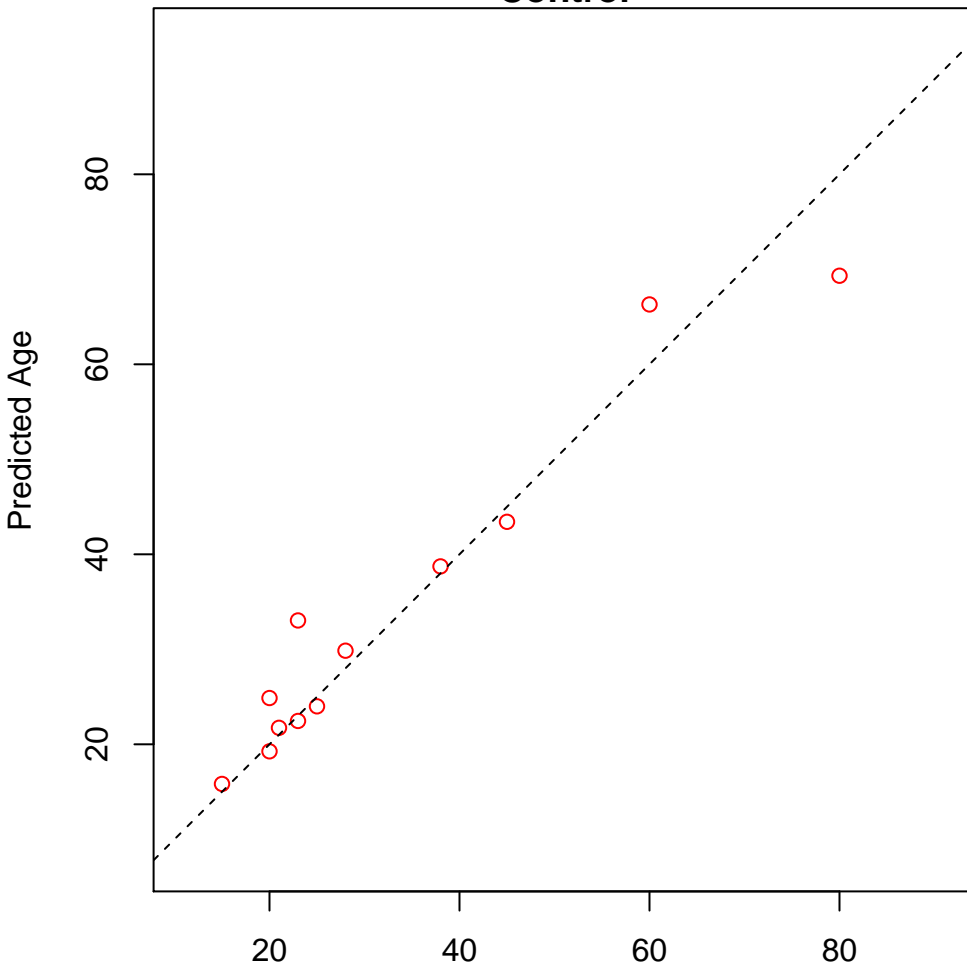
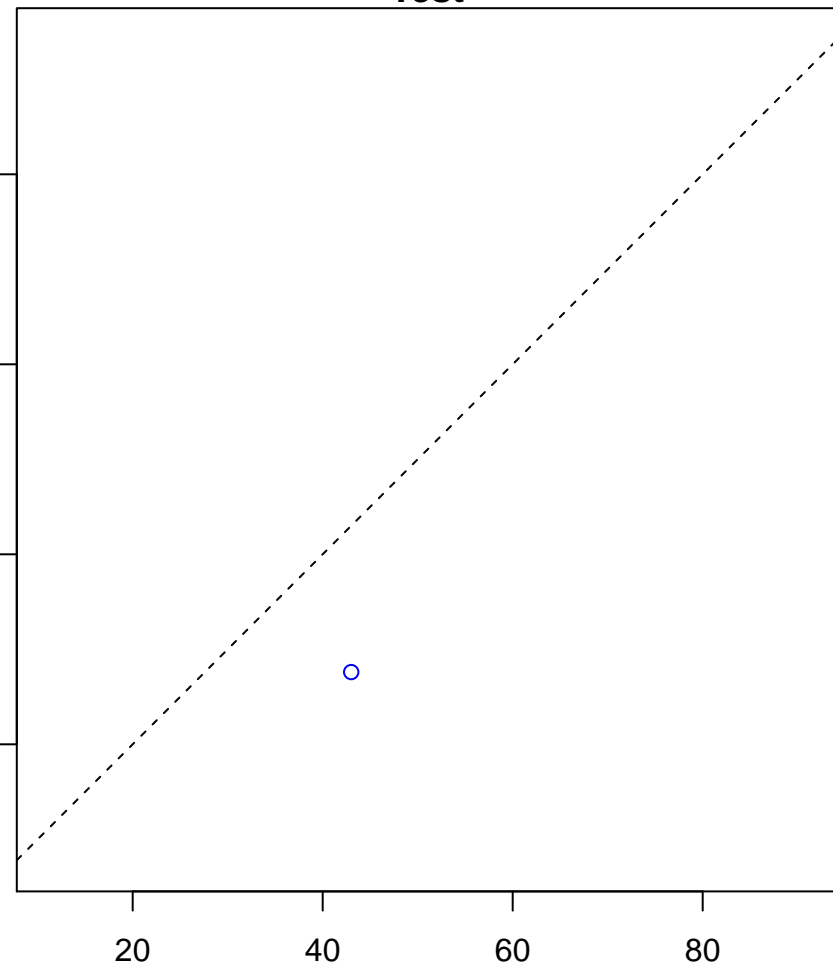


regulation of prostaglandin secretion (Score: 214.875015)

Control

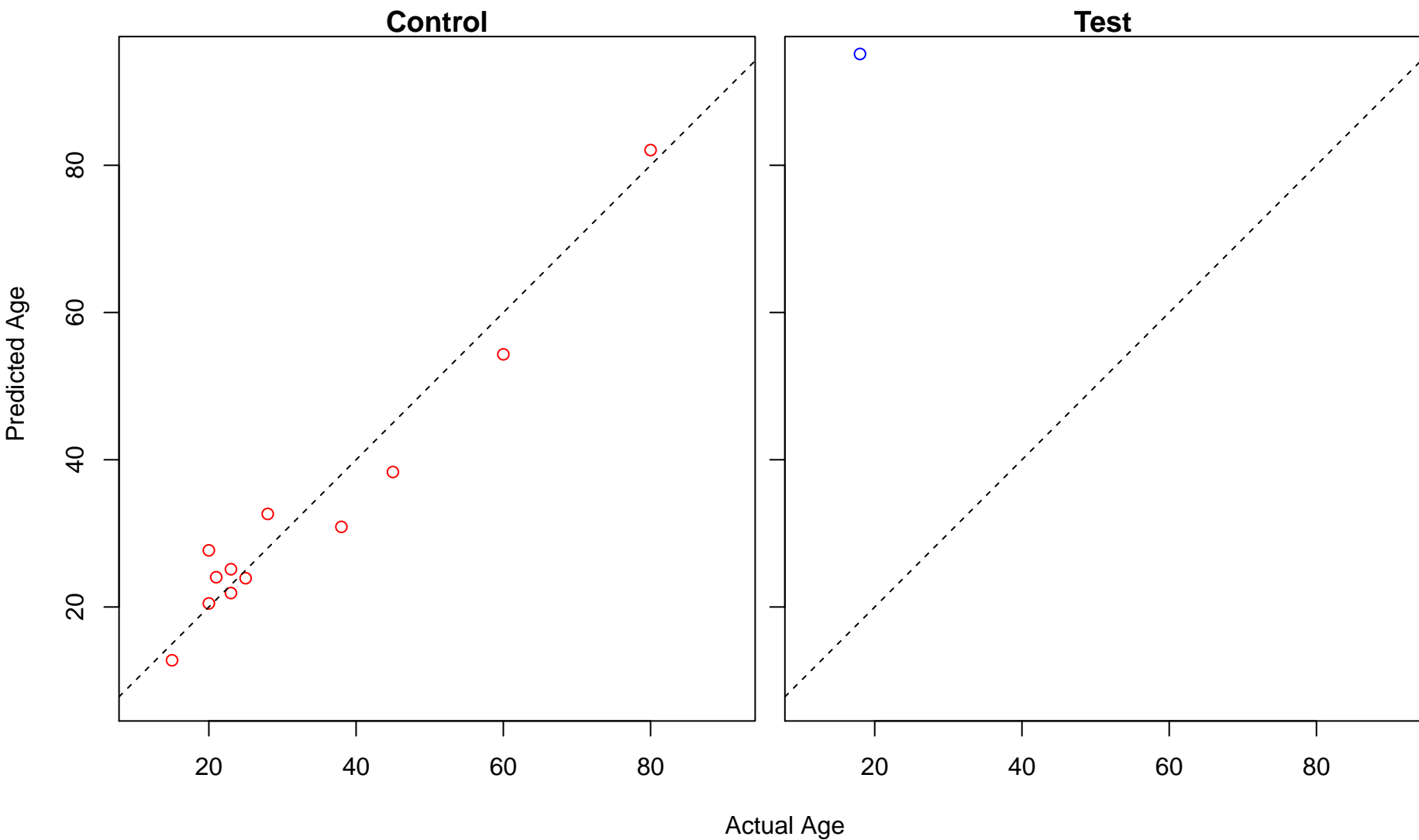


Test

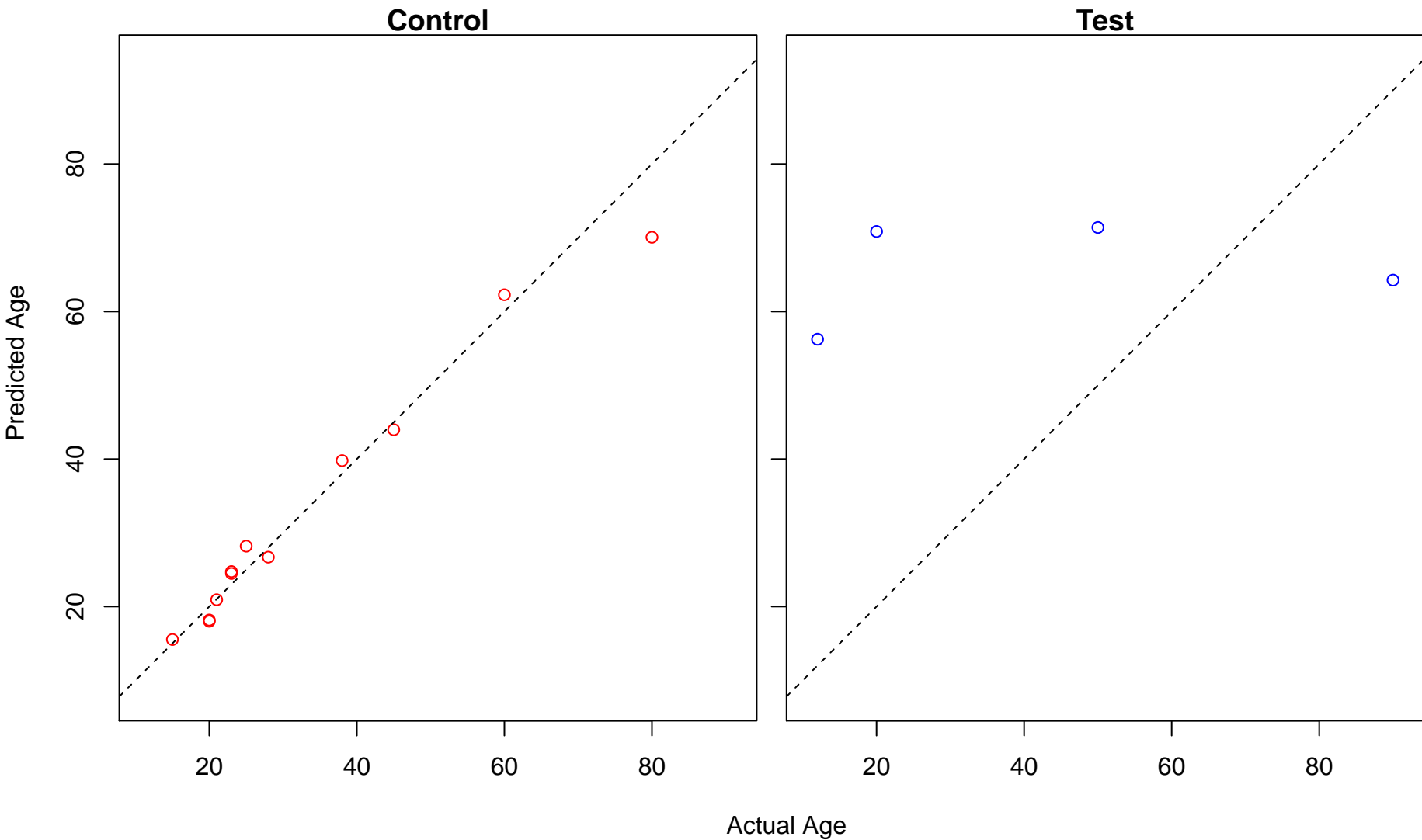


Actual Age

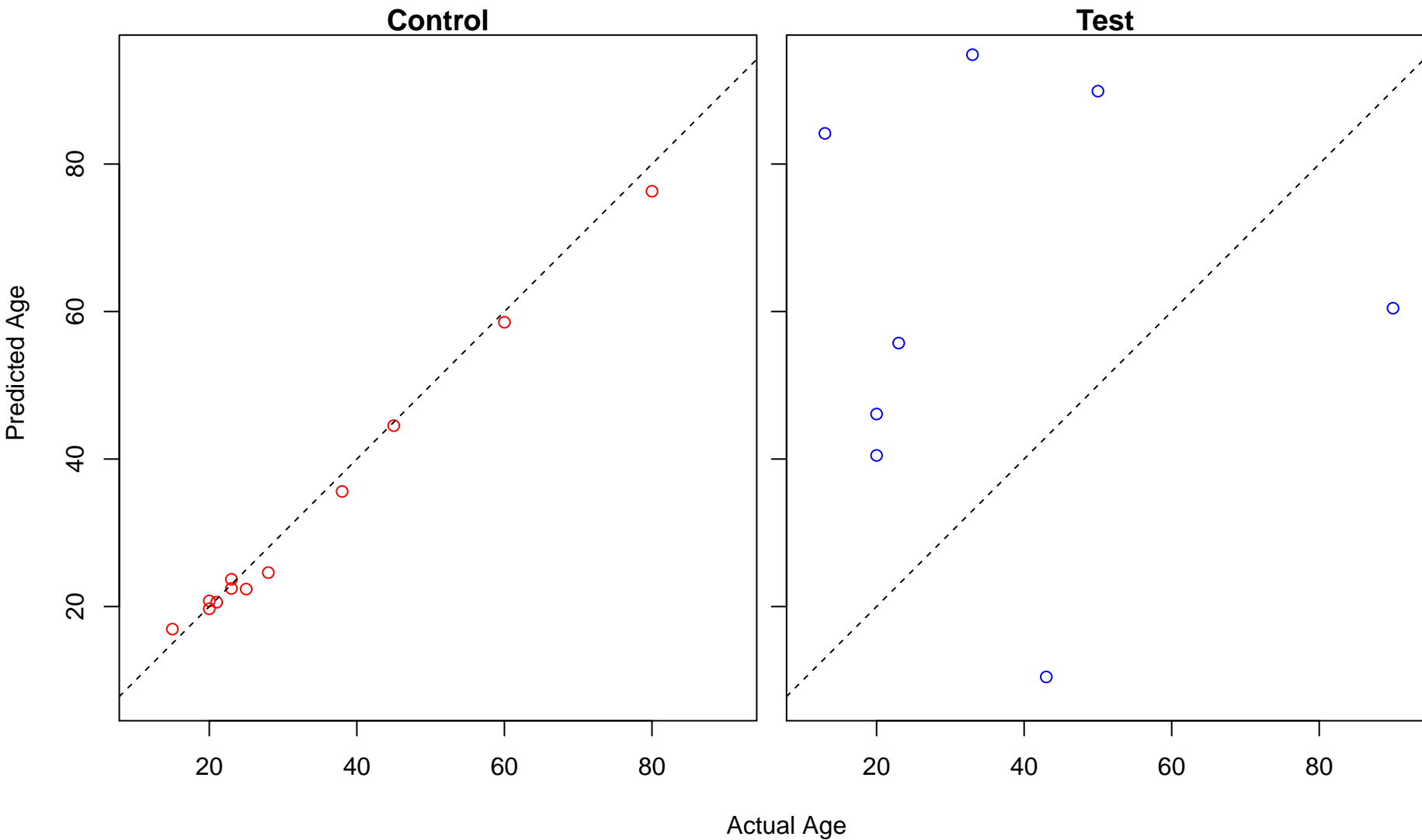
positive regulation of inositol phosphate biosynthetic process (Score: 209.102848)



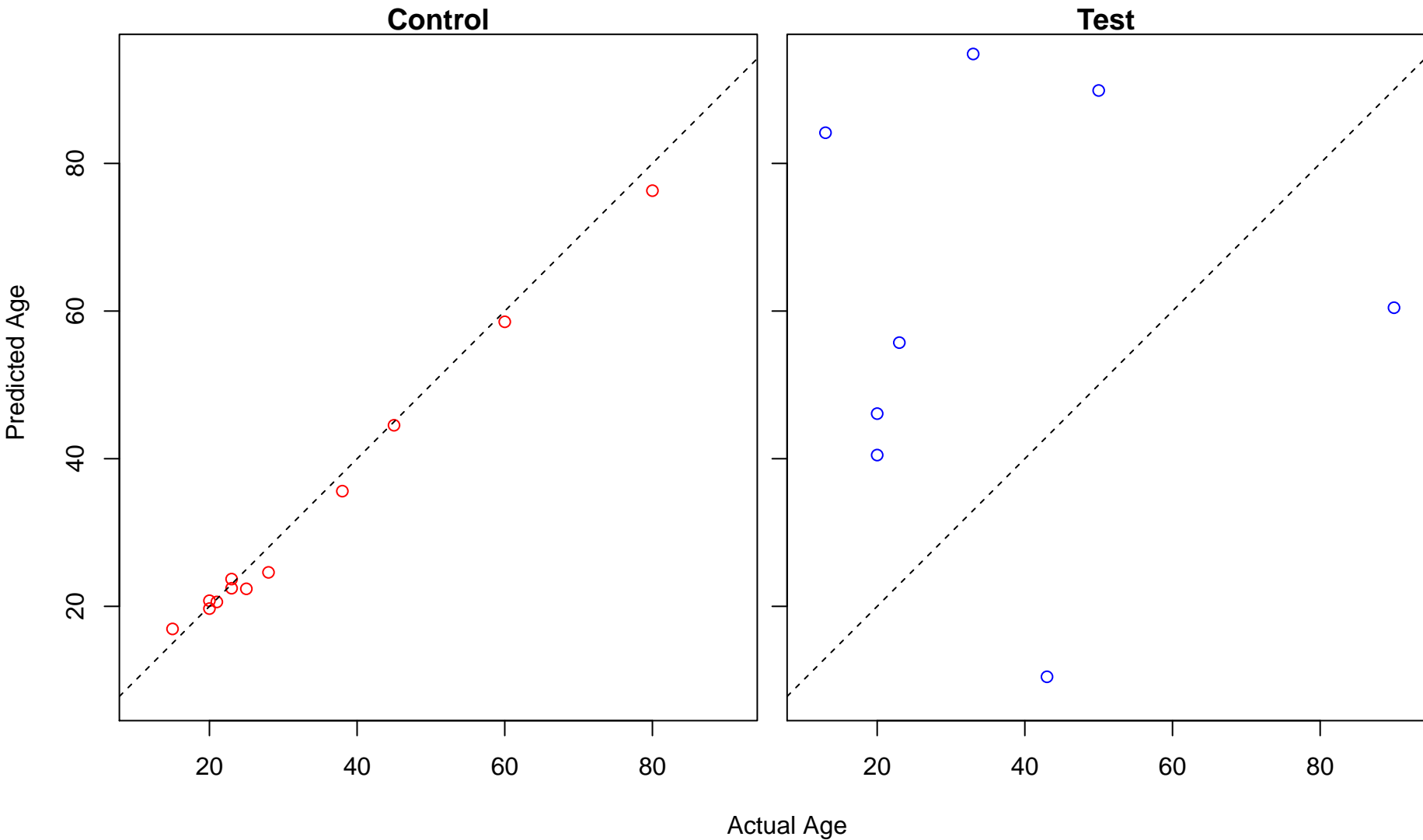
regulation of atrial cardiac muscle cell membrane repolarization (Score: 205.354090)



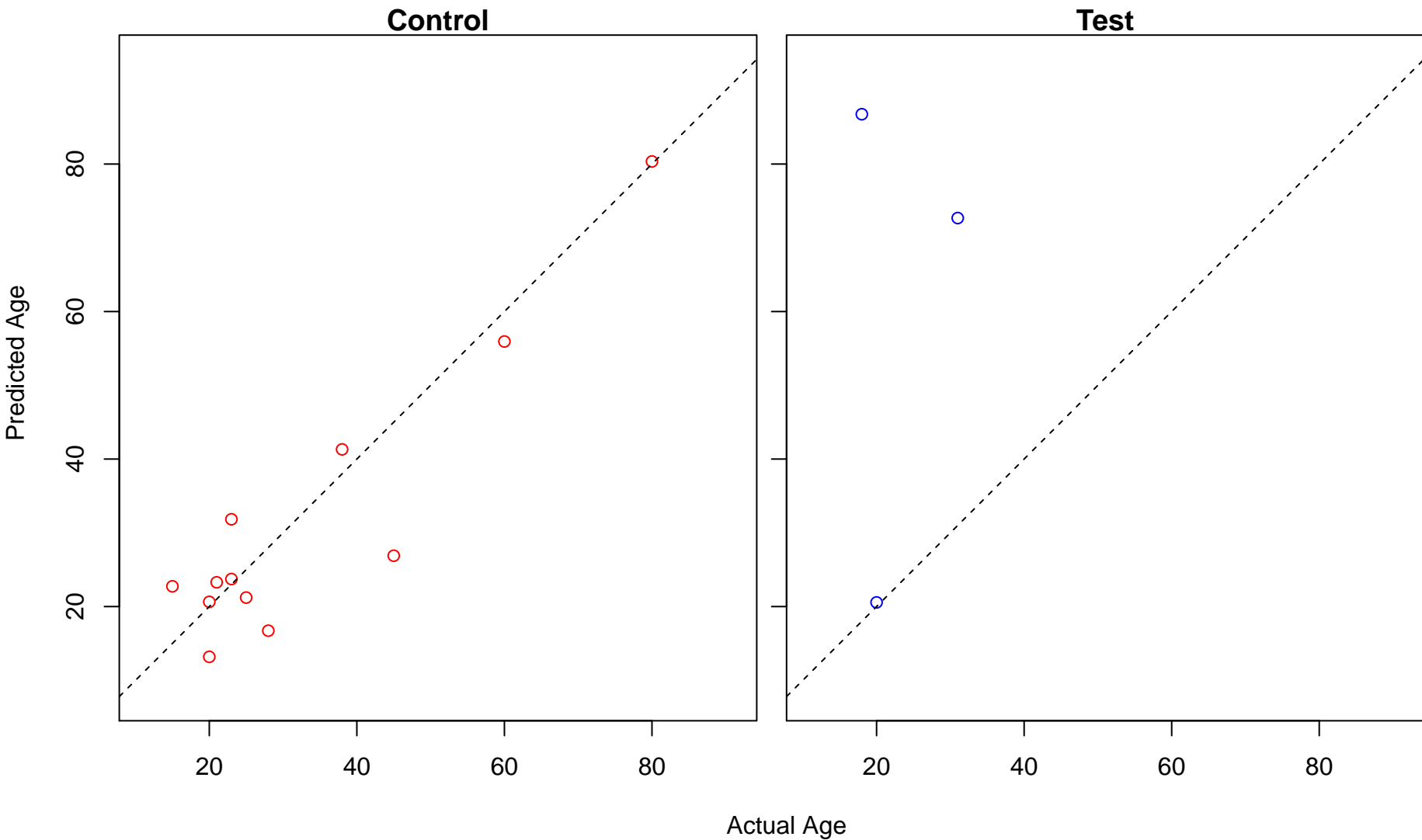
intrinsic apoptotic signaling pathway in response to oxidative stress (Score: 195.997826)



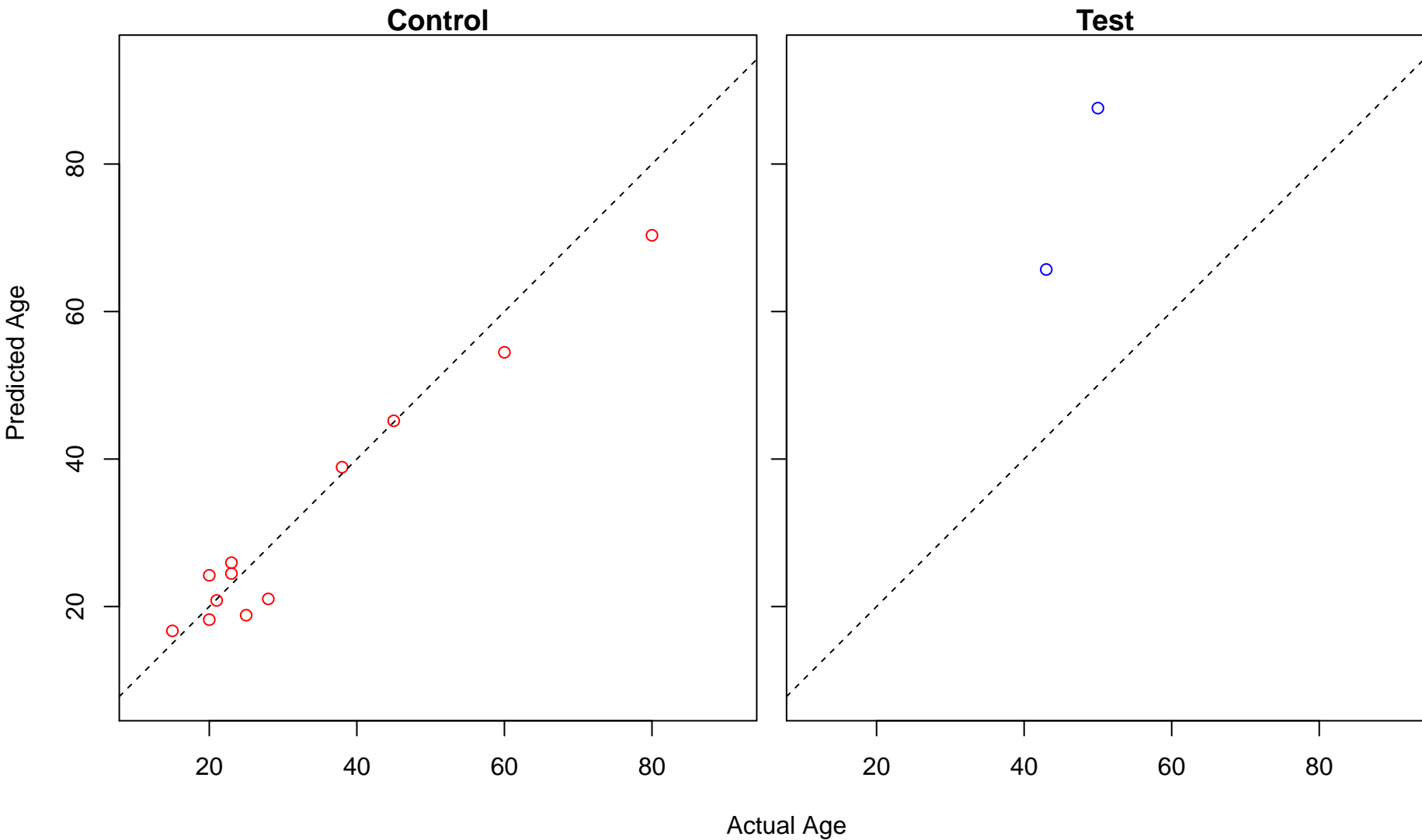
cell death in response to oxidative stress (Score: 195.997826)



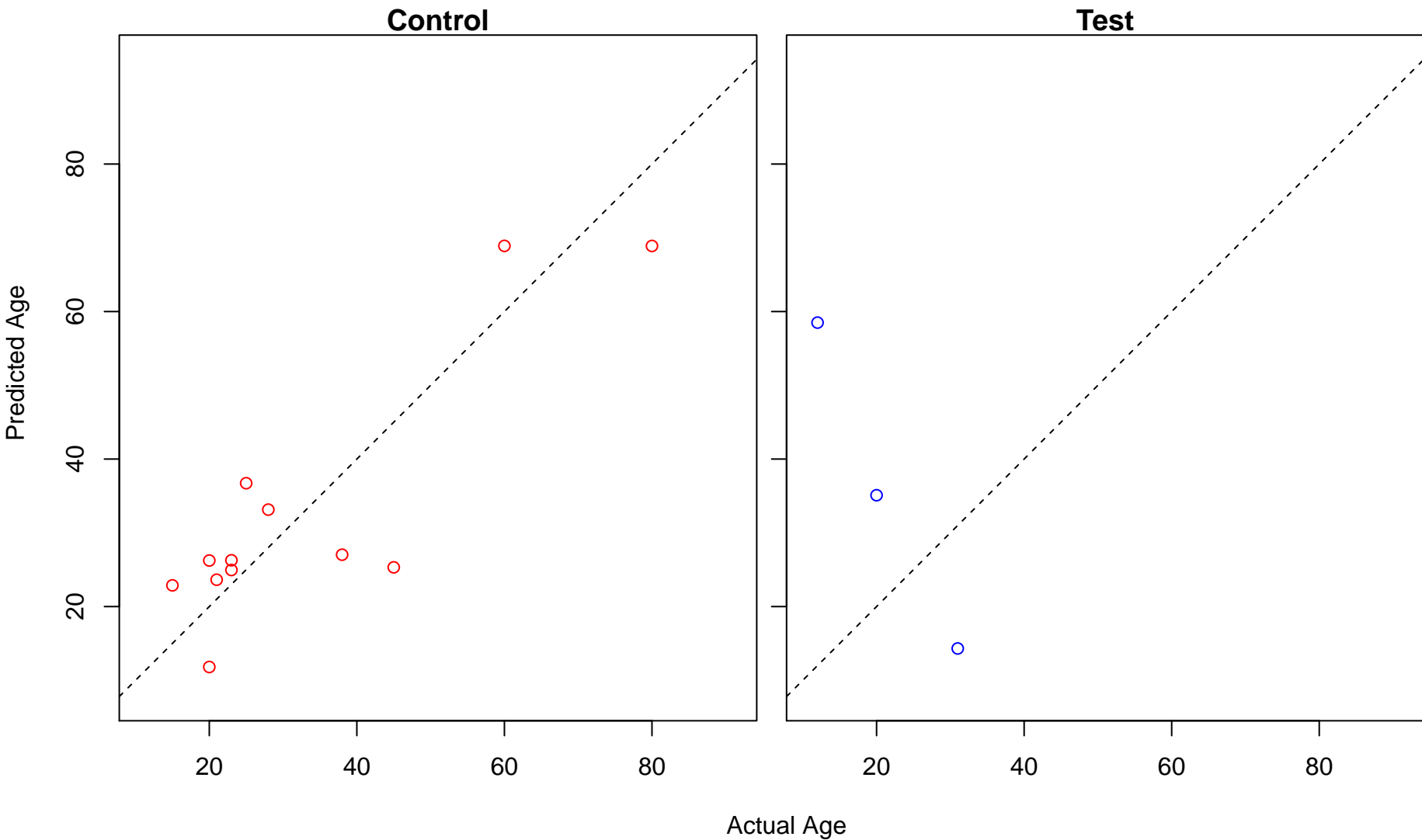
negative regulation of oligodendrocyte differentiation (Score: 169.094528)



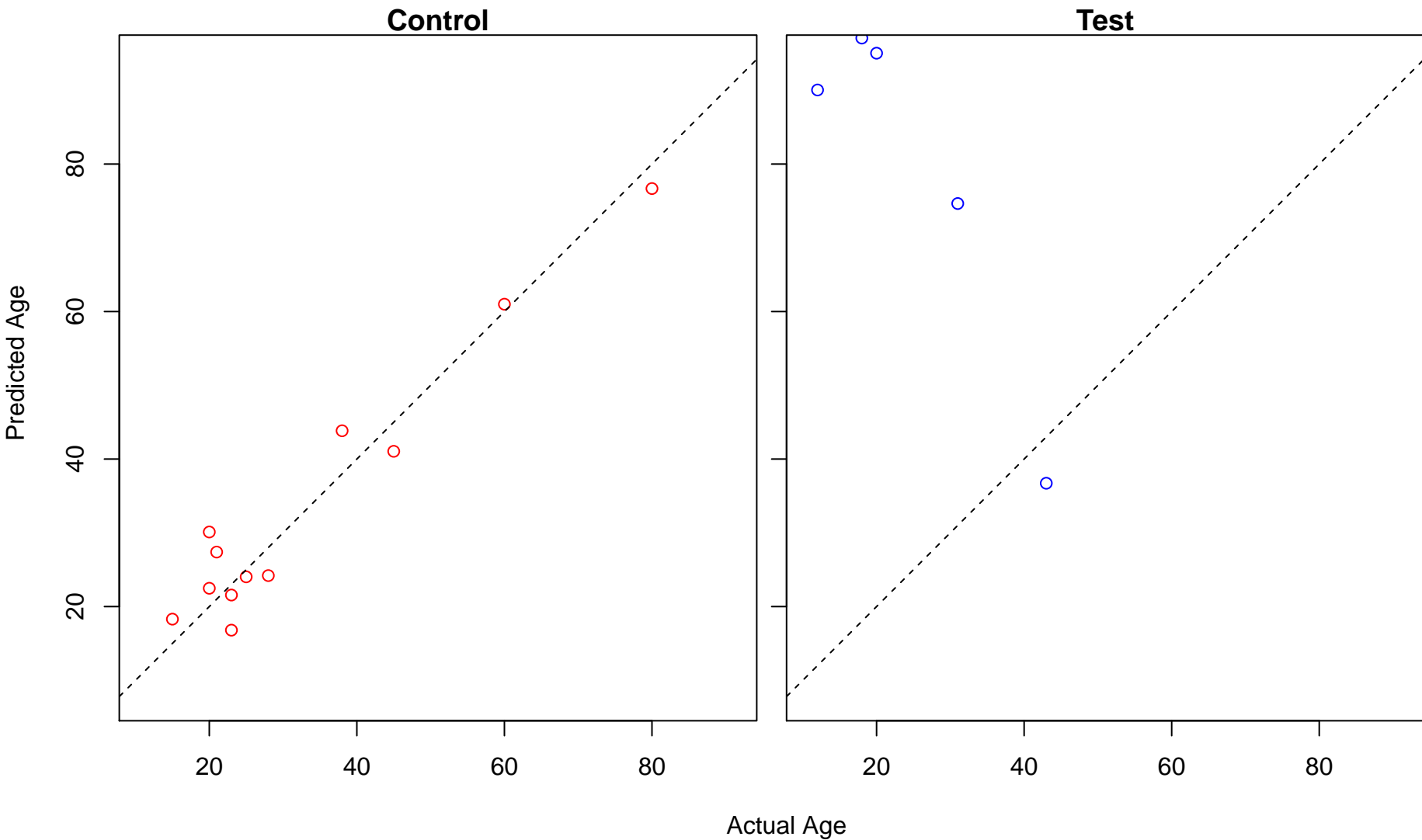
regulation of Golgi to plasma membrane protein transport (Score: 165.597795)



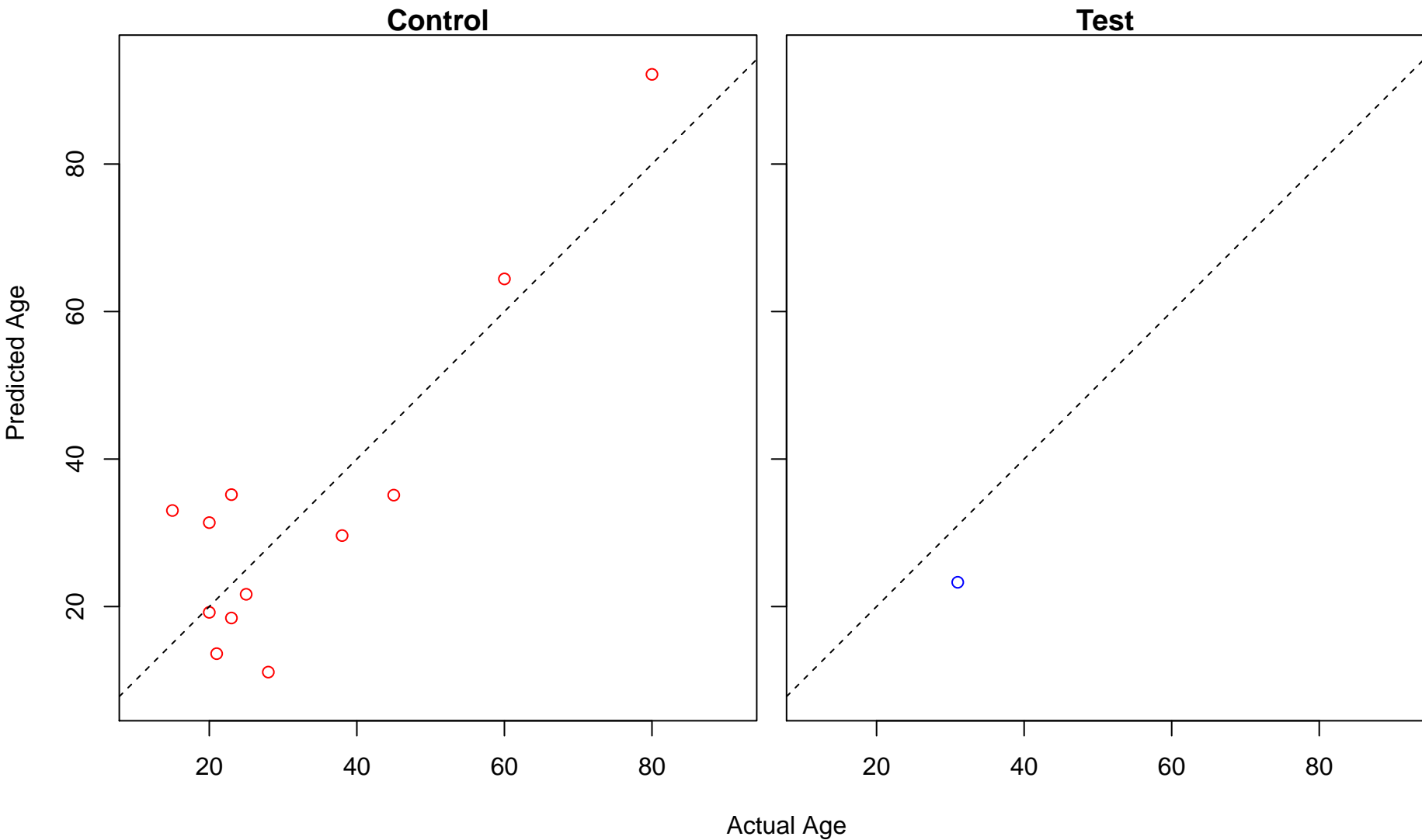
glutamine metabolic process (Score: 165.433179)



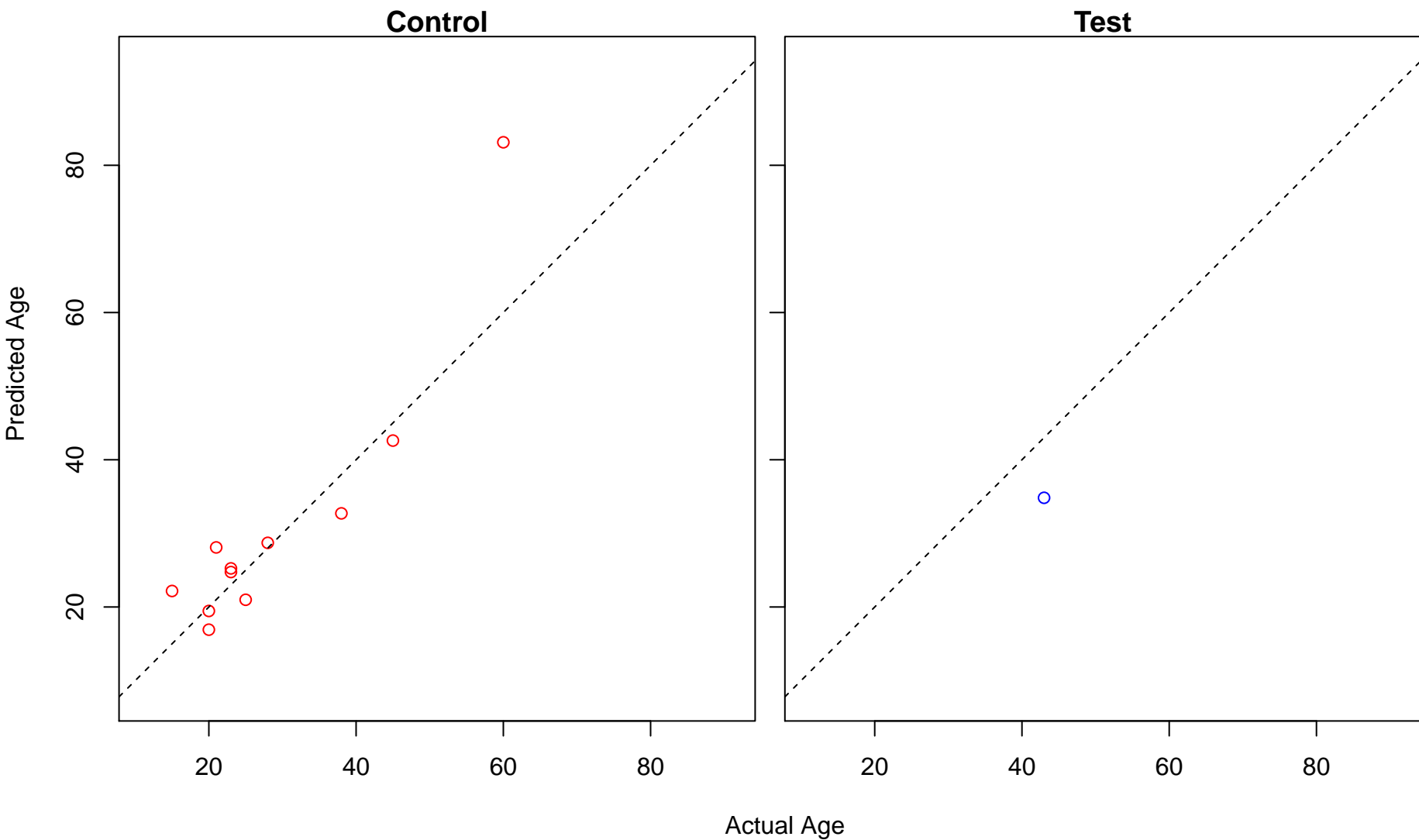
cell junction maintenance (Score: 146.208102)



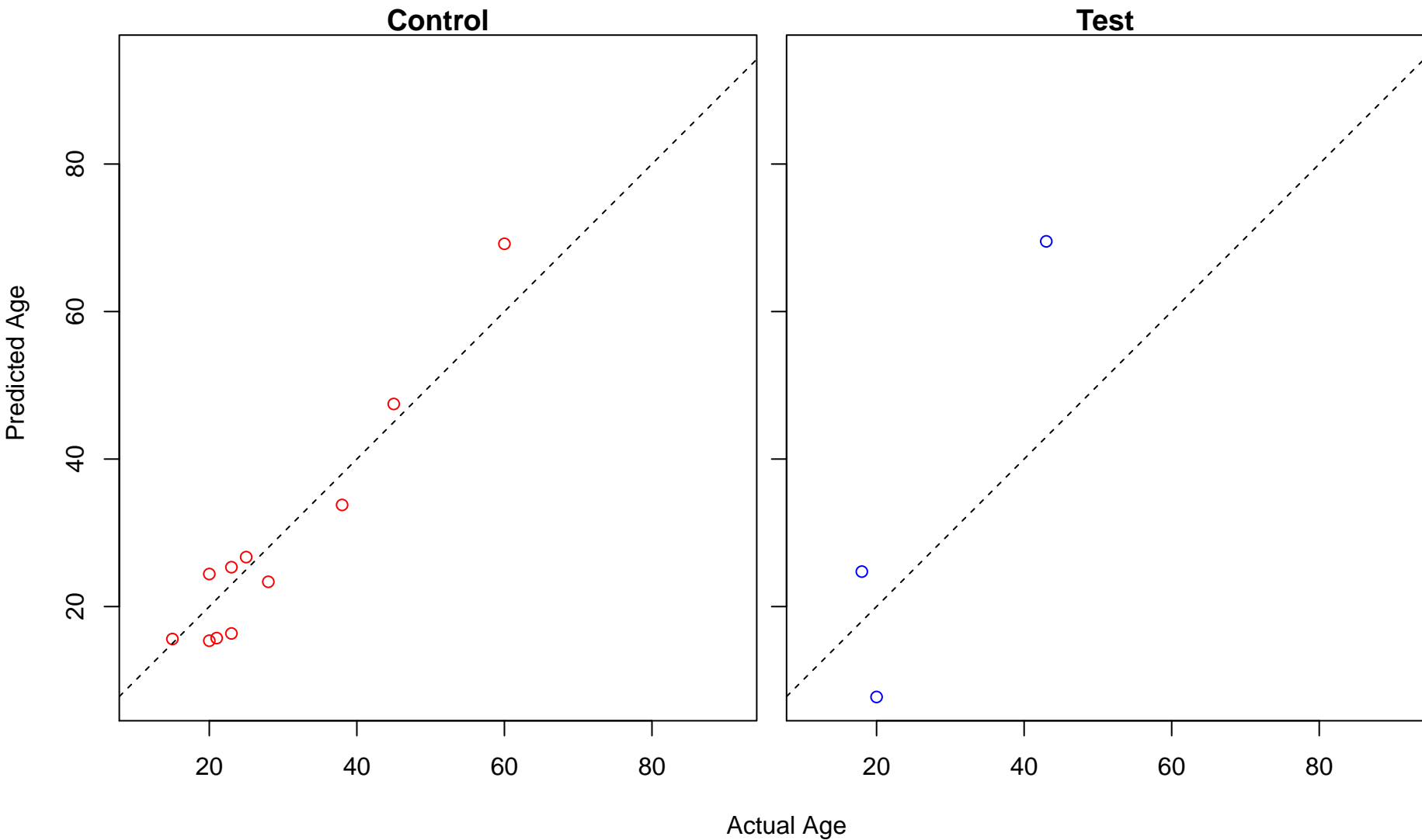
iris morphogenesis (Score: 144.039397)



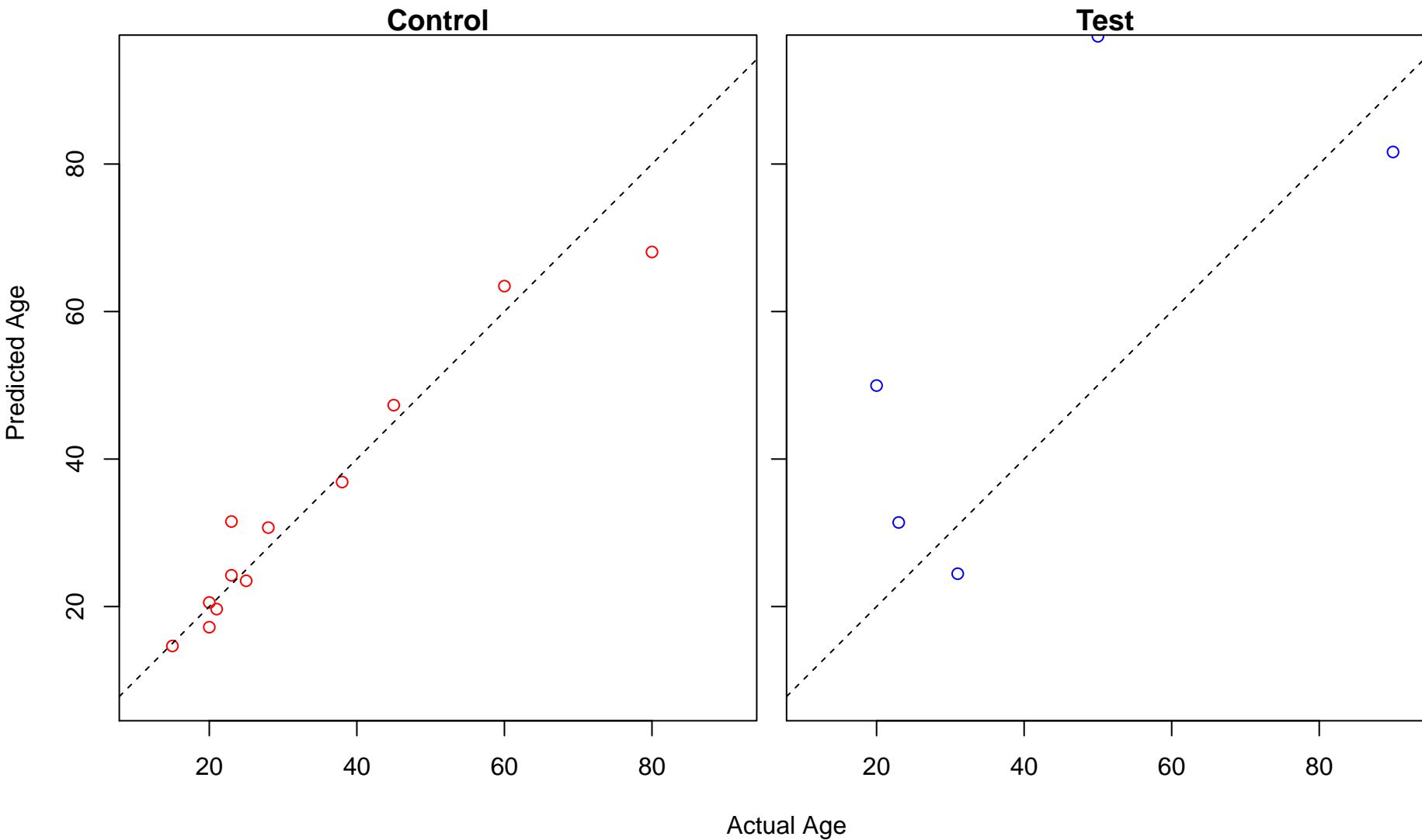
thrombin receptor signaling pathway (Score: 143.704115)



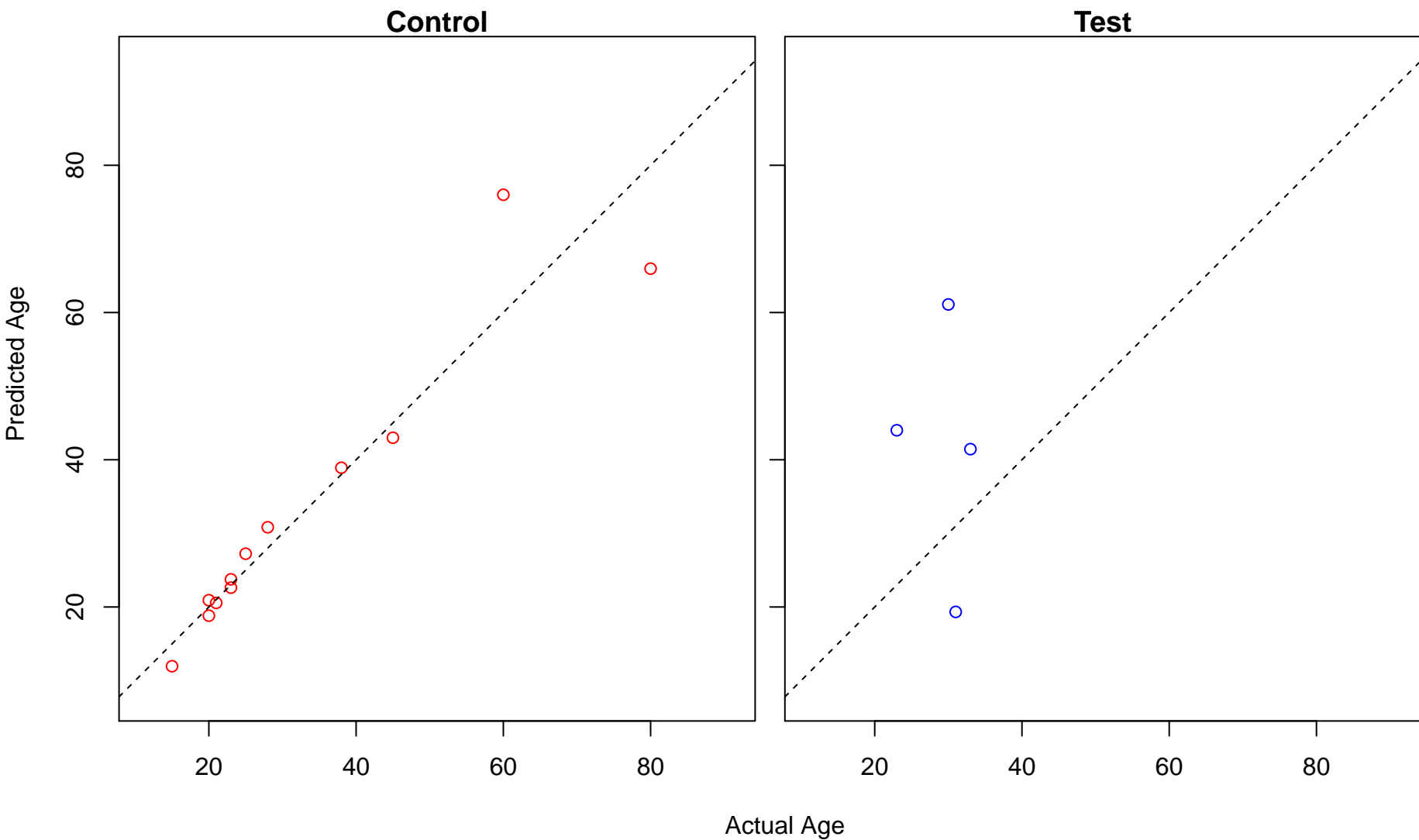
asymmetric neuroblast division (Score: 142.678551)



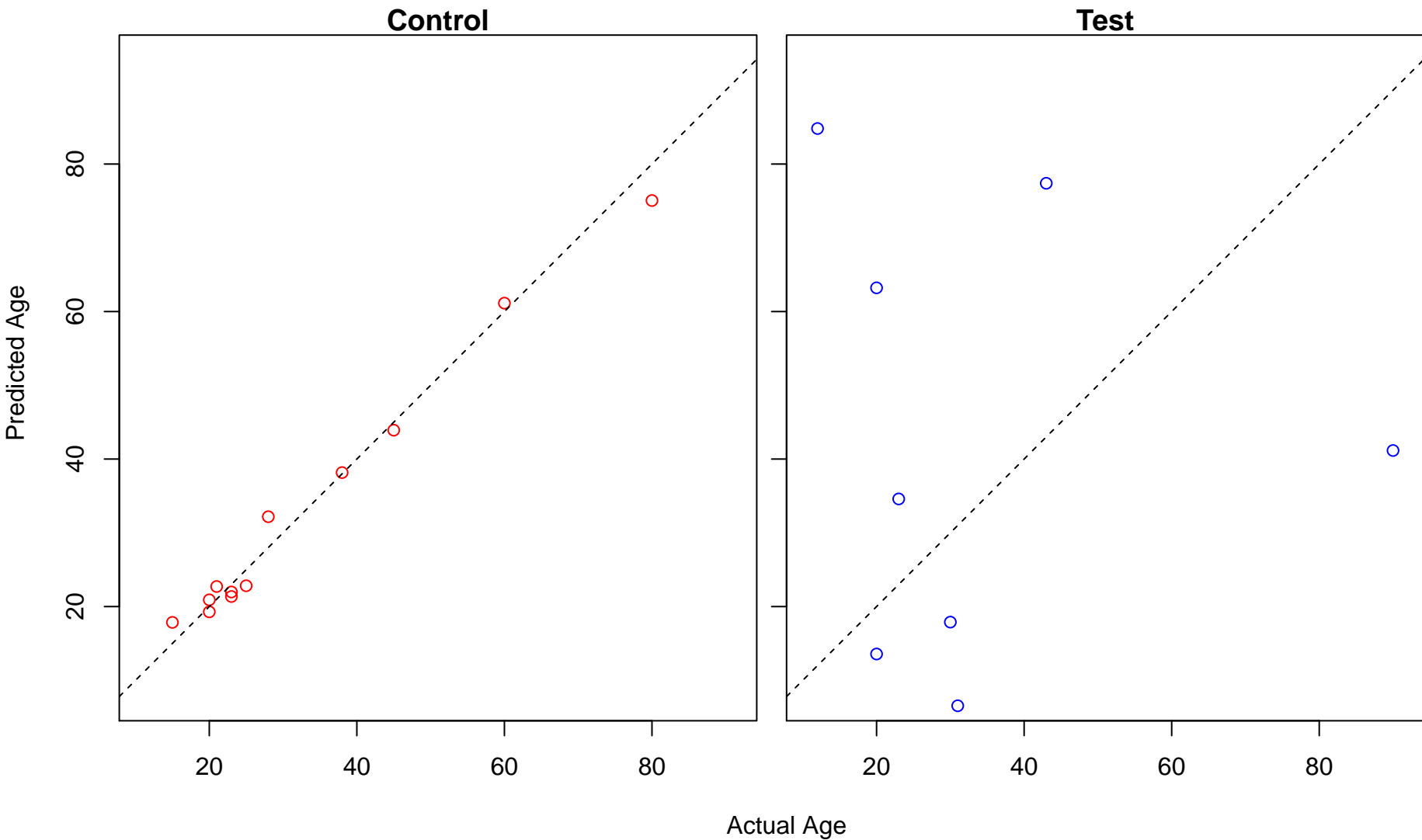
very-low-density lipoprotein particle assembly (Score: 140.634824)



positive regulation of histone ubiquitination (Score: 140.421702)

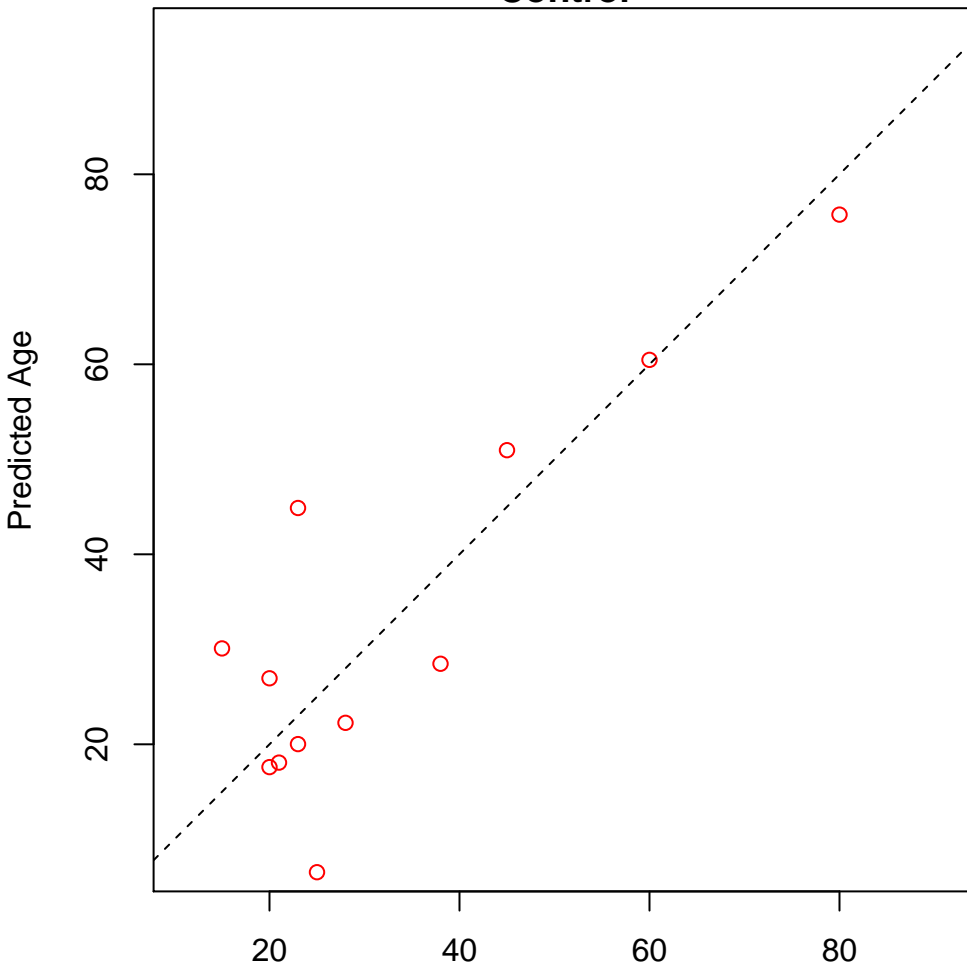


positive regulation of interleukin-6 secretion (Score: 139.896091)

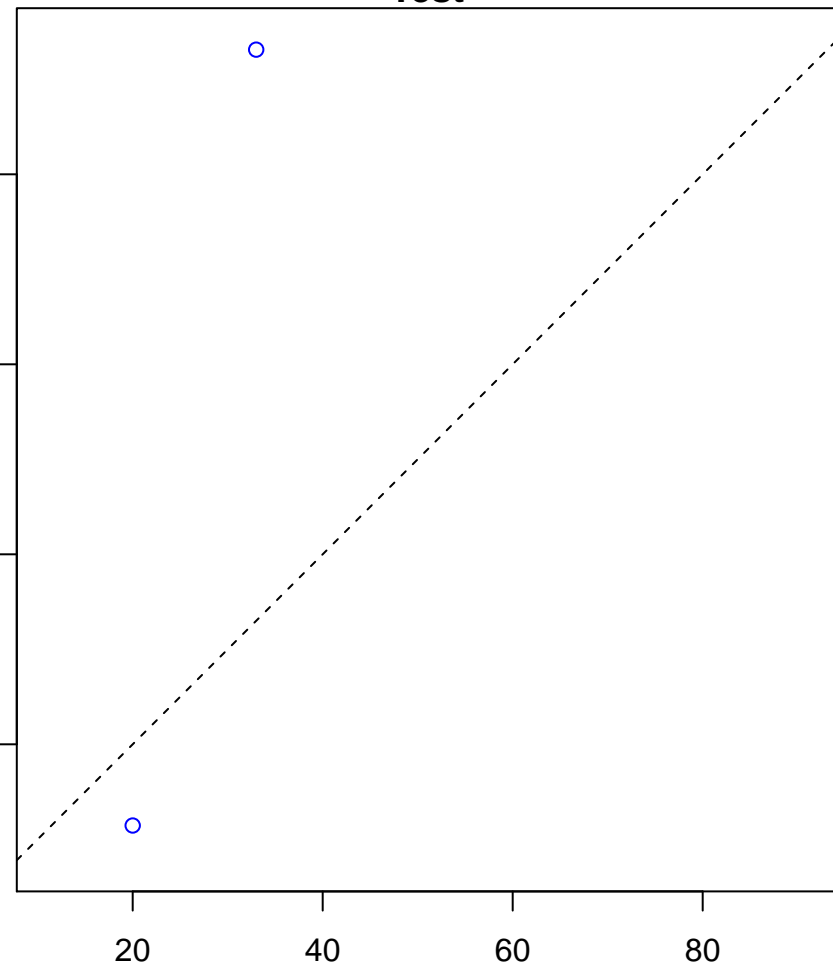


STAT protein import into nucleus (Score: 137.566115)

Control

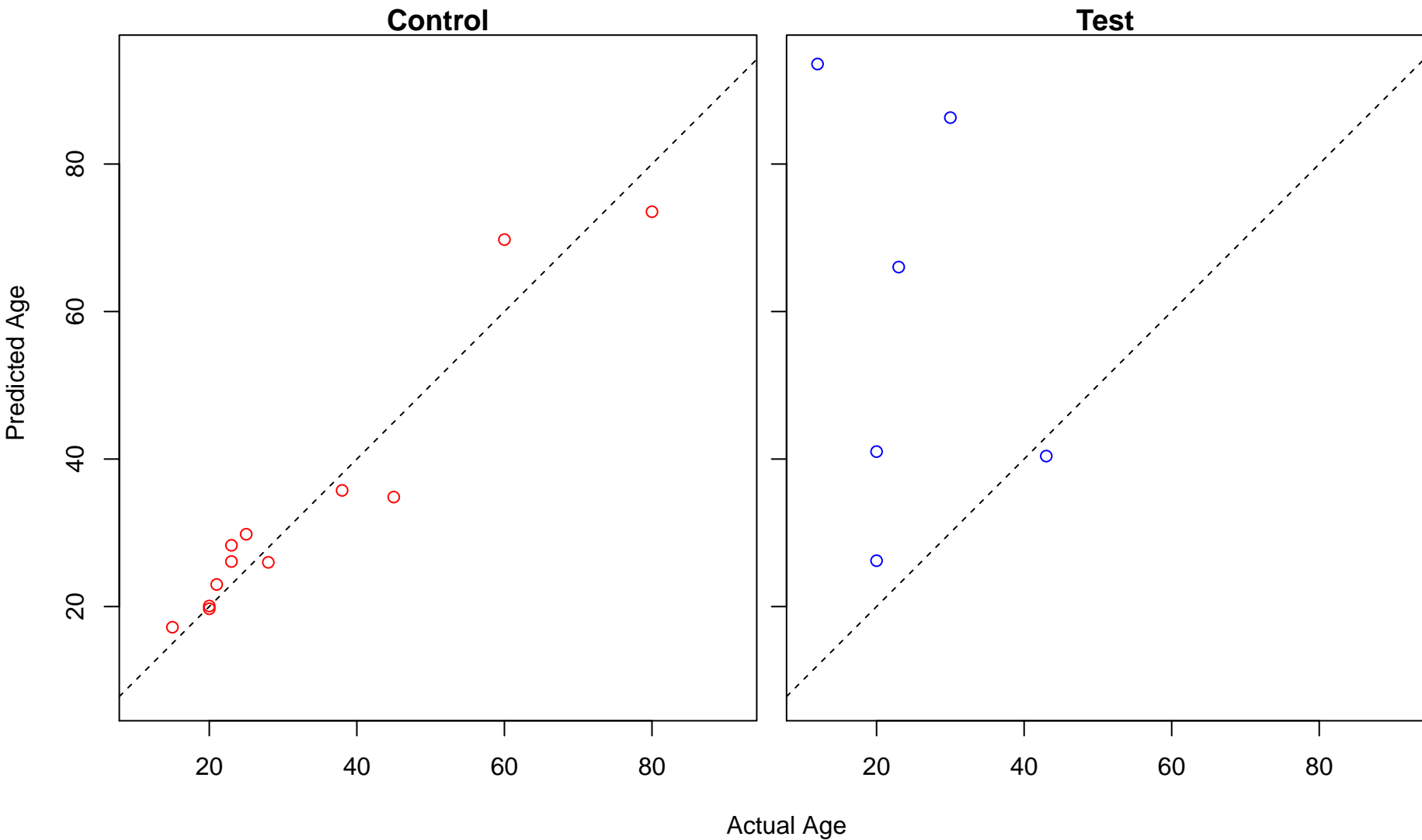


Test



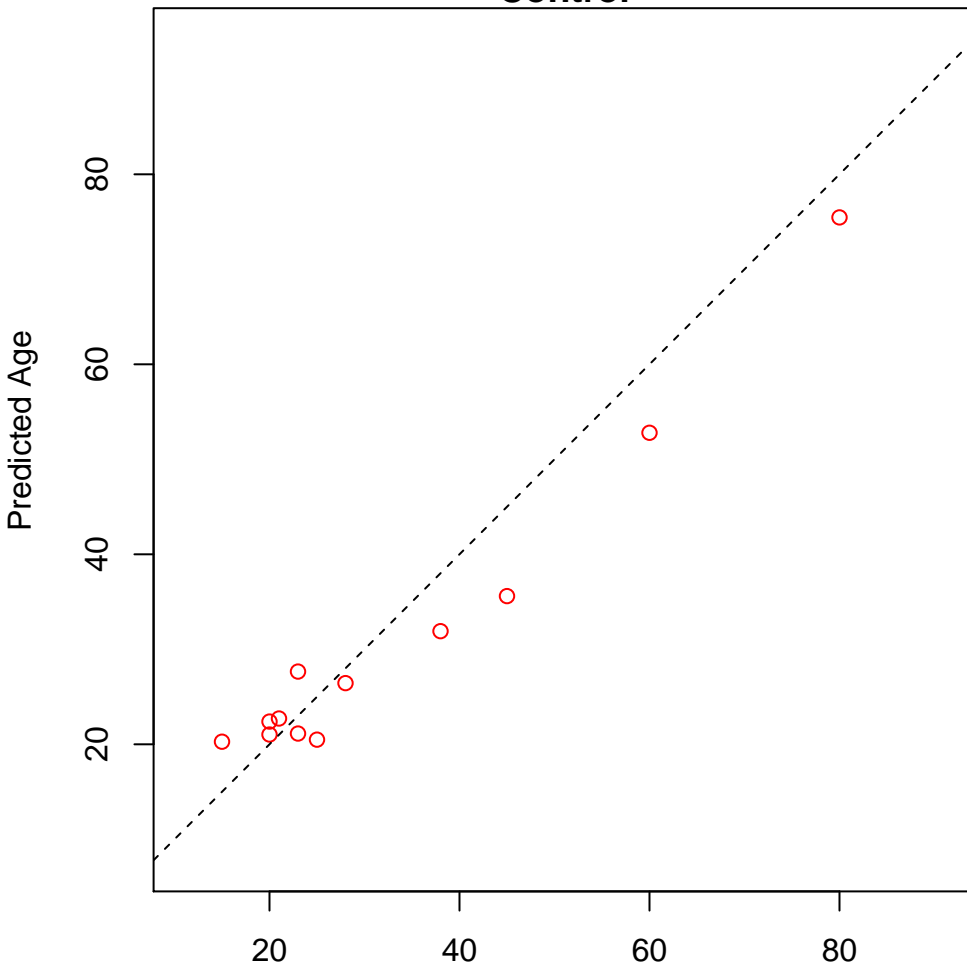
Actual Age

natural killer cell activation (Score: 136.690382)

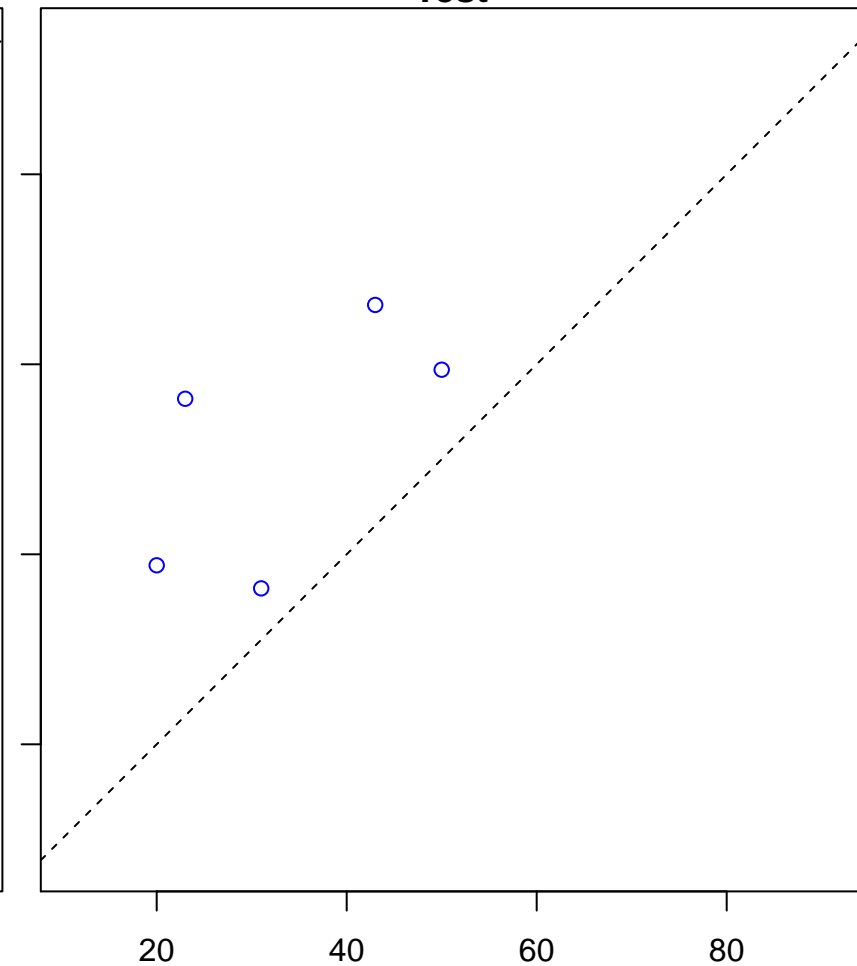


regulation of astrocyte differentiation (Score: 130.081145)

Control

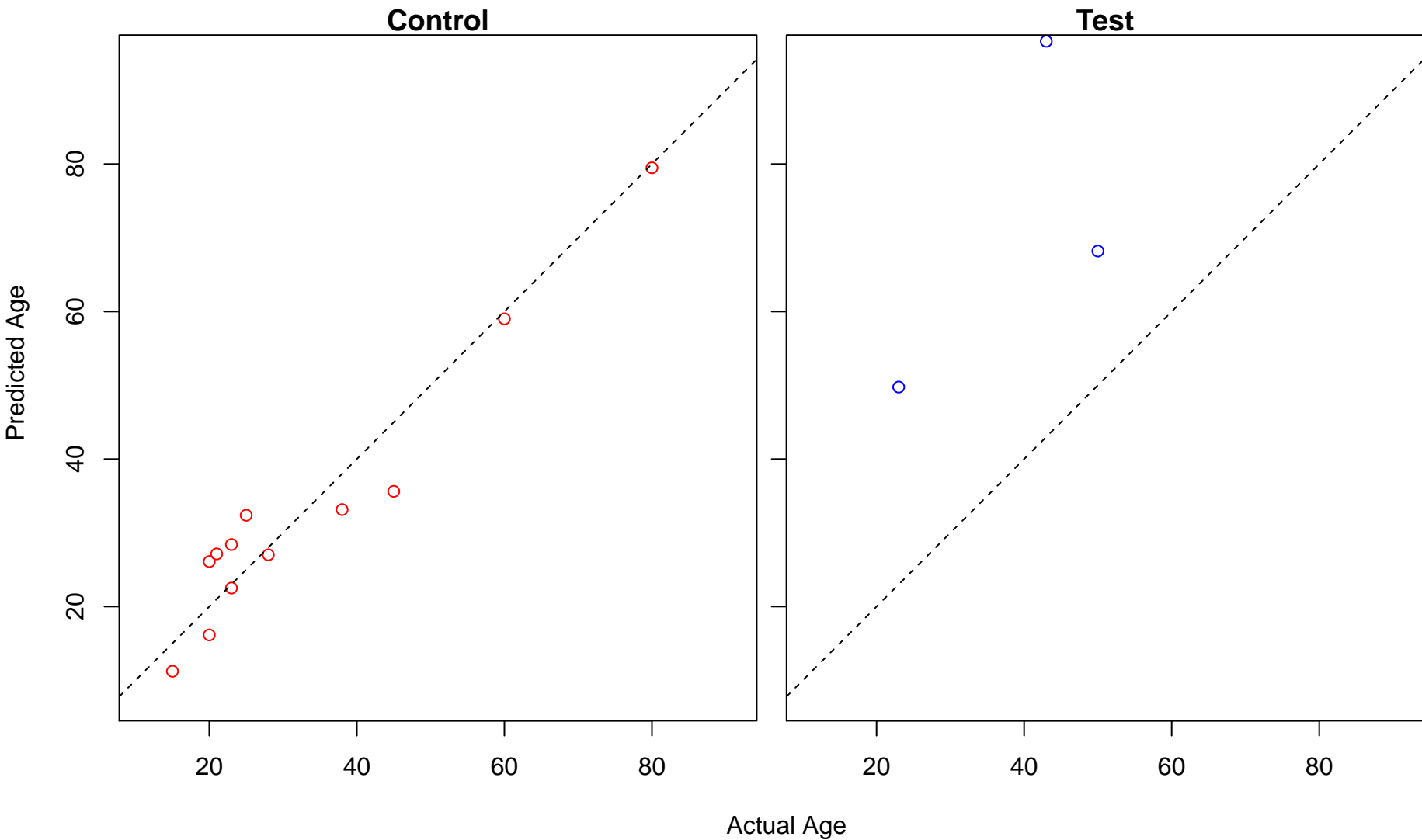


Test



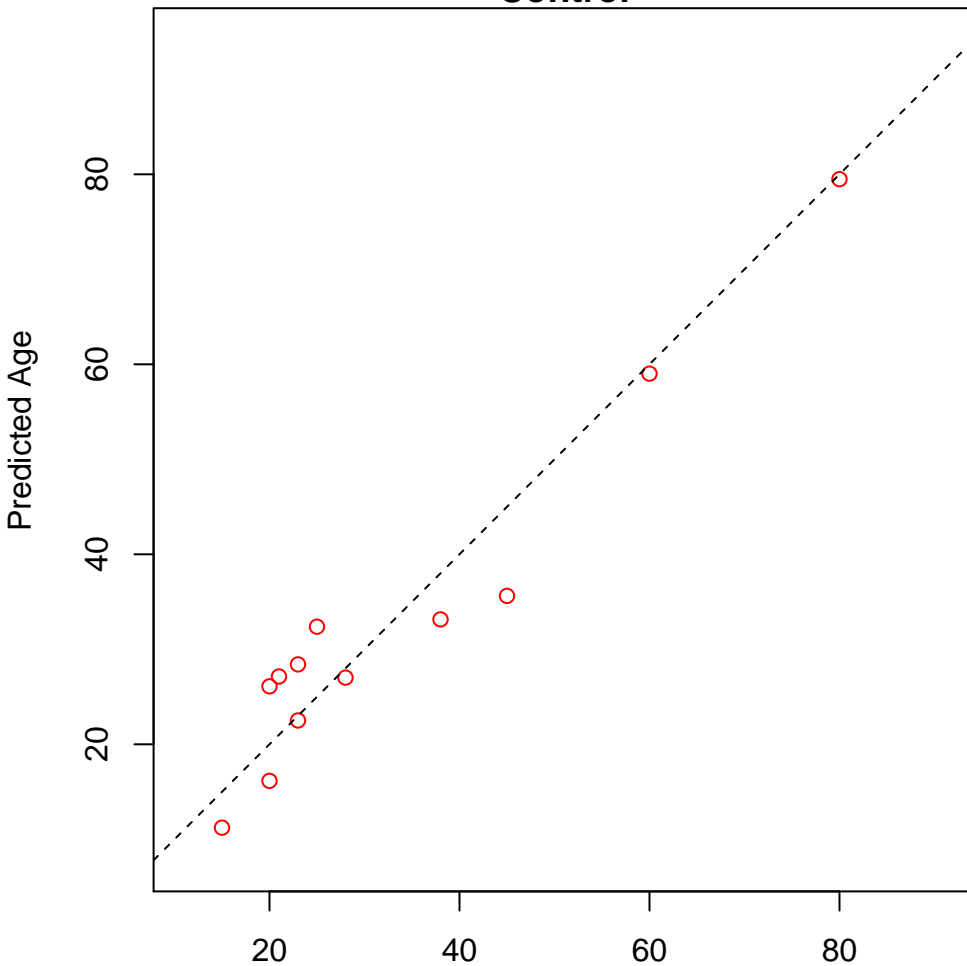
Actual Age

intracellular sterol transport (Score: 123.069330)

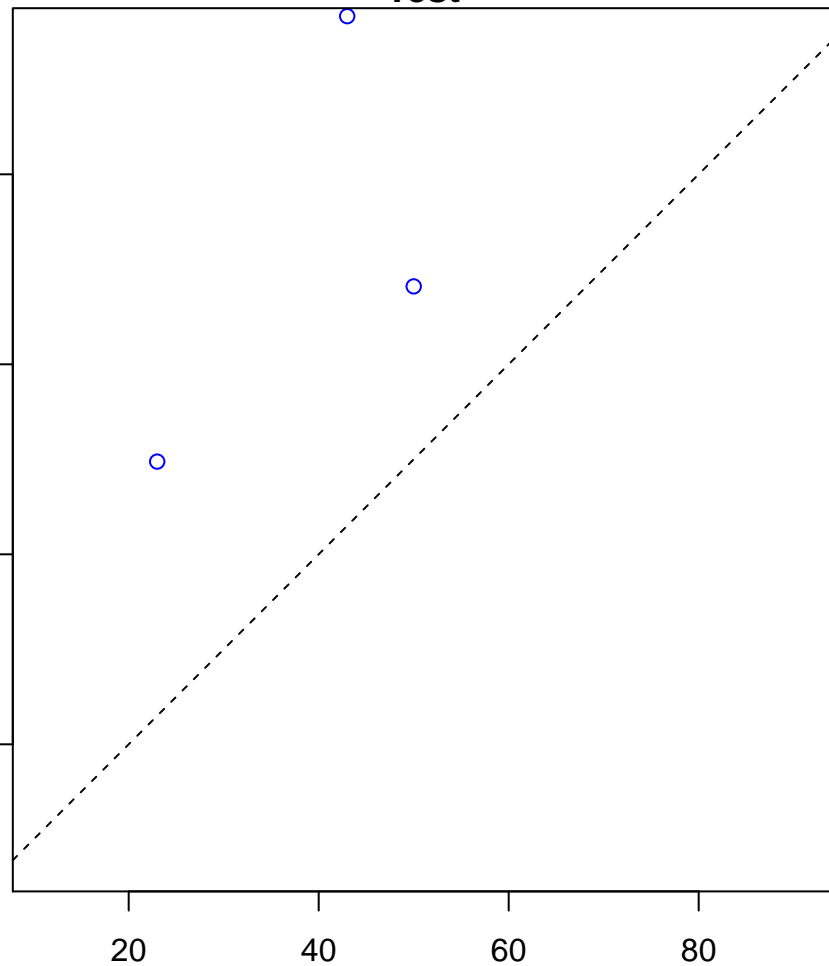


intracellular cholesterol transport (Score: 123.069330)

Control

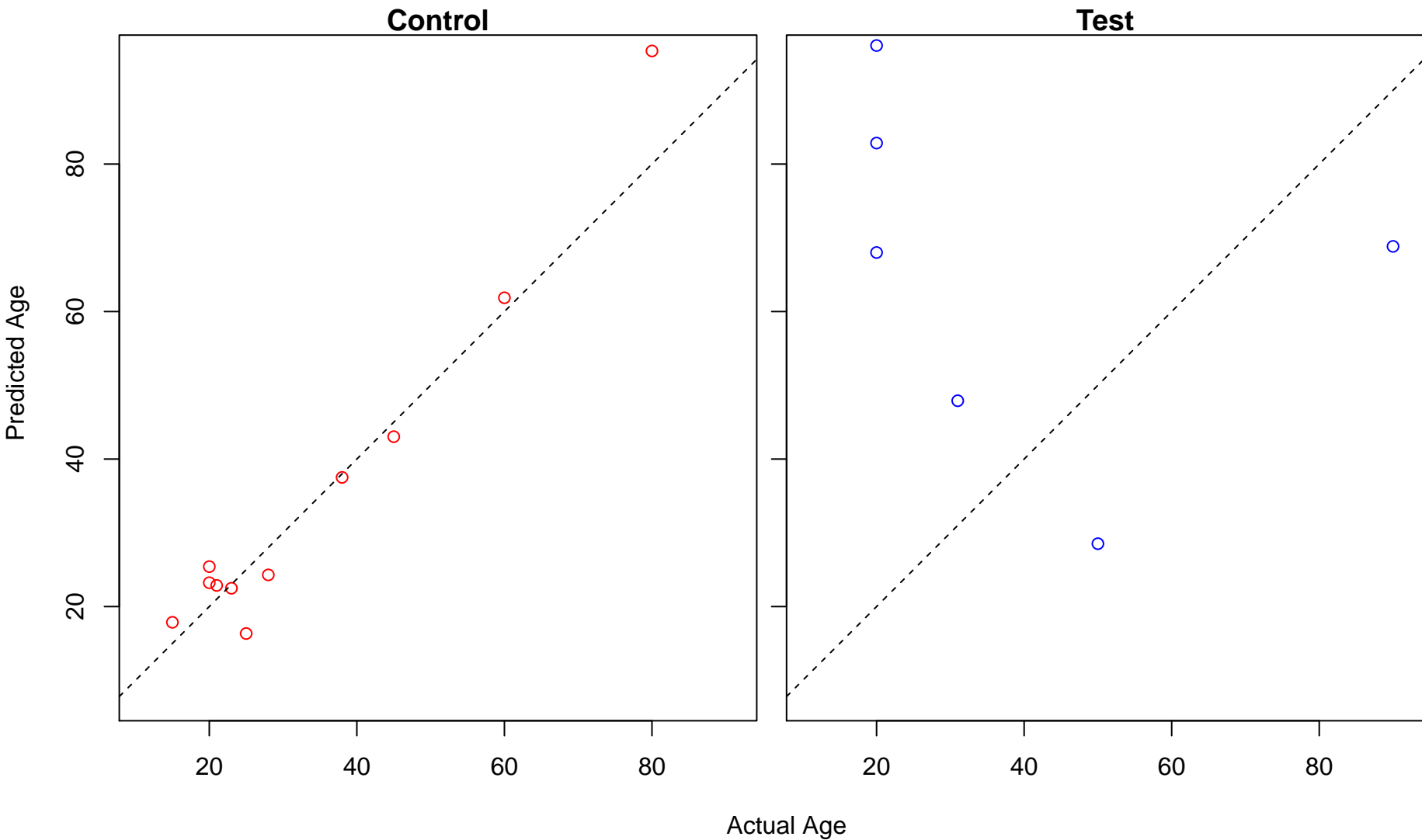


Test

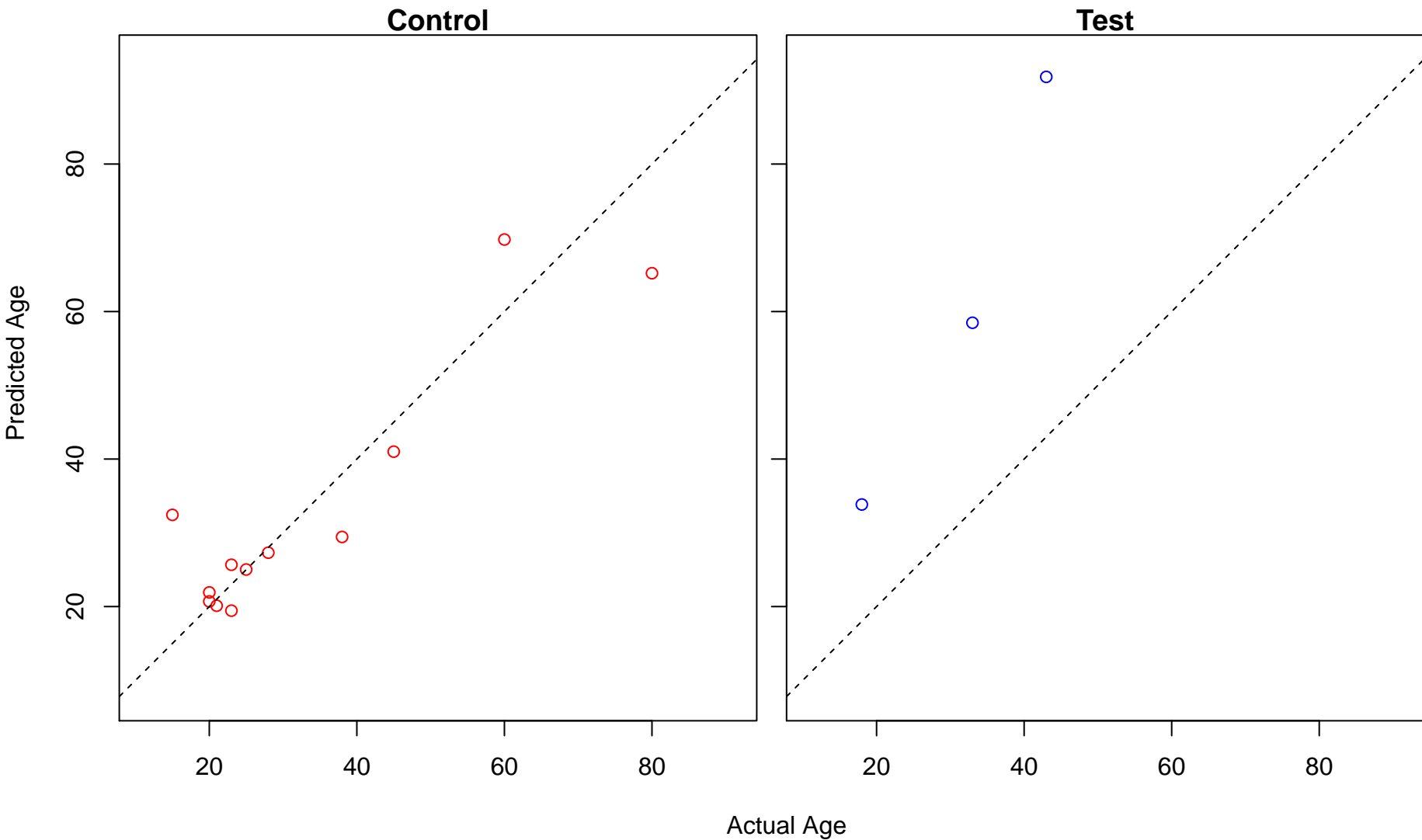


Actual Age

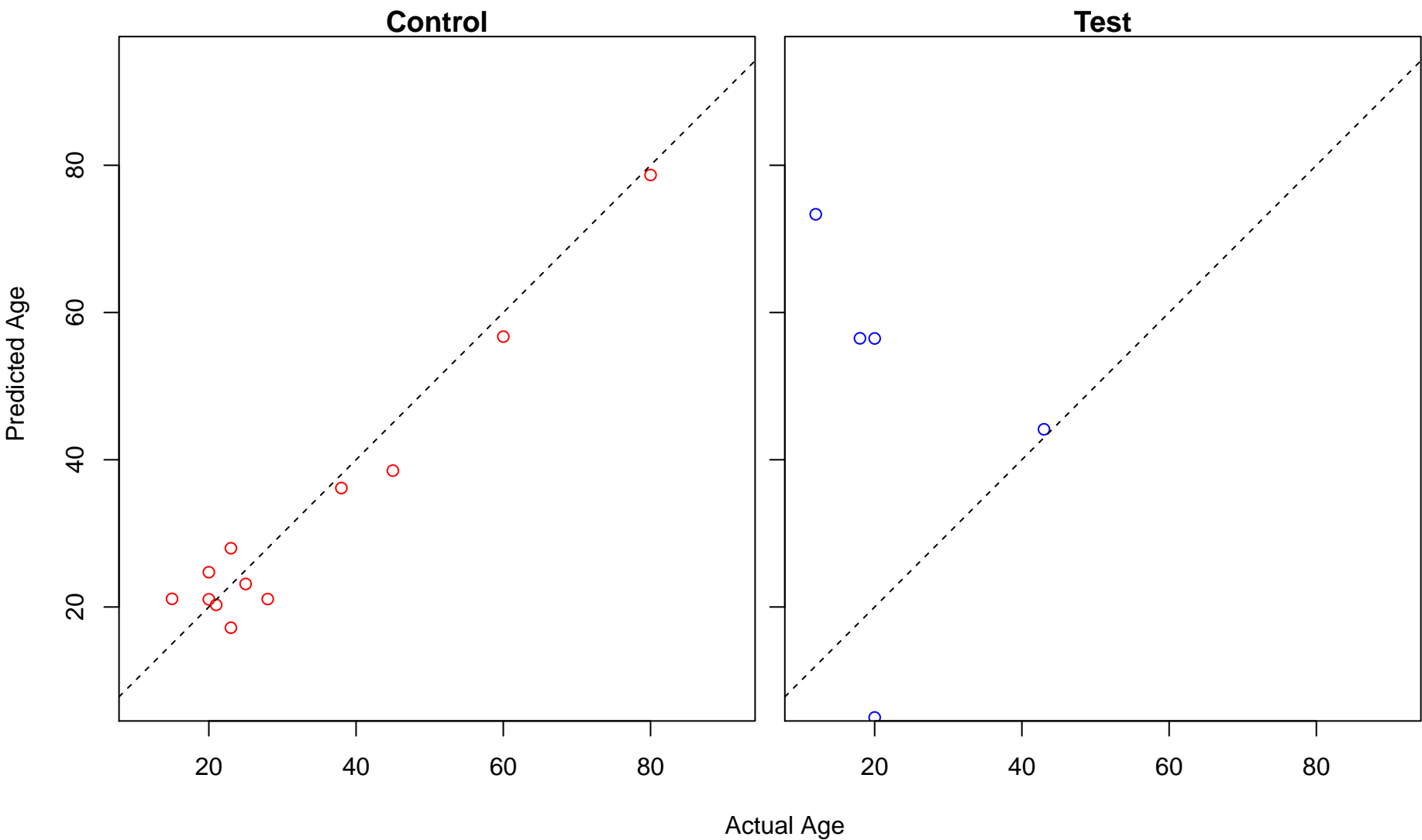
integrin activation (Score: 122.091760)



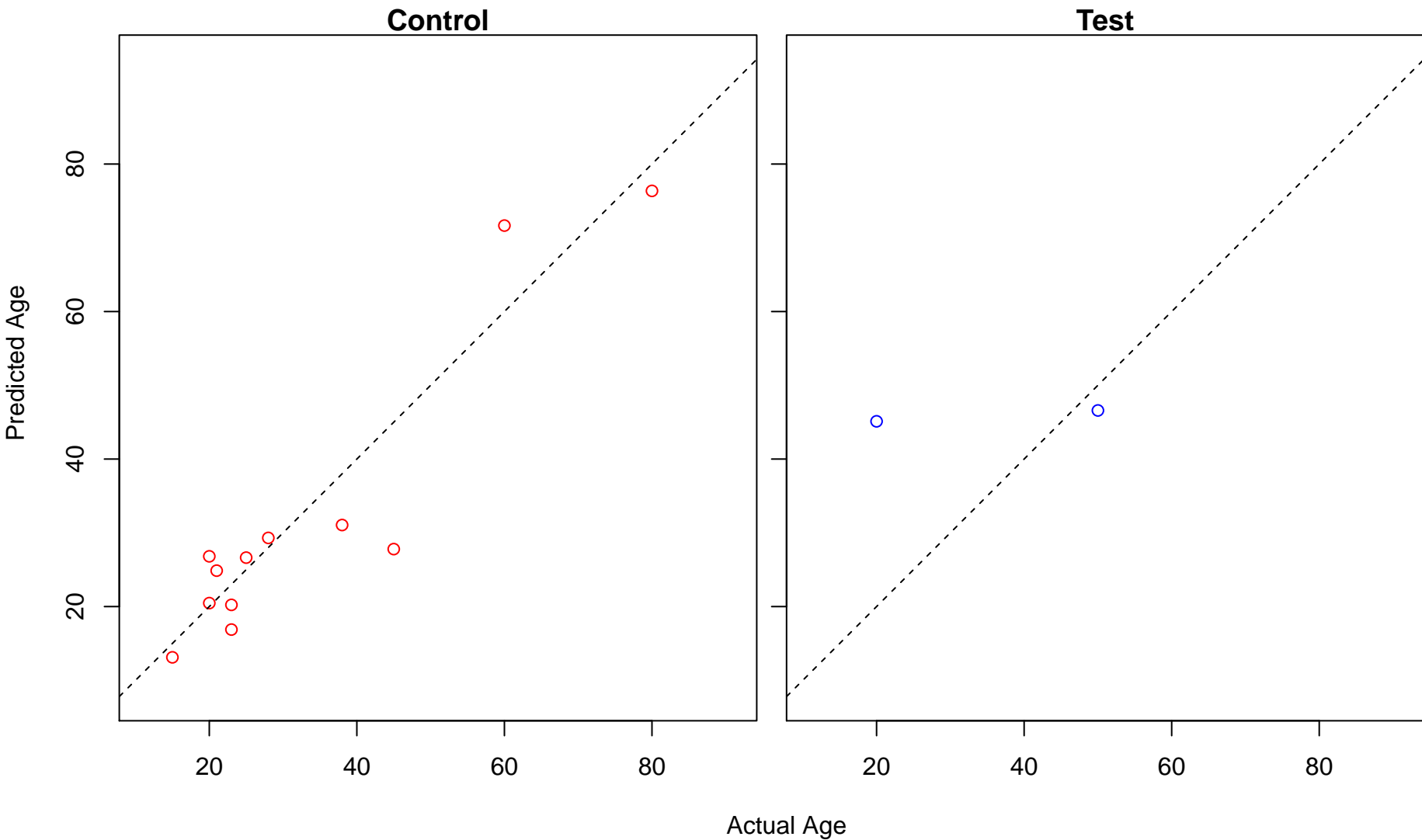
death-inducing signaling complex assembly (Score: 113.165768)



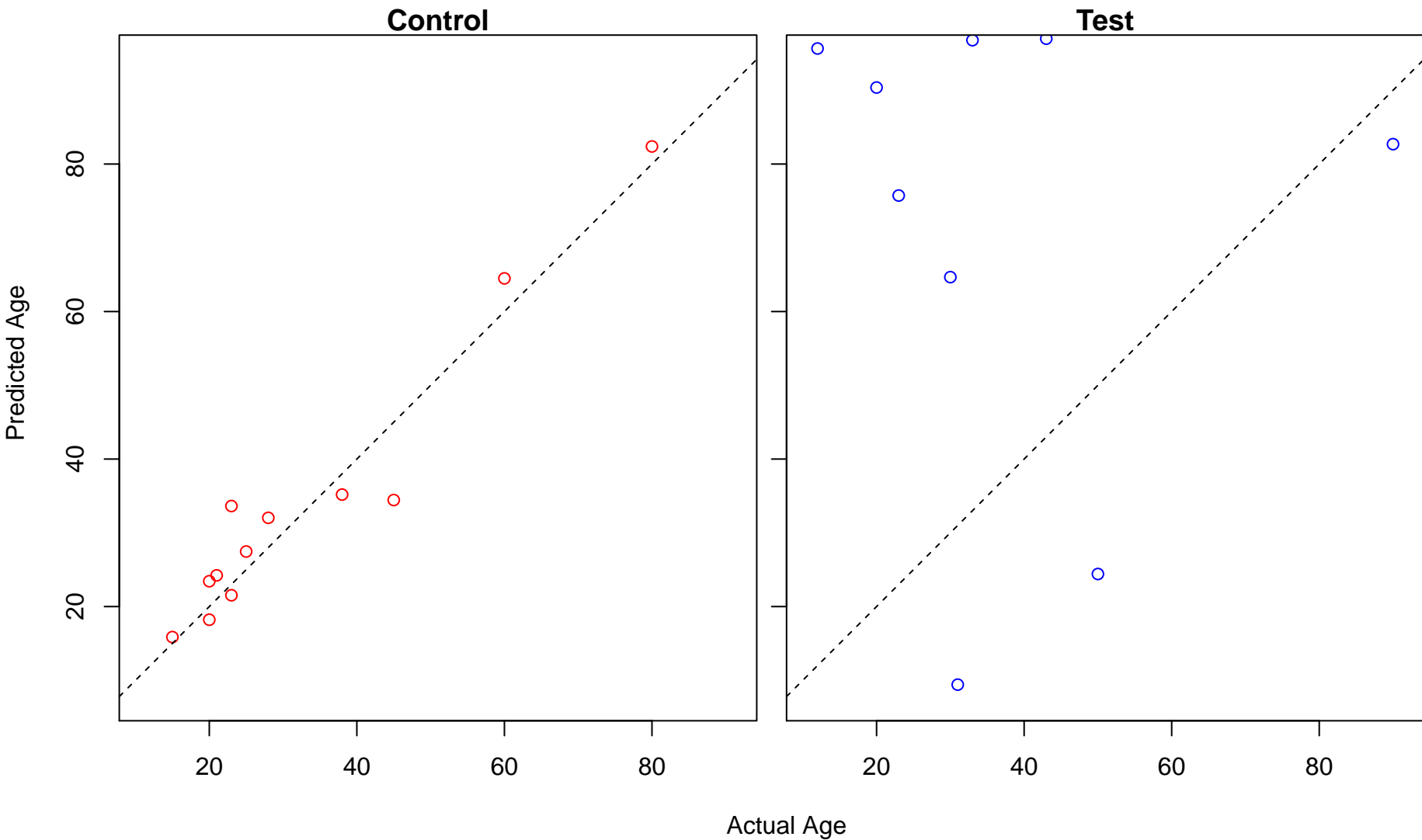
positive regulation of reactive oxygen species metabolic process (Score: 110.881533)



macropinocytosis (Score: 109.550476)

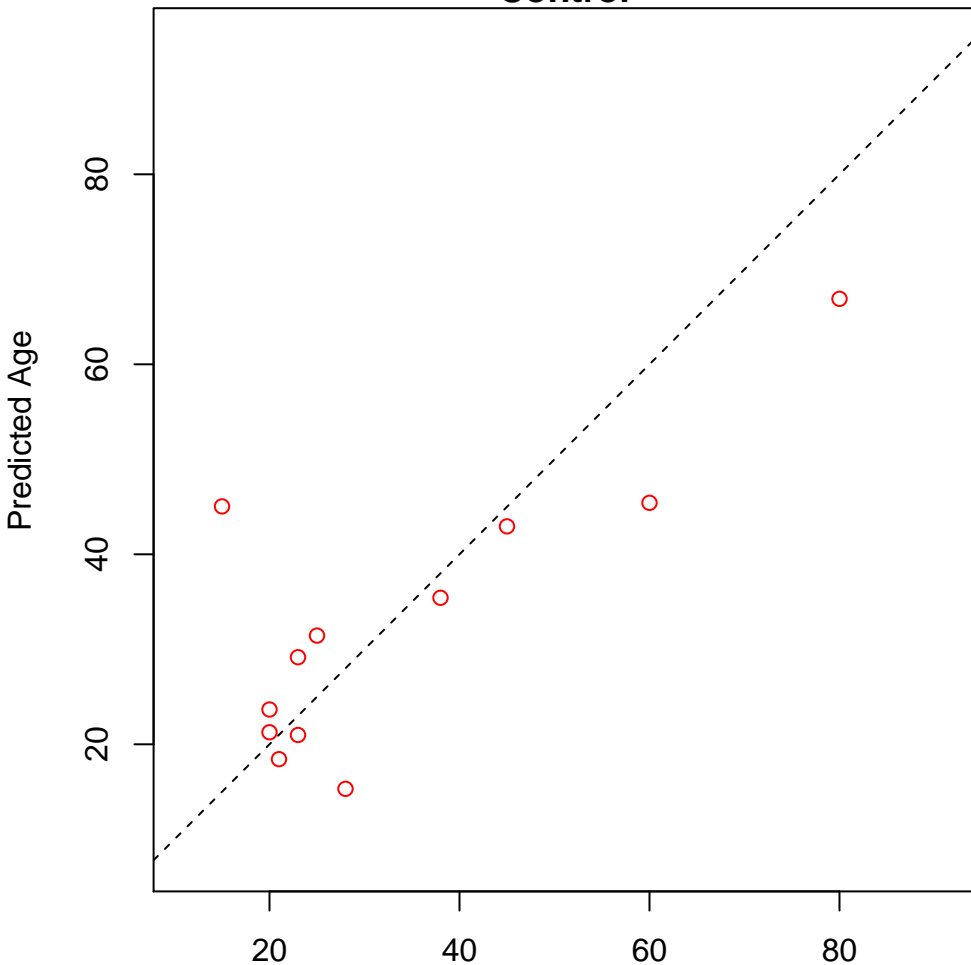


negative regulation of cholesterol storage (Score: 109.112044)

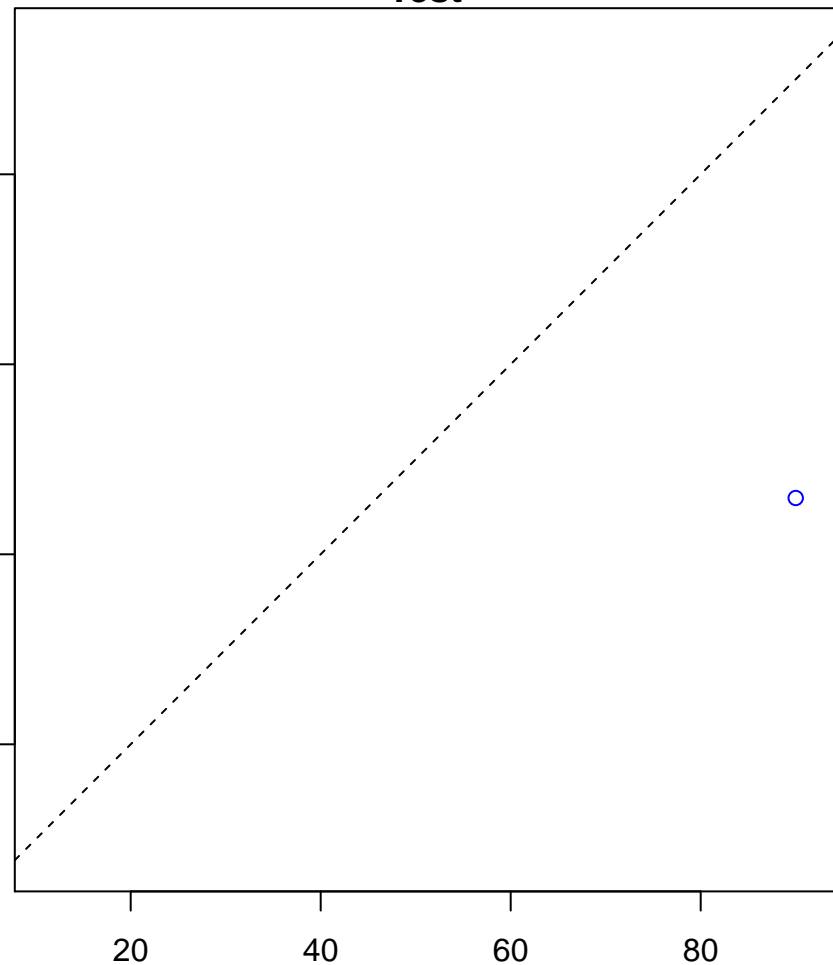


glucocorticoid biosynthetic process (Score: 105.811405)

Control

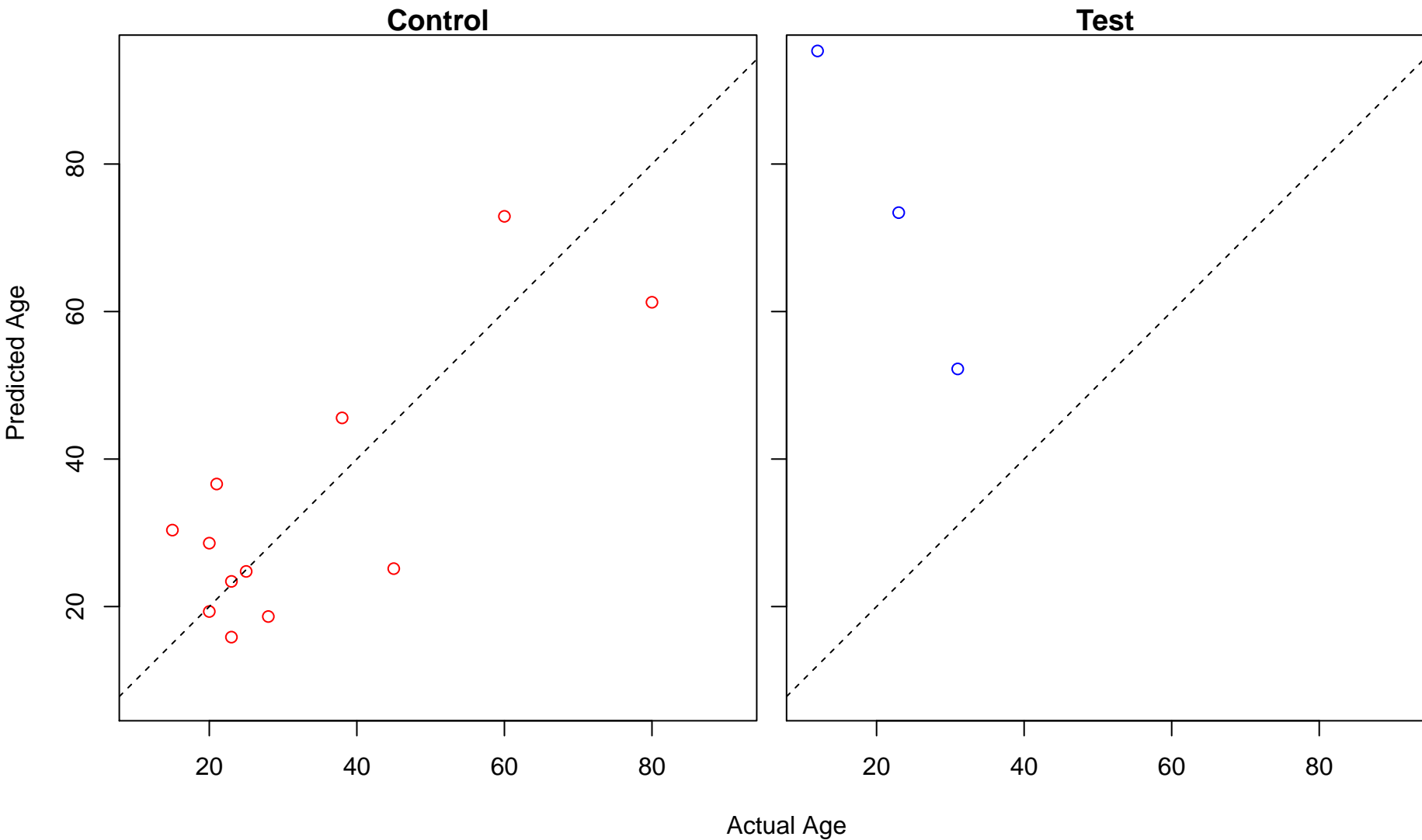


Test

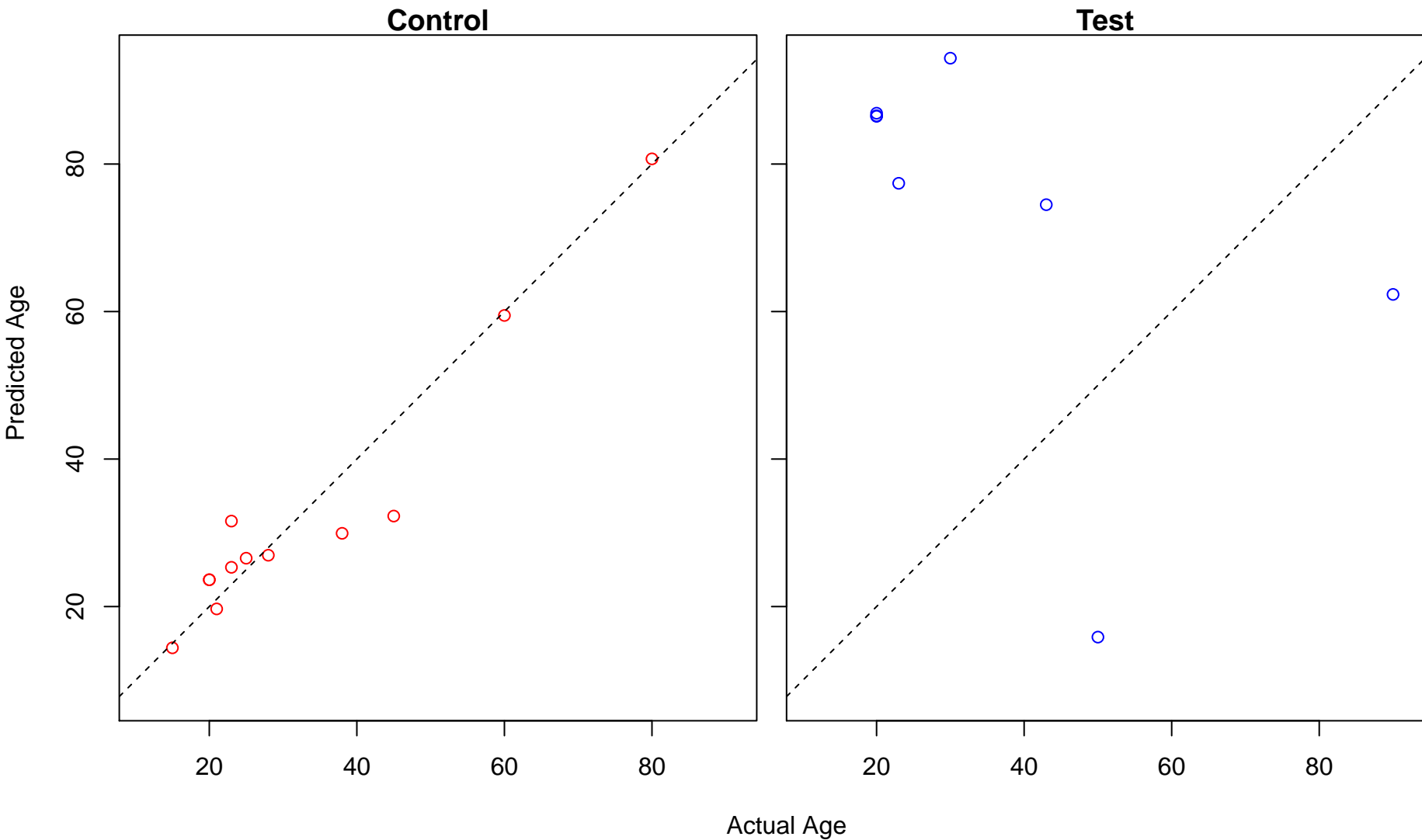


Actual Age

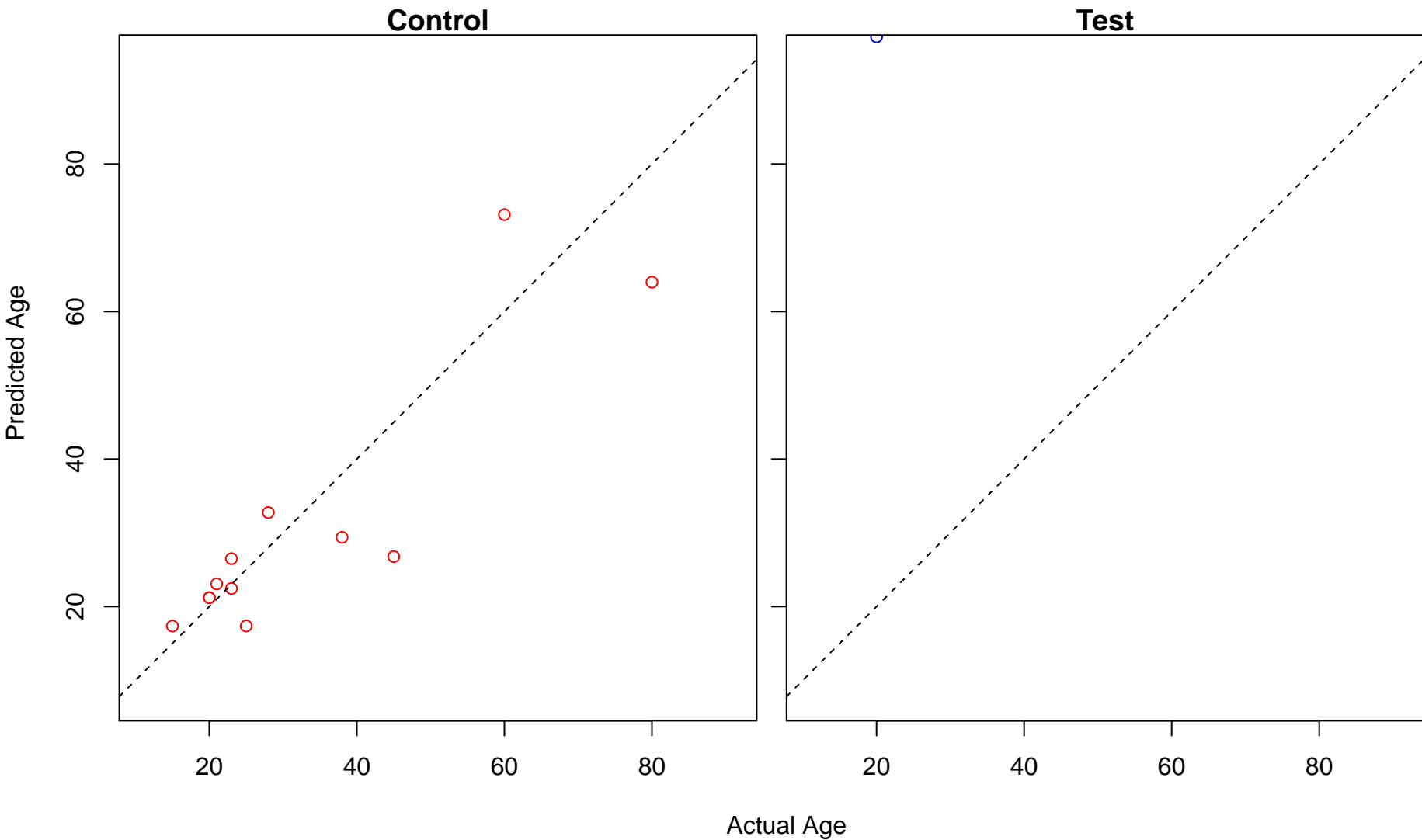
lens morphogenesis in camera-type eye (Score: 103.458447)



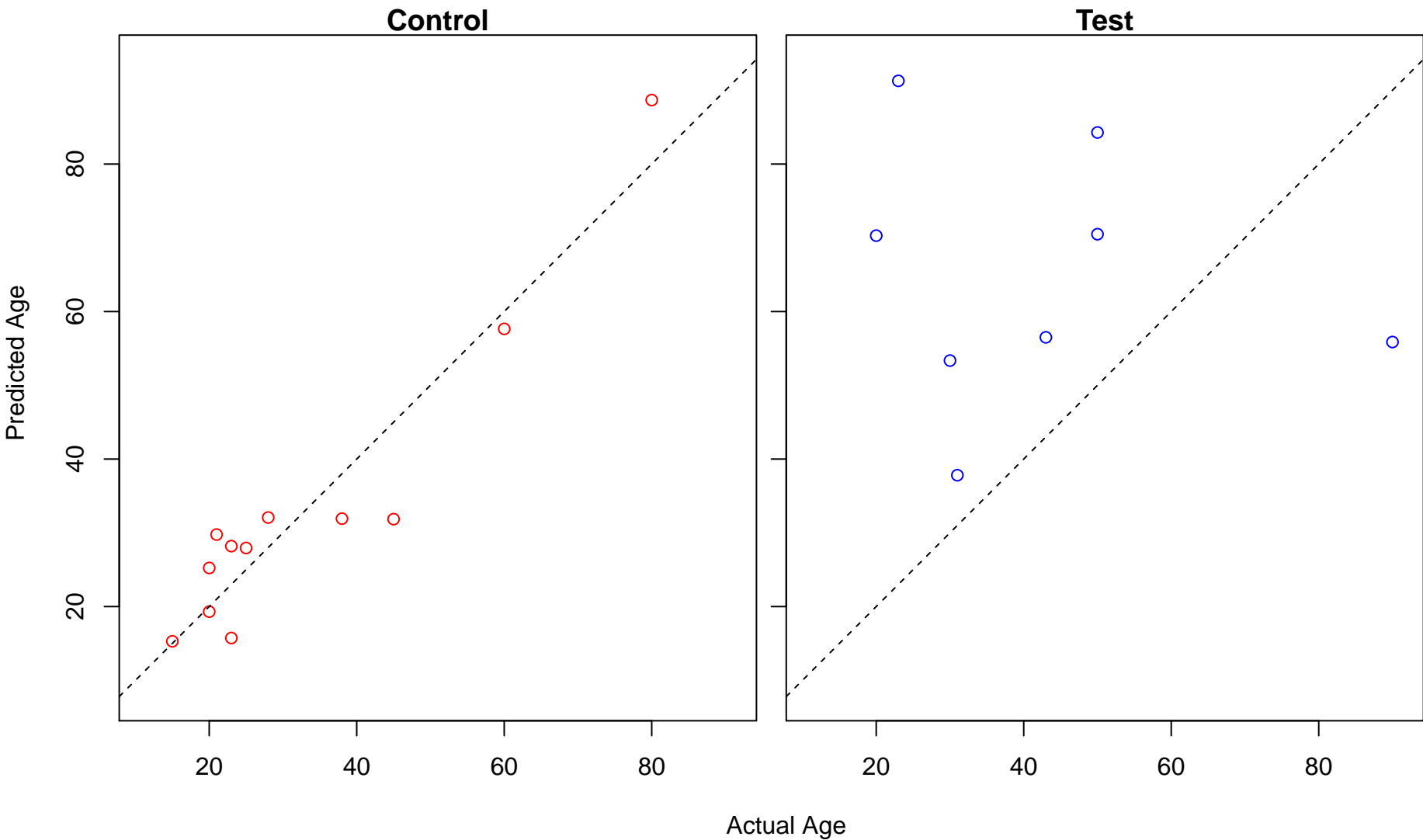
lipopolysaccharide-mediated signaling pathway (Score: 101.419118)



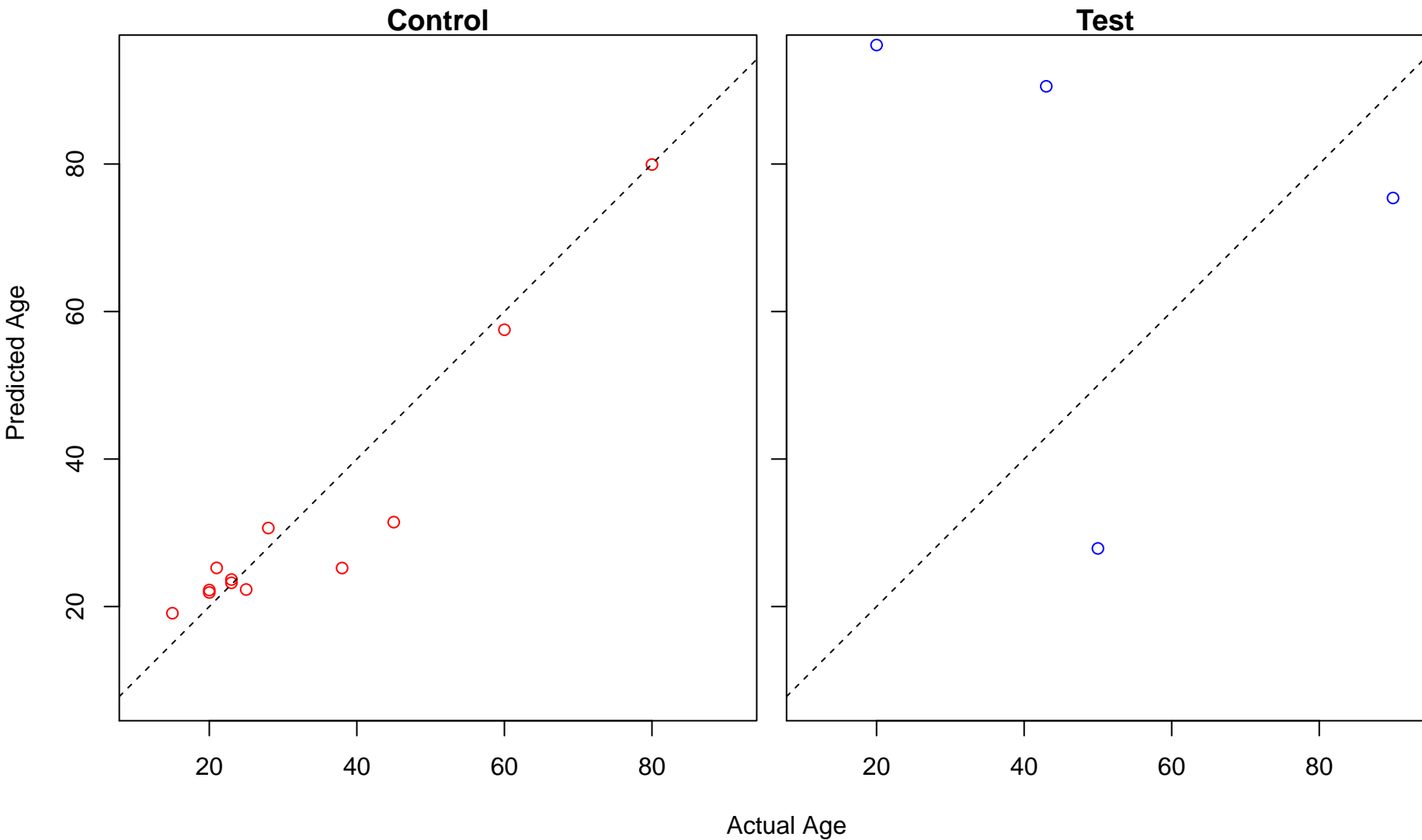
protein hydroxylation (Score: 101.148904)



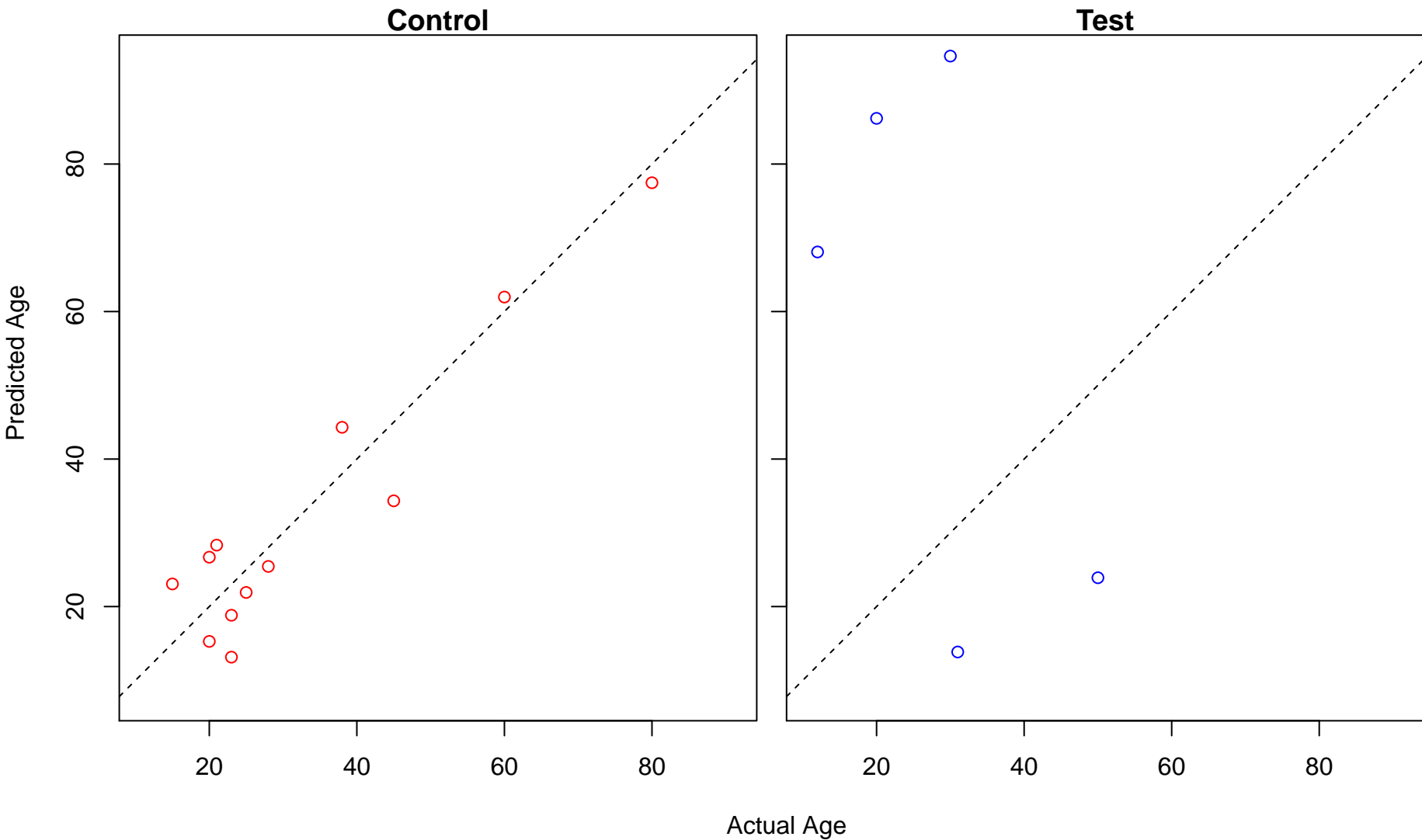
regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway (Score: 97.067)



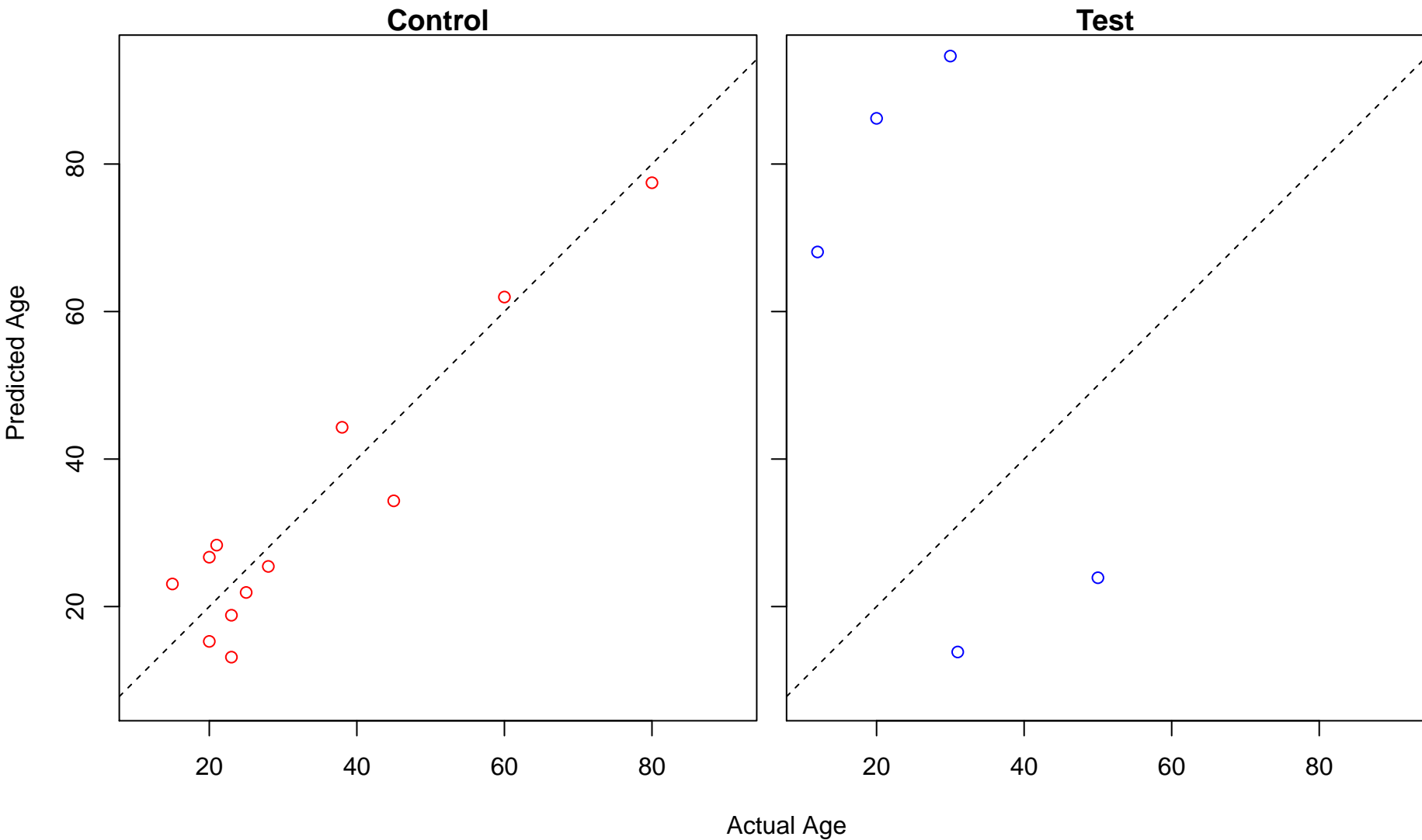
snRNA metabolic process (Score: 96.801041)



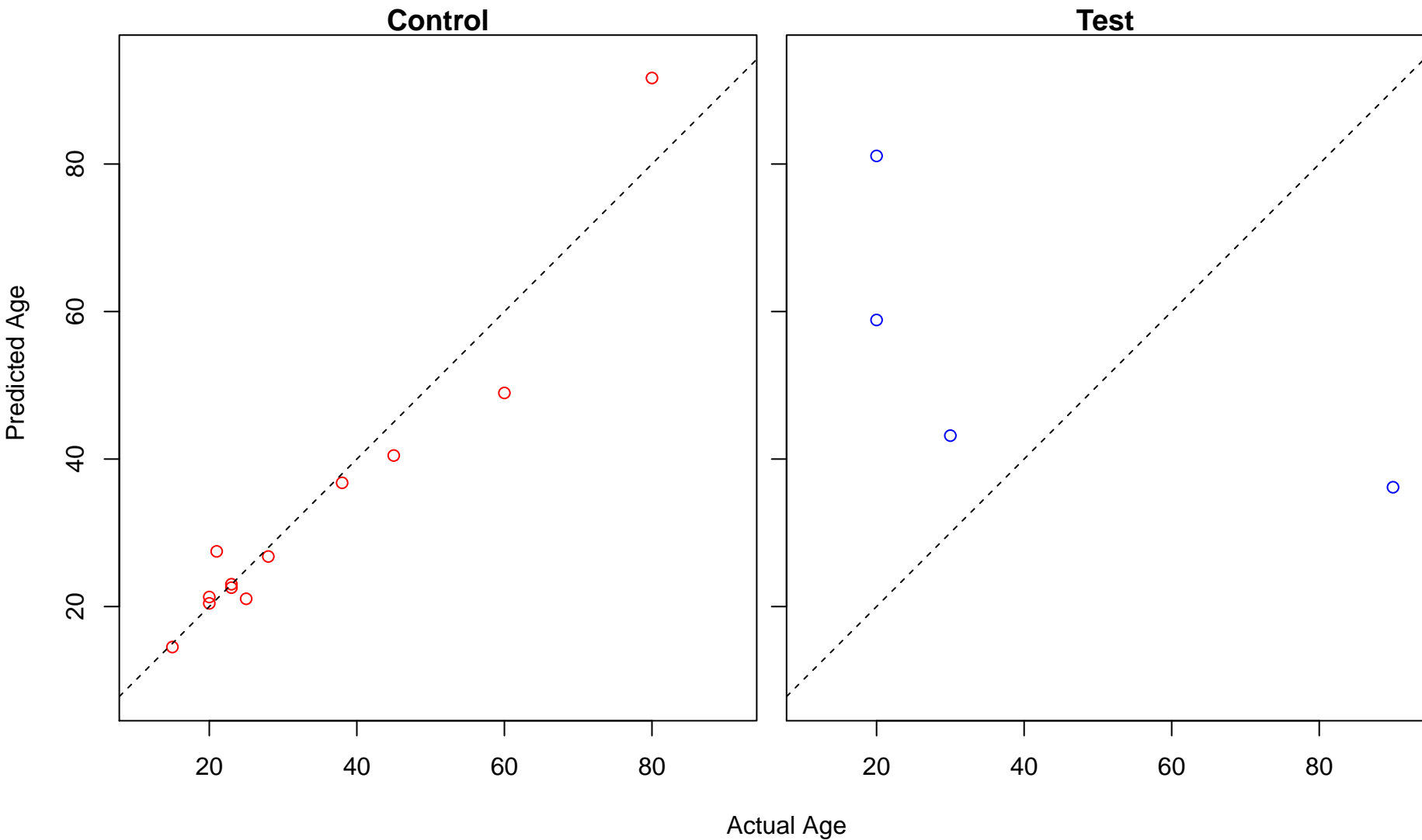
response to protozoan (Score: 95.150859)



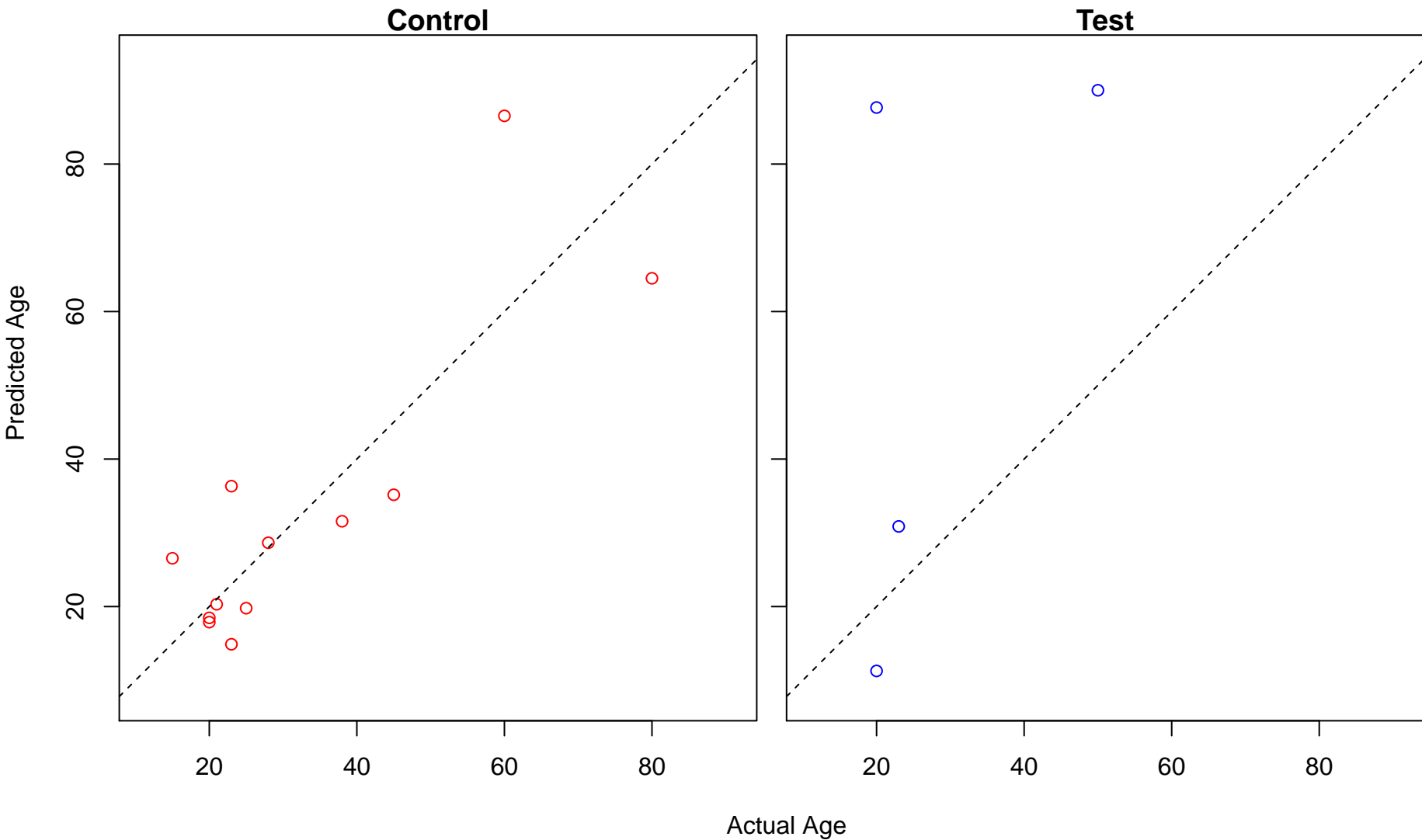
defense response to protozoan (Score: 95.150859)



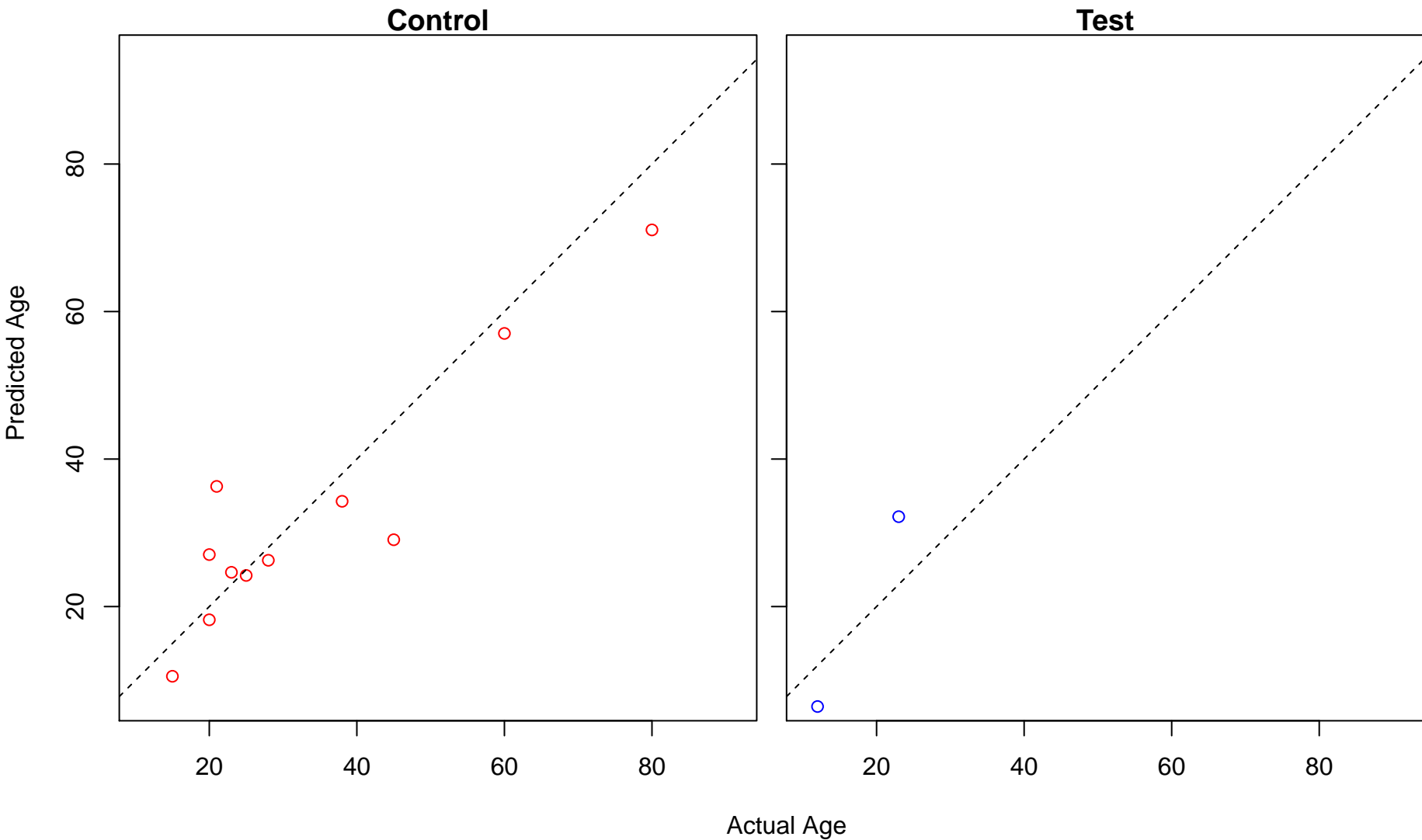
positive regulation of transcription initiation from RNA polymerase II promoter (Score: 92.946323)



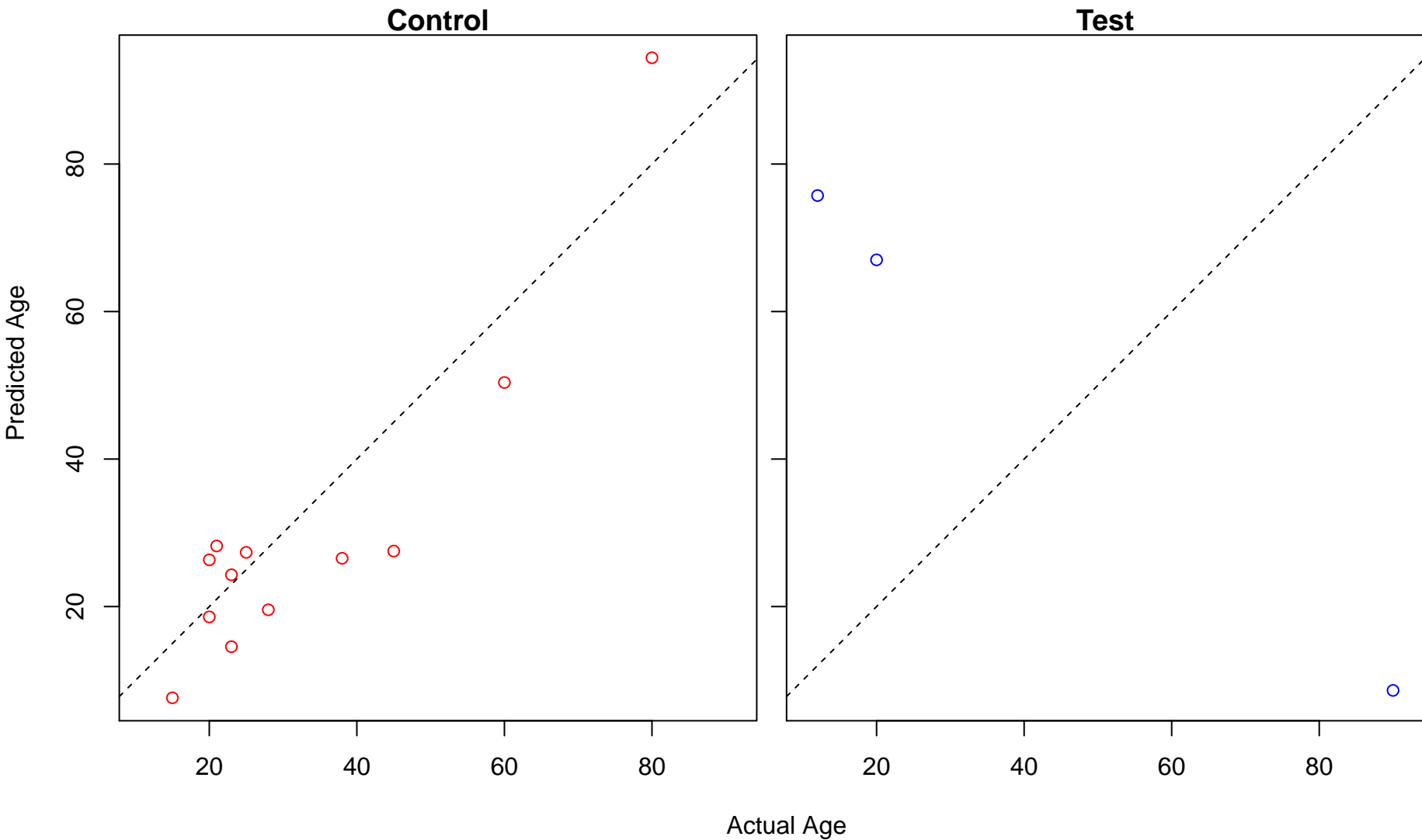
DNA cytosine deamination (Score: 92.679568)



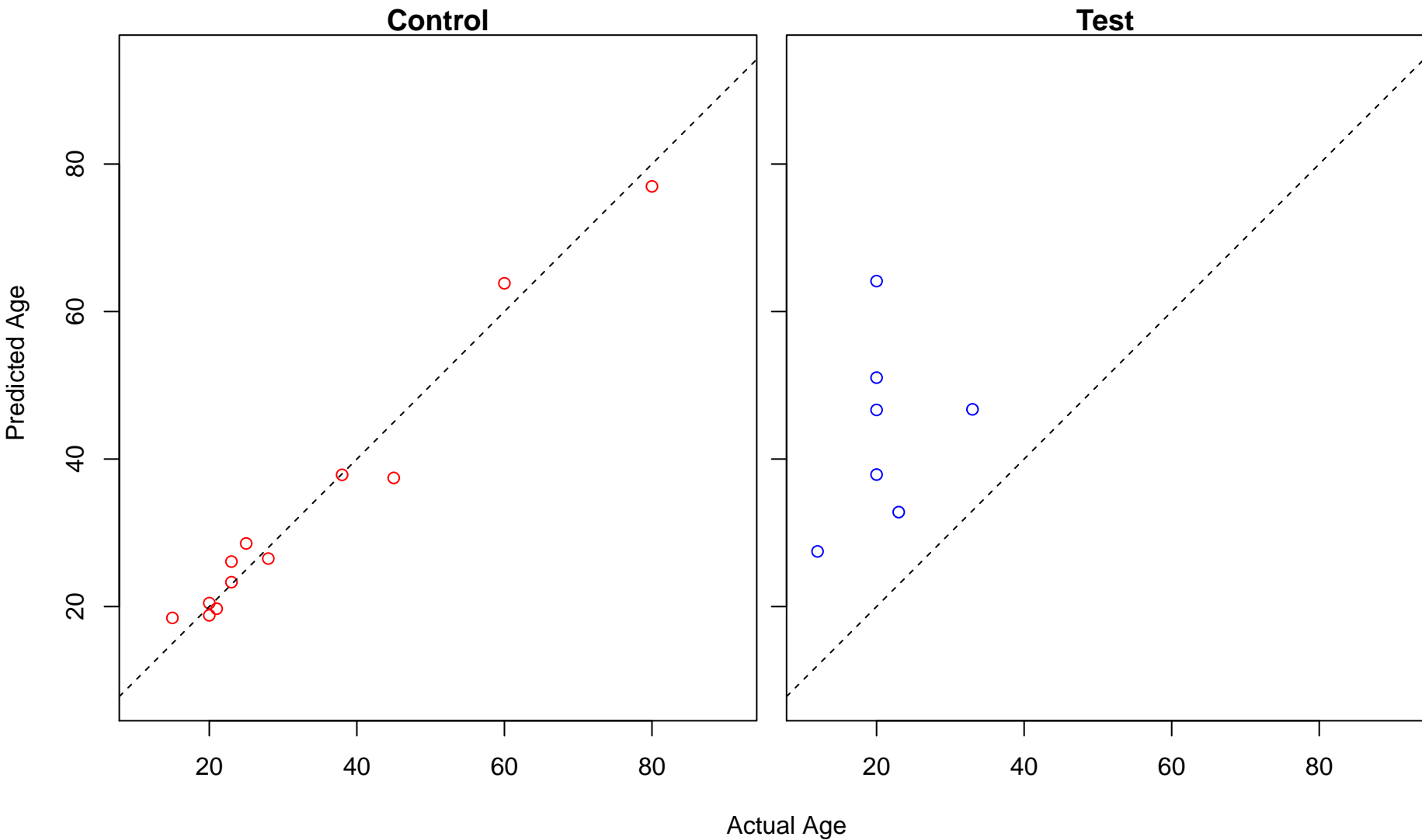
B cell proliferation (Score: 91.628026)



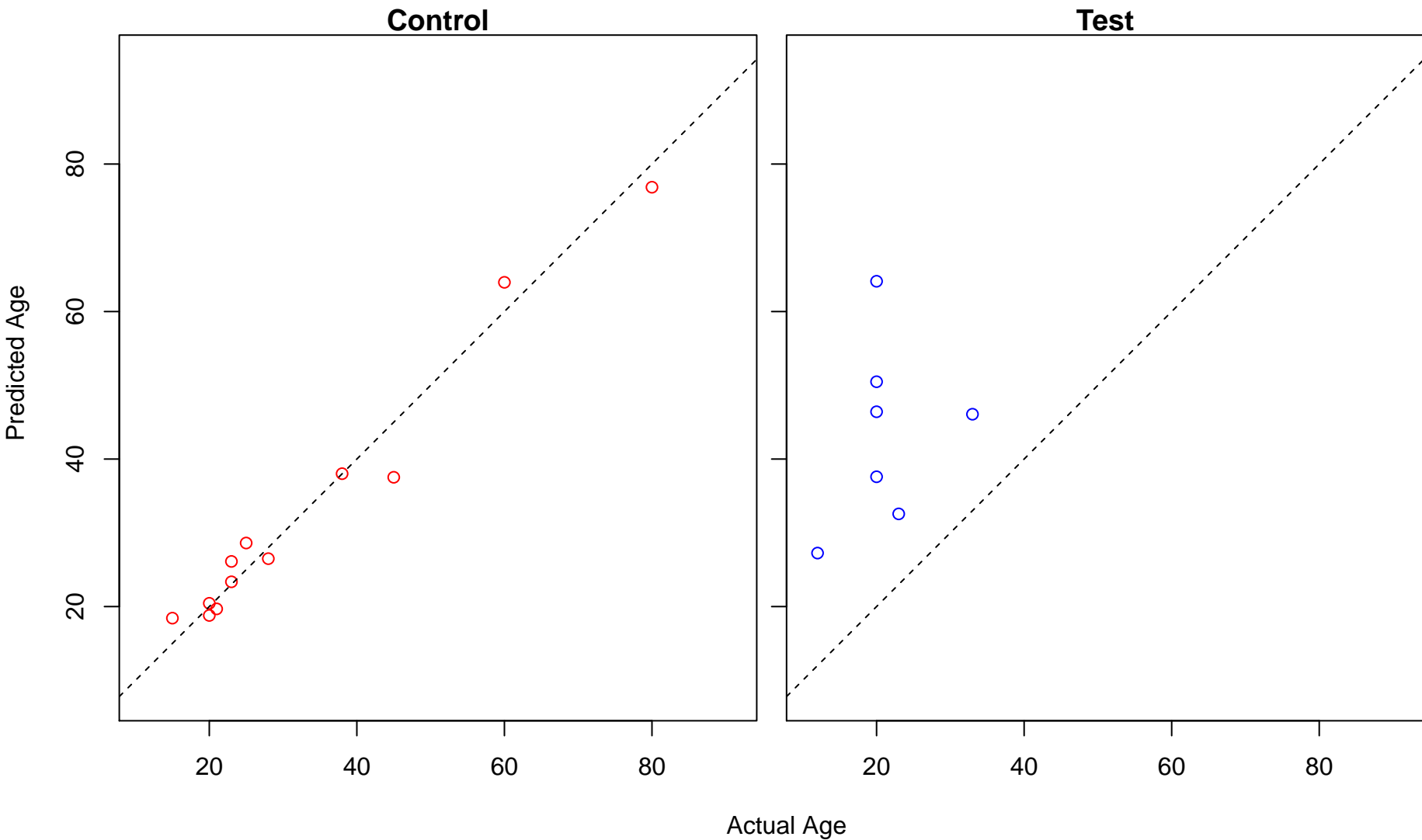
dicarboxylic acid catabolic process (Score: 91.599608)



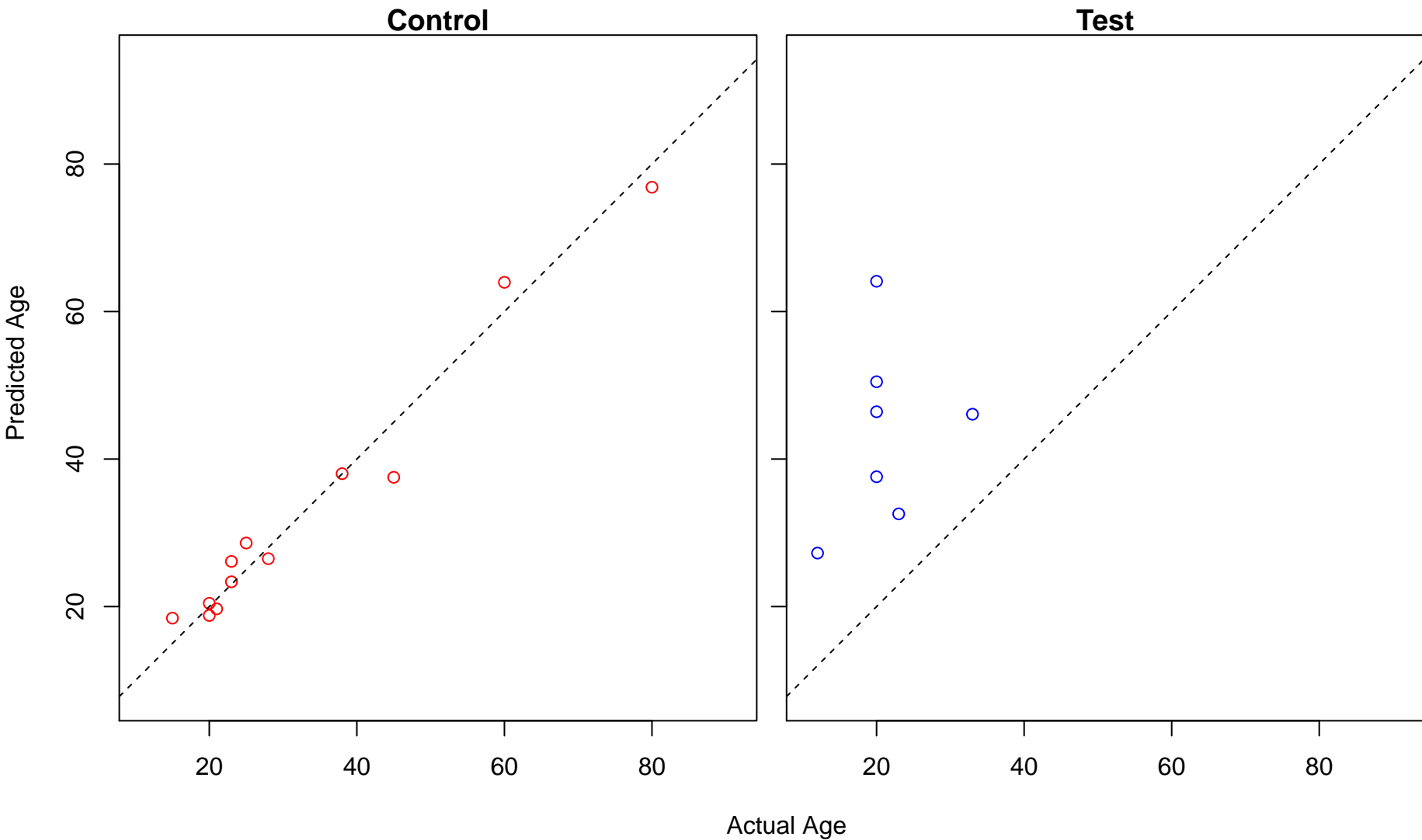
female sex differentiation (Score: 90.754863)



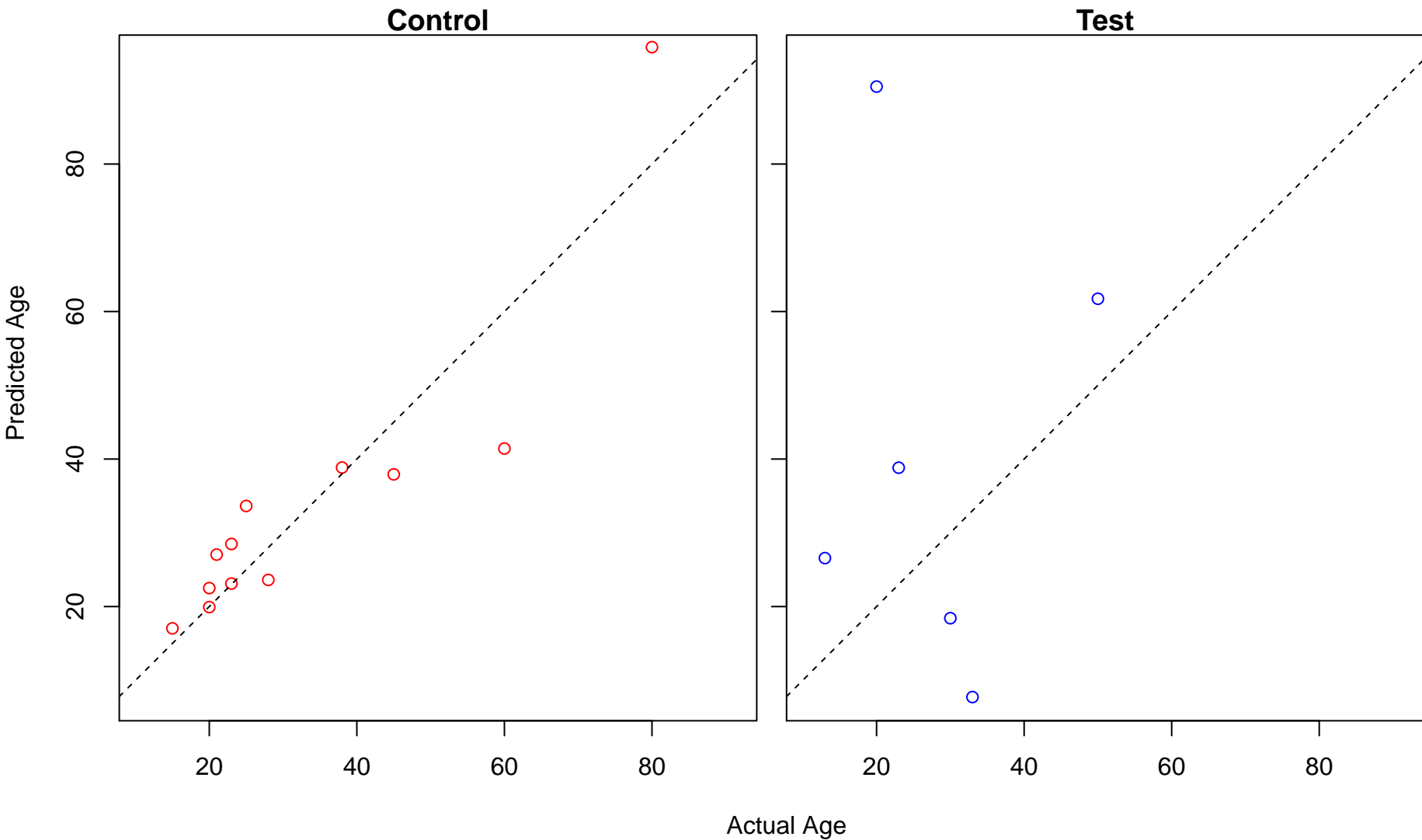
female gonad development (Score: 90.518008)



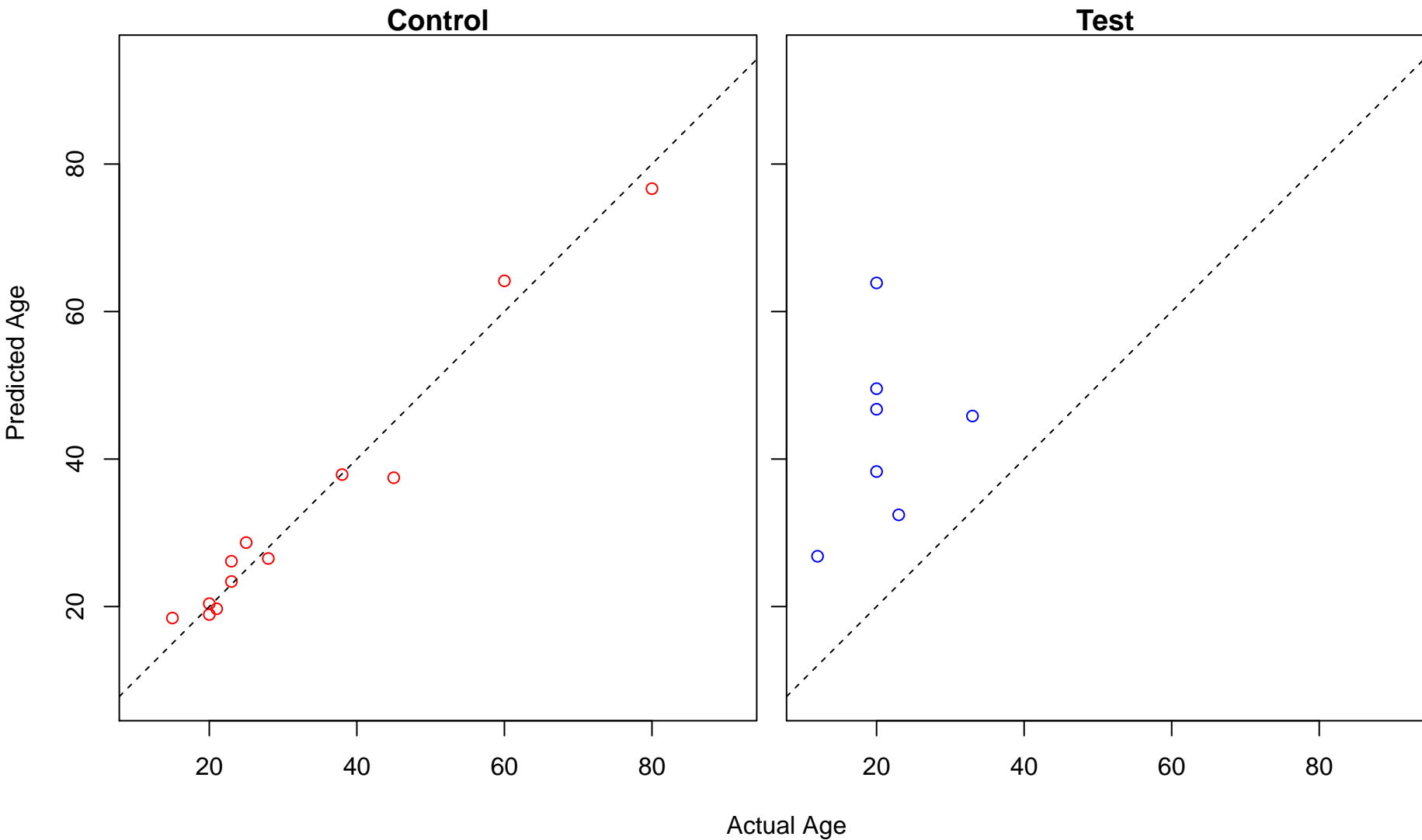
development of primary female sexual characteristics (Score: 90.518008)



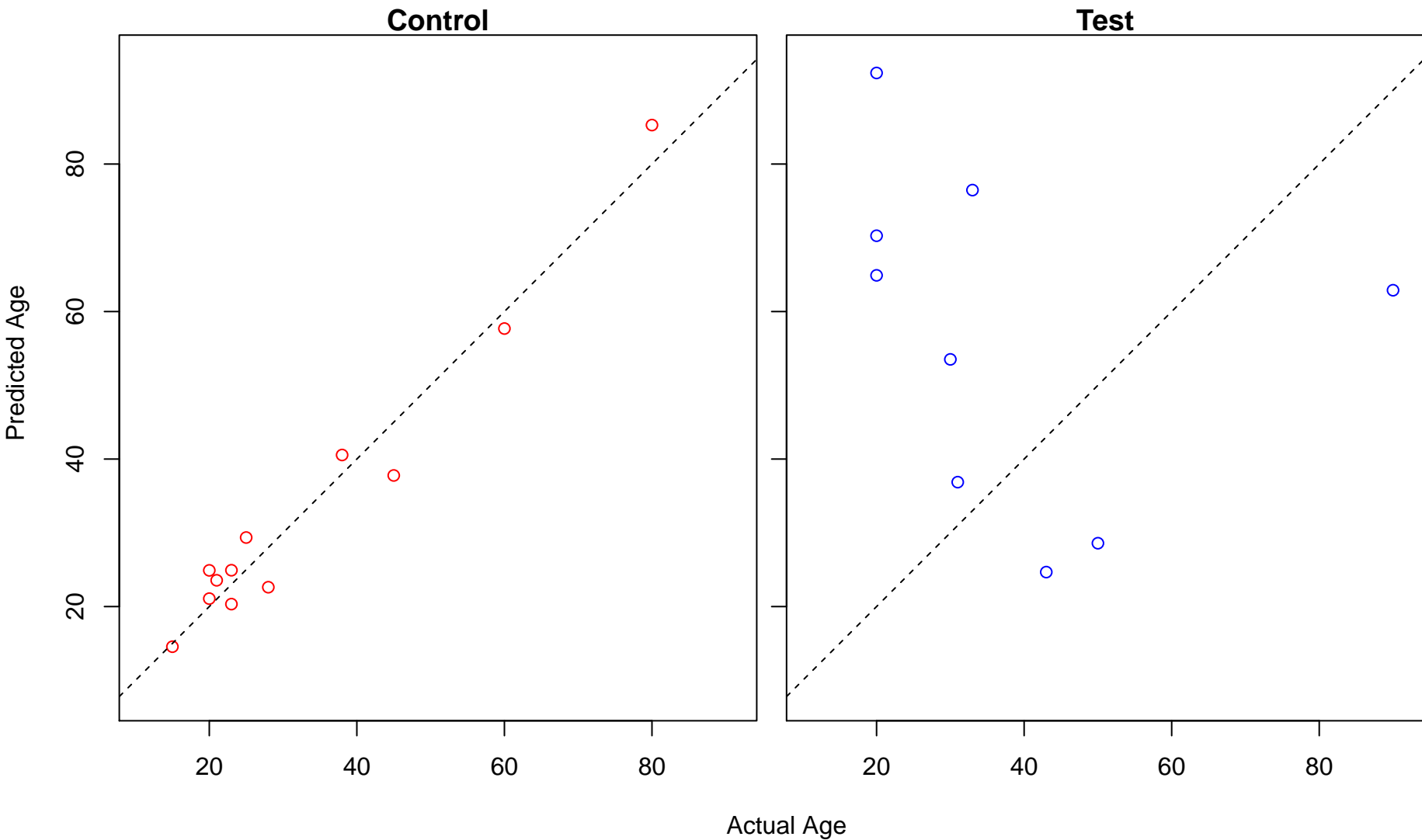
basement membrane organization (Score: 89.308007)



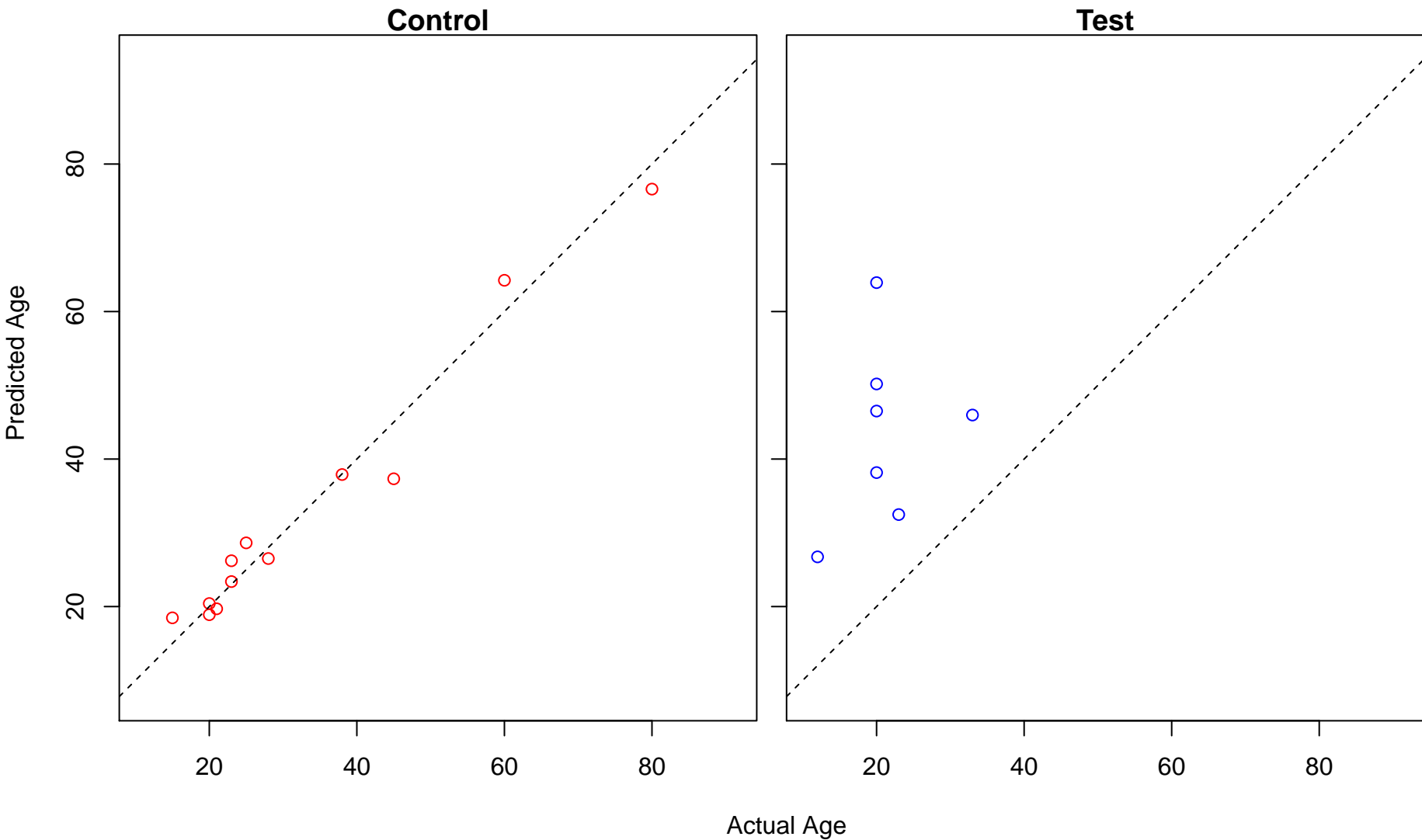
ovulation cycle process (Score: 89.012444)



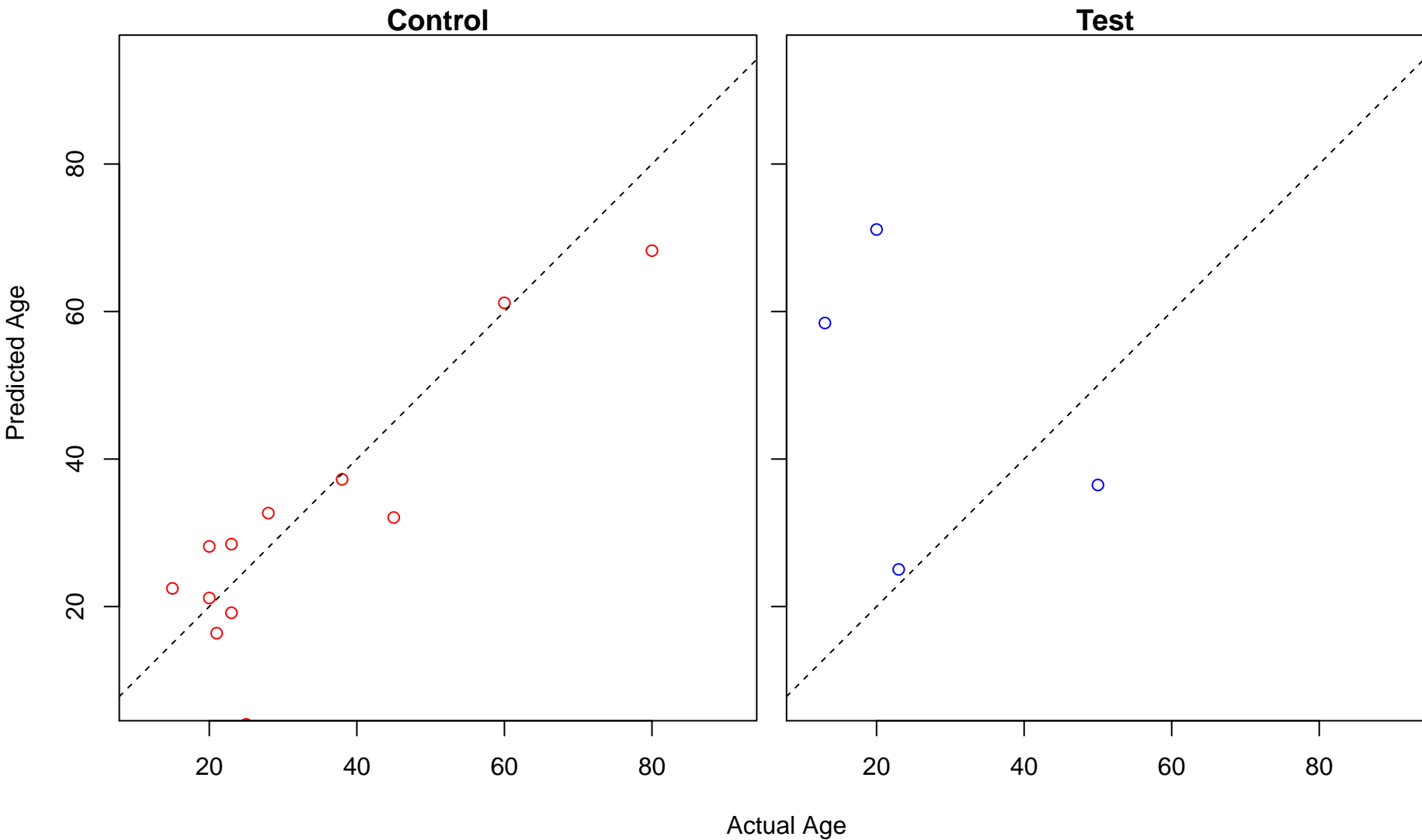
cell communication by electrical coupling (Score: 88.425009)



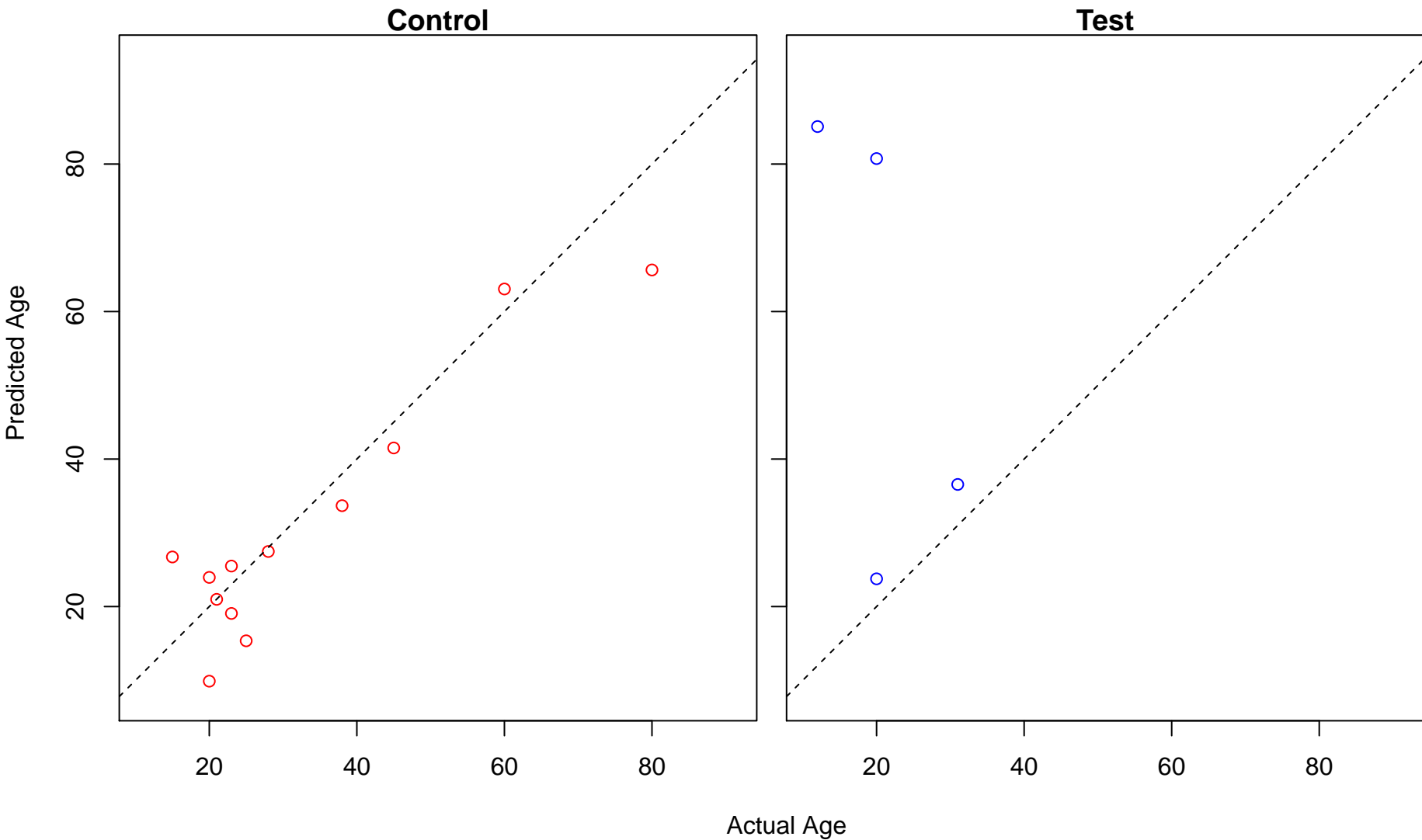
ovulation cycle (Score: 87.641716)



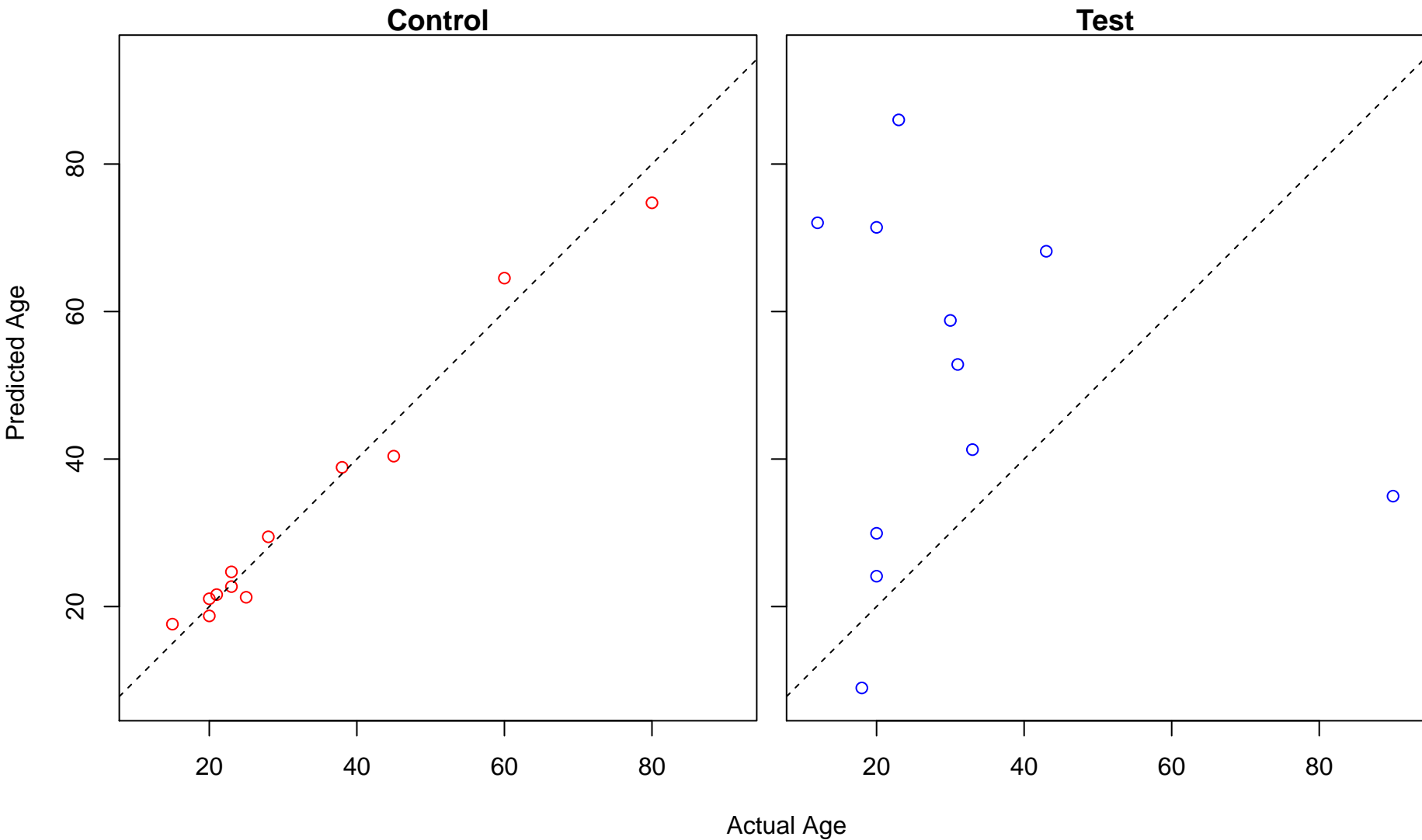
negative regulation of telomere capping (Score: 85.316799)



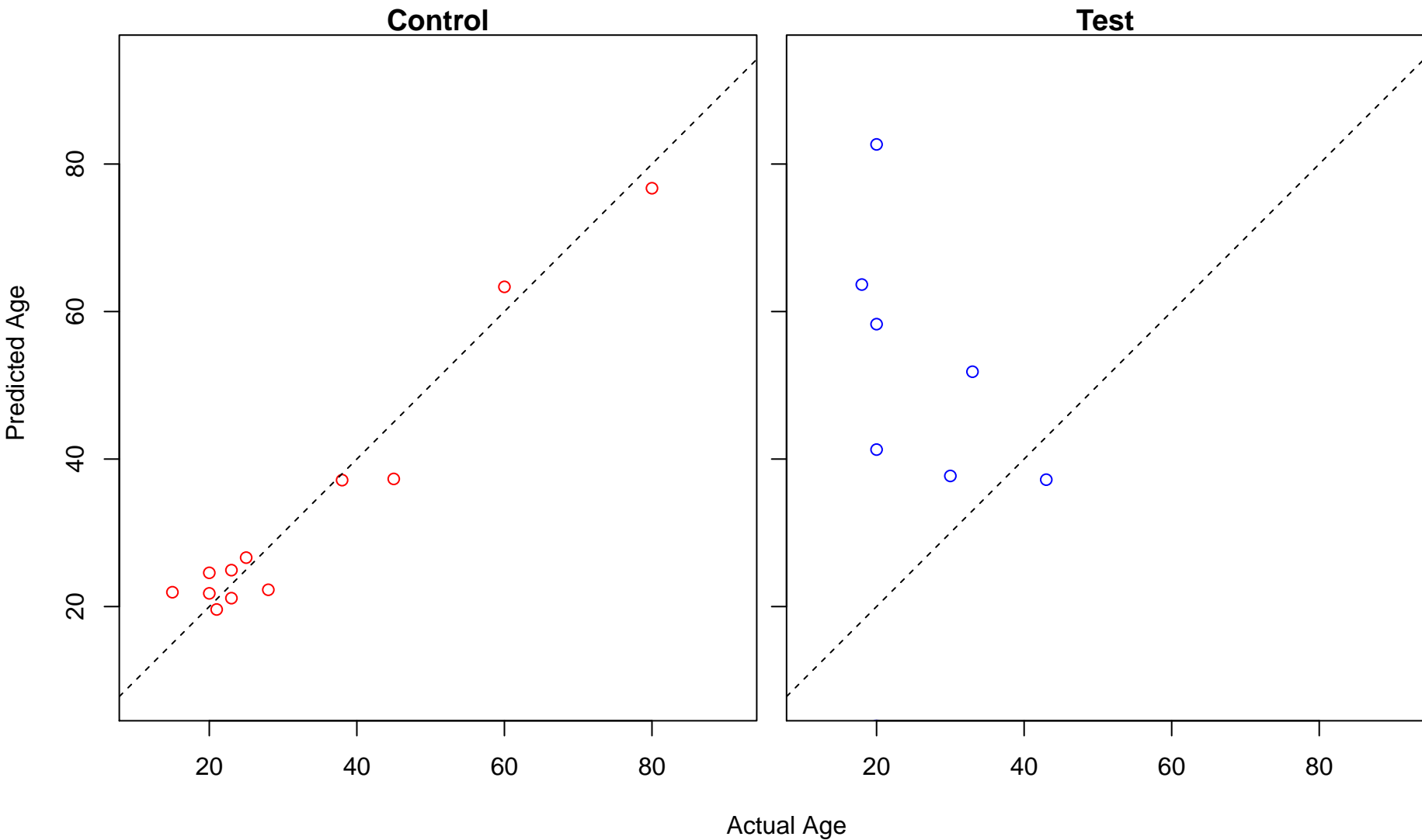
regulation of DNA methylation (Score: 83.269100)



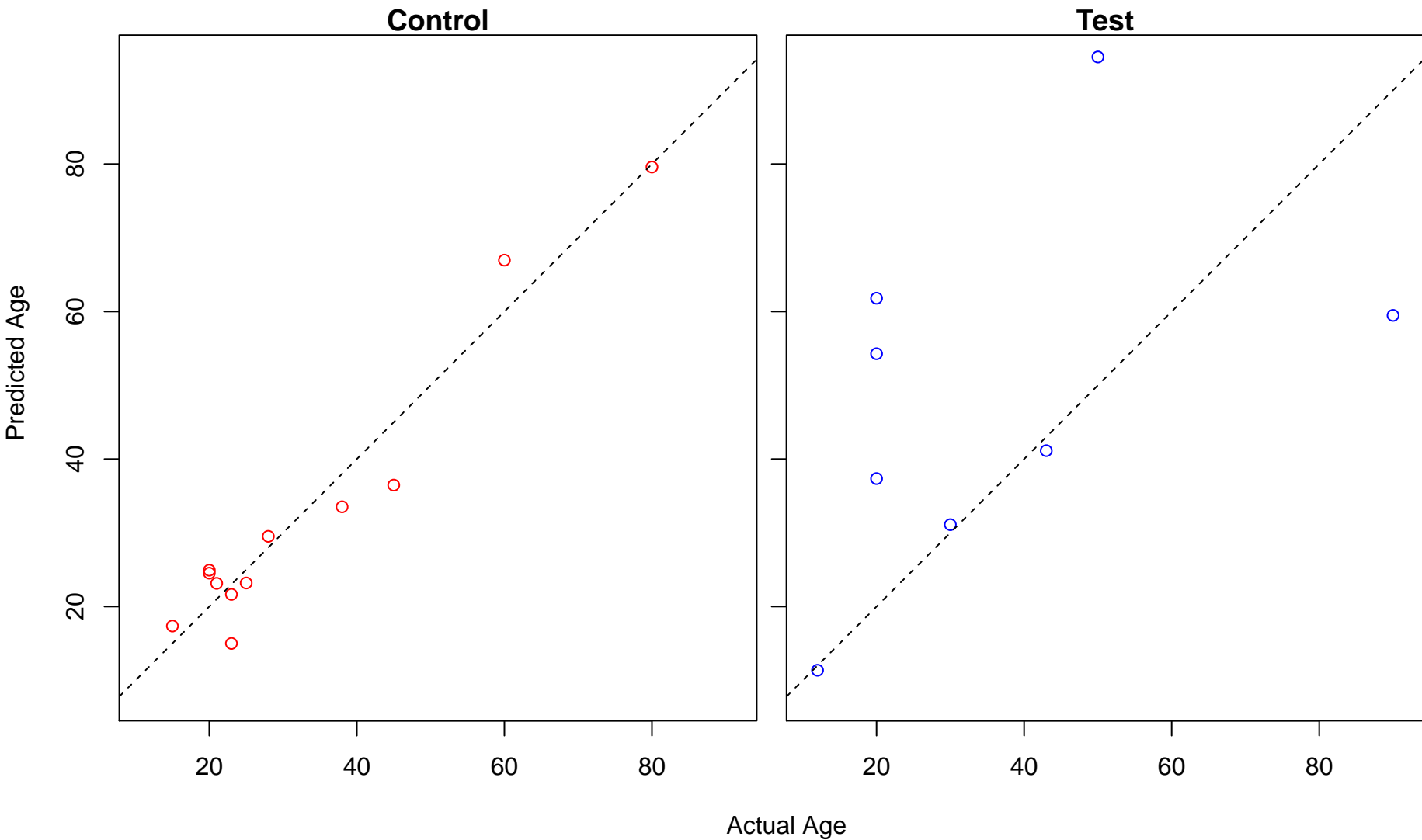
regulation of DNA-templated transcription, initiation (Score: 81.763986)



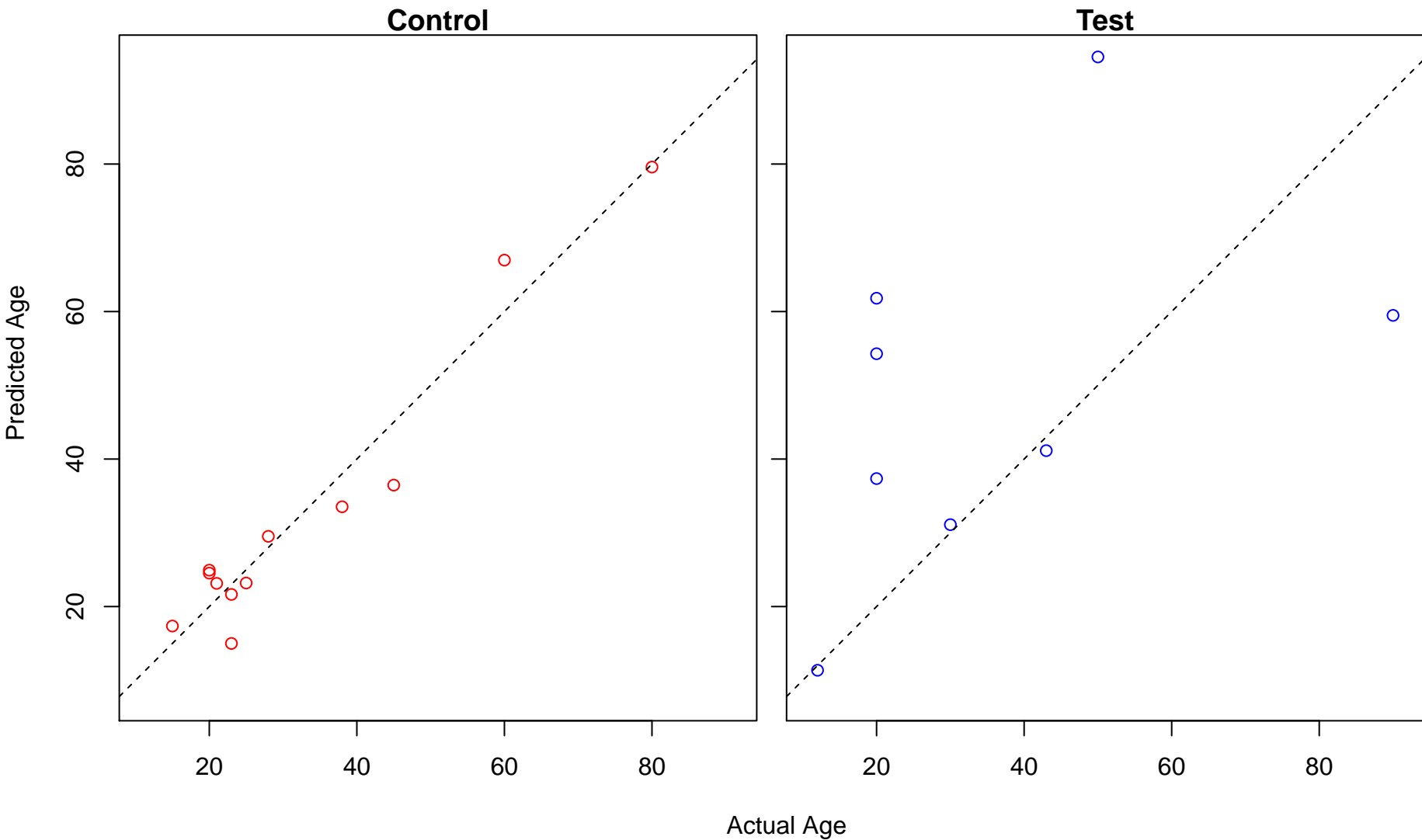
regulation of epidermal growth factor receptor signaling pathway (Score: 81.058945)



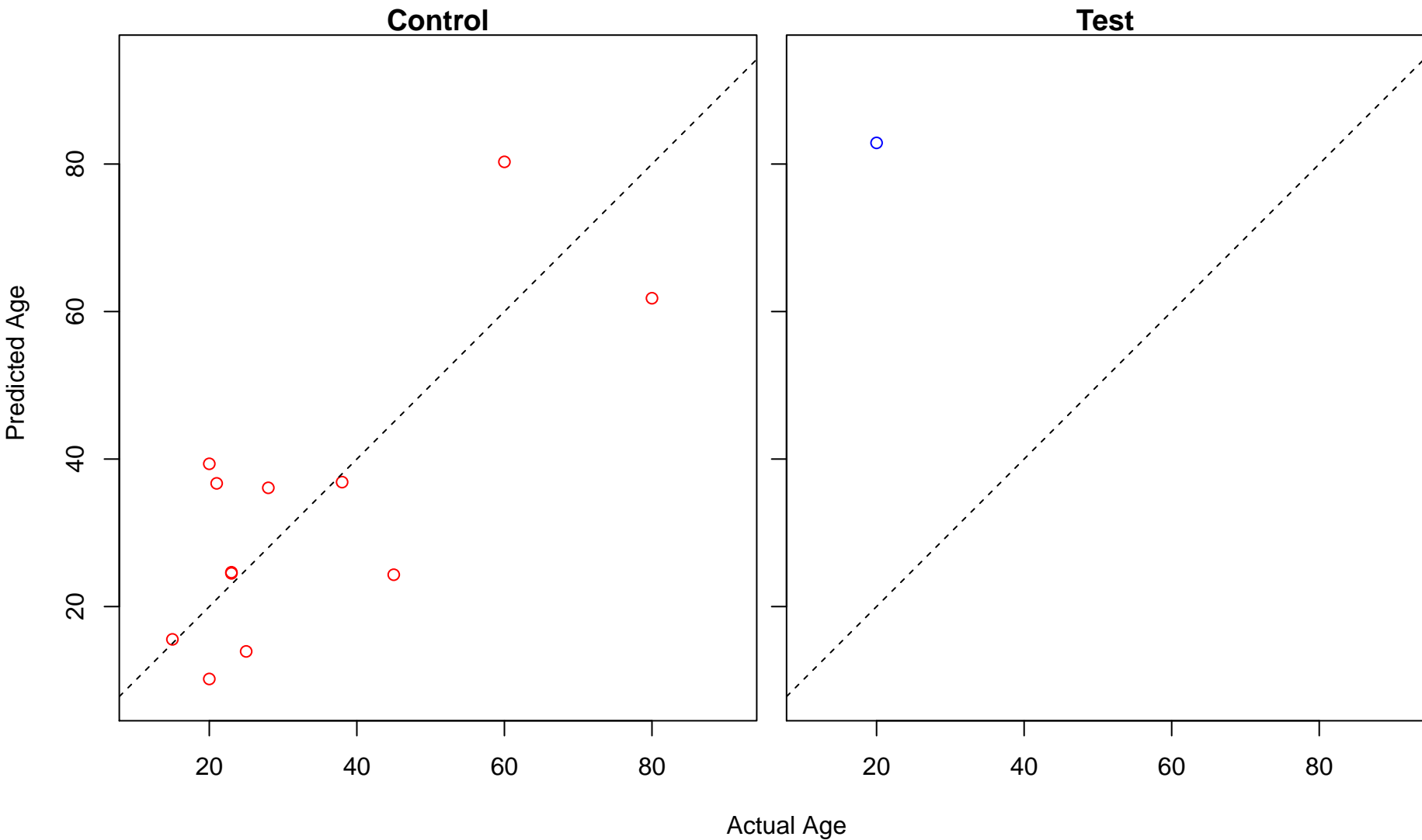
regulation of protein localization to plasma membrane (Score: 80.390587)



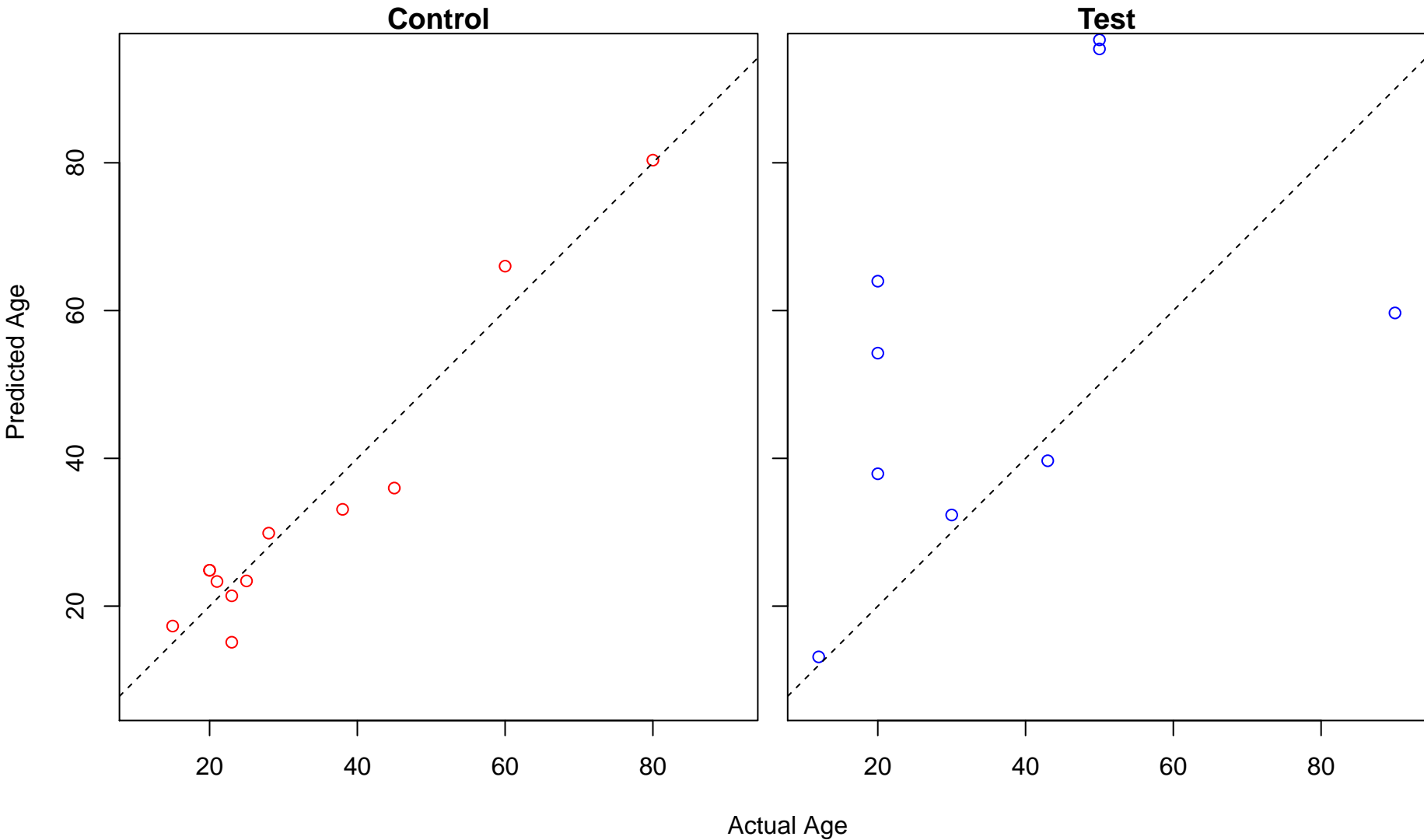
regulation of protein localization to cell periphery (Score: 80.390587)



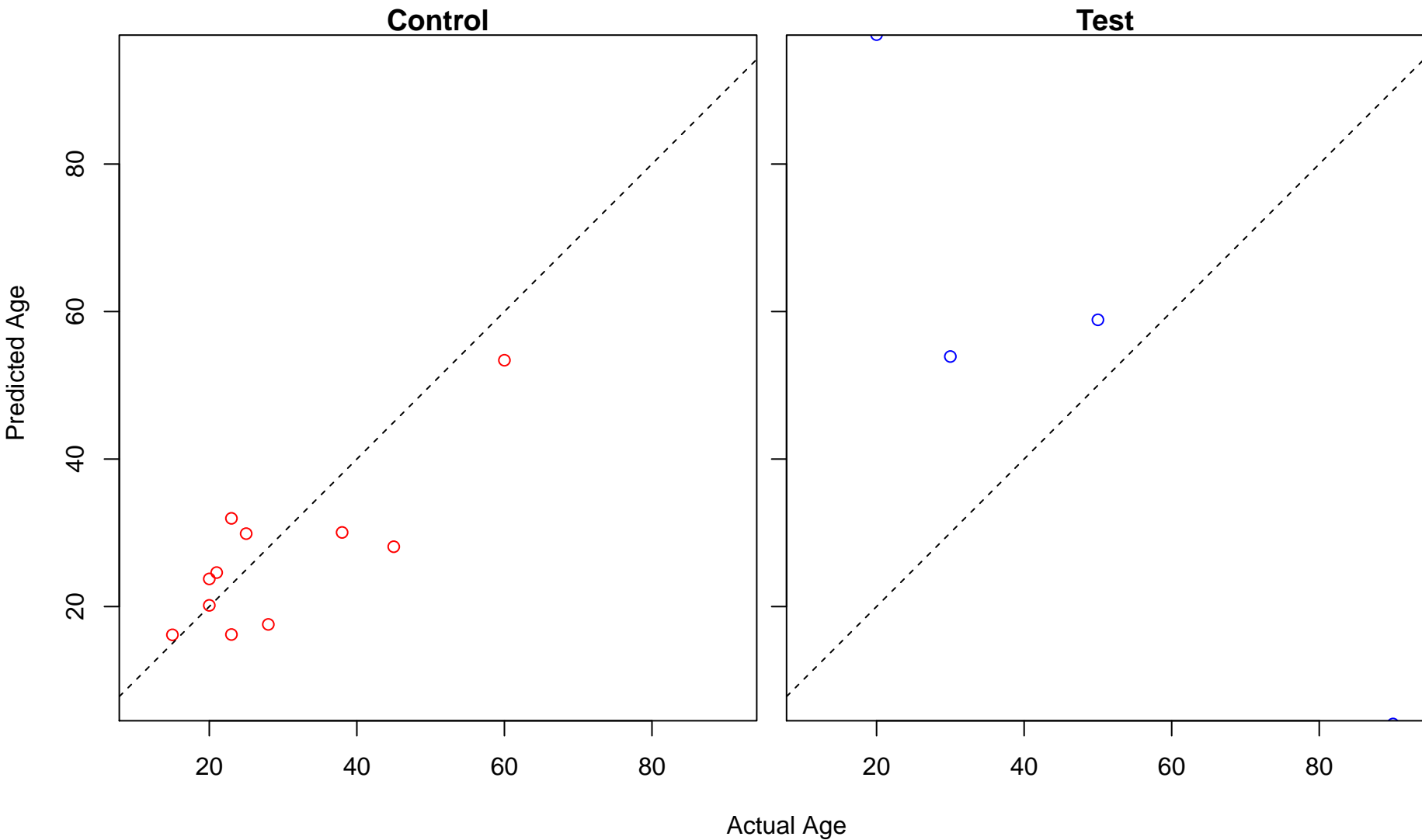
histone H4 deacetylation (Score: 79.304318)



regulation of plasma membrane organization (Score: 79.274092)

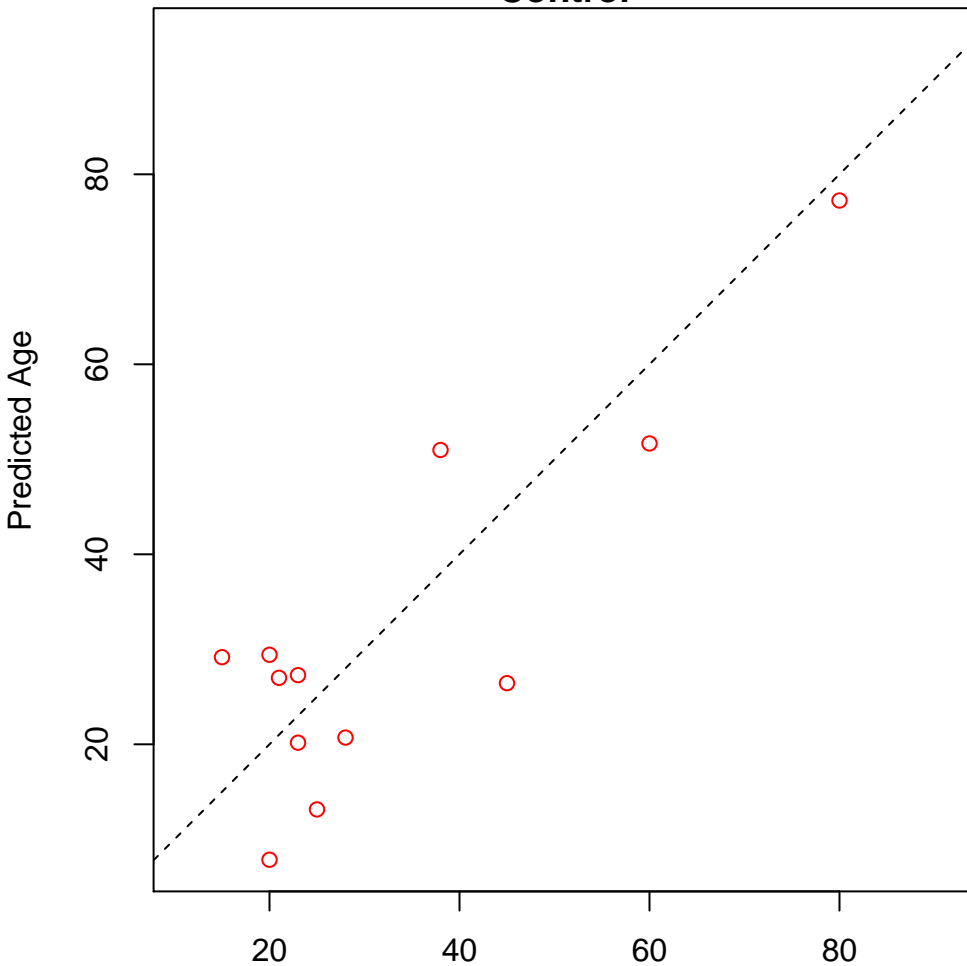


positive regulation of corticosteroid hormone secretion (Score: 77.831616)

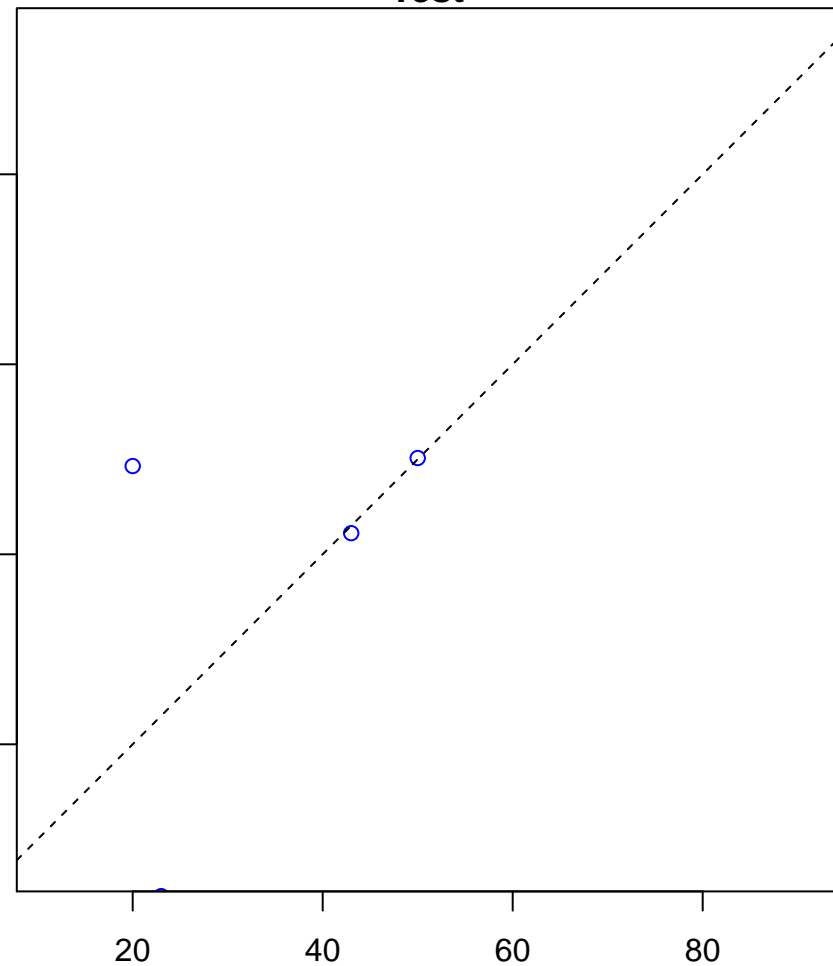


regulation of pro-B cell differentiation (Score: 75.430681)

Control



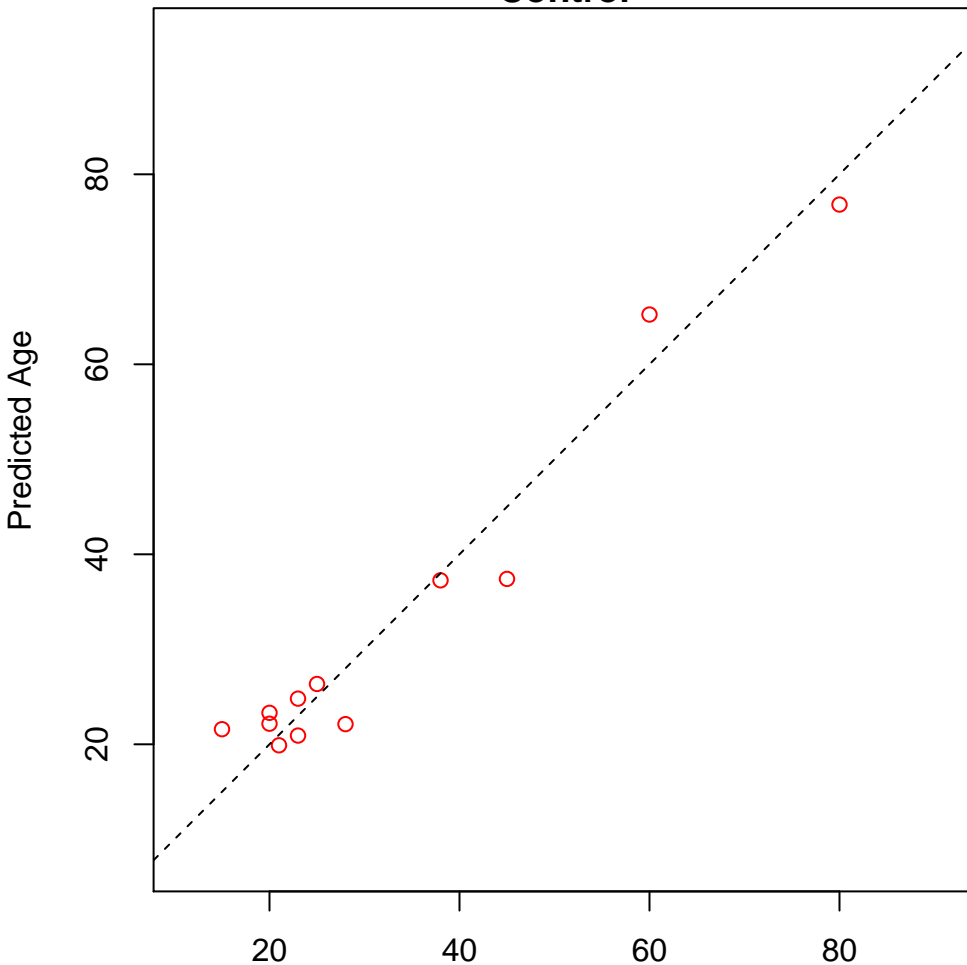
Test



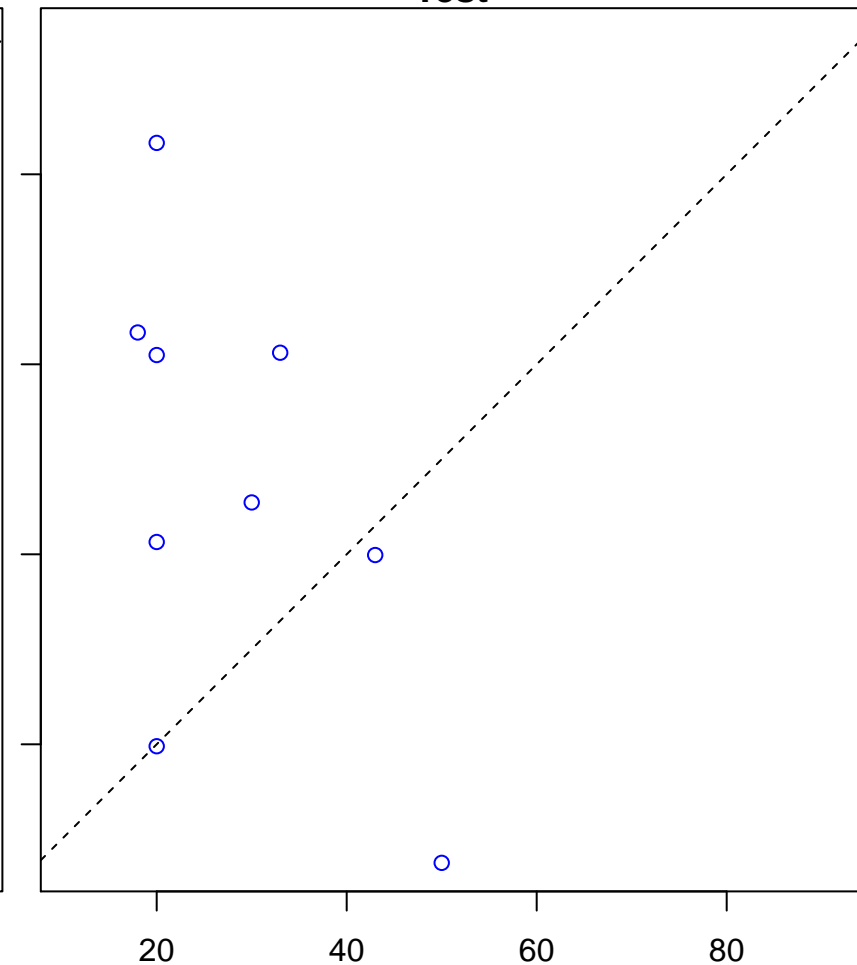
Actual Age

regulation of ERBB signaling pathway (Score: 75.096963)

Control

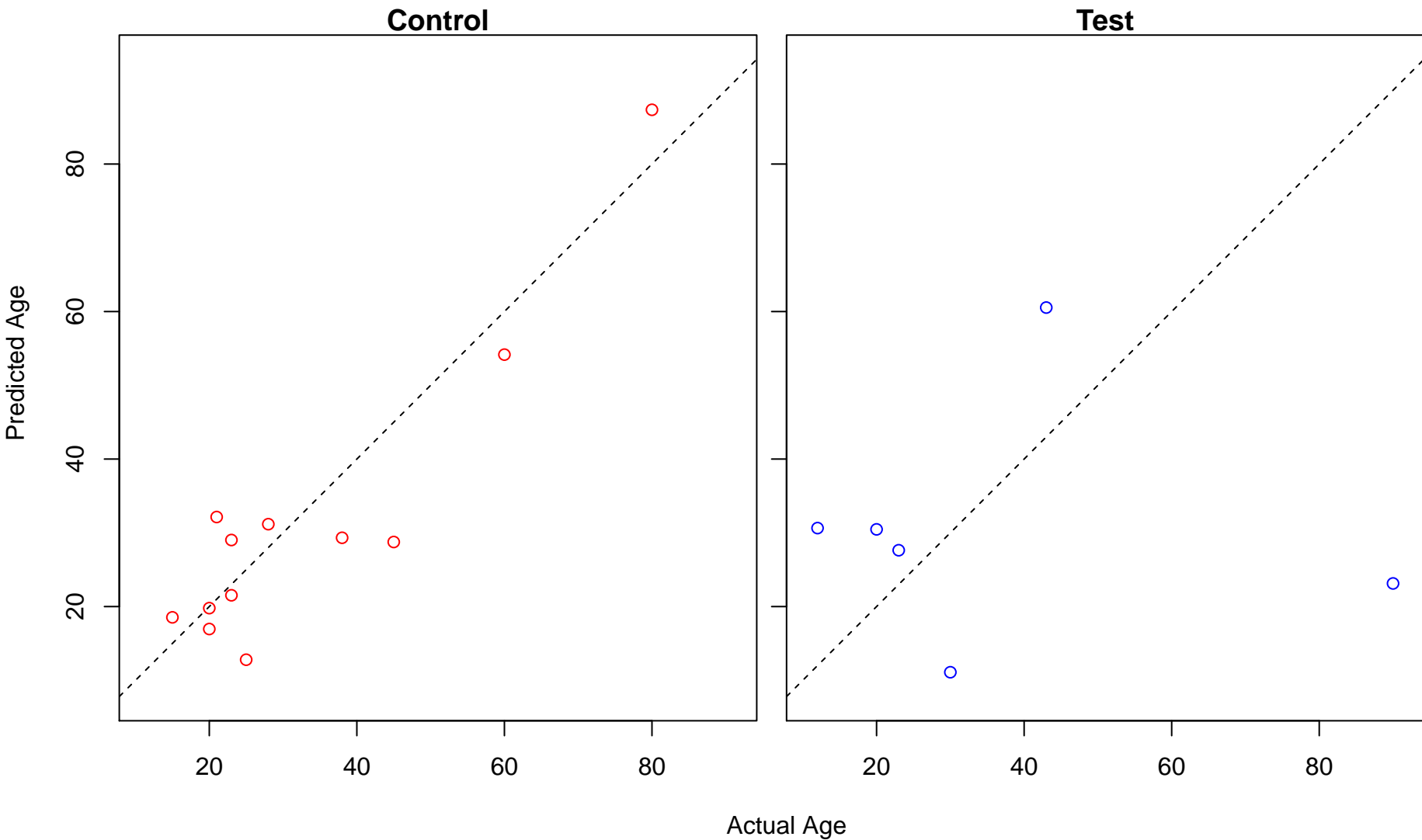


Test

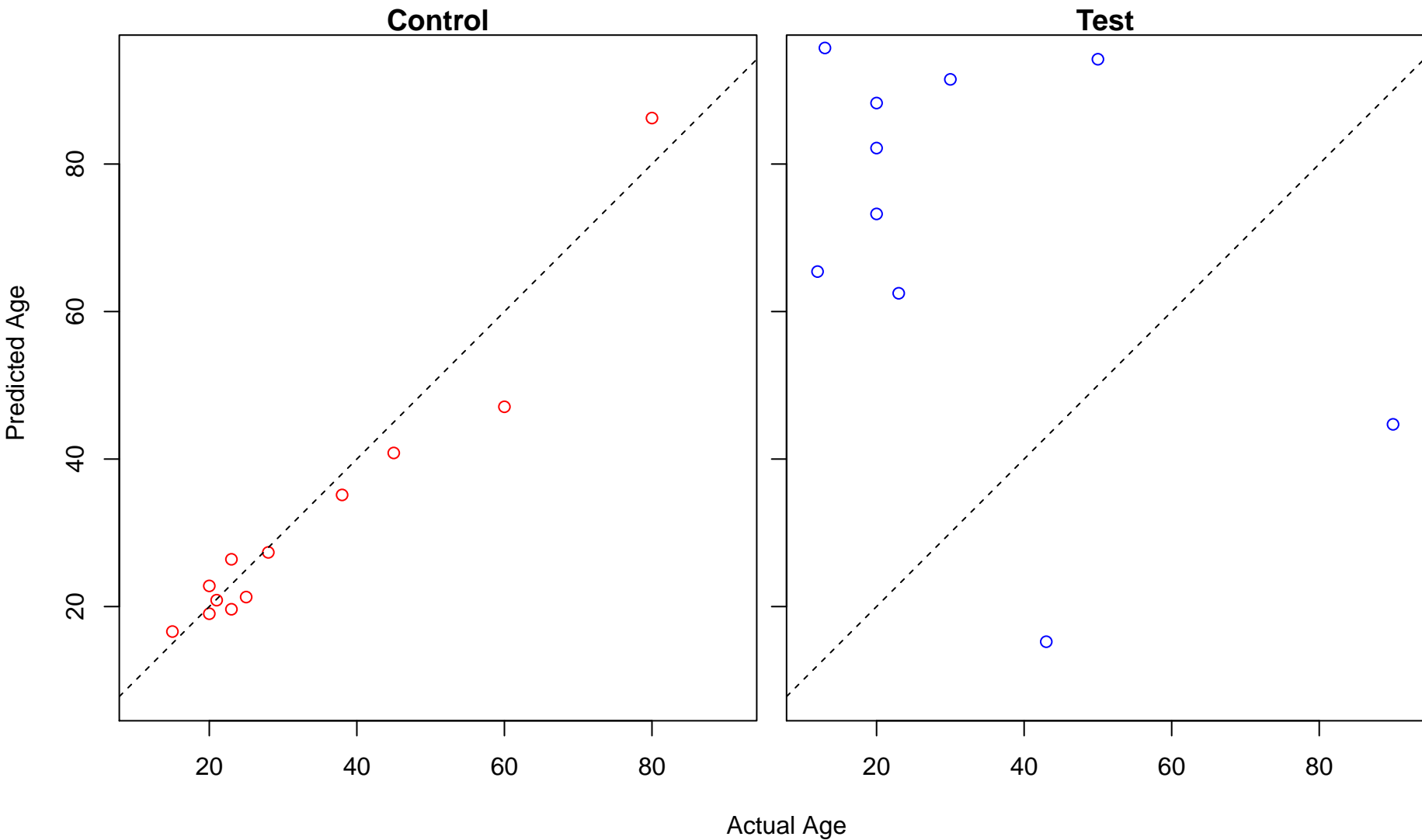


Actual Age

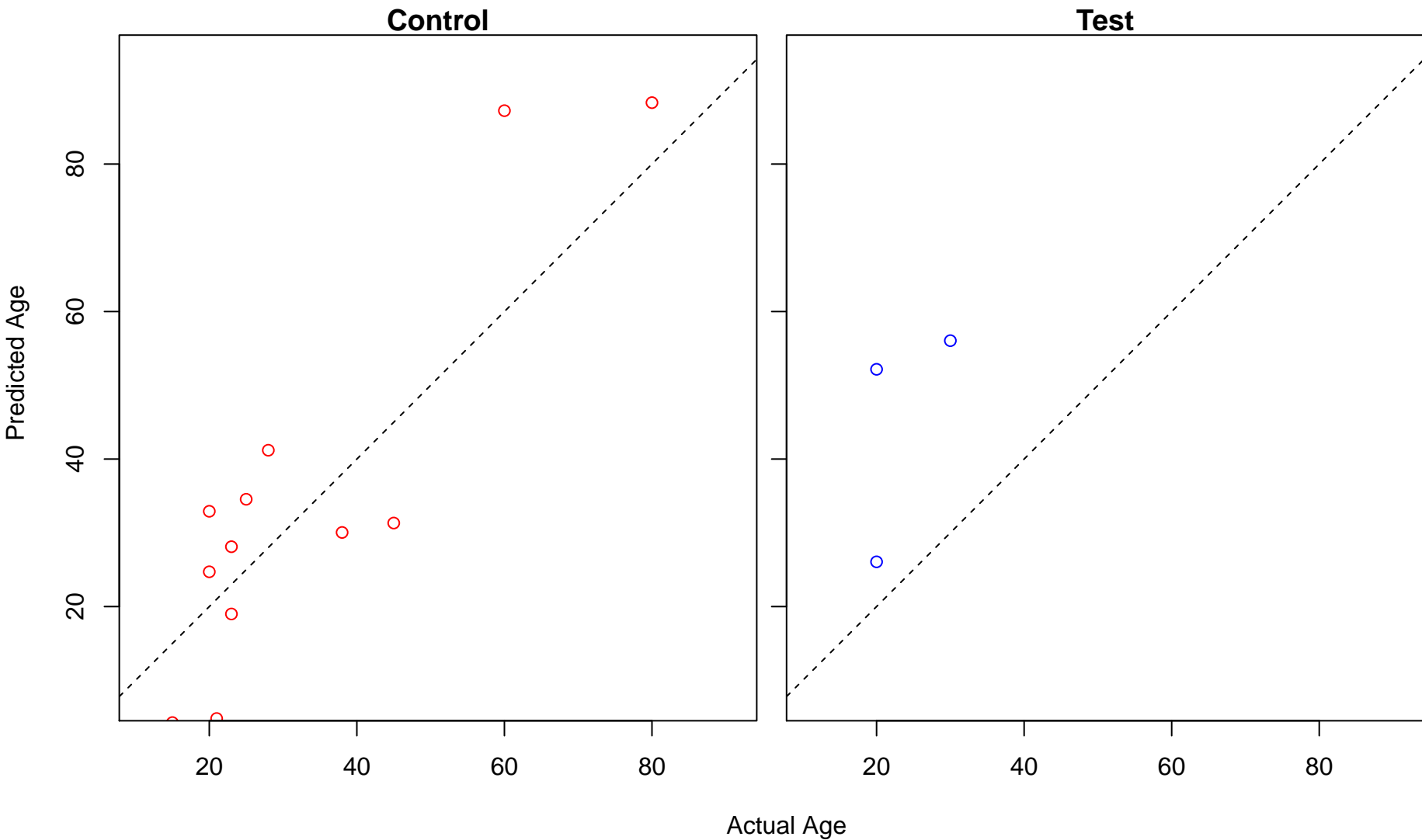
positive chemotaxis (Score: 74.543211)



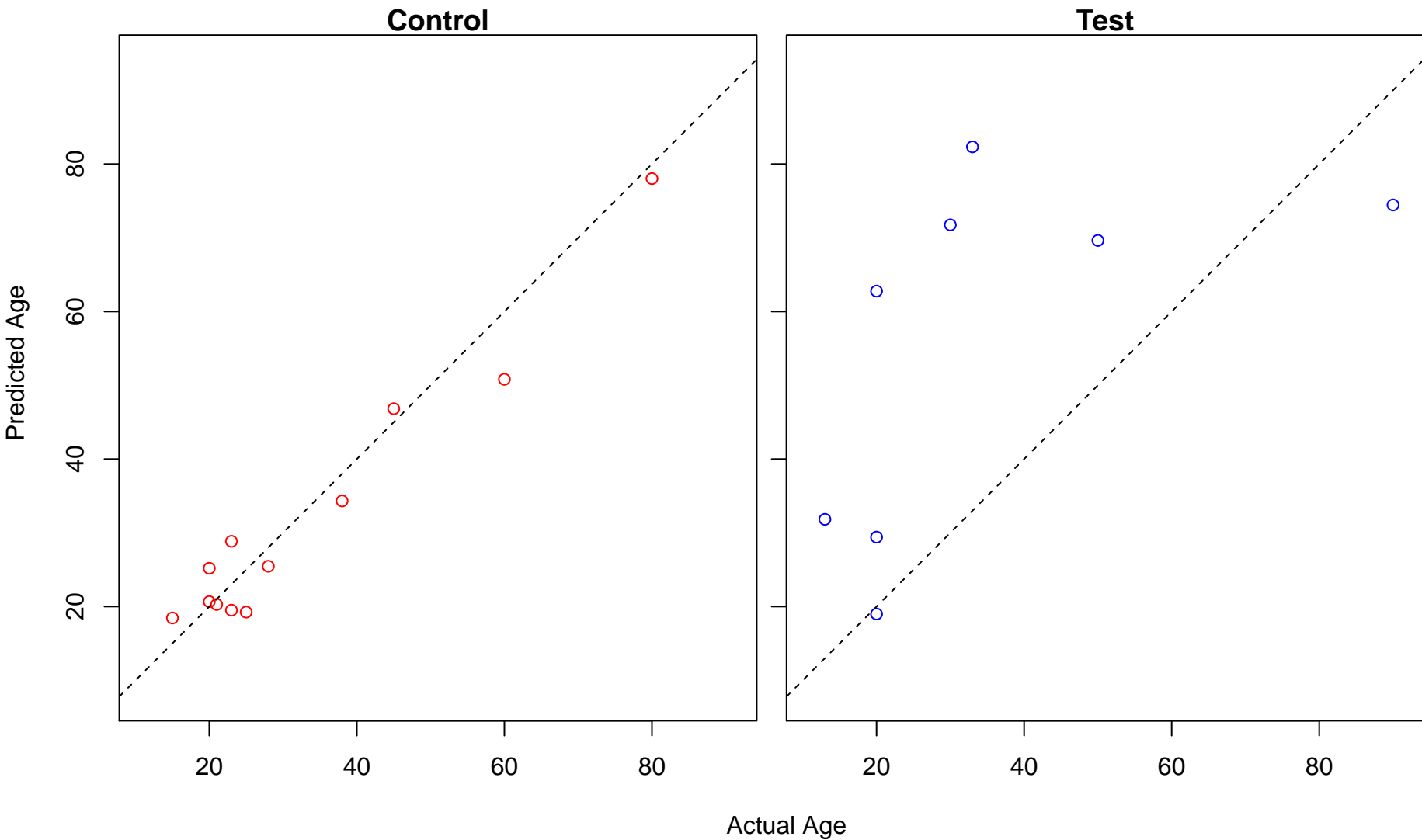
drug metabolic process (Score: 74.431588)



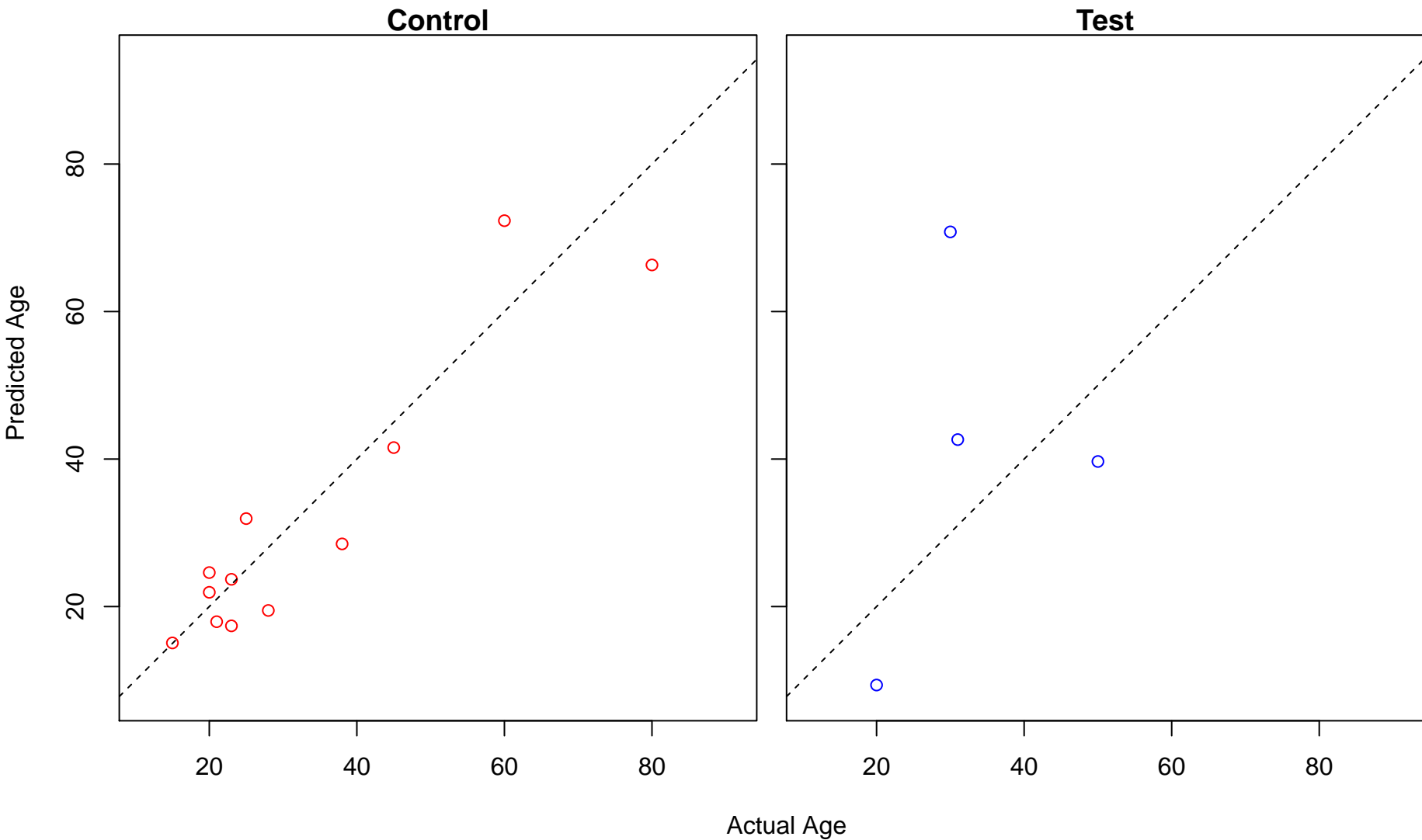
negative regulation of hydrogen peroxide-mediated programmed cell death (Score: 72.736345)



positive regulation of glial cell differentiation (Score: 72.474971)

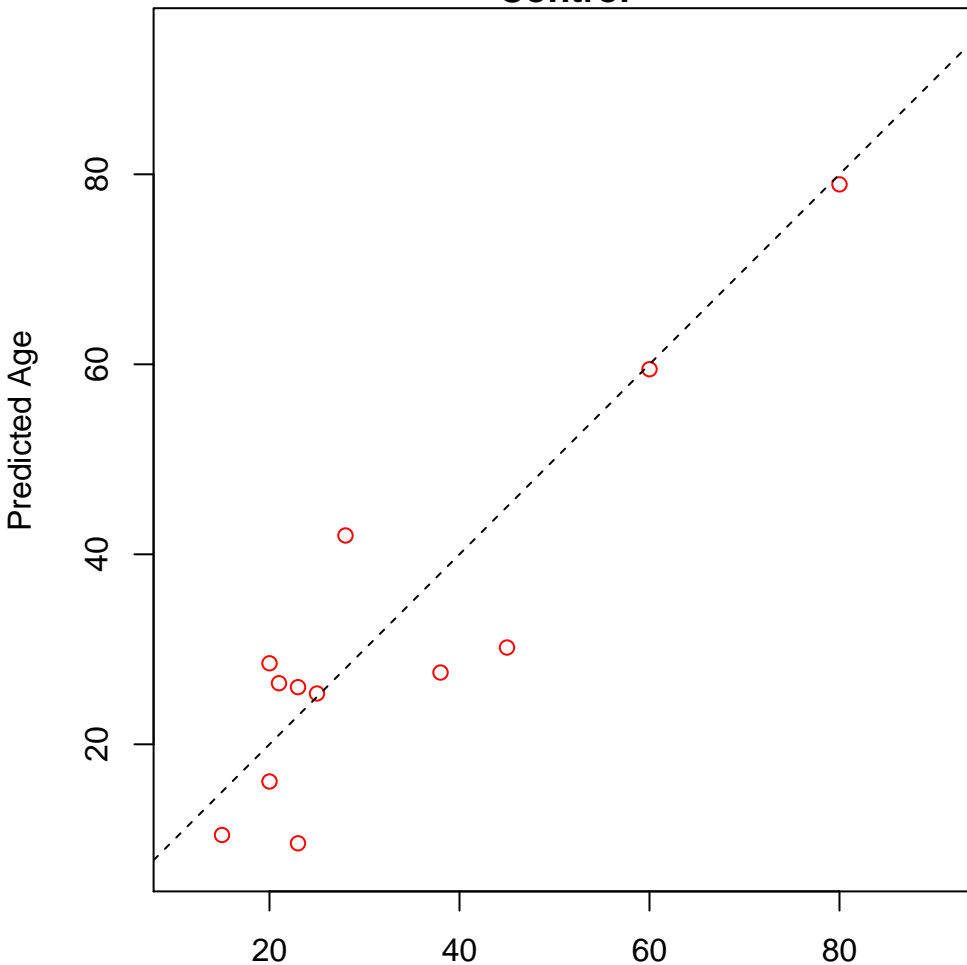


urate metabolic process (Score: 72.153828)

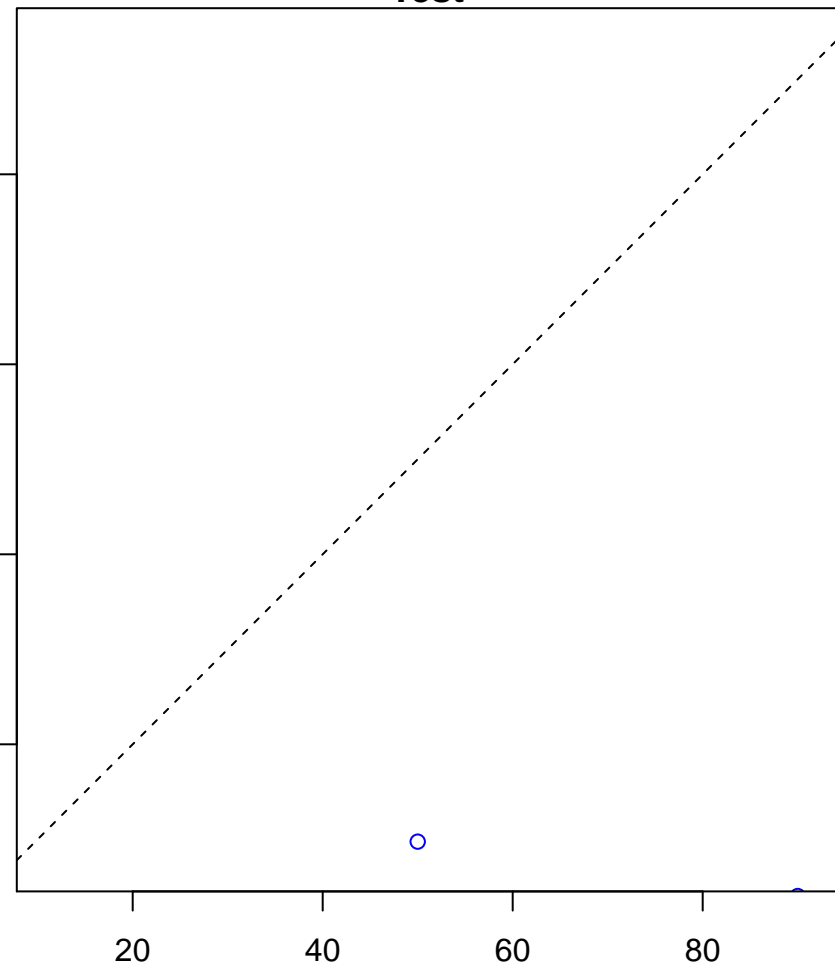


cardiac muscle cell proliferation (Score: 71.592558)

Control

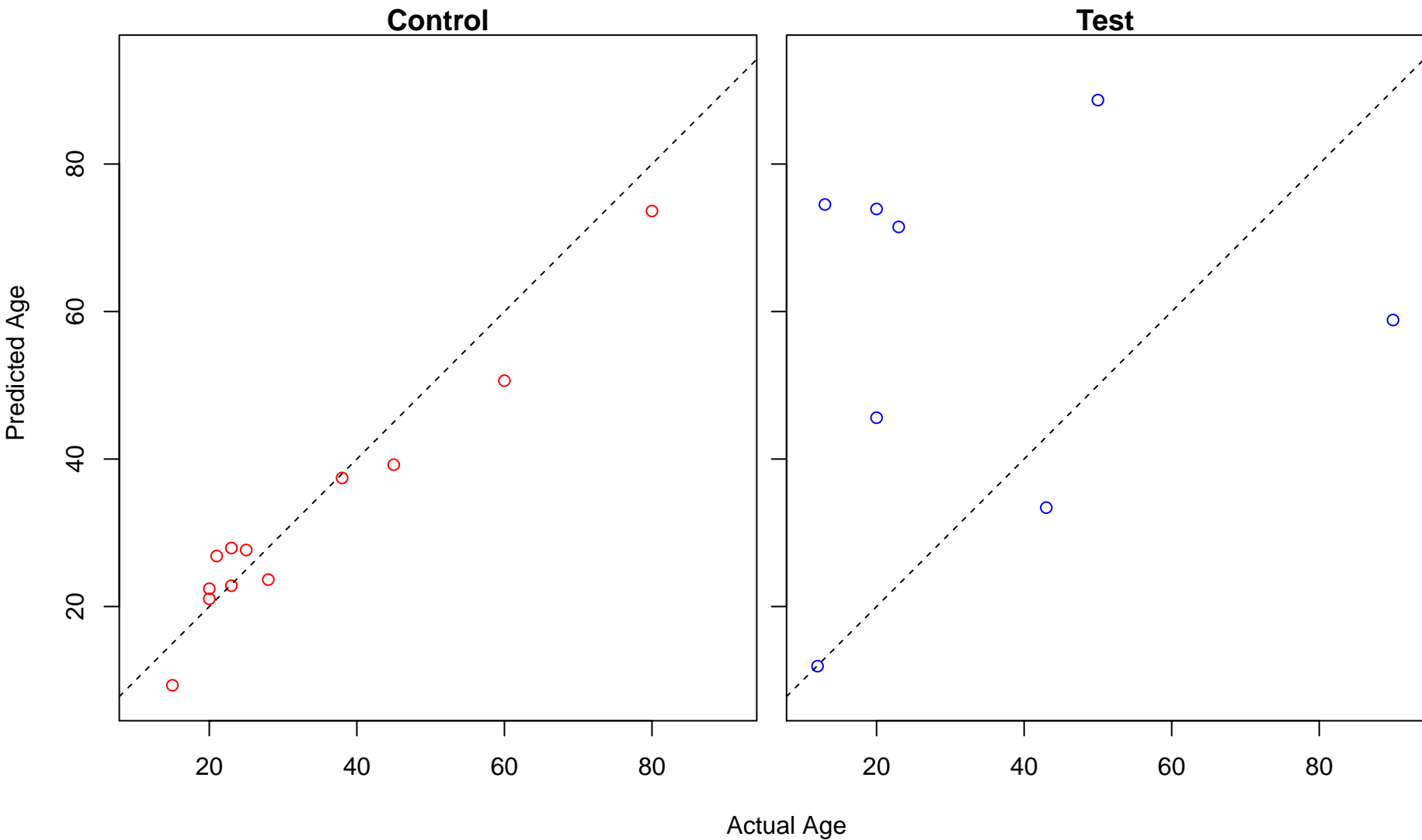


Test

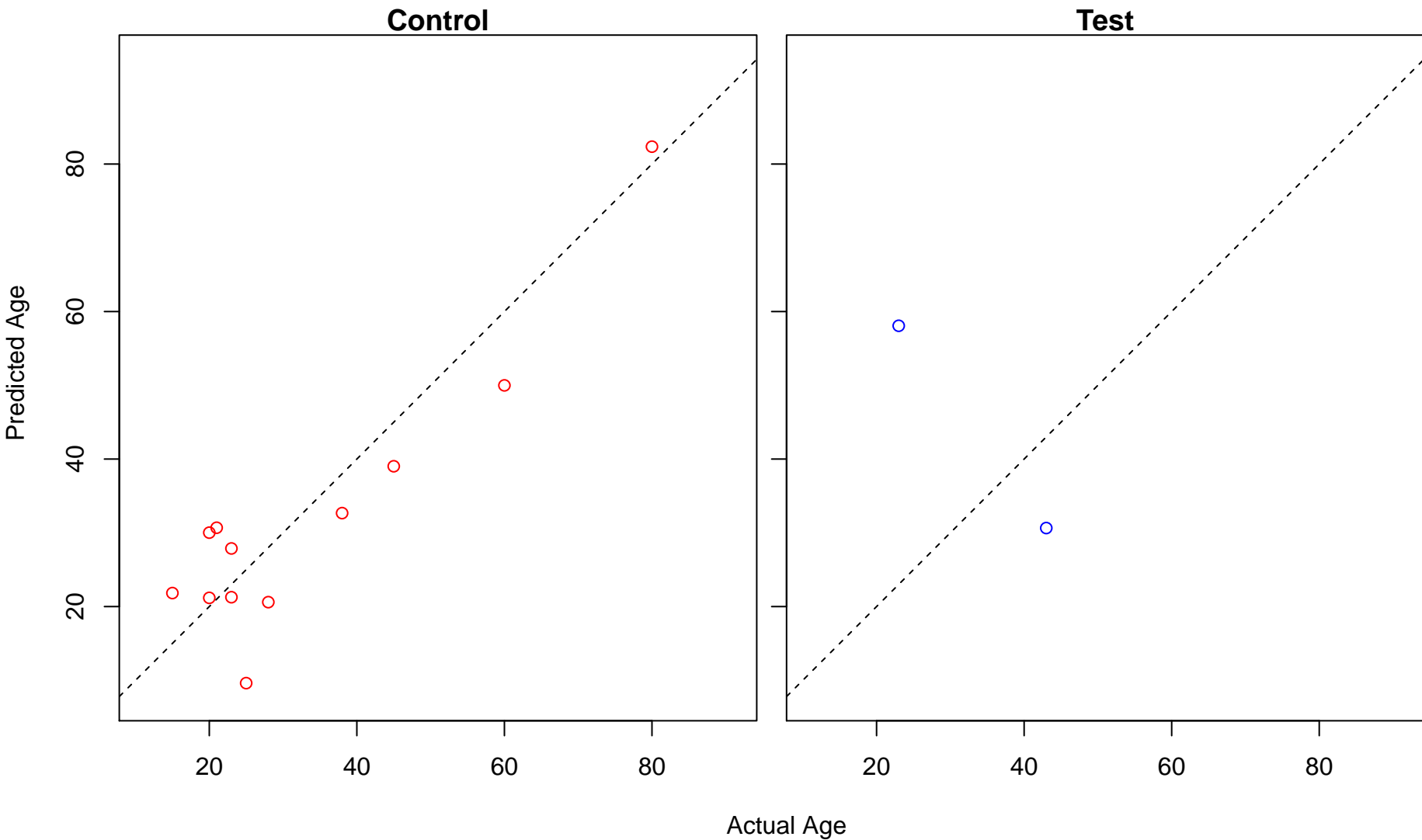


Actual Age

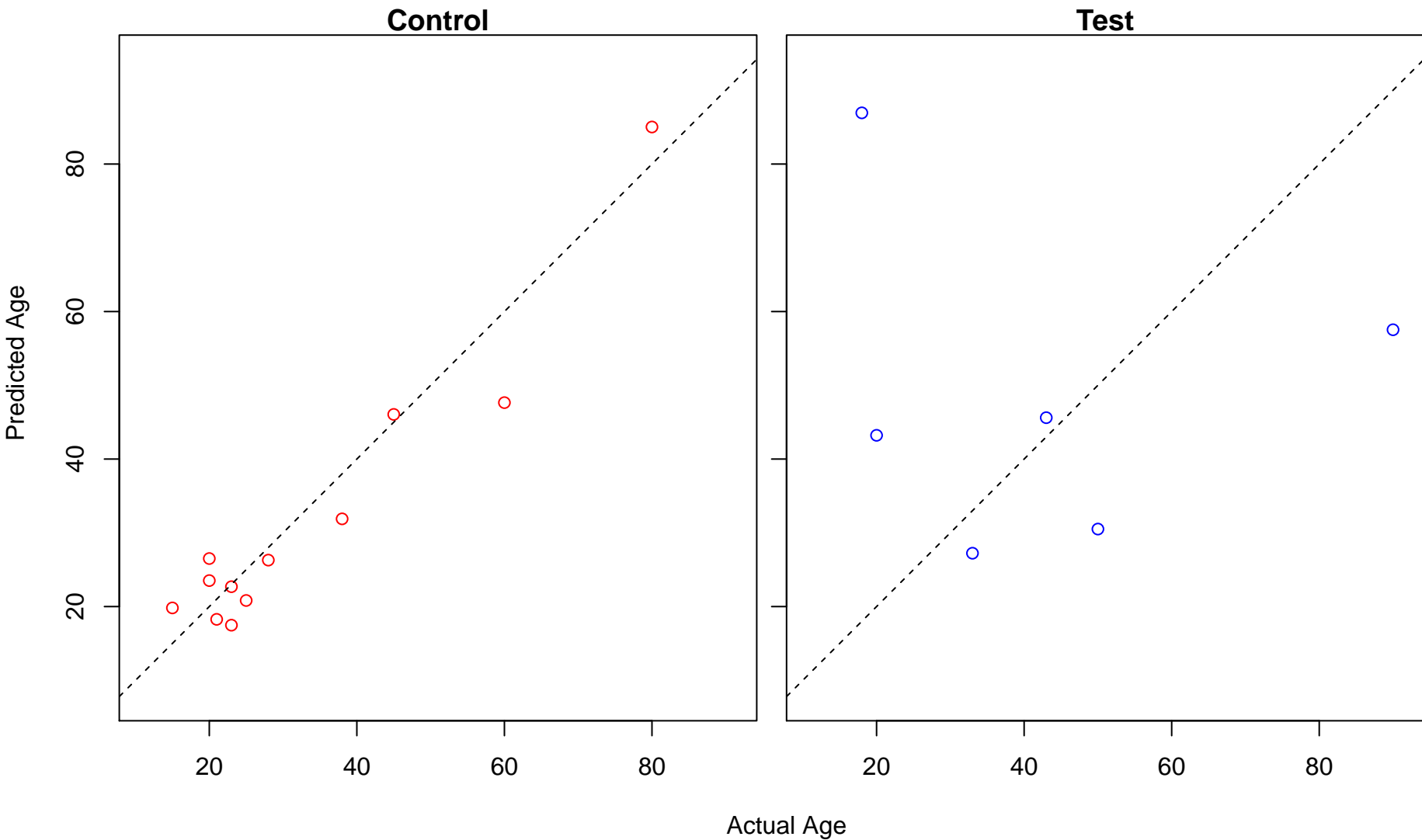
collagen fibril organization (Score: 71.308539)



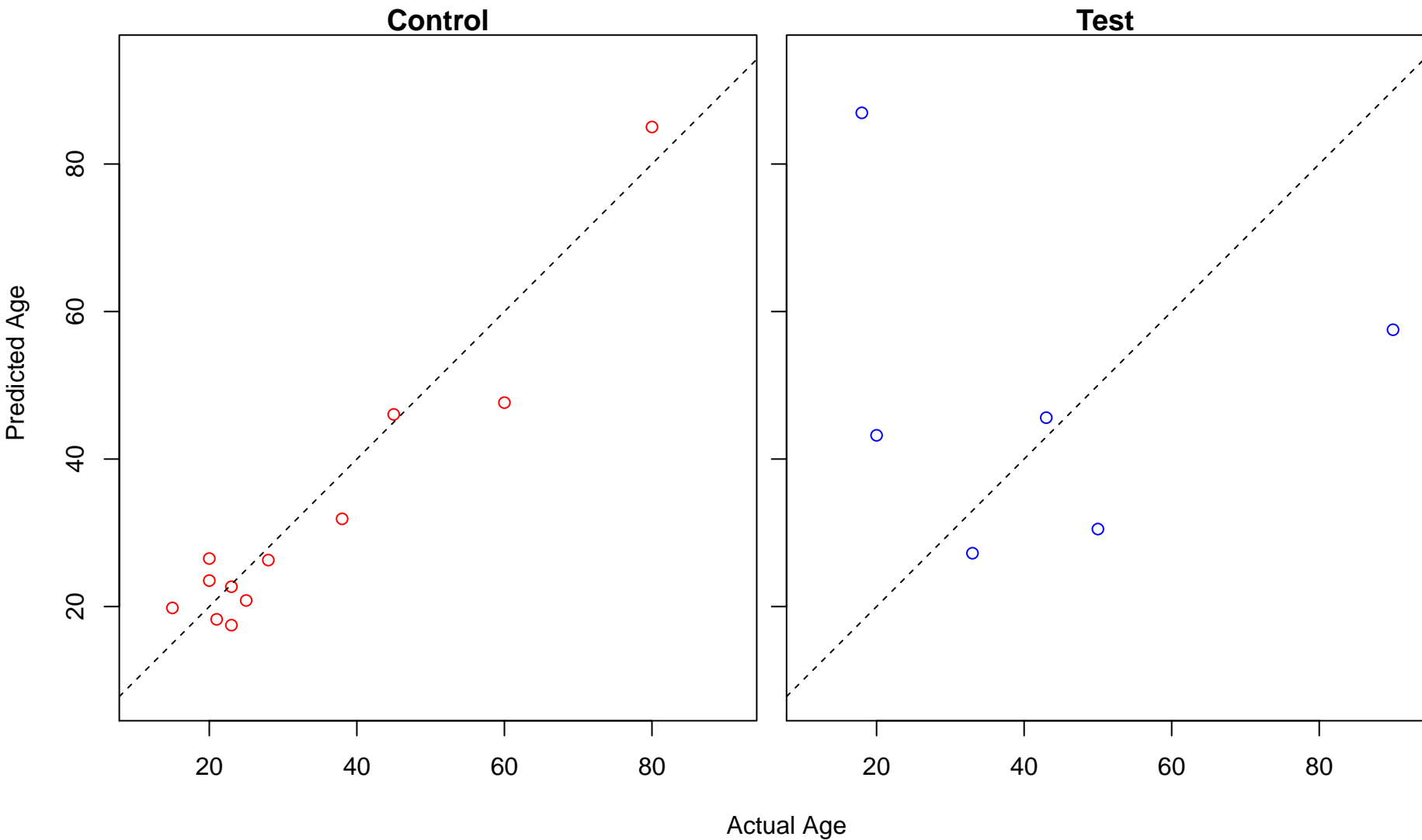
L-amino acid import (Score: 71.049009)



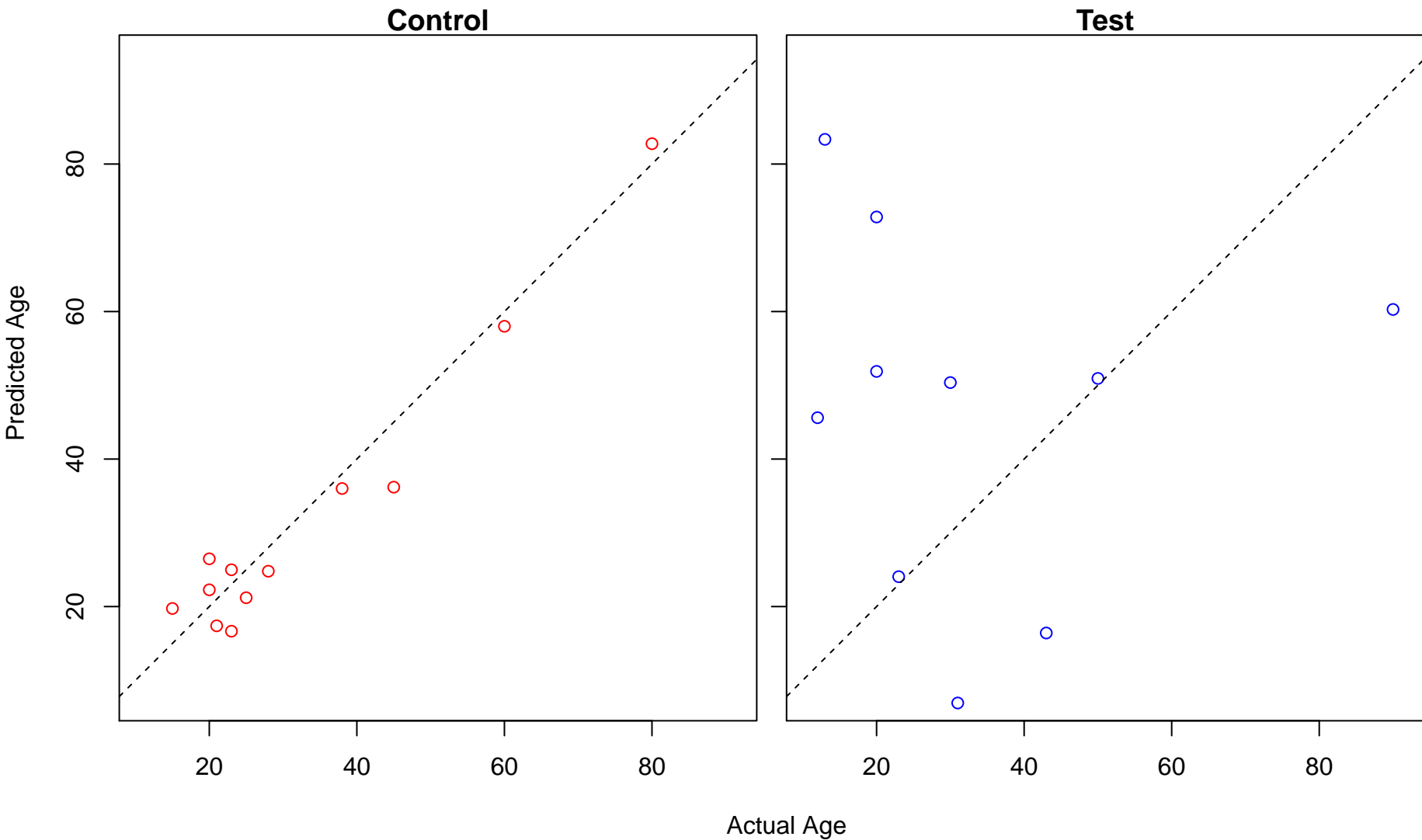
modulation by host of viral release from host cell (Score: 70.399605)



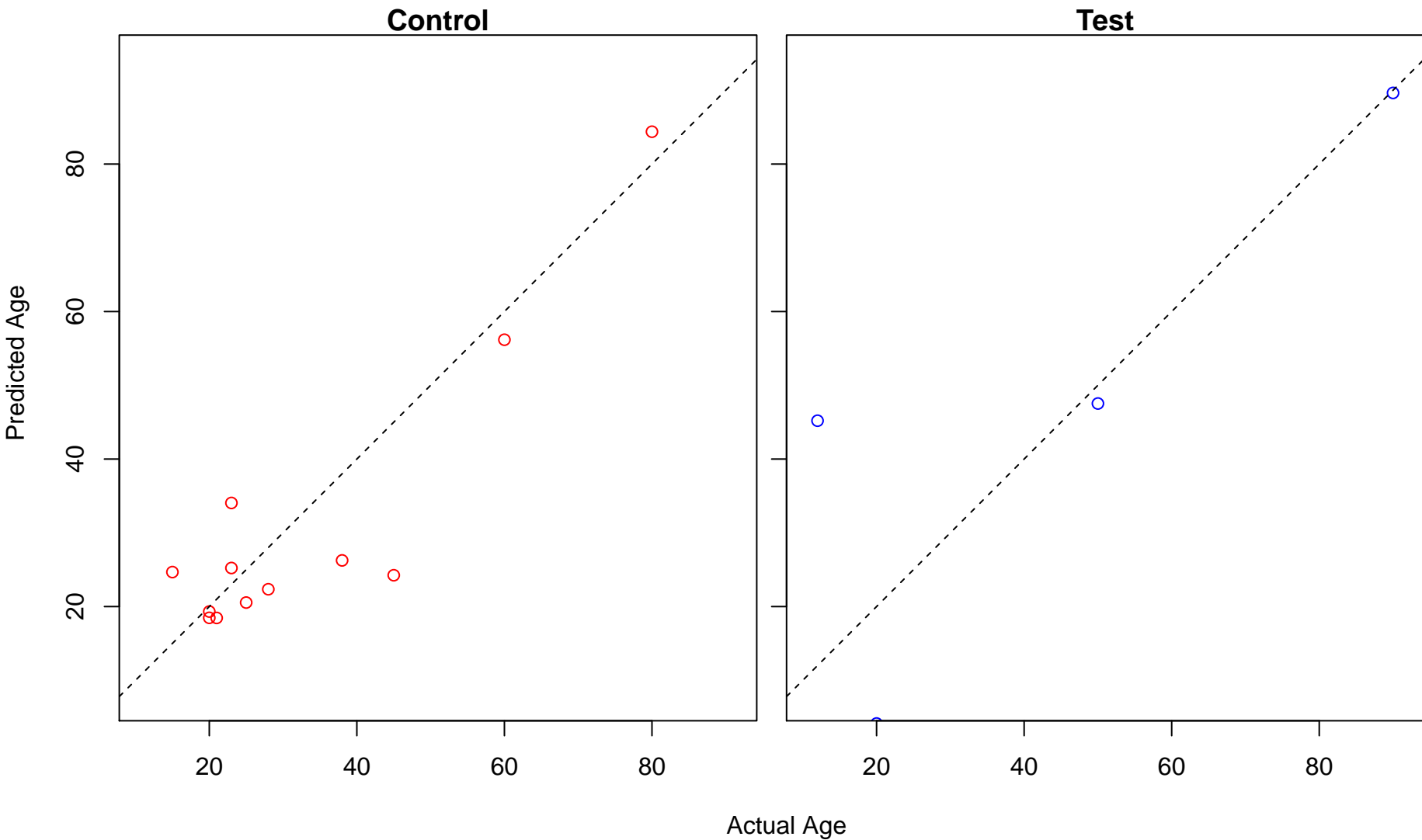
positive regulation by host of viral release from host cell (Score: 70.399605)



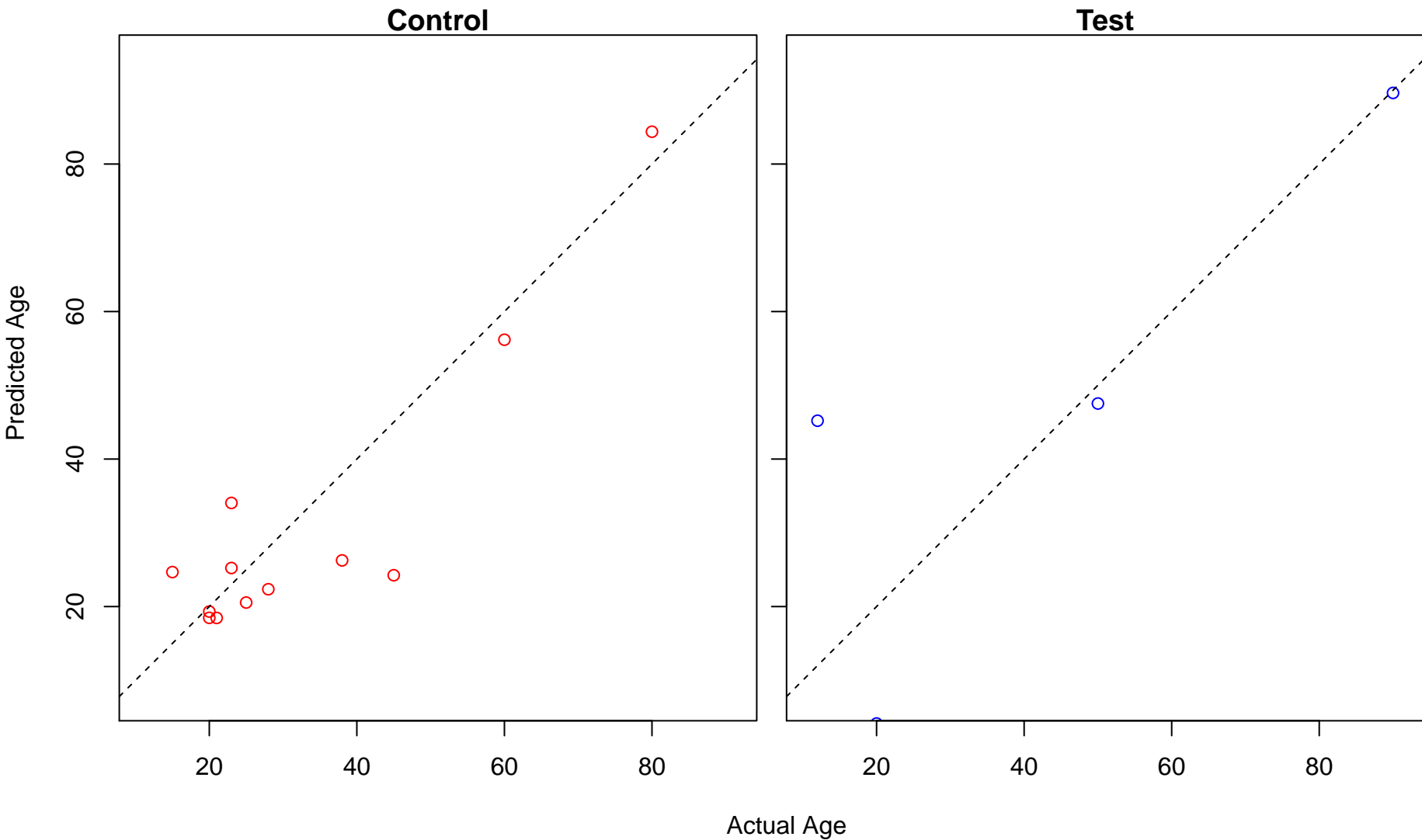
sister chromatid cohesion (Score: 69.569456)



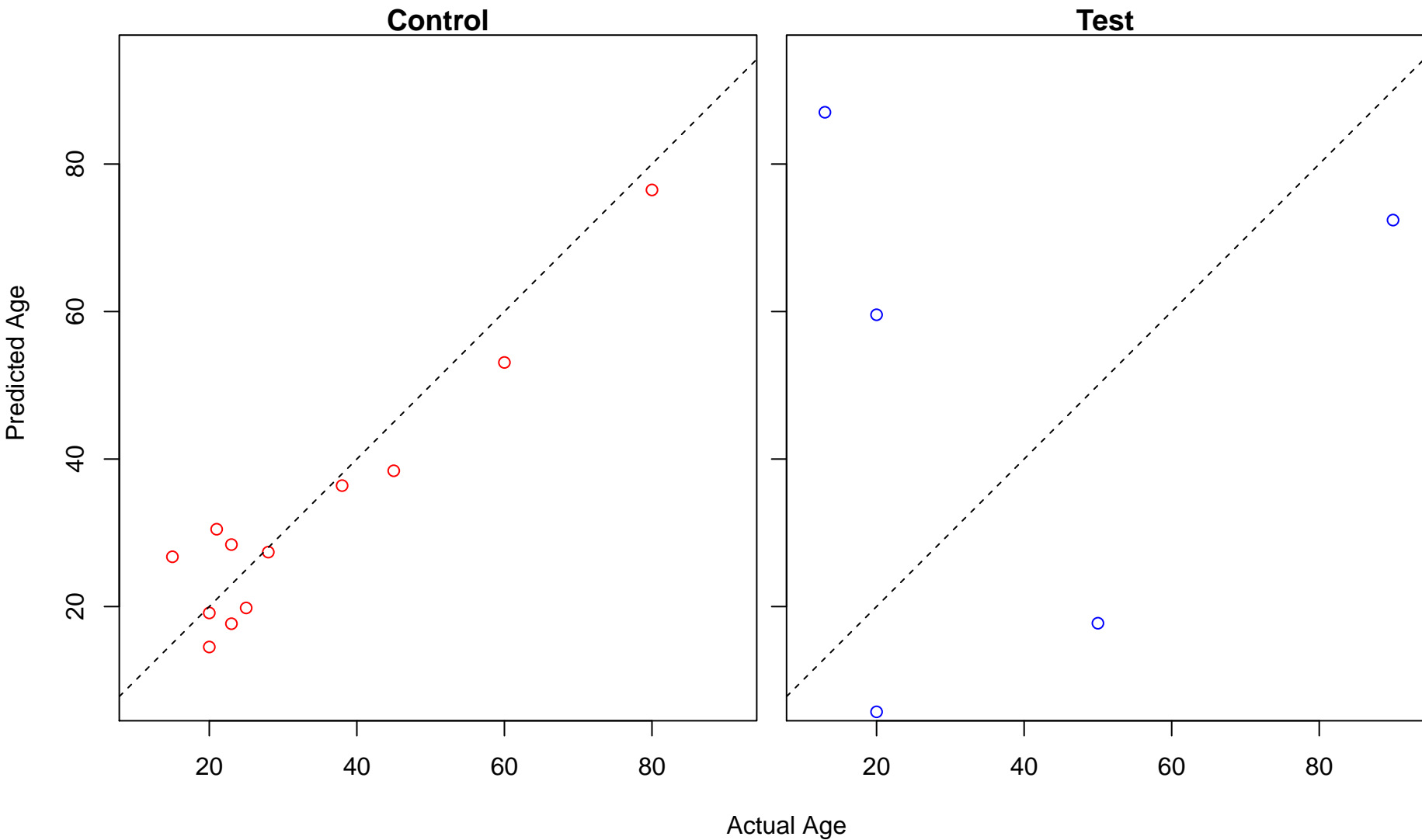
regulation of nuclear-transcribed mRNA poly(A) tail shortening (Score: 69.173298)



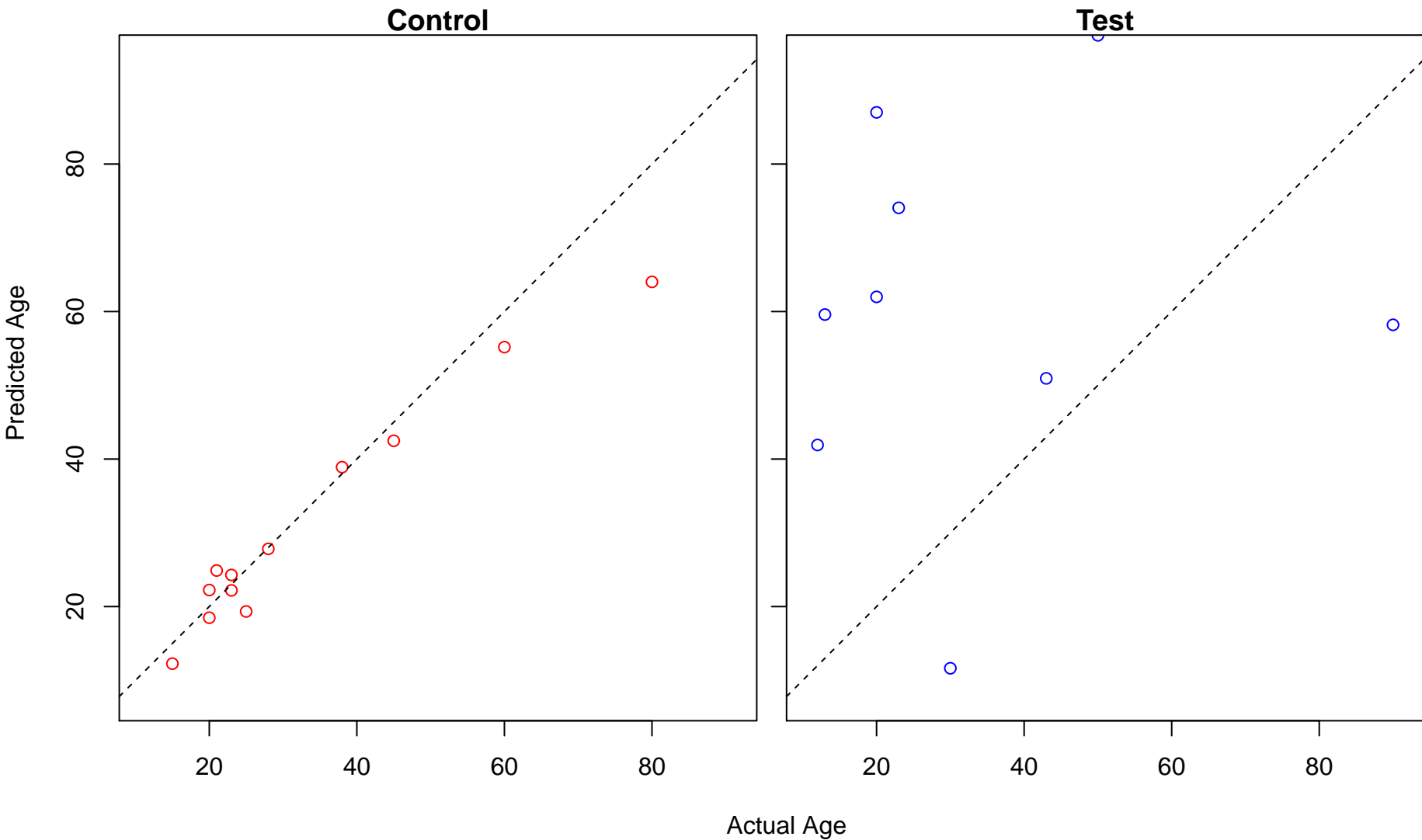
positive regulation of nuclear-transcribed mRNA poly(A) tail shortening (Score: 69.173298)



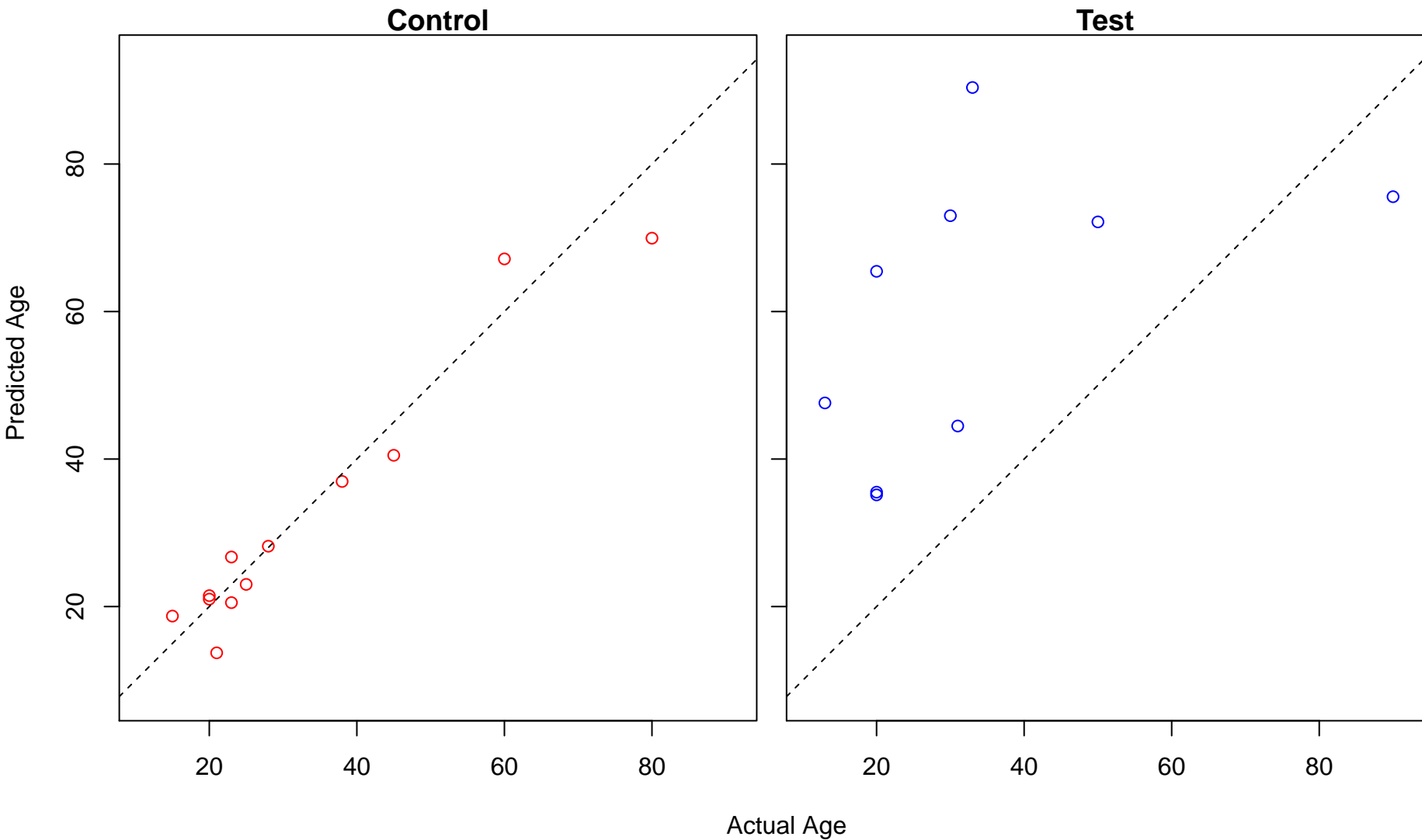
positive regulation of activin receptor signaling pathway (Score: 68.427293)



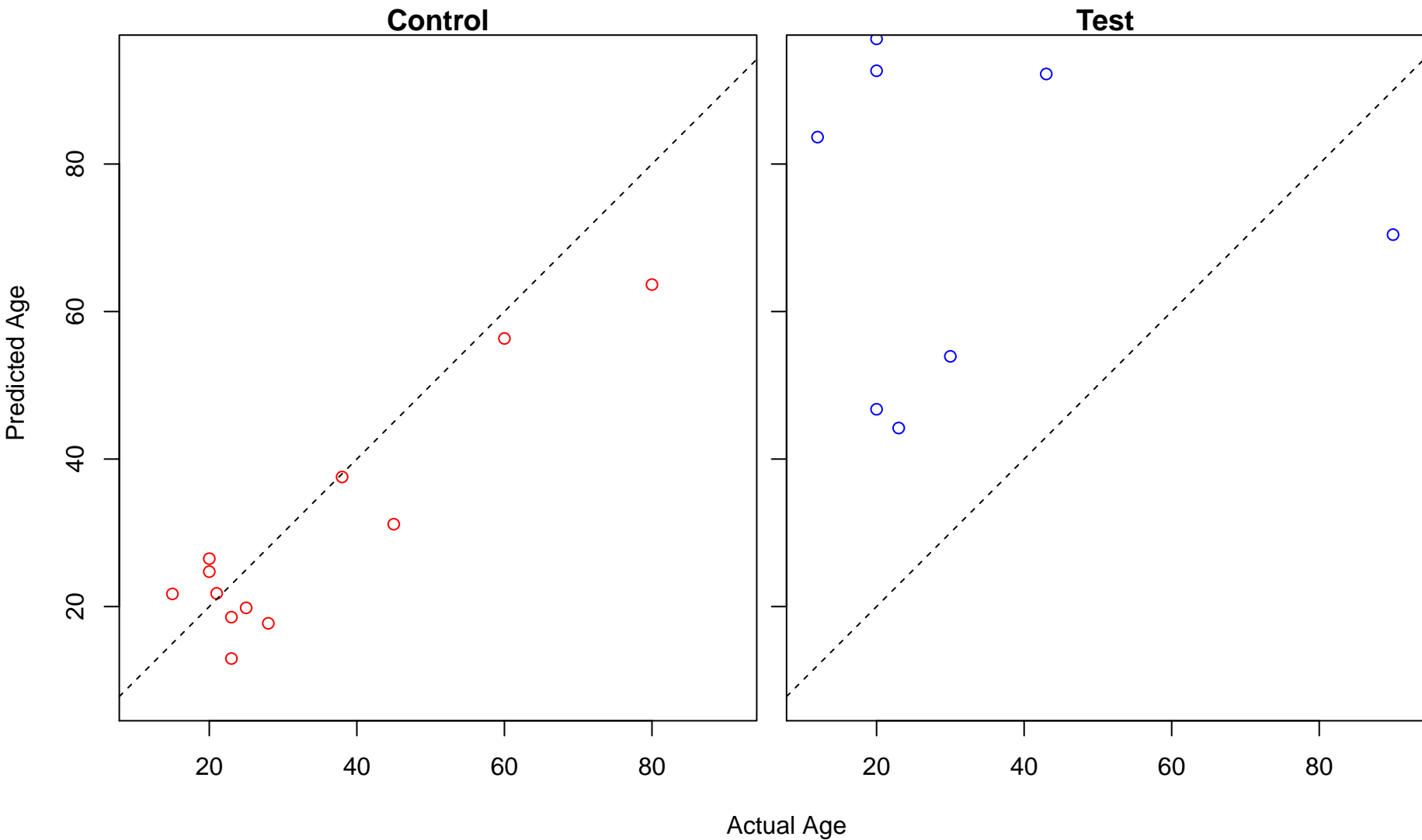
retina vasculature development in camera-type eye (Score: 68.356981)



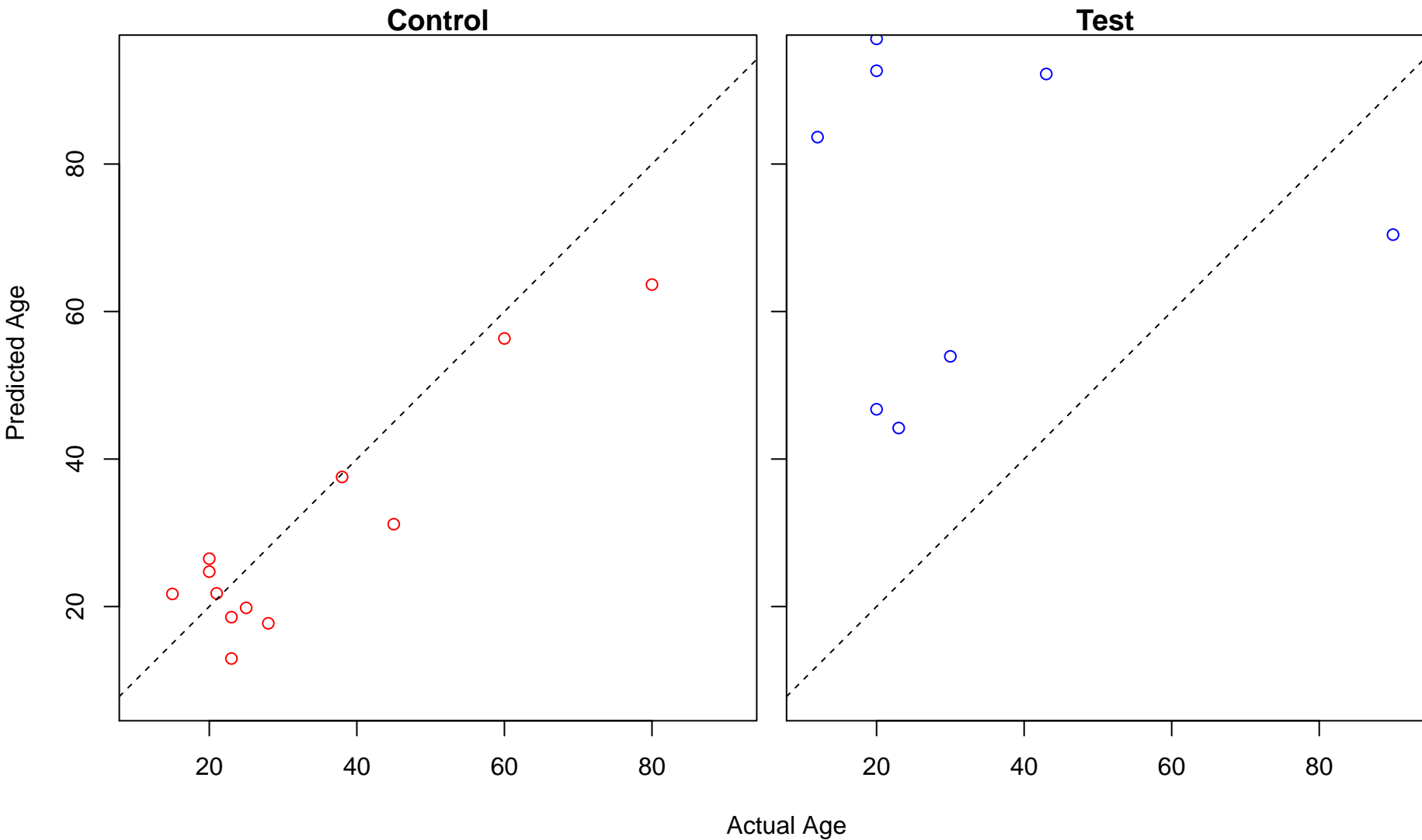
negative regulation of gliogenesis (Score: 68.256245)



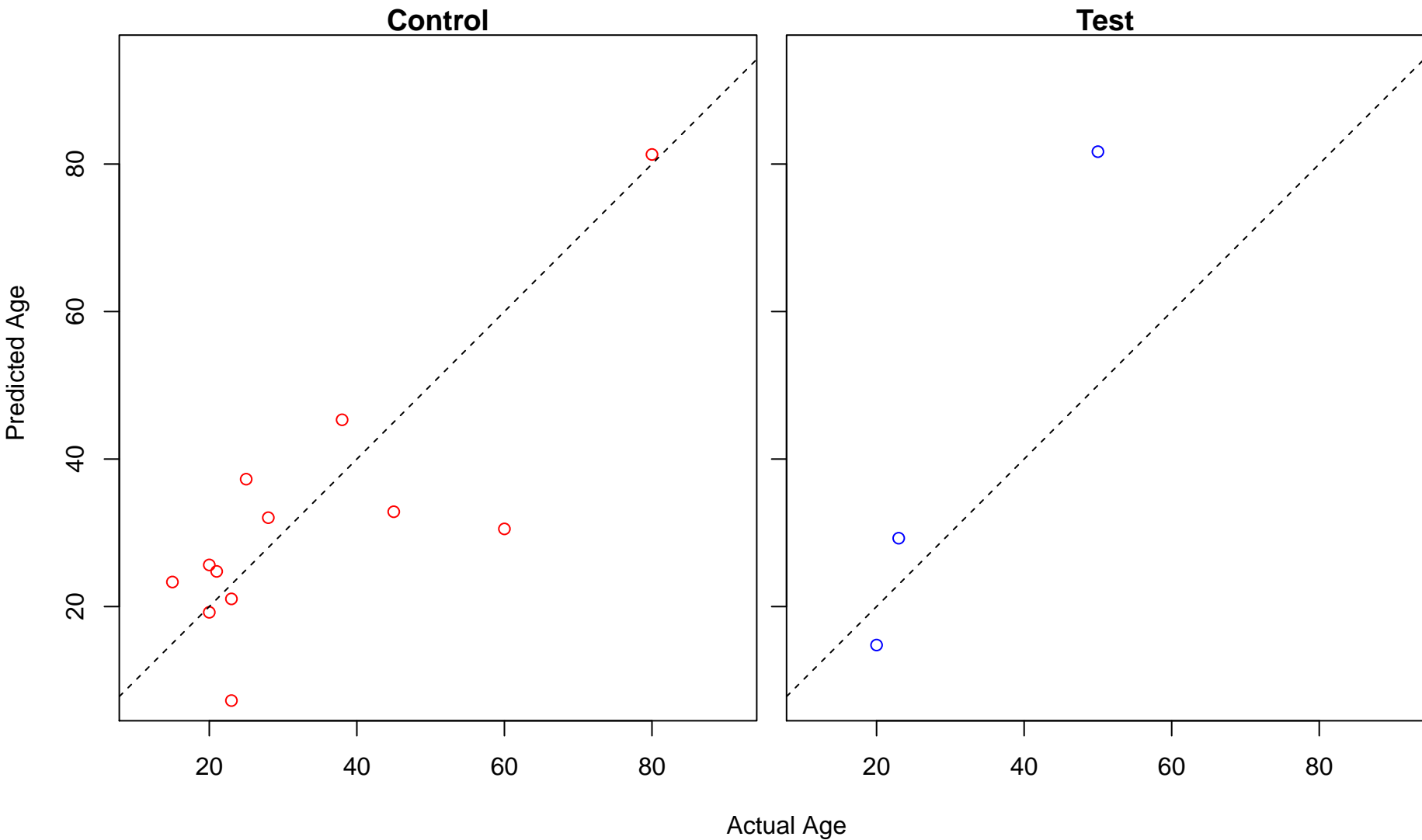
positive regulation of nitric oxide biosynthetic process (Score: 67.693907)



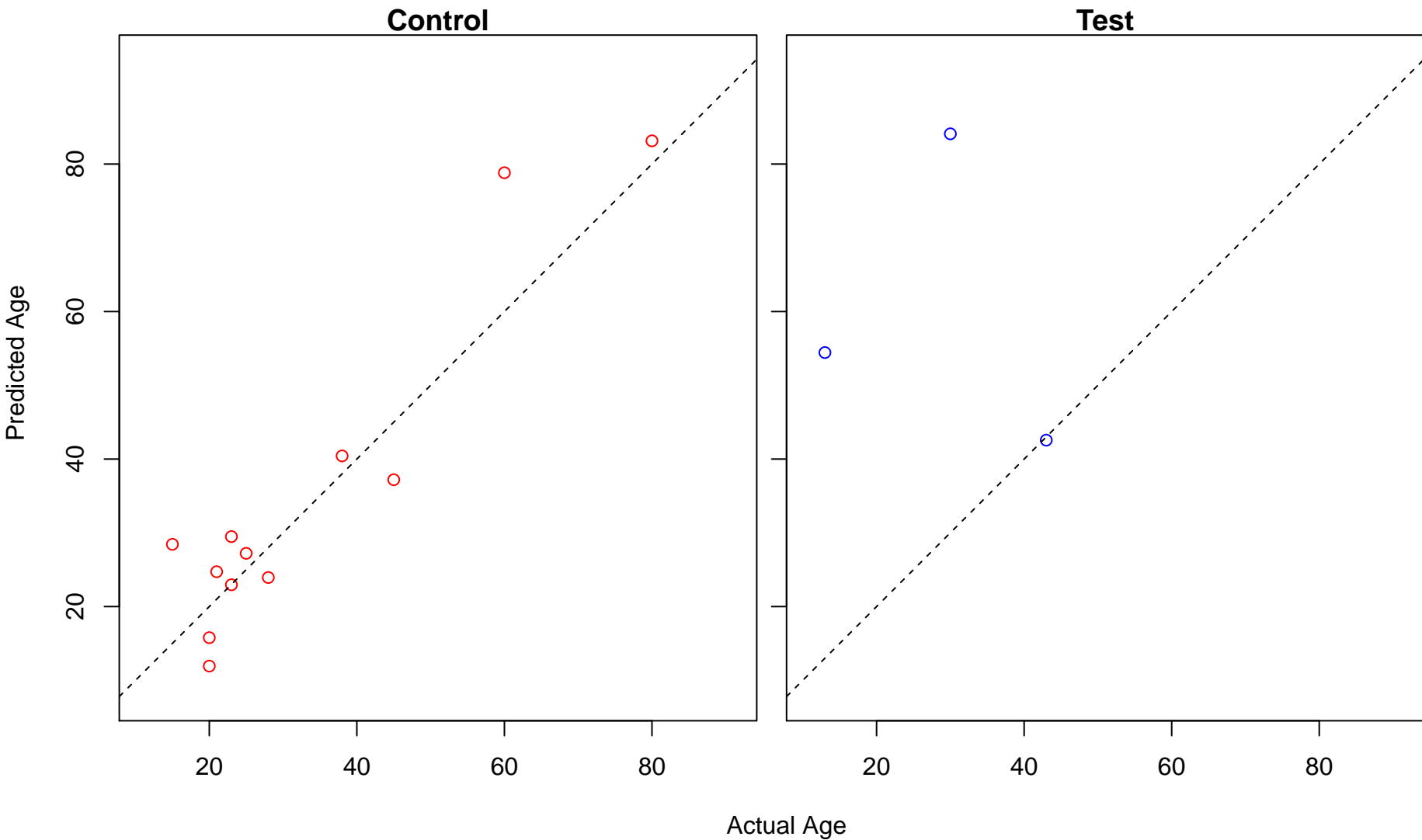
positive regulation of nitric oxide metabolic process (Score: 67.693907)



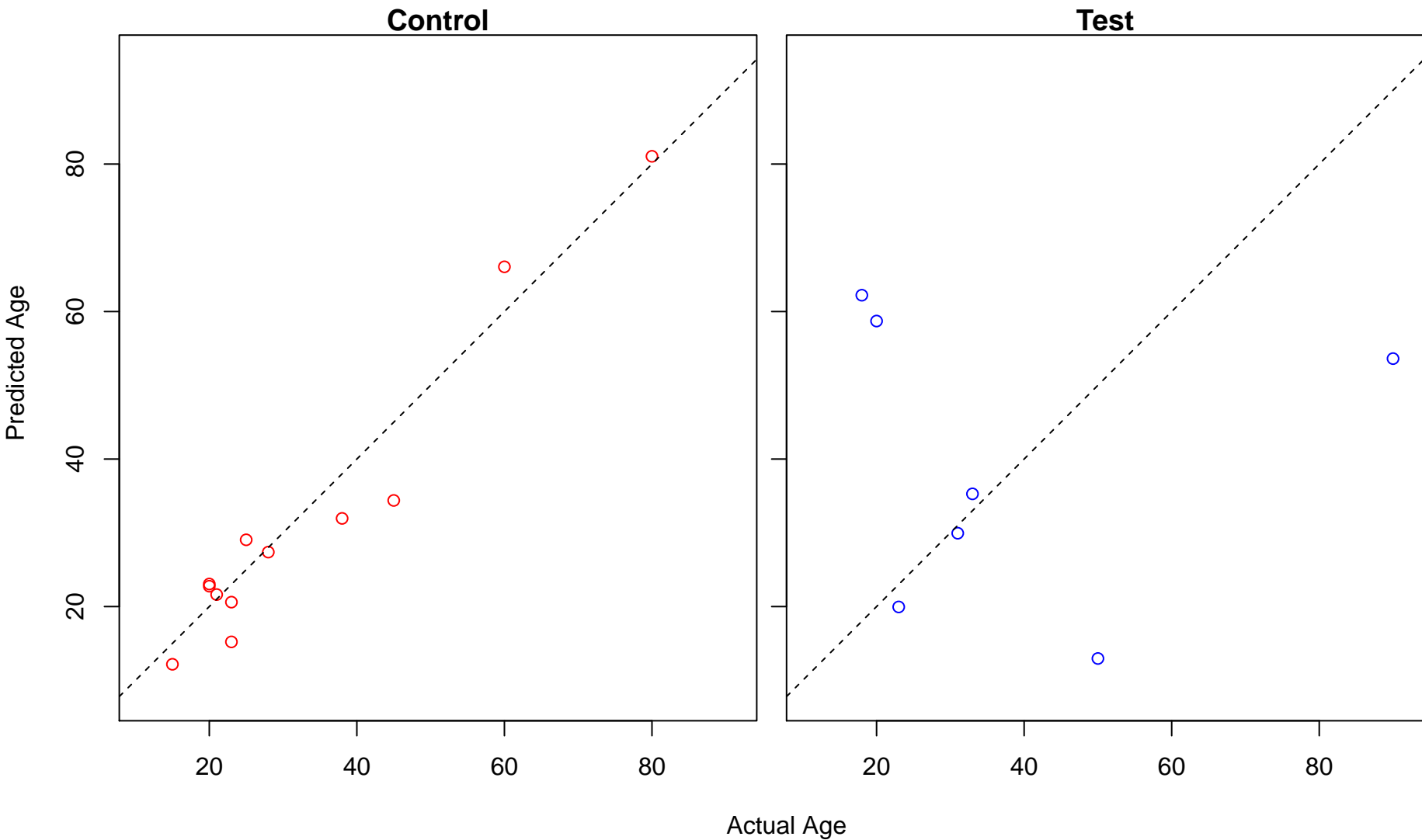
nucleoside triphosphate catabolic process (Score: 67.385557)



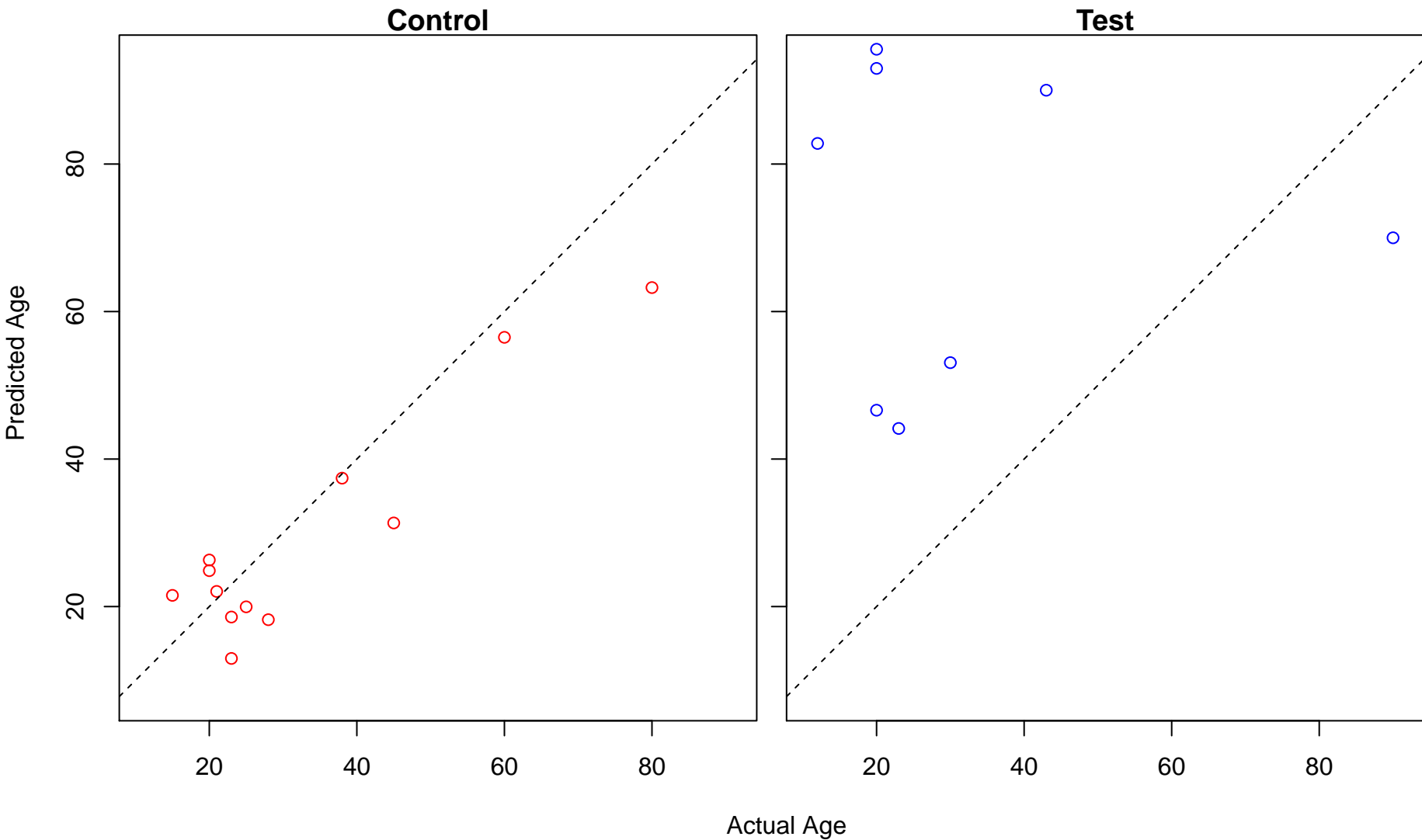
citrulline metabolic process (Score: 67.324768)



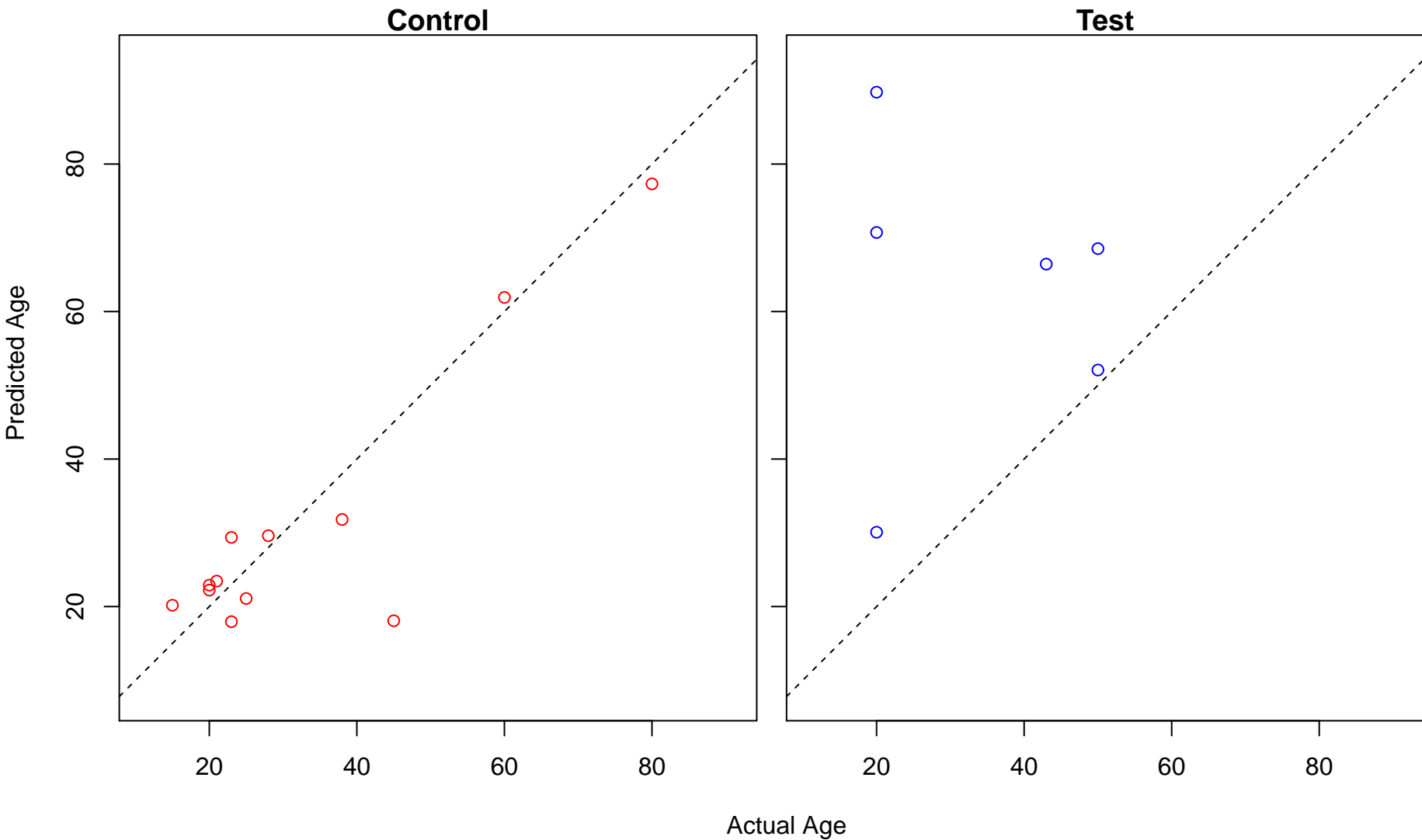
regulation of activated T cell proliferation (Score: 67.225955)



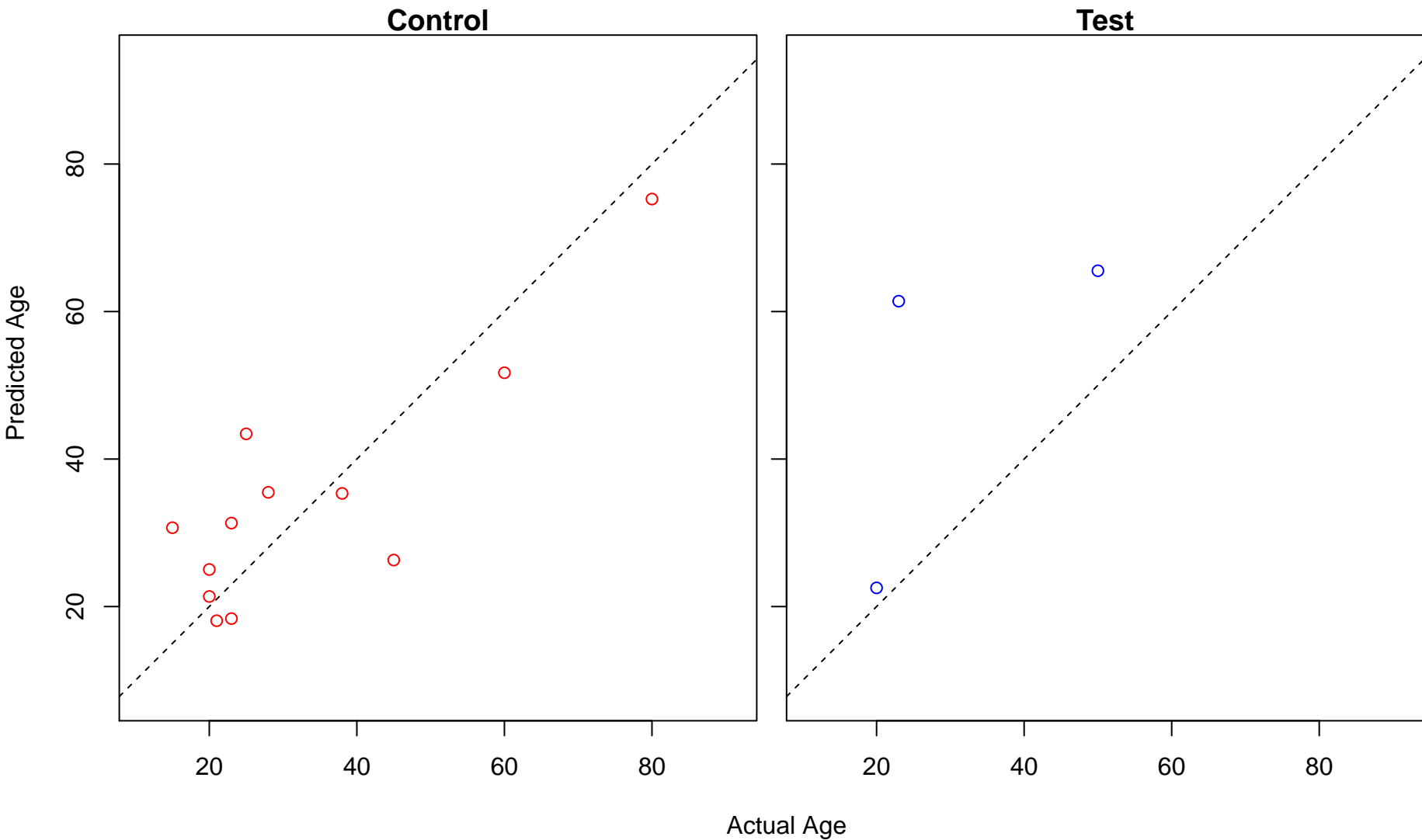
regulation of nitric oxide biosynthetic process (Score: 67.025666)



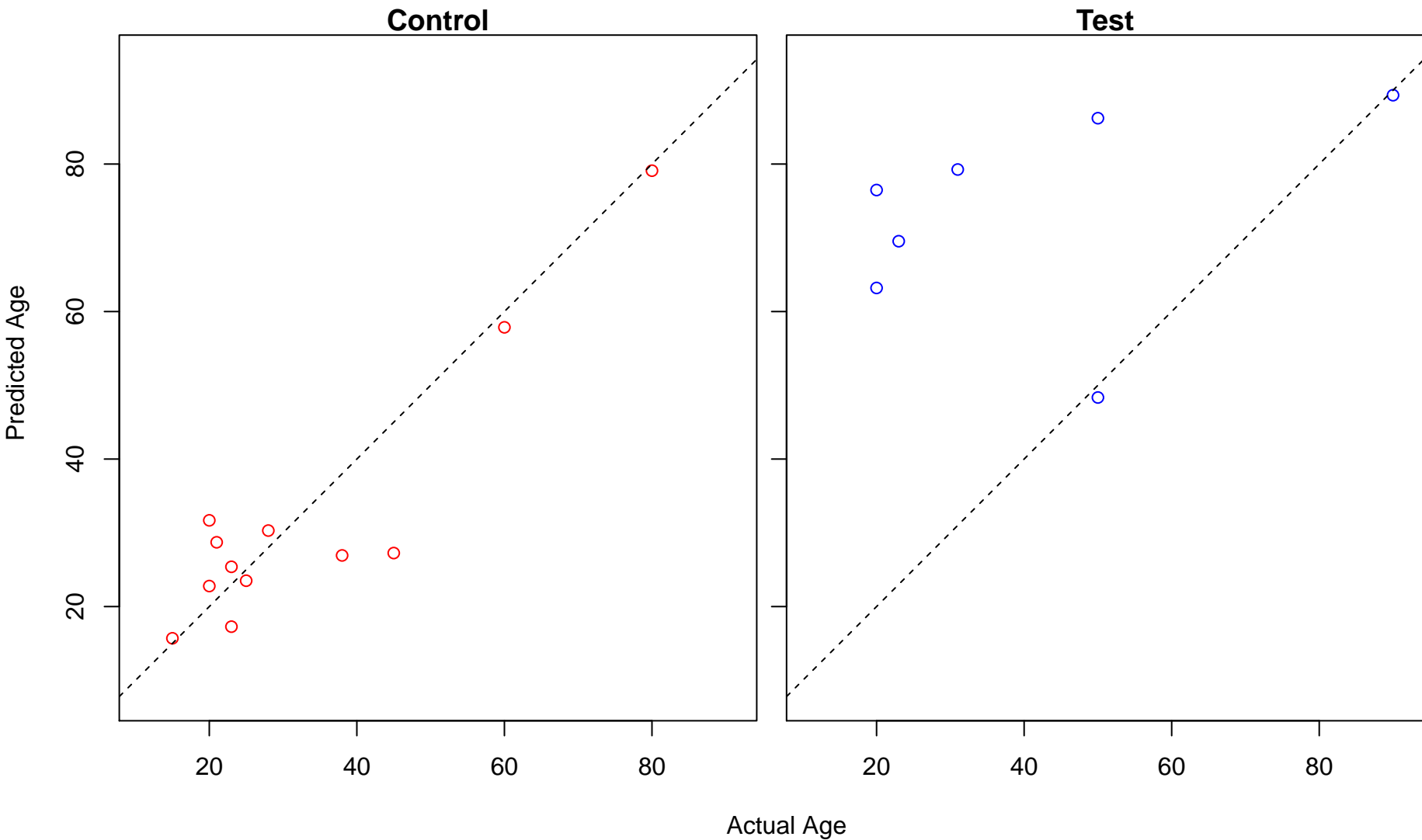
negative regulation of cellular response to insulin stimulus (Score: 66.728576)



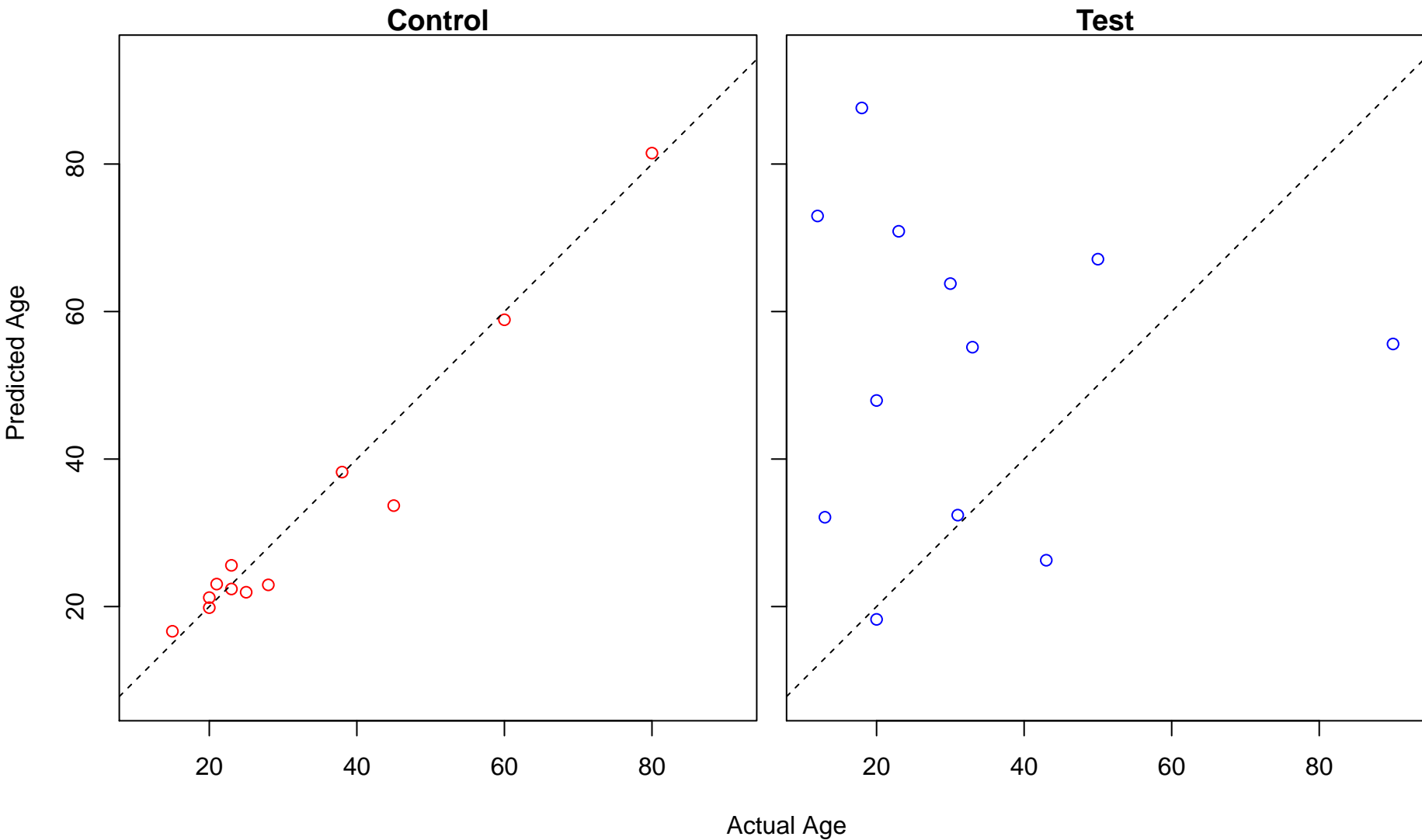
purine deoxyribonucleotide catabolic process (Score: 66.072160)



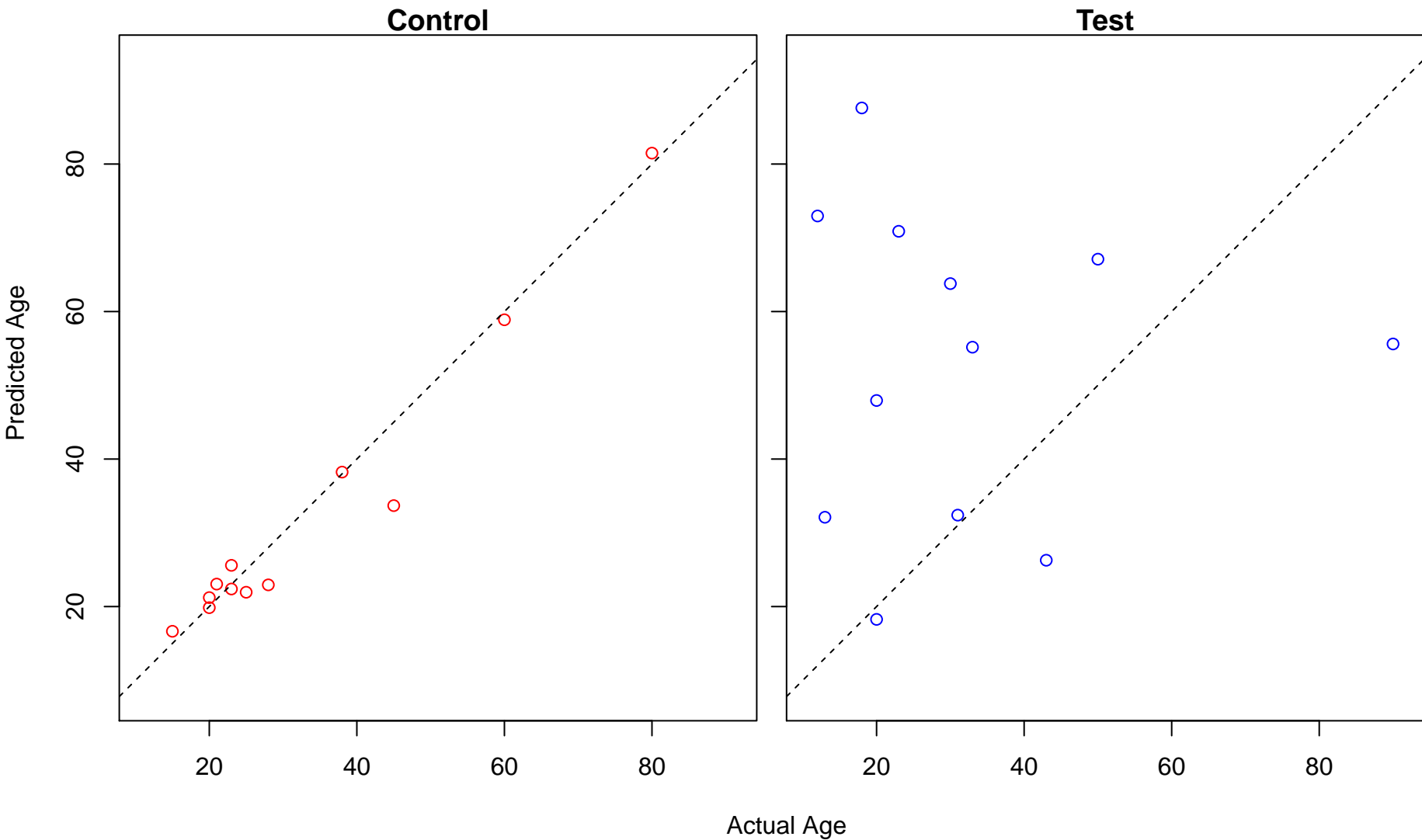
myoblast differentiation (Score: 65.057138)



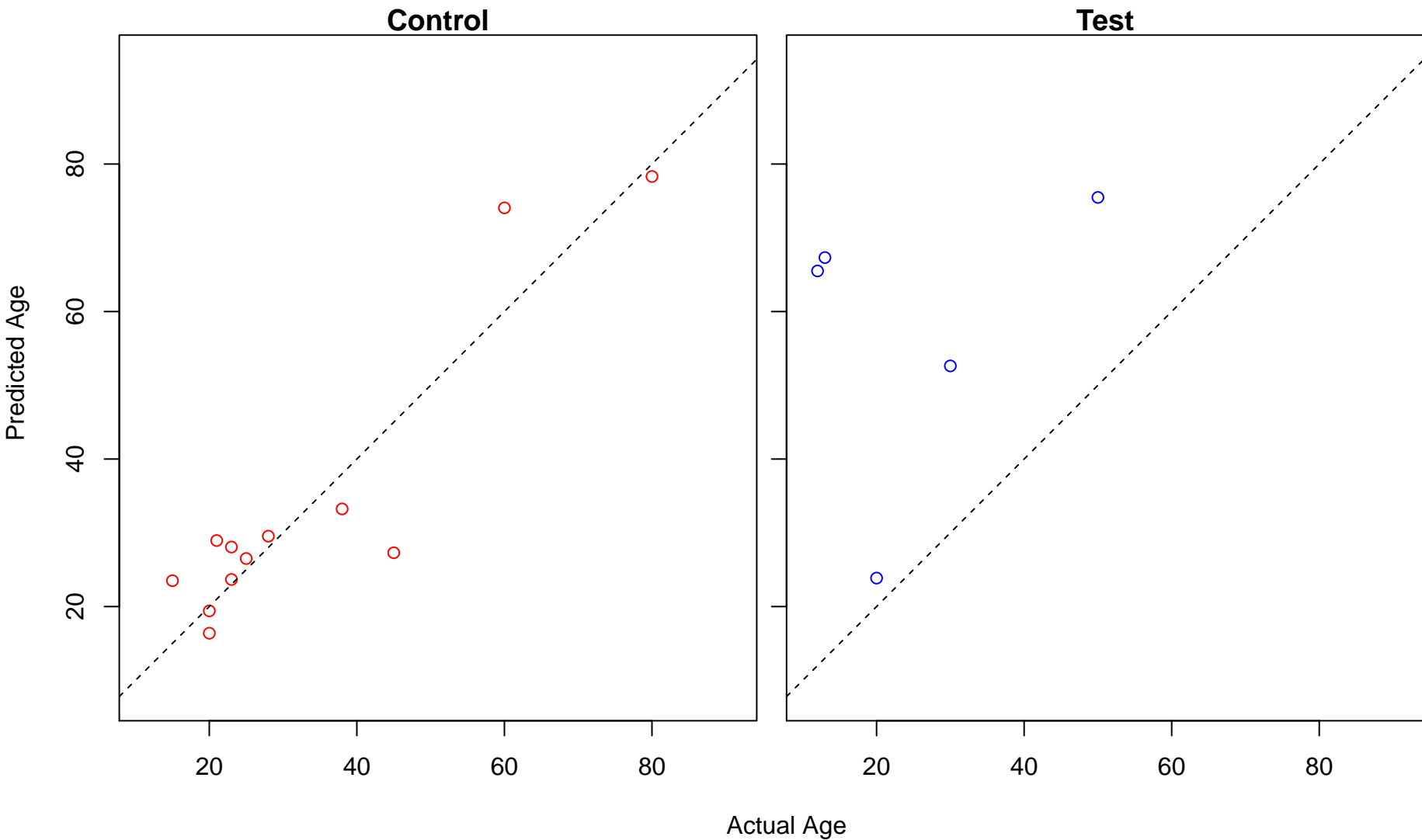
prostanoid metabolic process (Score: 64.905908)



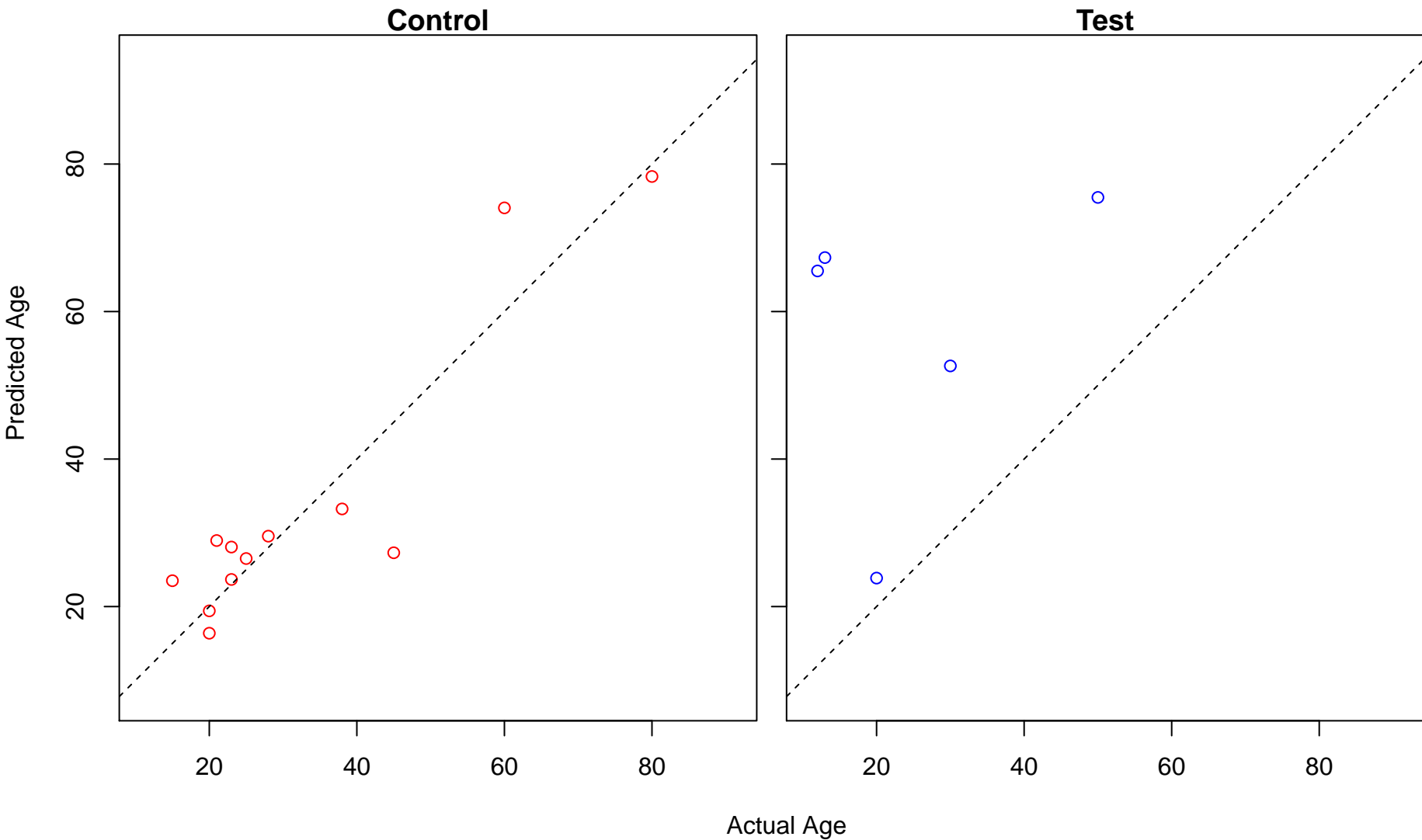
prostaglandin metabolic process (Score: 64.905908)



ectodermal placode formation (Score: 64.273041)

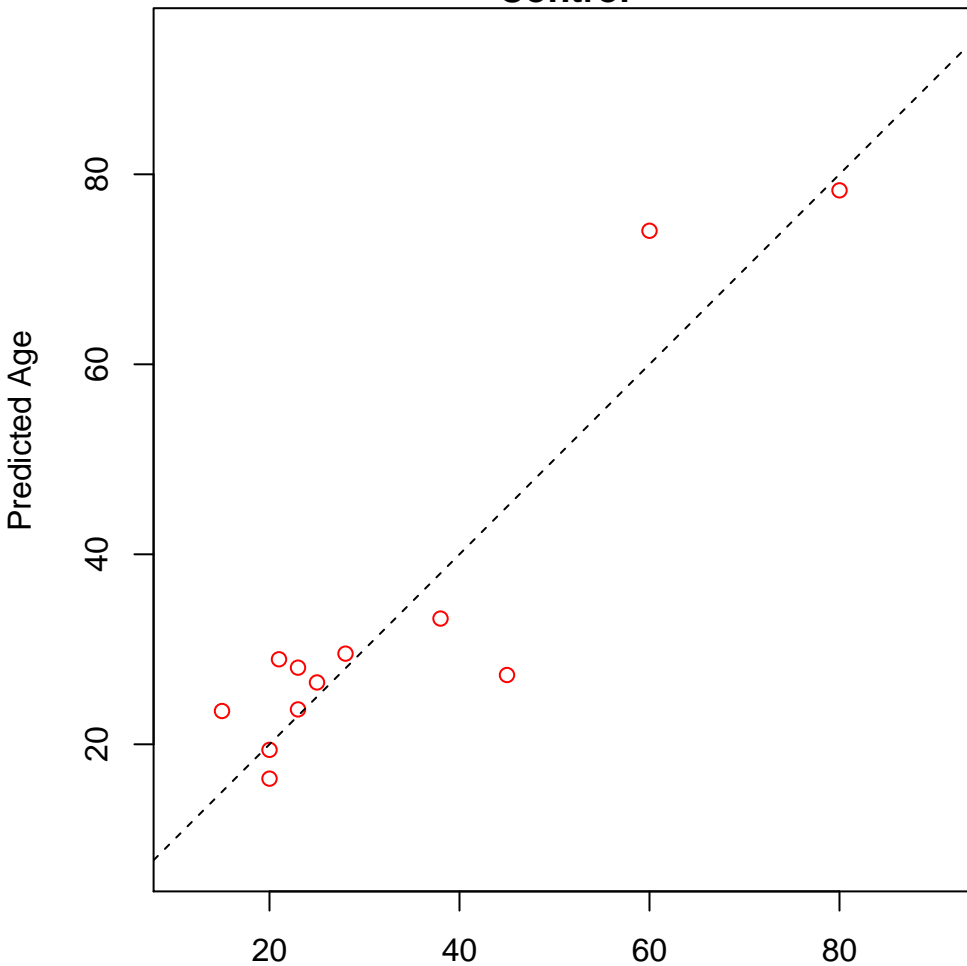


ectodermal placode development (Score: 64.273041)

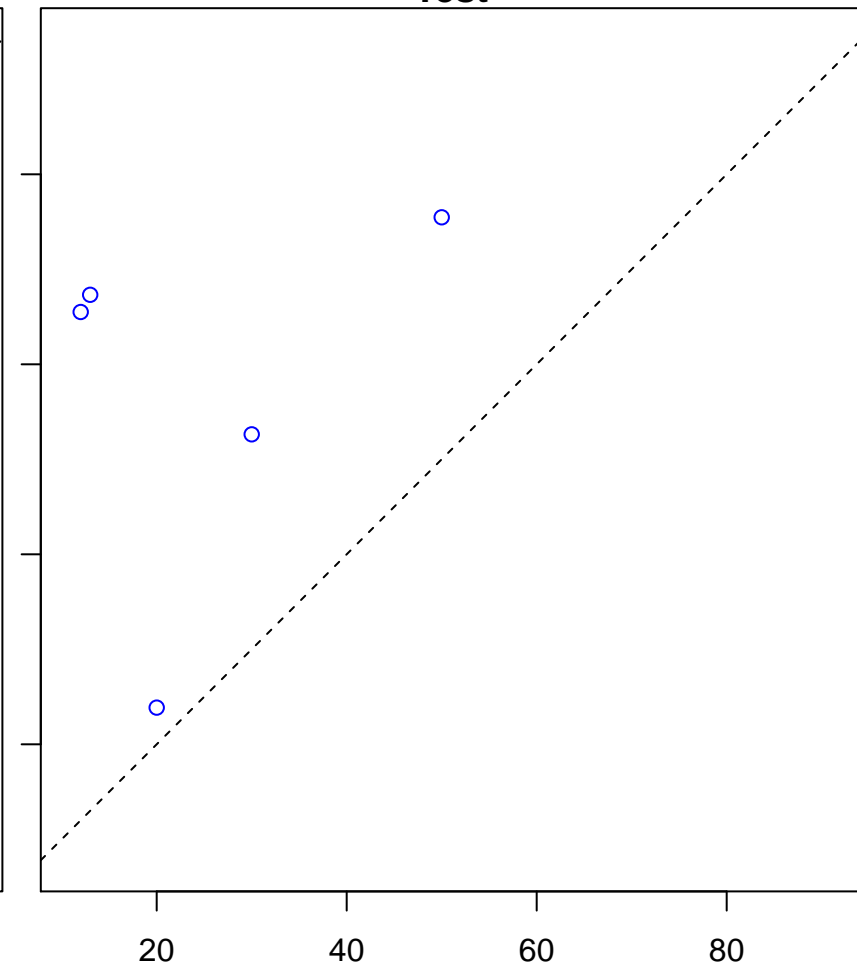


ectodermal placode morphogenesis (Score: 64.273041)

Control

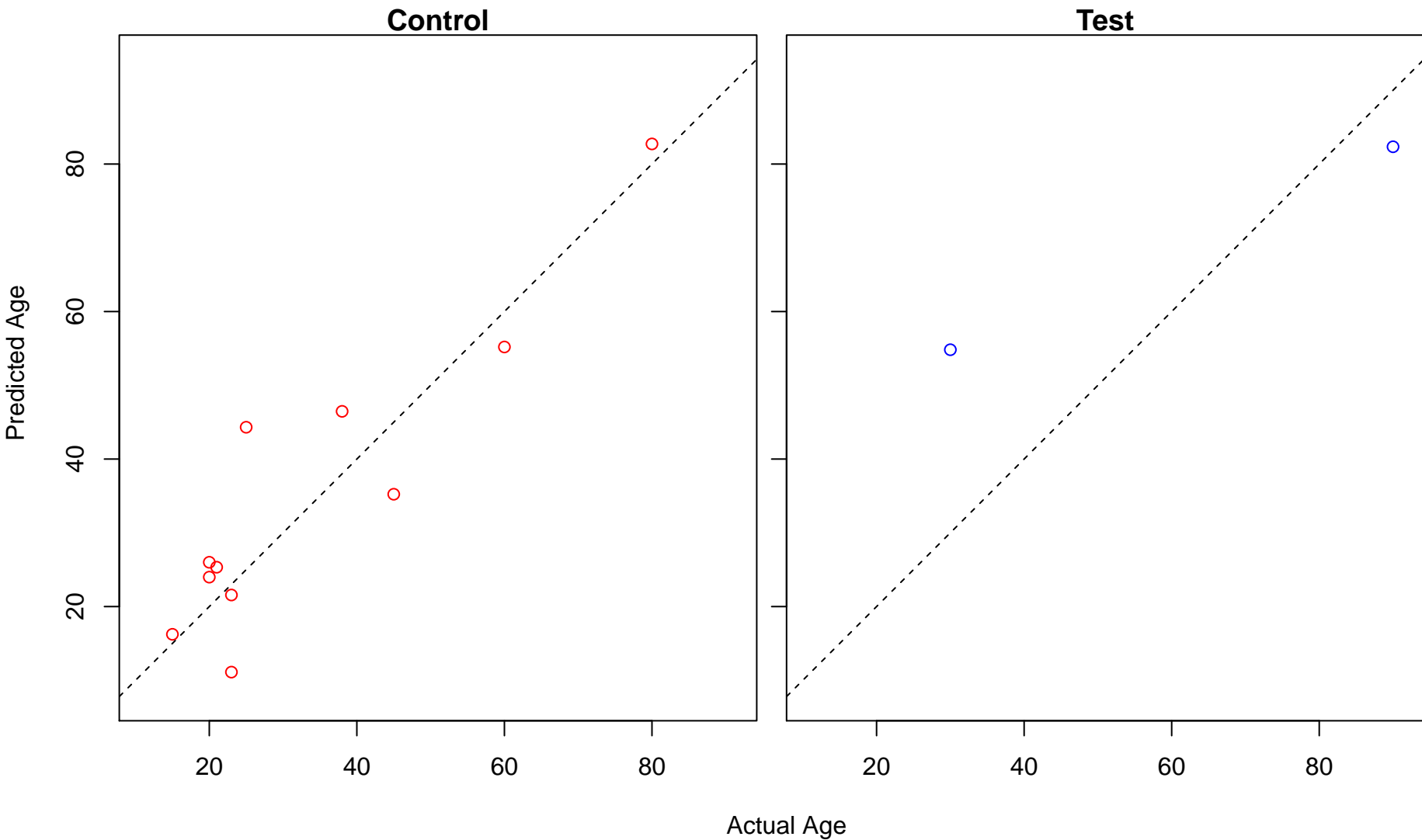


Test

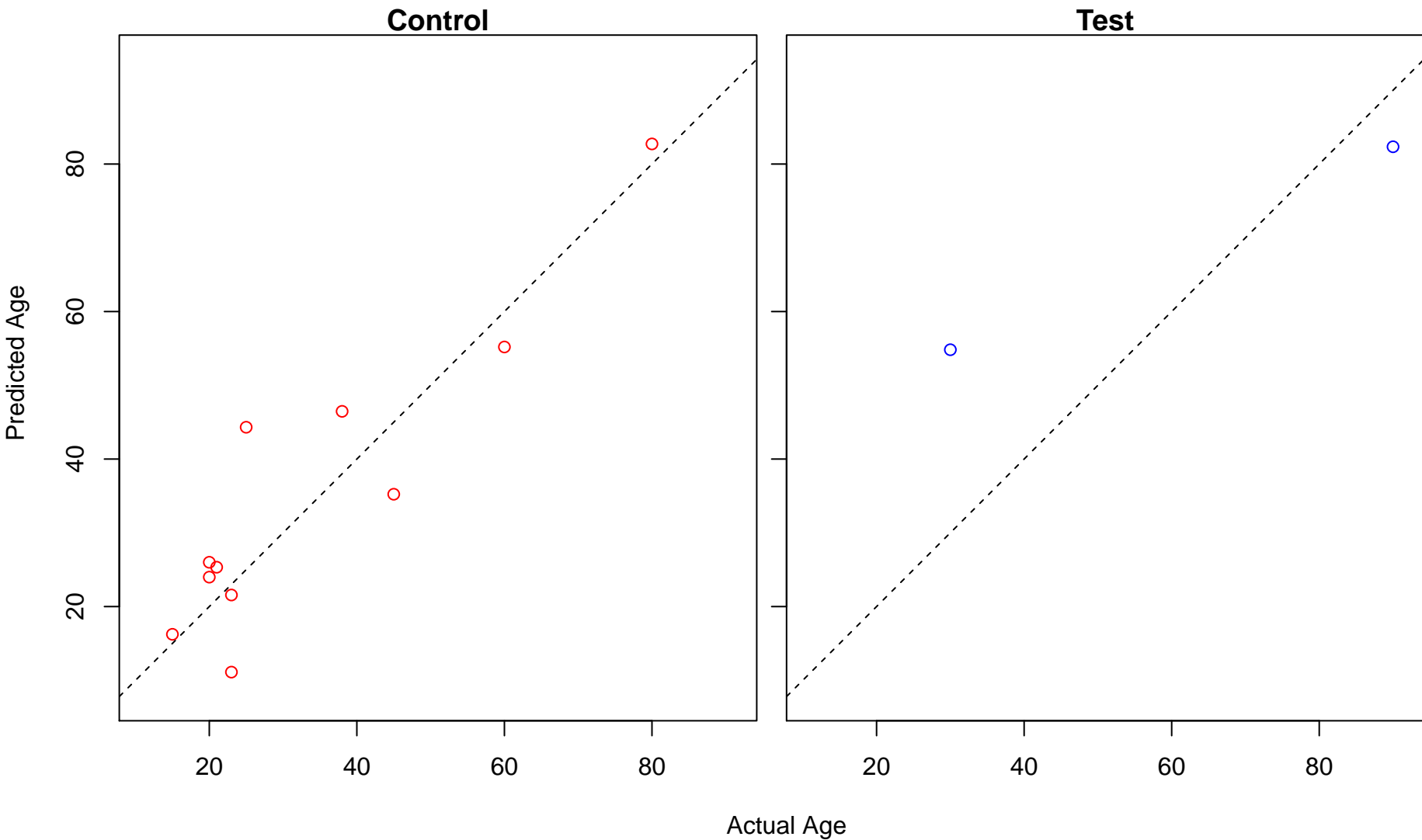


Actual Age

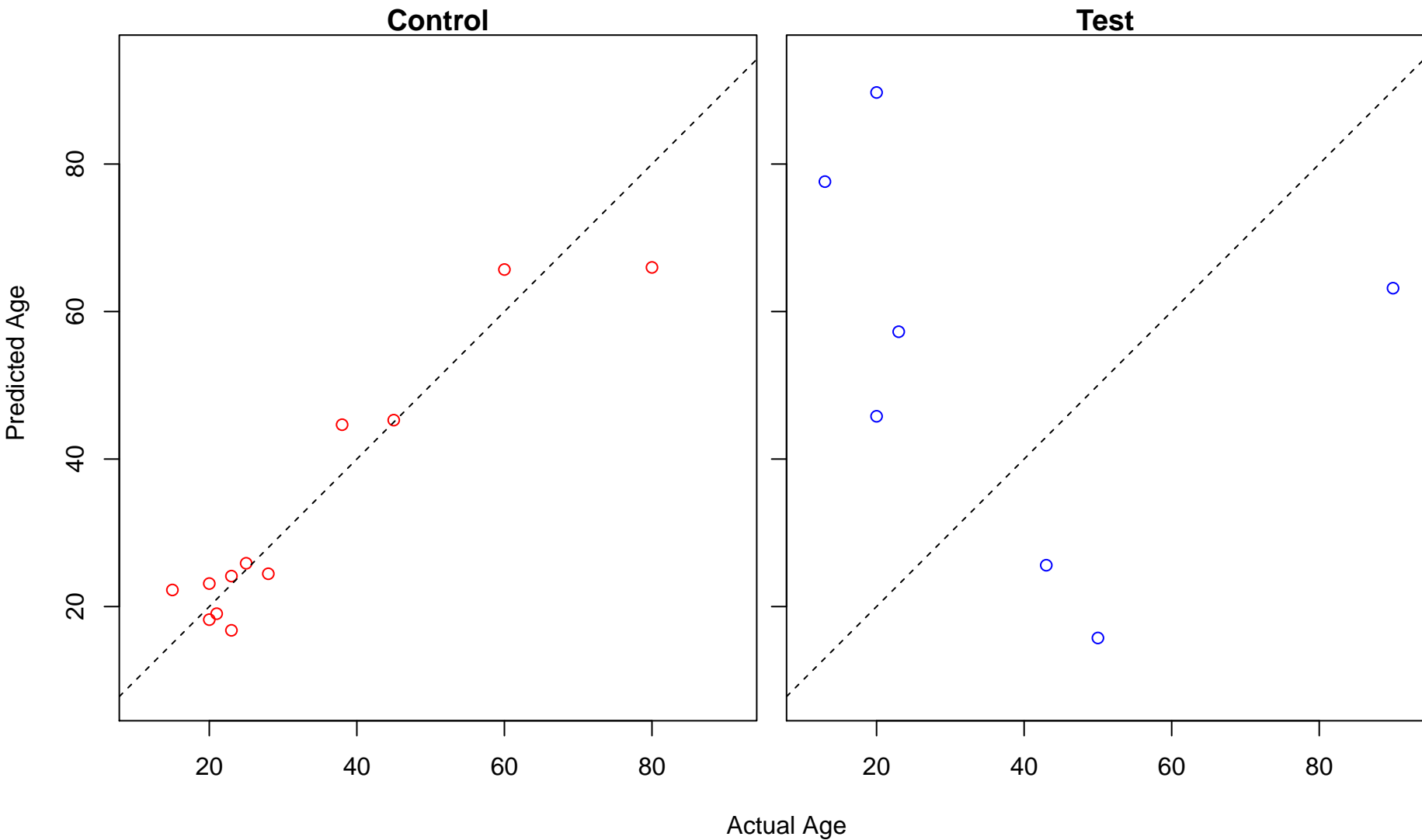
deoxyribonucleoside triphosphate metabolic process (Score: 62.854435)



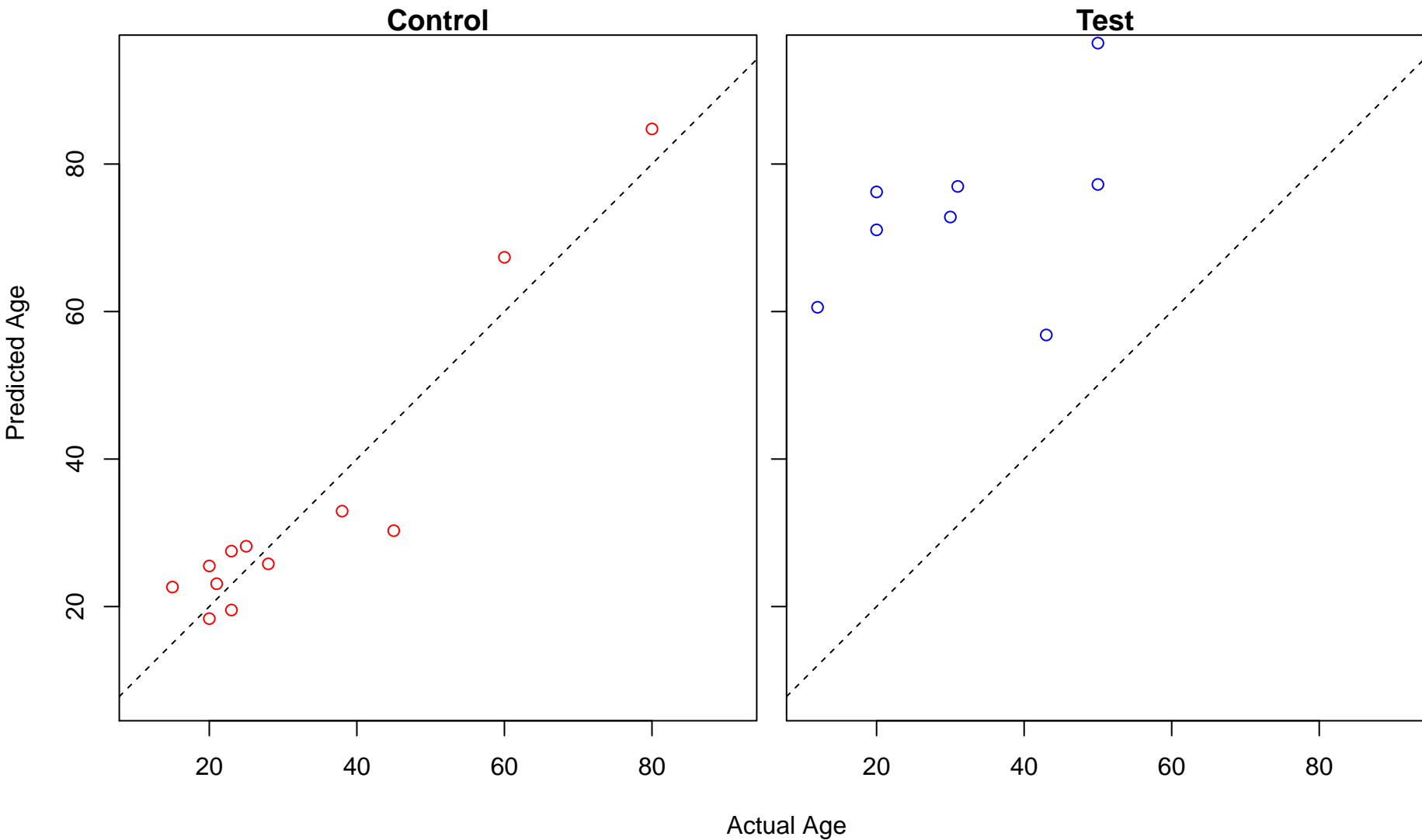
purine deoxyribonucleoside triphosphate metabolic process (Score: 62.854435)



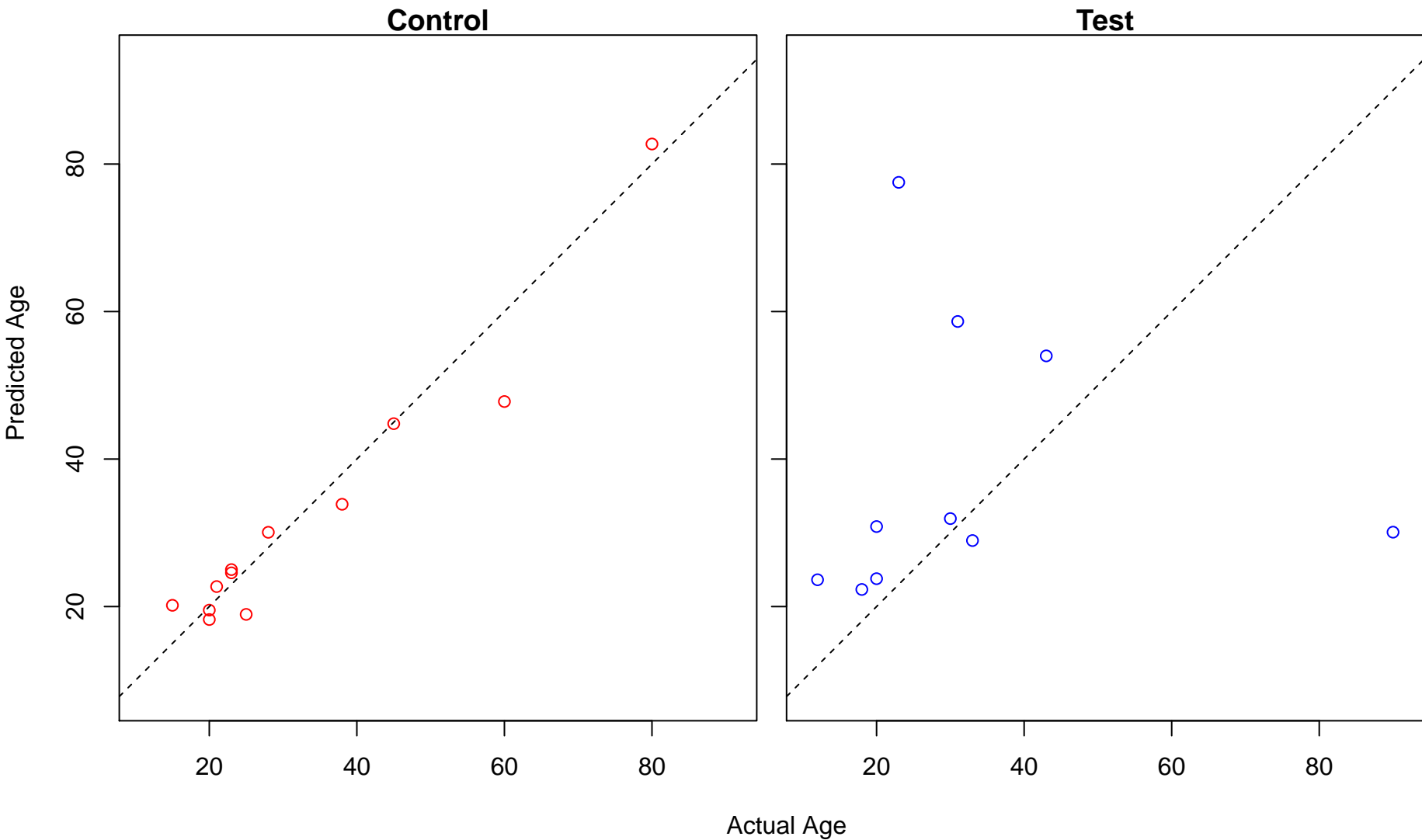
negative regulation of cell adhesion mediated by integrin (Score: 62.849798)



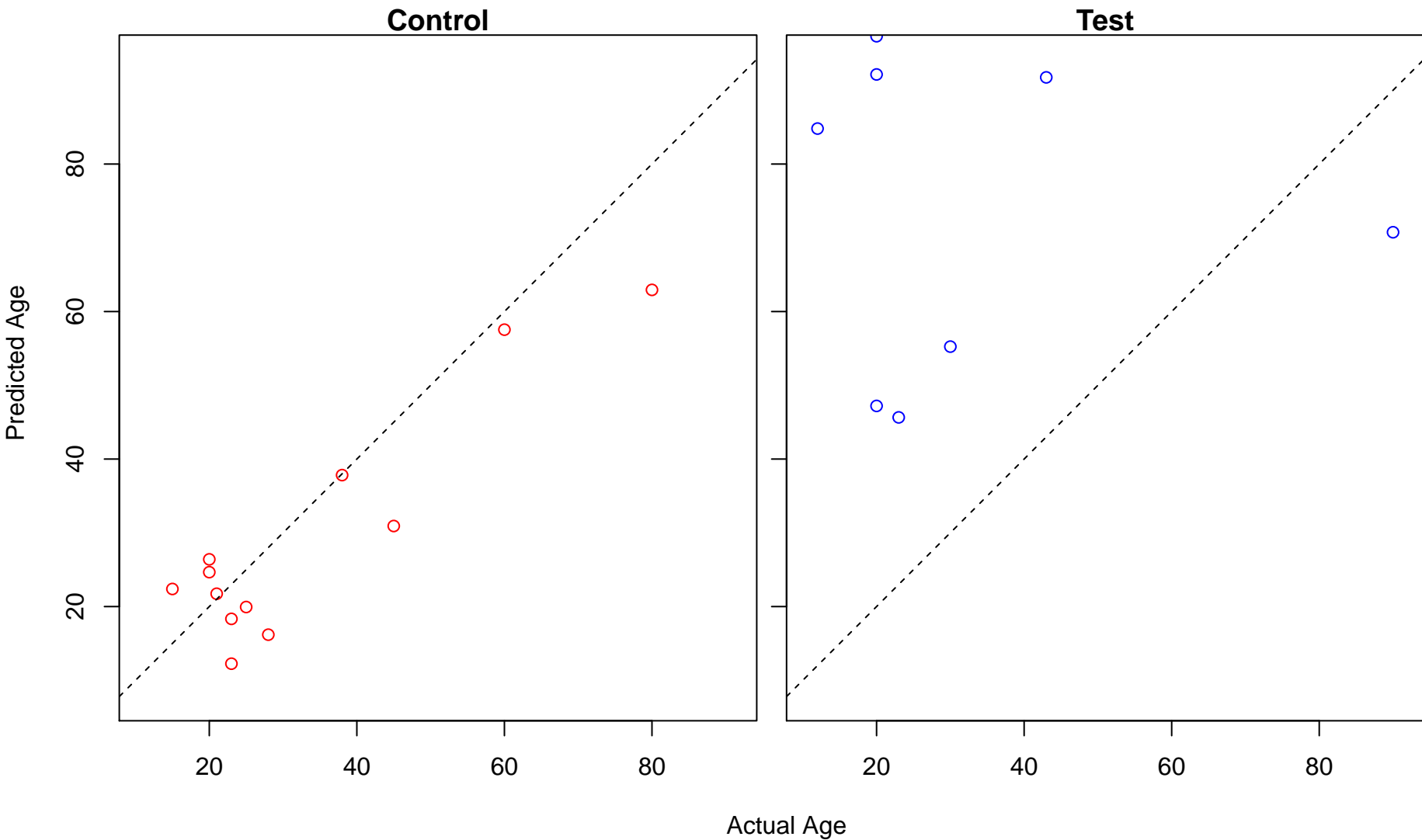
cytokinetic process (Score: 62.558641)



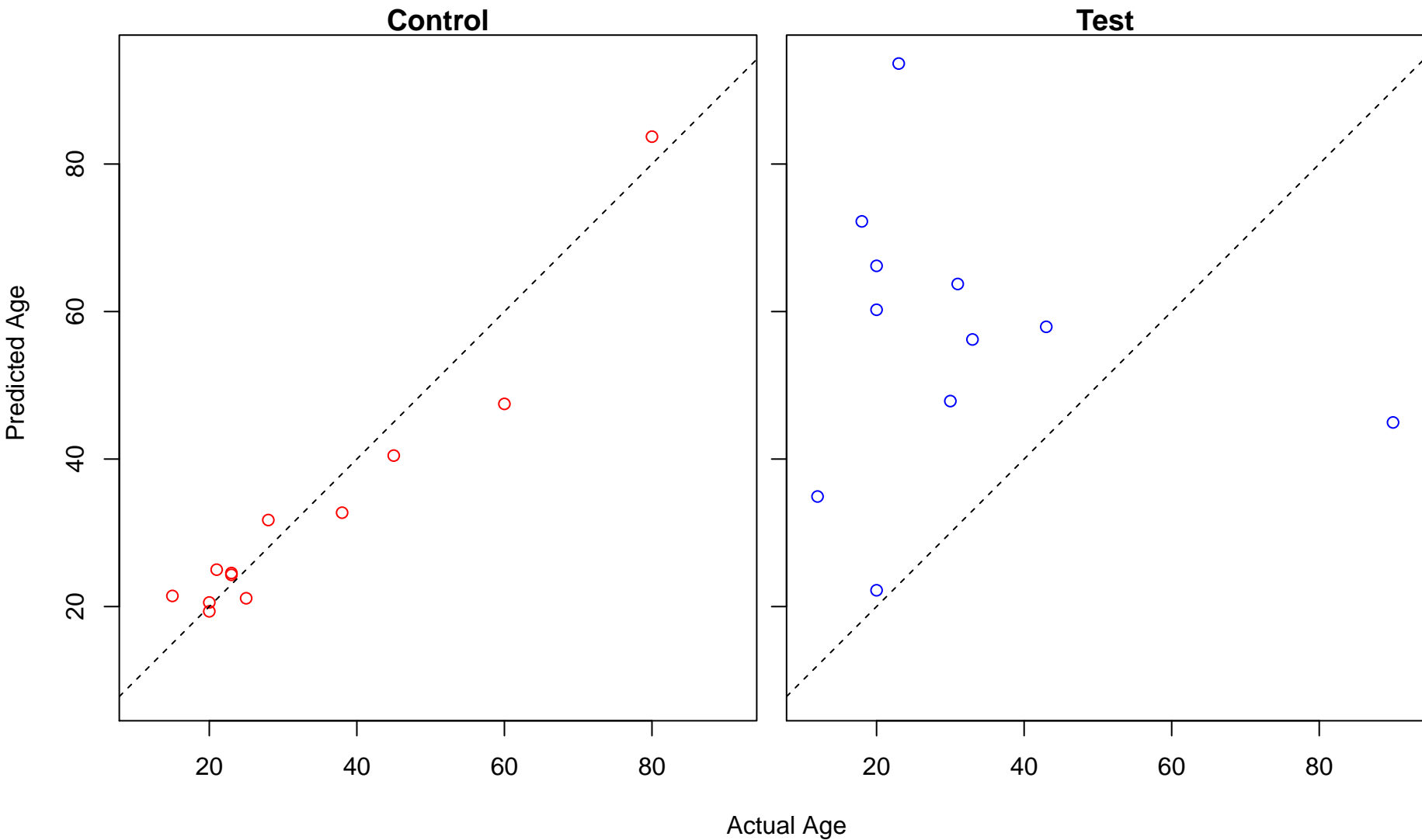
regulation of CD4-positive, alpha-beta T cell differentiation (Score: 62.446047)



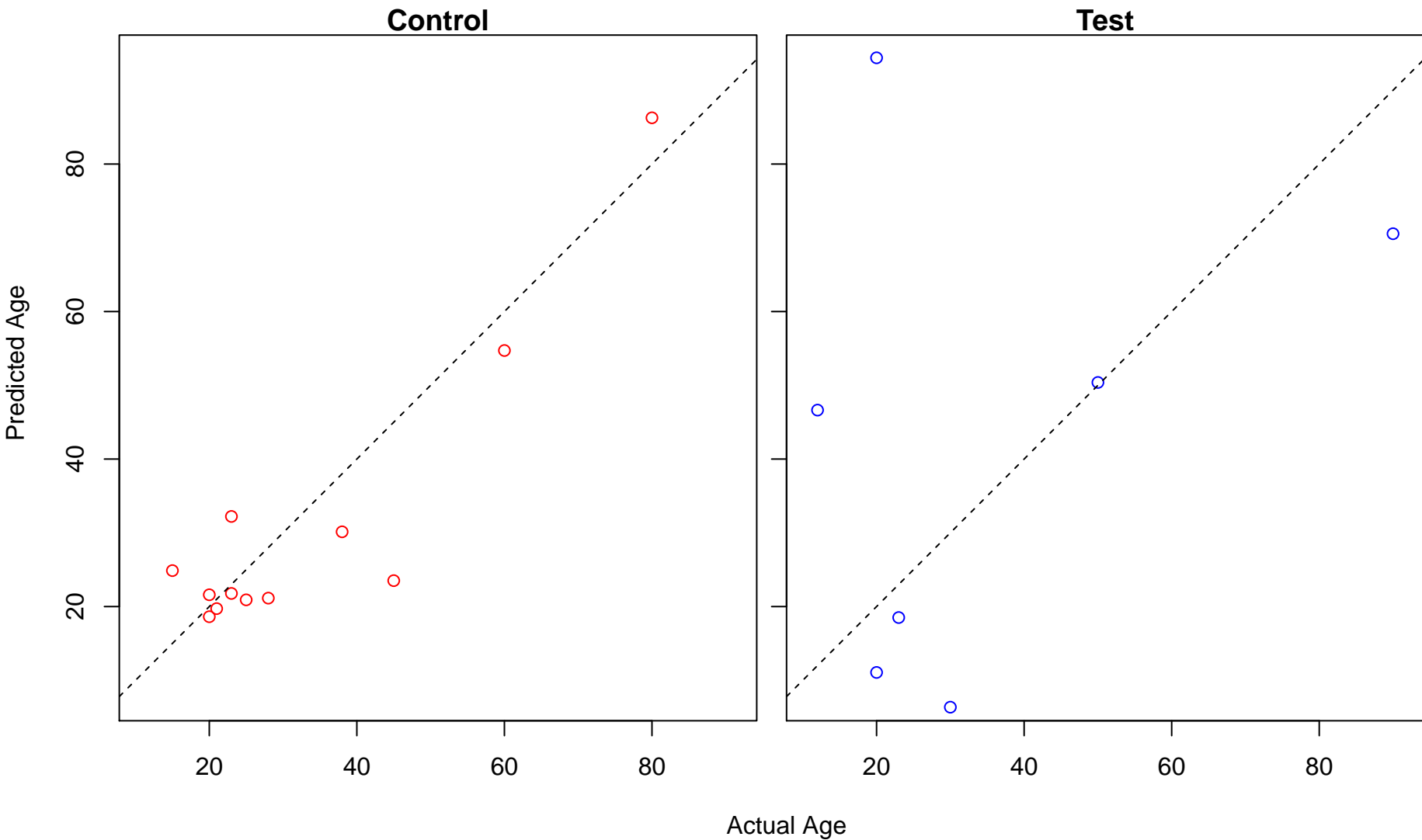
positive regulation of reactive oxygen species biosynthetic process (Score: 62.444329)



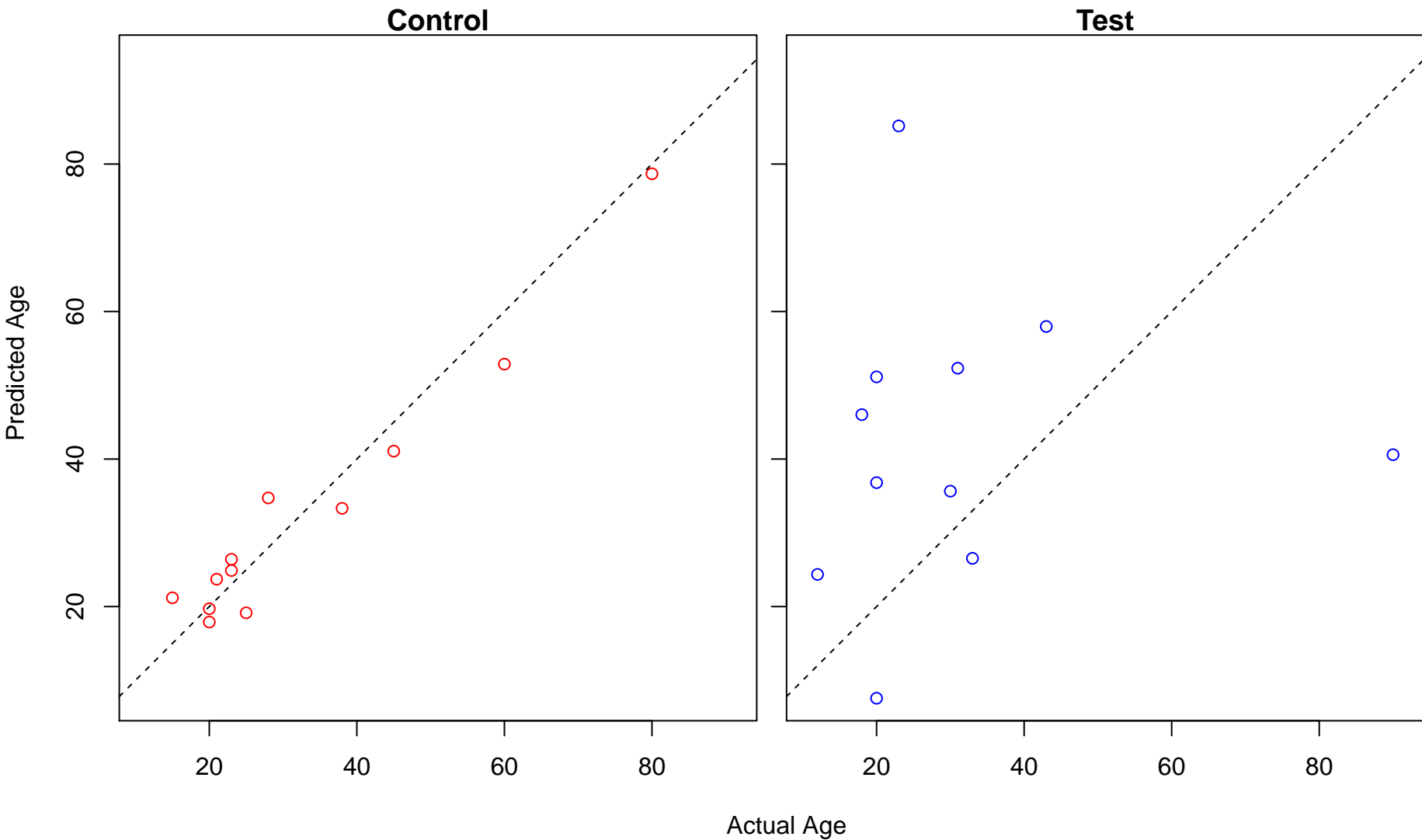
regulation of alpha-beta T cell differentiation (Score: 62.423703)



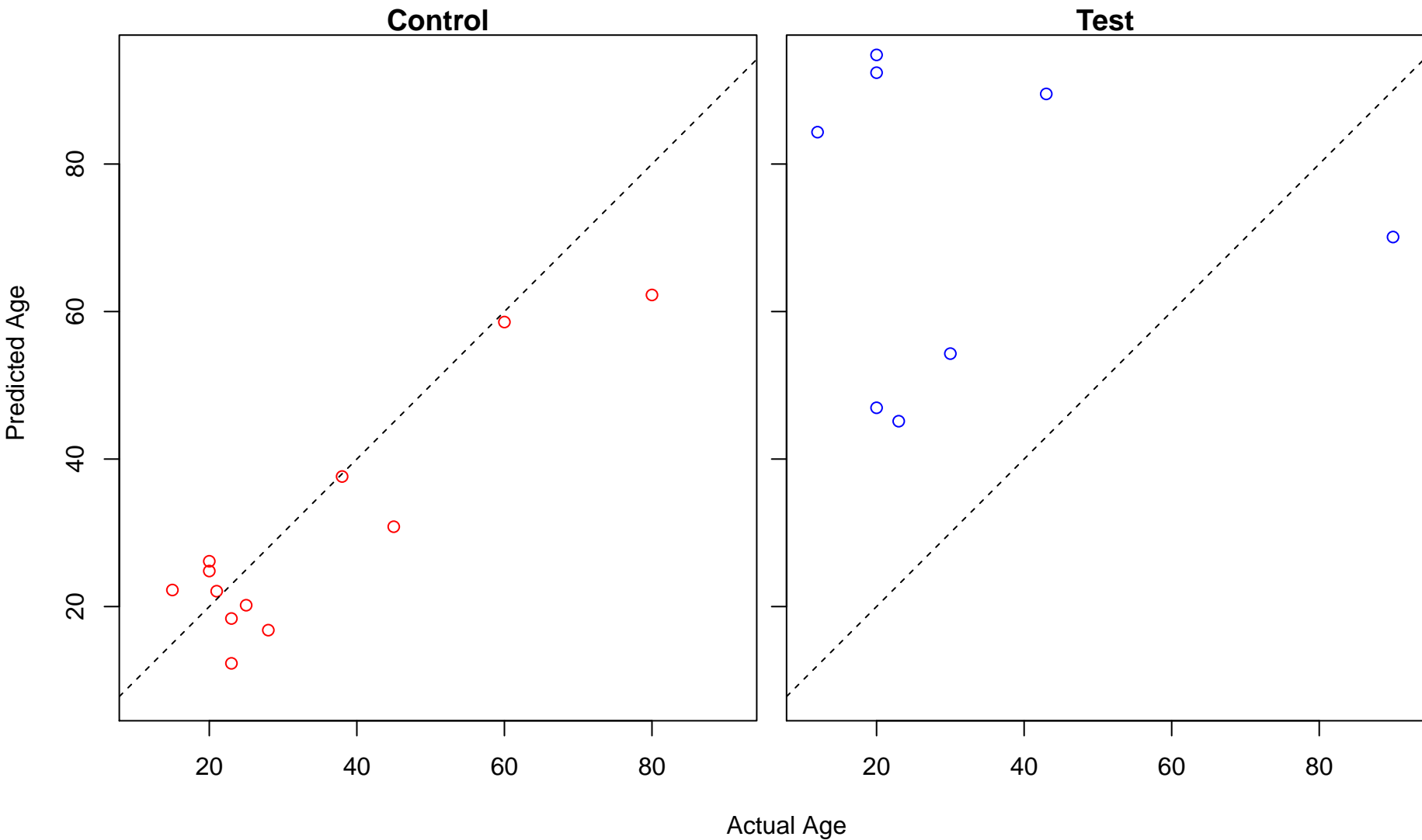
positive regulation of mRNA 3'-end processing (Score: 62.114208)



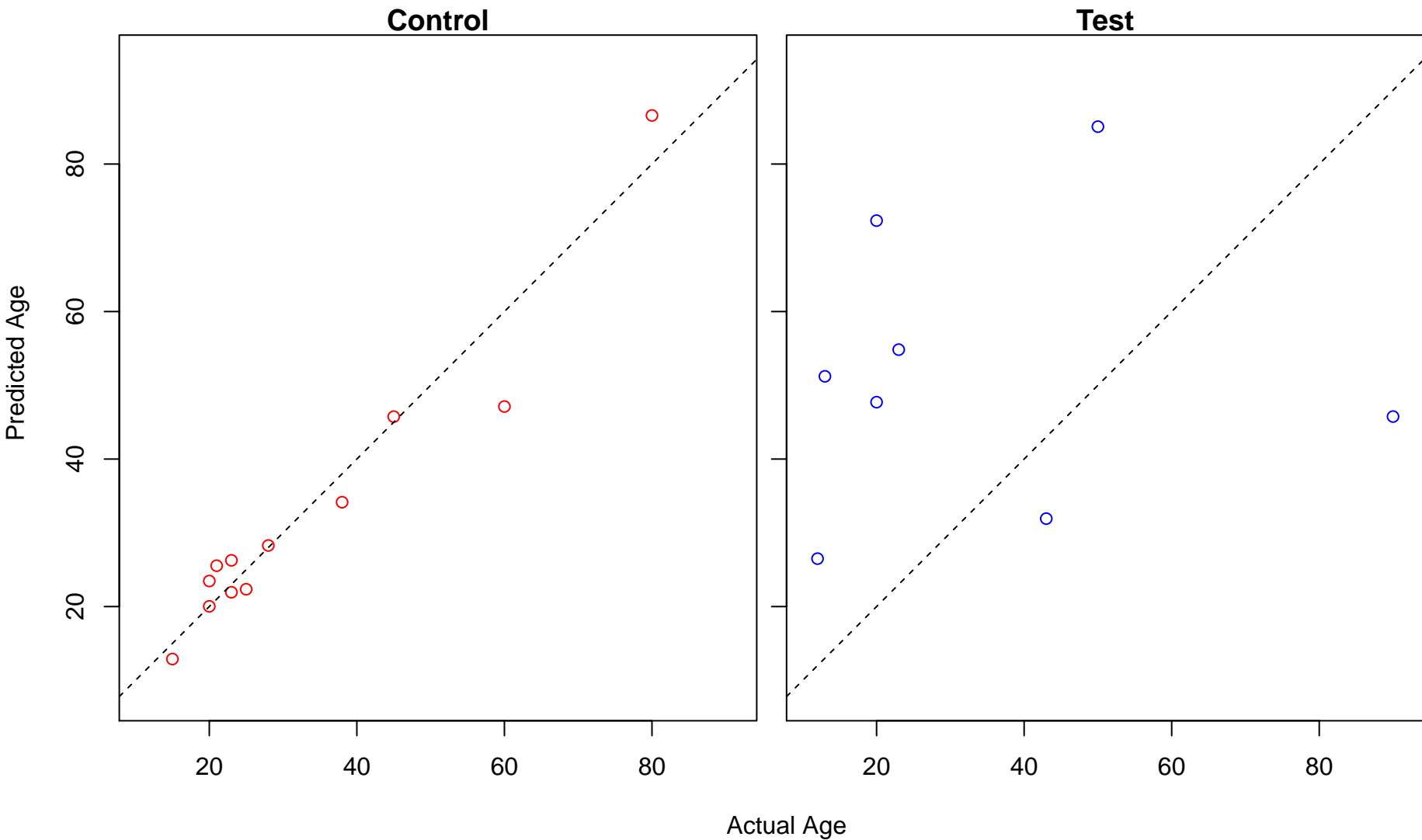
regulation of CD4-positive, alpha-beta T cell activation (Score: 60.725134)



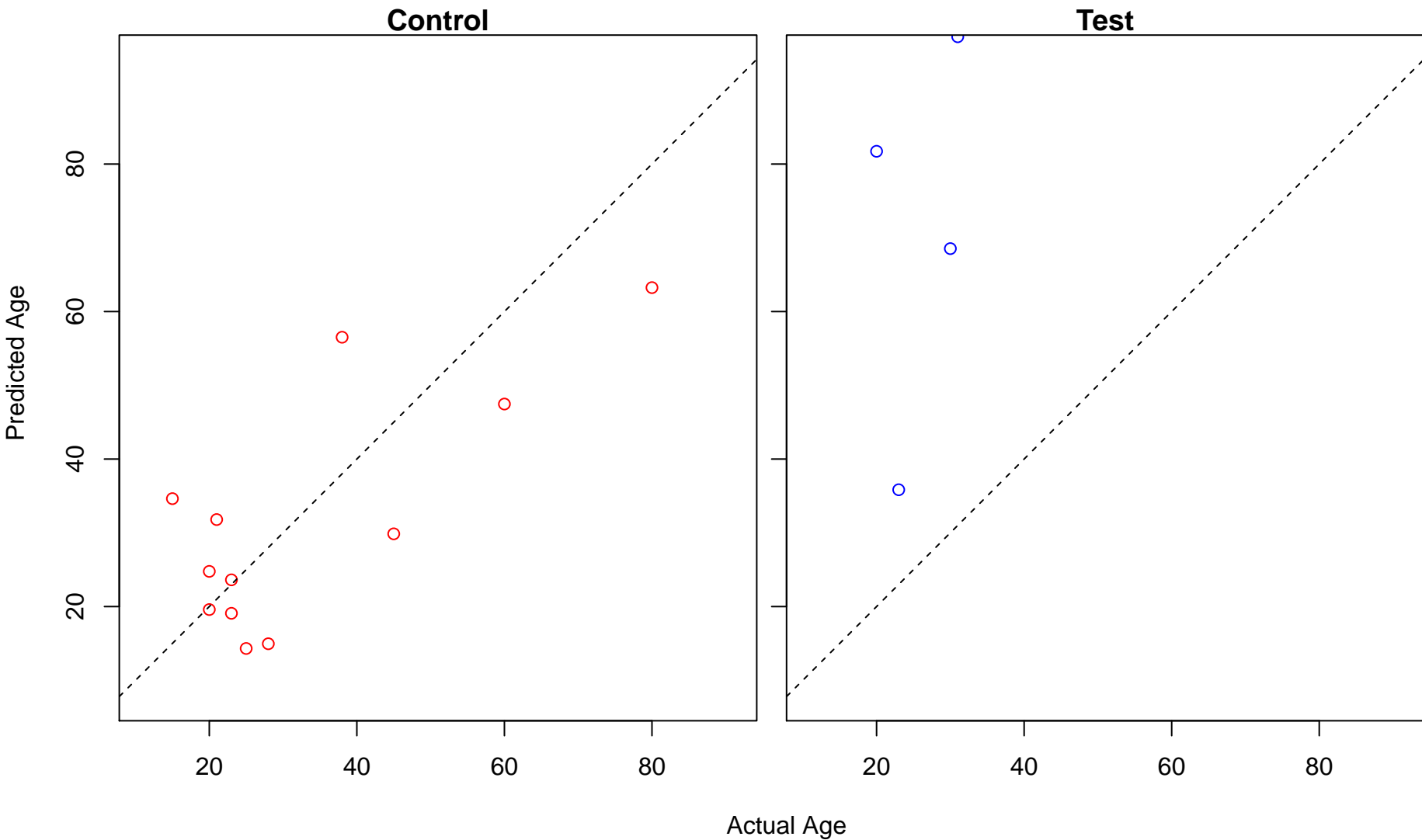
regulation of reactive oxygen species biosynthetic process (Score: 60.649562)



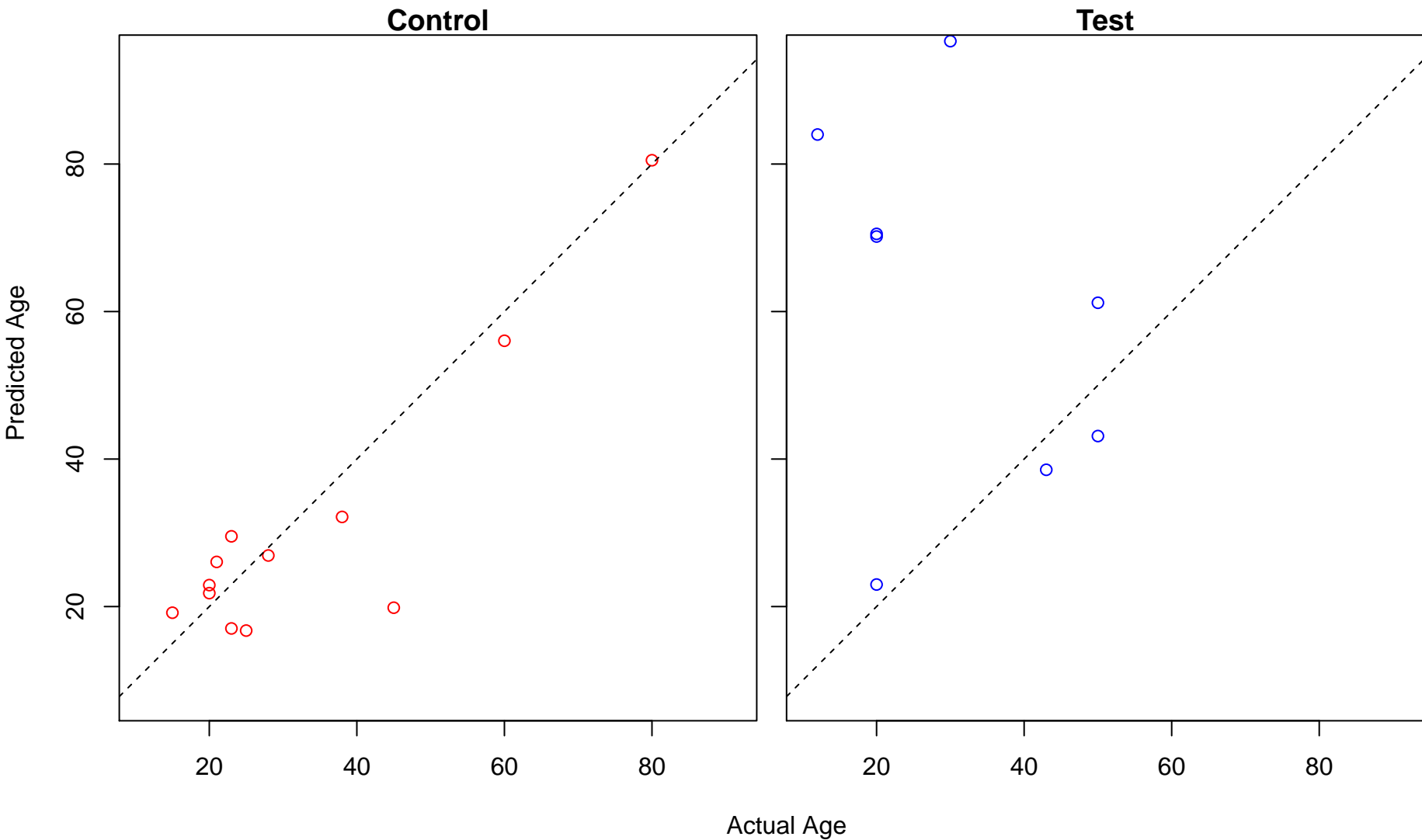
retina vasculature morphogenesis in camera-type eye (Score: 60.498586)



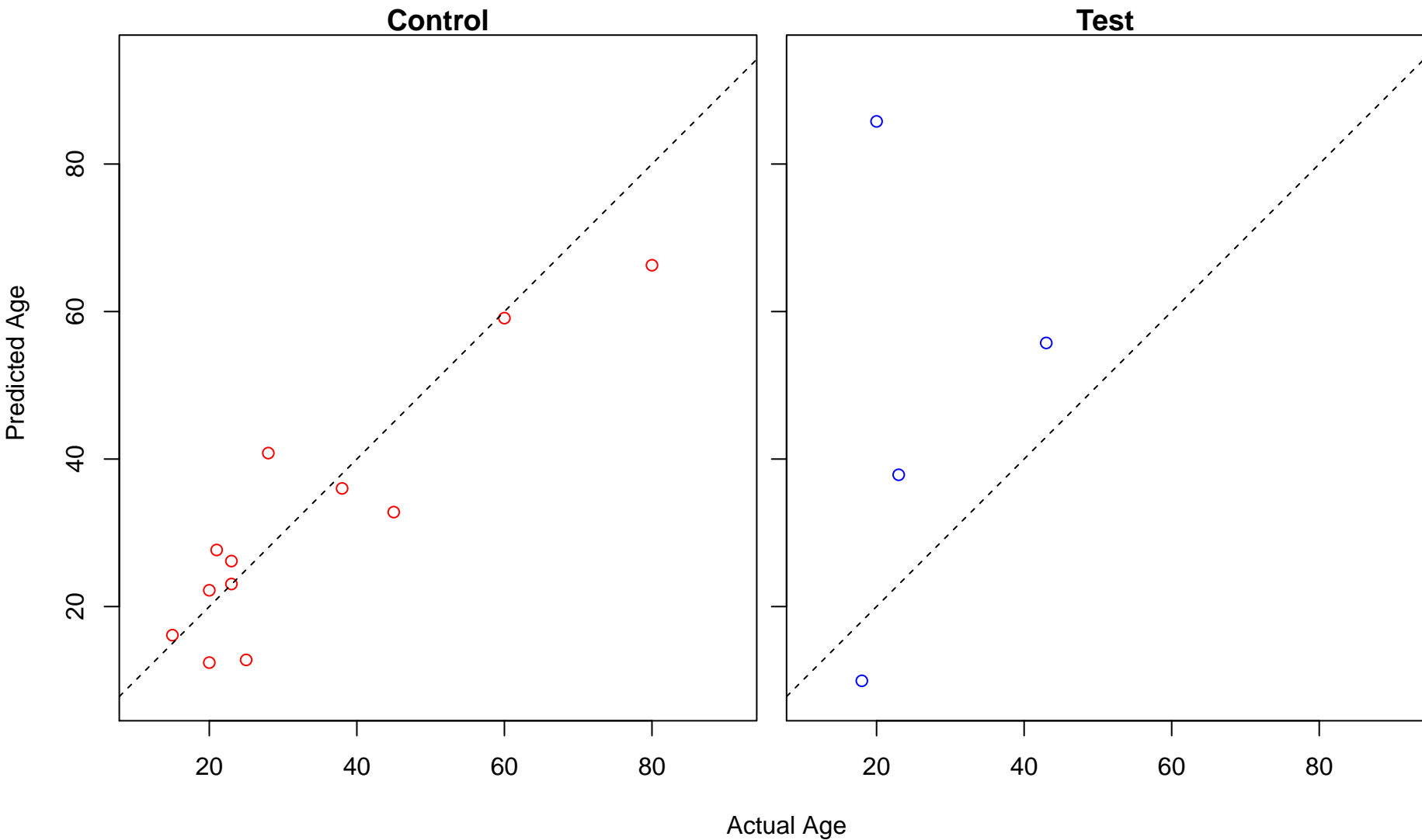
embryonic forelimb morphogenesis (Score: 60.234353)



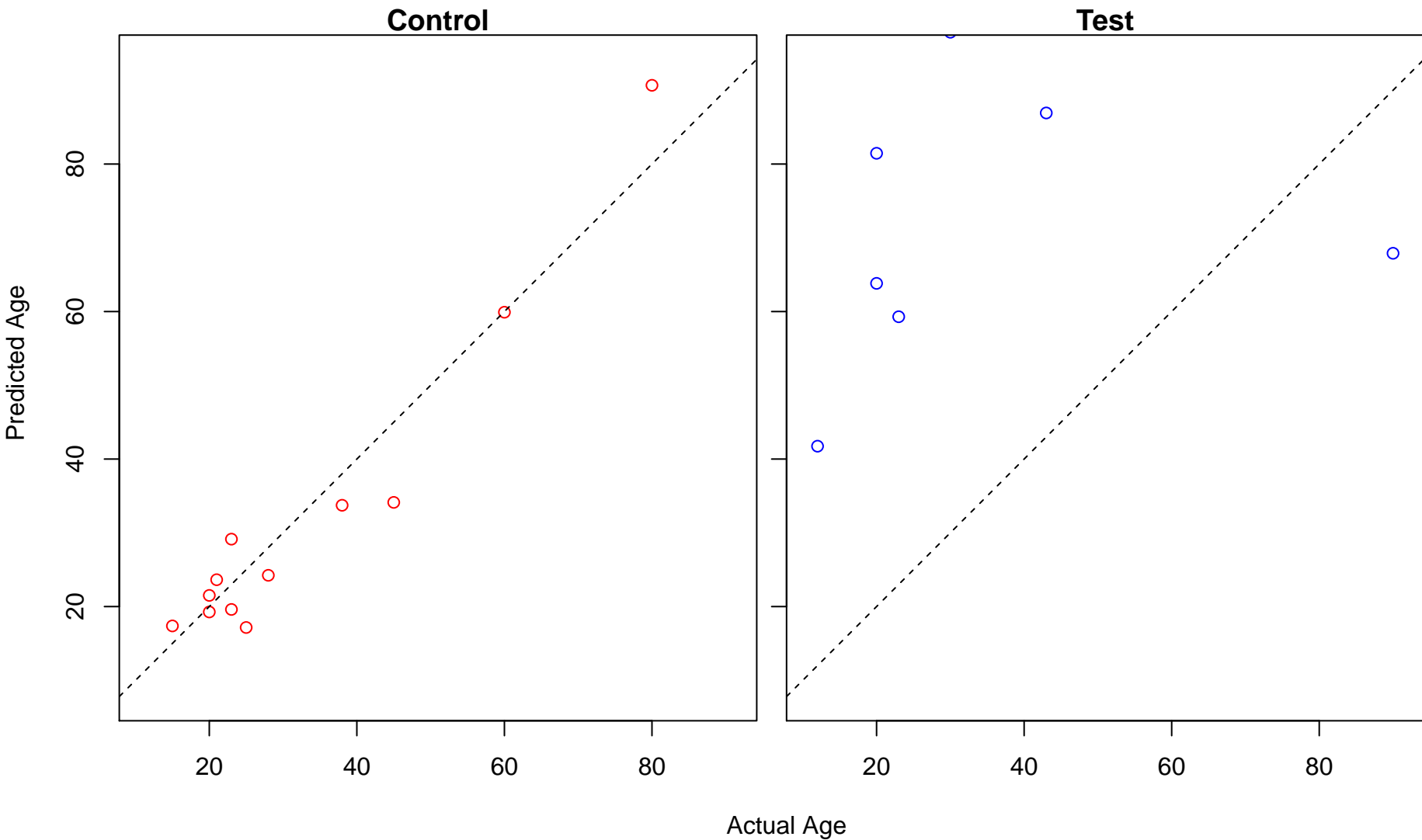
negative regulation of insulin receptor signaling pathway (Score: 58.697701)



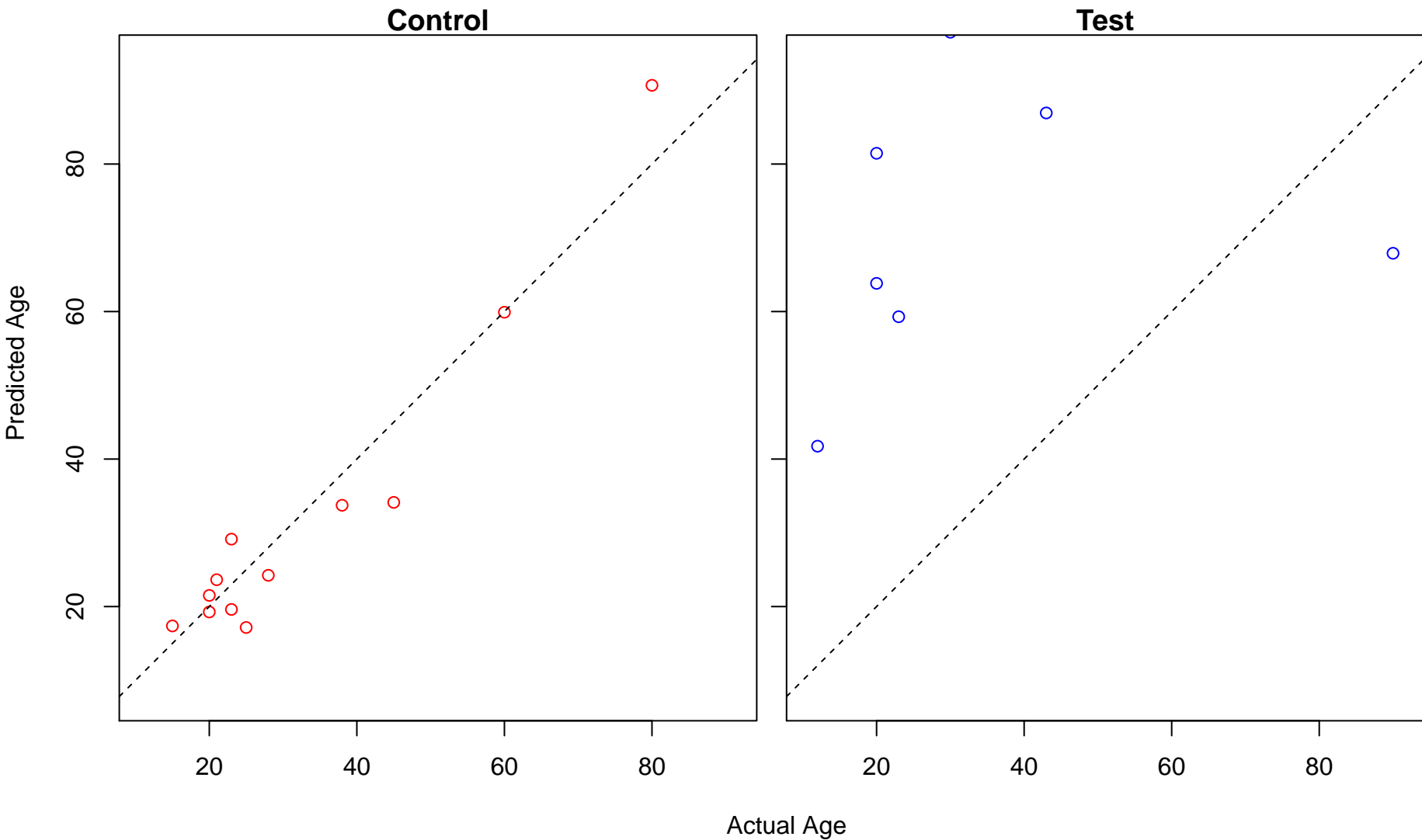
apoptotic cell clearance (Score: 58.568624)



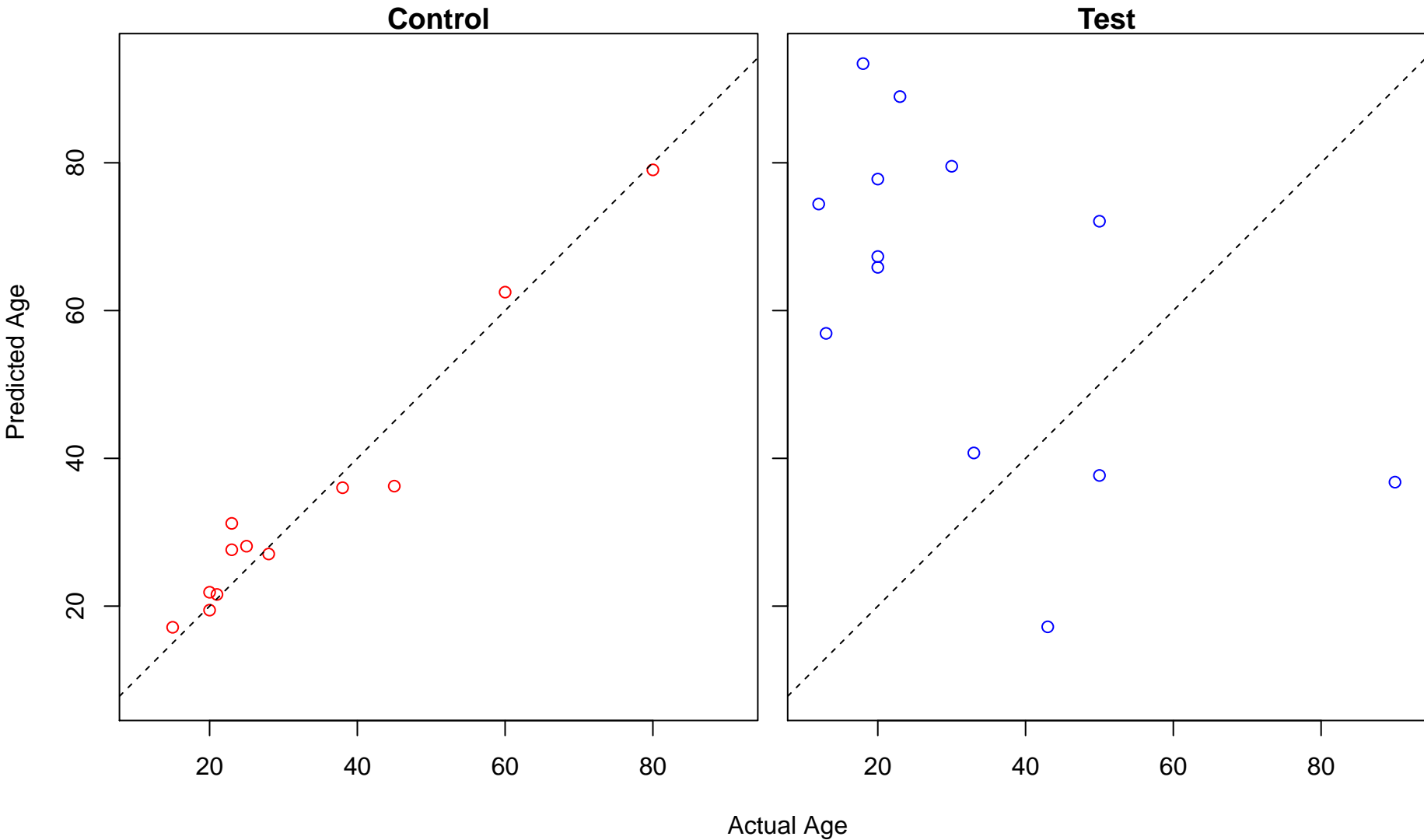
regulation of glial cell apoptotic process (Score: 58.340849)



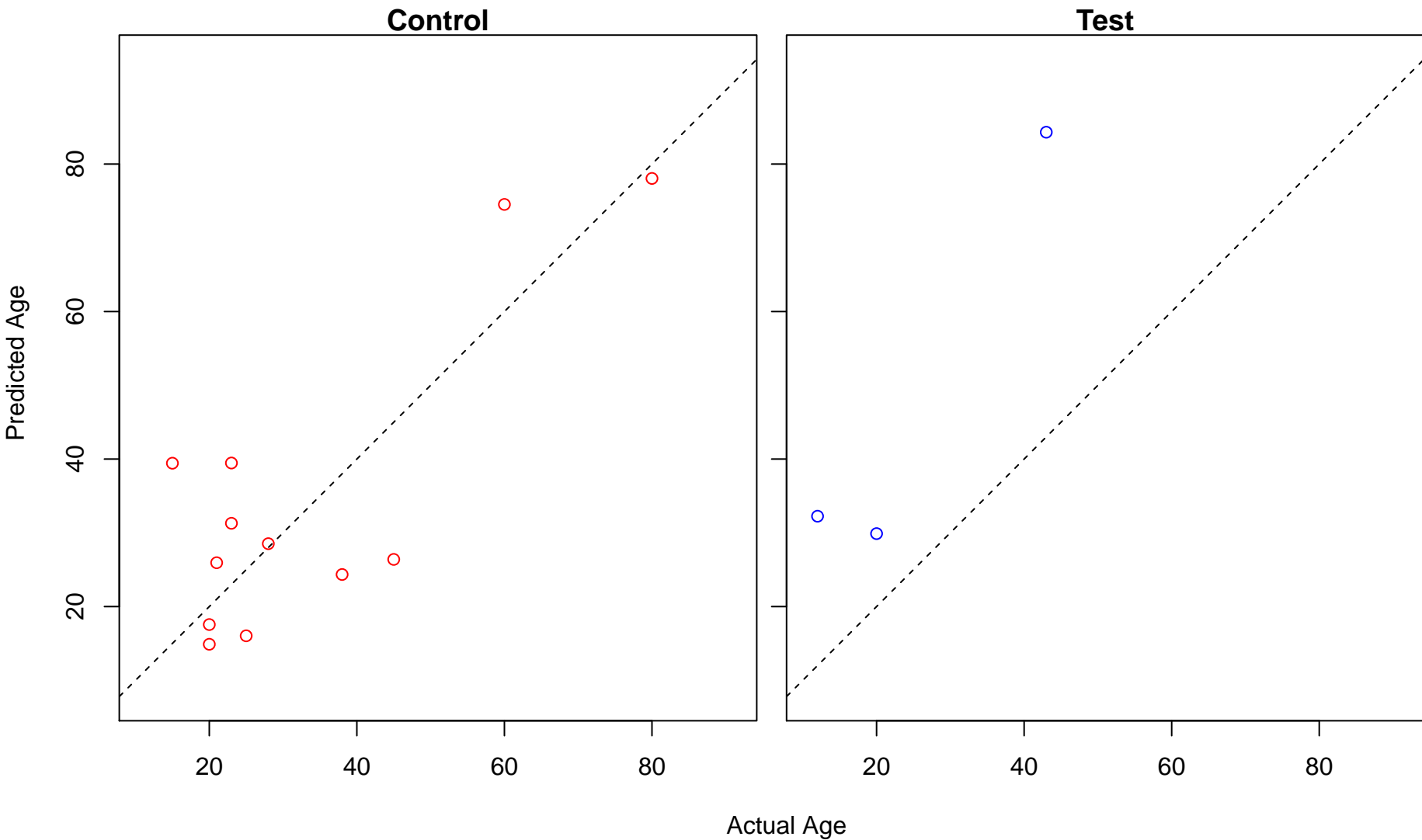
negative regulation of glial cell apoptotic process (Score: 58.340849)



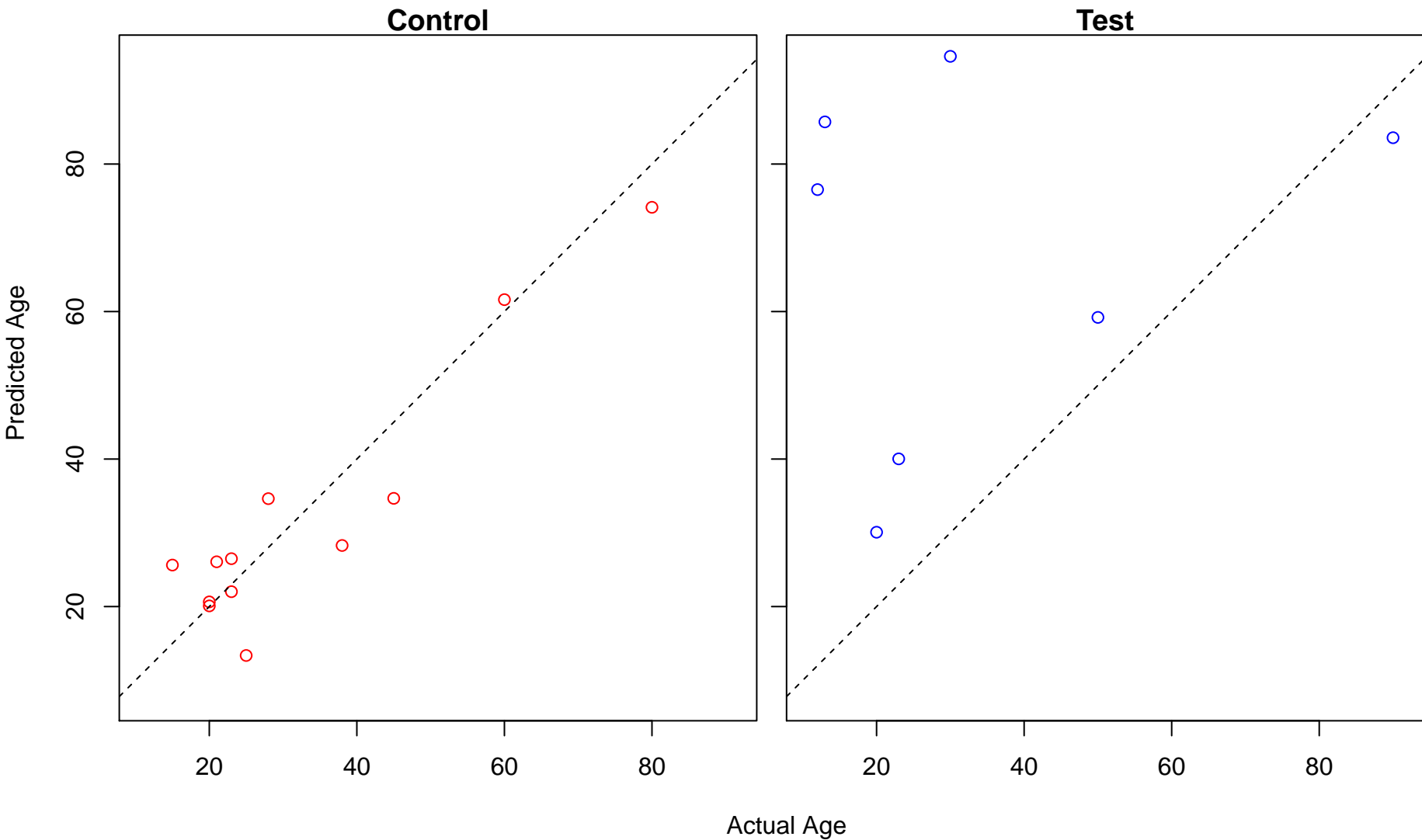
cytokine production involved in immune response (Score: 58.241078)



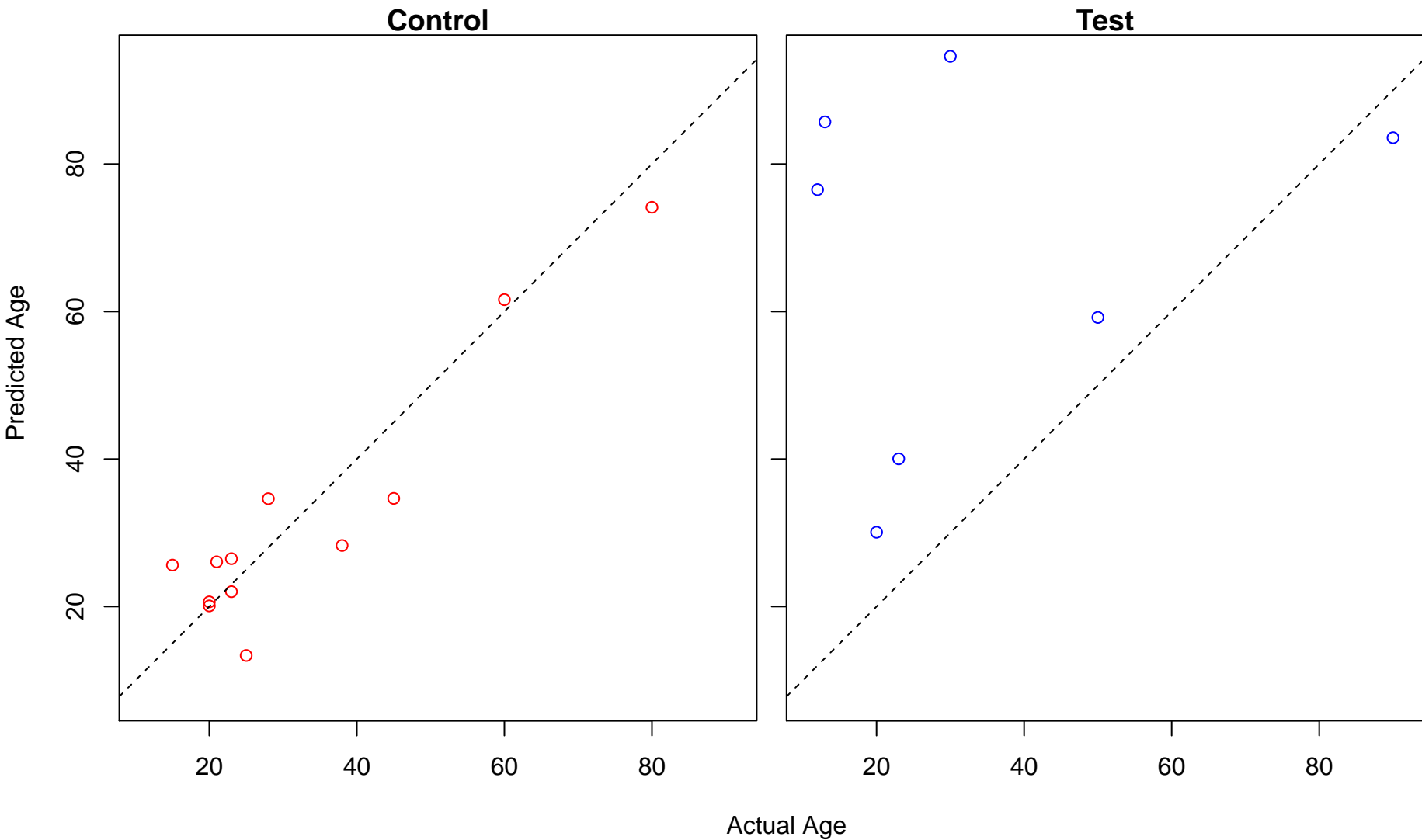
long-term memory (Score: 57.633470)



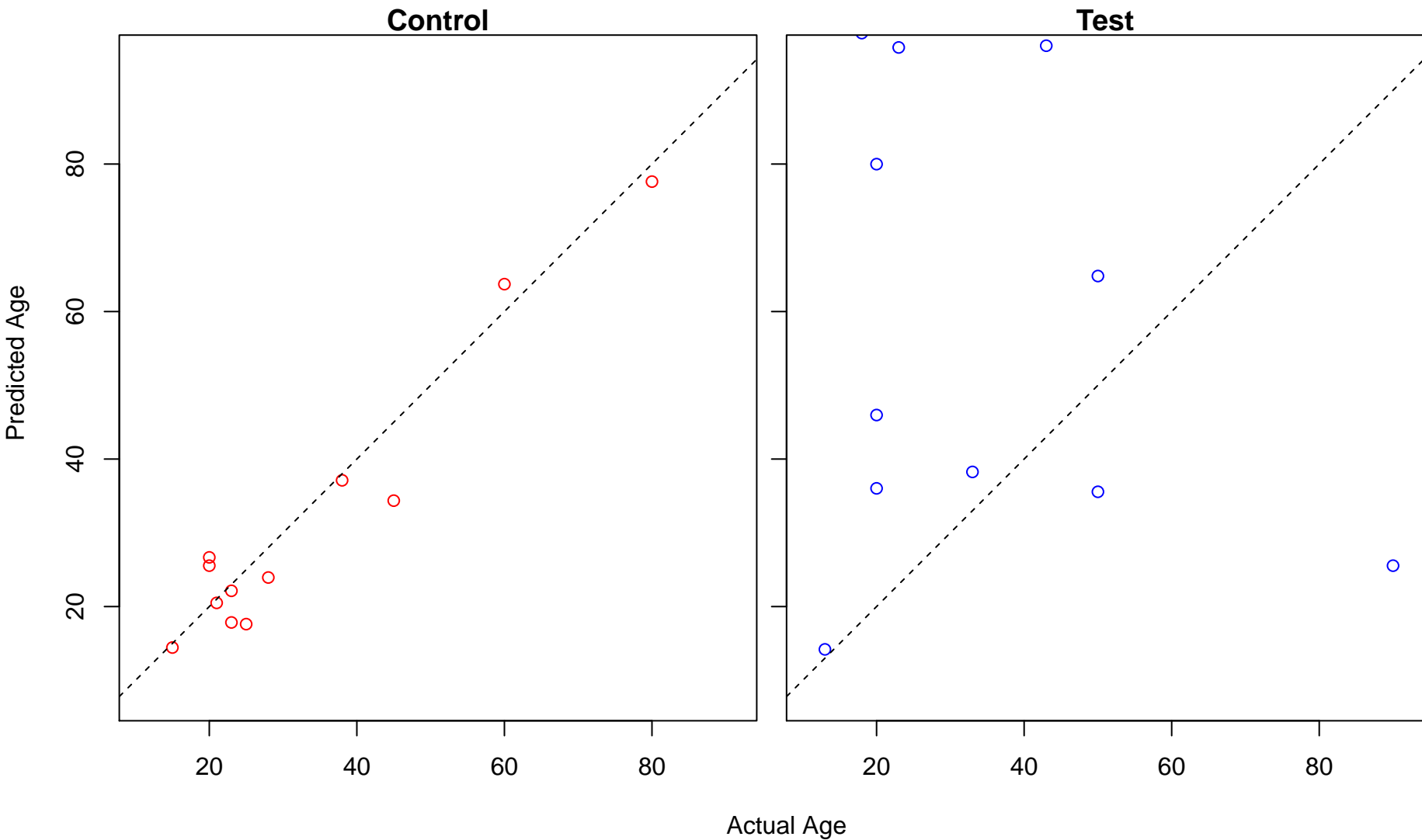
melanosome localization (Score: 57.353234)



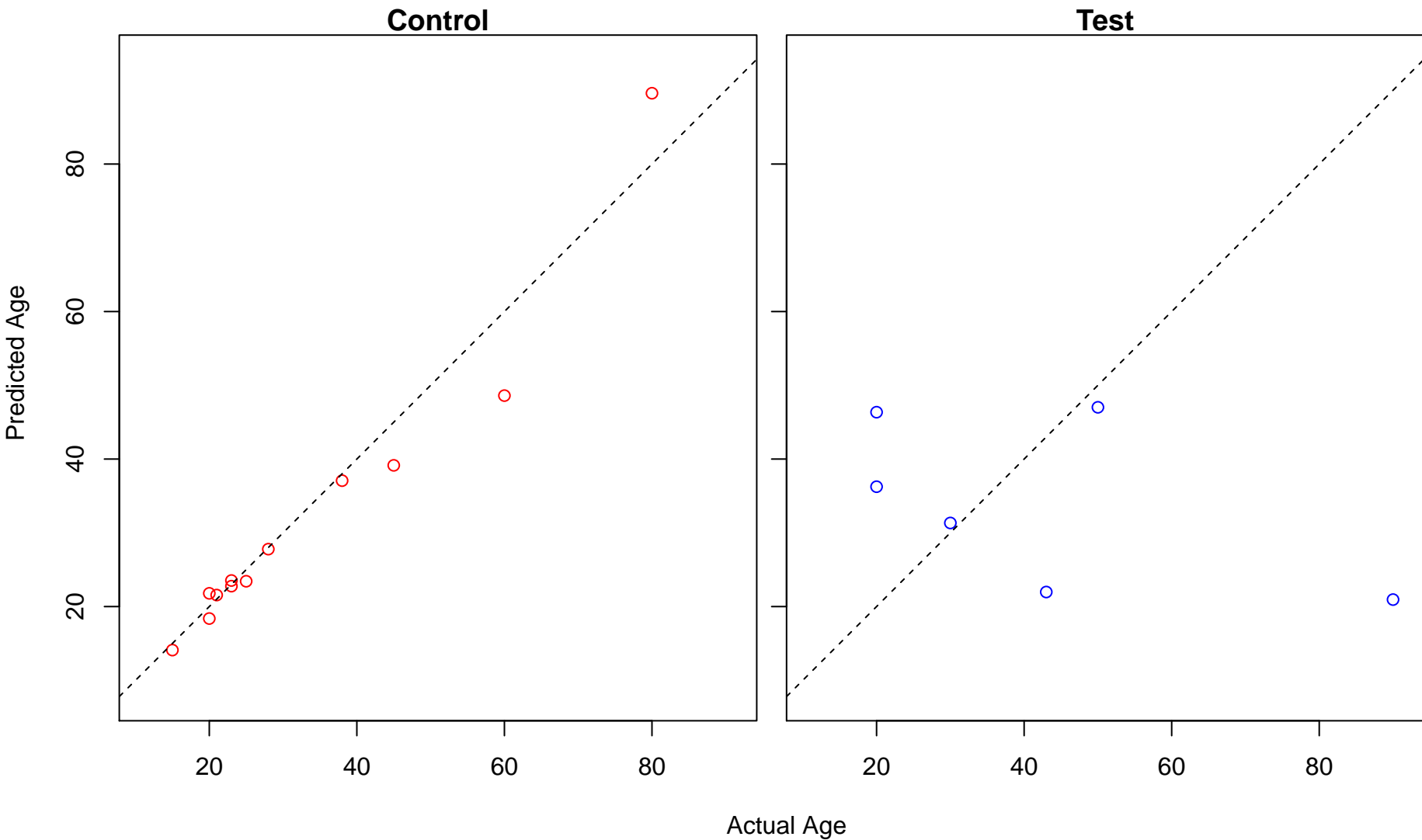
pigment granule localization (Score: 57.353234)



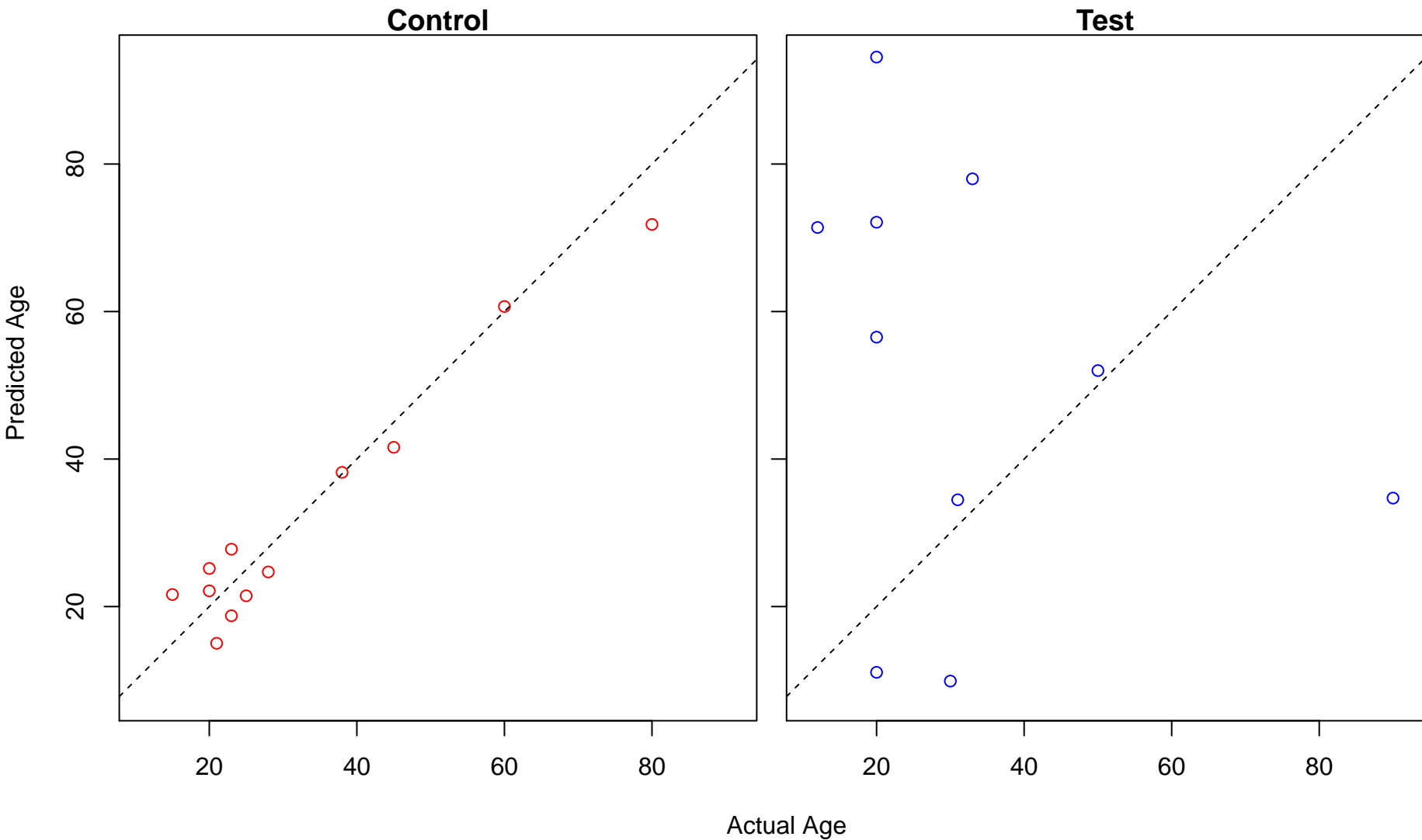
mitochondrial tRNA processing (Score: 56.707976)



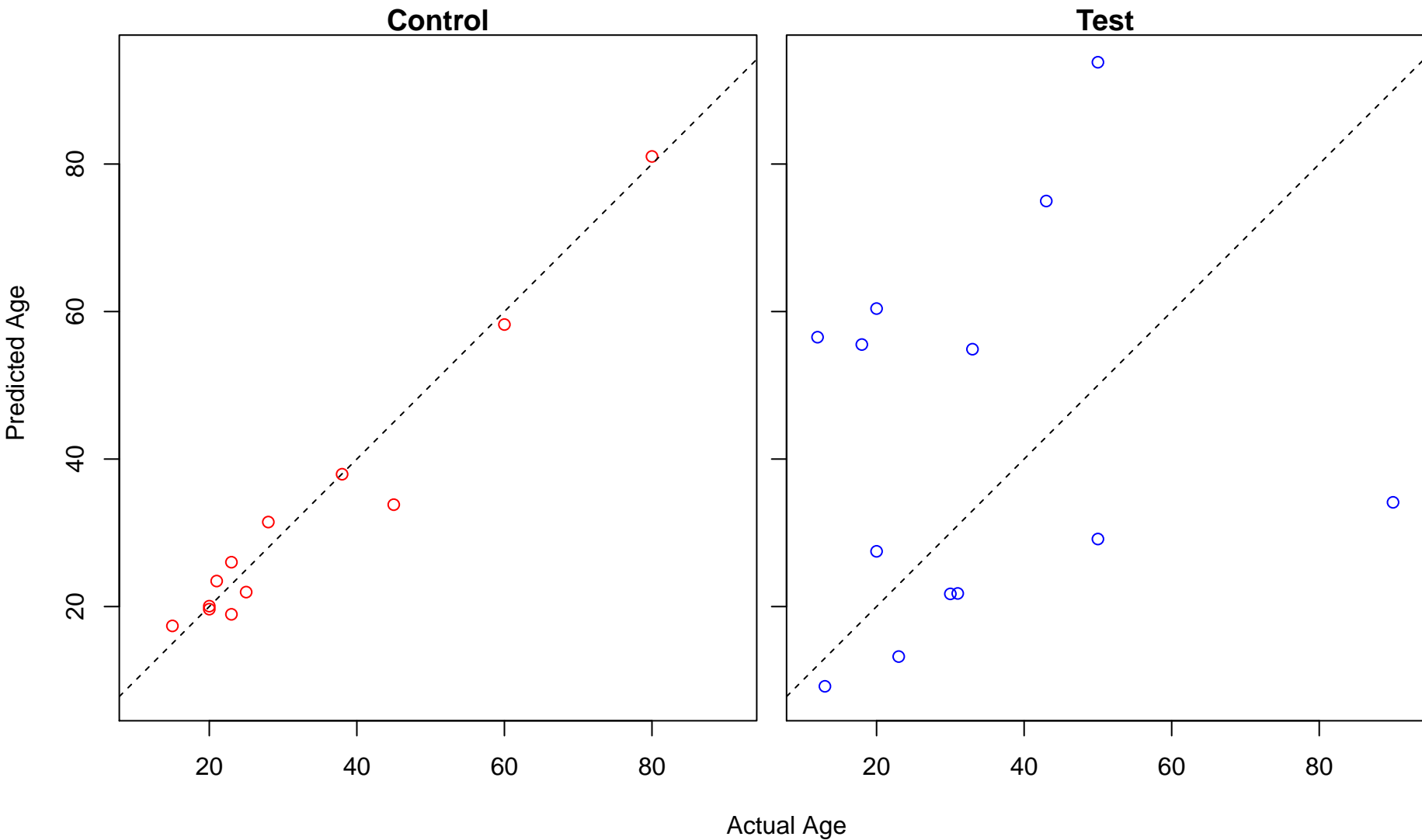
axis elongation (Score: 56.594257)



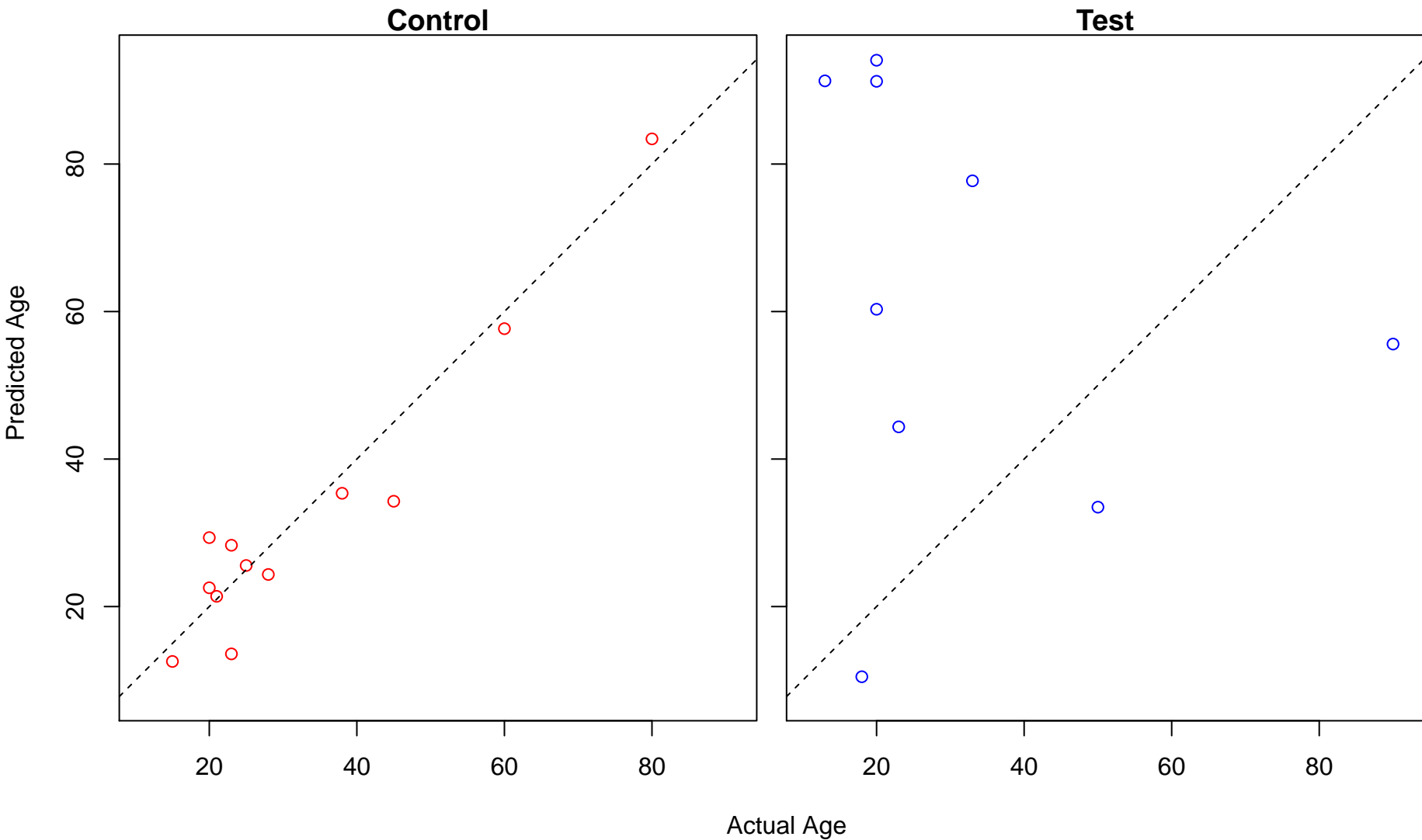
negative regulation of glial cell proliferation (Score: 56.320613)



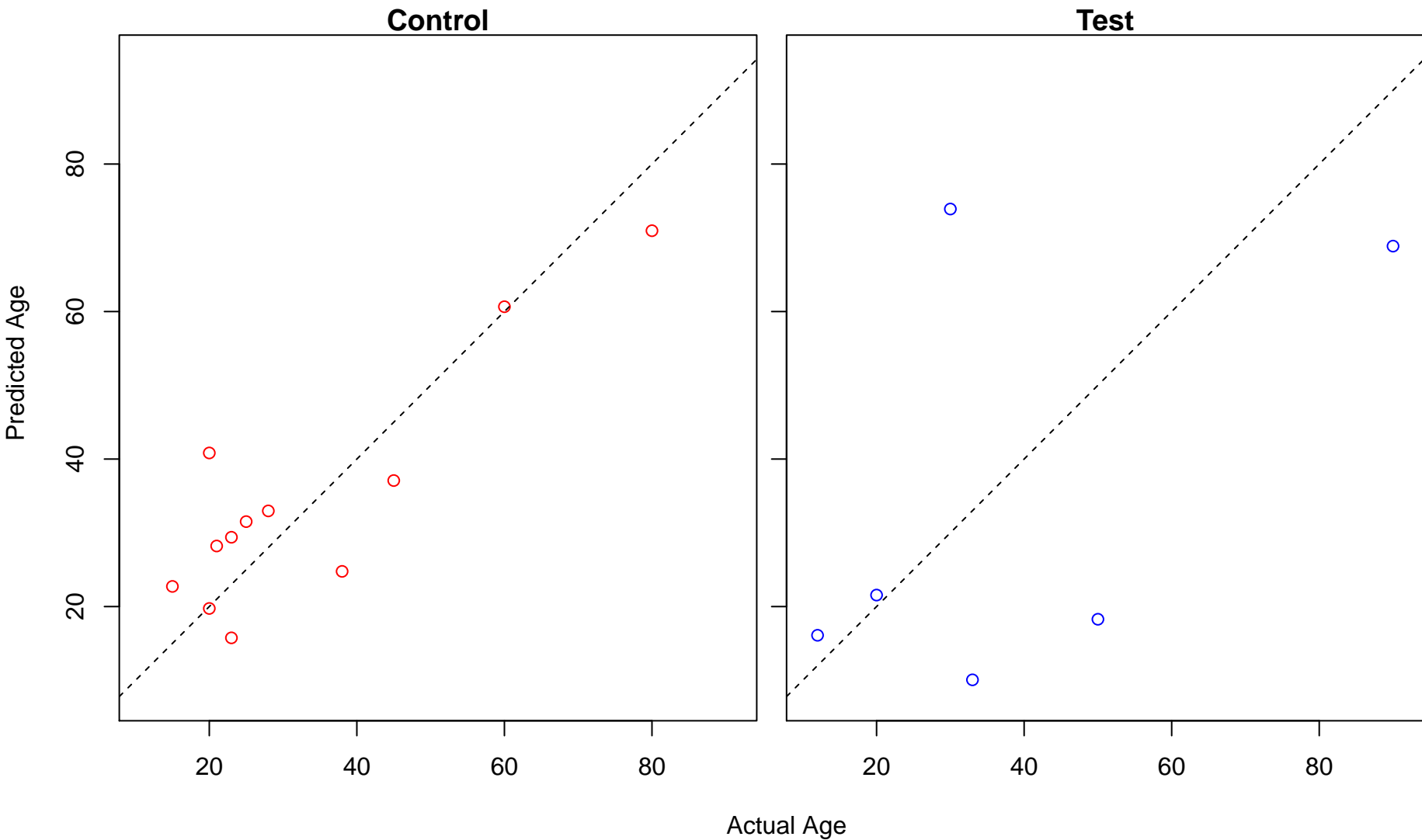
retinal metabolic process (Score: 55.467562)



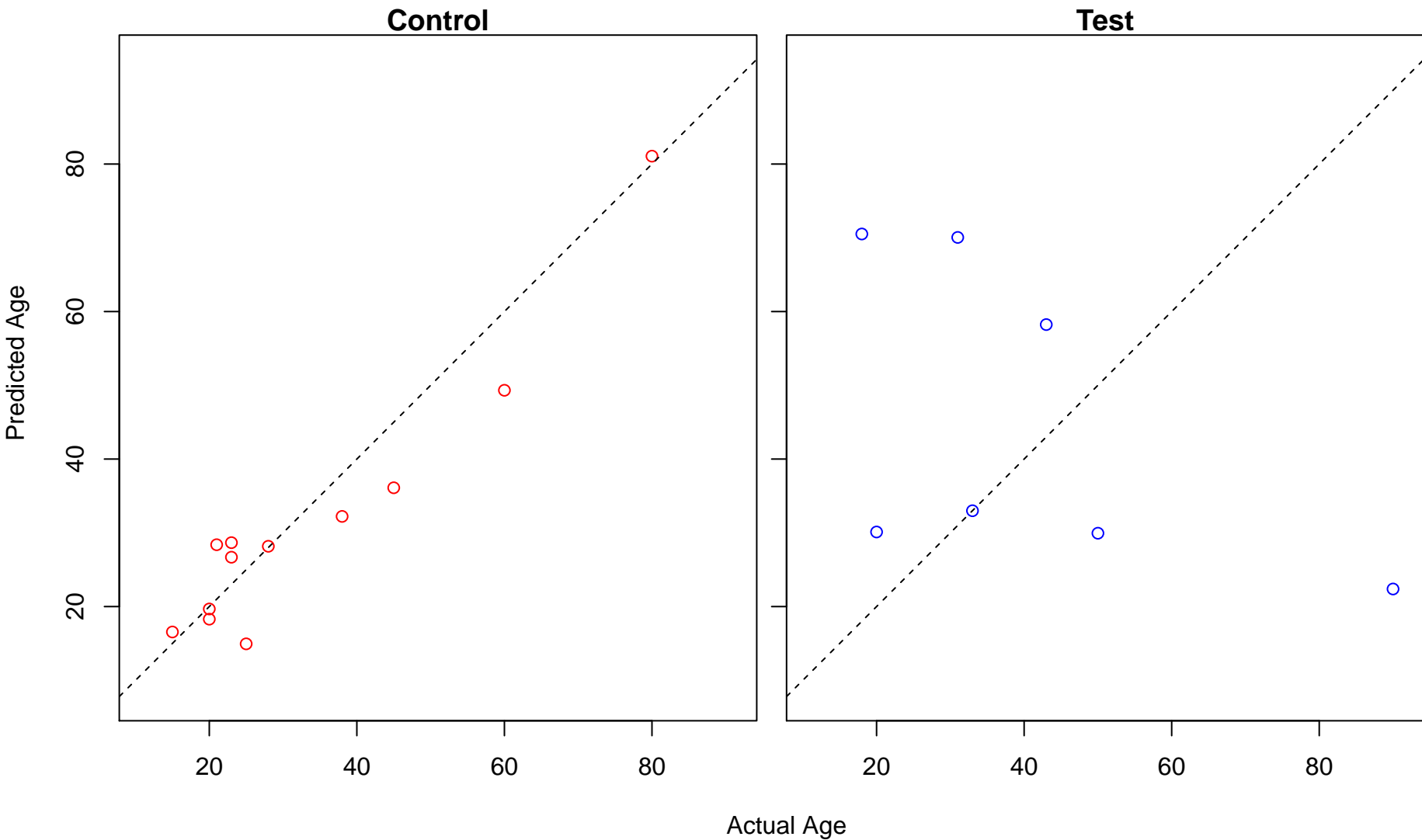
regulation of translation in response to stress (Score: 55.283857)



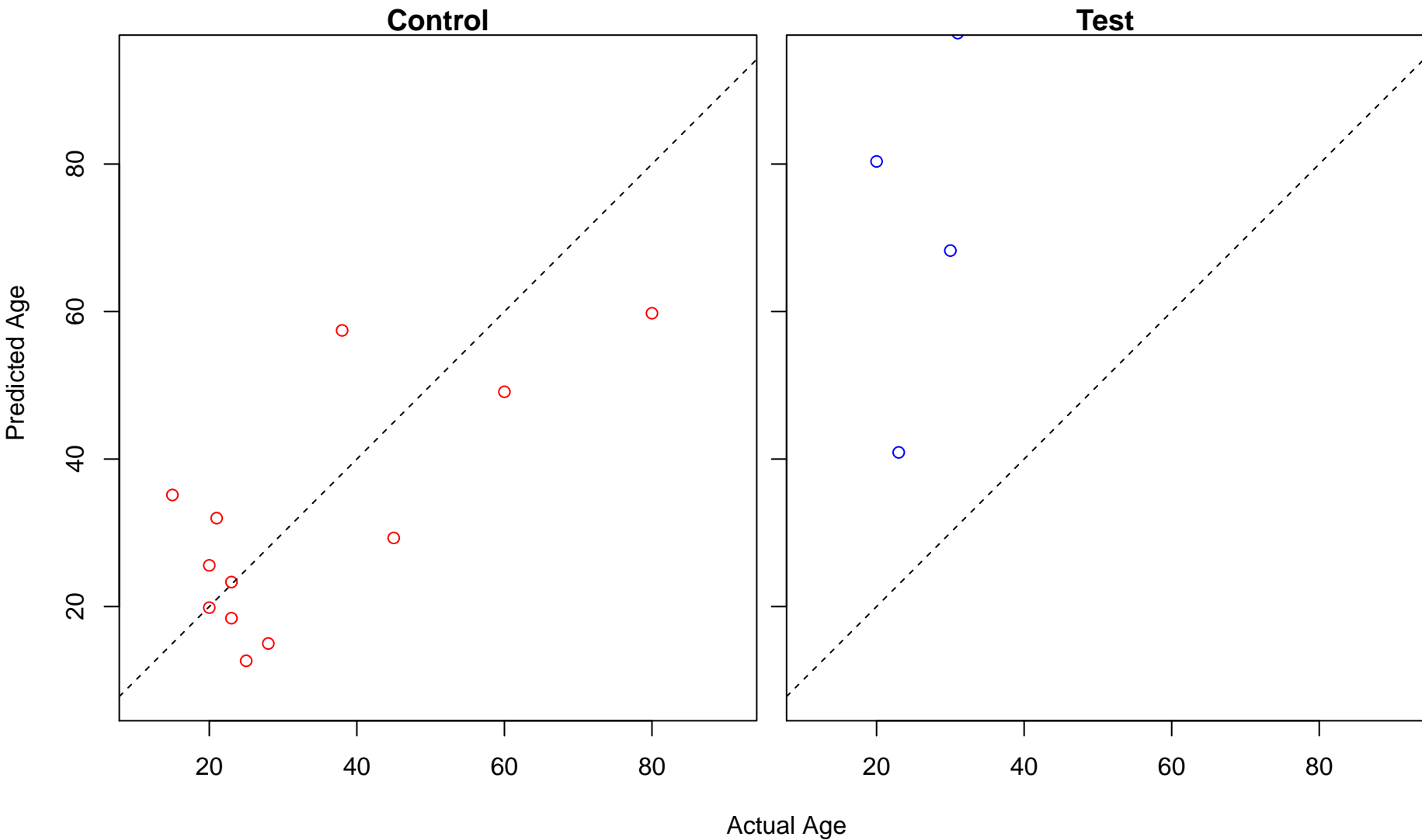
negative regulation of reactive oxygen species biosynthetic process (Score: 54.803012)



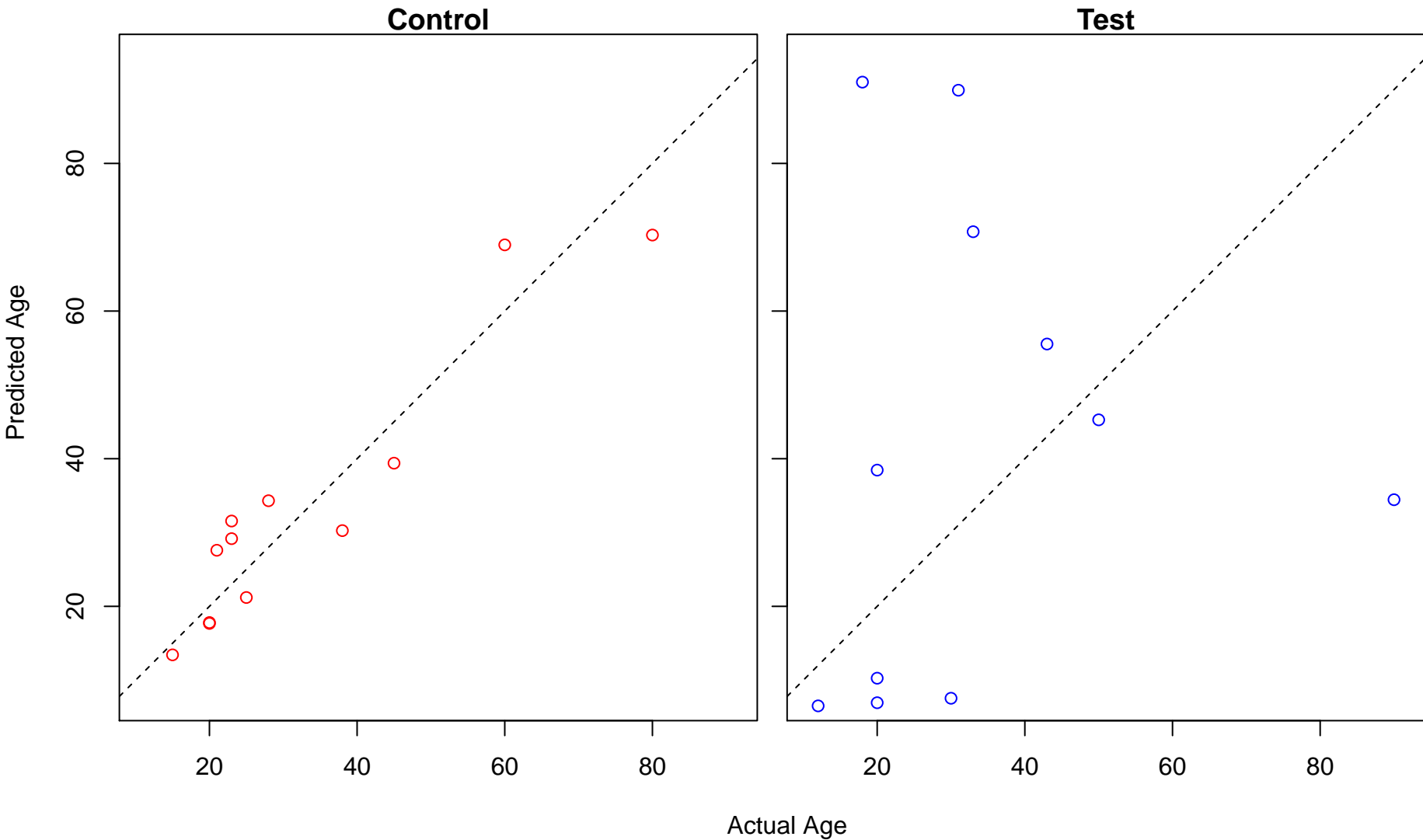
negative regulation of CD4-positive, alpha-beta T cell activation (Score: 54.627165)



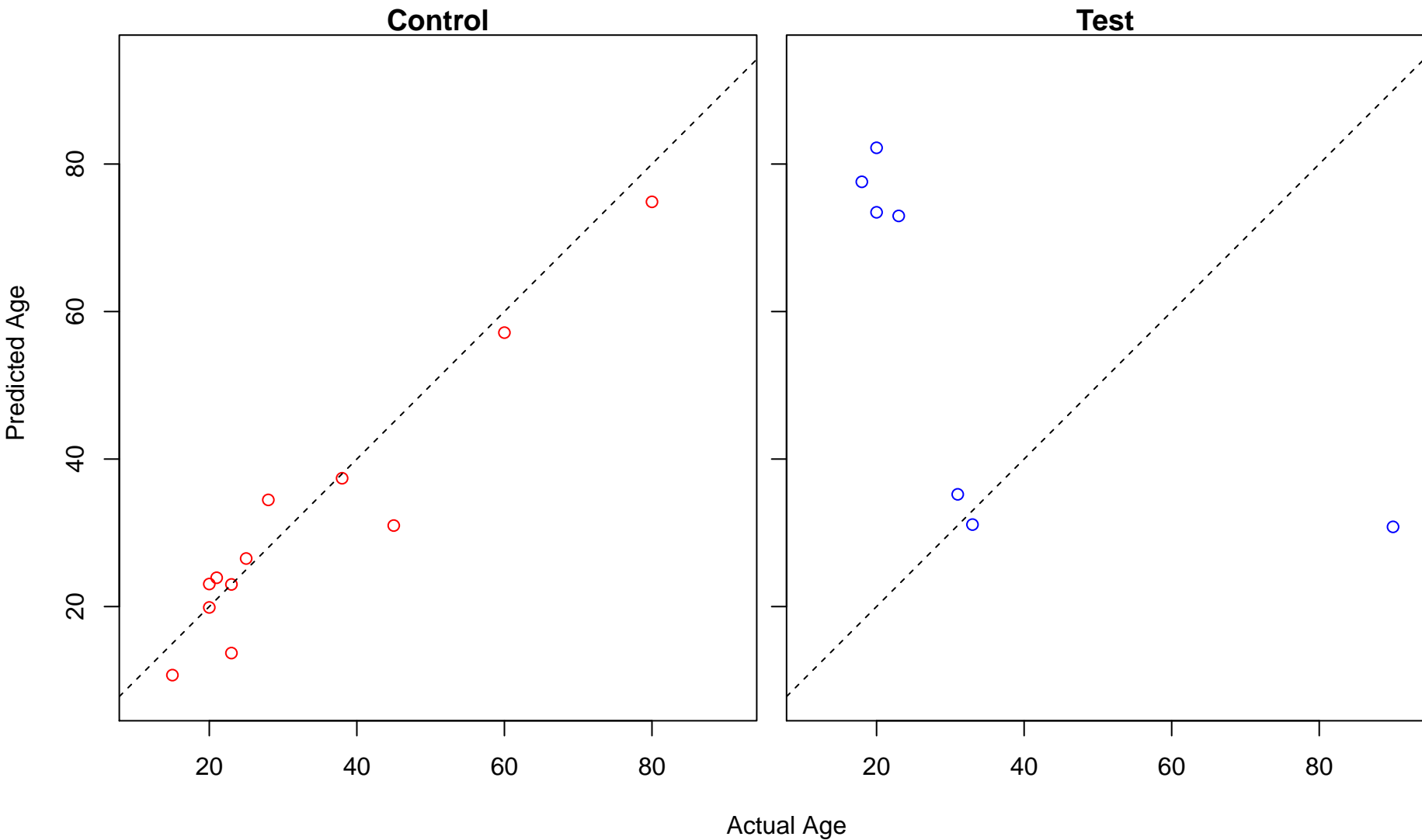
forelimb morphogenesis (Score: 54.522823)



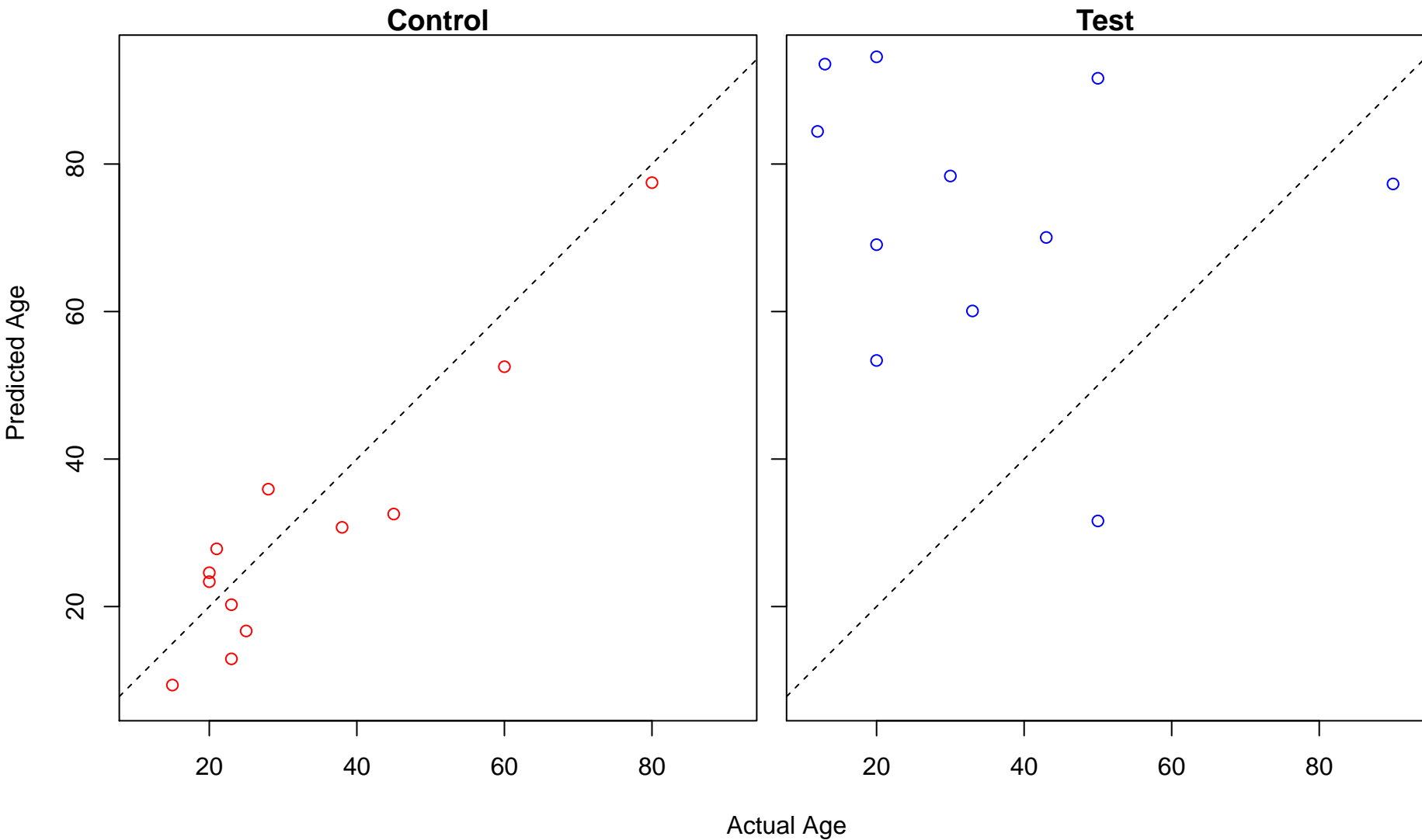
negative regulation of CD4-positive, alpha-beta T cell differentiation (Score: 53.809700)



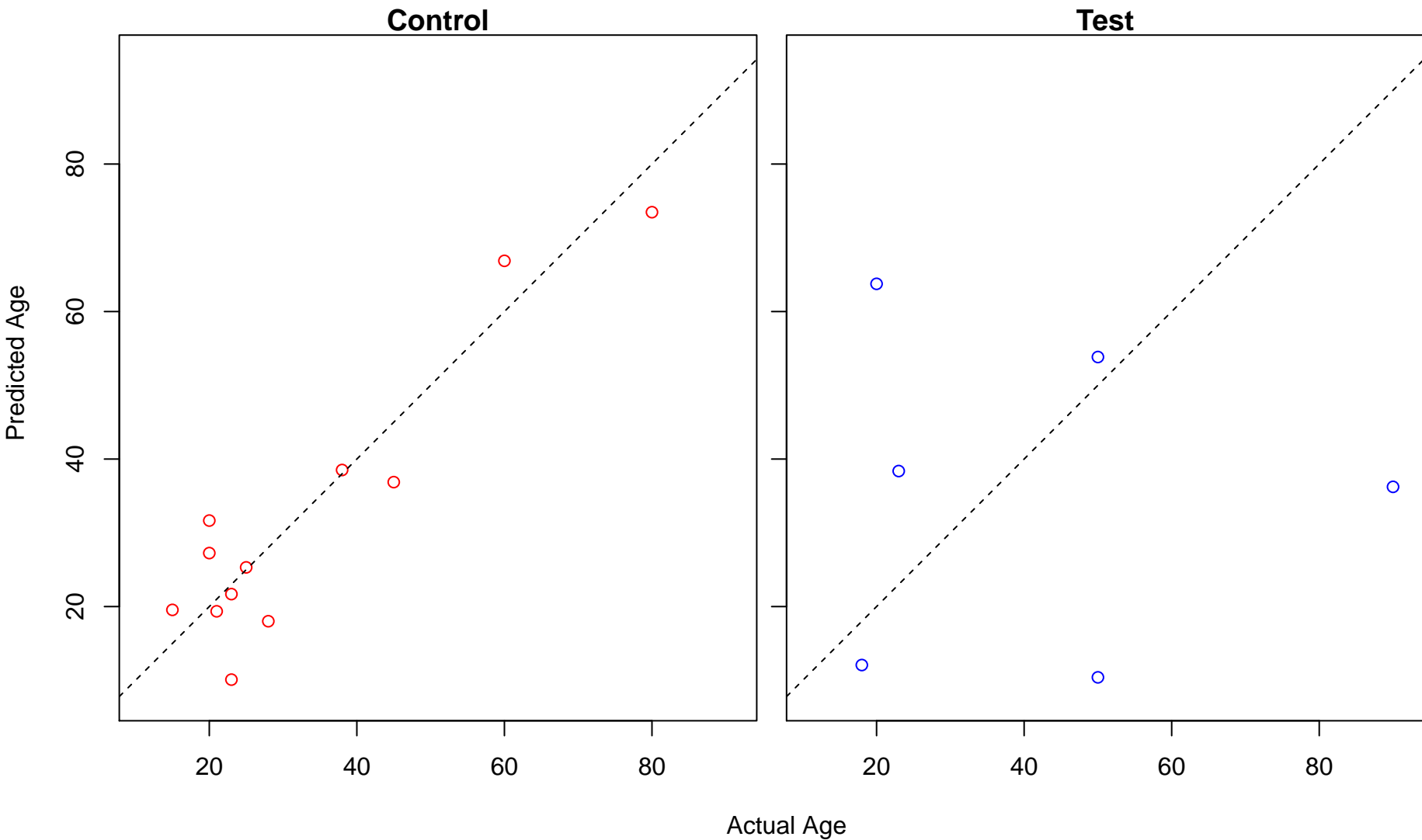
positive regulation of activated T cell proliferation (Score: 53.686749)



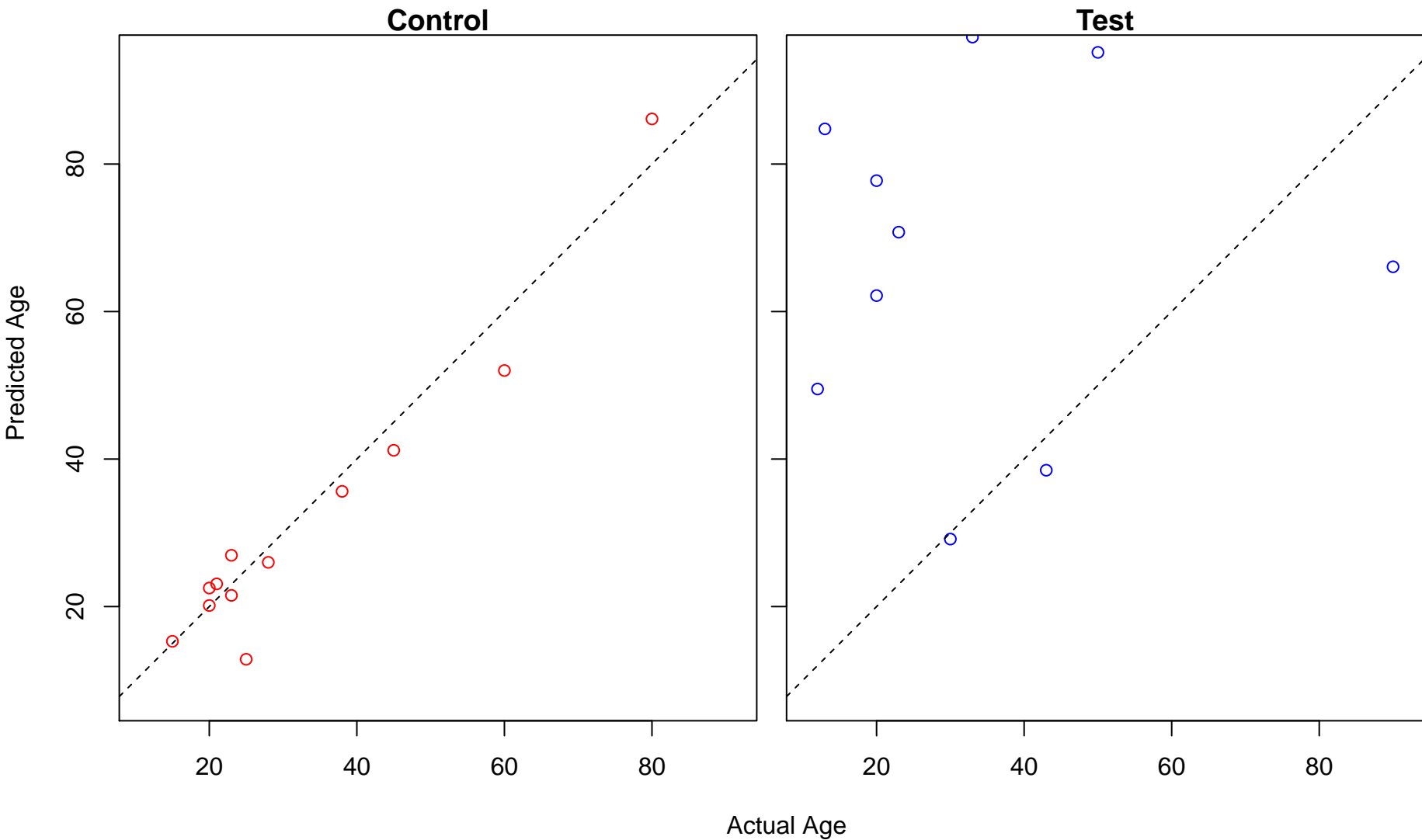
regulation of gastrulation (Score: 53.269388)



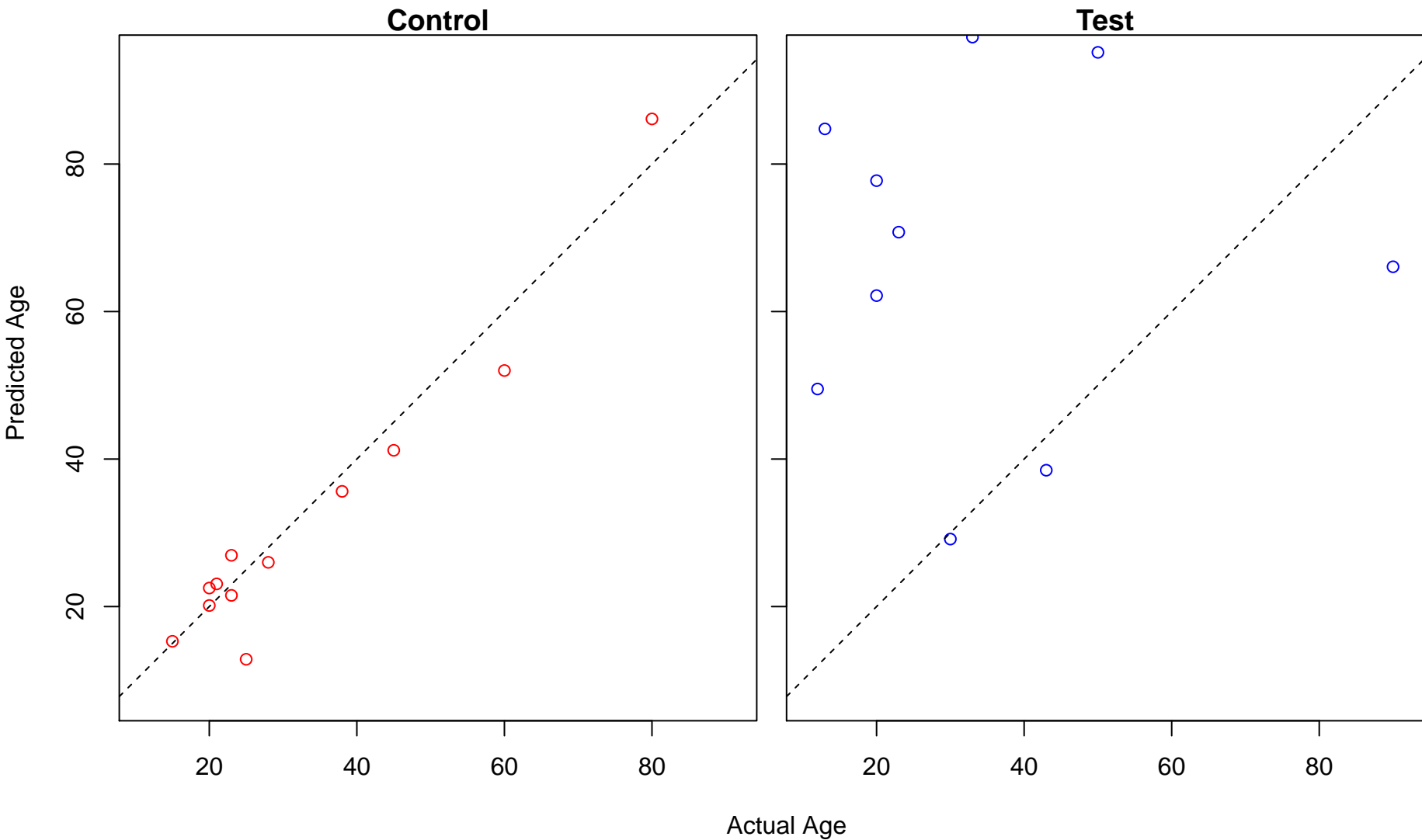
regulation of translational initiation in response to stress (Score: 53.183387)



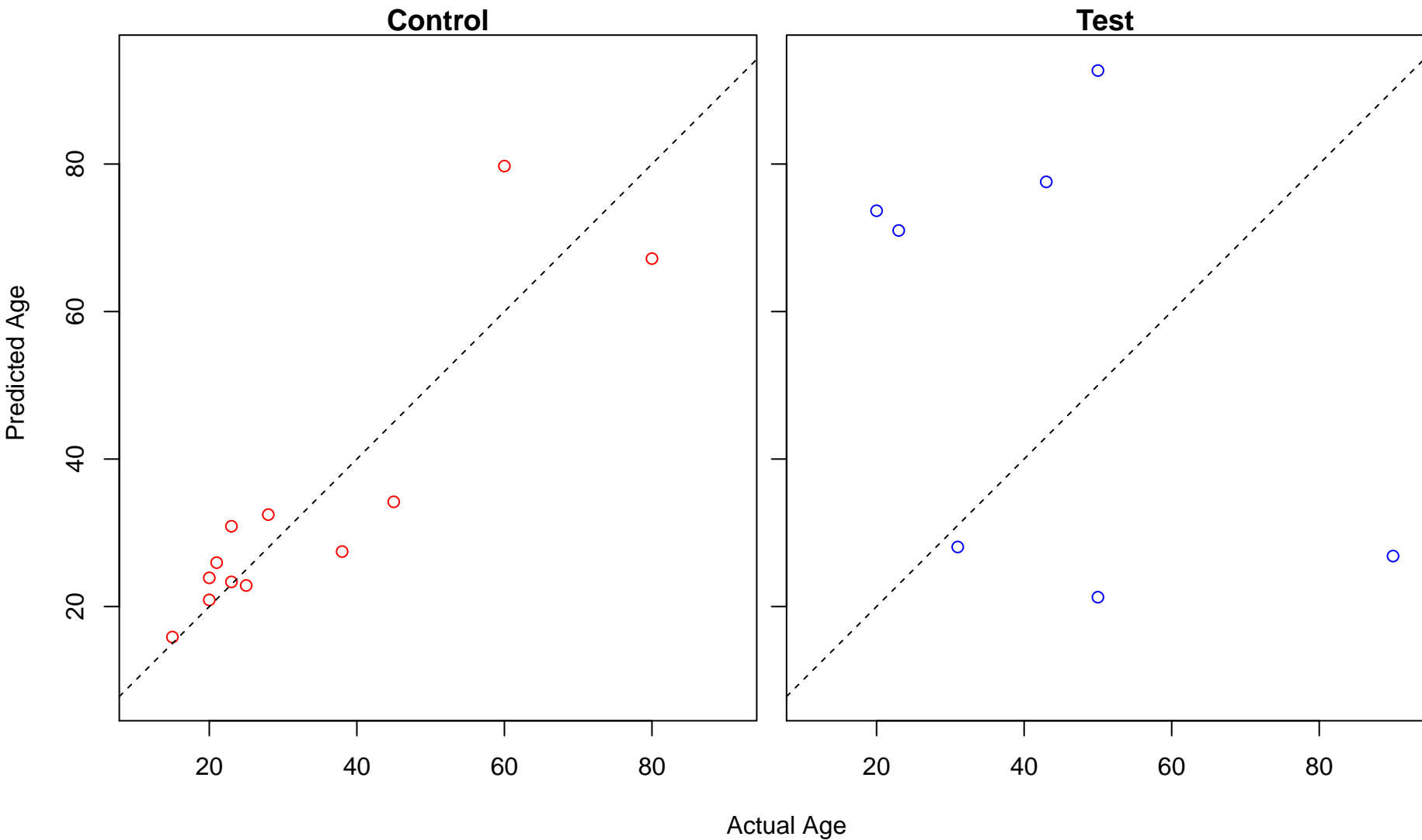
positive regulation of JAK-STAT cascade (Score: 52.724238)



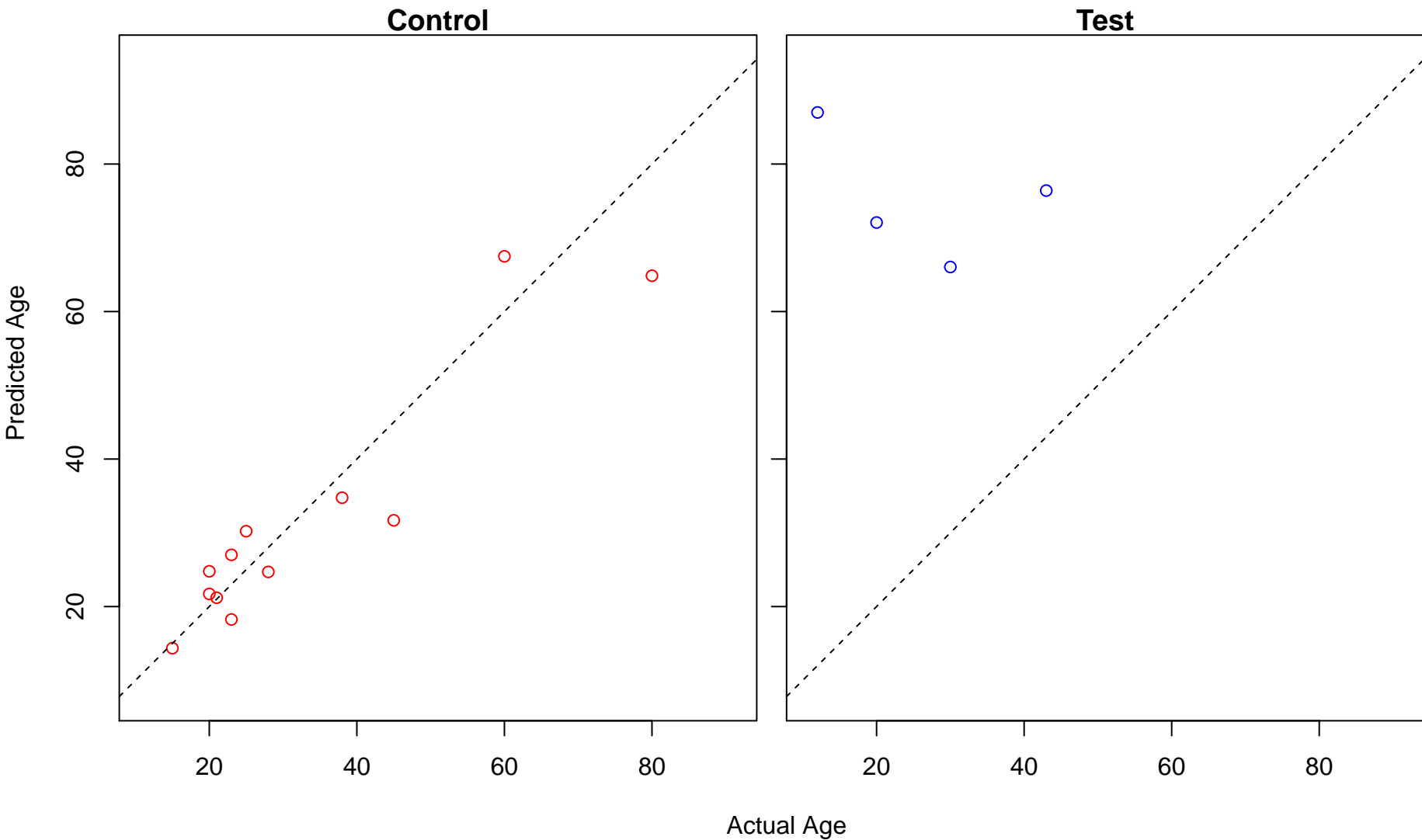
positive regulation of STAT cascade (Score: 52.724238)



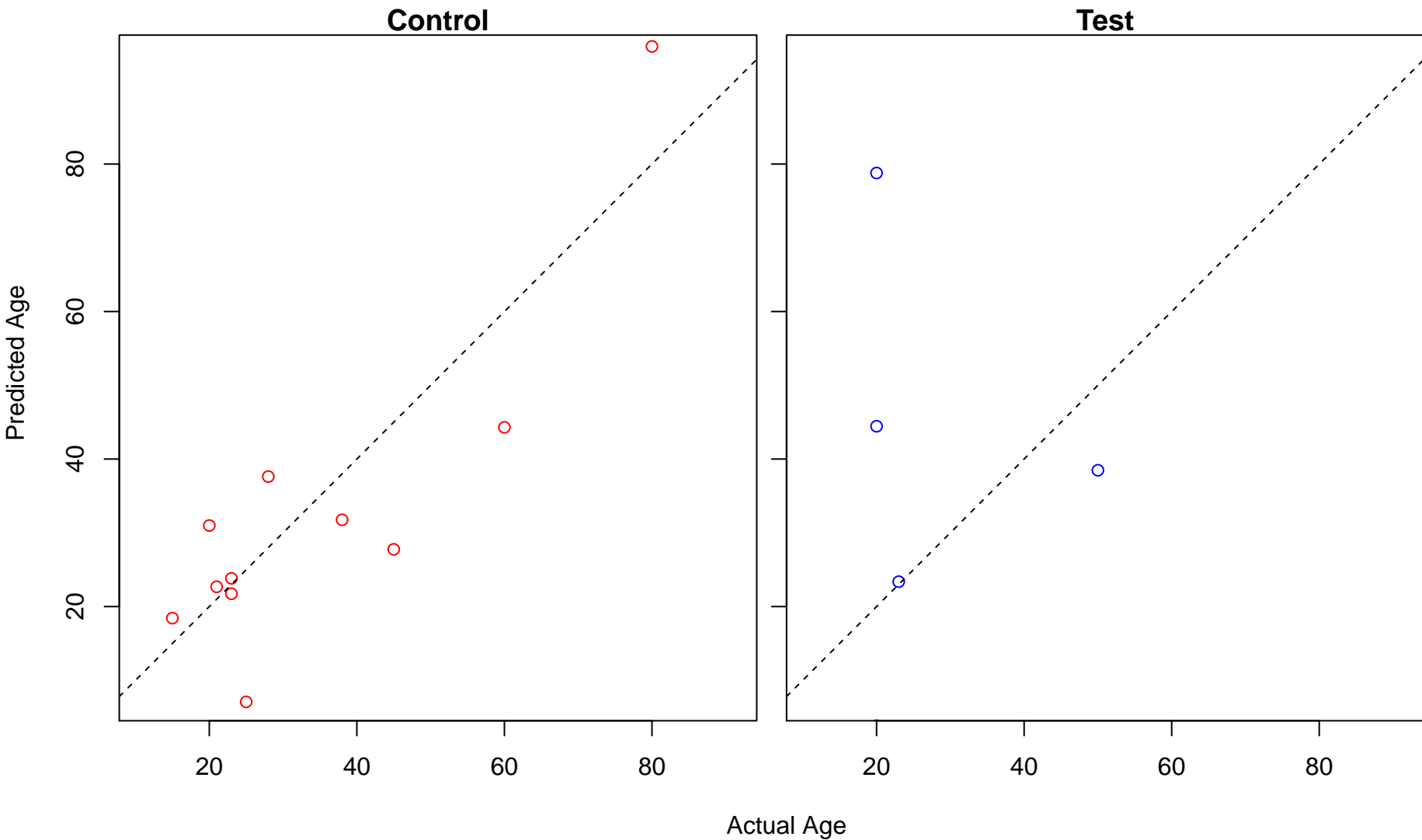
N-terminal protein amino acid modification (Score: 52.723771)



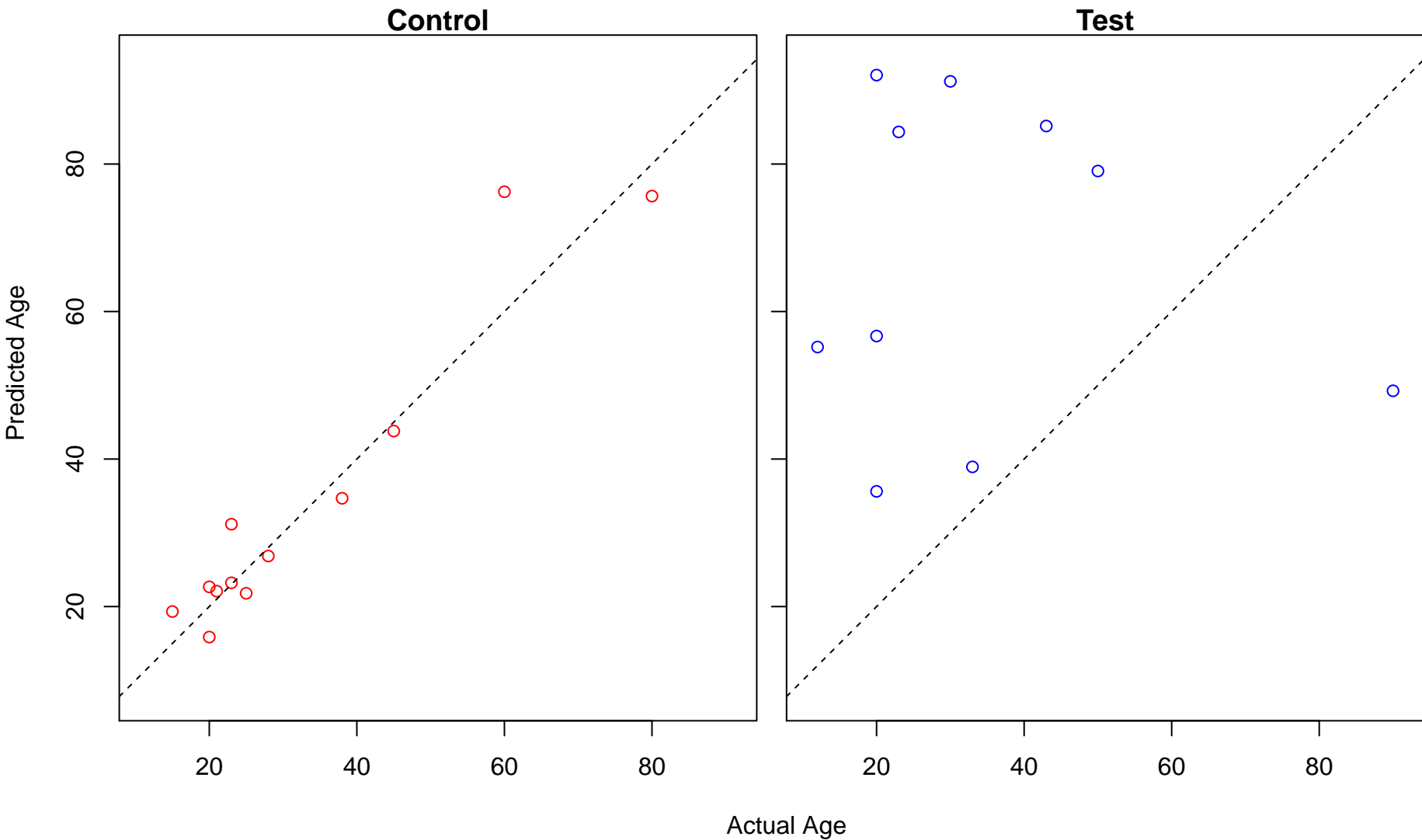
phosphatidylserine acyl-chain remodeling (Score: 52.288932)



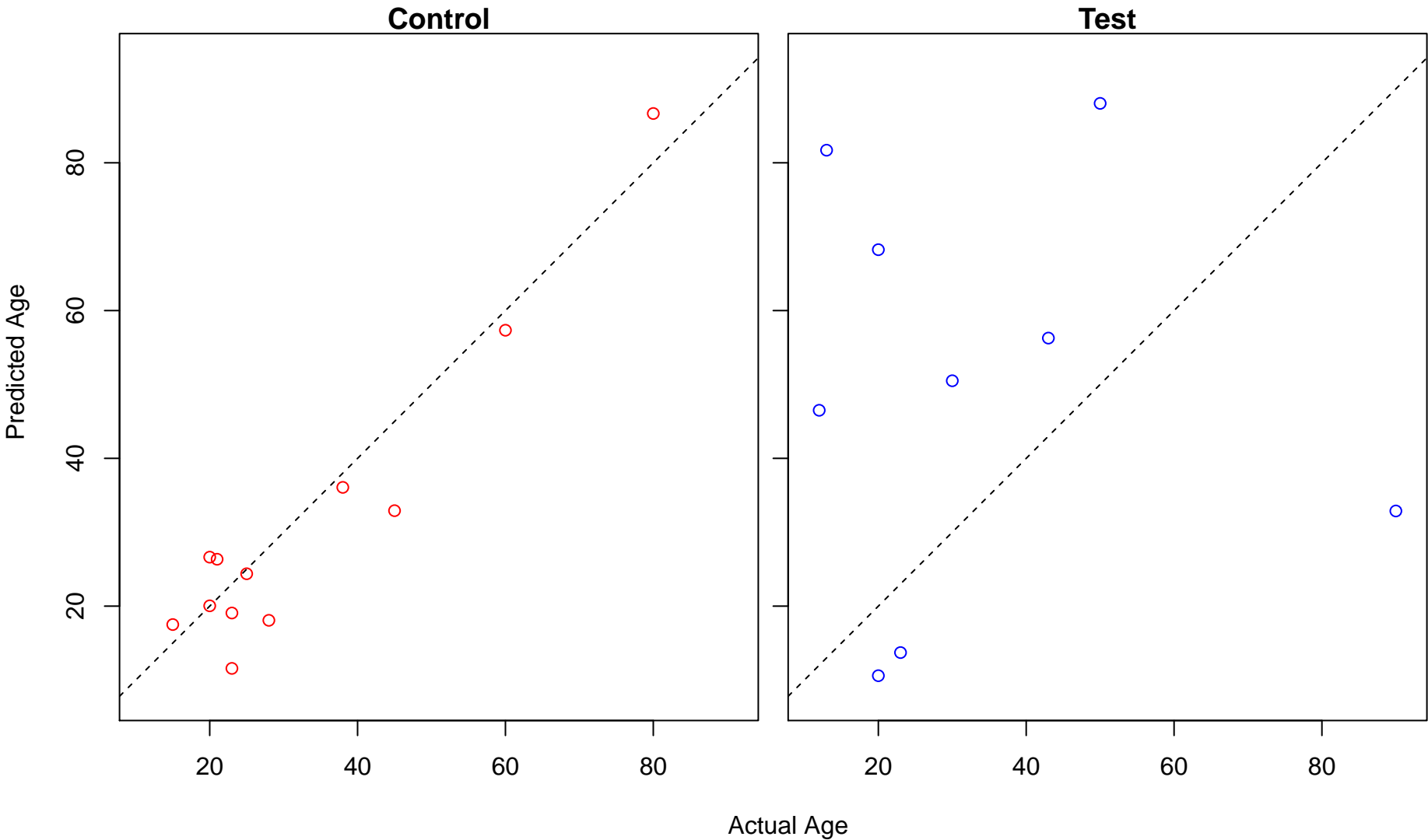
positive regulation of glomerulus development (Score: 52.230013)



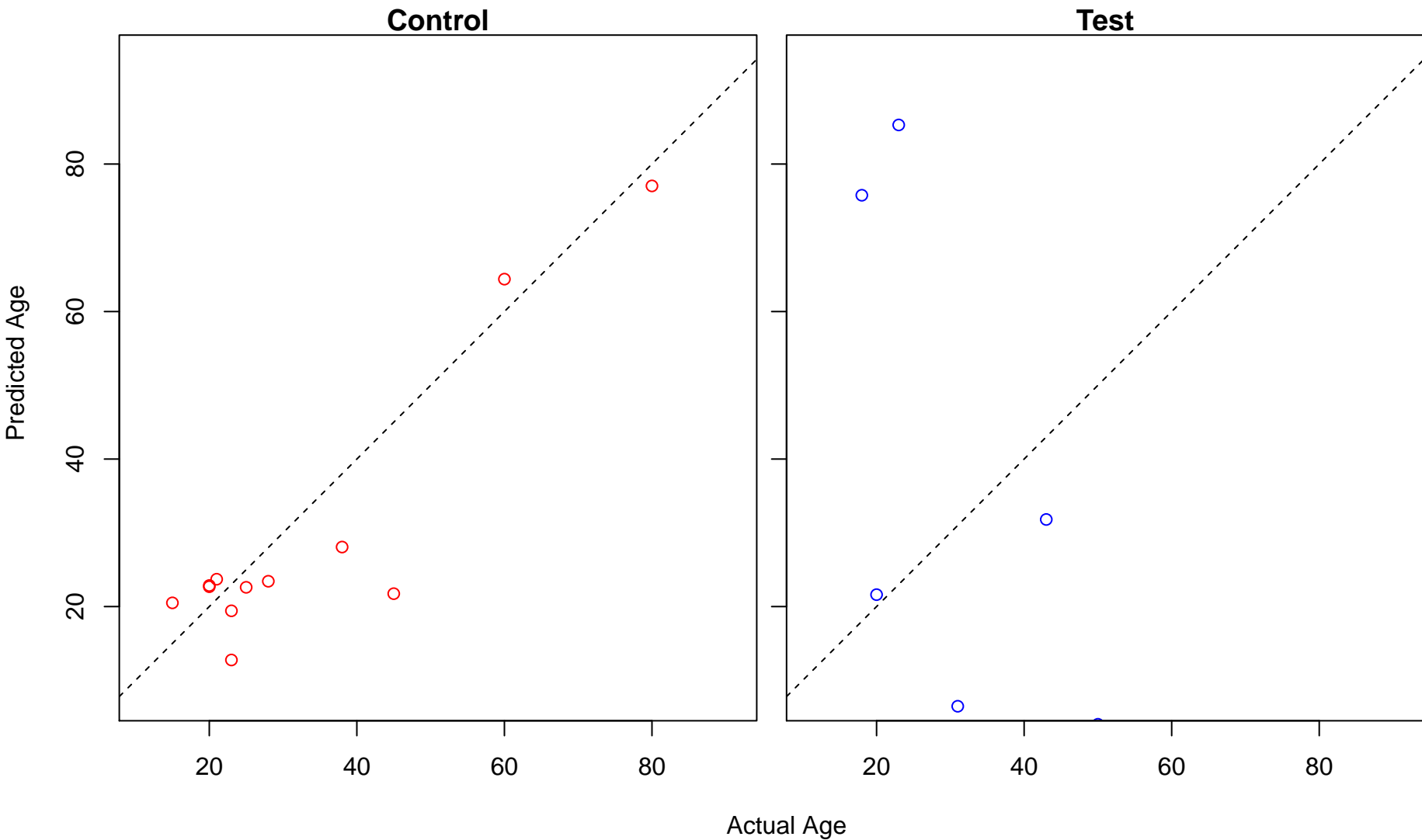
negative regulation of neurotransmitter transport (Score: 52.186701)



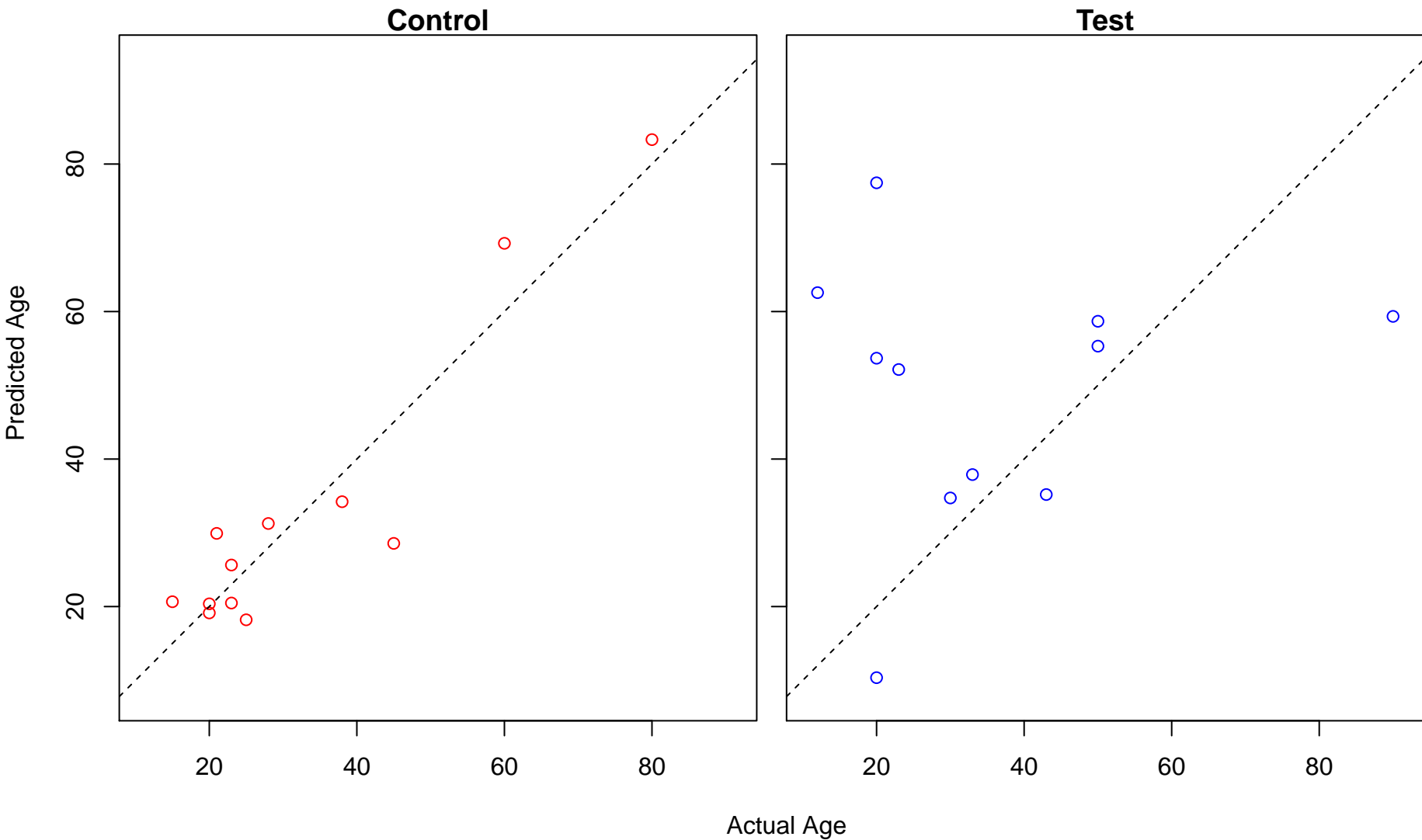
positive regulation of establishment of protein localization to plasma membrane (Score: 52.112899)



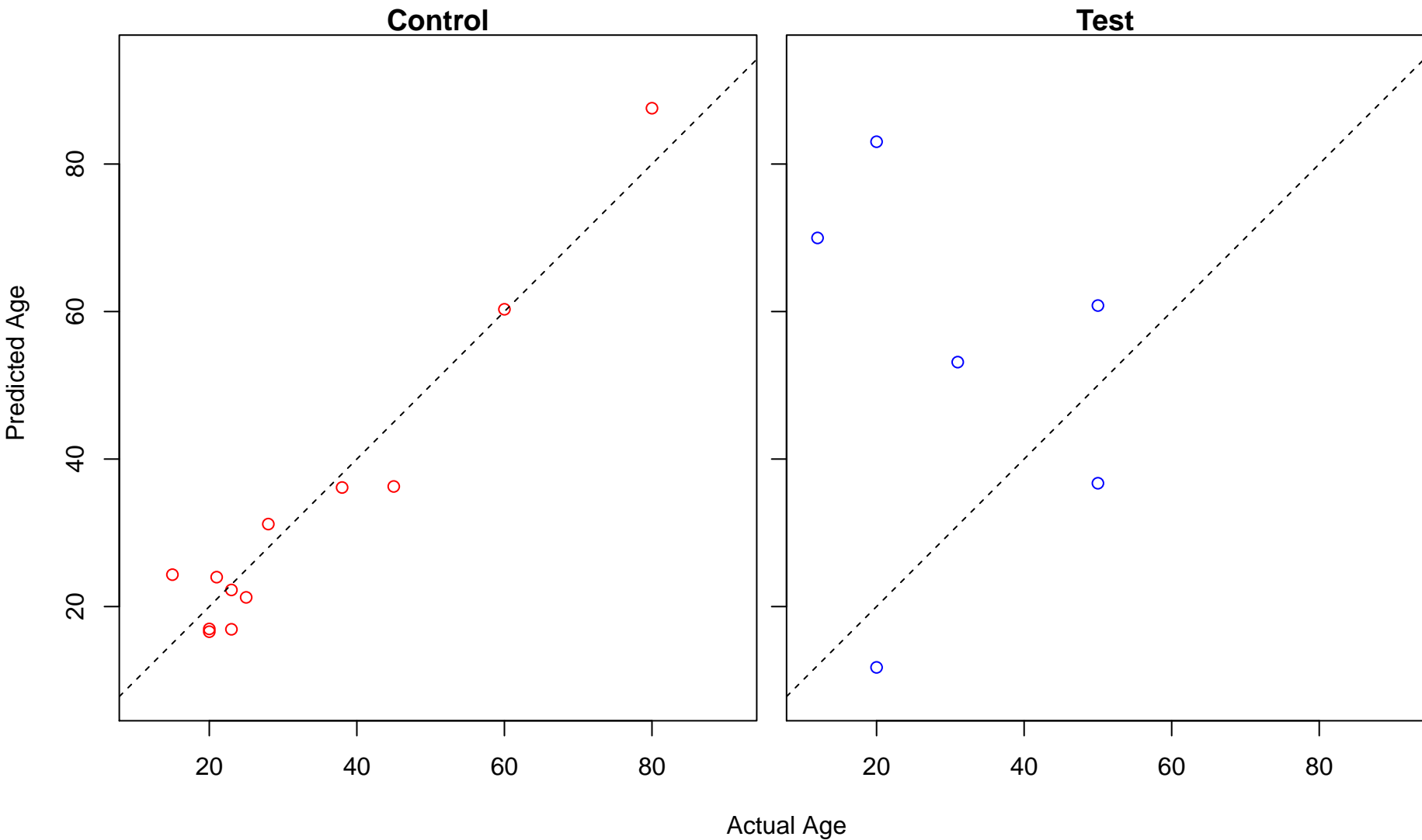
negative regulation of ATPase activity (Score: 52.104206)



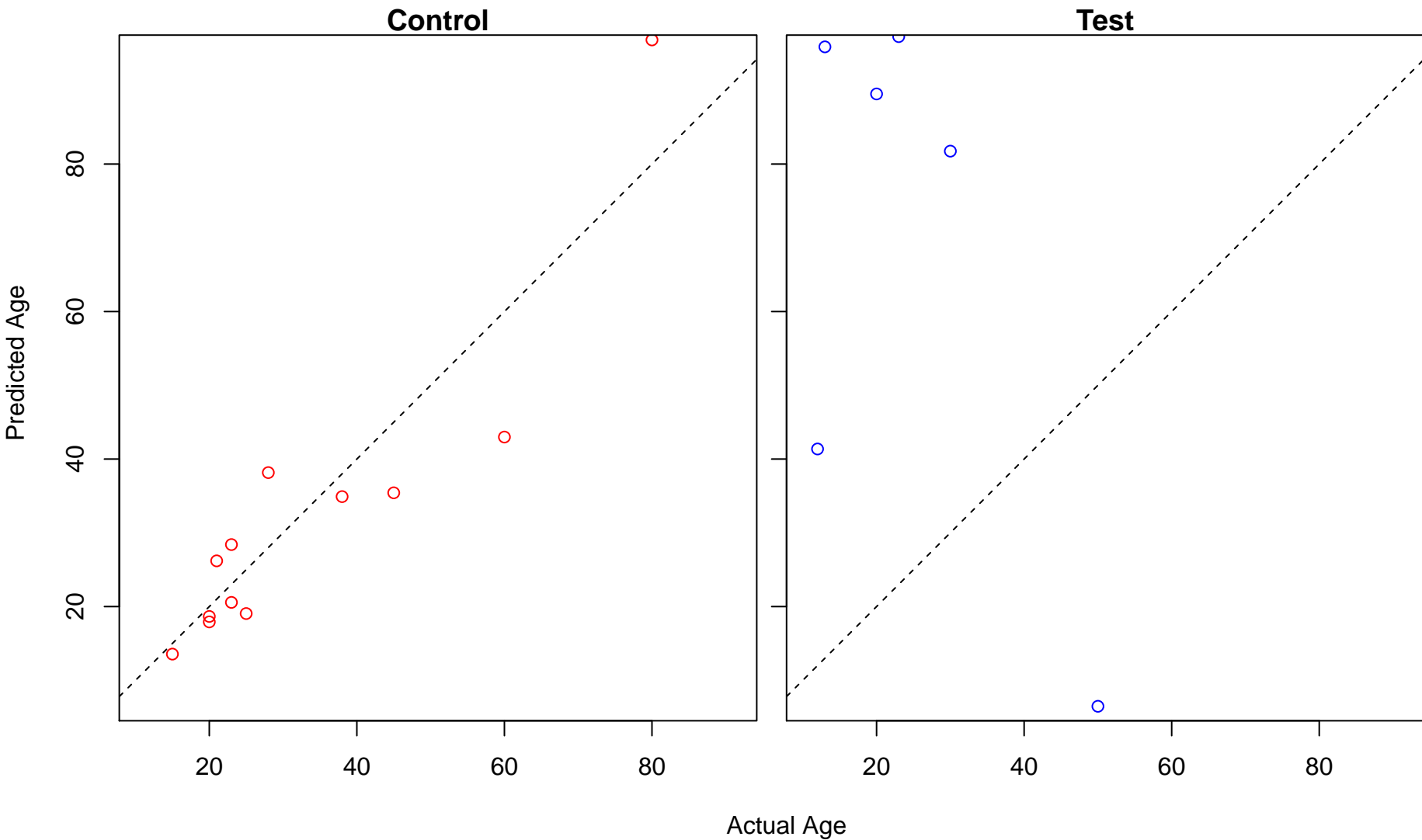
response to glucocorticoid (Score: 52.066391)



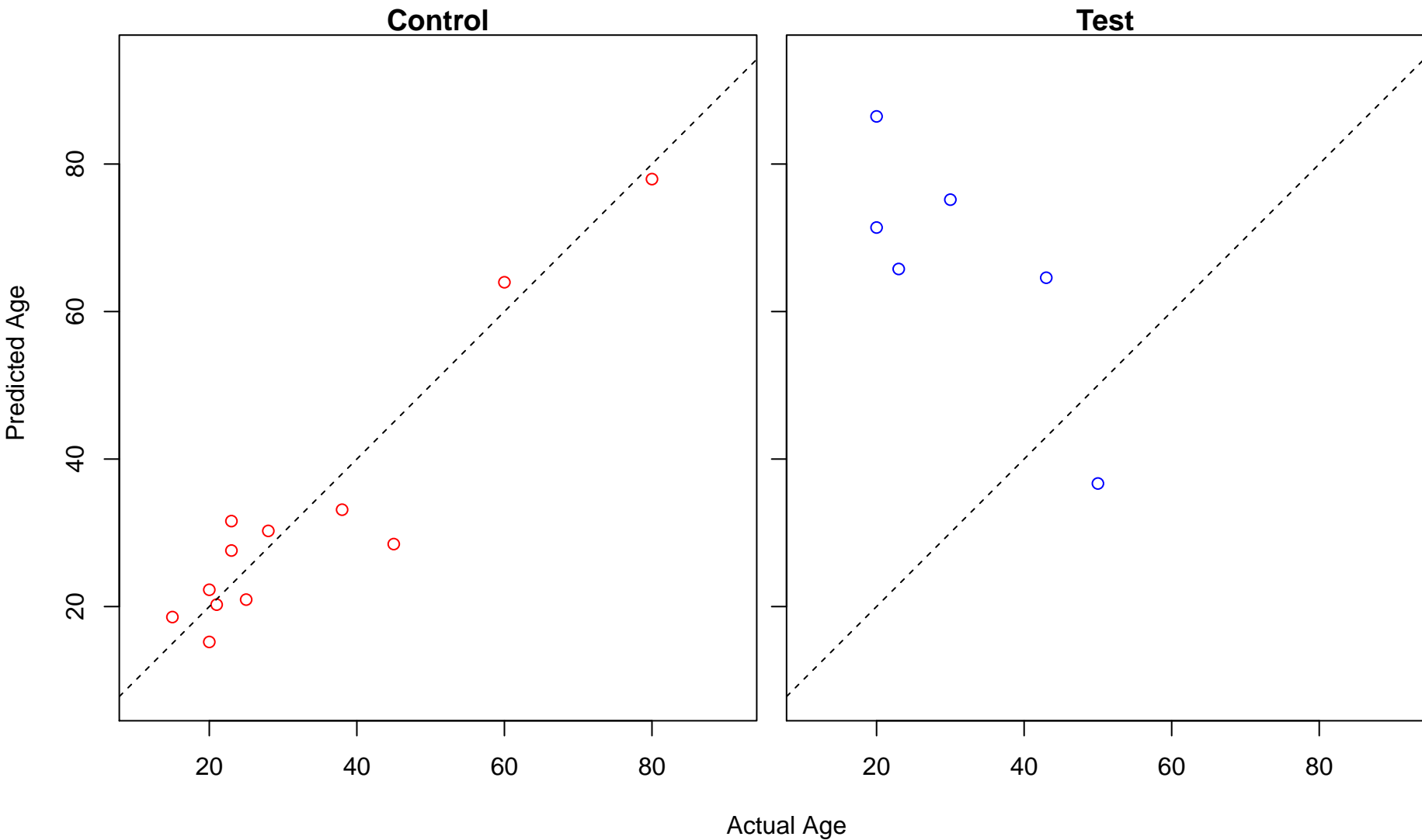
negative regulation of amine transport (Score: 51.914771)



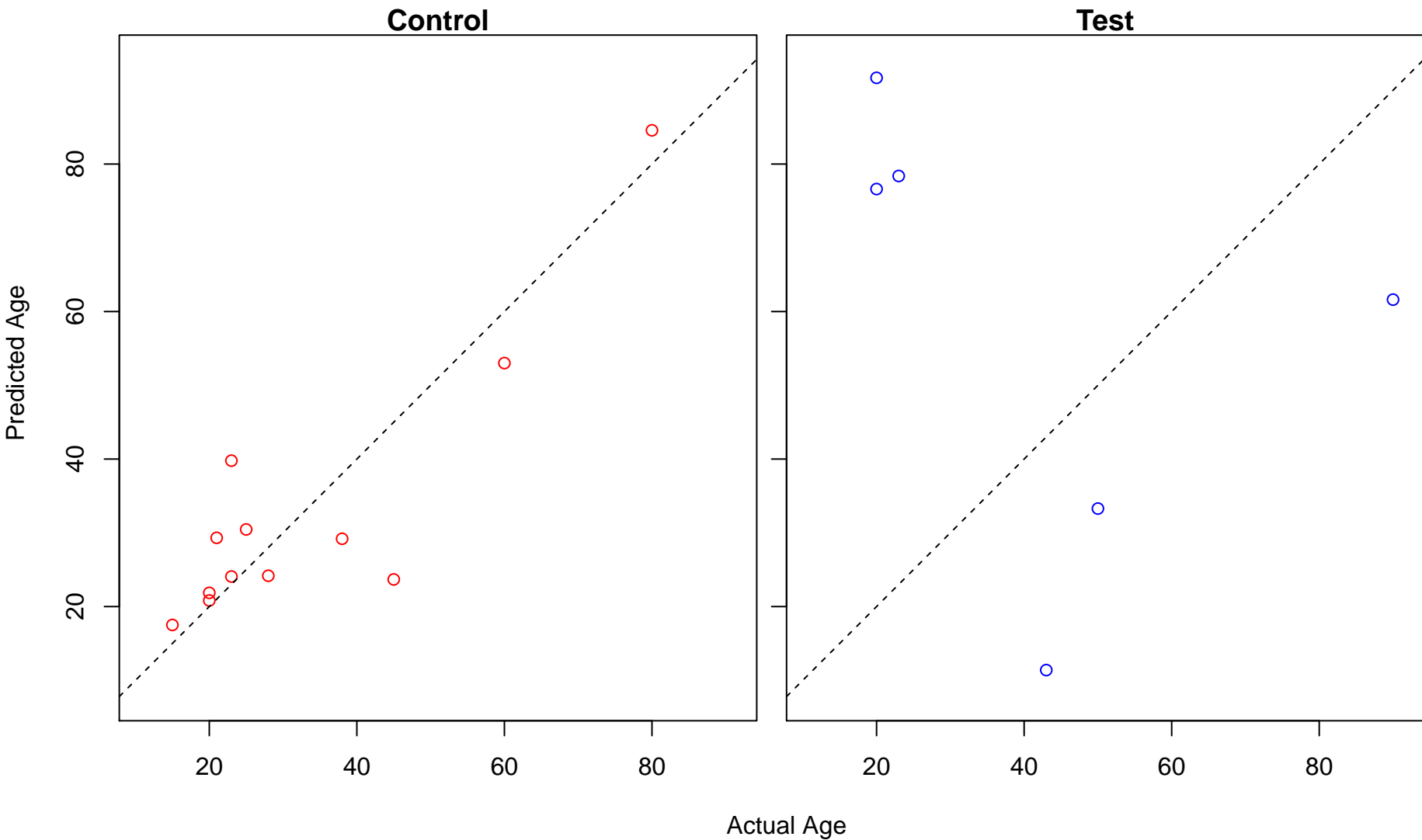
retrograde axonal transport (Score: 51.561185)



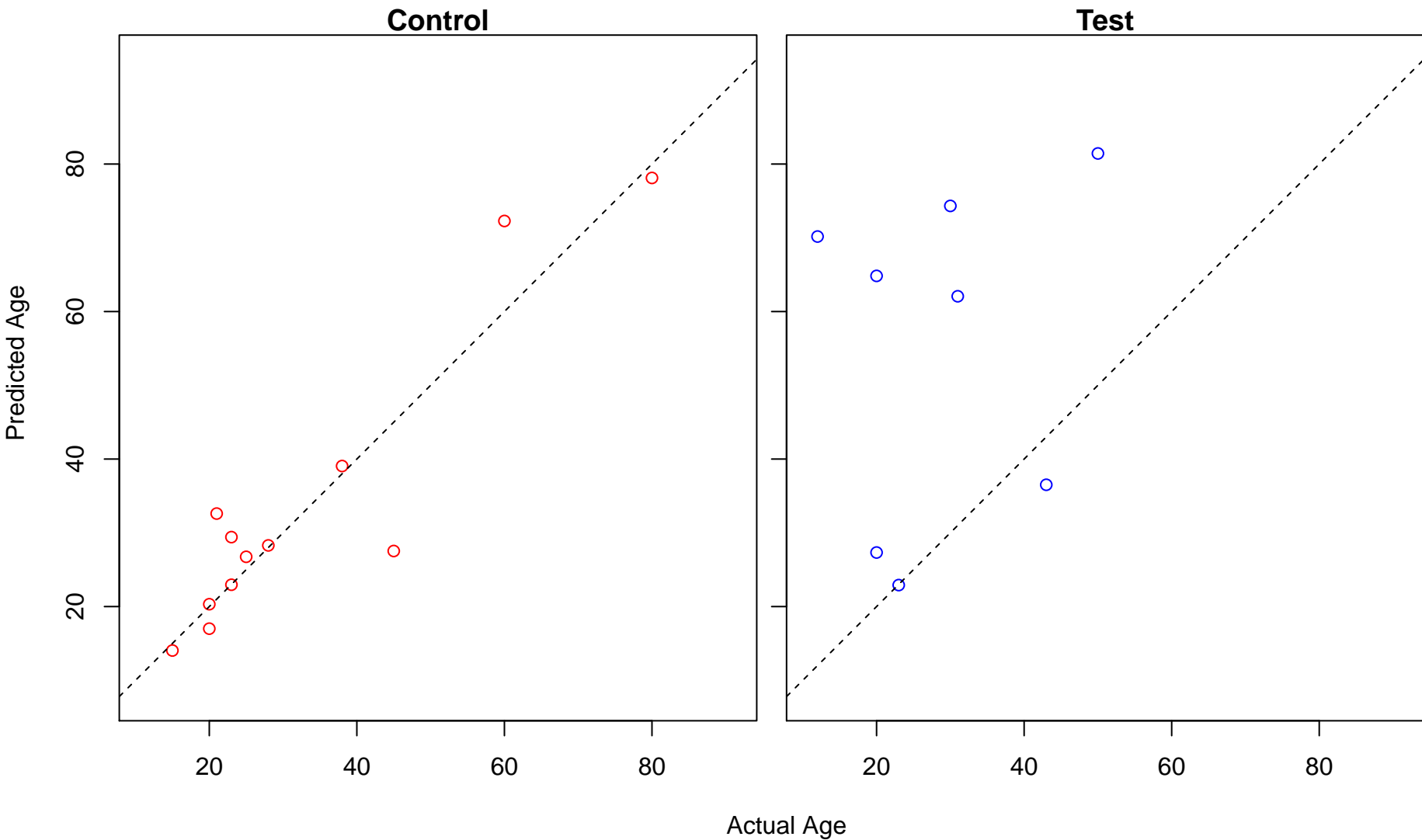
regulation of B cell receptor signaling pathway (Score: 51.426507)



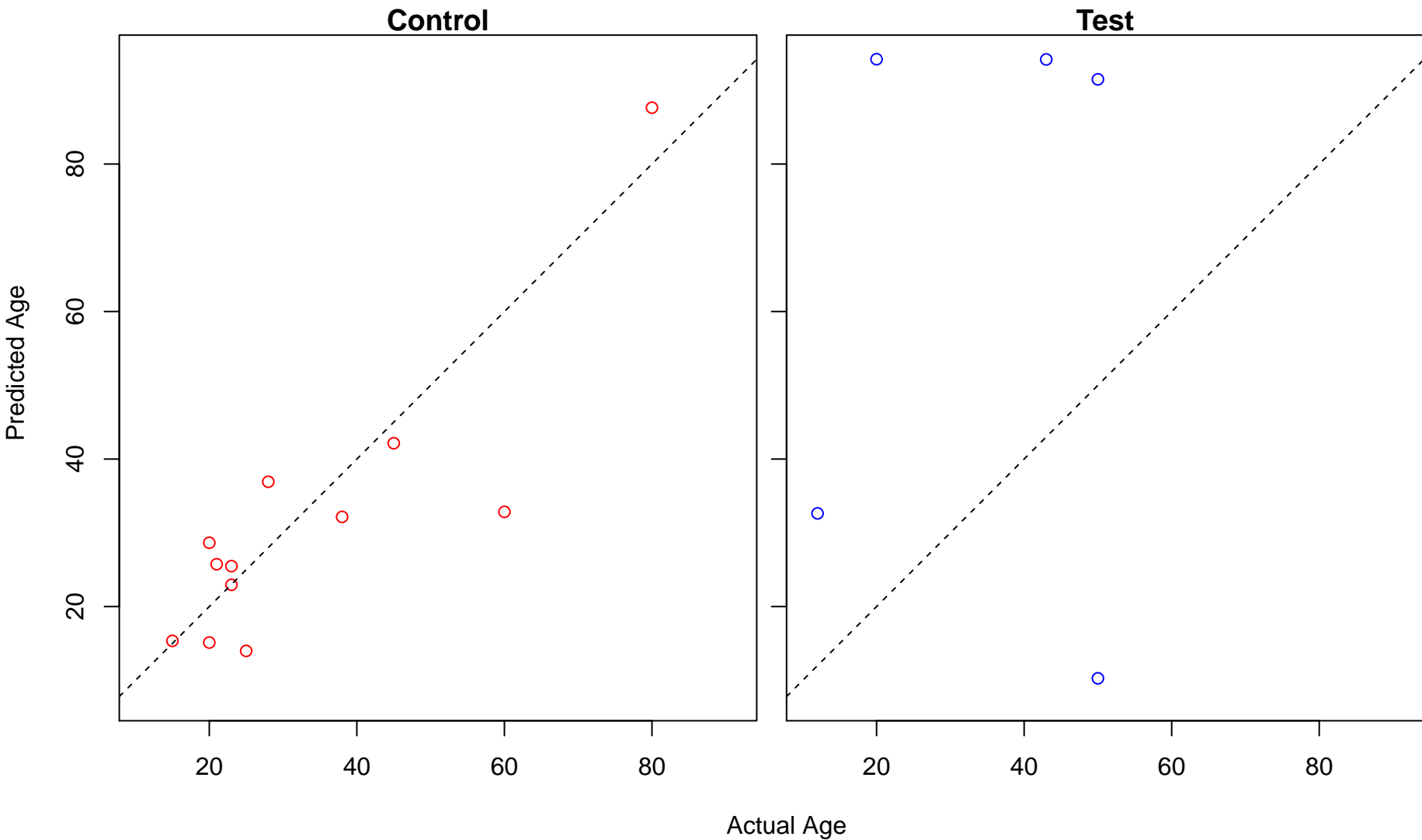
regulation of cholesterol efflux (Score: 51.231917)



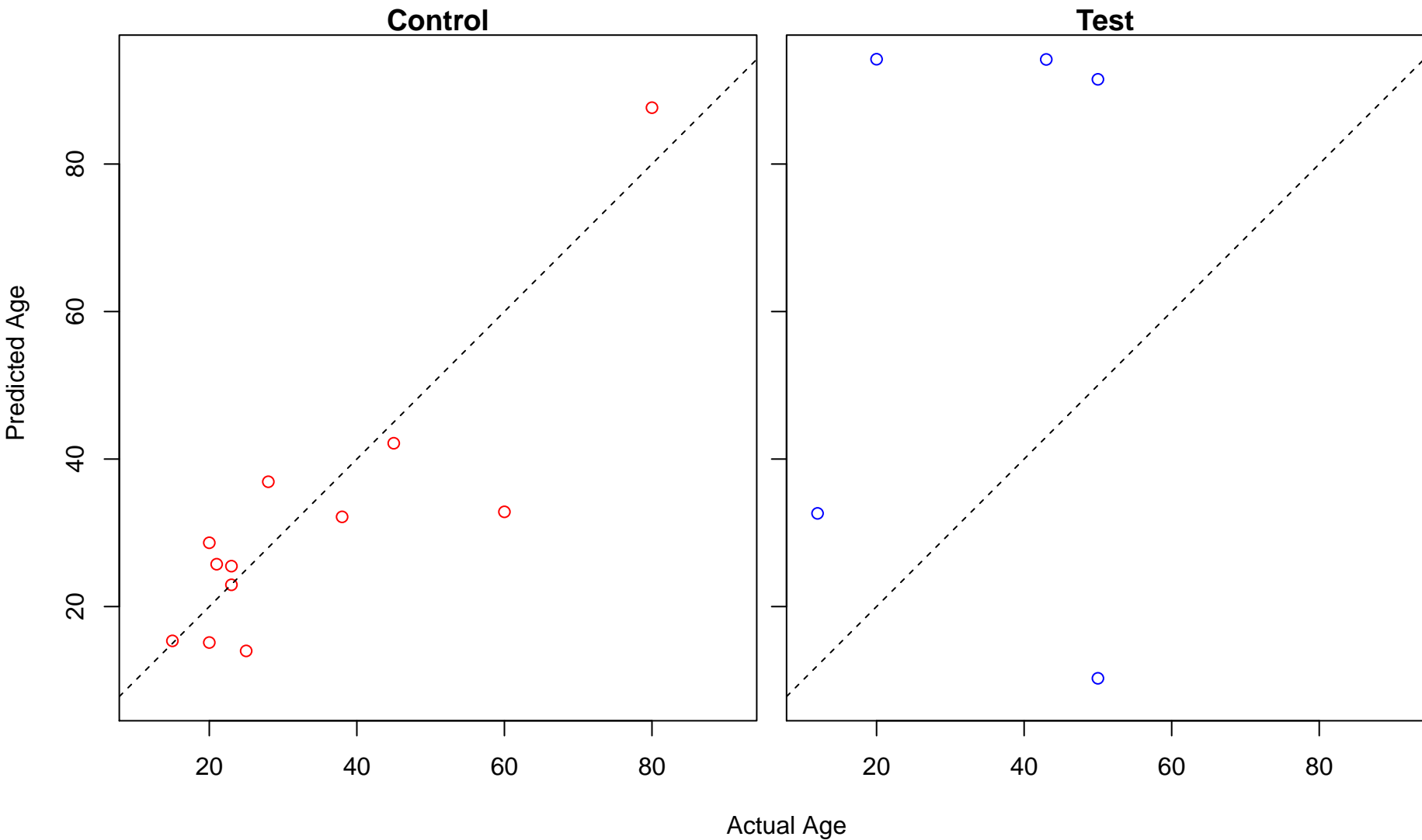
substrate-dependent cell migration, cell extension (Score: 51.094413)



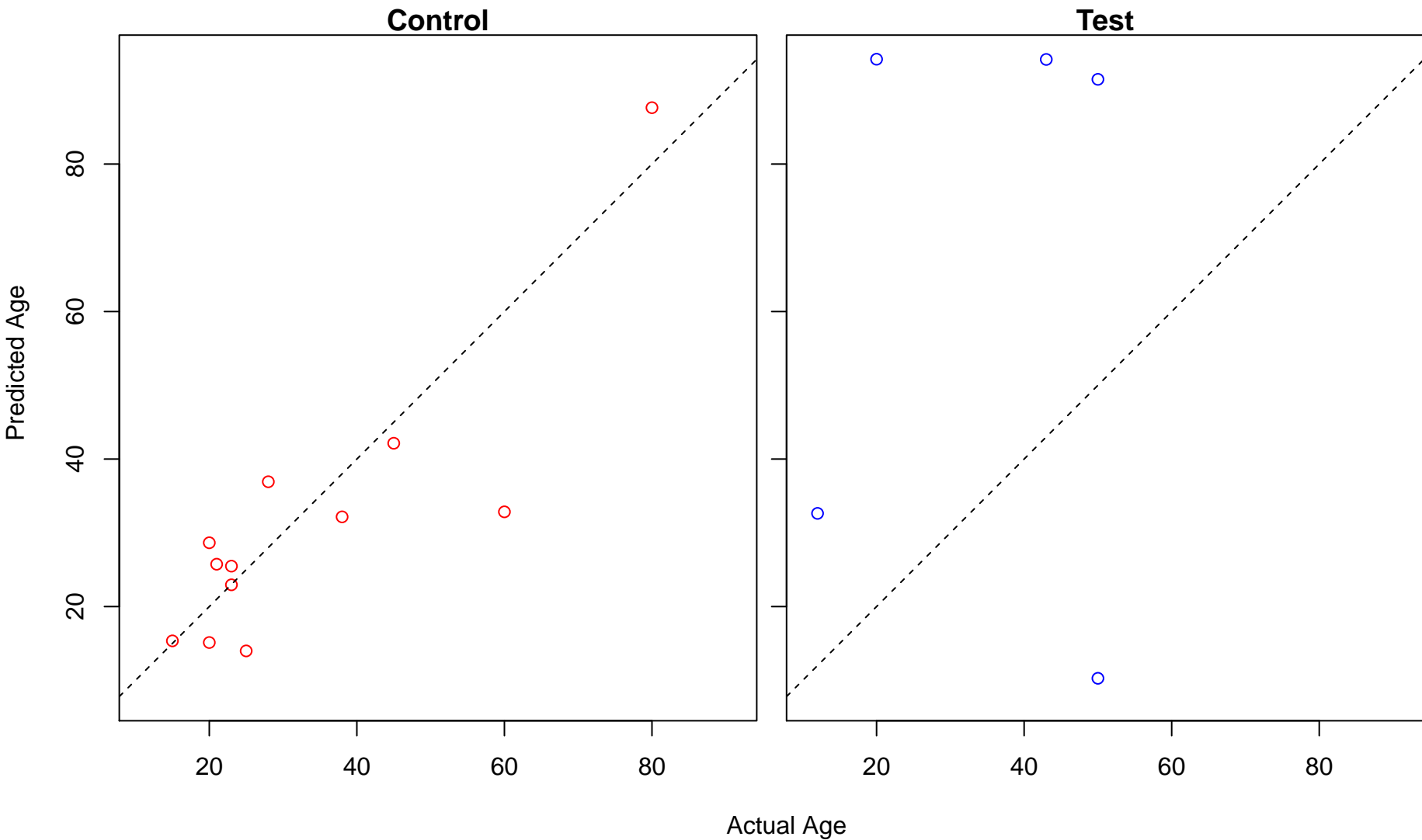
tryptophan catabolic process (Score: 50.809645)



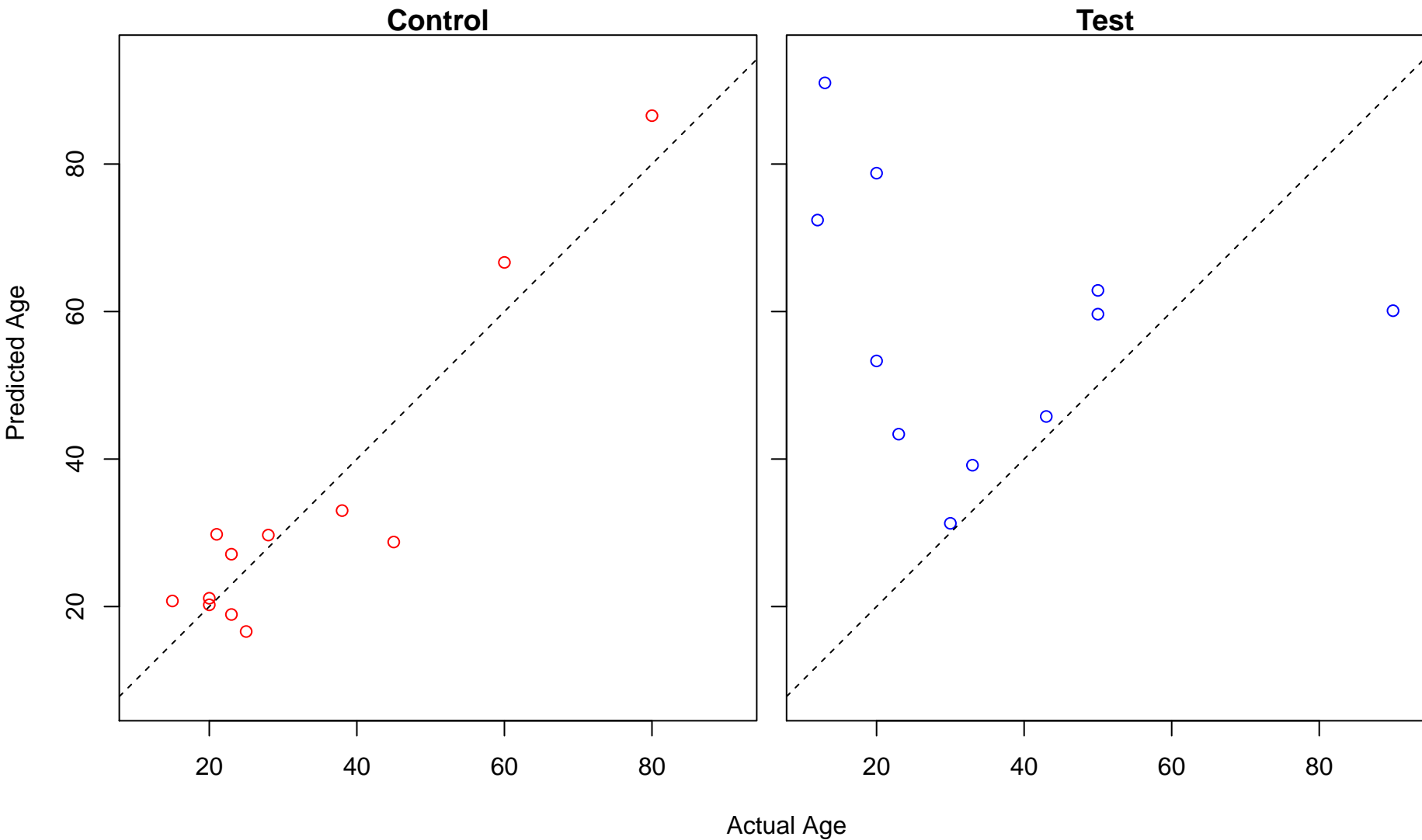
indole-containing compound catabolic process (Score: 50.809645)



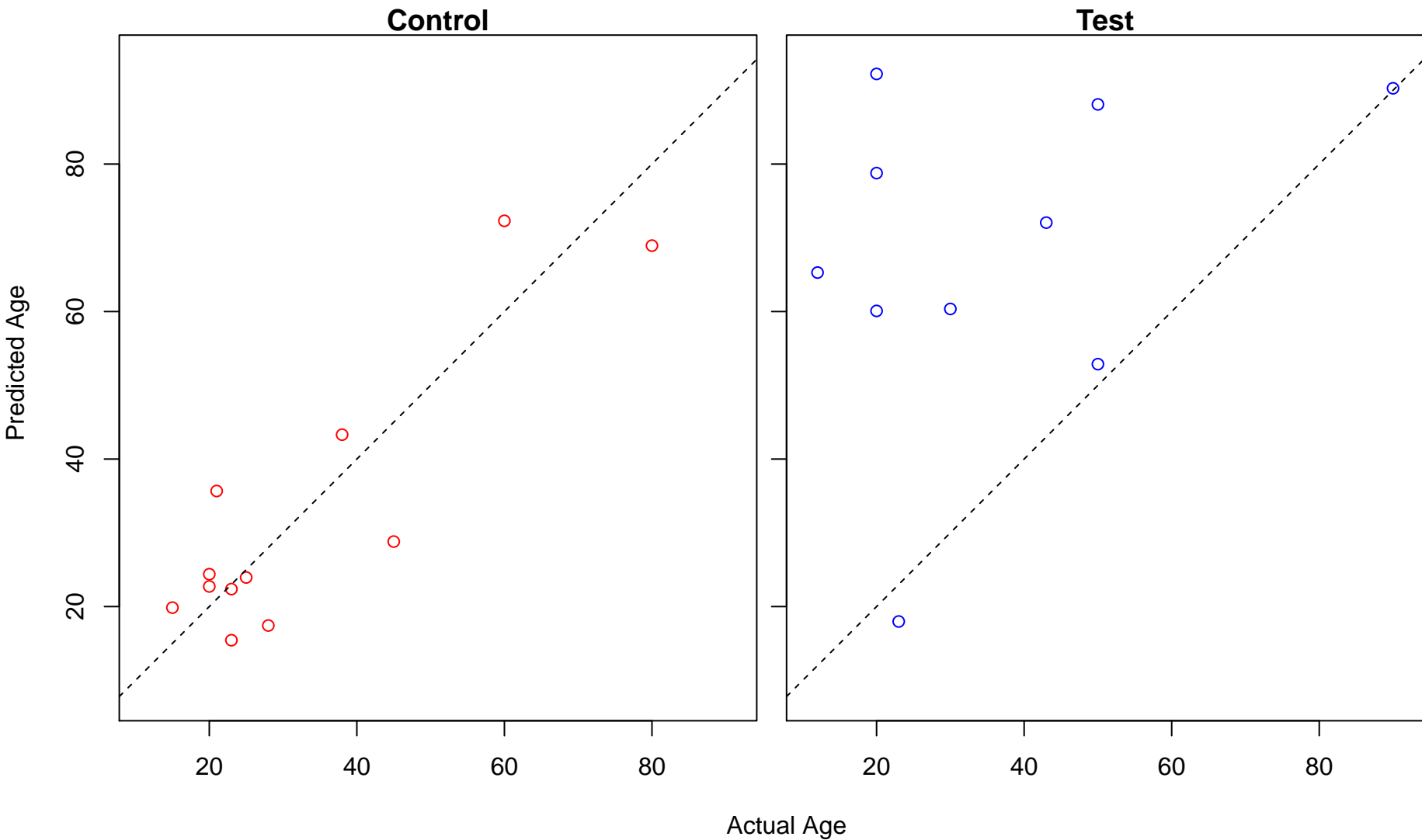
indolalkylamine catabolic process (Score: 50.809645)



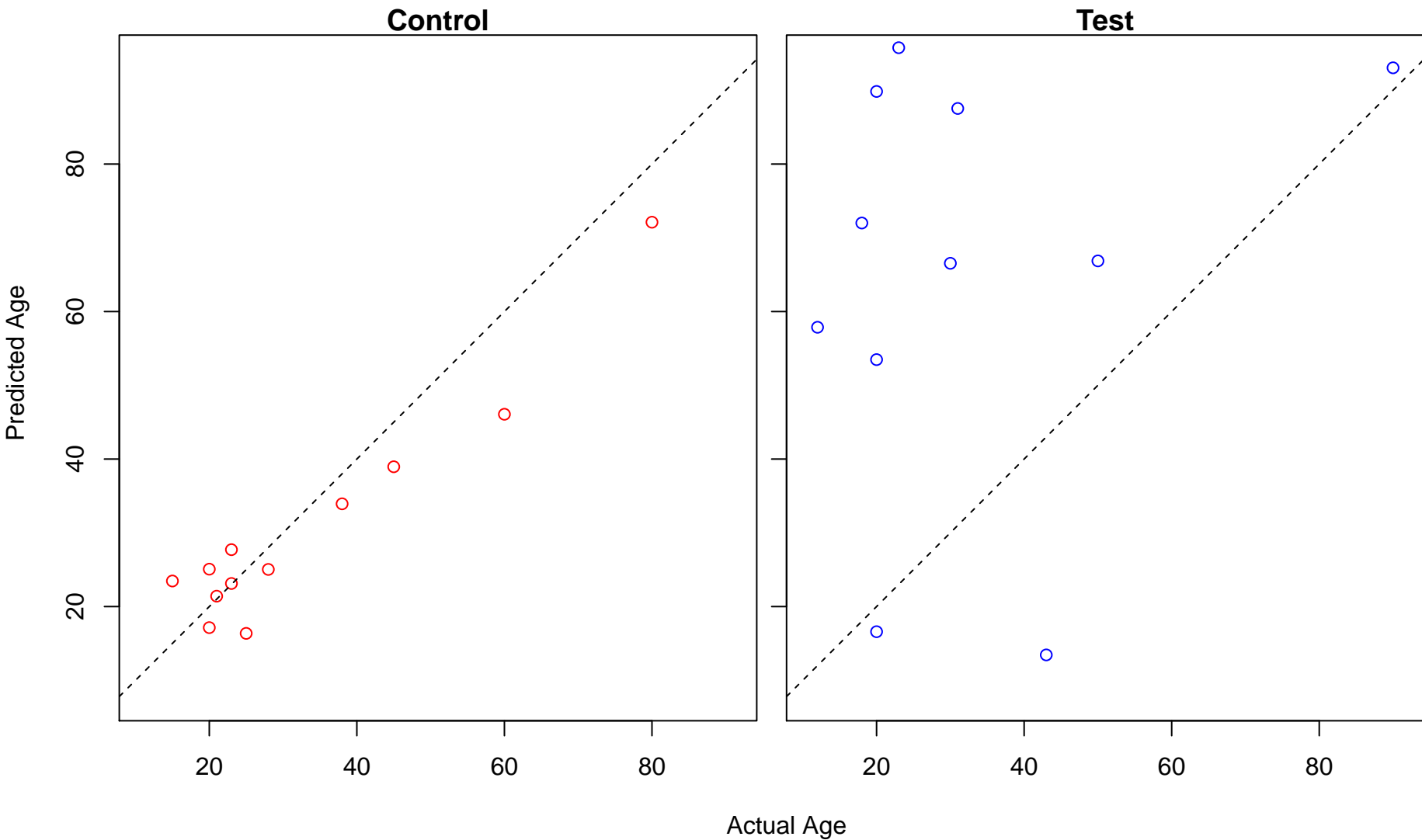
response to corticosteroid (Score: 50.600325)



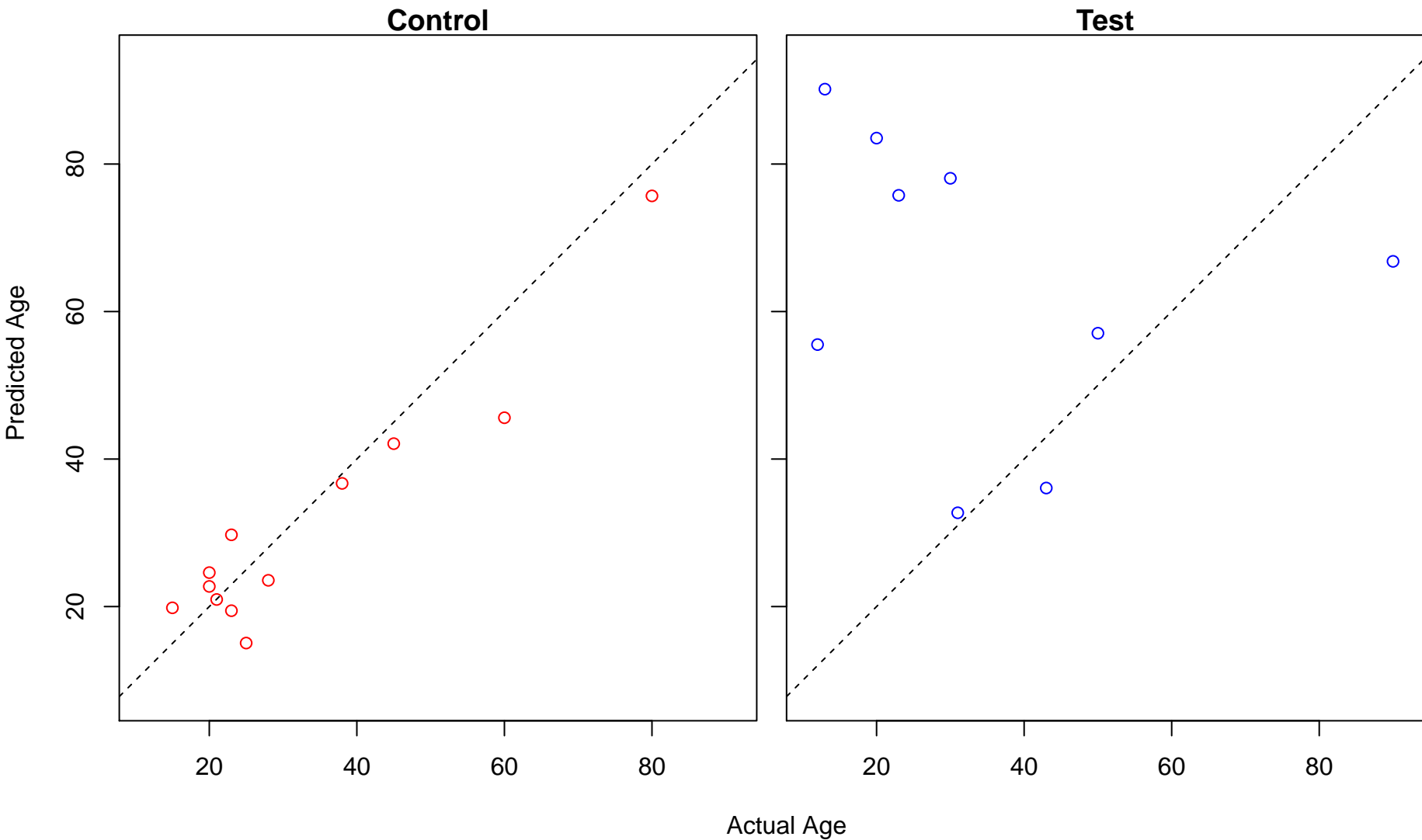
negative regulation of biomineral tissue development (Score: 49.258131)



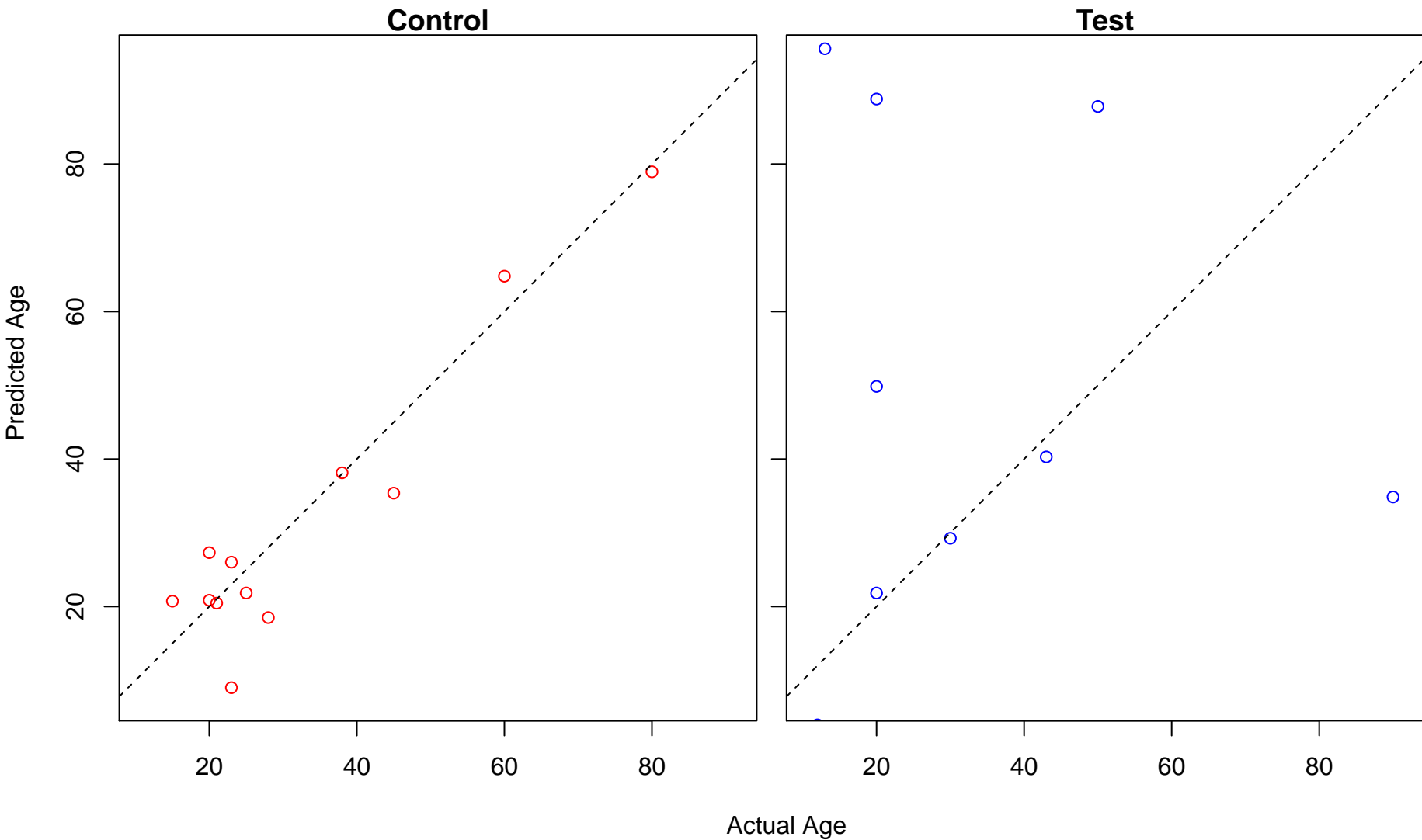
protein import (Score: 48.966817)



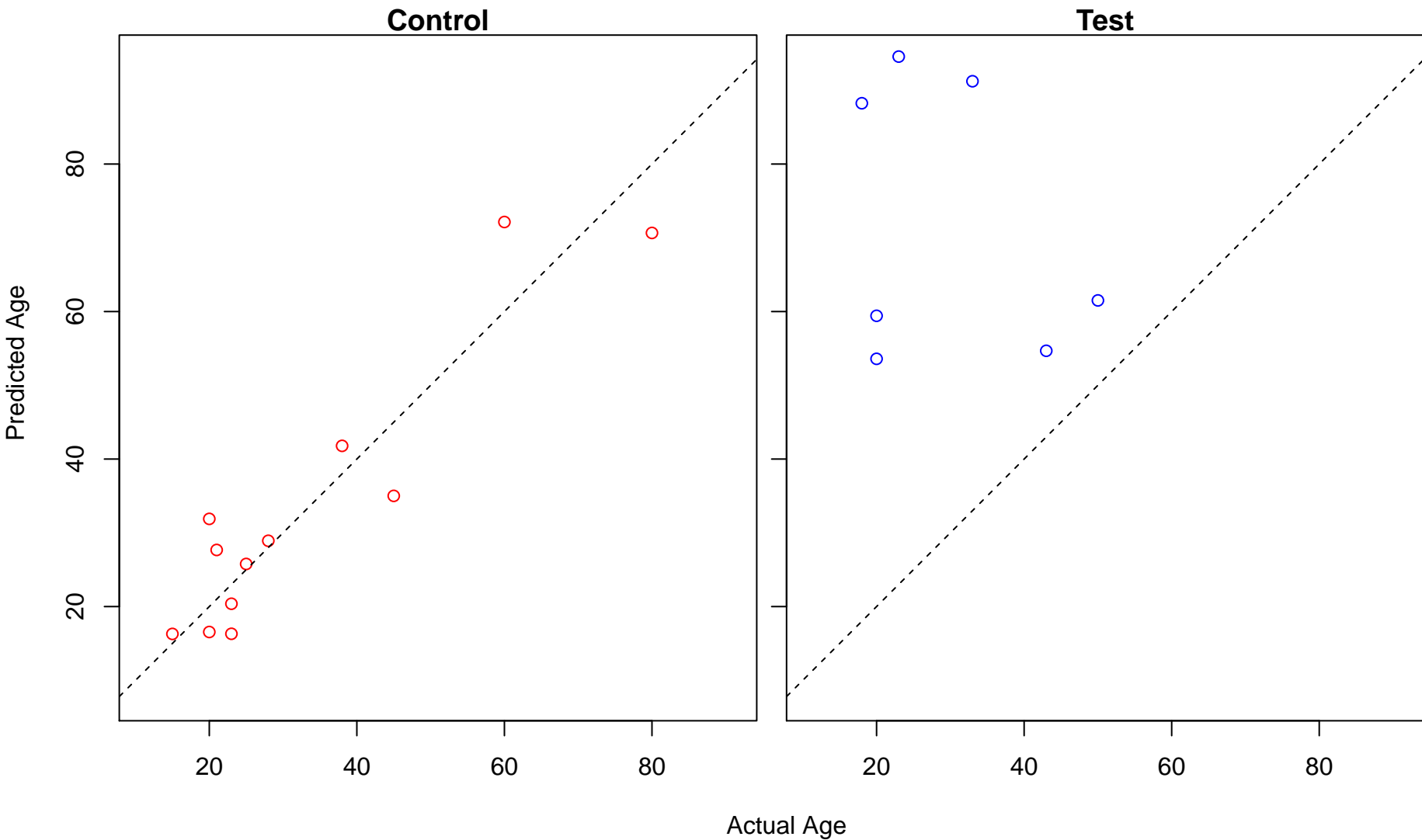
negative regulation of DNA-dependent DNA replication (Score: 48.823789)



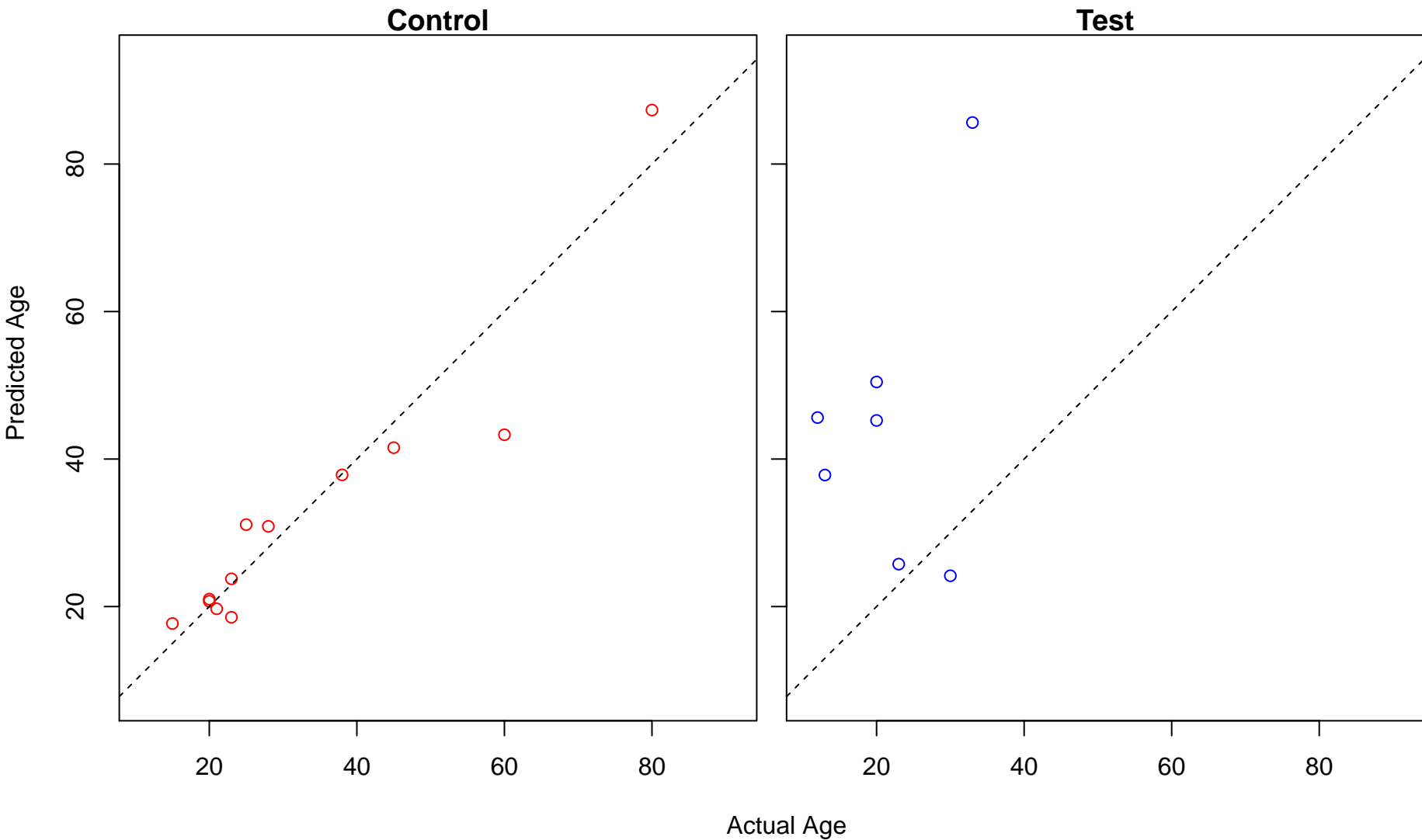
regulation of establishment of protein localization to plasma membrane (Score: 48.801231)



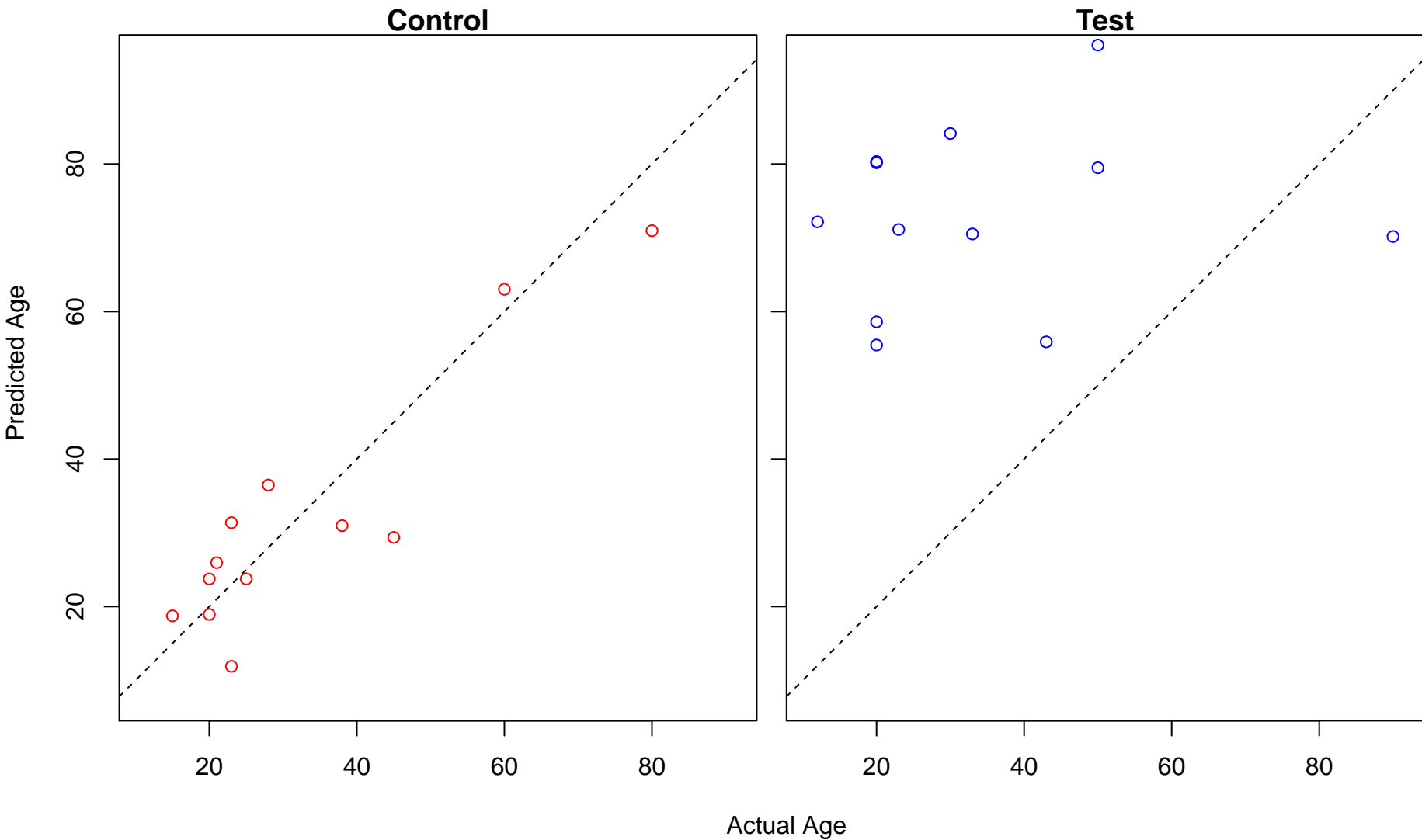
regulation of collateral sprouting (Score: 48.496108)



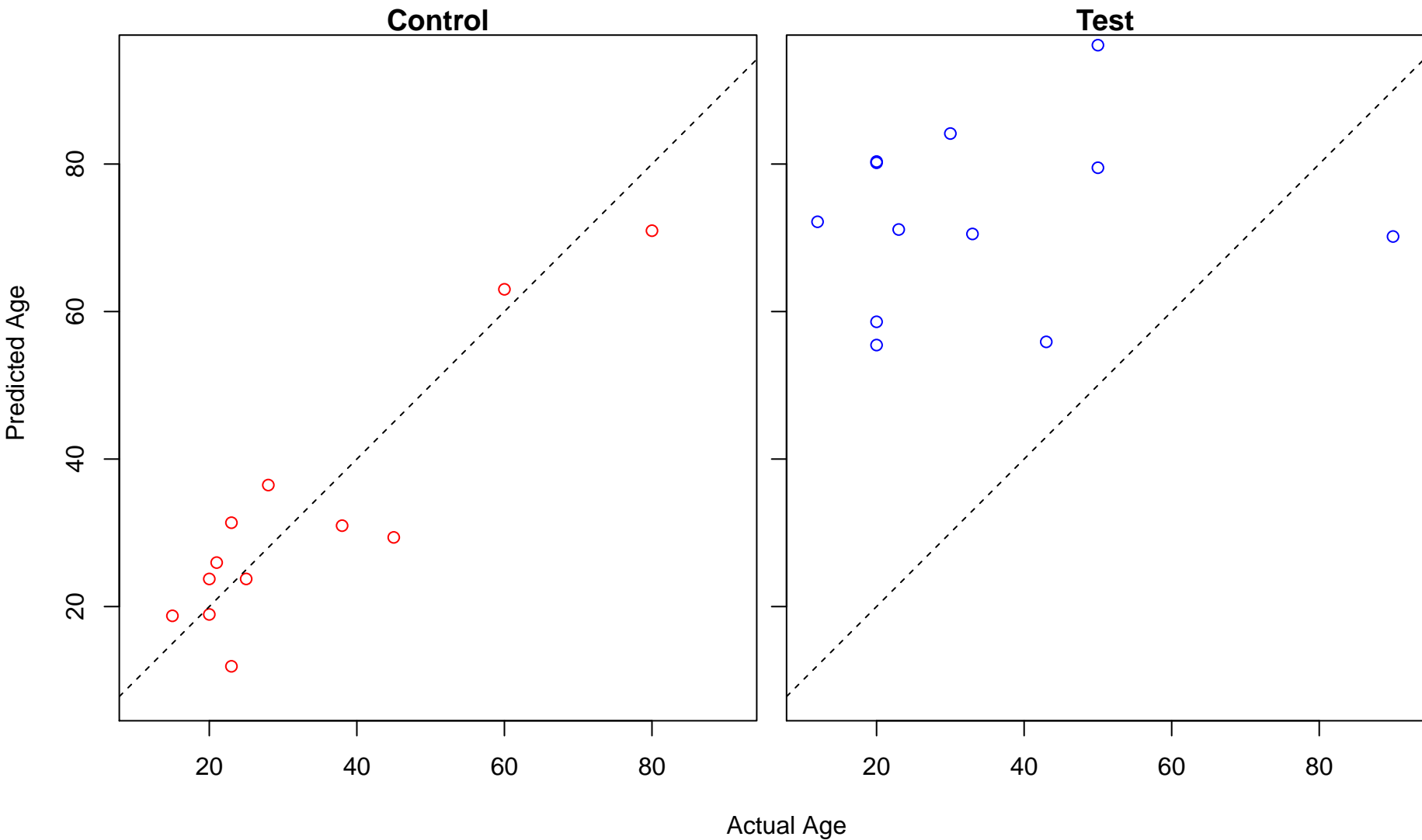
regulation of hyaluronan biosynthetic process (Score: 48.436197)



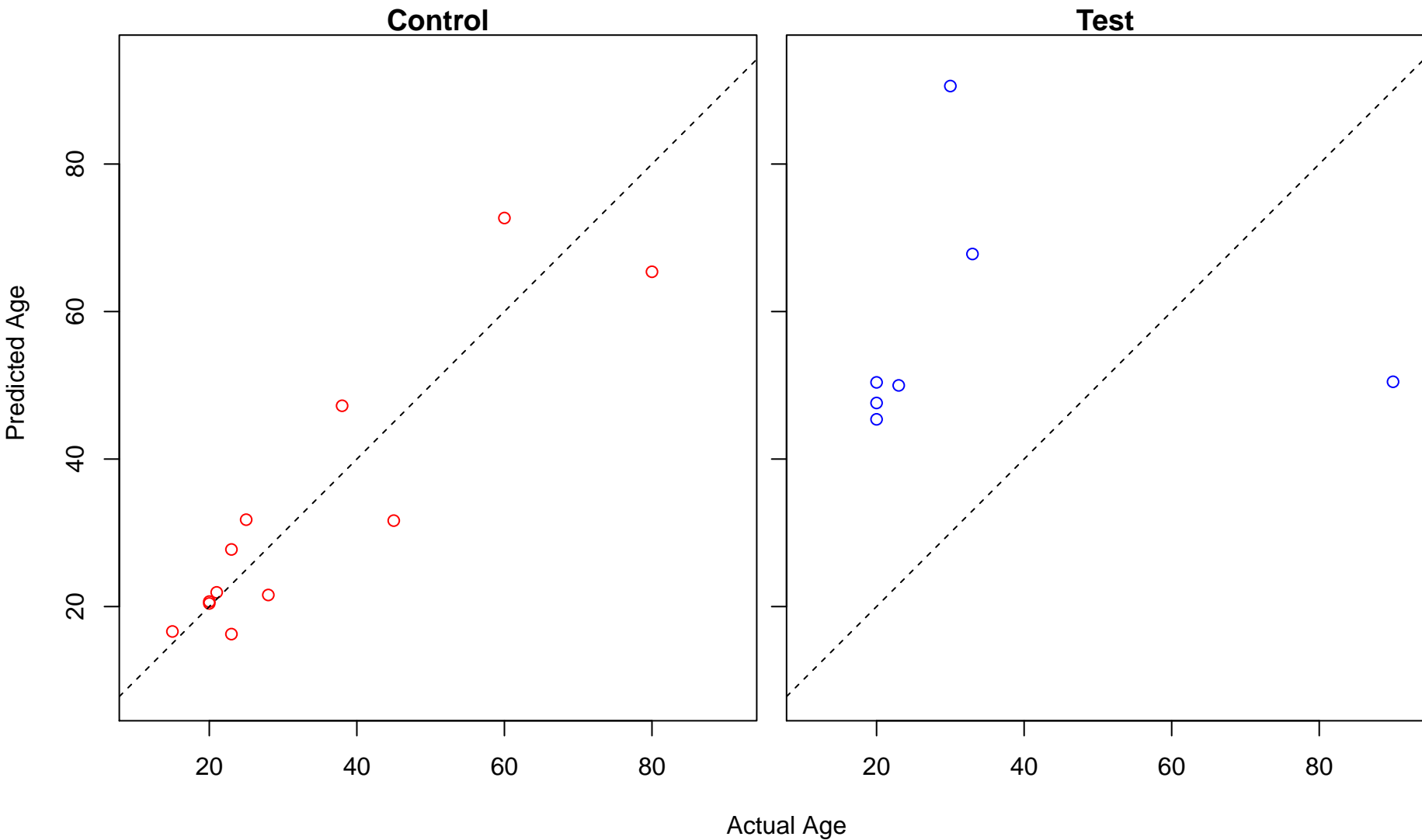
negative regulation of heterotypic cell-cell adhesion (Score: 48.403808)



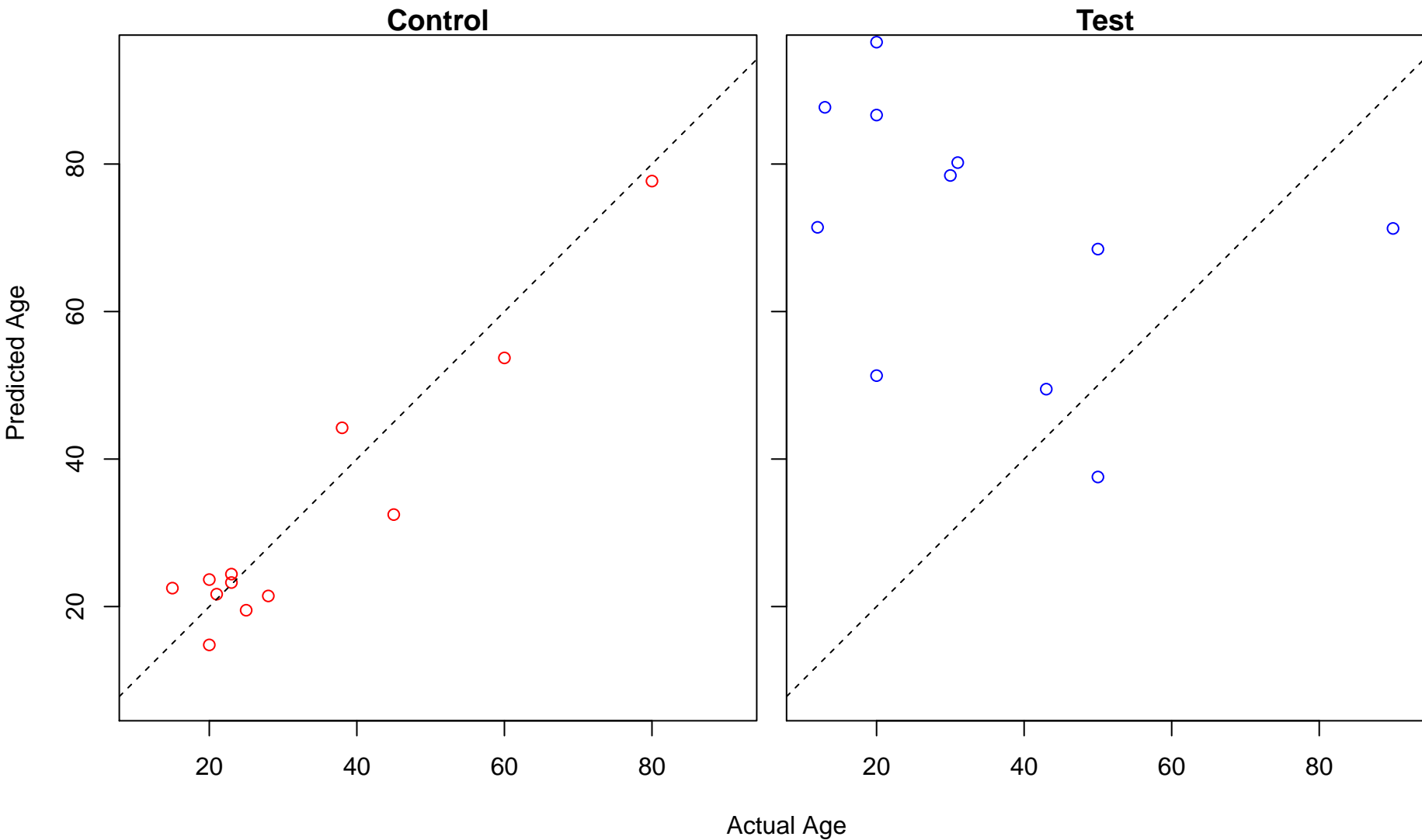
regulation of cell-cell adhesion involved in gastrulation (Score: 48.403808)



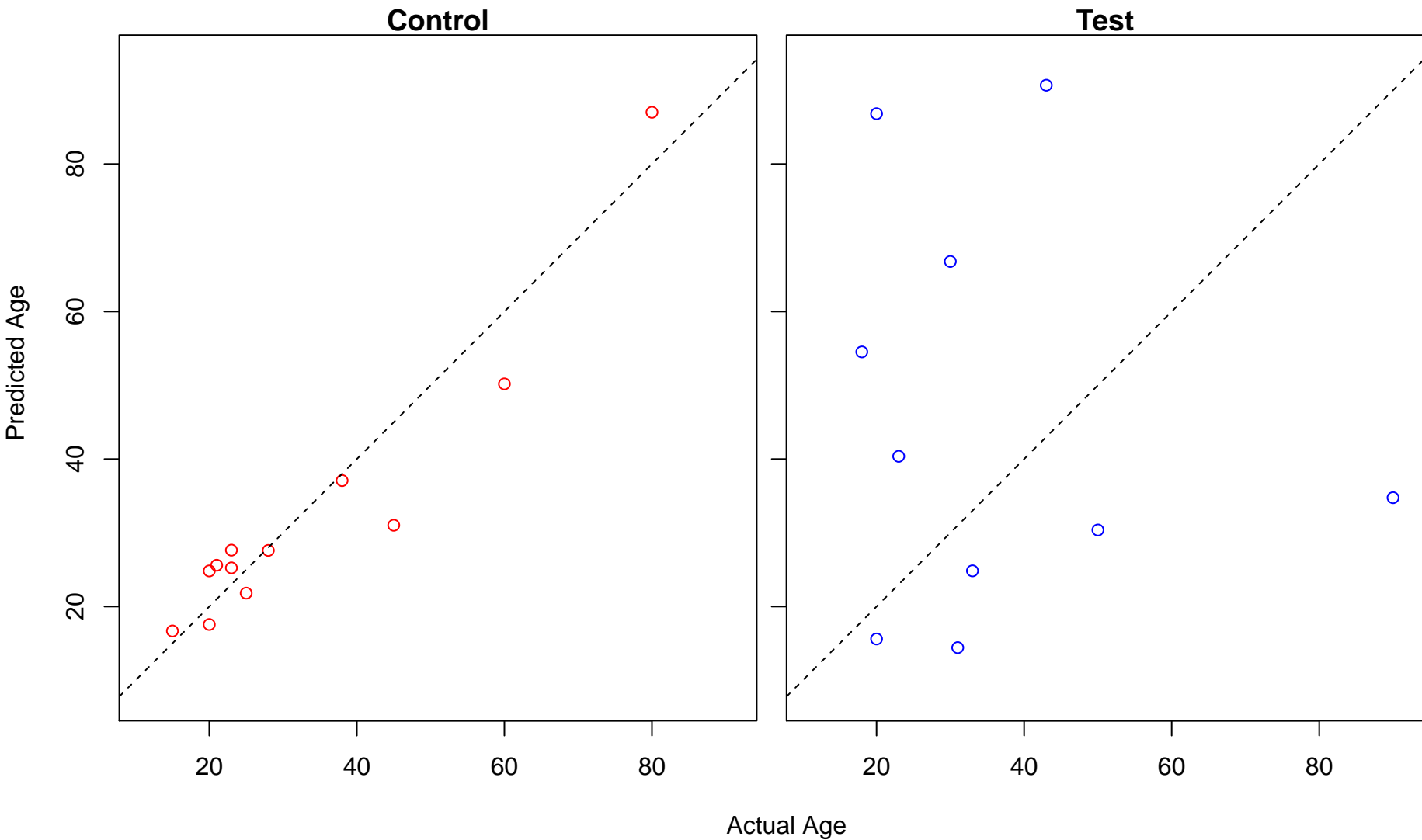
organic cation transport (Score: 48.347722)



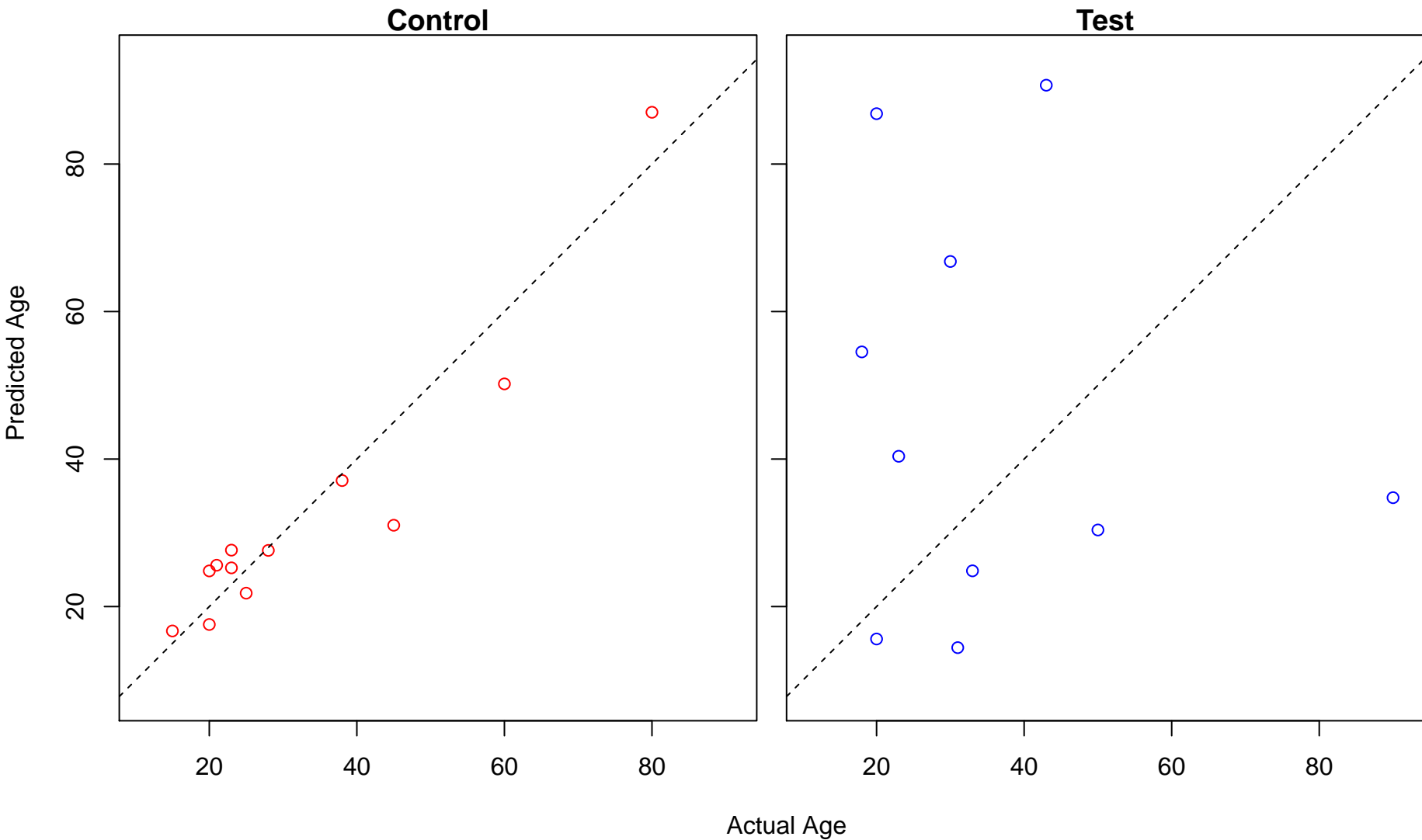
regulation of chromatin assembly or disassembly (Score: 47.744870)



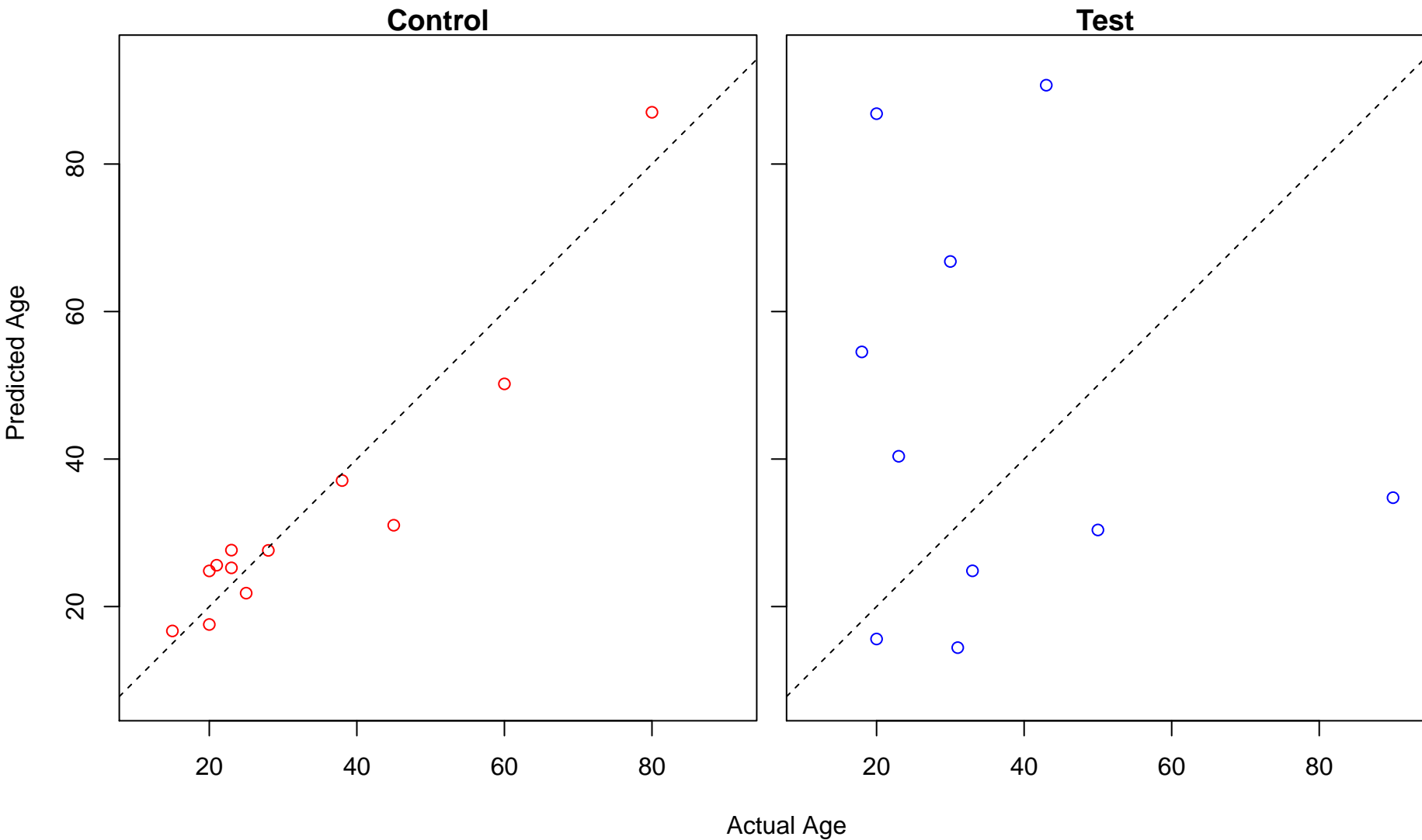
polyketide metabolic process (Score: 47.590807)



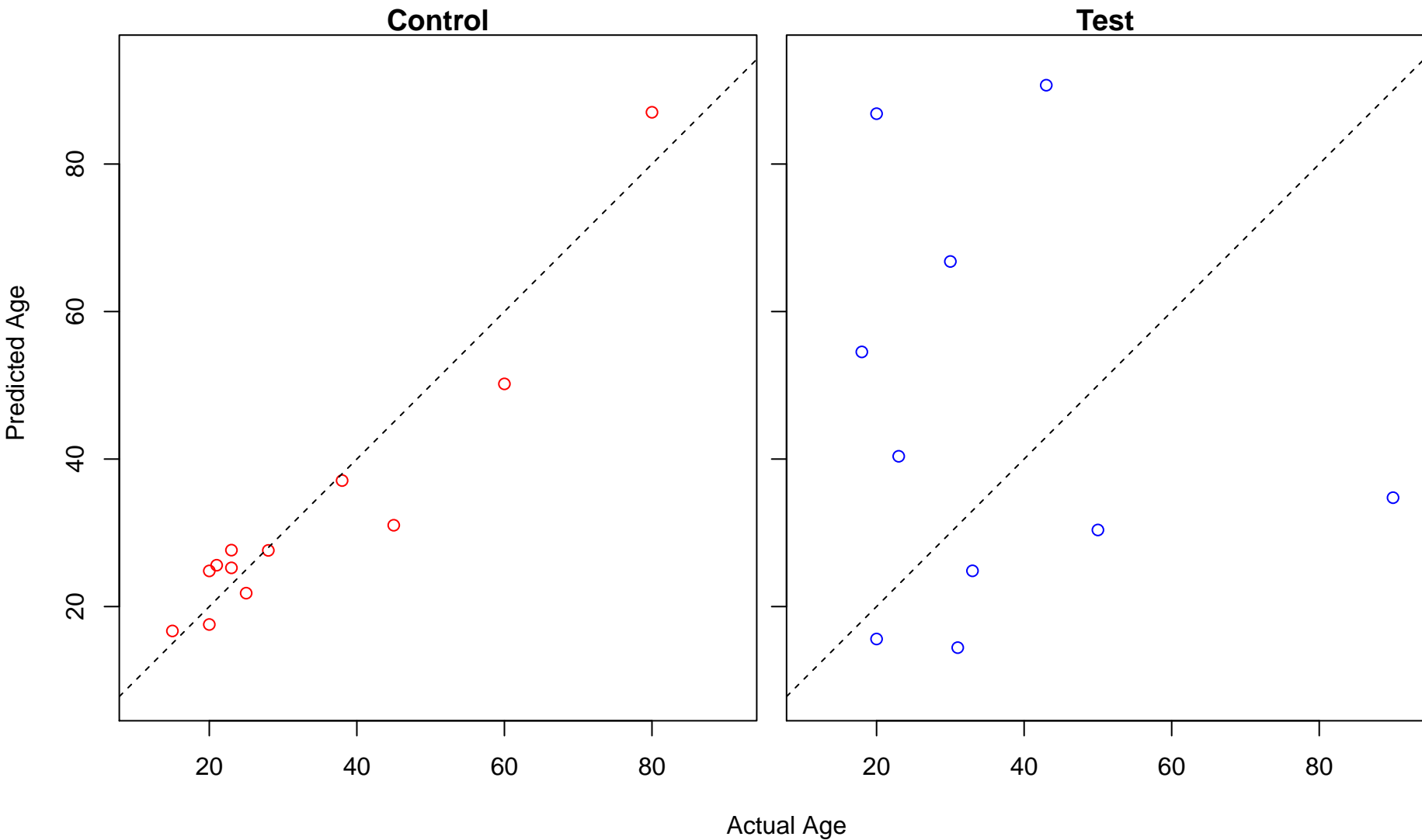
aminoglycoside antibiotic metabolic process (Score: 47.590807)



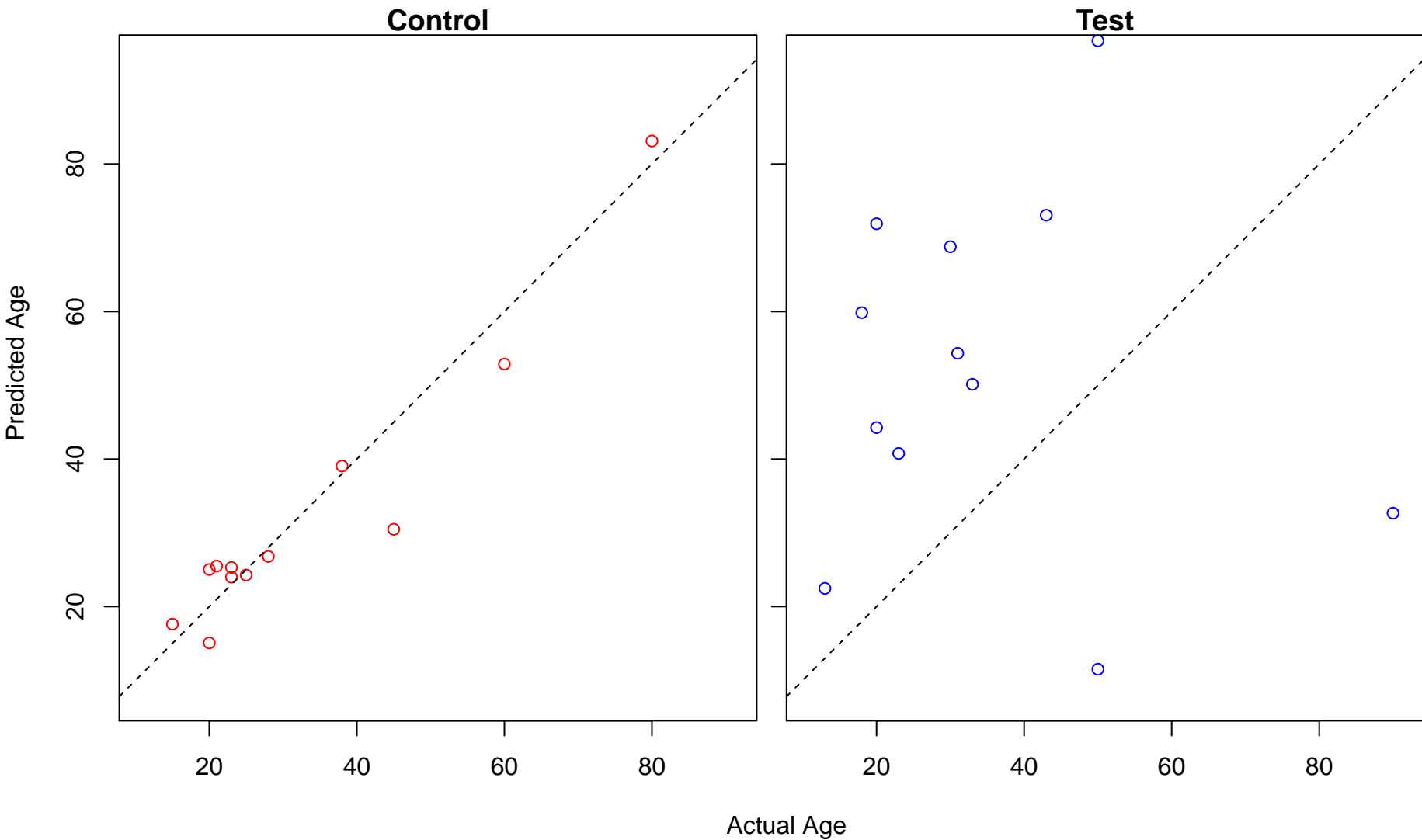
daunorubicin metabolic process (Score: 47.590807)



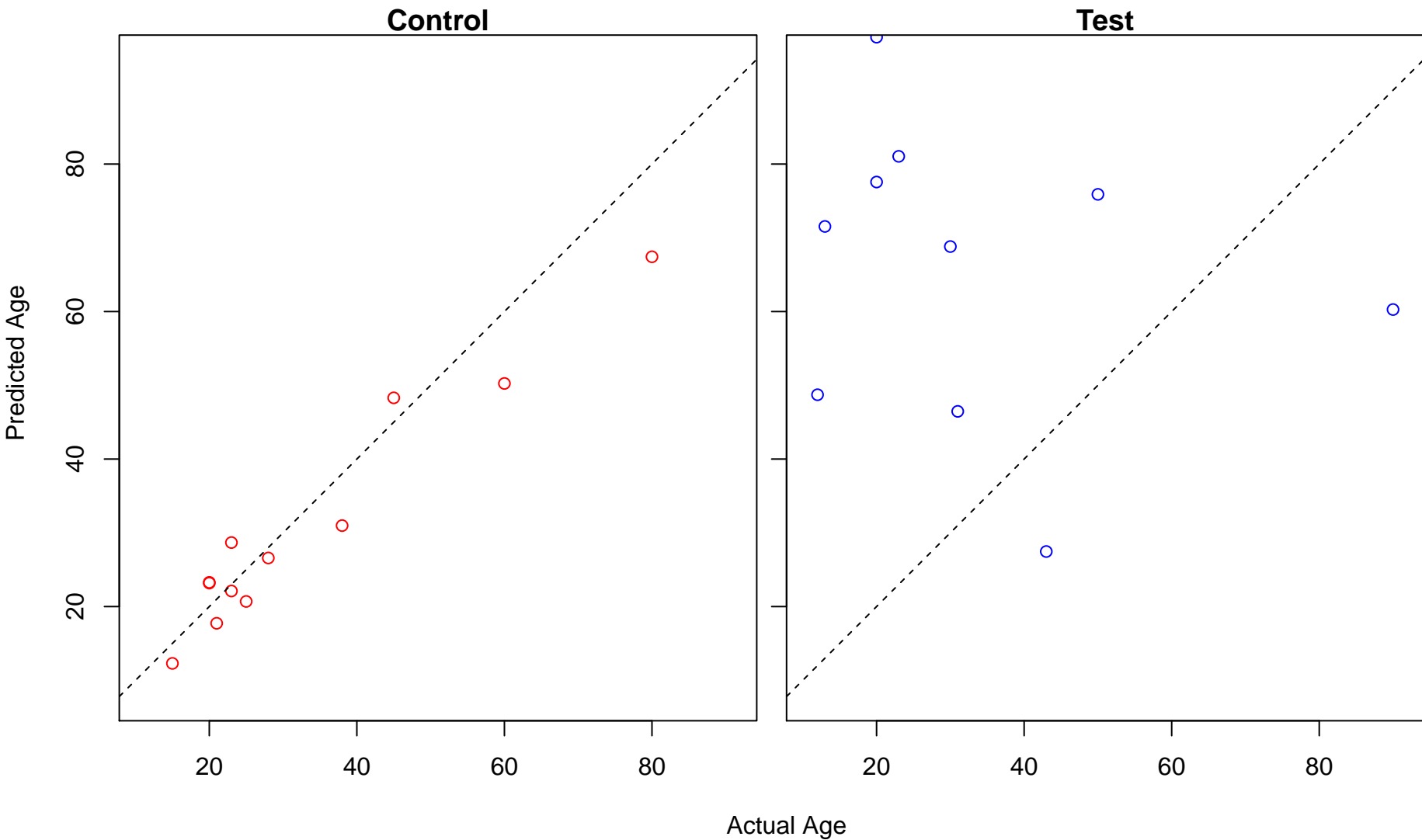
doxorubicin metabolic process (Score: 47.590807)



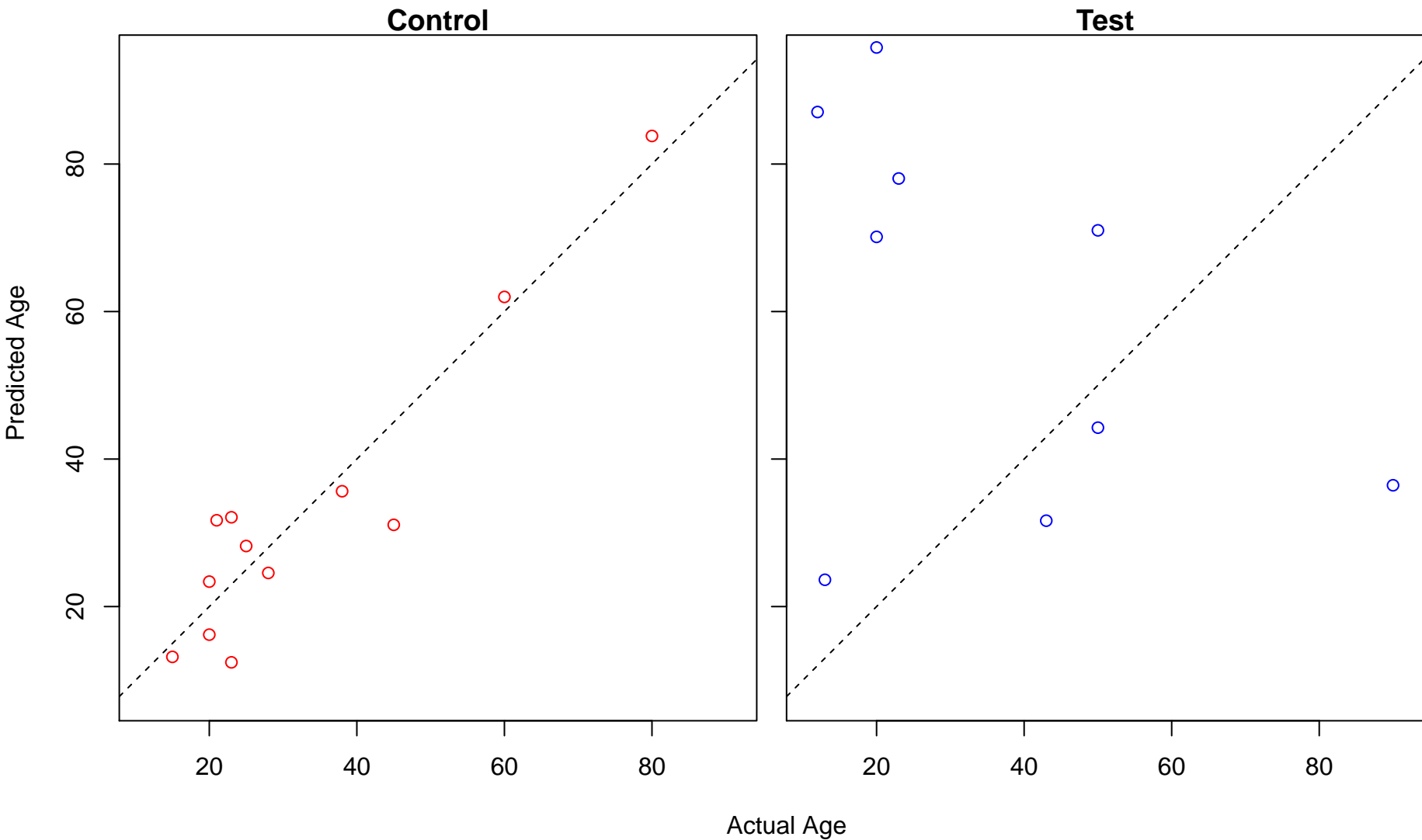
quinone metabolic process (Score: 47.500373)



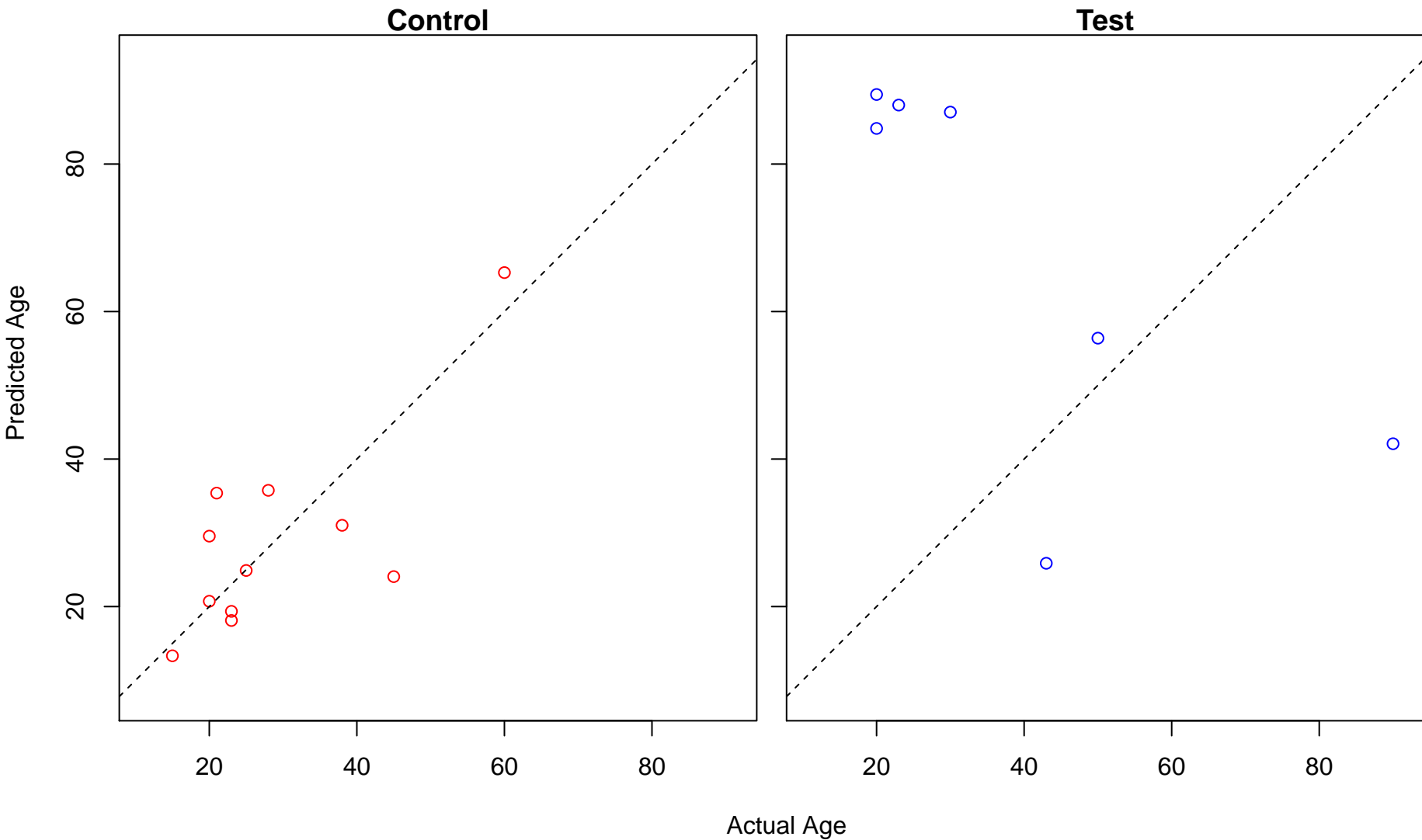
negative regulation of DNA endoreduplication (Score: 47.394734)



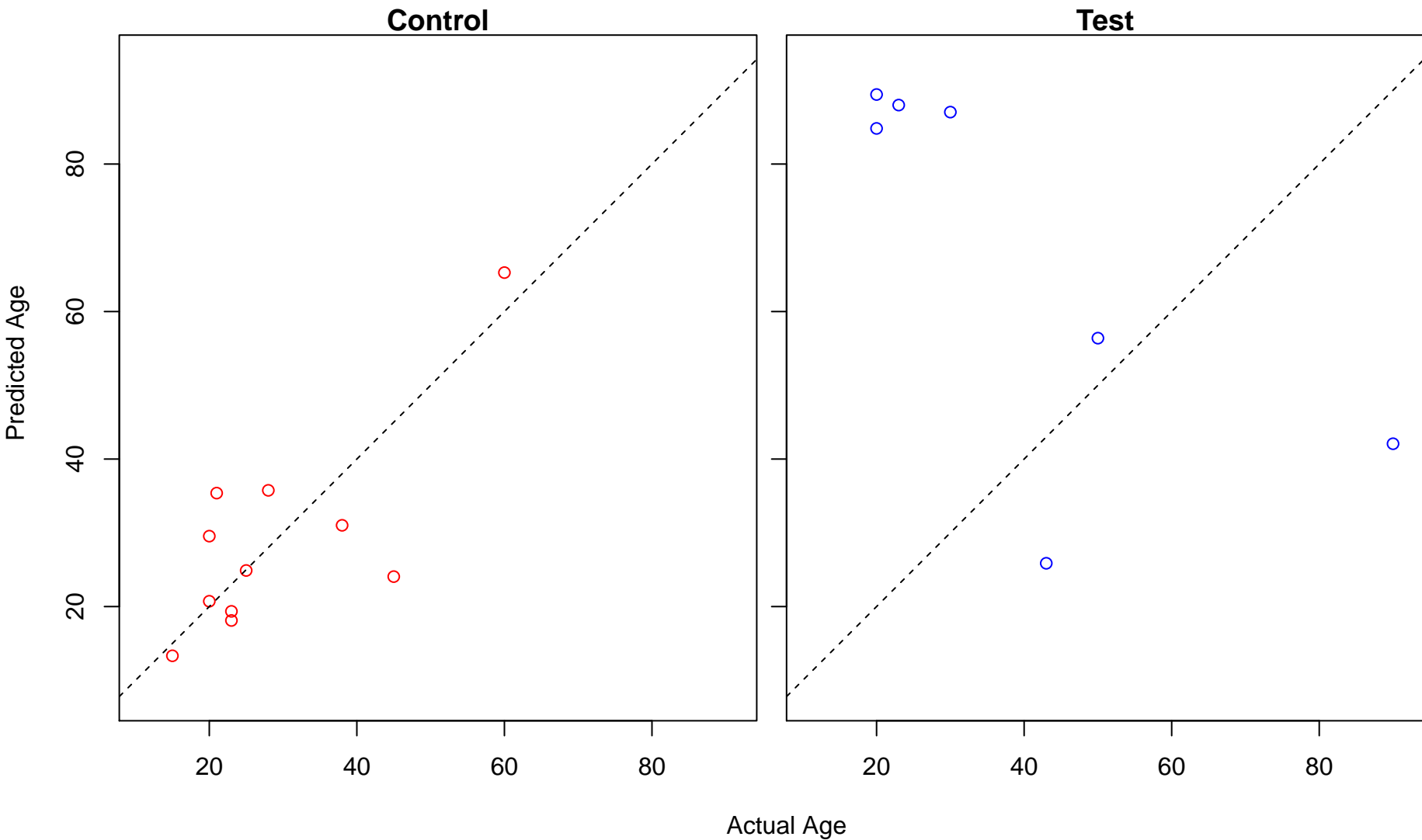
activation of anaphase-promoting complex activity (Score: 47.369859)



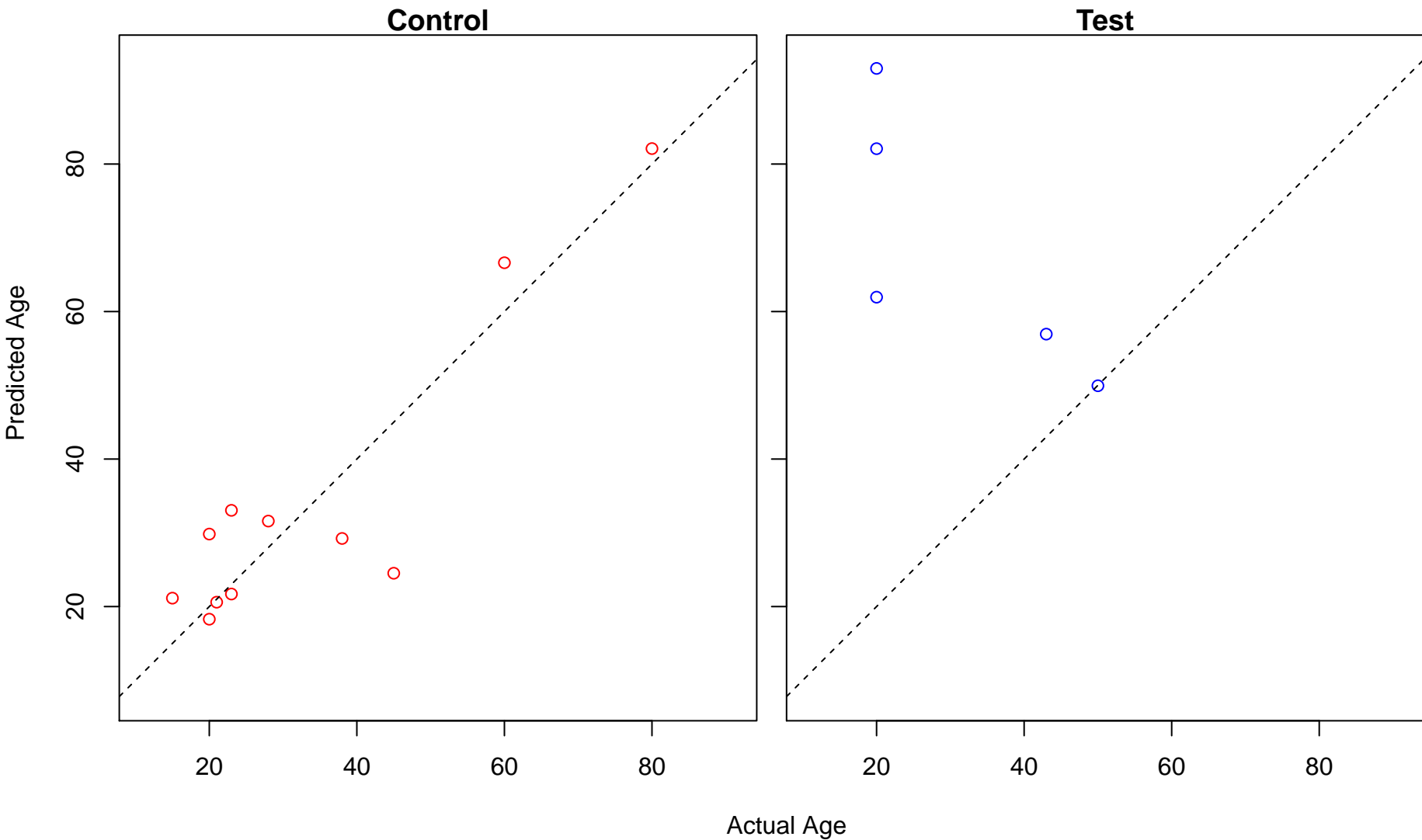
mononuclear cell proliferation (Score: 47.125167)



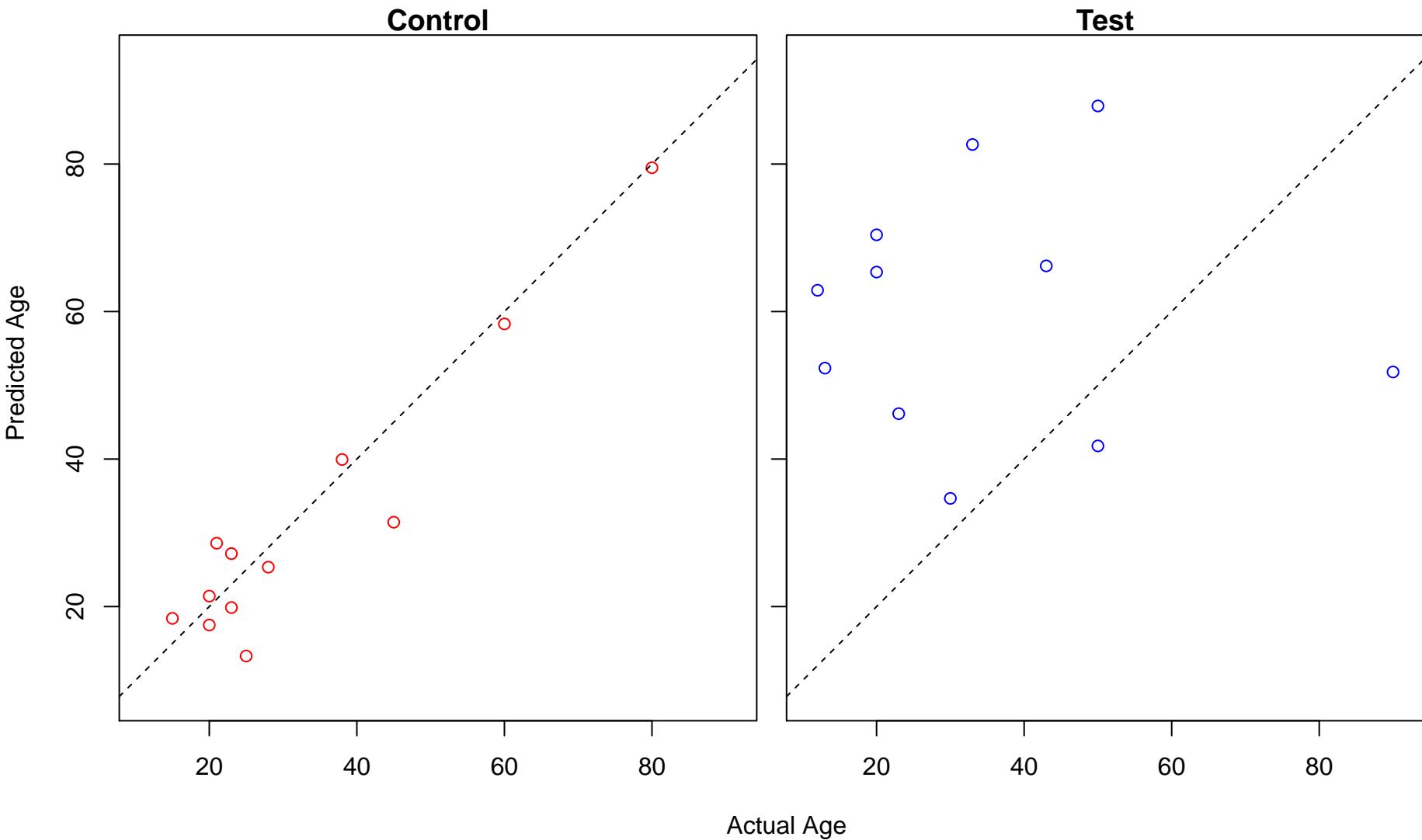
lymphocyte proliferation (Score: 47.125167)



response to cholesterol (Score: 46.901855)

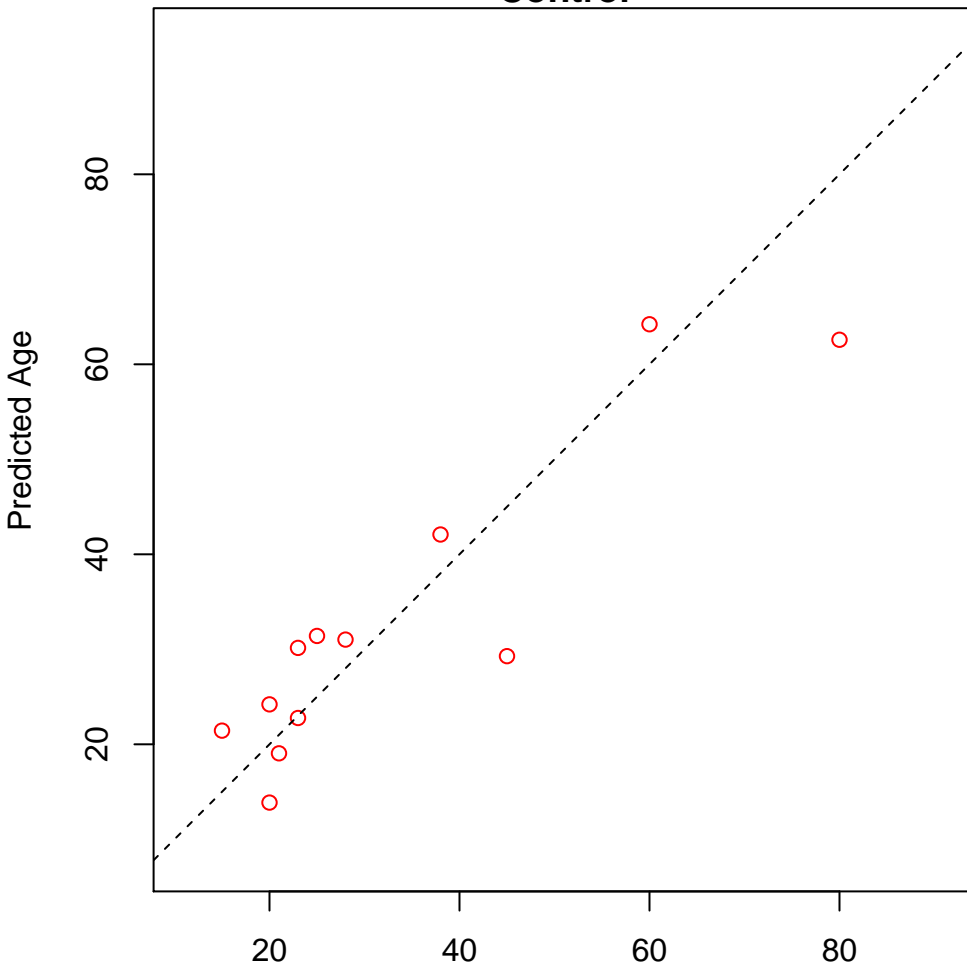


regulation of cell adhesion mediated by integrin (Score: 46.870571)

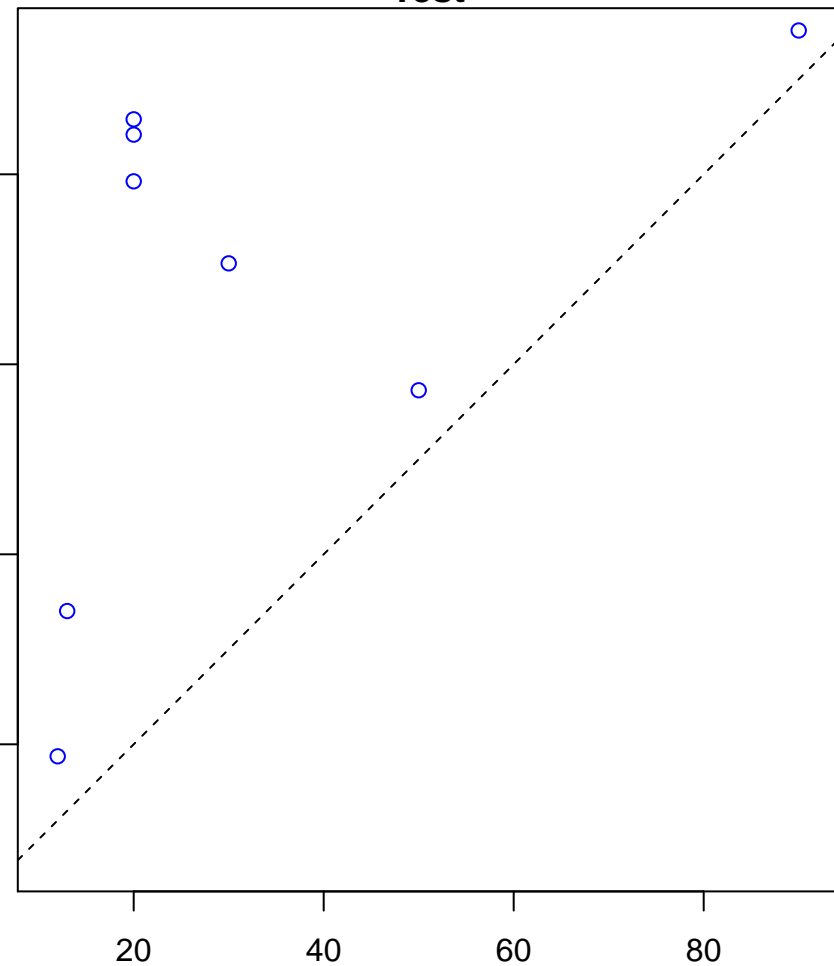


import across plasma membrane (Score: 46.717359)

Control

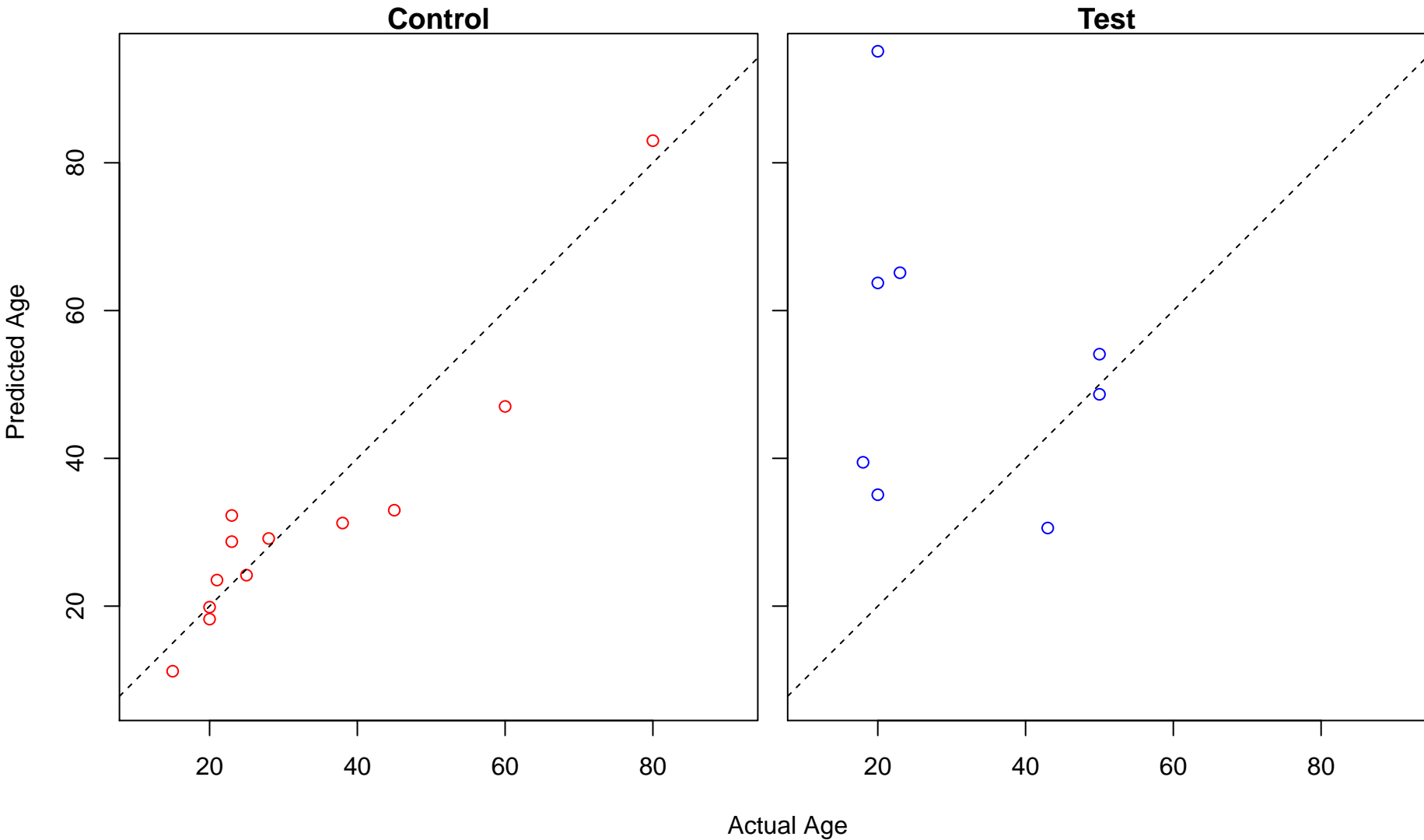


Test

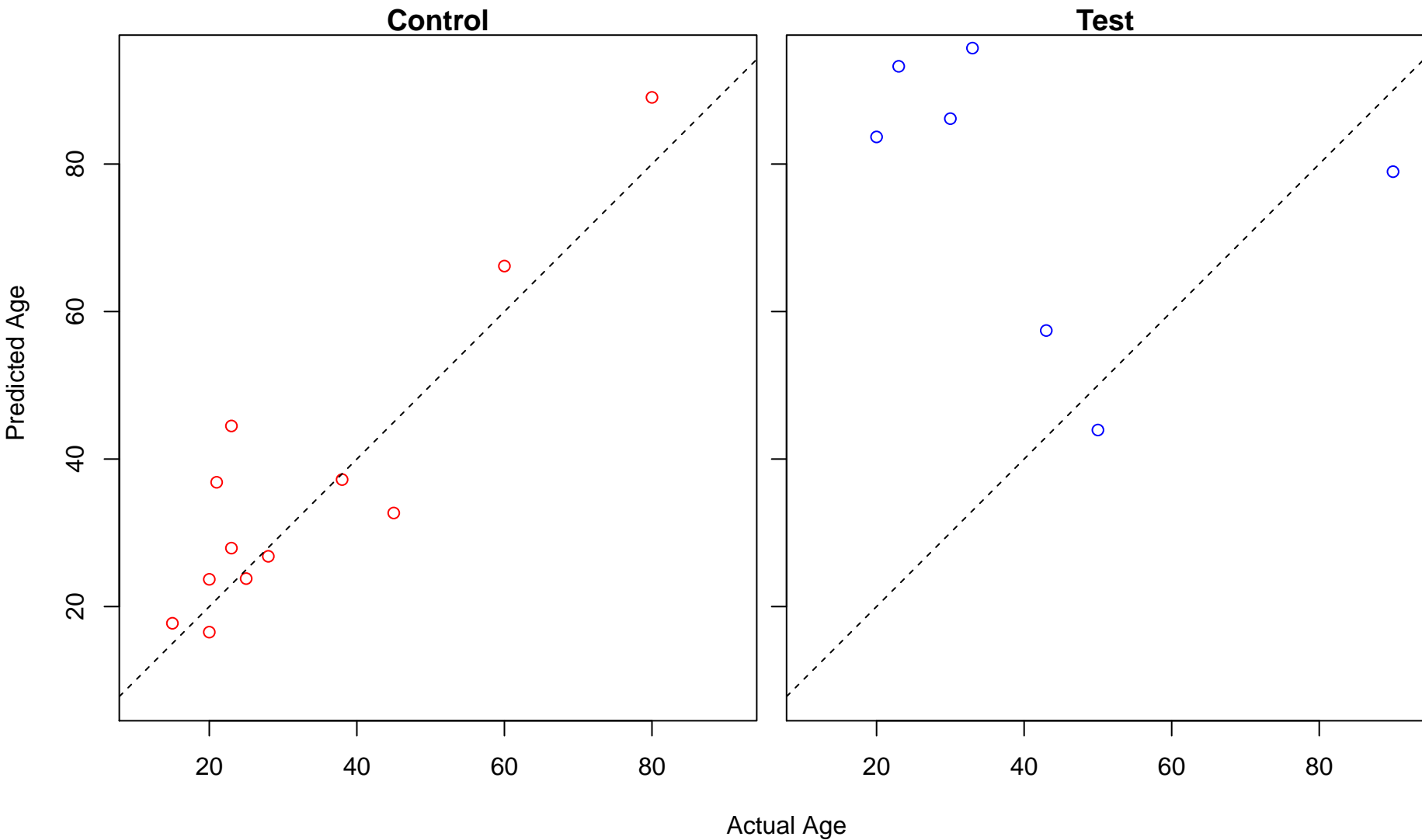


Actual Age

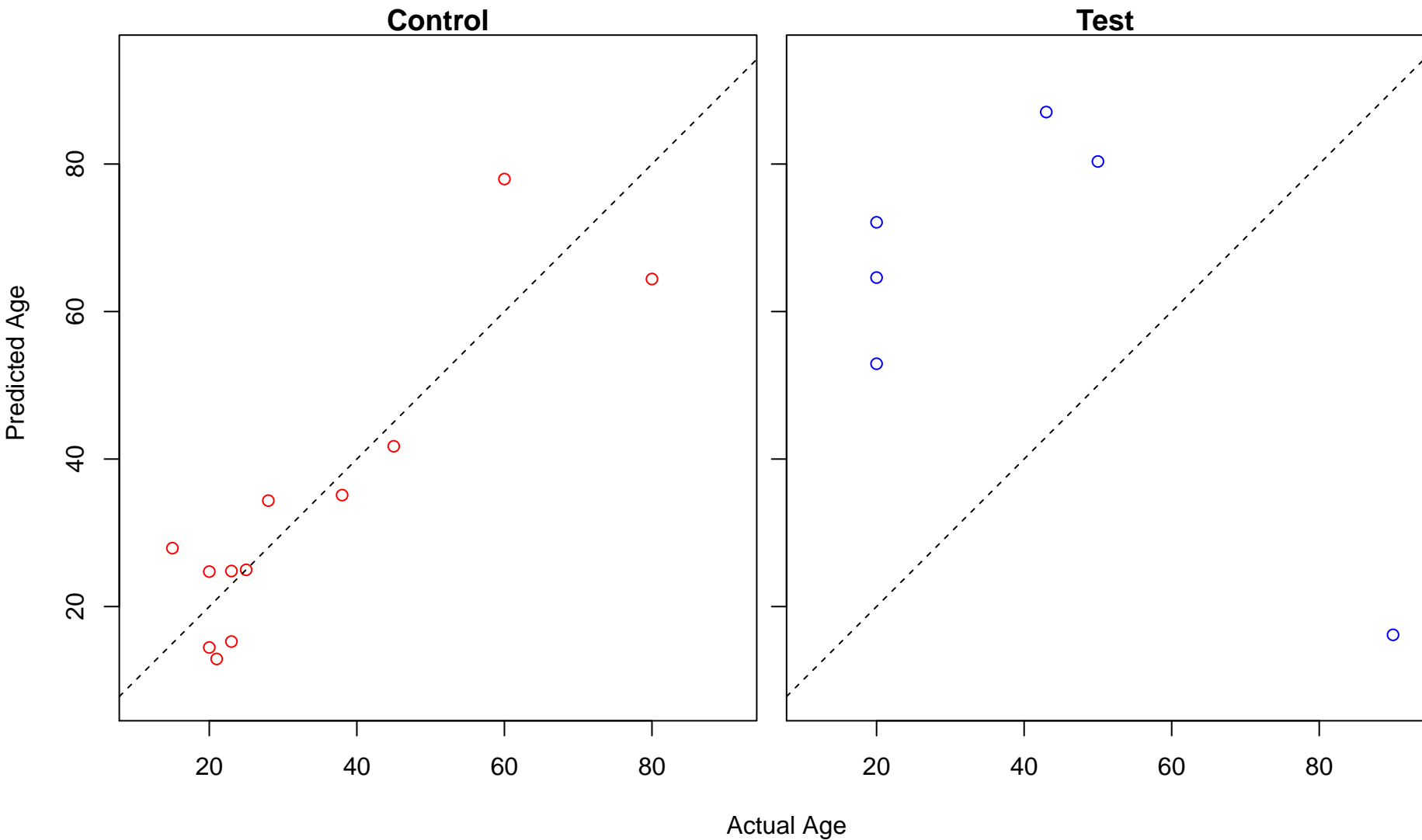
olfactory bulb interneuron differentiation (Score: 46.675596)



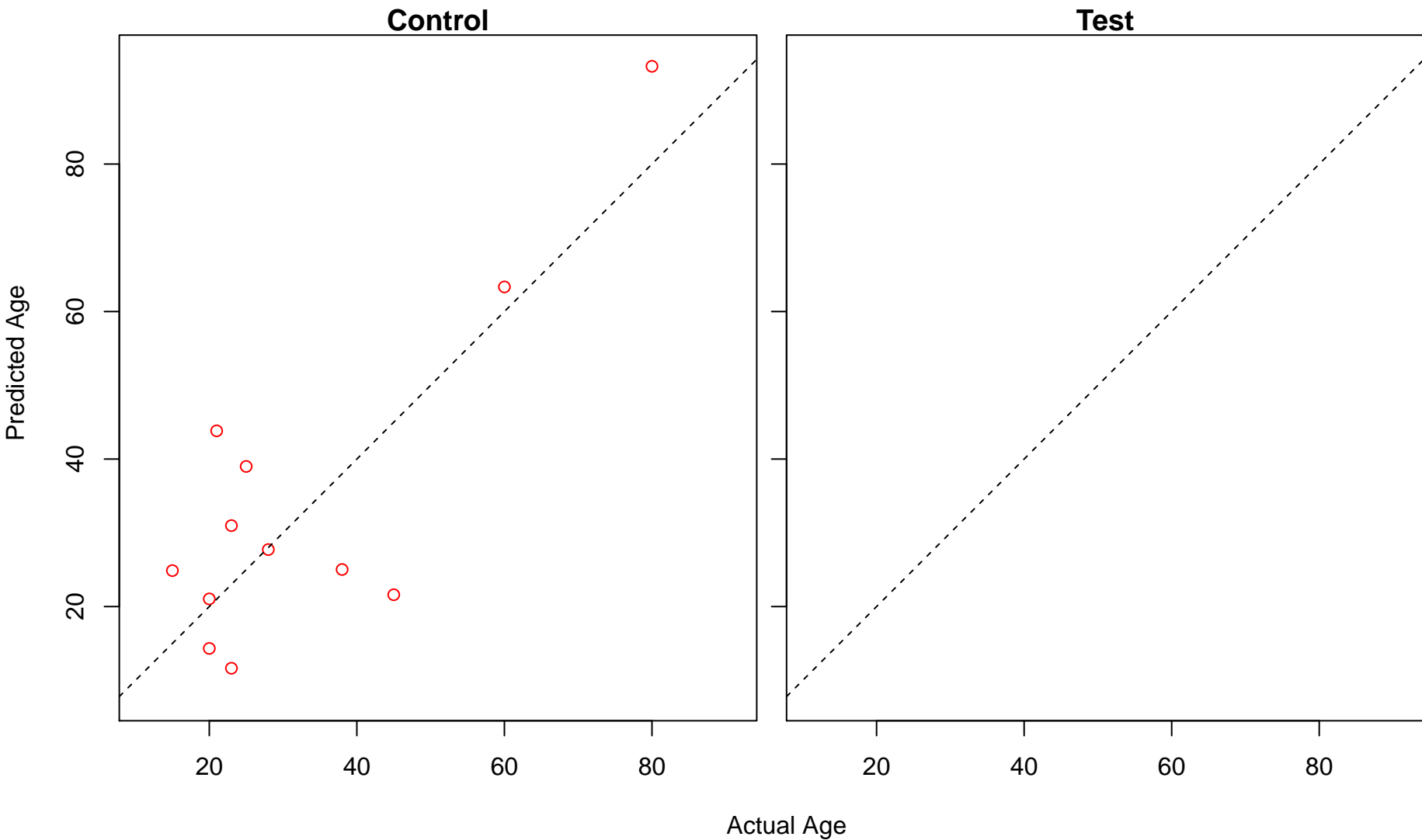
negative regulation of macrophage derived foam cell differentiation (Score: 46.501001)



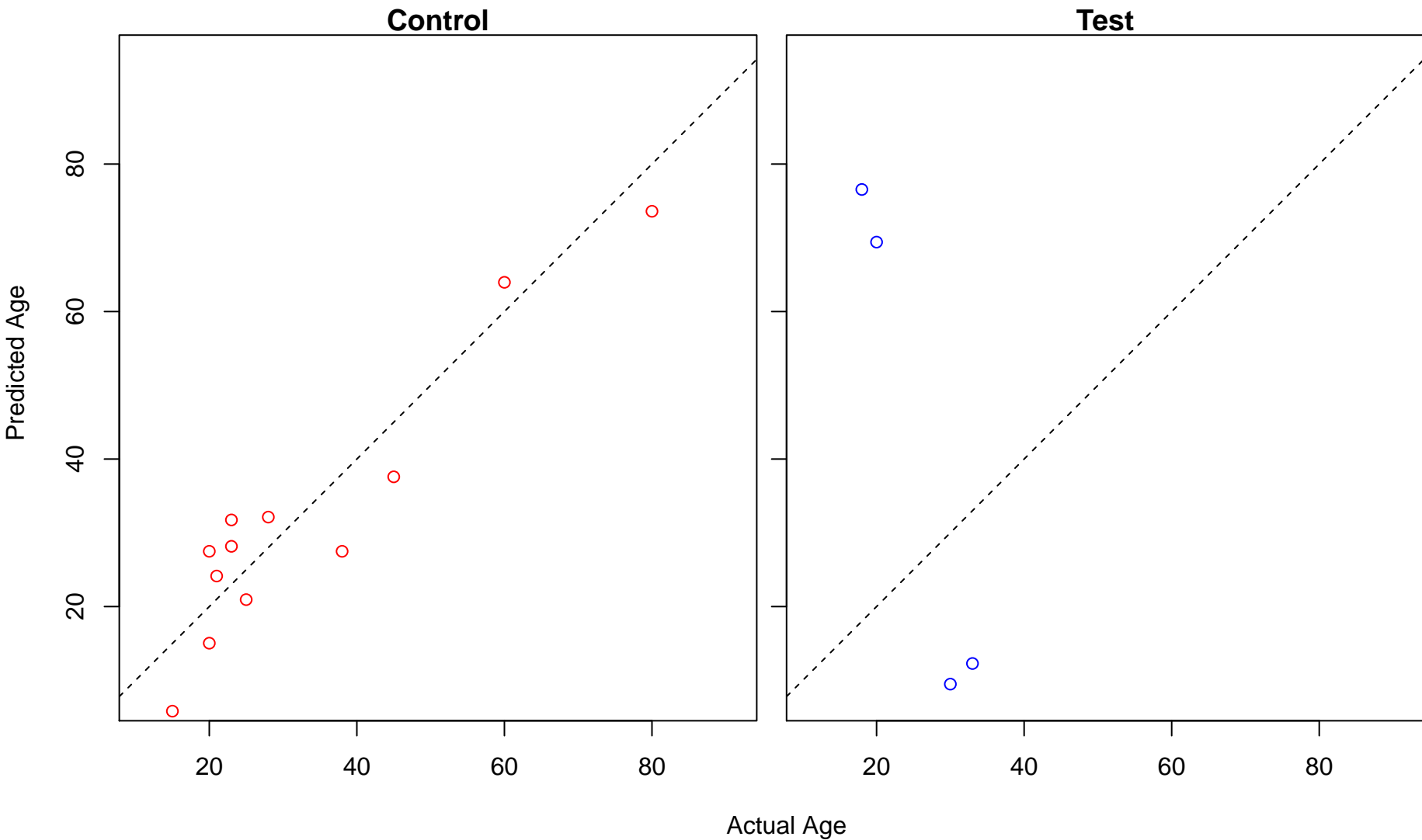
regulation of synaptic vesicle exocytosis (Score: 46.477898)



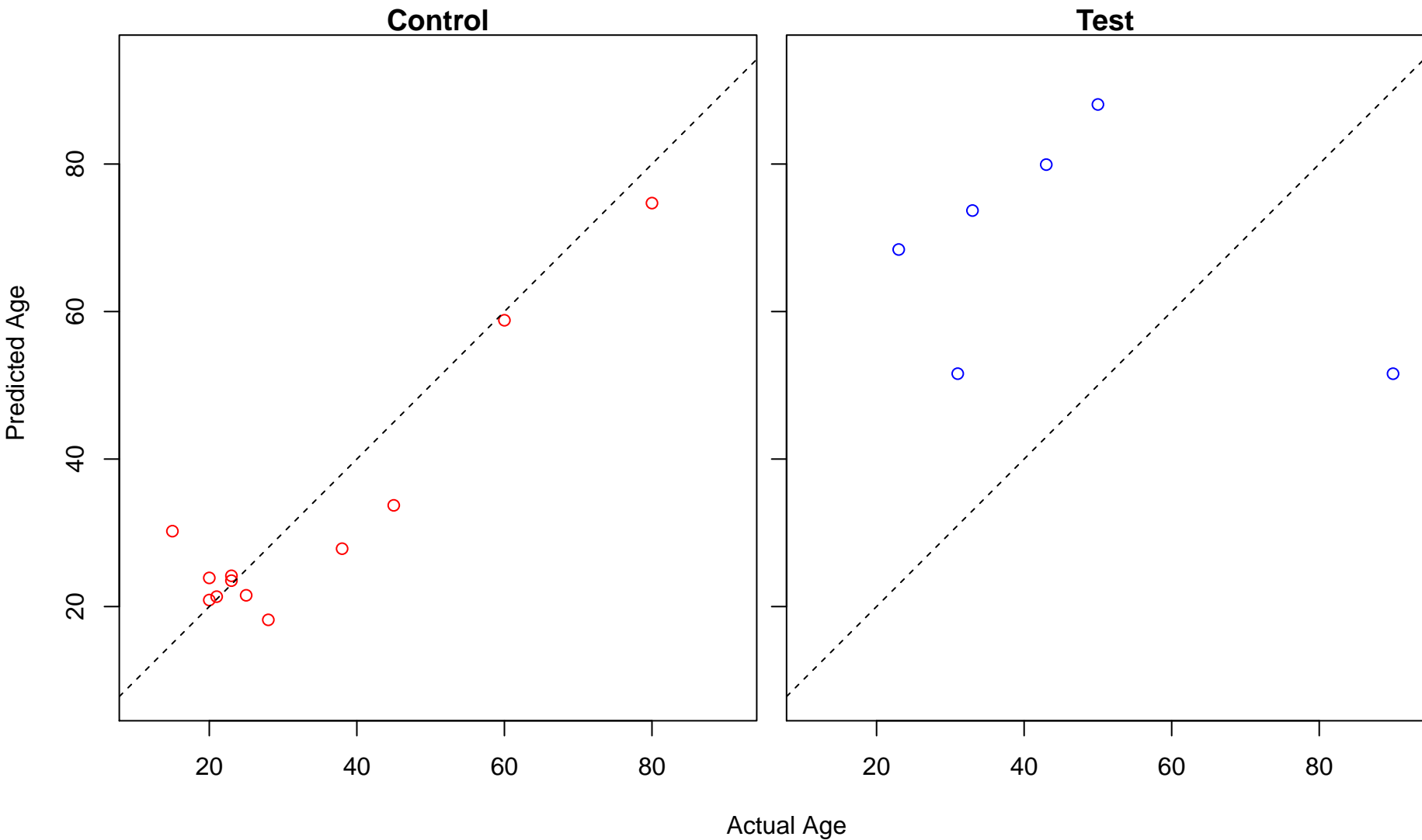
positive regulation of antigen receptor-mediated signaling pathway (Score: 46.375982)



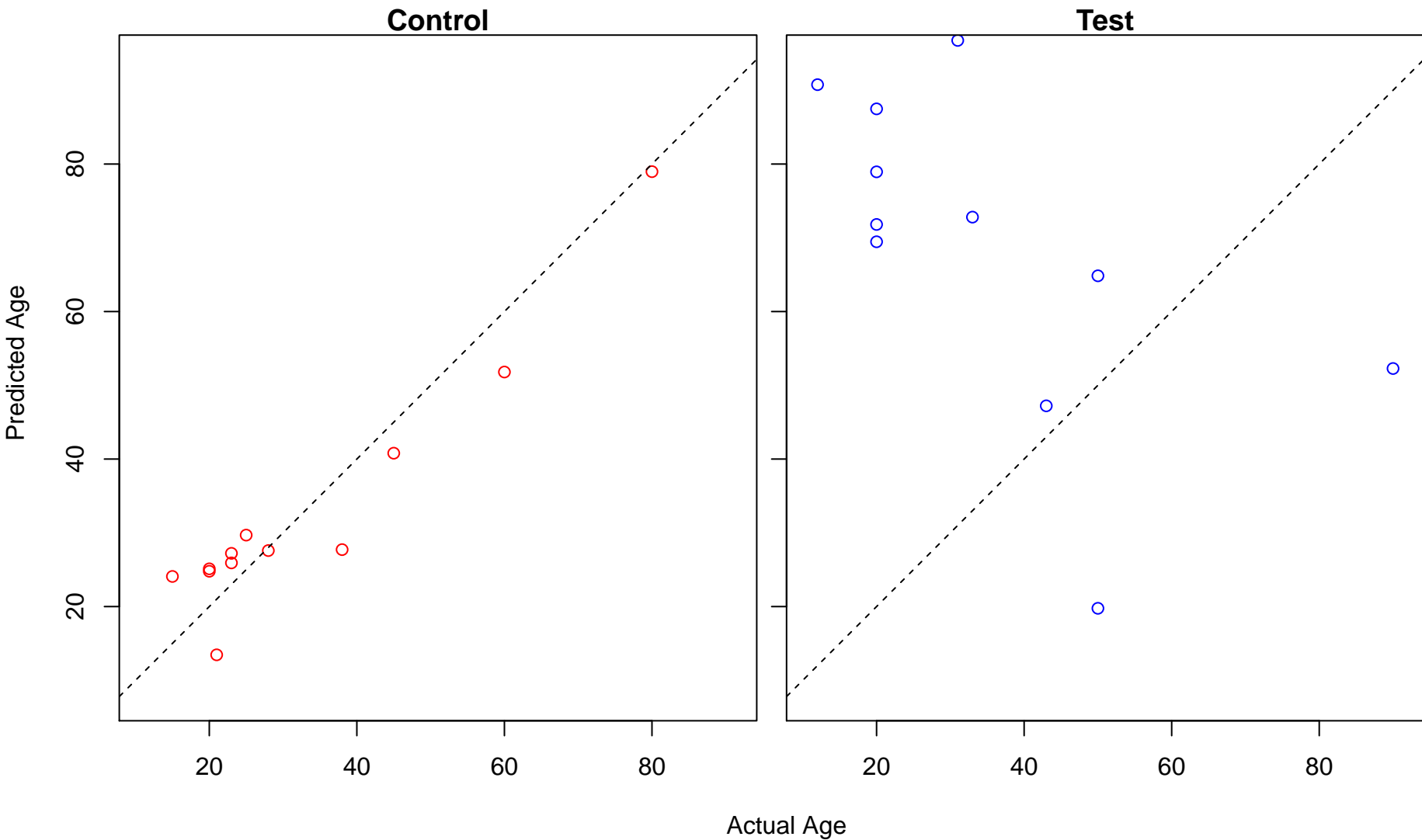
negative regulation of axon extension (Score: 46.124533)



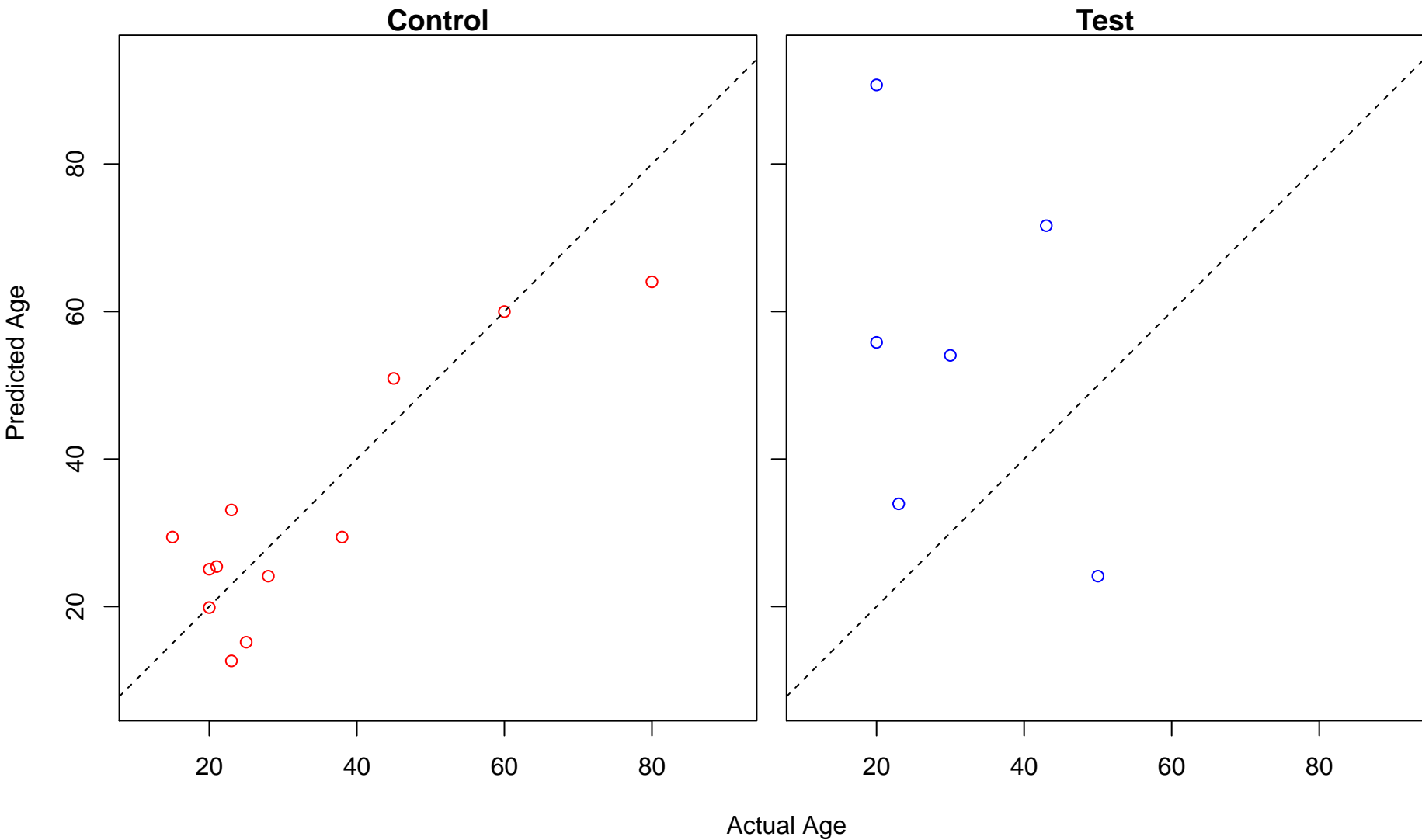
positive regulation of epidermal cell differentiation (Score: 45.781186)



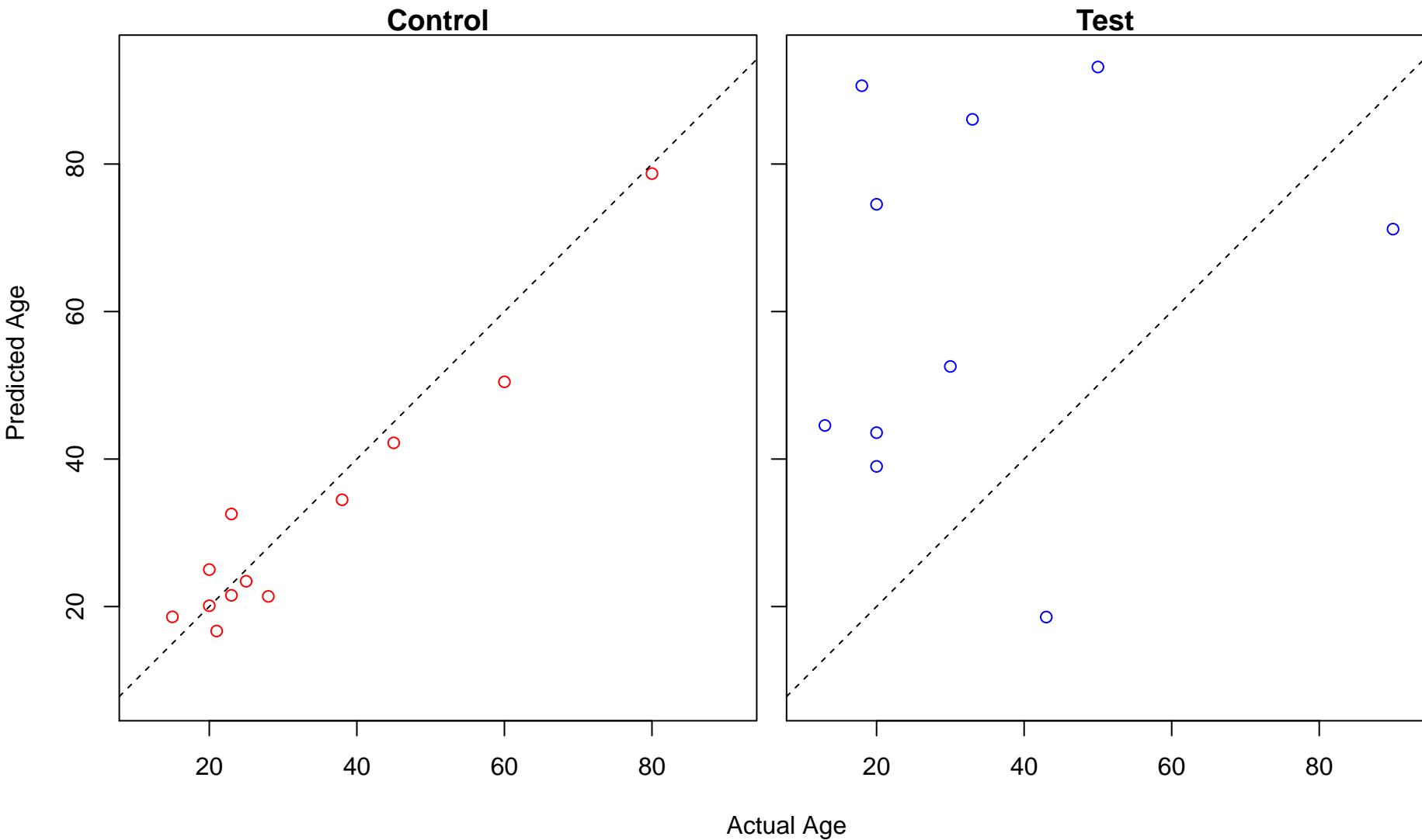
regulation of calcium ion-dependent exocytosis (Score: 45.632335)



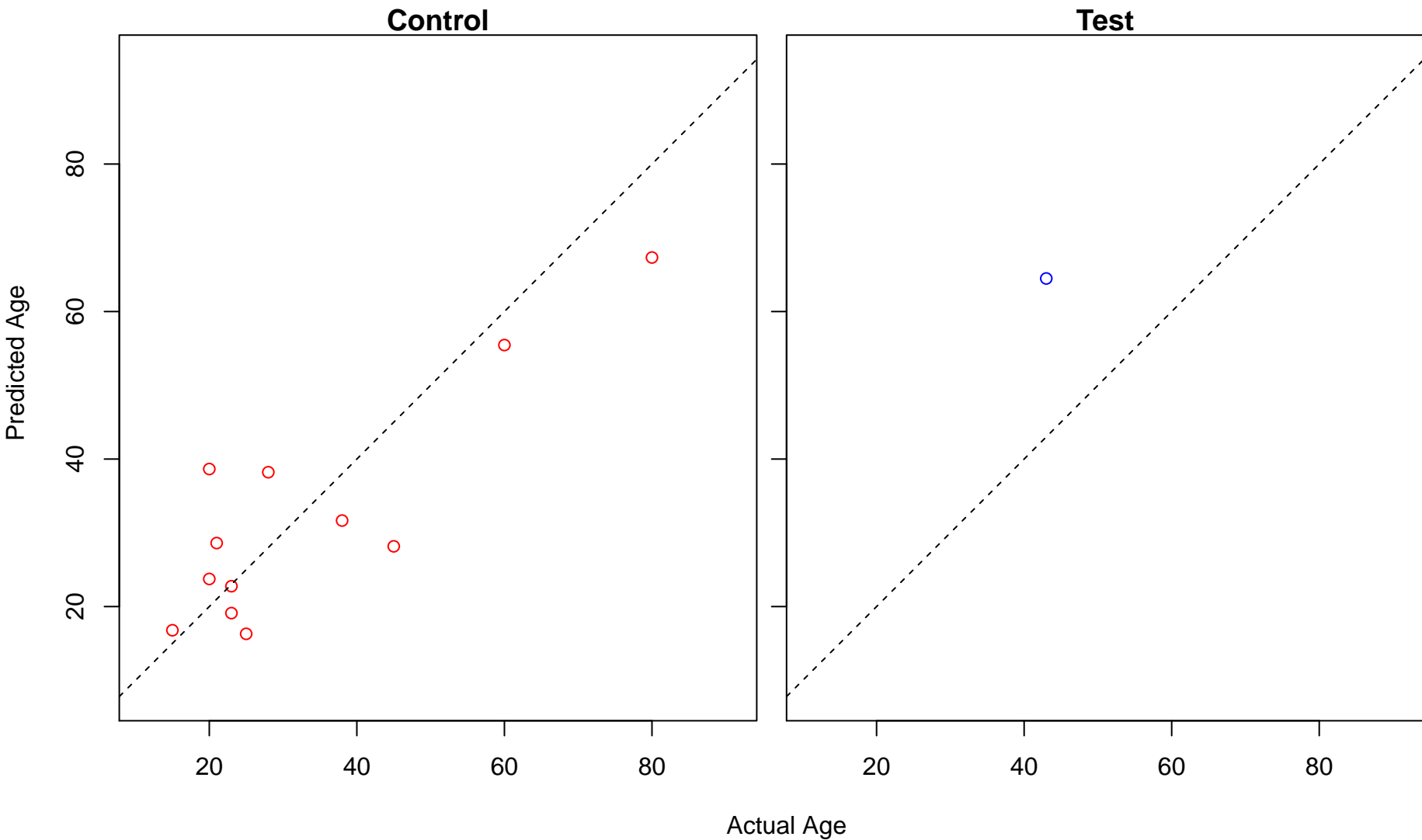
lens fiber cell development (Score: 45.361481)



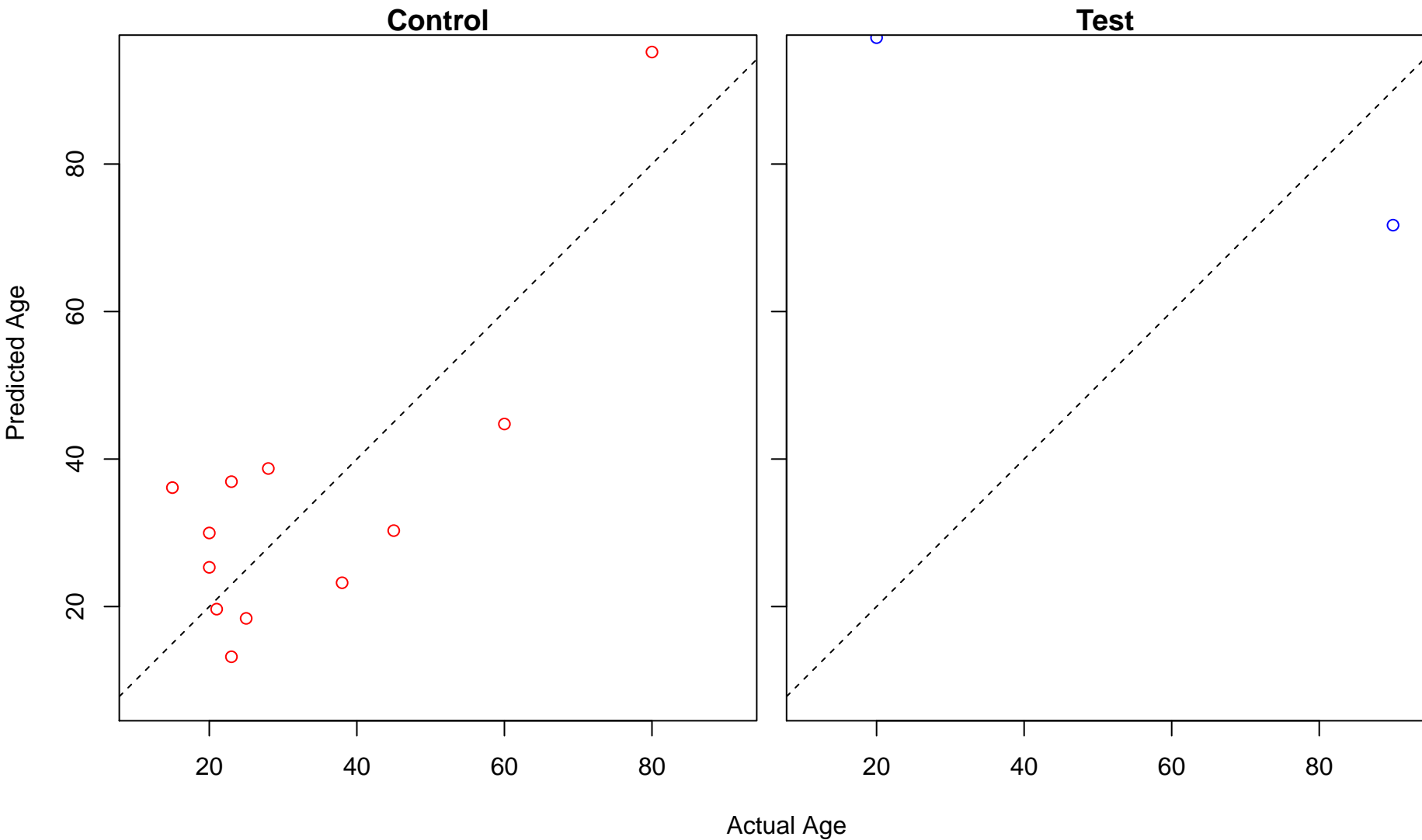
positive regulation of gliogenesis (Score: 45.090966)



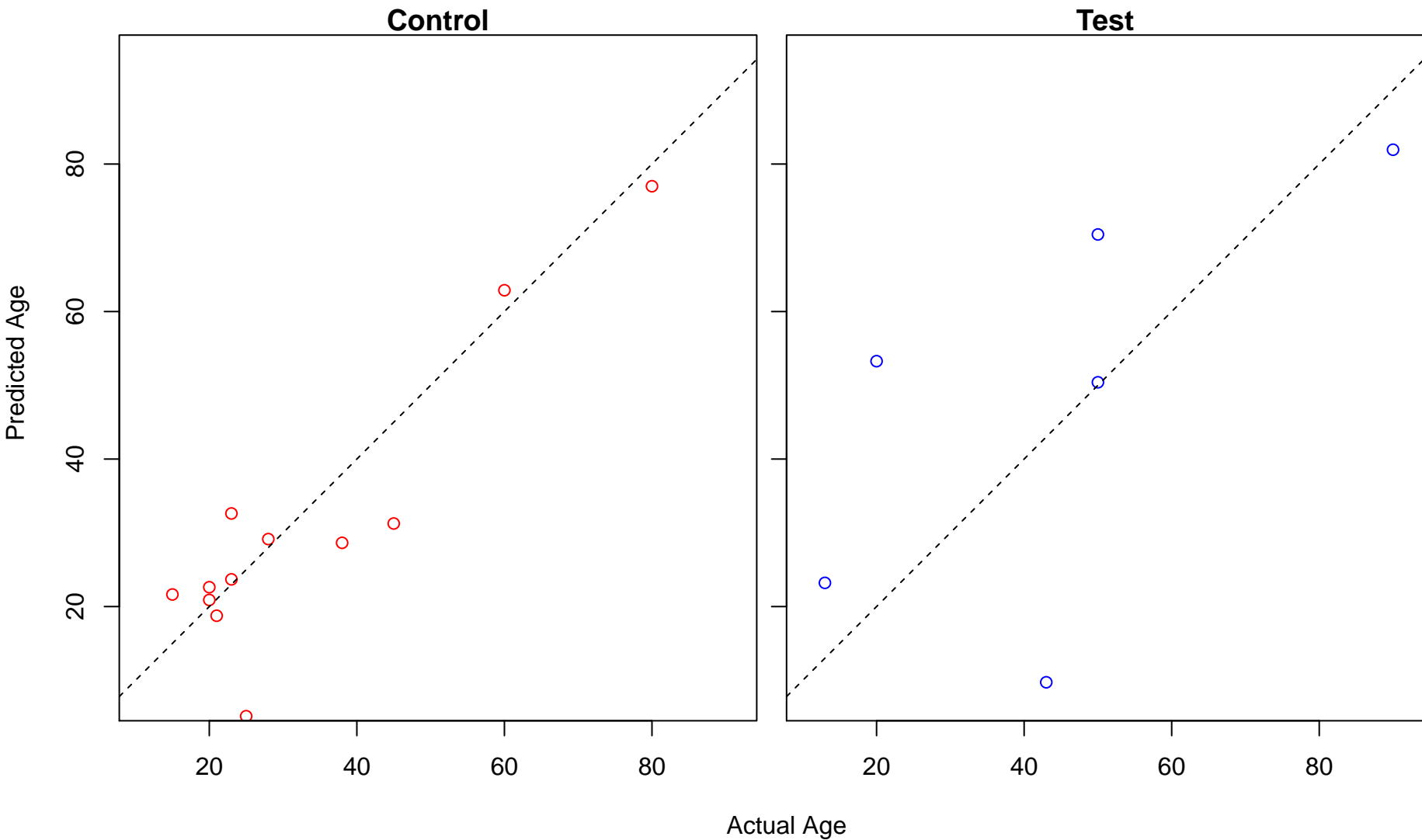
nuclear pore complex assembly (Score: 44.961862)



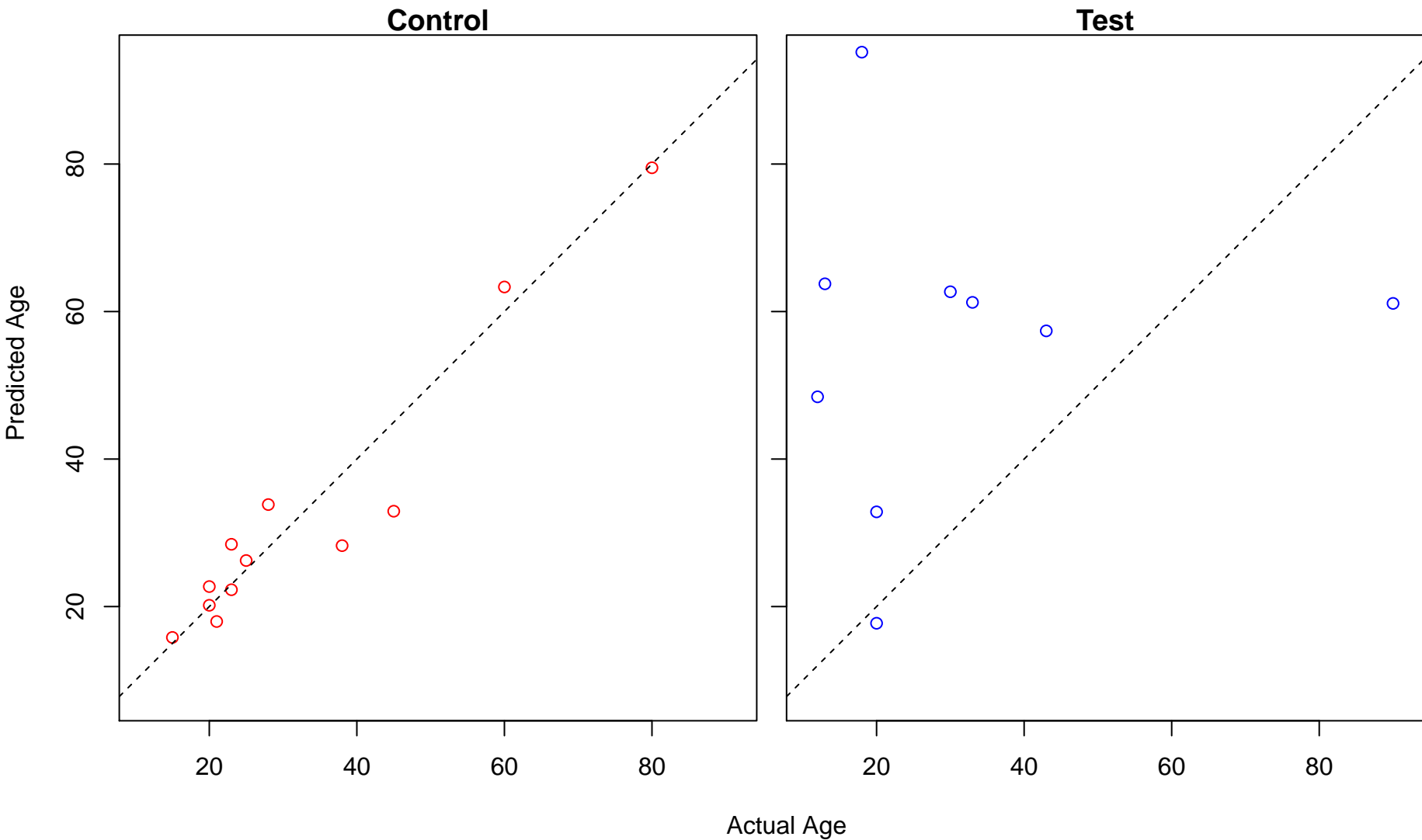
positive regulation of dendrite morphogenesis (Score: 44.817524)



cortical actin cytoskeleton organization (Score: 44.809747)

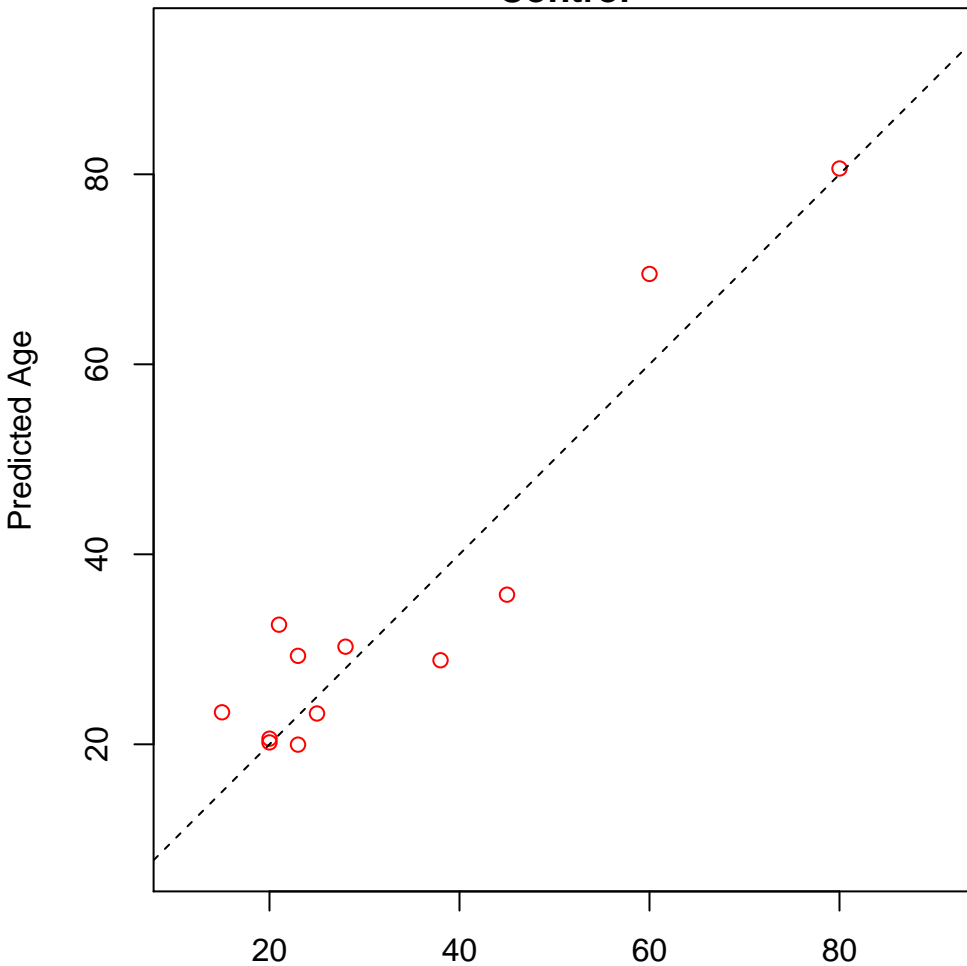


chromatin silencing (Score: 44.715306)

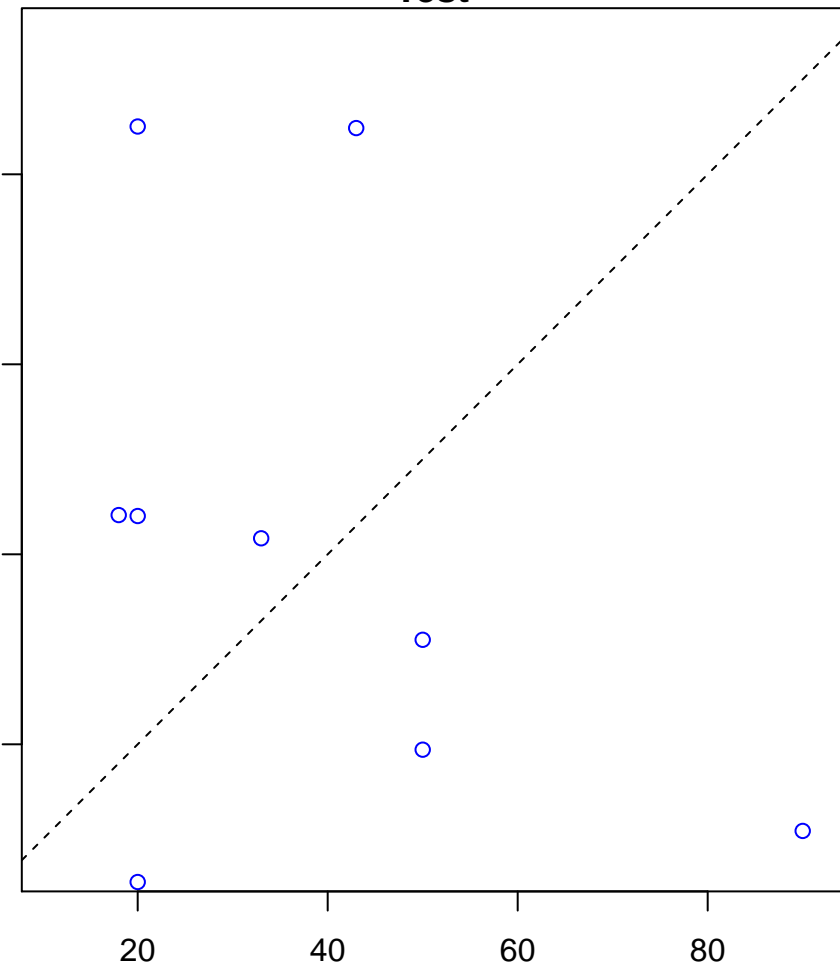


pharyngeal system development (Score: 44.632139)

Control

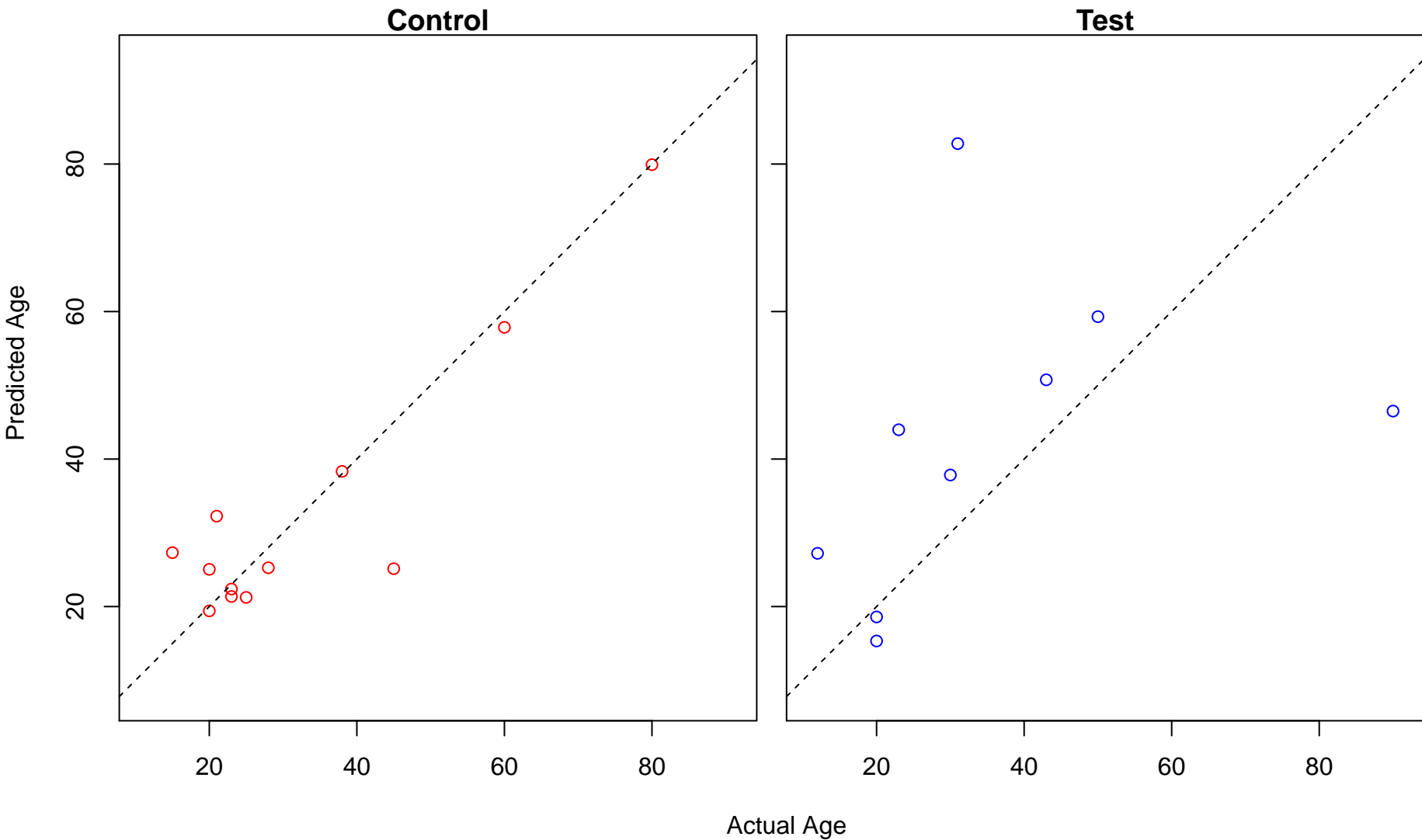


Test

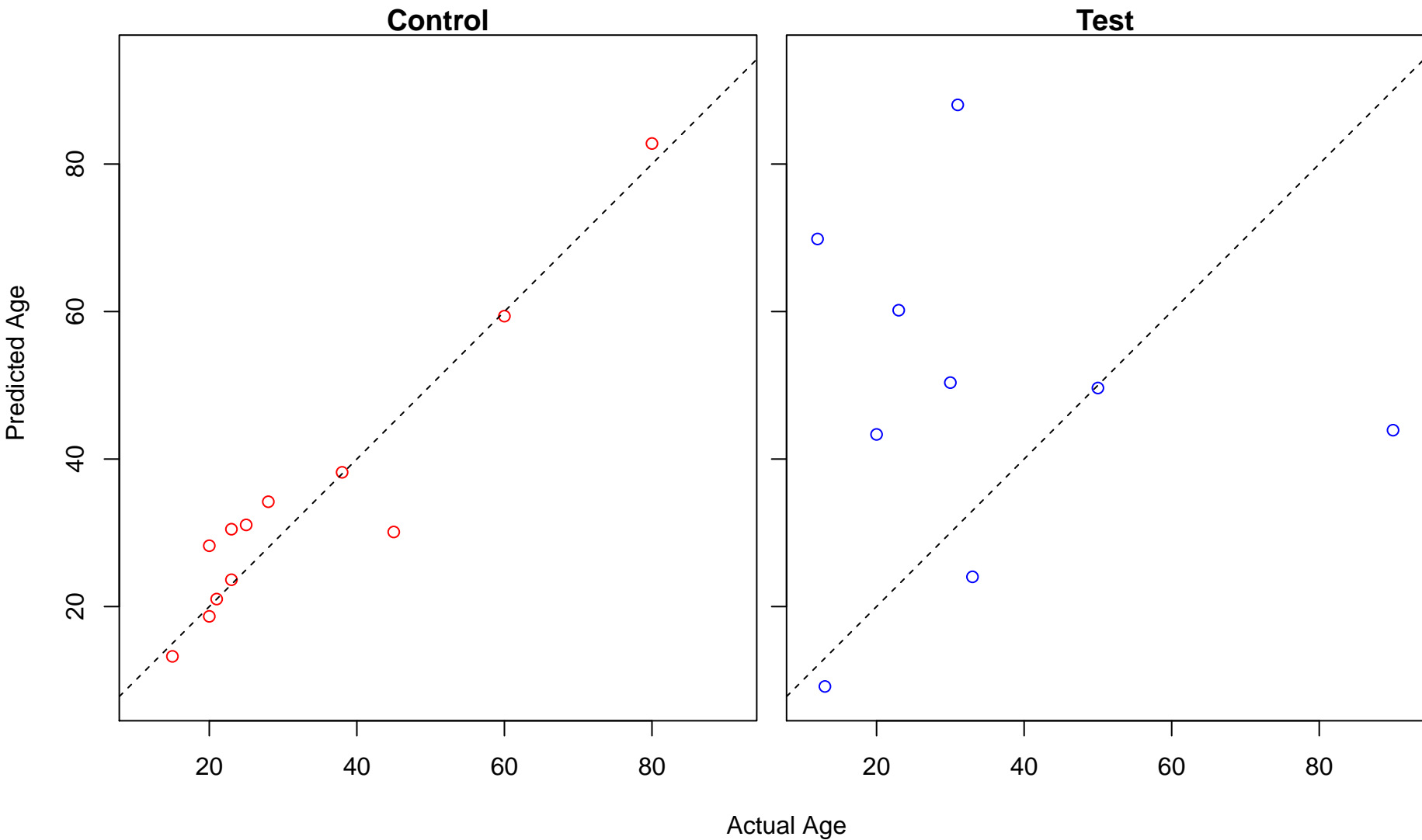


Actual Age

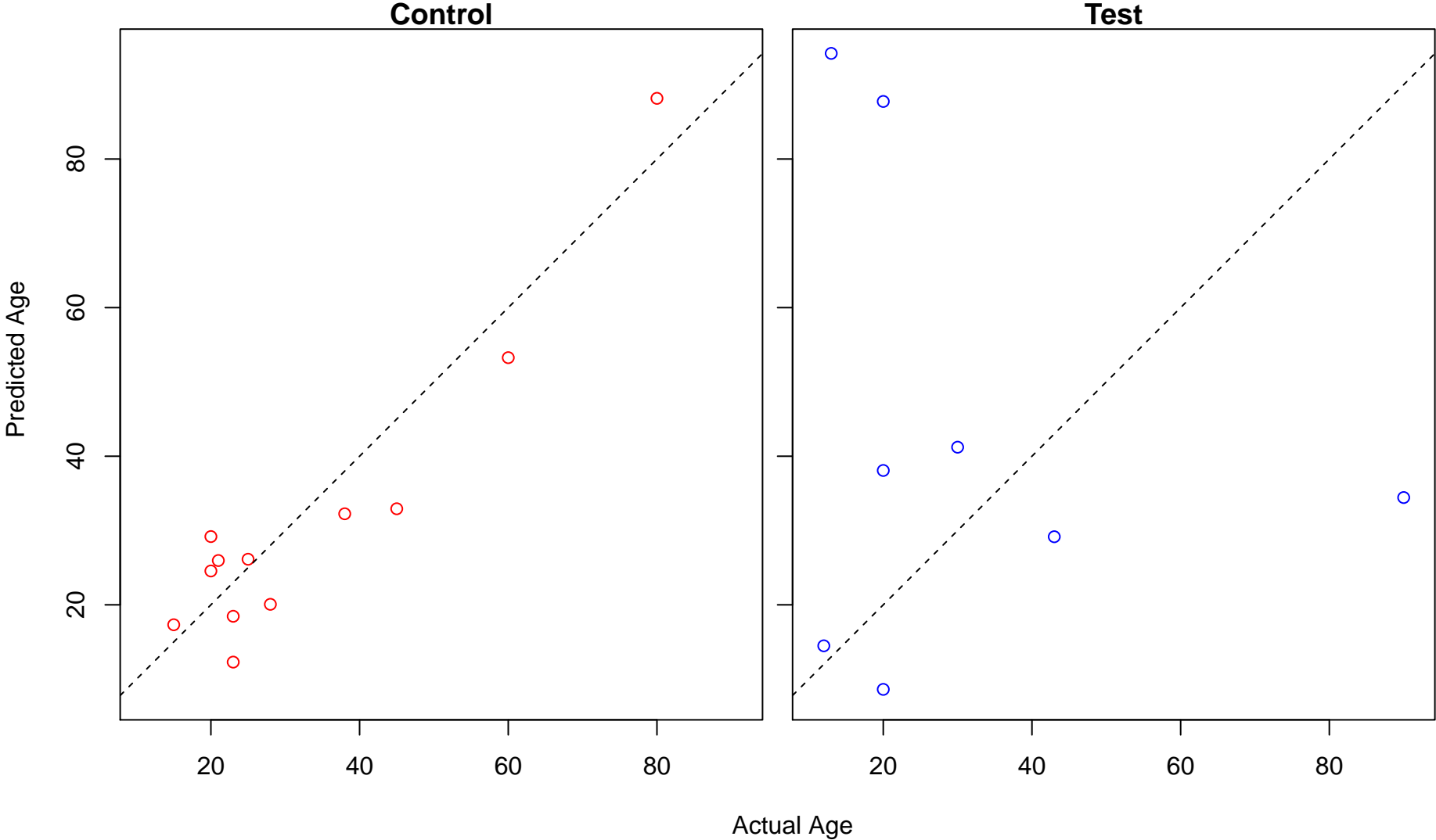
positive regulation of leukocyte migration (Score: 44.237713)



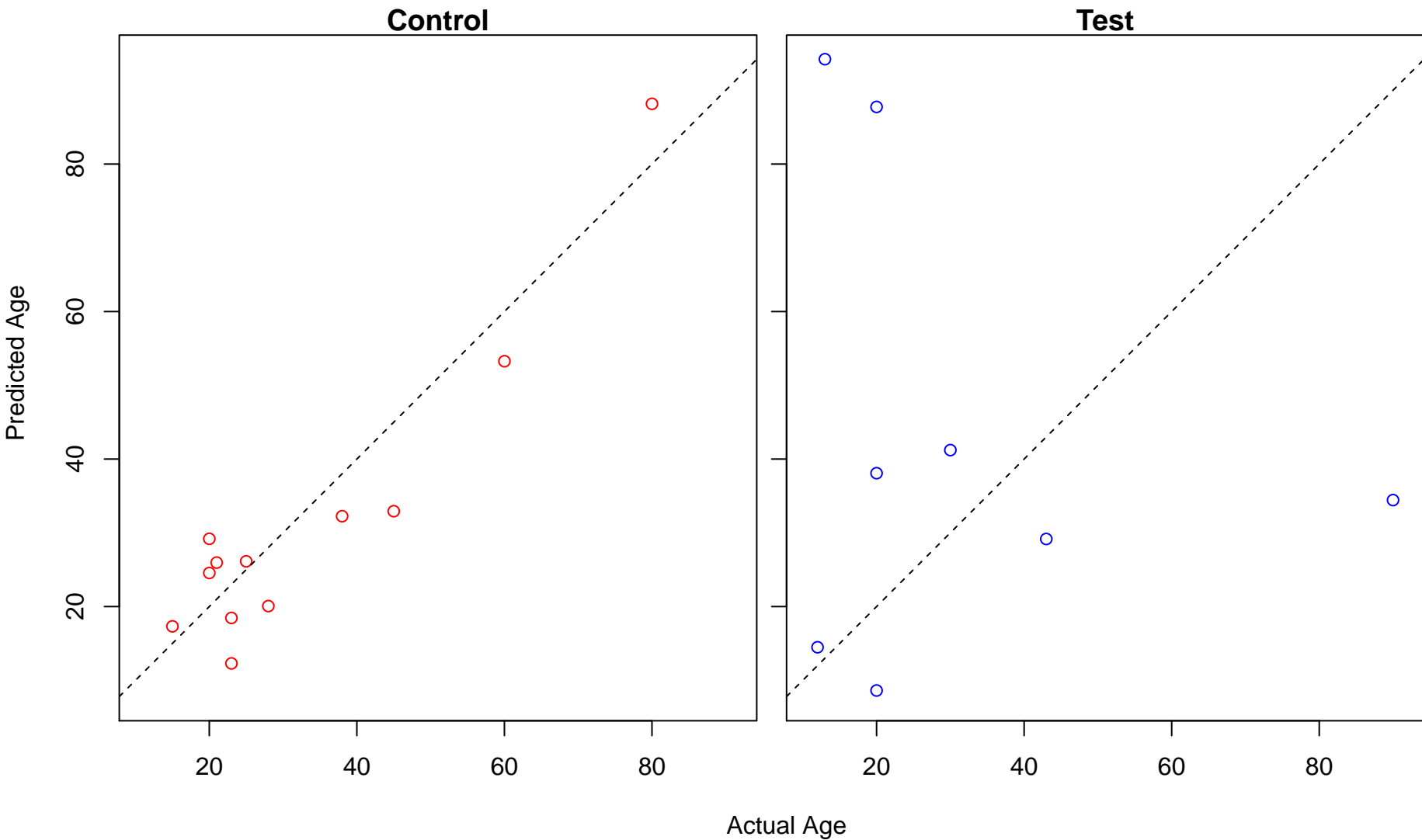
bile acid metabolic process (Score: 44.234350)



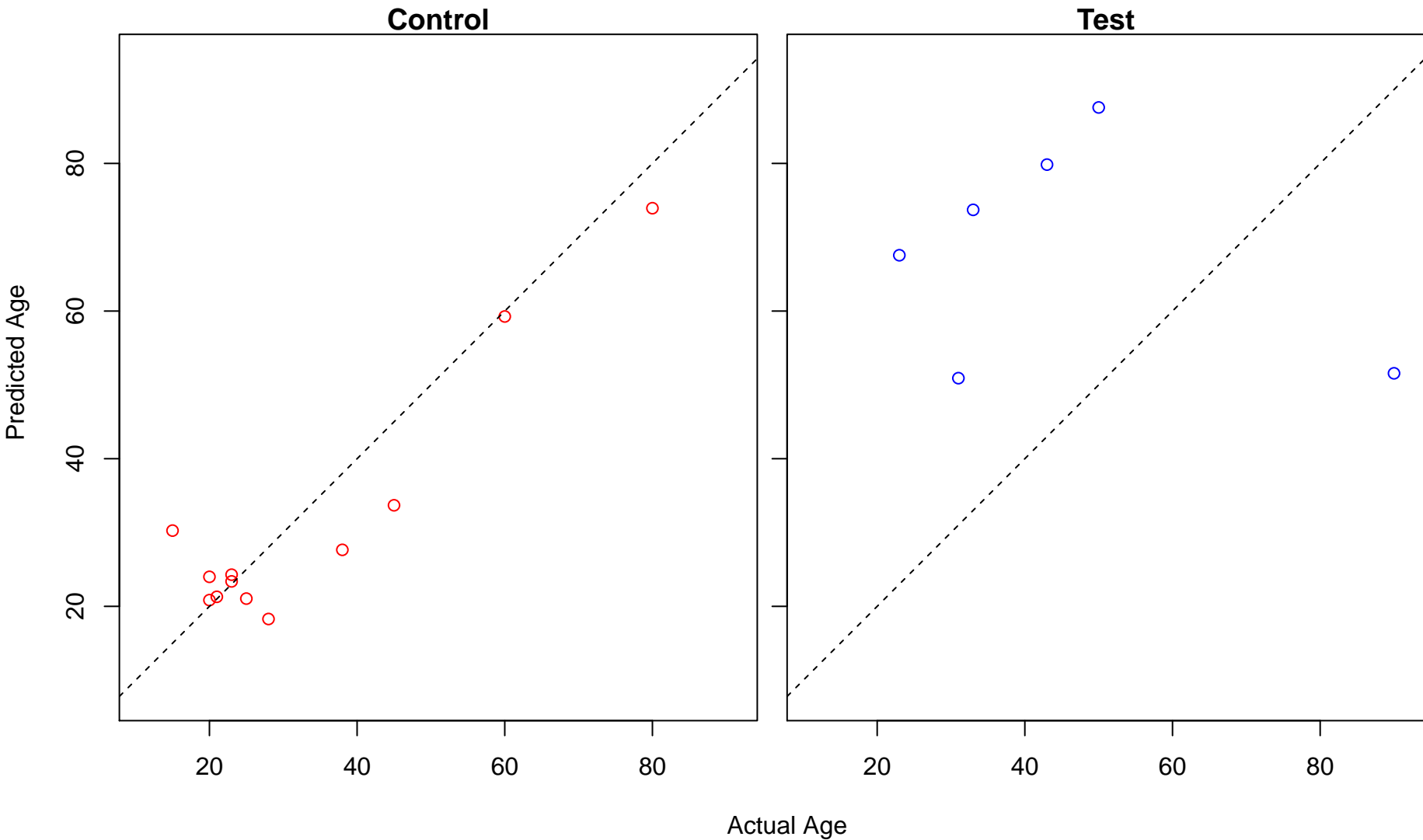
positive regulation of protein localization to plasma membrane (Score: 44.127701)



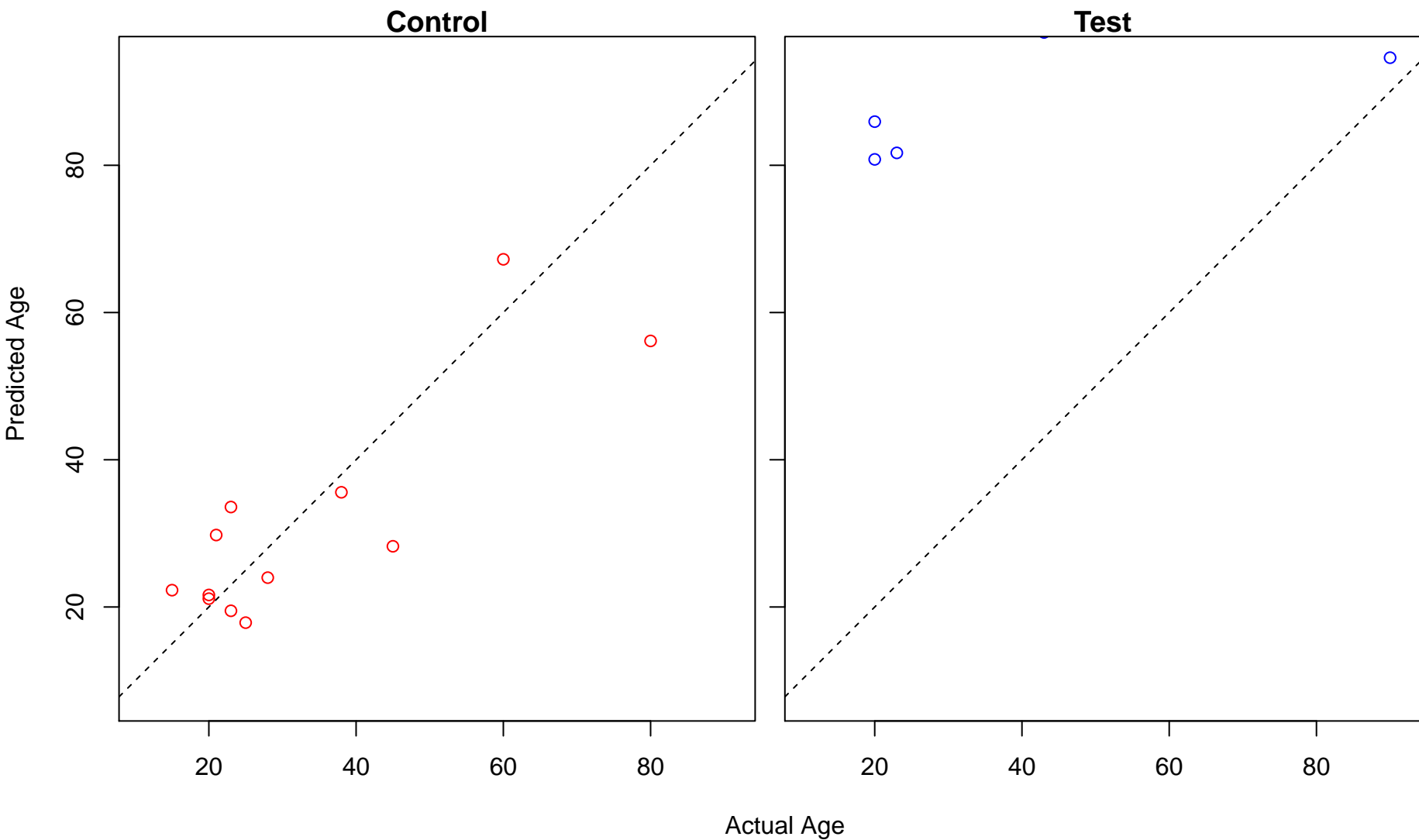
positive regulation of protein localization to cell periphery (Score: 44.127701)



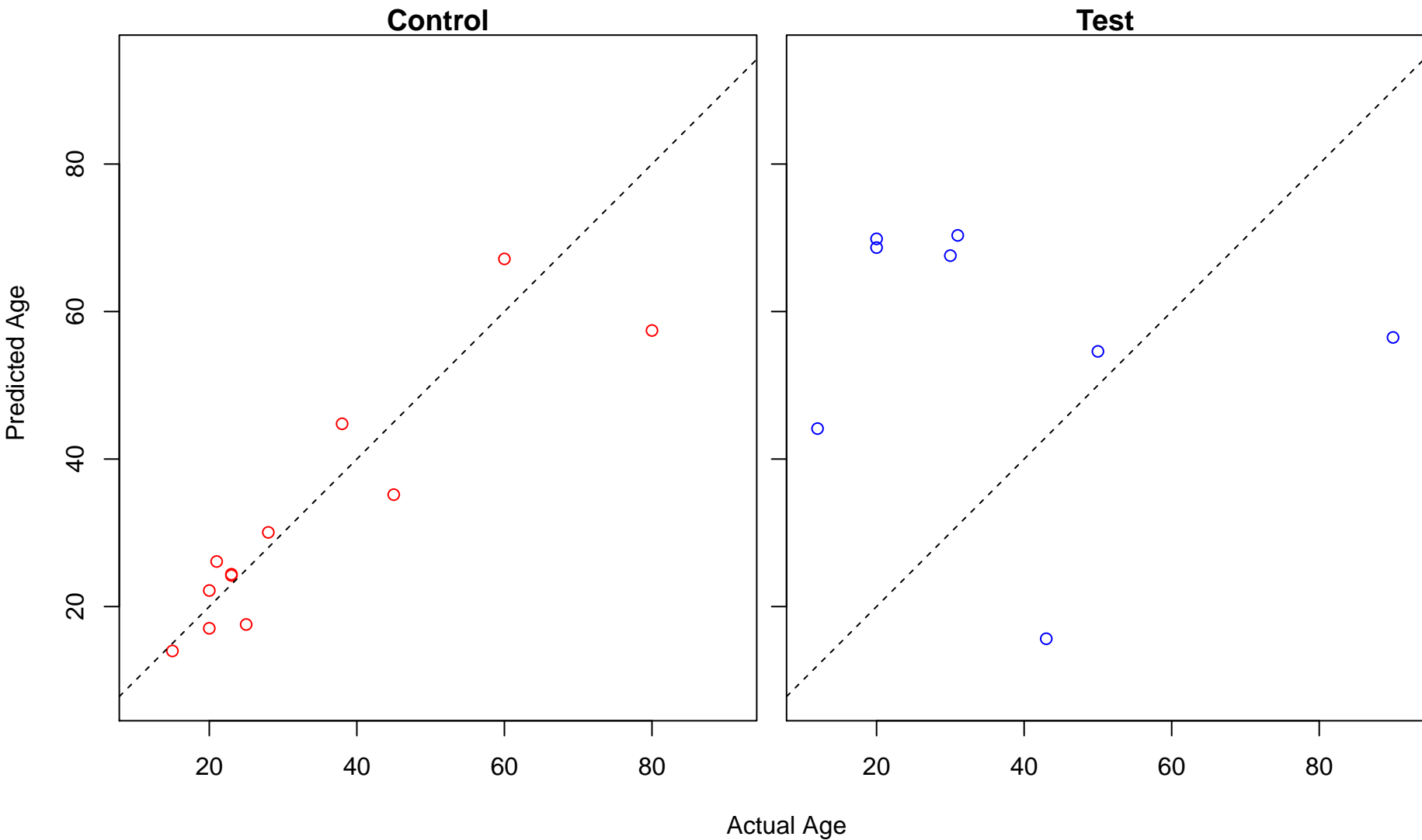
positive regulation of epidermis development (Score: 44.026898)



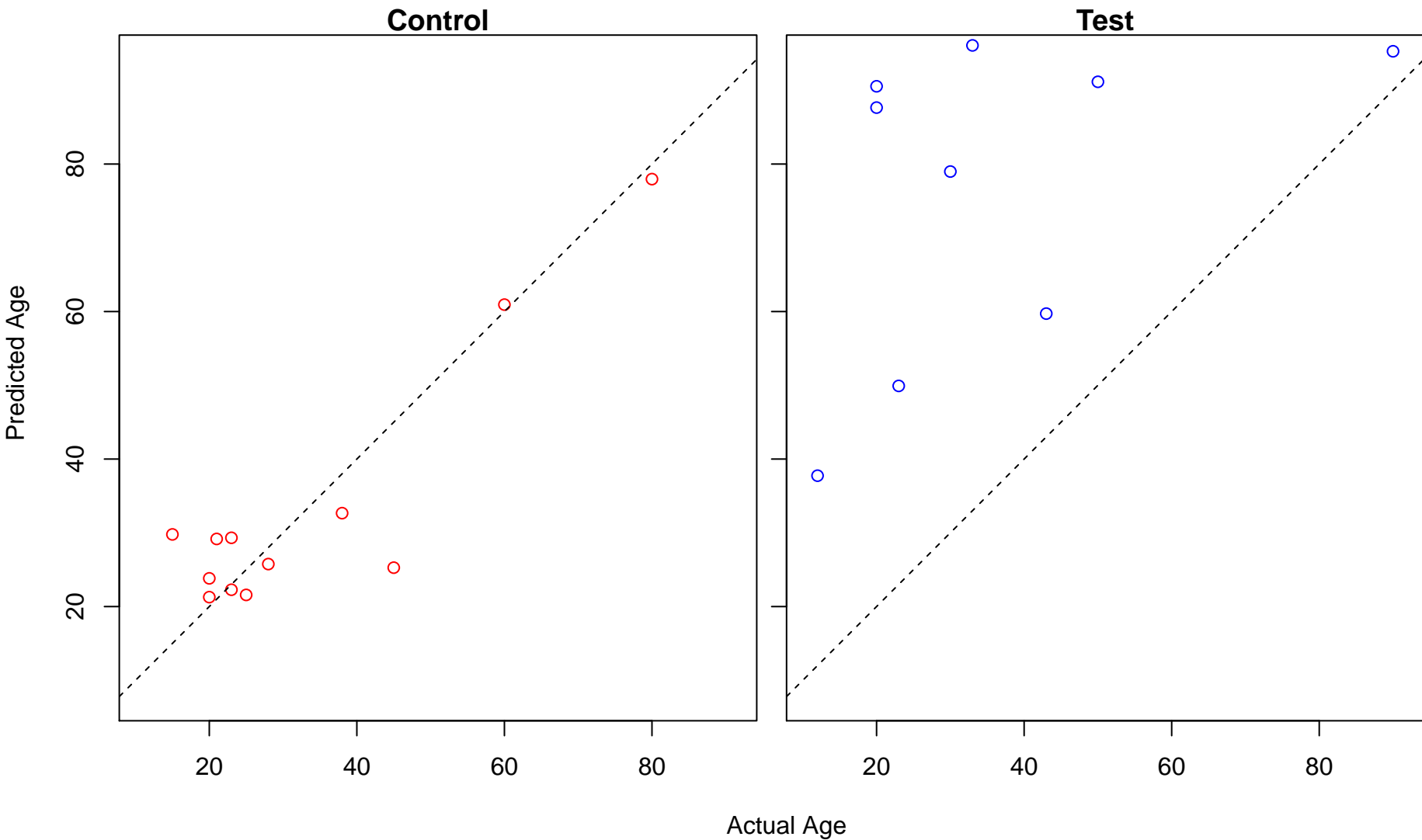
positive regulation of integrin activation (Score: 43.873236)



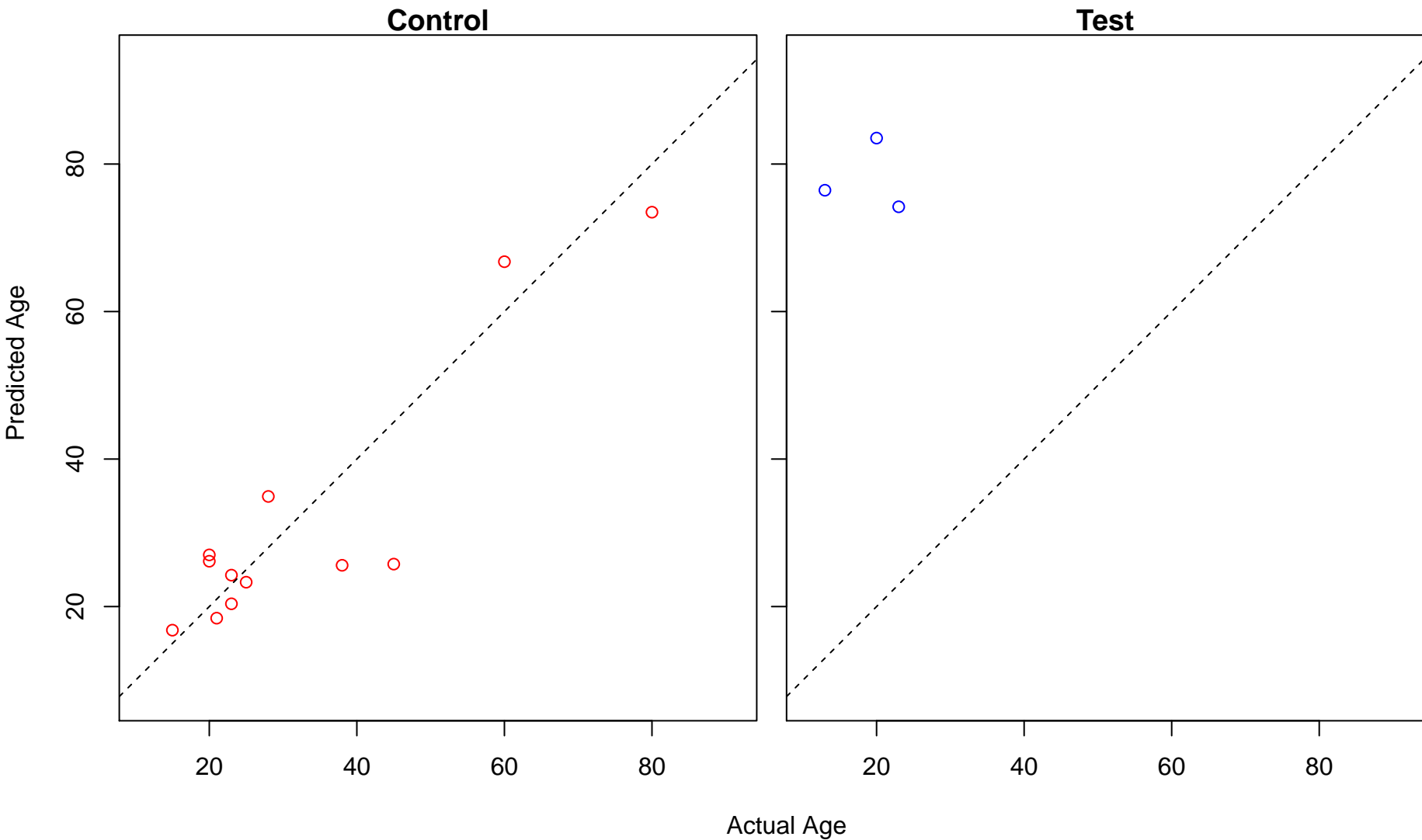
nuclear pore organization (Score: 43.856021)



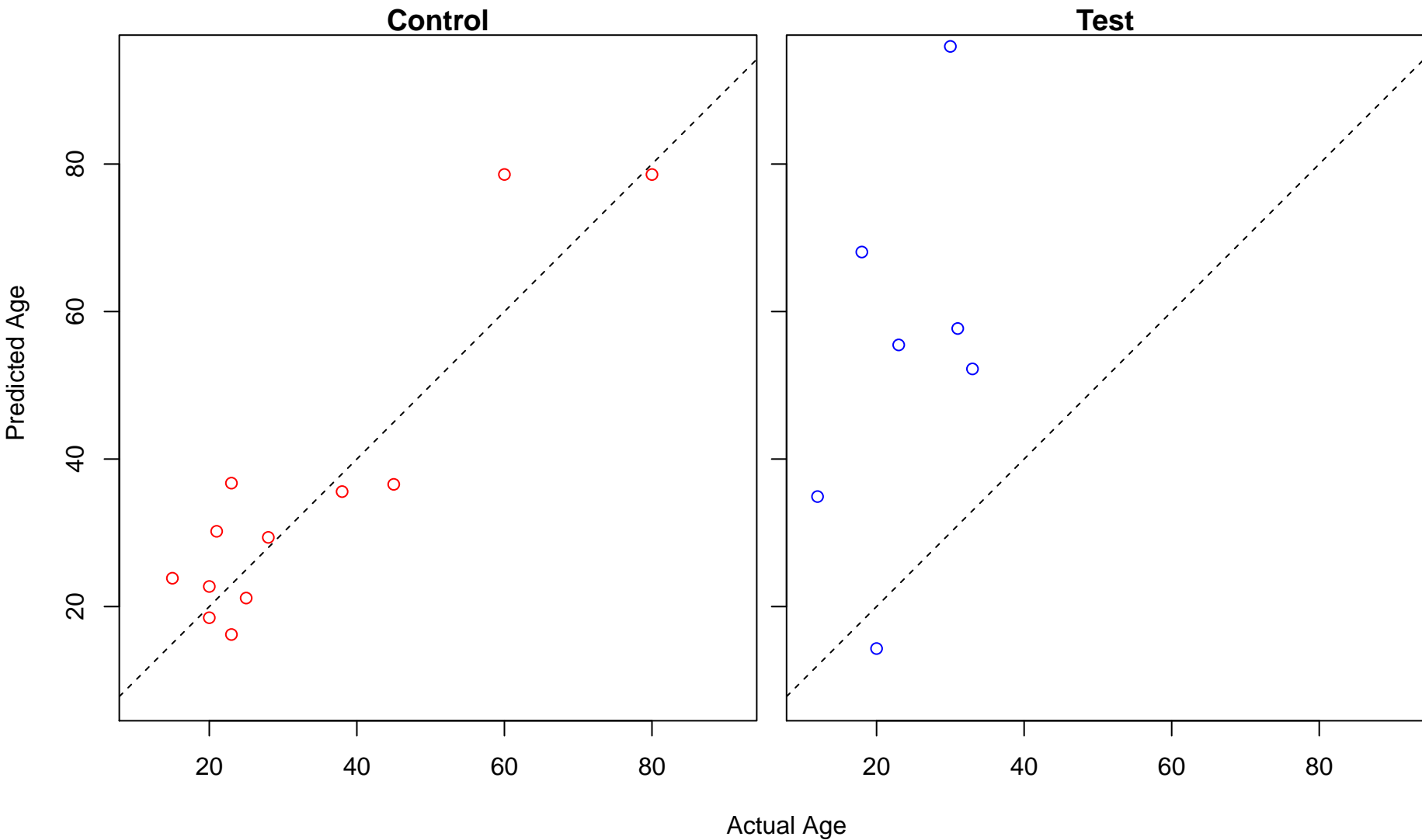
positive regulation of endocytosis (Score: 43.182615)



positive regulation of transcription from RNA polymerase I promoter (Score: 43.085988)

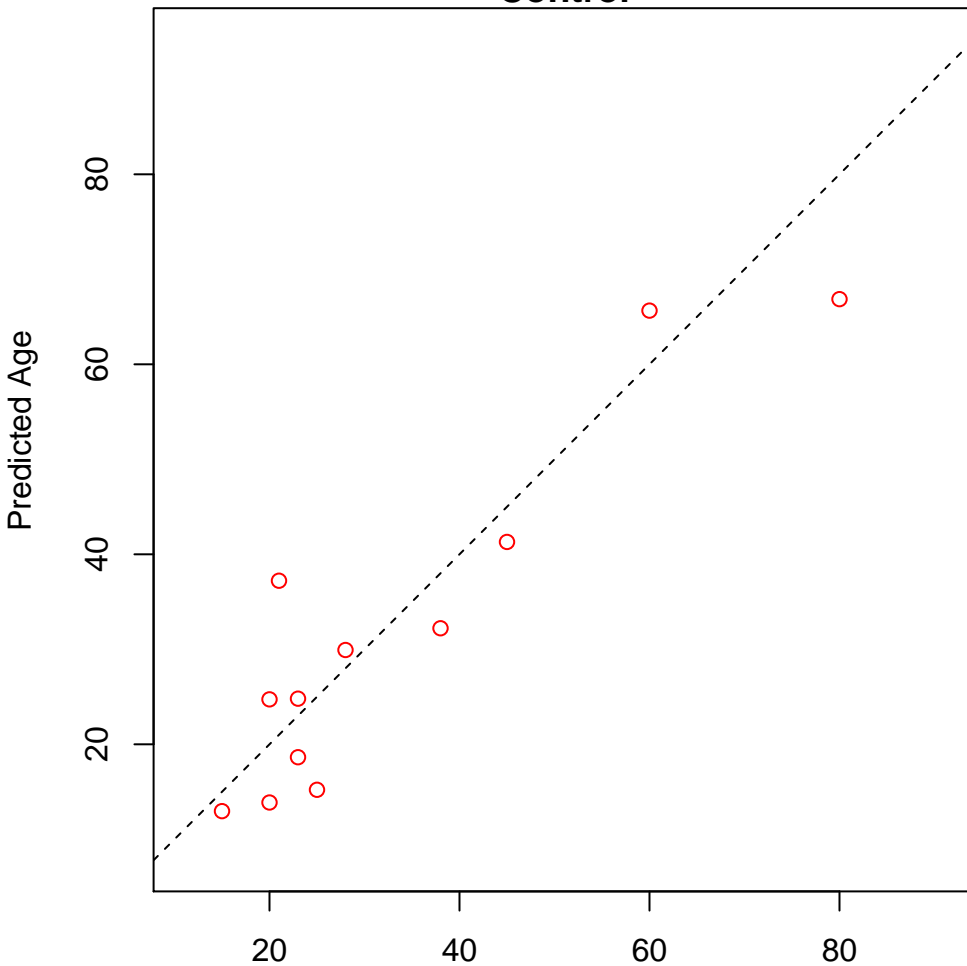


glycine metabolic process (Score: 42.654582)

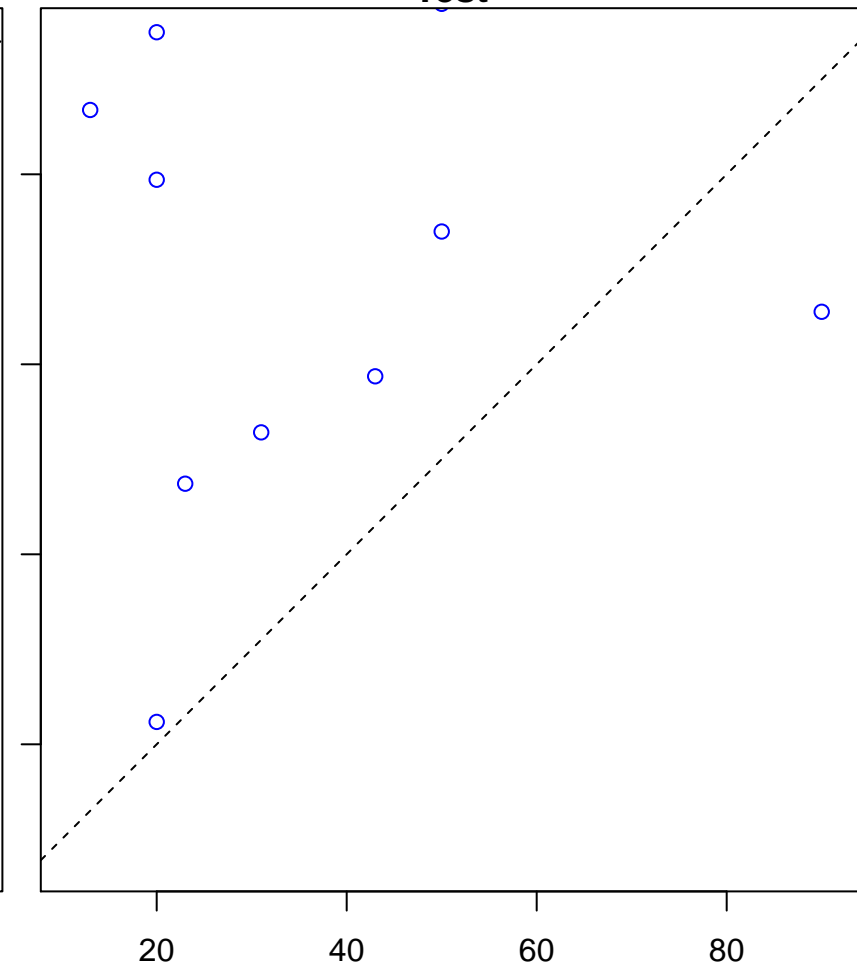


plasma lipoprotein particle assembly (Score: 42.002159)

Control

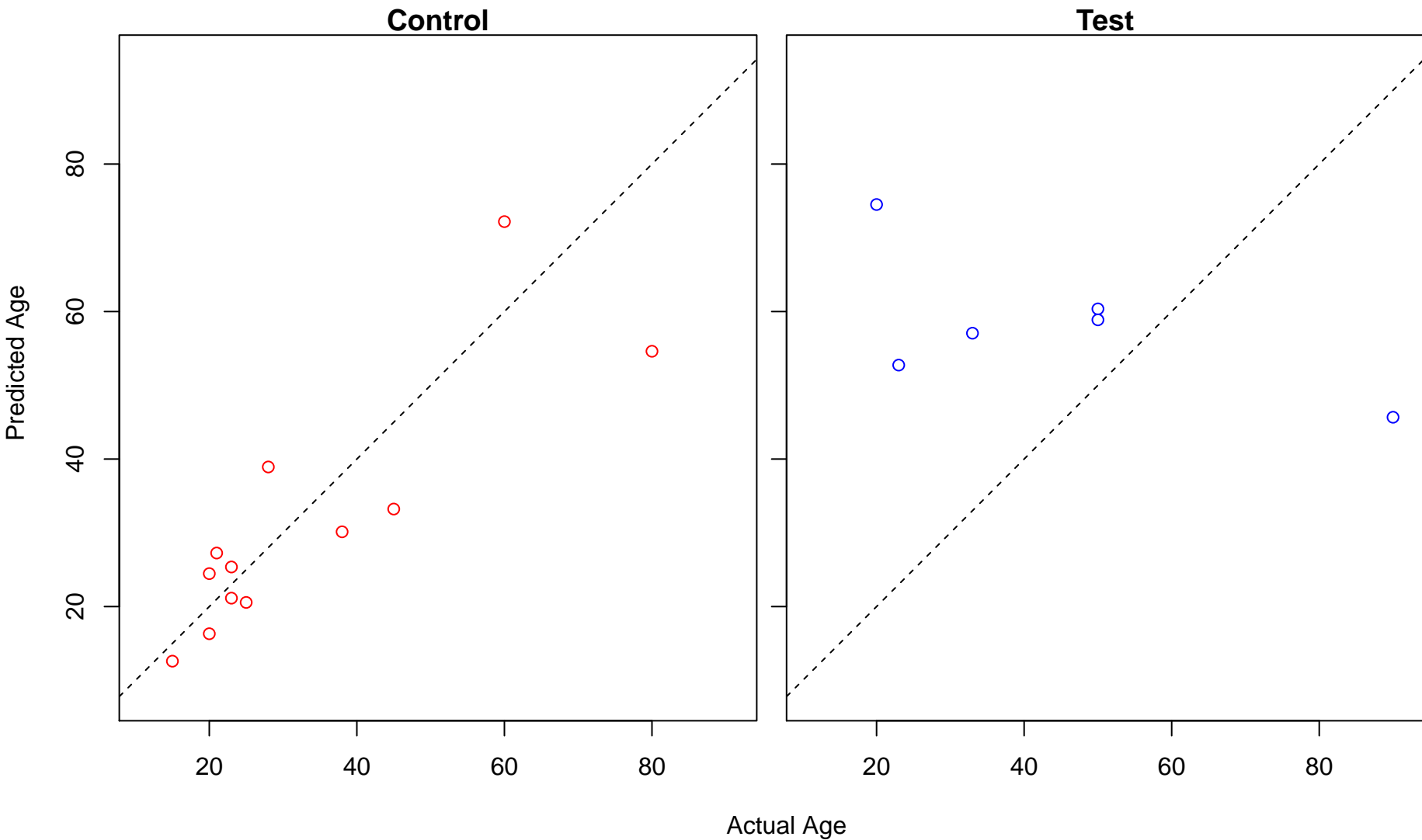


Test

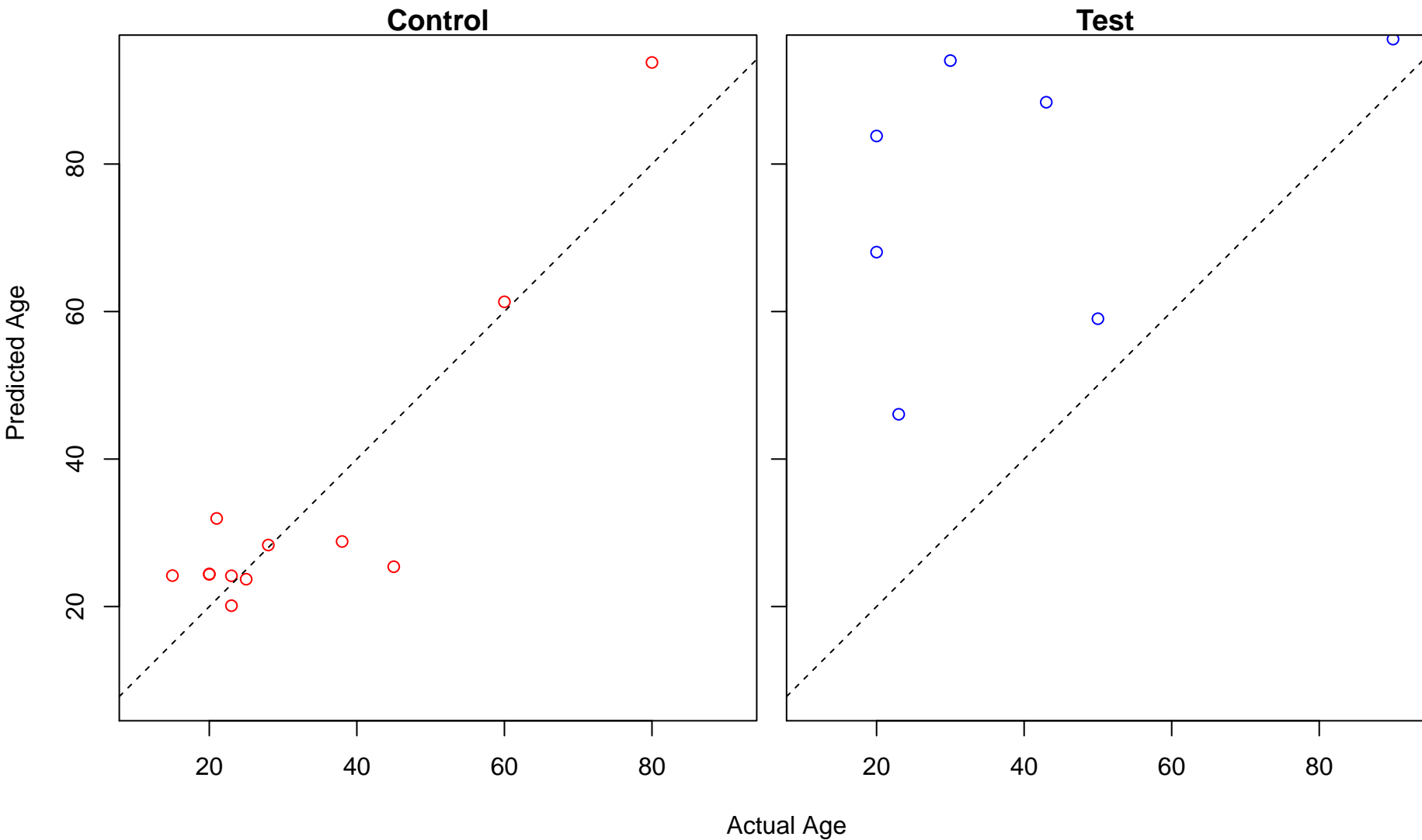


Actual Age

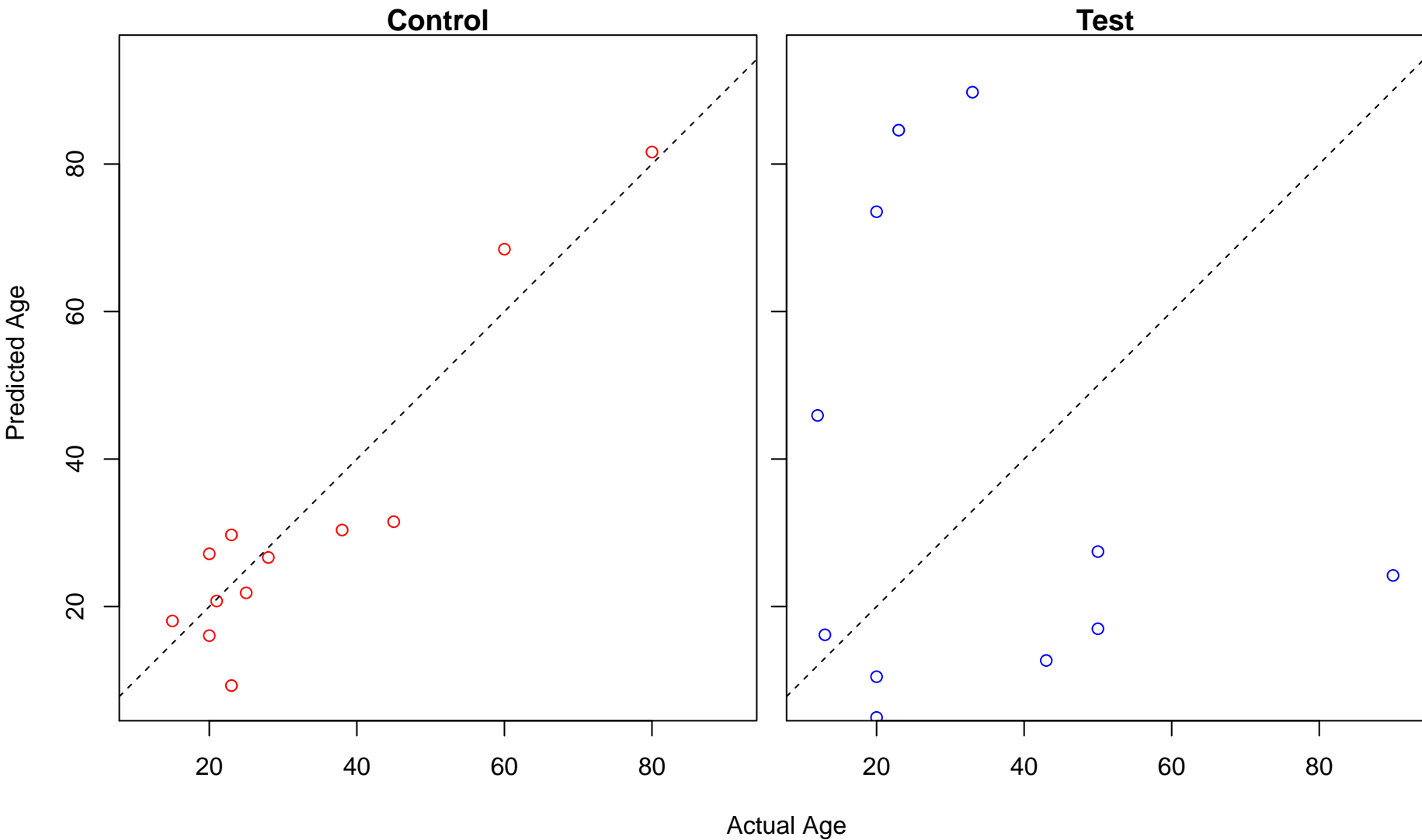
acute-phase response (Score: 41.902274)



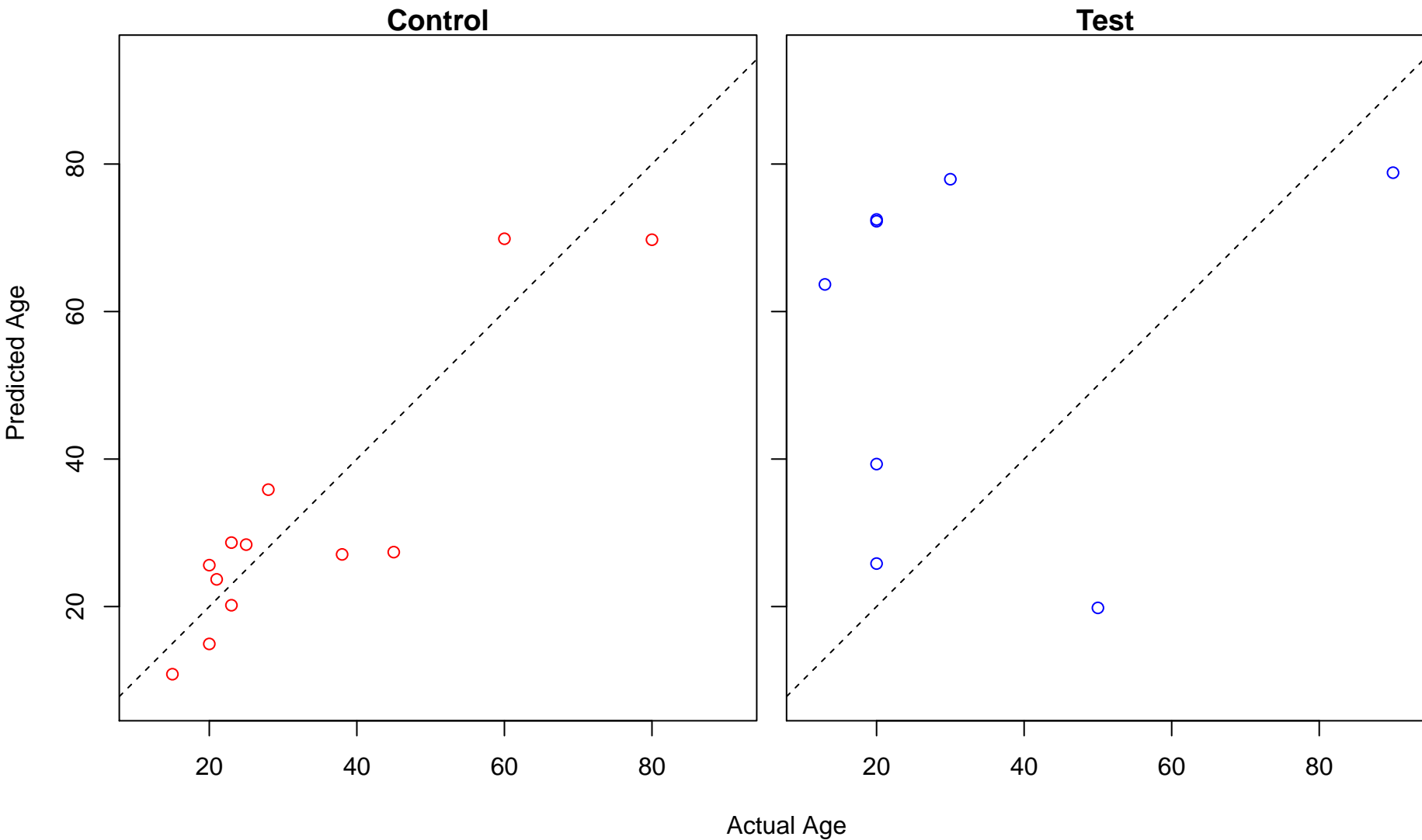
secretory granule organization (Score: 41.857412)



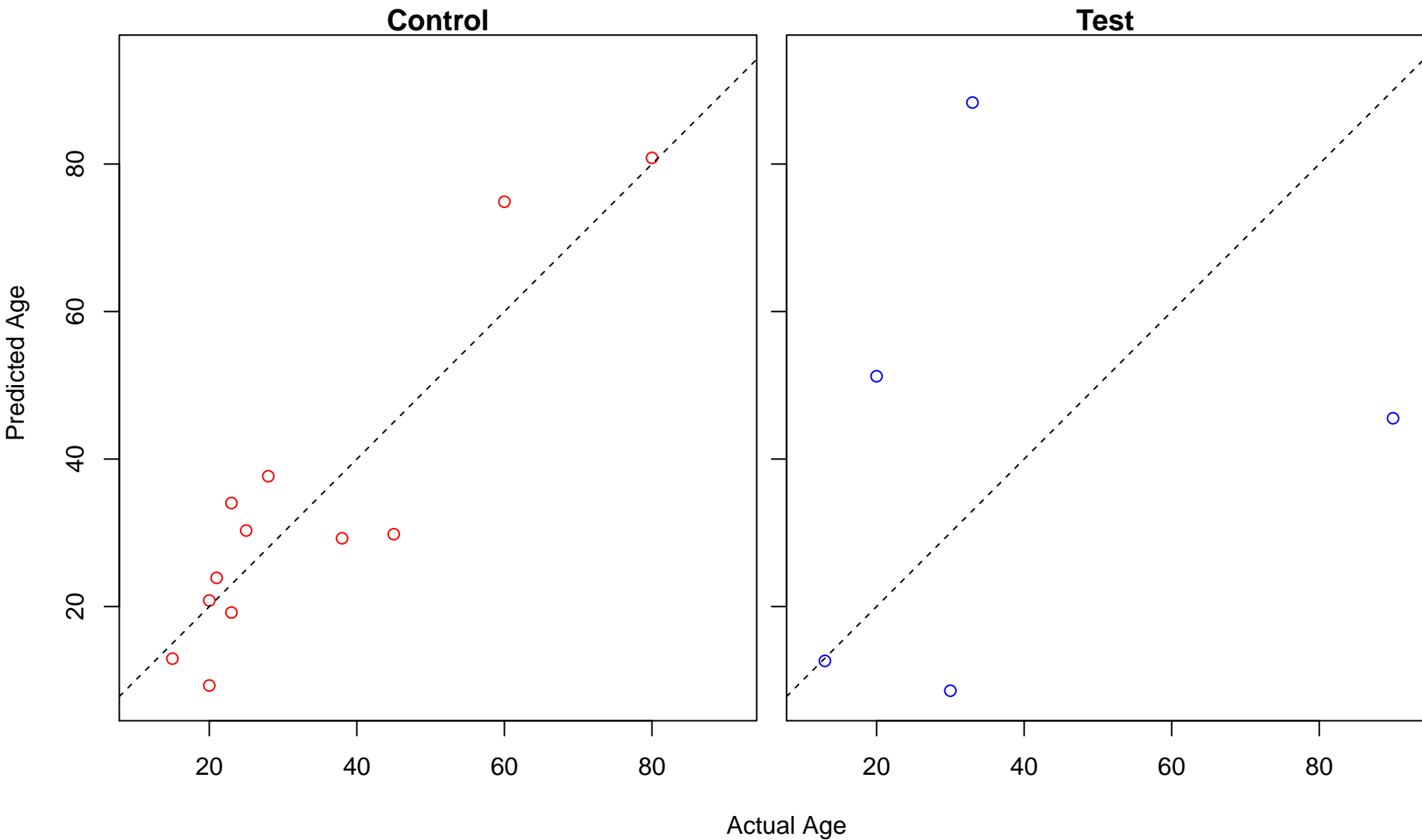
relaxation of cardiac muscle (Score: 41.462927)



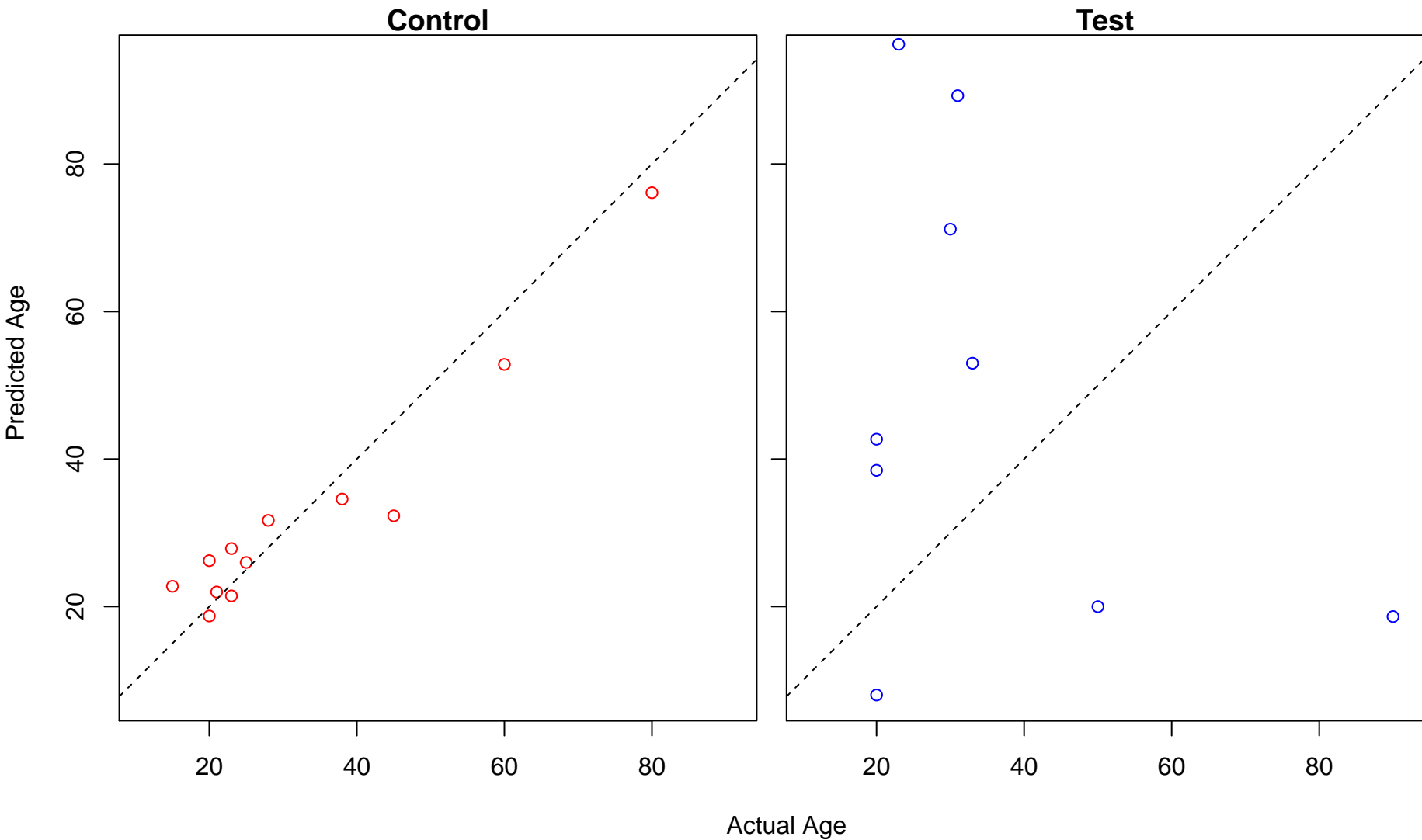
chemokine production (Score: 40.811028)



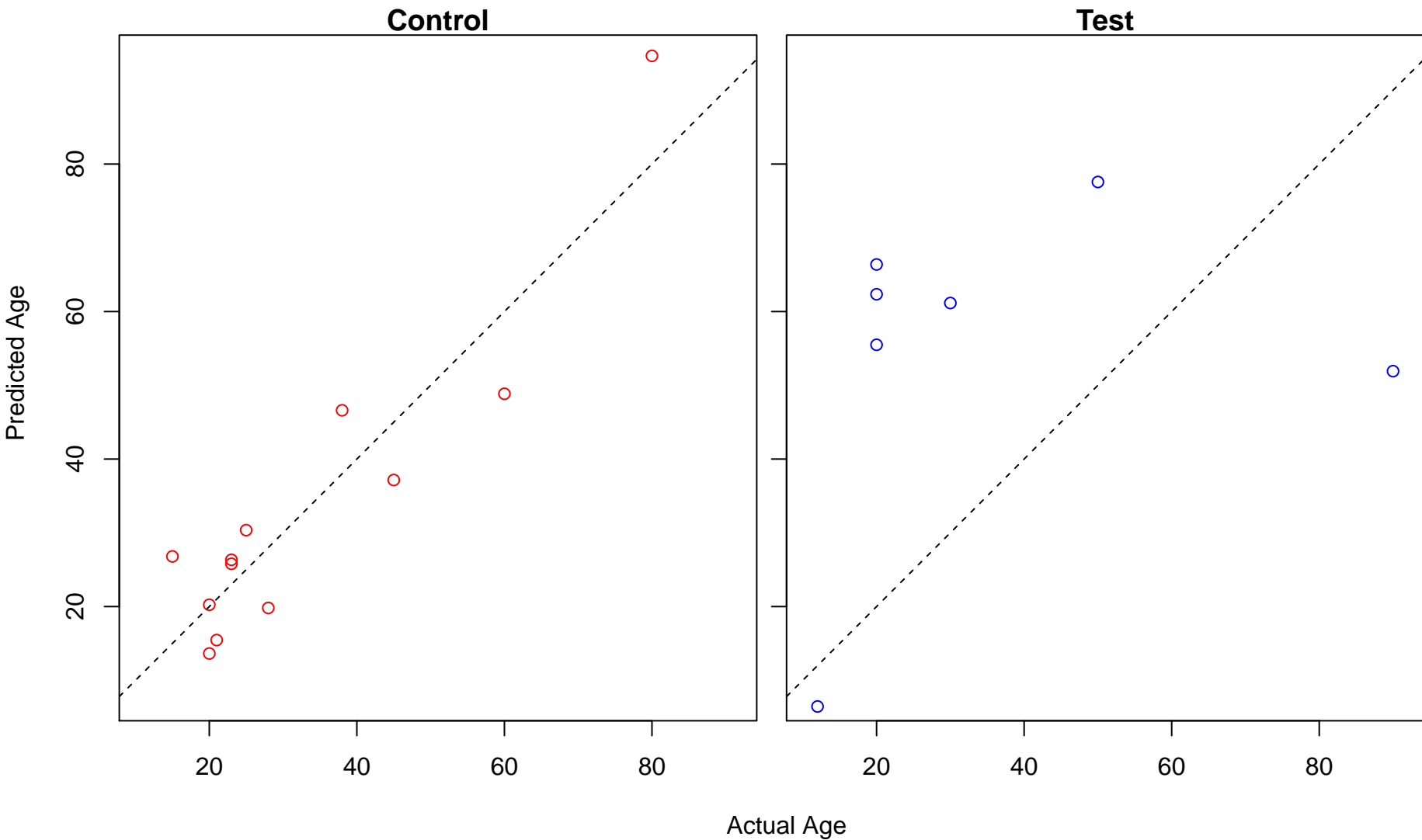
regulation of histone deacetylase activity (Score: 40.561859)



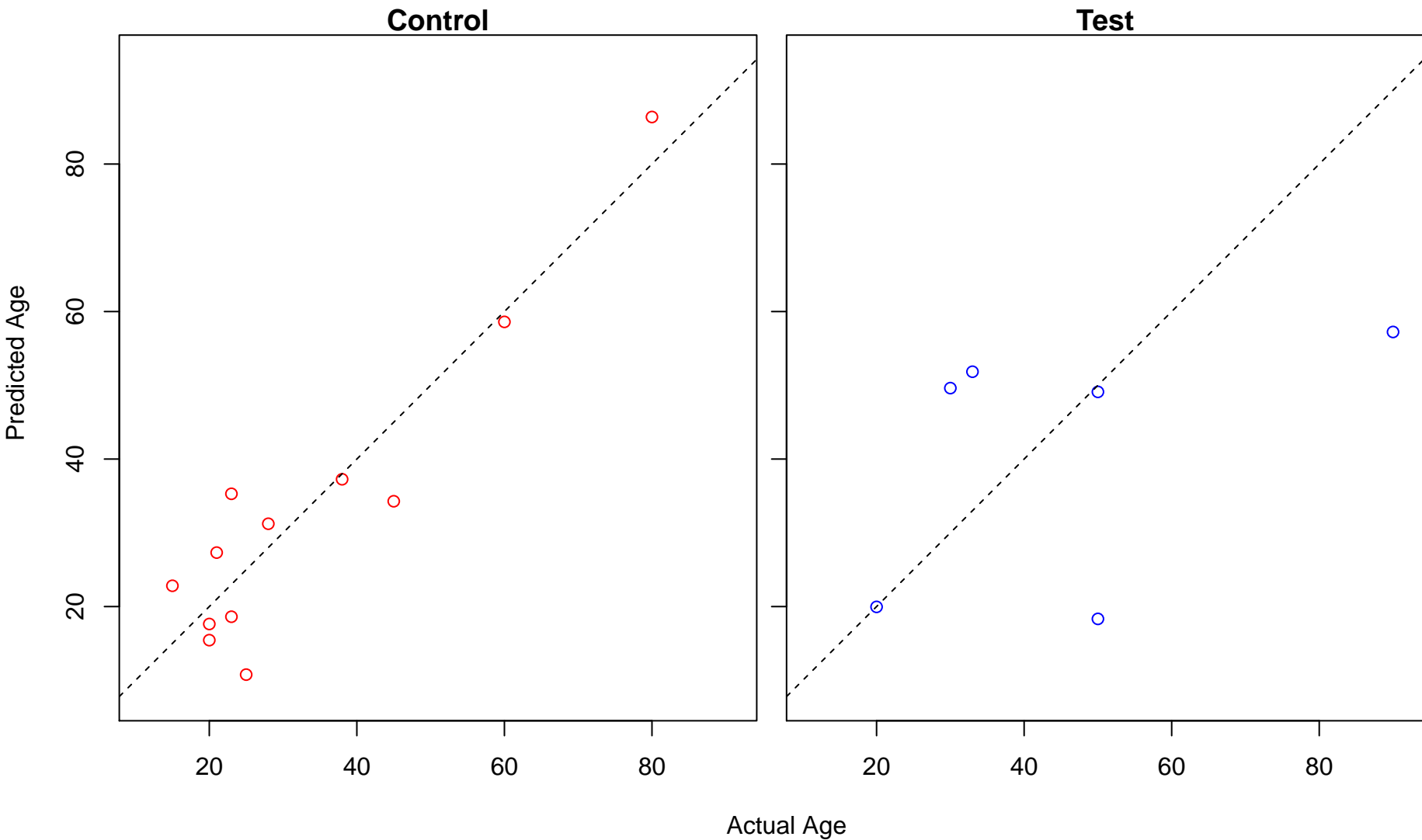
regulation of microtubule polymerization (Score: 40.349896)



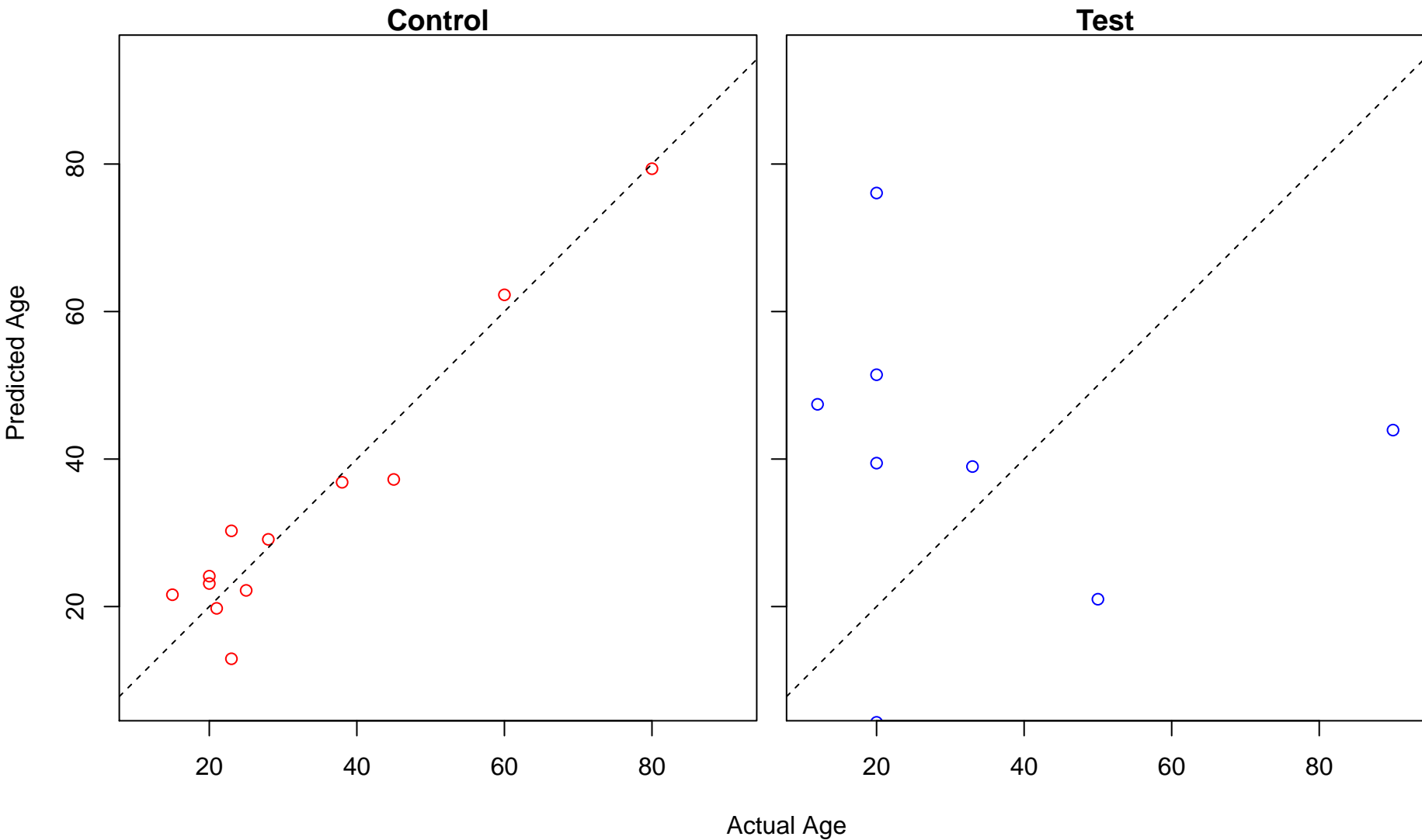
cyclooxygenase pathway (Score: 40.011630)



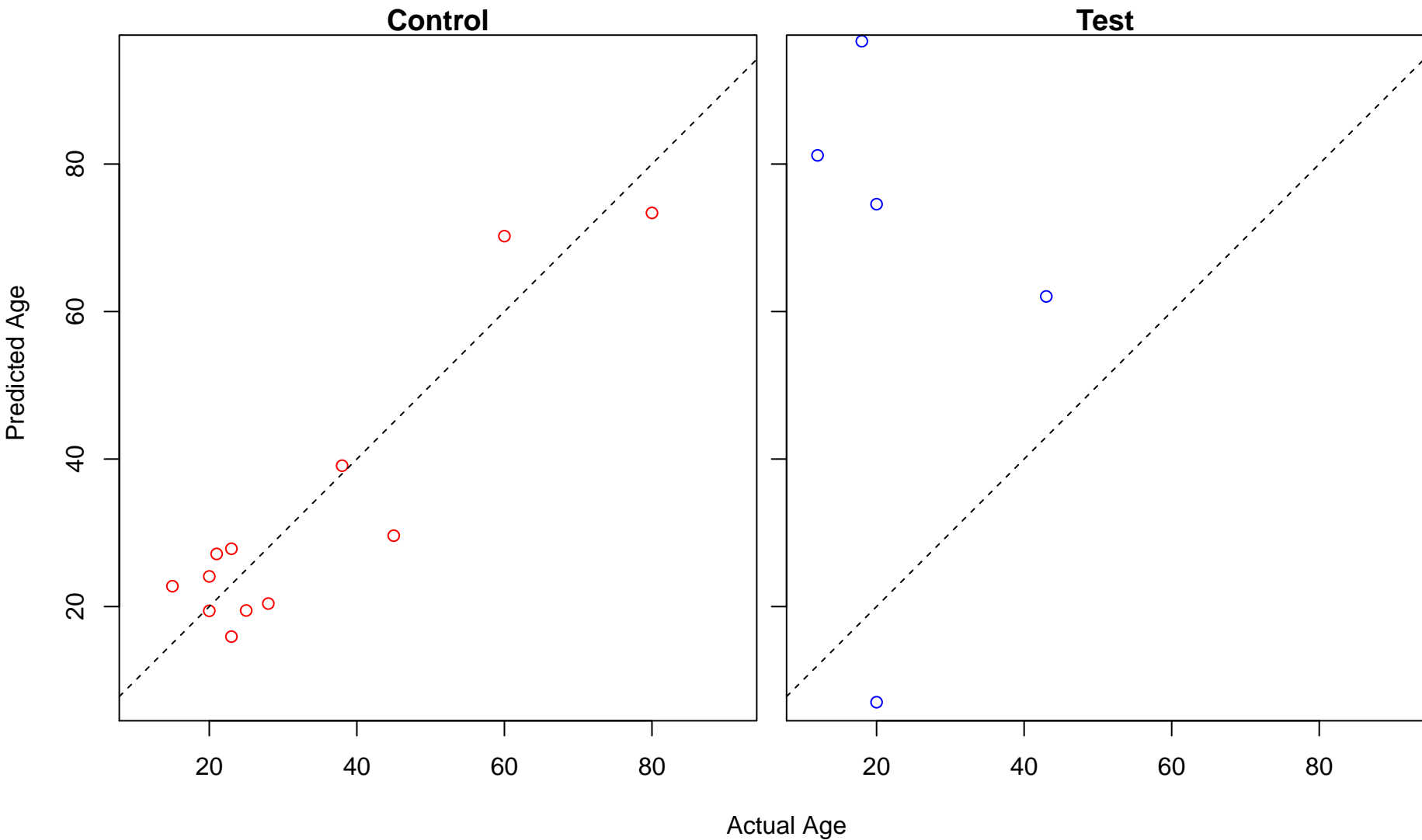
cellular response to interleukin-4 (Score: 39.852923)



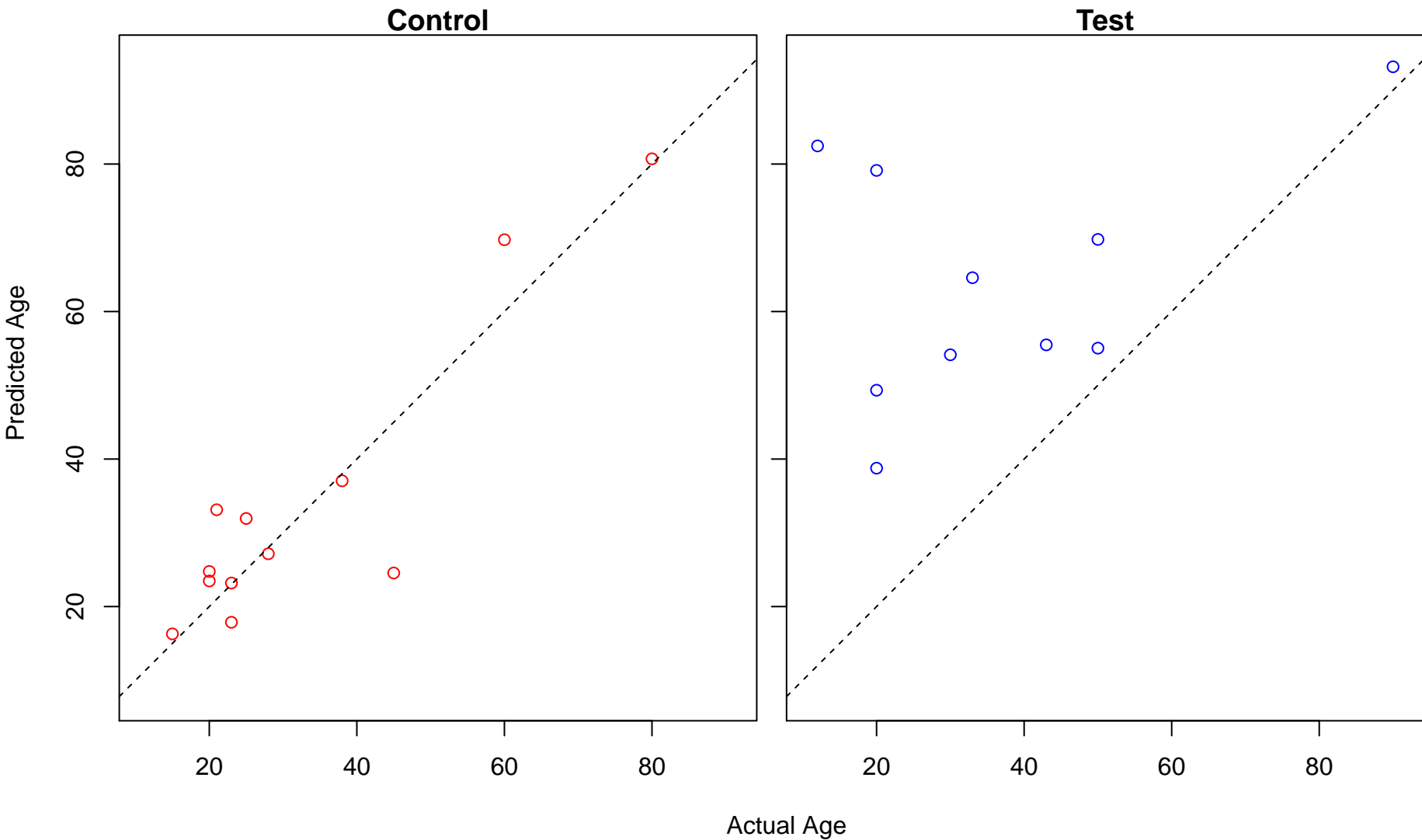
miRNA loading onto RISC involved in gene silencing by miRNA (Score: 39.515289)



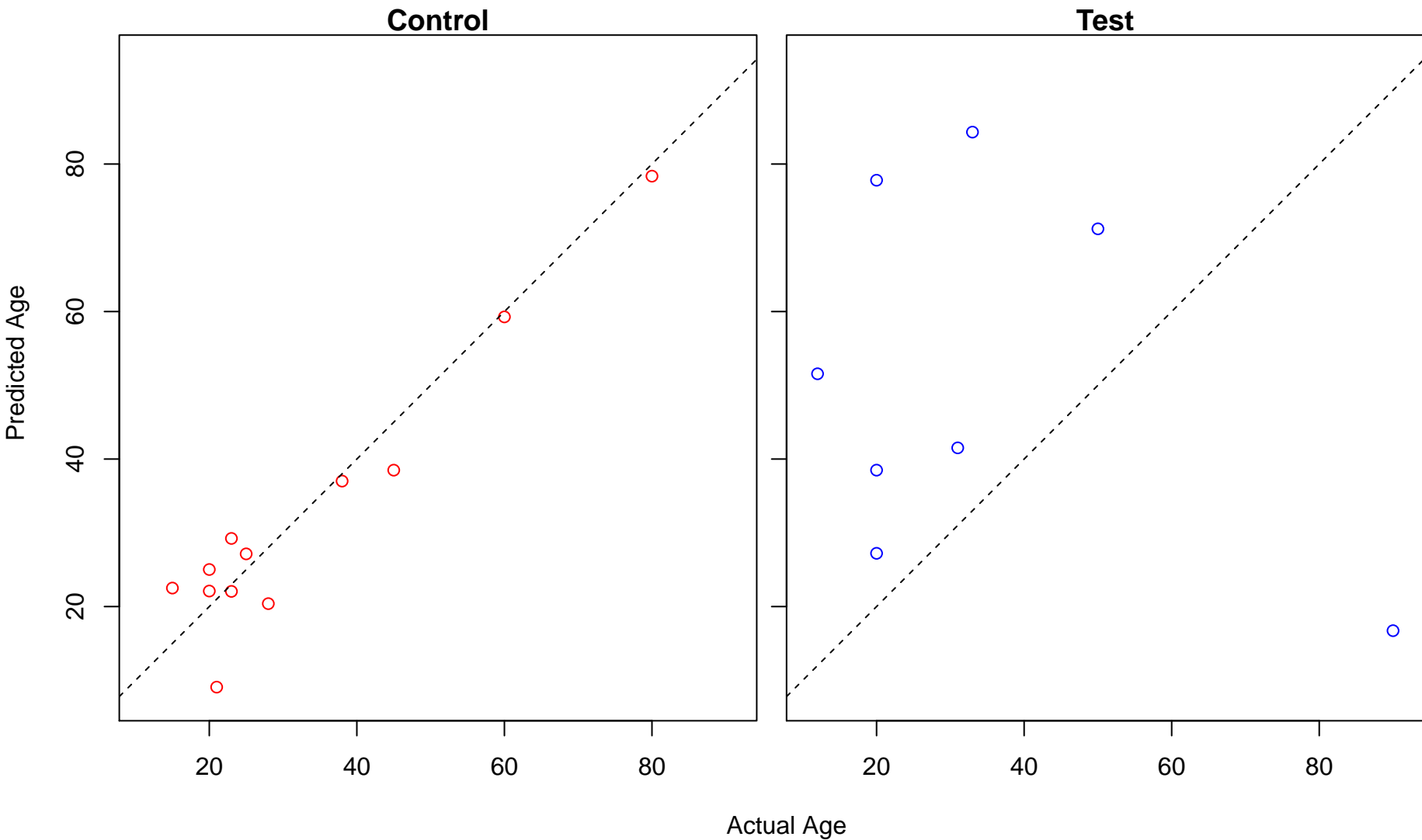
regulation of reactive oxygen species metabolic process (Score: 39.369204)



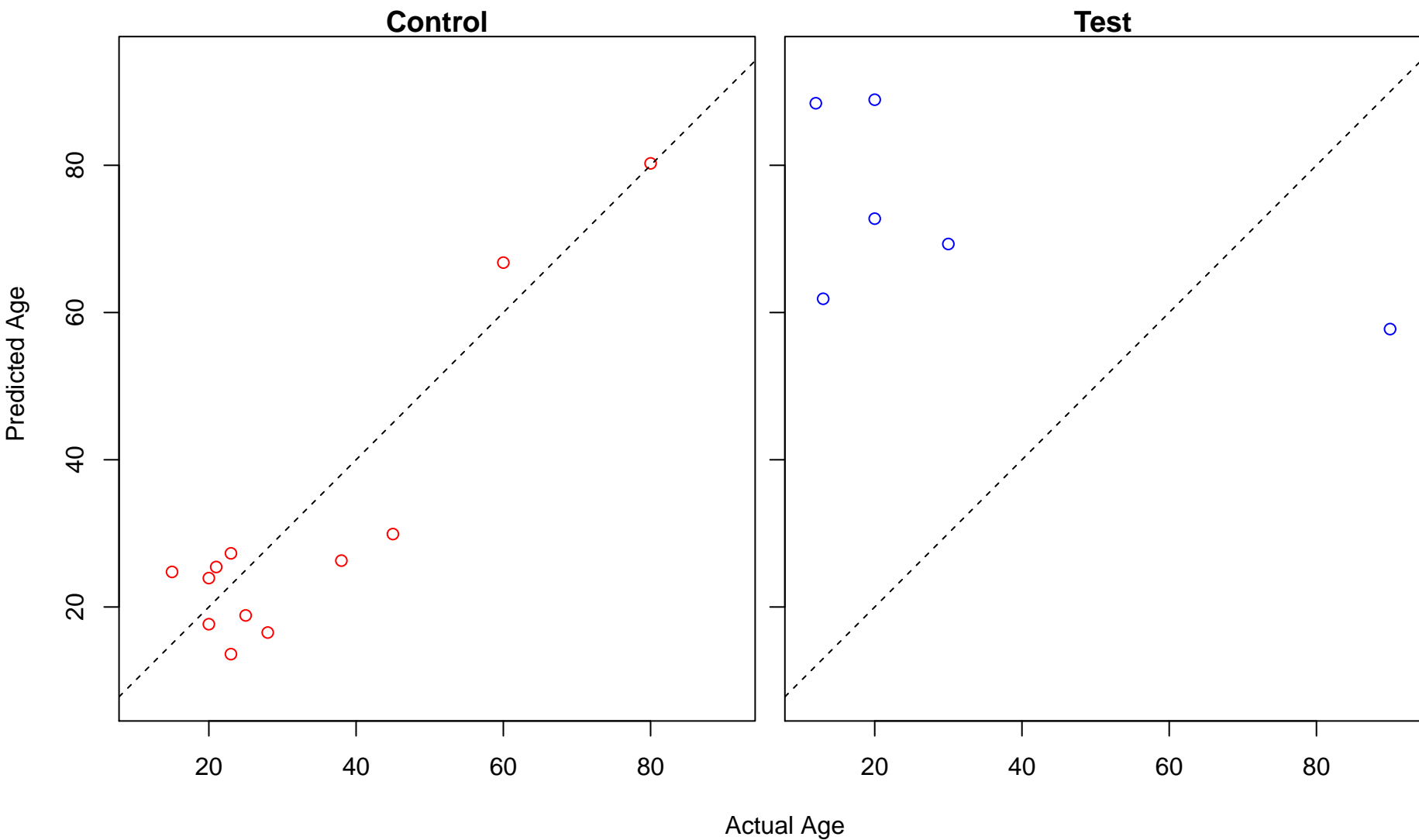
negative regulation of cytokine-mediated signaling pathway (Score: 39.278680)



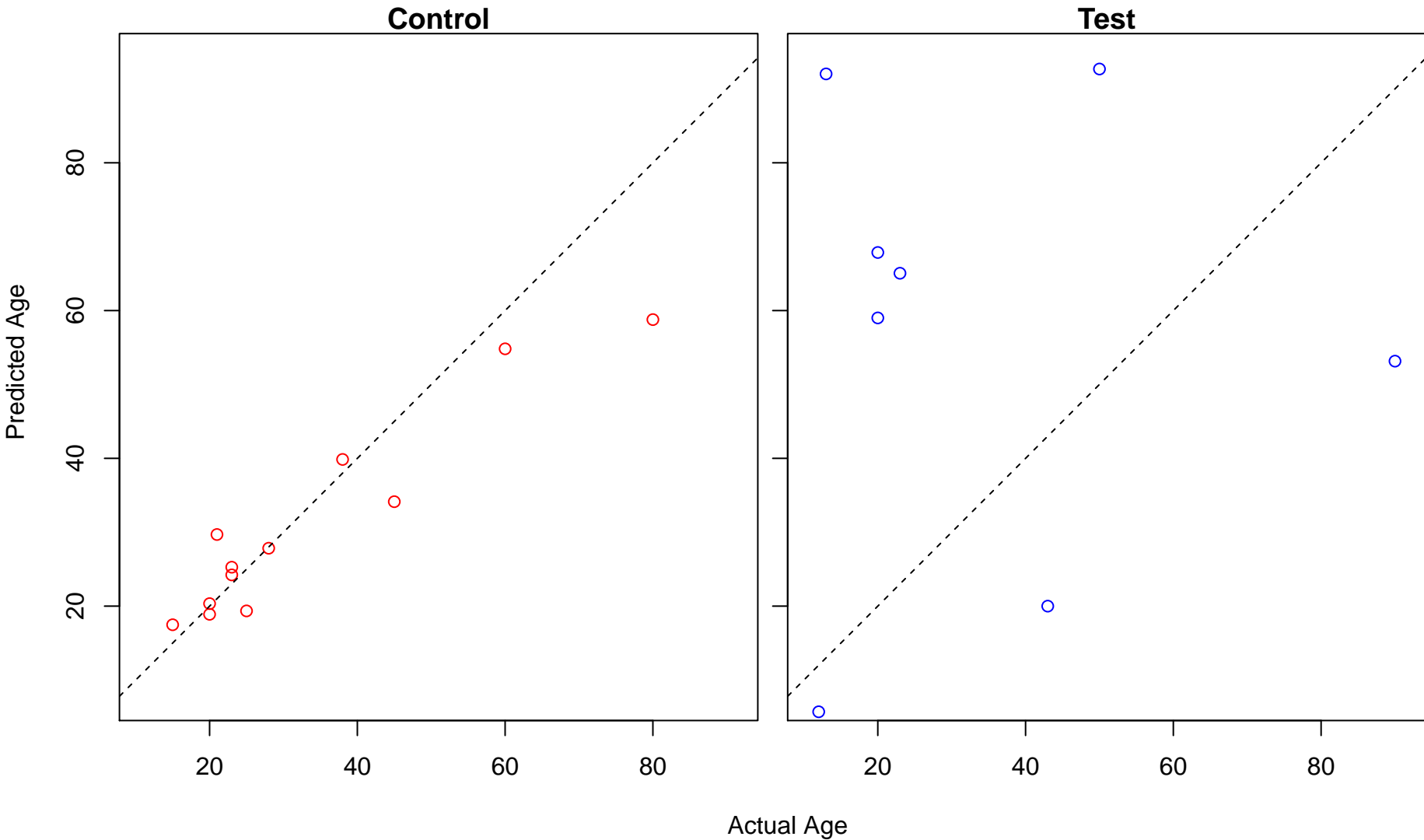
regulation of glial cell proliferation (Score: 38.989249)



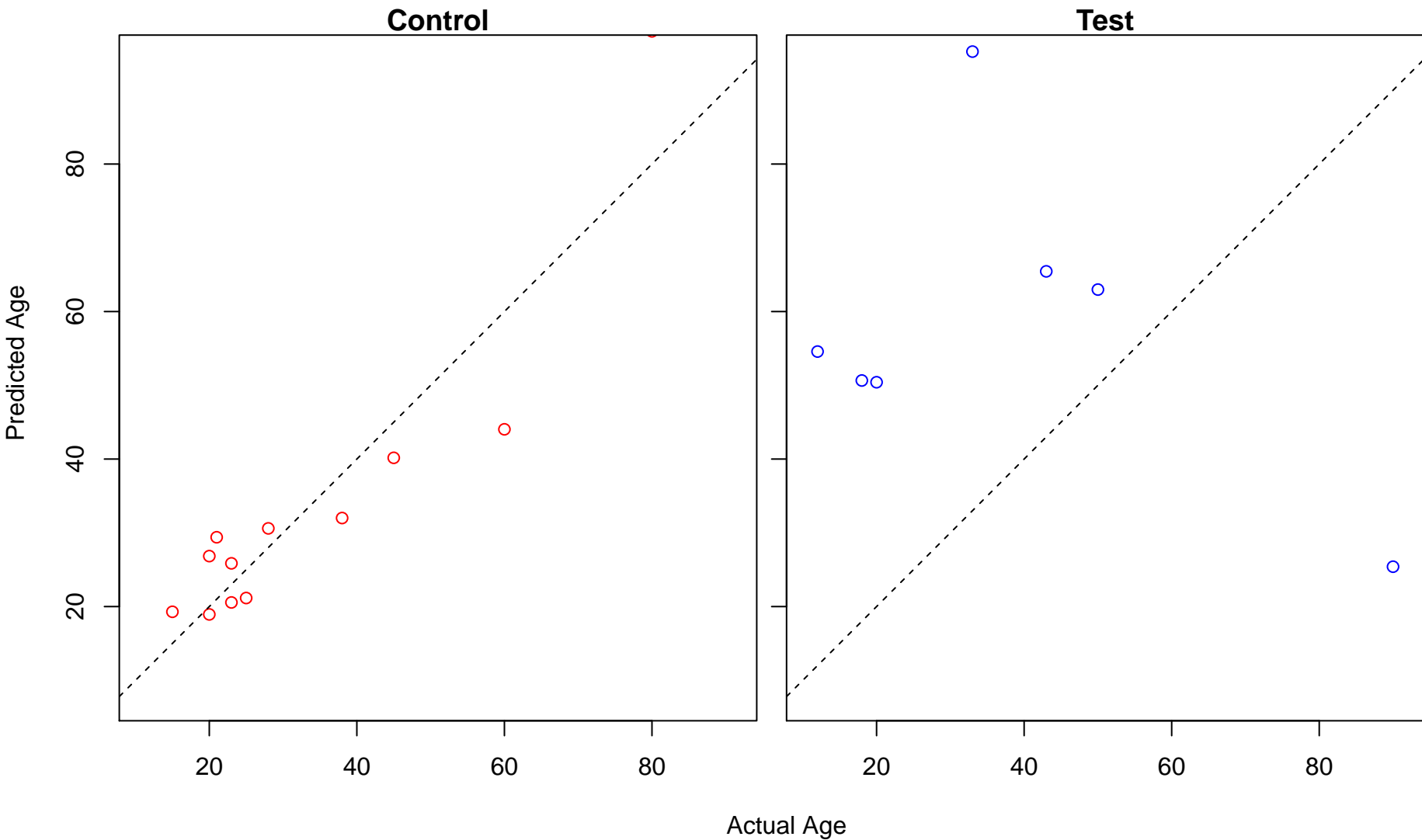
positive regulation of filopodium assembly (Score: 38.942631)



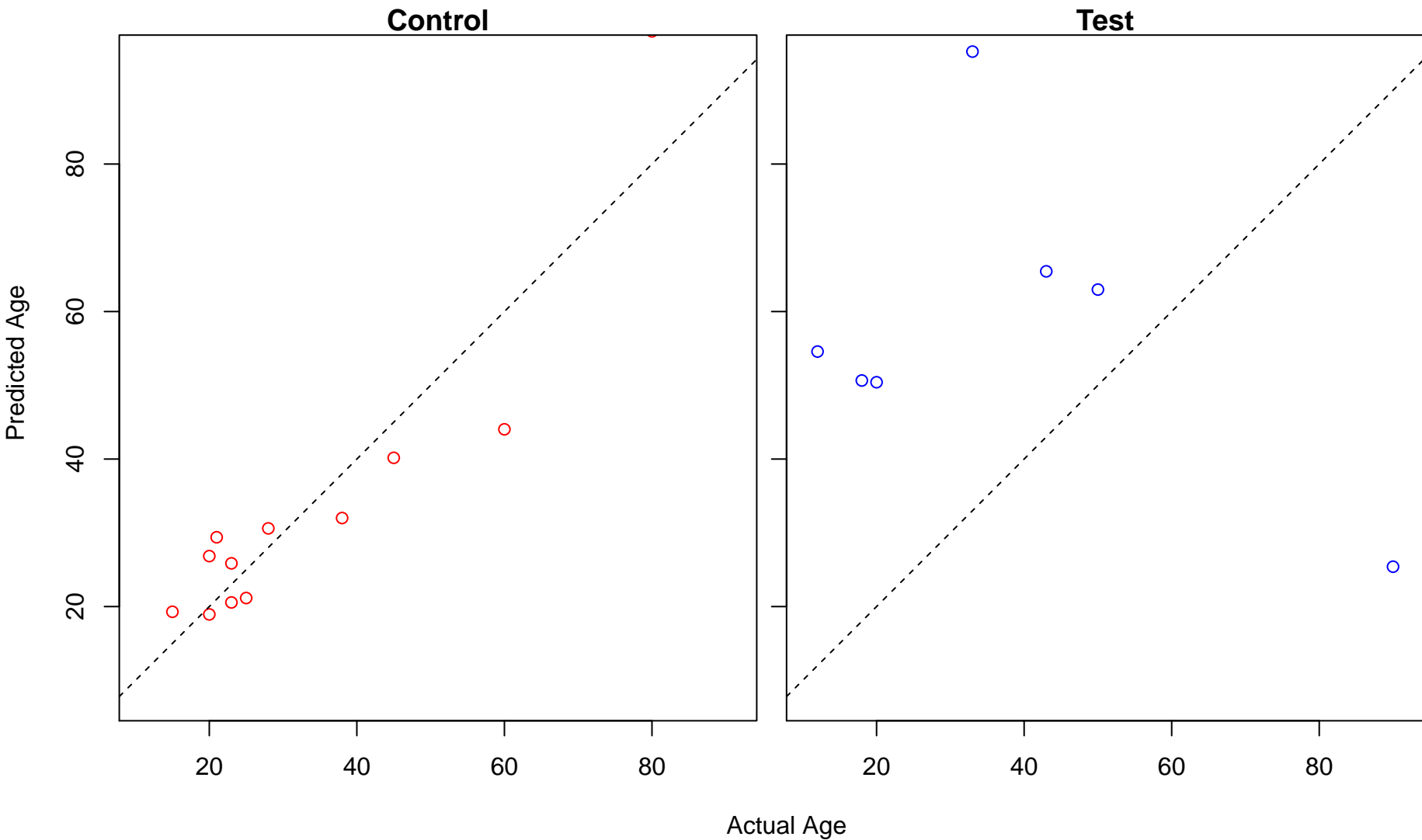
reactive oxygen species biosynthetic process (Score: 38.847982)



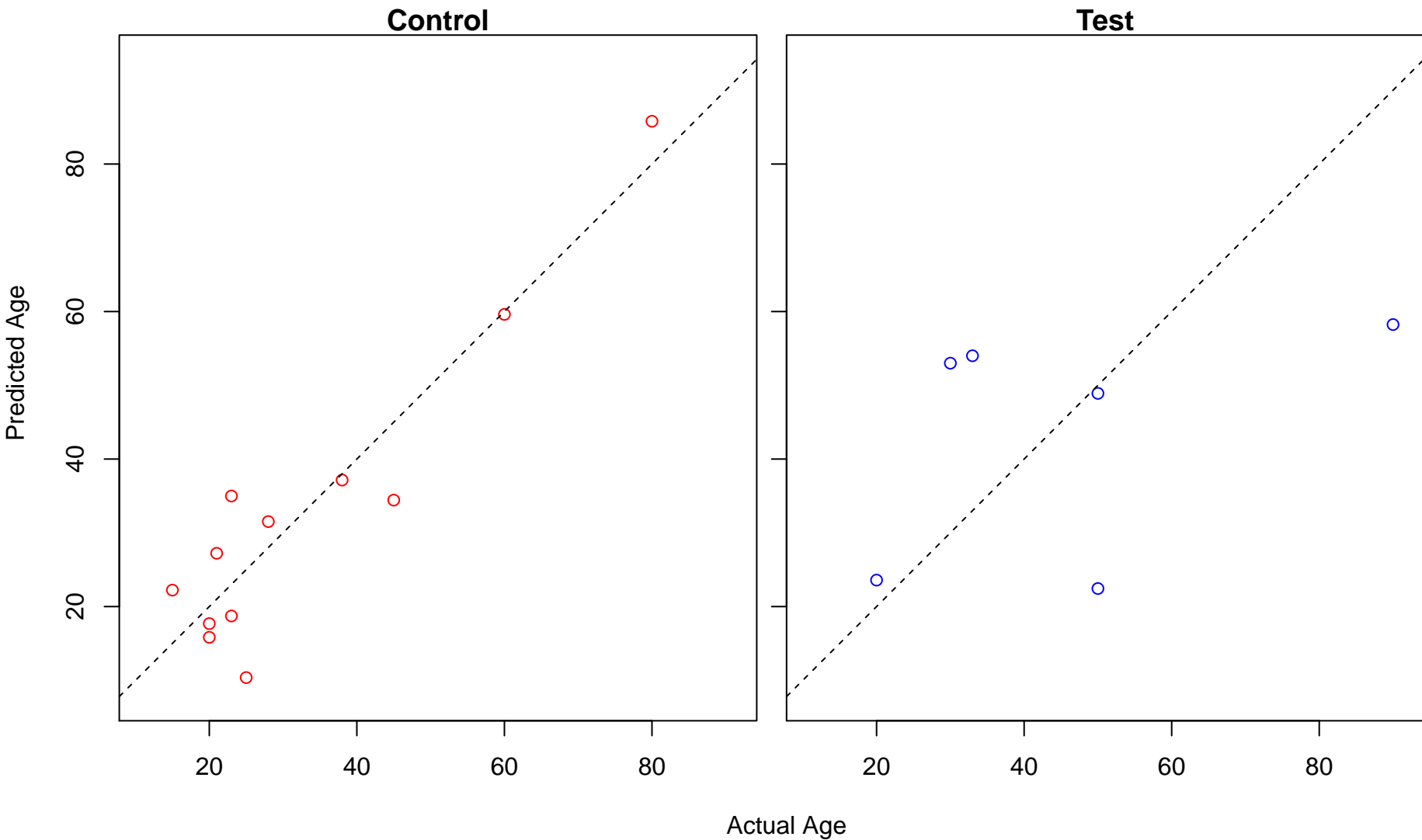
regulation of protein localization to Cajal body (Score: 38.759499)



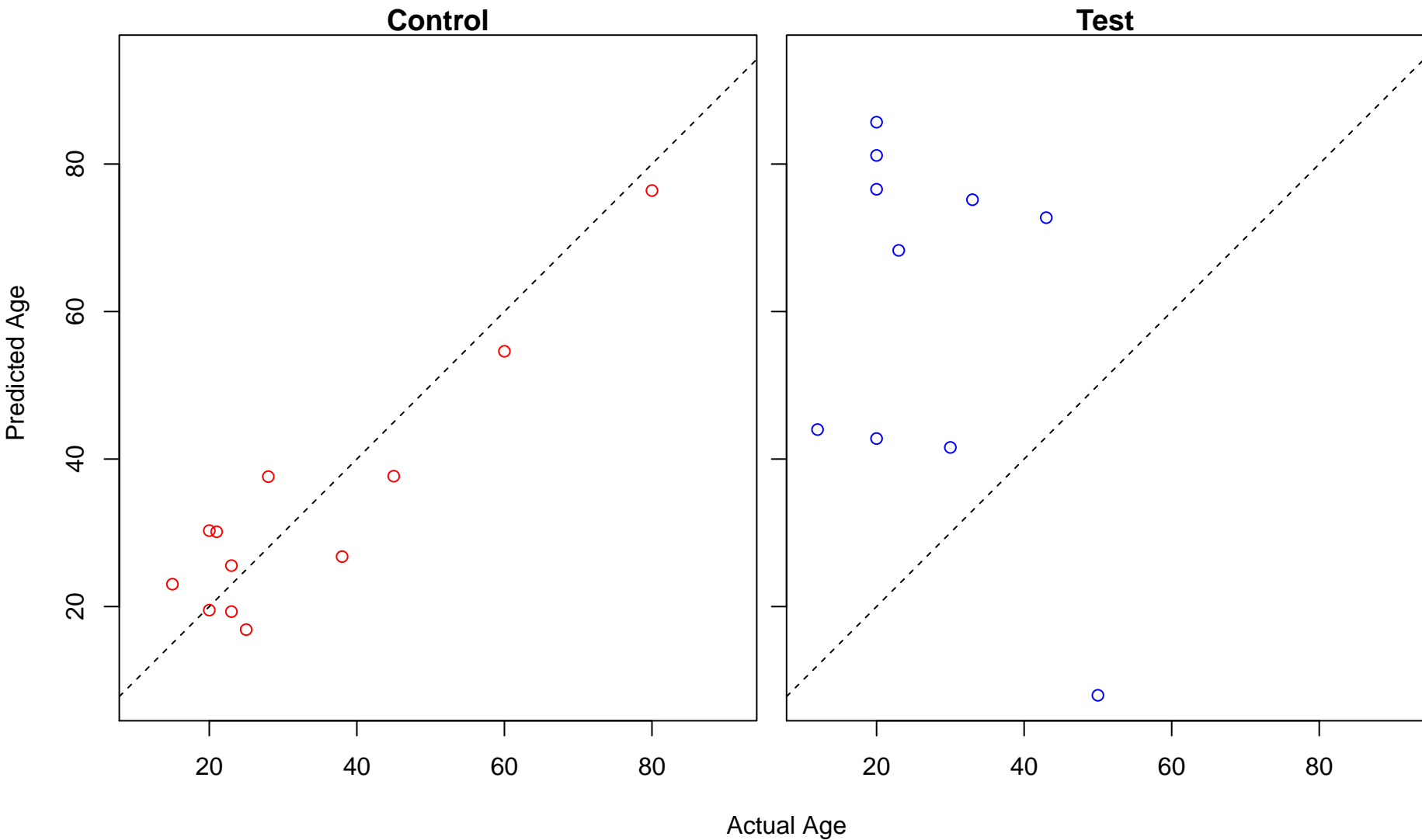
positive regulation of protein localization to Cajal body (Score: 38.759499)



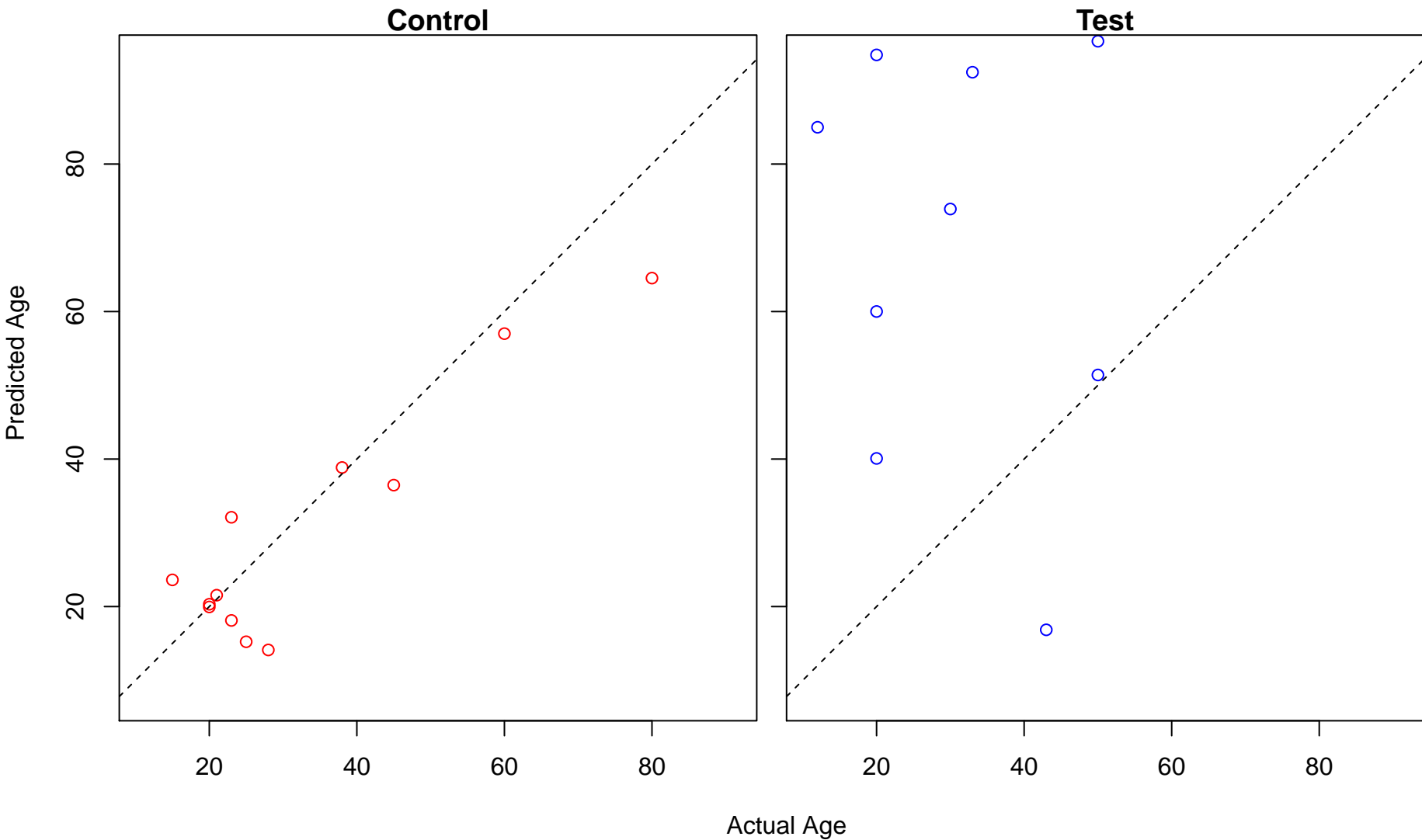
response to interleukin-4 (Score: 38.544283)



tissue remodeling (Score: 38.533023)

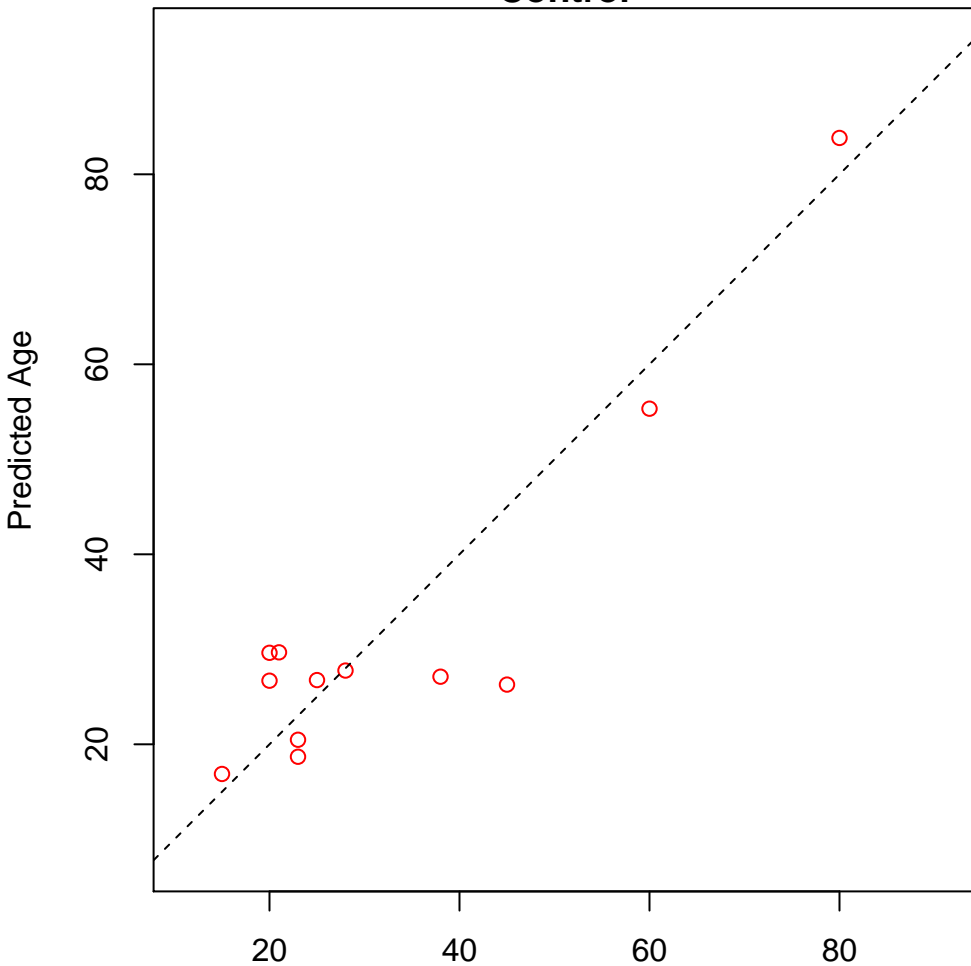


regulation of chemokine (C-X-C motif) ligand 2 production (Score: 38.393283)

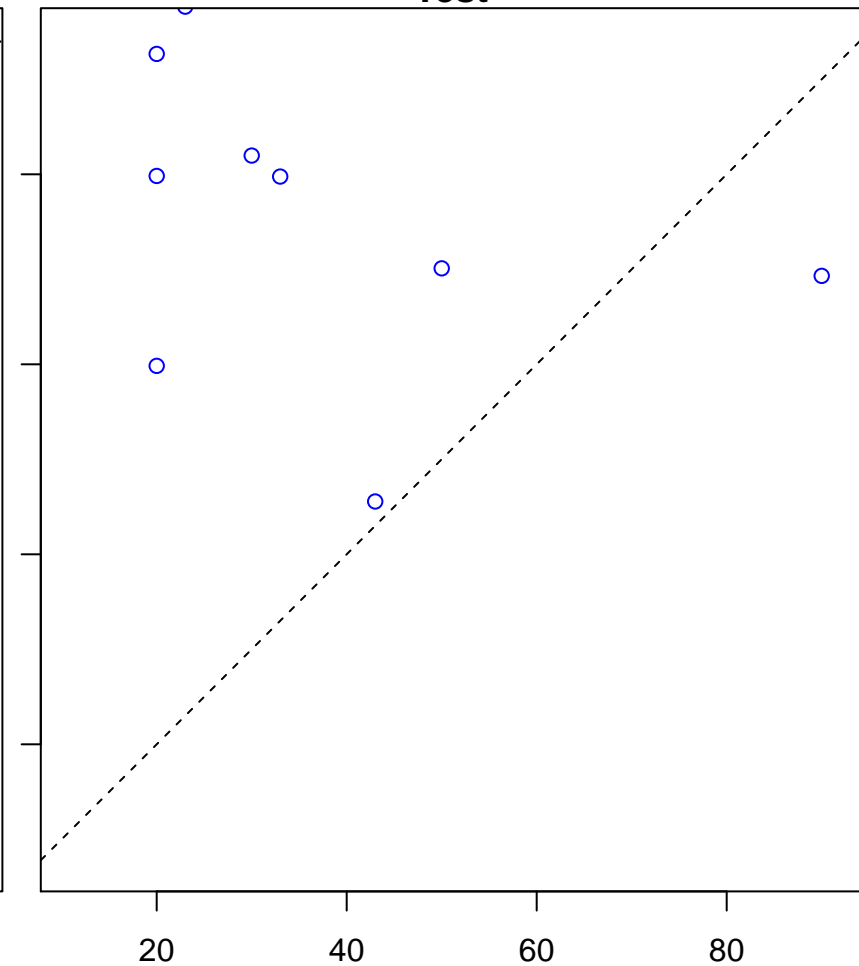


positive regulation of anion transport (Score: 38.367937)

Control

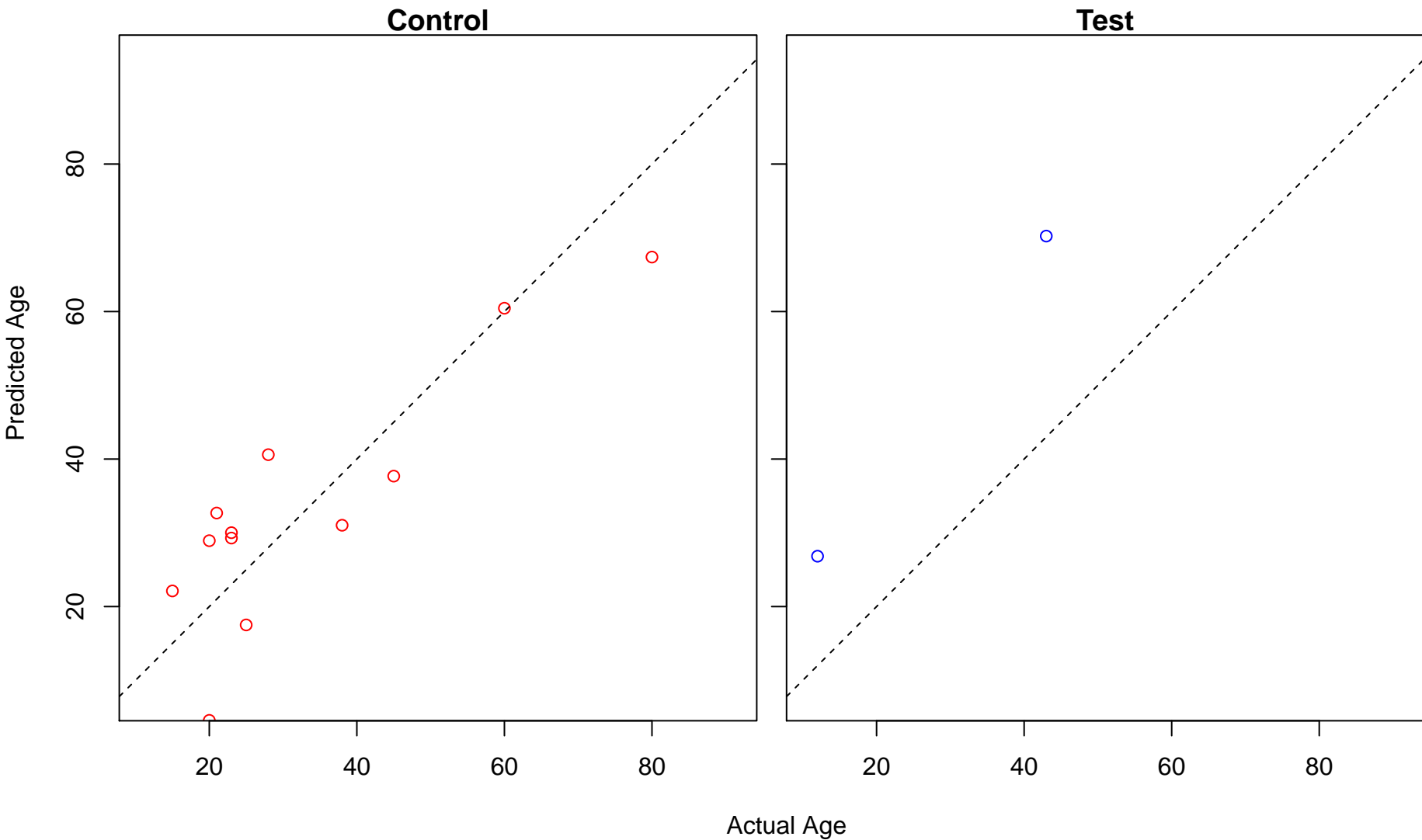


Test



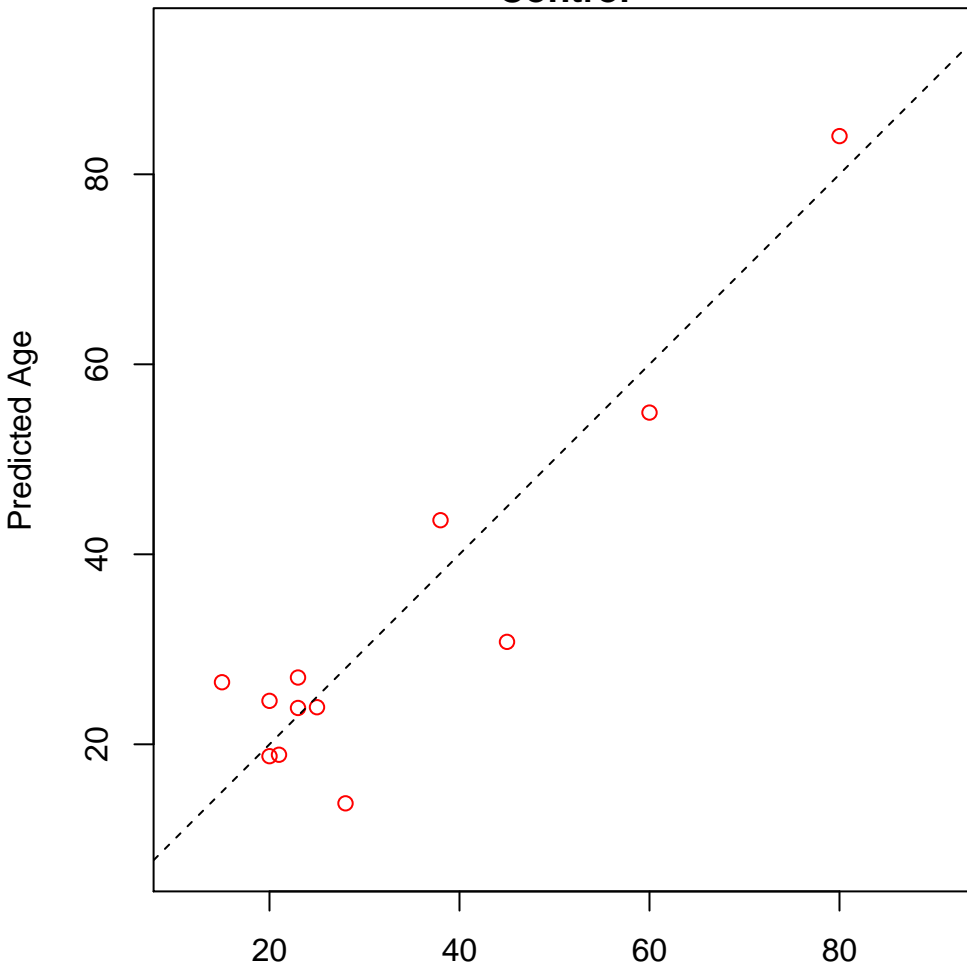
Actual Age

indolalkylamine metabolic process (Score: 38.207628)

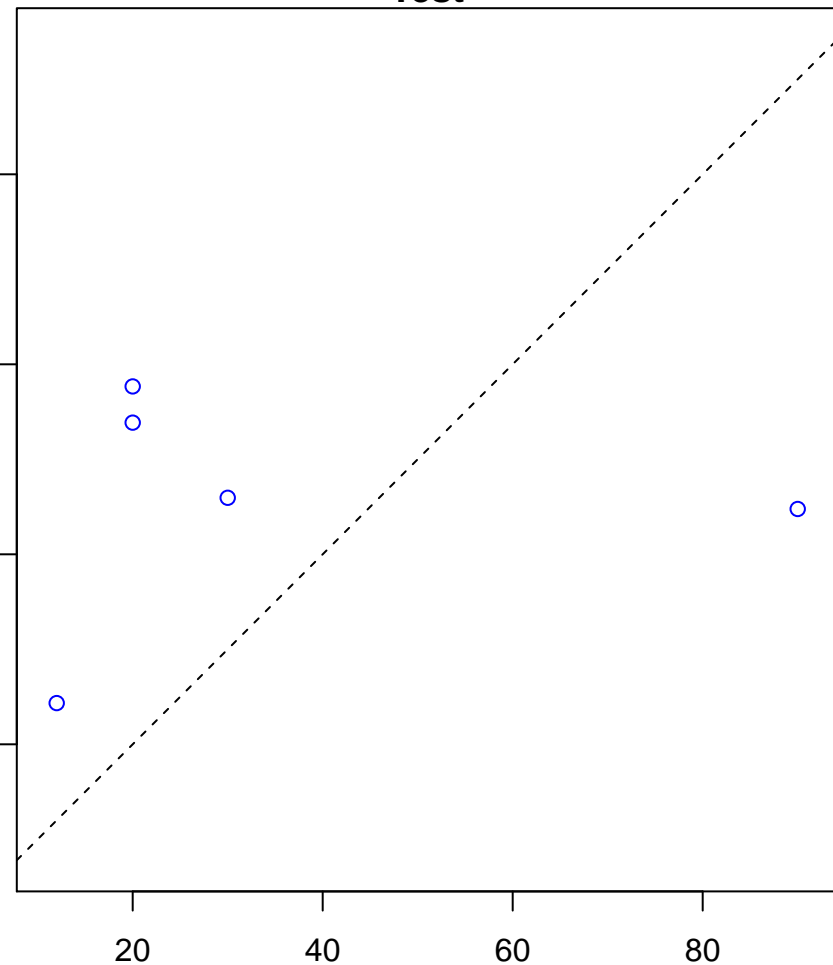


prostaglandin biosynthetic process (Score: 38.191319)

Control

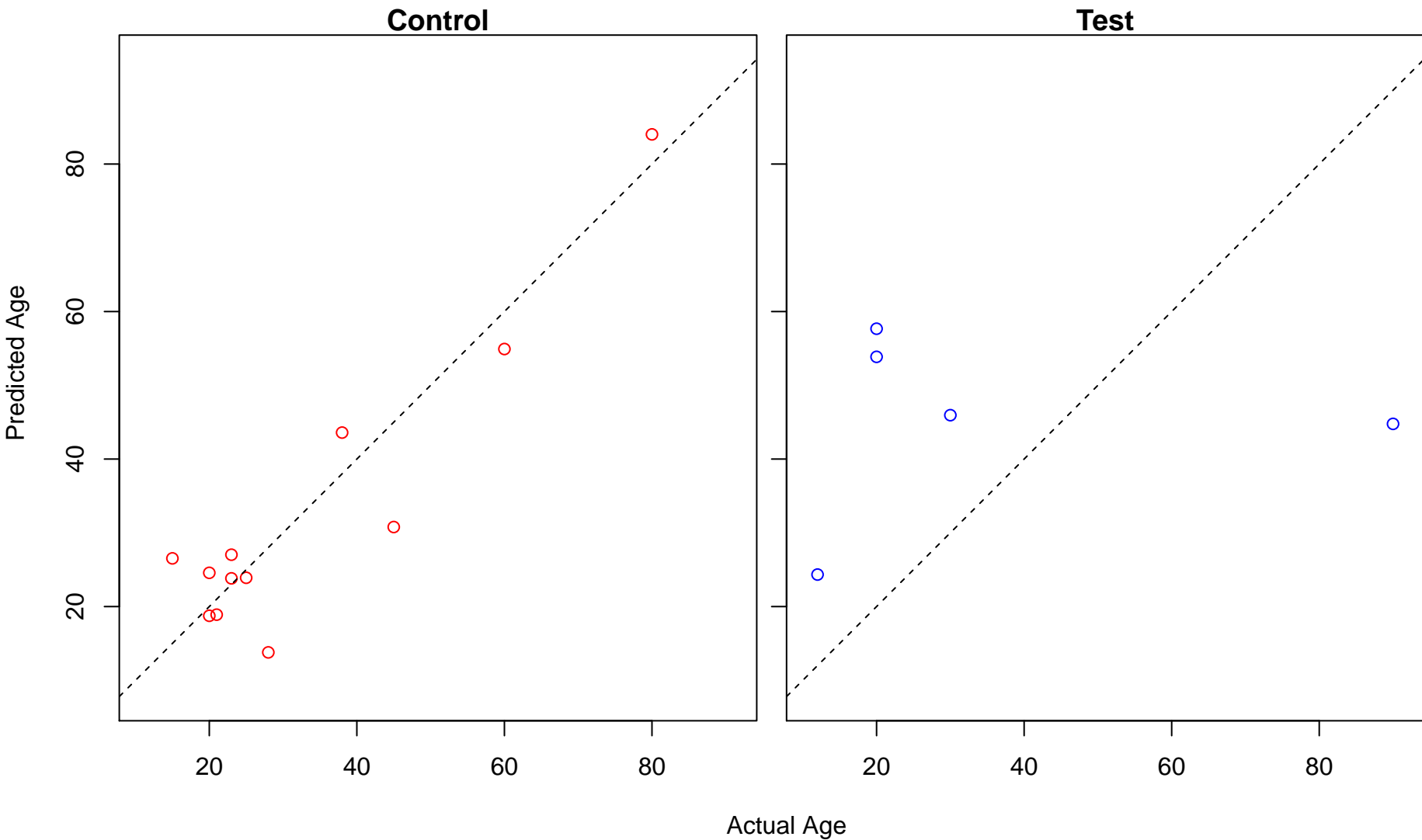


Test

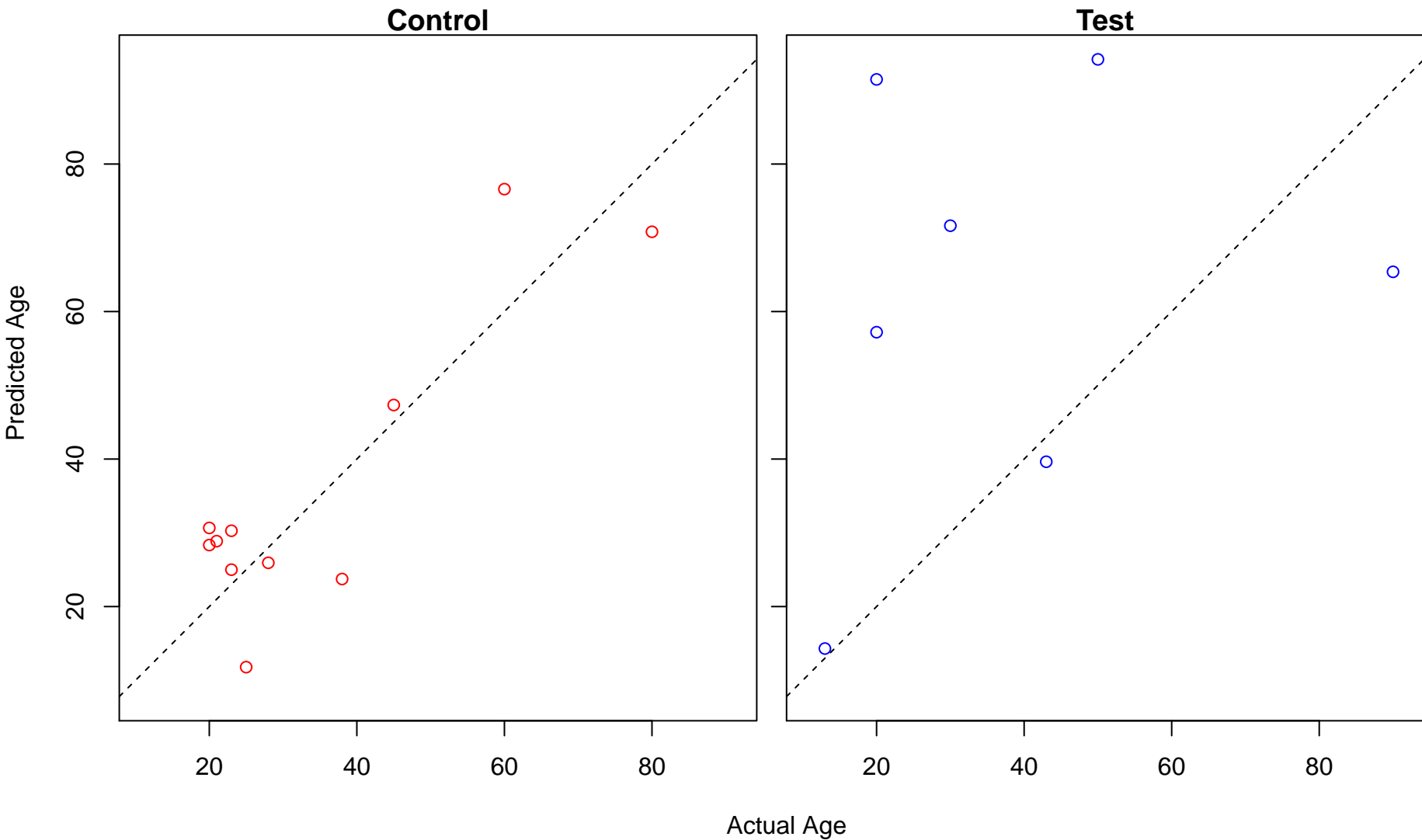


Actual Age

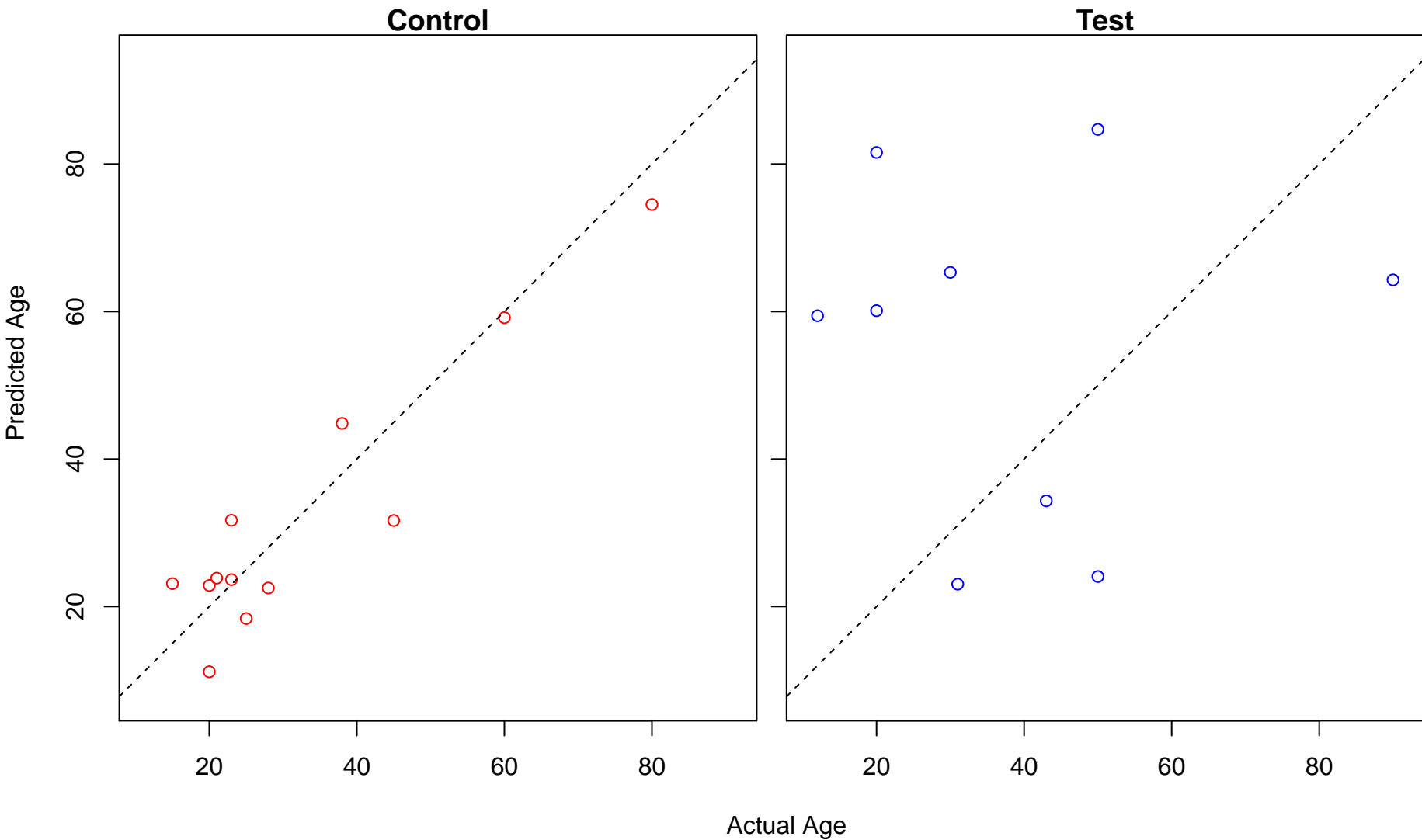
prostanoid biosynthetic process (Score: 38.191319)



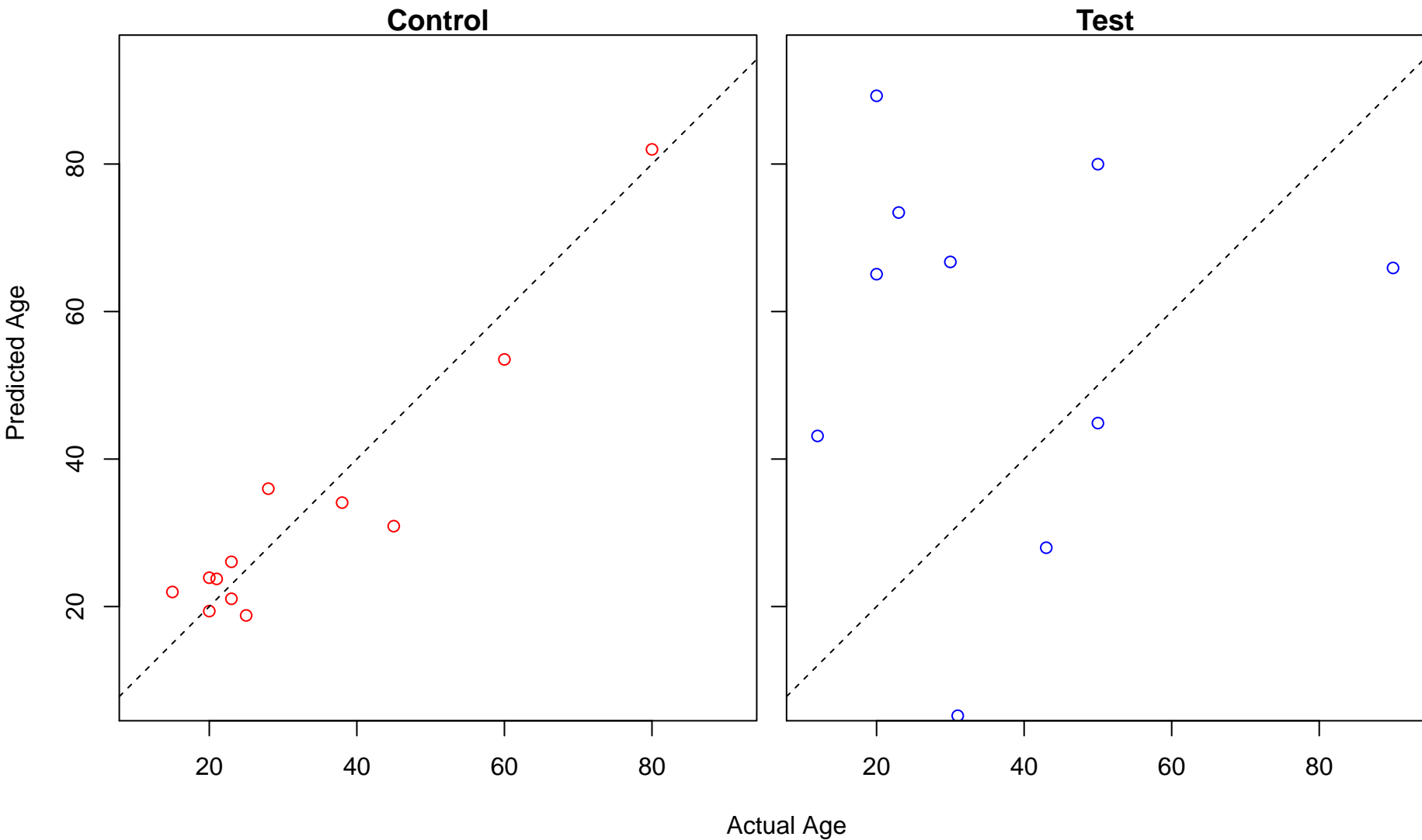
serotonin receptor signaling pathway (Score: 38.107069)



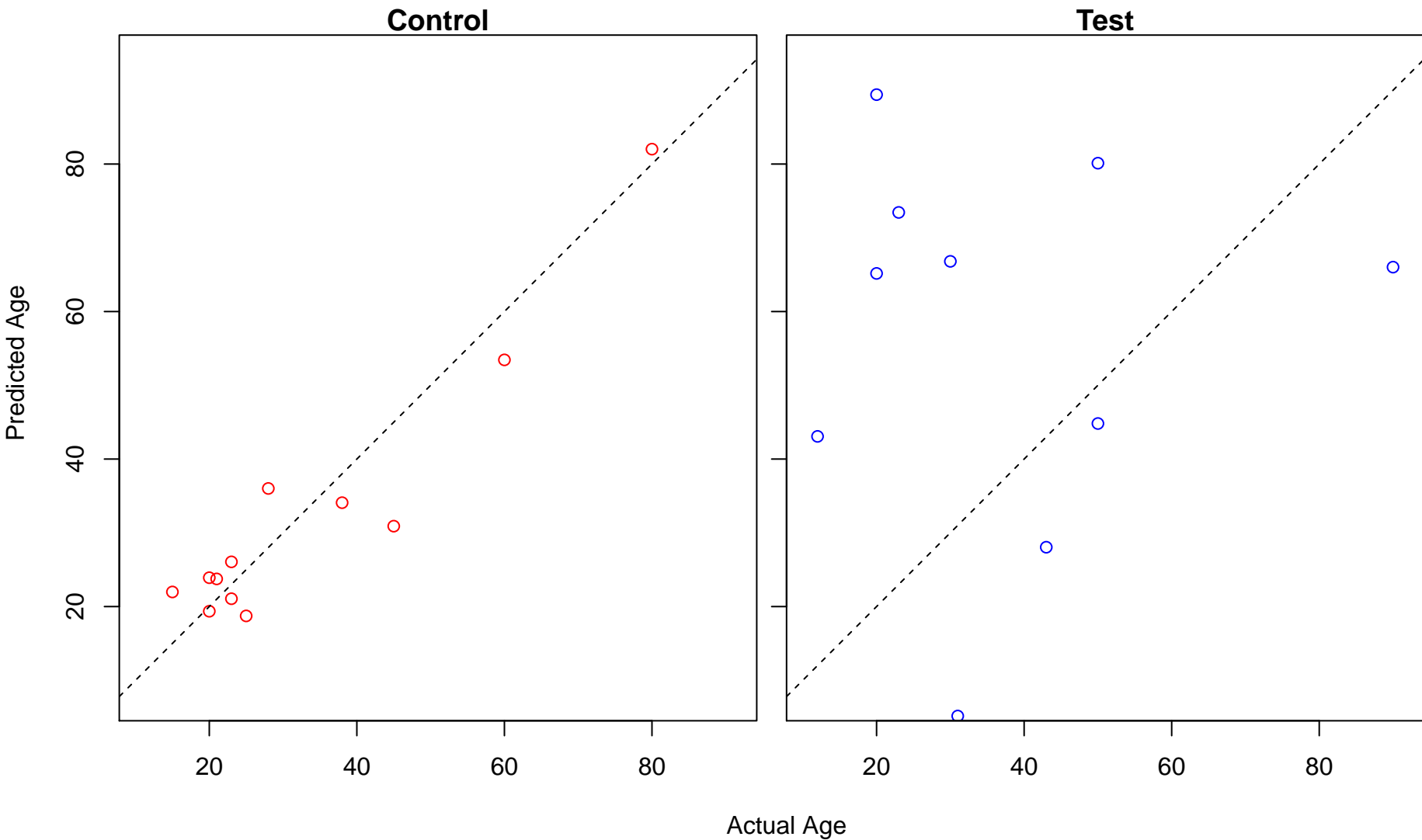
cellular response to interferon- α (Score: 38.046901)



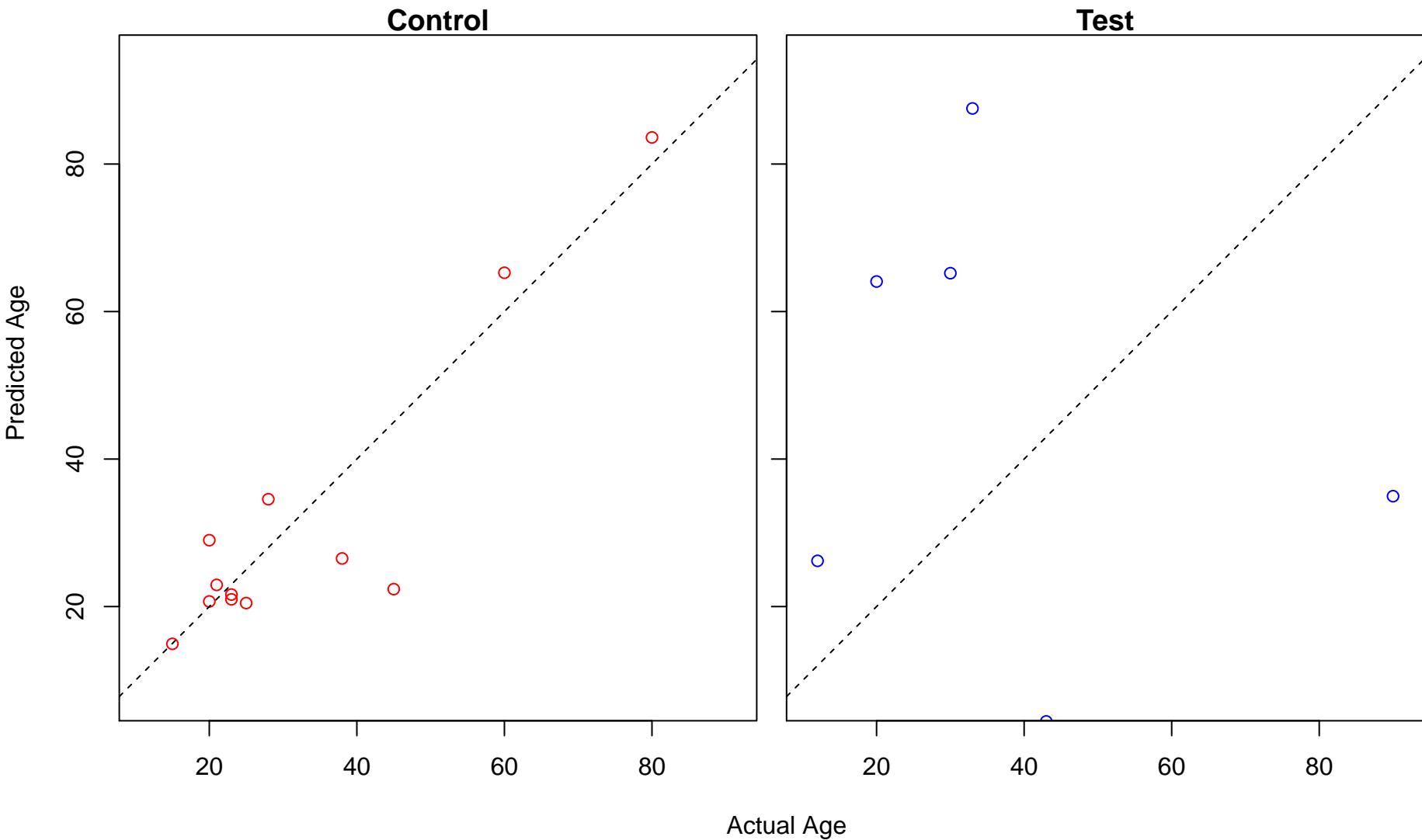
negative regulation of protein dephosphorylation (Score: 37.787831)



negative regulation of dephosphorylation (Score: 37.652843)

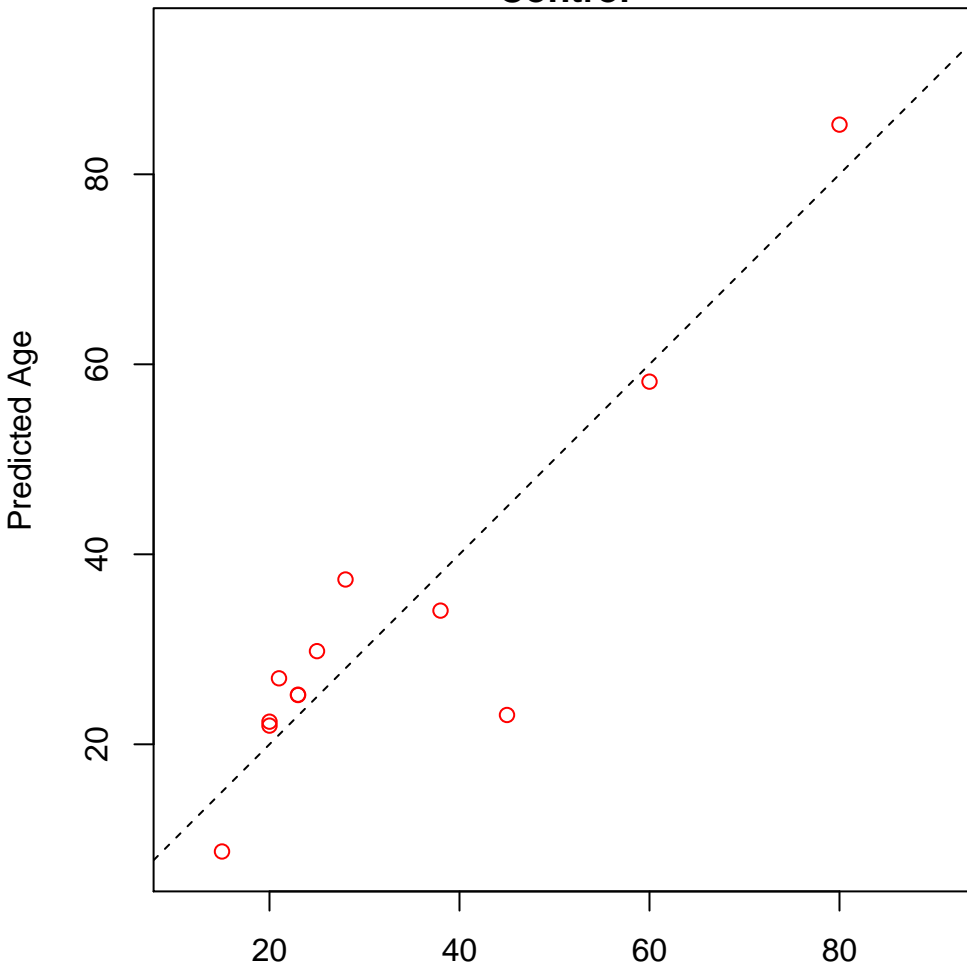


negative regulation of muscle cell differentiation (Score: 37.452237)

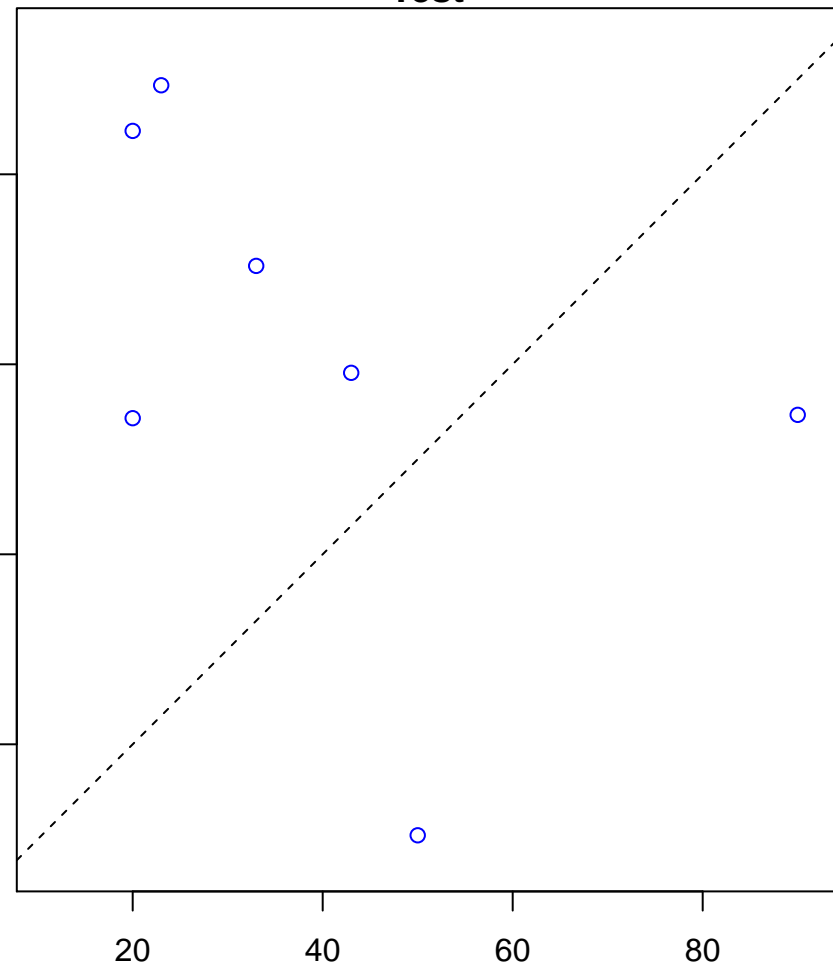


response to isoquinoline alkaloid (Score: 37.381668)

Control

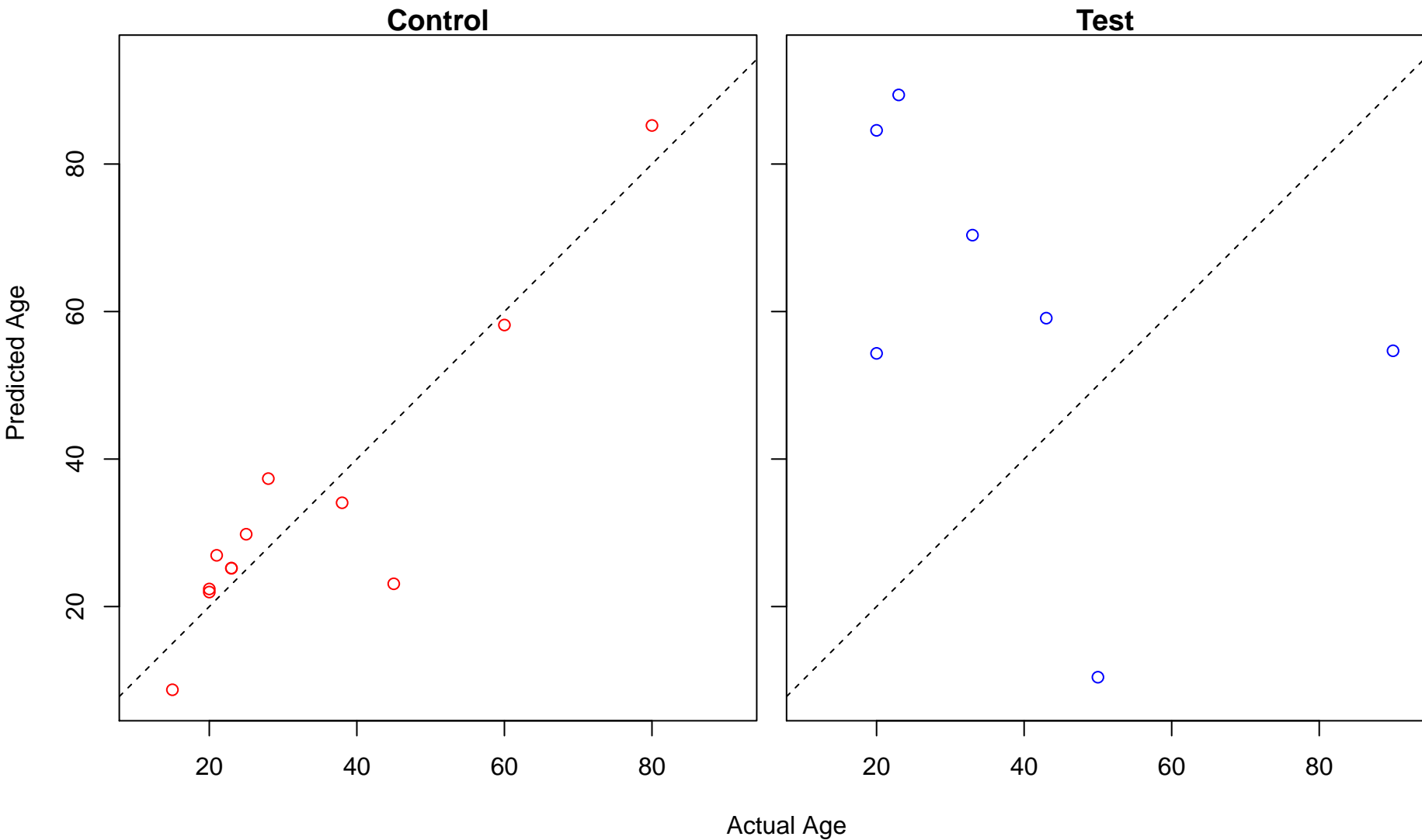


Test

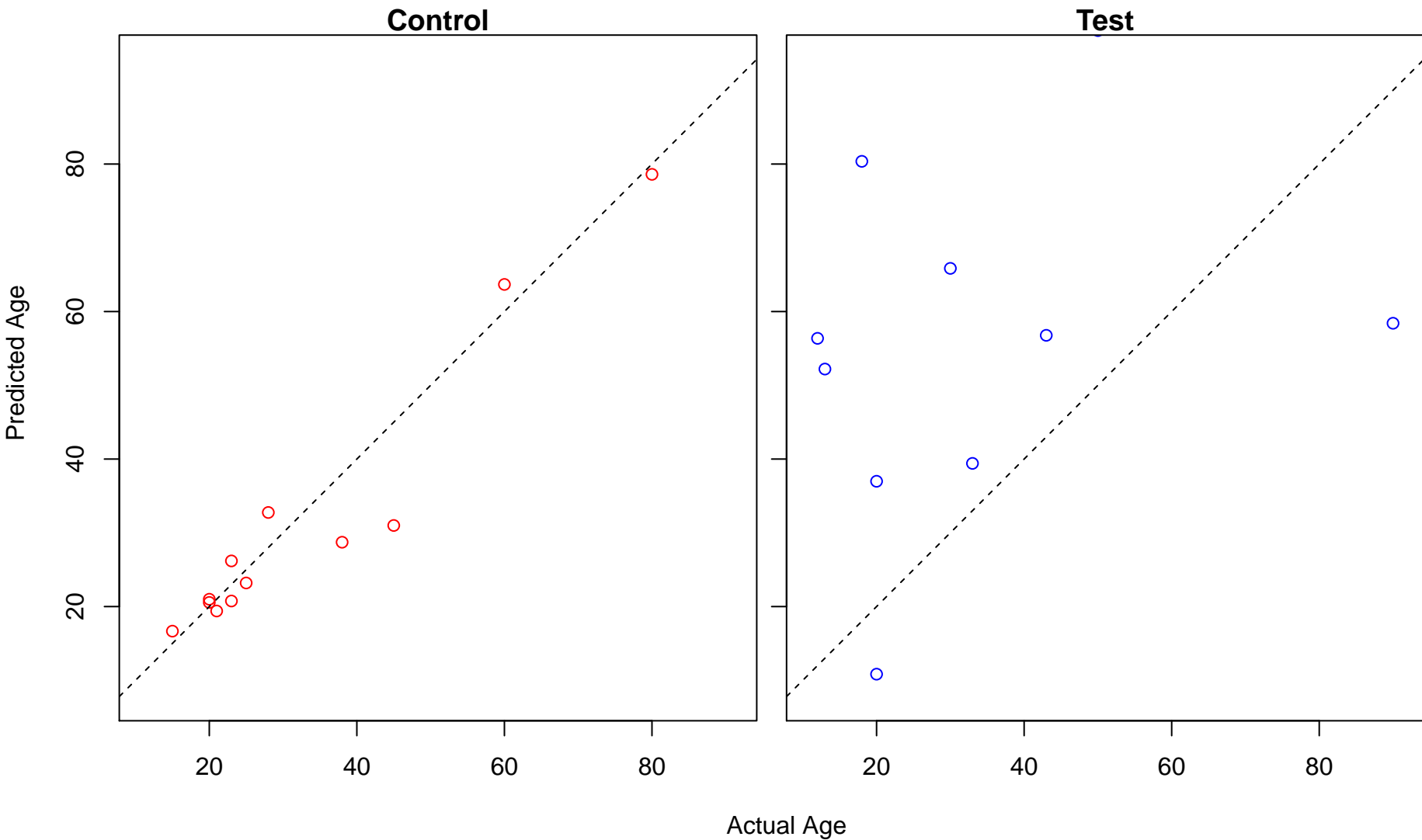


Actual Age

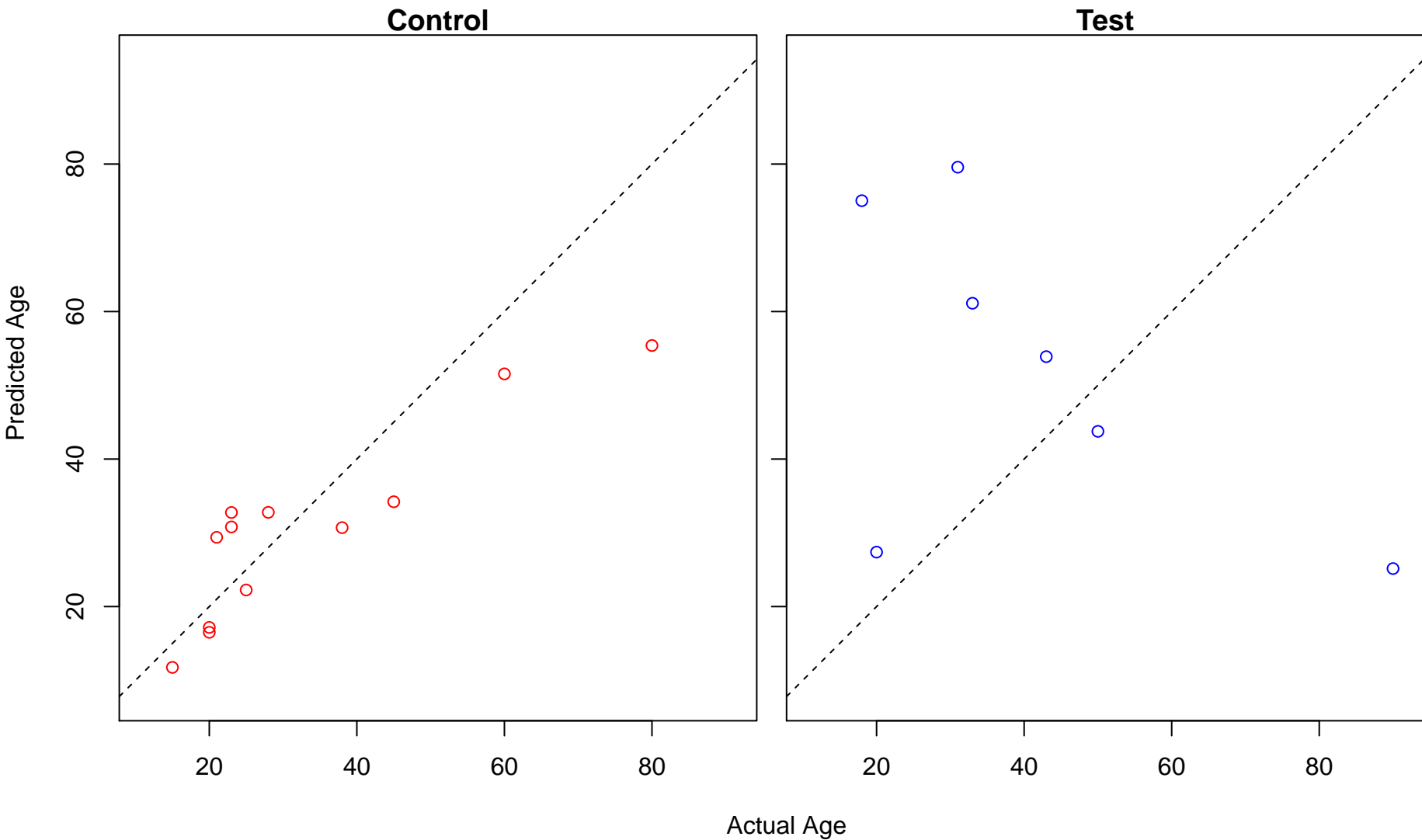
response to morphine (Score: 37.381668)



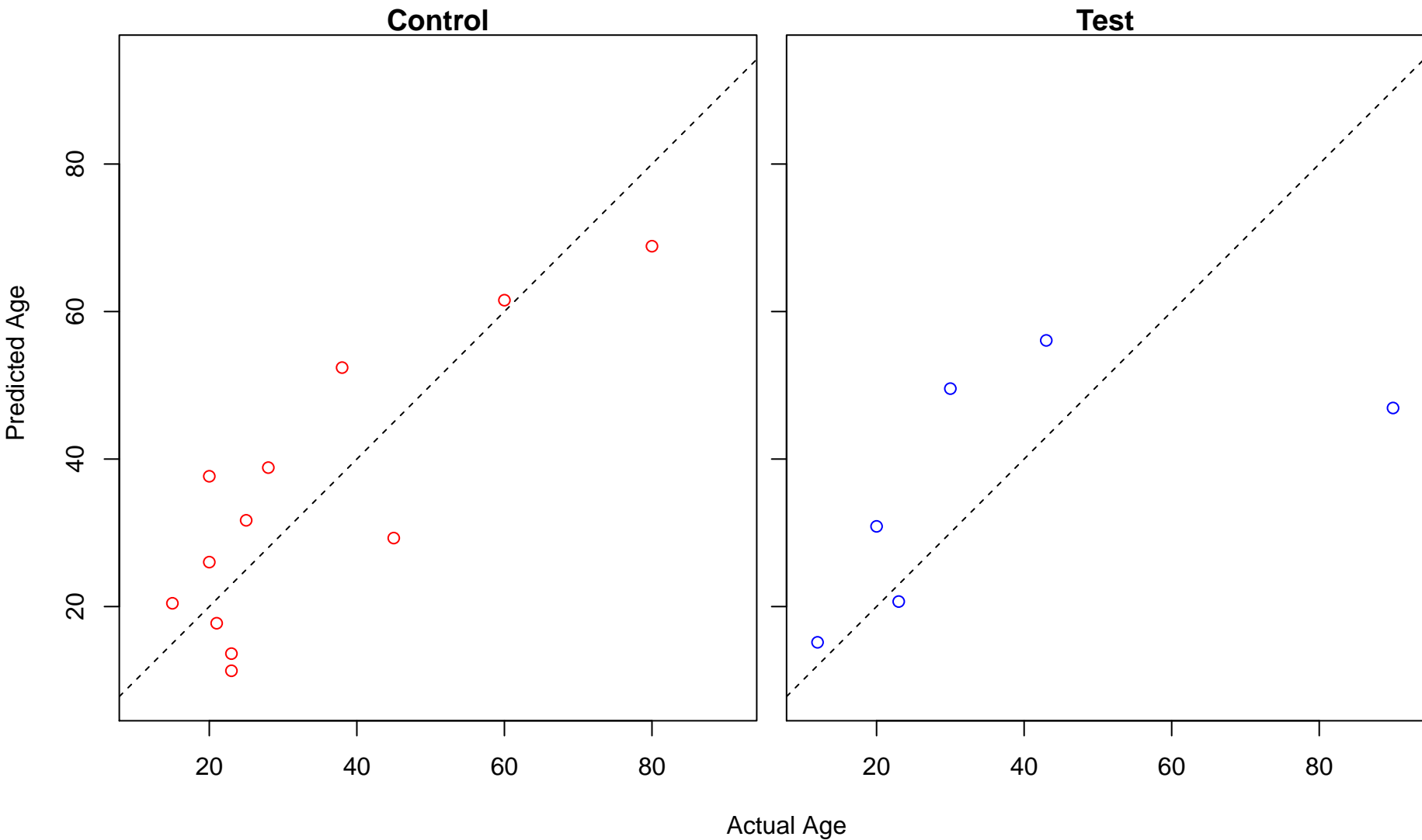
DNA methylation on cytosine (Score: 37.012109)



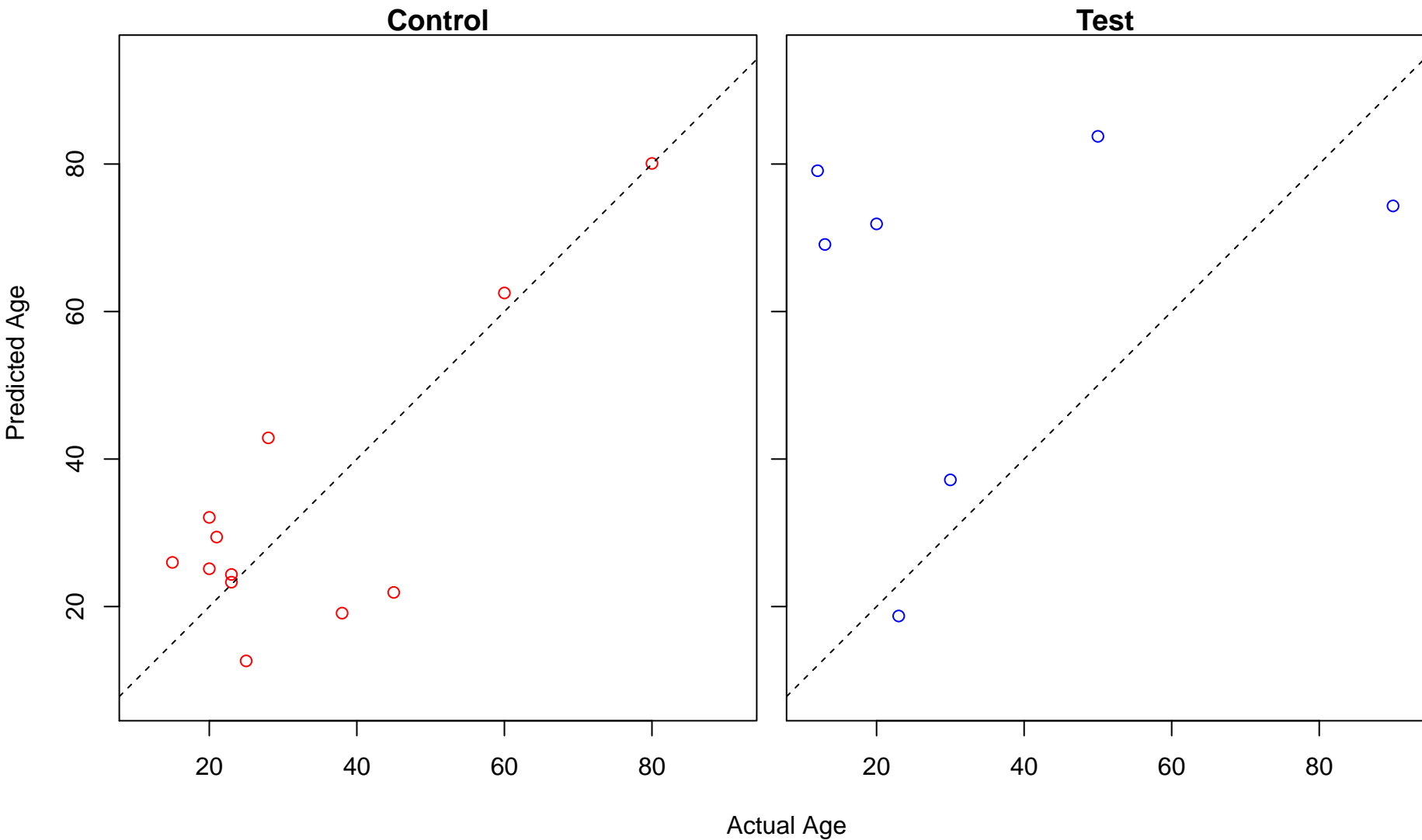
negative regulation of alpha-beta T cell differentiation (Score: 36.942771)



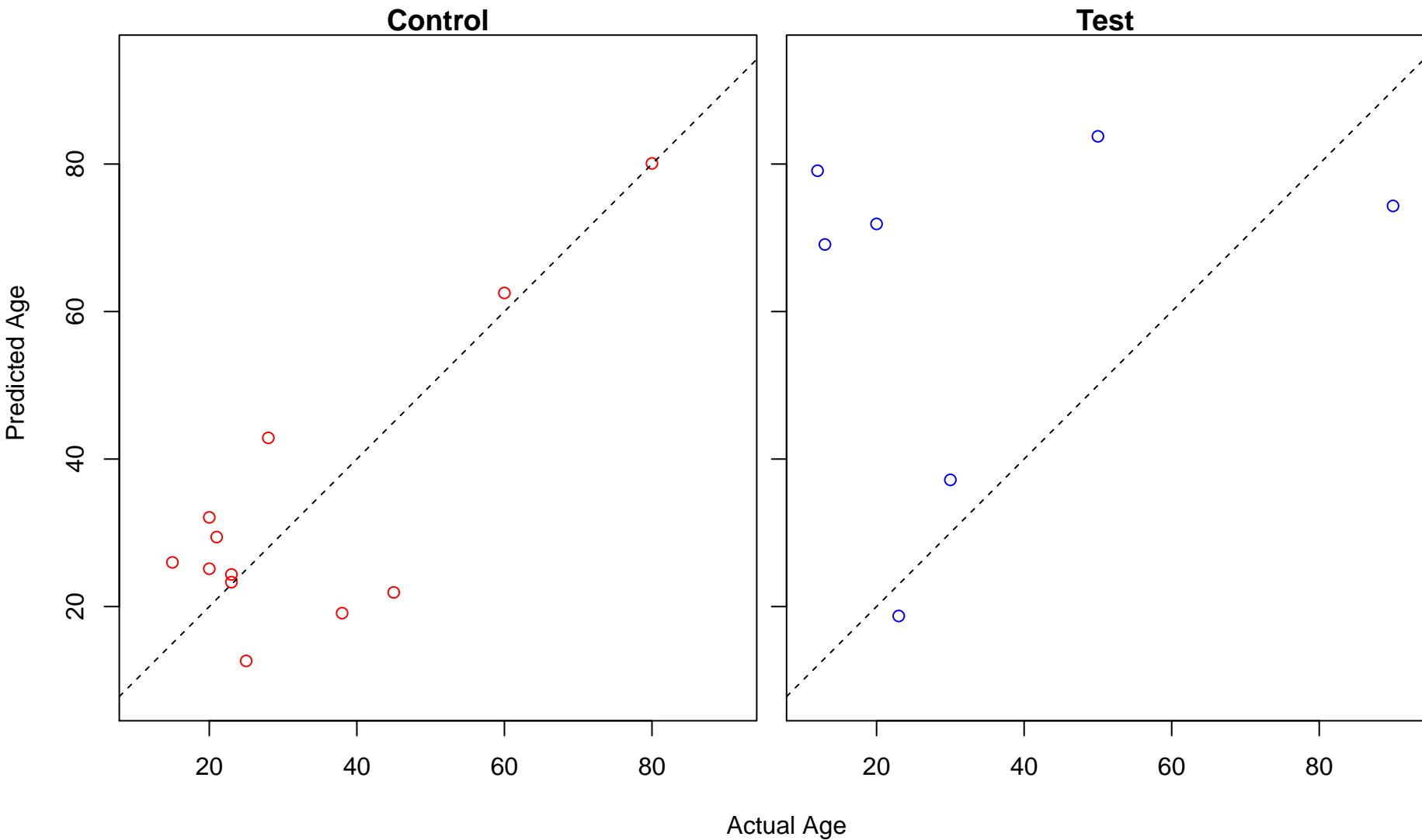
activation of JNKK activity (Score: 36.888439)



positive regulation of sphingolipid biosynthetic process (Score: 36.866372)

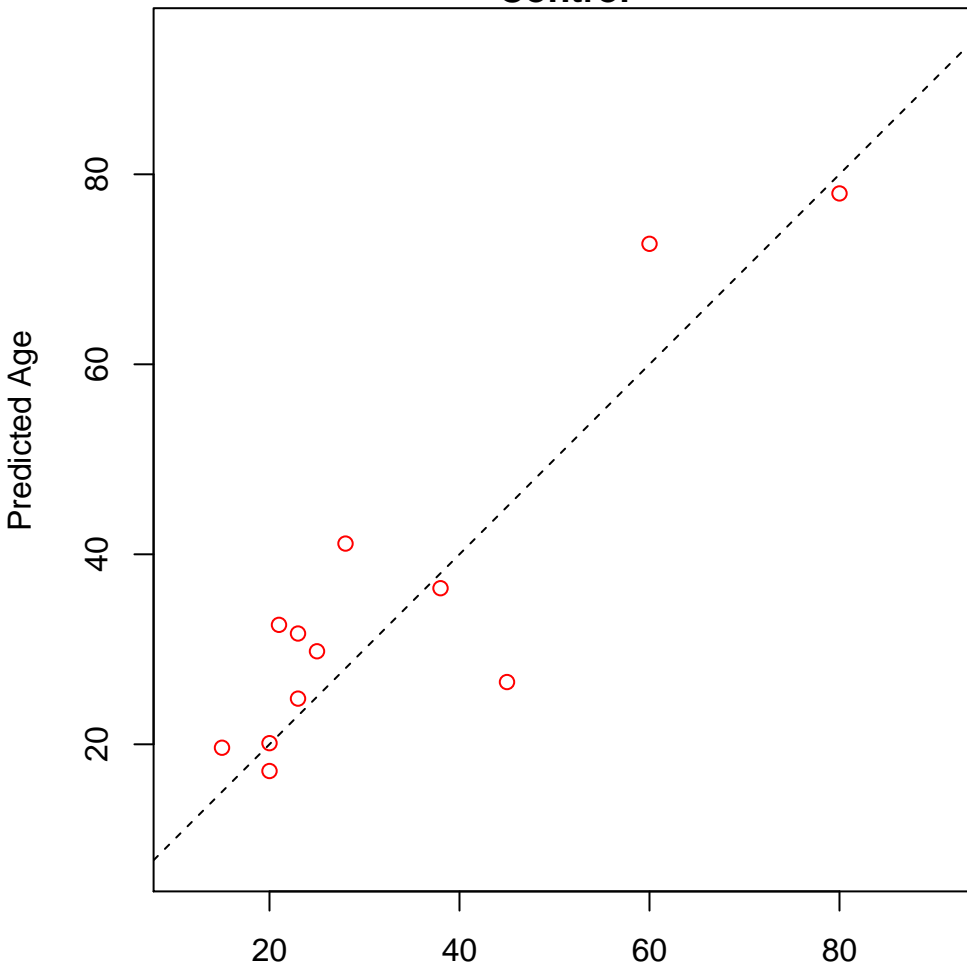


positive regulation of ceramide biosynthetic process (Score: 36.866372)

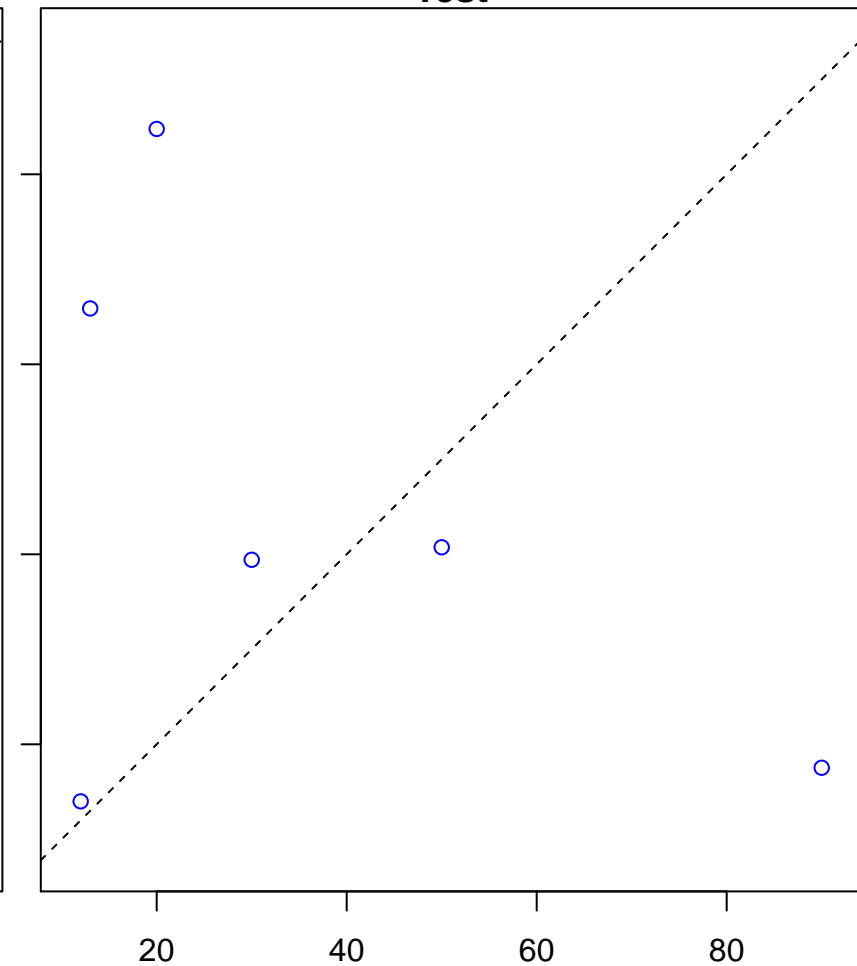


signal transduction in absence of ligand (Score: 36.849946)

Control

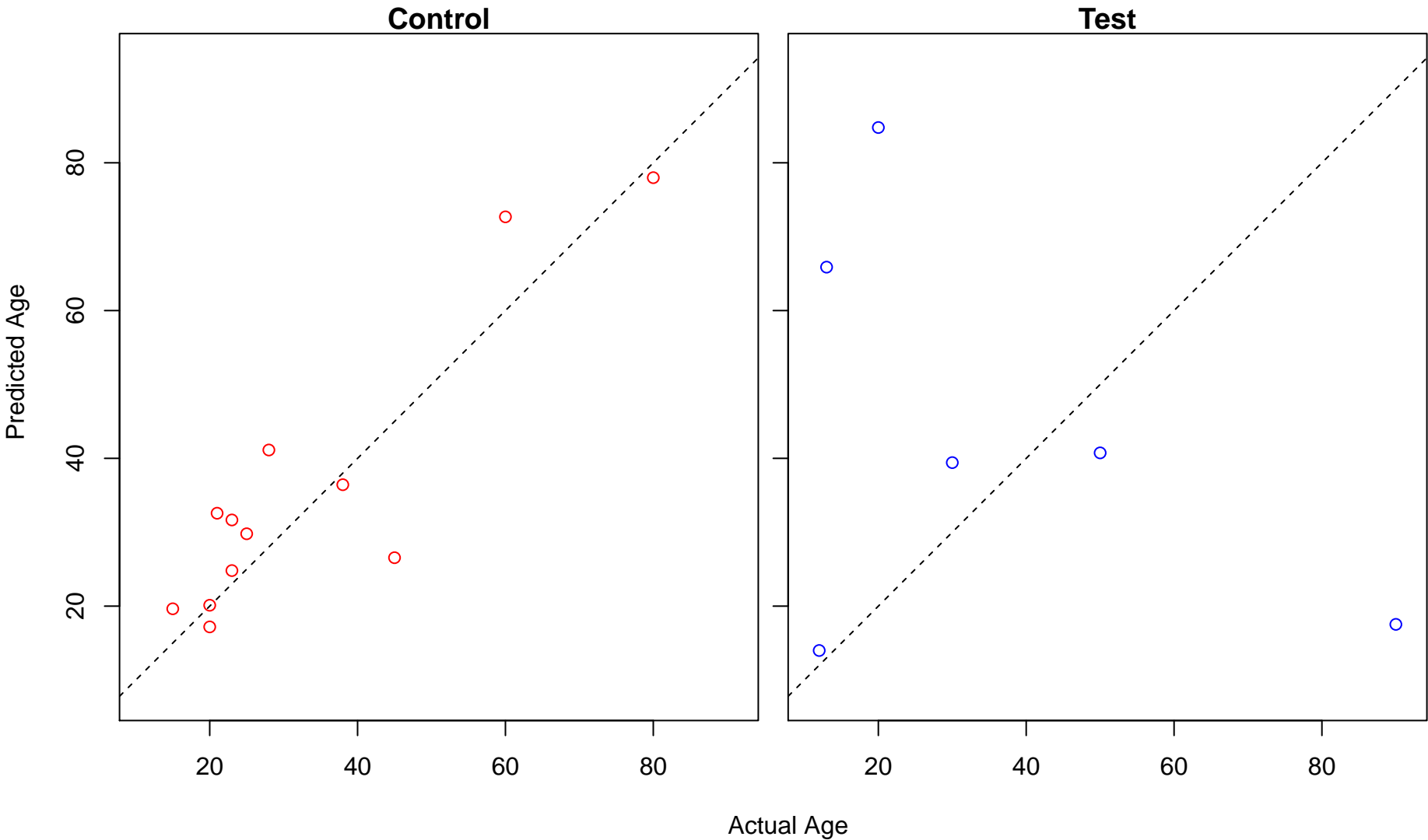


Test

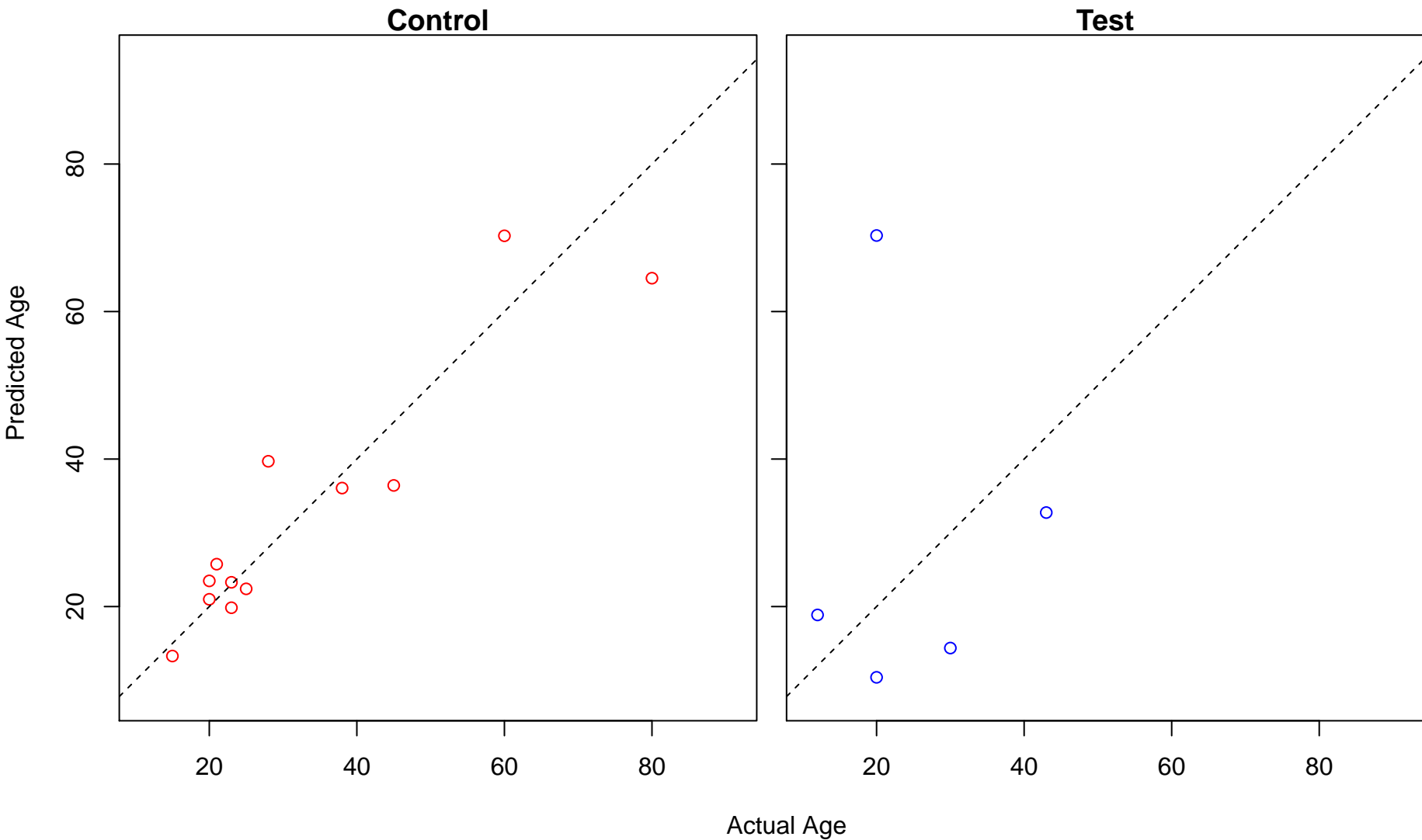


Actual Age

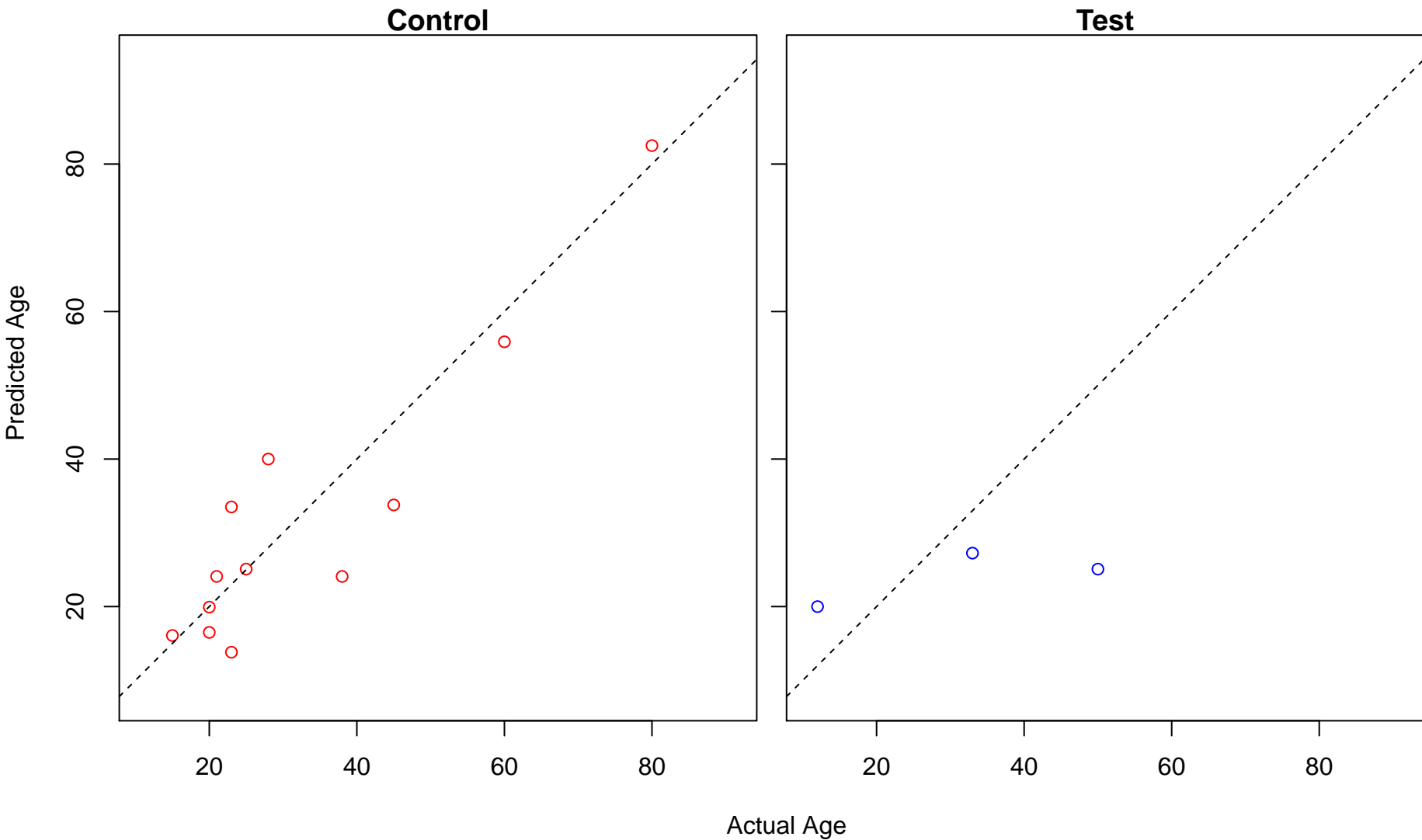
extrinsic apoptotic signaling pathway in absence of ligand (Score: 36.849946)



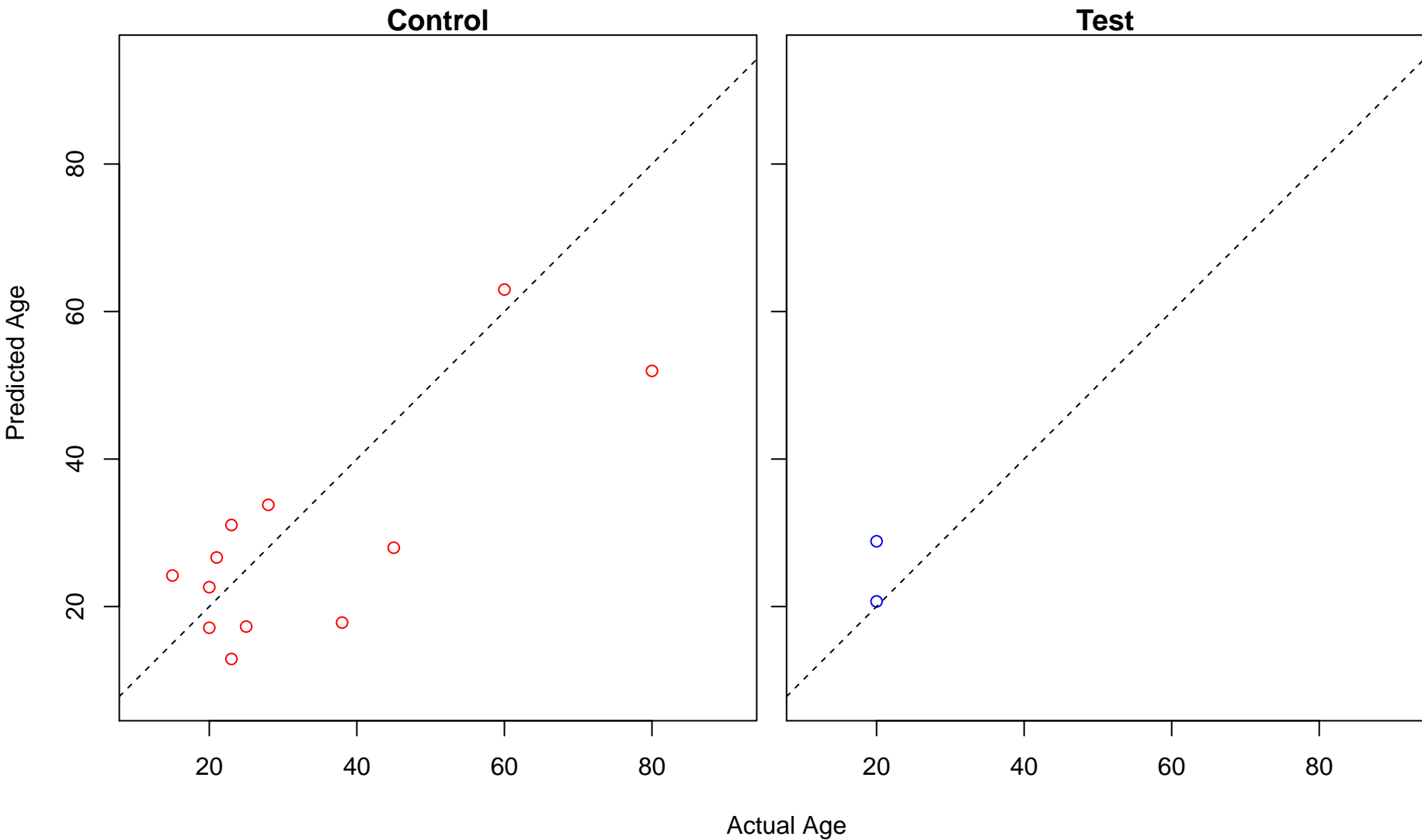
positive regulation of DNA repair (Score: 36.841230)



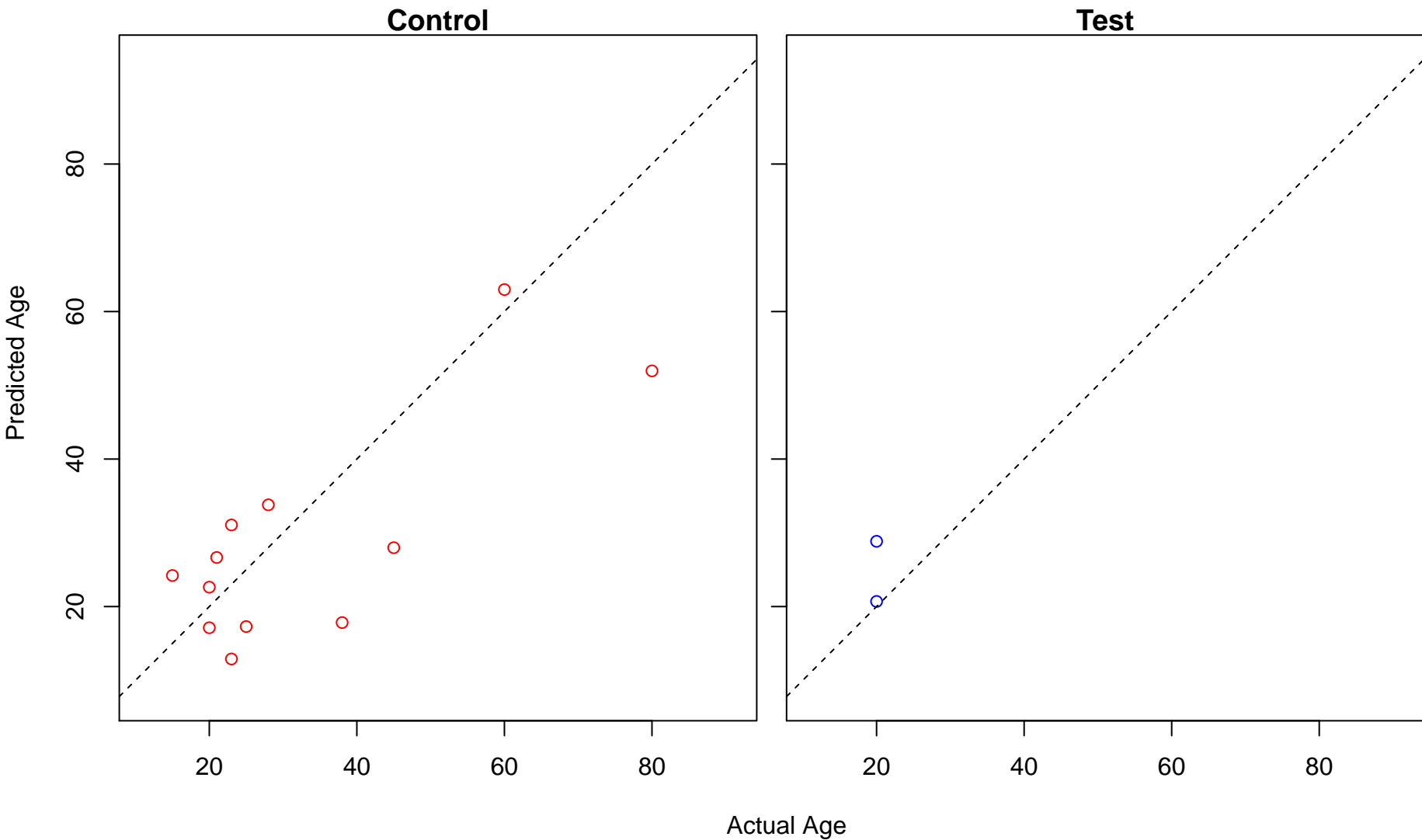
Golgi to endosome transport (Score: 36.784094)



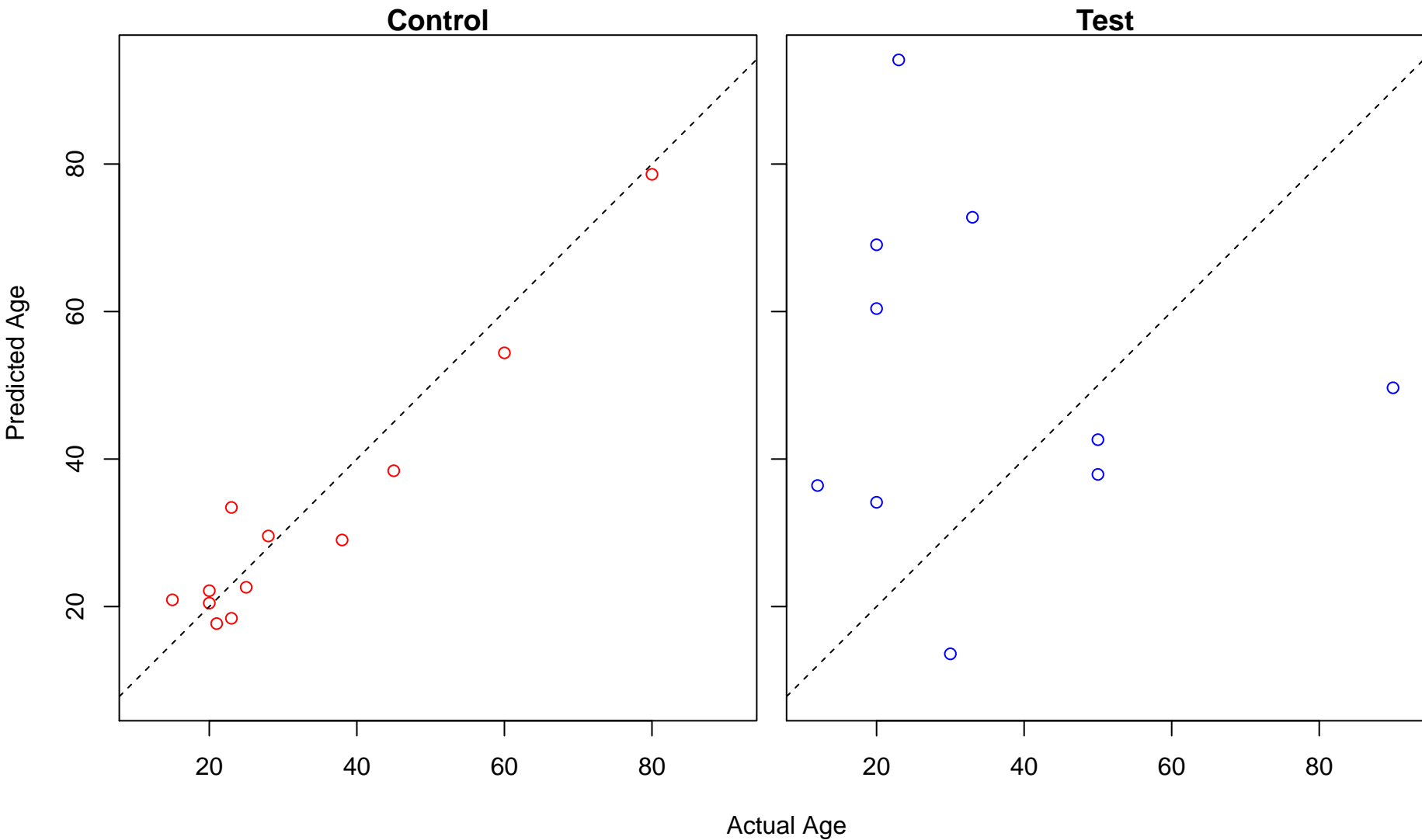
regulation of dopamine uptake involved in synaptic transmission (Score: 36.768556)



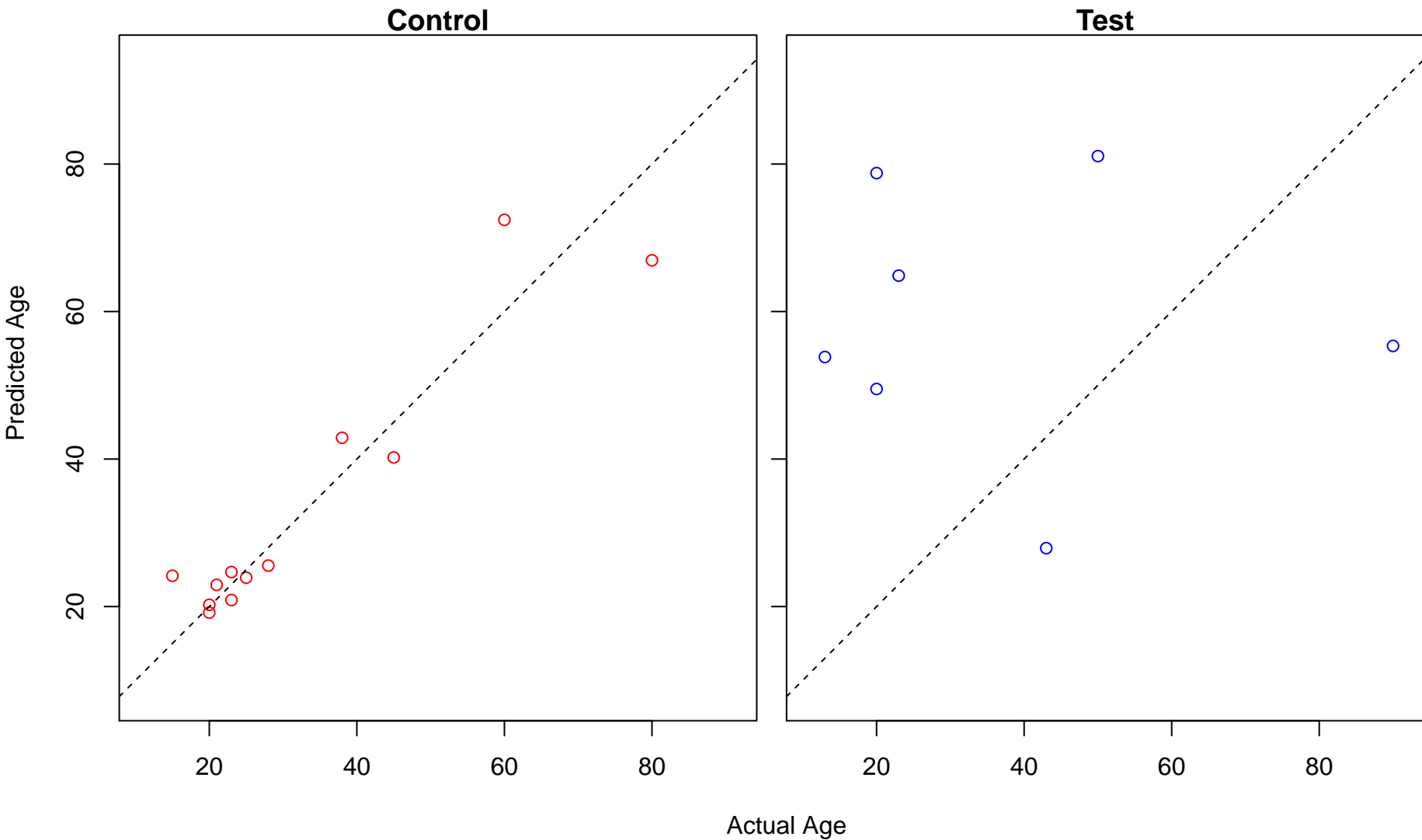
regulation of catecholamine uptake involved in synaptic transmission (Score: 36.768556)



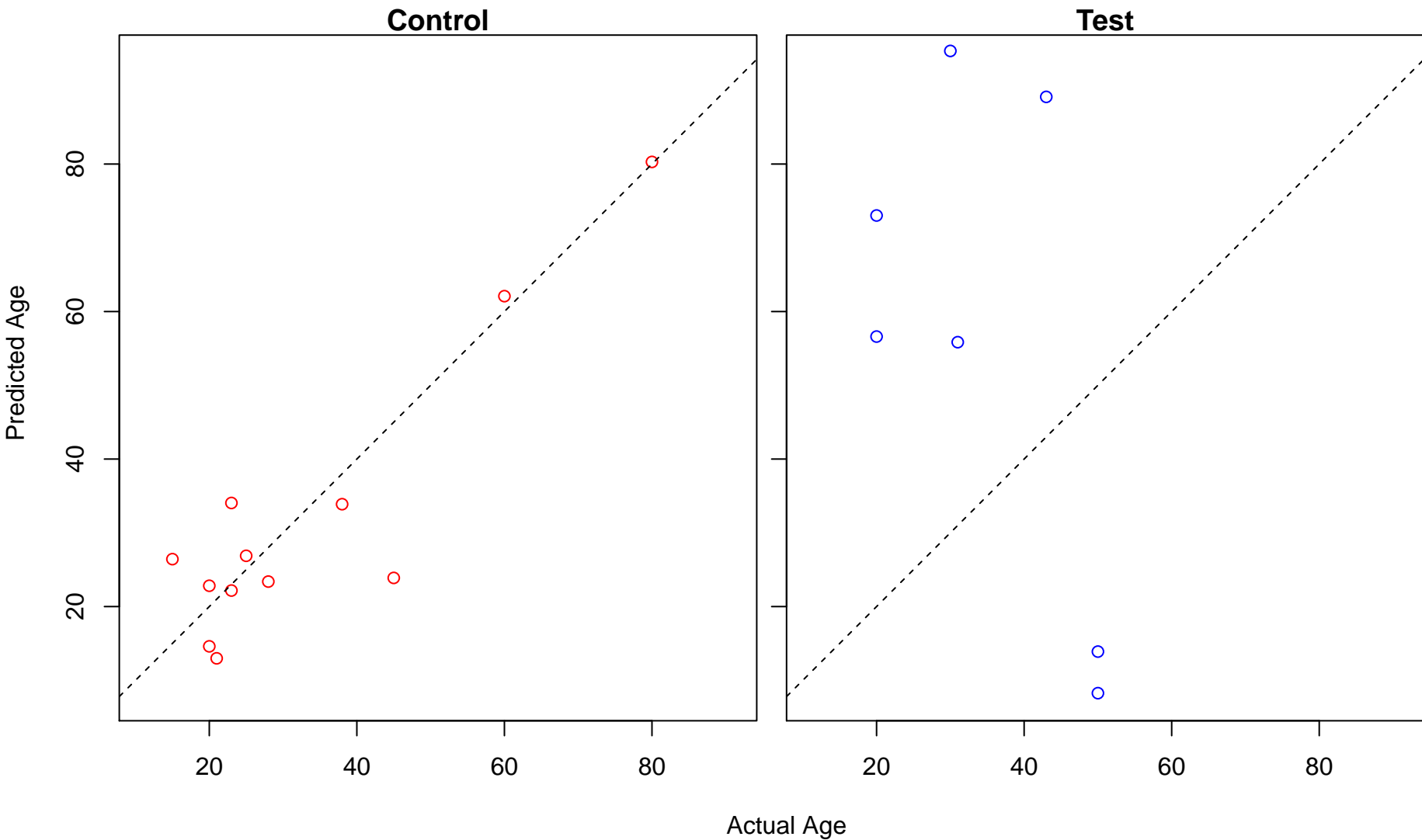
RNA interference (Score: 36.658312)



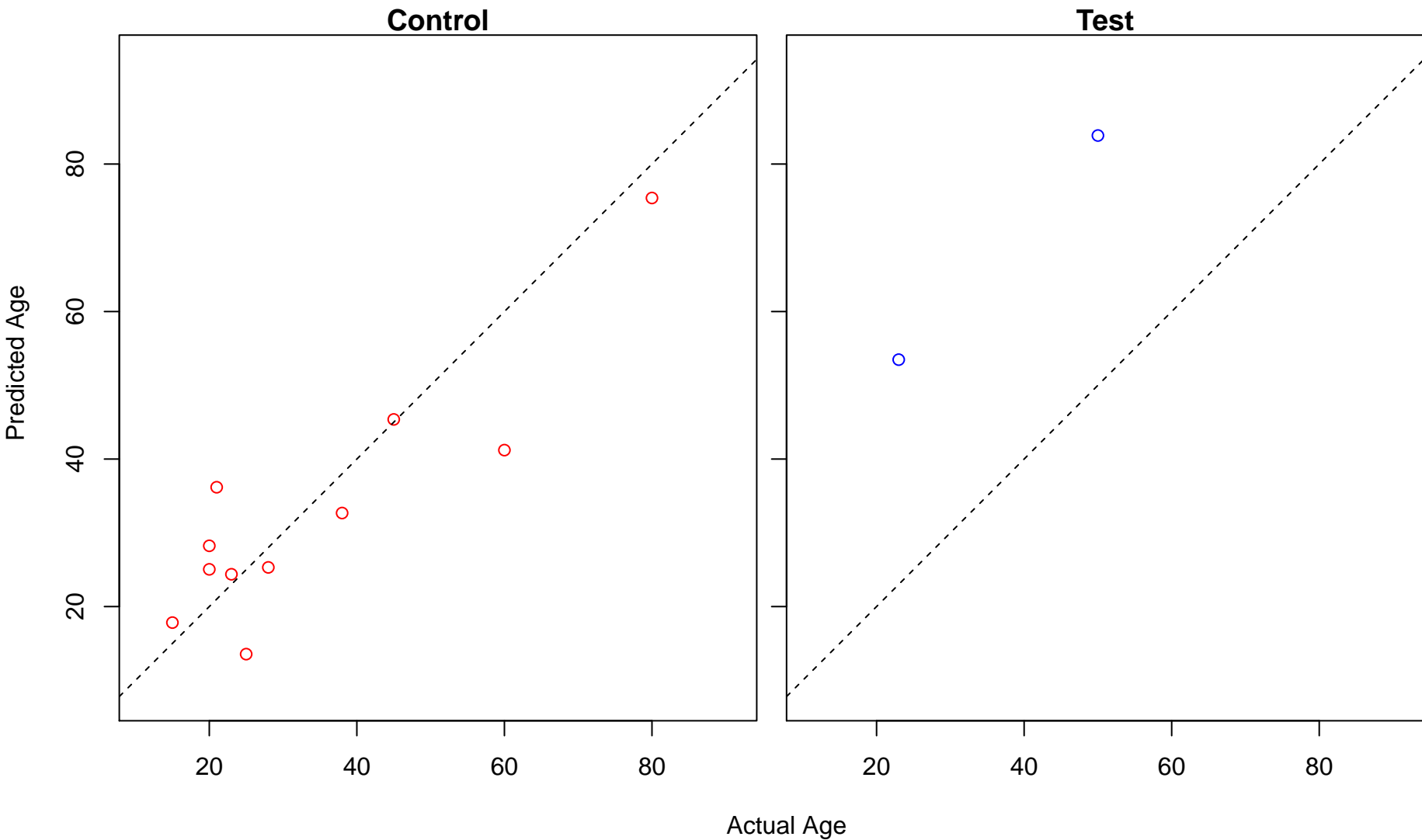
membrane lipid catabolic process (Score: 36.286509)



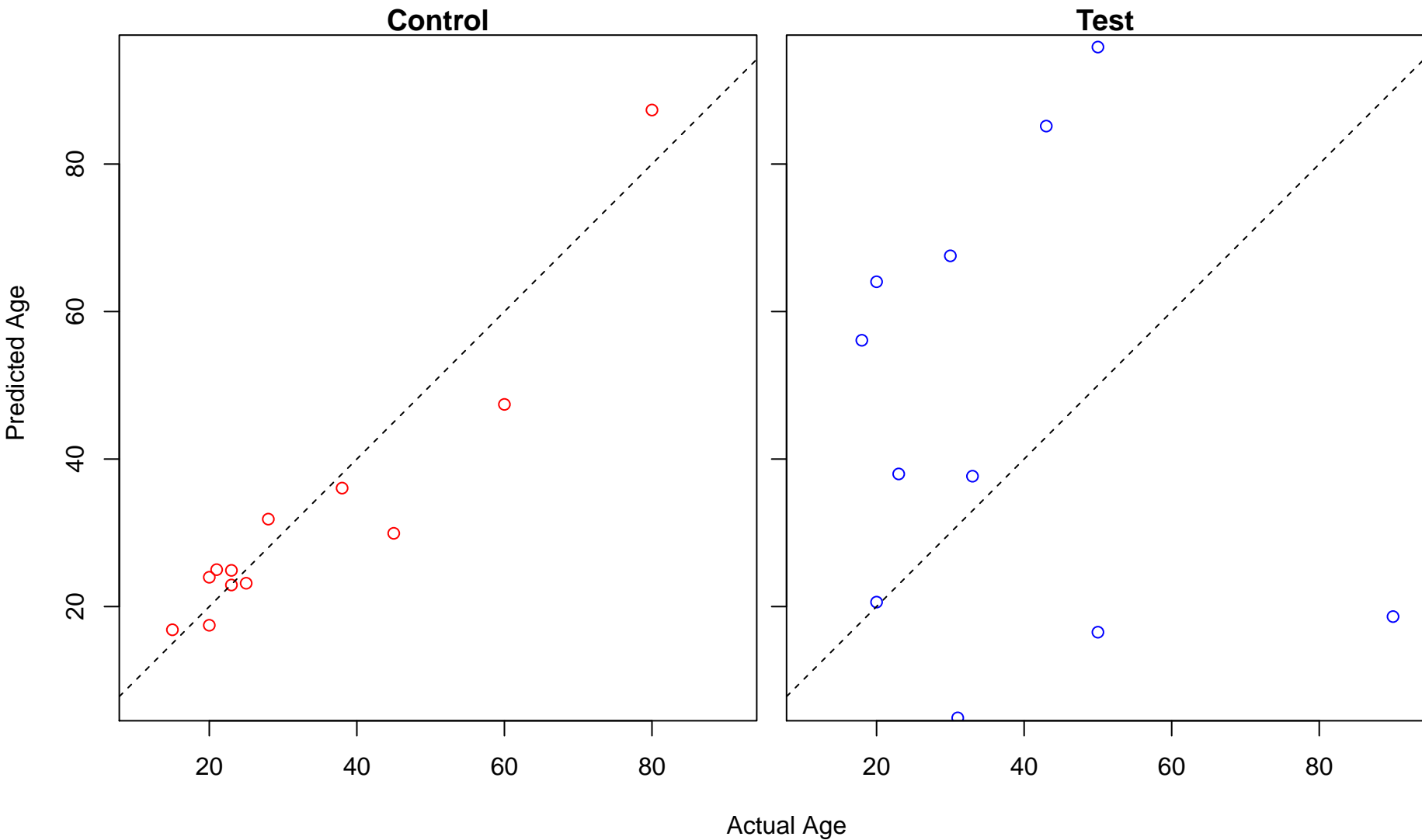
positive regulation of Arp2/3 complex-mediated actin nucleation (Score: 36.065196)



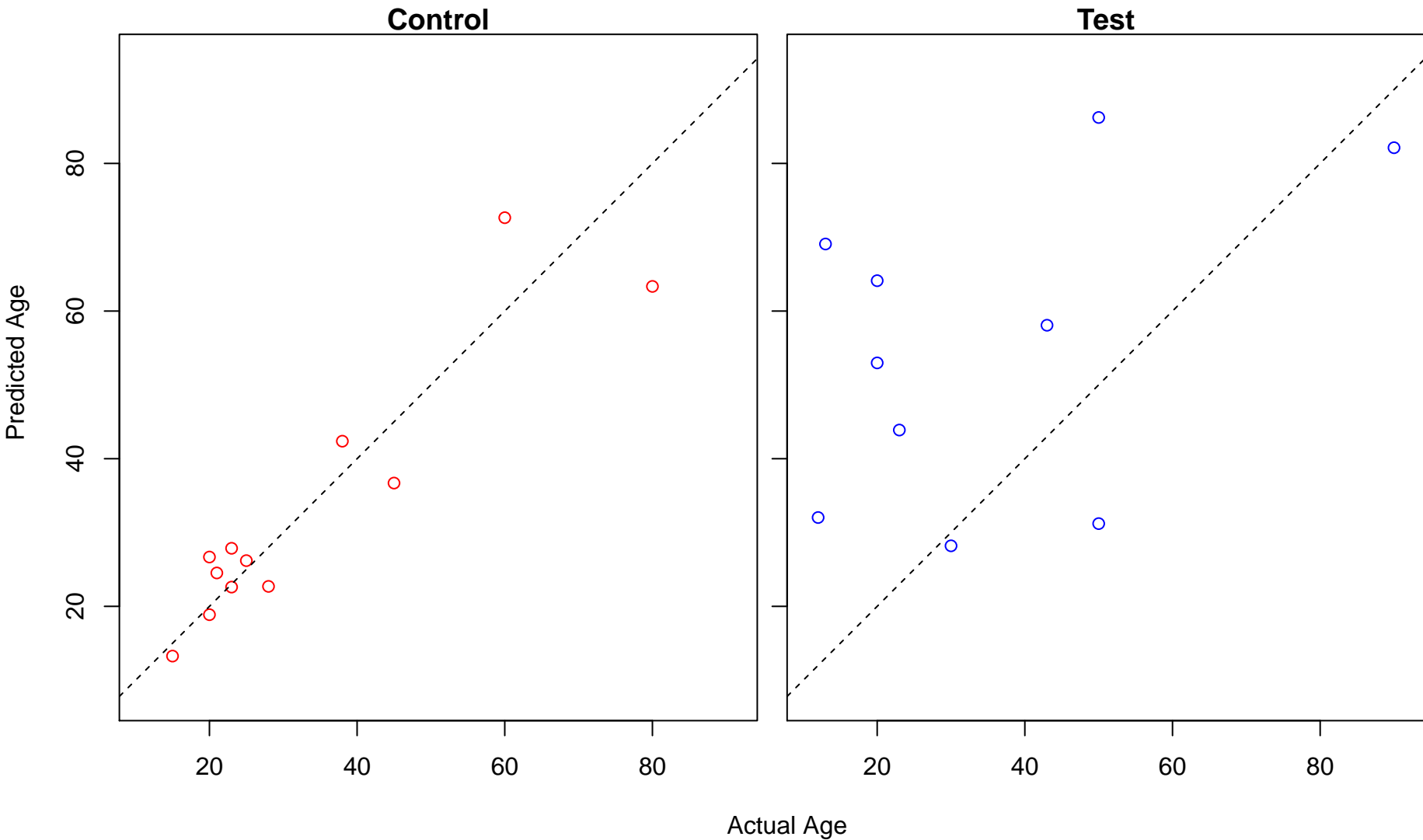
amino acid import (Score: 36.051688)



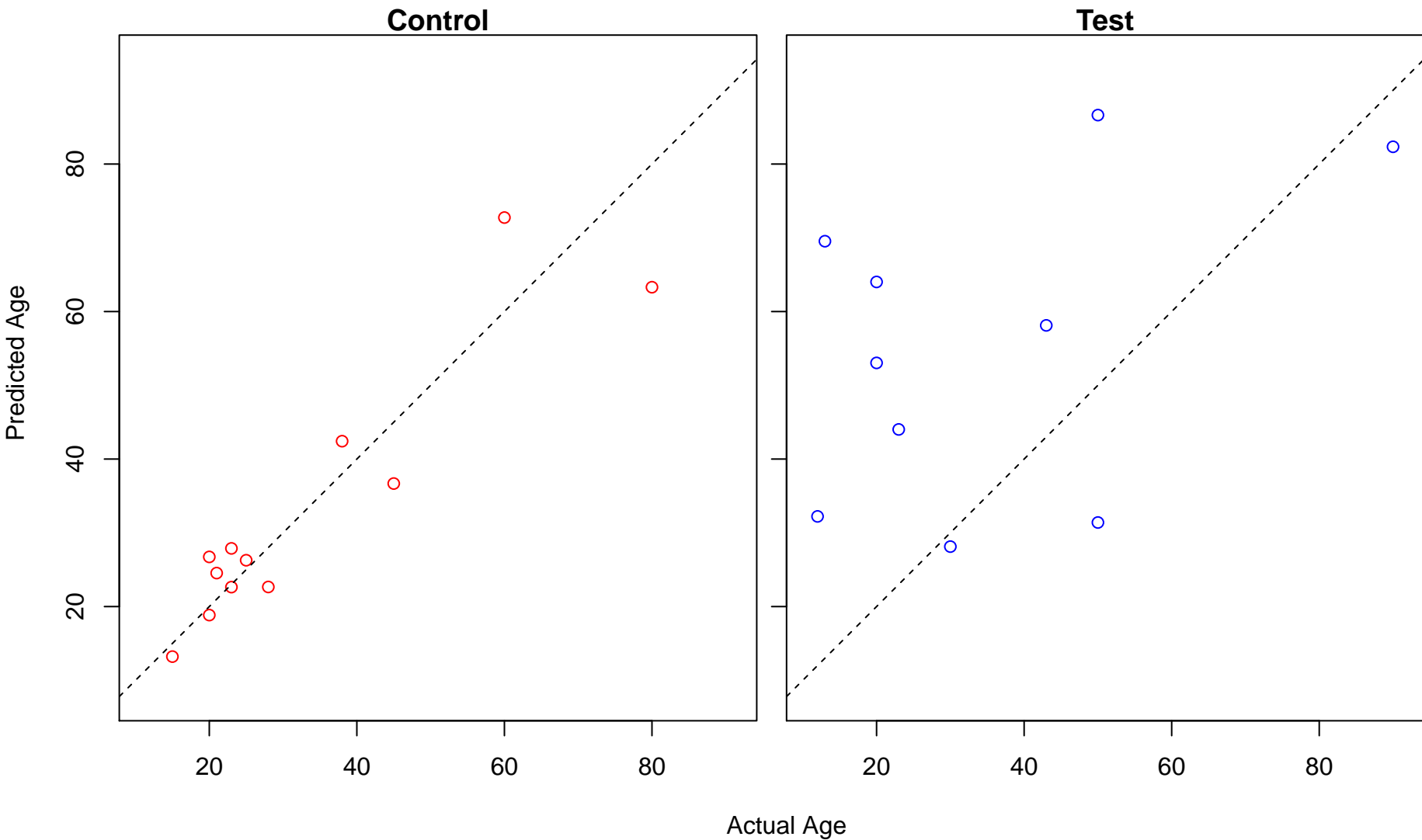
secondary metabolic process (Score: 35.502872)



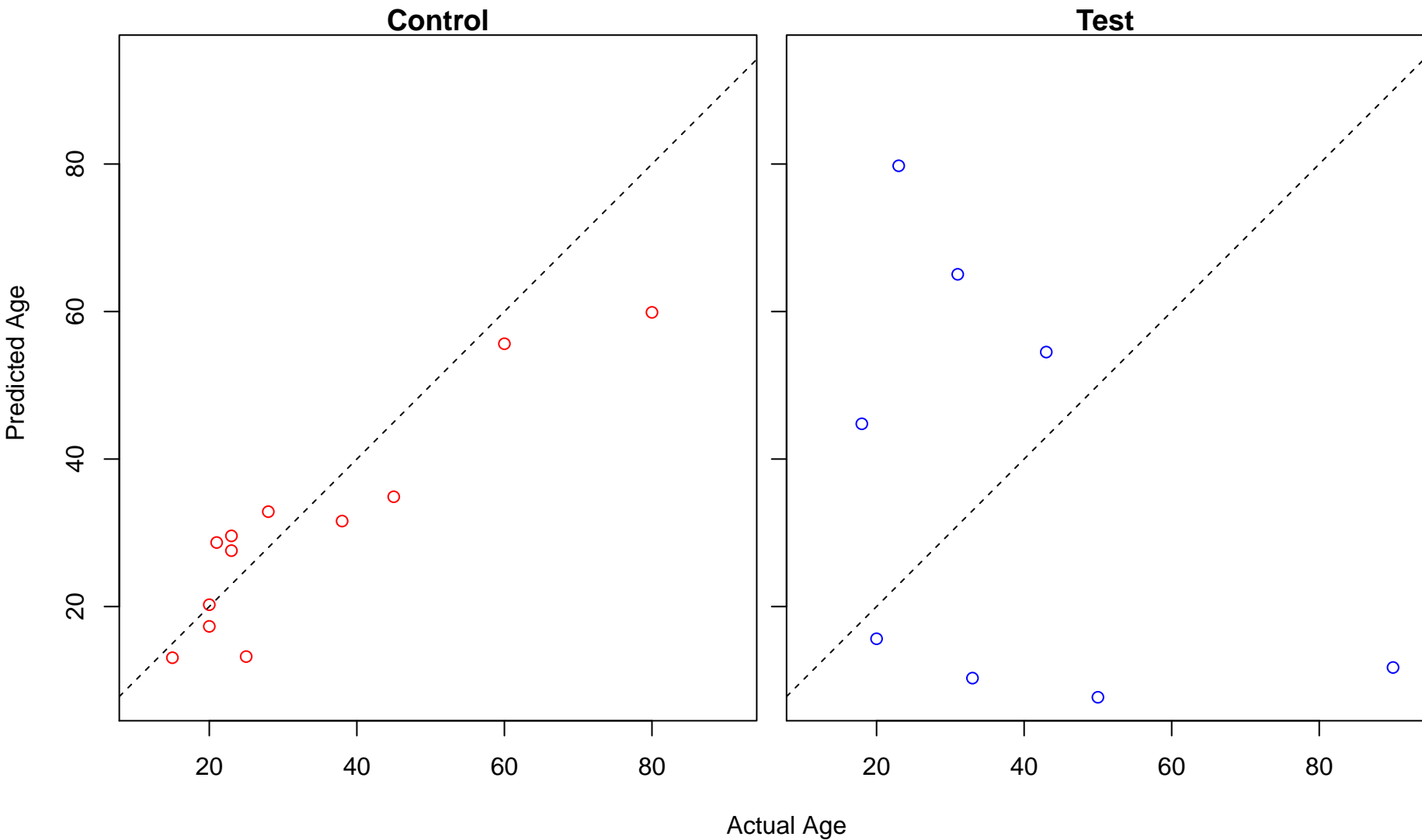
regulation of vascular endothelial growth factor production (Score: 35.313842)



positive regulation of vascular endothelial growth factor production (Score: 35.186502)

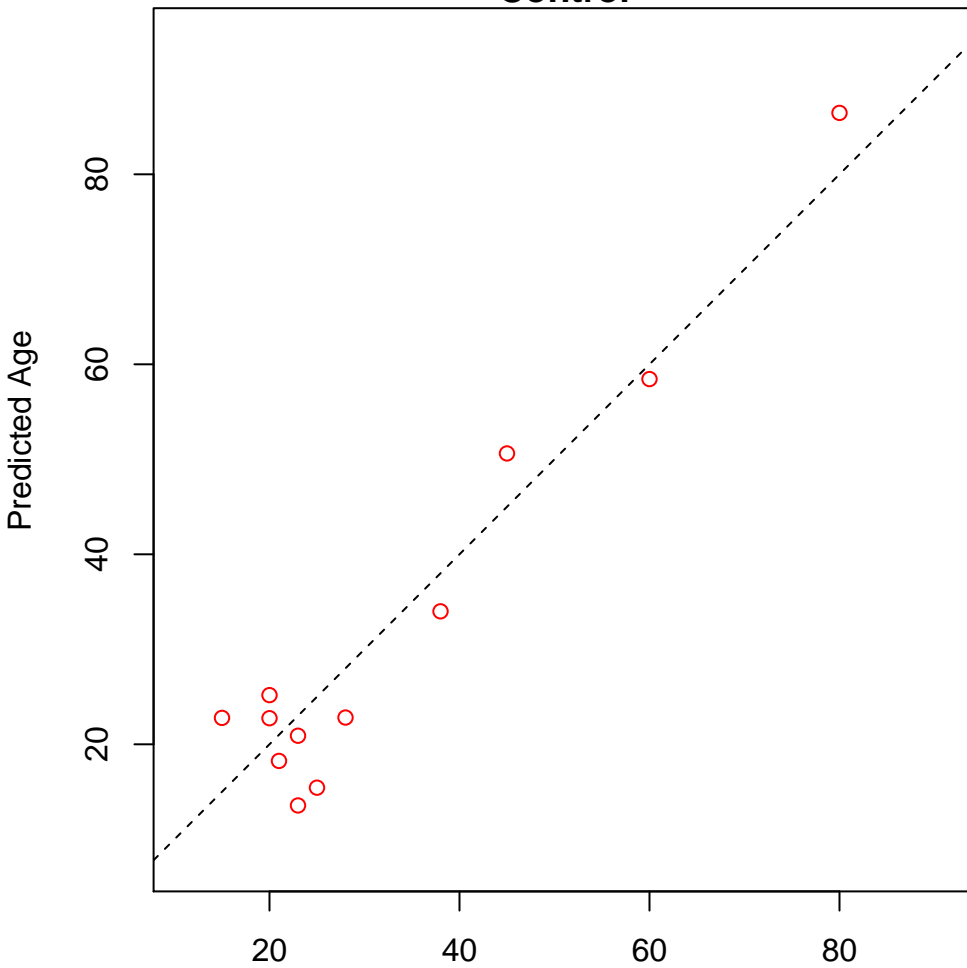


negative regulation of alpha-beta T cell activation (Score: 35.115540)

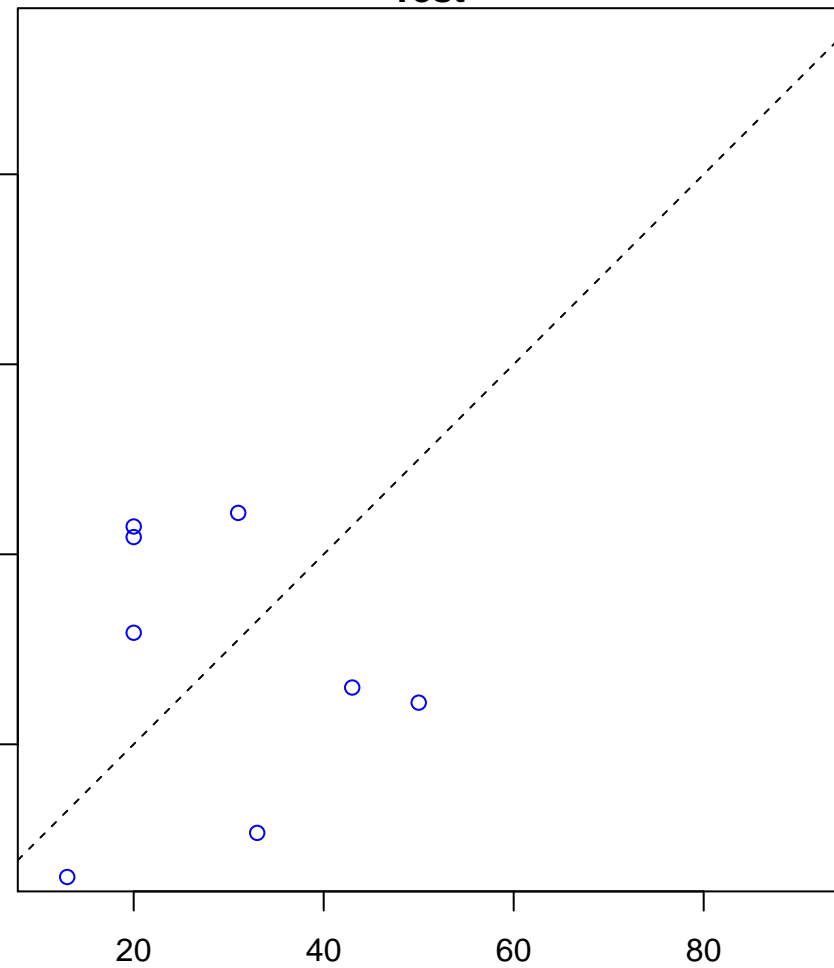


regulation of metanephros development (Score: 35.114198)

Control



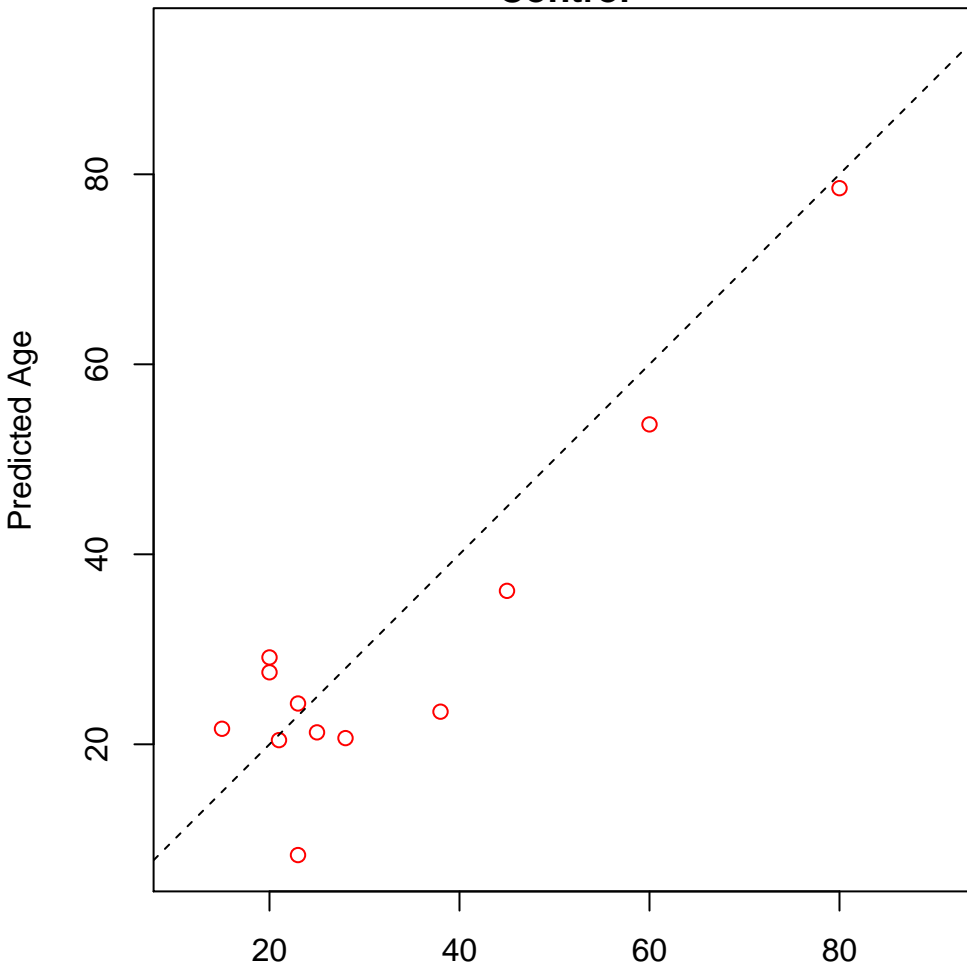
Test



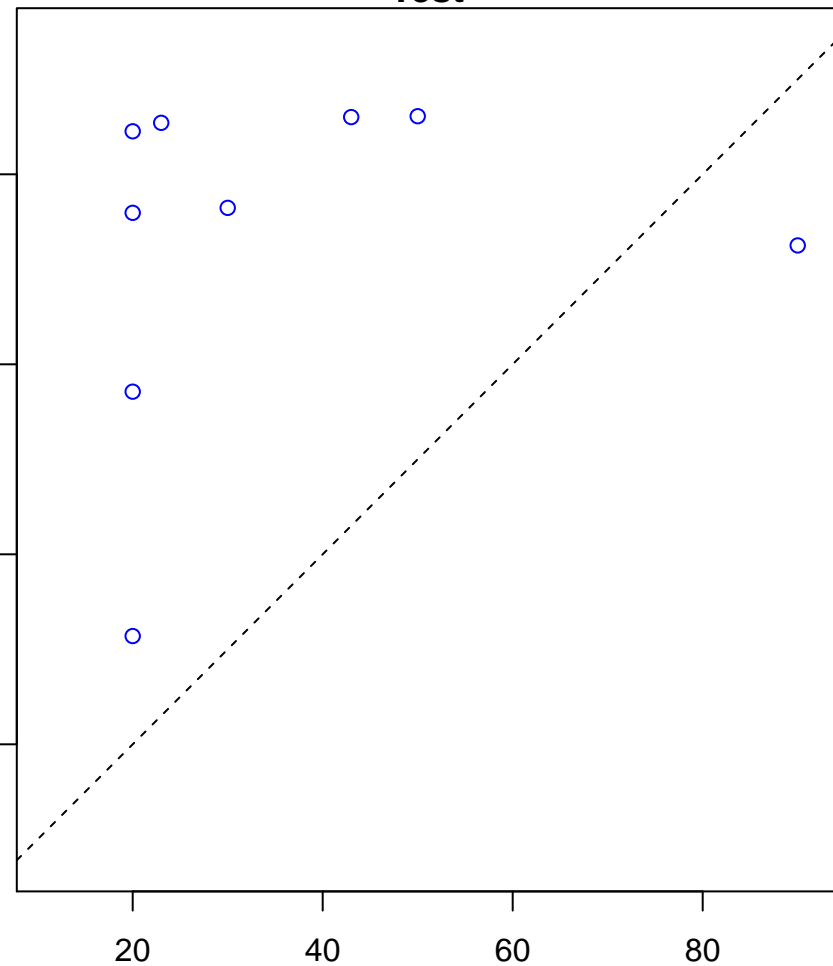
Actual Age

regulation of oxidoreductase activity (Score: 35.072034)

Control

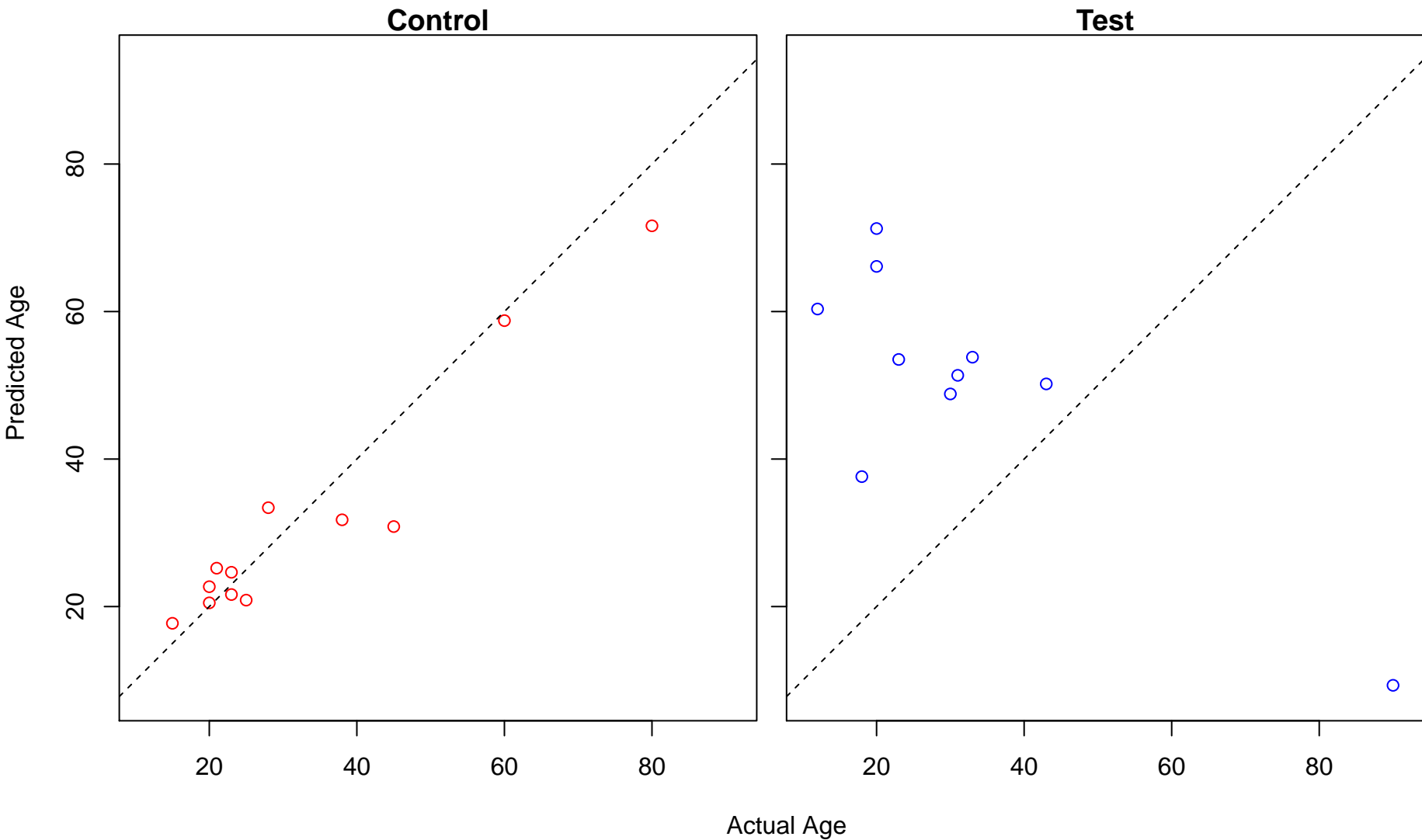


Test

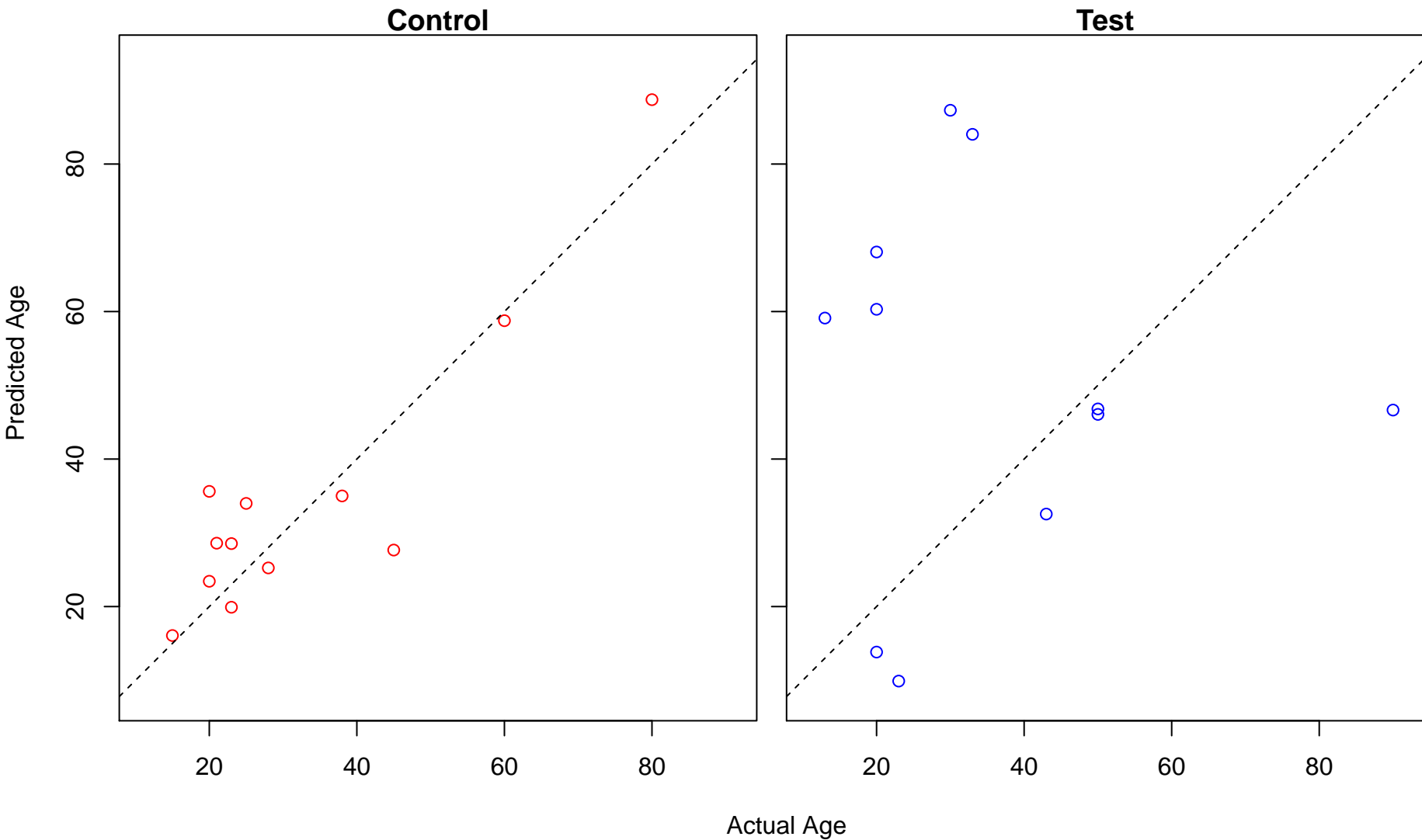


Actual Age

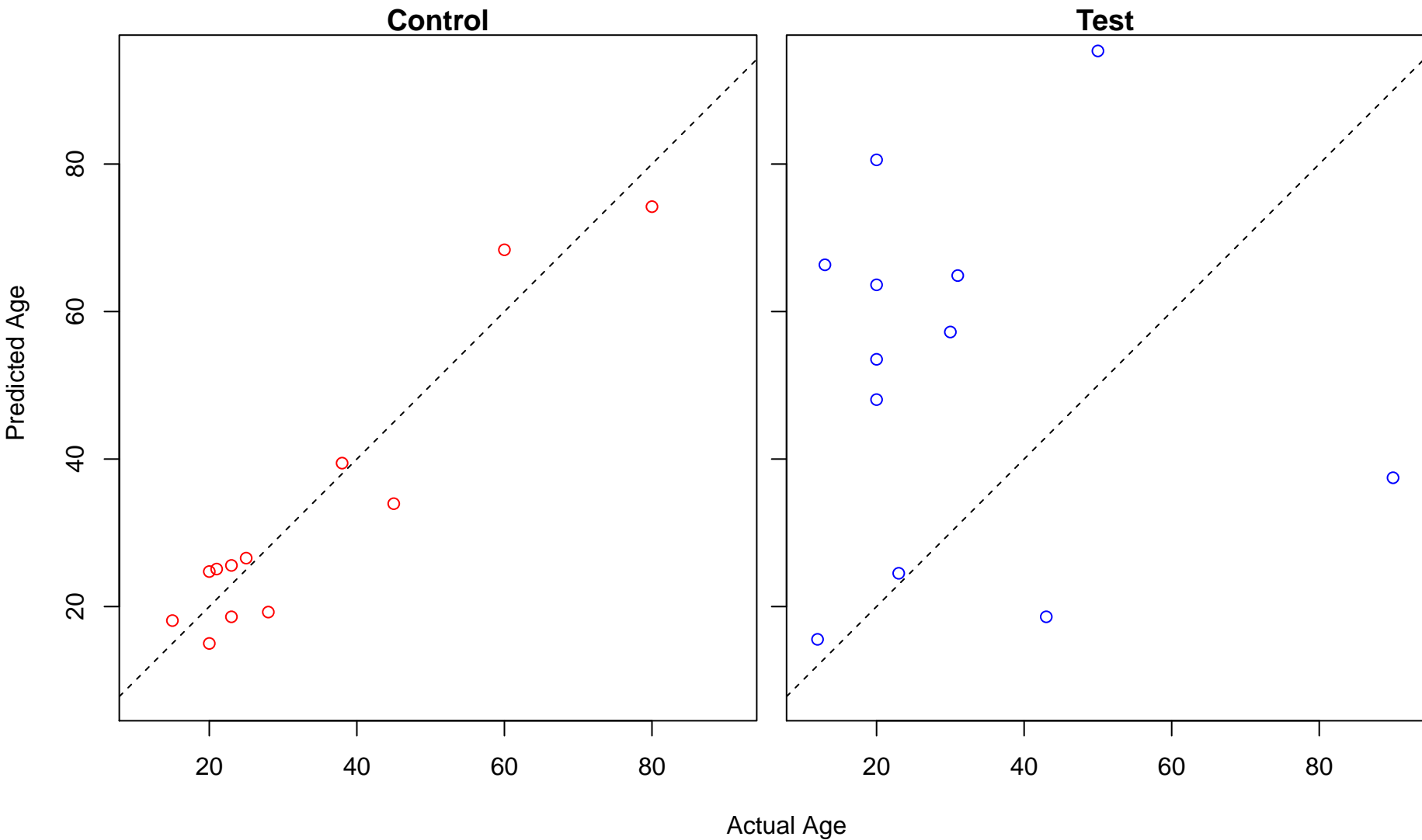
positive regulation of JNK cascade (Score: 34.957913)



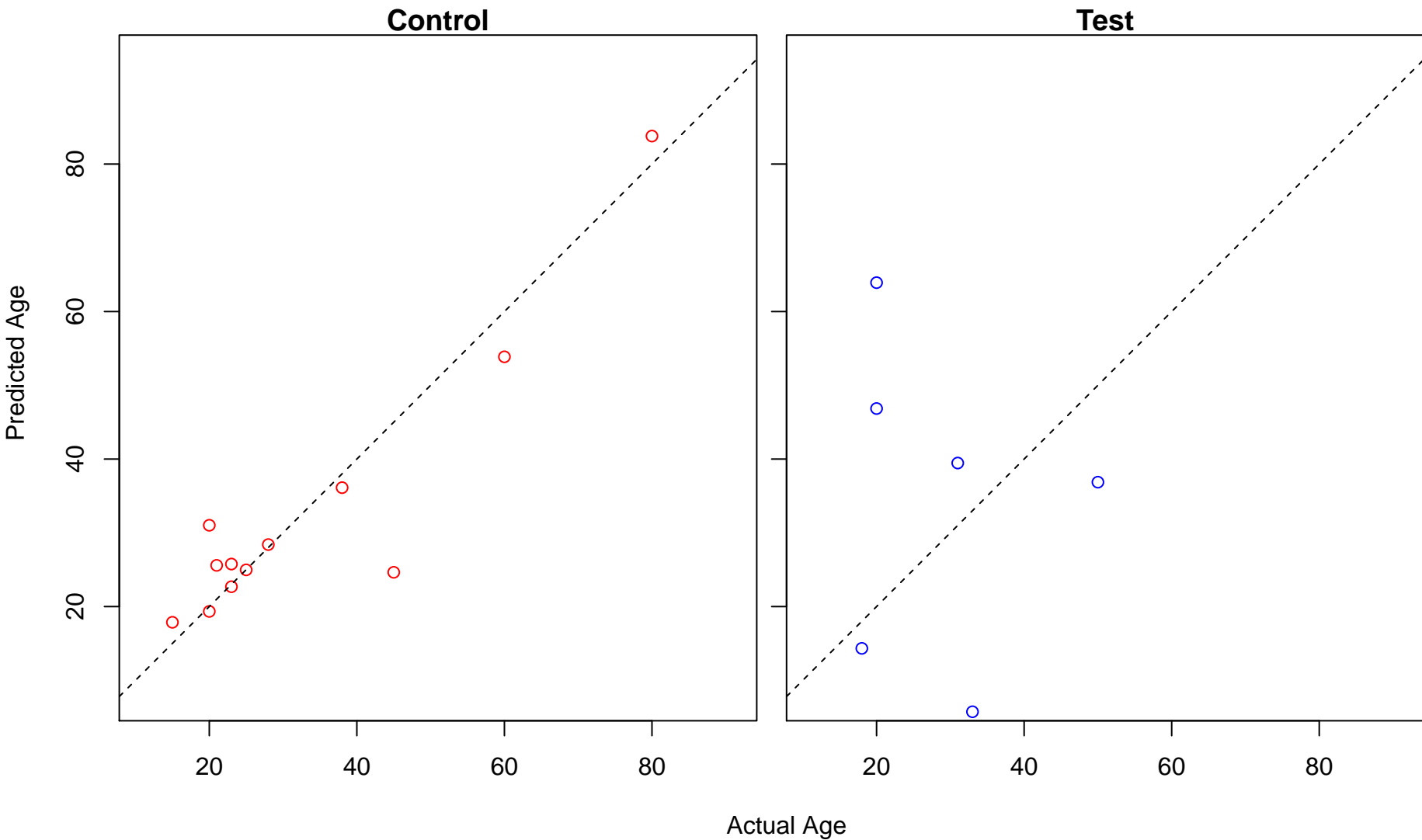
regulation of smooth muscle cell migration (Score: 34.881706)



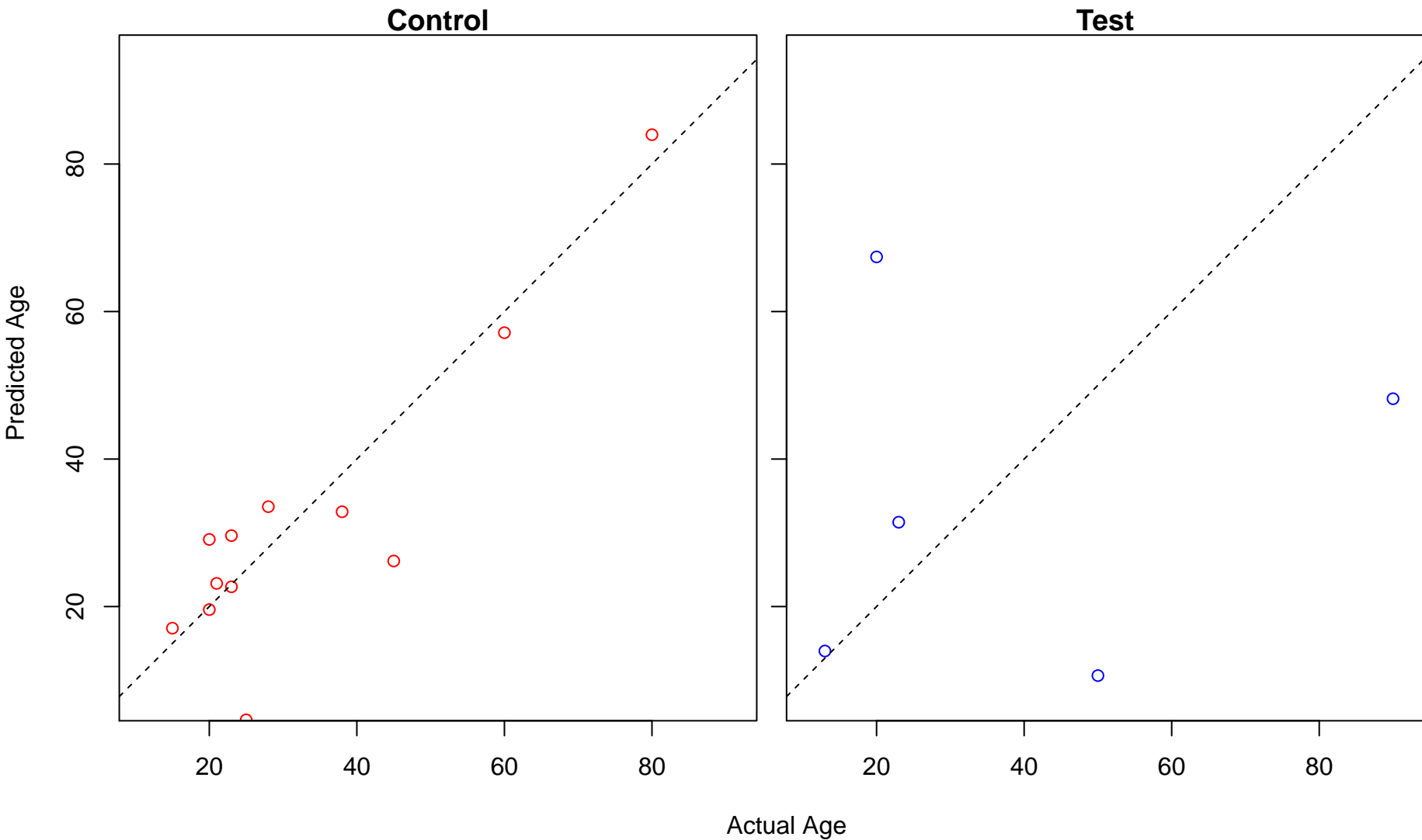
cell-cell adhesion via plasma-membrane adhesion molecules (Score: 34.803080)



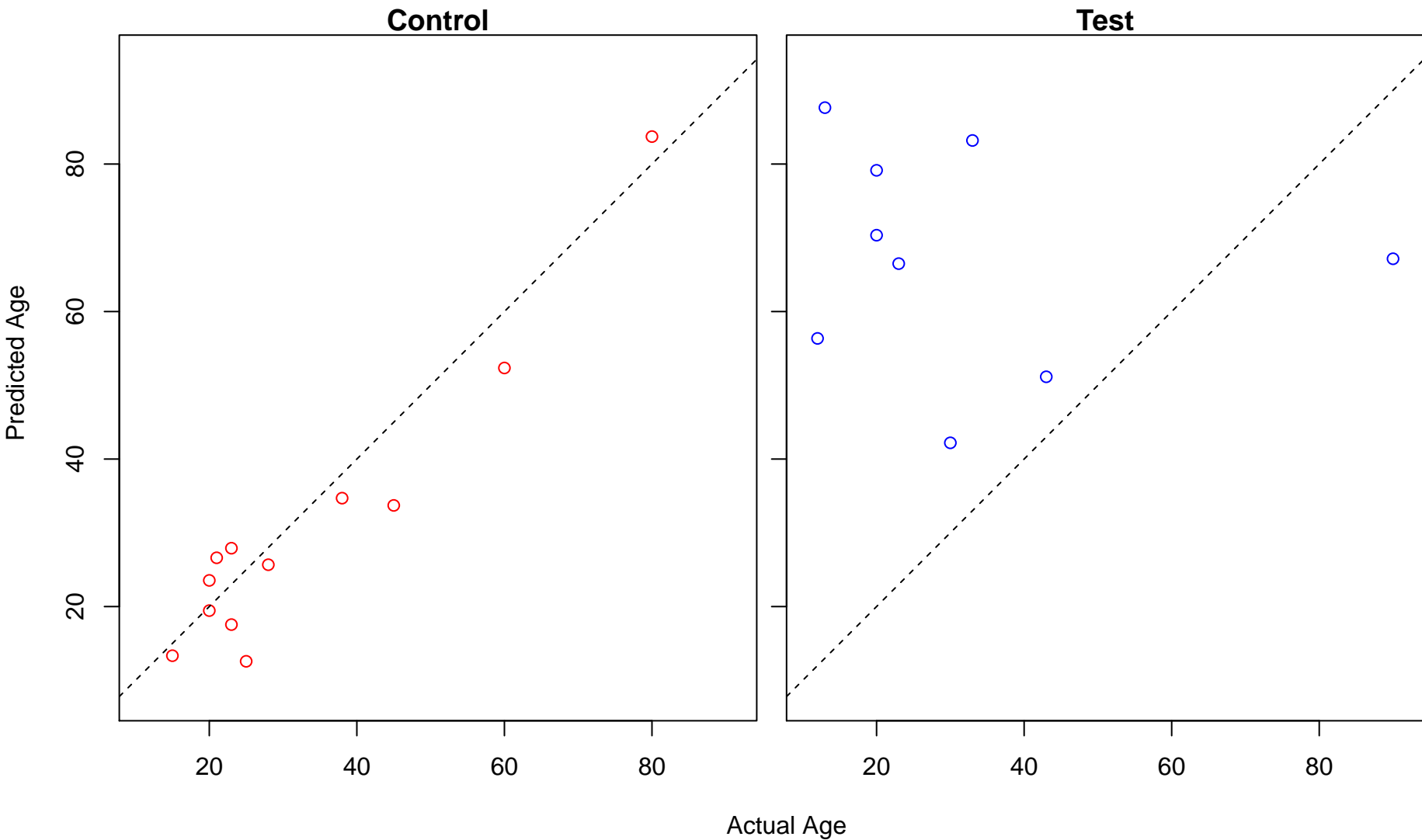
pyrimidine-containing compound transmembrane transport (Score: 34.786610)



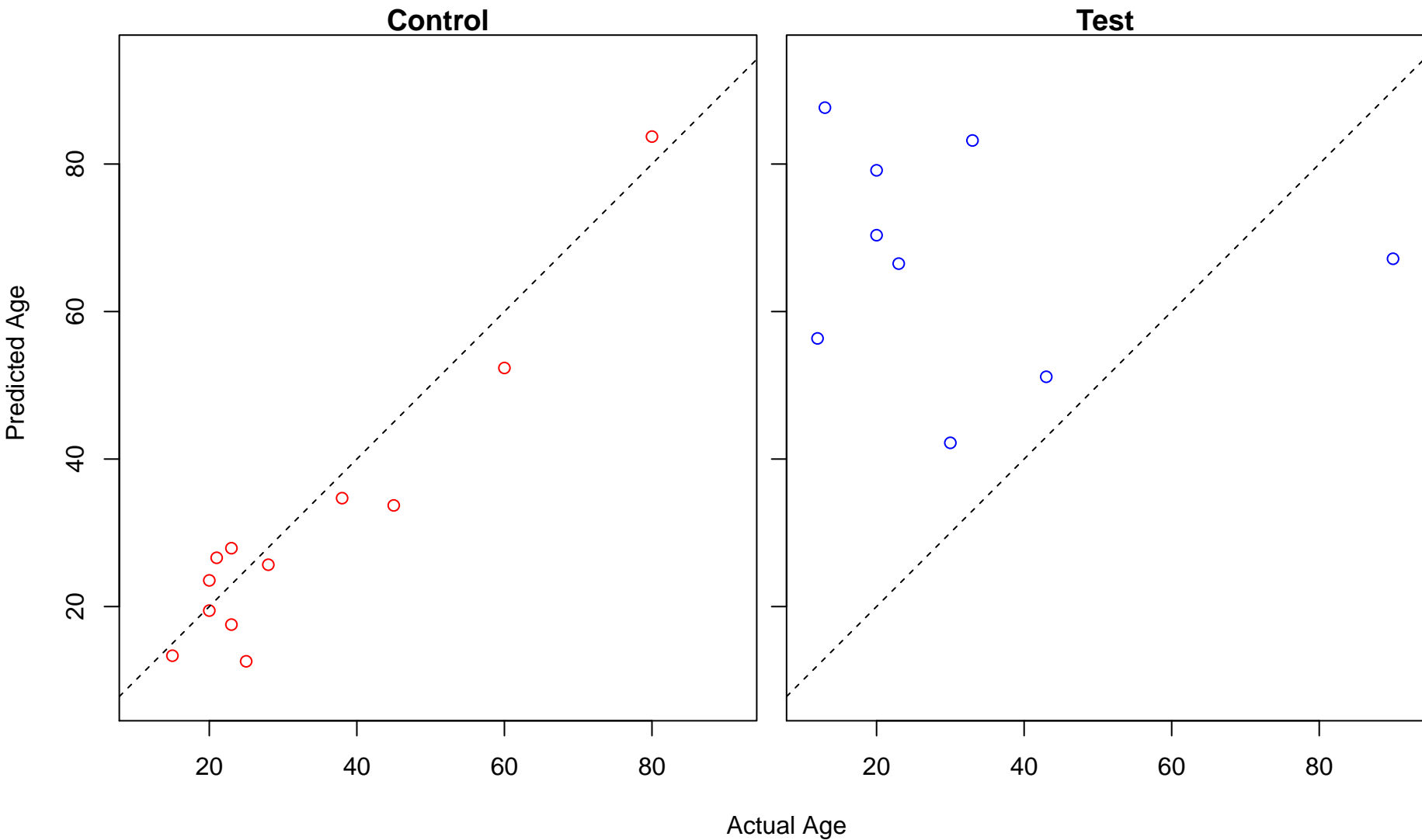
regulation of mononuclear cell migration (Score: 34.750216)



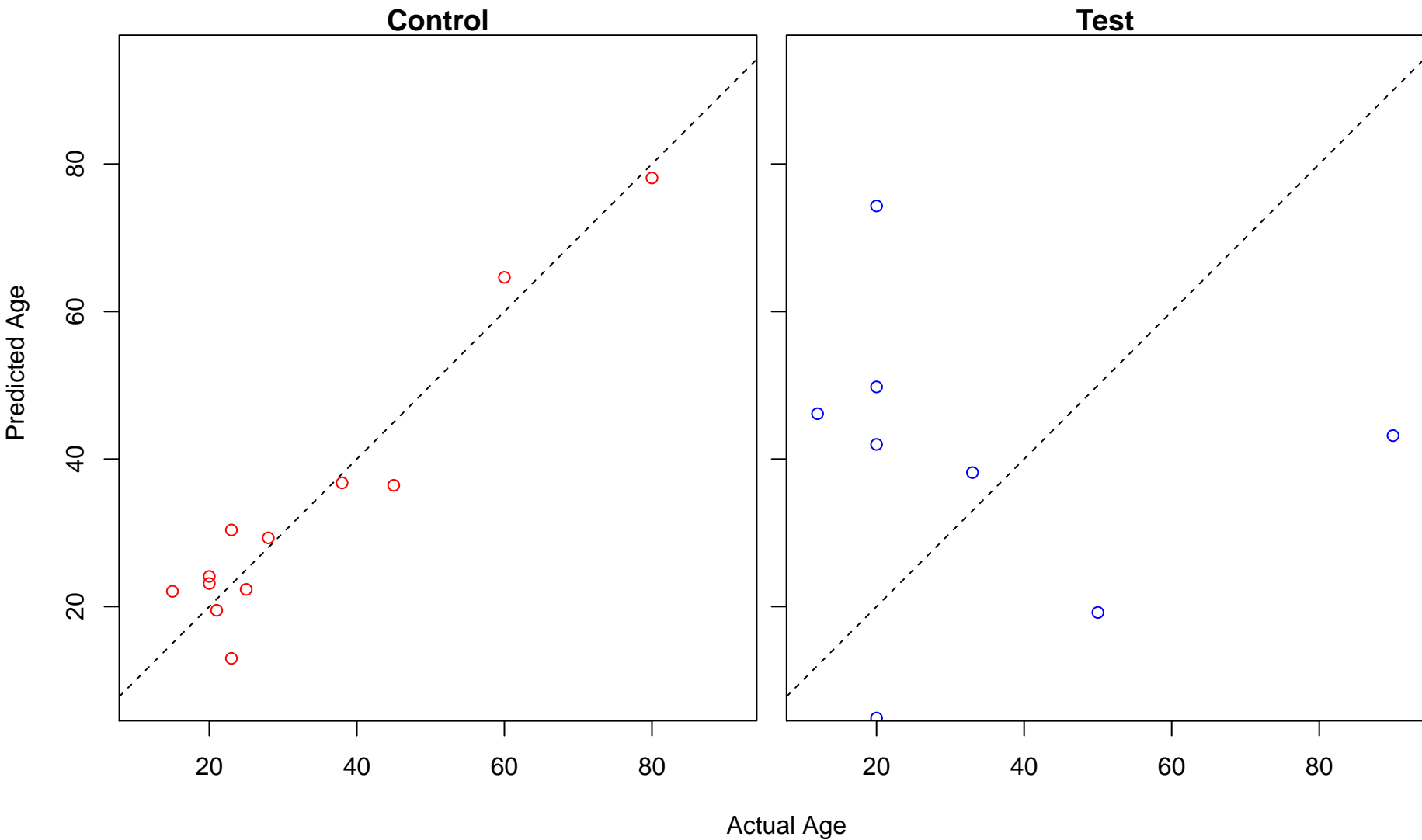
regulation of JAK-STAT cascade (Score: 34.729574)



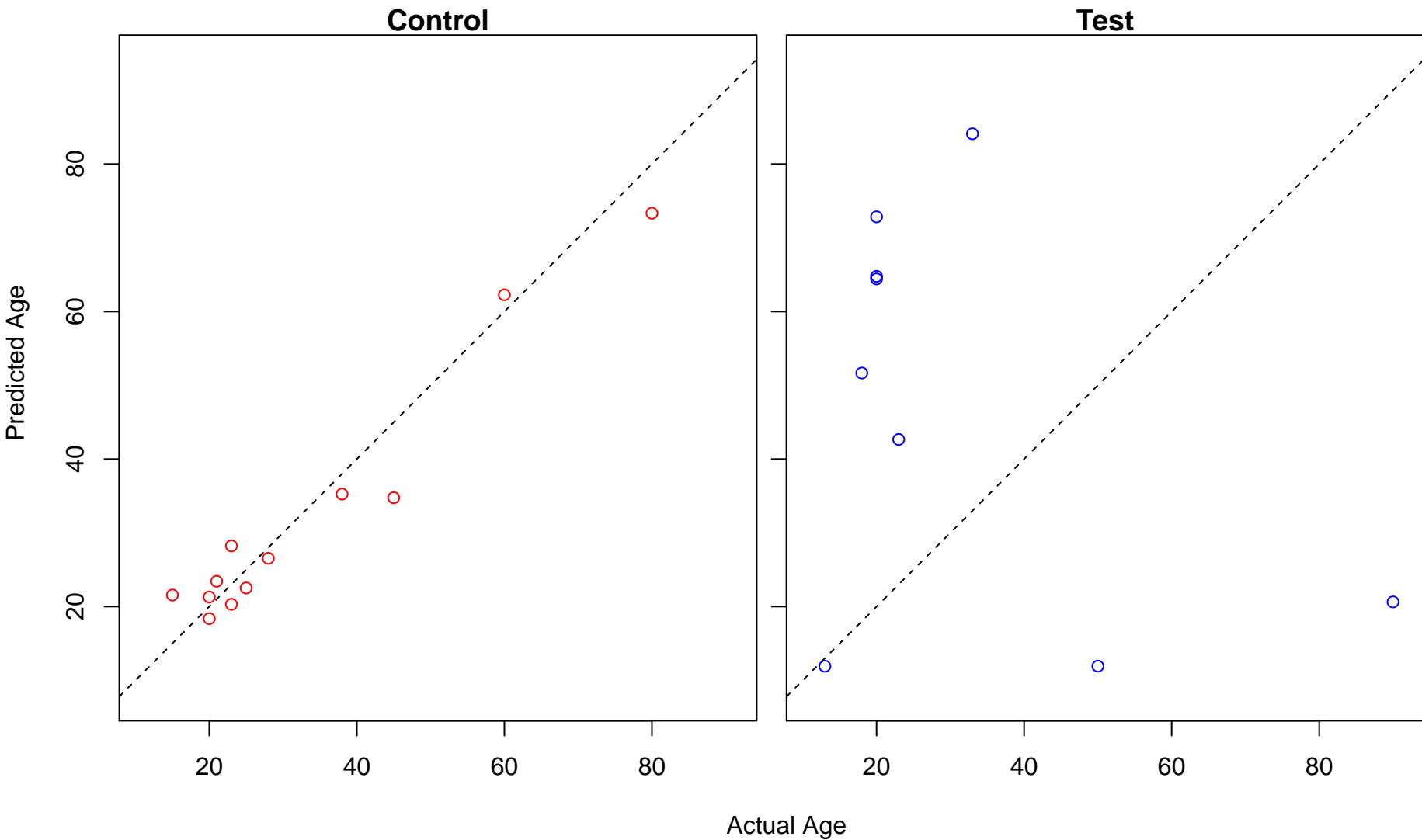
regulation of STAT cascade (Score: 34.729574)



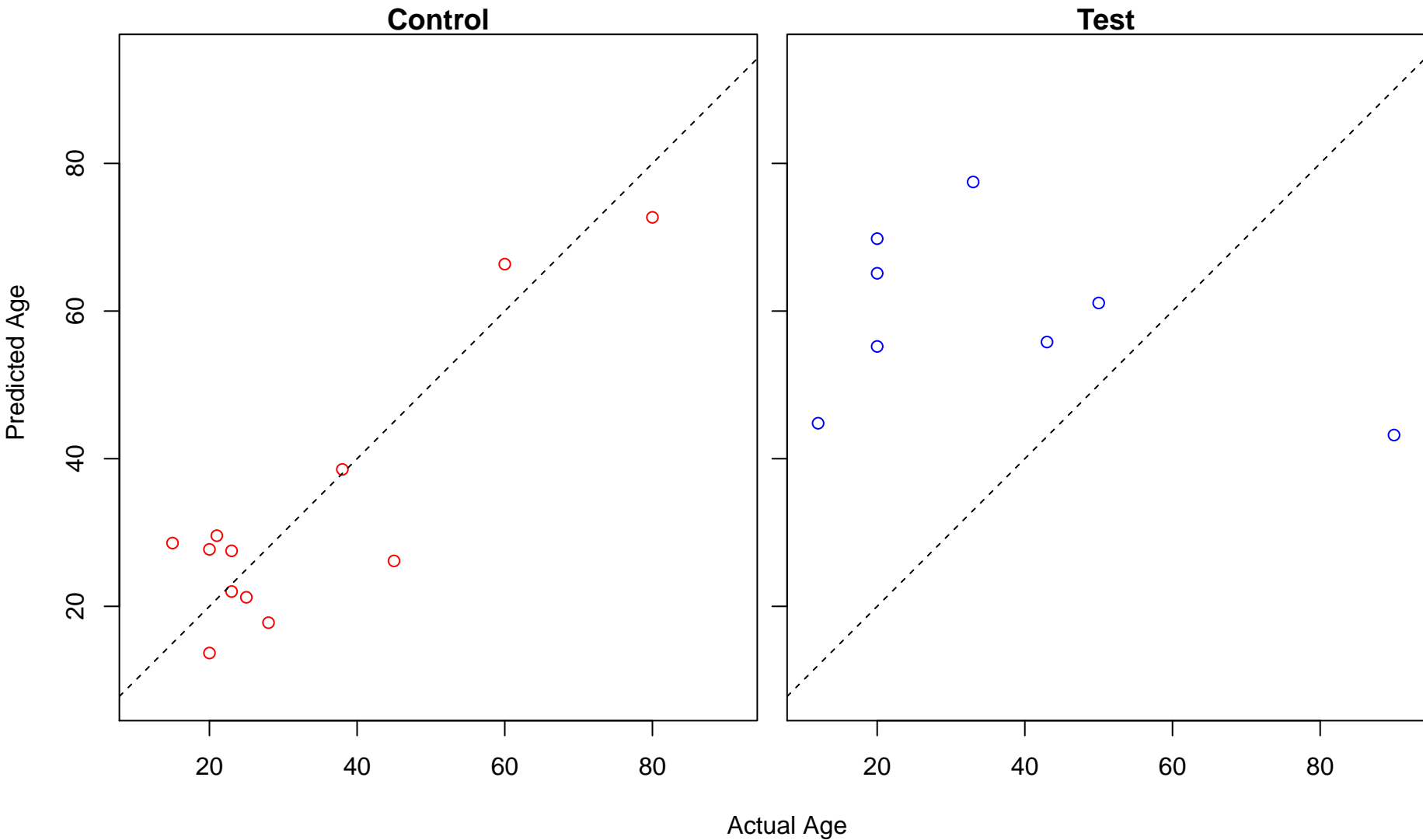
small RNA loading onto RISC (Score: 34.715043)



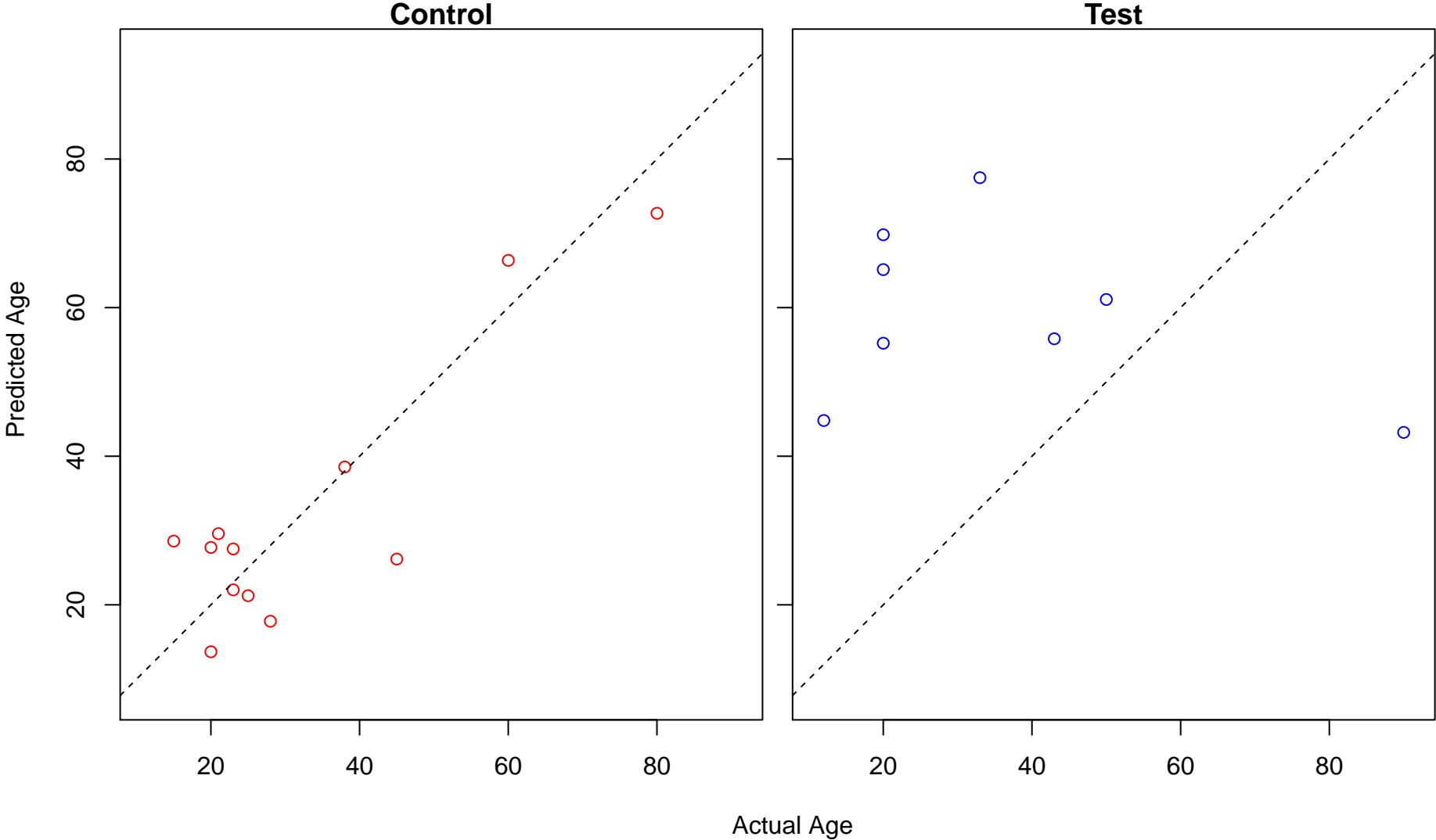
skeletal system morphogenesis (Score: 34.588080)



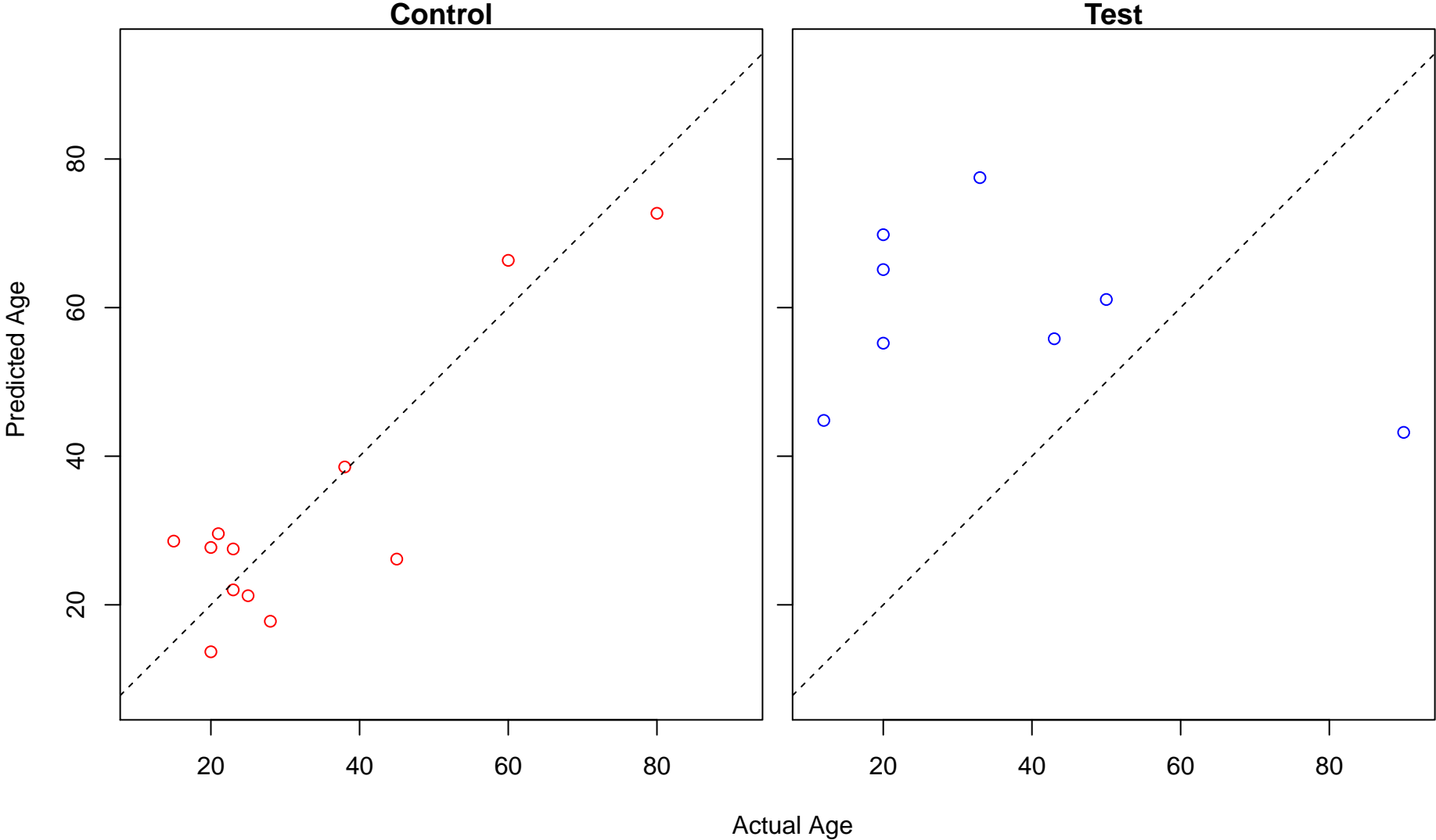
antigen processing and presentation of peptide antigen via MHC class II (Score: 34.490498)



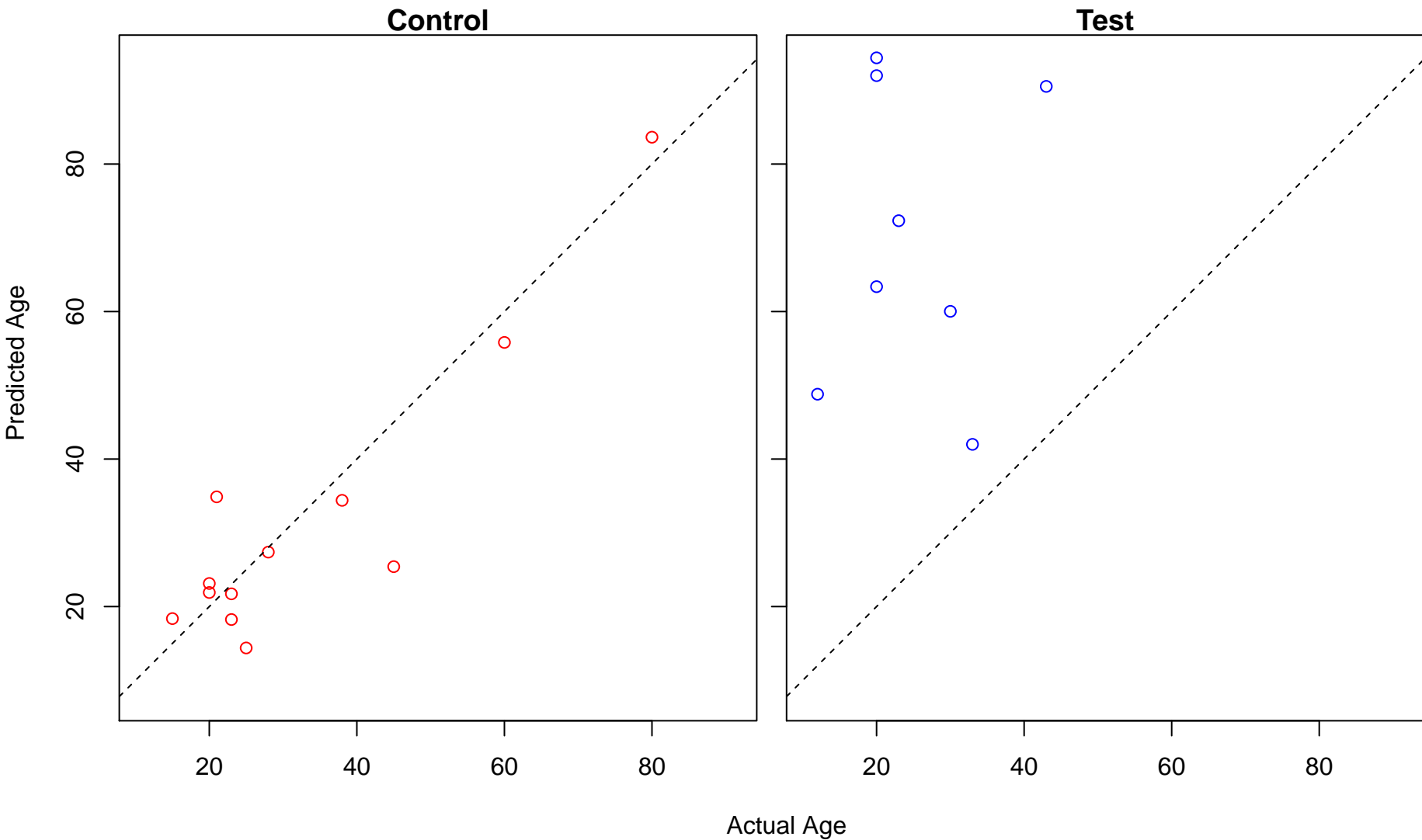
antigen processing and presentation of peptide or polysaccharide antigen via MHC class II (Score: 34.4)



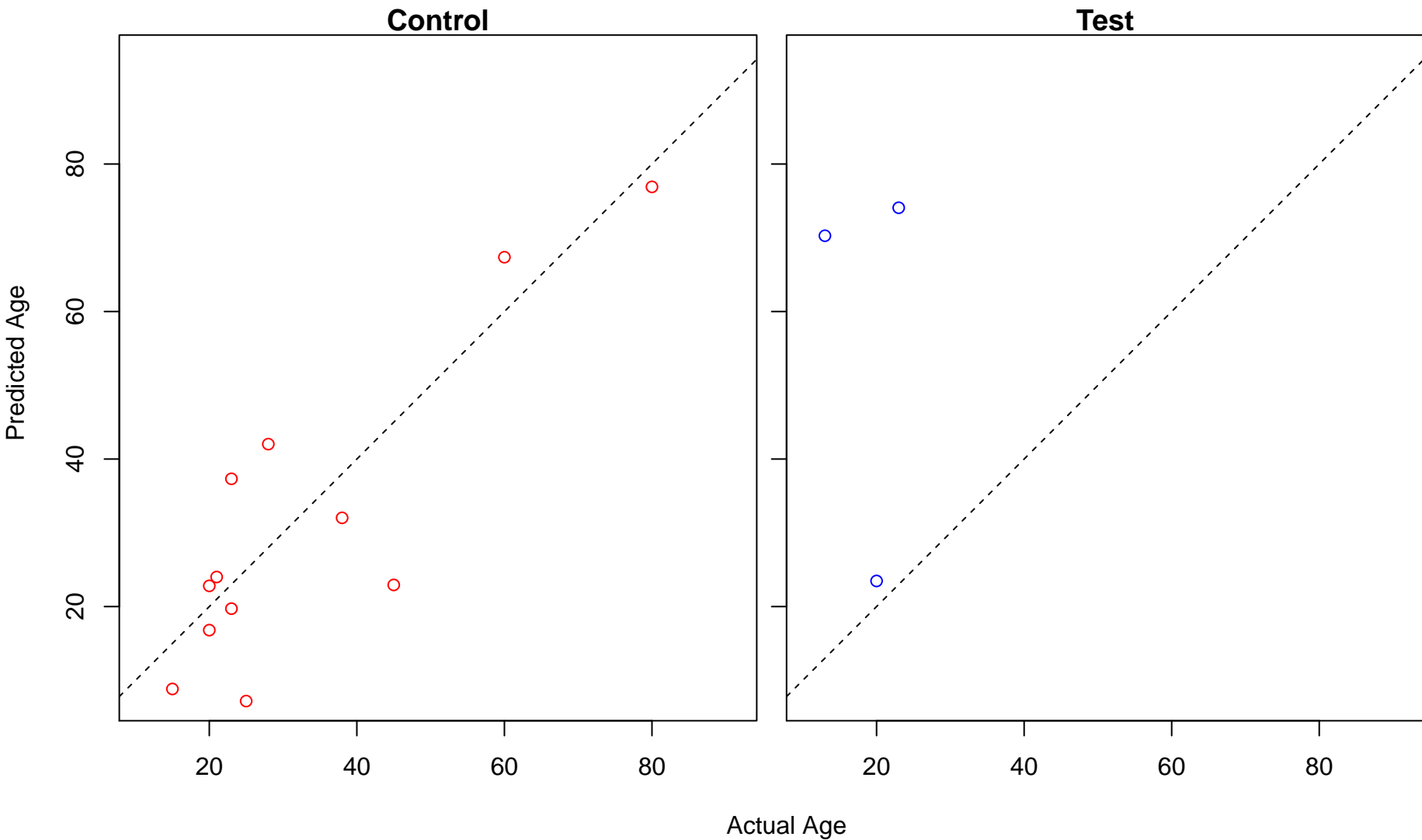
antigen processing and presentation of exogenous peptide antigen via MHC class II (Score: 34.4901)



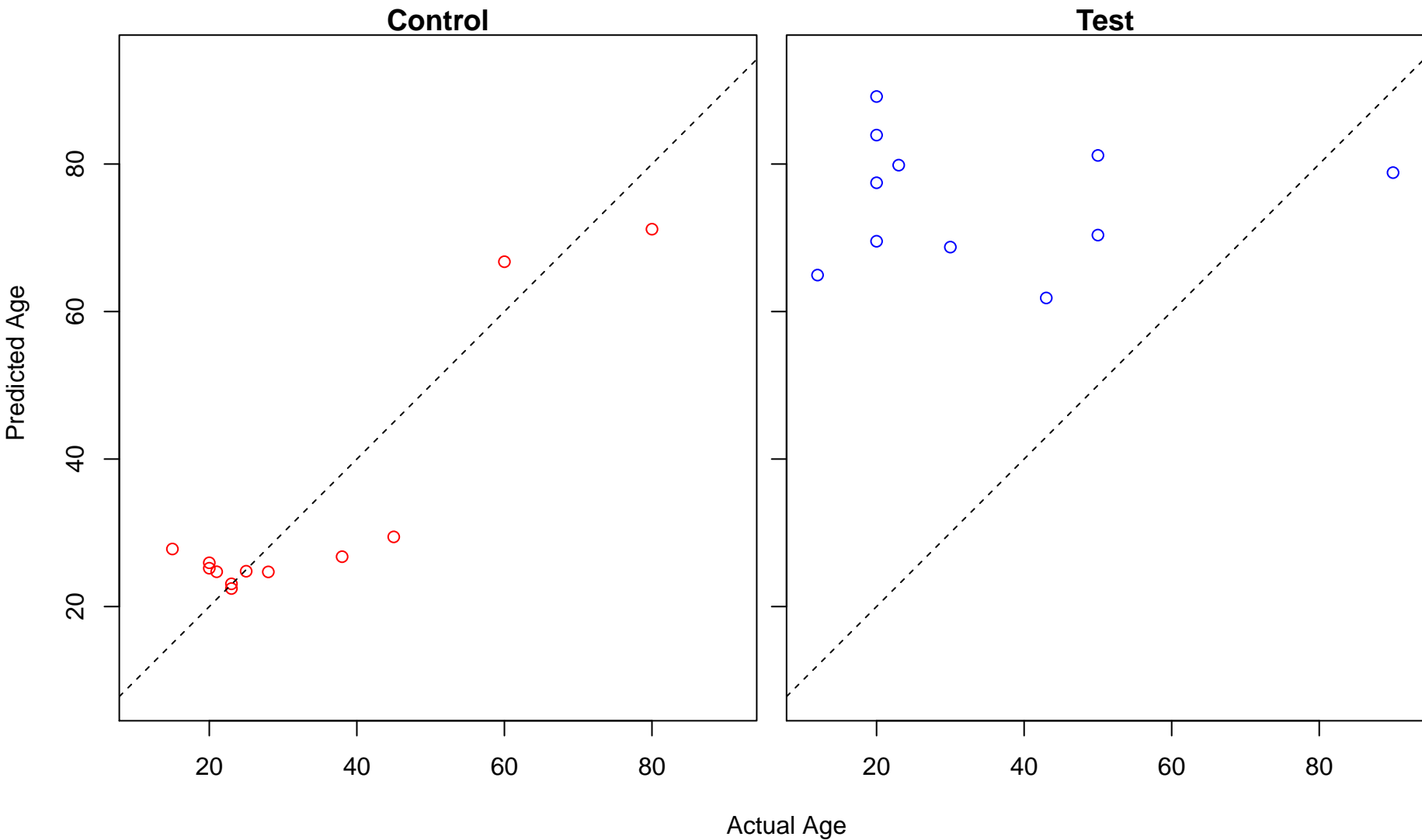
negative regulation of adaptive immune response (Score: 34.270438)



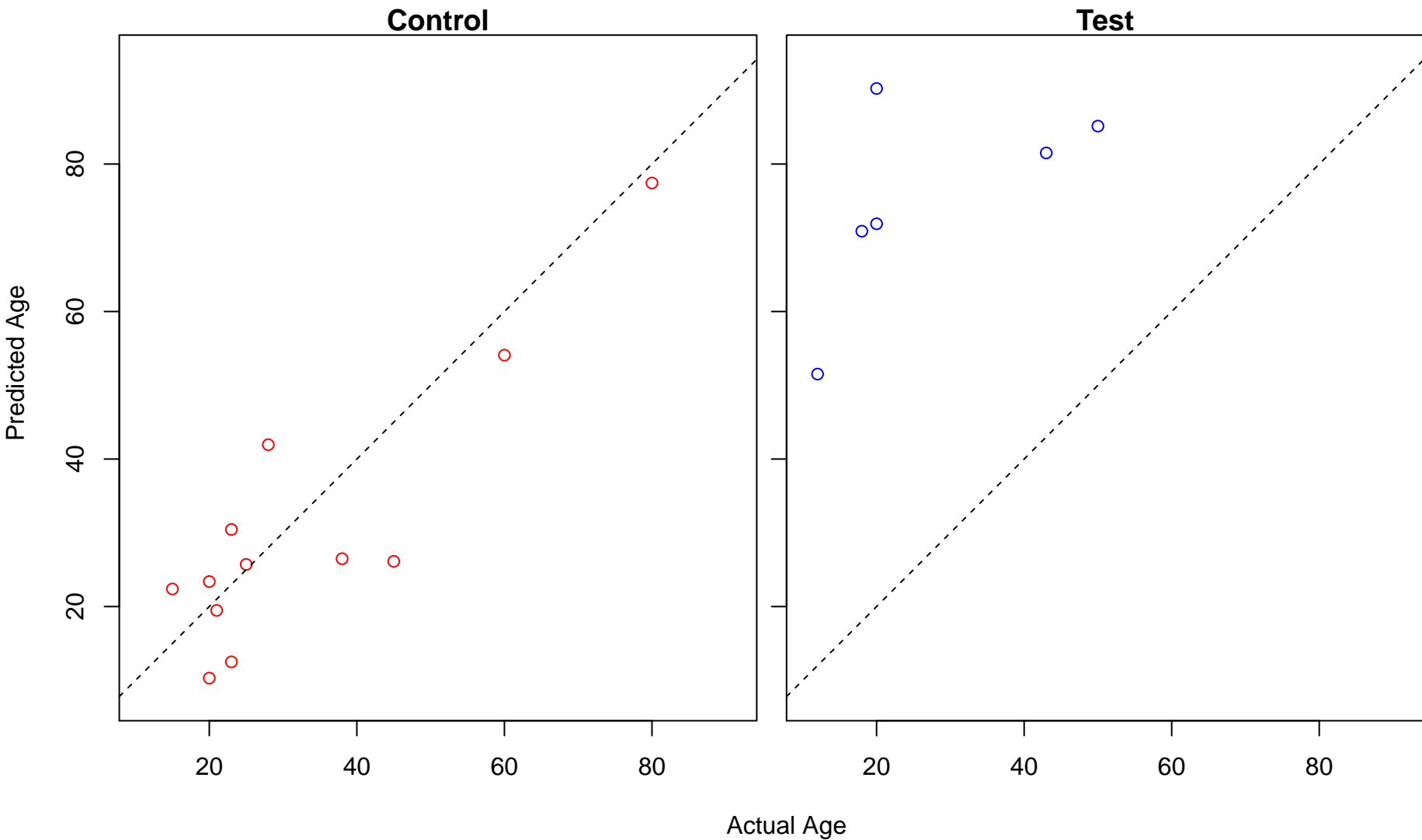
regulation of oxidative stress-induced neuron death (Score: 34.269221)



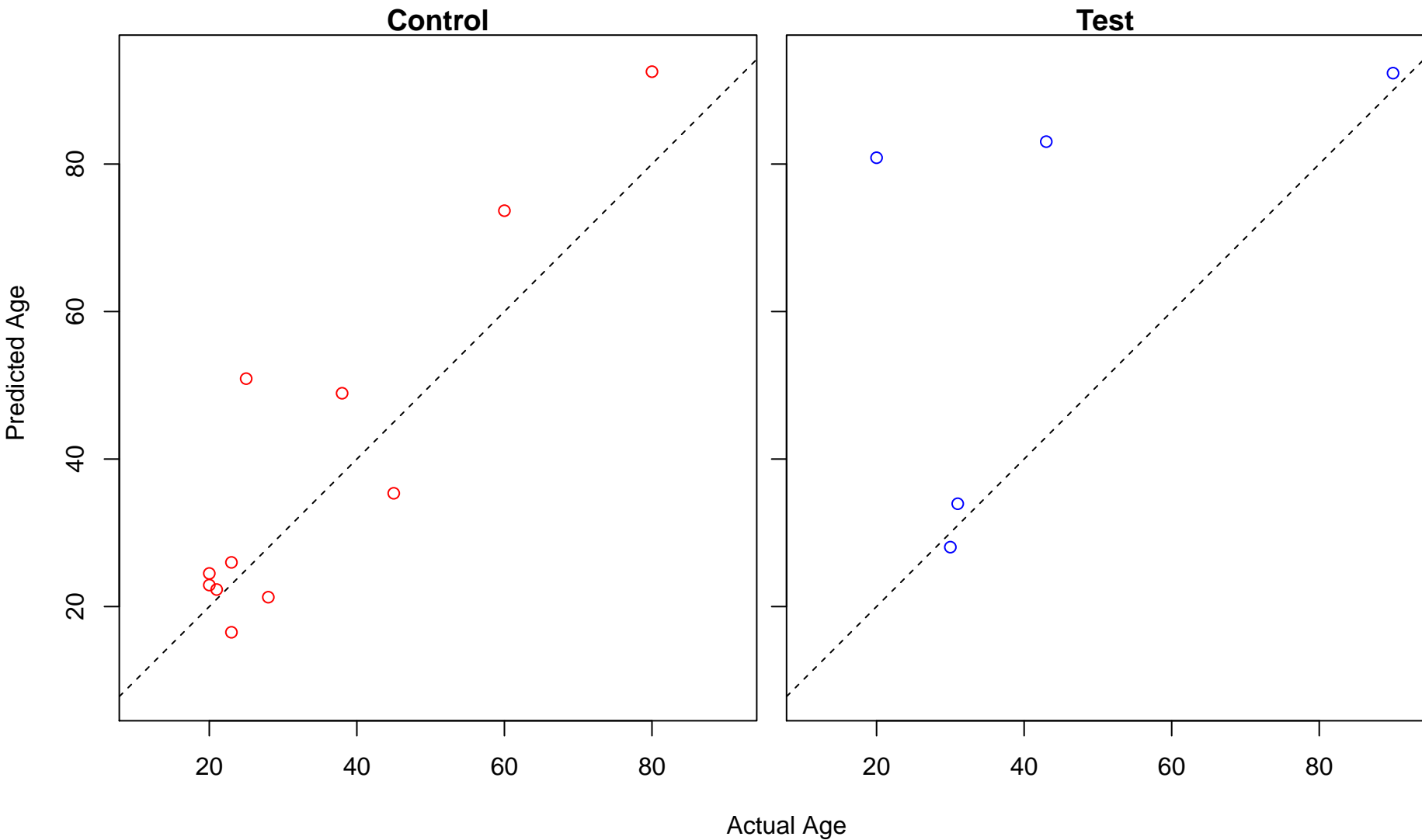
regulation of calcidiol 1-monooxygenase activity (Score: 34.074295)



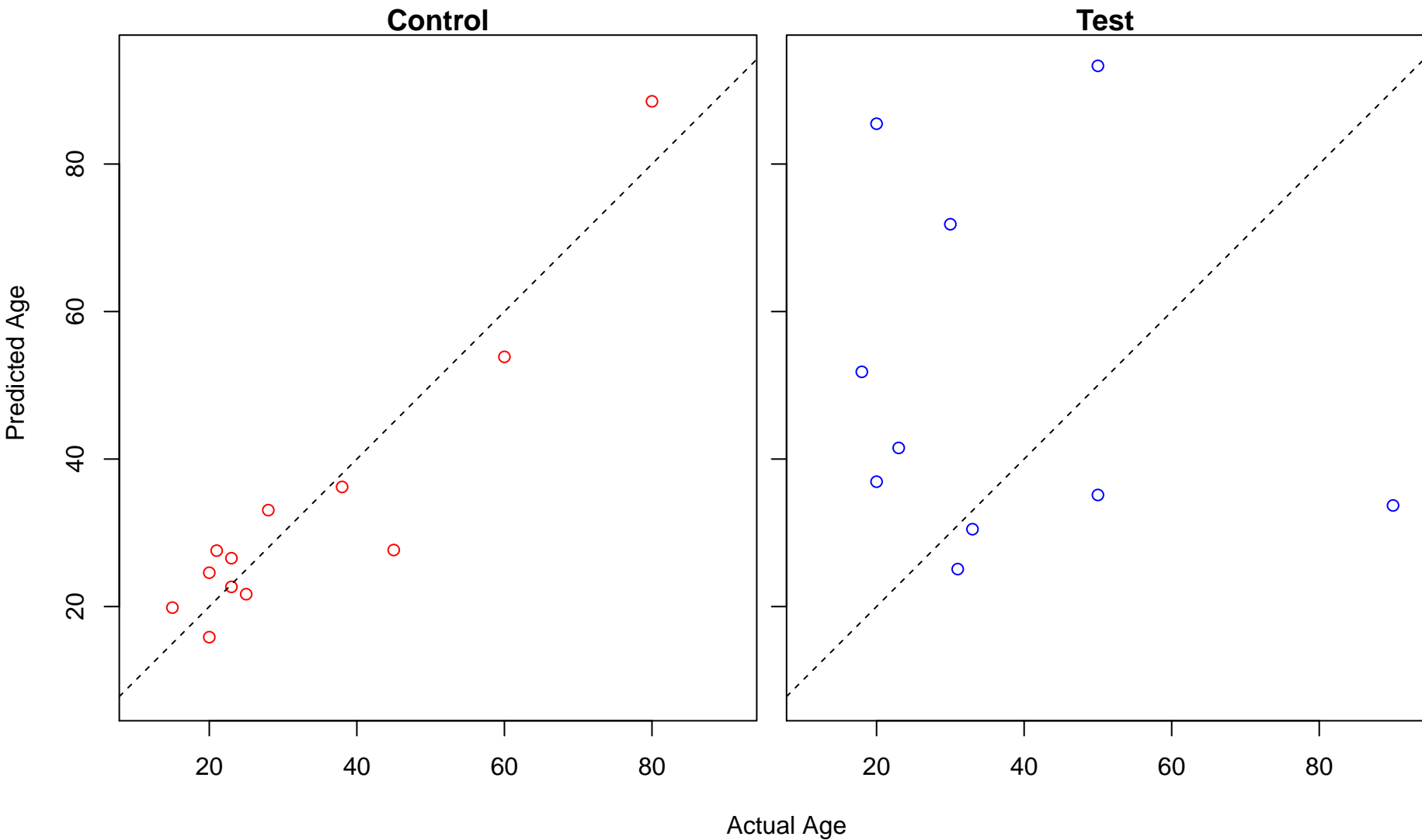
myeloid cell development (Score: 33.998565)



cartilage development involved in endochondral bone morphogenesis (Score: 33.881411)

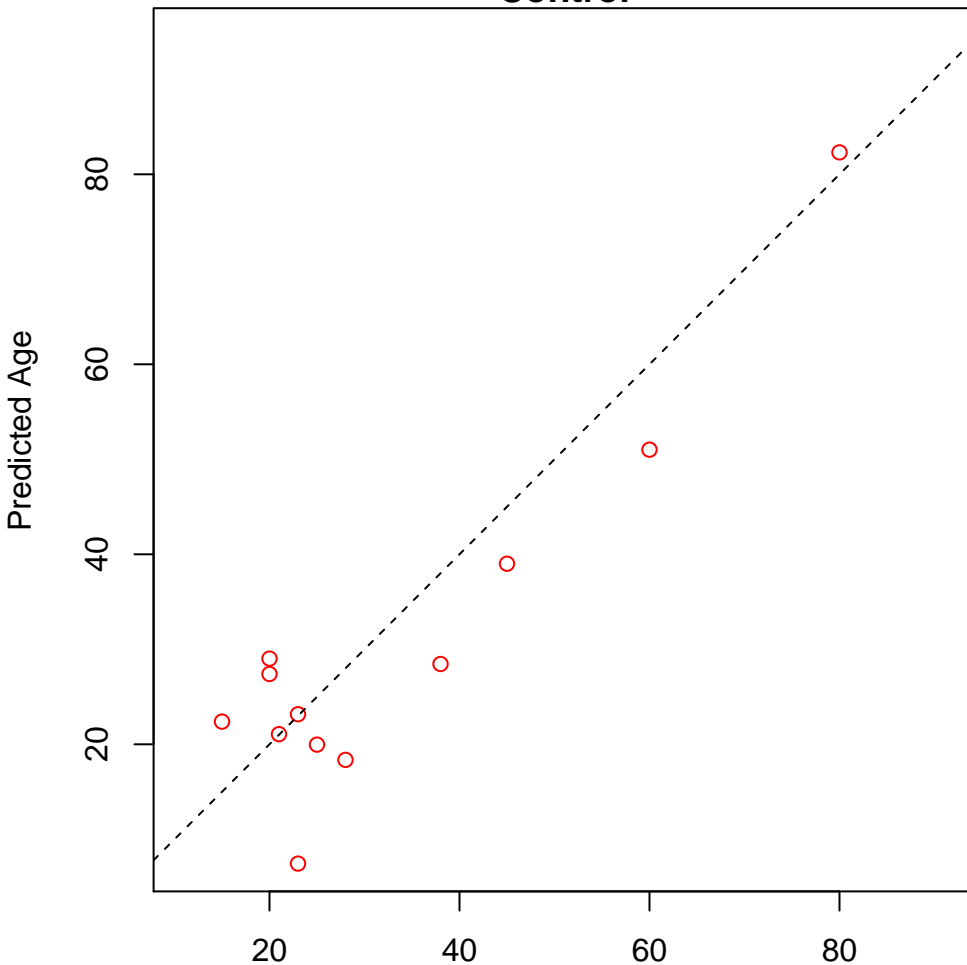


glycoside metabolic process (Score: 33.751748)

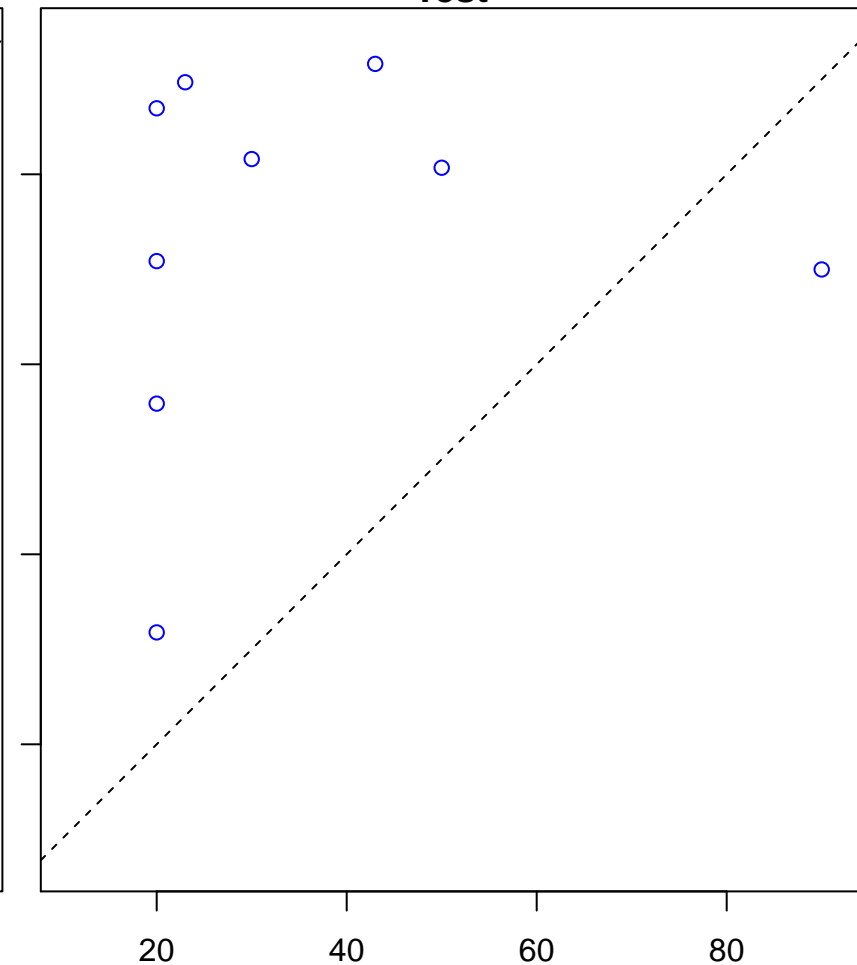


regulation of monooxygenase activity (Score: 33.693896)

Control

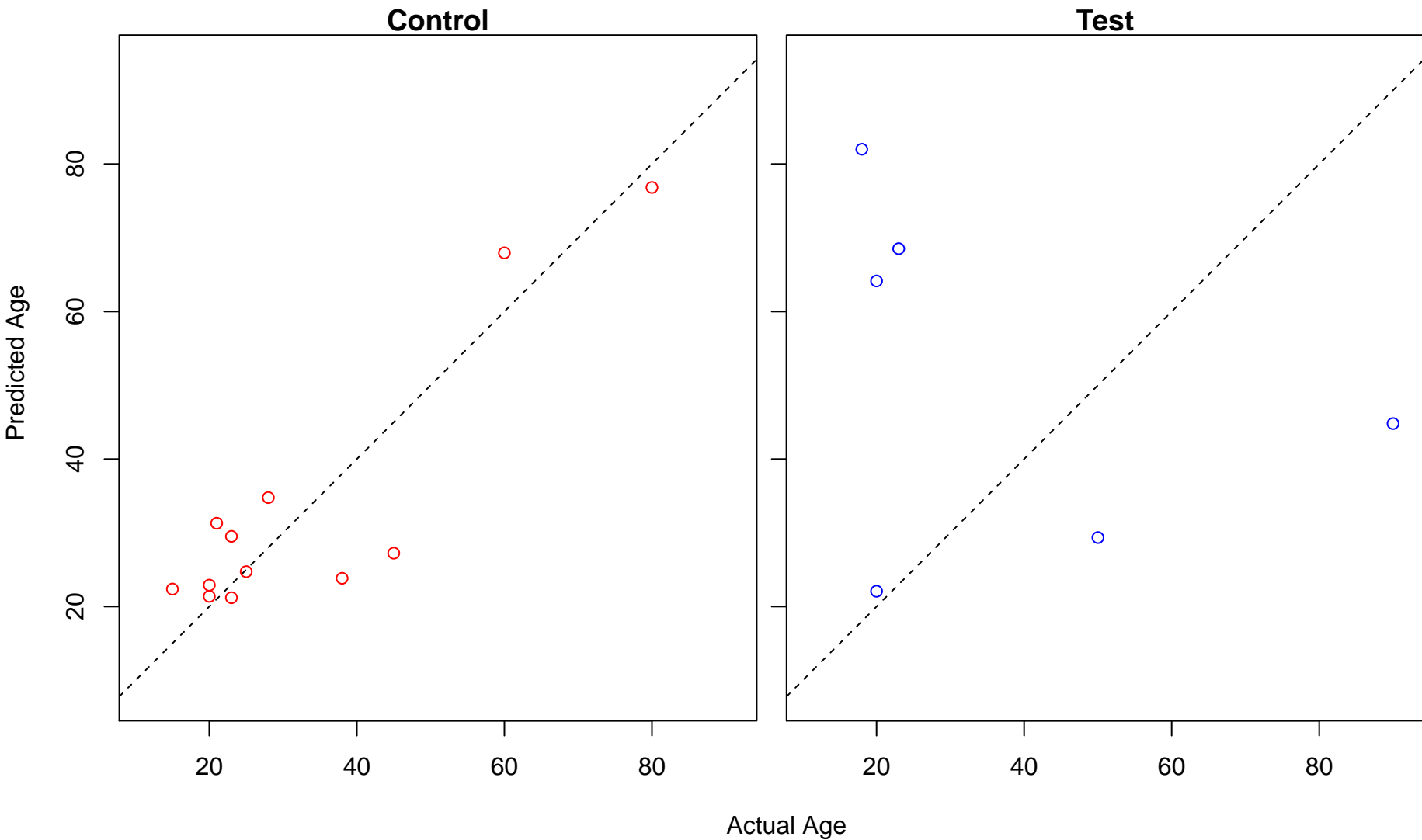


Test

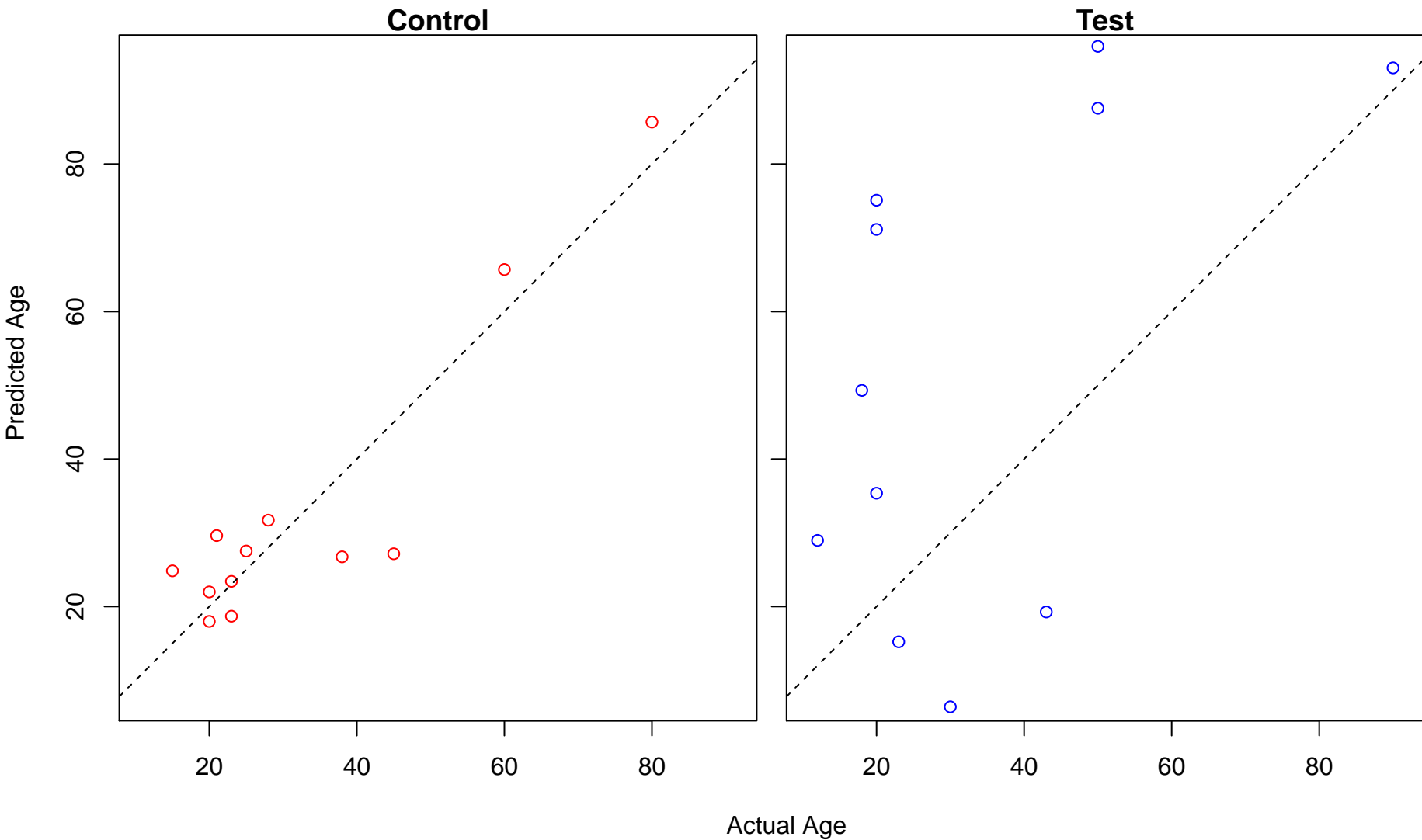


Actual Age

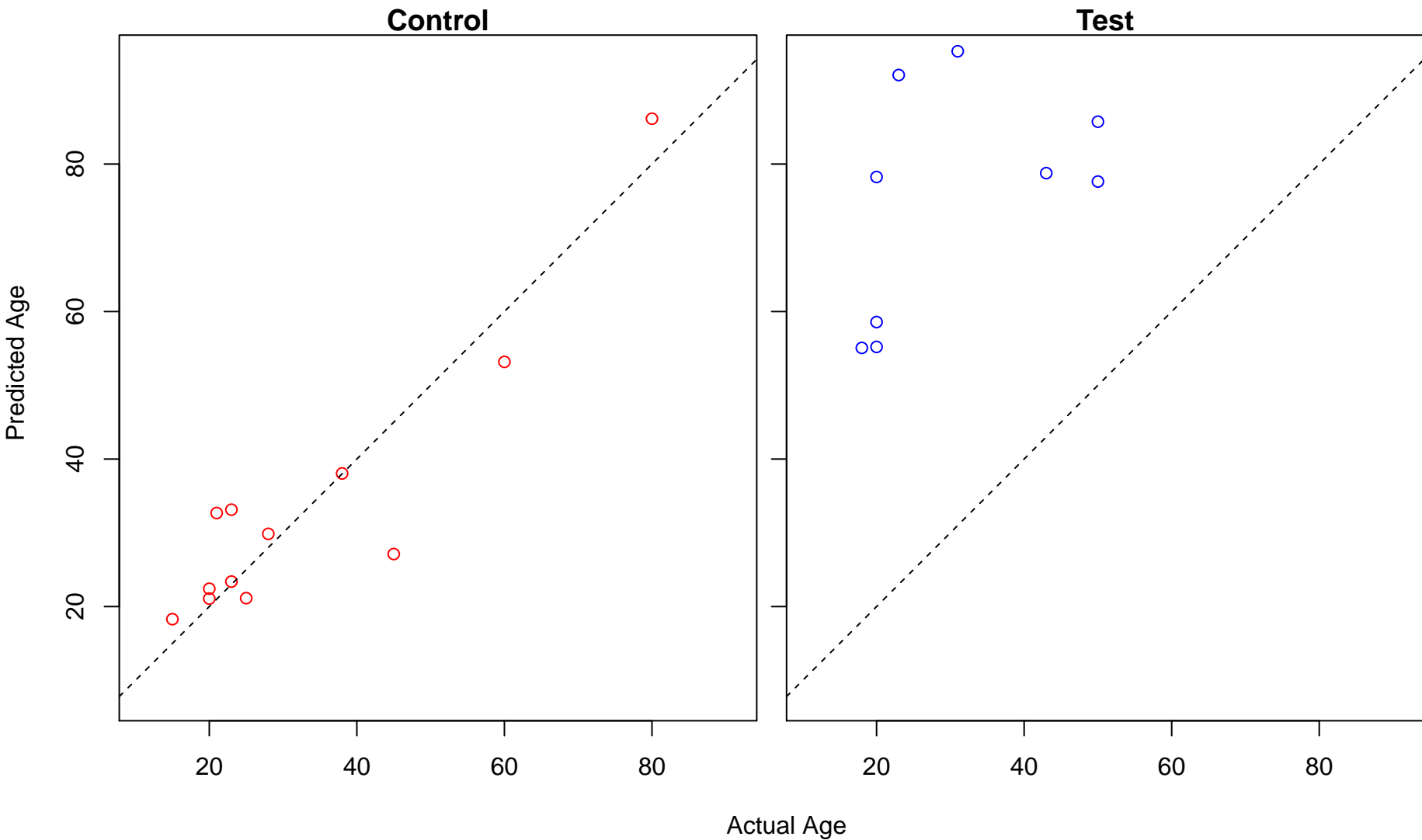
cell fate commitment (Score: 33.388767)



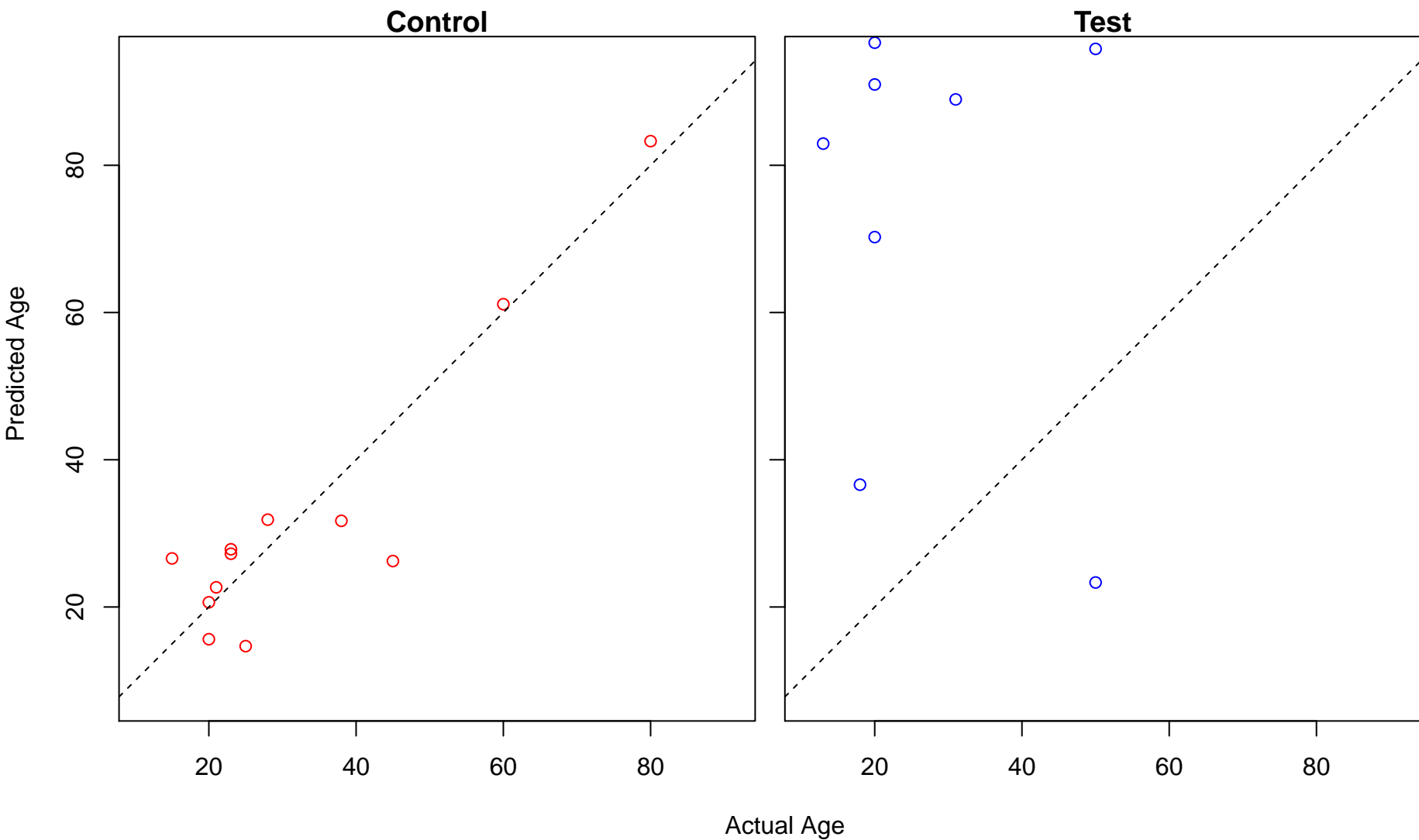
regulation of PERK-mediated unfolded protein response (Score: 33.381980)



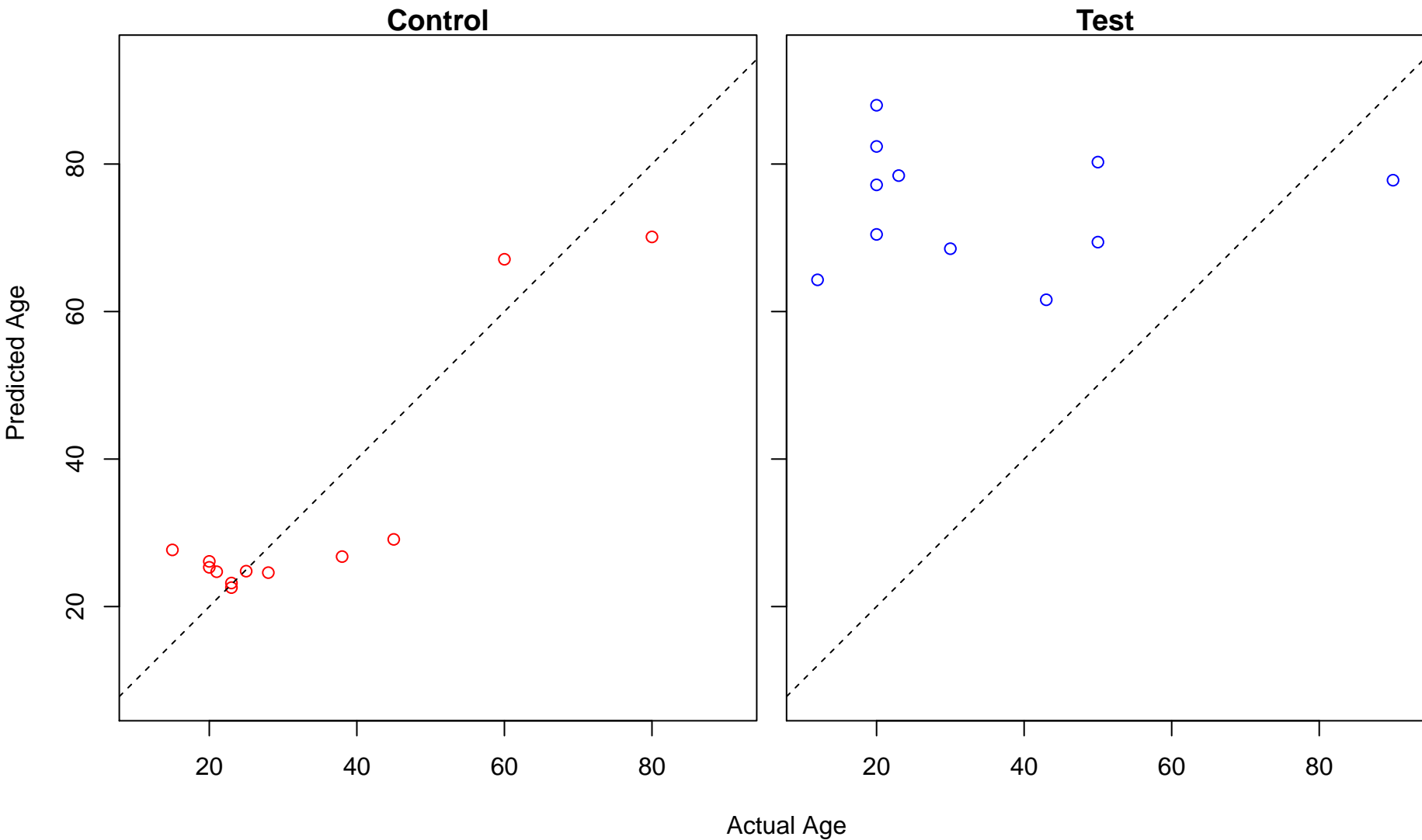
embryonic organ development (Score: 33.356929)



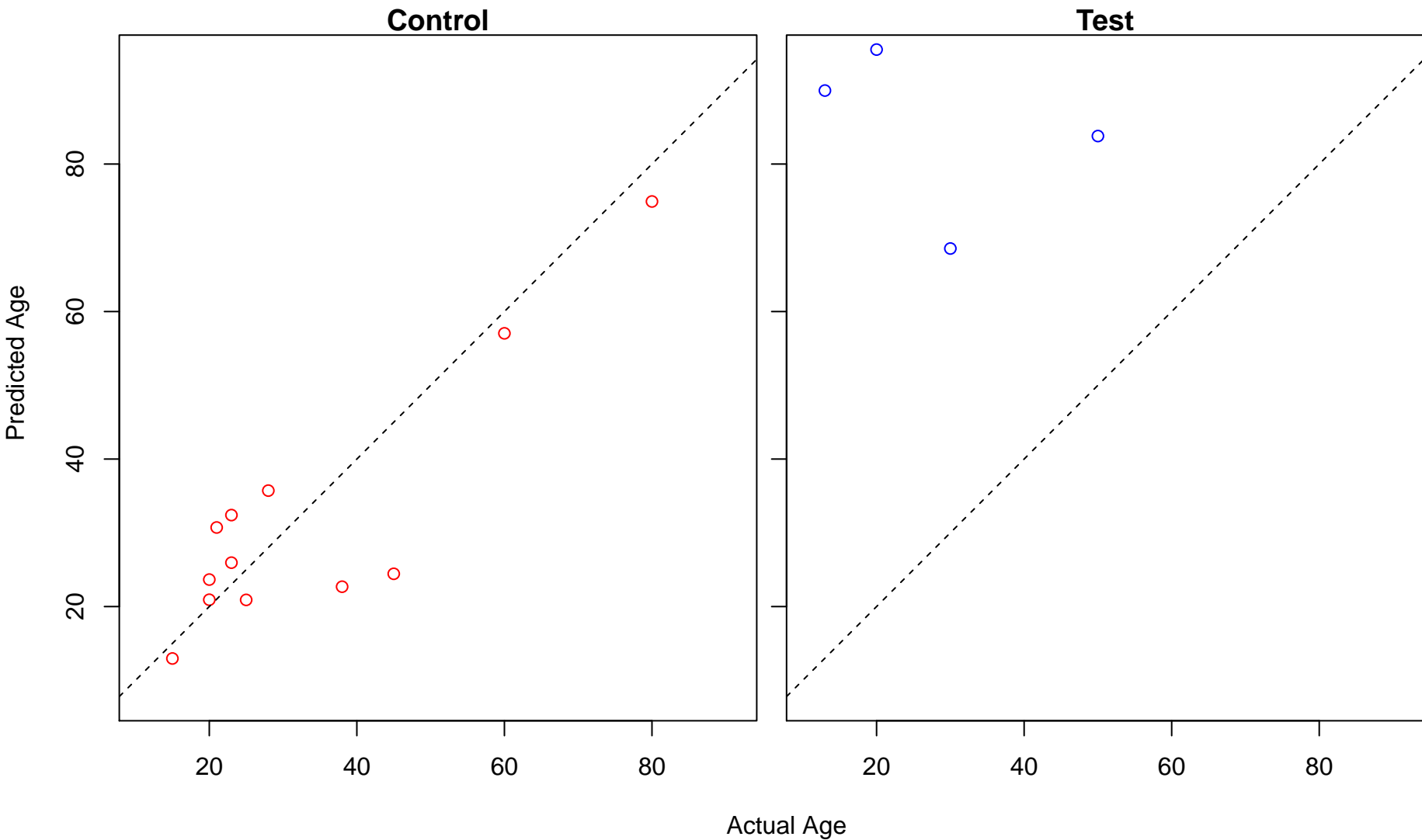
JUN phosphorylation (Score: 33.342501)



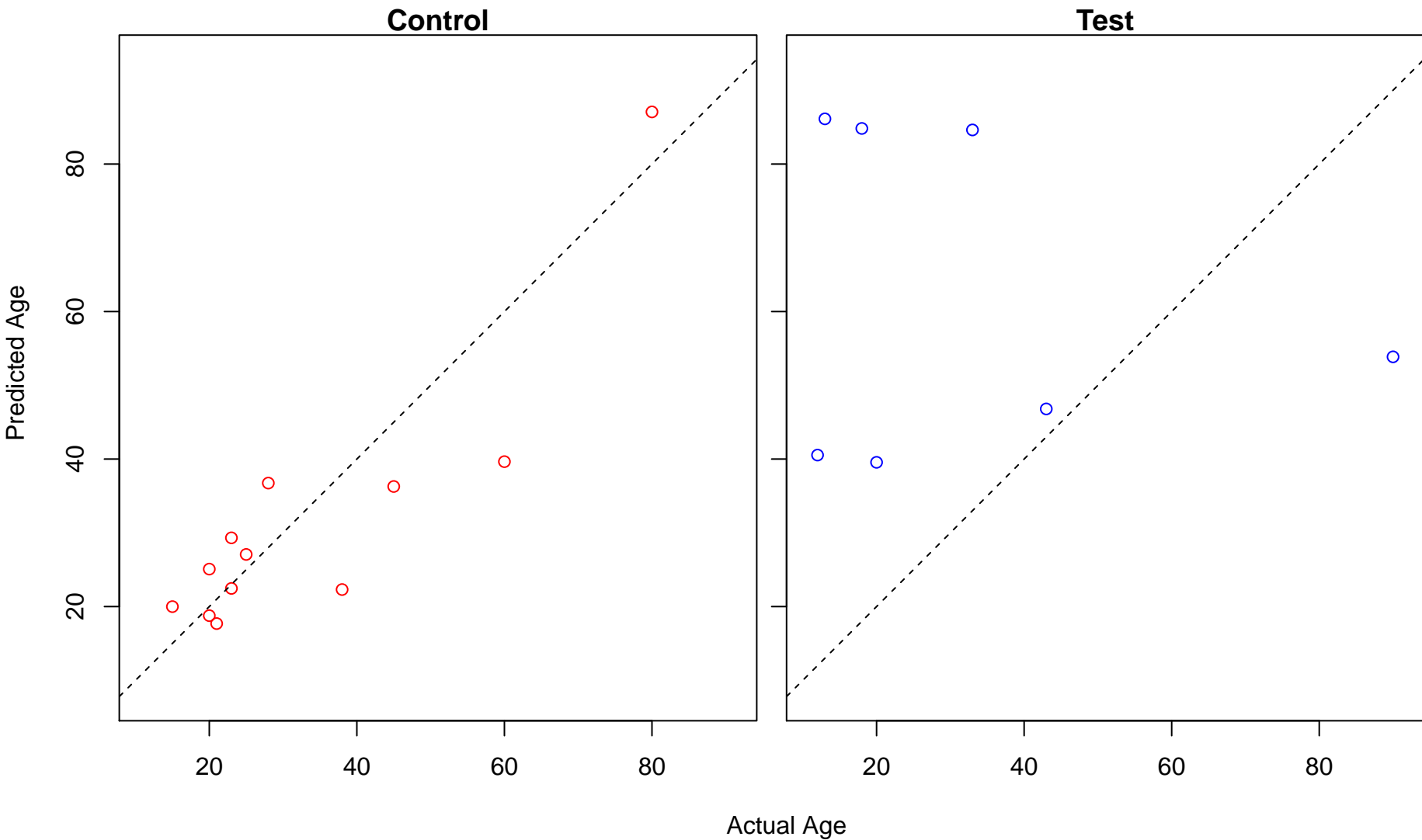
regulation of vitamin D biosynthetic process (Score: 32.952169)



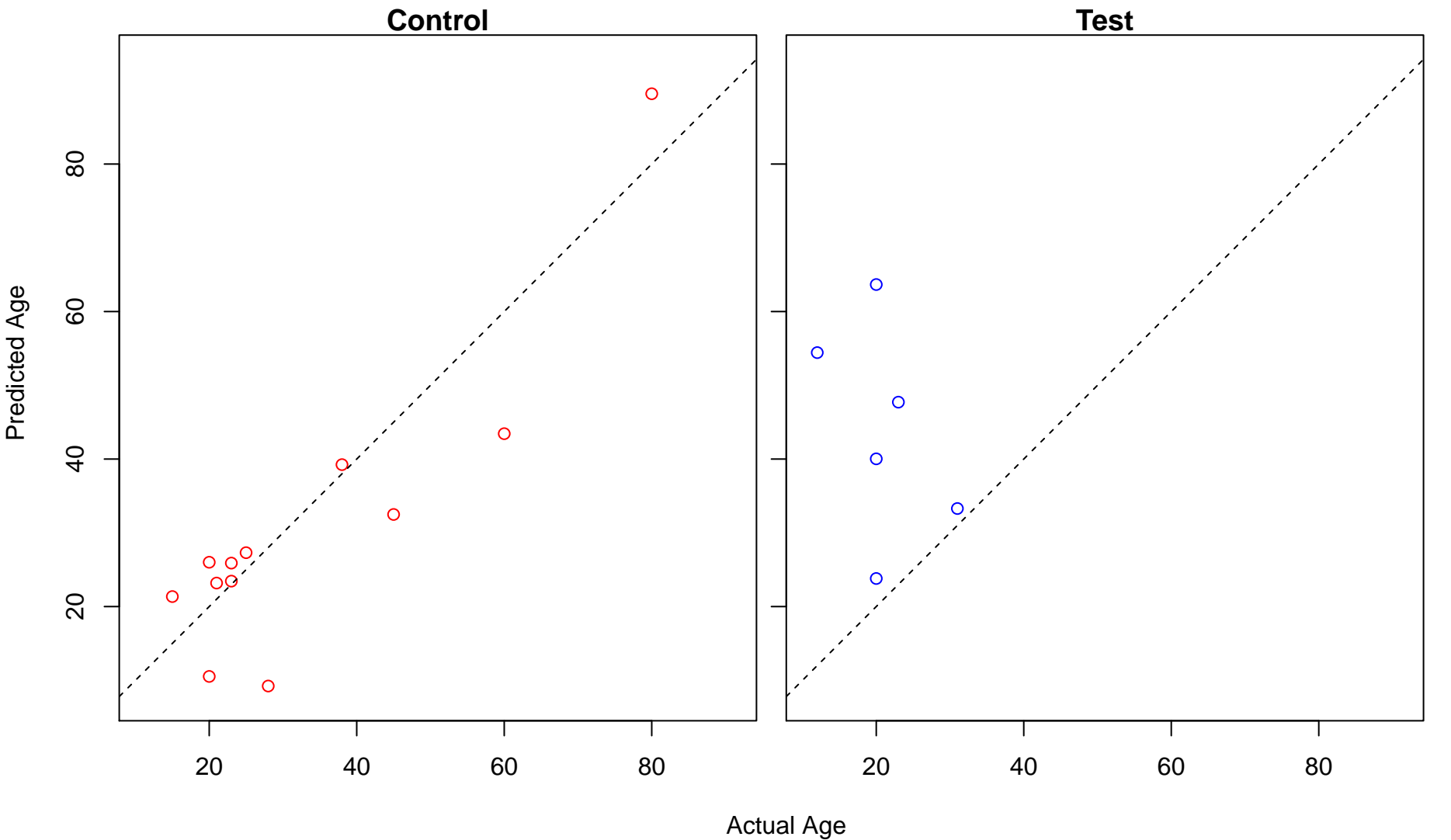
DNA replication checkpoint (Score: 32.765181)



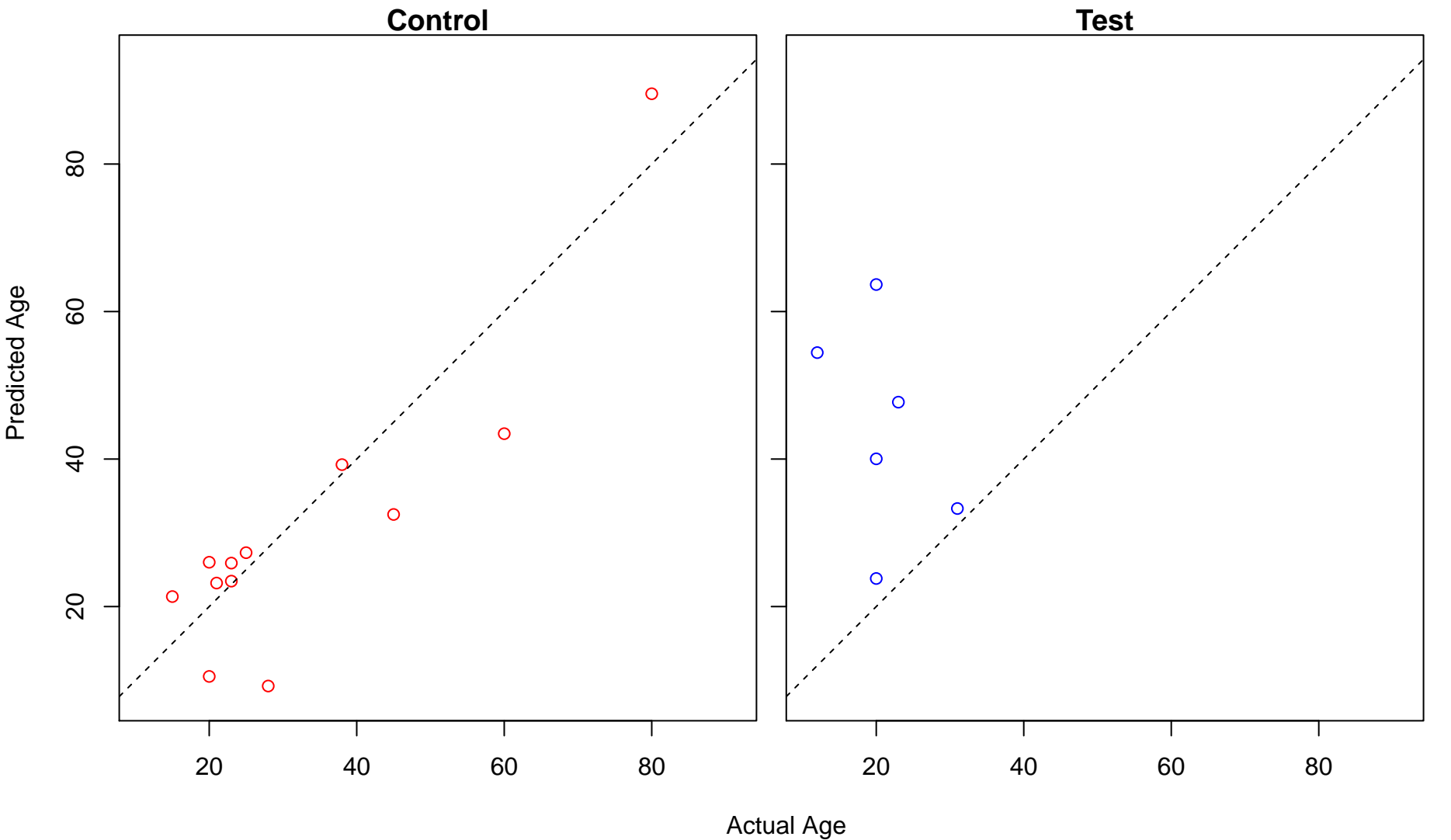
piRNA metabolic process (Score: 32.750282)



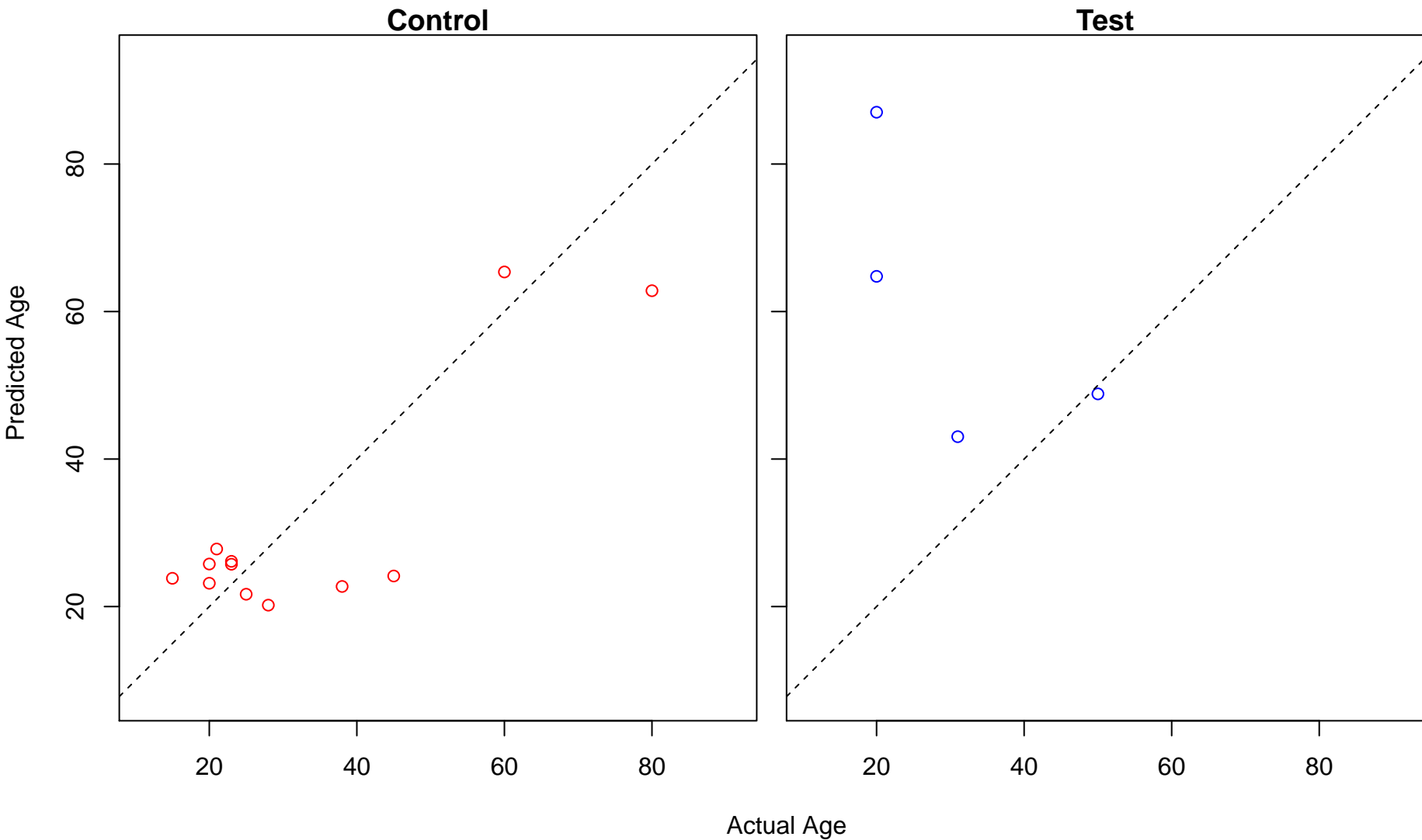
Evaluation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (Score



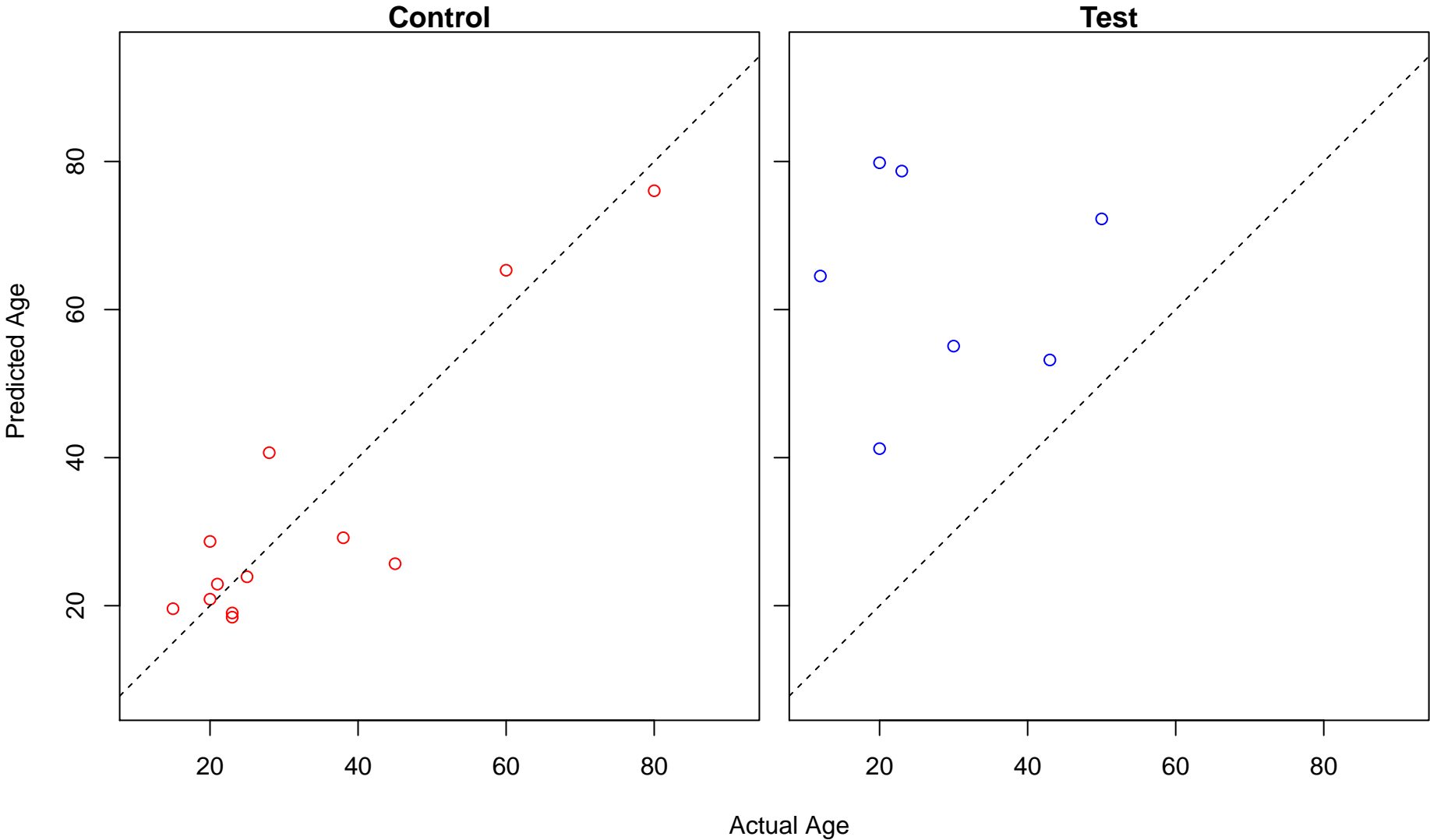
The regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (S



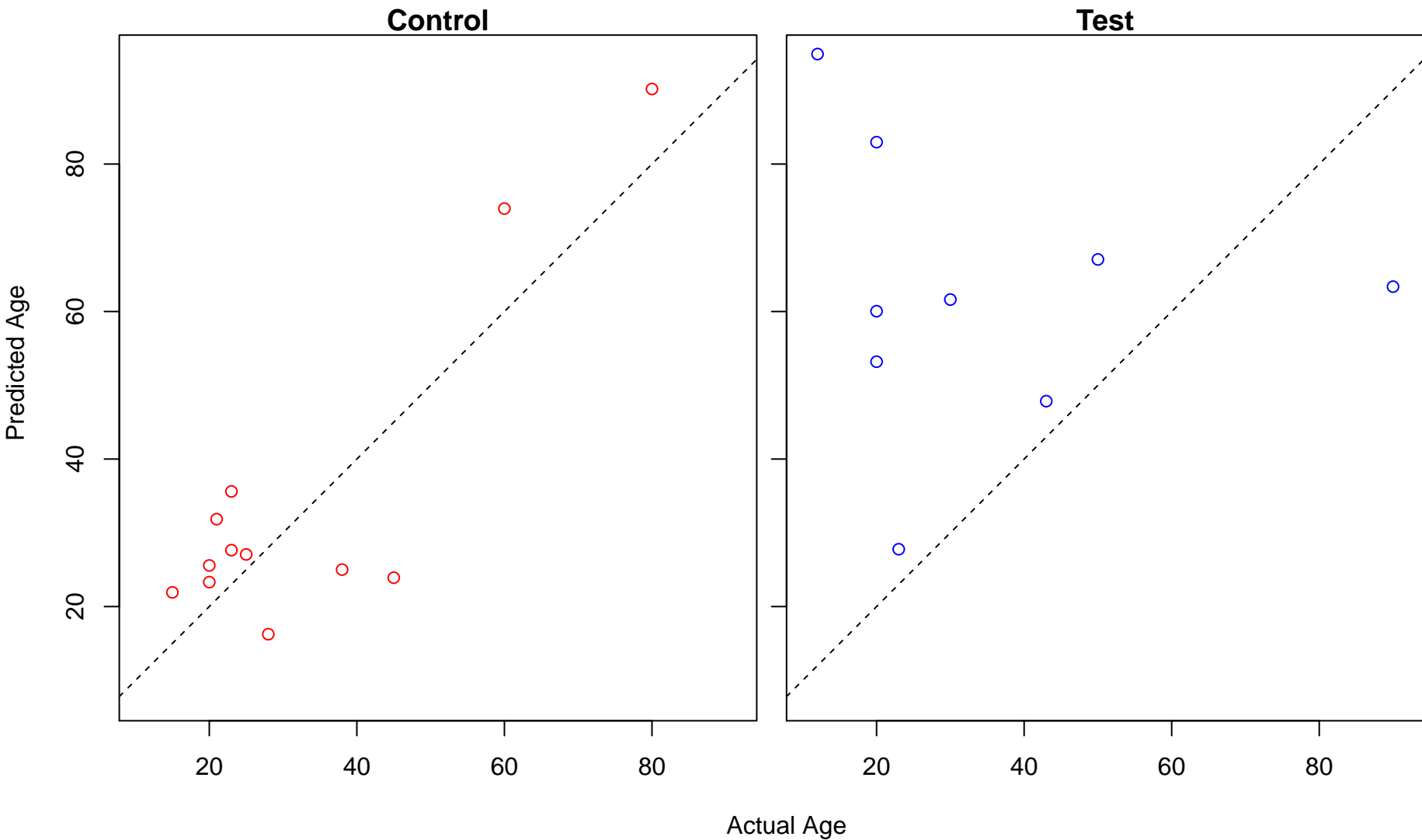
positive regulation of NFAT protein import into nucleus (Score: 32.403941)



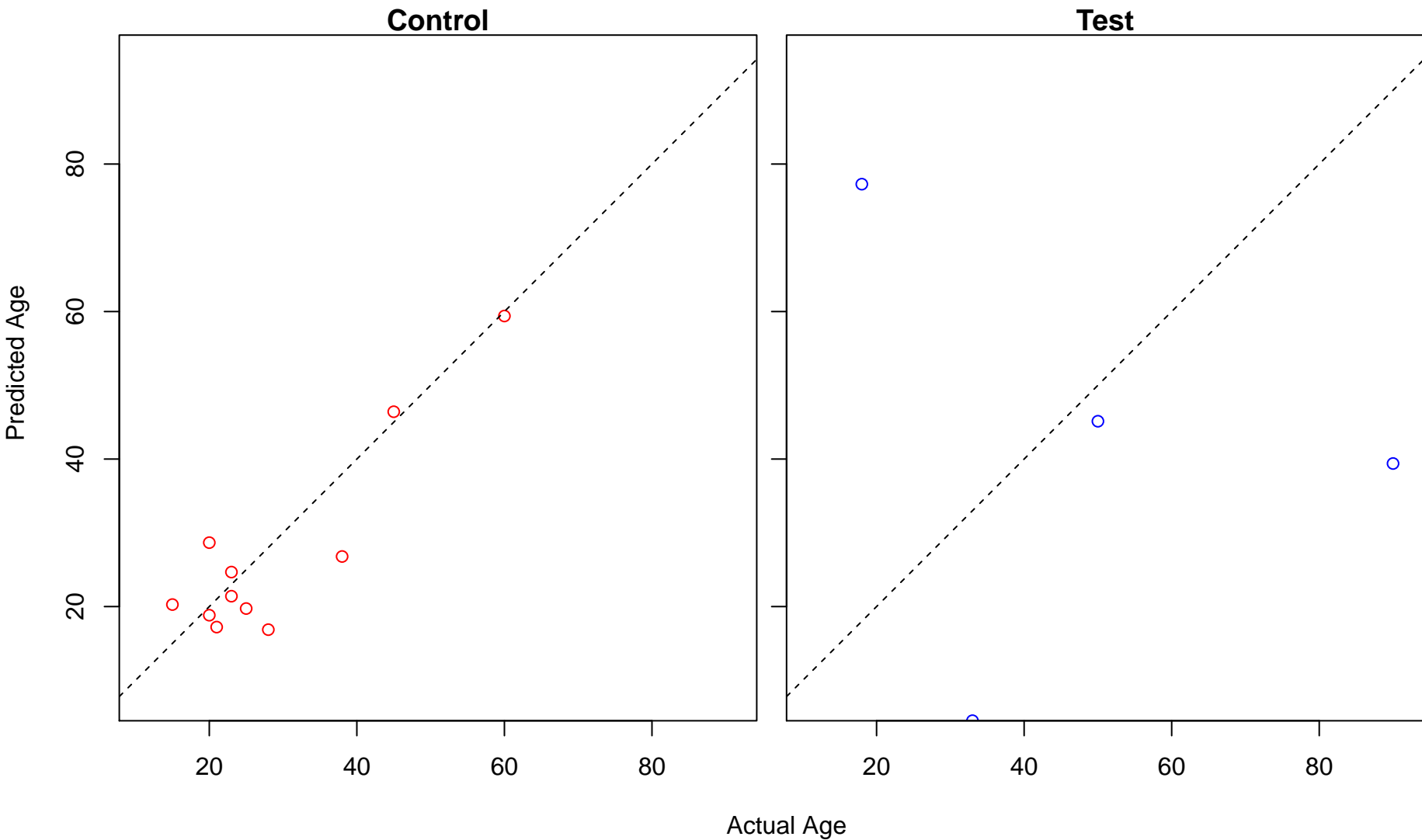
negative regulation of intracellular steroid hormone receptor signaling pathway (Score: 32.399991)



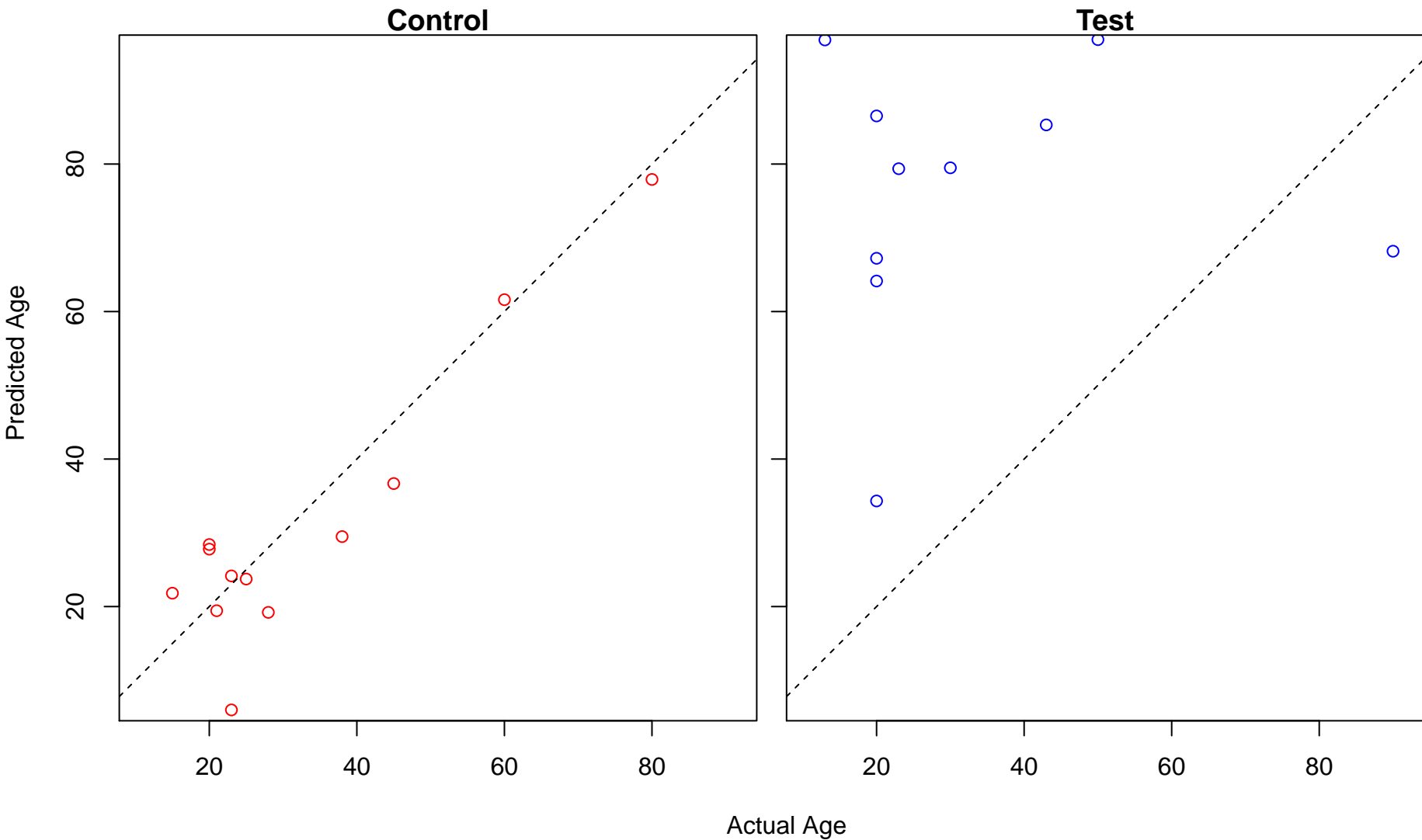
regulation of integrin activation (Score: 32.303029)



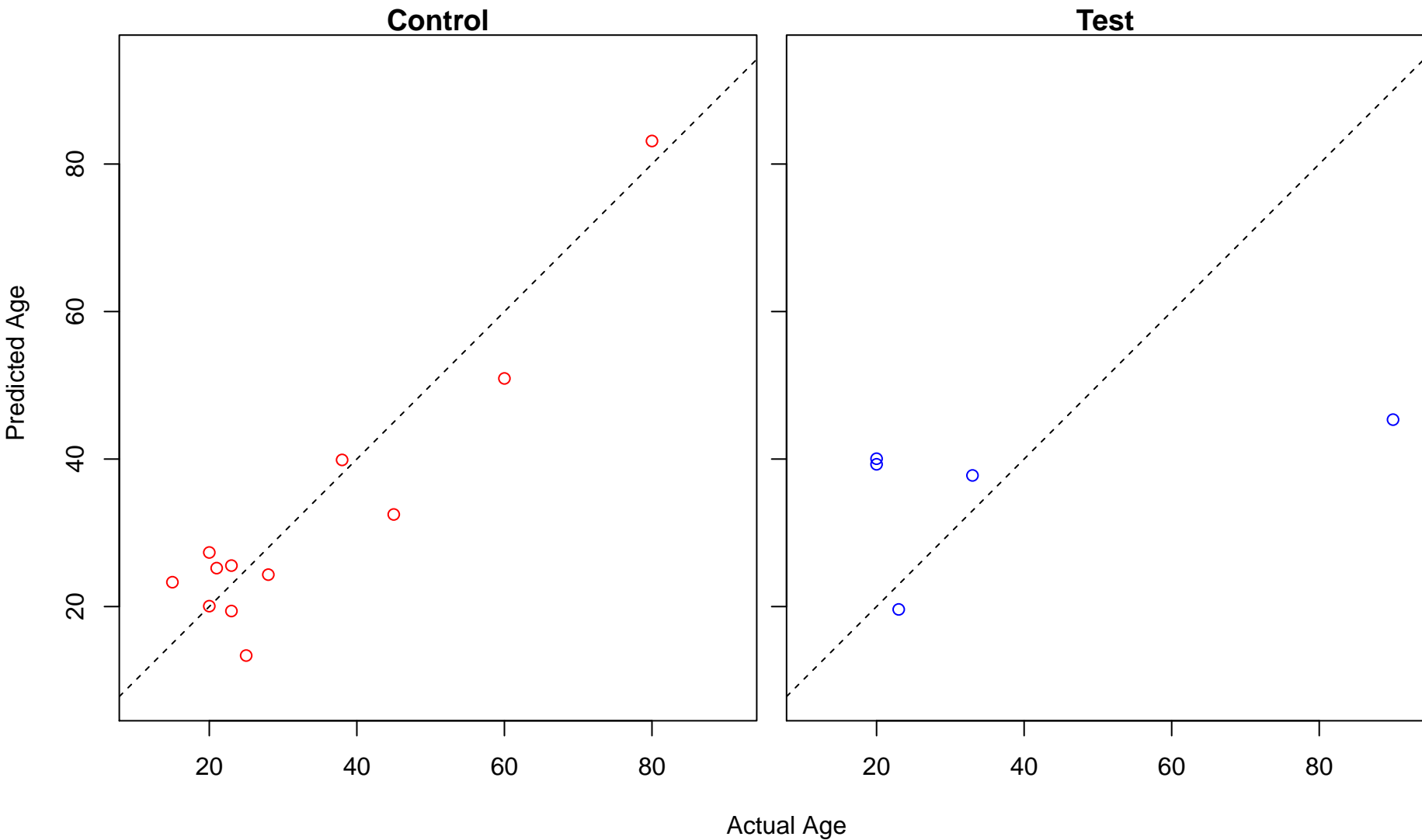
negative regulation of cAMP-mediated signaling (Score: 32.266204)



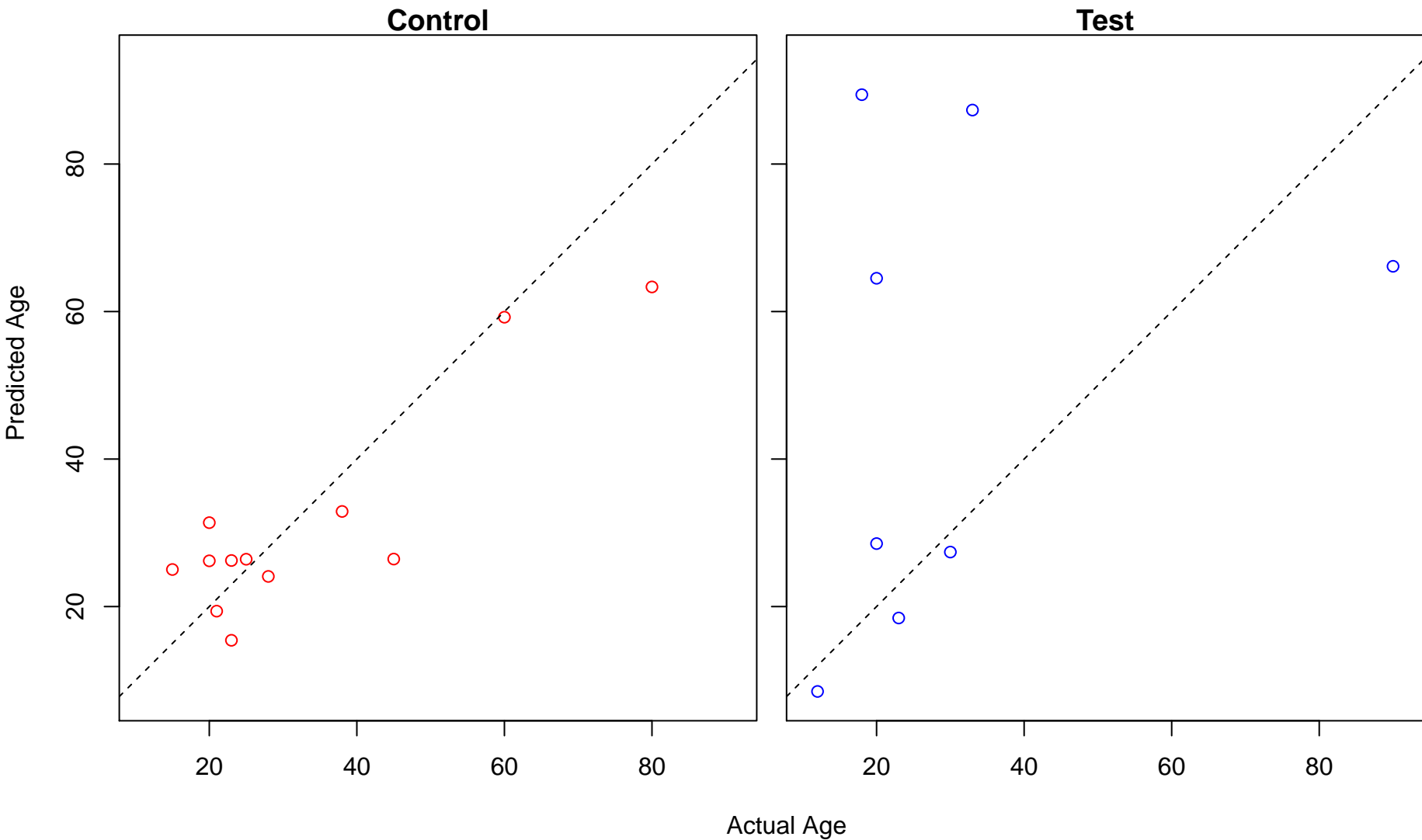
regulation of nitric-oxide synthase activity (Score: 32.235501)



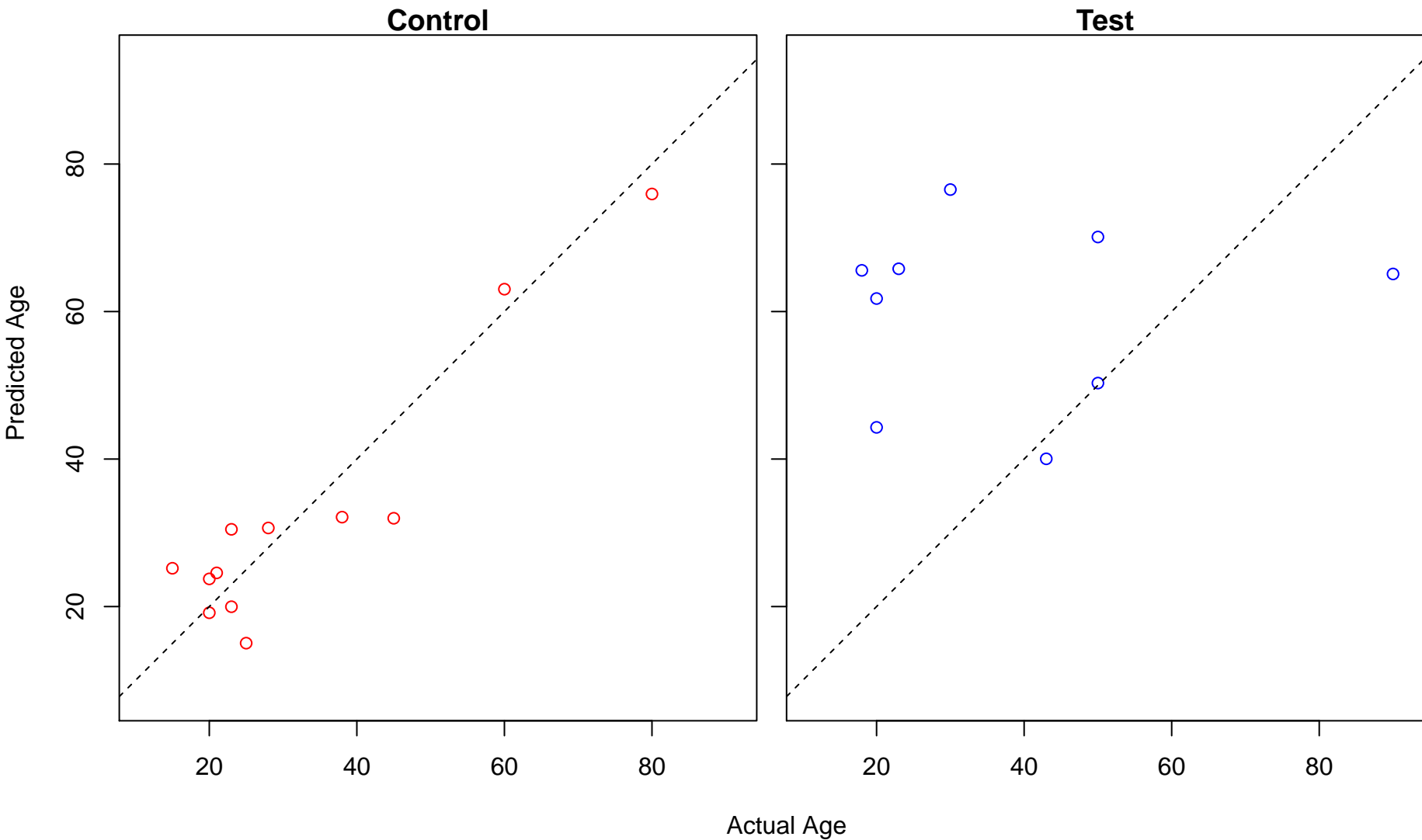
attachment of spindle microtubules to kinetochore (Score: 32.046937)



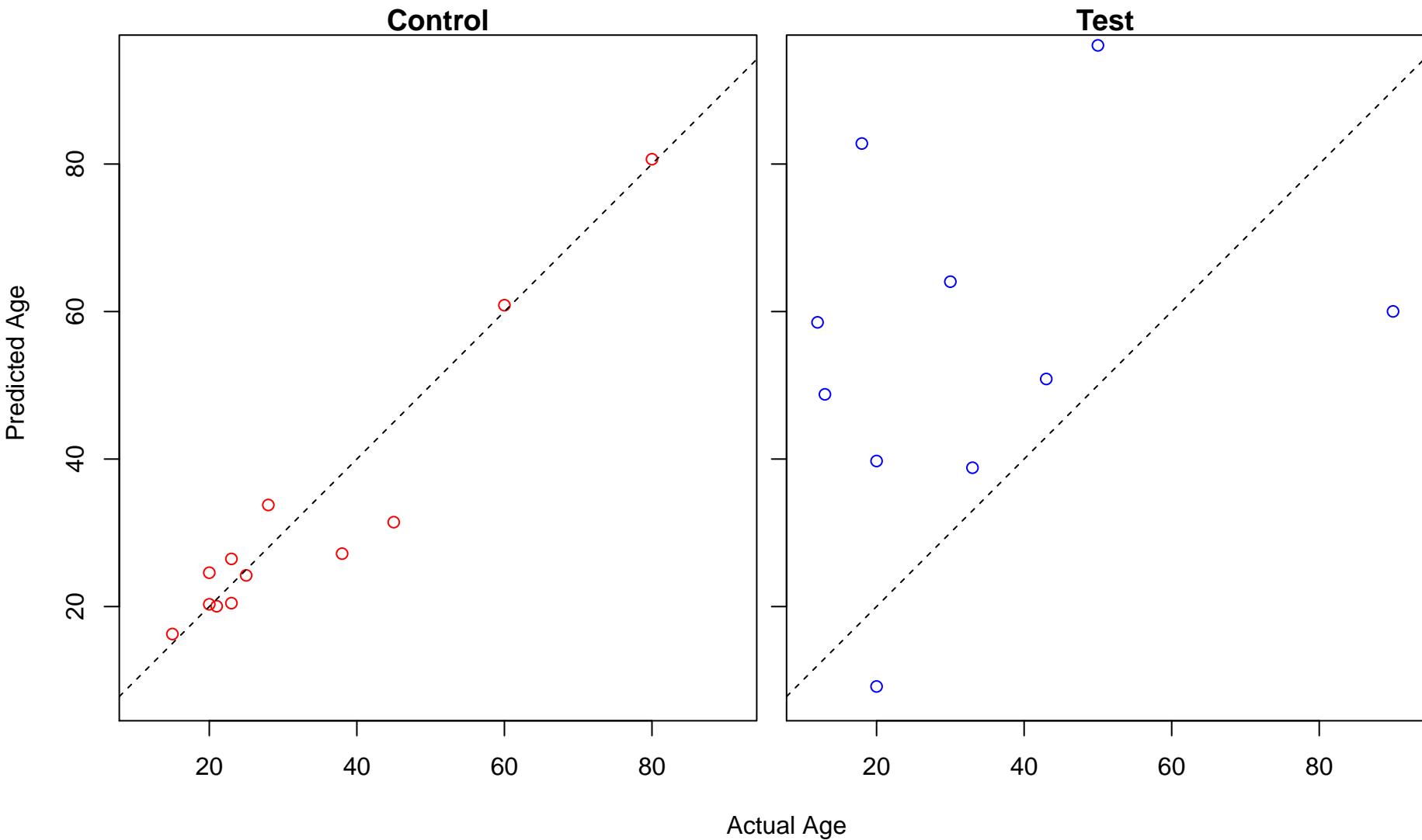
adherens junction assembly (Score: 32.032502)



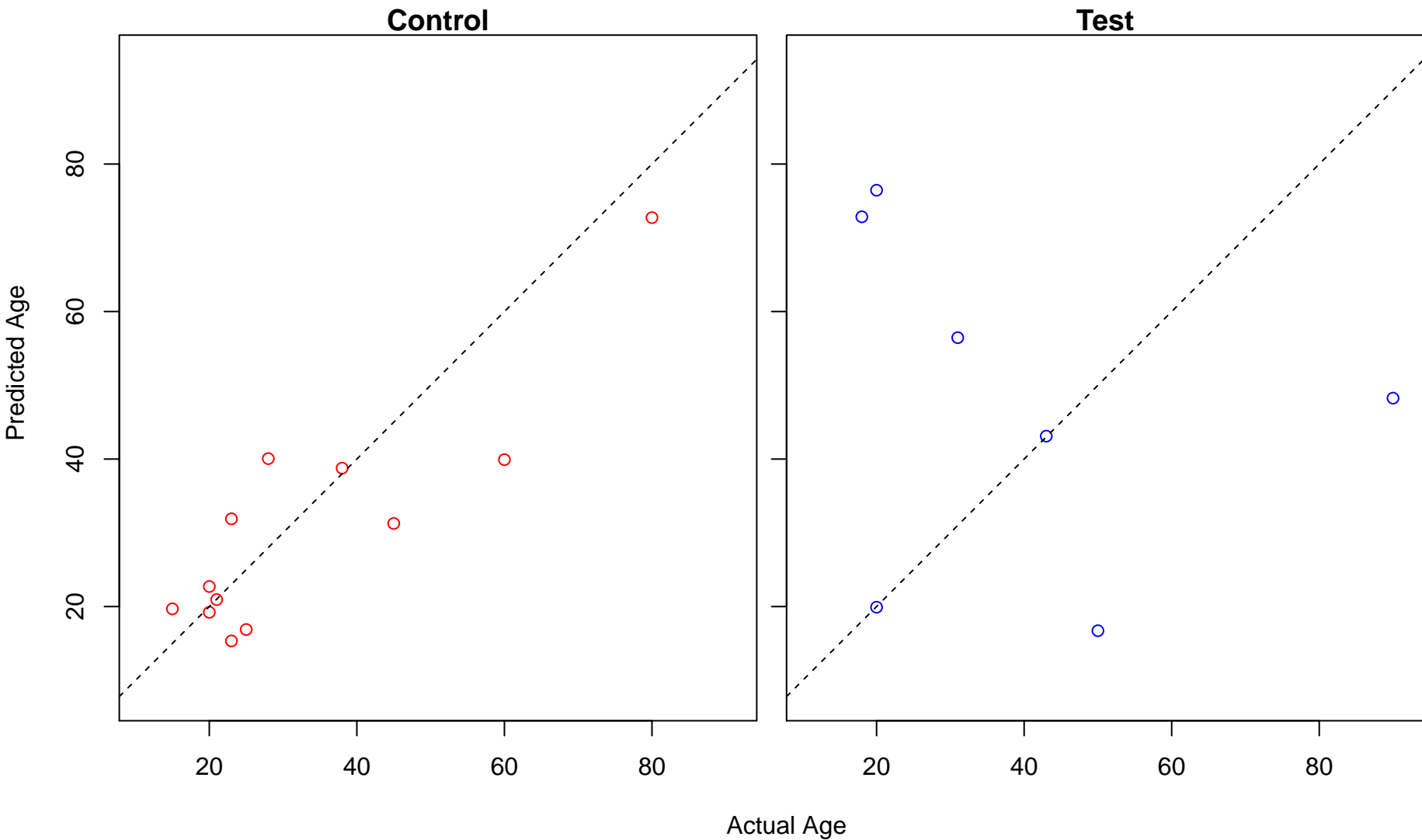
regulation of ossification (Score: 31.972088)



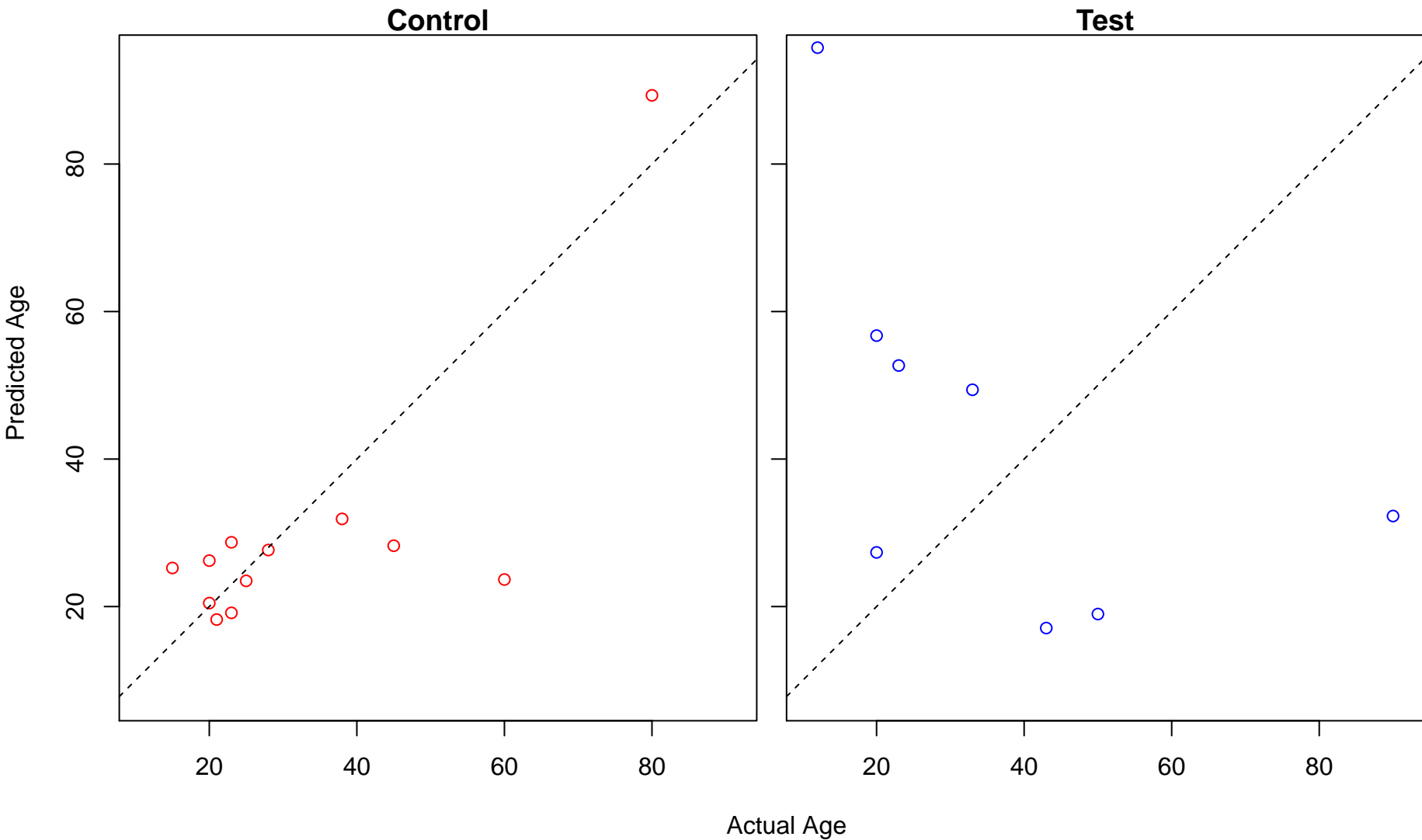
chromatin silencing at rDNA (Score: 31.794273)



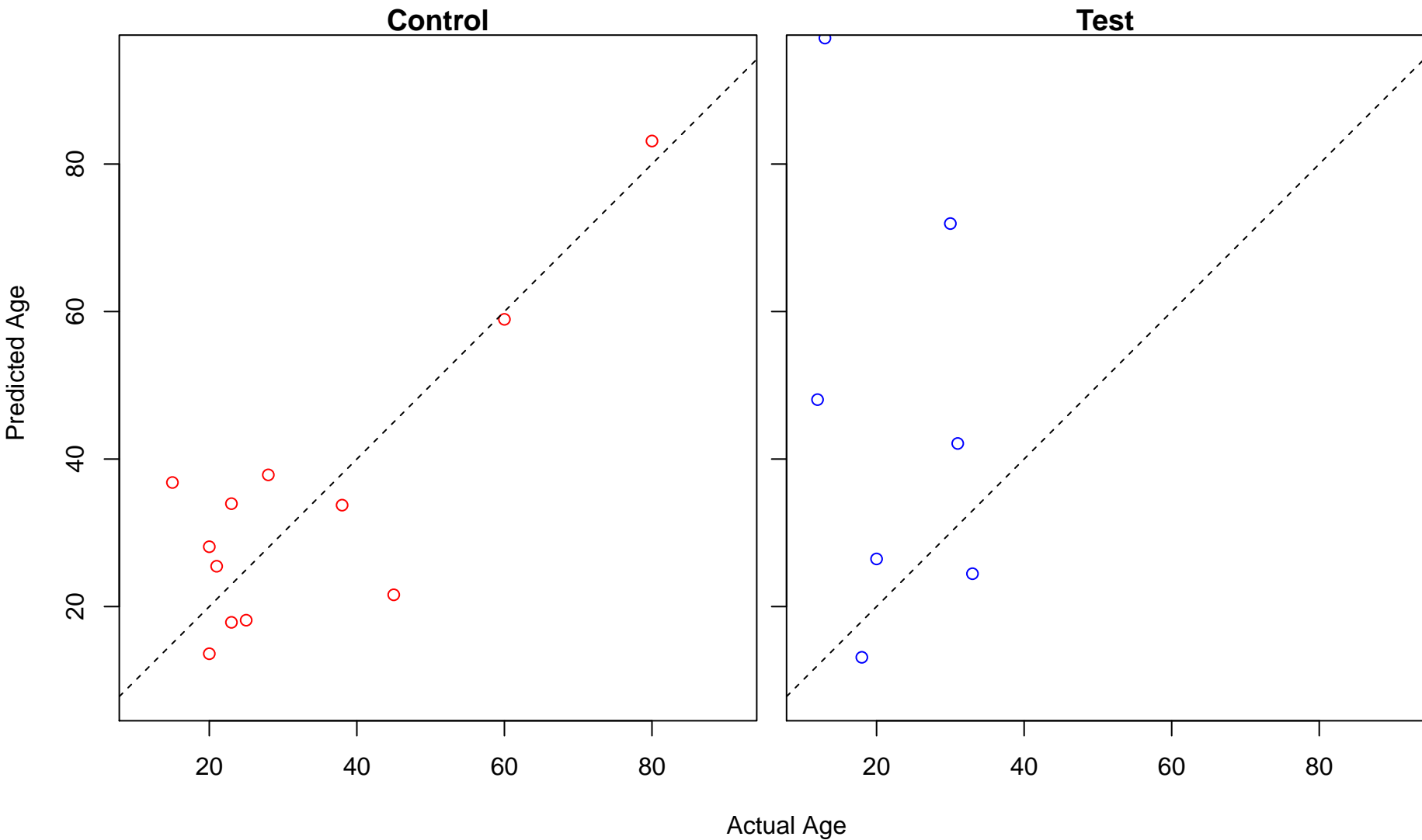
ceramide transport (Score: 31.768922)



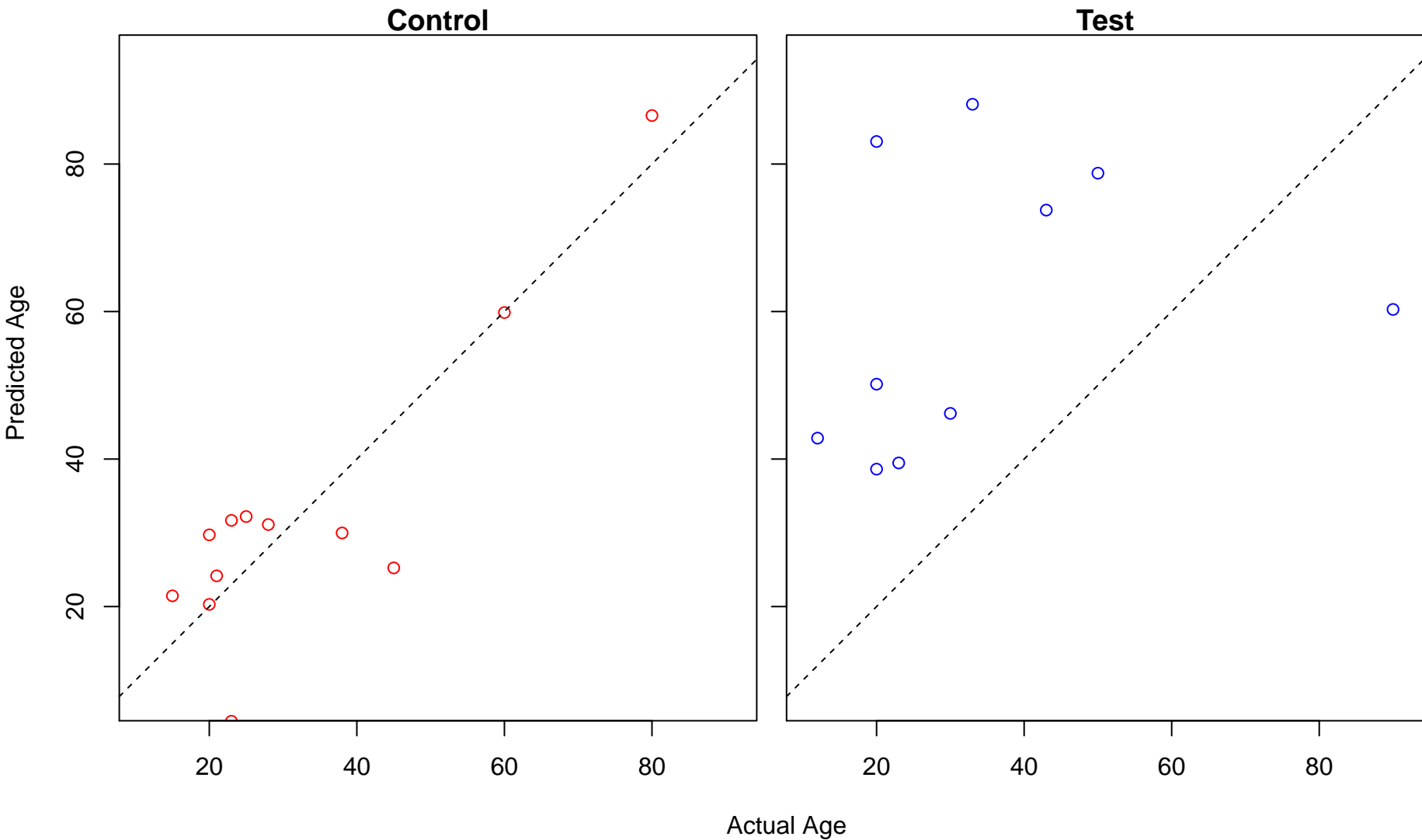
chemosensory behavior (Score: 31.765874)



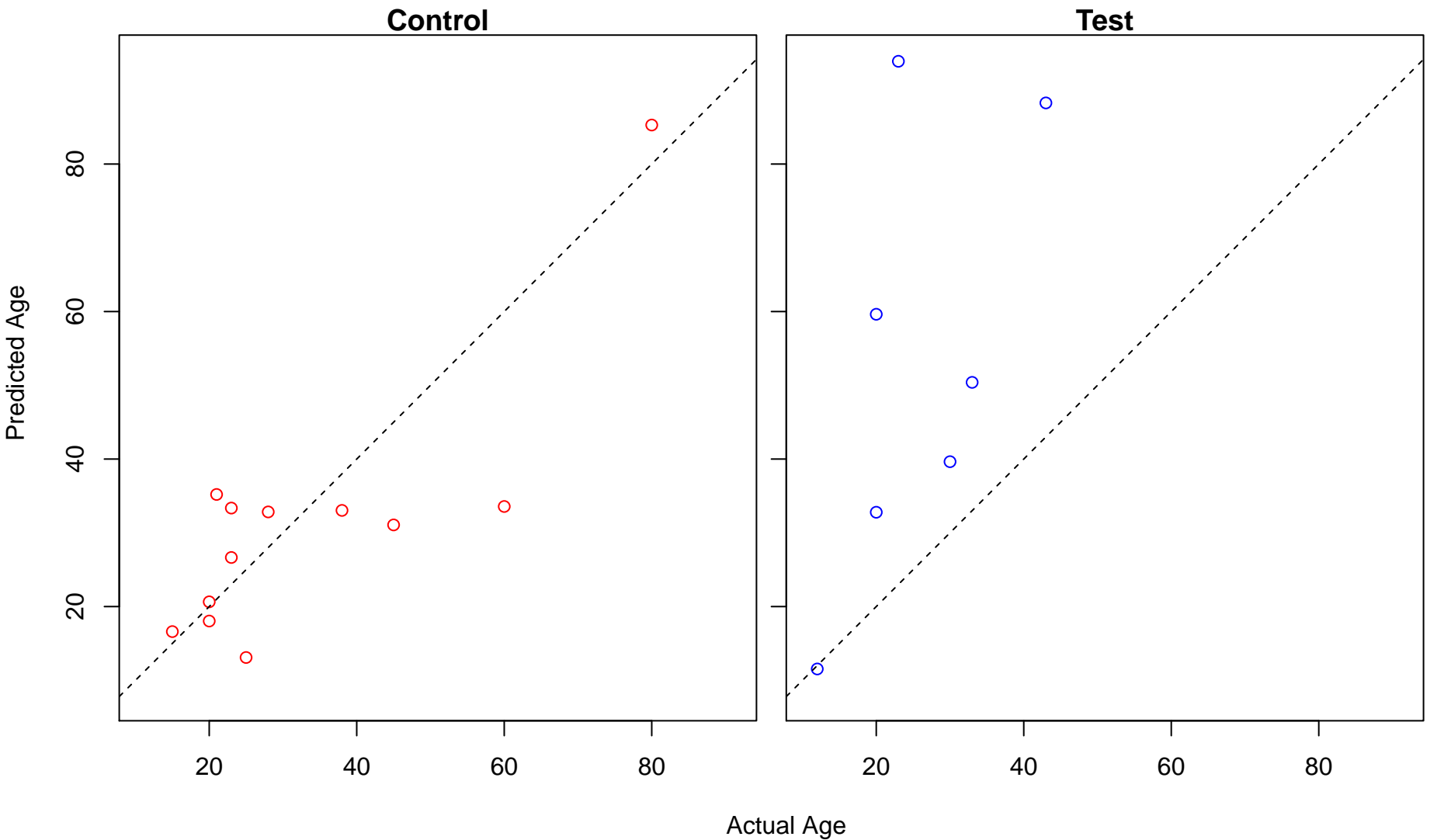
positive regulation of peptidyl-serine phosphorylation (Score: 31.705613)



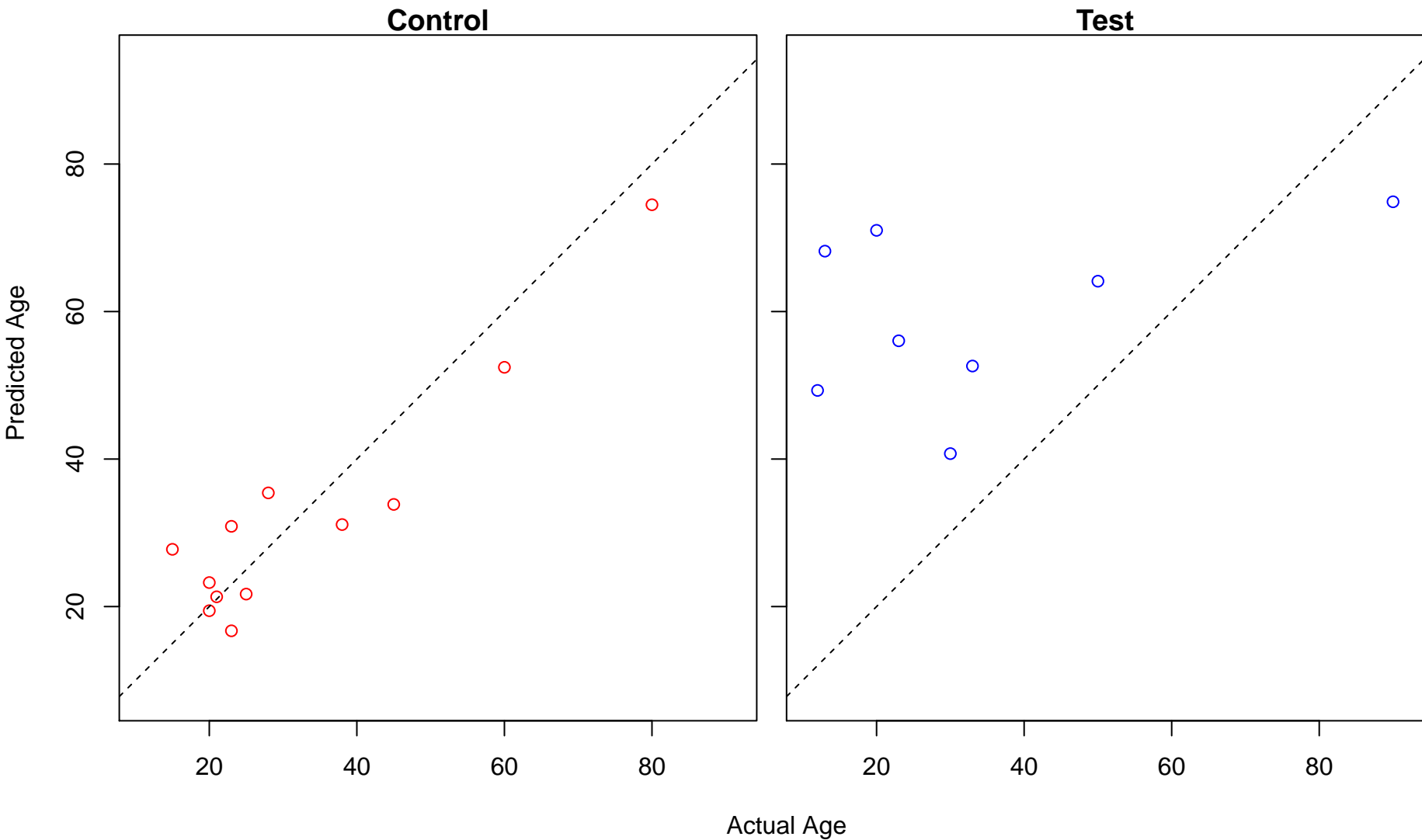
positive regulation of phagocytosis (Score: 31.631357)



ve immune response based on somatic recombination of immune receptors built from immunoglobulin su

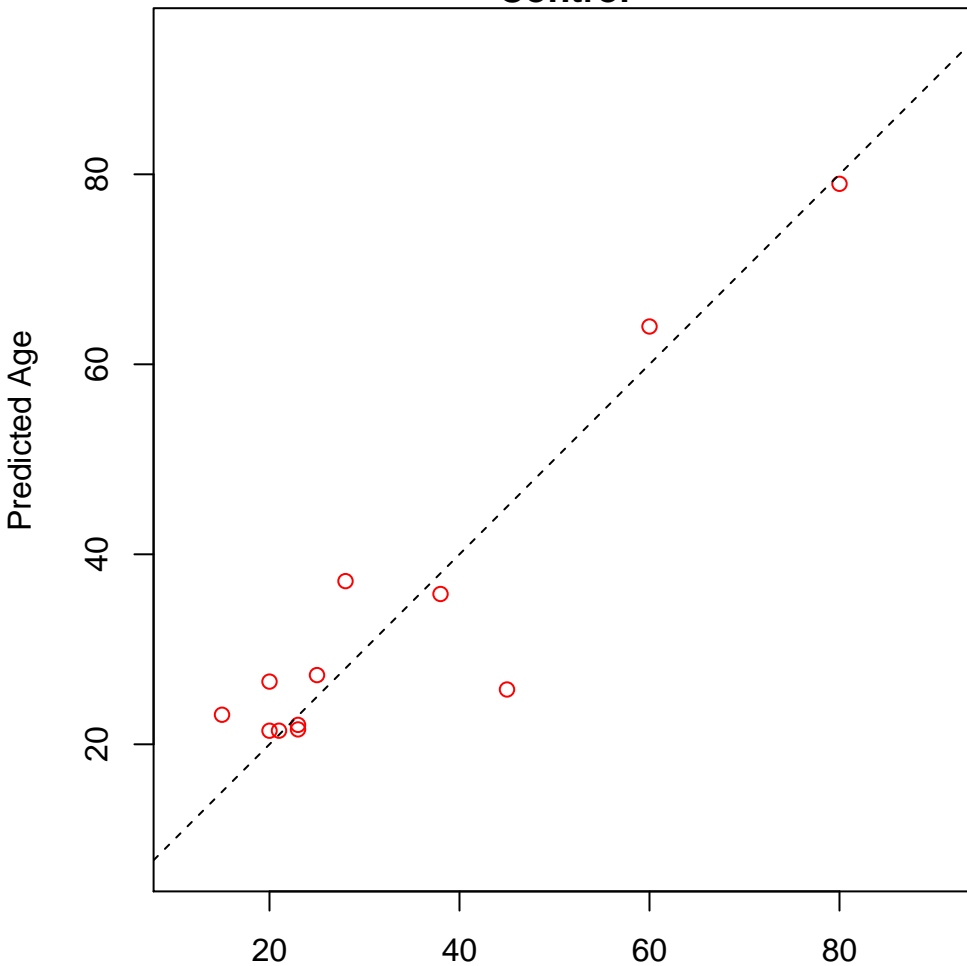


response to dsRNA (Score: 31.534590)

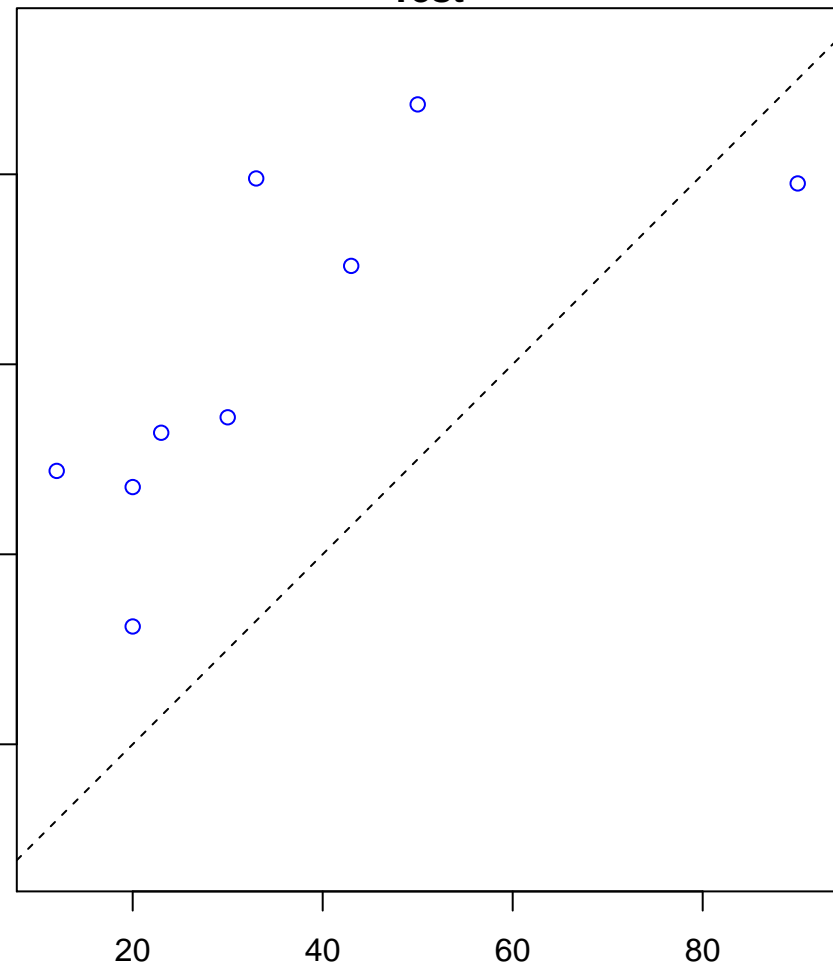


regulation of dendritic cell chemotaxis (Score: 31.423687)

Control

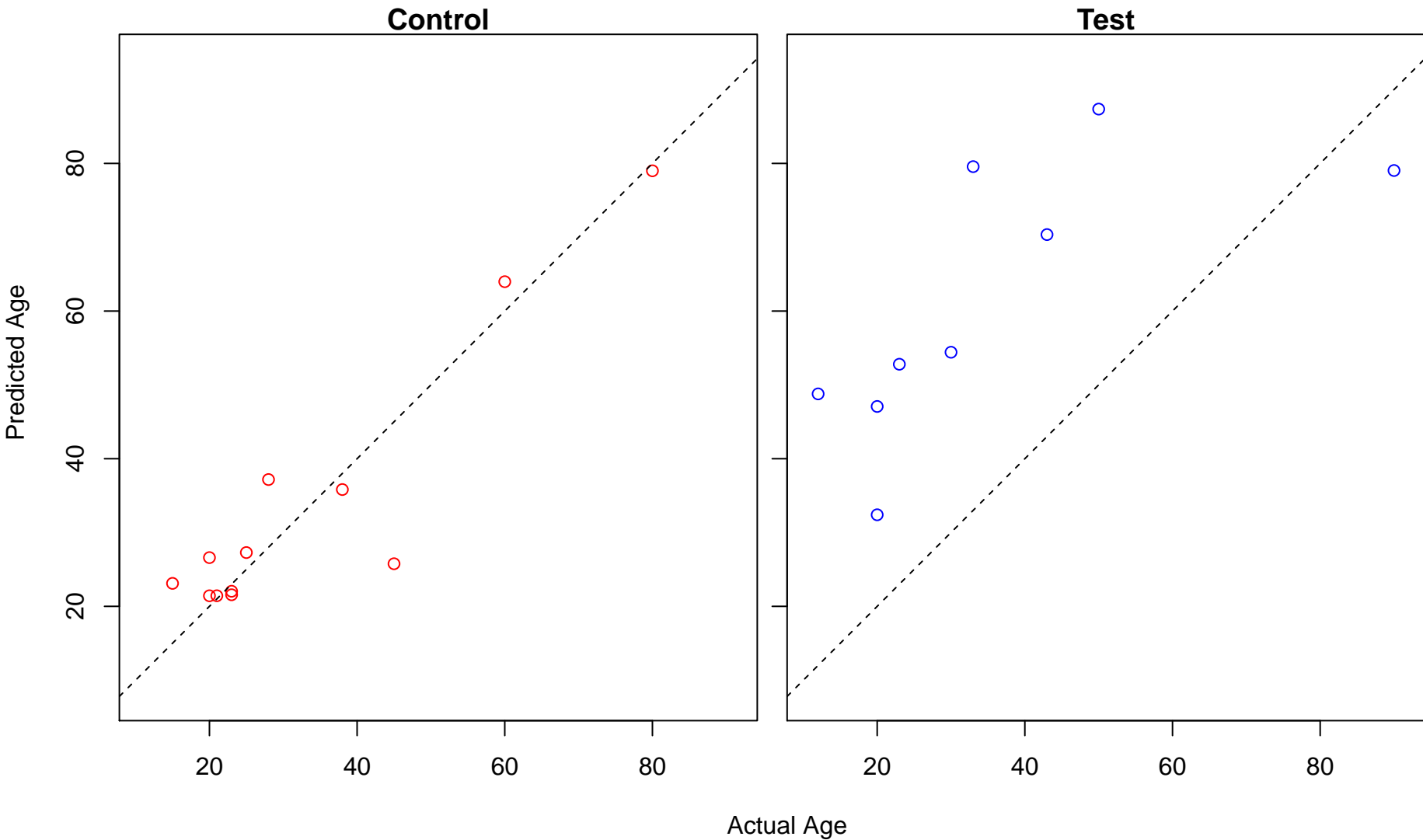


Test

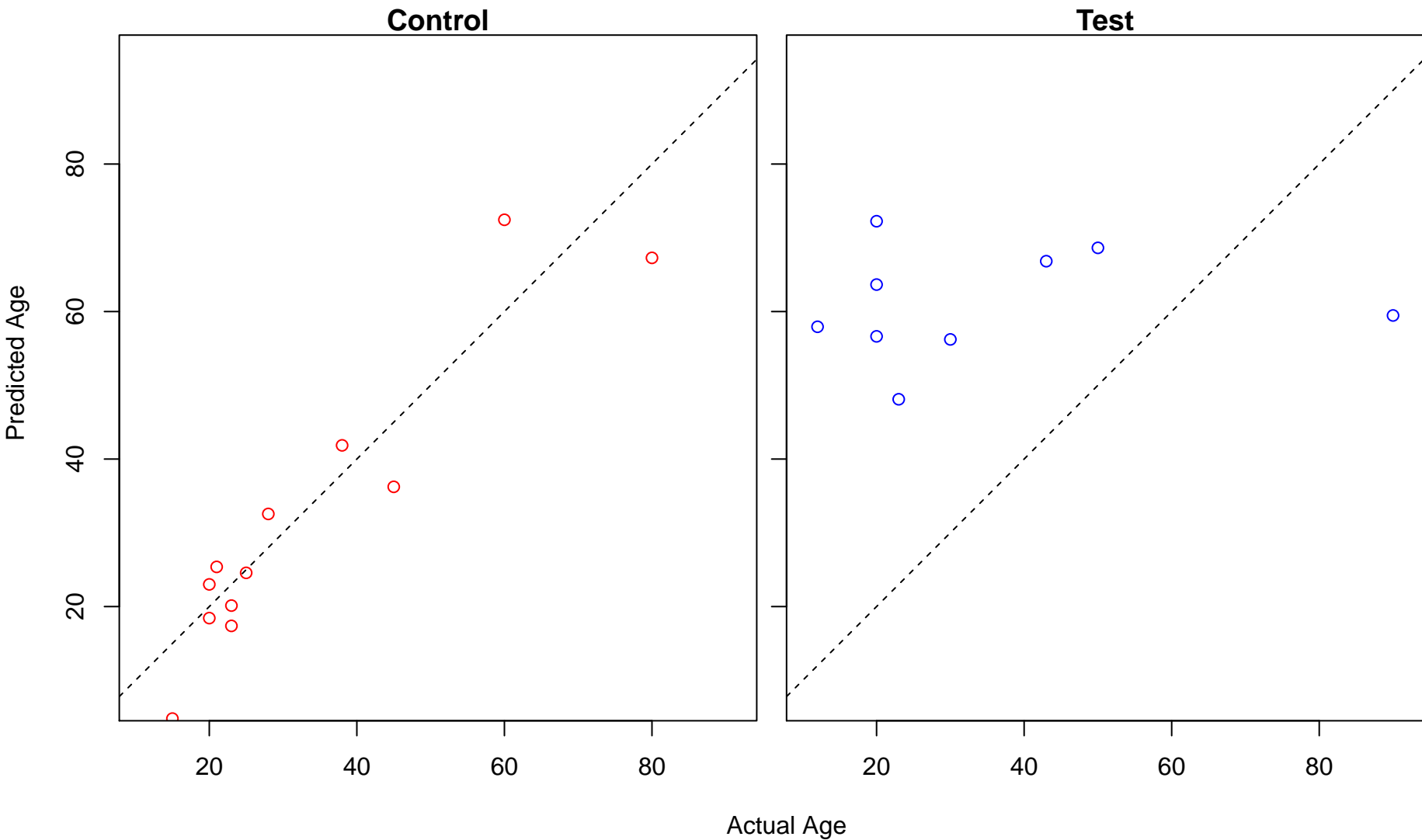


Actual Age

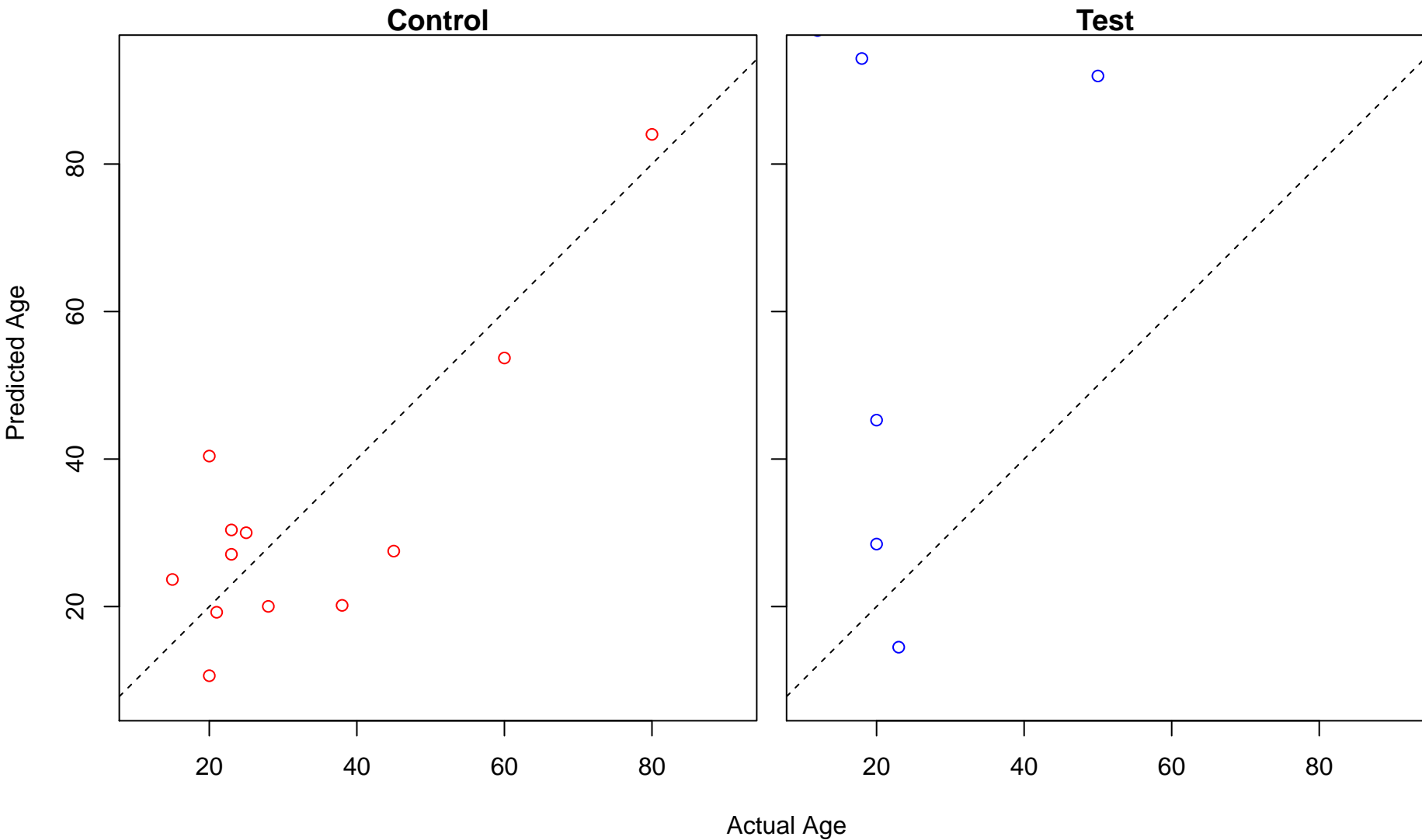
positive regulation of dendritic cell chemotaxis (Score: 31.423687)



phosphatidylinositol acyl-chain remodeling (Score: 31.385180)

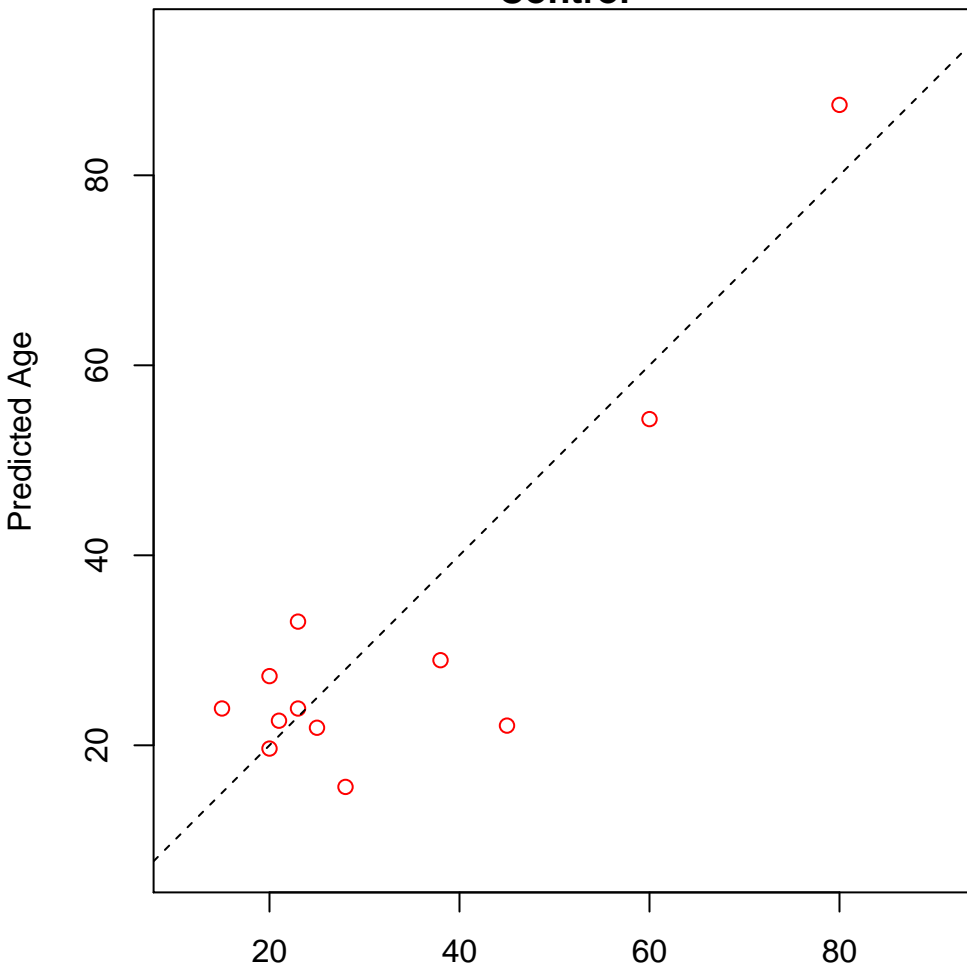


detection of chemical stimulus involved in sensory perception of bitter taste (Score: 31.254083)

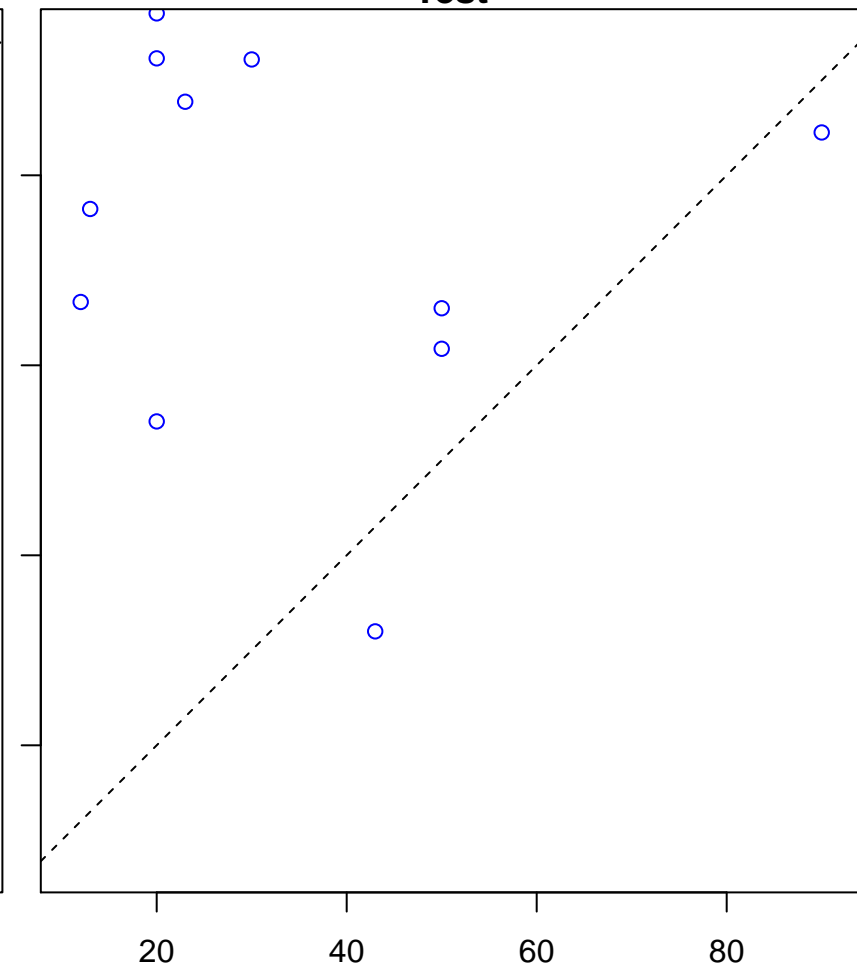


regulation of mRNA 3'-end processing (Score: 31.216865)

Control

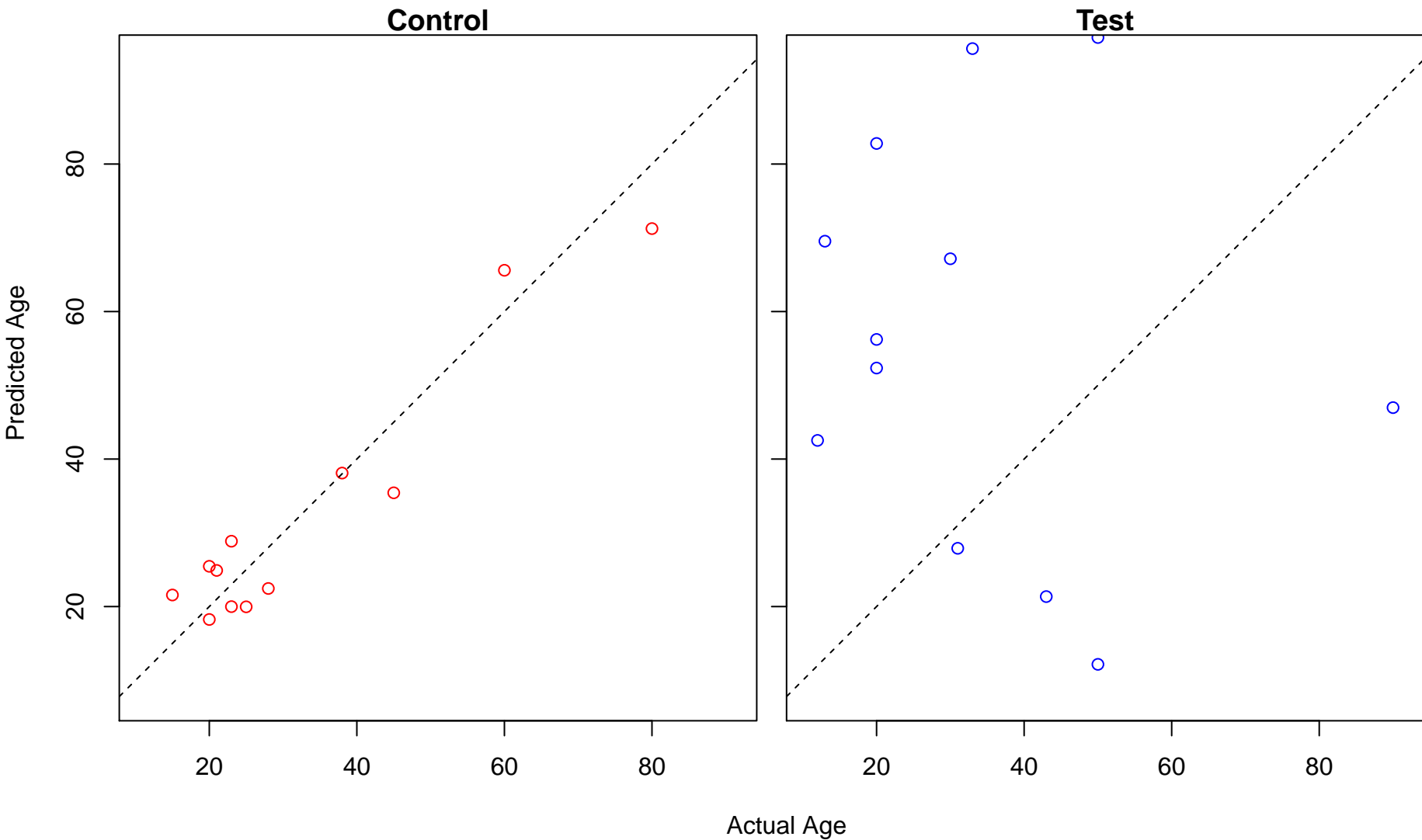


Test

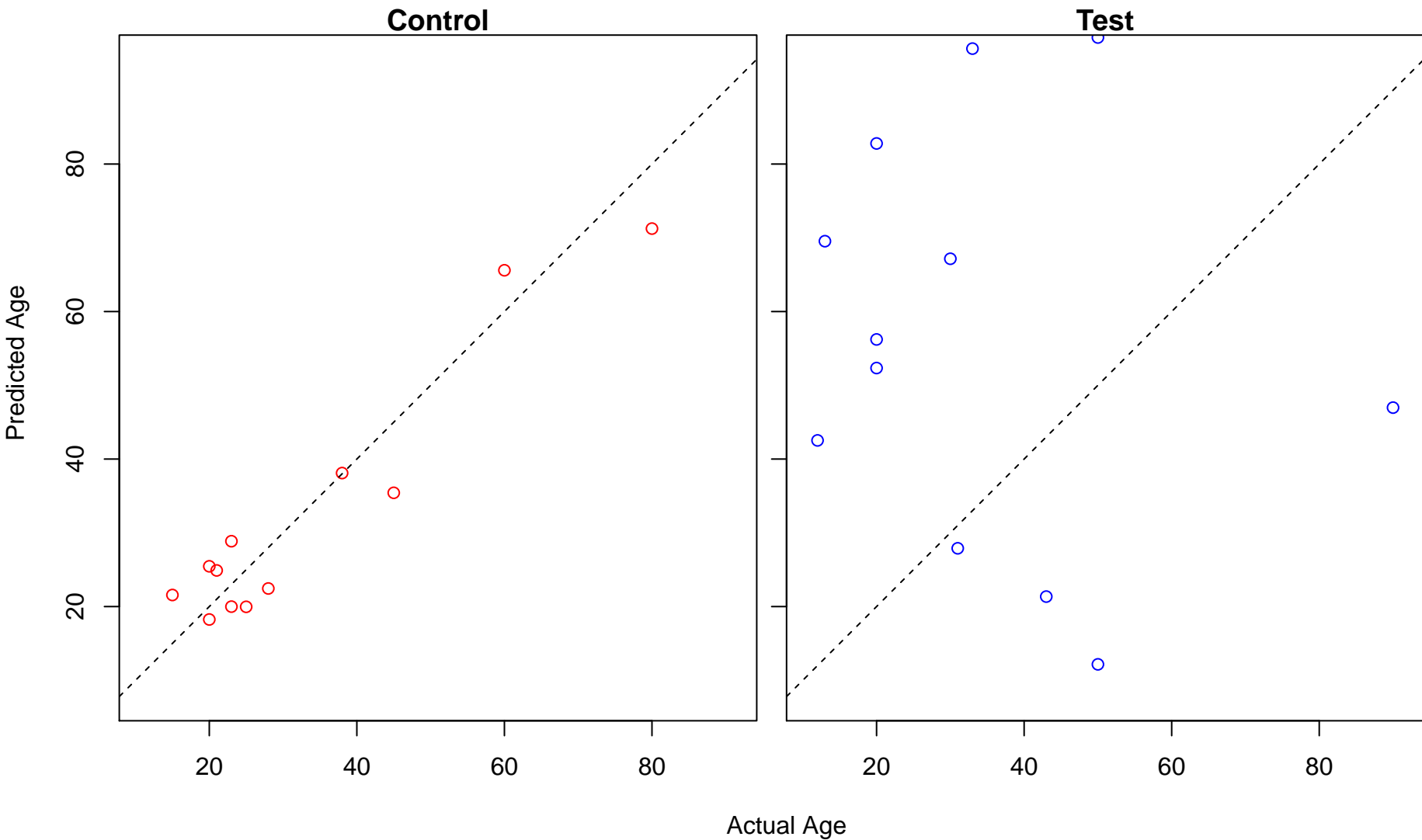


Actual Age

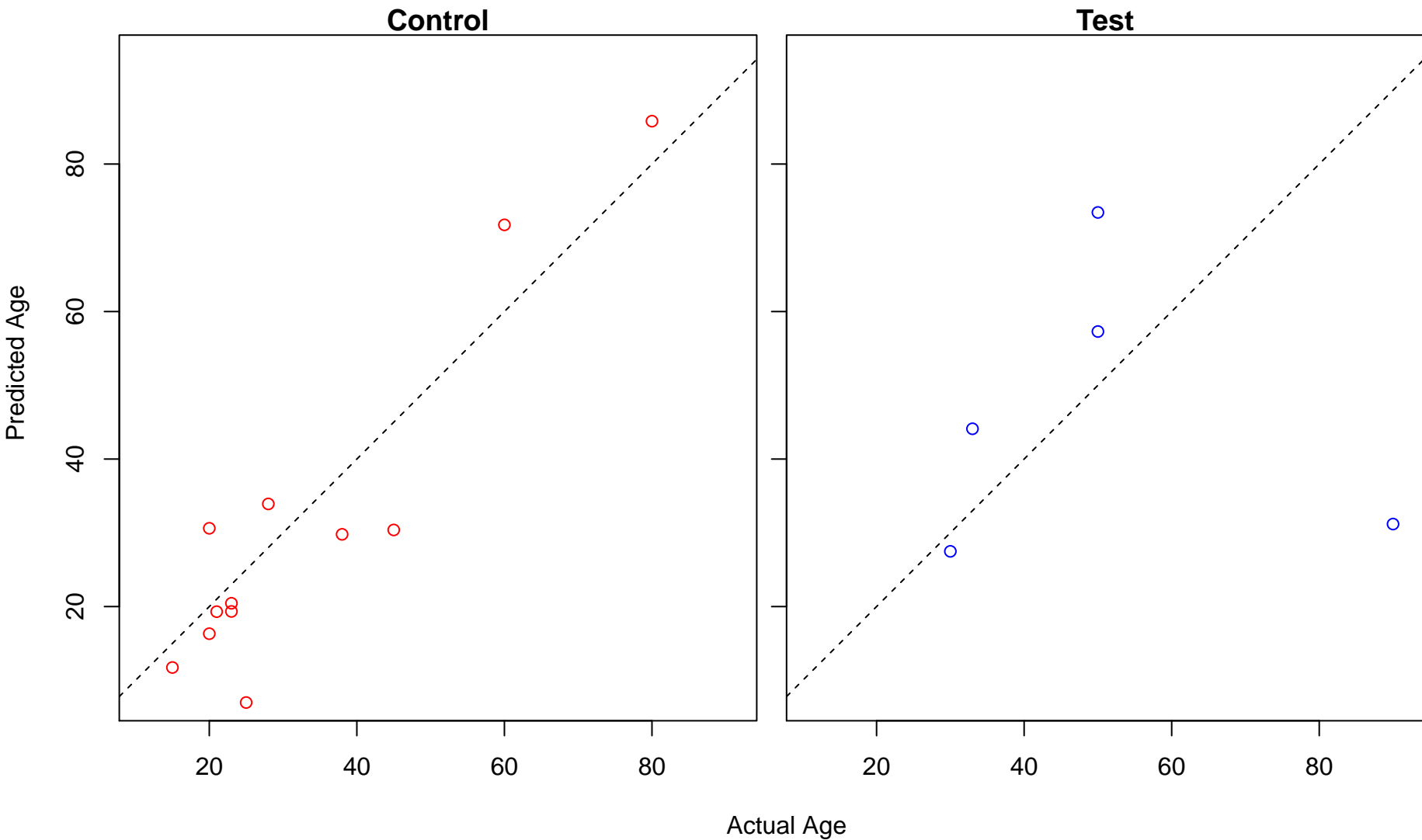
regulation of mitotic cell cycle spindle assembly checkpoint (Score: 31.175407)



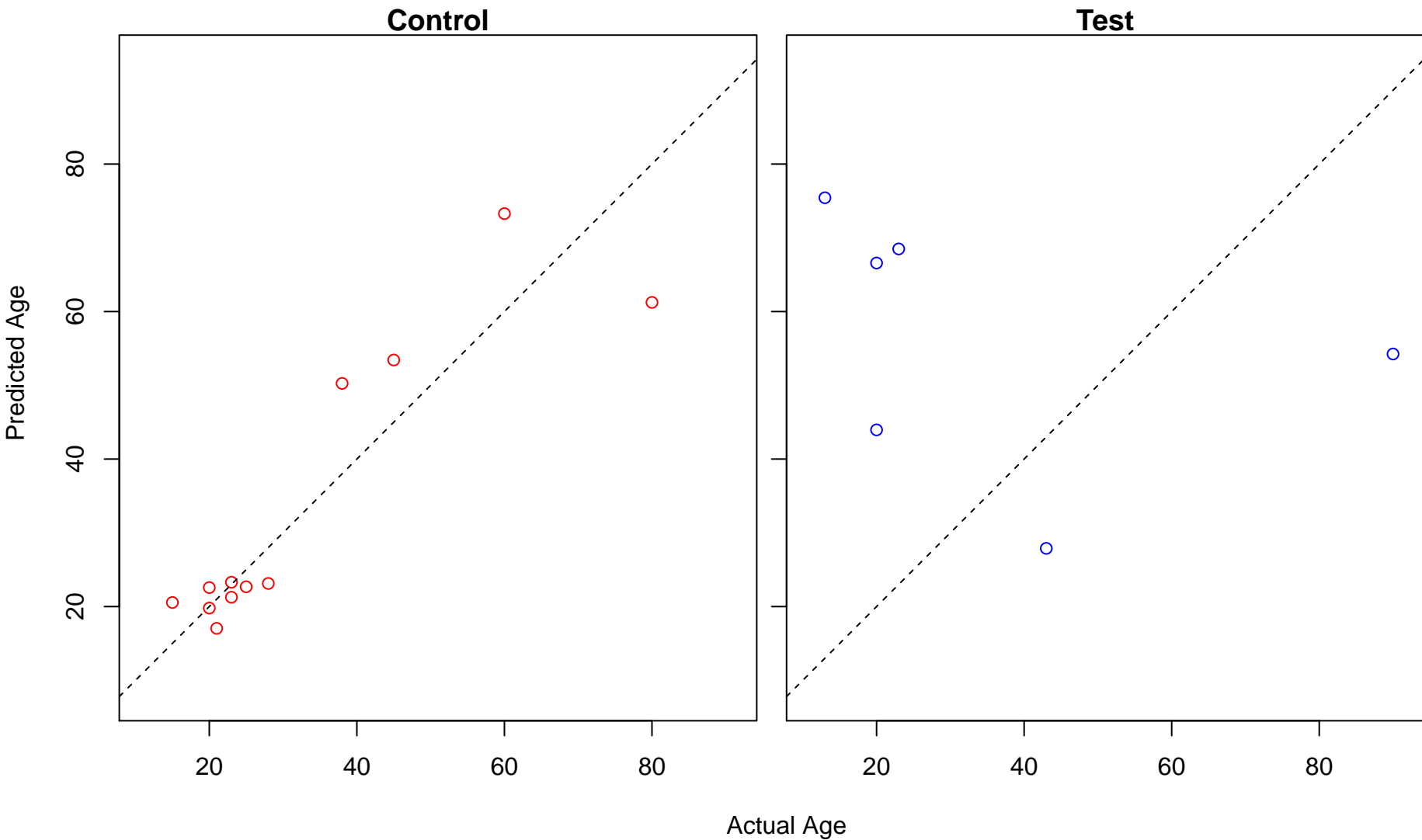
regulation of mitotic spindle checkpoint (Score: 31.175407)



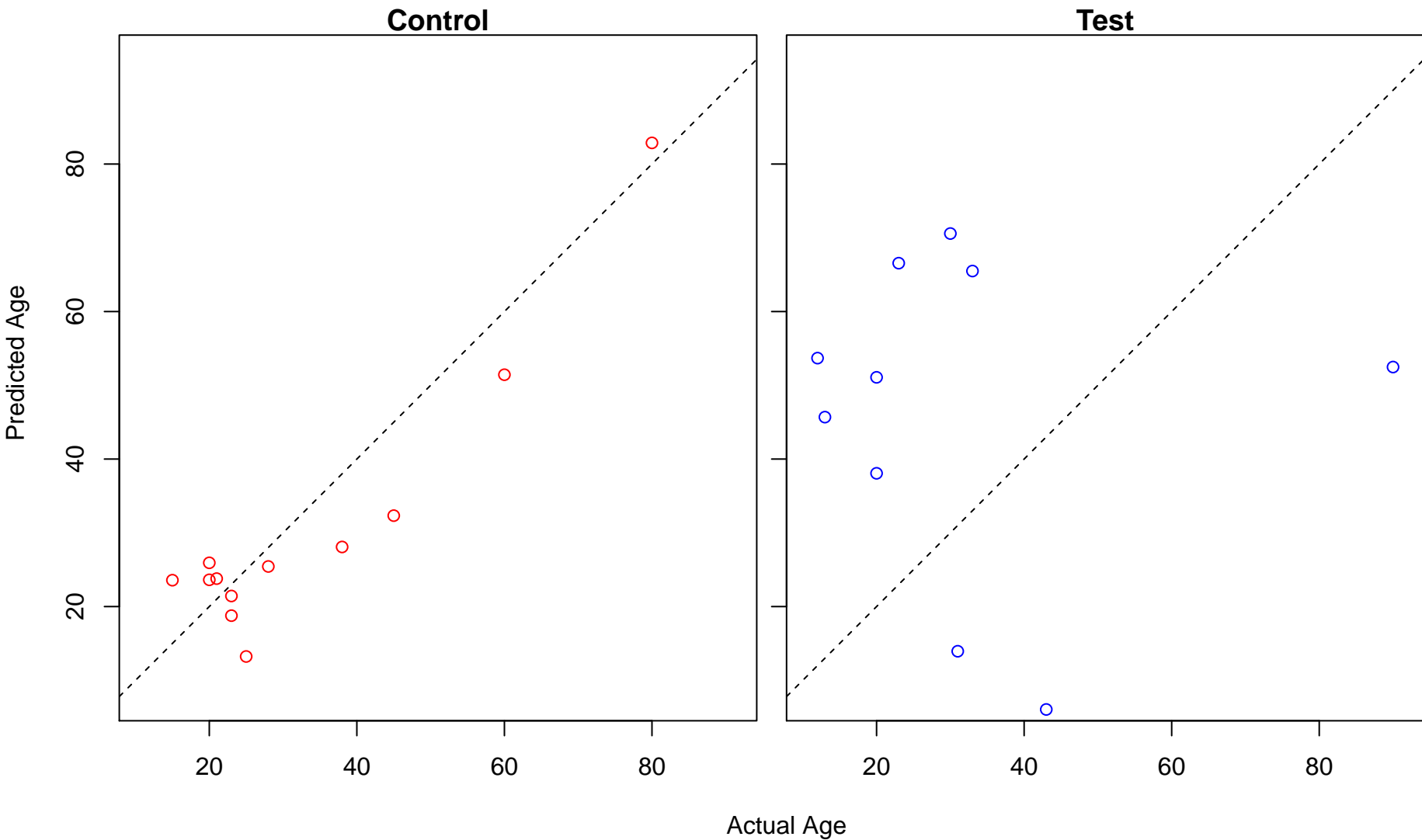
negative regulation of myotube differentiation (Score: 31.171100)



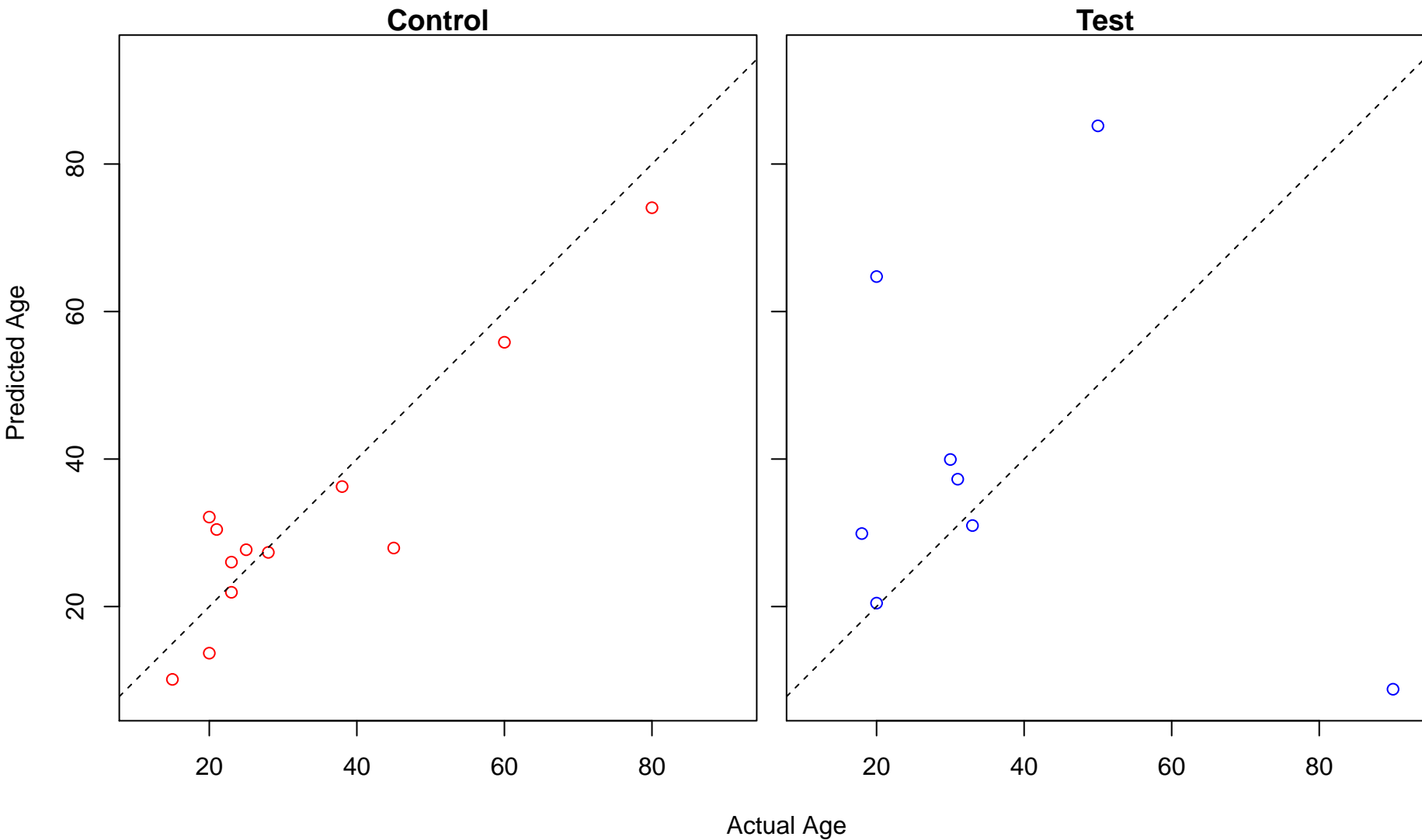
retinol metabolic process (Score: 31.138160)



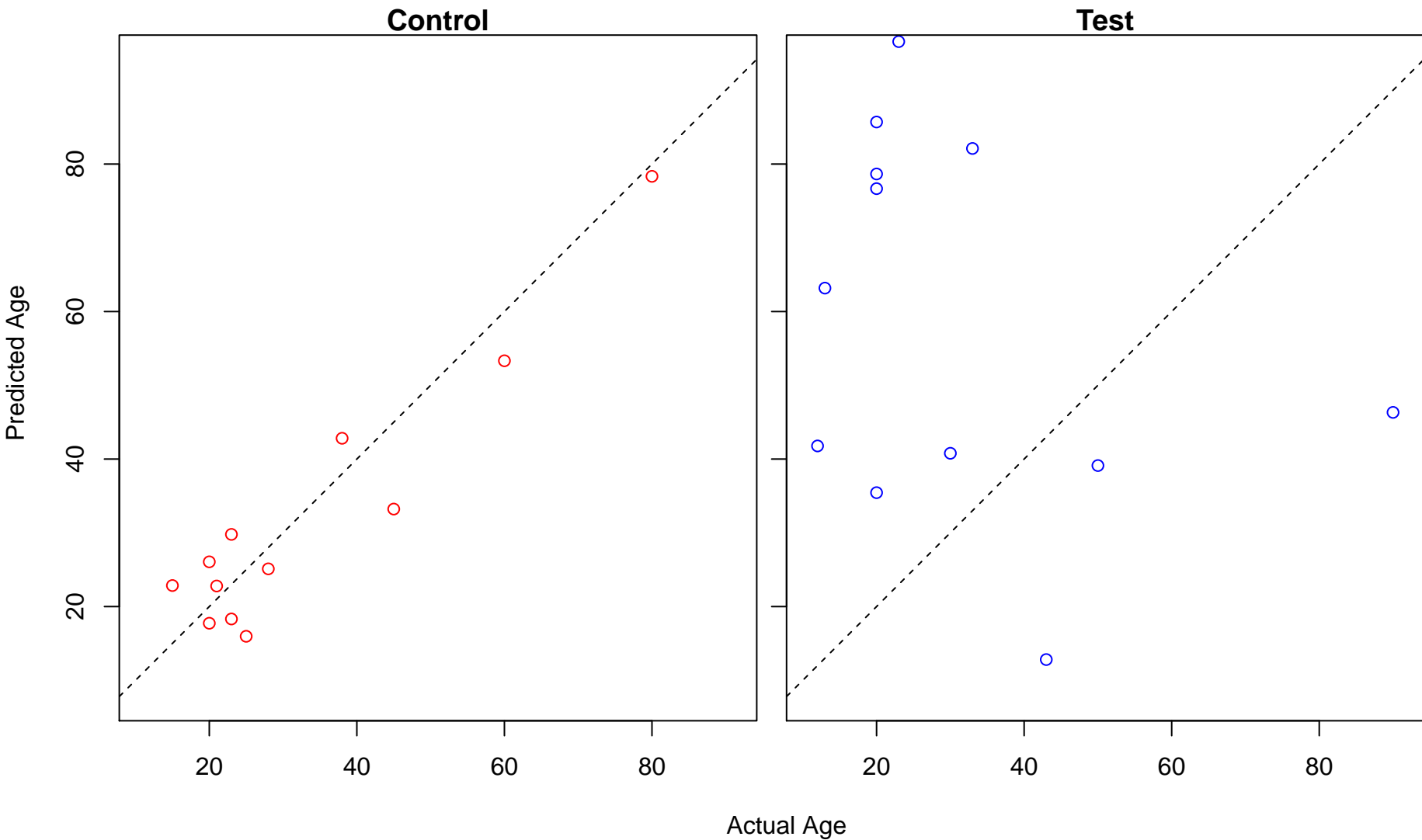
protein autoubiquitination (Score: 31.071598)



C21-steroid hormone metabolic process (Score: 31.070584)

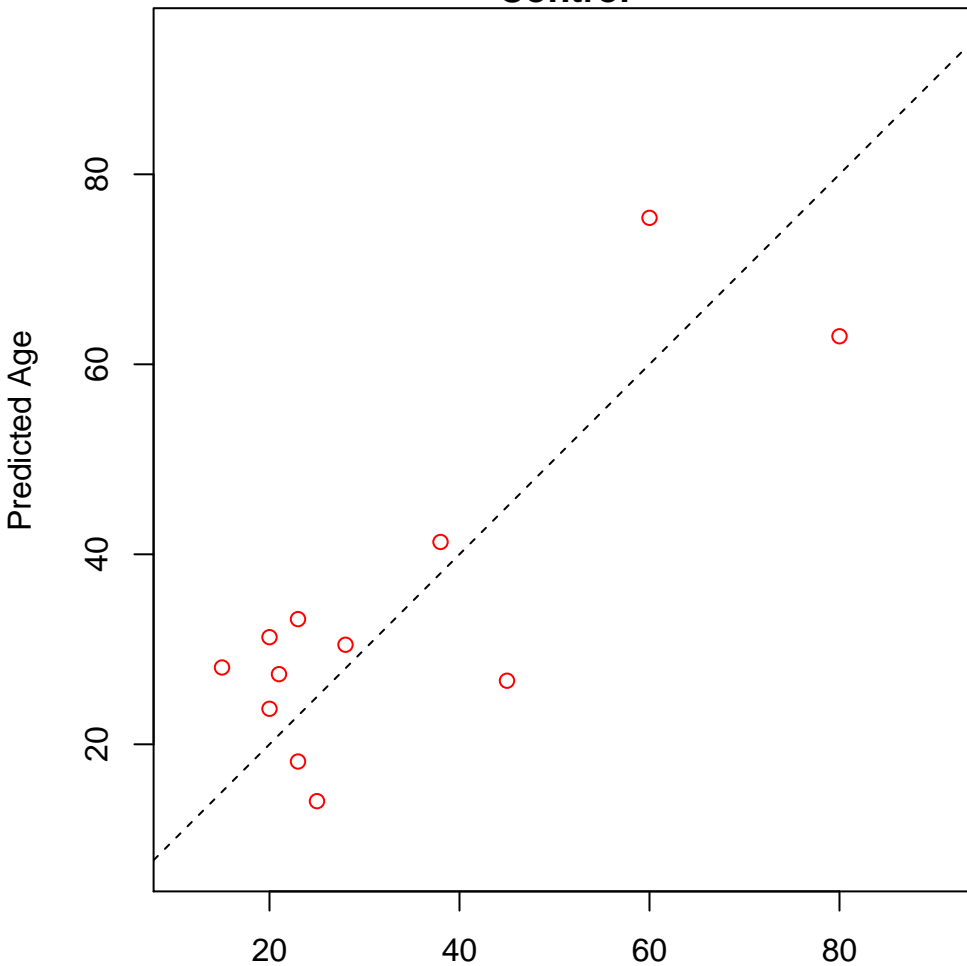


response to interferon-alpha (Score: 30.965193)

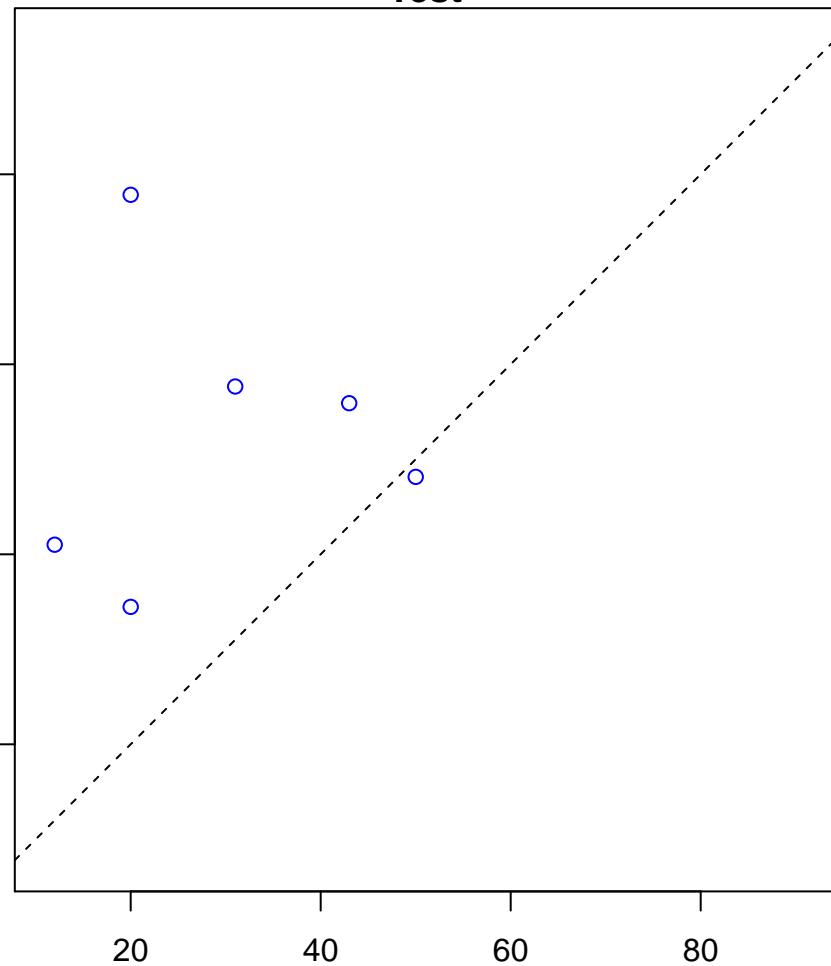


positive regulation of insulin secretion (Score: 30.606315)

Control

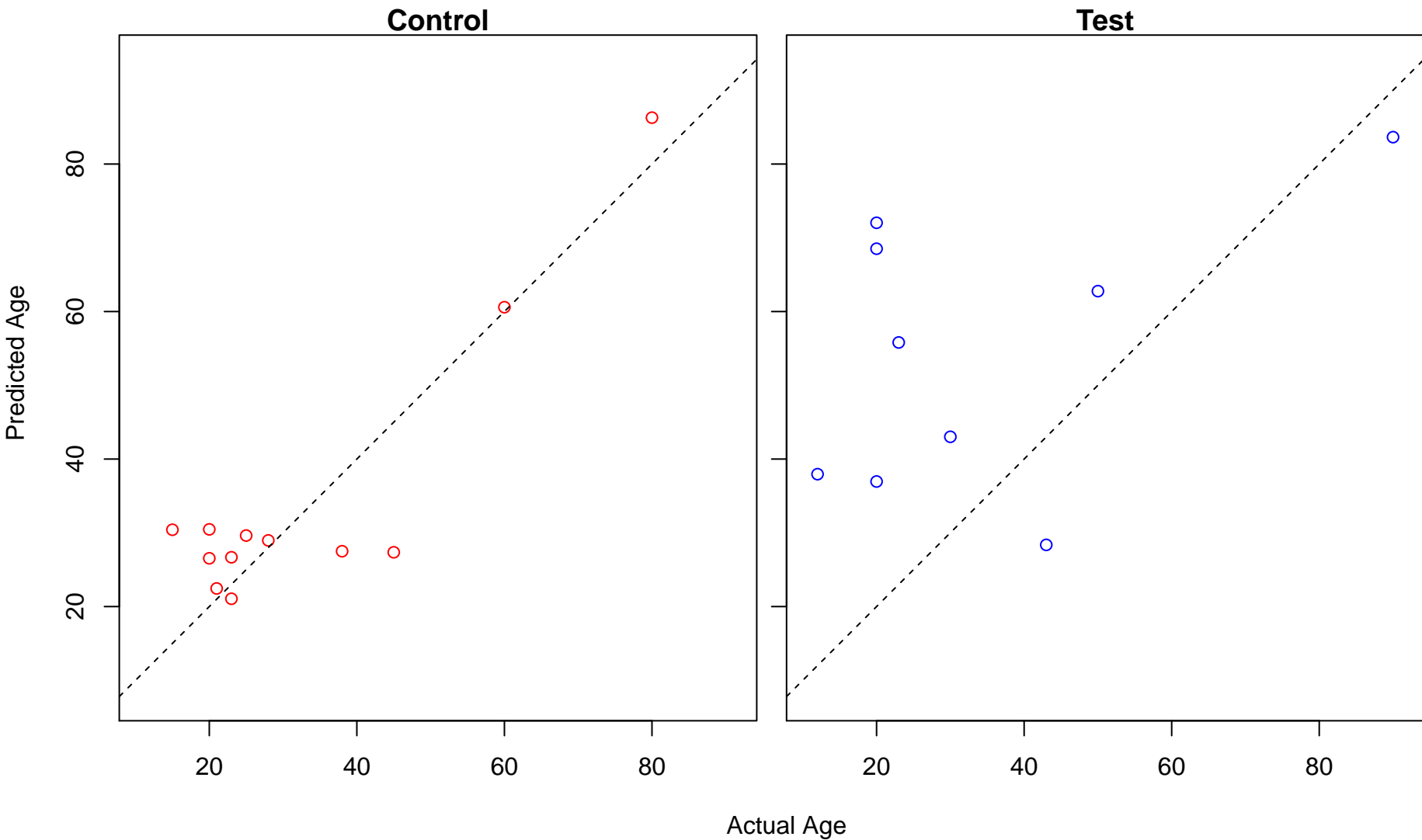


Test



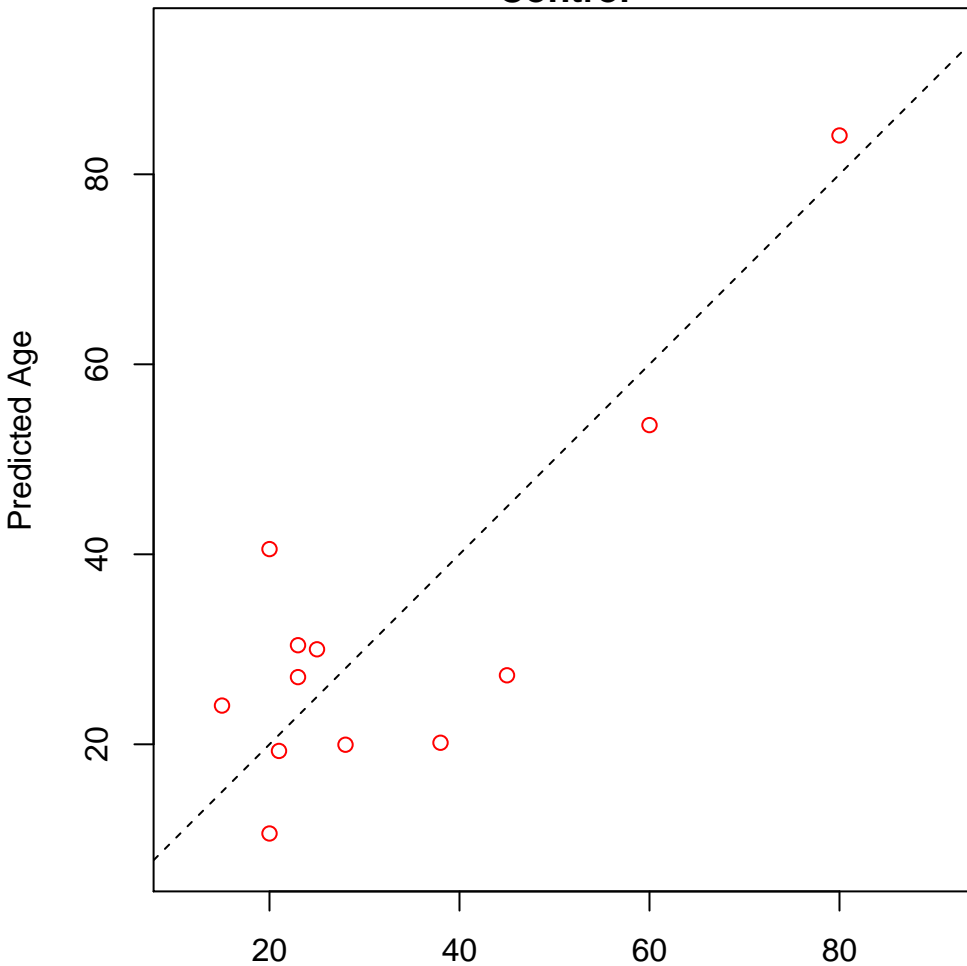
Actual Age

regulation of cell division (Score: 30.580449)

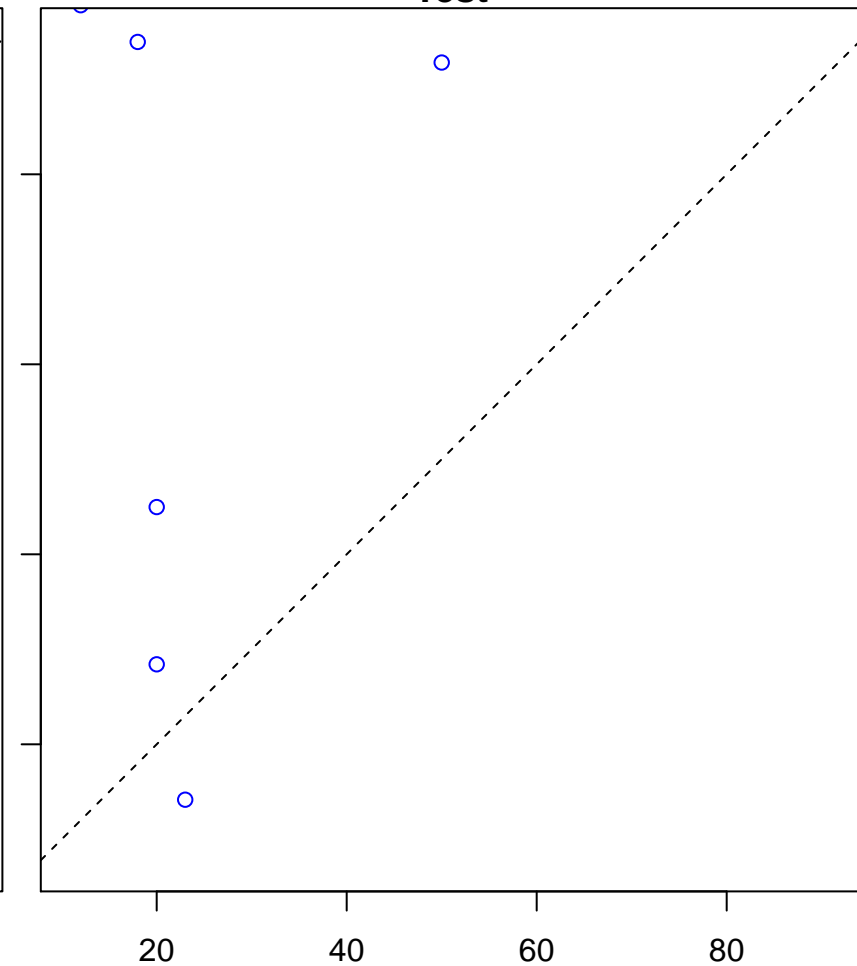


sensory perception of bitter taste (Score: 30.551202)

Control

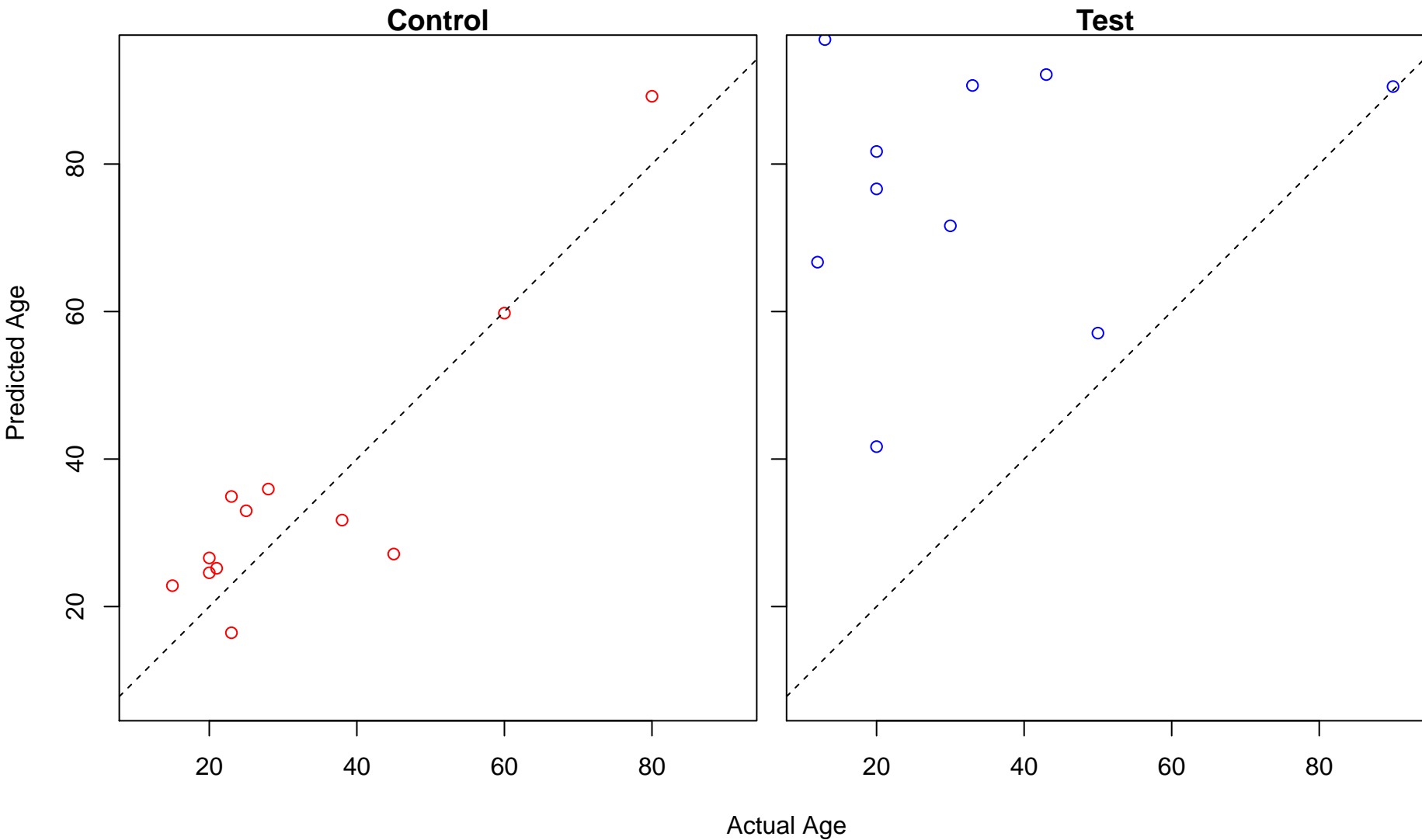


Test

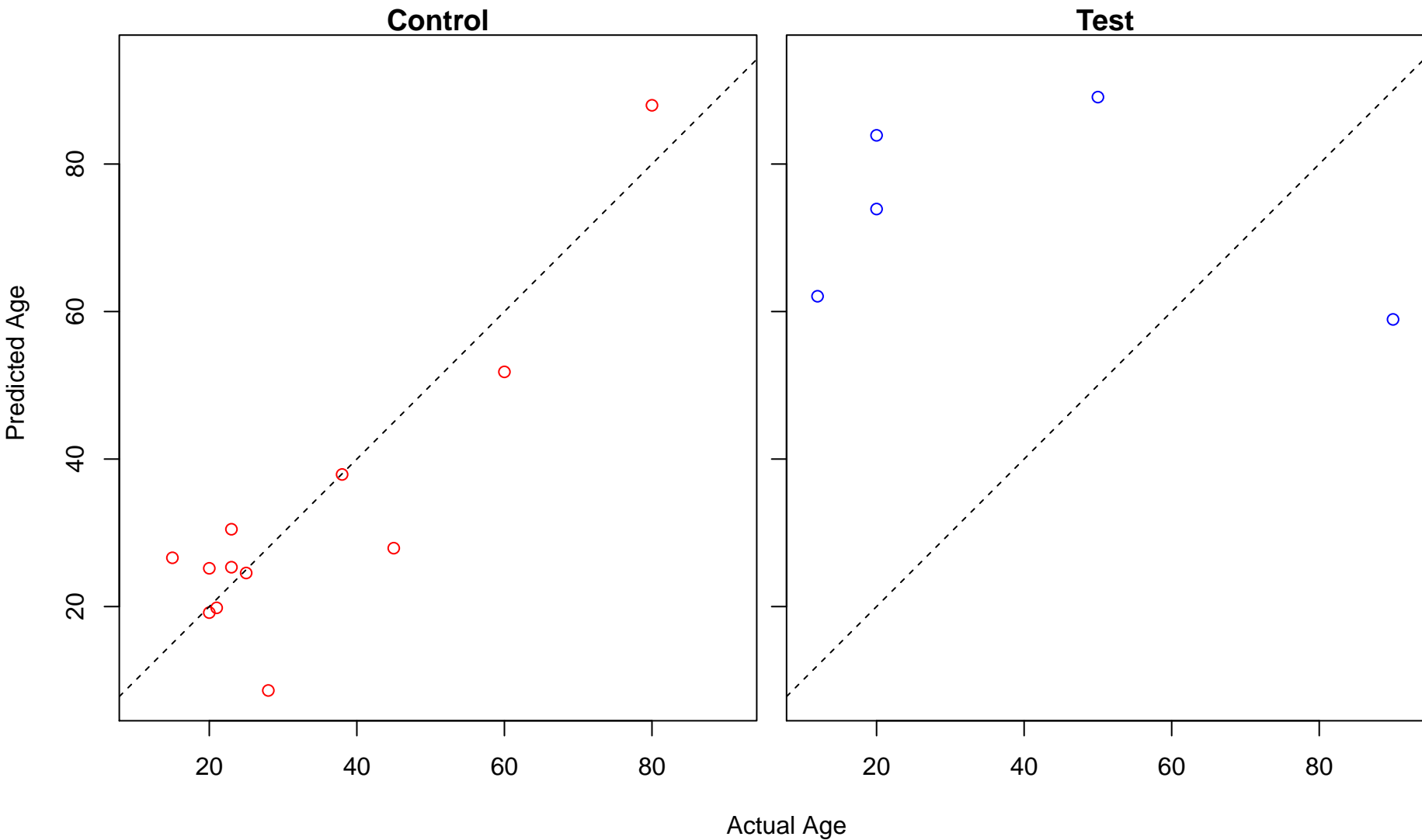


Actual Age

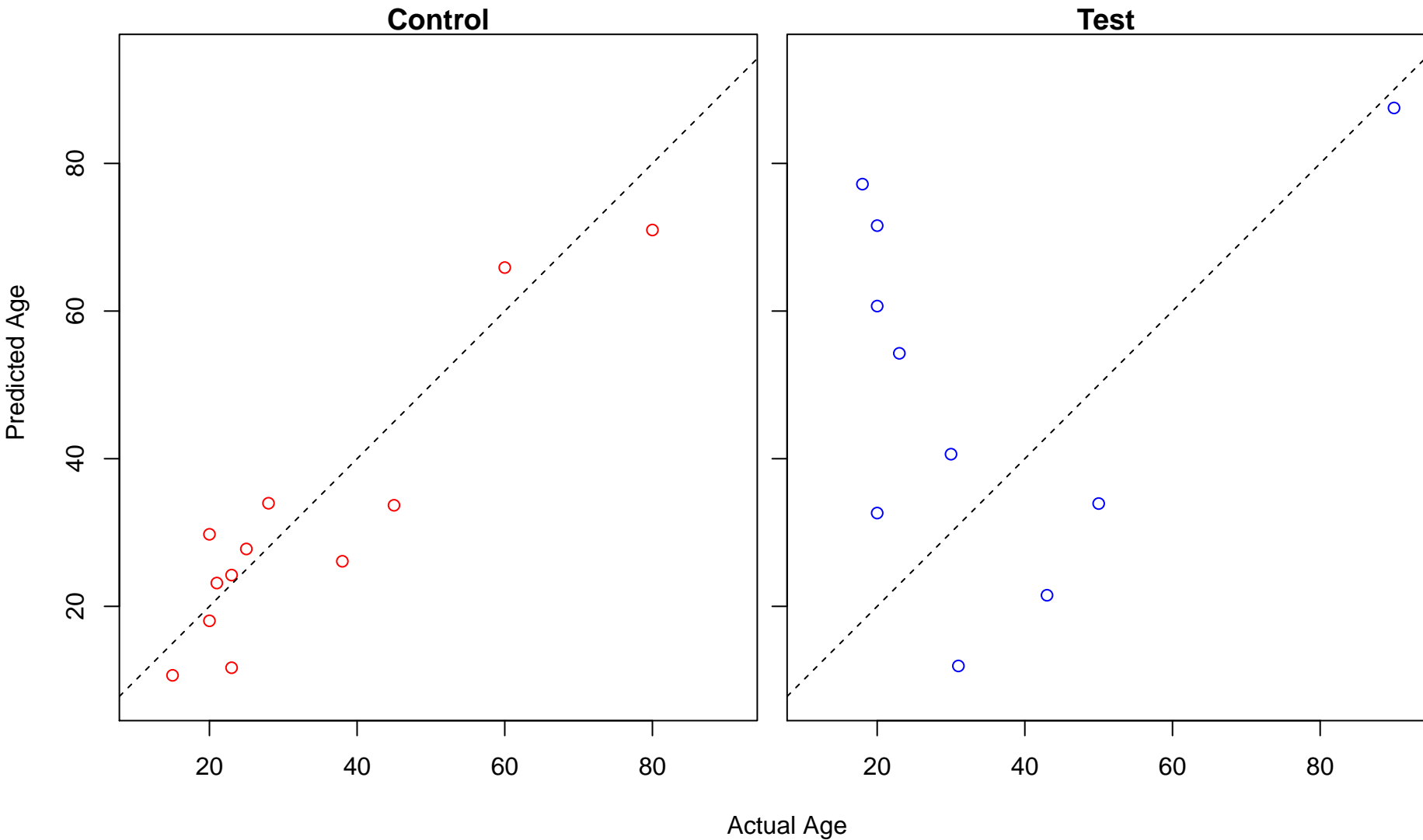
sequestering of metal ion (Score: 30.494756)



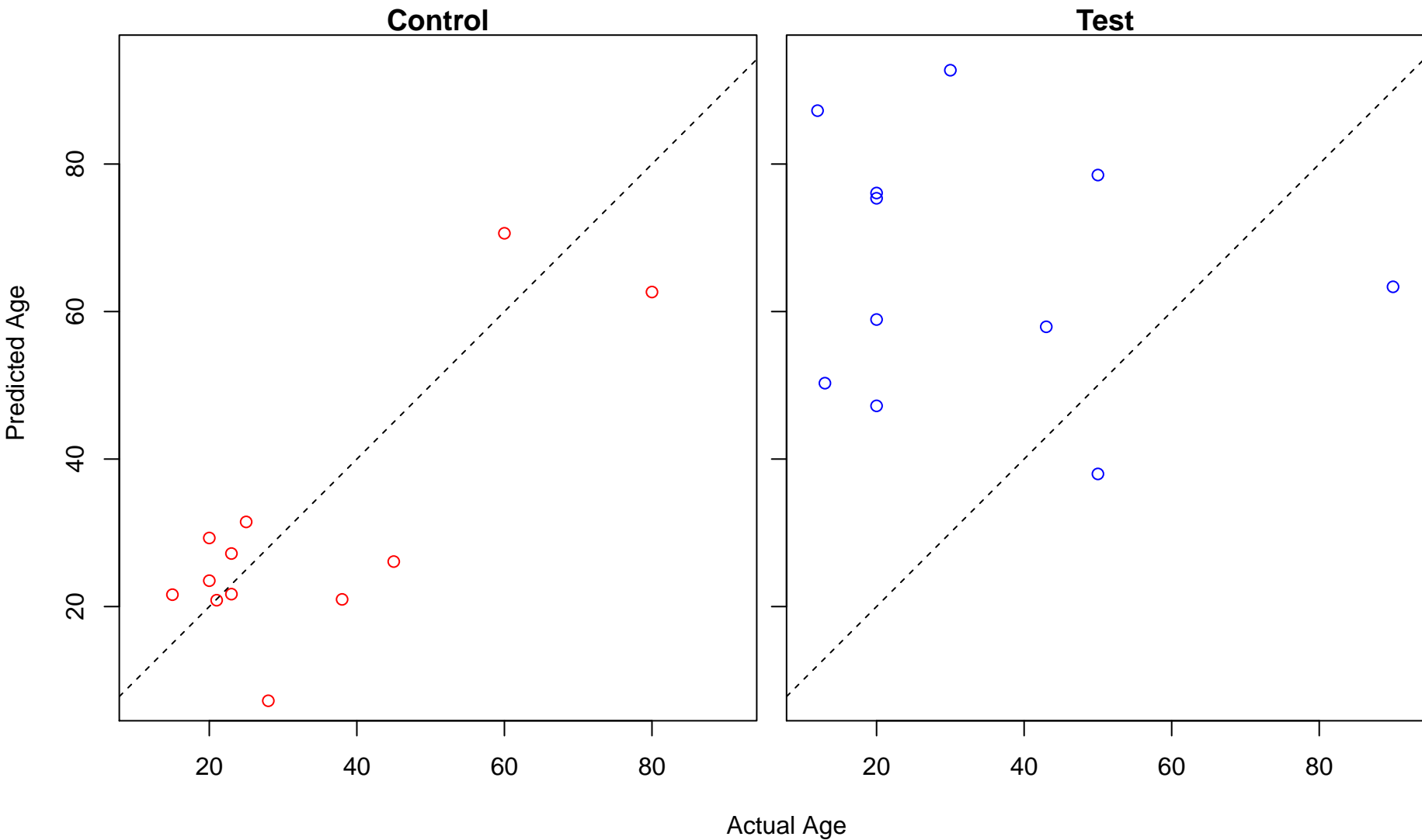
fatty acid biosynthetic process (Score: 30.403187)



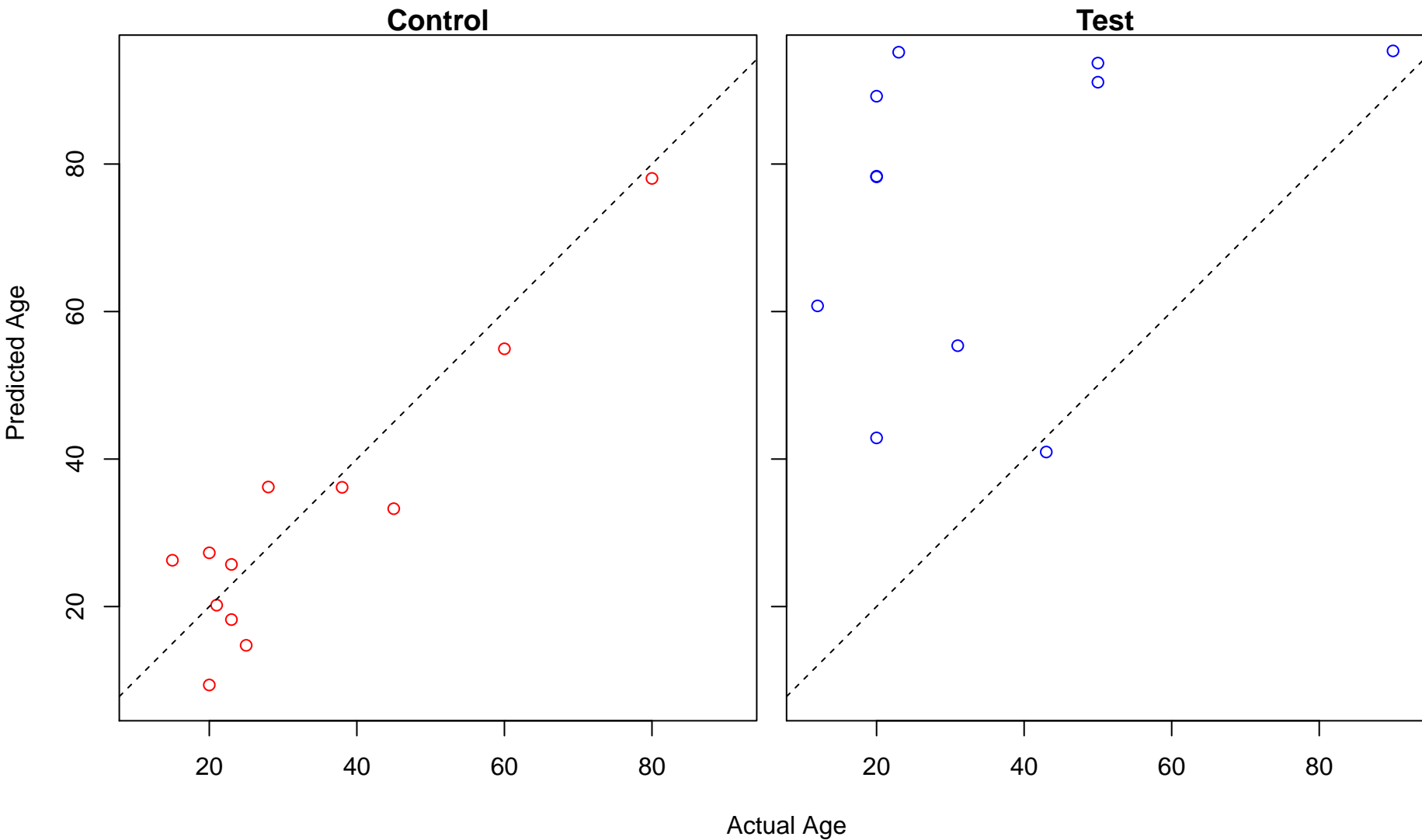
negative regulation of toll-like receptor signaling pathway (Score: 30.401711)



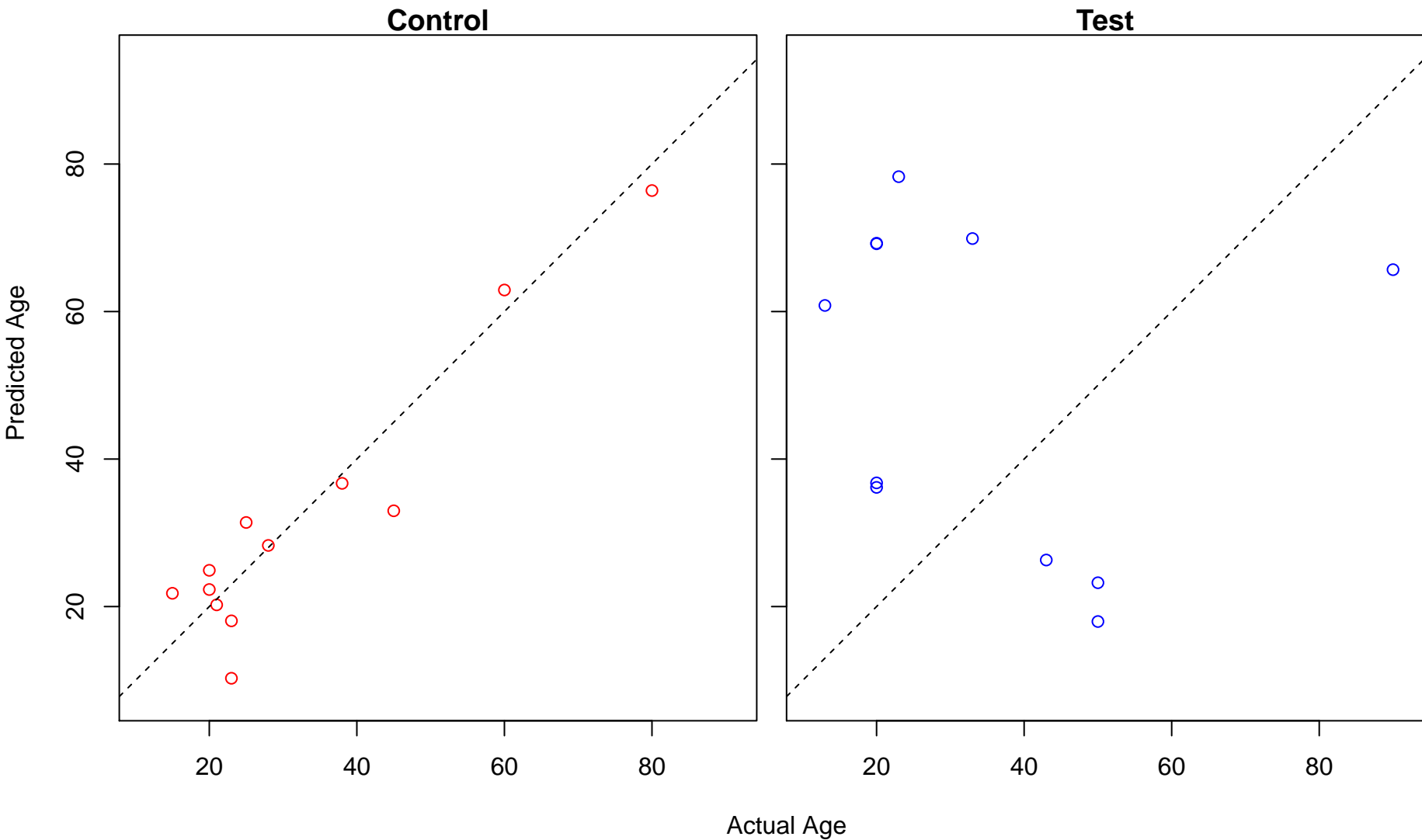
positive regulation of organic acid transport (Score: 30.201623)



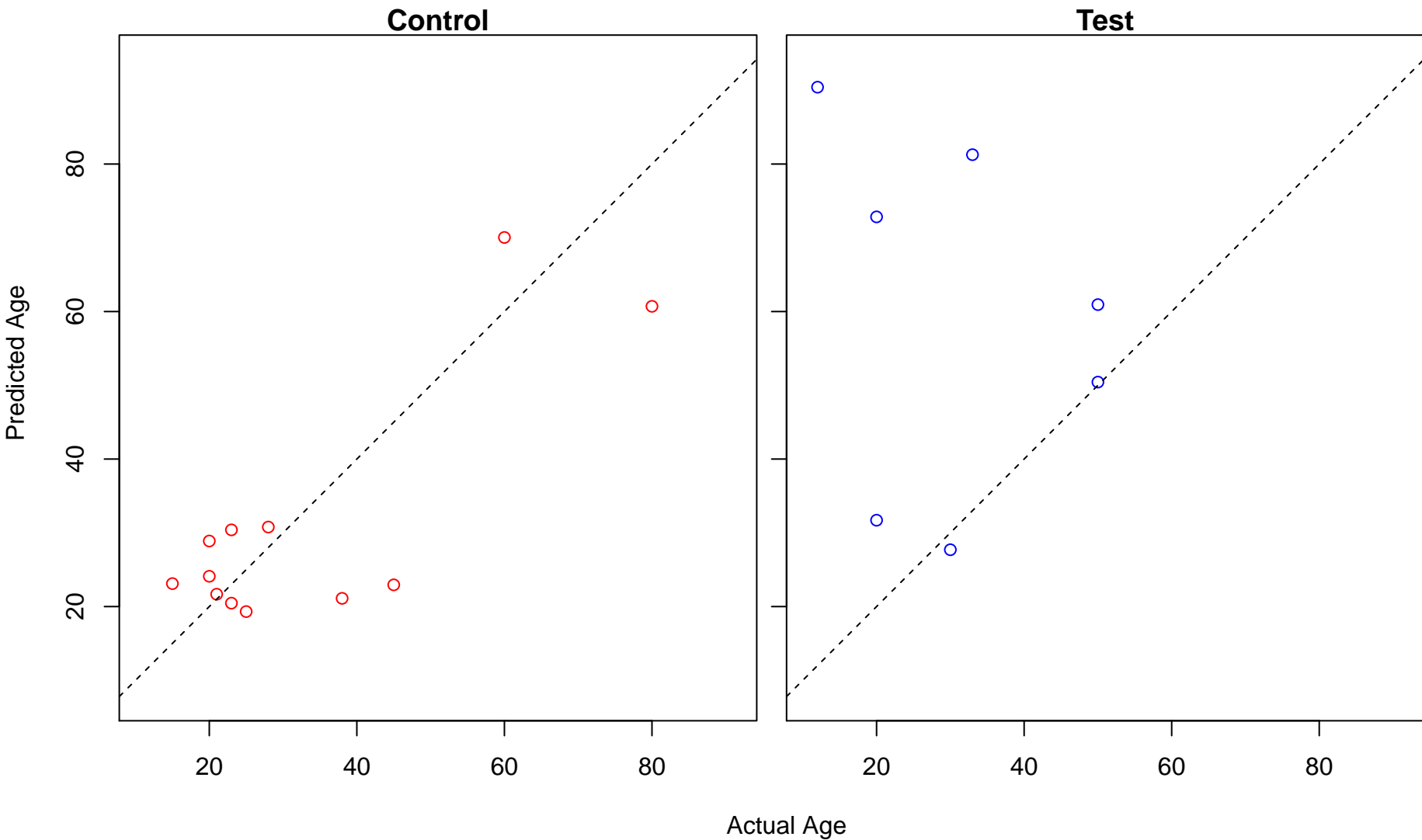
regulation of monocyte differentiation (Score: 29.737725)



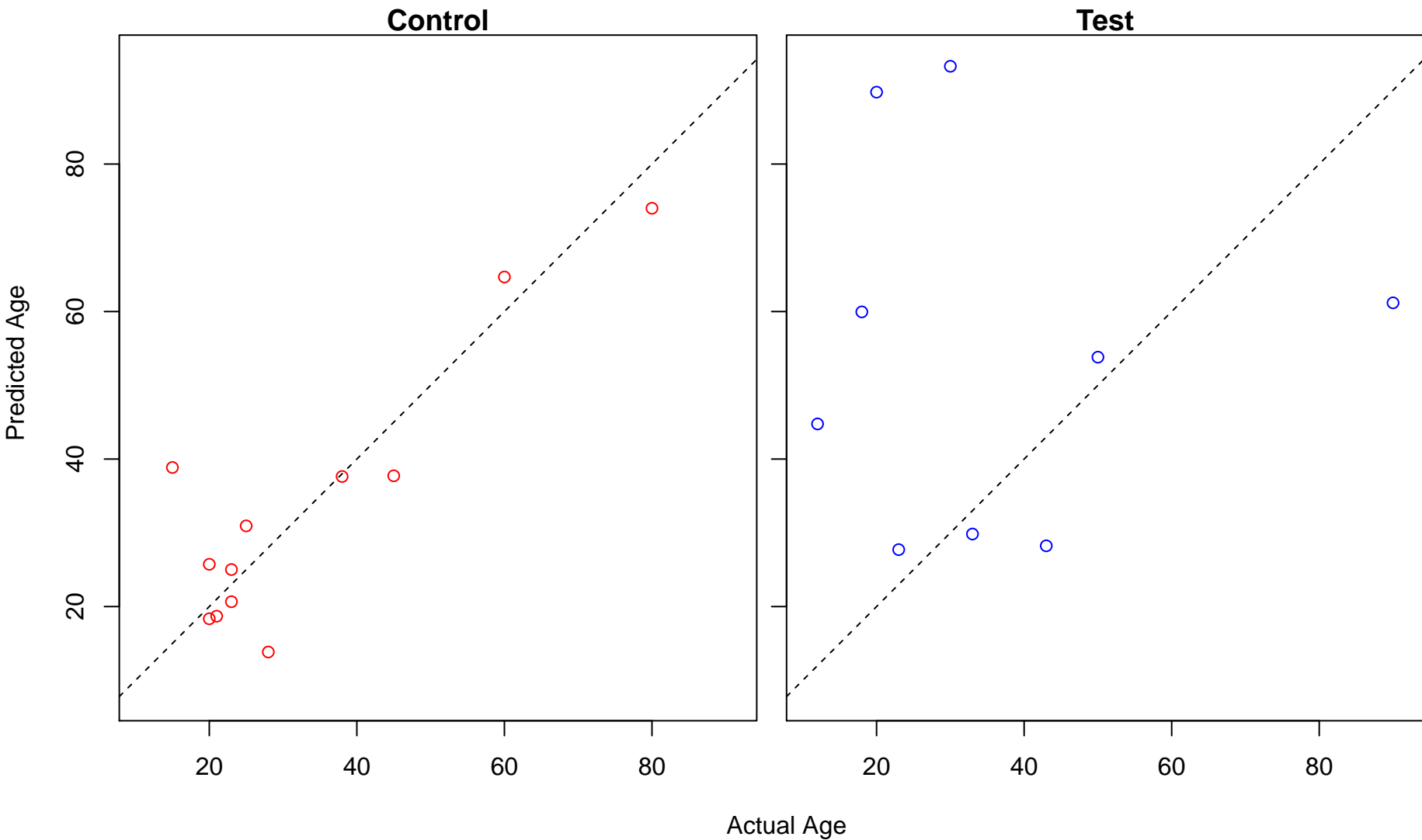
positive regulation of tyrosine phosphorylation of Stat3 protein (Score: 29.668310)



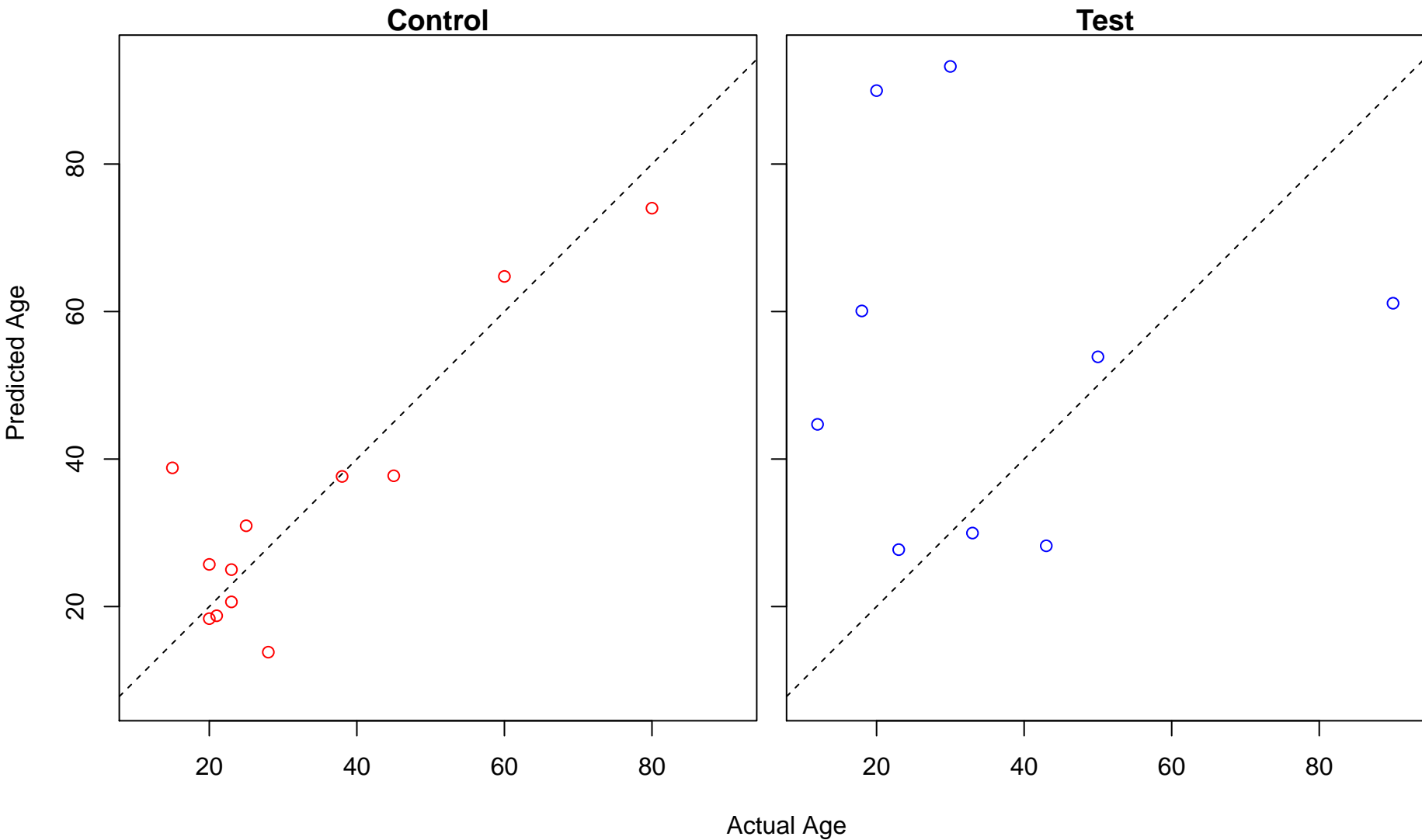
regulation of muscle adaptation (Score: 29.662656)



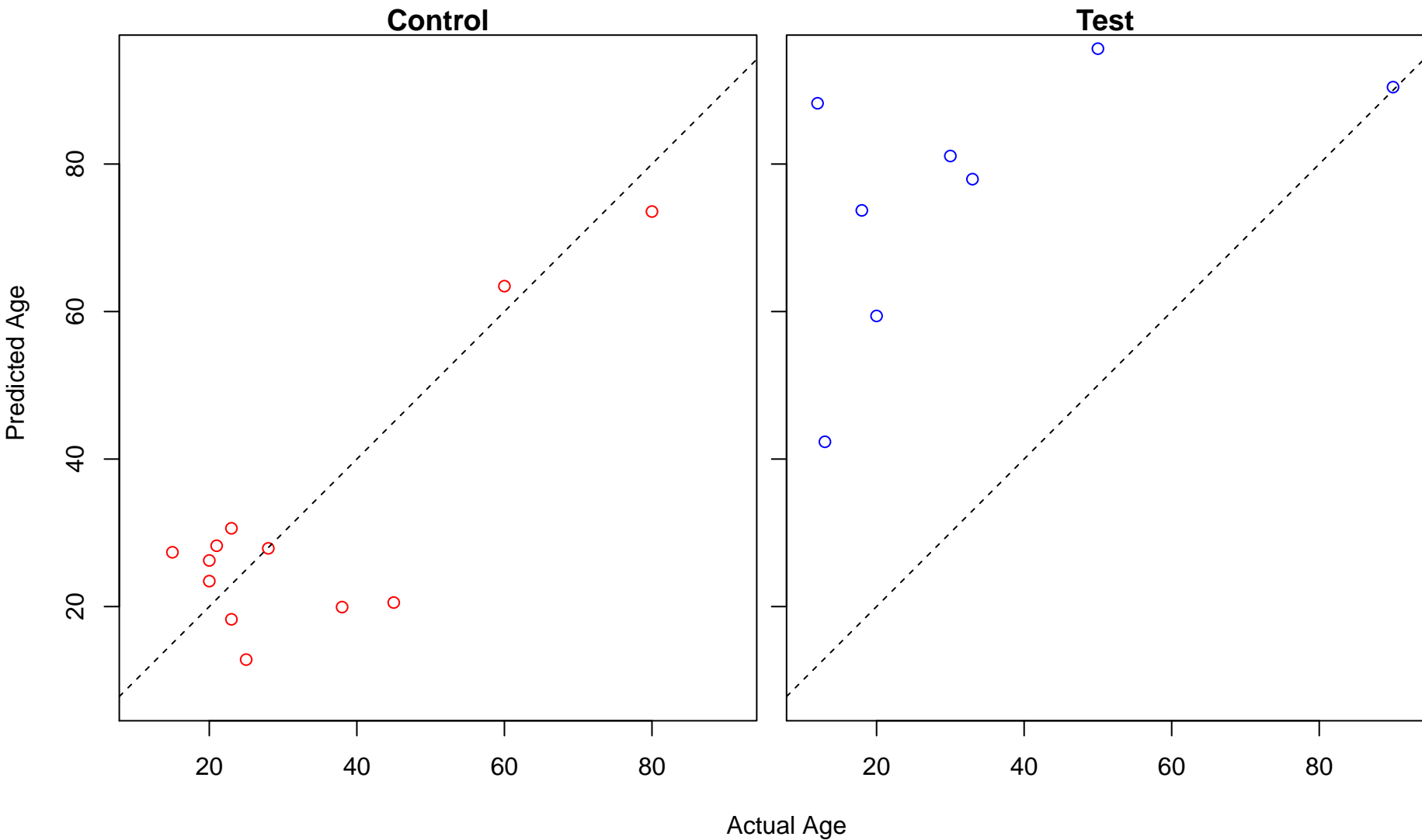
positive regulation of tumor necrosis factor superfamily cytokine production (Score: 29.655942)



positive regulation of tumor necrosis factor production (Score: 29.624146)

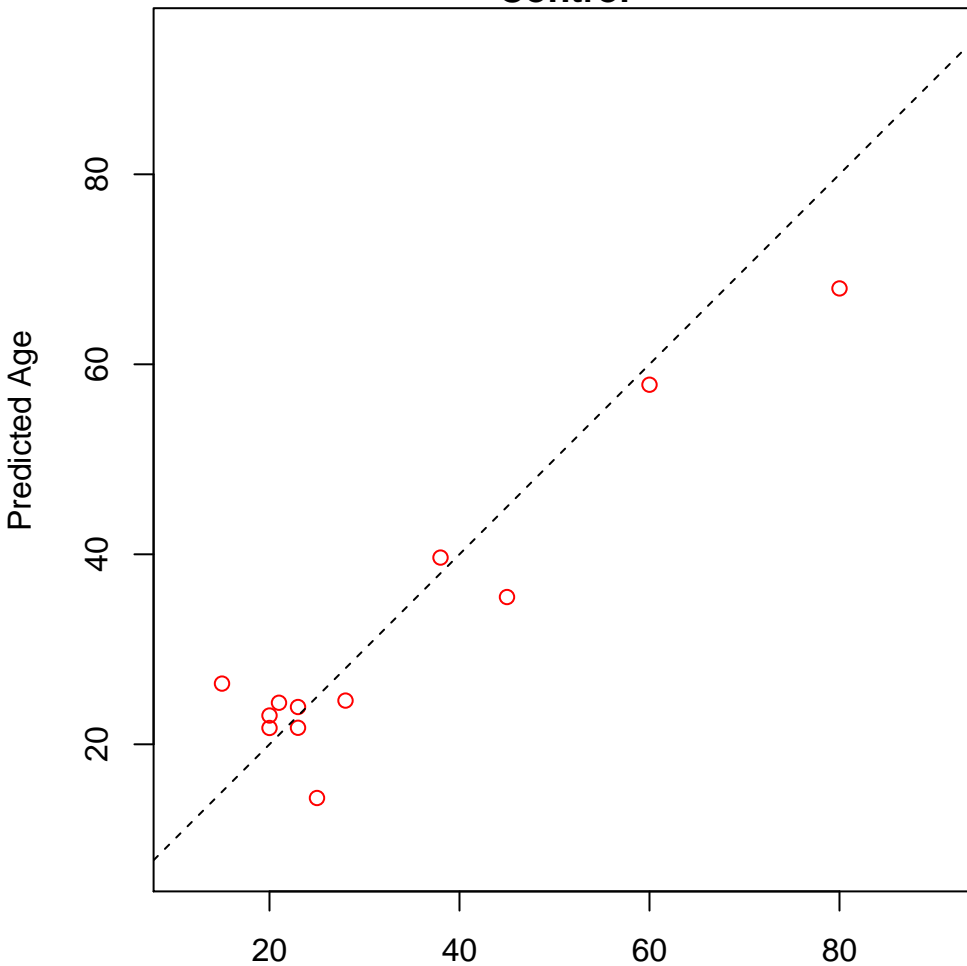


positive regulation of transcription factor import into nucleus (Score: 29.553198)

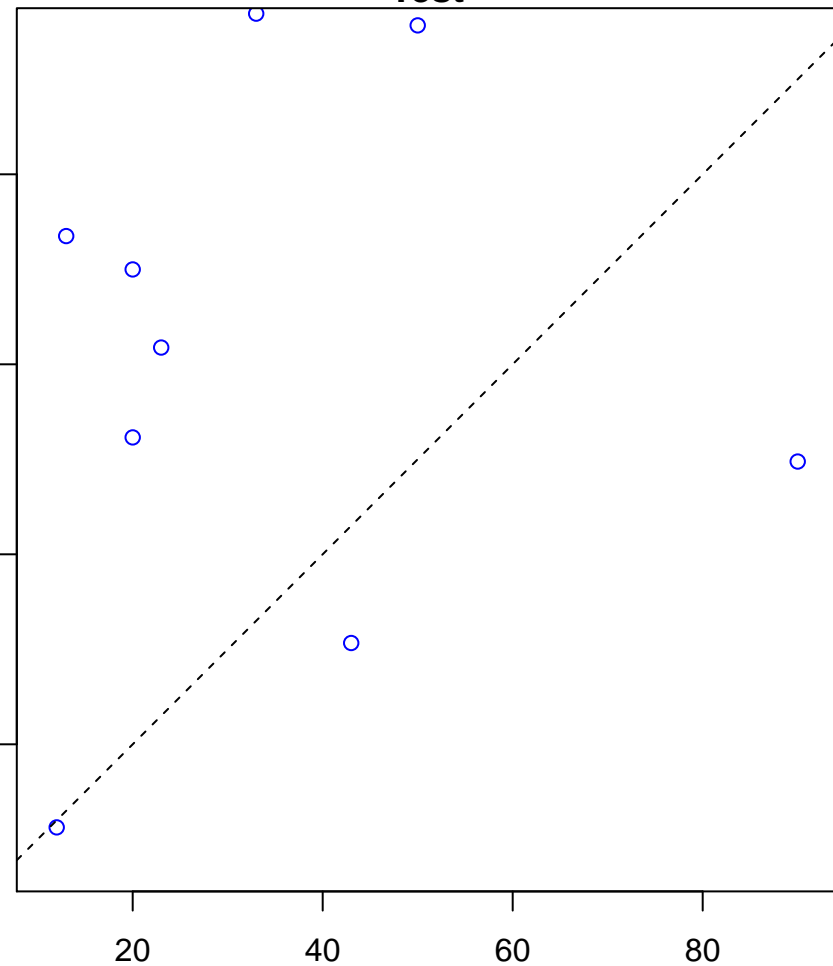


retina development in camera-type eye (Score: 29.519195)

Control

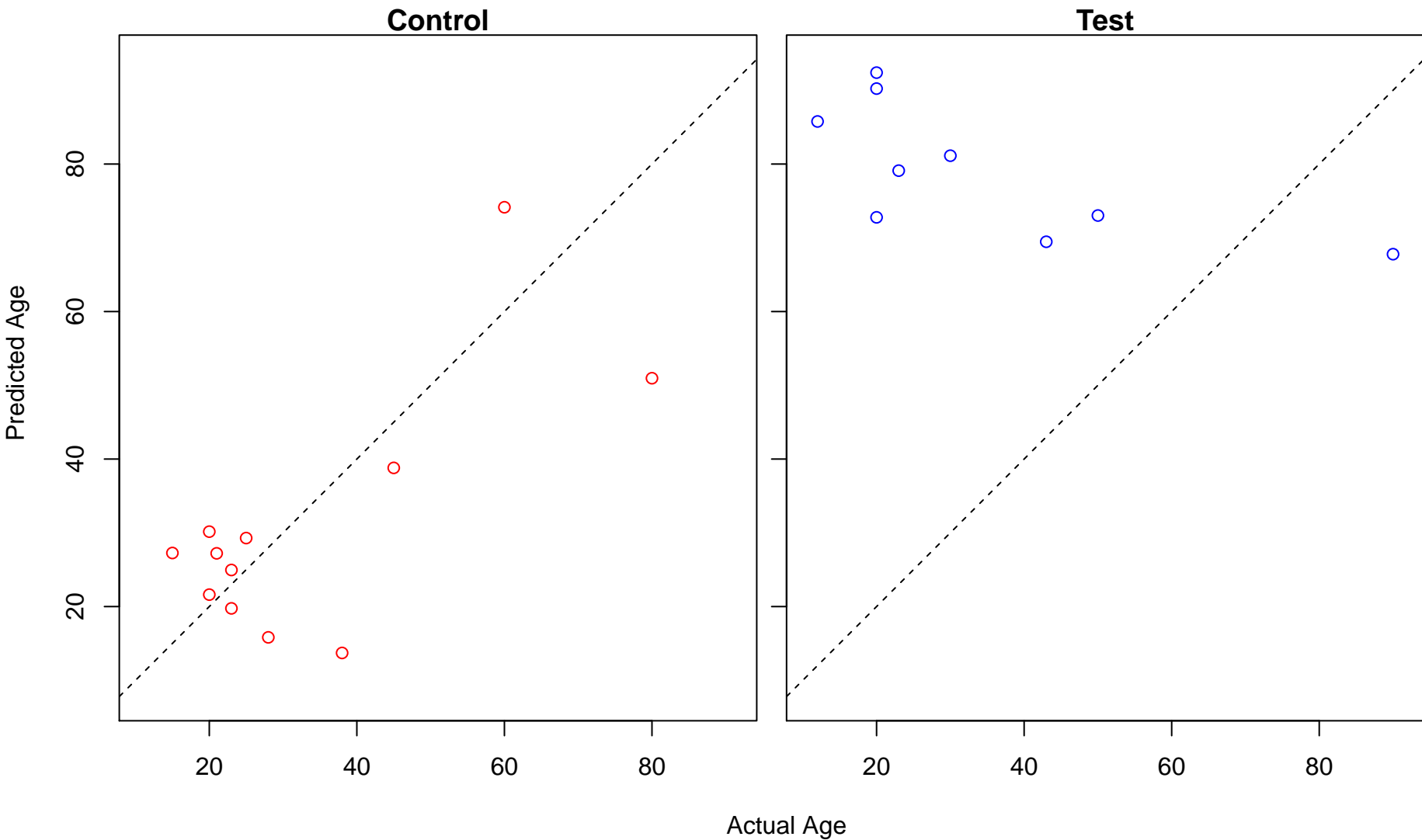


Test

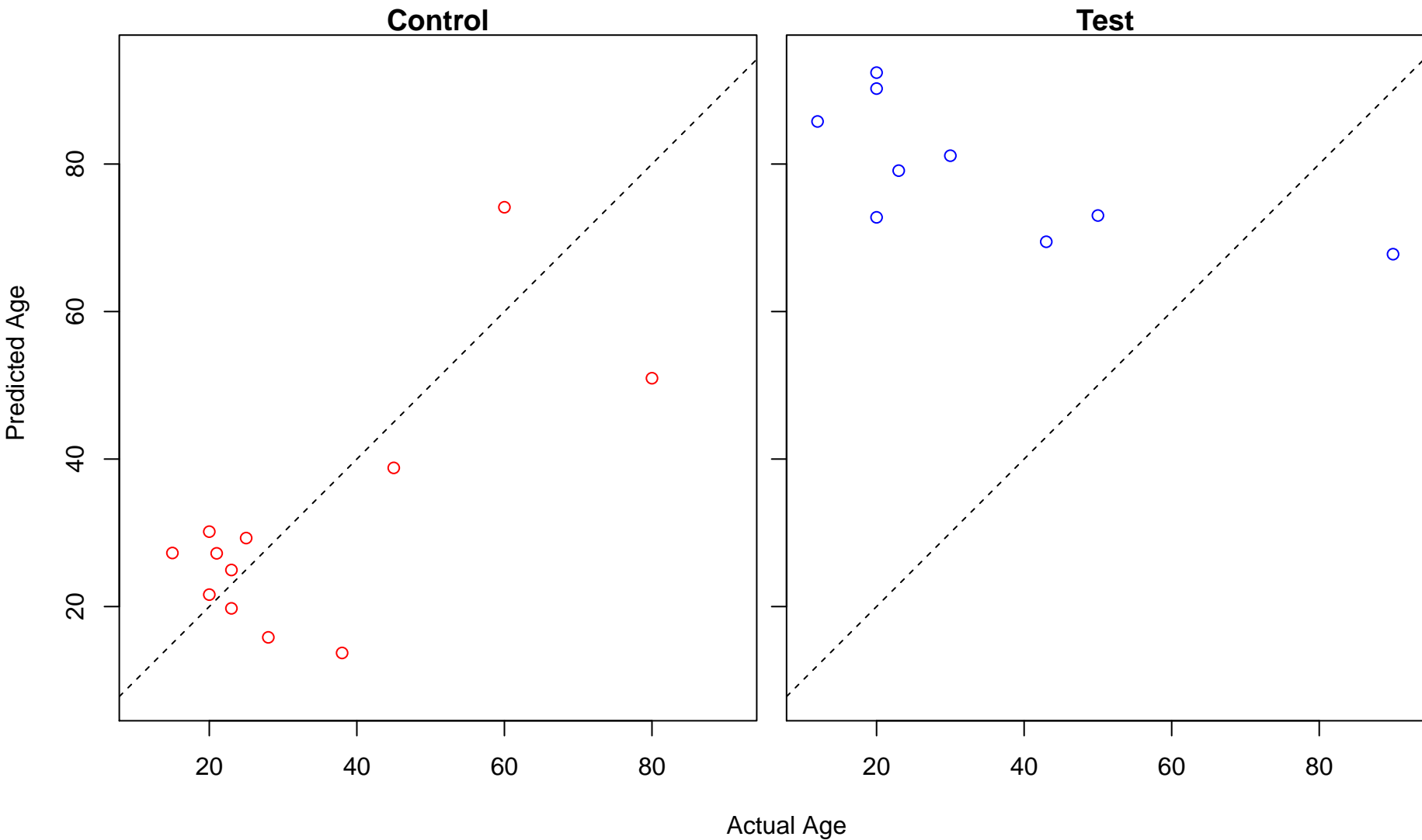


Actual Age

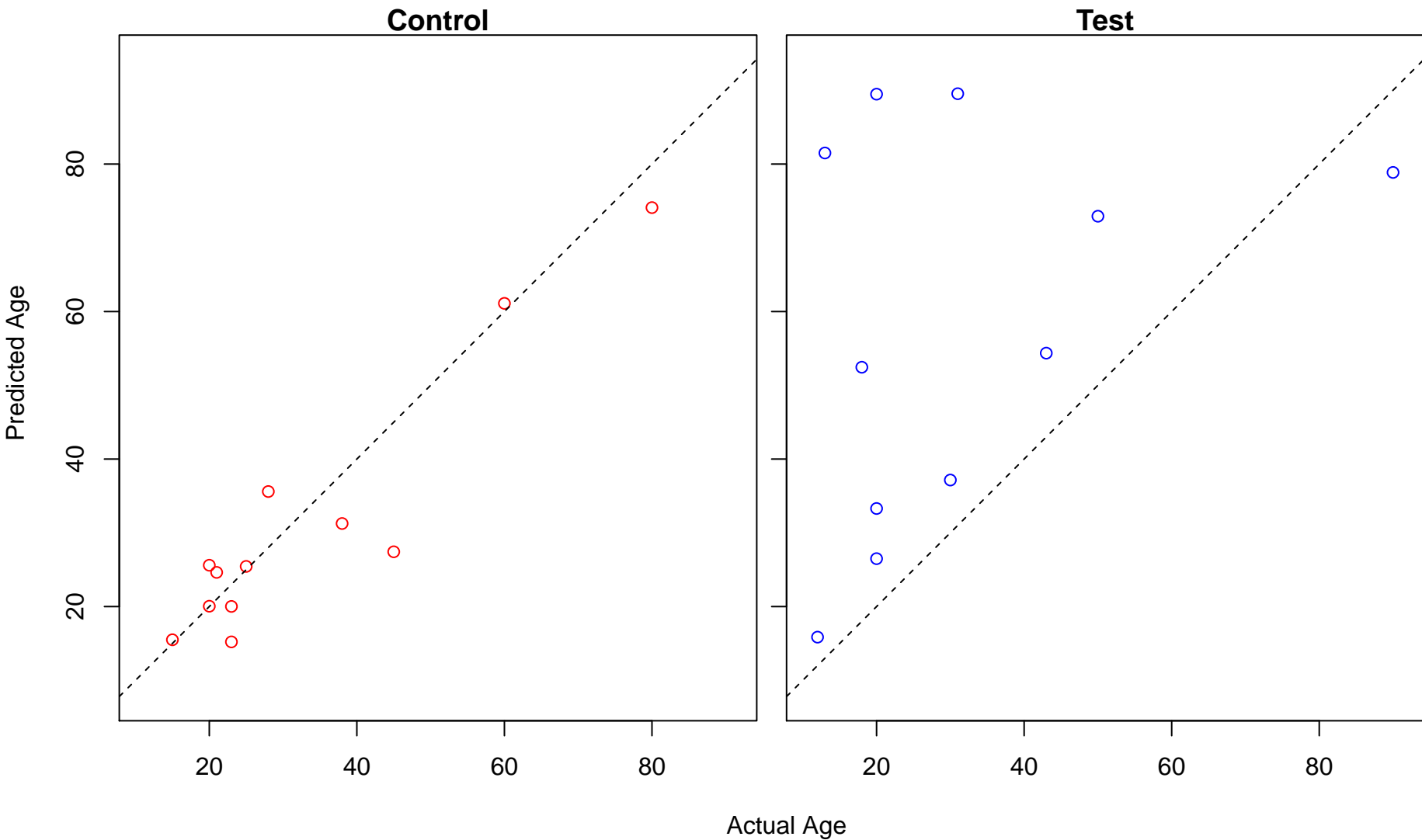
positive regulation of icosanoid secretion (Score: 29.382616)



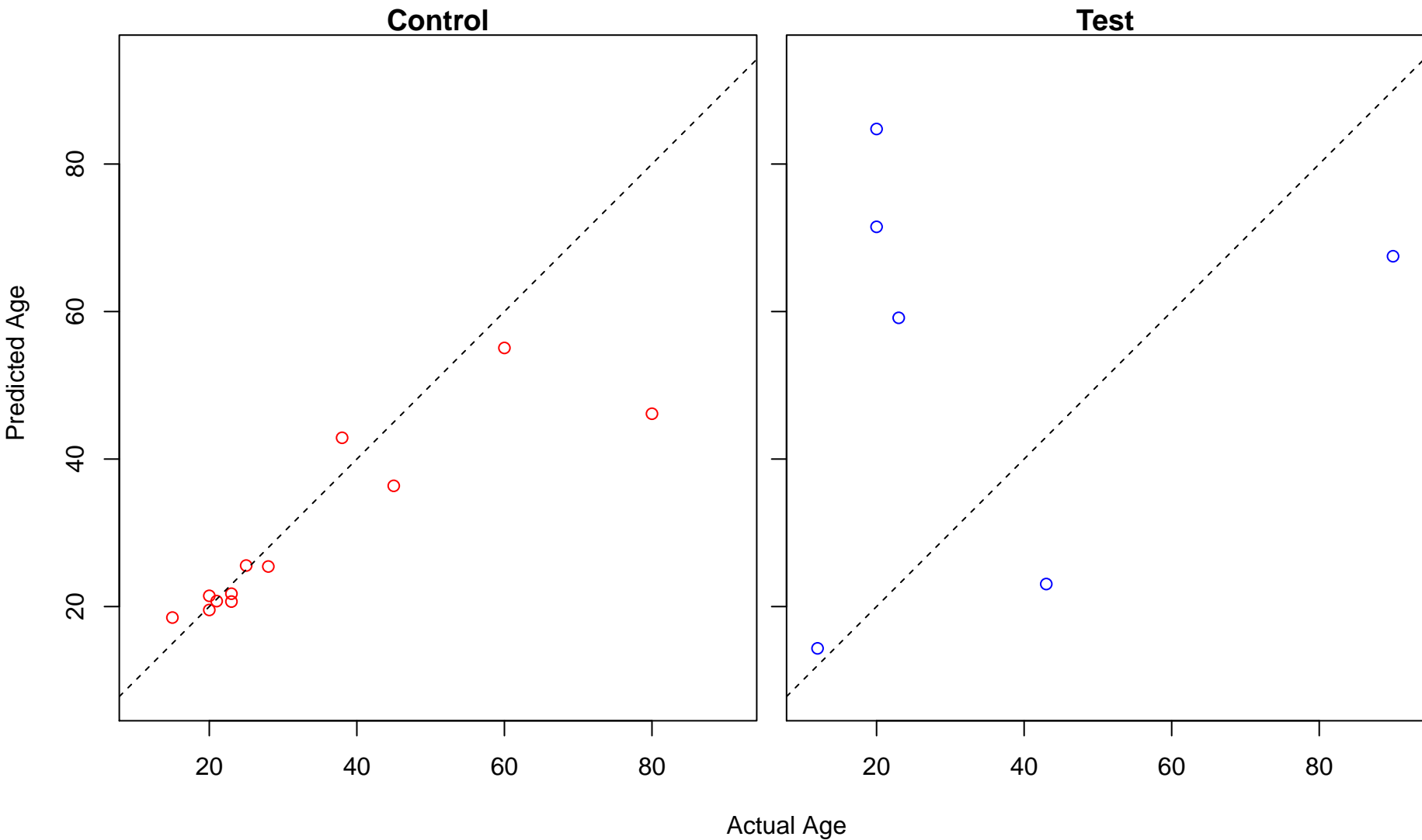
positive regulation of fatty acid transport (Score: 29.382616)



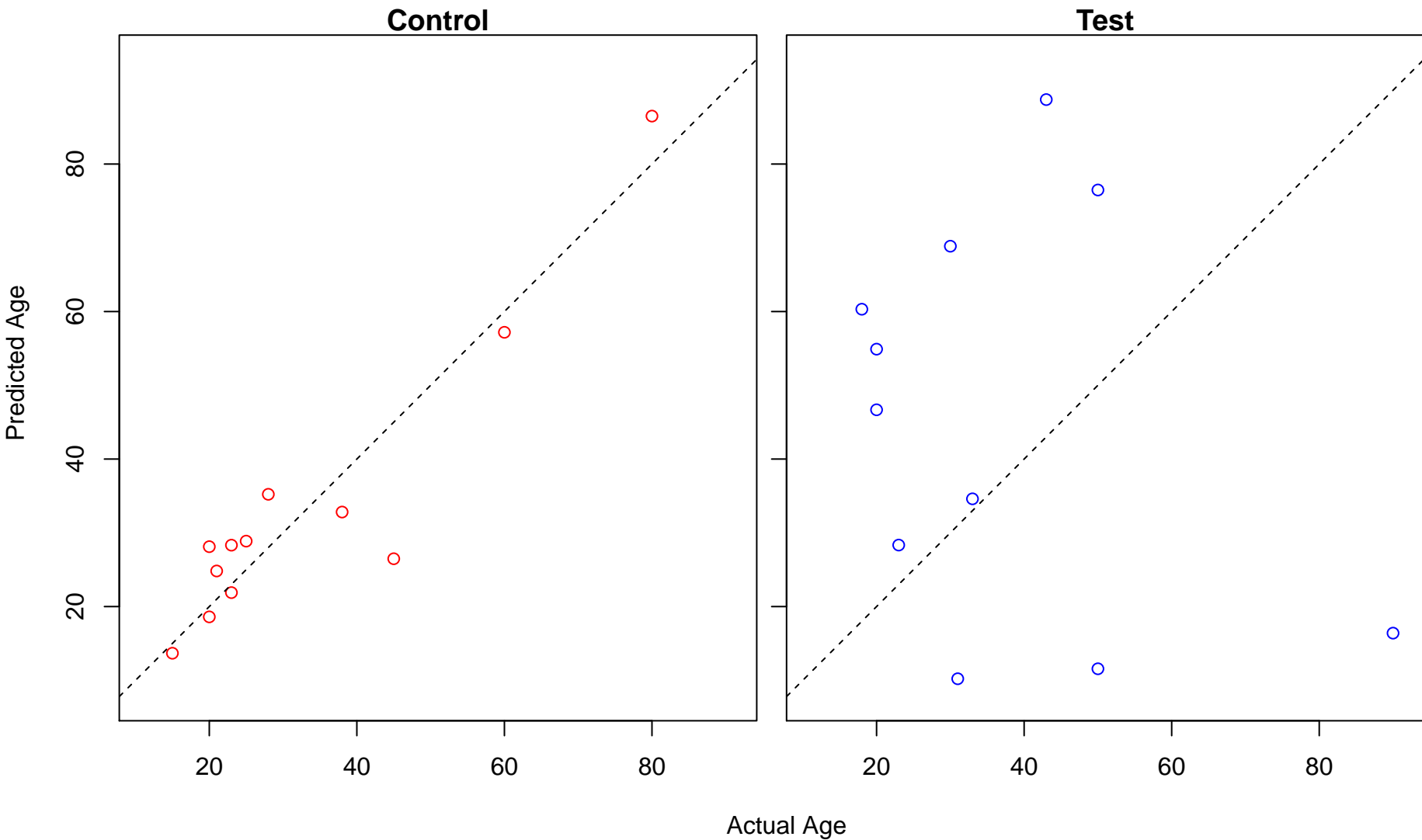
negative regulation of glucocorticoid receptor signaling pathway (Score: 29.346513)



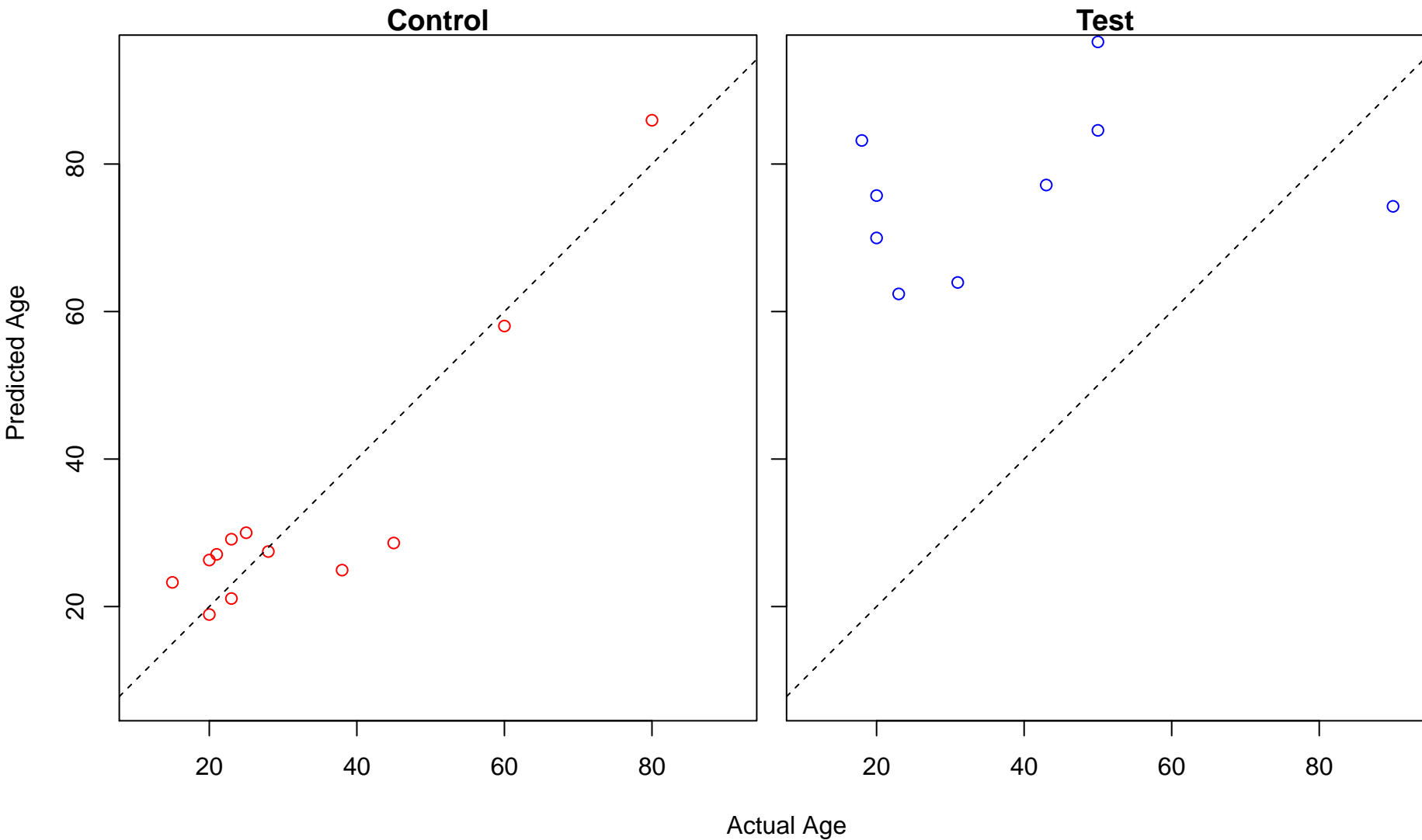
nitric oxide biosynthetic process (Score: 29.289053)



ammonium ion metabolic process (Score: 29.162767)

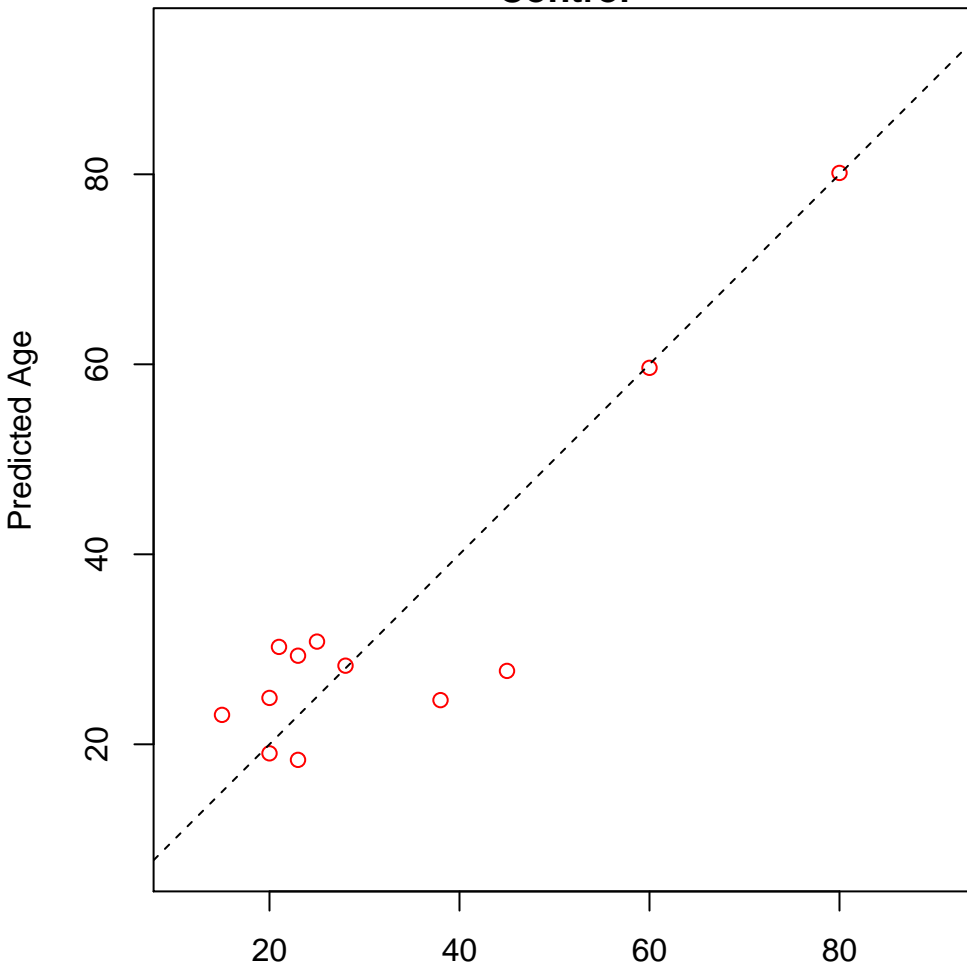


placenta blood vessel development (Score: 29.116869)

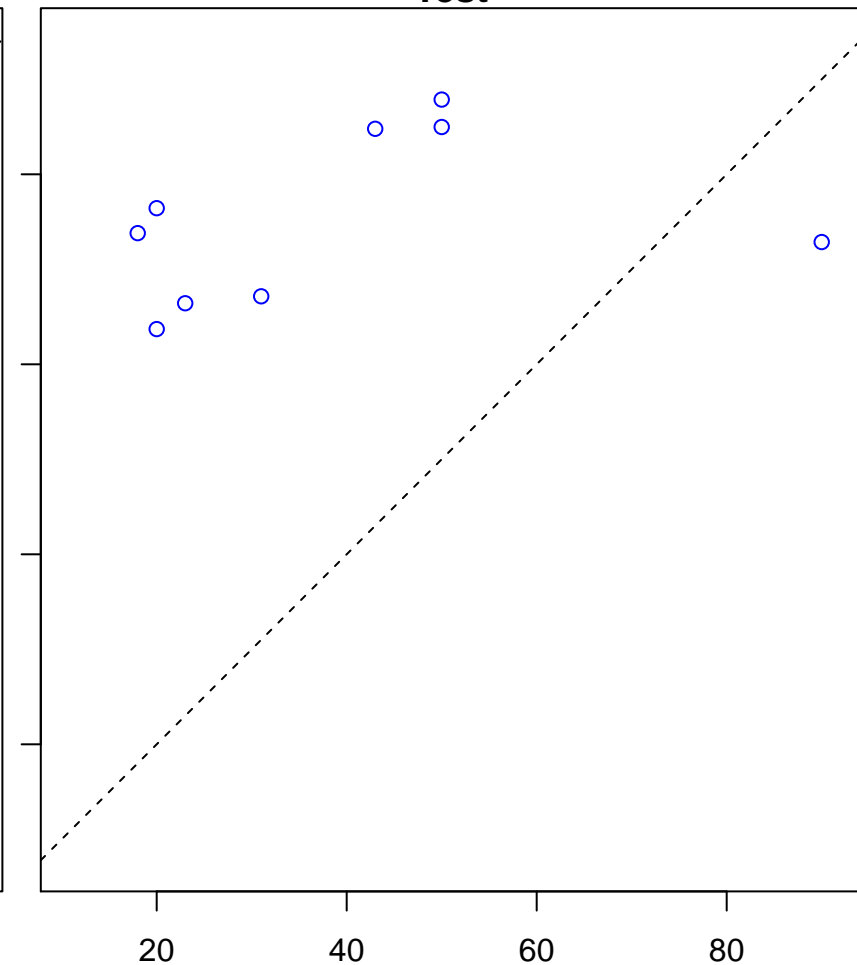


endocardial cushion morphogenesis (Score: 29.024772)

Control

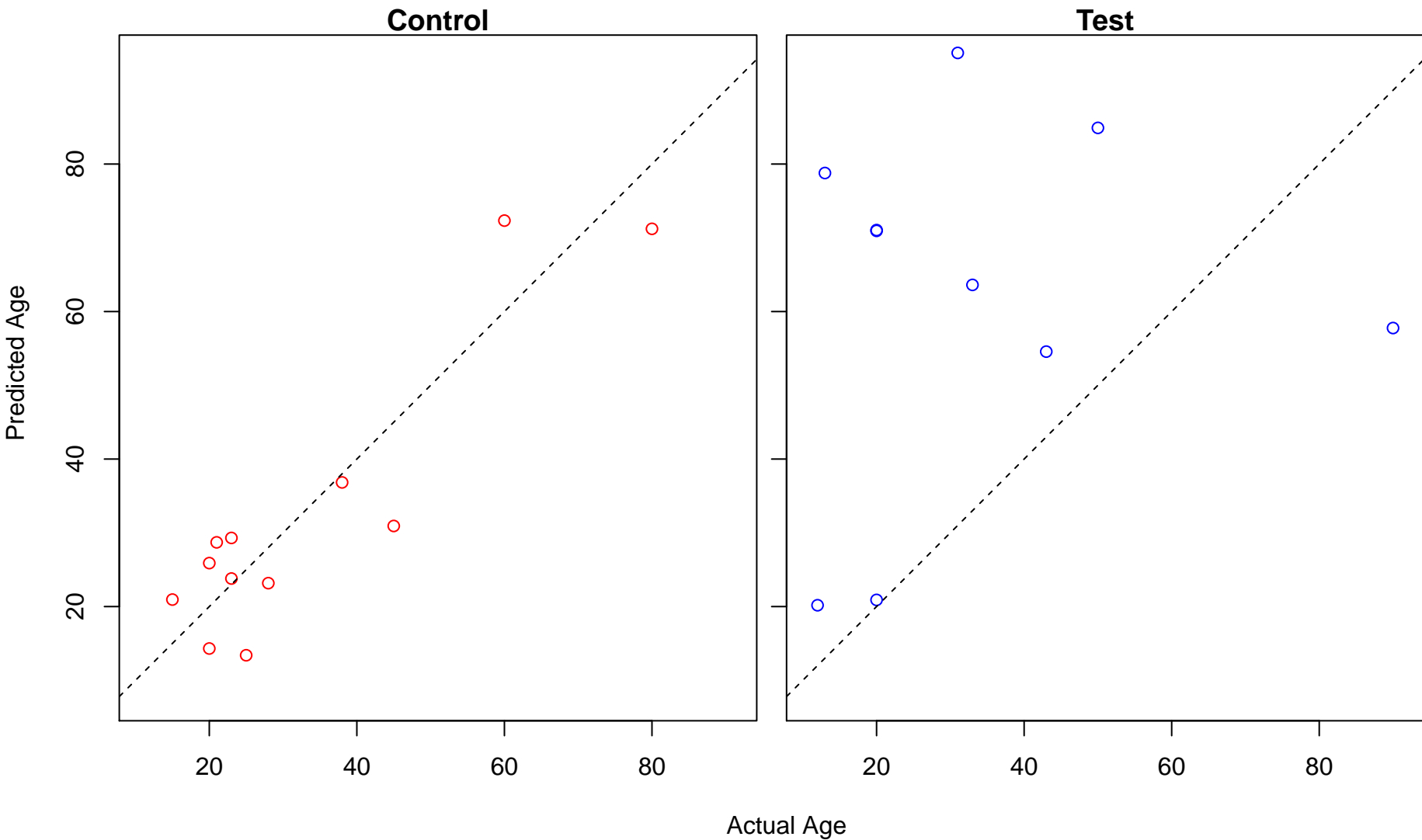


Test

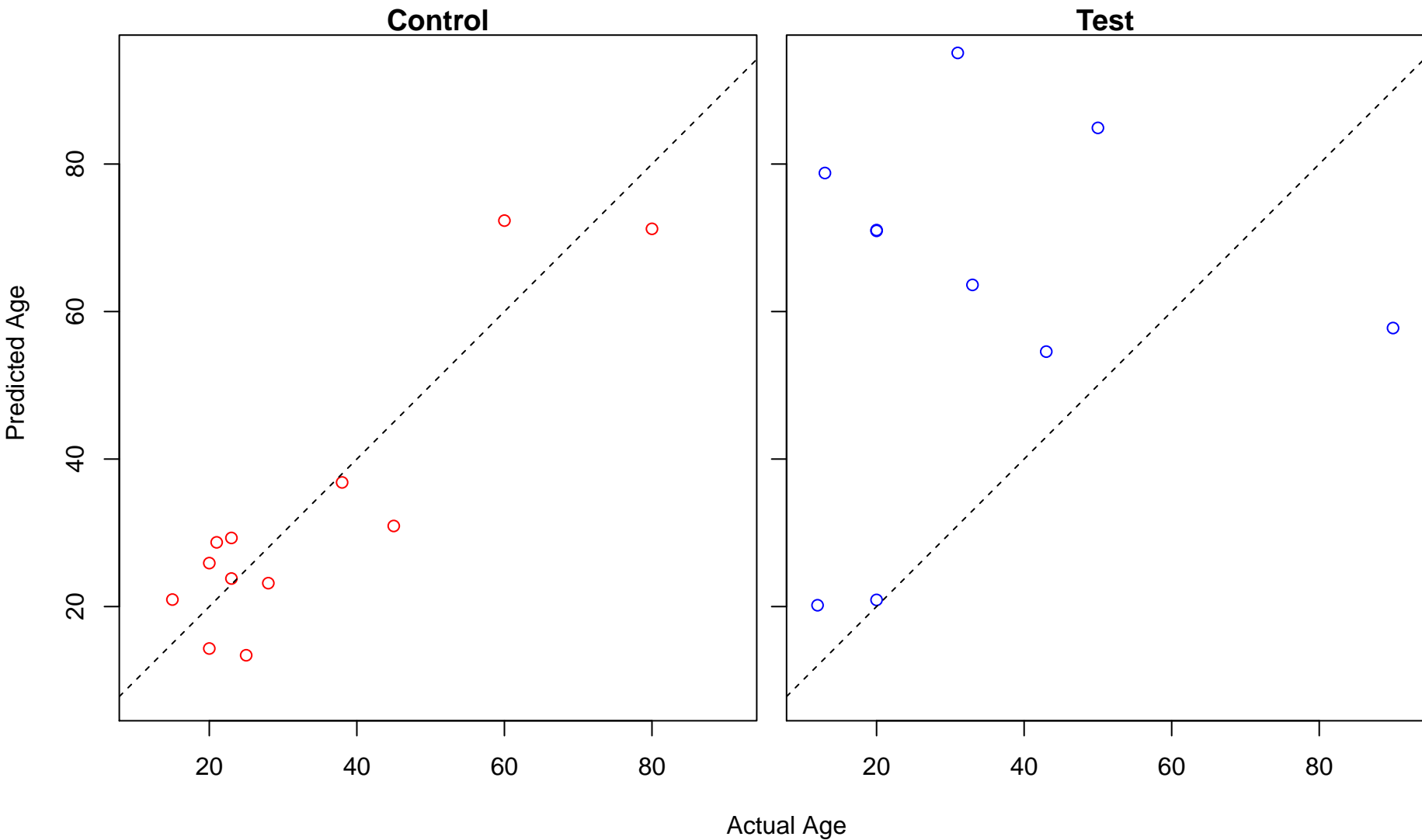


Actual Age

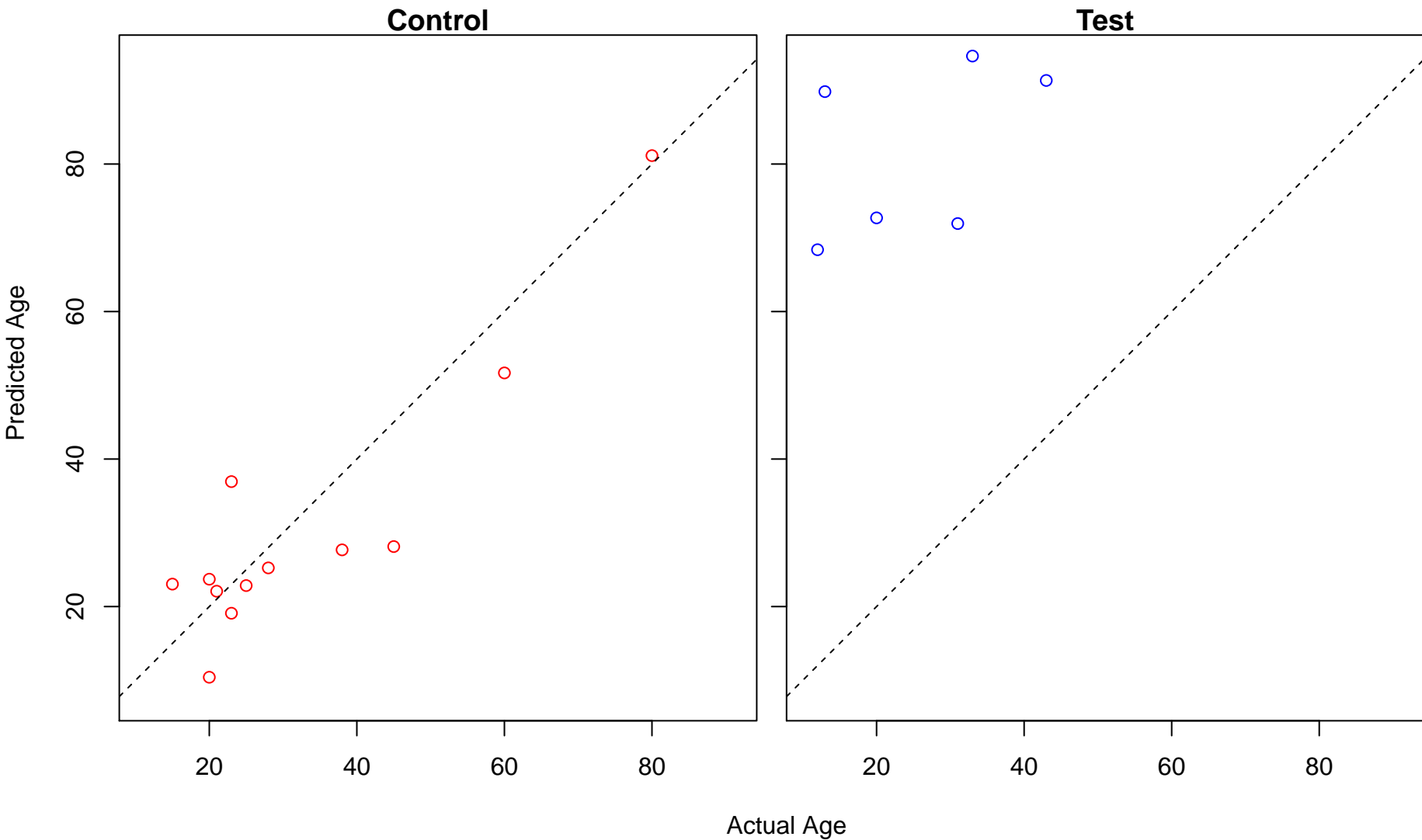
lymphocyte costimulation (Score: 28.849635)



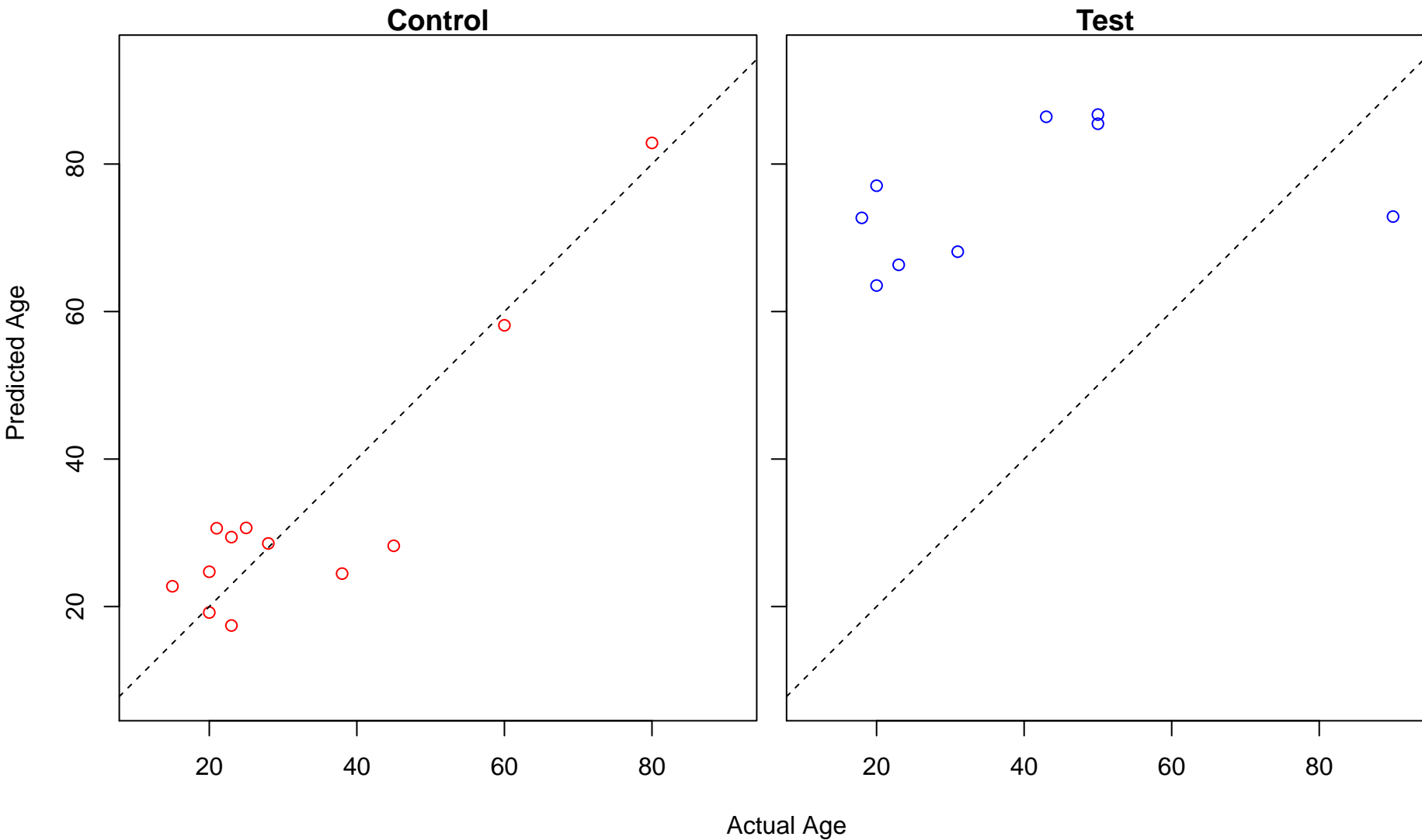
T cell costimulation (Score: 28.849635)



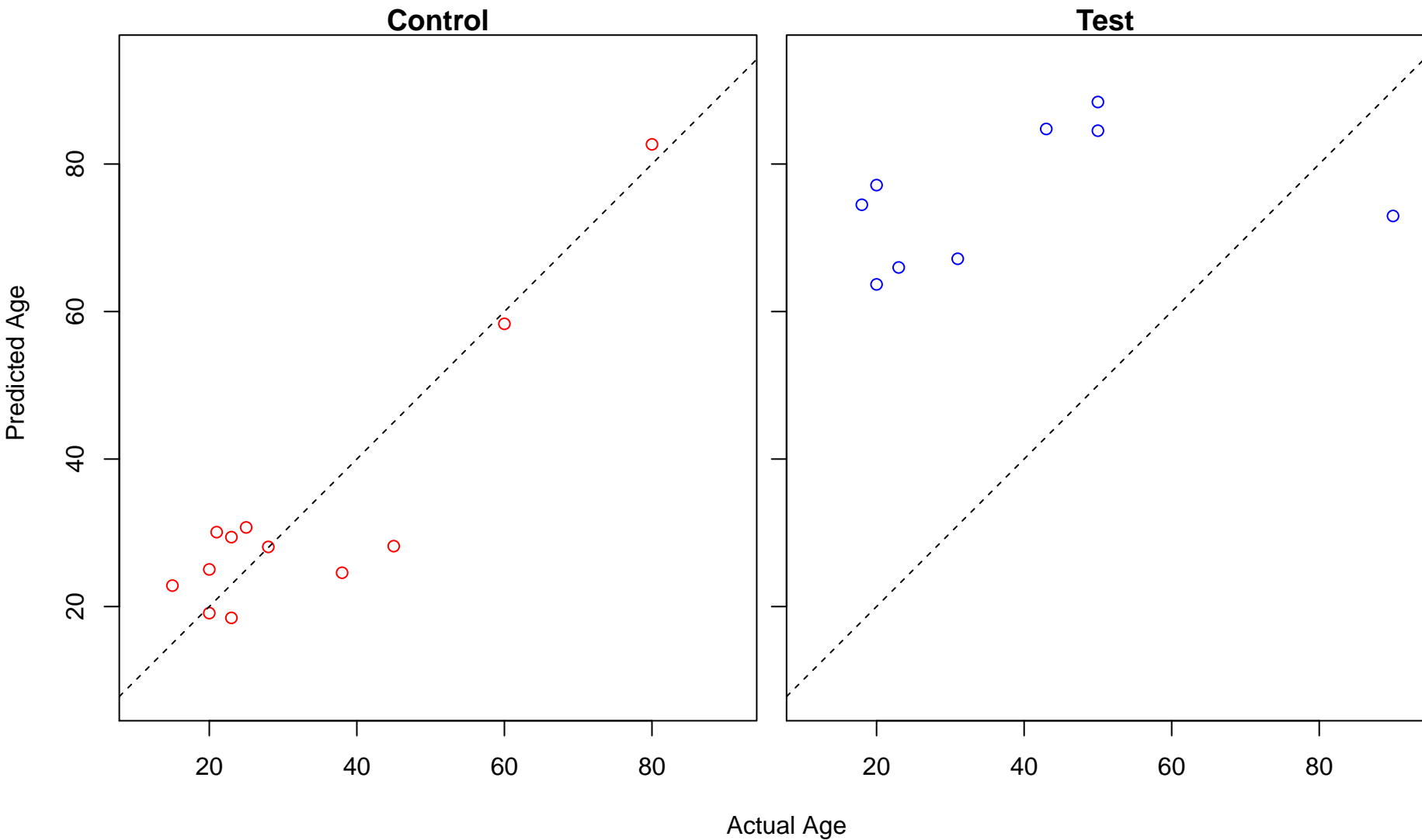
regulation of receptor internalization (Score: 28.846872)



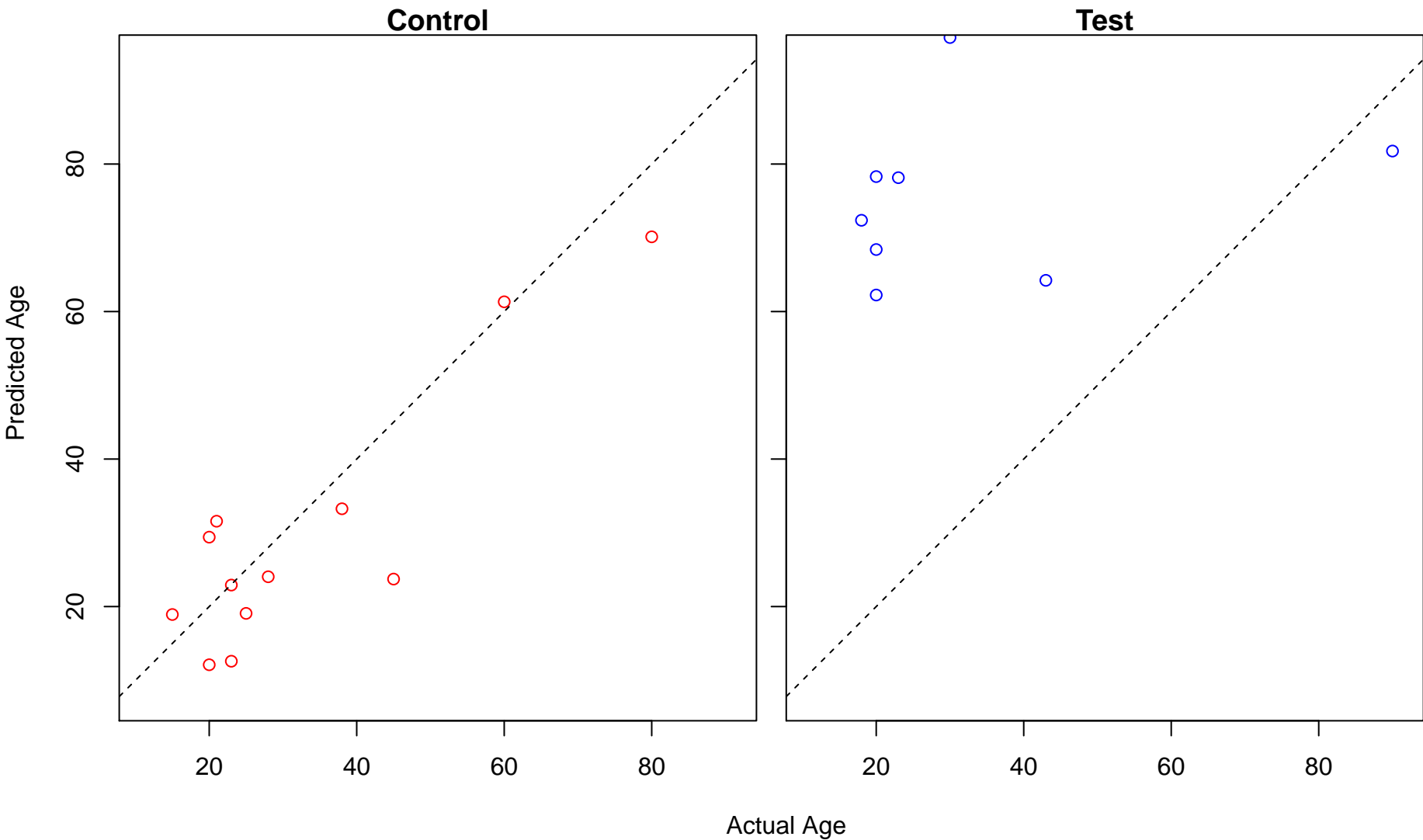
epithelial to mesenchymal transition involved in endocardial cushion formation (Score: 28.833583)



endocardial cushion formation (Score: 28.824671)

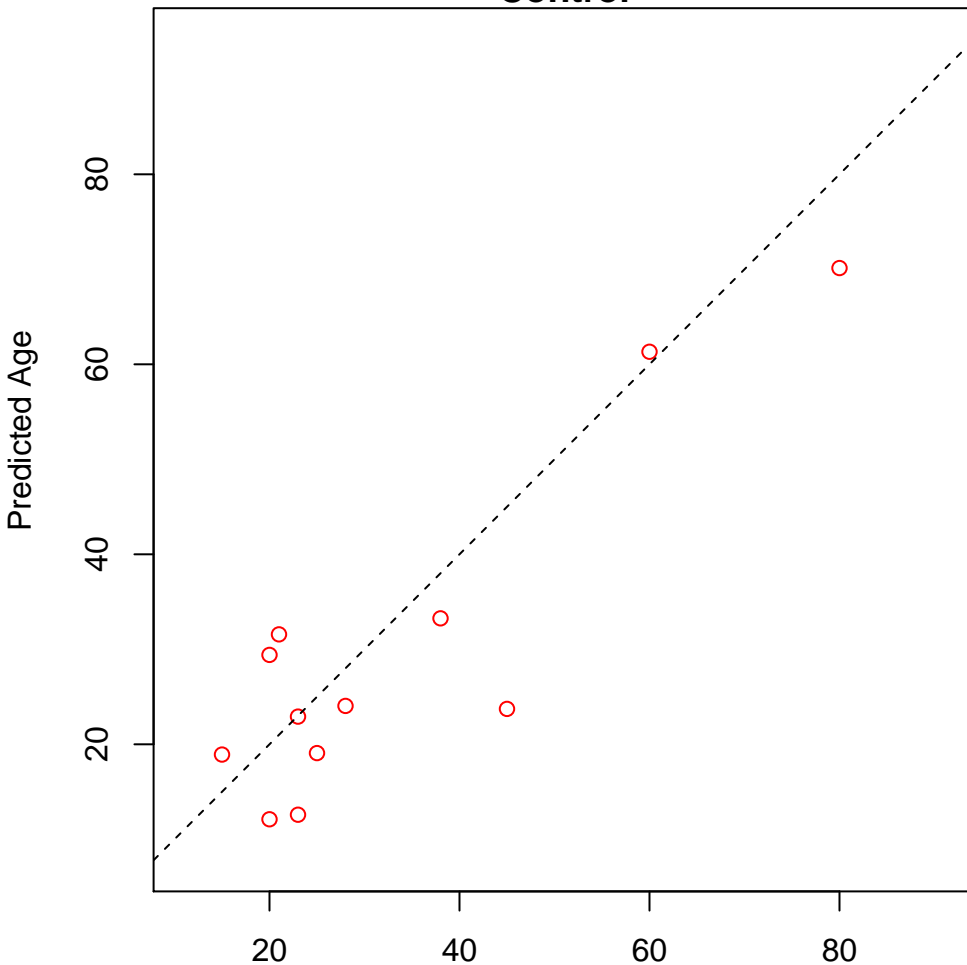


immune response–regulating cell surface receptor signaling pathway involved in phagocytosis (Score: 28

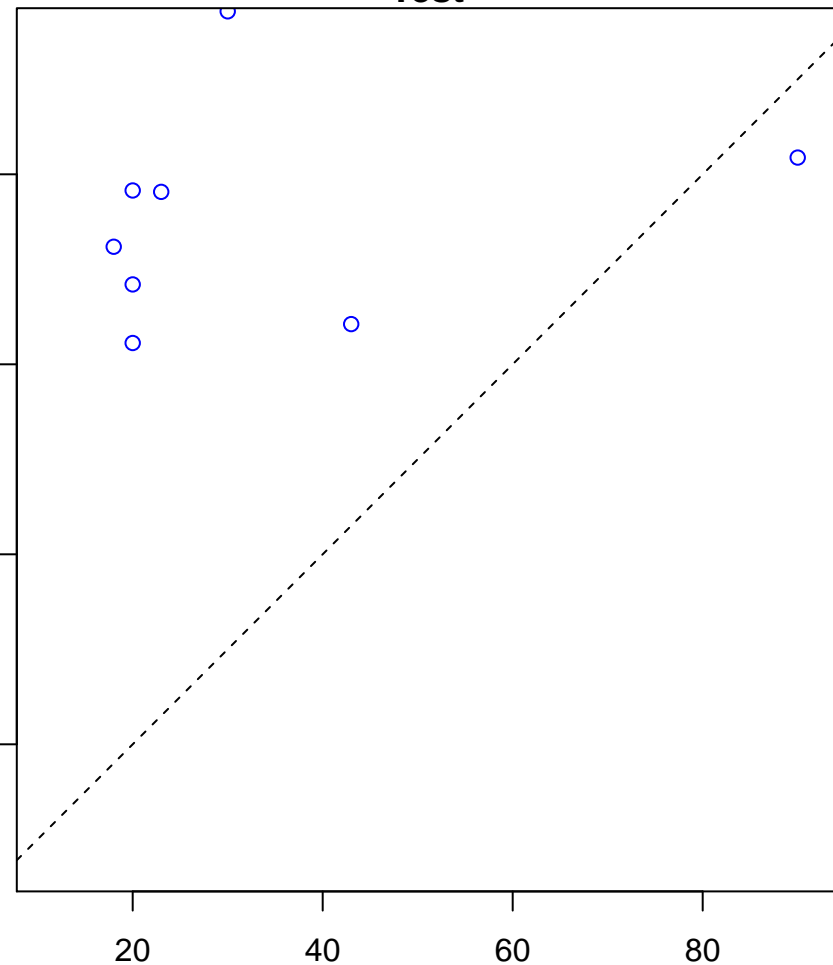


Fc-gamma receptor signaling pathway (Score: 28.811387)

Control

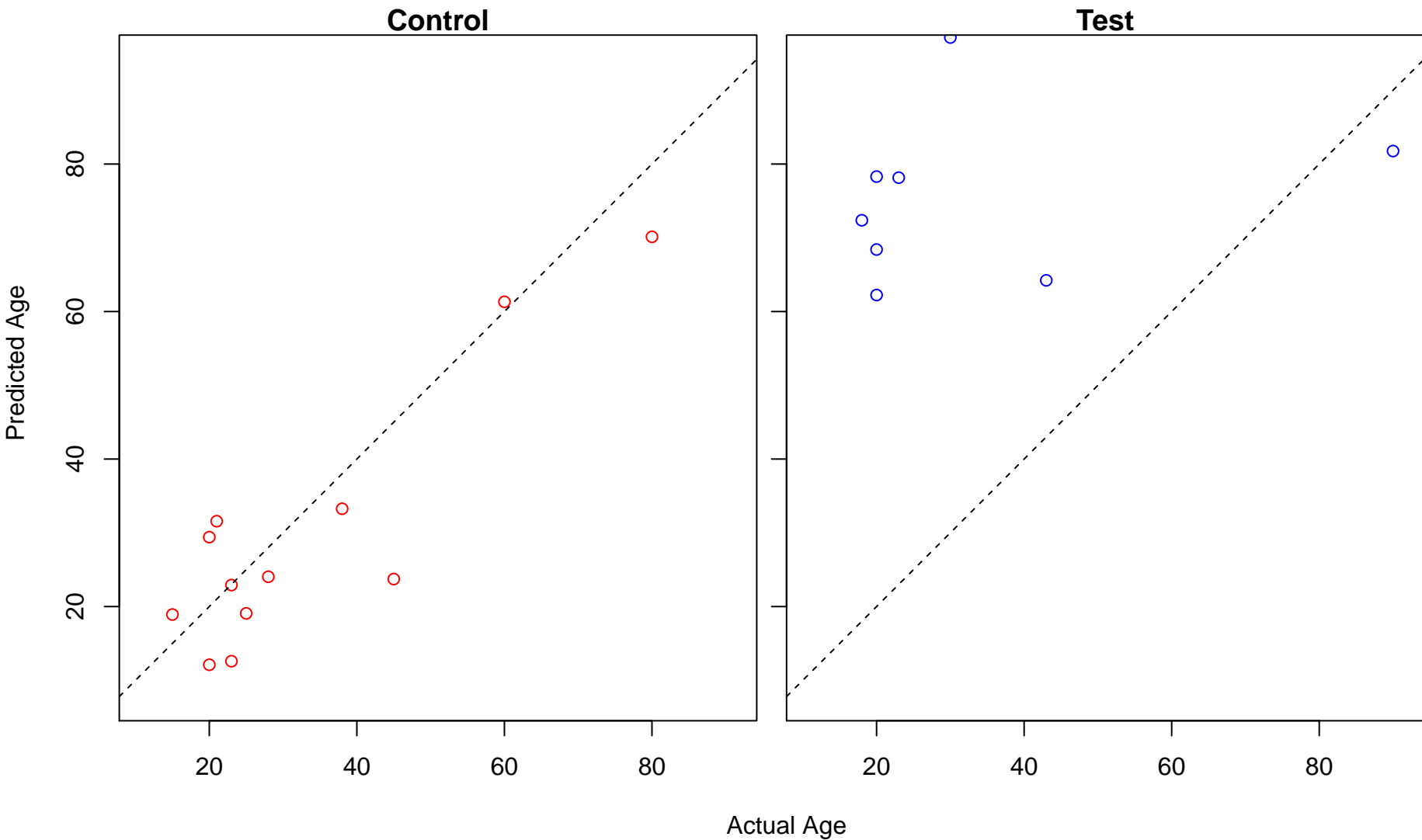


Test

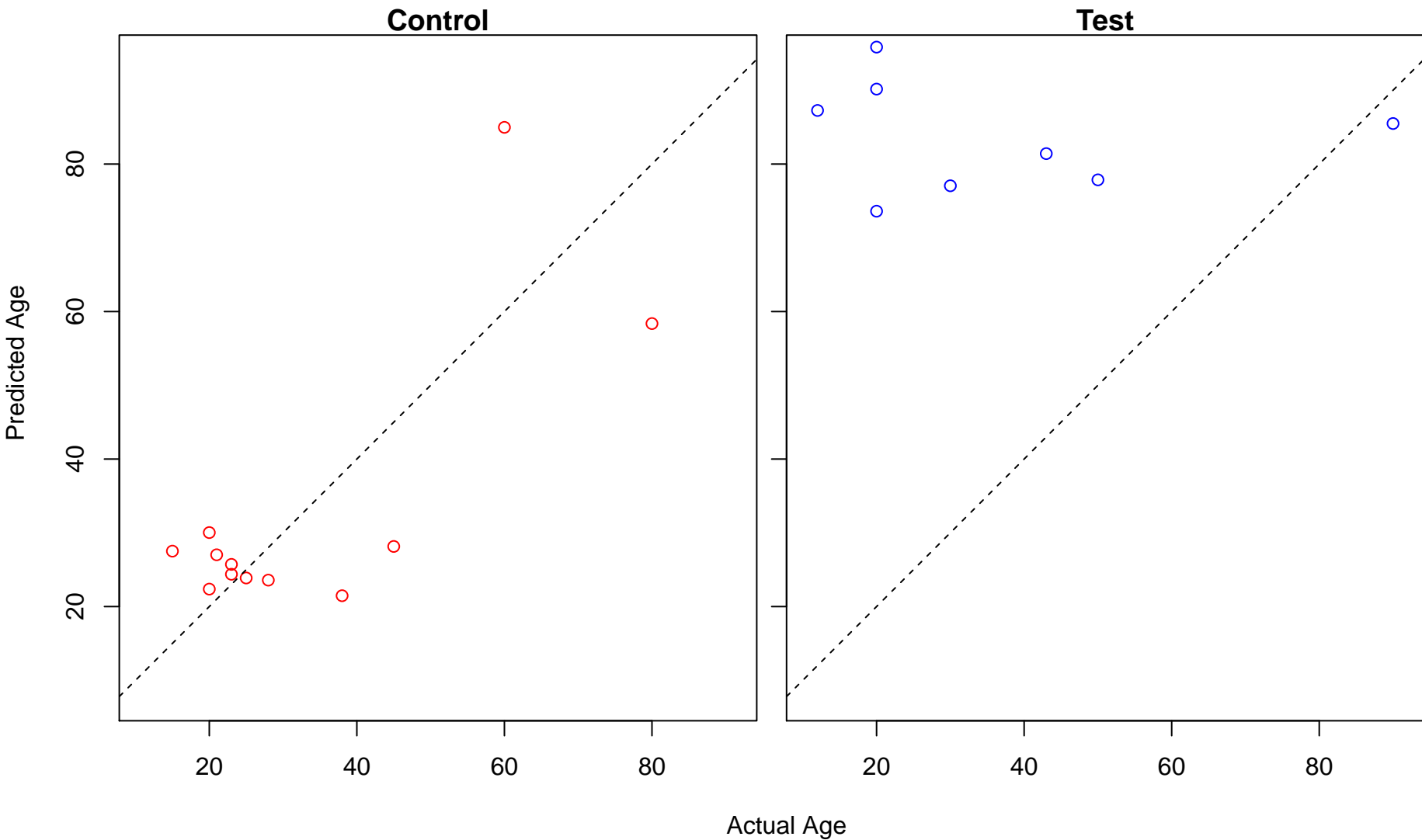


Actual Age

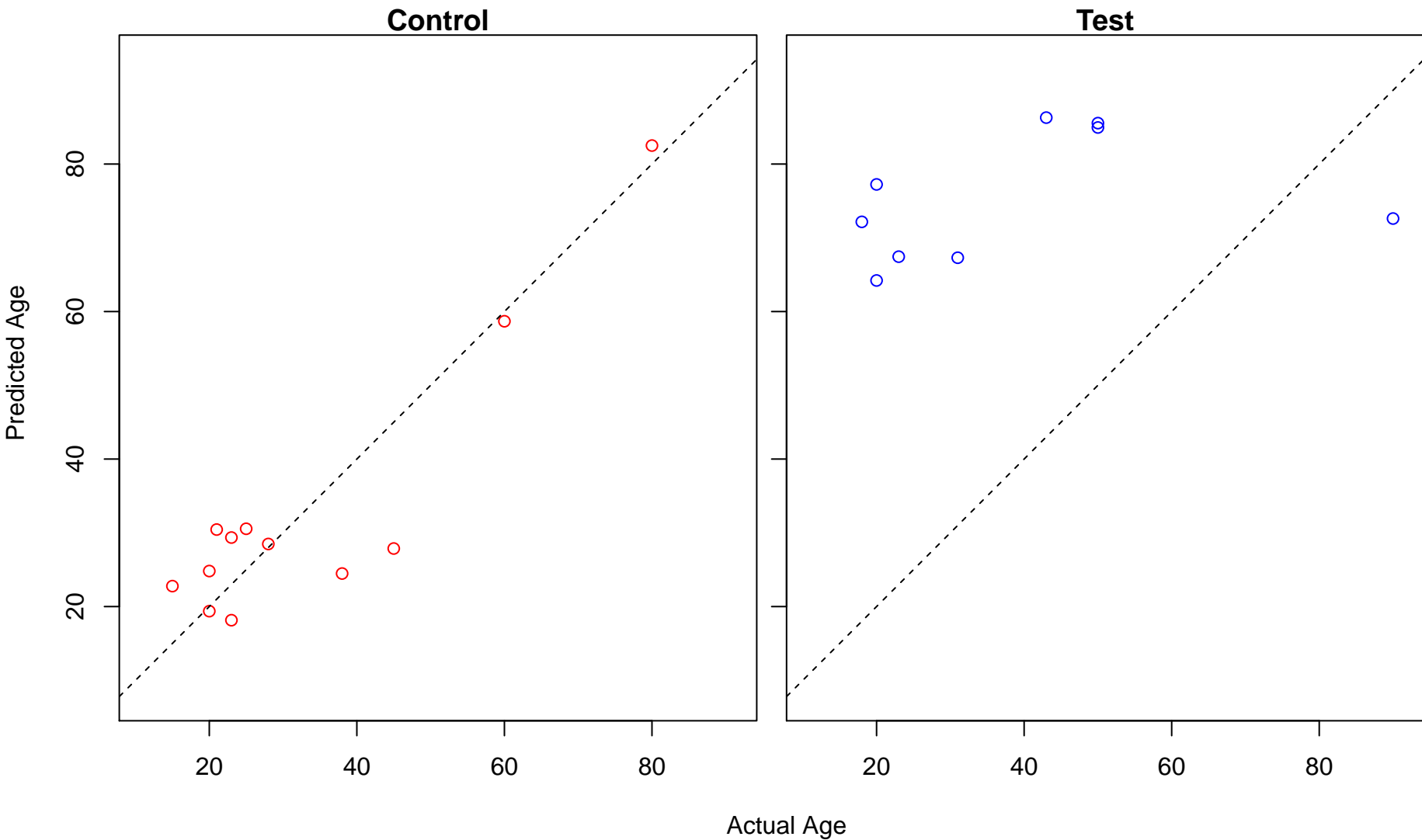
Fc-gamma receptor signaling pathway involved in phagocytosis (Score: 28.811387)



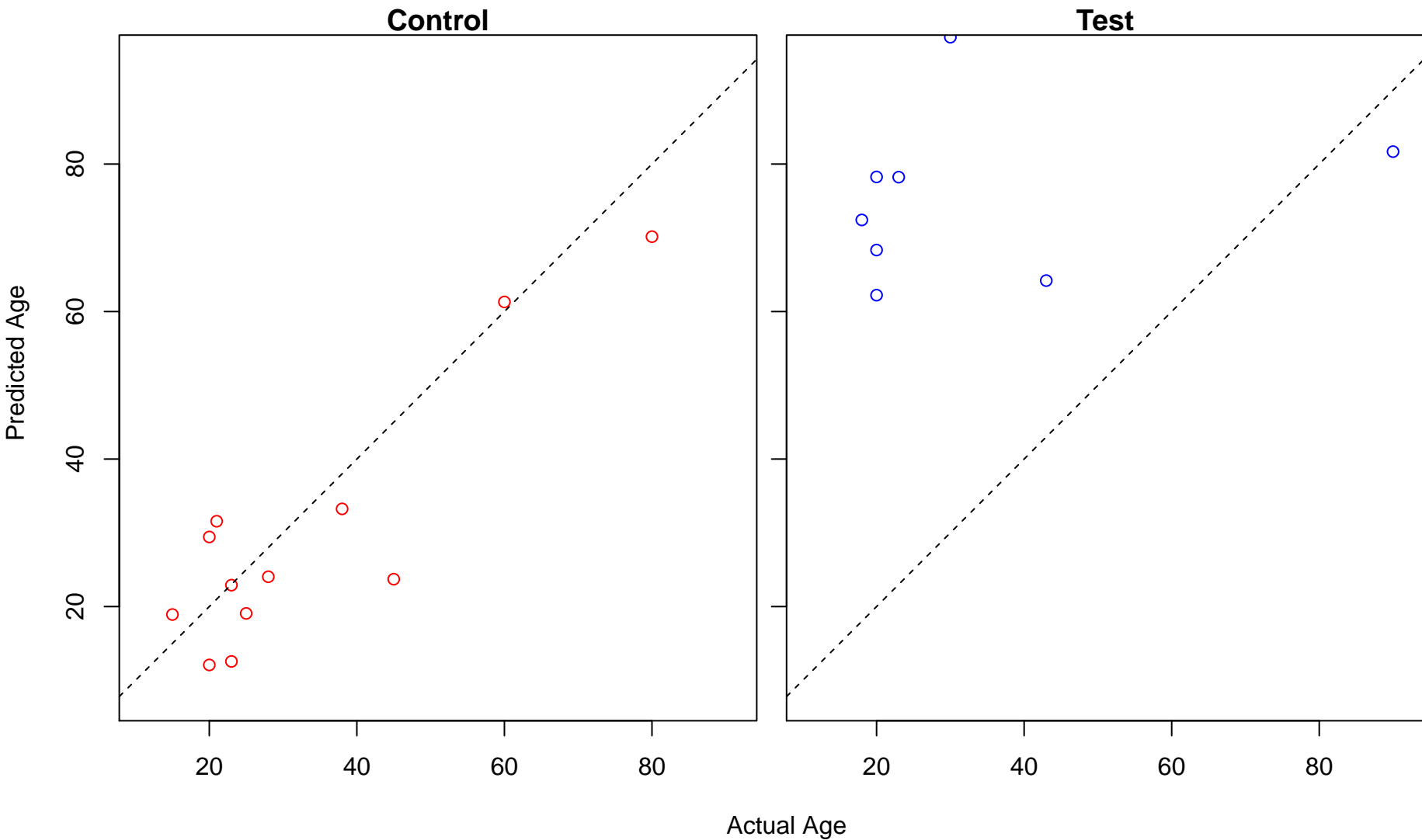
hyaluronan biosynthetic process (Score: 28.805045)



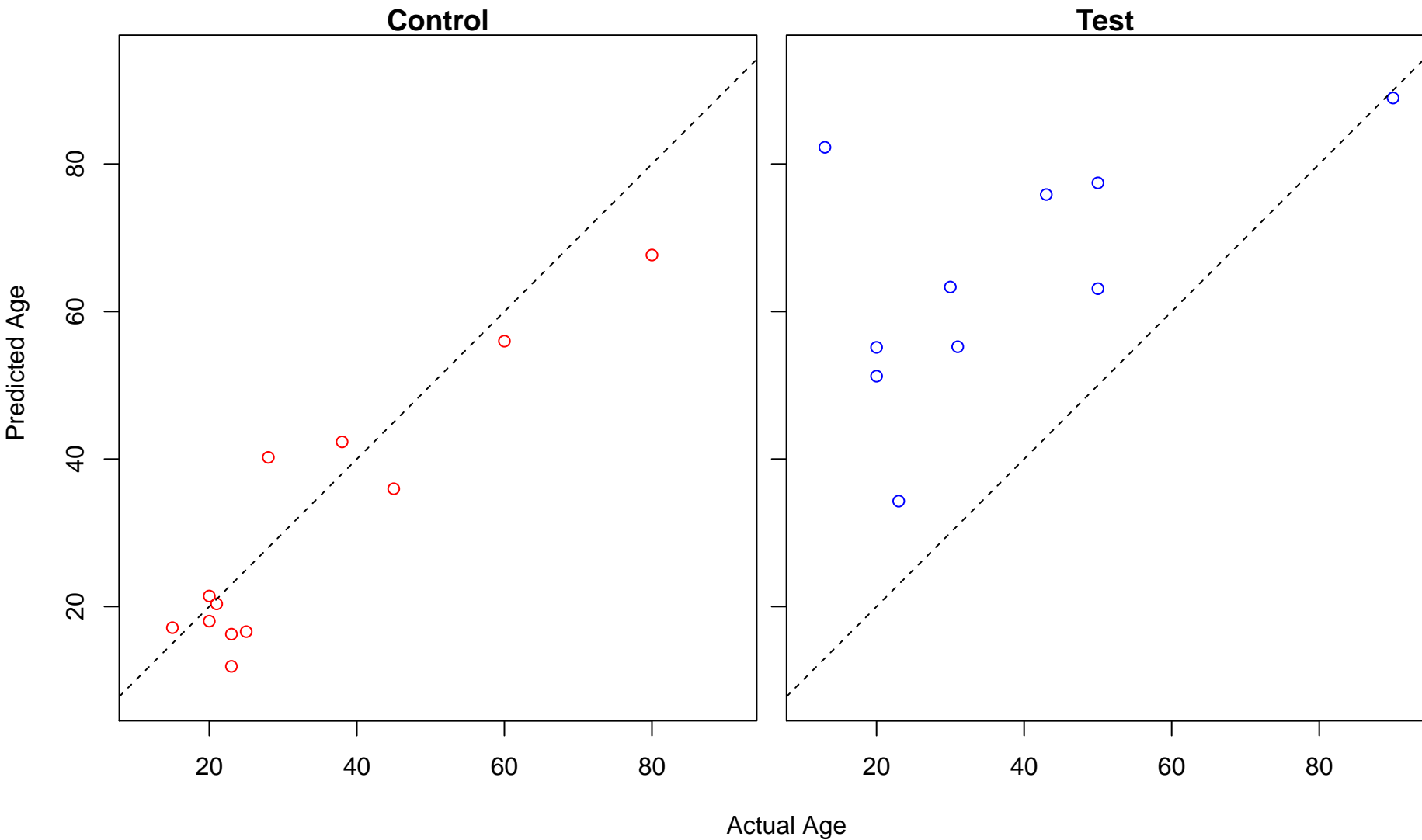
cardiac epithelial to mesenchymal transition (Score: 28.795320)



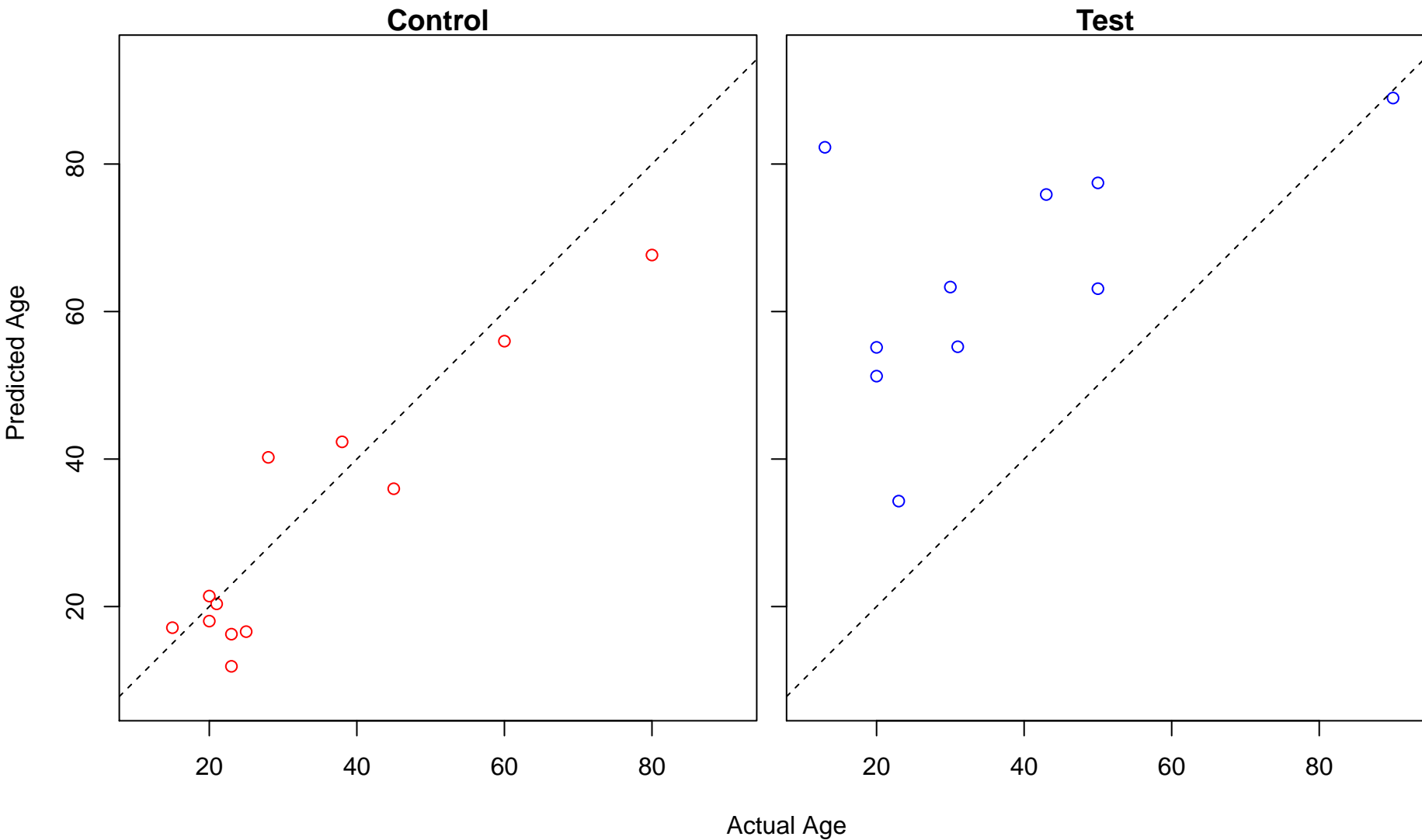
Fc receptor mediated stimulatory signaling pathway (Score: 28.767983)



olfactory bulb development (Score: 28.690293)

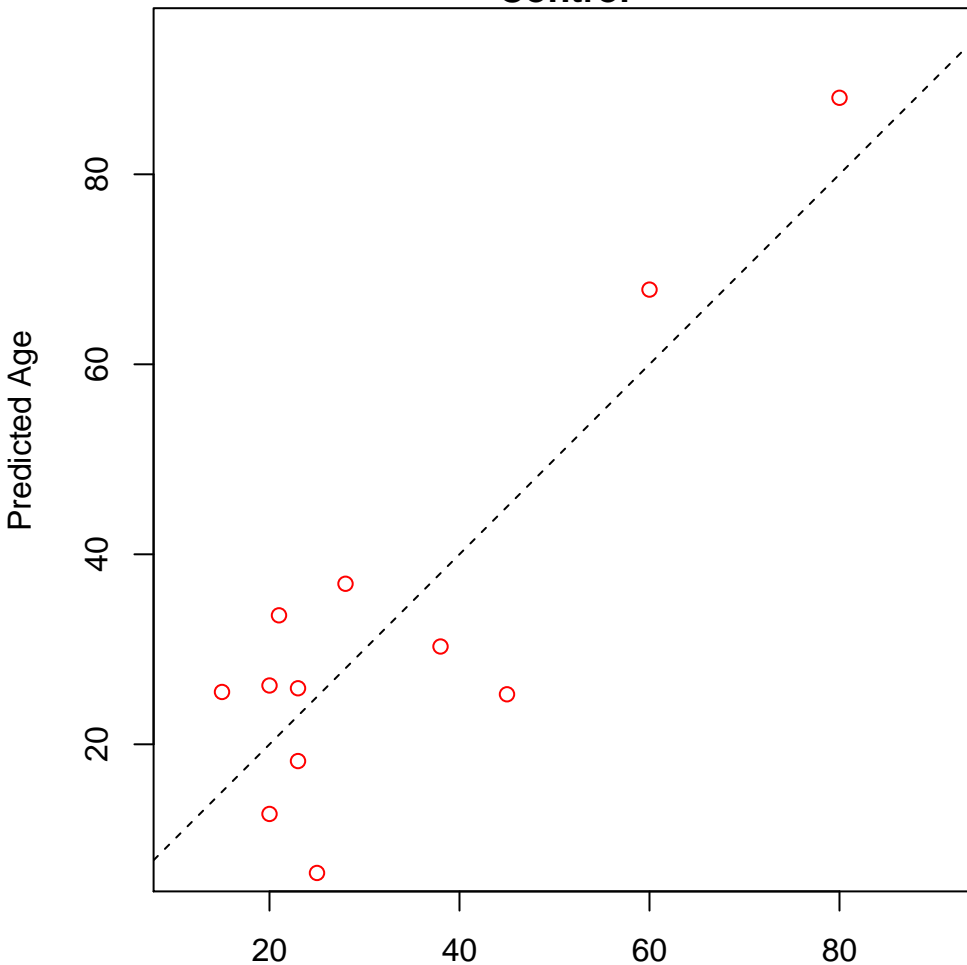


olfactory lobe development (Score: 28.690293)

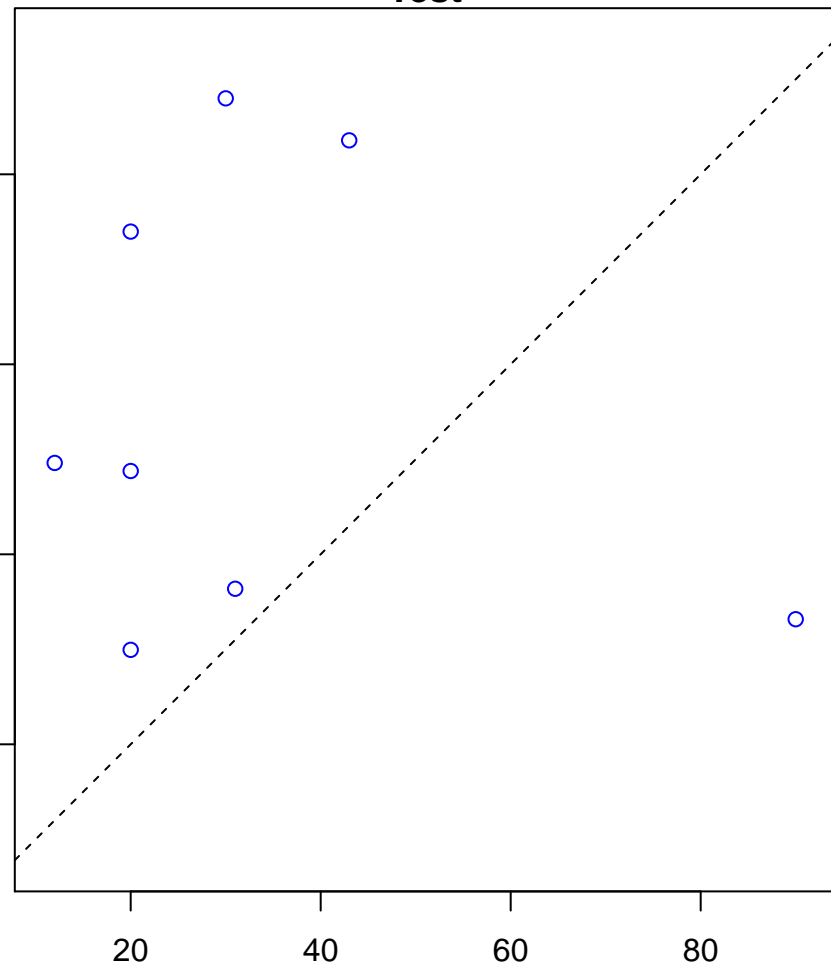


sympathetic ganglion development (Score: 28.464677)

Control

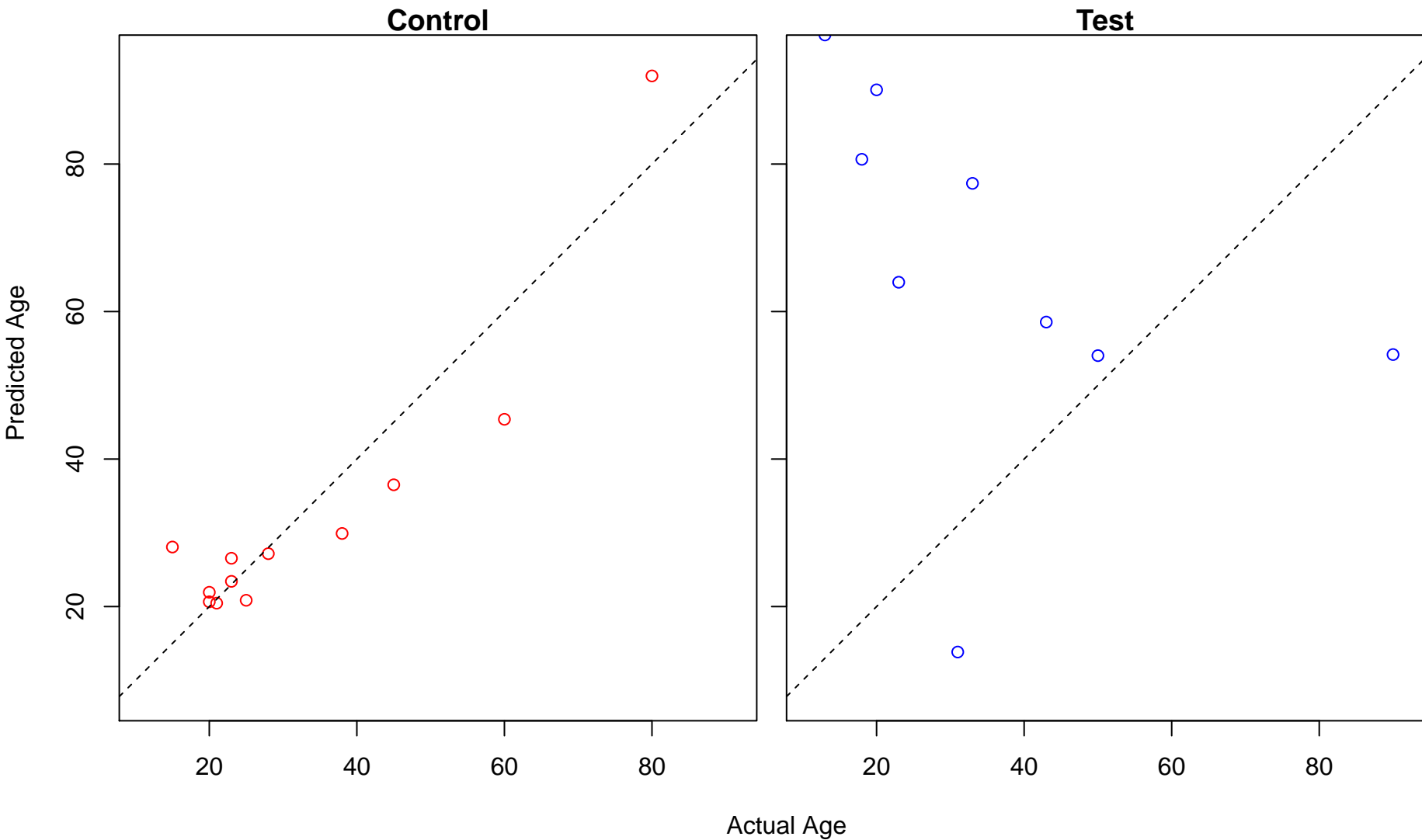


Test

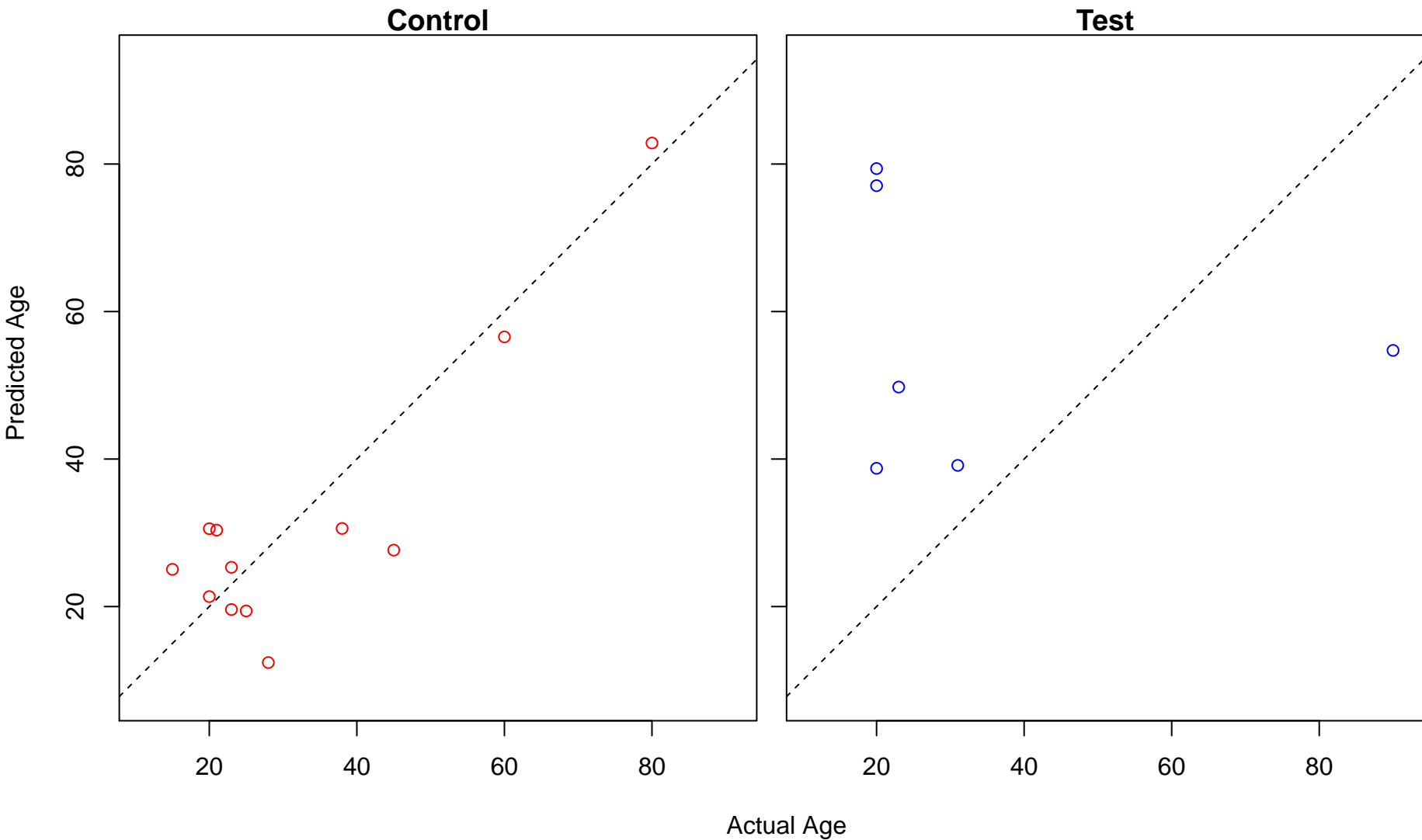


Actual Age

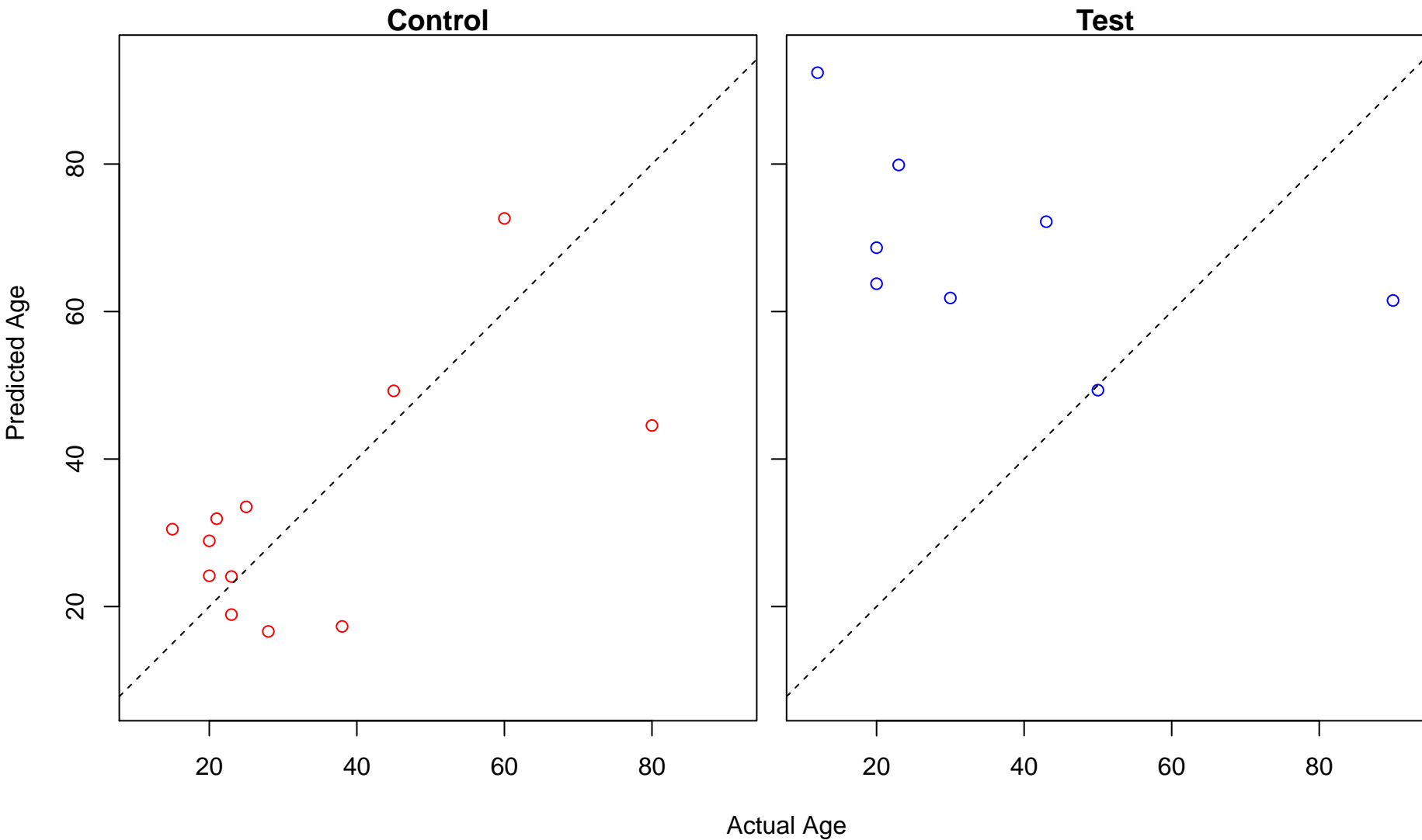
positive regulation of keratinocyte differentiation (Score: 28.432578)



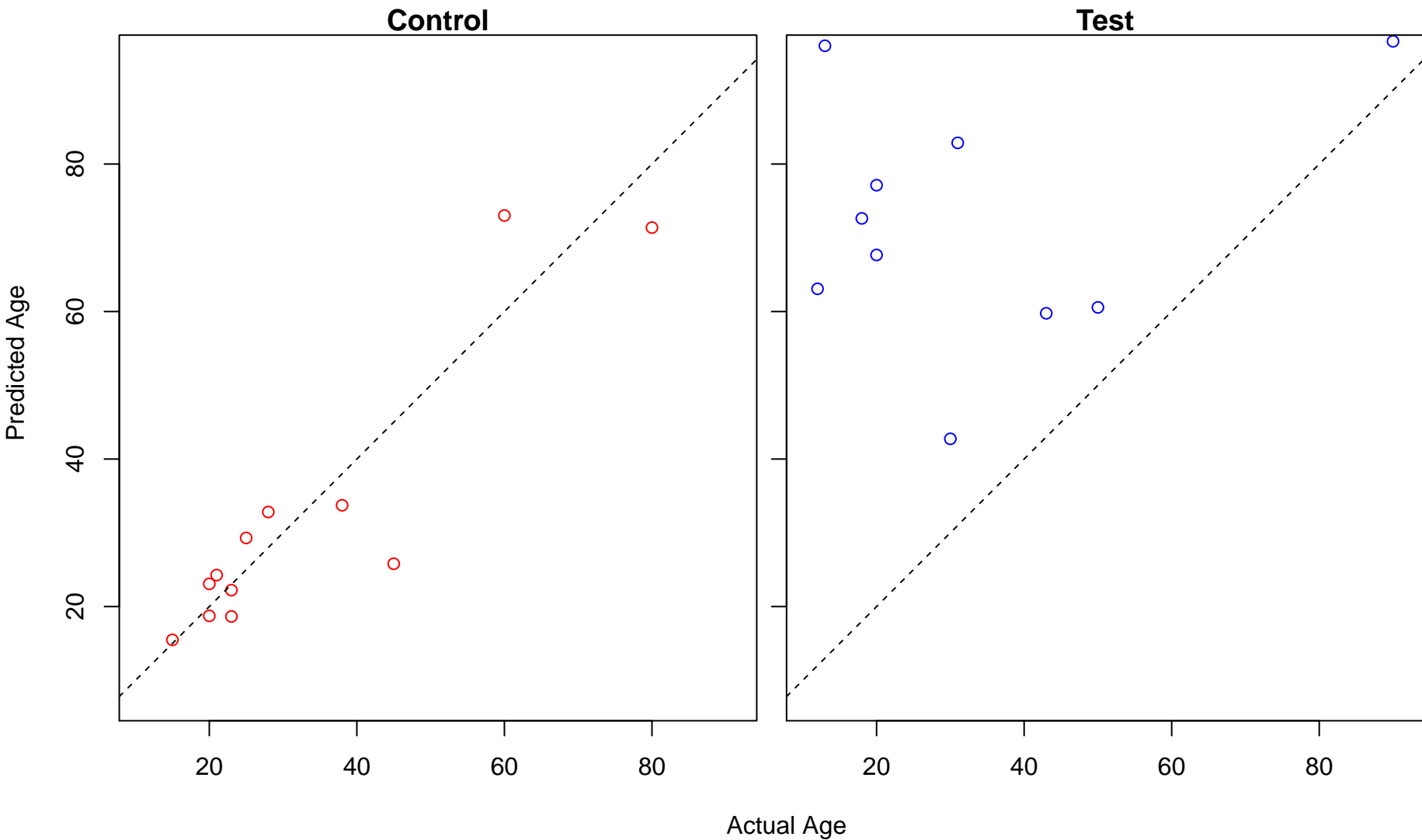
organelle membrane fusion (Score: 28.430890)



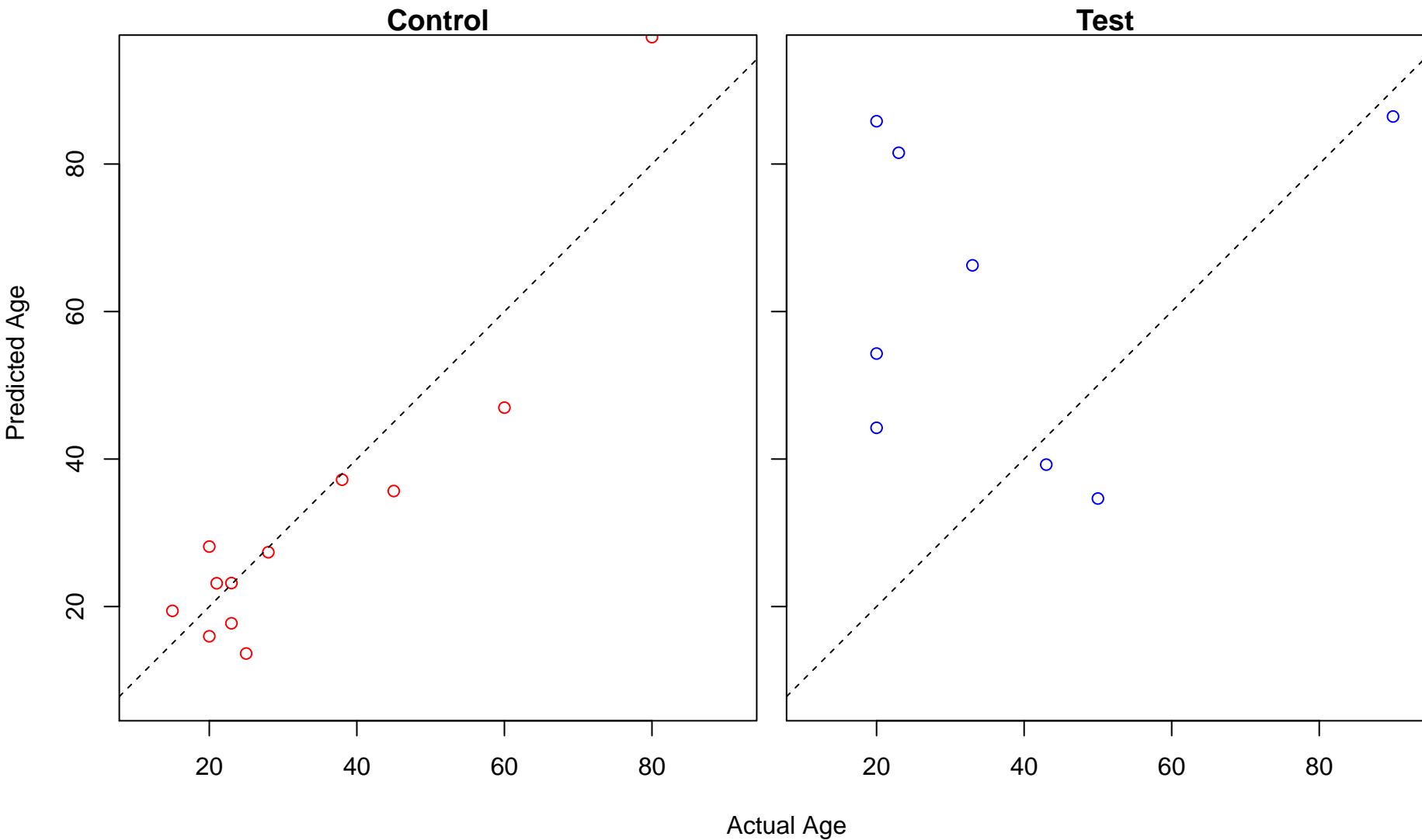
positive regulation of interleukin-2 biosynthetic process (Score: 28.424824)



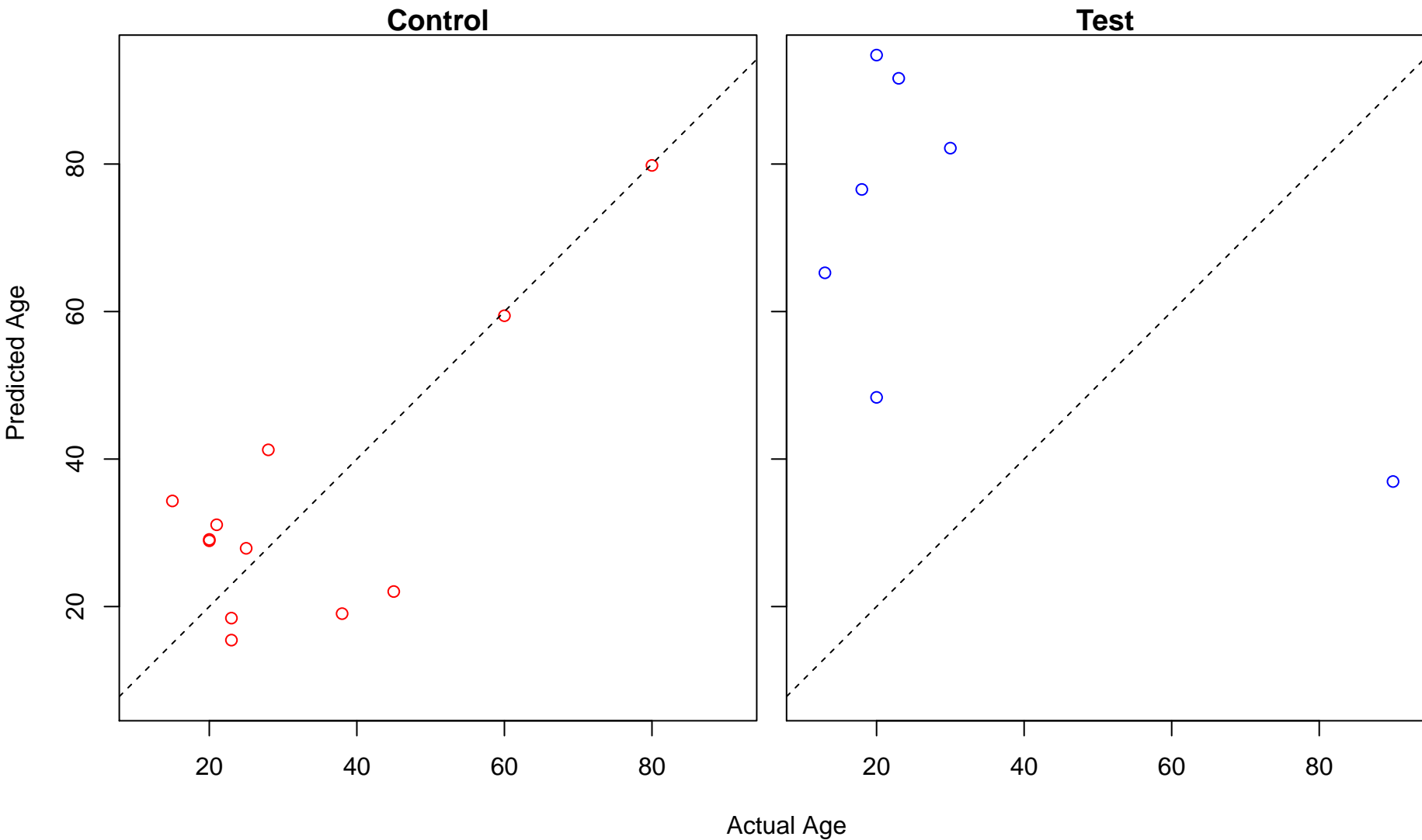
regulation of glucocorticoid receptor signaling pathway (Score: 28.392294)



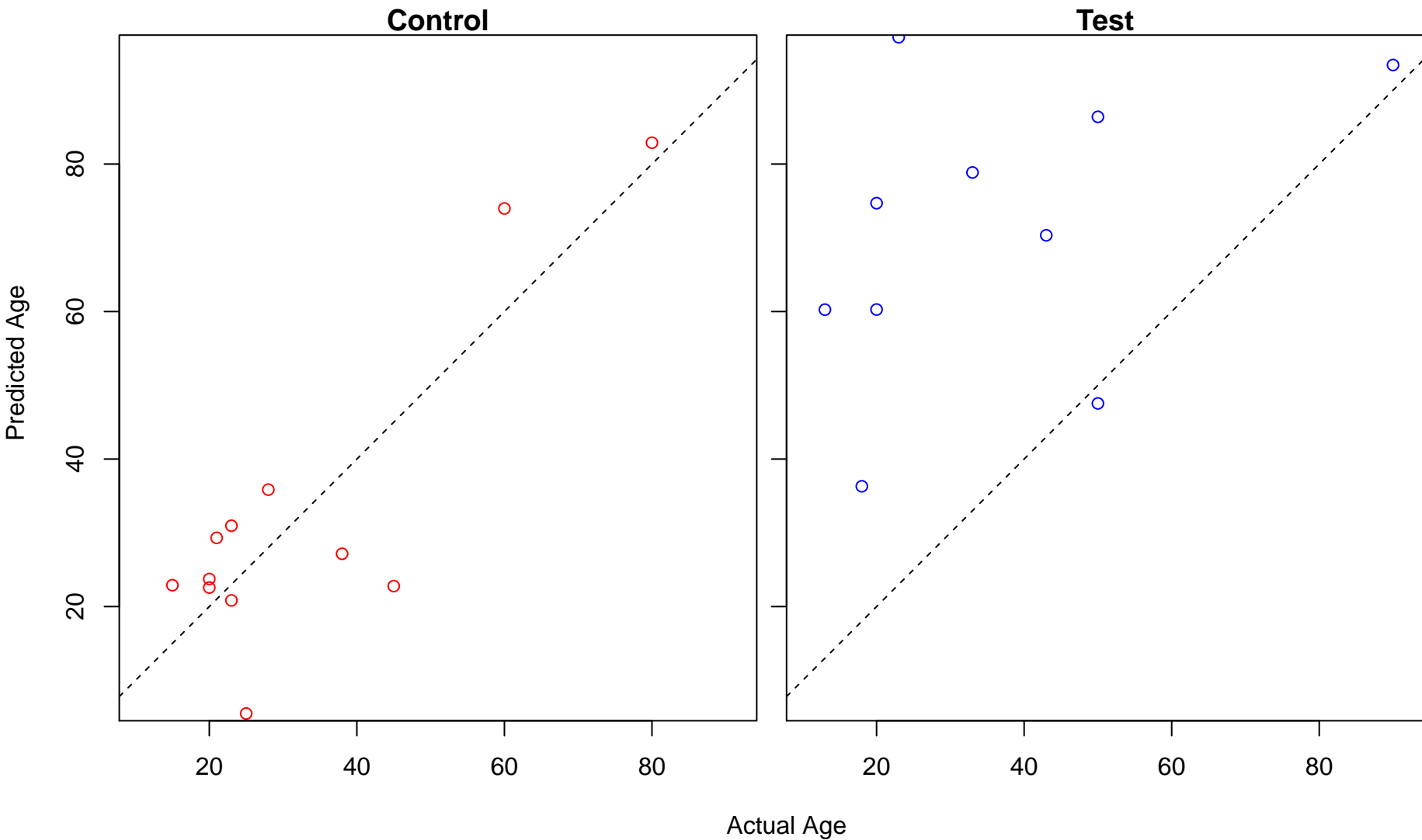
regulation of tyrosine phosphorylation of STAT protein (Score: 28.354426)



positive regulation of interleukin-8 production (Score: 28.319681)

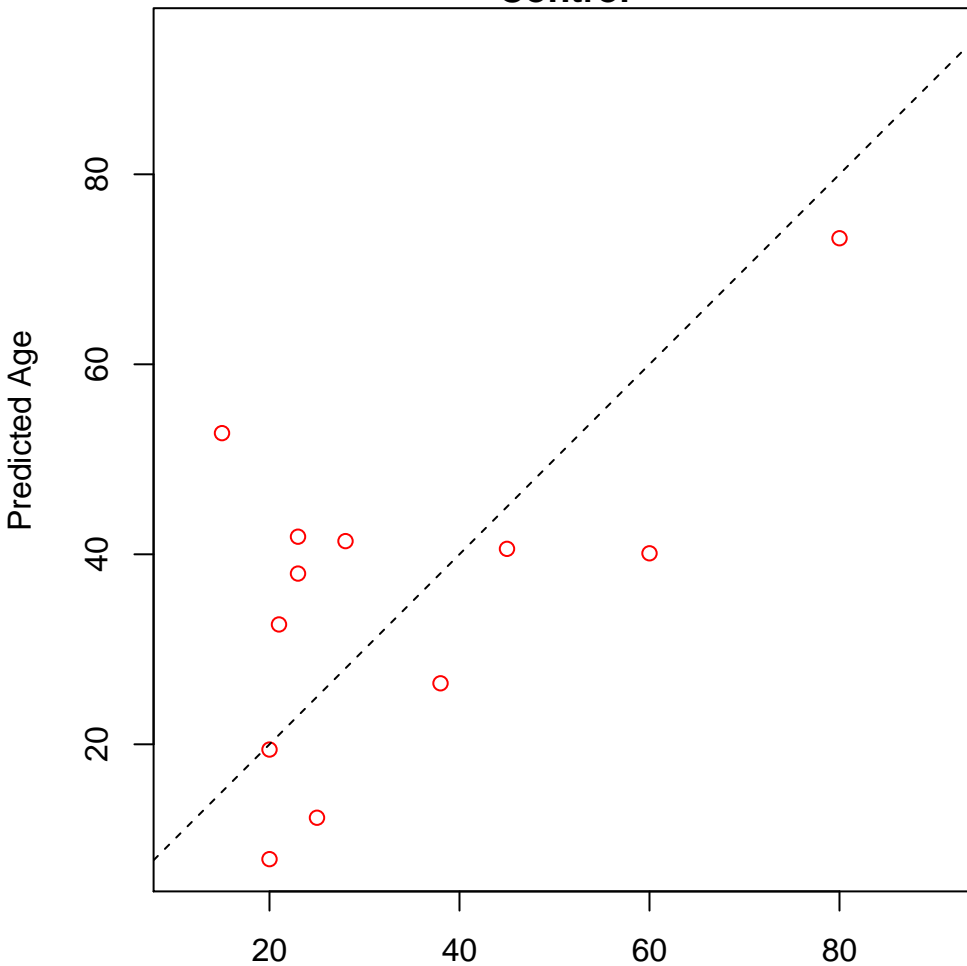


sensory perception of pain (Score: 28.297055)

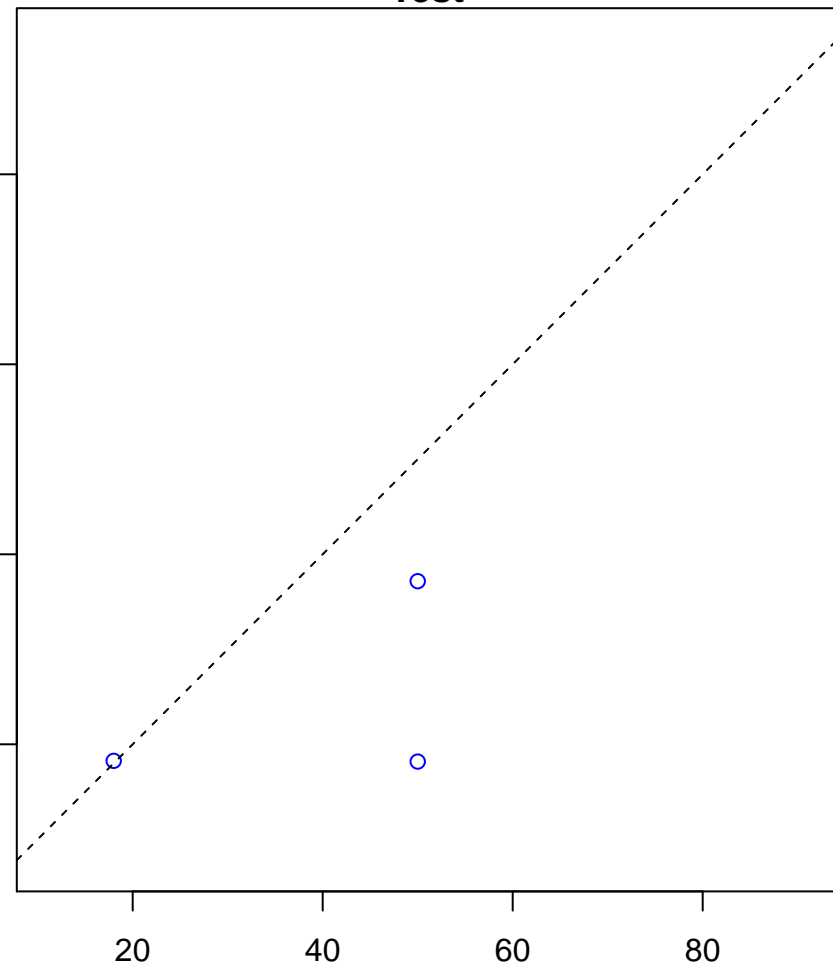


mineralocorticoid biosynthetic process (Score: 28.288881)

Control



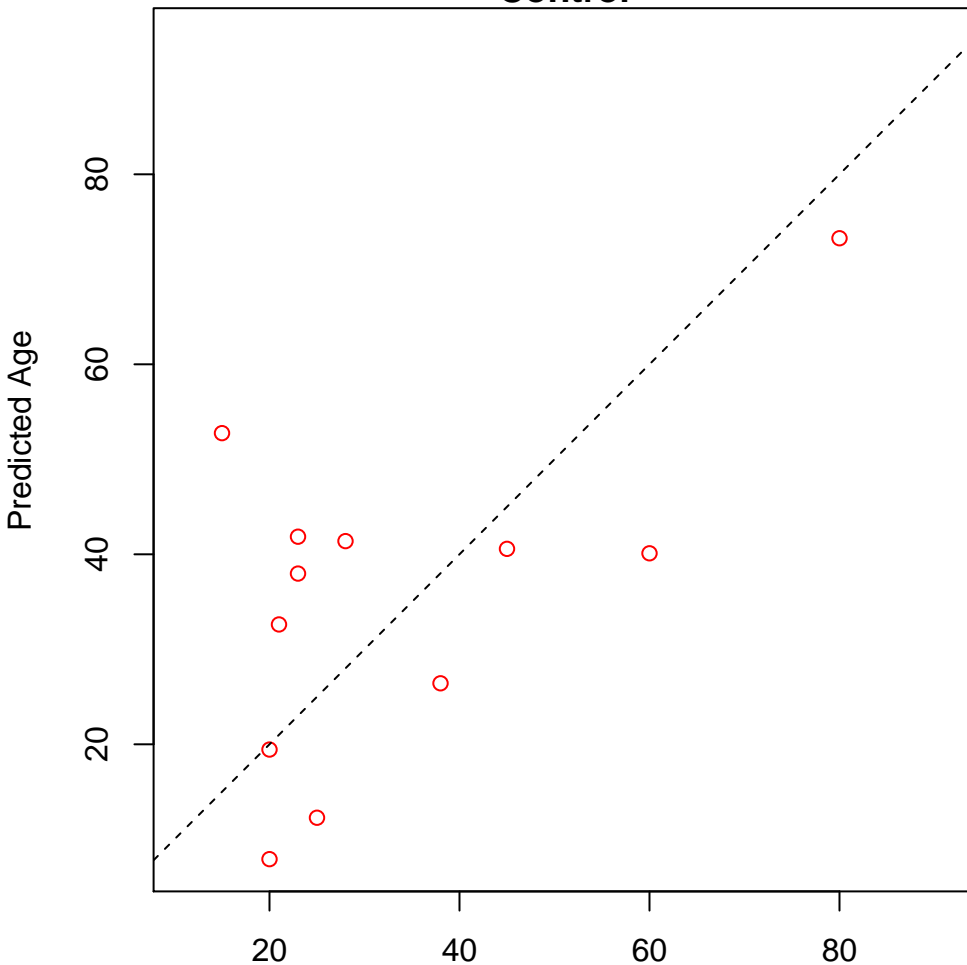
Test



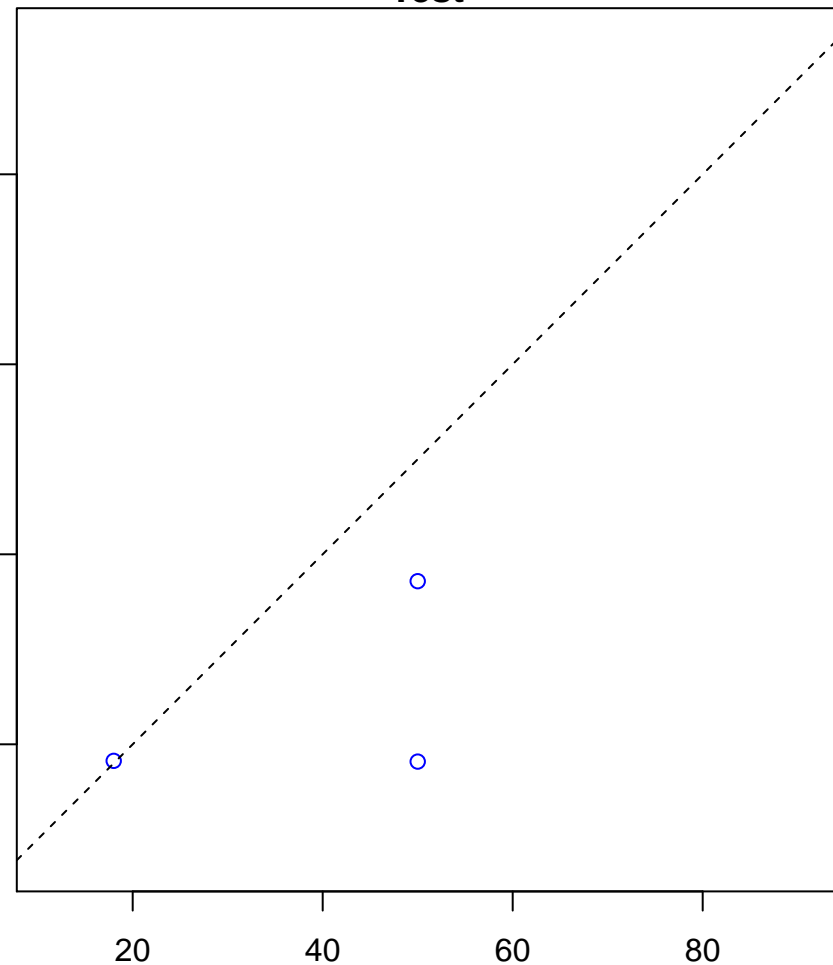
Actual Age

mineralocorticoid metabolic process (Score: 28.288881)

Control

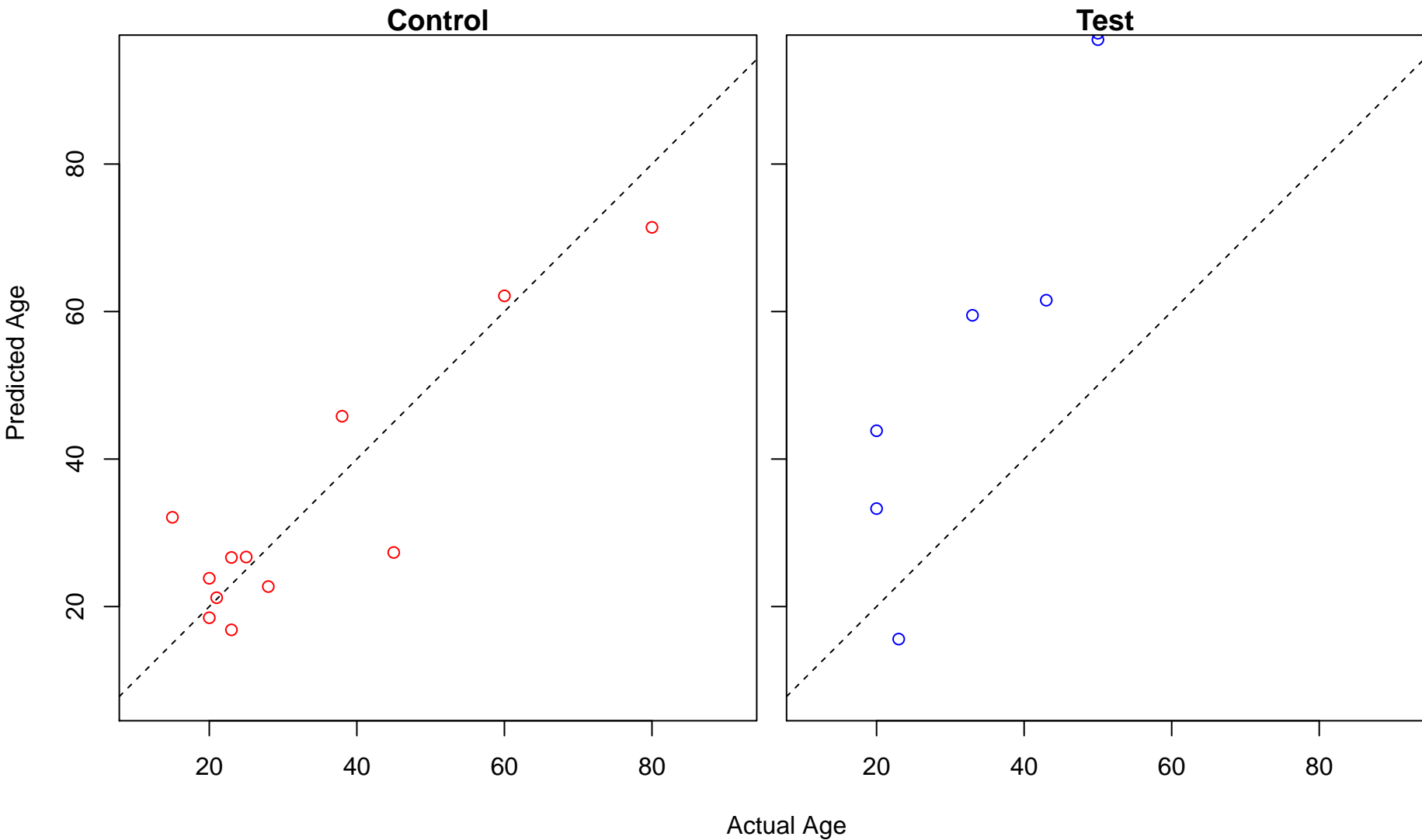


Test



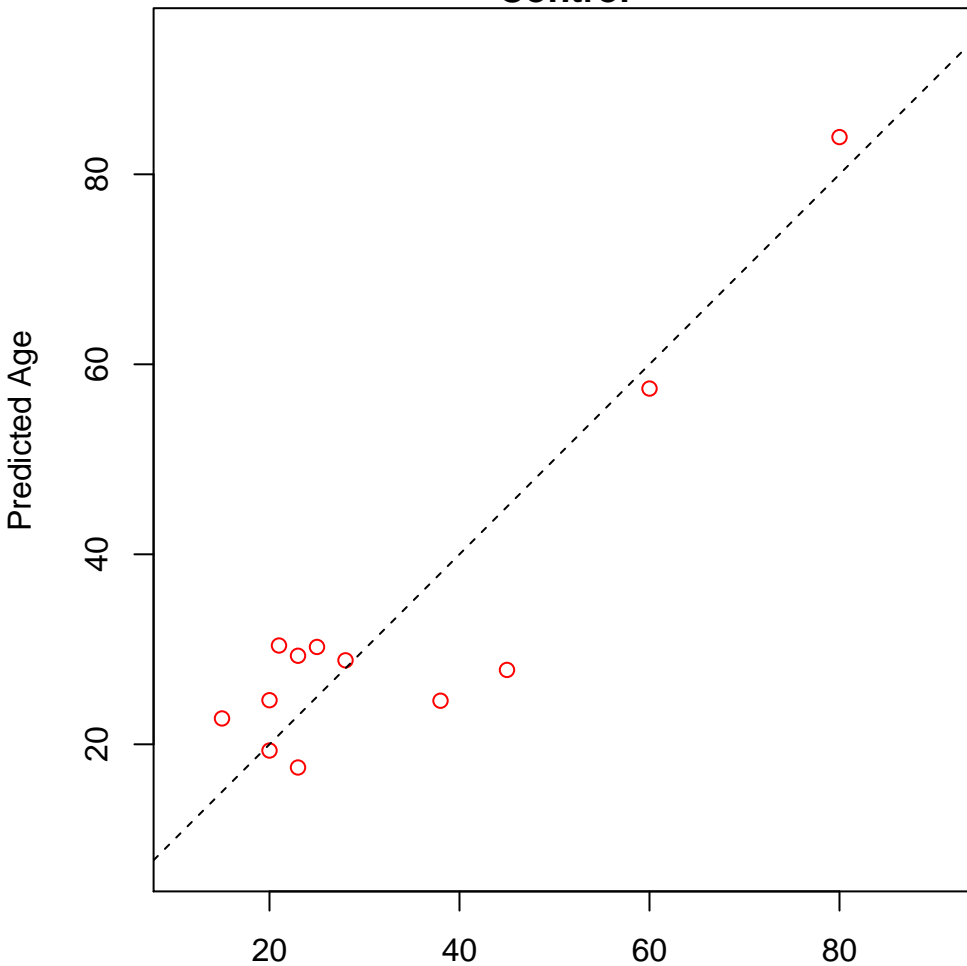
Actual Age

ammonium transport (Score: 28.262278)

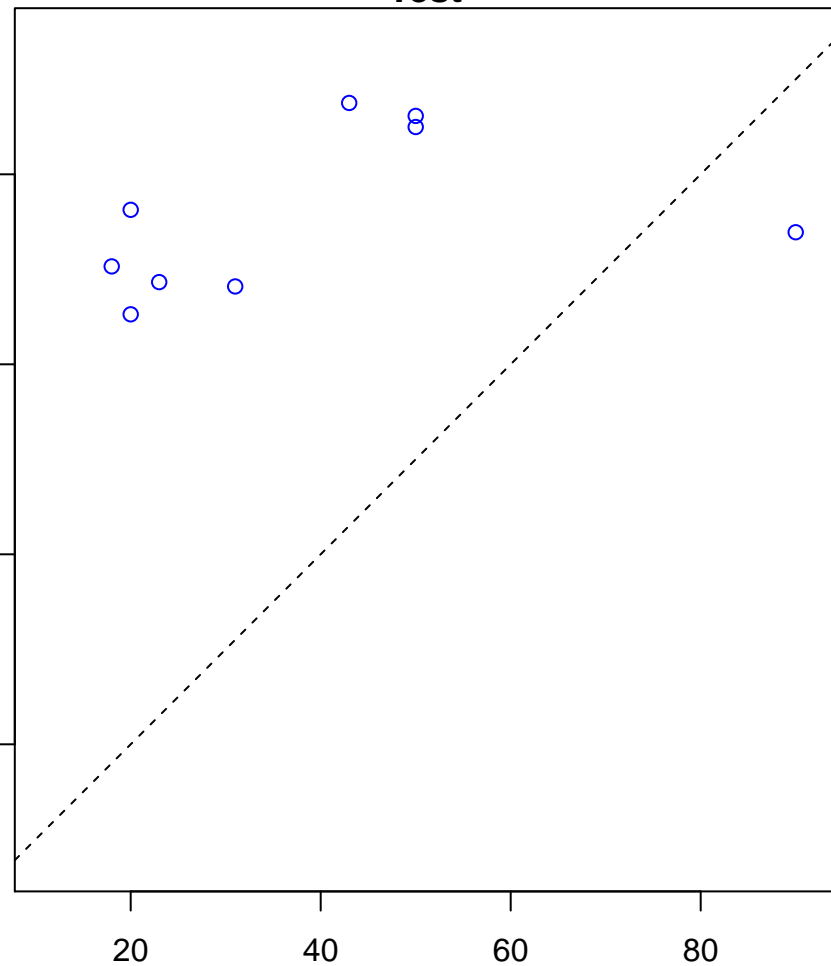


blood vessel endothelial cell differentiation (Score: 28.261530)

Control

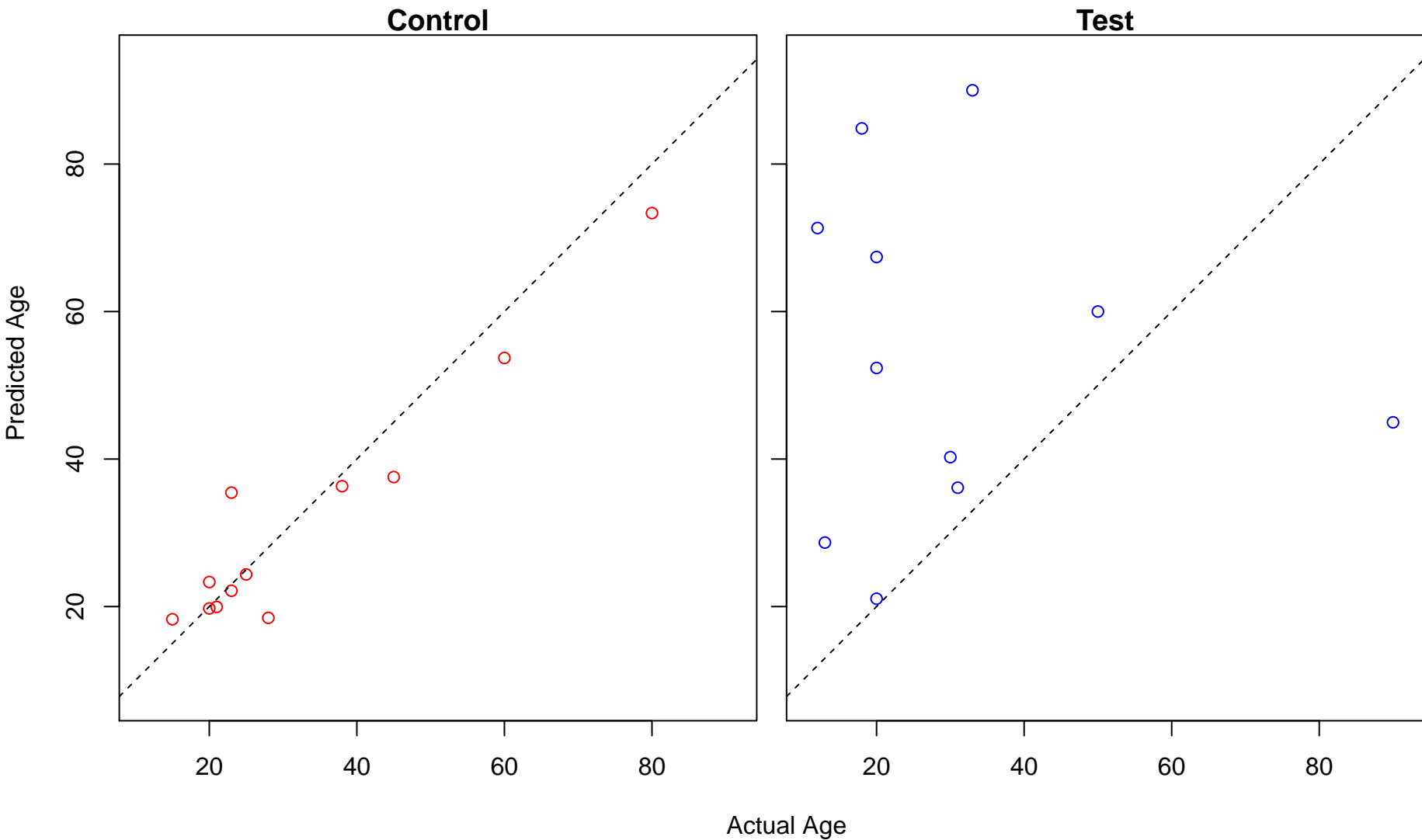


Test

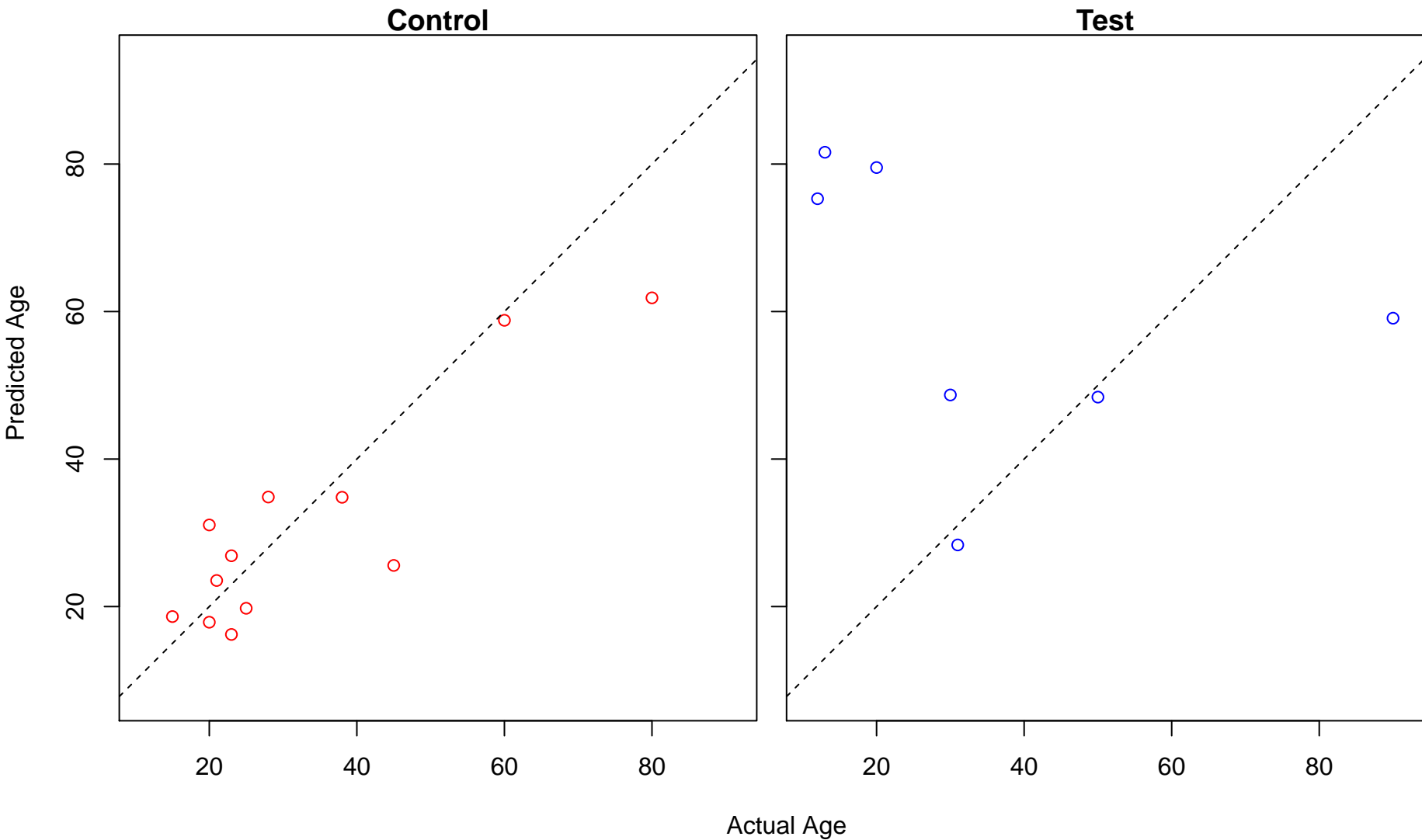


Actual Age

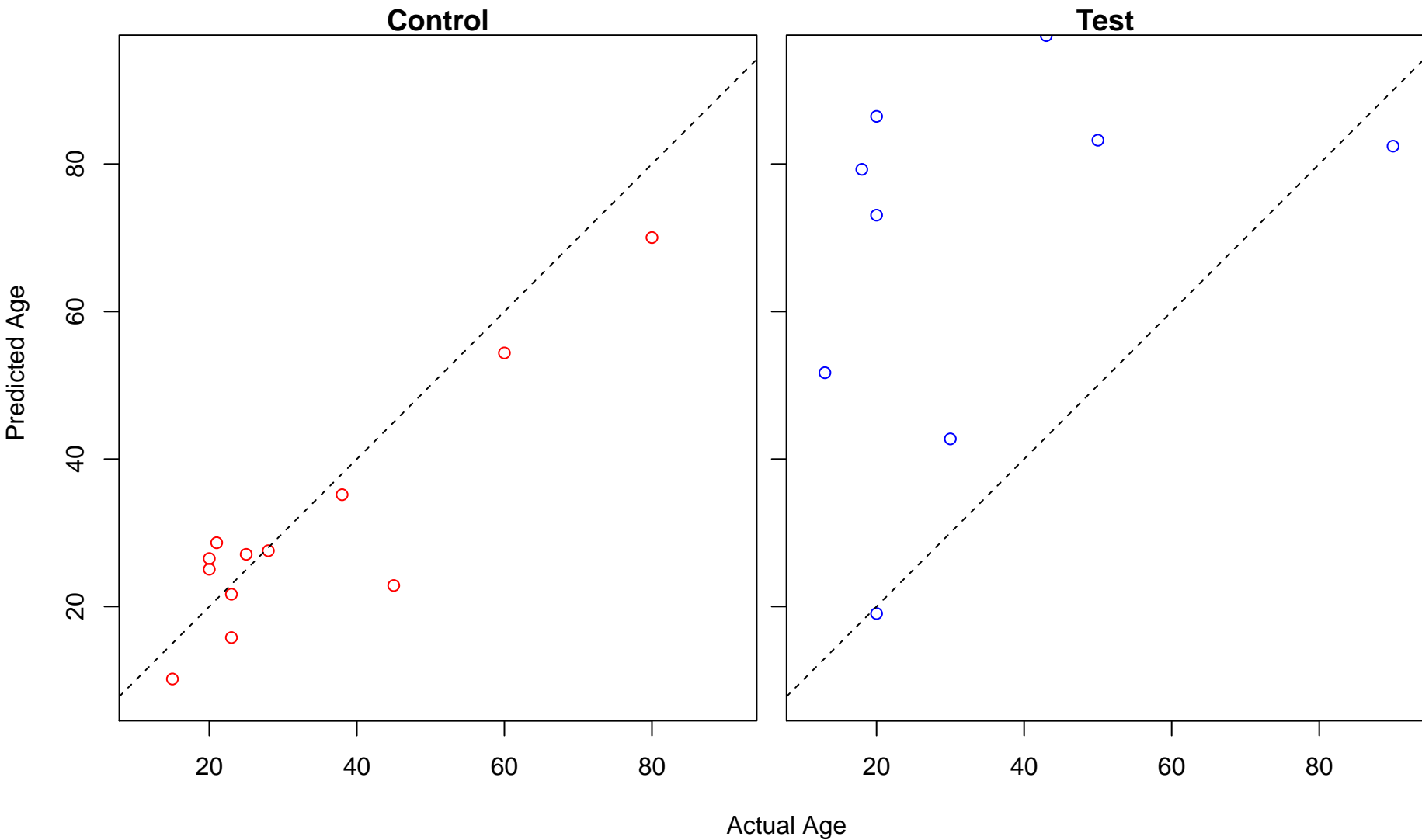
regulation of gliogenesis (Score: 28.218440)



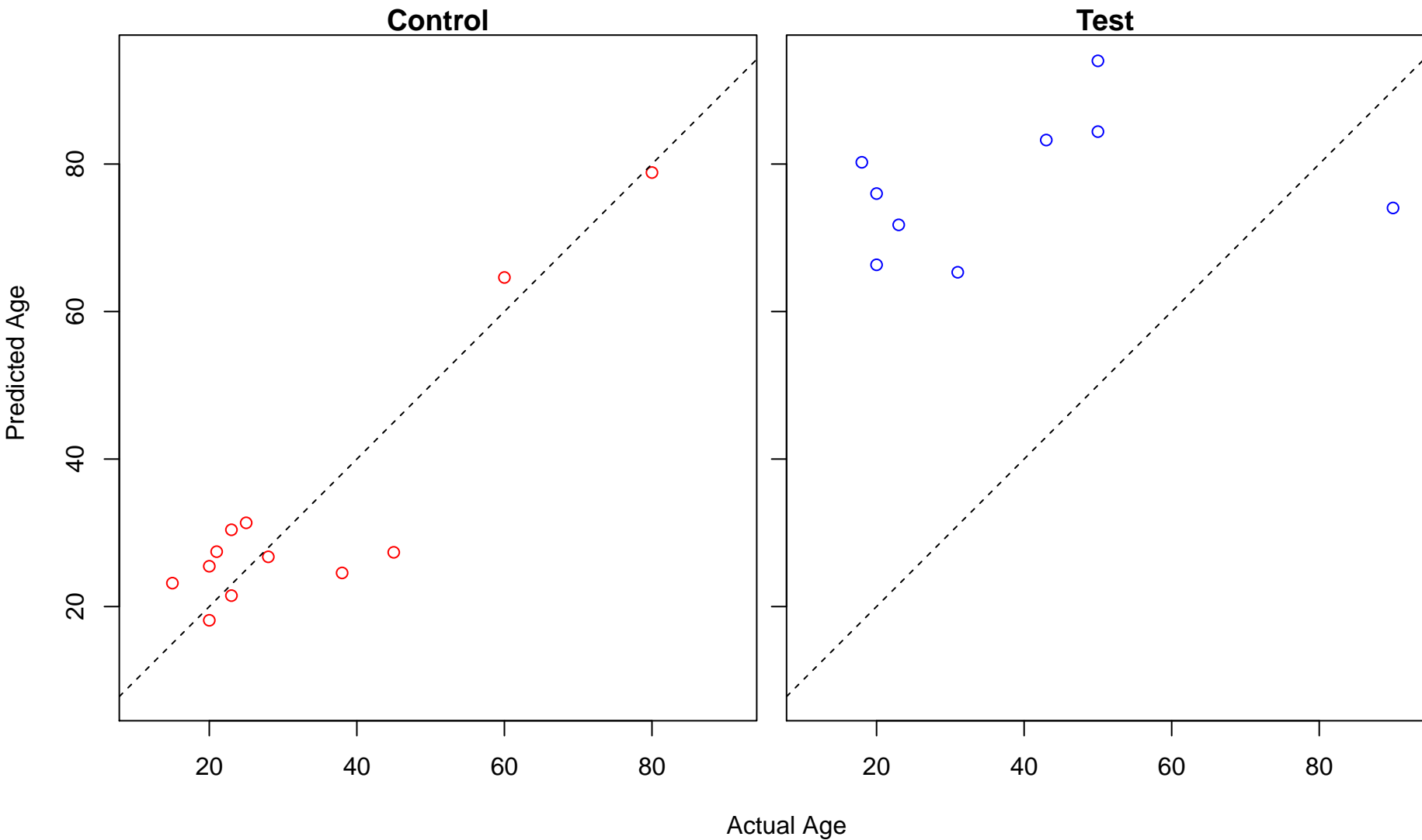
GTP metabolic process (Score: 28.158149)



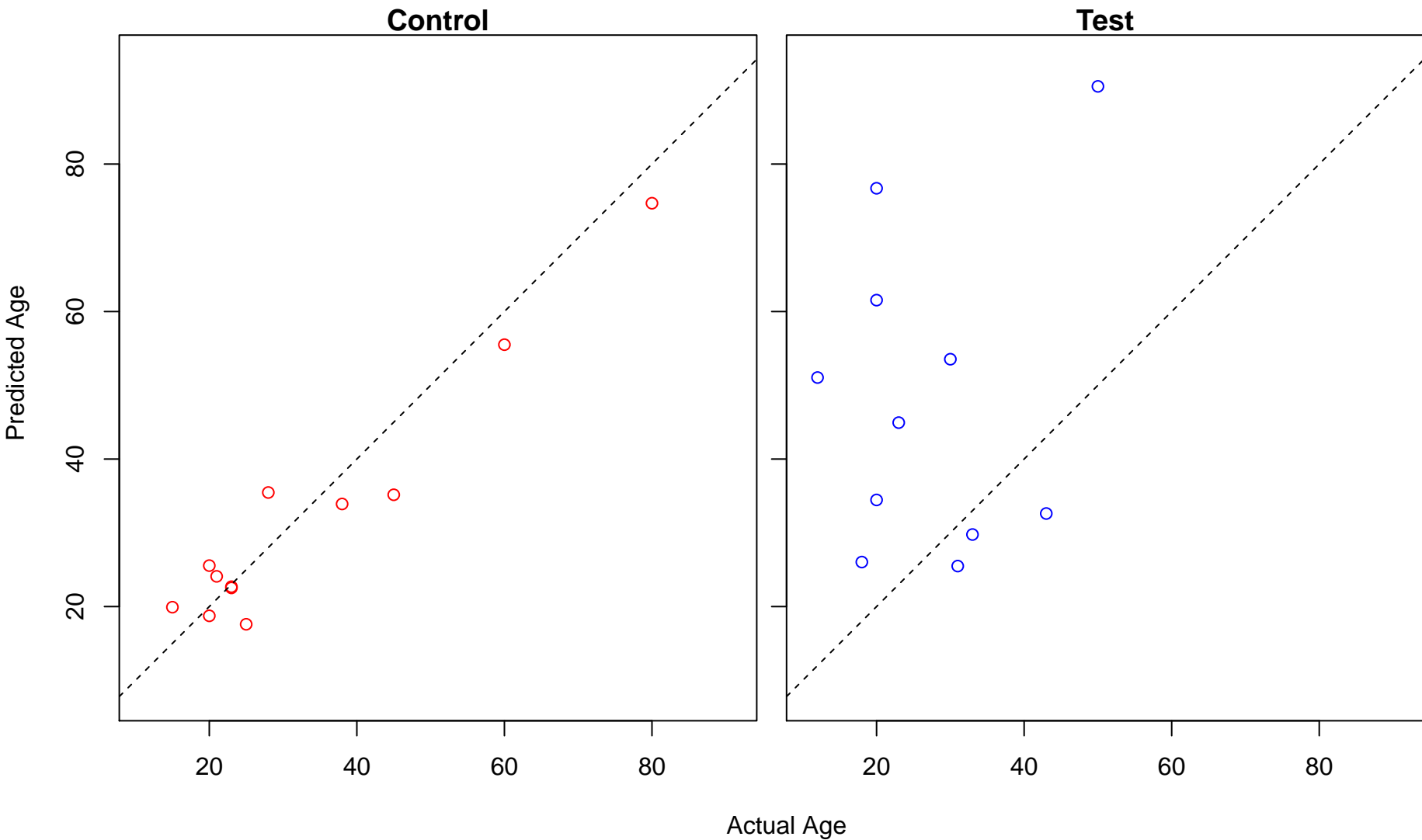
cellular response to interferon-beta (Score: 28.156491)



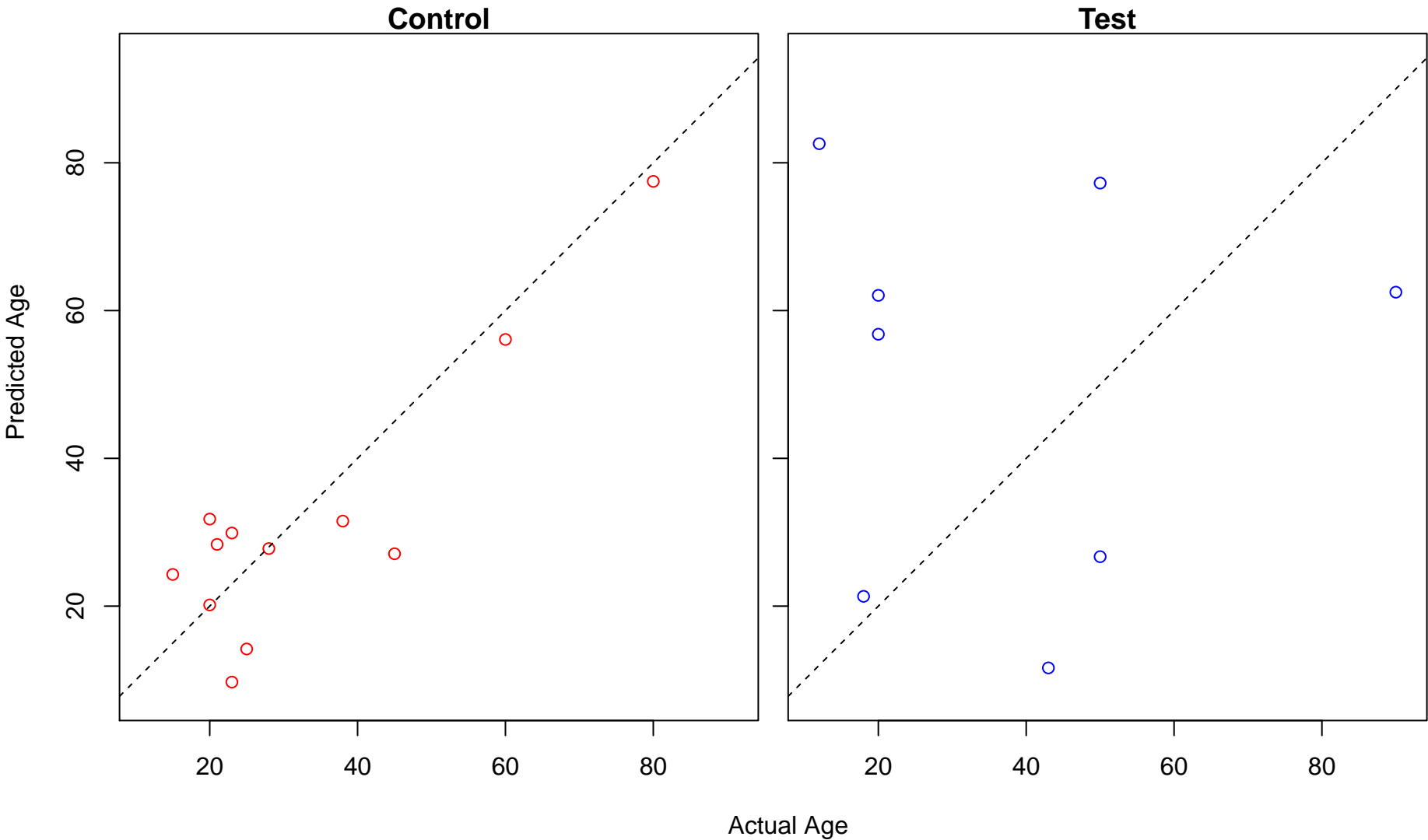
cell fate specification (Score: 28.104851)



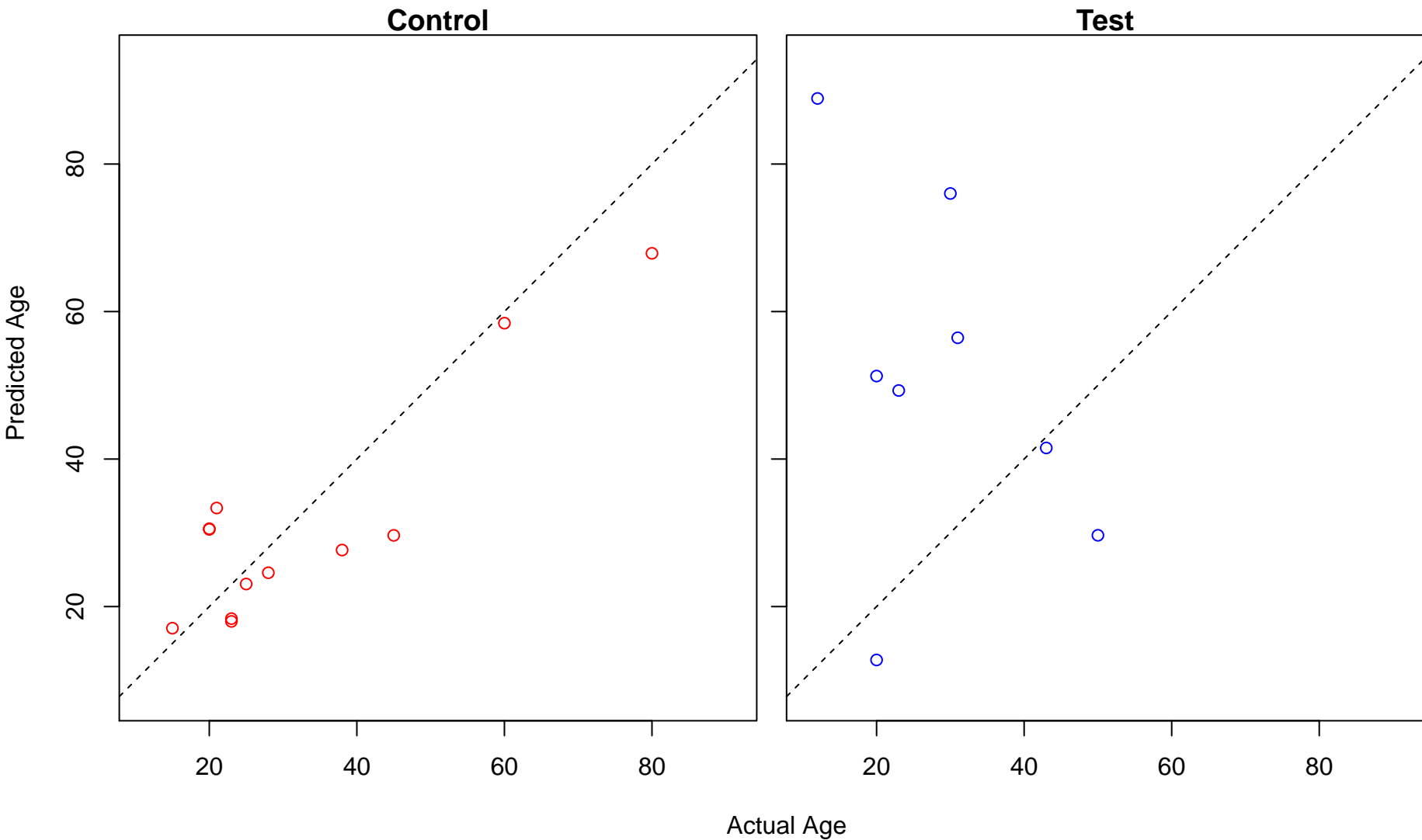
regulation of DNA repair (Score: 28.086106)



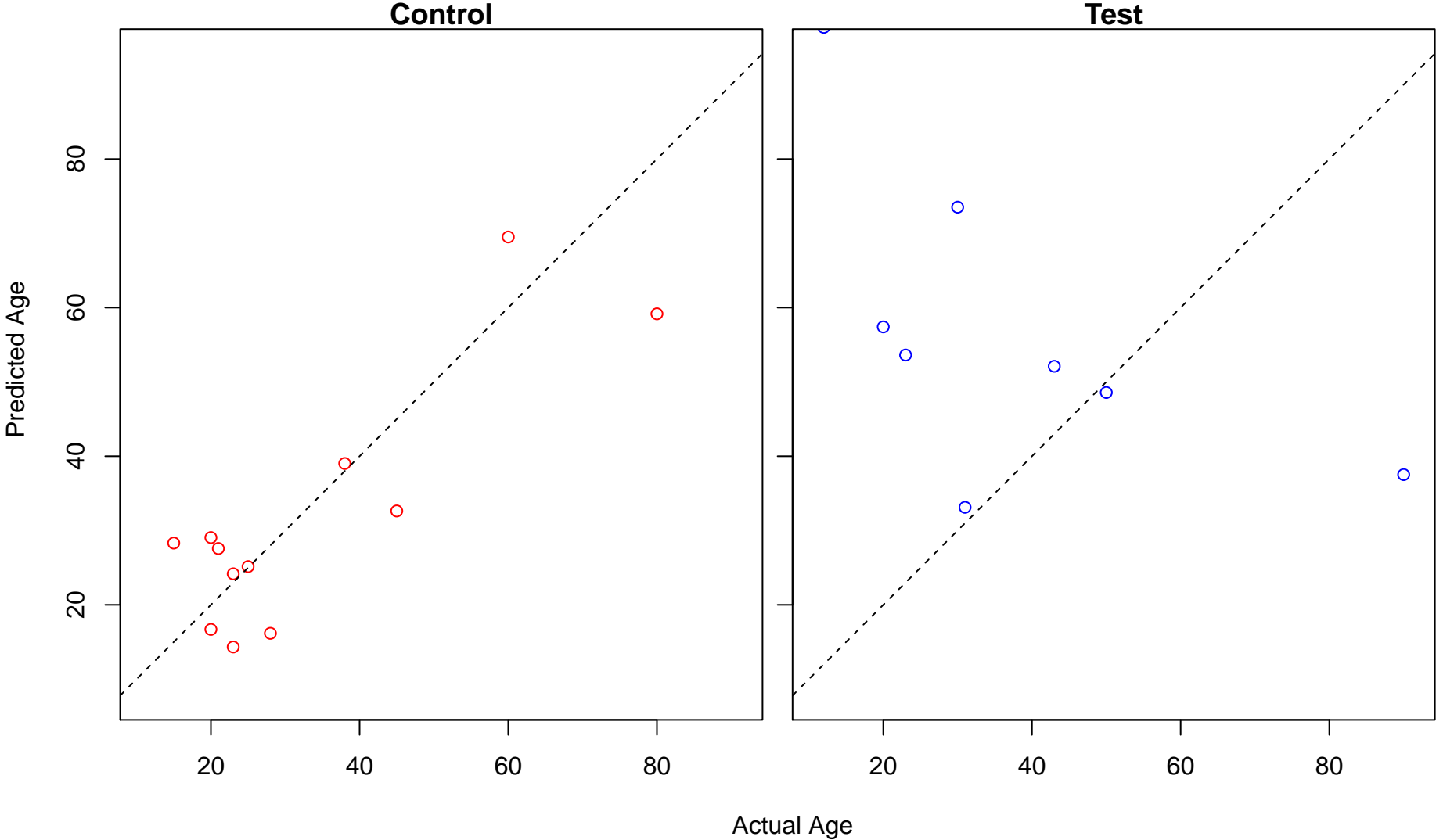
JAK-STAT cascade involved in growth hormone signaling pathway (Score: 28.014454)



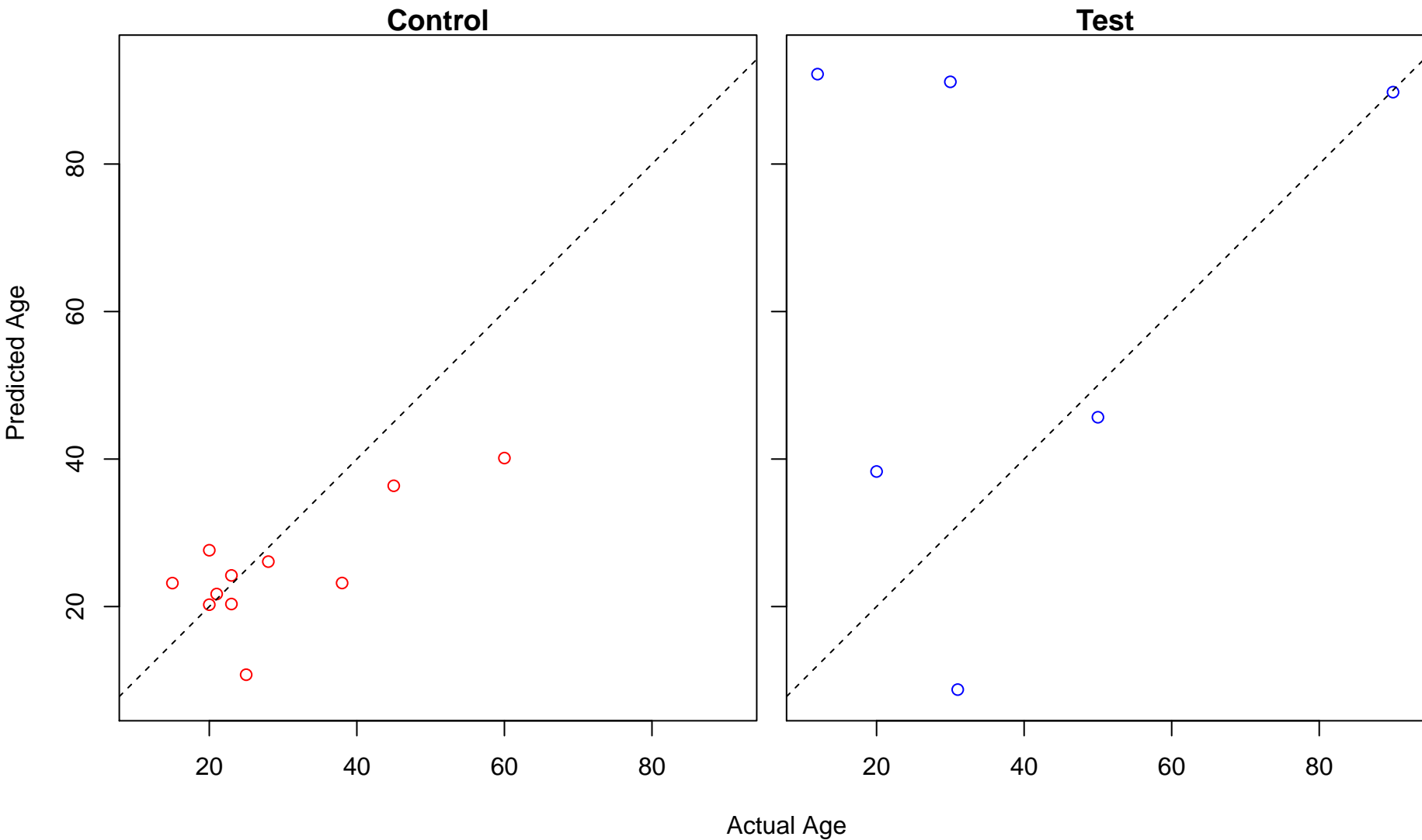
carbohydrate transmembrane transport (Score: 27.999907)



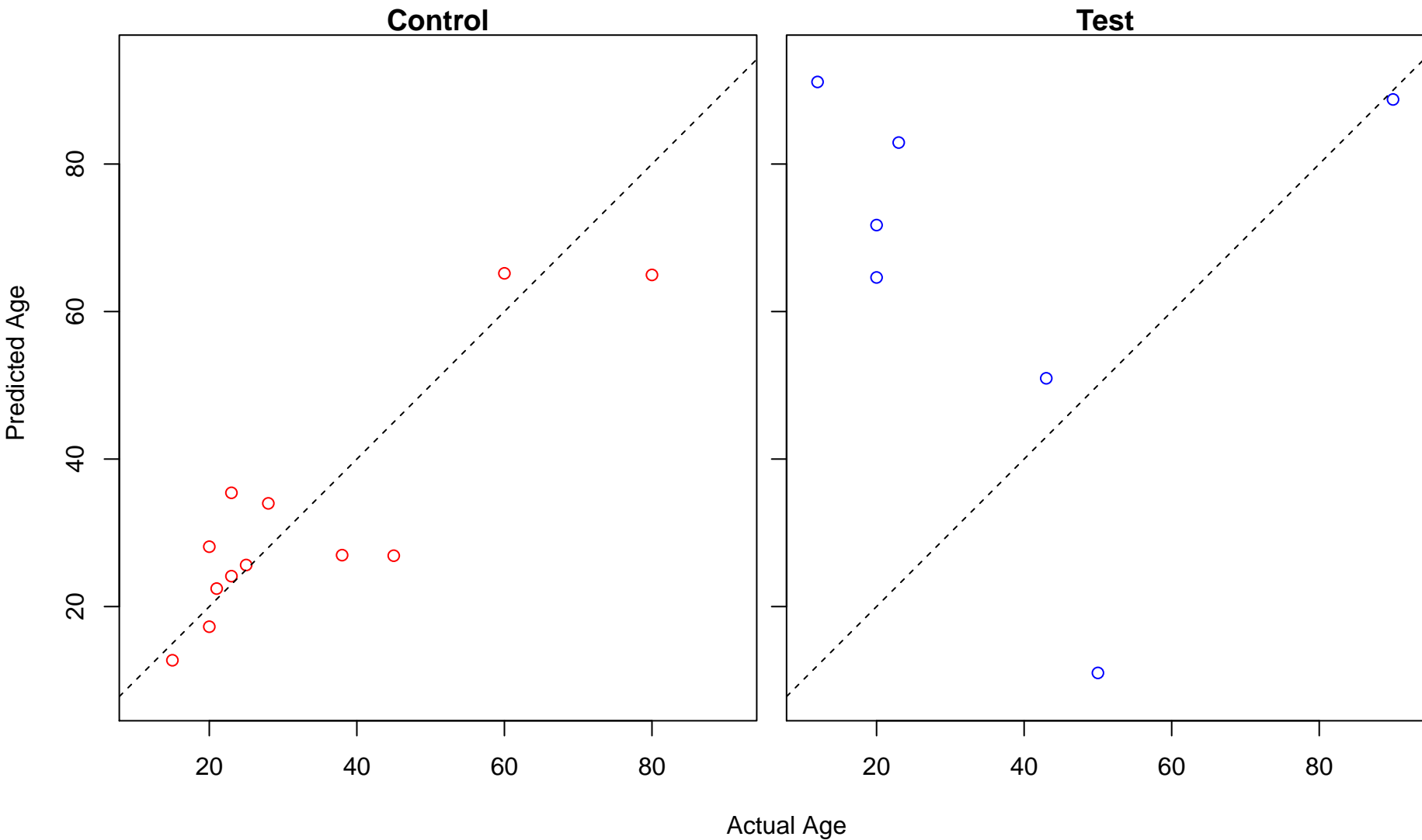
ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway (Score: 27.9)



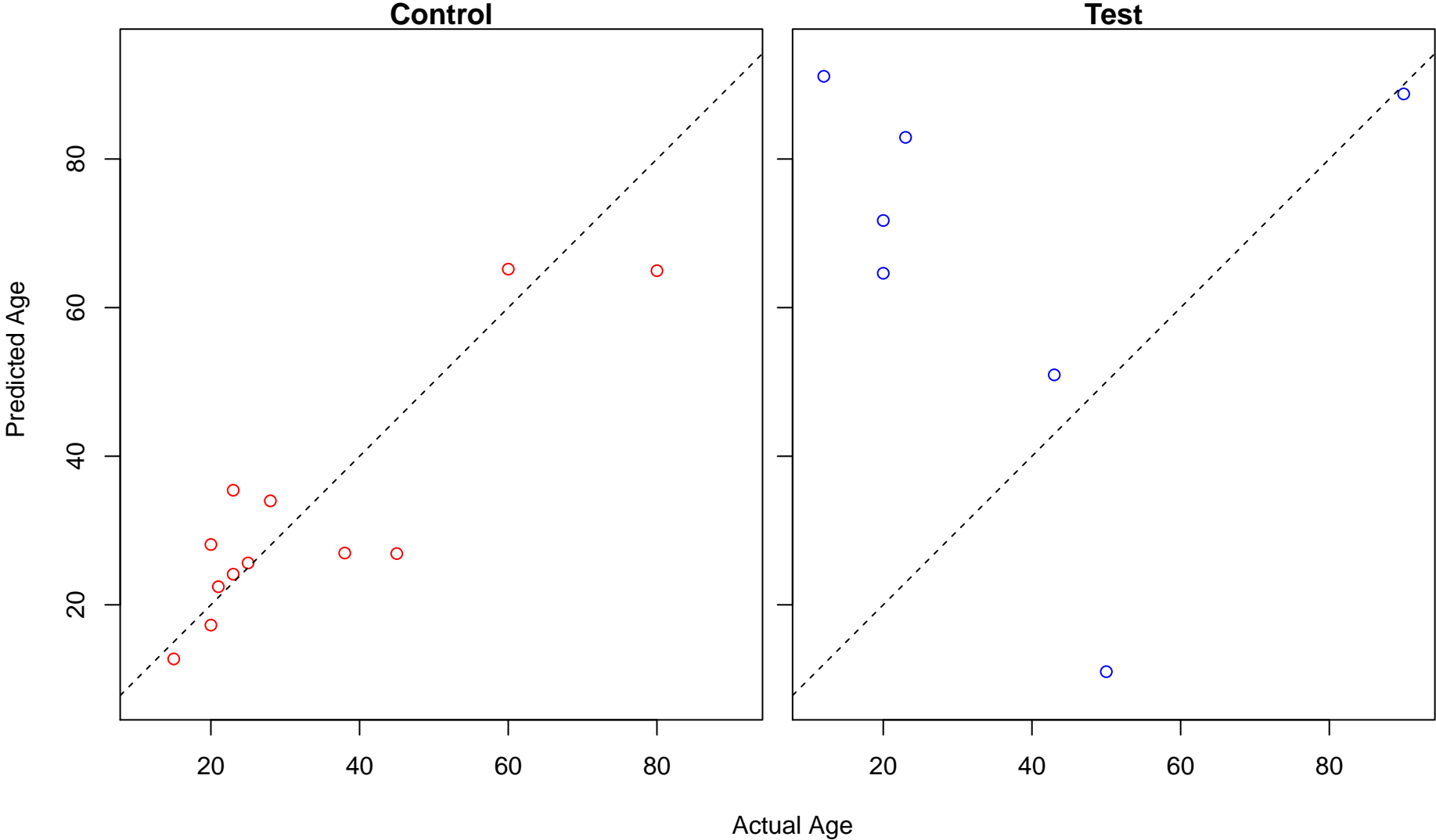
negative regulation of defense response to virus (Score: 27.849226)



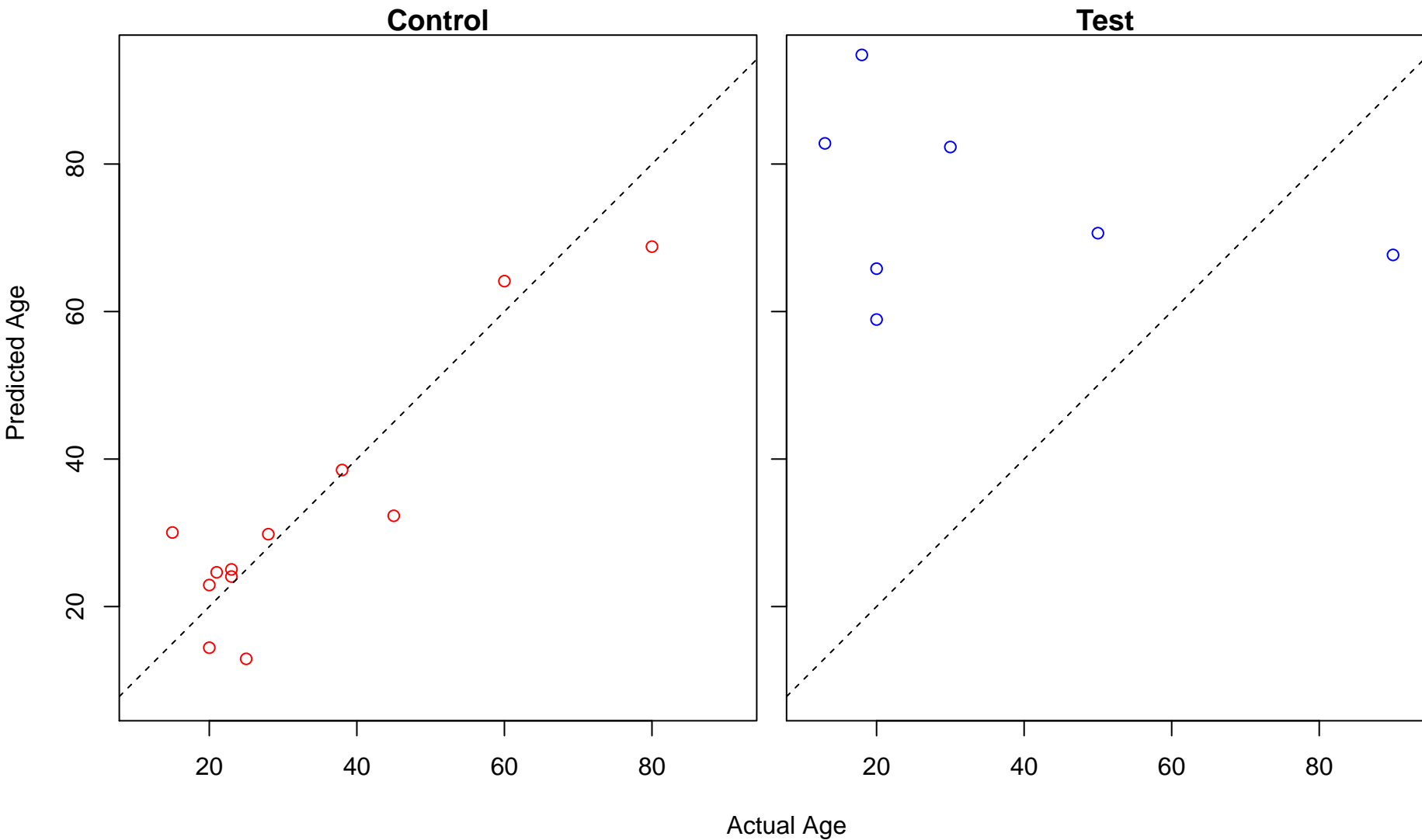
immune response-inhibiting signal transduction (Score: 27.83910)



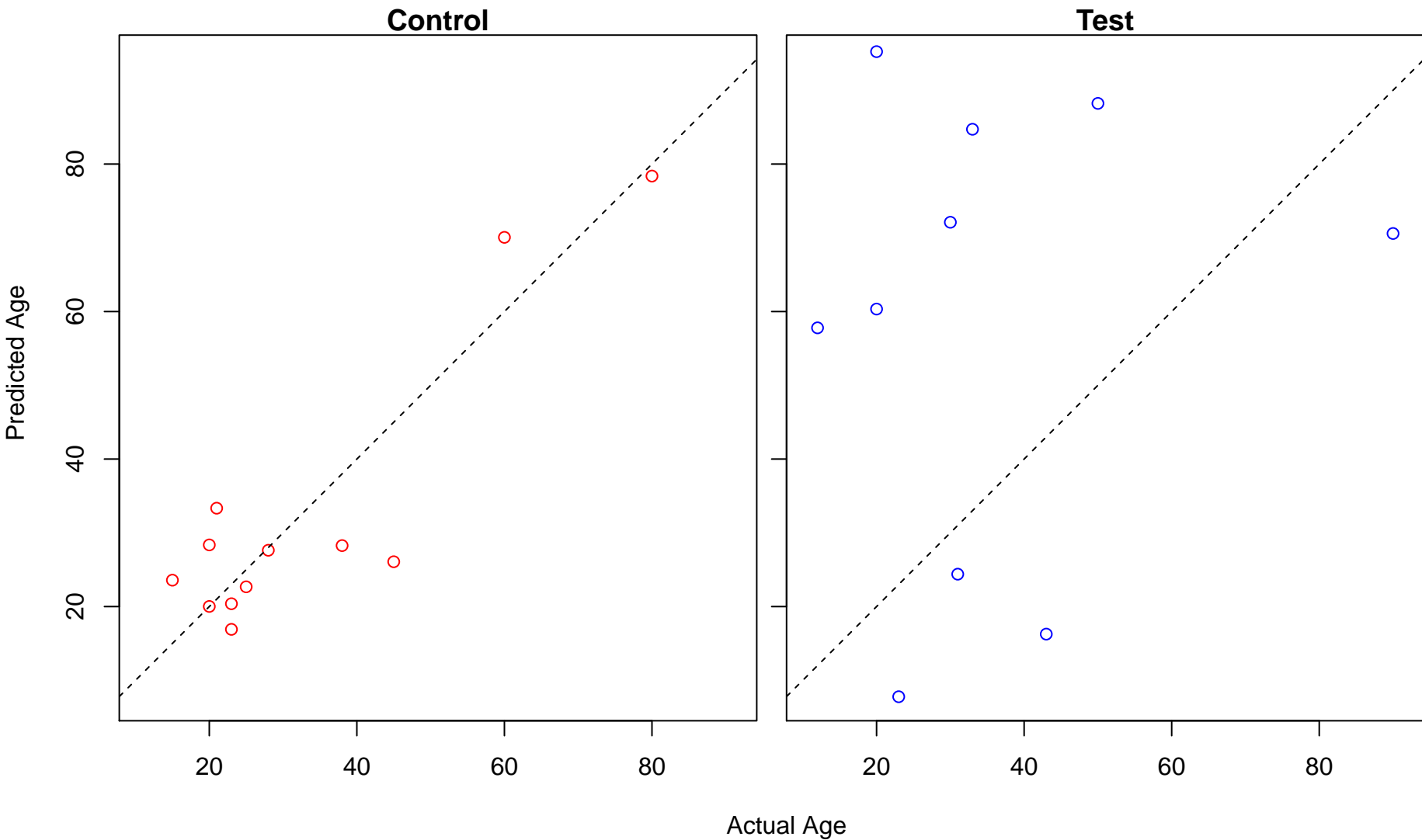
immune response–inhibiting cell surface receptor signaling pathway (Score: 27.838910)



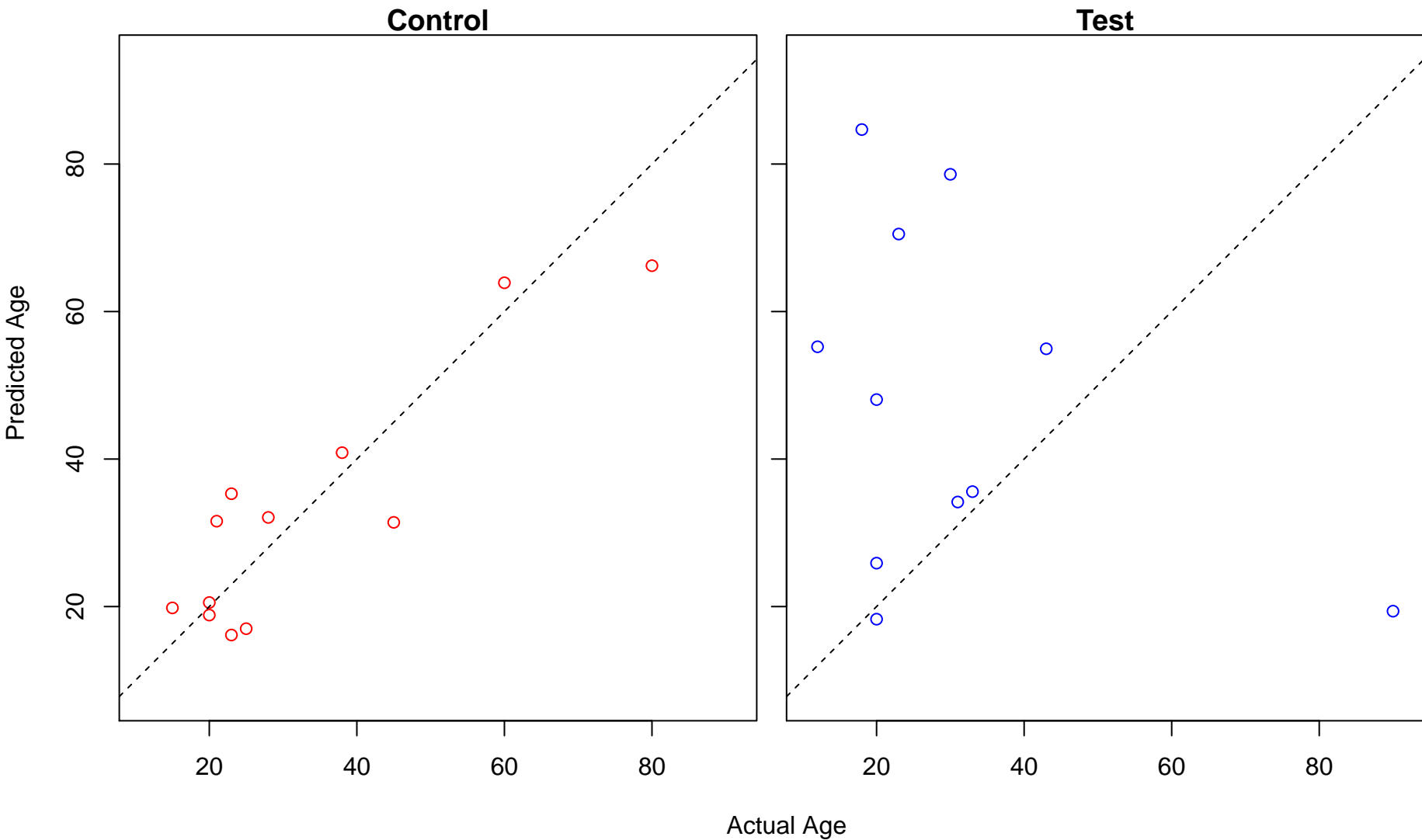
axoneme assembly (Score: 27.834277)



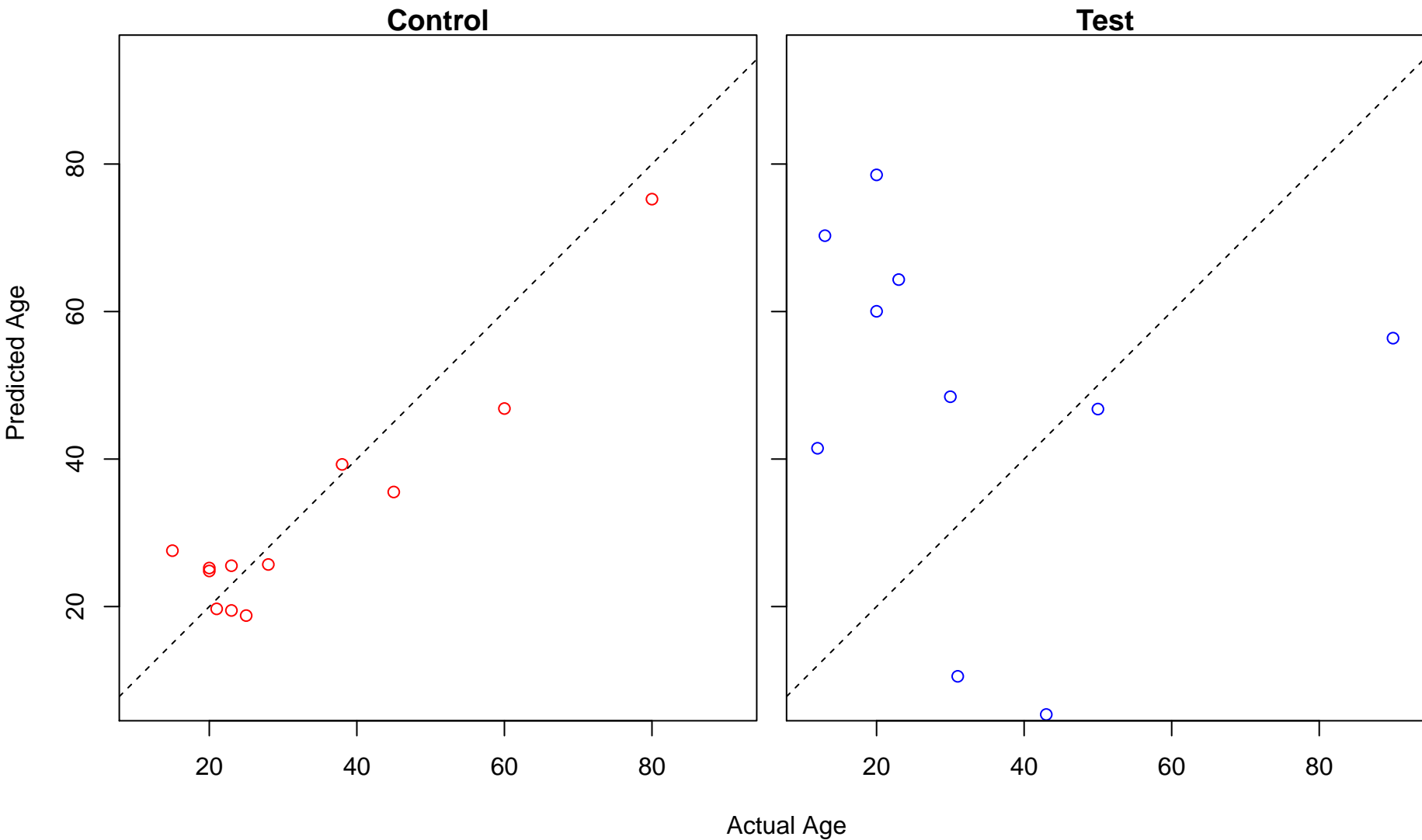
cellular pigmentation (Score: 27.783332)



negative regulation of endothelial cell migration (Score: 27.728083)

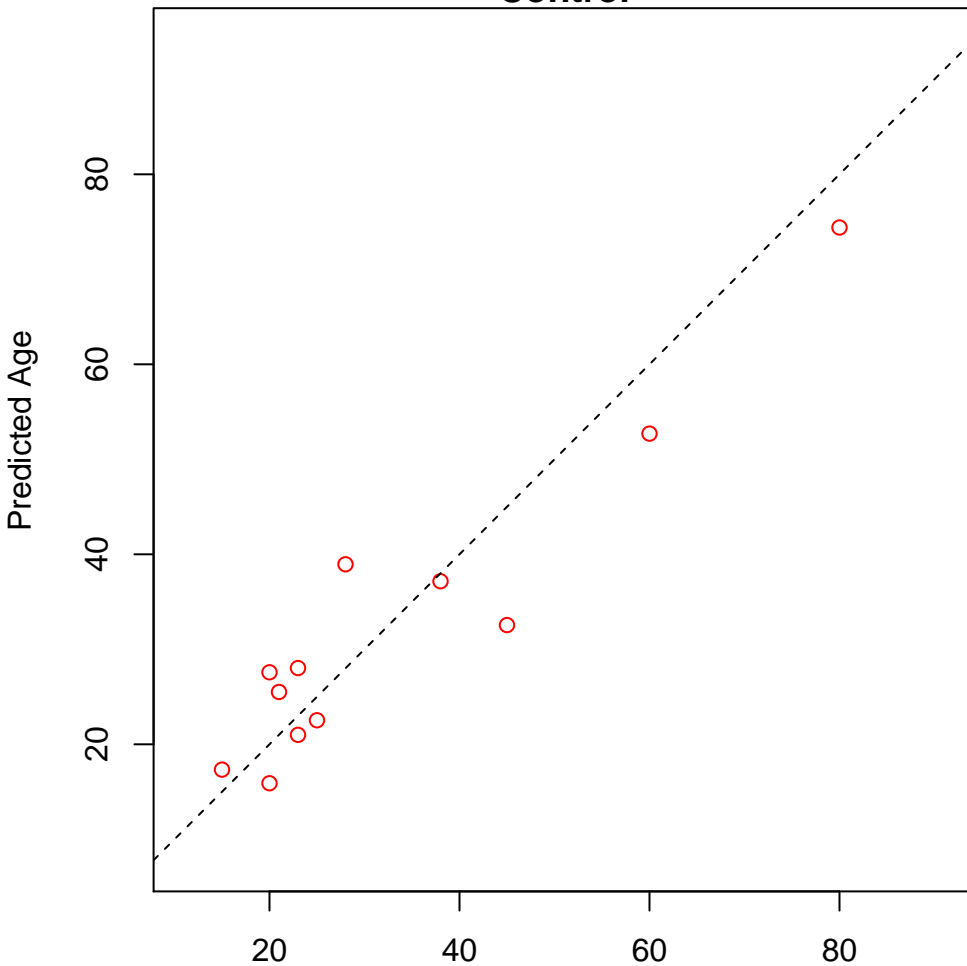


regulation of DNA-dependent DNA replication (Score: 27.723538)

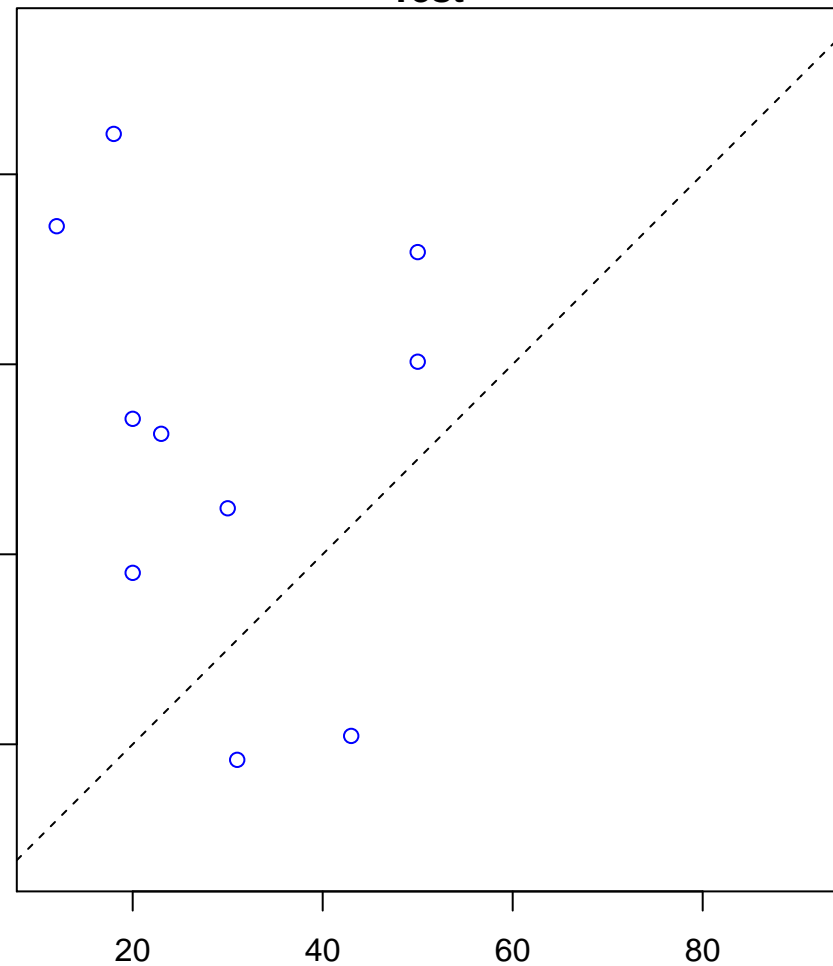


G2/M transition of mitotic cell cycle (Score: 27.712286)

Control

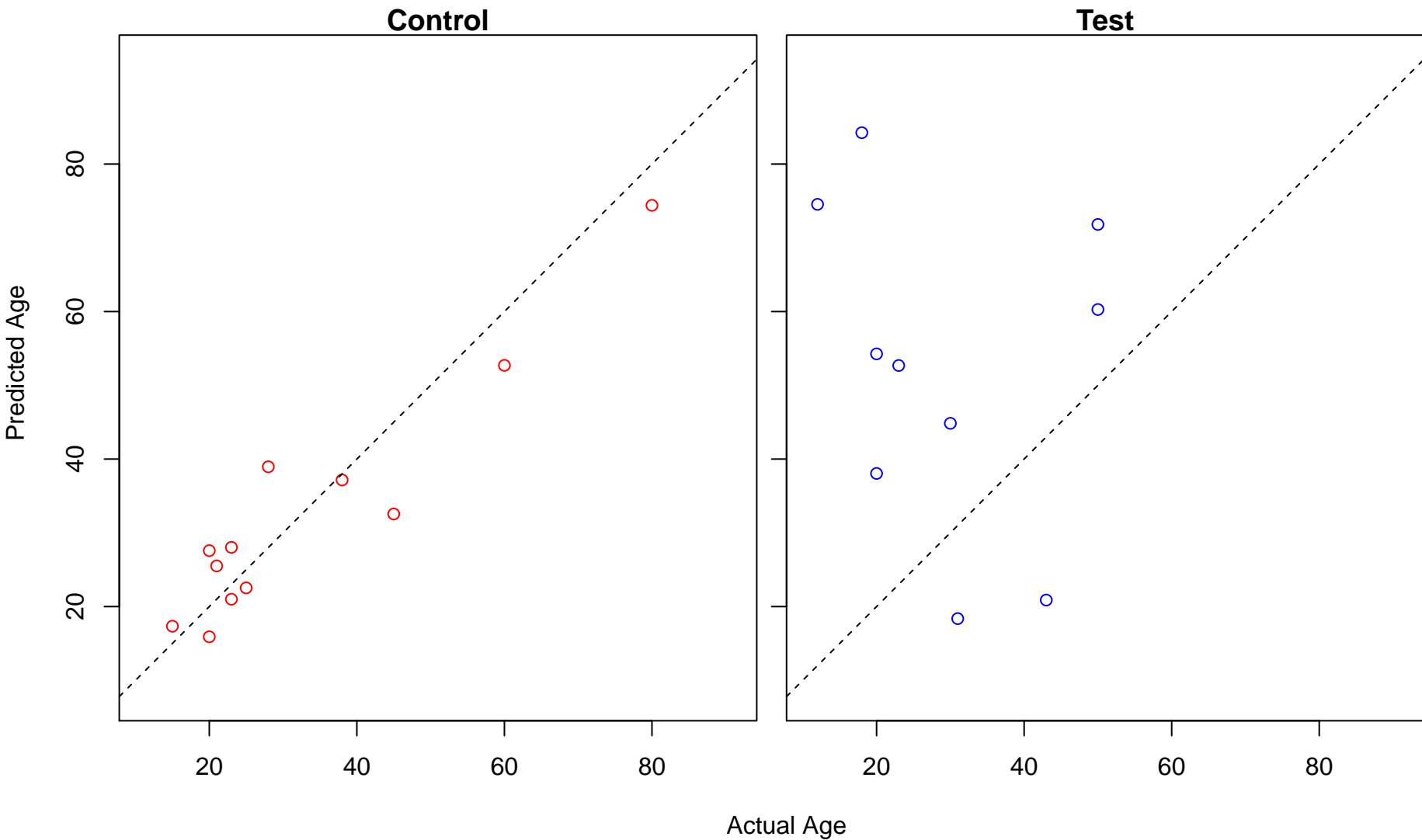


Test

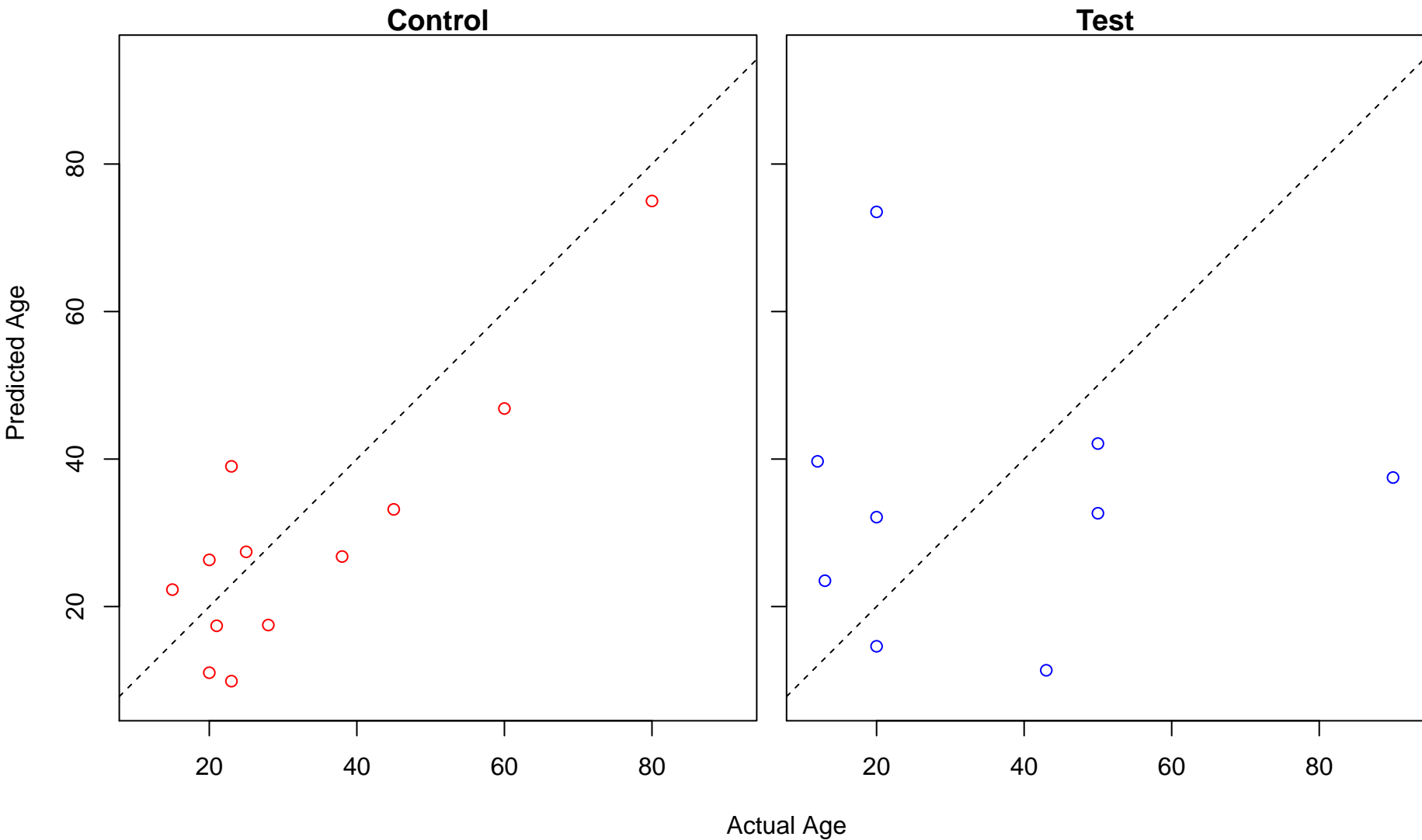


Actual Age

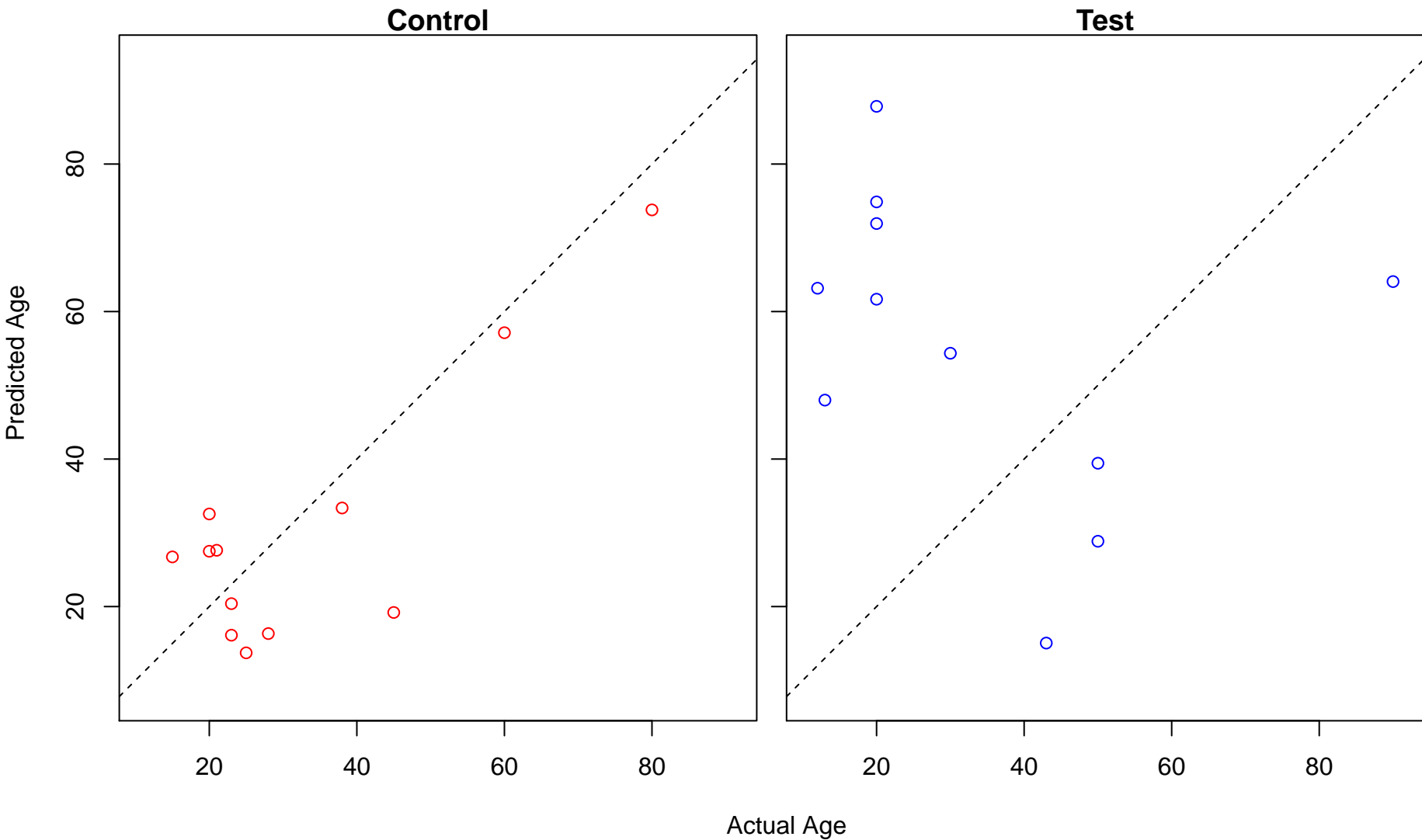
cell cycle G2/M phase transition (Score: 27.712286)



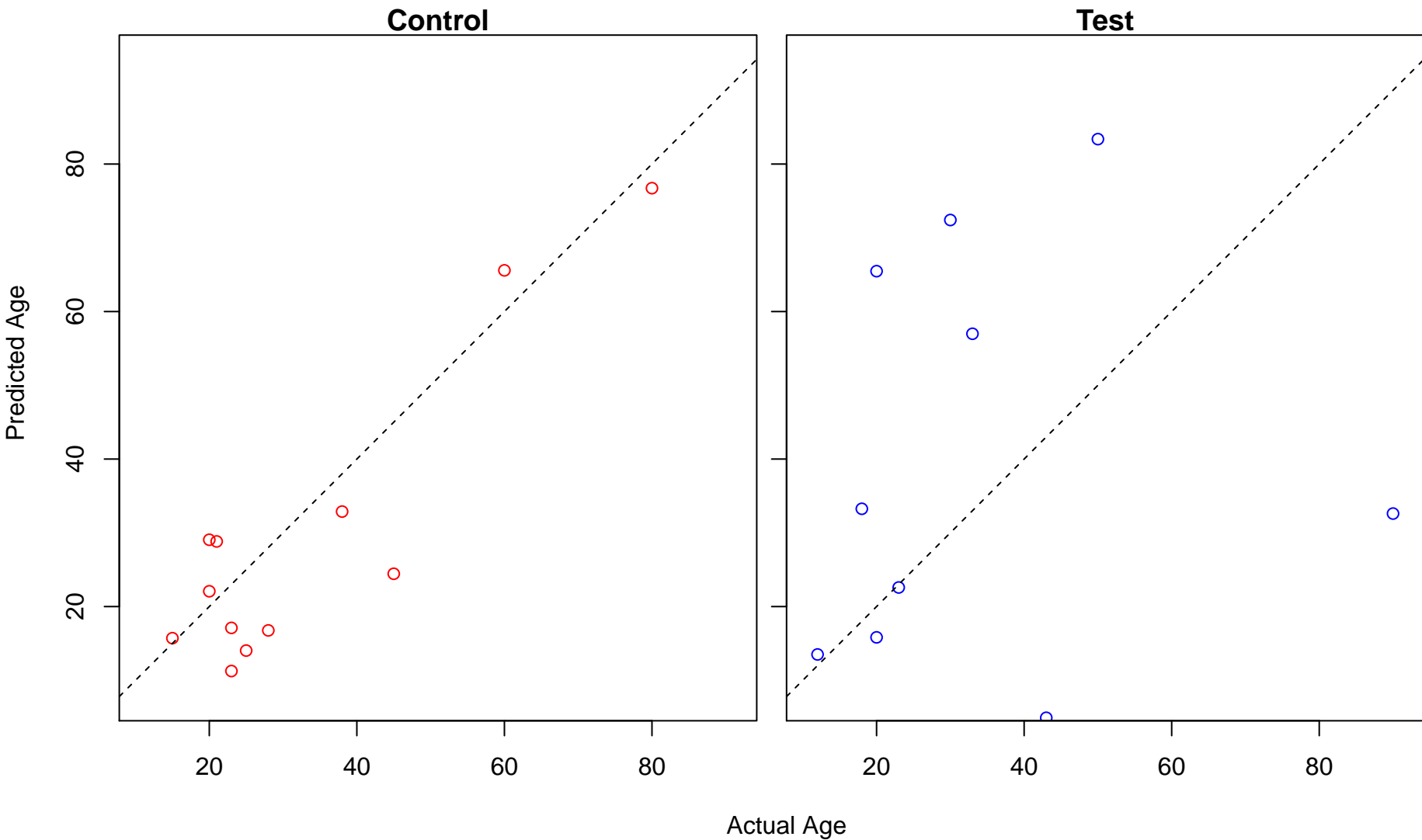
relaxation of muscle (Score: 27.682593)



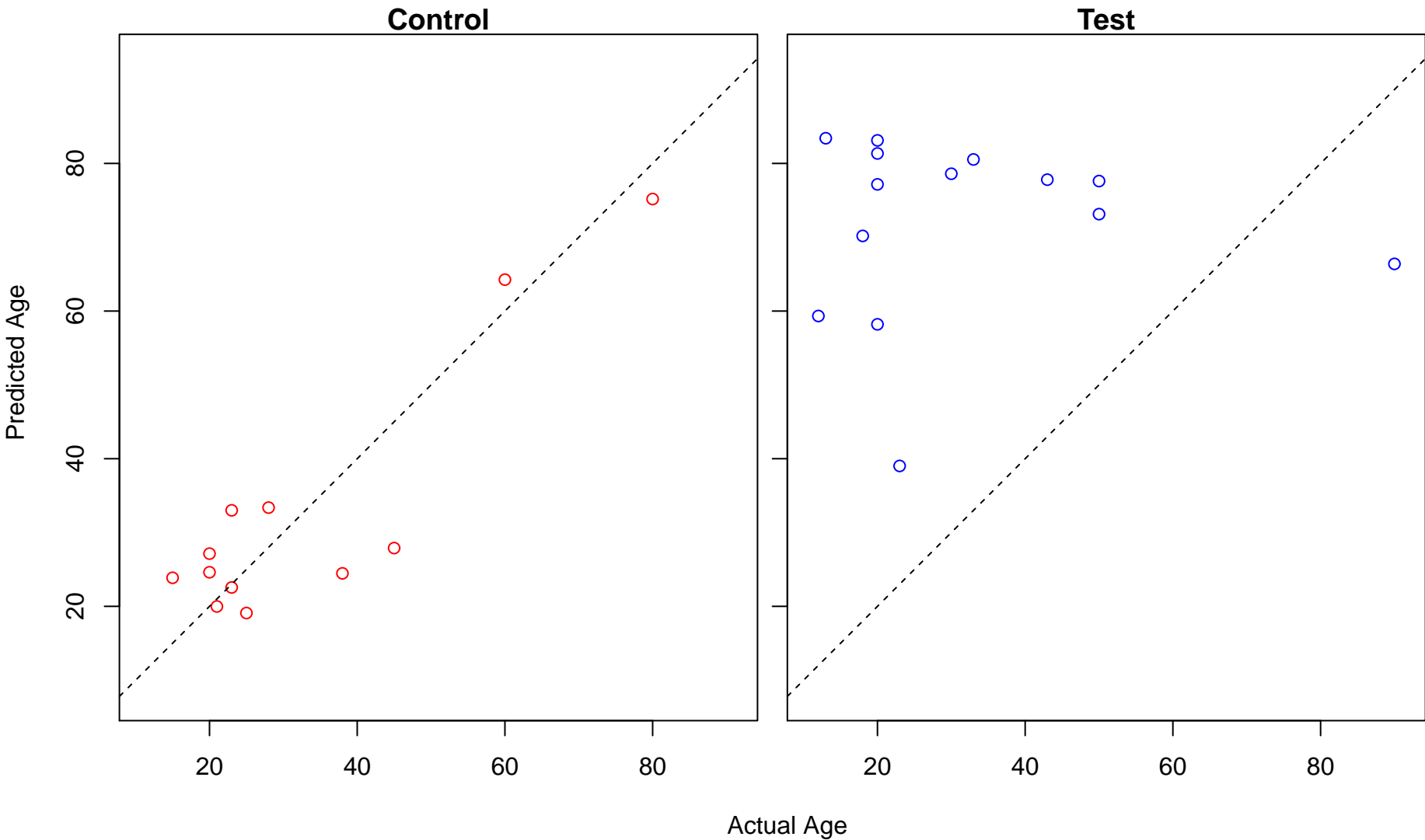
regulation of glucose transport (Score: 27.675032)



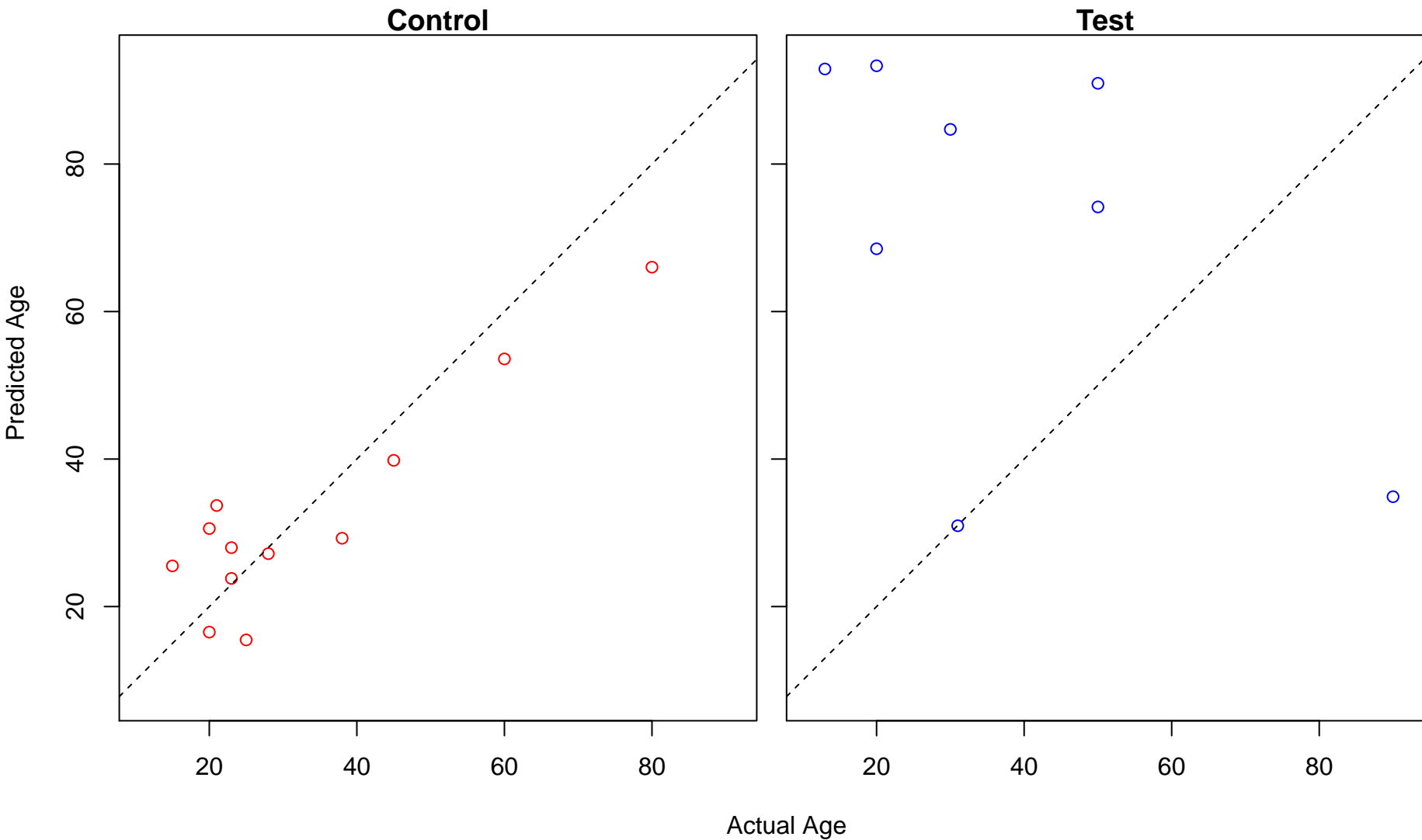
positive regulation of lipid transport (Score: 27.571257)



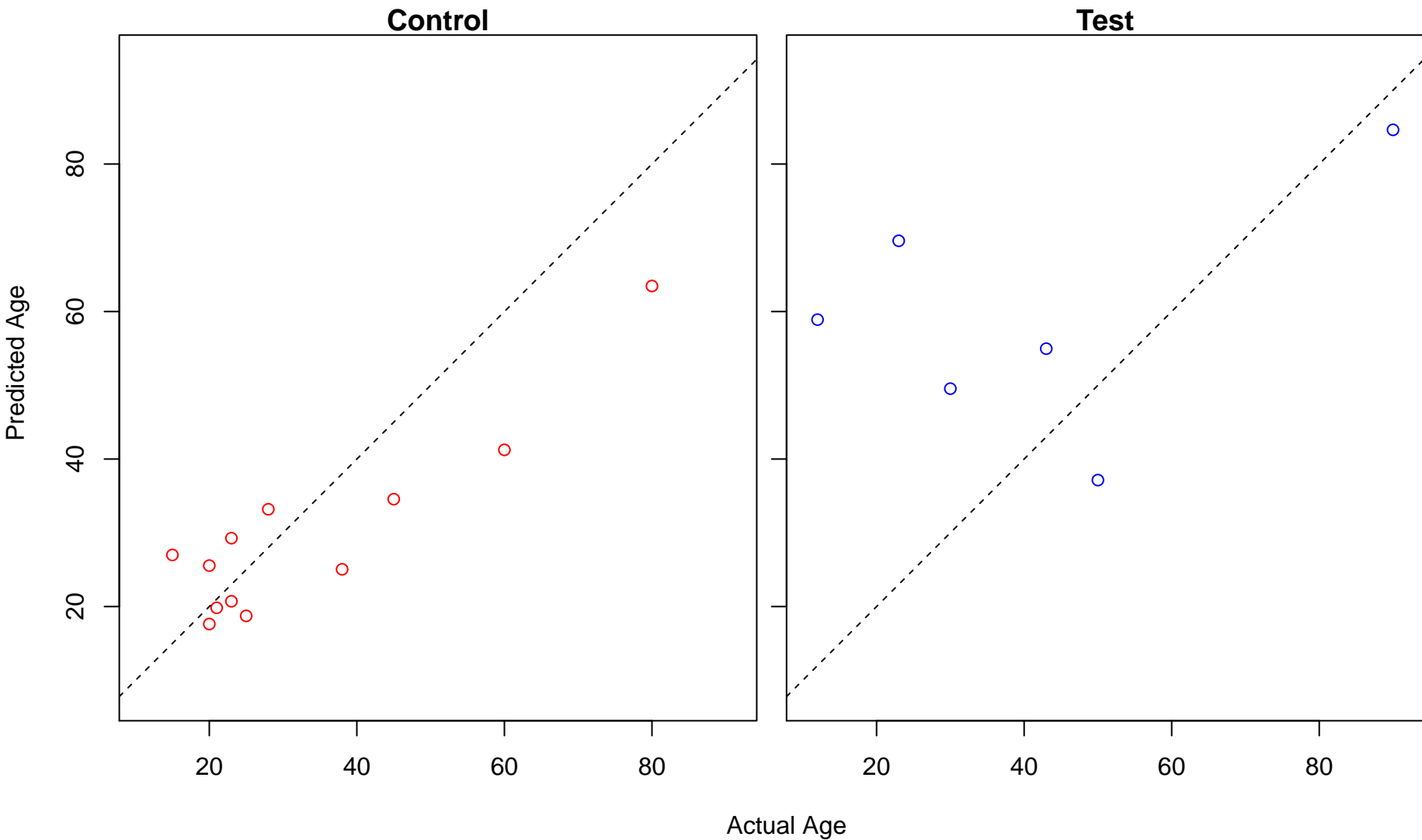
phospholipase C-activating G-protein coupled receptor signaling pathway (Score: 27.511541)



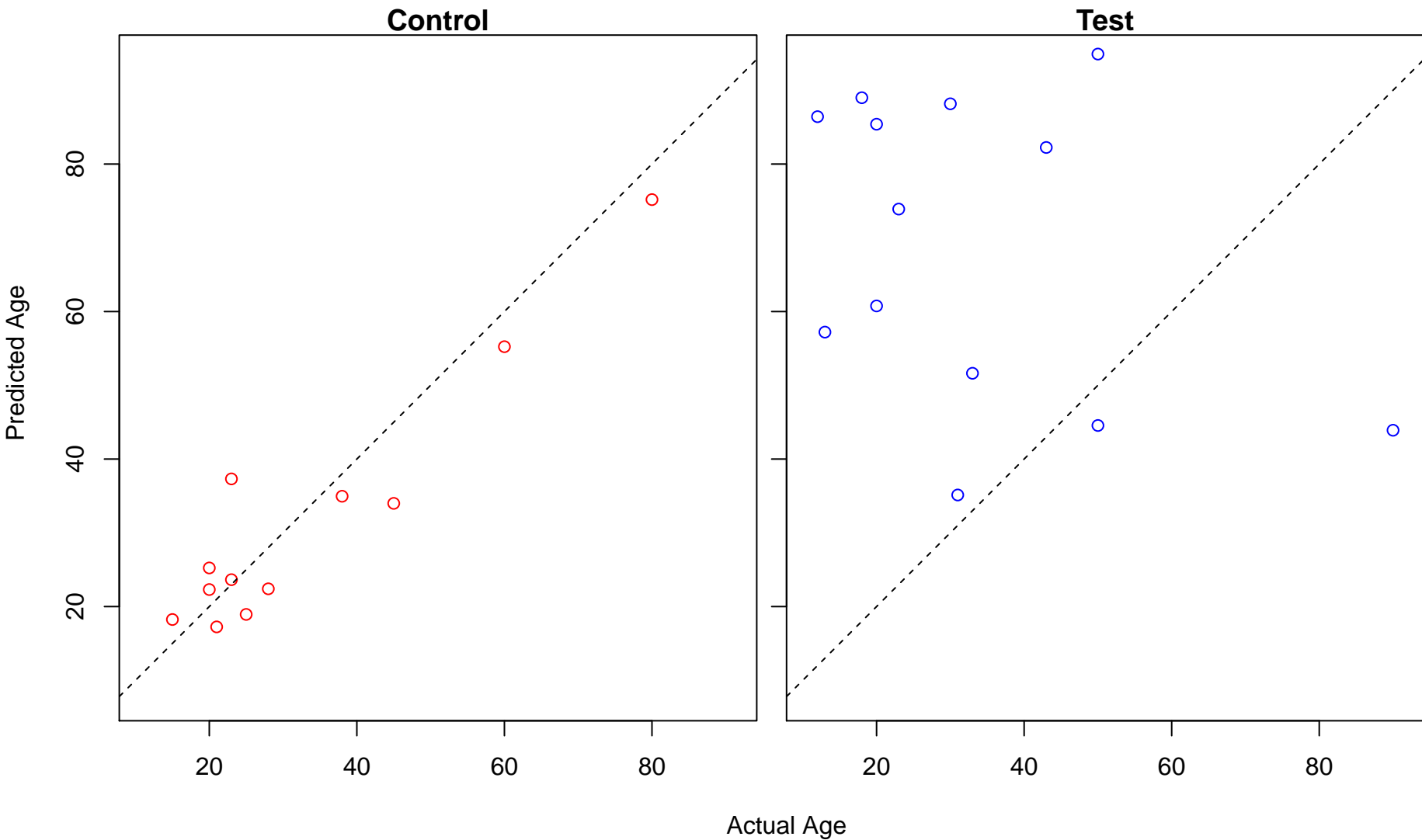
protein ufmylation (Score: 27.391926)



copper ion transport (Score: 27.378439)

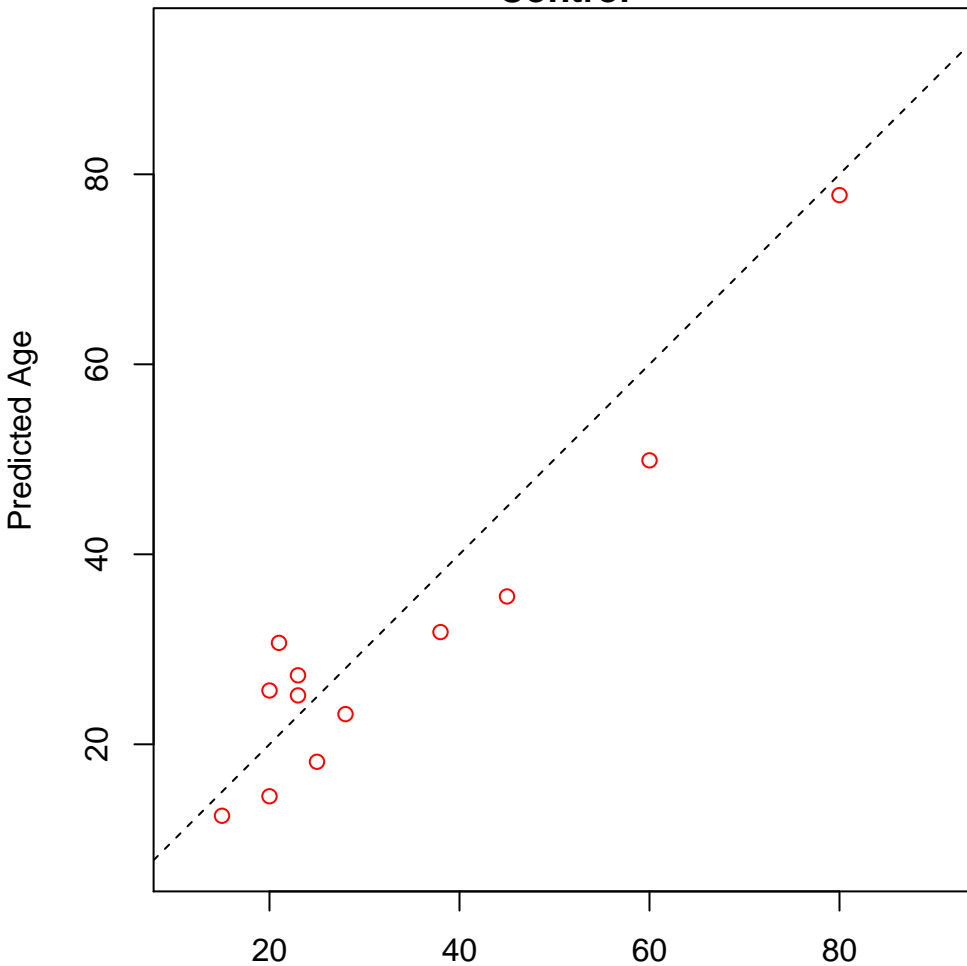


monocarboxylic acid transport (Score: 27.319175)

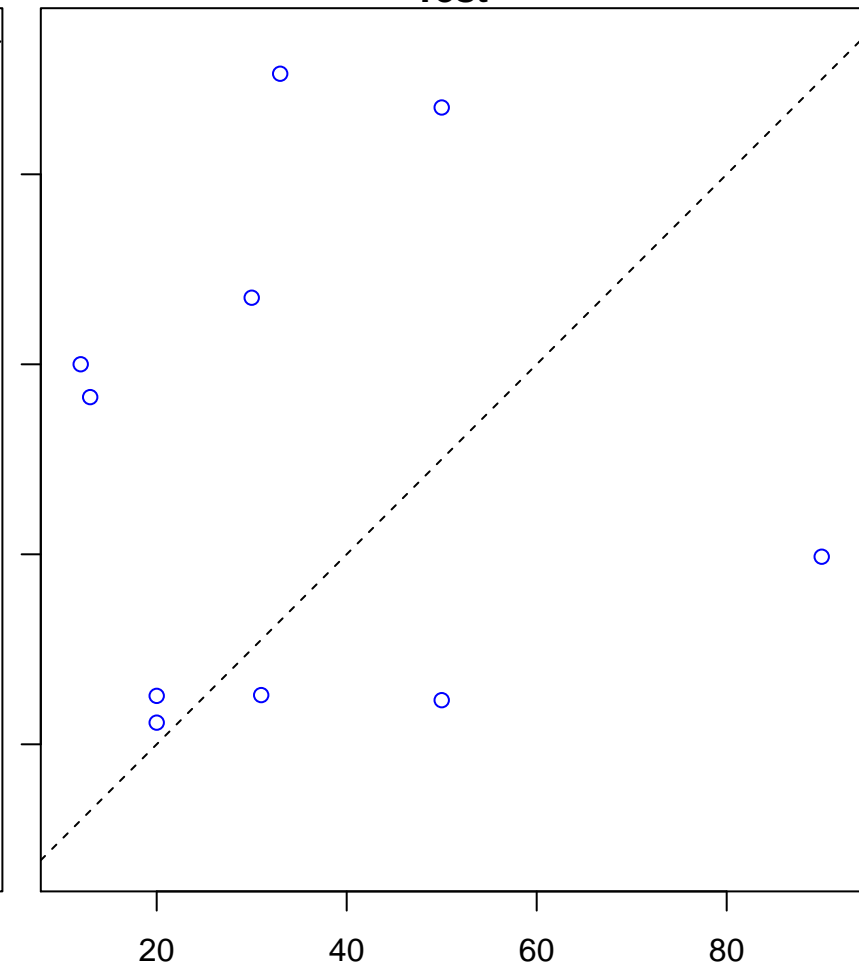


multivesicular body sorting pathway (Score: 27.314799)

Control

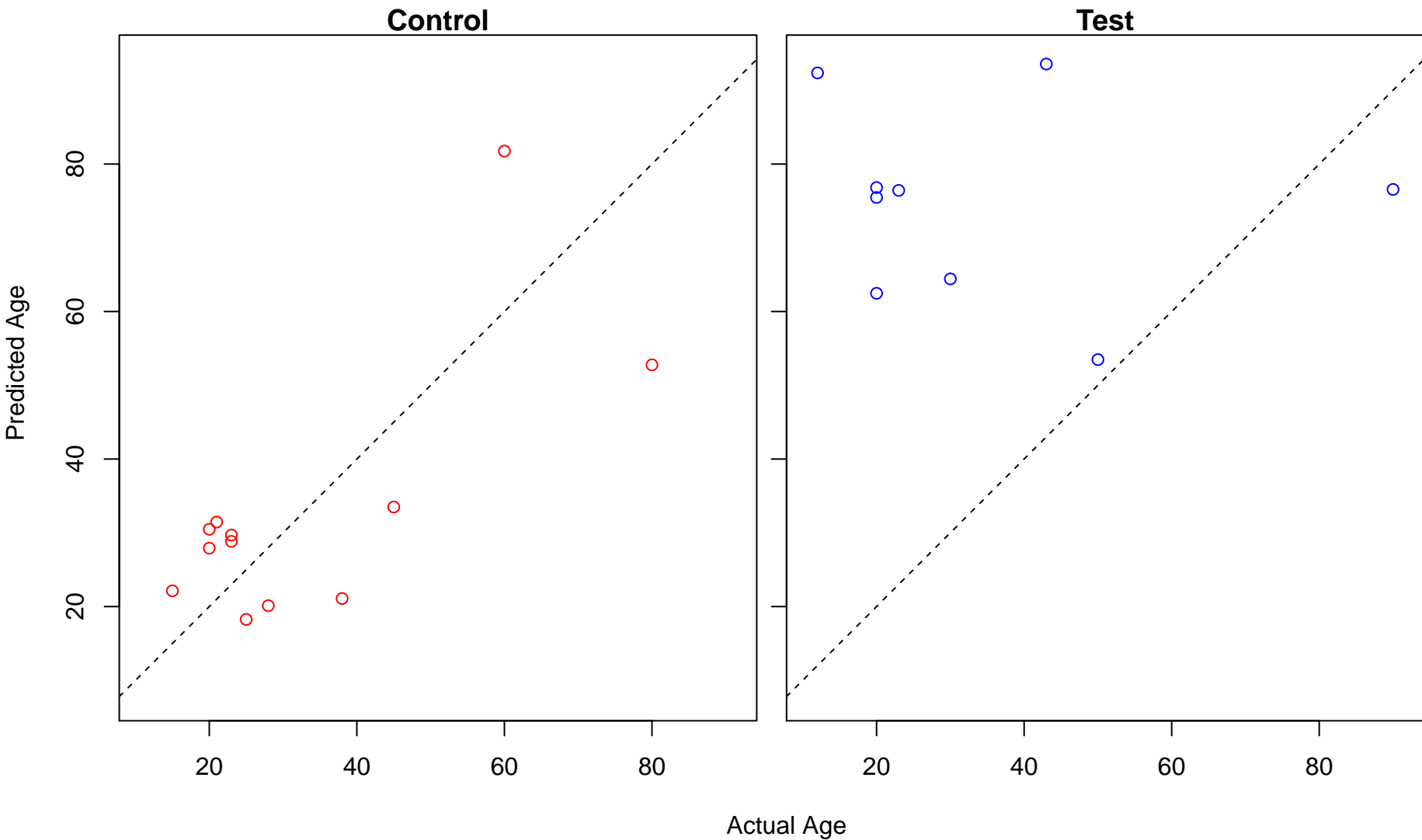


Test



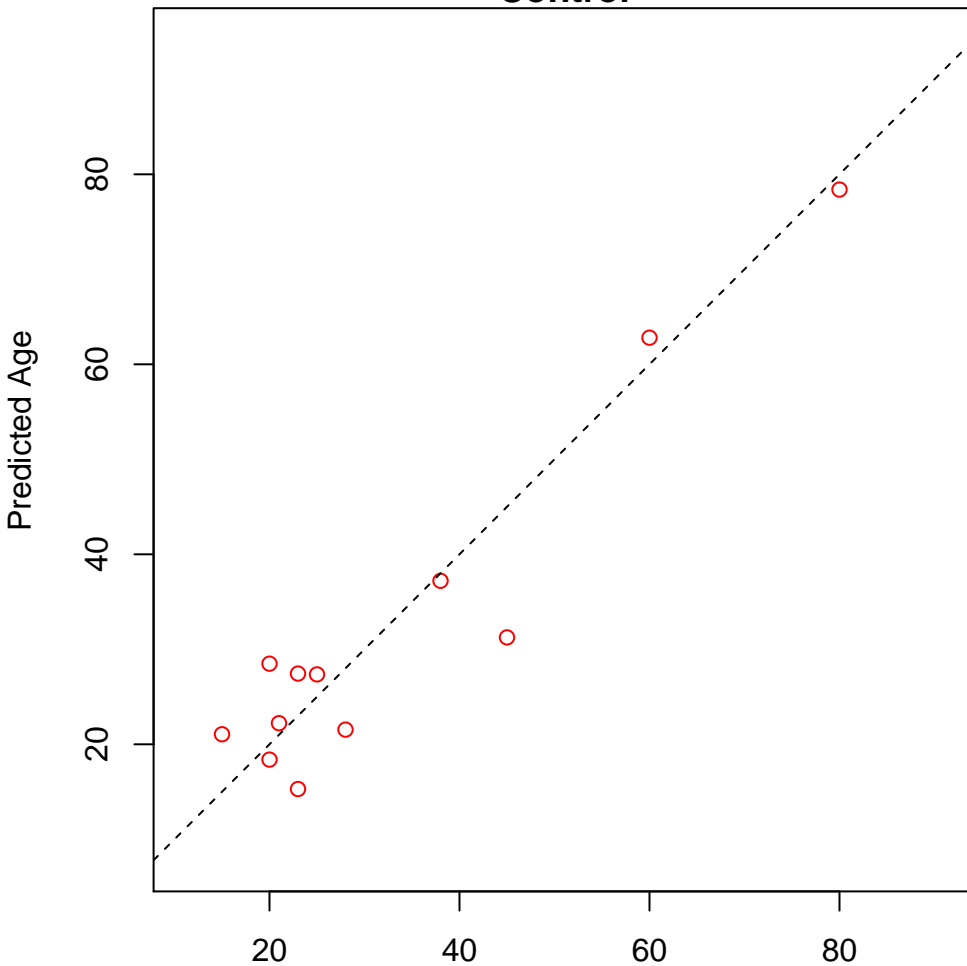
Actual Age

regulation of interleukin-2 biosynthetic process (Score: 27.290743)

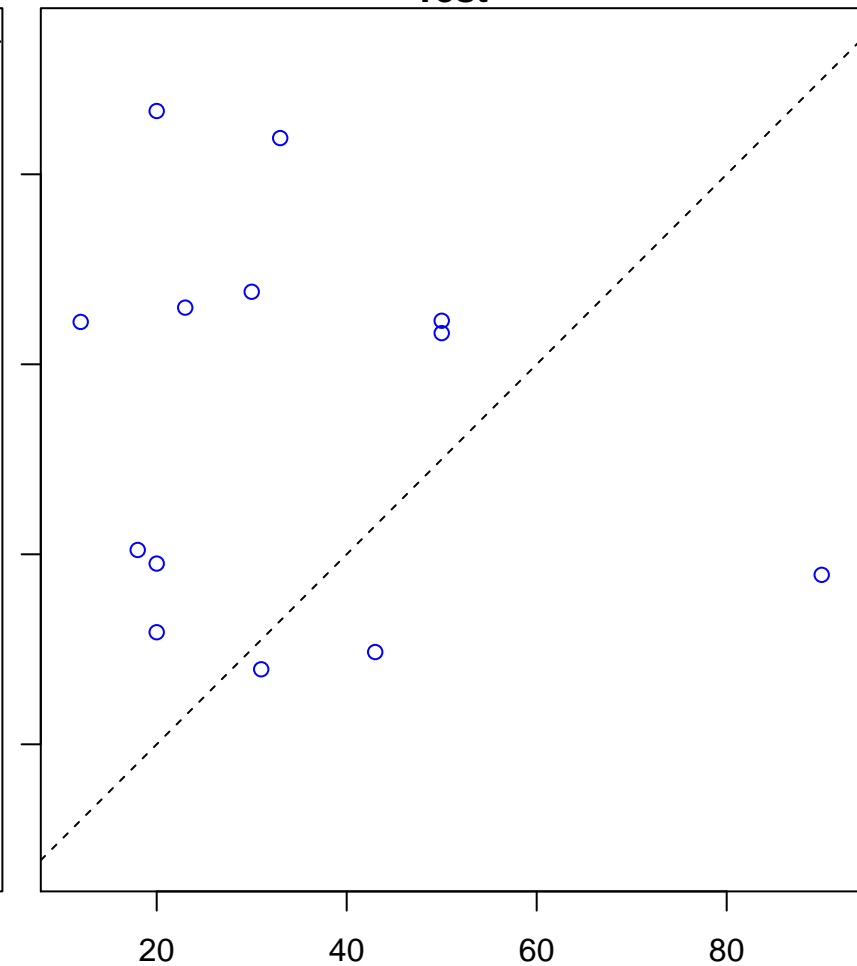


protein localization to mitochondrion (Score: 27.280712)

Control

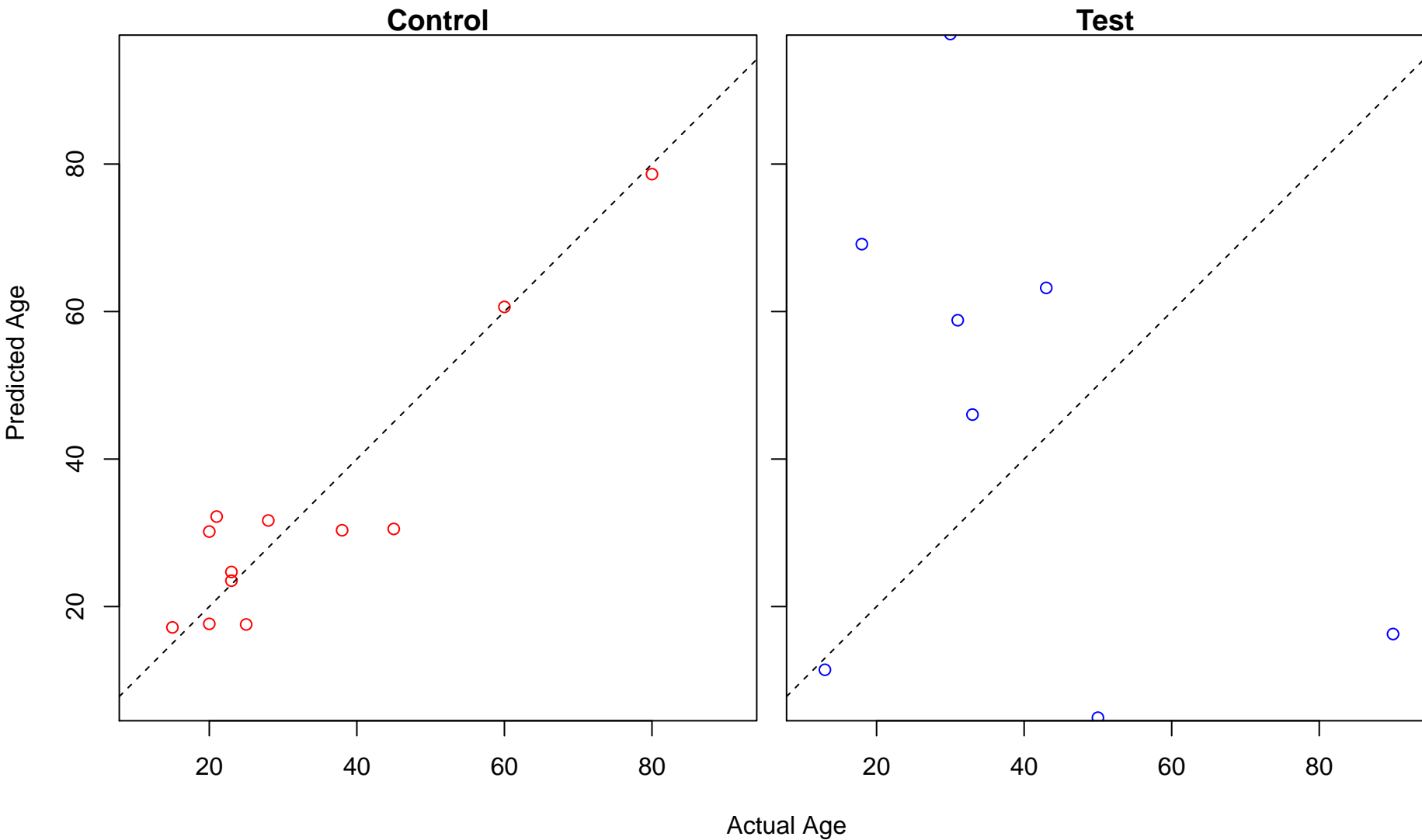


Test

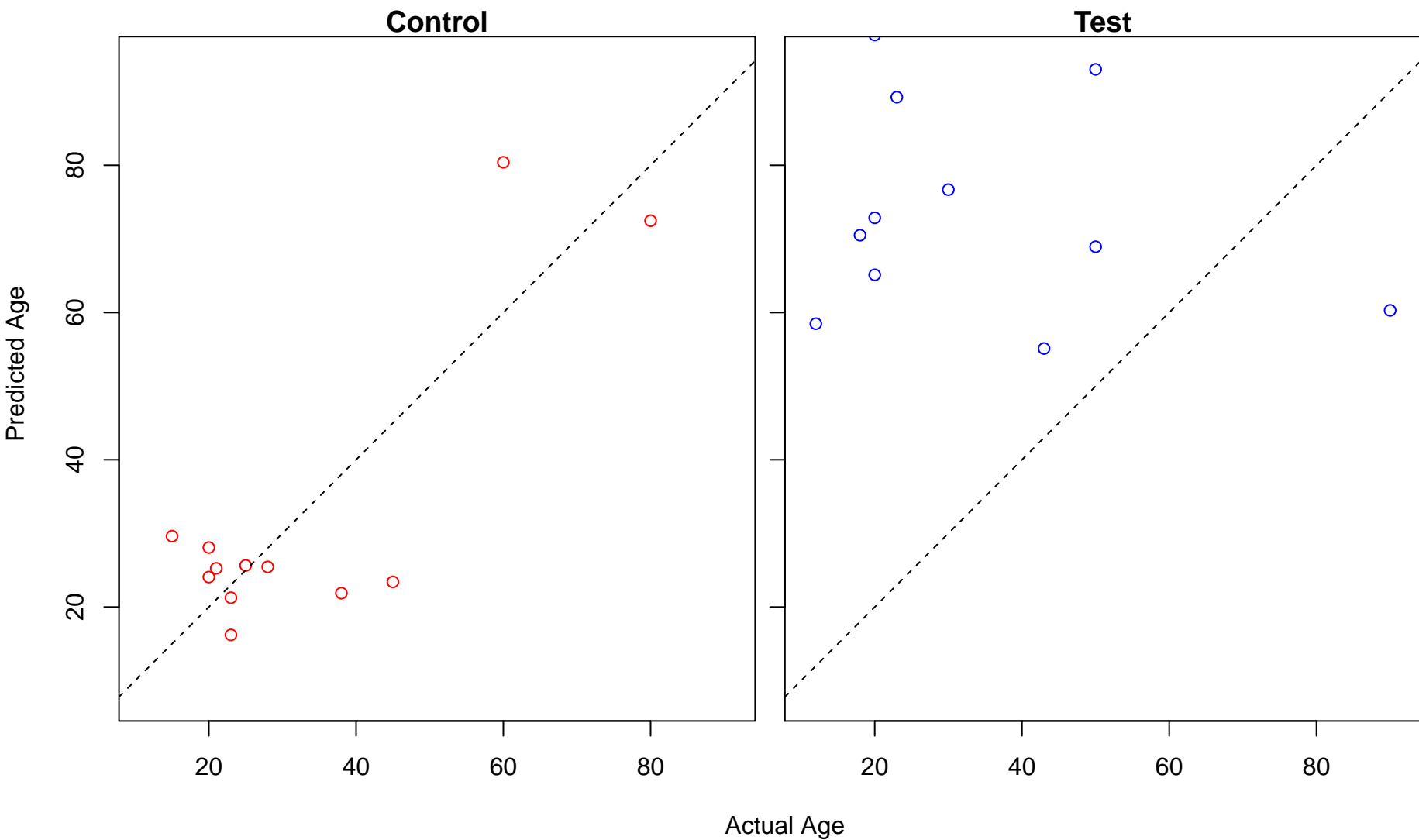


Actual Age

regulation of voltage-gated calcium channel activity (Score: 27.203968)

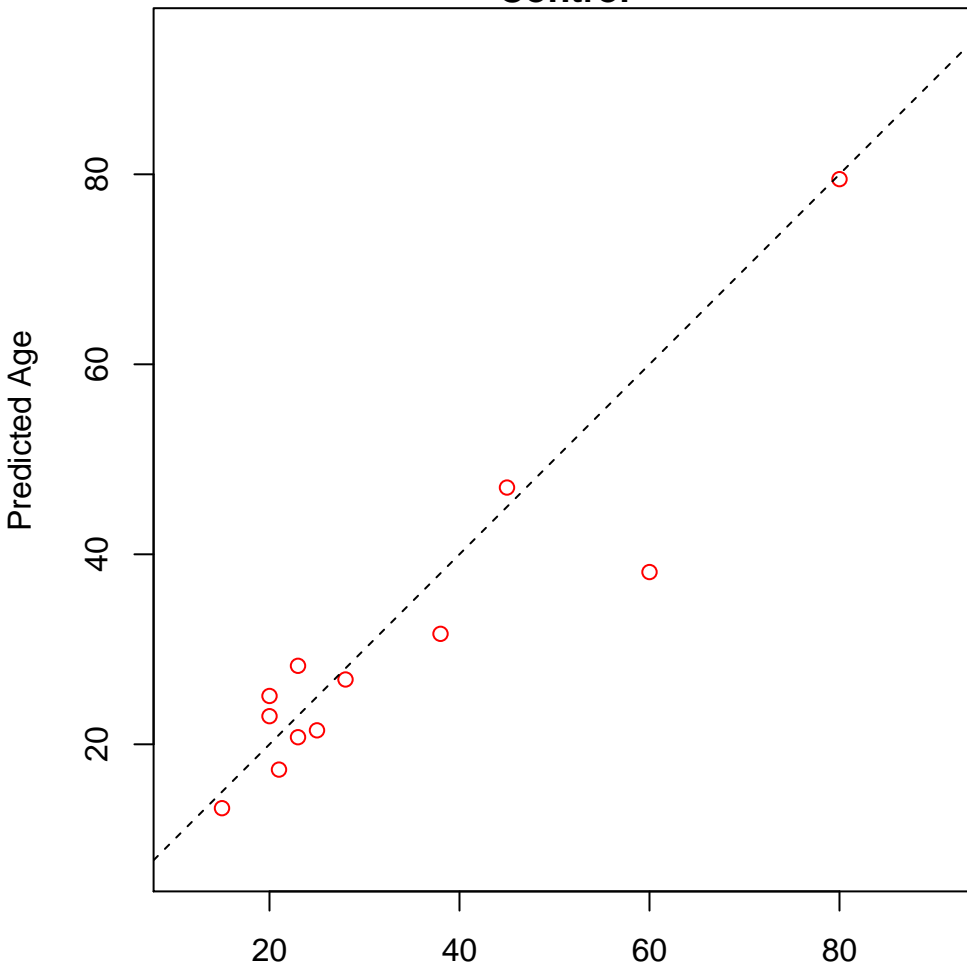


positive regulation of membrane protein ectodomain proteolysis (Score: 27.077468)

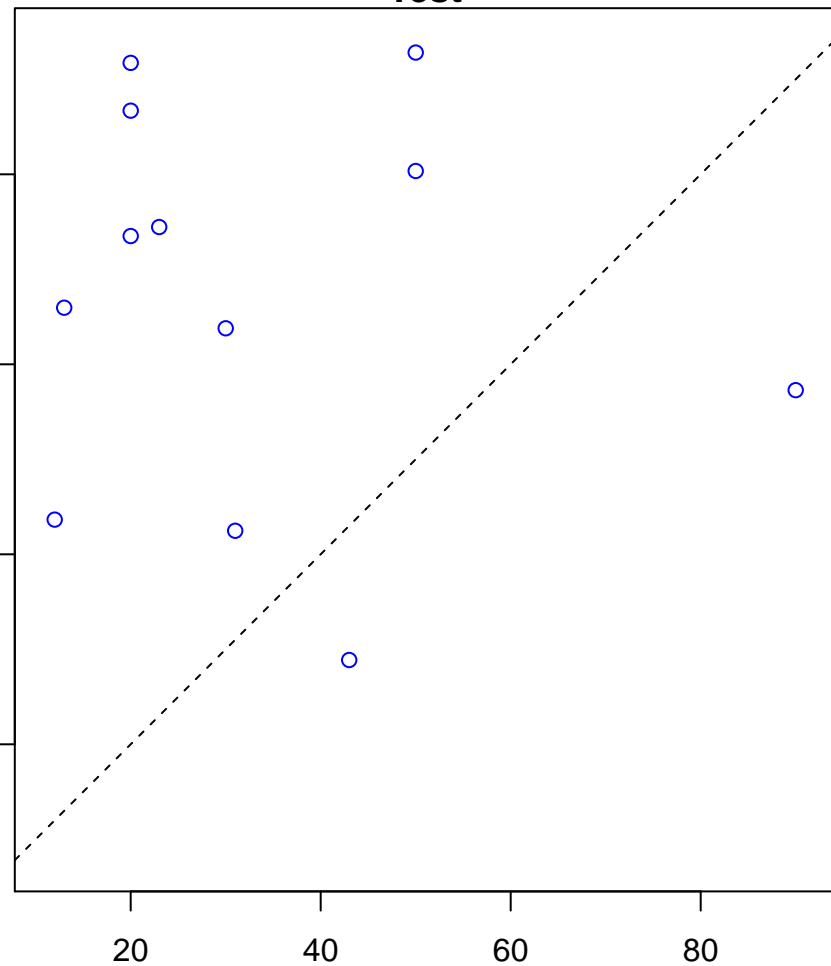


regulation of DNA endoreduplication (Score: 27.051367)

Control

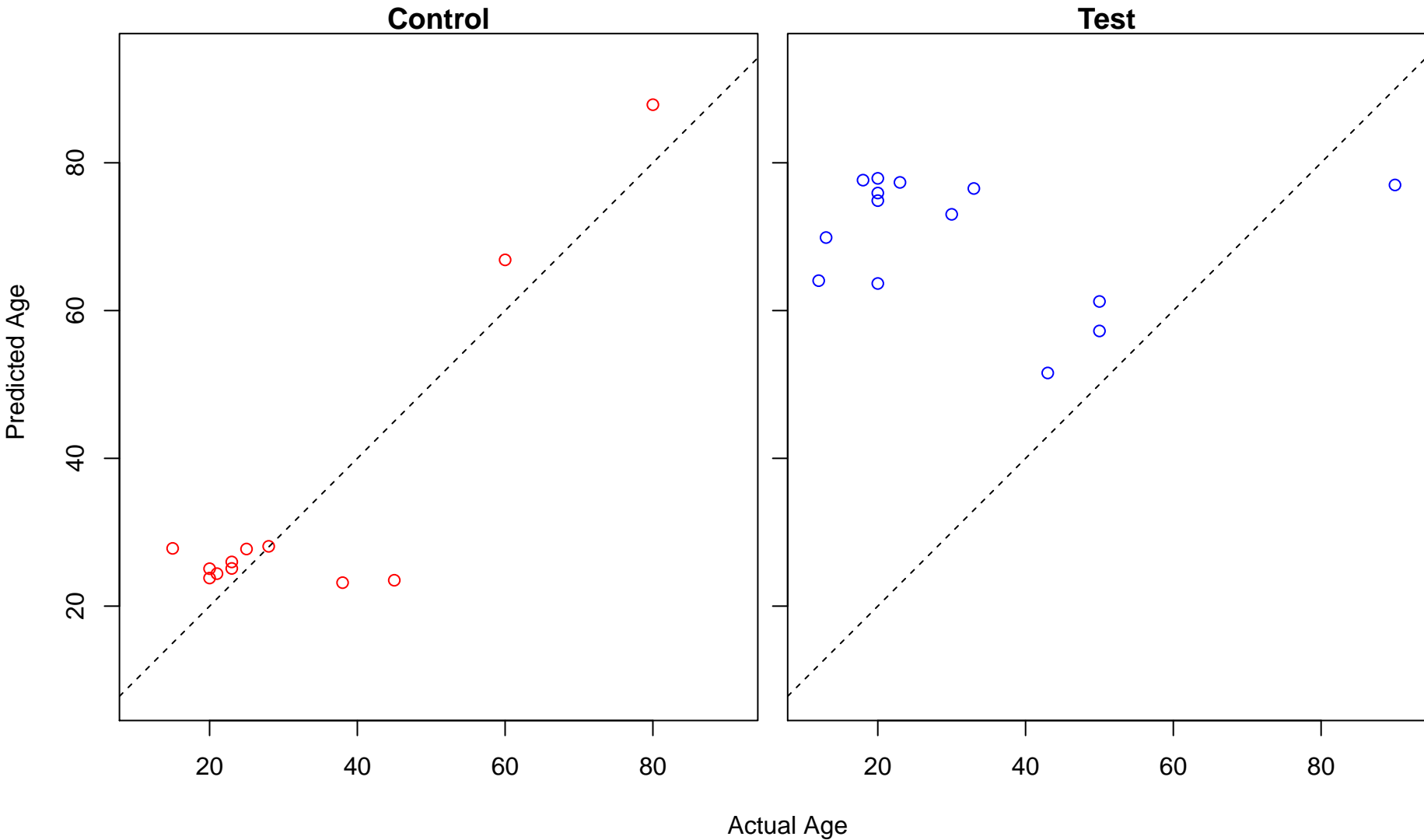


Test

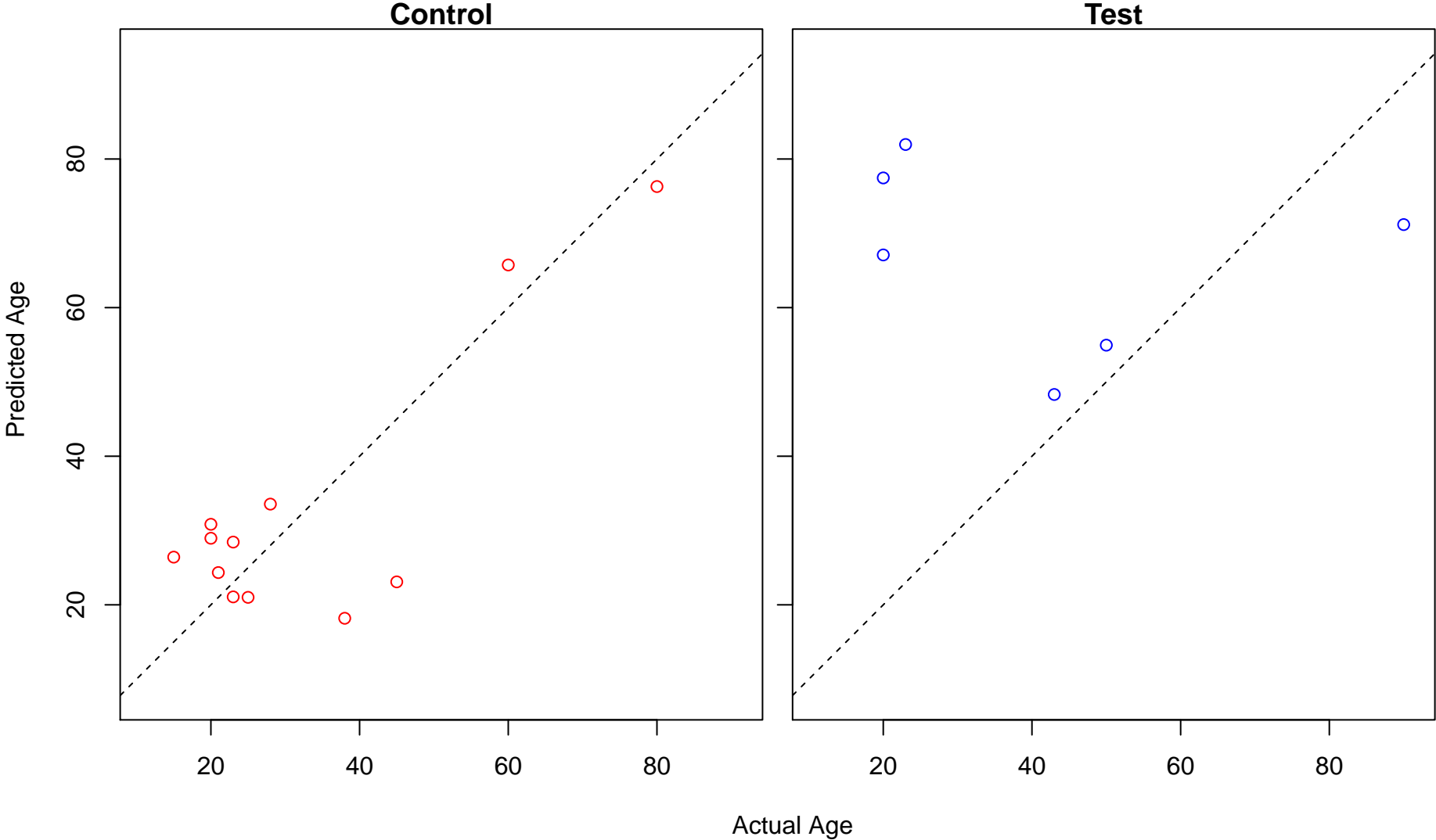


Actual Age

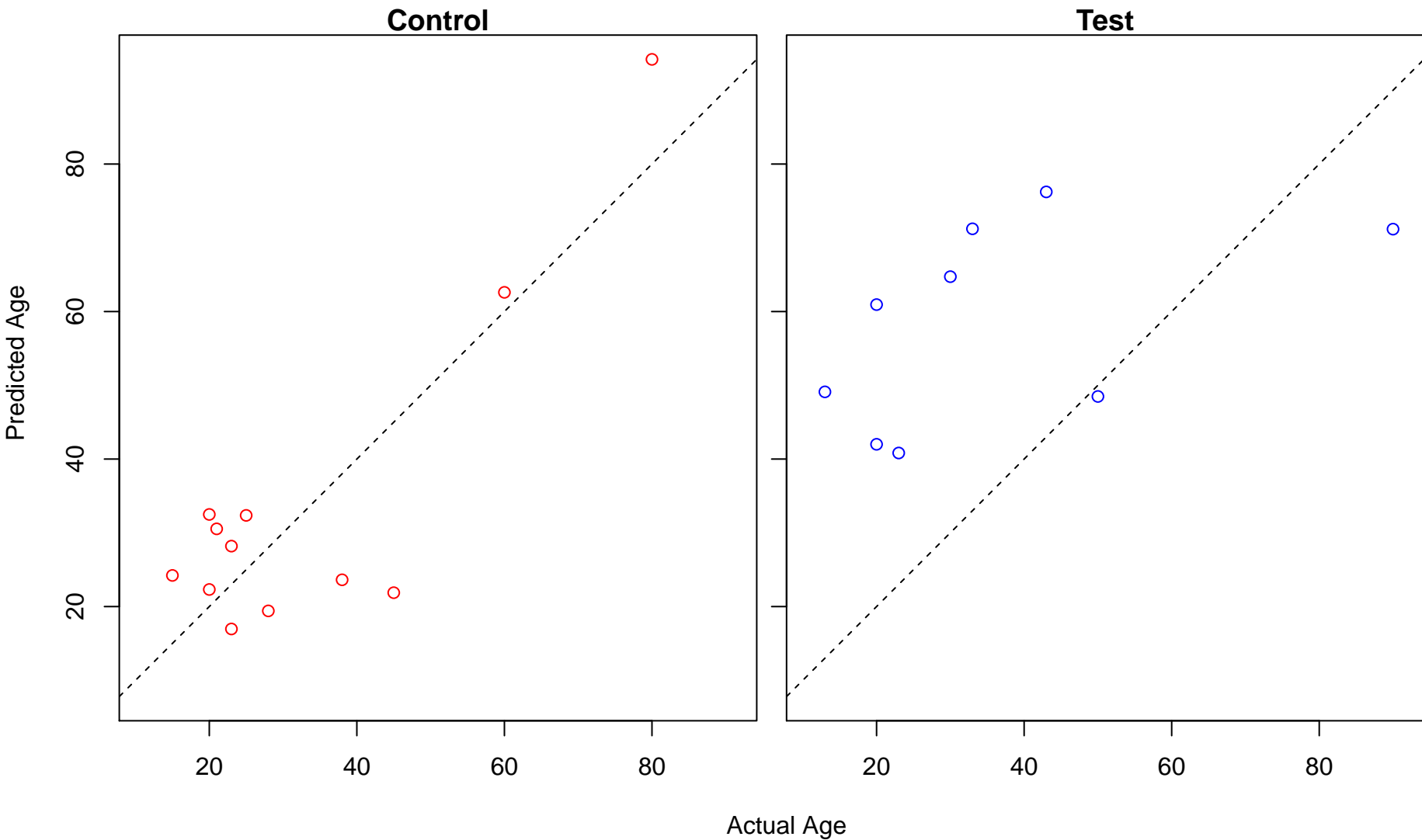
regulation of NF-kappaB import into nucleus (Score: 27.030625)



positive regulation of endothelial cell proliferation (Score: 26.945535)

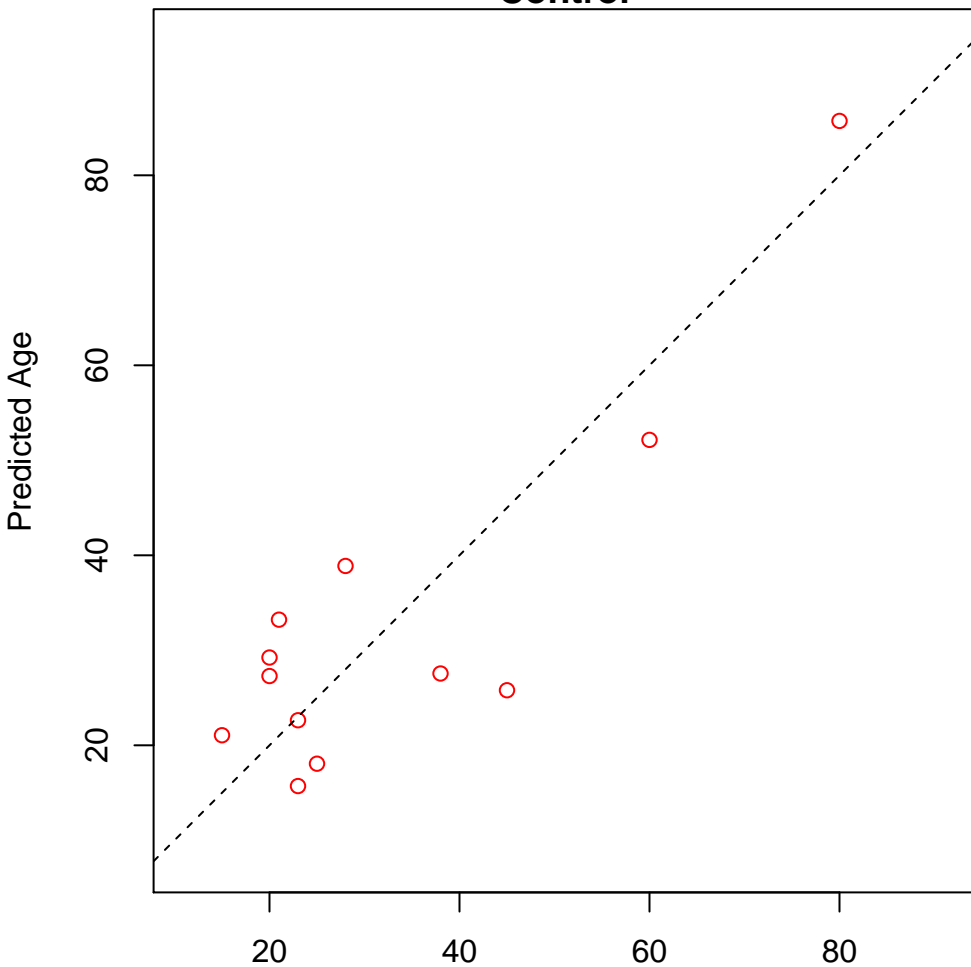


regulation of steroid biosynthetic process (Score: 26.912795)

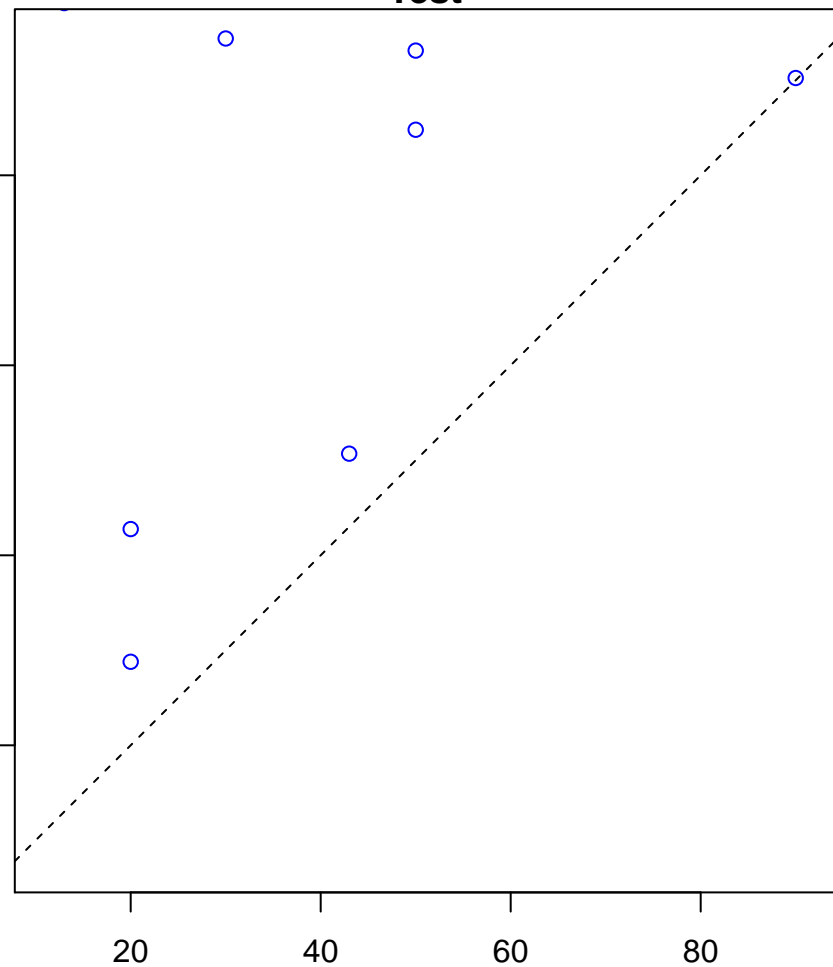


regulation of NIK/NF-kappaB signaling (Score: 26.751931)

Control

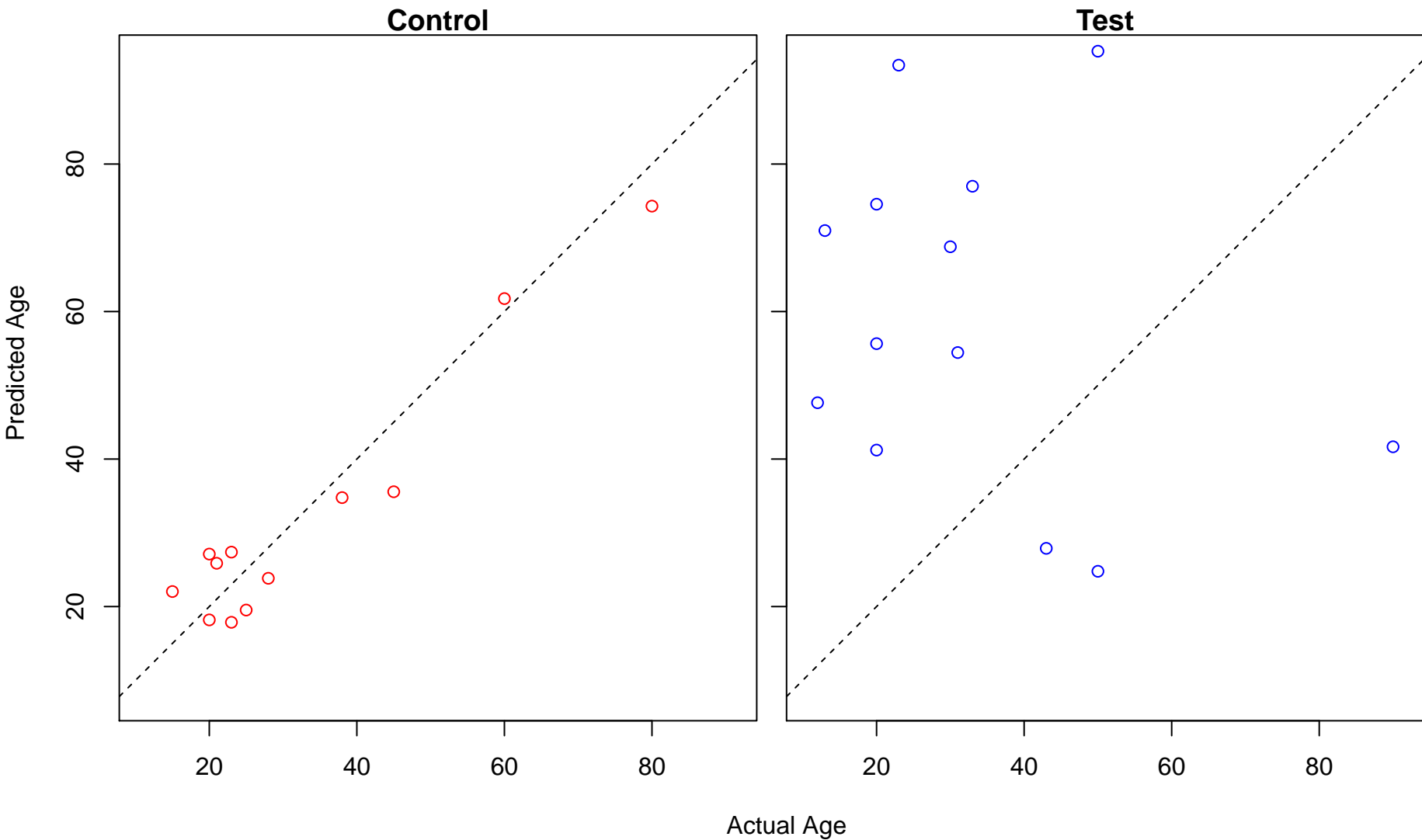


Test

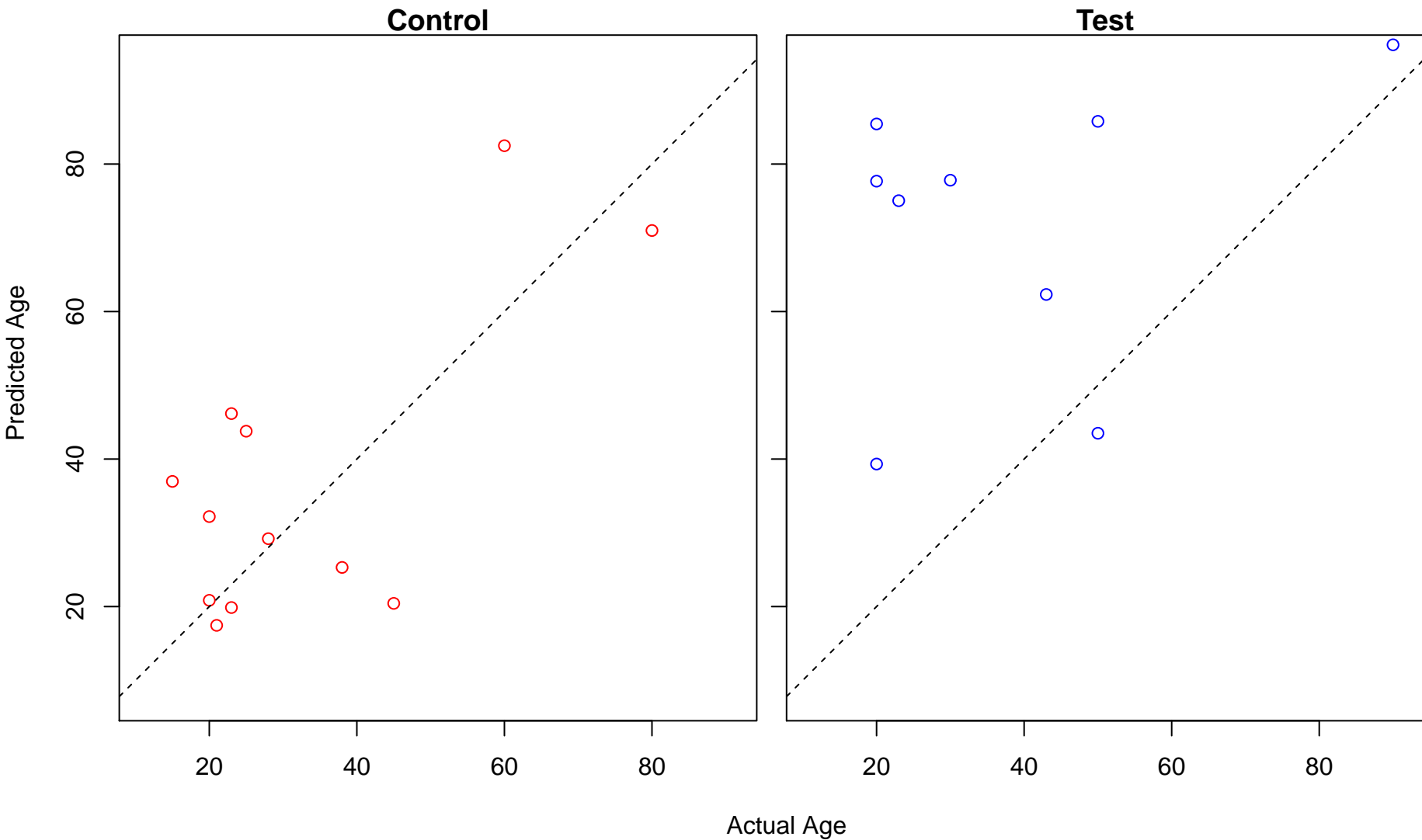


Actual Age

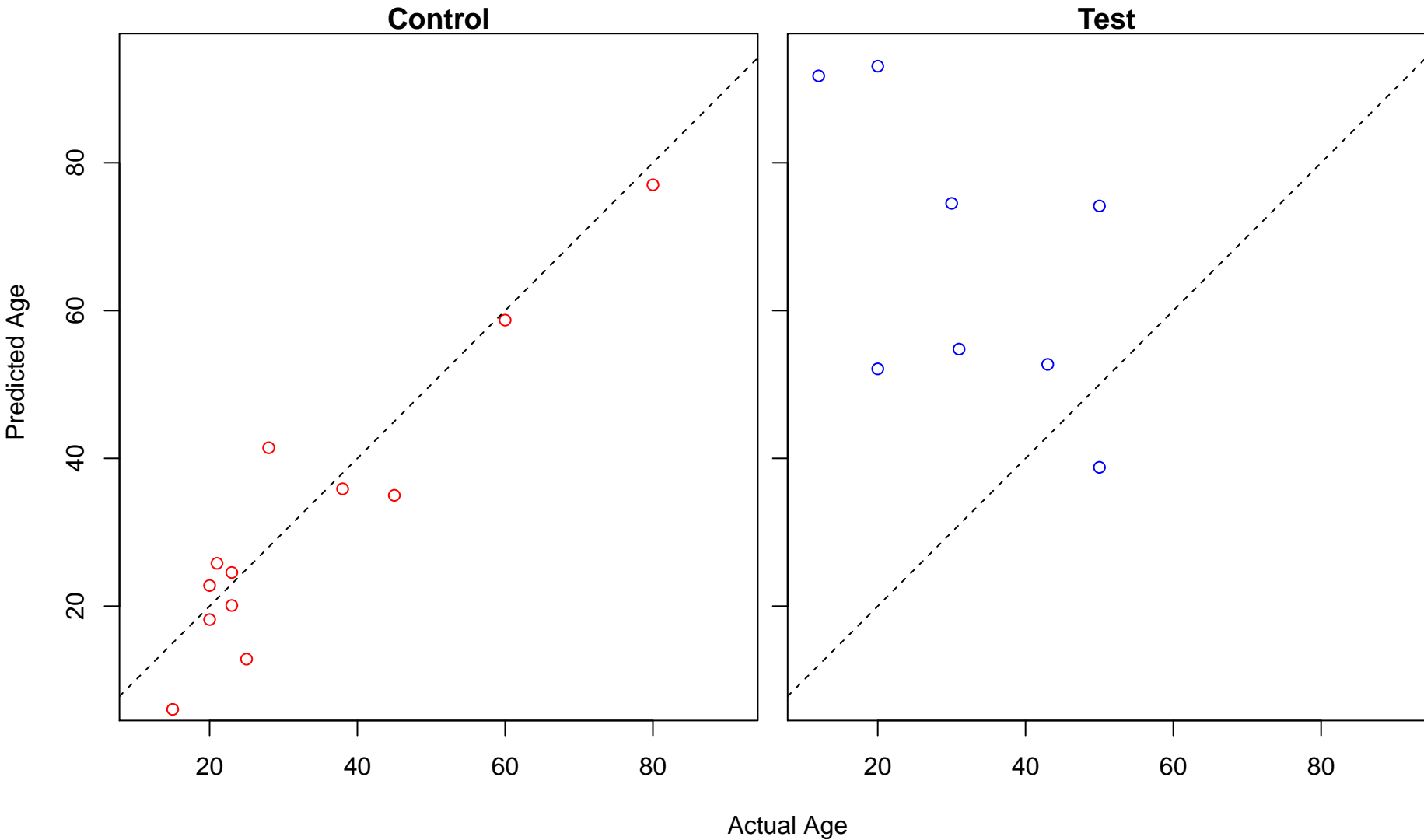
regulation of spindle checkpoint (Score: 26.739271)



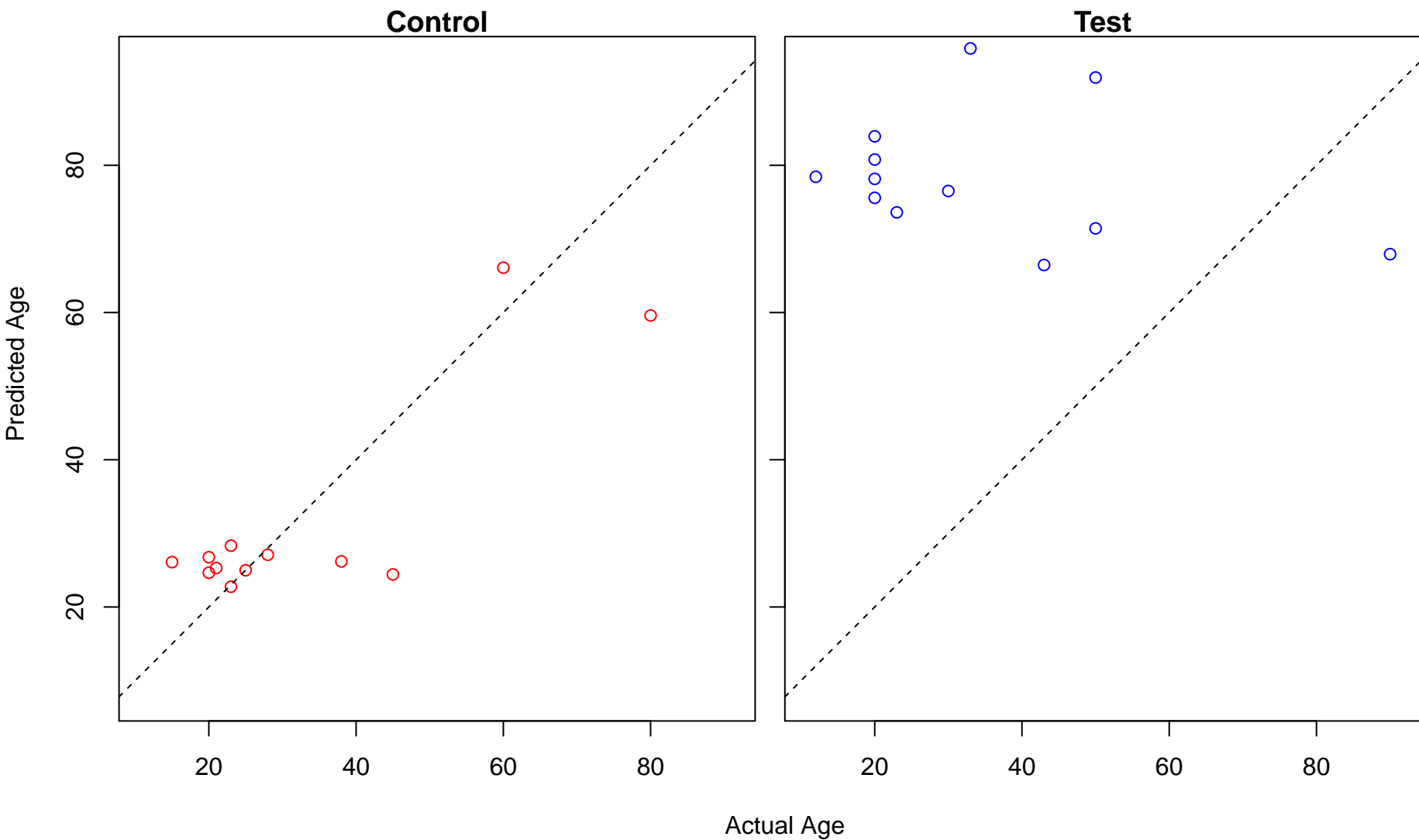
negative regulation of lipid catabolic process (Score: 26.663632)



regulation of lipoprotein metabolic process (Score: 26.492855)

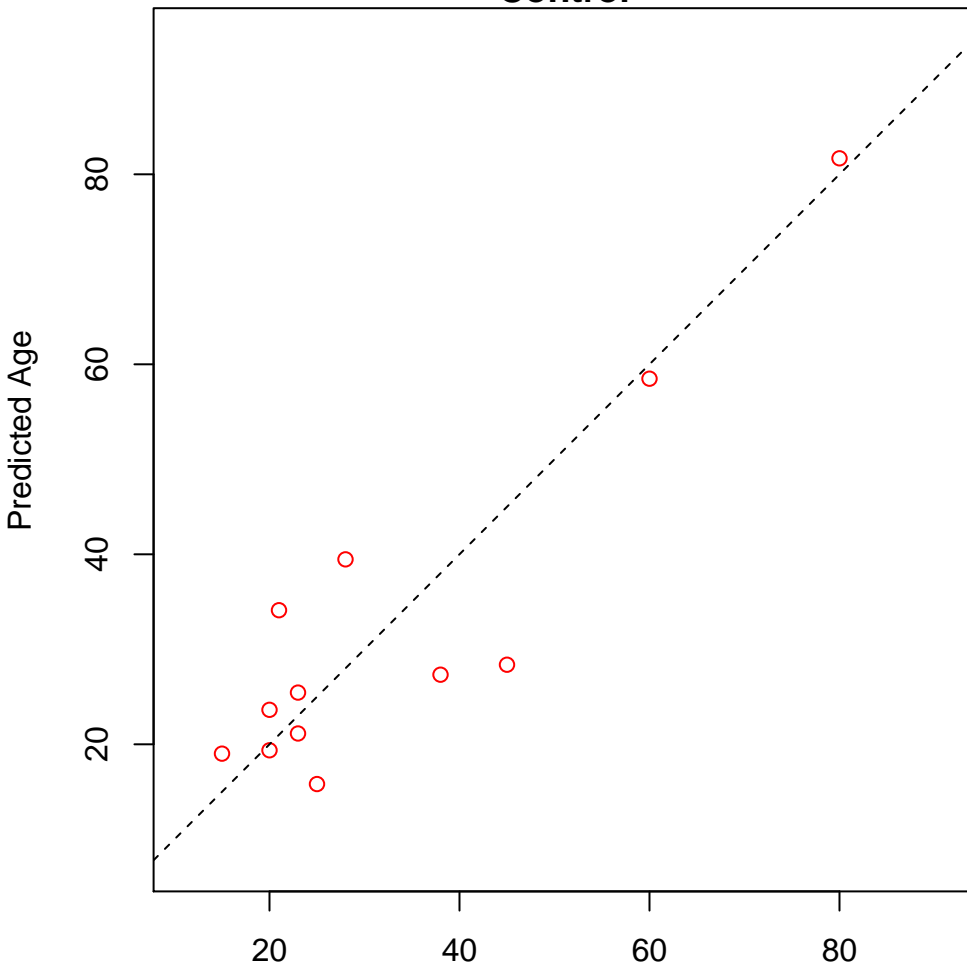


positive regulation of NF-kappaB import into nucleus (Score: 26.431777)

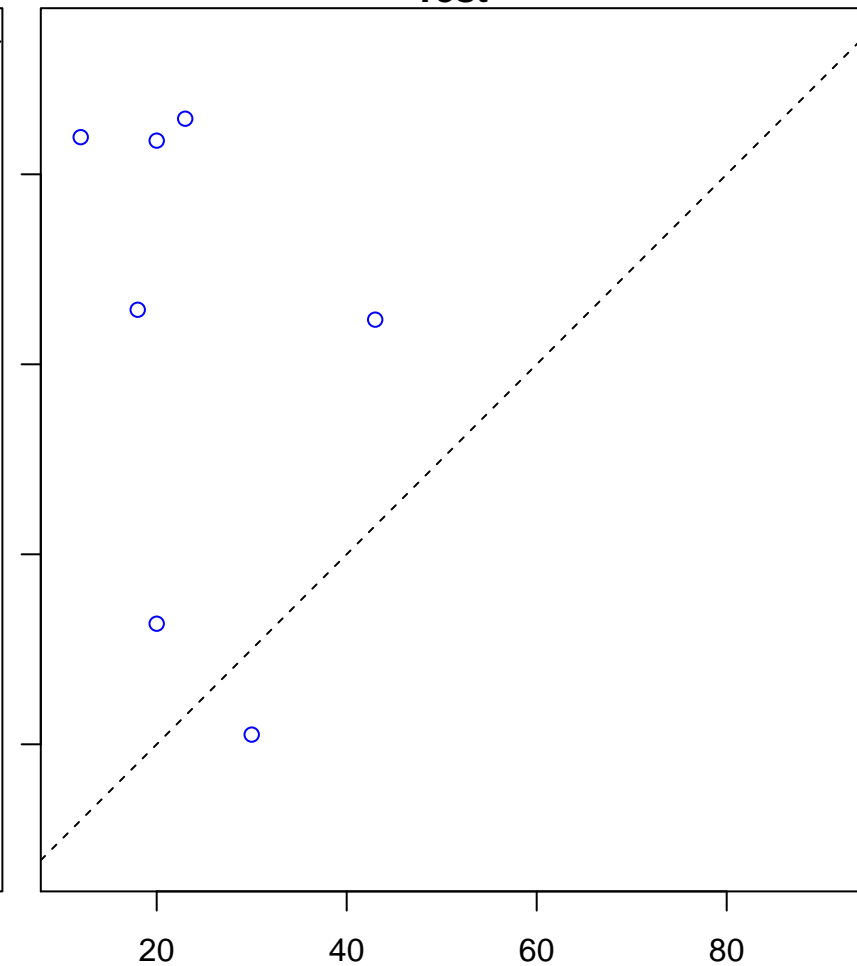


base conversion or substitution editing (Score: 26.372882)

Control

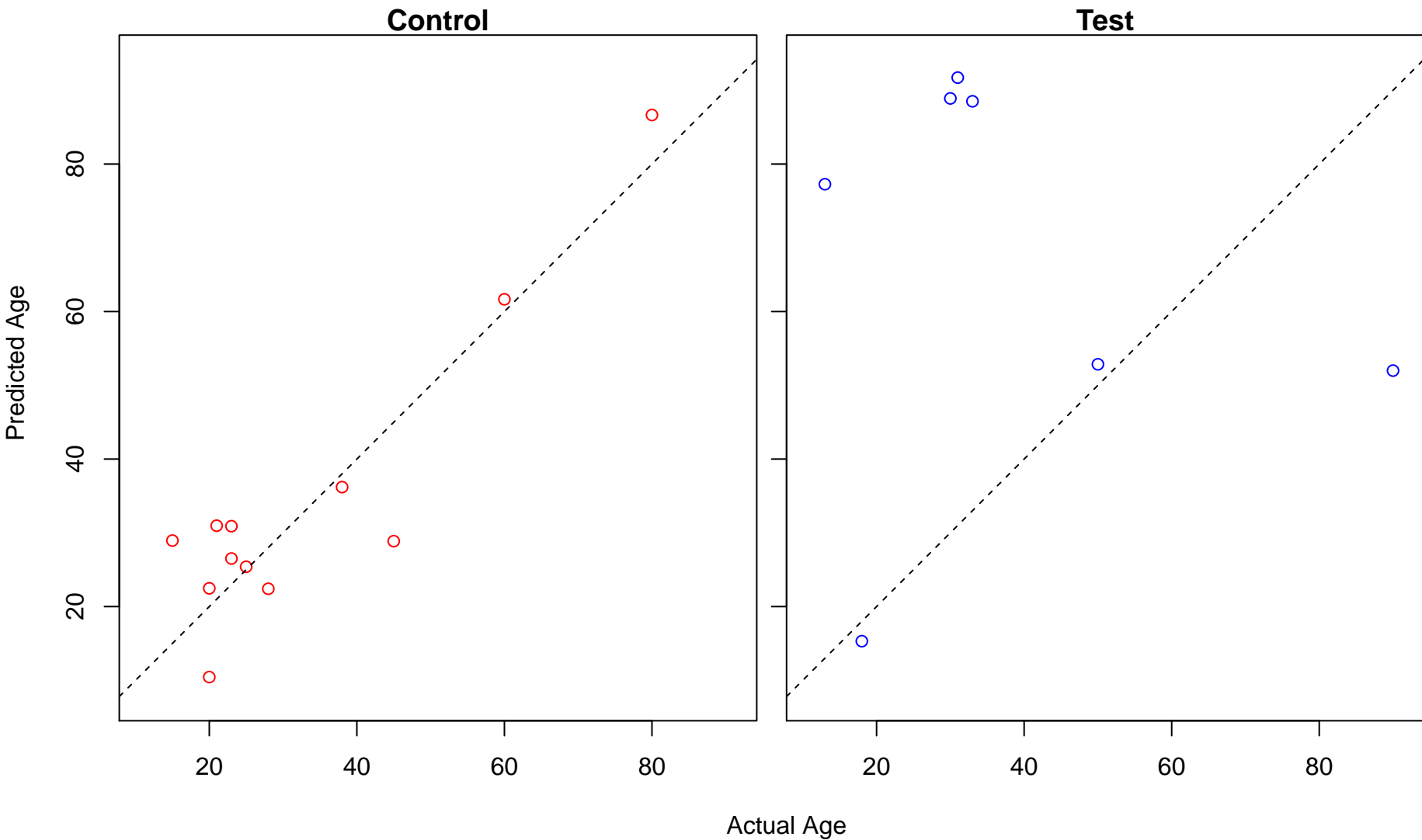


Test

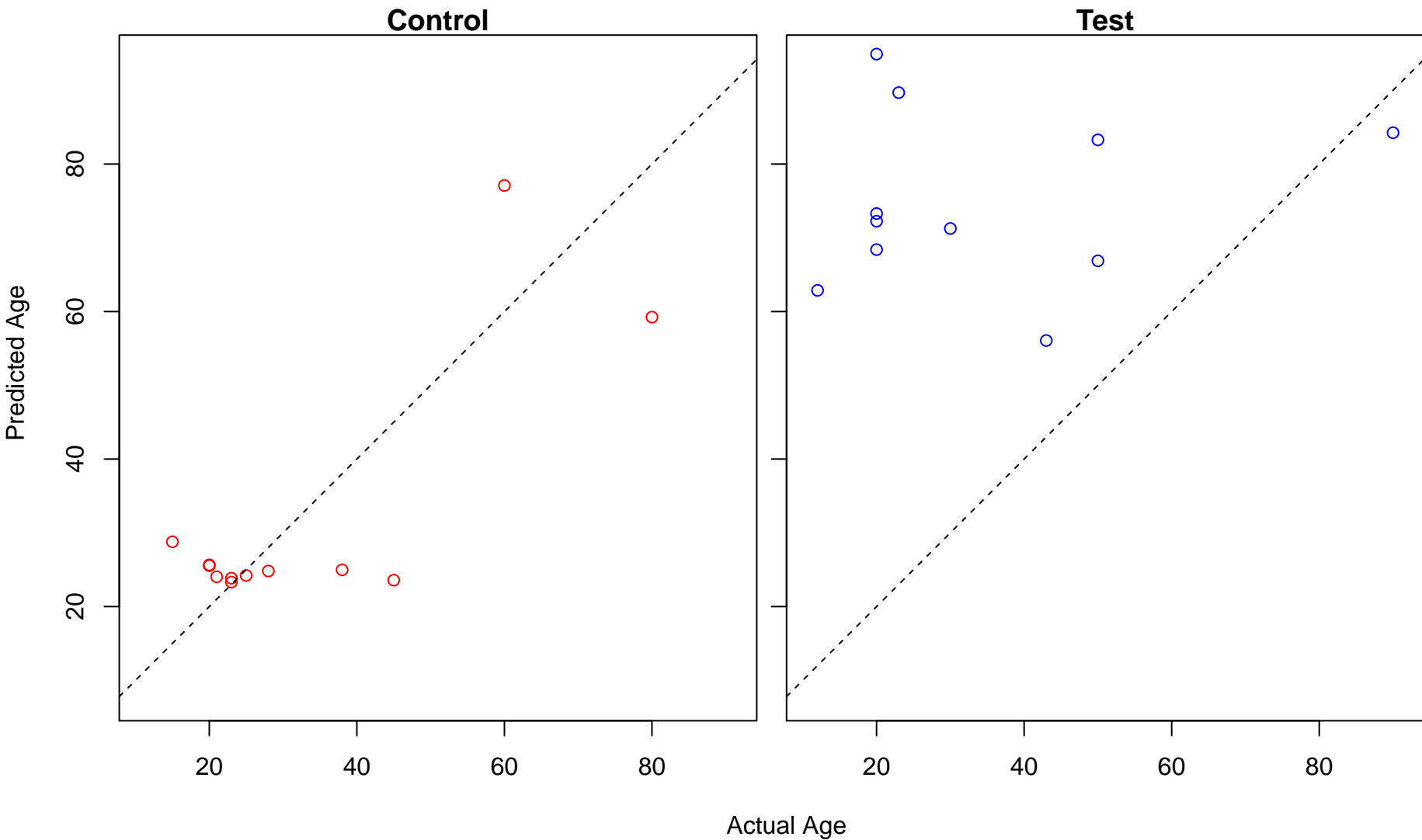


Actual Age

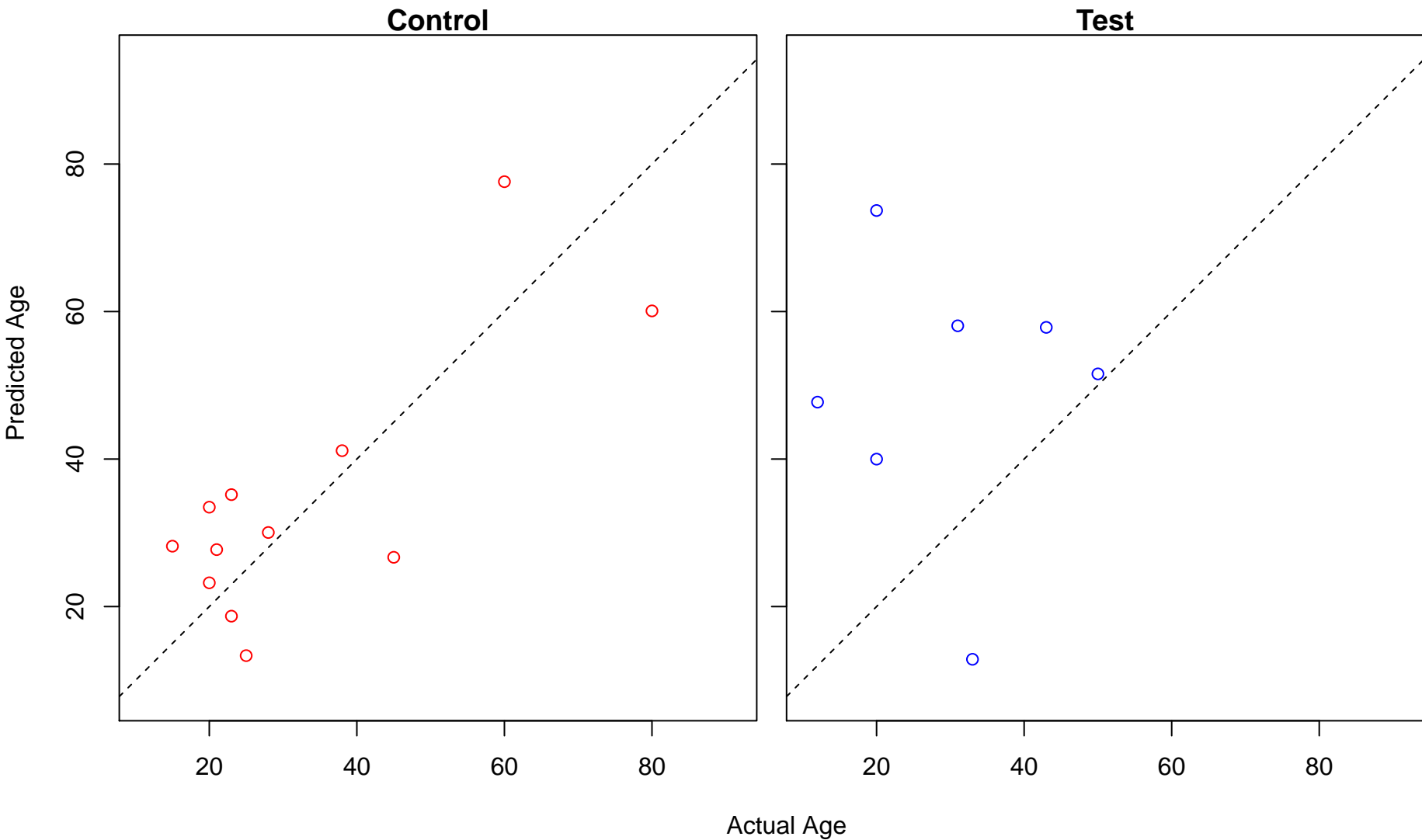
negative regulation of ruffle assembly (Score: 26.356472)



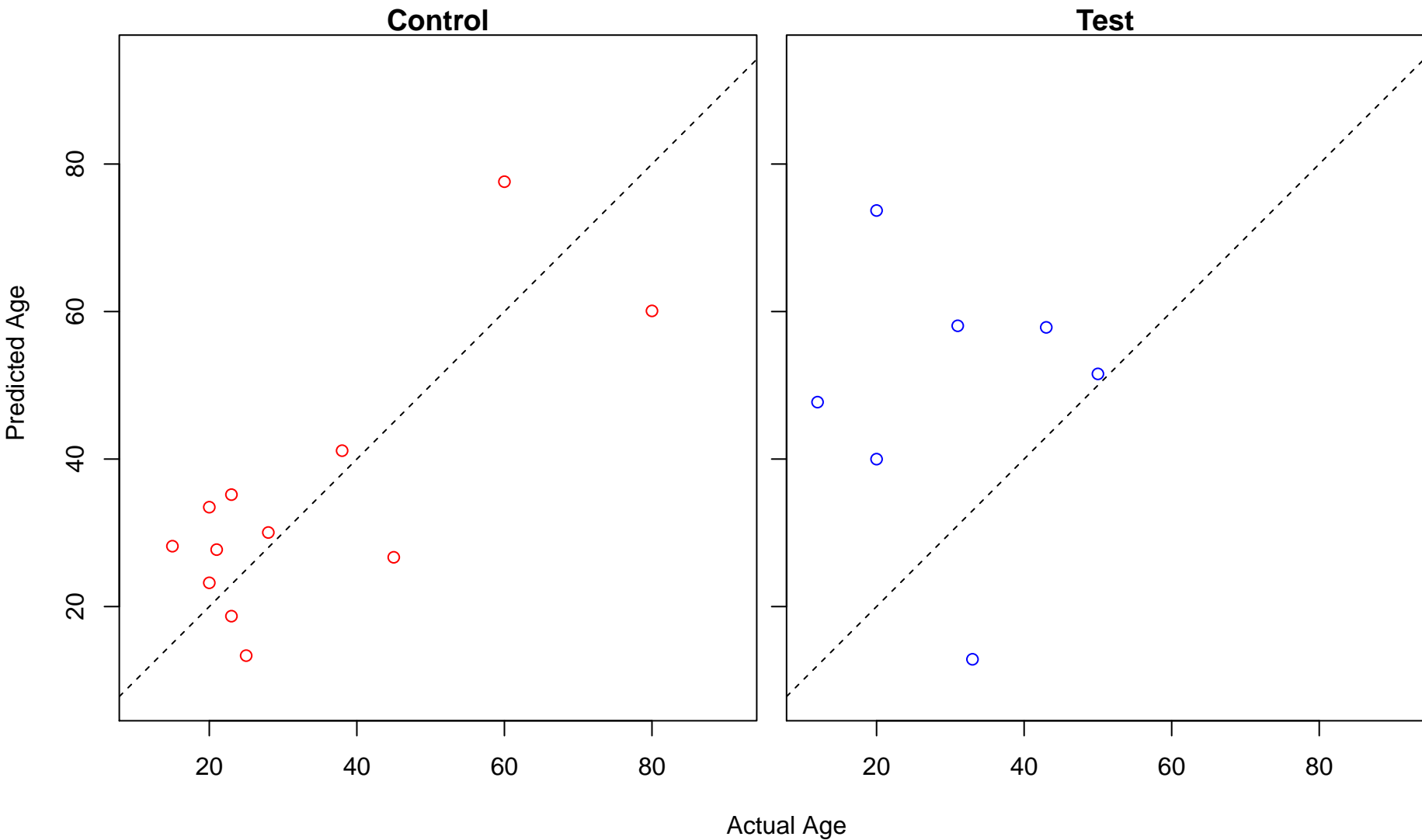
regulation of vitamin metabolic process (Score: 26.349972)



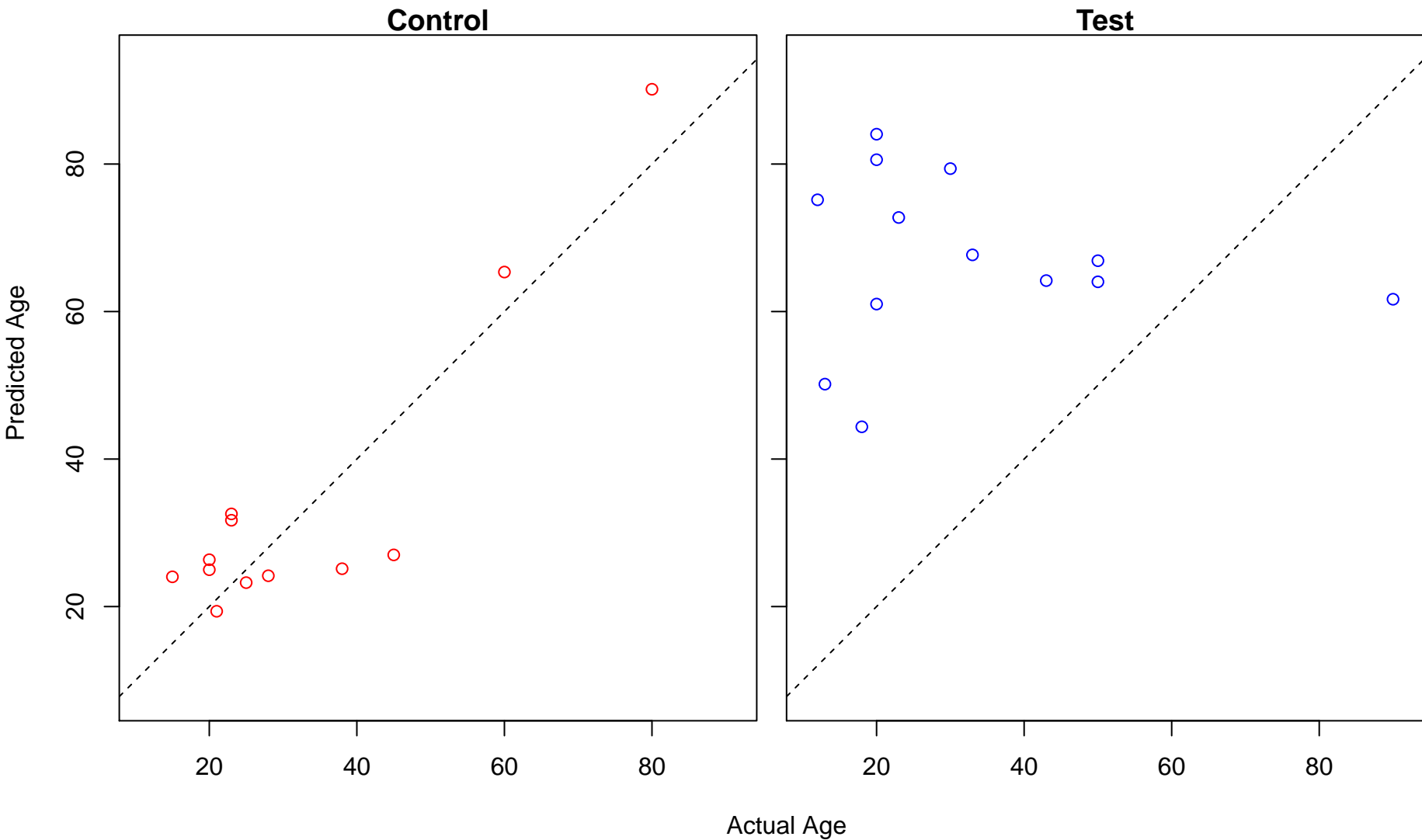
positive regulation of peptide secretion (Score: 26.320929)



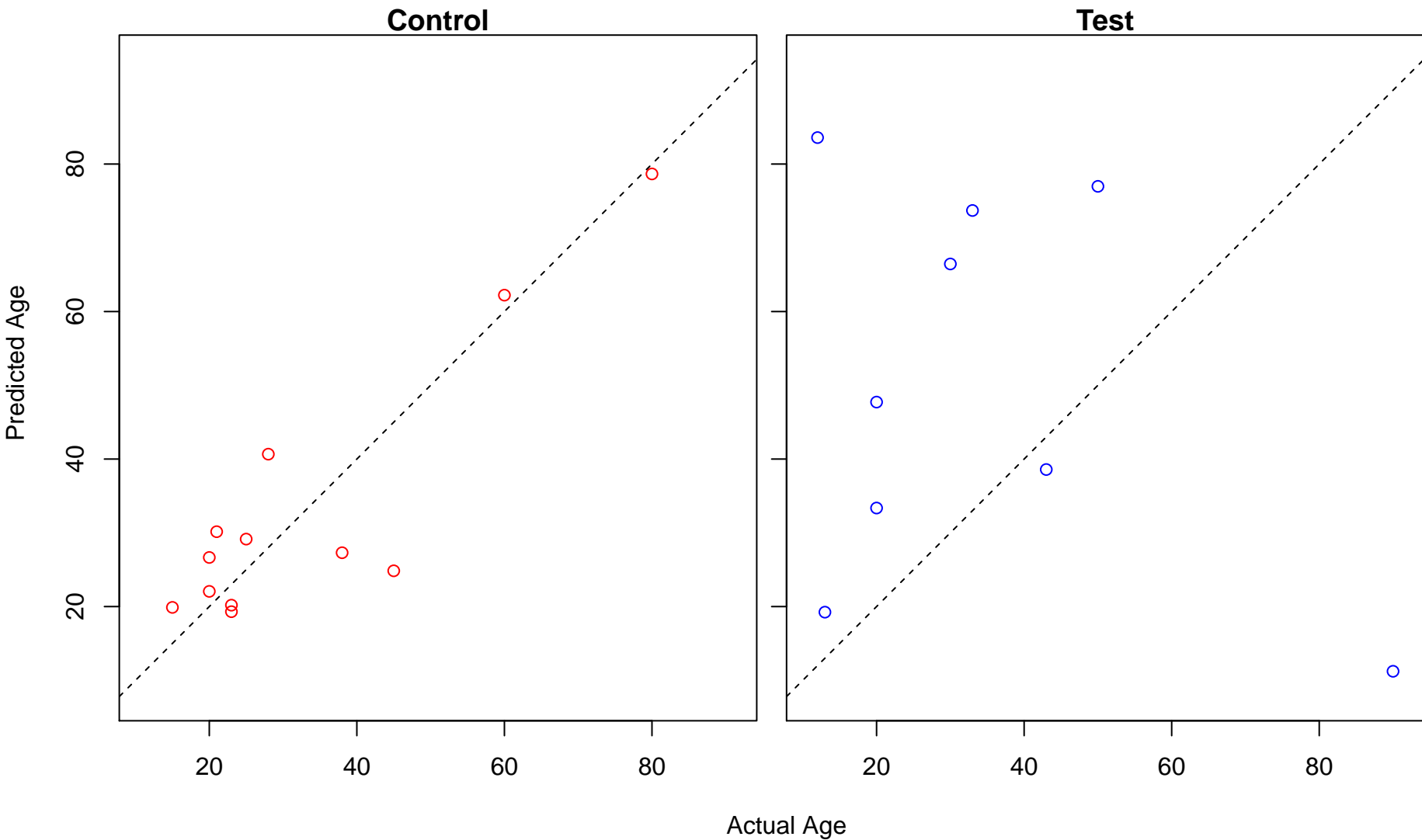
positive regulation of peptide hormone secretion (Score: 26.320929)



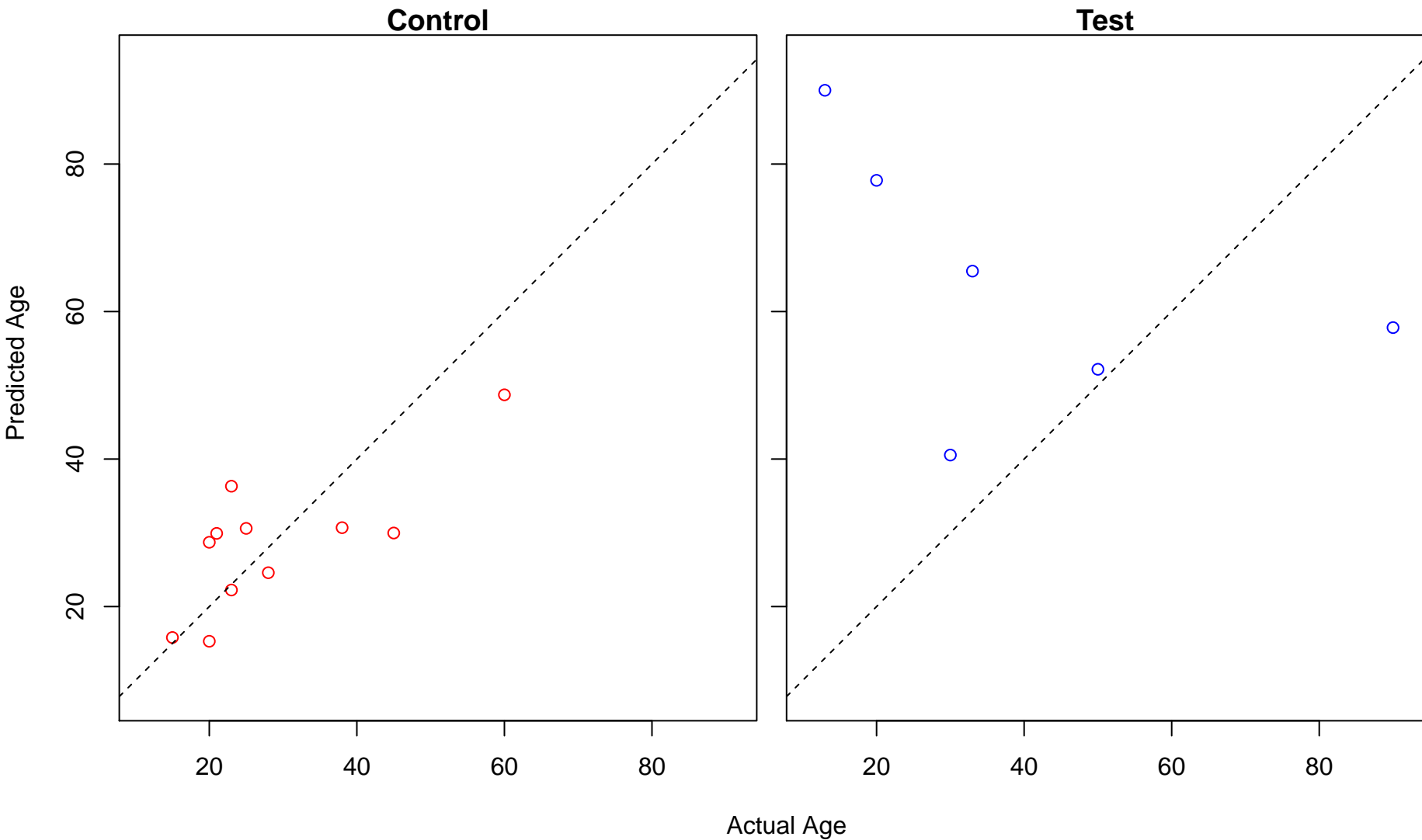
nitric oxide mediated signal transduction (Score: 26.317142)



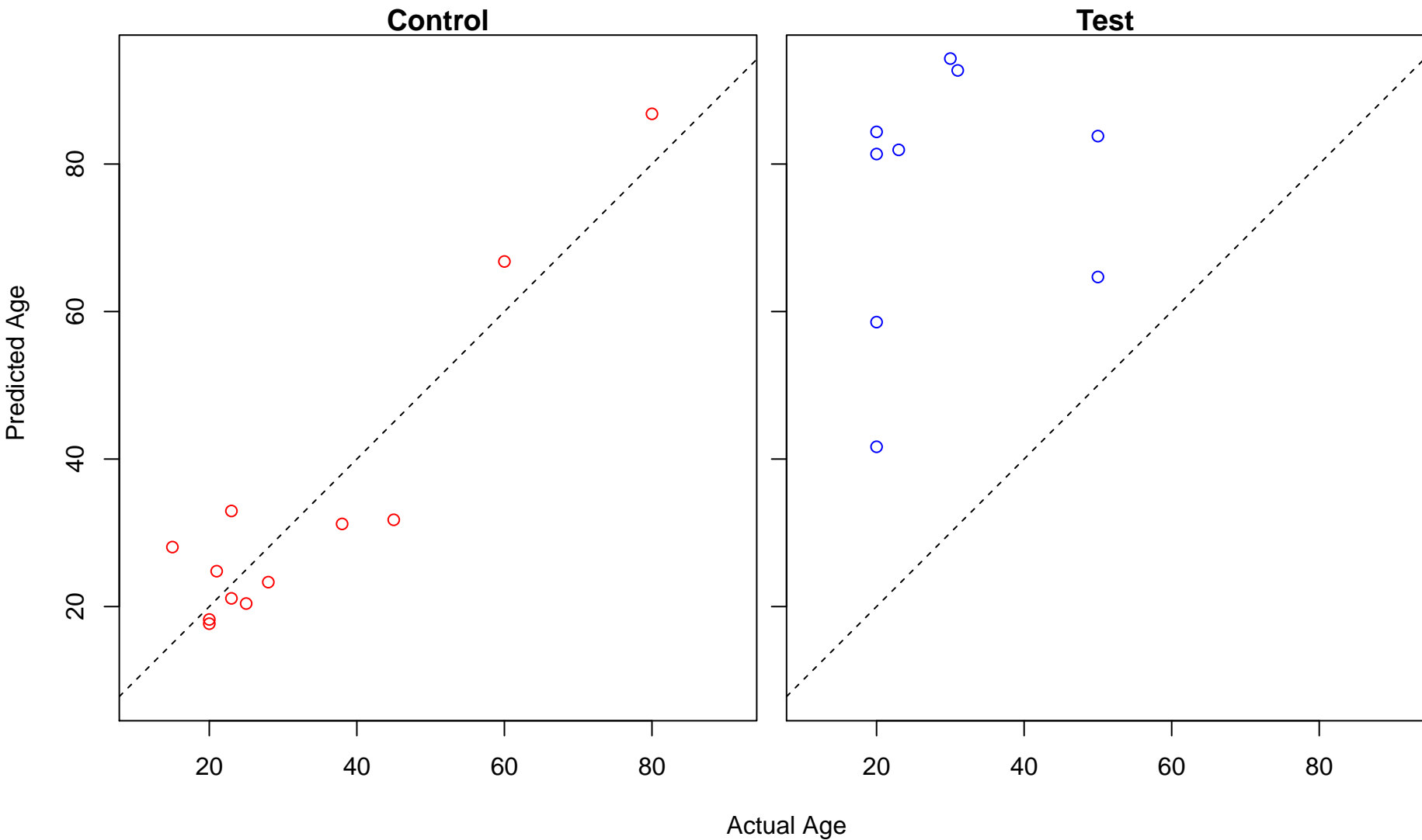
leukocyte cell-cell adhesion (Score: 26.314950)



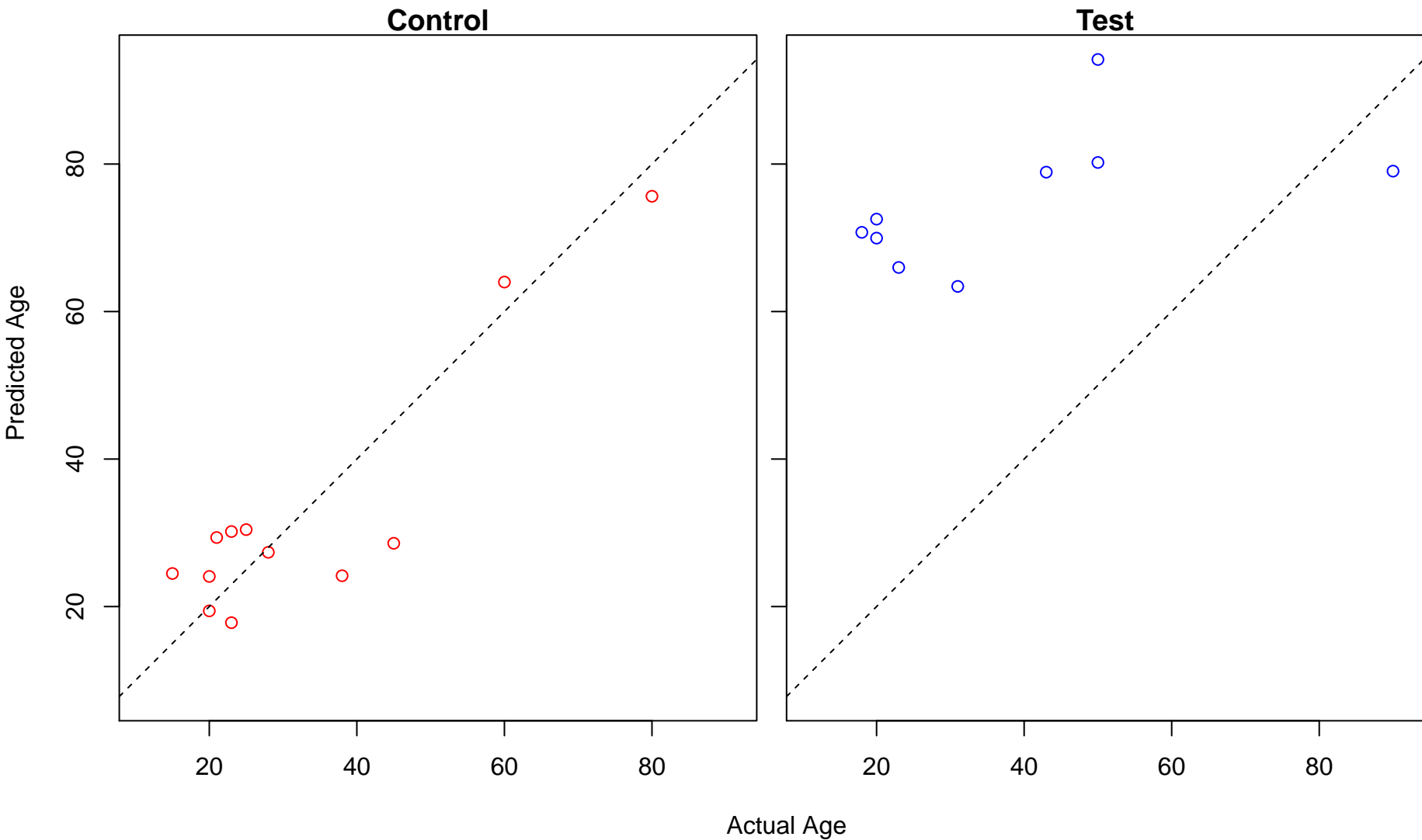
digestive system process (Score: 26.288200)



histone arginine methylation (Score: 26.112228)

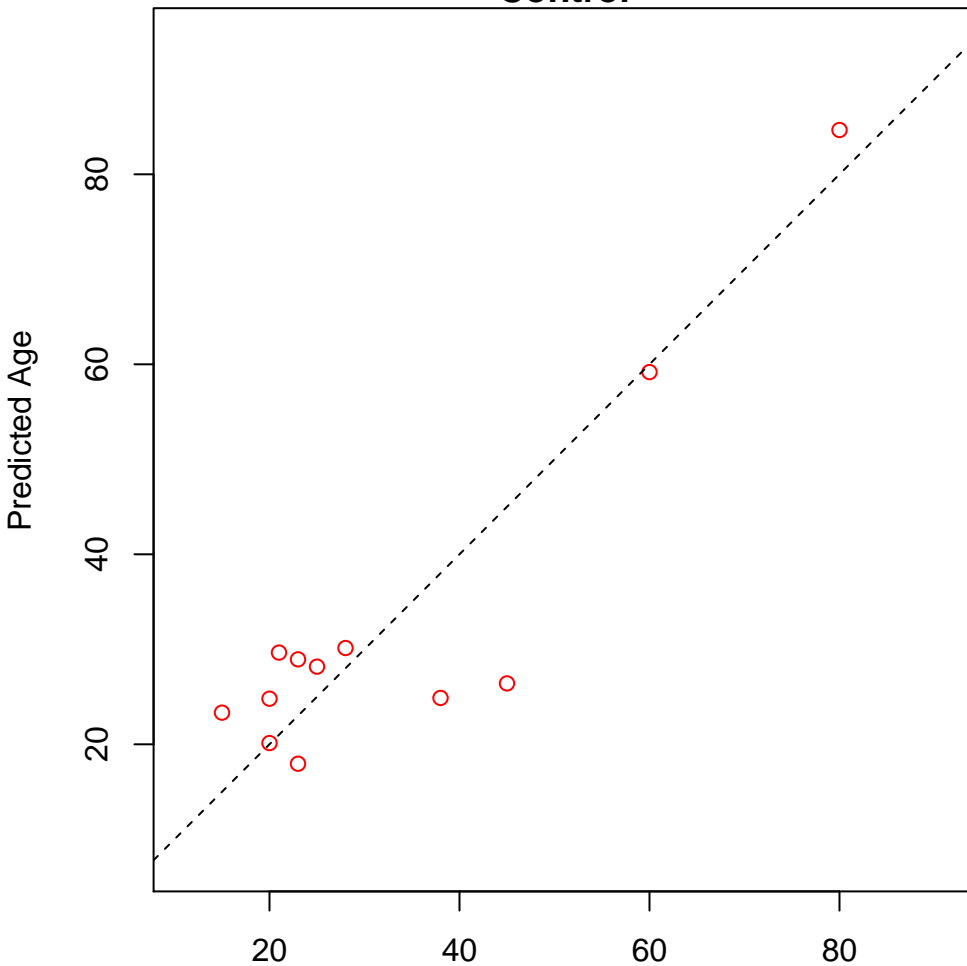


aorta development (Score: 26.091864)

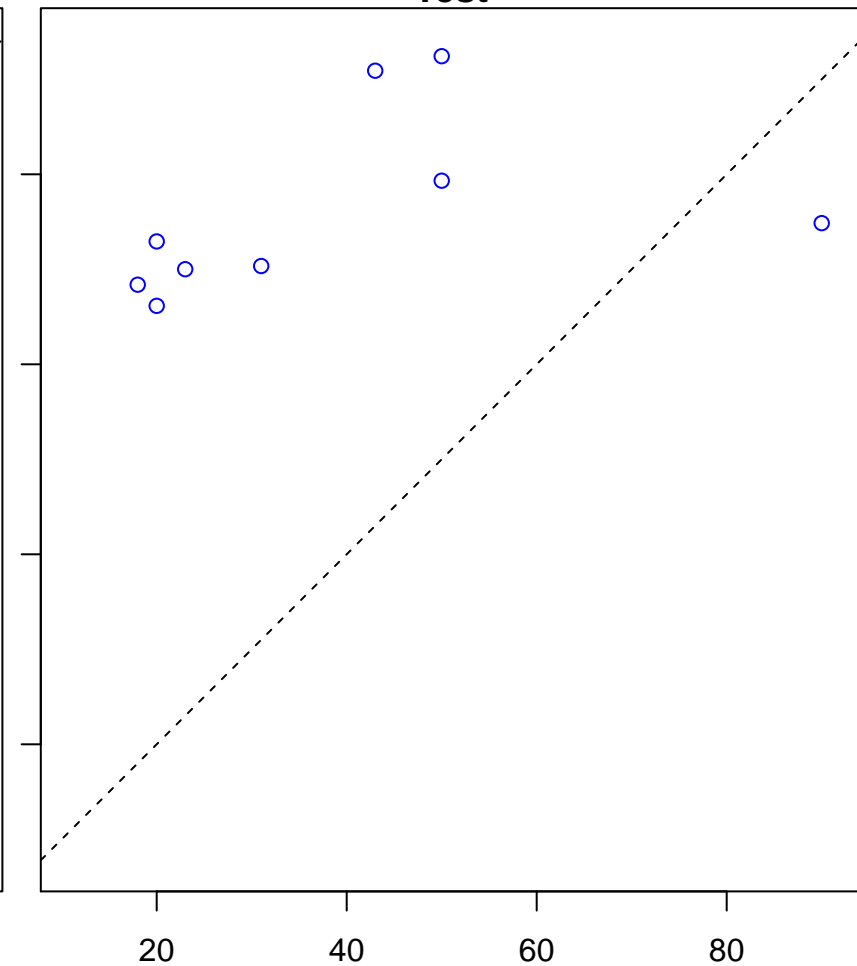


embryonic placenta development (Score: 26.077843)

Control

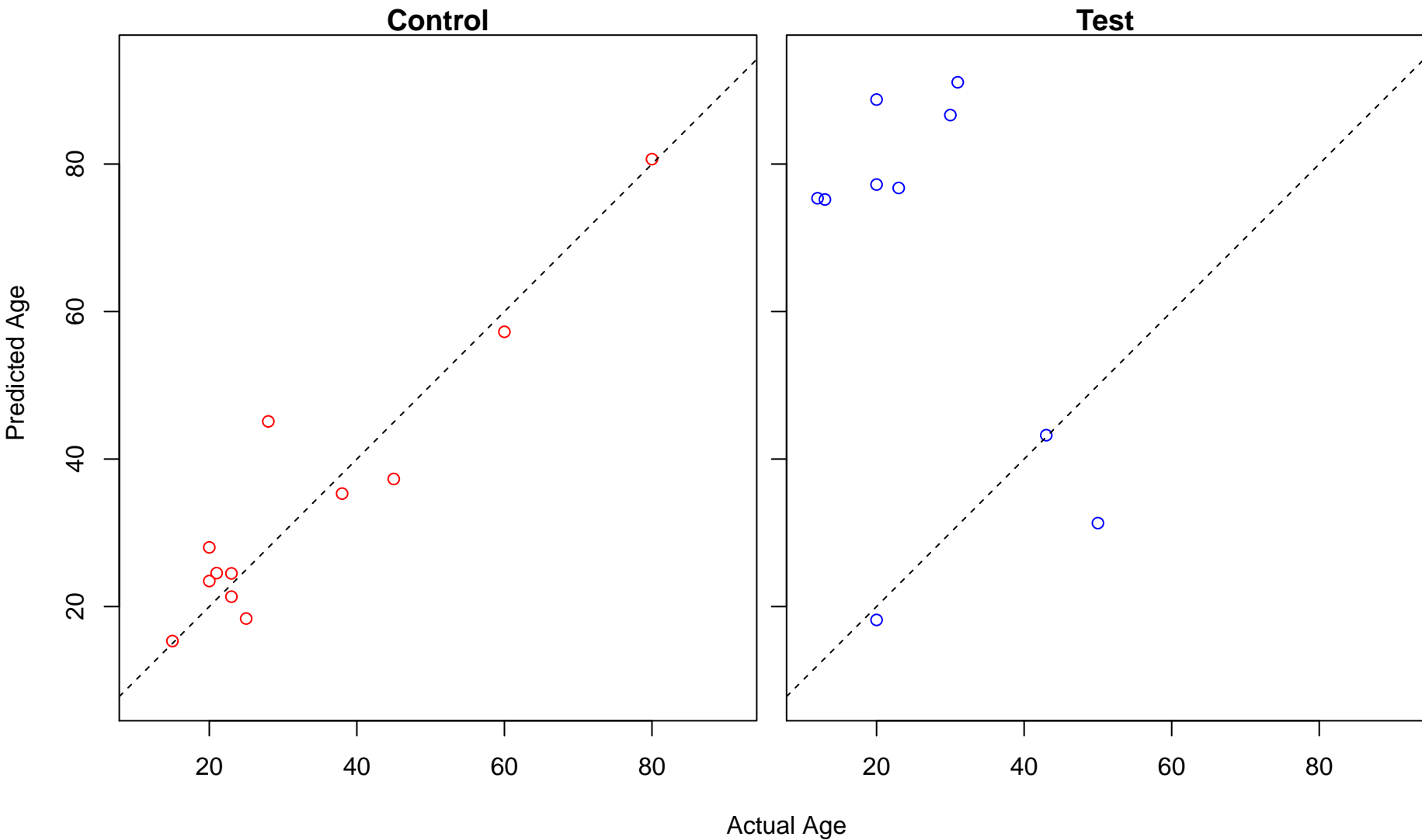


Test

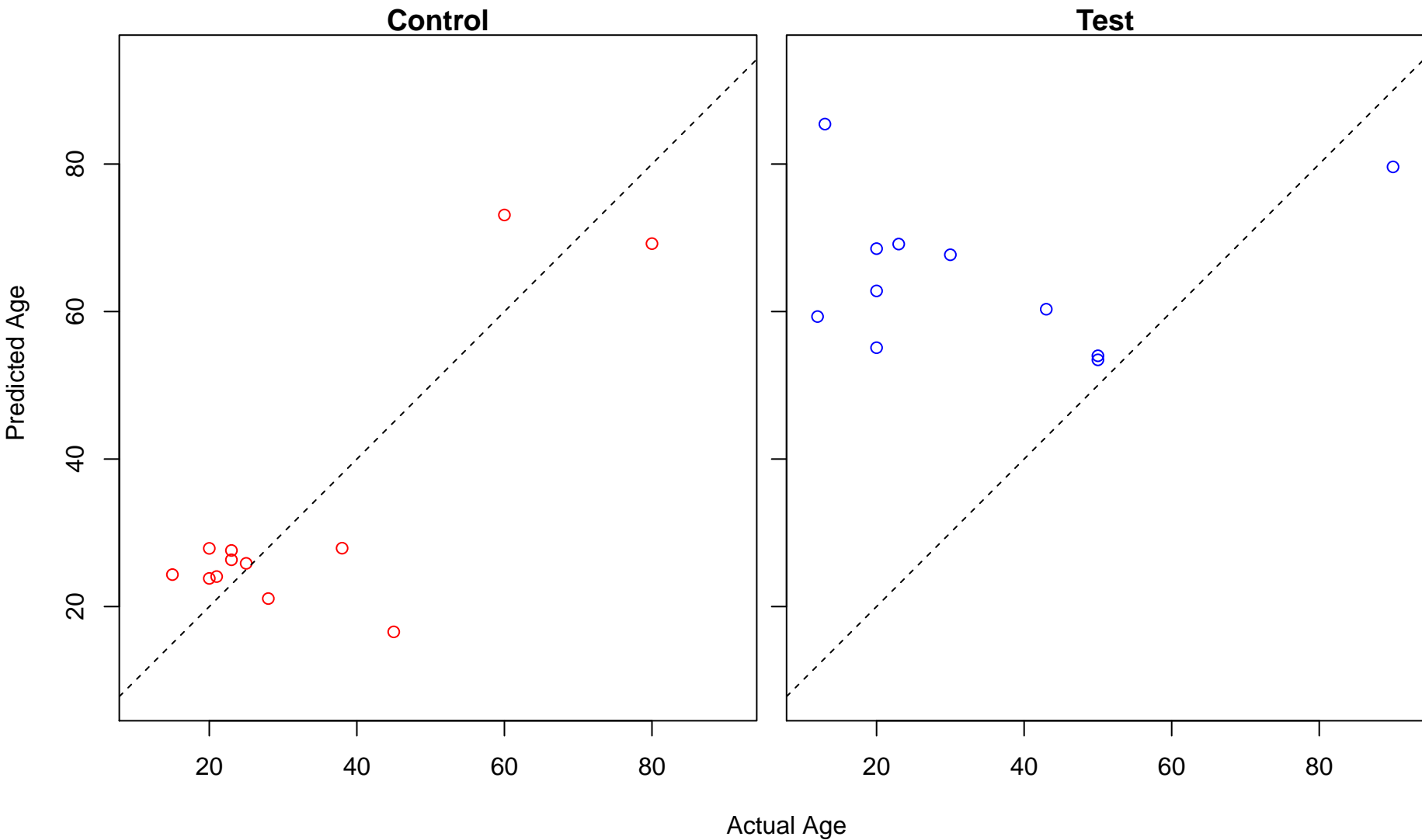


Actual Age

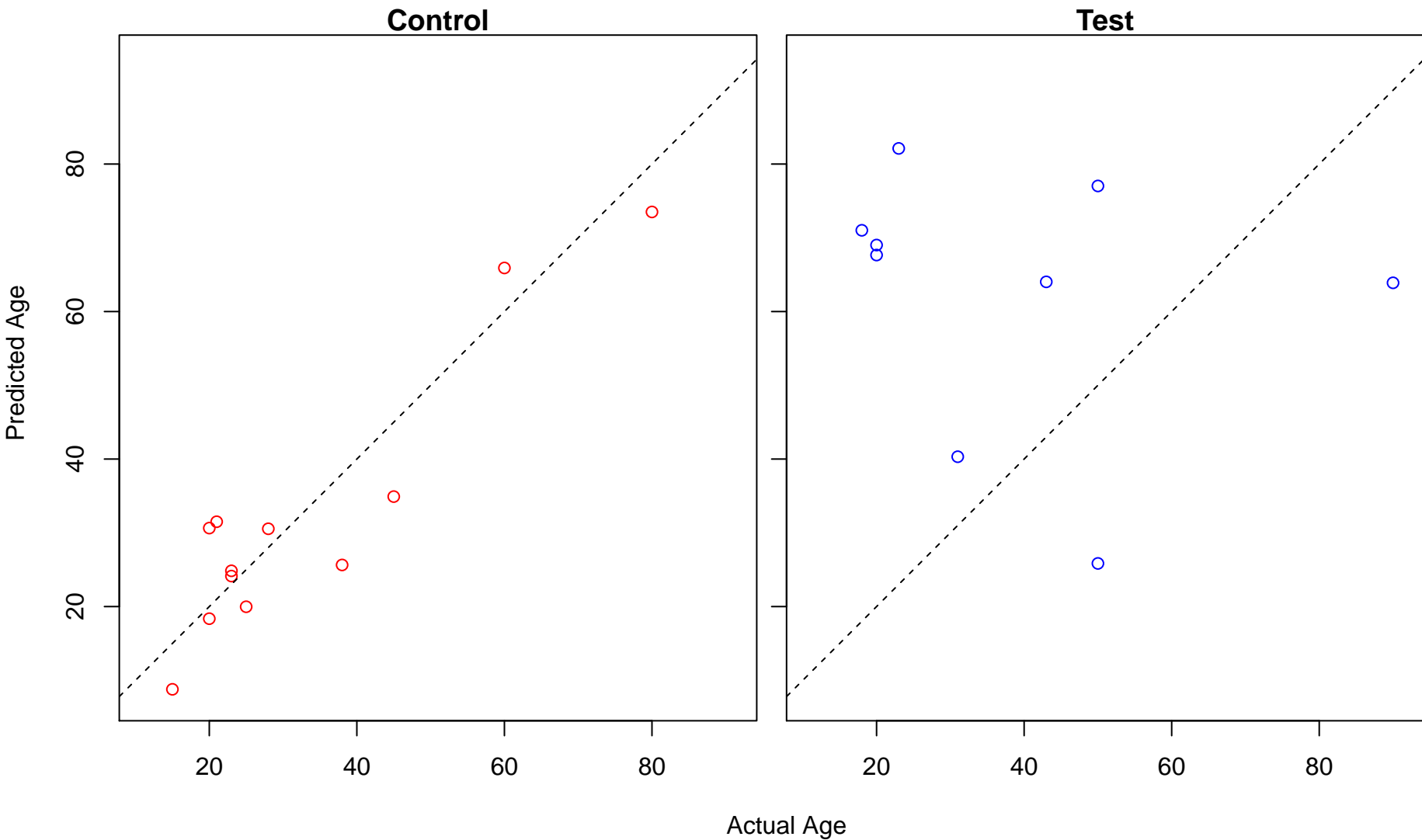
anterograde axonal transport (Score: 26.030732)



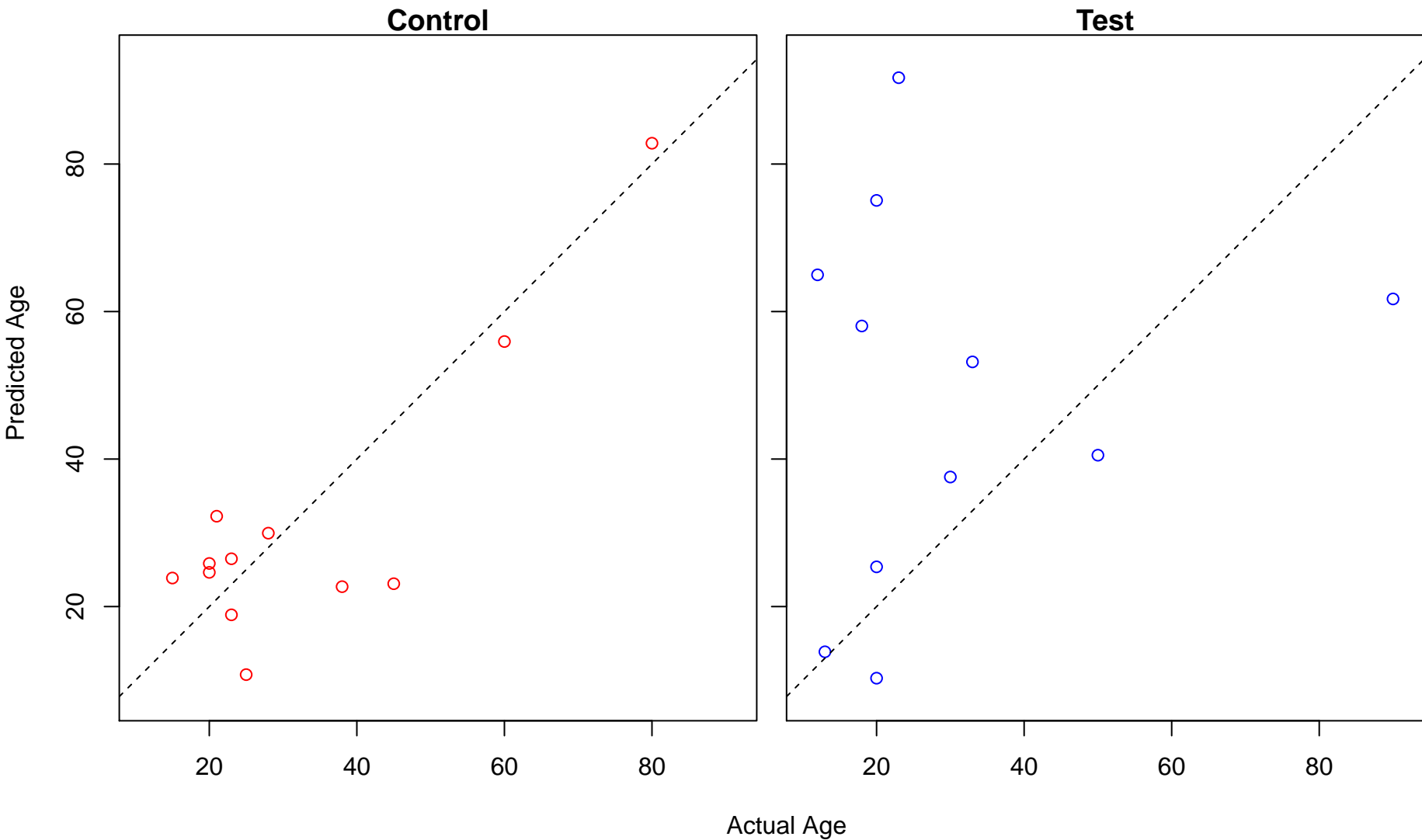
negative regulation of glucose transport (Score: 26.022100)



mesenchyme morphogenesis (Score: 25.965903)

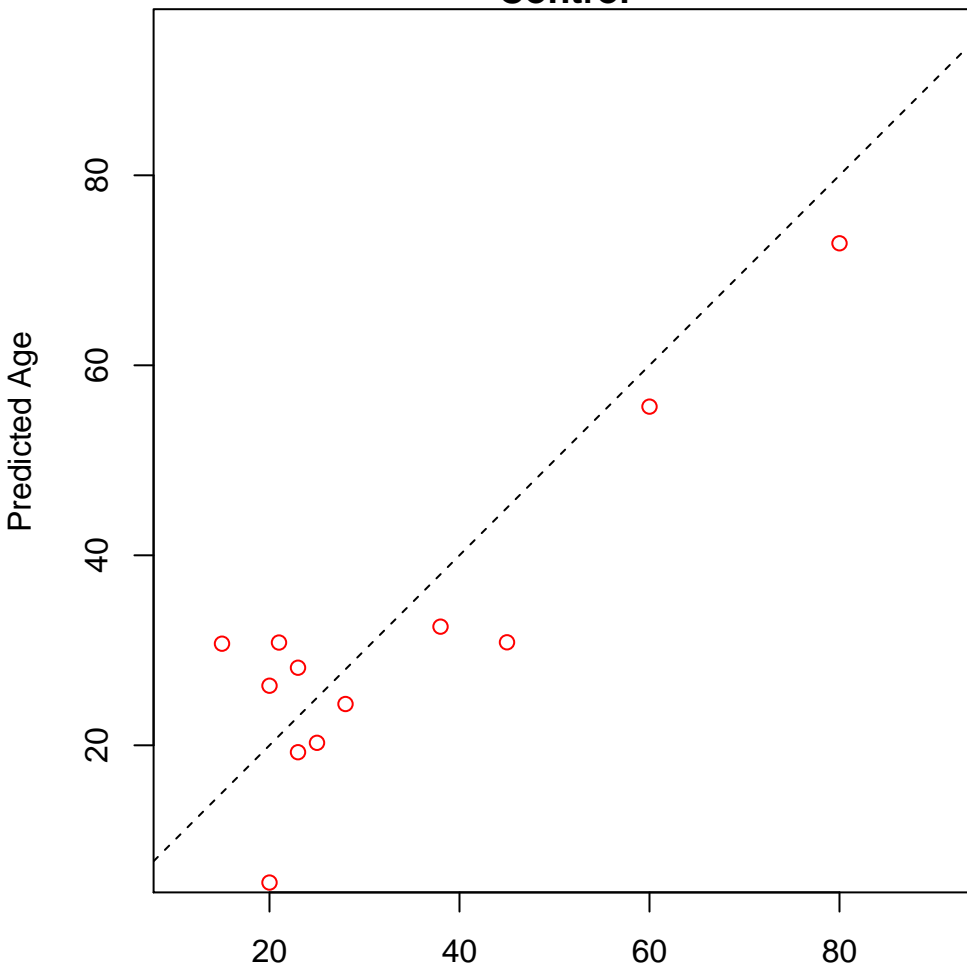


regulation of transcription factor import into nucleus (Score: 25.960175)

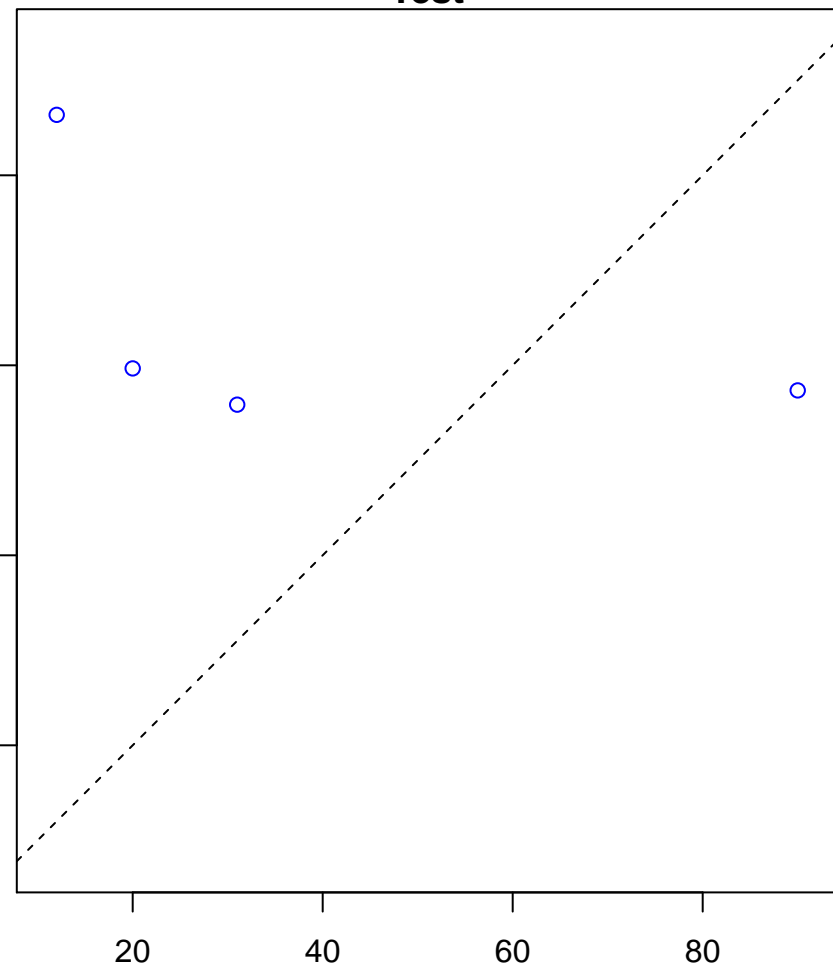


regulation of pseudopodium assembly (Score: 25.955191)

Control

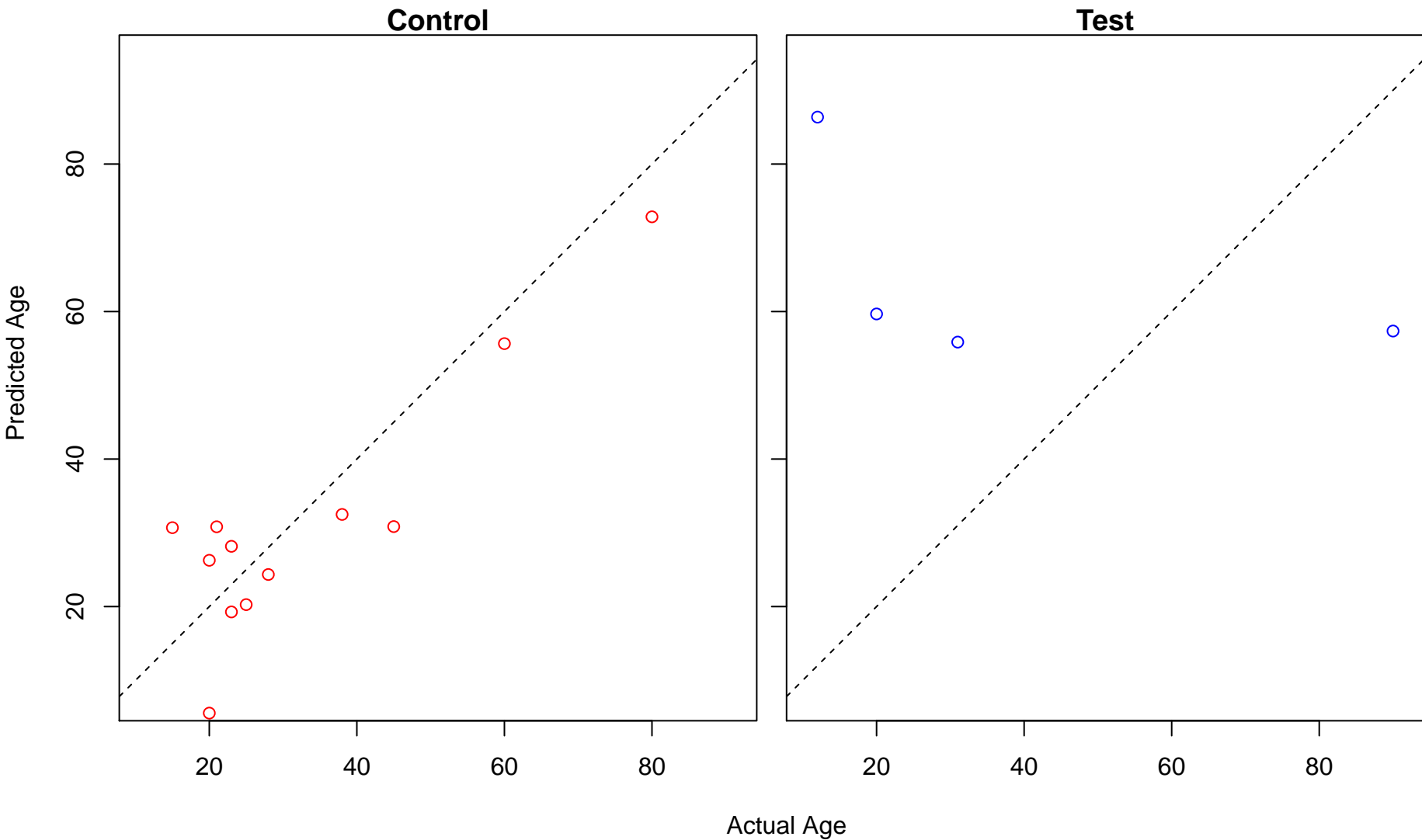


Test

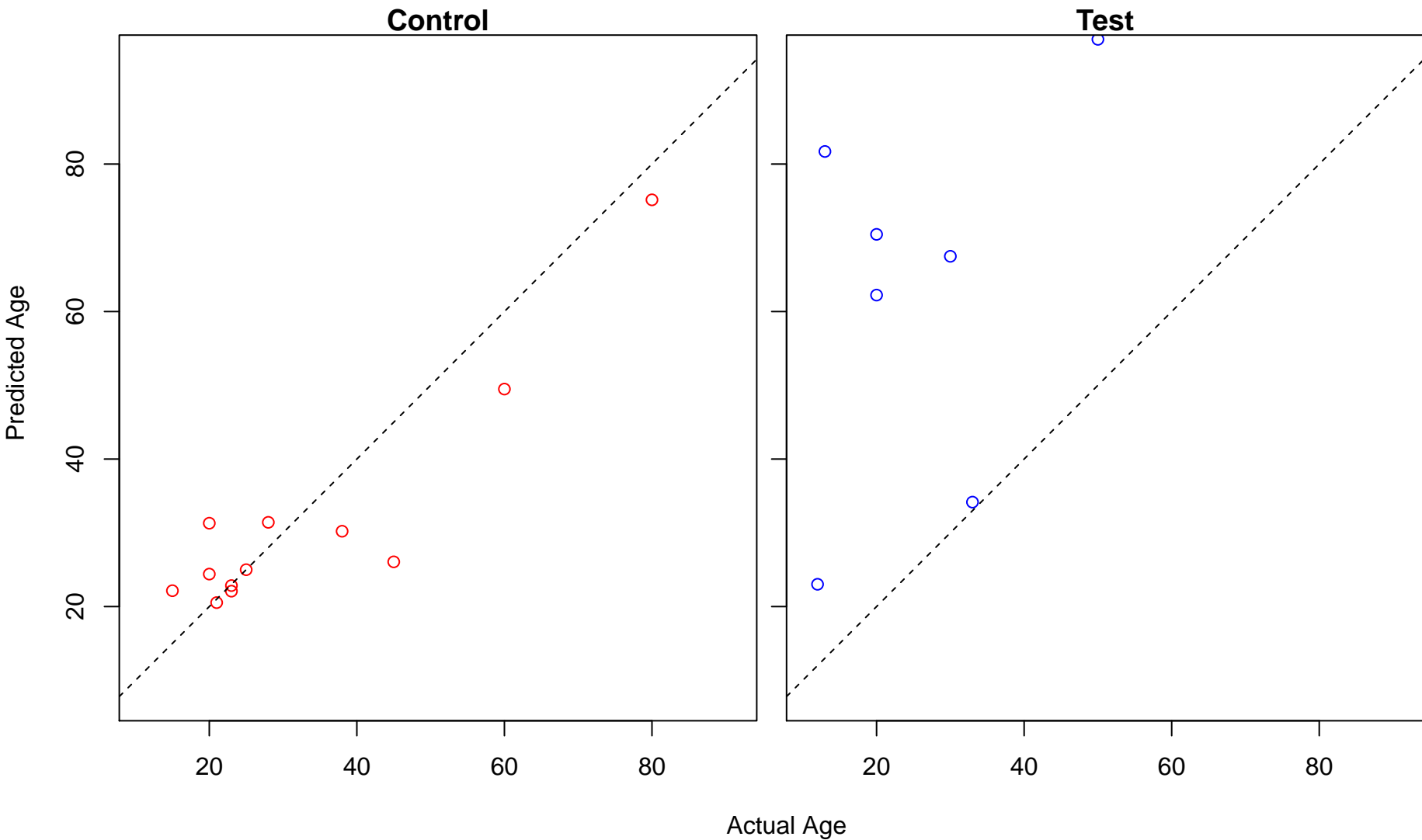


Actual Age

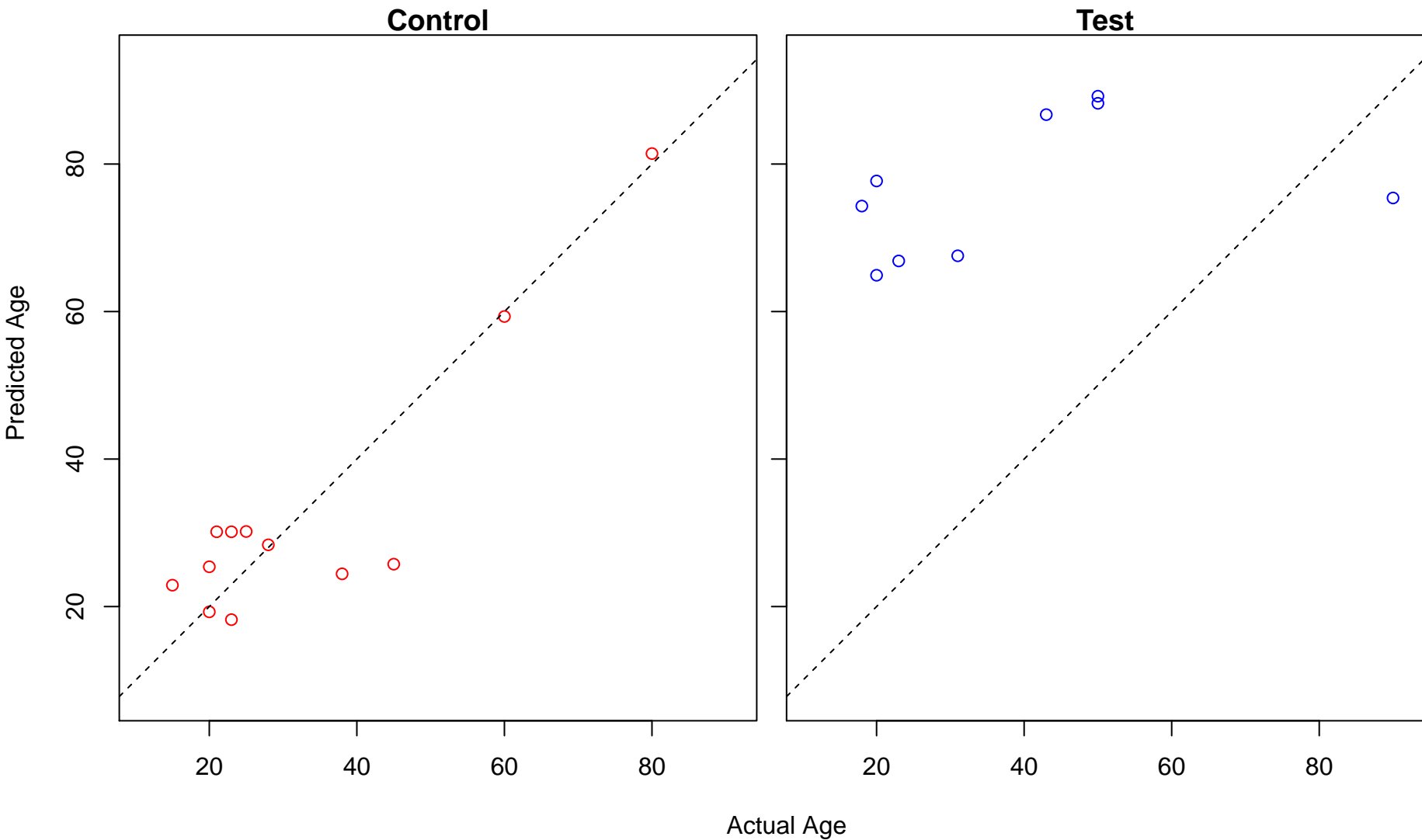
positive regulation of pseudopodium assembly (Score: 25.955191)



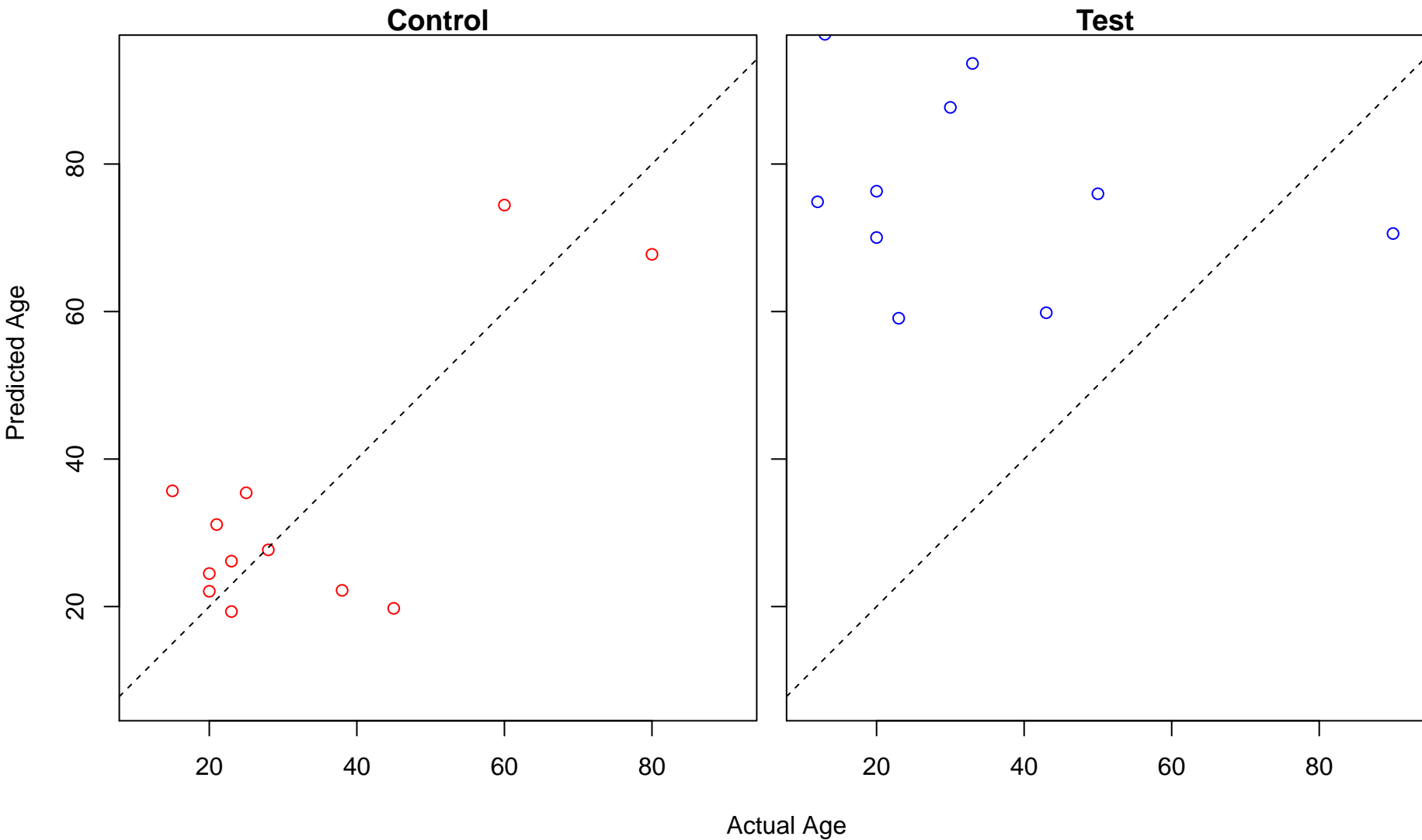
negative regulation of viral transcription (Score: 25.940588)



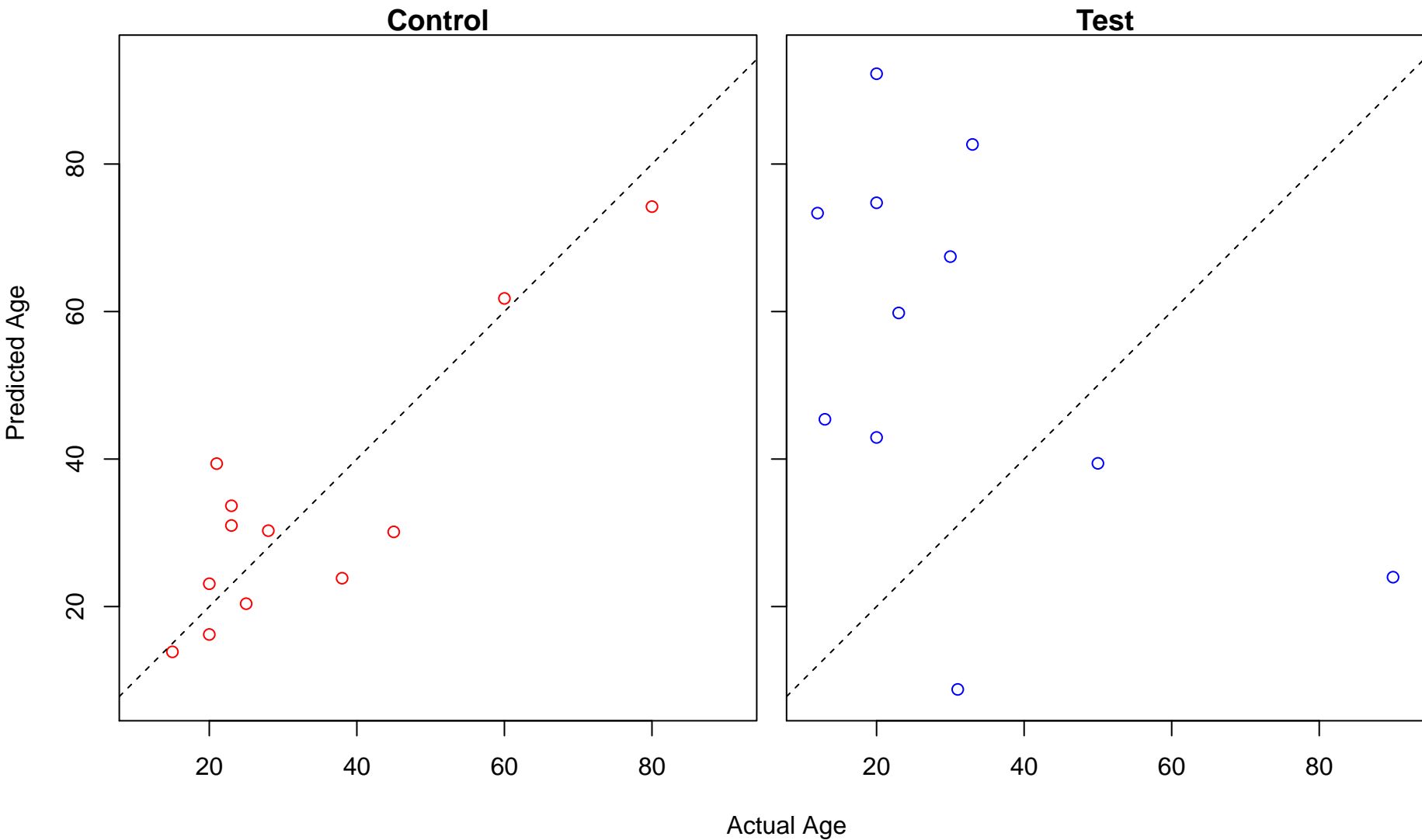
labyrinthine layer development (Score: 25.880959)



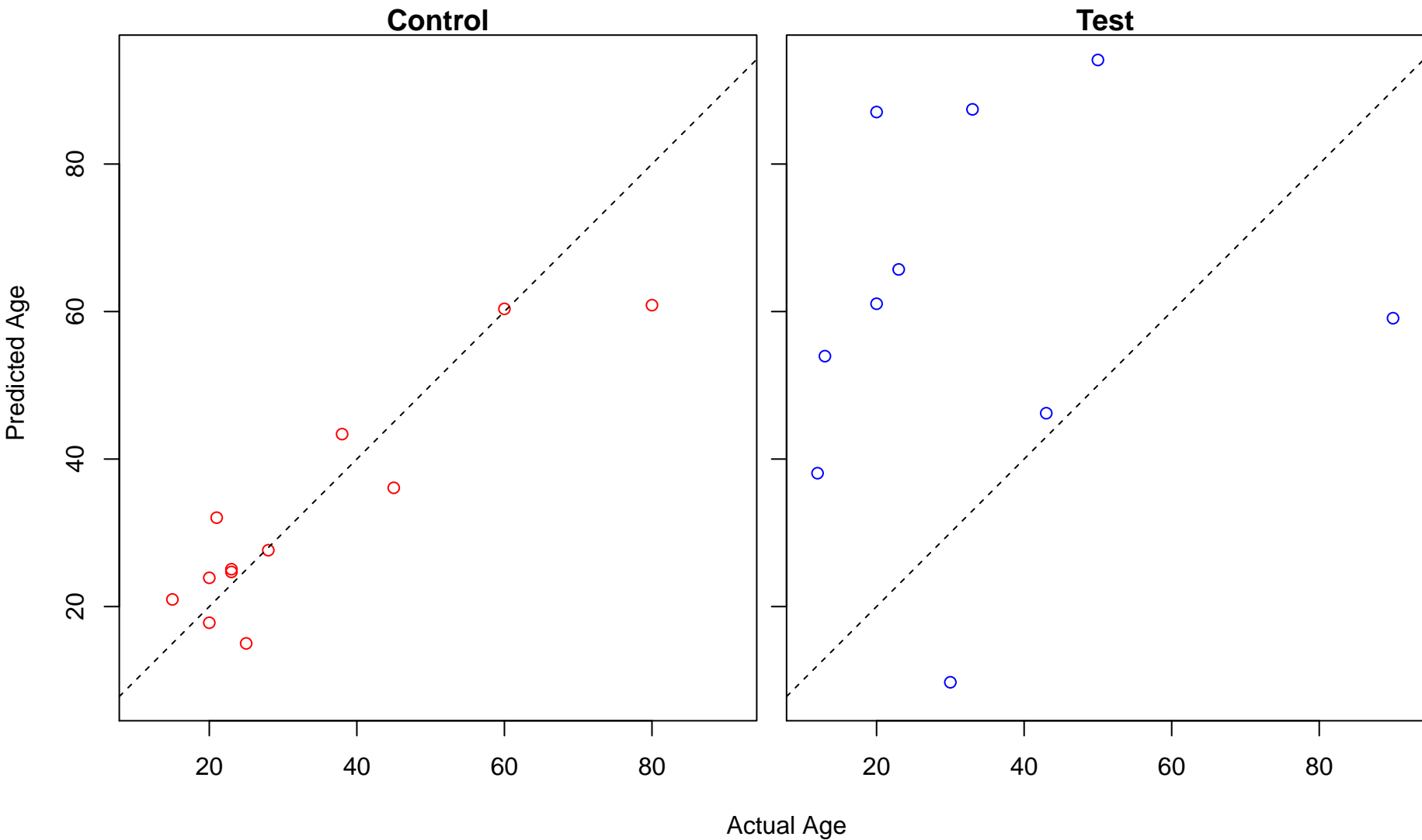
hyaluronan metabolic process (Score: 25.834159)



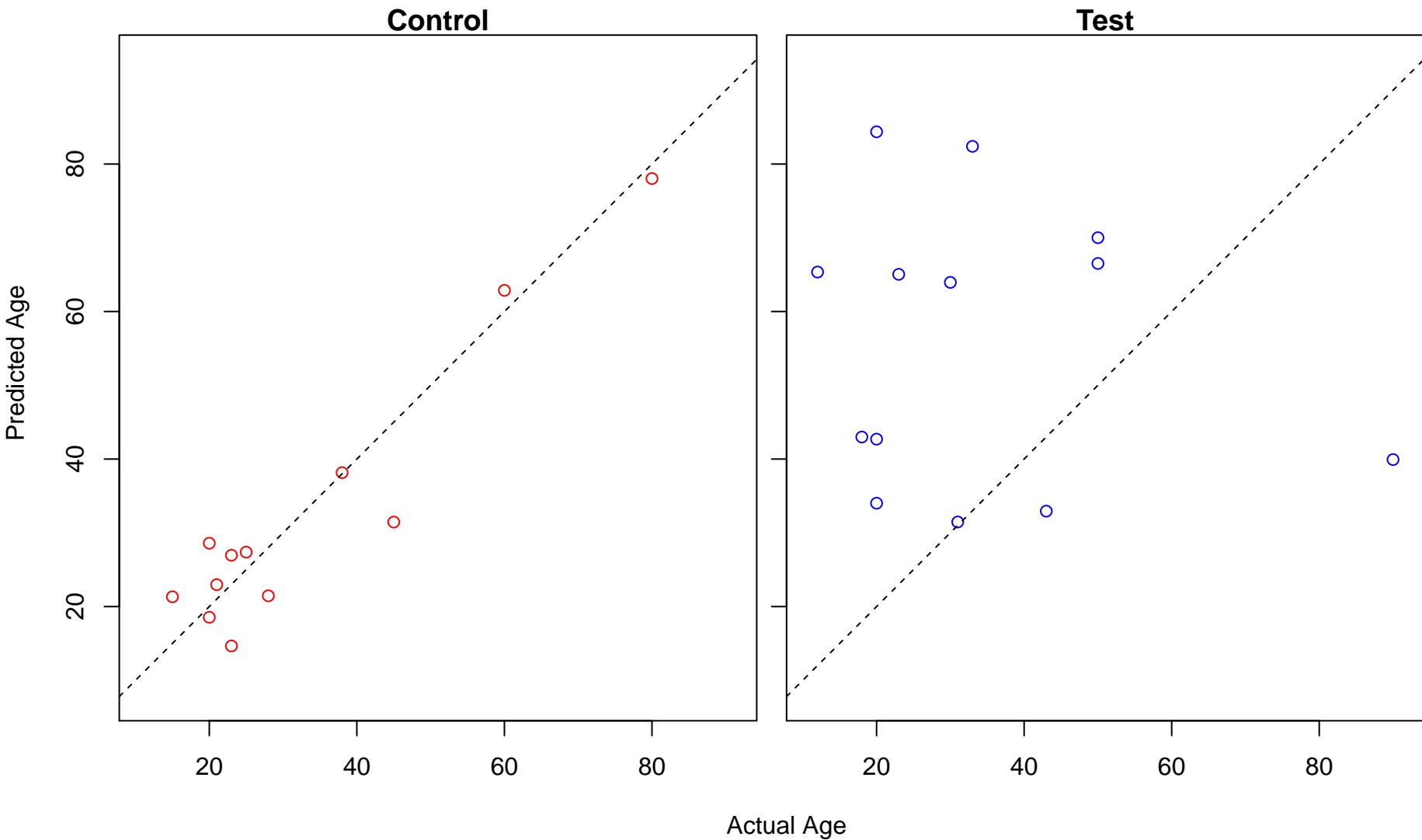
protein repair (Score: 25.808622)



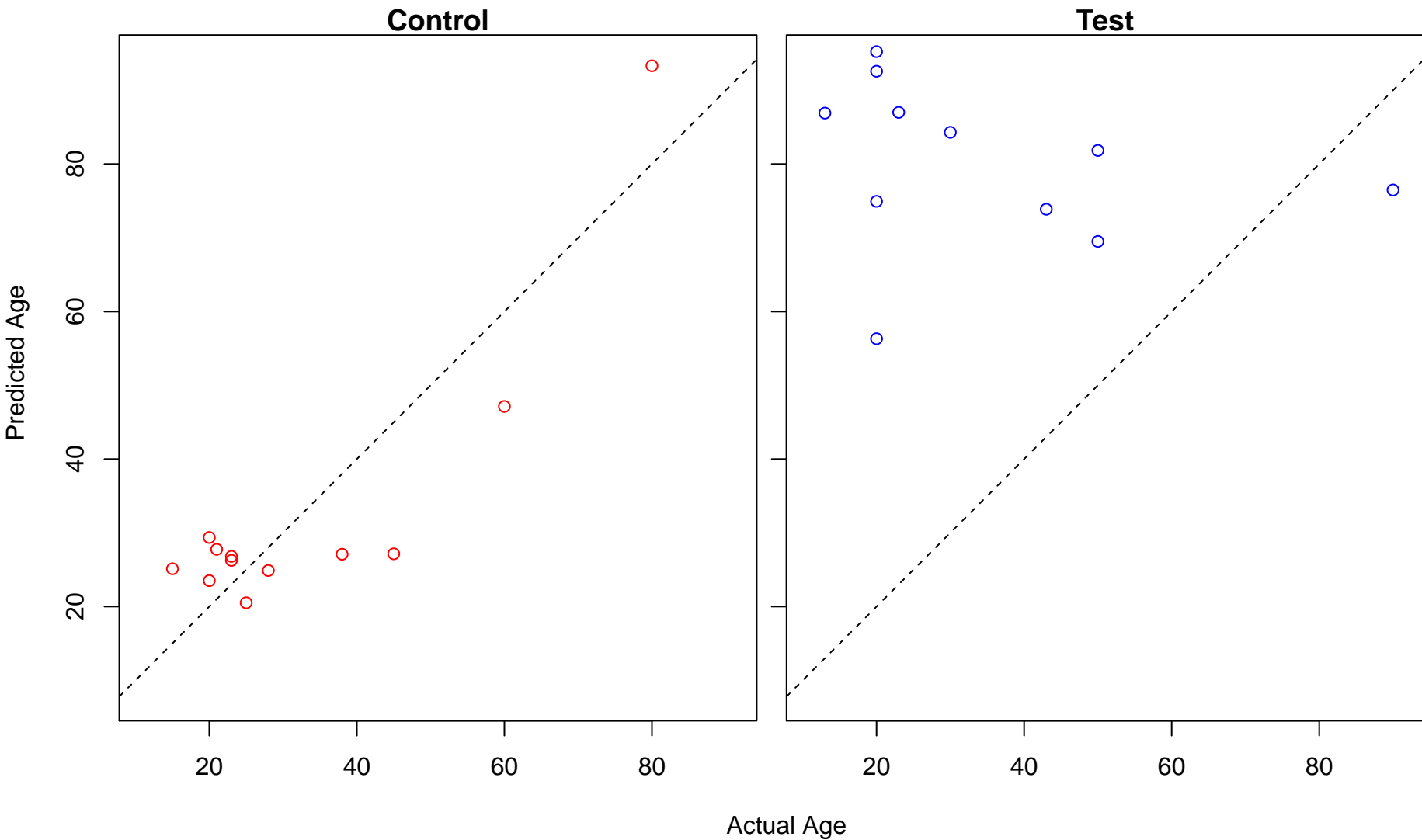
epoxygenase P450 pathway (Score: 25.789559)



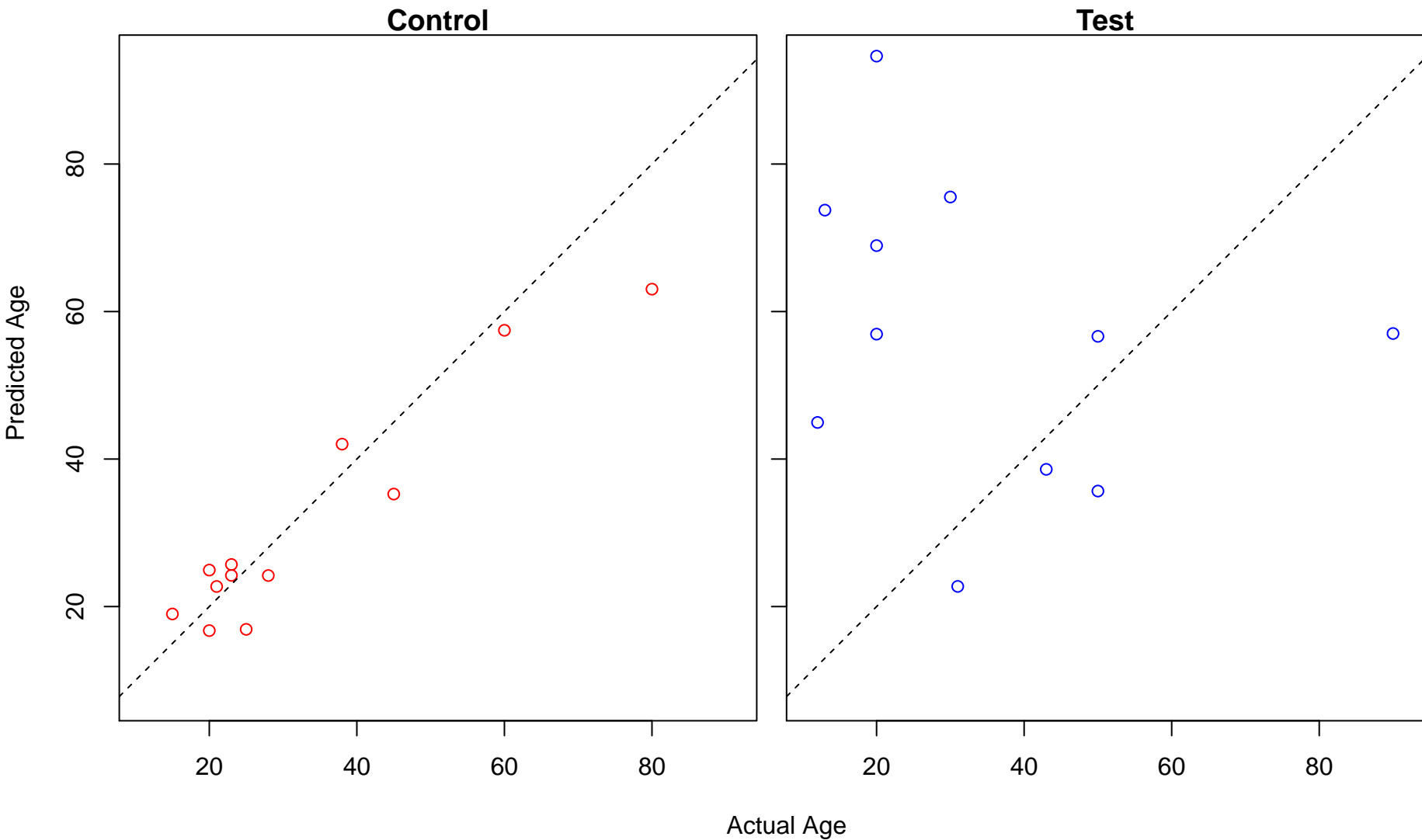
establishment of protein localization to mitochondrion (Score: 25.742479)



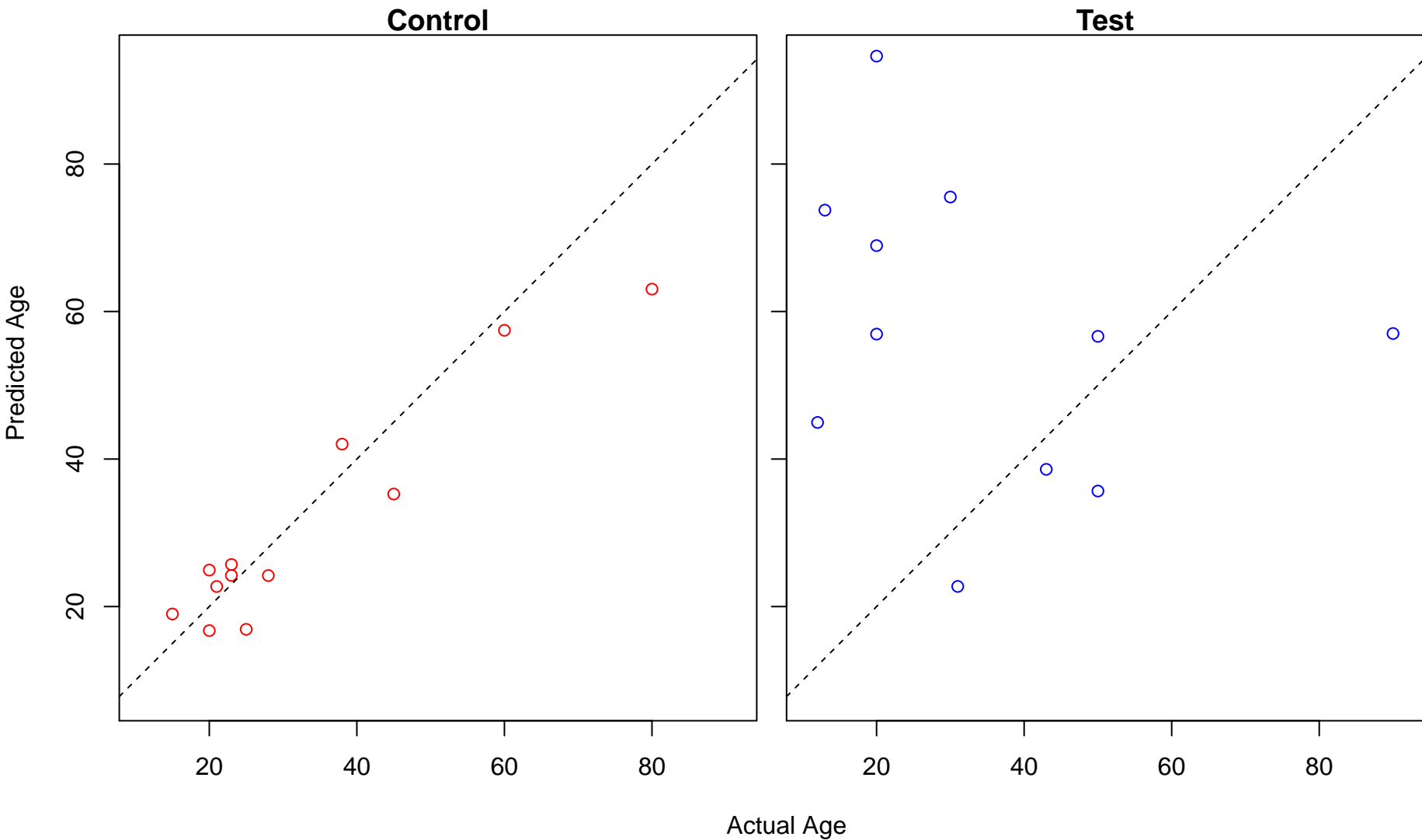
oxygen homeostasis (Score: 25.685277)



positive regulation of spindle checkpoint (Score: 25.546698)

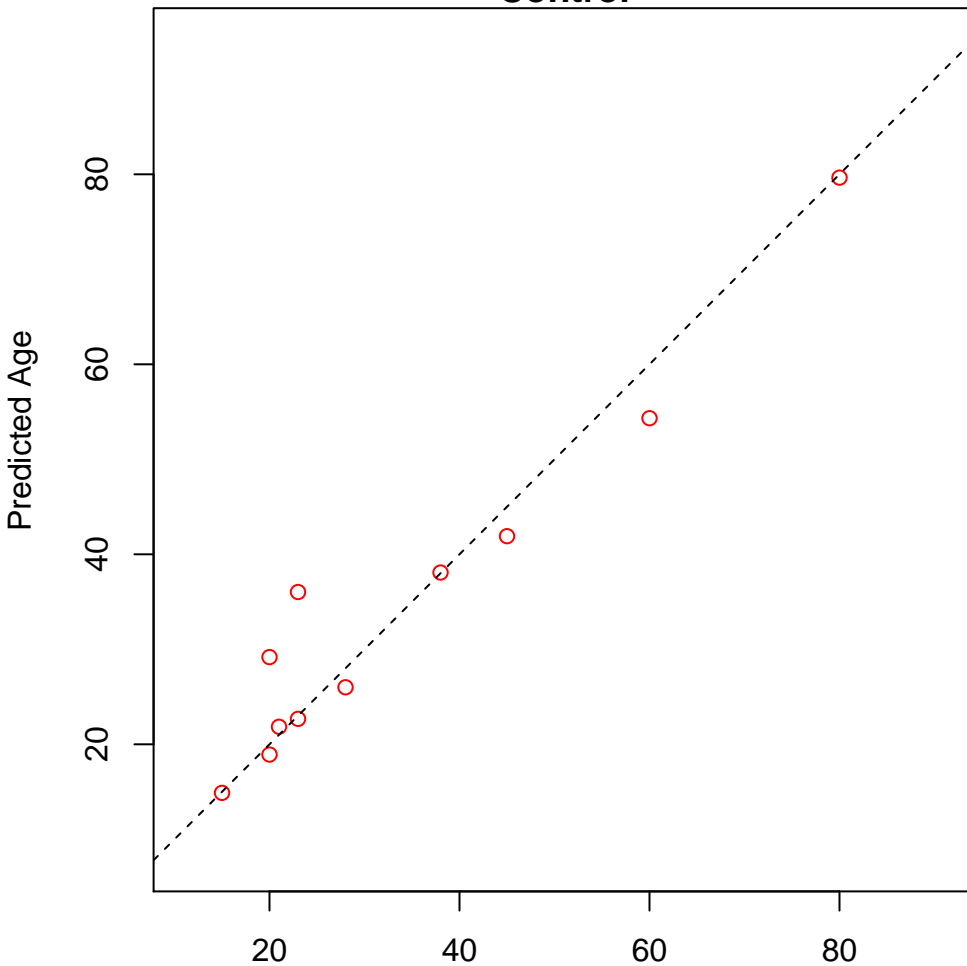


positive regulation of cell cycle checkpoint (Score: 25.546698)

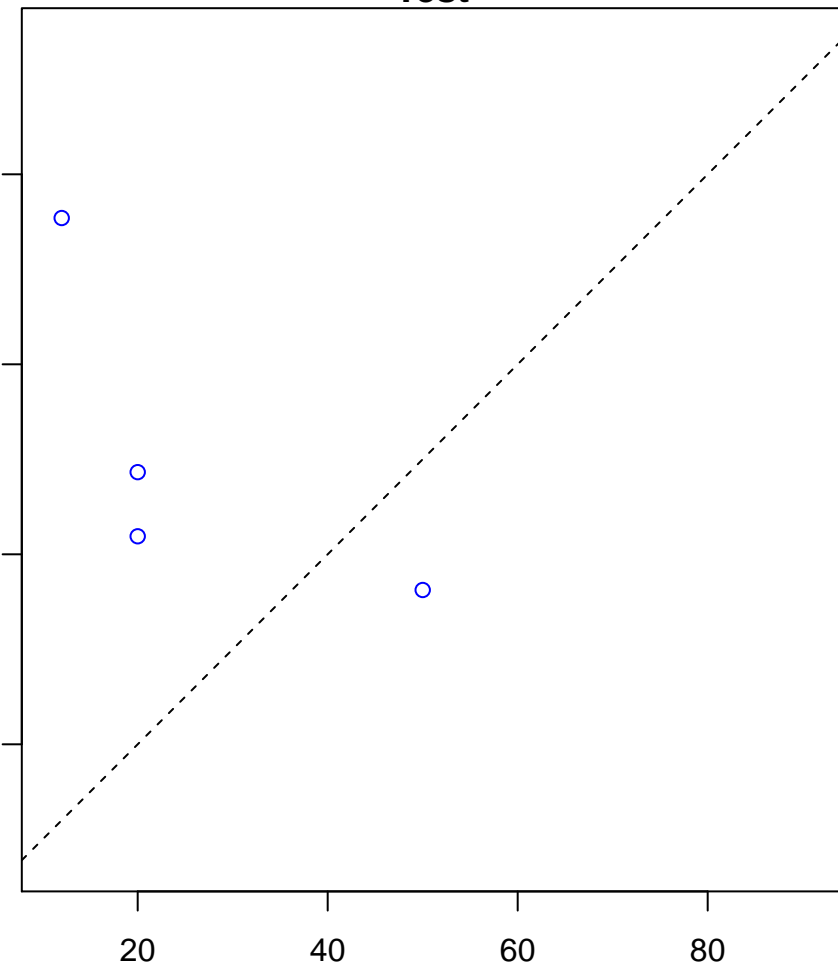


regulation of histone phosphorylation (Score: 25.475267)

Control



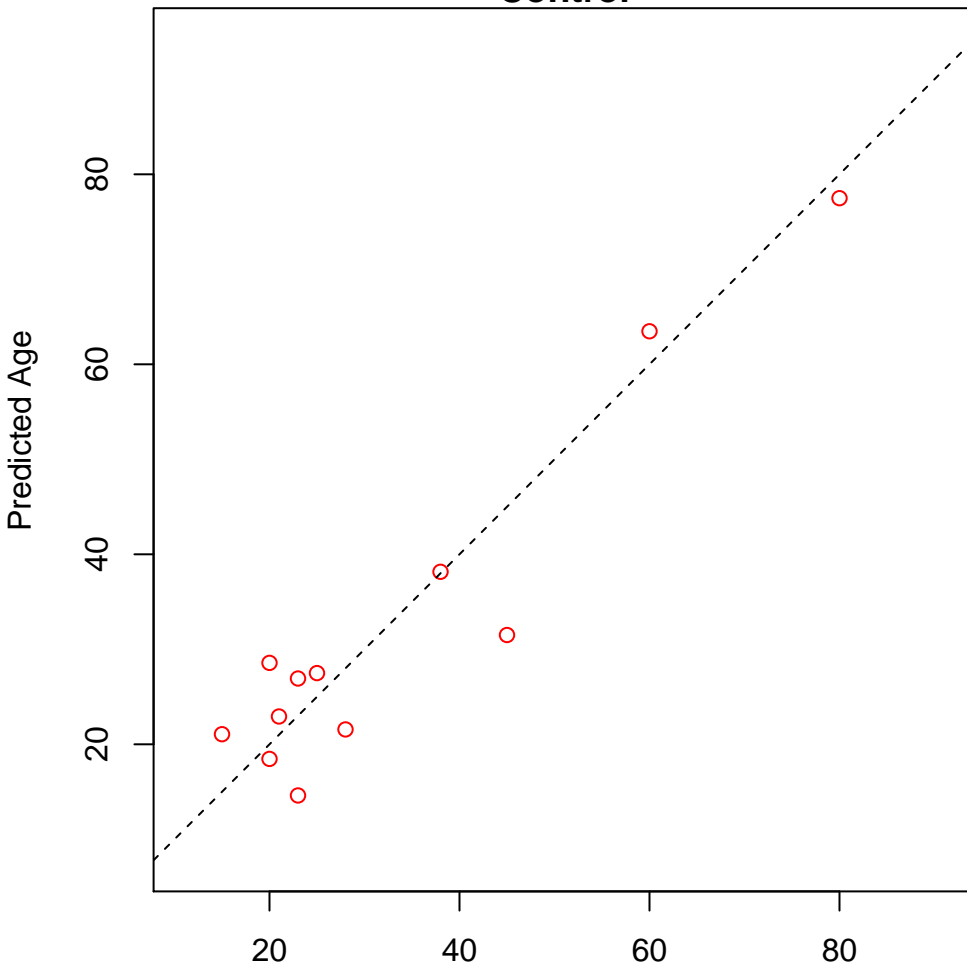
Test



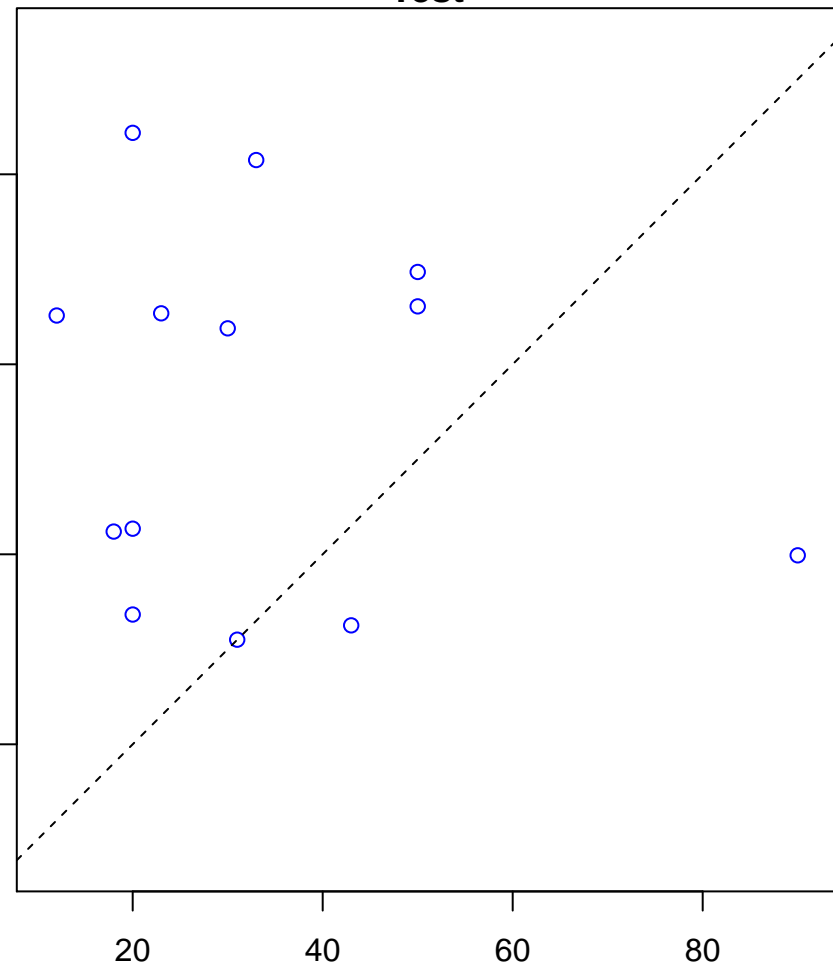
Actual Age

protein targeting to mitochondrion (Score: 25.443567)

Control

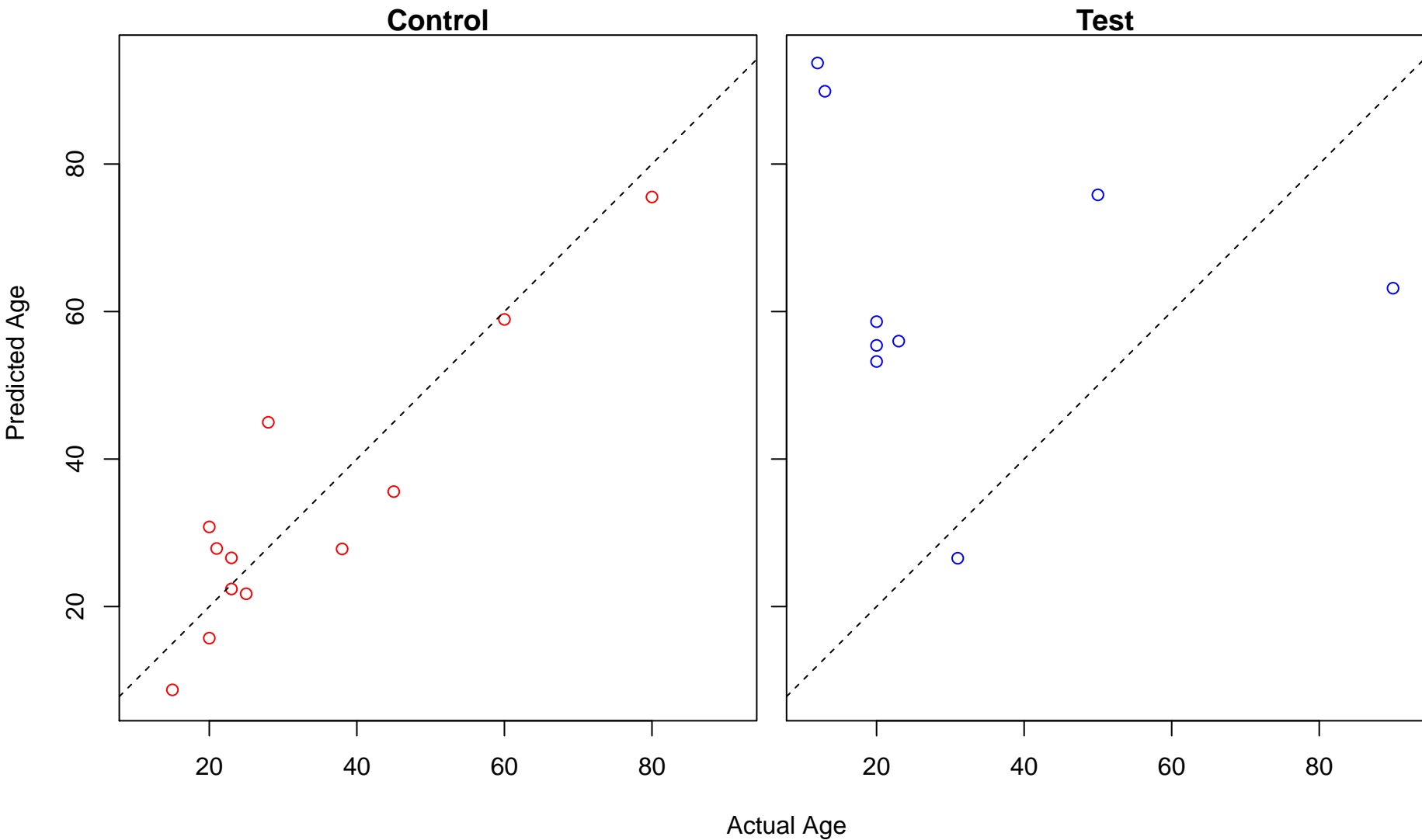


Test

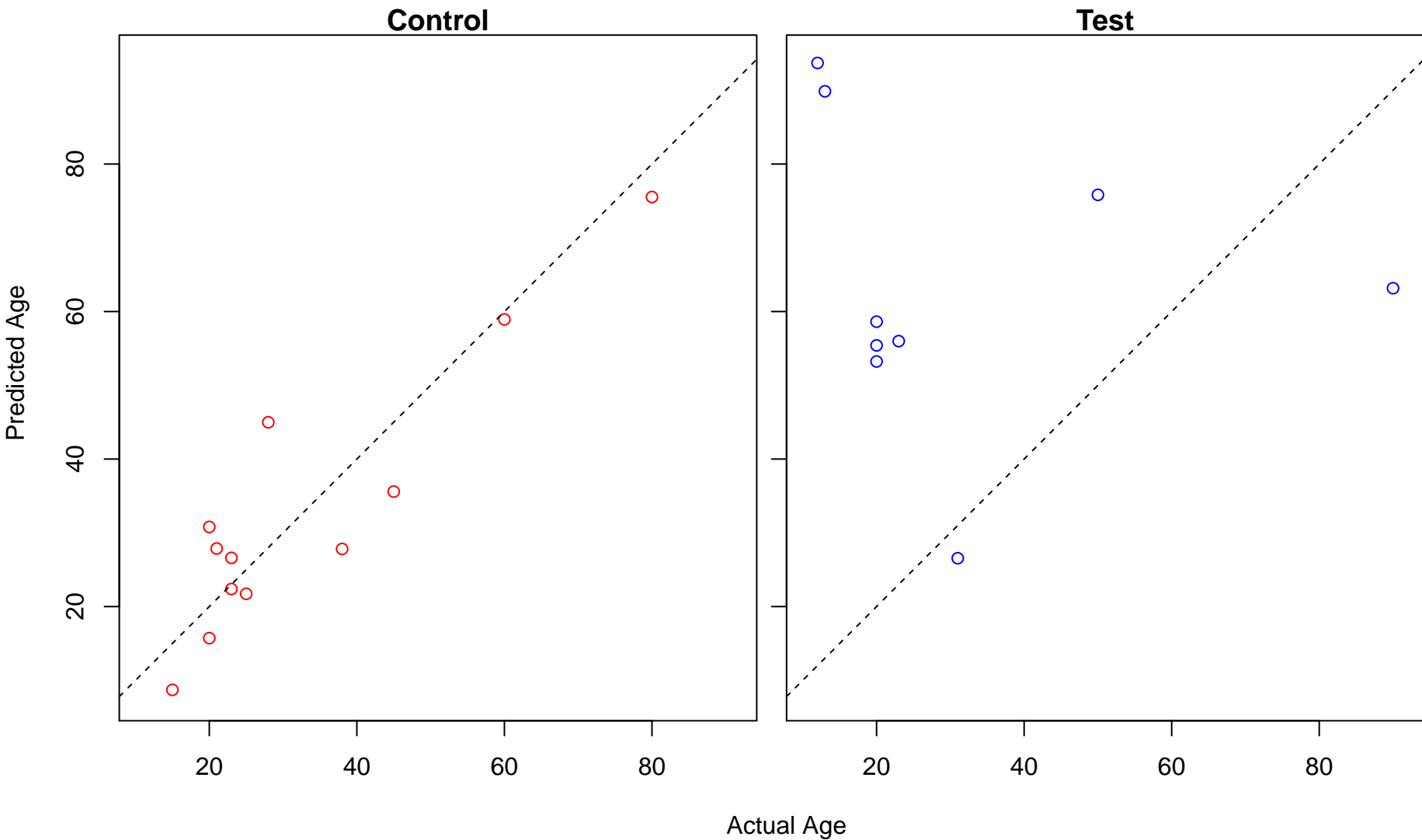


Actual Age

autophagosome maturation (Score: 25.378774)

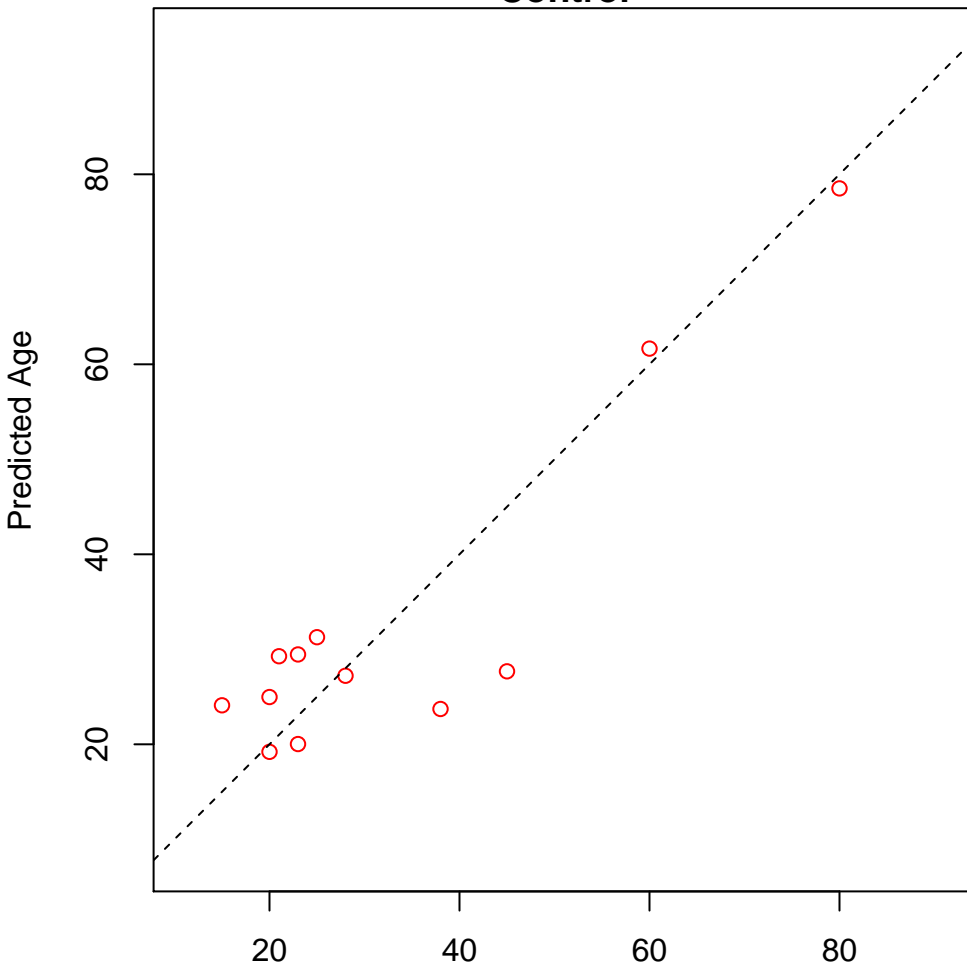


vacuole fusion (Score: 25.378774)

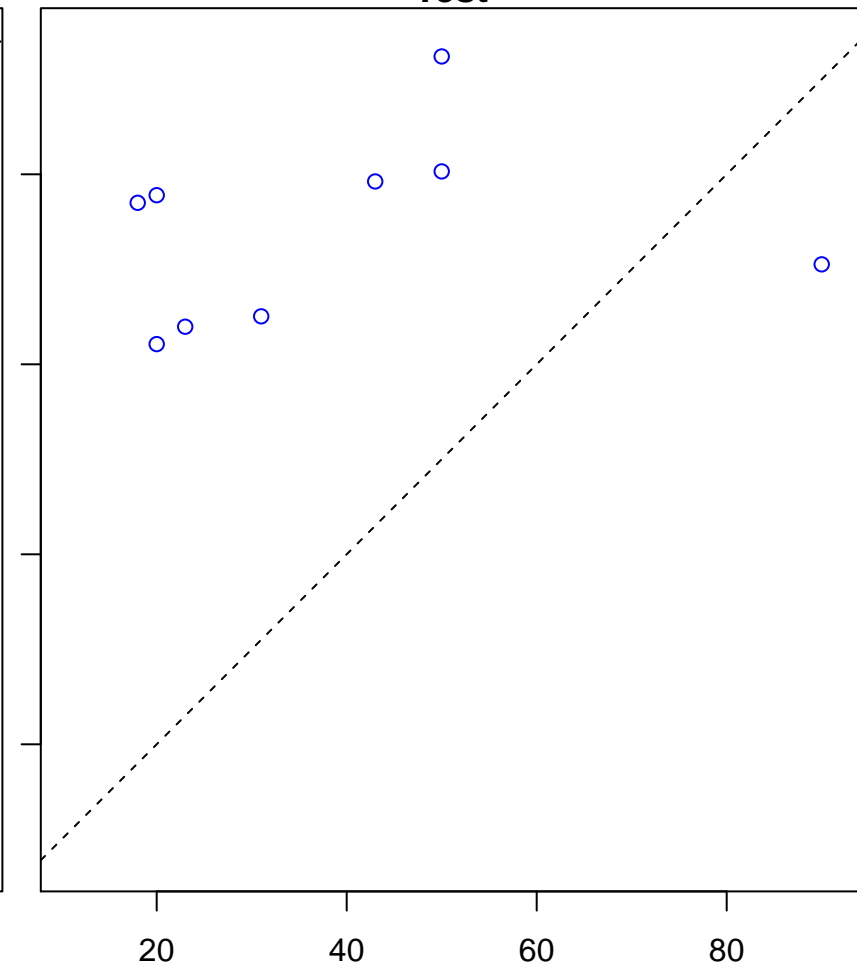


endocardial cushion development (Score: 25.376488)

Control

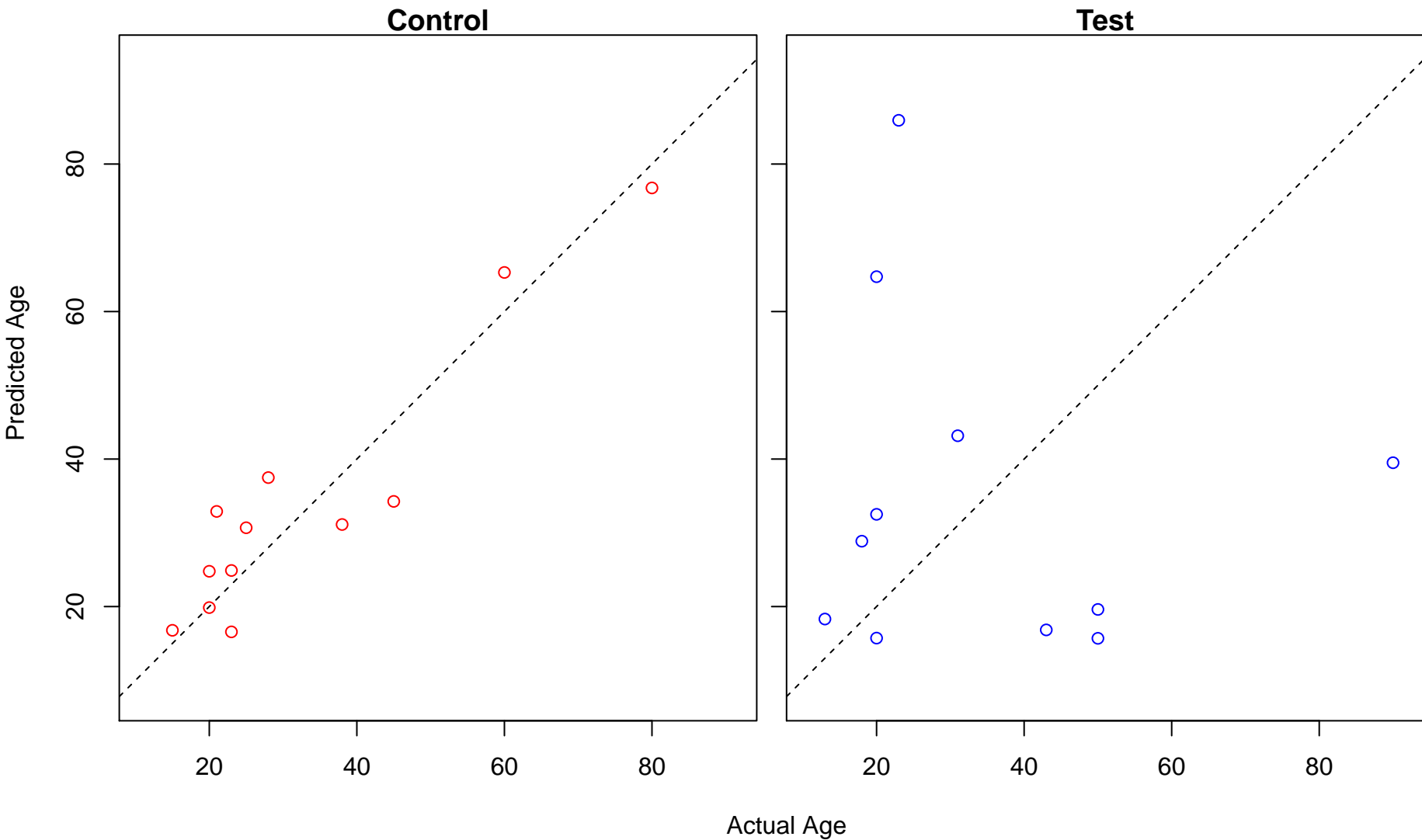


Test



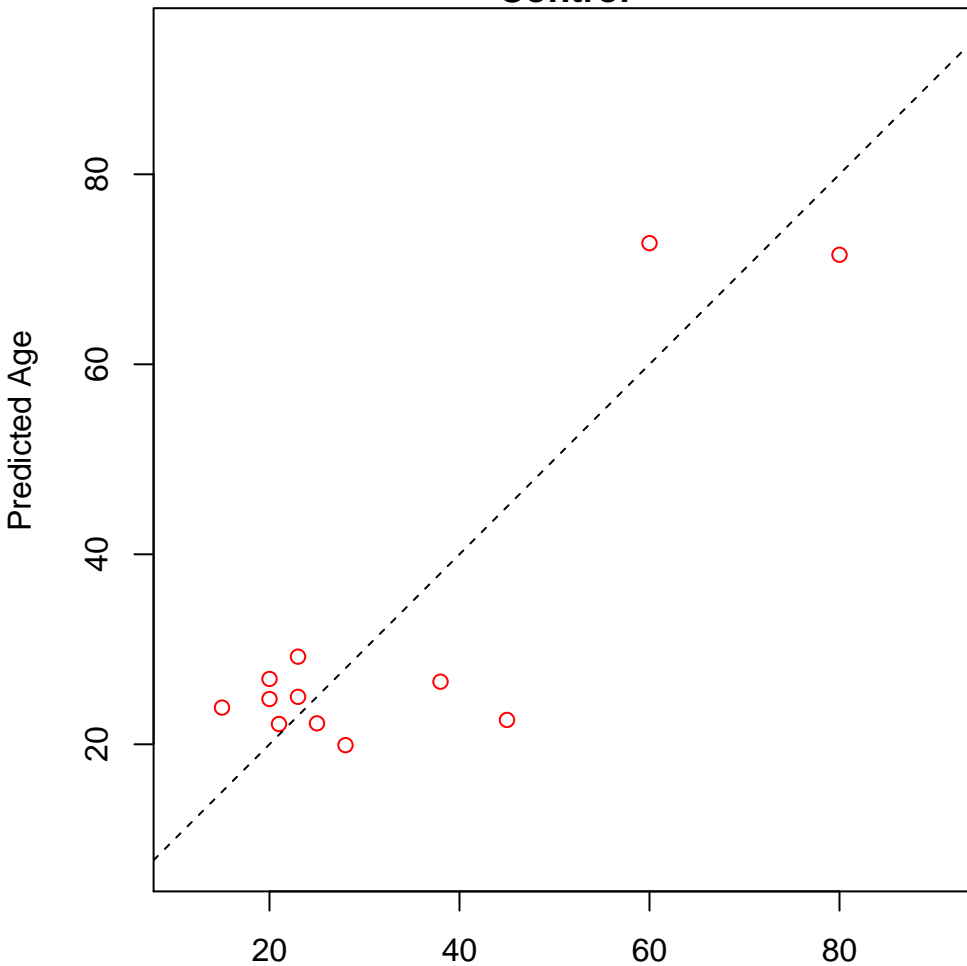
Actual Age

cobalamin metabolic process (Score: 25.283249)

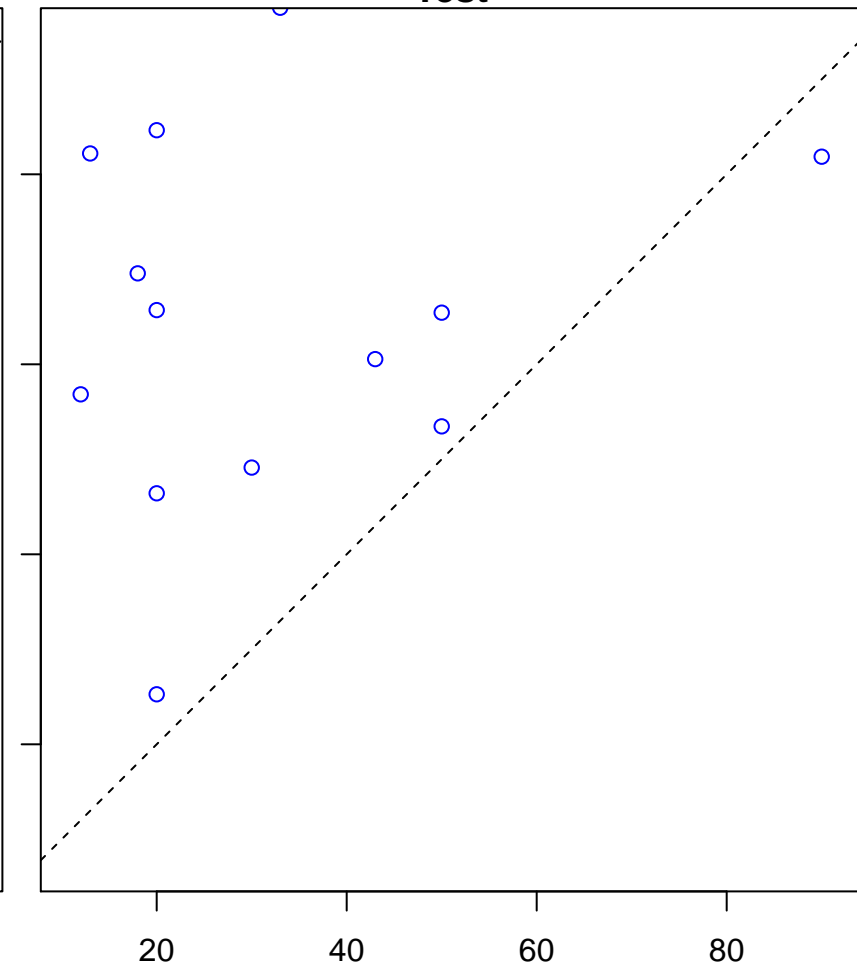


response to mechanical stimulus (Score: 25.221005)

Control

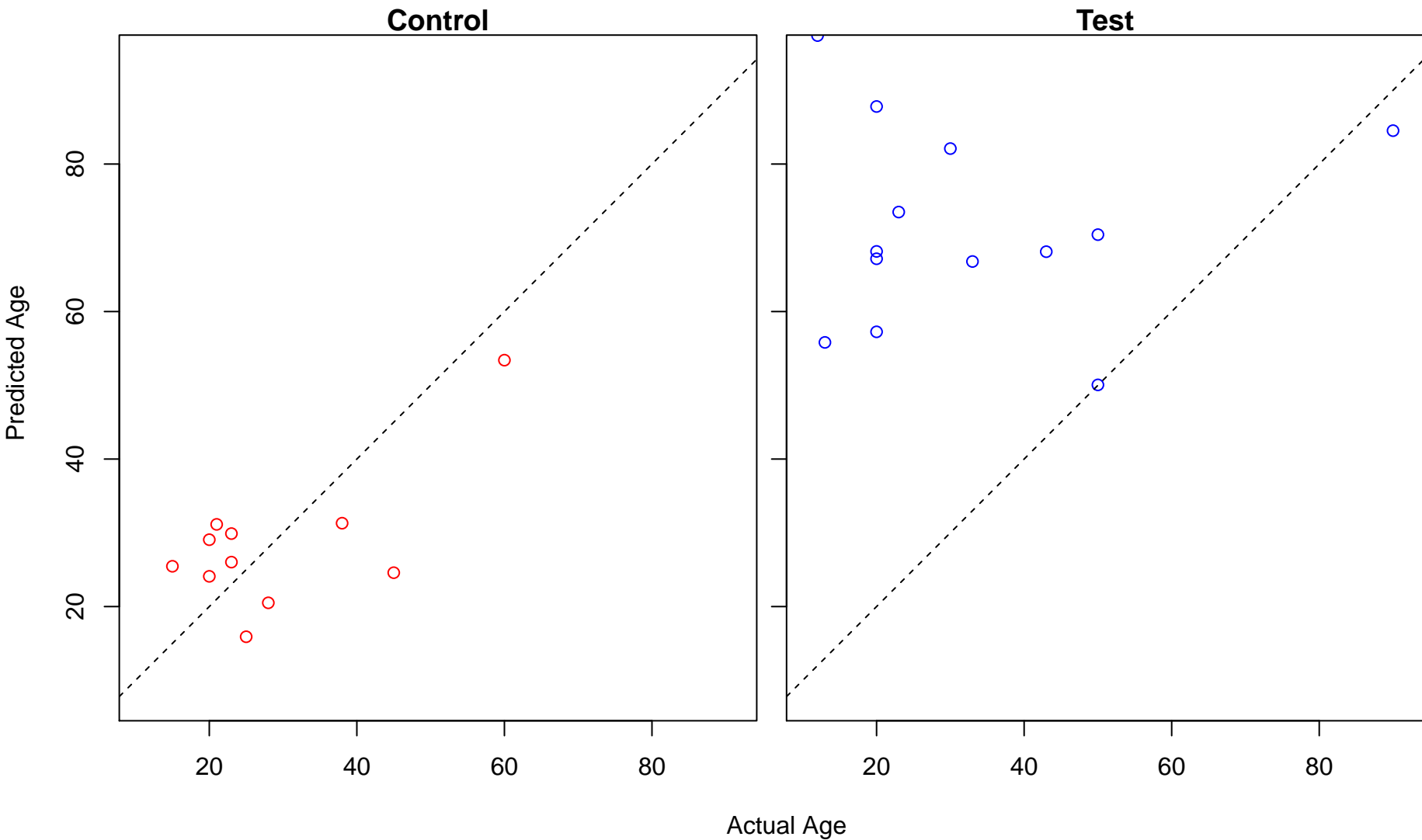


Test

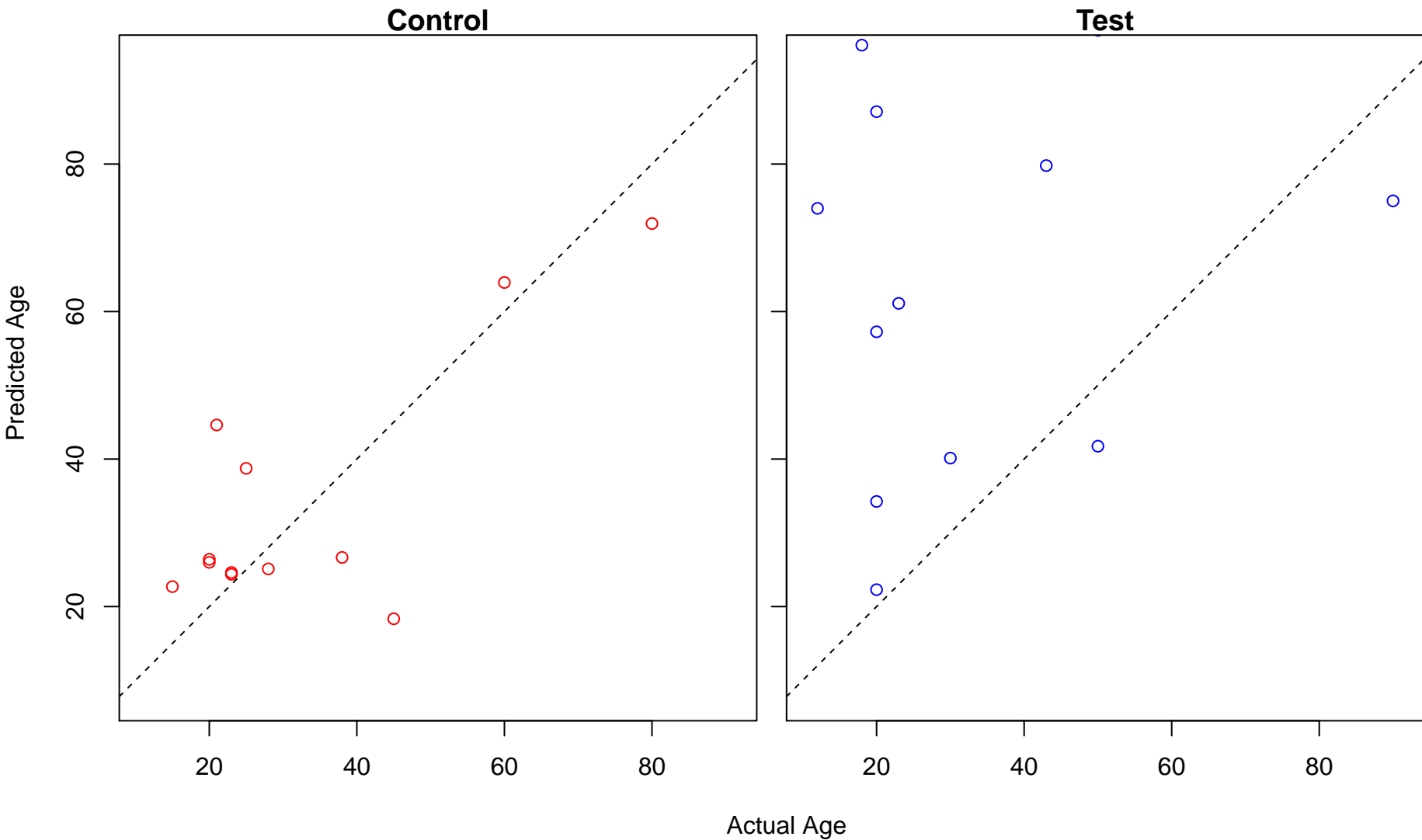


Actual Age

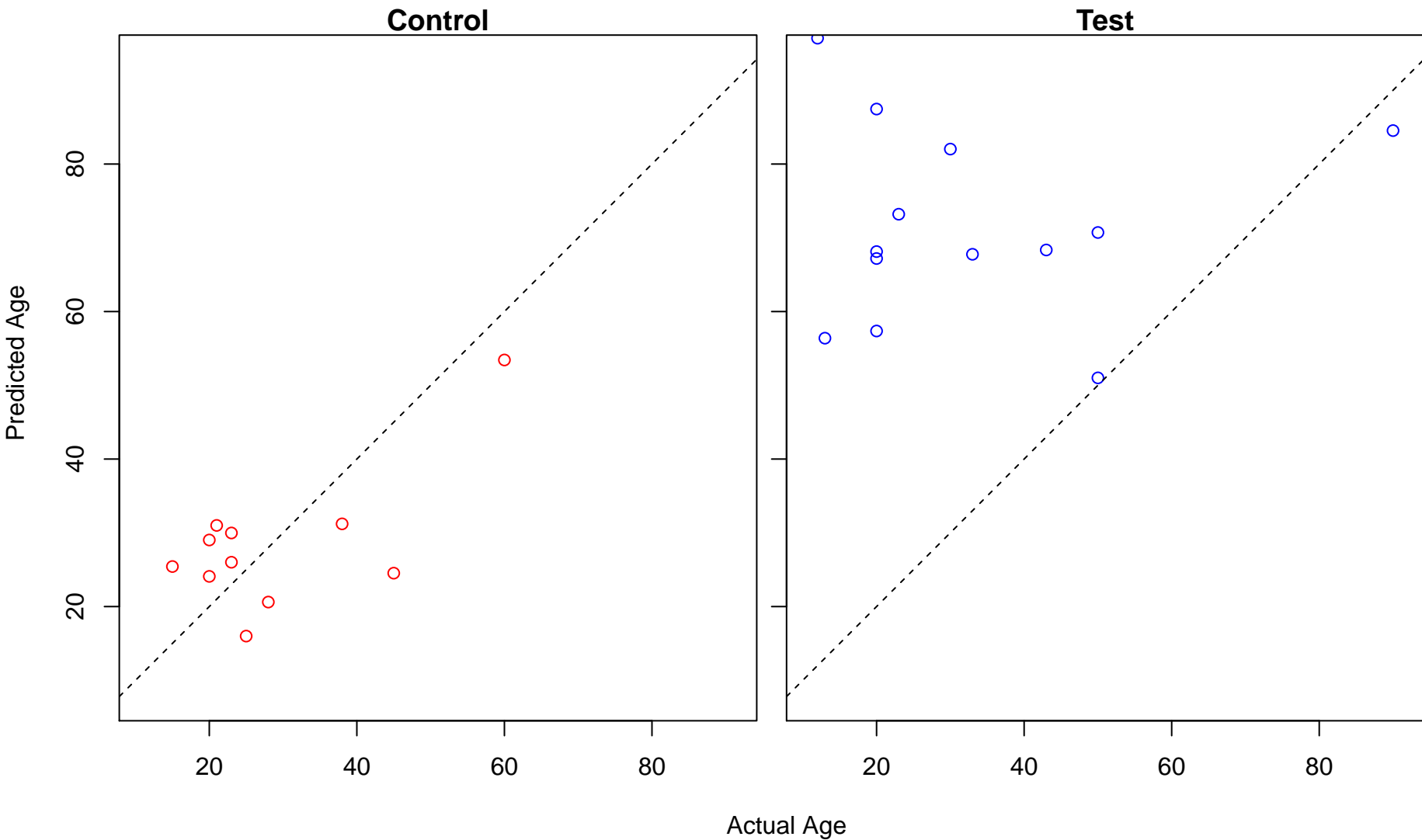
cellular zinc ion homeostasis (Score: 25.054061)



regulation of natural killer cell chemotaxis (Score: 25.019999)

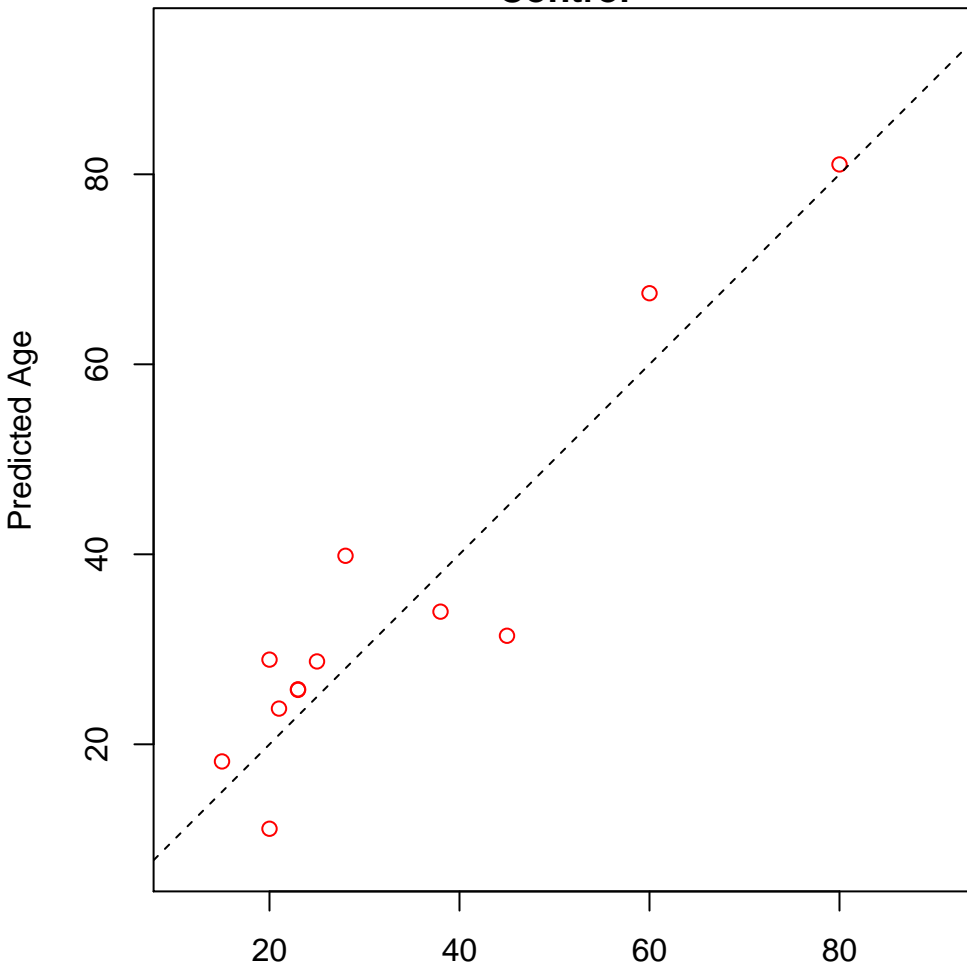


zinc ion homeostasis (Score: 25.009798)

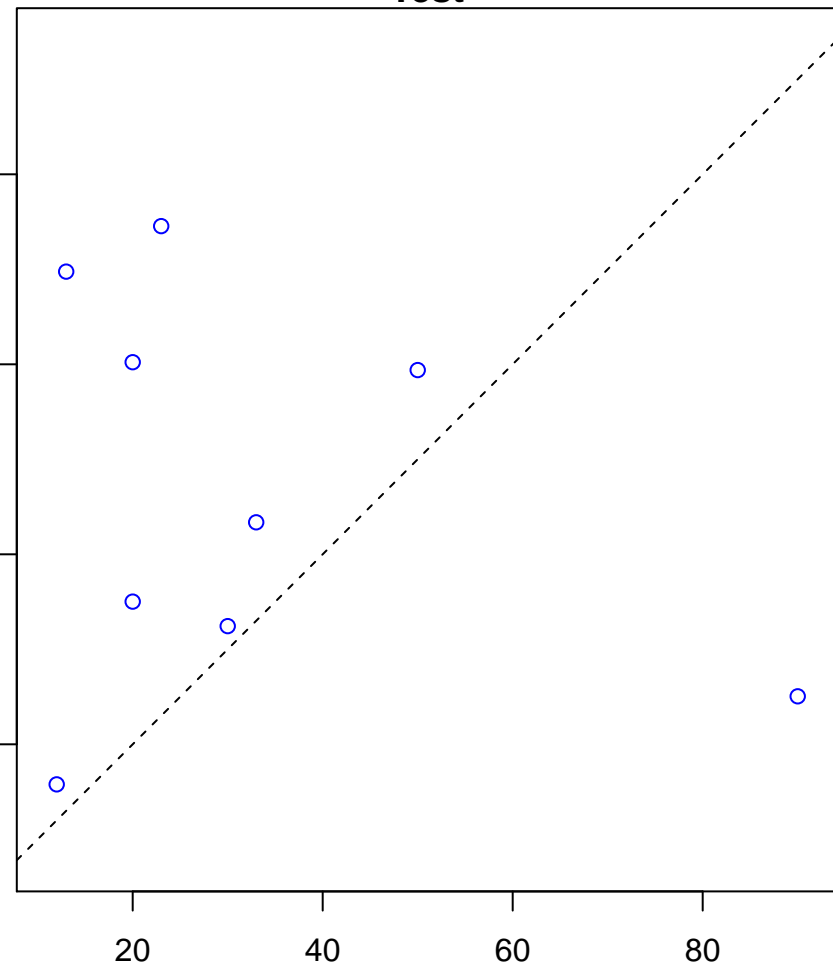


ribose phosphate metabolic process (Score: 24.975787)

Control

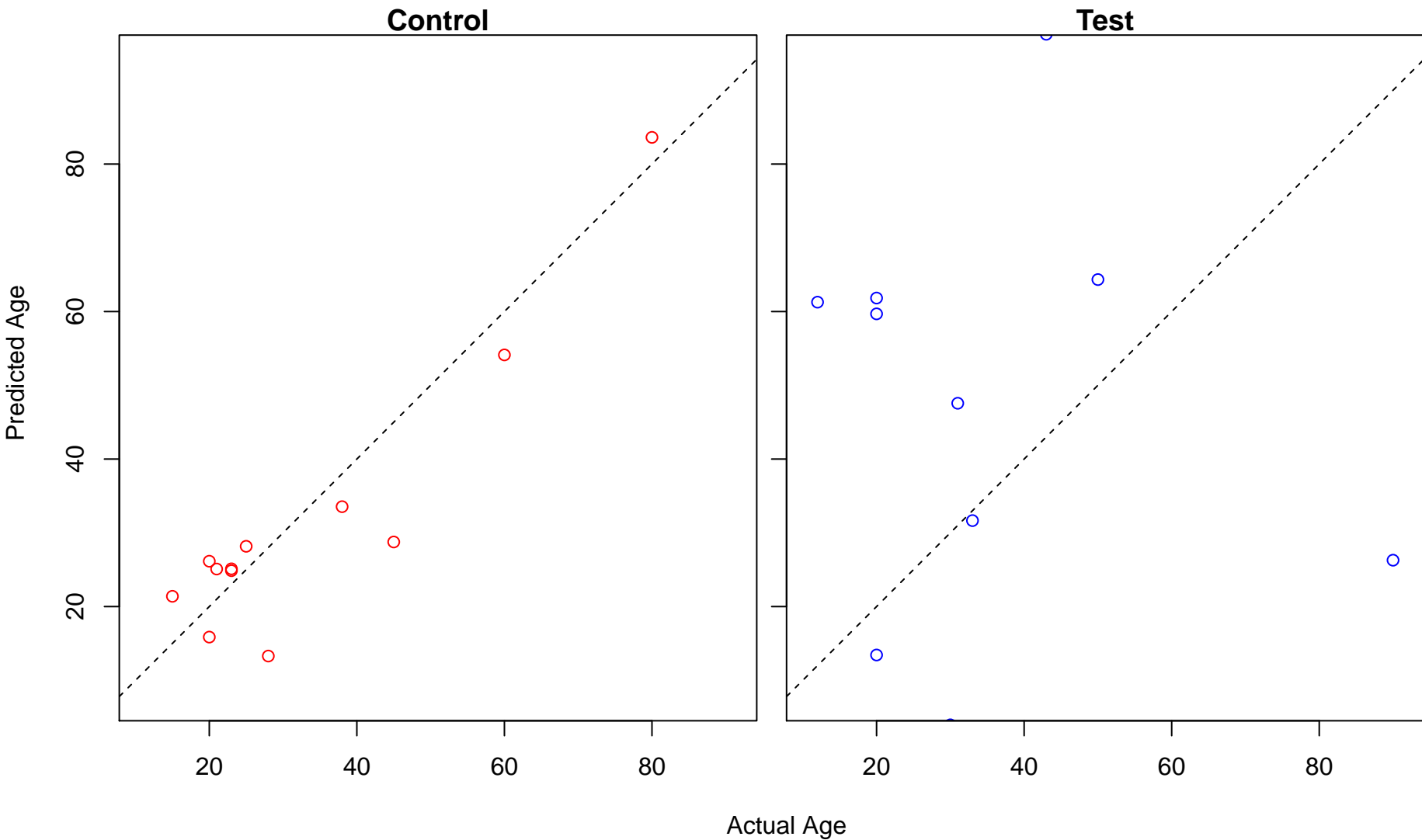


Test

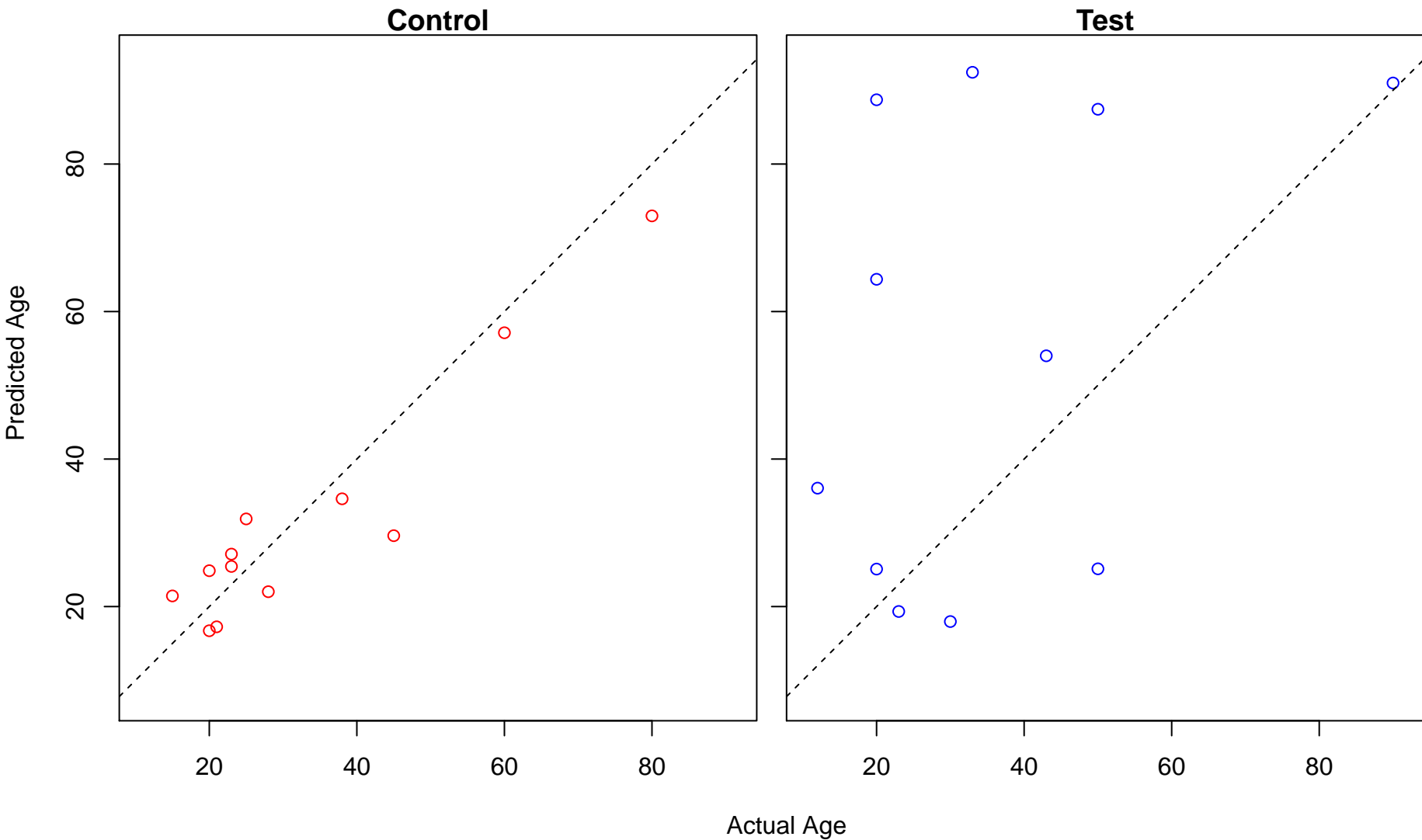


Actual Age

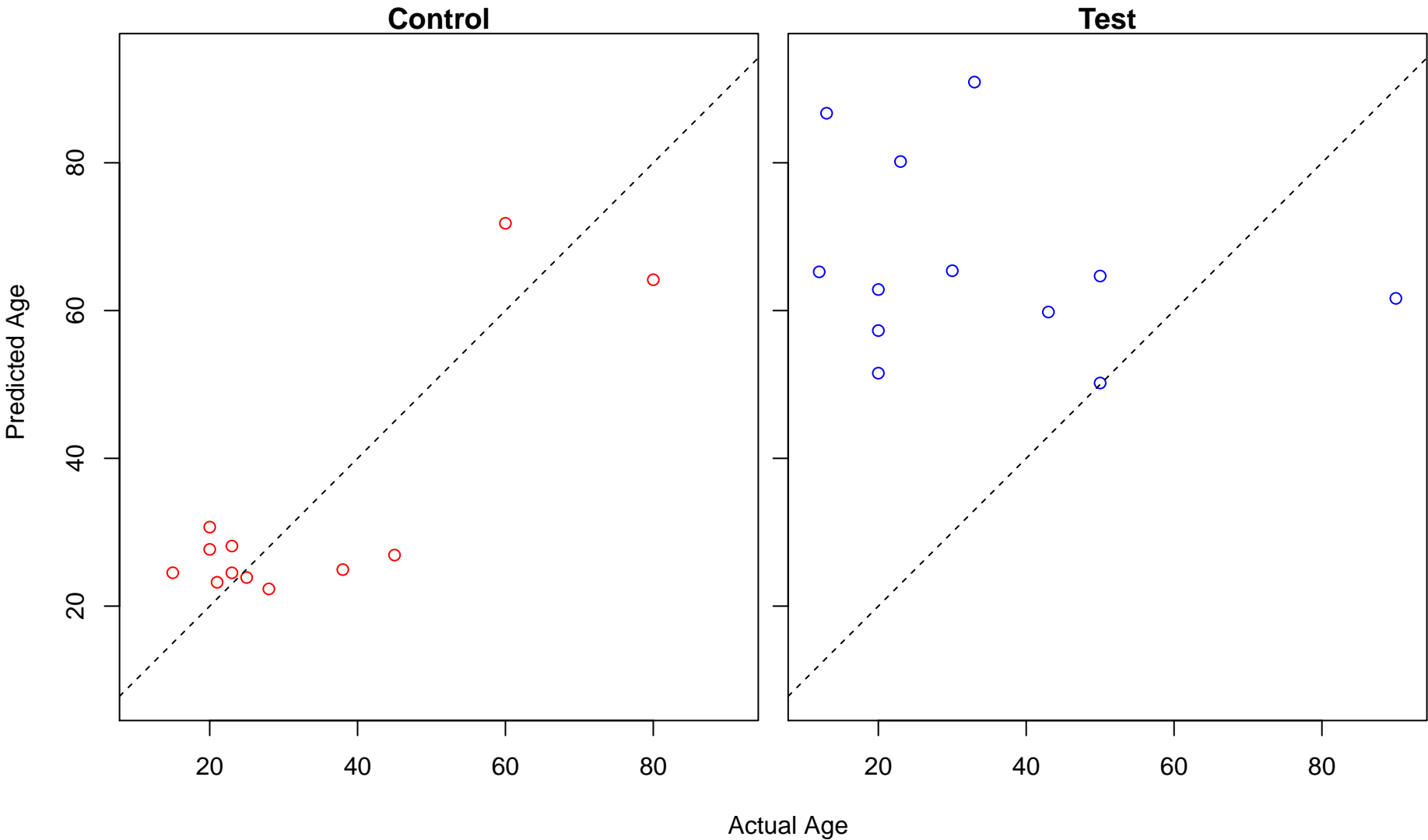
regulation of respiratory gaseous exchange (Score: 24.943130)



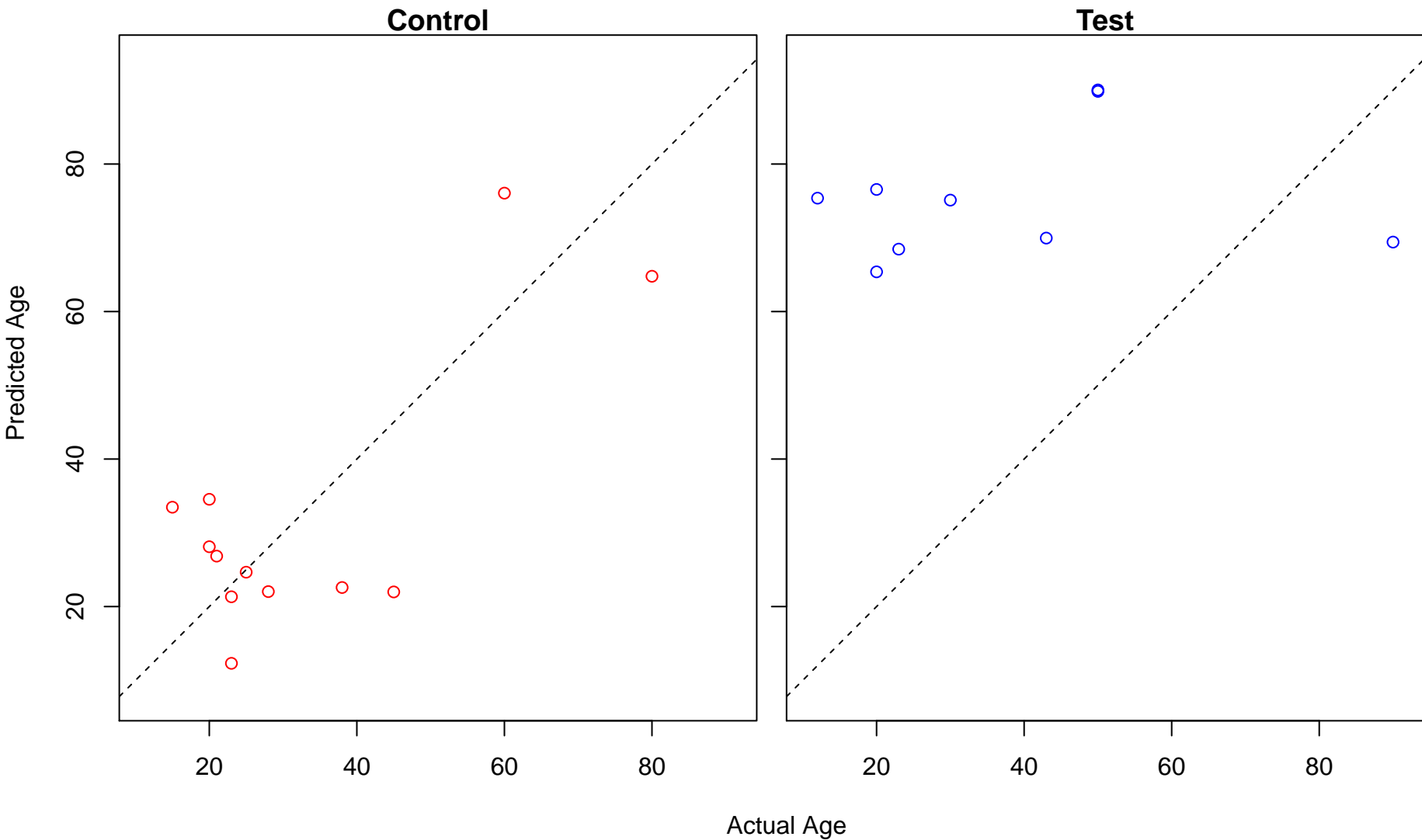
negative regulation of histone modification (Score: 24.923304)



positive regulation of granulocyte macrophage colony-stimulating factor production (Score: 24.8687)

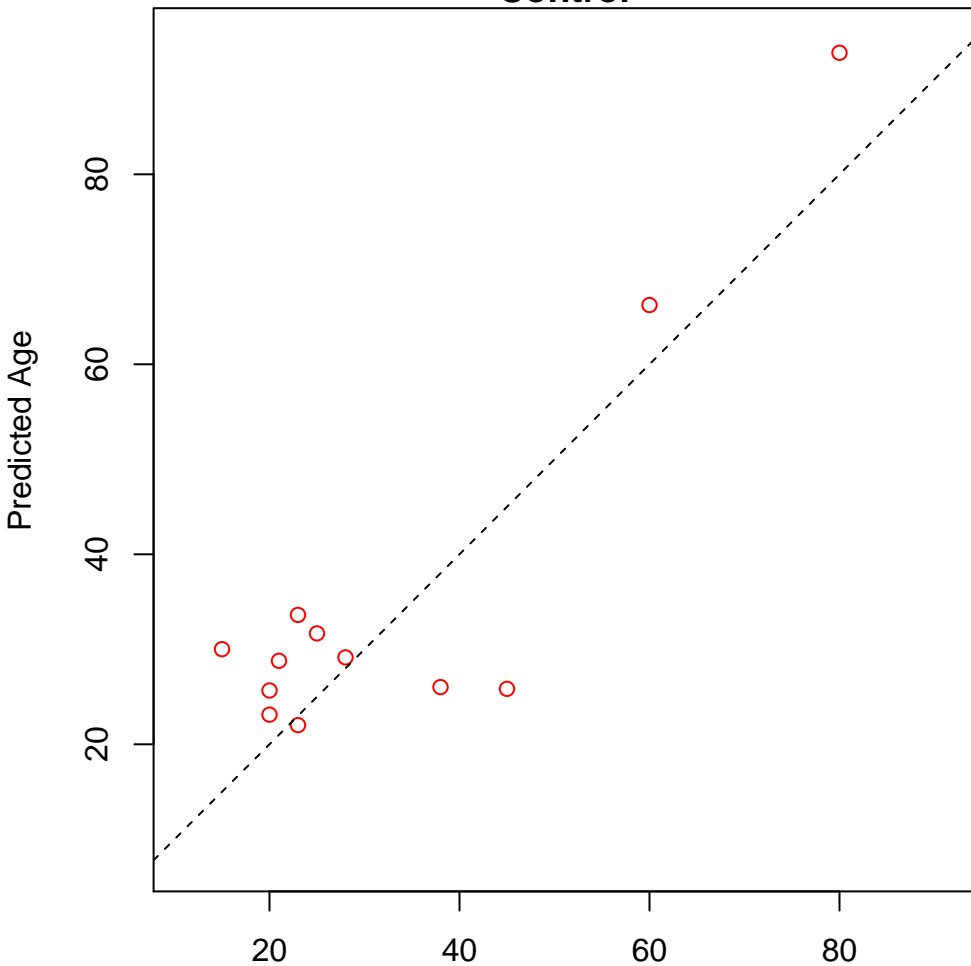


regulation of organic acid transport (Score: 24.854975)

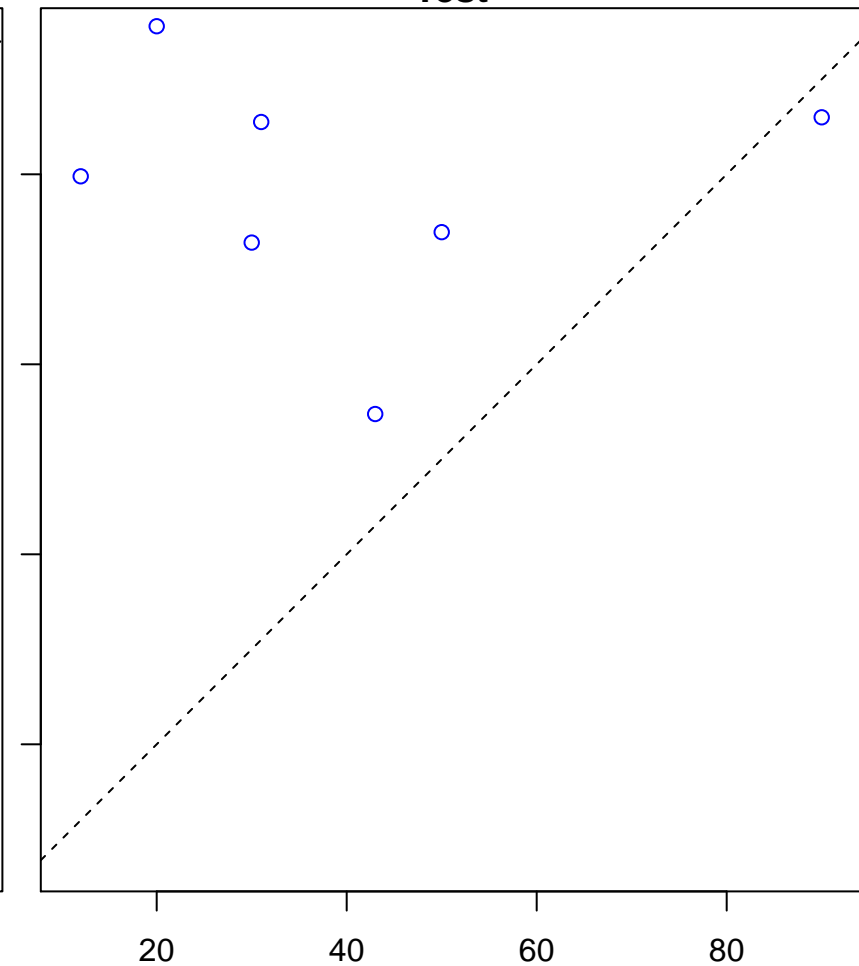


peptidyl-tyrosine dephosphorylation (Score: 24.803128)

Control



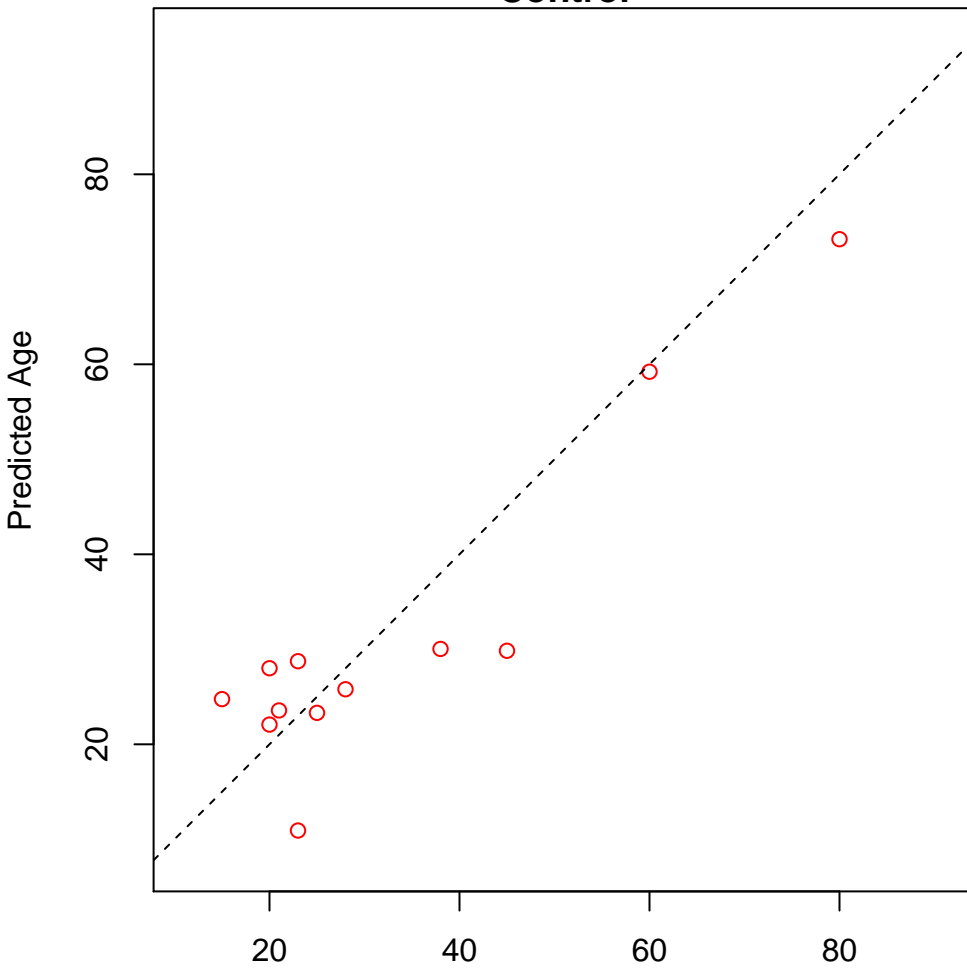
Test



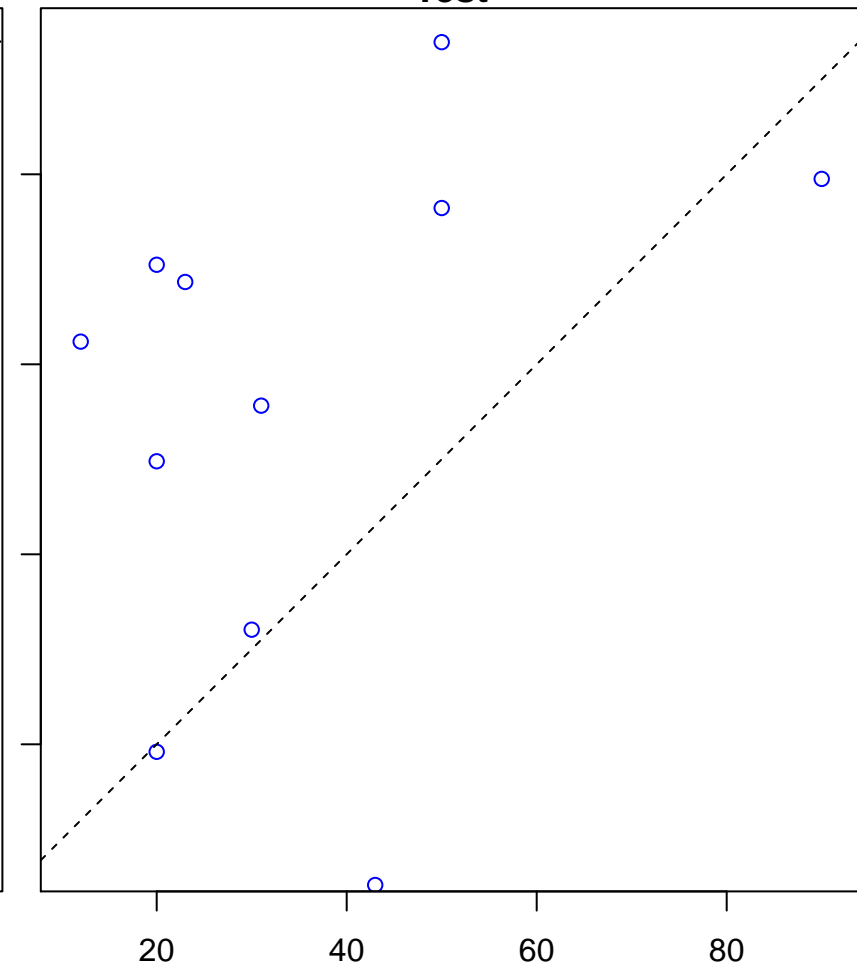
Actual Age

mitochondrial membrane organization (Score: 24.792570)

Control

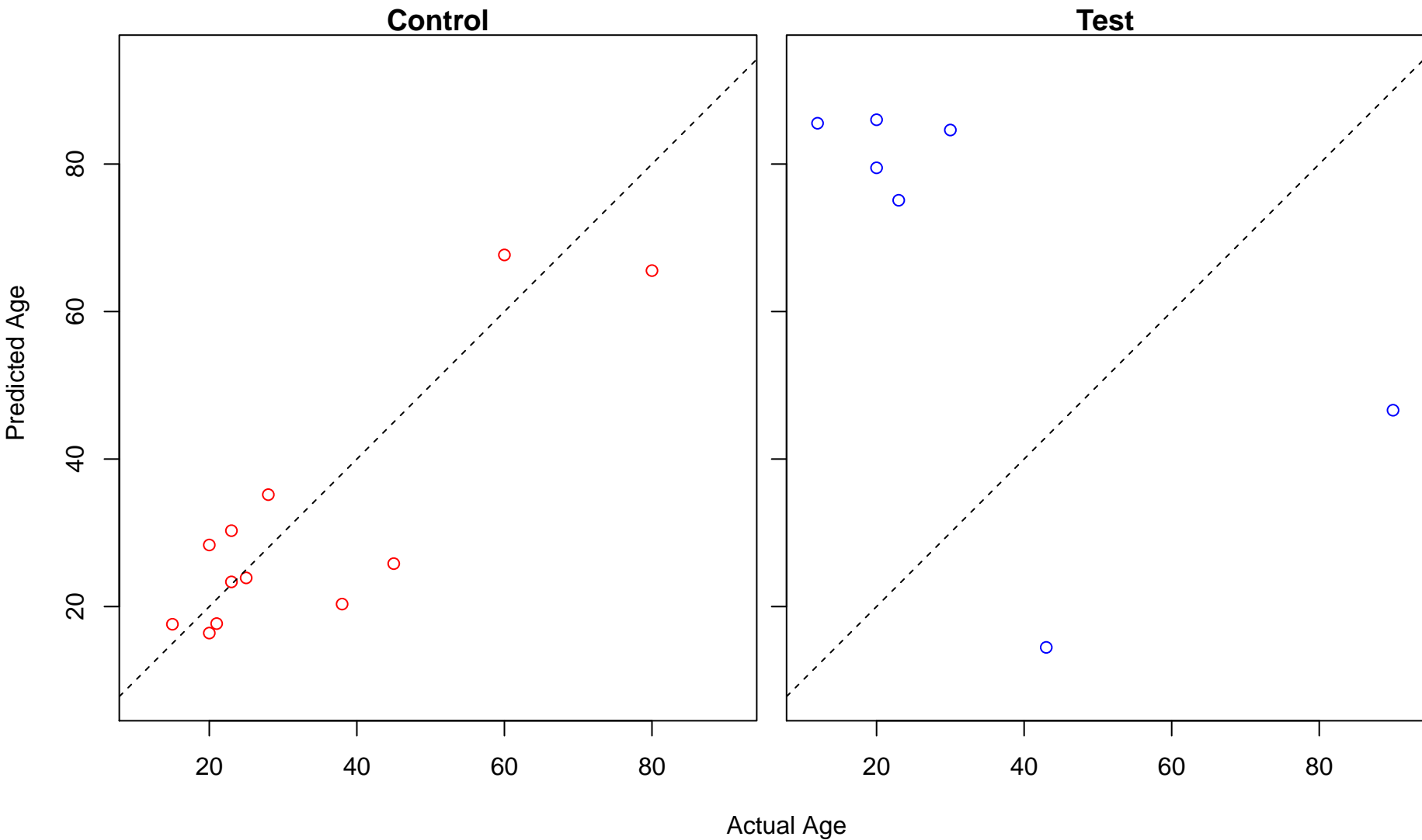


Test

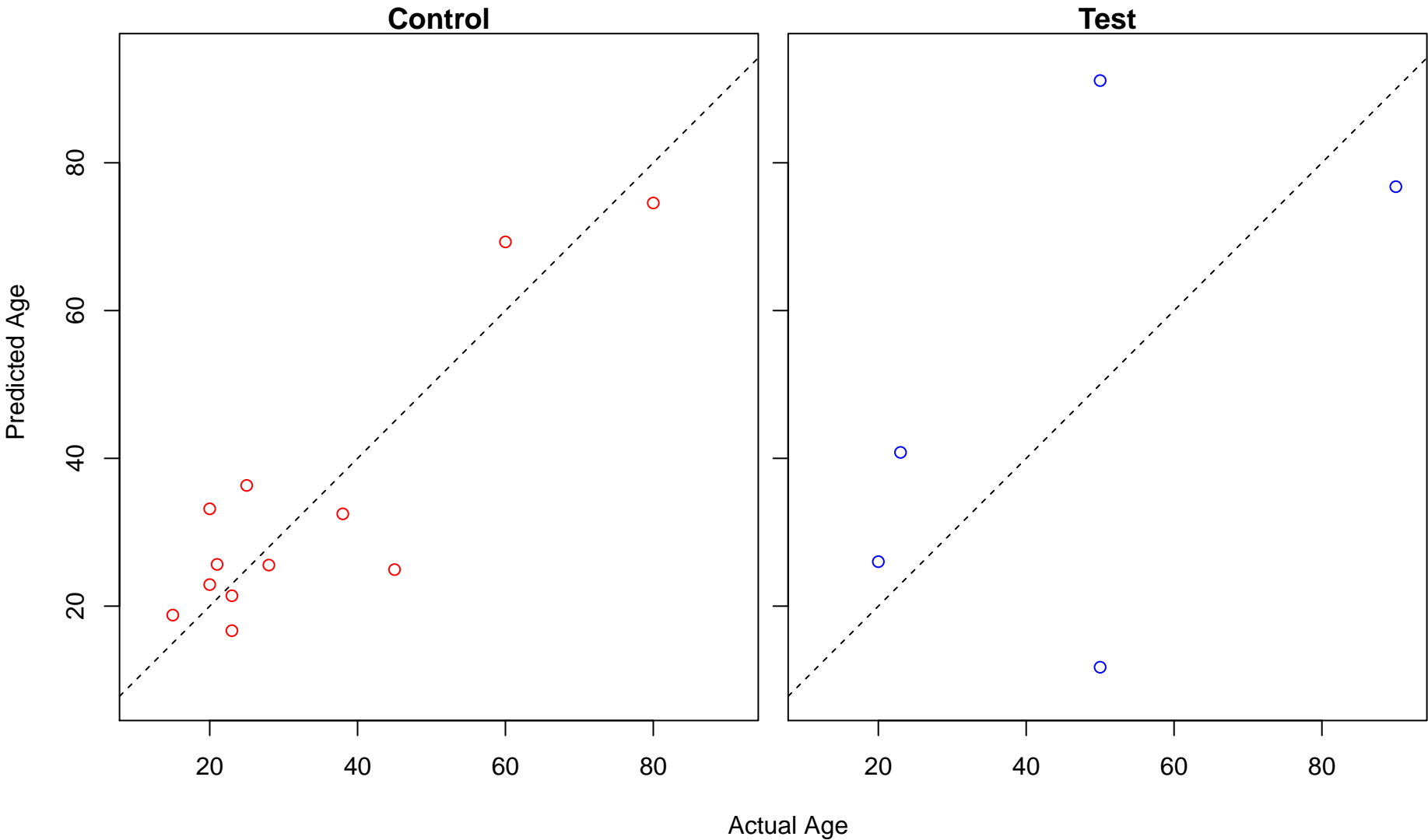


Actual Age

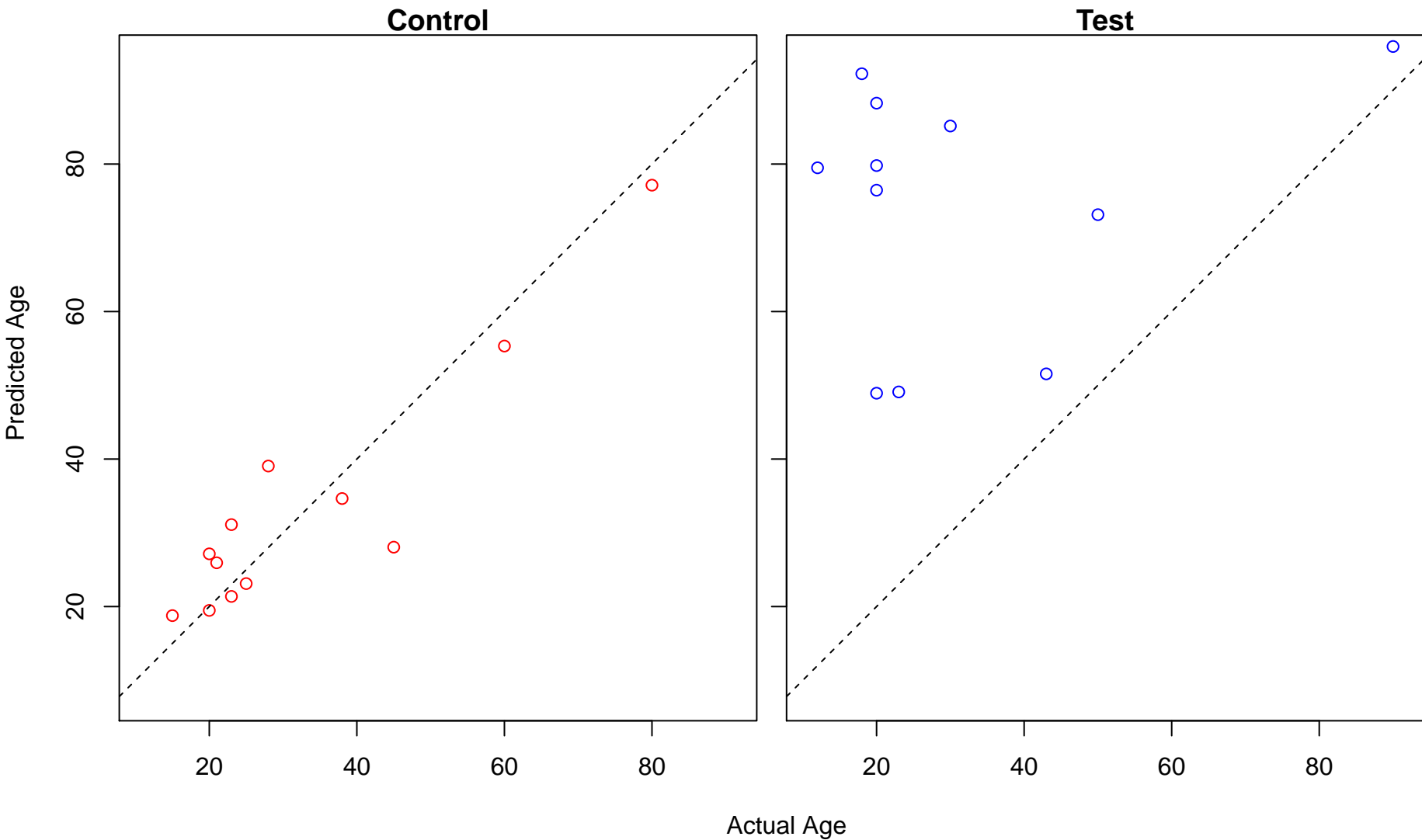
autophagosome assembly (Score: 24.772956)



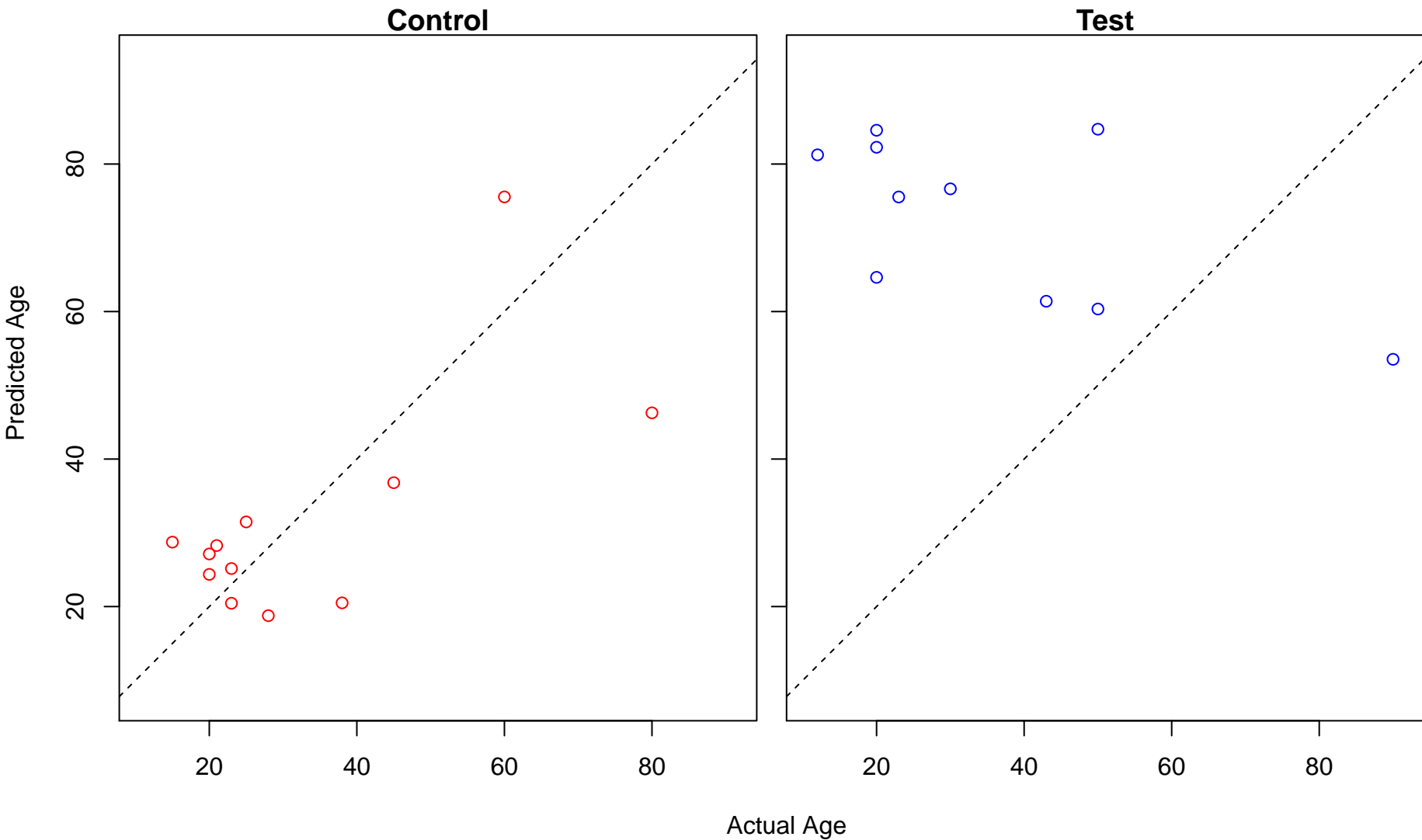
positive regulation of sequence-specific DNA binding transcription factor activity (Score: 24.76865)



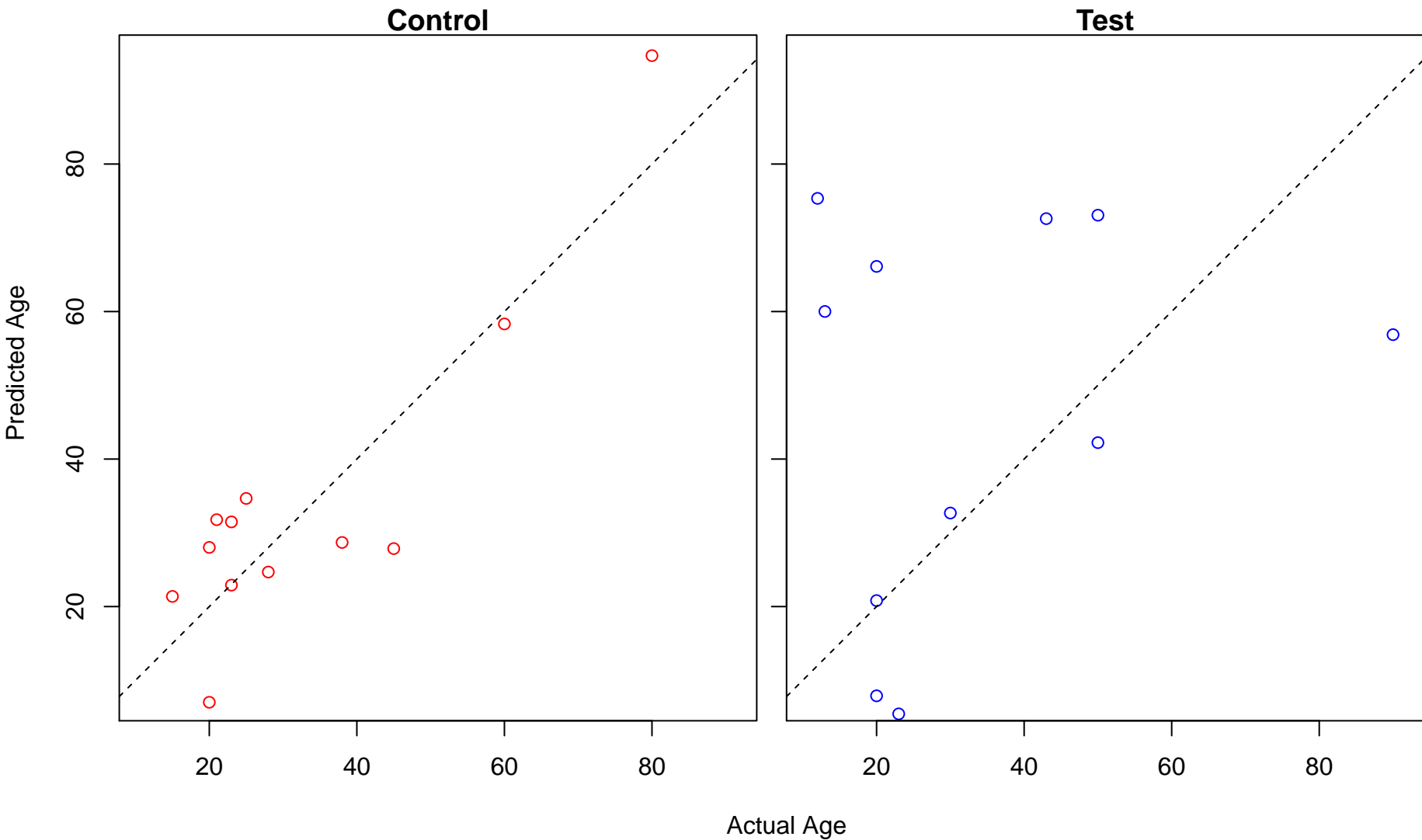
embryo development (Score: 24.741967)



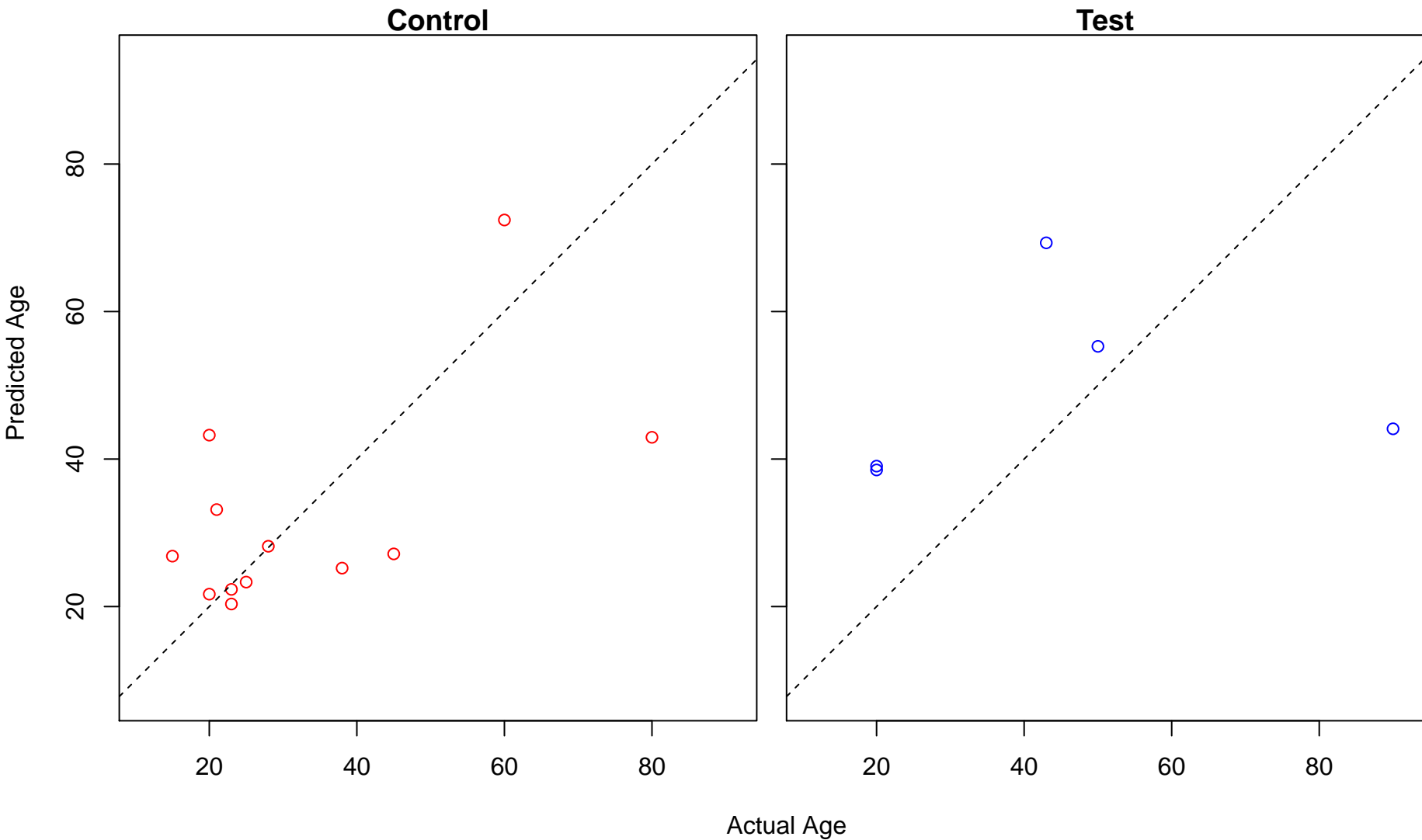
positive regulation of acute inflammatory response (Score: 24.705008)



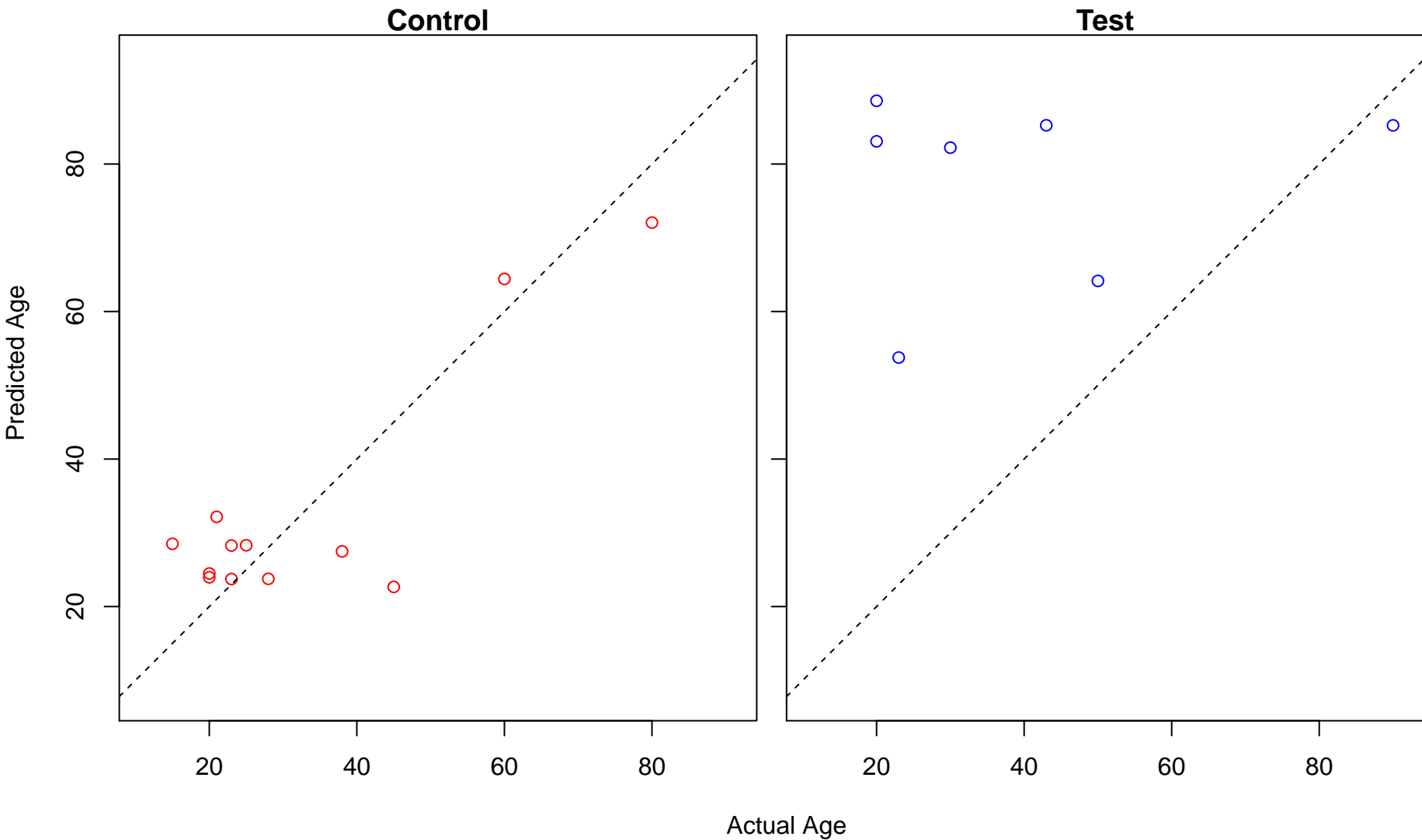
release of cytochrome c from mitochondria (Score: 24.602483)



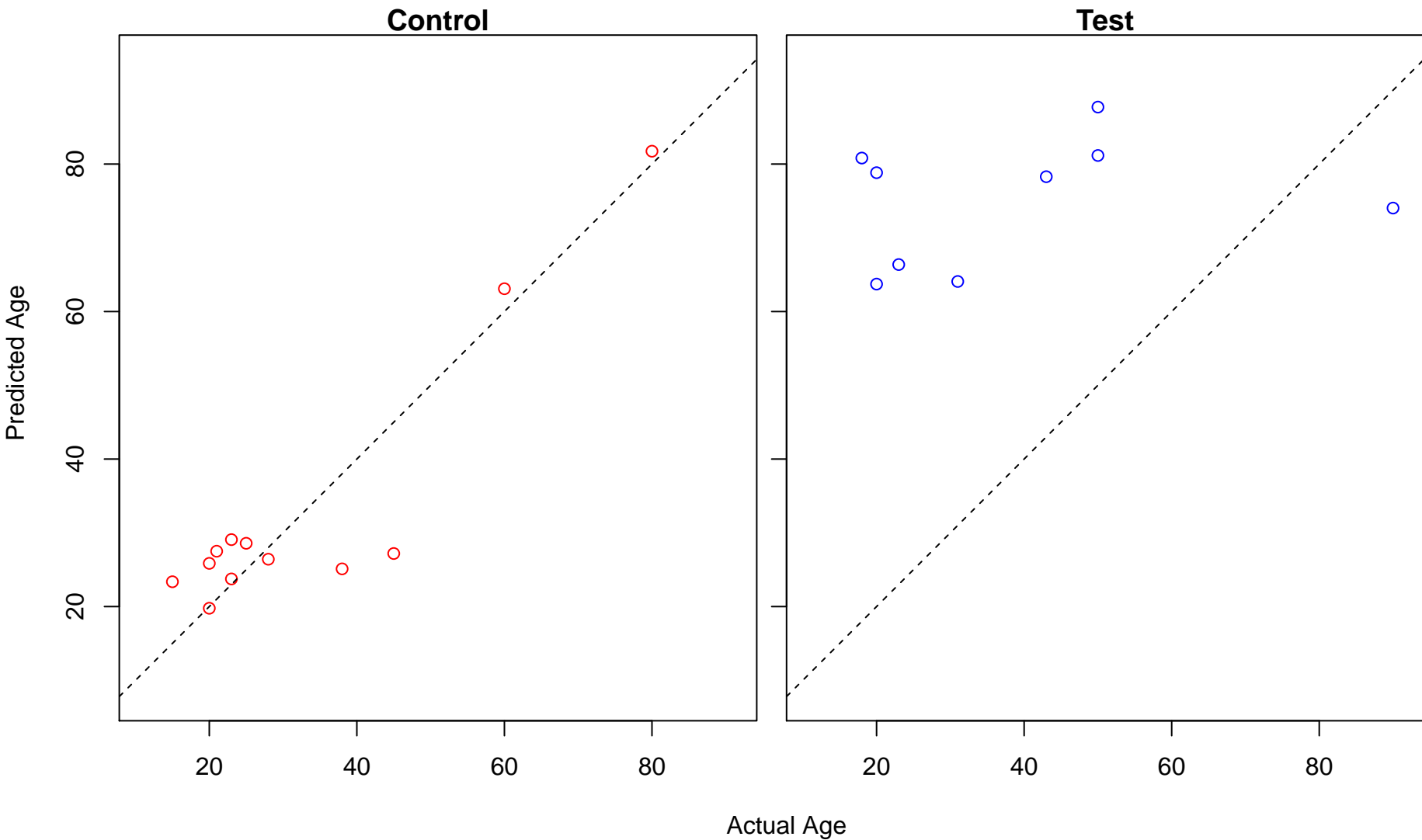
leukocyte migration involved in inflammatory response (Score: 24.499448)



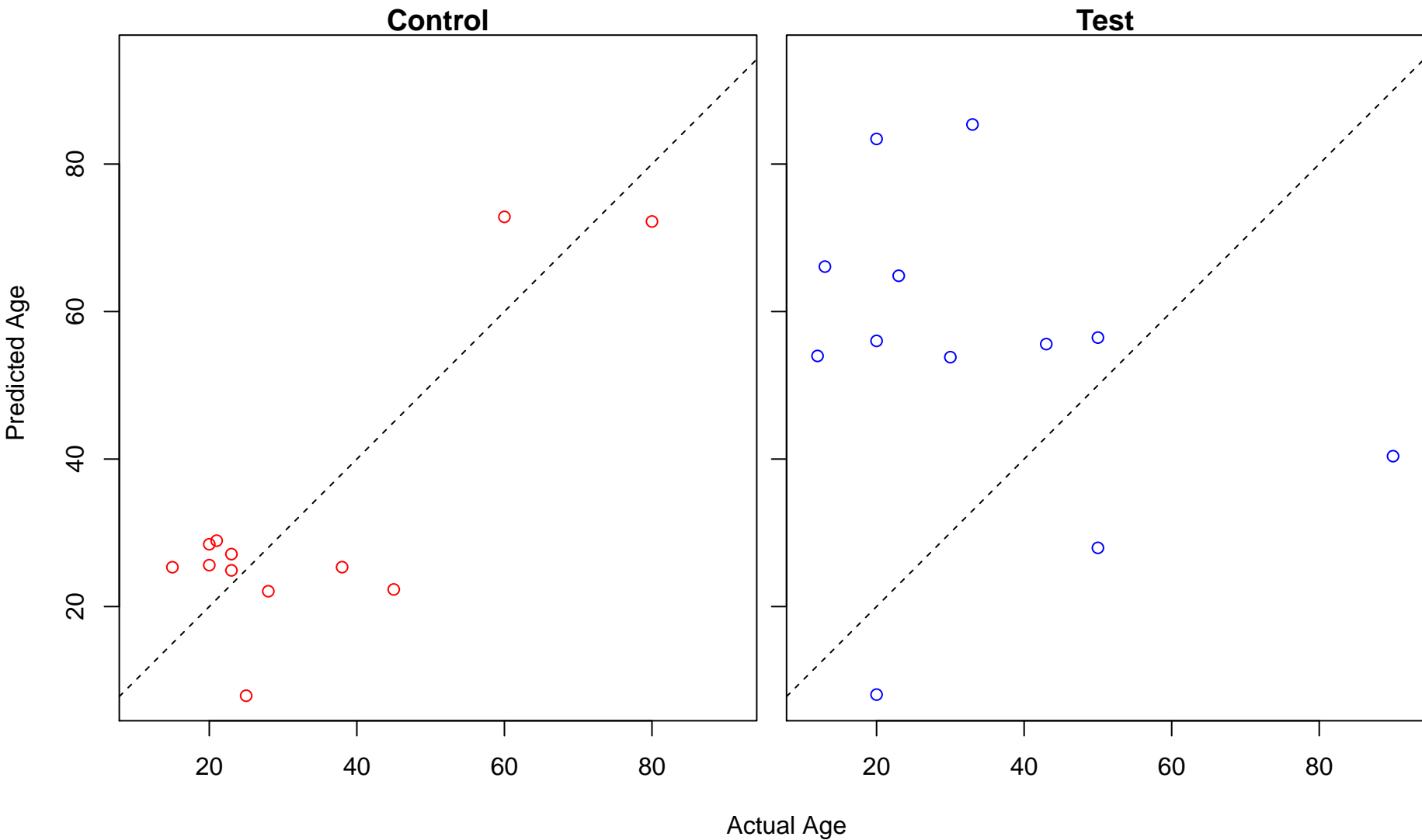
negative regulation of bone mineralization (Score: 24.467189)



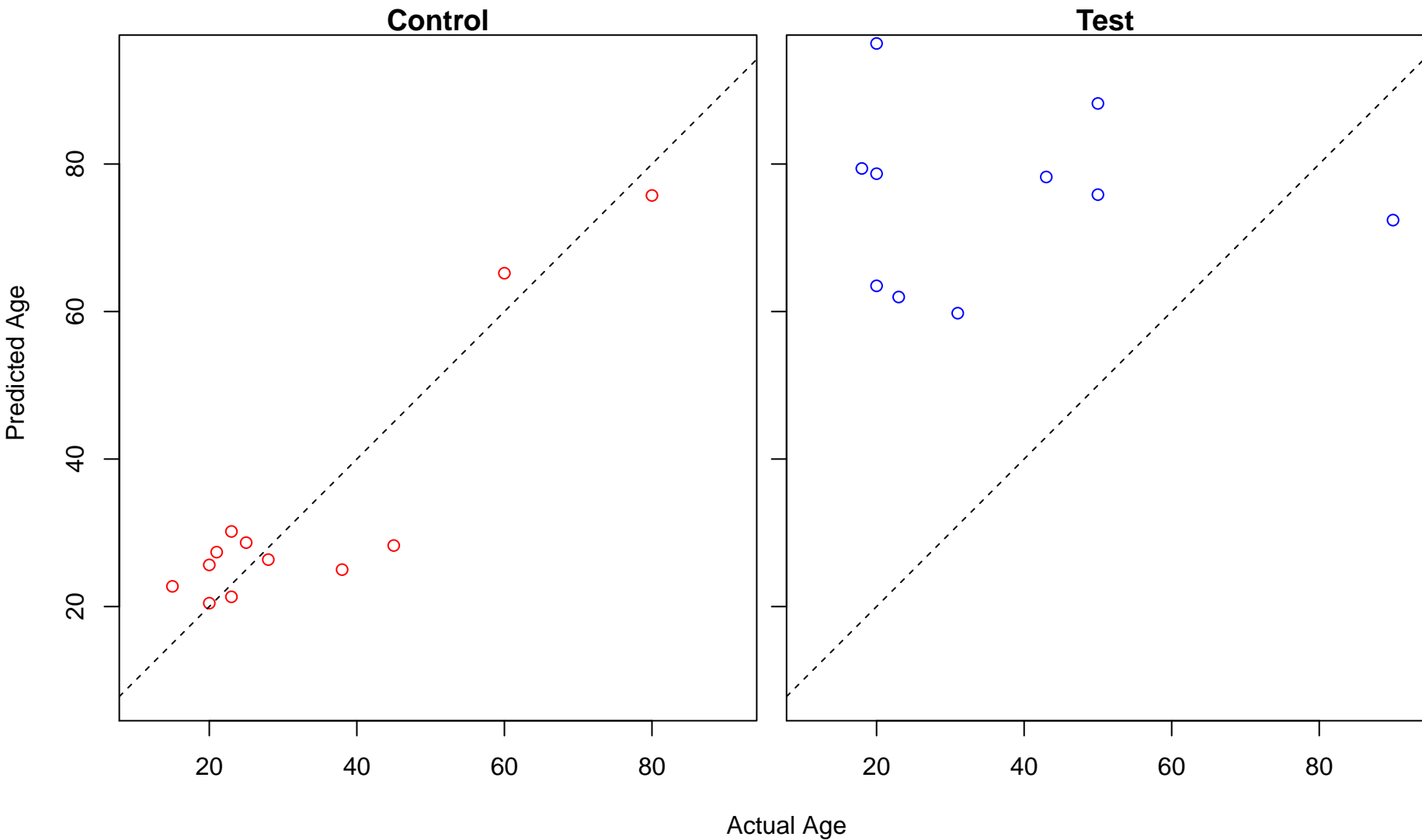
positive regulation of BMP signaling pathway (Score: 24.466857)



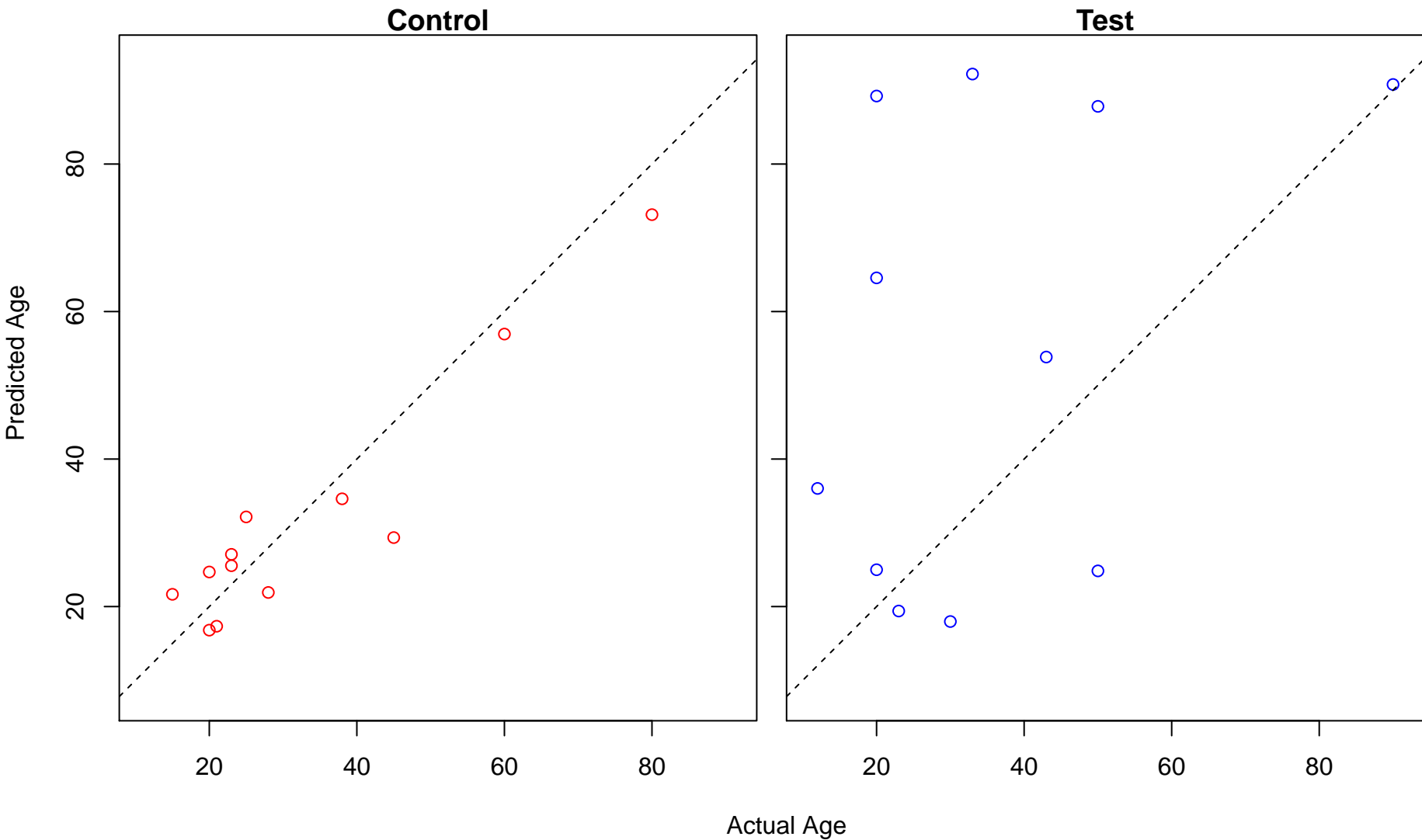
regulation of endothelial cell differentiation (Score: 24.413167)



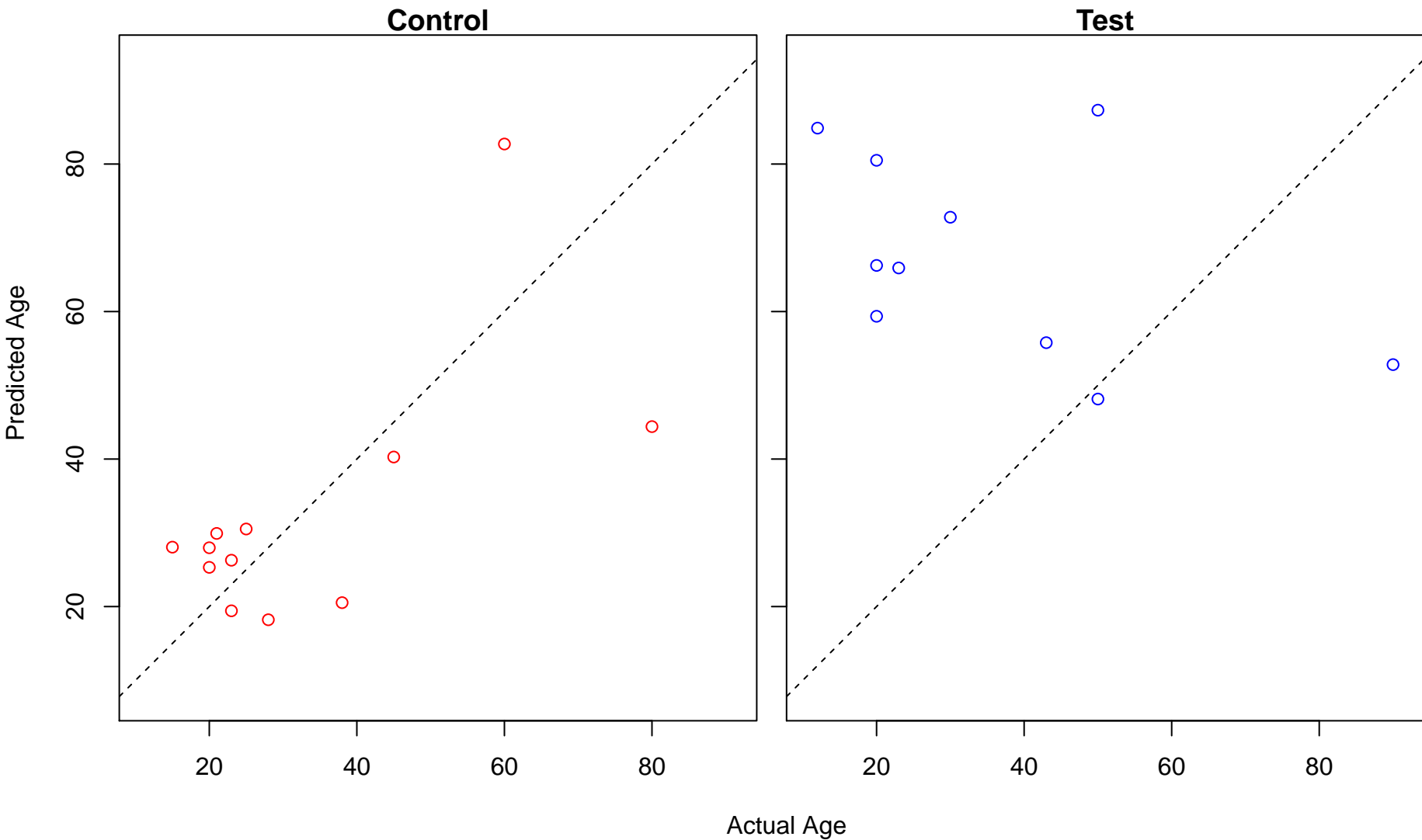
endocardium morphogenesis (Score: 24.394035)



negative regulation of chromatin modification (Score: 24.383088)

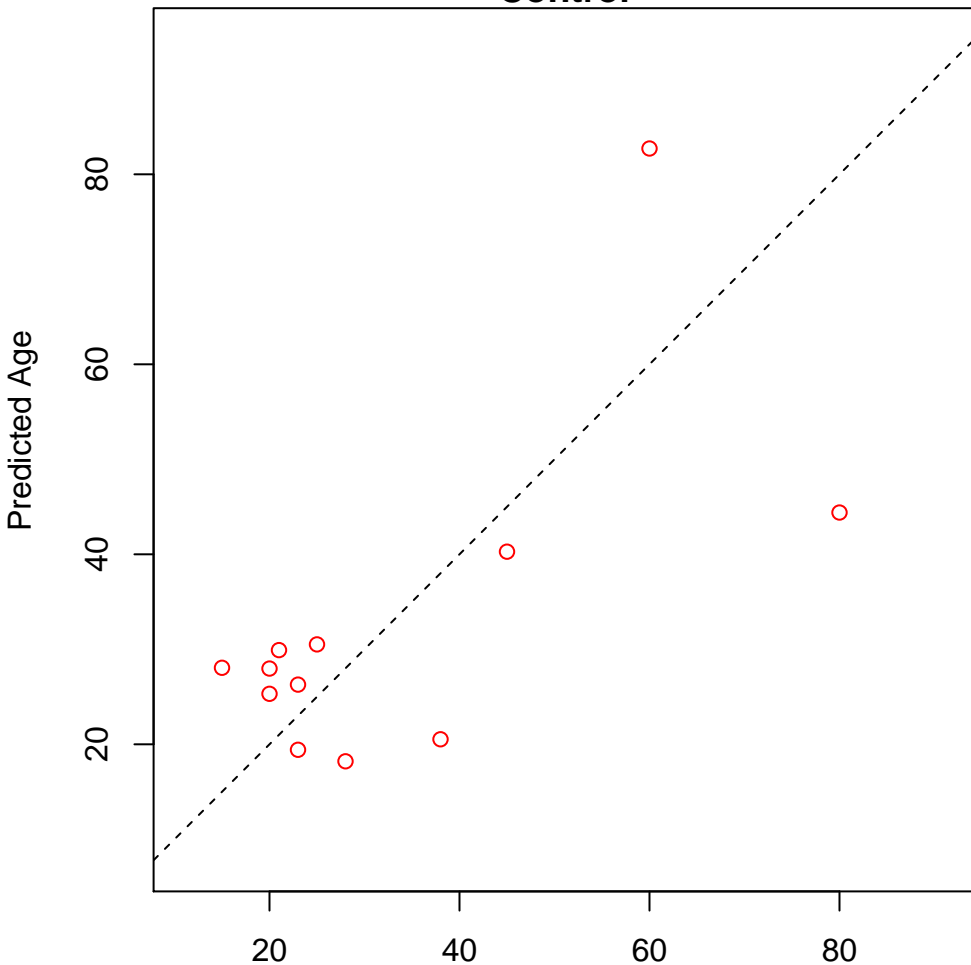


regulation of fever generation (Score: 24.352352)

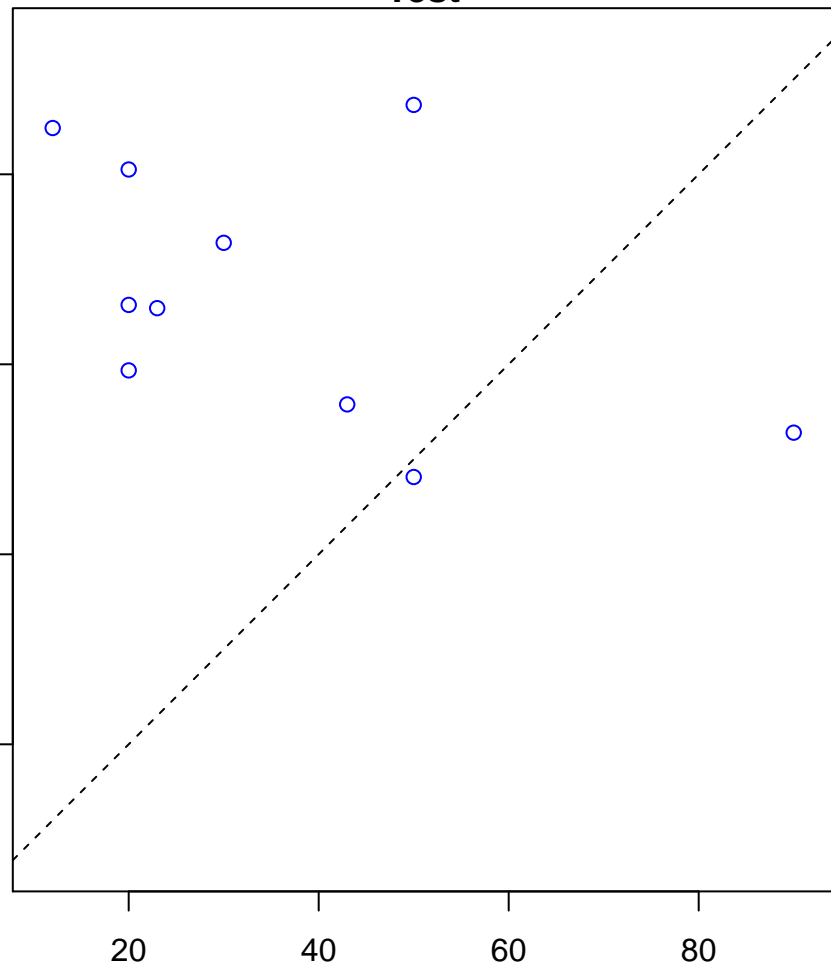


positive regulation of fever generation (Score: 24.352352)

Control

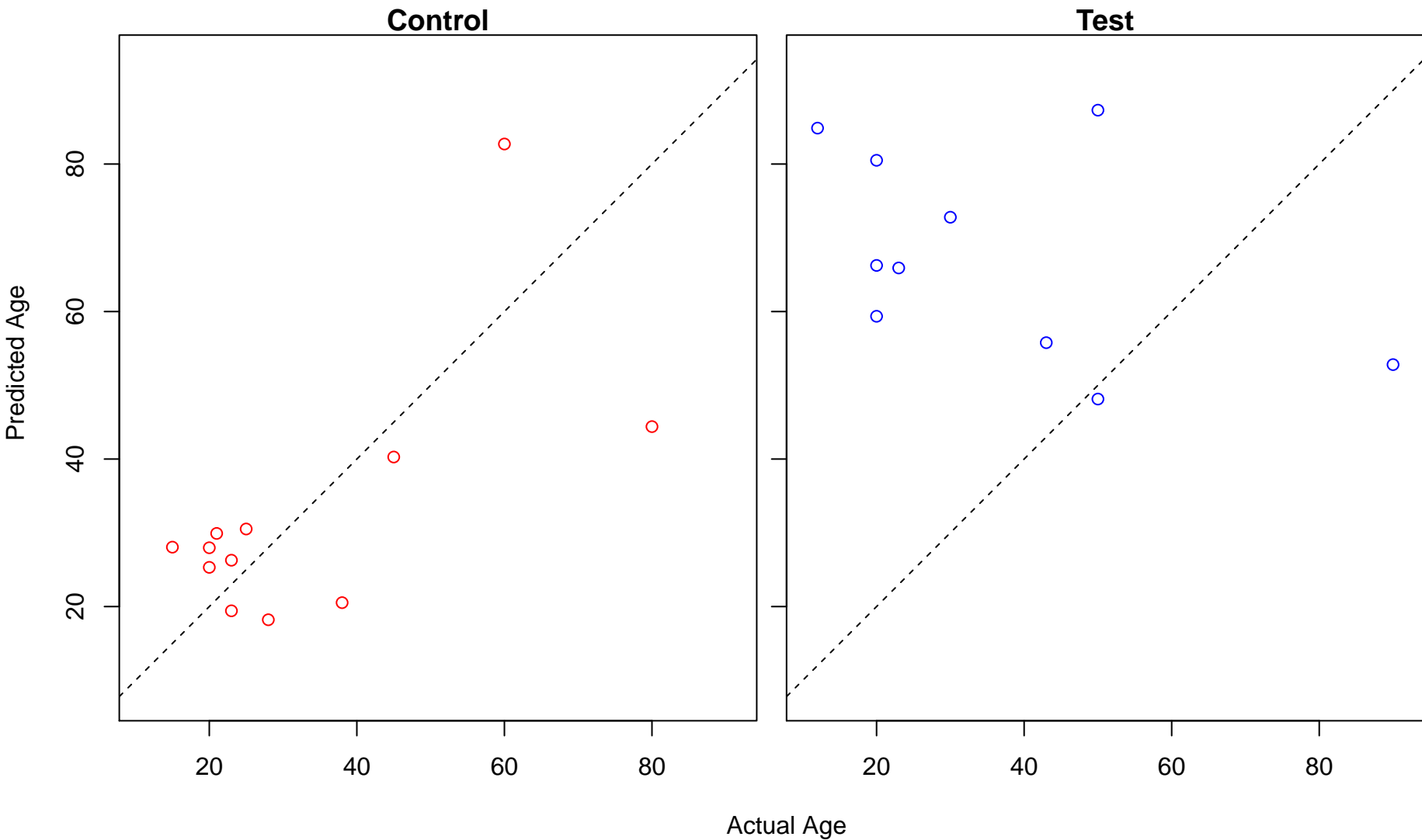


Test



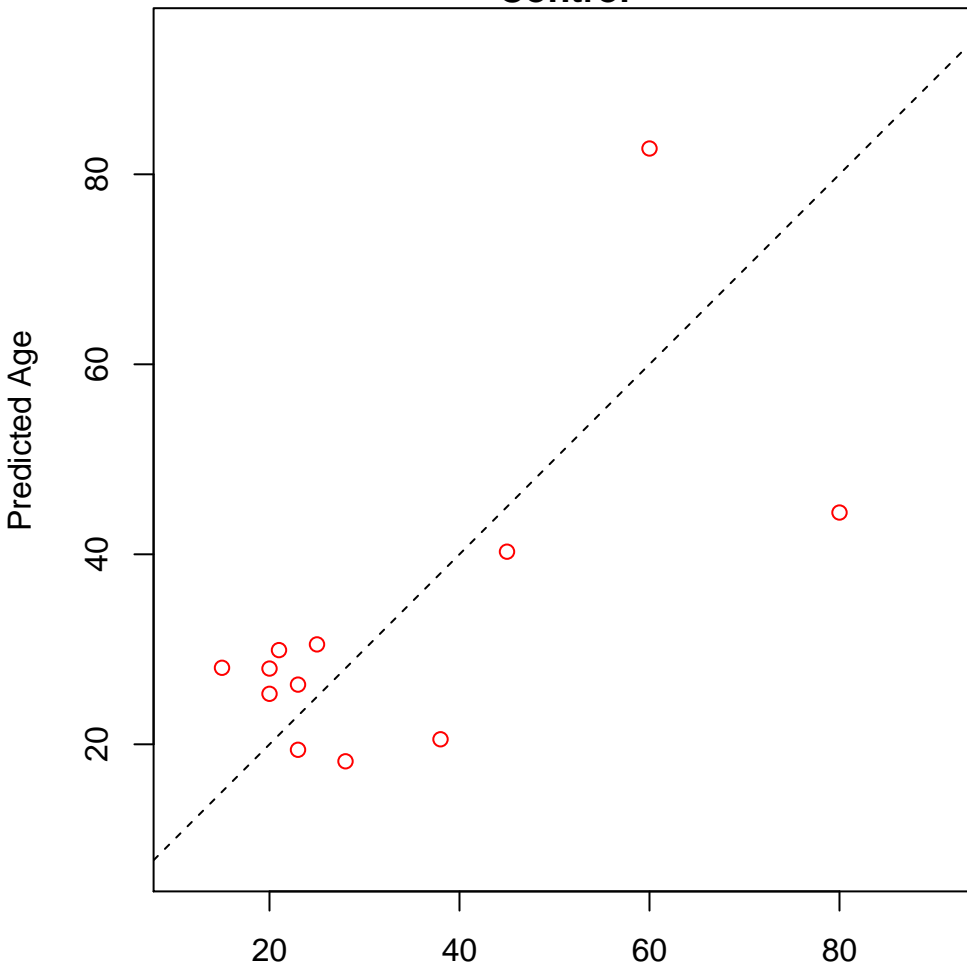
Actual Age

regulation of heat generation (Score: 24.352352)

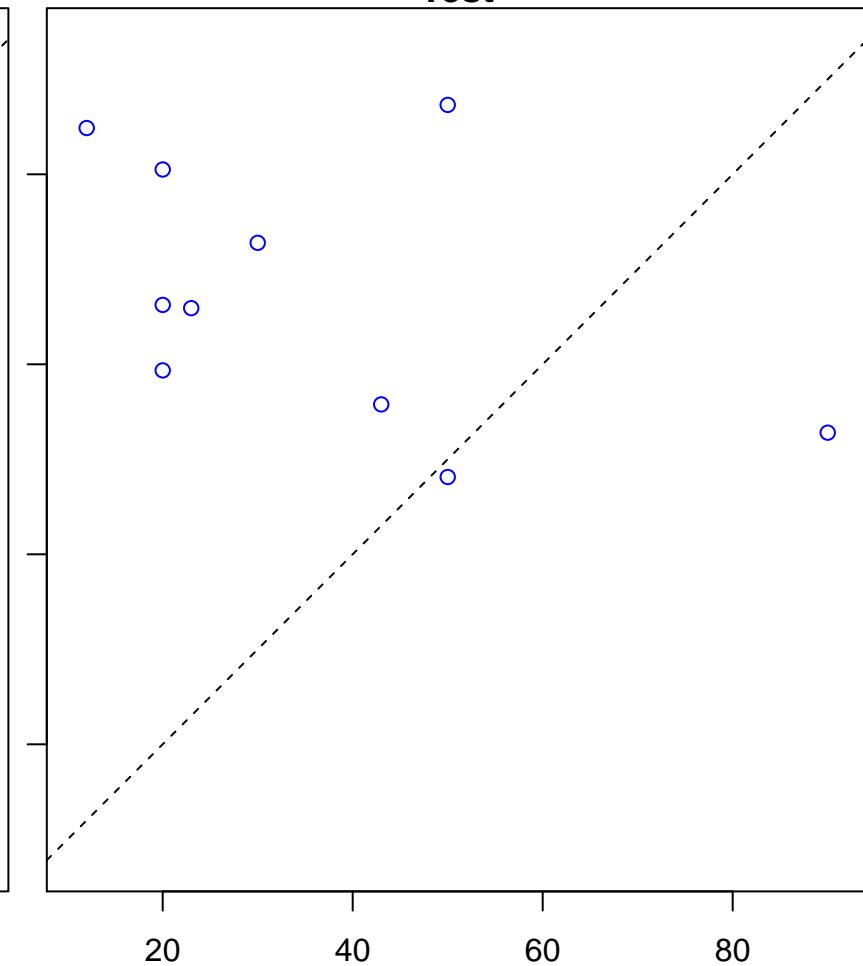


positive regulation of heat generation (Score: 24.352352)

Control

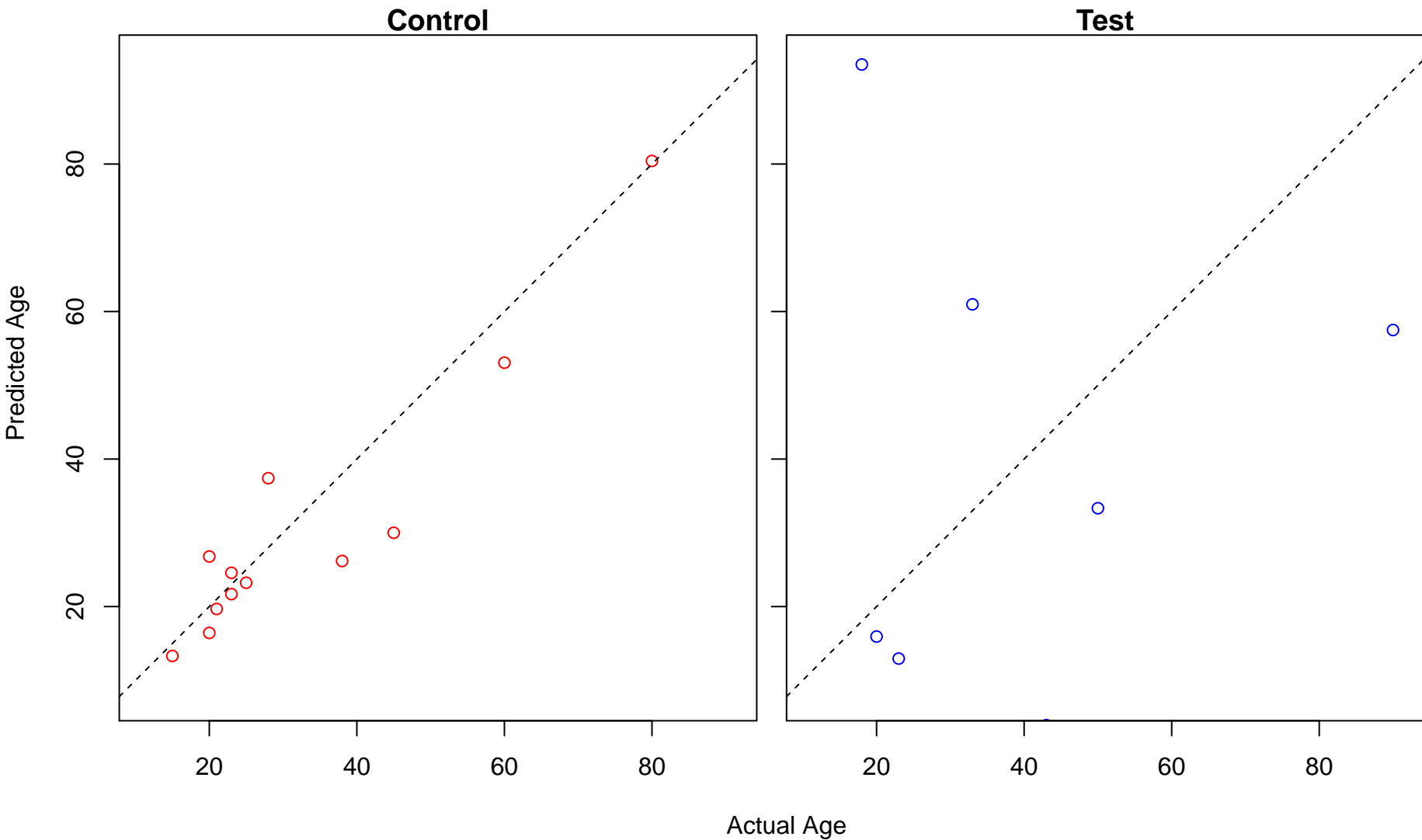


Test

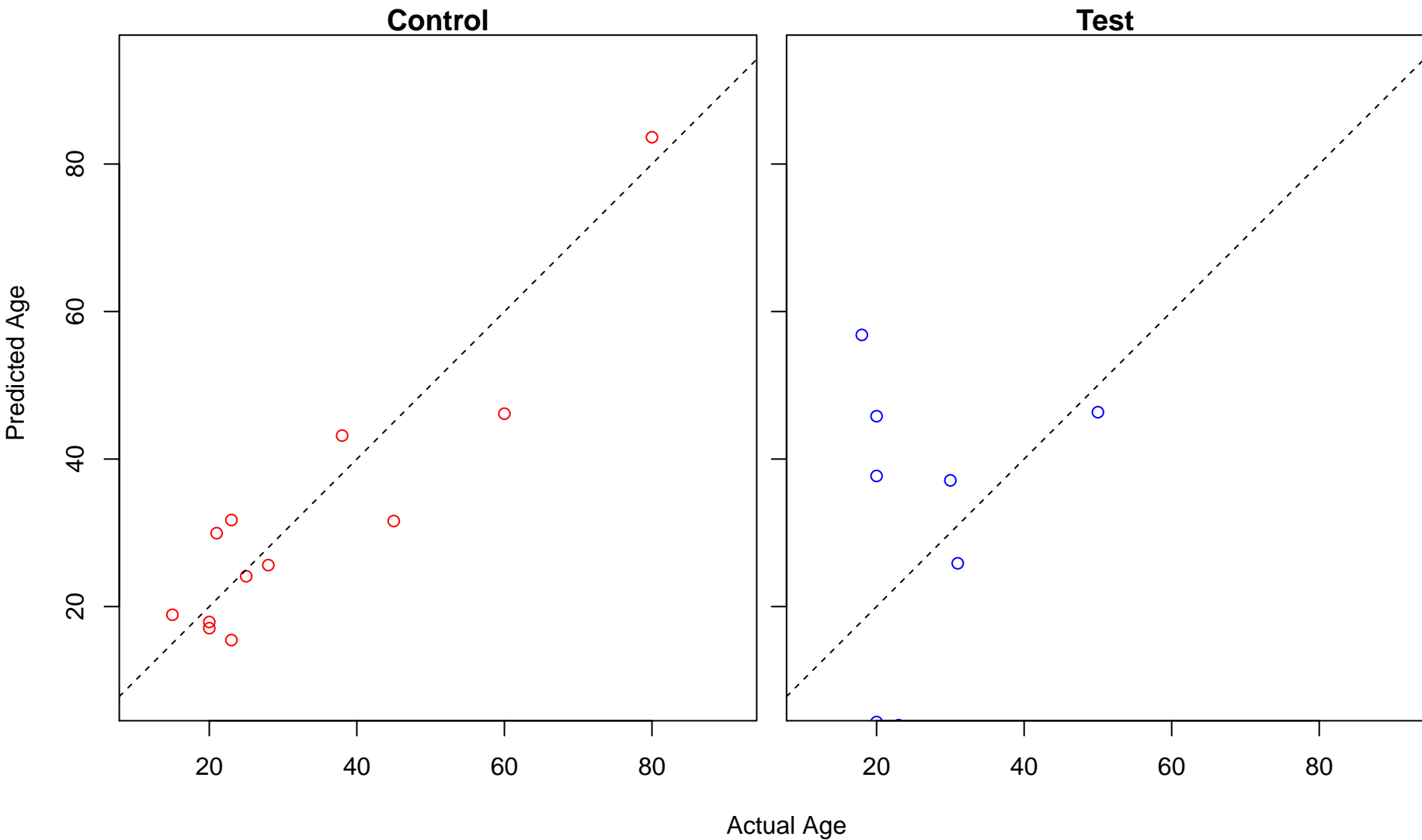


Actual Age

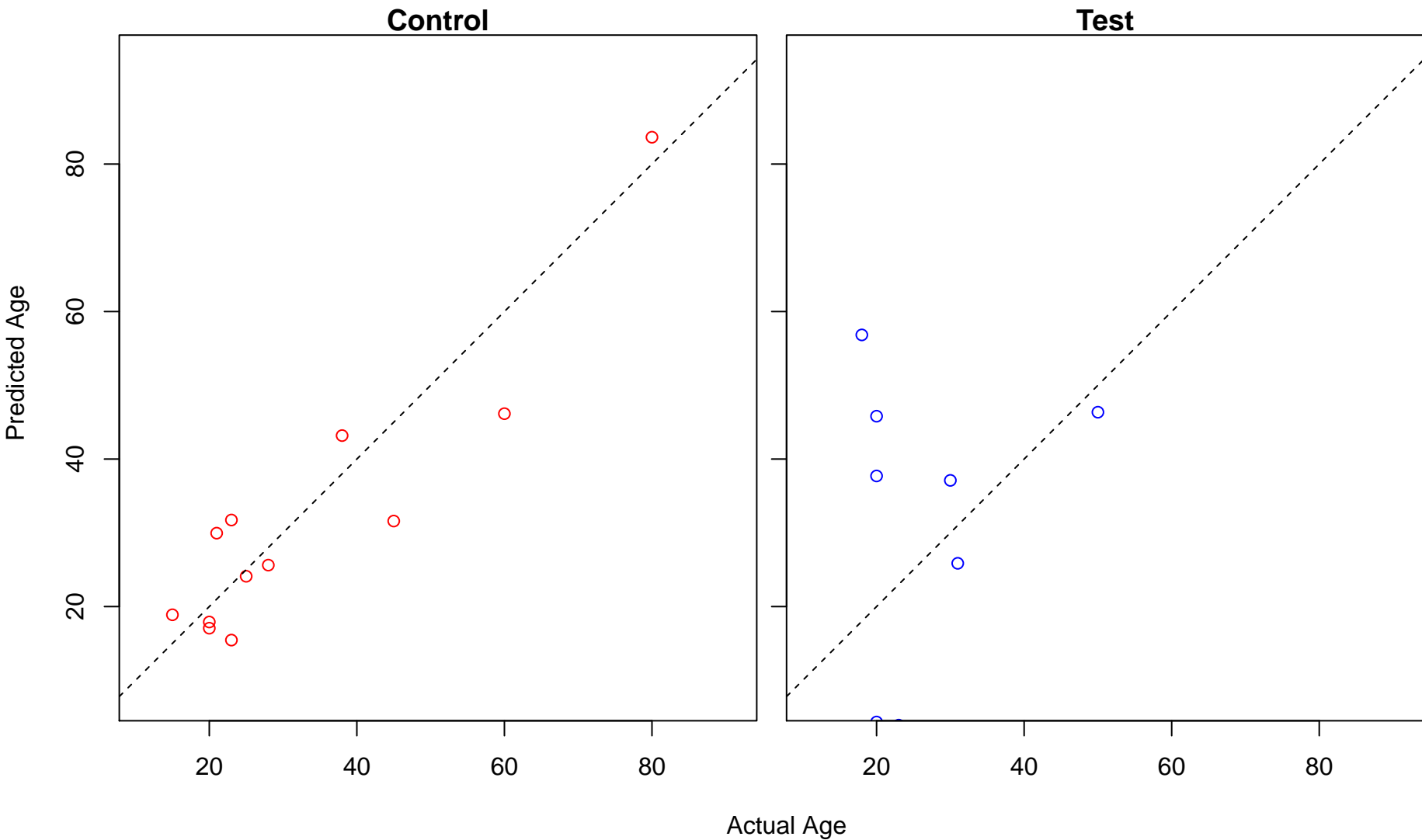
tissue regeneration (Score: 24.346360)



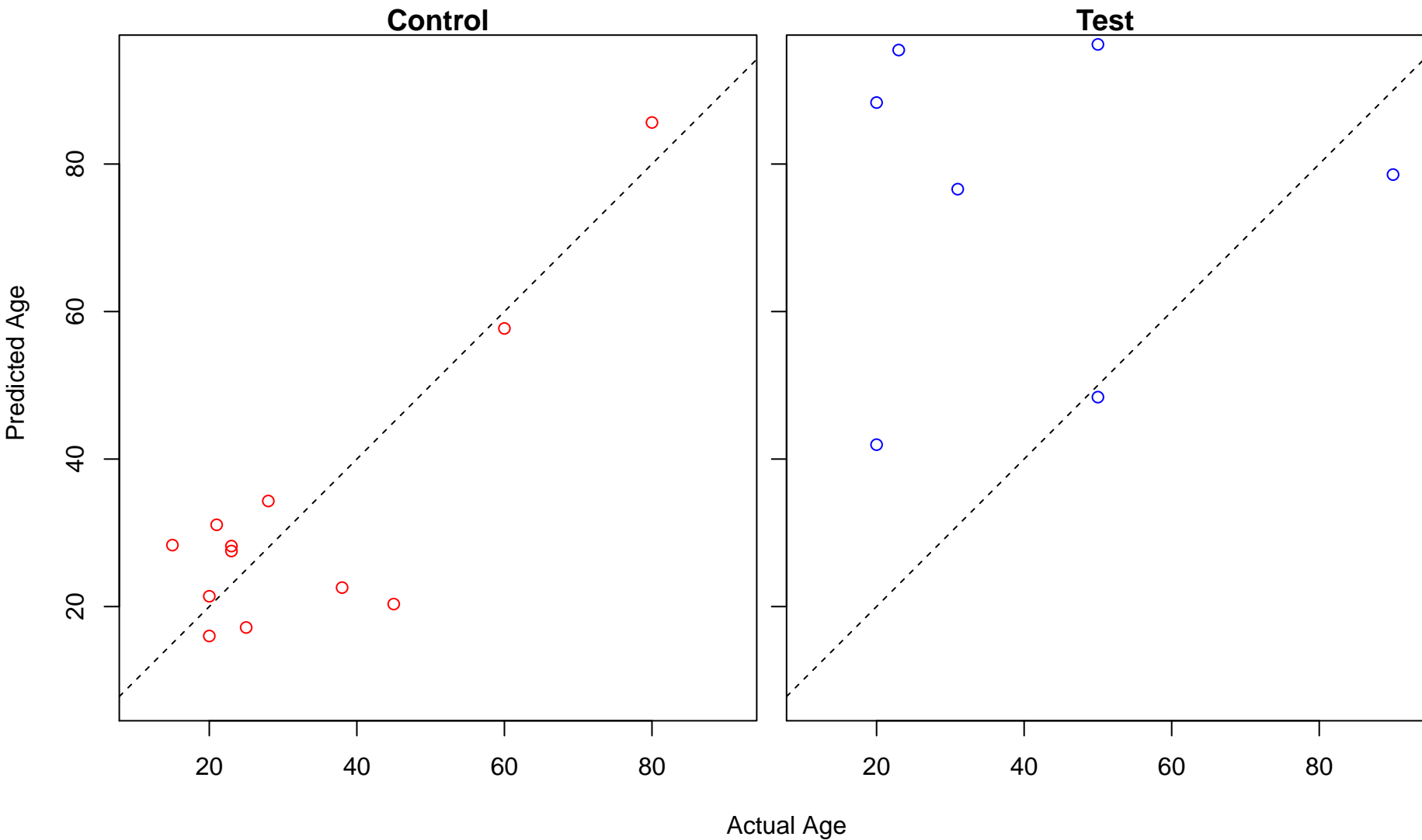
regulation of water loss via skin (Score: 24.290193)



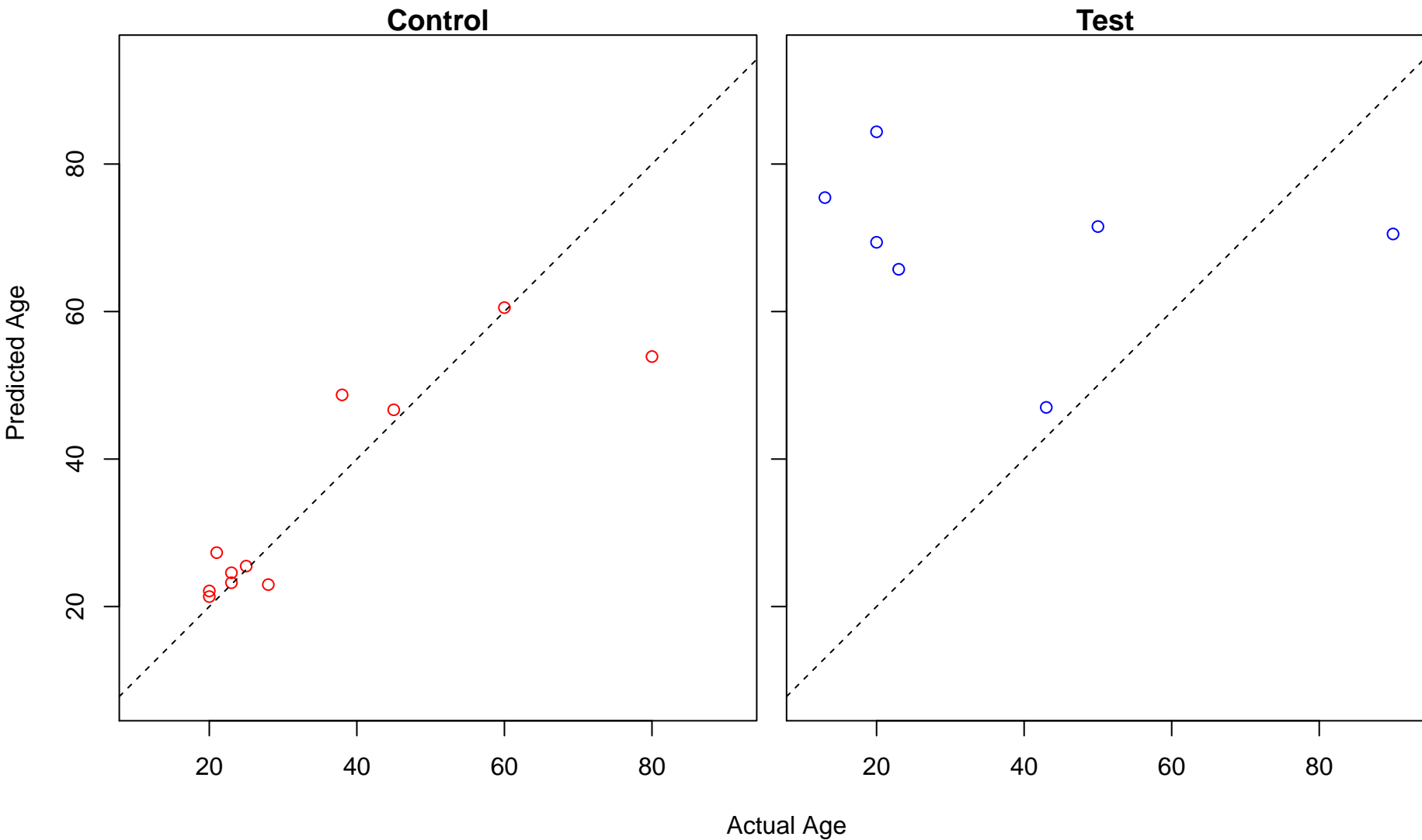
establishment of skin barrier (Score: 24.290193)



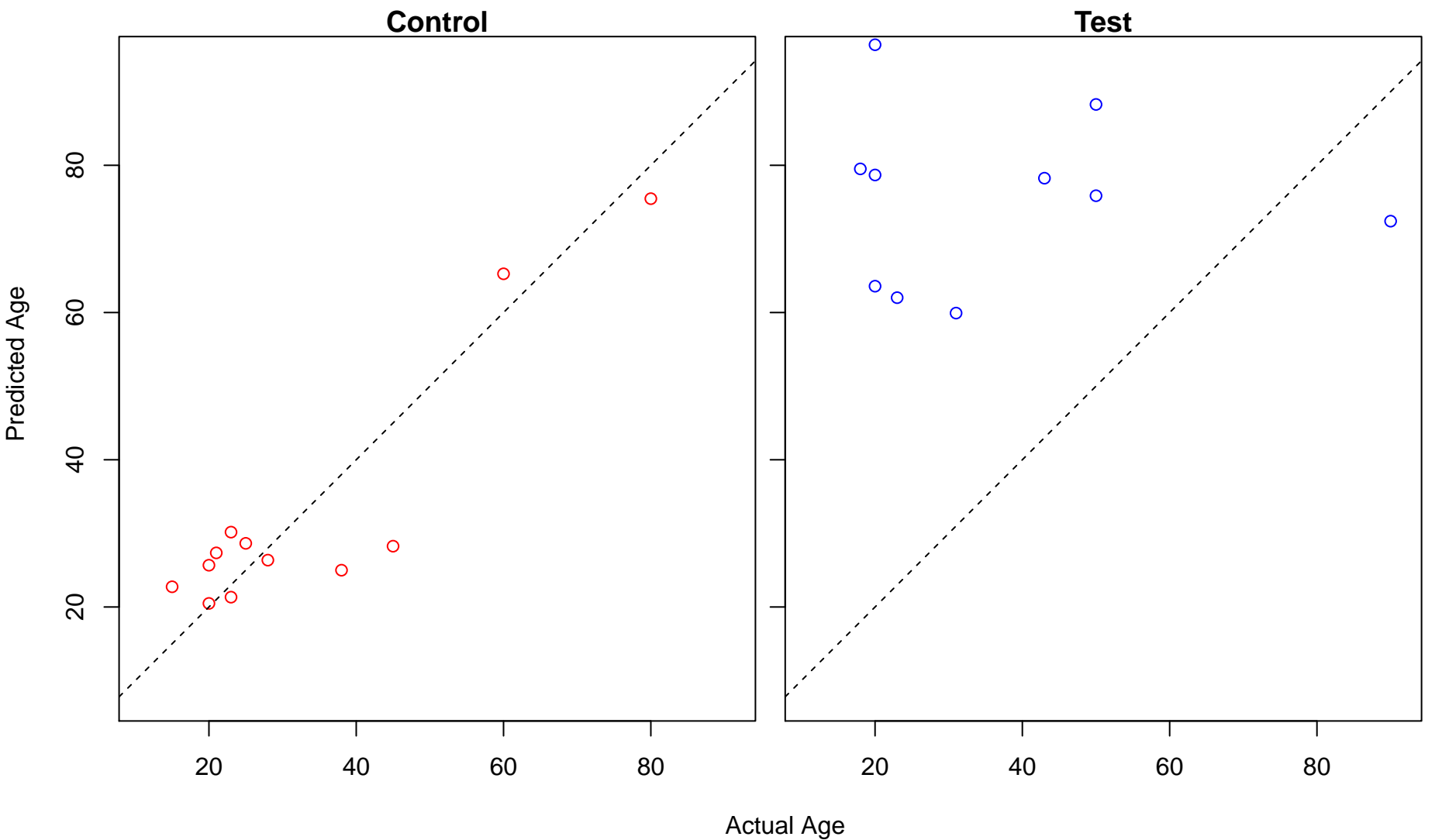
regulation of cytoplasmic mRNA processing body assembly (Score: 24.272963)



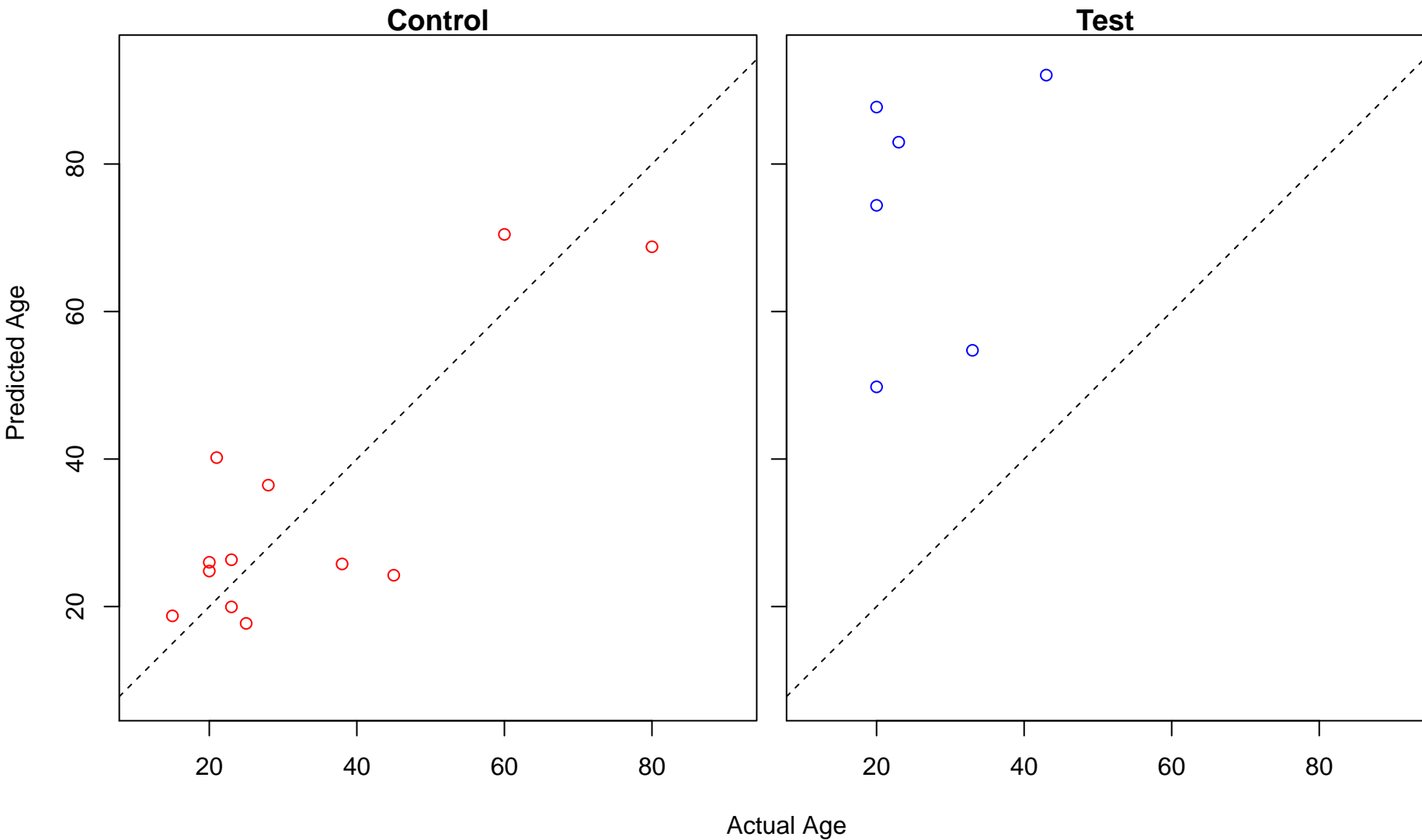
omega-hydroxylase P450 pathway (Score: 24.260689)



n of transcription from RNA polymerase II promoter involved in myocardial precursor cell differentiation (S

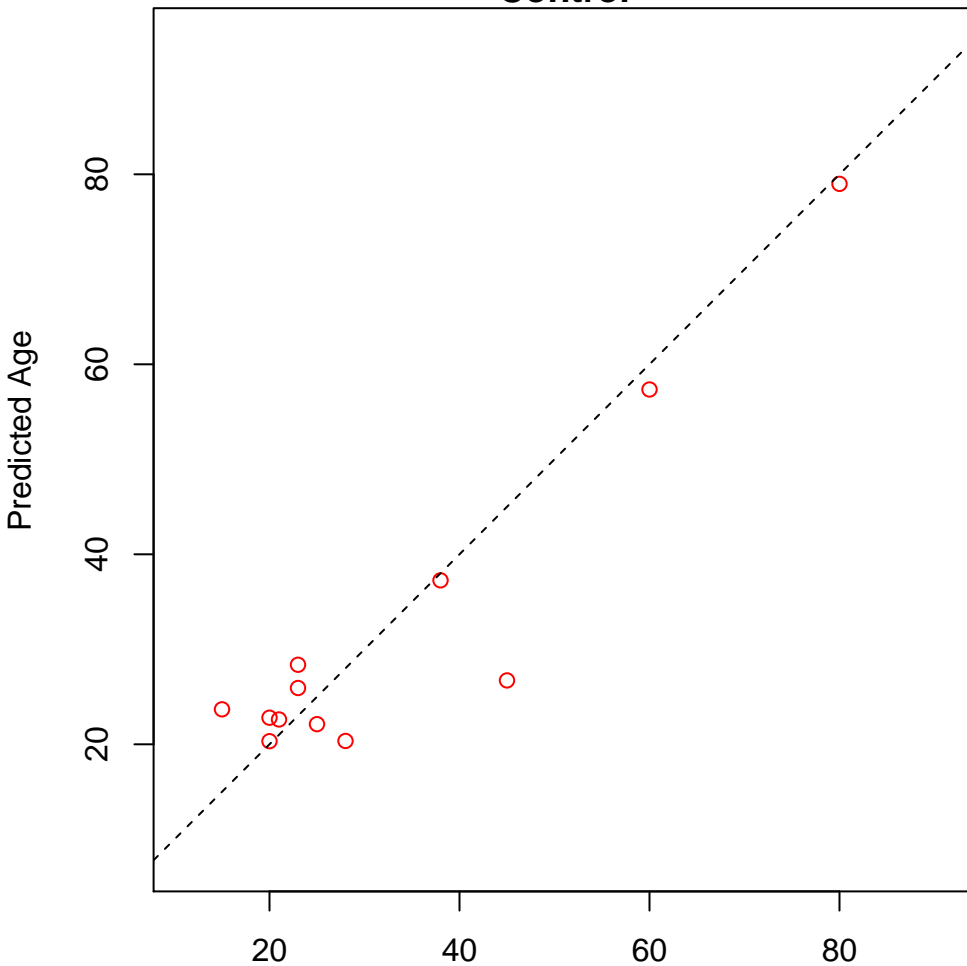


negative regulation of peptidyl-tyrosine phosphorylation (Score: 24.245519)

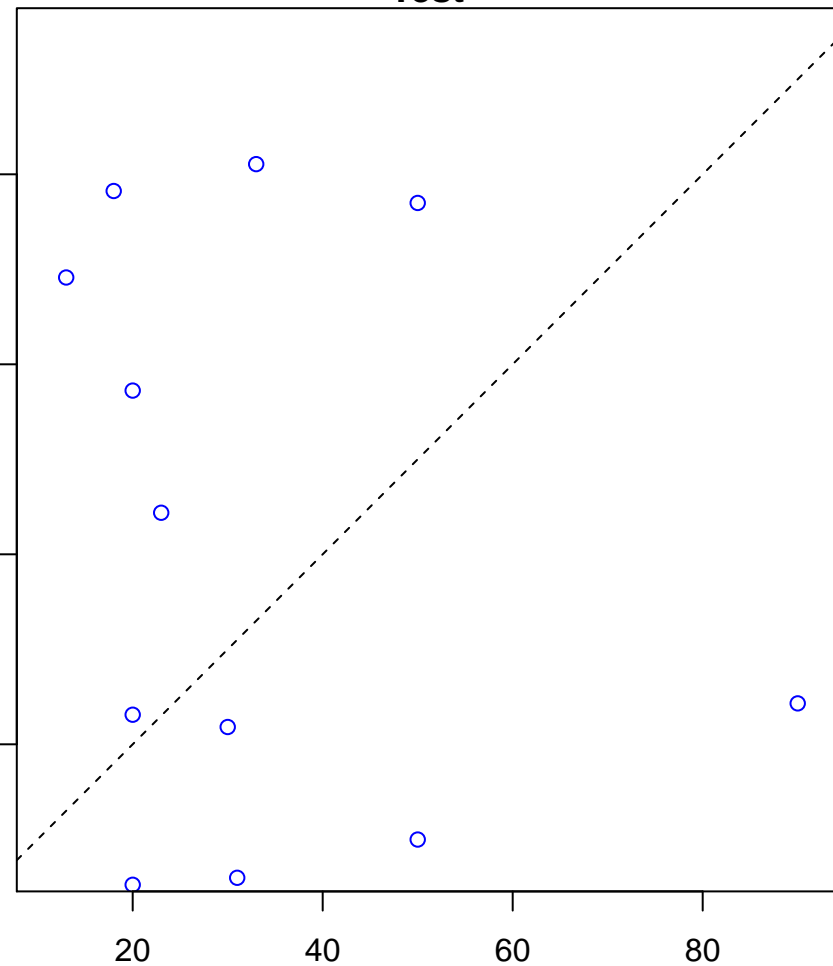


divalent inorganic cation homeostasis (Score: 24.238529)

Control

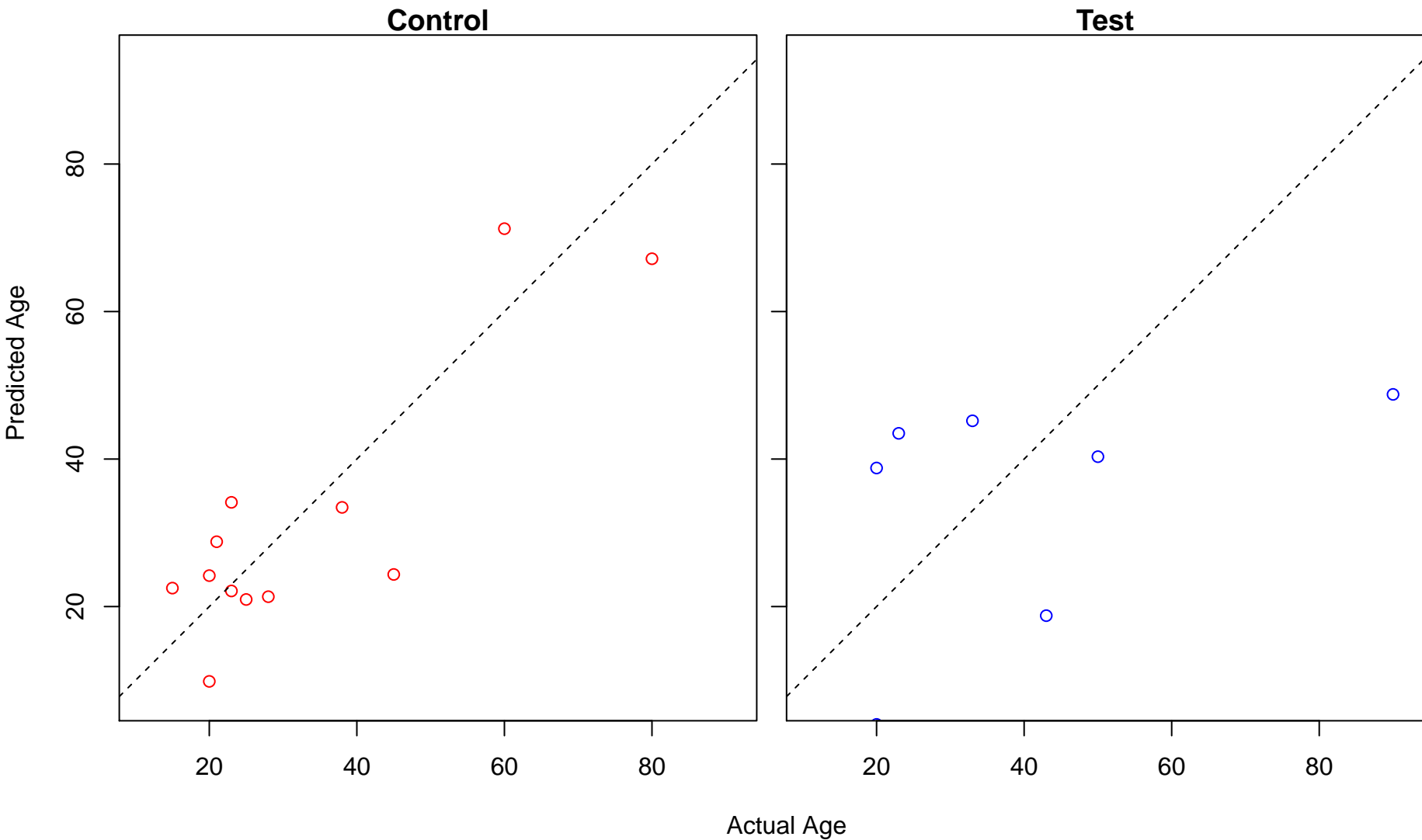


Test



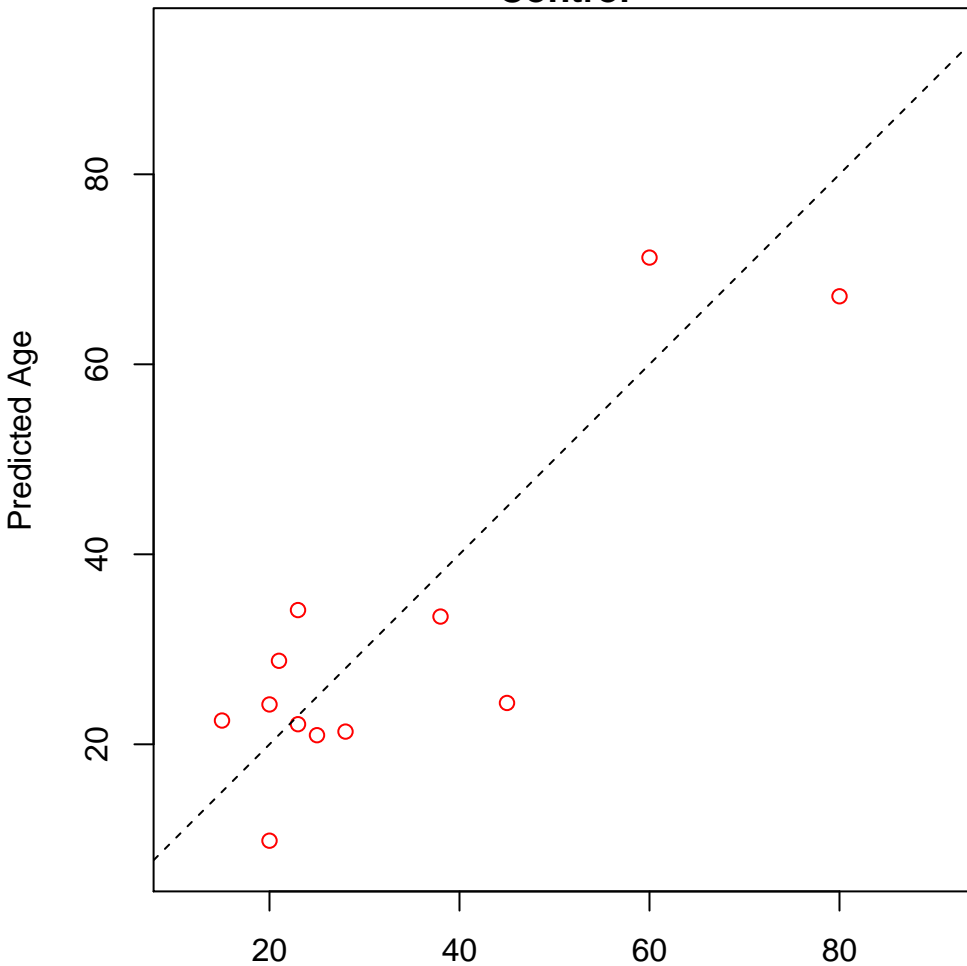
Actual Age

response to interleukin-3 (Score: 24.231376)

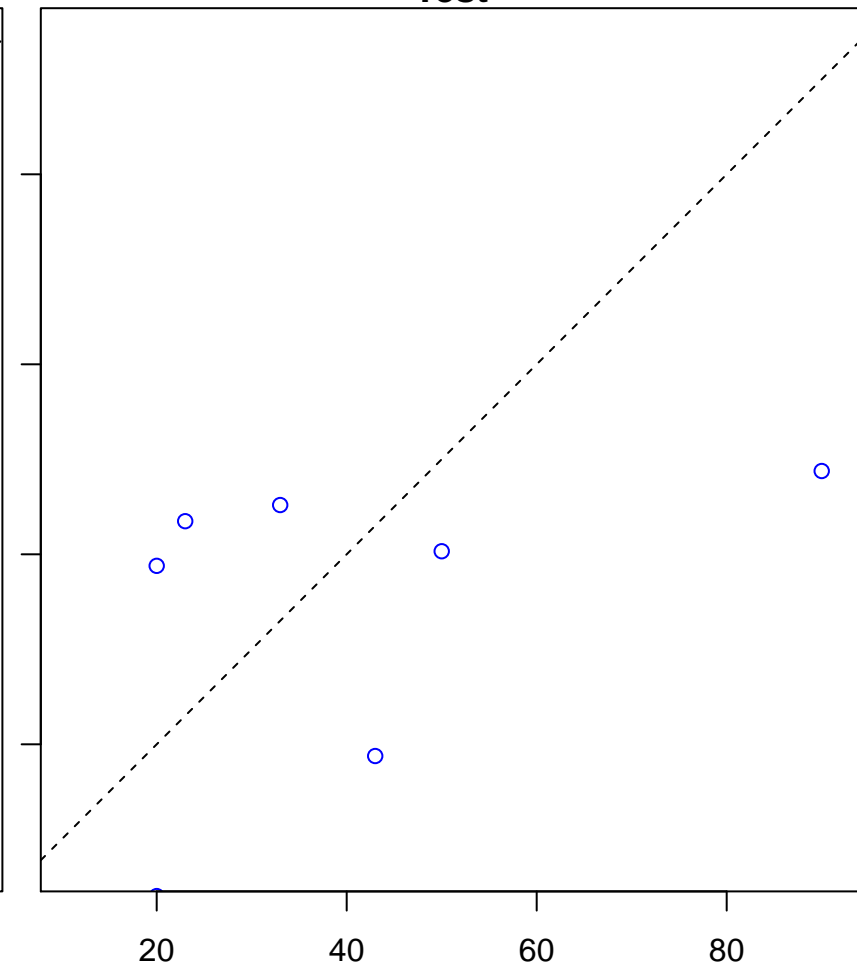


cellular response to interleukin-3 (Score: 24.231376)

Control



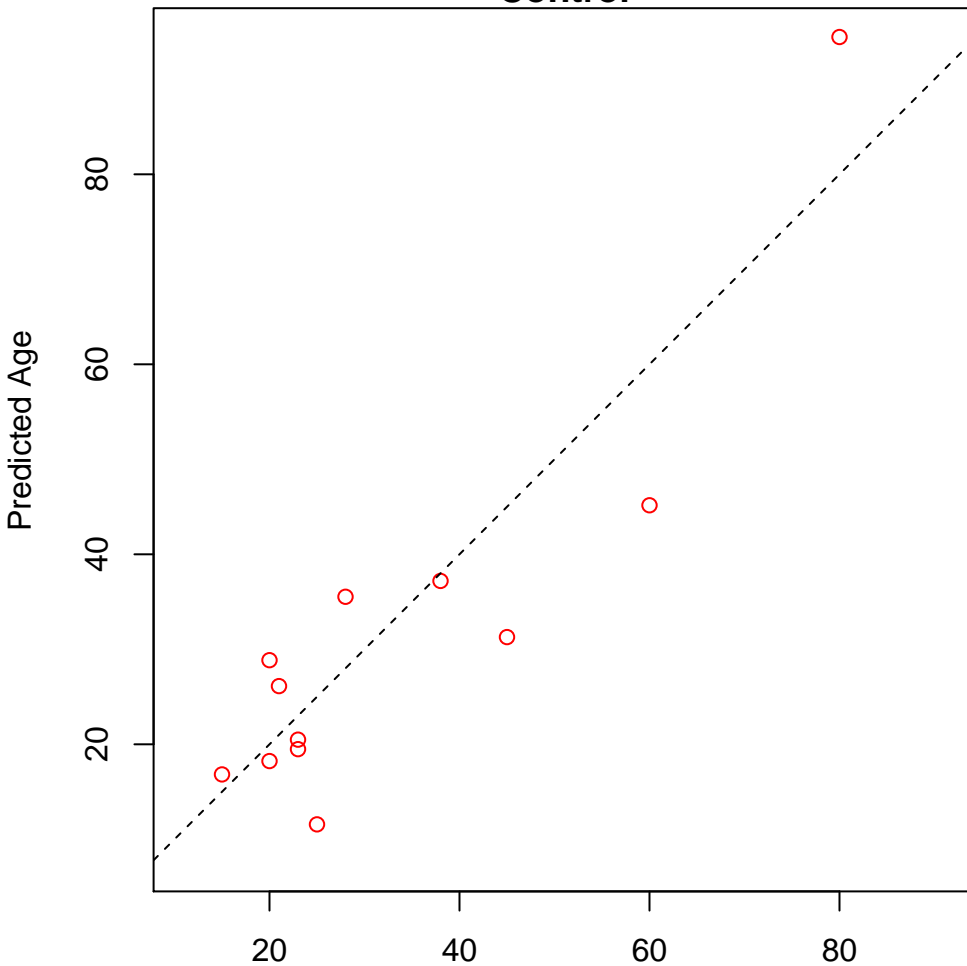
Test



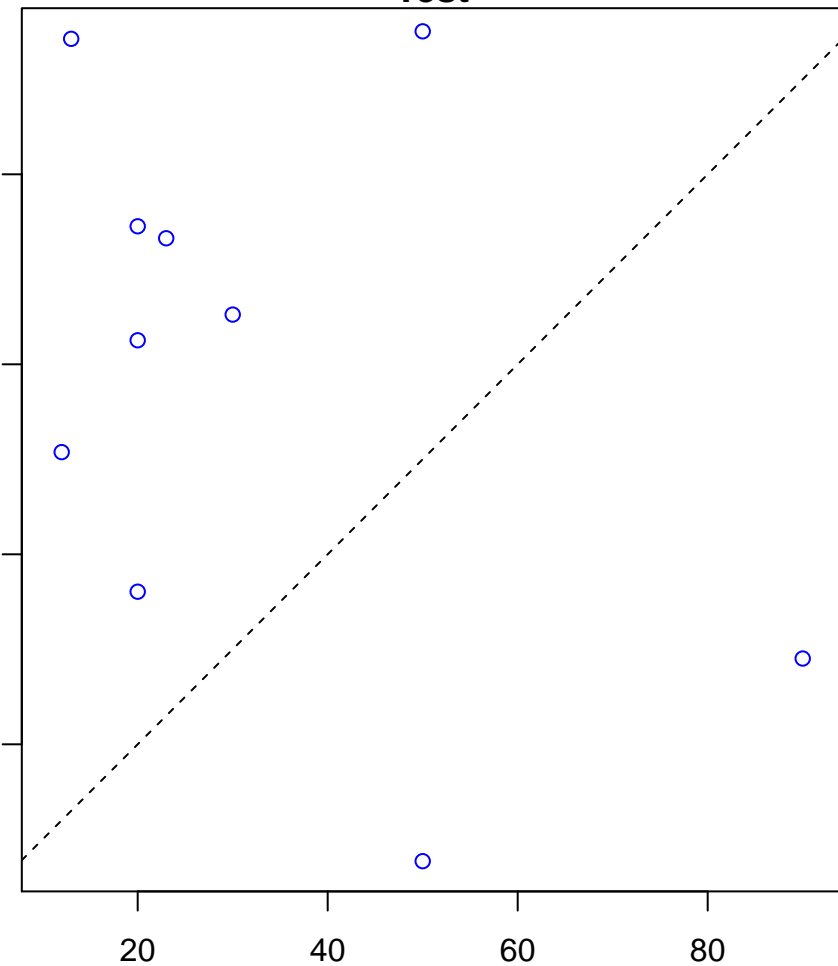
Actual Age

natural killer cell mediated cytotoxicity (Score: 24.221846)

Control

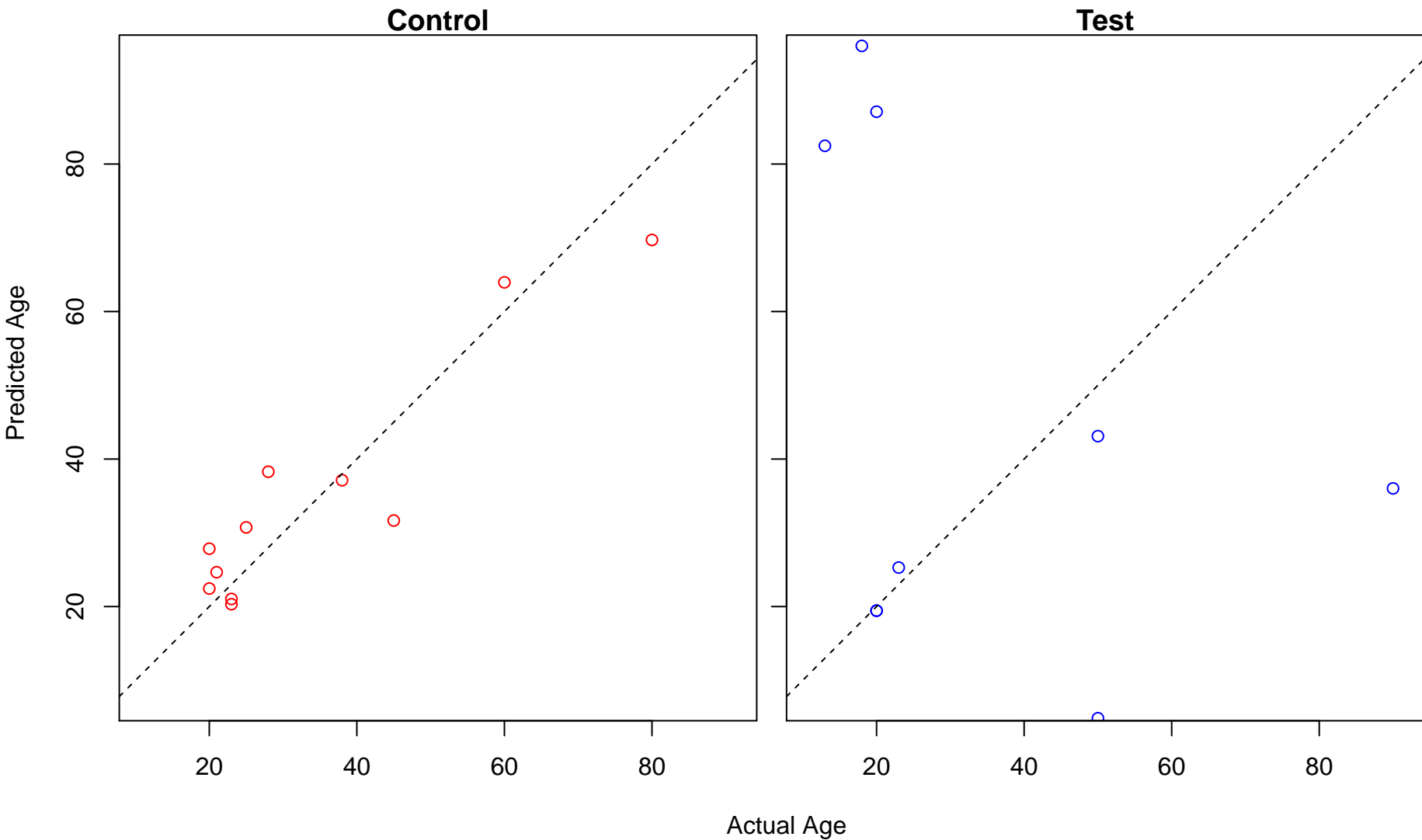


Test

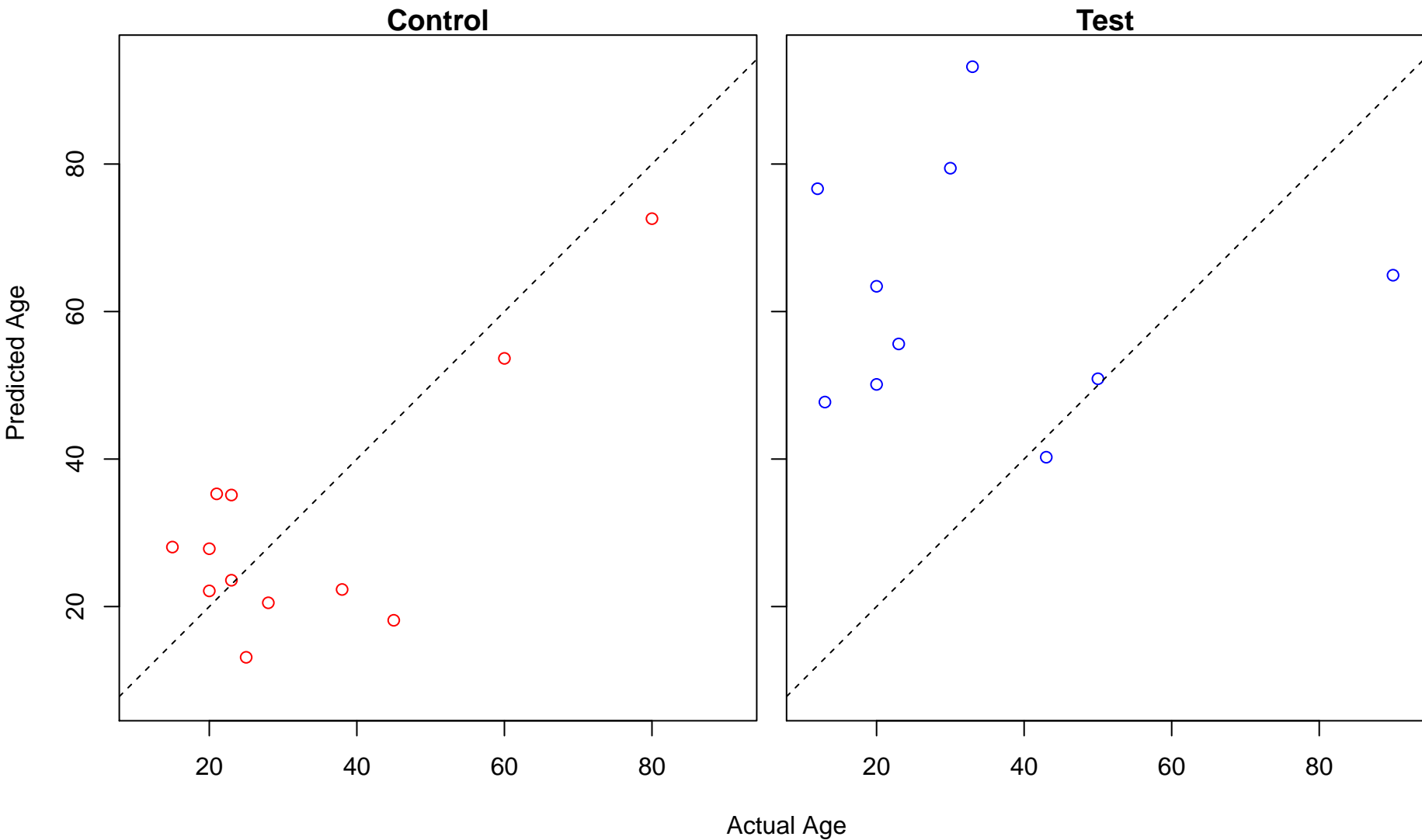


Actual Age

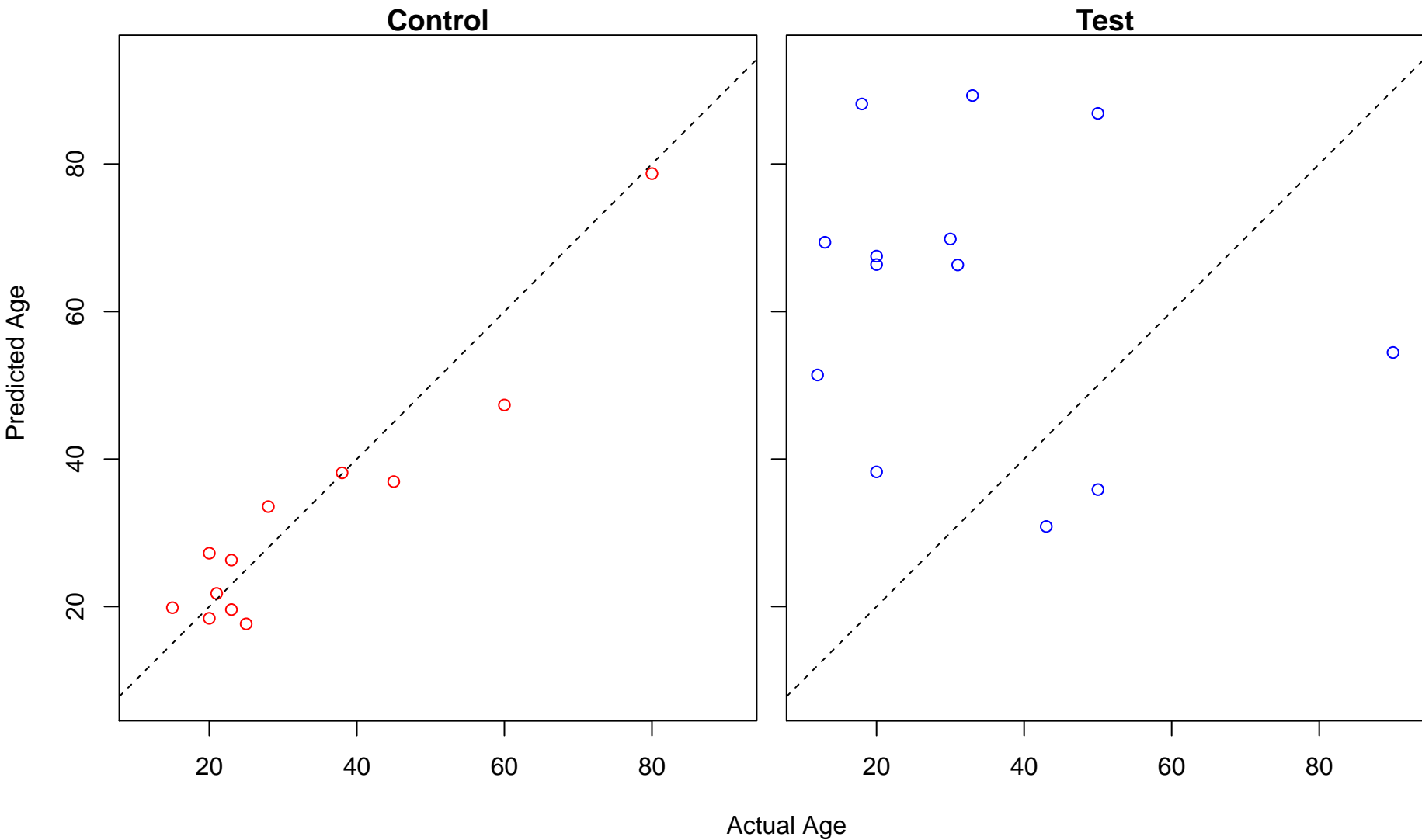
negative regulation of cyclin-dependent protein kinase activity (Score: 24.188735)



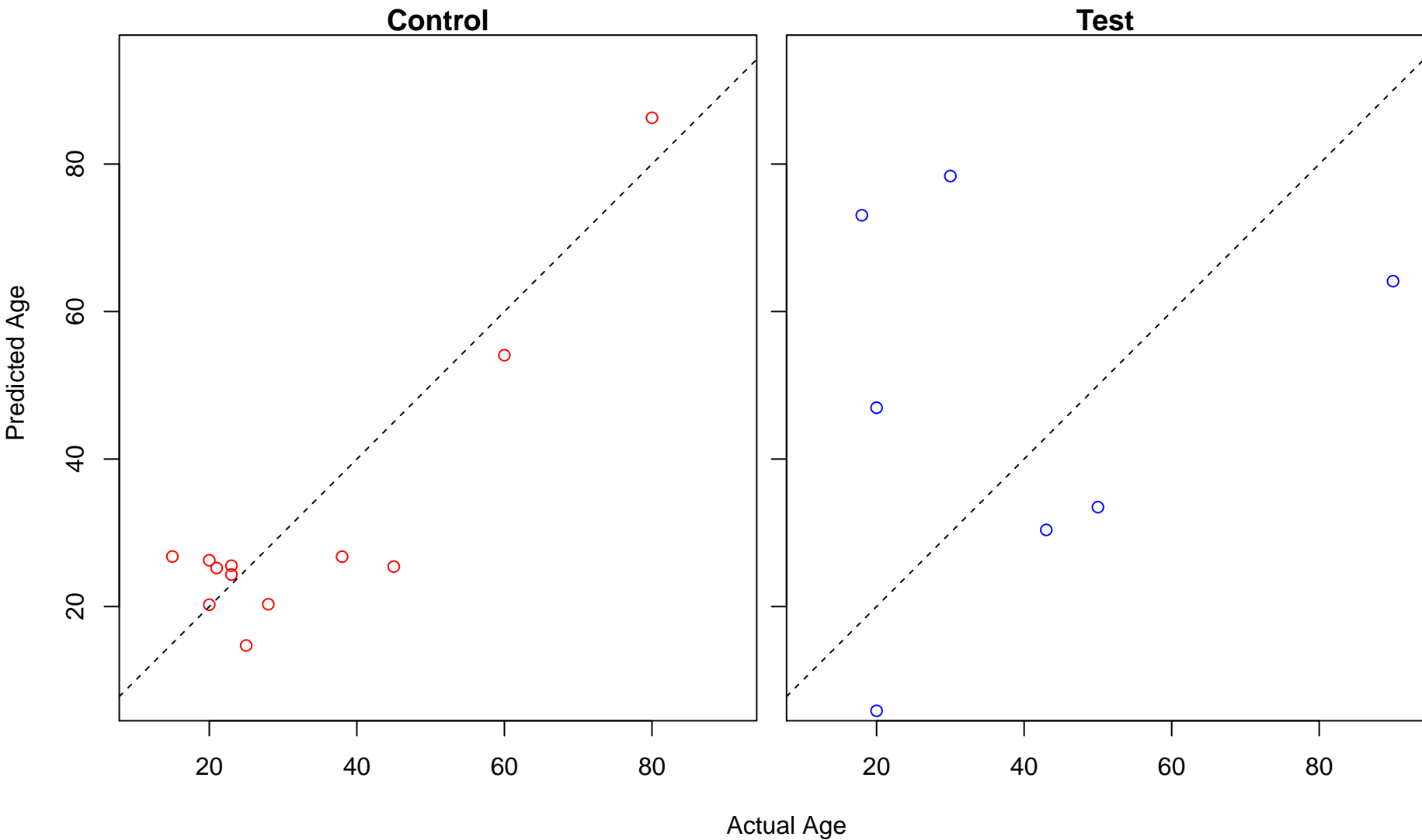
hematopoietic progenitor cell differentiation (Score: 24.155863)



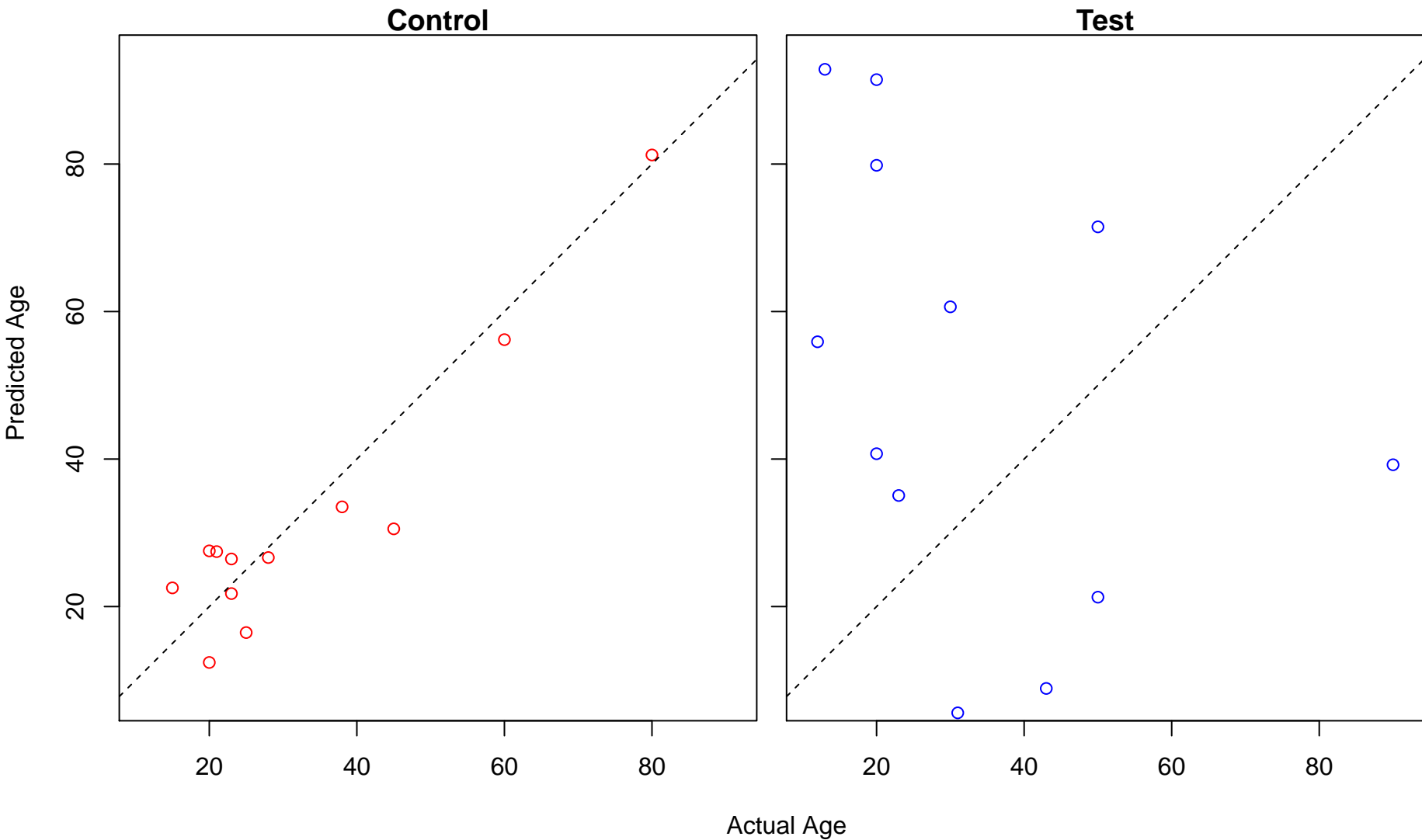
regulation of cell cycle checkpoint (Score: 24.032717)



cellular response to biotic stimulus (Score: 24.029468)

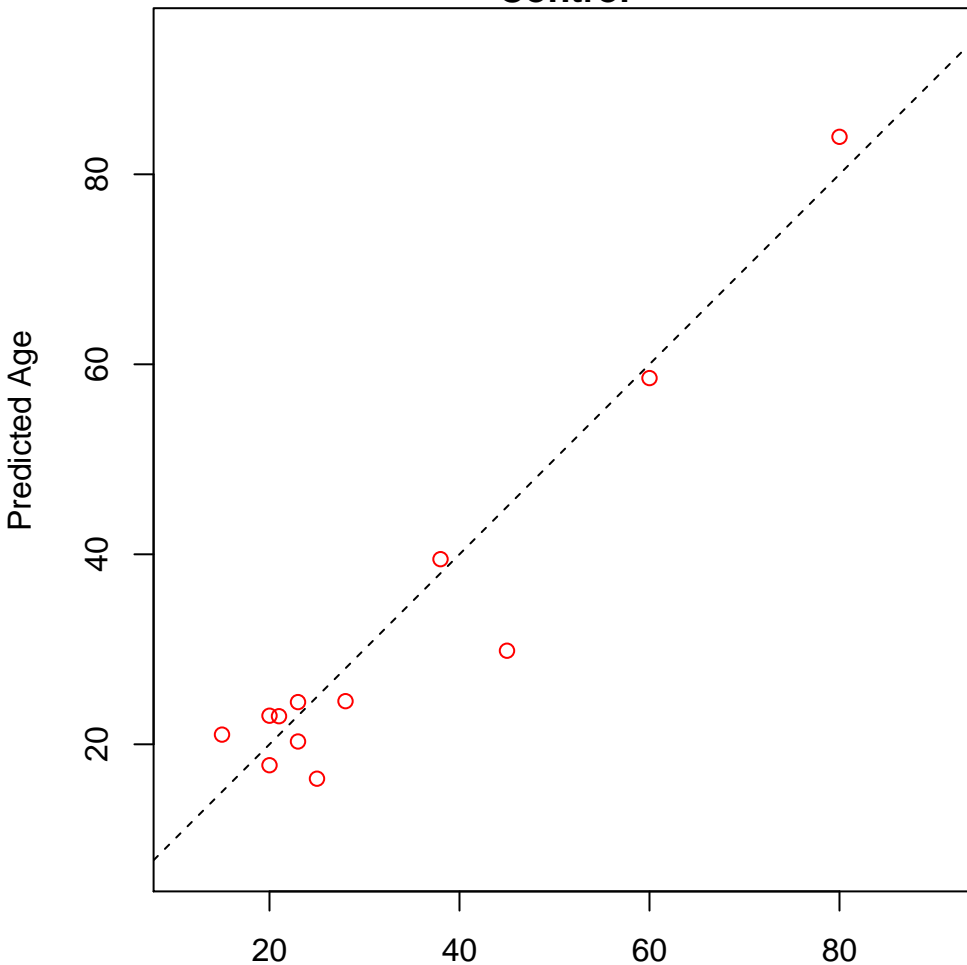


negative regulation of phosphatase activity (Score: 24.021689)

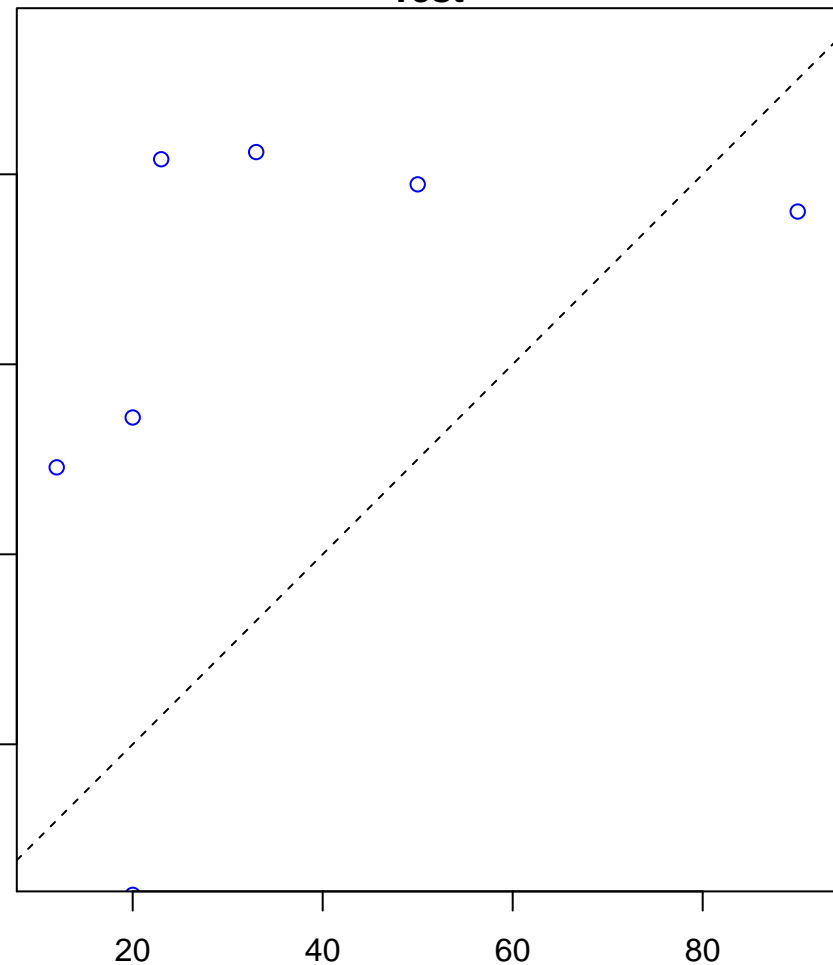


metanephric nephron development (Score: 23.922178)

Control

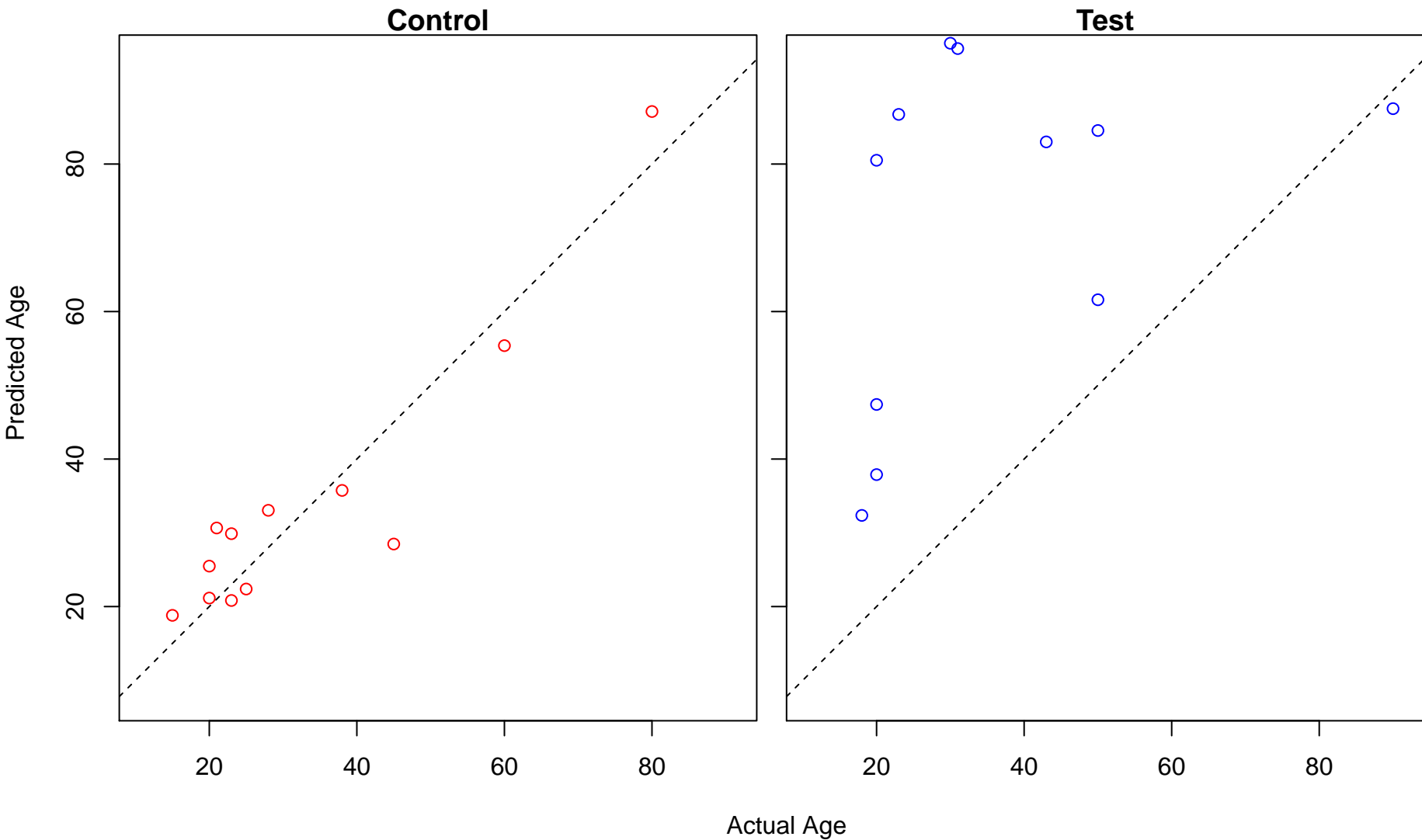


Test

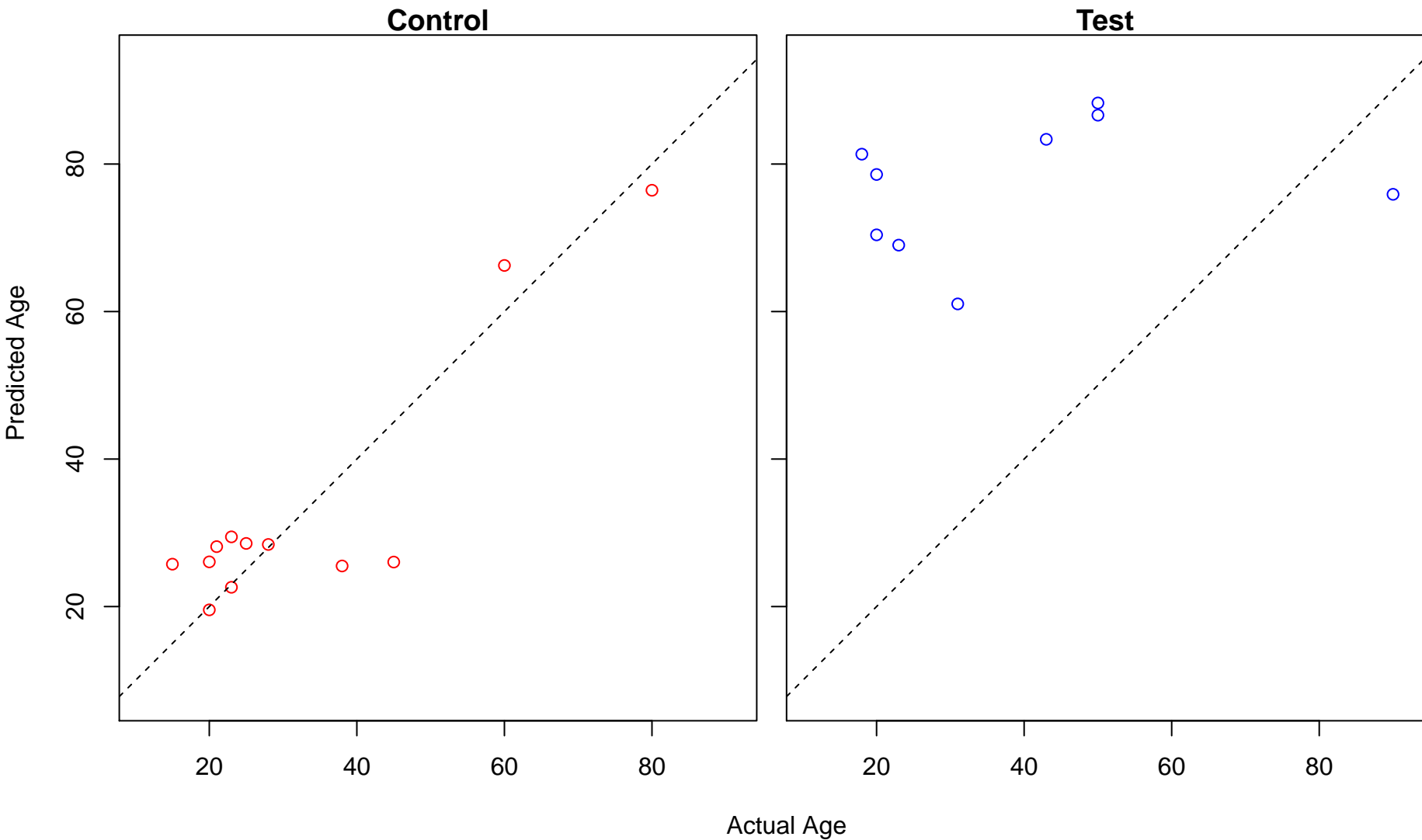


Actual Age

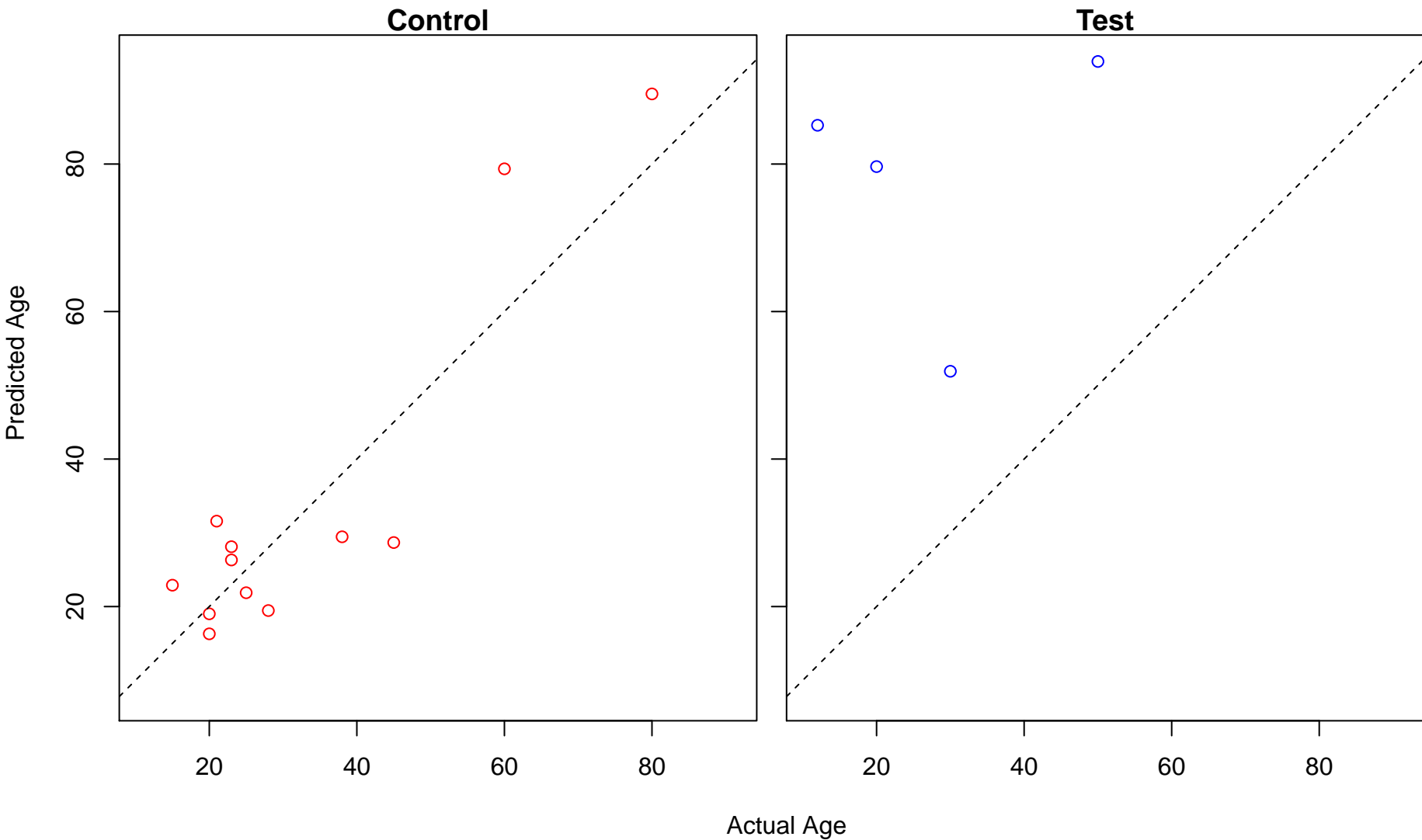
heart morphogenesis (Score: 23.903849)



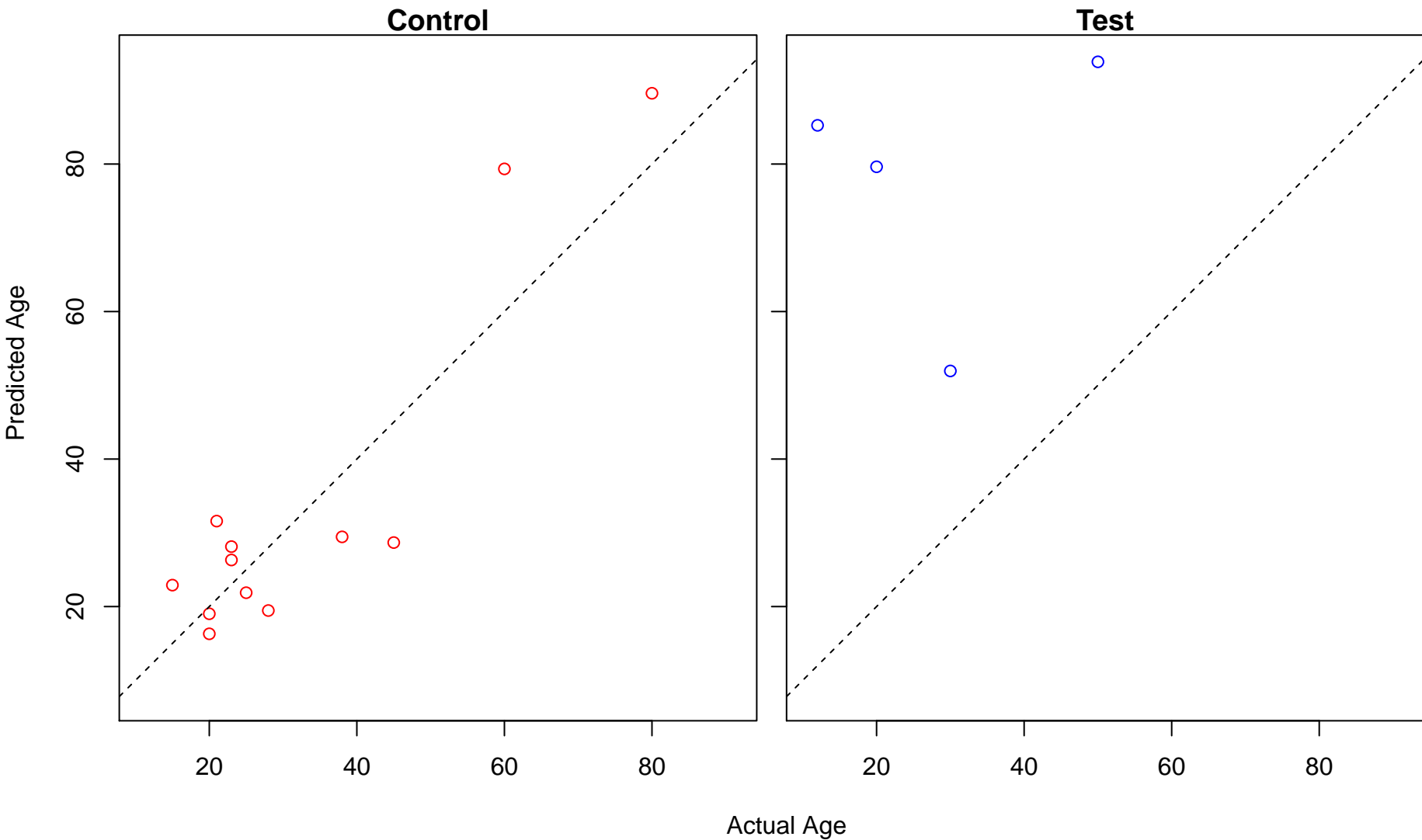
in utero embryonic development (Score: 23.876152)



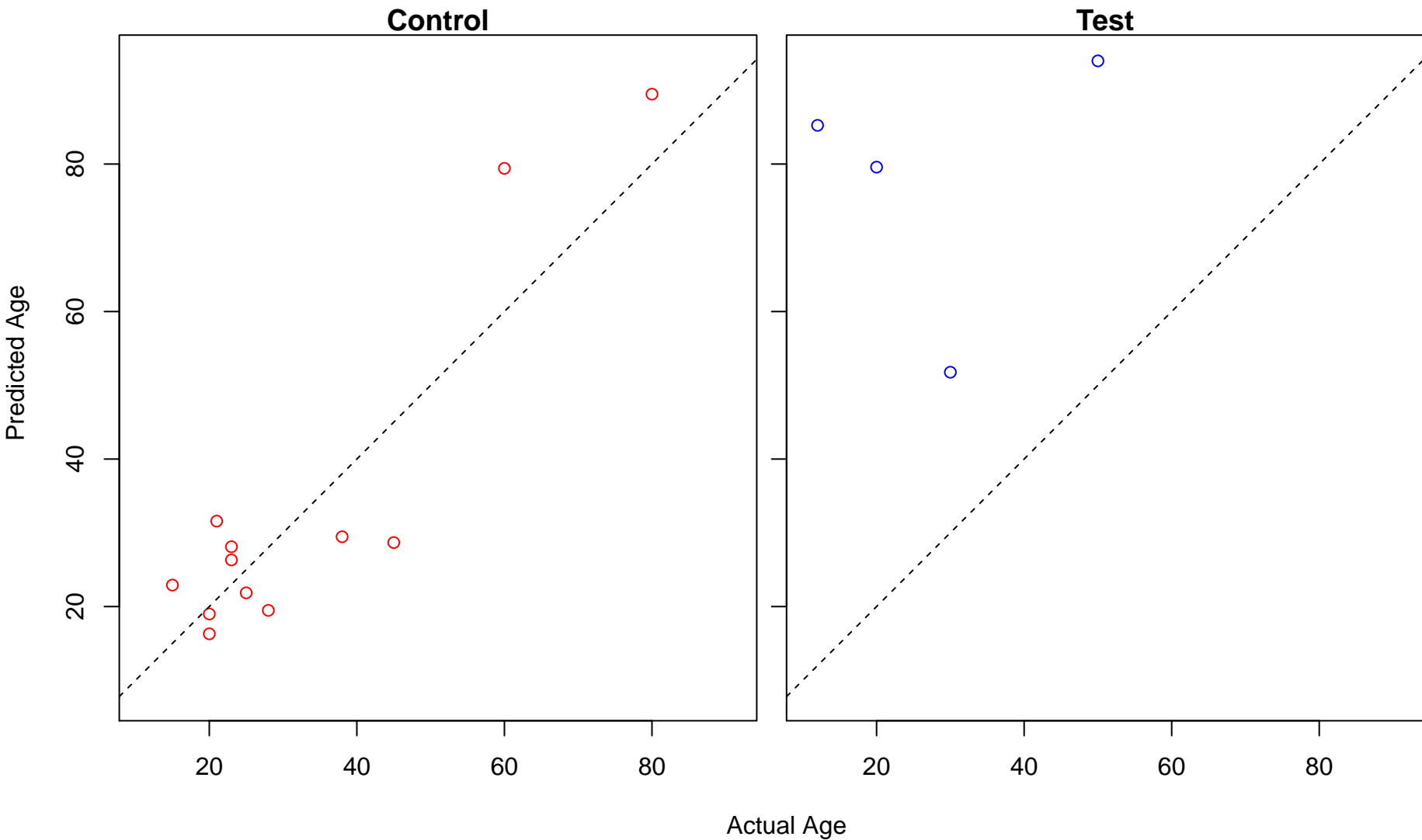
regulation of muscle tissue development (Score: 23.847181)



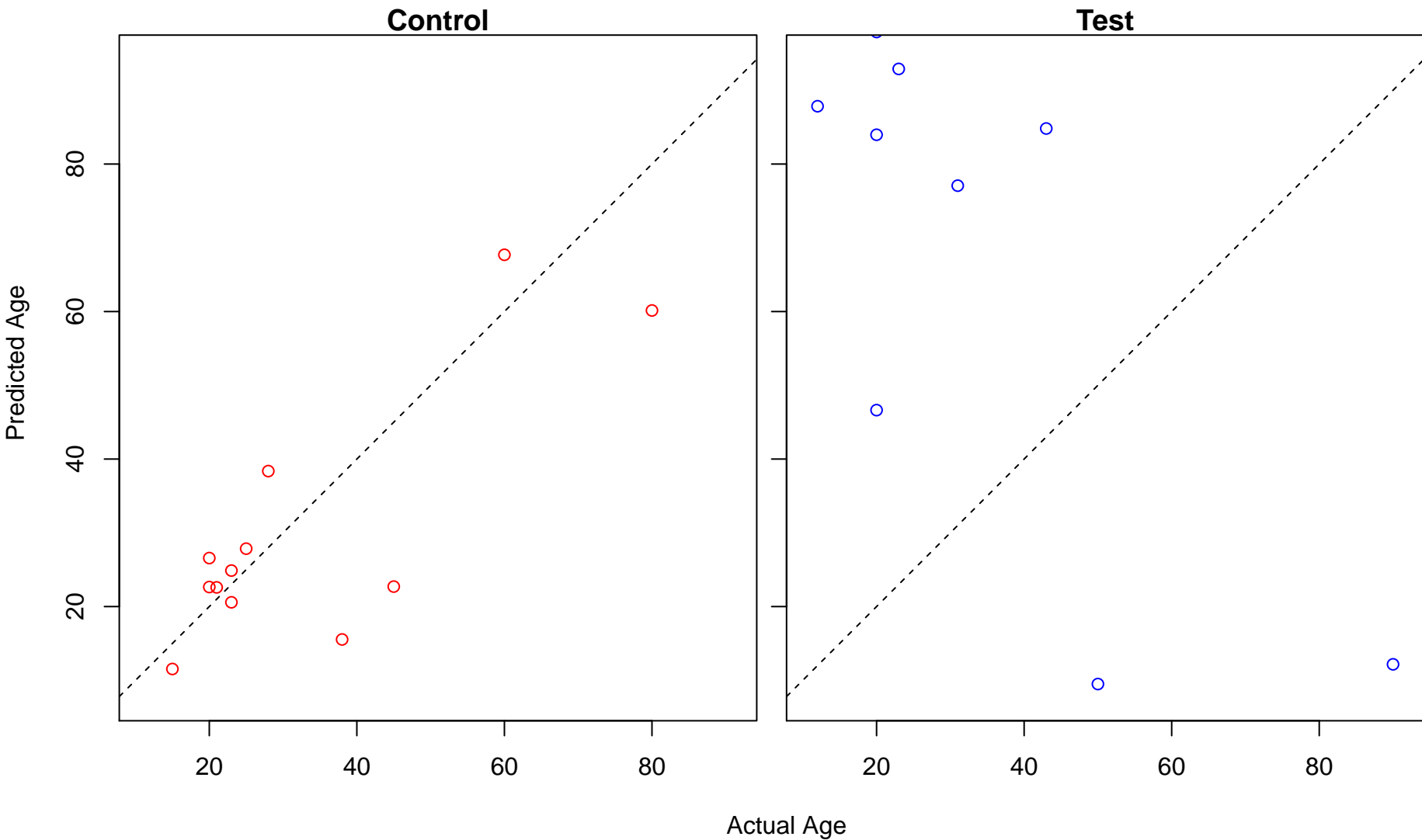
regulation of muscle organ development (Score: 23.803923)



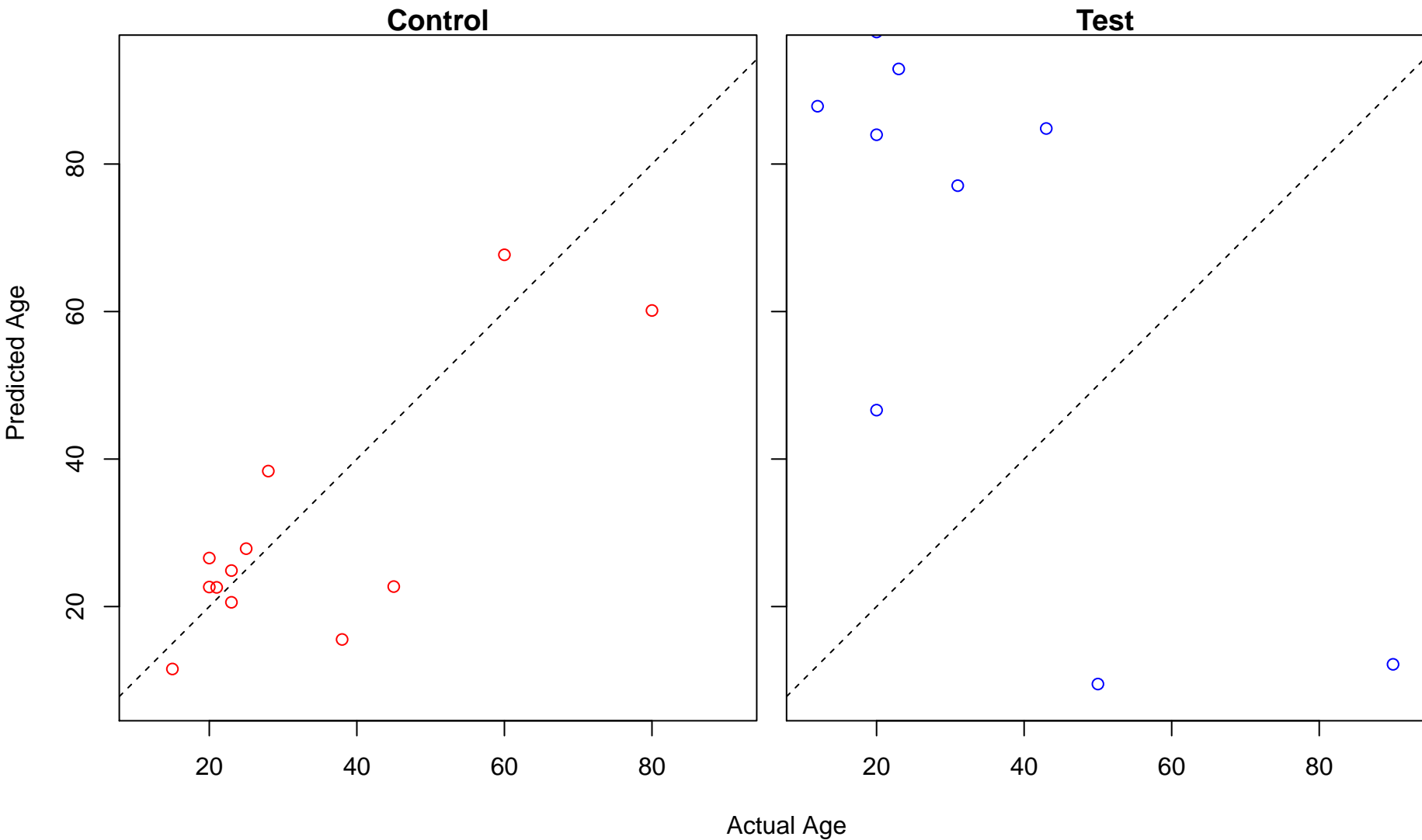
regulation of striated muscle tissue development (Score: 23.800135)



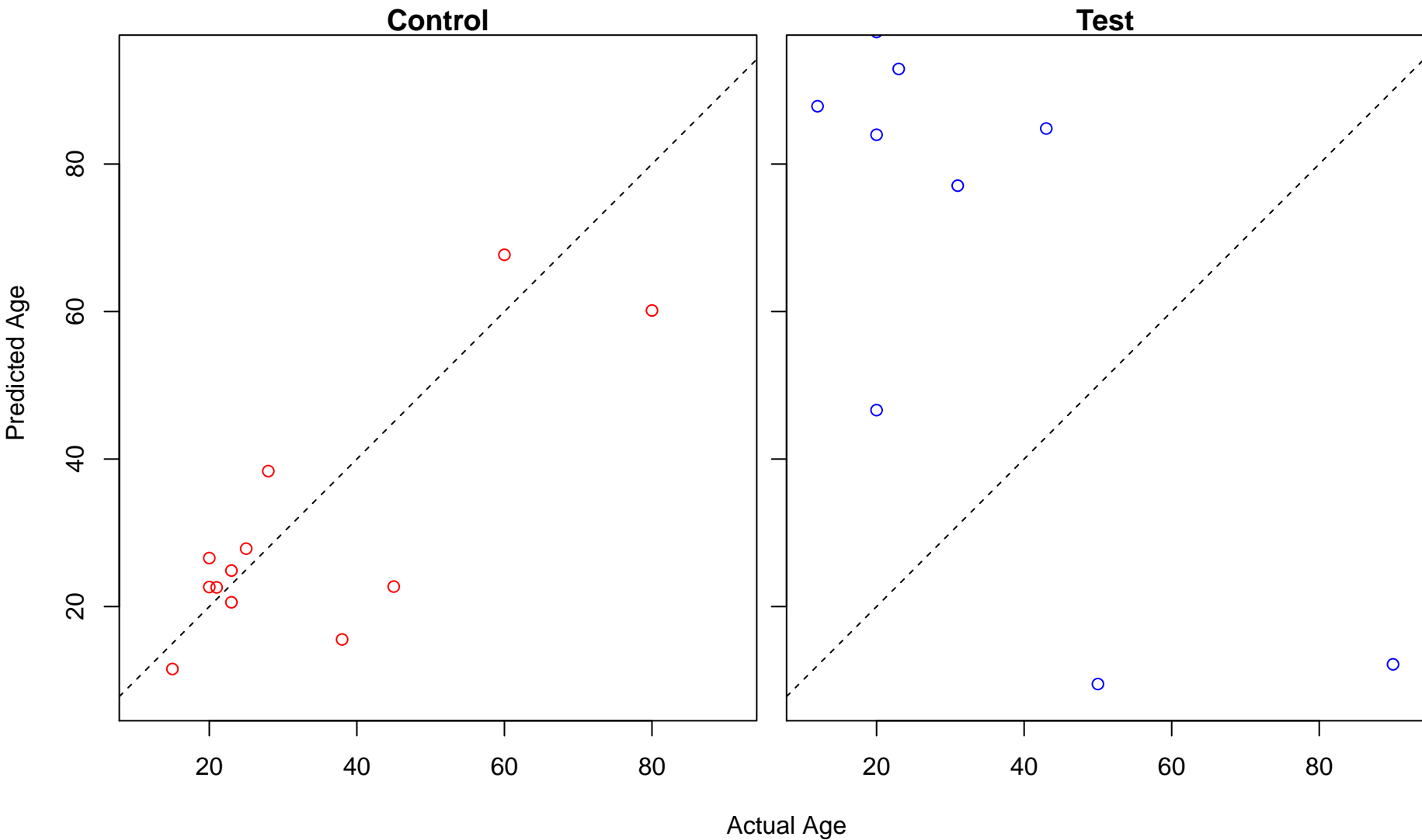
nucleoside biphosphate metabolic process (Score: 23.761033)



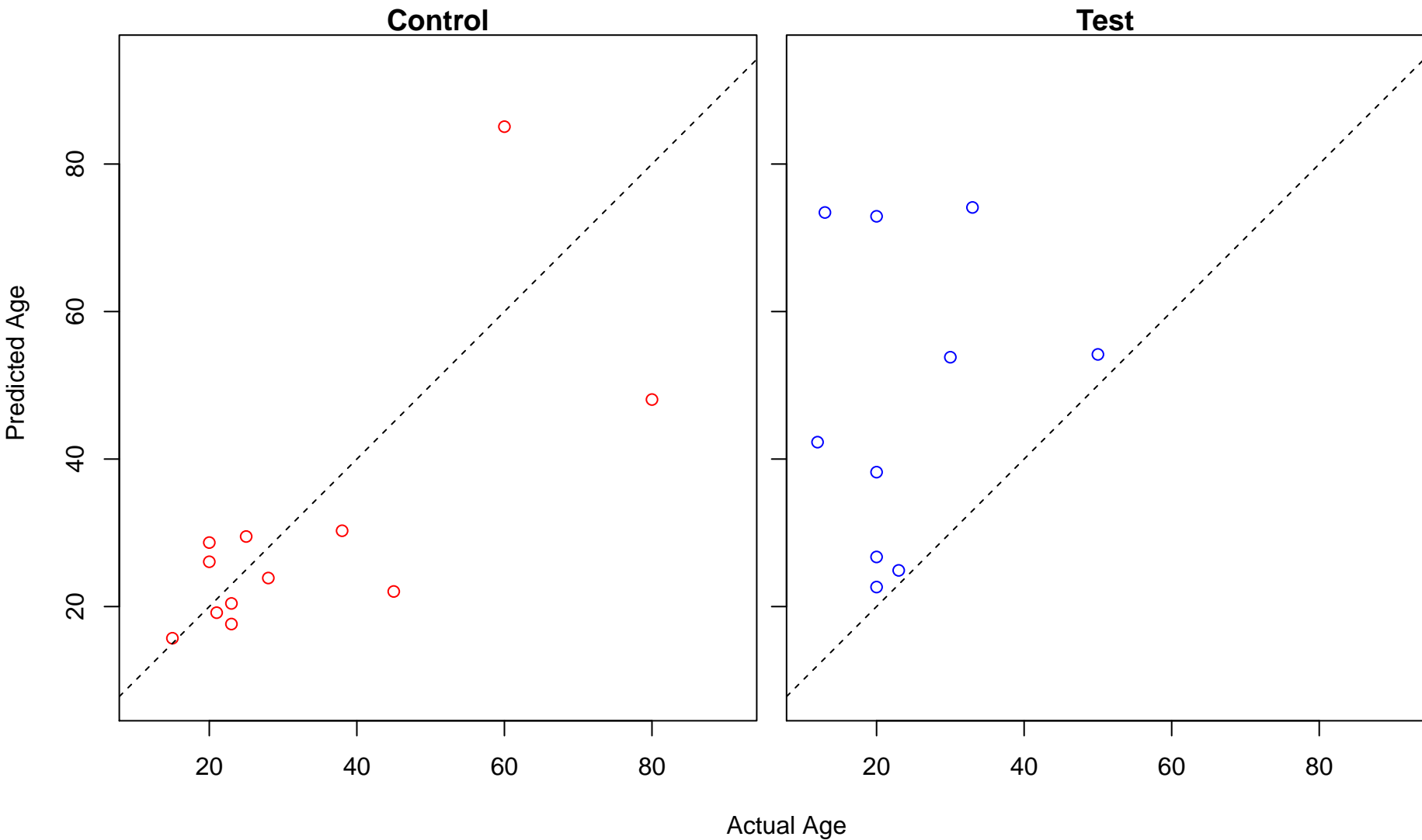
ribonucleoside biphosphate metabolic process (Score: 23.761033)



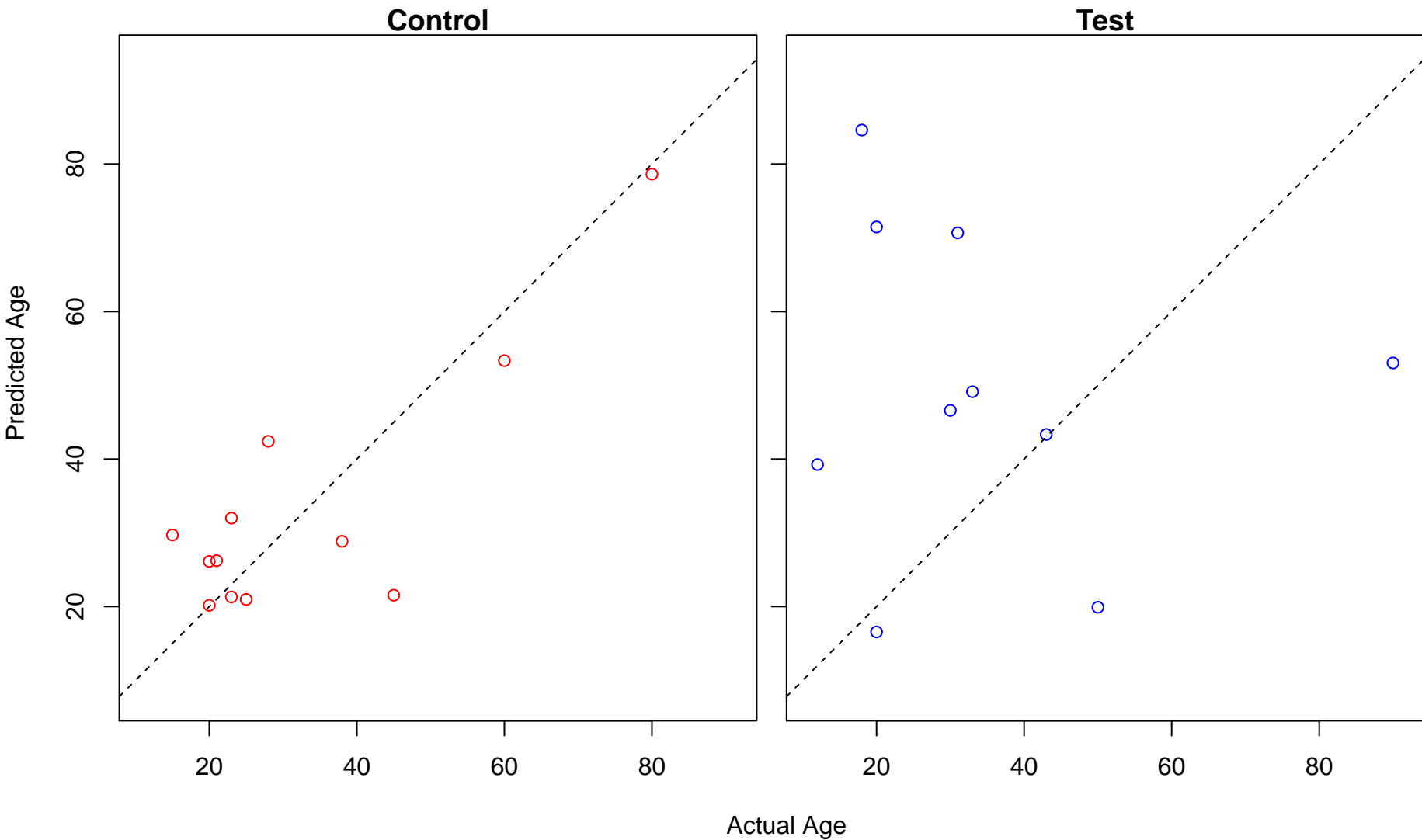
purine nucleoside biphosphate metabolic process (Score: 23.761033)



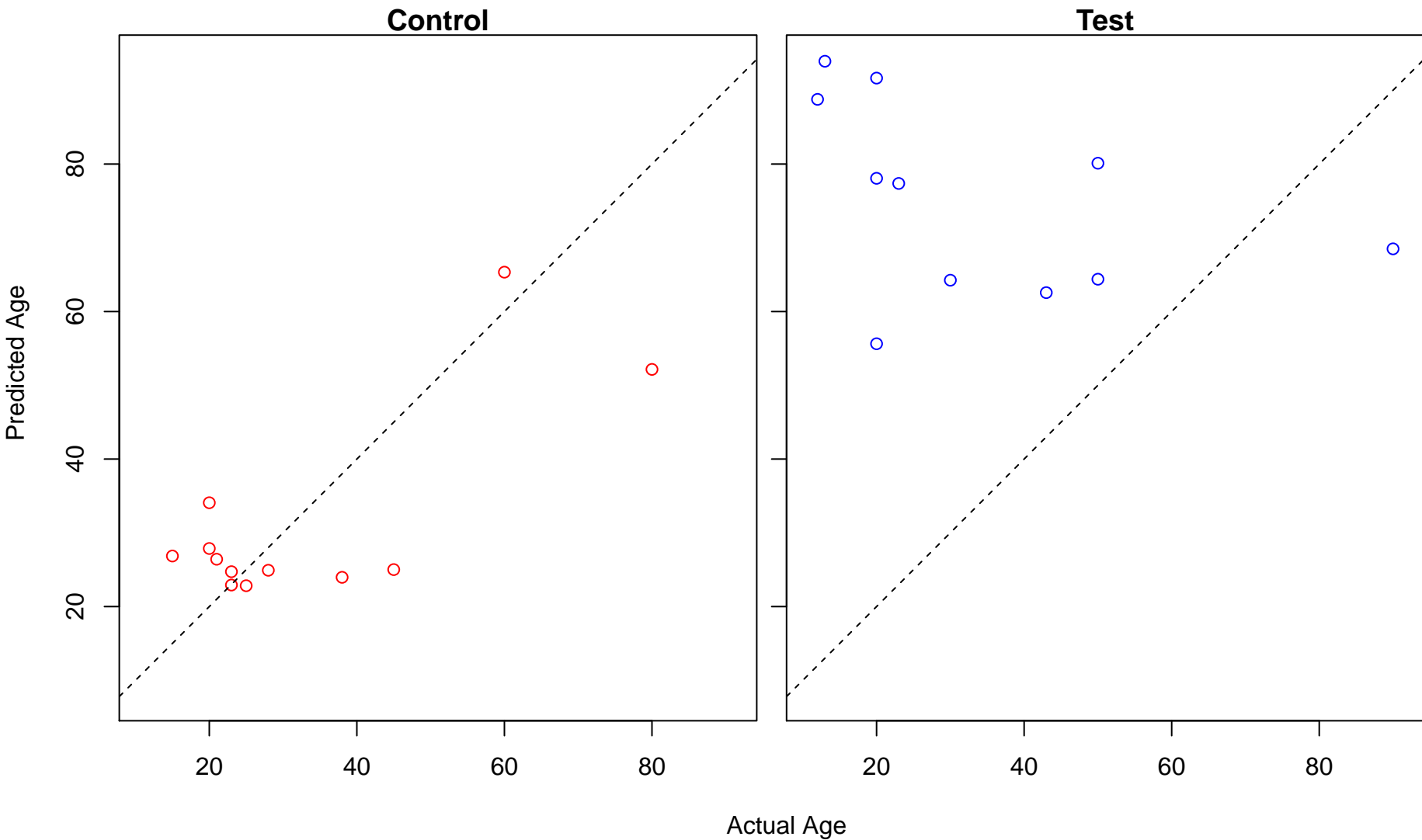
regulation of icosanoid secretion (Score: 23.714667)



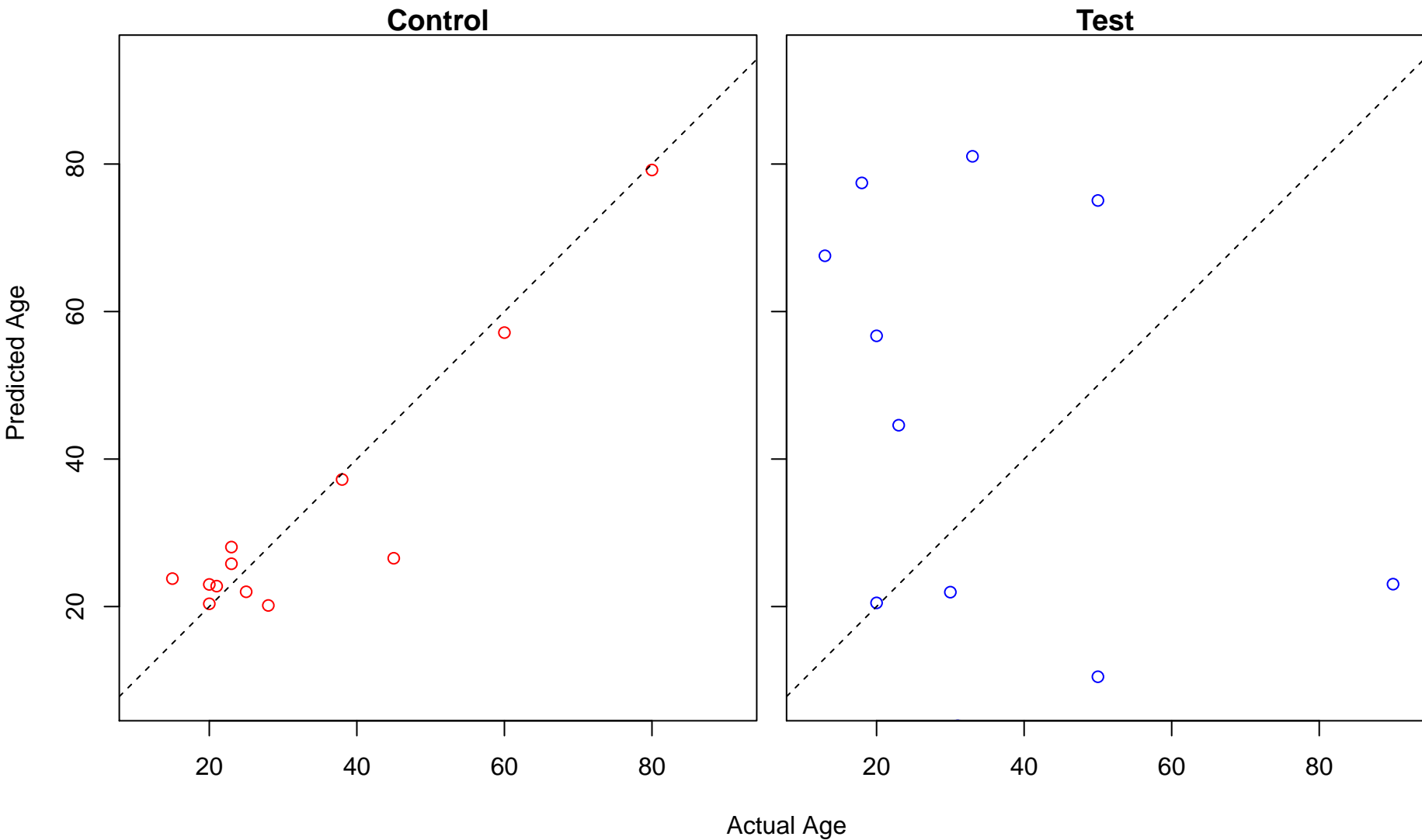
positive regulation of ERK1 and ERK2 cascade (Score: 23.697743)



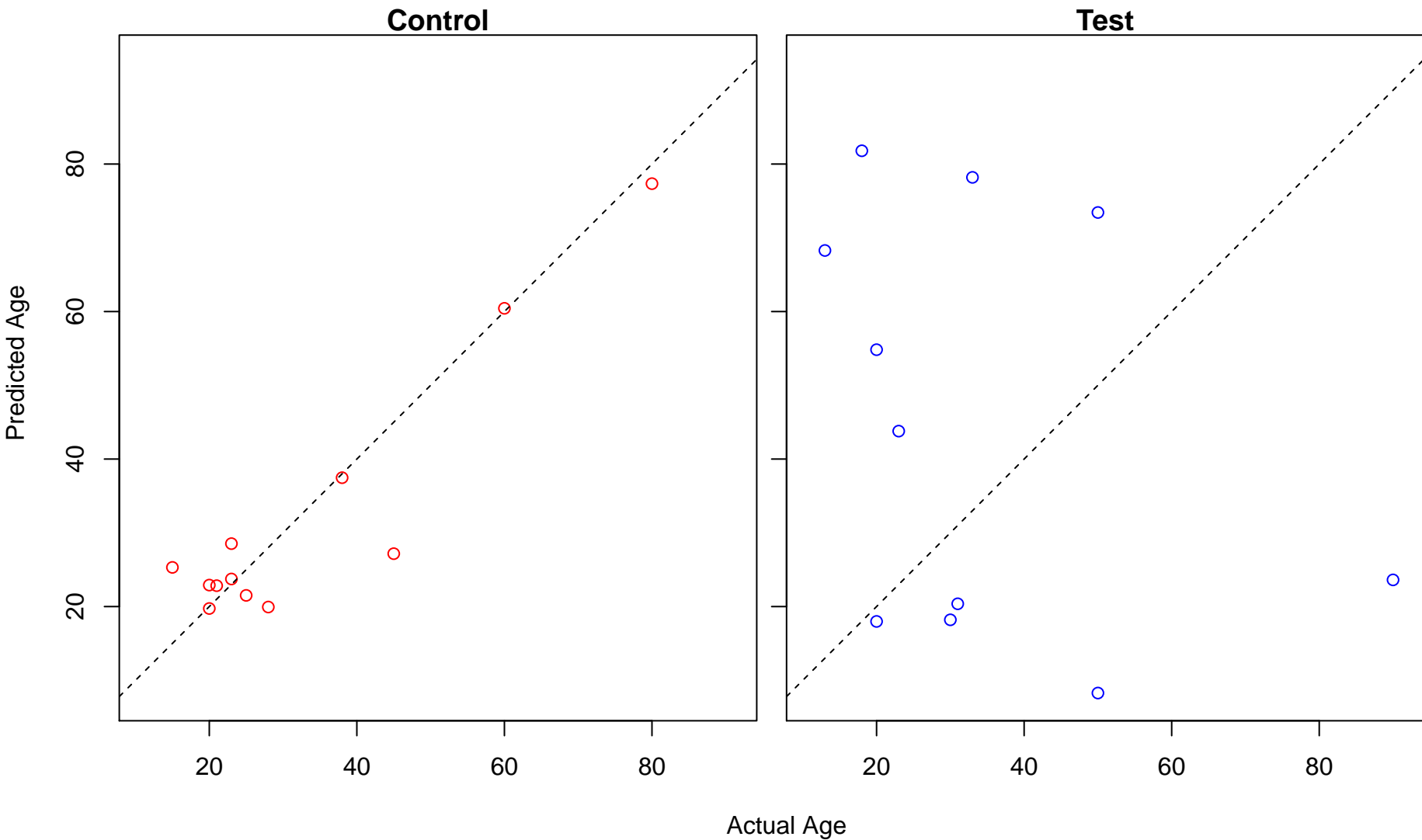
neurological system process involved in regulation of systemic arterial blood pressure (Score: 23.695)



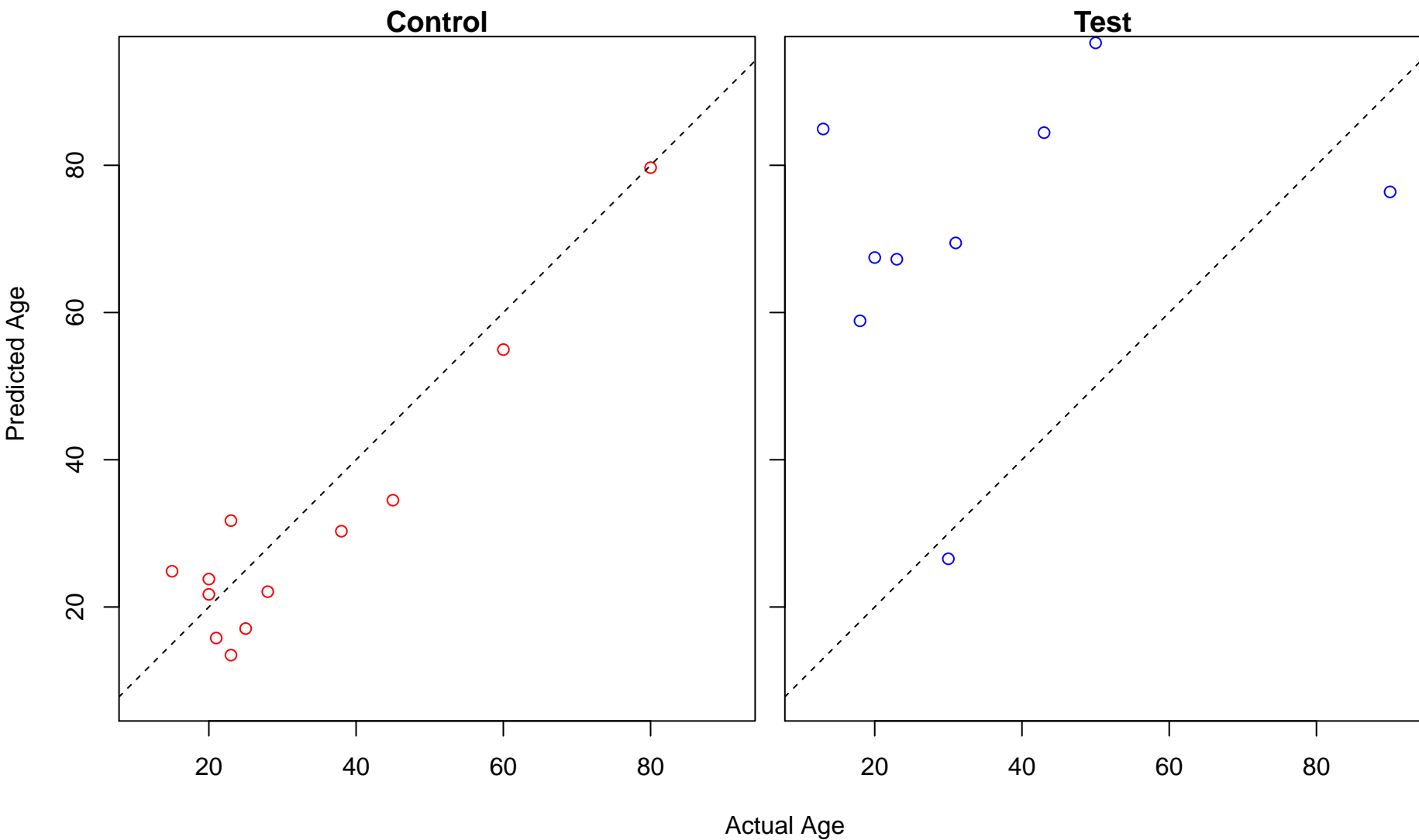
cellular divalent inorganic cation homeostasis (Score: 23.688800)



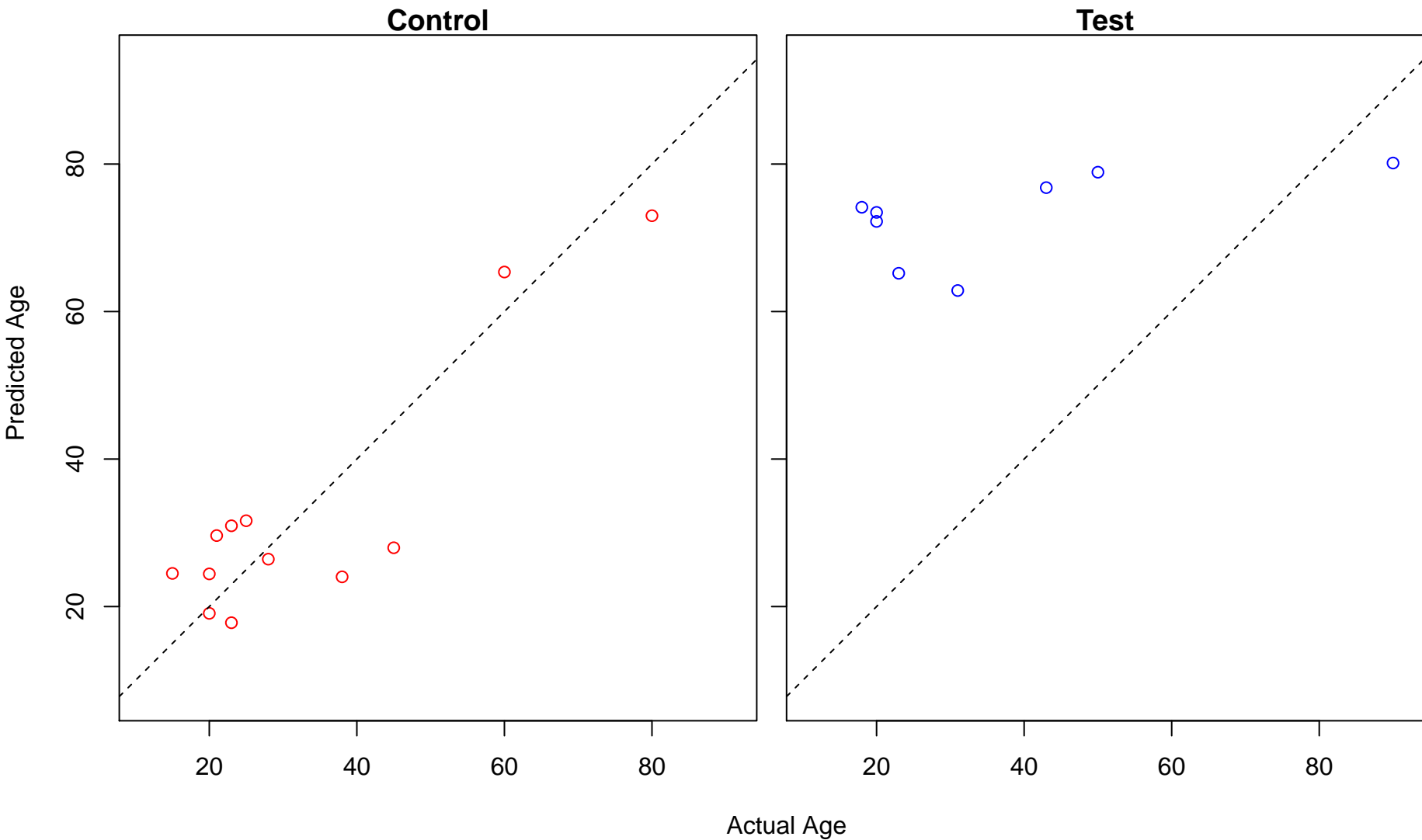
calcium ion homeostasis (Score: 23.668907)



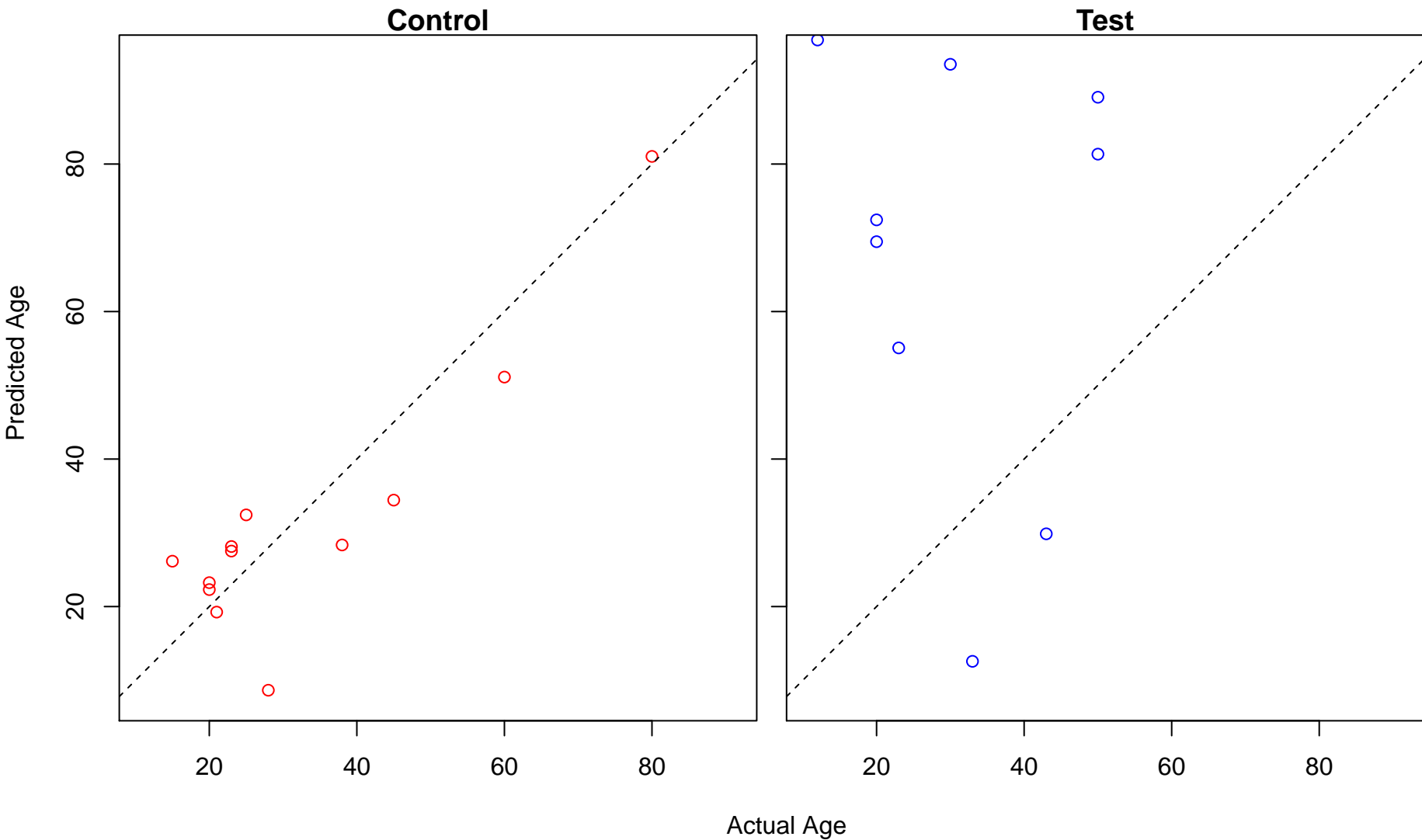
pyrimidine nucleotide catabolic process (Score: 23.646816)



aorta morphogenesis (Score: 23.603399)

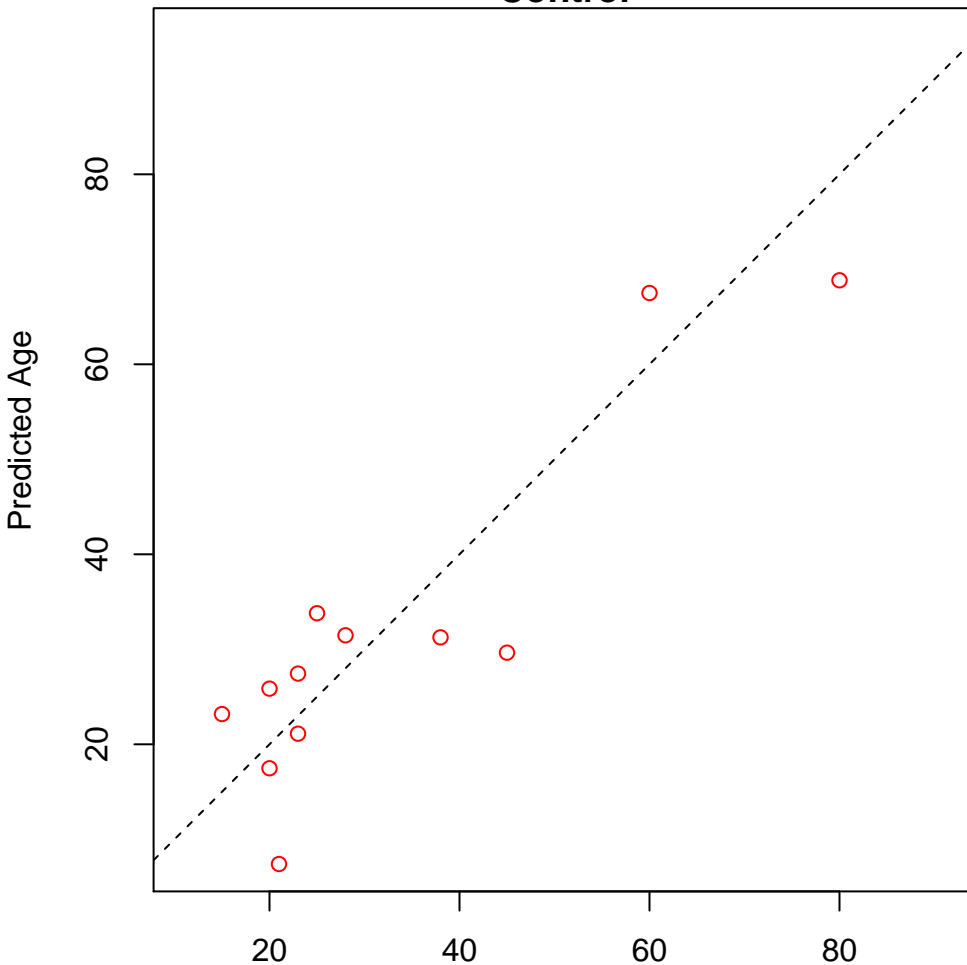


fructose 1,6-bisphosphate metabolic process (Score: 23.511340)

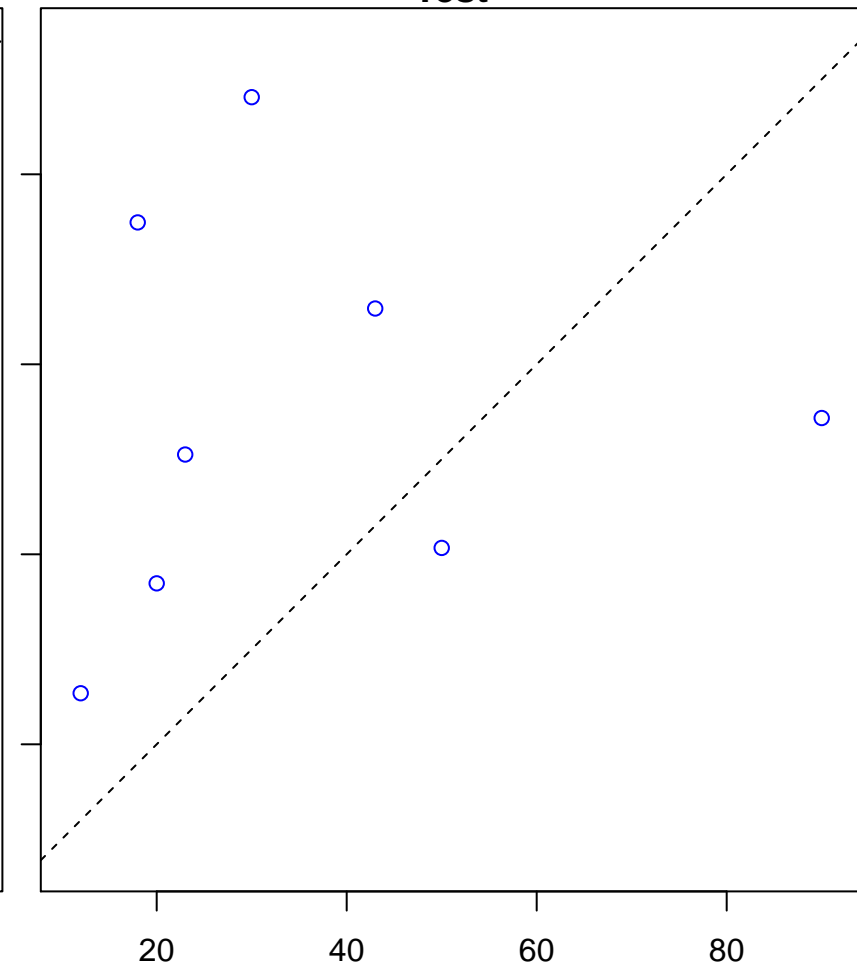


RNA secondary structure unwinding (Score: 23.507553)

Control

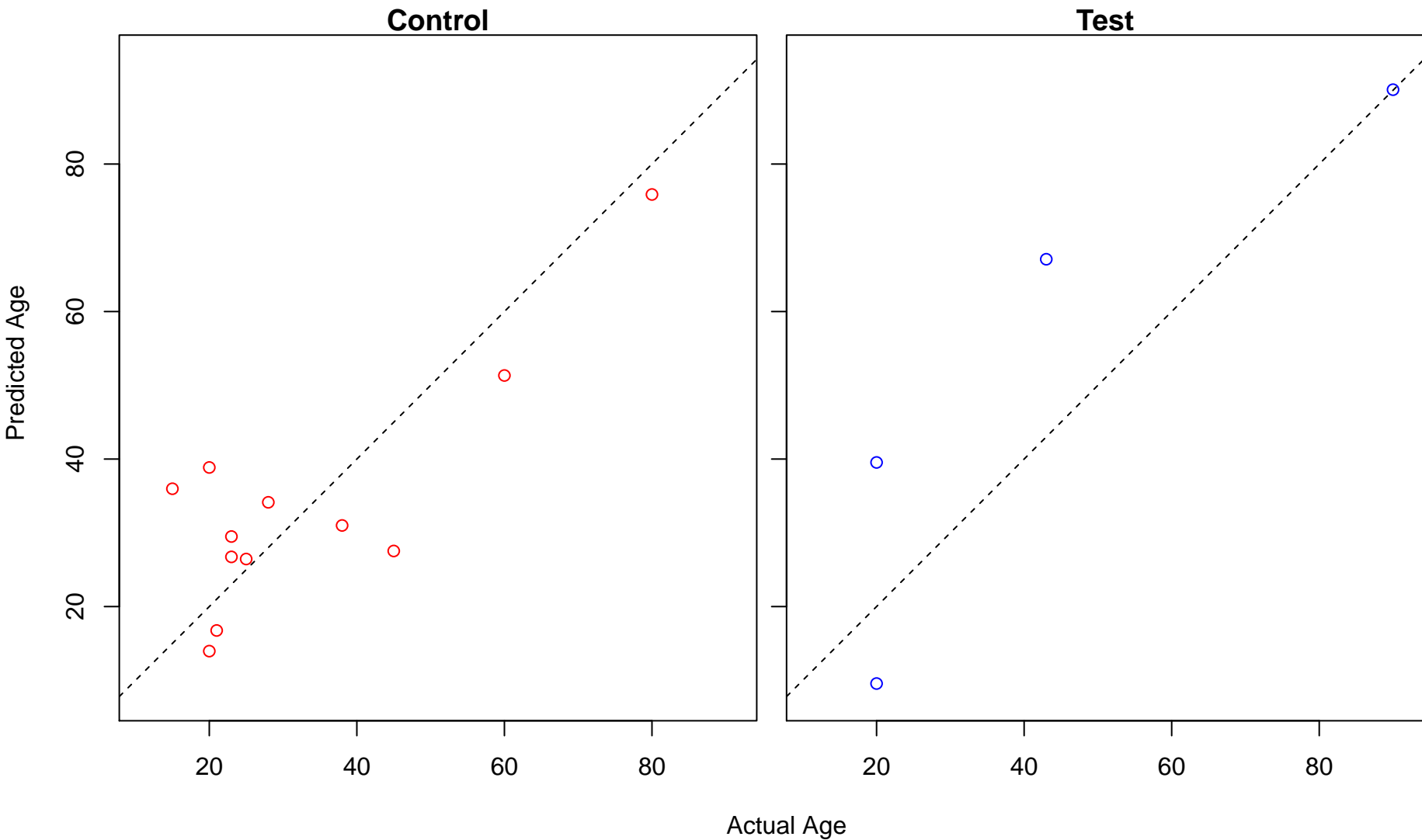


Test

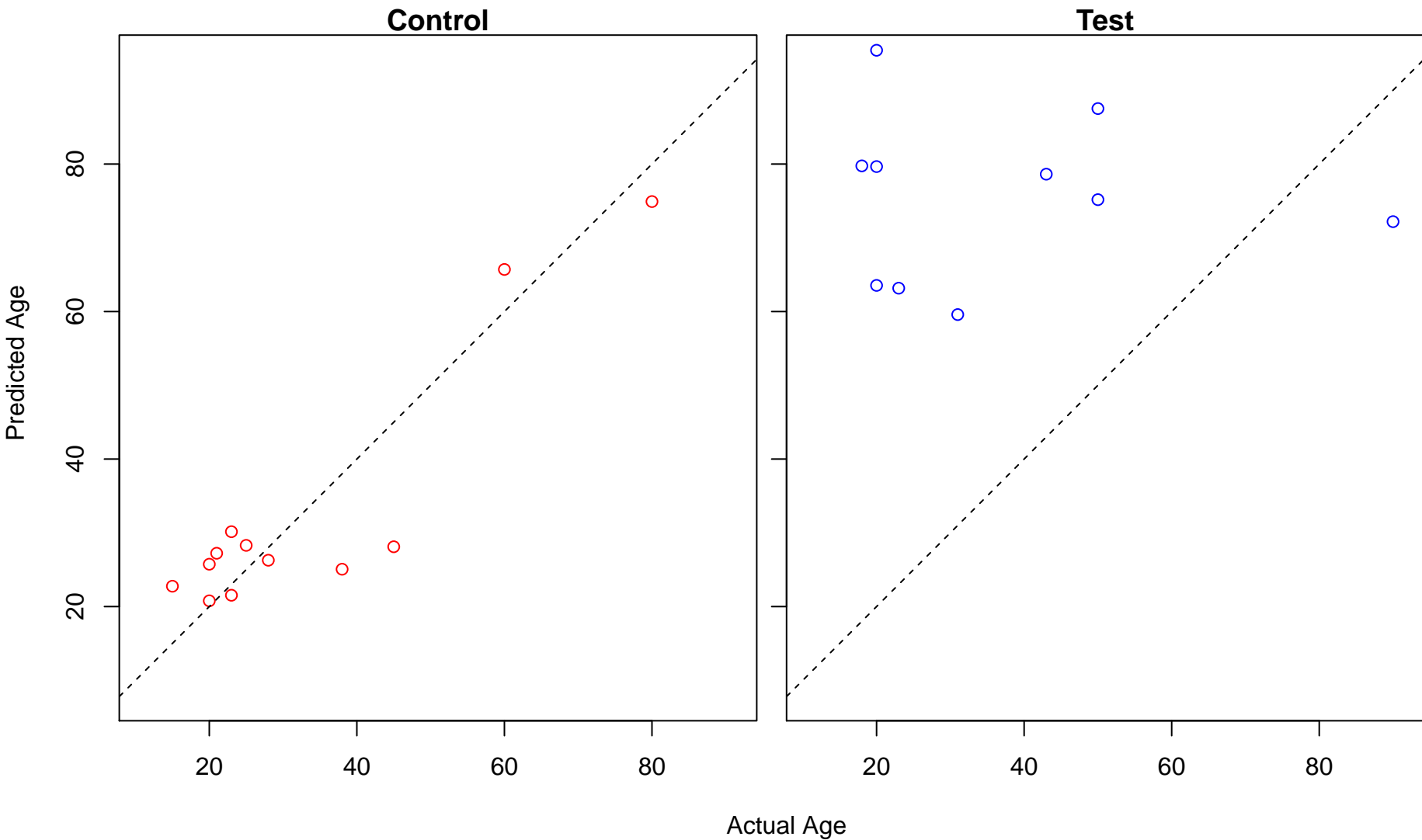


Actual Age

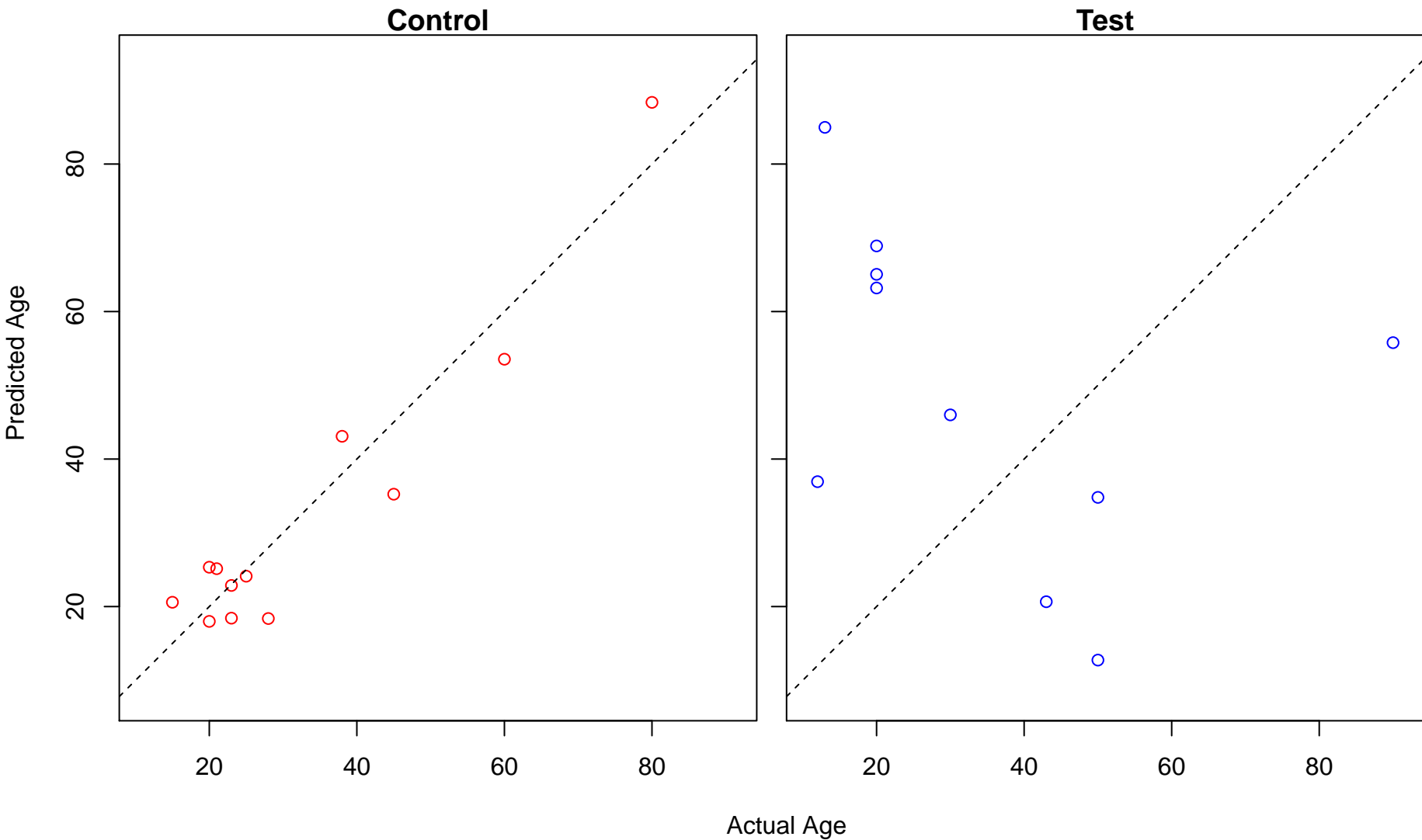
GDP metabolic process (Score: 23.446073)



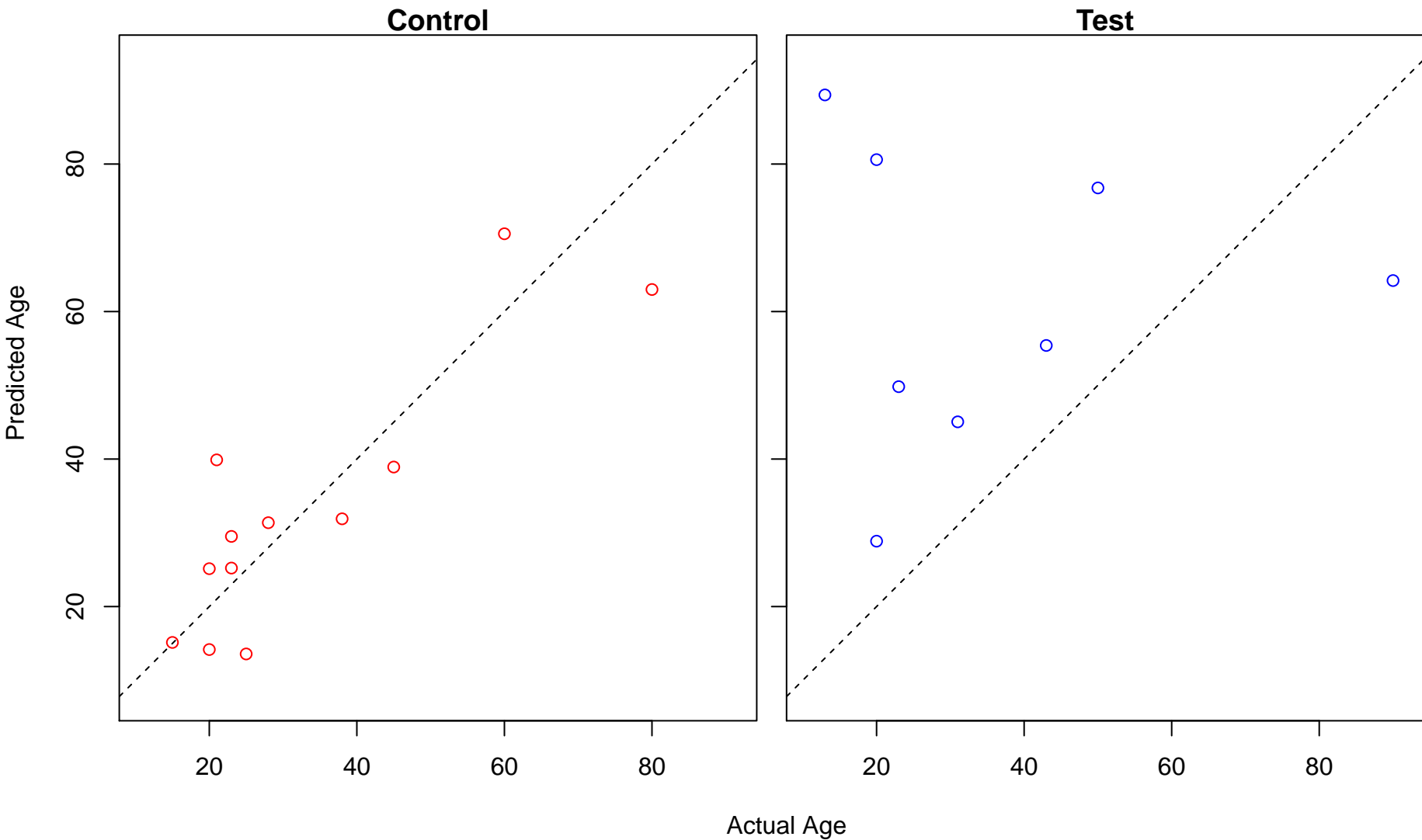
cardiac muscle cell myoblast differentiation (Score: 23.410432)



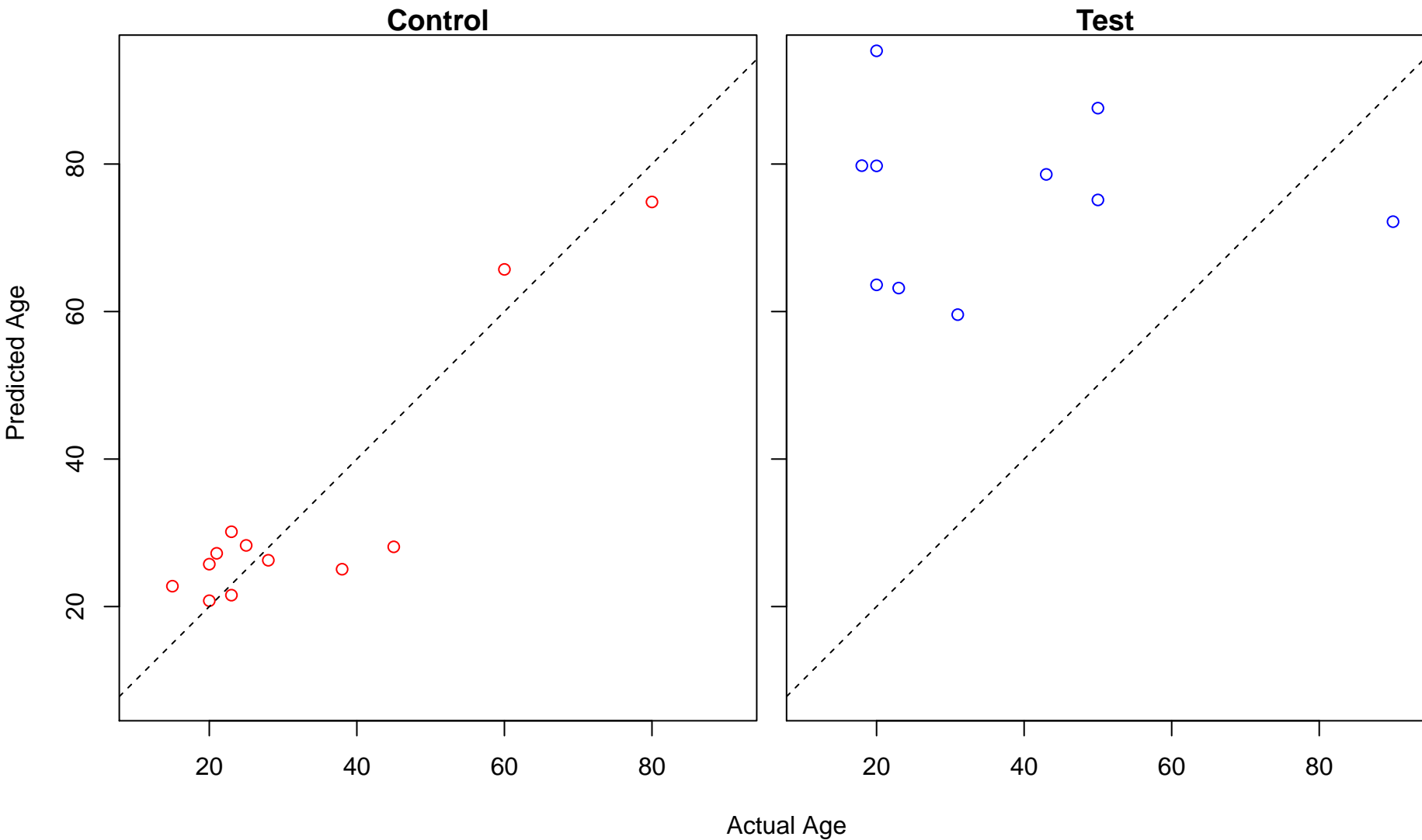
positive regulation of protein export from nucleus (Score: 23.402764)



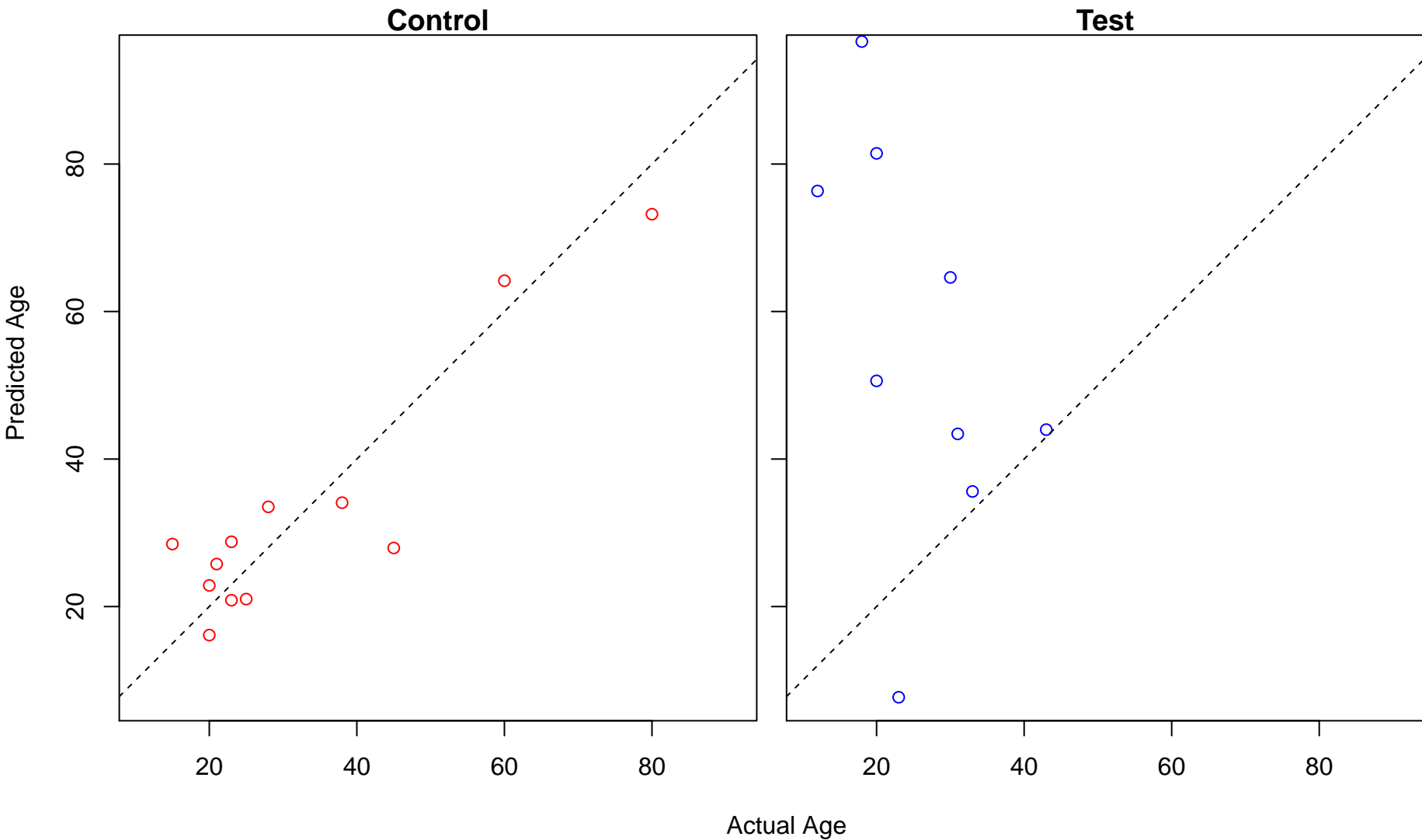
protein-lipid complex assembly (Score: 23.374143)



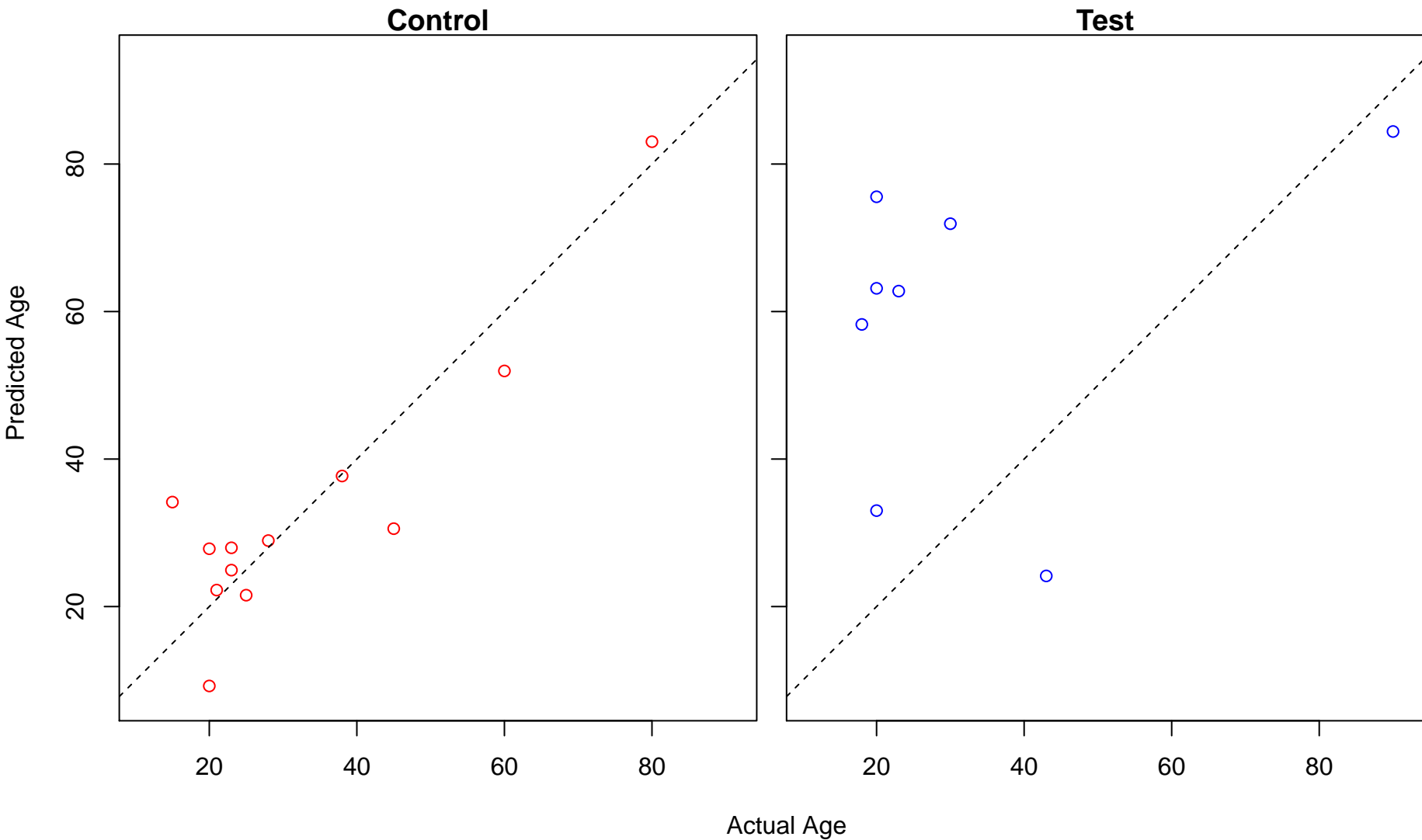
cardioblast differentiation (Score: 23.361732)



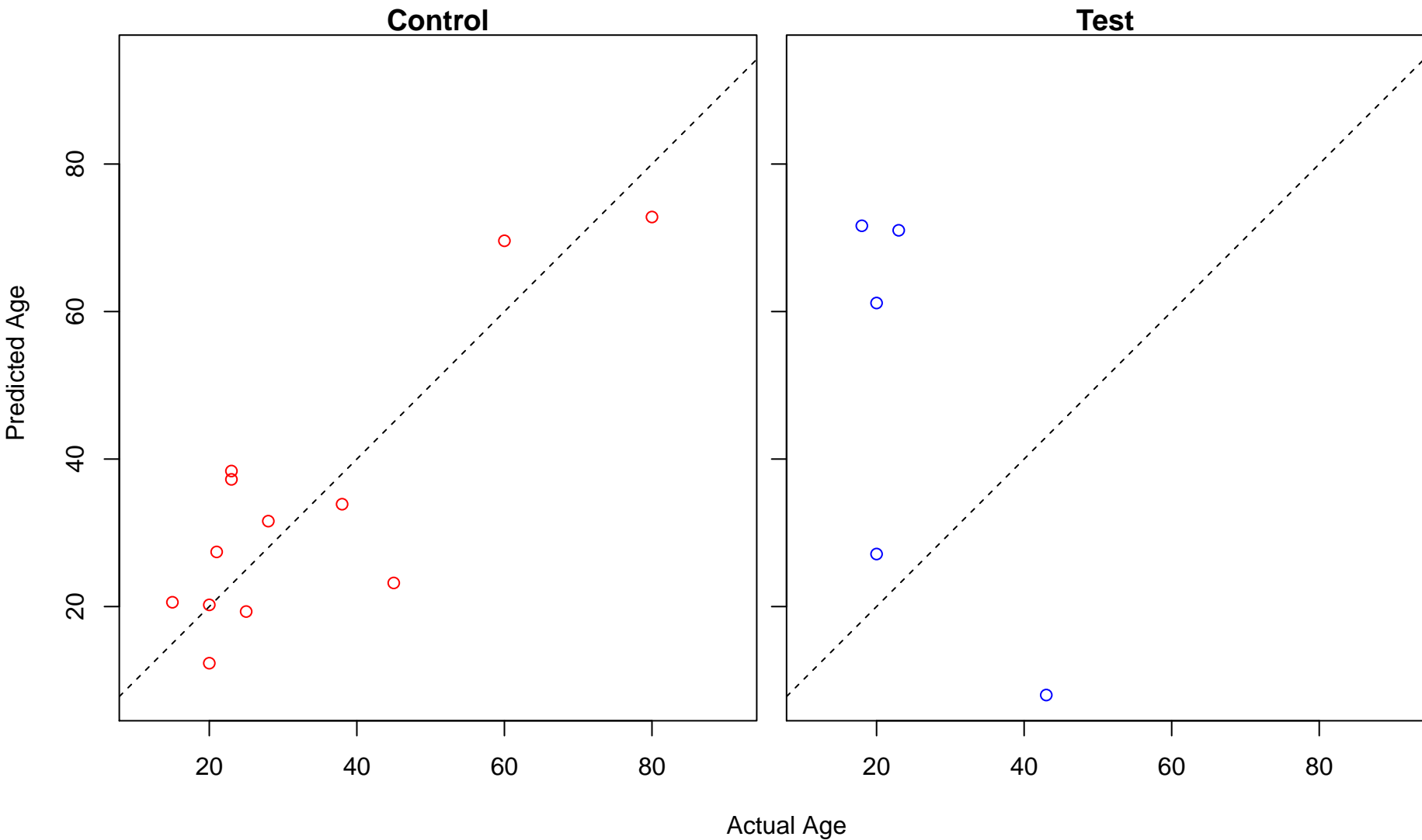
protein secretion (Score: 23.297981)



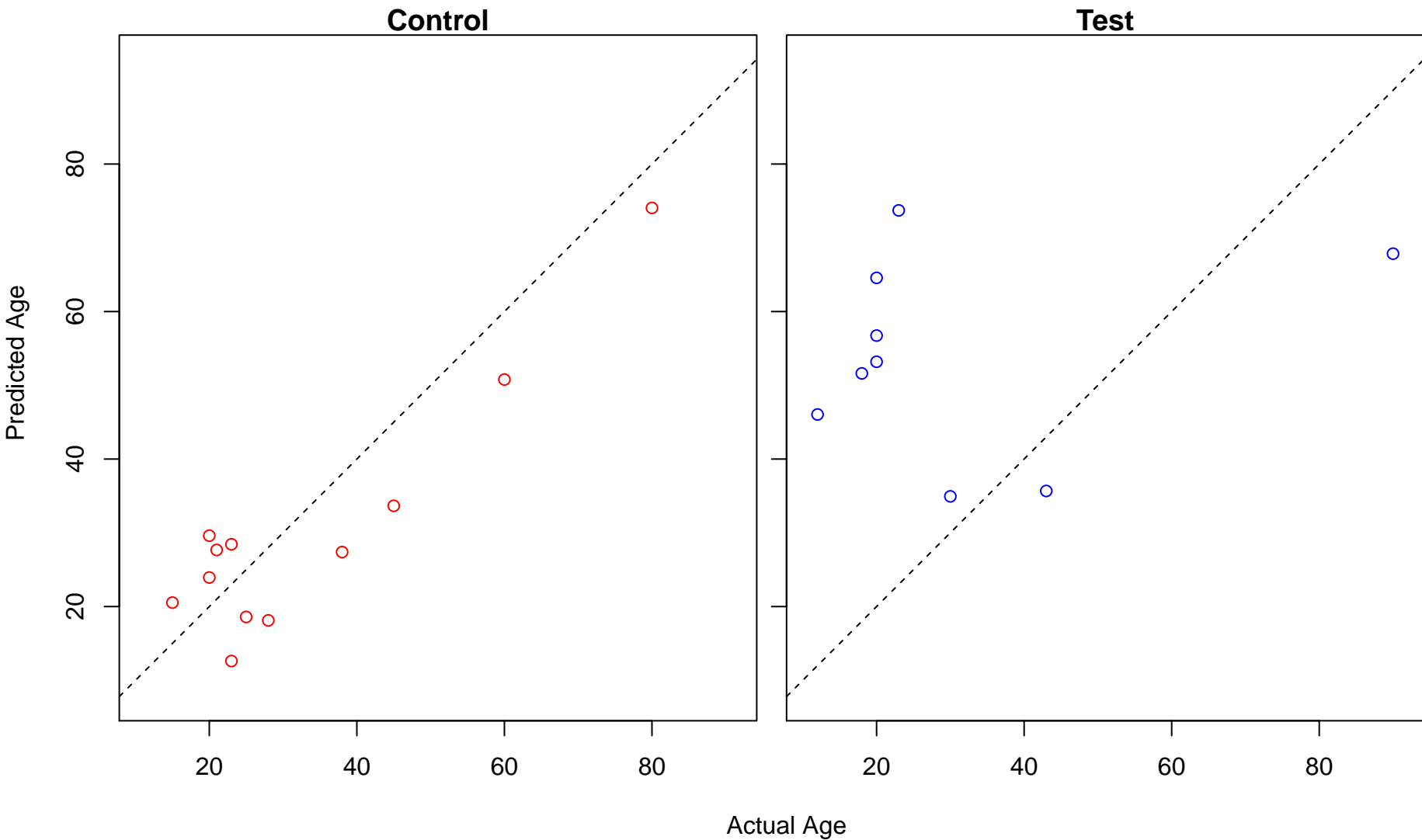
regulation of toll-like receptor 4 signaling pathway (Score: 23.251235)



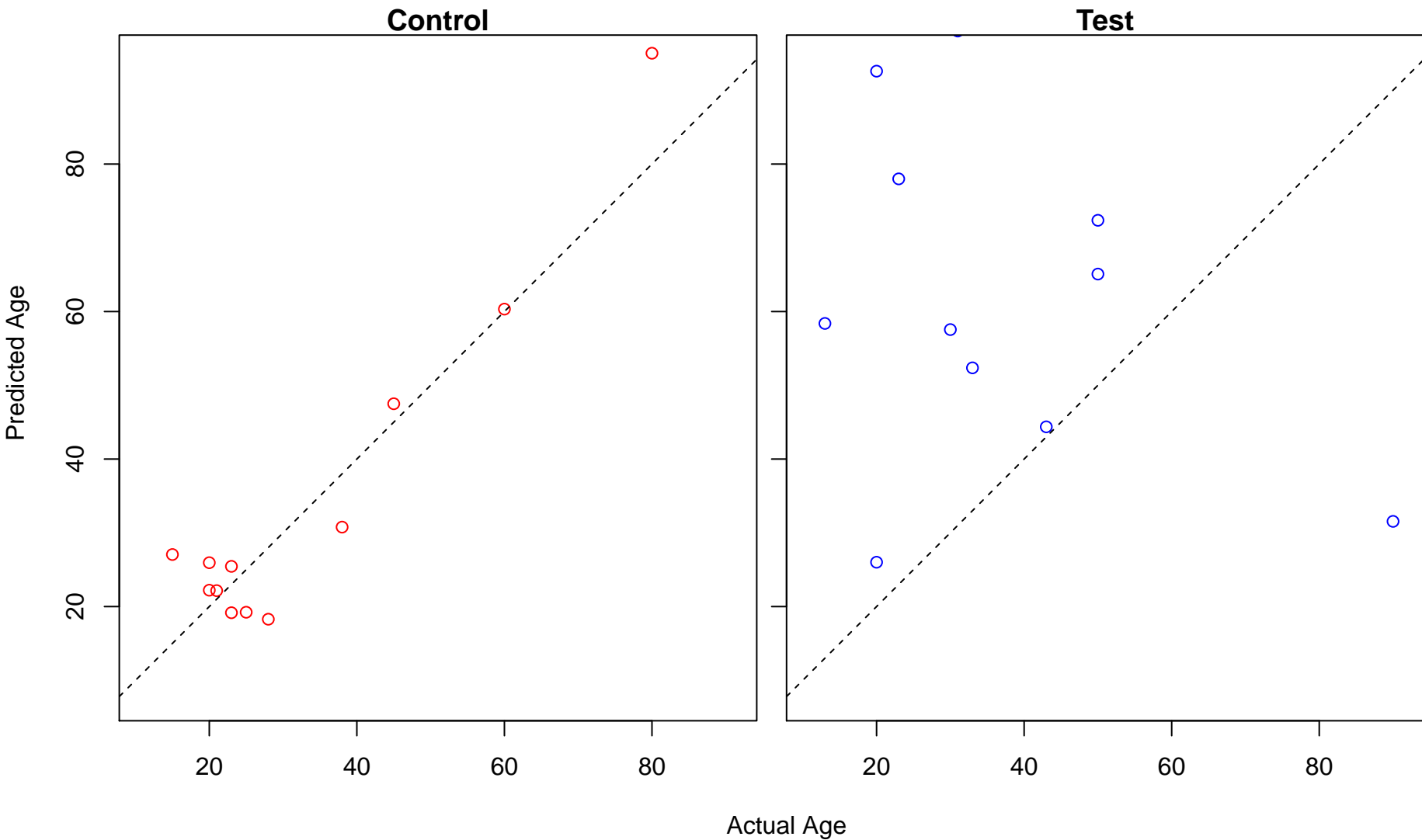
angiotensin maturation (Score: 23.203429)



response to cold (Score: 23.106594)

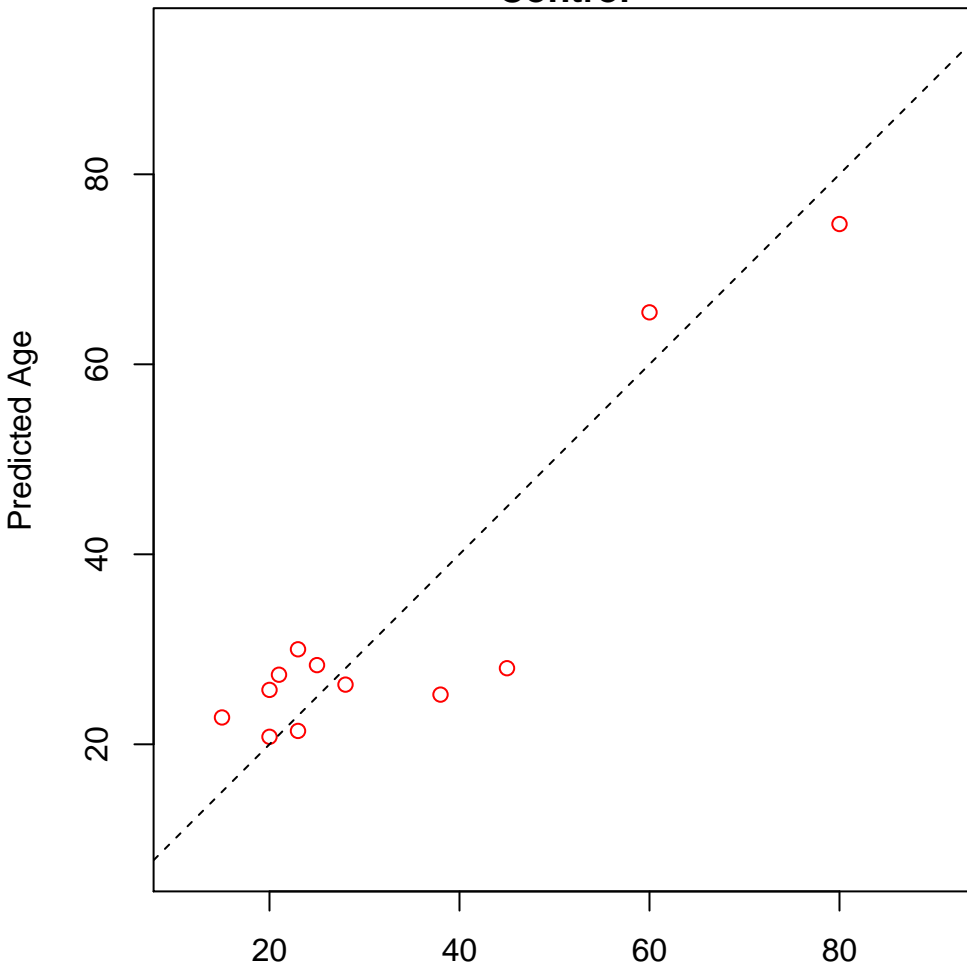


sperm motility (Score: 23.080125)

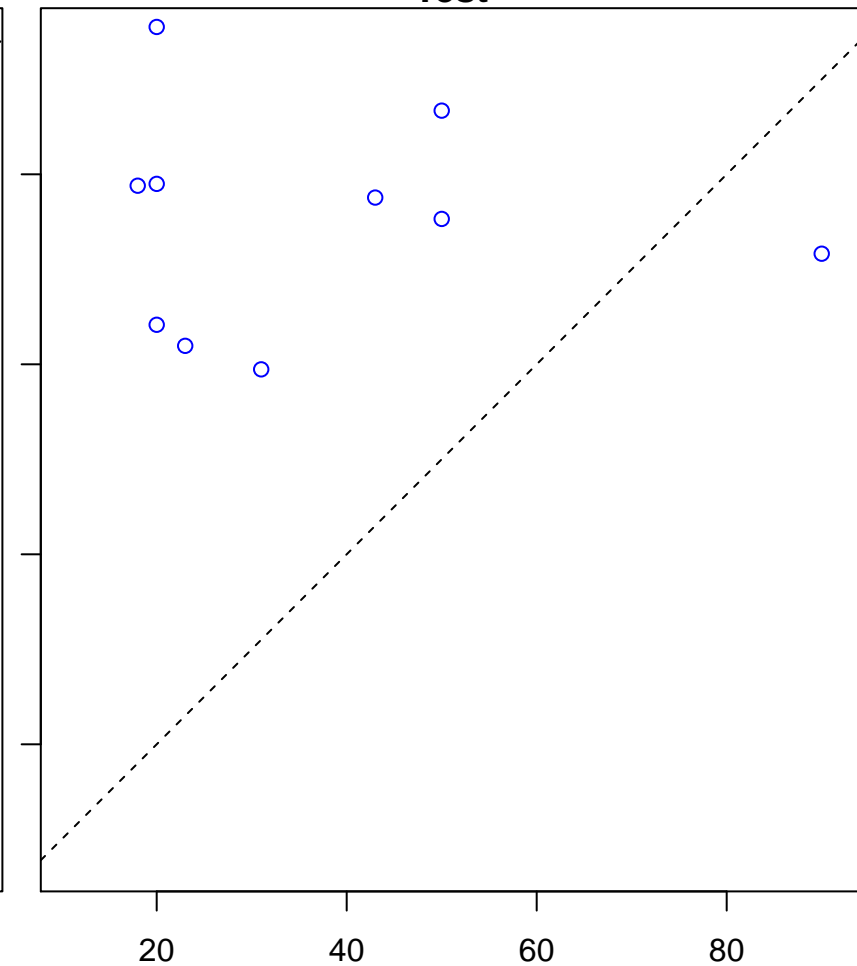


cardiac left ventricle morphogenesis (Score: 23.078482)

Control



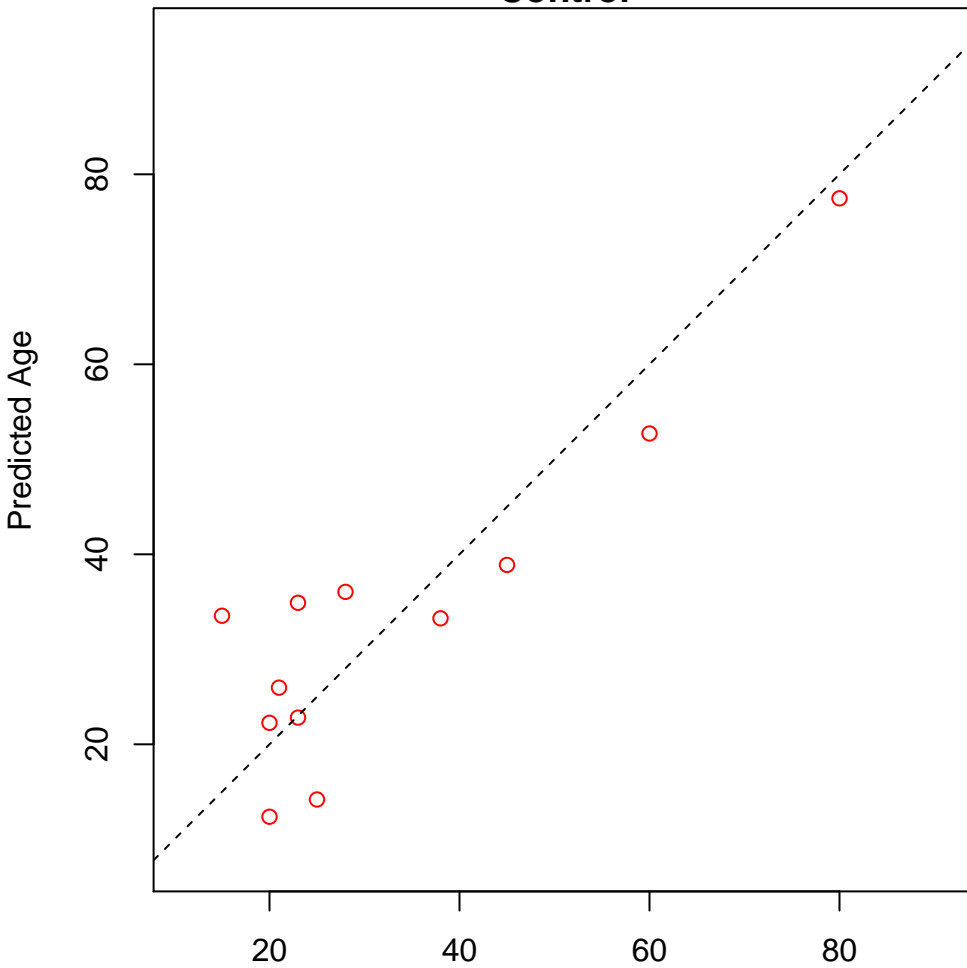
Test



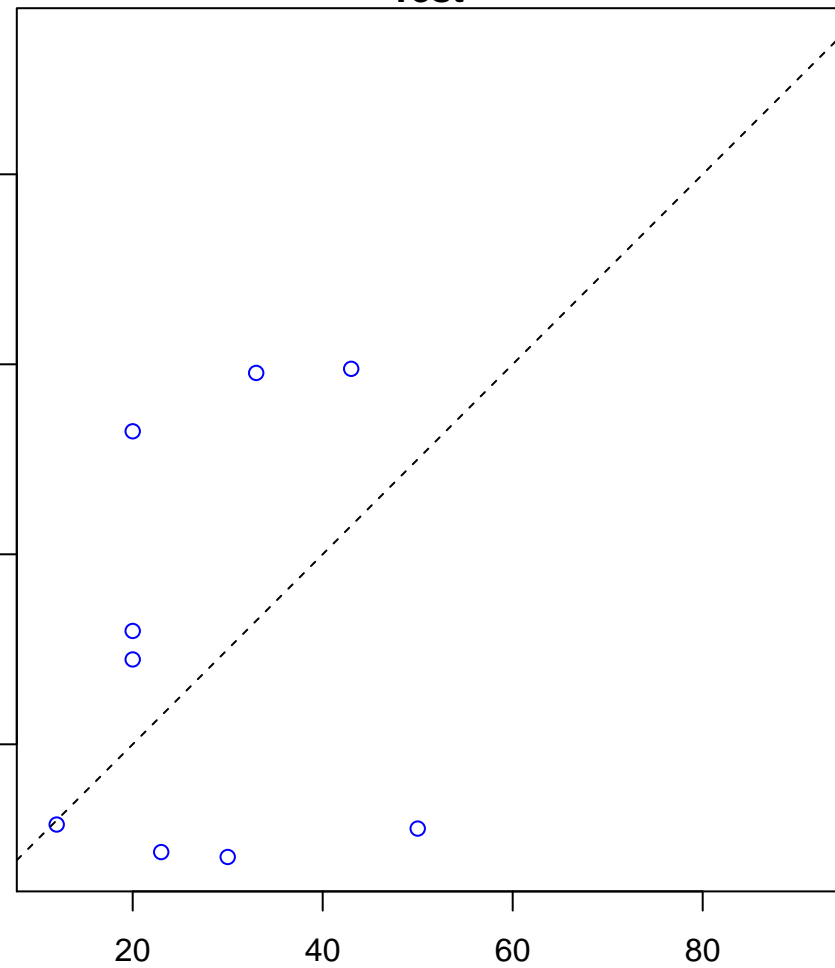
Actual Age

regulation of interleukin-1 production (Score: 23.067869)

Control

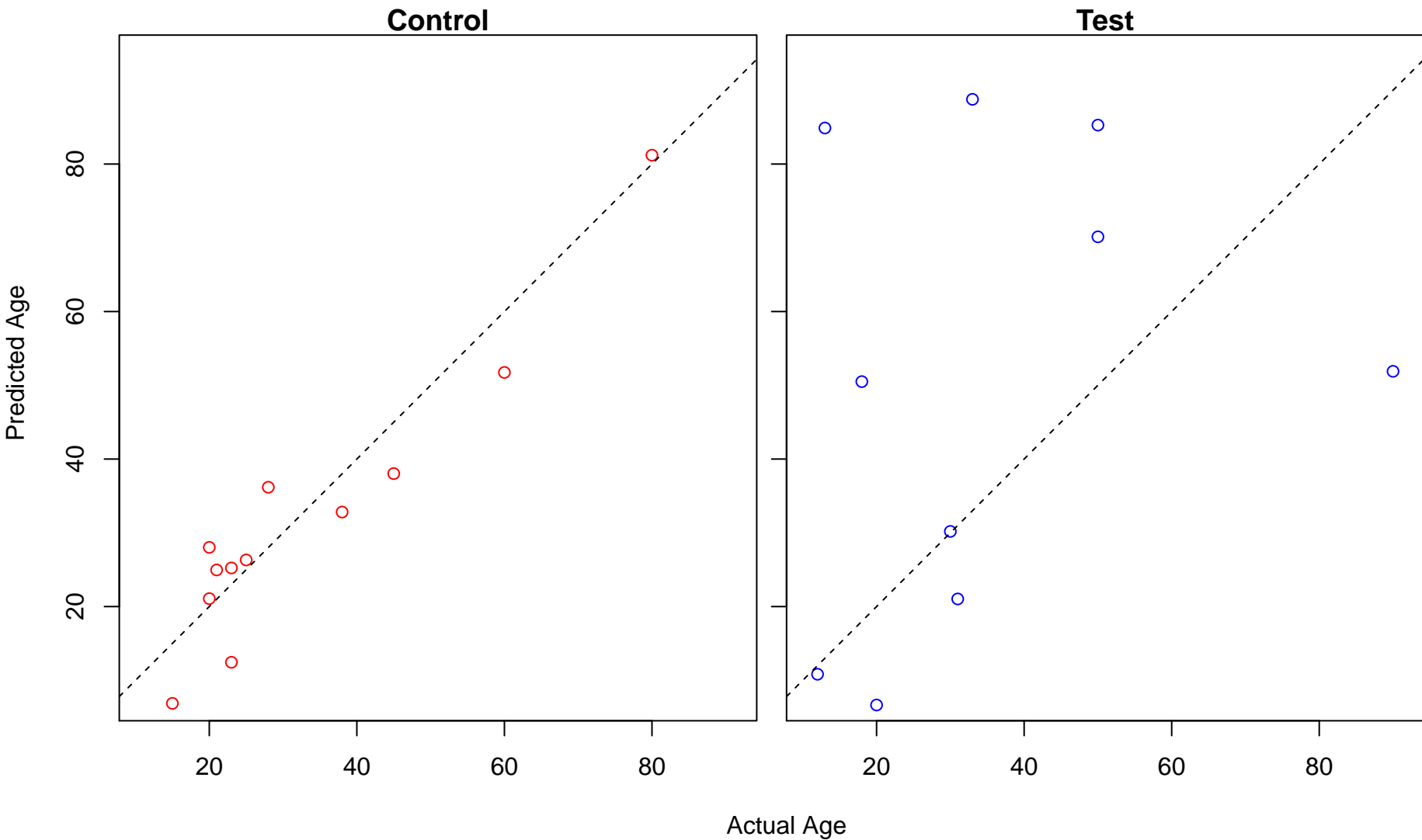


Test

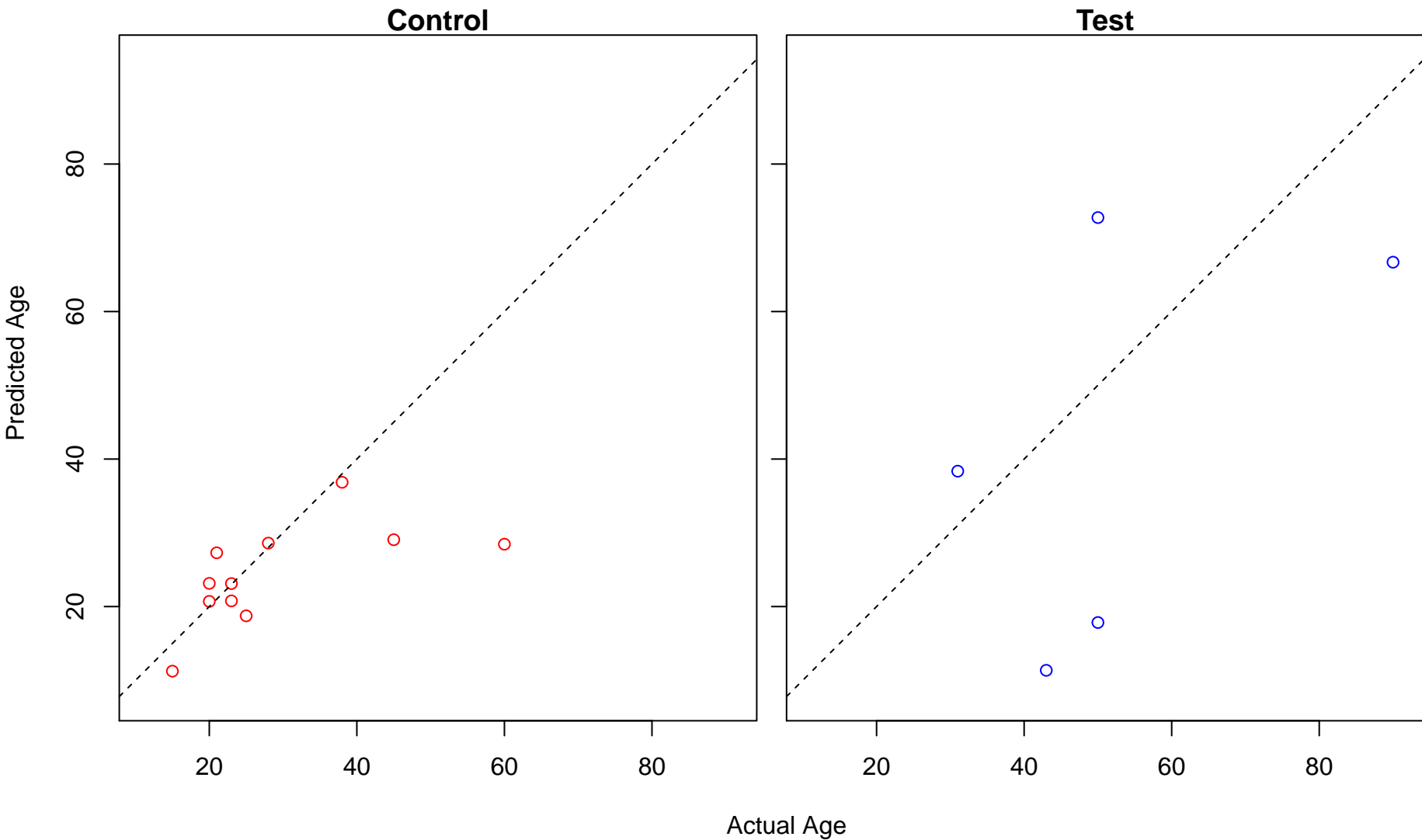


Actual Age

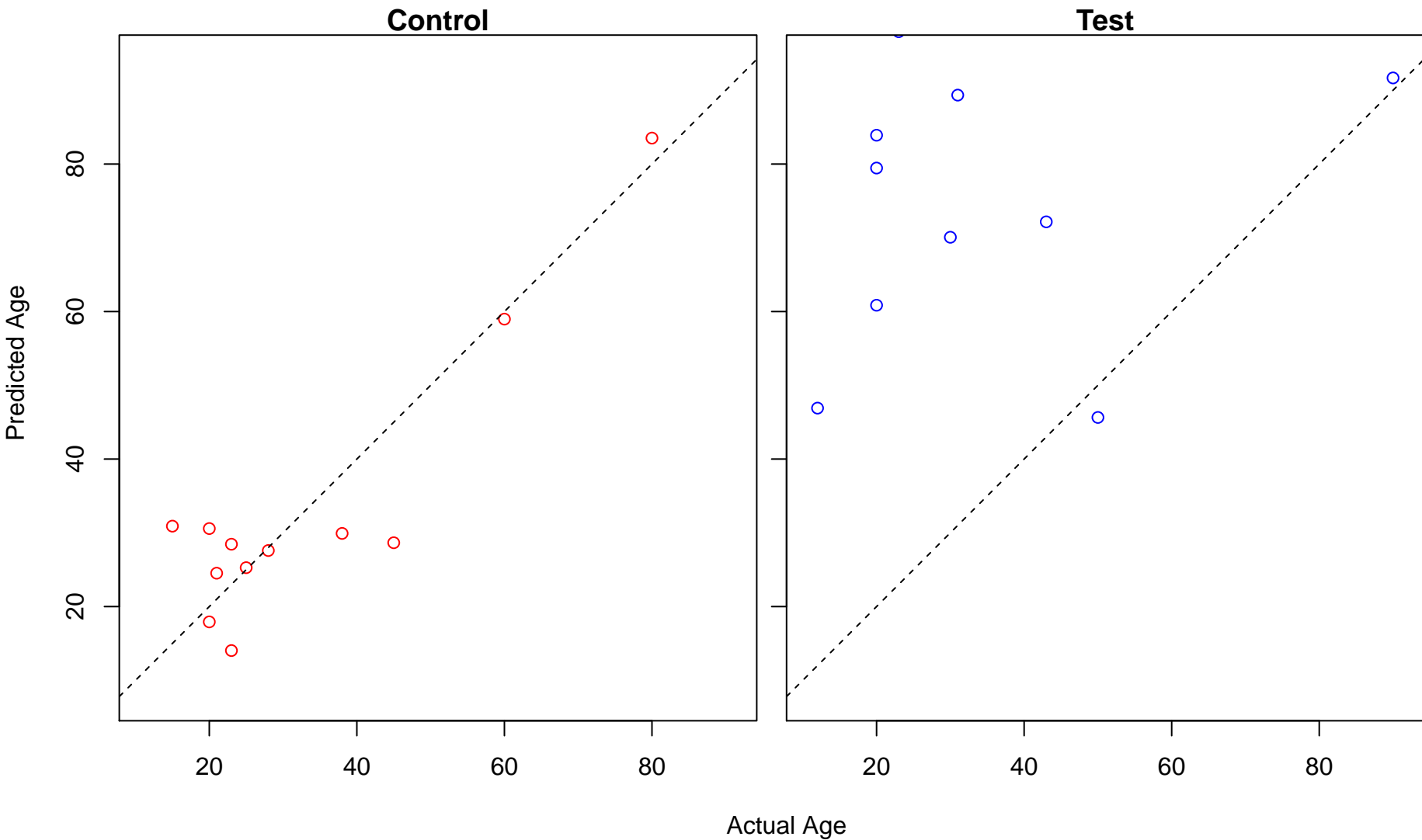
negative regulation of sprouting angiogenesis (Score: 23.013277)



face morphogenesis (Score: 22.928135)

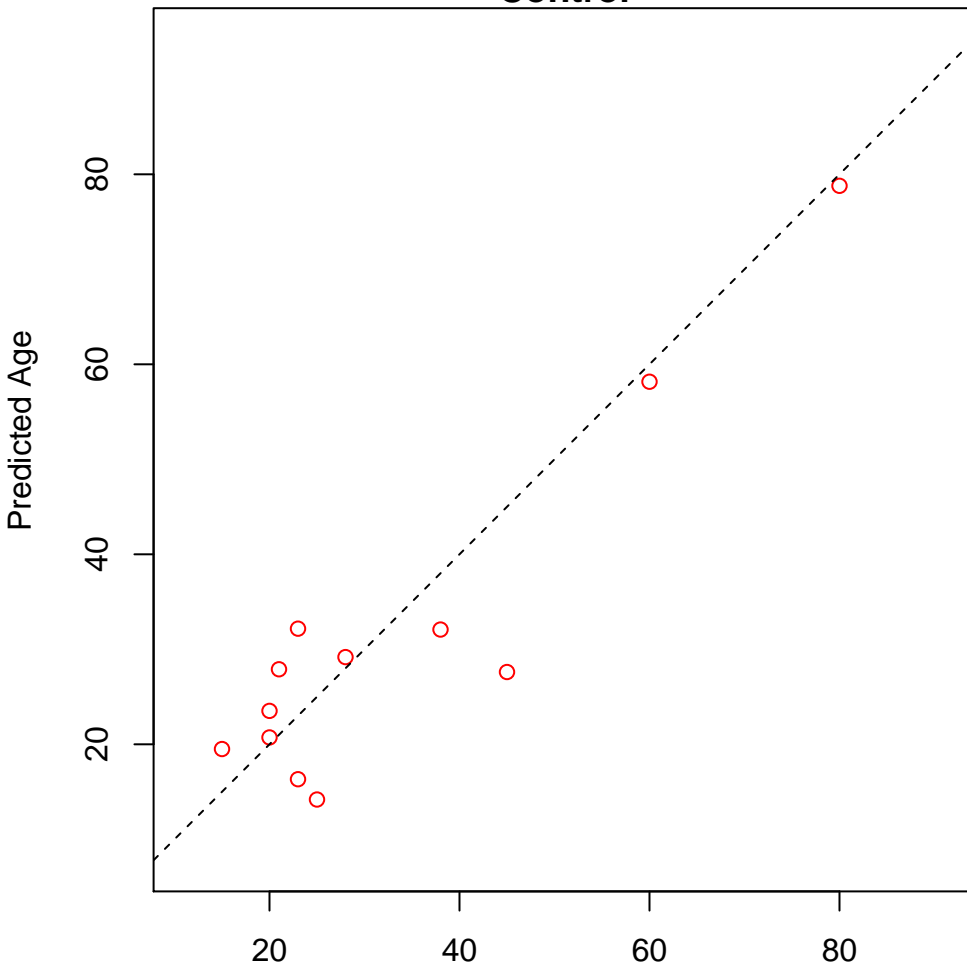


ventricular system development (Score: 22.906512)

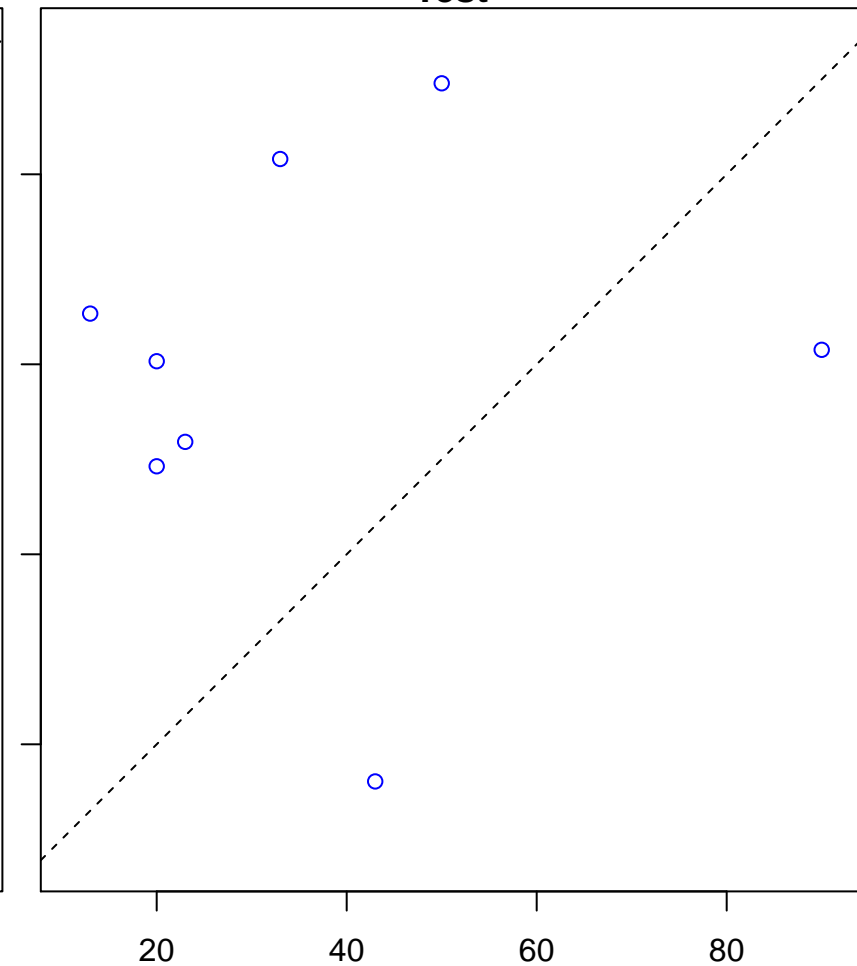


cellular response to hydrogen peroxide (Score: 22.857972)

Control

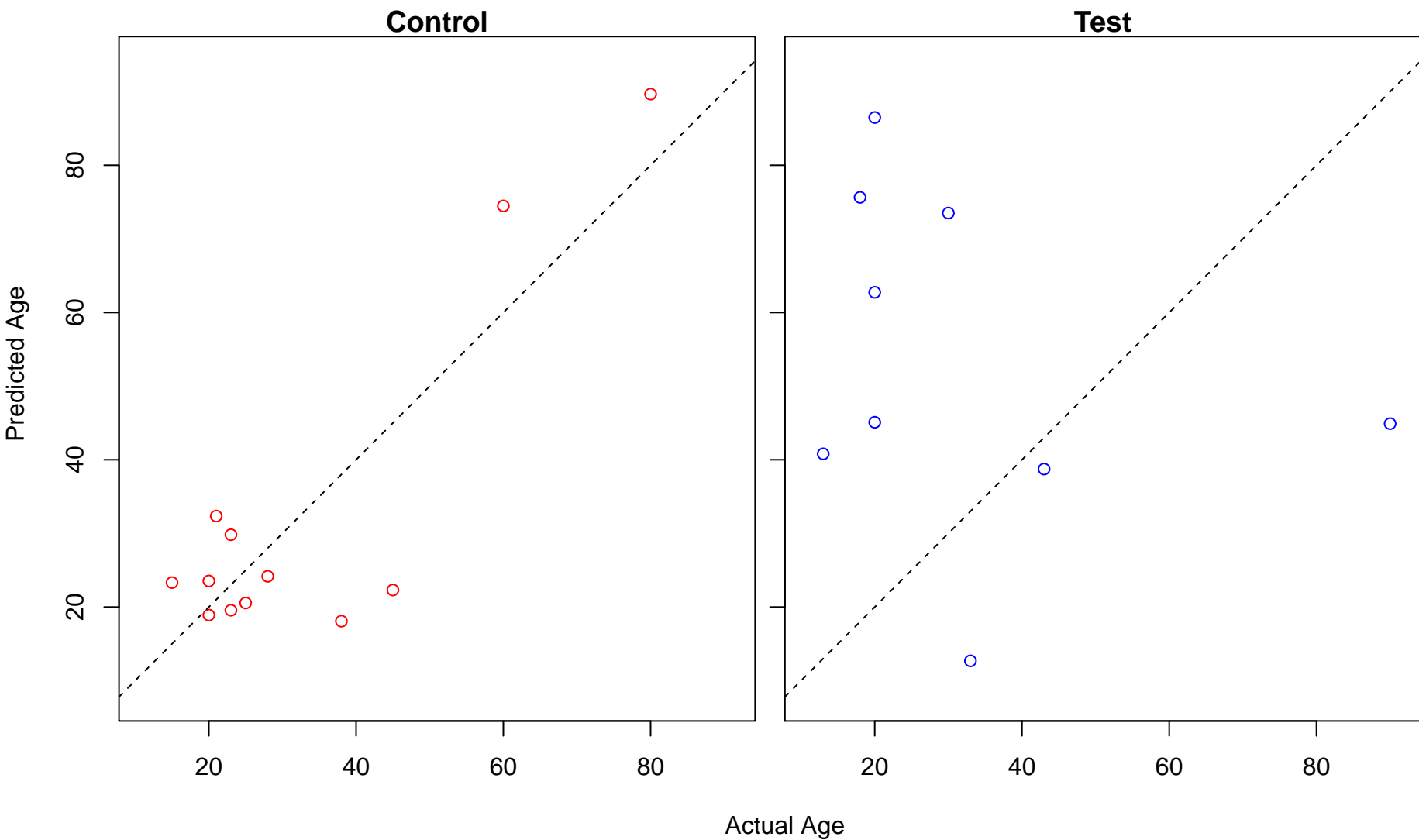


Test

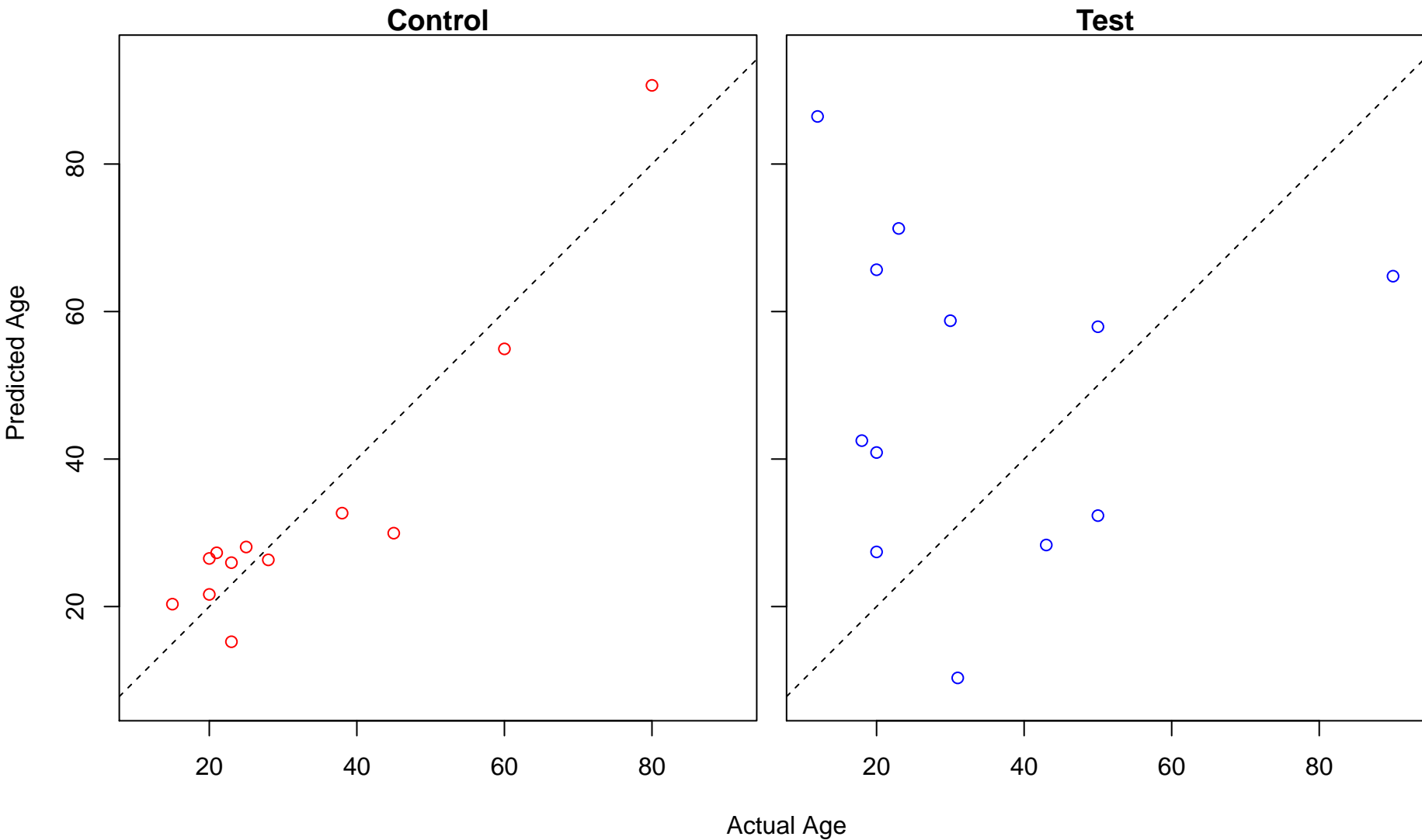


Actual Age

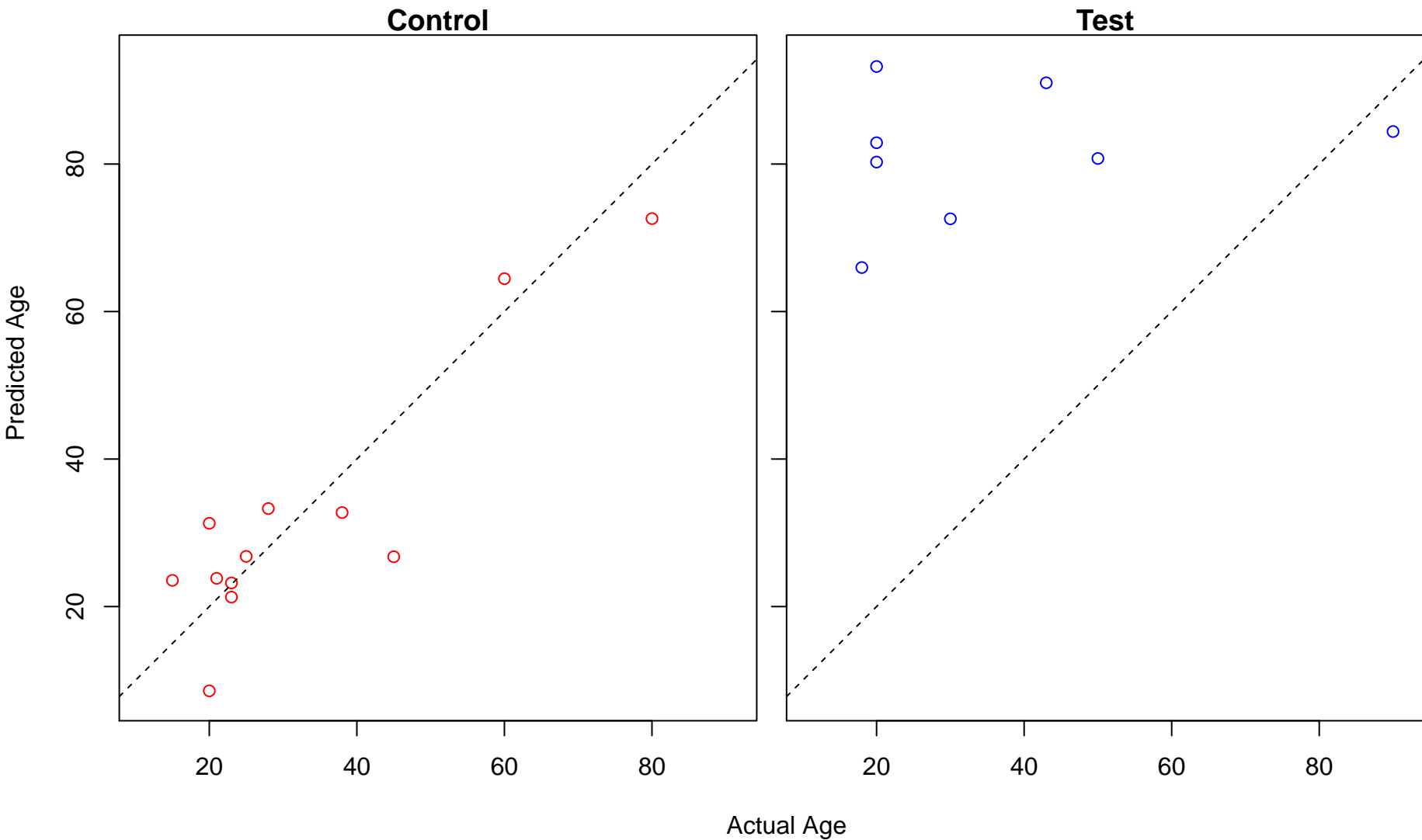
phosphatidylinositol dephosphorylation (Score: 22.851331)



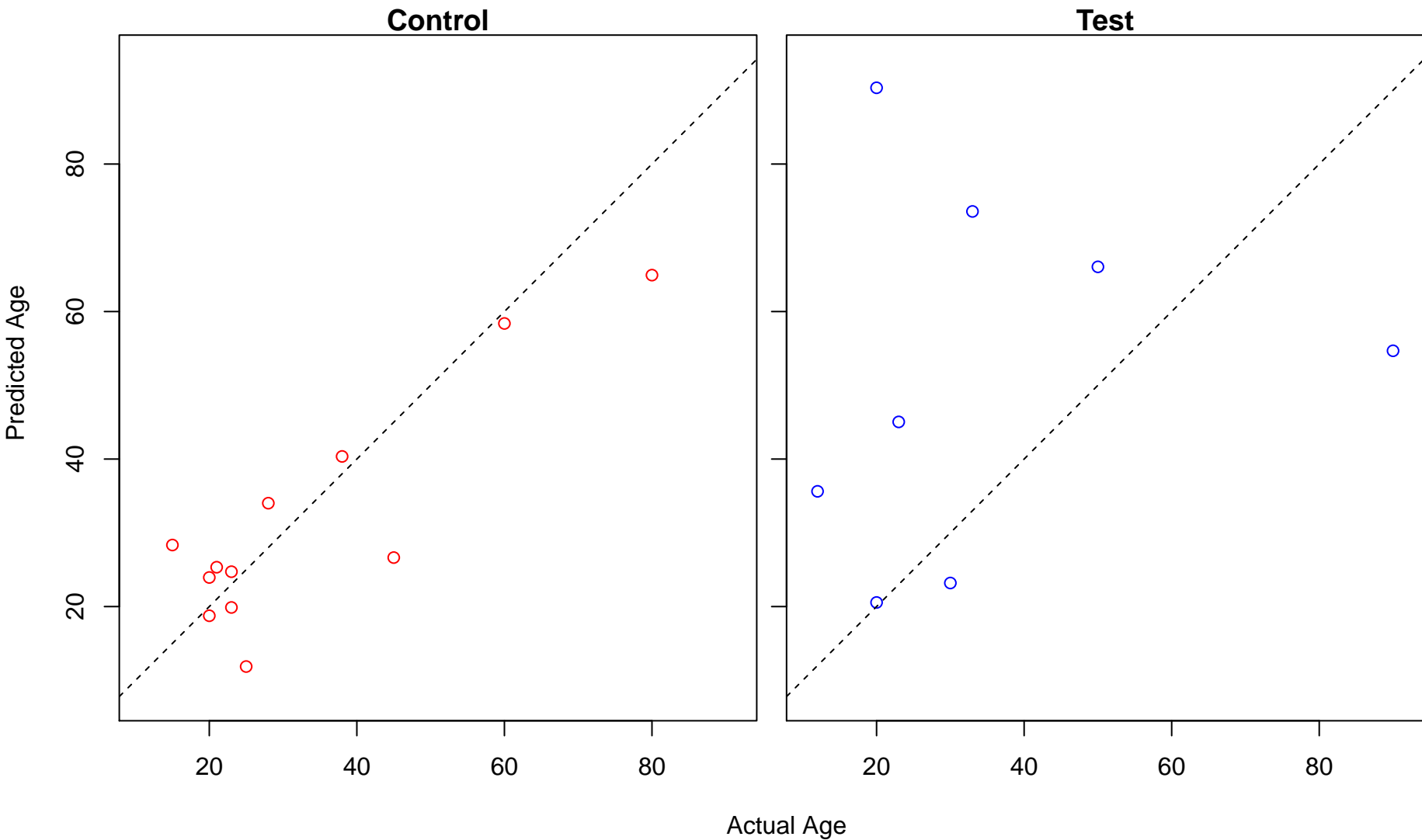
mitochondrial transport (Score: 22.843229)



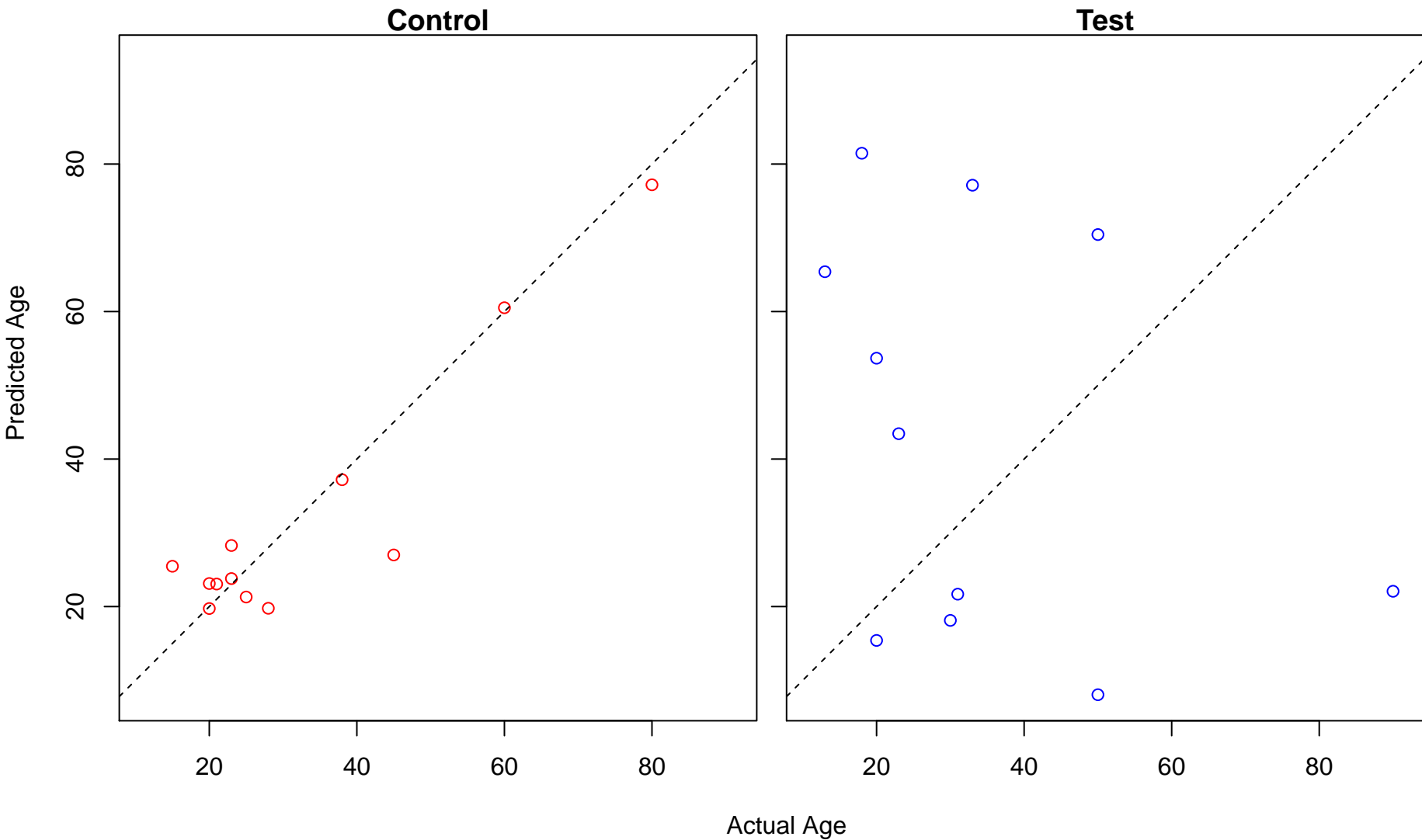
negative regulation of pathway-restricted SMAD protein phosphorylation (Score: 22.800900)



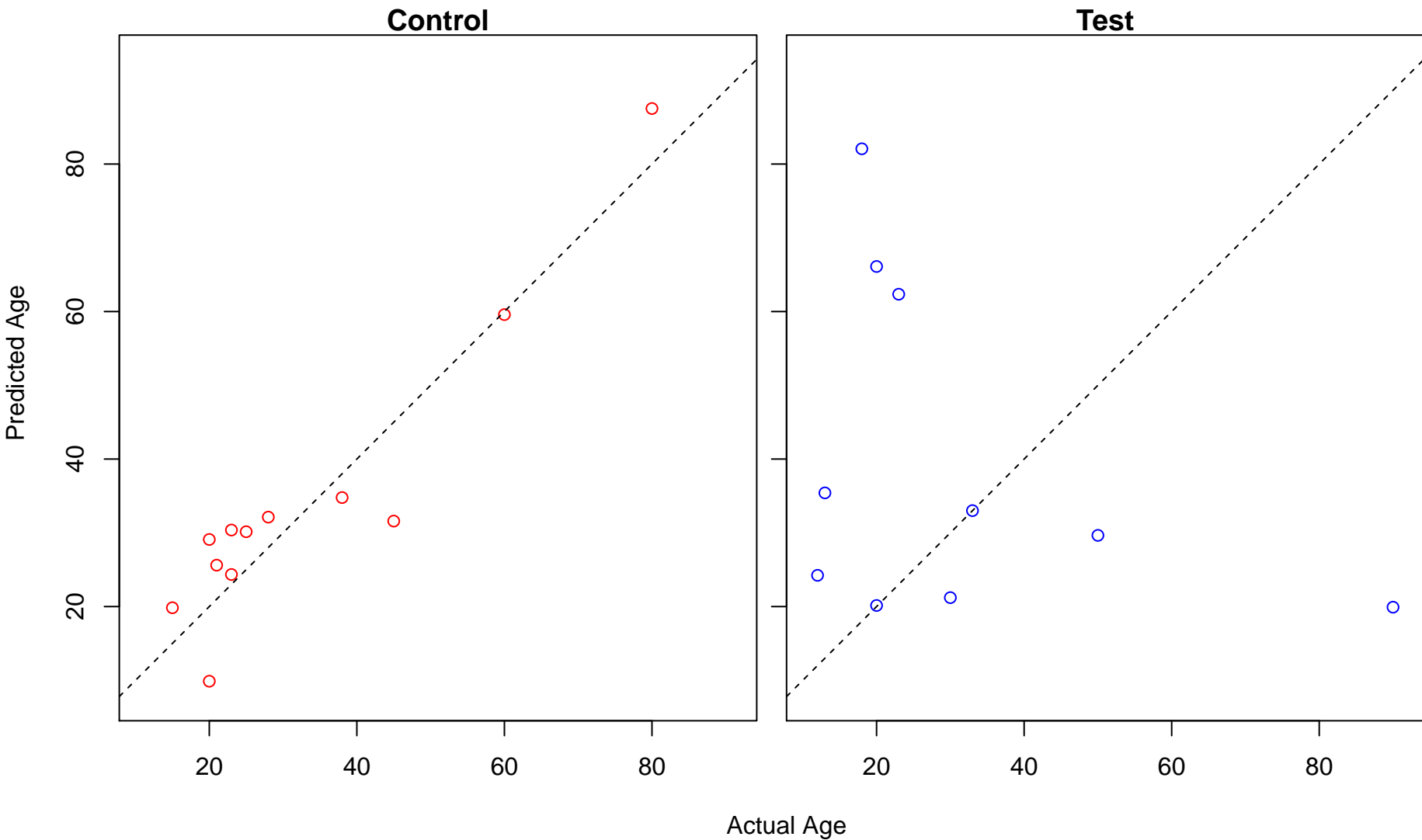
microtubule cytoskeleton organization involved in mitosis (Score: 22.792773)



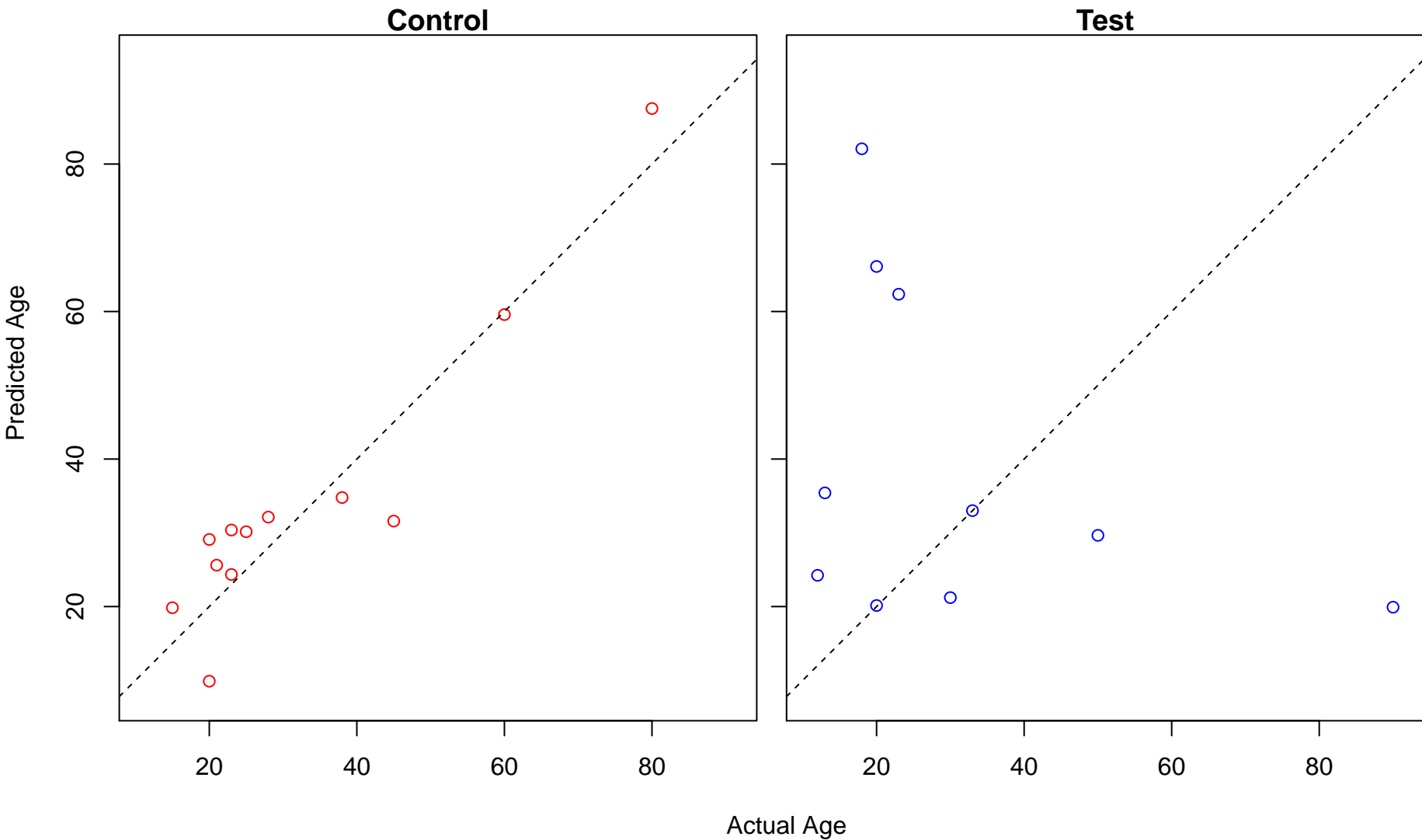
cellular calcium ion homeostasis (Score: 22.776341)



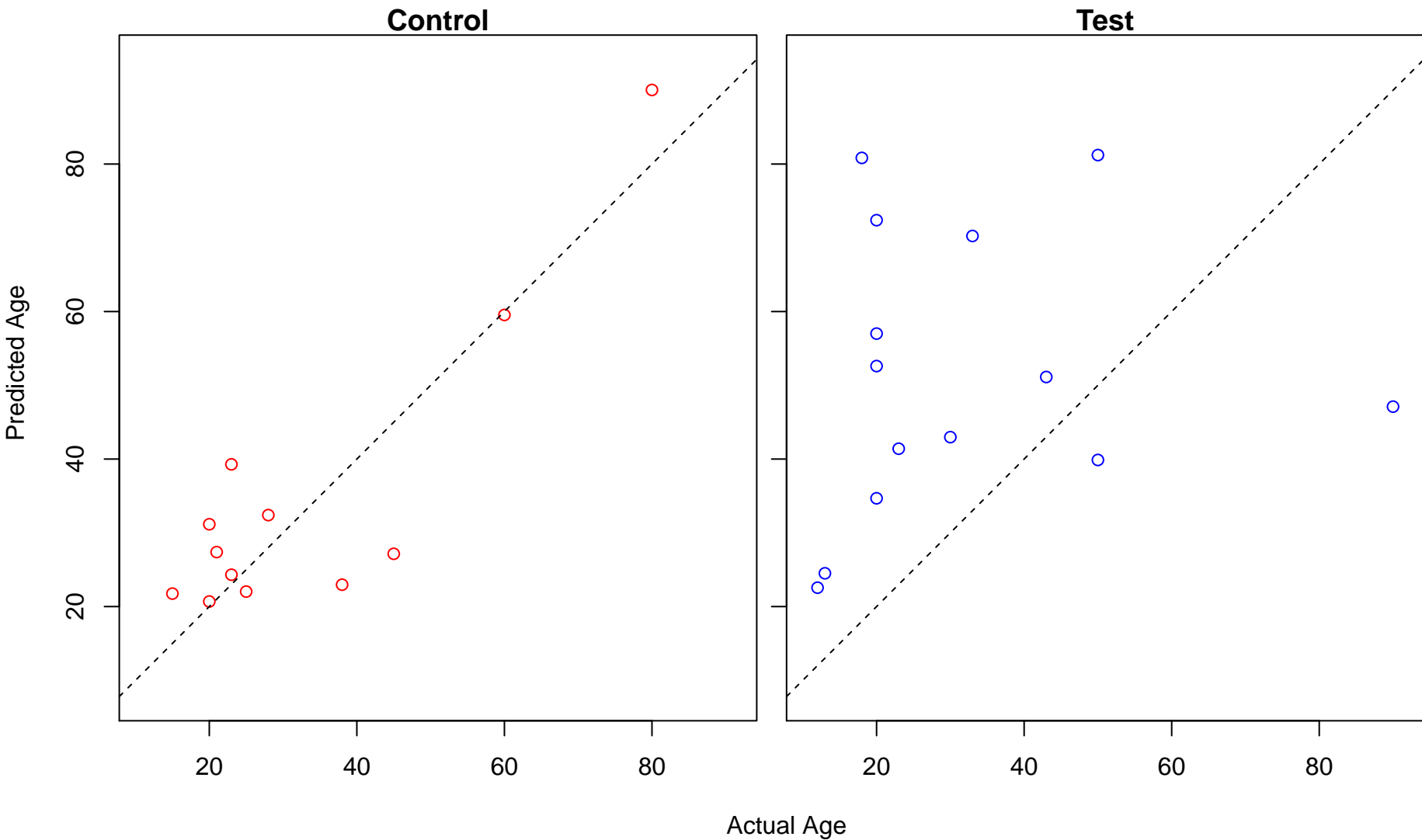
purine ribonucleoside triphosphate metabolic process (Score: 22.772646)



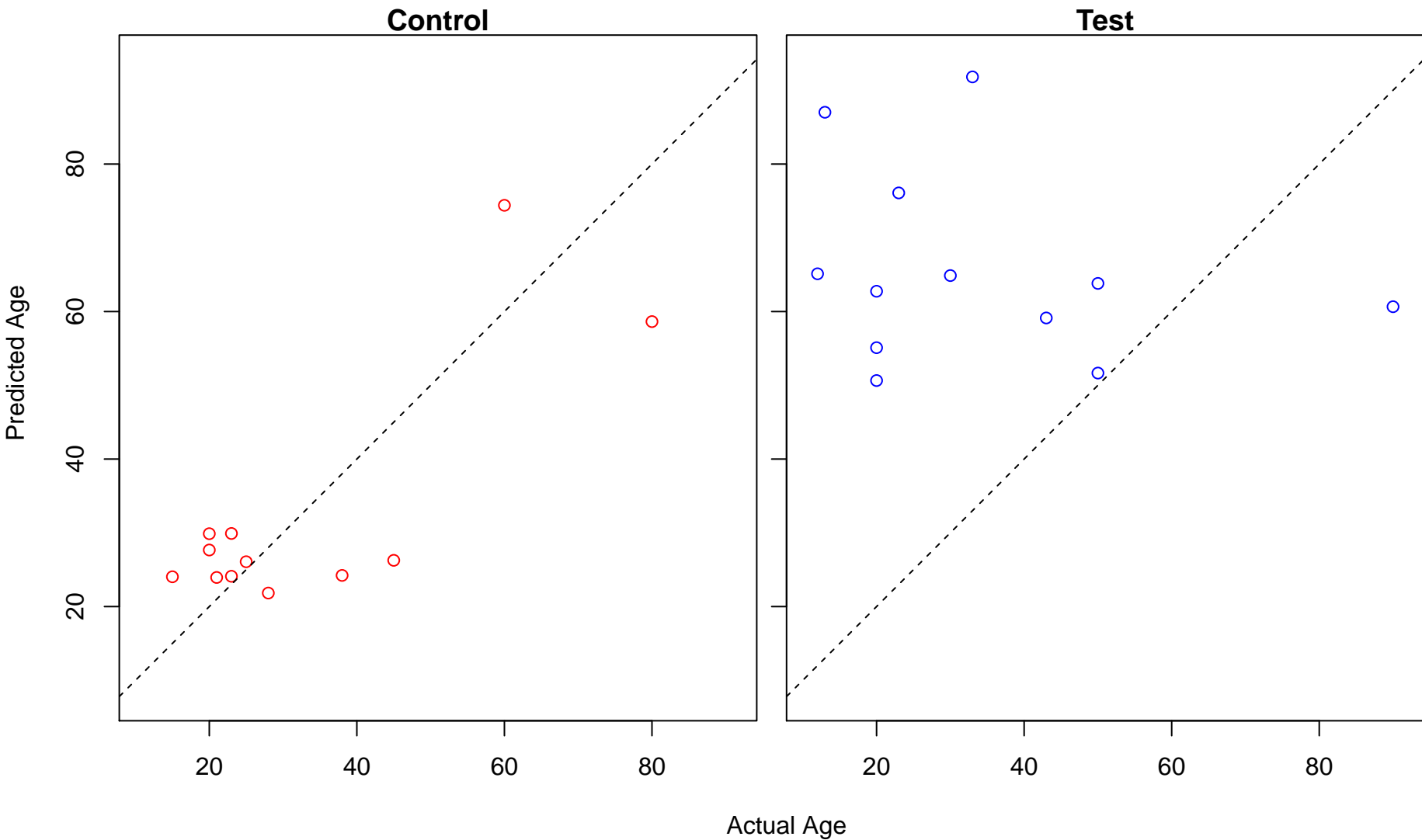
ribonucleoside triphosphate metabolic process (Score: 22.772492)



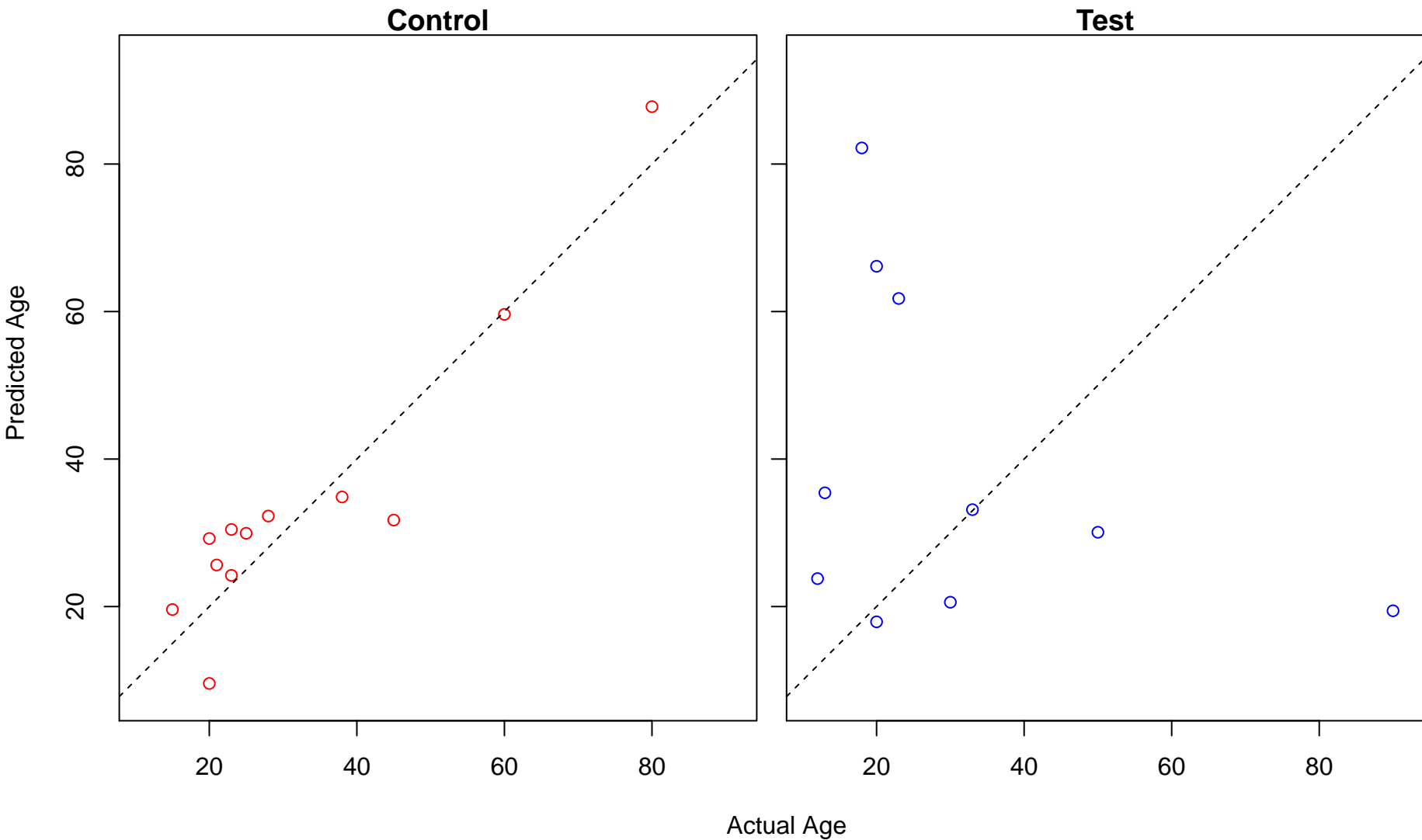
positive regulation of steroid metabolic process (Score: 22.751059)



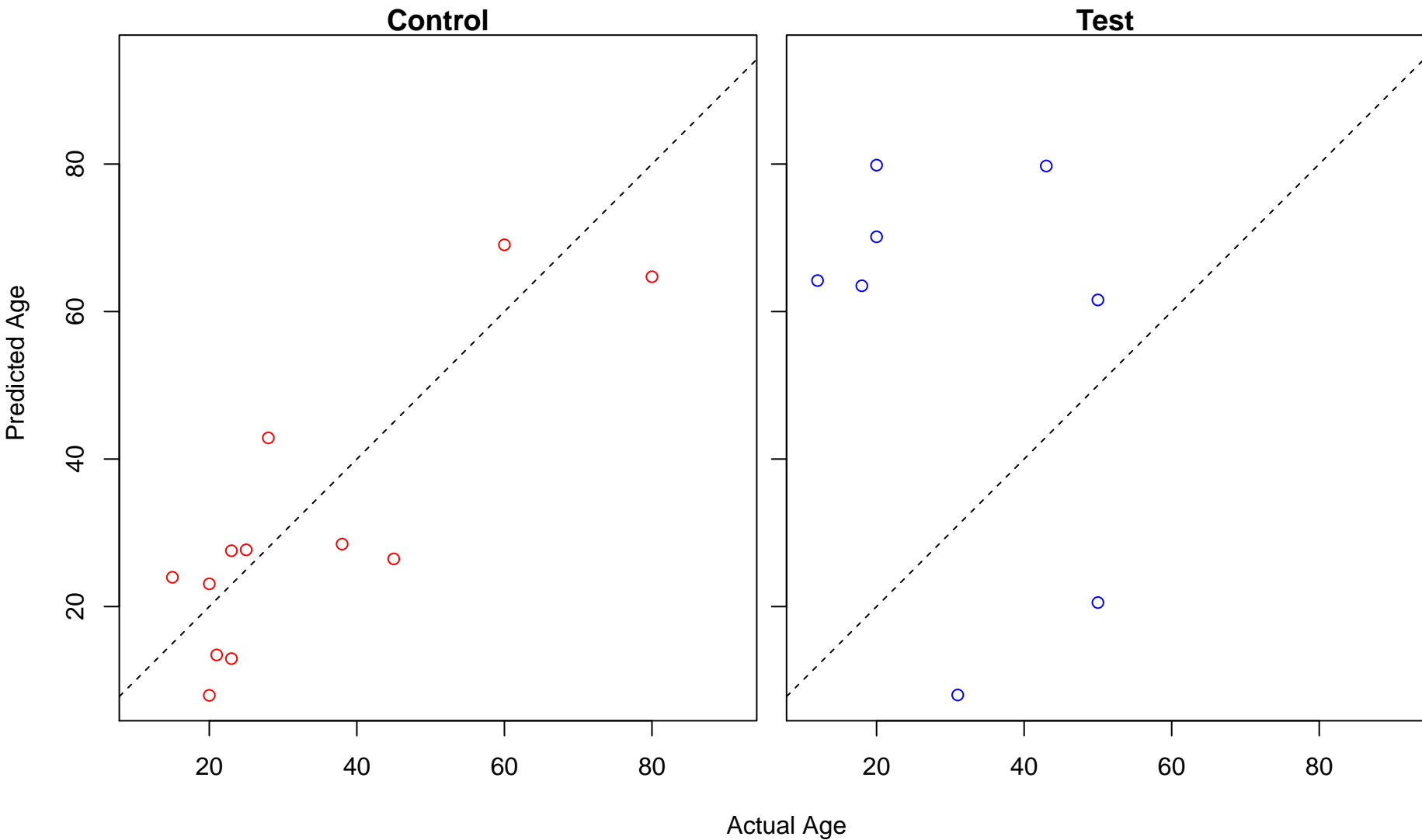
regulation of granulocyte macrophage colony-stimulating factor production (Score: 22.676928)



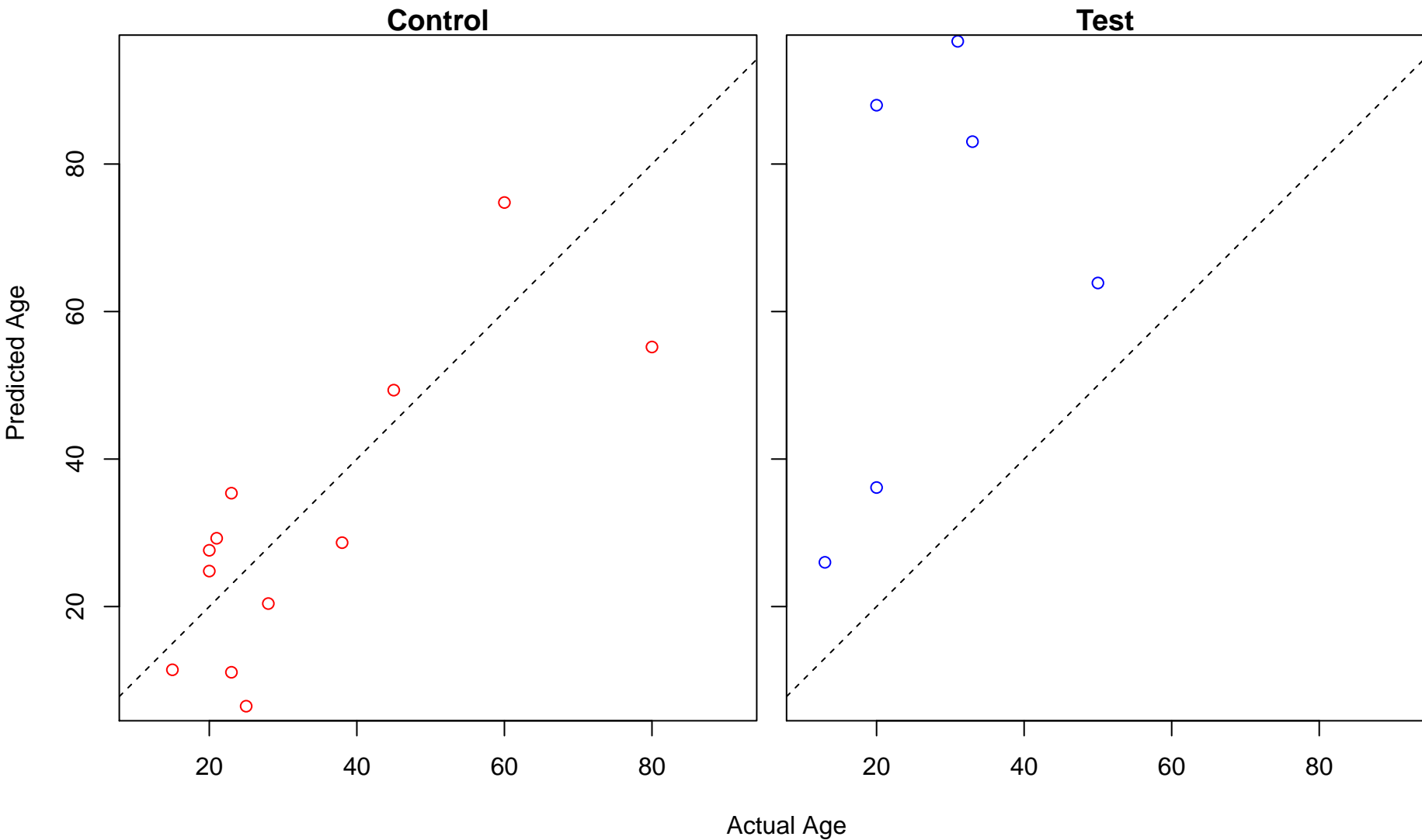
ATP metabolic process (Score: 22.670547)



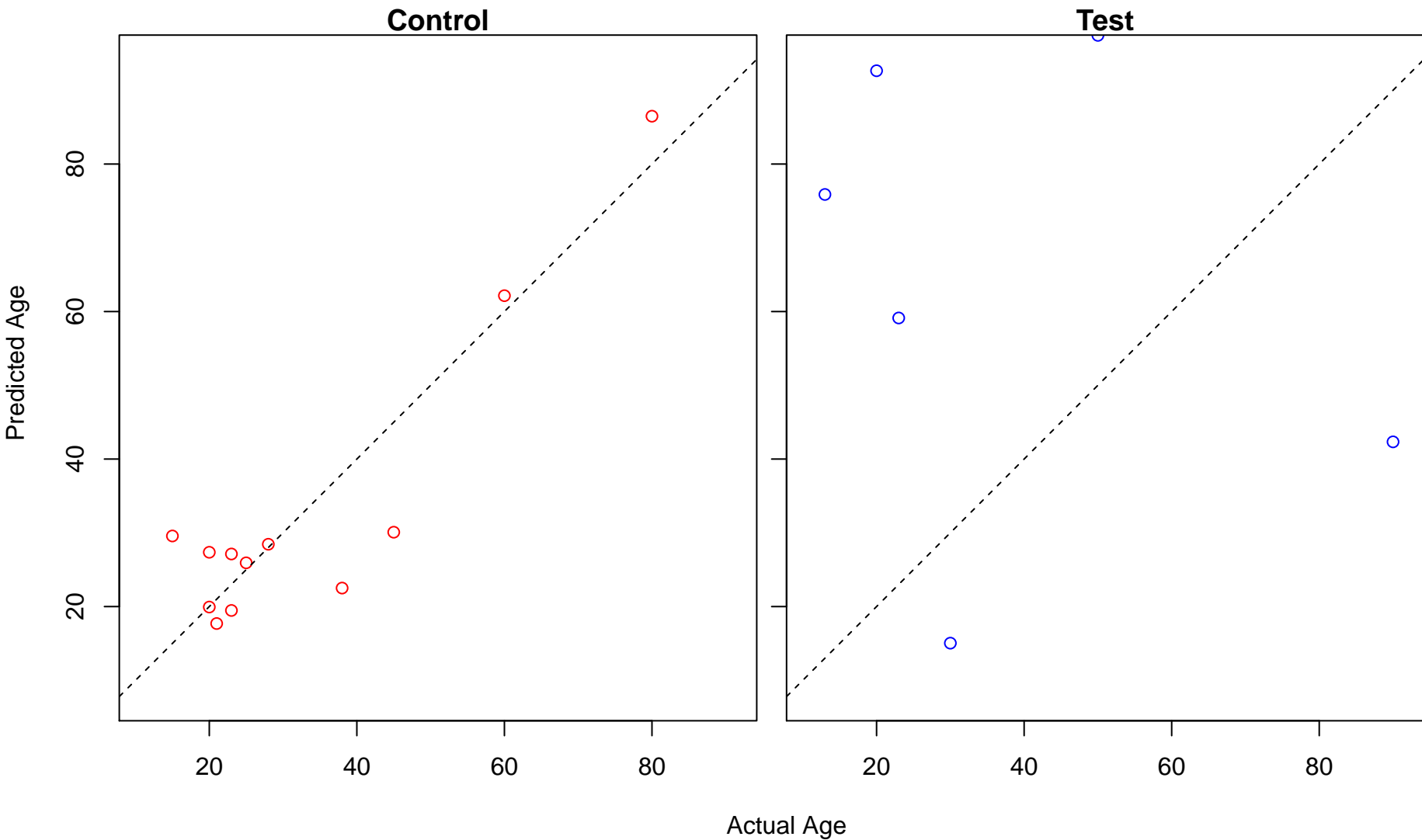
bone cell development (Score: 22.608539)



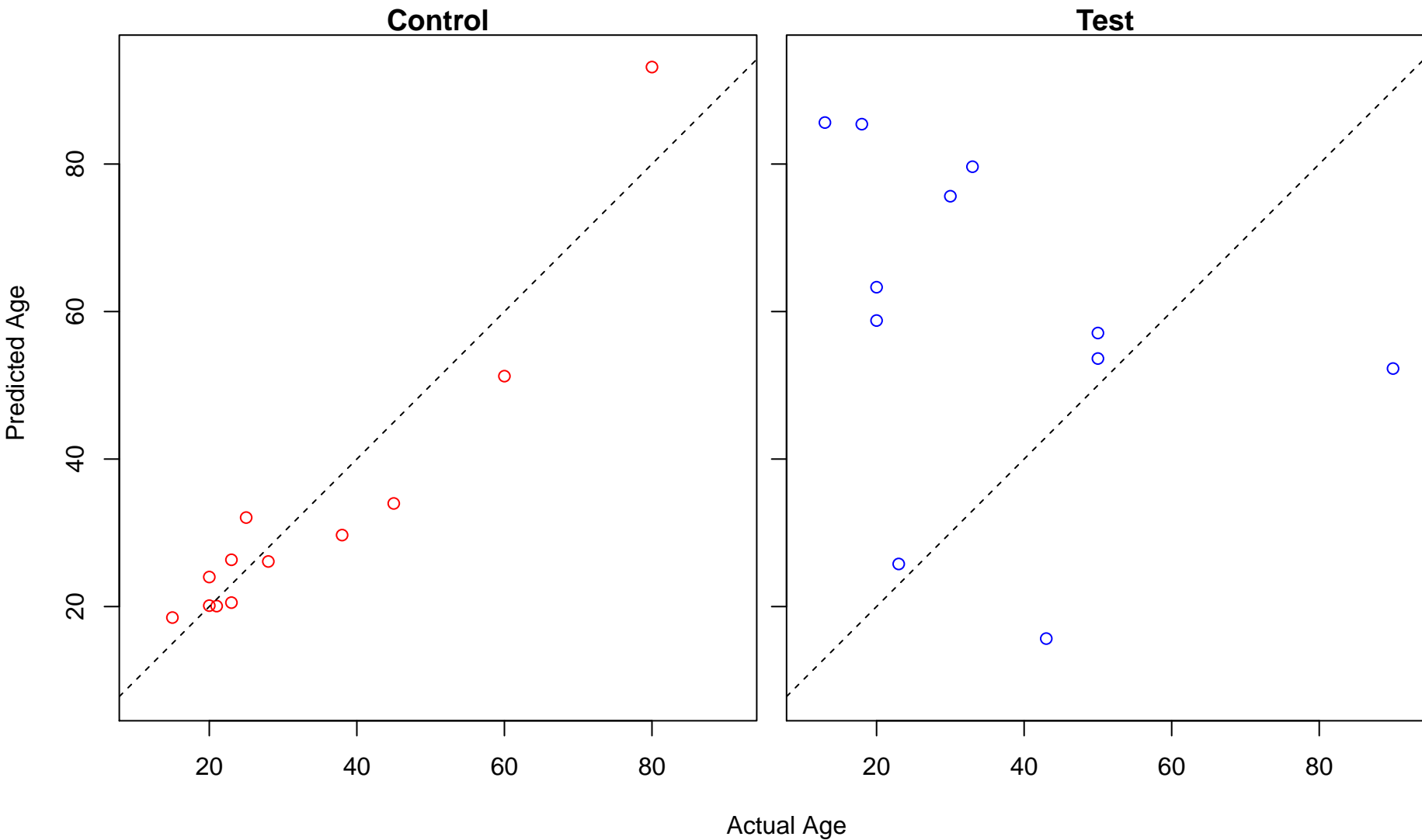
mRNA transcription from RNA polymerase II promoter (Score: 22.598200)



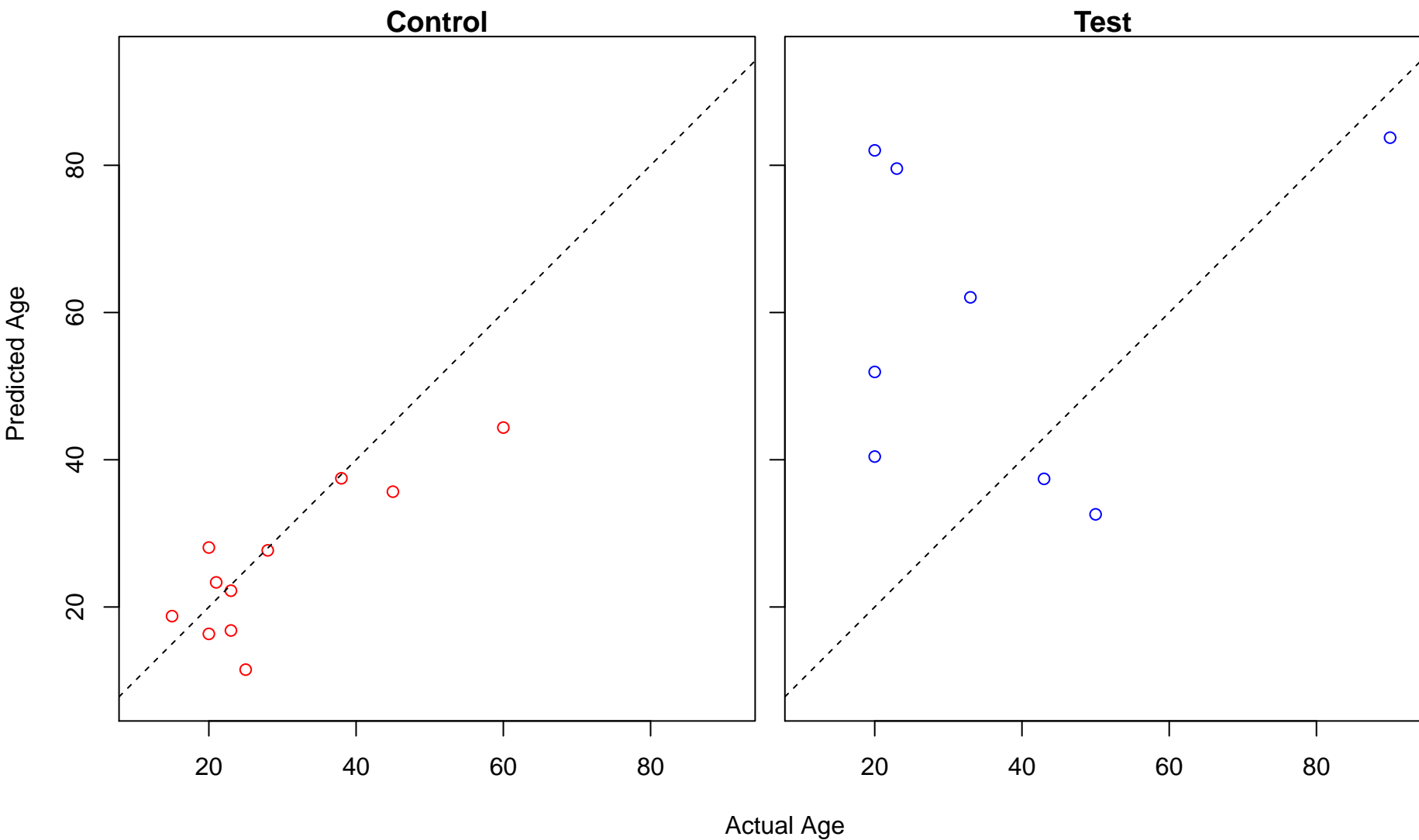
negative regulation of cell division (Score: 22.414099)



synapse assembly (Score: 22.406531)

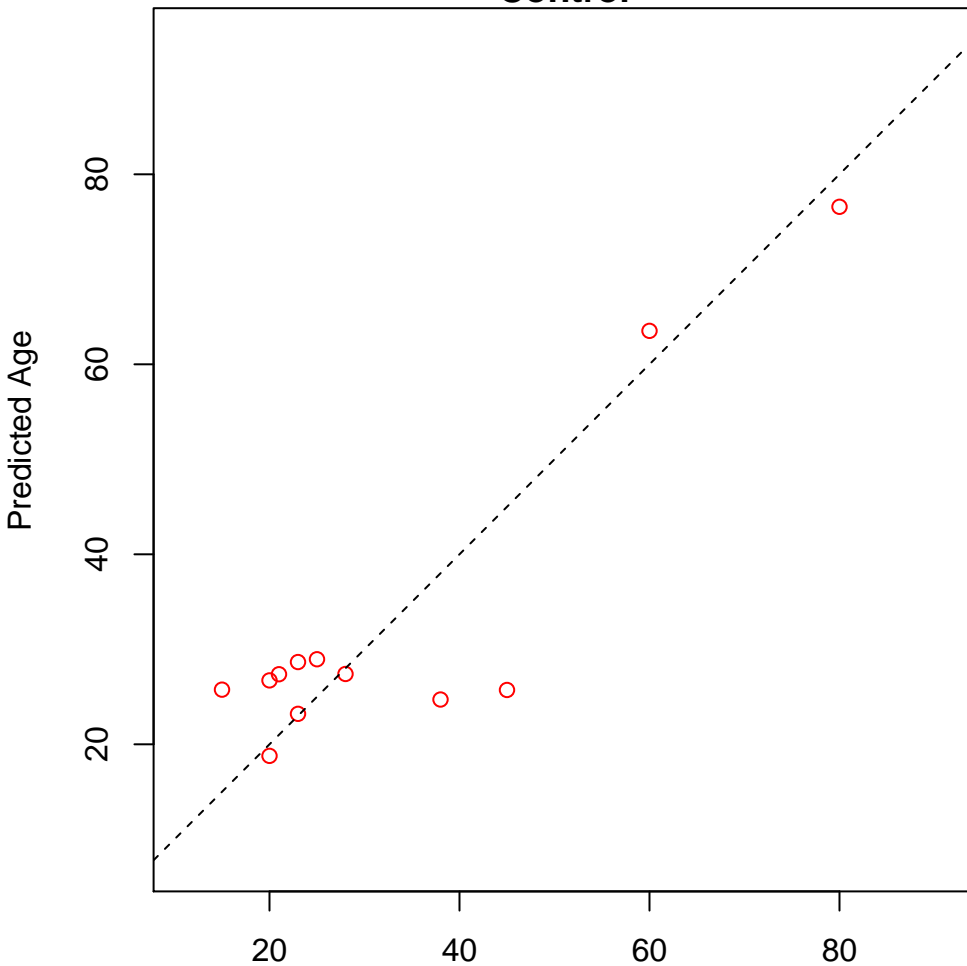


positive regulation of tyrosine phosphorylation of STAT protein (Score: 22.400157)

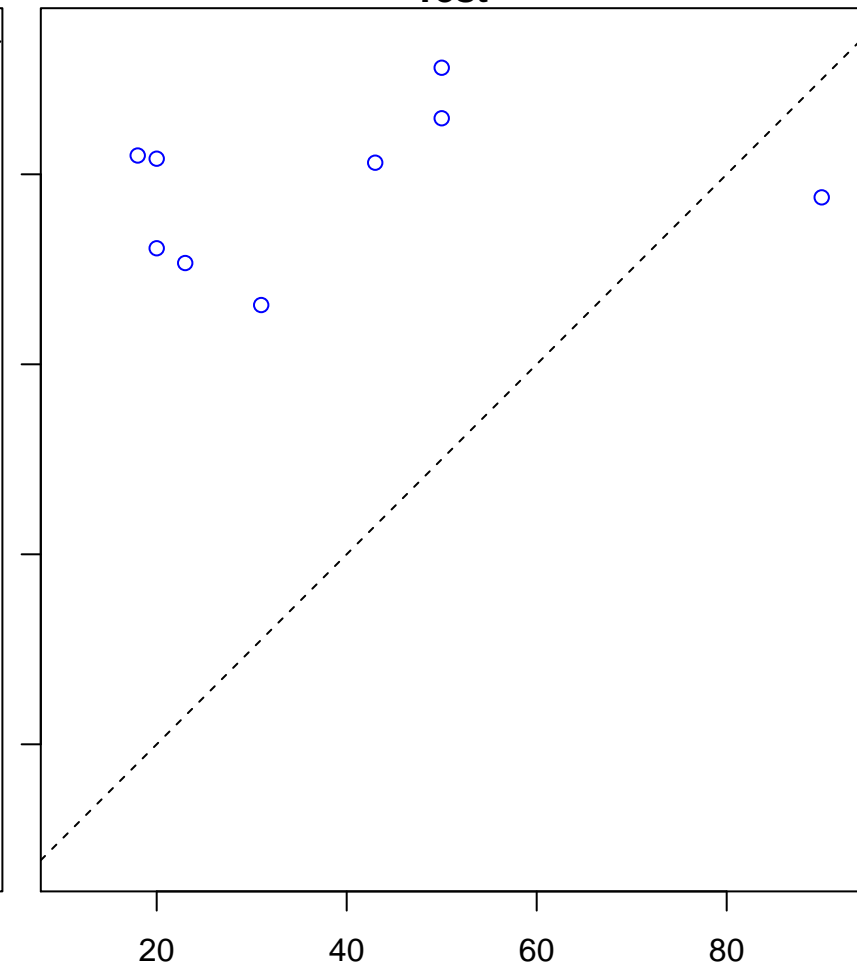


regulation of BMP signaling pathway (Score: 22.352318)

Control

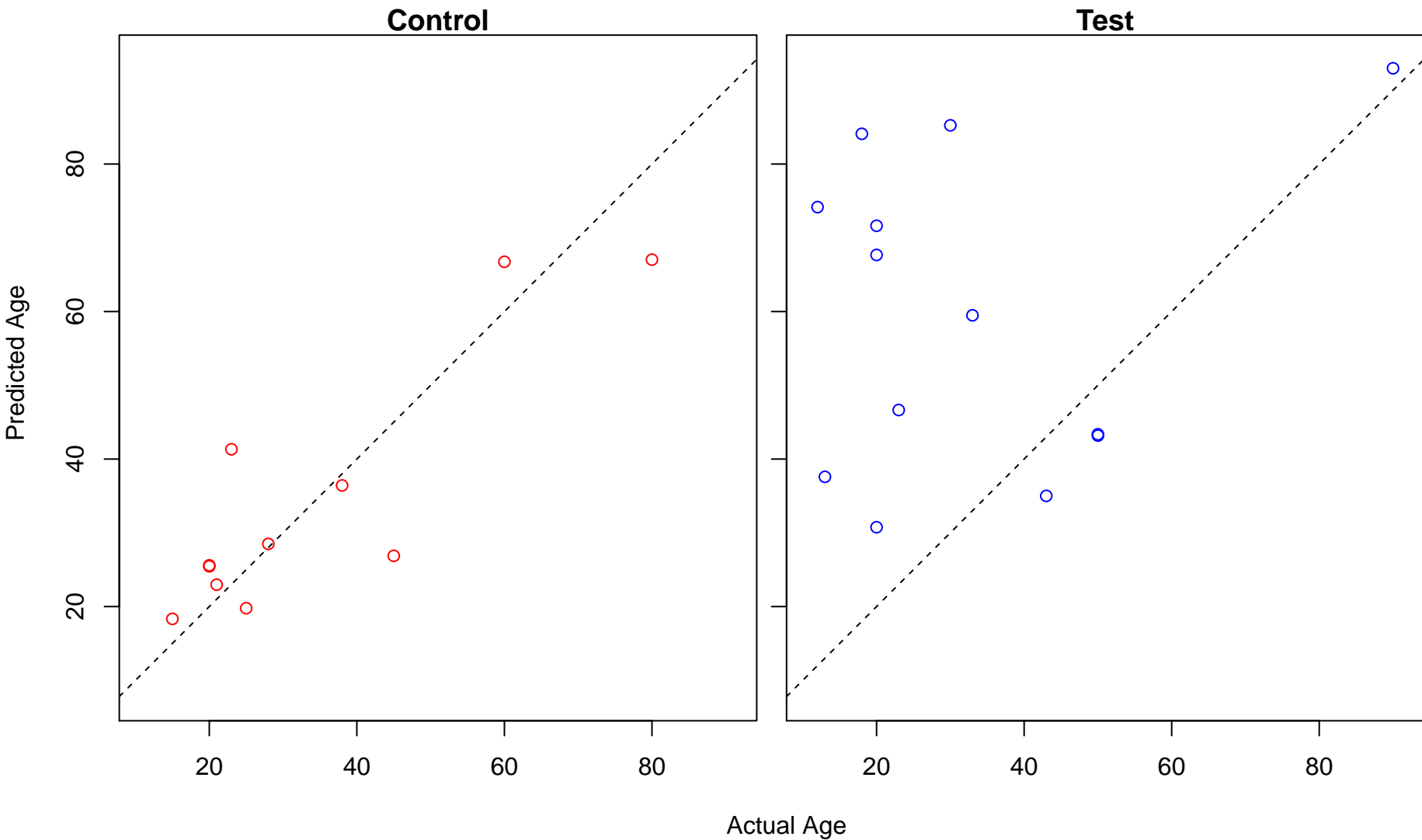


Test

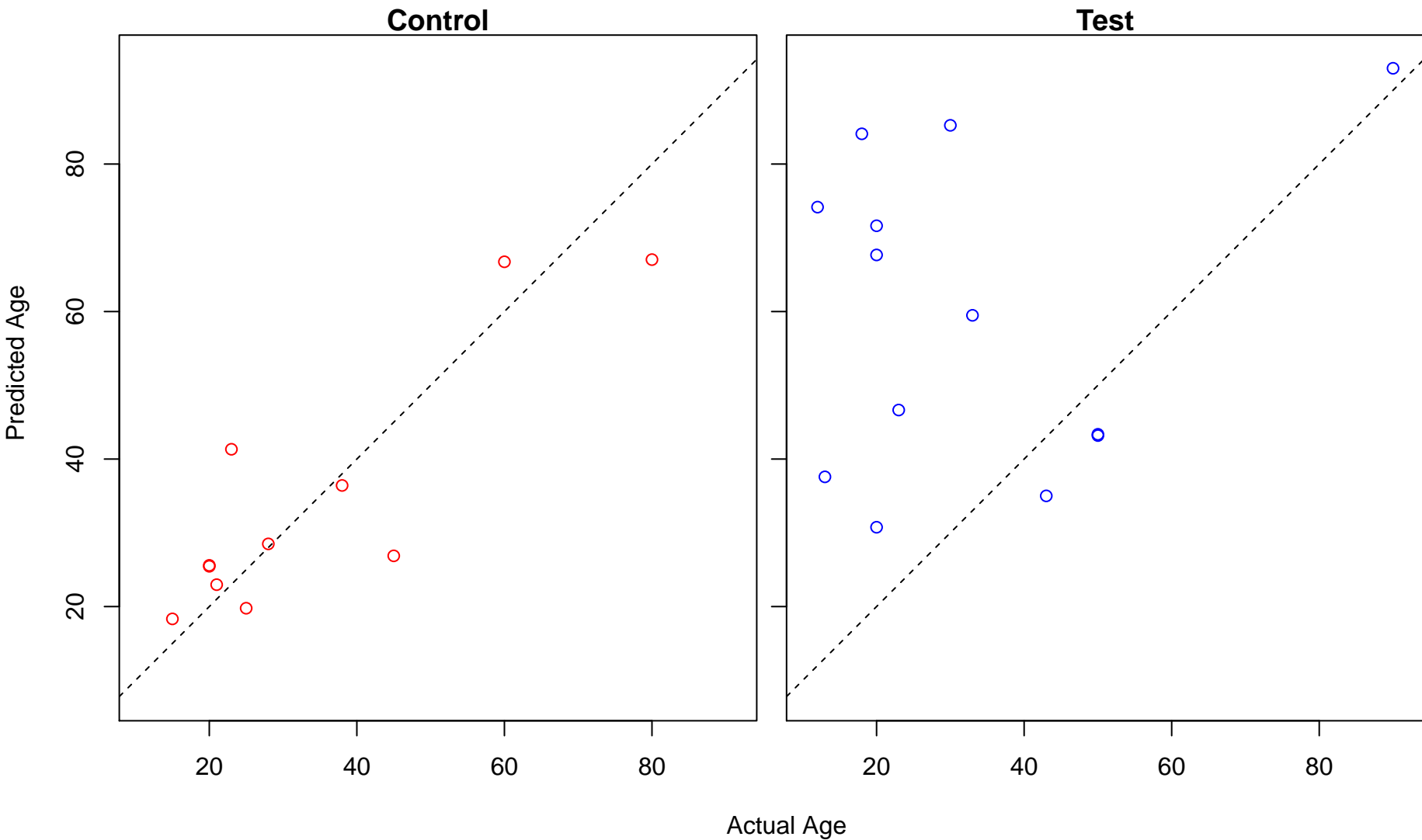


Actual Age

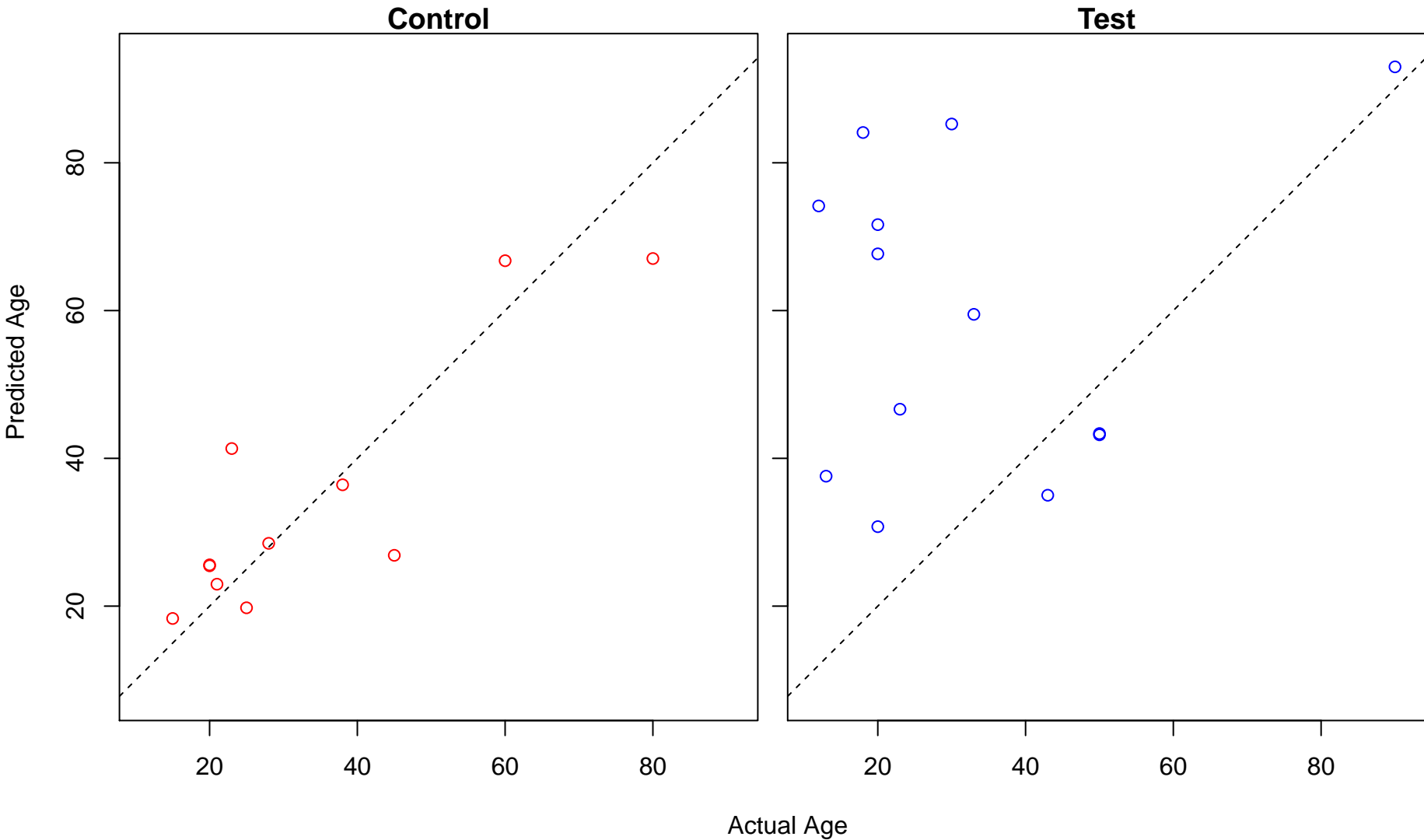
miRNA mediated inhibition of translation (Score: 22.348167)



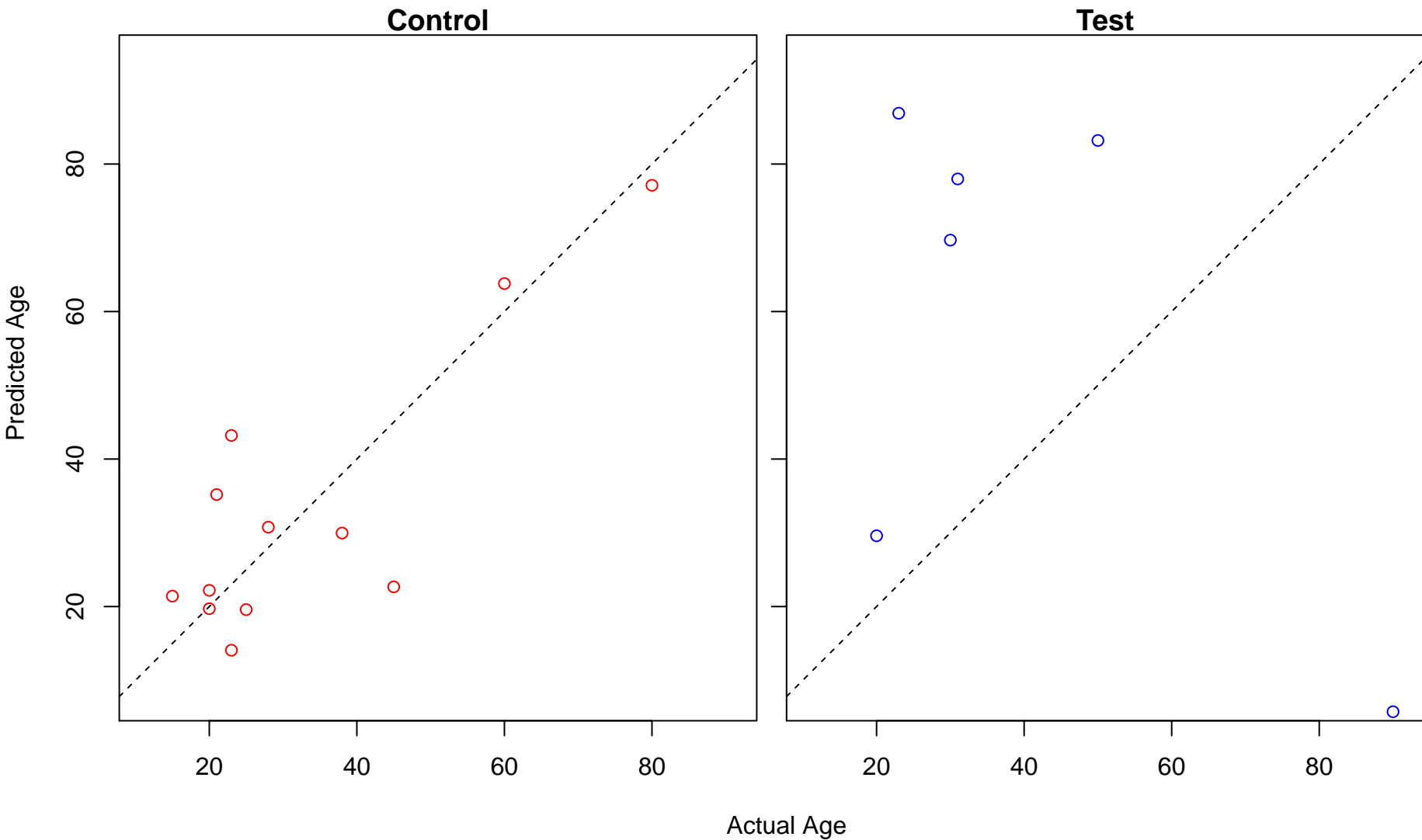
negative regulation of translation, ncRNA-mediated (Score: 22.348167)



regulation of translation, ncRNA-mediated (Score: 22.348167)

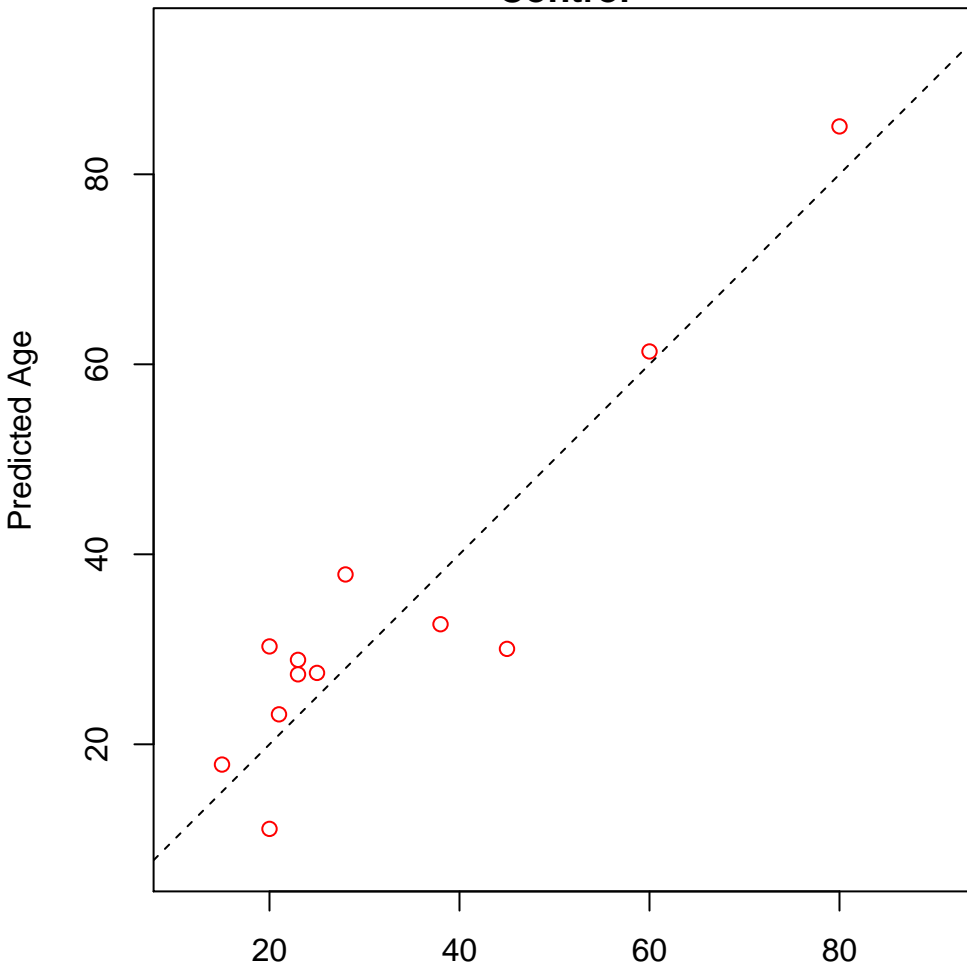


abscission (Score: 22.164366)

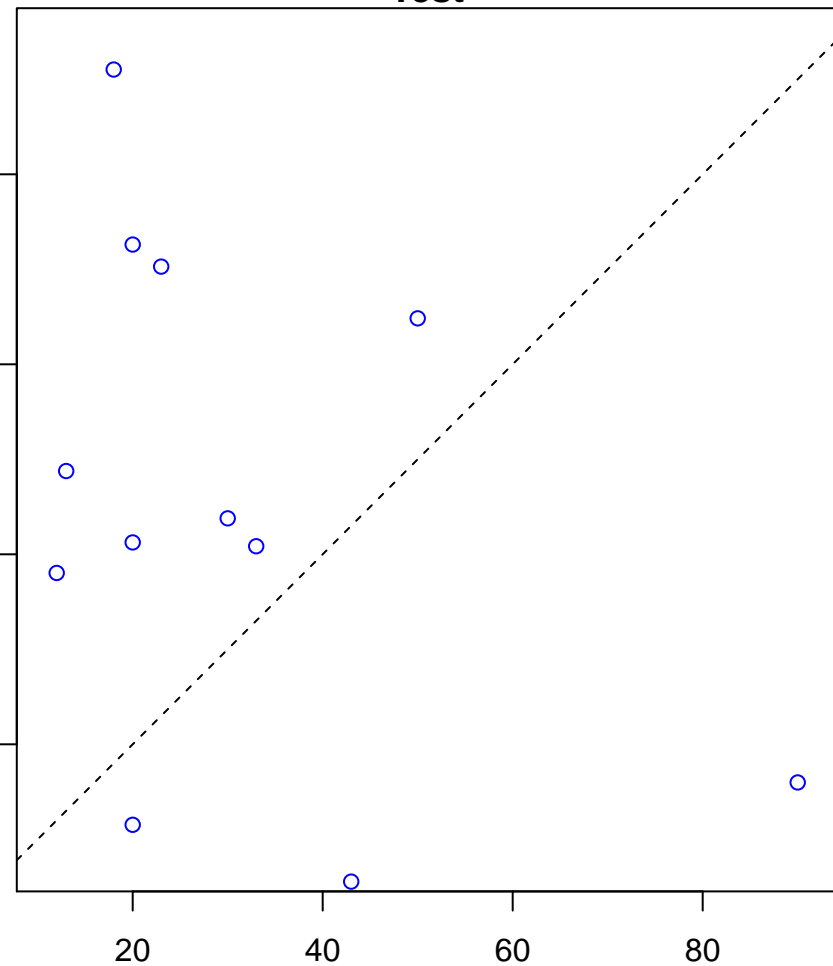


glycosyl compound metabolic process (Score: 22.111910)

Control

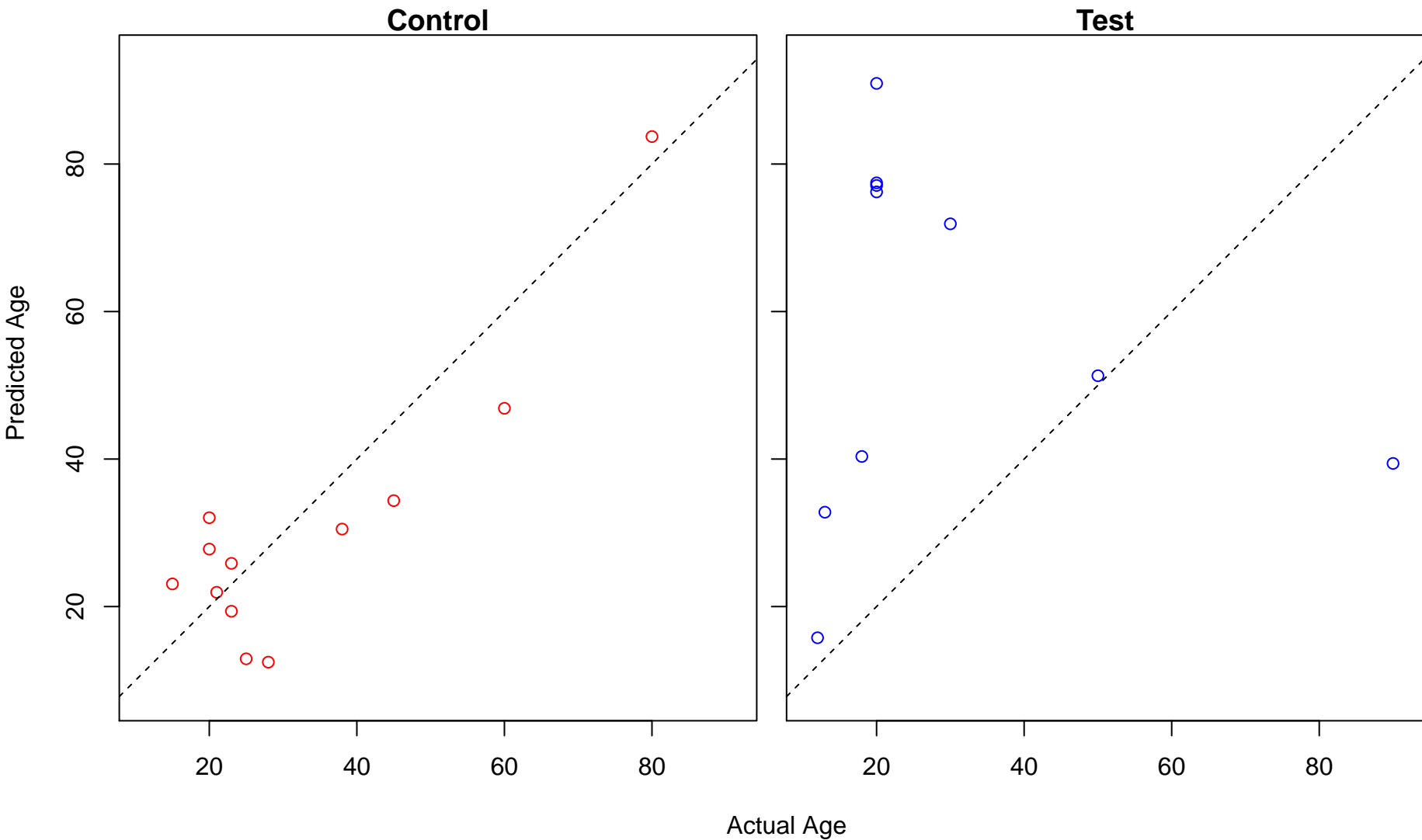


Test

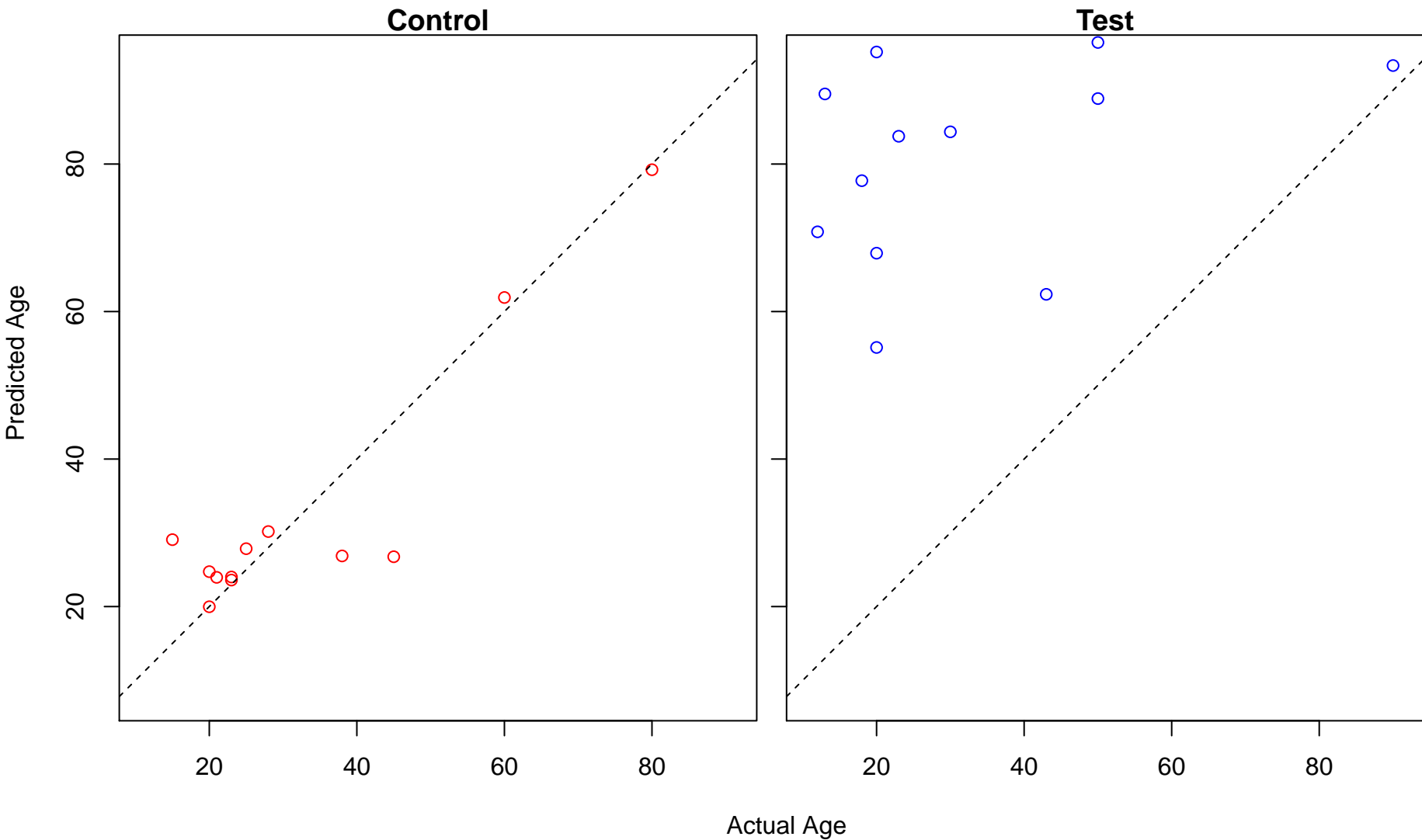


Actual Age

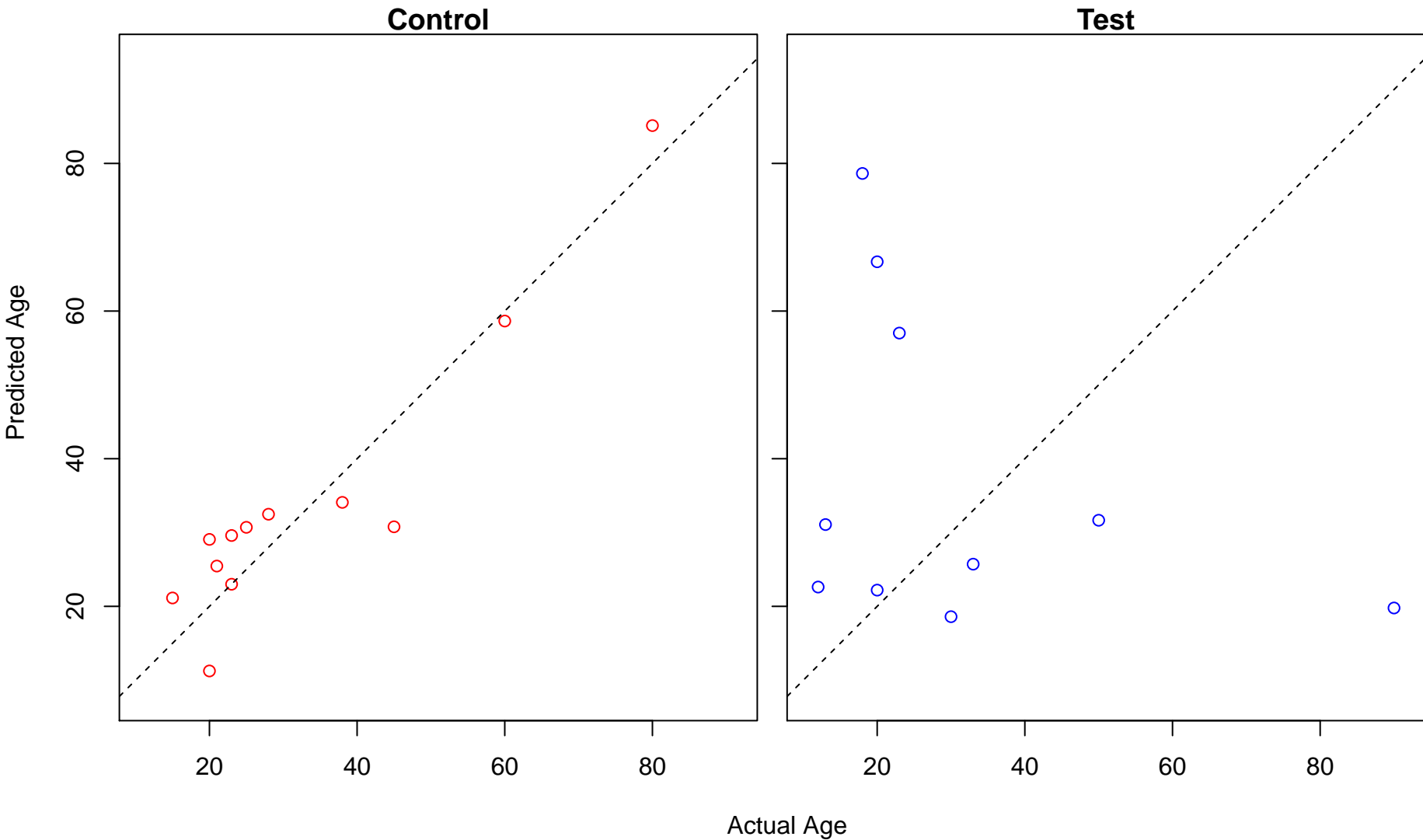
membrane depolarization during action potential (Score: 22.099985)



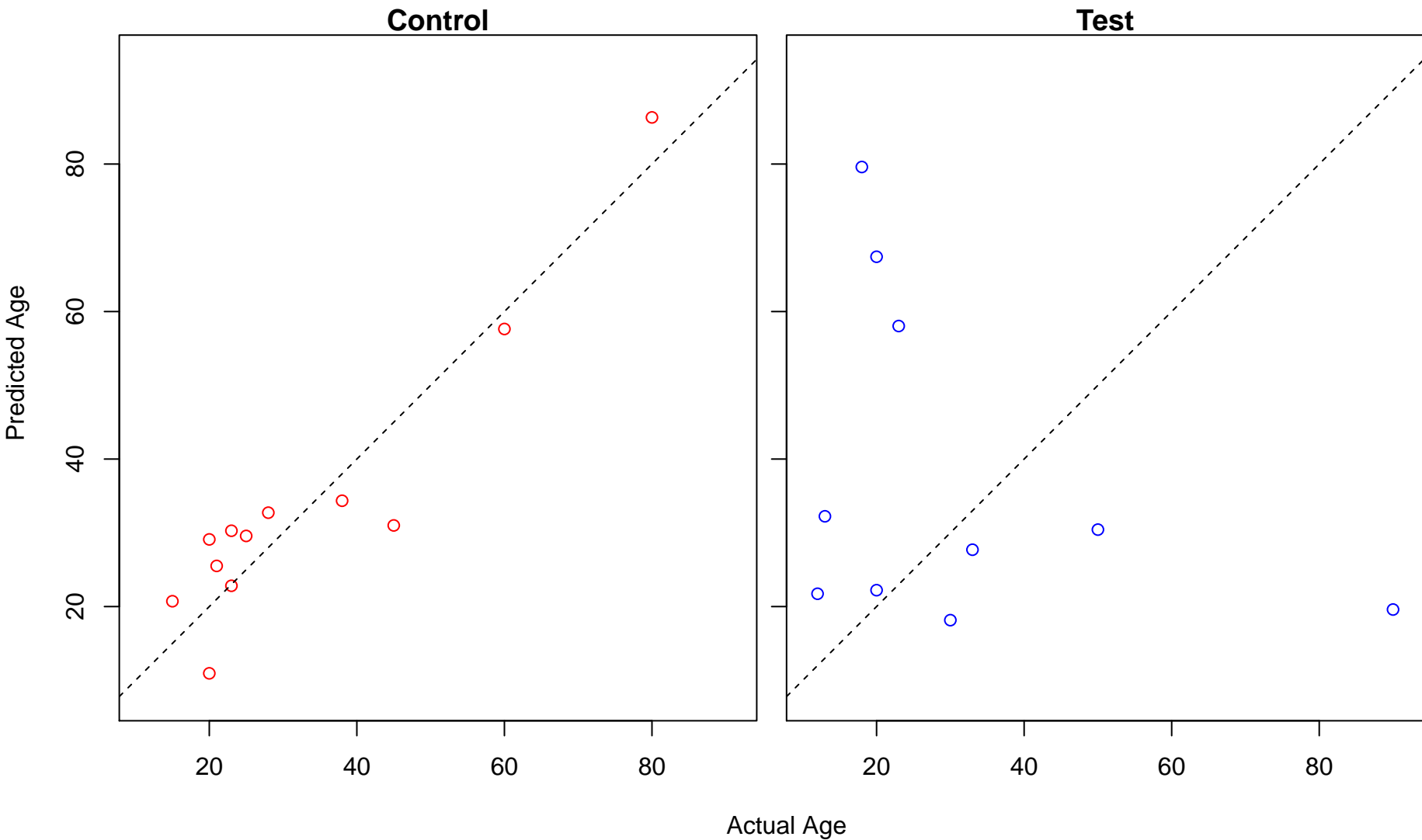
interleukin-4-mediated signaling pathway (Score: 22.008950)



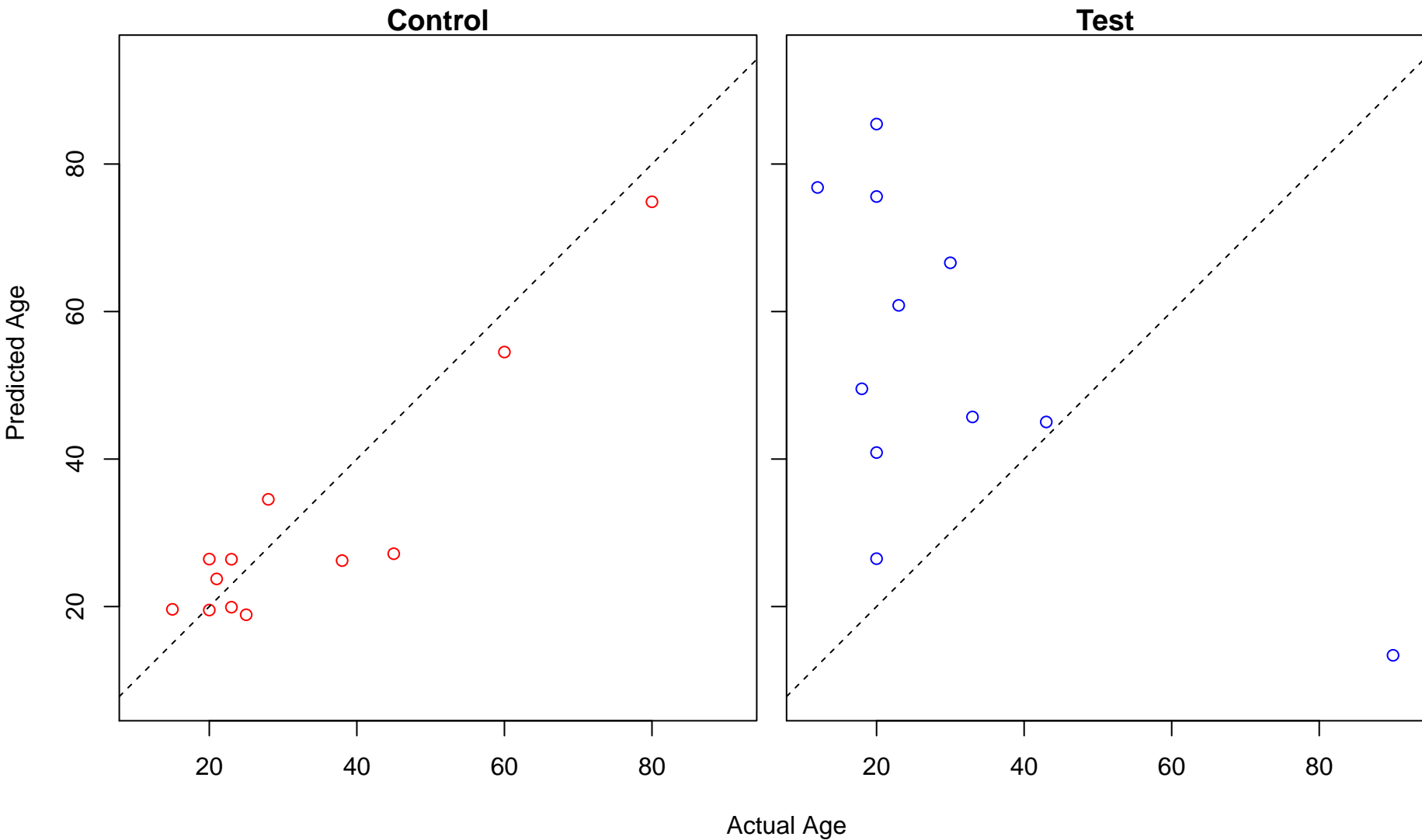
nucleoside triphosphate metabolic process (Score: 21.991303)



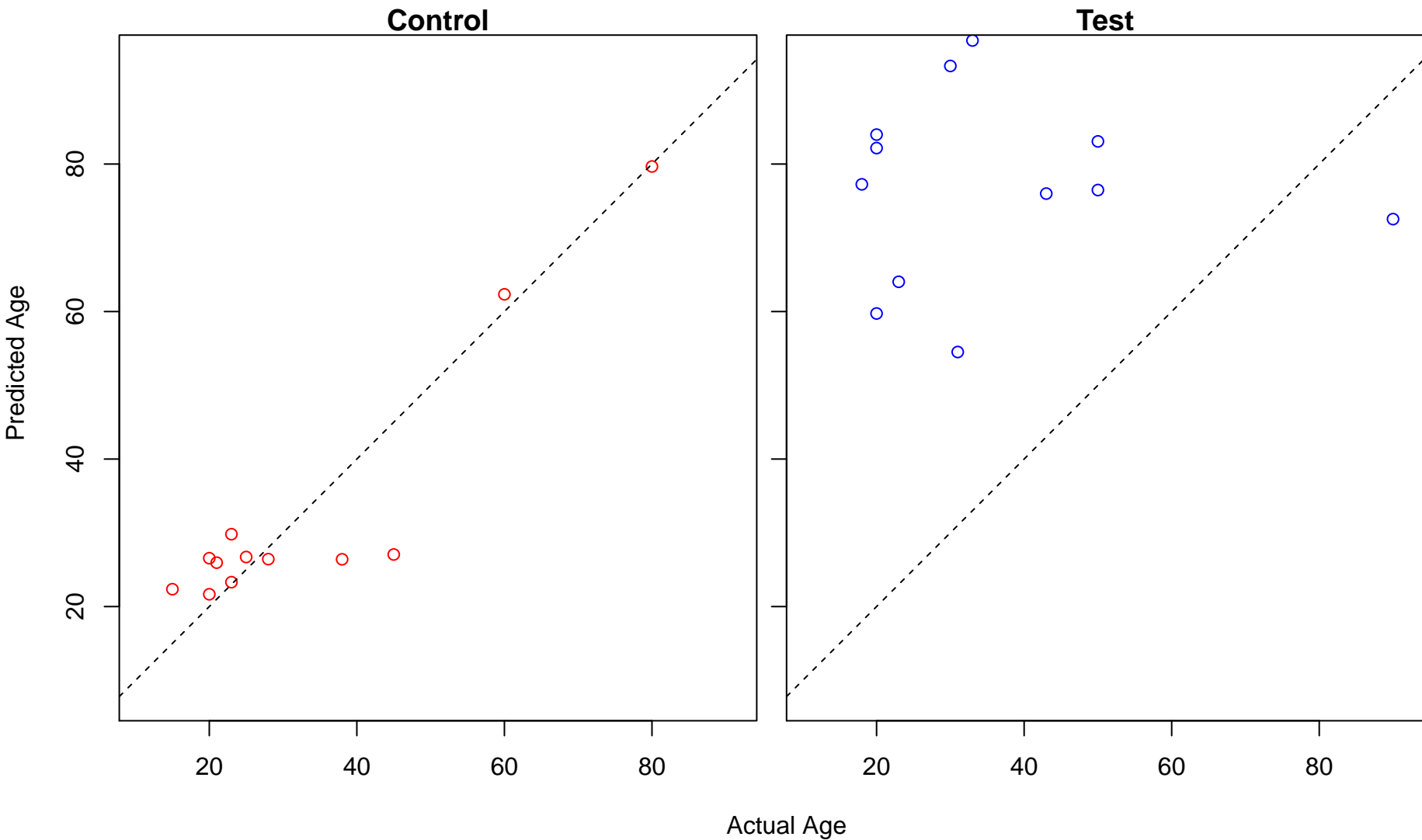
purine nucleoside triphosphate metabolic process (Score: 21.976101)



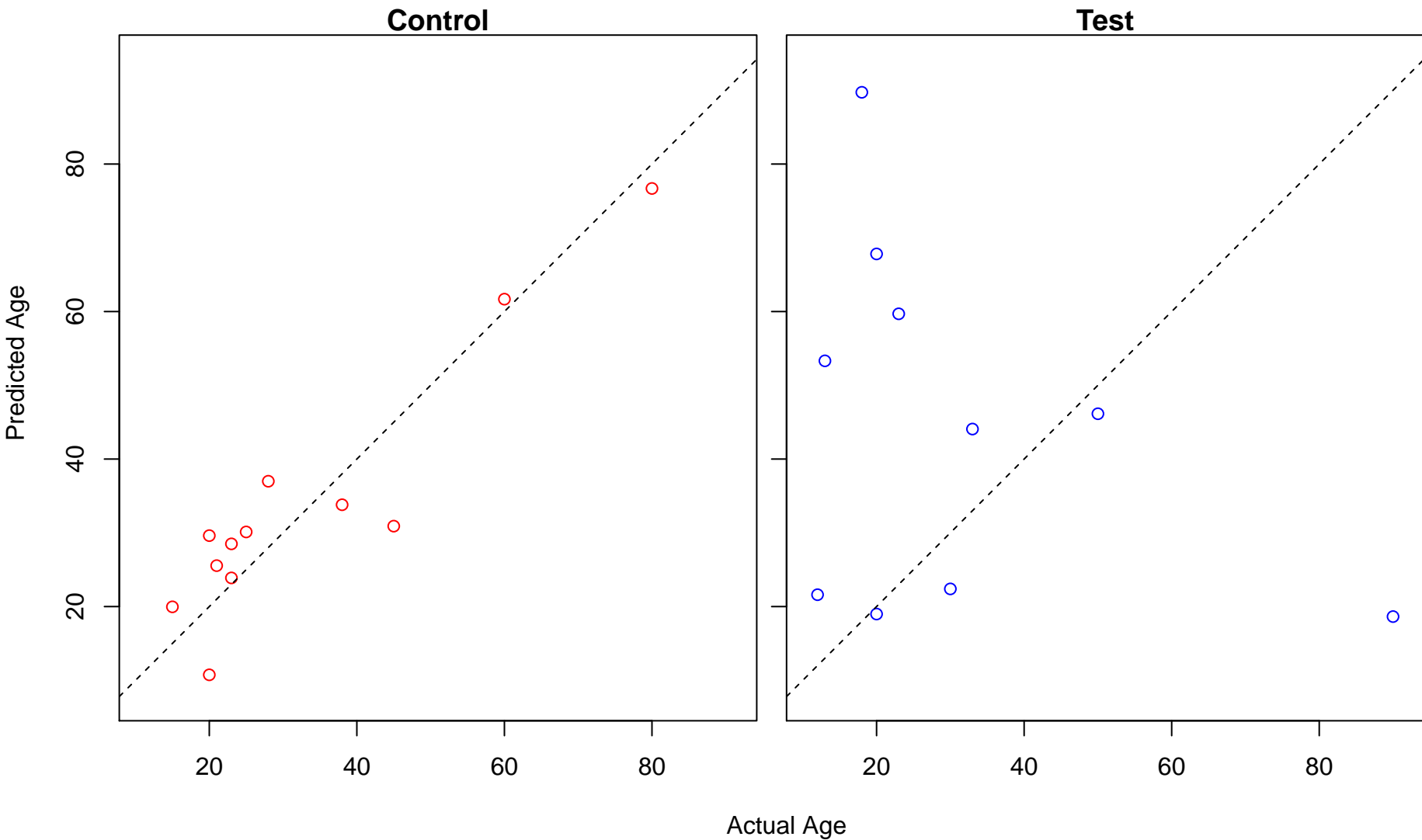
positive regulation of stress-activated protein kinase signaling cascade (Score: 21.854891)



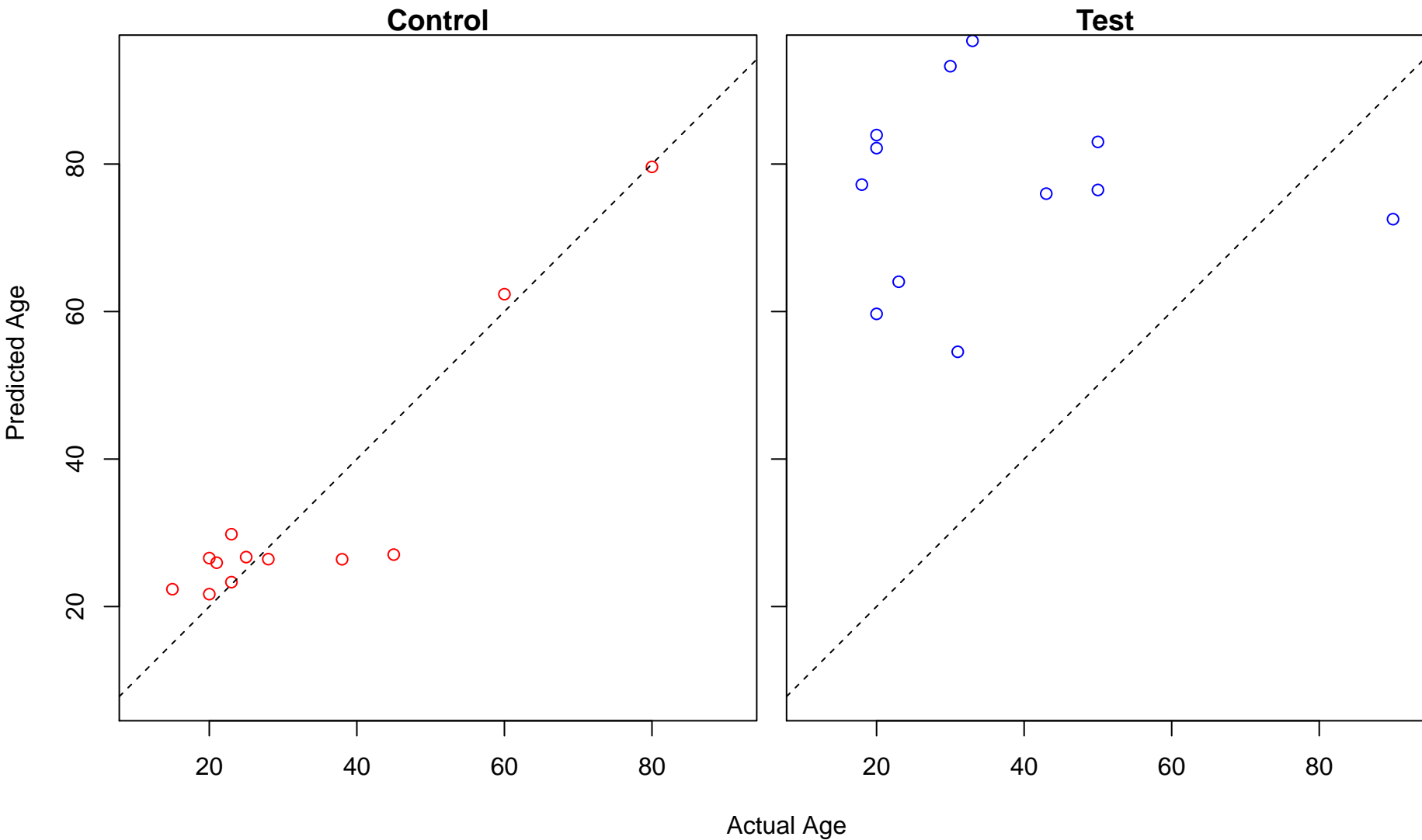
positive regulation of cardiac muscle cell proliferation (Score: 21.847114)



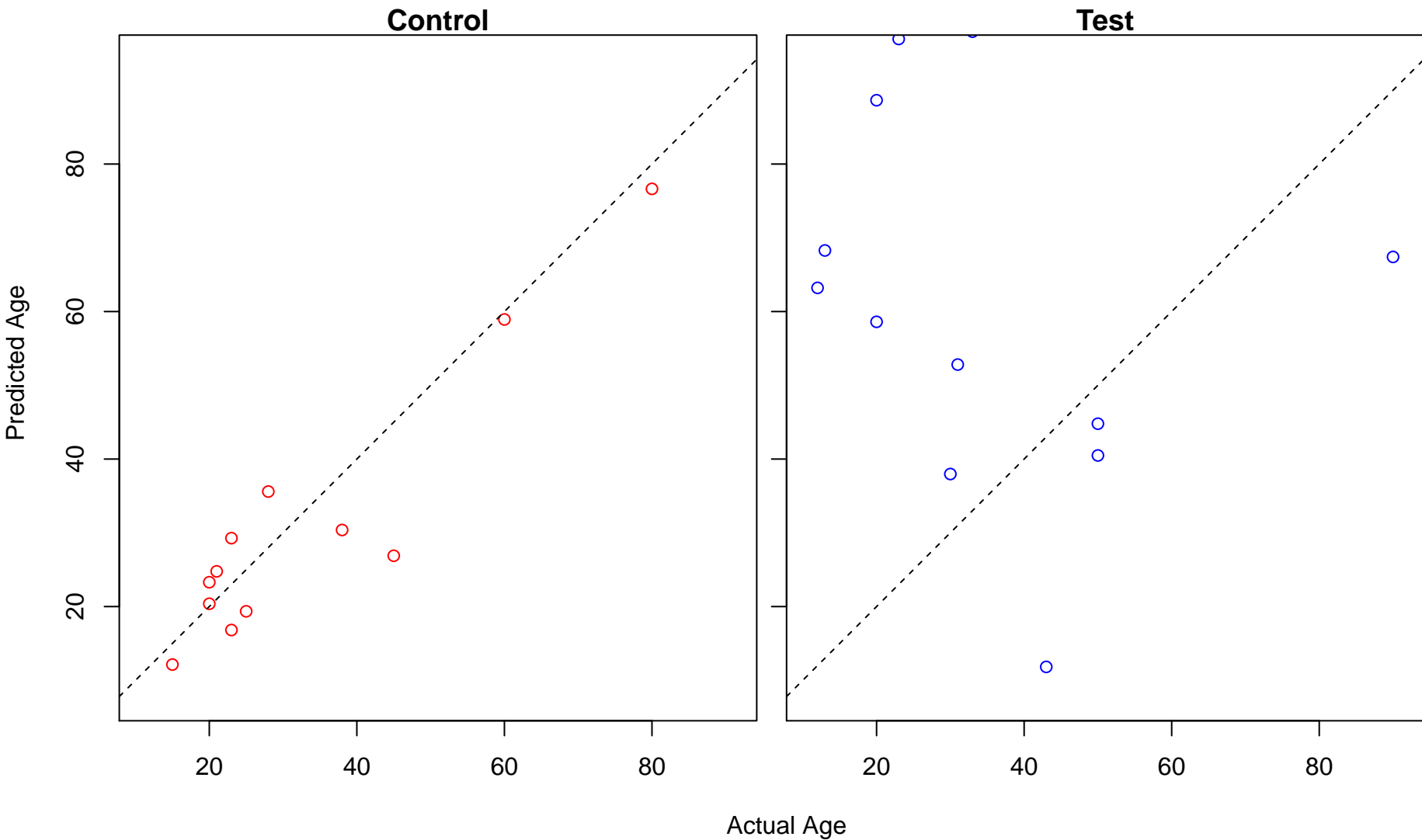
ribonucleotide metabolic process (Score: 21.810358)



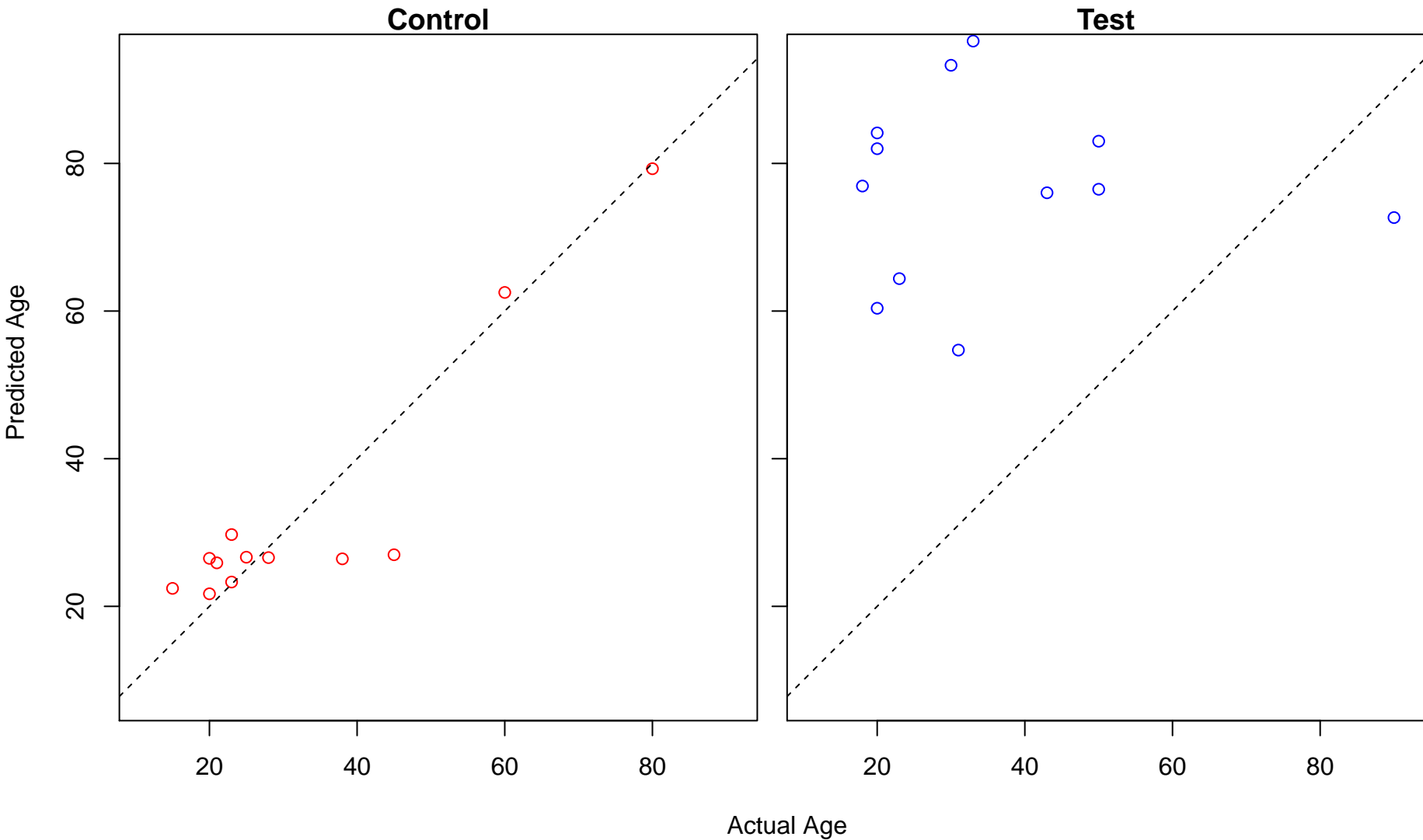
positive regulation of cardiac muscle tissue growth (Score: 21.792631)



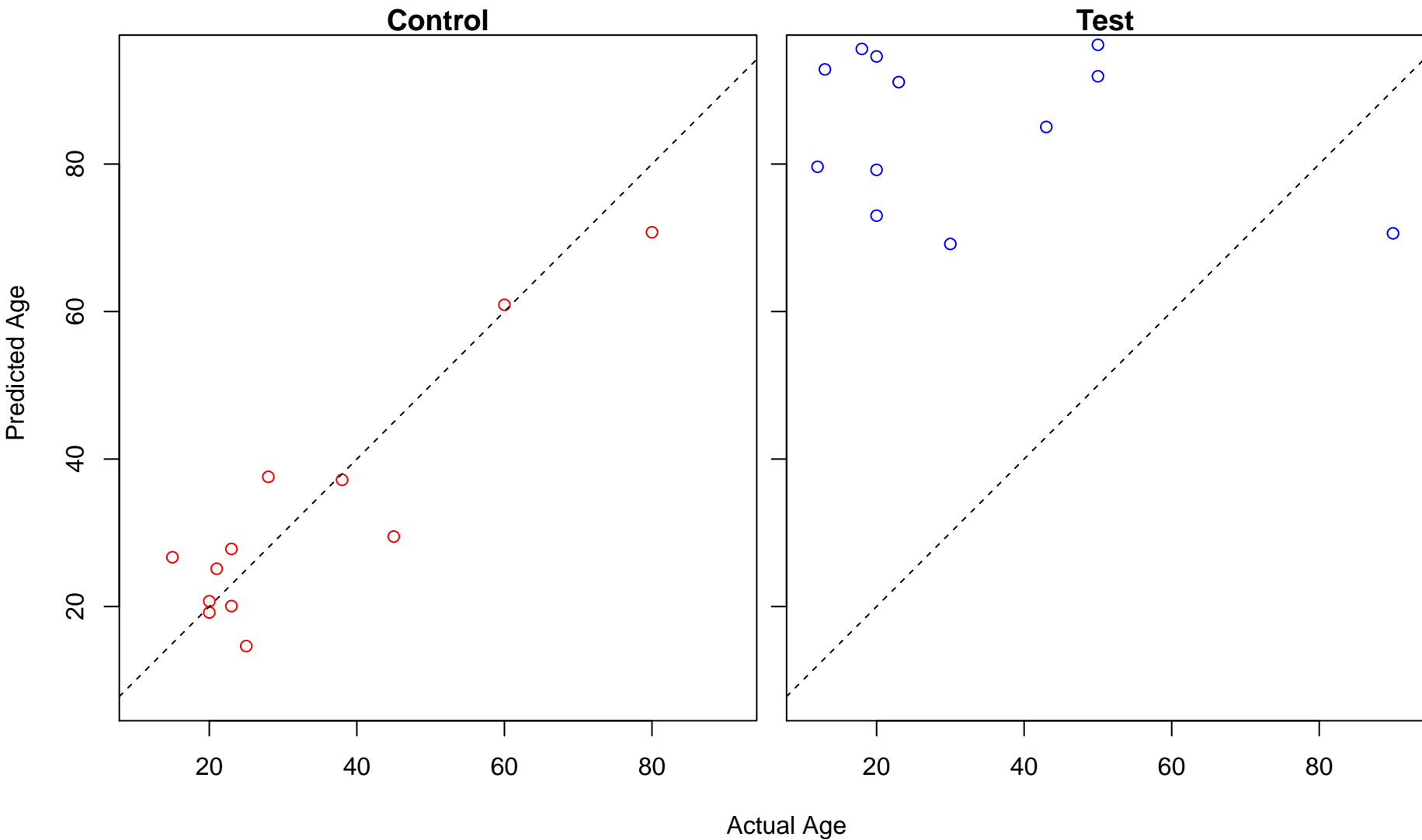
endocytic recycling (Score: 21.754592)



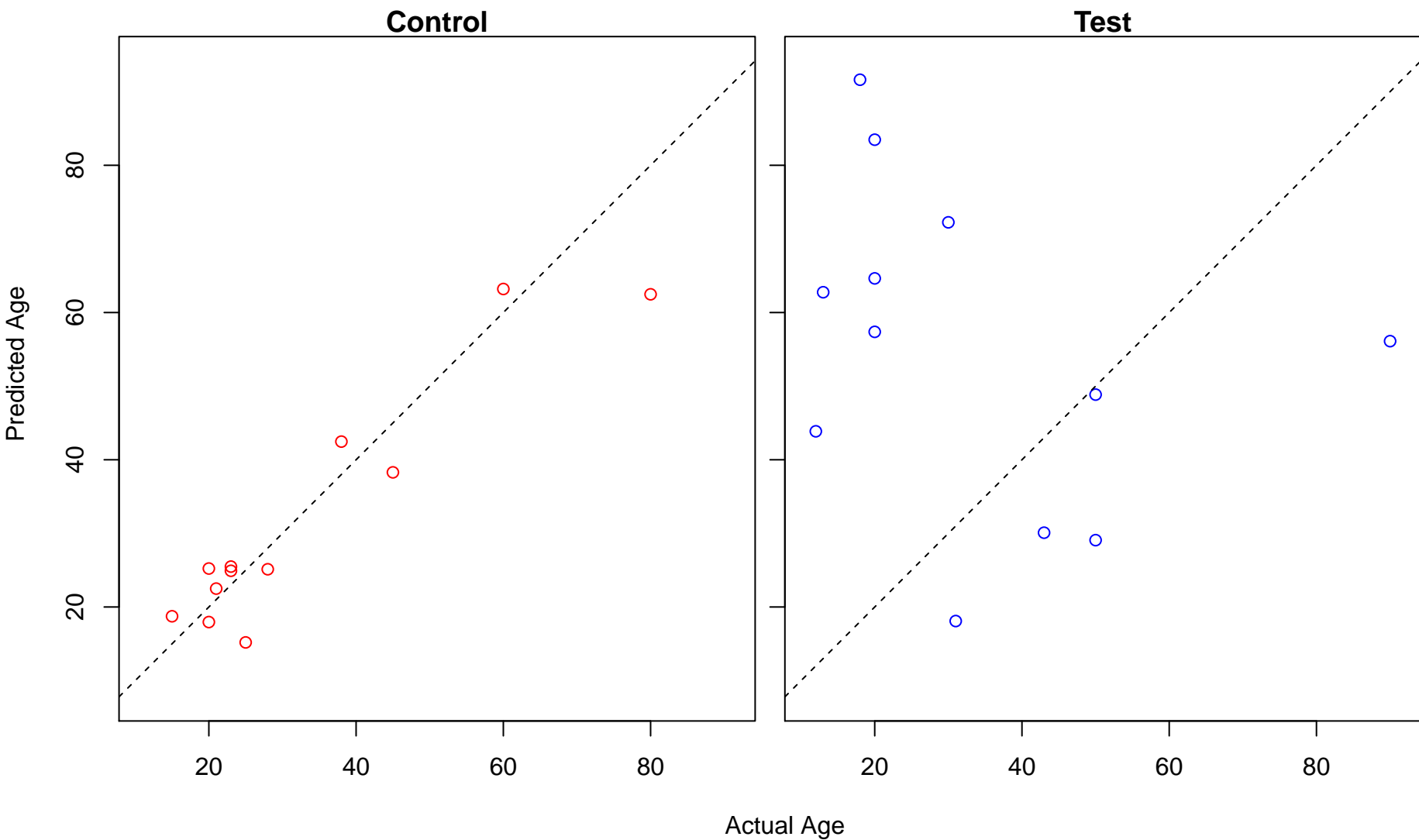
regulation of cardiac muscle cell proliferation (Score: 21.732239)



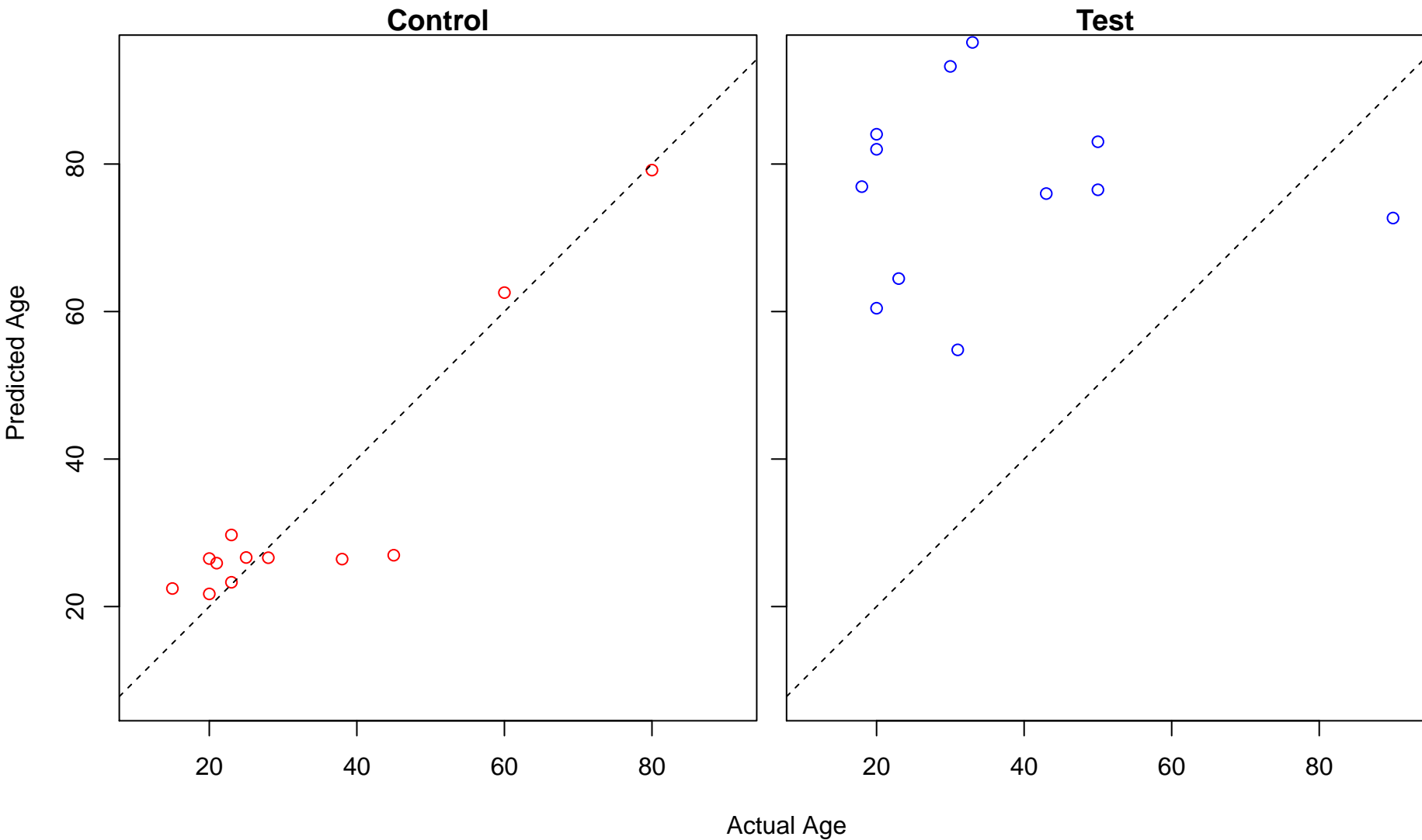
pattern specification process (Score: 21.701247)



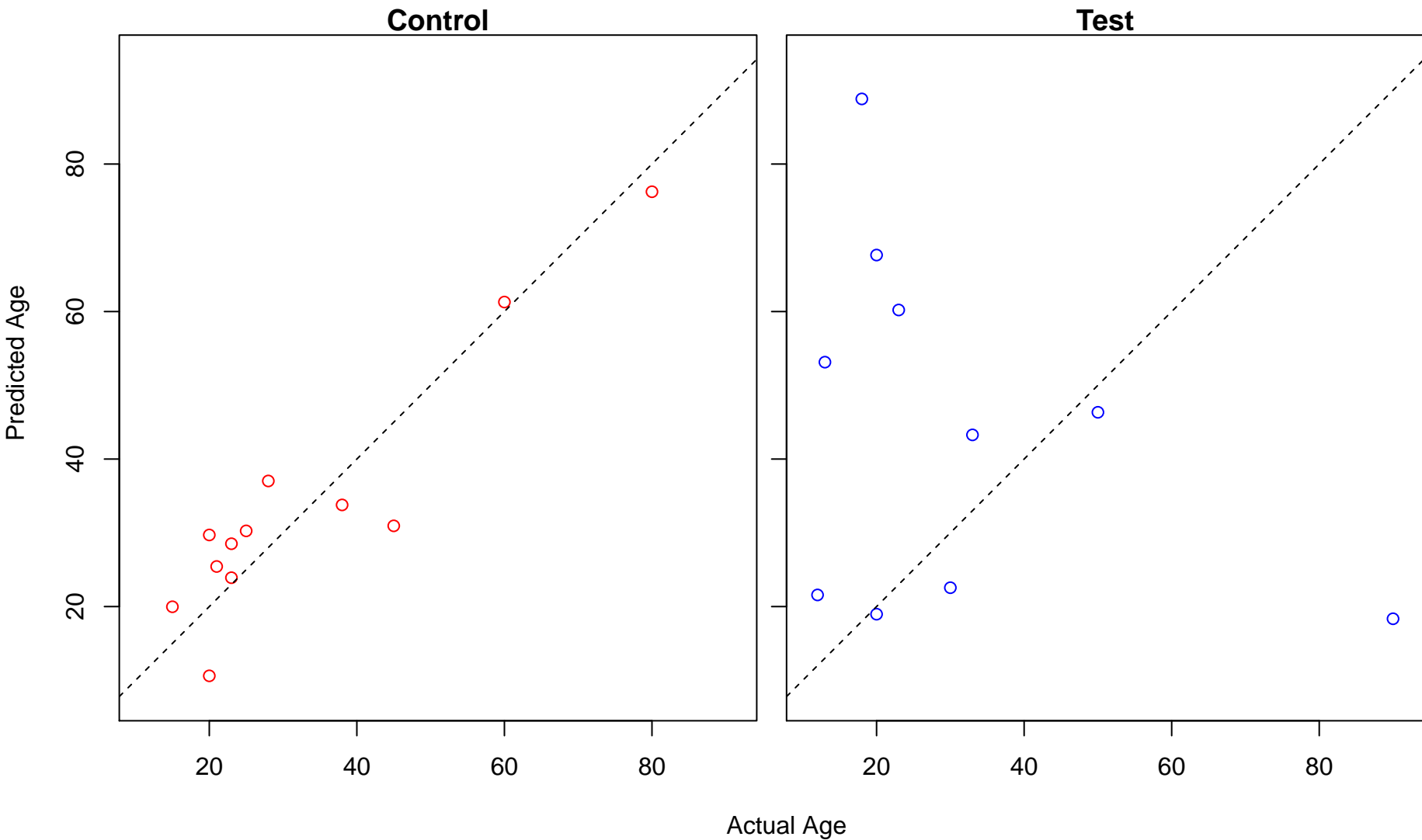
positive regulation of mitotic cell cycle spindle assembly checkpoint (Score: 21.65831)



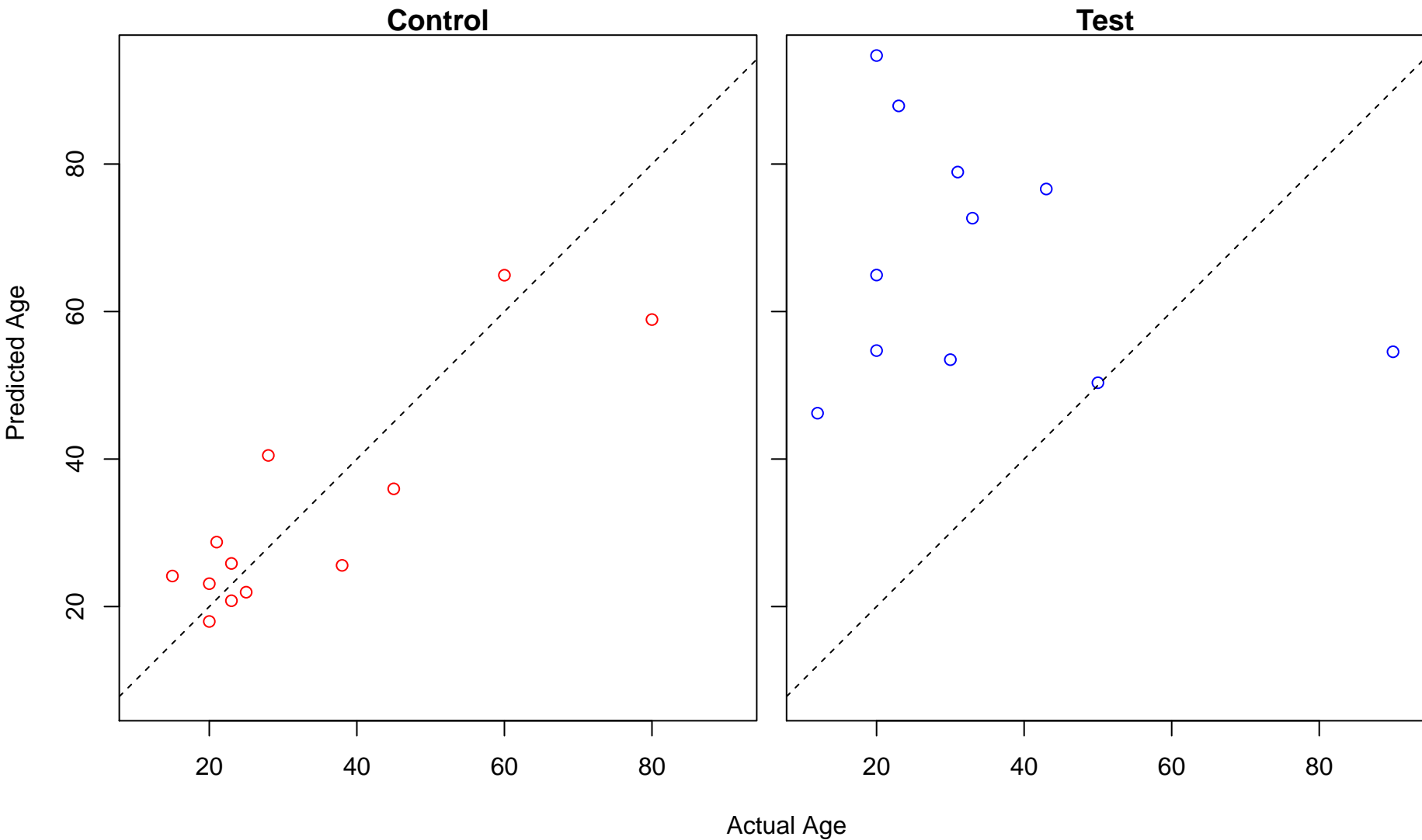
regulation of cardiac muscle tissue growth (Score: 21.645647)



purine ribonucleotide metabolic process (Score: 21.639575)

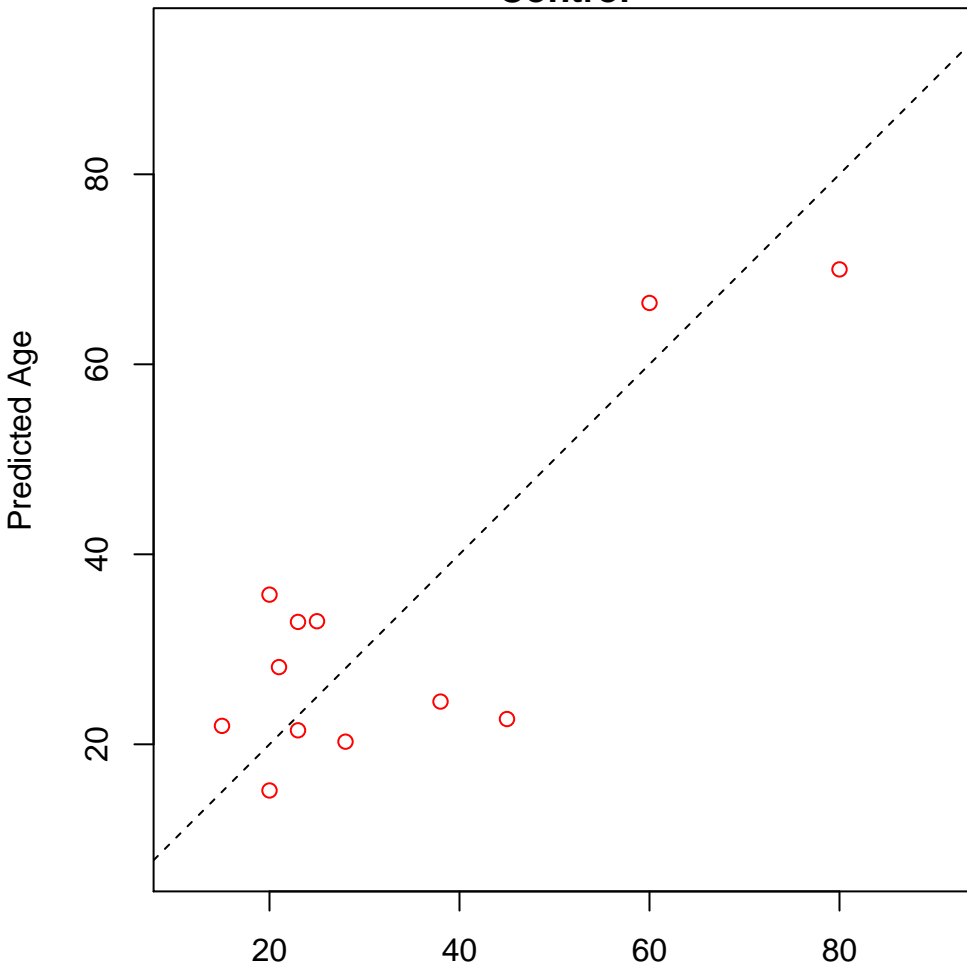


negative regulation of lymphocyte differentiation (Score: 21.63511)

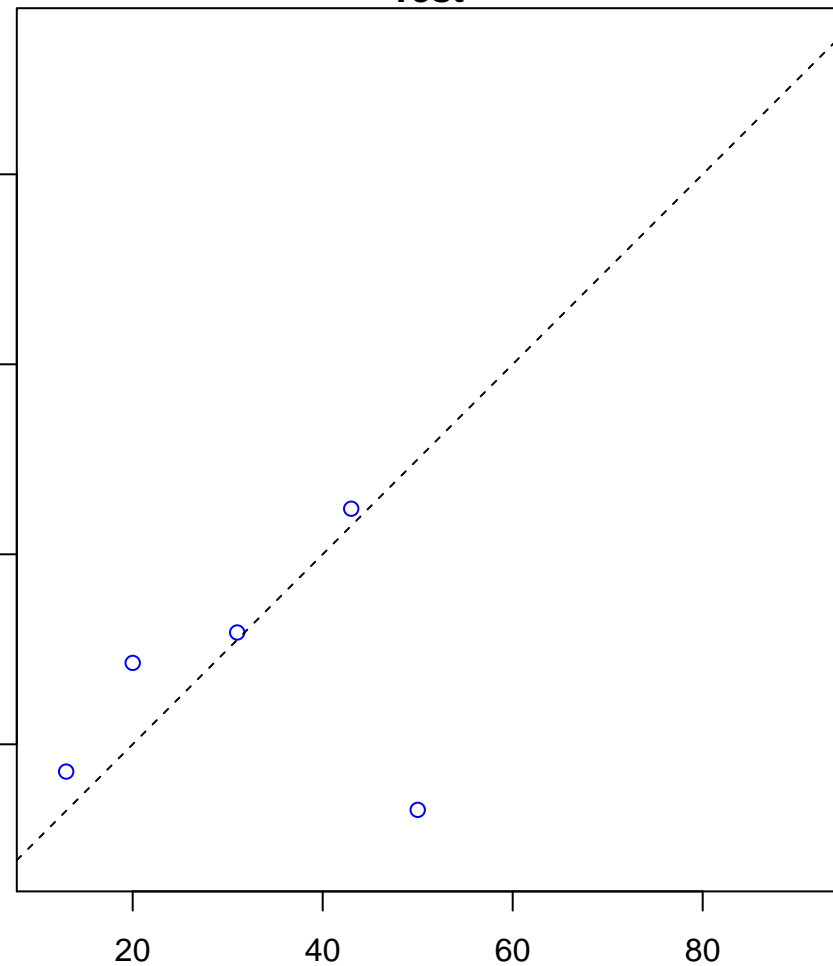


one-carbon metabolic process (Score: 21.602280)

Control

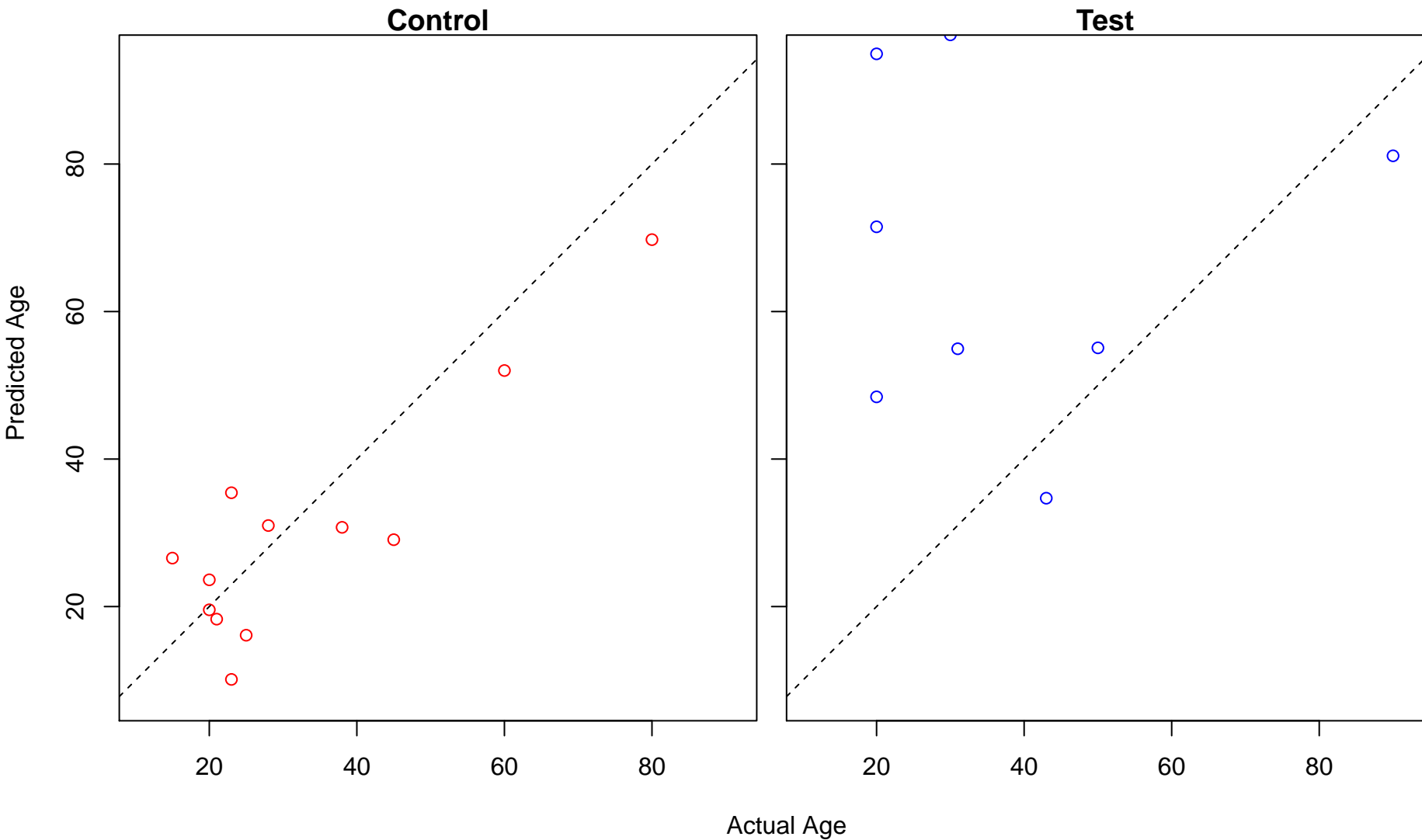


Test

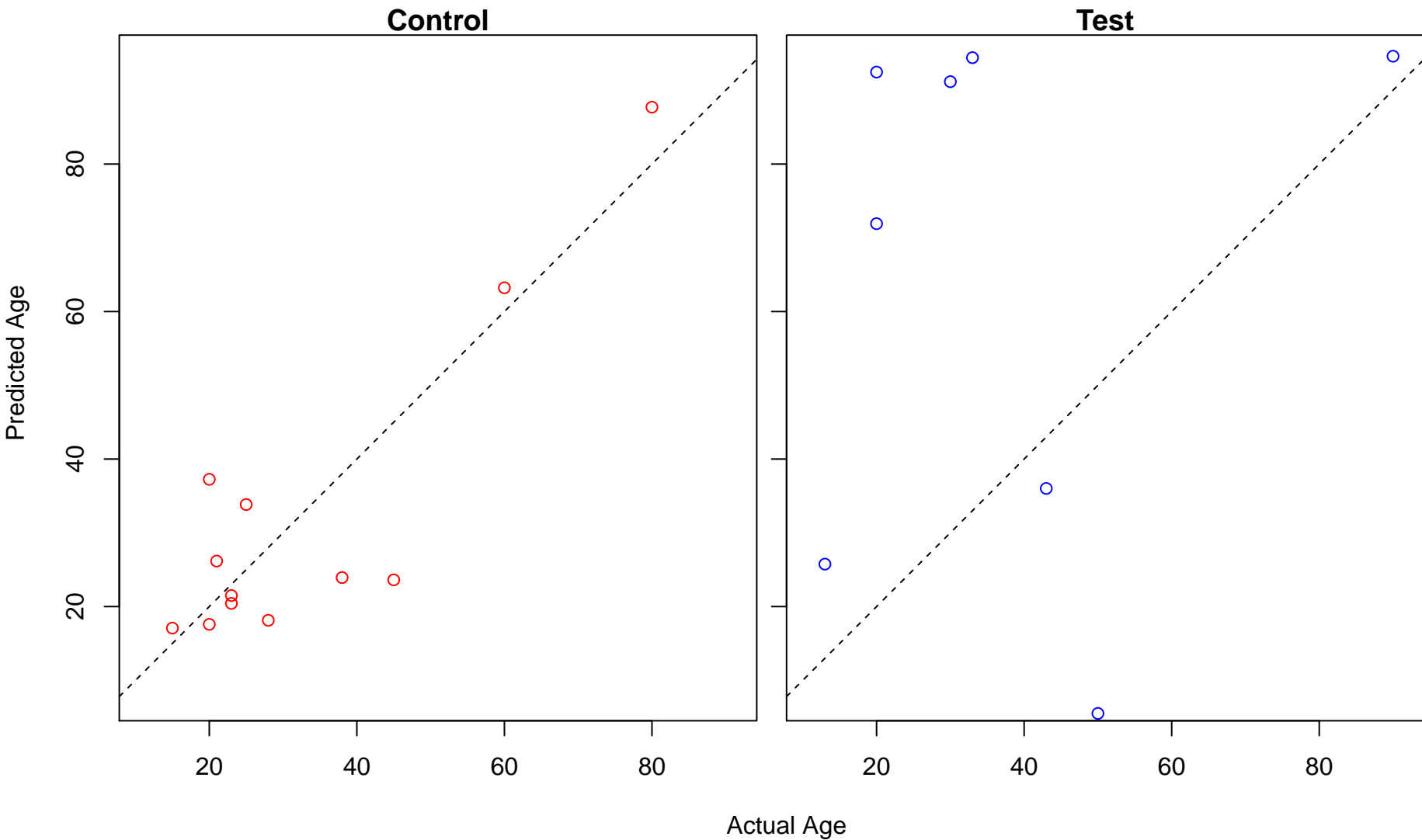


Actual Age

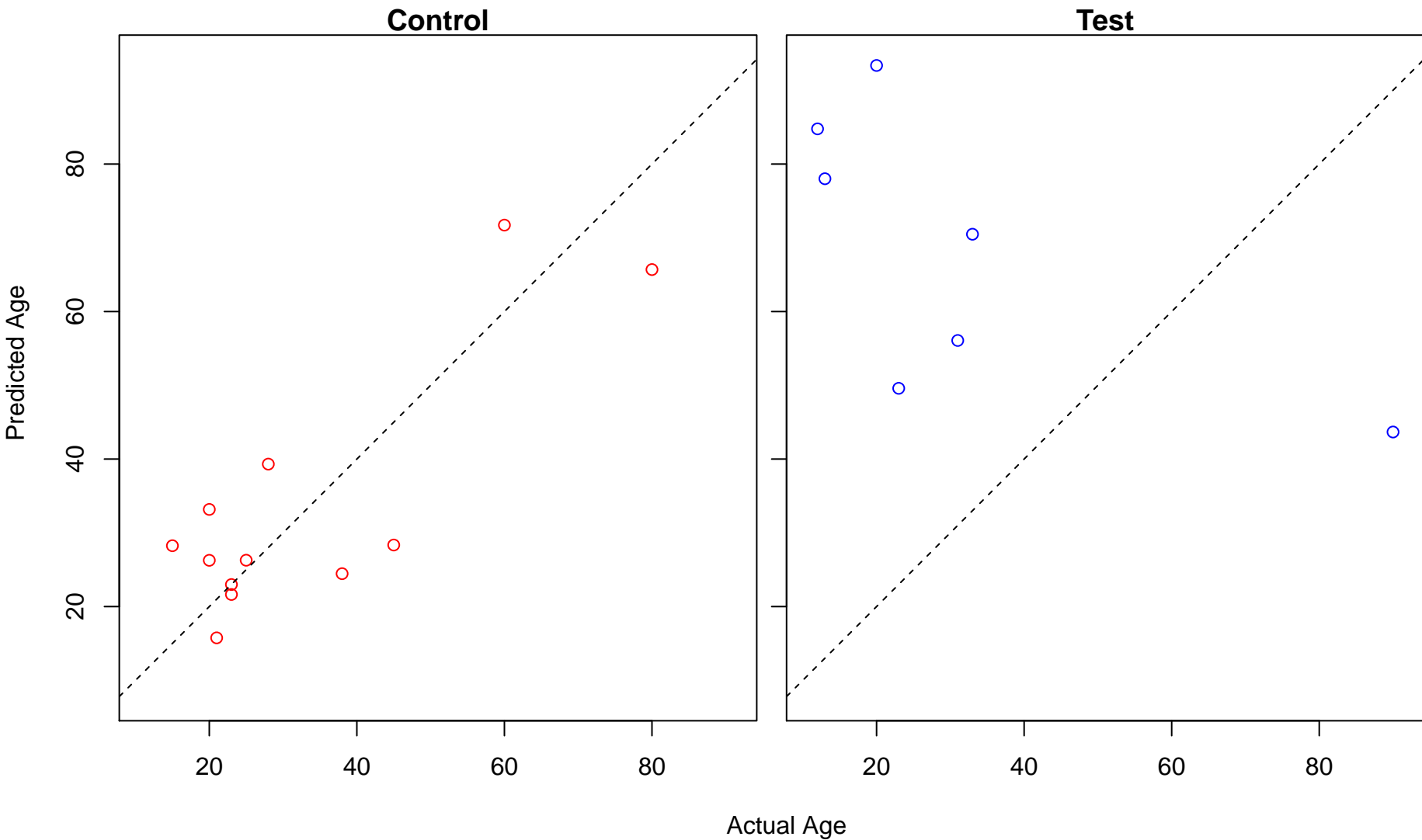
depyrimidination (Score: 21.560106)



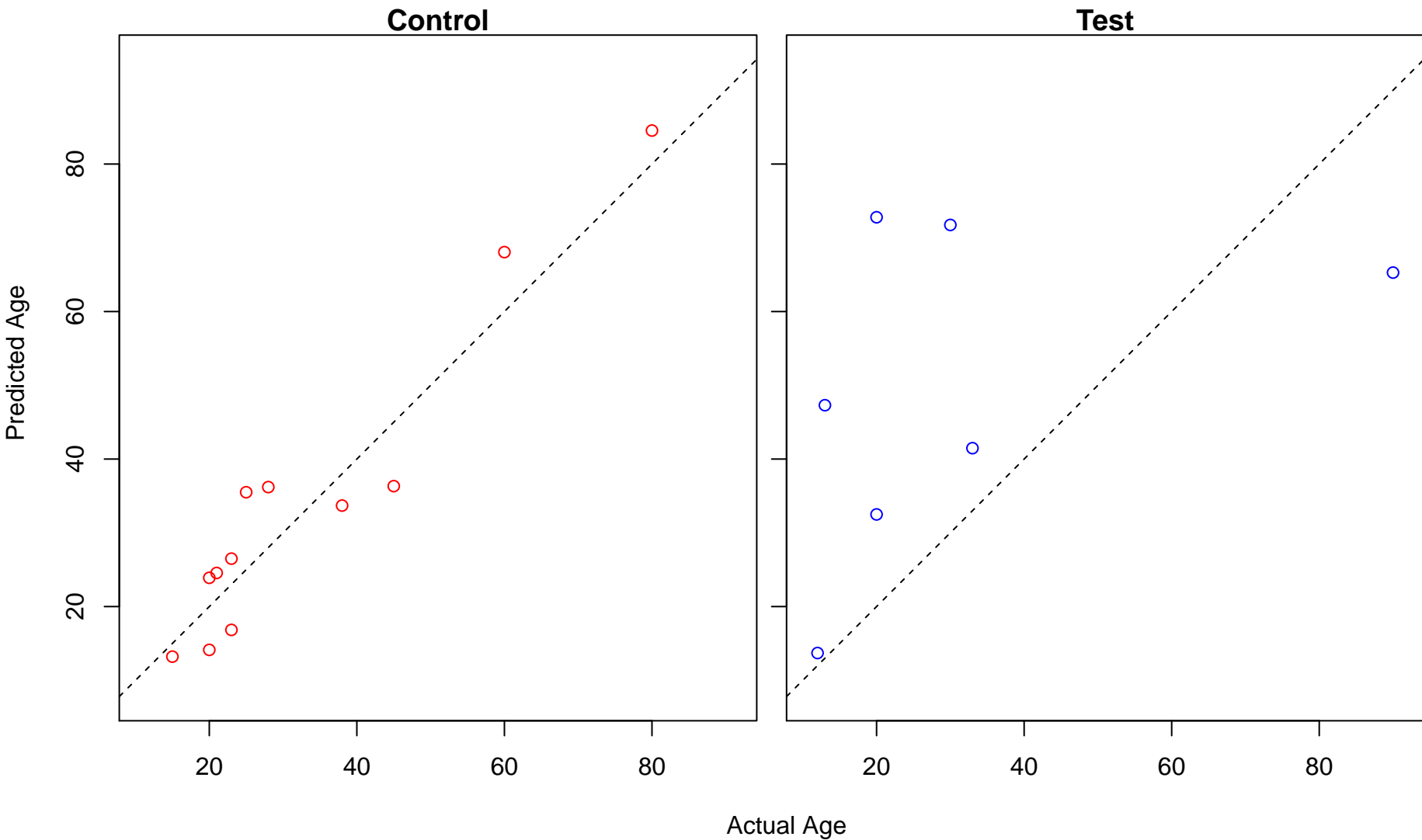
tetrahydrofolate interconversion (Score: 21.553137)



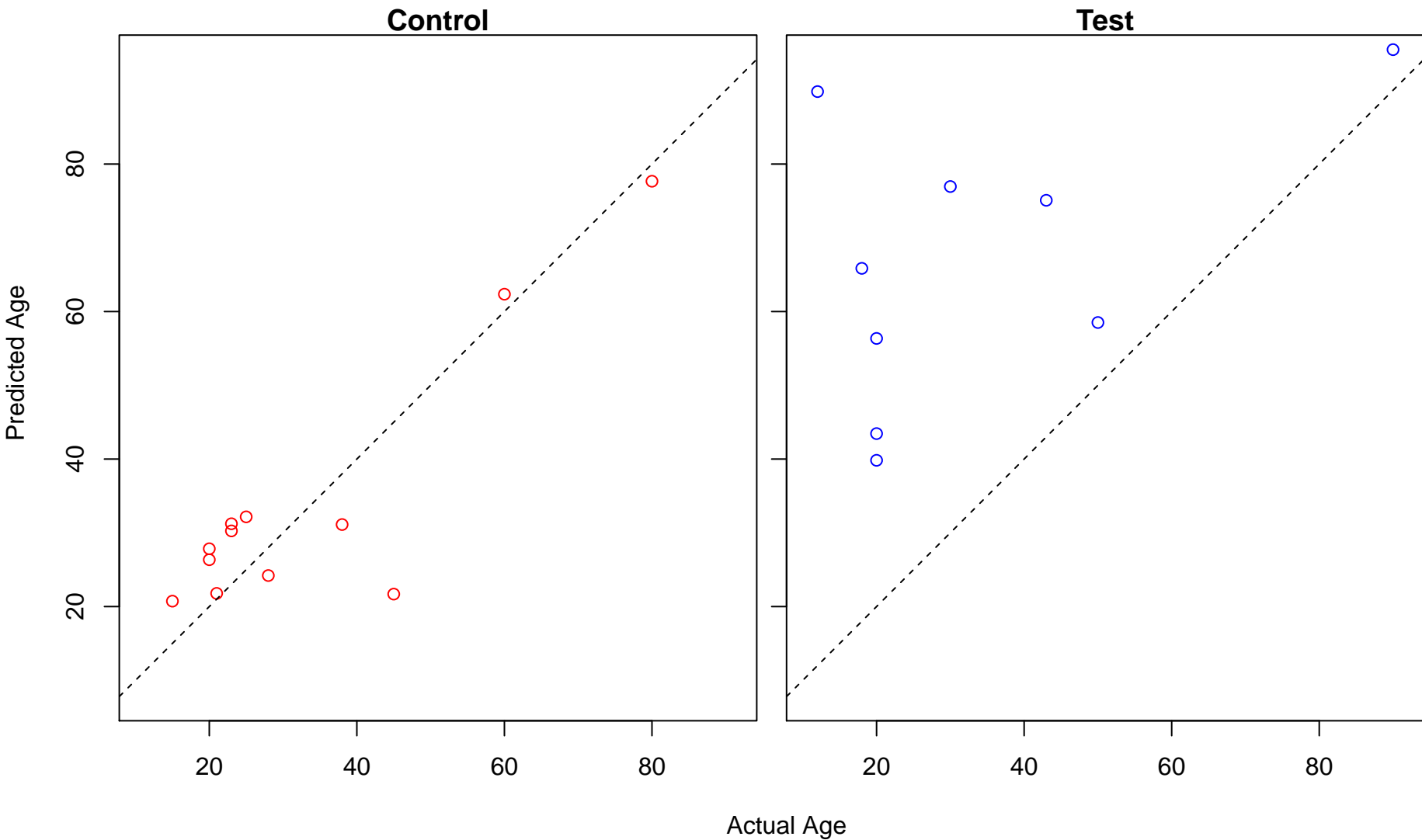
negative regulation of microtubule polymerization or depolymerization (Score: 21.384320)



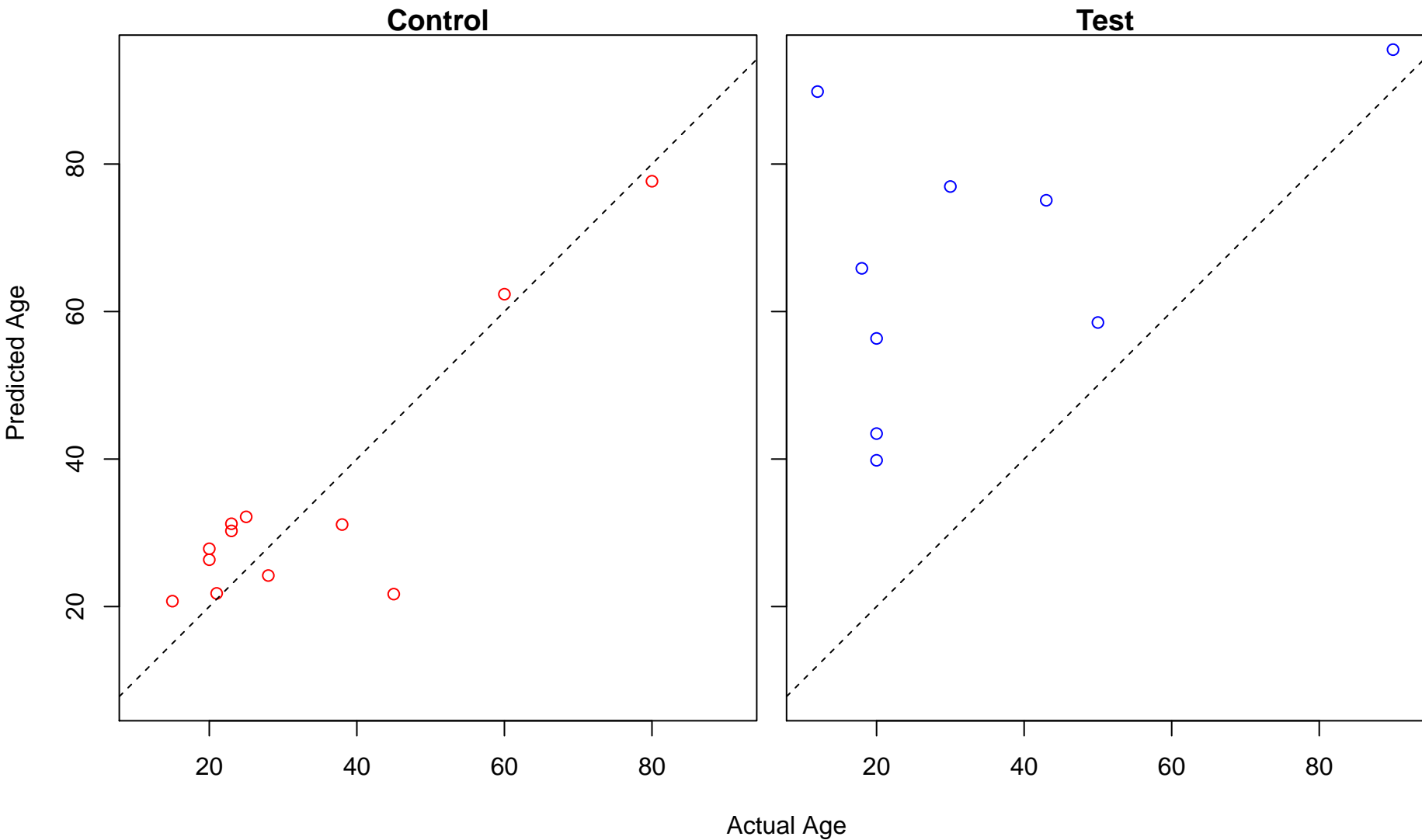
positive regulation of CREB transcription factor activity (Score: 21.374588)



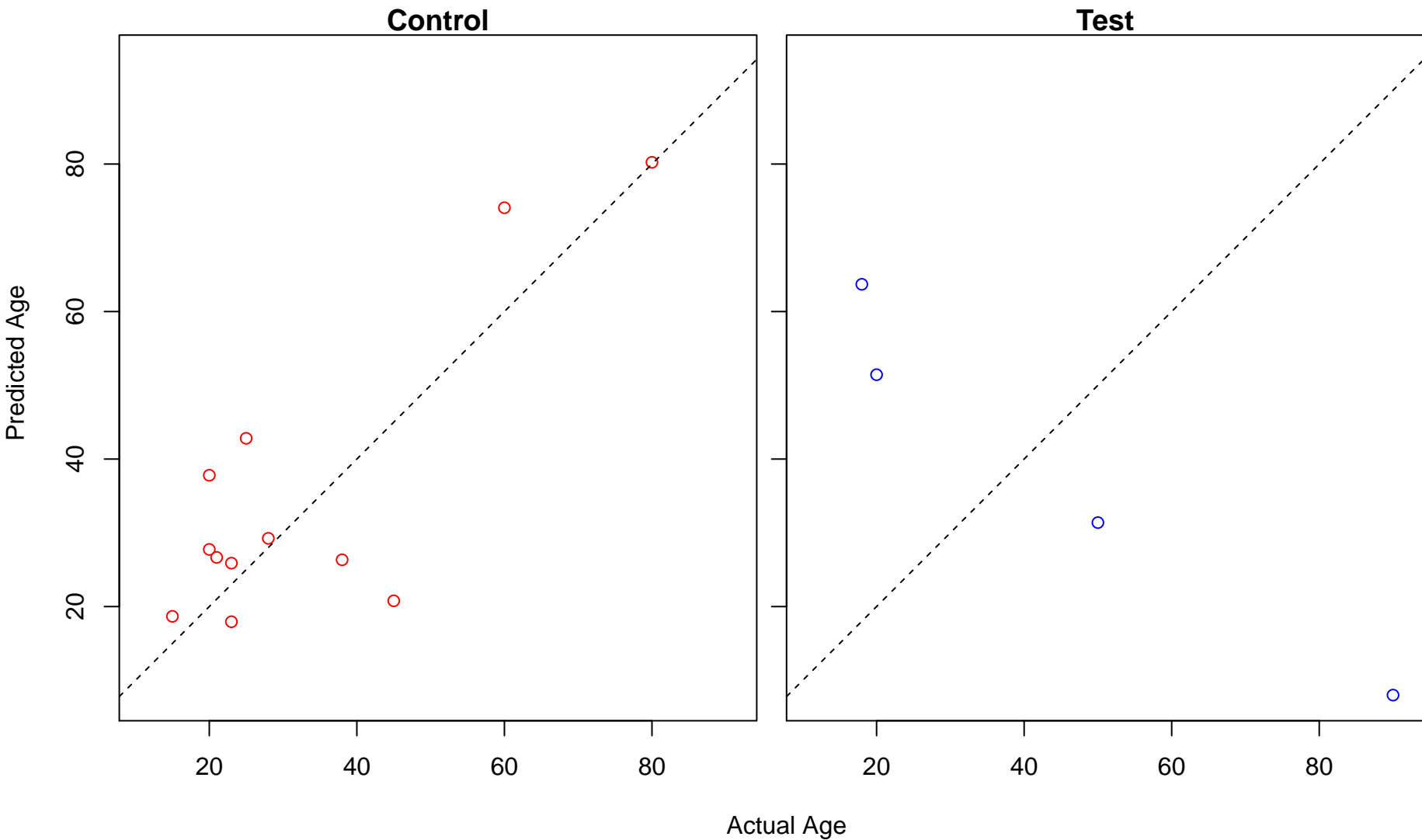
response to activity (Score: 21.366705)



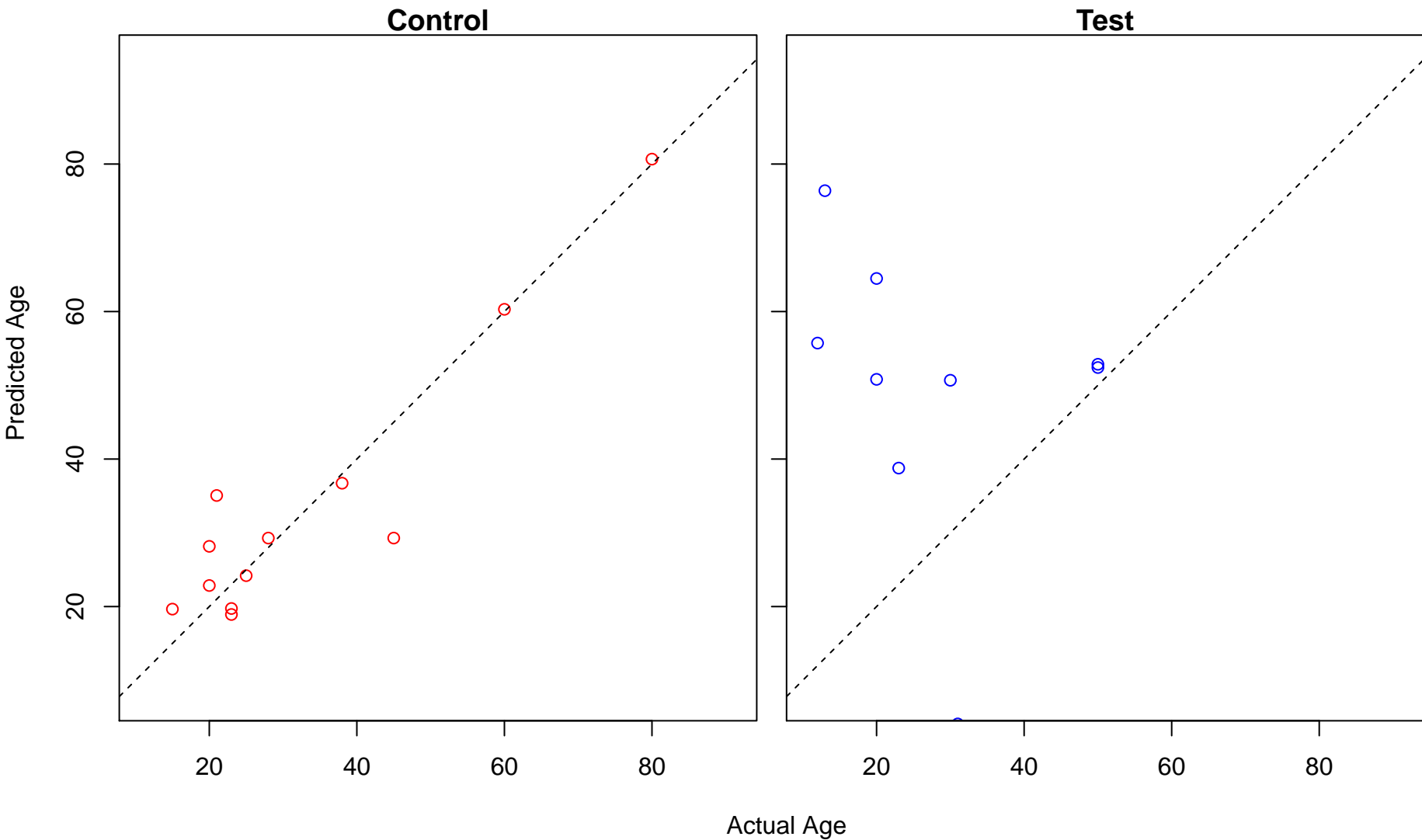
response to muscle activity (Score: 21.366705)



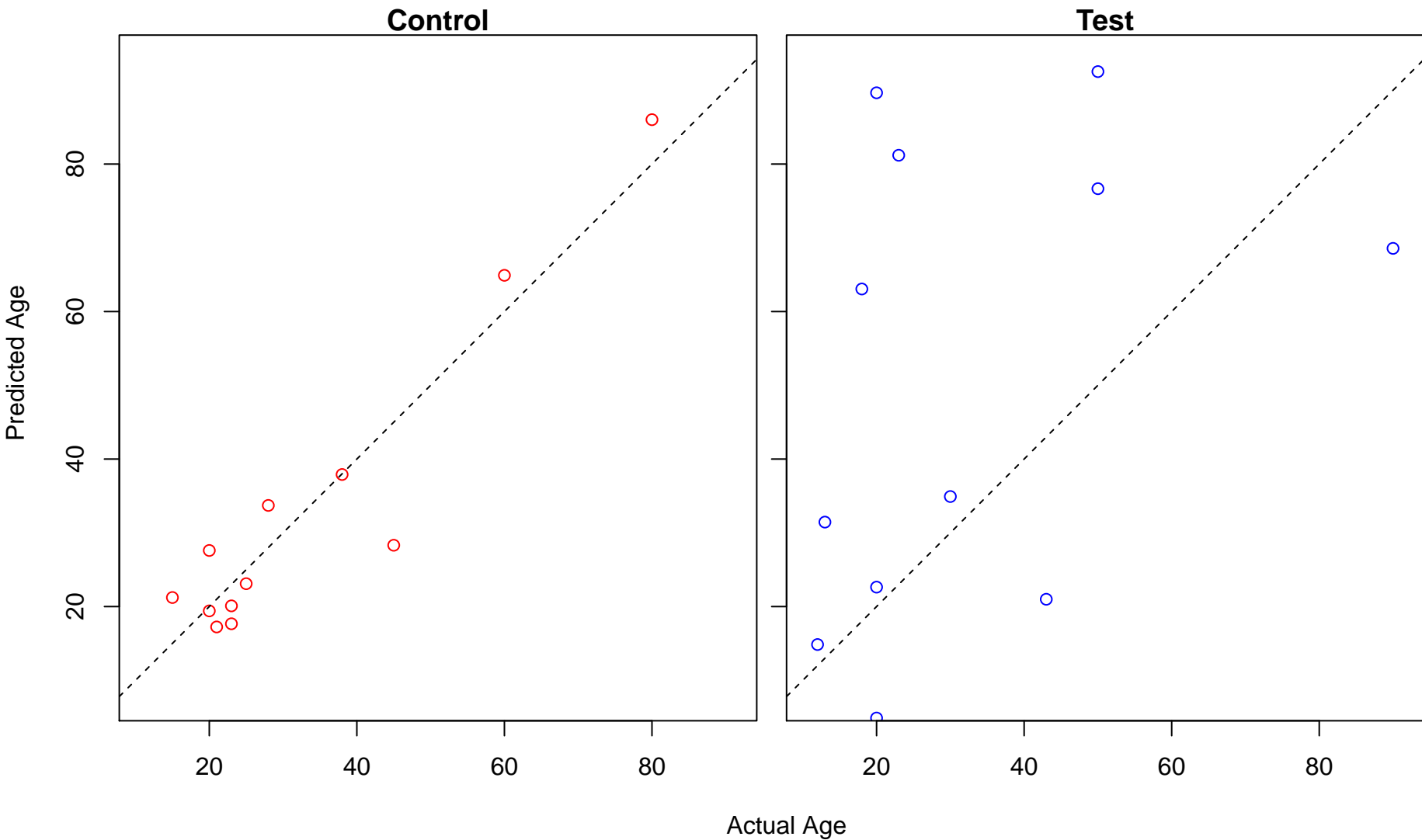
positive regulation of protein homodimerization activity (Score: 21.365434)



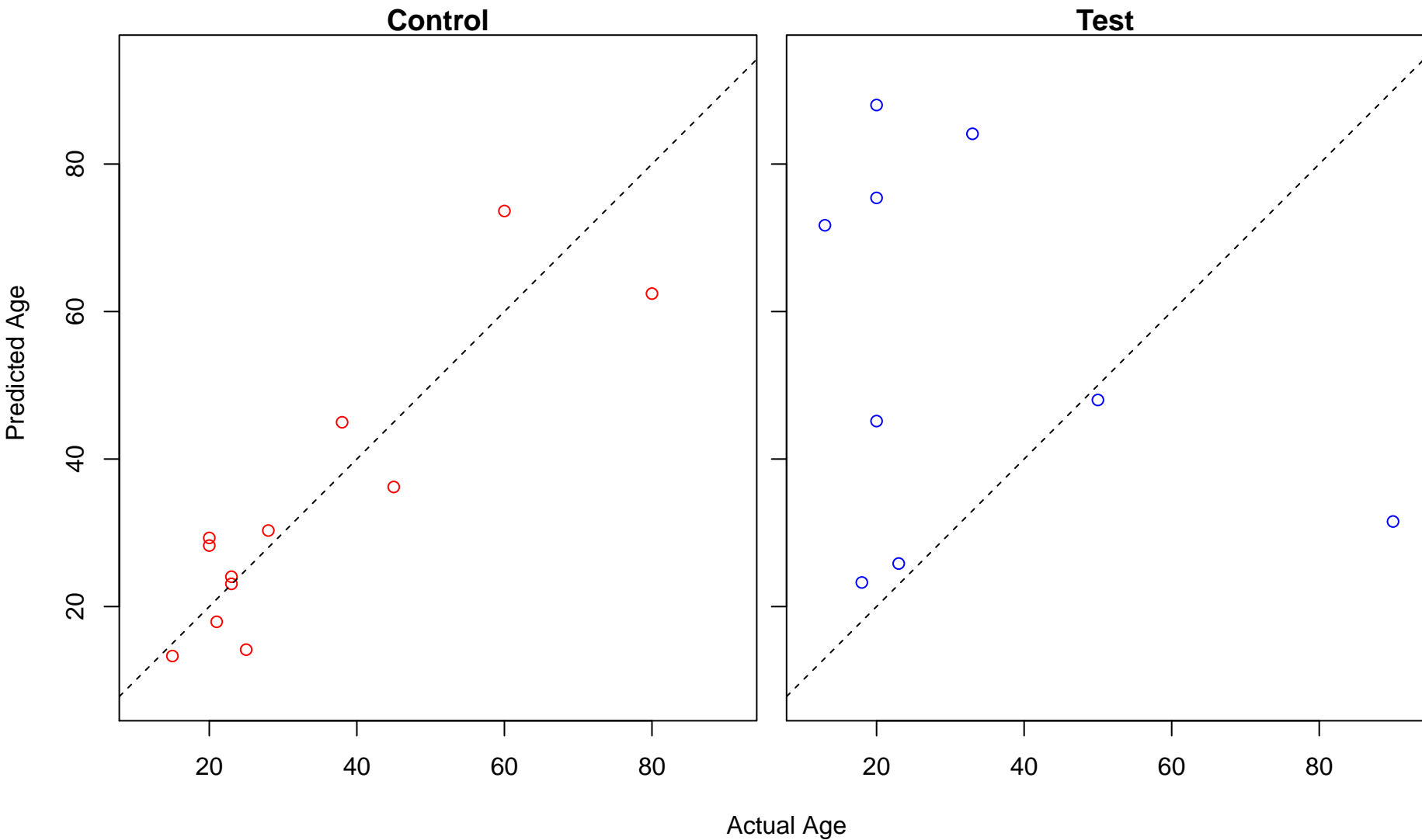
positive regulation of cellular carbohydrate metabolic process (Score: 21.358859)



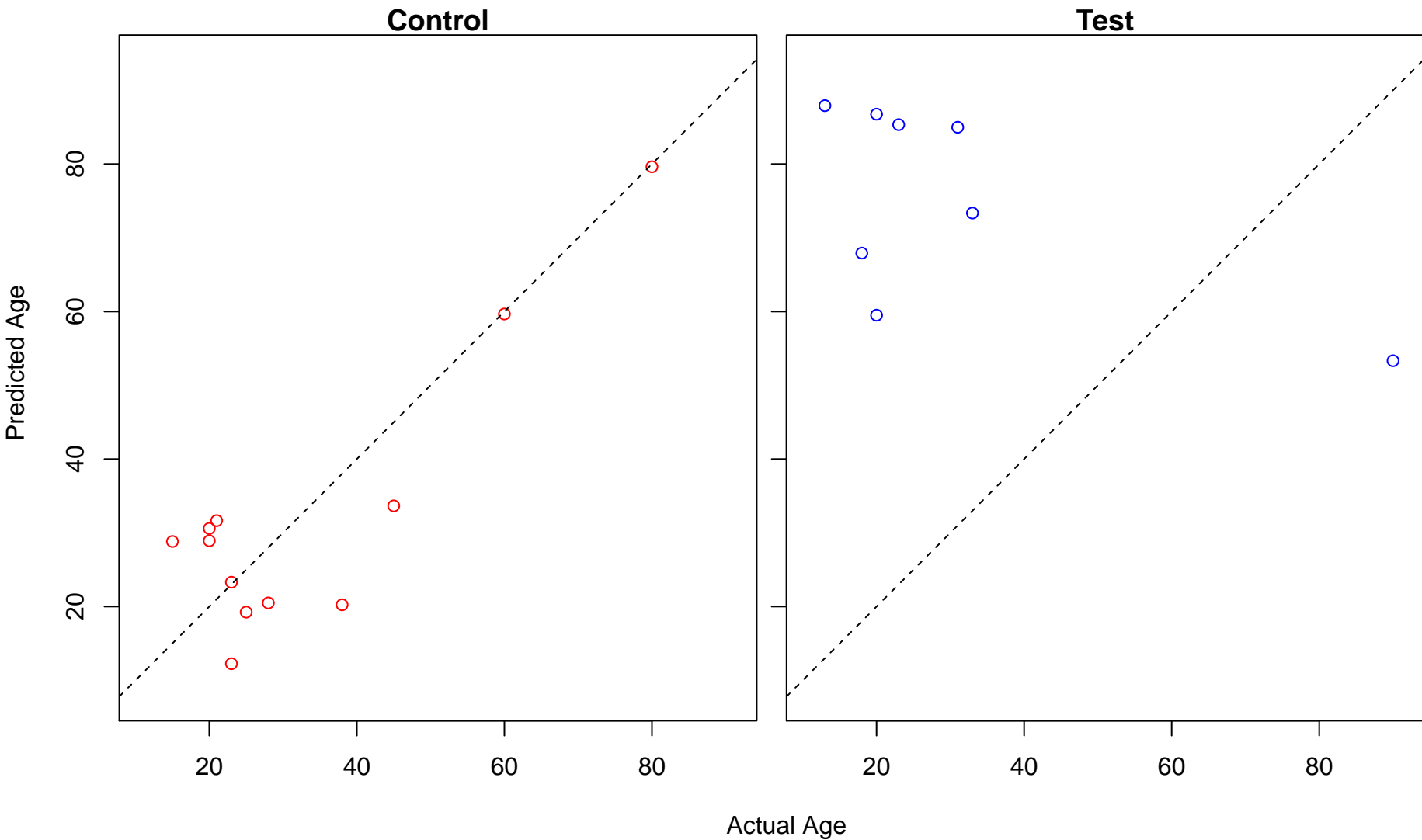
digestive tract morphogenesis (Score: 21.355657)



cellular response to cold (Score: 21.297972)

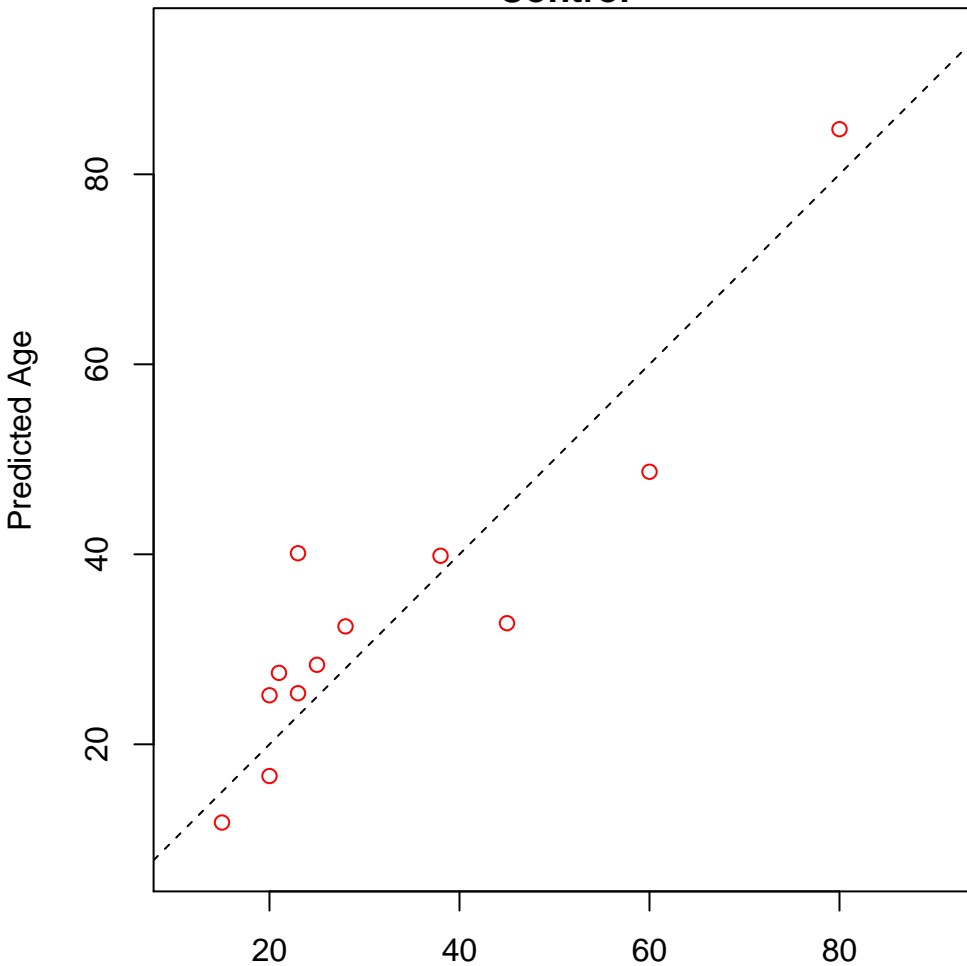


heme transport (Score: 21.291237)

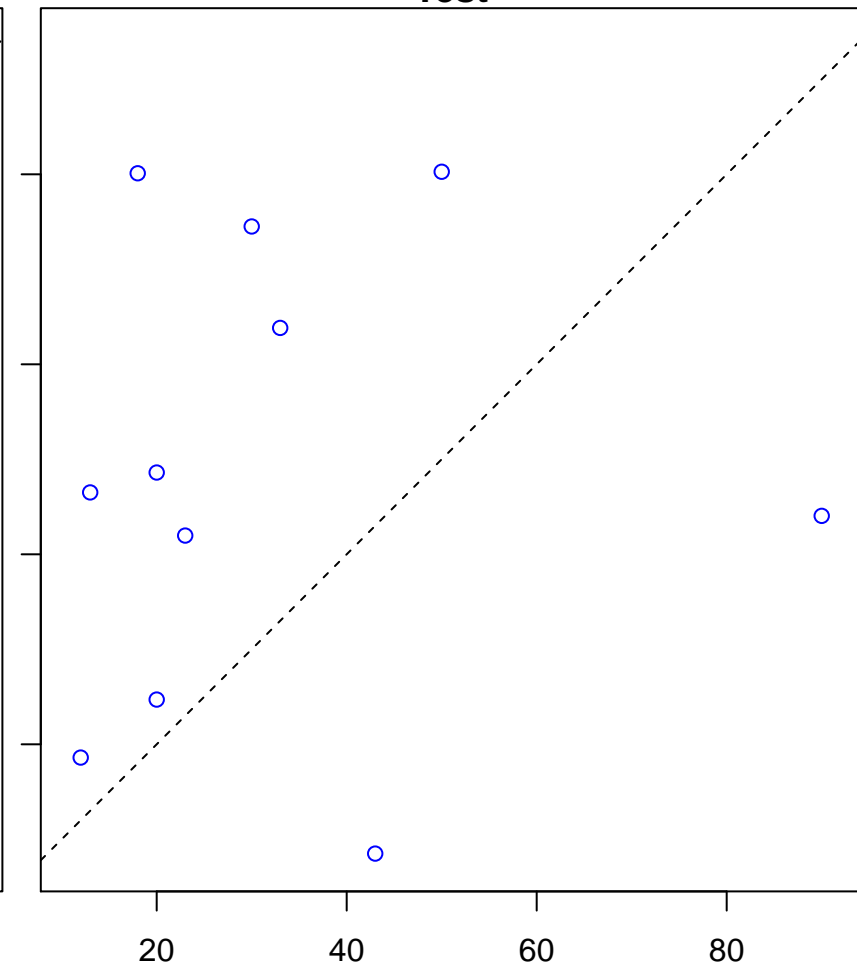


fat-soluble vitamin metabolic process (Score: 21.28663)

Control

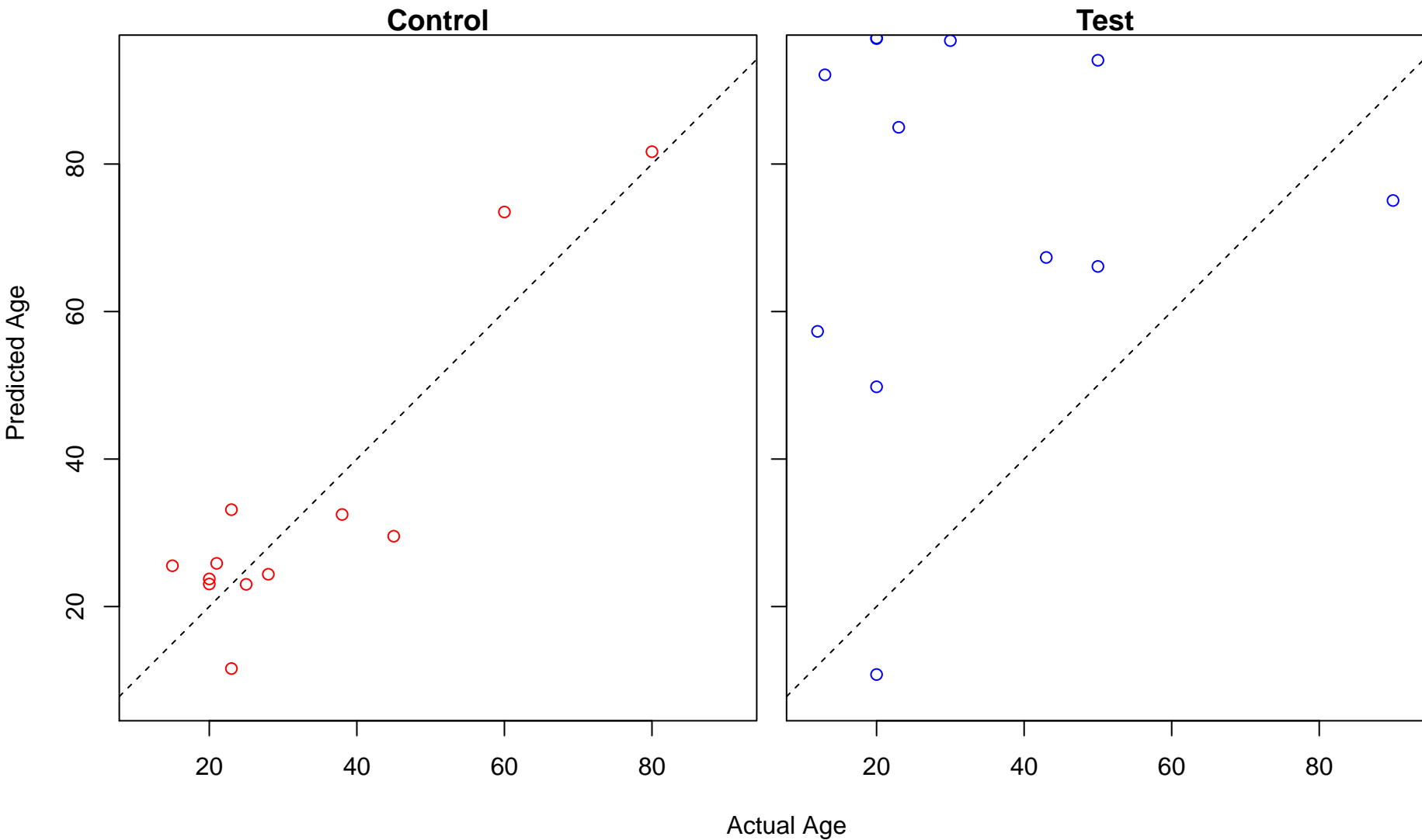


Test

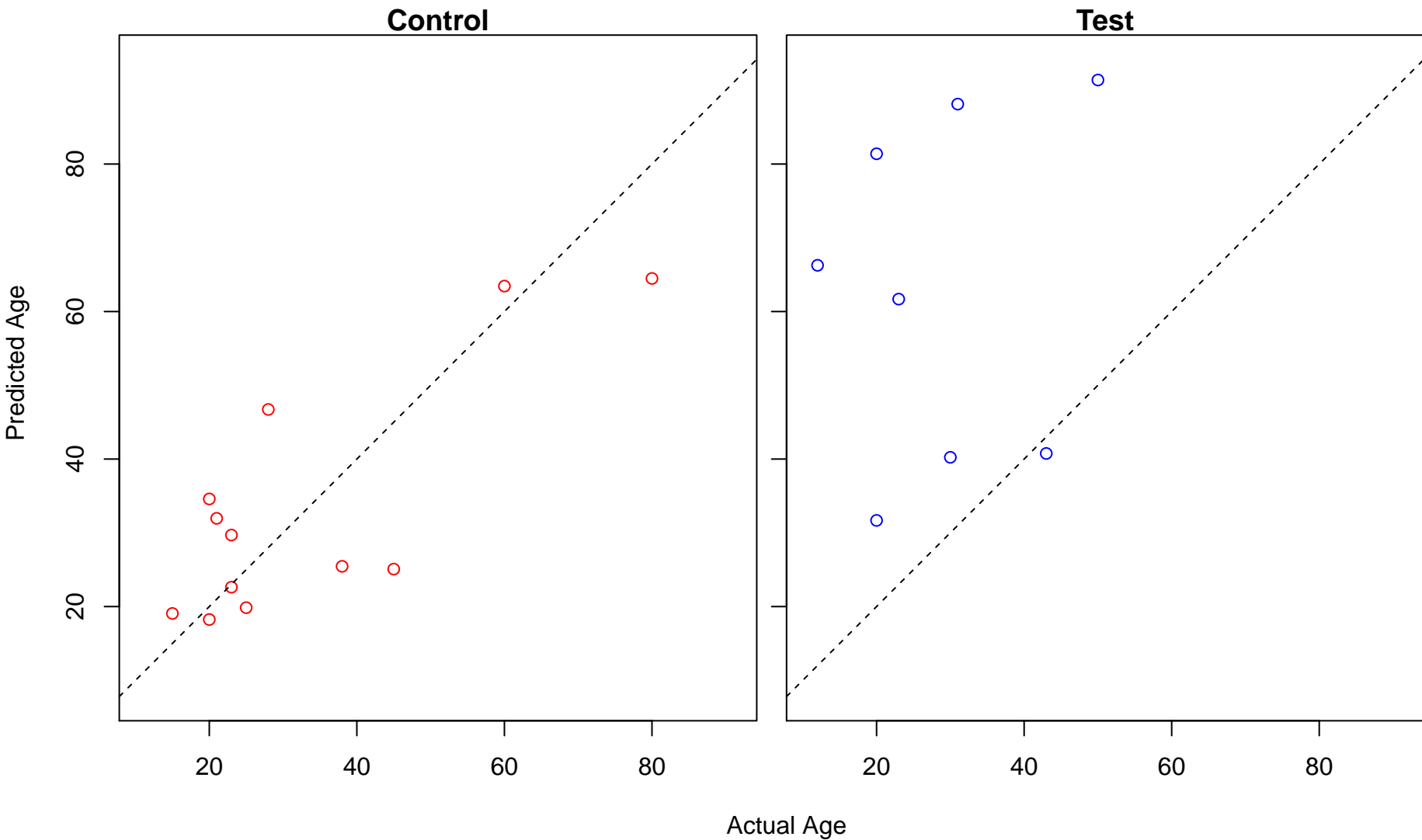


Actual Age

negative regulation of phosphatidylinositol 3-kinase signaling (Score: 21.249734)

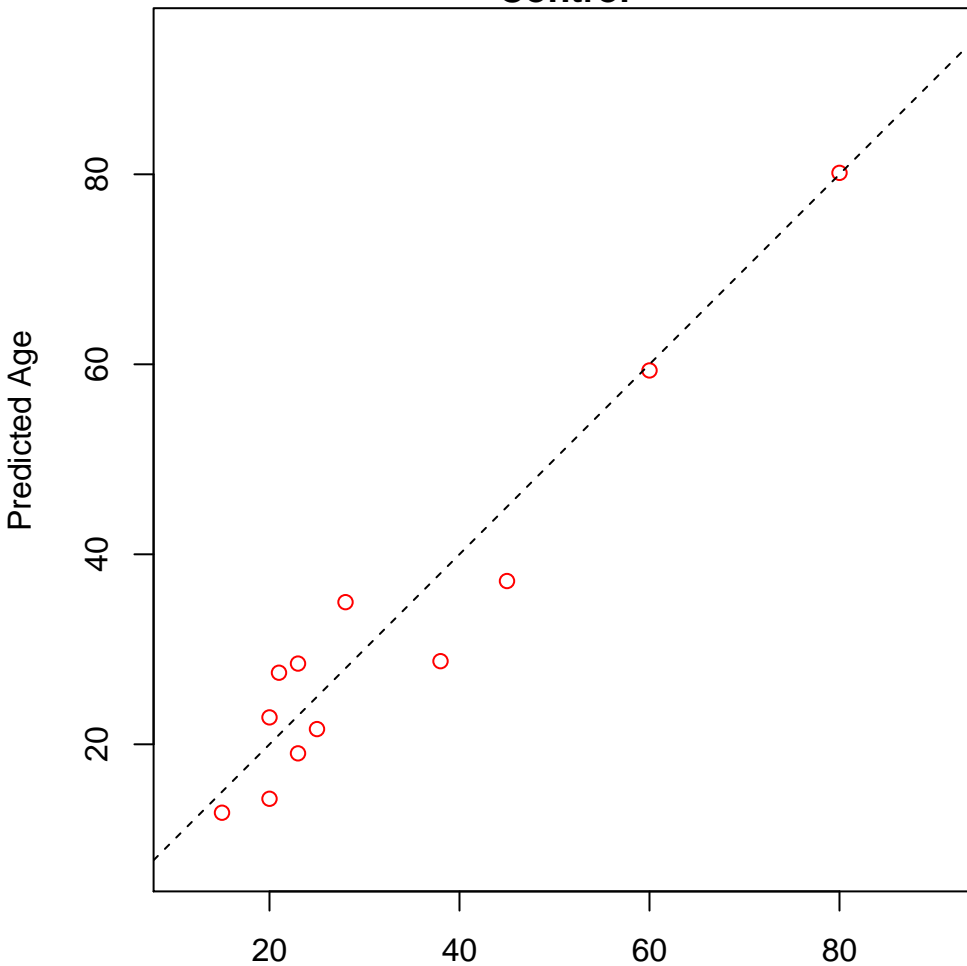


cellular response to tumor necrosis factor (Score: 21.246735)

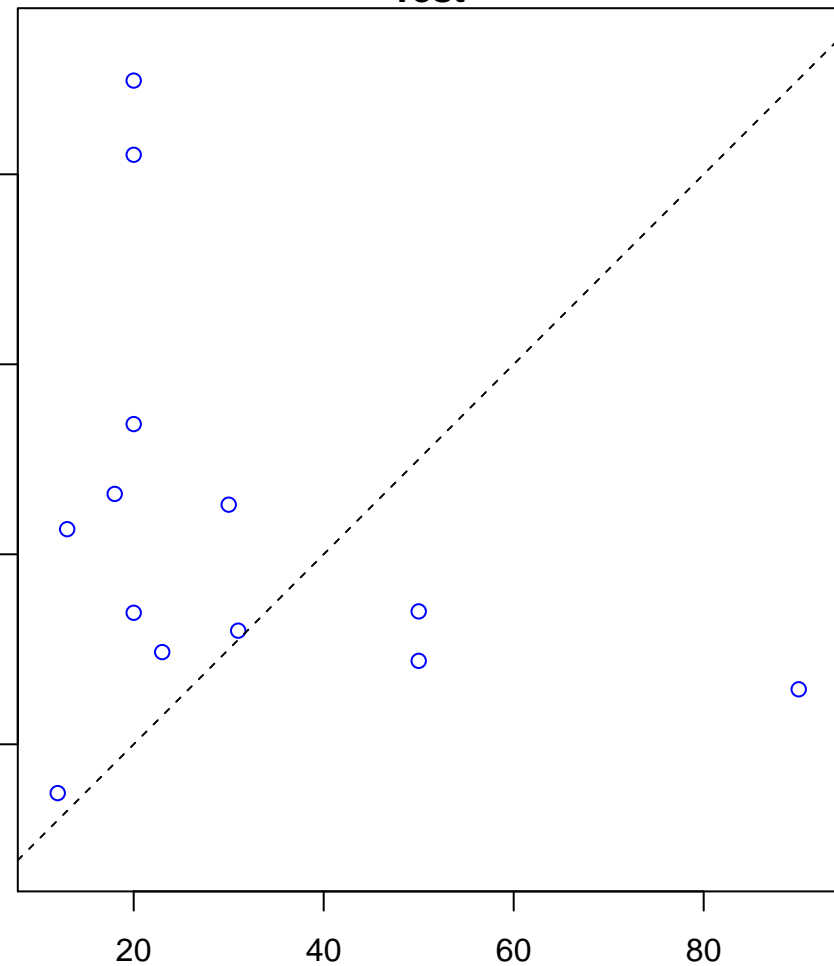


nucleotide transmembrane transport (Score: 21.232892)

Control

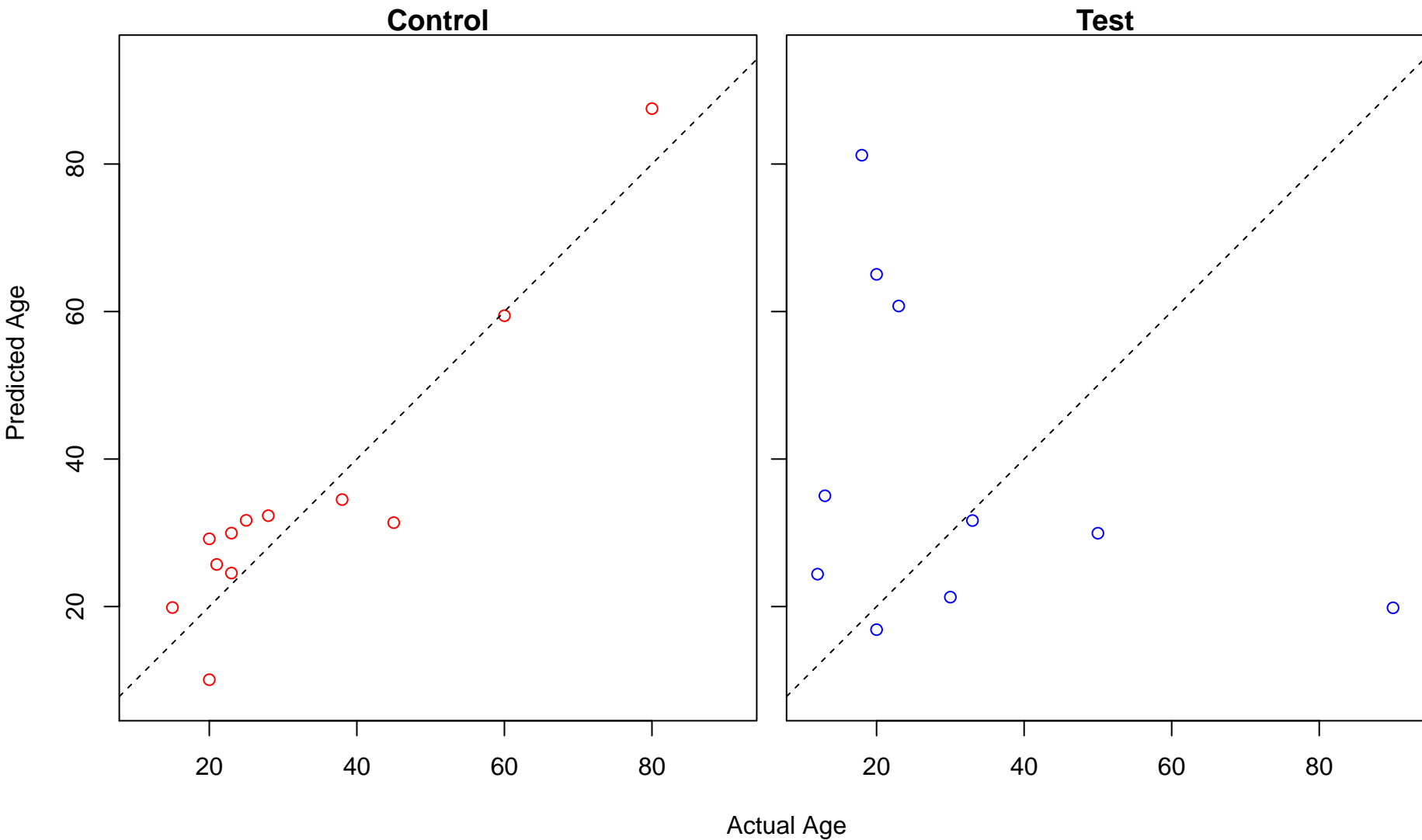


Test

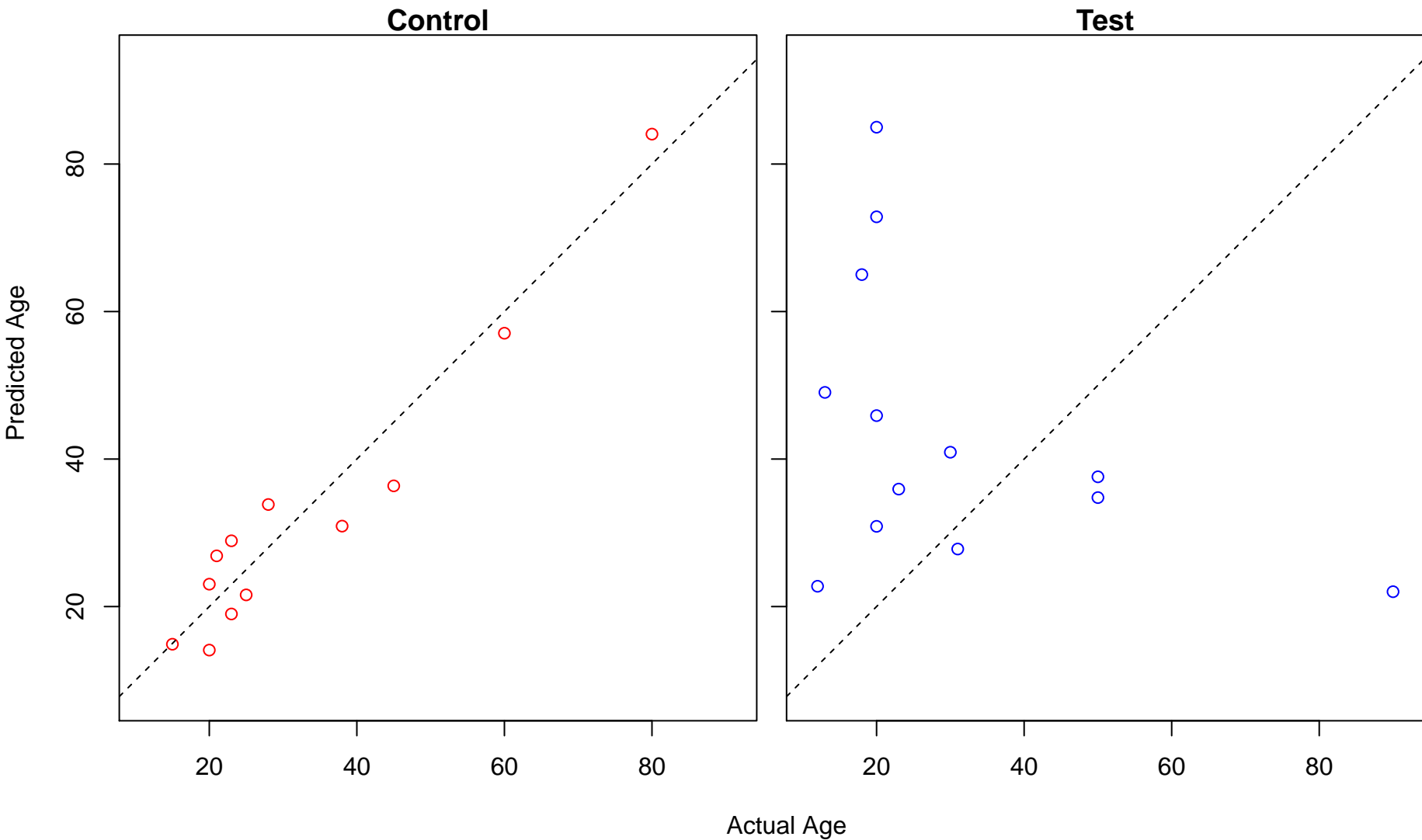


Actual Age

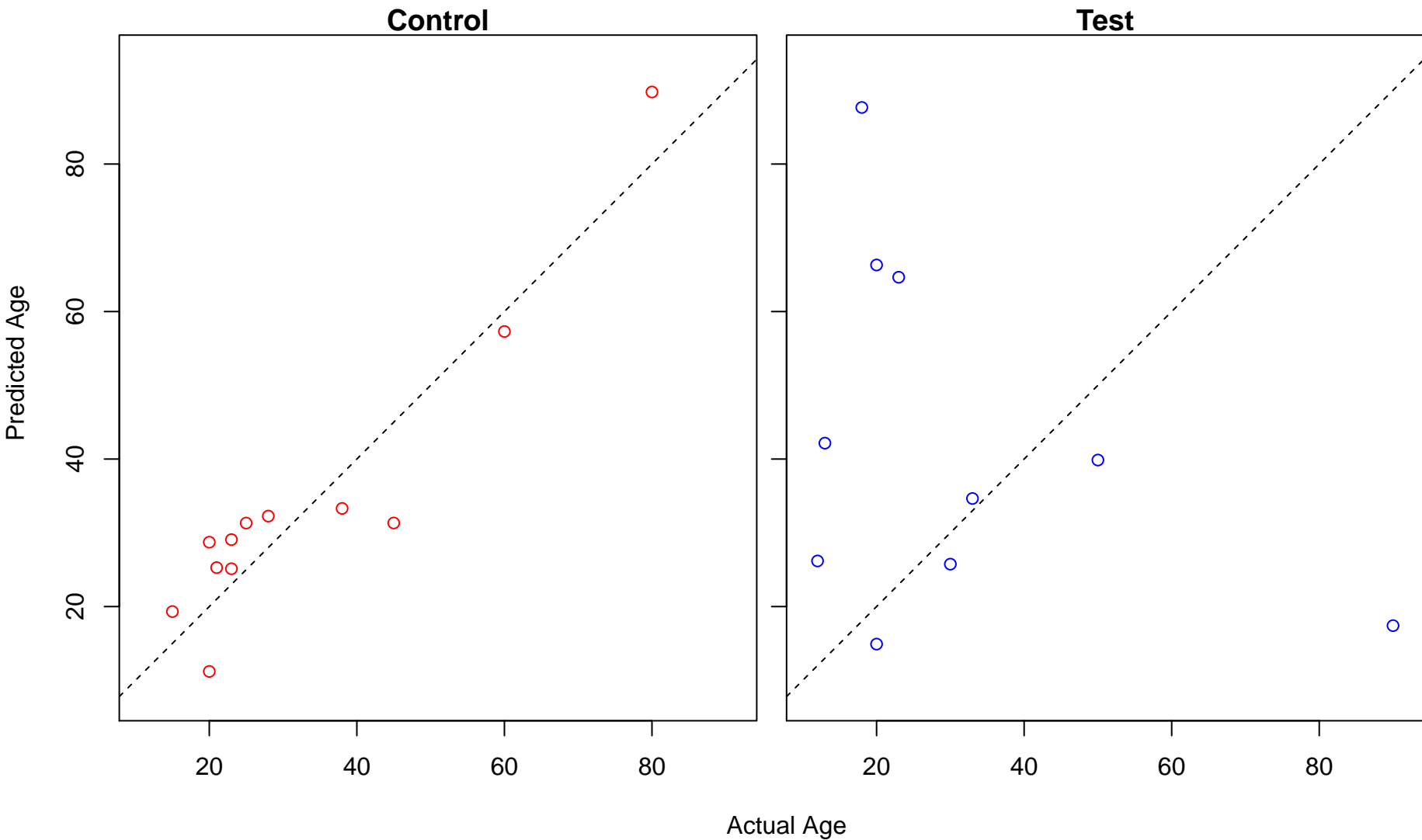
nucleoside monophosphate metabolic process (Score: 21.183520)



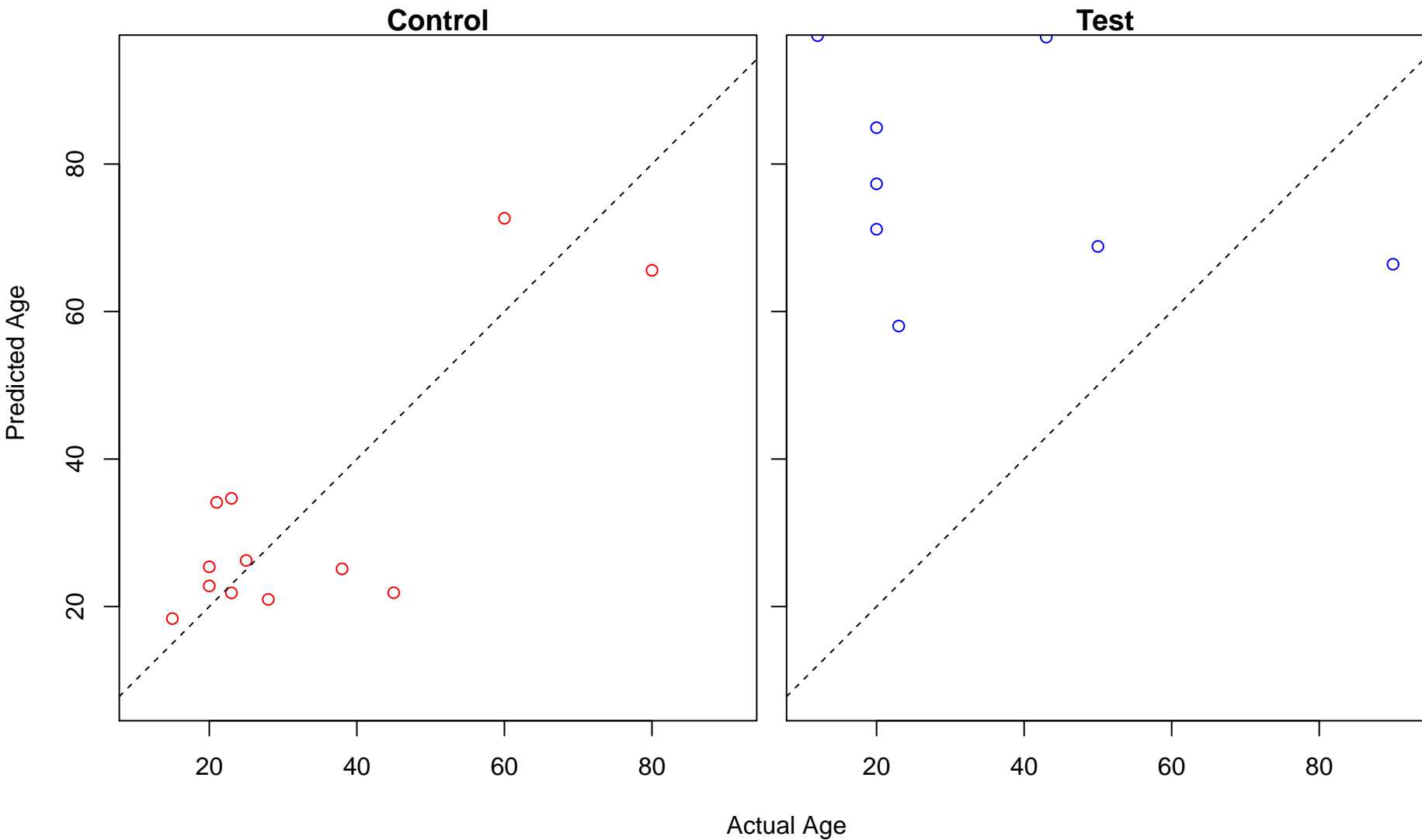
nucleotide transport (Score: 21.114663)



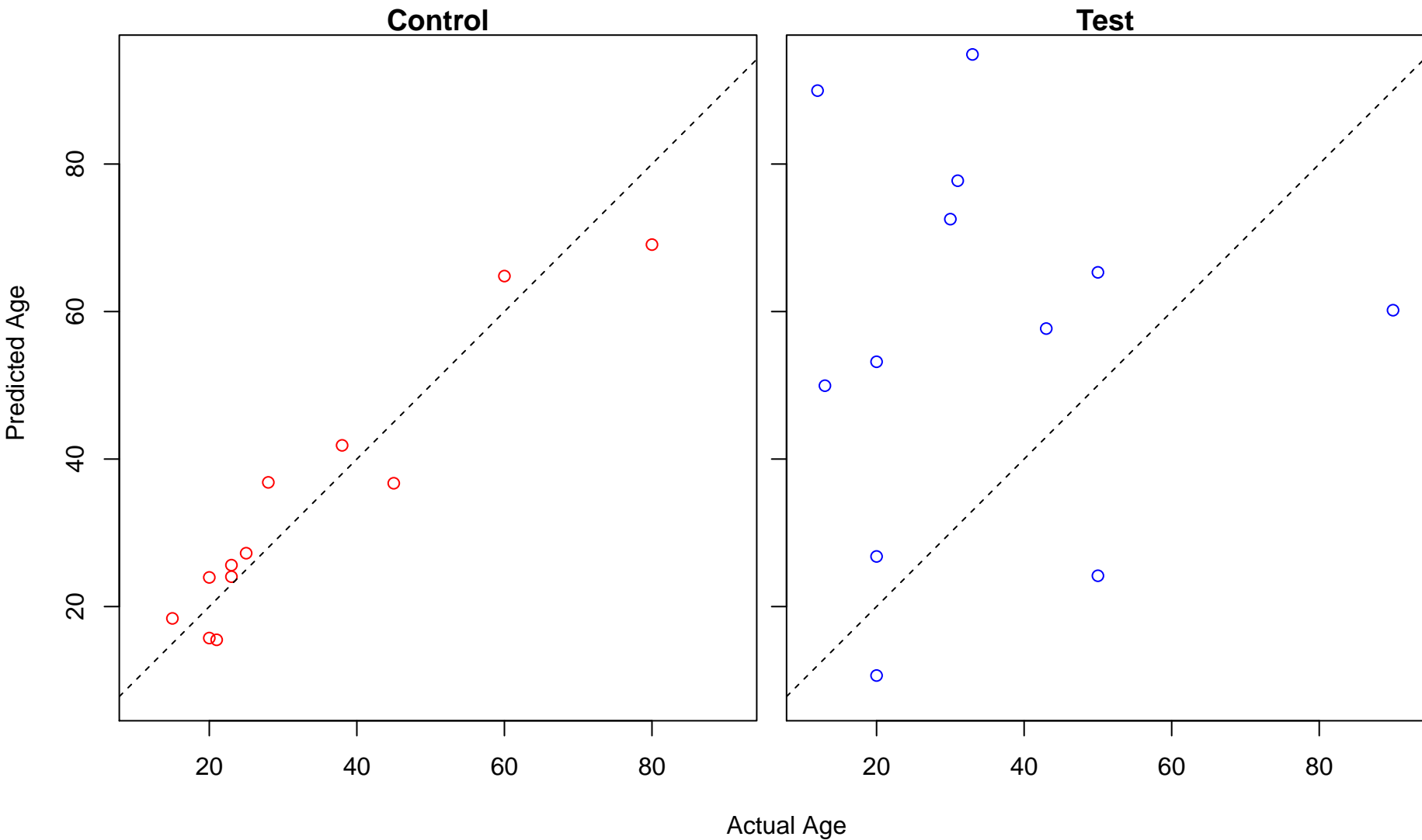
ribonucleoside metabolic process (Score: 21.061686)



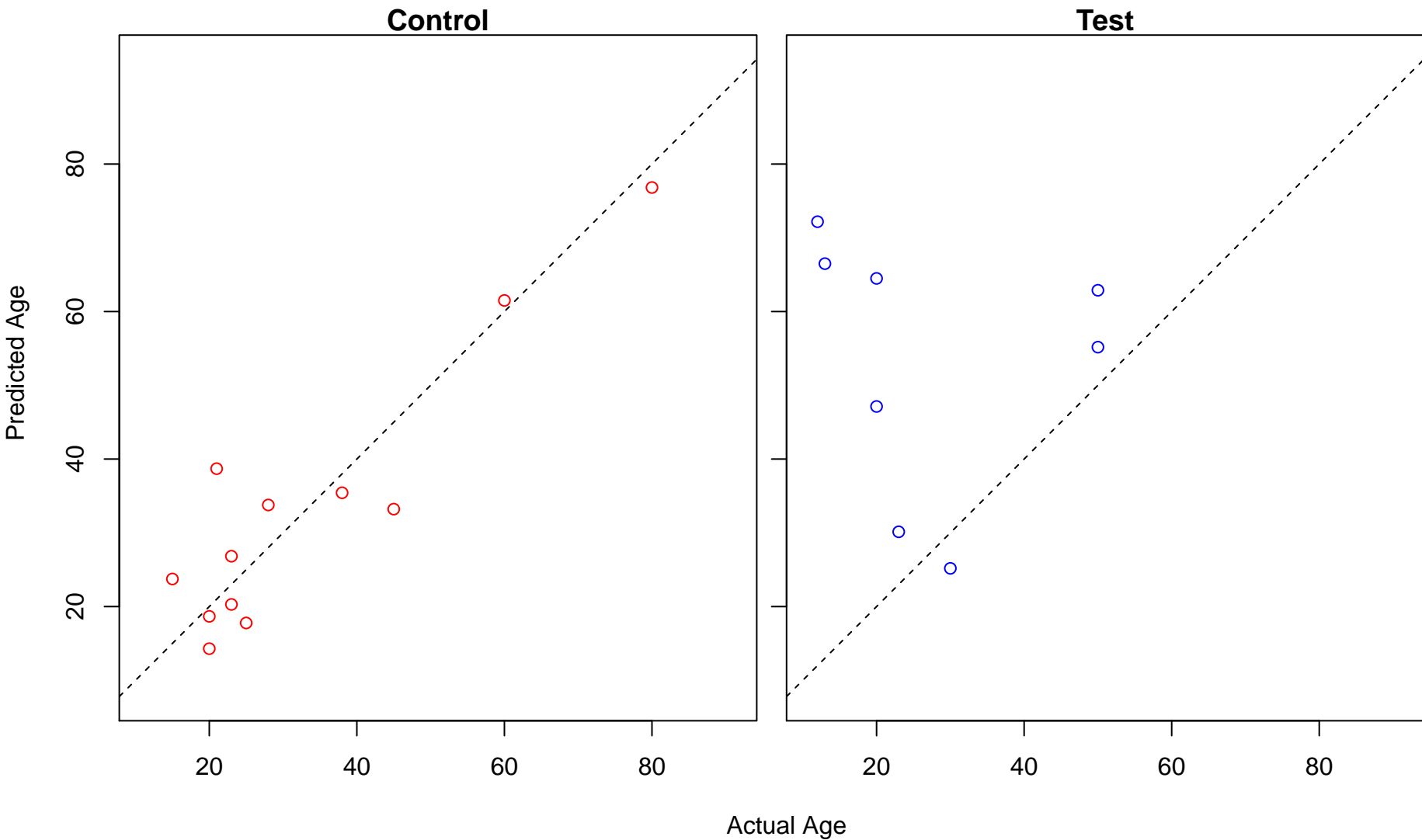
positive regulation of steroid biosynthetic process (Score: 21.010407)



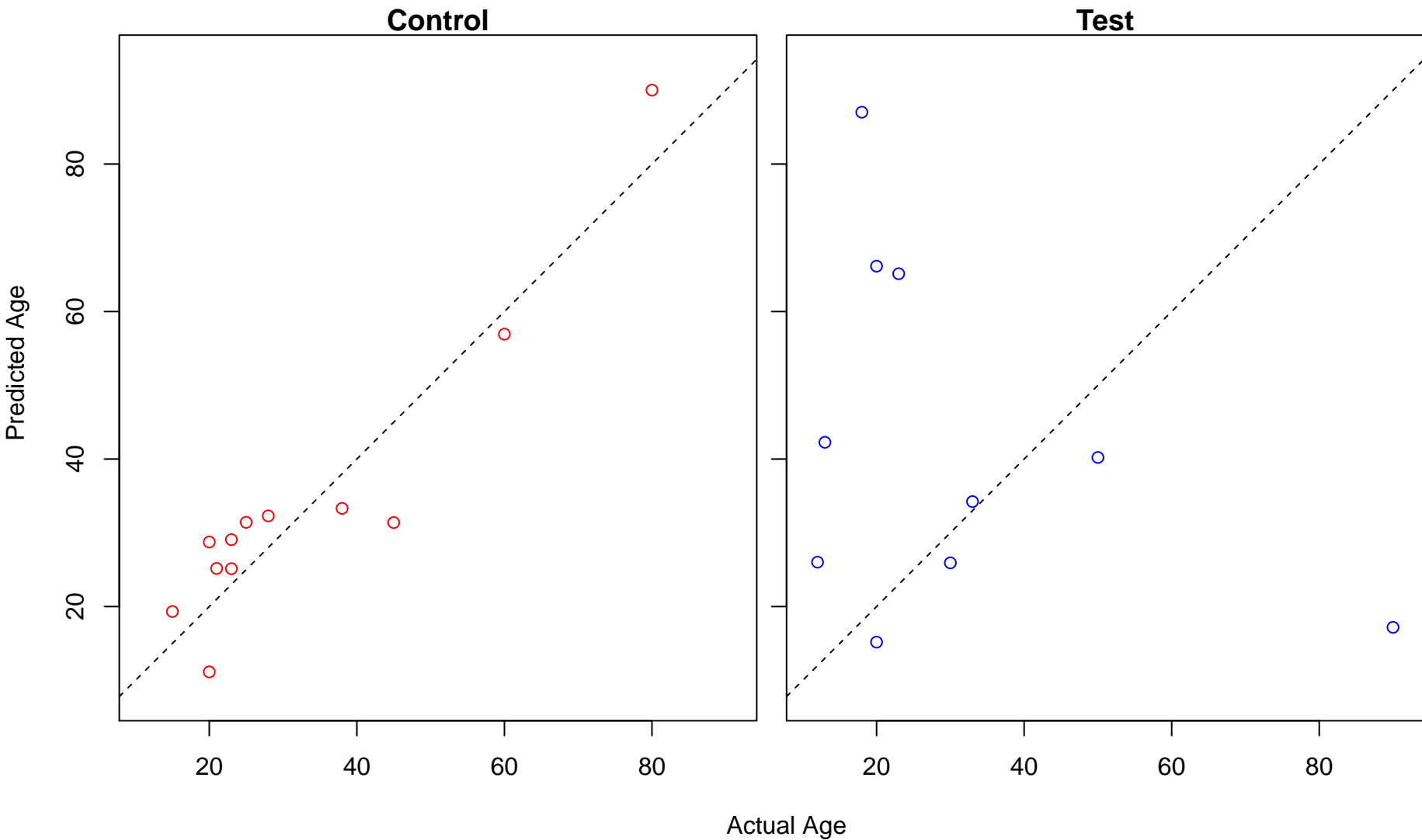
regulation of DNA damage checkpoint (Score: 20.992448)



positive regulation of glucose metabolic process (Score: 20.935562)

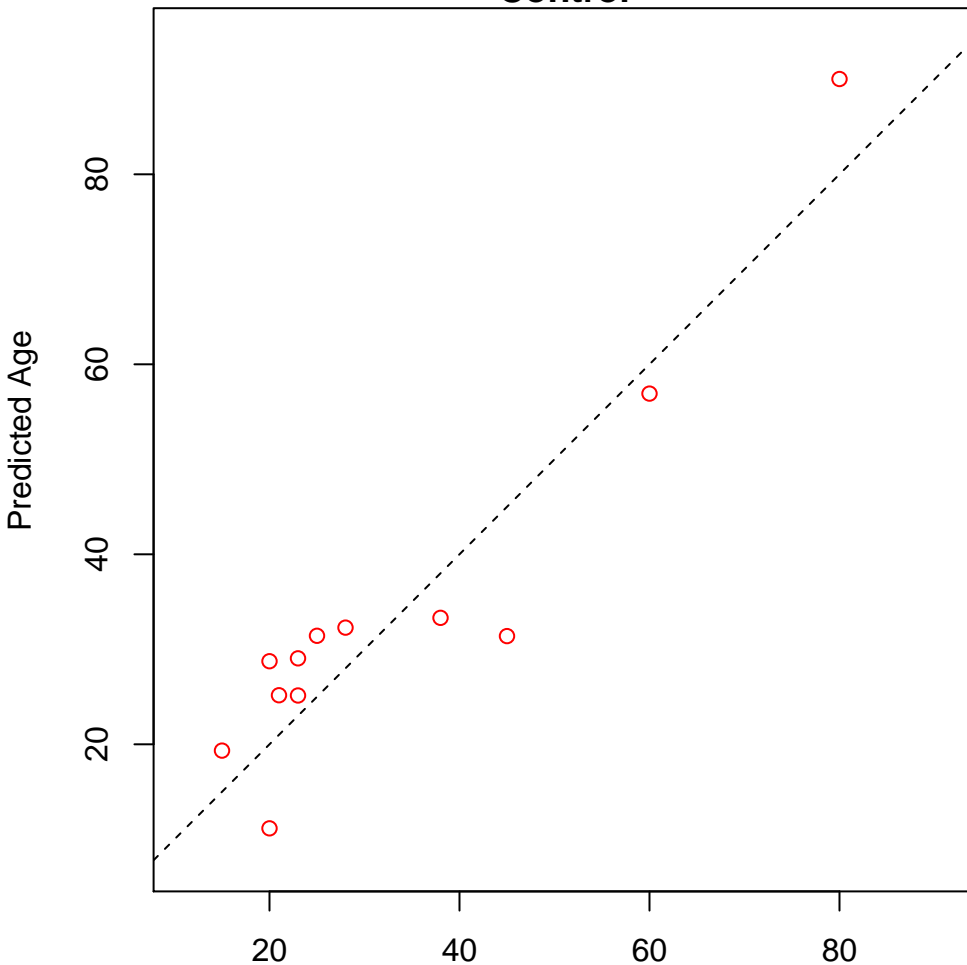


purine ribonucleoside metabolic process (Score: 20.921698)

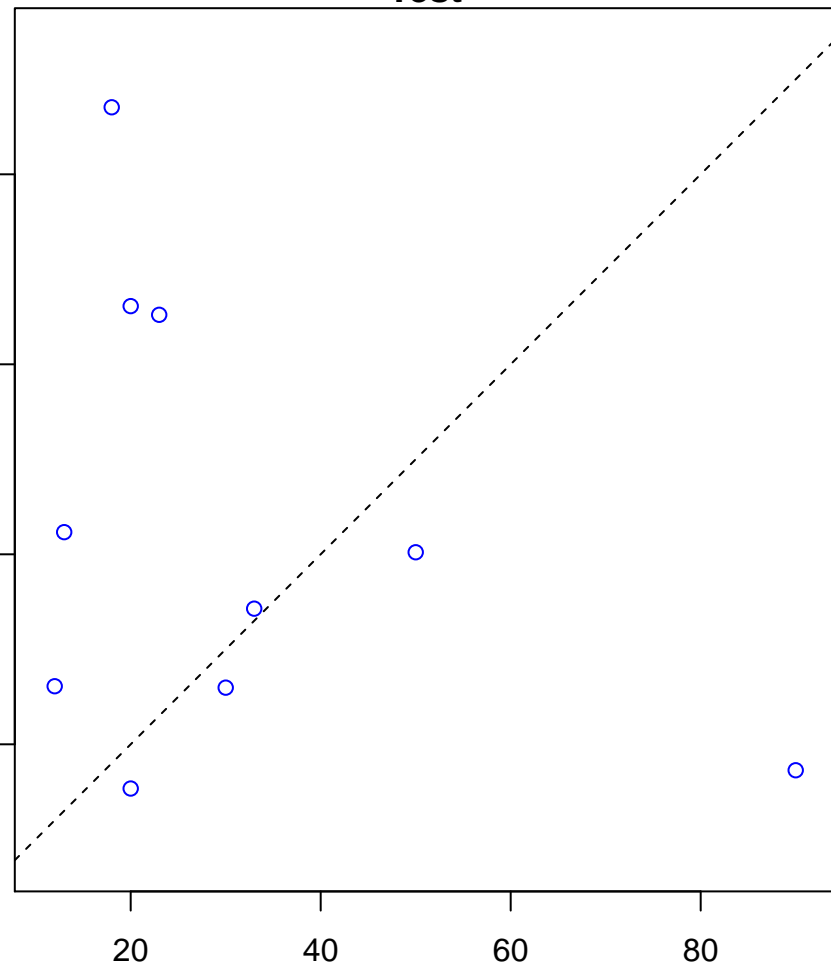


purine nucleoside metabolic process (Score: 20.912317)

Control



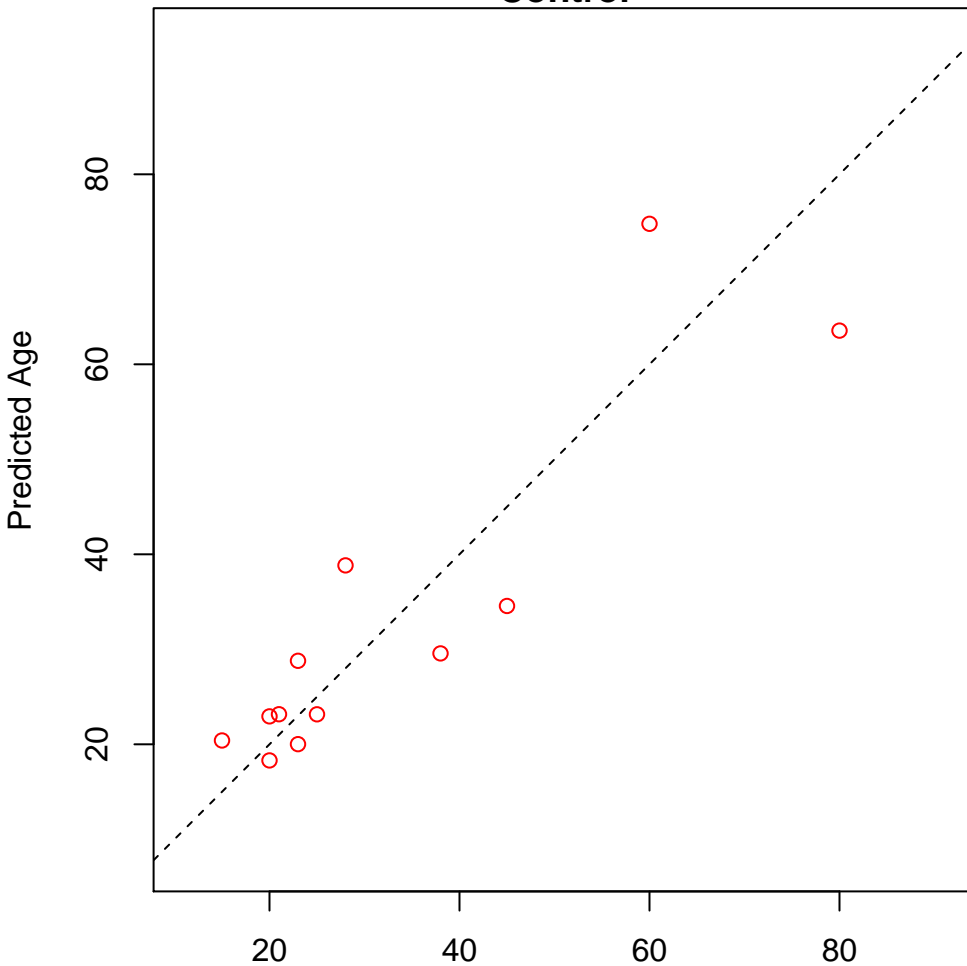
Test



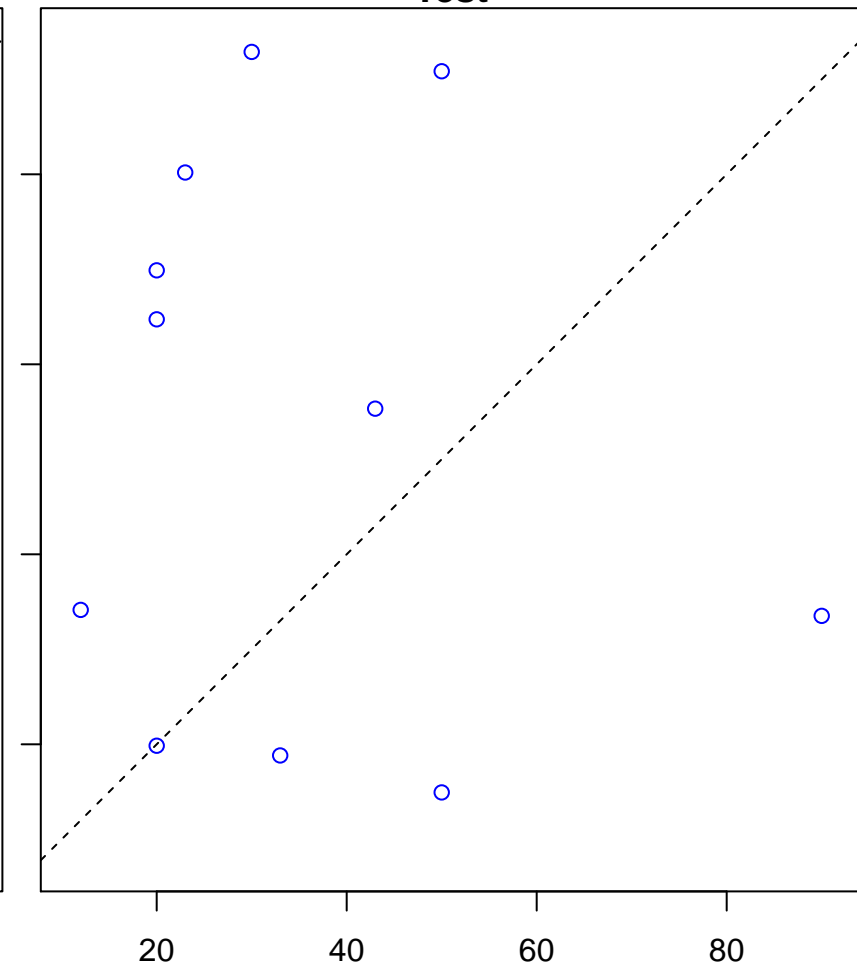
Actual Age

regulation of neurotransmitter uptake (Score: 20.880490)

Control

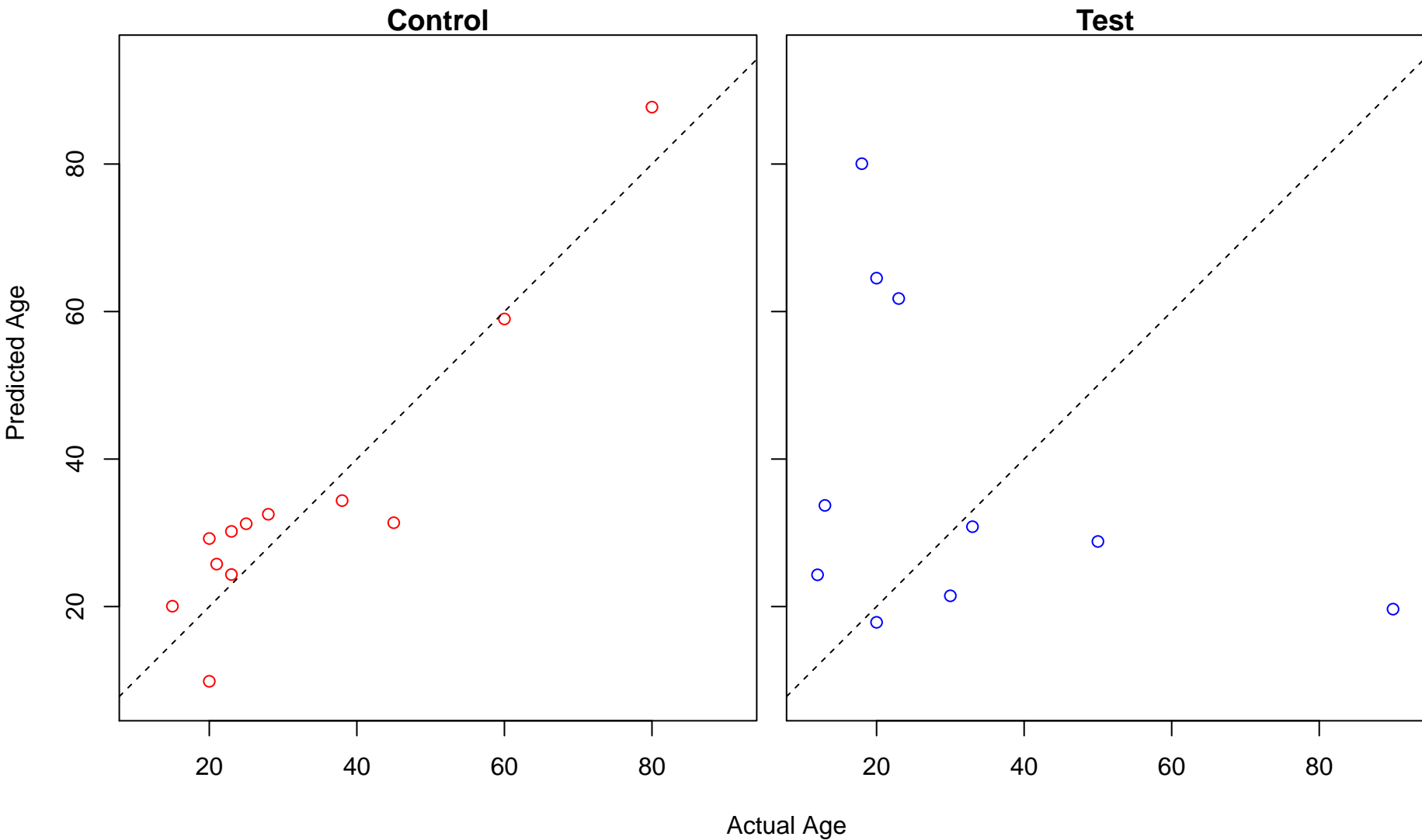


Test

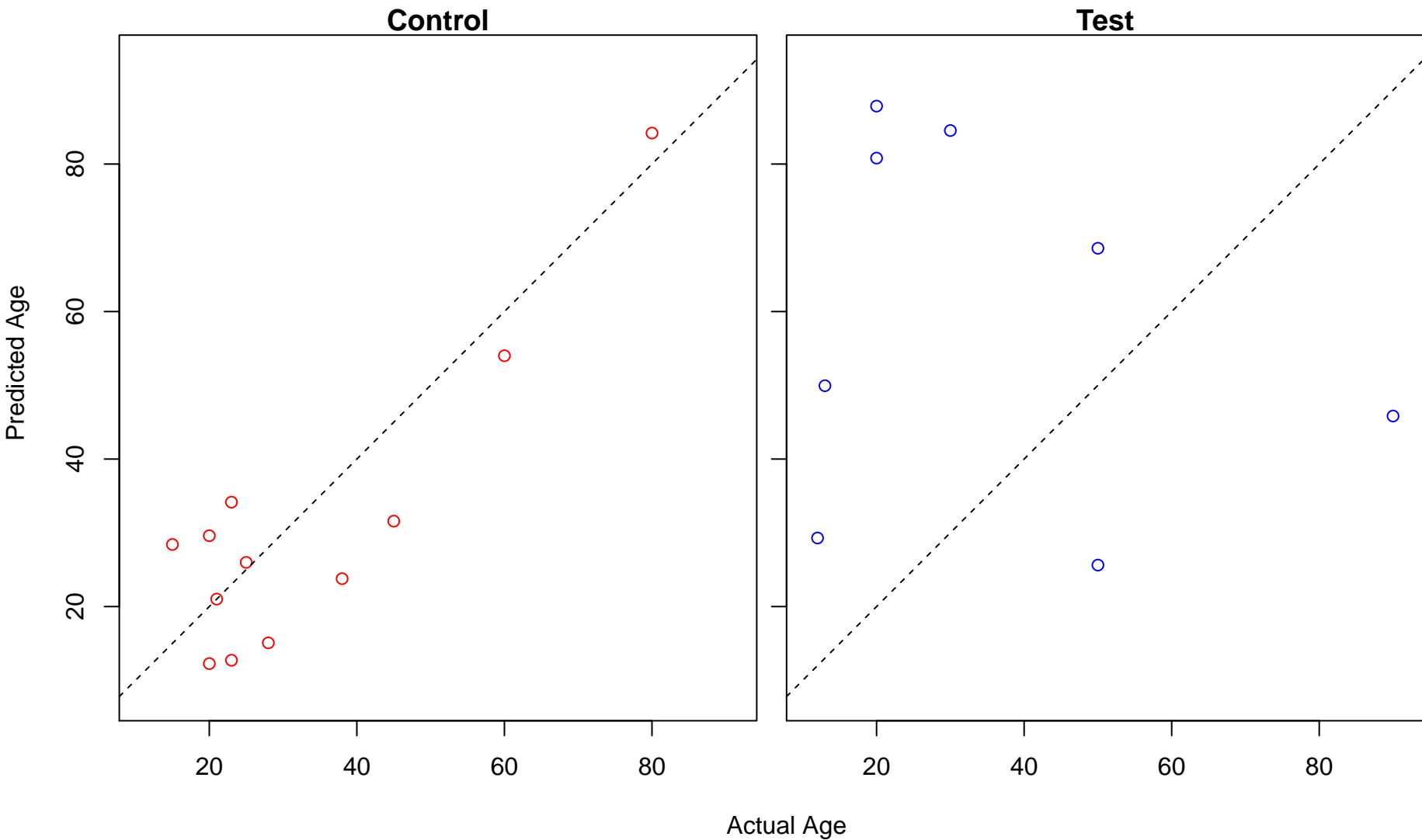


Actual Age

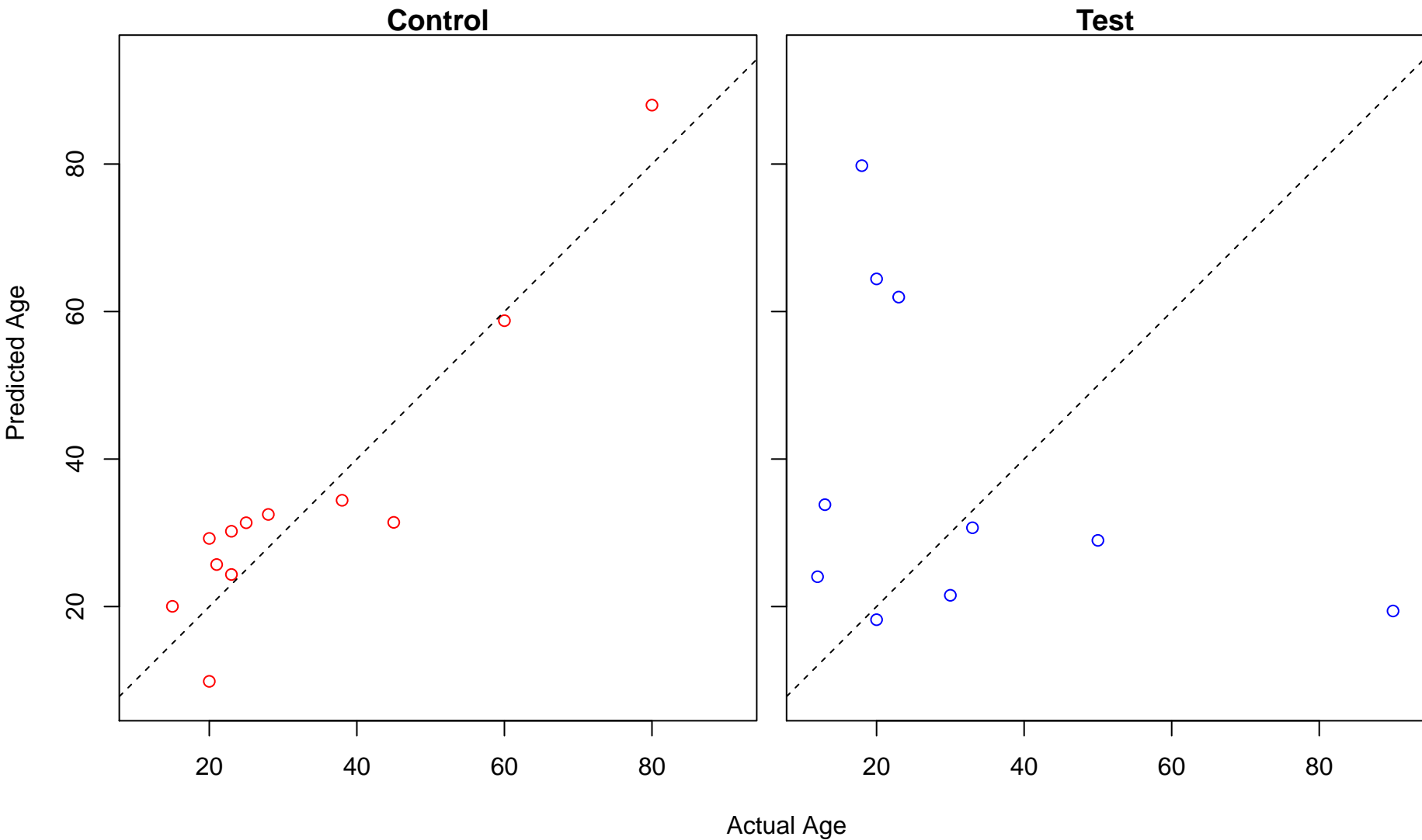
ribonucleoside monophosphate metabolic process (Score: 20.864617)



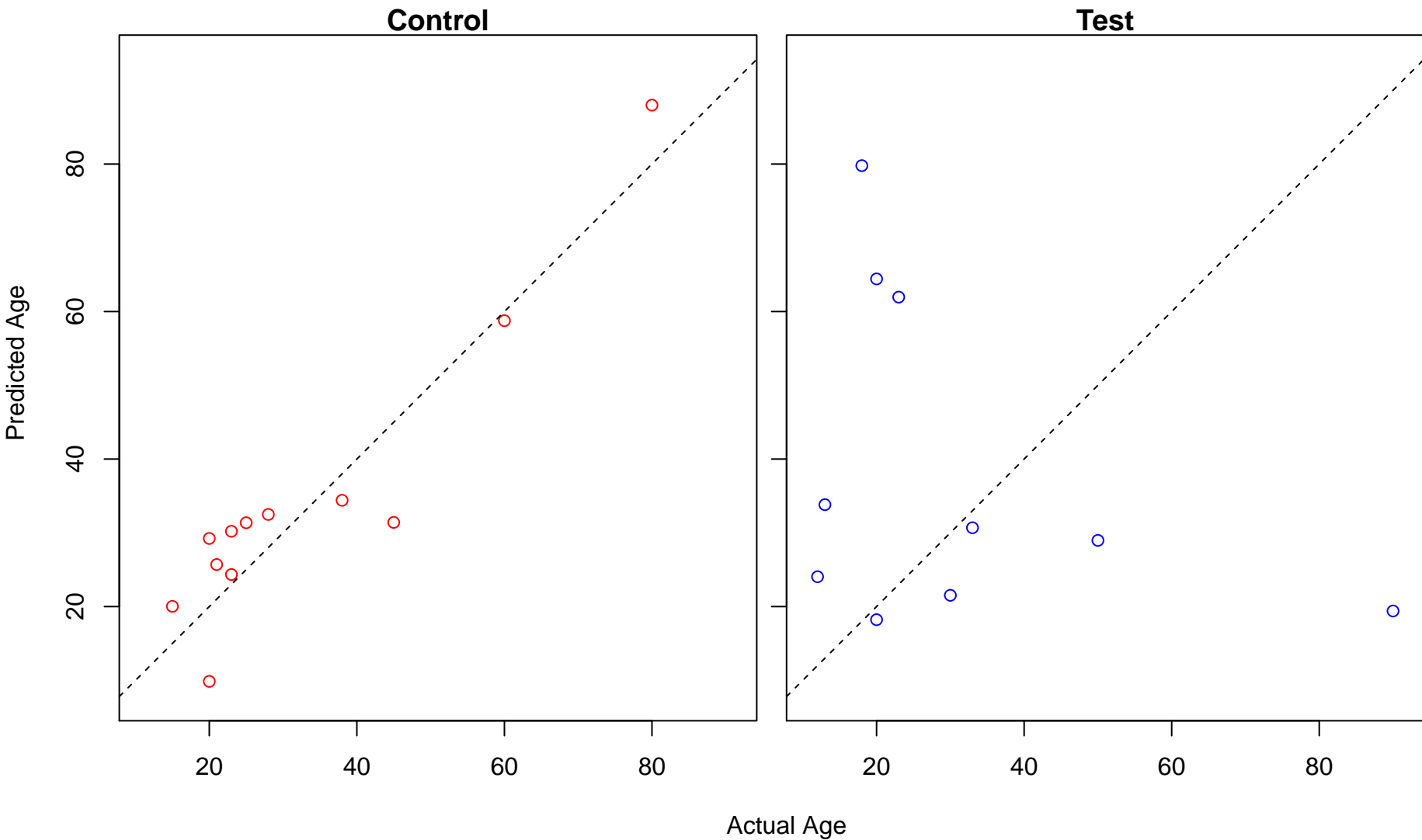
regulation of alternative mRNA splicing, via spliceosome (Score: 20.836093)



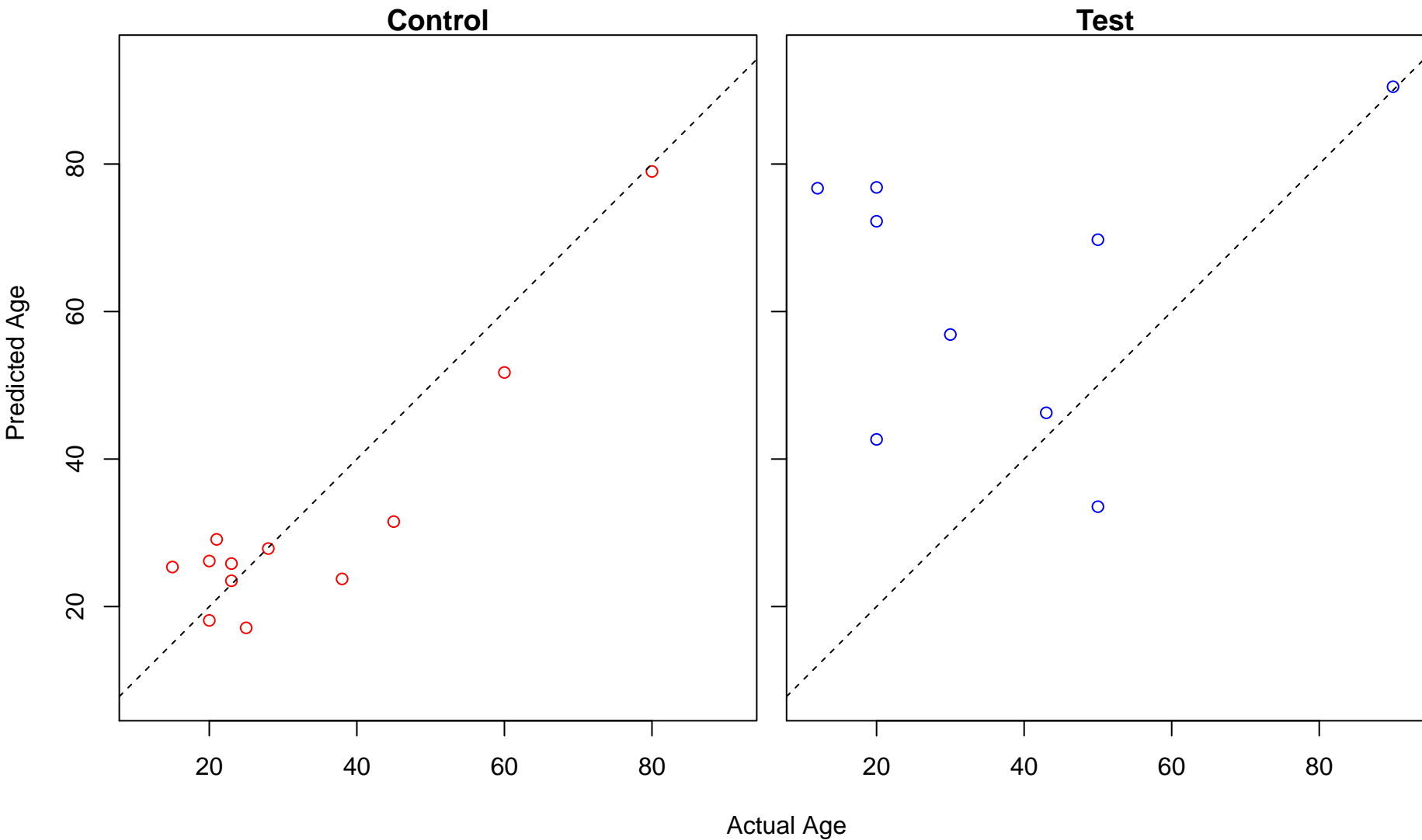
purine nucleoside monophosphate metabolic process (Score: 20.795730)



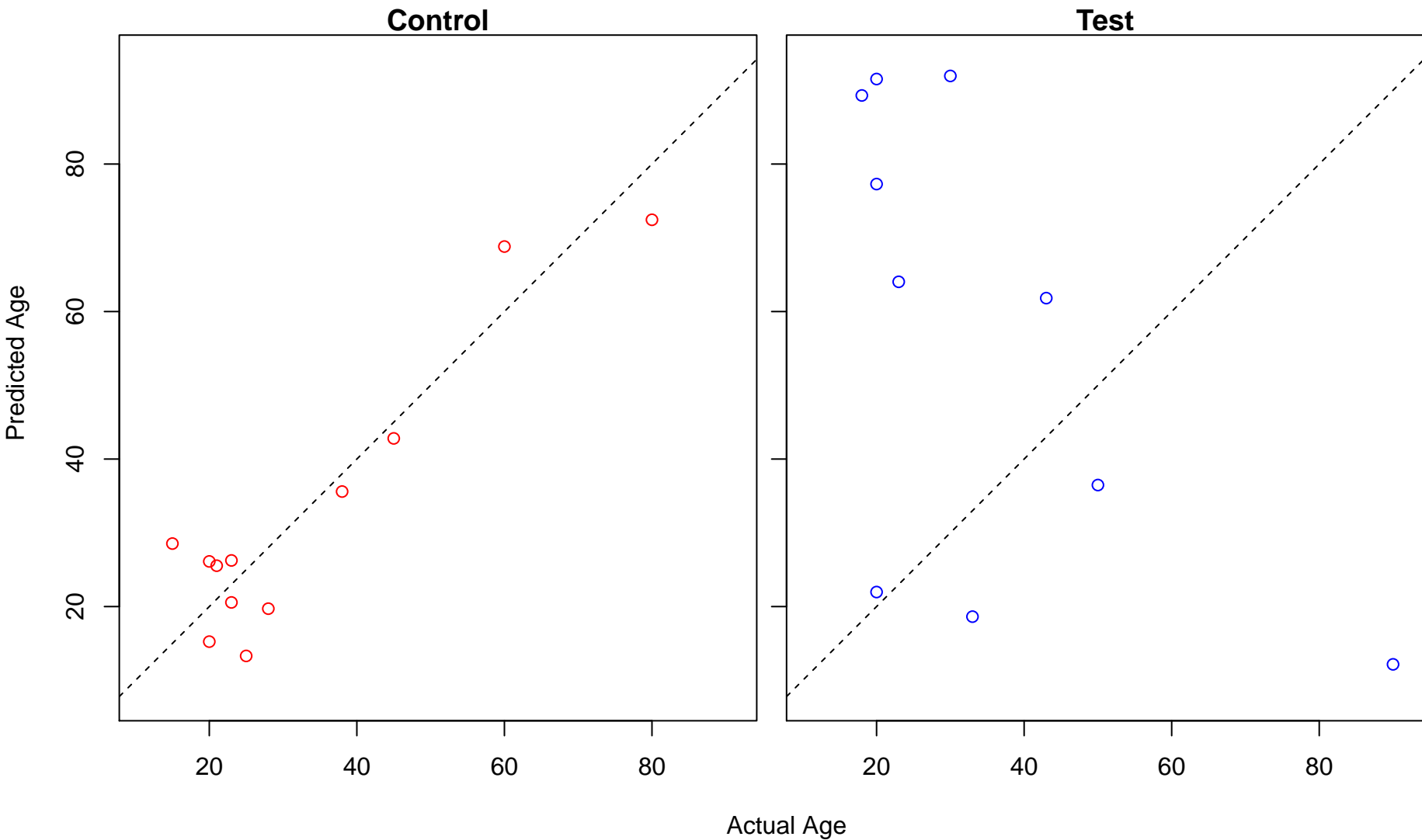
purine ribonucleoside monophosphate metabolic process (Score: 20.795730)



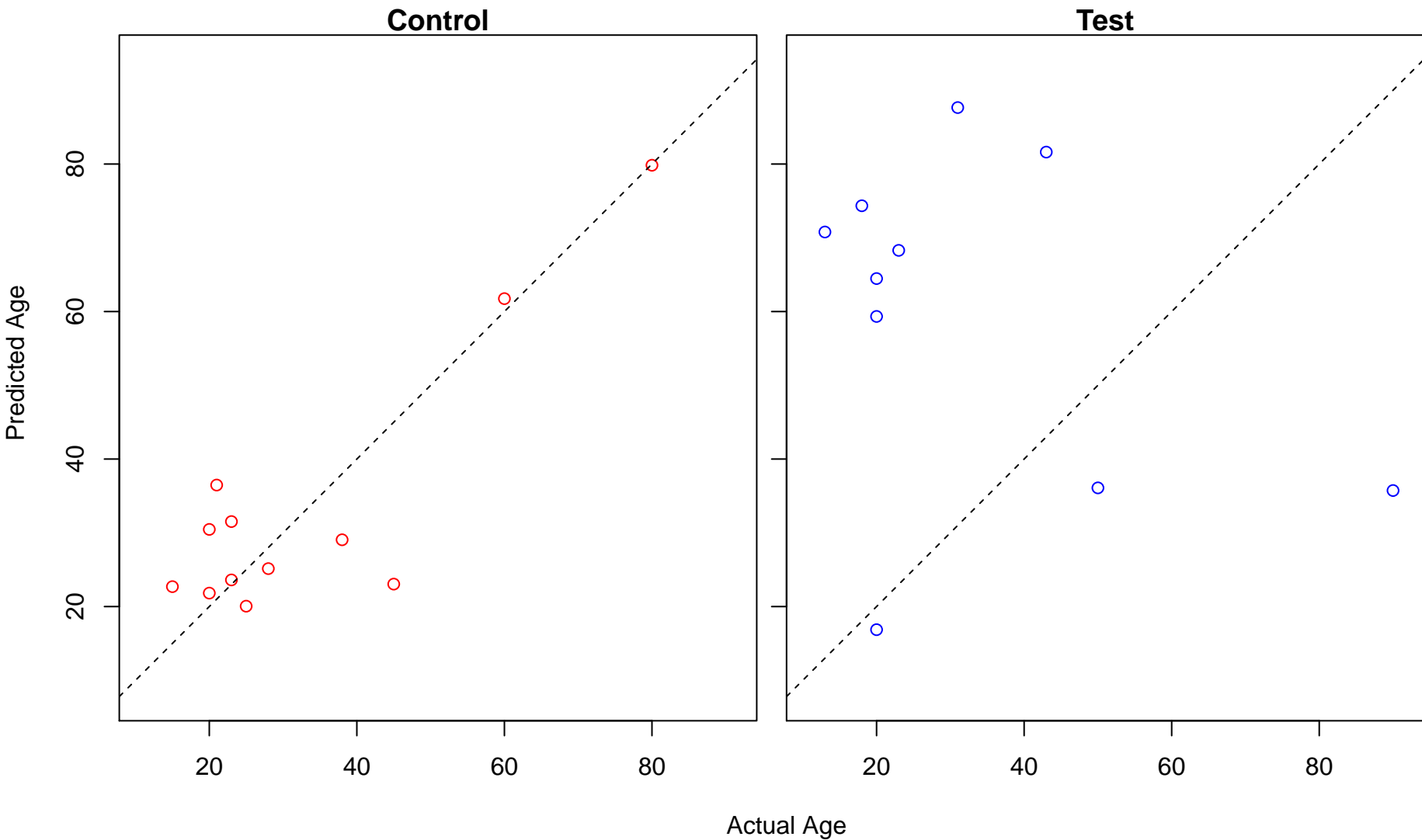
response to redox state (Score: 20.759752)



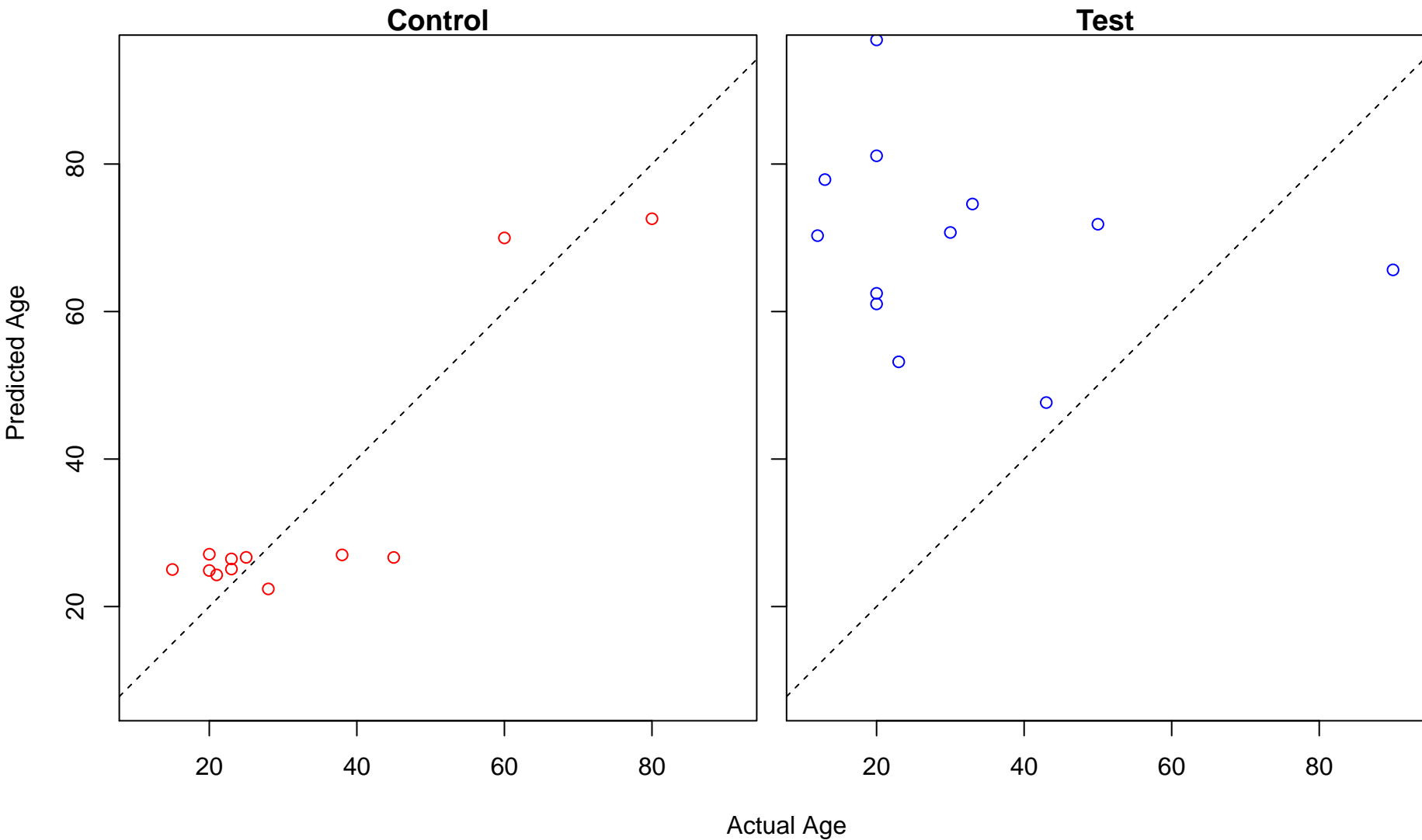
RNA 5'-end processing (Score: 20.748275)



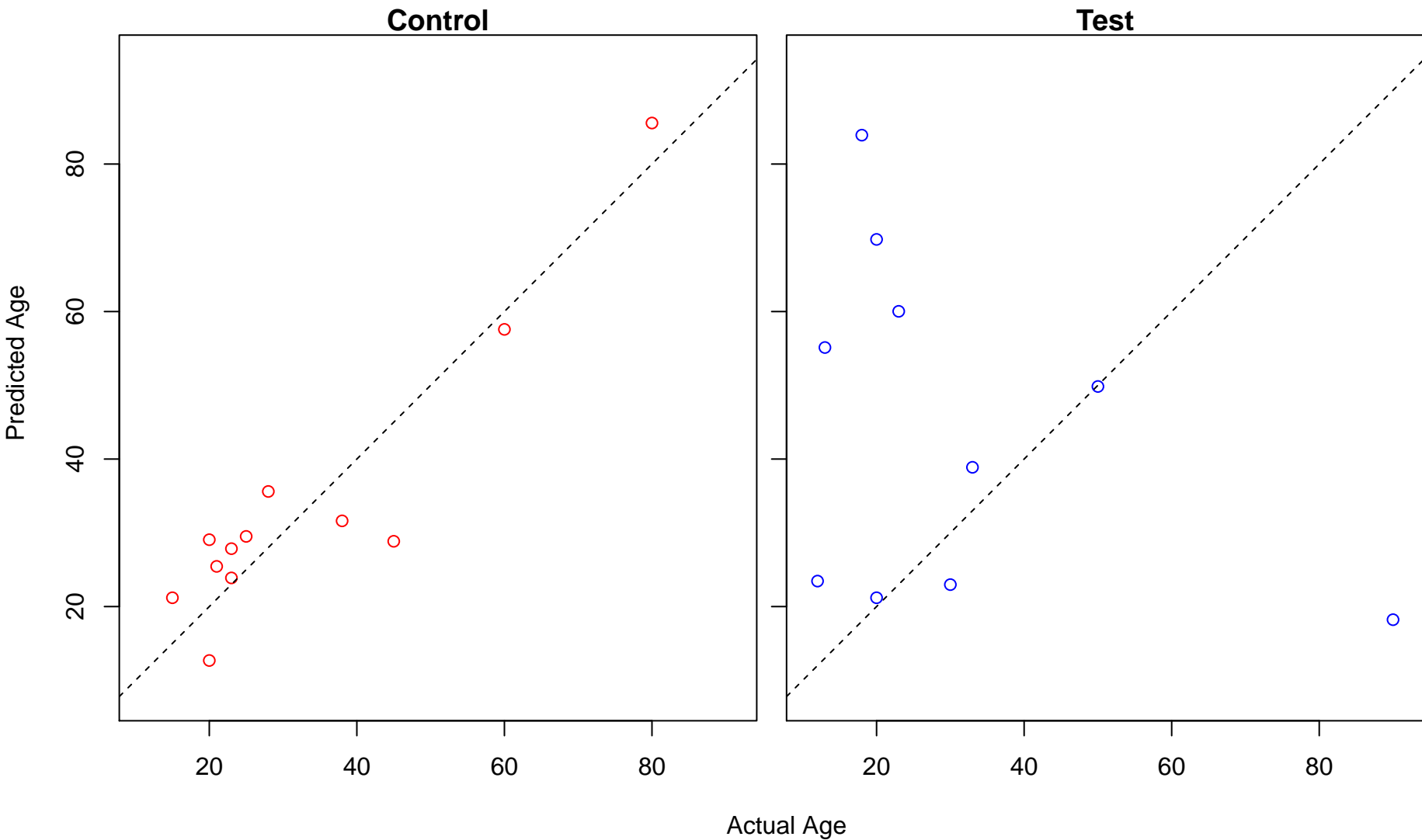
formation of primary germ layer (Score: 20.717488)



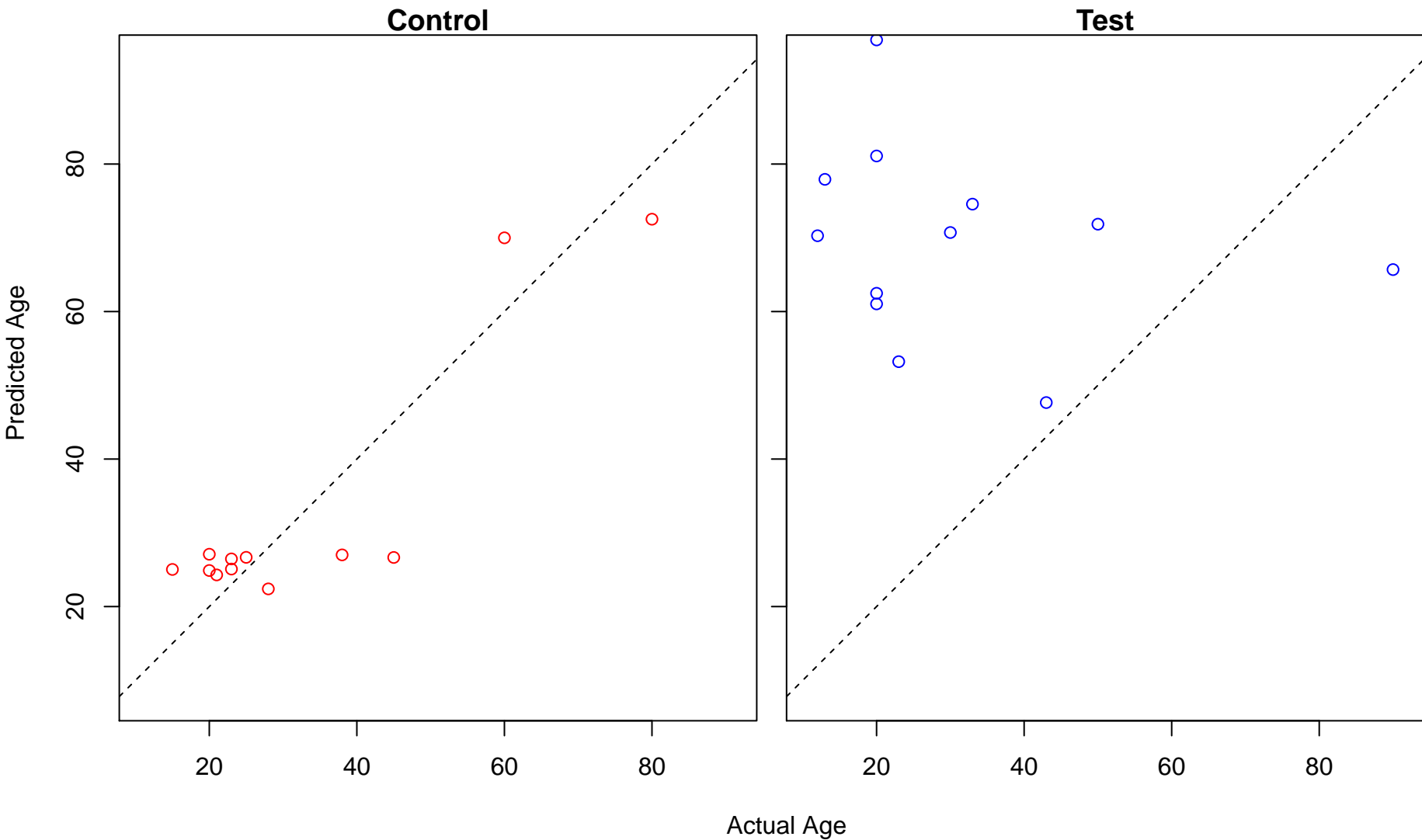
positive regulation of cardiac muscle contraction (Score: 20.703589)



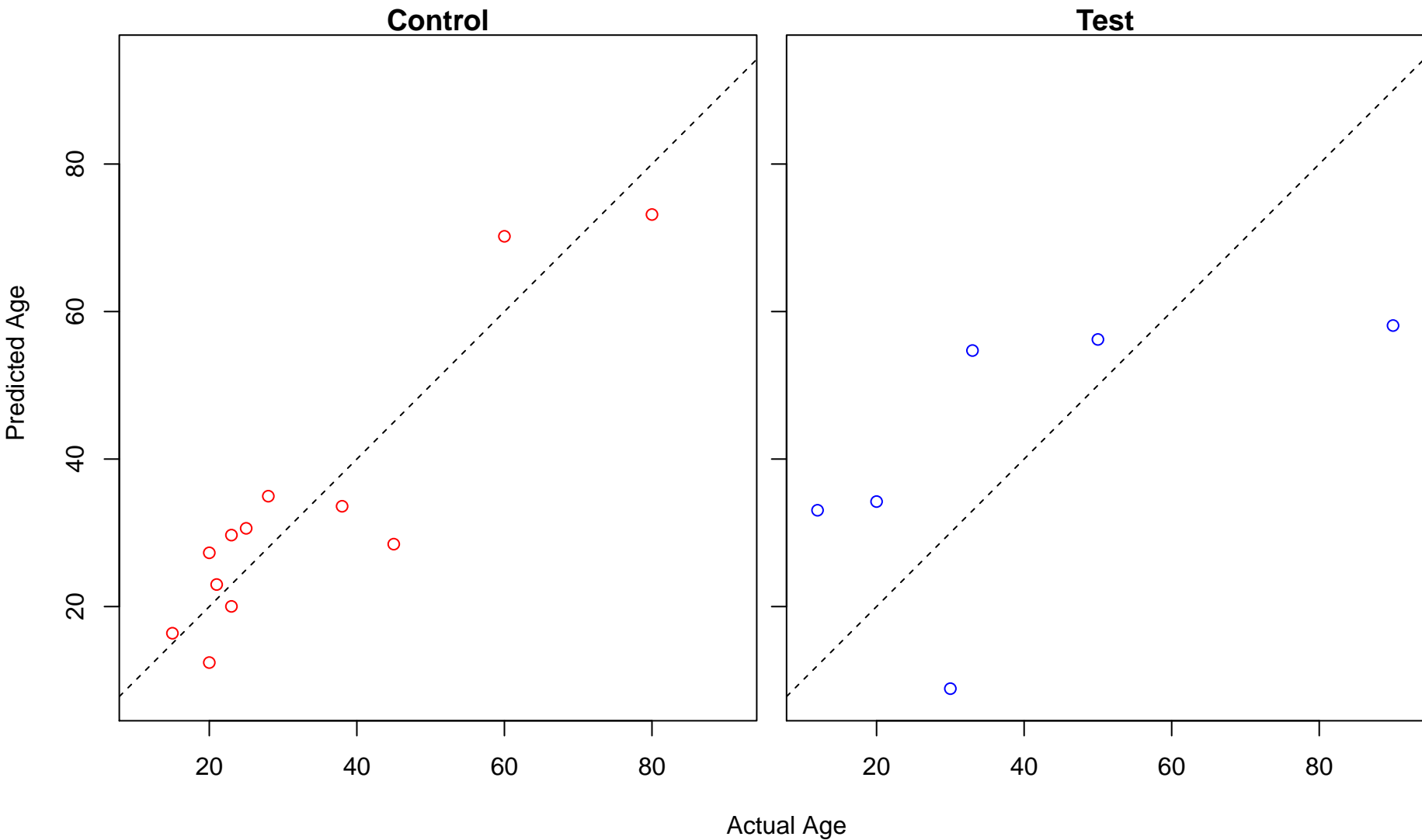
purine-containing compound metabolic process (Score: 20.676342)



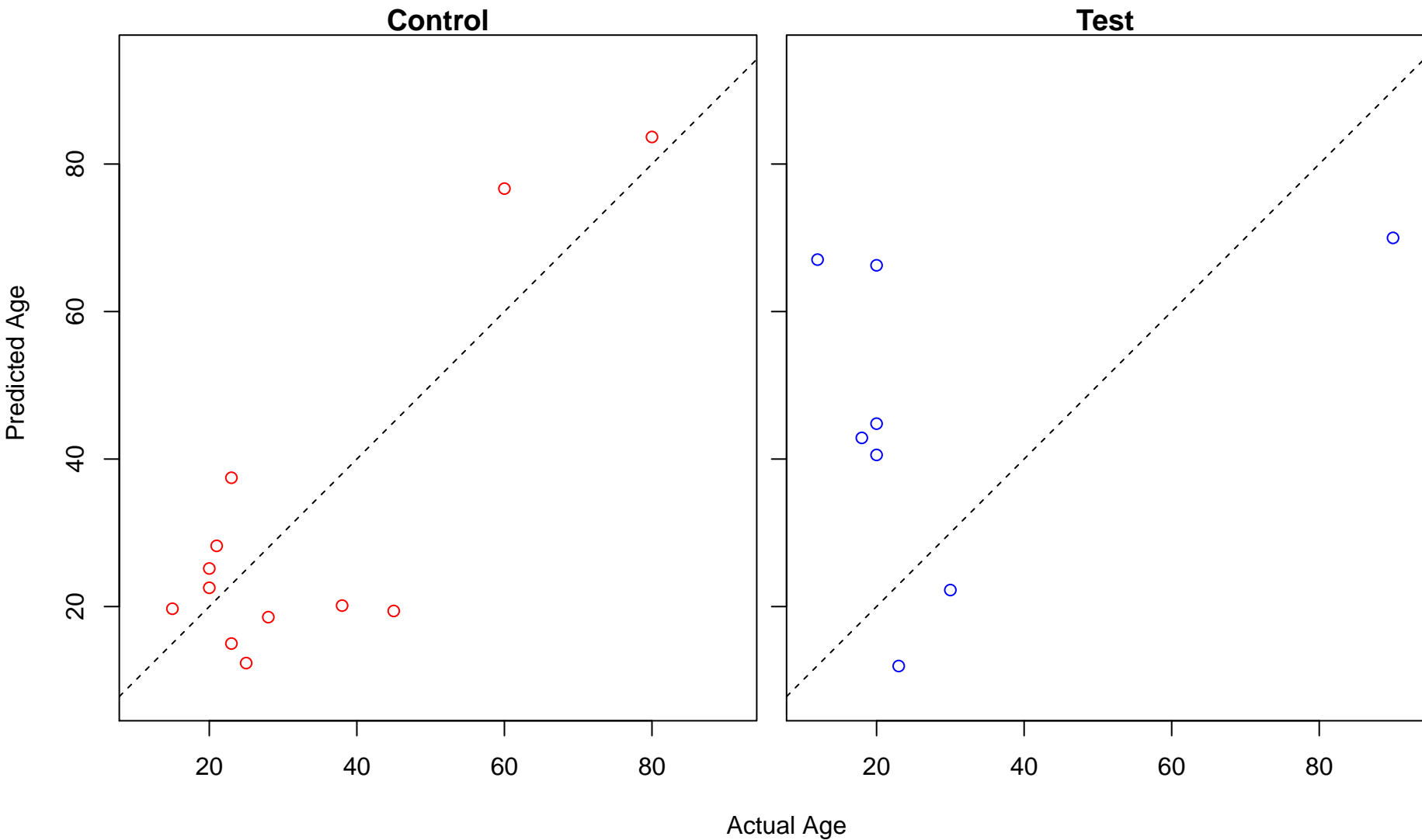
positive regulation of striated muscle contraction (Score: 20.653283)



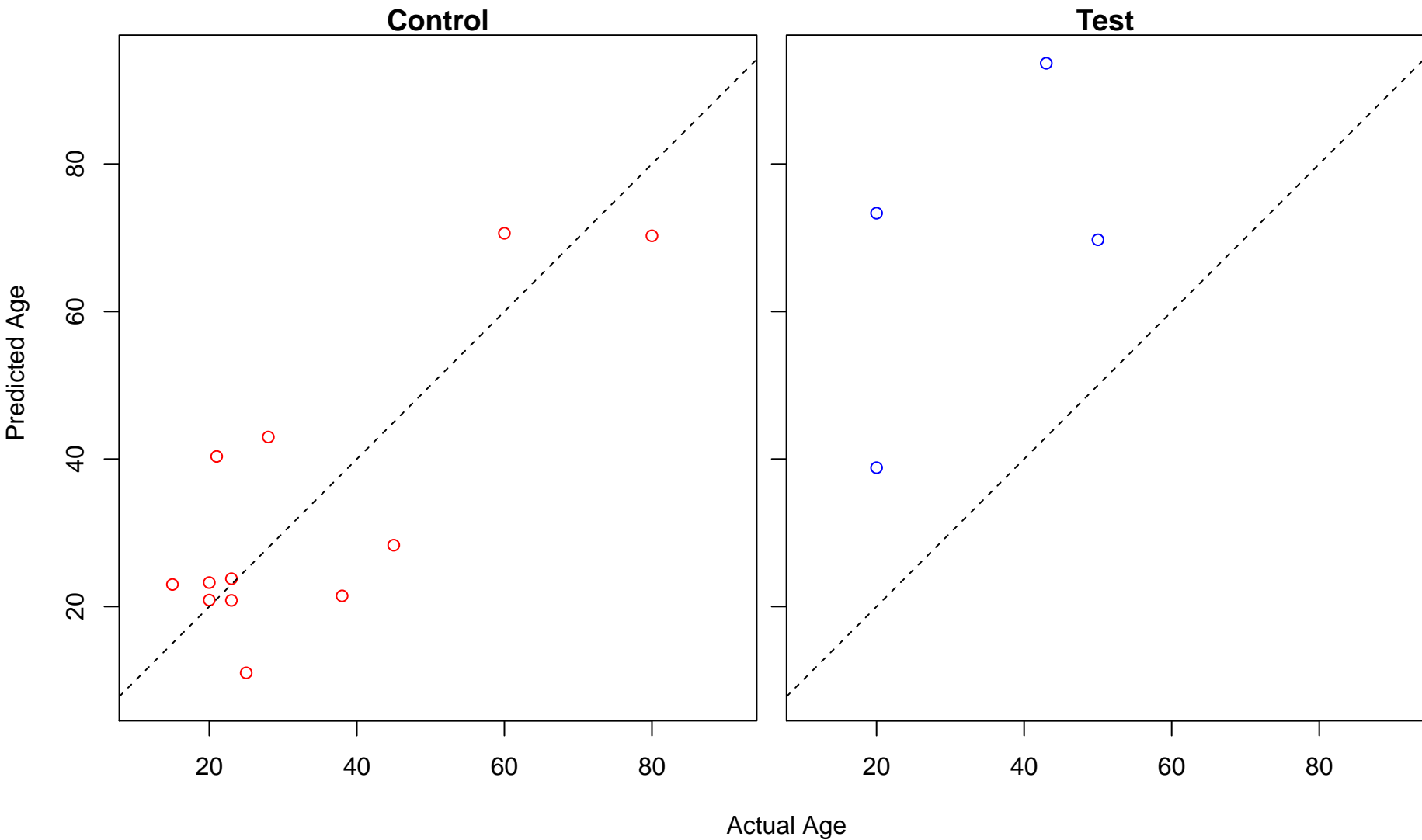
regeneration (Score: 20.647876)



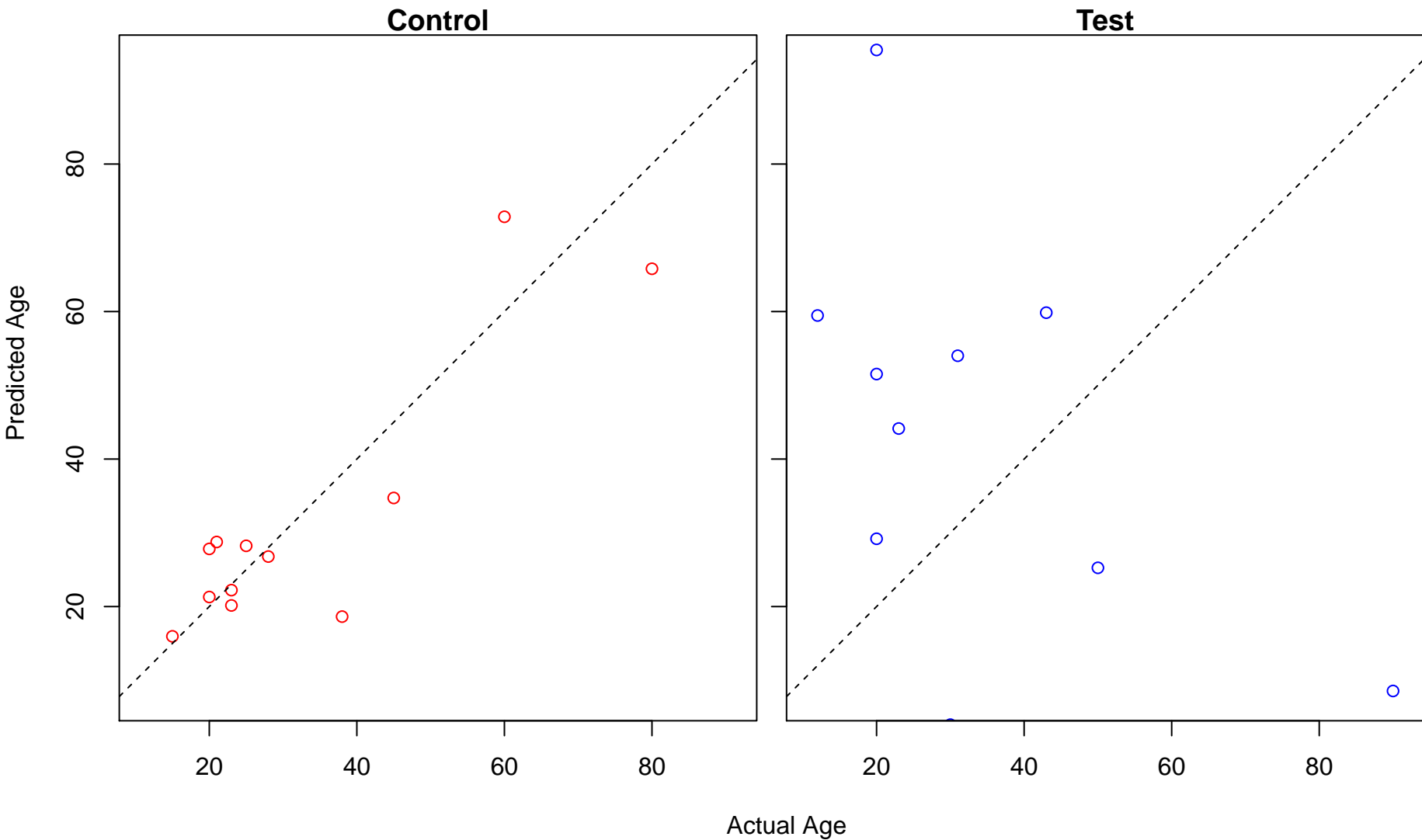
cellular glucuronidation (Score: 20.635914)



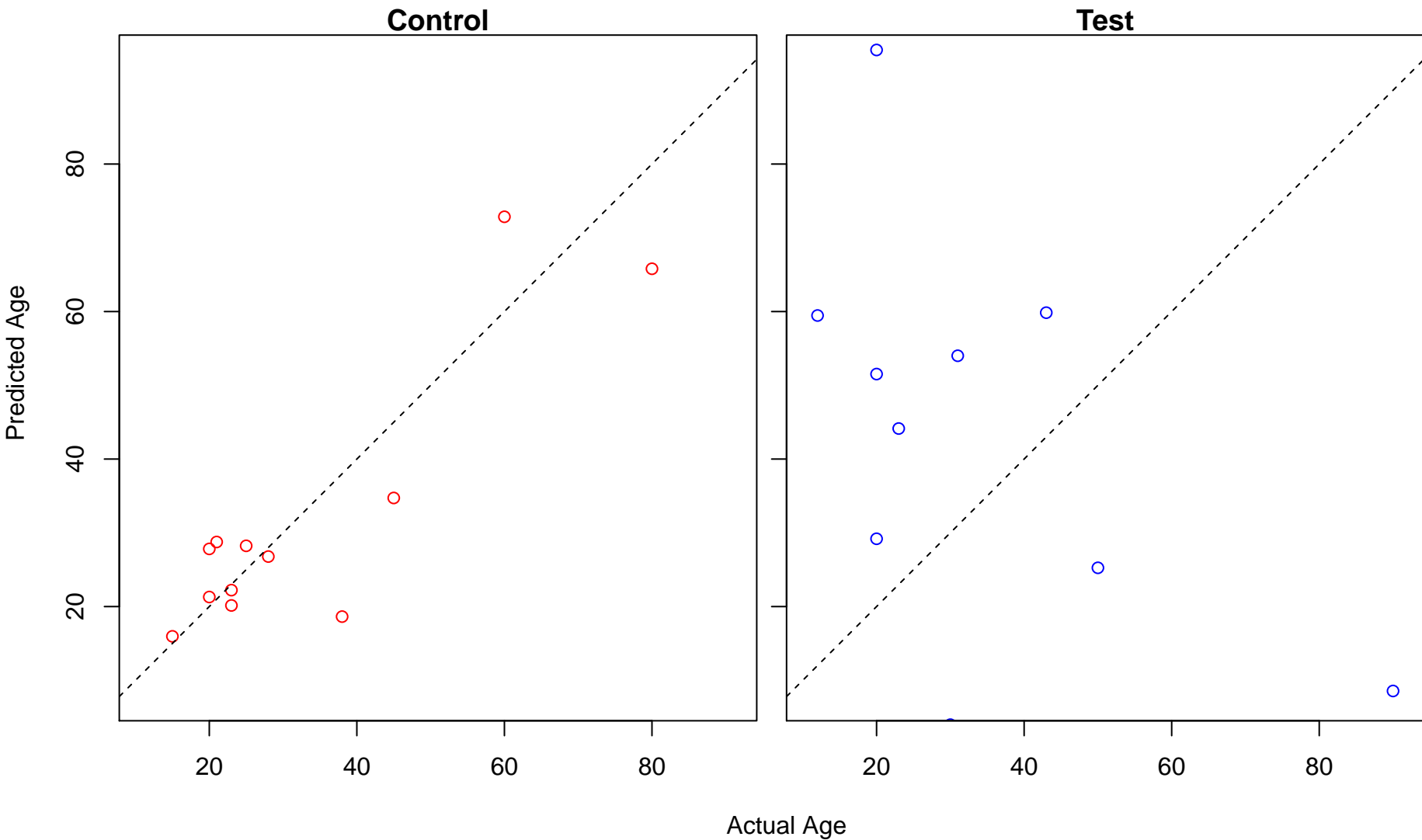
peptidyl-proline hydroxylation (Score: 20.628297)



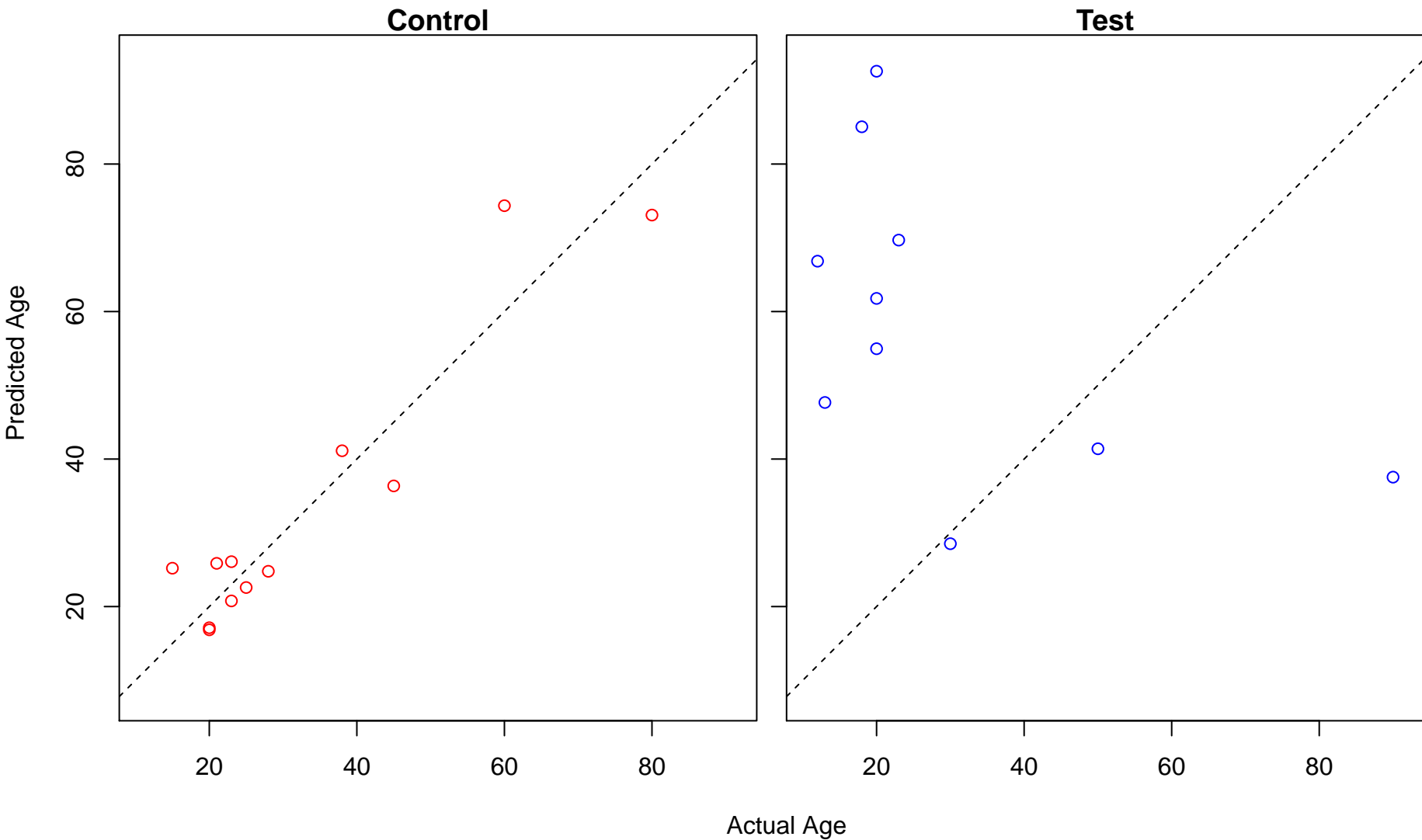
purine ribonucleoside bisphosphate biosynthetic process (Score: 20.604779)



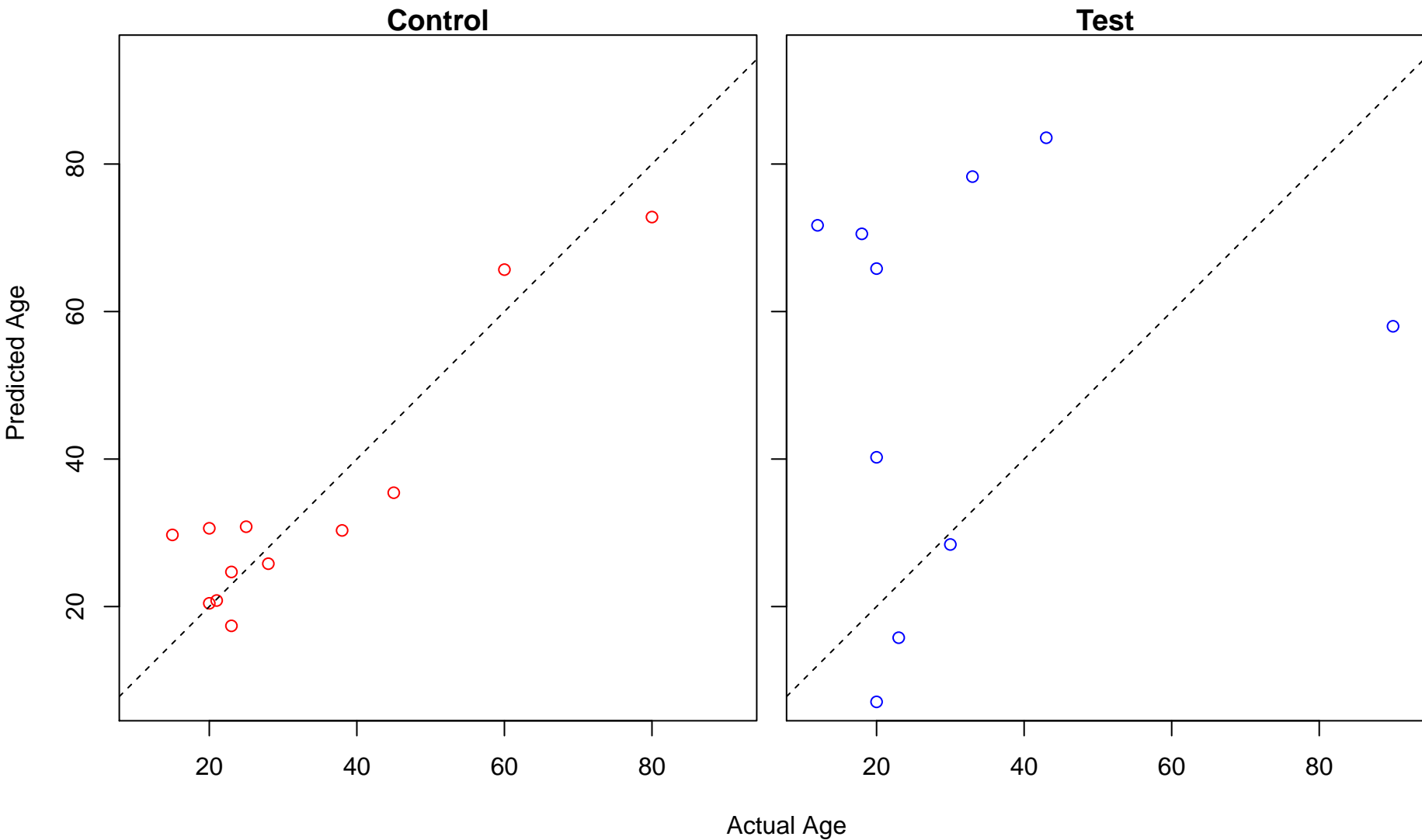
3'-phosphoadenosine 5'-phosphosulfate biosynthetic process (Score: 20.604779)



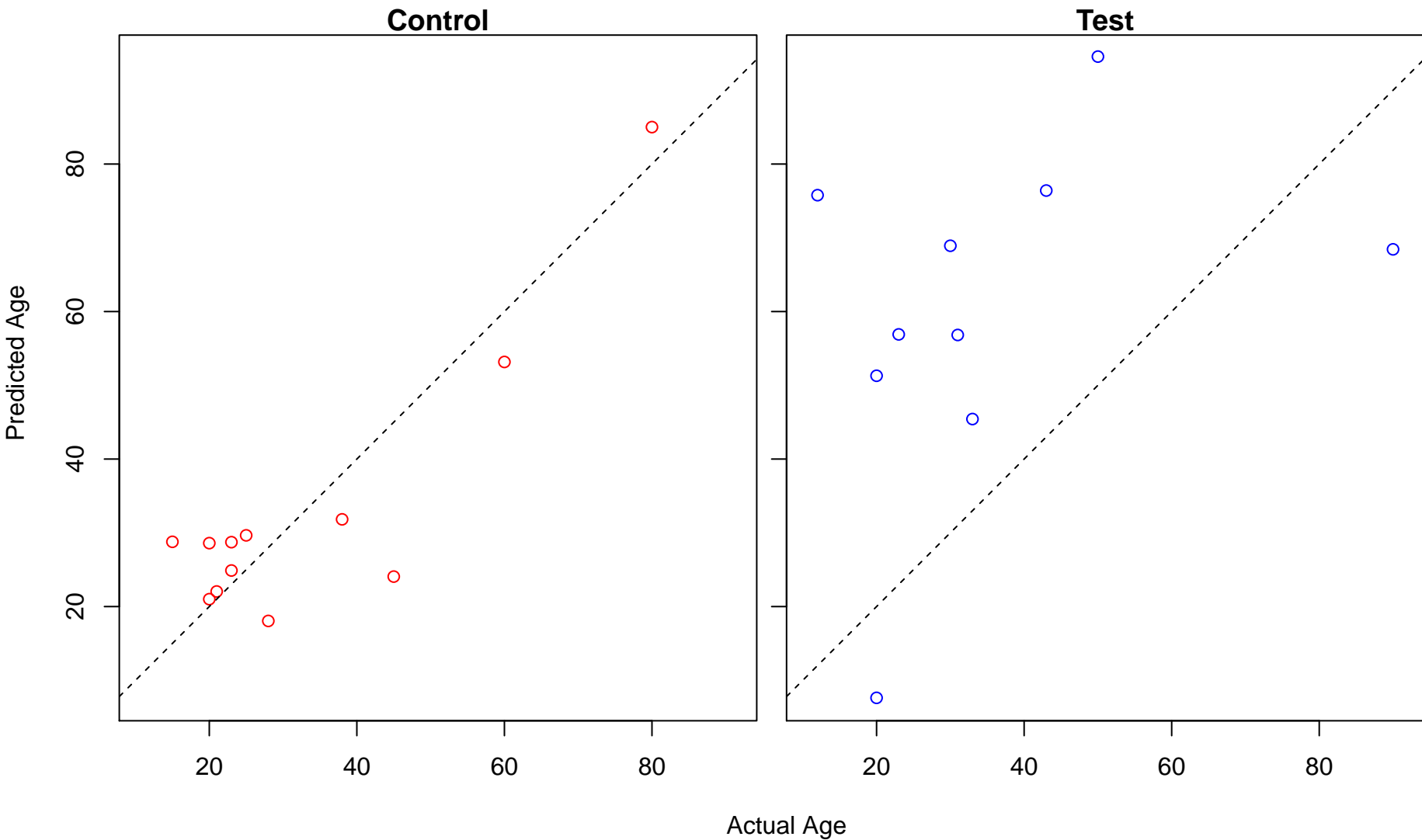
oogenesis (Score: 20.547366)



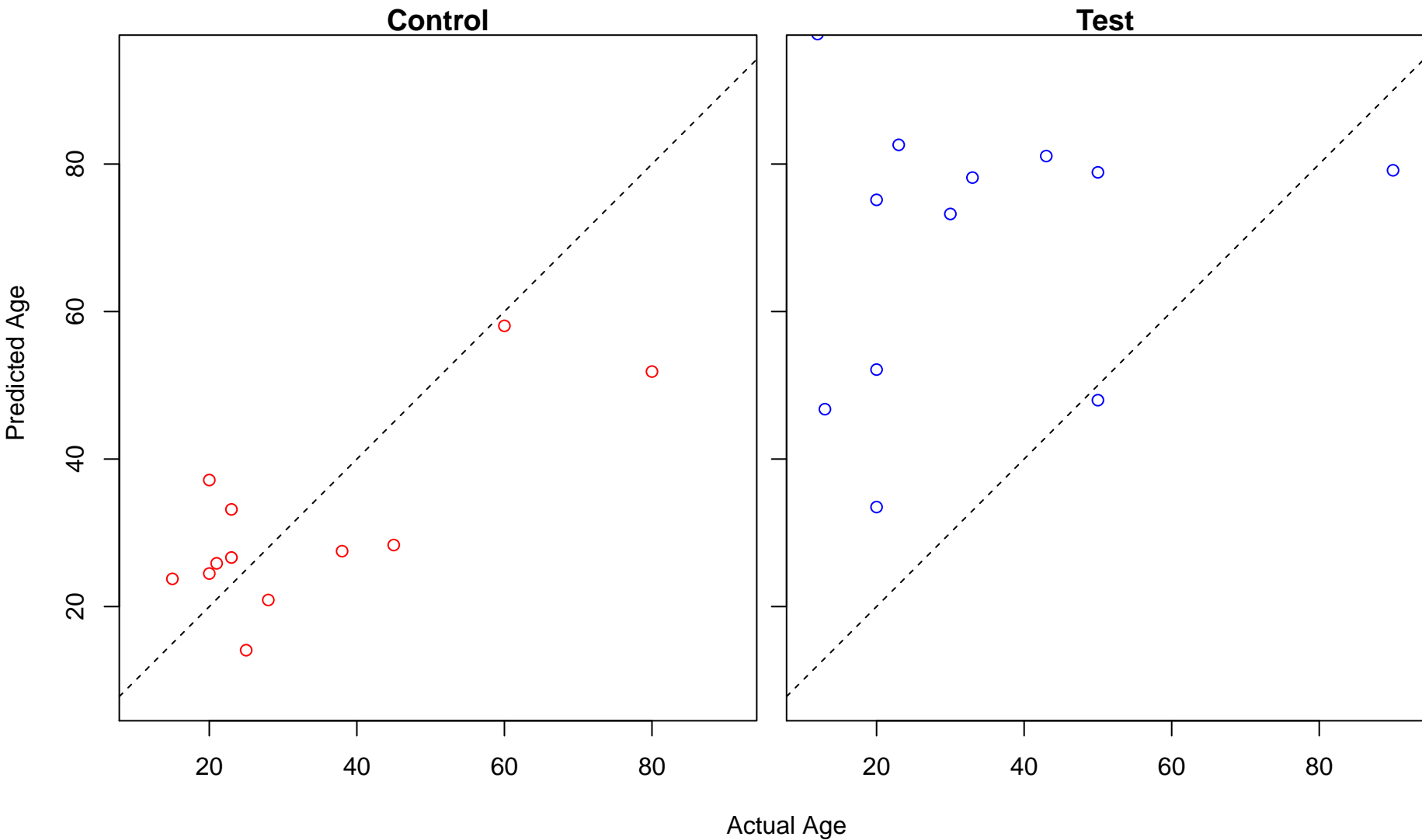
negative regulation of cell-substrate adhesion (Score: 20.538663)



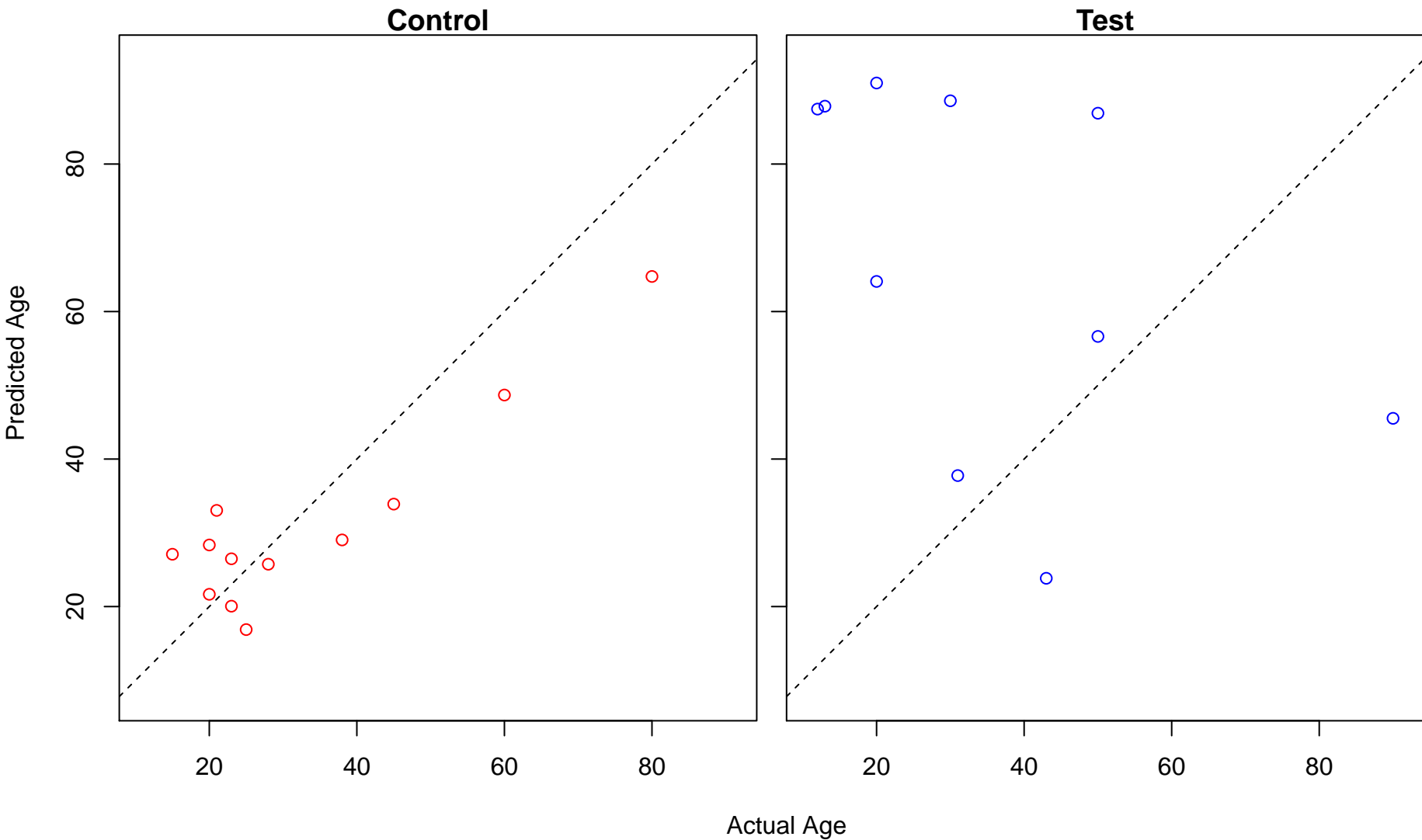
regulation of pinocytosis (Score: 20.532401)



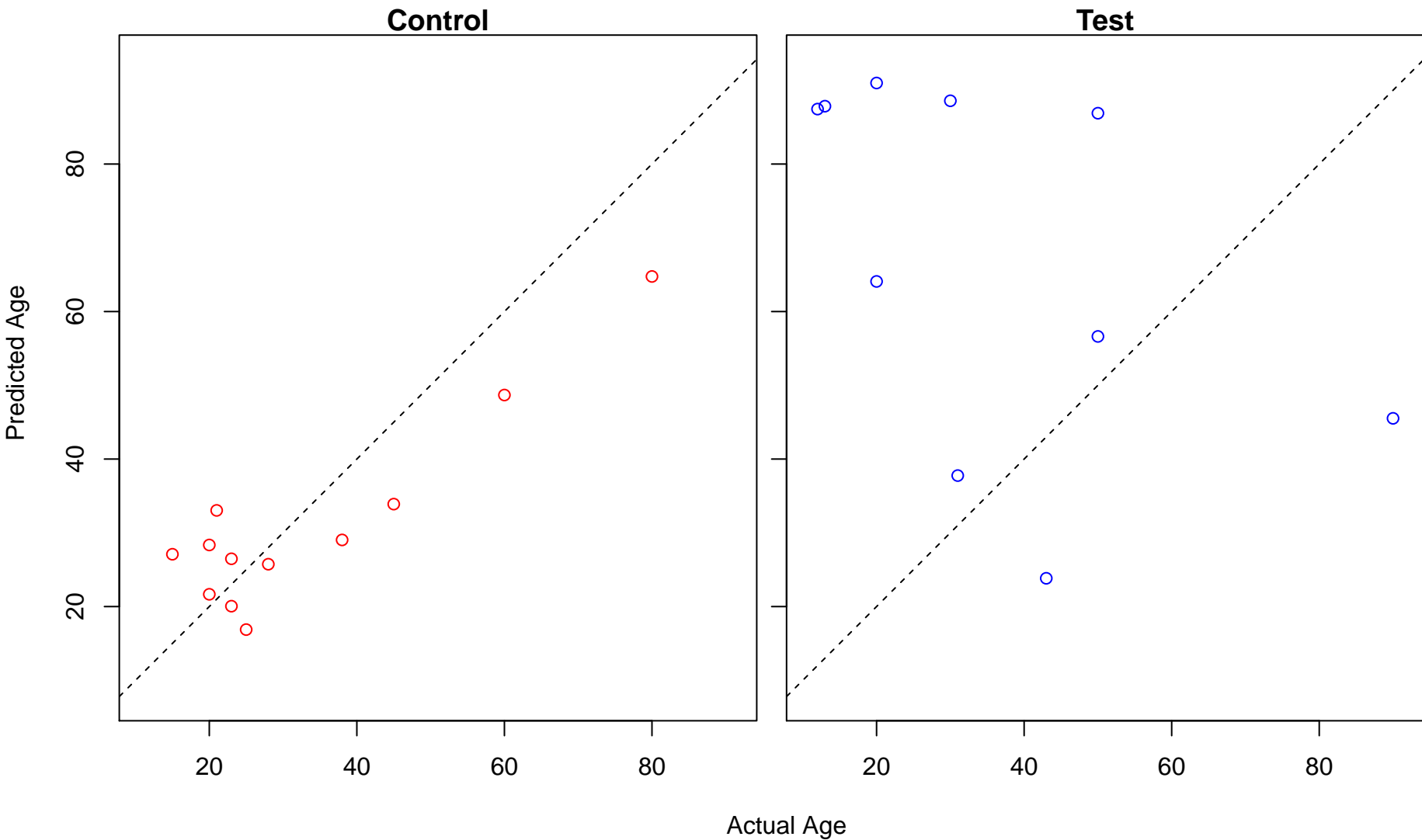
positive regulation of nitric-oxide synthase biosynthetic process (Score: 20.504001)



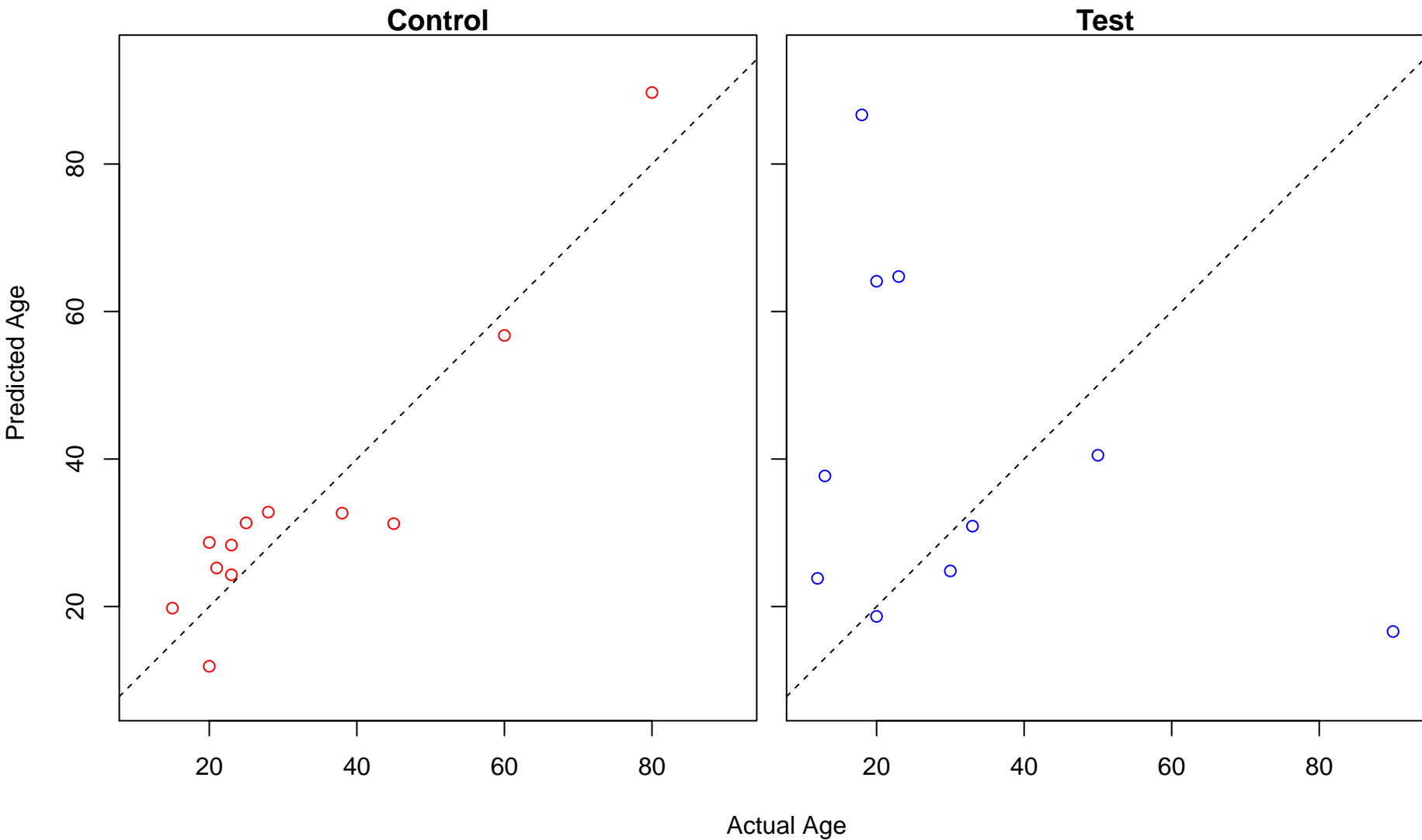
protein polyufmylation (Score: 20.415950)



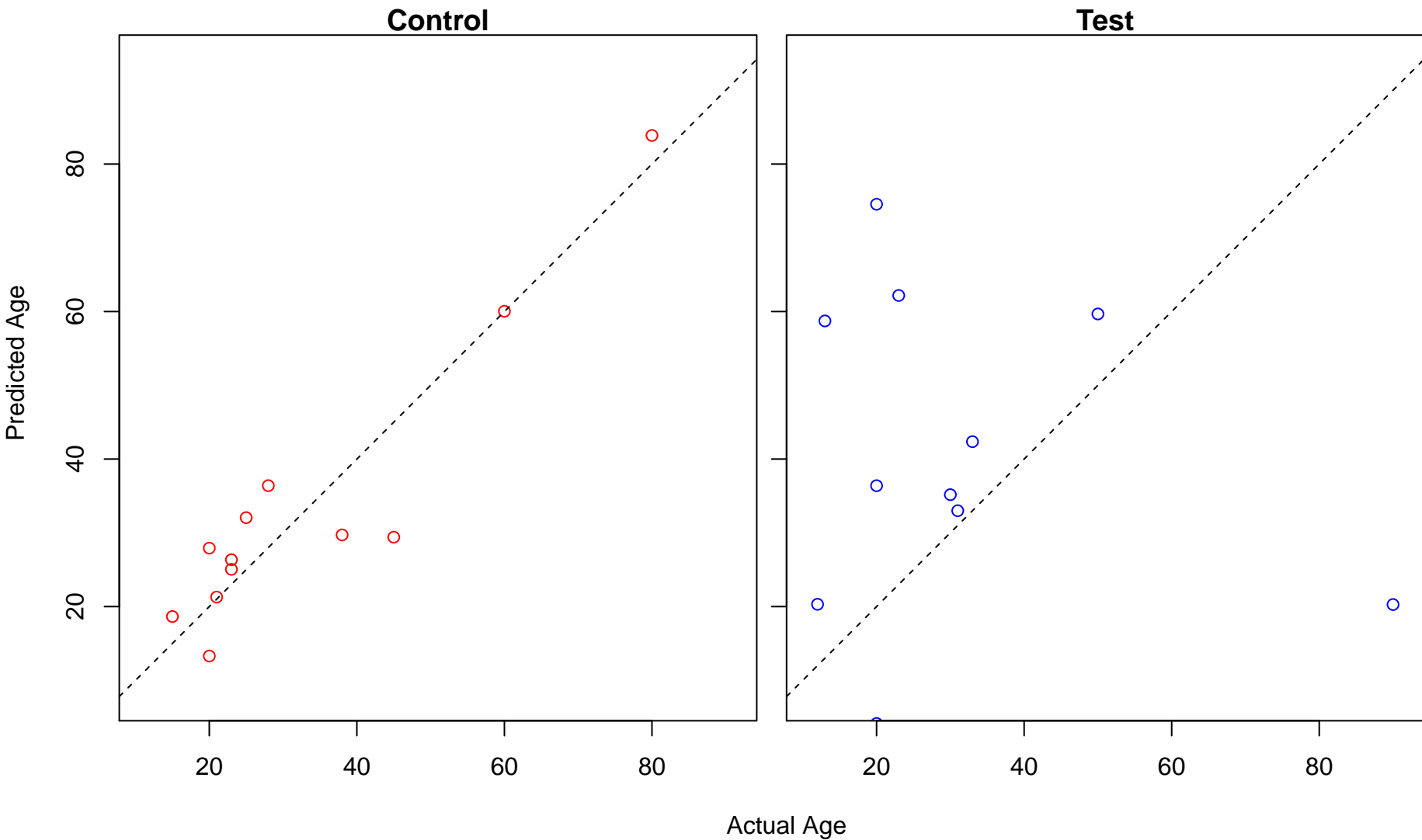
protein K69-linked ufmylation (Score: 20.415950)



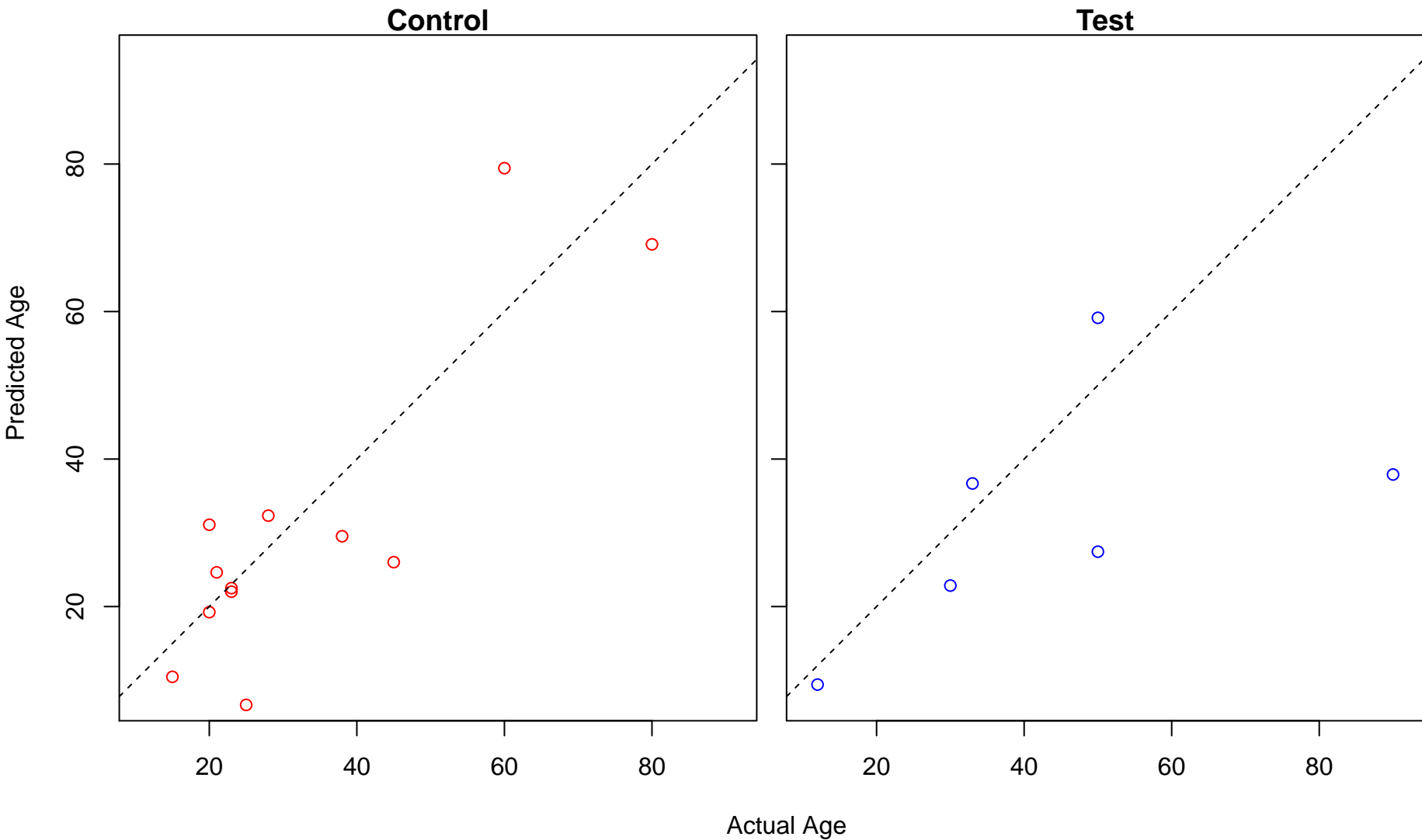
nucleoside metabolic process (Score: 20.347400)



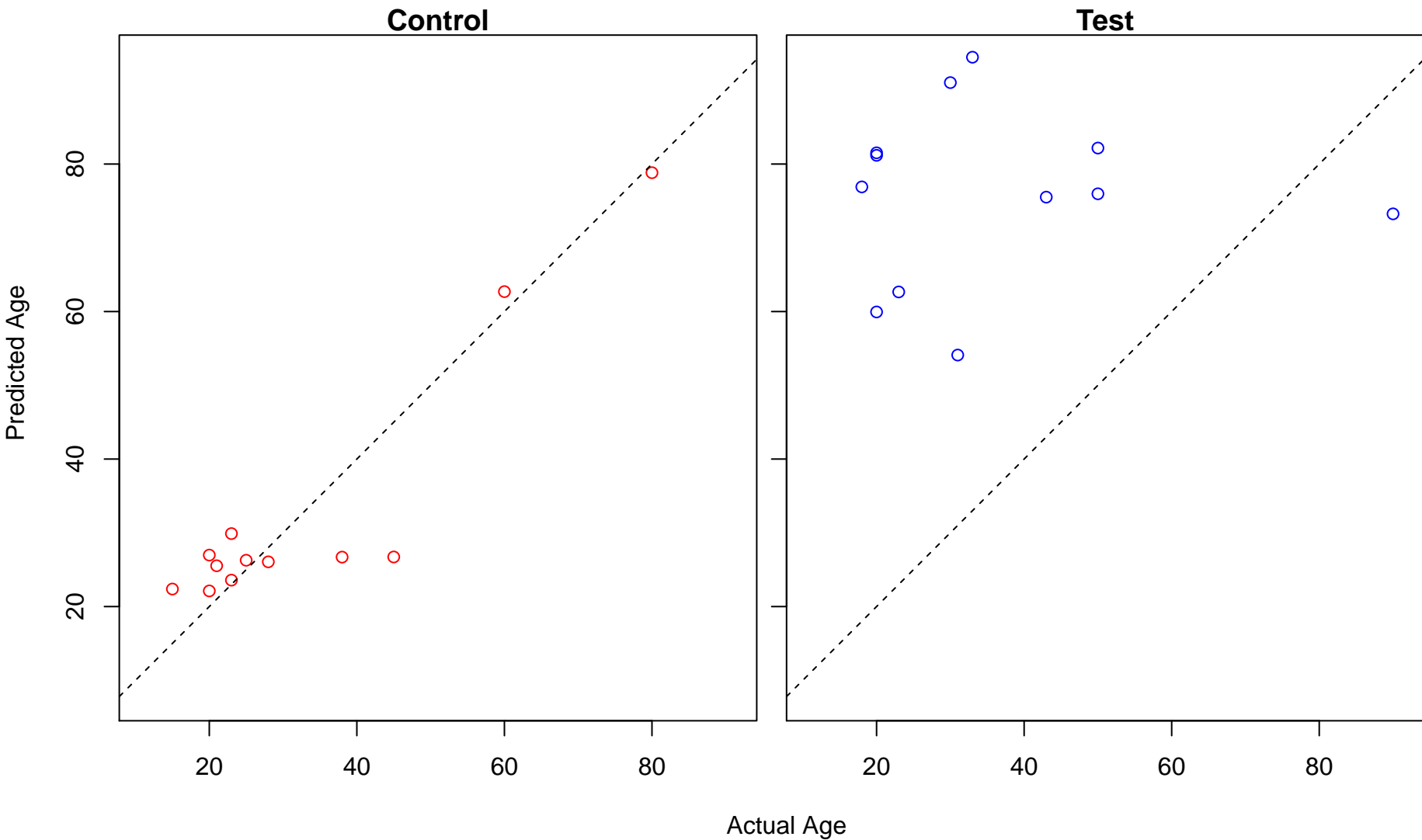
nucleotide metabolic process (Score: 20.322220)



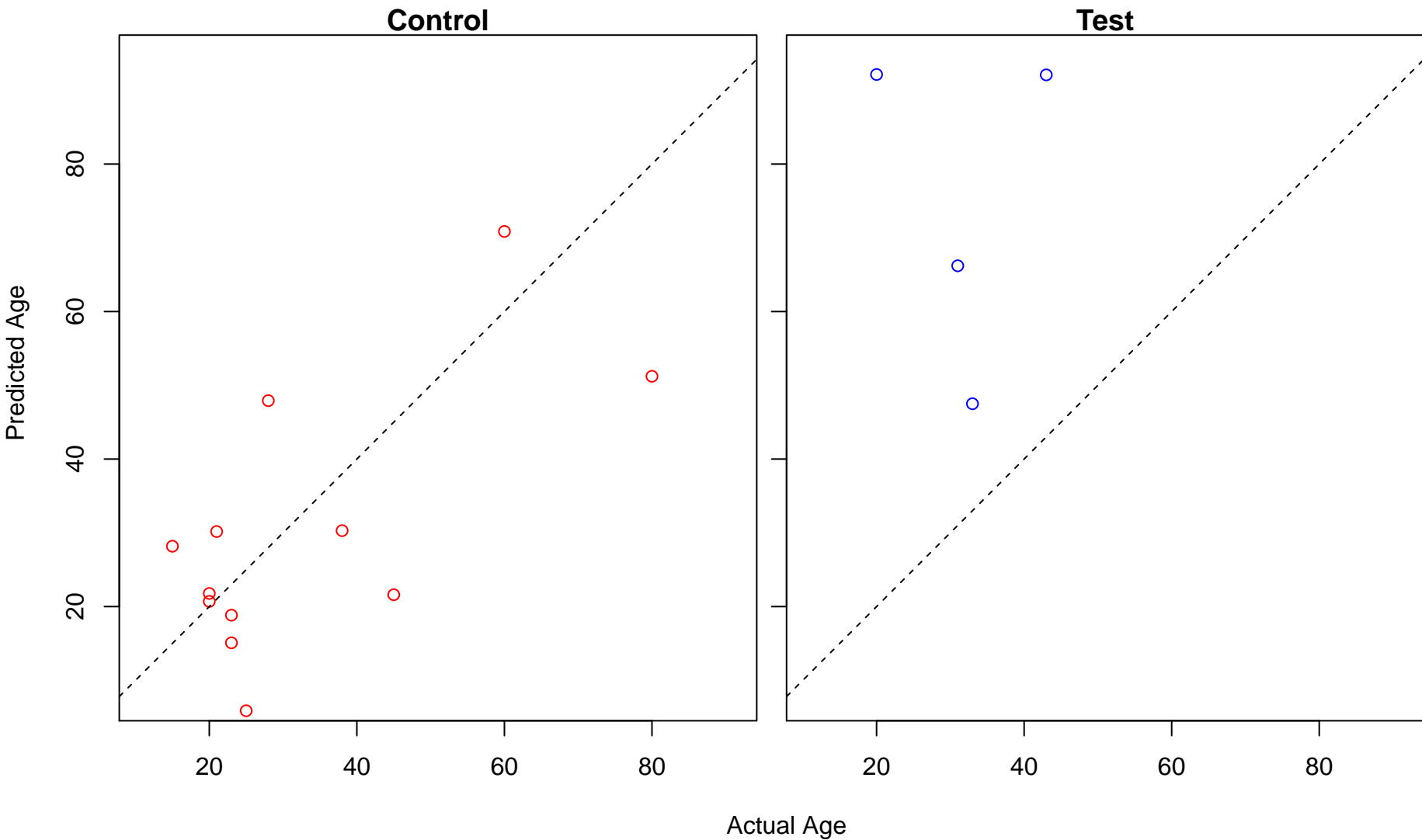
negative regulation of striated muscle cell differentiation (Score: 20.291977)



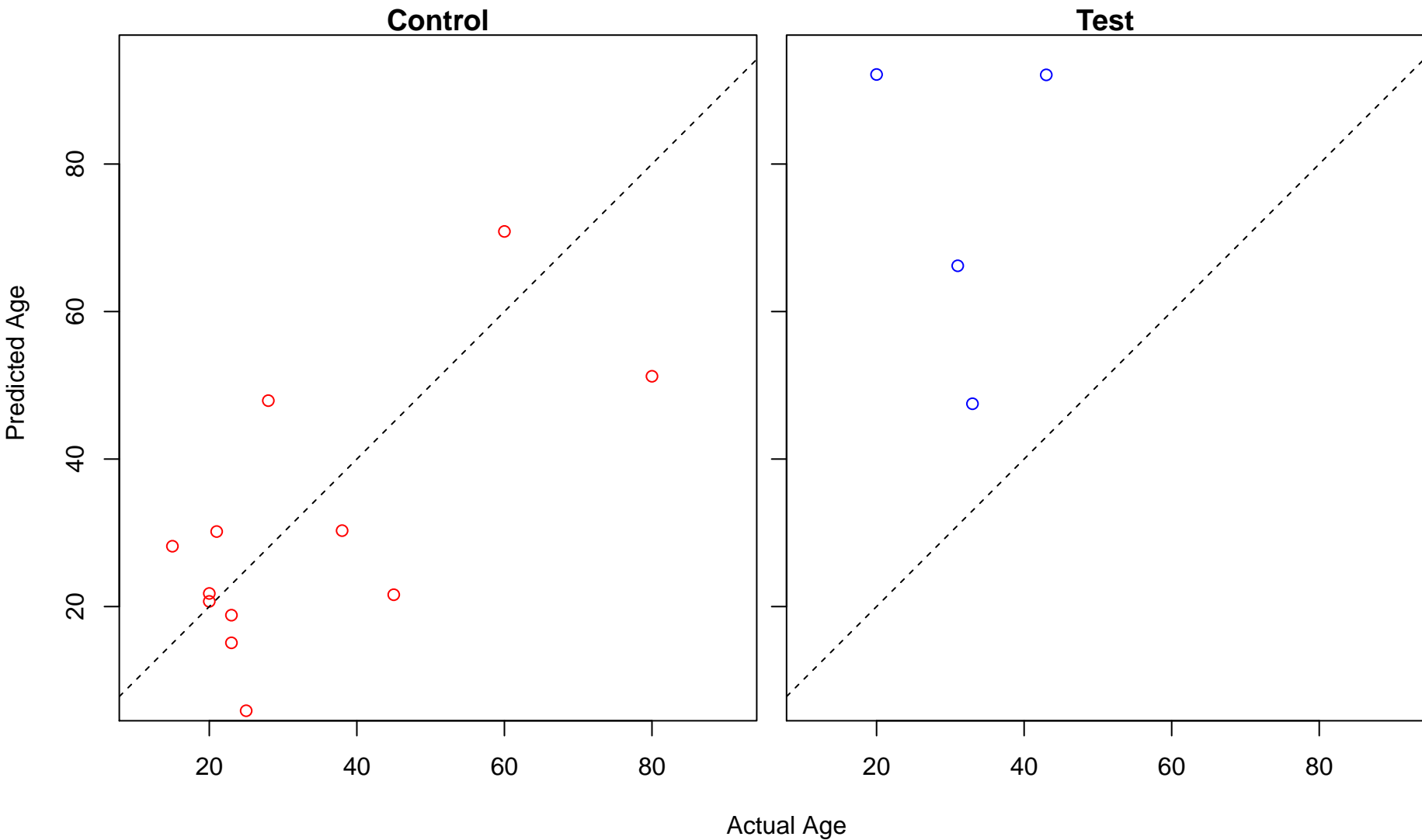
positive regulation of cardiac muscle tissue development (Score: 20.225099)



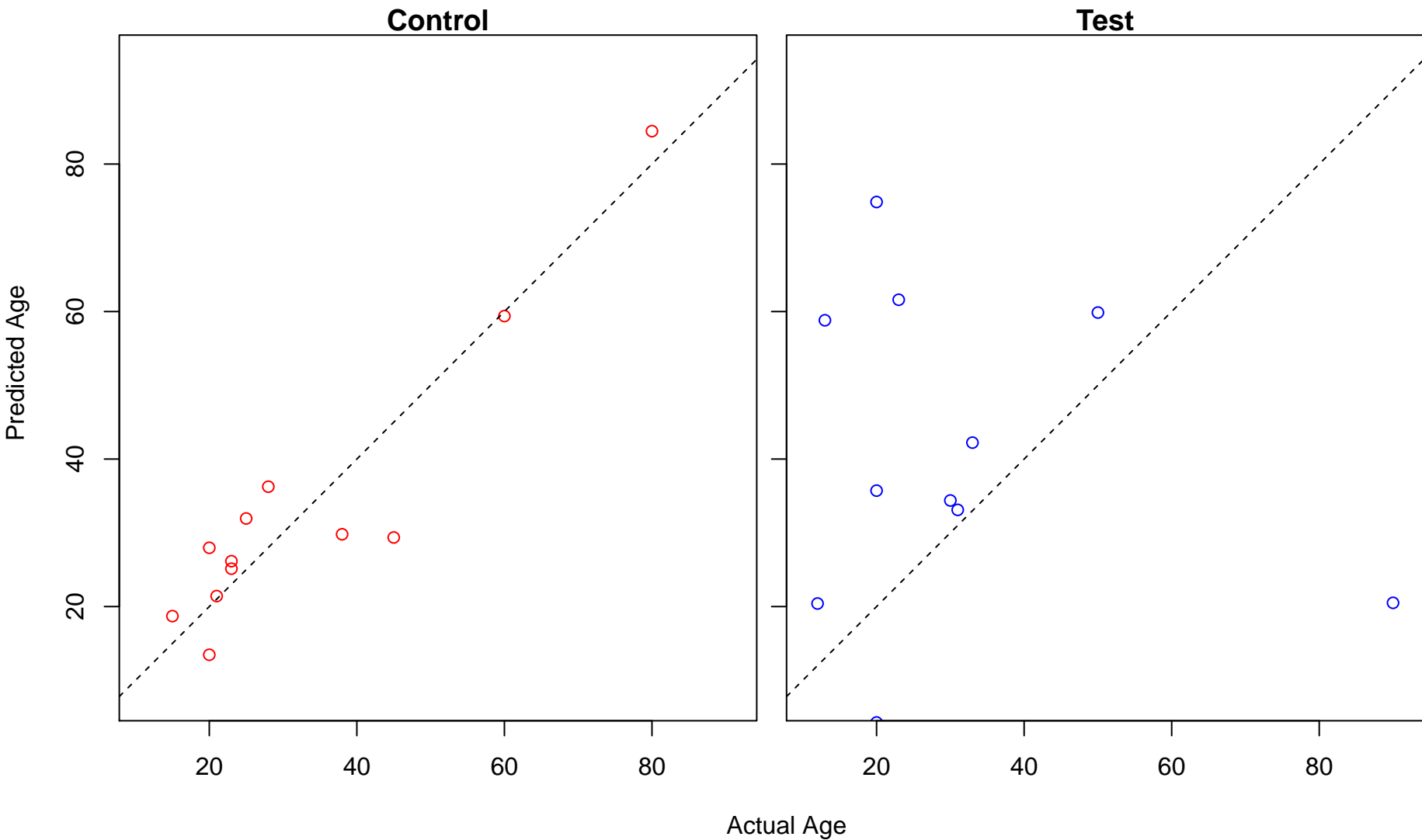
negative regulation of sterol transport (Score: 20.182907)



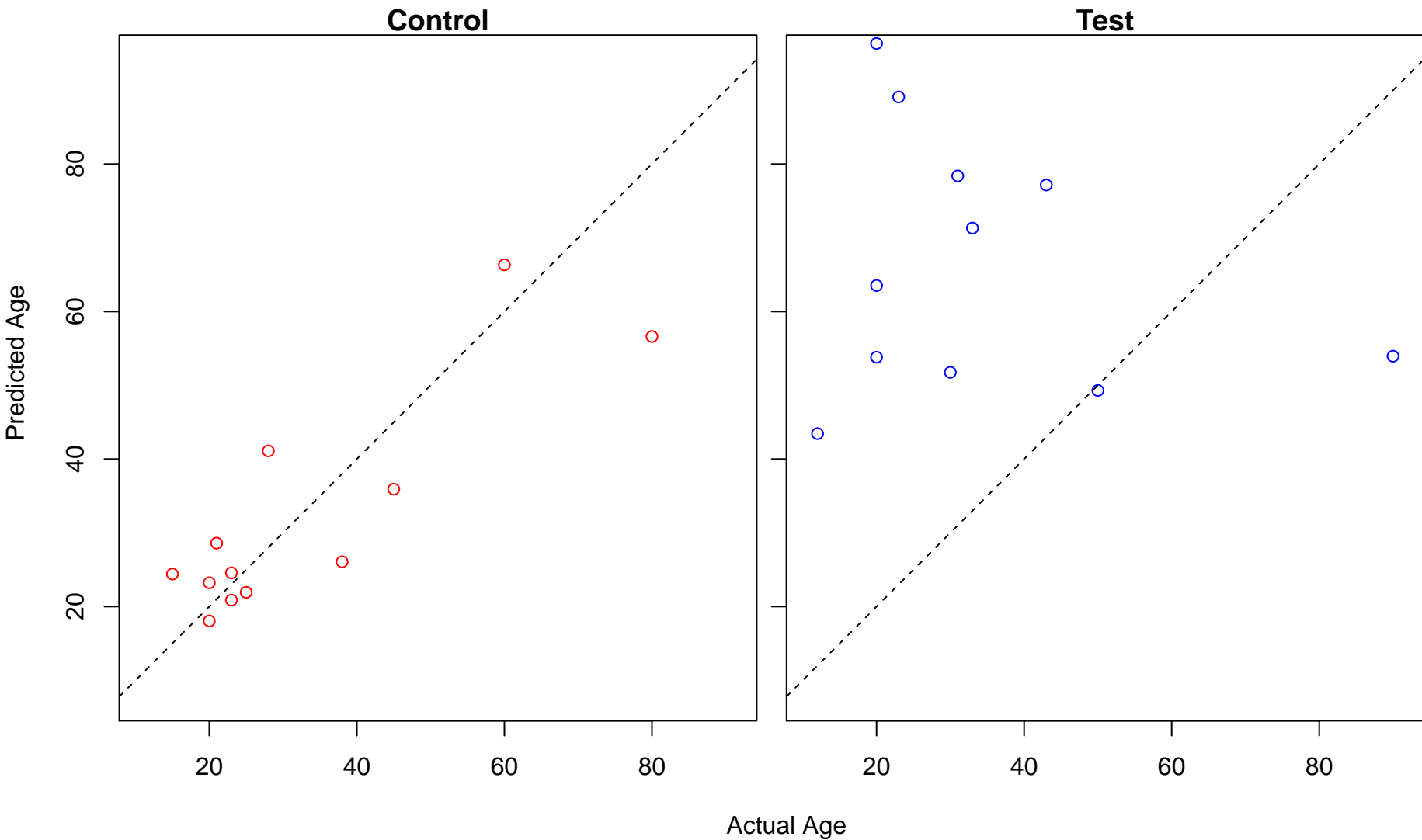
negative regulation of cholesterol transport (Score: 20.182907)



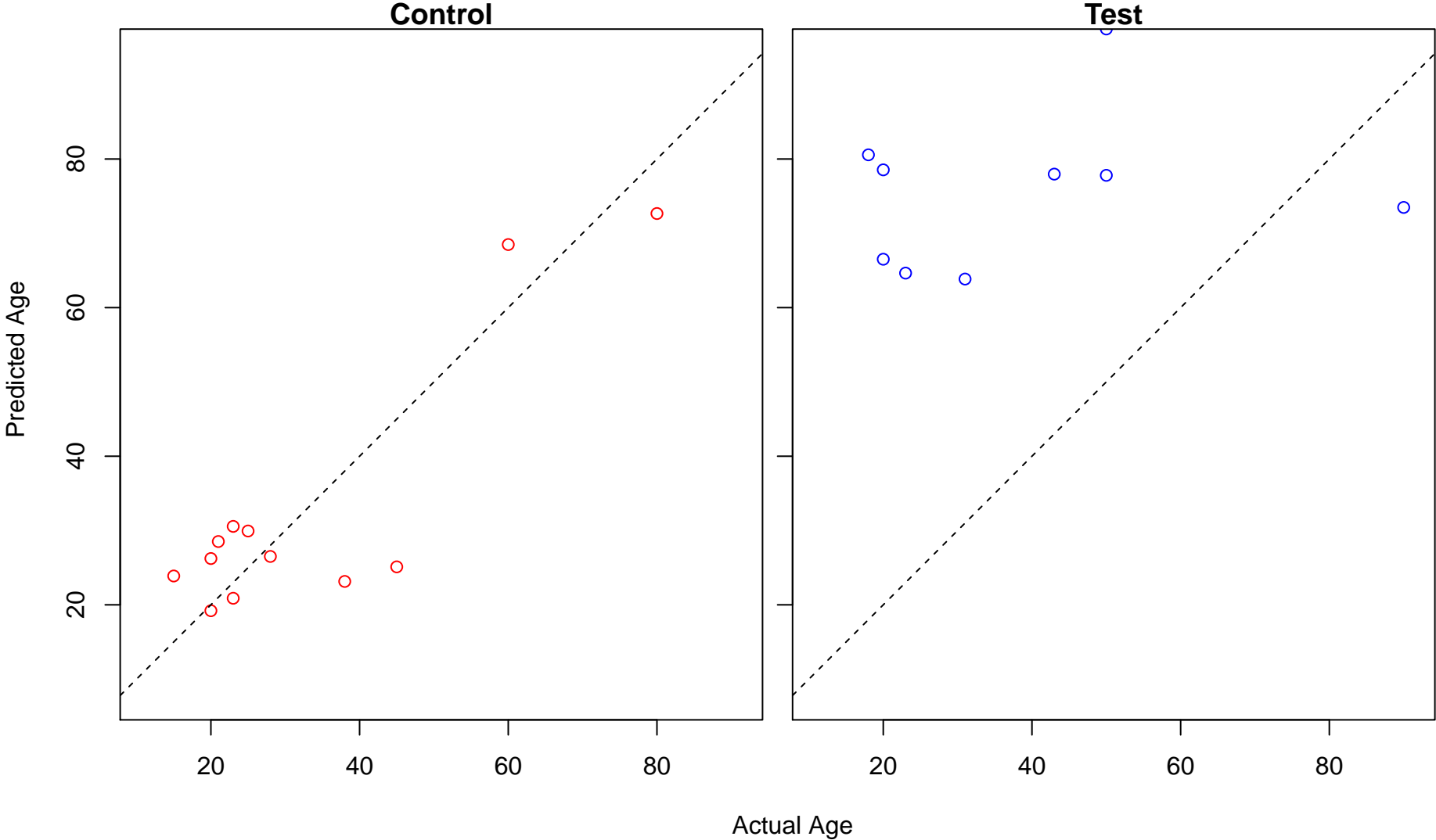
nucleoside phosphate metabolic process (Score: 20.179354)



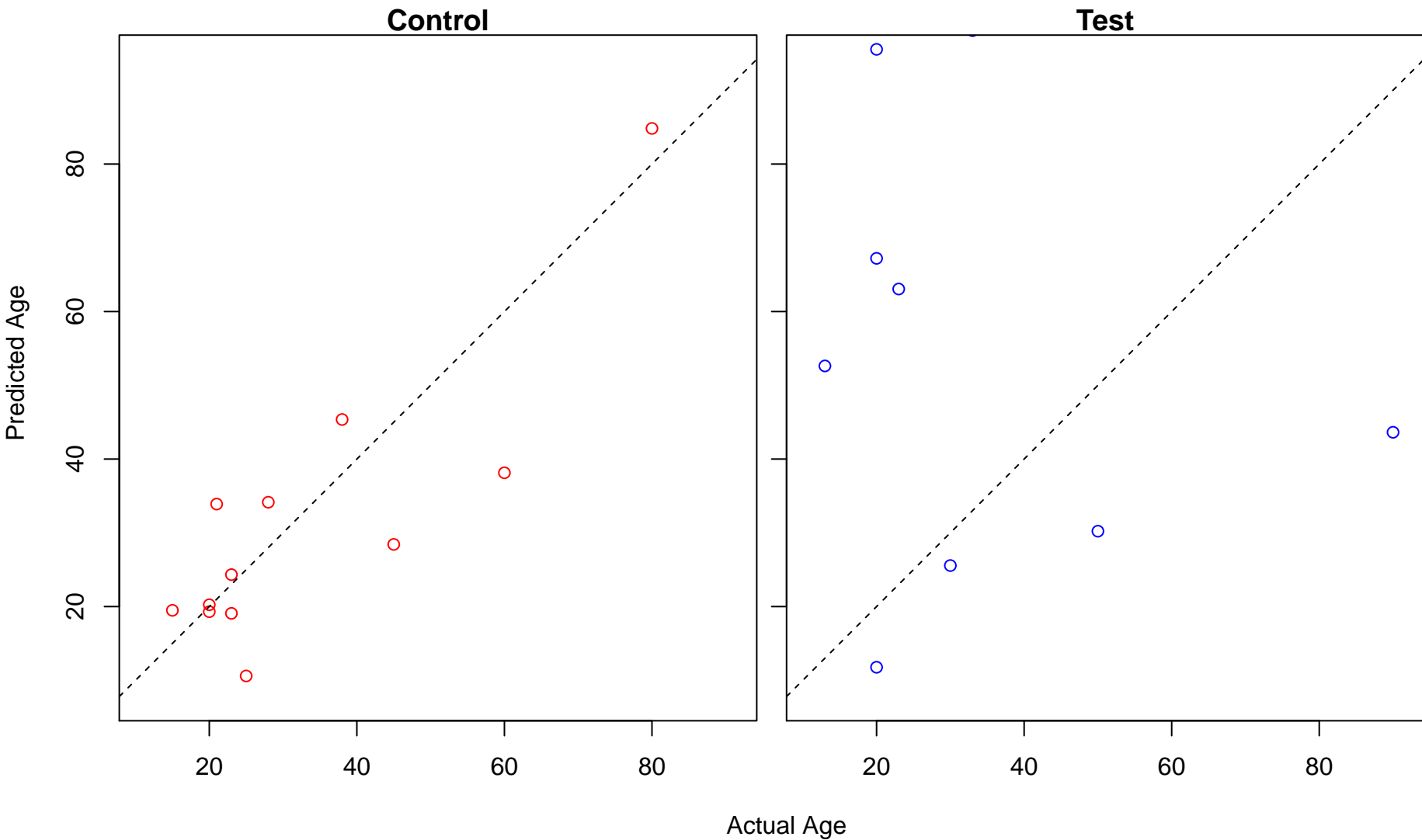
negative regulation of T cell differentiation (Score: 20.133422)



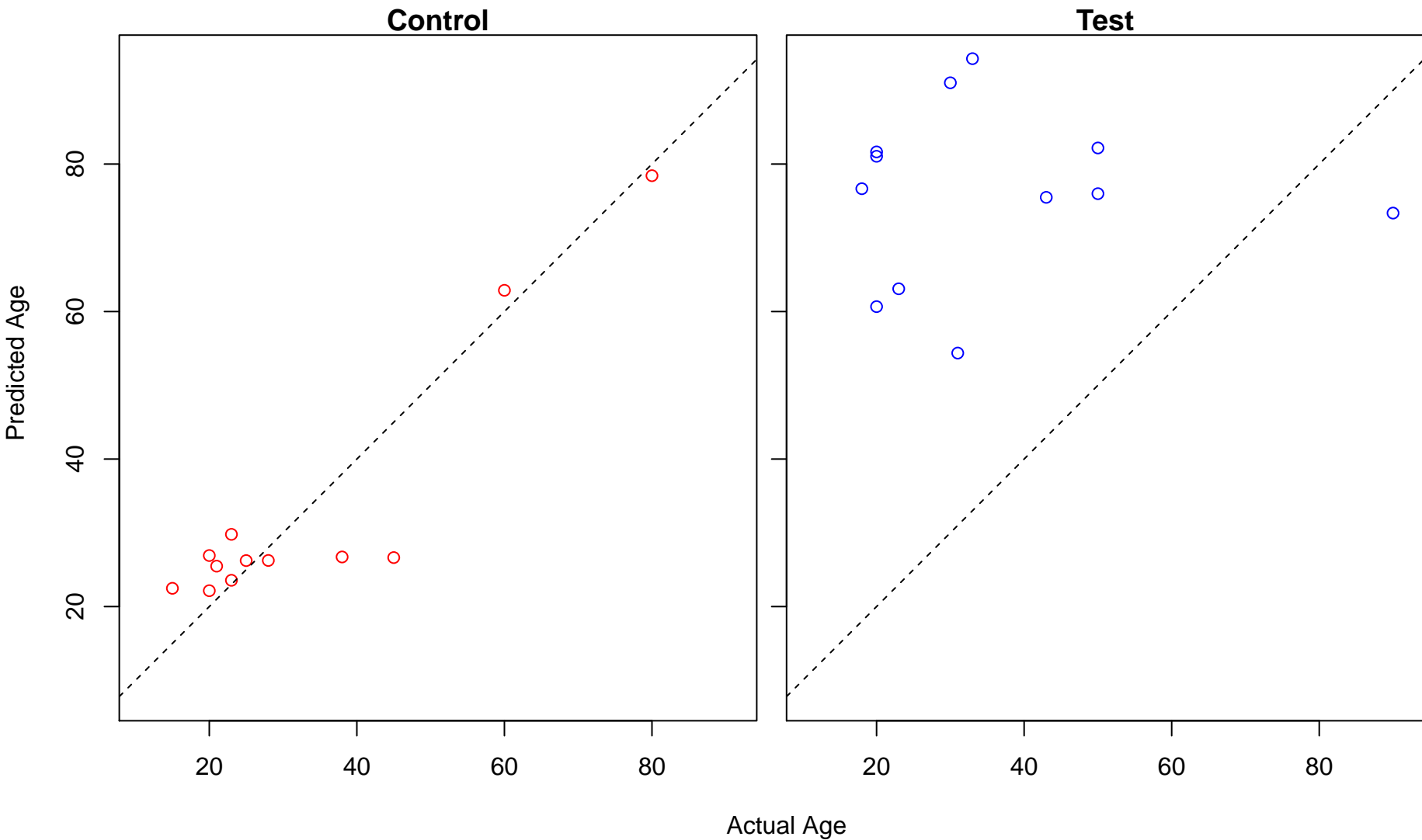
regulation of transcription from RNA polymerase II promoter involved in heart development (Score: 20.1)



myotube differentiation (Score: 20.091414)

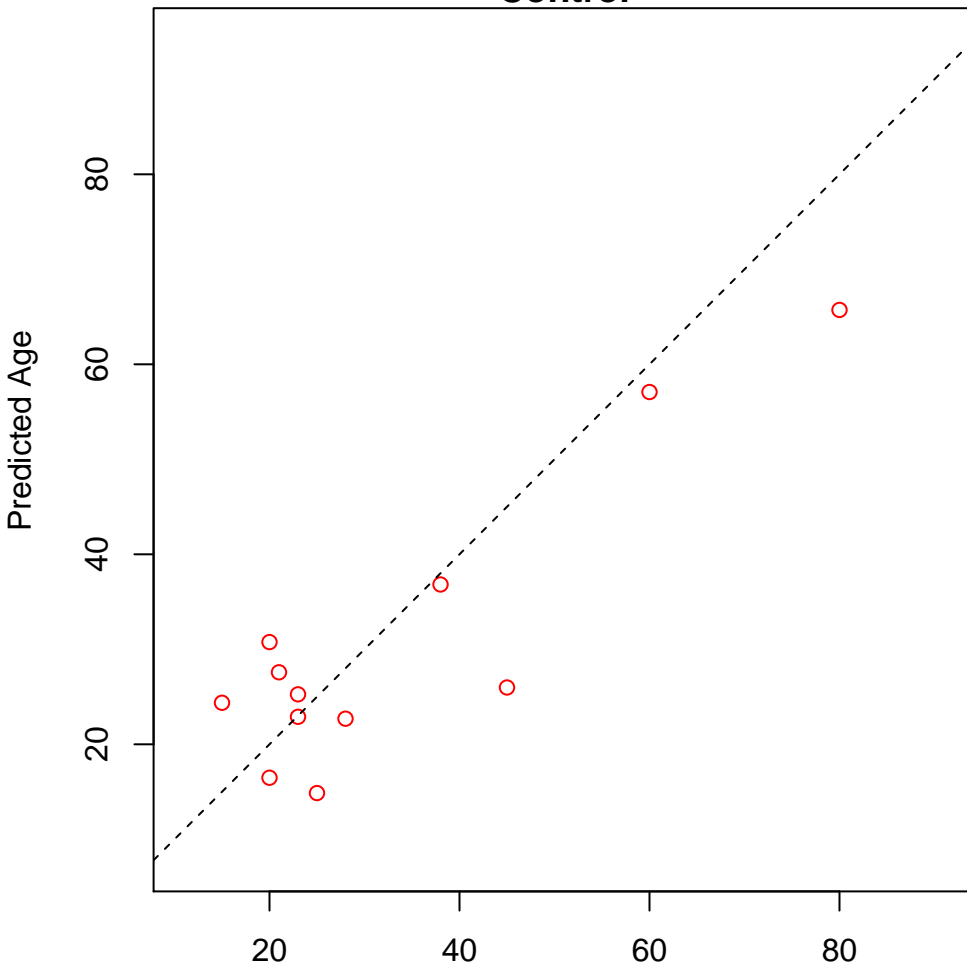


regulation of cardiac muscle tissue development (Score: 20.079302)

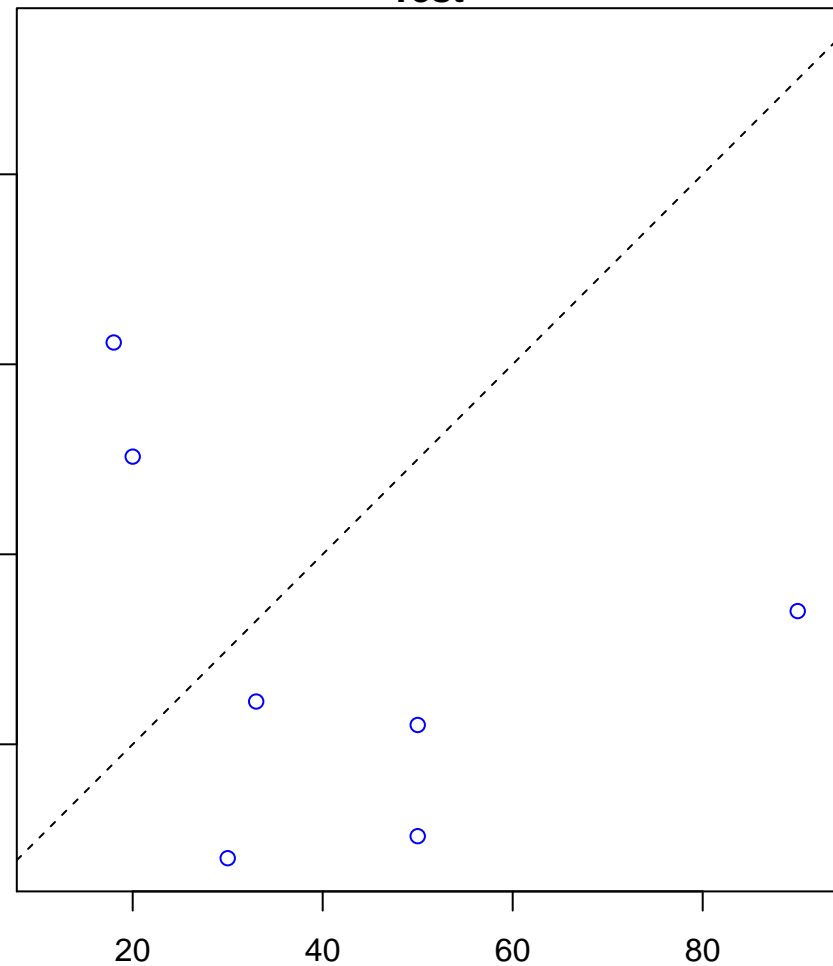


skeletal muscle tissue development (Score: 20.053871)

Control

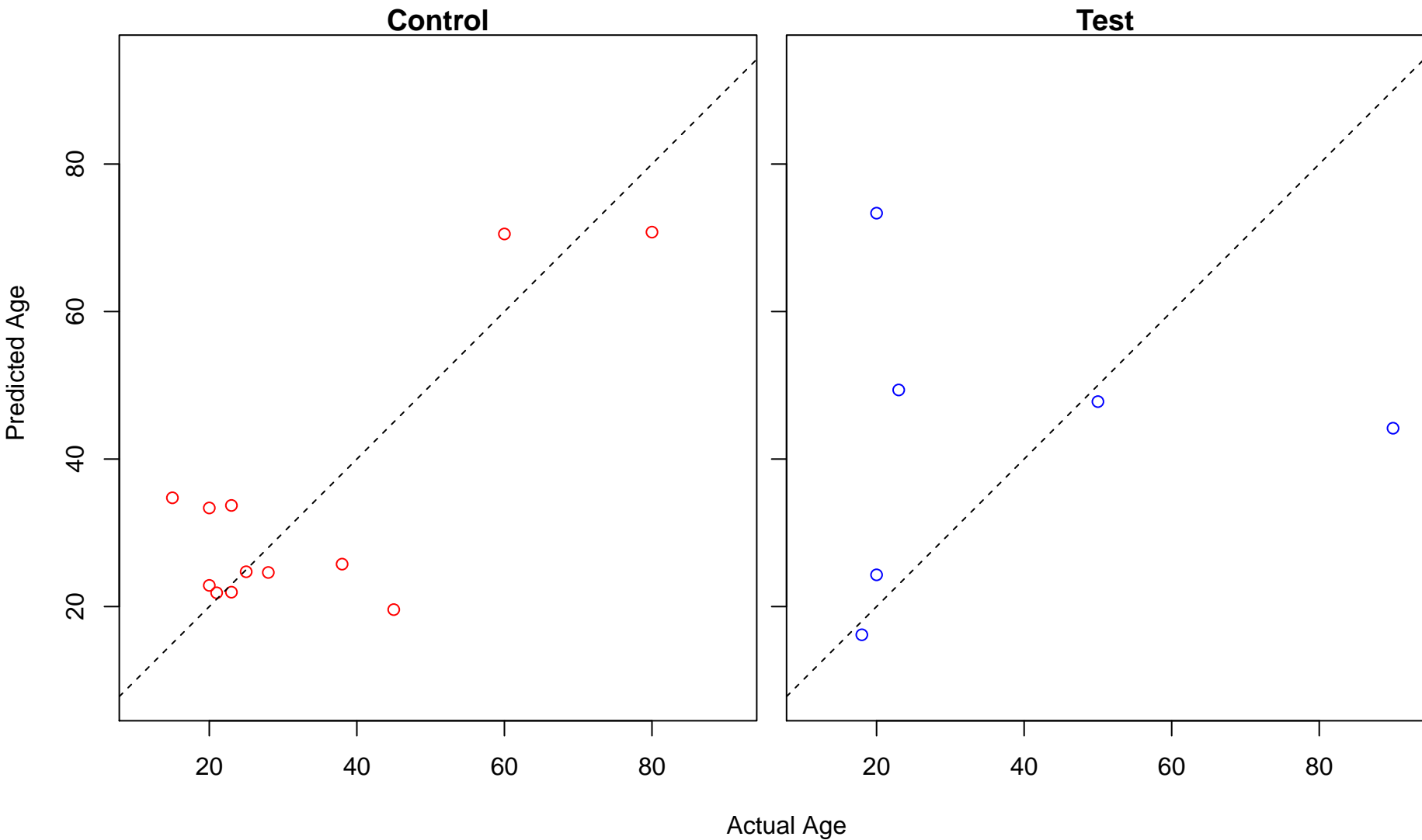


Test

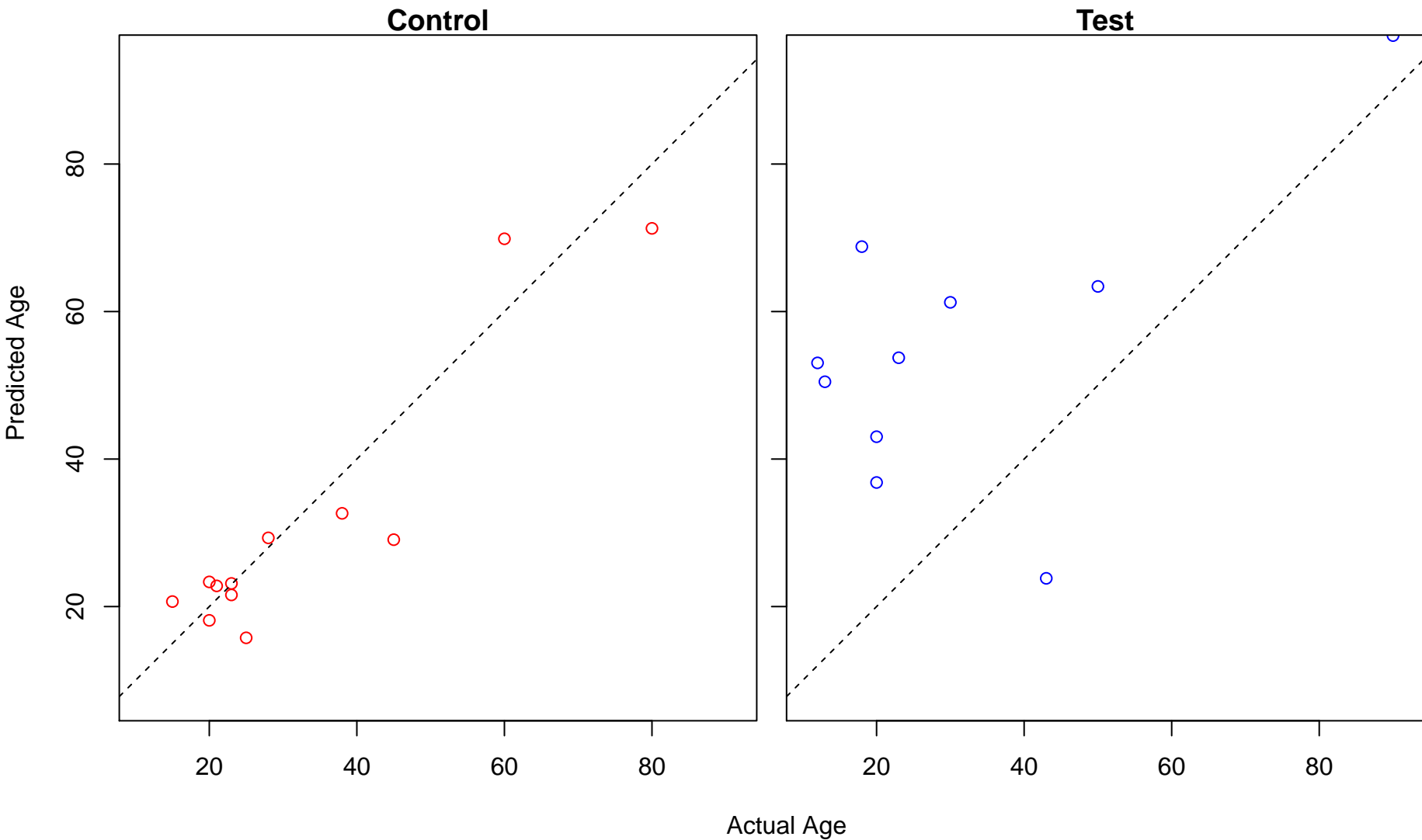


Actual Age

ureter development (Score: 20.019508)

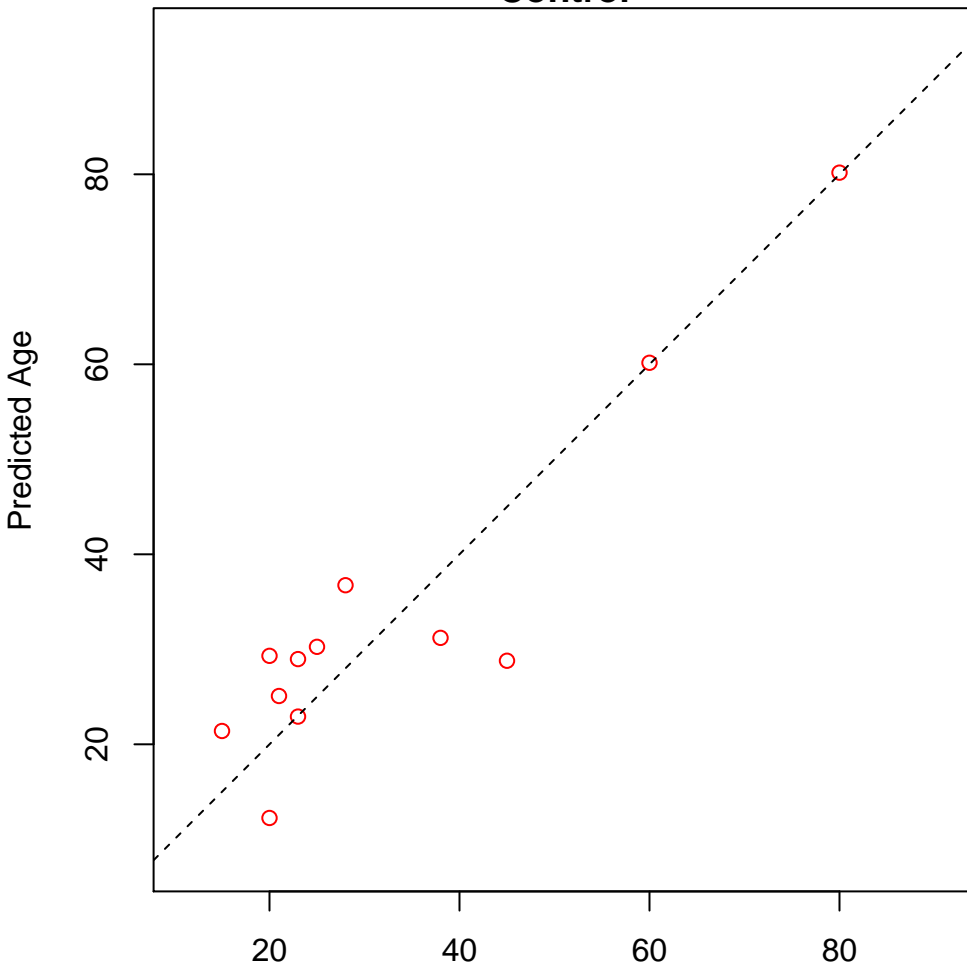


activation of NF-kappaB-inducing kinase activity (Score: 20.015456)

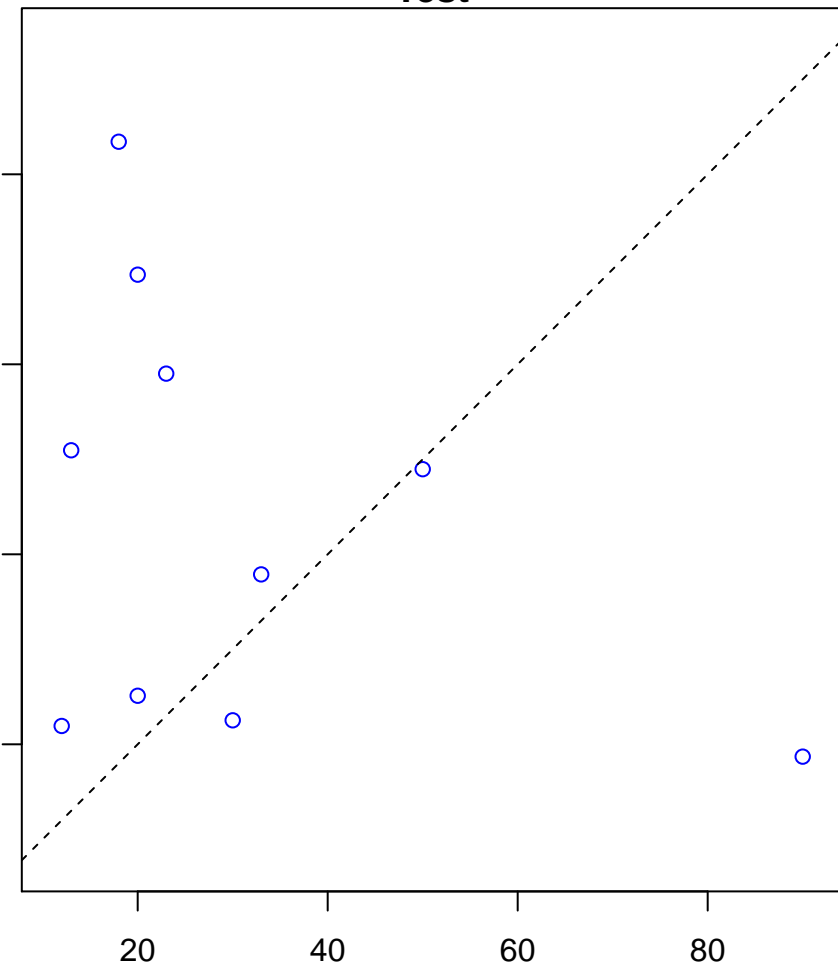


purine nucleotide metabolic process (Score: 19.970000)

Control

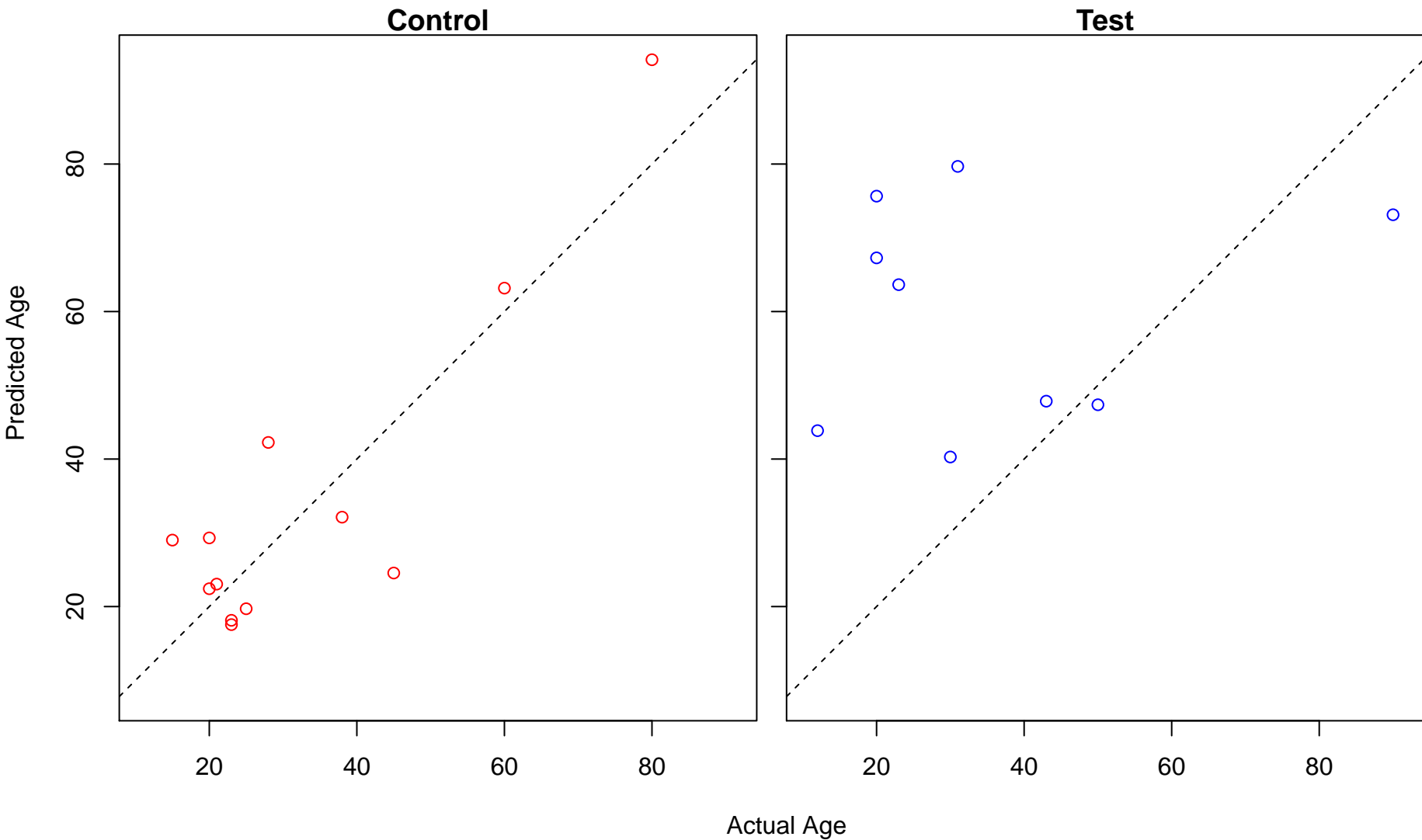


Test

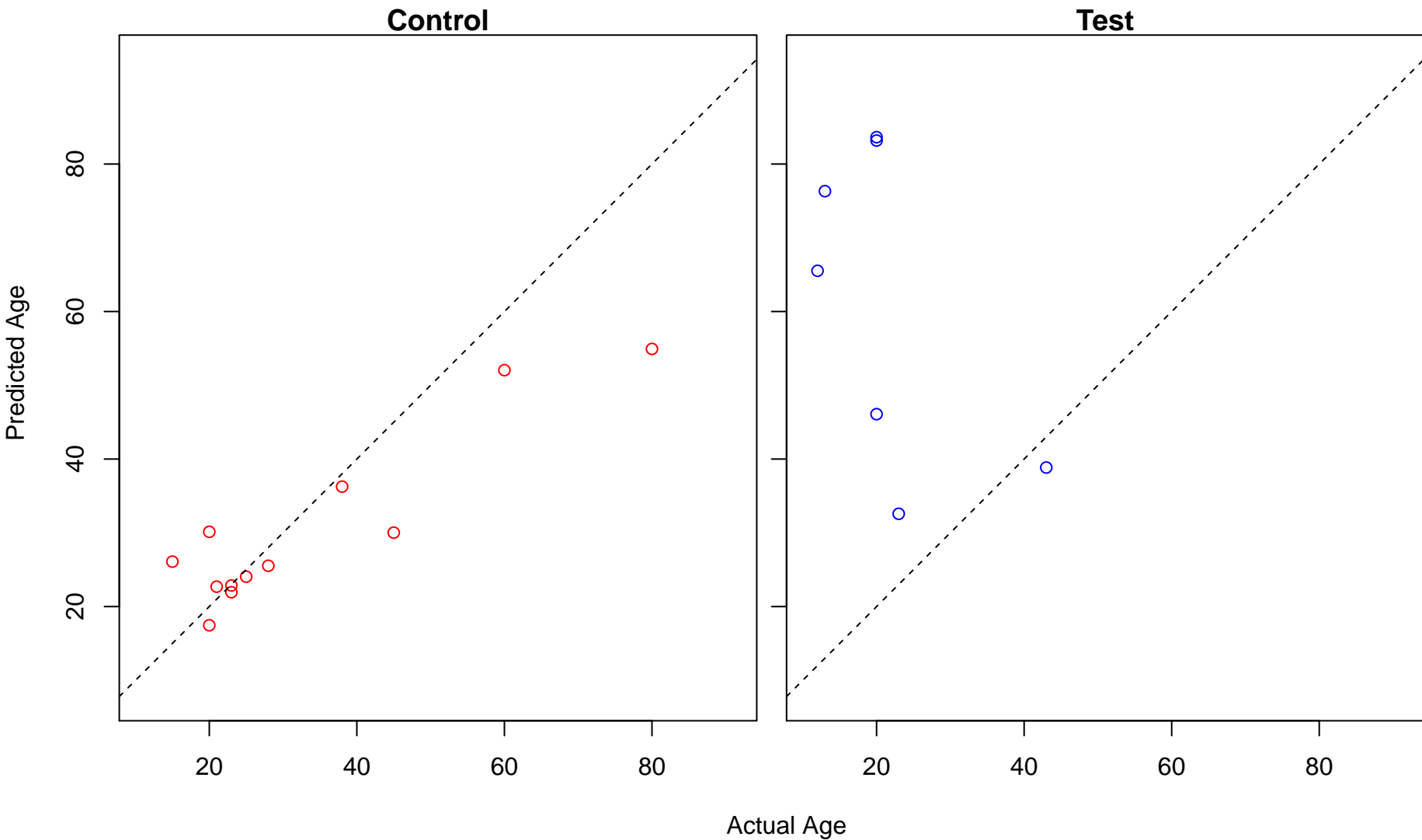


Actual Age

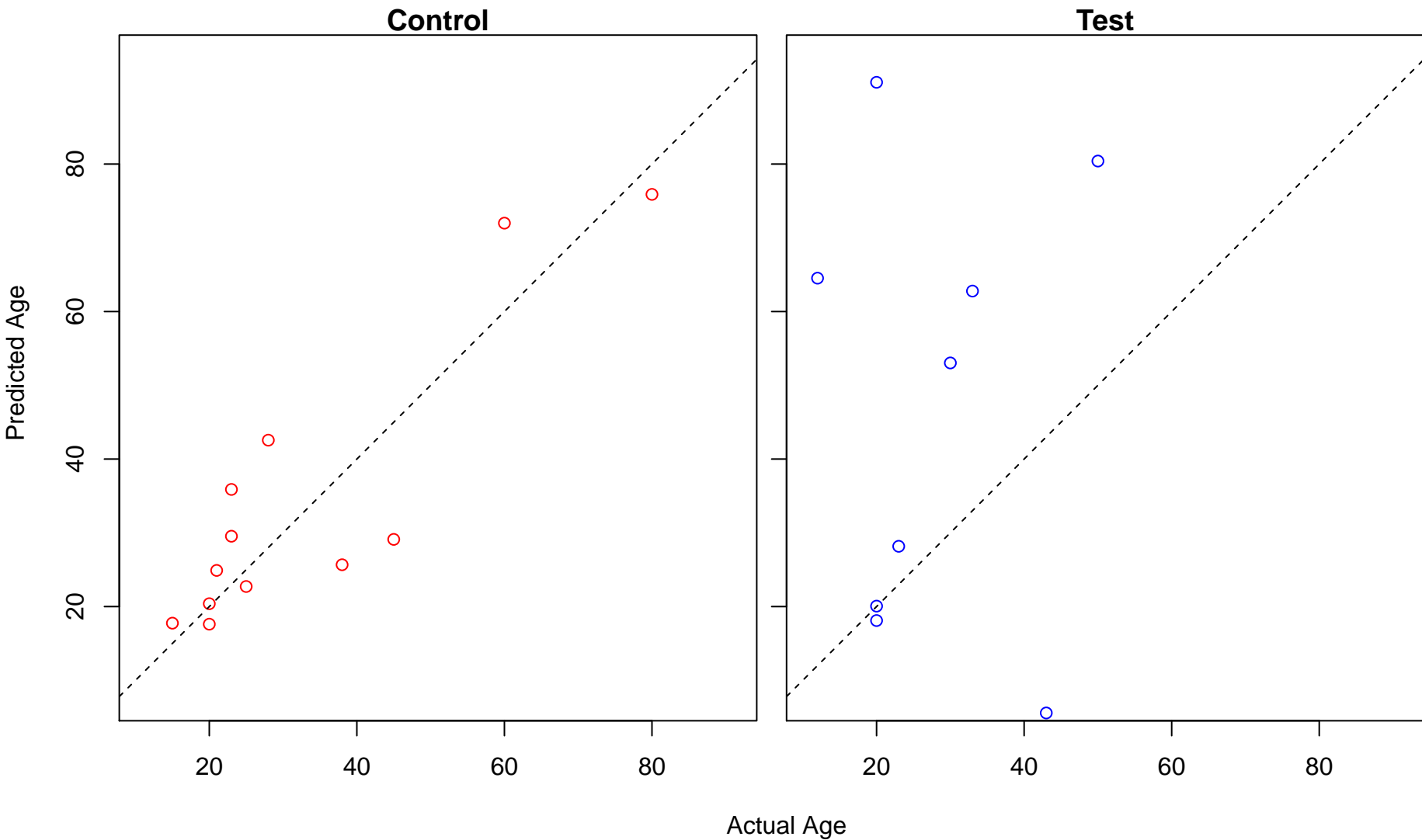
ATF6-mediated unfolded protein response (Score: 19.954592)



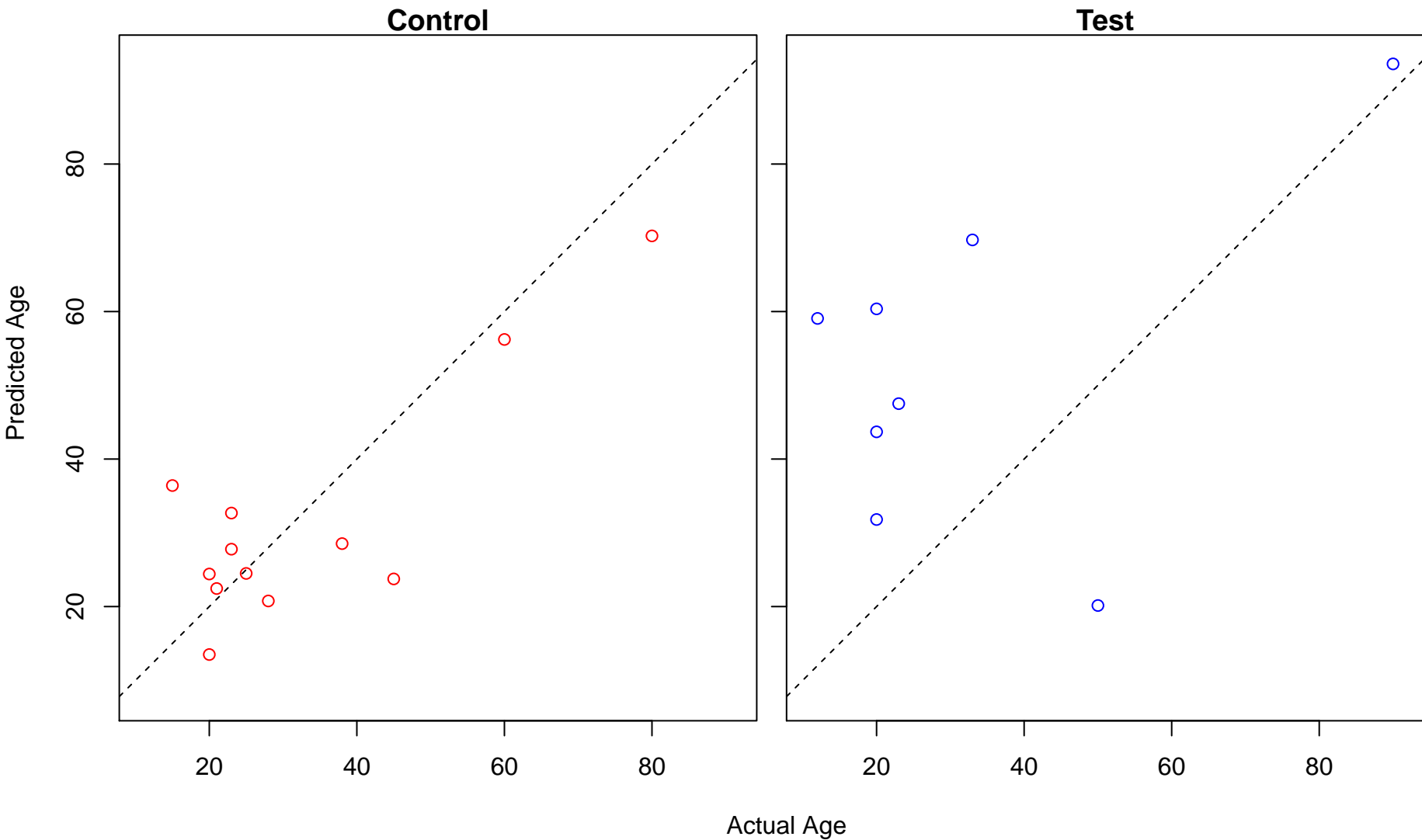
insulin-like growth factor receptor signaling pathway (Score: 19.949908)



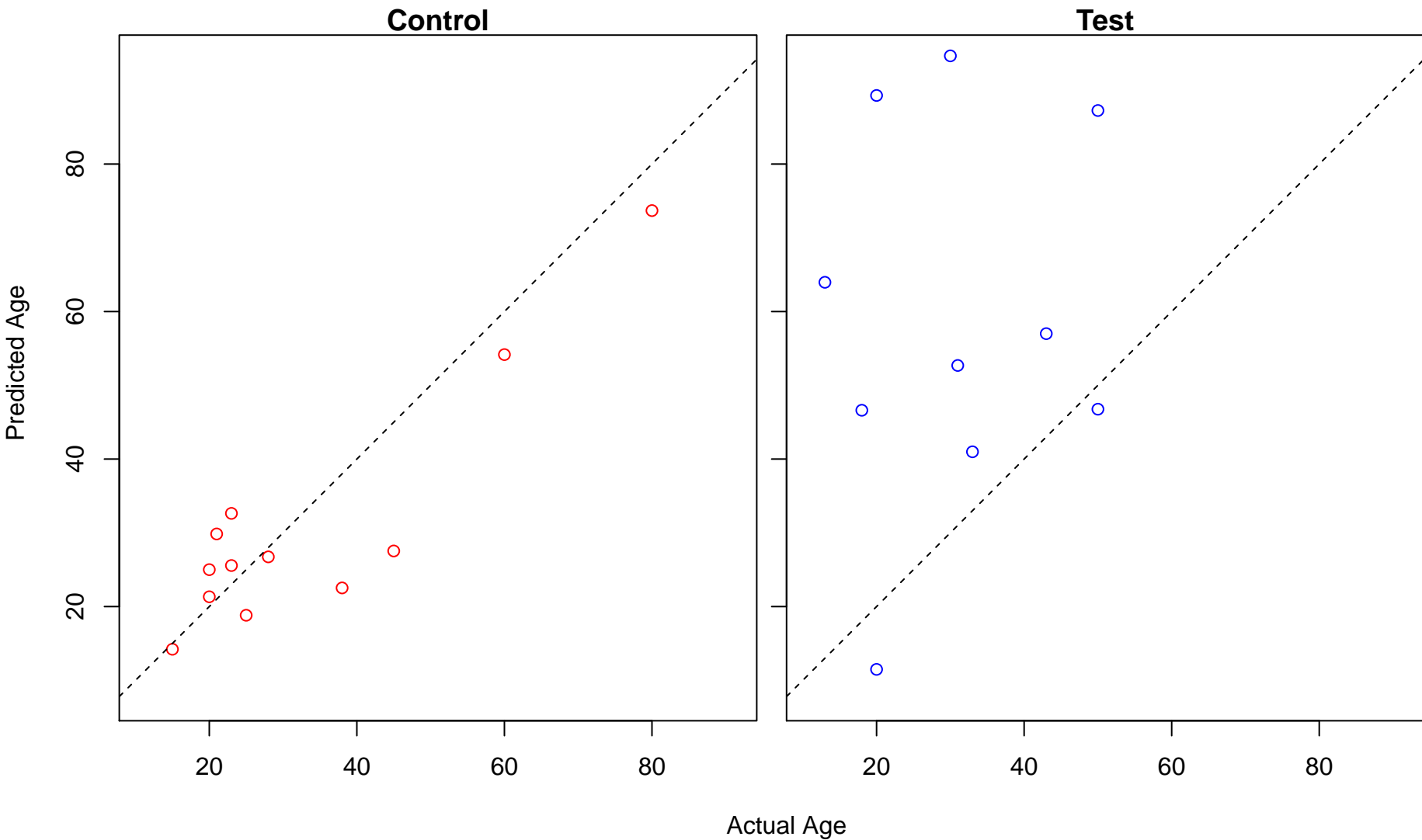
rhythmic process (Score: 19.907747)



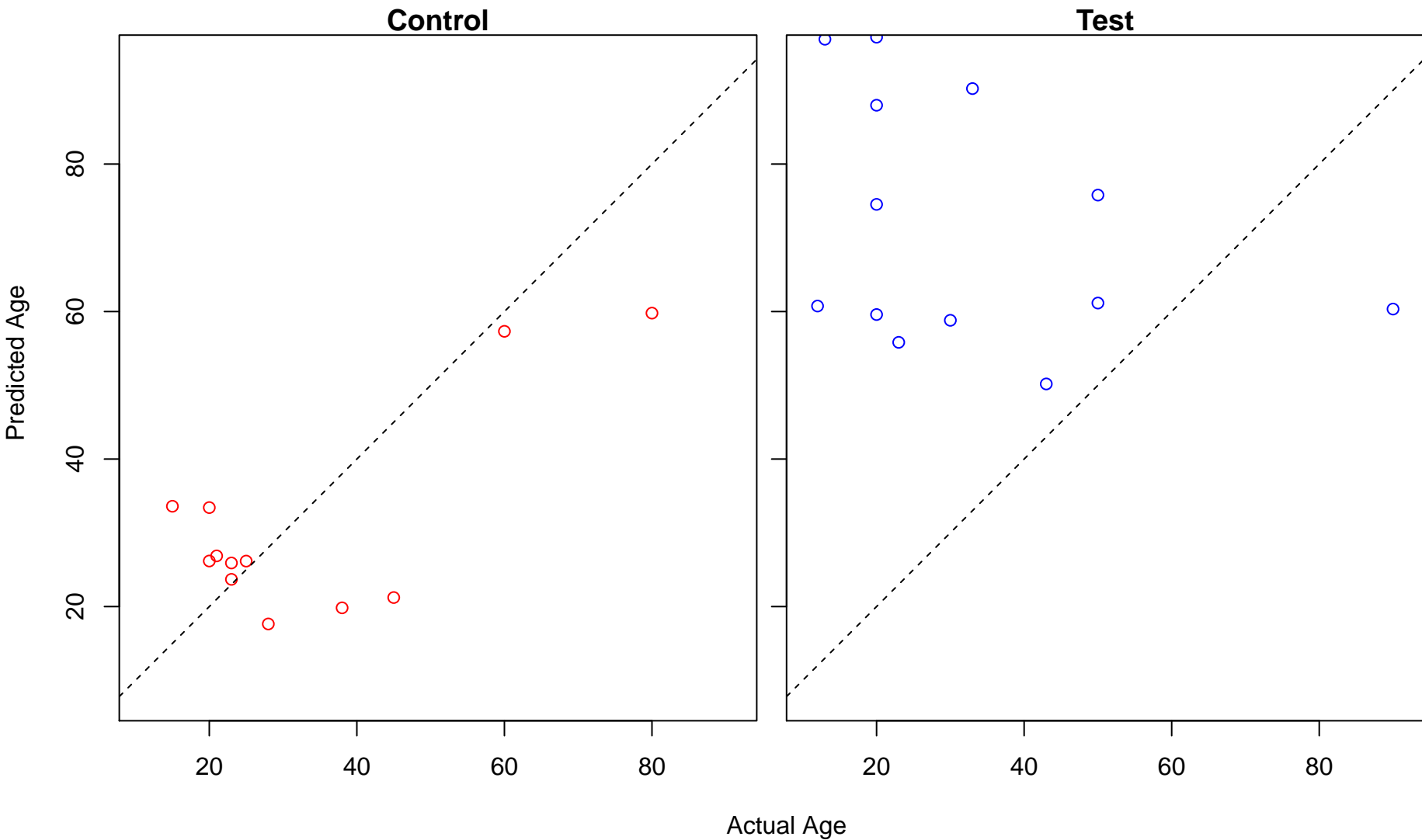
negative regulation of receptor-mediated endocytosis (Score: 19.897364)



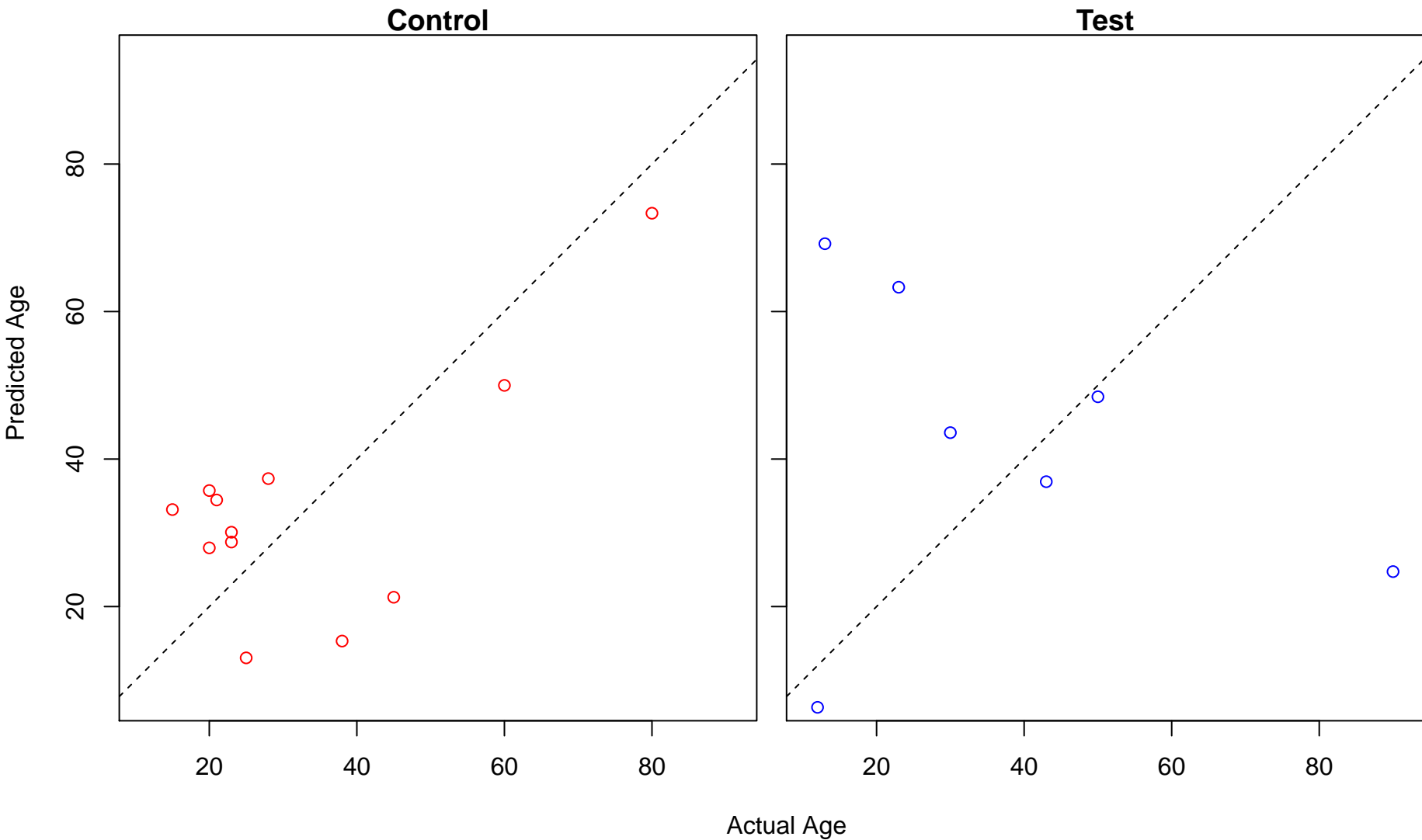
regulation of circadian sleep/wake cycle (Score: 19.874538)



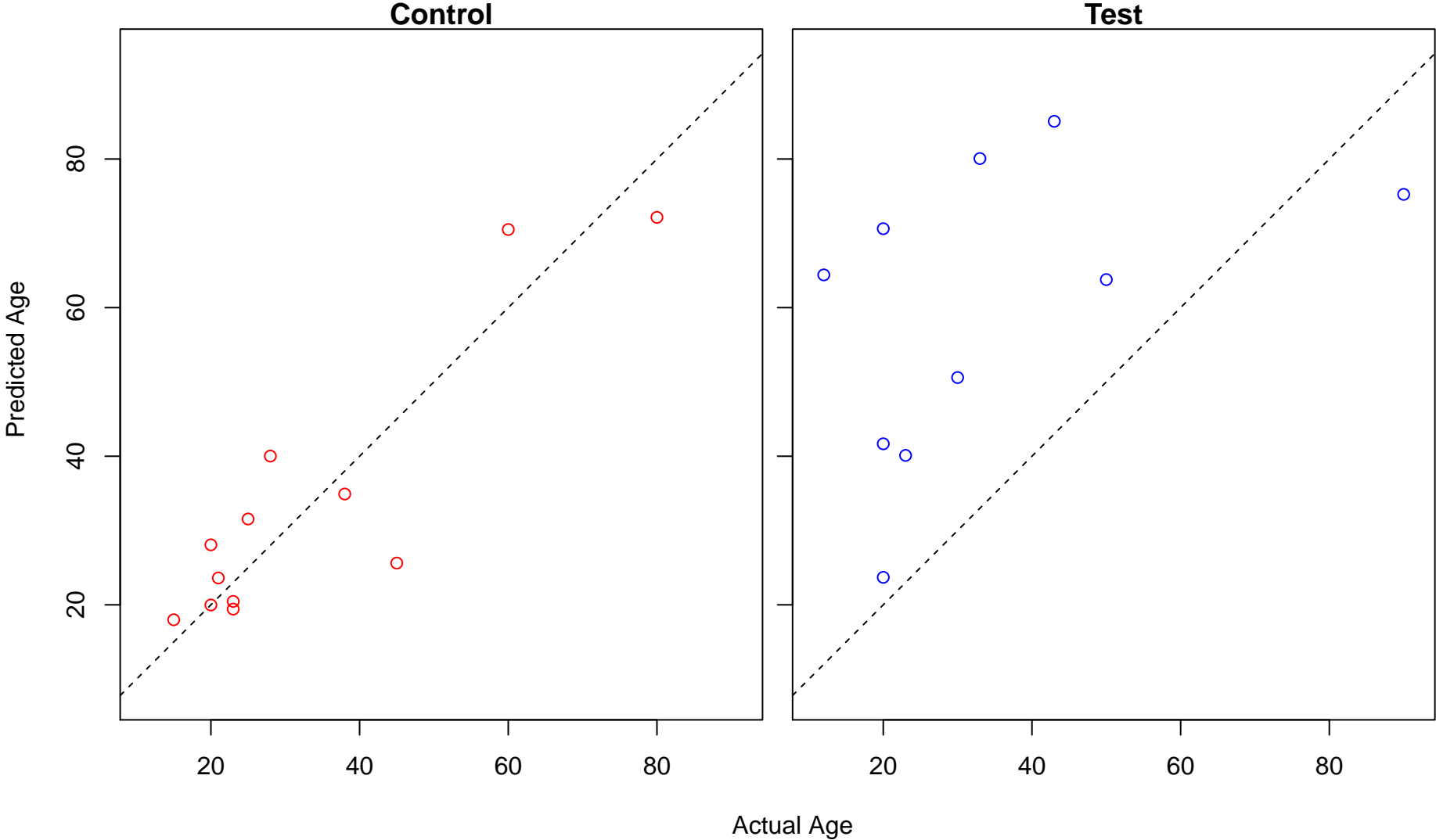
positive regulation of monooxygenase activity (Score: 19.833475)



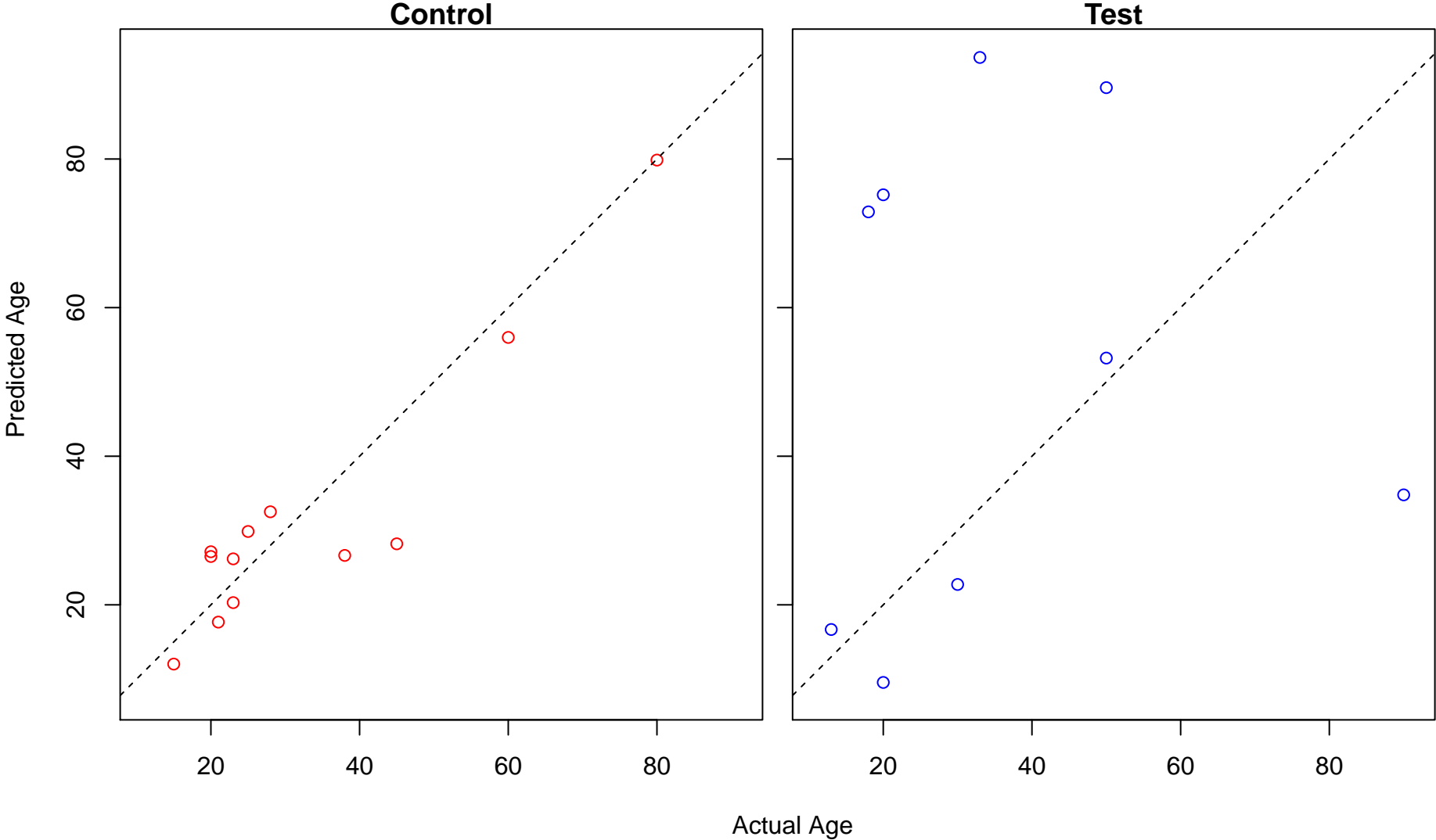
positive regulation of oxidoreductase activity (Score: 19.829288)



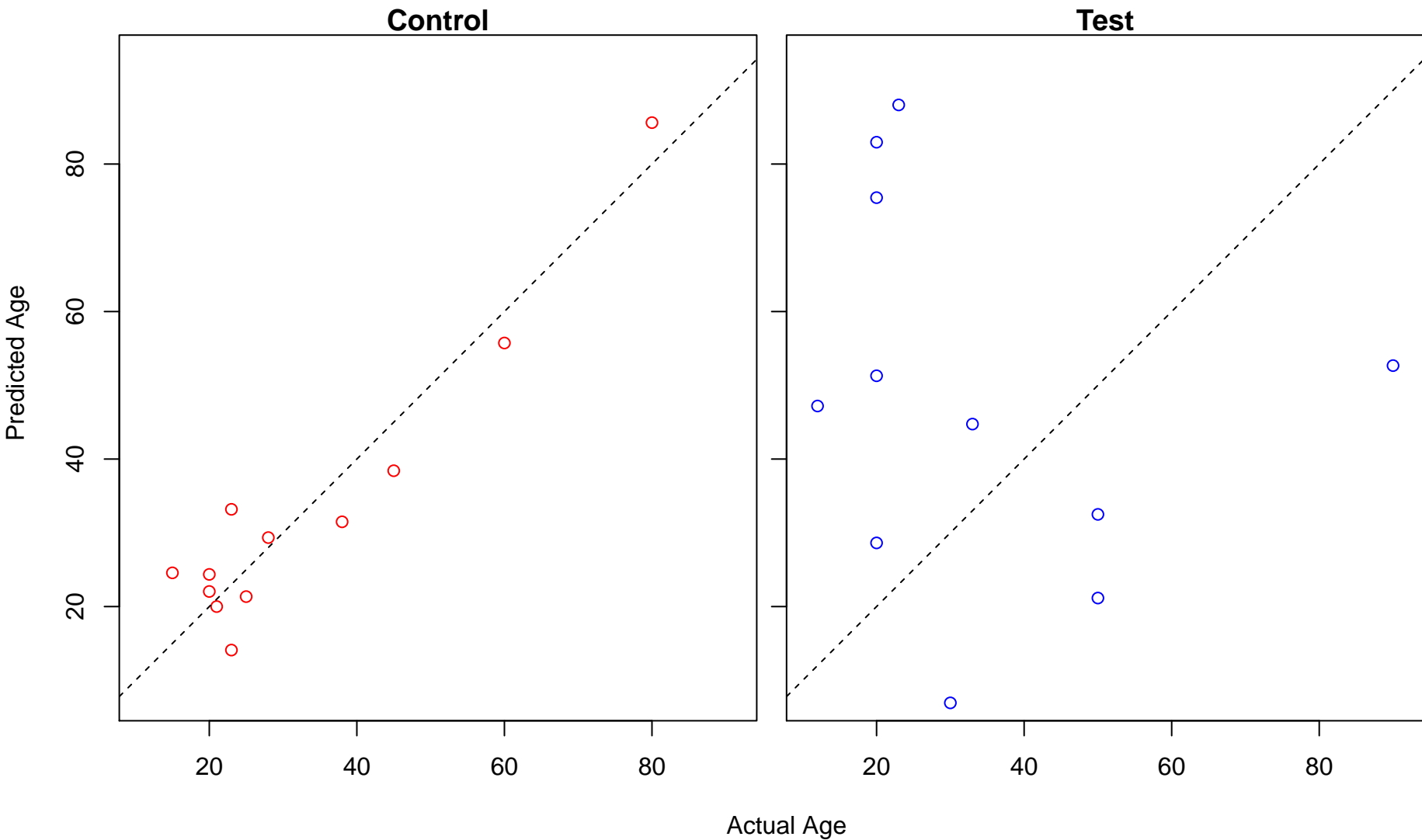
negative regulation of retinoic acid receptor signaling pathway (Score: 19.821912)



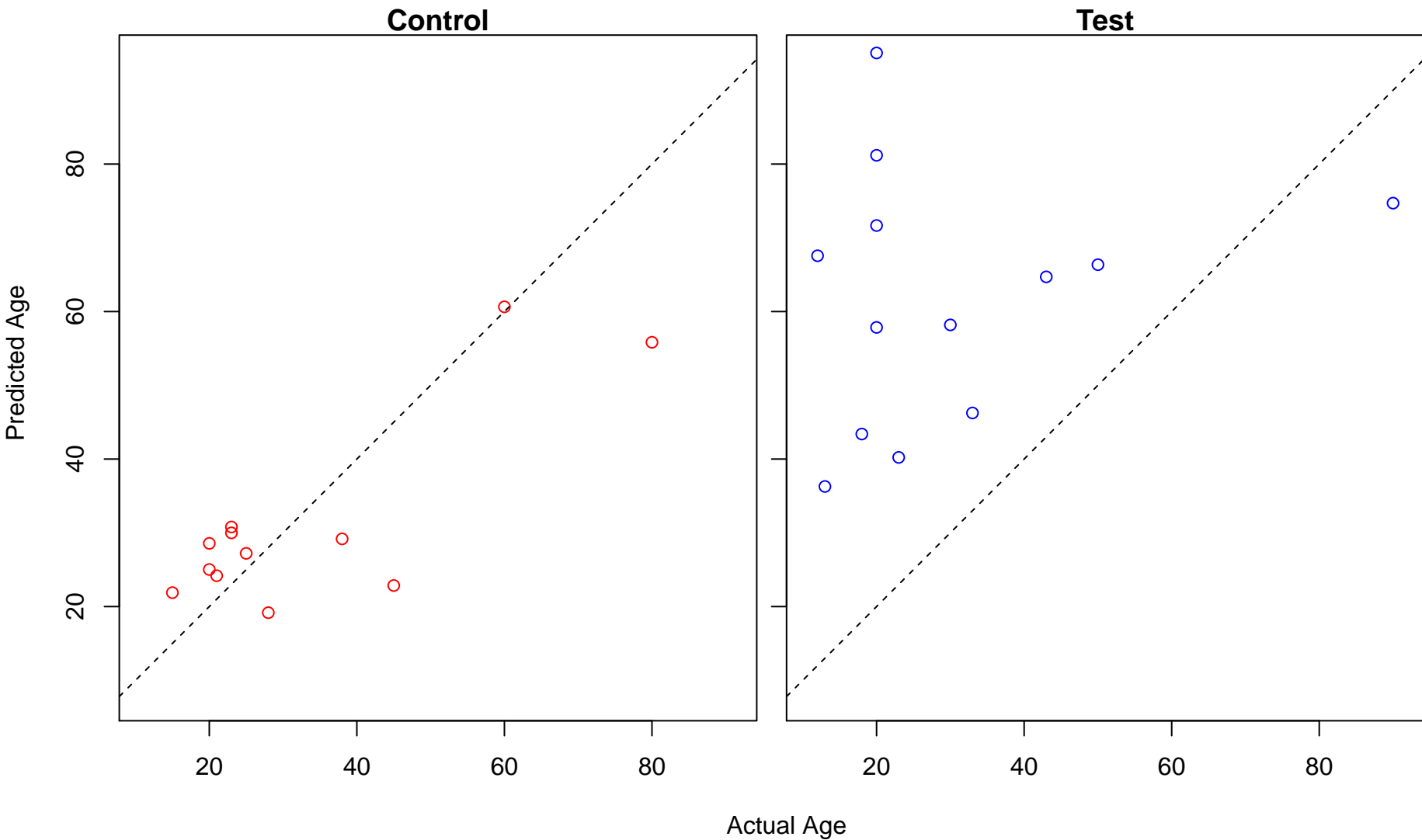
activation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 19.7)



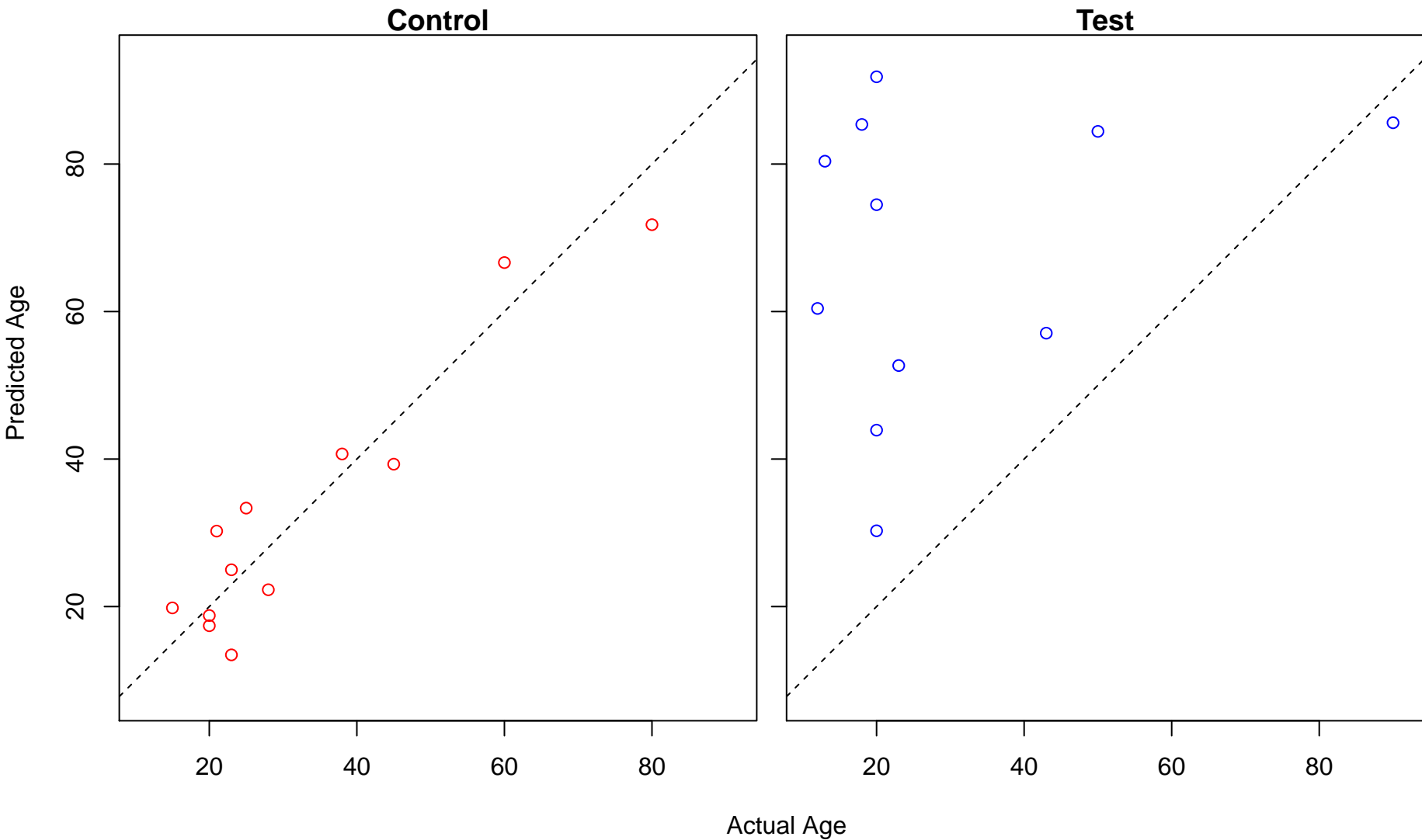
pre-miRNA processing (Score: 19.782513)



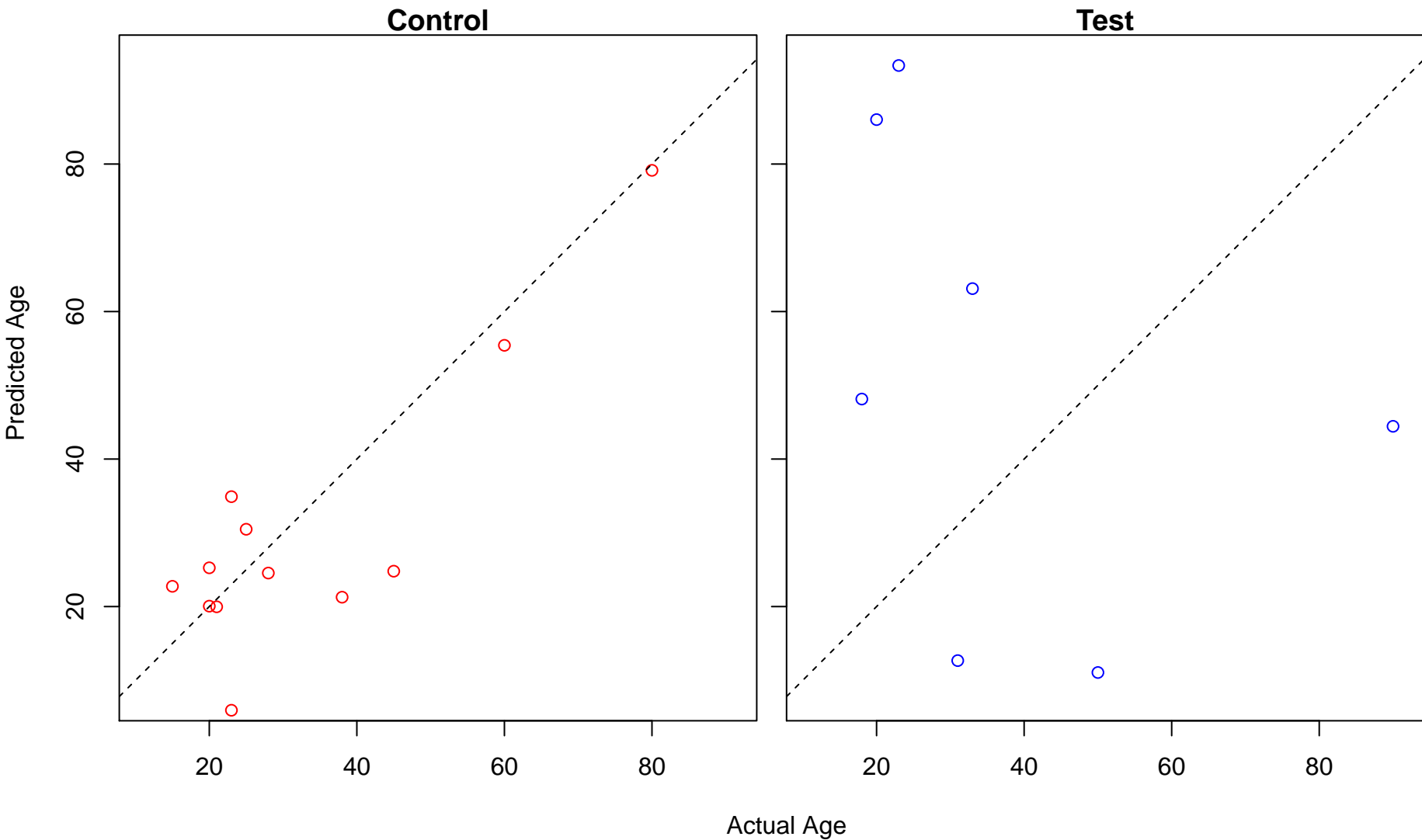
positive regulation of smooth muscle contraction (Score: 19.774378)



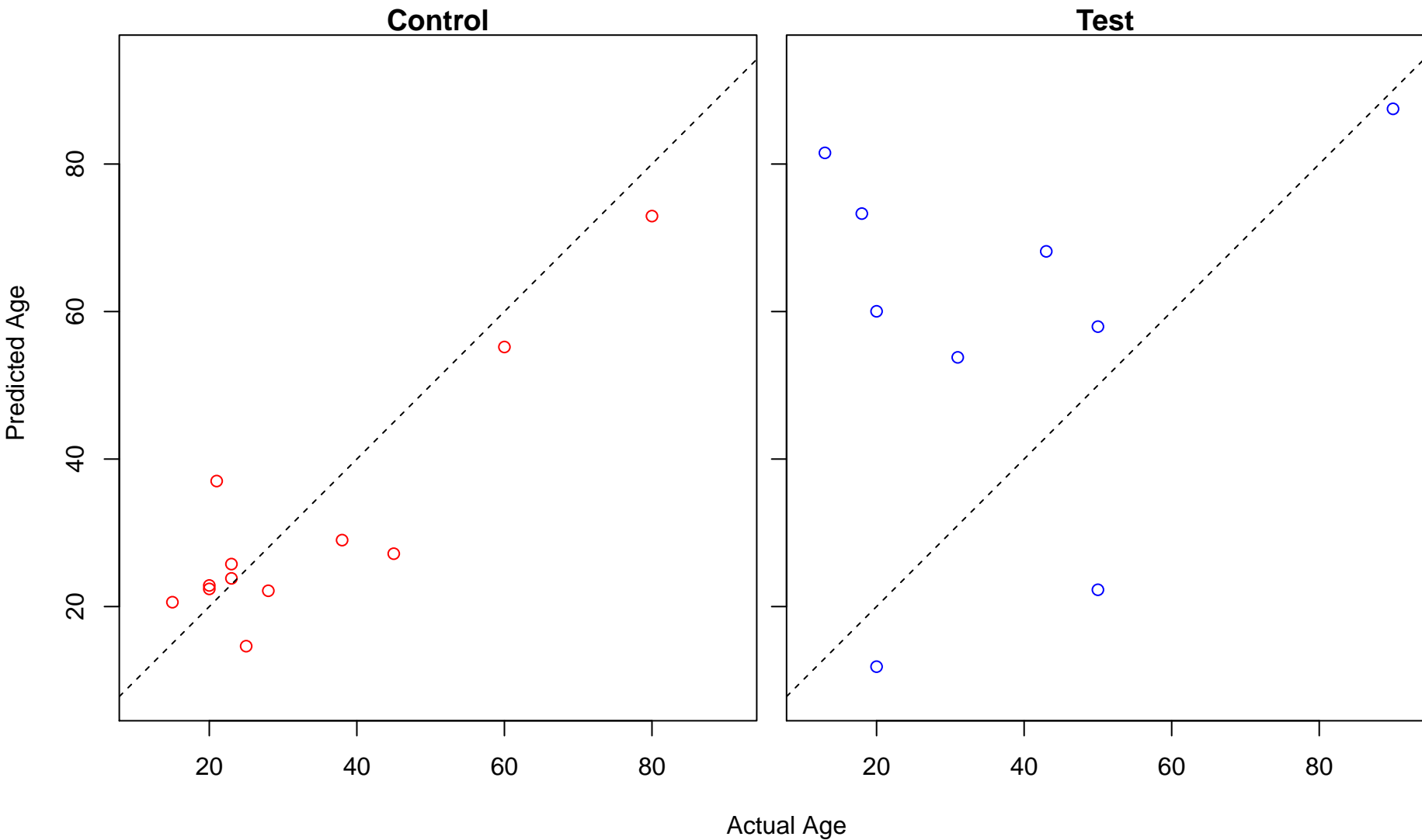
interferon-gamma secretion (Score: 19.732549)



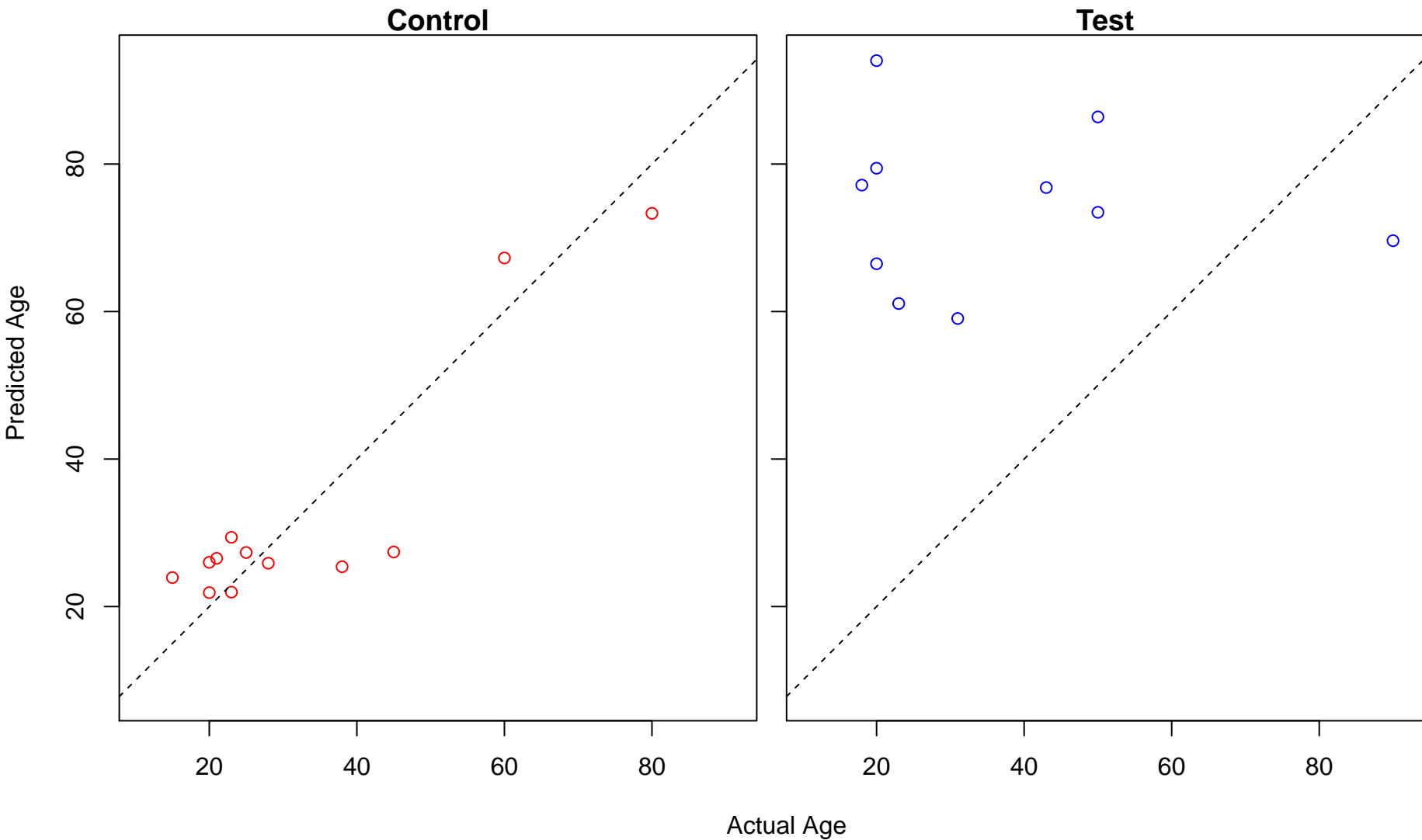
centrosome localization (Score: 19.682775)



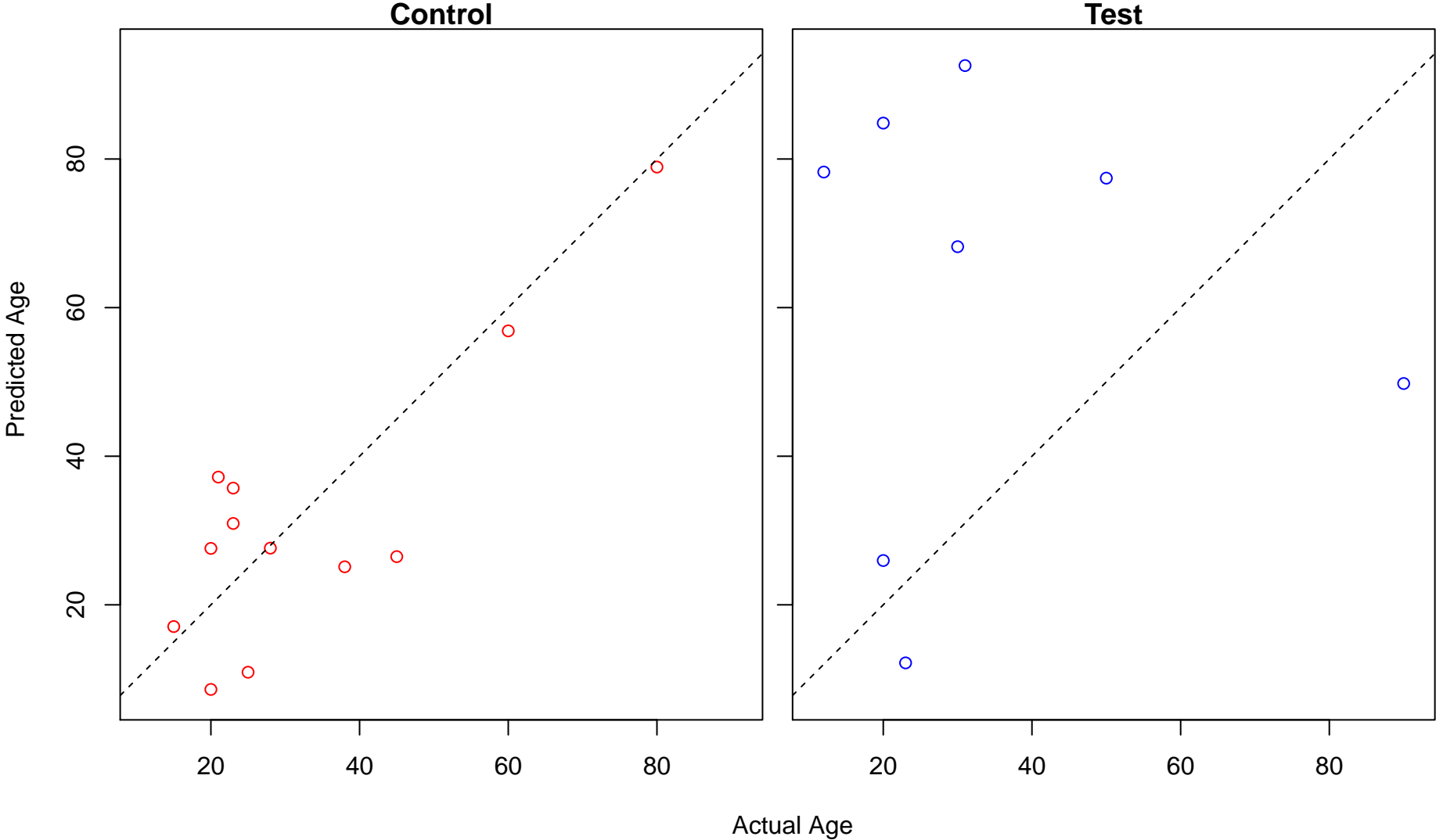
DNA replication initiation (Score: 19.601015)



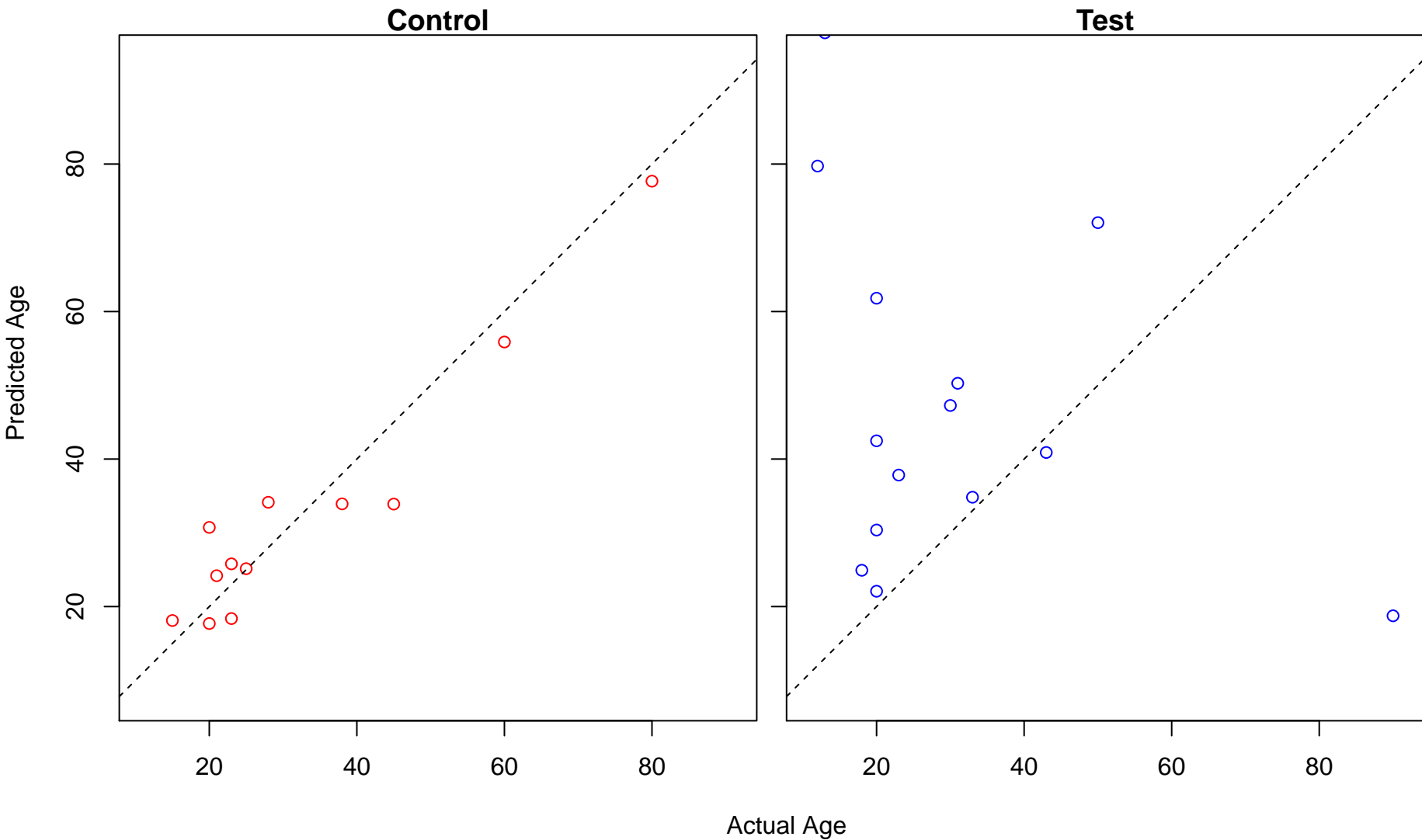
endocardium development (Score: 19.597819)



regulation of cell migration involved in sprouting angiogenesis (Score: 19.485709)



positive regulation of response to DNA damage stimulus (Score: 19.357309)

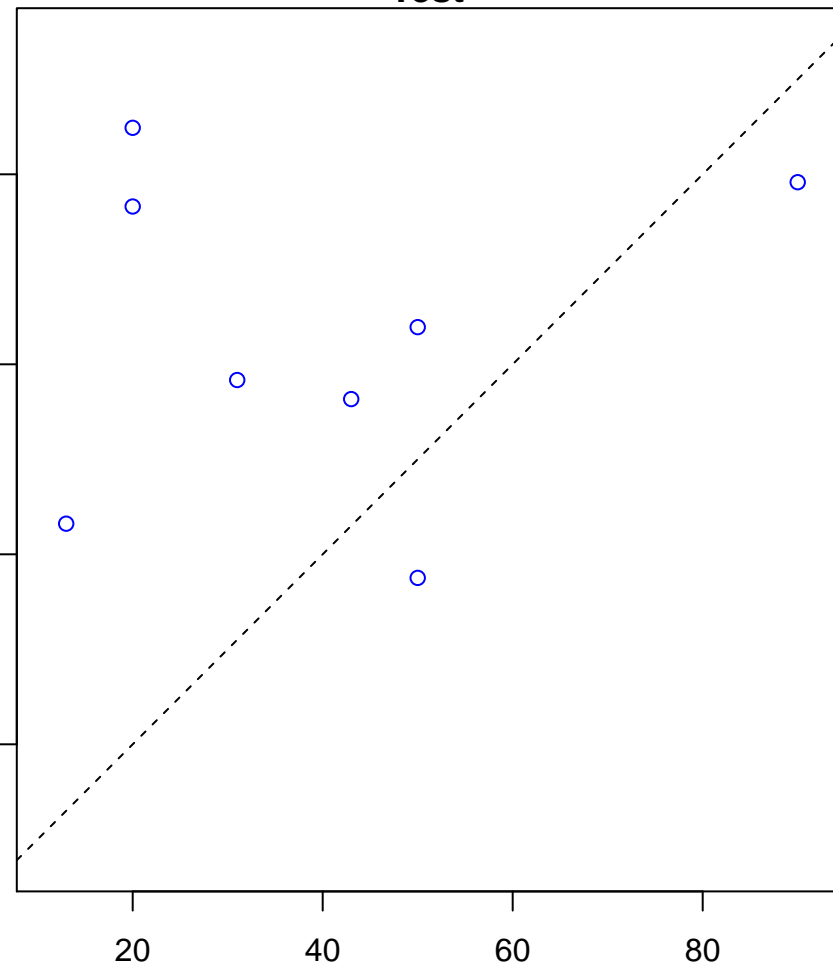
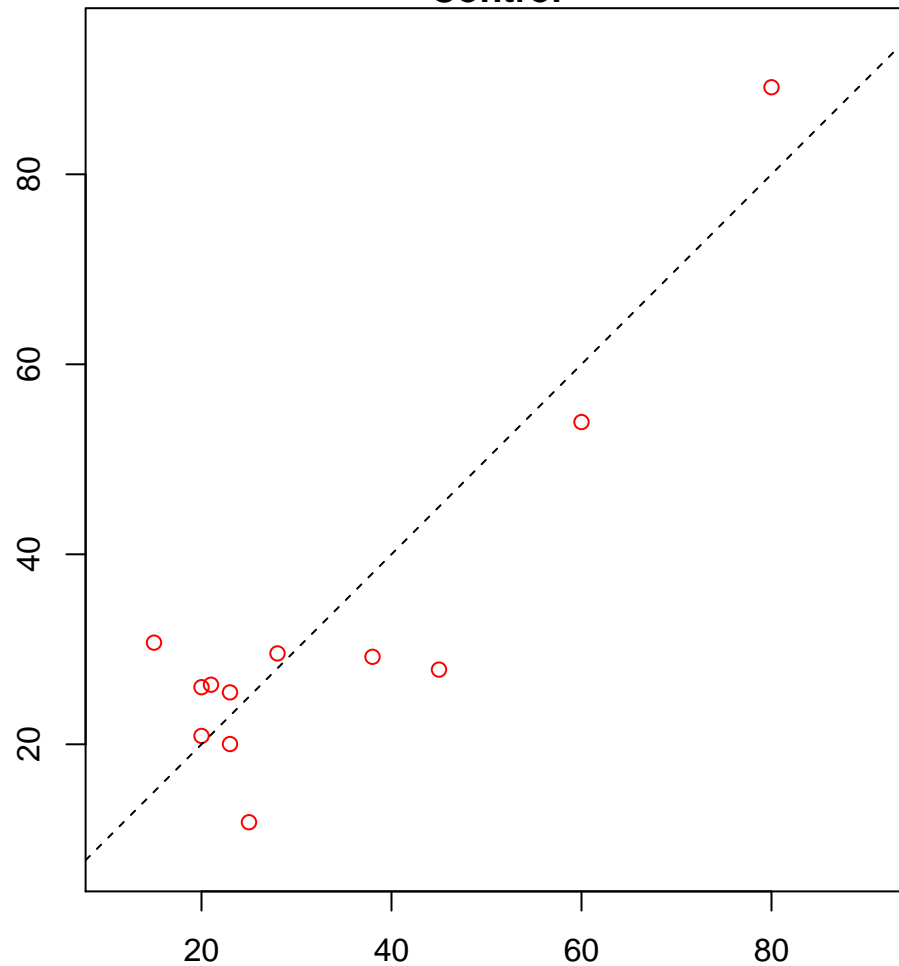


positive regulation of macroautophagy (Score: 19.253620)

Control

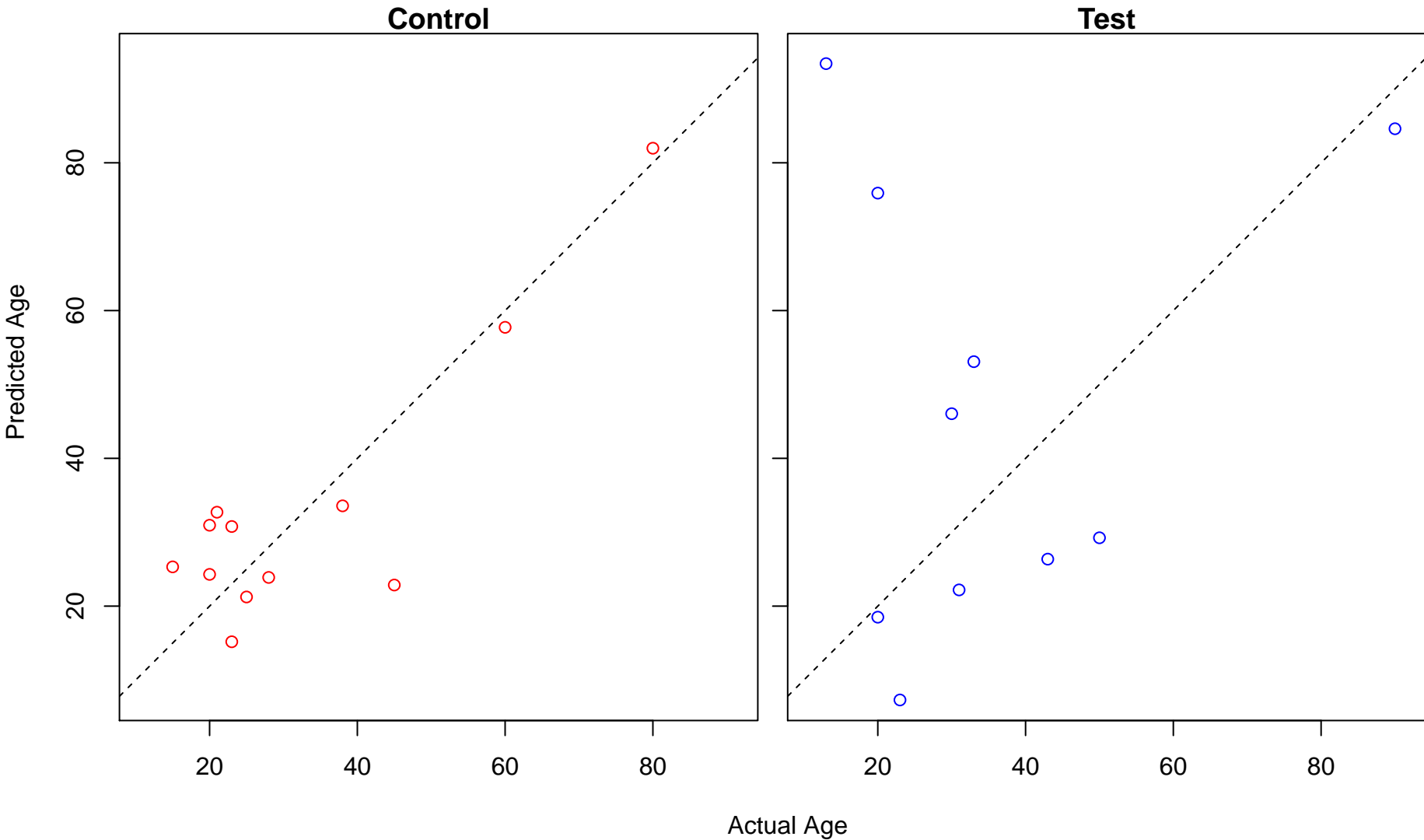
Test

Predicted Age

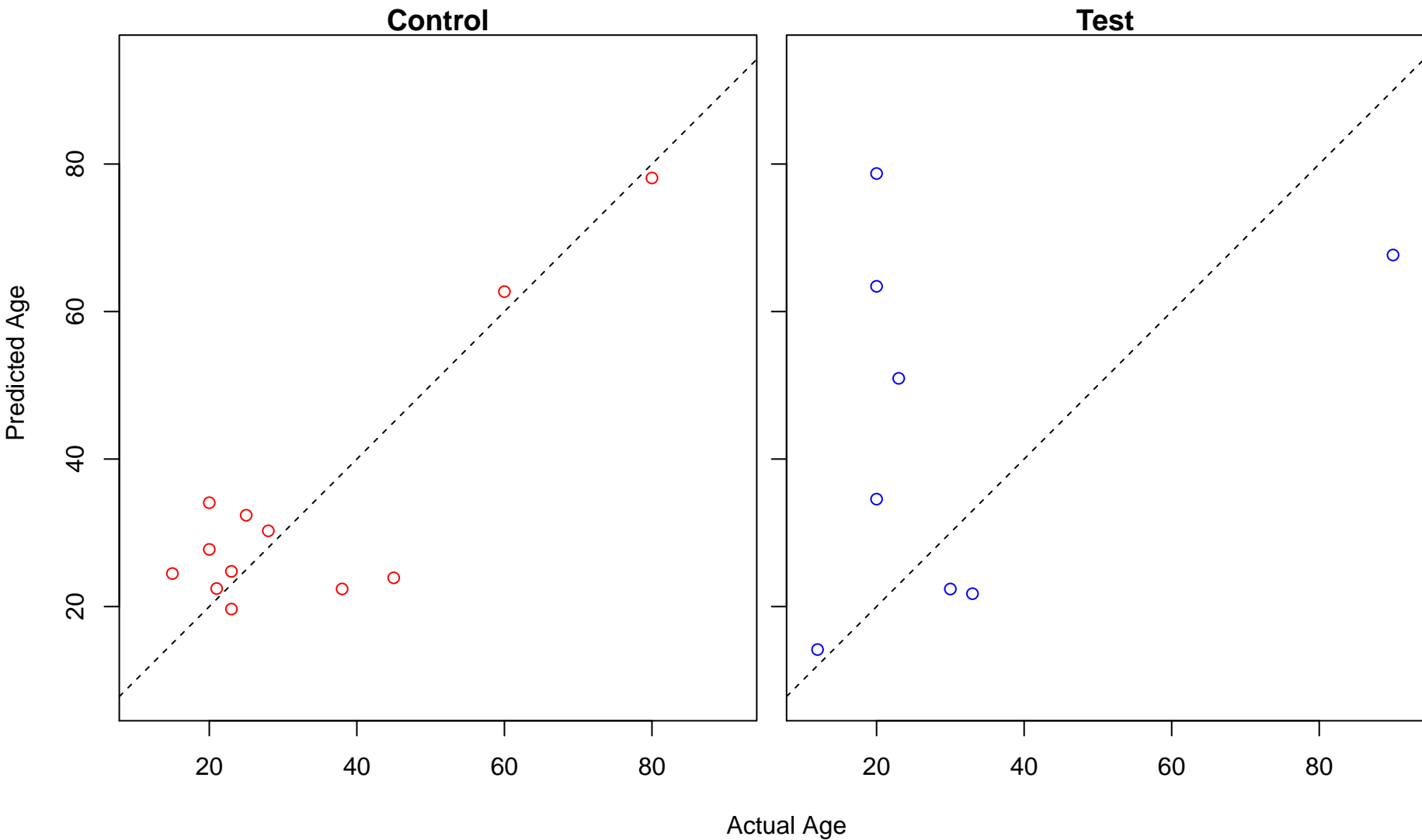


Actual Age

phosphatidylcholine biosynthetic process (Score: 19.232852)

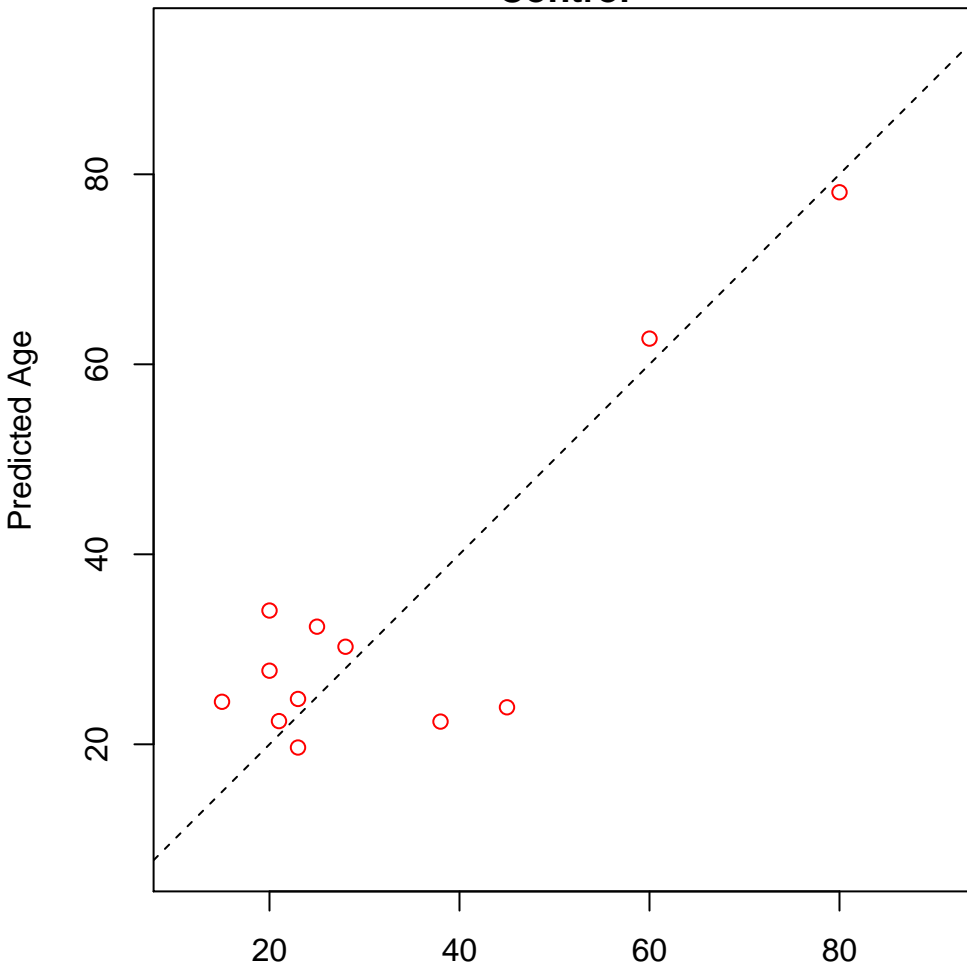


protein nitrosylation (Score: 19.212395)

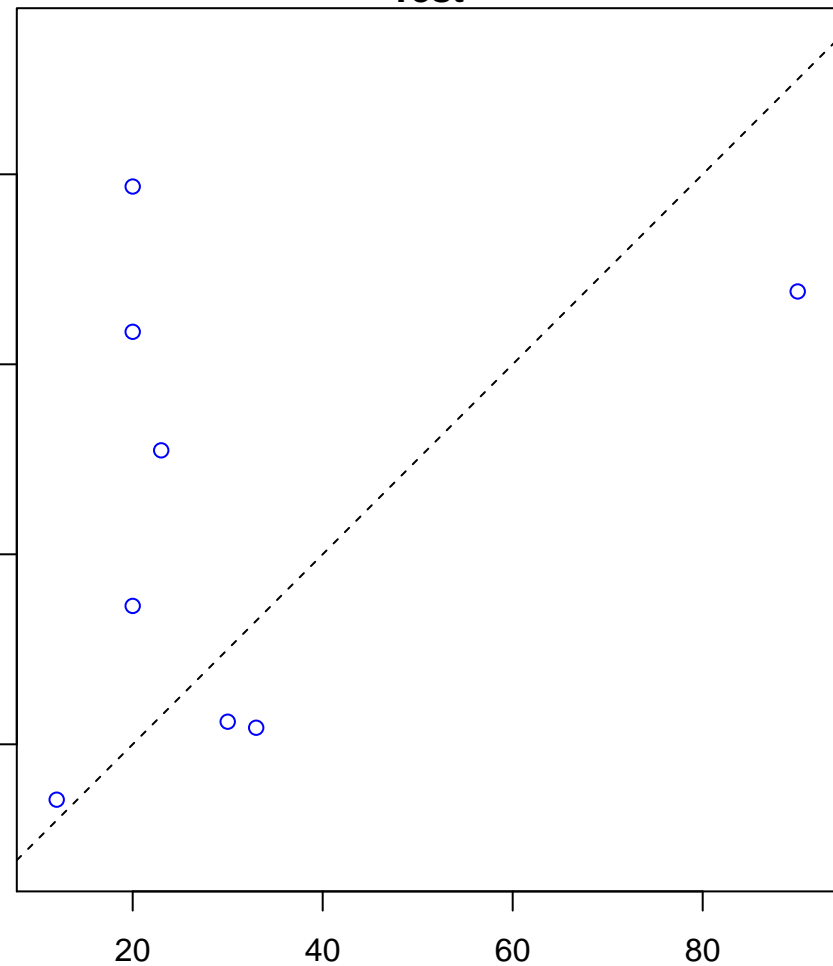


peptidyl-cysteine S-nitrosylation (Score: 19.212395)

Control

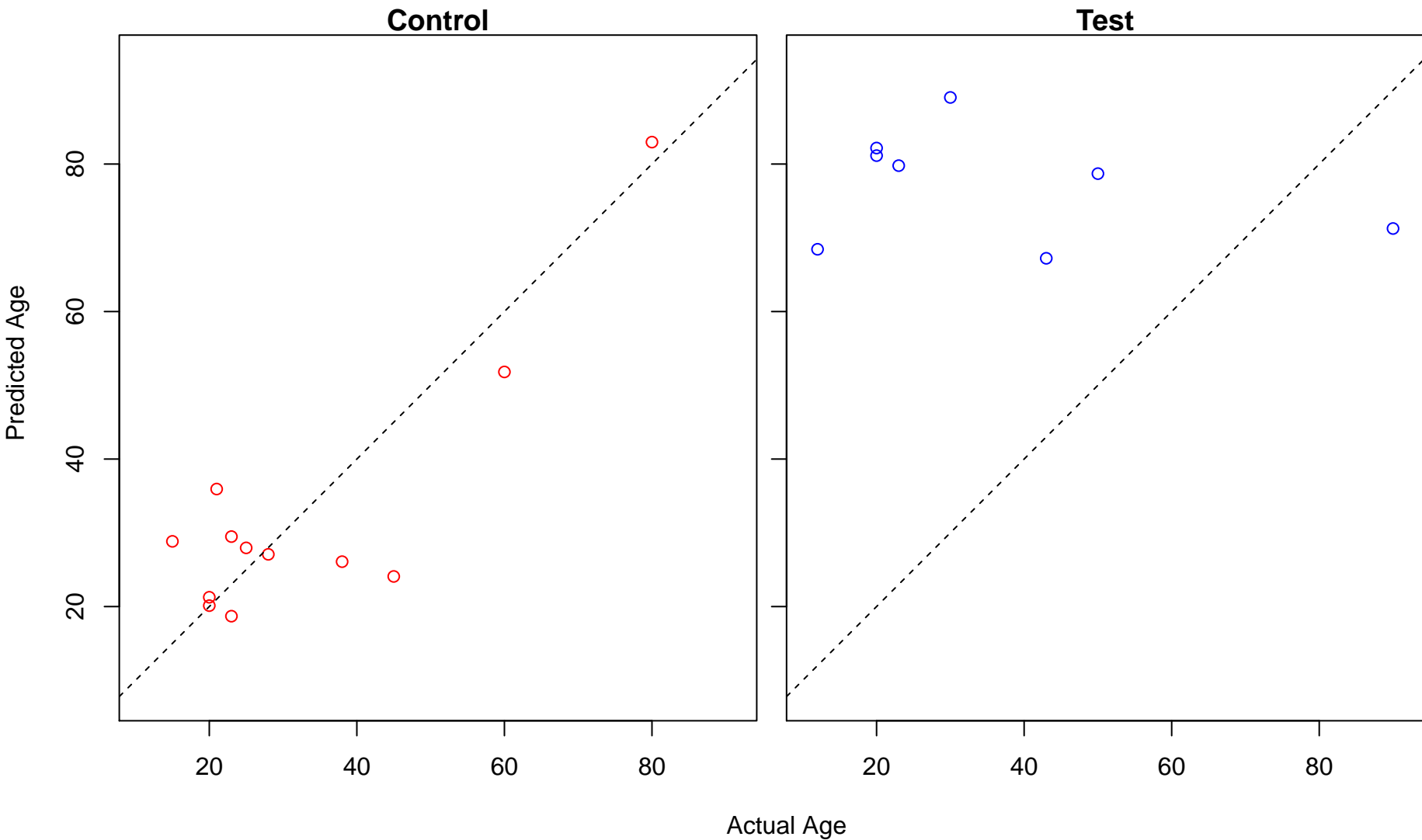


Test

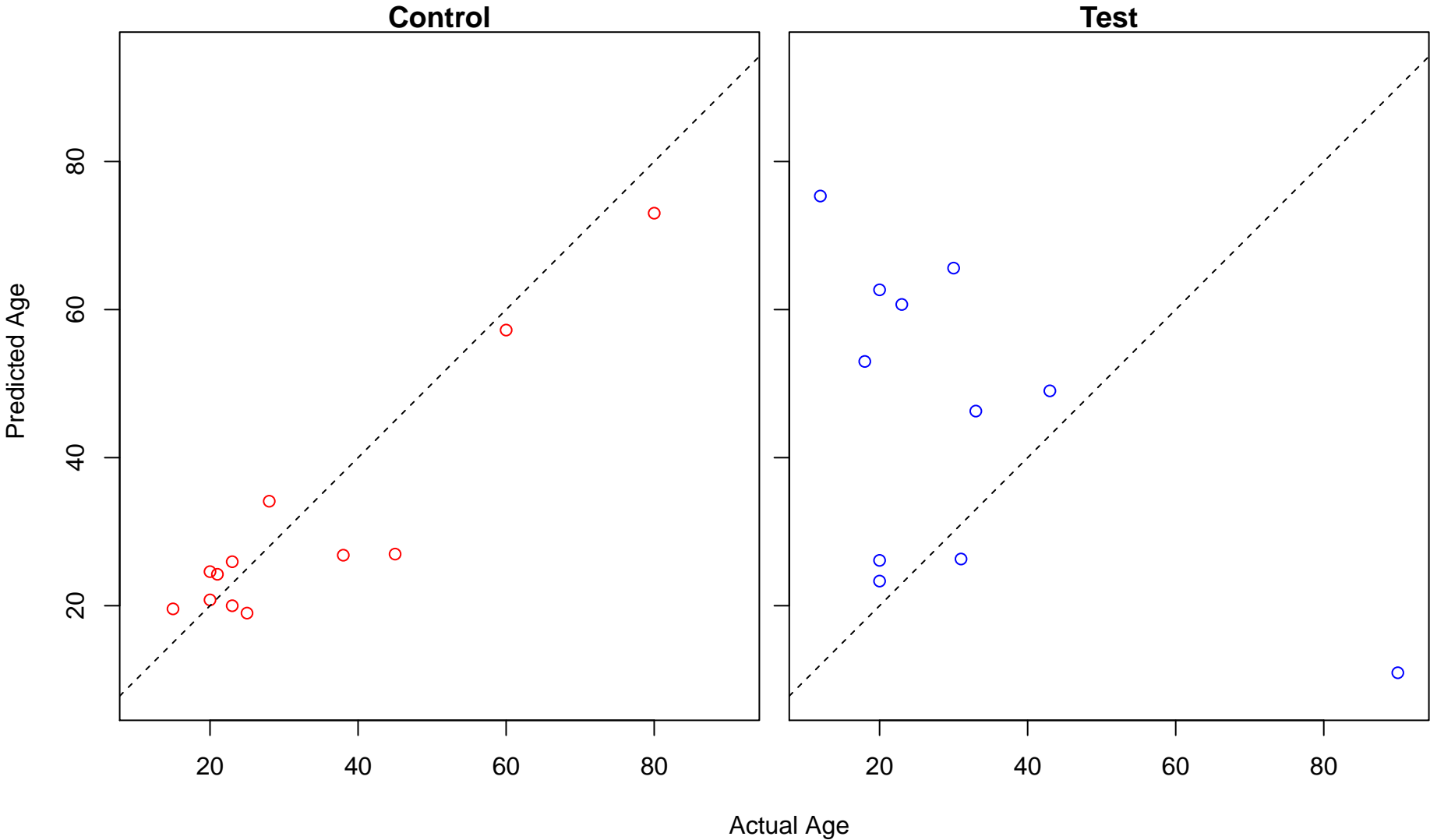


Actual Age

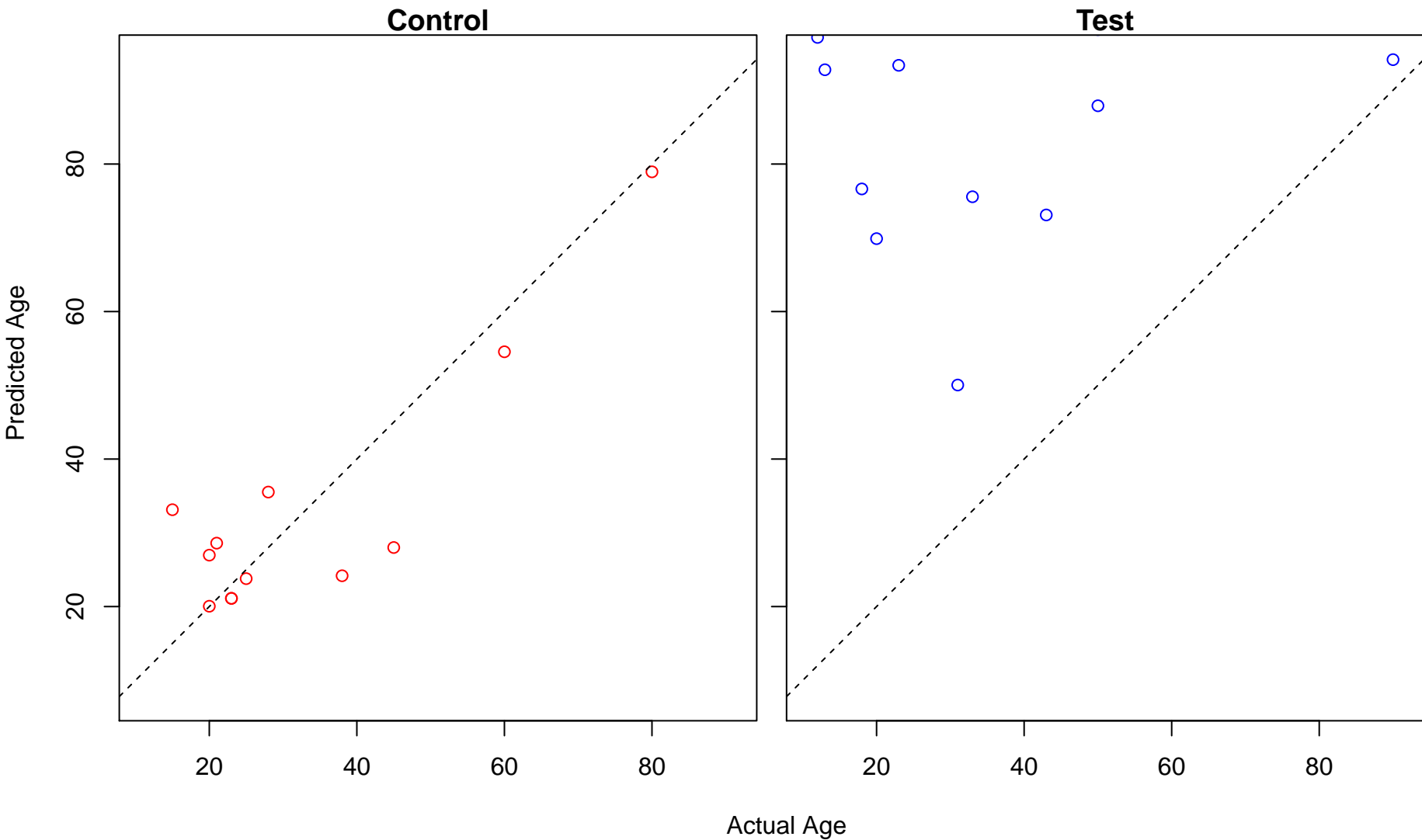
regulation of cholesterol storage (Score: 19.100915)



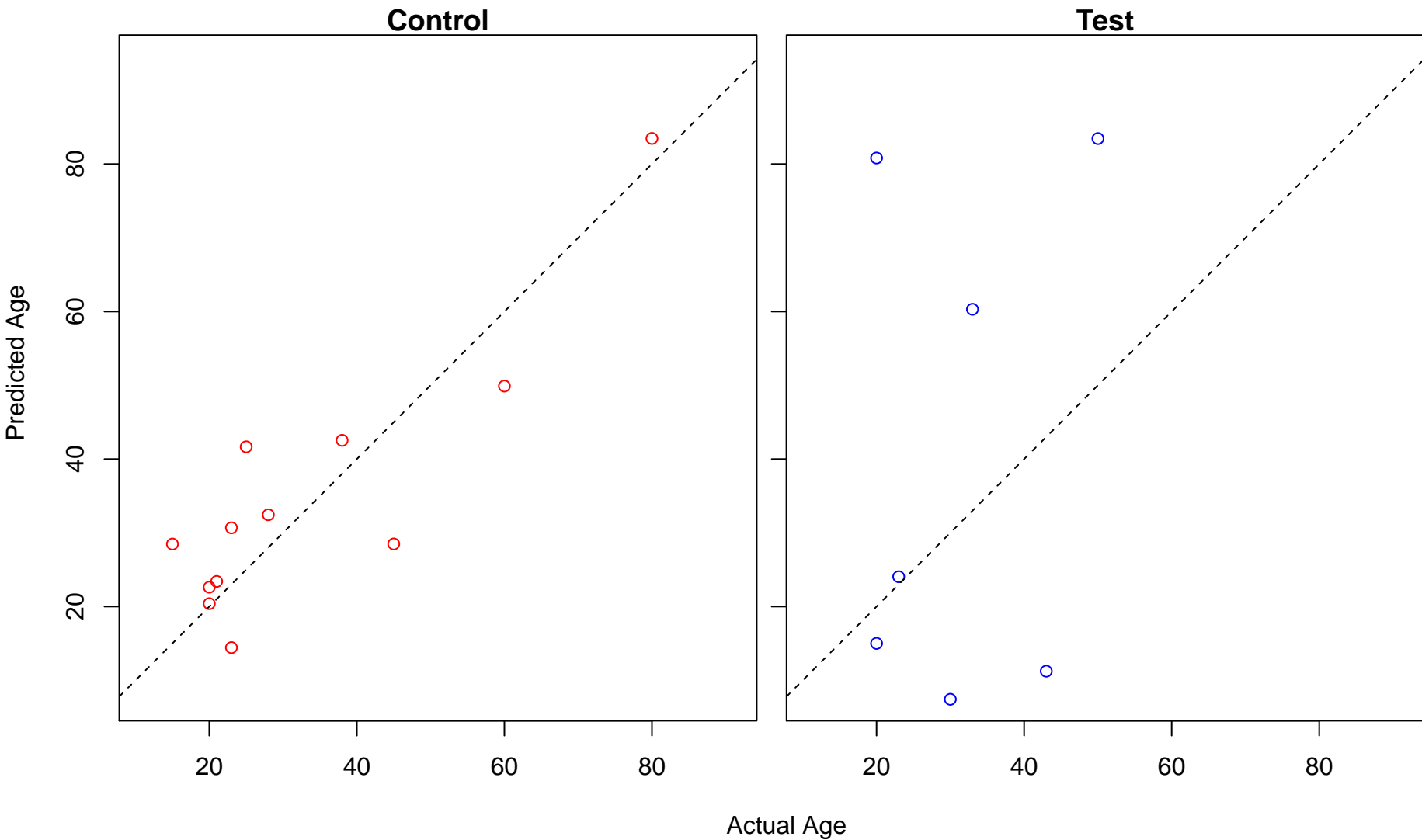
positive regulation of stress-activated MAPK cascade (Score: 19.099803)



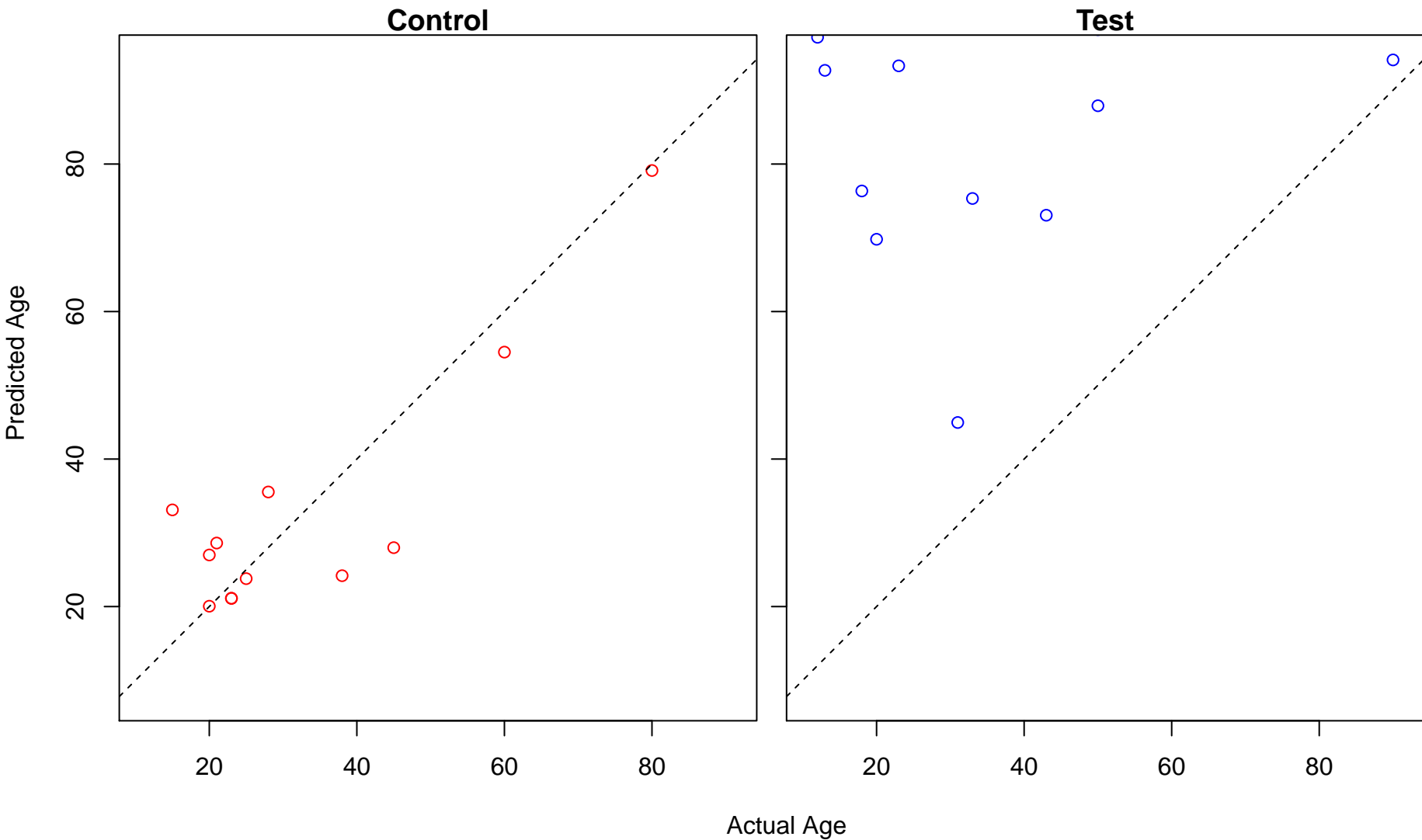
regulation of monocyte chemotactic protein-1 production (Score: 19.097580)



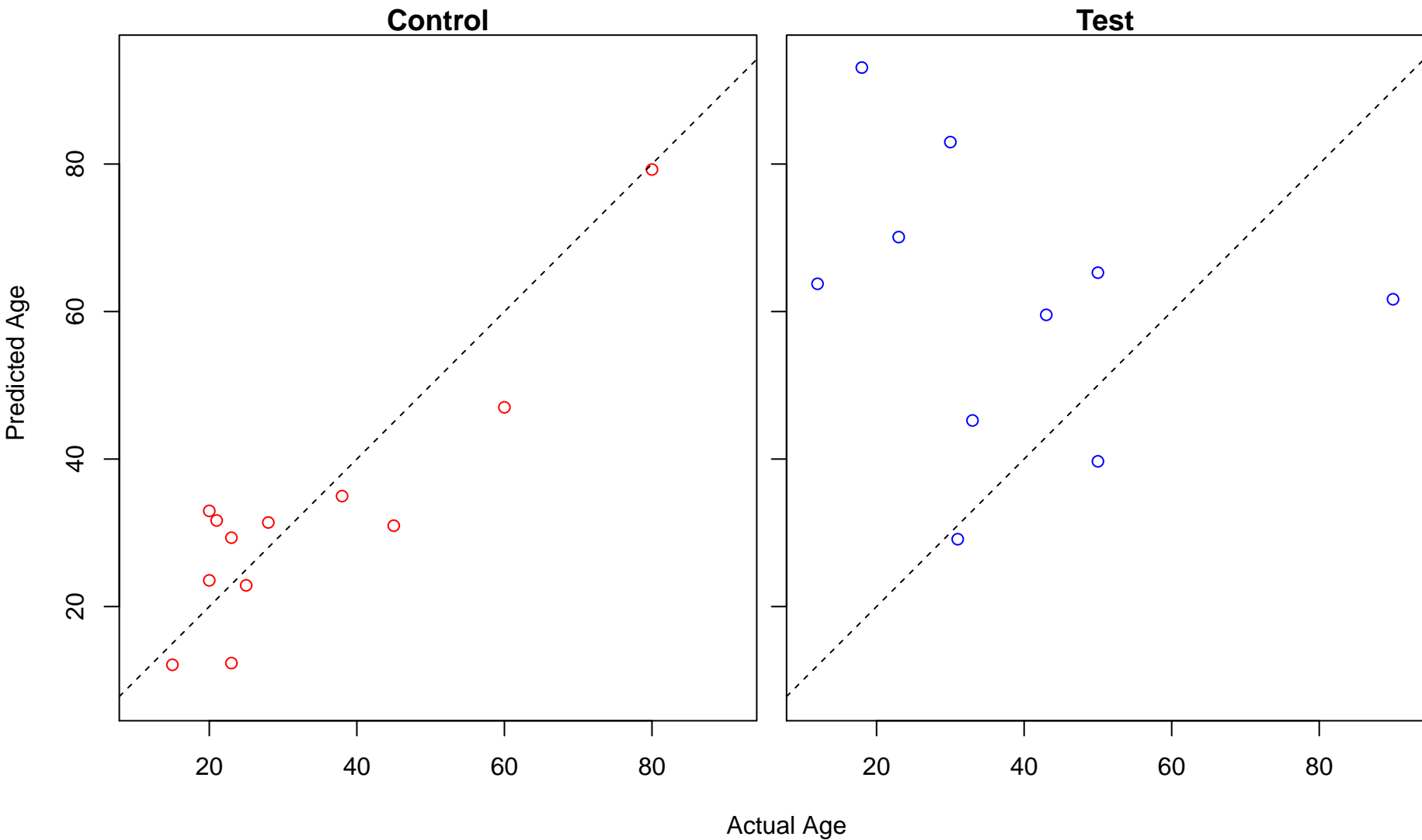
regulation of respiratory burst (Score: 19.087932)



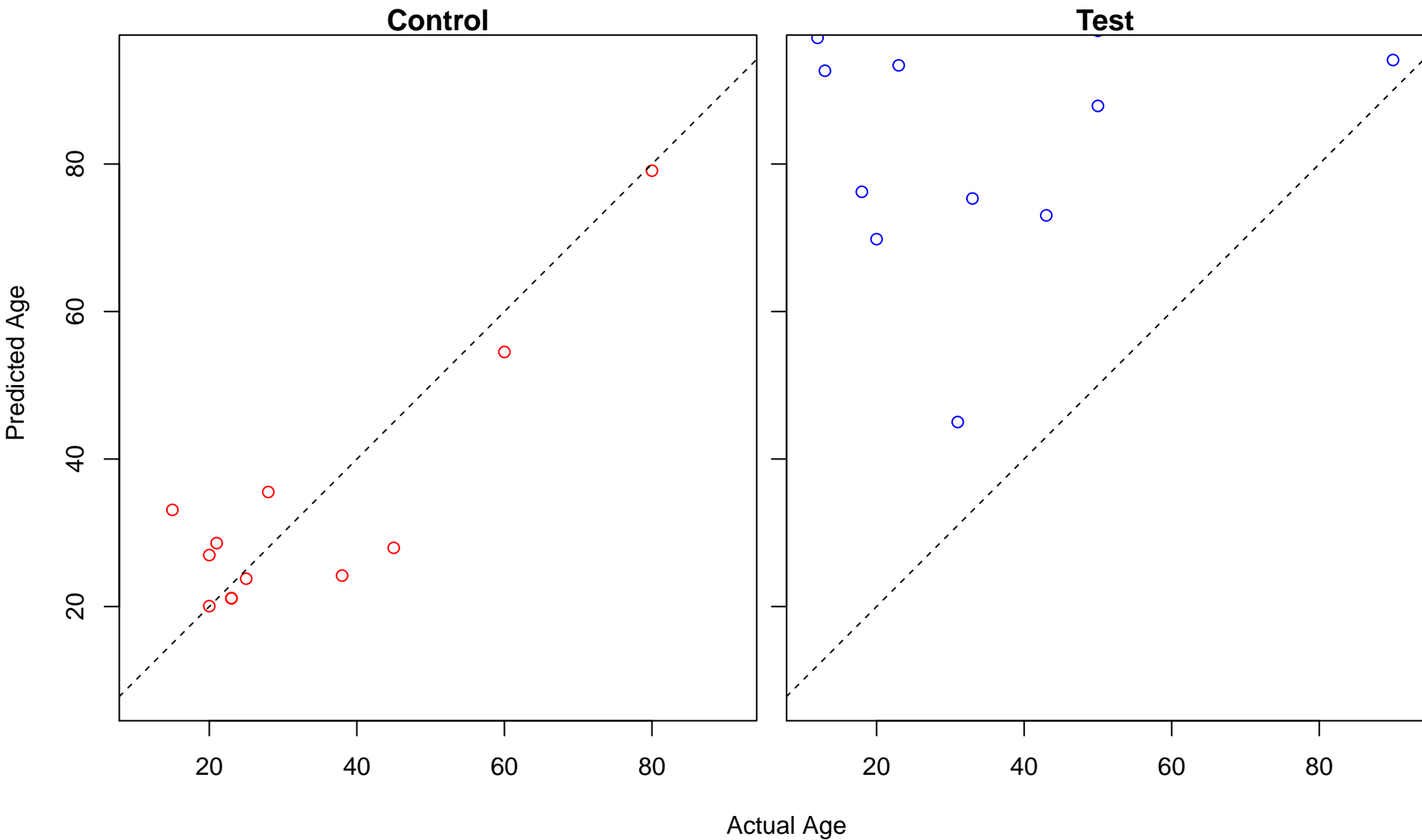
negative regulation of interleukin-1 beta production (Score: 19.039809)



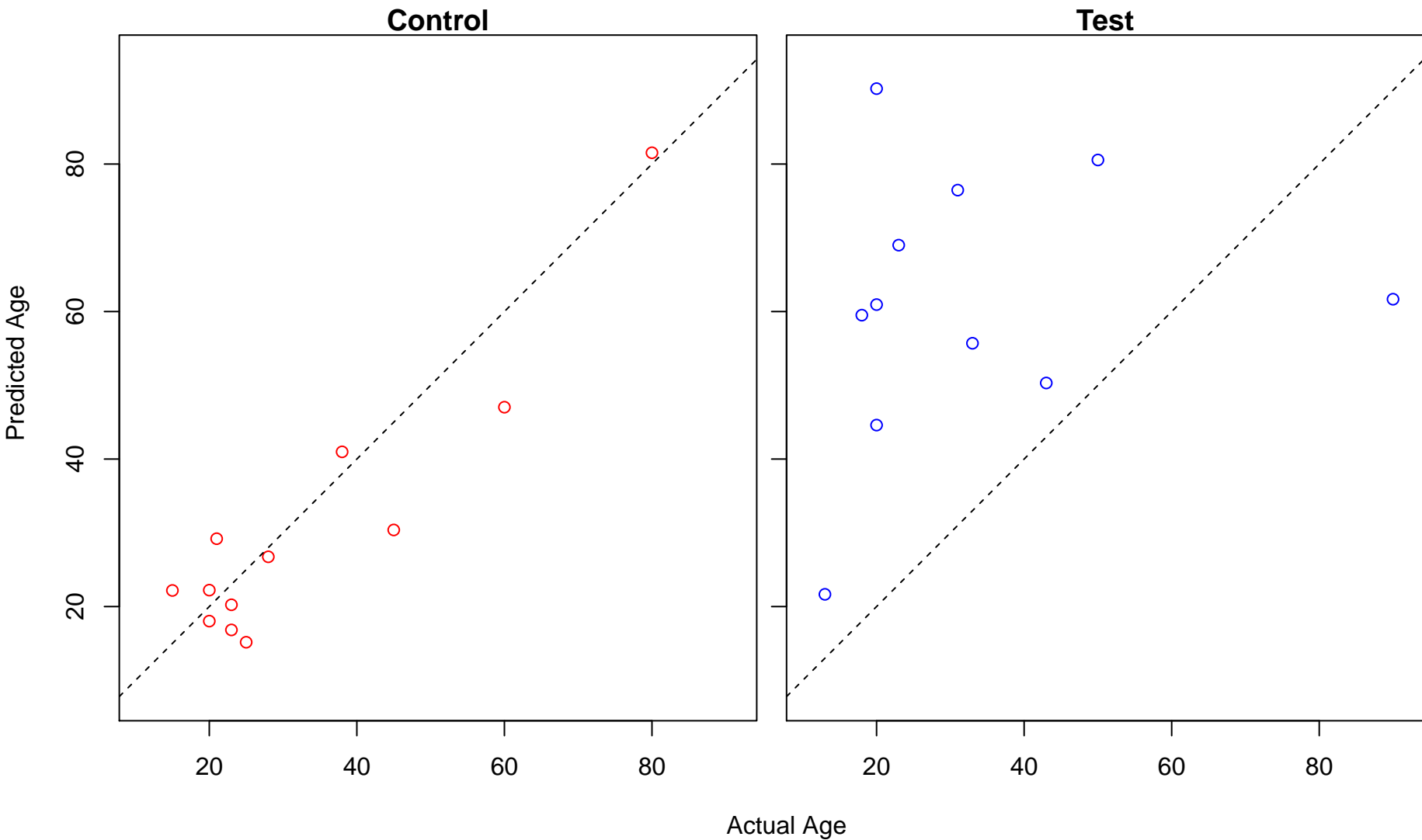
regulation of protein kinase B signaling (Score: 19.038165)



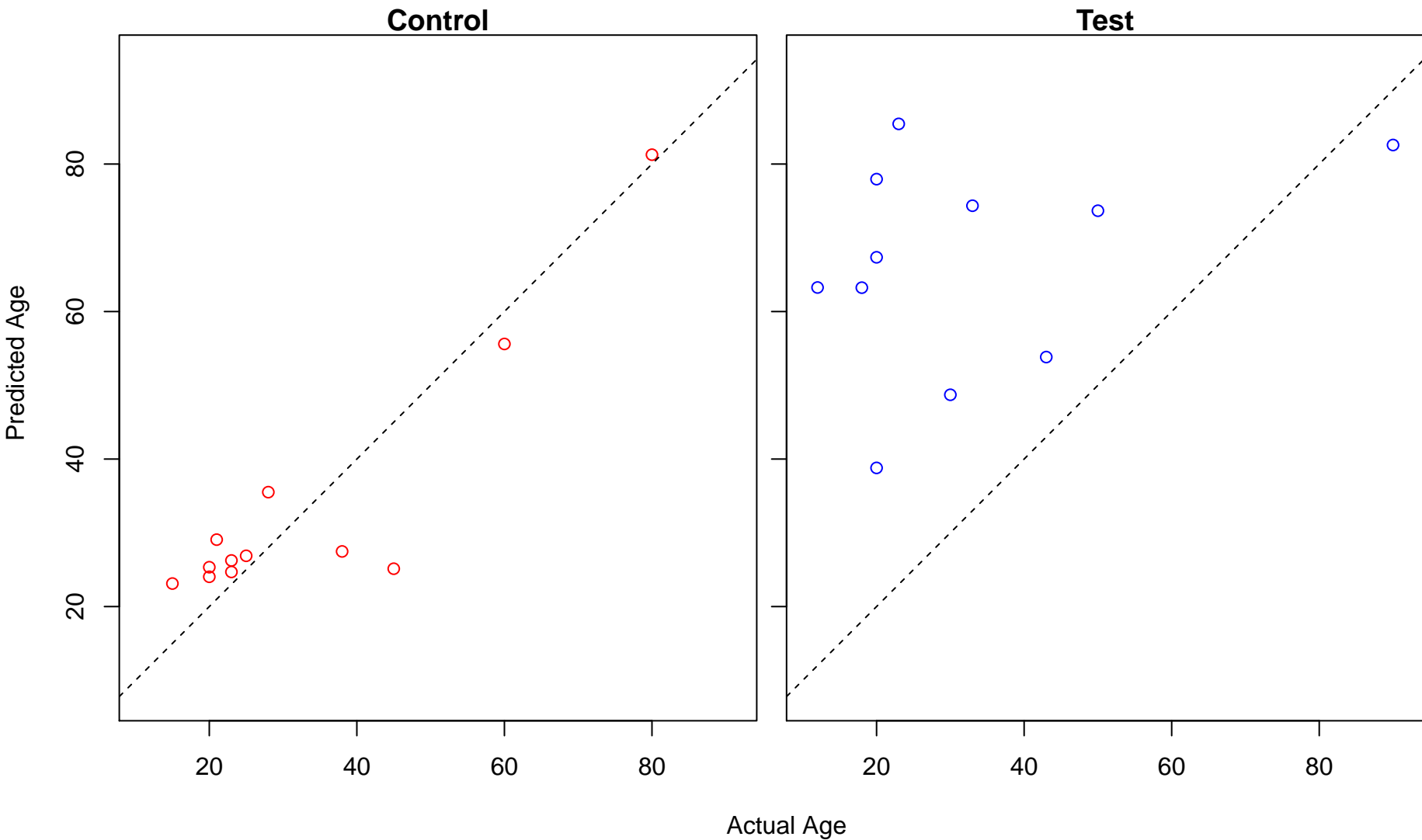
negative regulation of interleukin-1 production (Score: 19.001882)



chemical synaptic transmission, postsynaptic (Score: 18.902603)

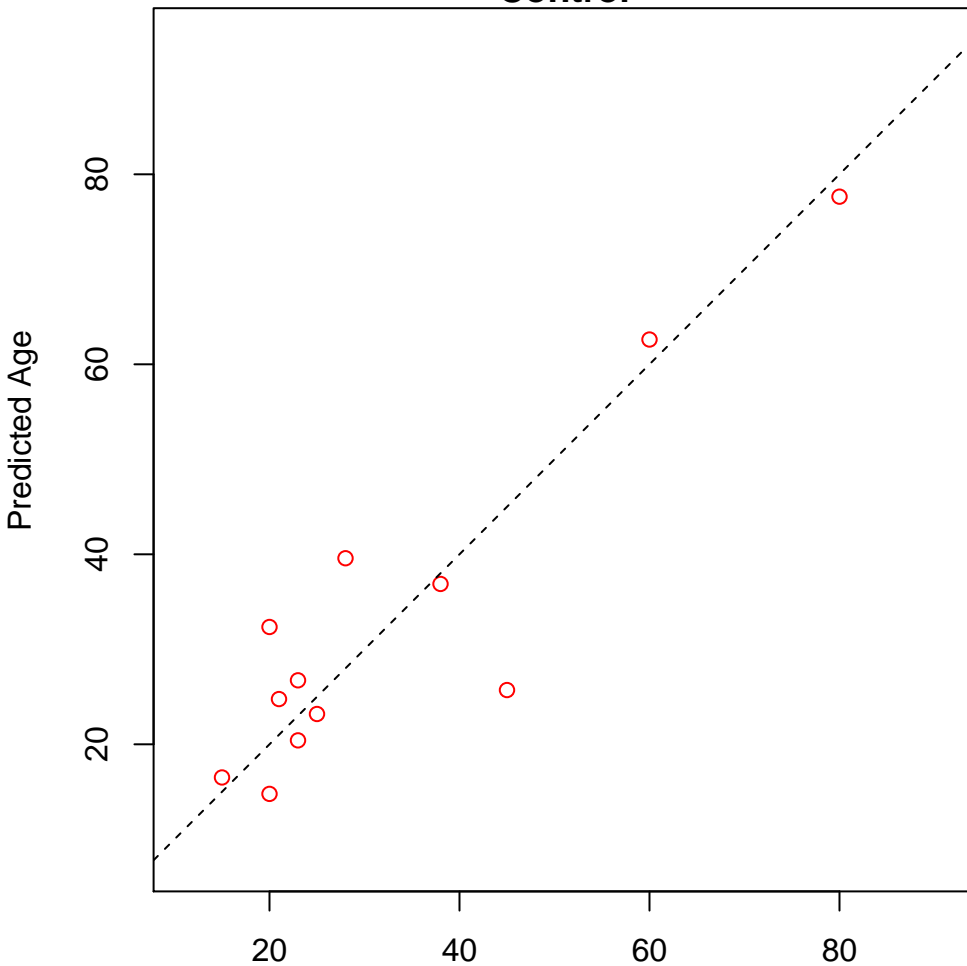


organ morphogenesis (Score: 18.889818)

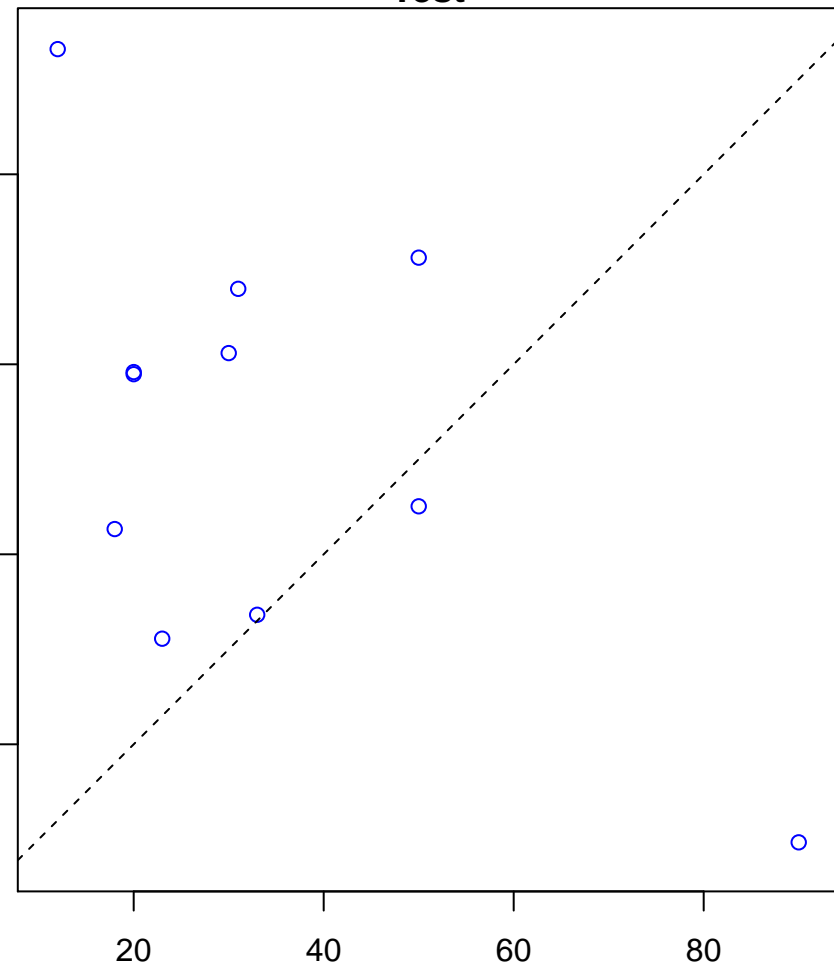


progesterone metabolic process (Score: 18.888295)

Control

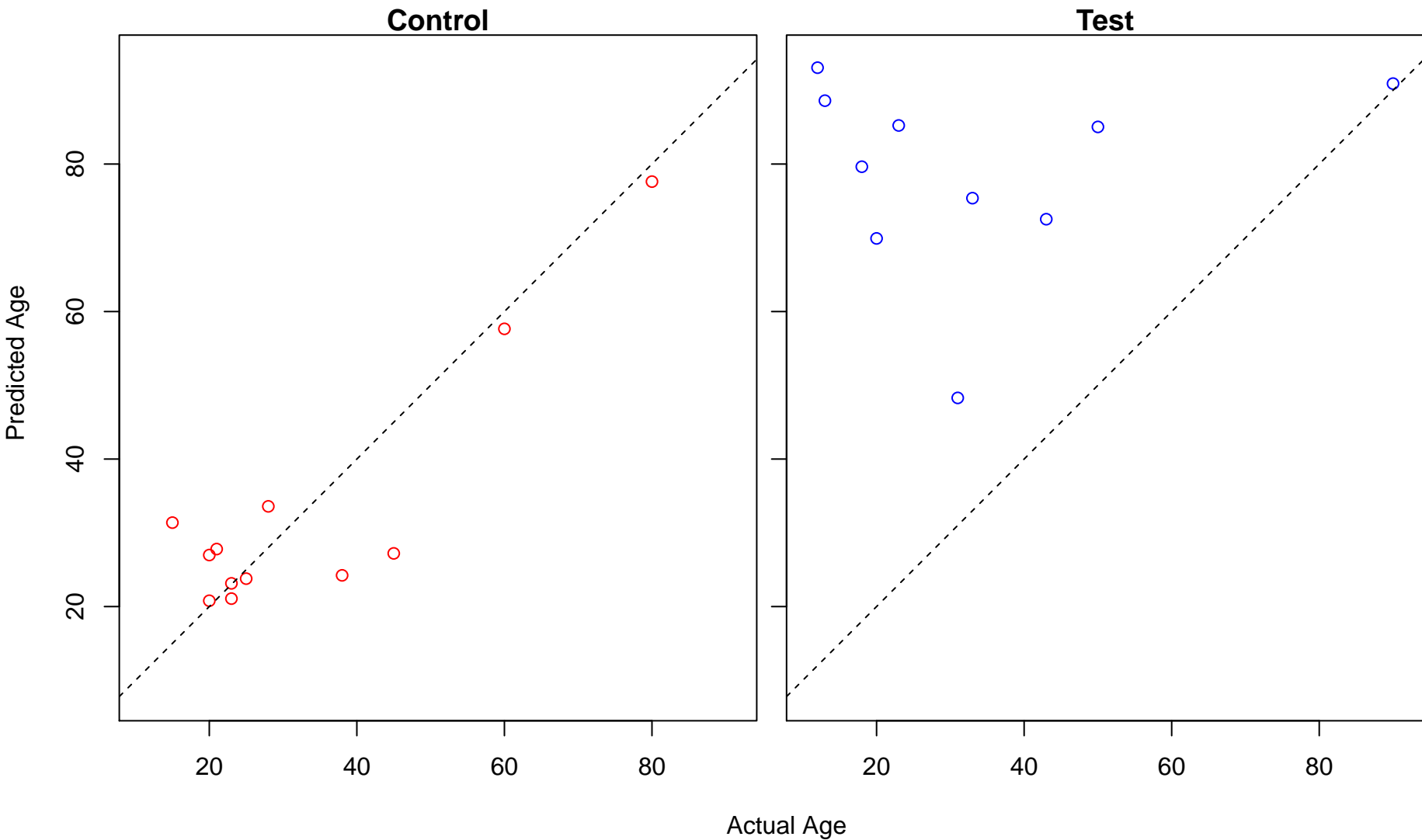


Test



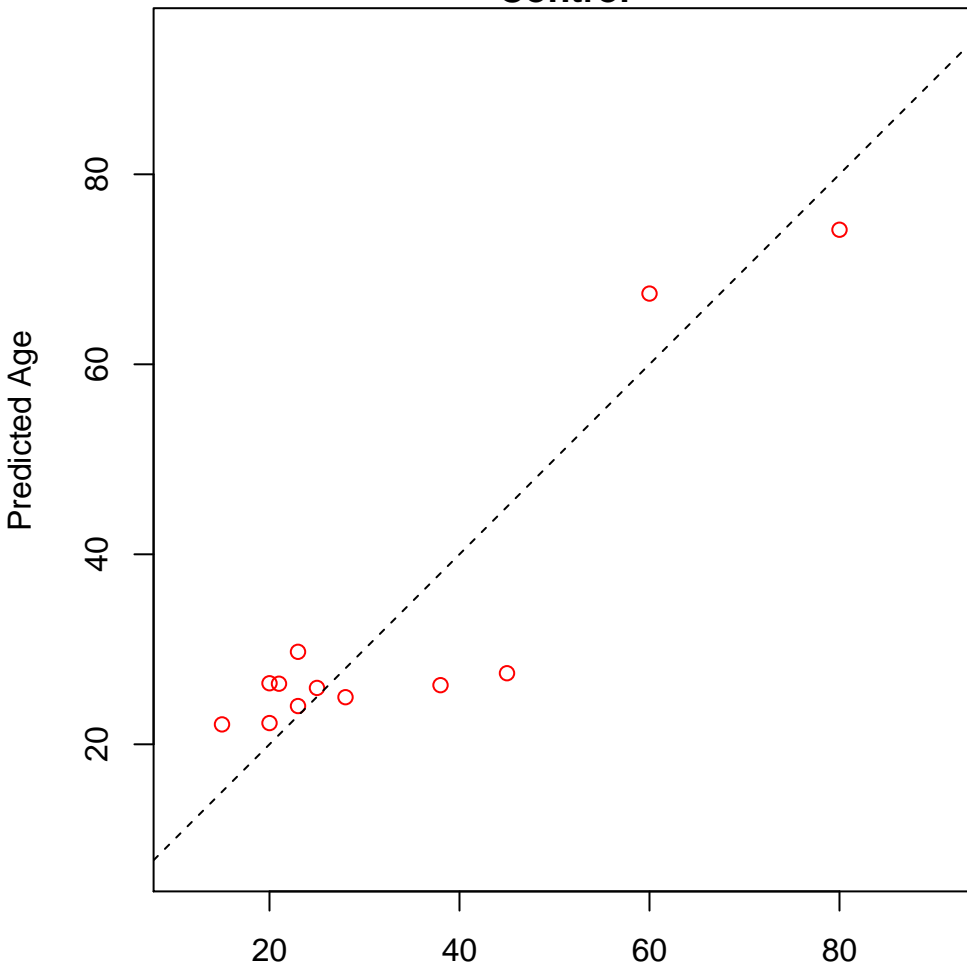
Actual Age

negative regulation of chemokine production (Score: 18.838064)

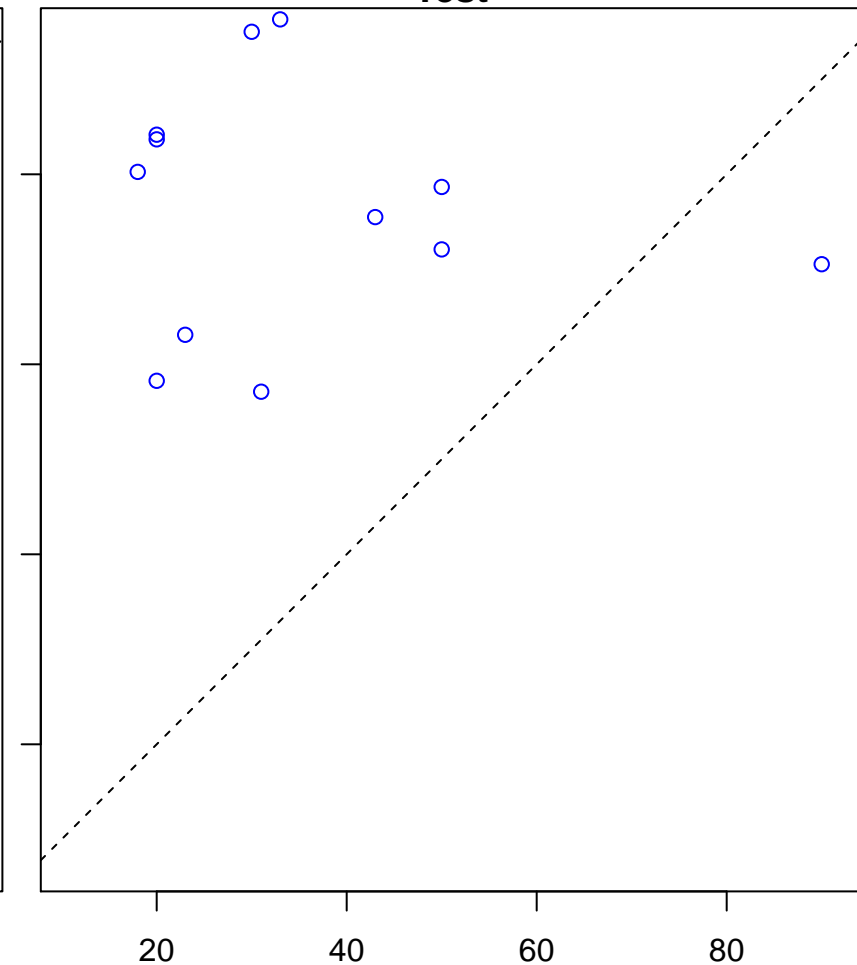


atrioventricular canal development (Score: 18.837767)

Control

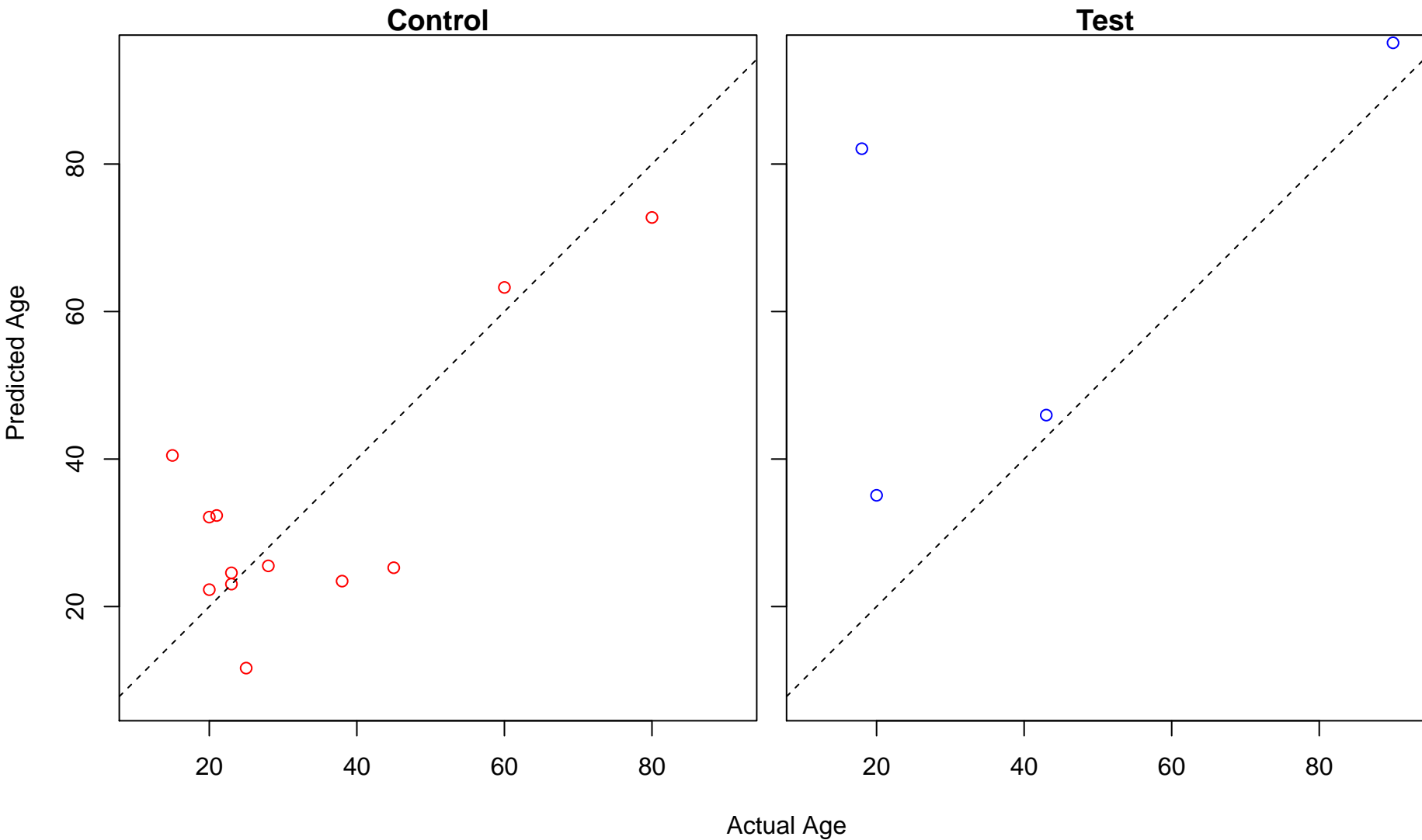


Test

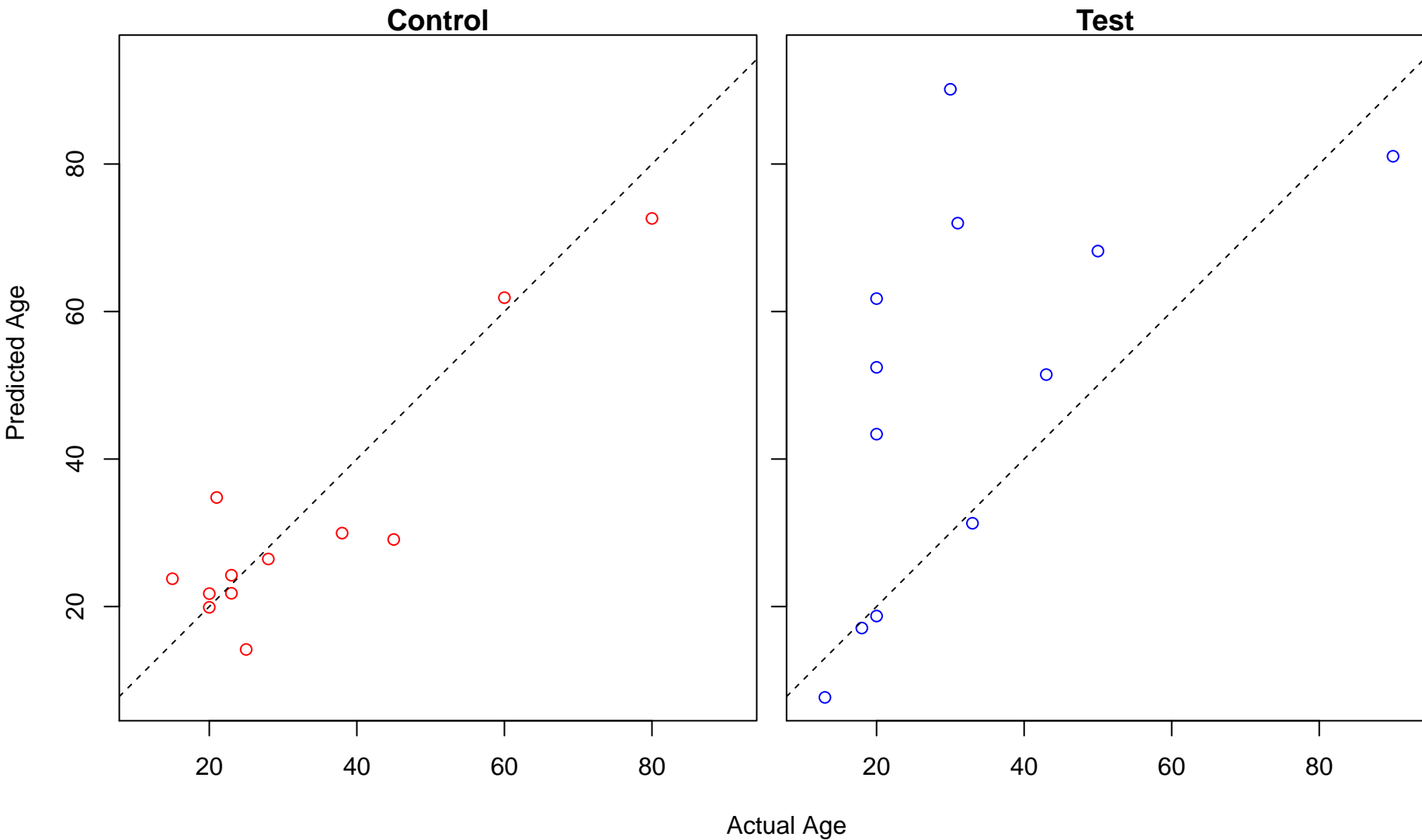


Actual Age

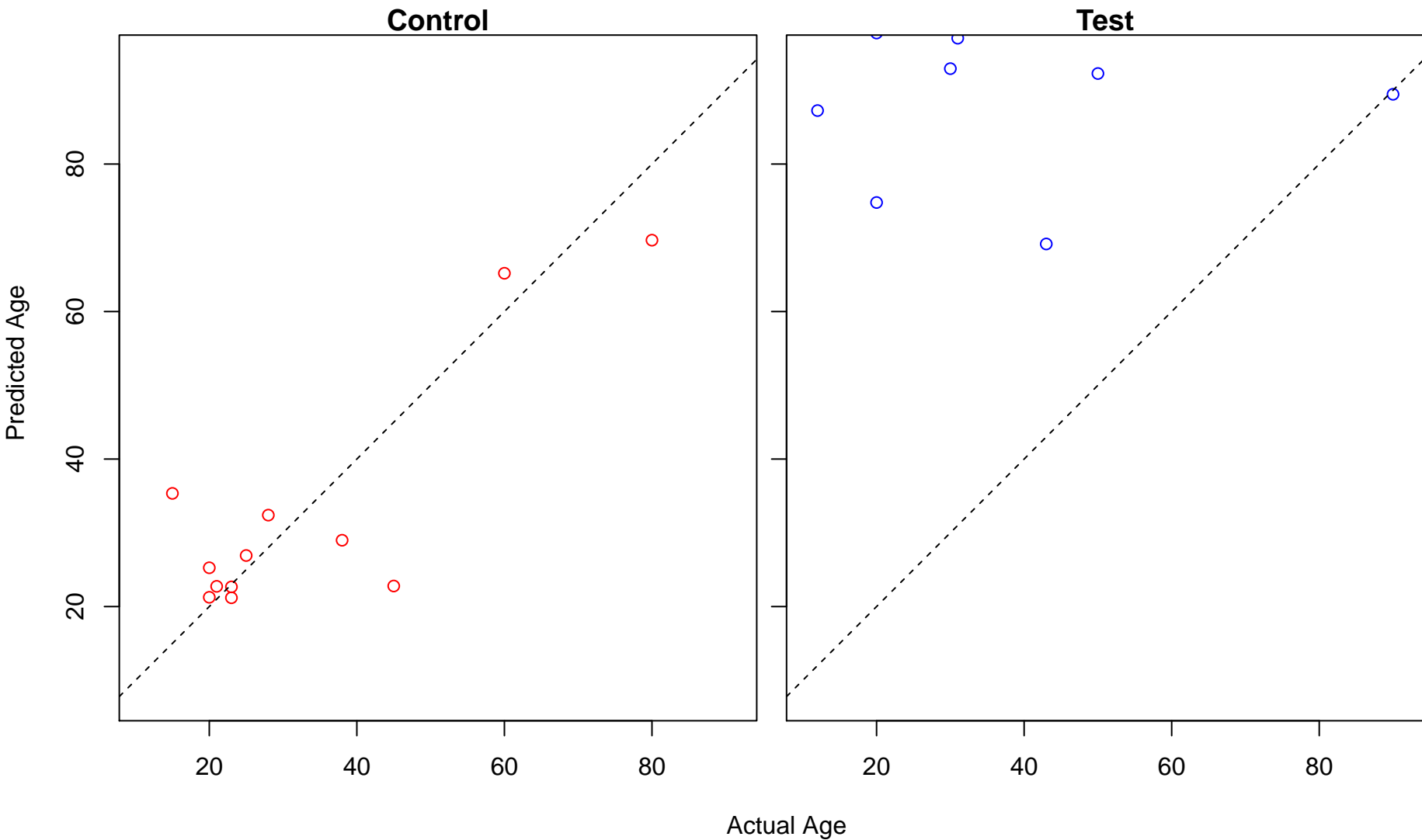
membrane depolarization (Score: 18.828641)



positive regulation of regulated secretory pathway (Score: 18.781717)

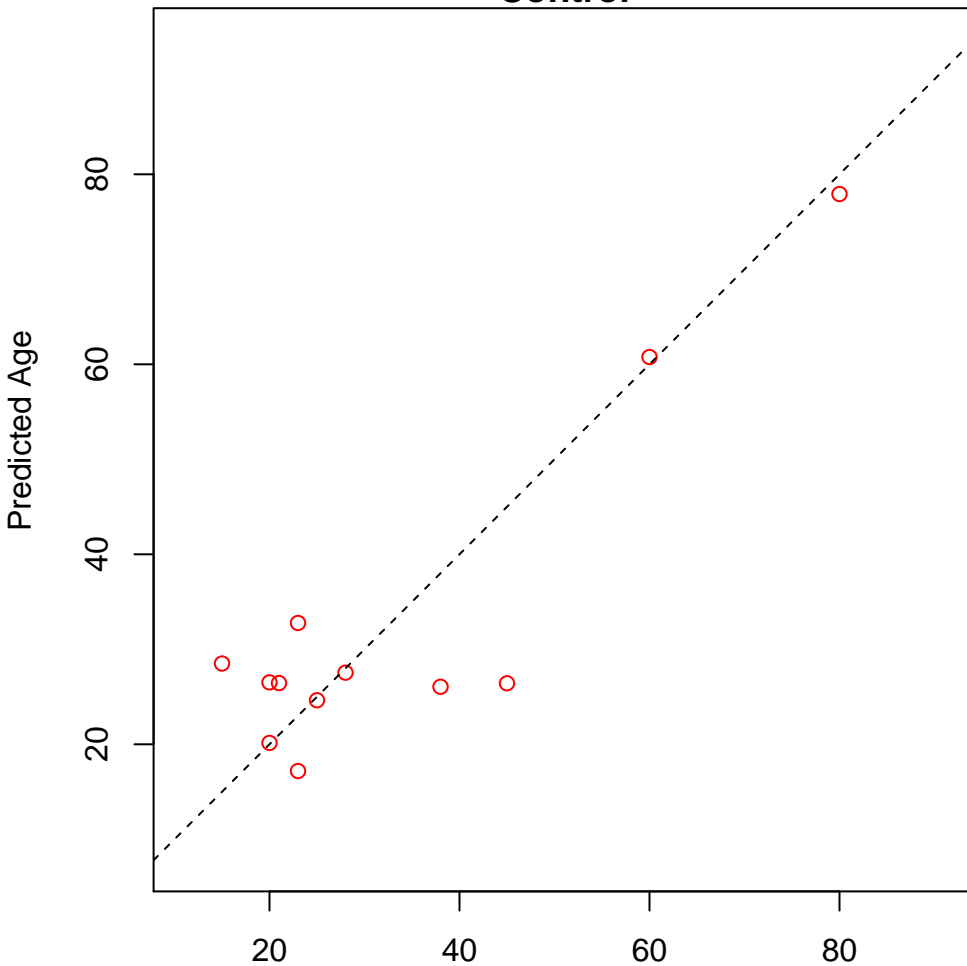


chromatin-mediated maintenance of transcription (Score: 18.729907)

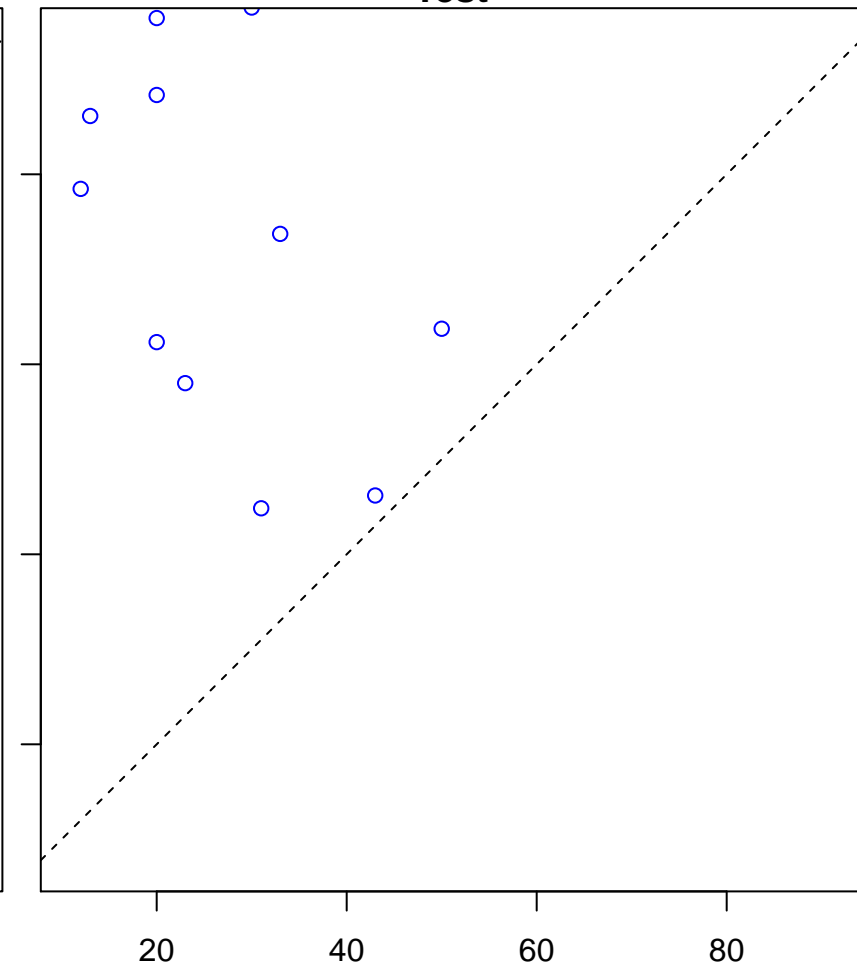


transformed cell apoptotic process (Score: 18.726142)

Control

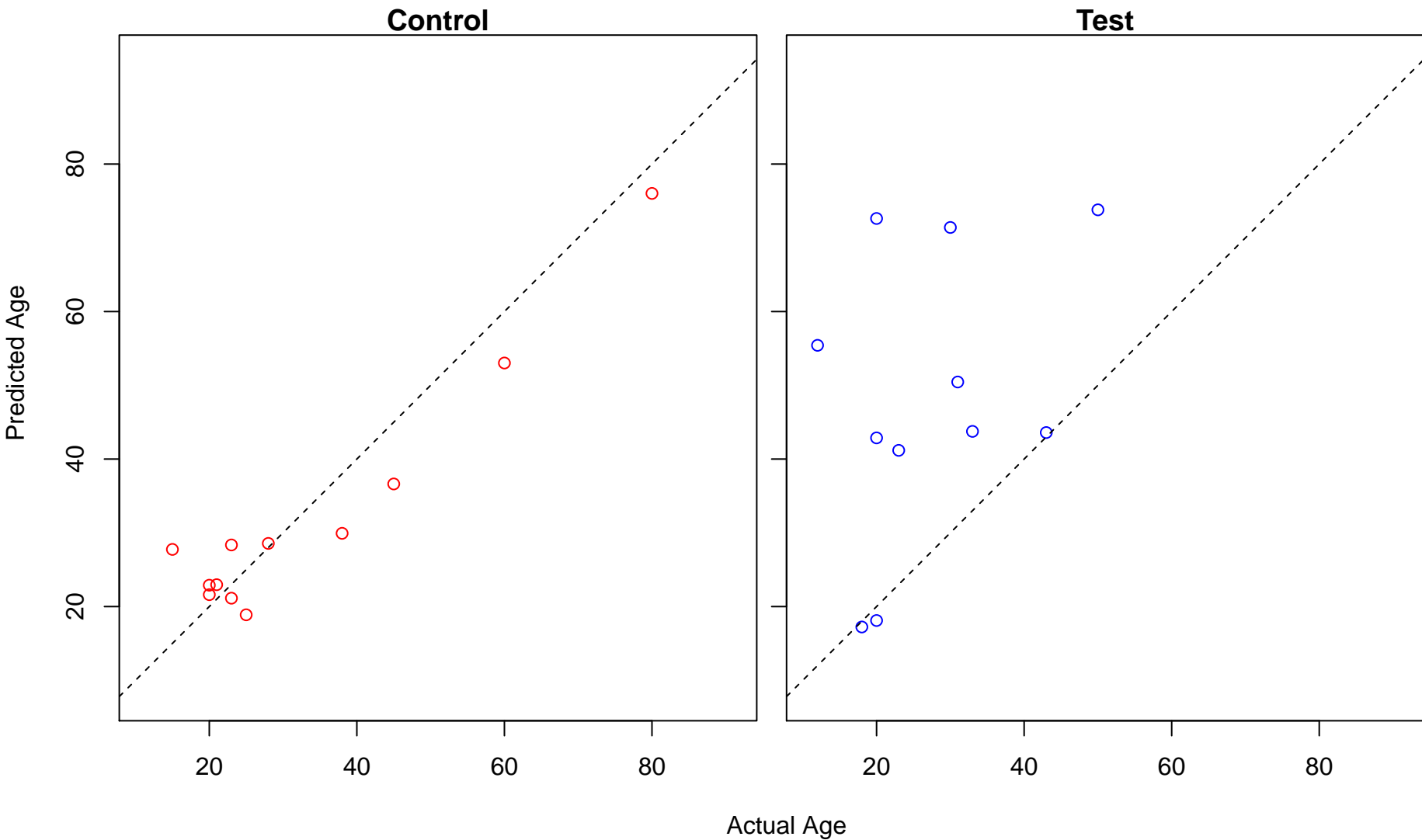


Test

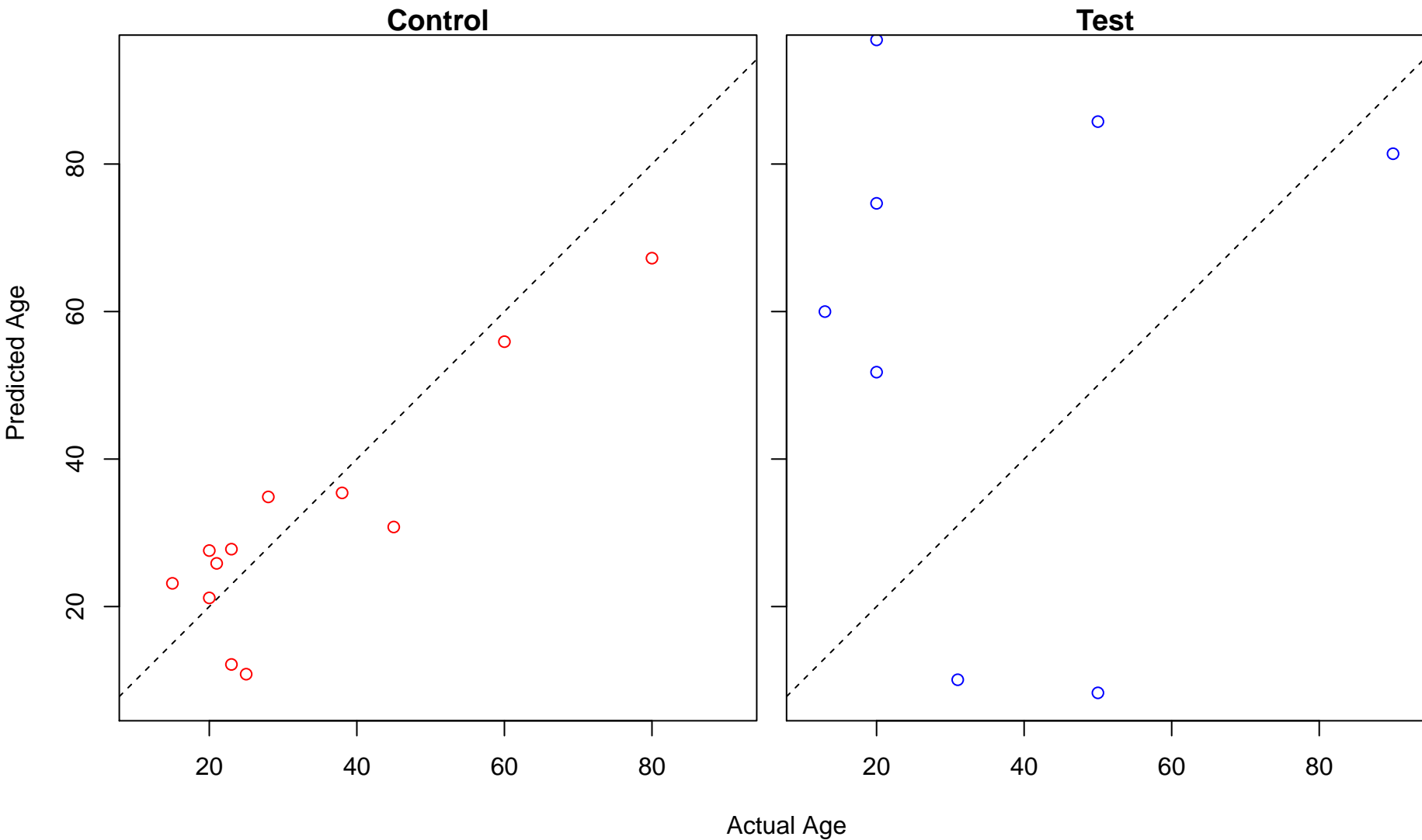


Actual Age

DNA geometric change (Score: 18.717495)

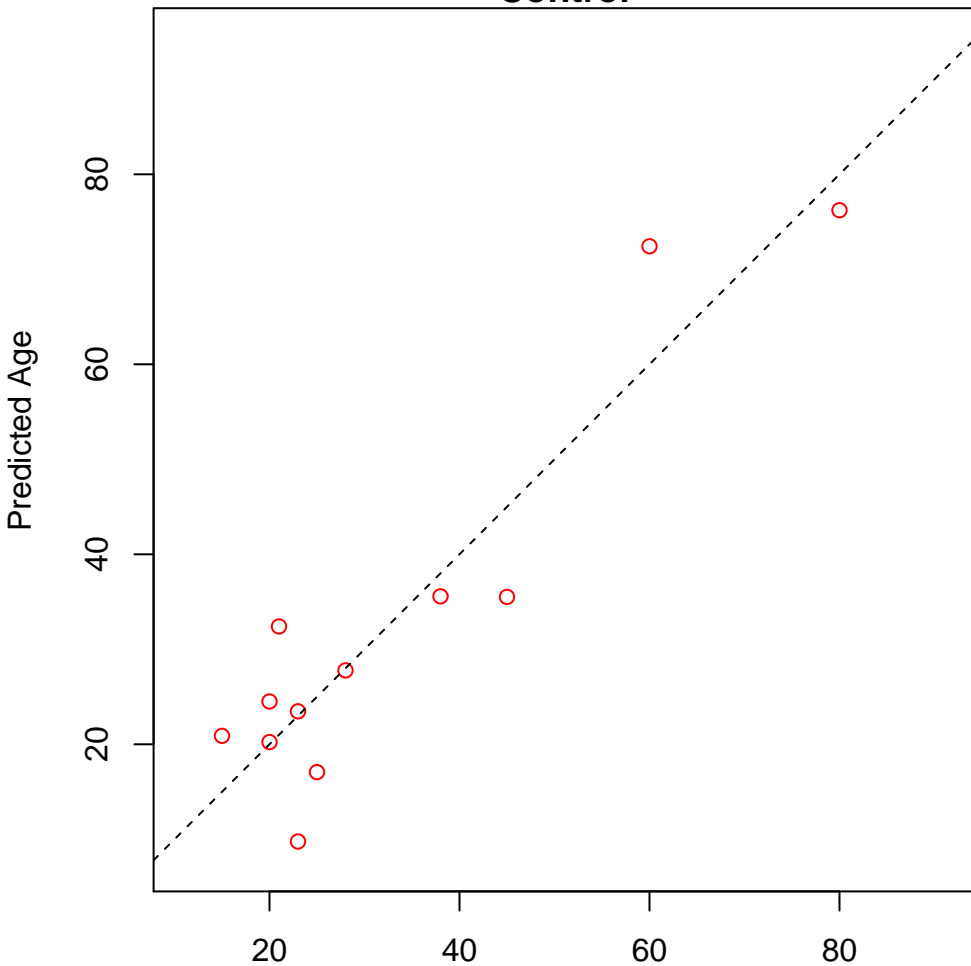


regulation of nuclear cell cycle DNA replication (Score: 18.714093)

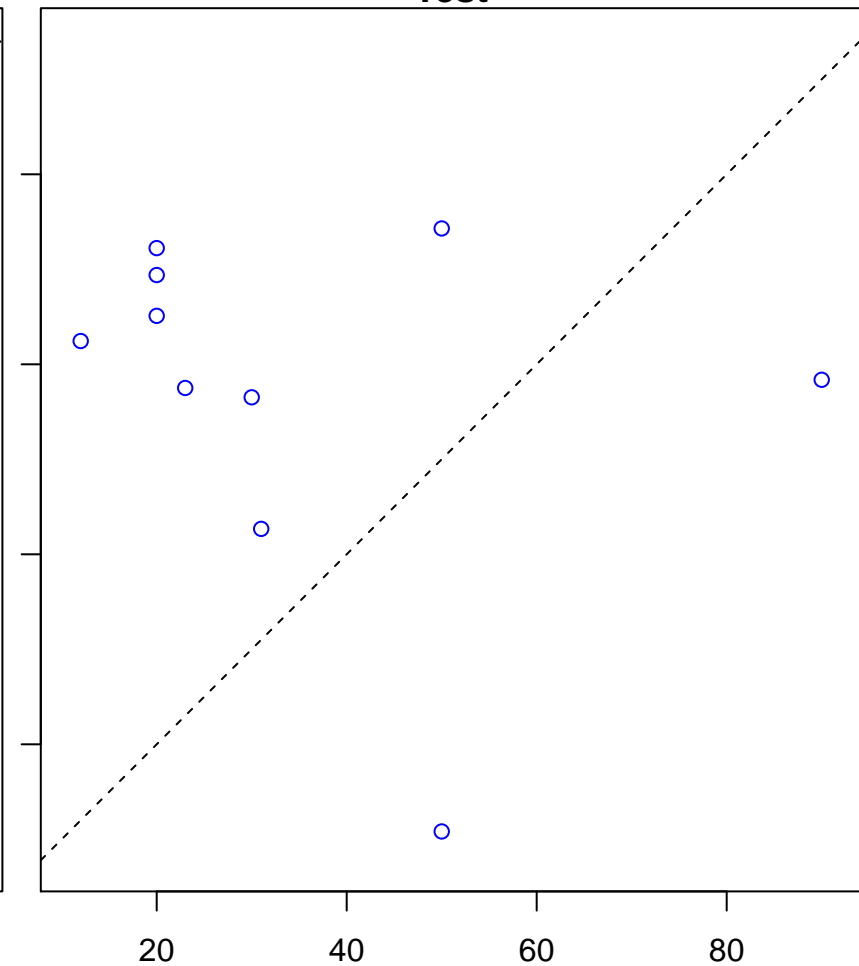


mitochondrial genome maintenance (Score: 18.709157)

Control



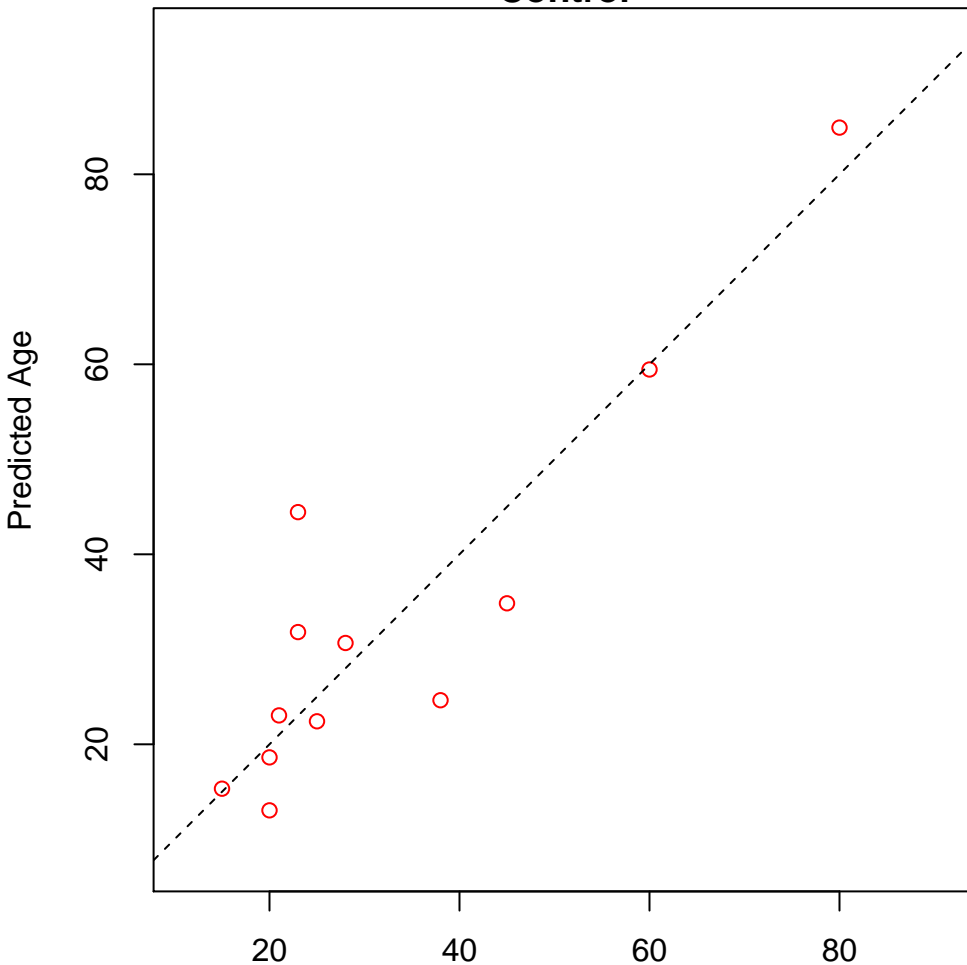
Test



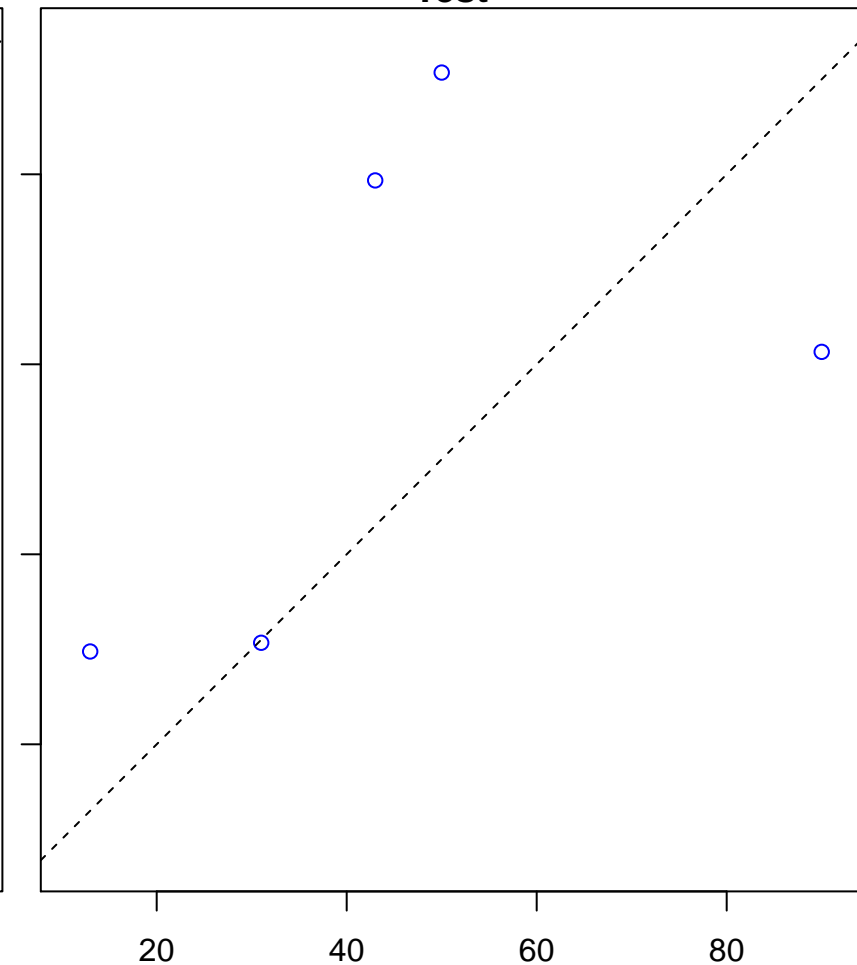
Actual Age

protein localization to endosome (Score: 18.647387)

Control

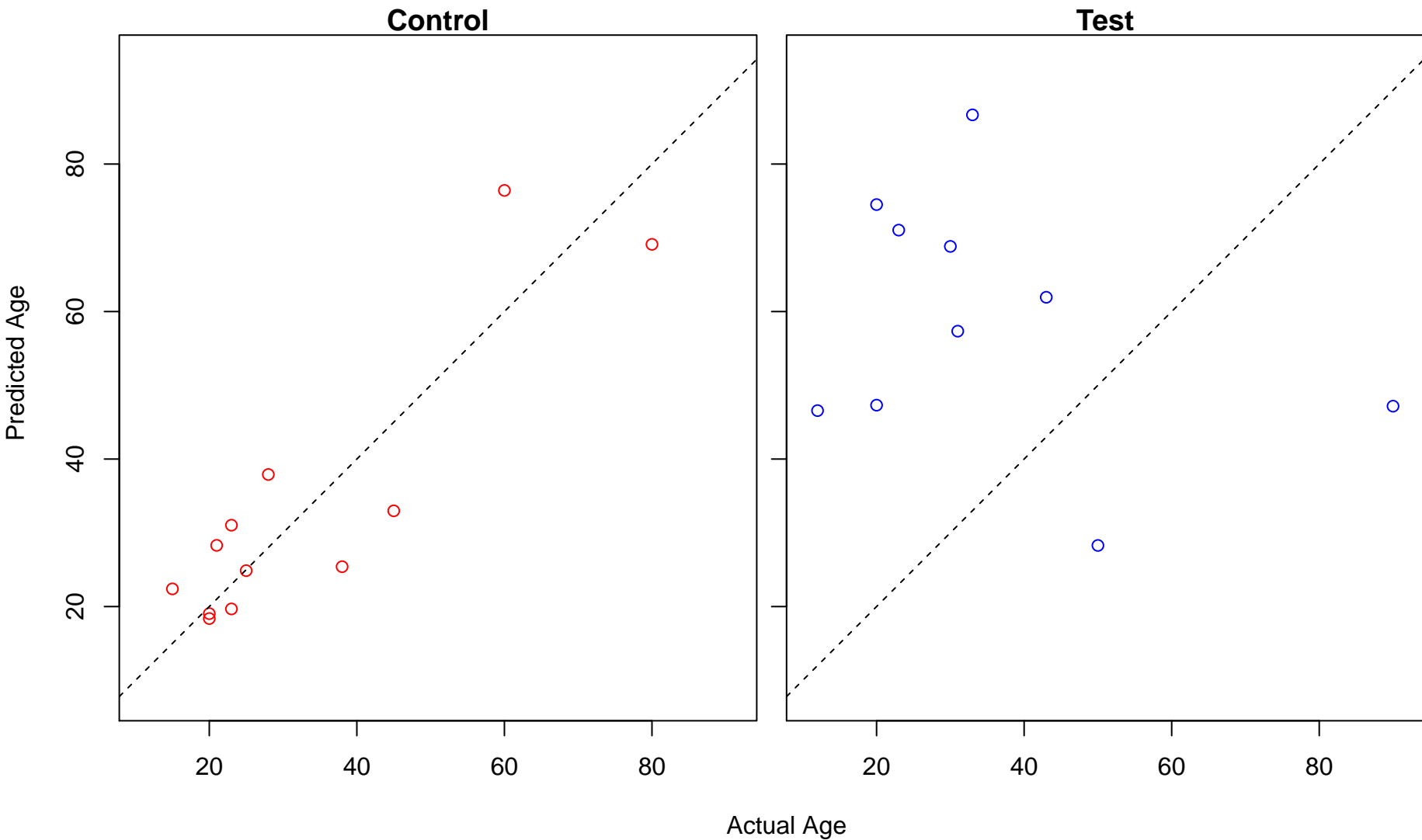


Test



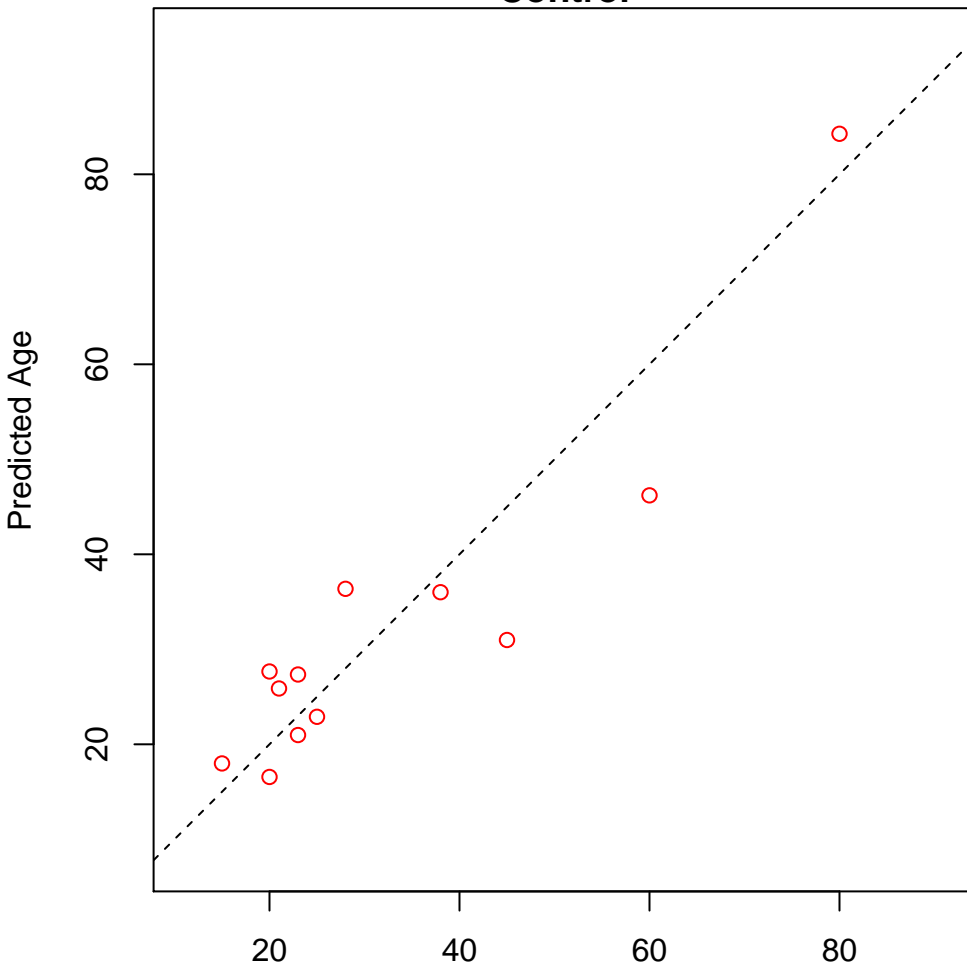
Actual Age

alpha-beta T cell differentiation (Score: 18.633813)

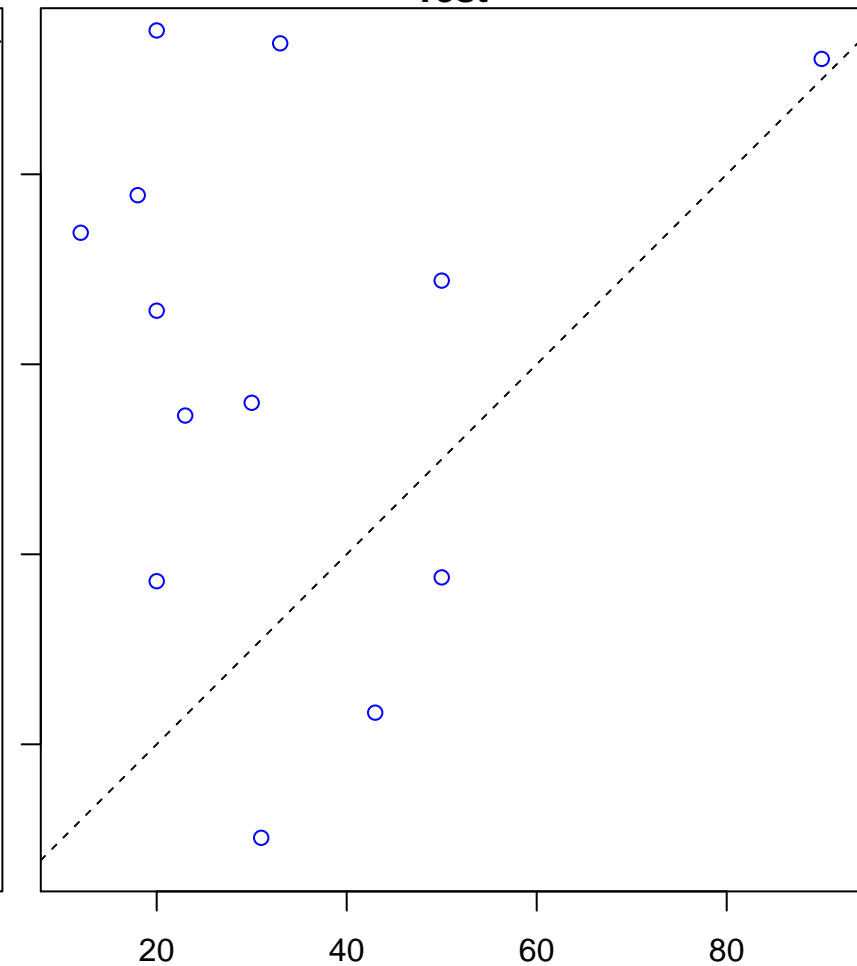


mitotic cell cycle phase transition (Score: 18.631156)

Control

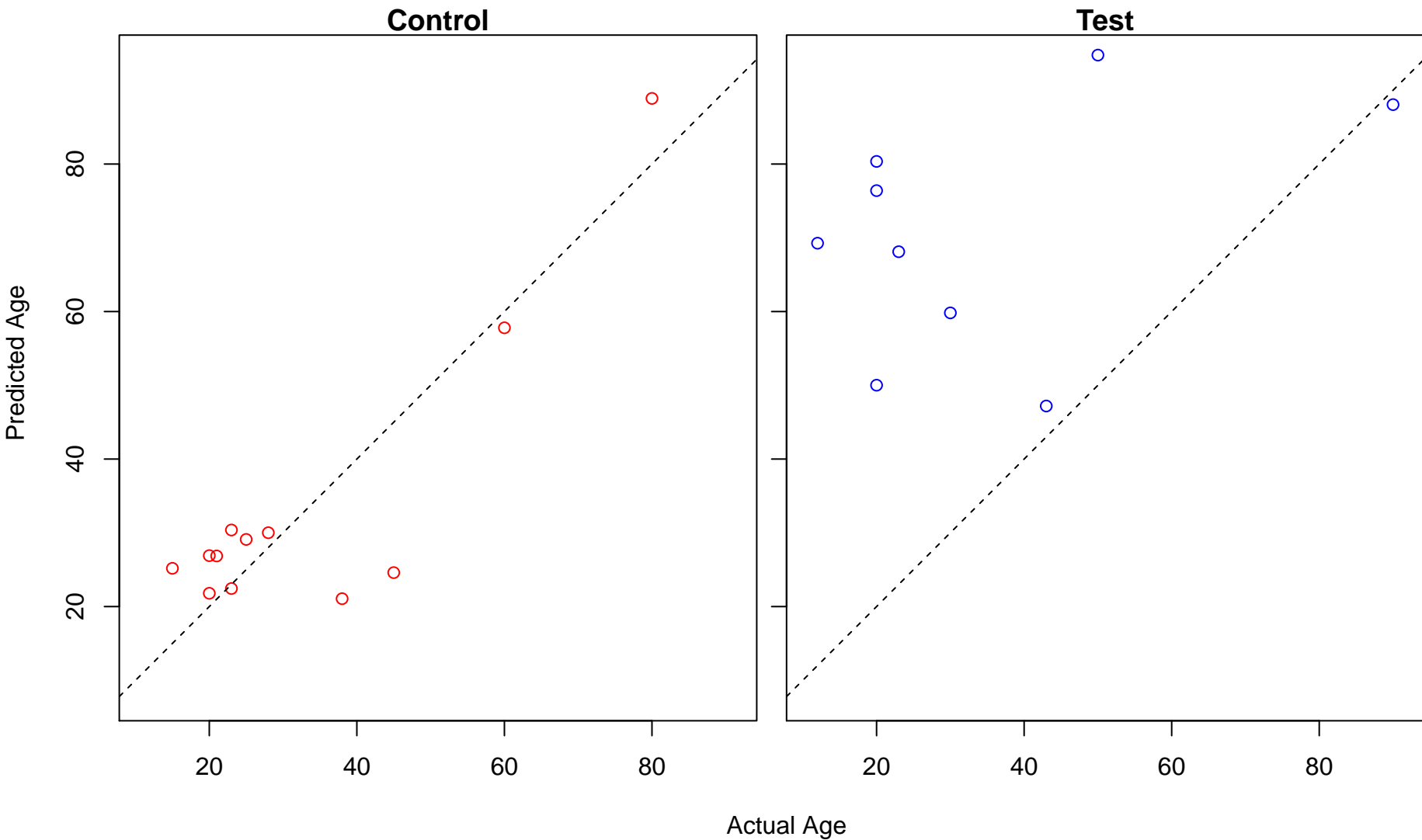


Test

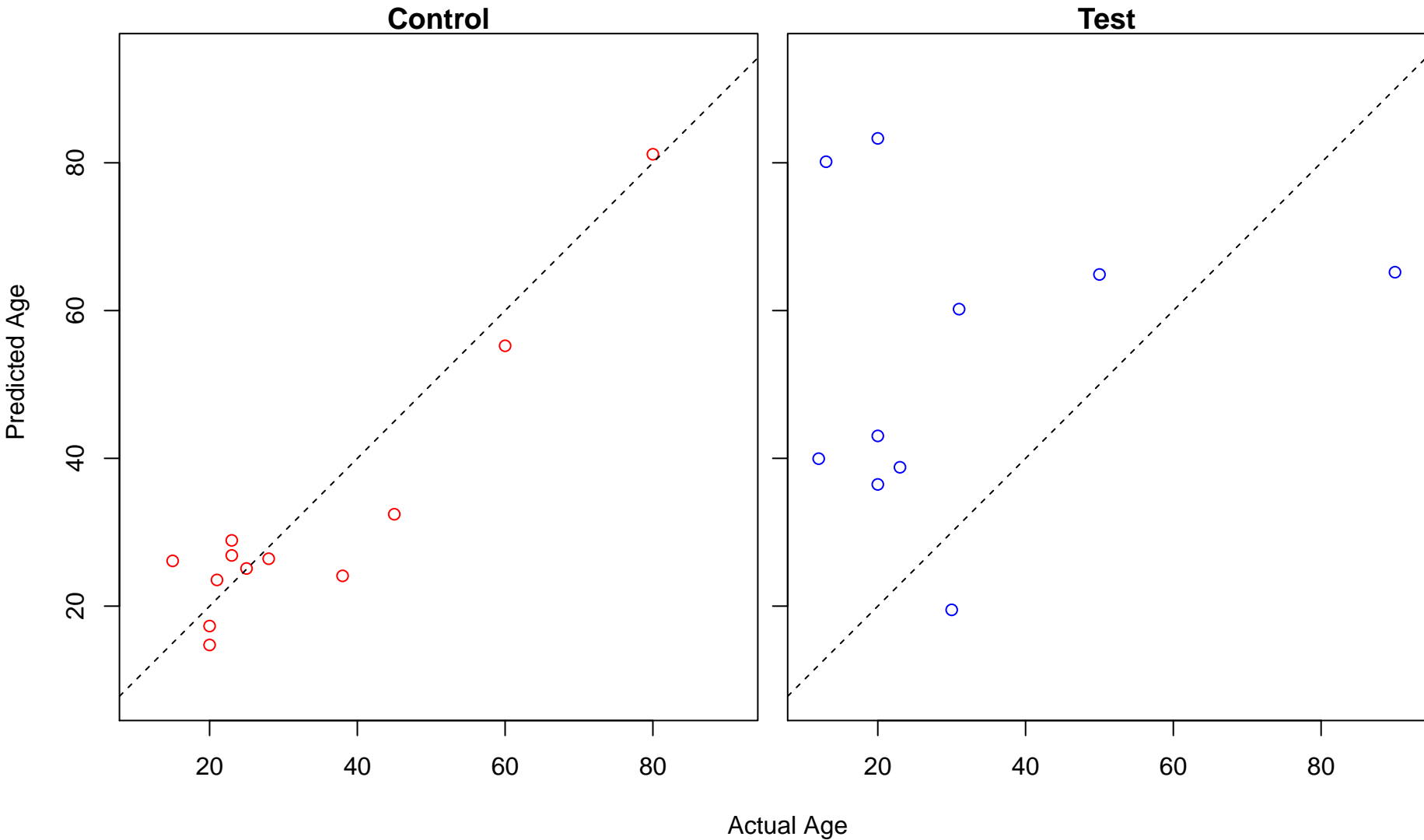


Actual Age

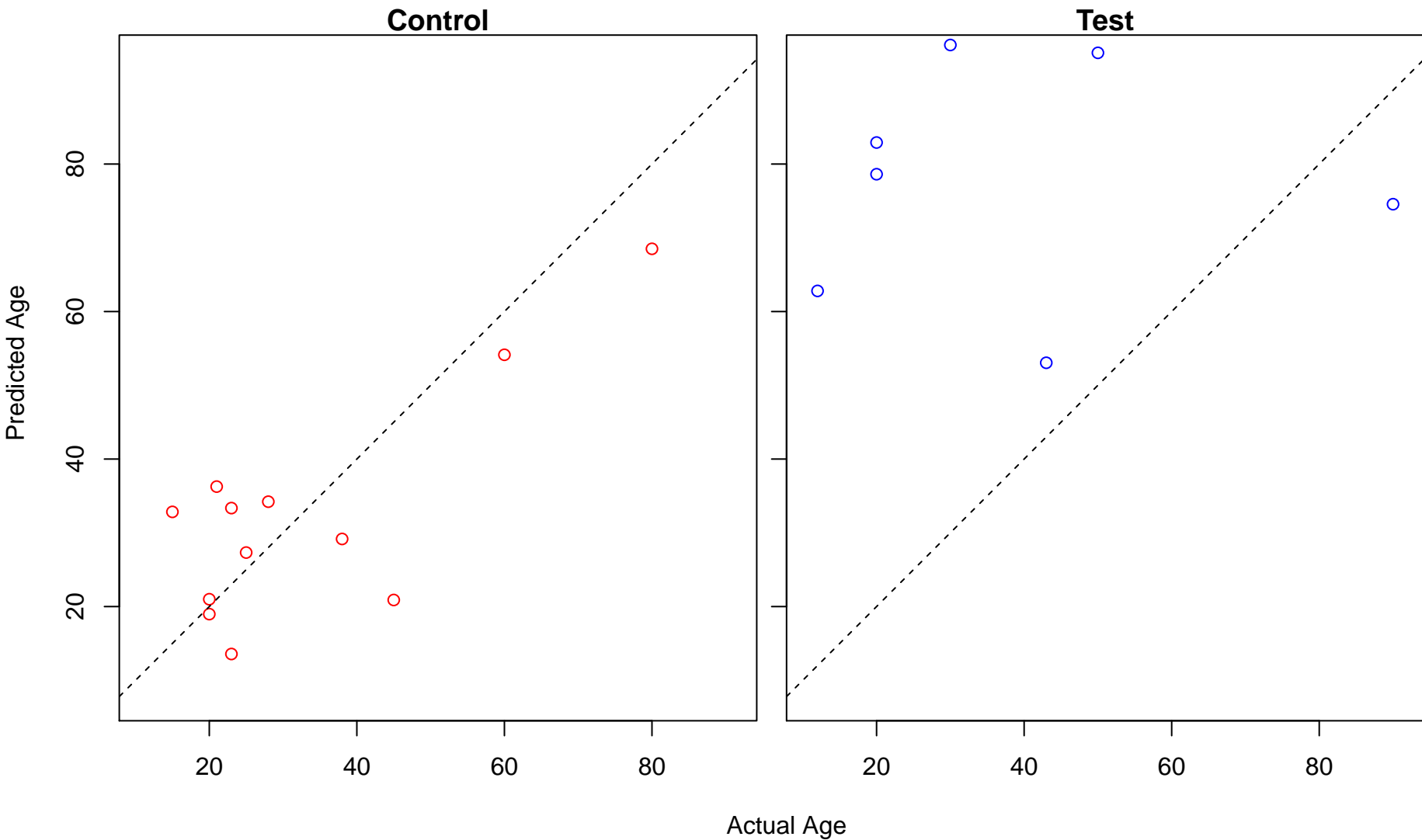
histone ubiquitination (Score: 18.620945)



developmental growth involved in morphogenesis (Score: 18.600781)

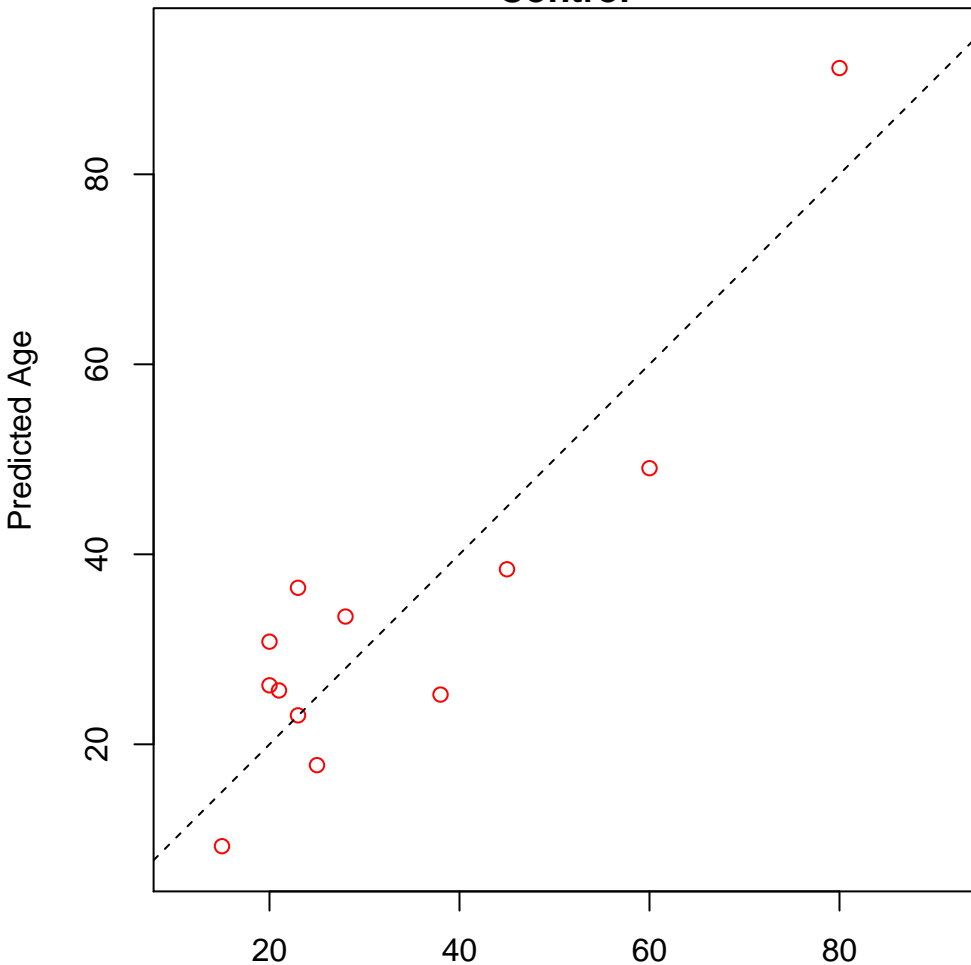


positive regulation of cholesterol storage (Score: 18.587559)

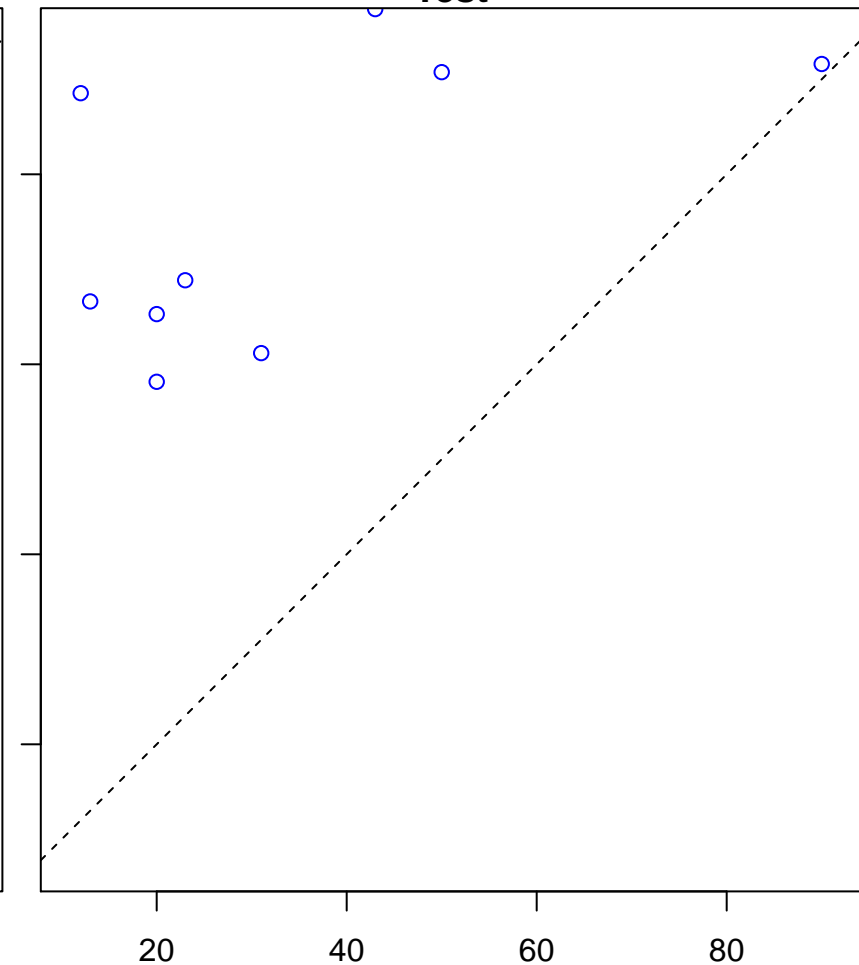


renal system vasculature development (Score: 18.567234)

Control

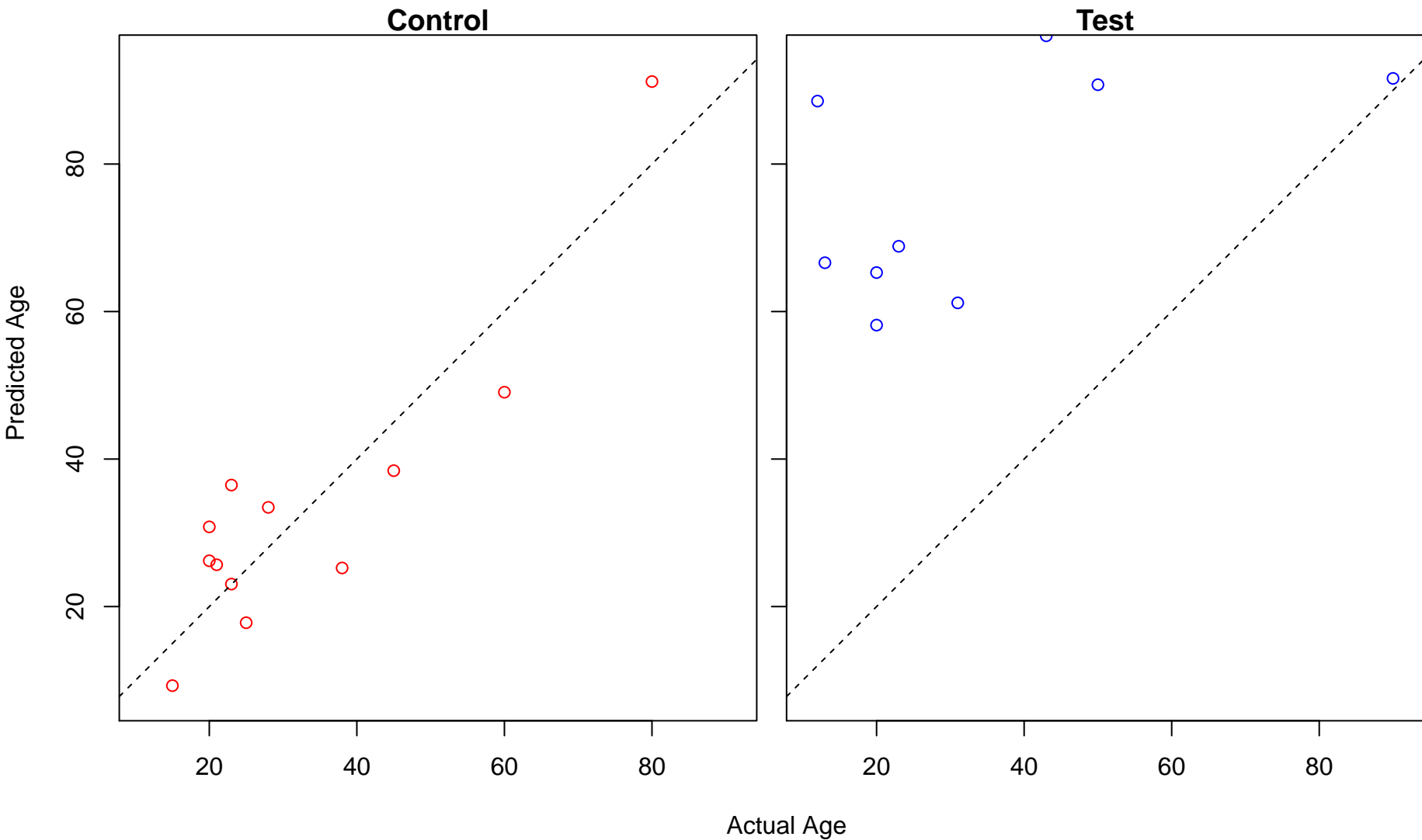


Test

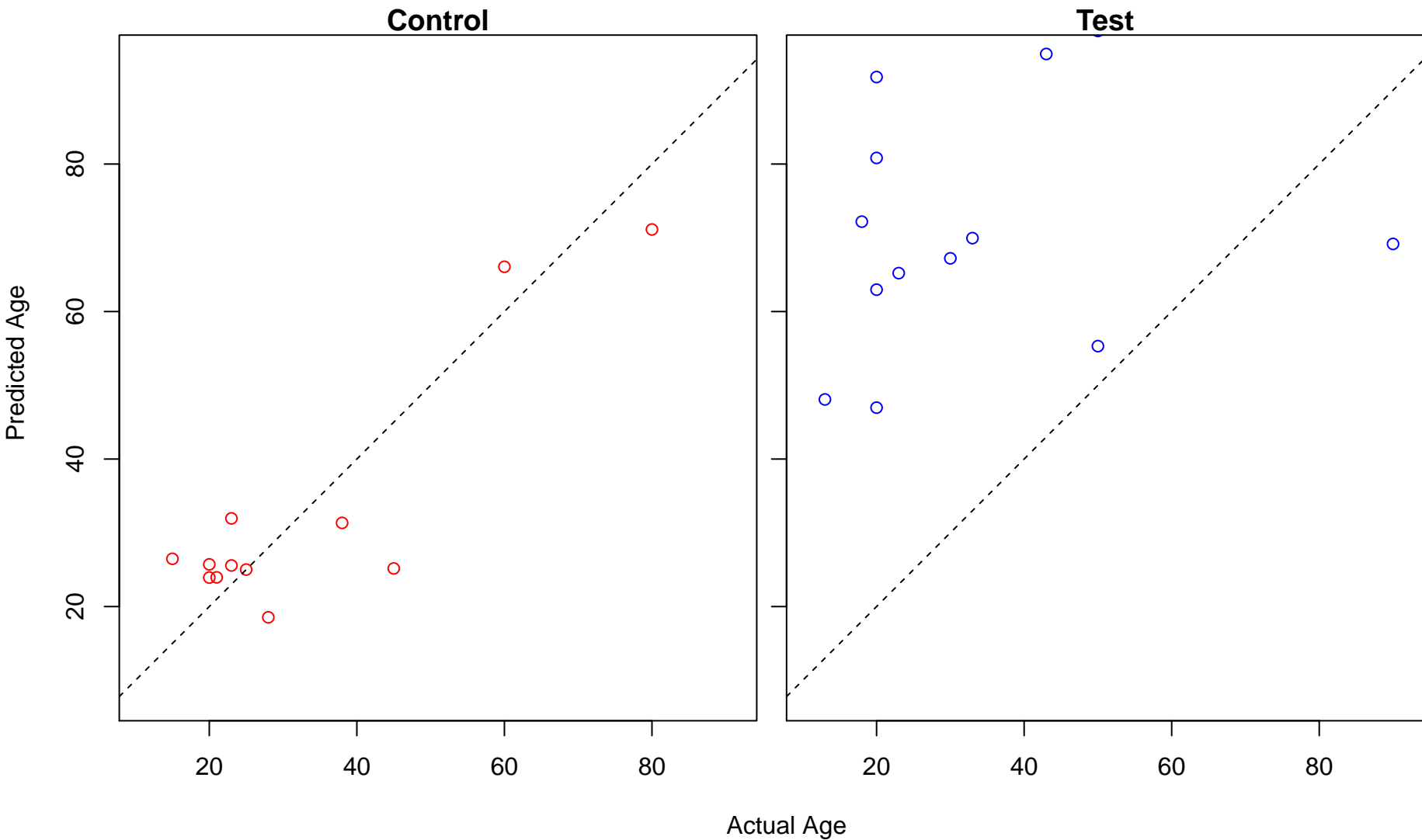


Actual Age

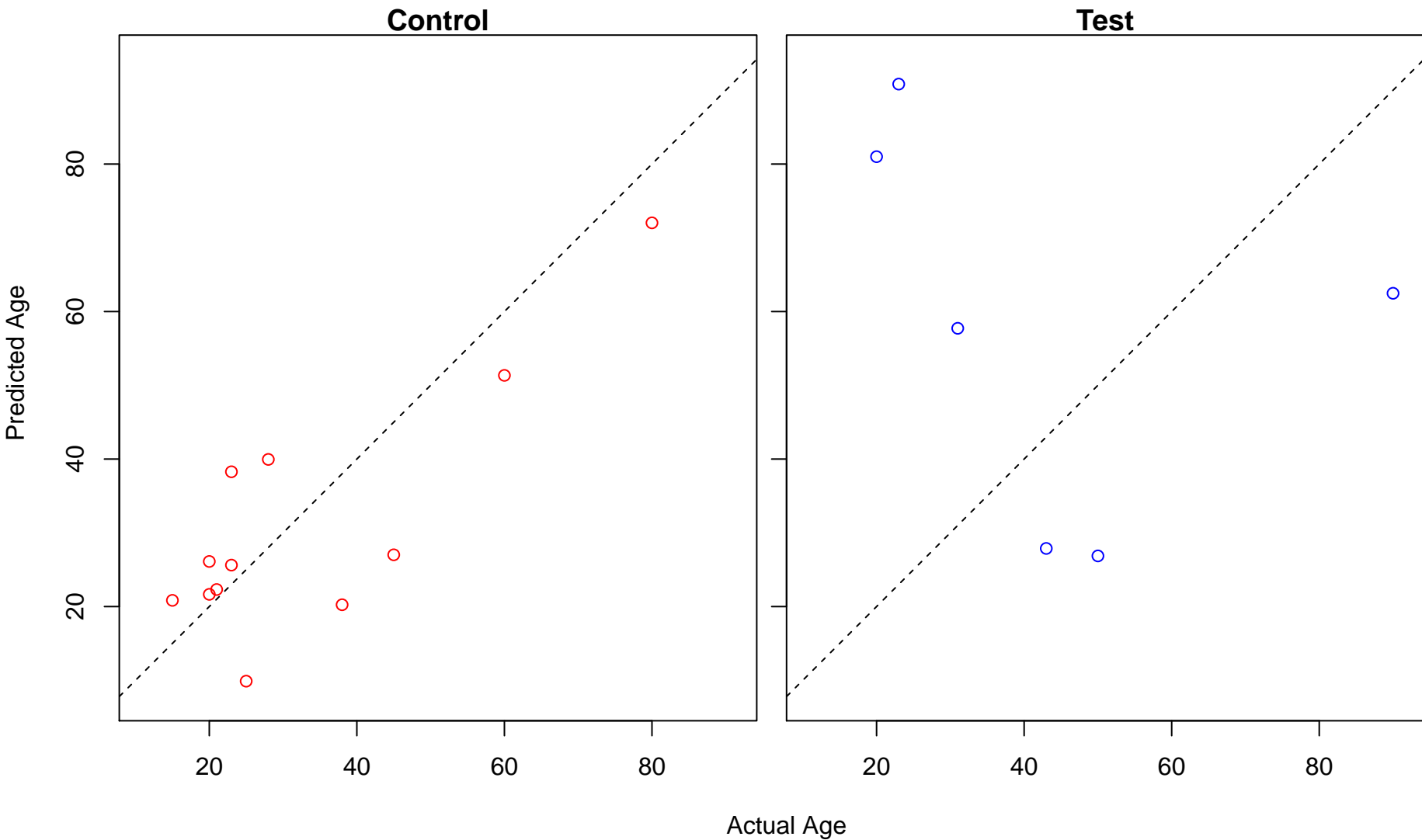
kidney vasculature development (Score: 18.567234)



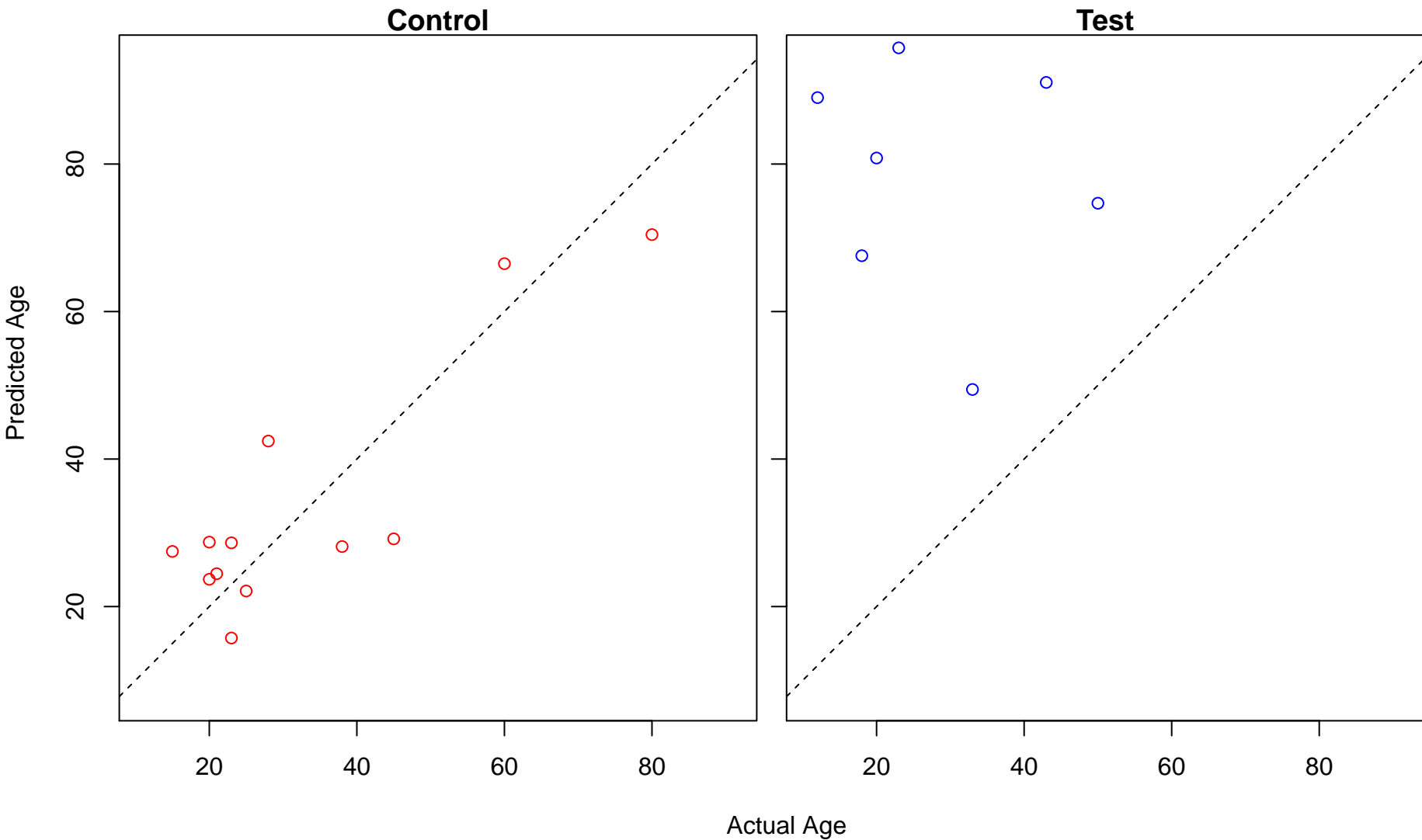
polysaccharide digestion (Score: 18.526013)



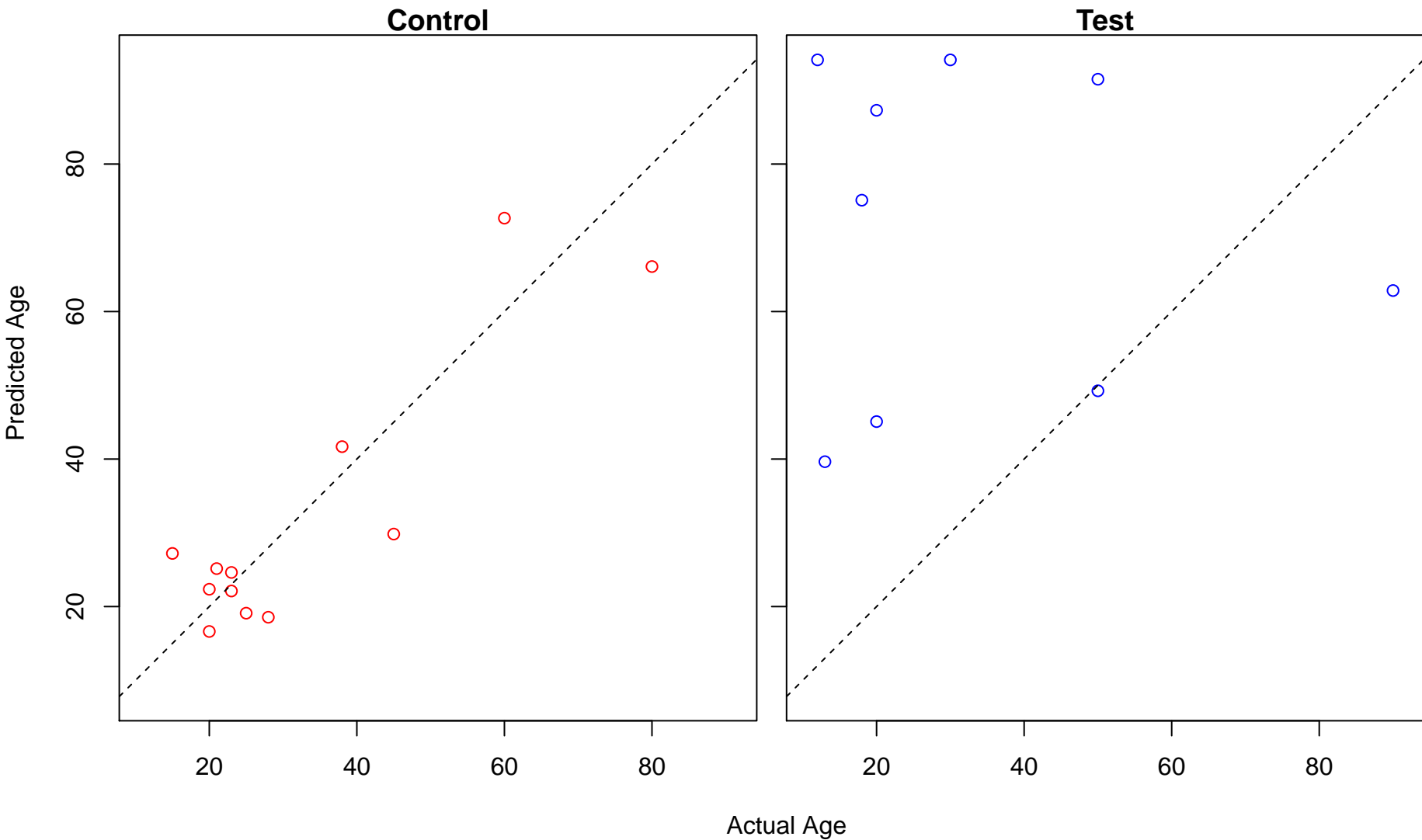
glutamate receptor signaling pathway (Score: 18.494239)



negative regulation of BMP signaling pathway (Score: 18.414064)

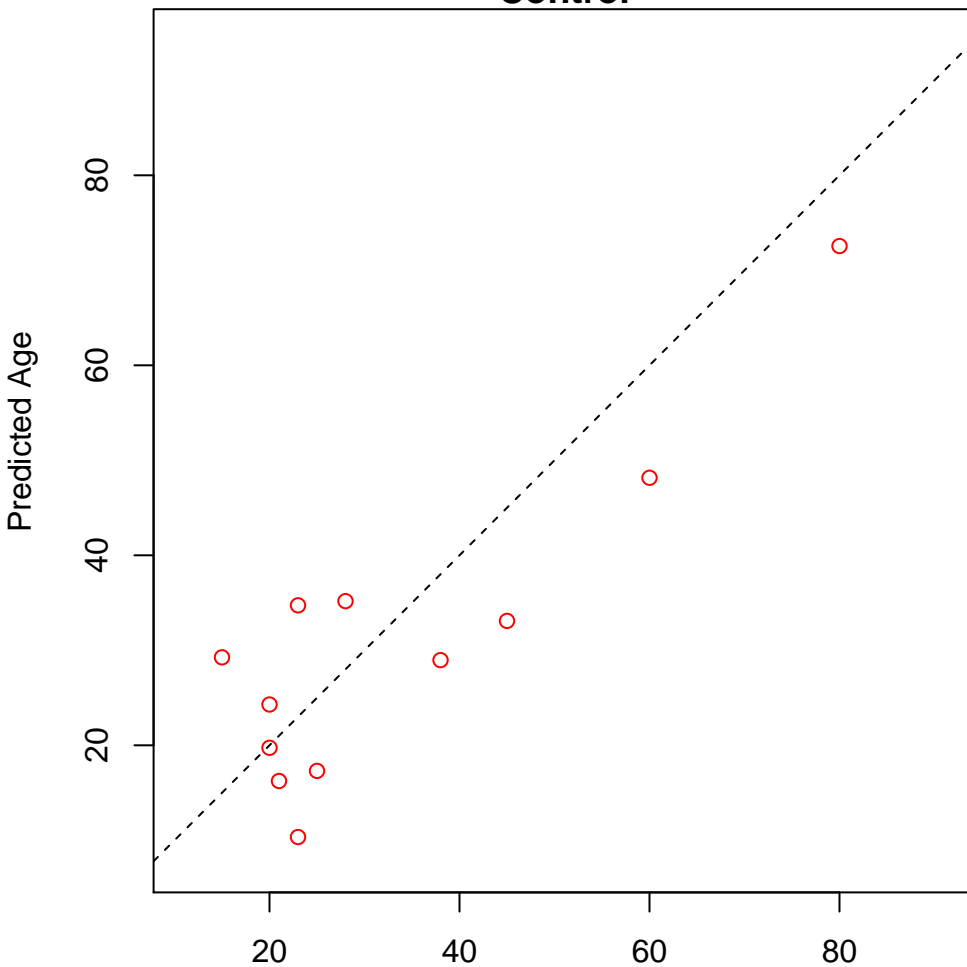


microtubule bundle formation (Score: 18.367377)

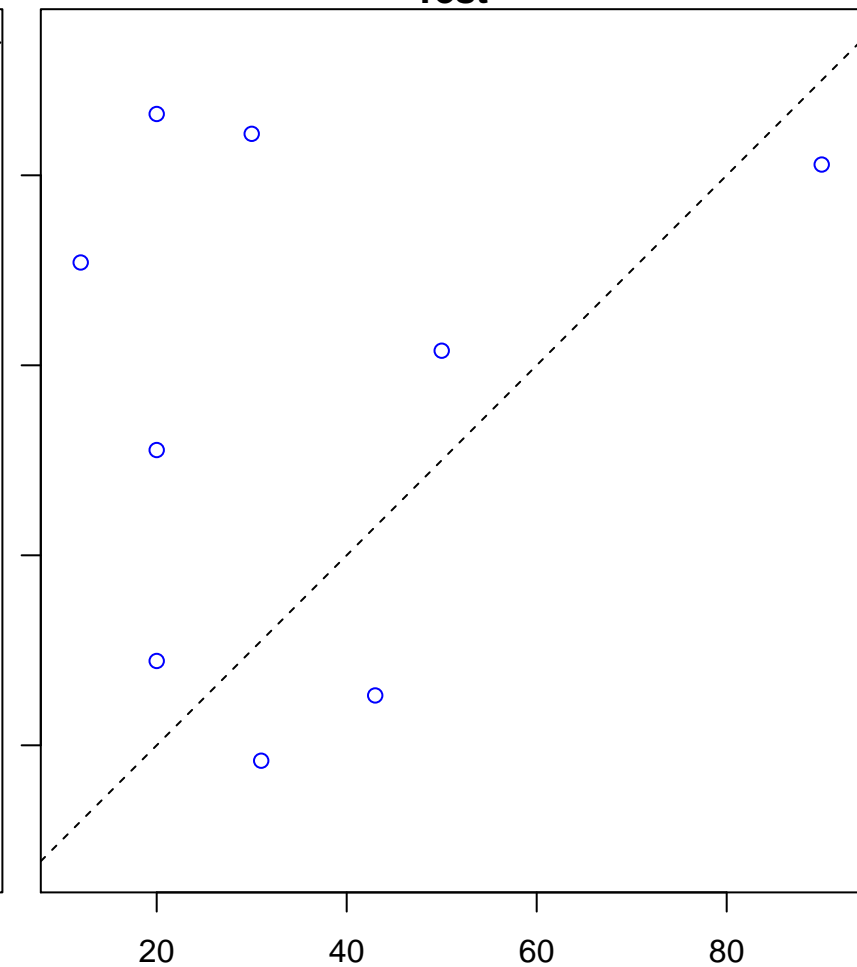


base-excision repair, AP site formation (Score: 18.235020)

Control

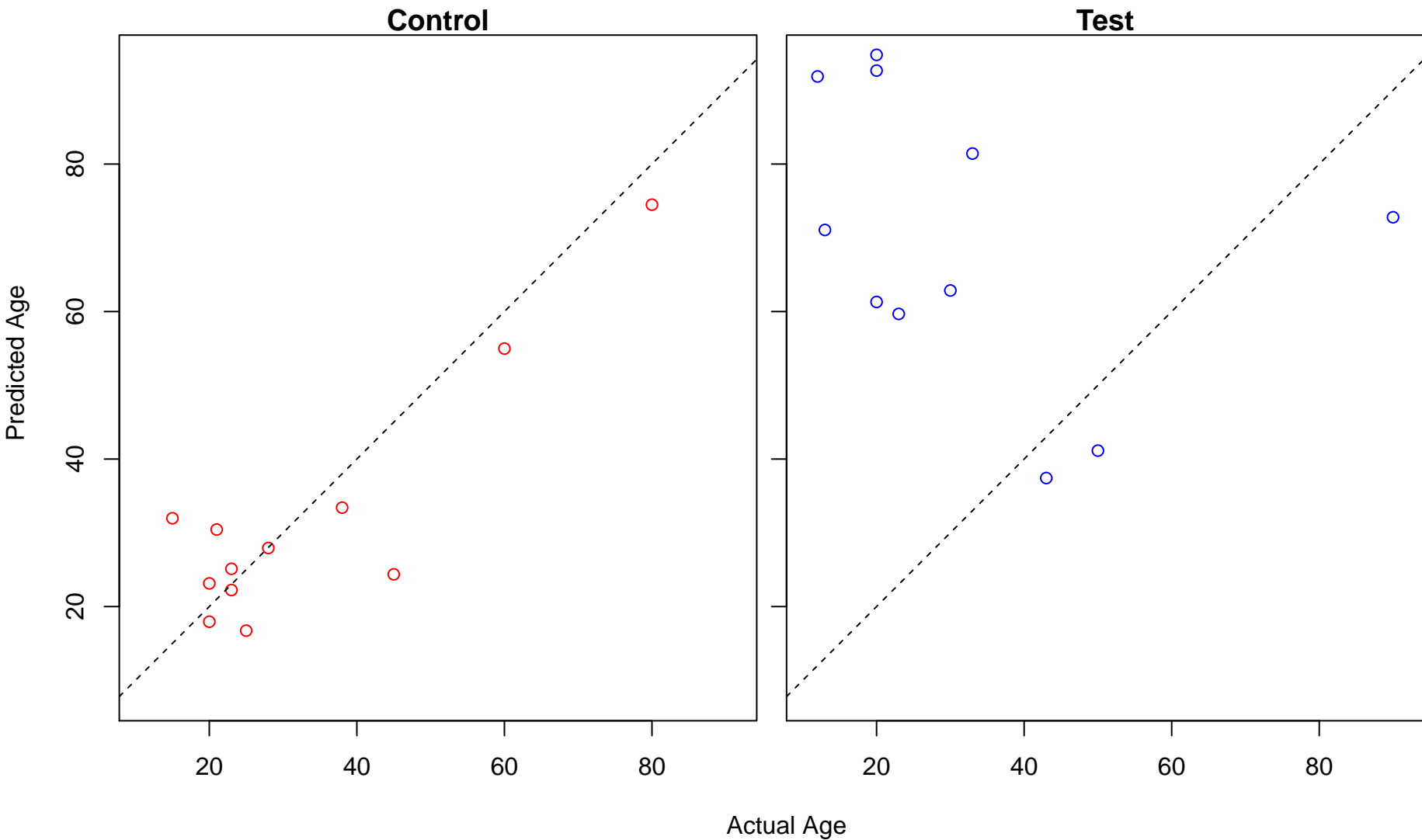


Test

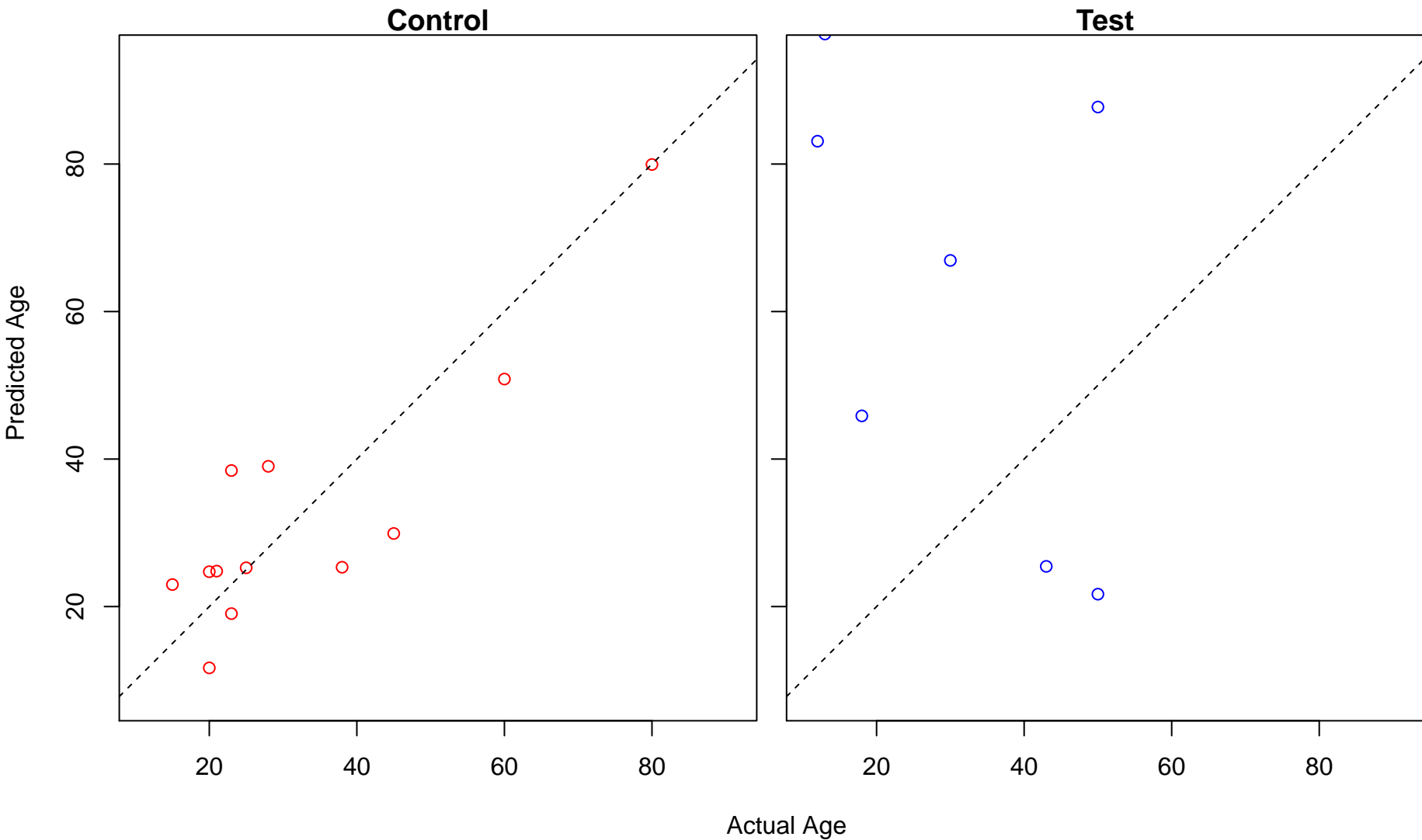


Actual Age

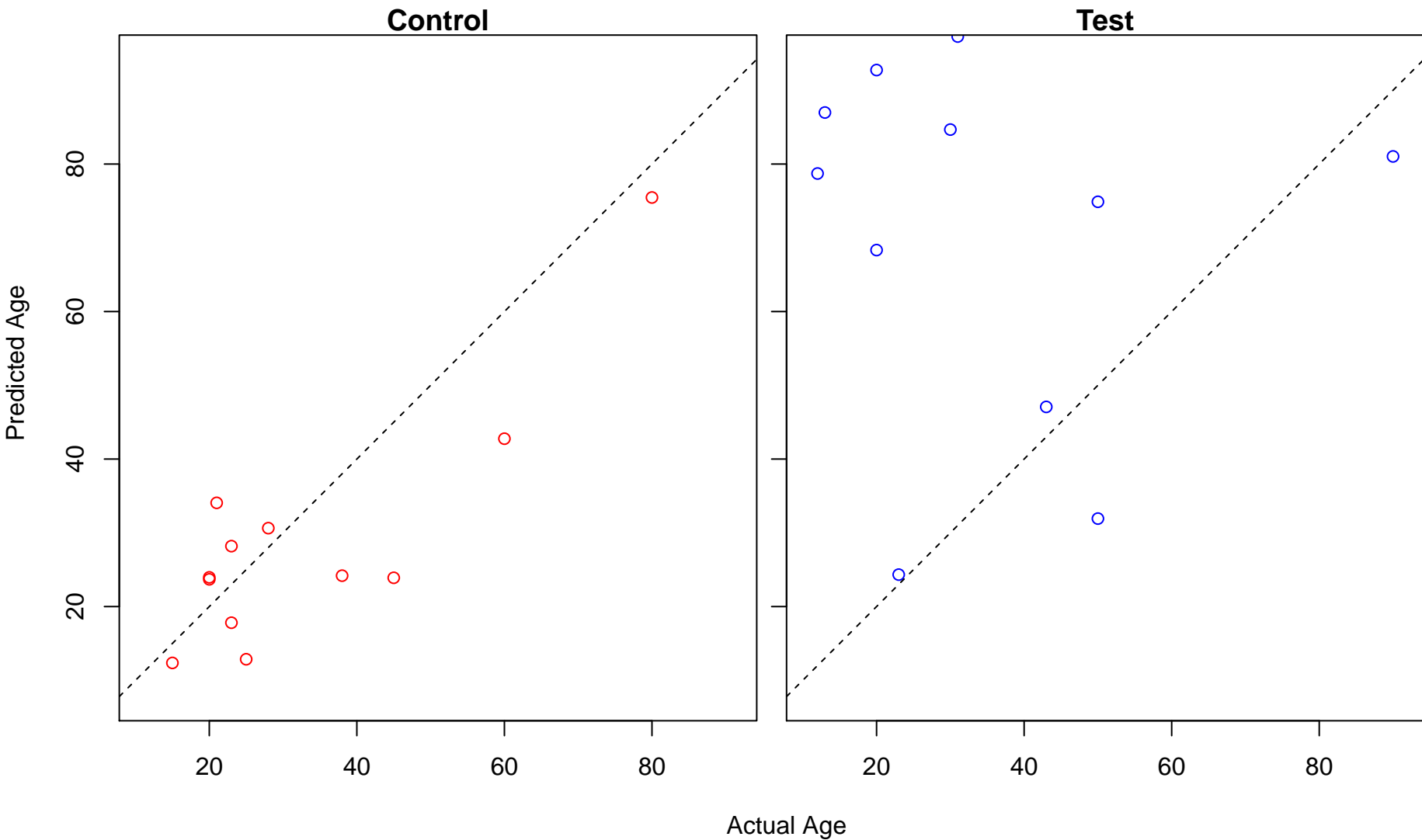
positive regulation of interleukin-4 production (Score: 18.216516)



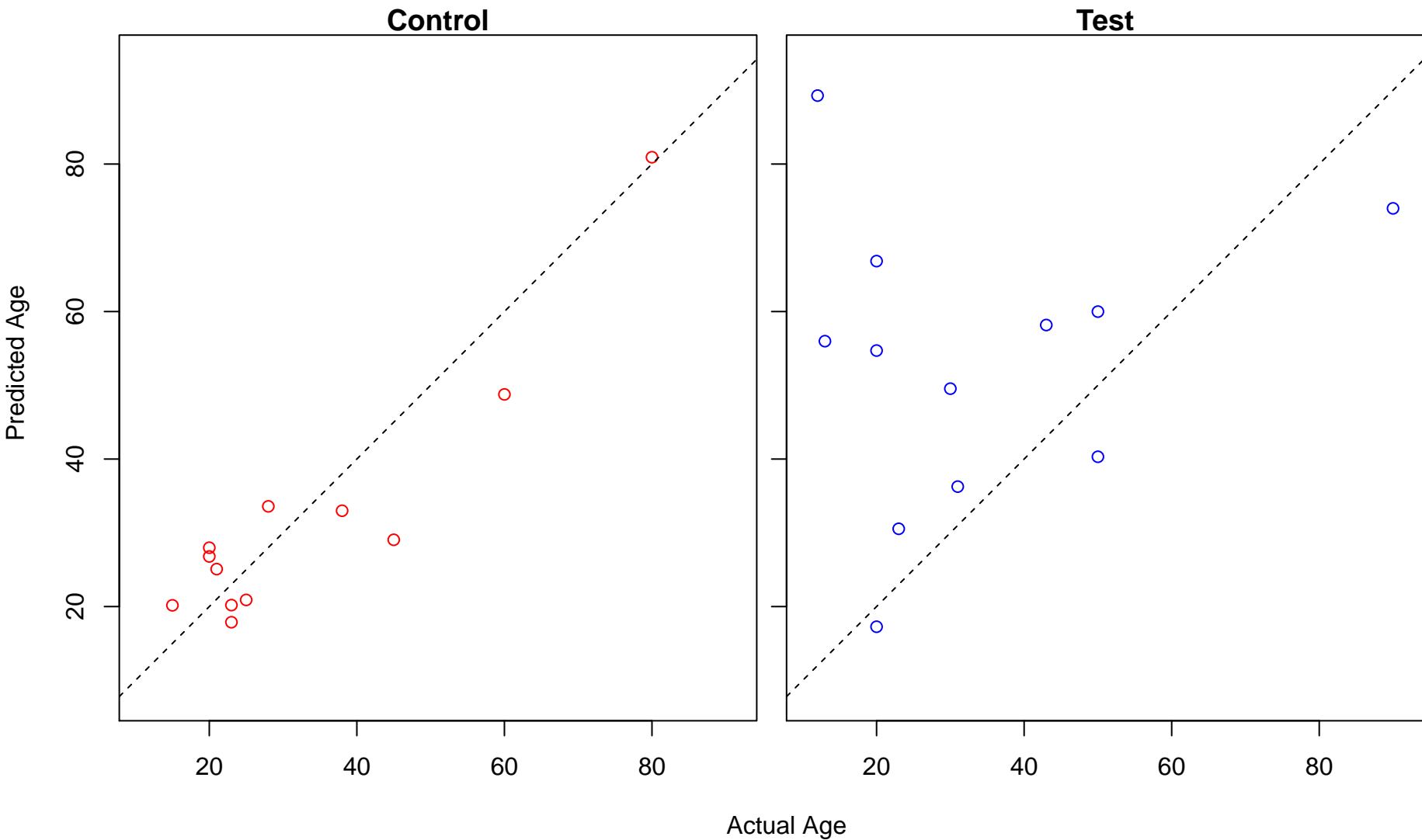
striated muscle contraction (Score: 18.203161)



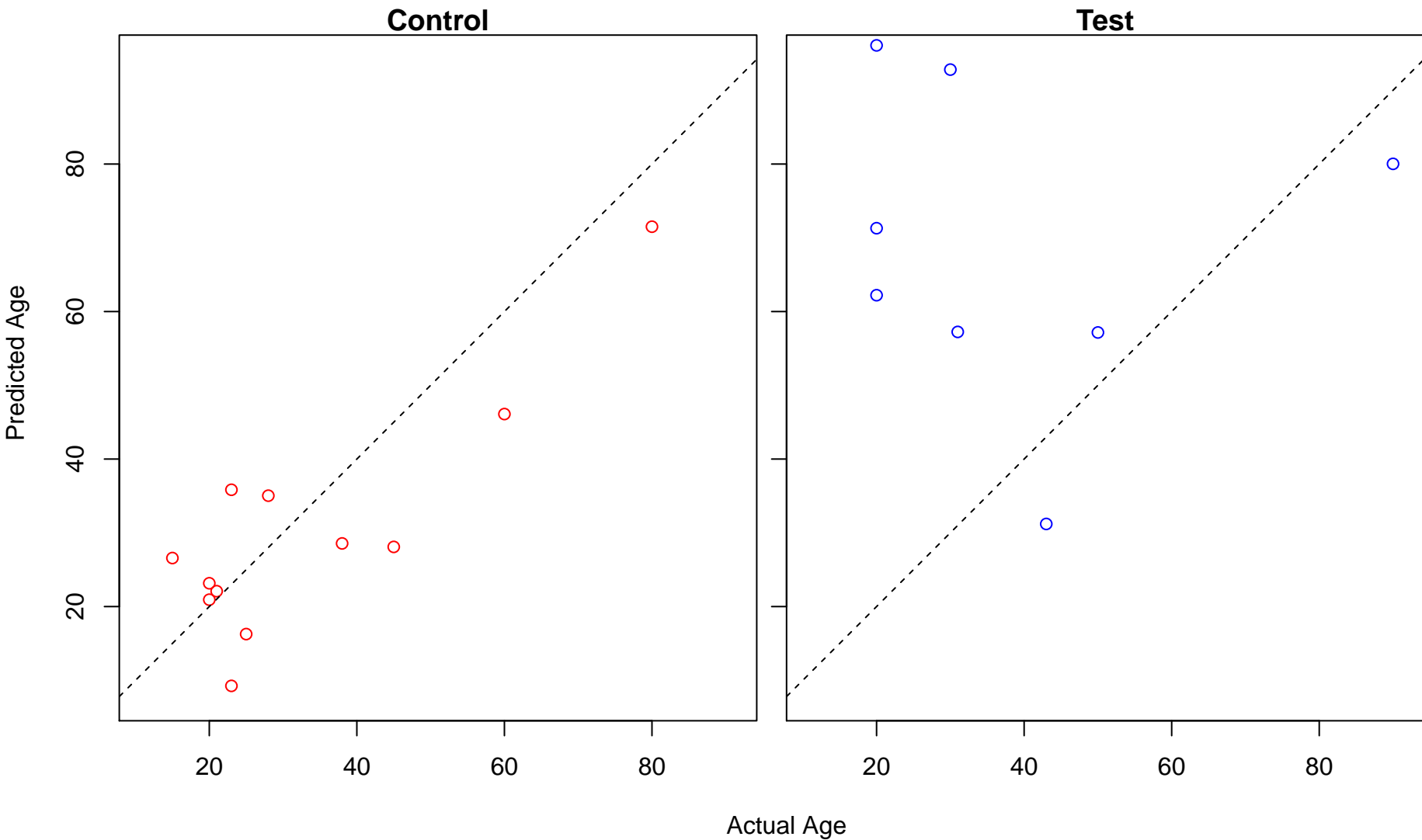
brain morphogenesis (Score: 18.196367)



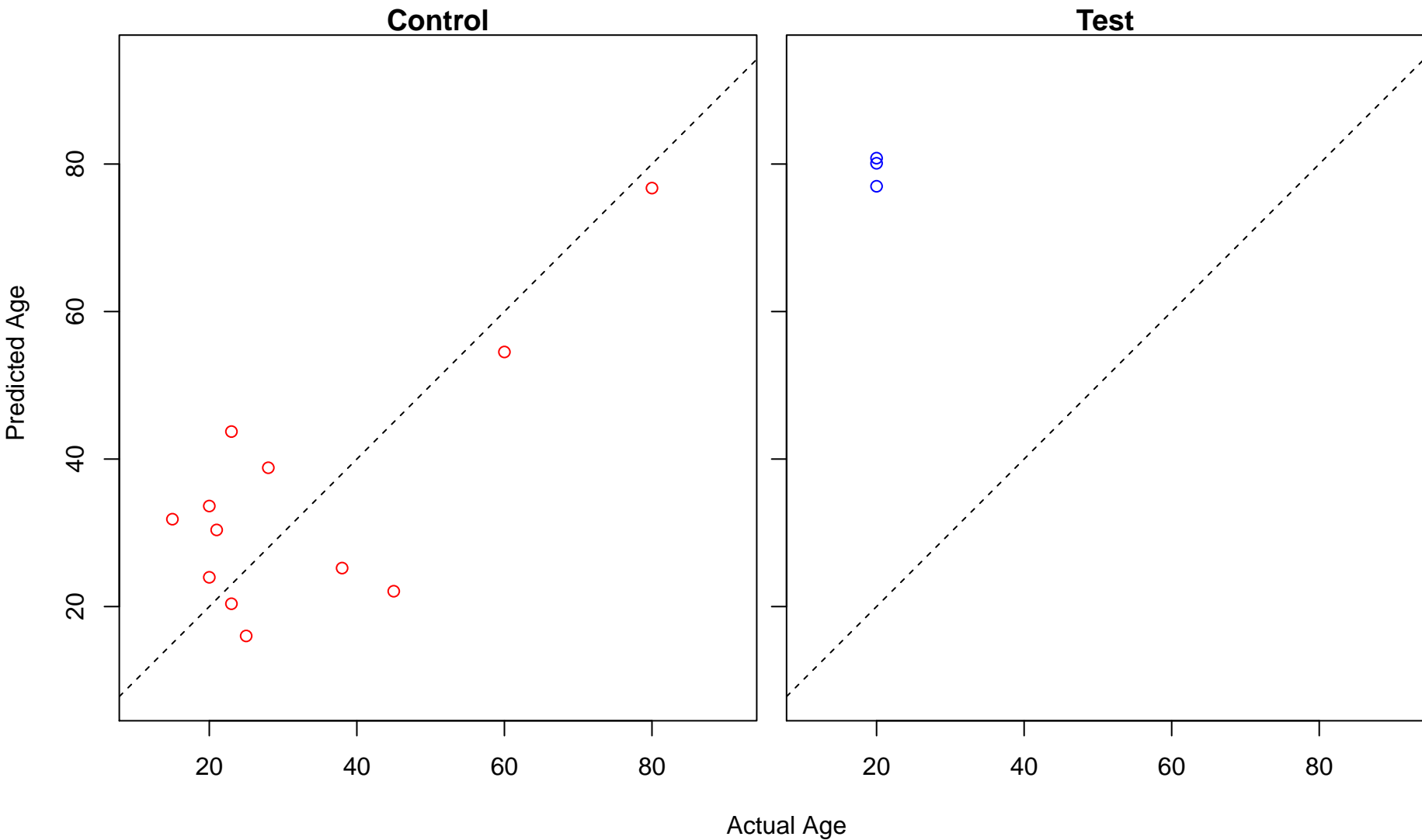
pyrimidine-containing compound metabolic process (Score: 18.167497)



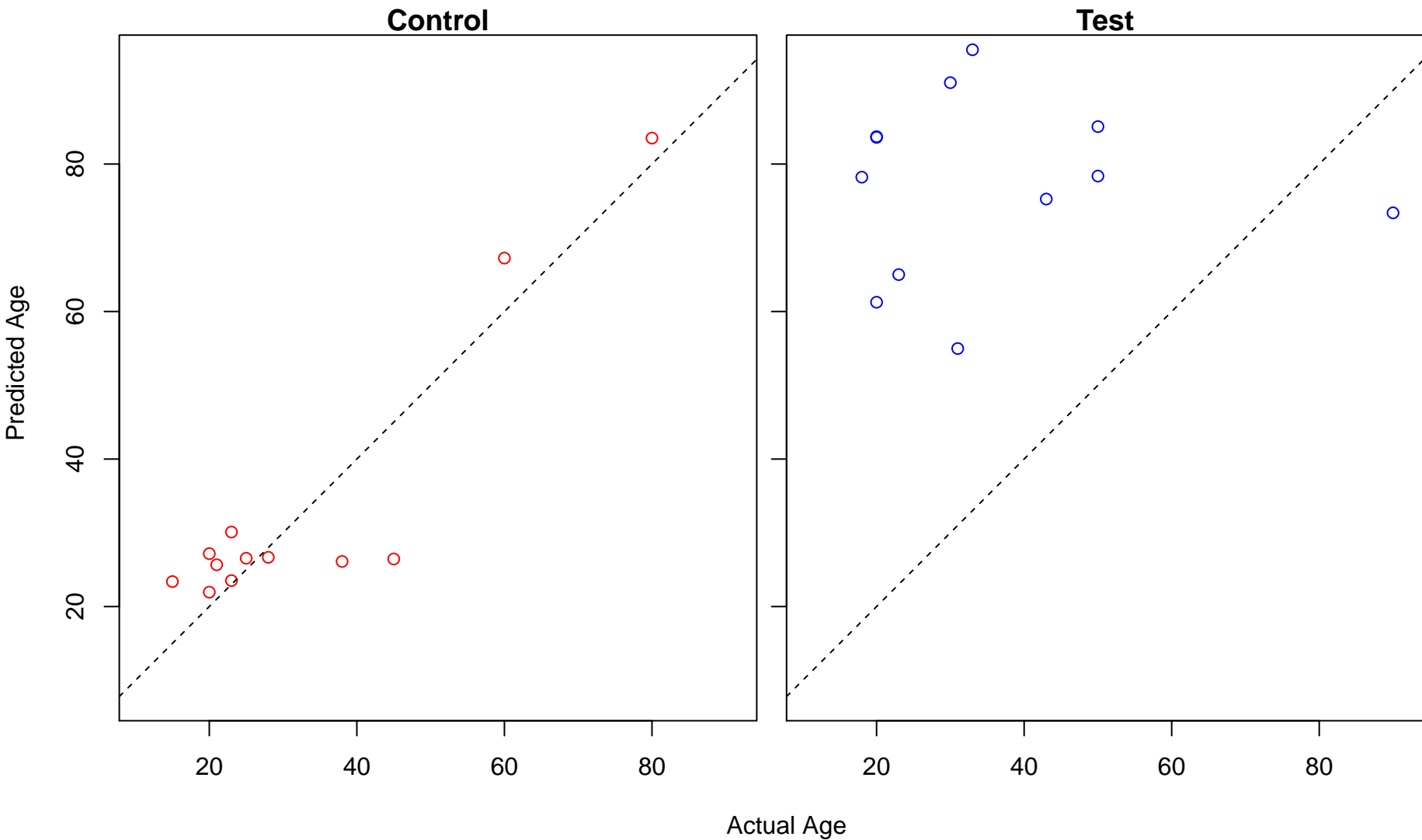
pyrimidine deoxyribonucleotide metabolic process (Score: 18.147425)



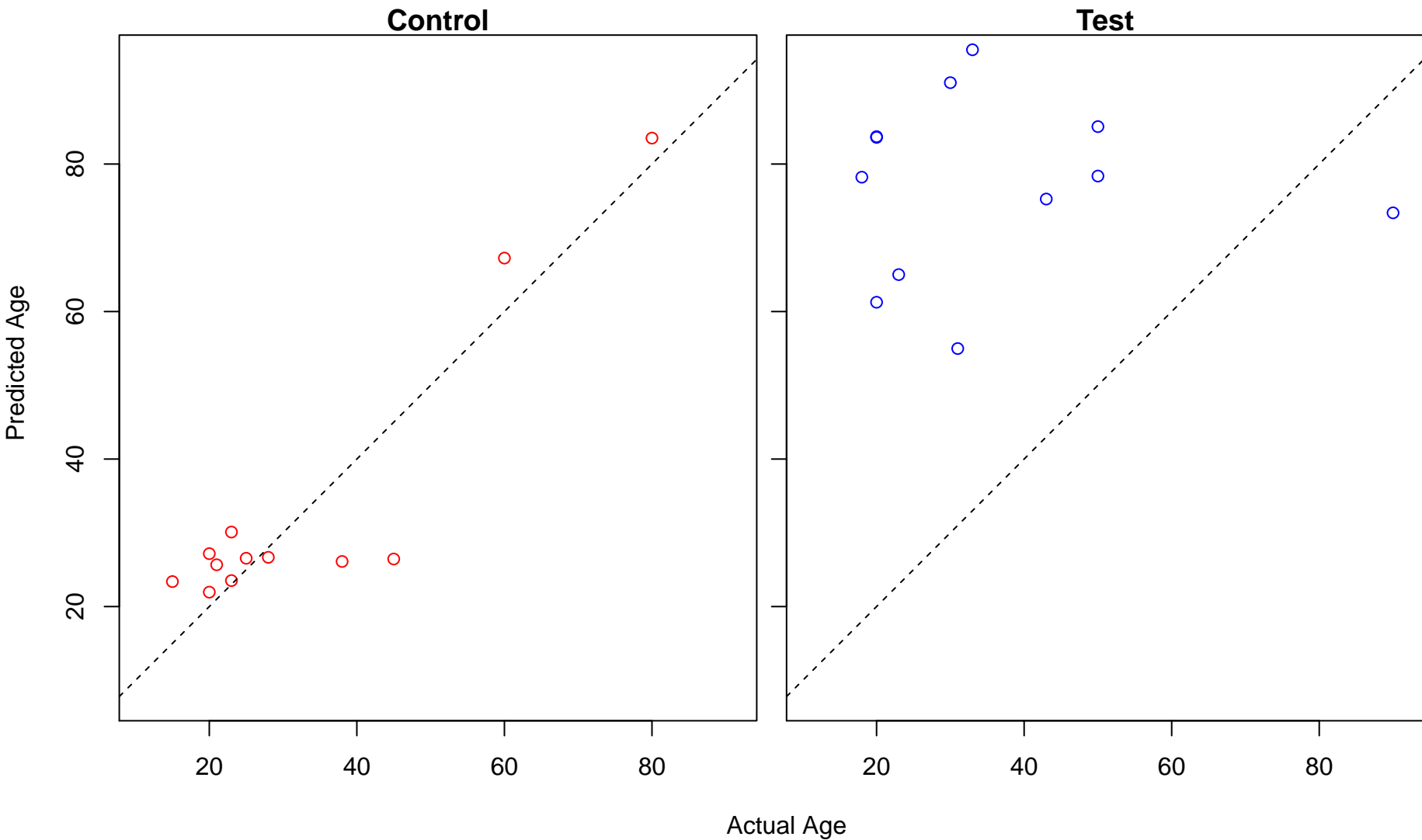
thiamine-containing compound metabolic process (Score: 18.144860)



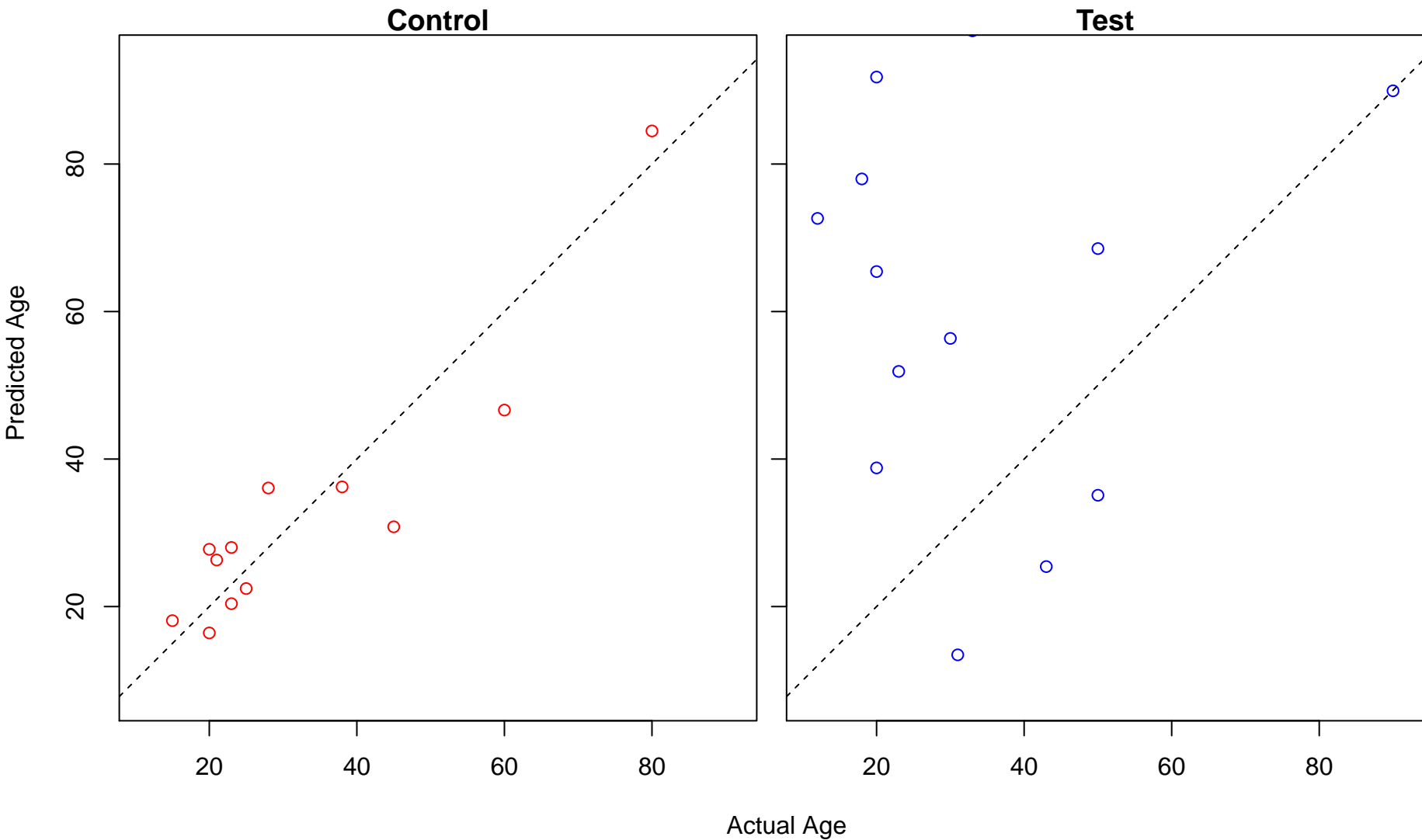
positive regulation of organ growth (Score: 18.139269)



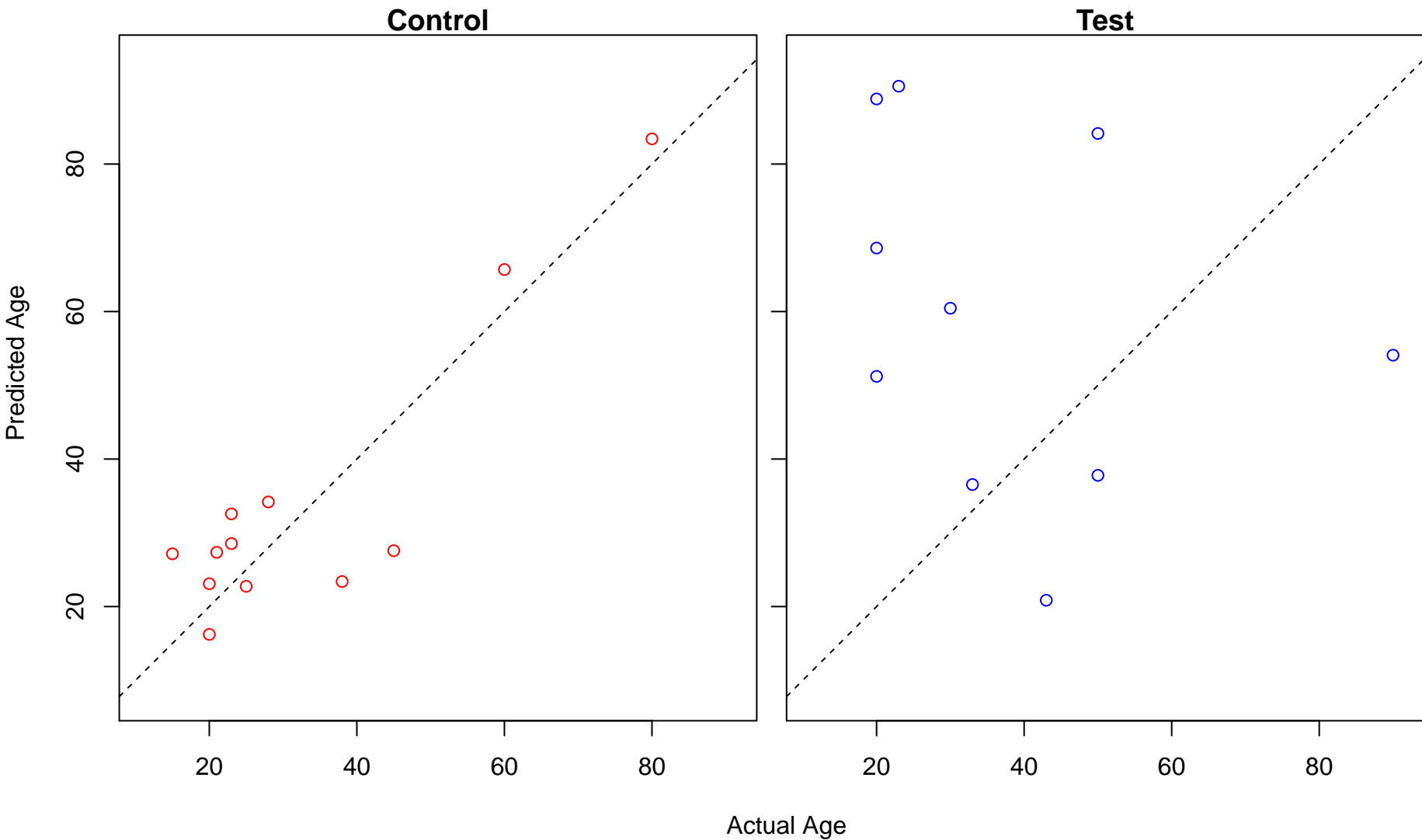
positive regulation of heart growth (Score: 18.139269)



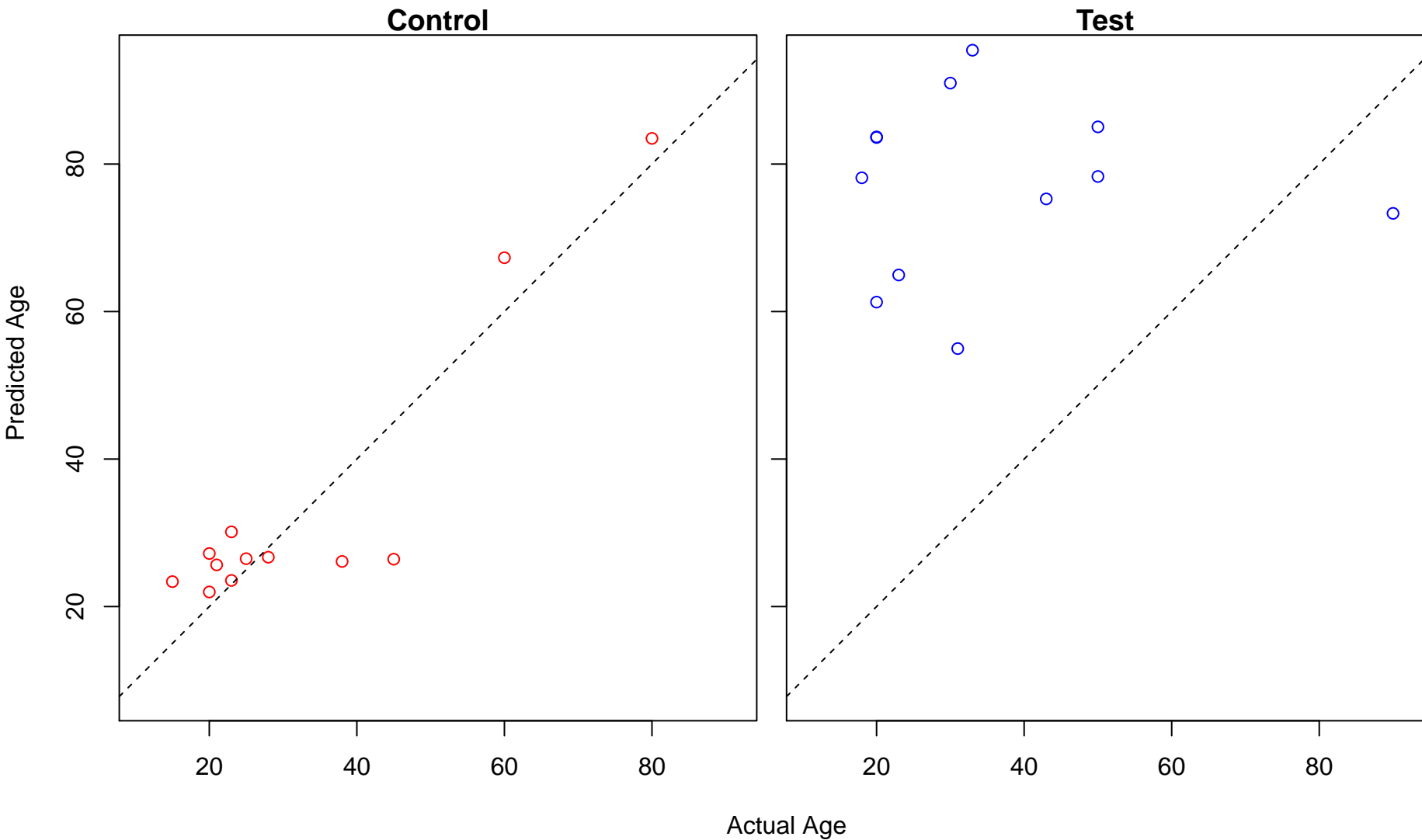
cell cycle phase transition (Score: 18.107612)



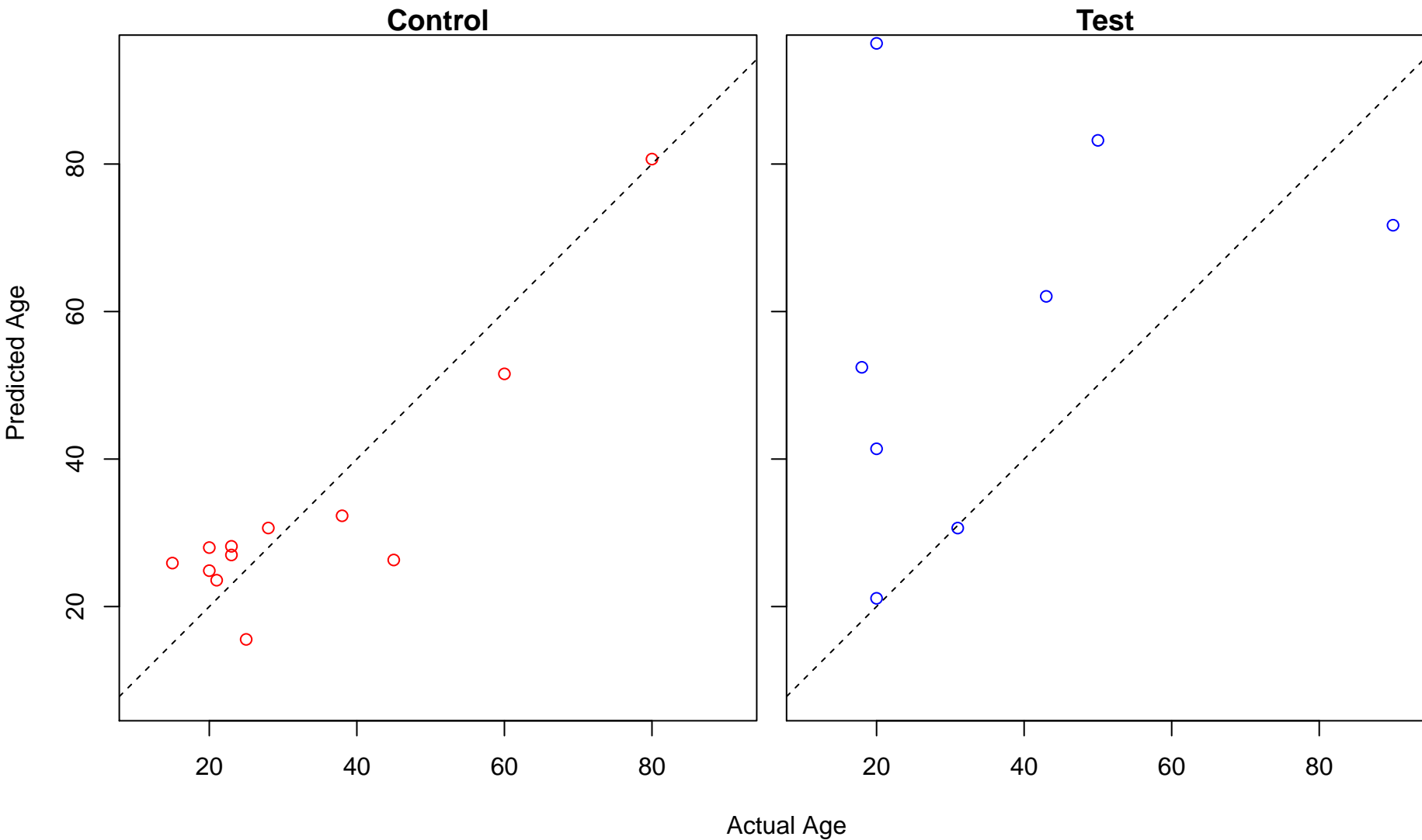
regulation of Notch signaling pathway (Score: 18.103242)



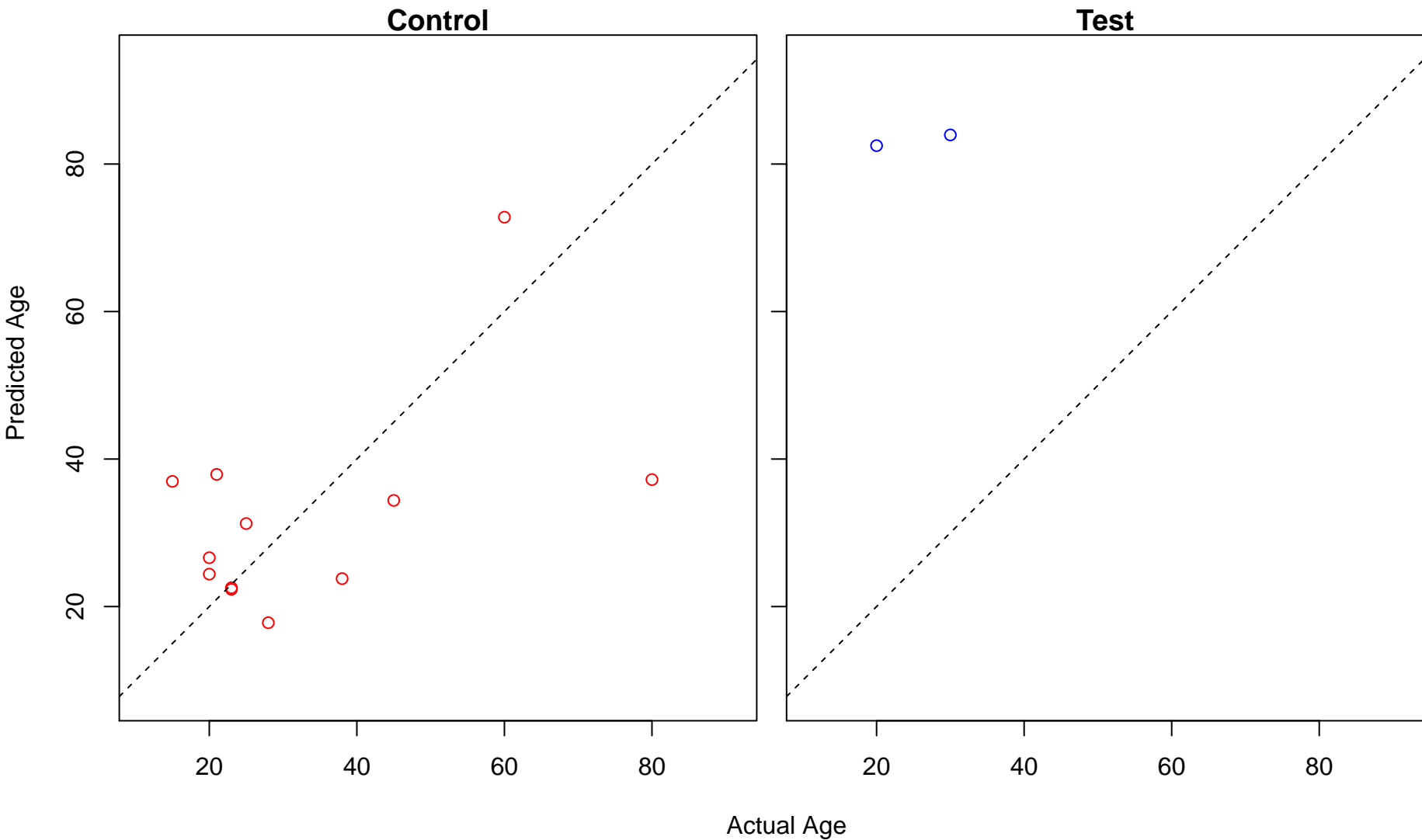
regulation of heart growth (Score: 18.085699)



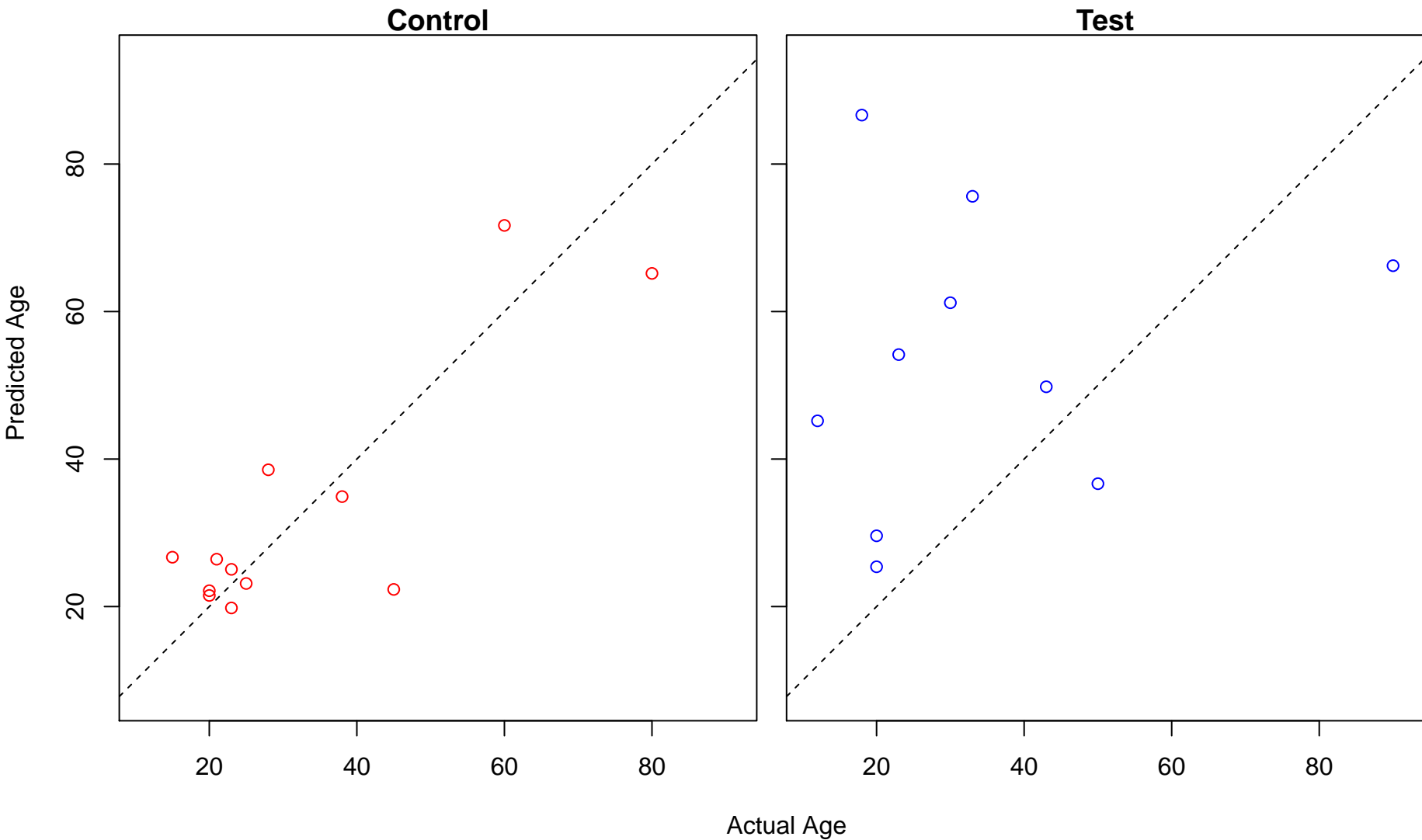
lung epithelium development (Score: 18.058603)



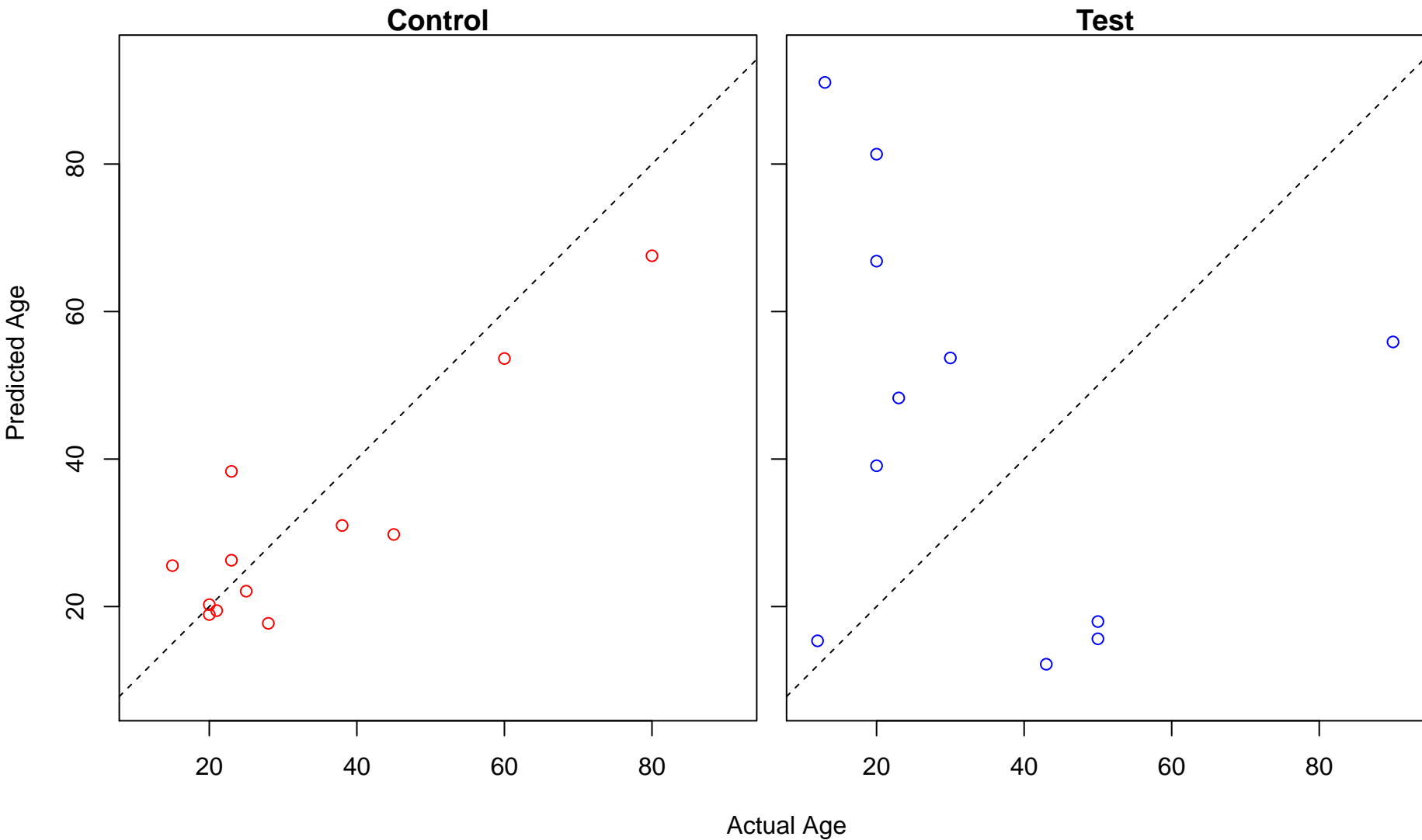
sensory perception of sweet taste (Score: 18.039355)



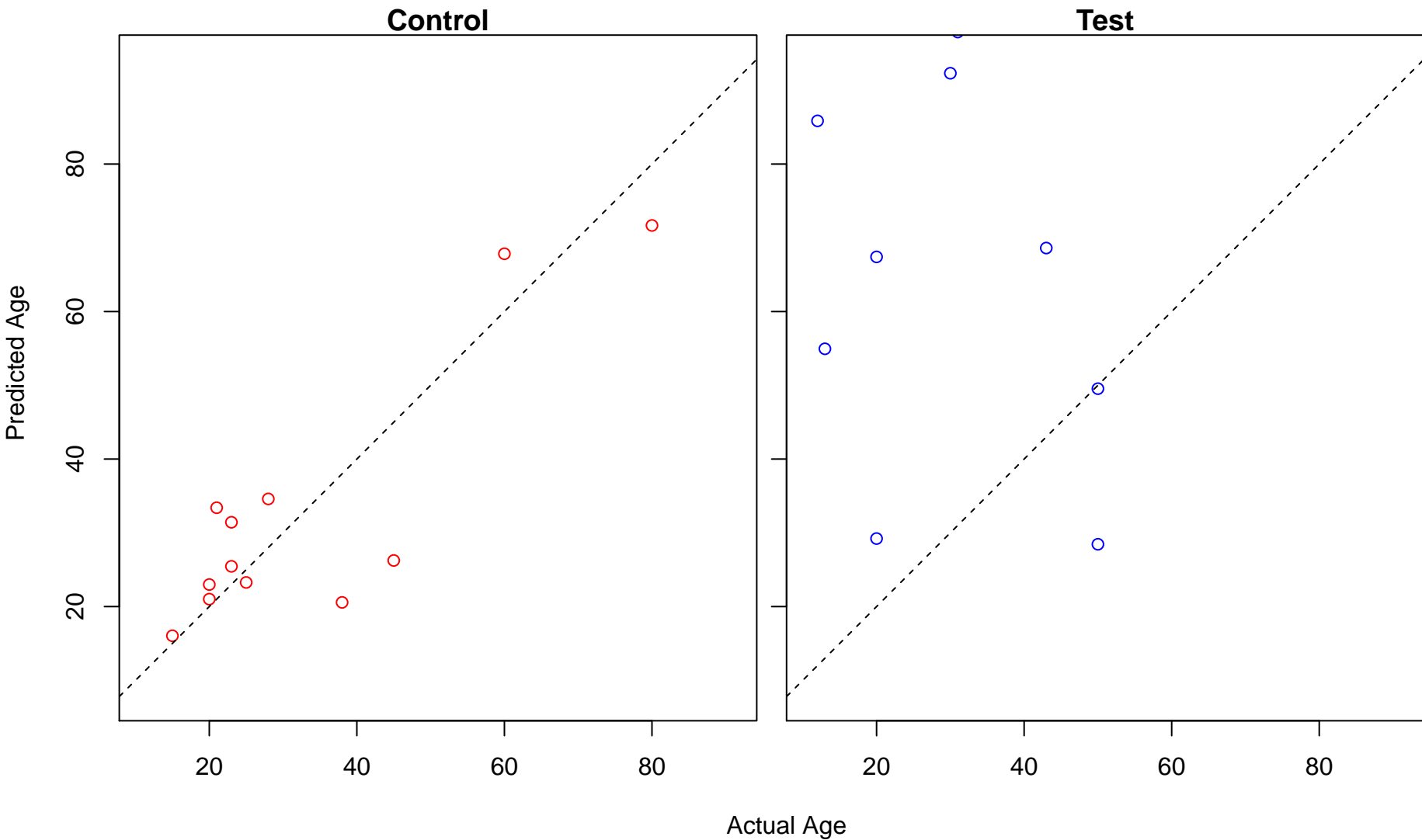
regulation of leukocyte chemotaxis (Score: 17.984683)



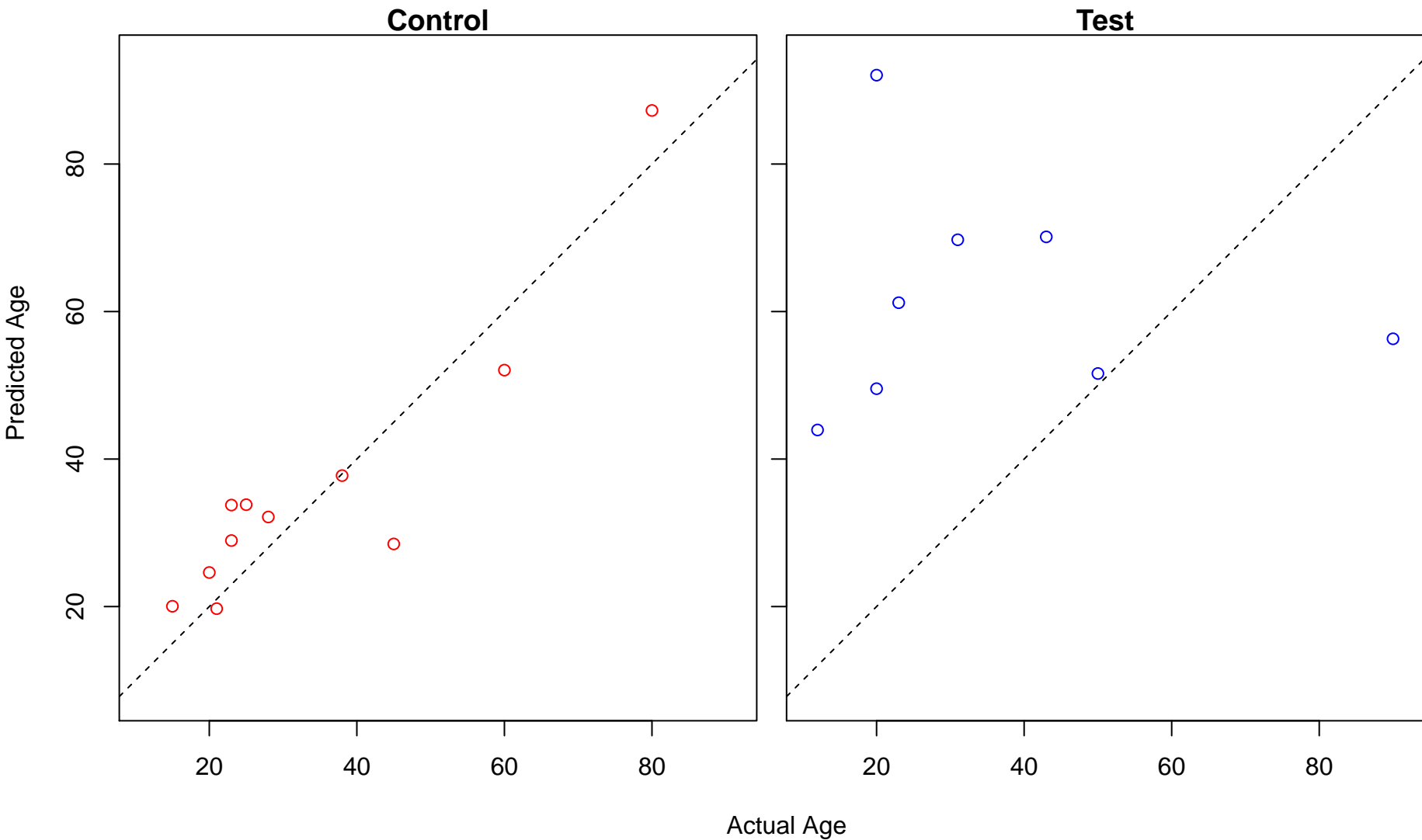
cell communication involved in cardiac conduction (Score: 17.951403)



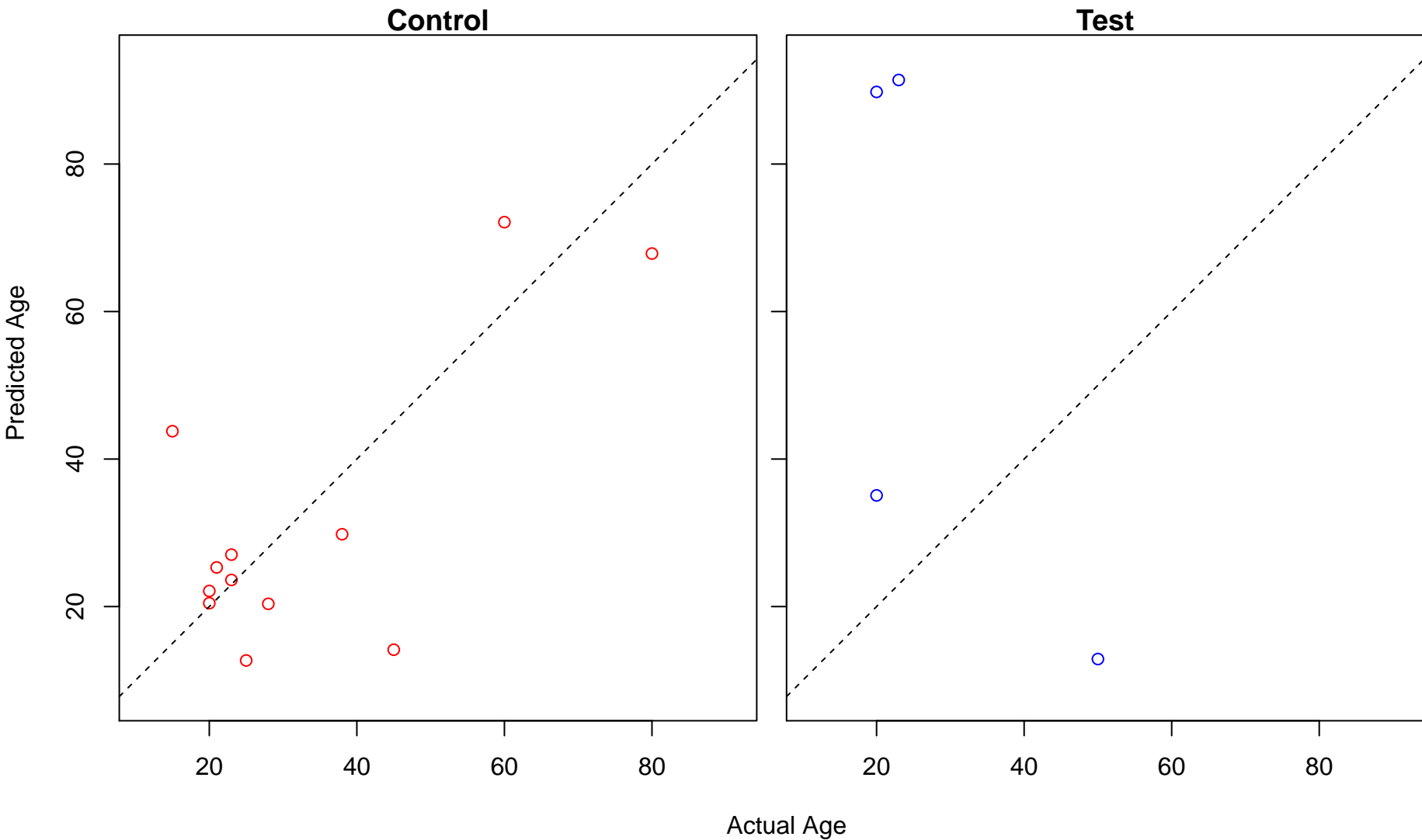
positive regulation of cell junction assembly (Score: 17.942159)



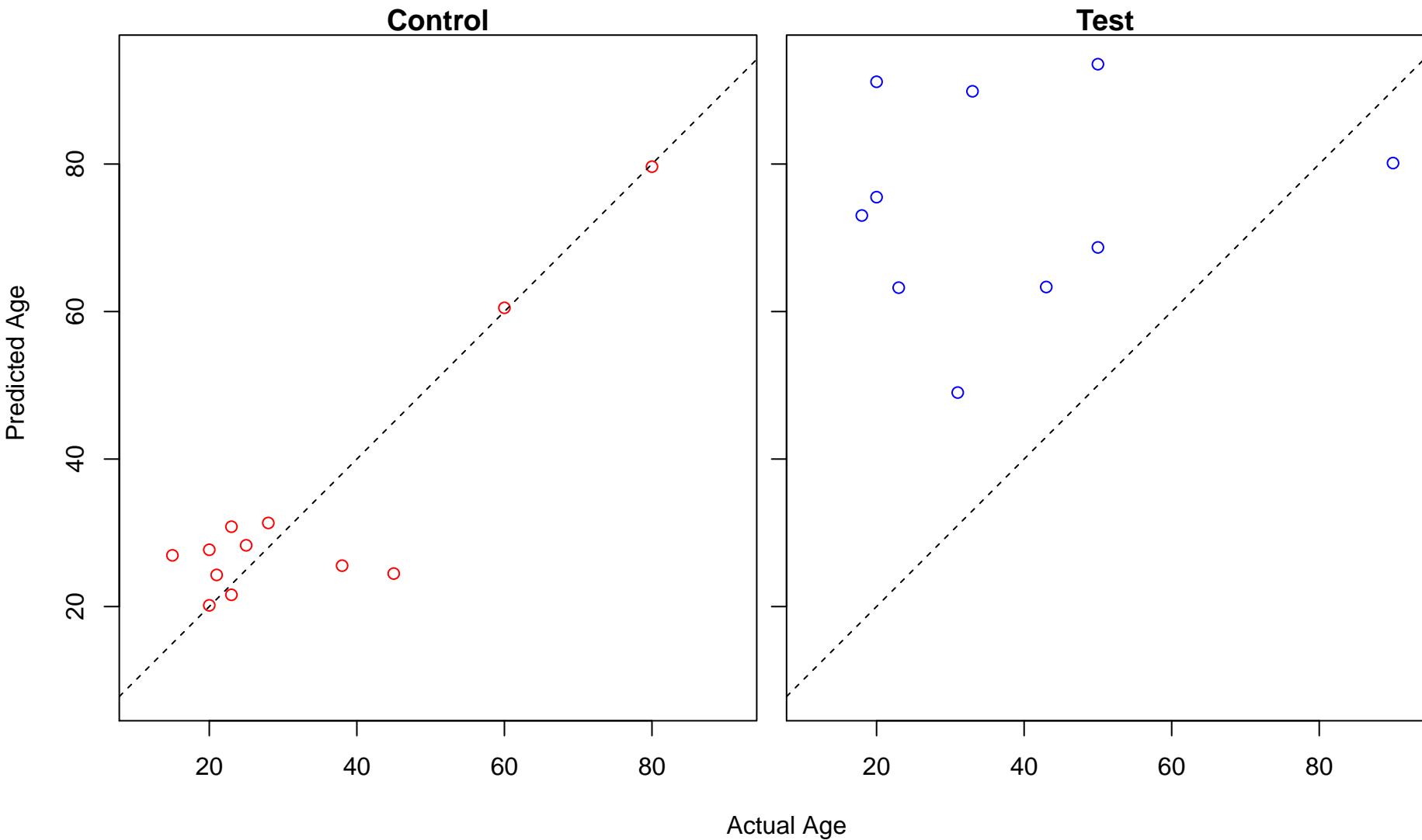
vitamin K metabolic process (Score: 17.896372)



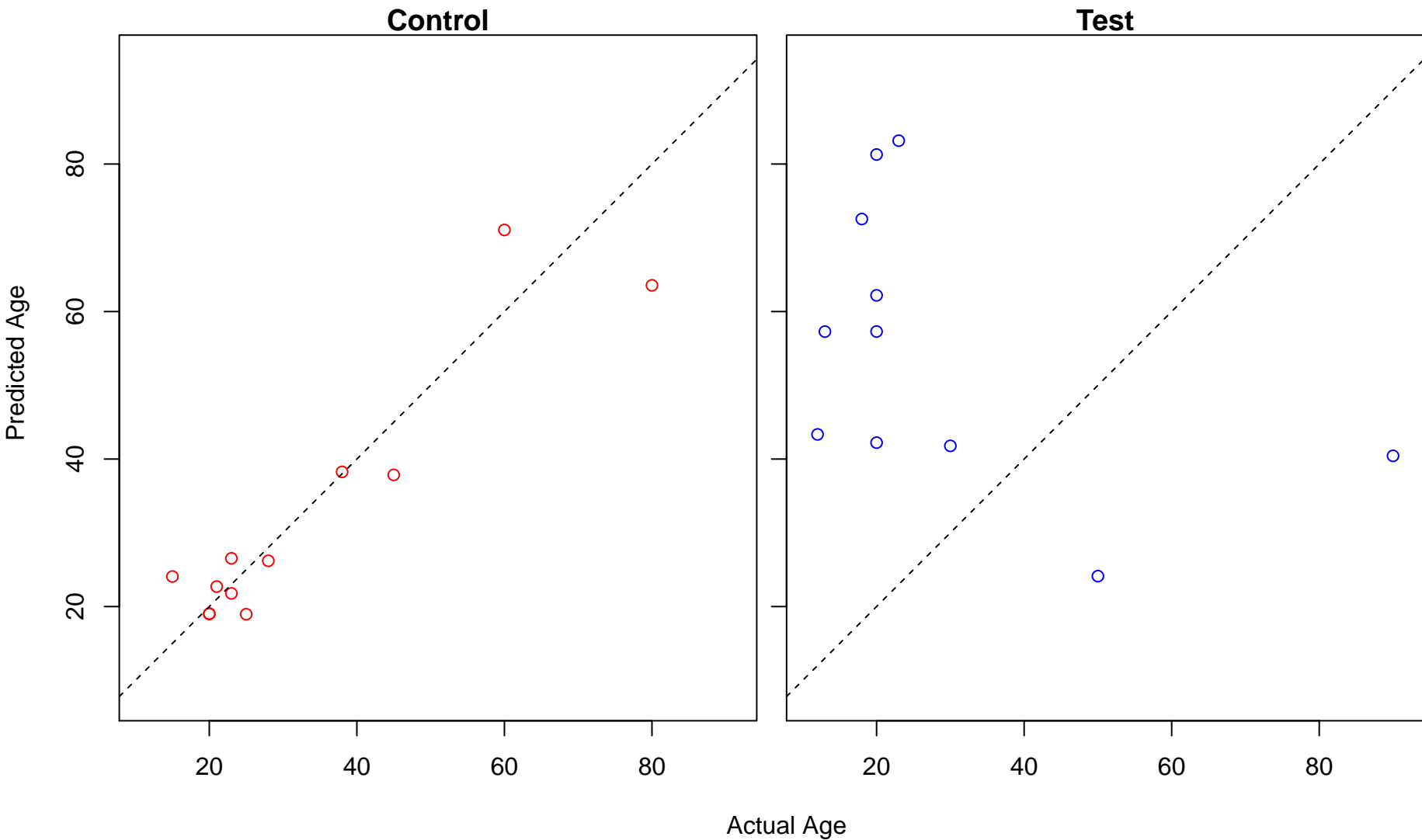
negative regulation of oxidative stress-induced cell death (Score: 17.891333)



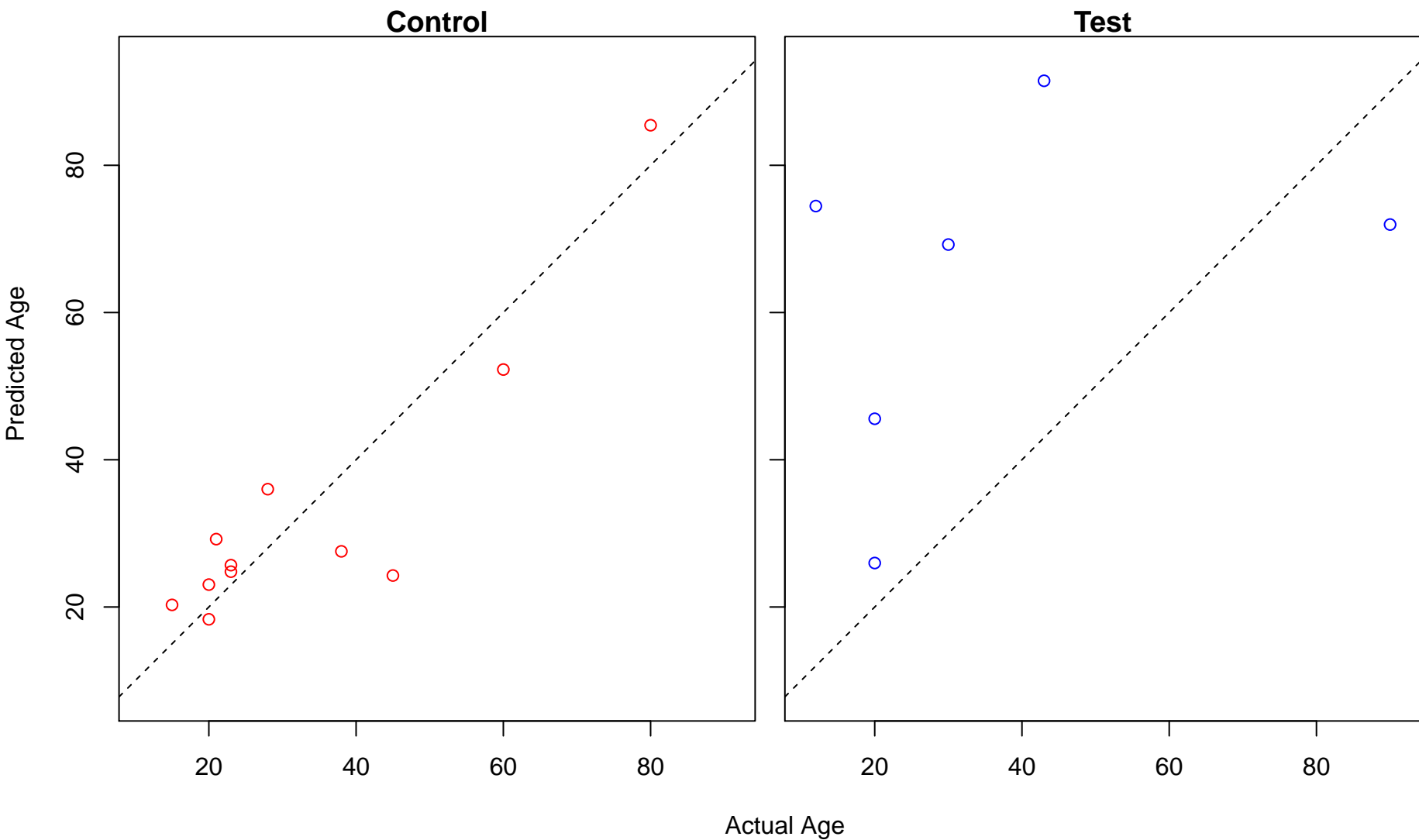
artery morphogenesis (Score: 17.868251)



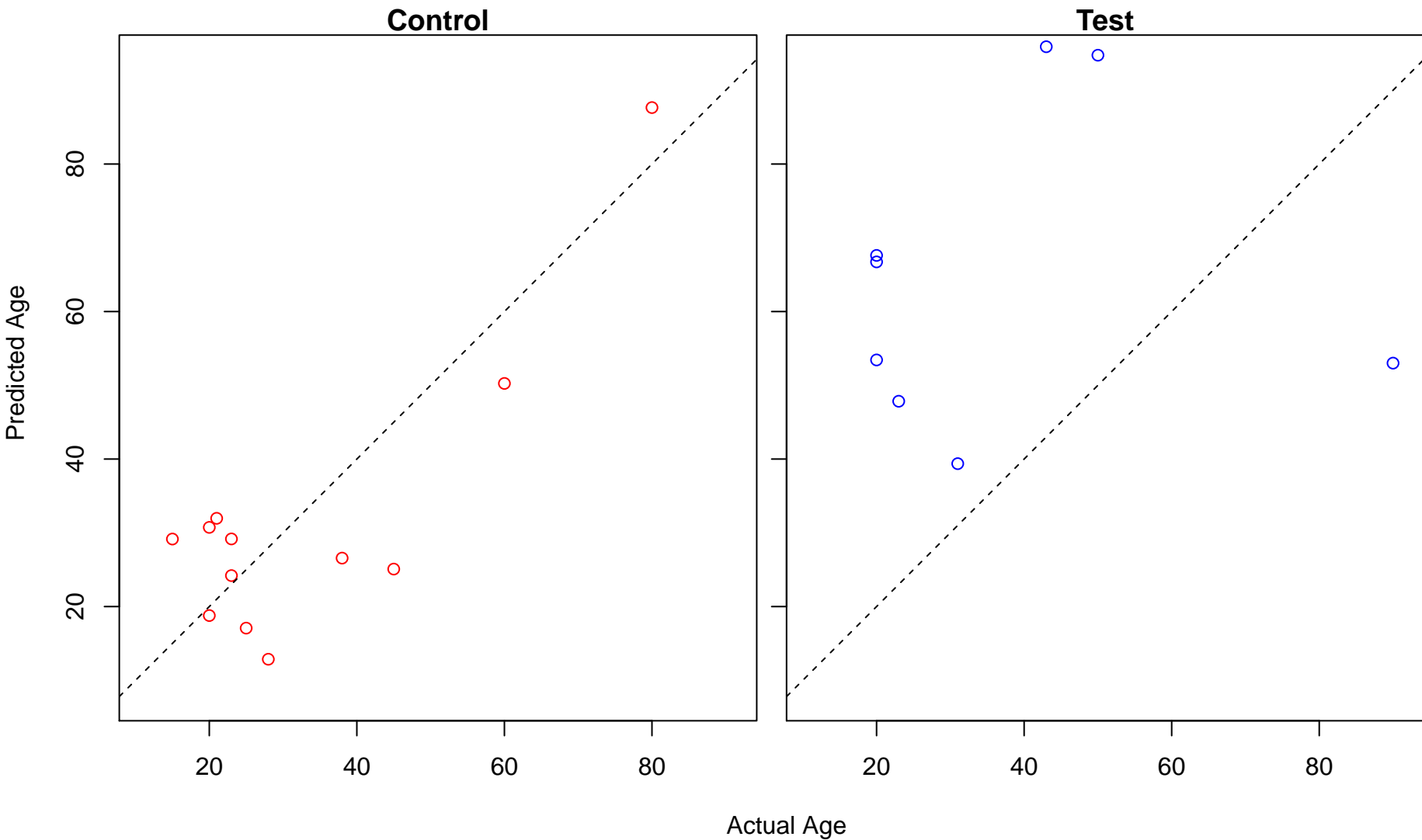
chondrocyte differentiation (Score: 17.857955)



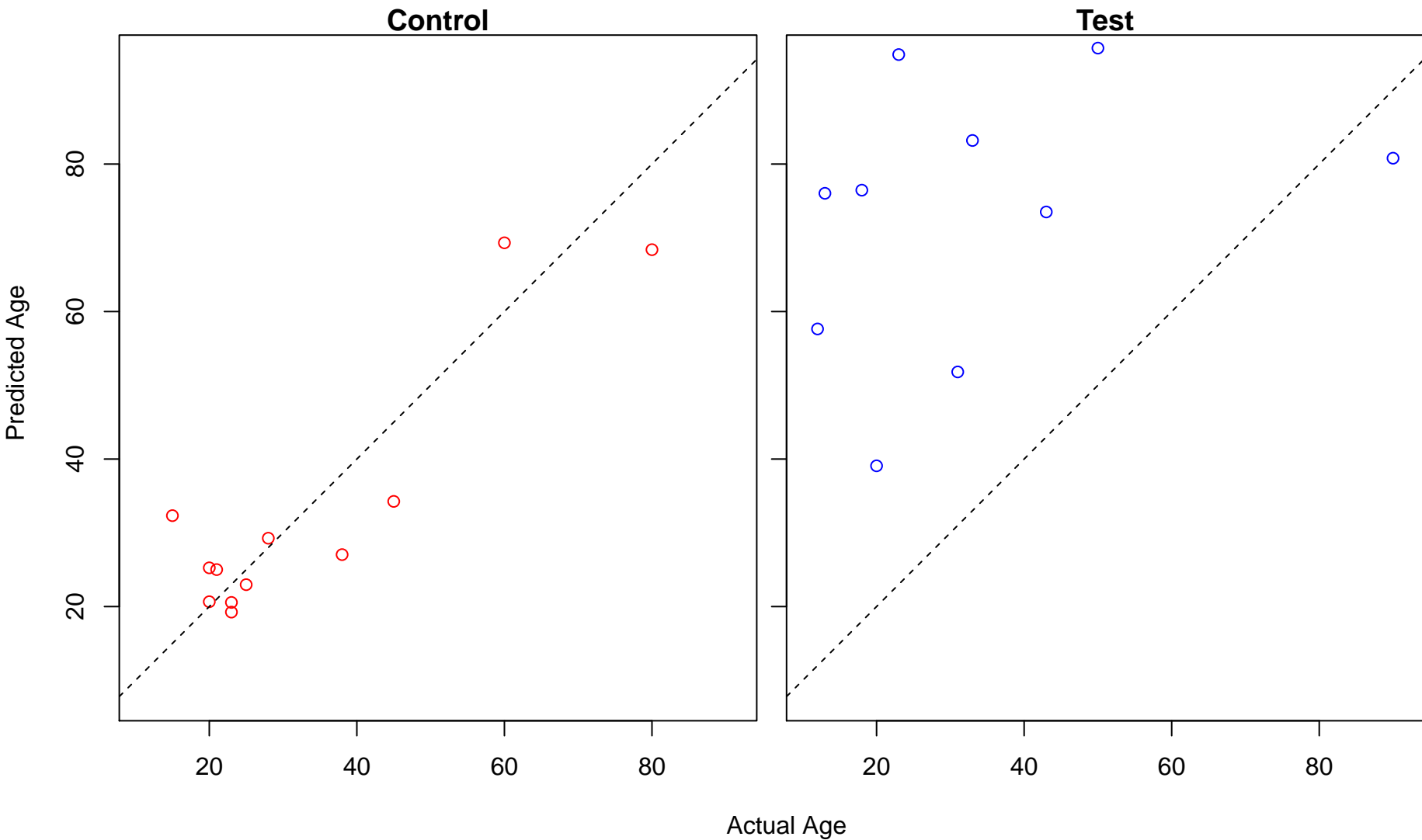
positive regulation of JUN kinase activity (Score: 17.809880)



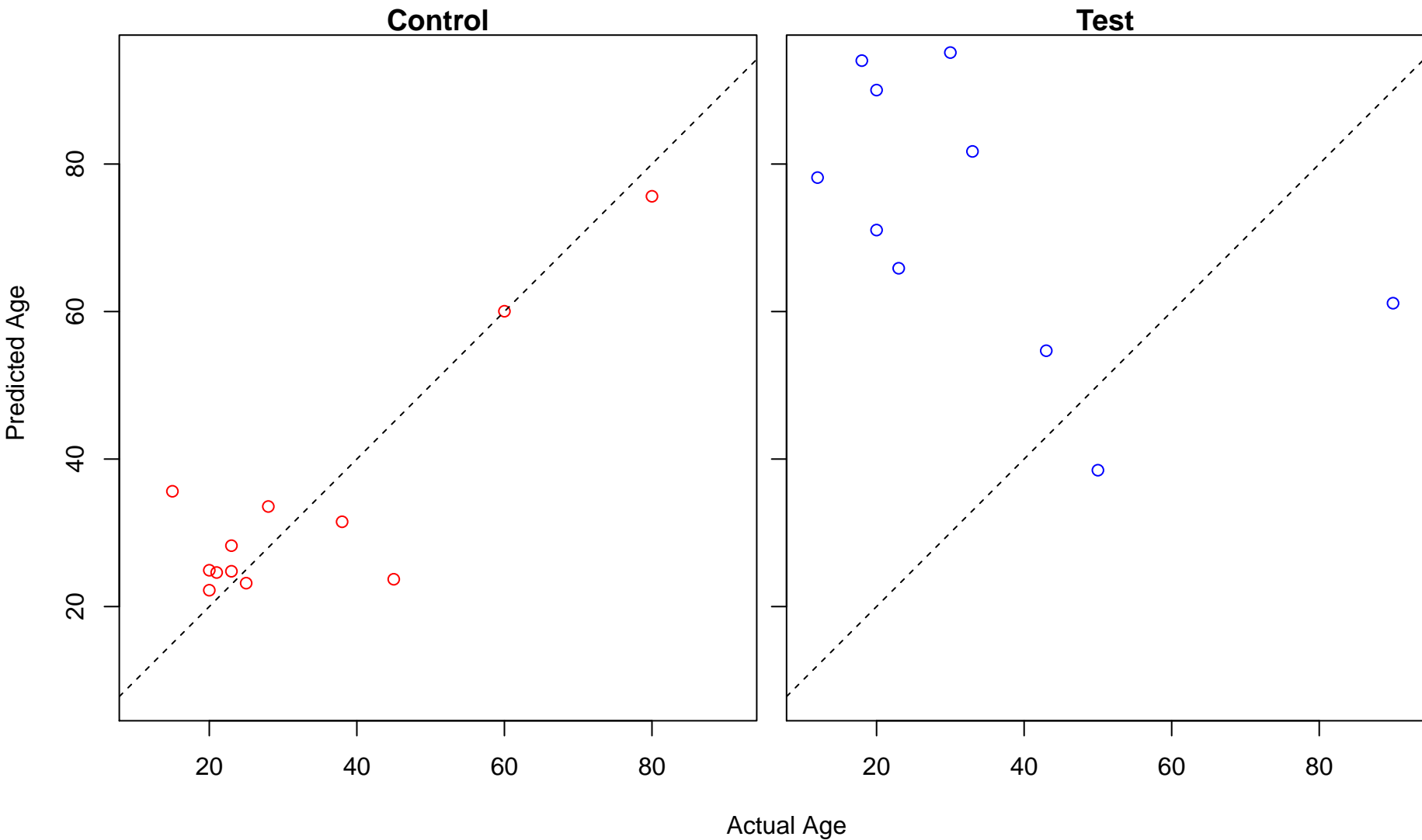
organelle fusion (Score: 17.801262)



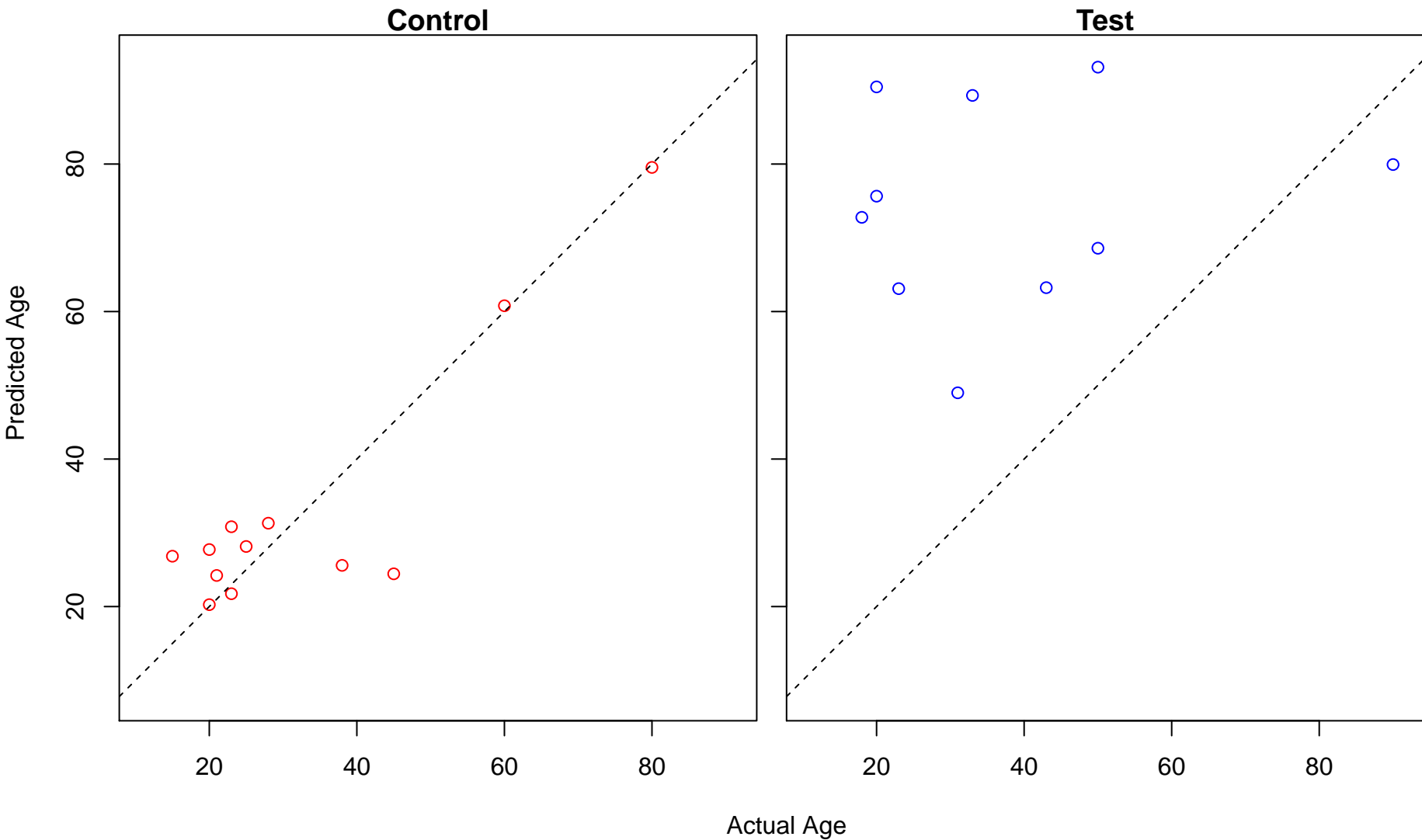
creatine metabolic process (Score: 17.730498)



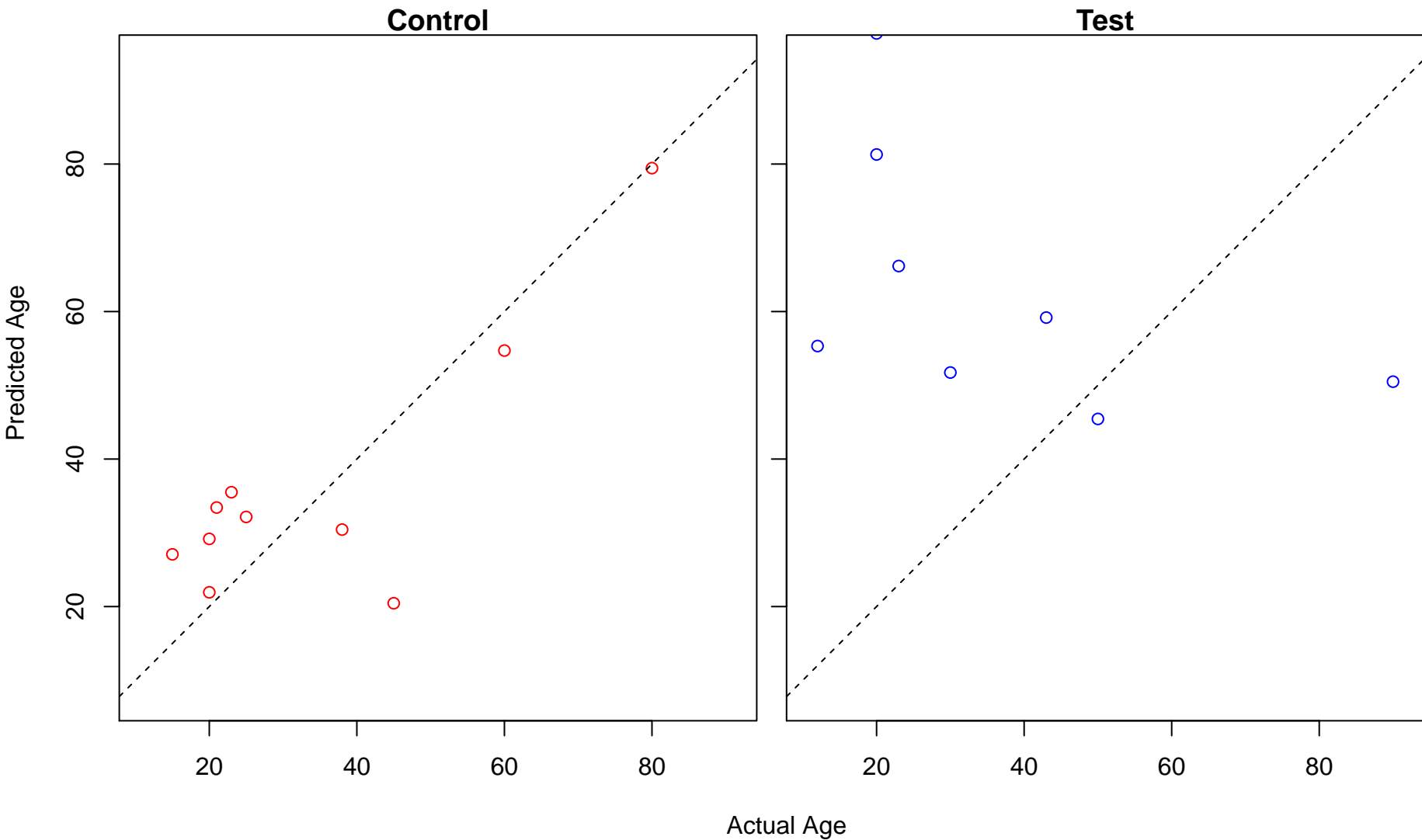
positive regulation of response to external stimulus (Score: 17.728770)



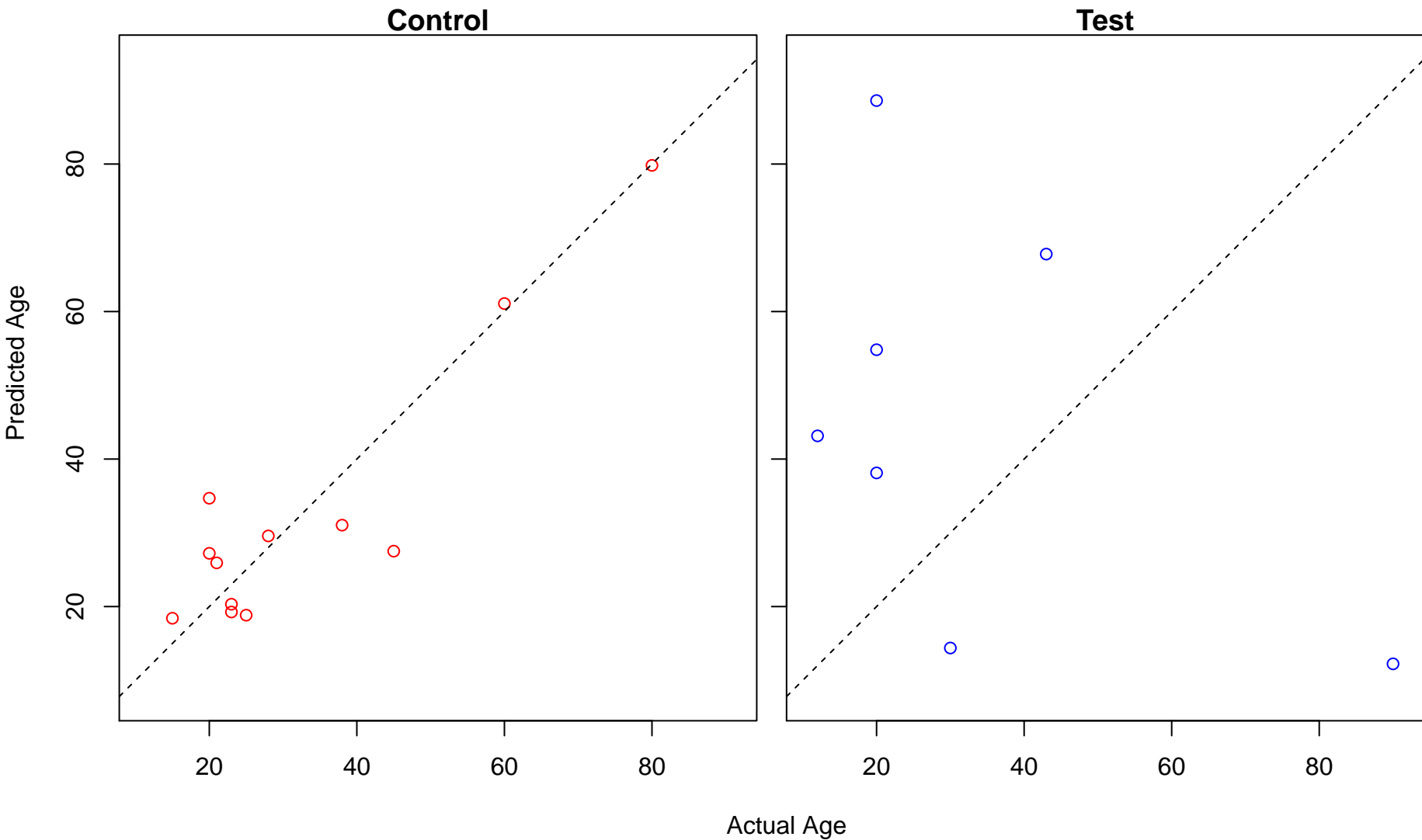
artery development (Score: 17.681718)



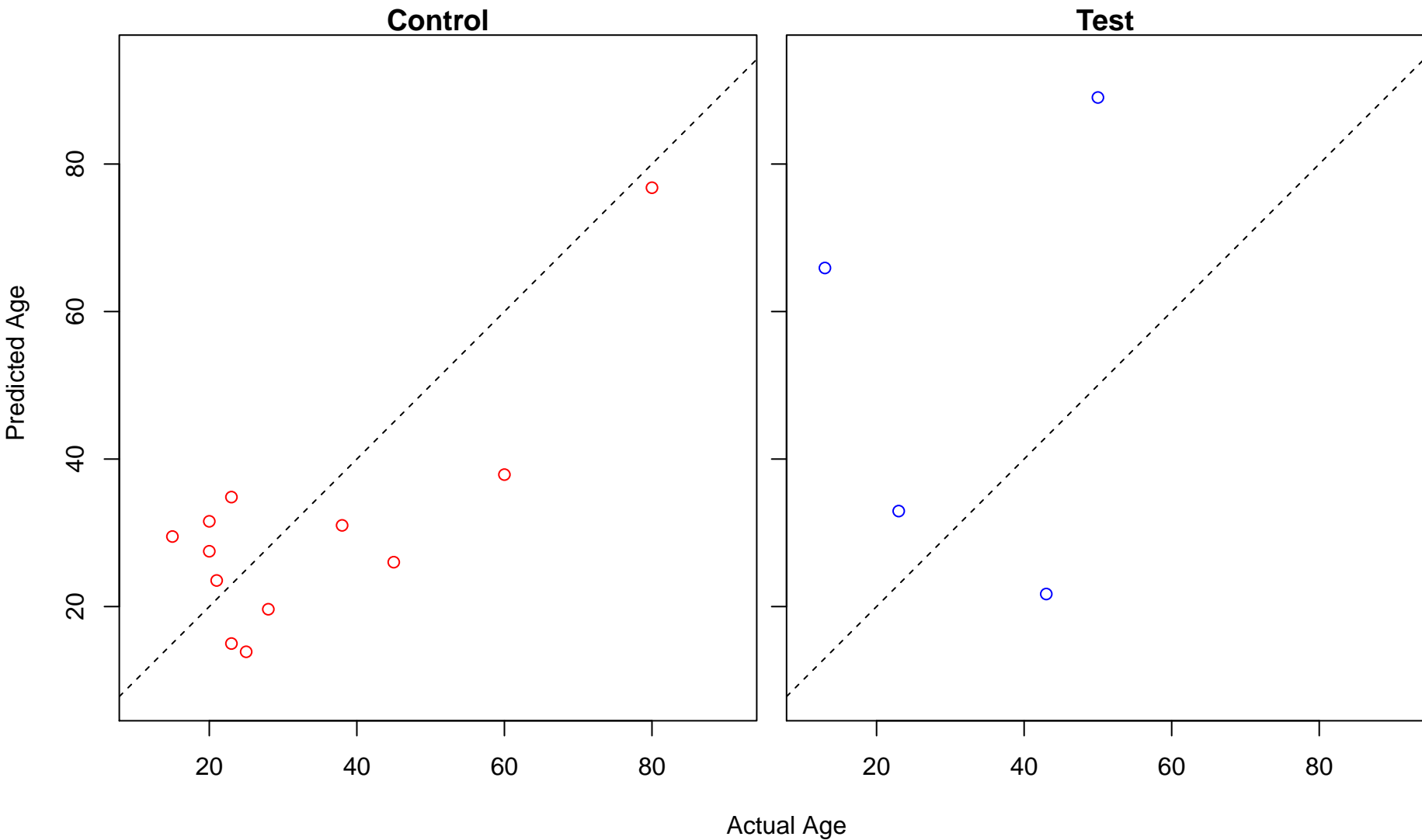
nucleobase transport (Score: 17.667308)



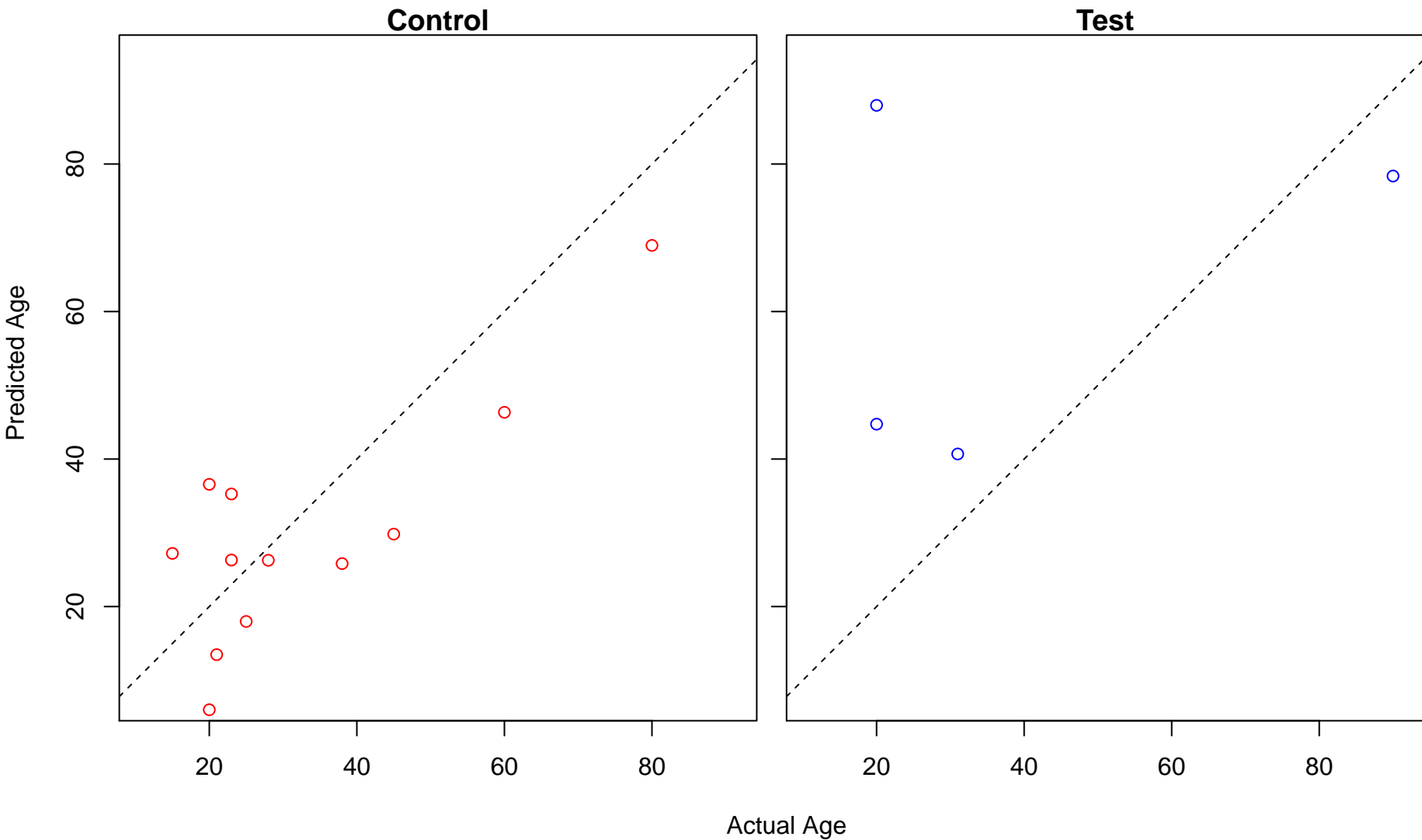
ketone biosynthetic process (Score: 17.666594)



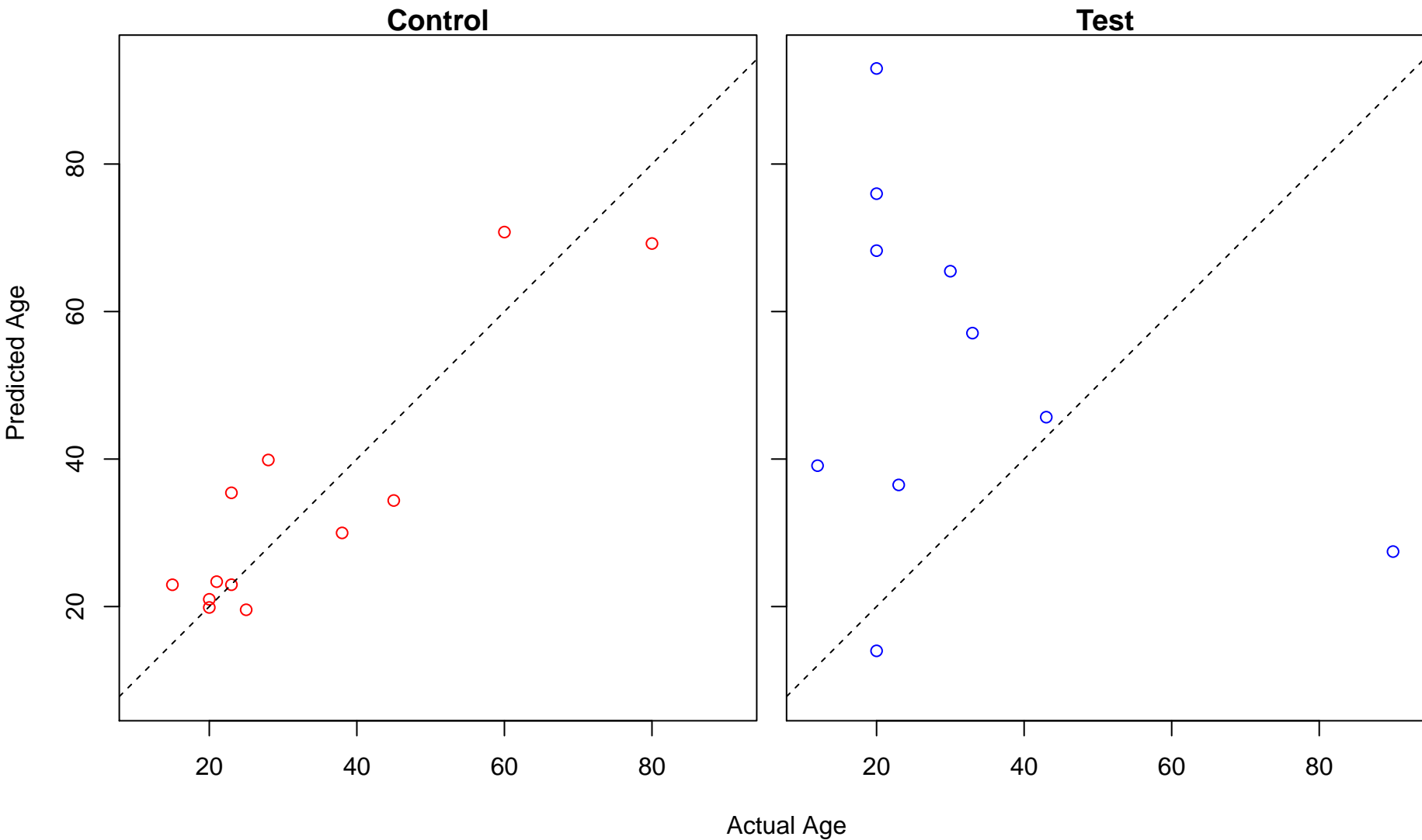
positive regulation of dendritic cell antigen processing and presentation (Score: 17.653576)



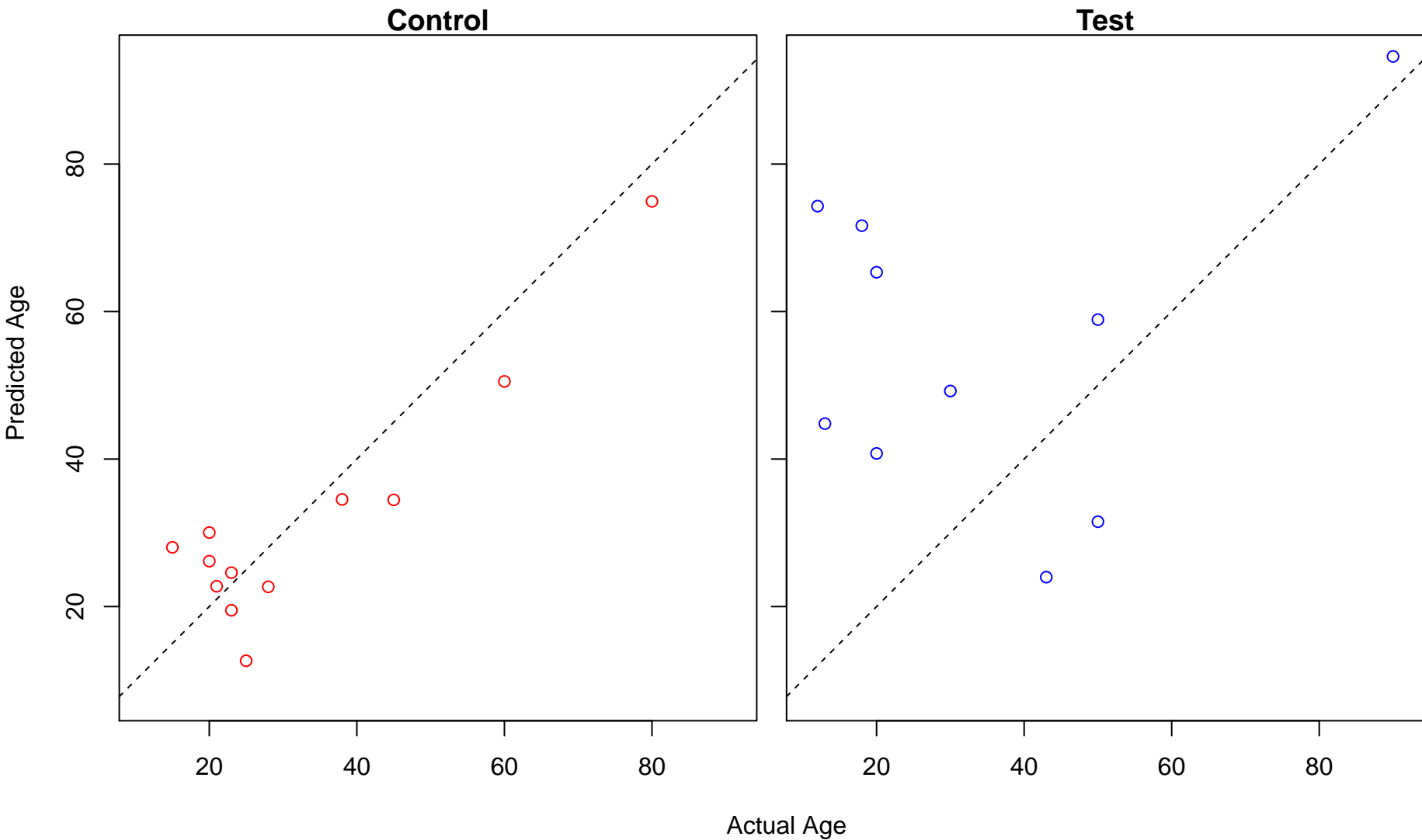
positive regulation of megakaryocyte differentiation (Score: 17.597662)



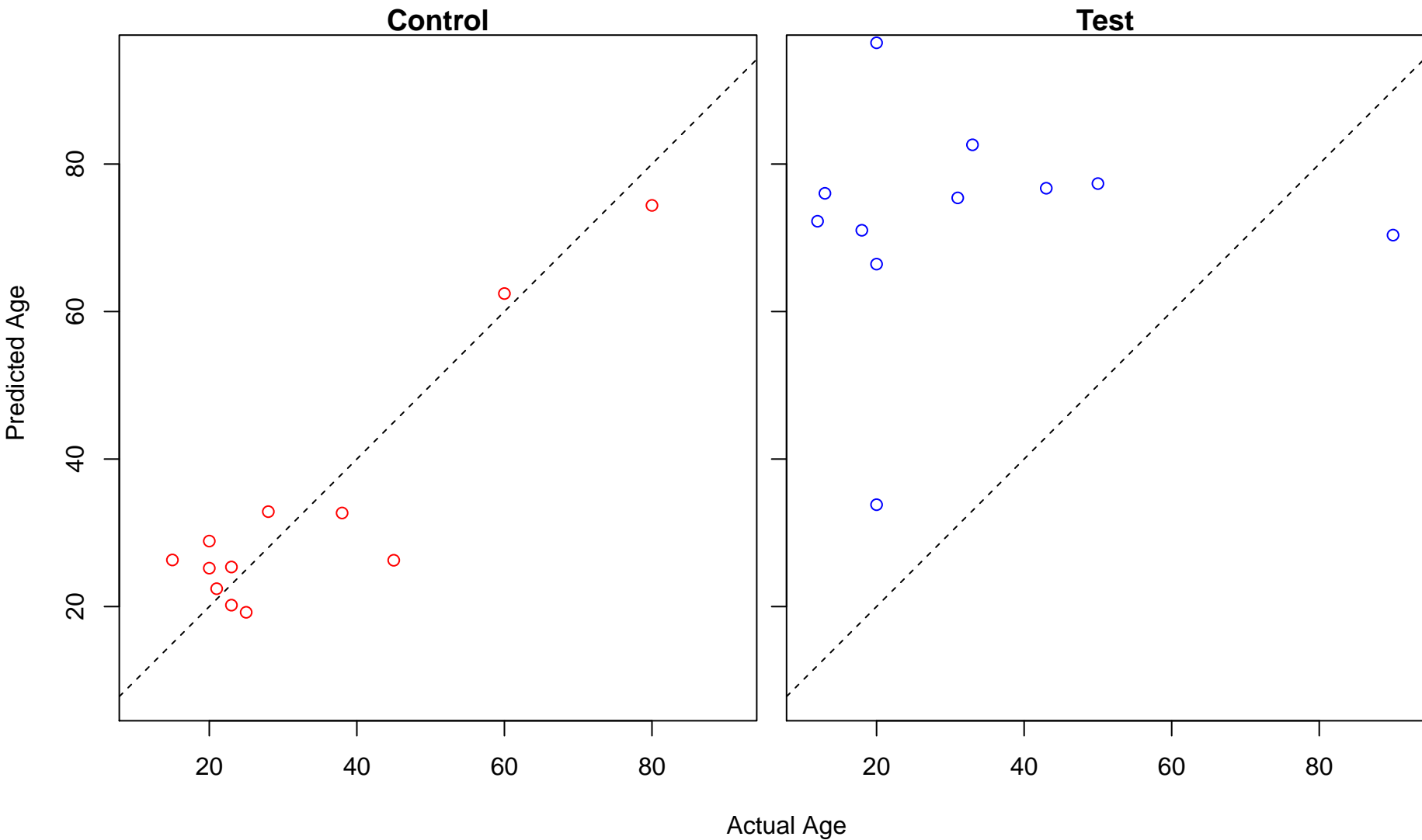
lymphocyte differentiation (Score: 17.528430)



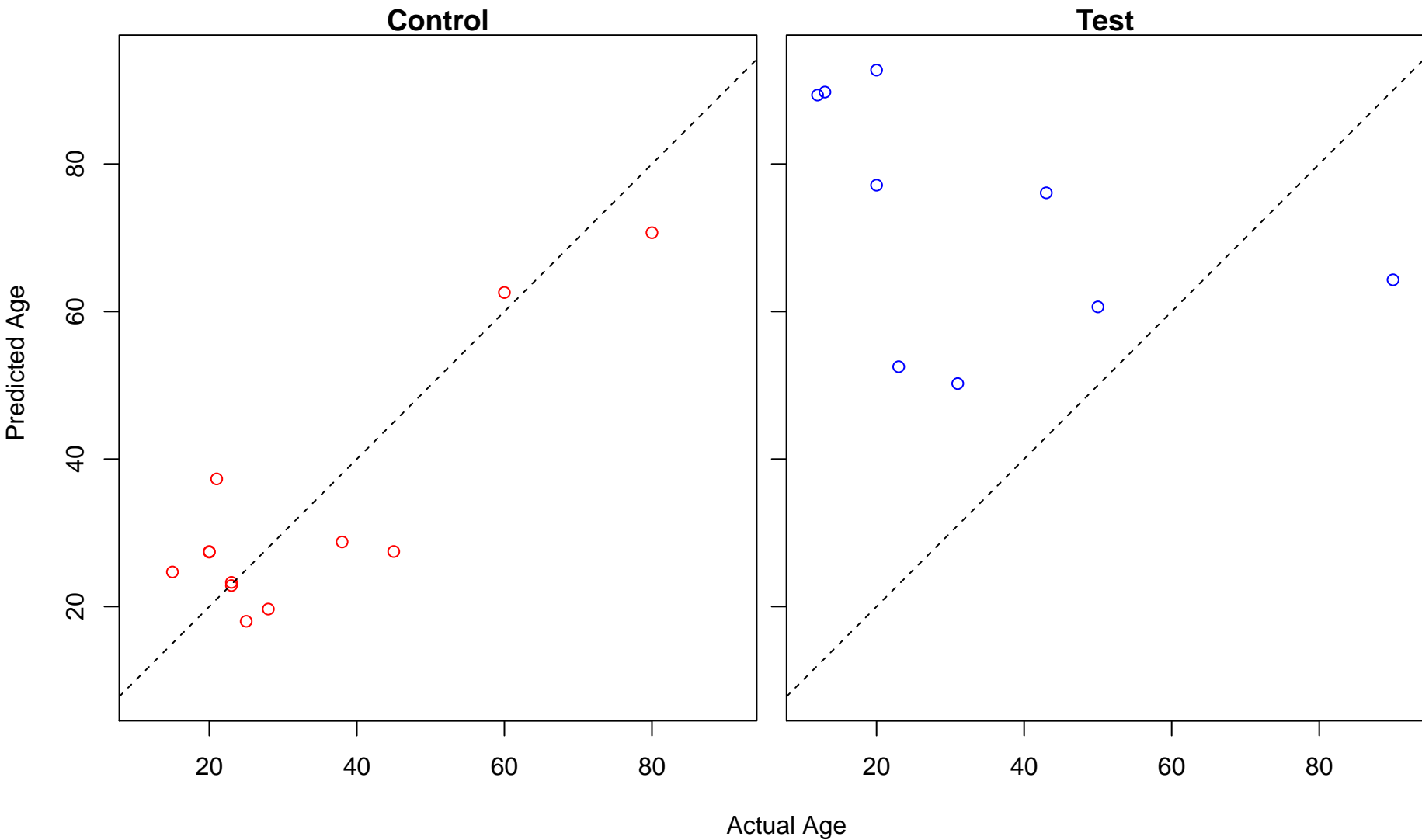
defense response to virus (Score: 17.508107)



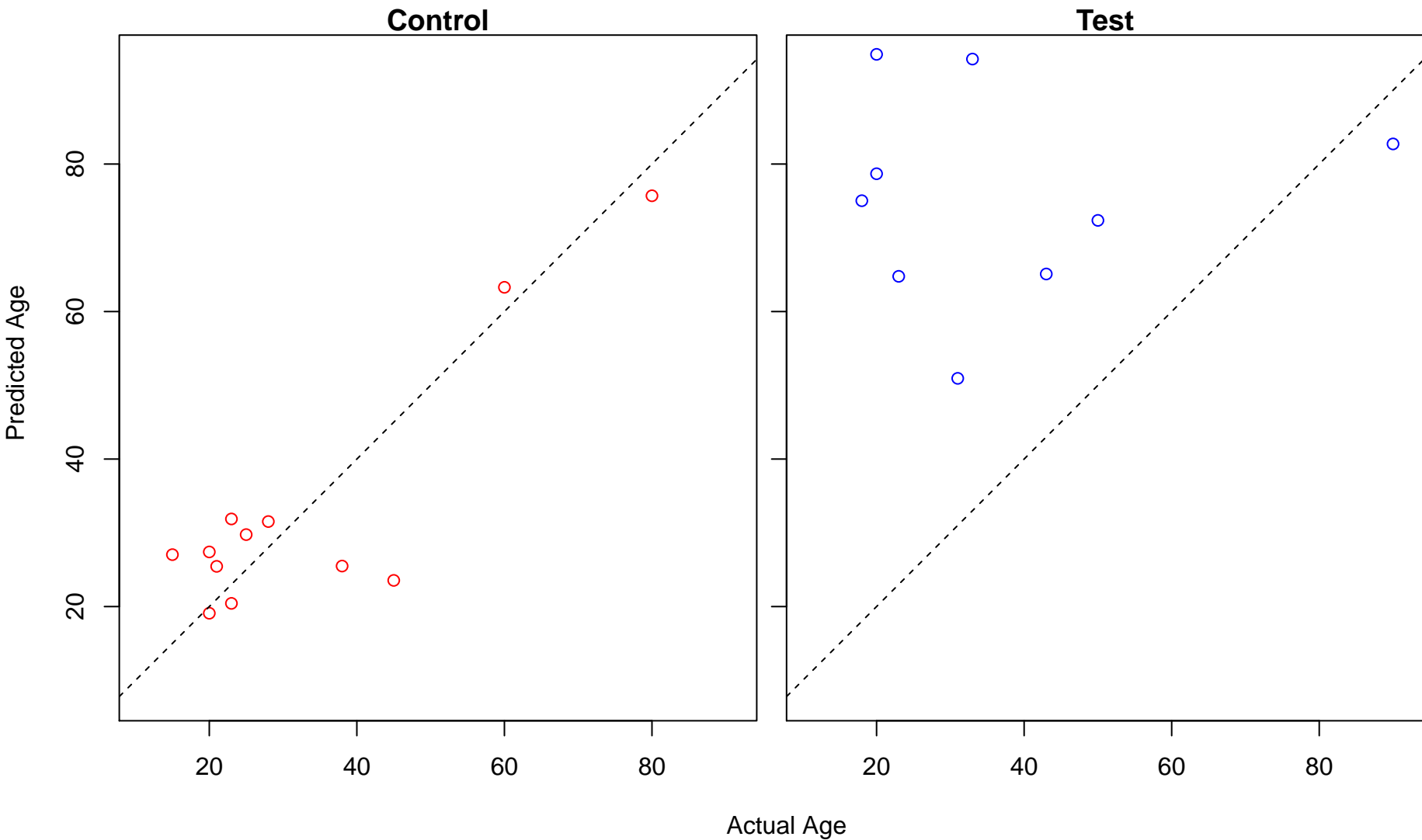
exit from mitosis (Score: 17.408387)



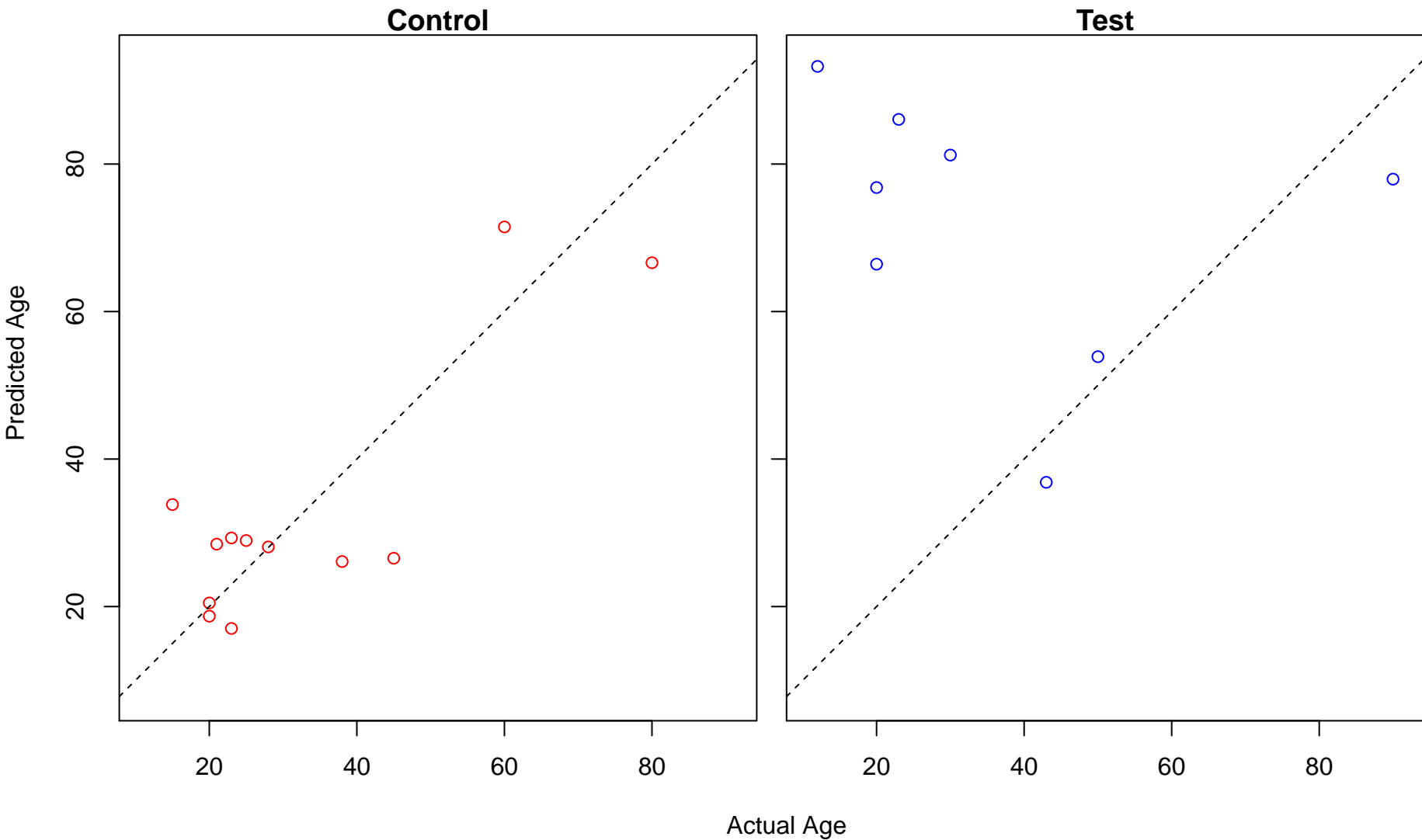
myotube cell development (Score: 17.387945)



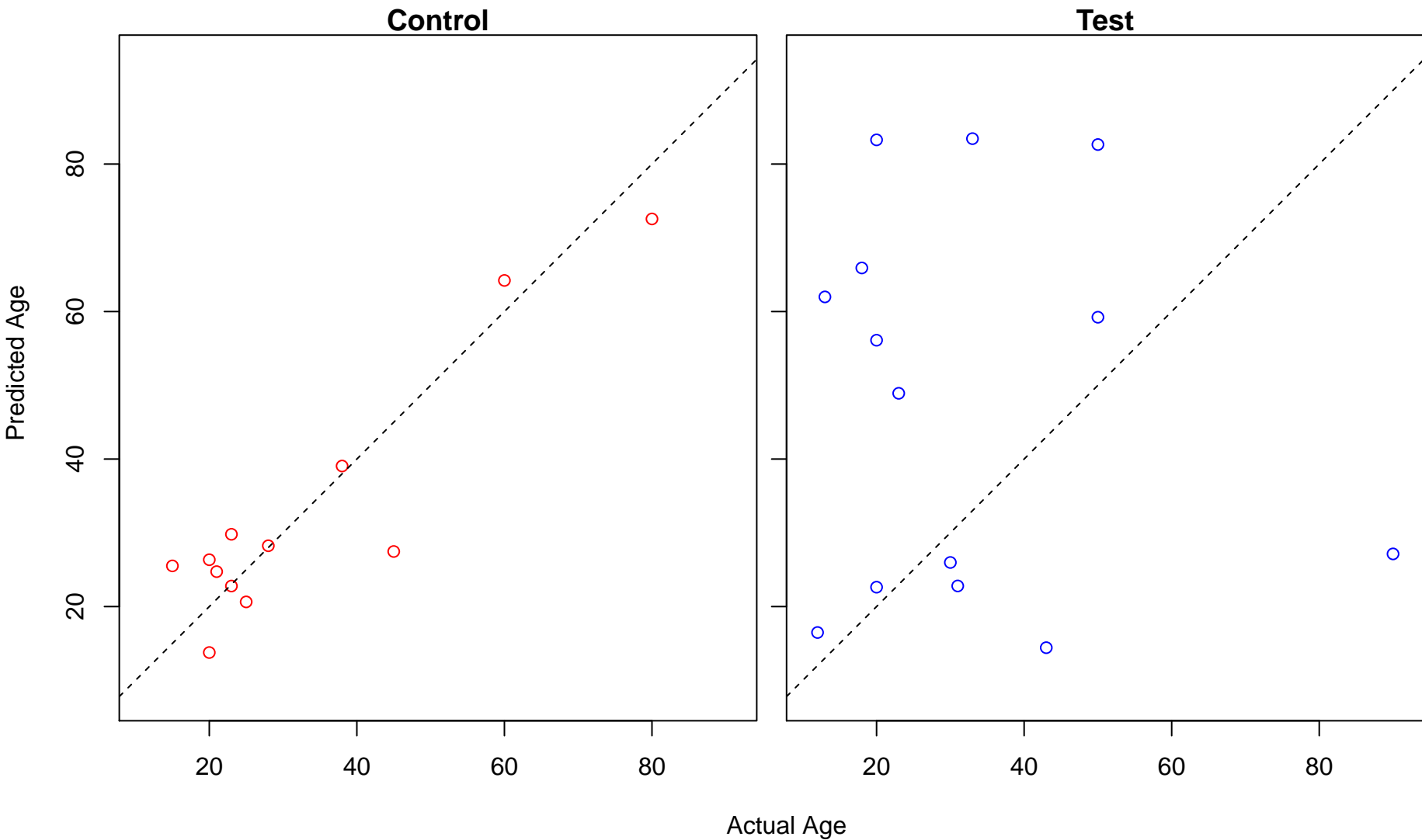
outflow tract morphogenesis (Score: 17.371943)



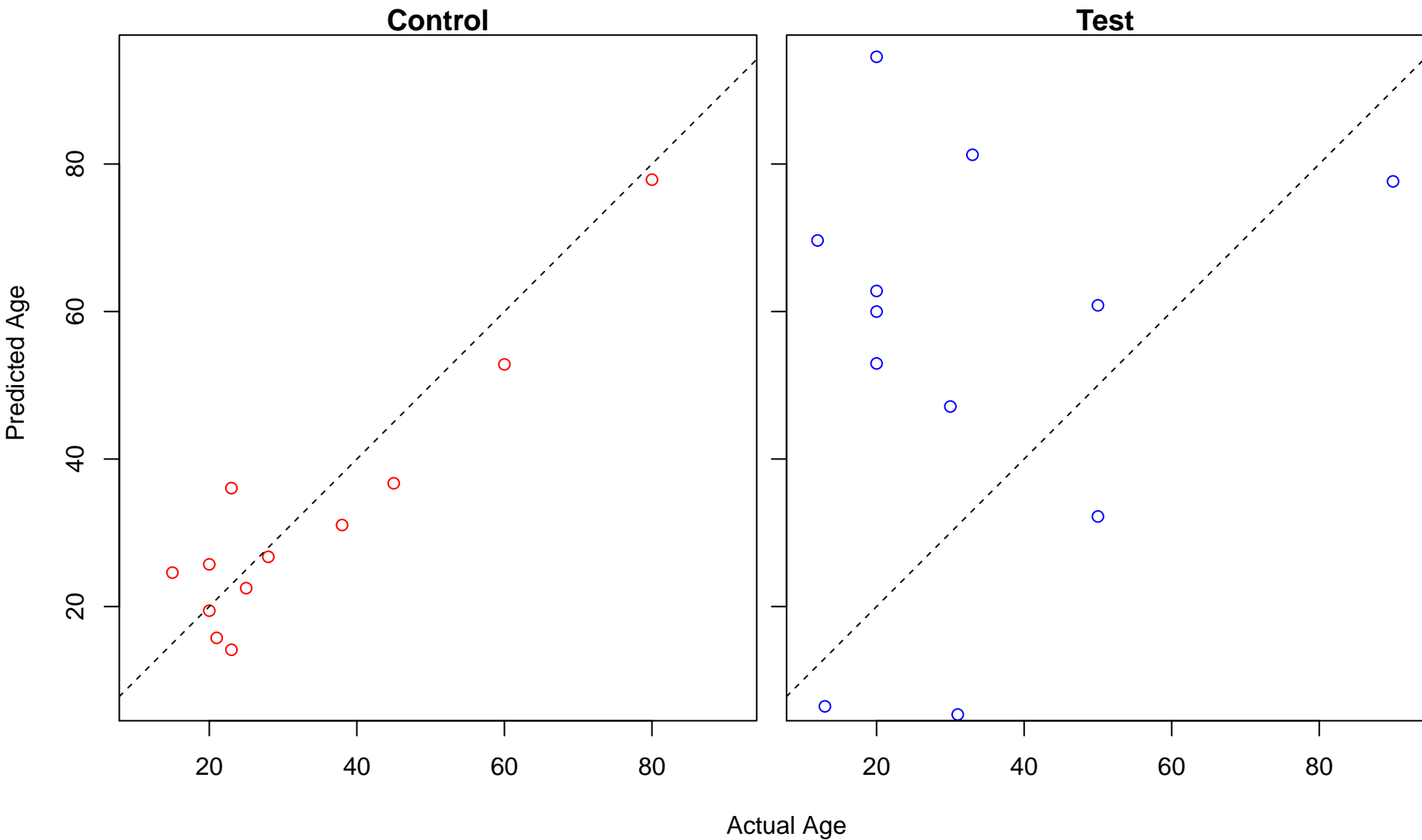
ovarian follicle development (Score: 17.359843)



regulation of calcium ion transport (Score: 17.290554)

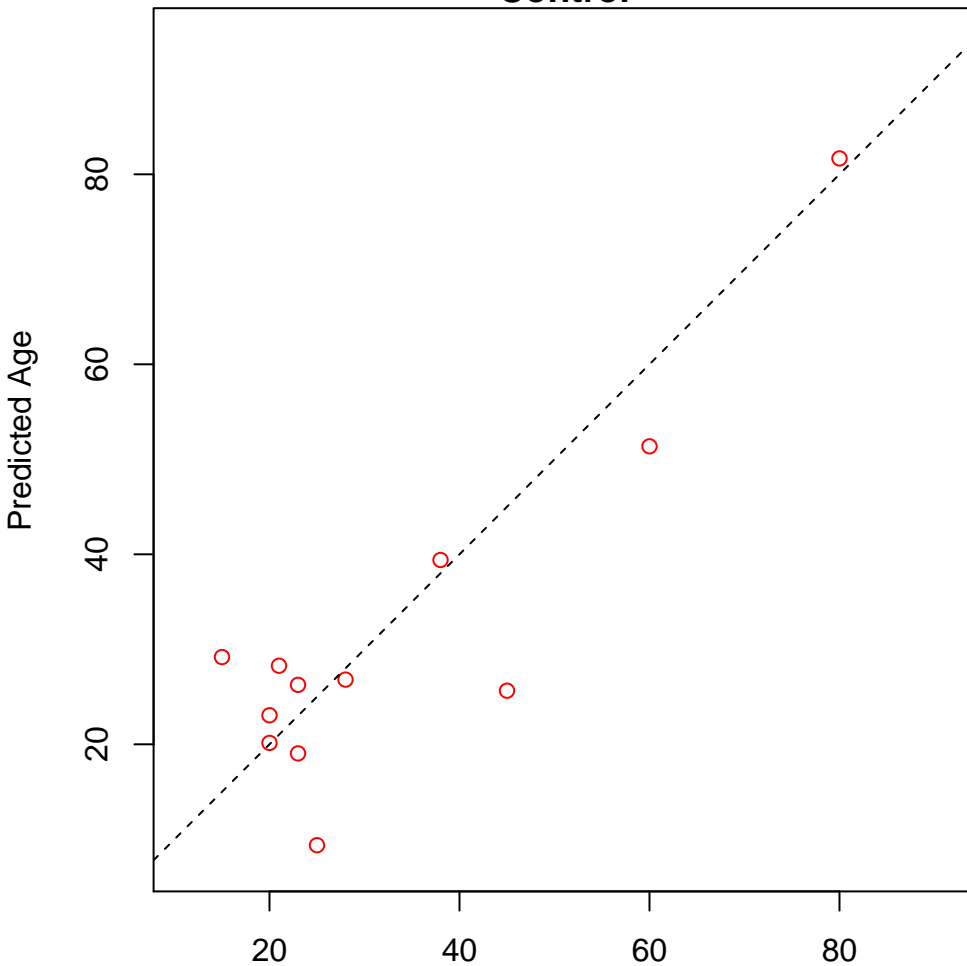


production of siRNA involved in RNA interference (Score: 17.279336)

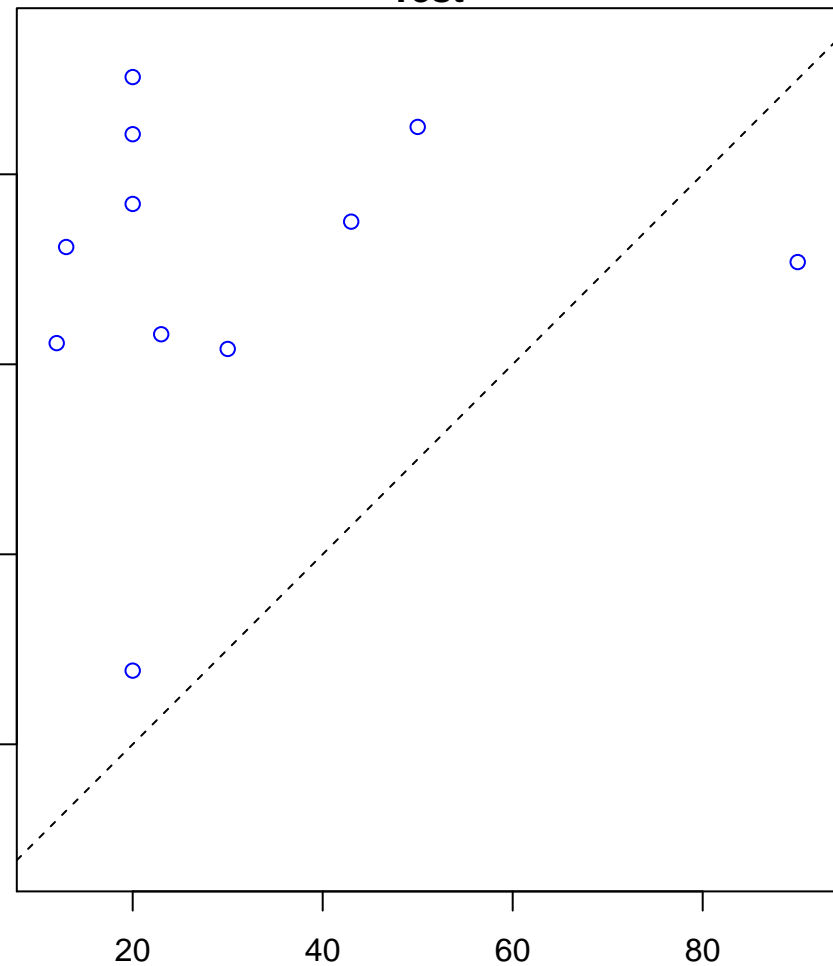


microtubule-based movement (Score: 17.274839)

Control

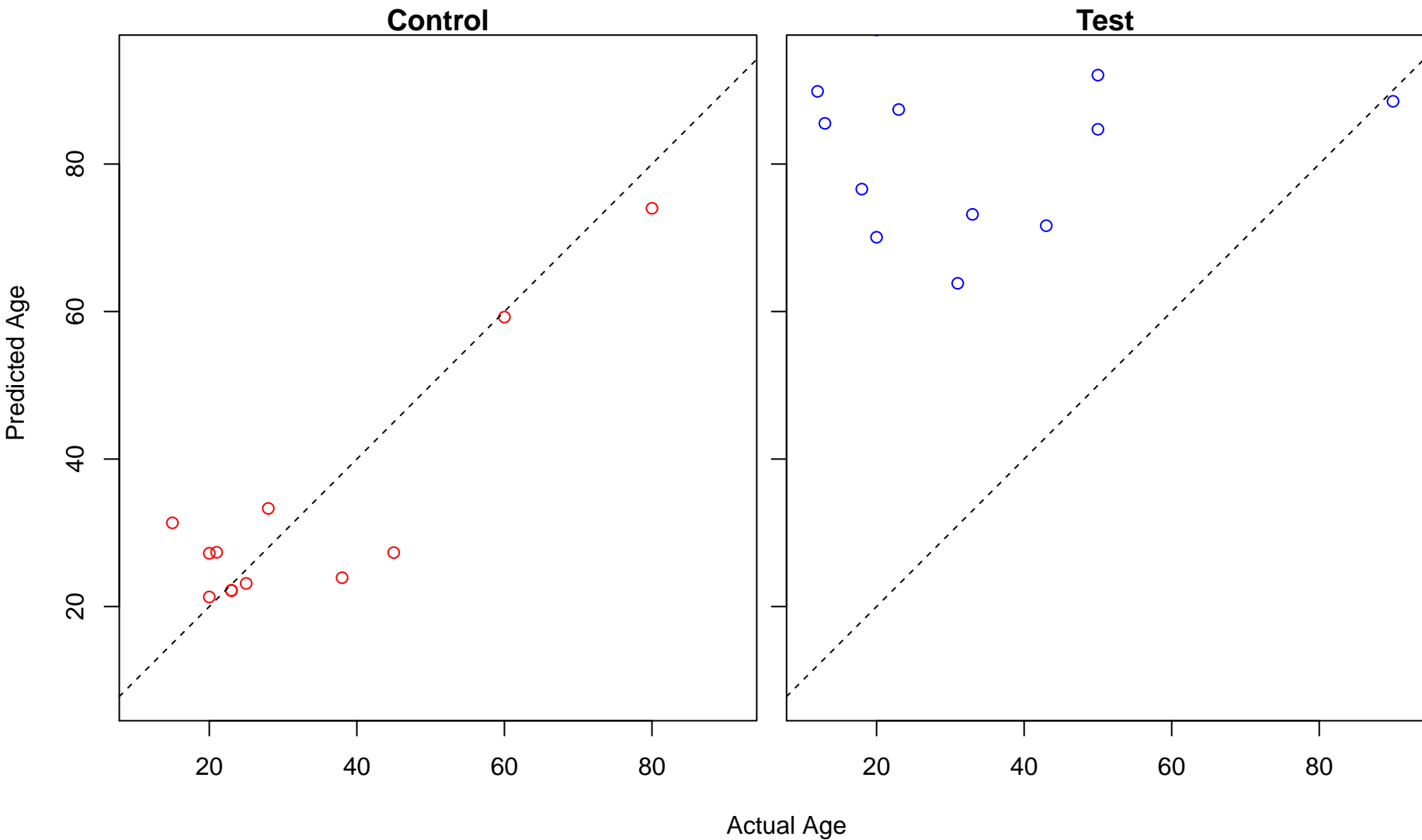


Test

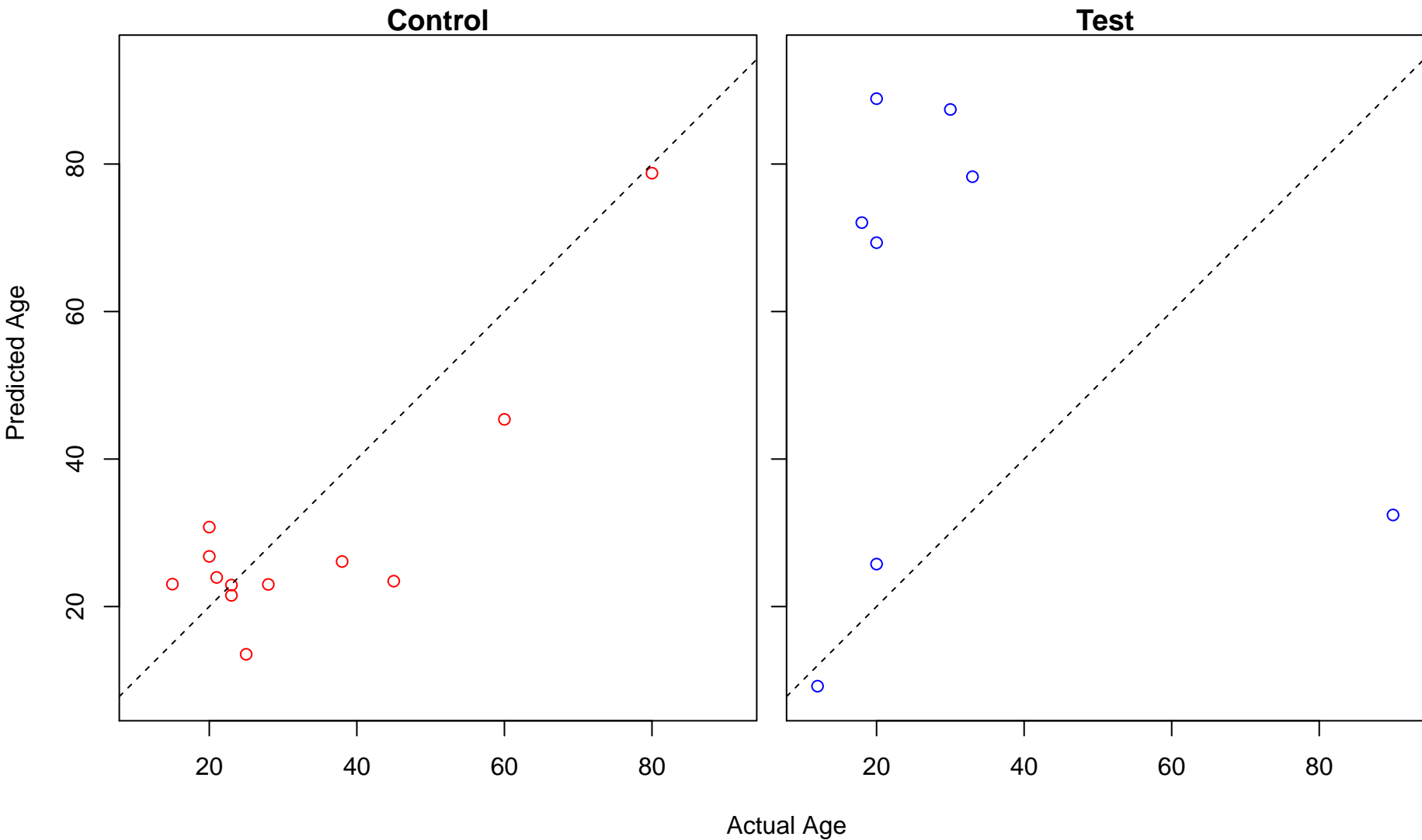


Actual Age

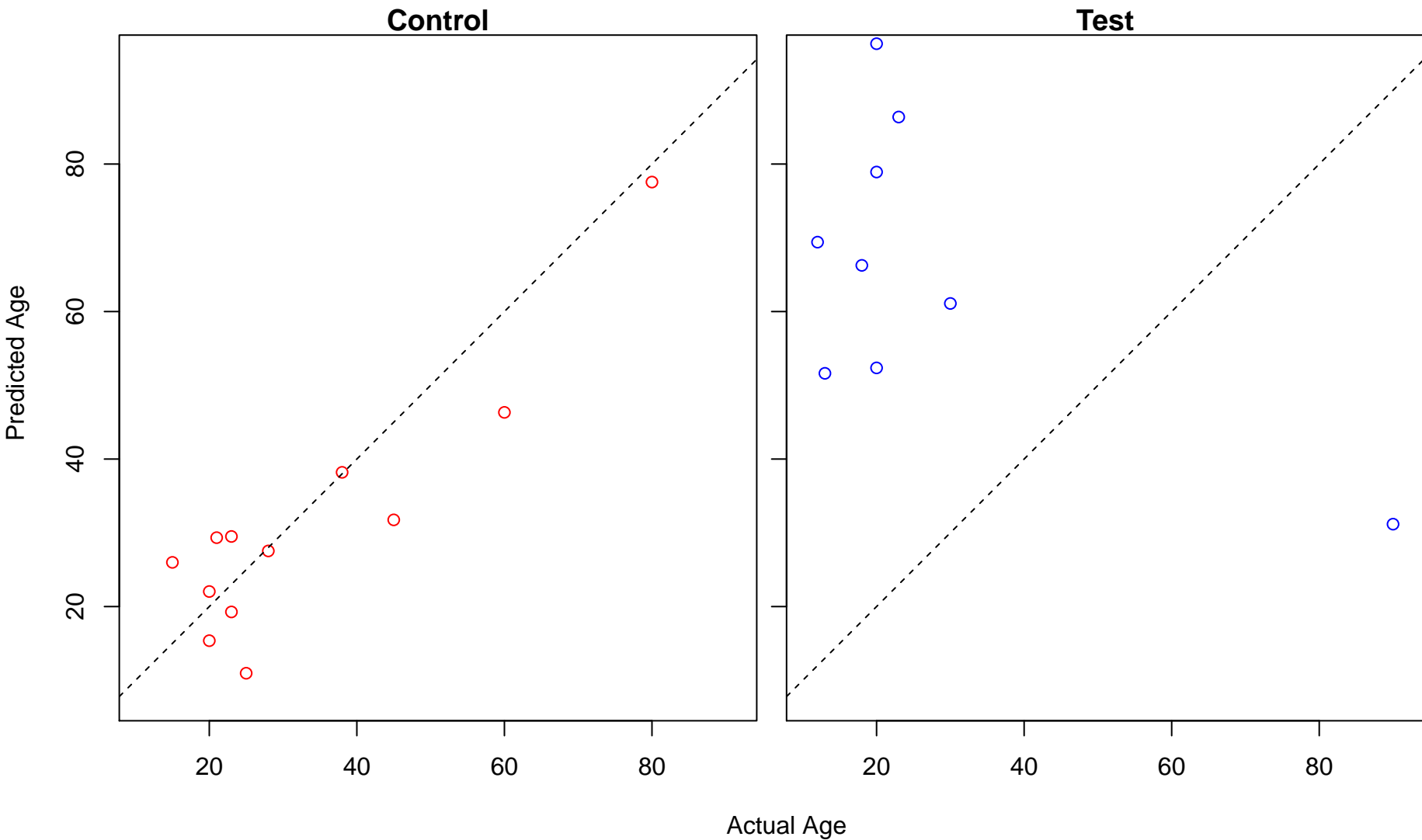
negative regulation of tumor necrosis factor production (Score: 17.267244)



positive regulation of apoptotic signaling pathway (Score: 17.208038)

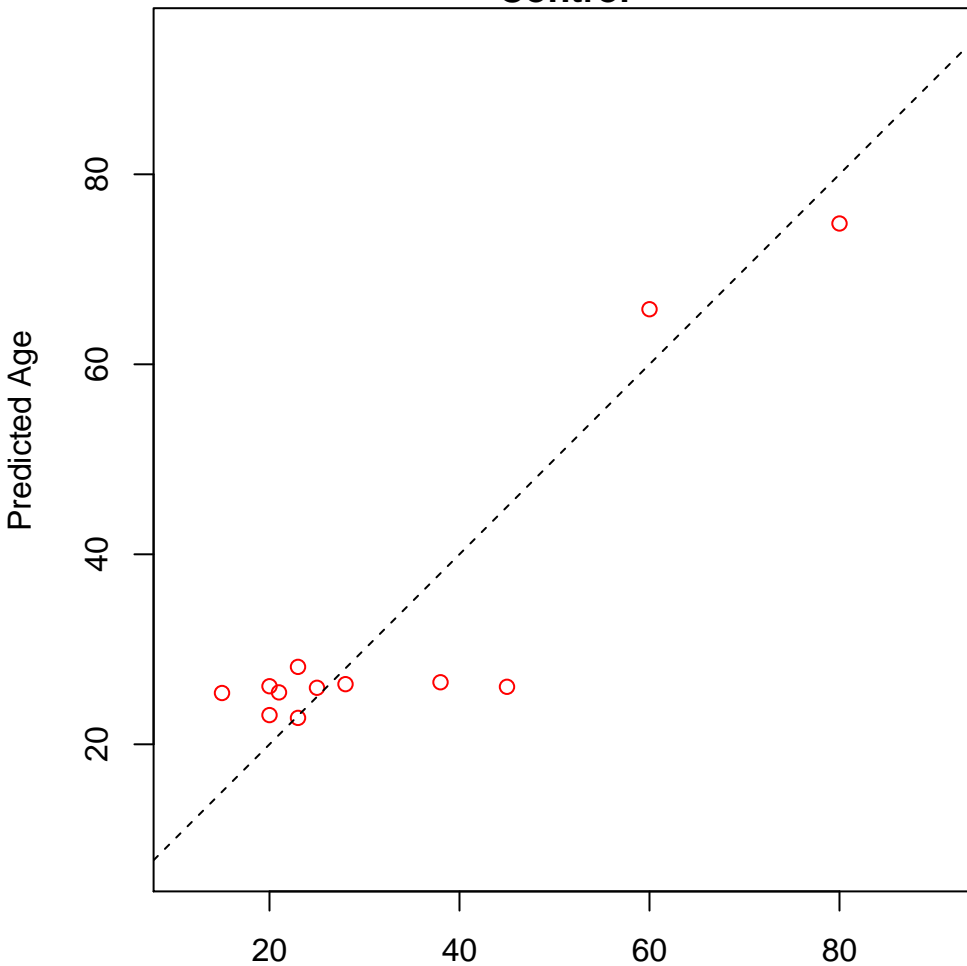


proteoglycan metabolic process (Score: 17.196140)

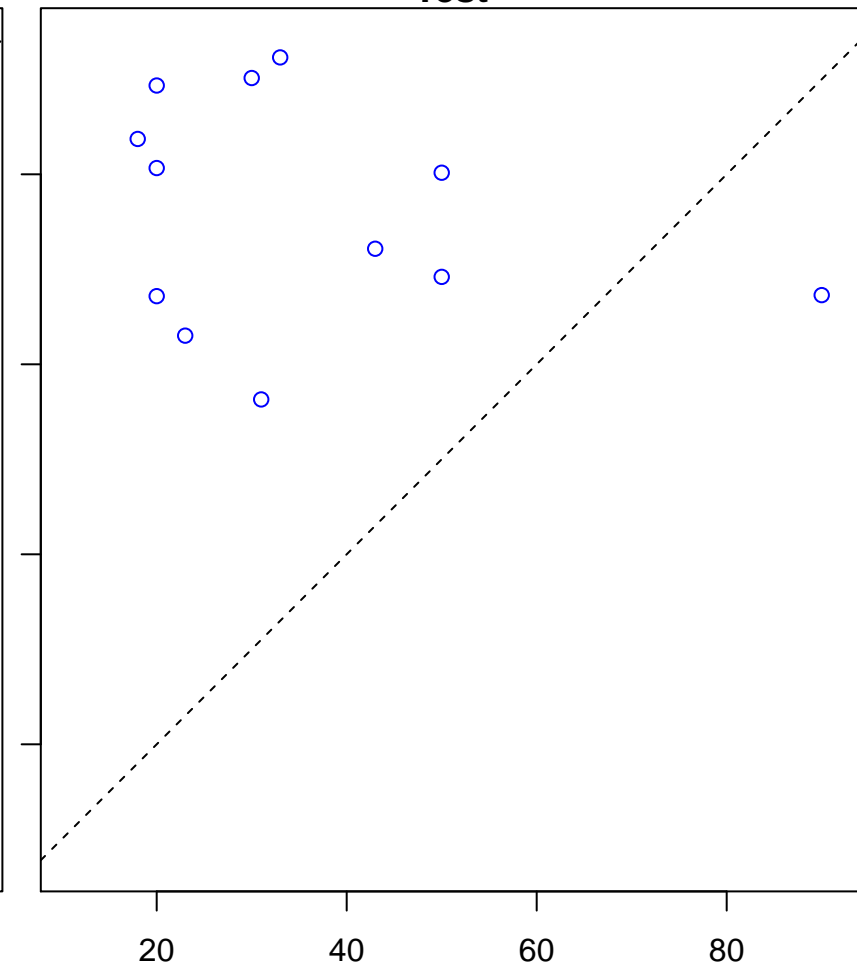


endothelial cell fate commitment (Score: 17.189966)

Control

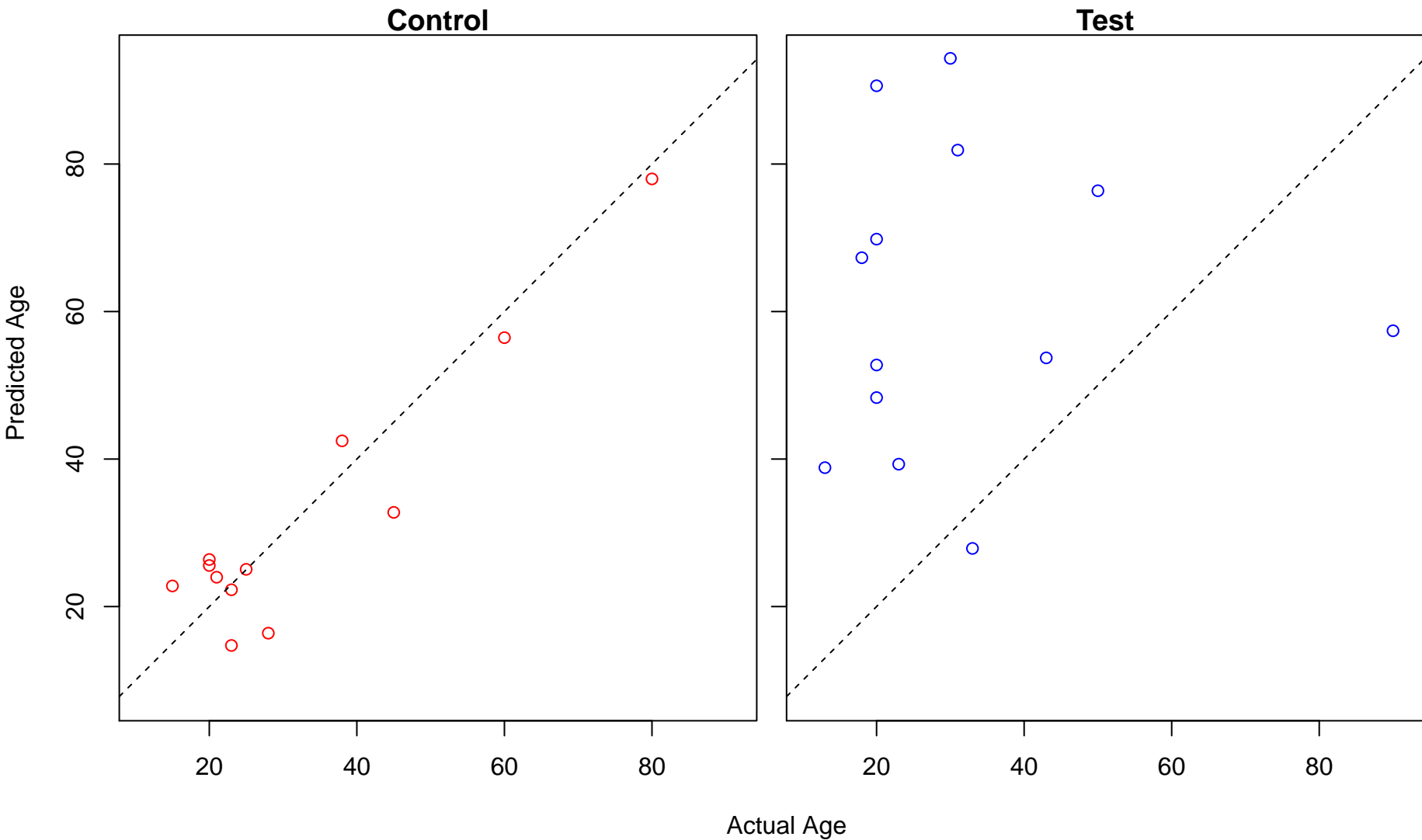


Test

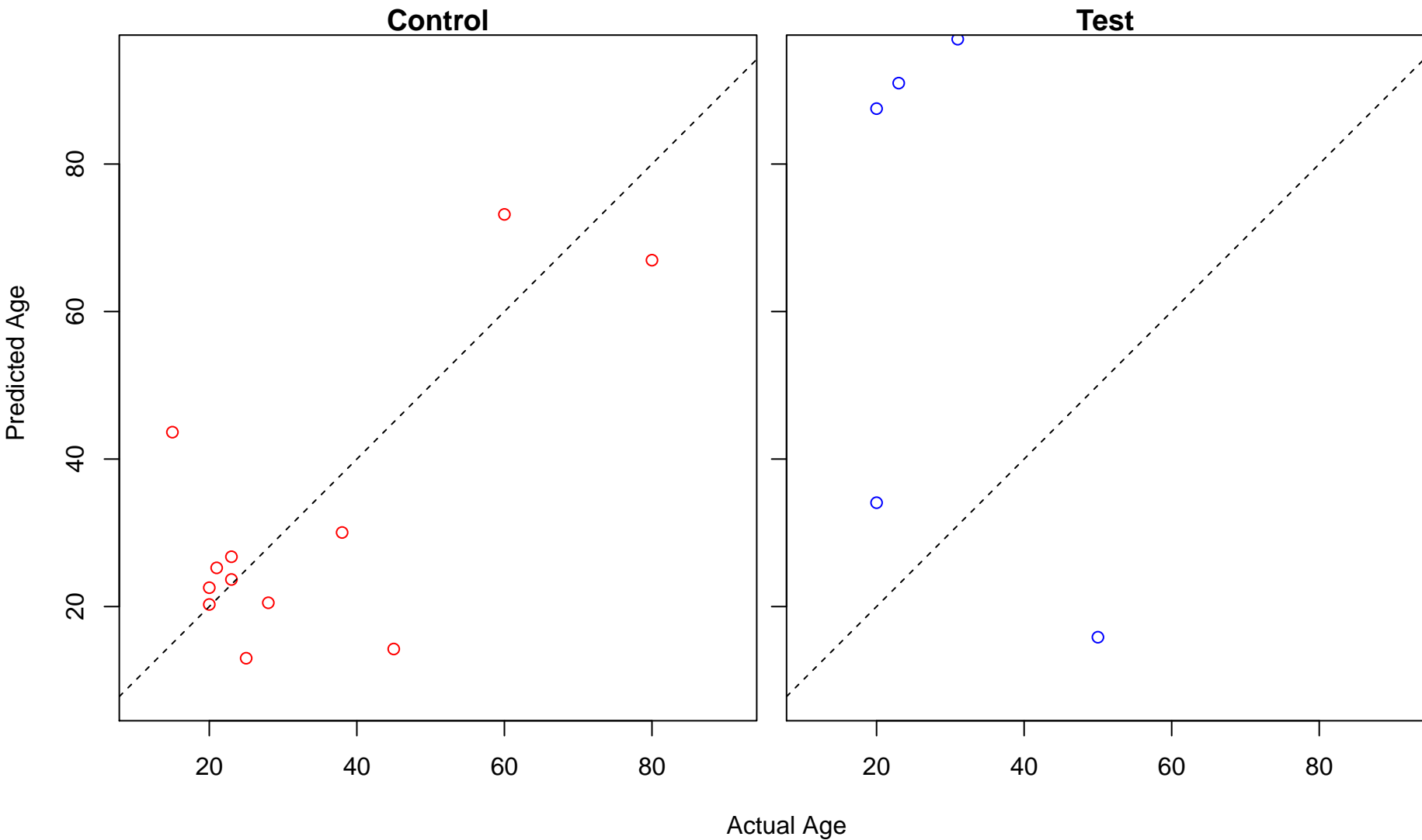


Actual Age

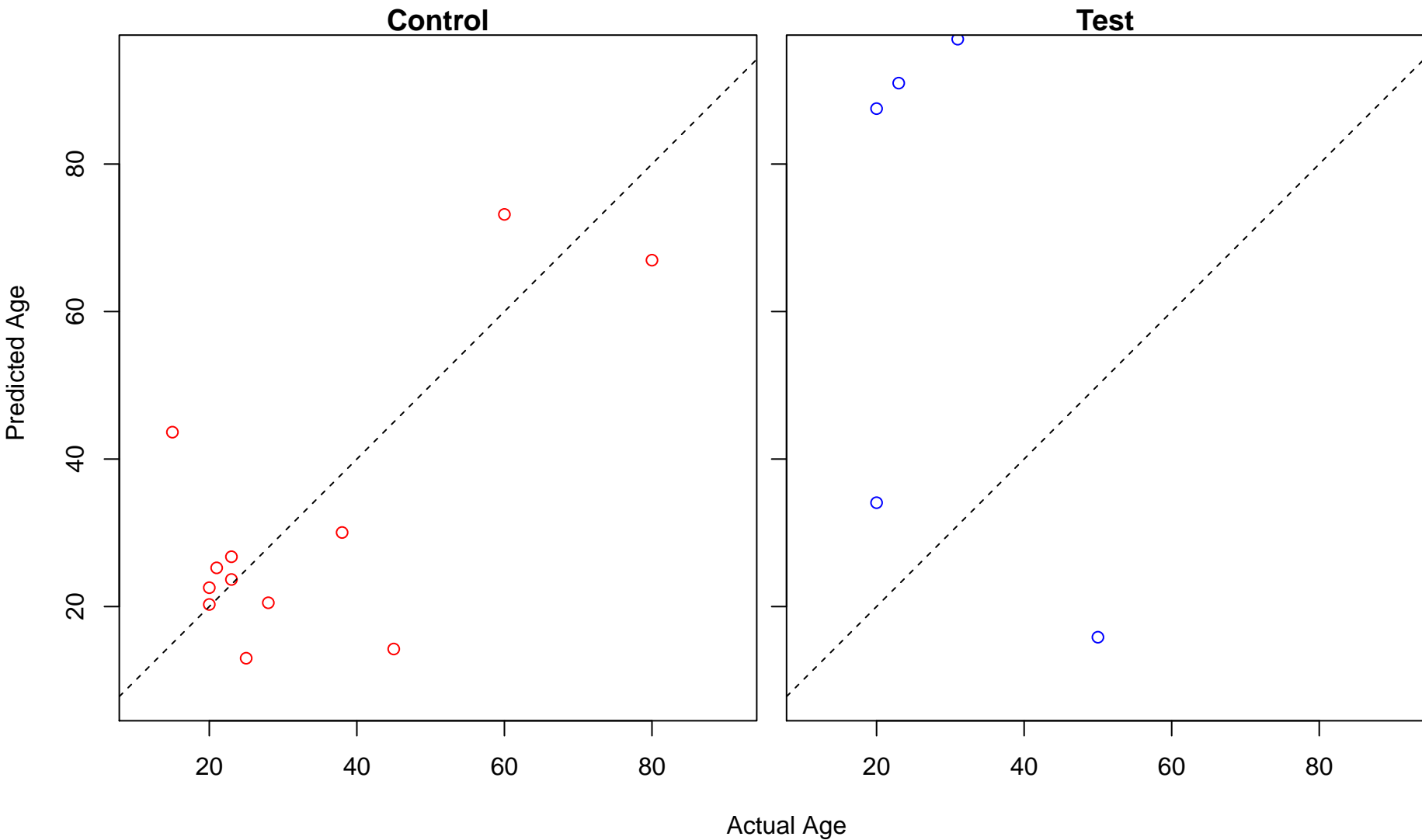
cellular response to ammonium ion (Score: 17.183431)



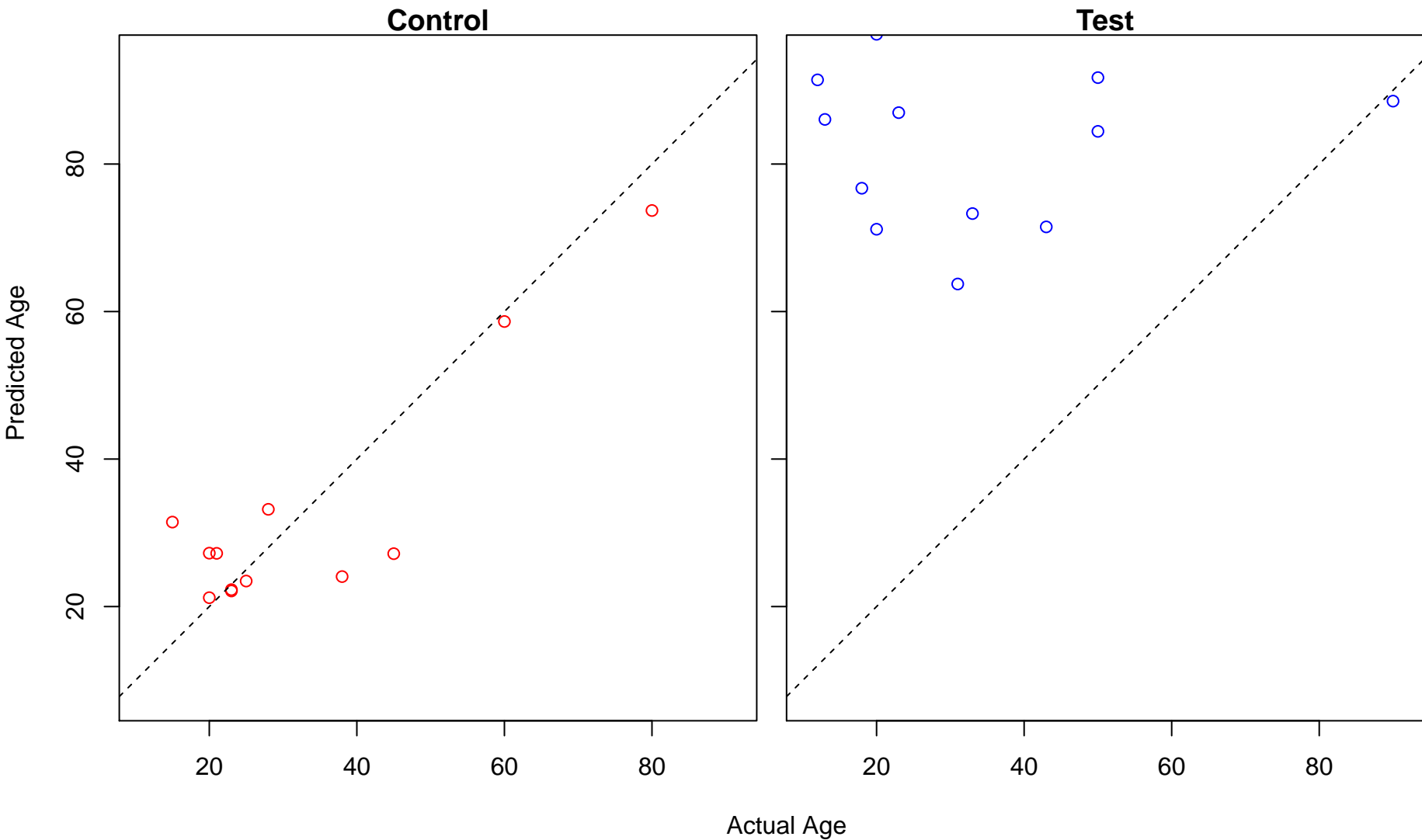
negative regulation of cellular response to oxidative stress (Score: 17.178321)



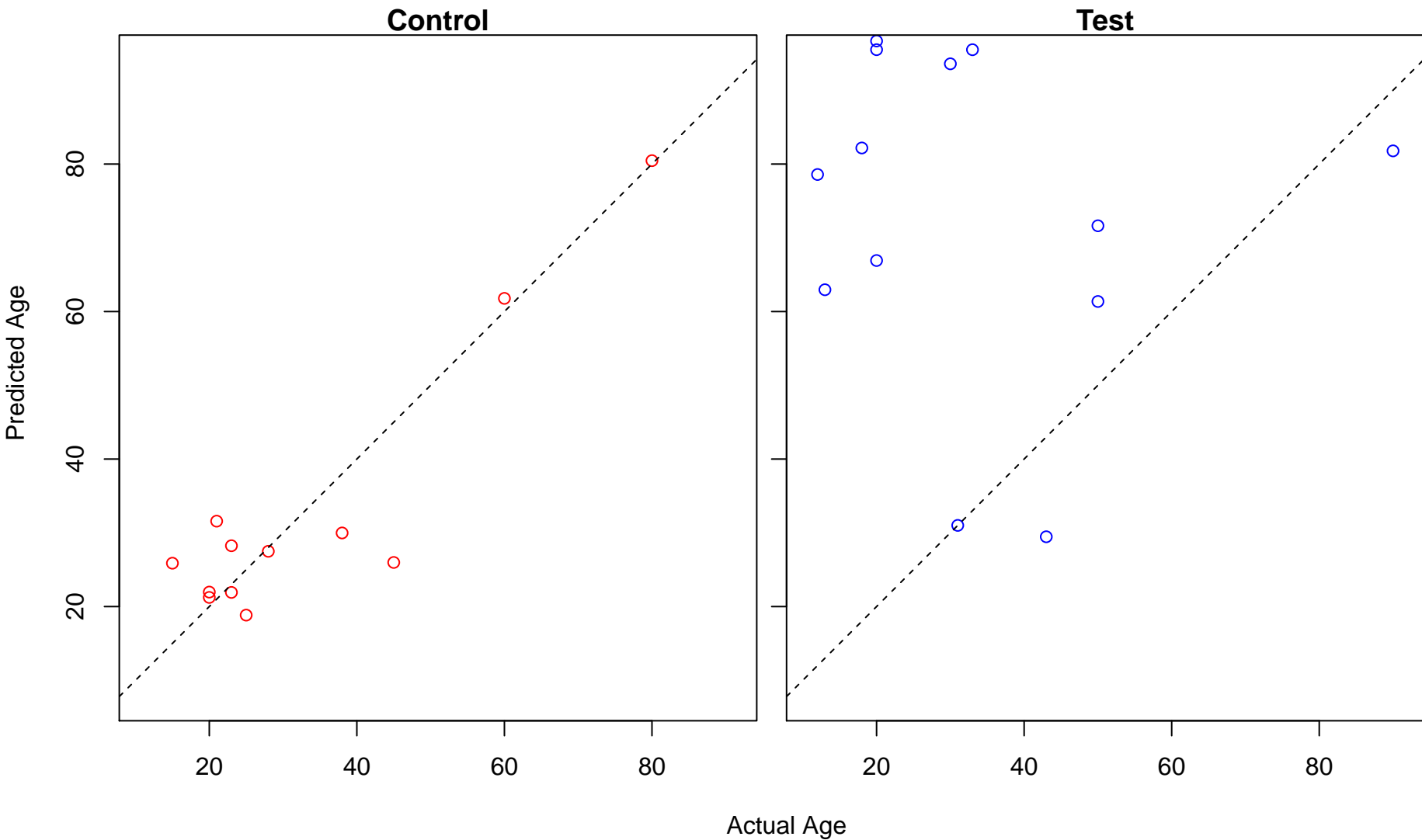
negative regulation of response to oxidative stress (Score: 17.178321)



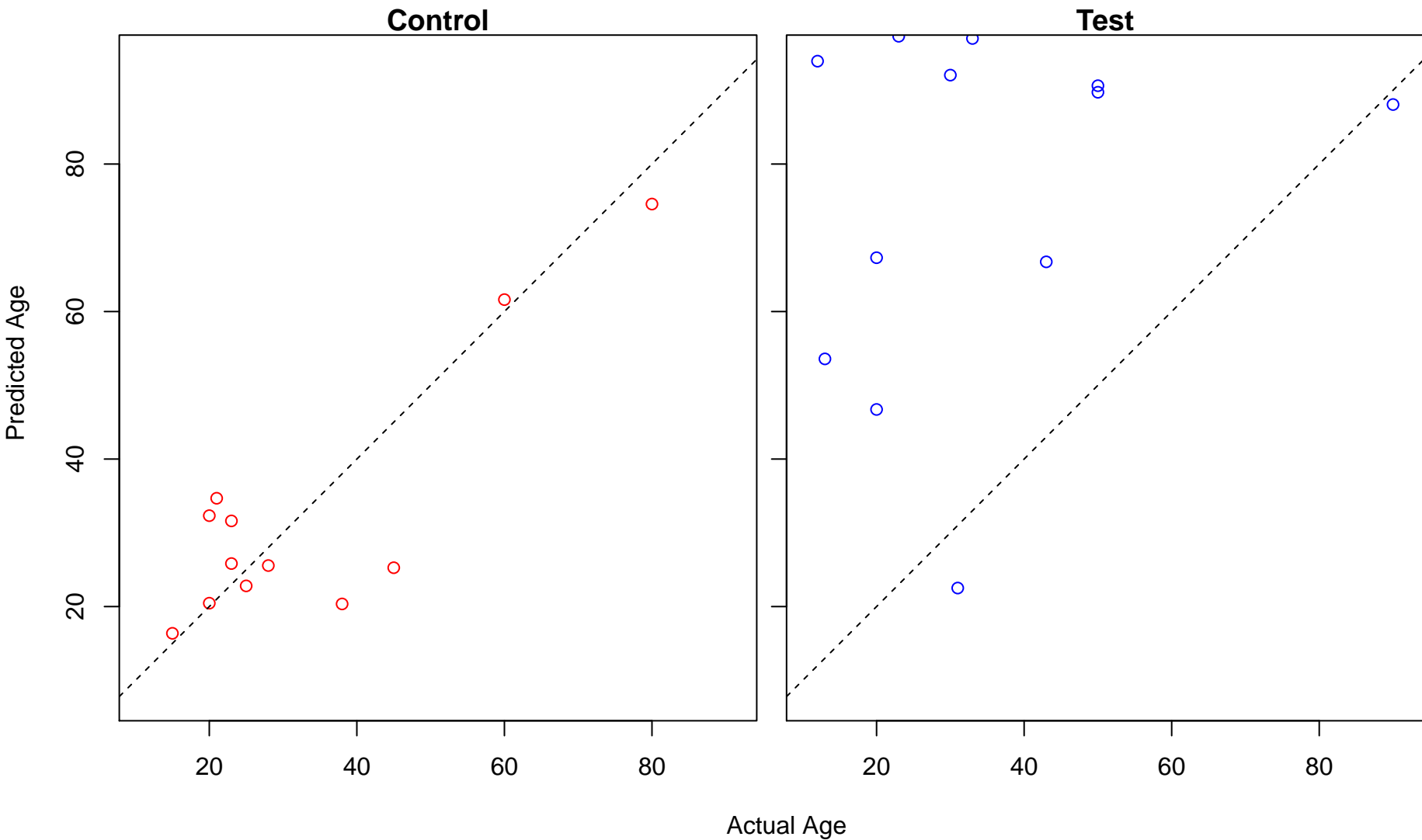
negative regulation of tumor necrosis factor superfamily cytokine production (Score: 17.175505)



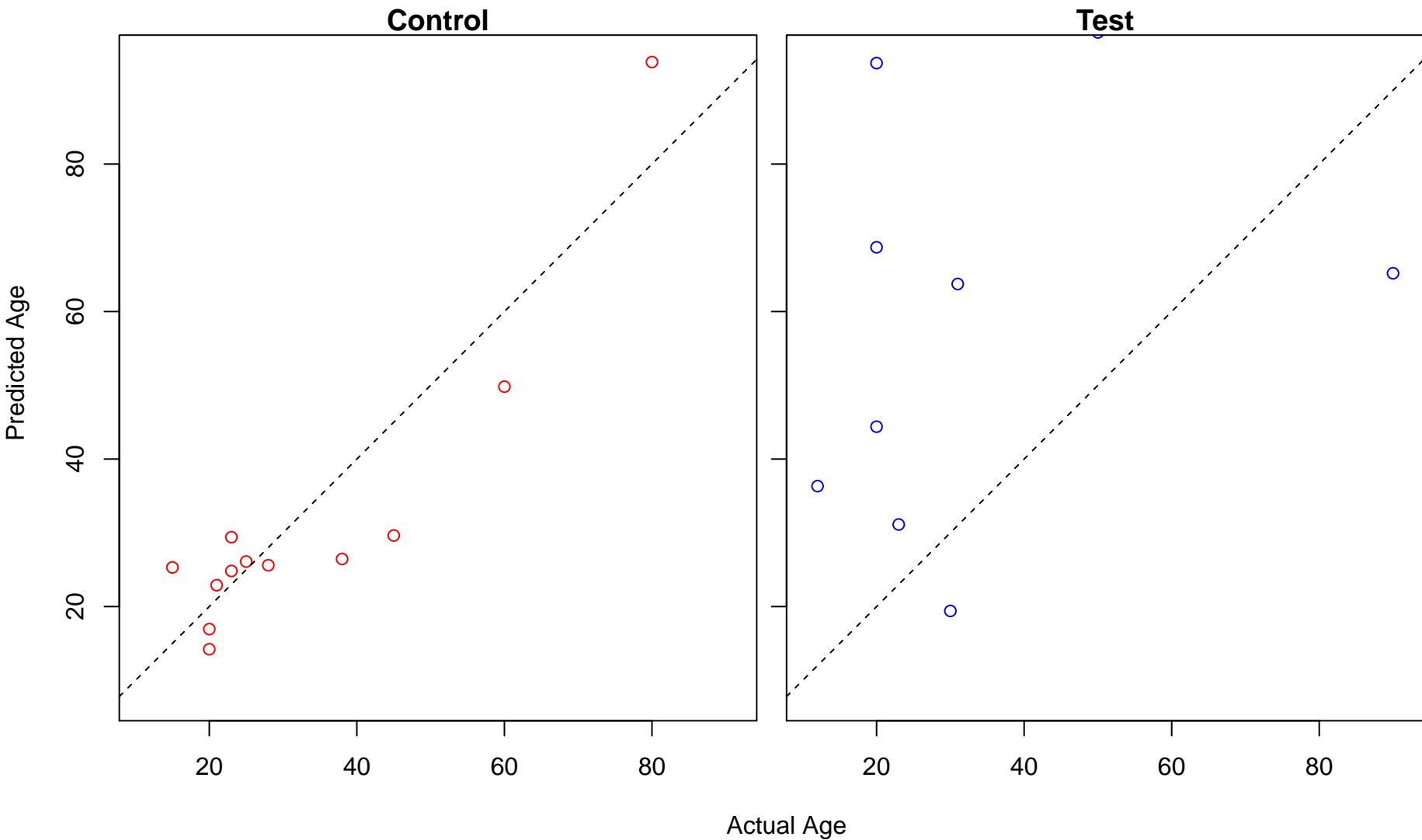
regulation of cellular component size (Score: 17.161499)



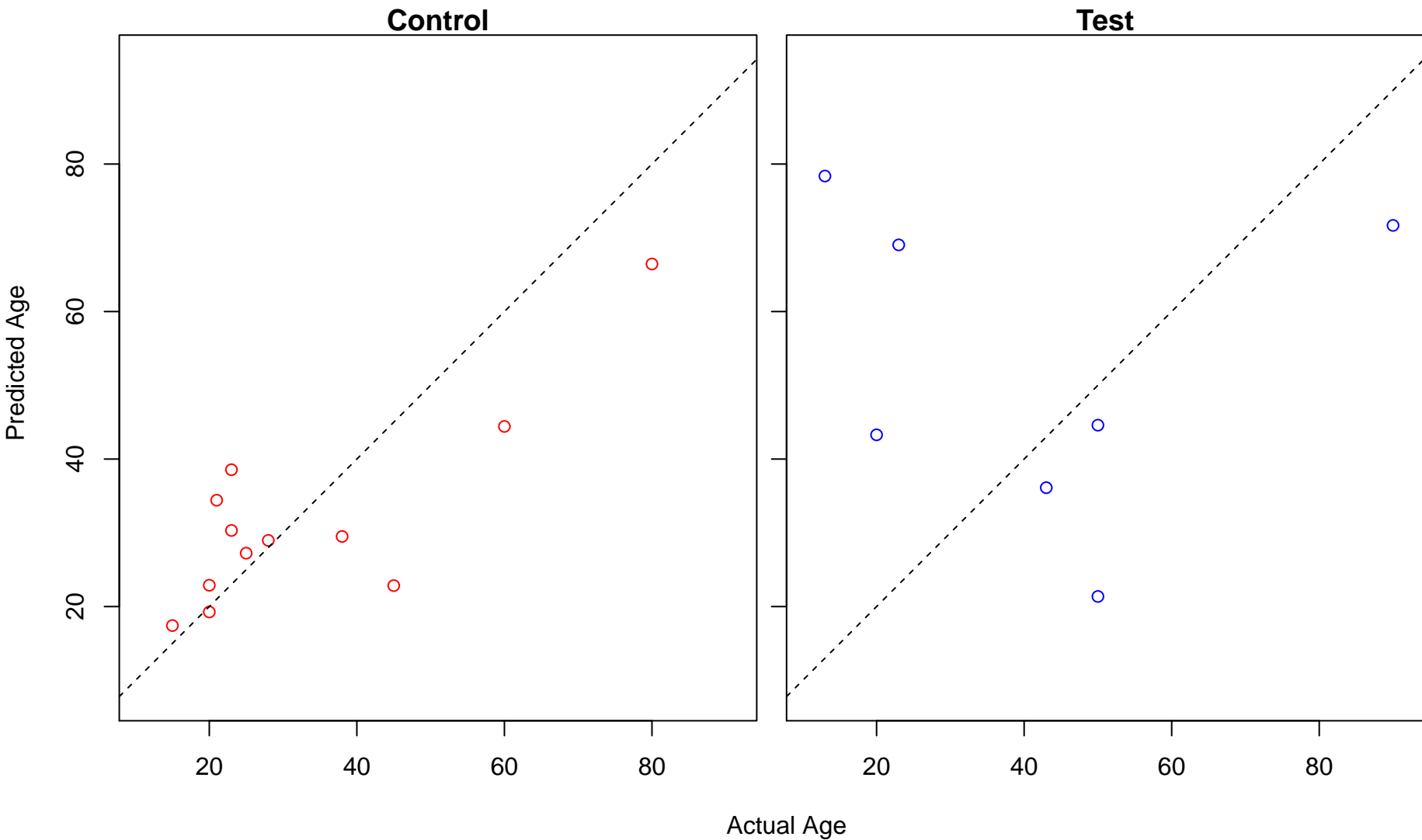
positive regulation of G-protein coupled receptor protein signaling pathway (Score: 17.147447)



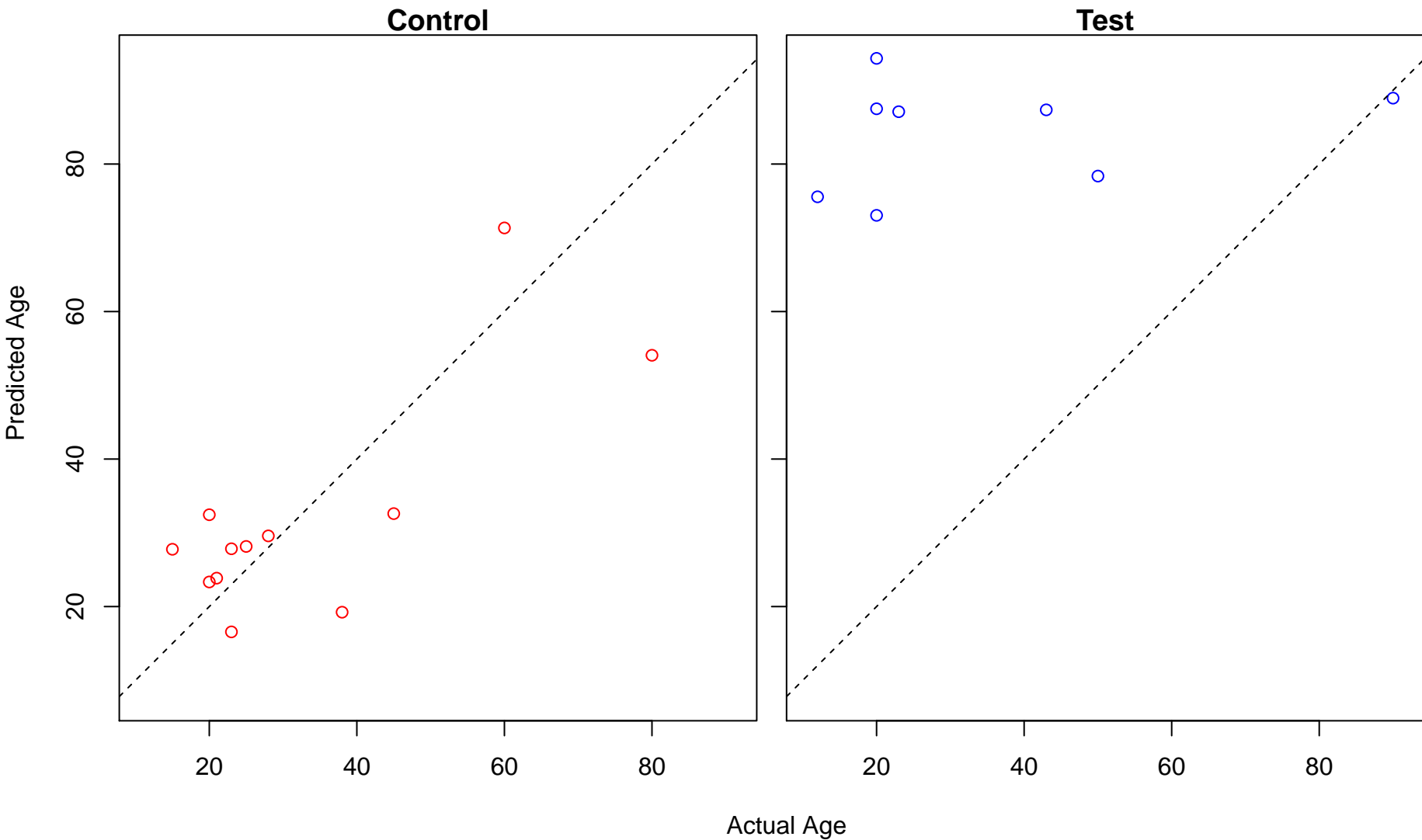
axon extension (Score: 17.124815)



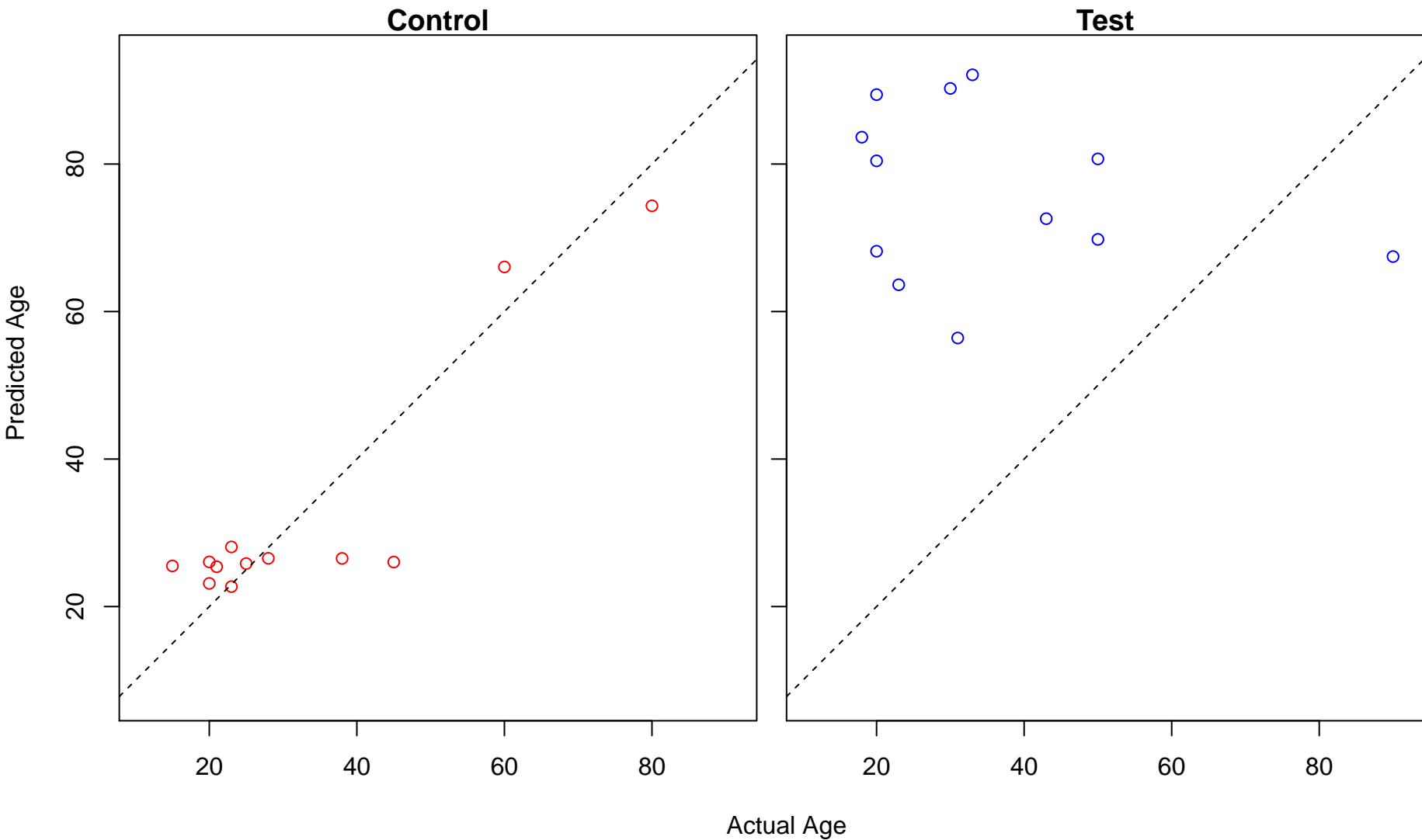
B cell receptor signaling pathway (Score: 17.079059)



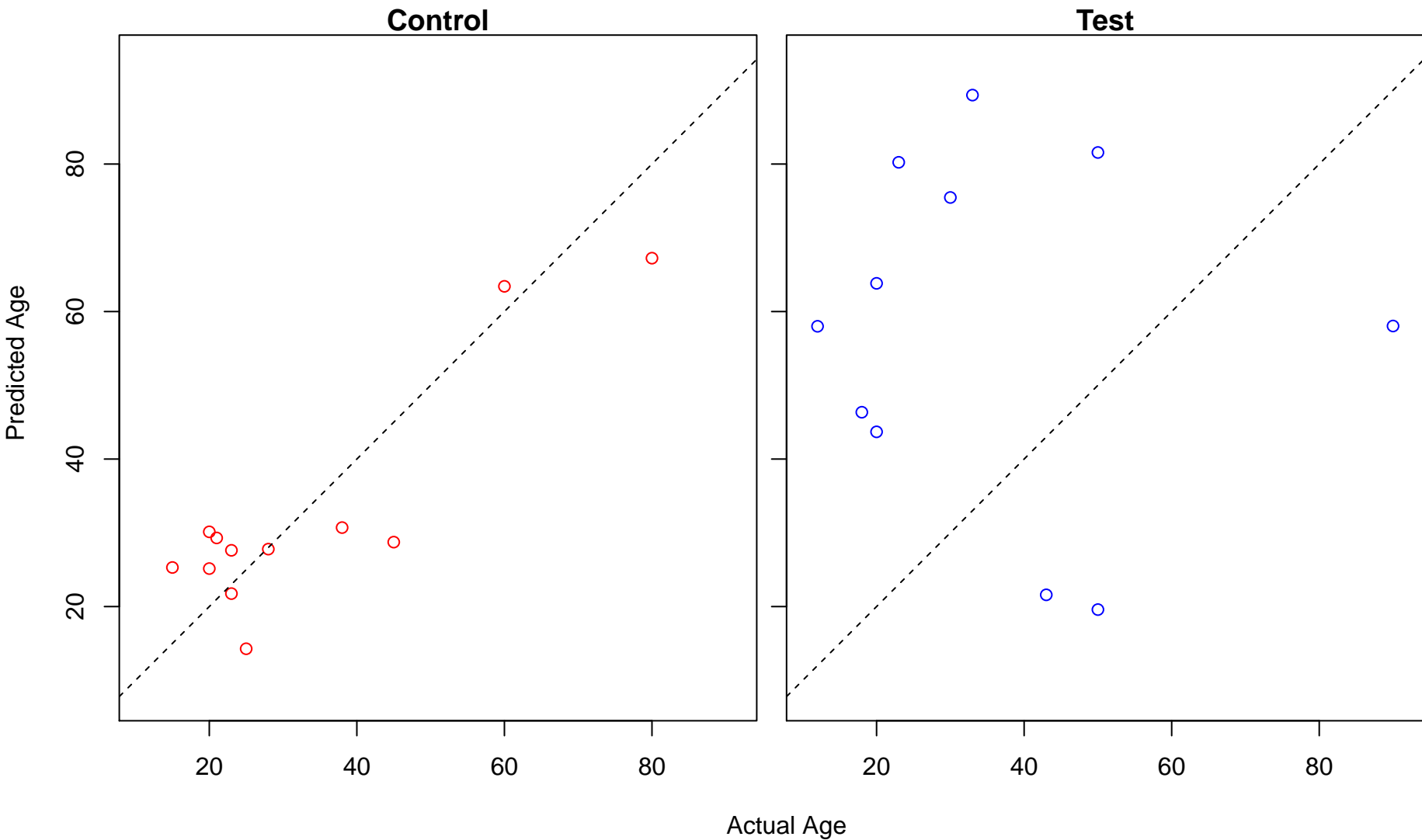
tooth mineralization (Score: 17.058642)



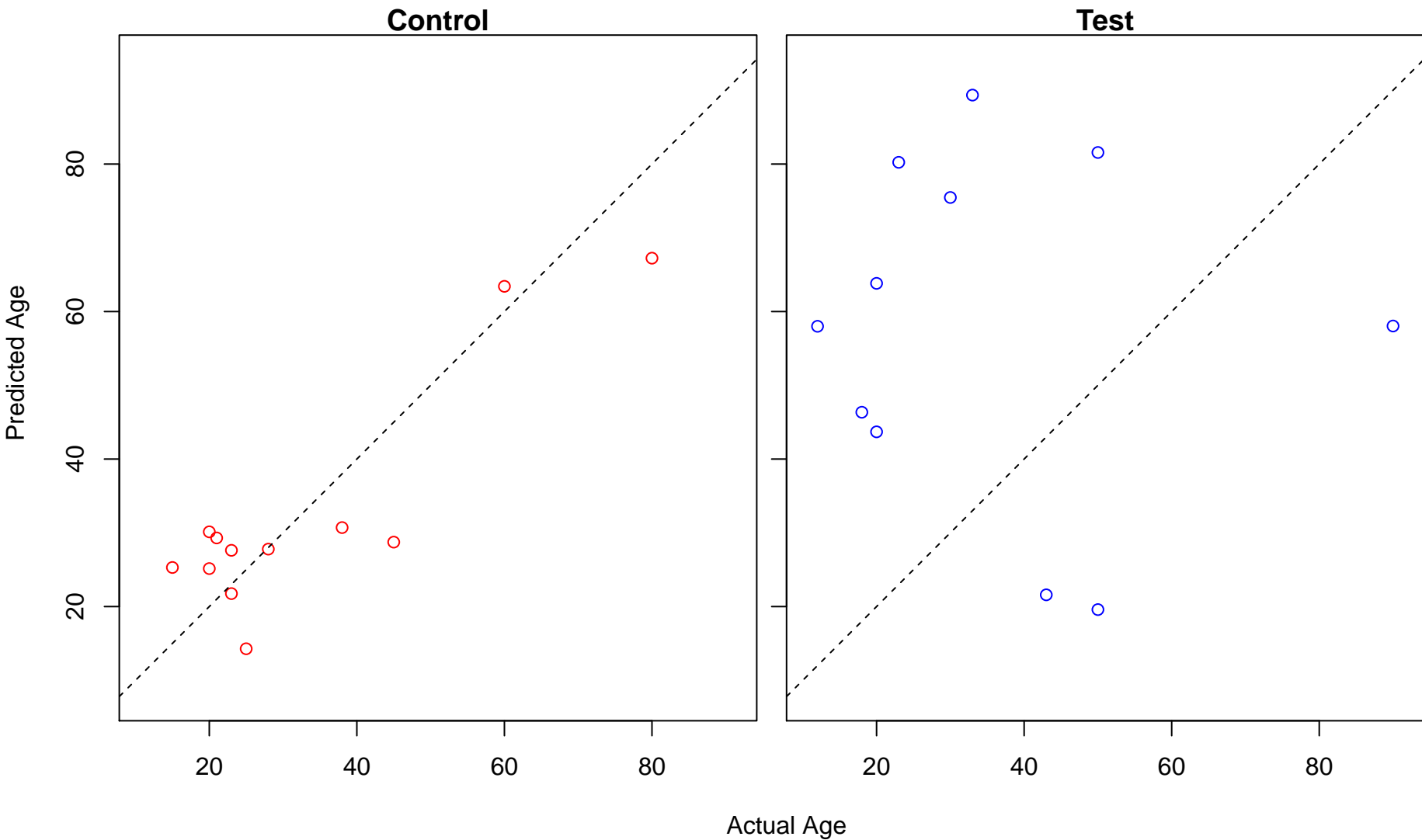
epithelial cell fate commitment (Score: 17.052279)



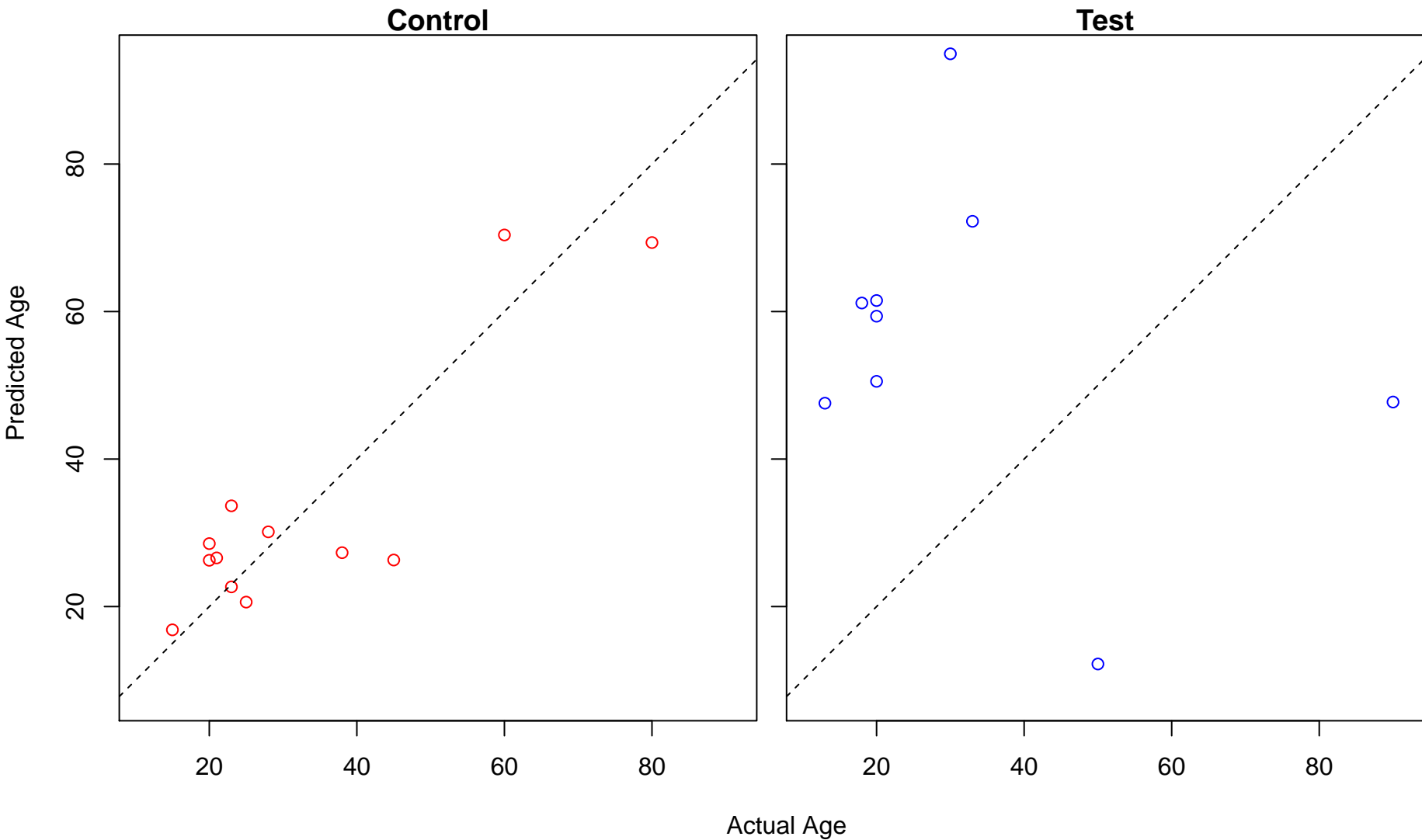
growth hormone receptor signaling pathway (Score: 17.047883)



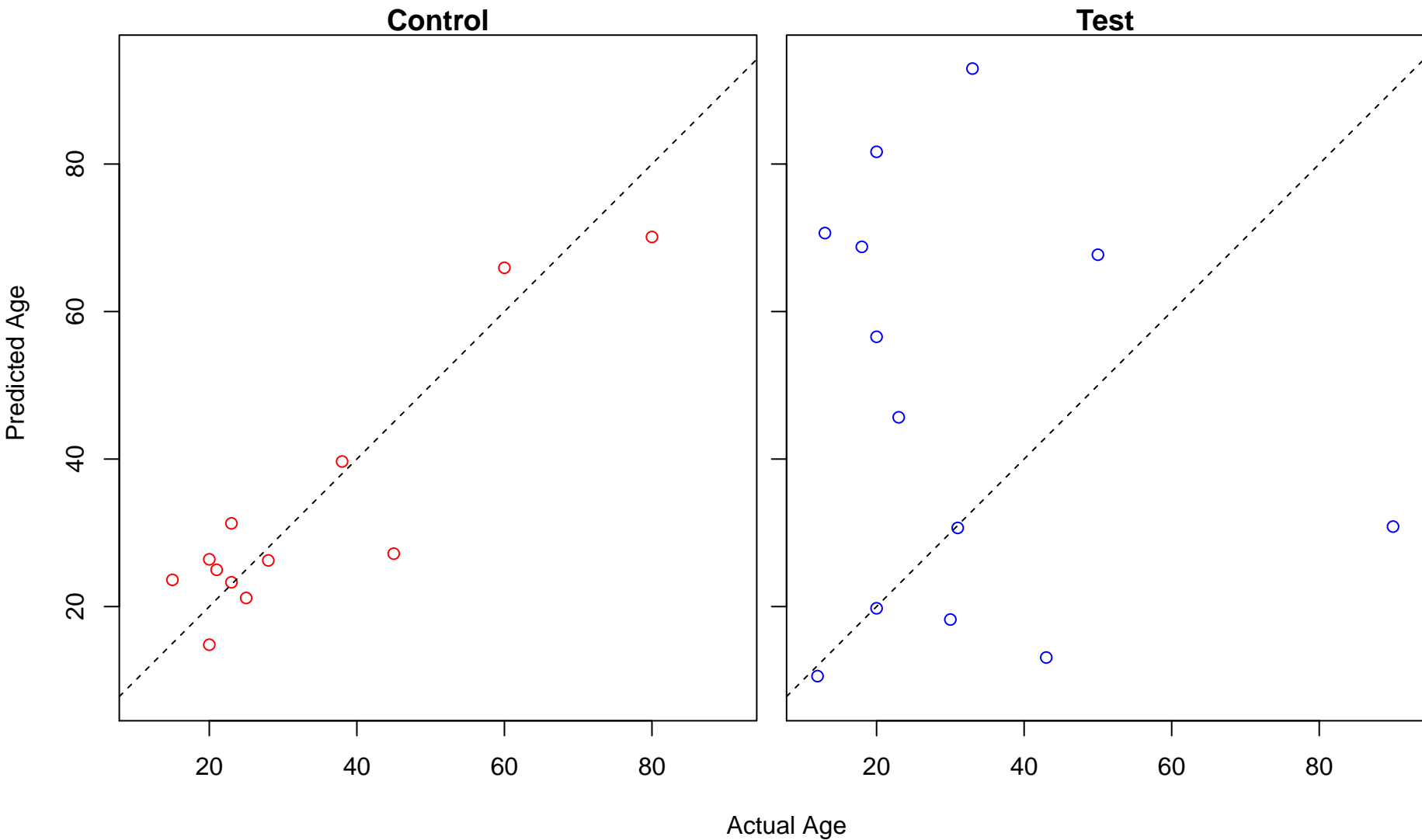
cellular response to growth hormone stimulus (Score: 17.047883)



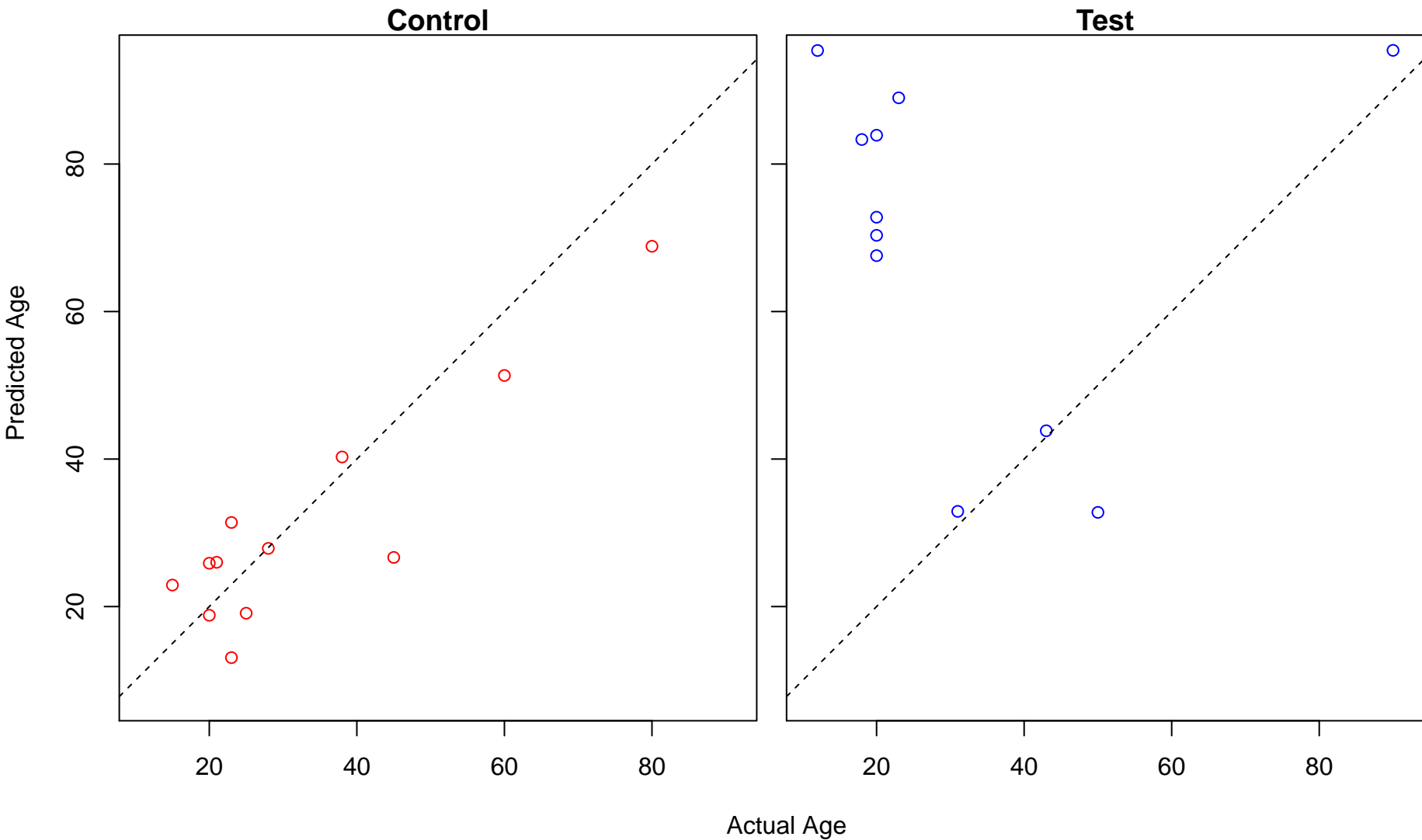
reelin-mediated signaling pathway (Score: 17.039234)



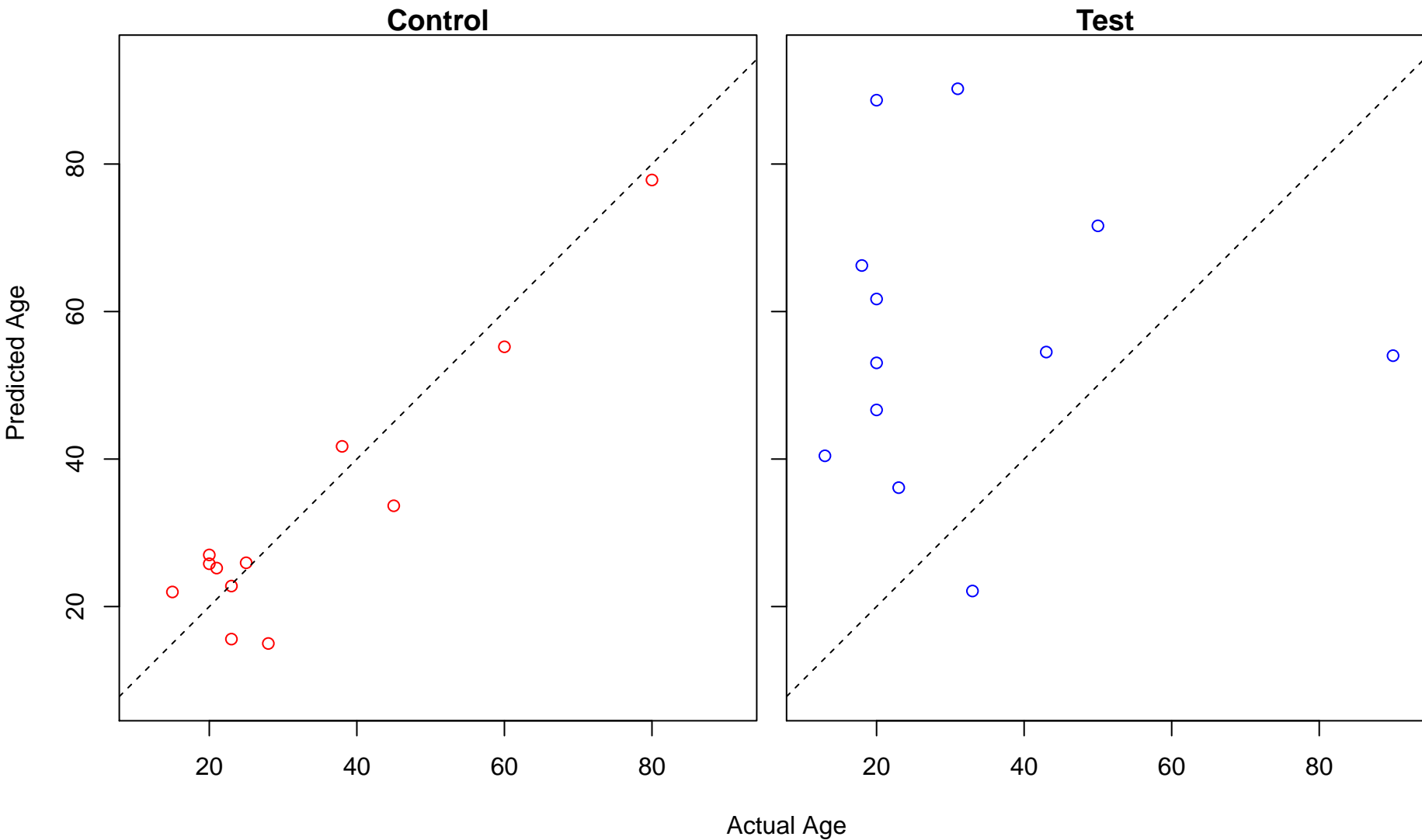
positive regulation of calcium ion transport (Score: 17.036080)



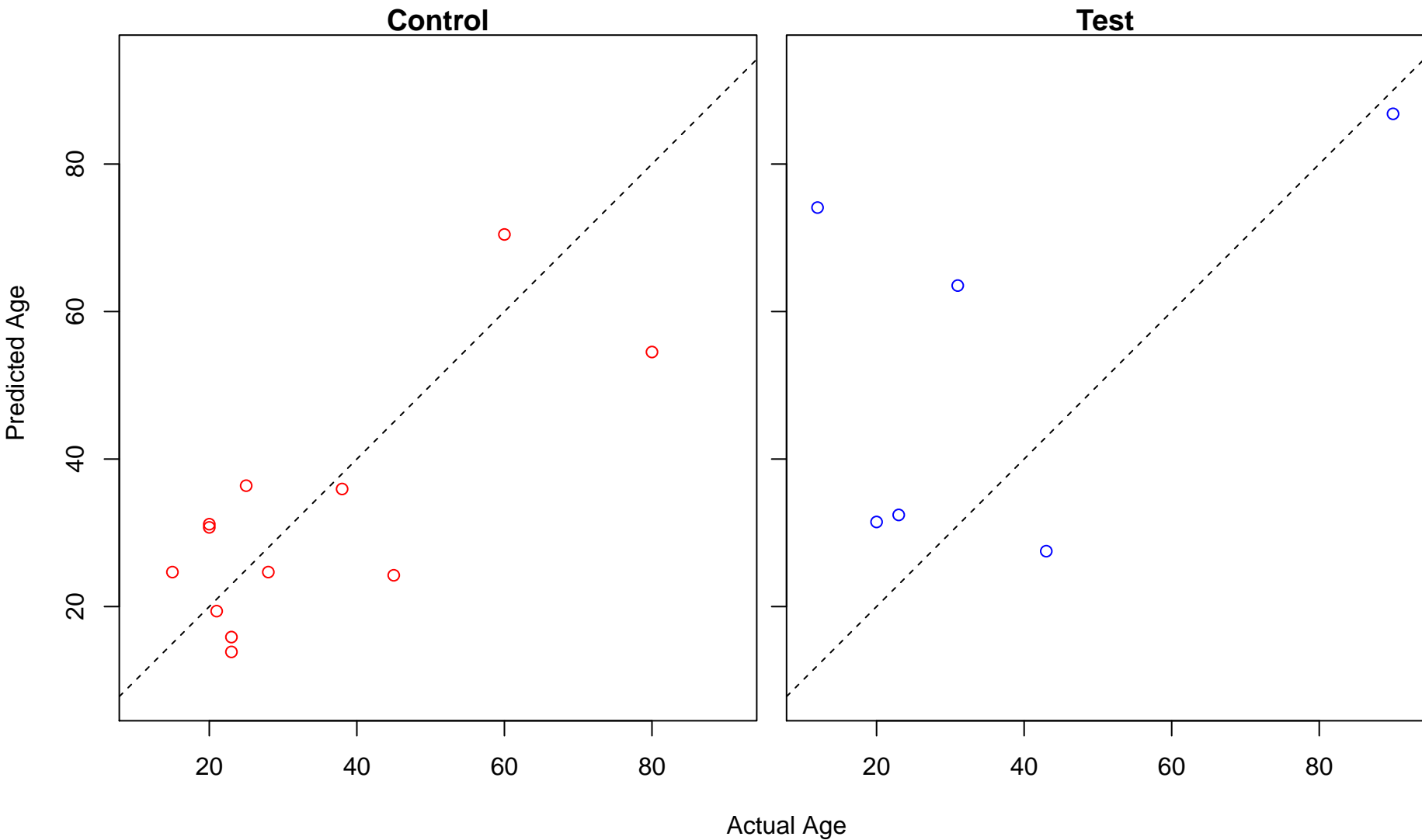
sprouting angiogenesis (Score: 17.023414)



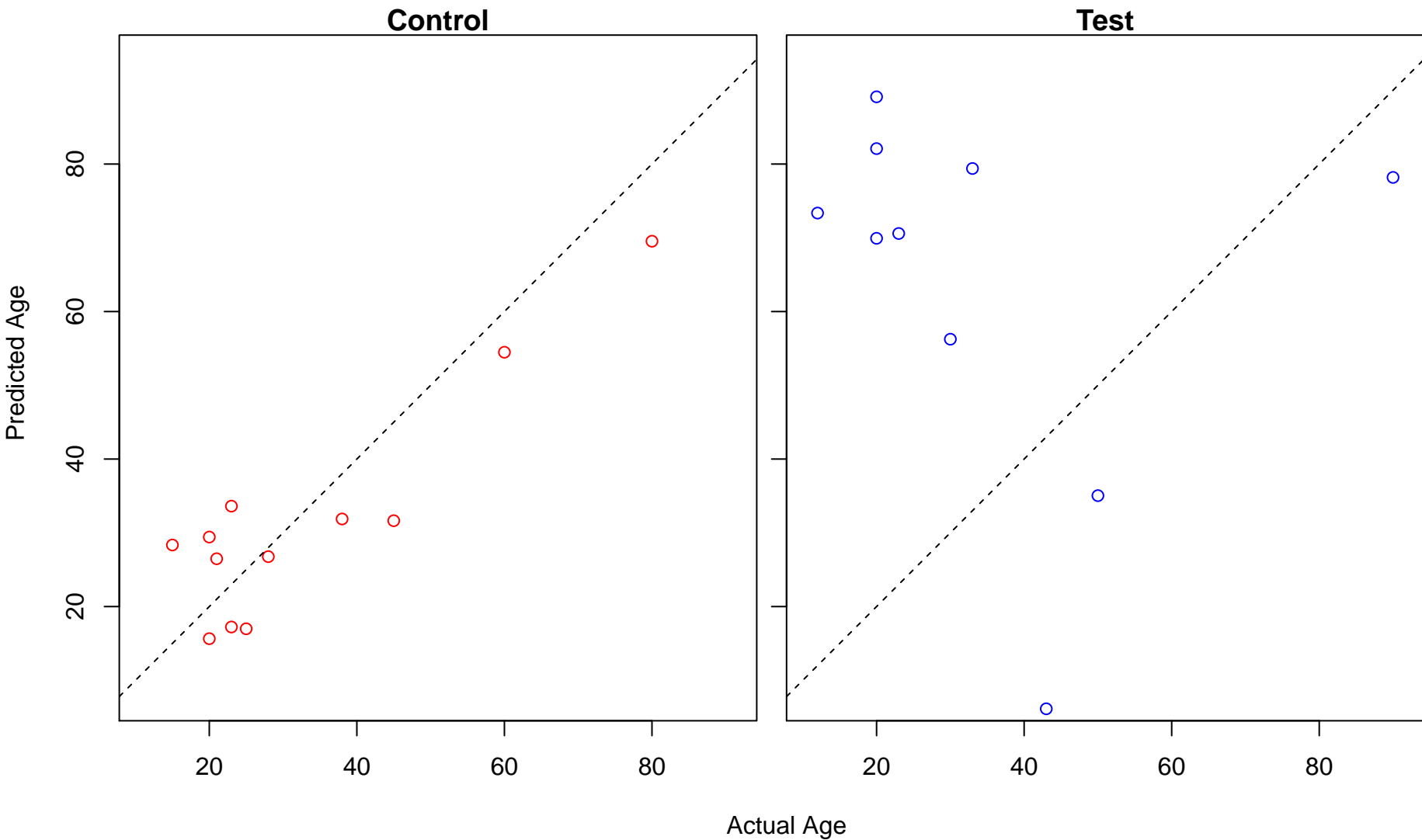
cellular response to histamine (Score: 17.013417)



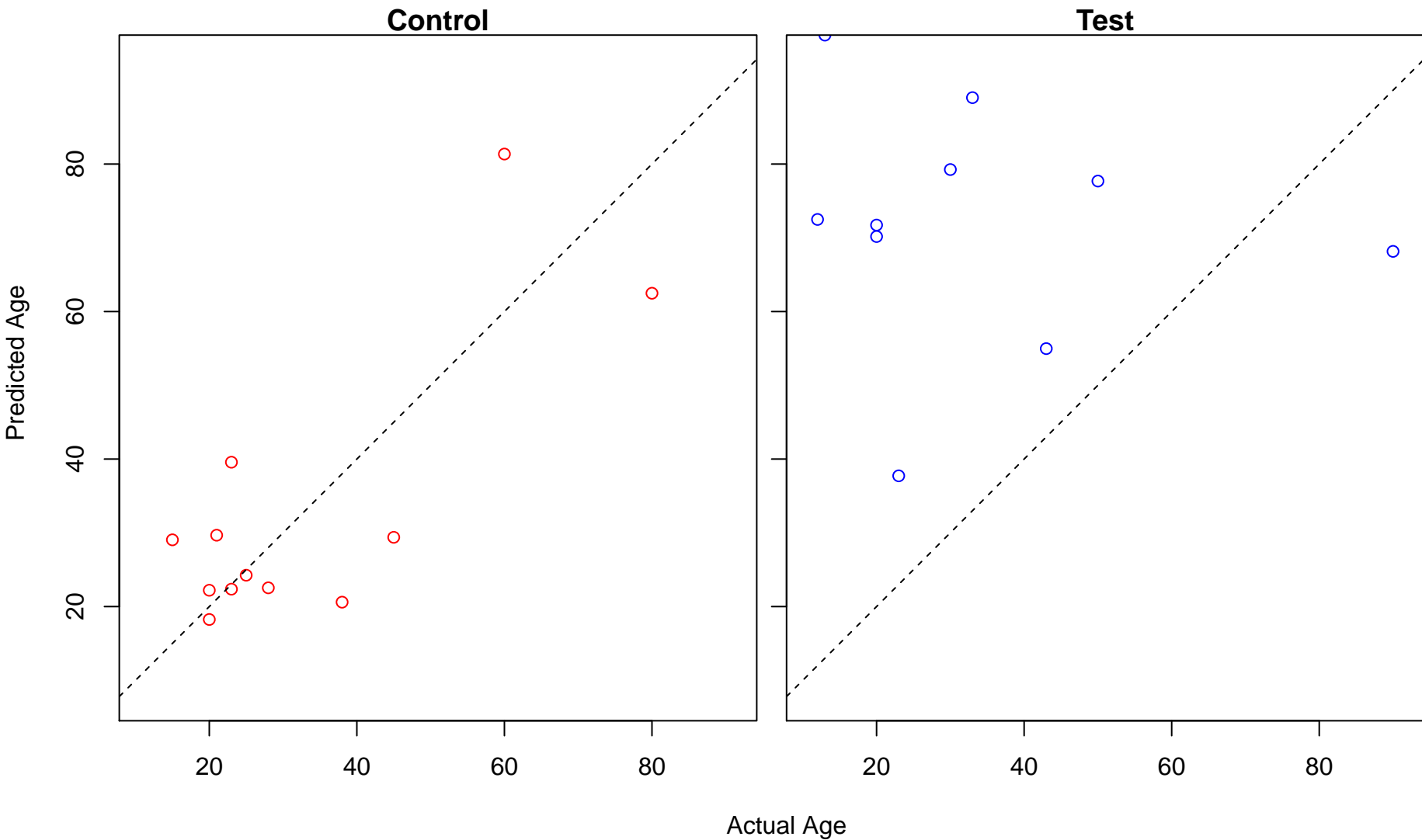
GDP-mannose metabolic process (Score: 17.010953)



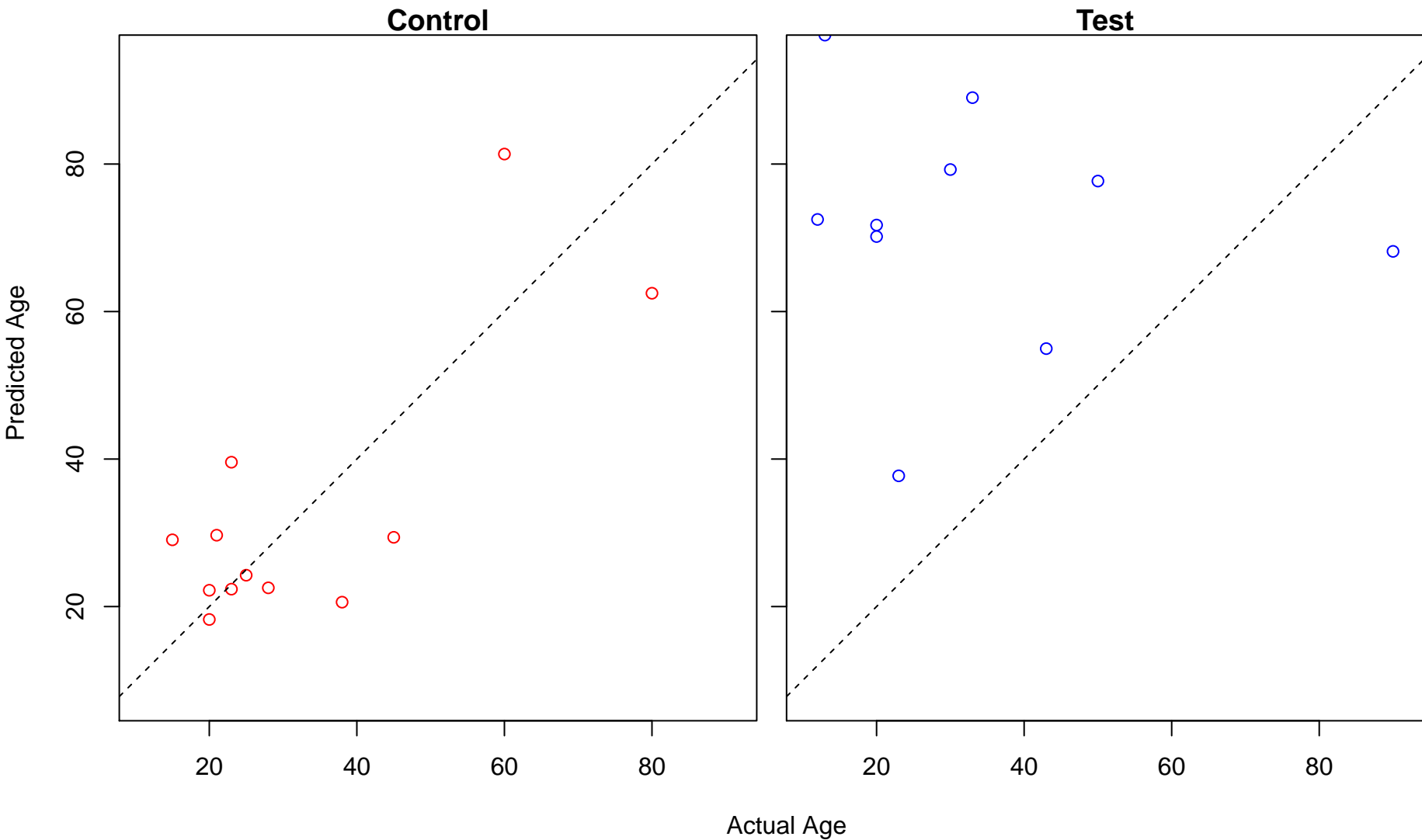
nuclear import (Score: 16.975923)



negative regulation of blood coagulation (Score: 16.942552)

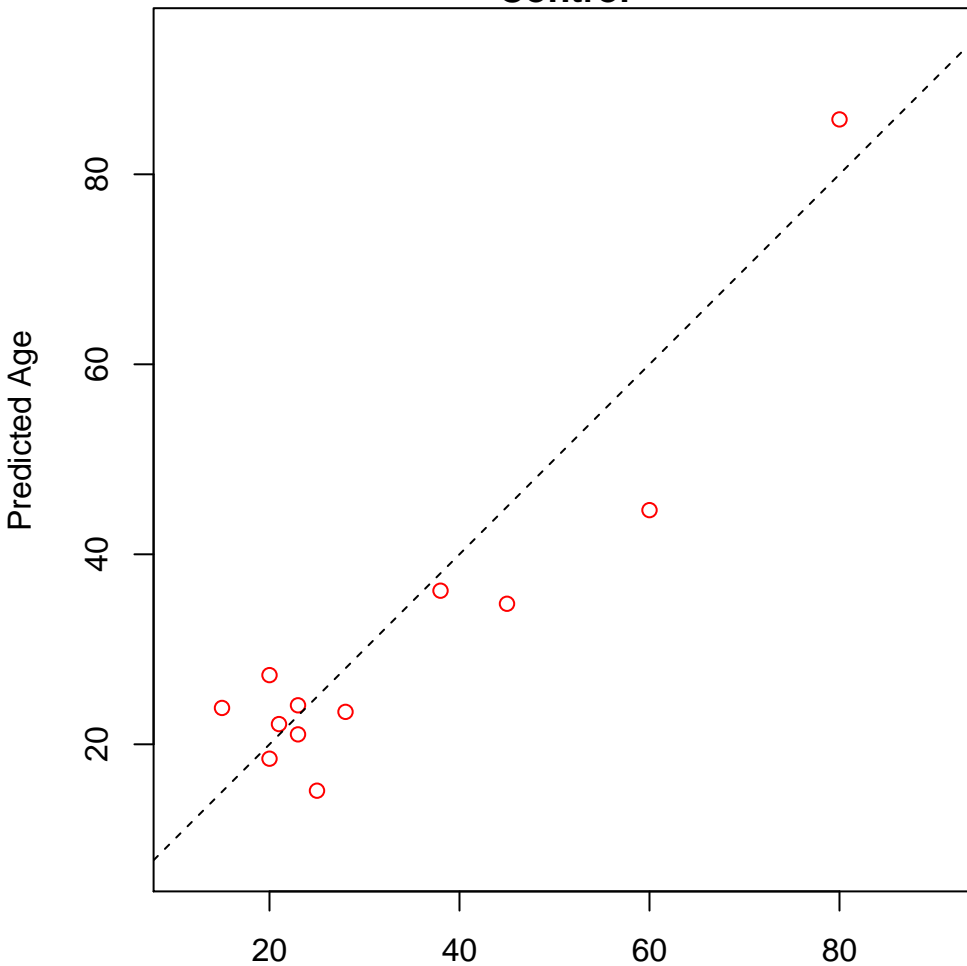


negative regulation of hemostasis (Score: 16.942552)

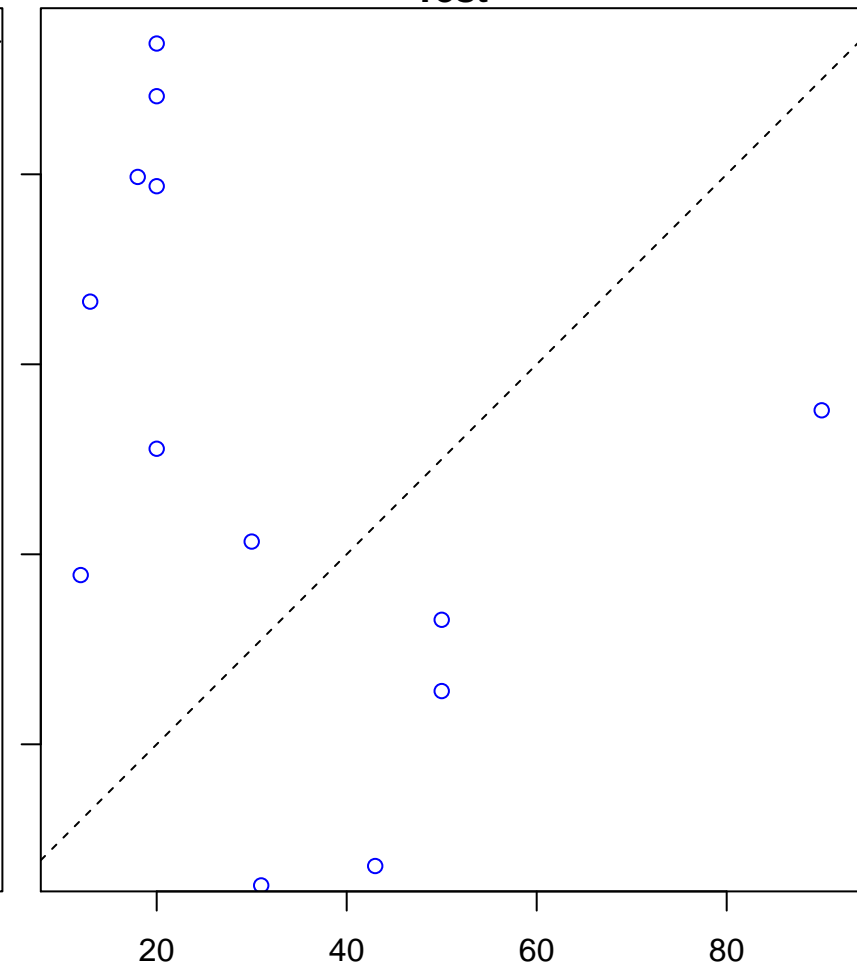


regulation of RNA export from nucleus (Score: 16.903580)

Control

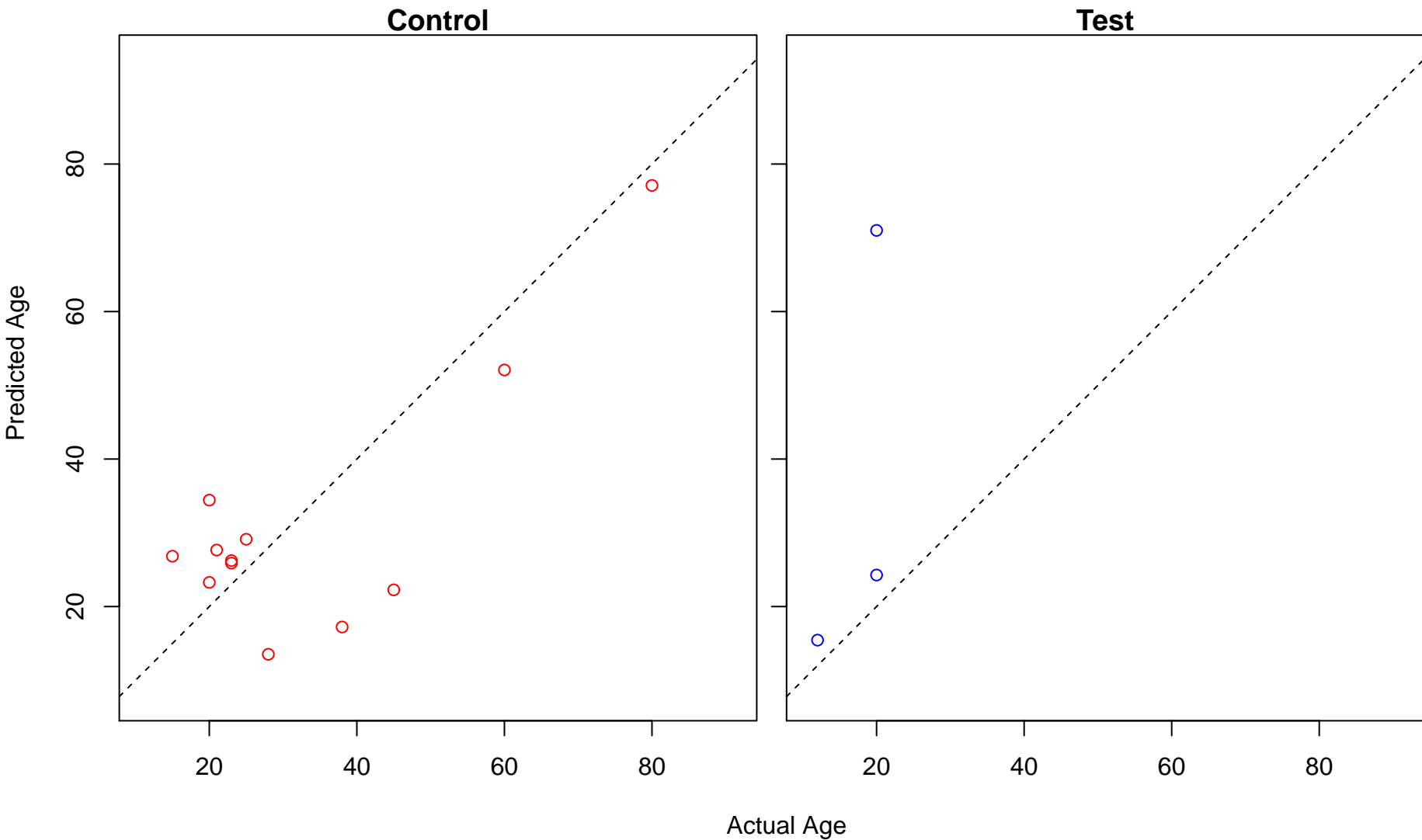


Test

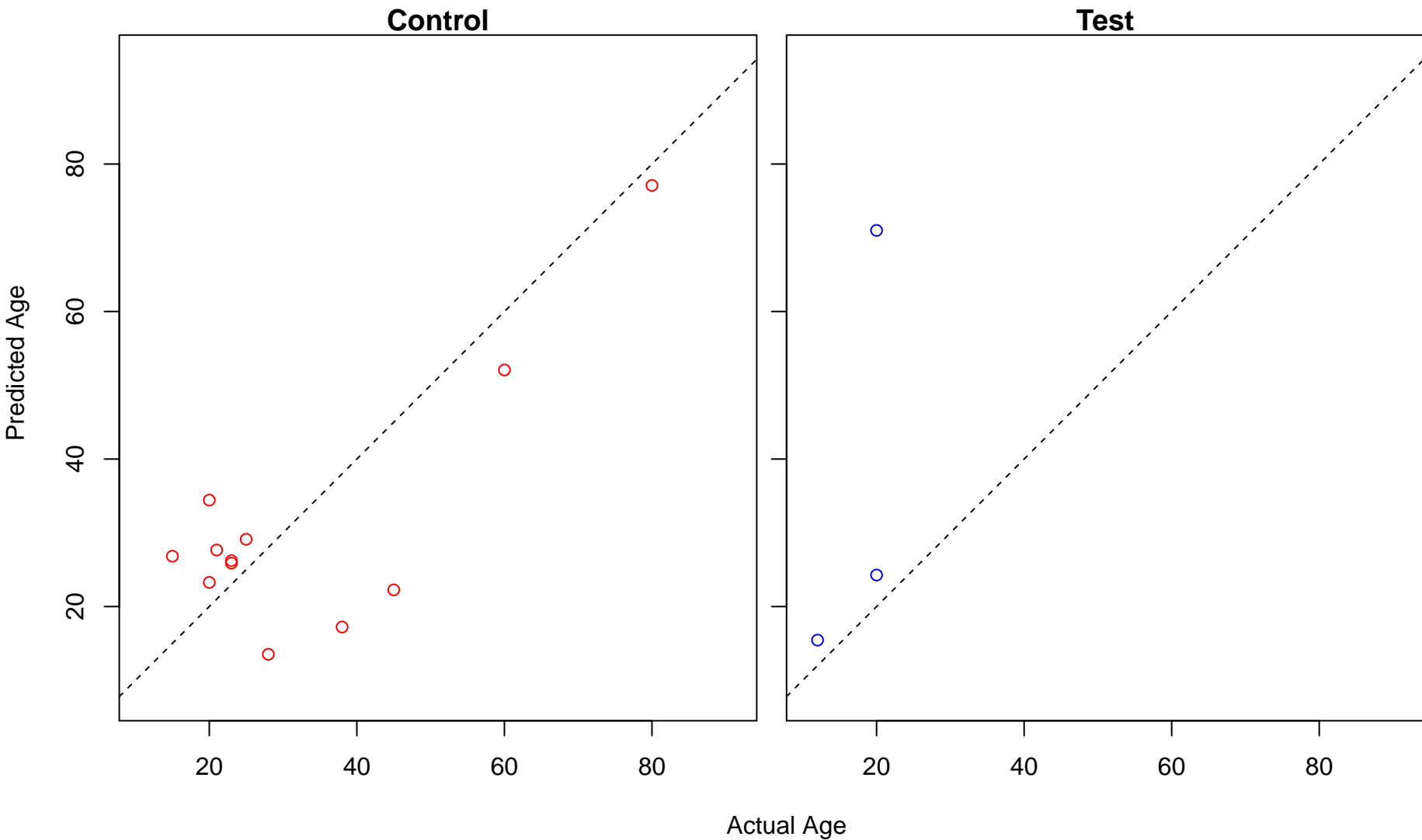


Actual Age

heart valve development (Score: 16.891699)

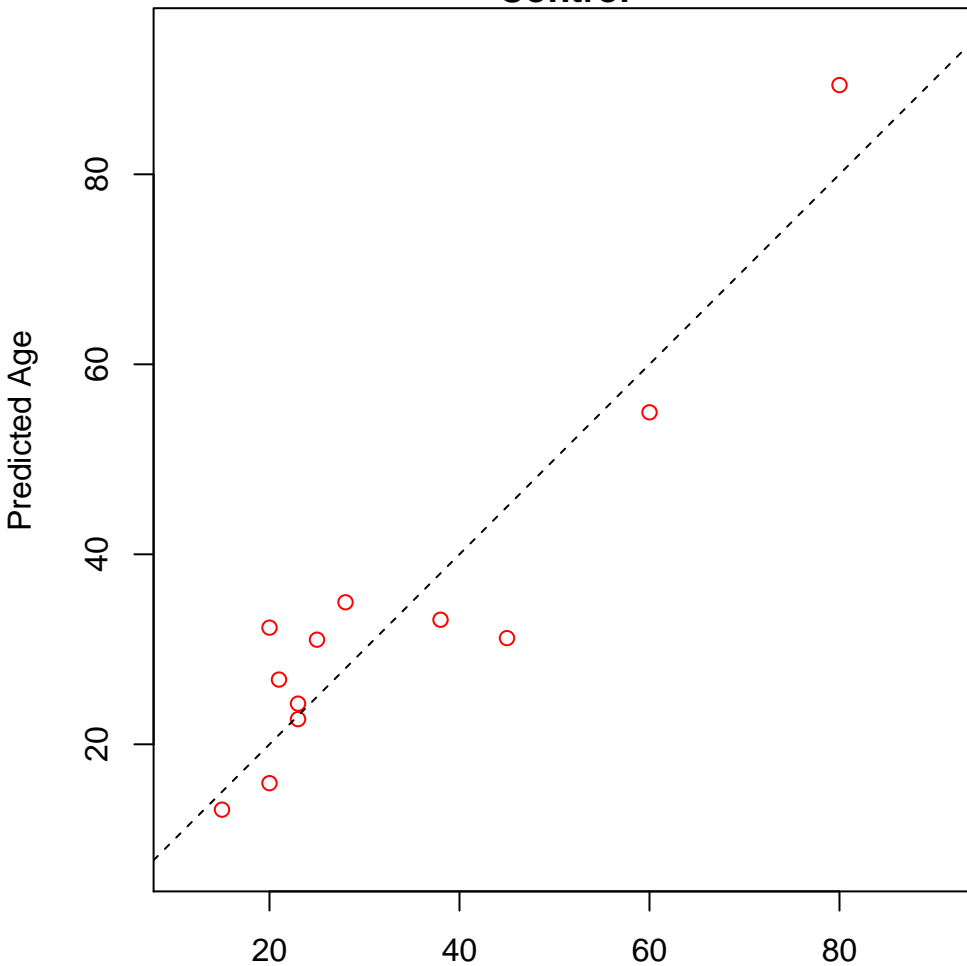


heart valve morphogenesis (Score: 16.891699)

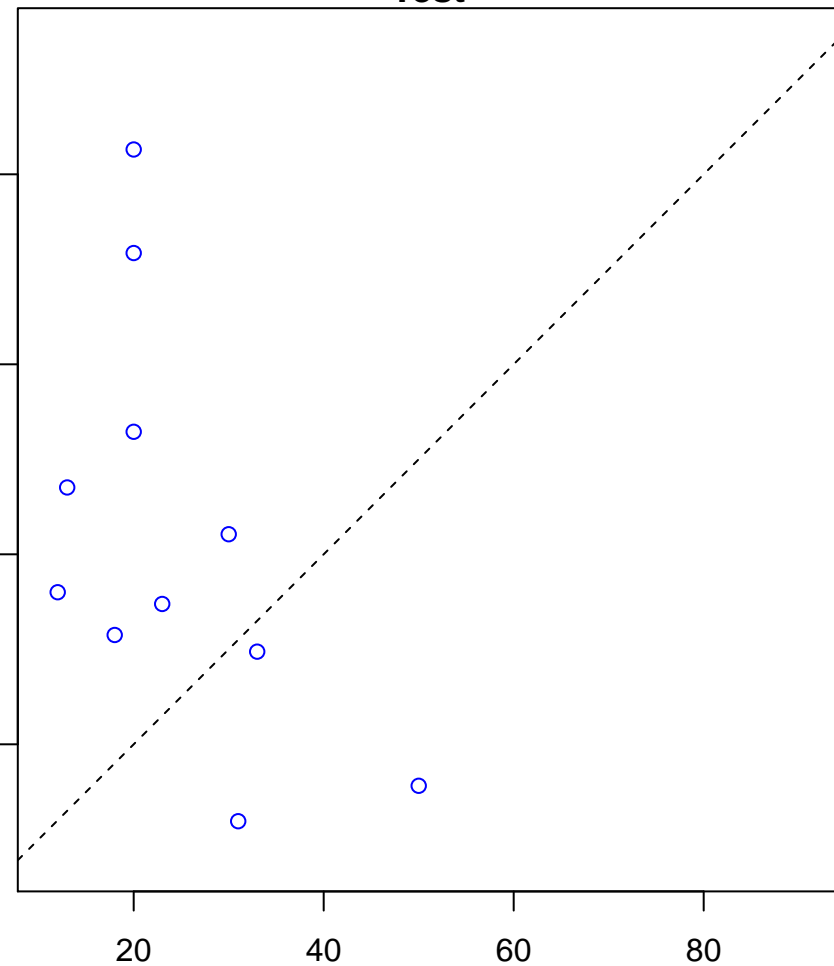


cellular response to estradiol stimulus (Score: 16.861927)

Control

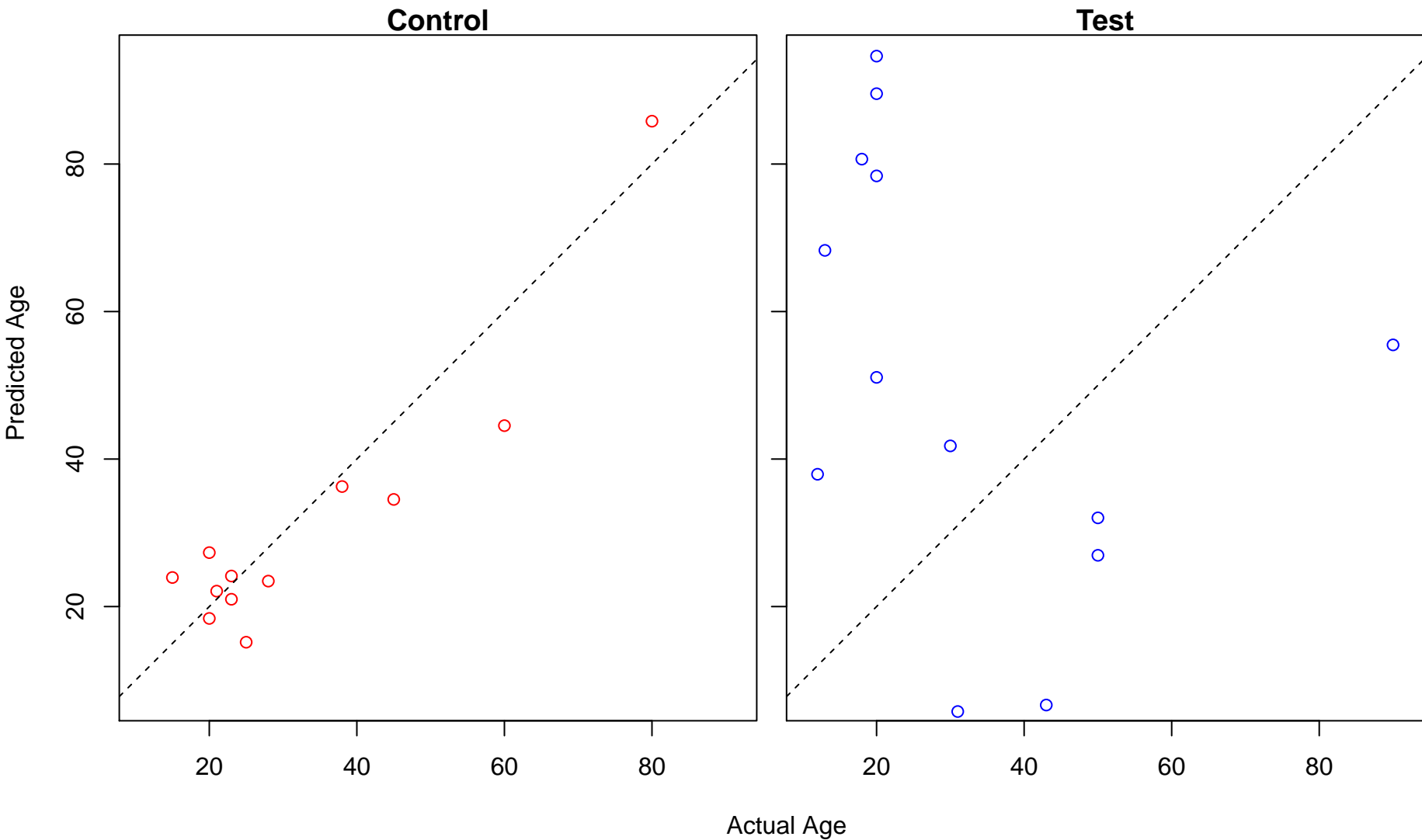


Test

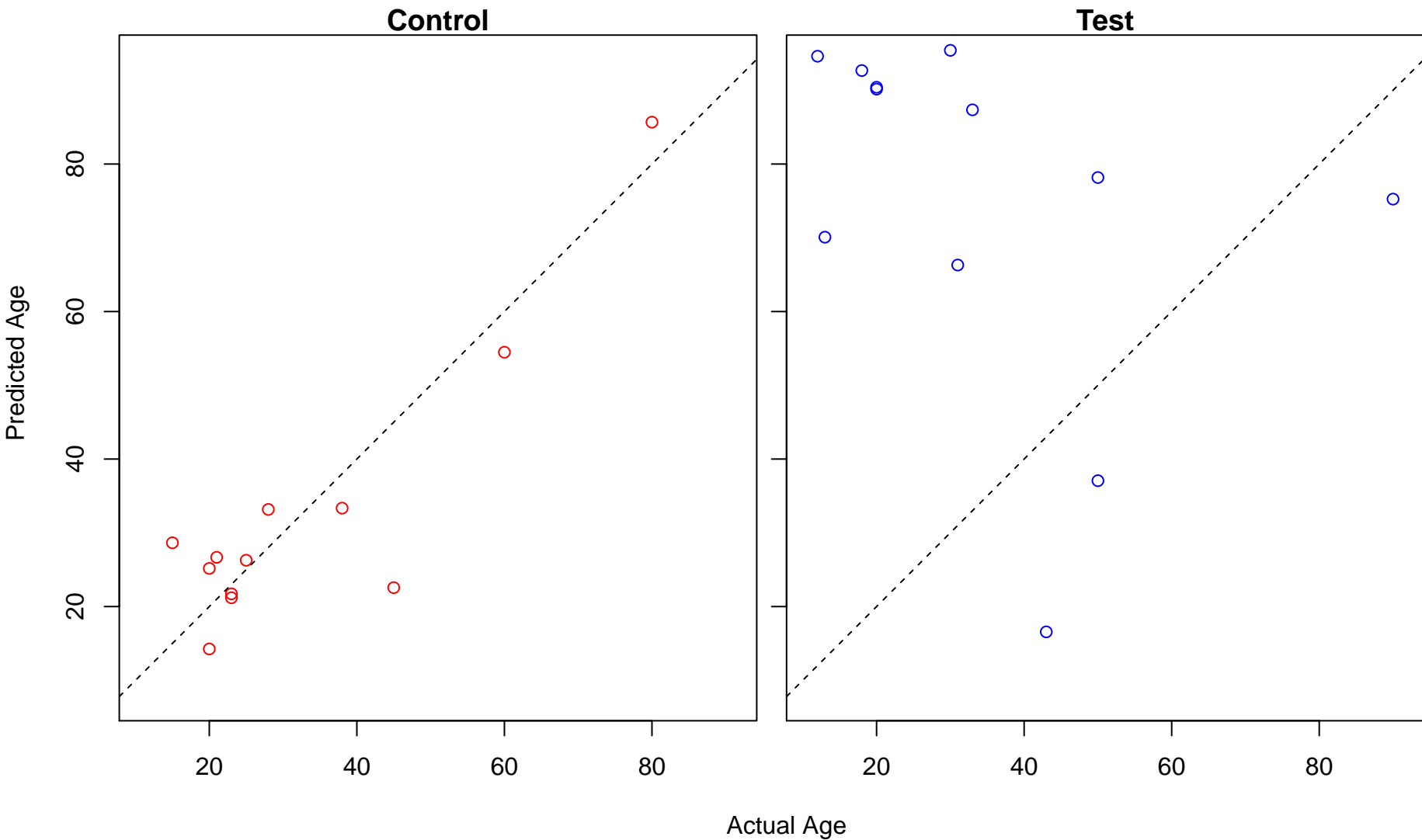


Actual Age

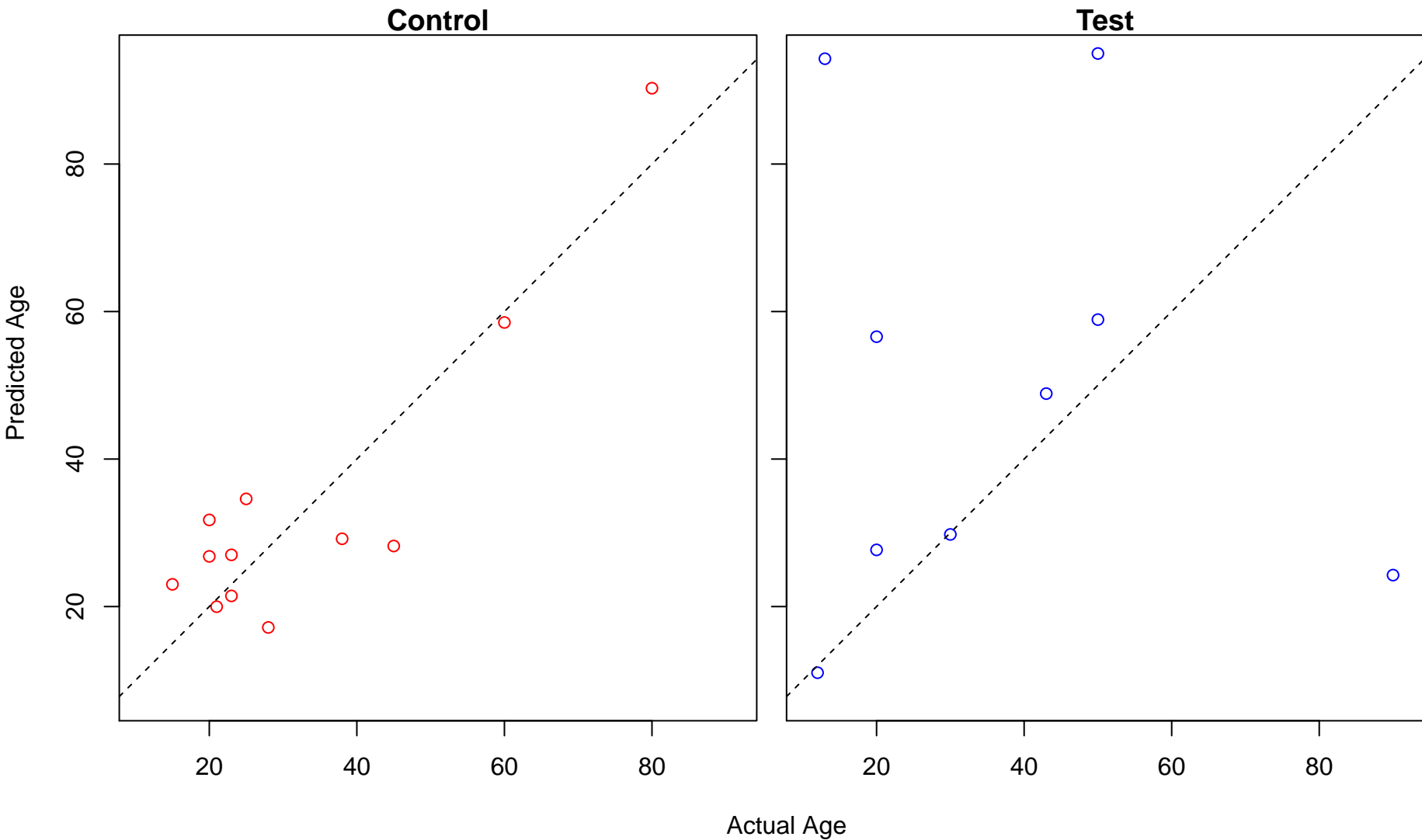
regulation of nucleobase-containing compound transport (Score: 16.858022)



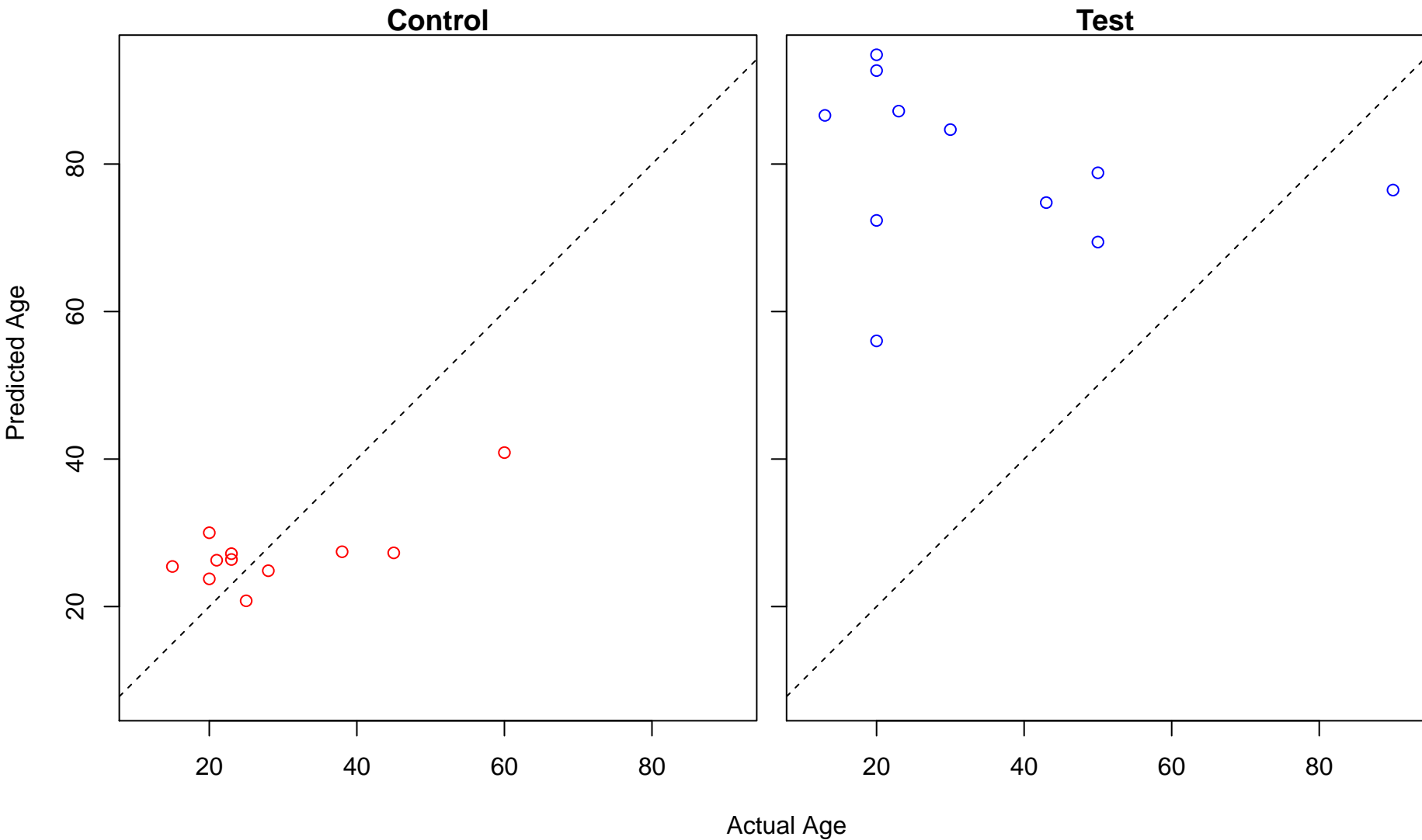
response to interleukin-2 (Score: 16.845444)



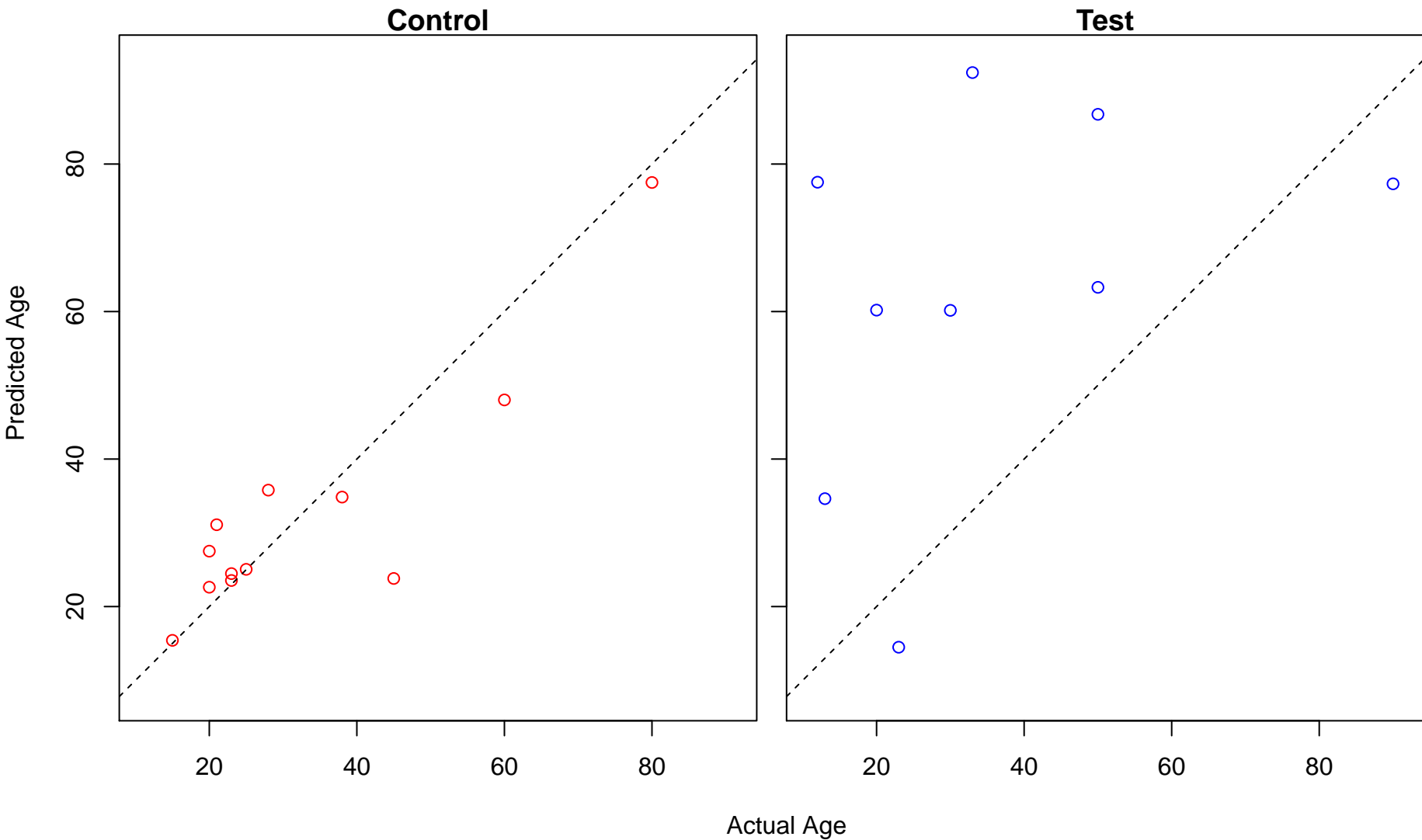
body fluid secretion (Score: 16.831010)



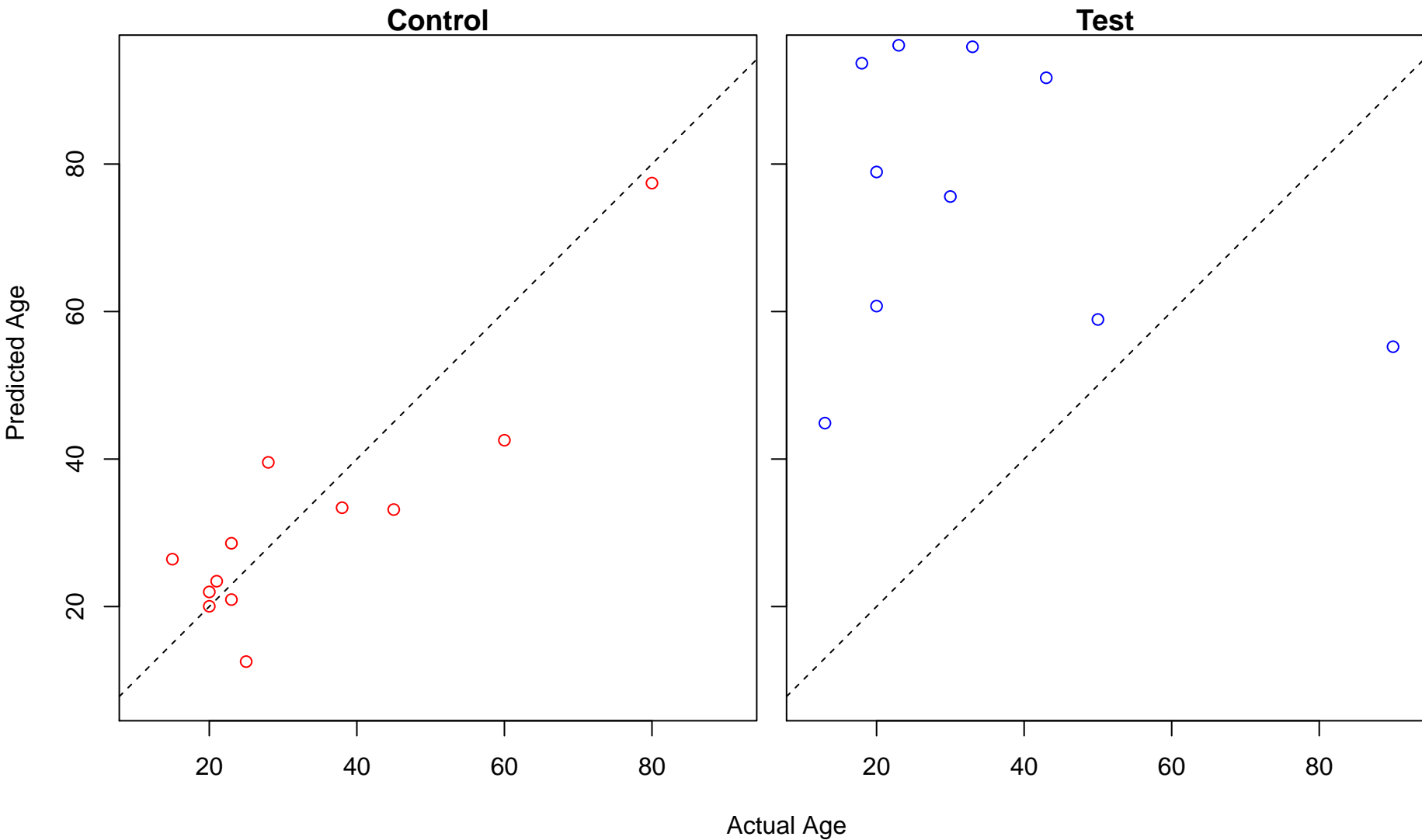
gas homeostasis (Score: 16.788875)



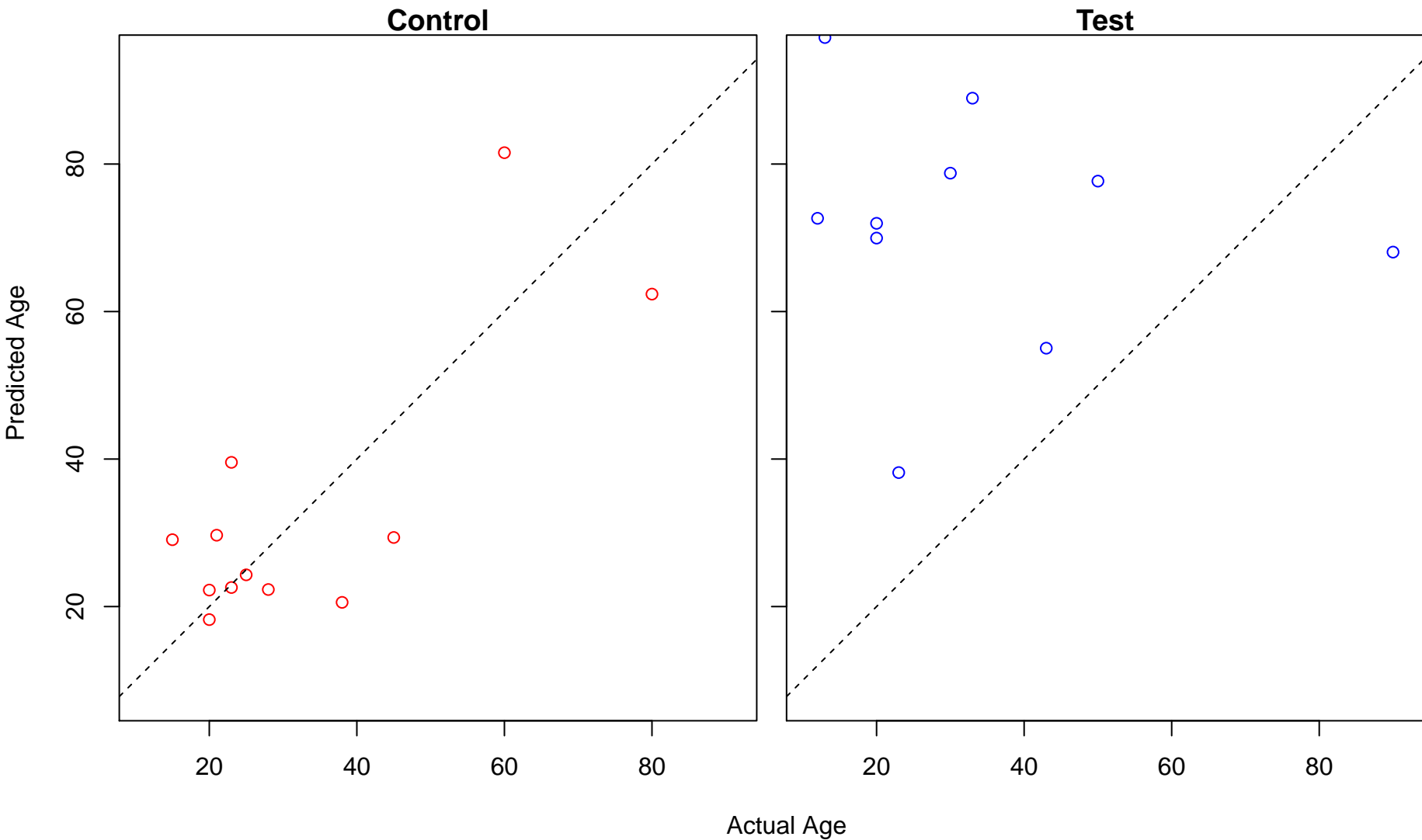
nucleobase metabolic process (Score: 16.774957)



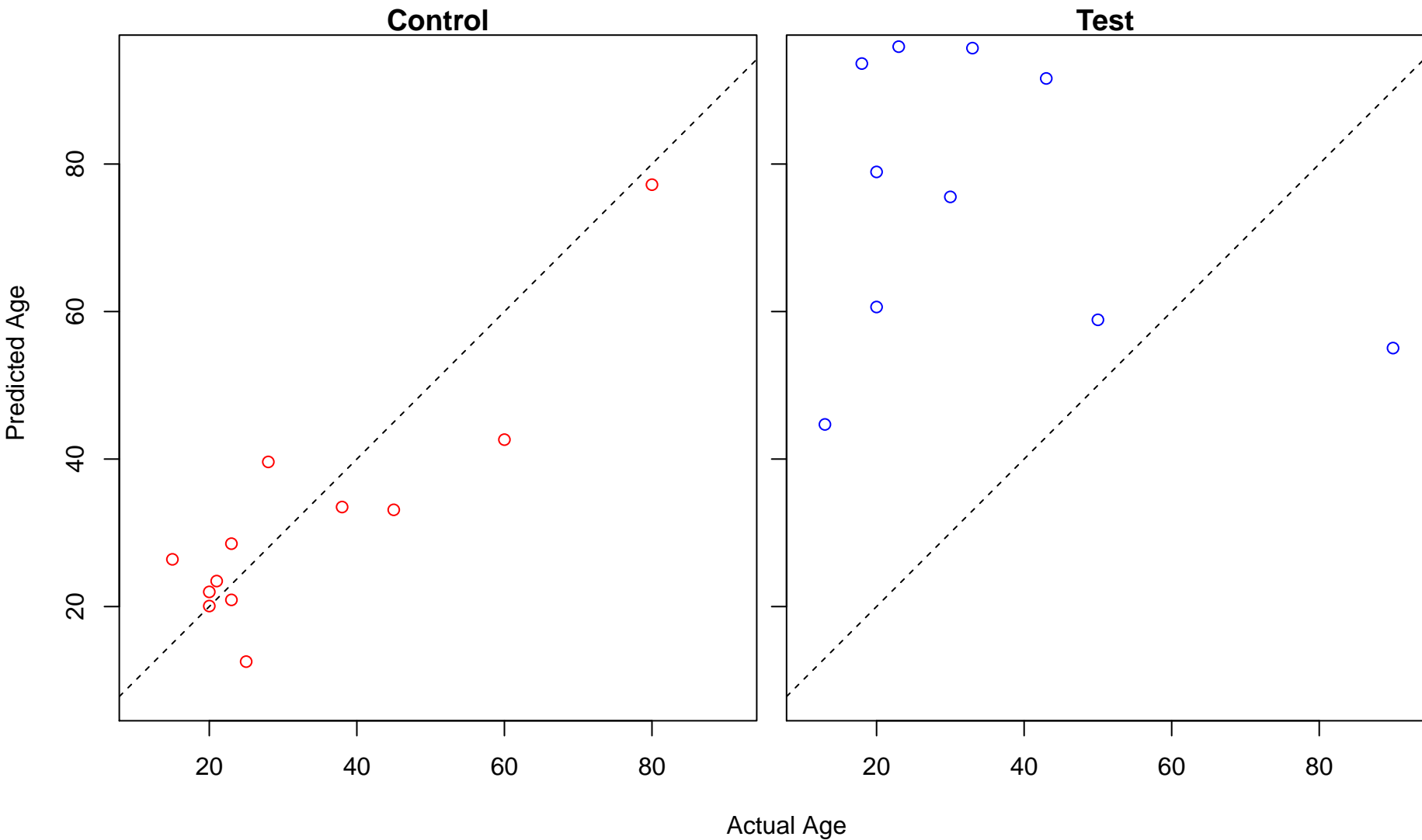
specification of symmetry (Score: 16.761175)



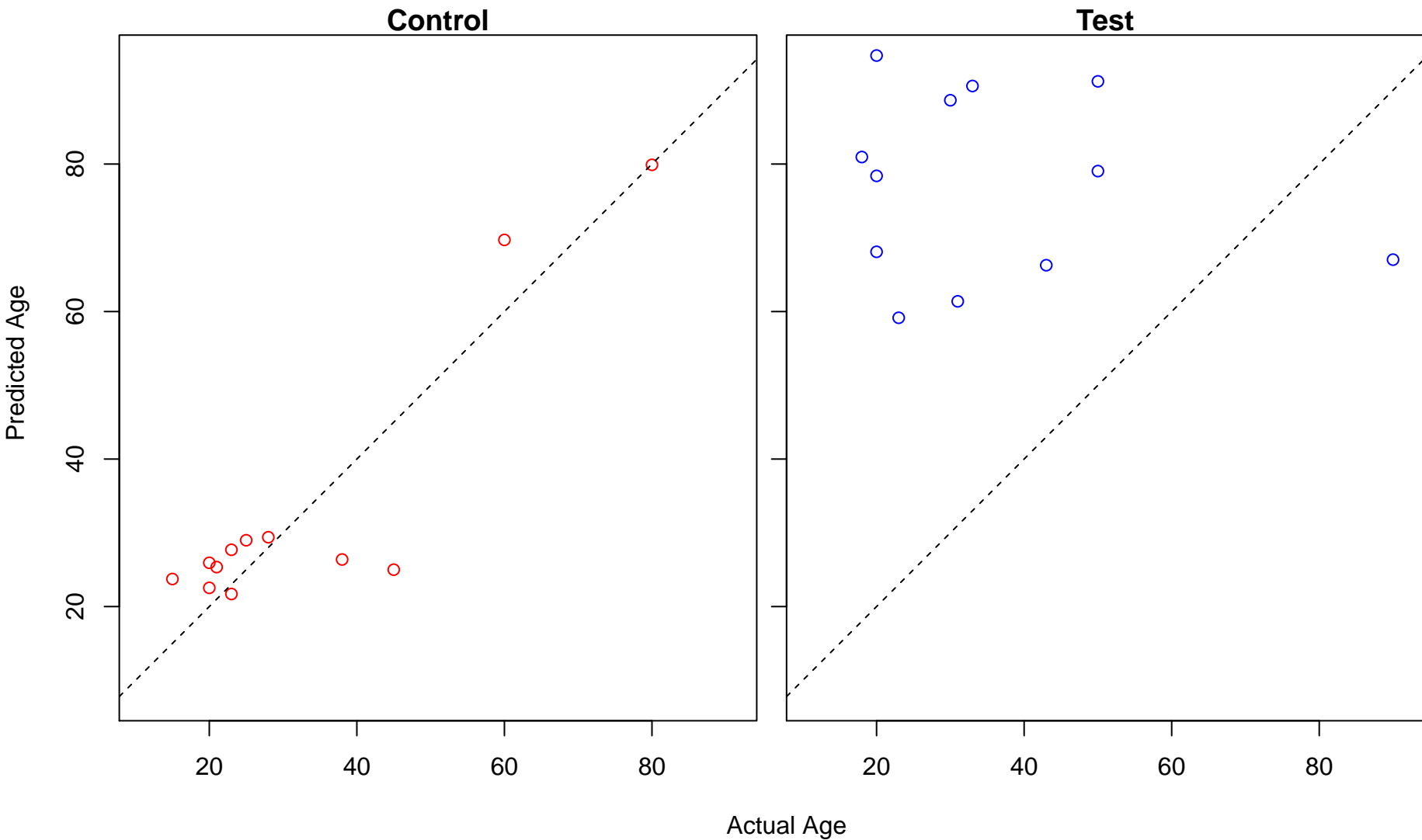
negative regulation of coagulation (Score: 16.755242)



determination of bilateral symmetry (Score: 16.753846)

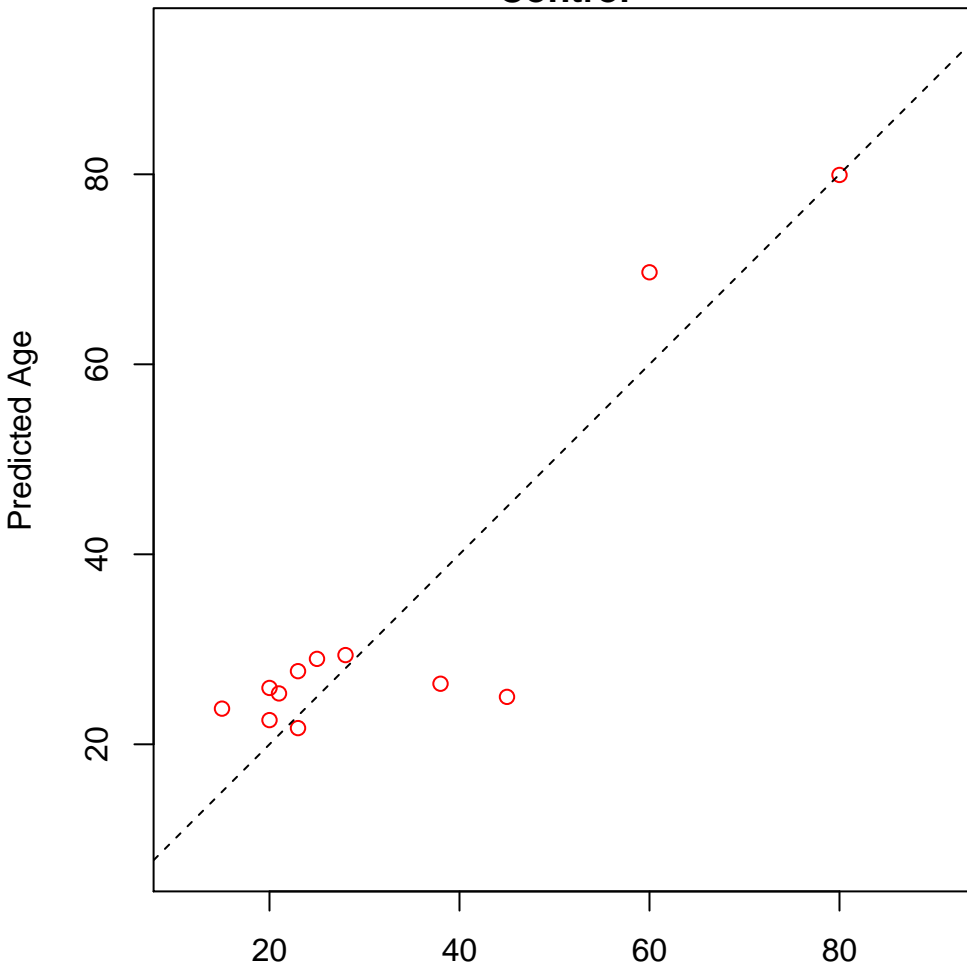


ventricular cardiac muscle tissue morphogenesis (Score: 16.731359)

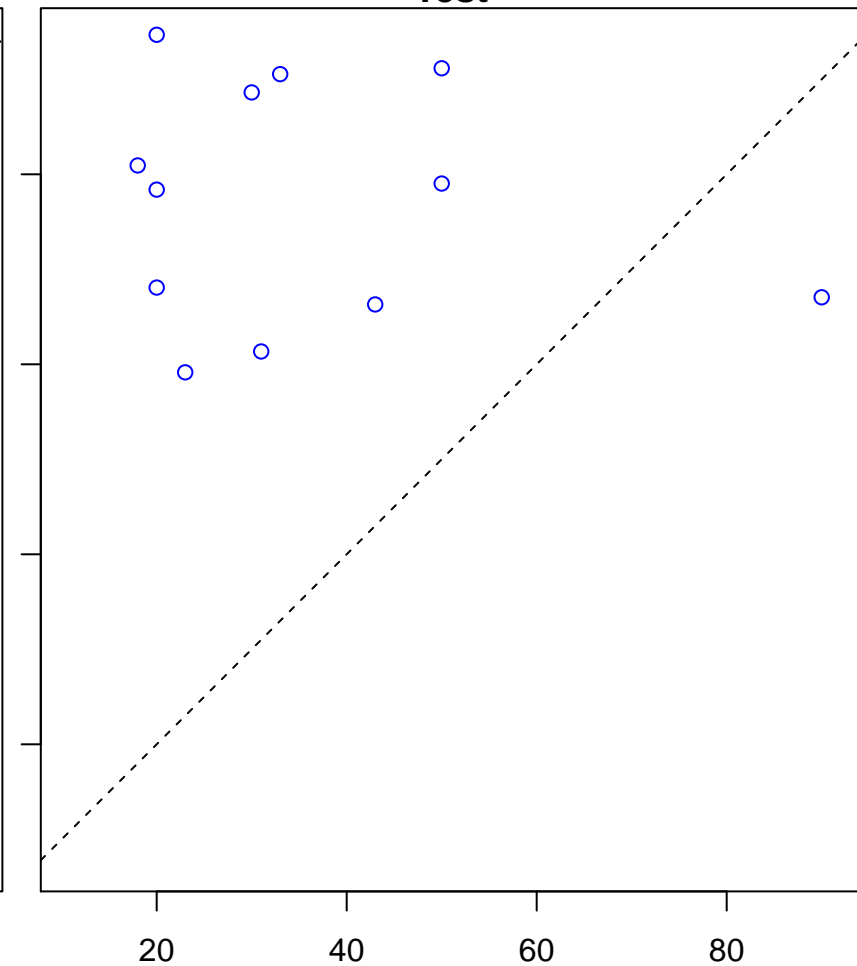


cardiac muscle tissue morphogenesis (Score: 16.716050)

Control

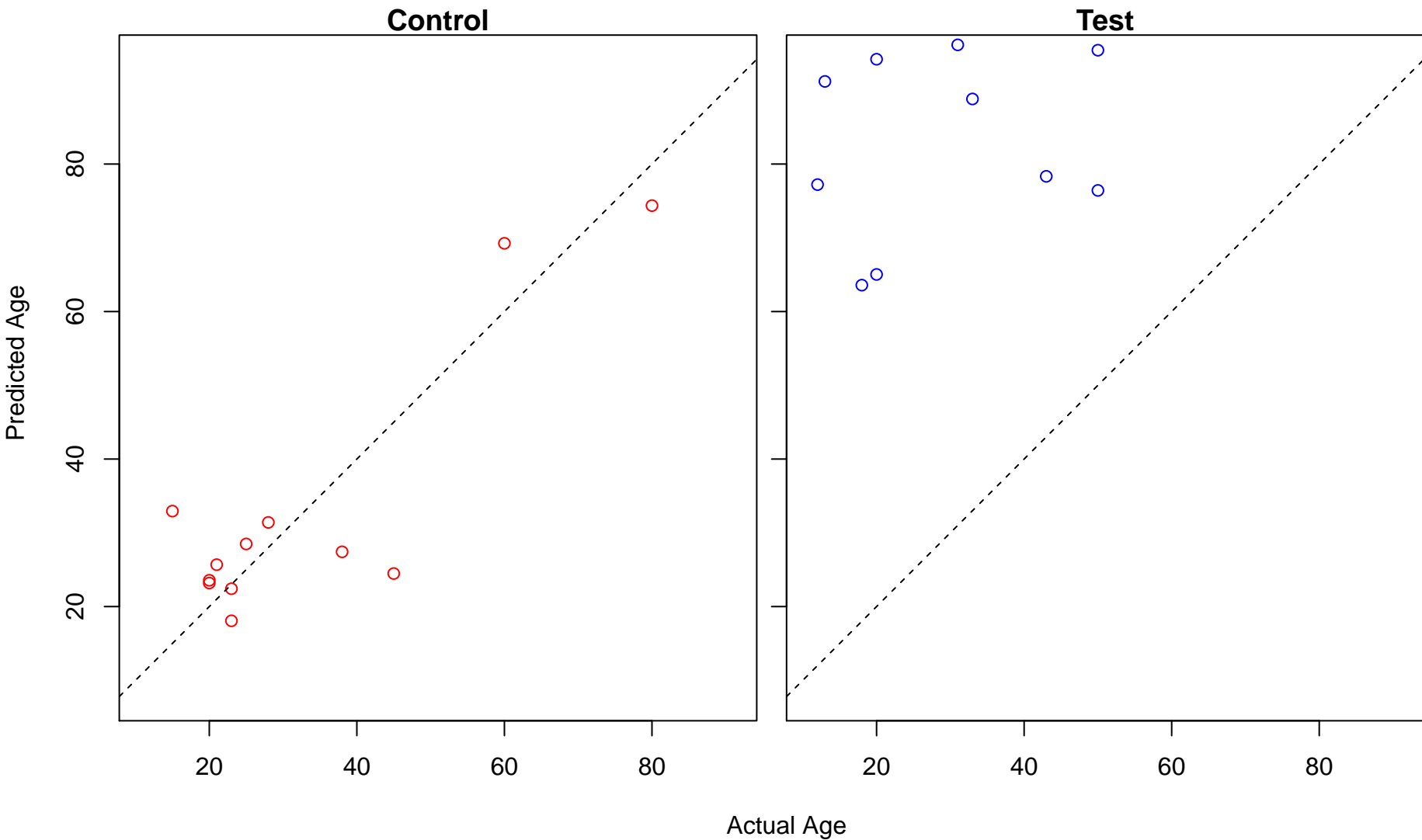


Test

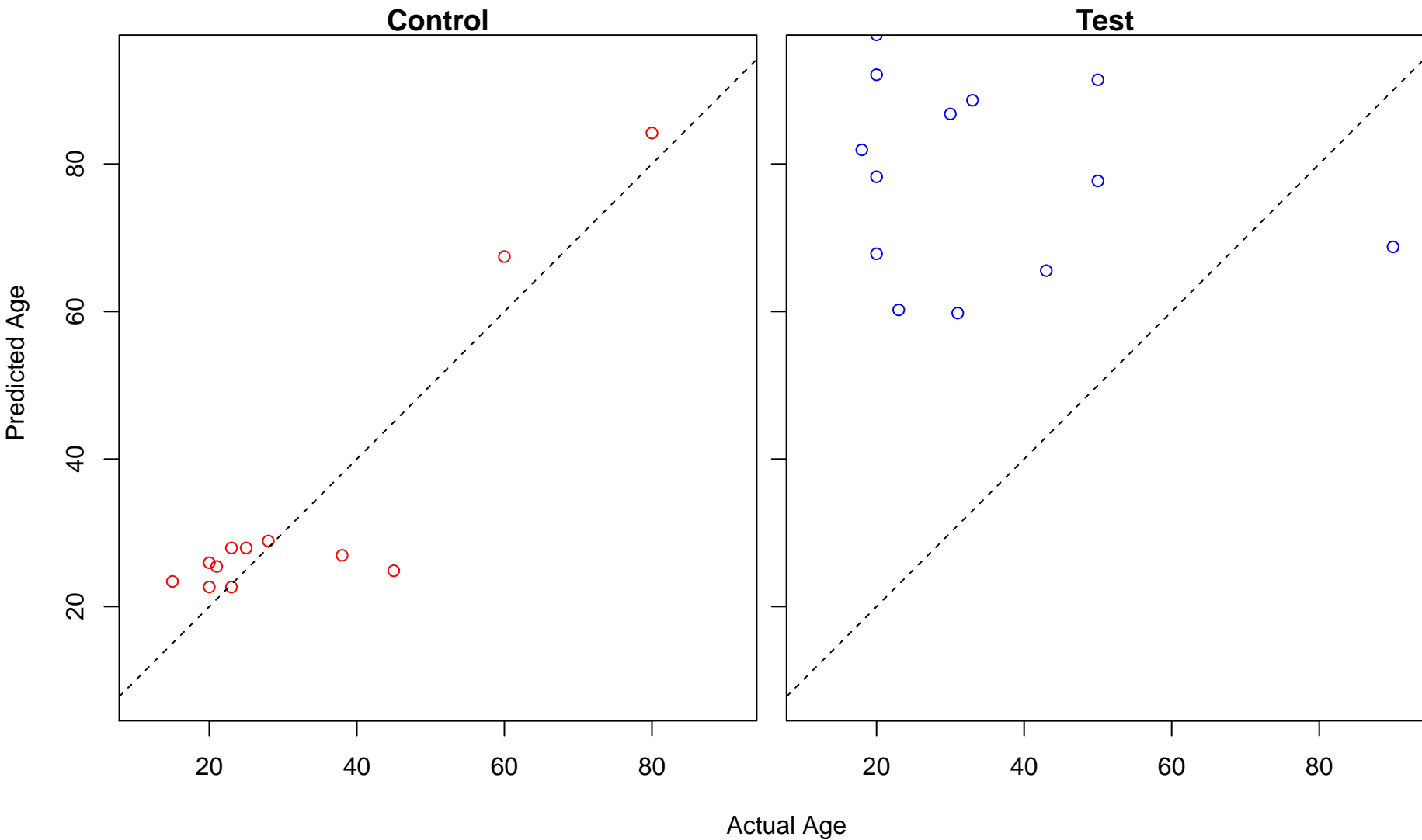


Actual Age

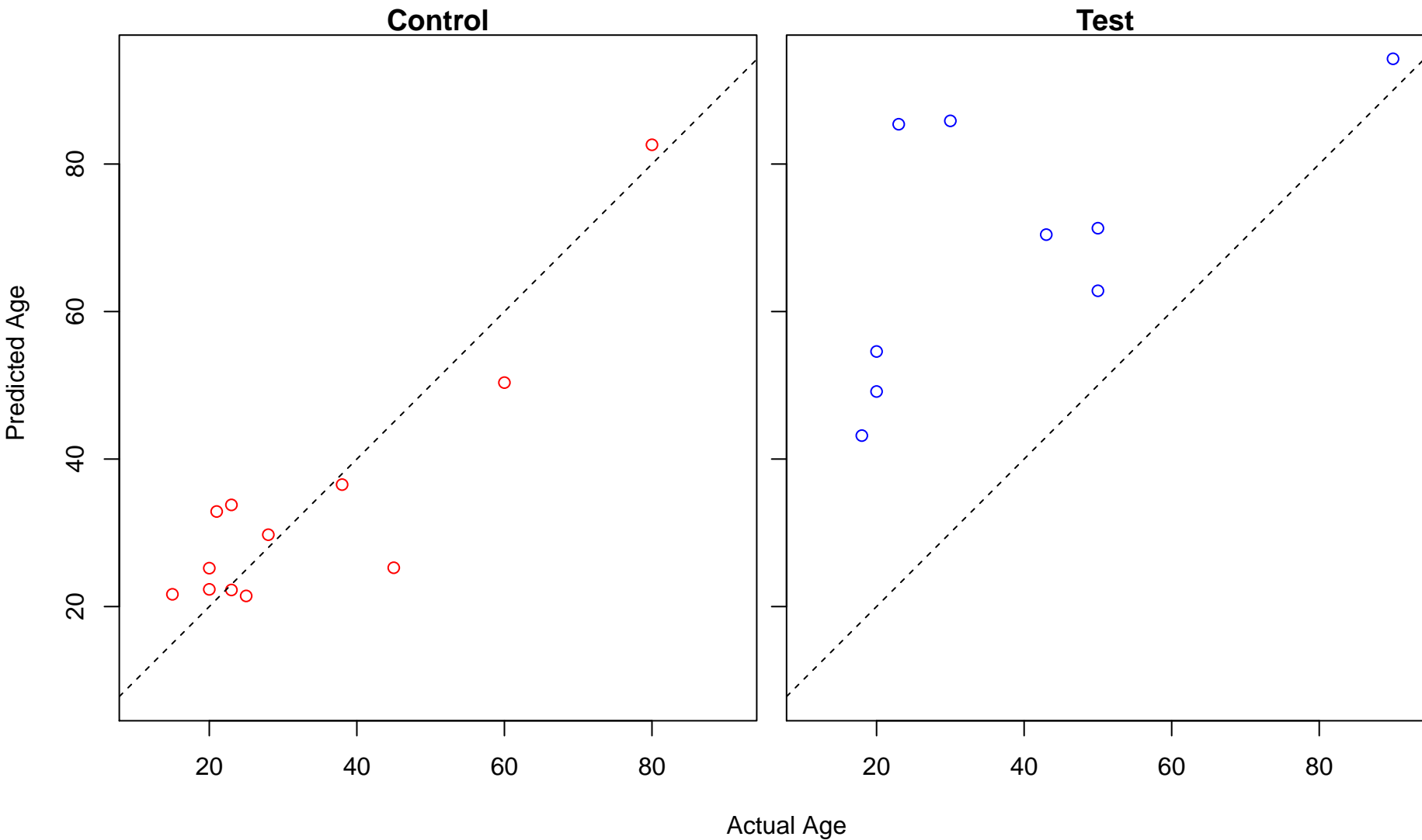
negative regulation of protein targeting to membrane (Score: 16.686563)



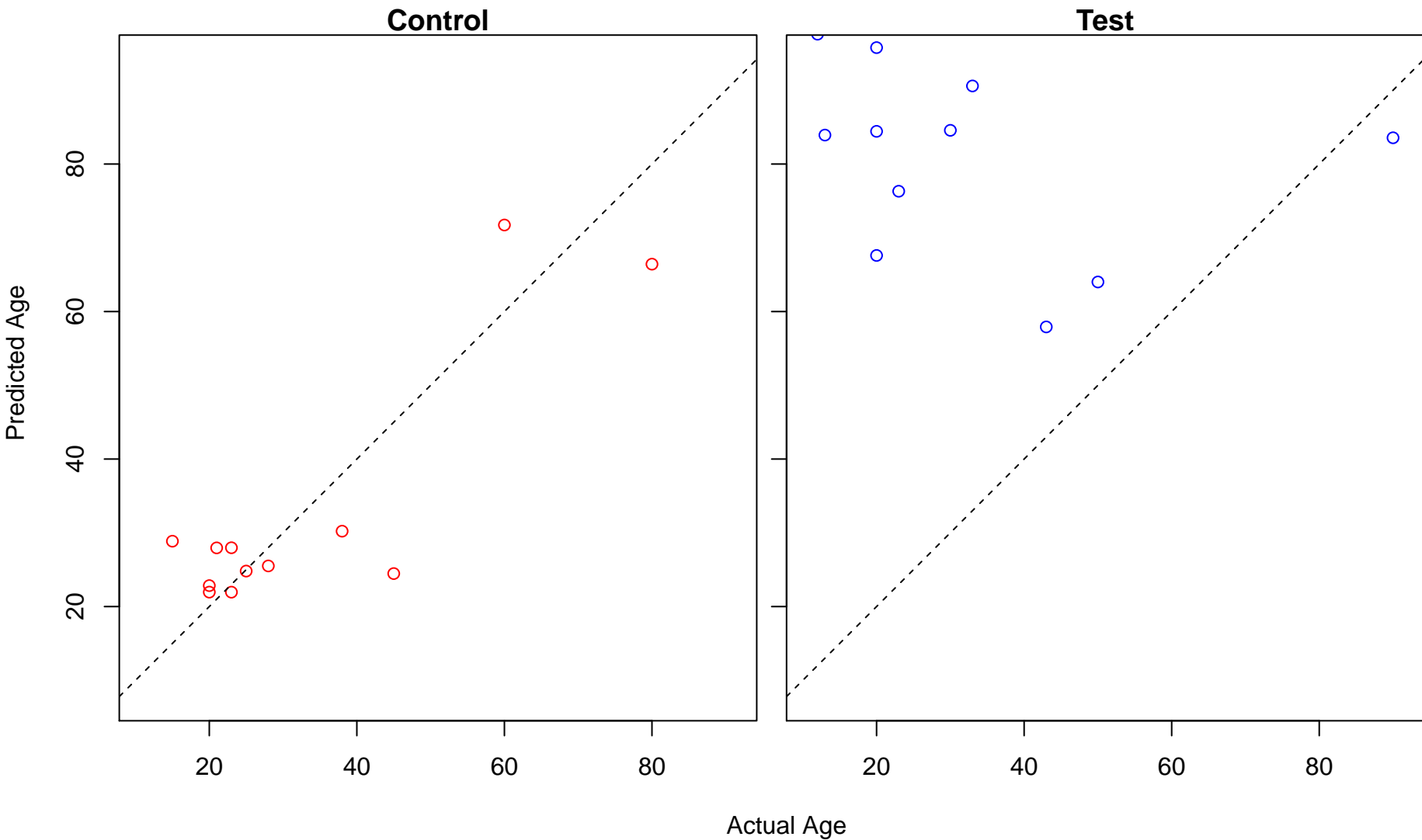
ventricular cardiac muscle tissue development (Score: 16.676209)



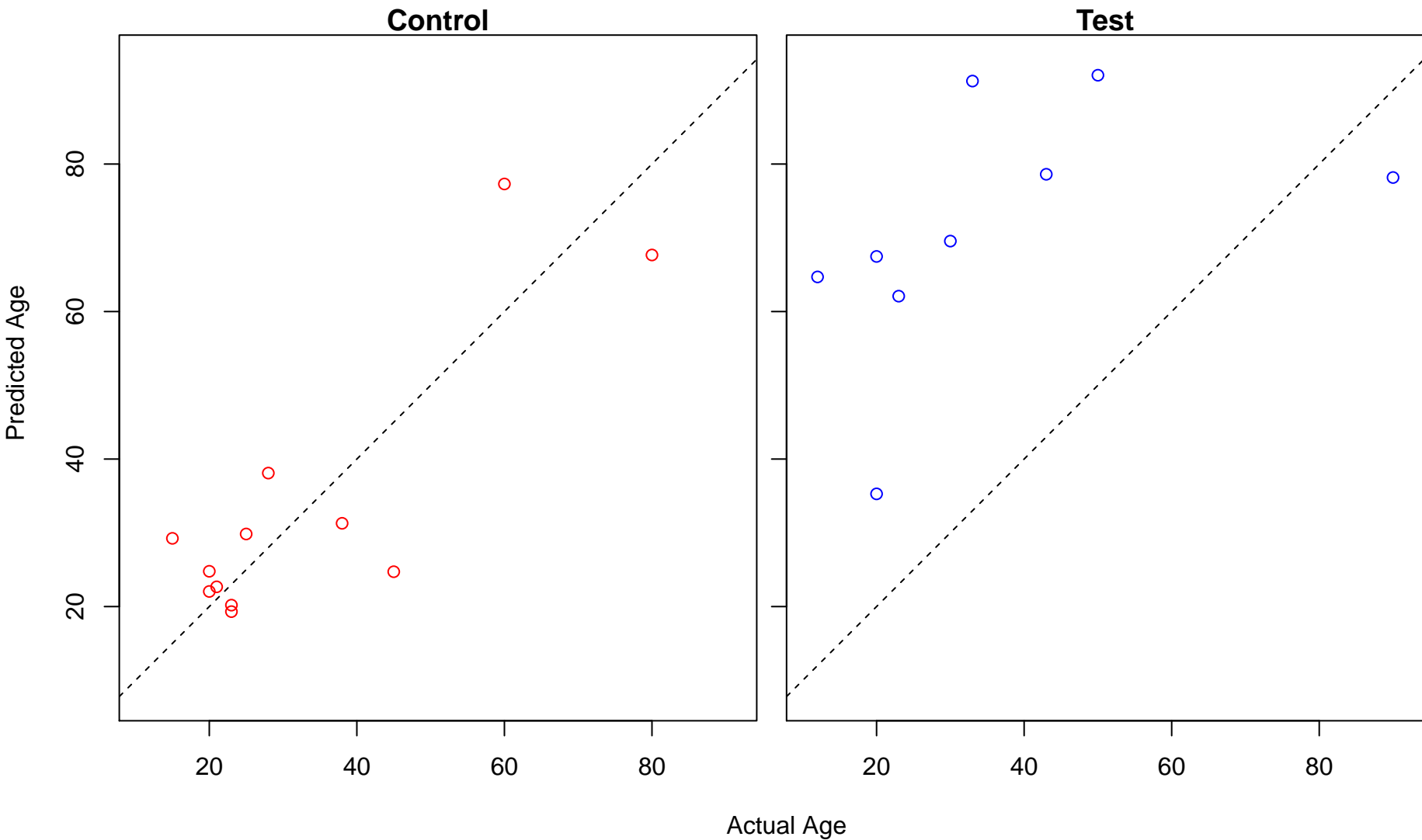
epithelial tube morphogenesis (Score: 16.670663)



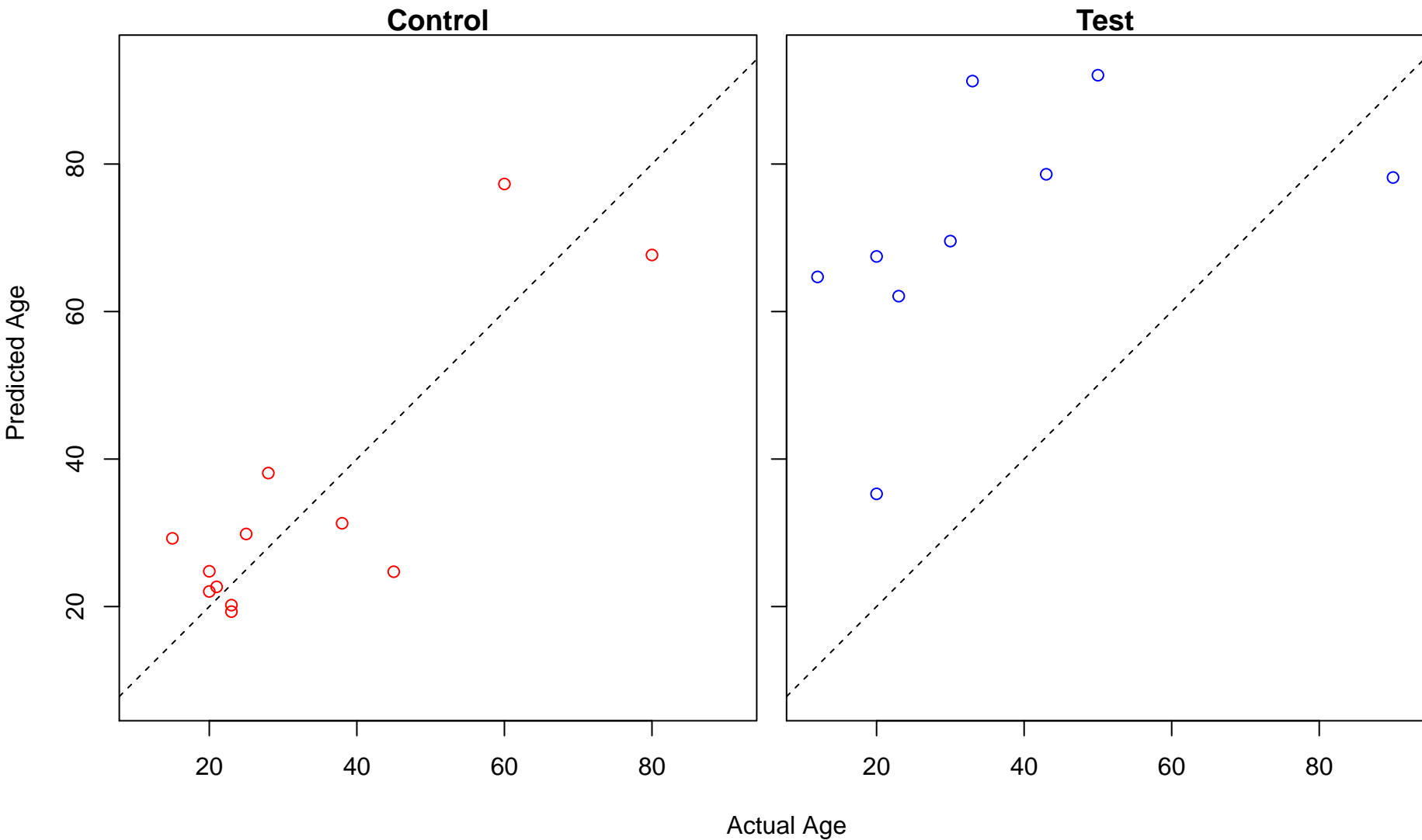
regulation of transcription involved in cell fate commitment (Score: 16.658888)



corticosteroid receptor signaling pathway (Score: 16.638916)

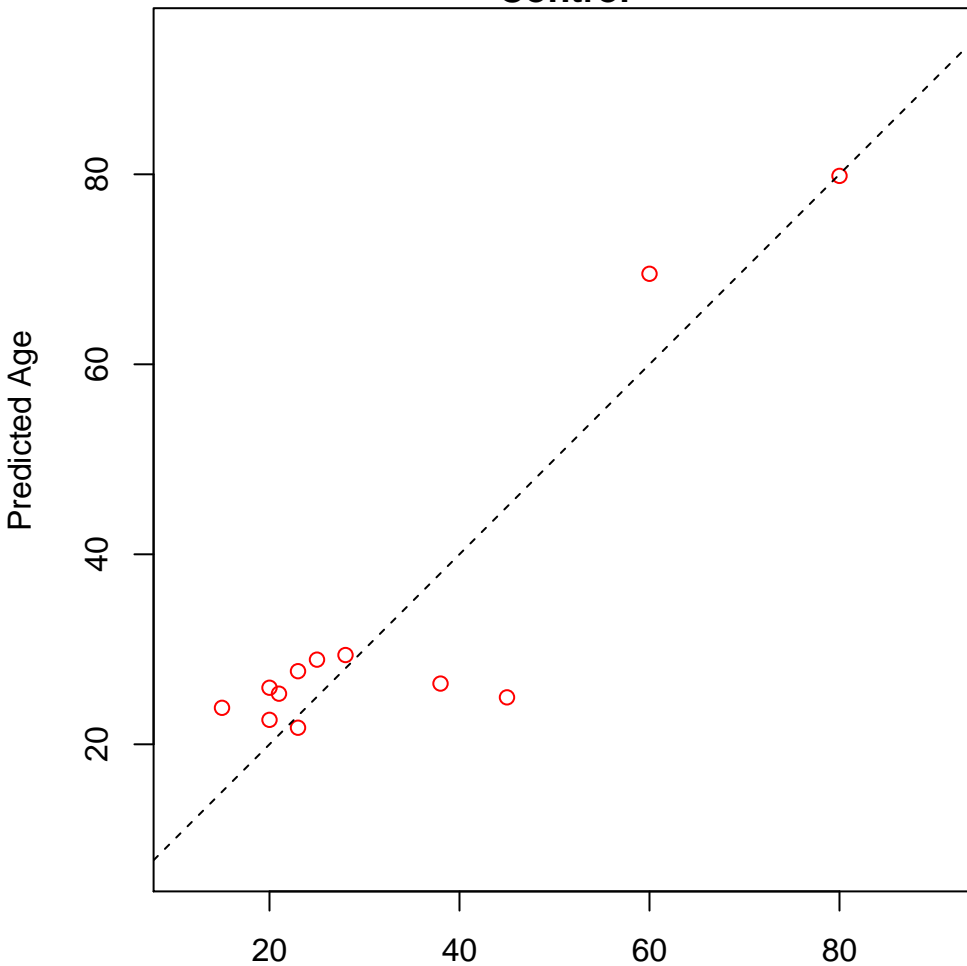


glucocorticoid receptor signaling pathway (Score: 16.638916)

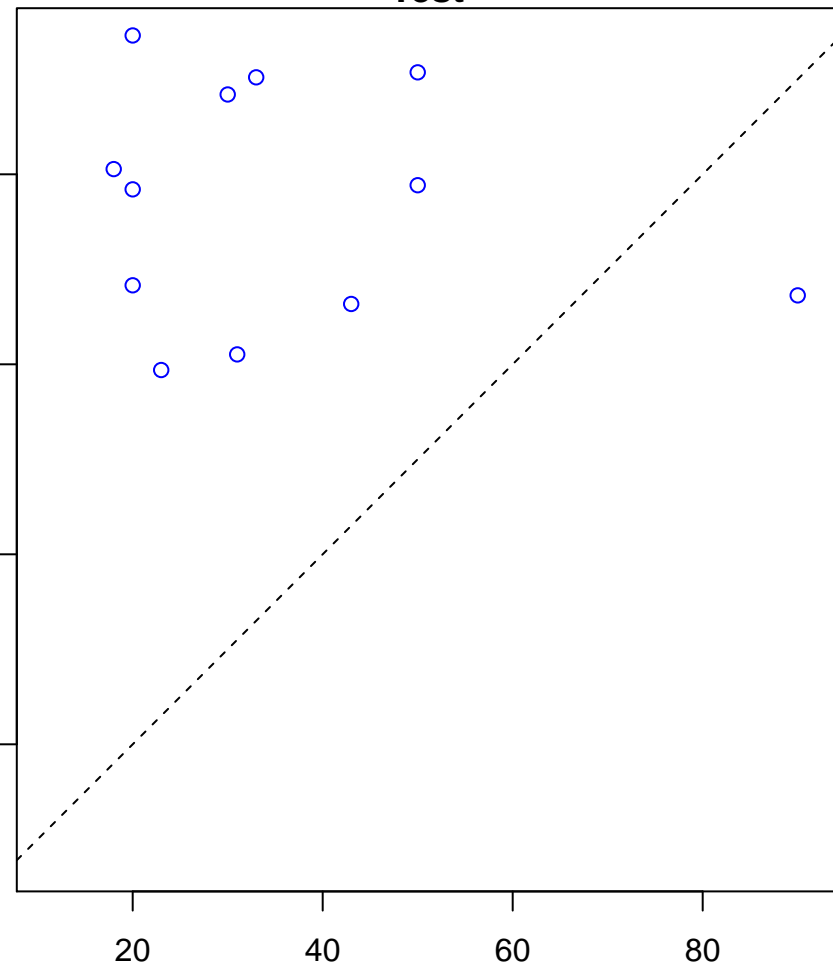


muscle organ morphogenesis (Score: 16.632903)

Control

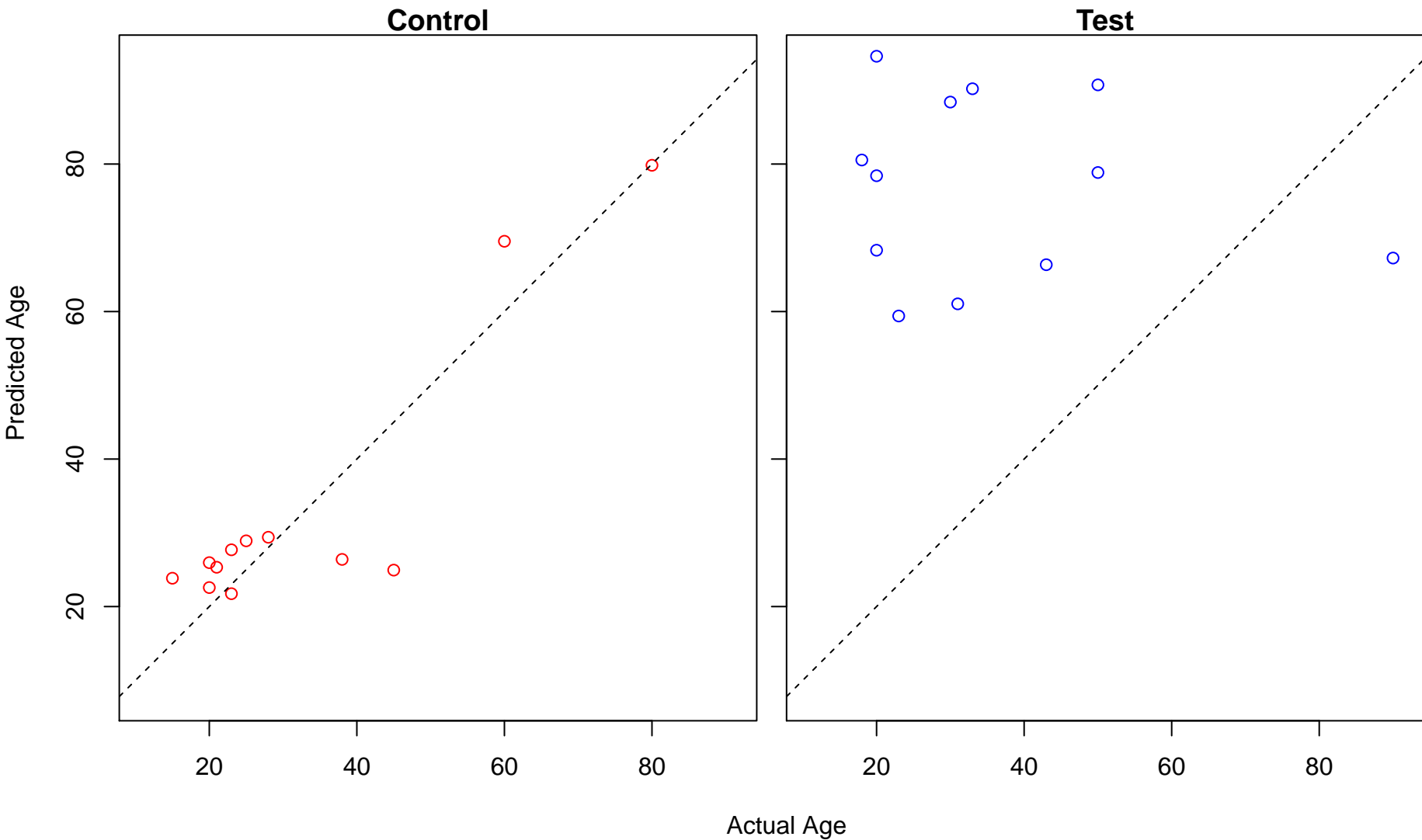


Test

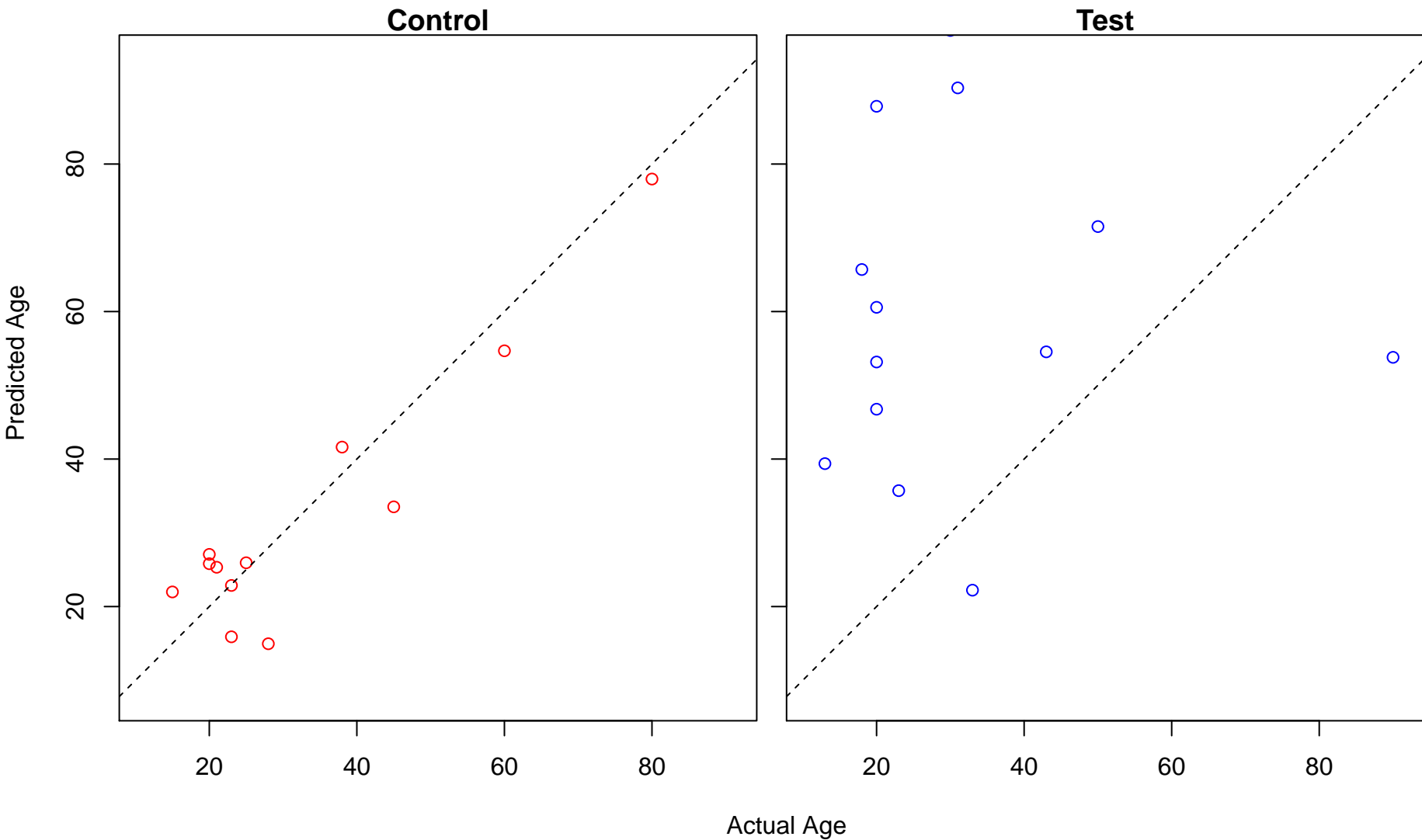


Actual Age

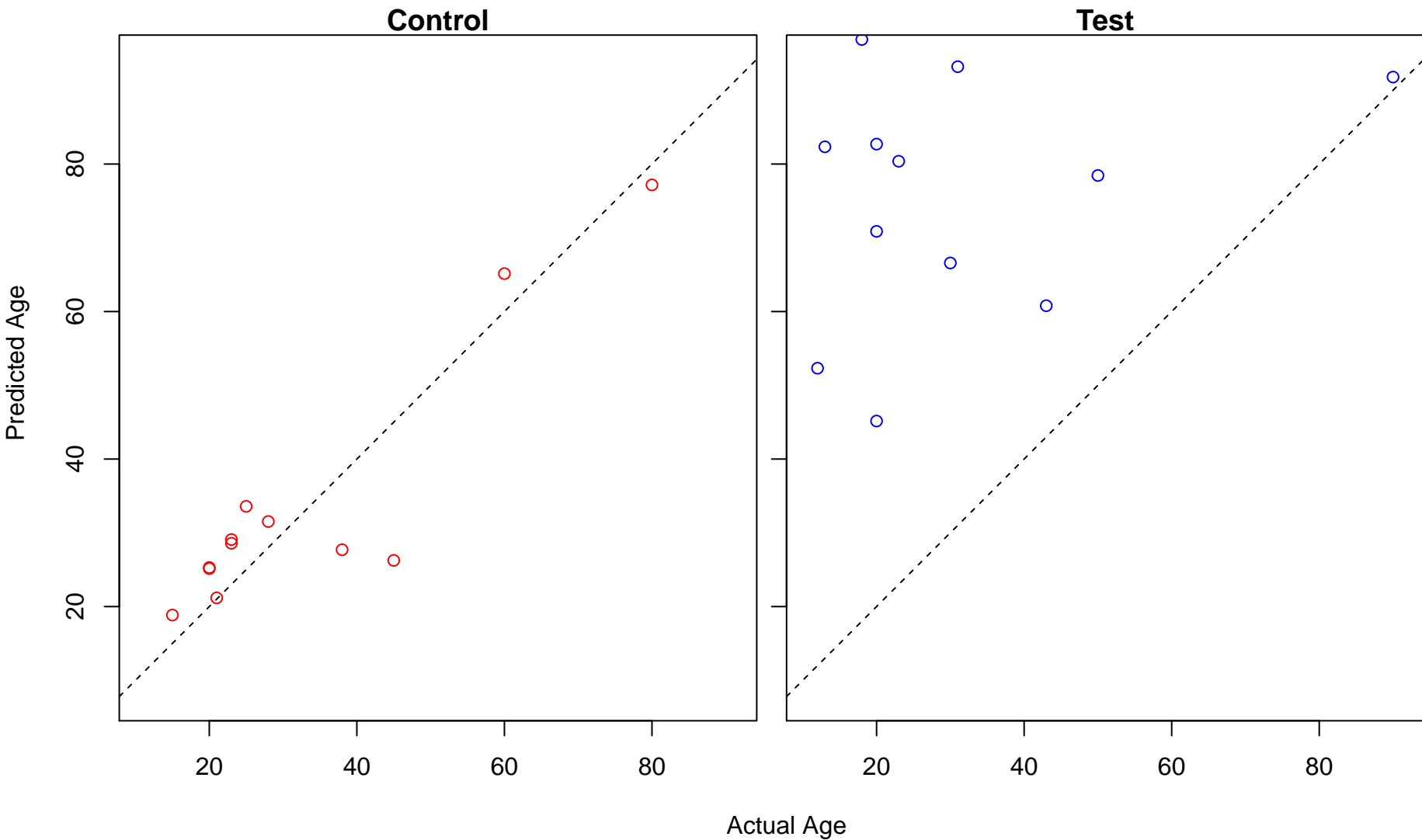
muscle tissue morphogenesis (Score: 16.632903)



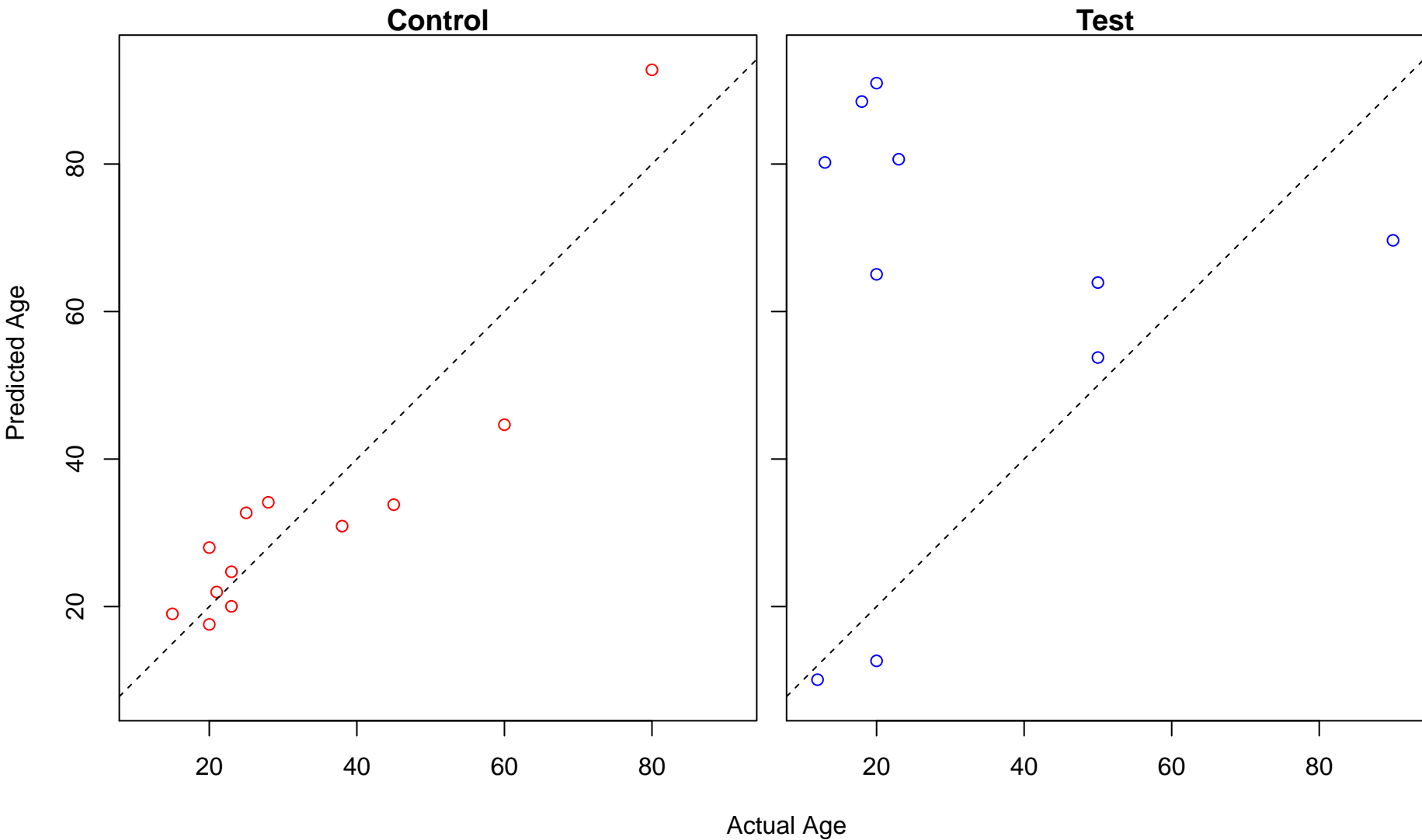
response to histamine (Score: 16.618165)



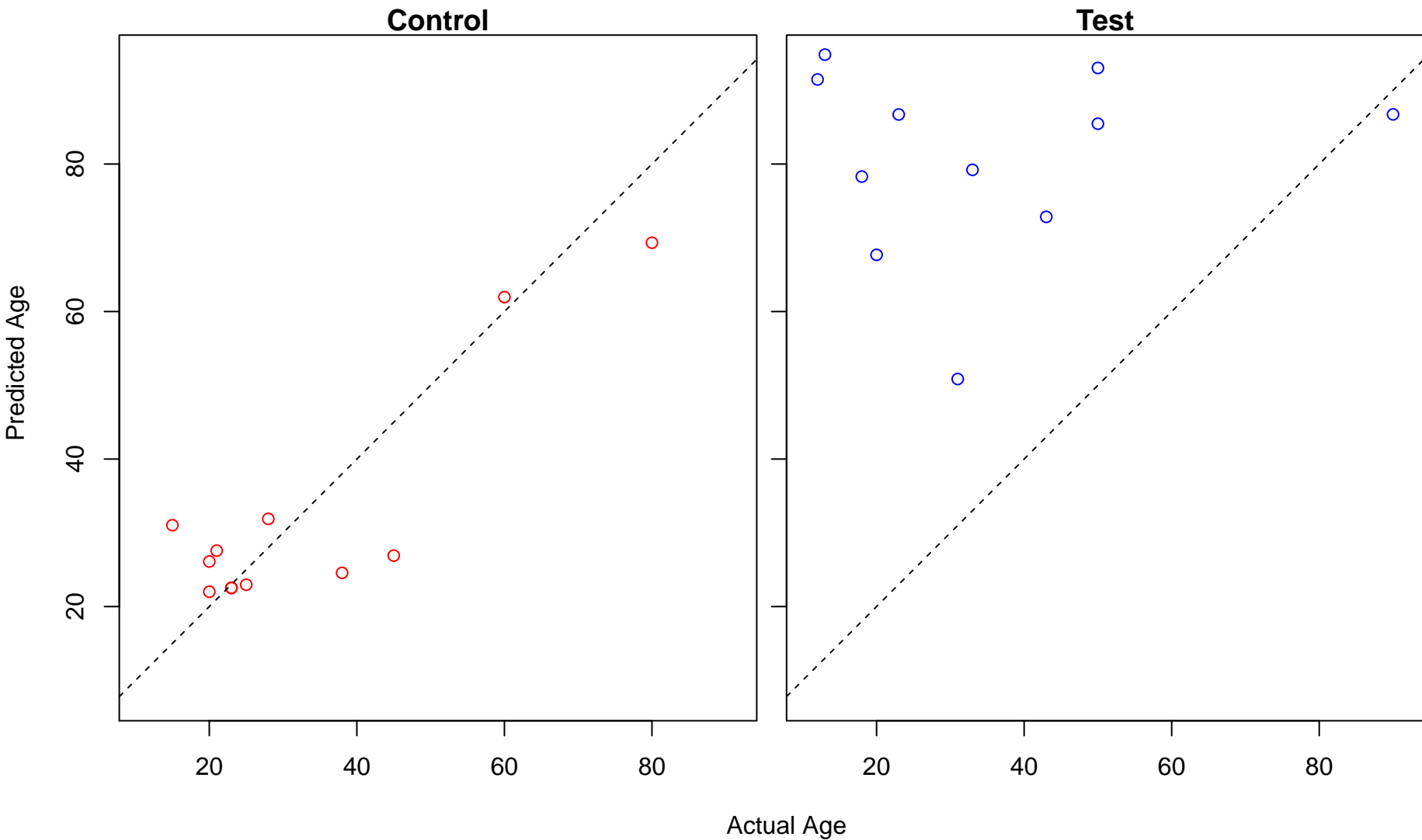
positive regulation of ruffle assembly (Score: 16.573381)



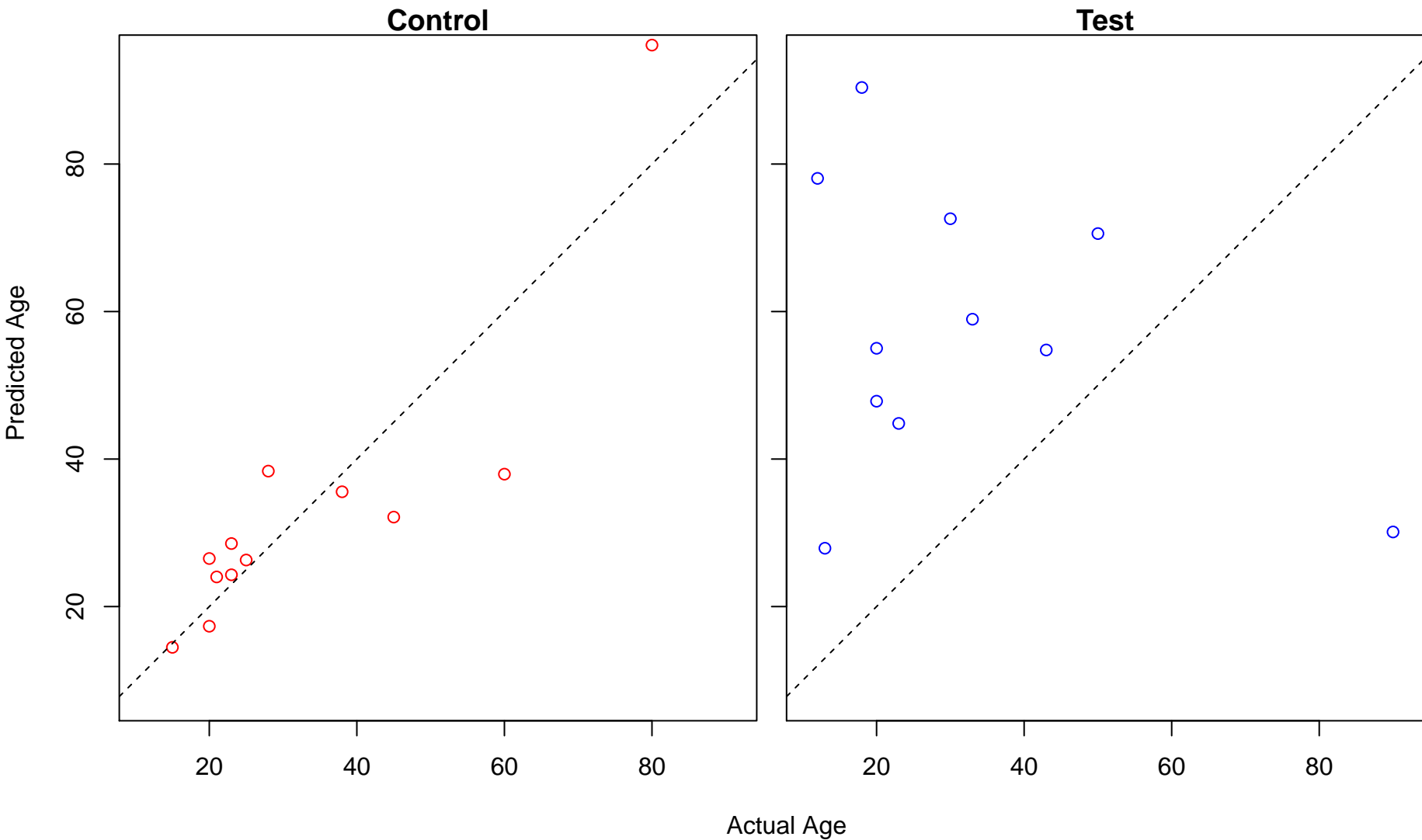
negative regulation of monooxygenase activity (Score: 16.572882)



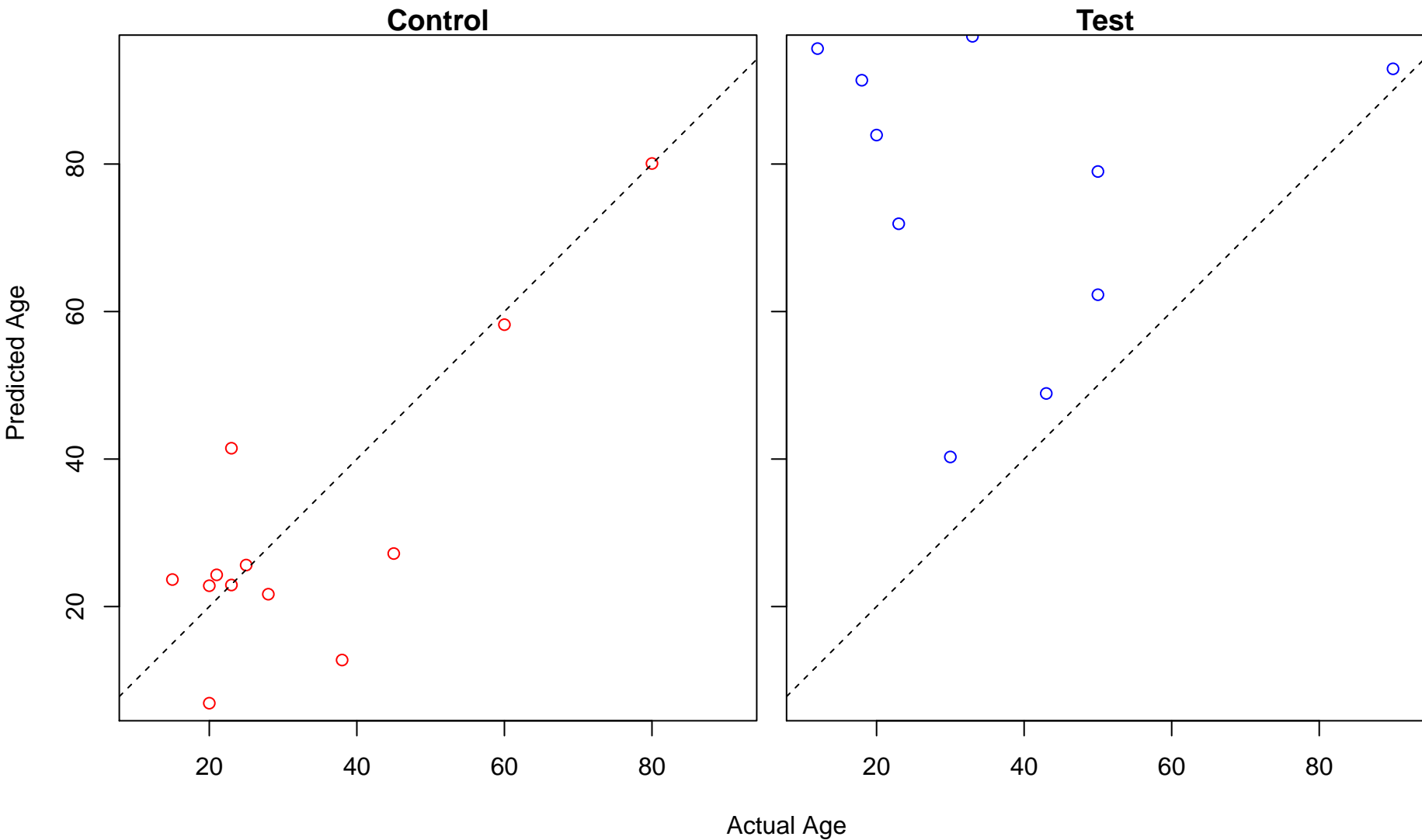
regulation of interleukin-1 beta production (Score: 16.509813)



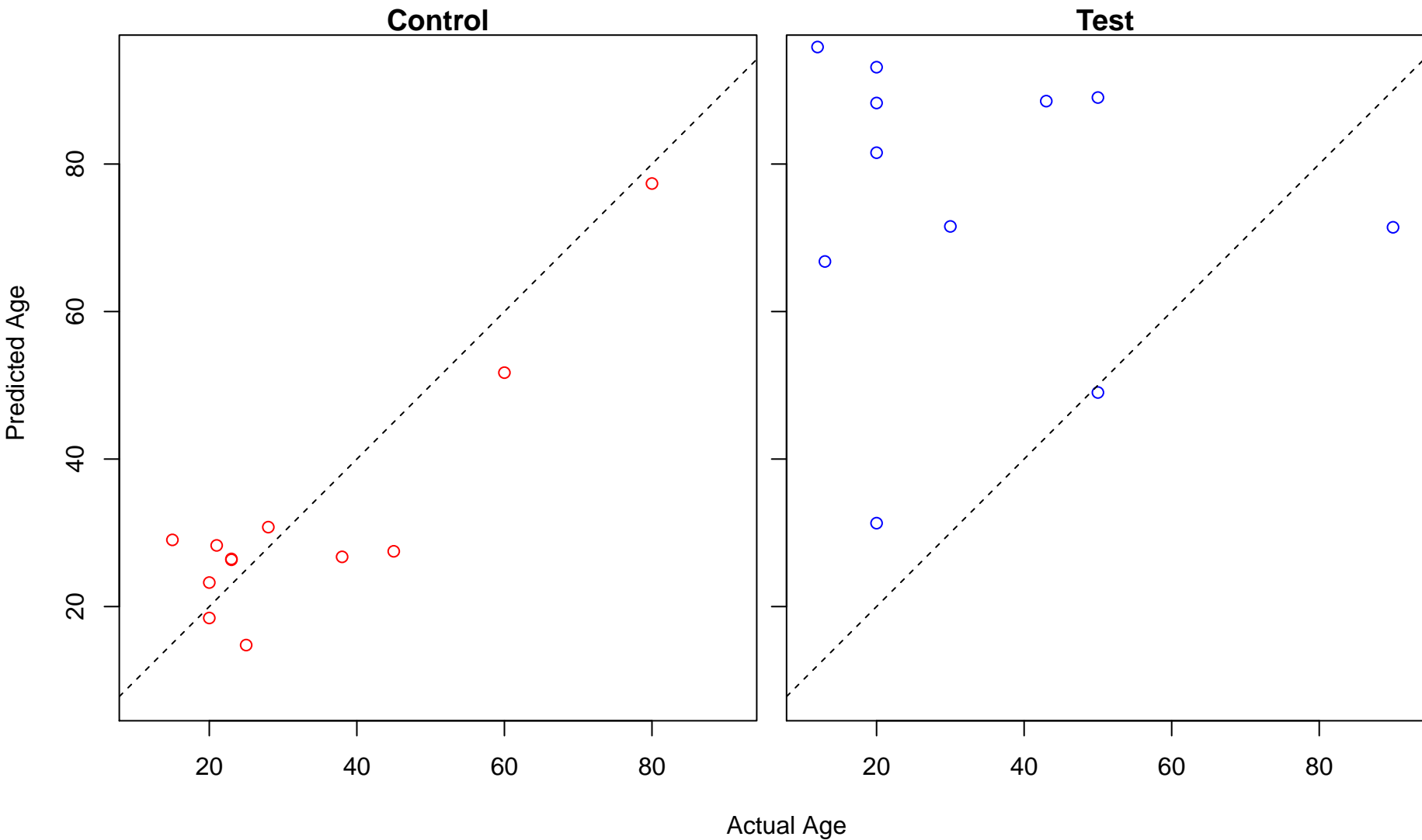
vitamin metabolic process (Score: 16.482628)



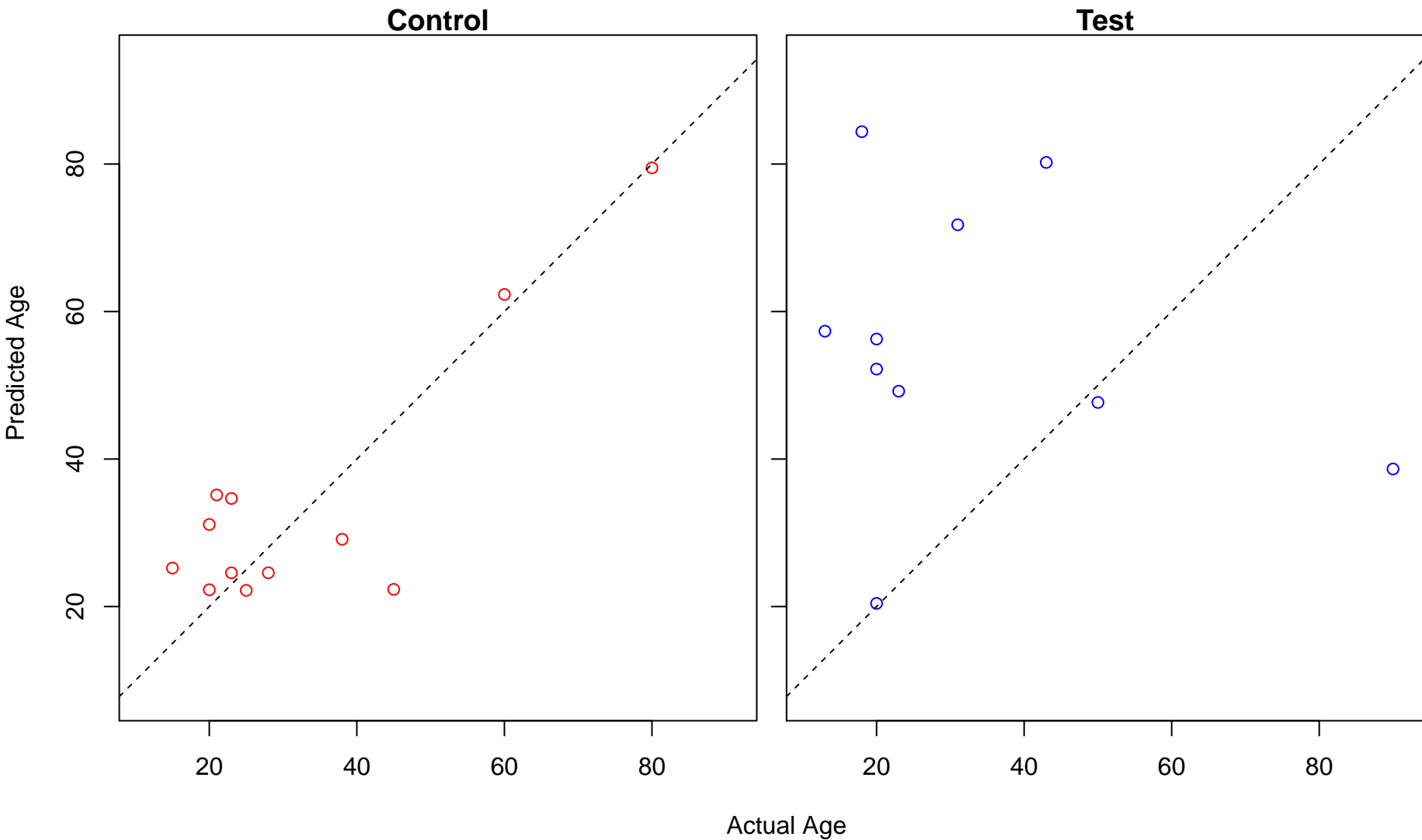
potassium ion import (Score: 16.474080)



cilium assembly (Score: 16.462624)

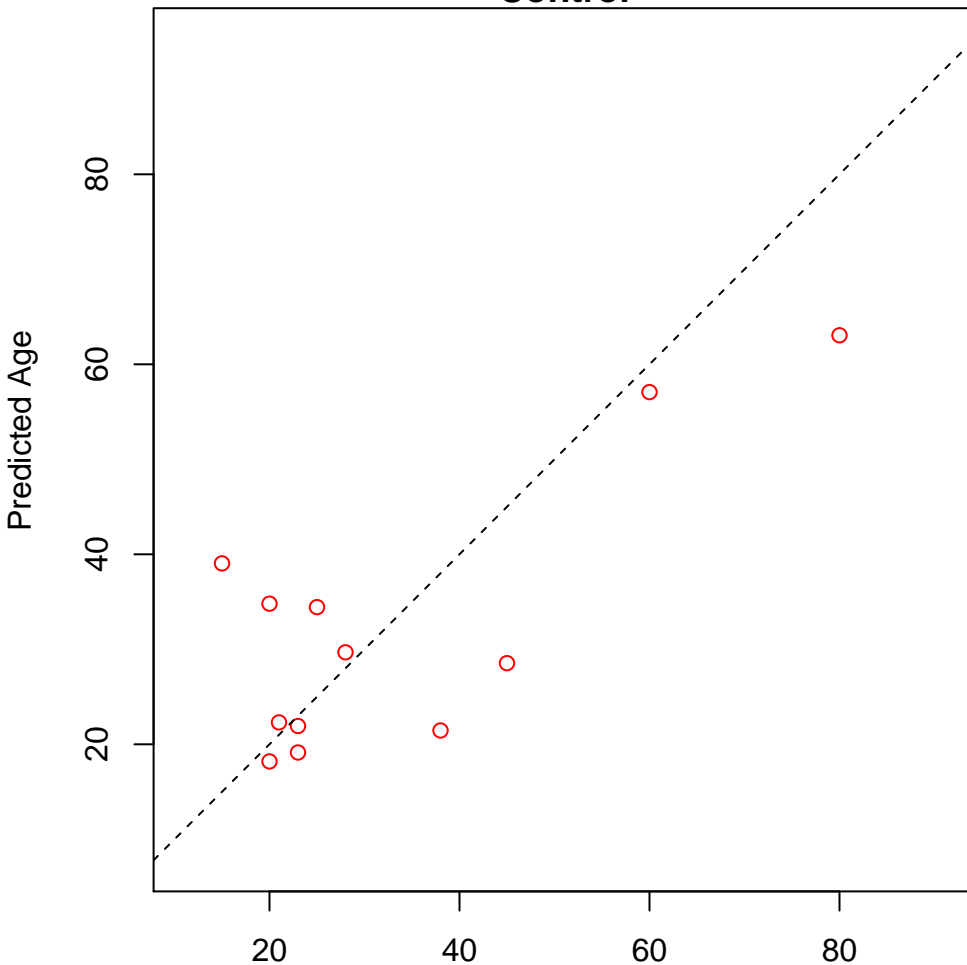


gastrulation (Score: 16.440560)

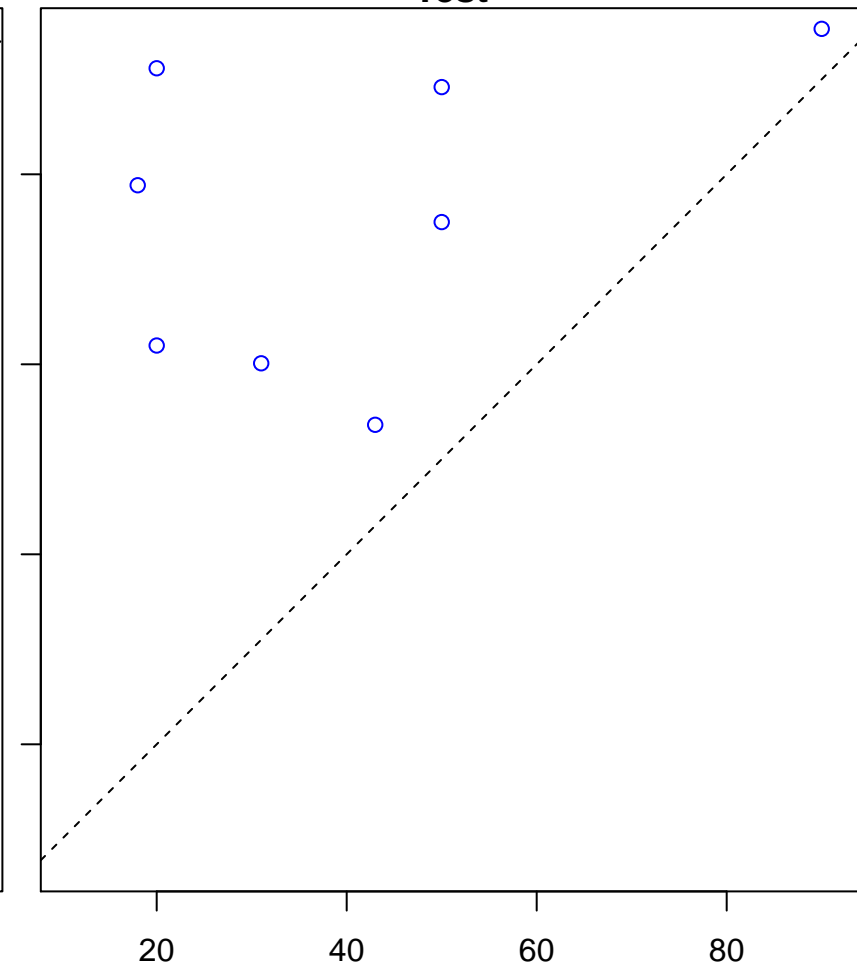


acylglycerol acyl-chain remodeling (Score: 16.407696)

Control

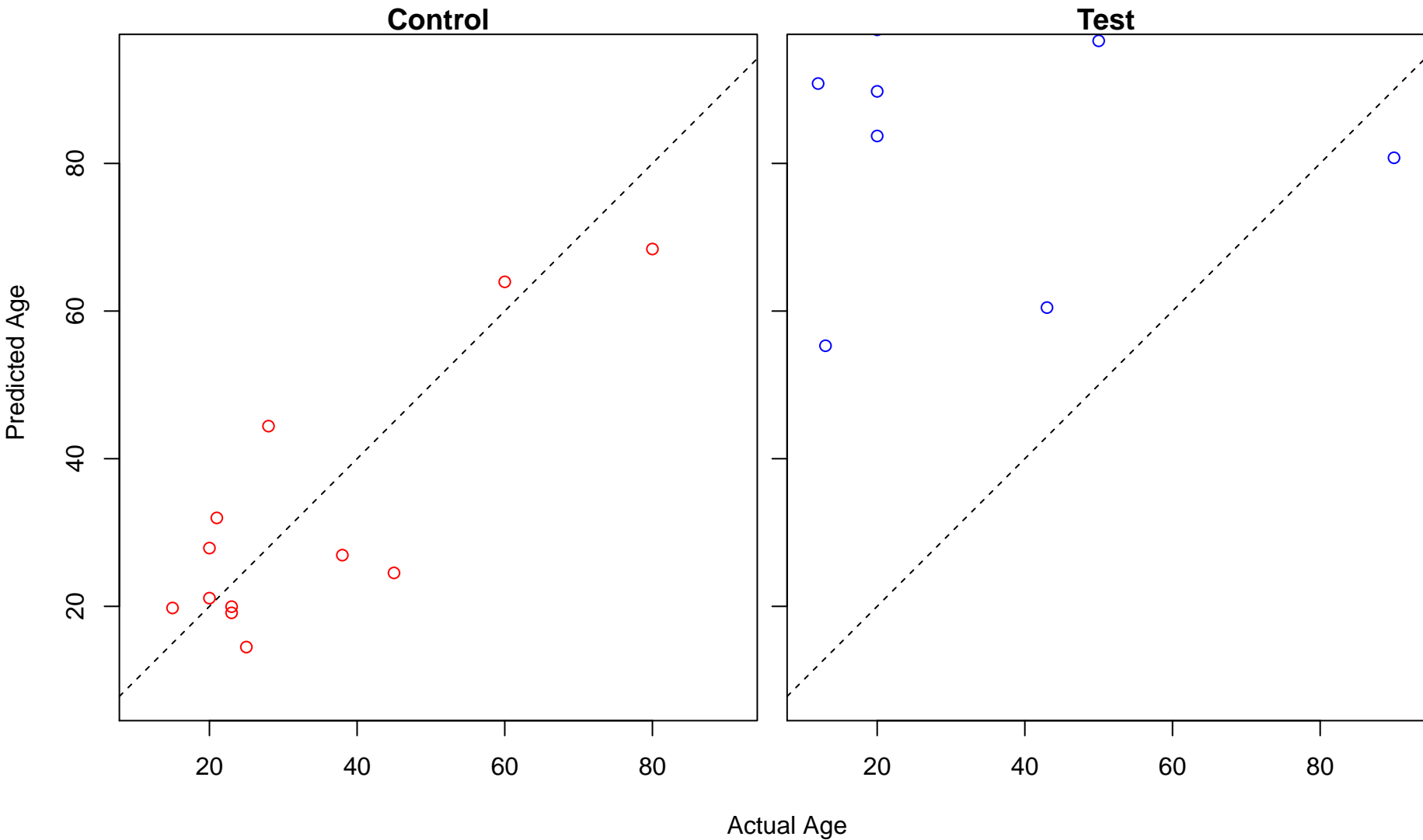


Test



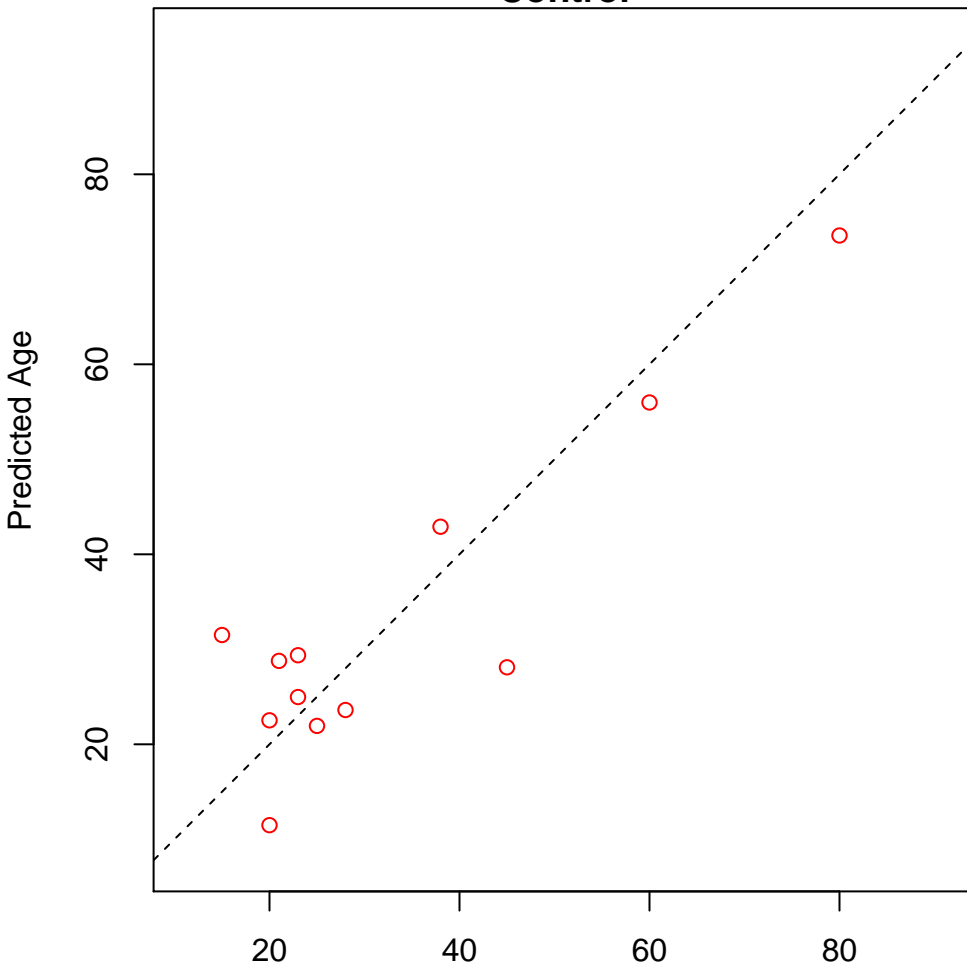
Actual Age

positive regulation of protein complex assembly (Score: 16.397830)

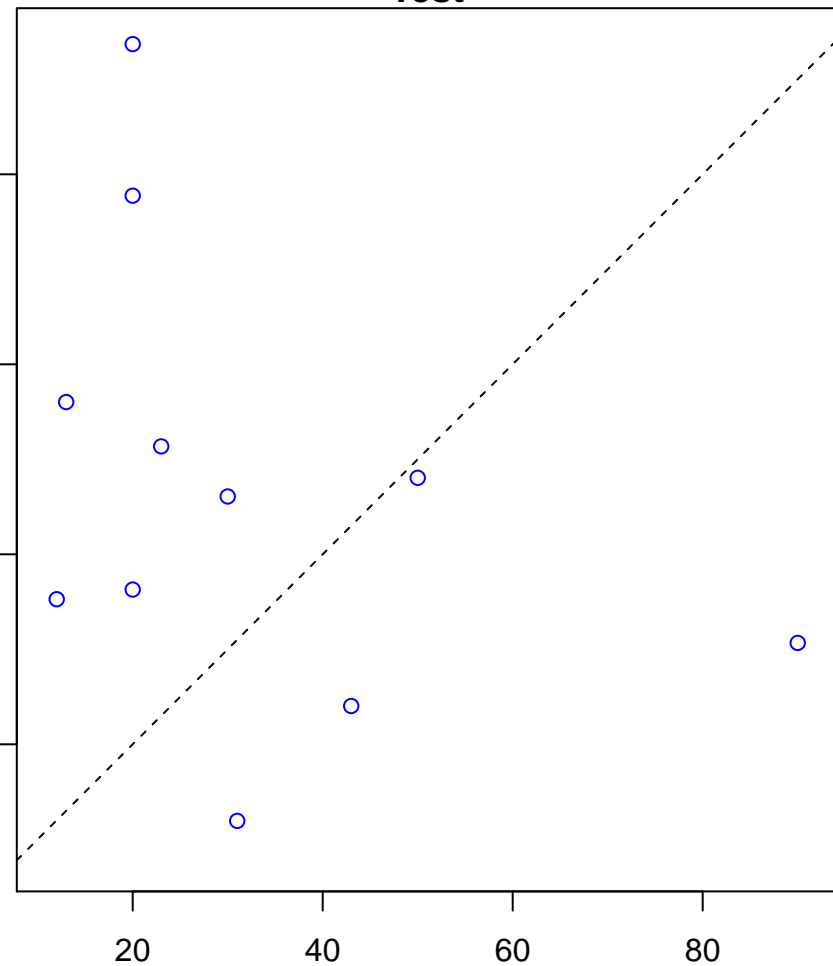


regulation of transmembrane transport (Score: 16.380658)

Control



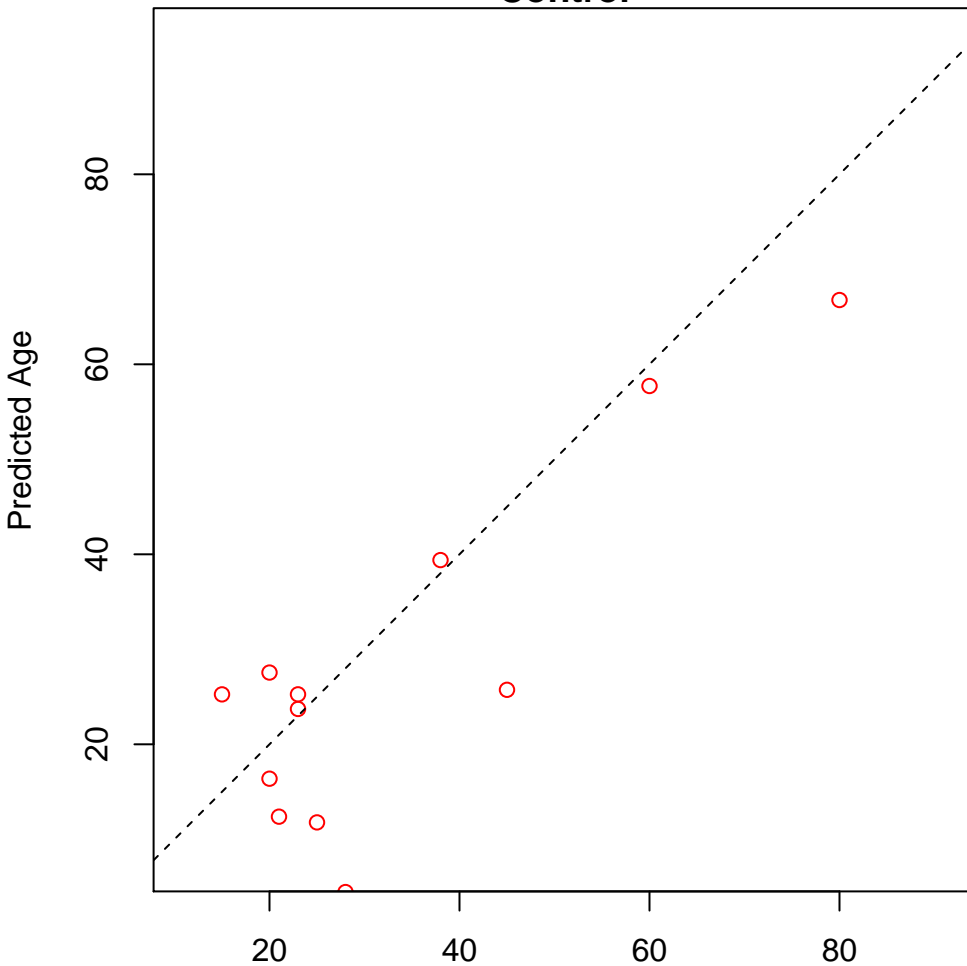
Test



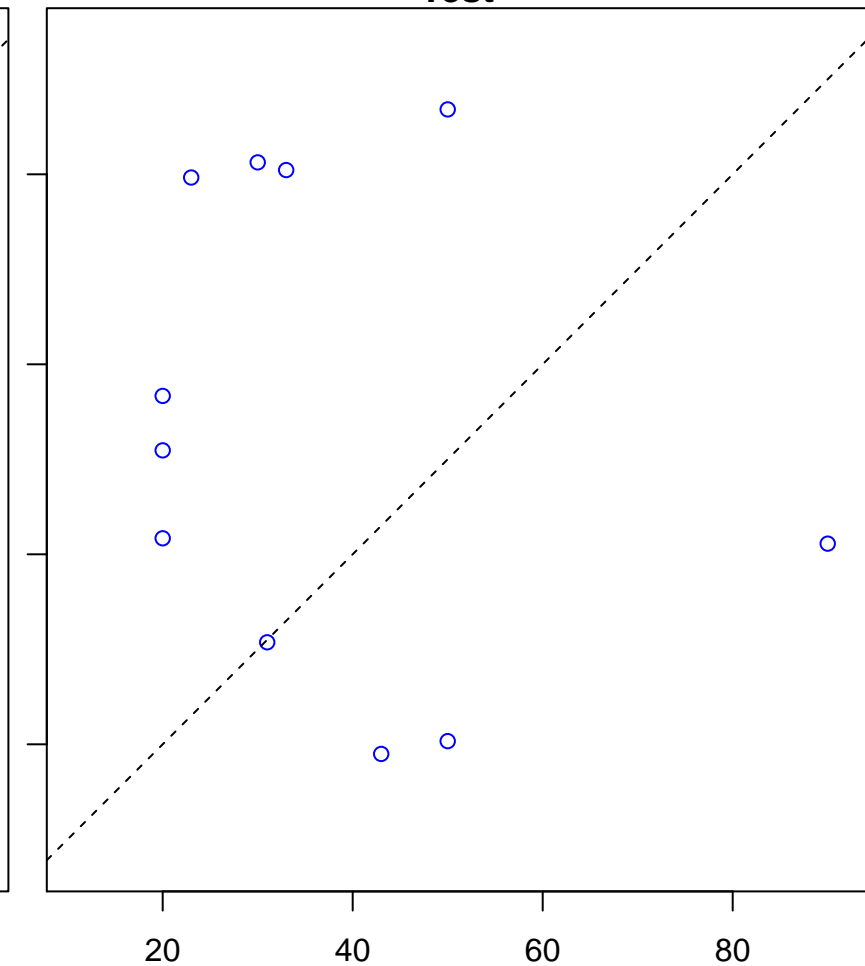
Actual Age

regulation of platelet aggregation (Score: 16.358696)

Control

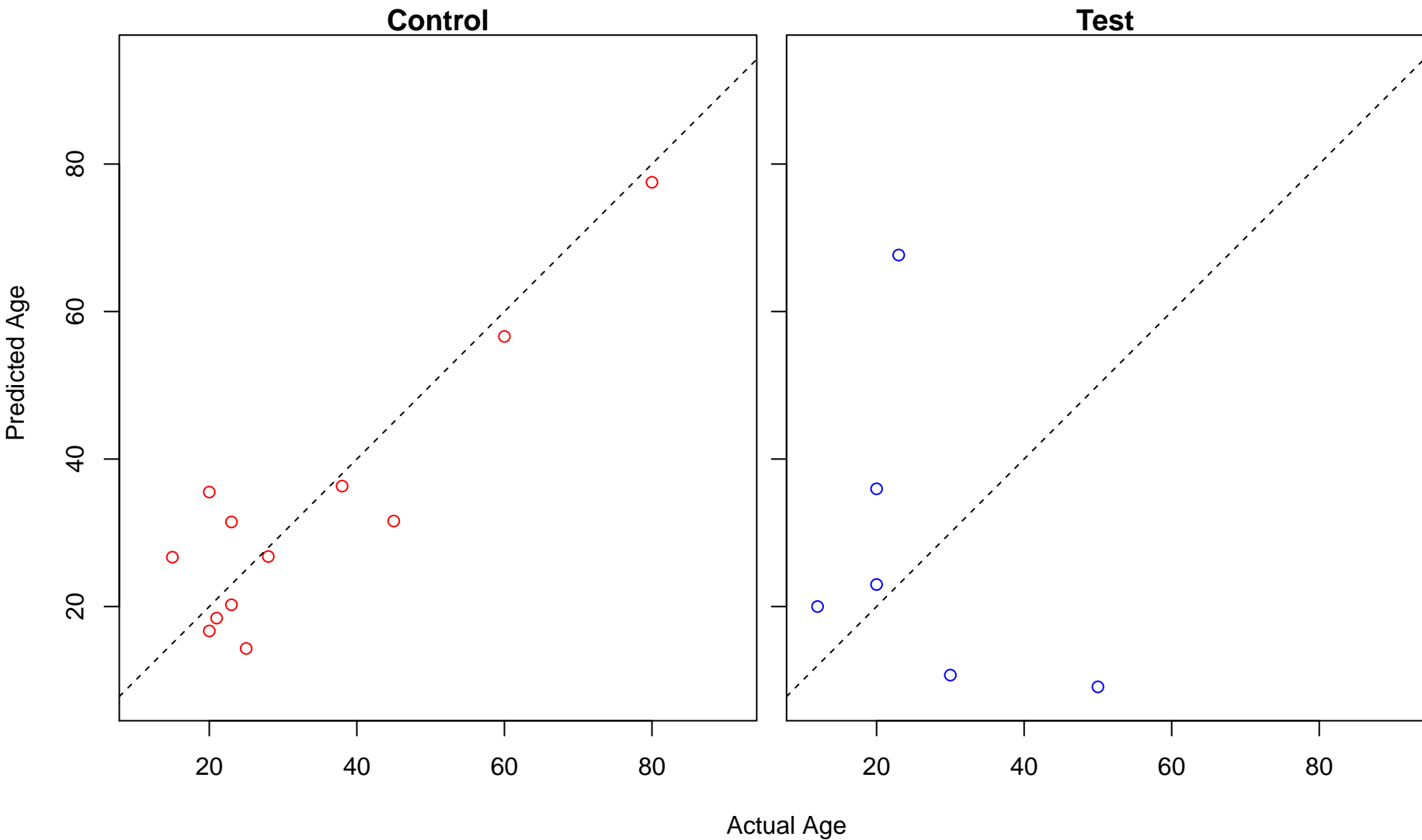


Test

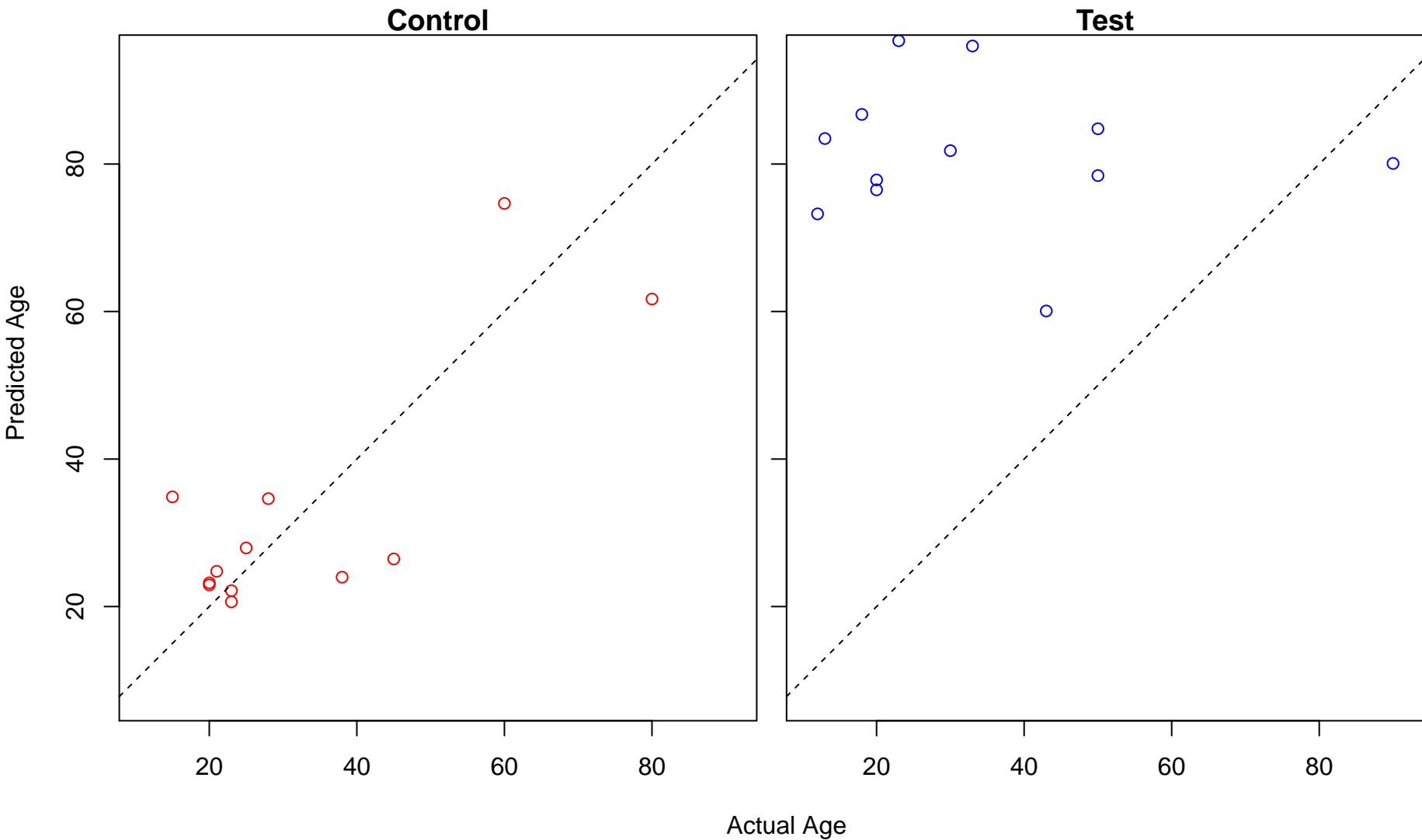


Actual Age

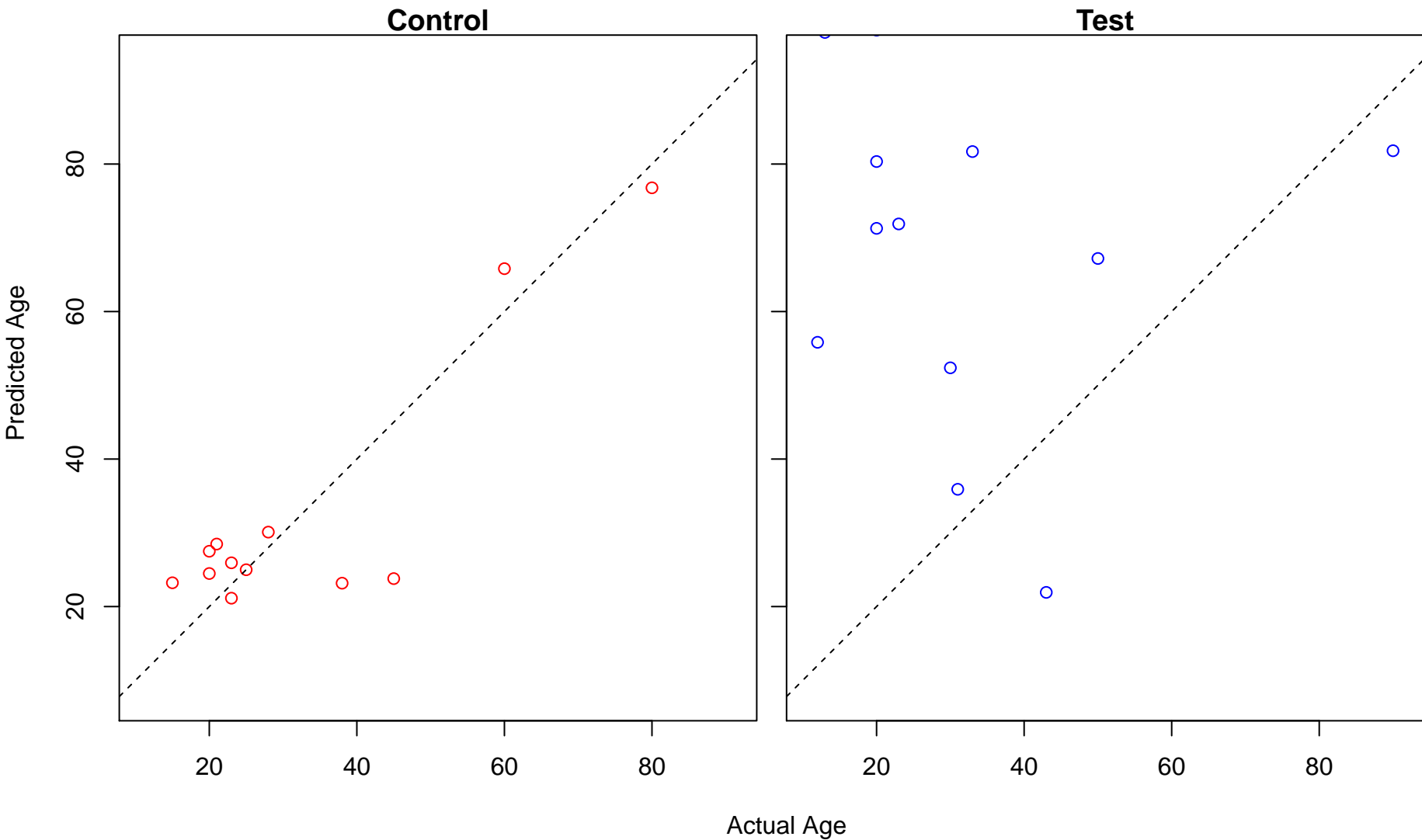
Schwann cell differentiation (Score: 16.358617)



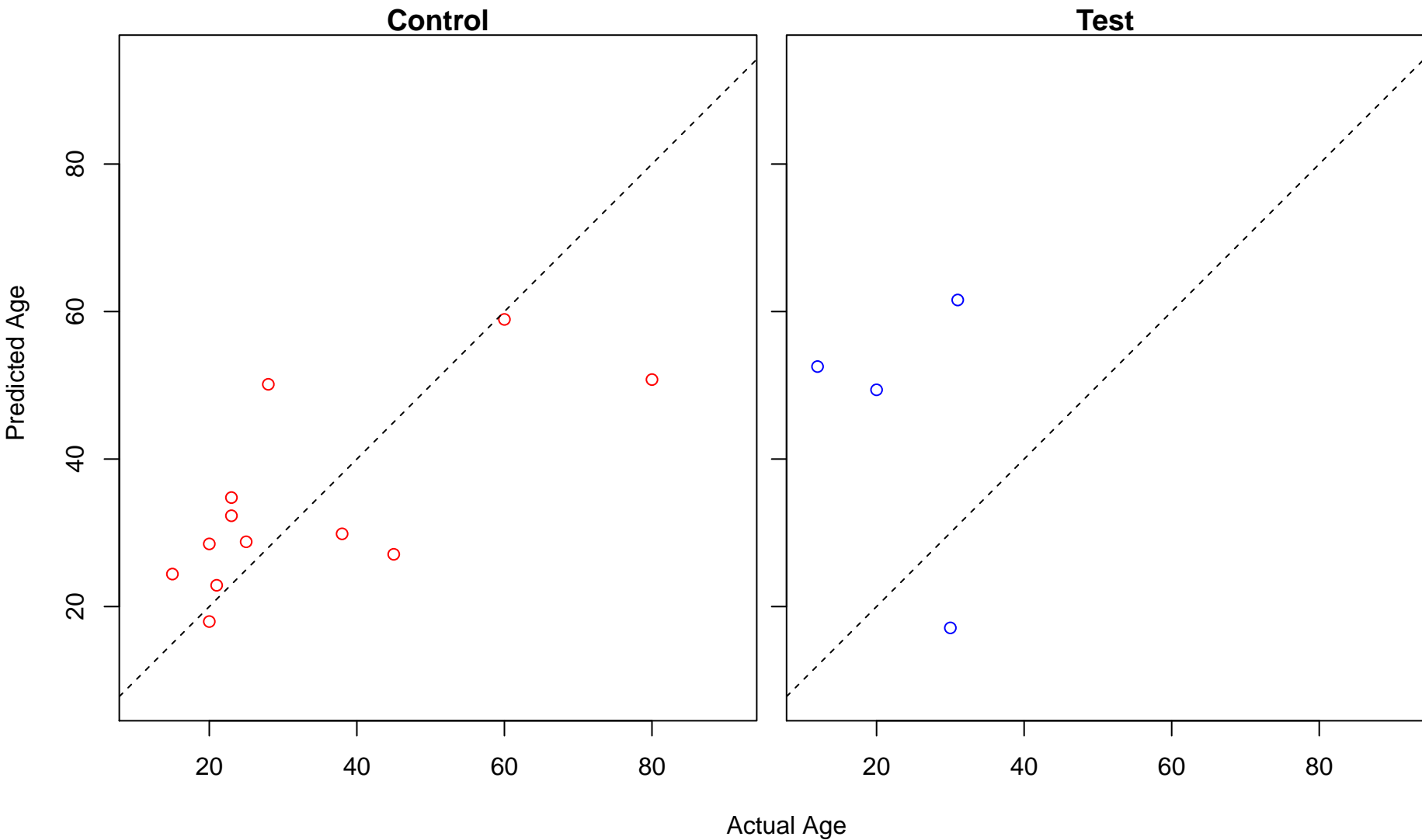
positive regulation of heterotypic cell-cell adhesion (Score: 16.353200)



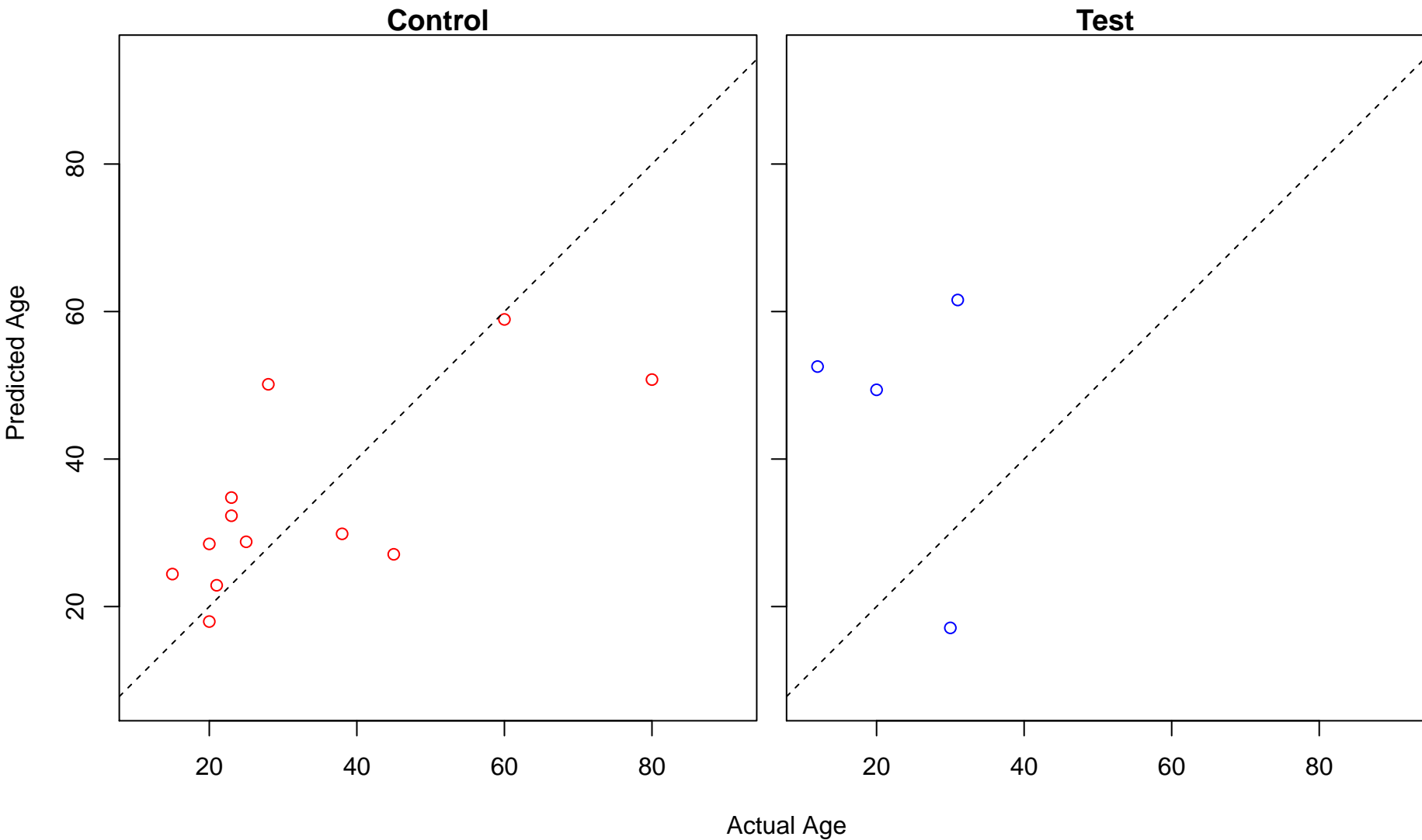
ribosomal large subunit biogenesis (Score: 16.332308)



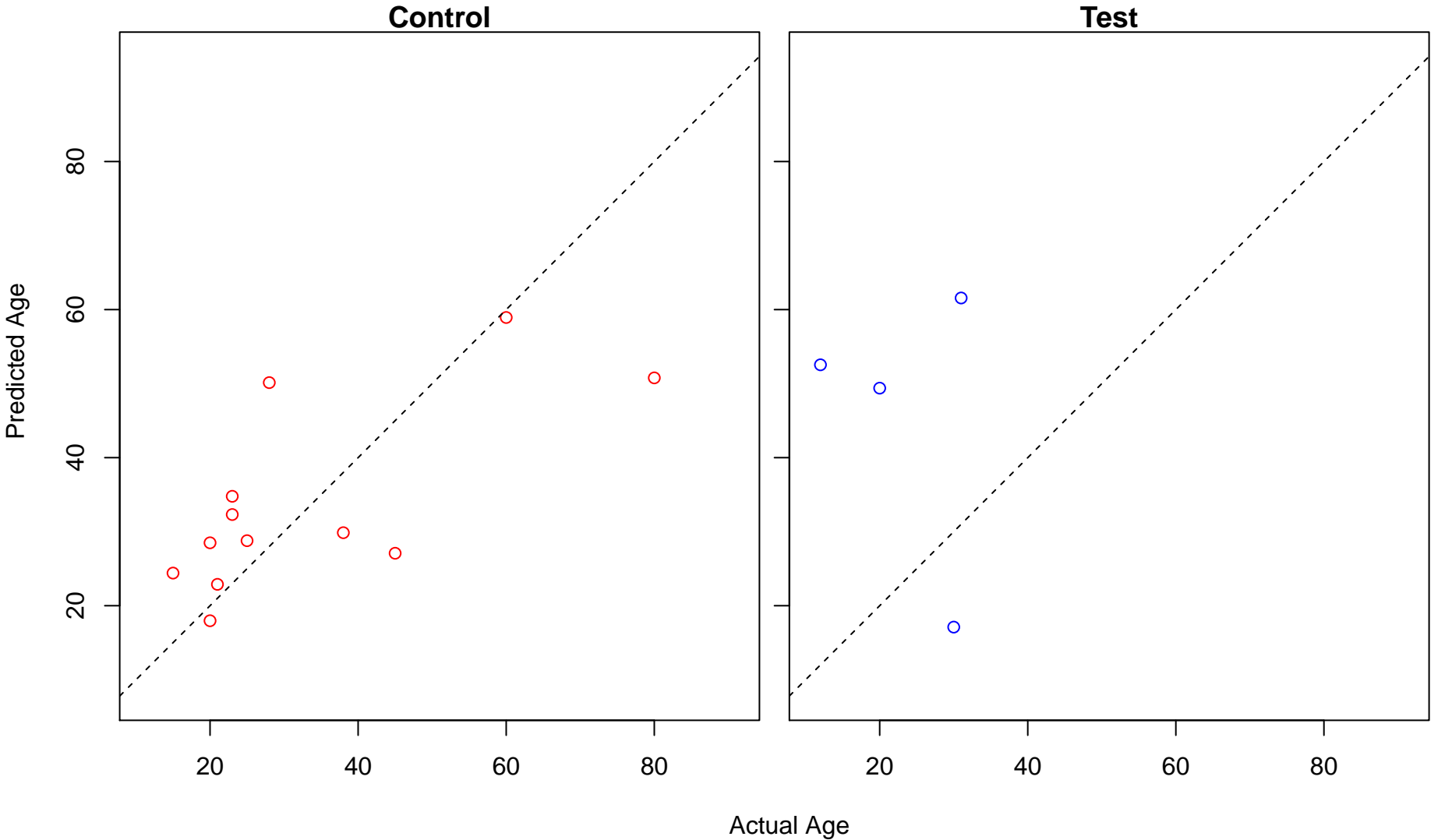
regulation of natural killer cell mediated immune response to tumor cell (Score: 16.306453)



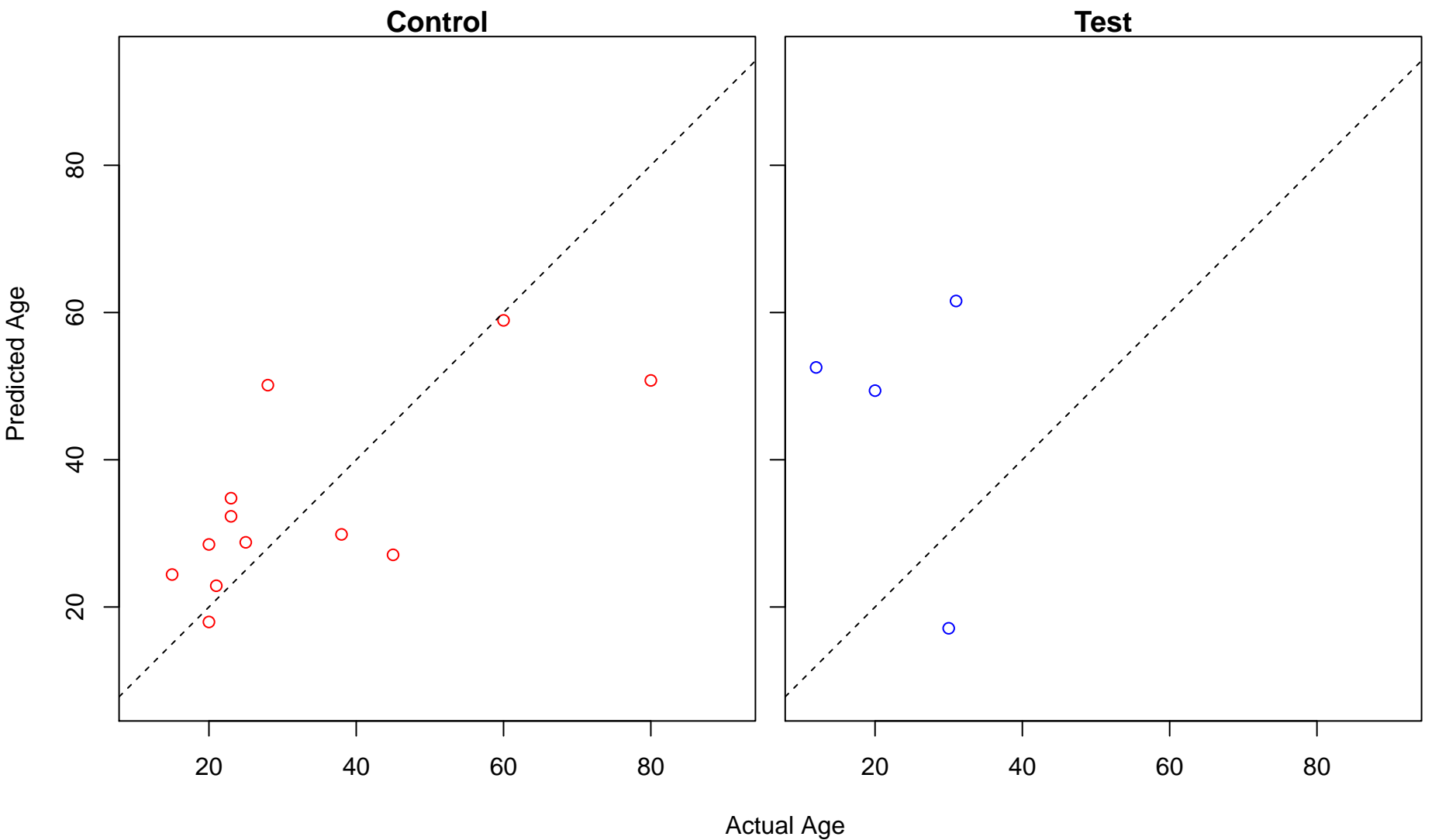
positive regulation of natural killer cell mediated immune response to tumor cell (Score: 16.306453)



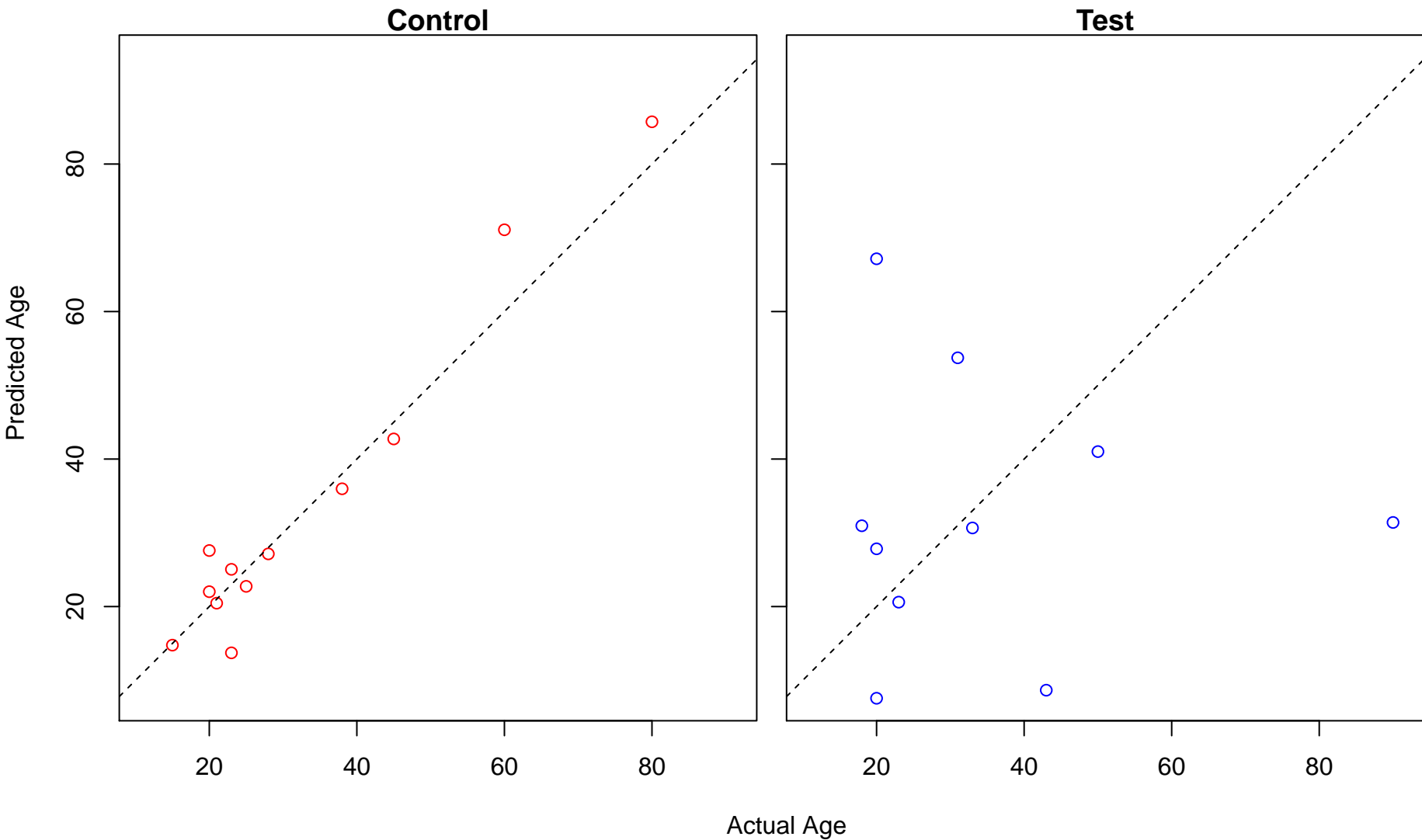
regulation of natural killer cell mediated cytotoxicity directed against tumor cell target (Score: 16.306)



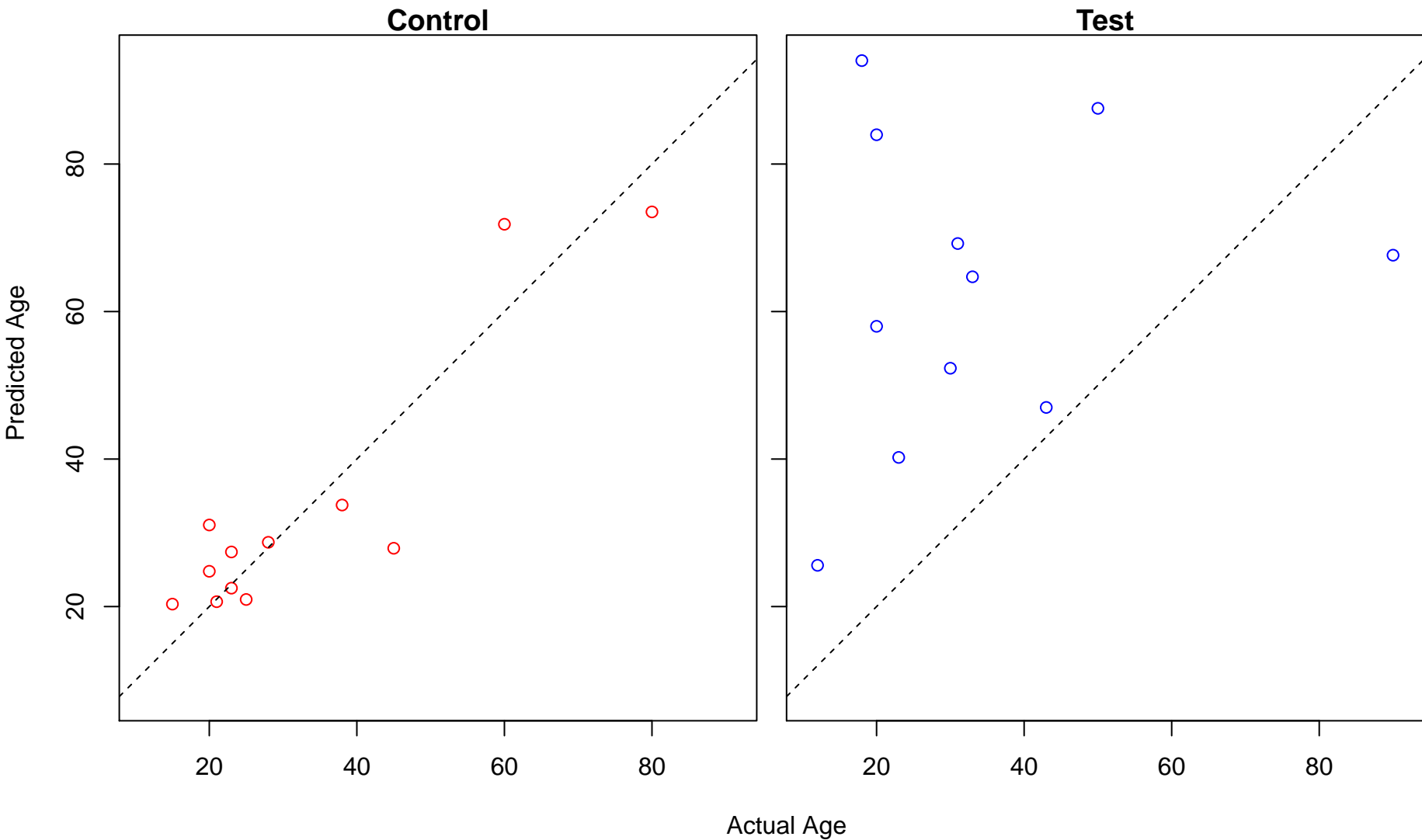
positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target (Score: 16)



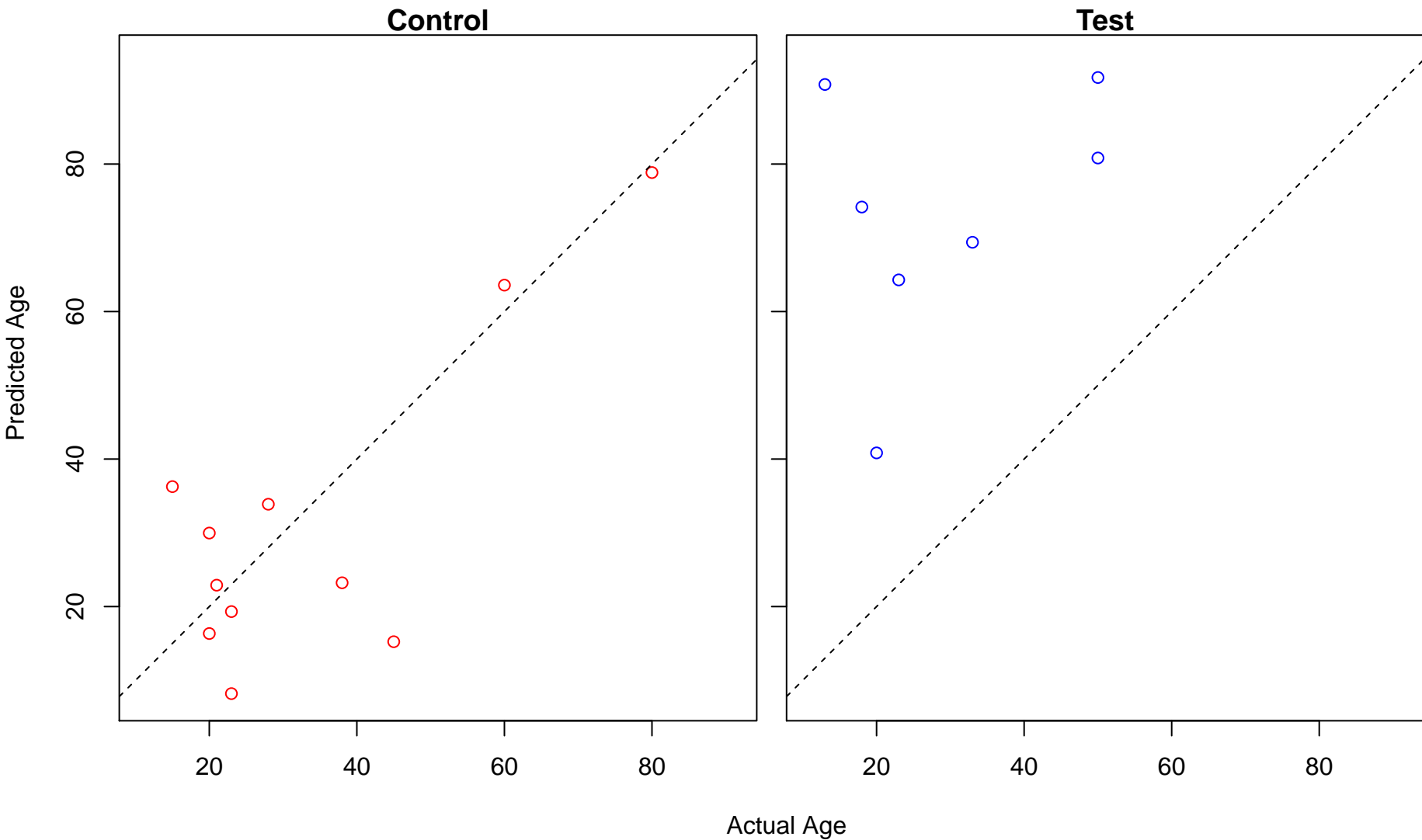
vitamin D metabolic process (Score: 16.287581)



protein hexamerization (Score: 16.275476)

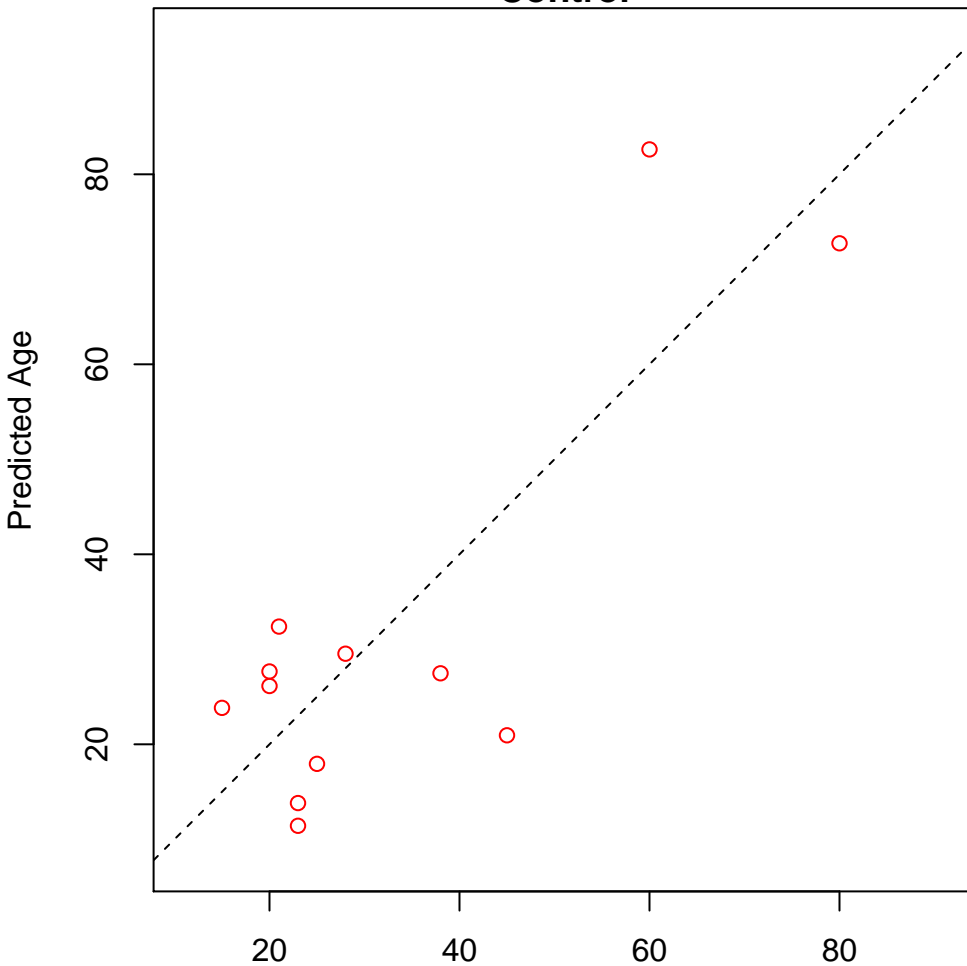


regulation of tumor necrosis factor biosynthetic process (Score: 16.205301)

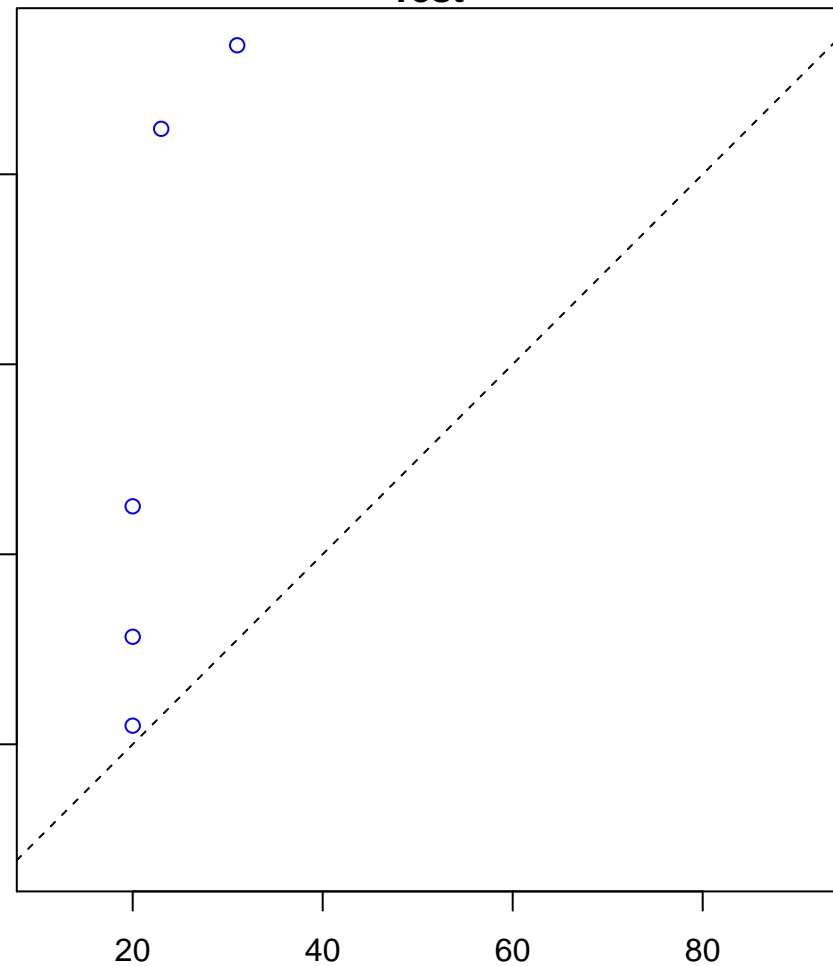


response to arsenic-containing substance (Score: 16.155932)

Control

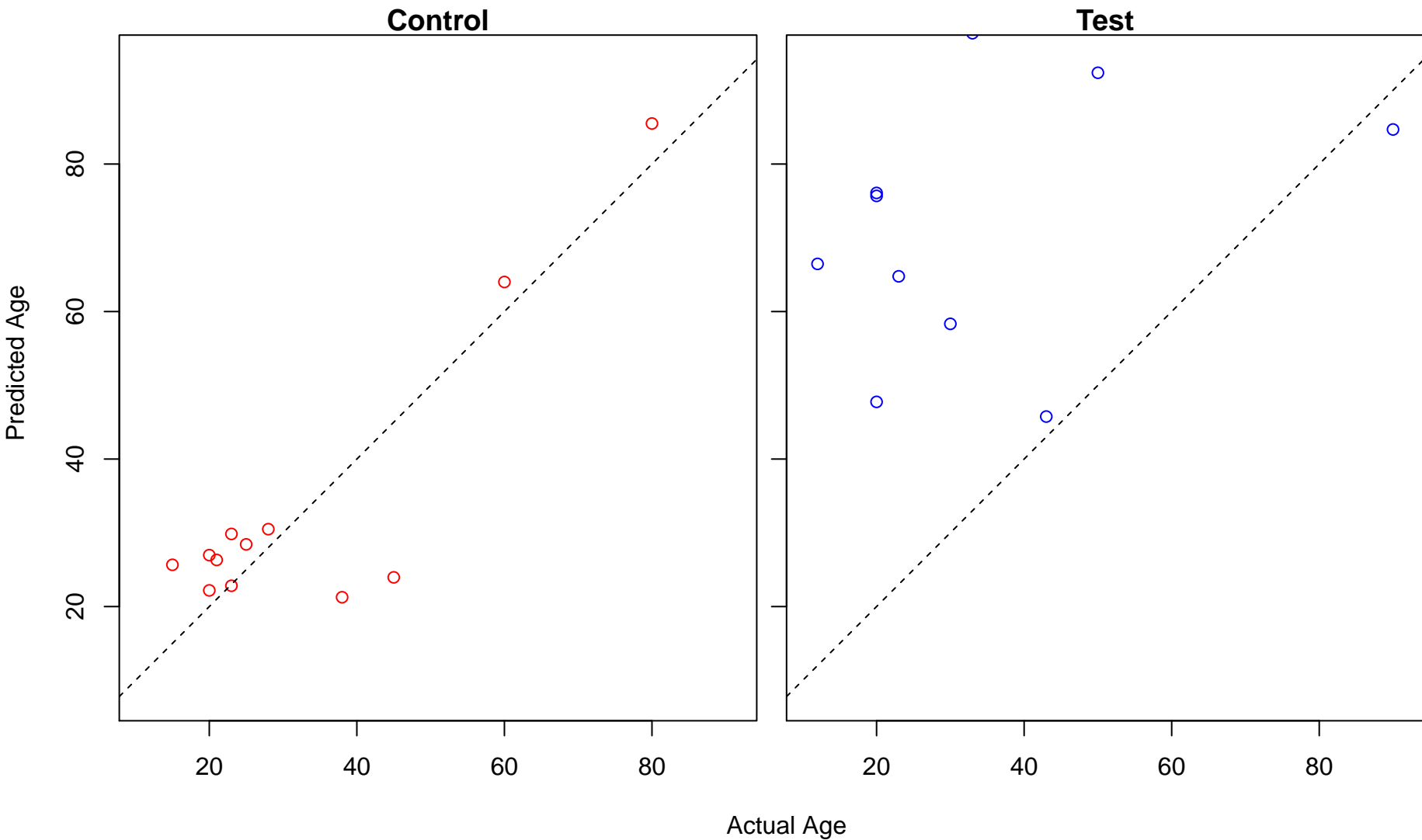


Test

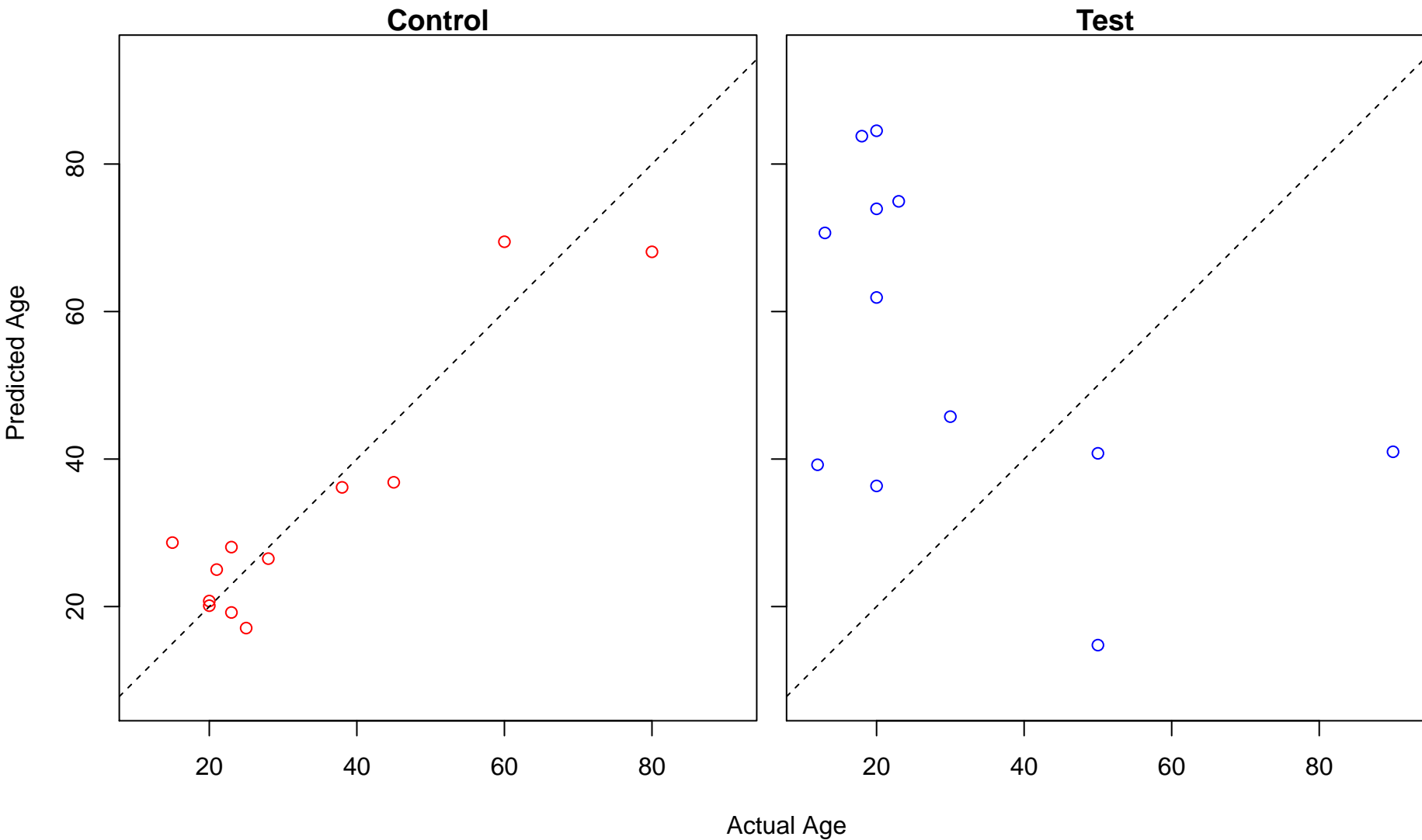


Actual Age

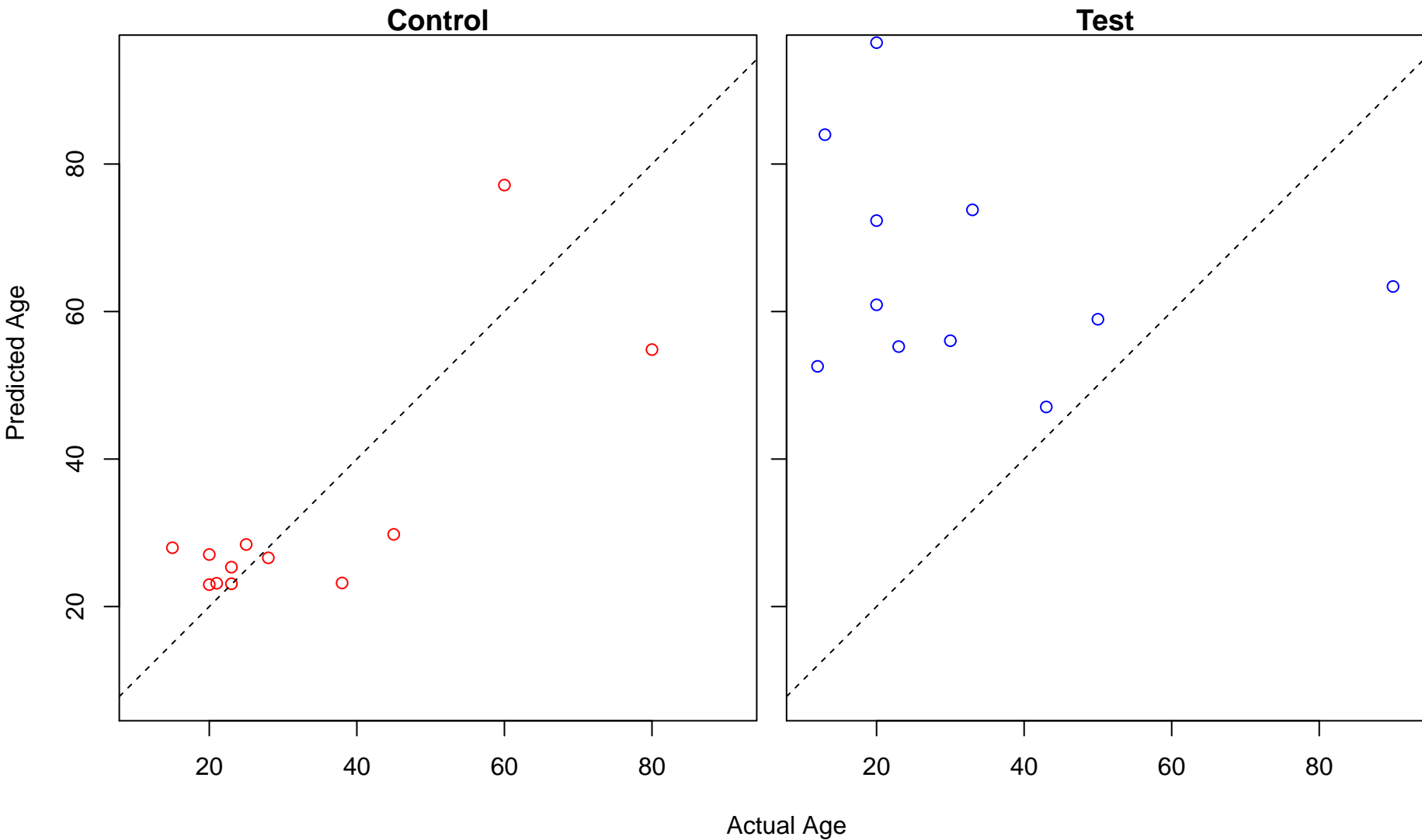
protein monoubiquitination (Score: 16.132456)



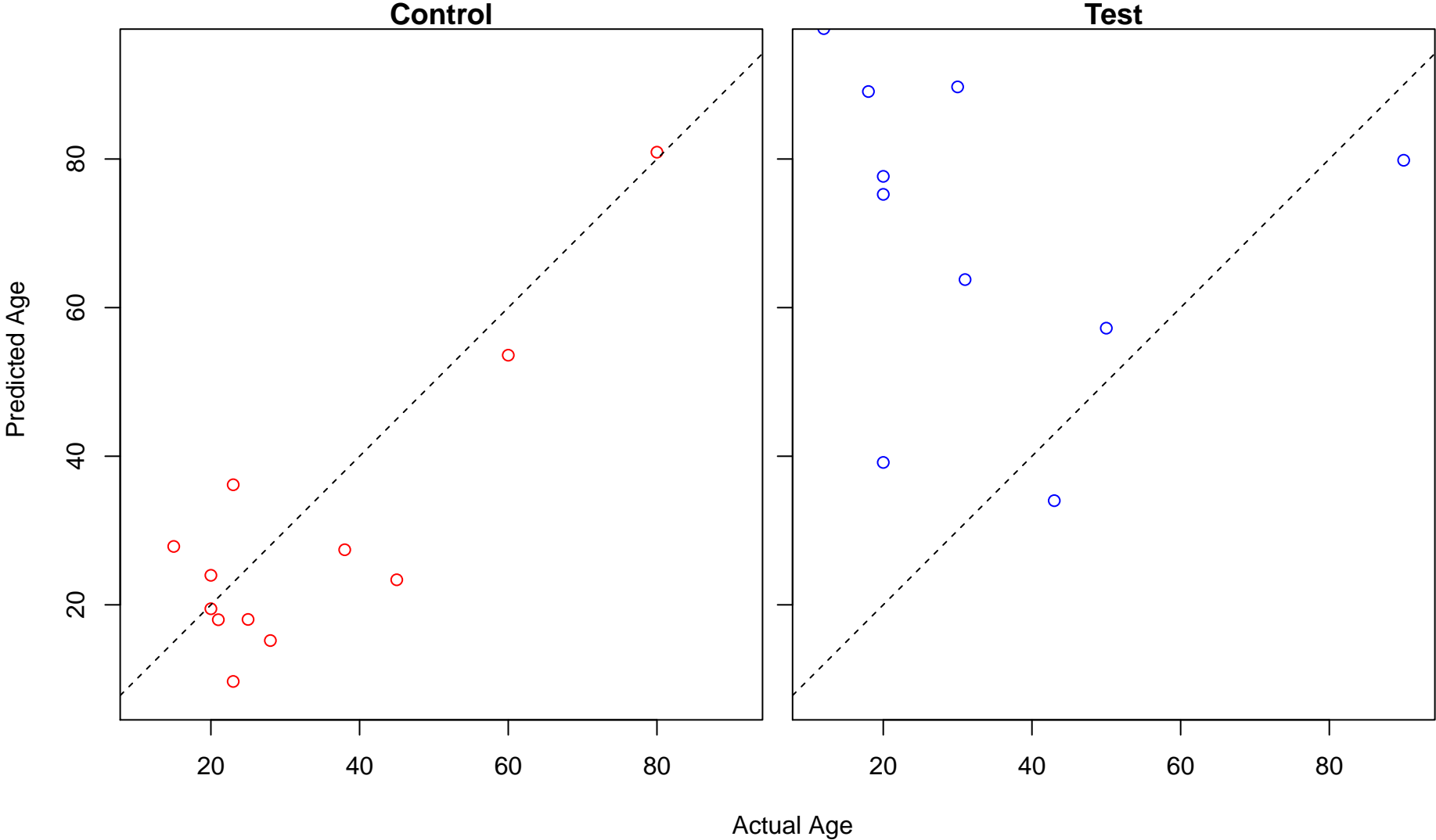
cartilage development (Score: 16.129171)



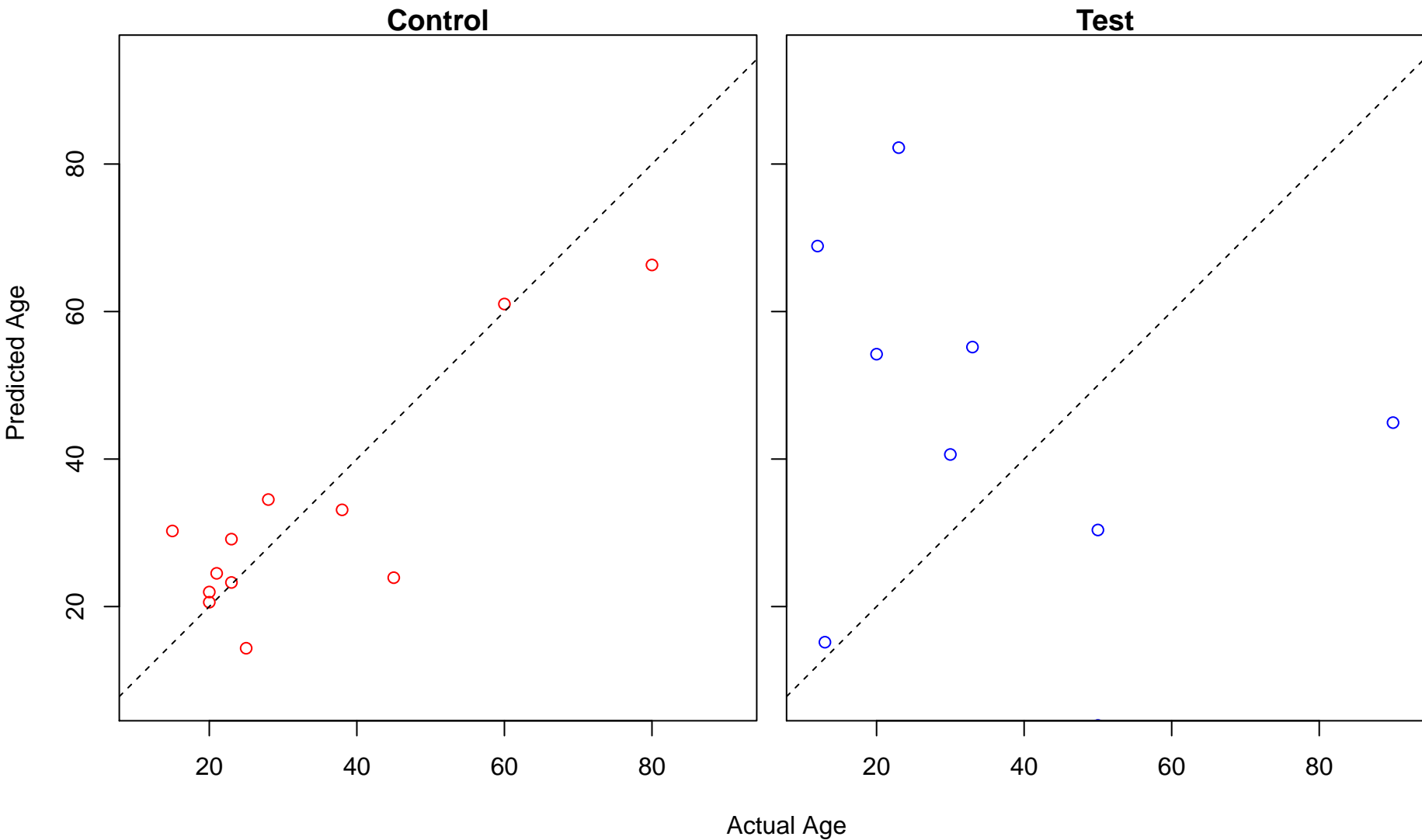
negative regulation of phospholipase activity (Score: 16.122996)



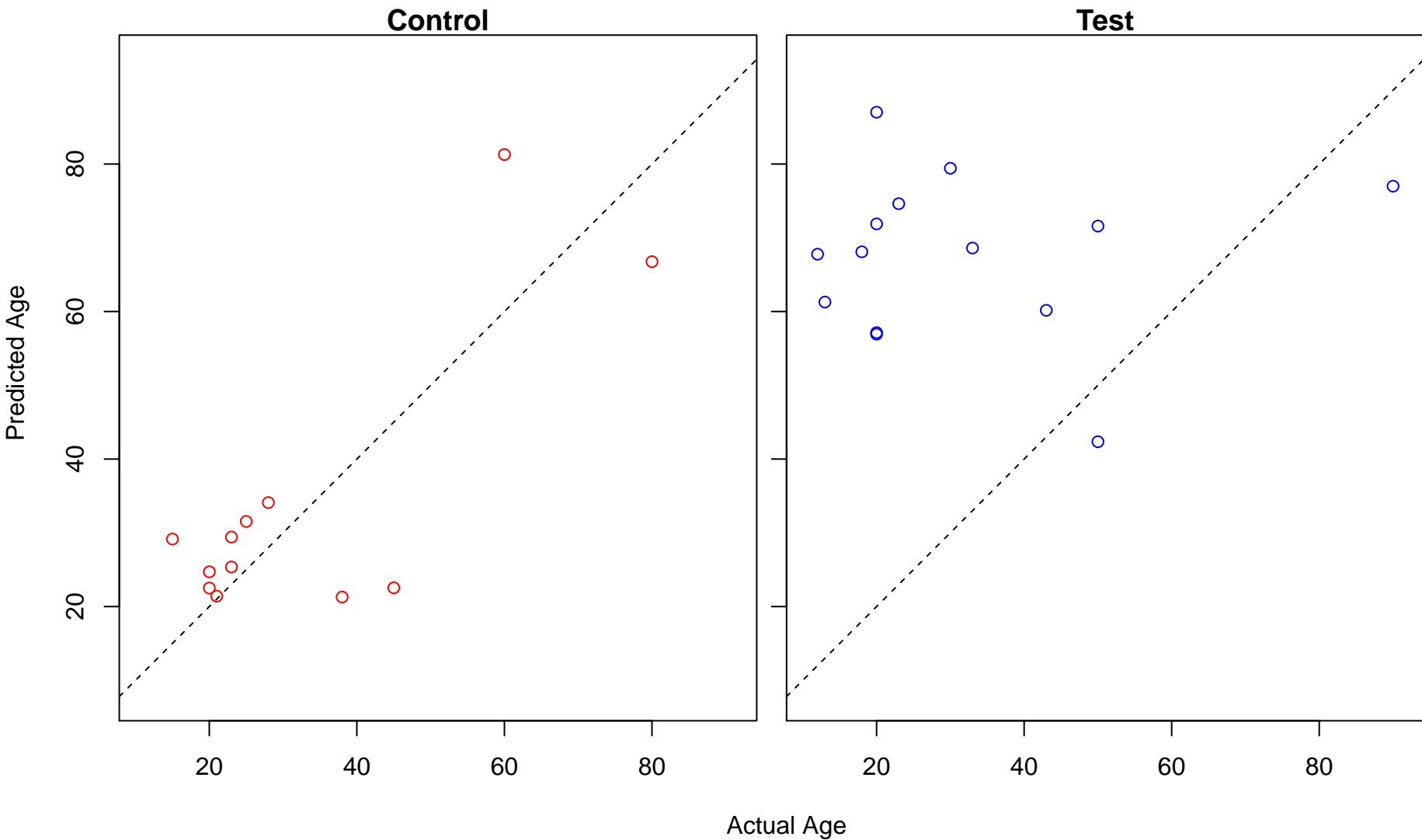
pyrimidine deoxyribonucleotide catabolic process (Score: 16.113777)



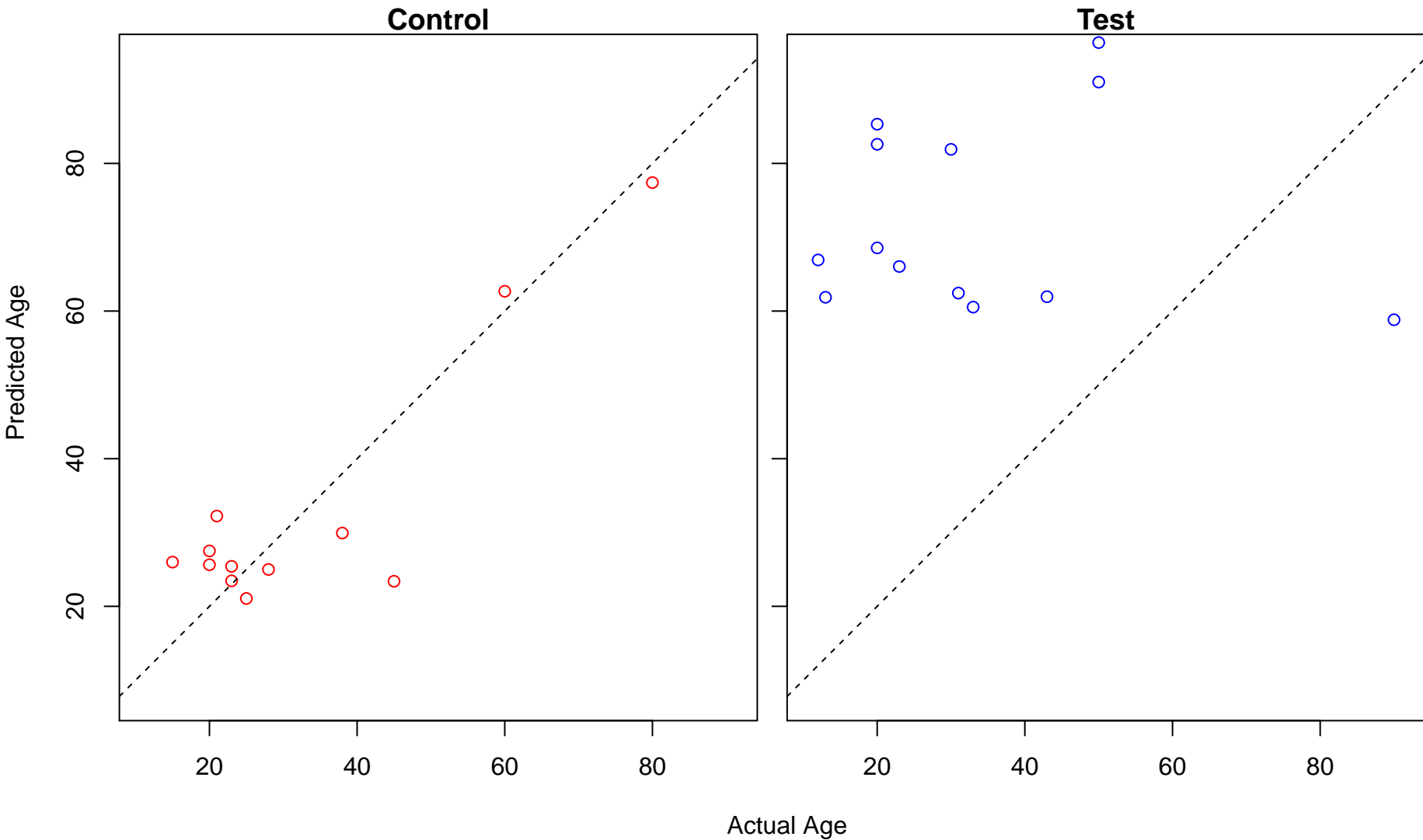
mitotic spindle organization (Score: 16.067625)



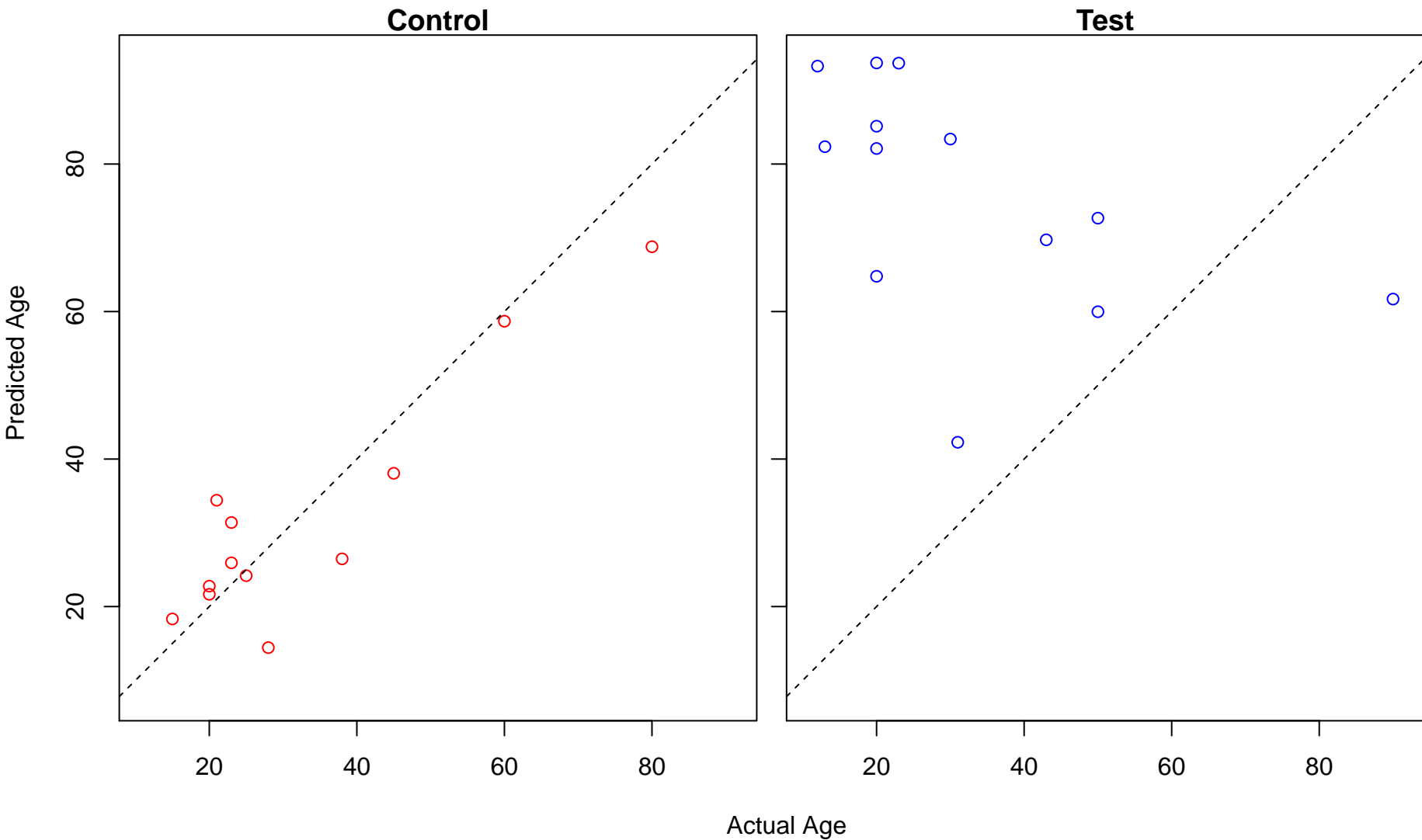
negative regulation of lipopolysaccharide-mediated signaling pathway (Score: 16.066704)



embryonic eye morphogenesis (Score: 16.052694)

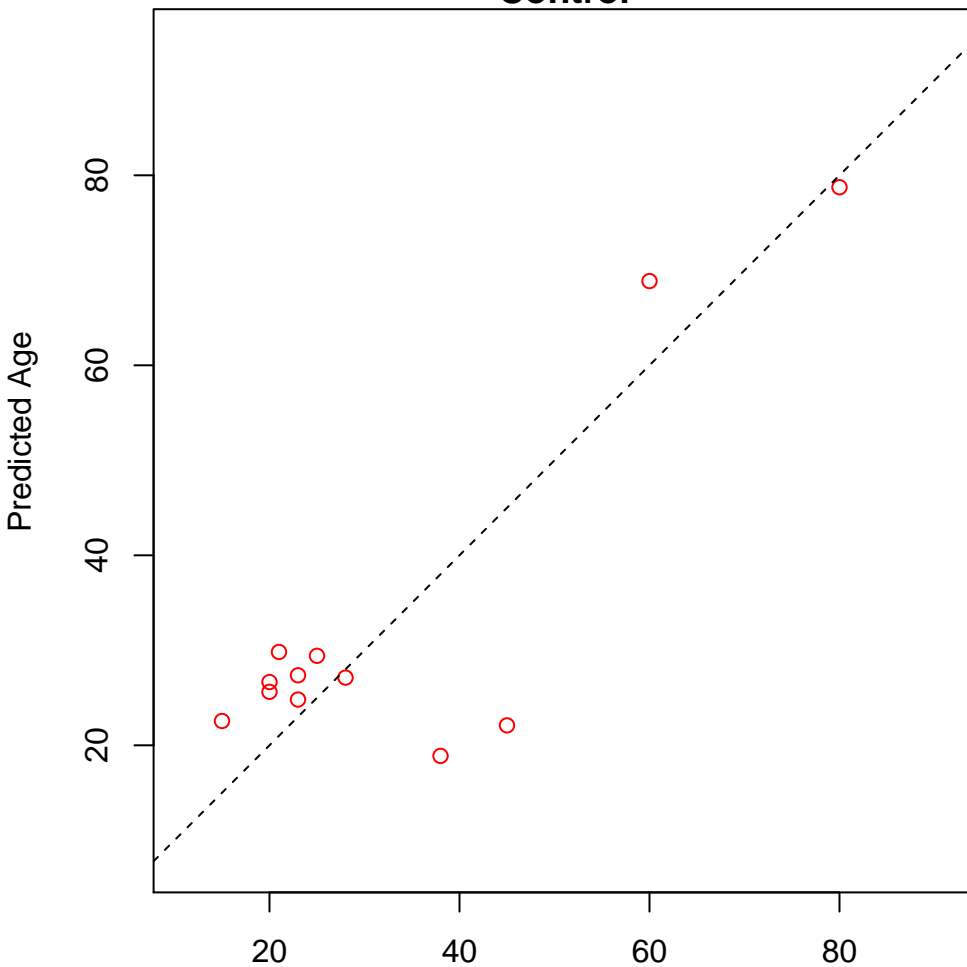


type 2 immune response (Score: 15.957004)

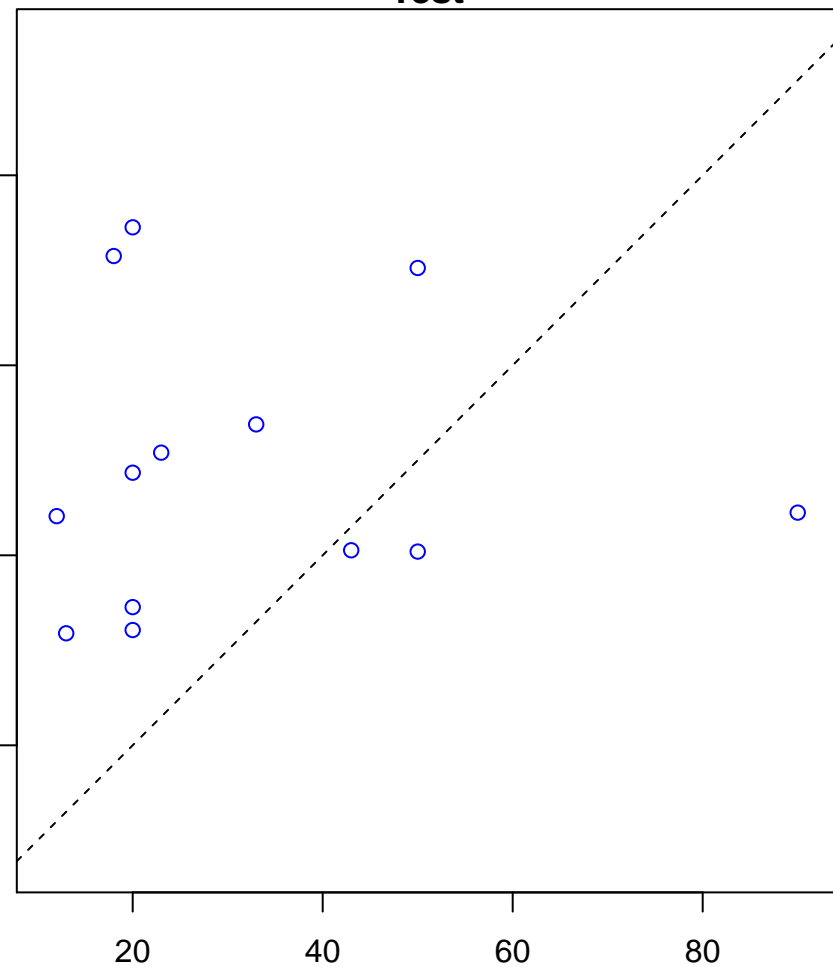


protein K11-linked deubiquitination (Score: 15.935408)

Control

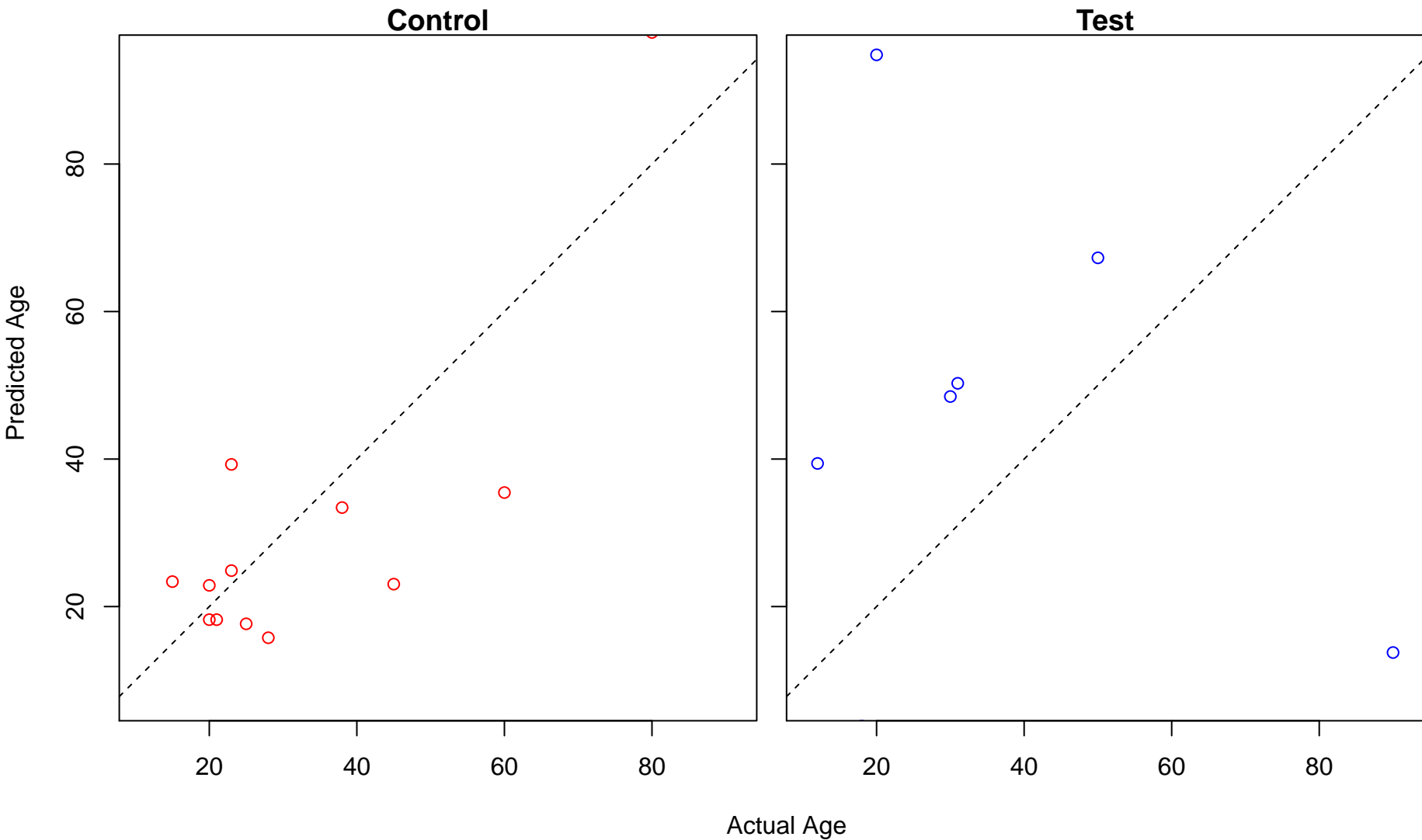


Test



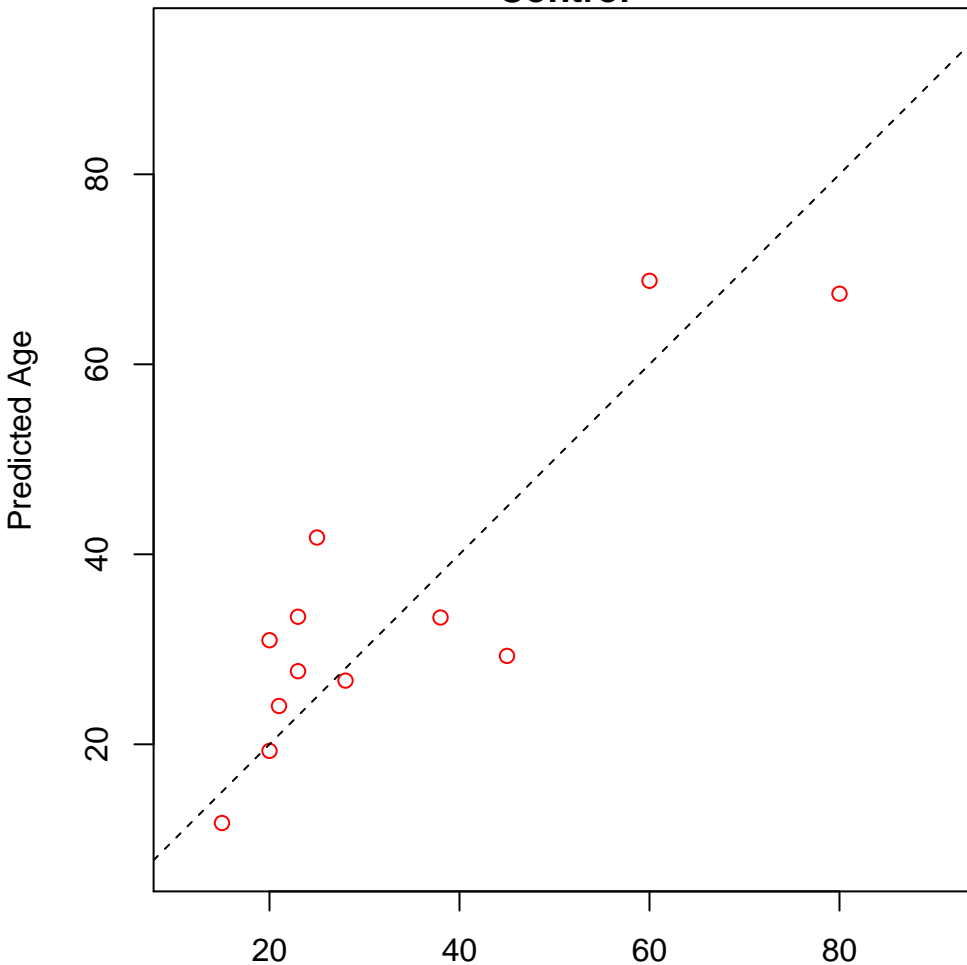
Actual Age

regulation of developmental pigmentation (Score: 15.927904)

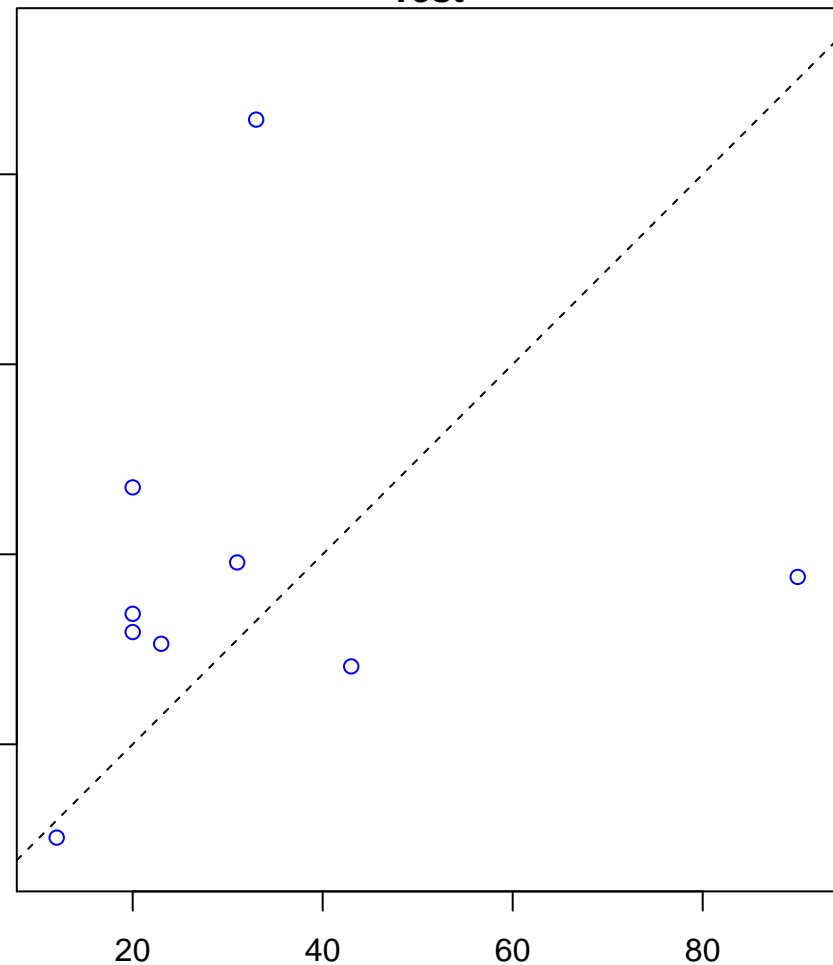


glomerular mesangium development (Score: 15.916483)

Control



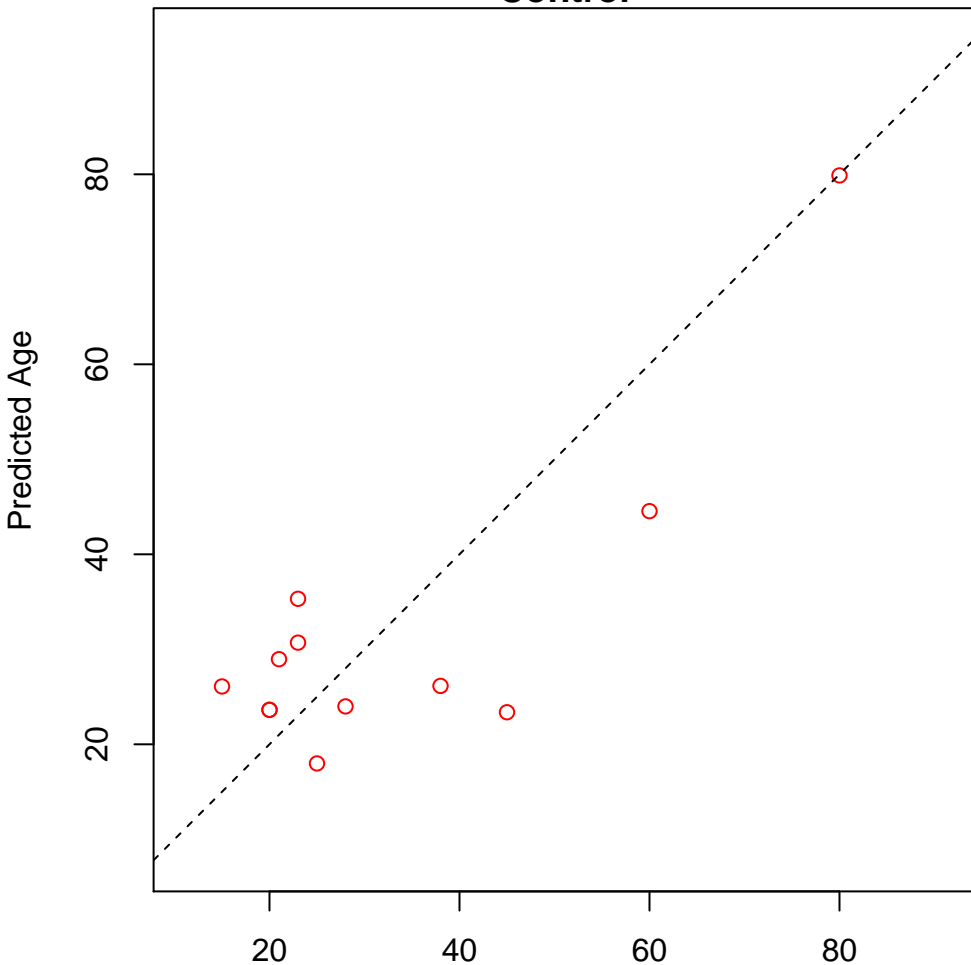
Test



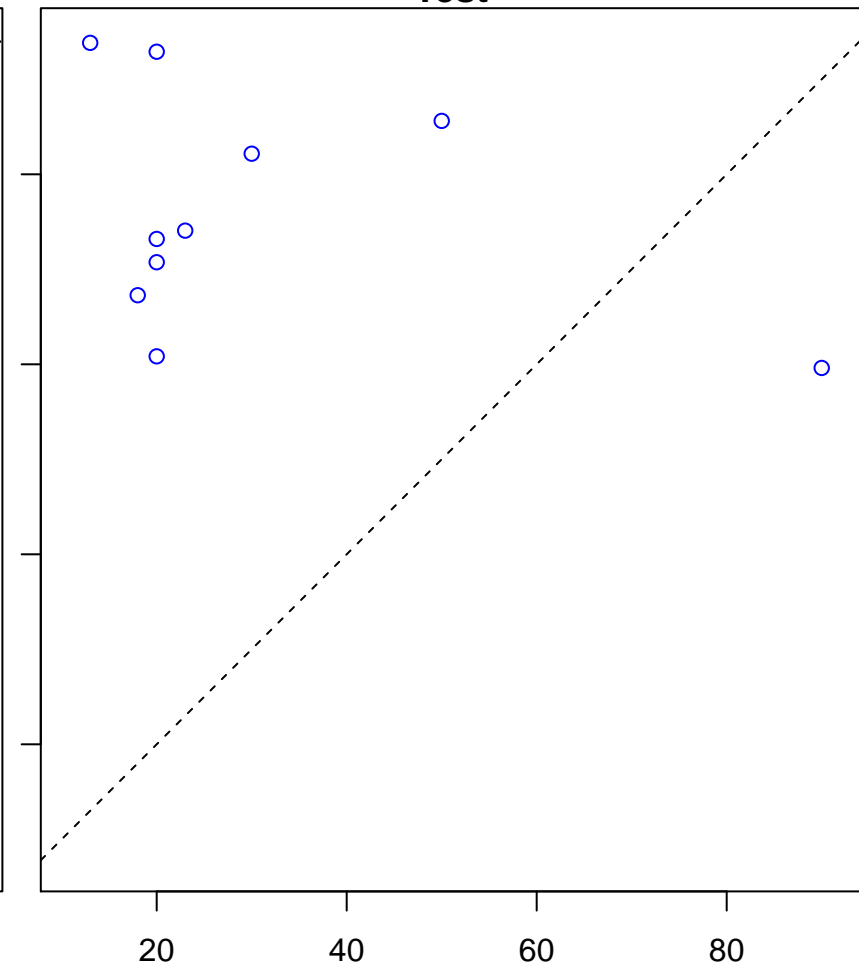
Actual Age

response to hepatocyte growth factor (Score: 15.912523)

Control

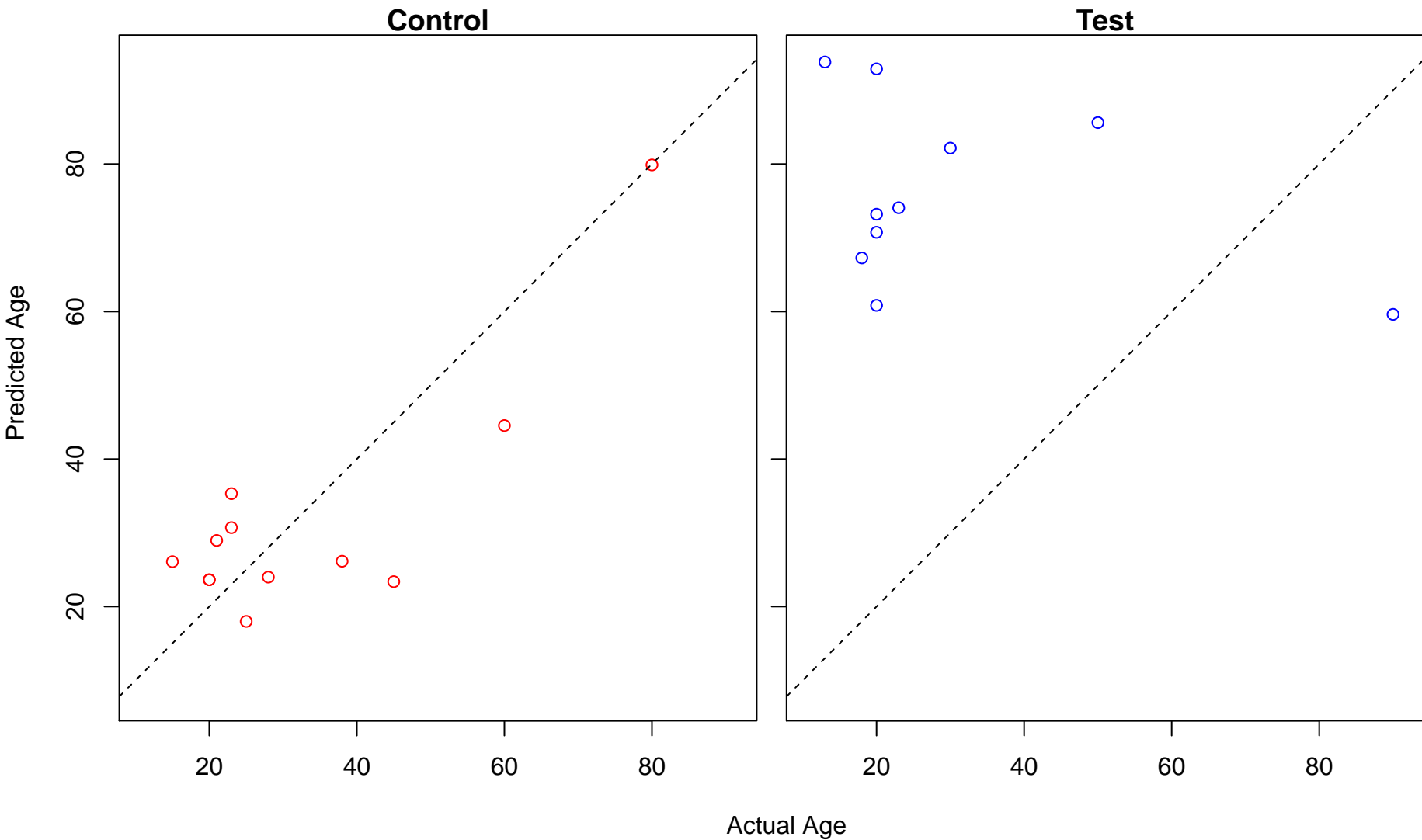


Test

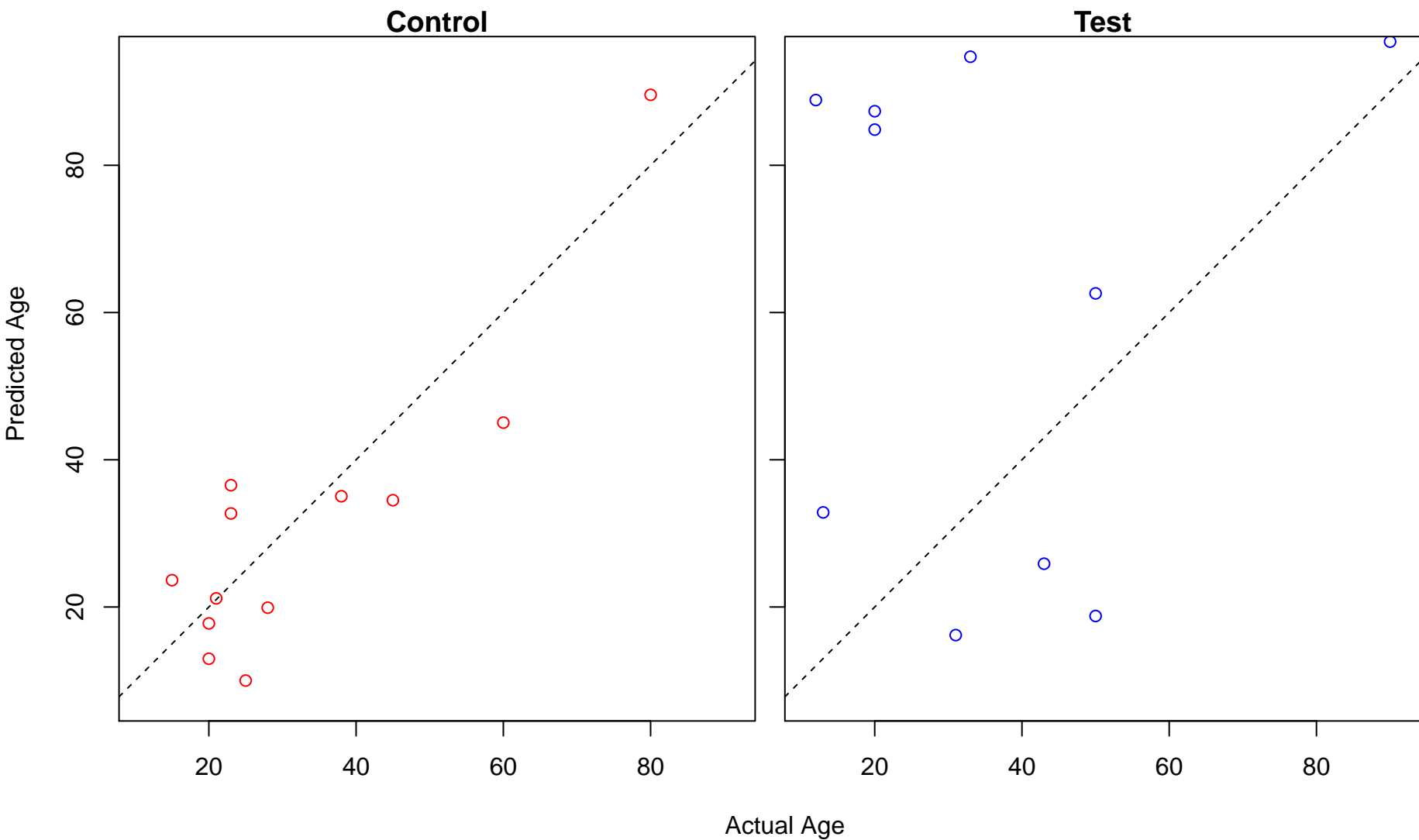


Actual Age

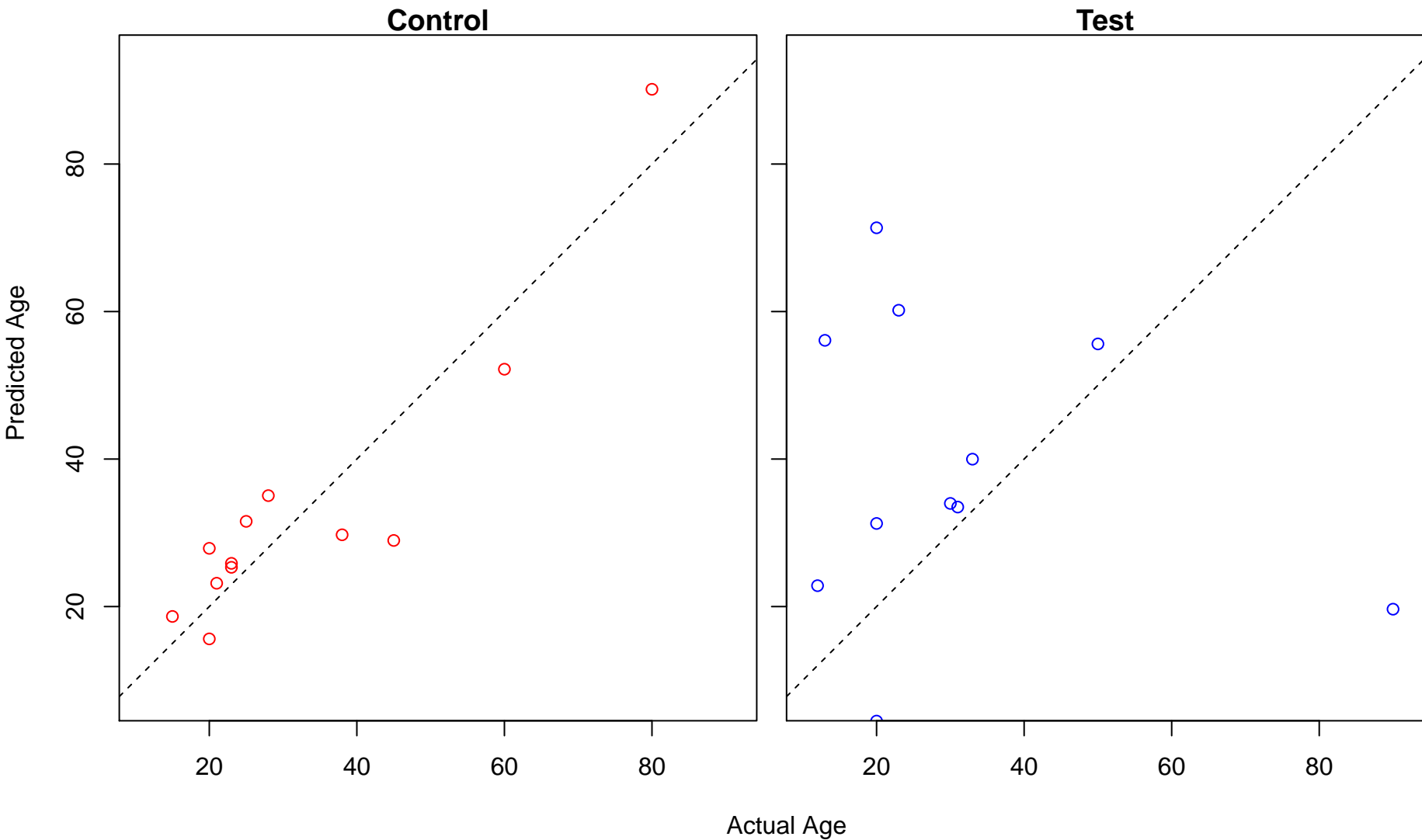
cellular response to hepatocyte growth factor stimulus (Score: 15.912523)



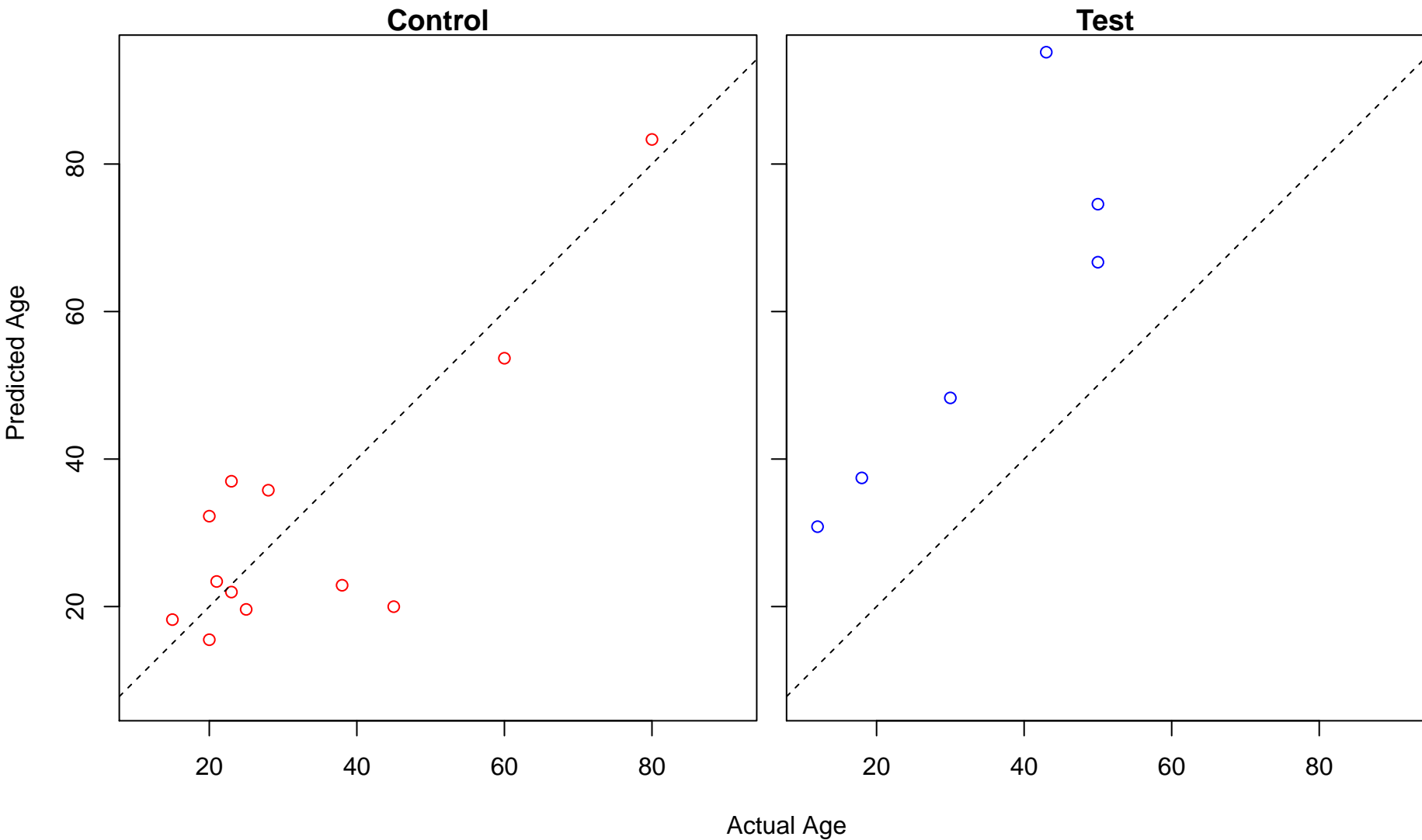
positive regulation of actin nucleation (Score: 15.899857)



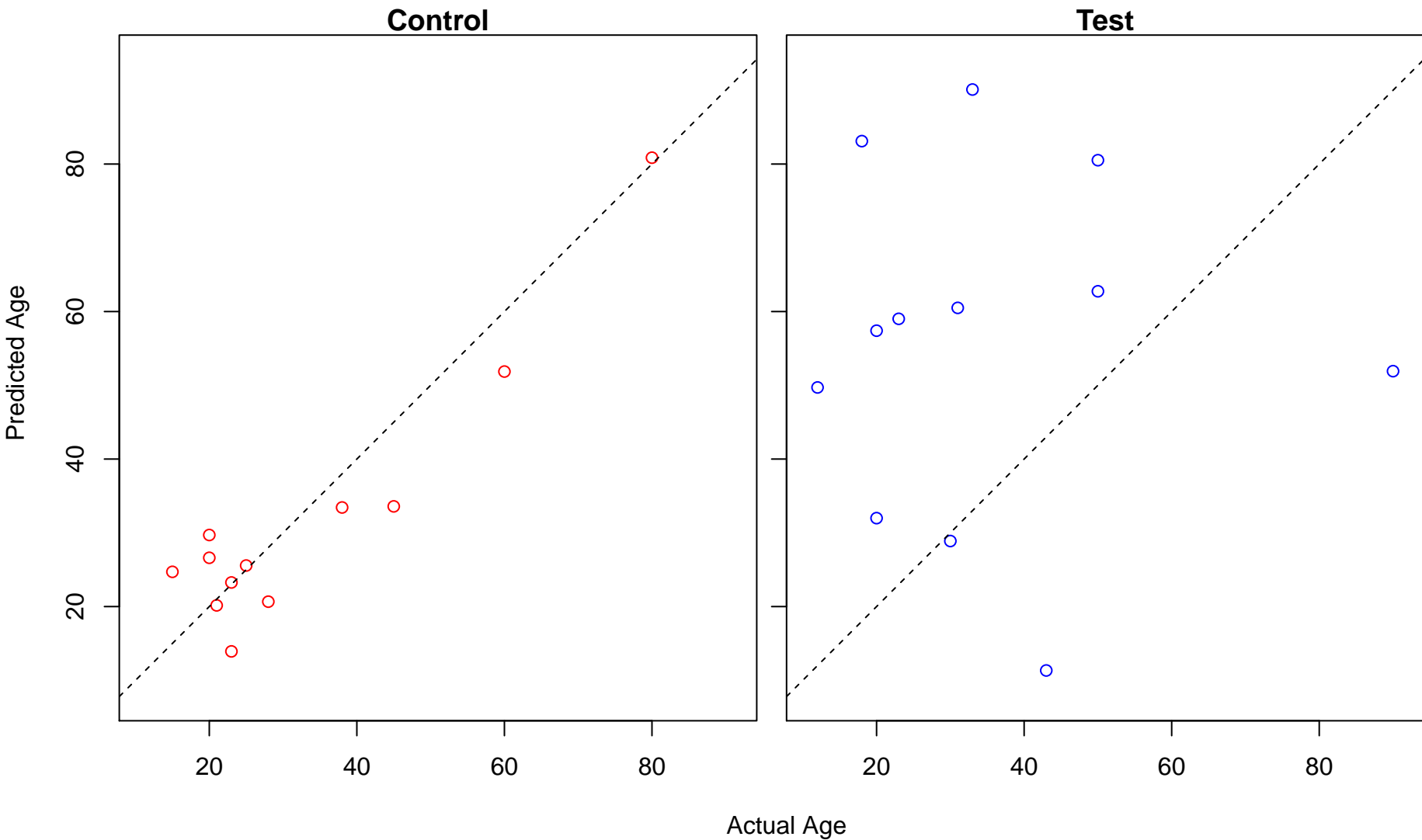
nucleobase-containing small molecule metabolic process (Score: 15.868633)



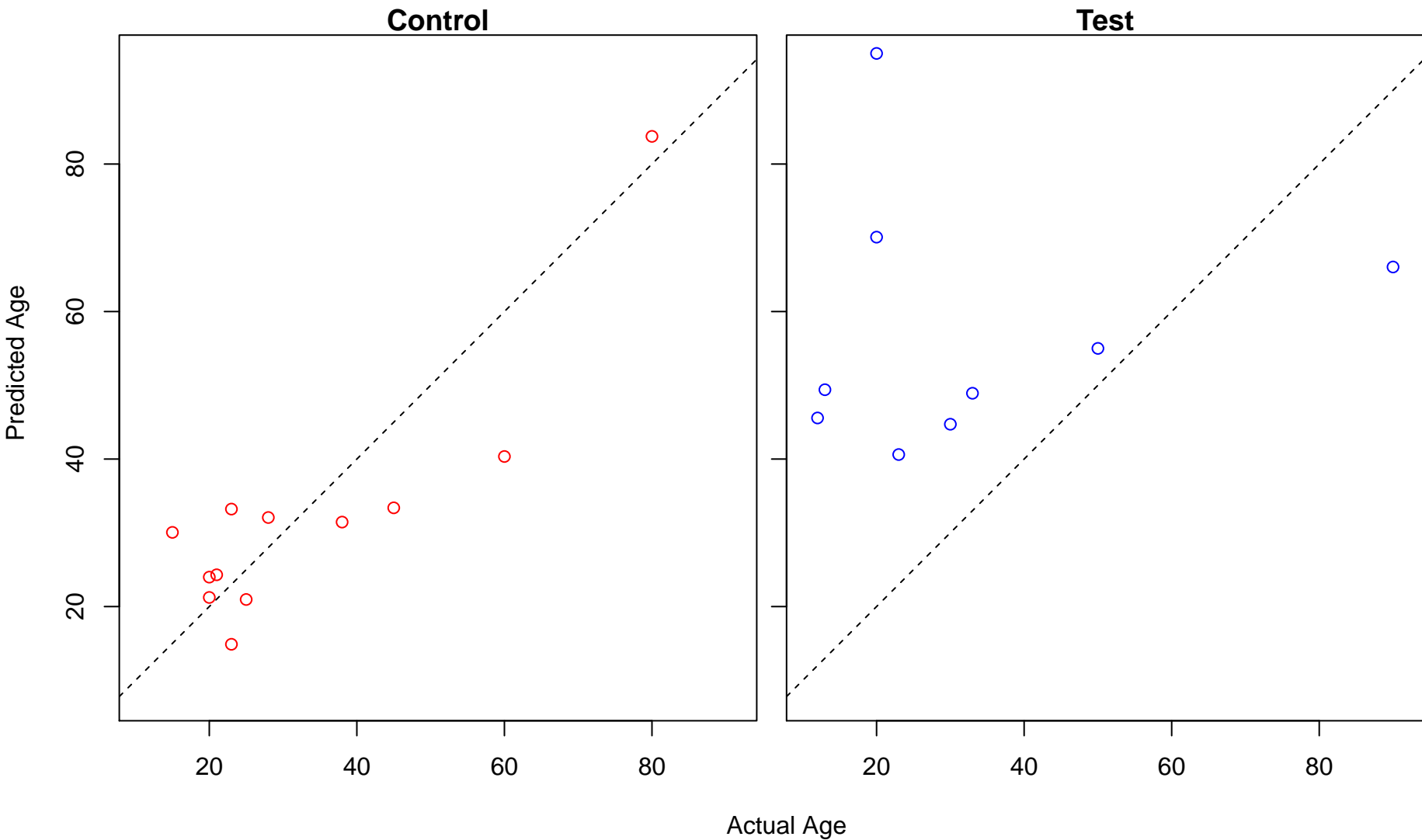
positive regulation of fibroblast apoptotic process (Score: 15.863983)



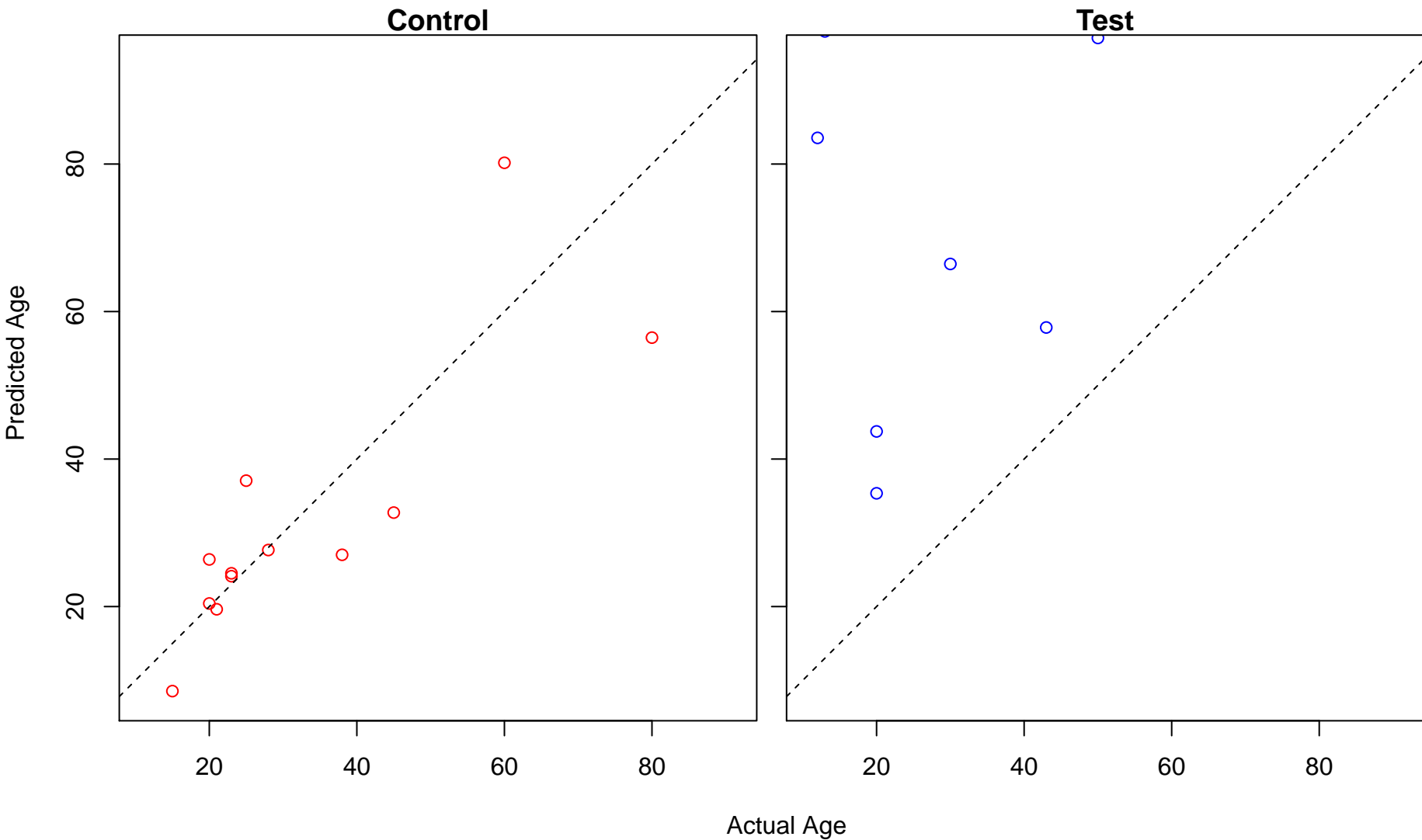
response to heat (Score: 15.845253)



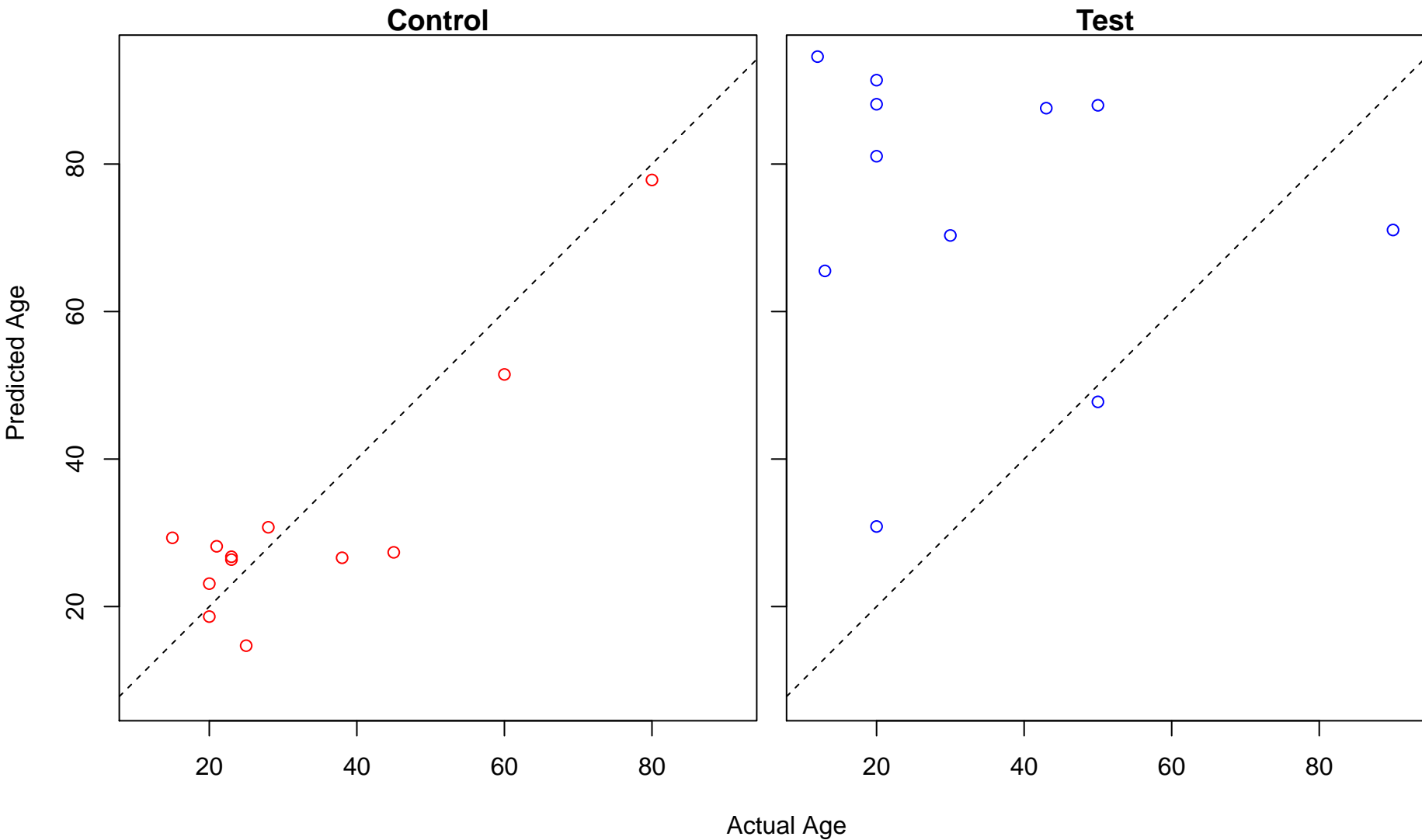
cellular response to dsRNA (Score: 15.833241)



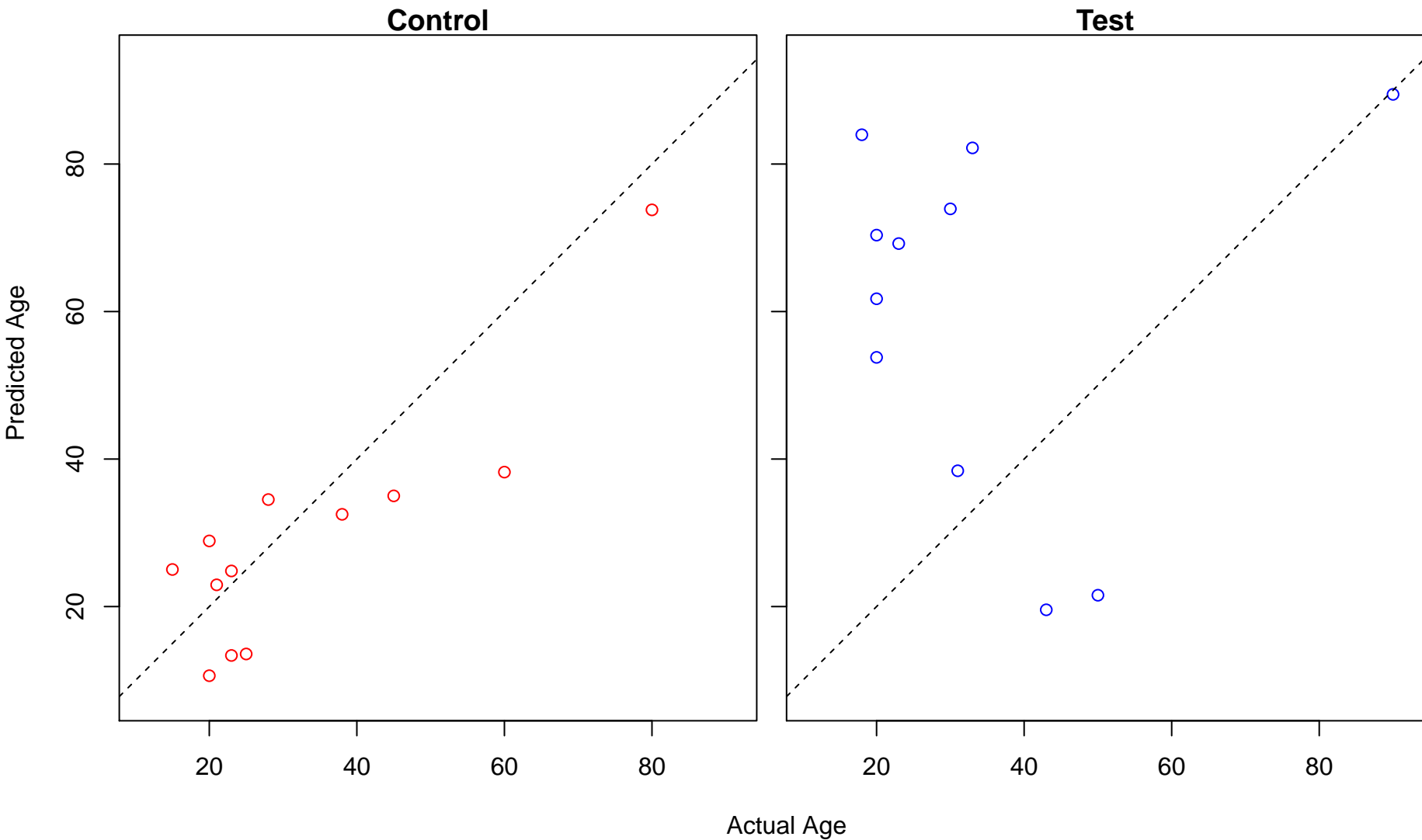
phosphatidylethanolamine acyl-chain remodeling (Score: 15.769880)



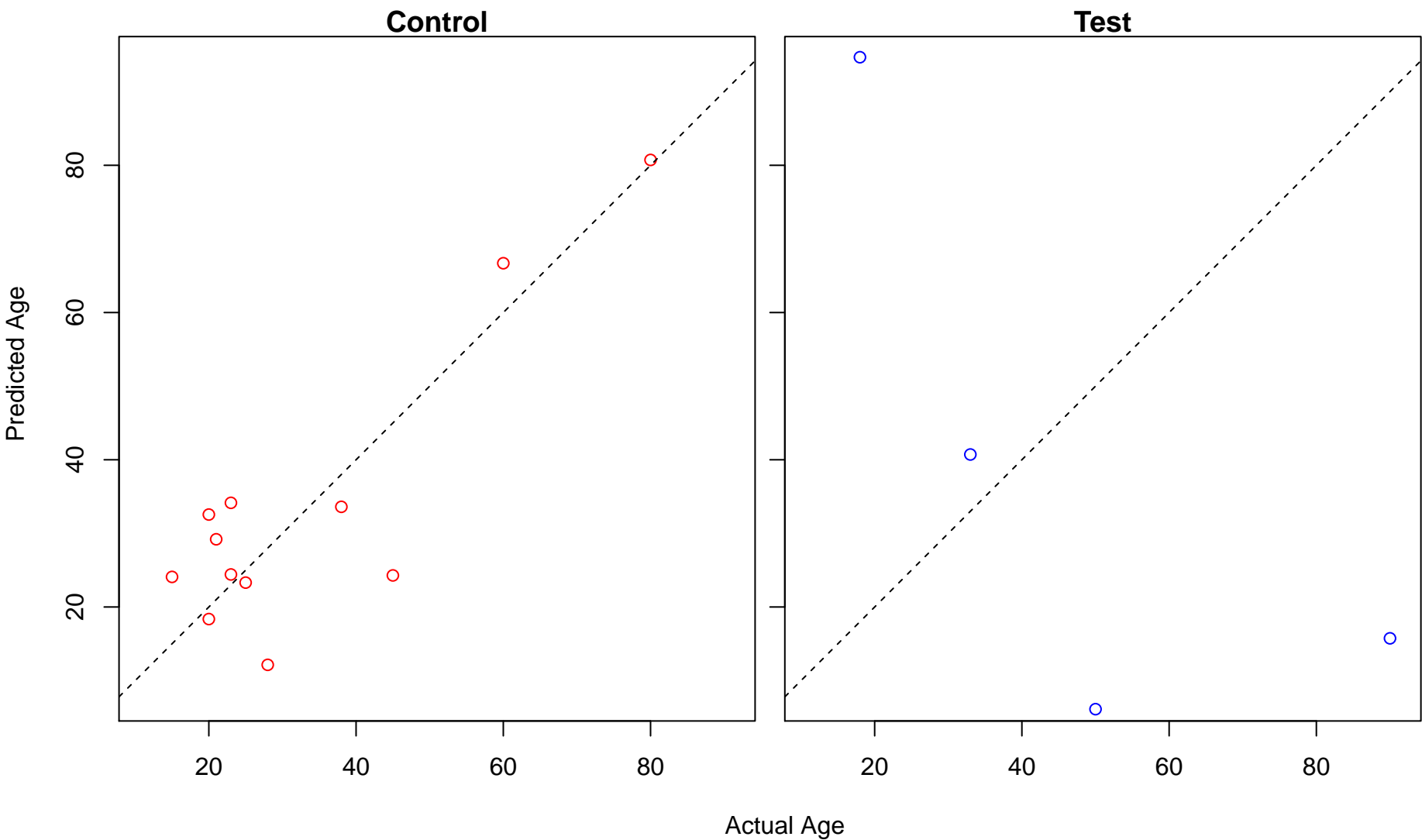
cilium organization (Score: 15.768858)



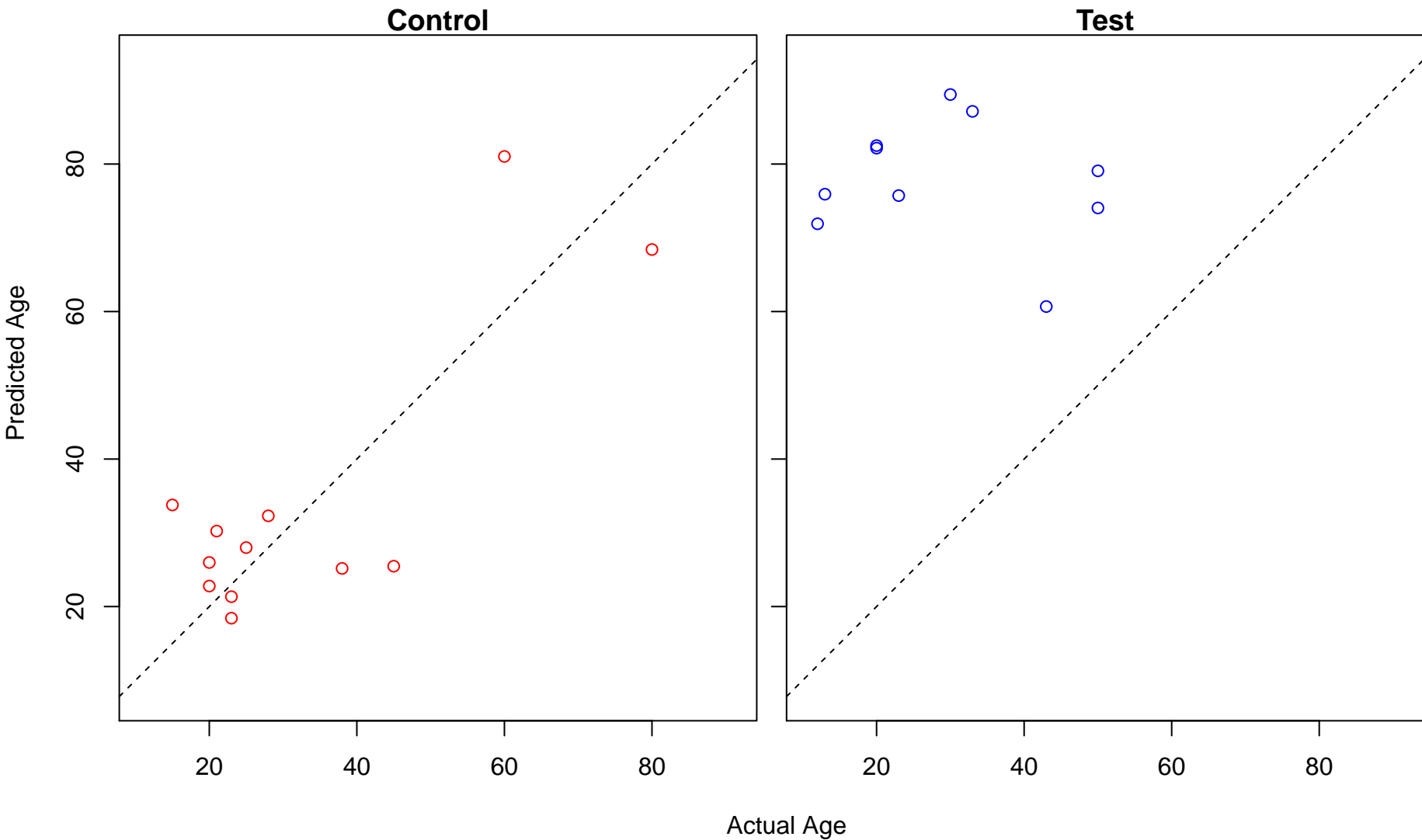
regulation of toll-like receptor 2 signaling pathway (Score: 15.768845)



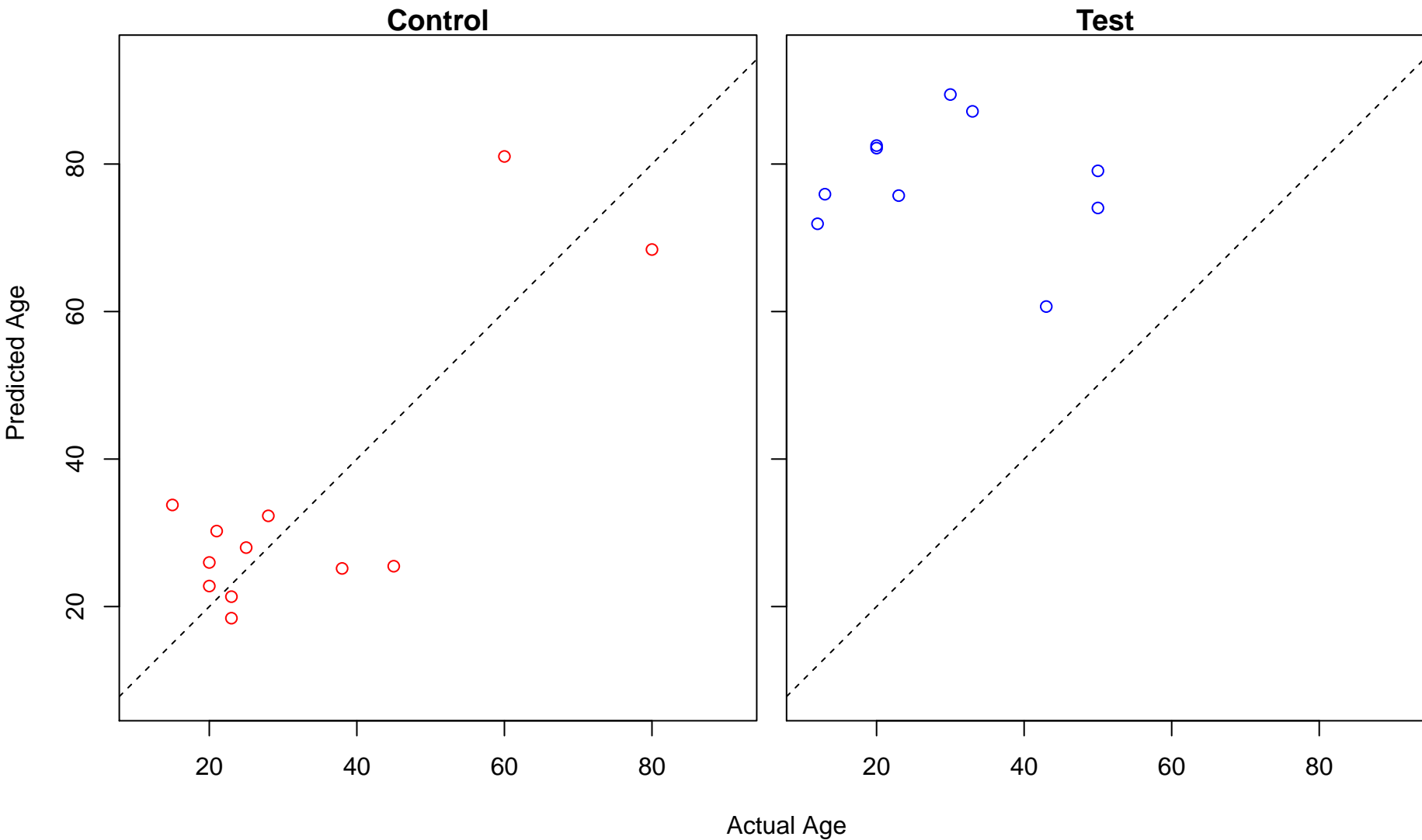
regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score: 15.



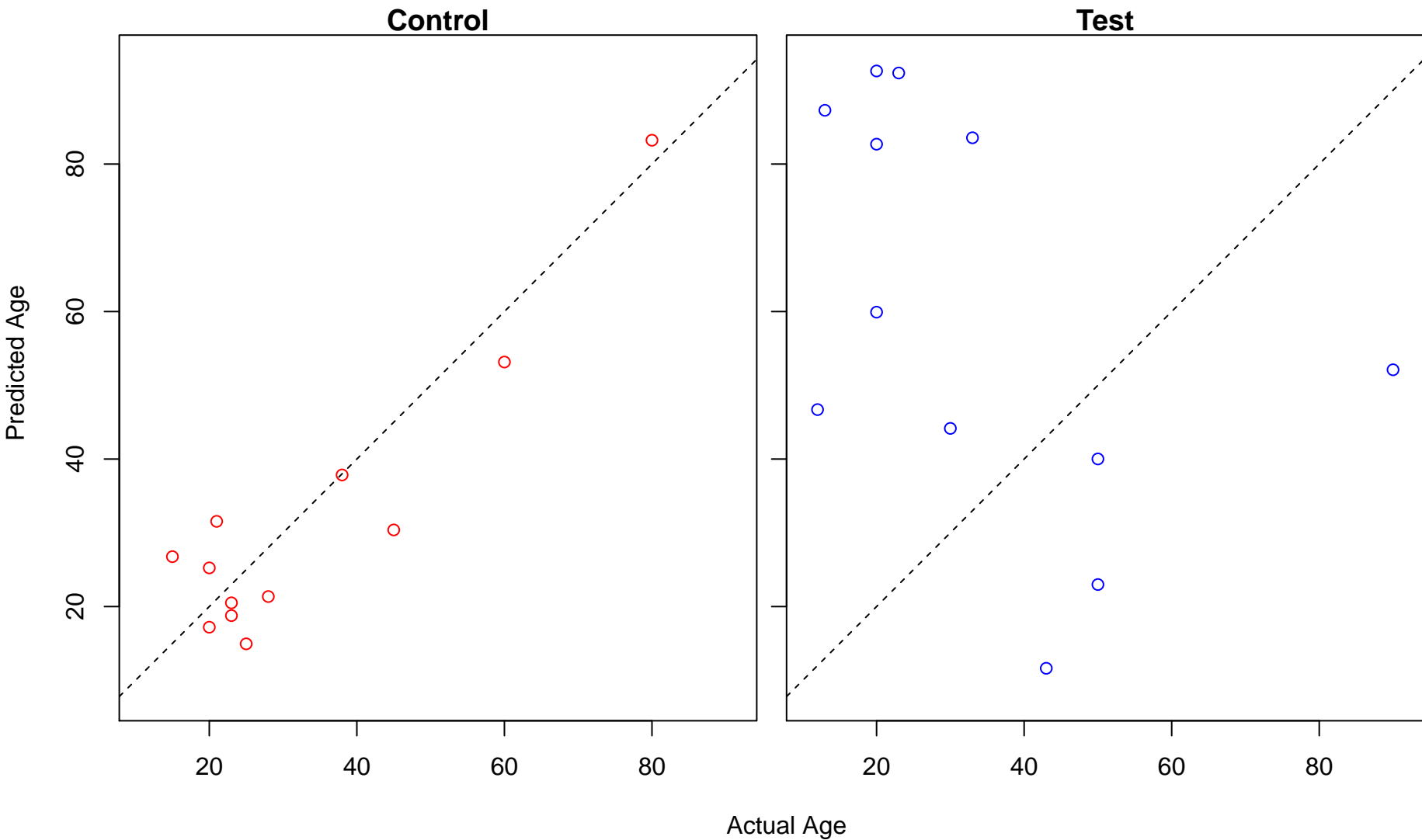
negative regulation of nucleoside metabolic process (Score: 15.705059)



negative regulation of ATP metabolic process (Score: 15.705059)

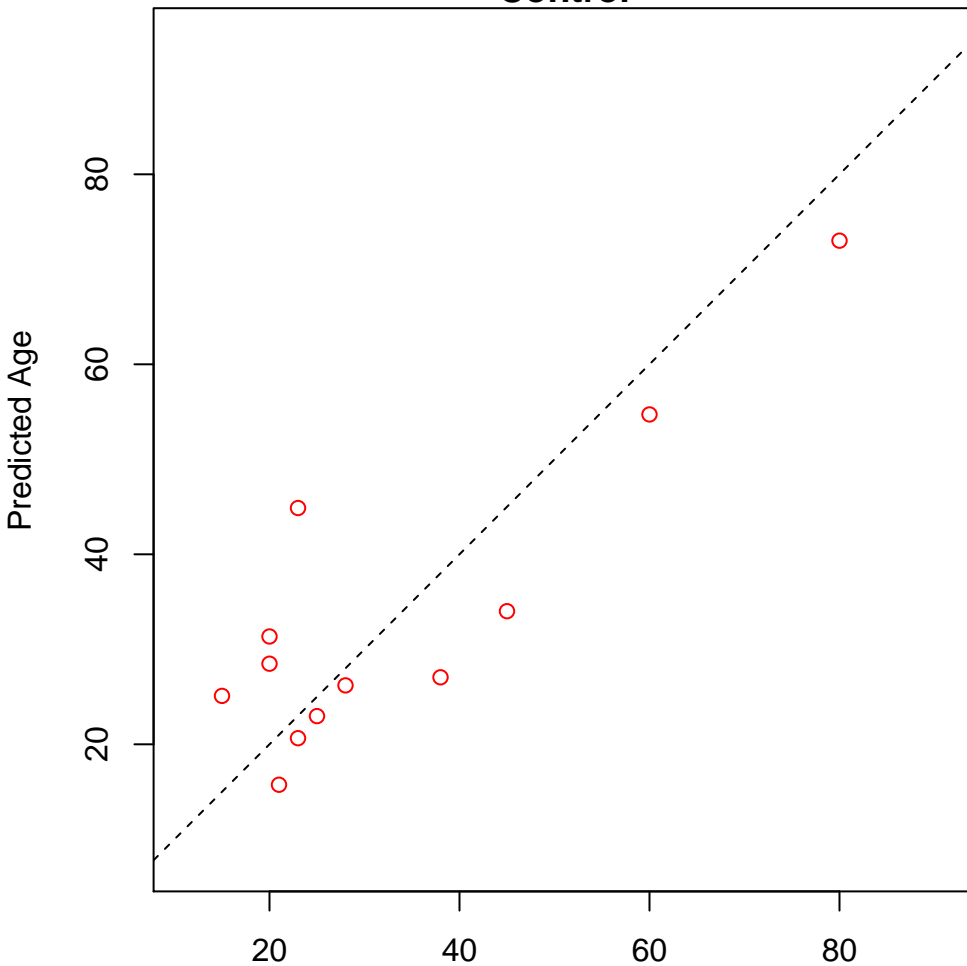


regulation of protein export from nucleus (Score: 15.700980)

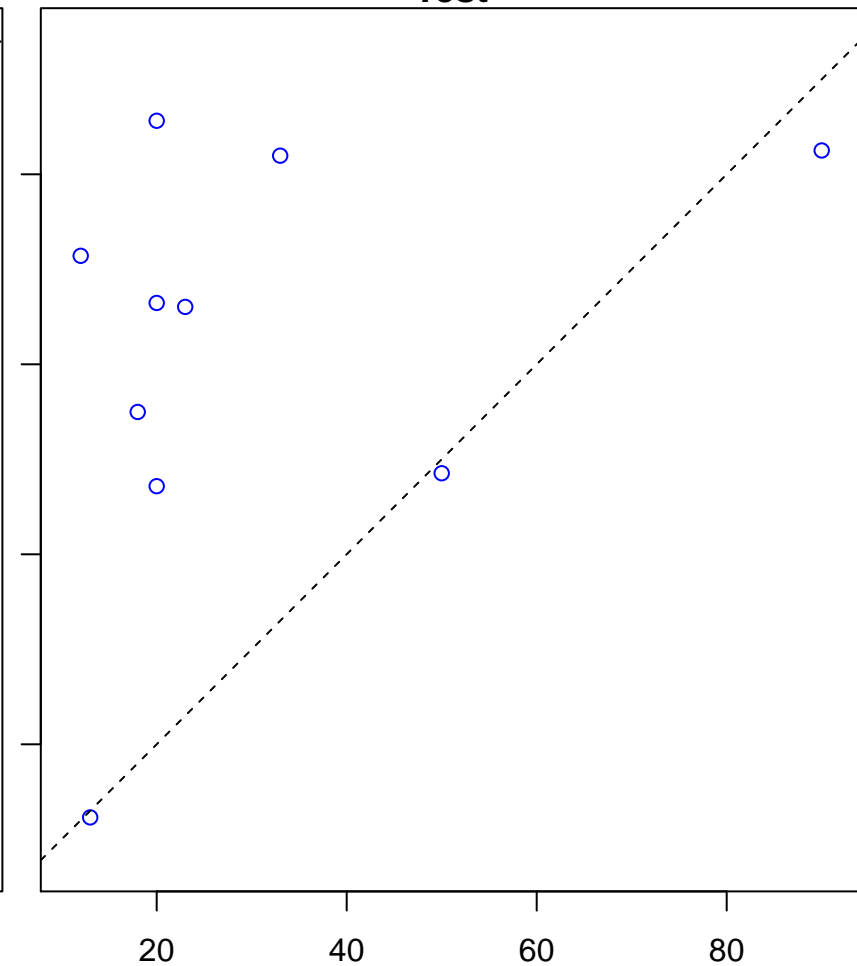


respiratory gaseous exchange (Score: 15.688583)

Control

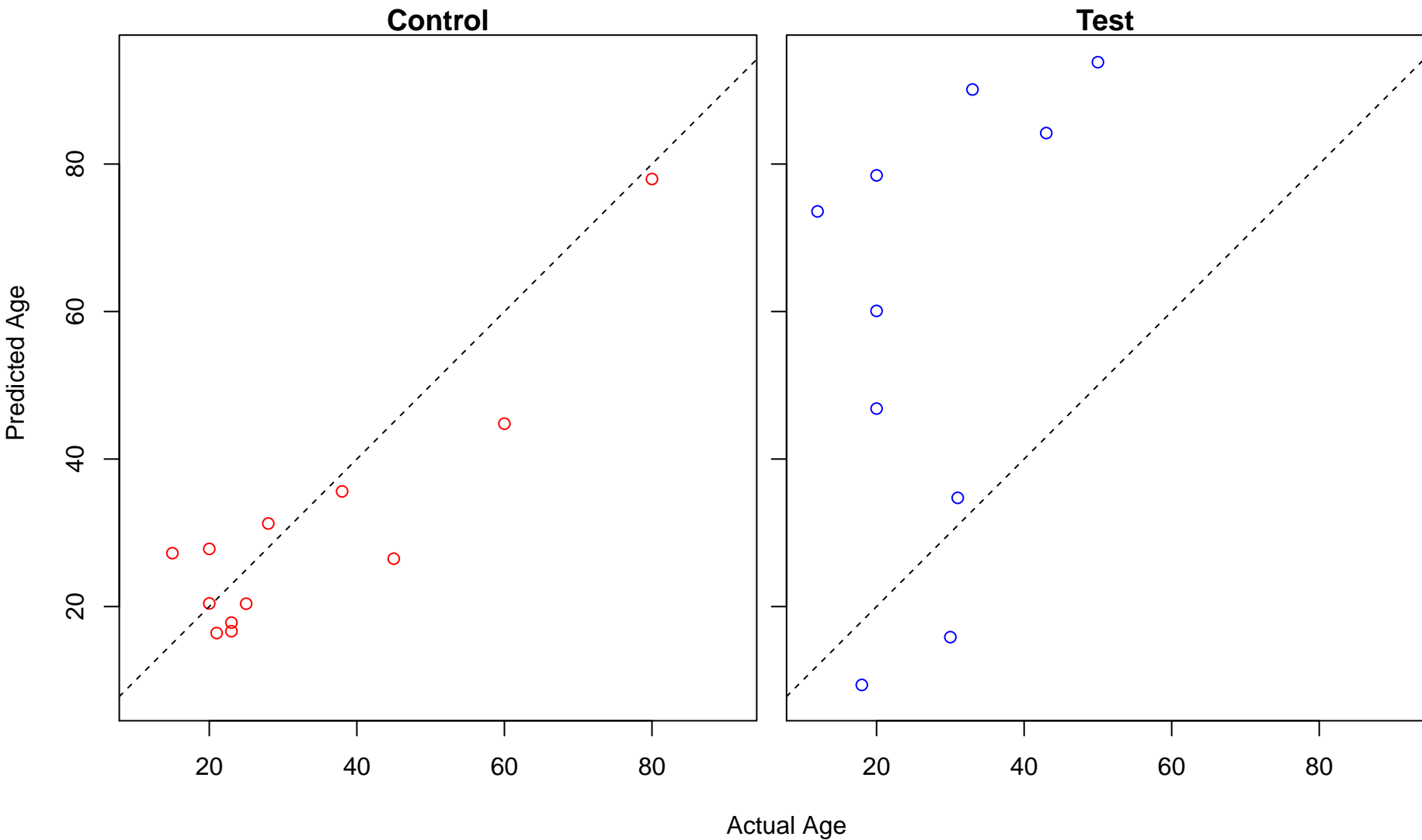


Test

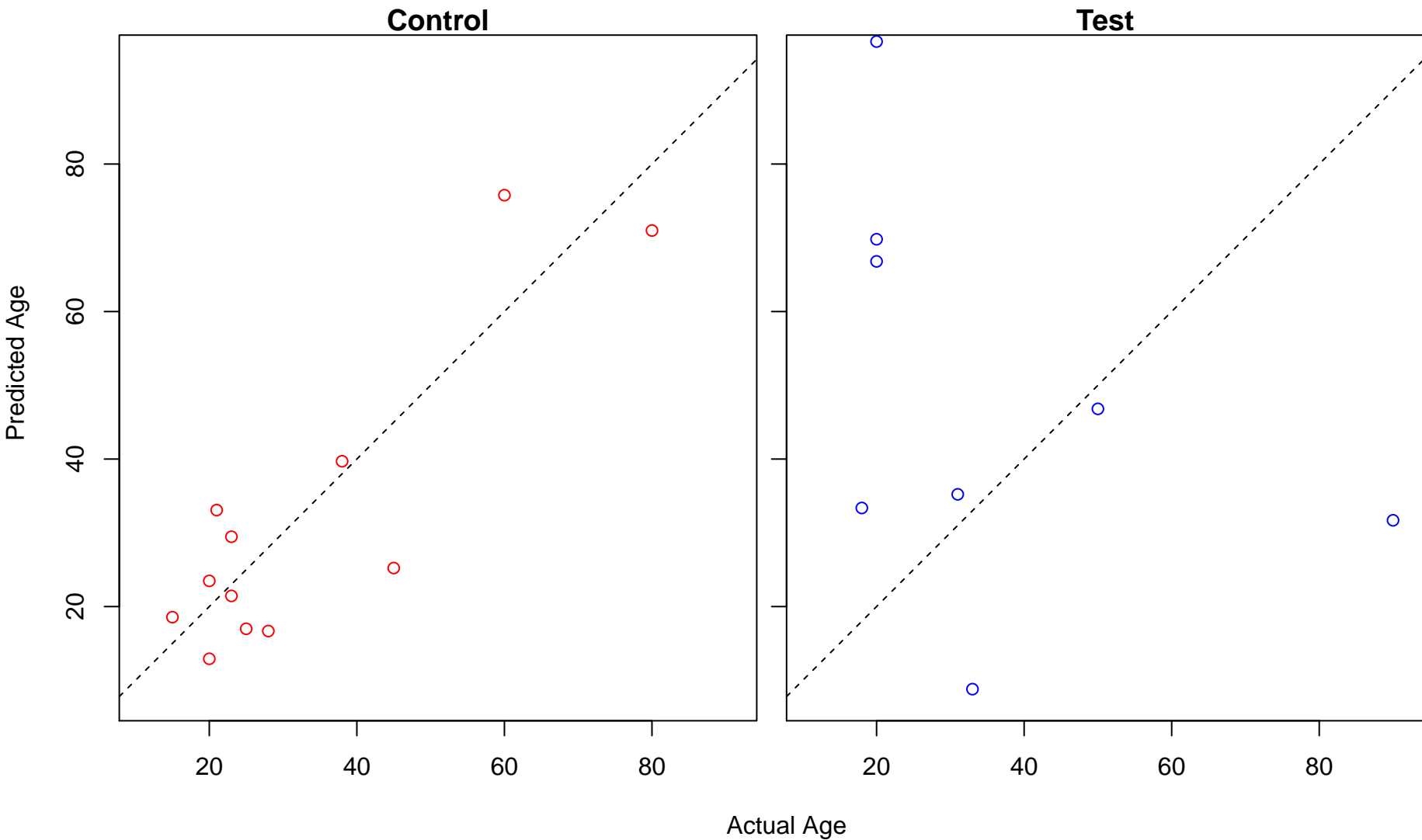


Actual Age

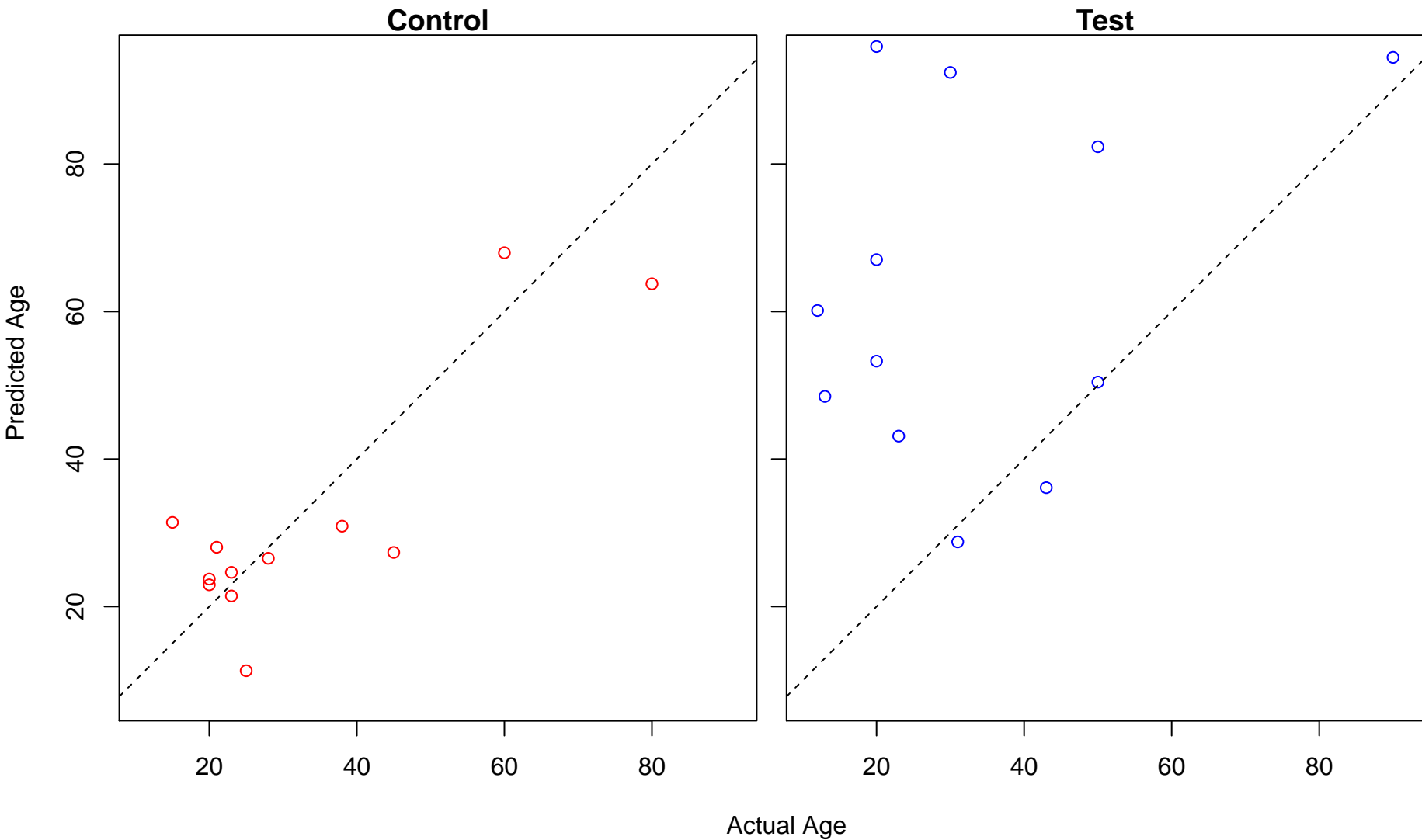
nephron tubule morphogenesis (Score: 15.658526)



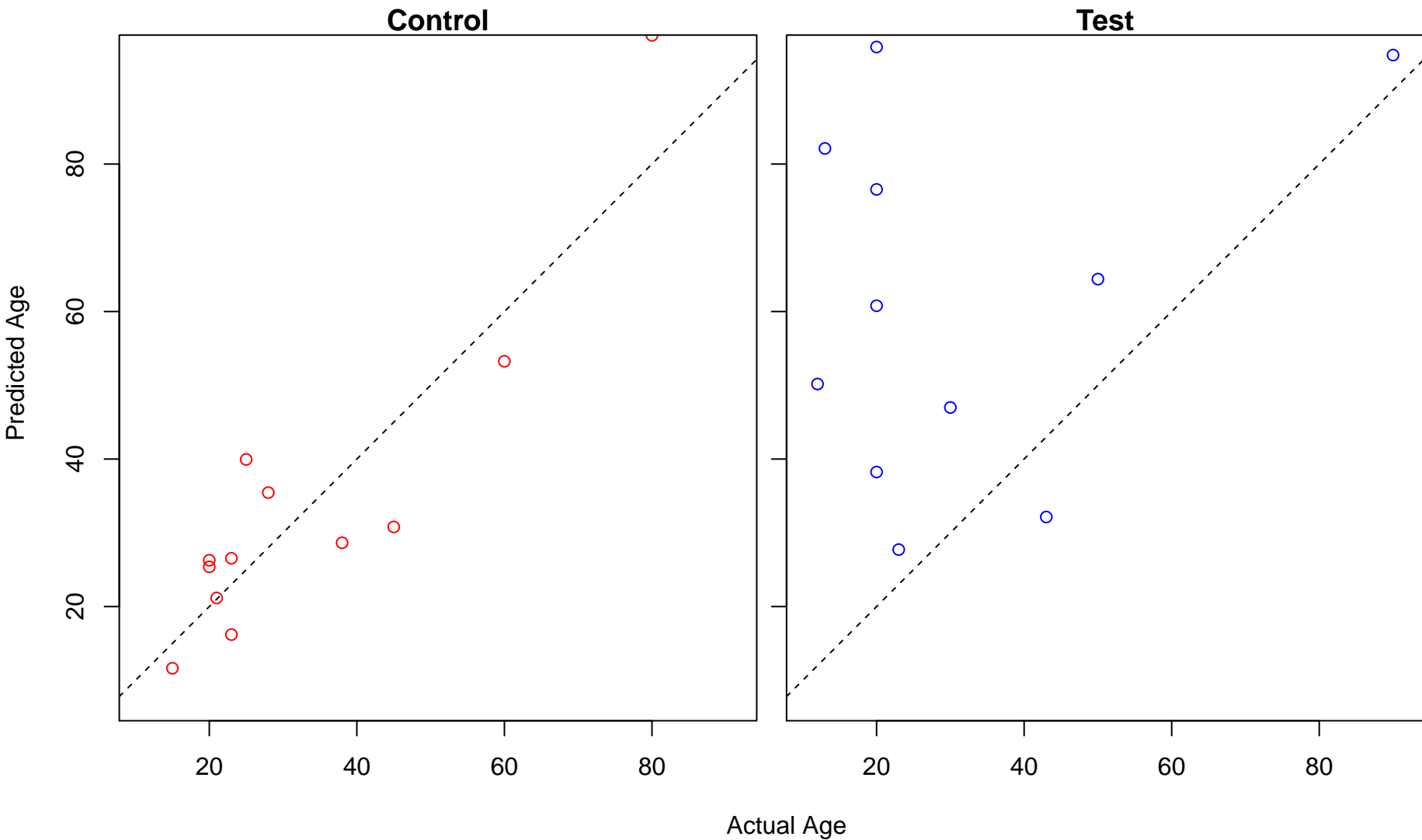
regulation of interferon-gamma-mediated signaling pathway (Score: 15.610087)



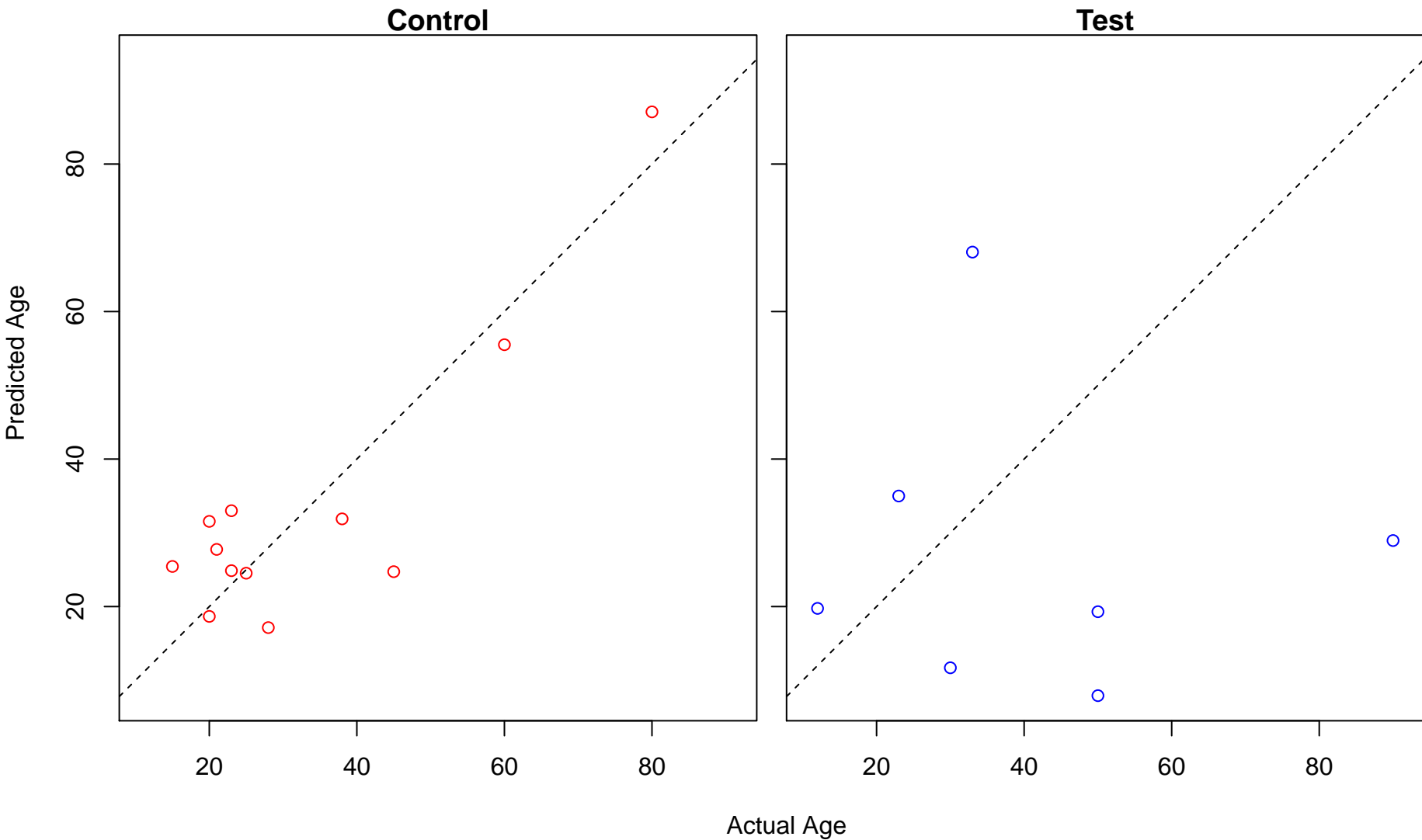
metaphase plate congression (Score: 15.600193)



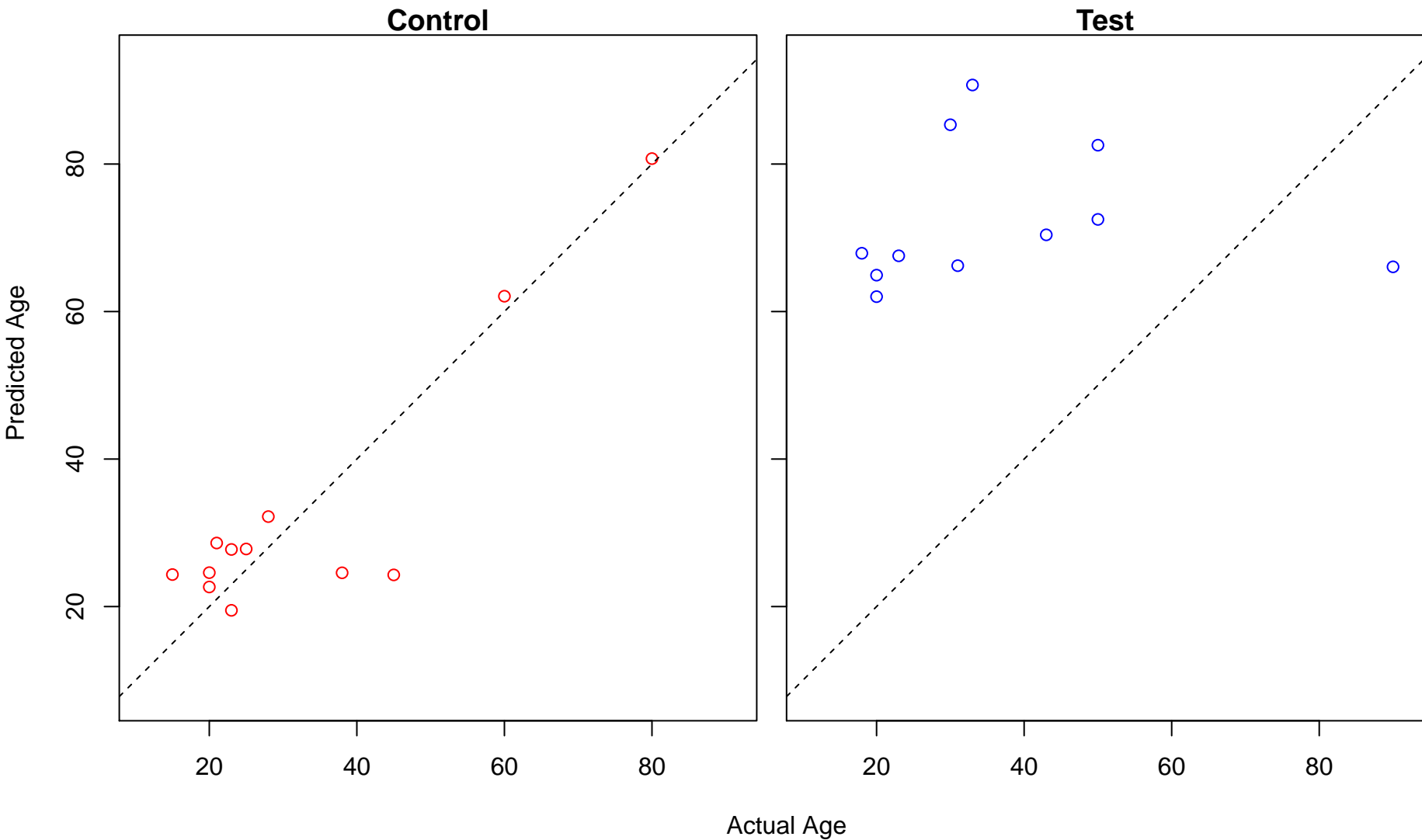
regulation of developmental growth (Score: 15.599491)



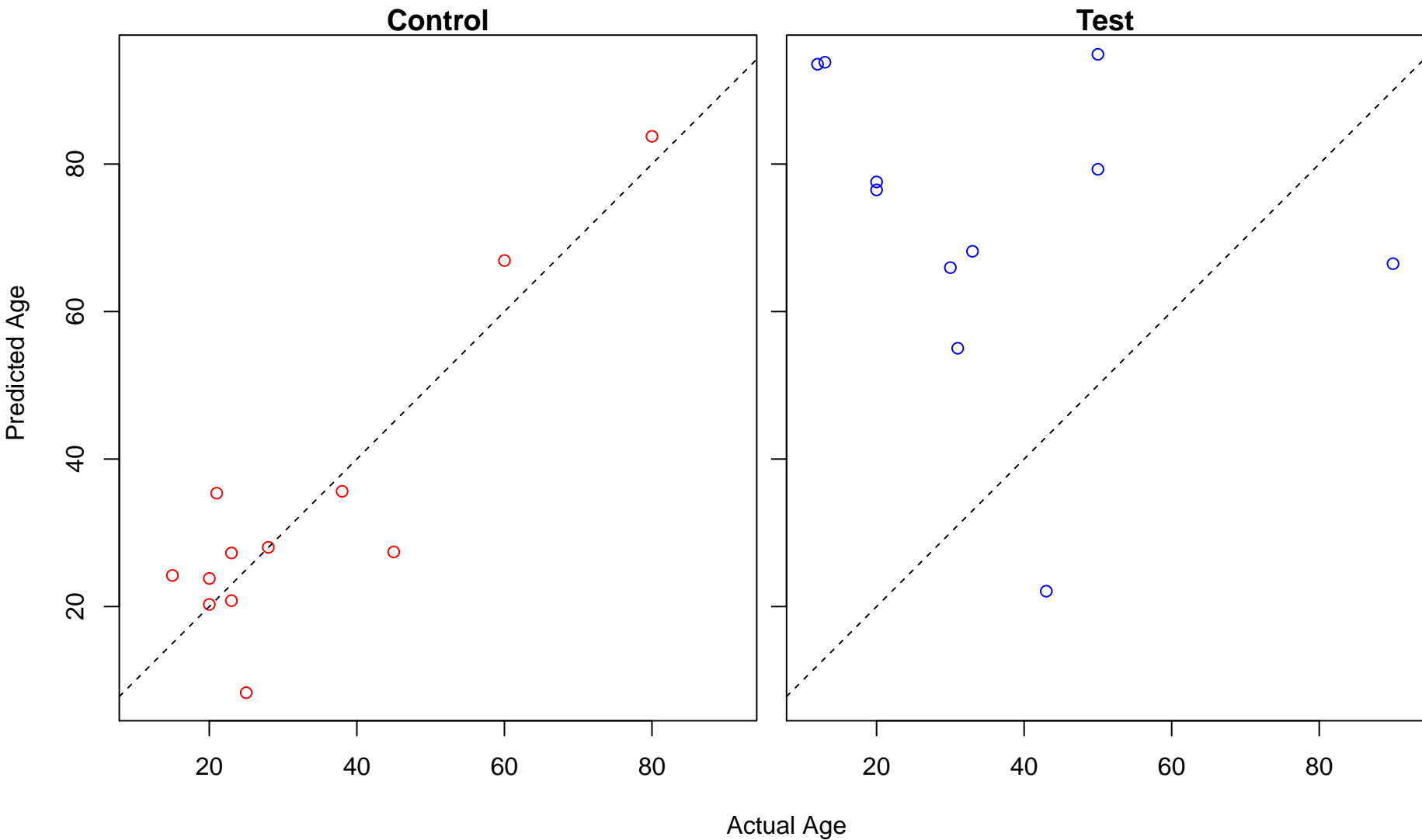
positive regulation of protein modification by small protein conjugation or removal (Score: 15.43870)



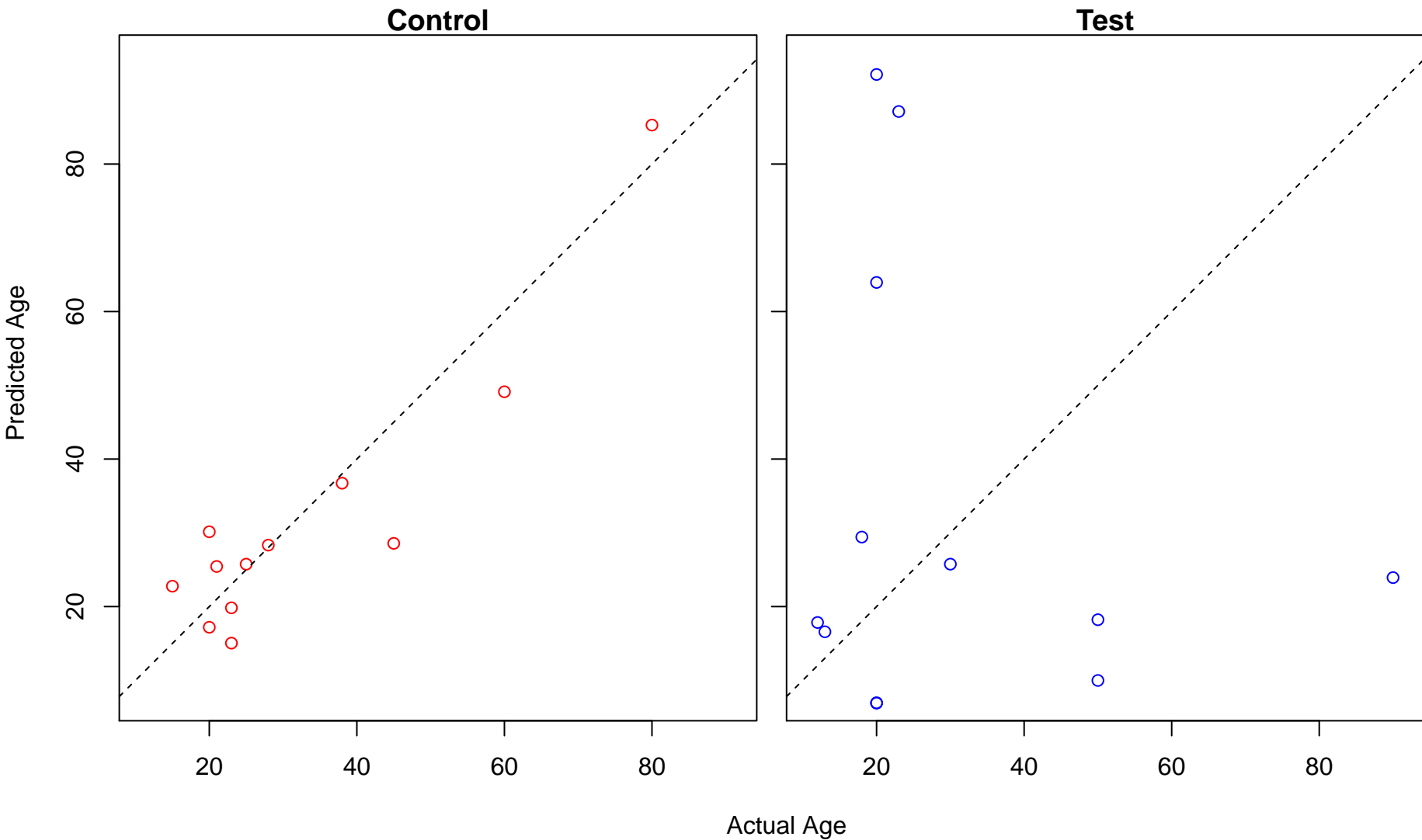
heart trabecula morphogenesis (Score: 15.43143)



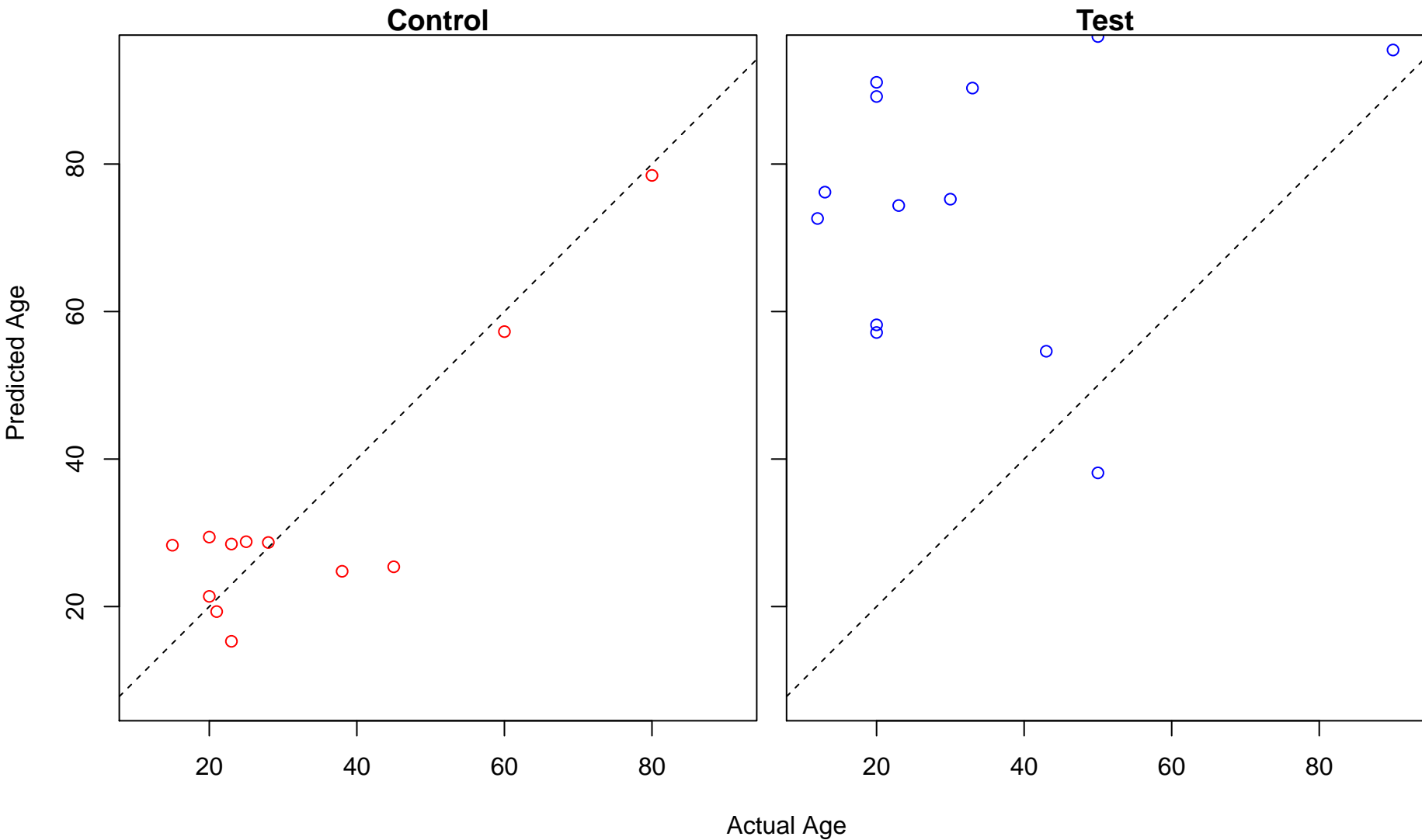
leukemia inhibitory factor signaling pathway (Score: 15.424807)



regulation of protein import (Score: 15.424787)

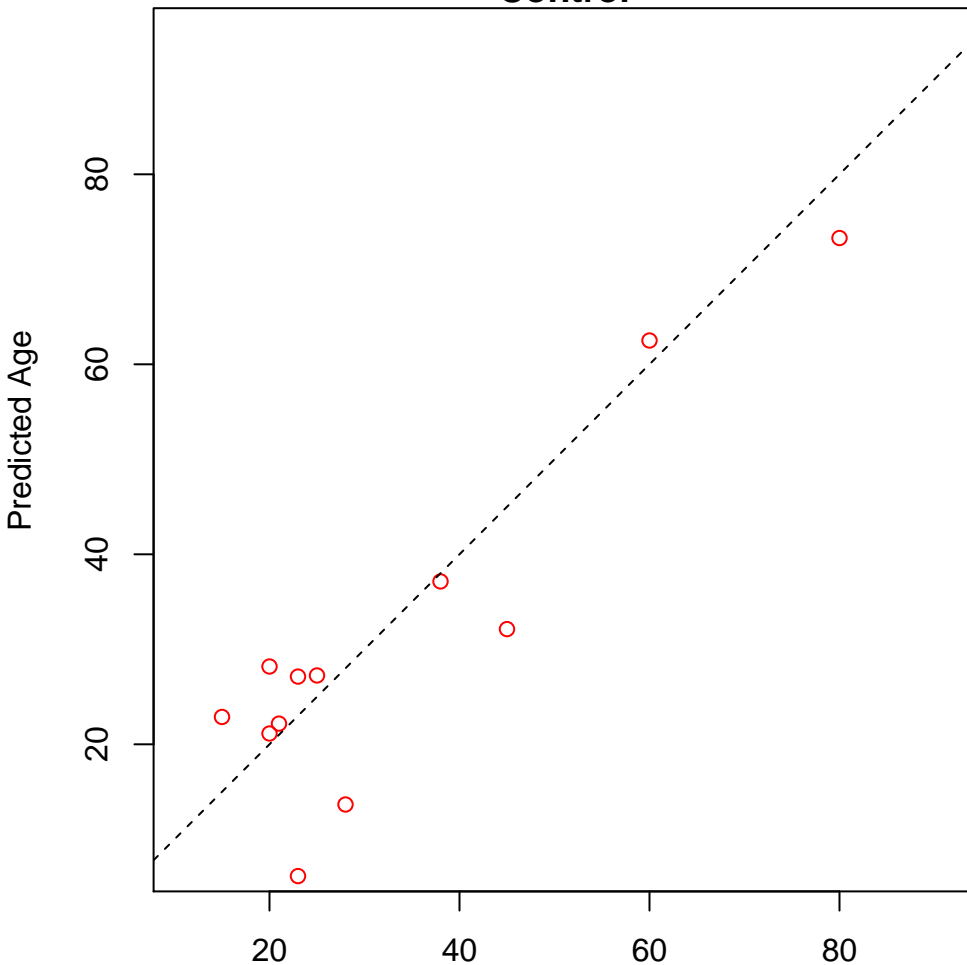


Rap protein signal transduction (Score: 15.340177)

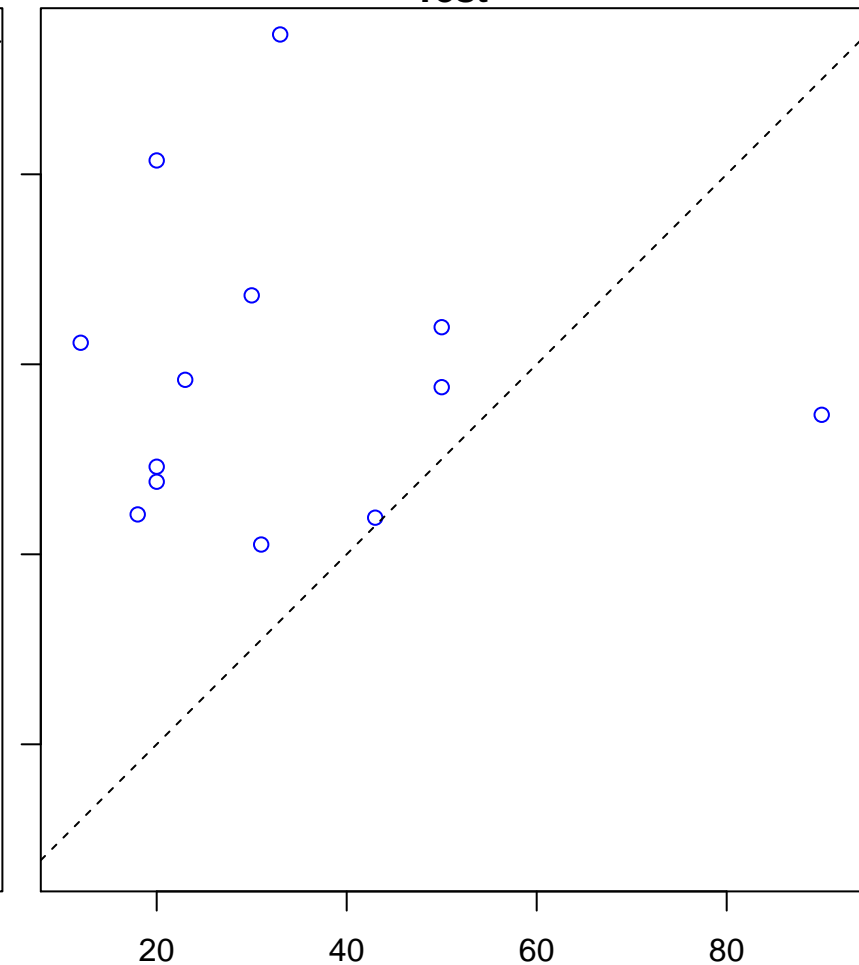


protein transmembrane transport (Score: 15.259927)

Control

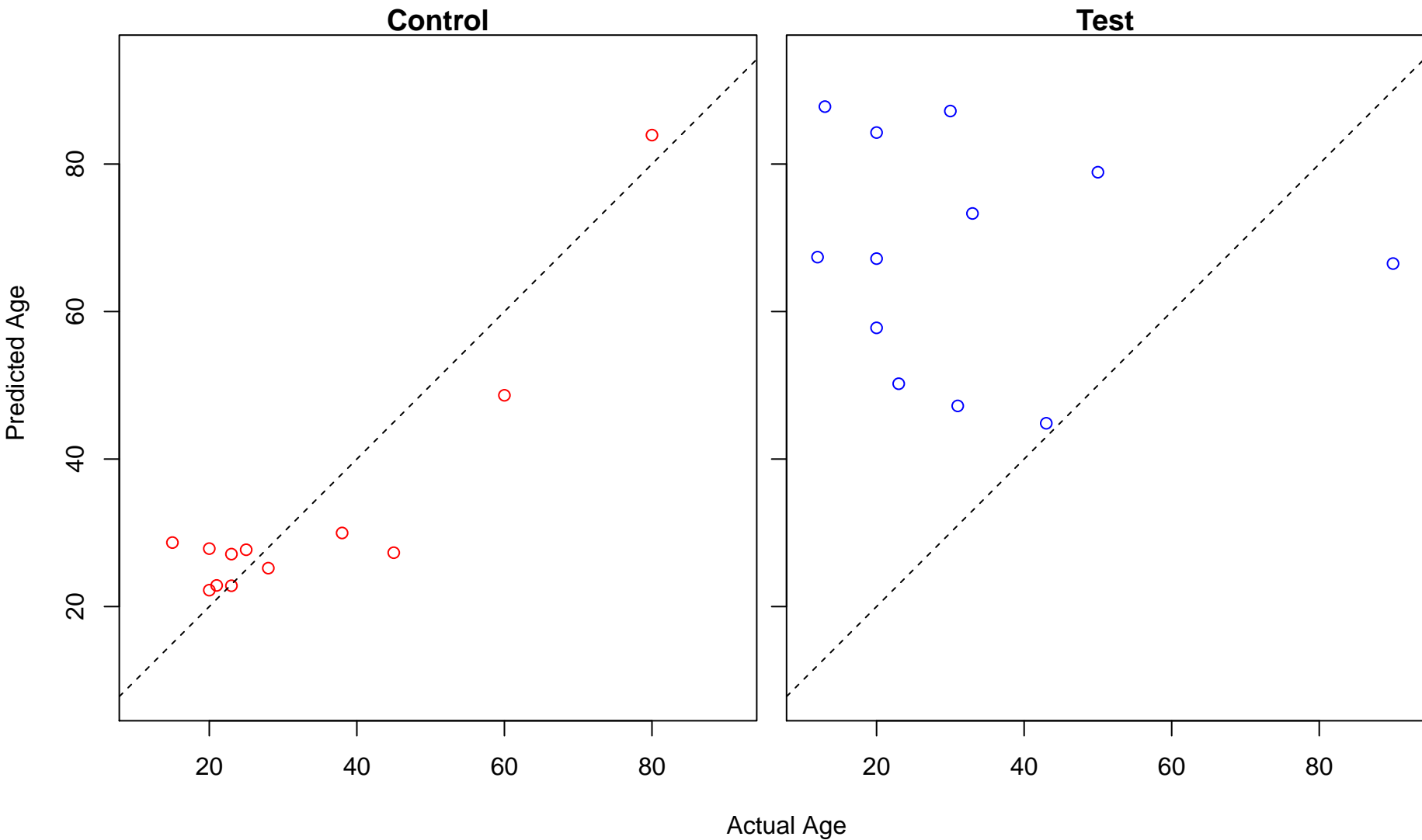


Test

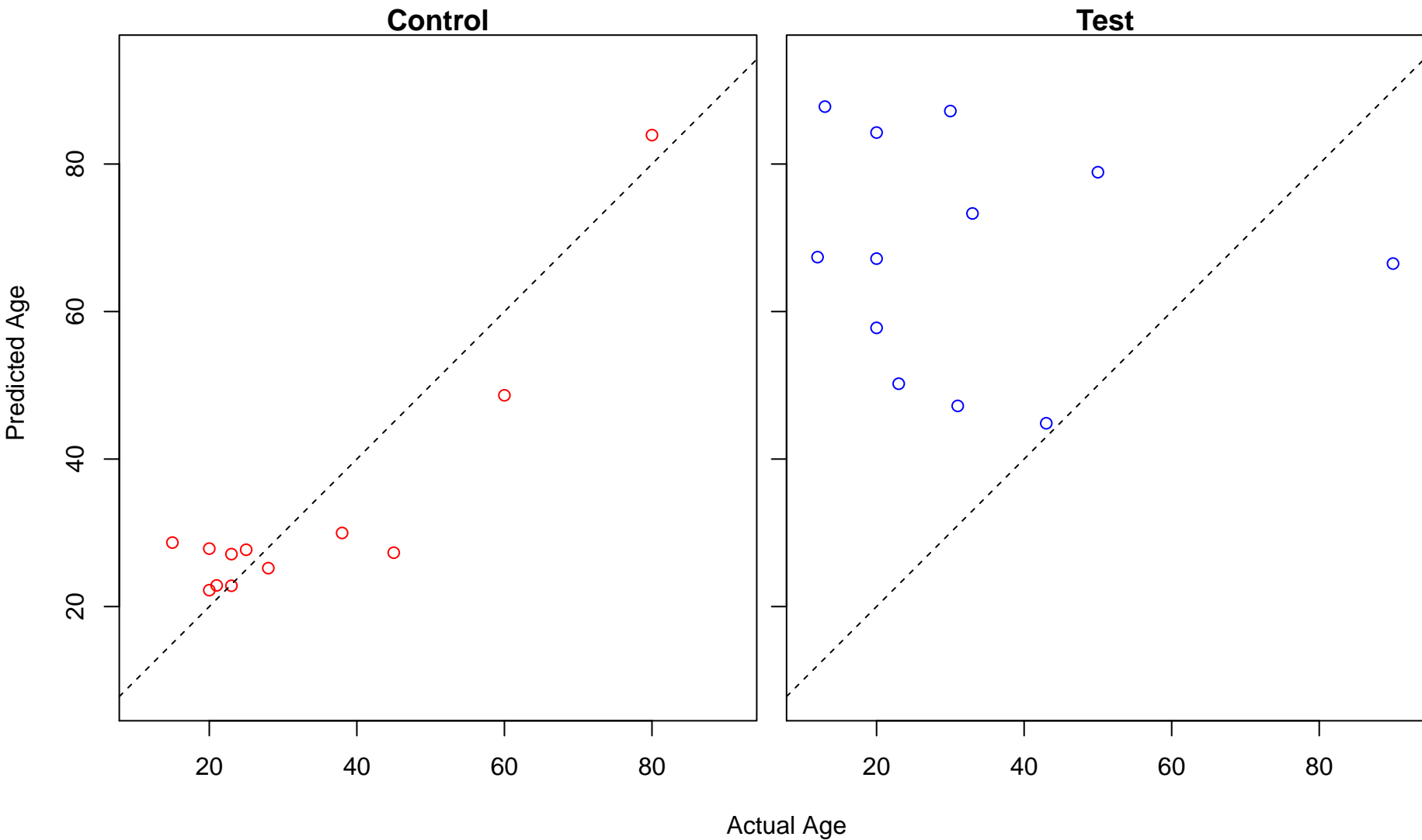


Actual Age

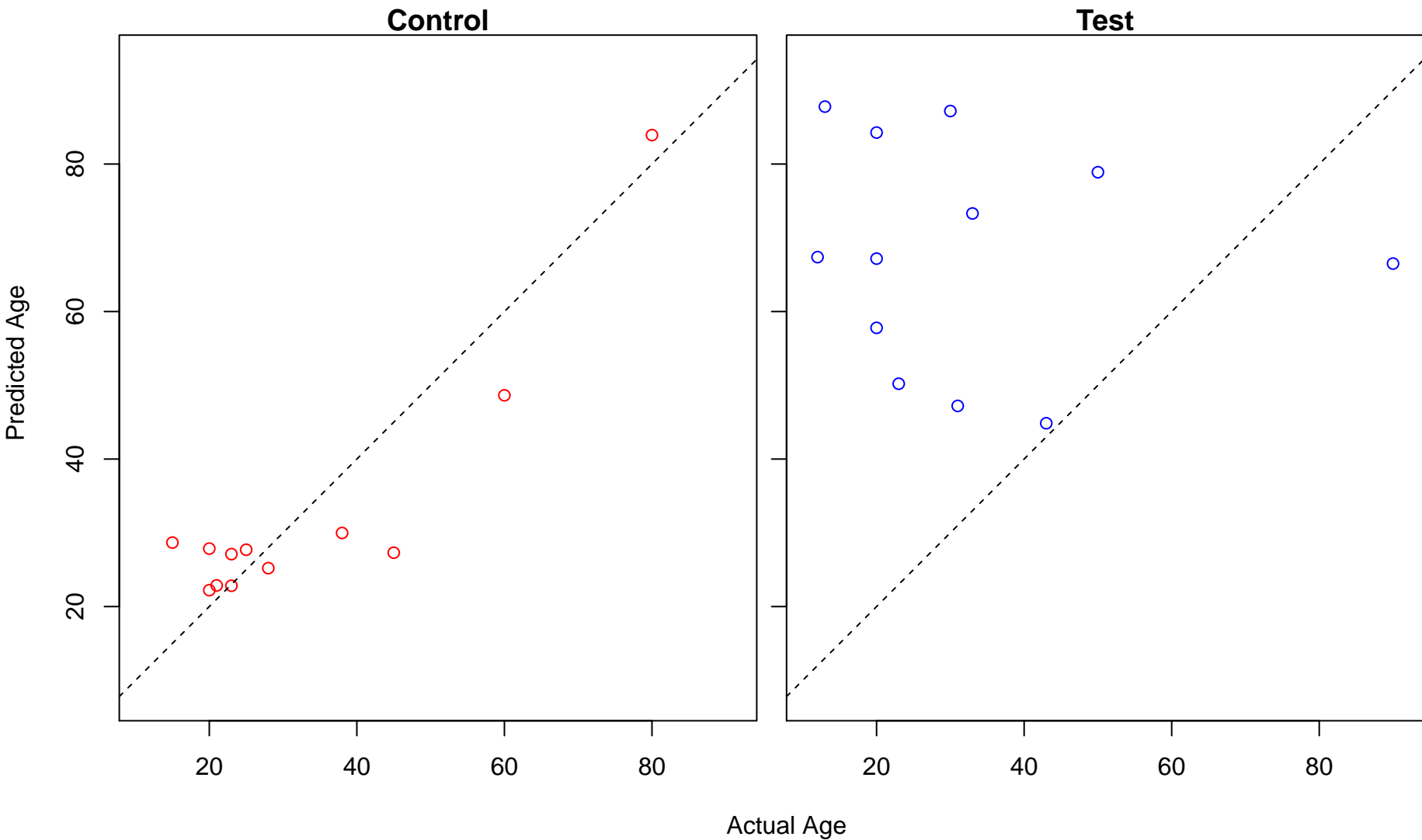
atrial cardiac muscle cell action potential (Score: 15.227984)



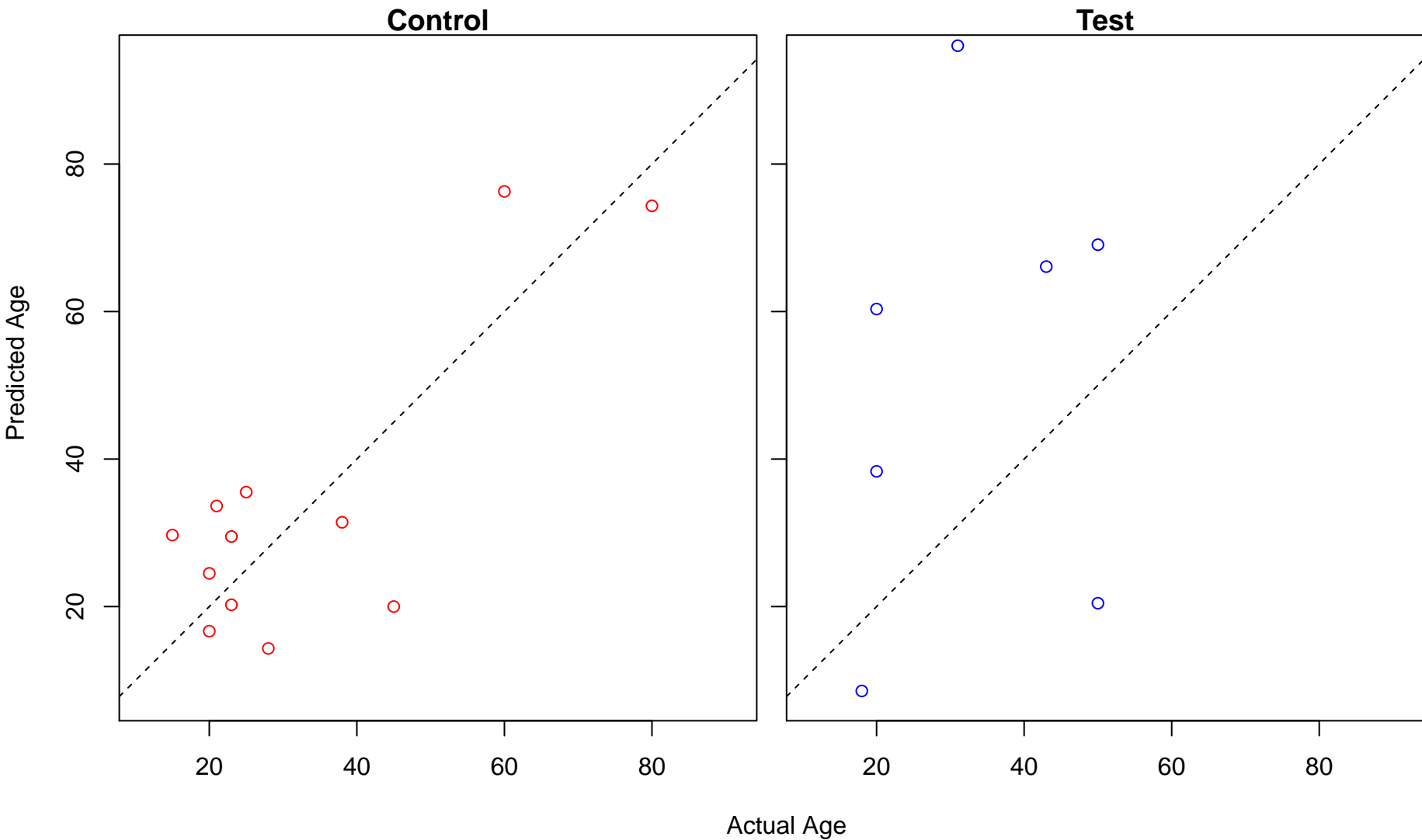
atrial cardiac muscle cell to AV node cell signaling (Score: 15.227984)



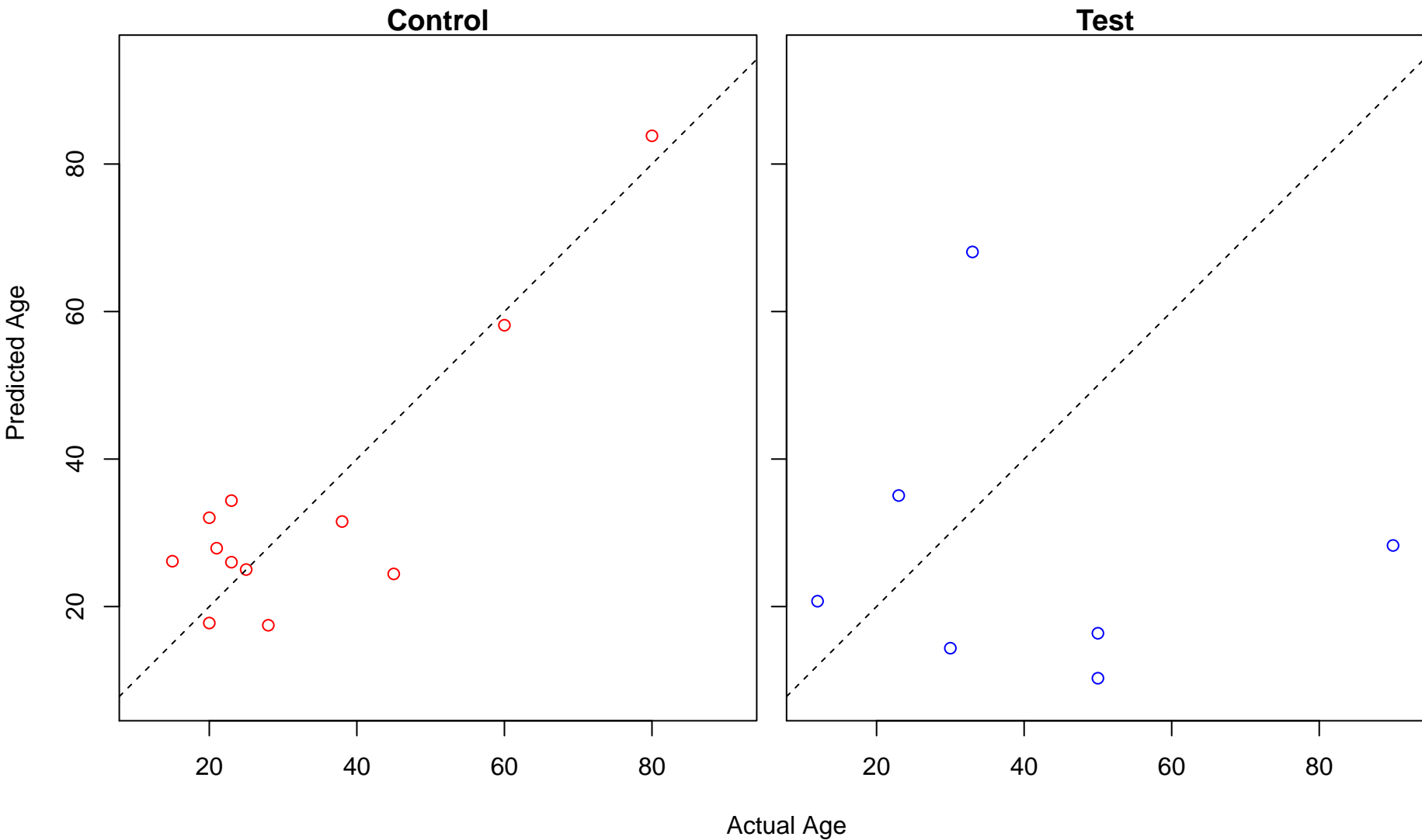
atrial cardiac muscle cell to AV node cell communication (Score: 15.227984)



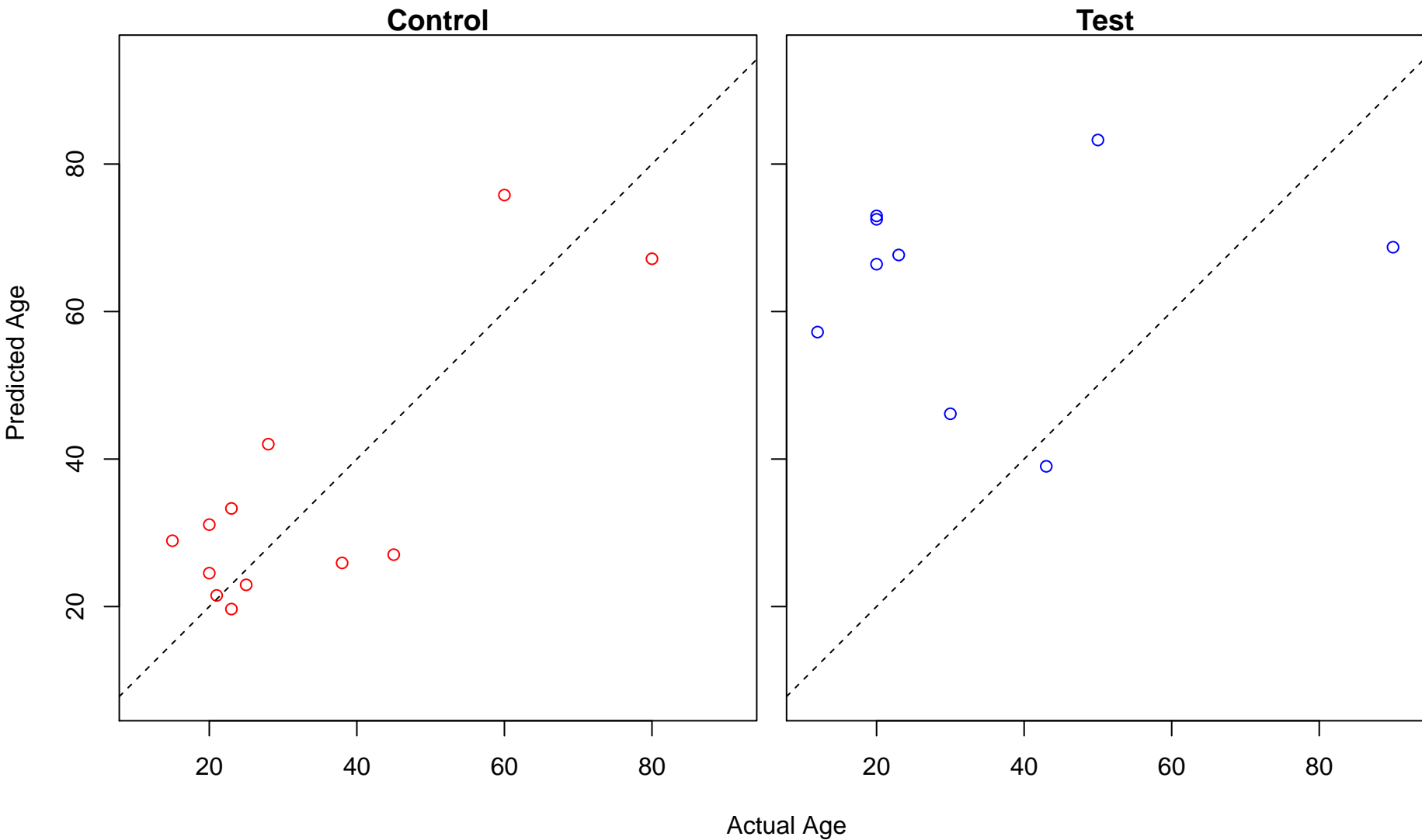
protein destabilization (Score: 15.215973)



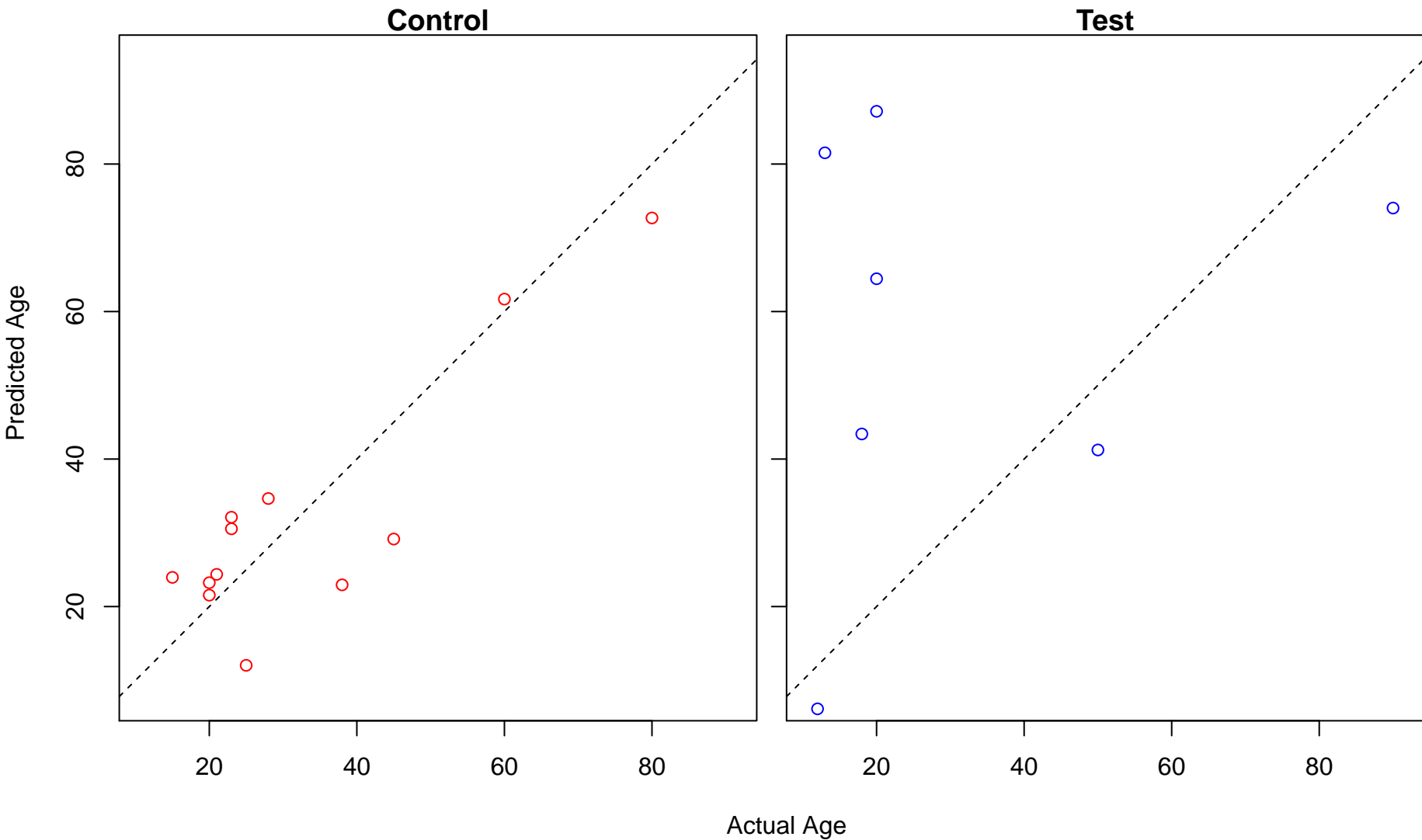
positive regulation of protein ubiquitination (Score: 15.198984)



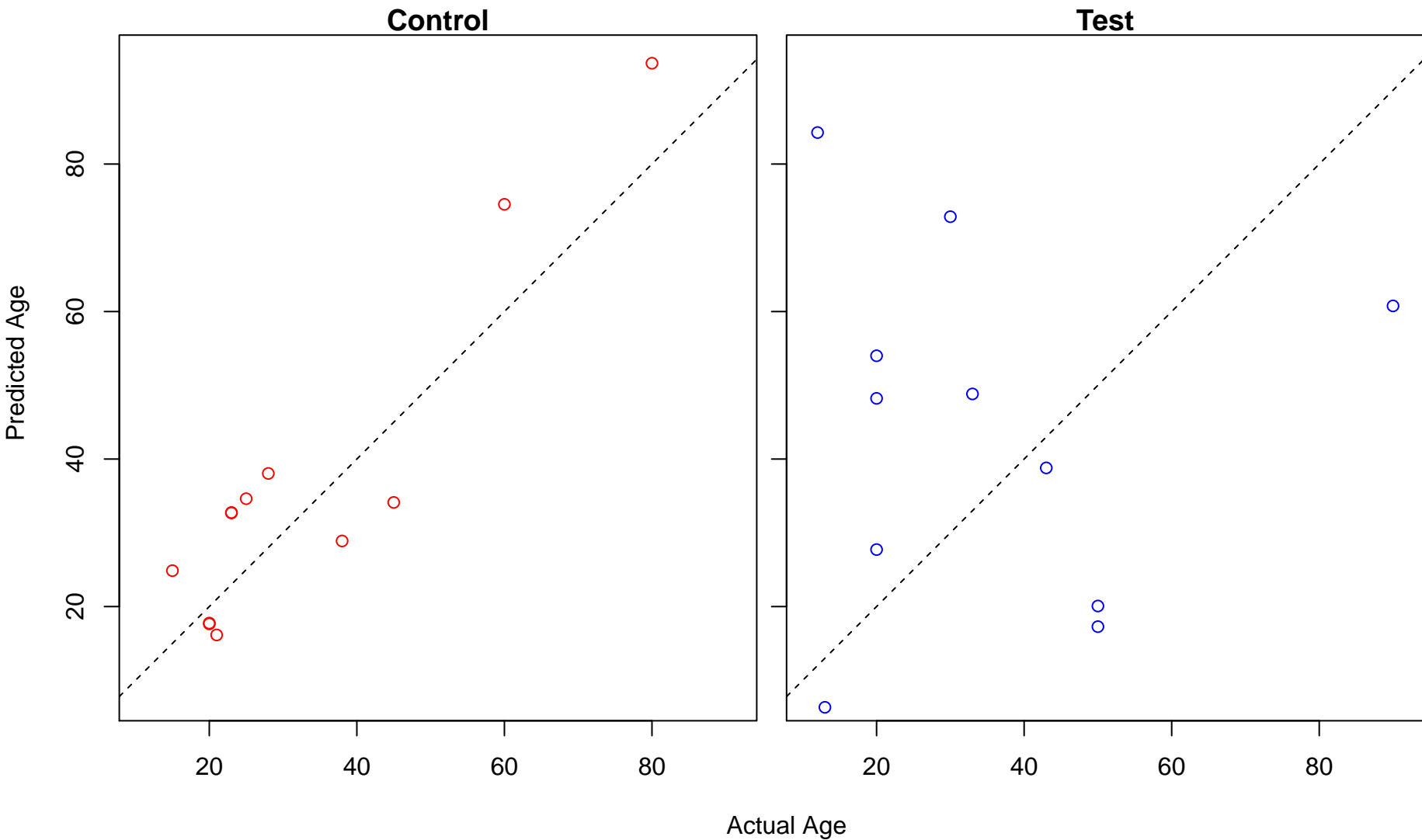
regulation of cell cycle process (Score: 15.187442)



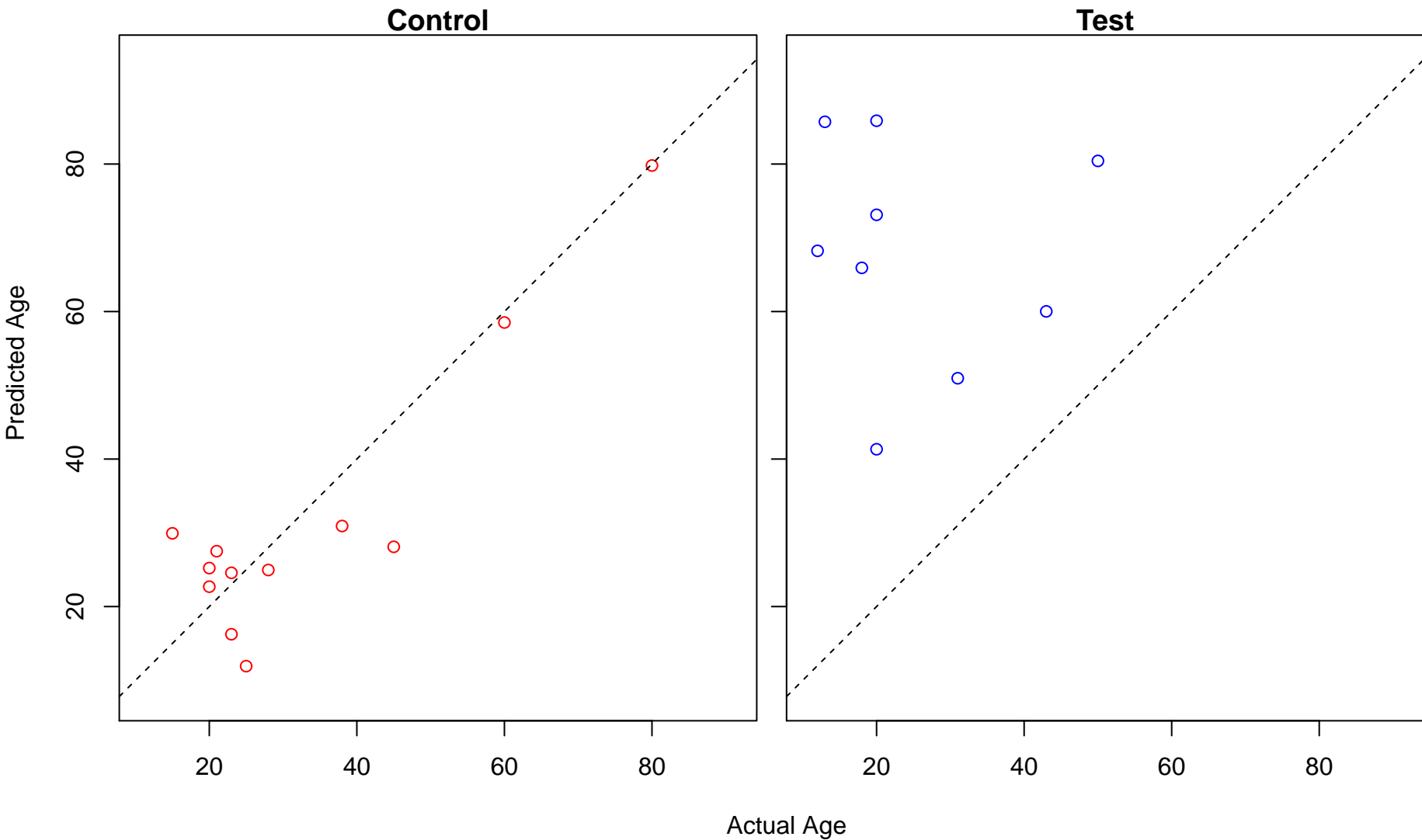
negative regulation of B cell apoptotic process (Score: 15.184716)



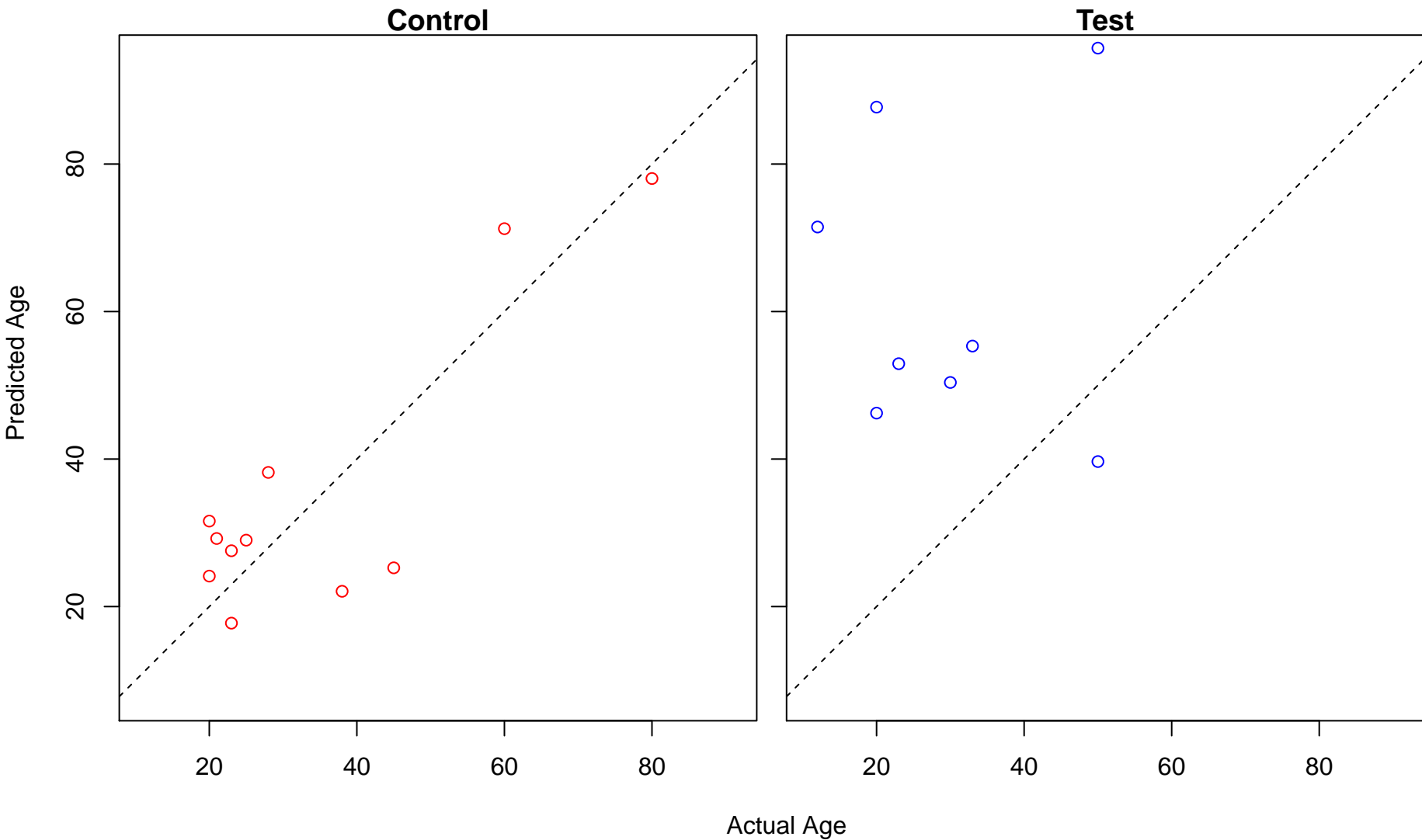
Rac protein signal transduction (Score: 15.162765)



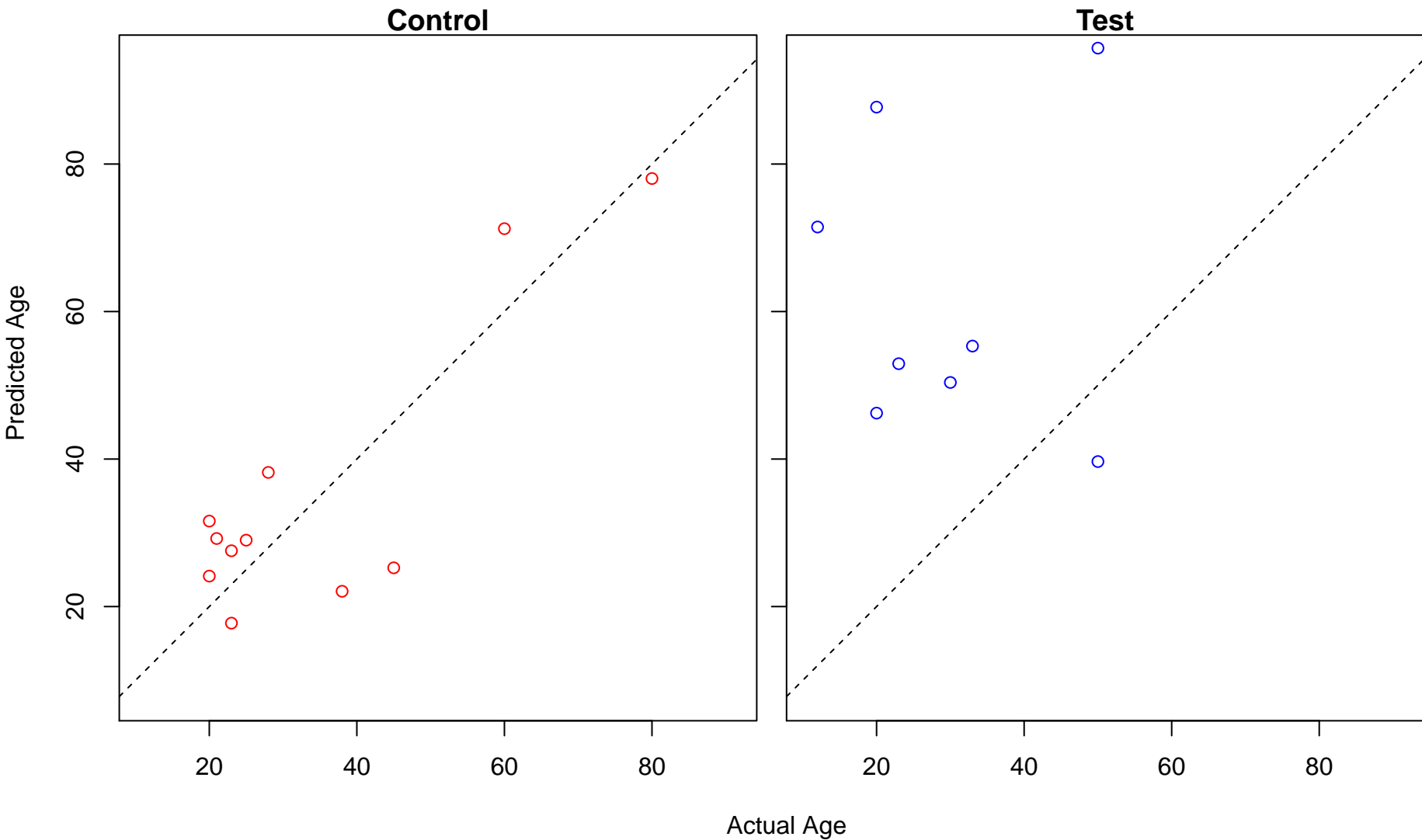
response to ionizing radiation (Score: 15.162053)



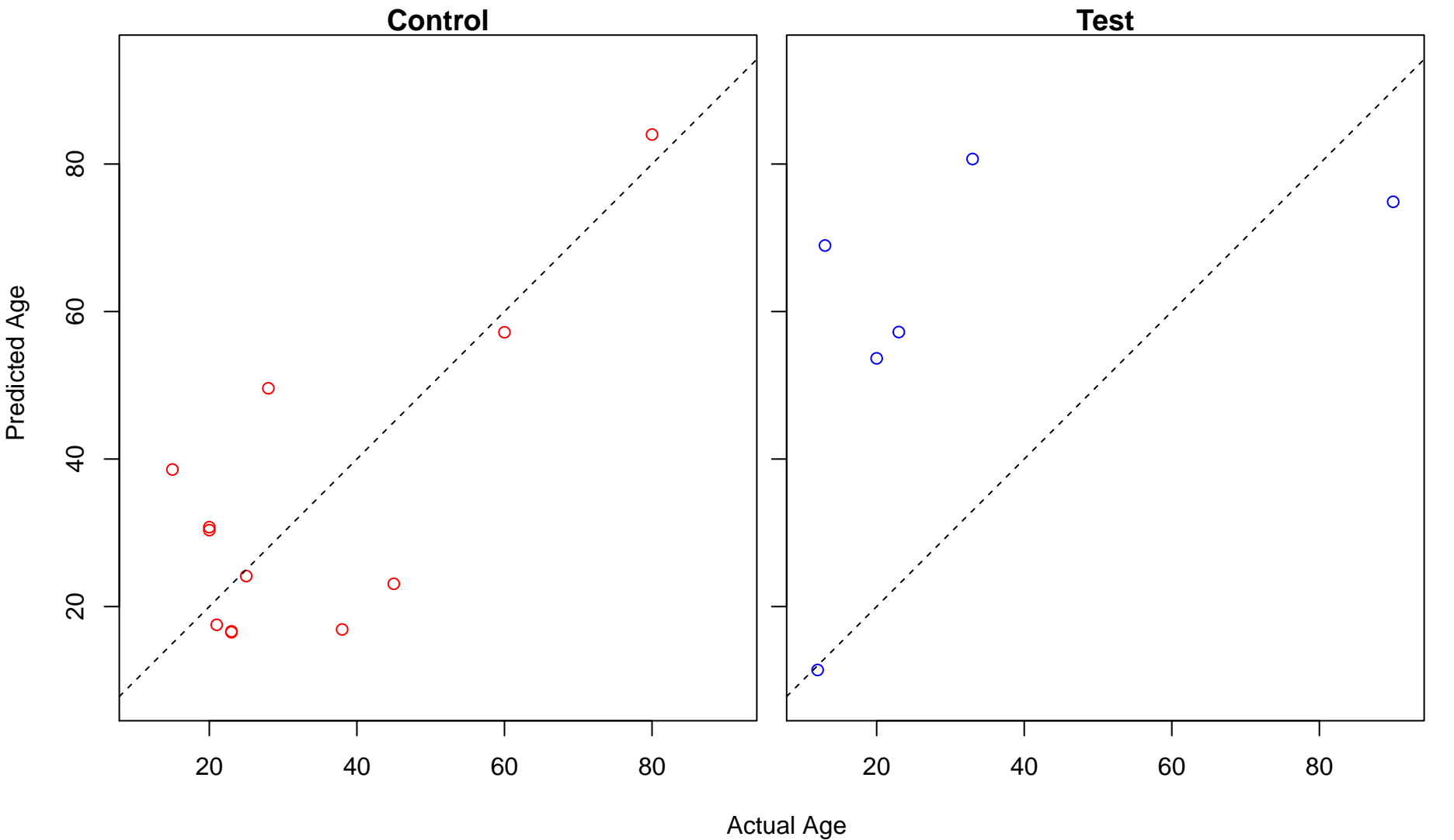
positive regulation of nucleoside metabolic process (Score: 15.154552)



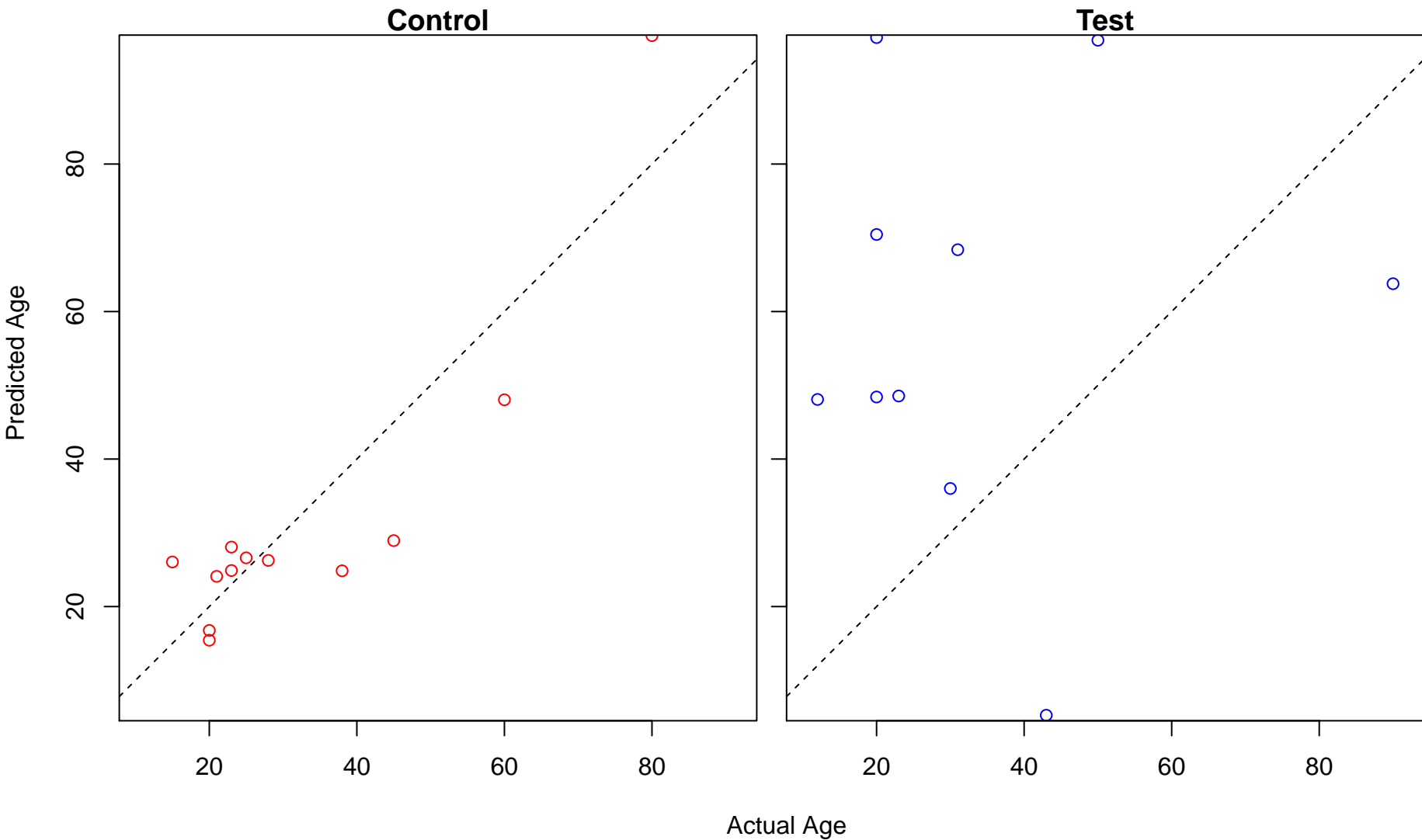
positive regulation of ATP metabolic process (Score: 15.154552)



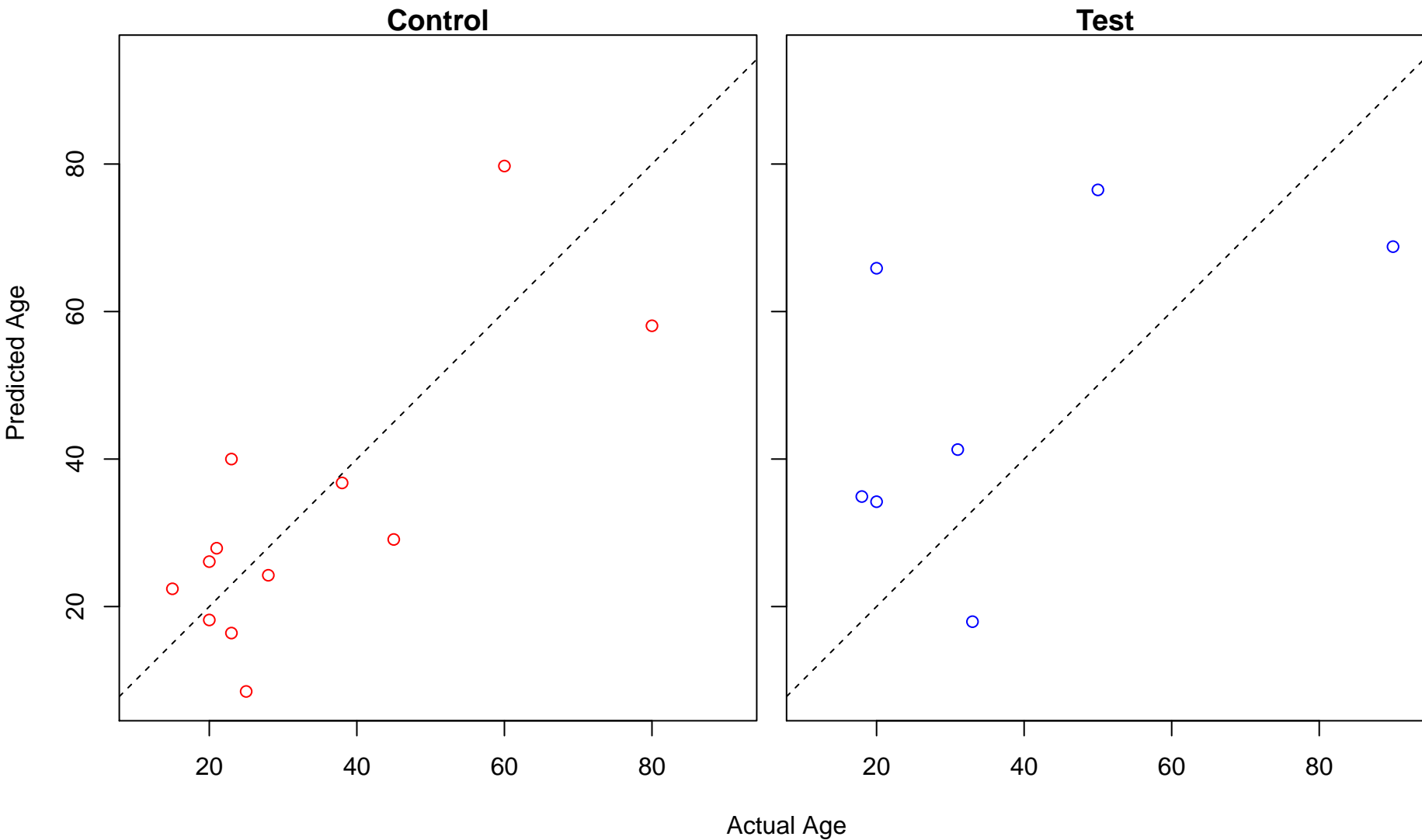
ulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (Score



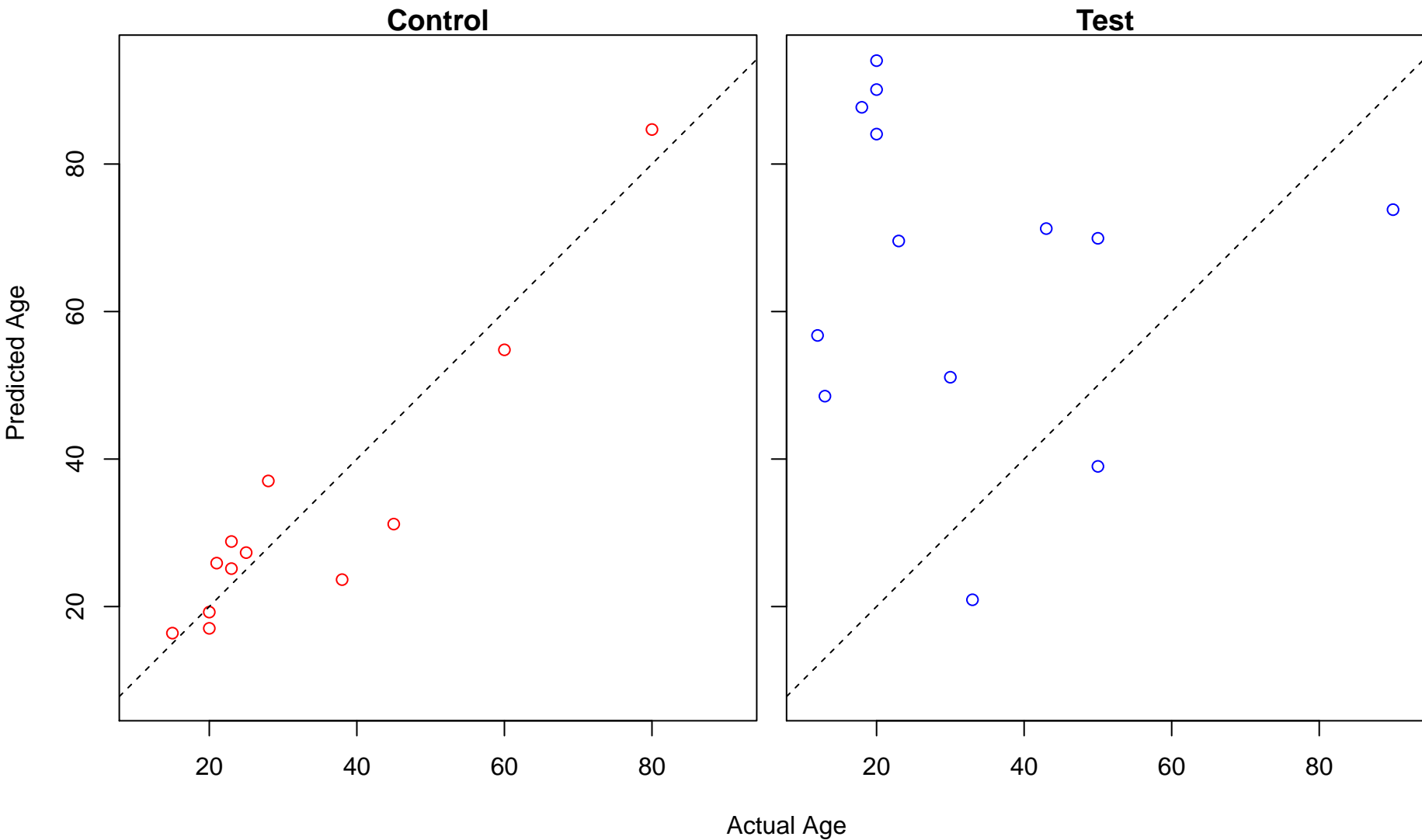
neuron projection extension (Score: 15.134233)



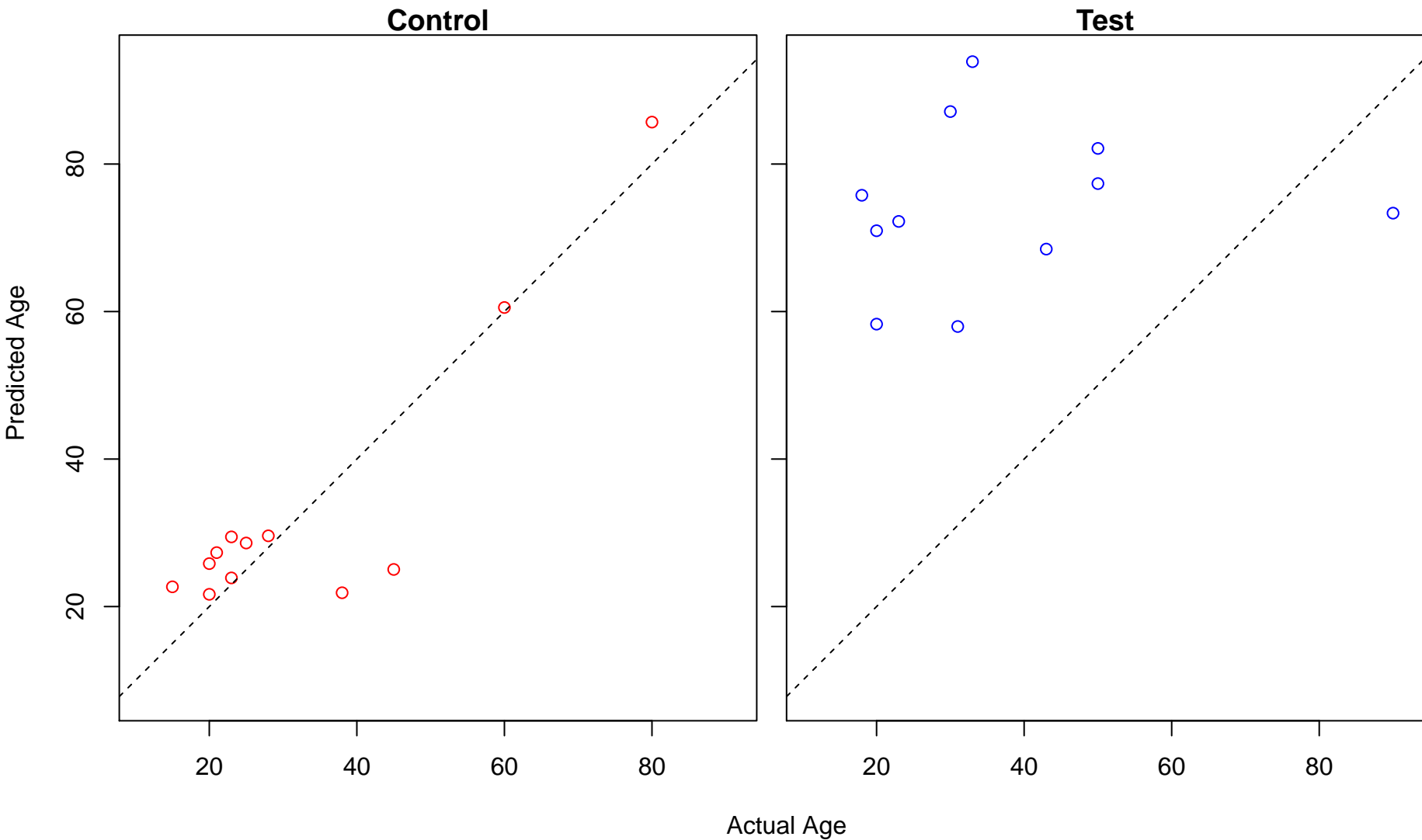
positive regulation of embryonic development (Score: 15.121202)



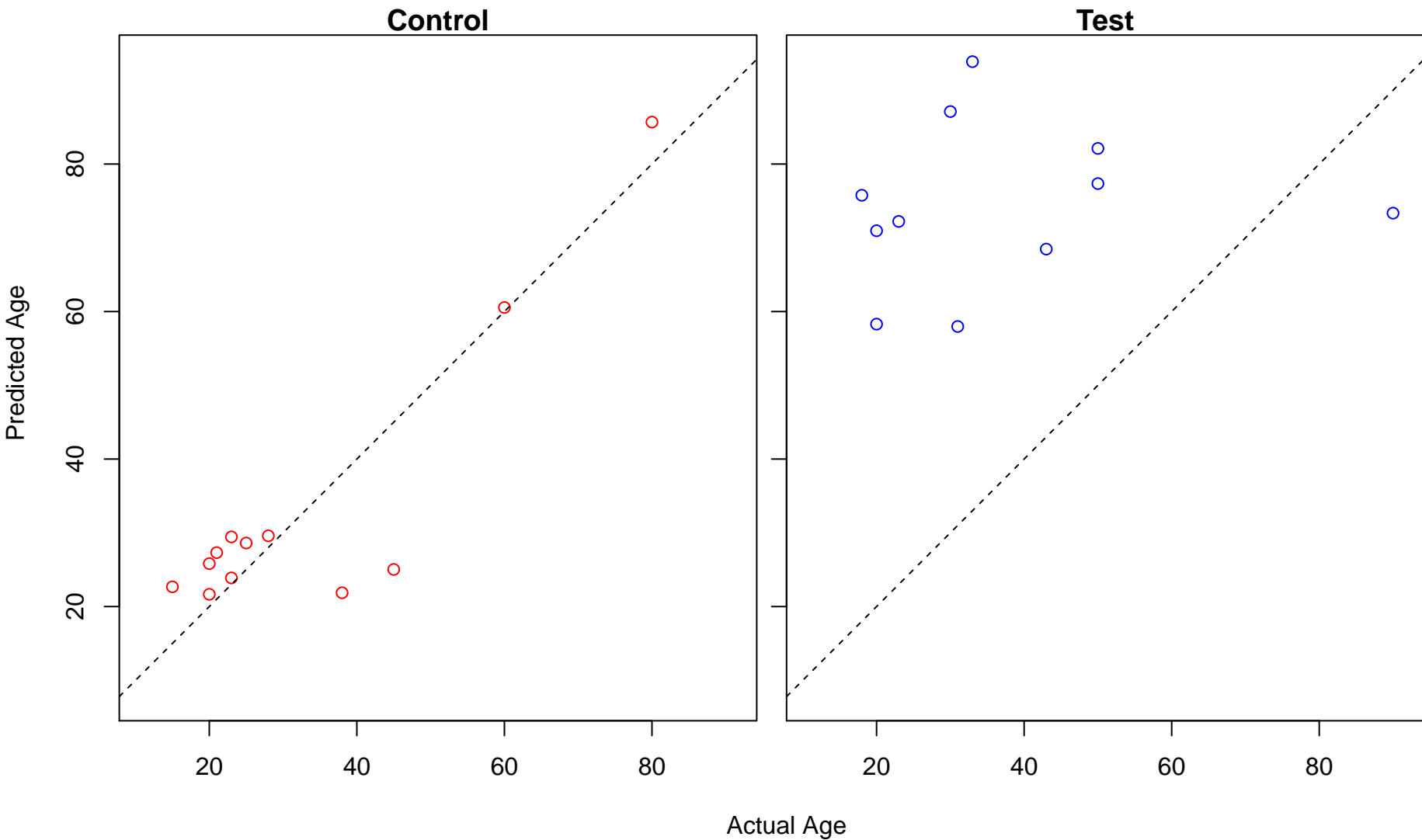
cellular response to ketone (Score: 15.118243)



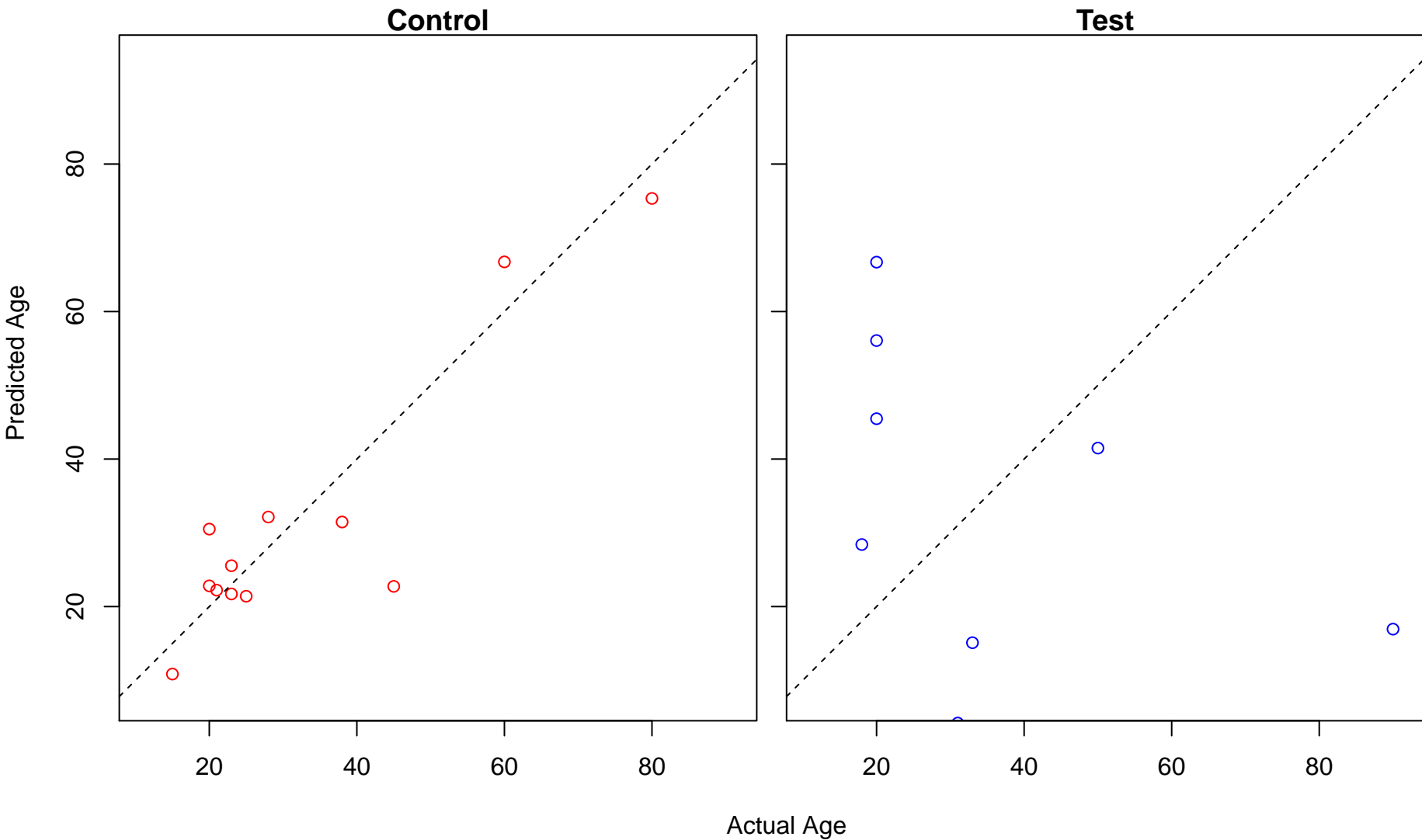
positive regulation of striated muscle tissue development (Score: 15.100970)



positive regulation of muscle organ development (Score: 15.100970)

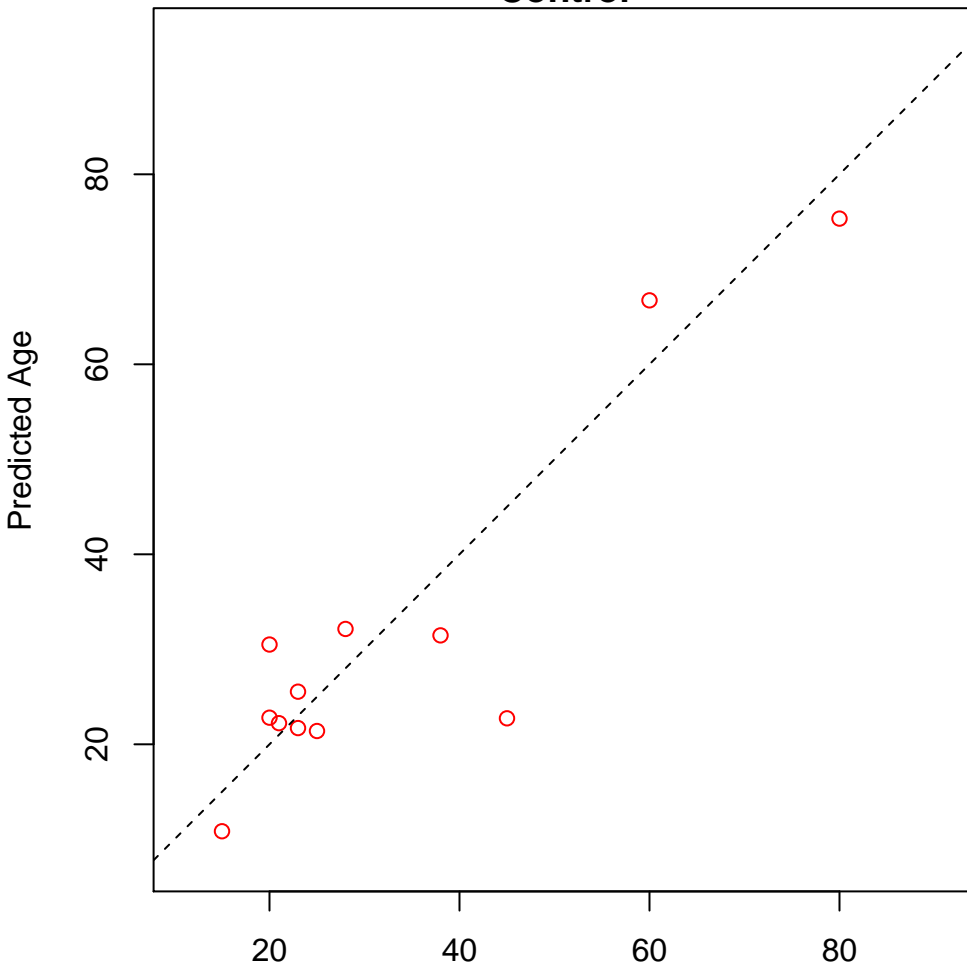


nucleotide-sugar transport (Score: 15.100567)

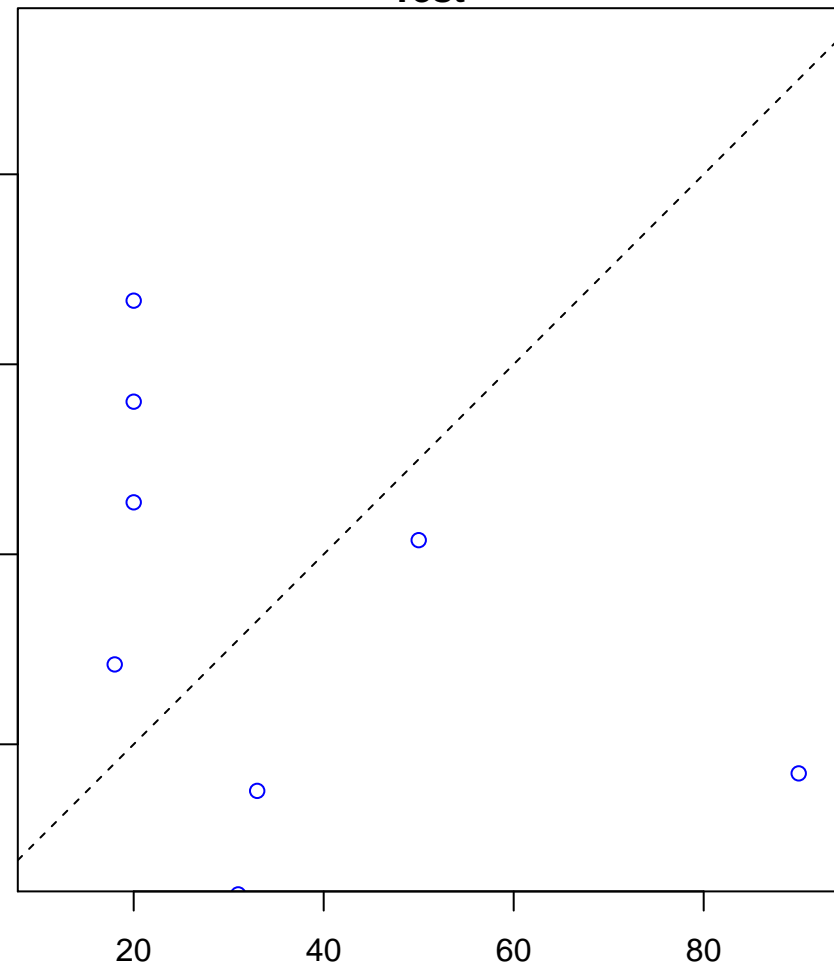


pyrimidine nucleotide–sugar transport (Score: 15.100567)

Control

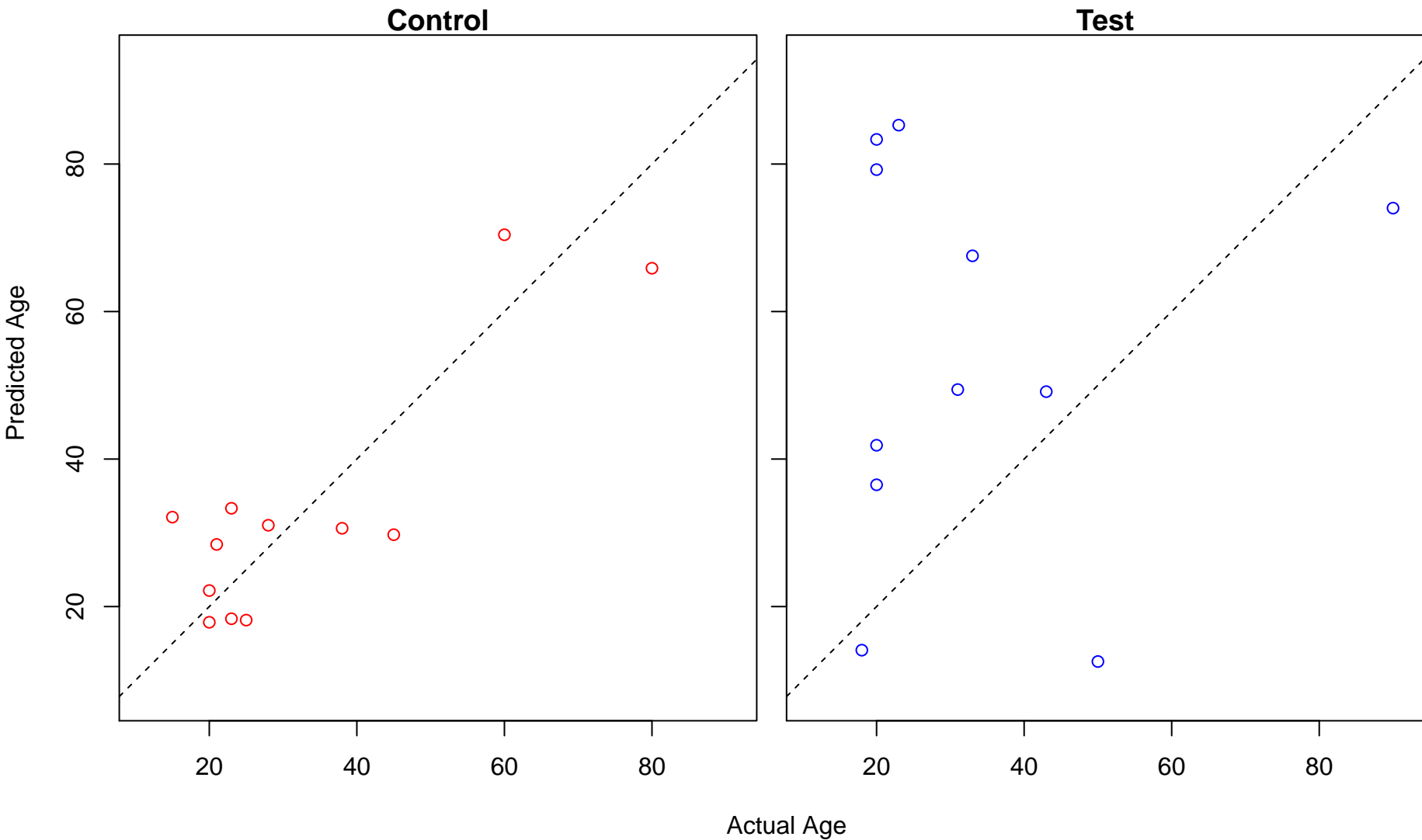


Test

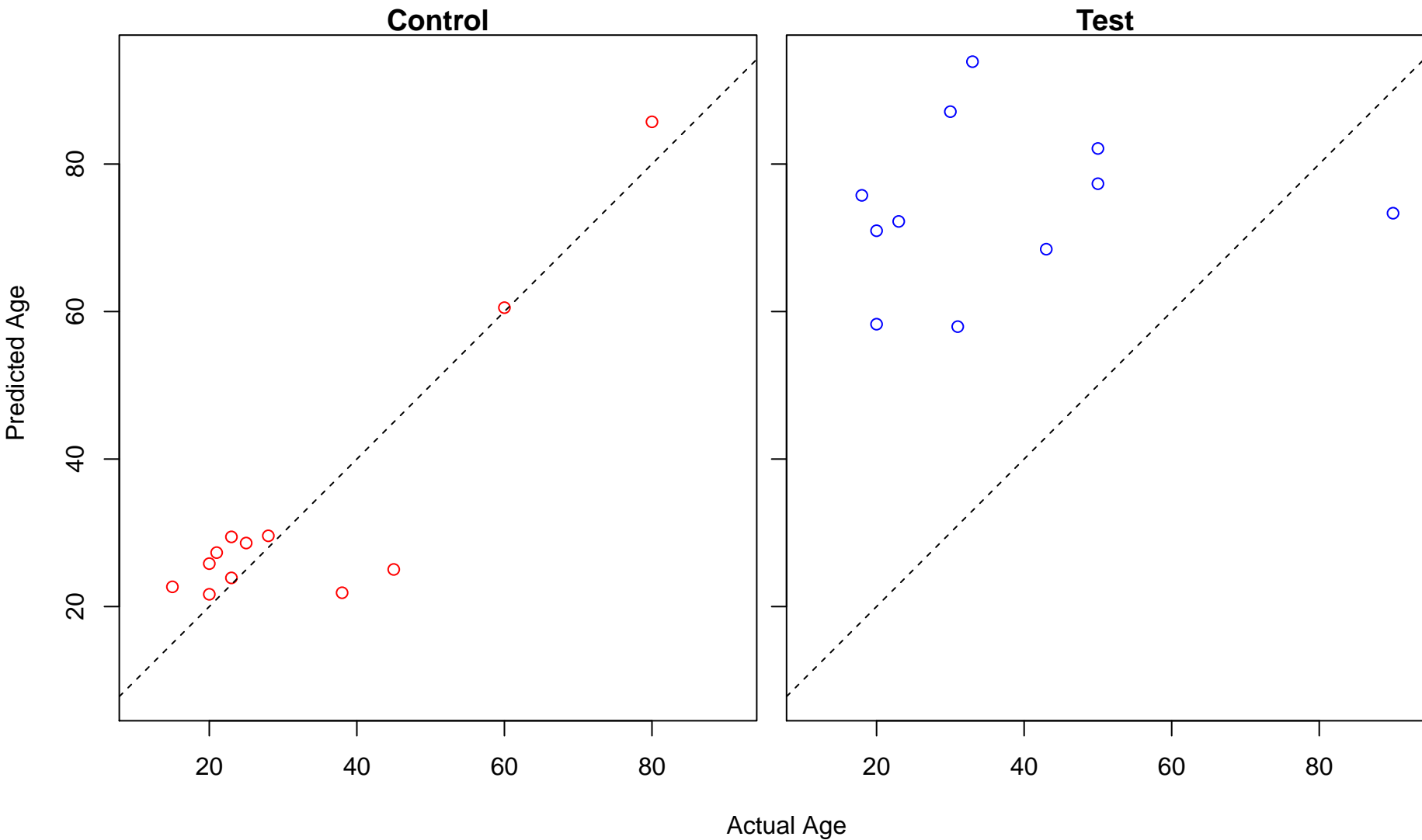


Actual Age

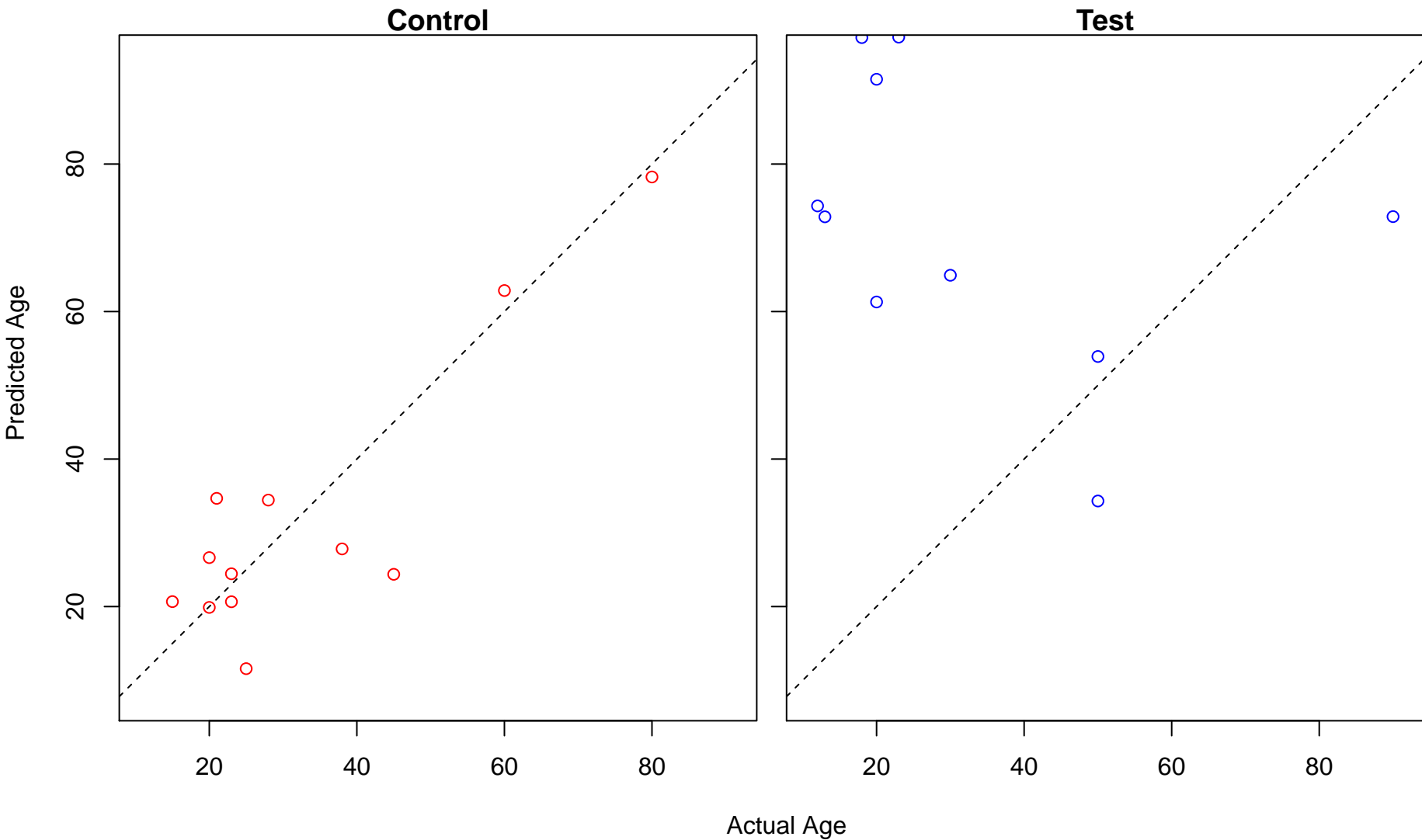
regulation of DNA binding (Score: 15.097064)



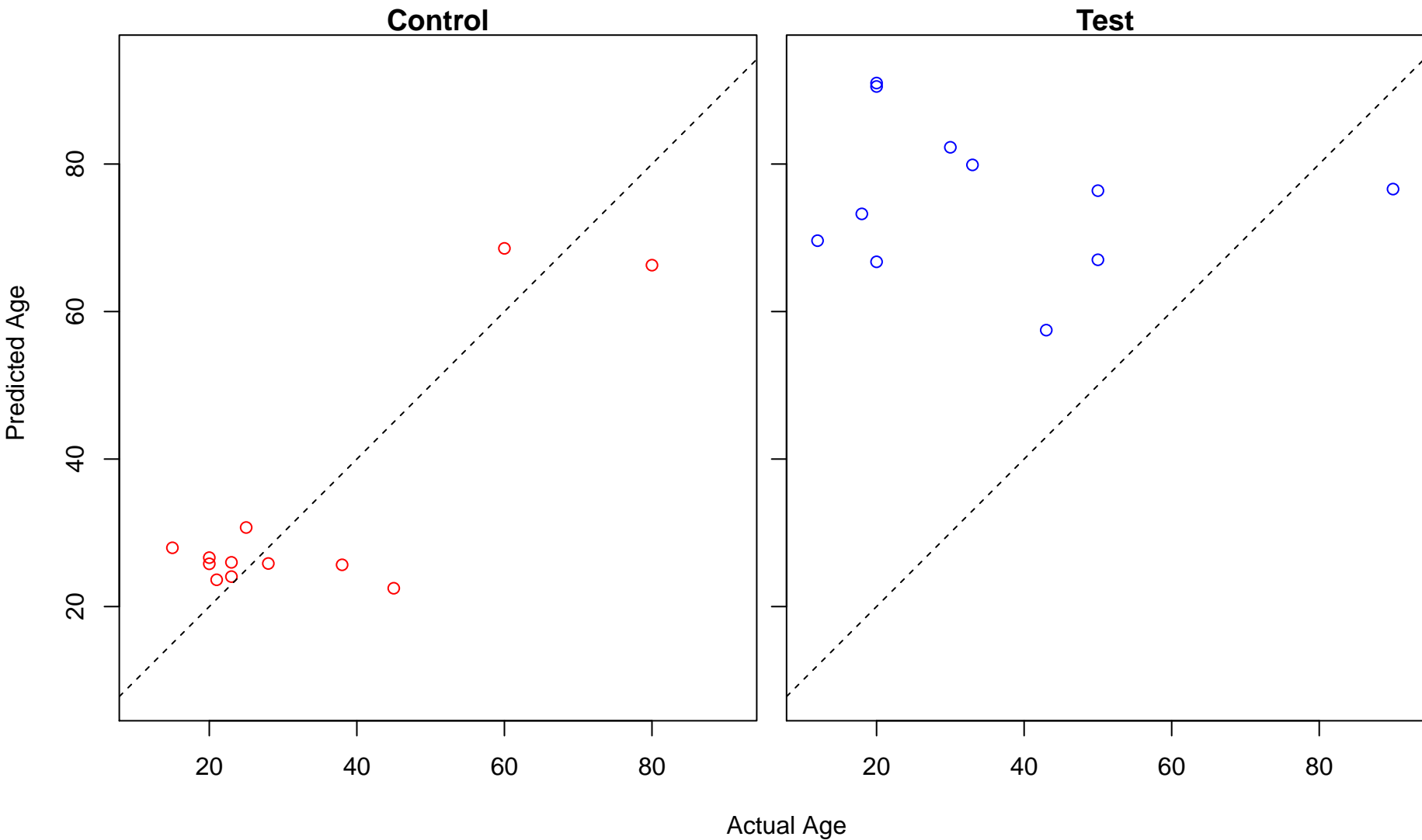
positive regulation of muscle tissue development (Score: 15.091777)



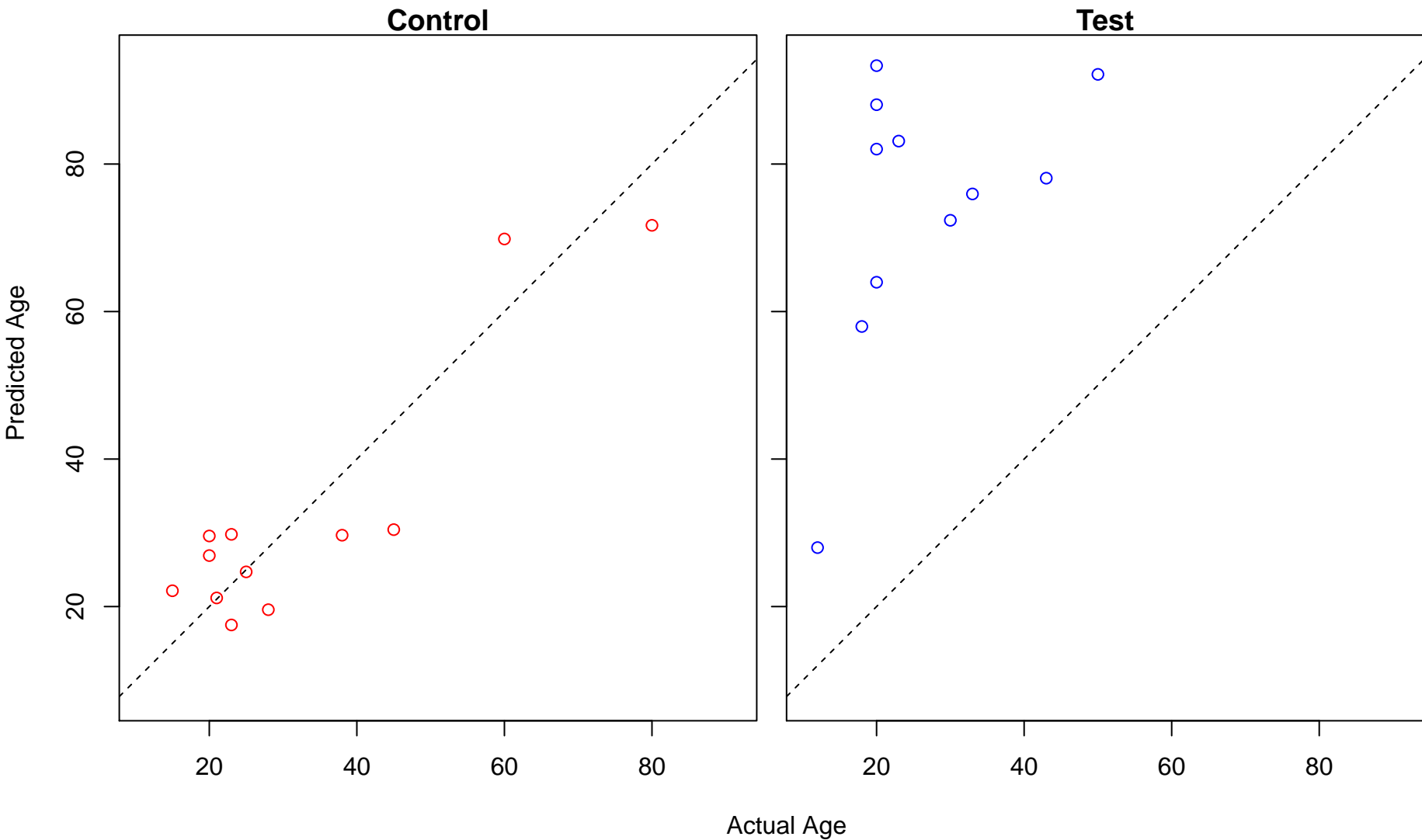
DNA-dependent DNA replication (Score: 15.089710)



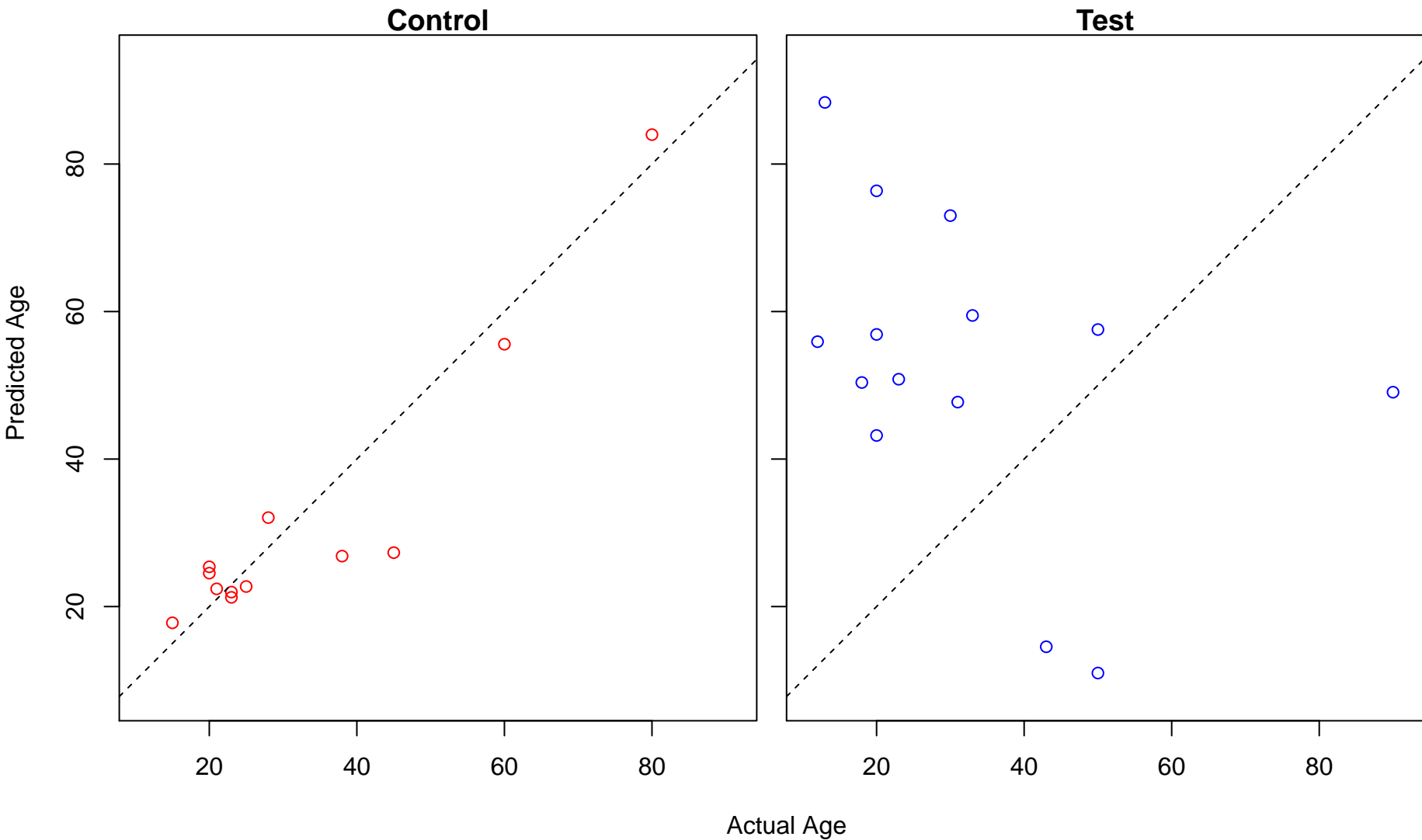
positive regulation of cellular extravasation (Score: 15.060269)



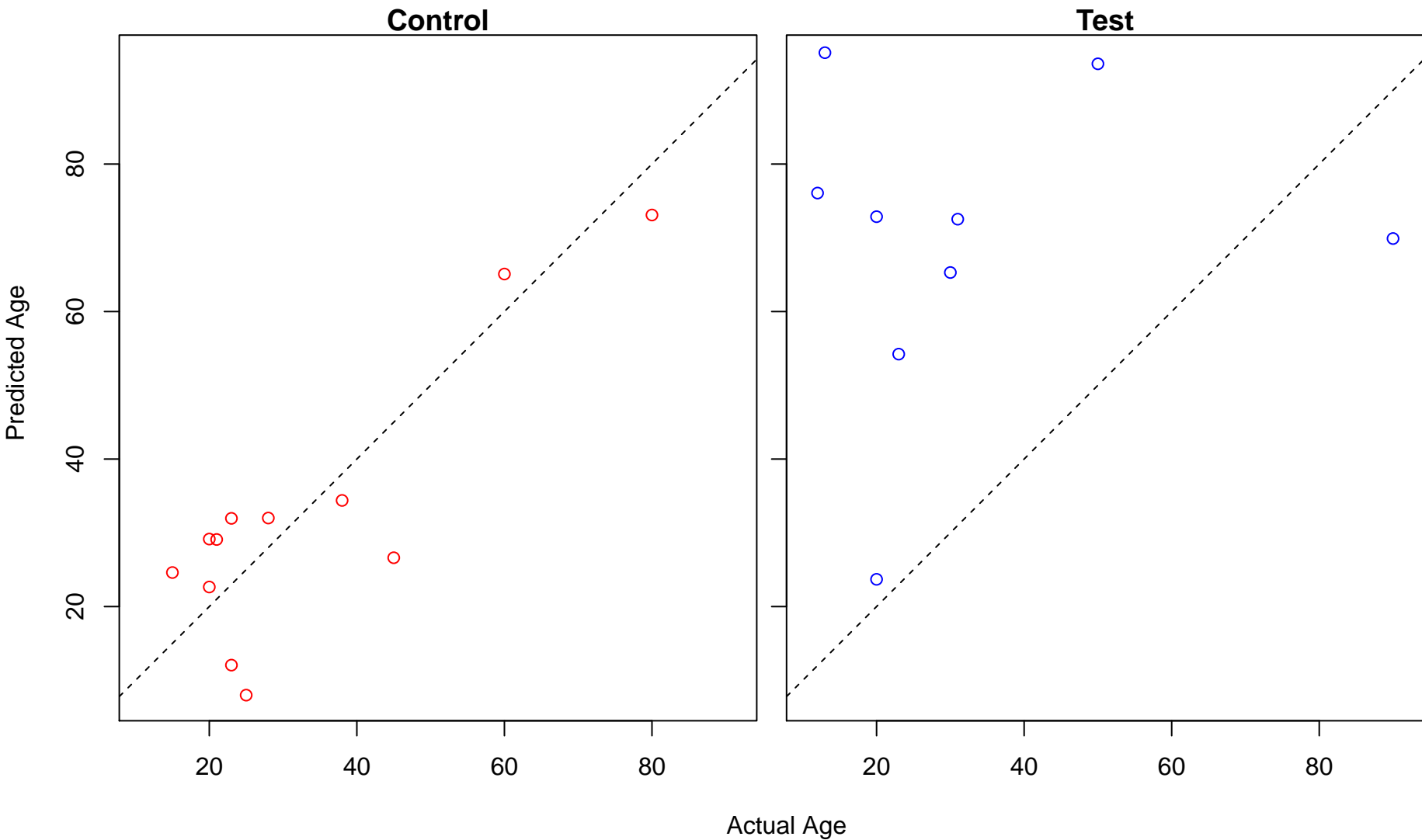
ncRNA 3'-end processing (Score: 15.019858)



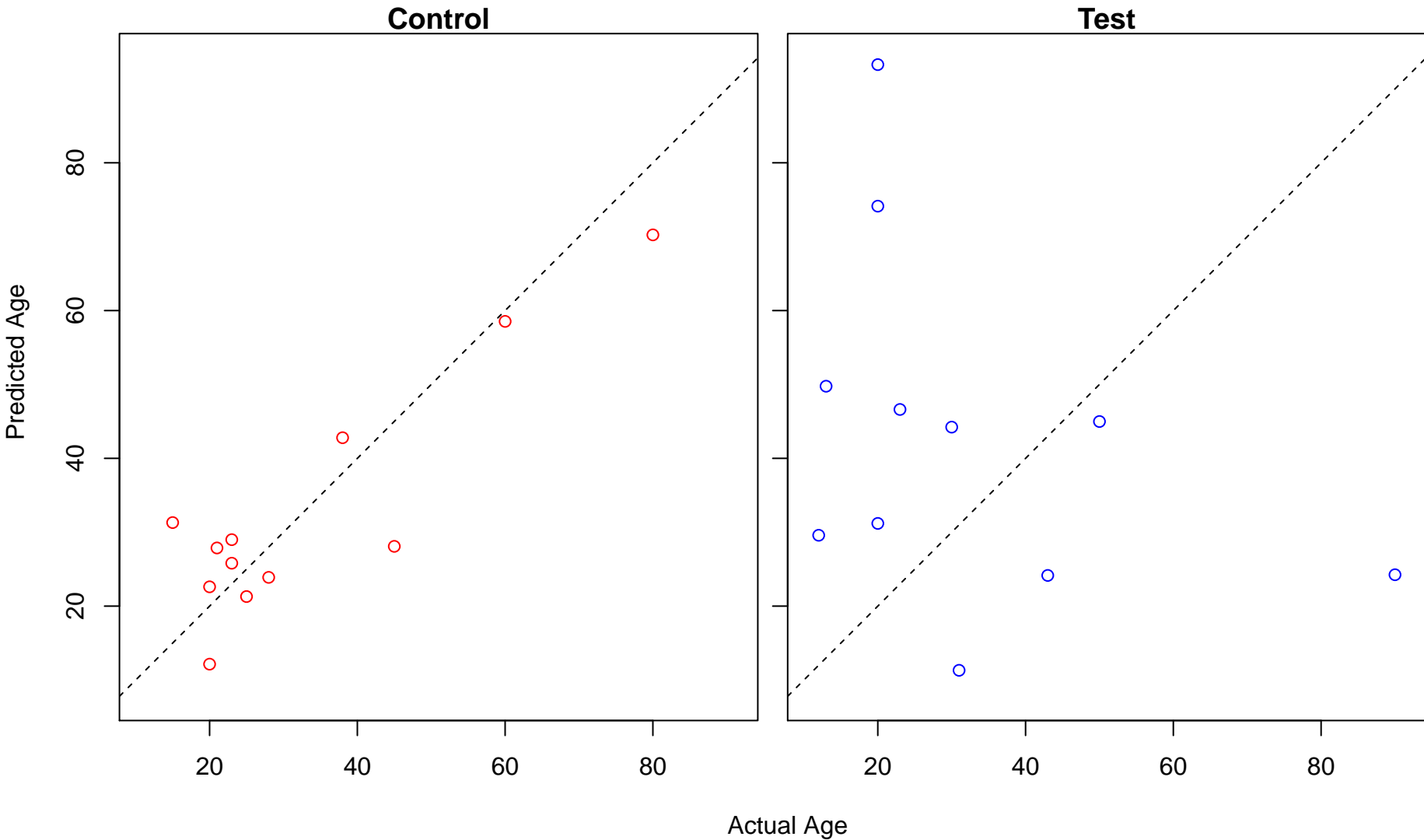
regulation of JNK cascade (Score: 15.016216)



negative regulation of cell migration involved in sprouting angiogenesis (Score: 14.992339)

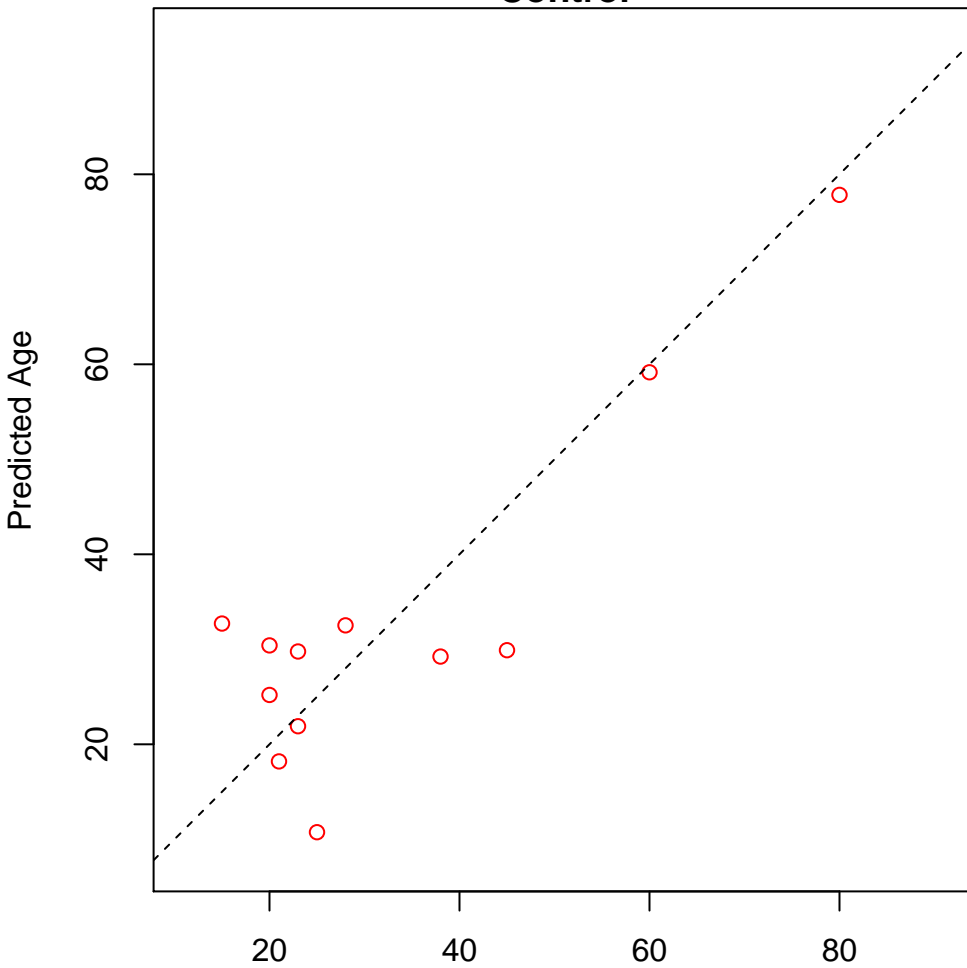


regulation of ion transmembrane transport (Score: 14.928216)

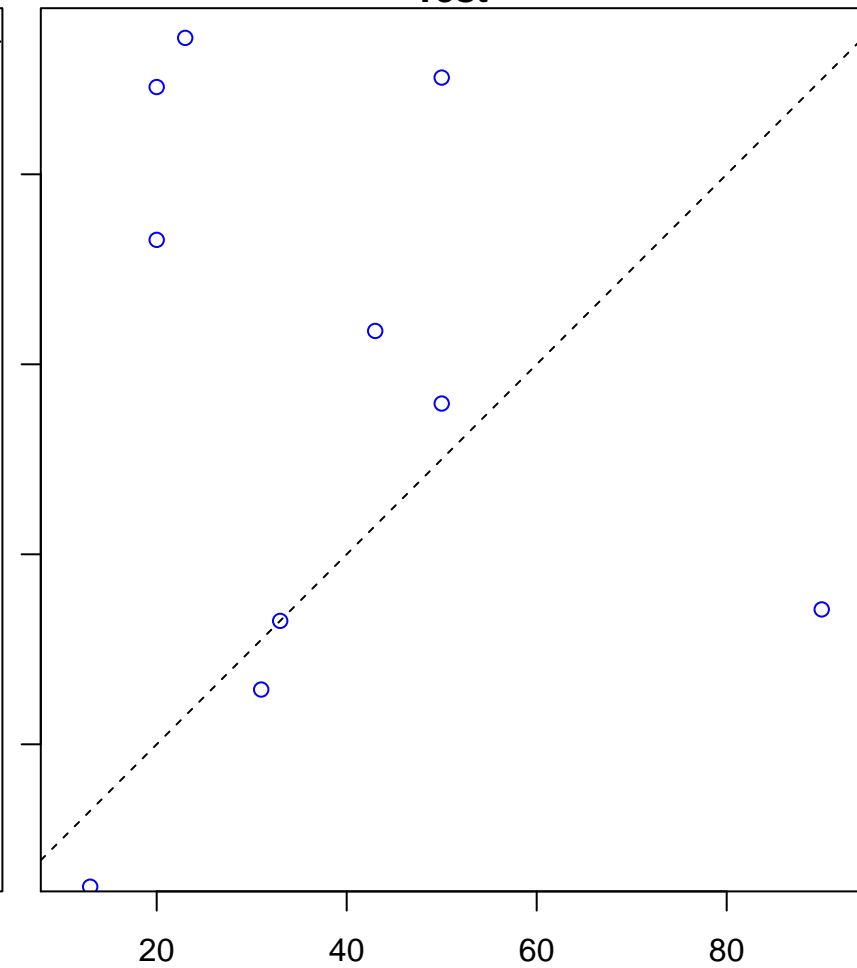


mitochondrial RNA metabolic process (Score: 14.925416)

Control

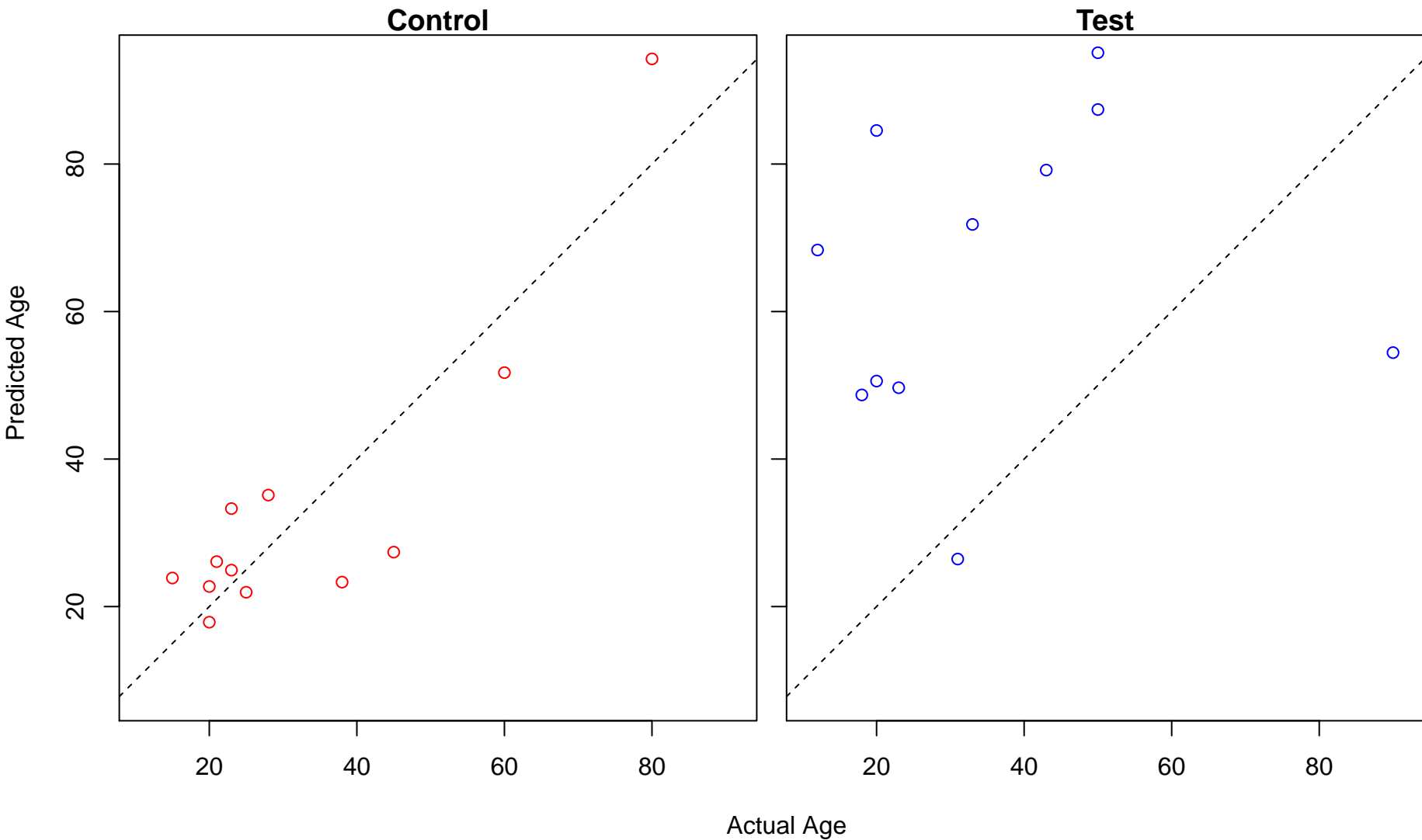


Test

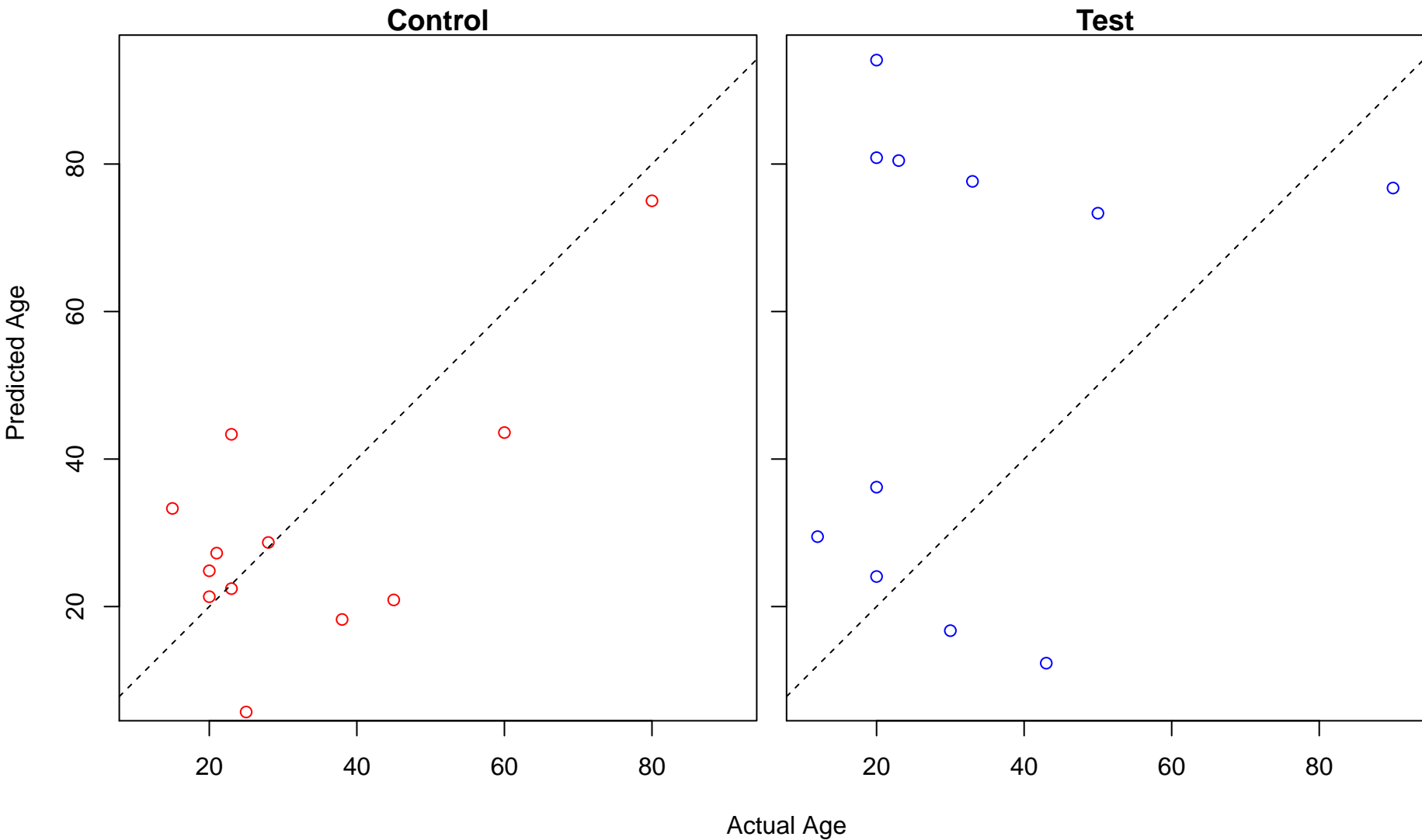


Actual Age

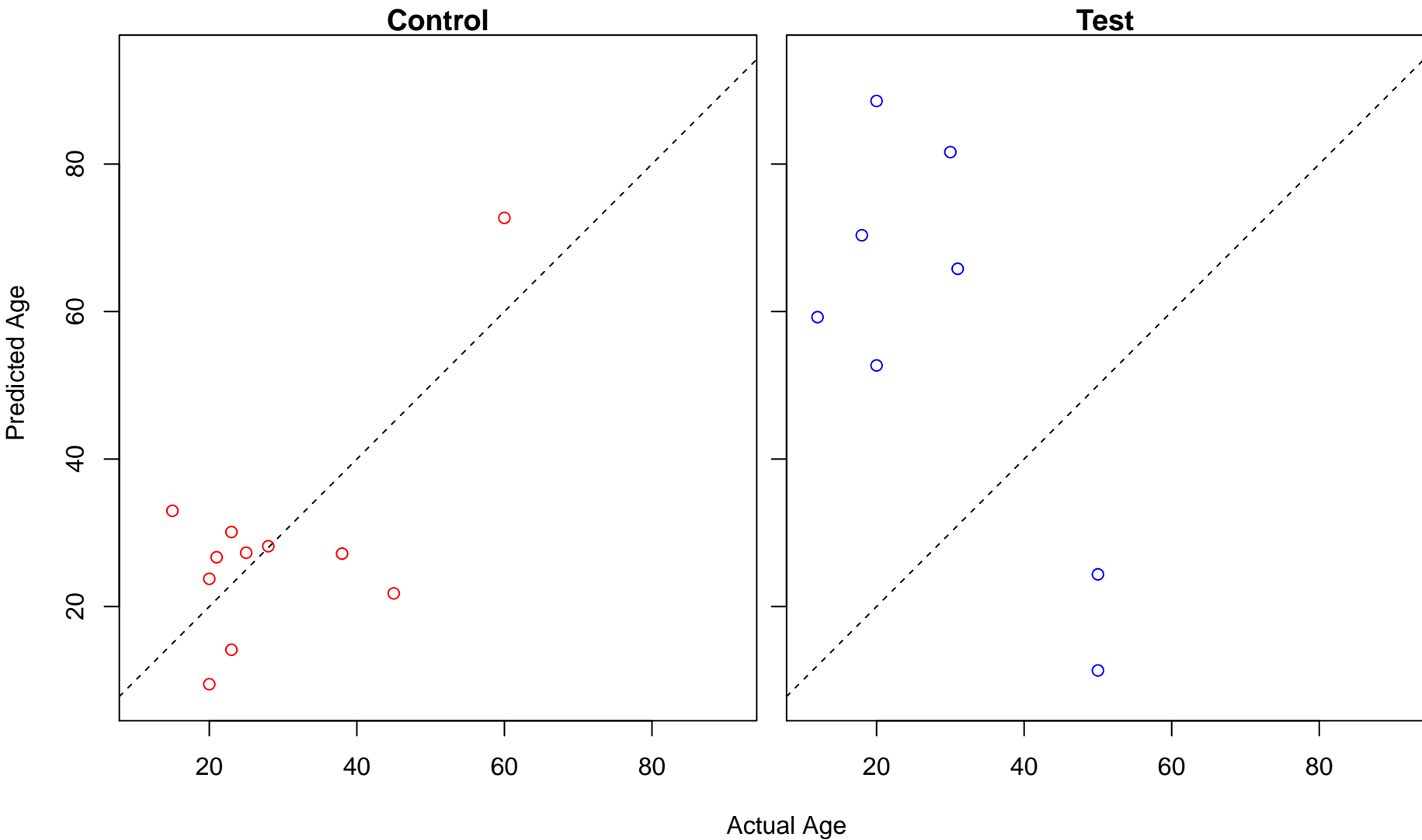
digestion (Score: 14.890272)



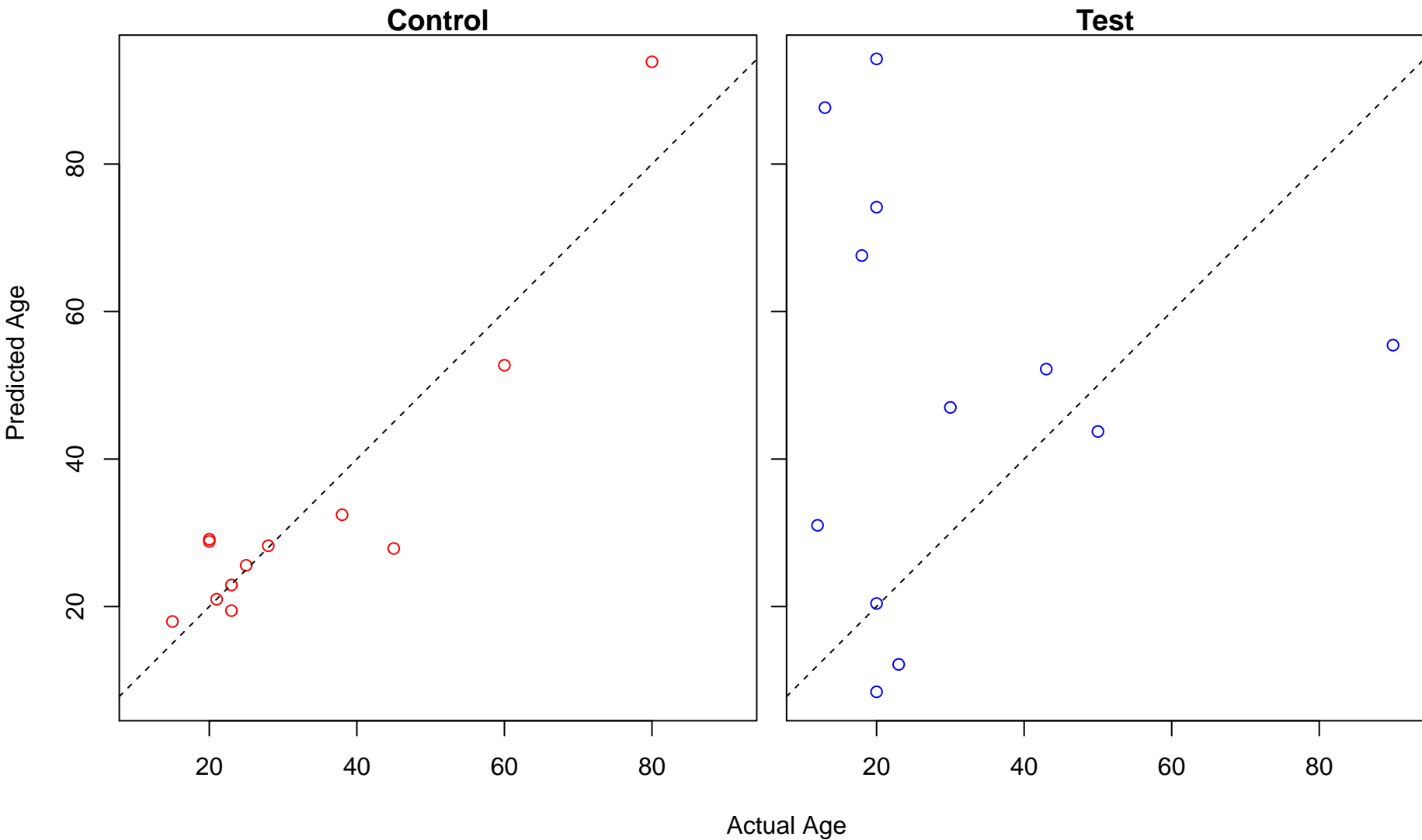
positive regulation of lipid storage (Score: 14.866076)



positive regulation of neural precursor cell proliferation (Score: 14.829385)

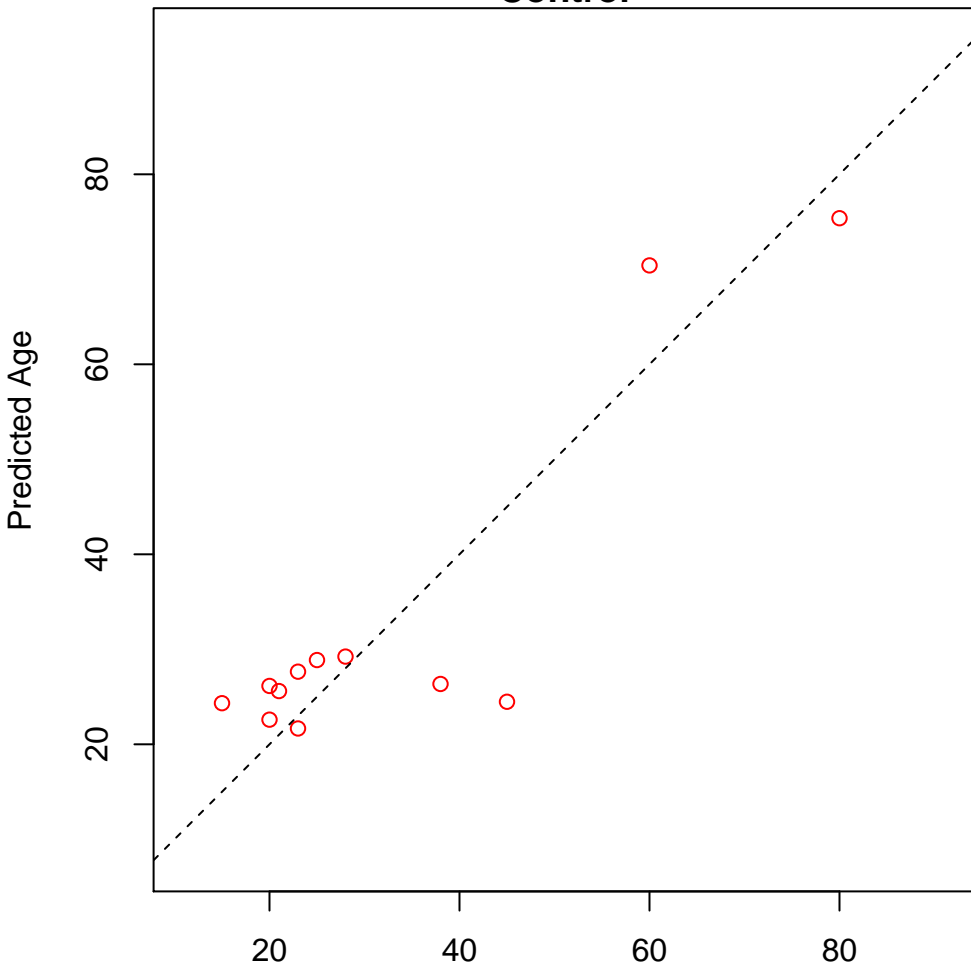


tube development (Score: 14.813494)

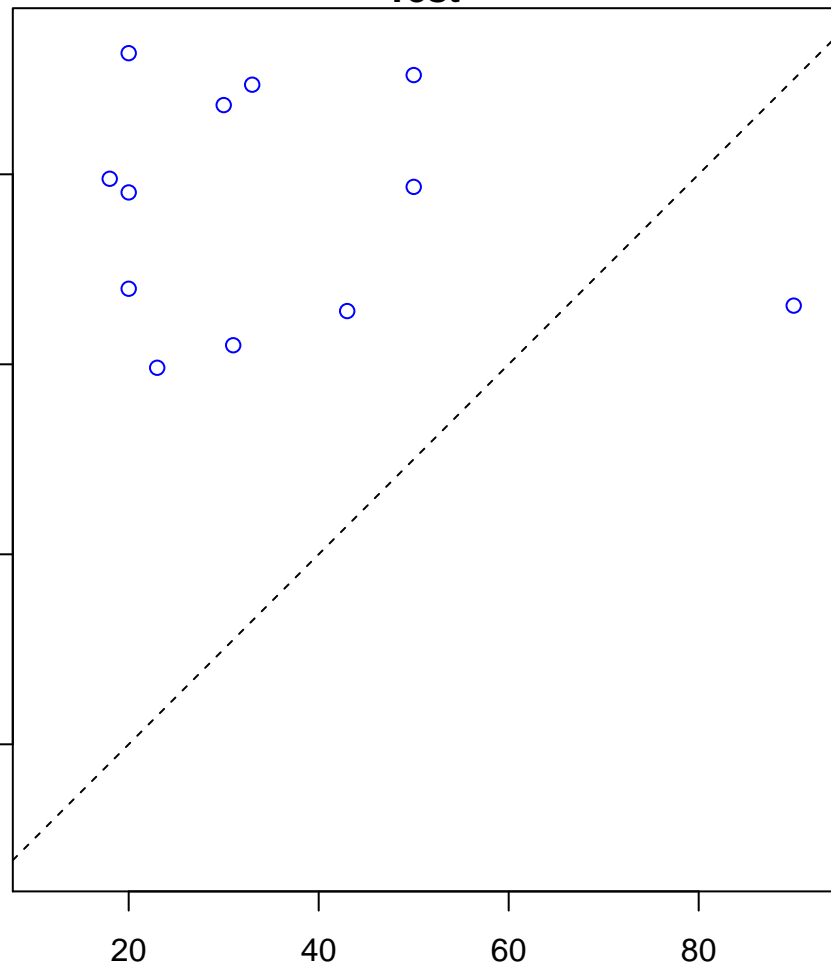


cardiac ventricle morphogenesis (Score: 14.768786)

Control



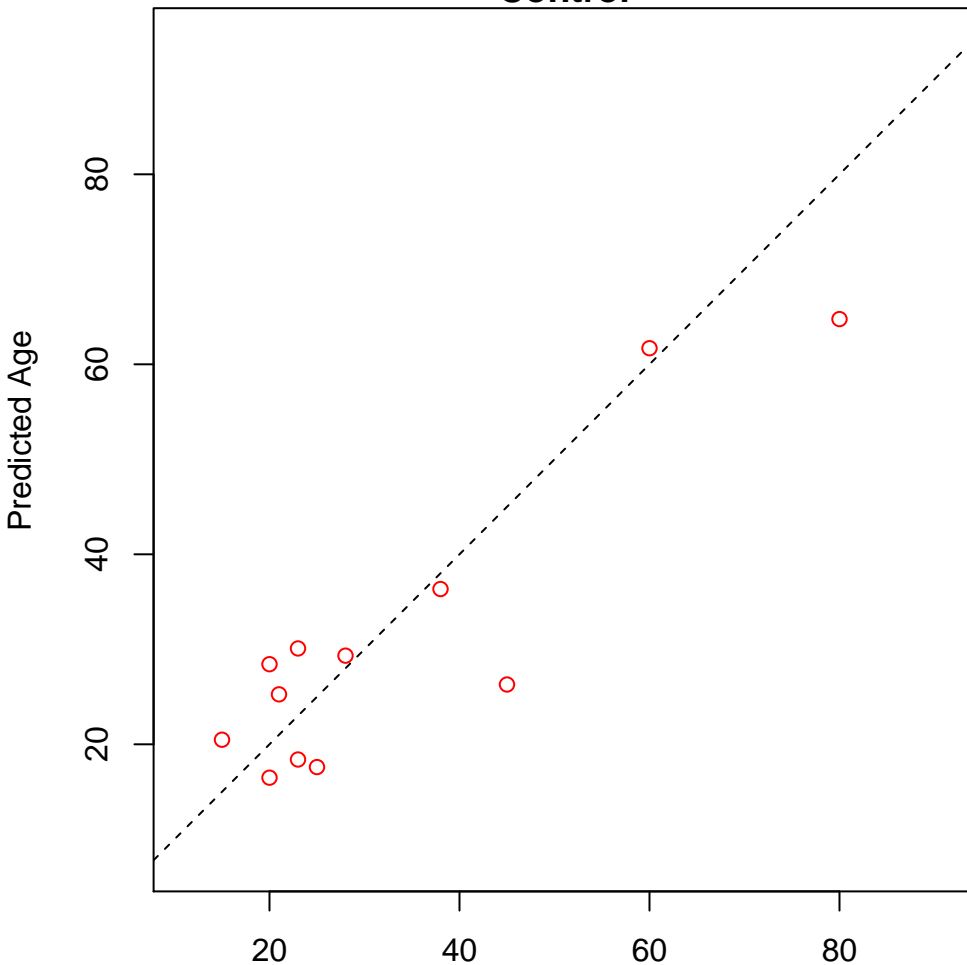
Test



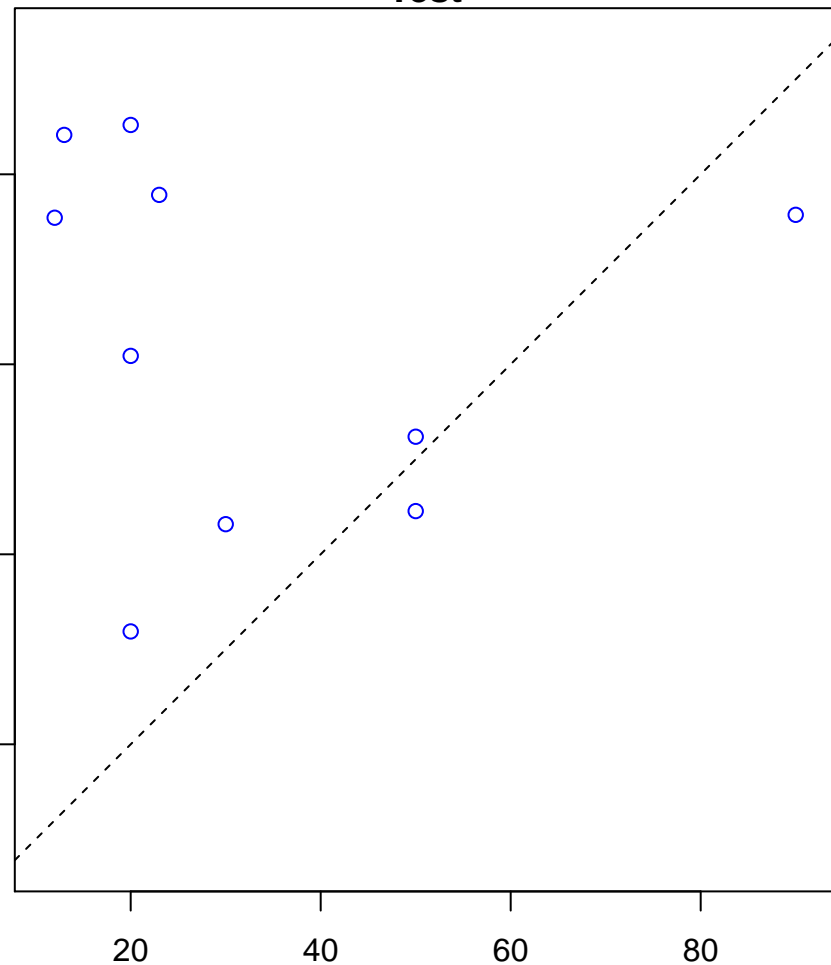
Actual Age

peptidyl-threonine phosphorylation (Score: 14.768712)

Control

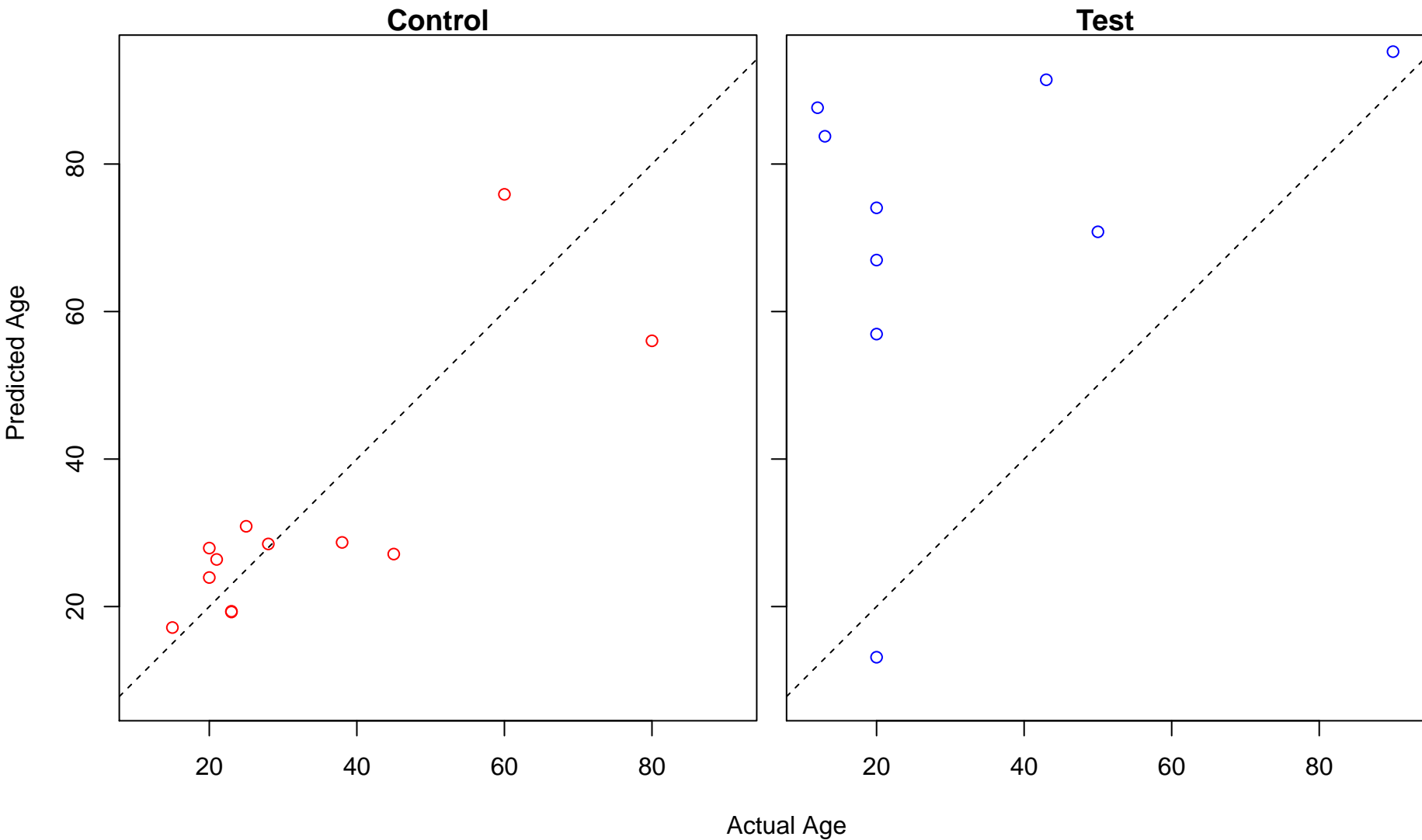


Test

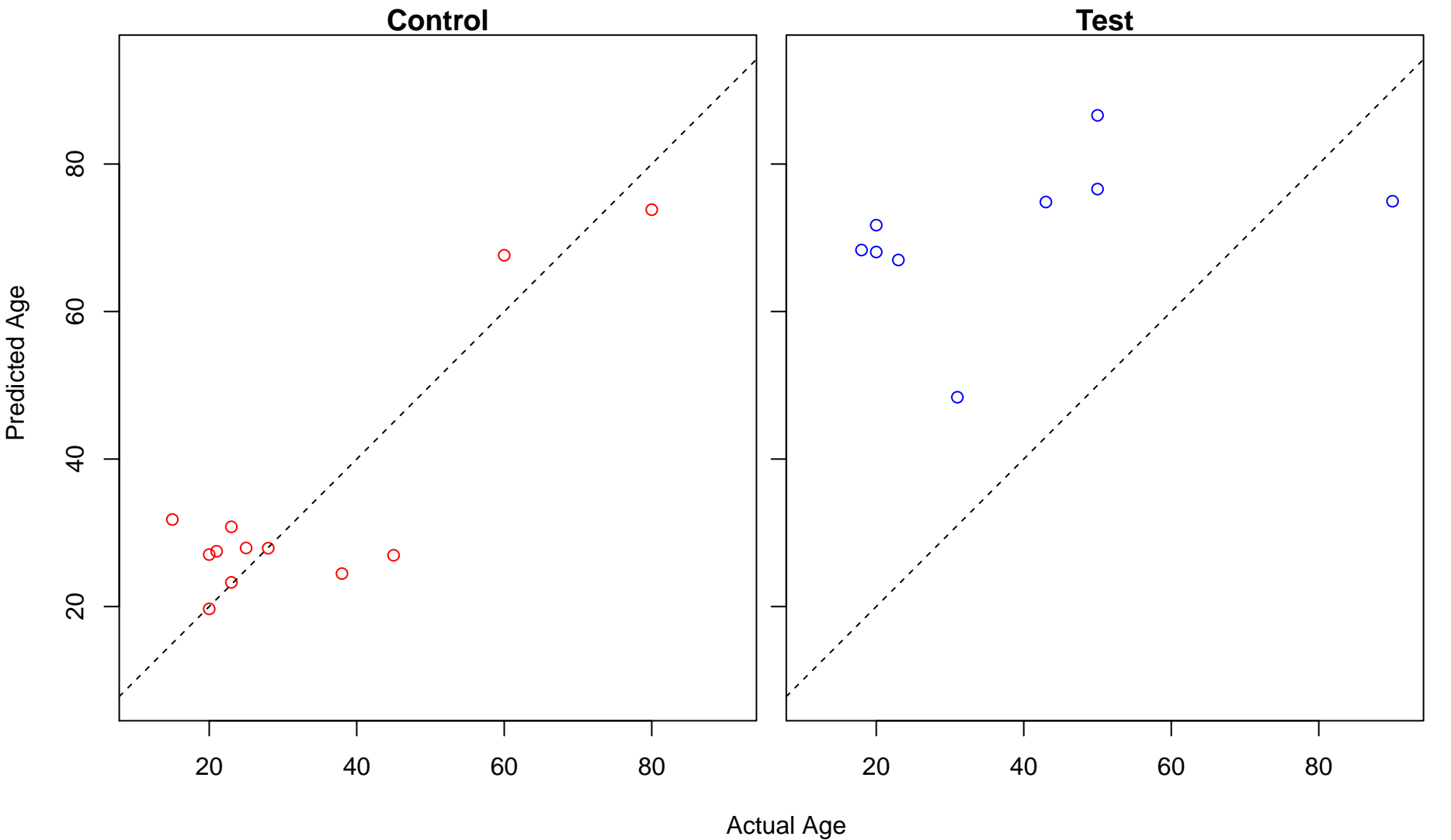


Actual Age

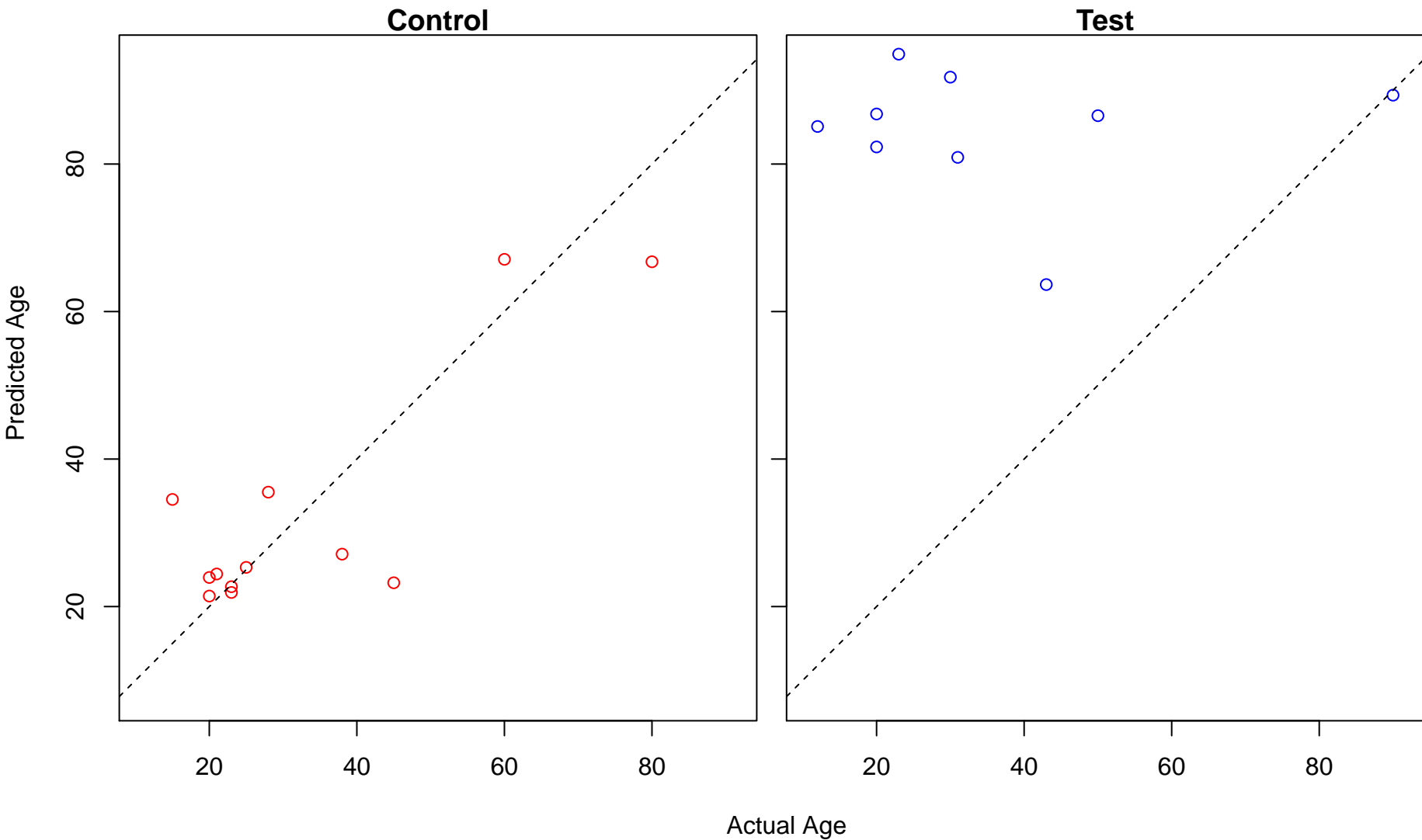
cell aging (Score: 14.749150)



Validation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimuli

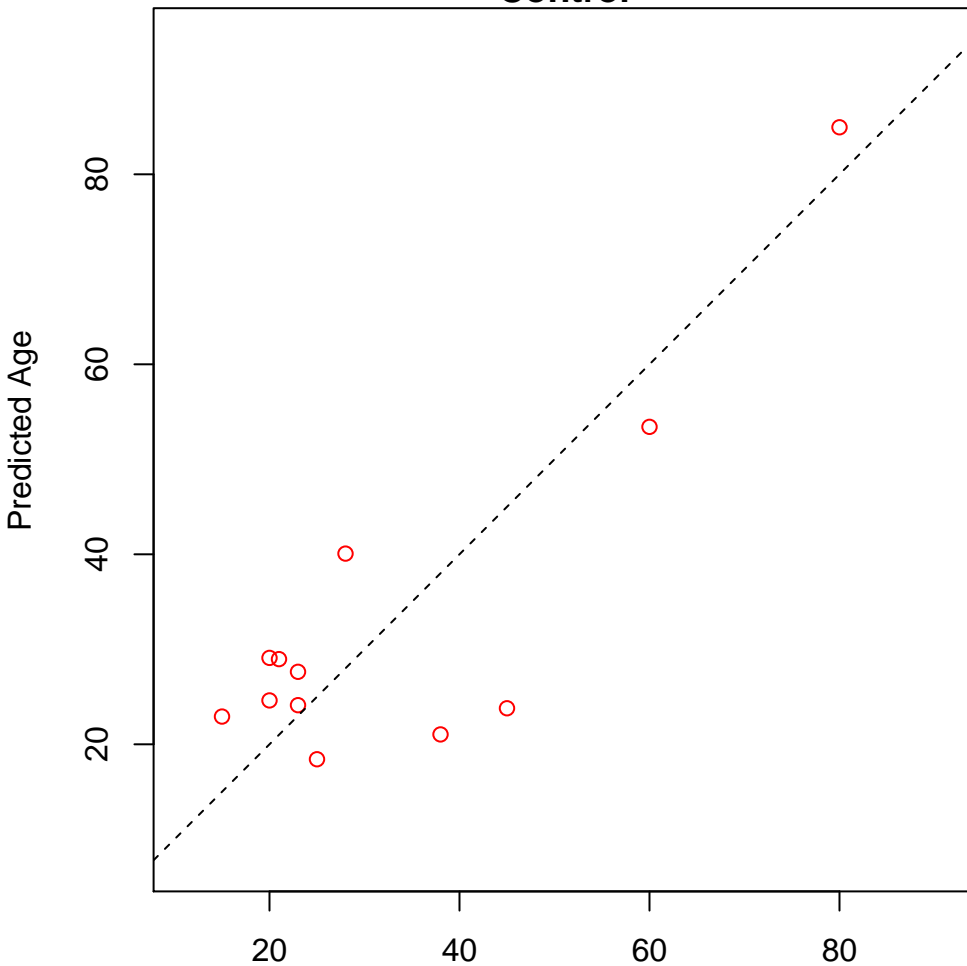


intracellular estrogen receptor signaling pathway (Score: 14.687412)

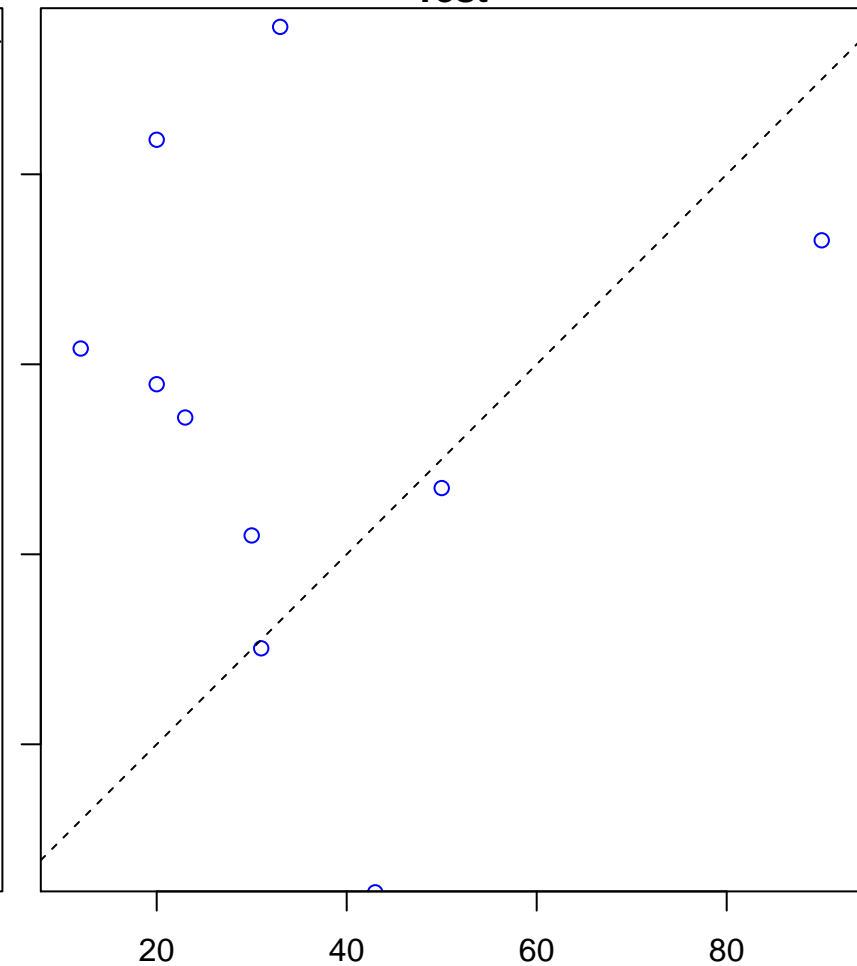


ribonucleoprotein complex biogenesis (Score: 14.682509)

Control

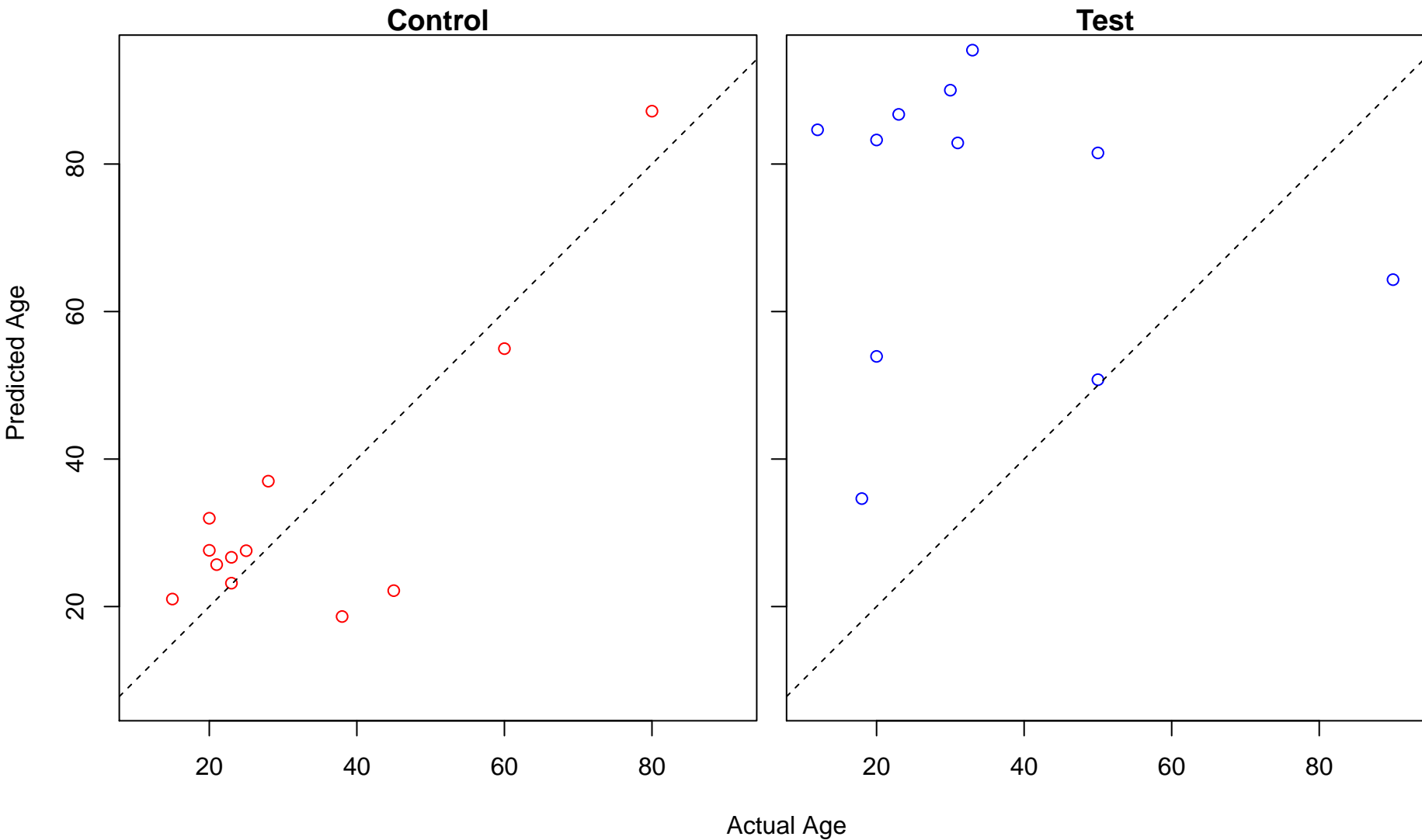


Test



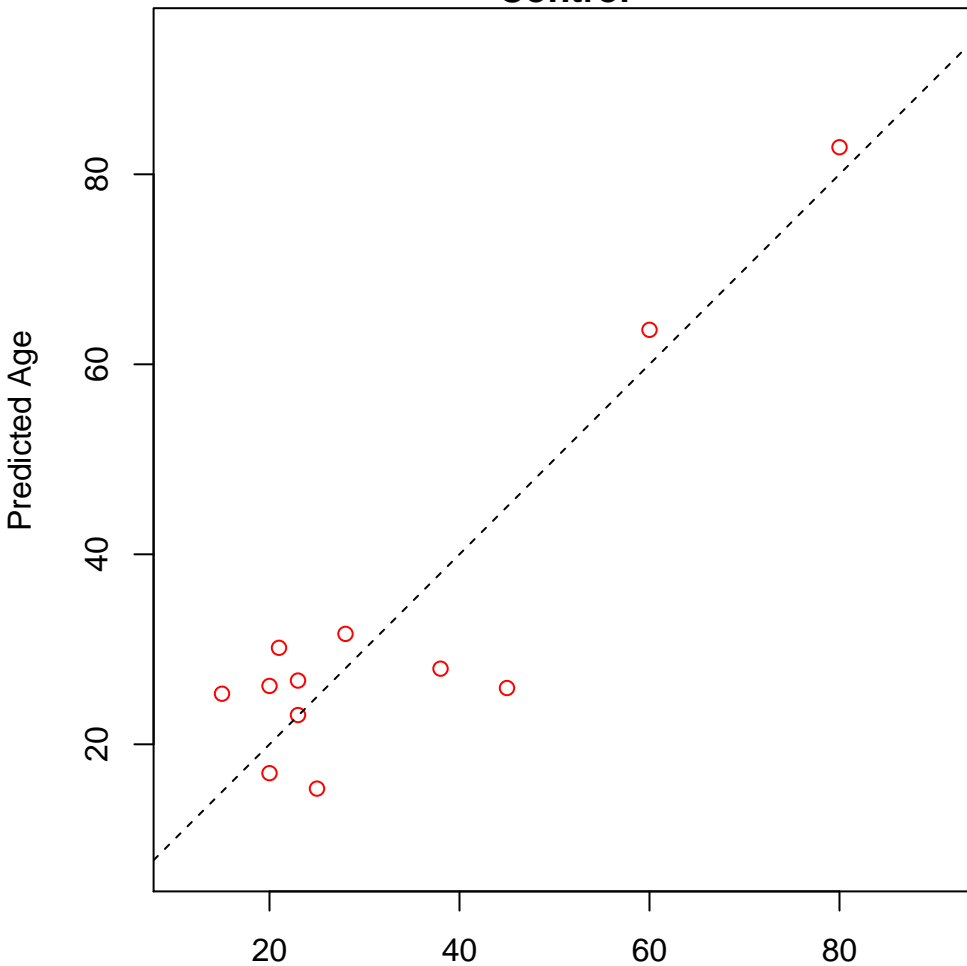
Actual Age

negative regulation of Notch signaling pathway (Score: 14.672553)

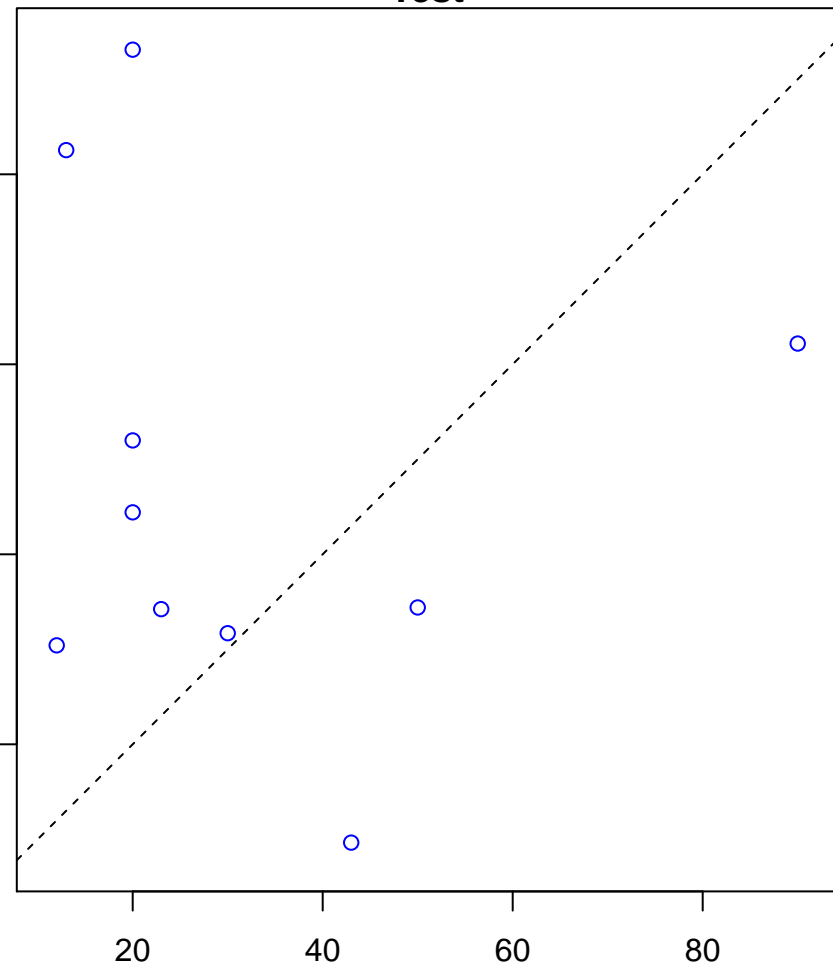


peptidyl-serine phosphorylation (Score: 14.662183)

Control

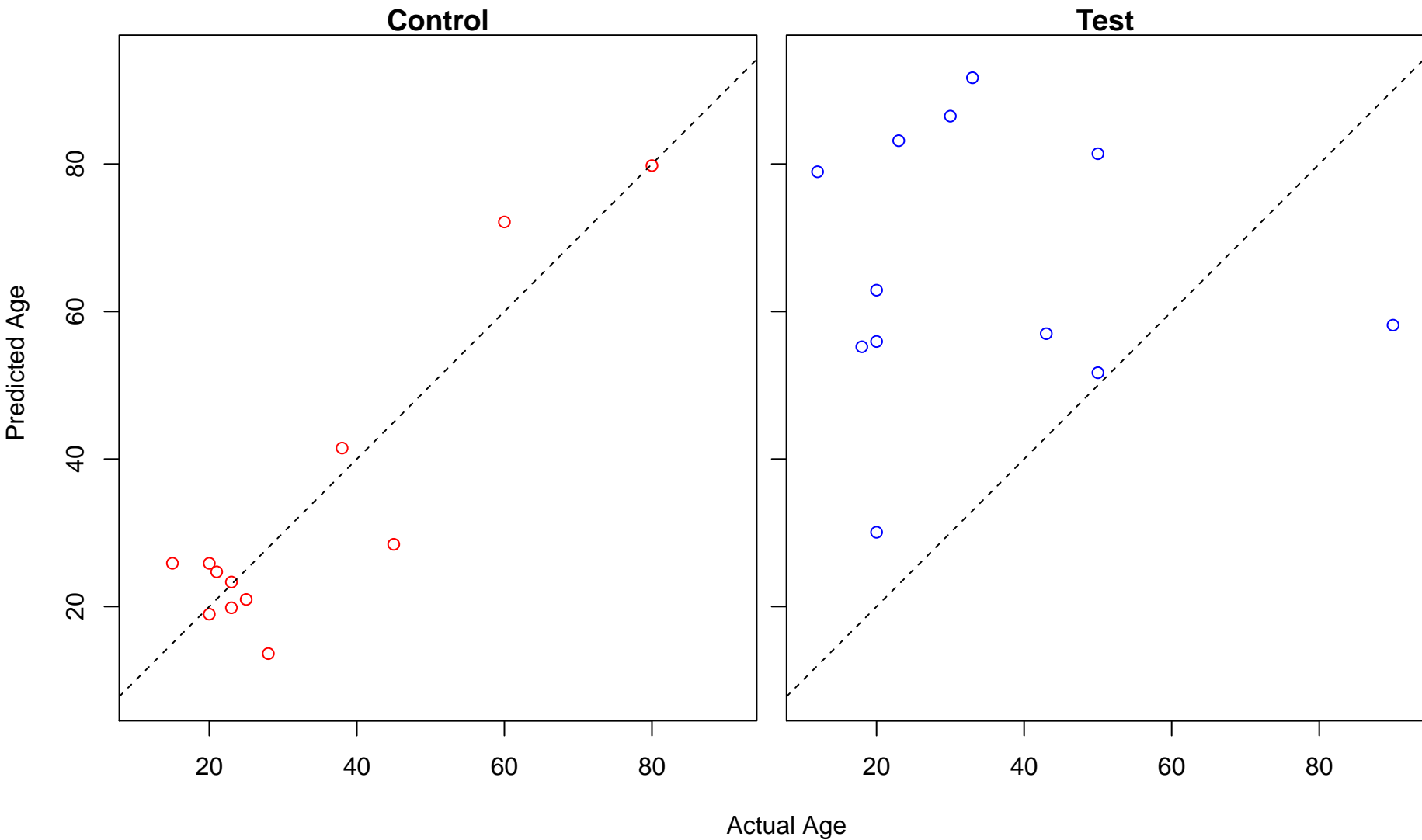


Test

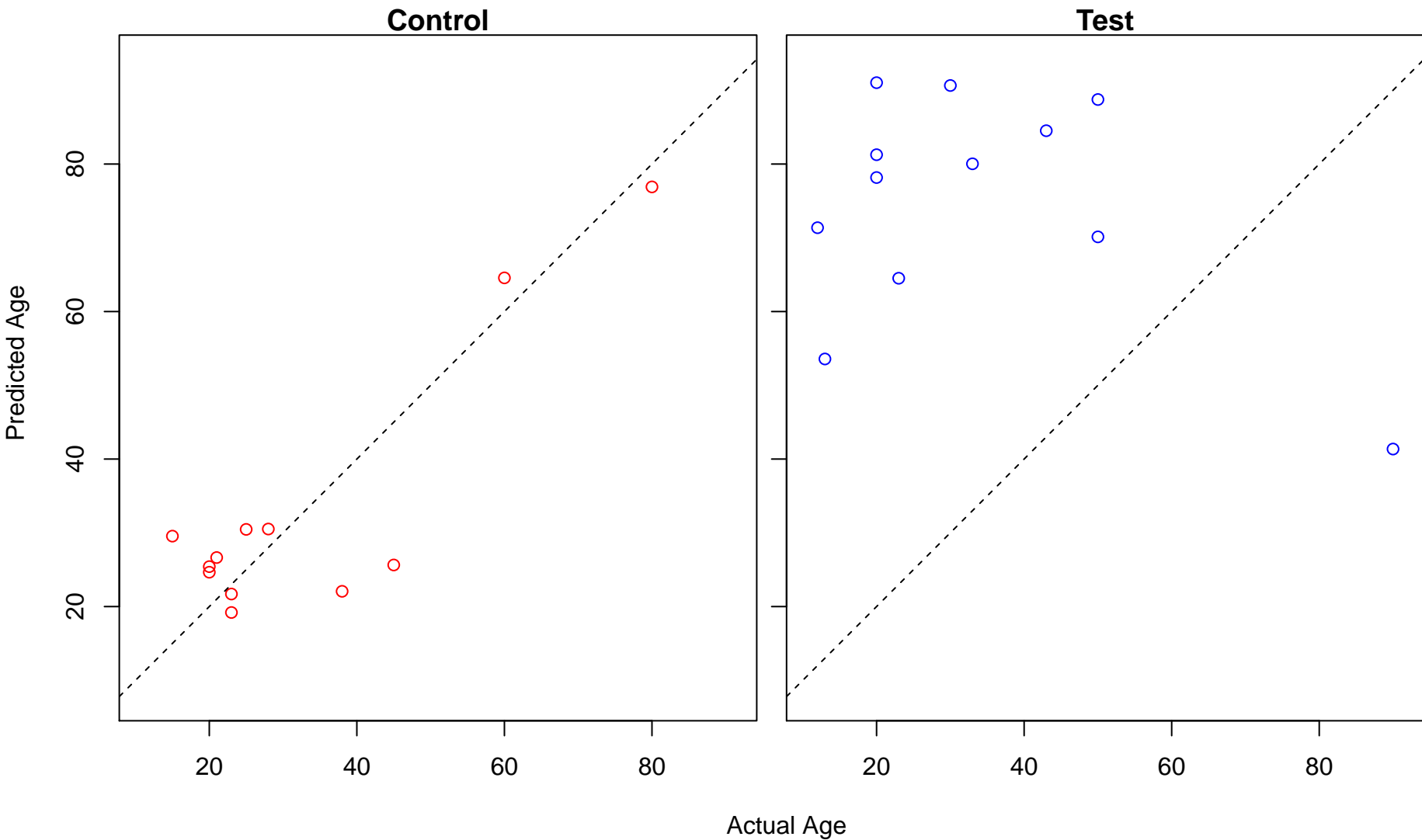


Actual Age

cellular protein complex assembly (Score: 14.639134)

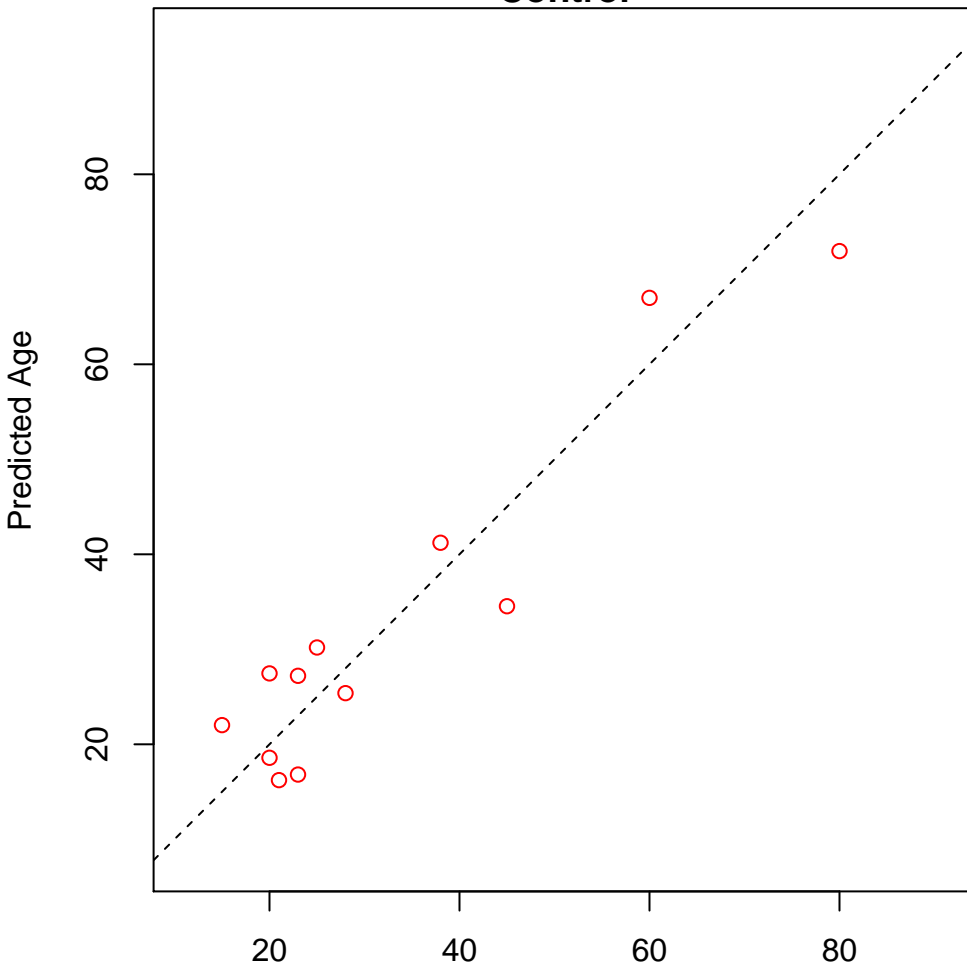


maintenance of protein localization in endoplasmic reticulum (Score: 14.633650)

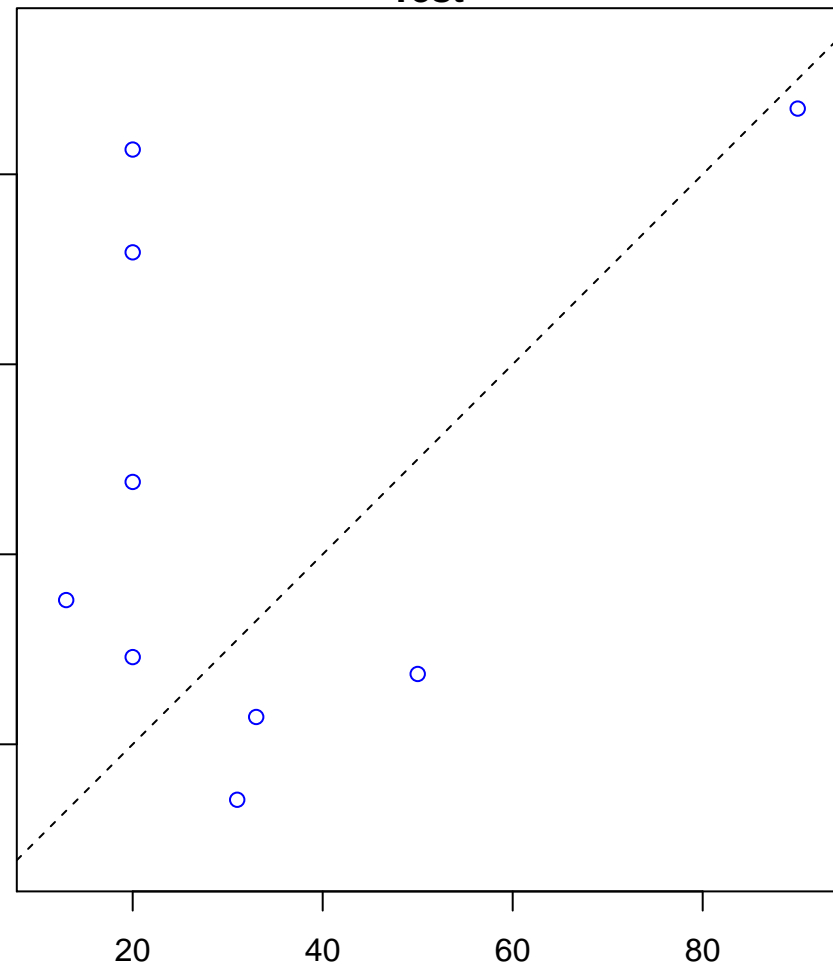


homocysteine metabolic process (Score: 14.589179)

Control

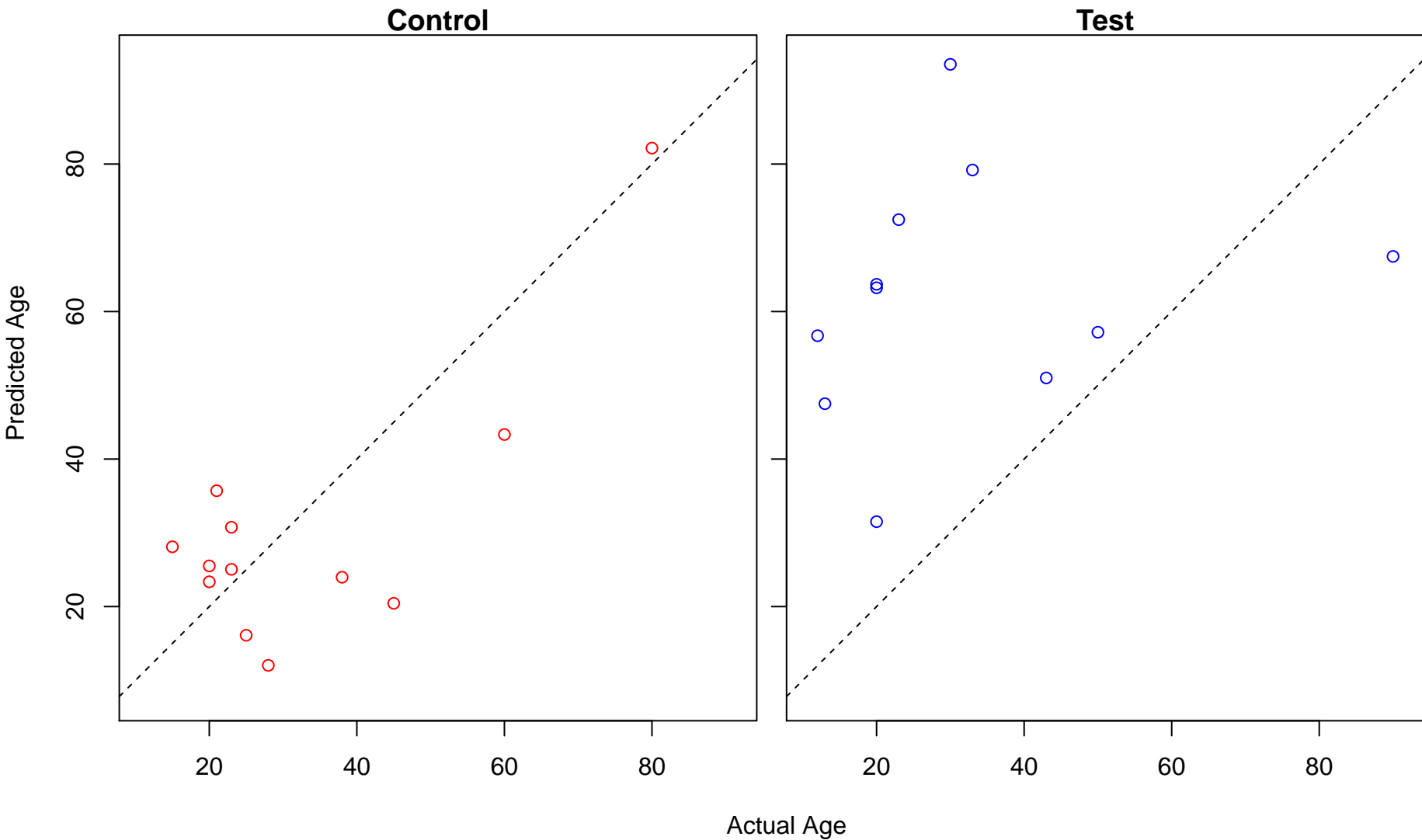


Test



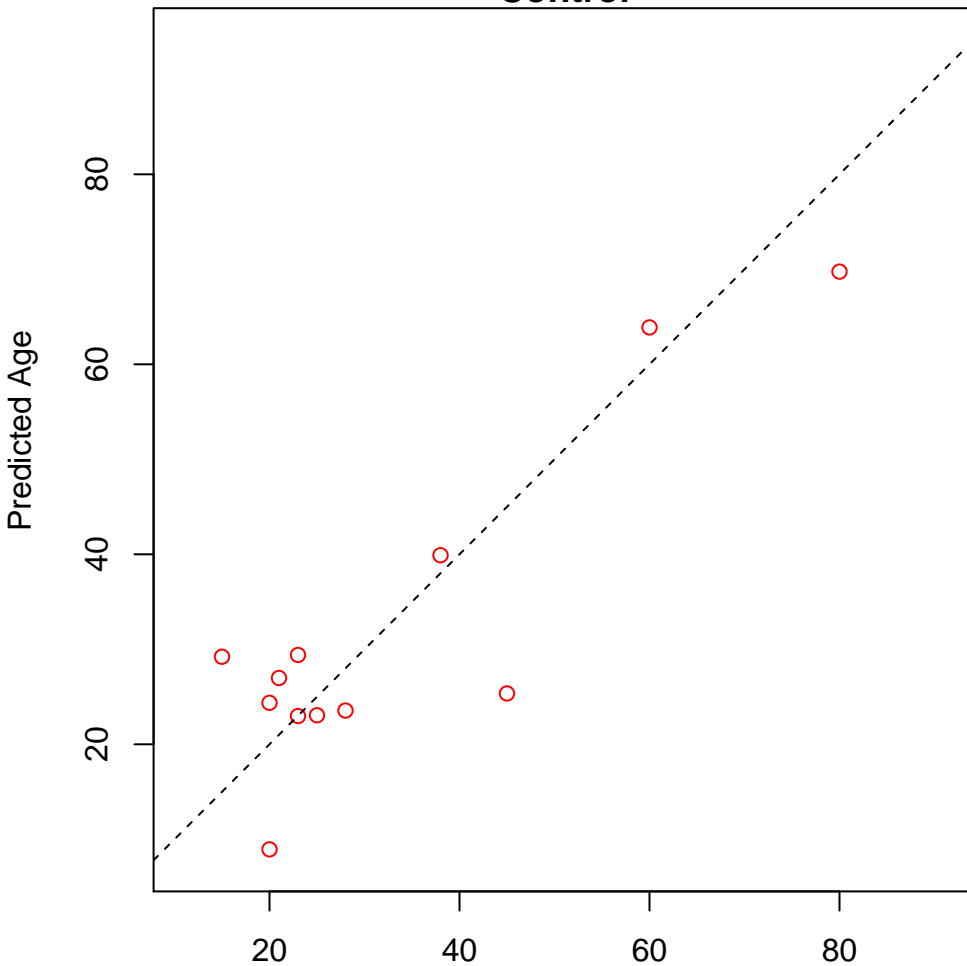
Actual Age

attachment of GPI anchor to protein (Score: 14.579951)

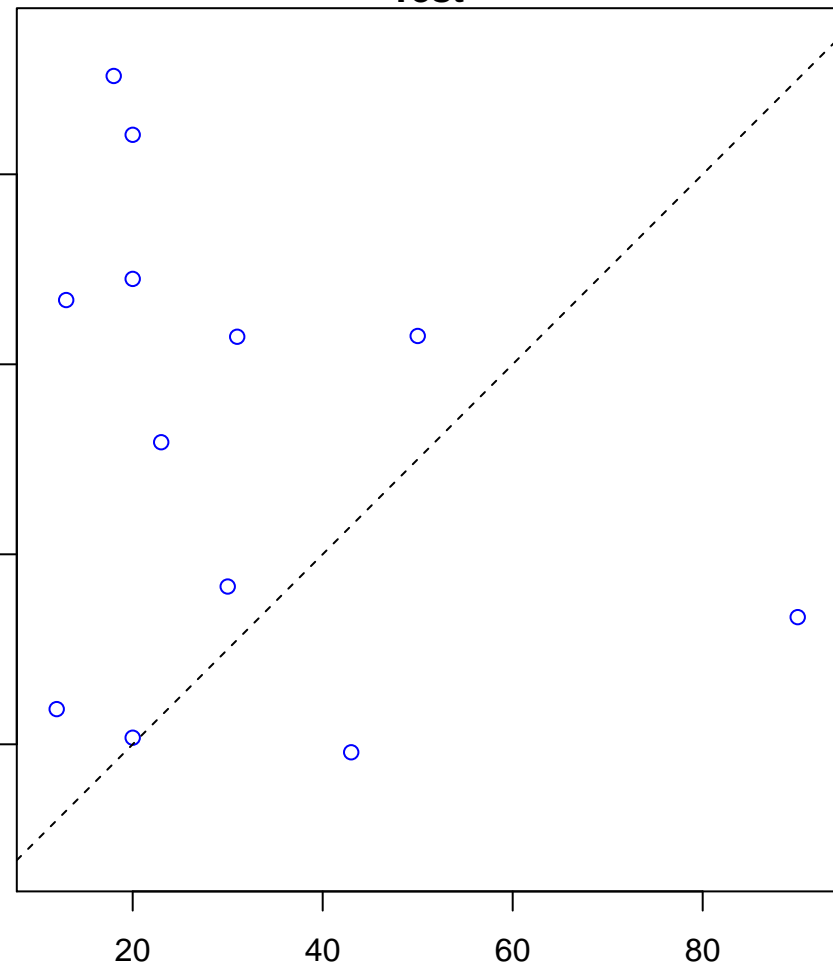


positive regulation of ion transport (Score: 14.577773)

Control

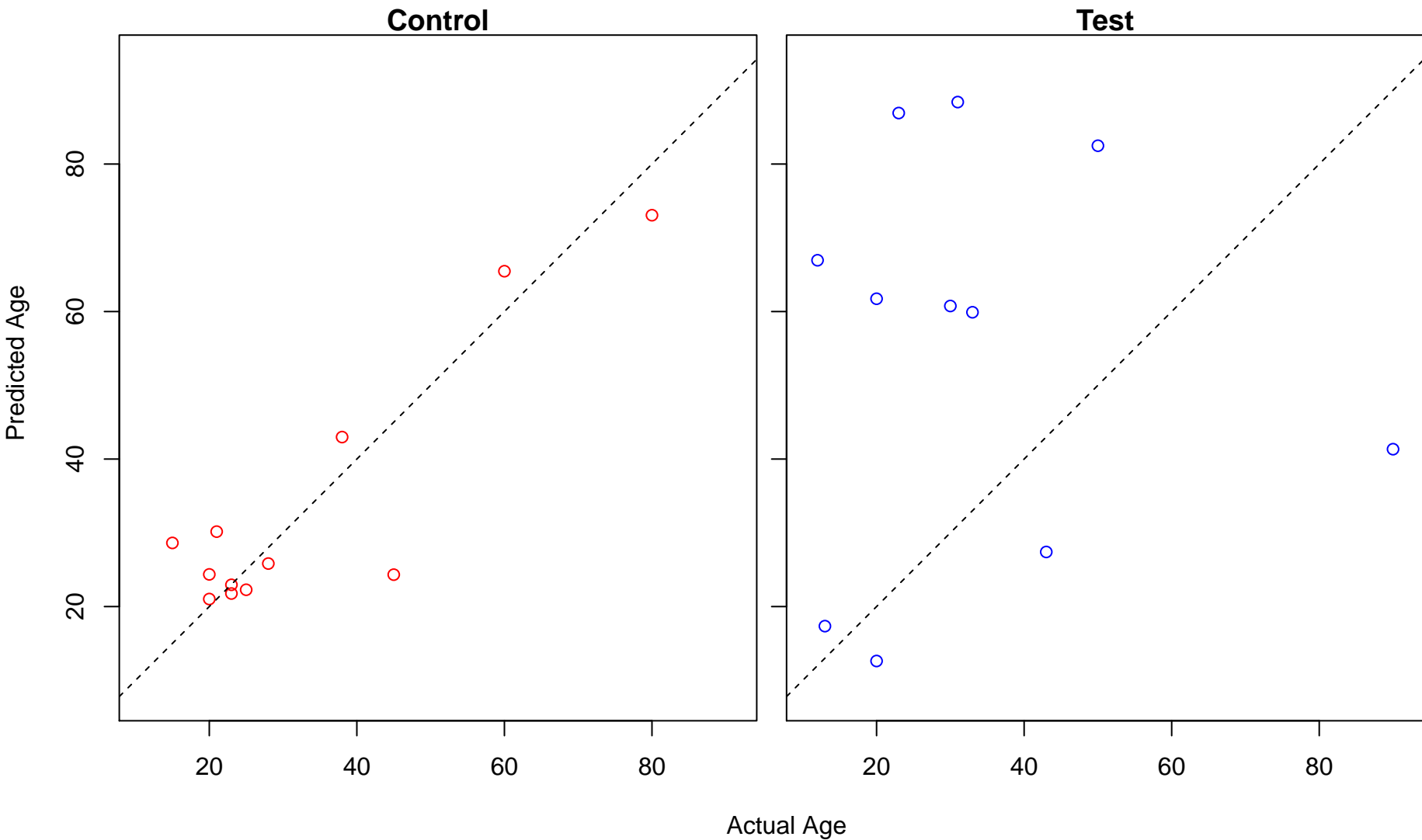


Test



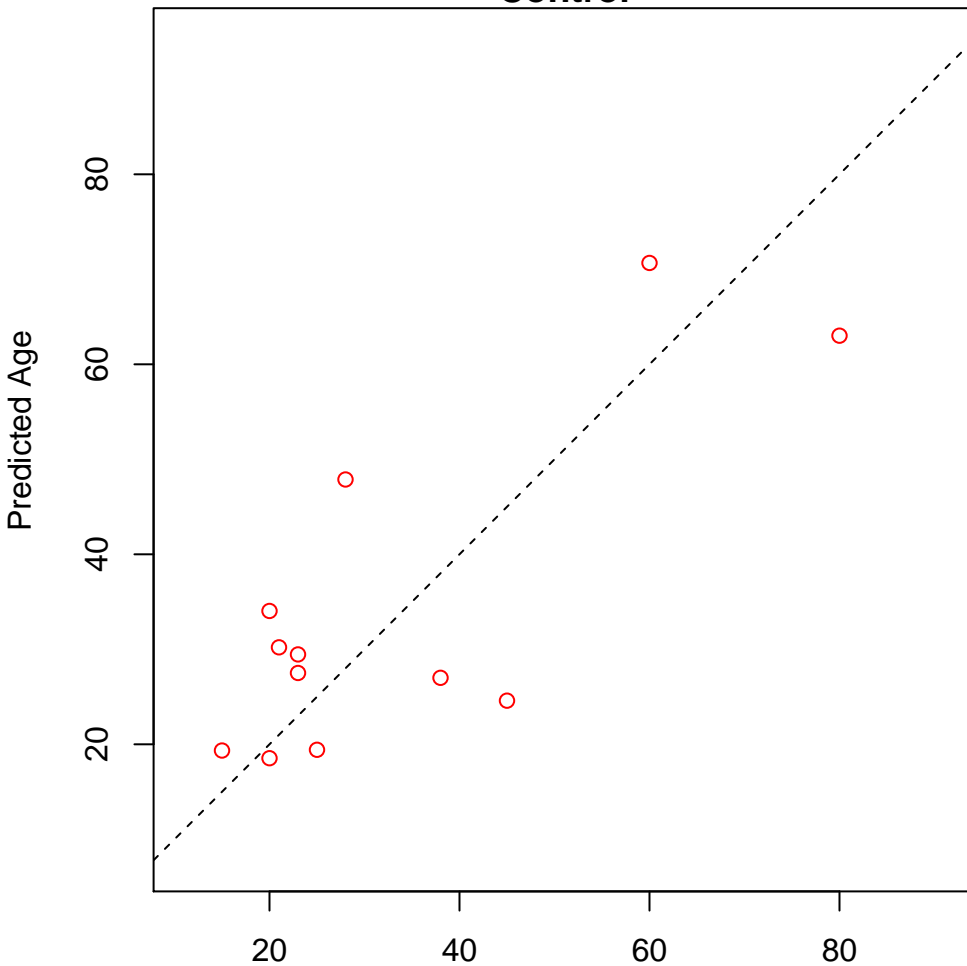
Actual Age

adherens junction organization (Score: 14.568731)

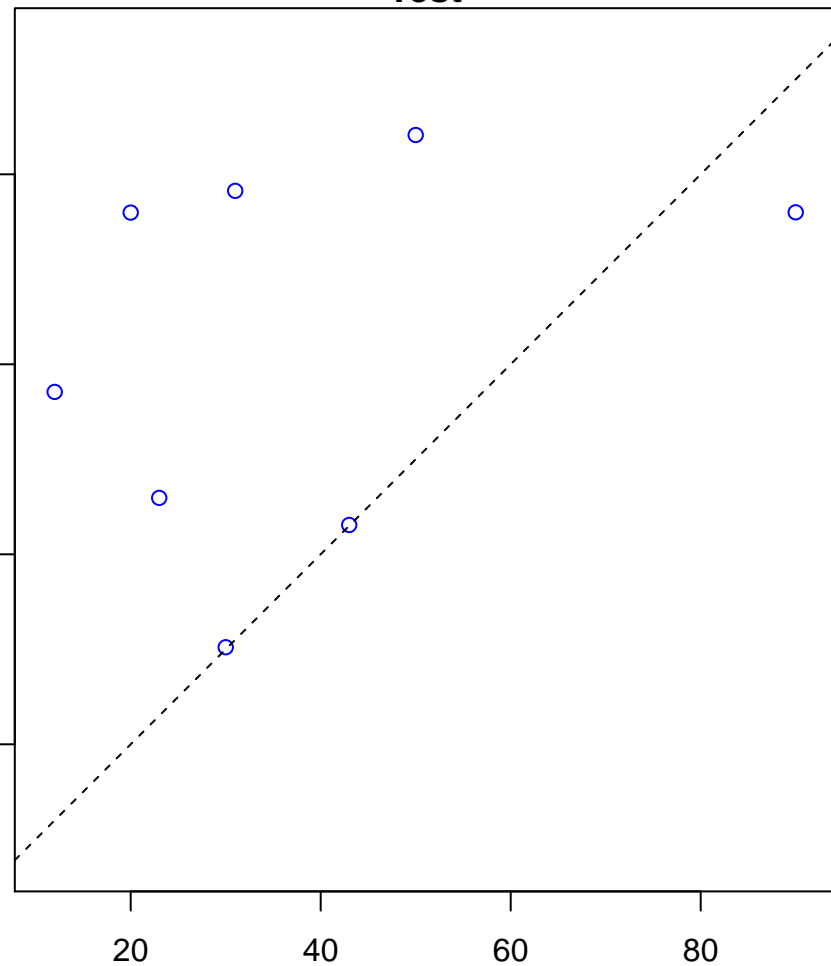


response to tumor necrosis factor (Score: 14.538586)

Control

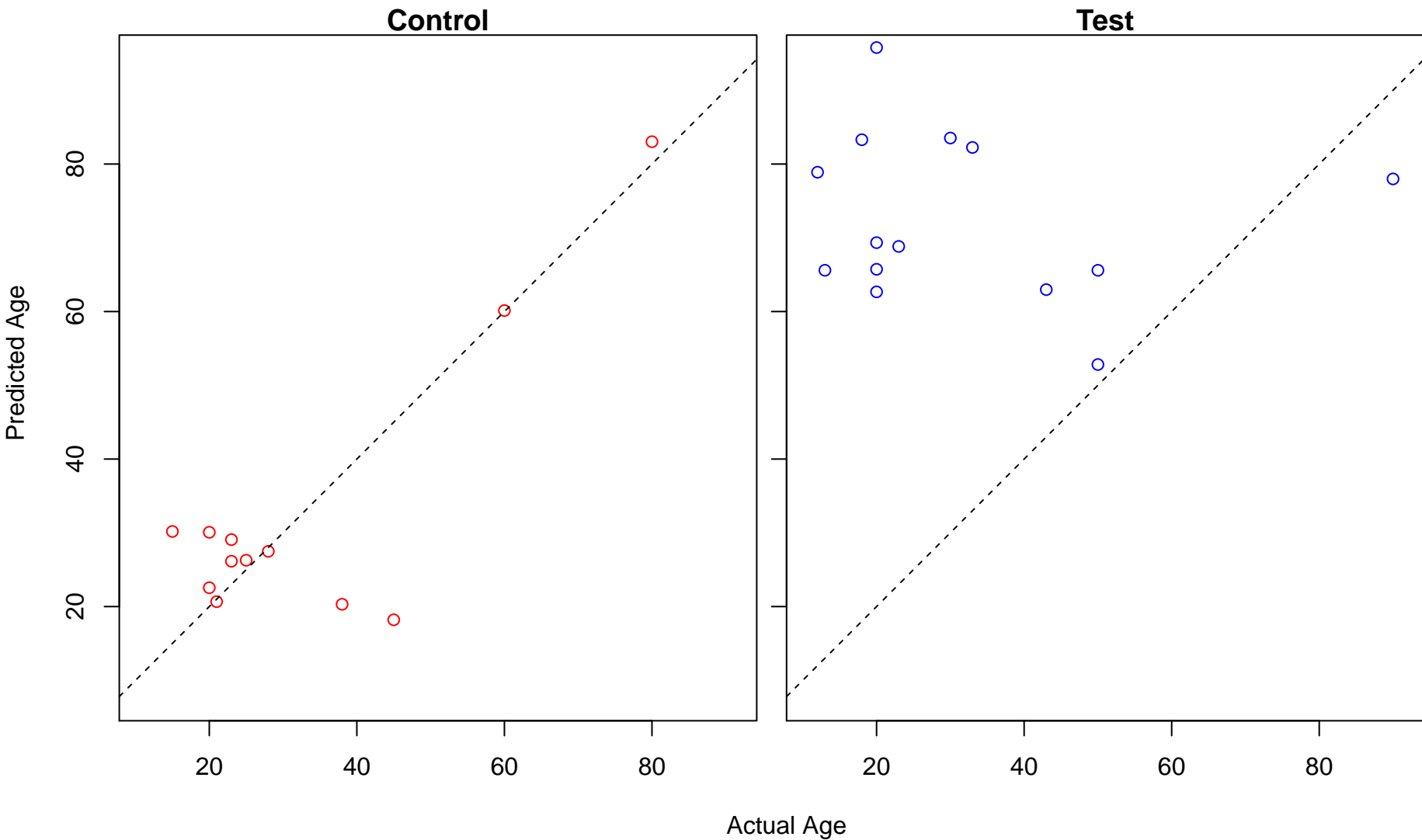


Test

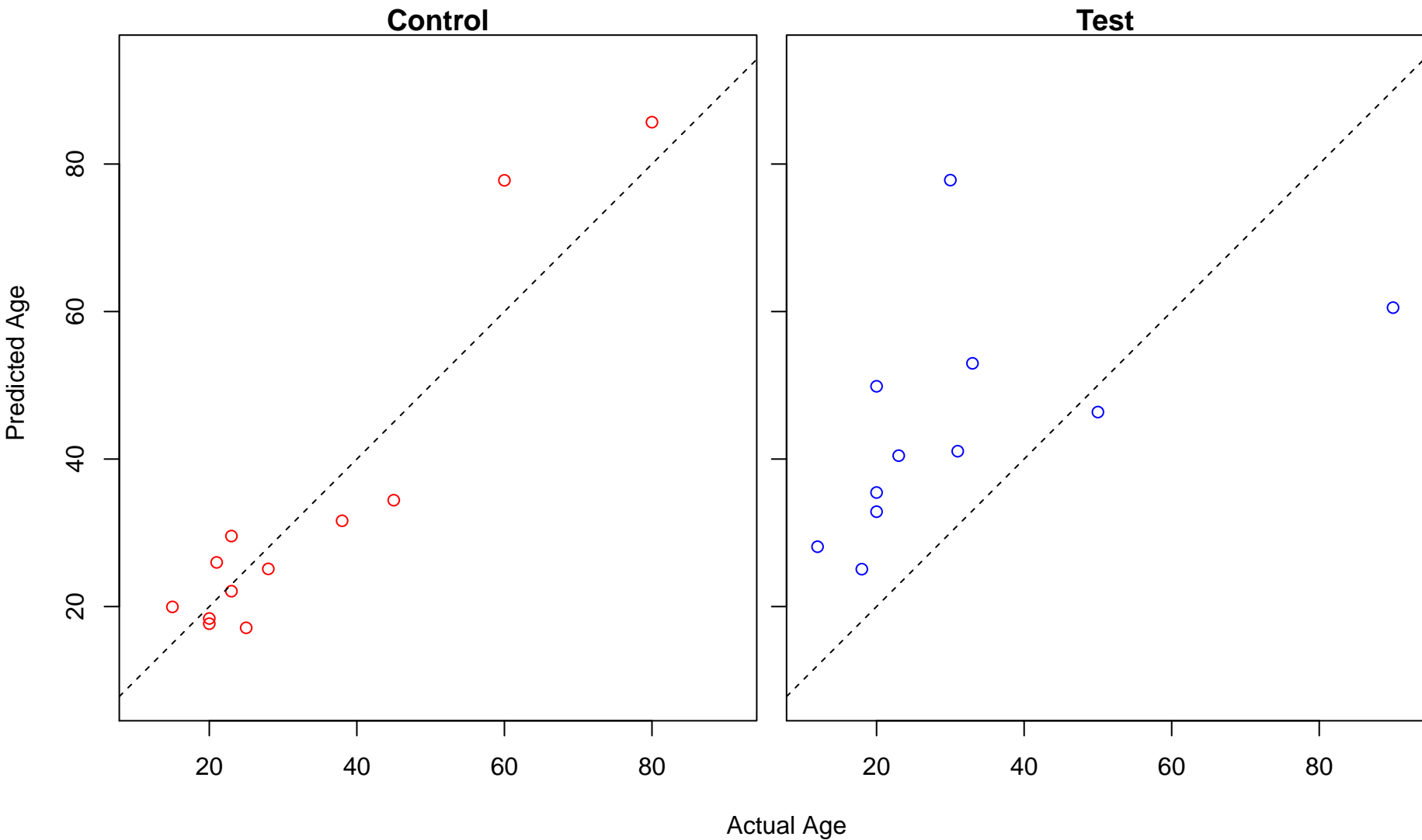


Actual Age

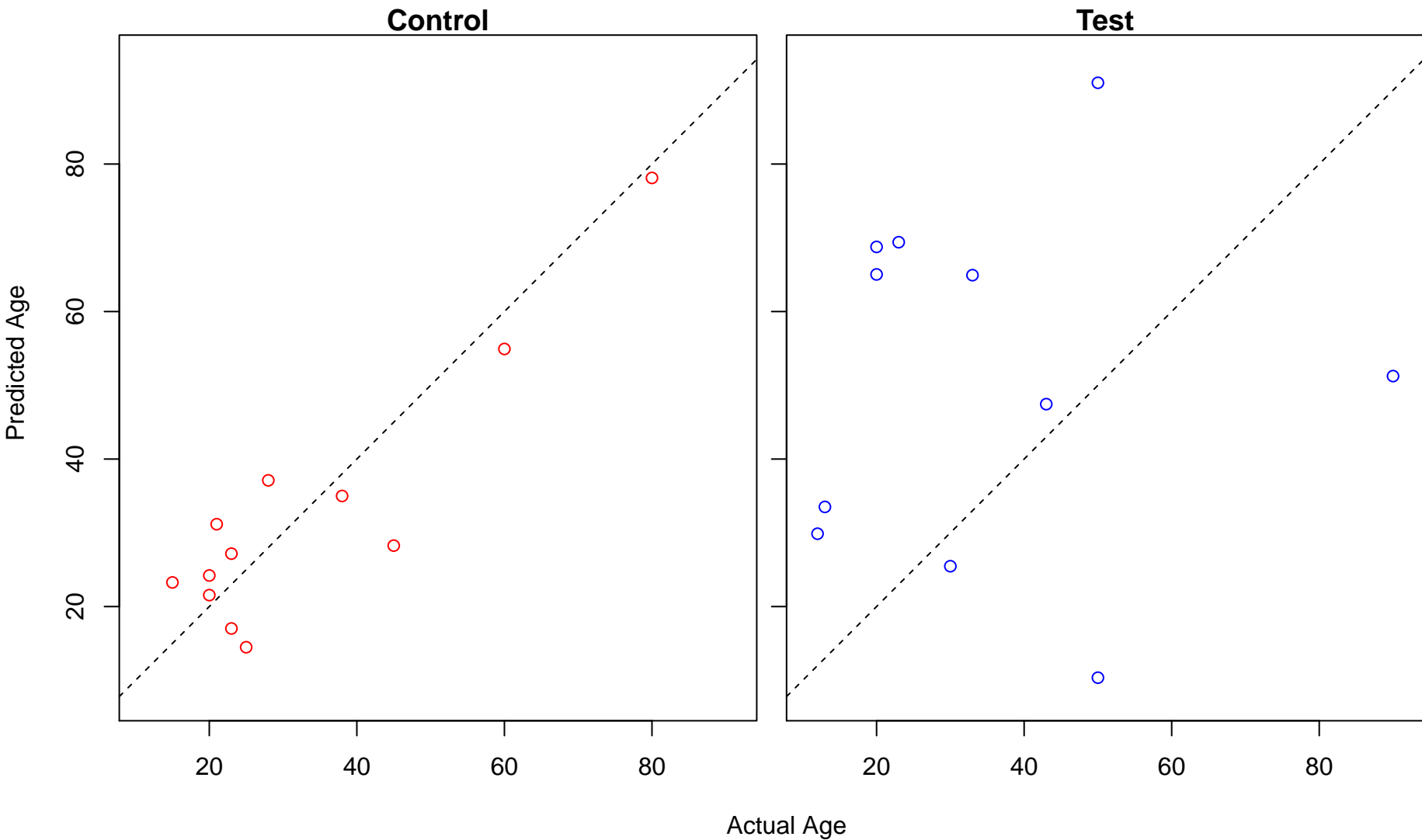
regulation of lipopolysaccharide-mediated signaling pathway (Score: 14.509398)



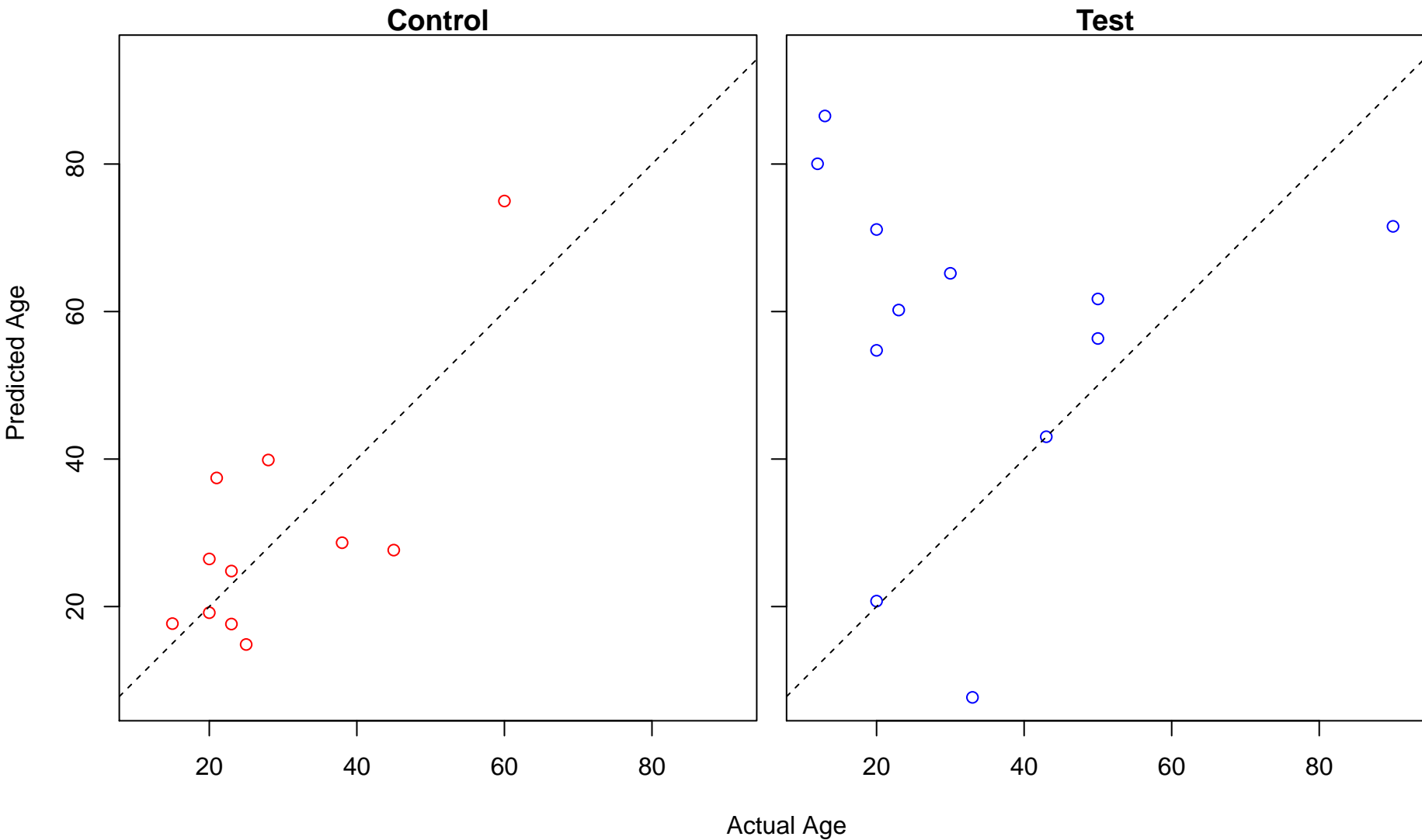
regulation of establishment of cell polarity (Score: 14.501596)



camera-type eye development (Score: 14.499660)

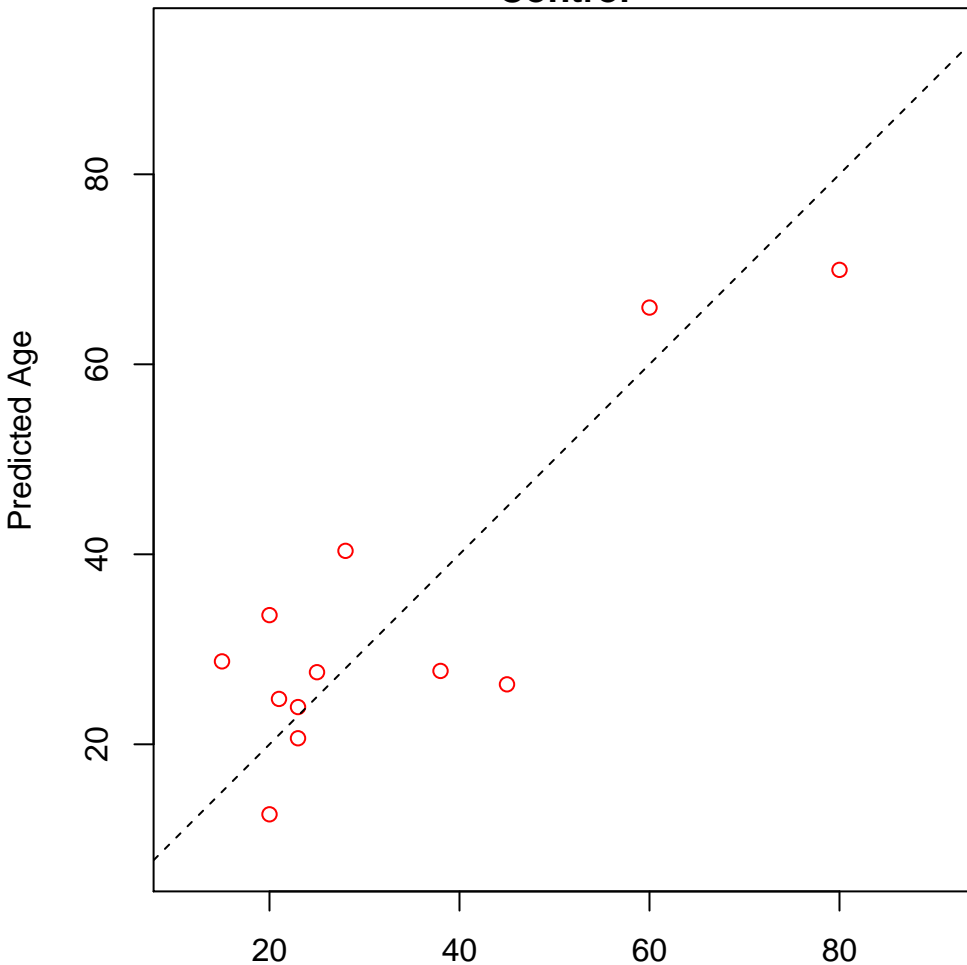


regulation of viral entry into host cell (Score: 14.497771)

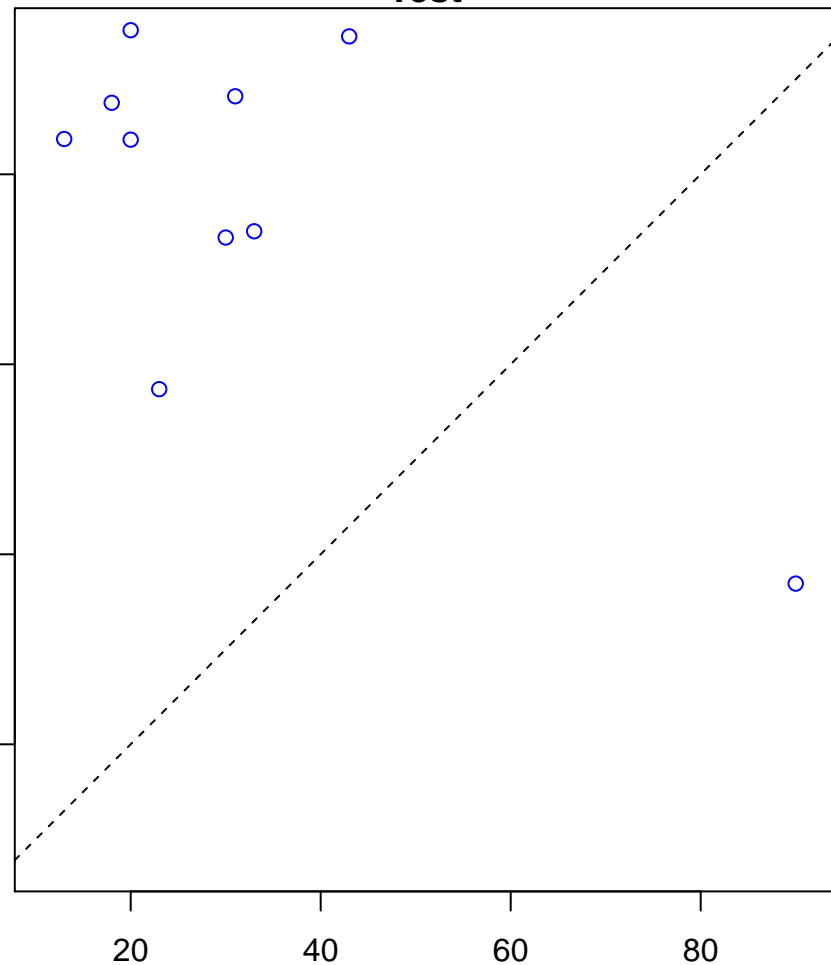


anterior/posterior axis specification (Score: 14.459430)

Control

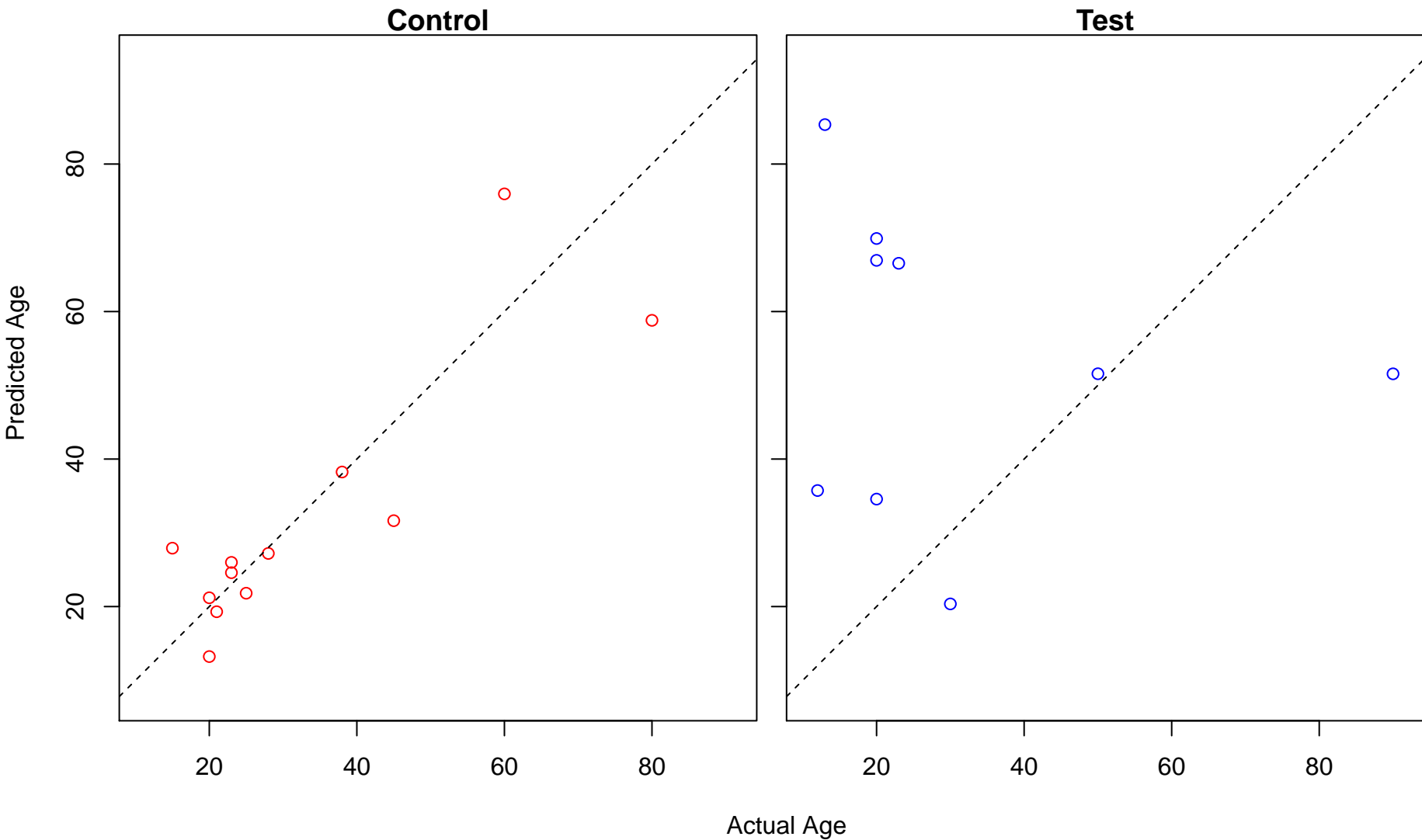


Test

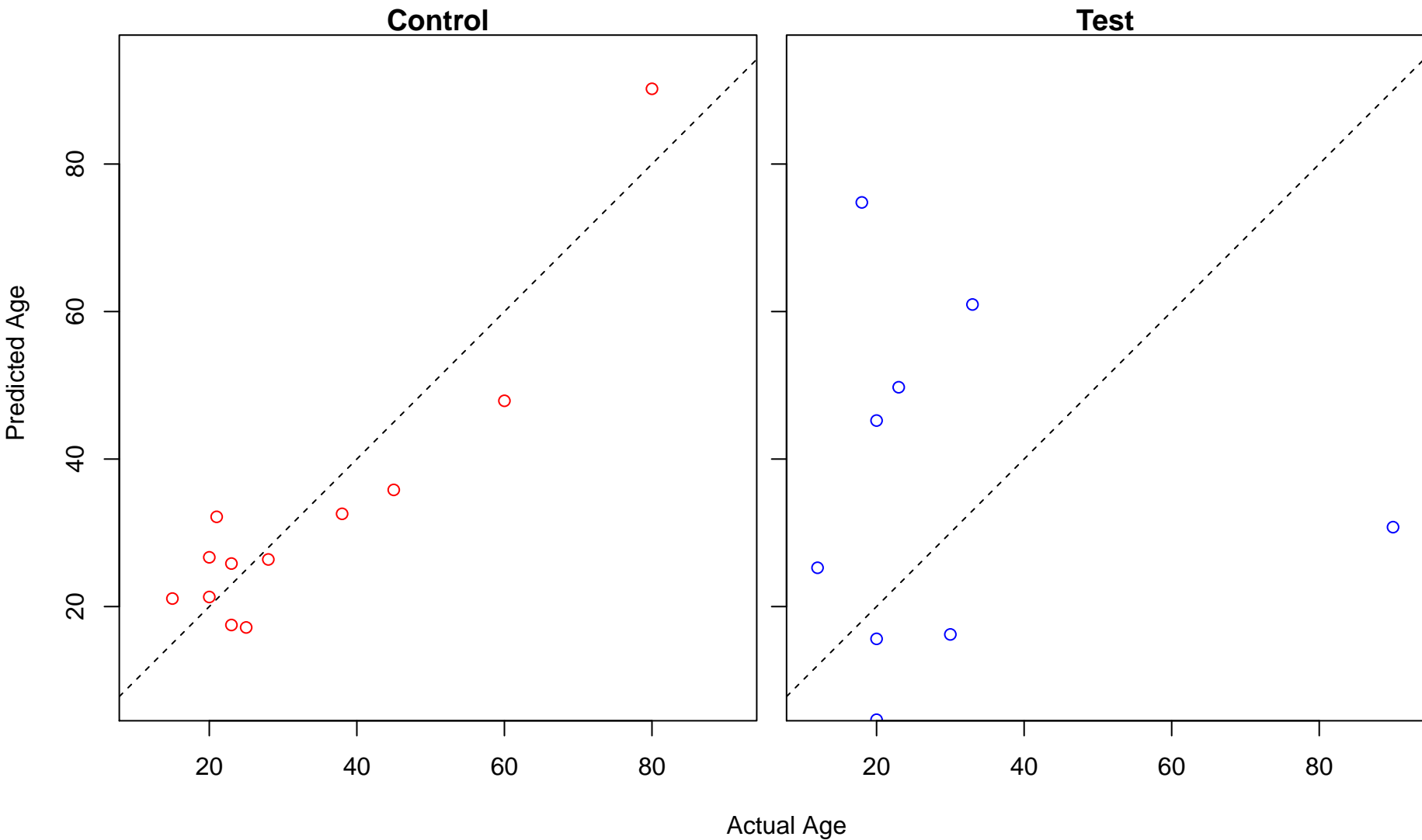


Actual Age

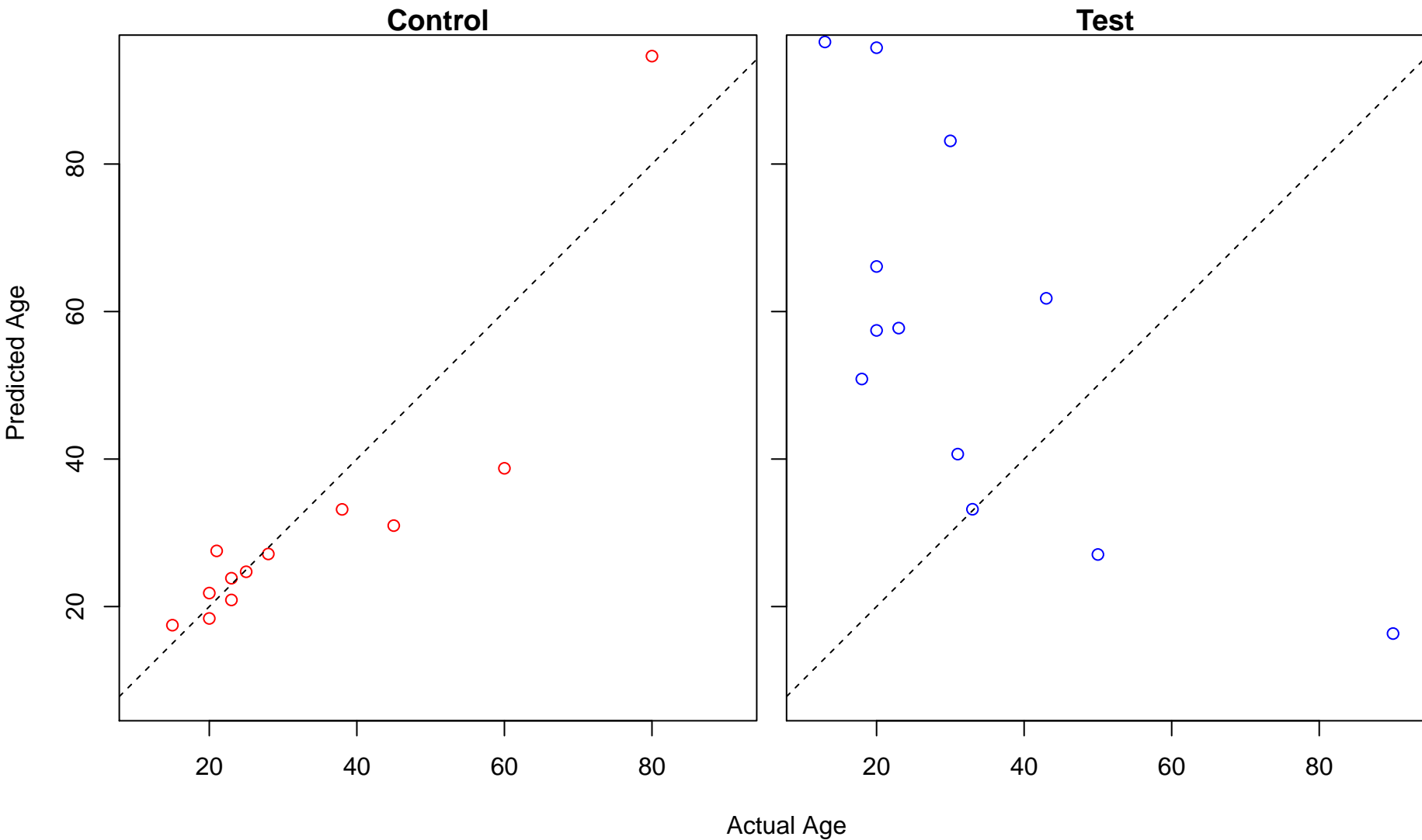
regulation of biomineral tissue development (Score: 14.436470)



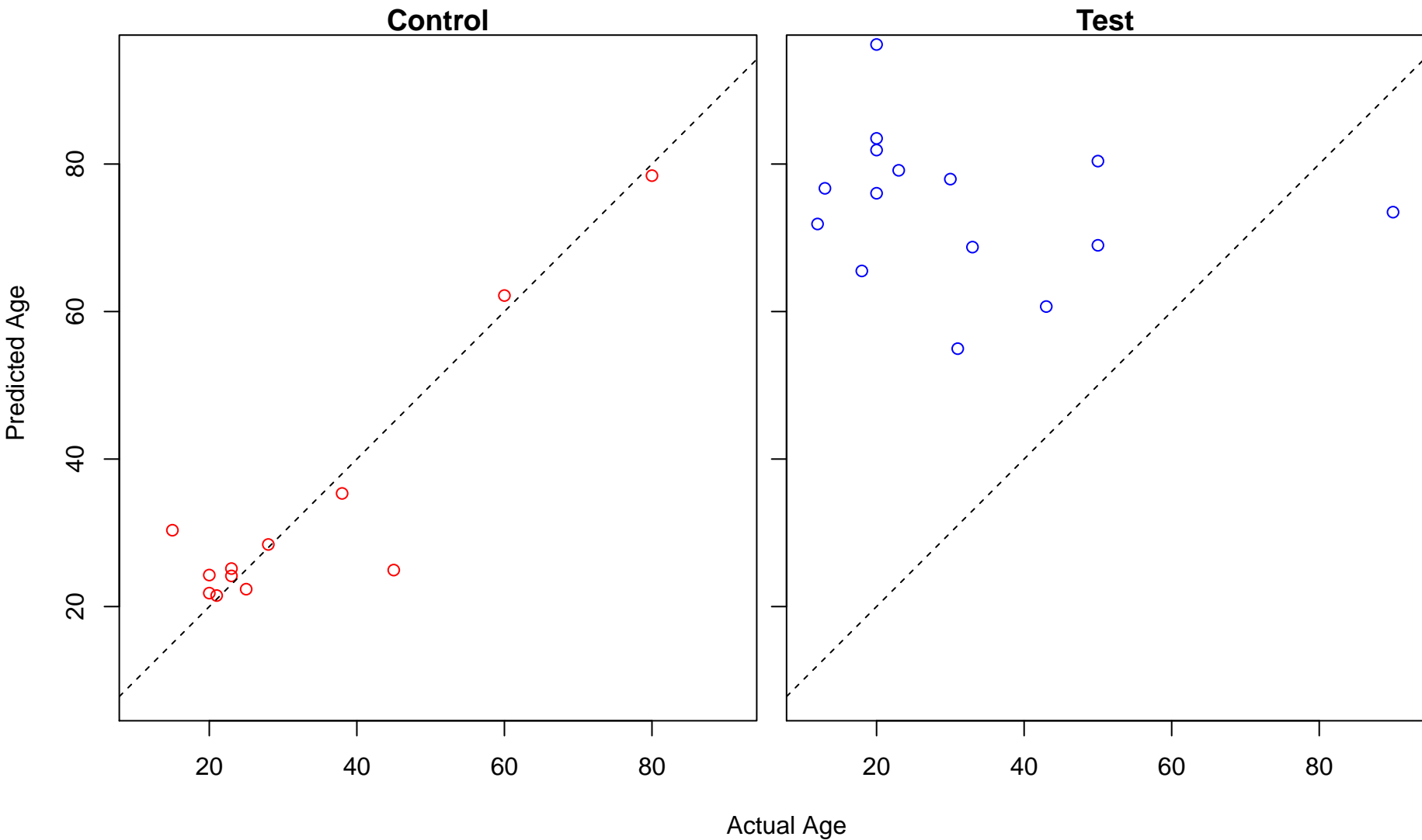
monoubiquitinated protein deubiquitination (Score: 14.412662)



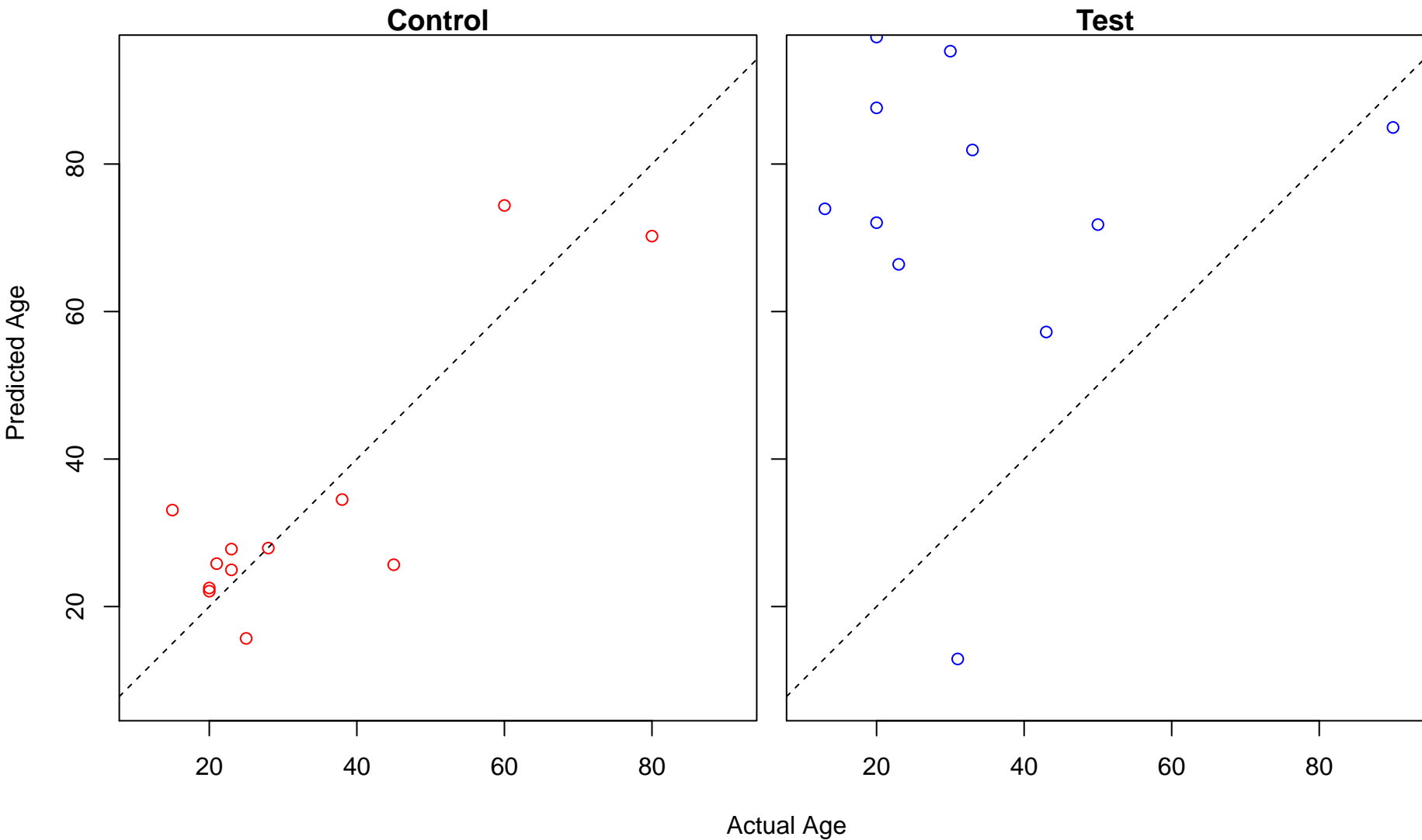
negative regulation of epithelial cell migration (Score: 14.321028)



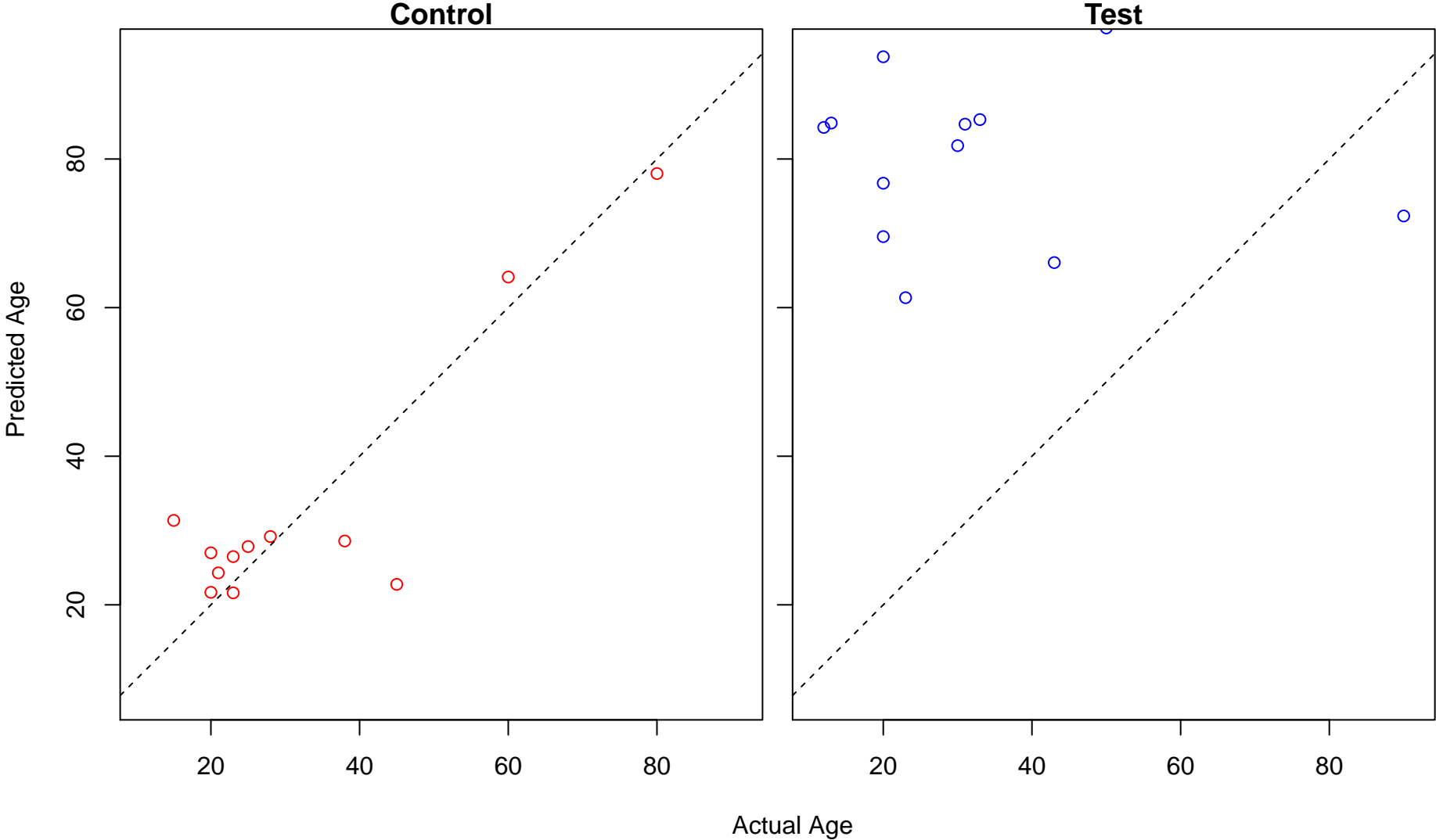
negative regulation of leukocyte chemotaxis (Score: 14.305507)



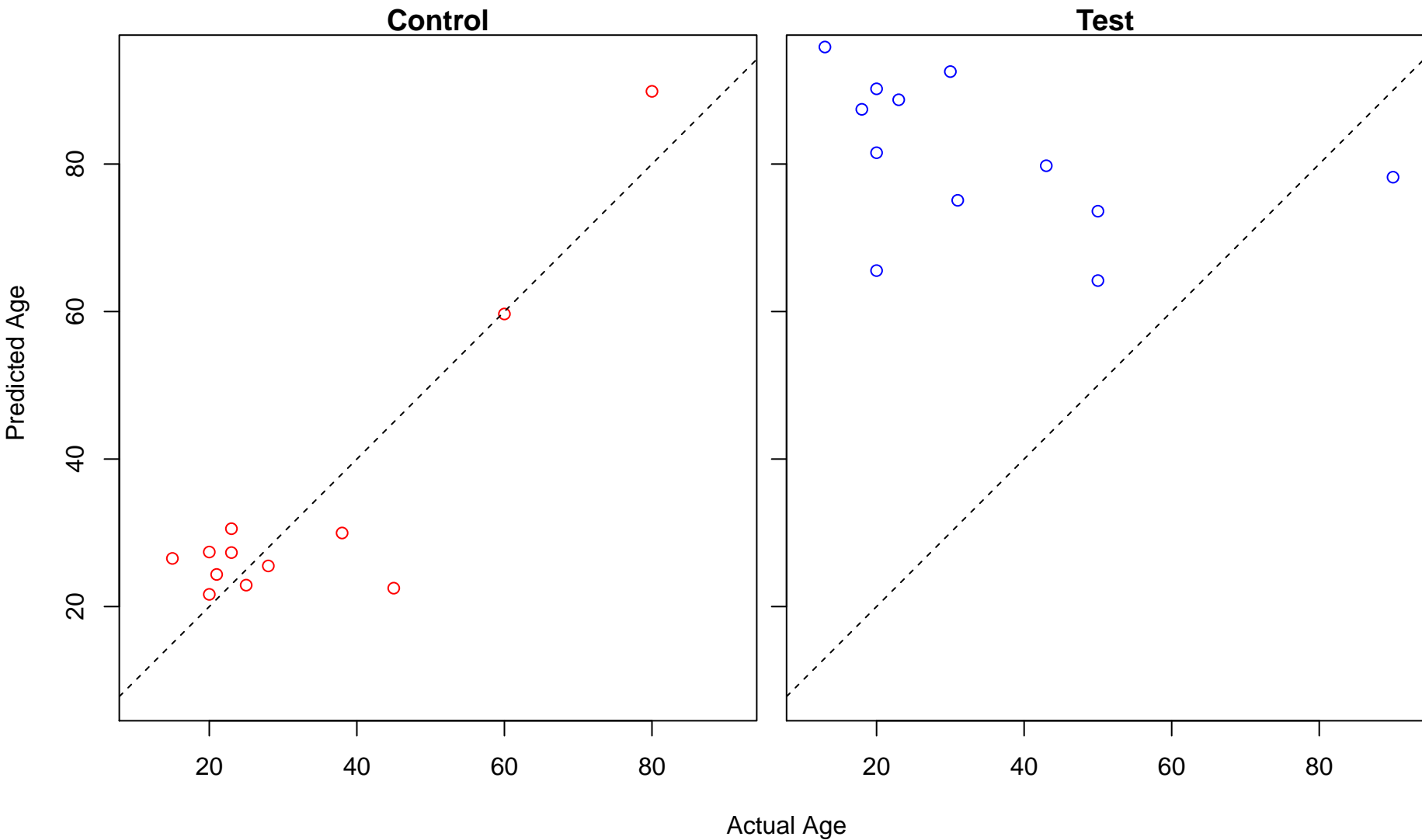
chronic inflammatory response (Score: 14.269863)



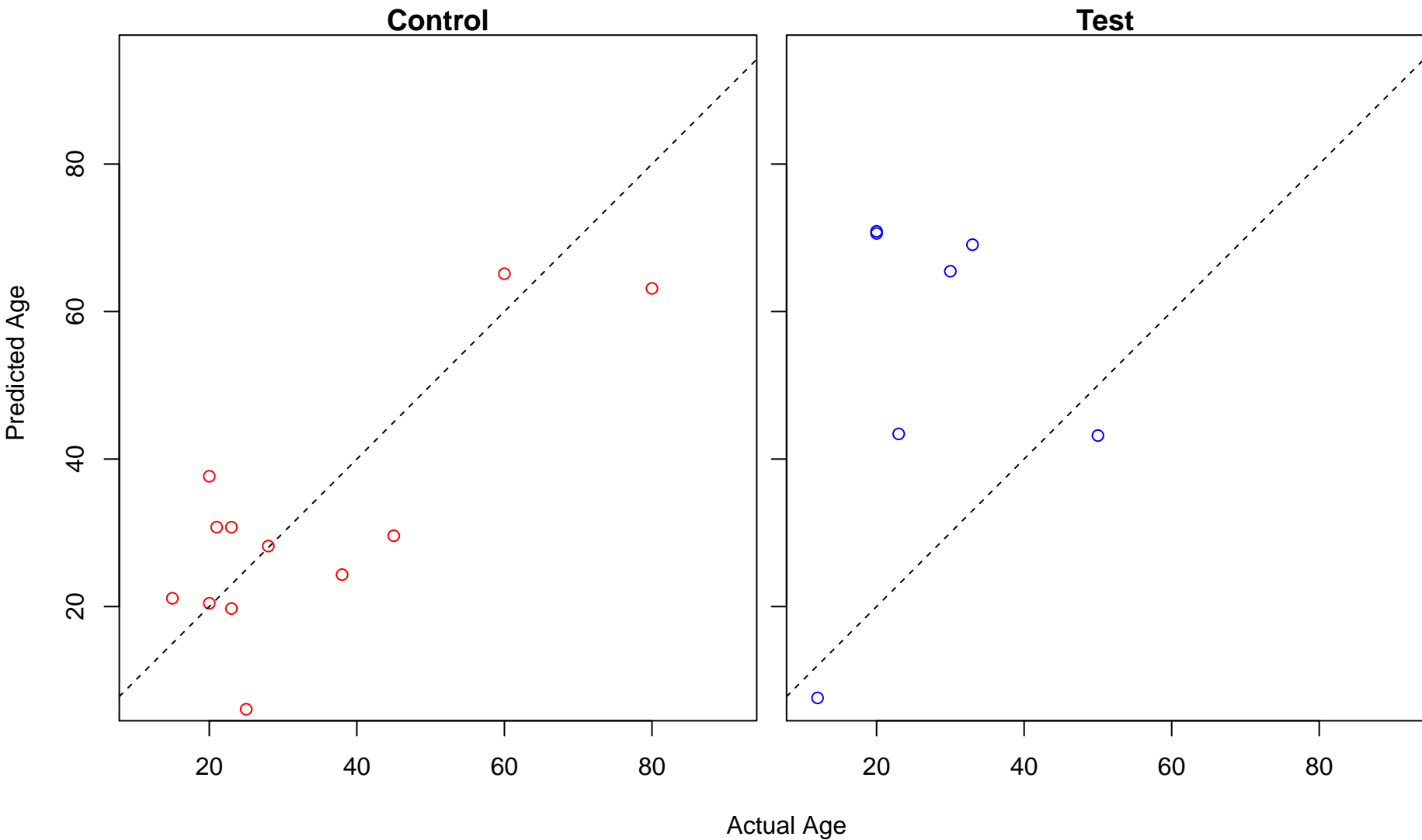
positive regulation of transcription from RNA polymerase II promoter in response to stress (Score: 14.2)



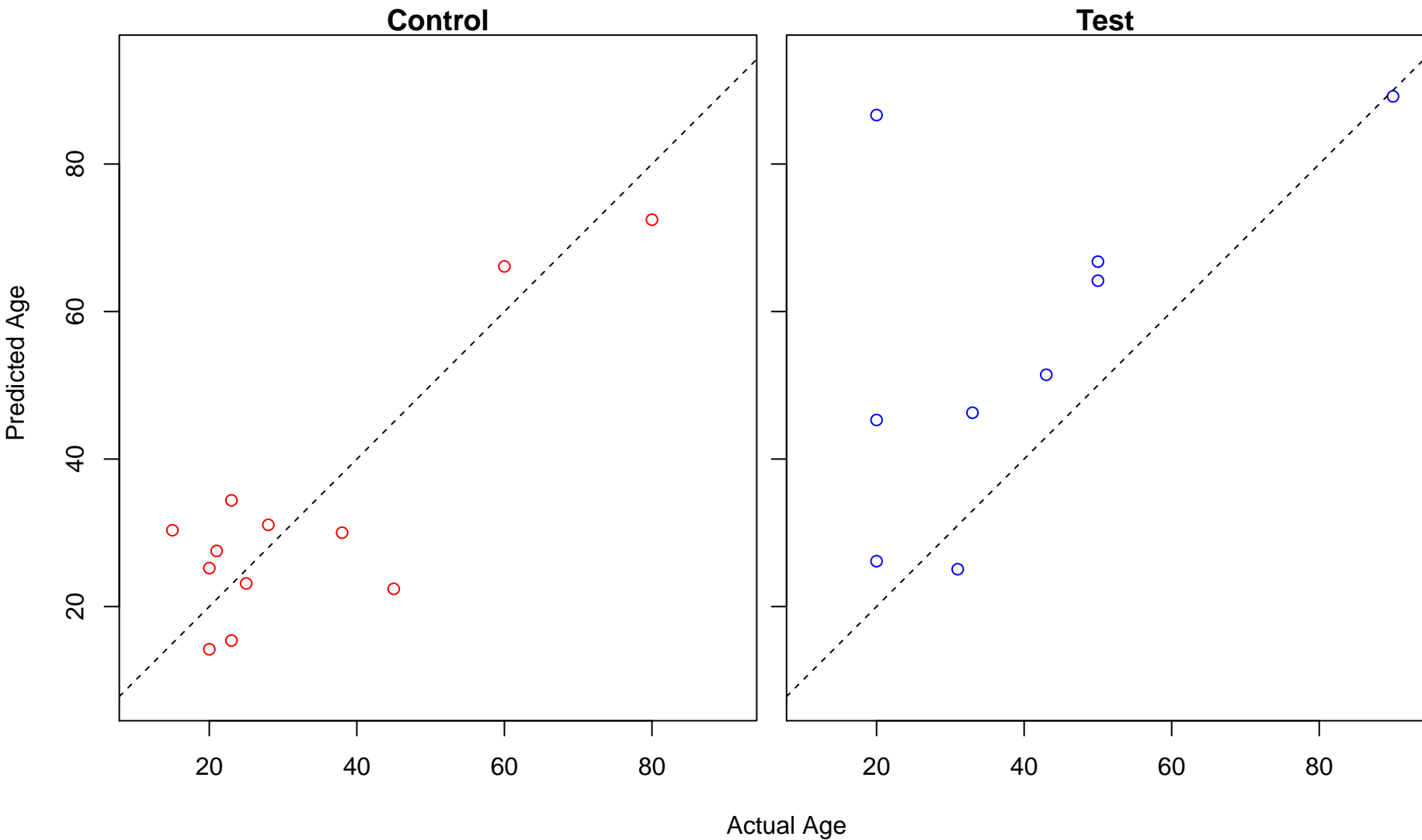
positive regulation of macrophage differentiation (Score: 14.237644)



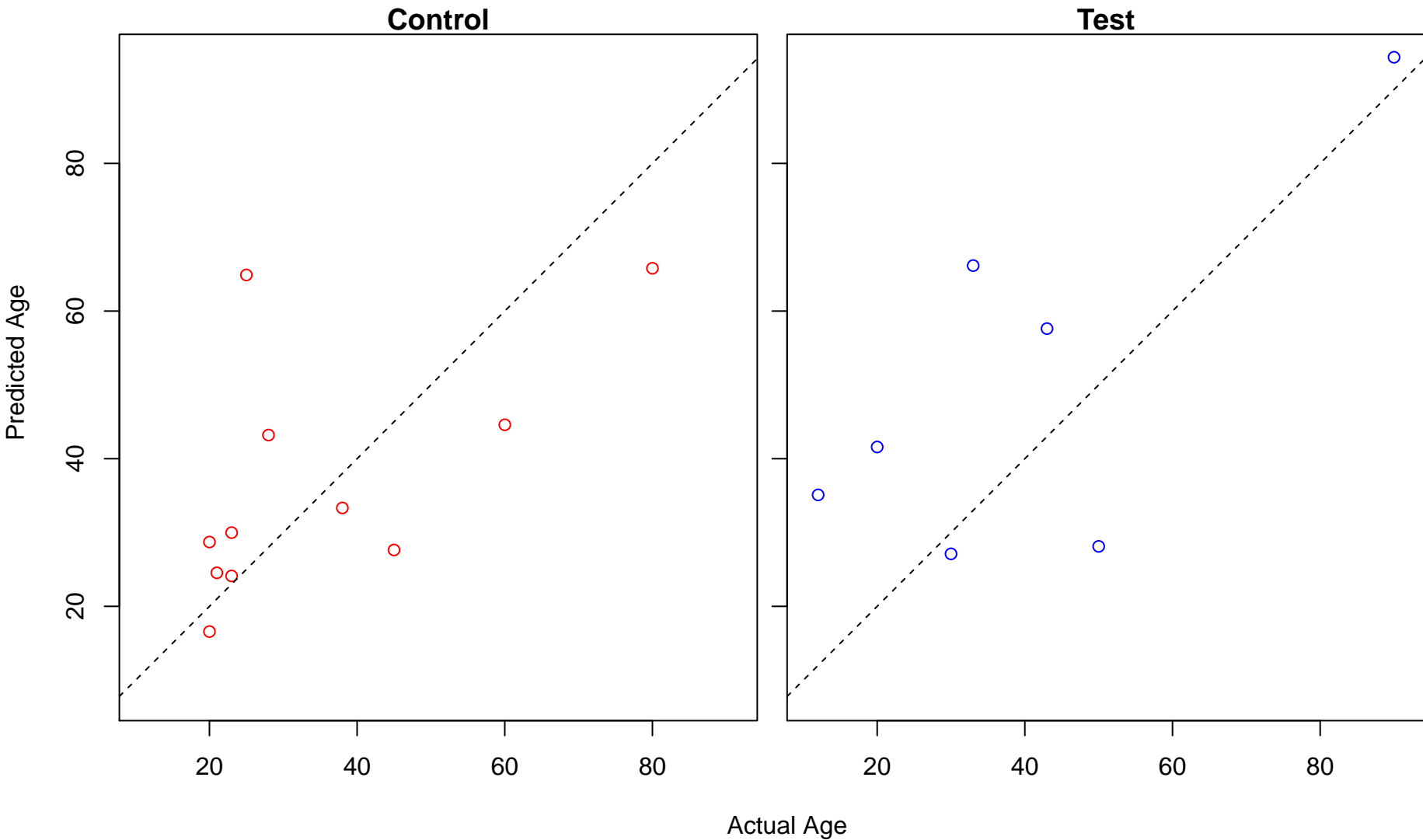
positive regulation of myeloid cell apoptotic process (Score: 14.231134)



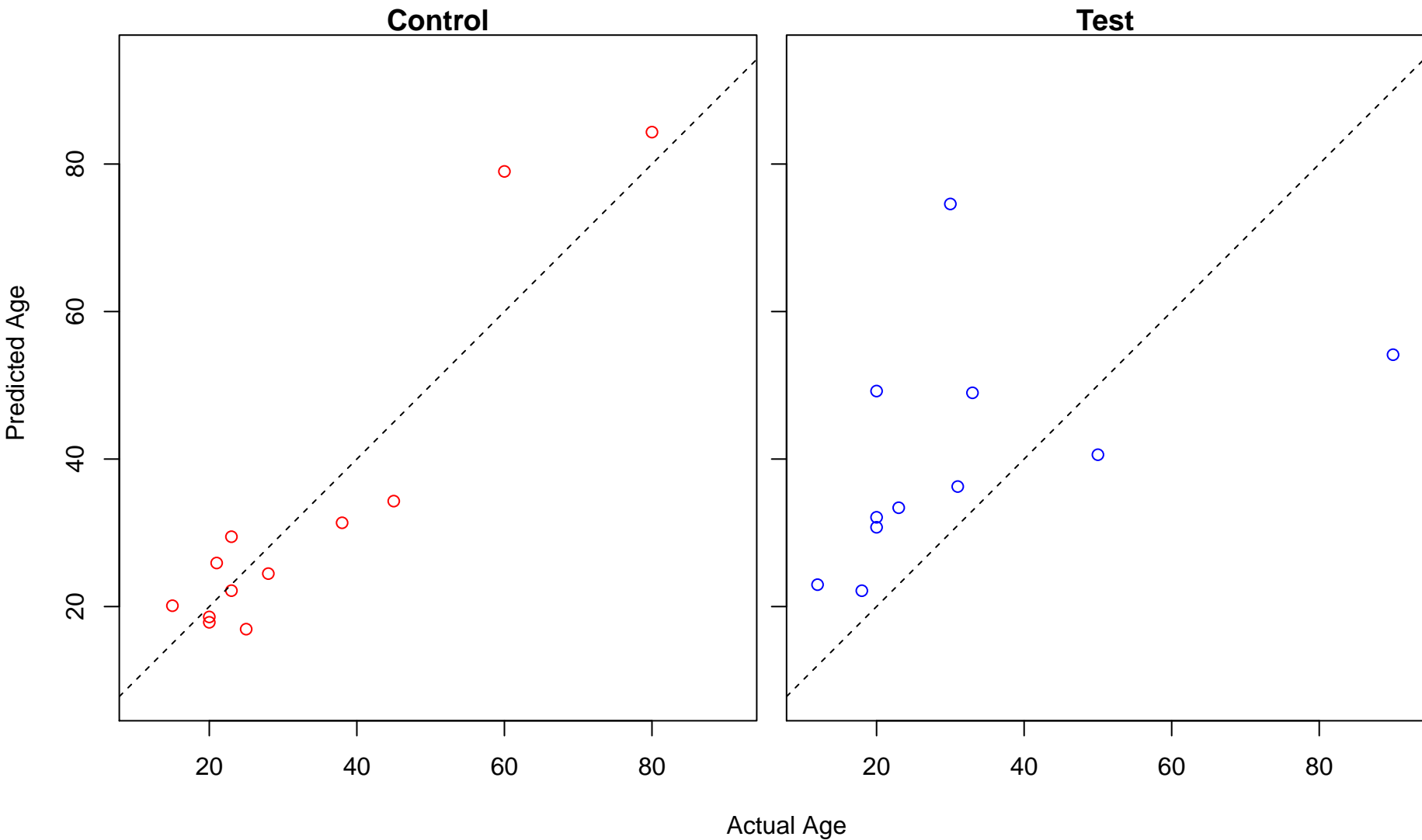
neuronal stem cell population maintenance (Score: 14.220083)



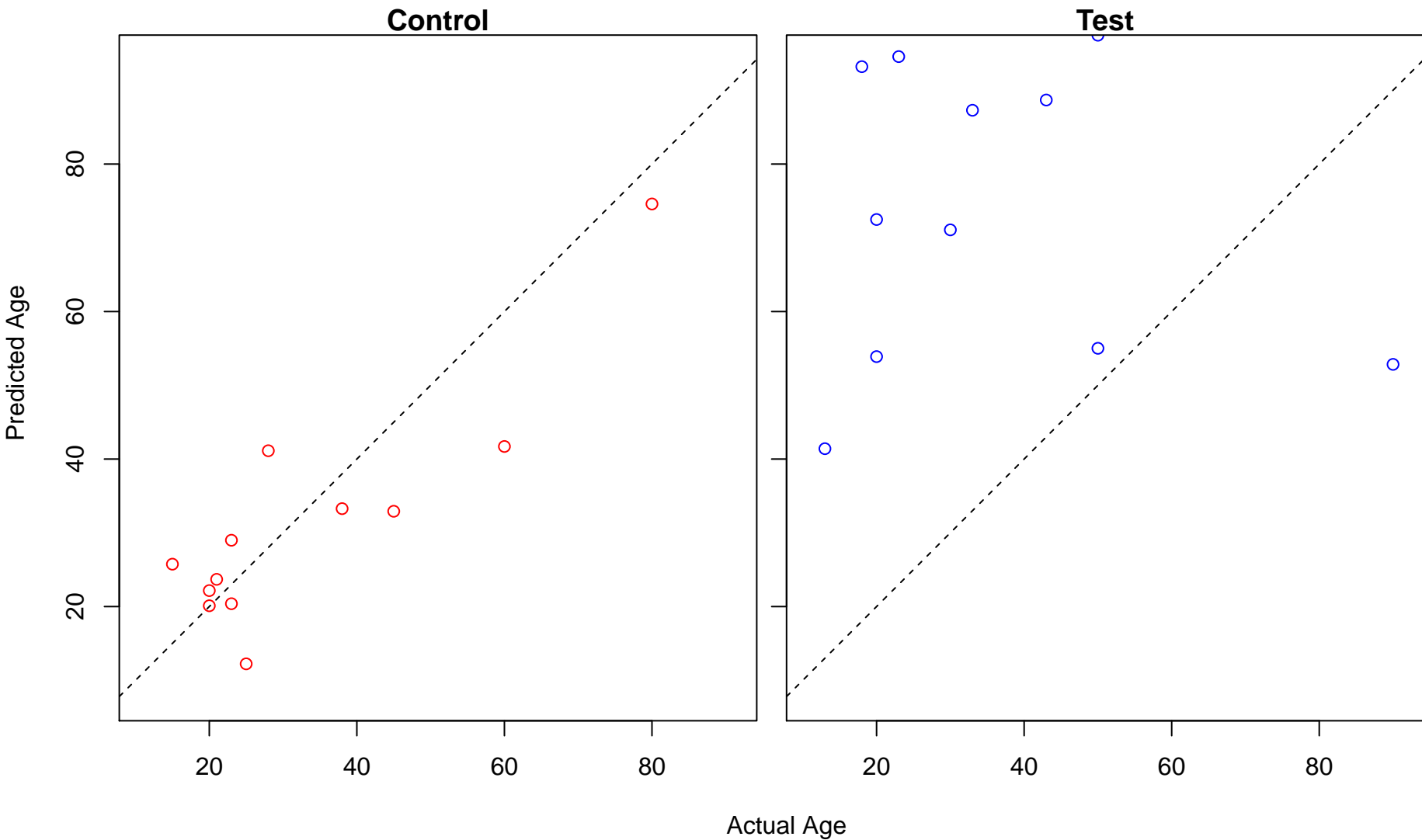
positive regulation of insulin receptor signaling pathway (Score: 14.196732)



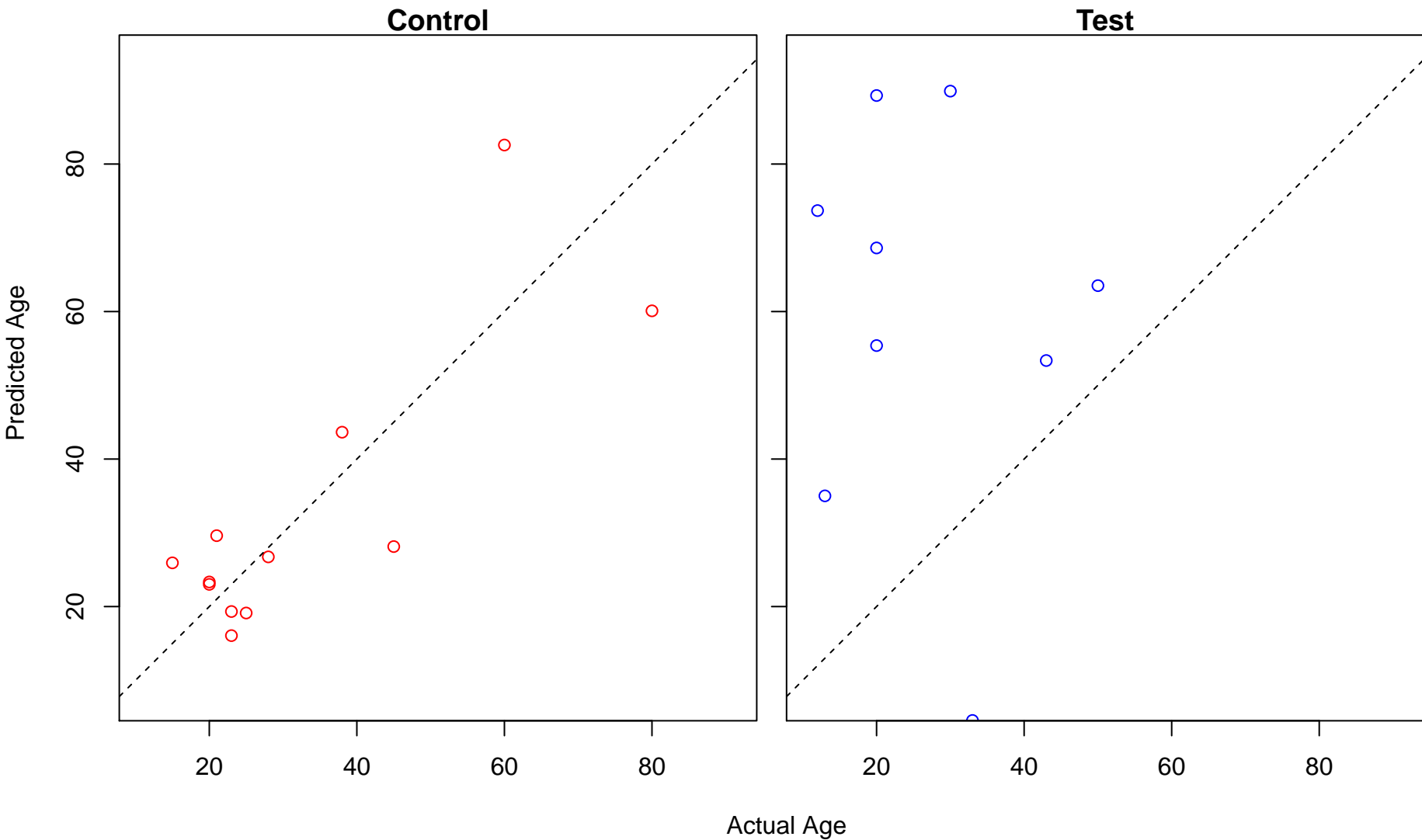
regulation of establishment or maintenance of cell polarity (Score: 14.187435)



determination of left/right symmetry (Score: 14.153081)

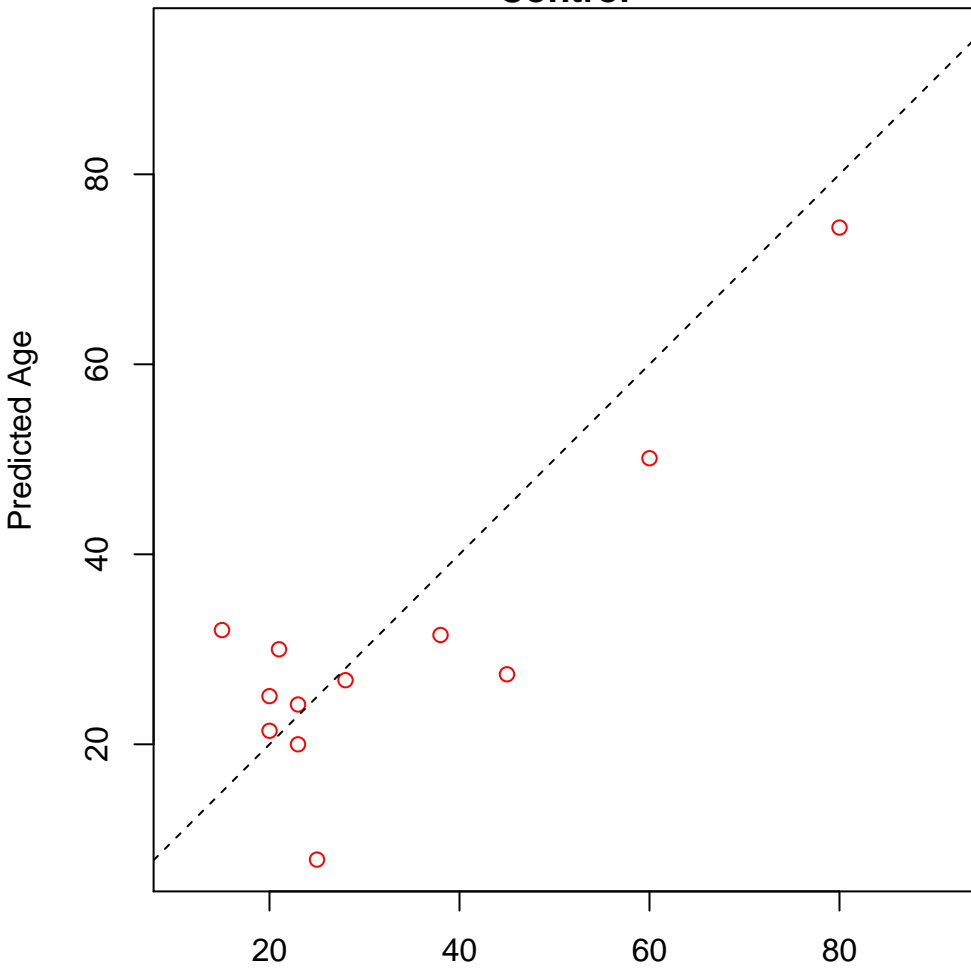


positive regulation of protein homooligomerization (Score: 14.140674)

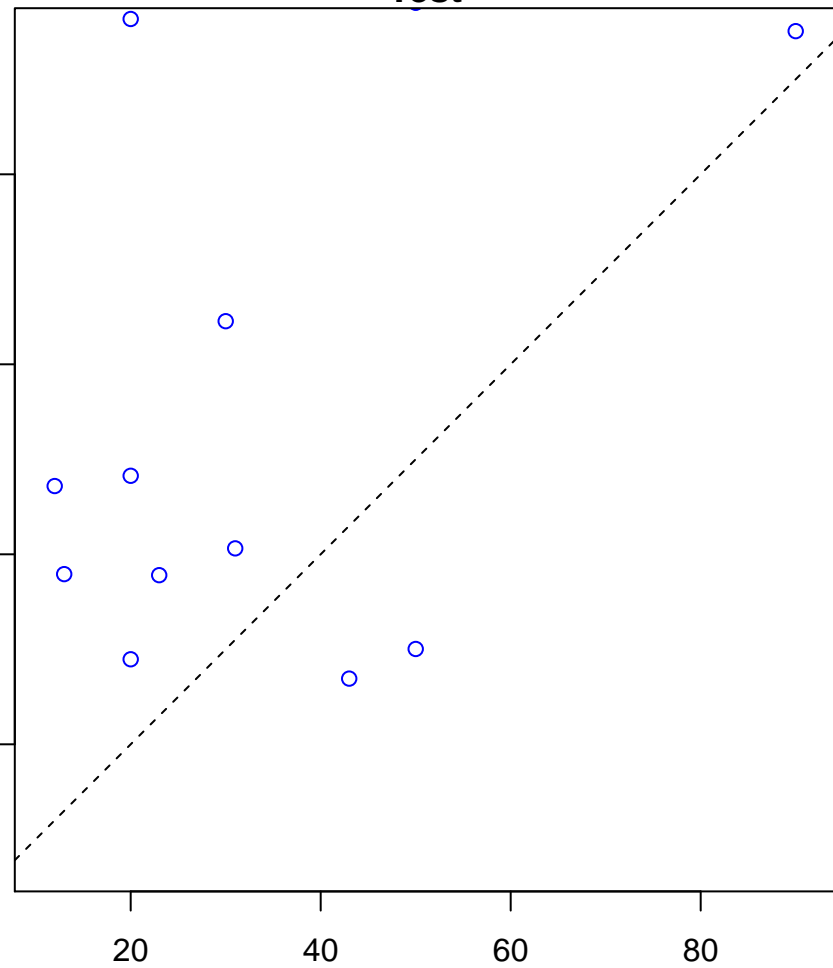


mitotic metaphase plate congression (Score: 14.137191)

Control

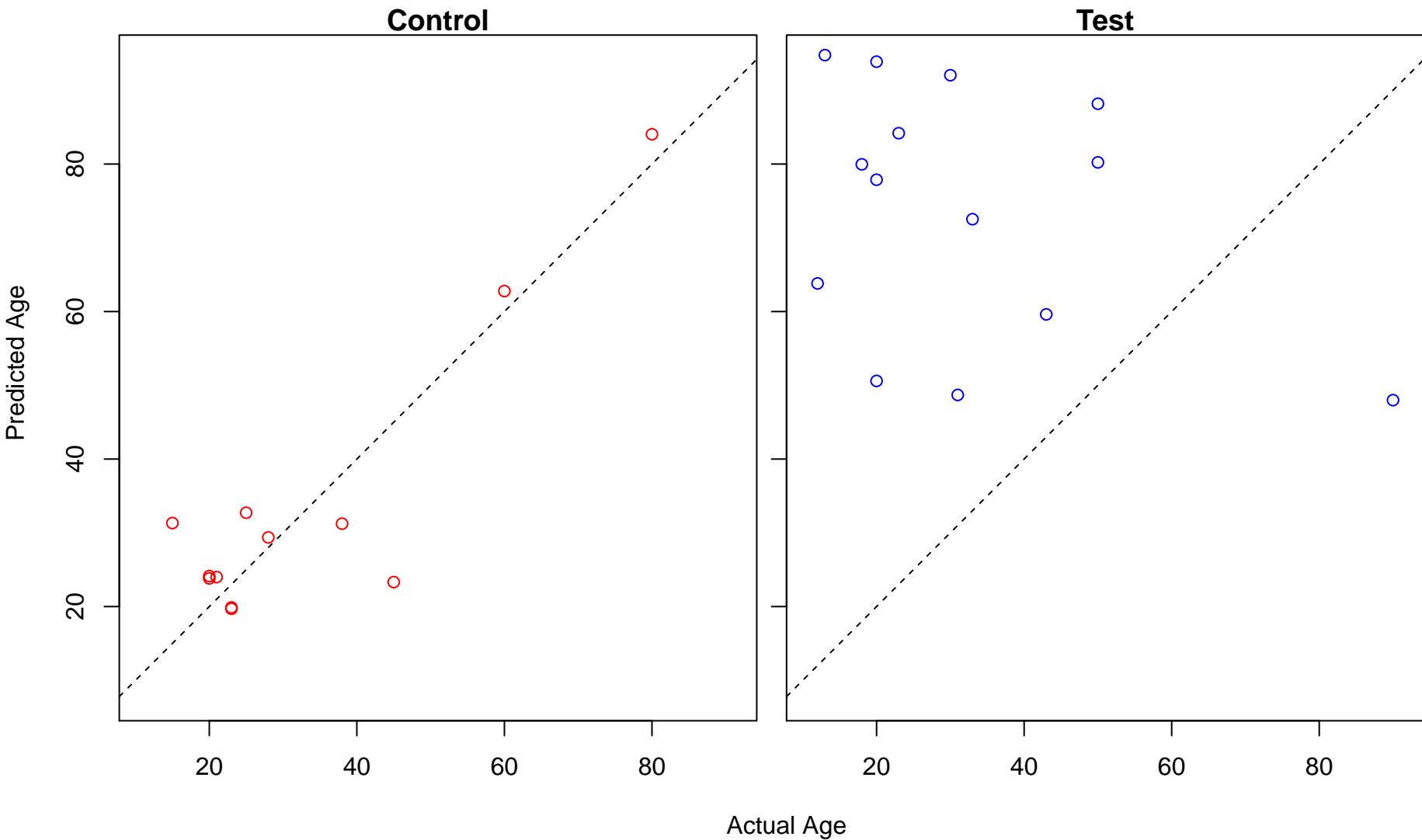


Test

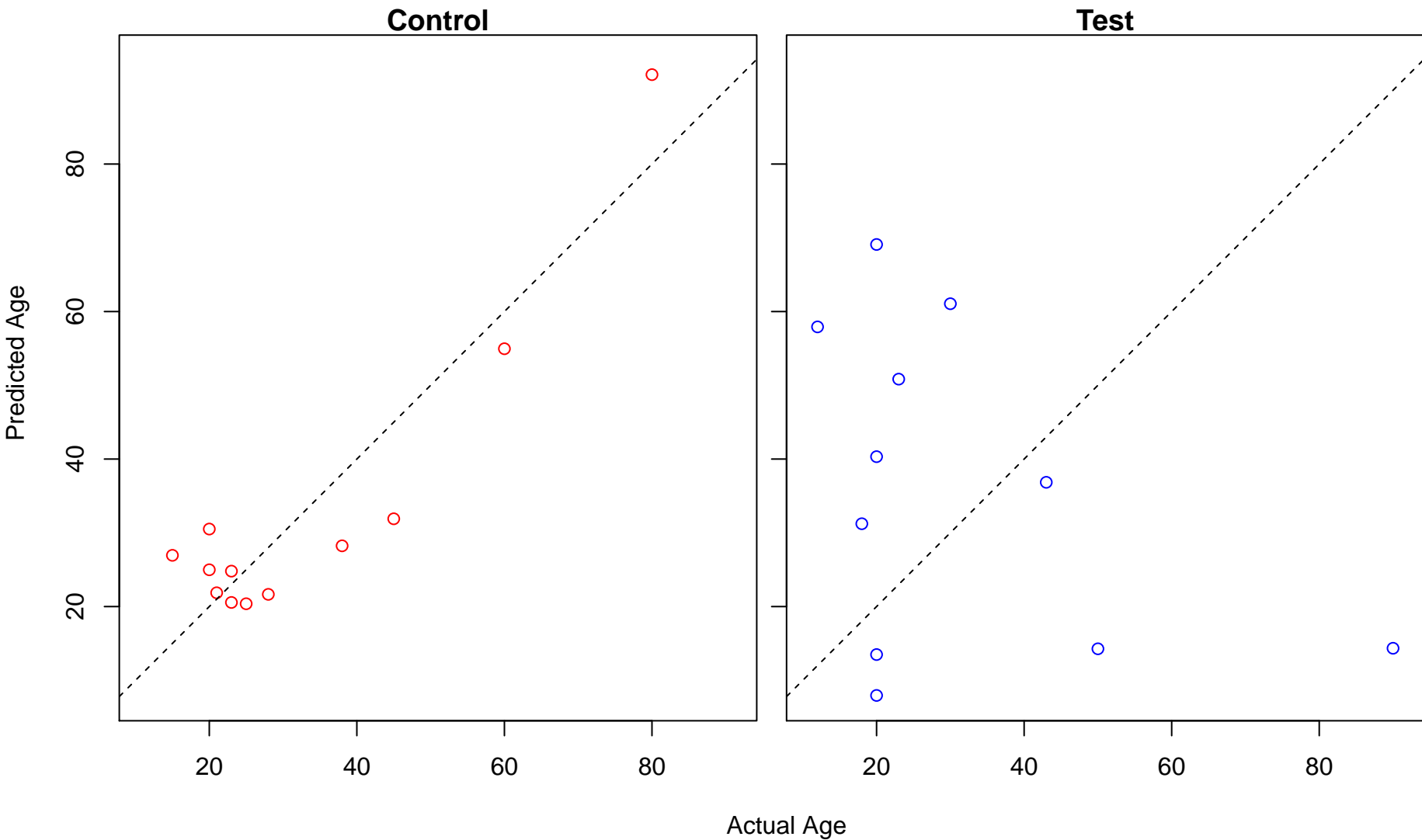


Actual Age

glutamine transport (Score: 14.127977)

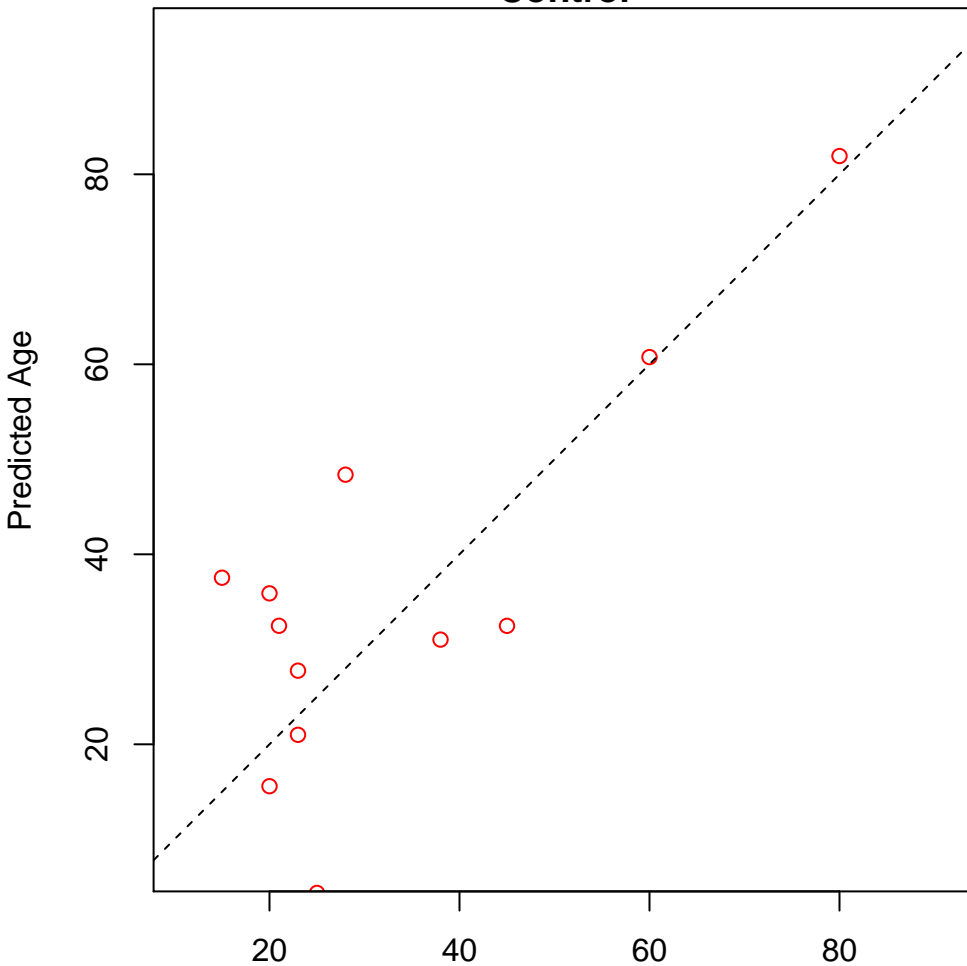


hormone biosynthetic process (Score: 14.124971)

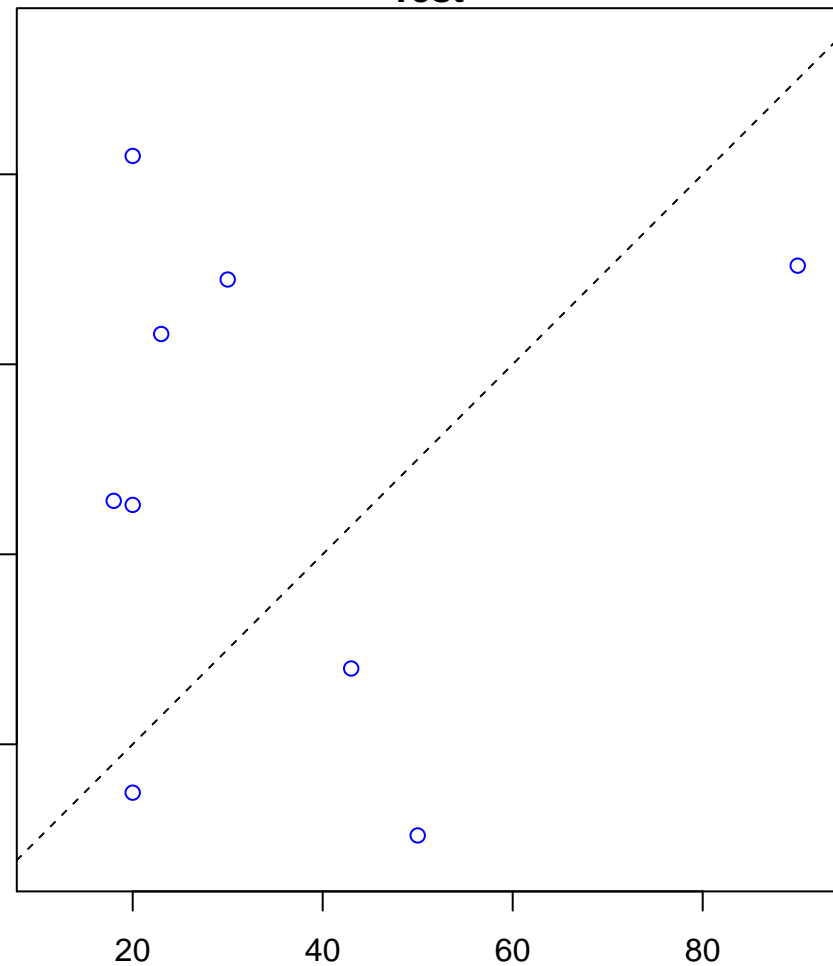


regulation of mast cell degranulation (Score: 14.098440)

Control

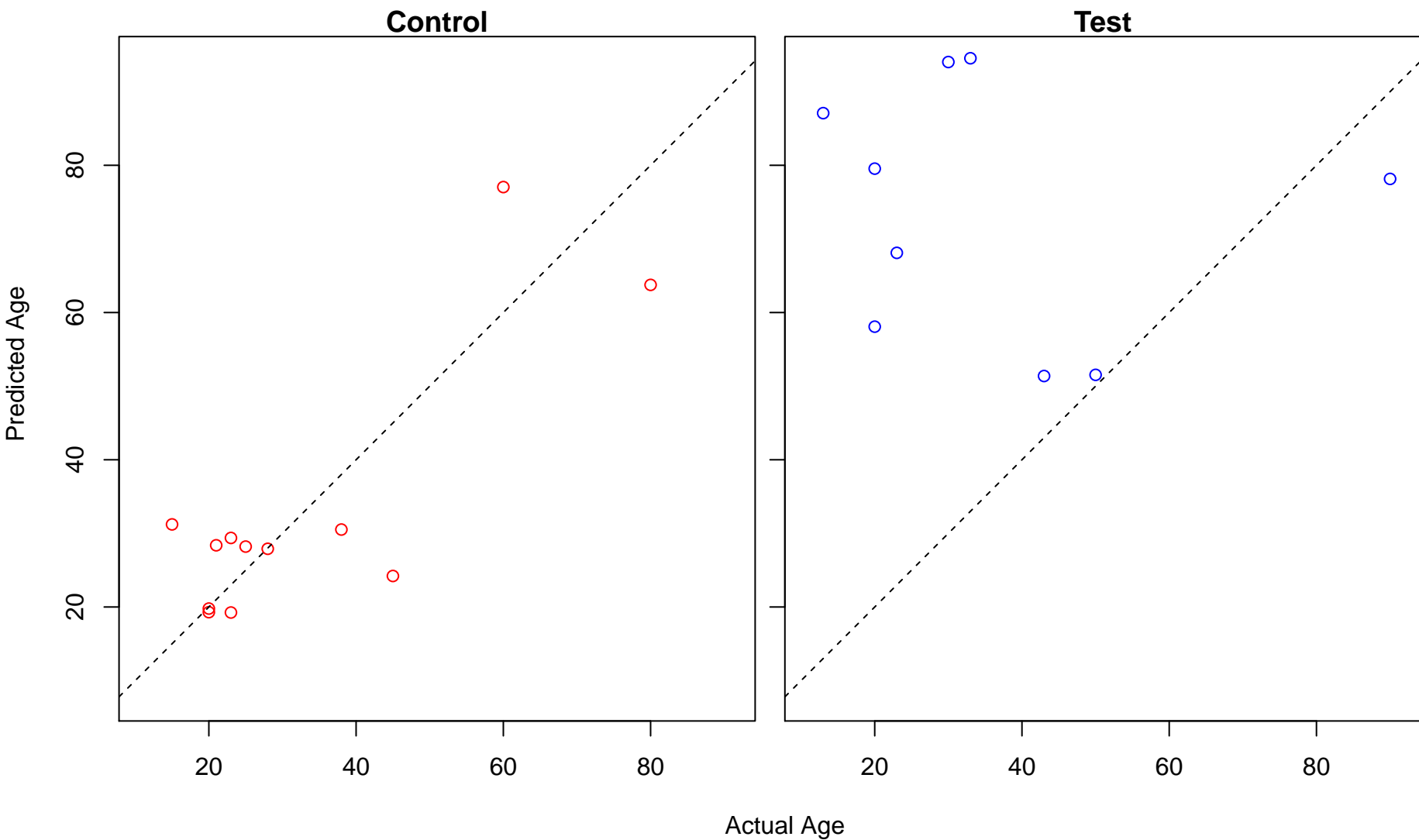


Test



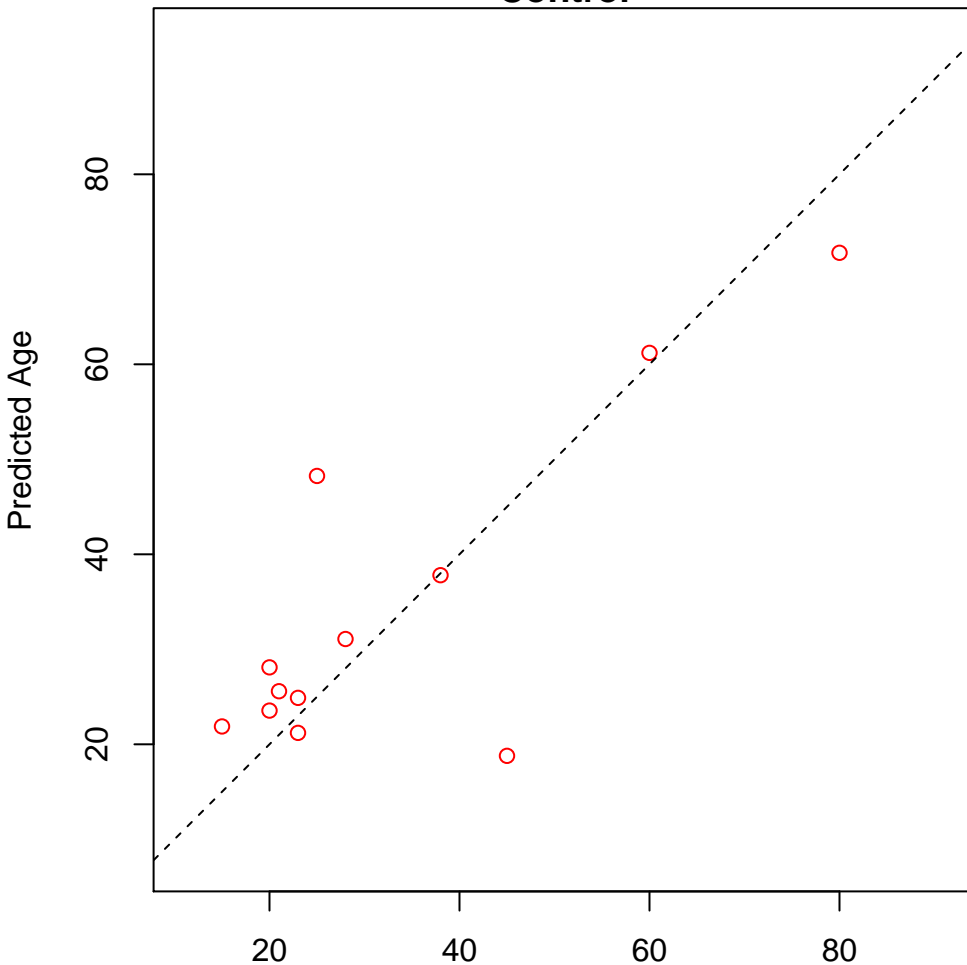
Actual Age

CD4-positive, alpha-beta T cell activation (Score: 14.076720)

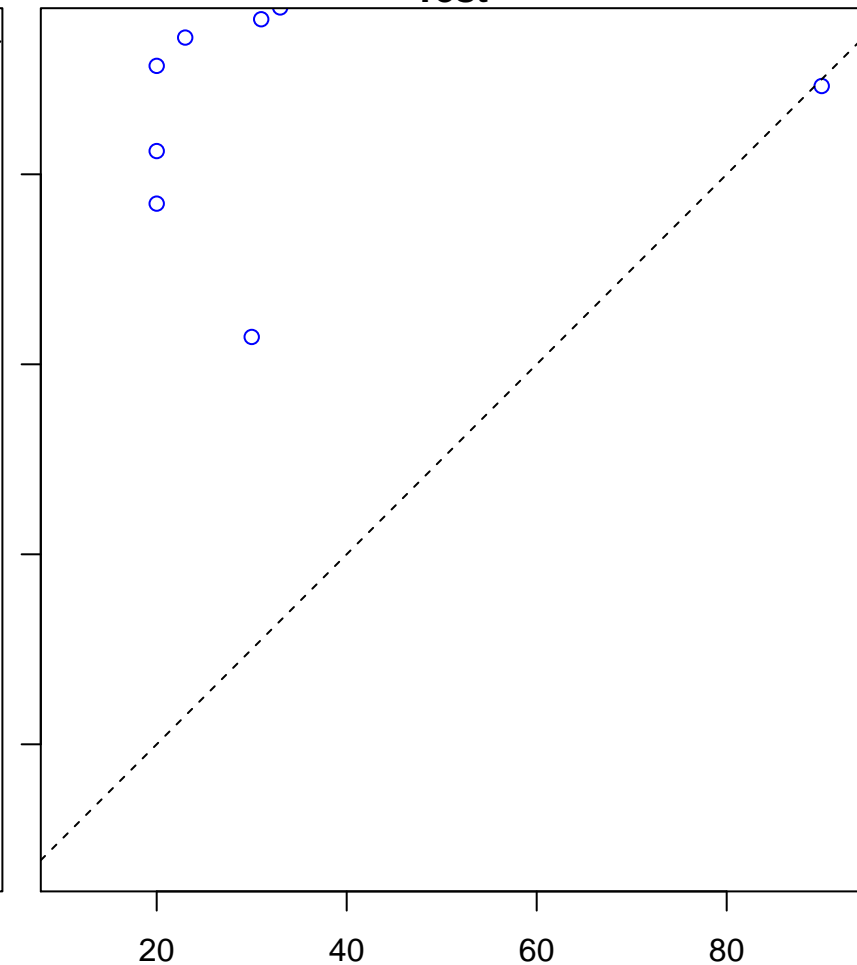


regulation of macrophage chemotaxis (Score: 14.070038)

Control

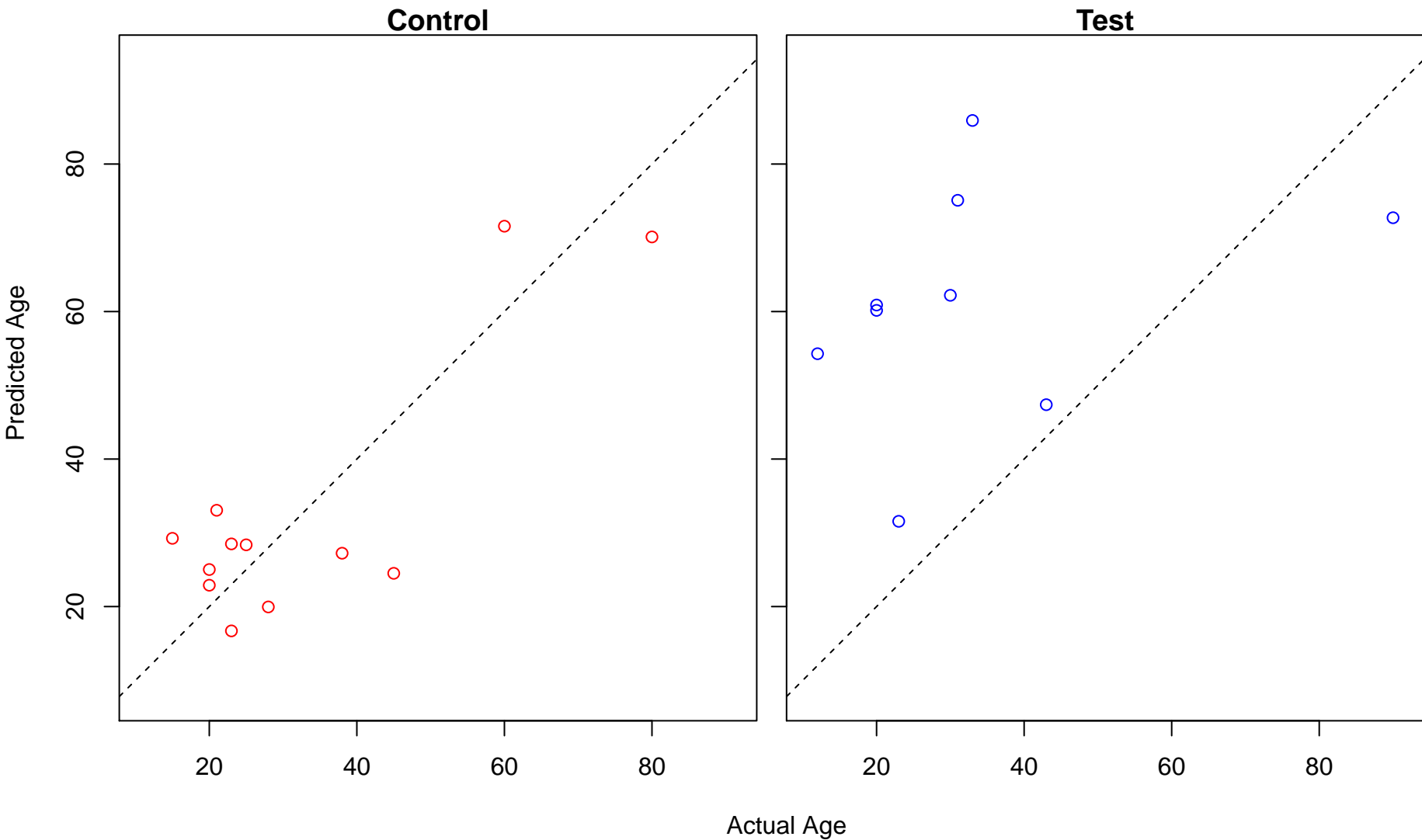


Test

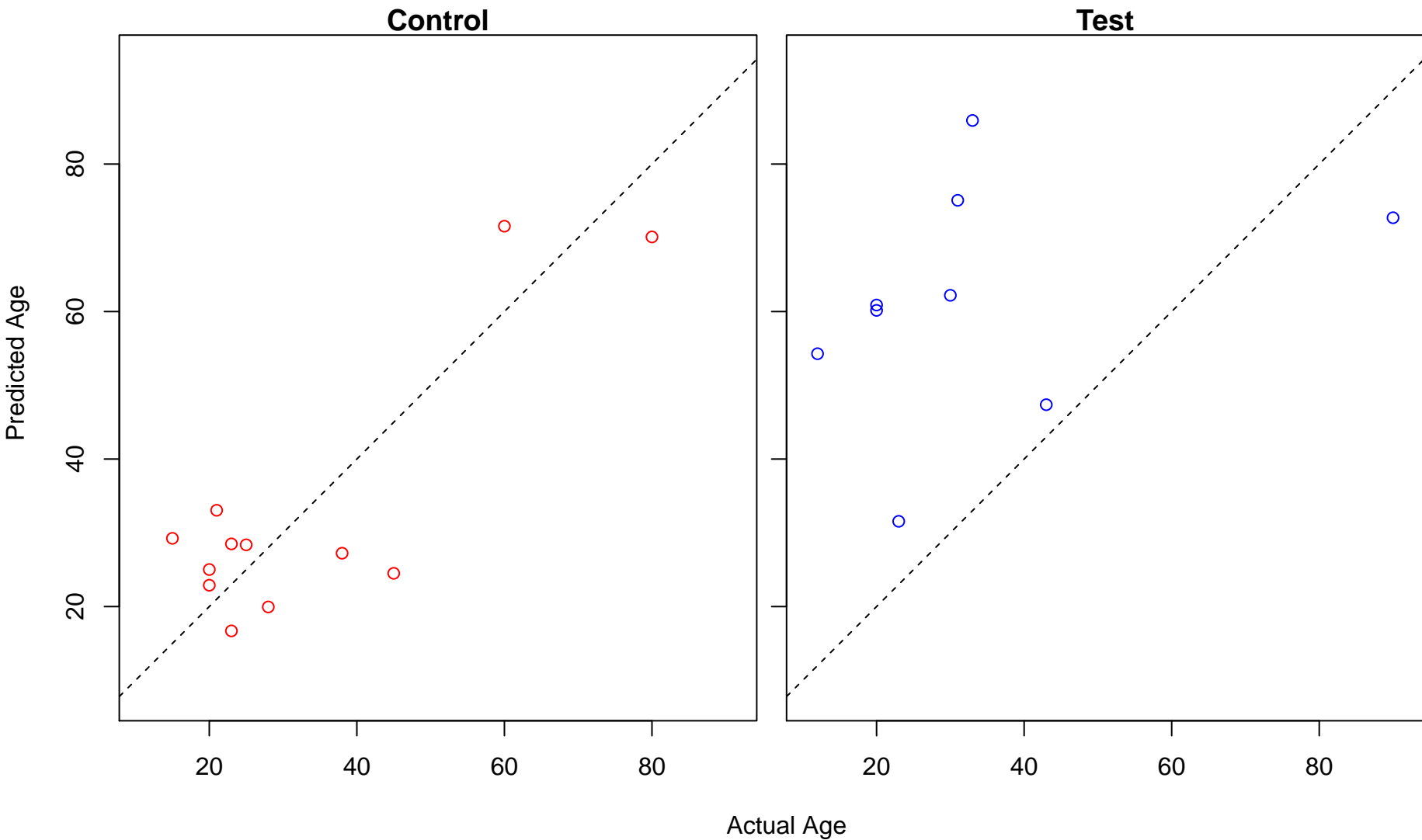


Actual Age

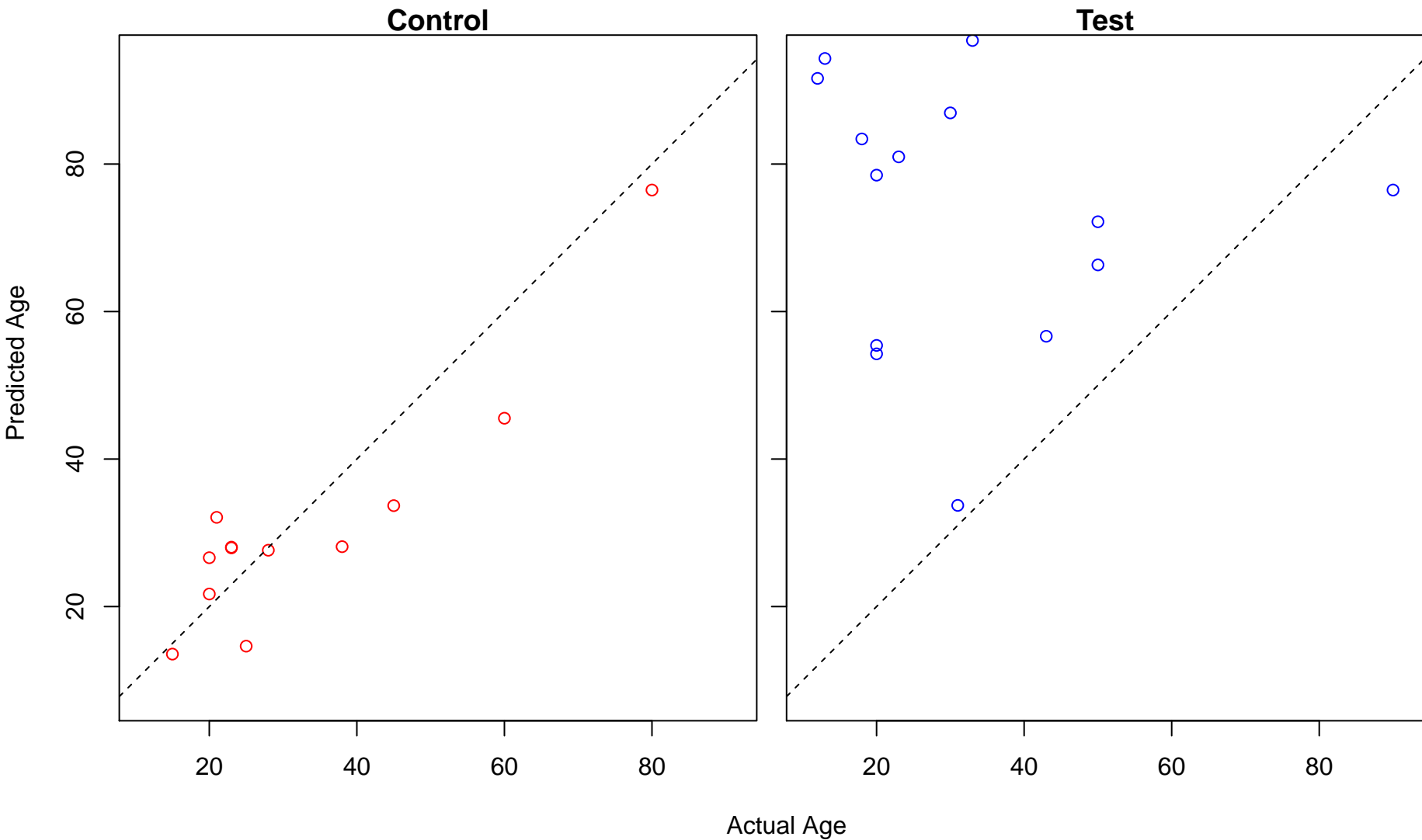
pigment accumulation (Score: 14.054450)



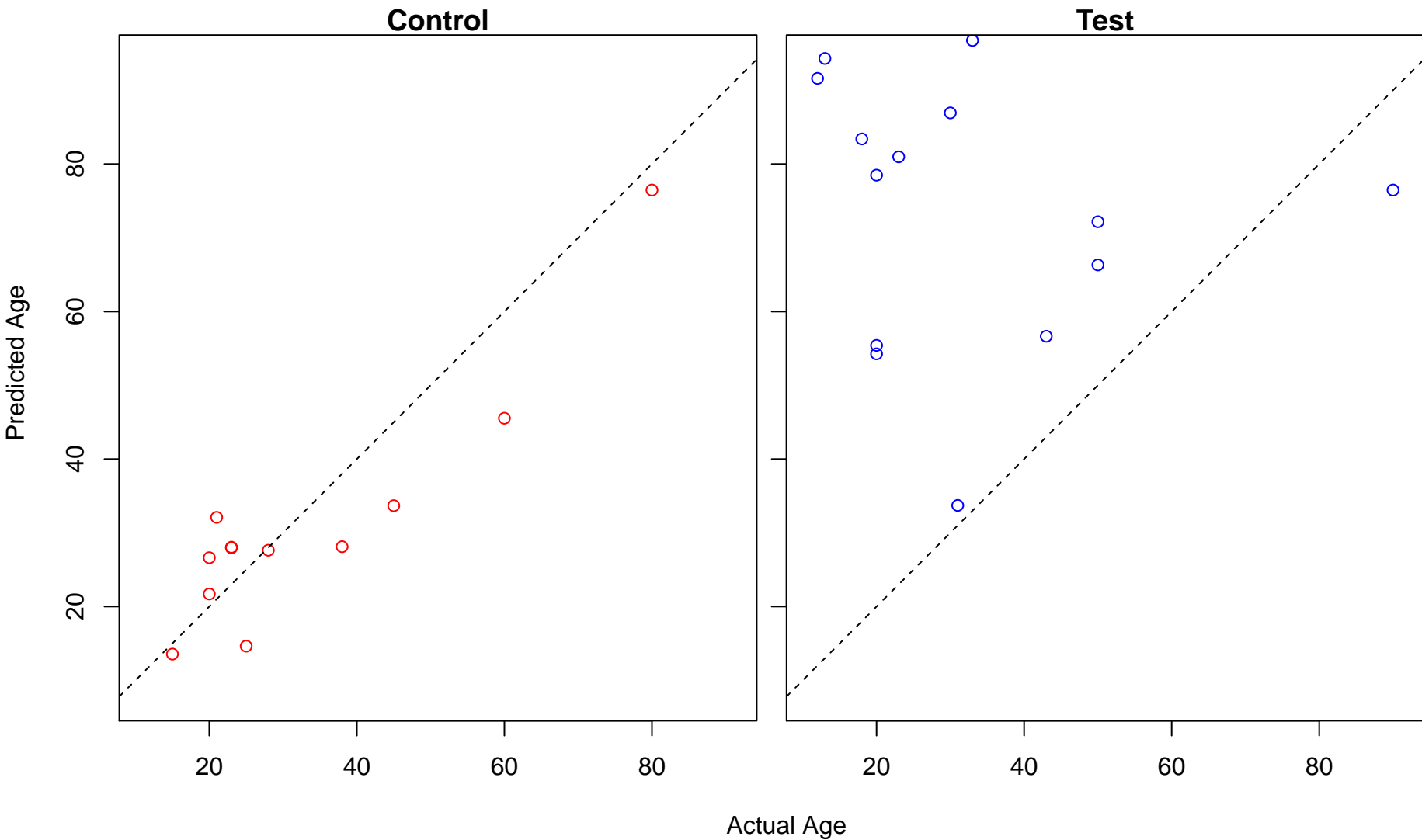
cellular pigment accumulation (Score: 14.054450)



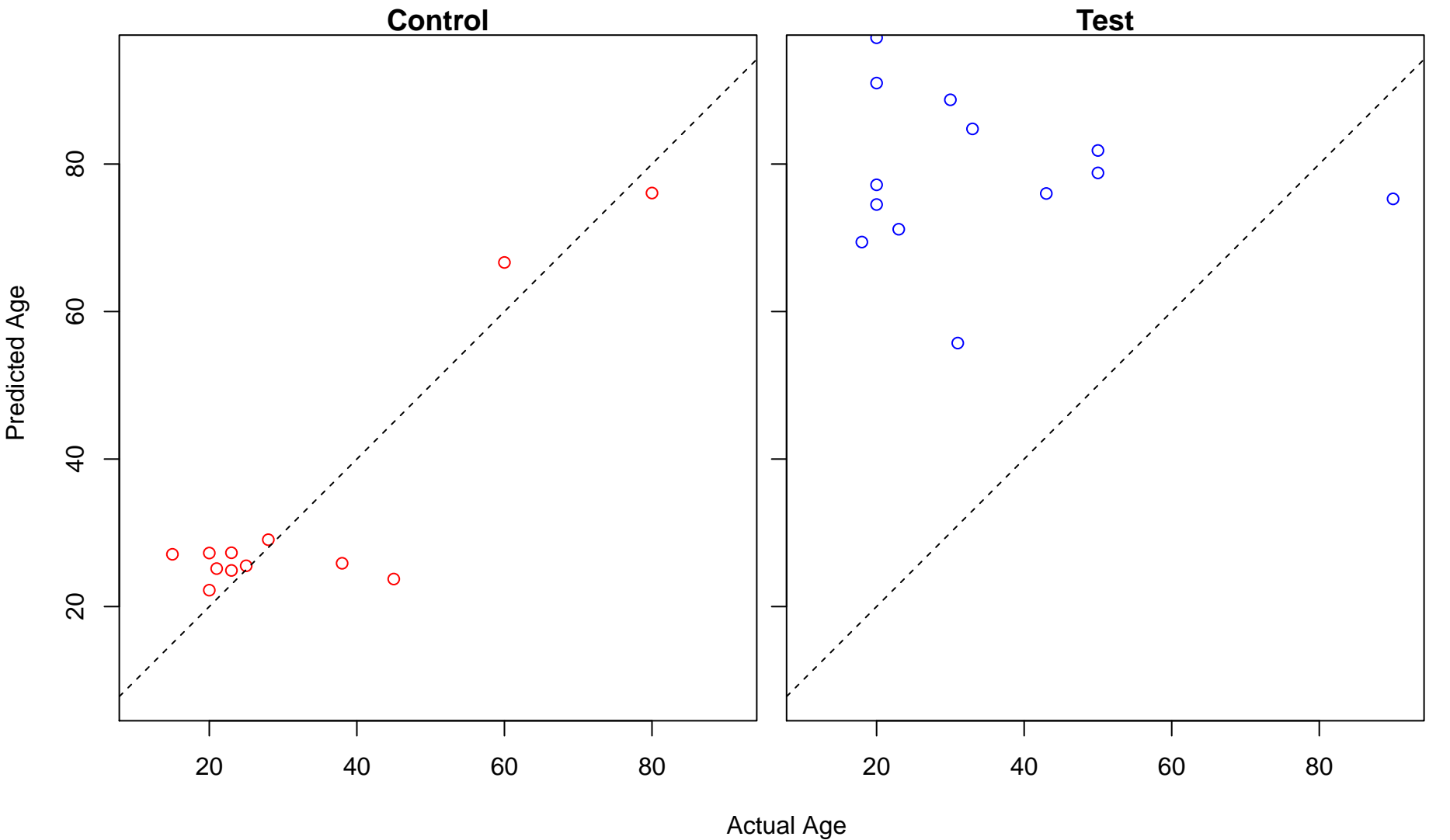
subpallium development (Score: 14.053435)



striatum development (Score: 14.053435)

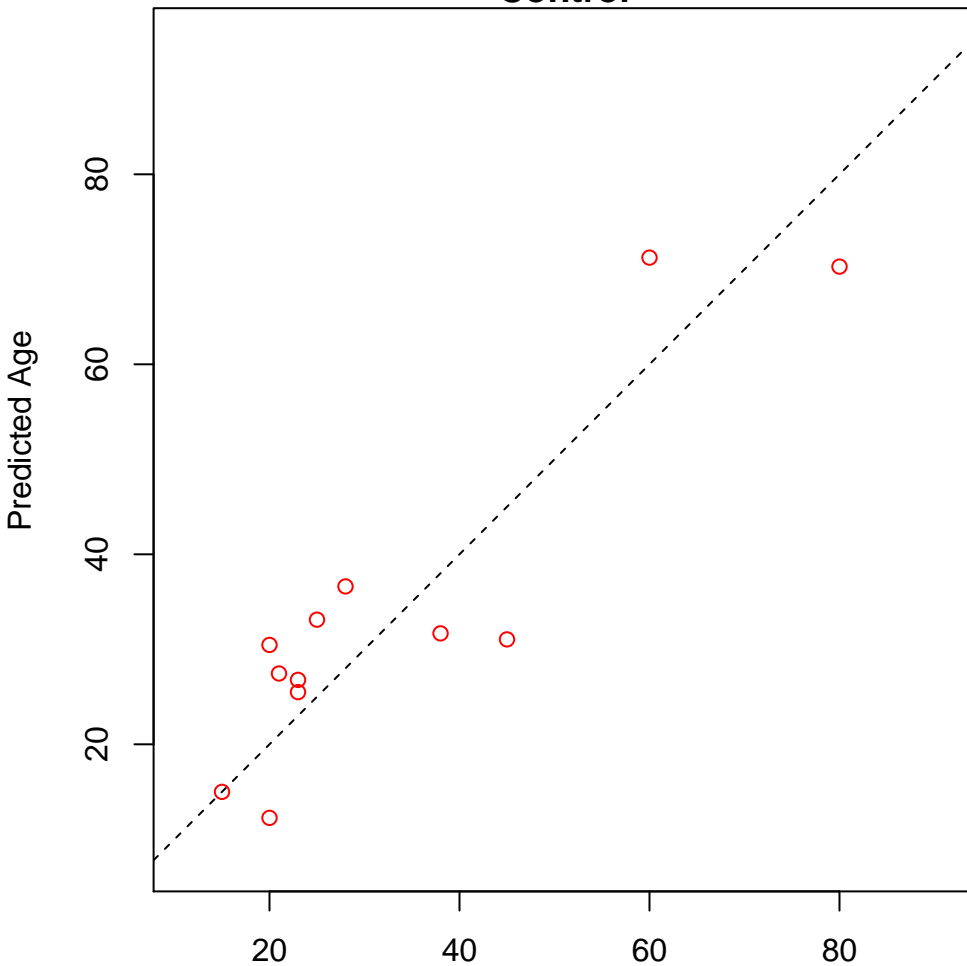


positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 1

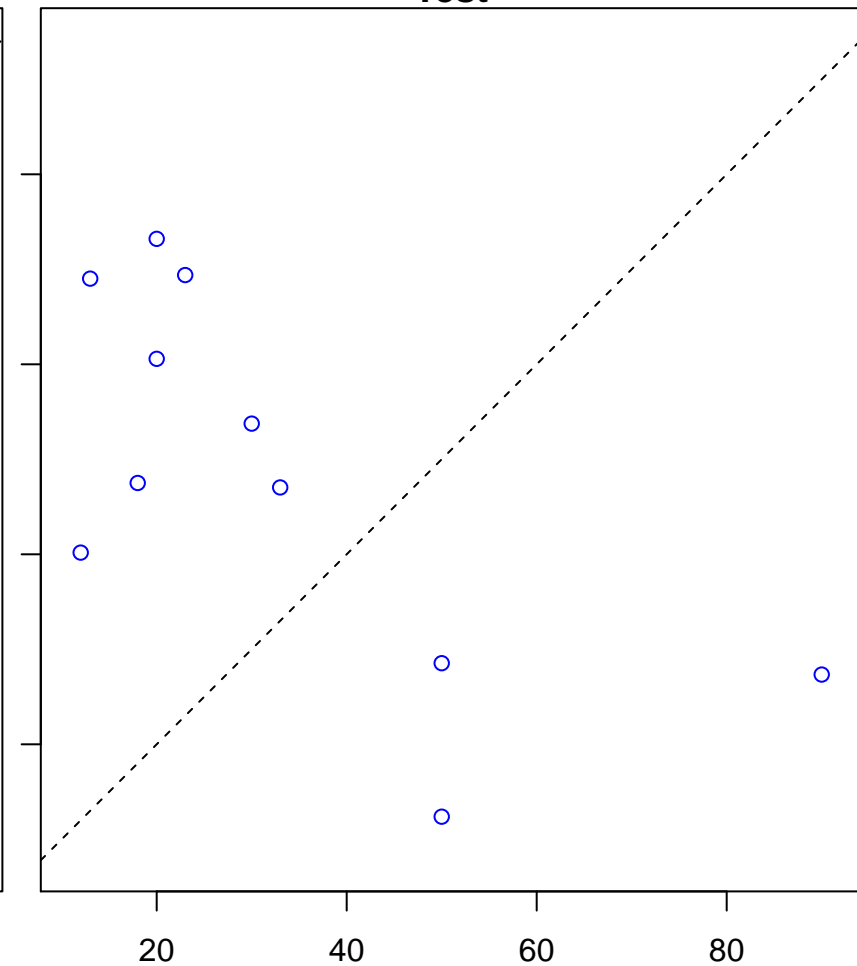


cellular response to estrogen stimulus (Score: 14.017134)

Control



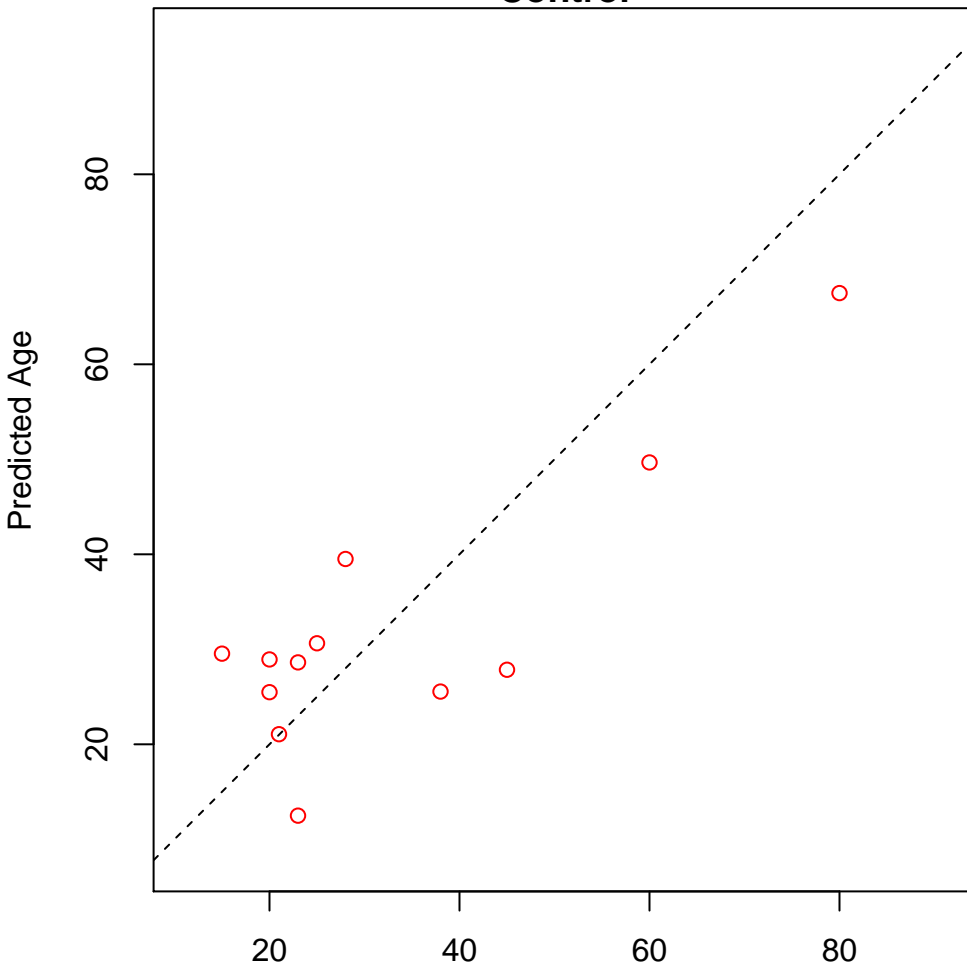
Test



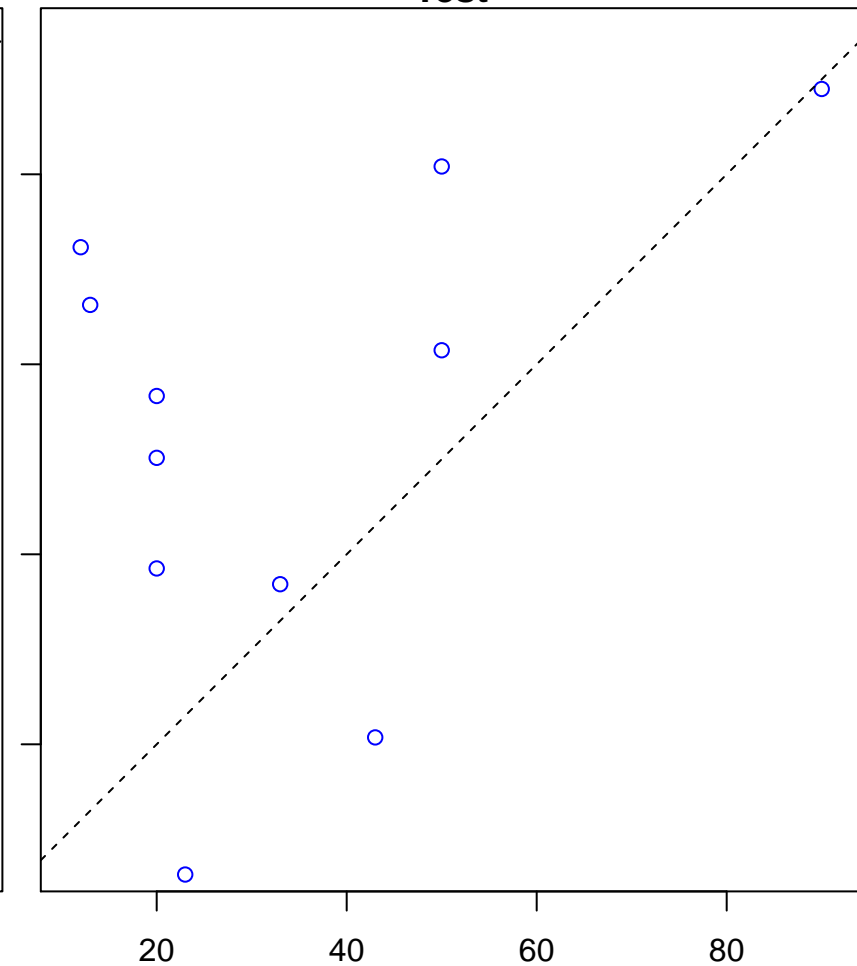
Actual Age

response to exogenous dsRNA (Score: 13.989314)

Control

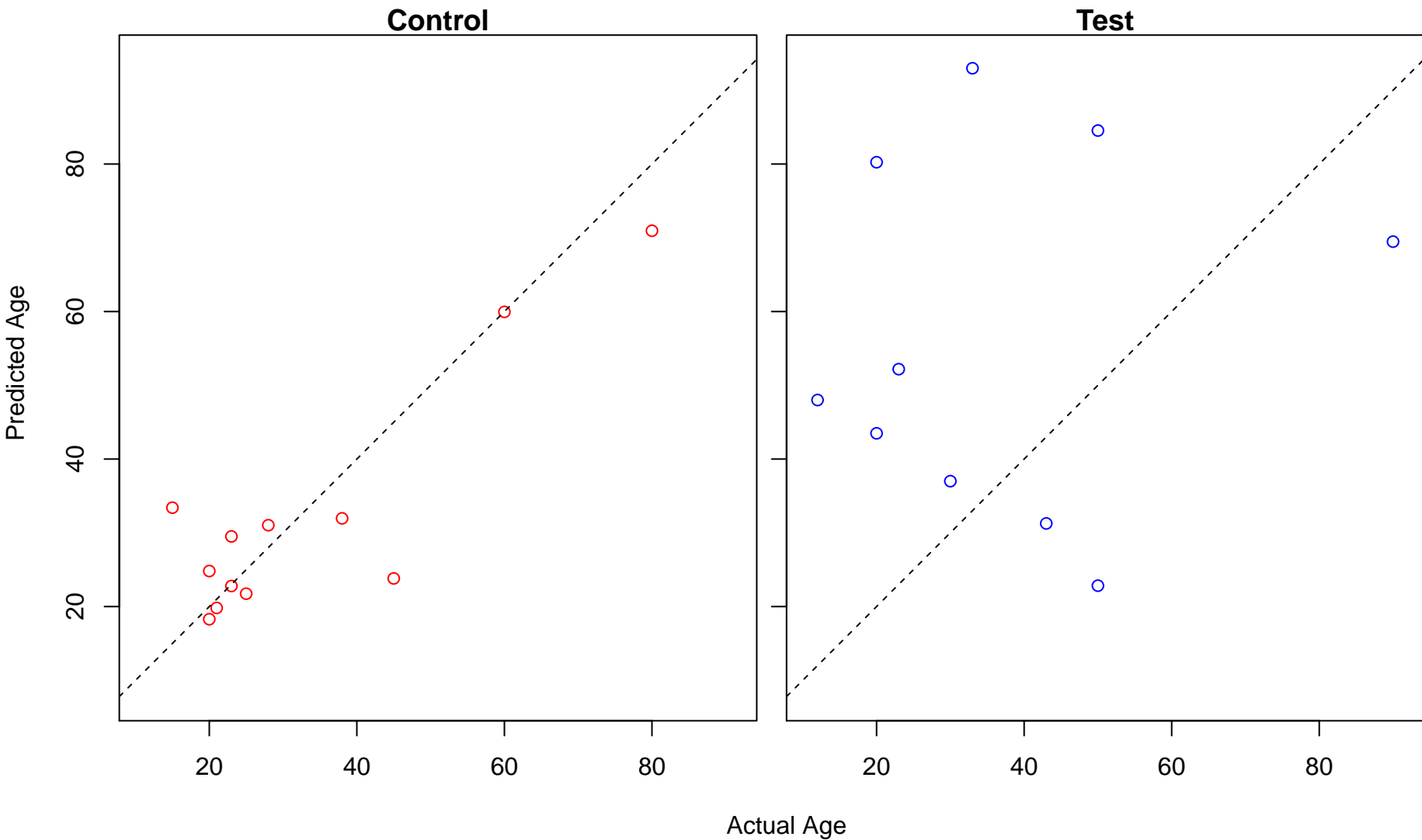


Test

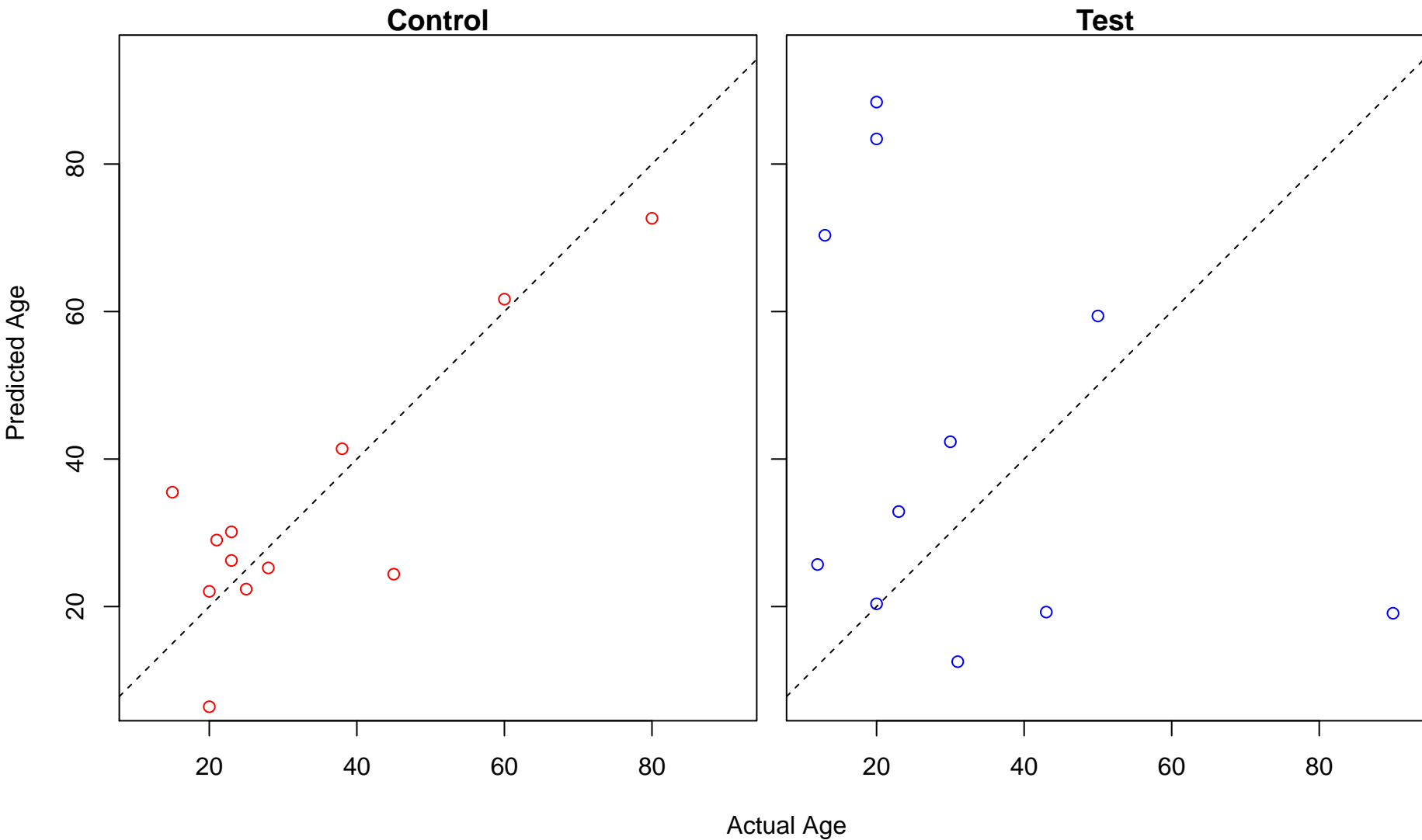


Actual Age

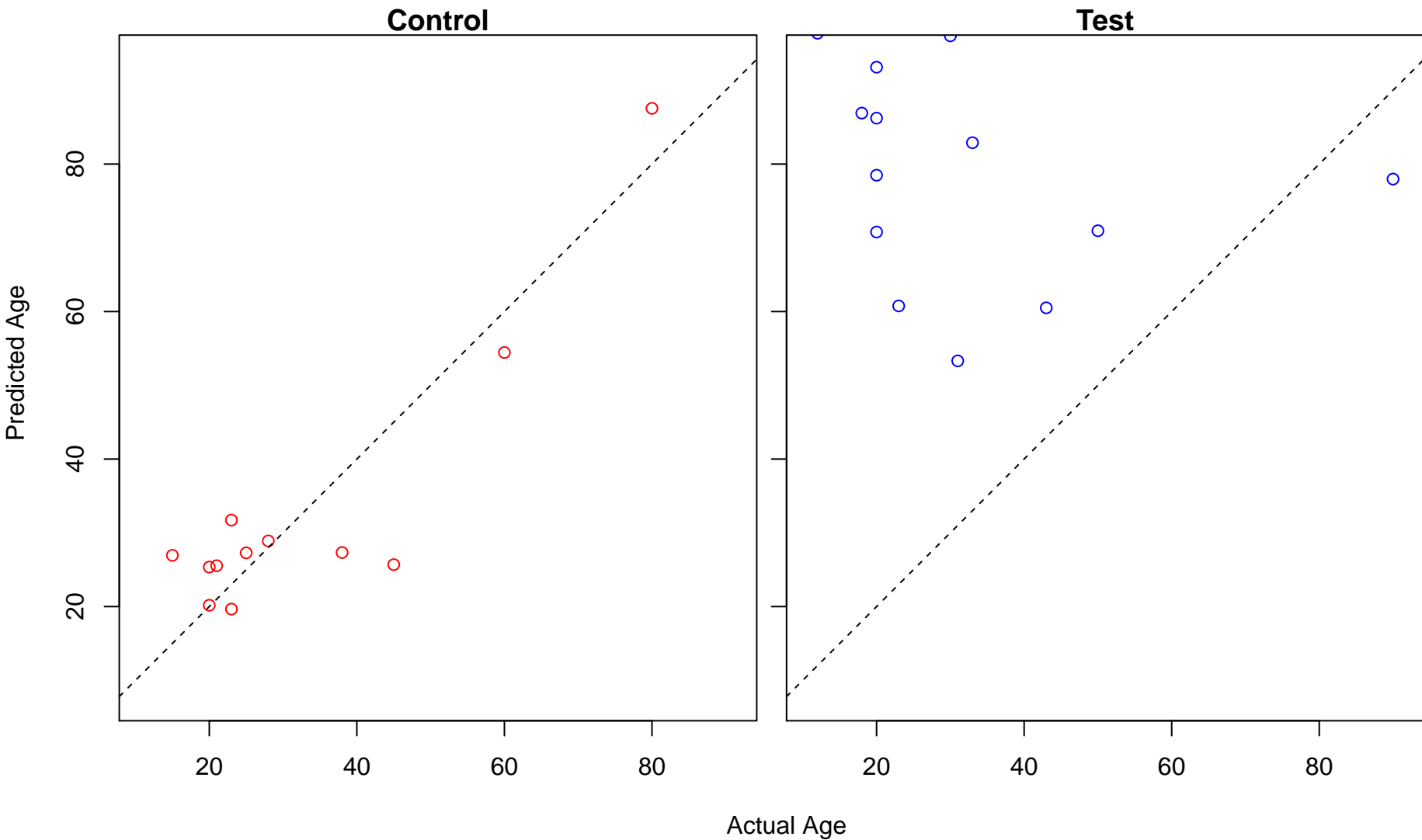
regulation of chromatin organization (Score: 13.977487)



regulation of metal ion transport (Score: 13.943379)

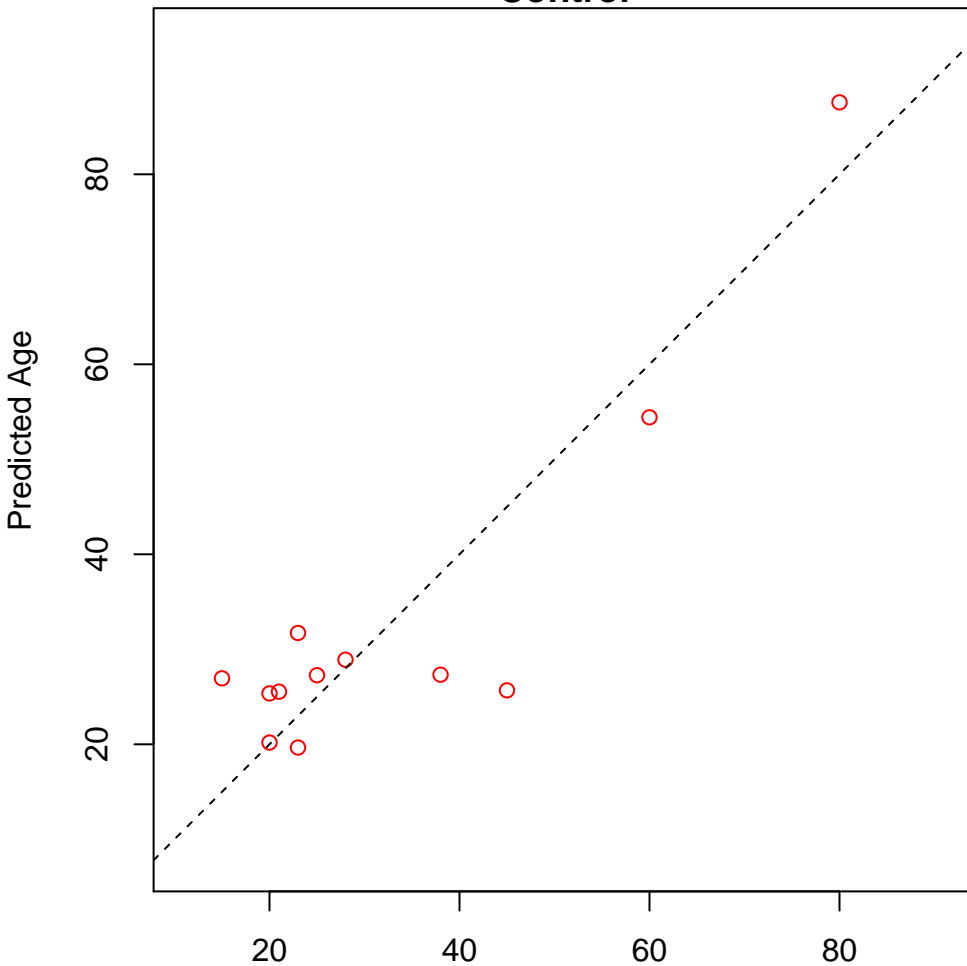


endothelial tube morphogenesis (Score: 13.941556)

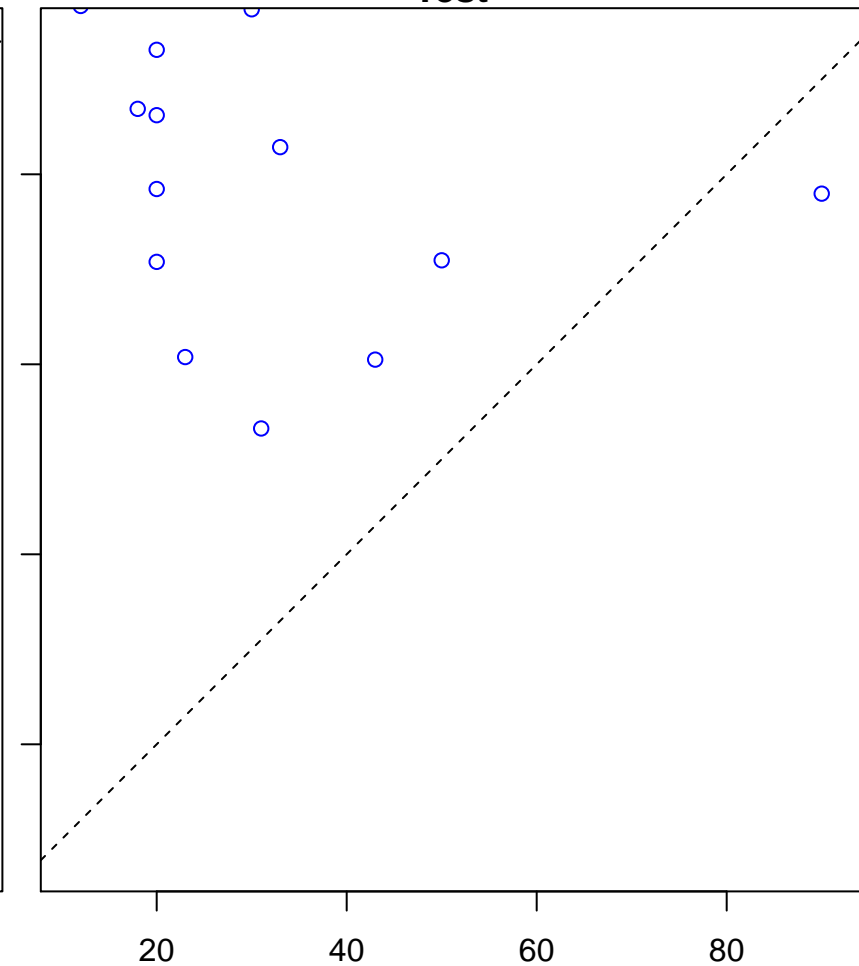


morphogenesis of an endothelium (Score: 13.922453)

Control



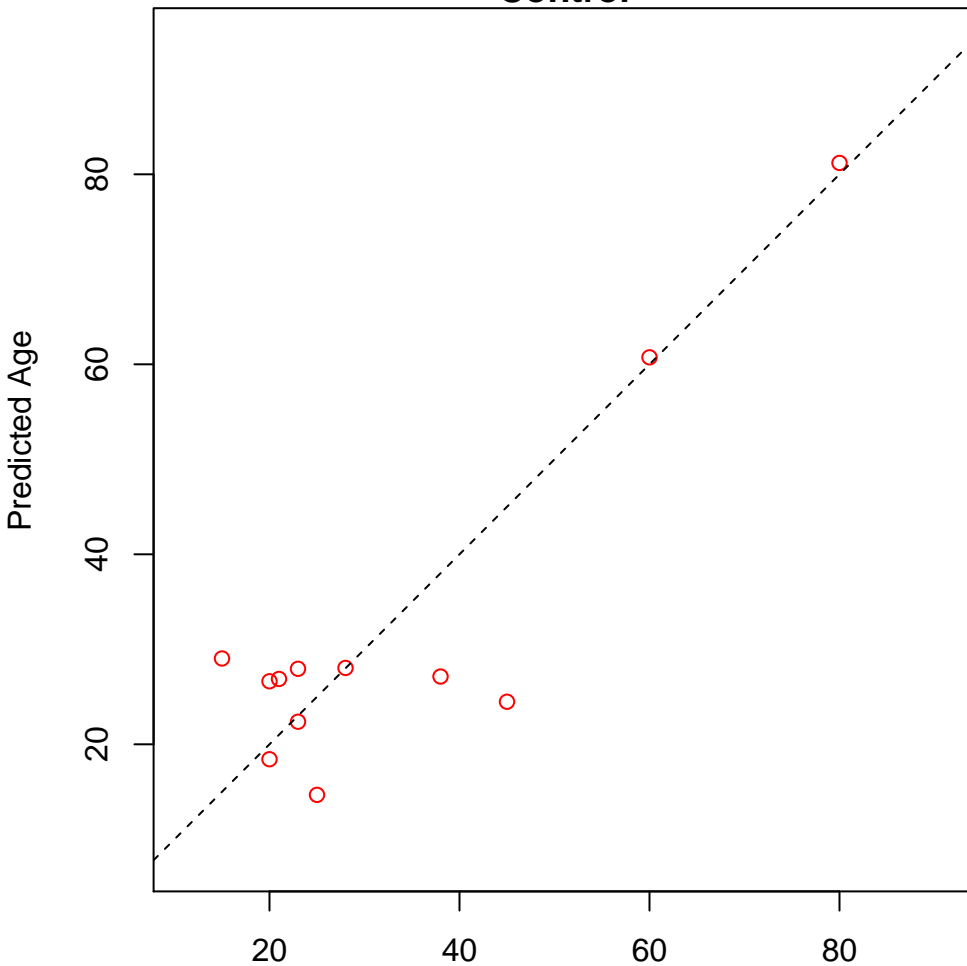
Test



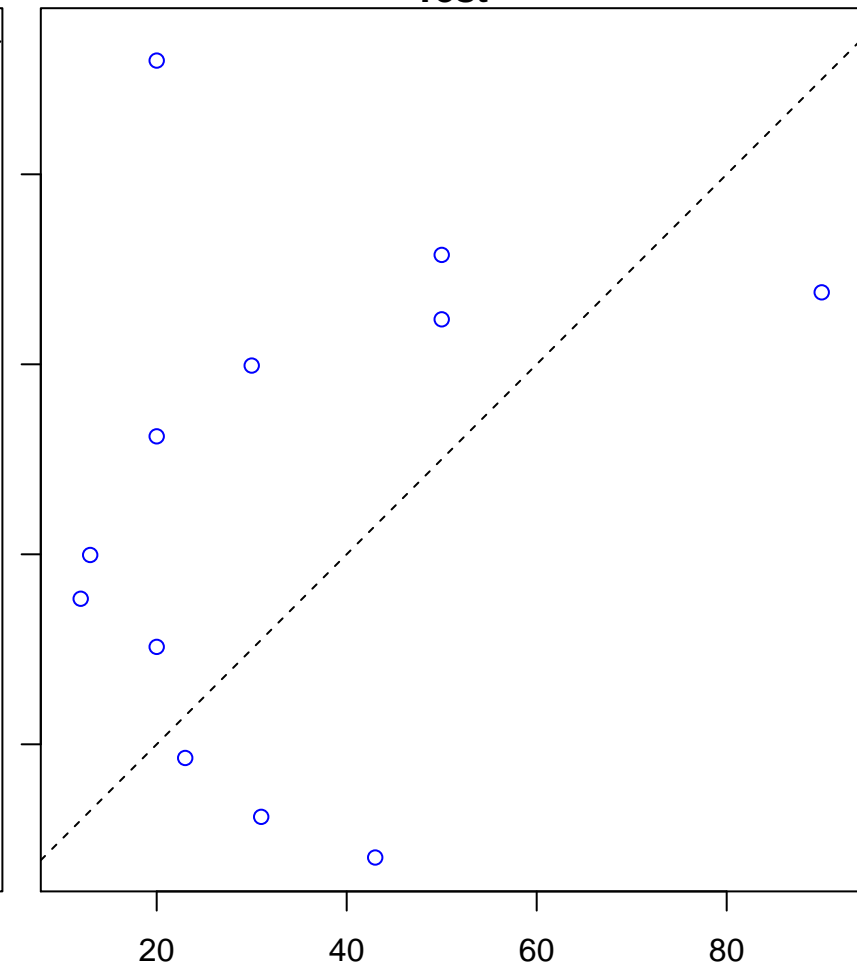
Actual Age

nuclear chromosome segregation (Score: 13.914294)

Control

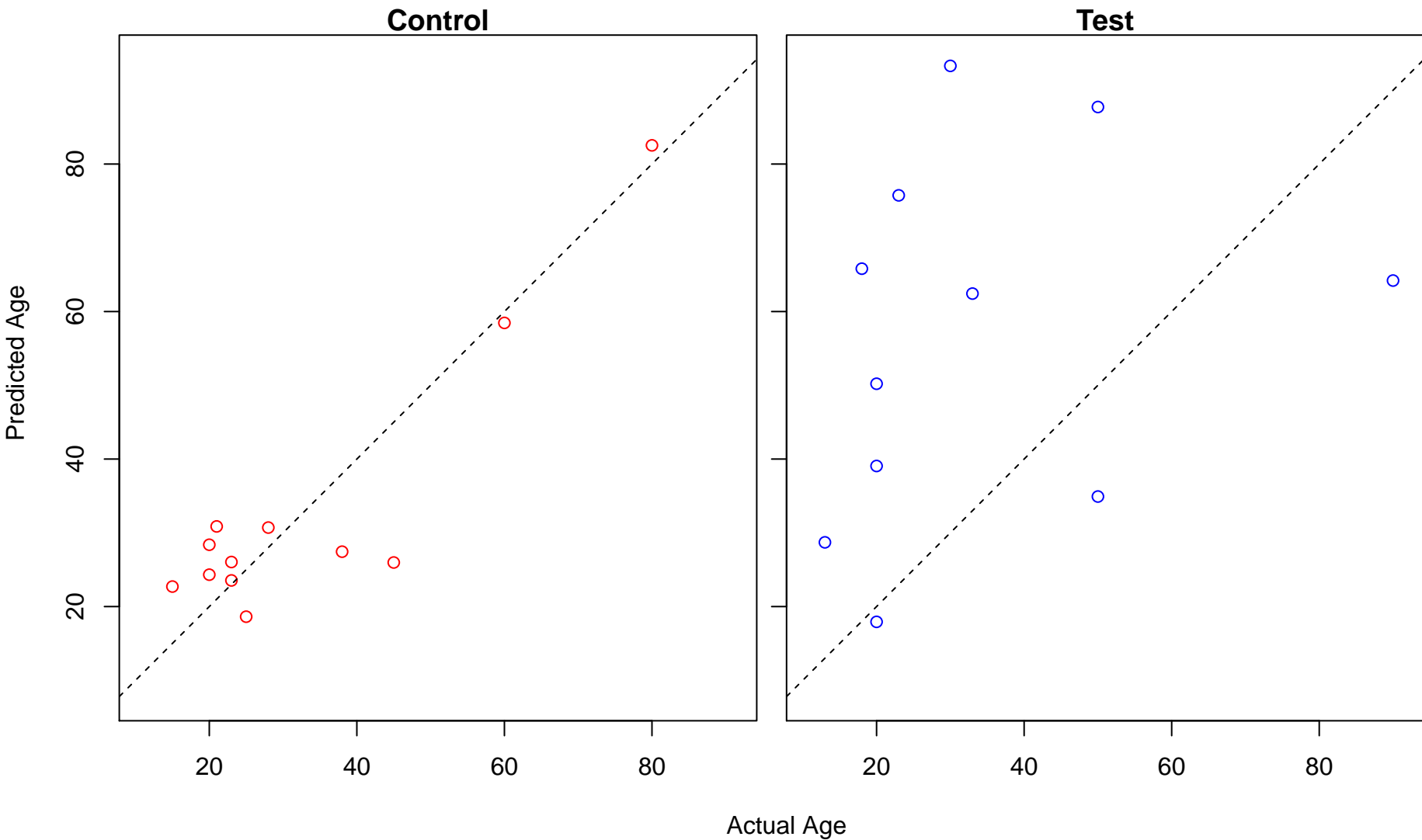


Test

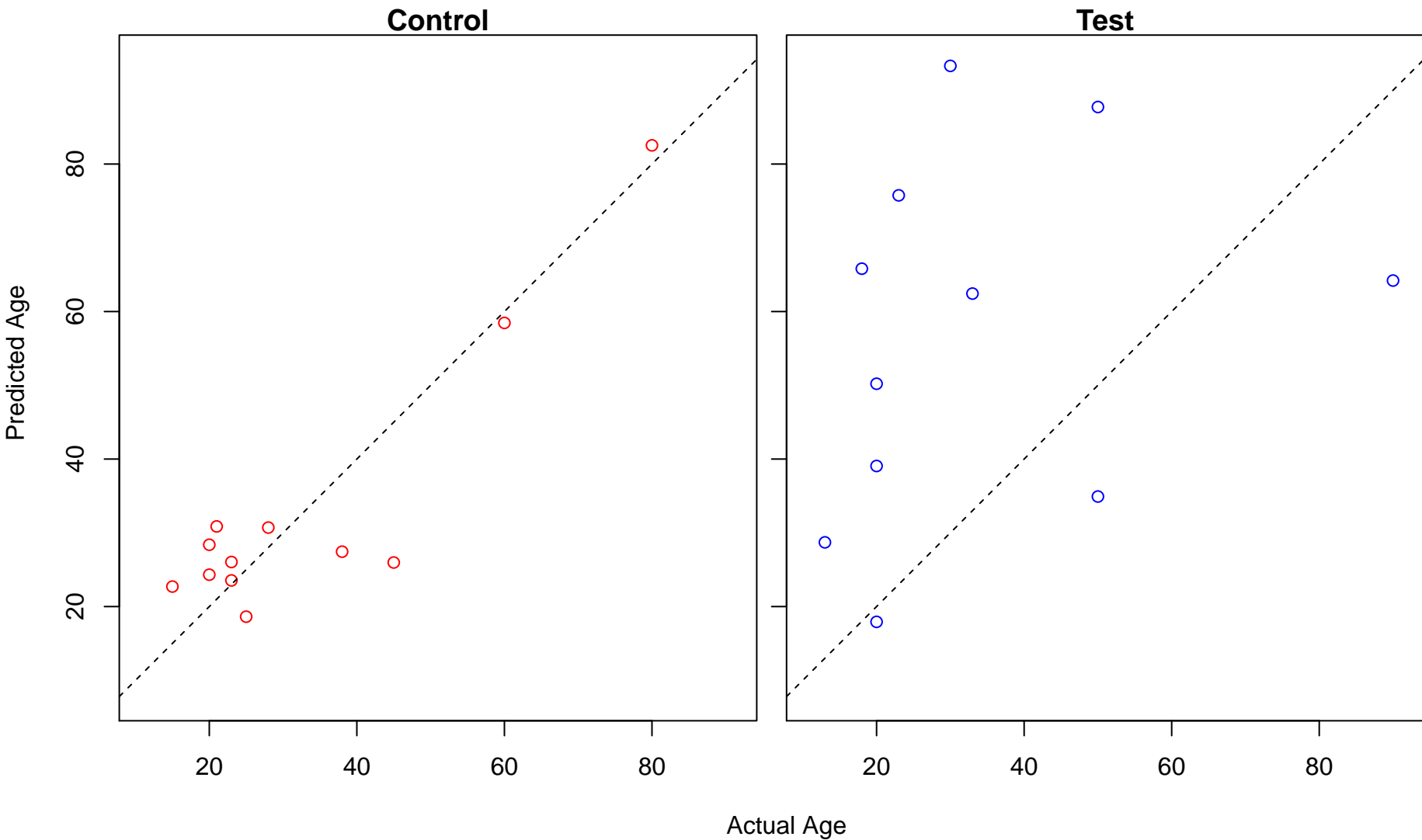


Actual Age

regulation of transposition (Score: 13.899935)

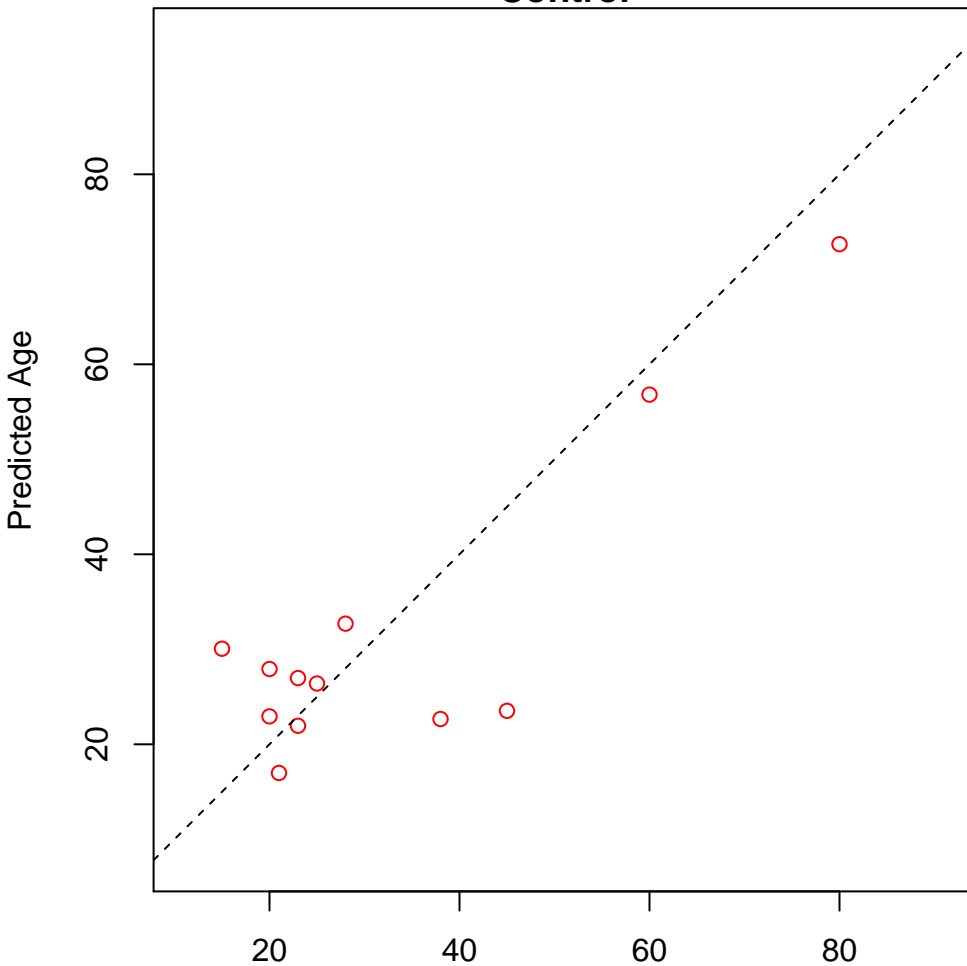


negative regulation of transposition (Score: 13.899935)

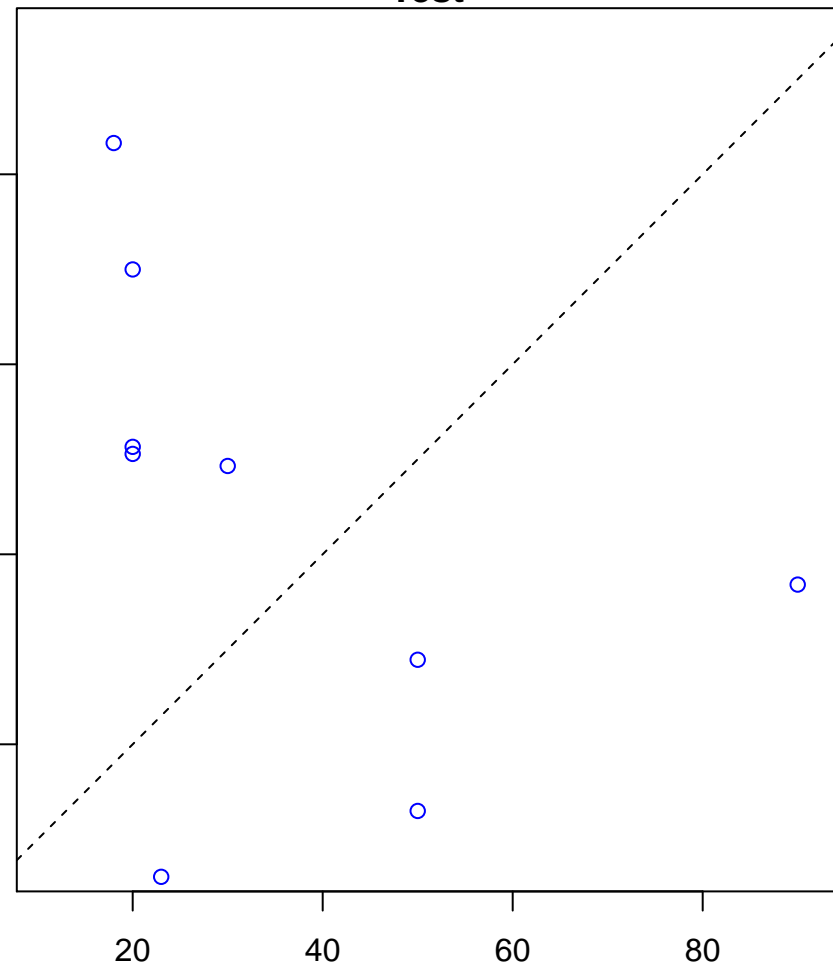


protein K48-linked deubiquitination (Score: 13.895916)

Control

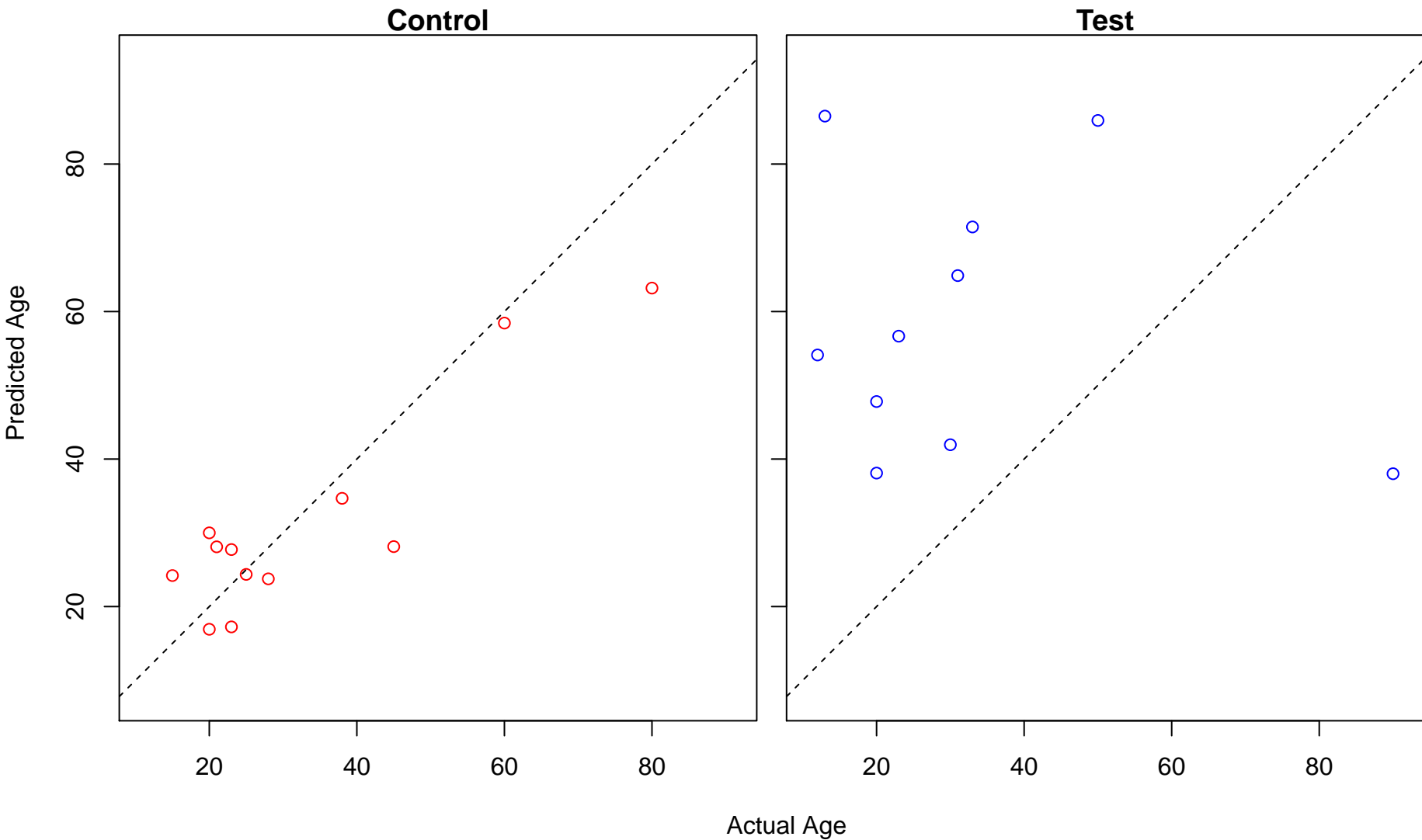


Test

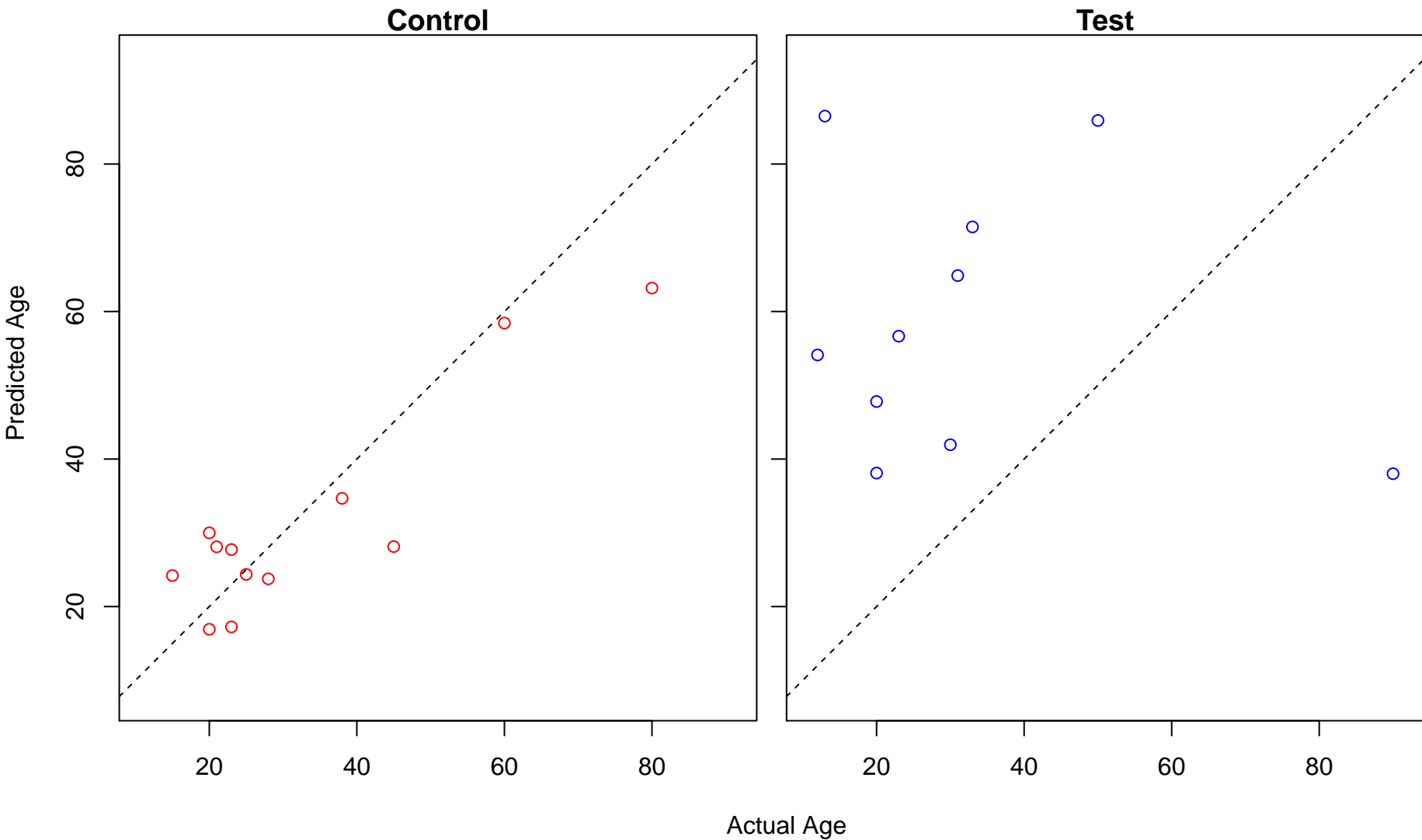


Actual Age

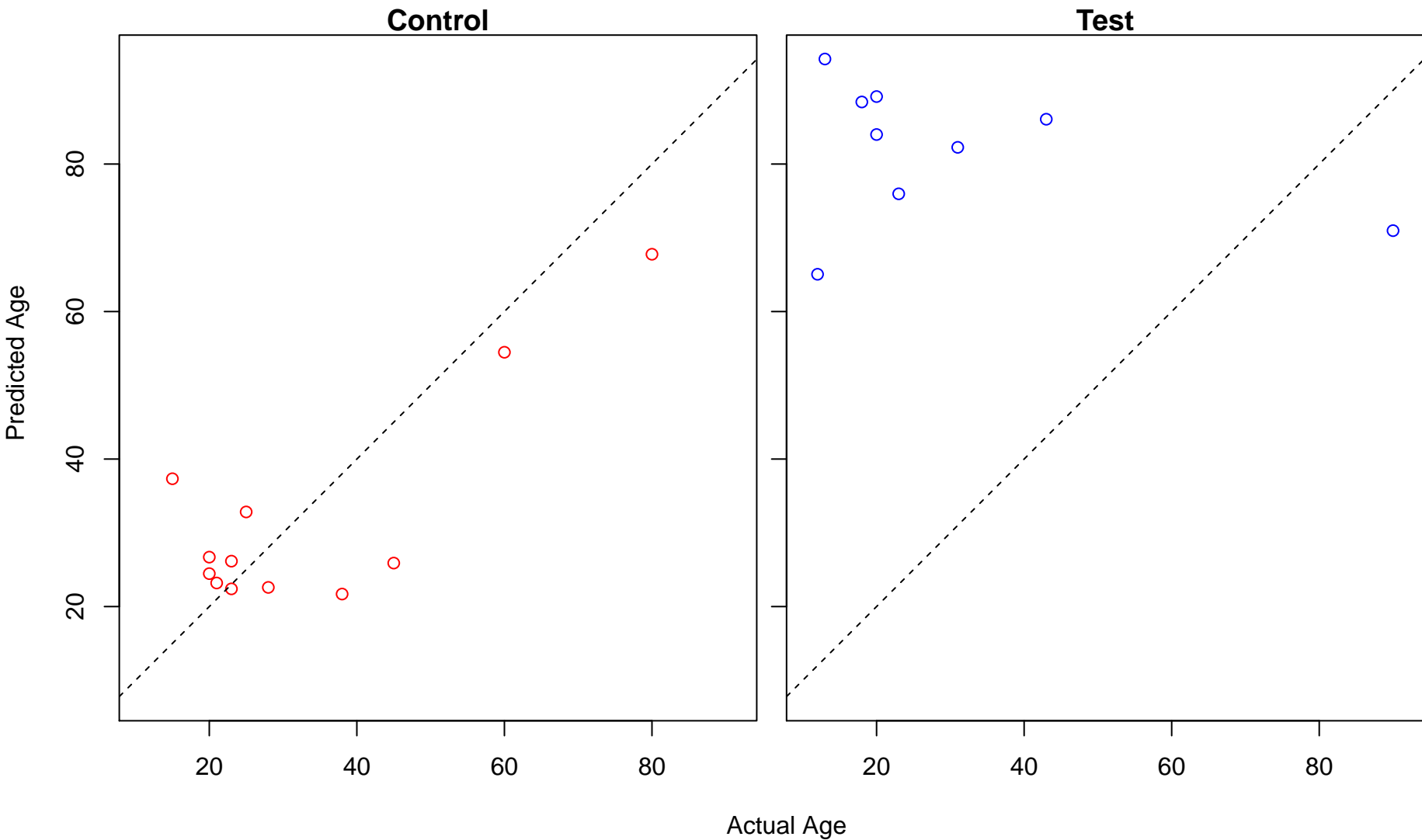
response to epinephrine (Score: 13.884023)



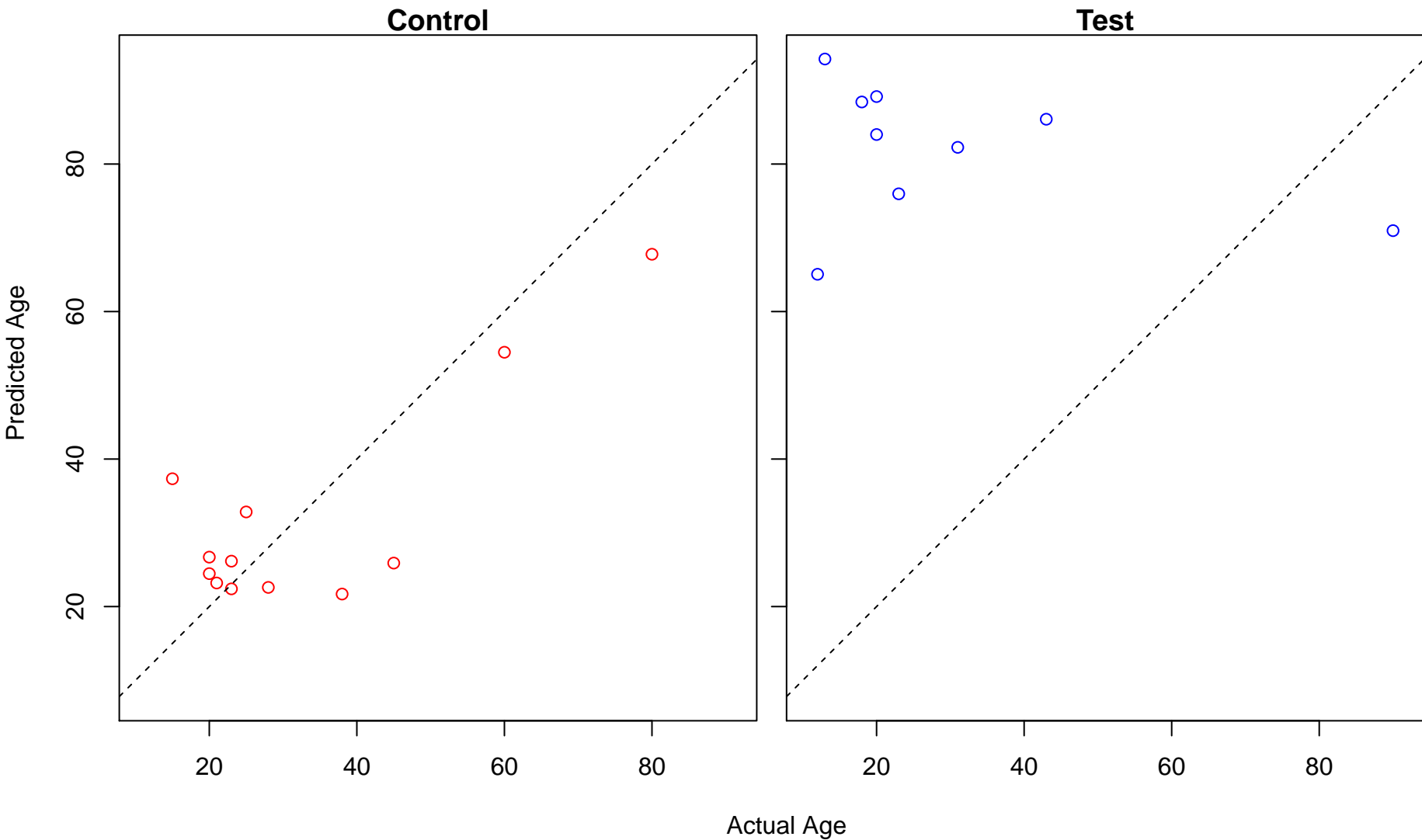
cellular response to epinephrine stimulus (Score: 13.884023)



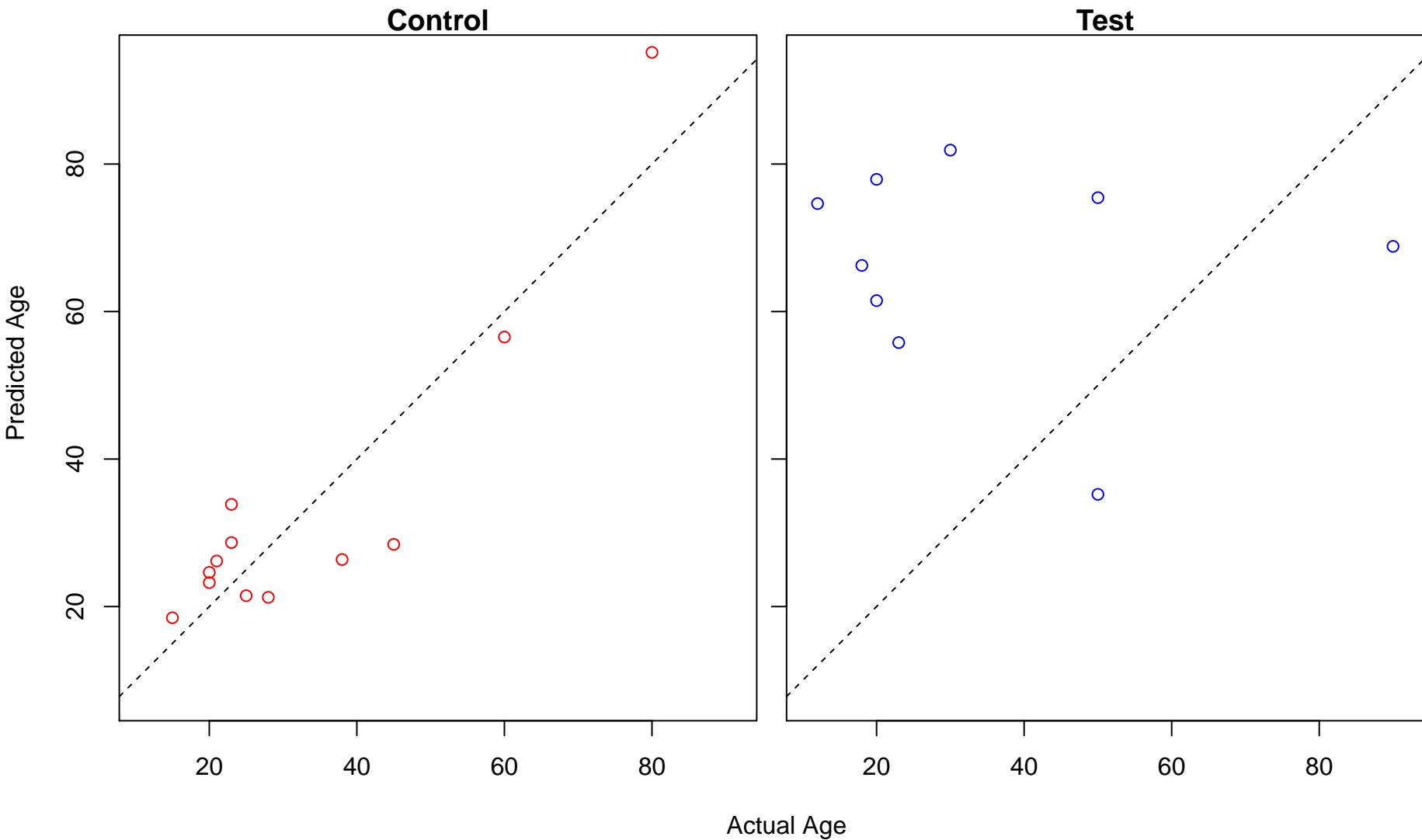
protein localization to extracellular region (Score: 13.866477)



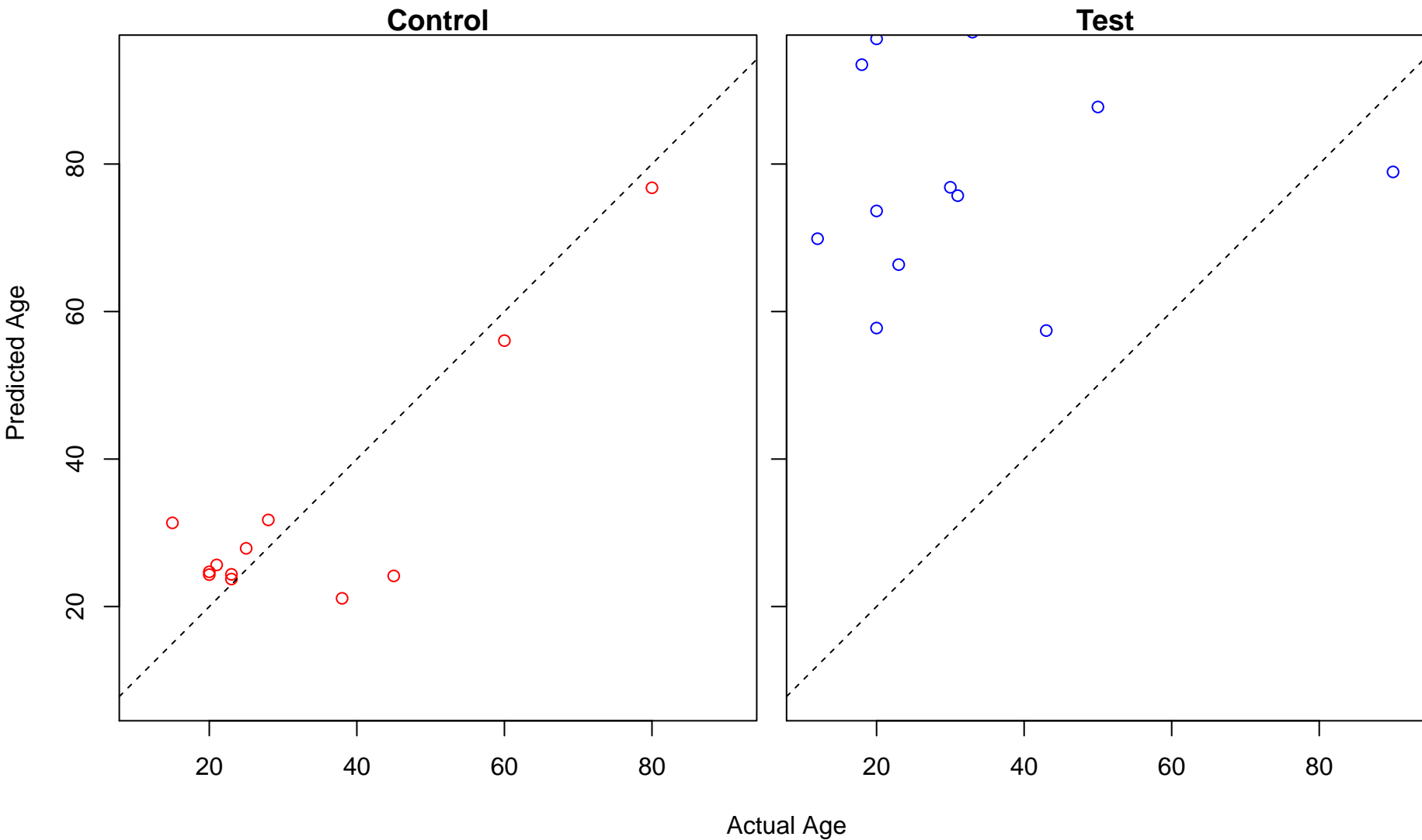
maintenance of protein location in extracellular region (Score: 13.866477)



peptidyl-arginine methylation (Score: 13.862809)

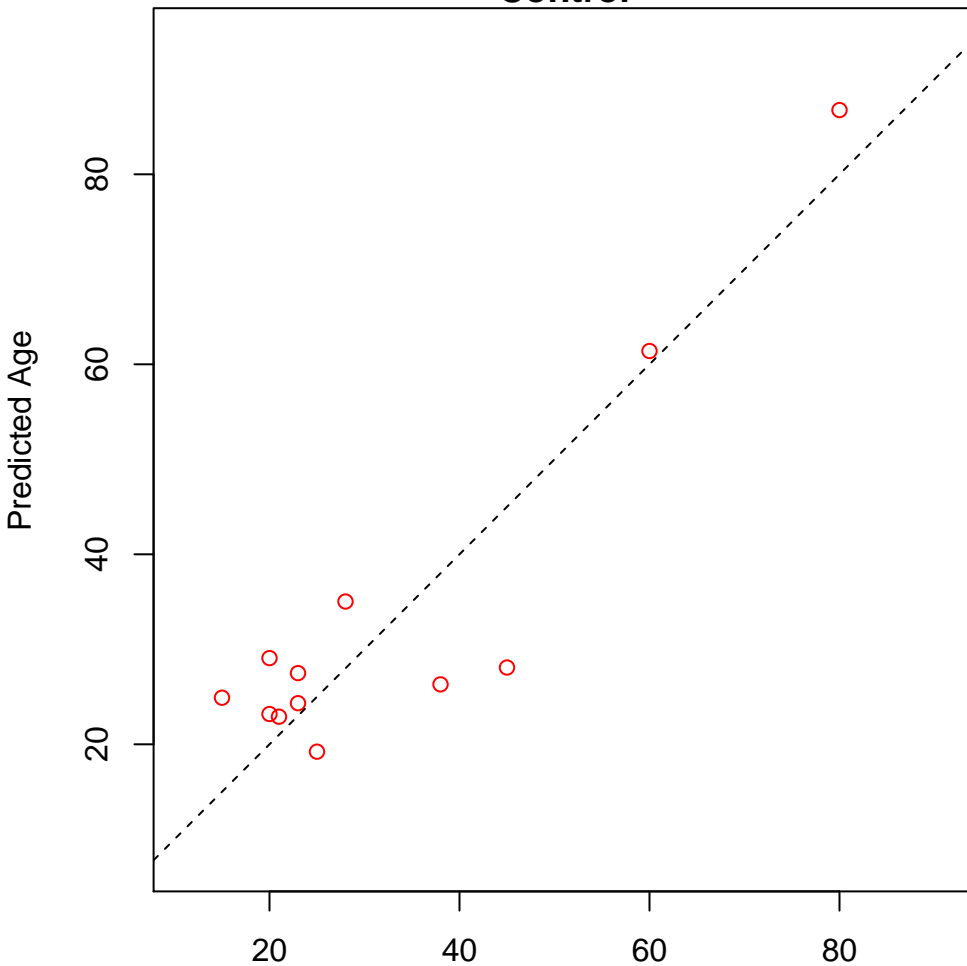


negative regulation of DNA metabolic process (Score: 13.840083)

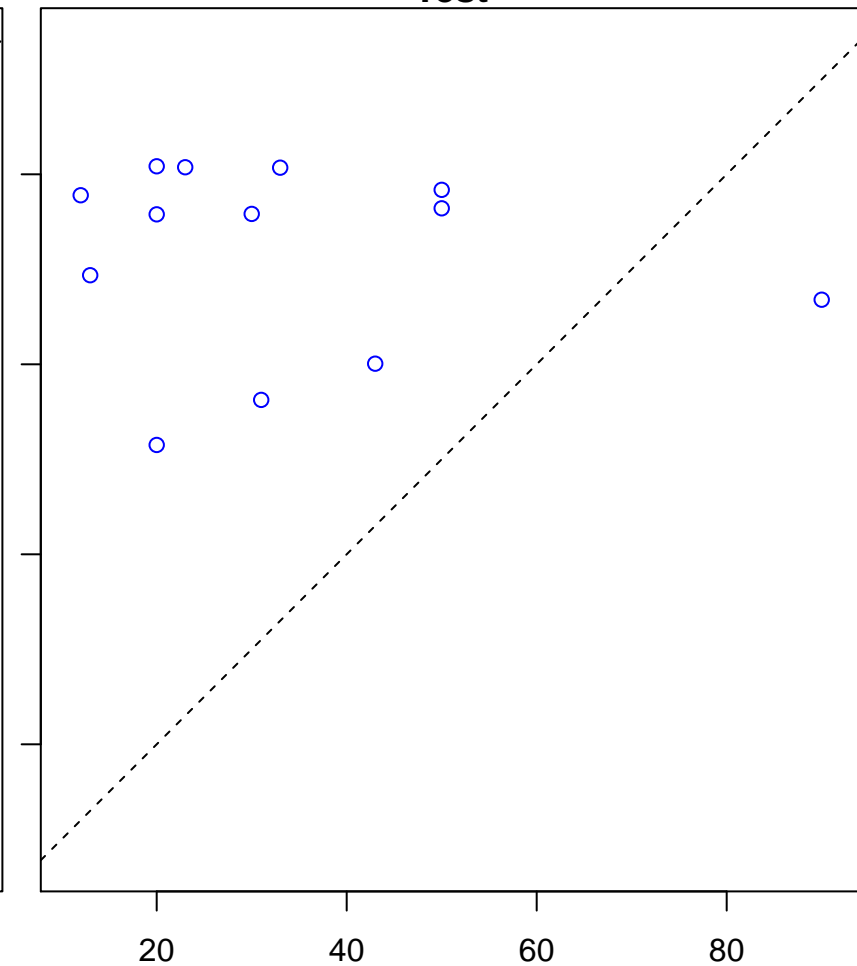


peptidyl-methionine modification (Score: 13.832272)

Control



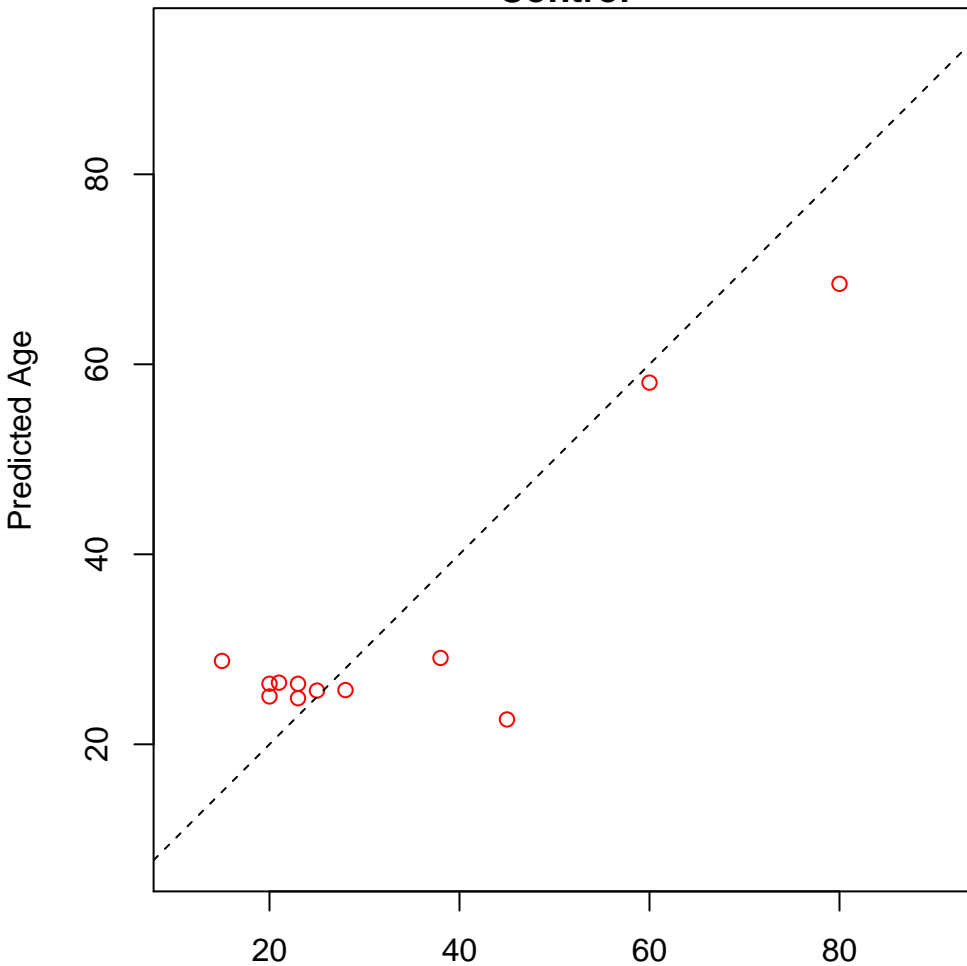
Test



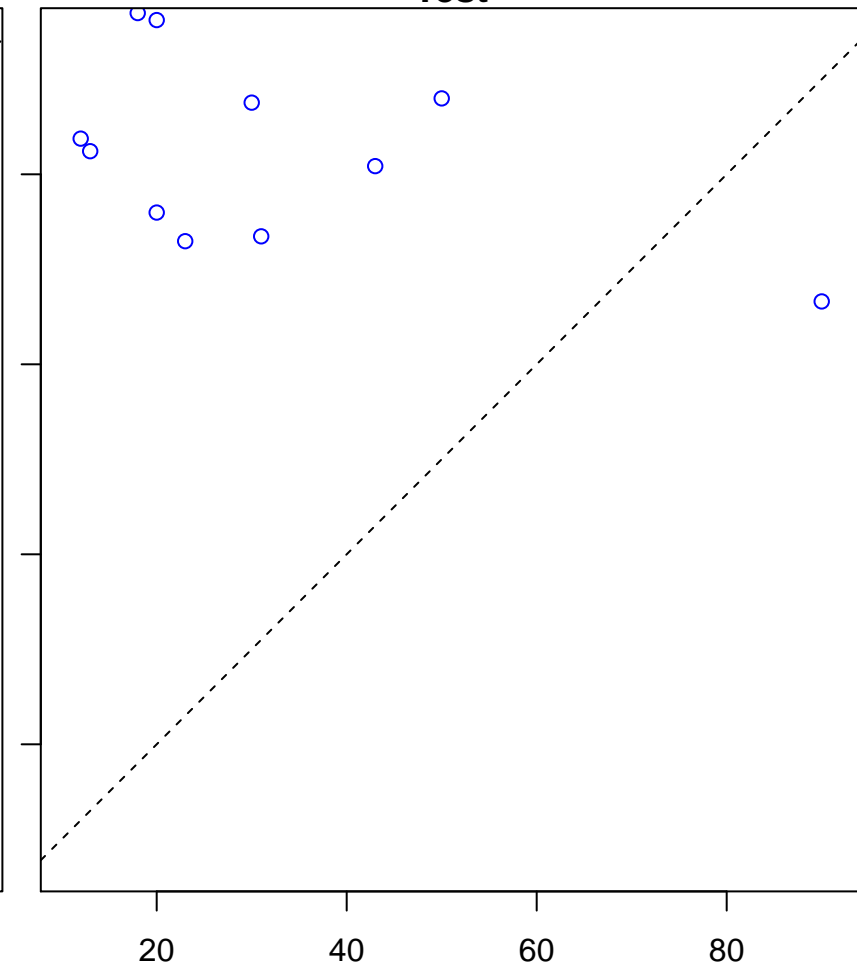
Actual Age

glycosaminoglycan catabolic process (Score: 13.807538)

Control

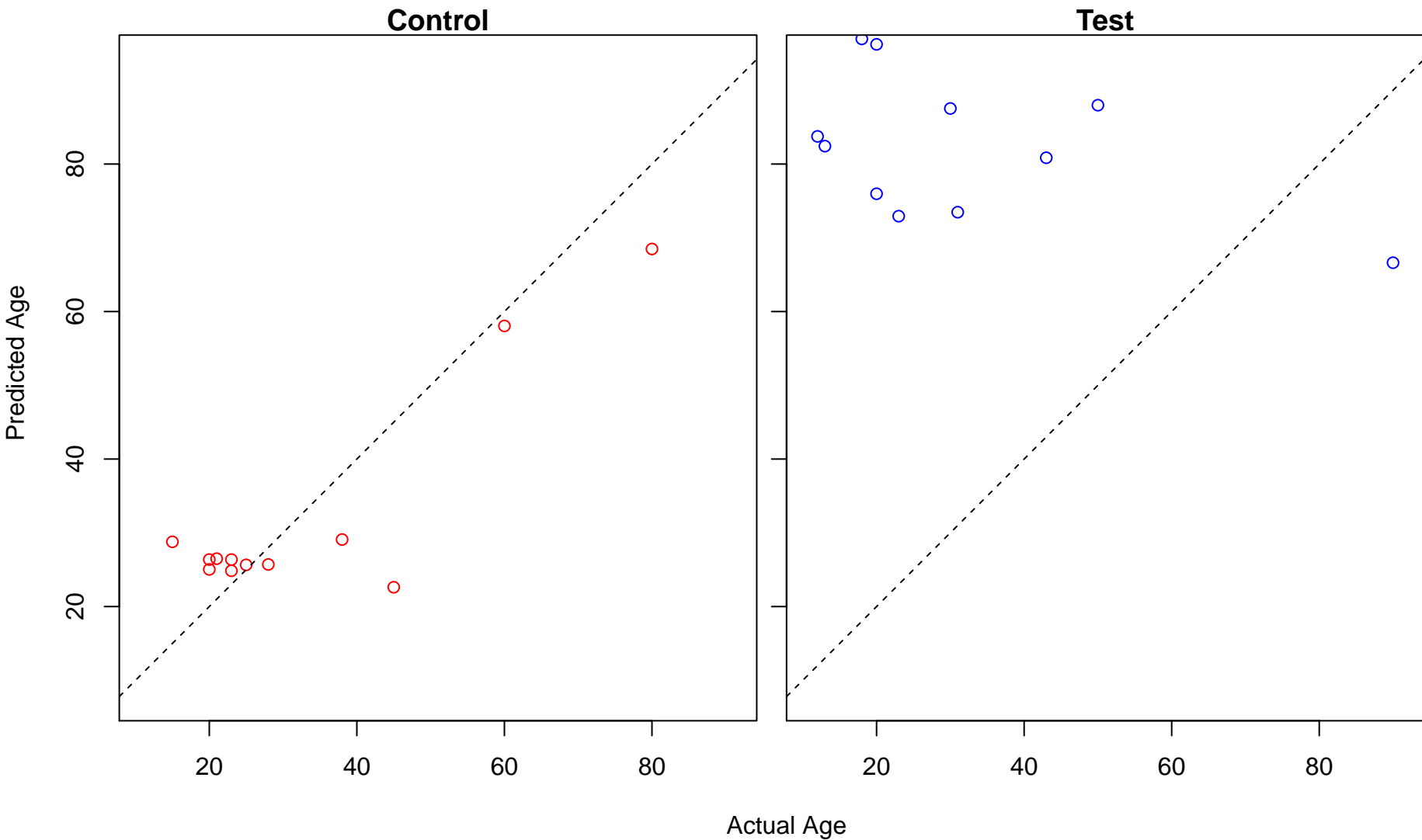


Test

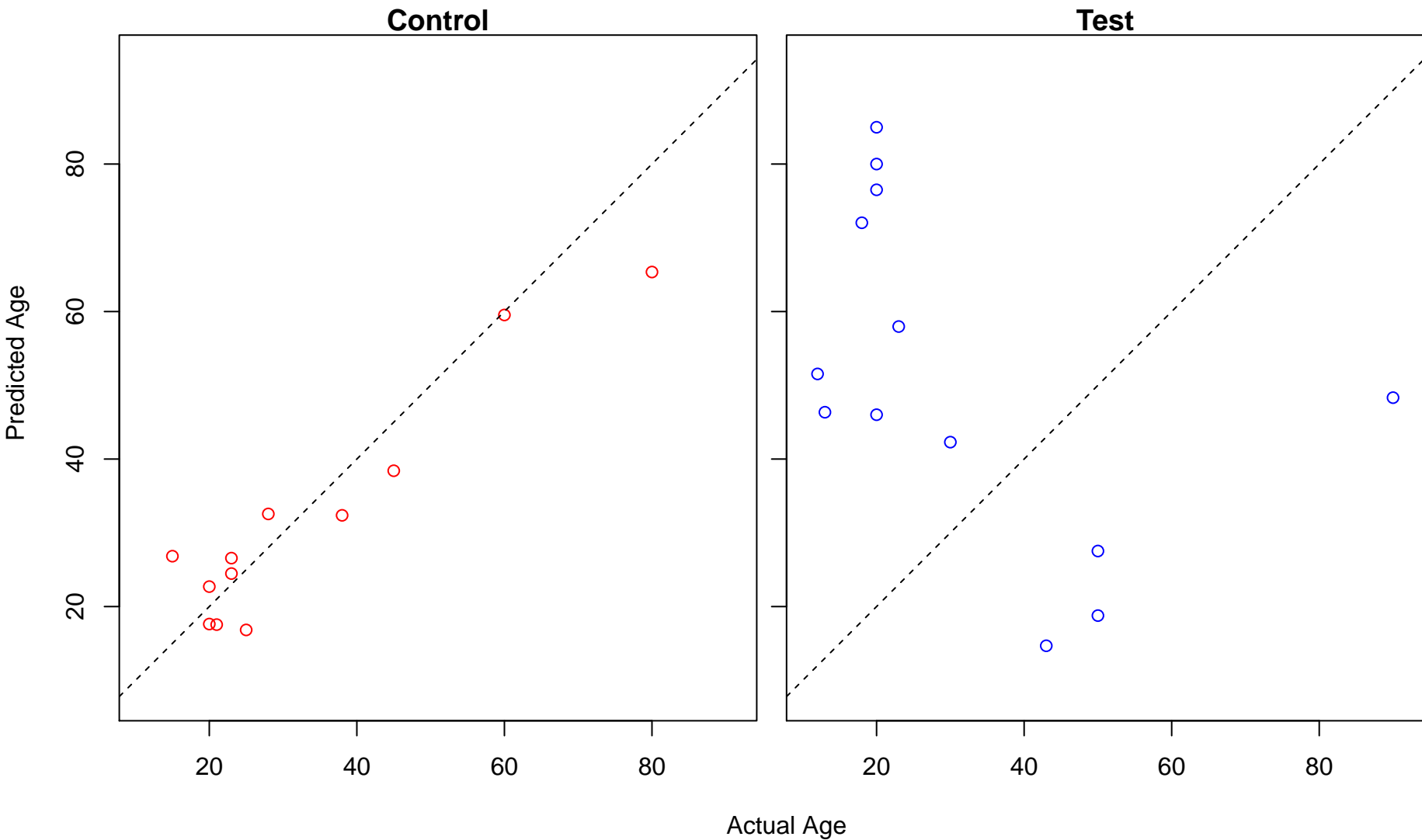


Actual Age

aminoglycan catabolic process (Score: 13.804468)

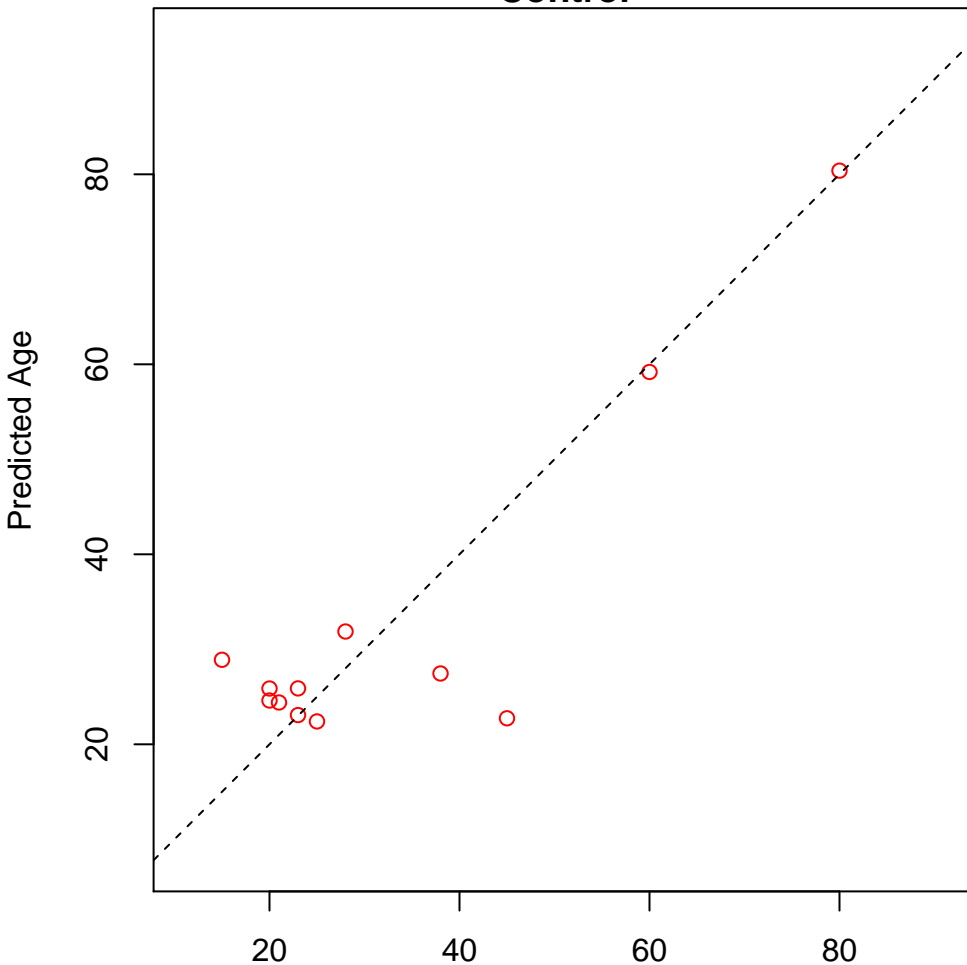


germ cell development (Score: 13.797352)

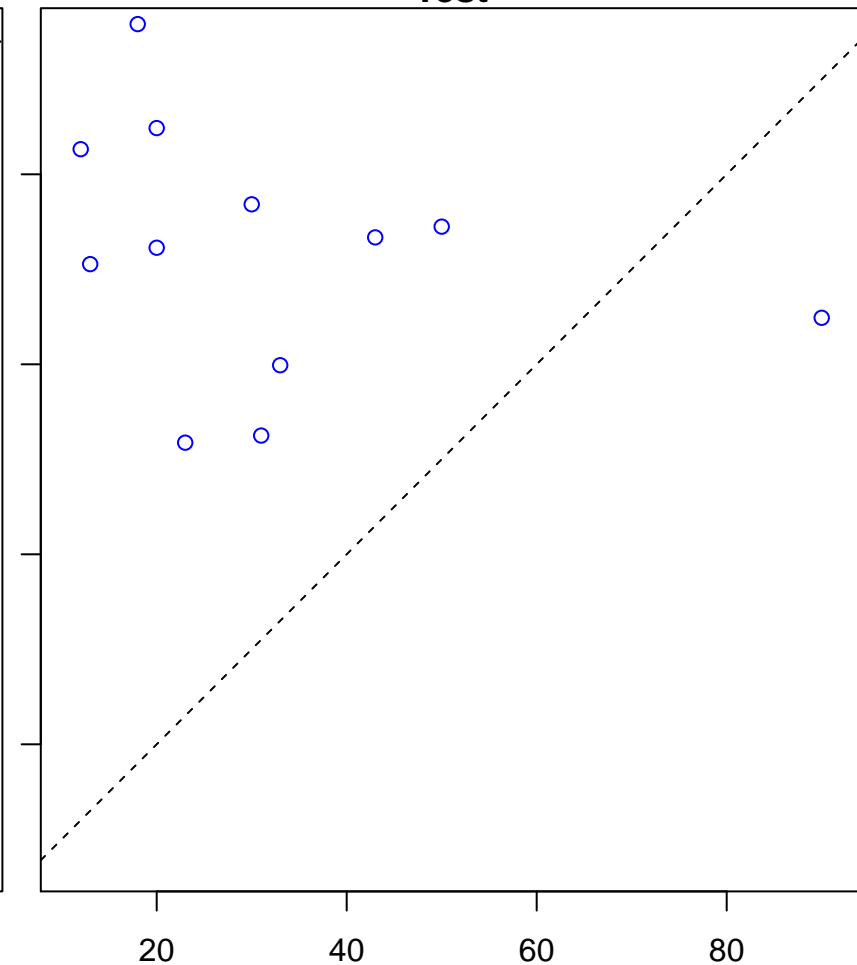


regulation of mitochondrial translation (Score: 13.781578)

Control

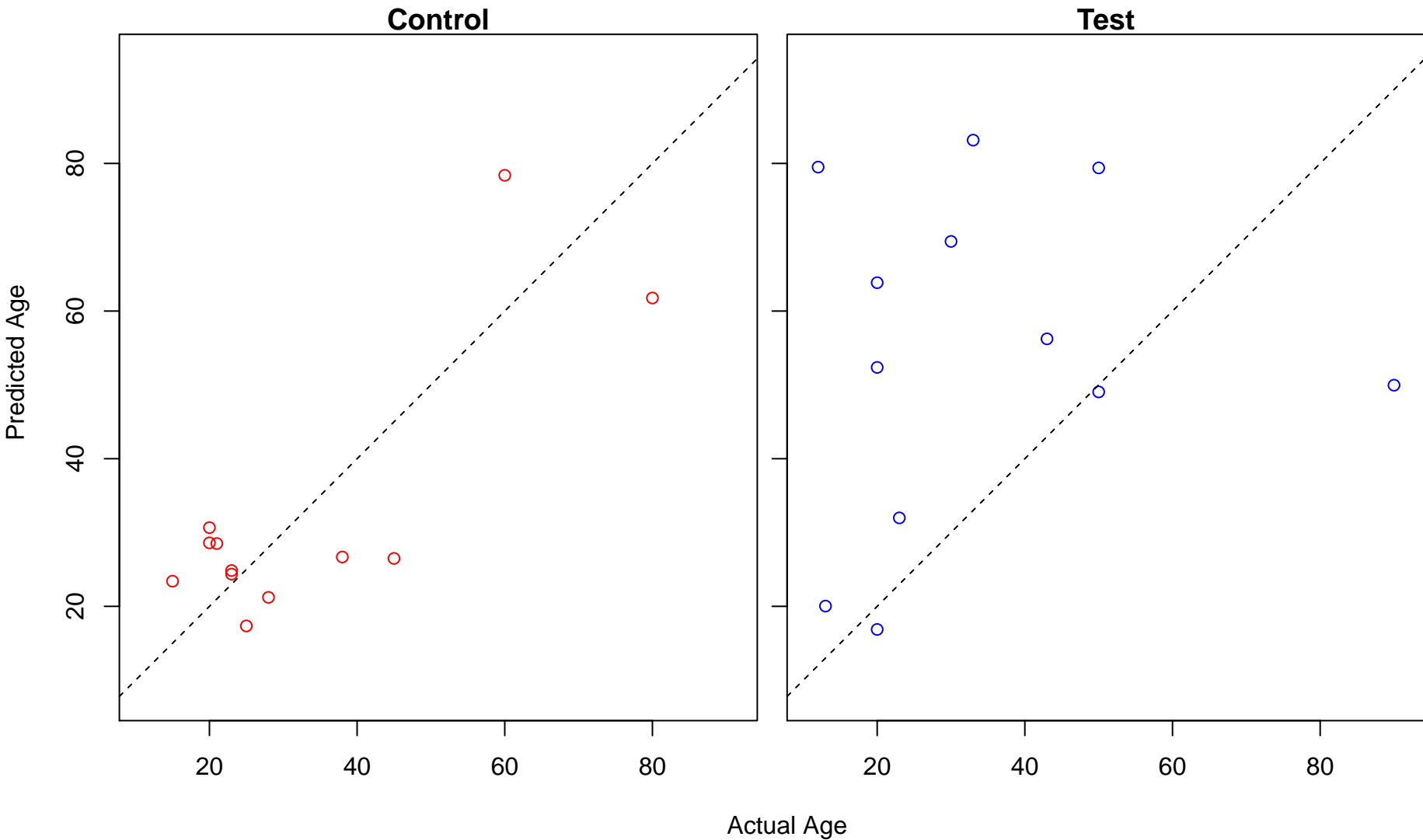


Test

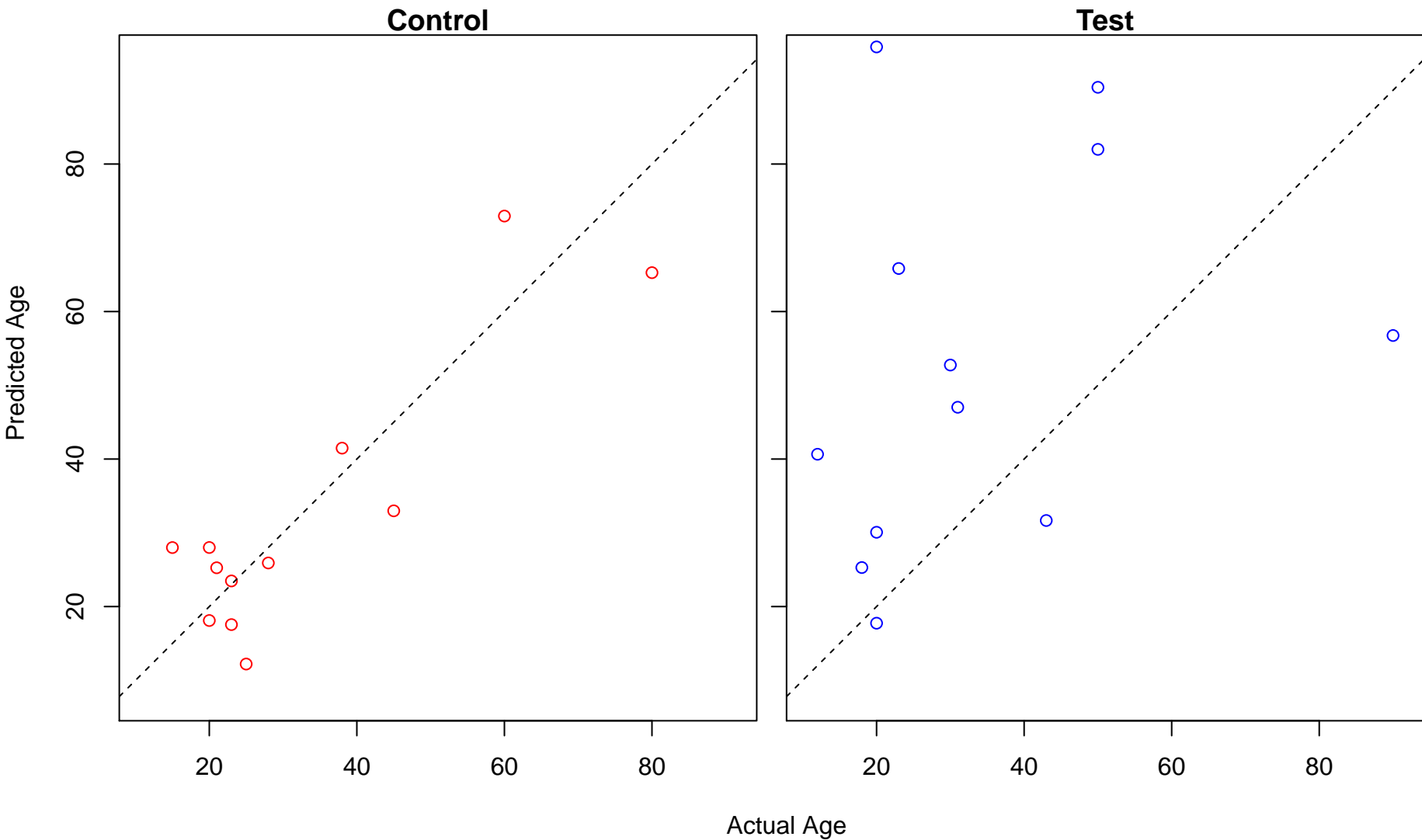


Actual Age

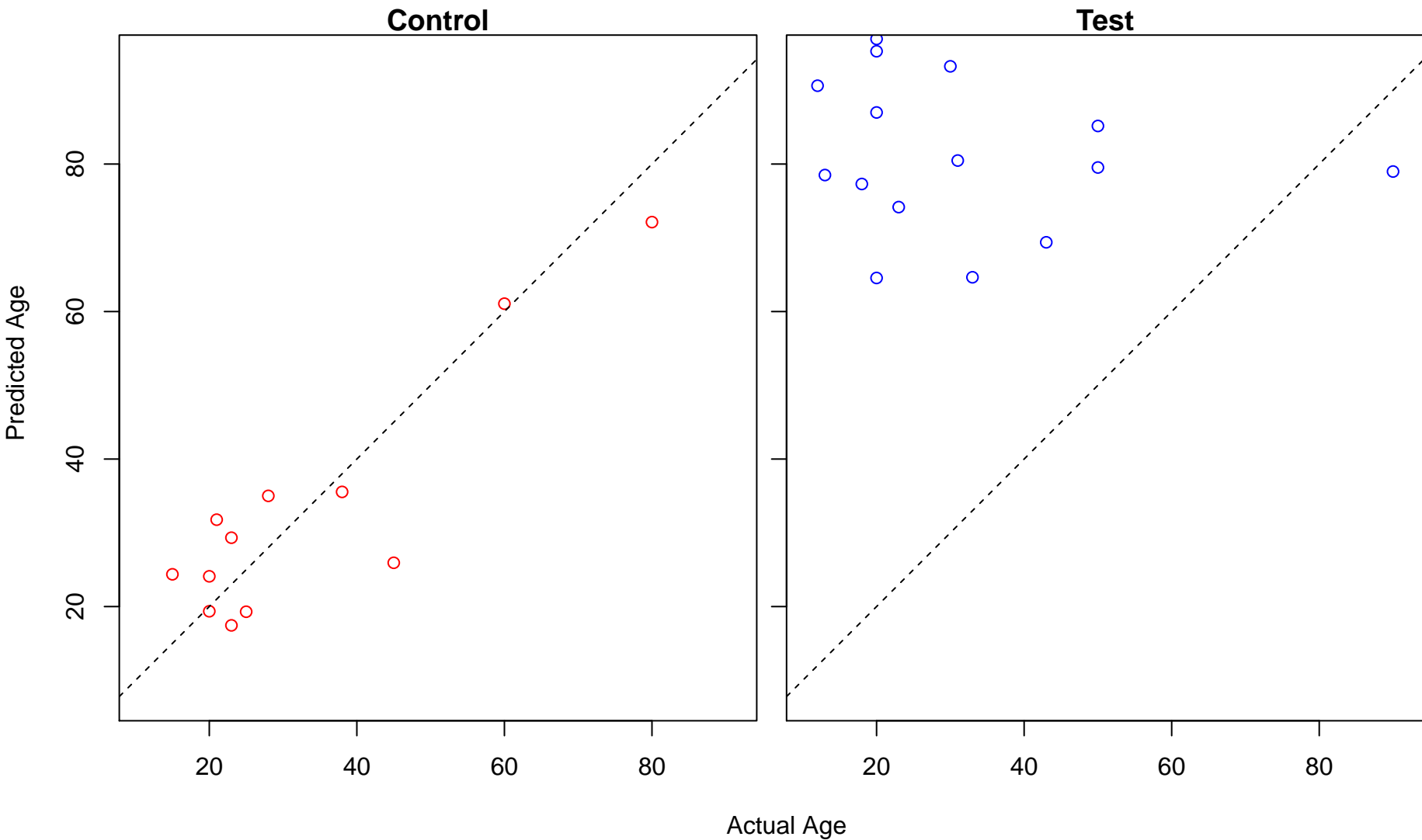
regulation of alcohol biosynthetic process (Score: 13.771753)



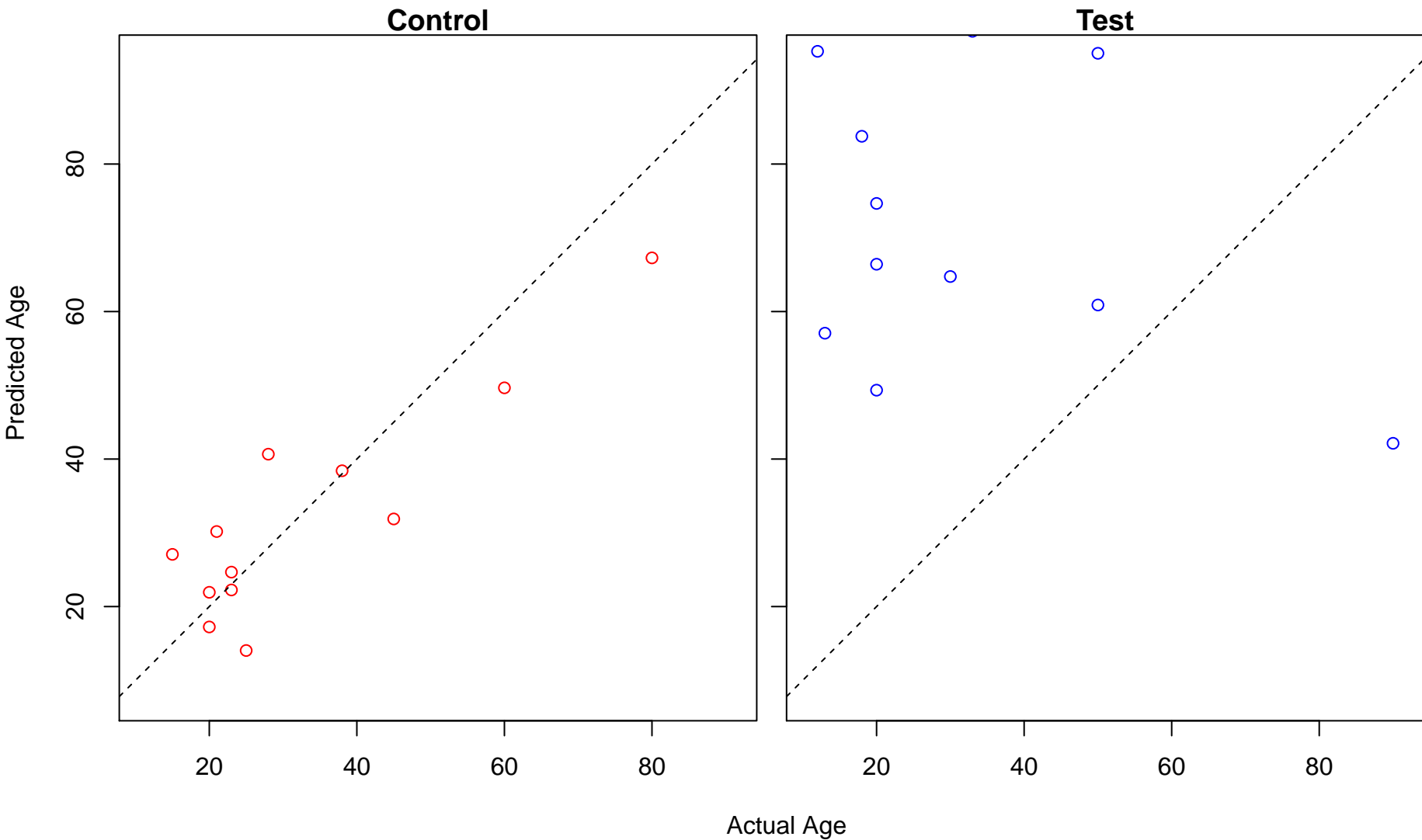
response to antibiotic (Score: 13.764062)



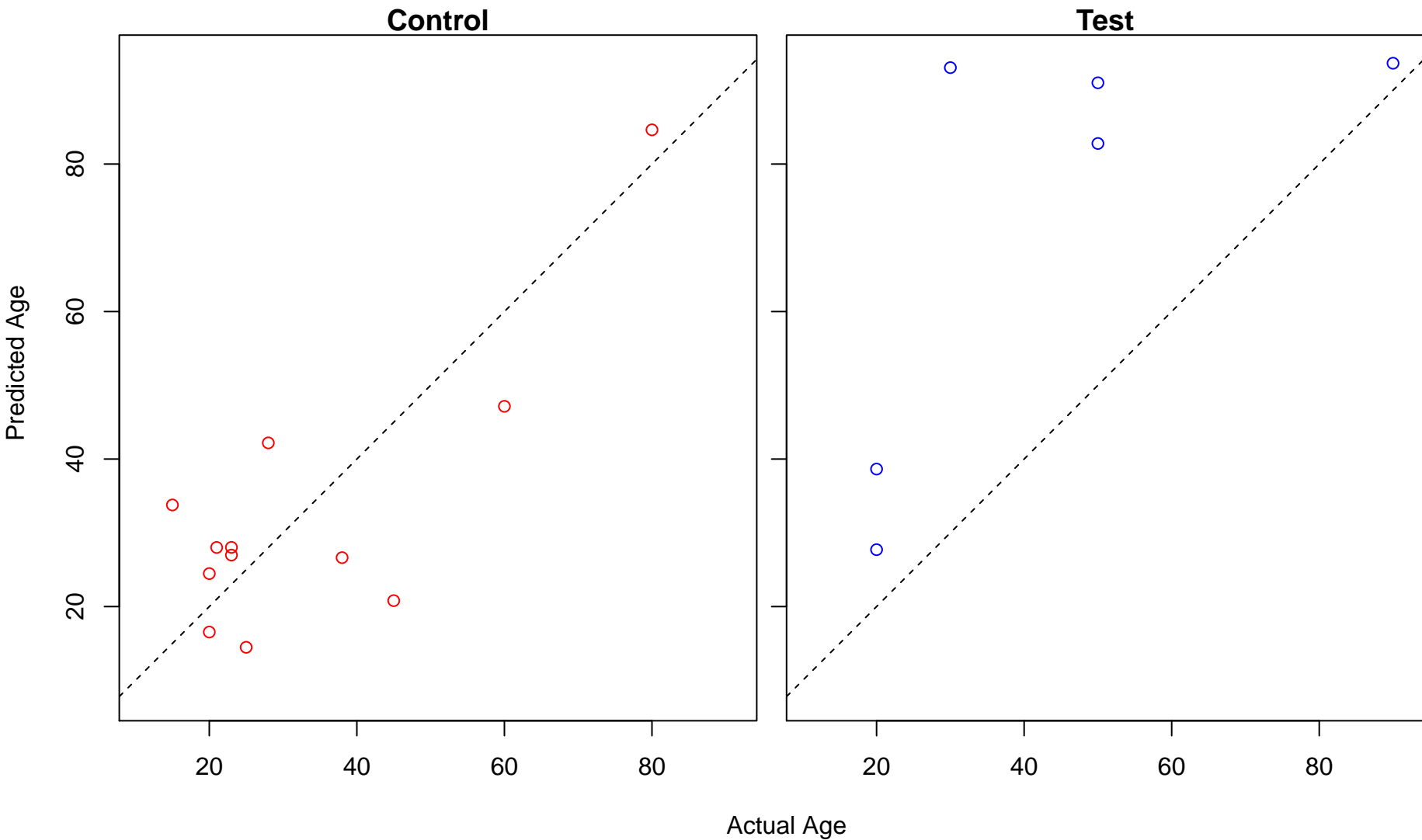
tissue morphogenesis (Score: 13.731871)



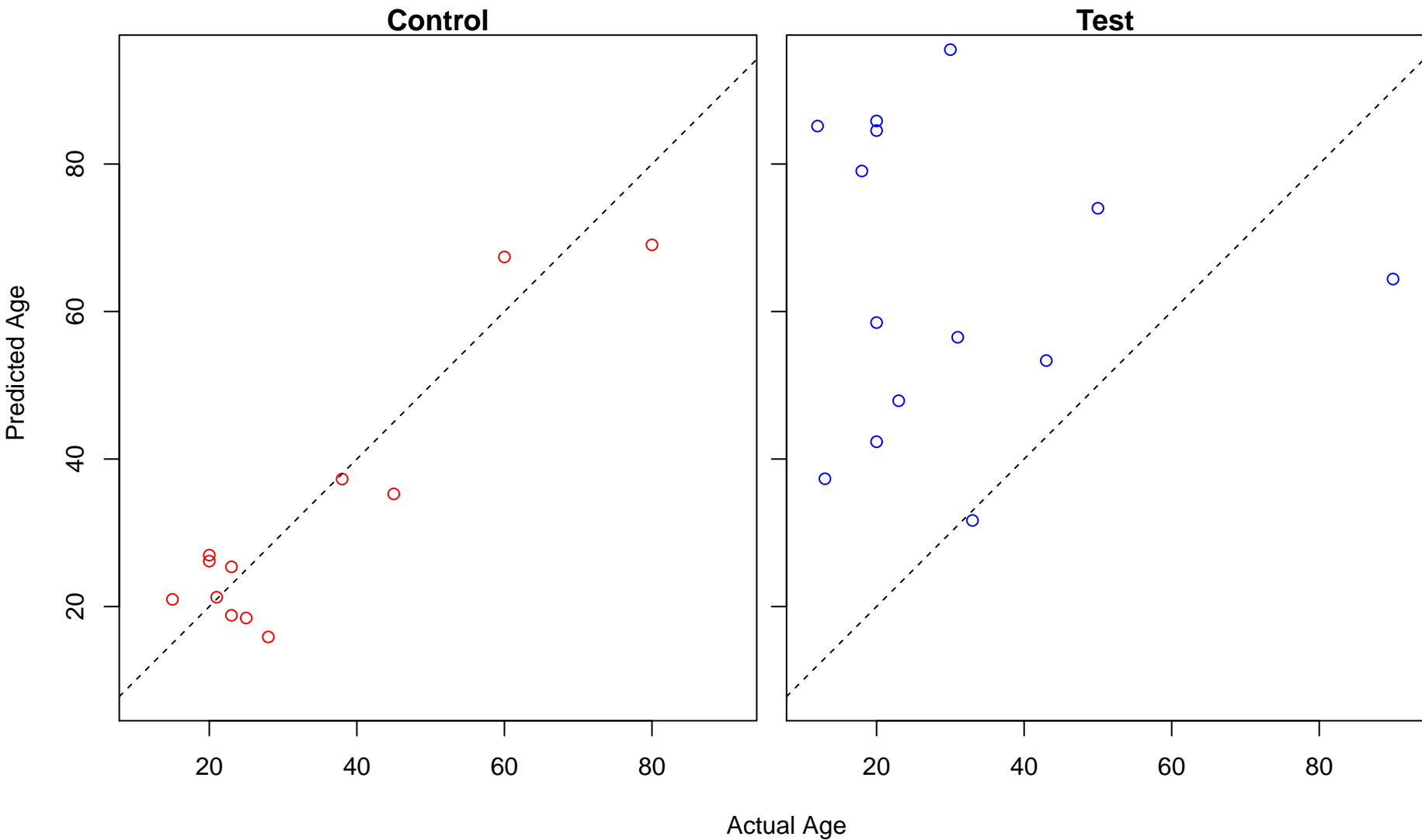
axonemal dynein complex assembly (Score: 13.724723)



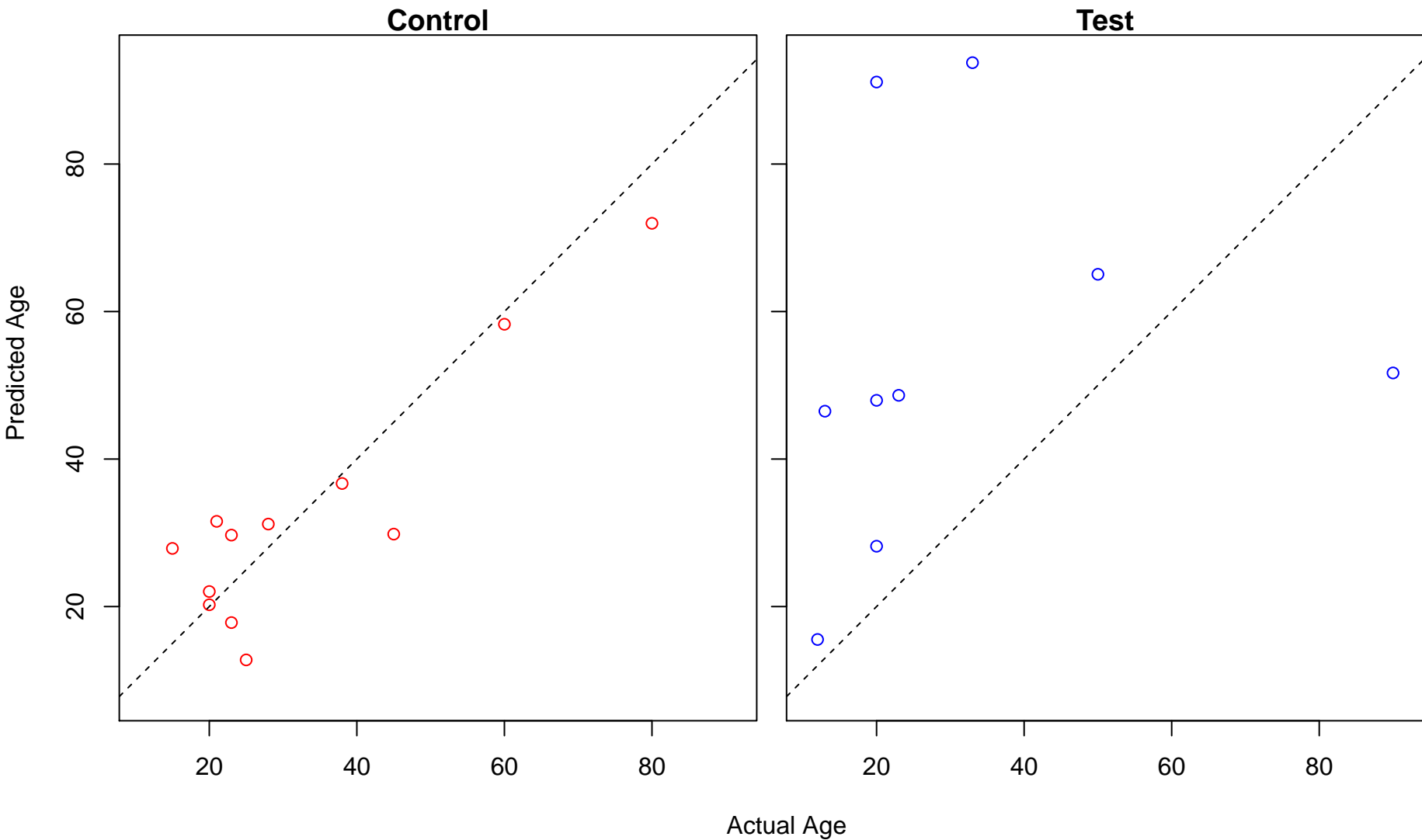
regulation of mitophagy (Score: 13.694230)



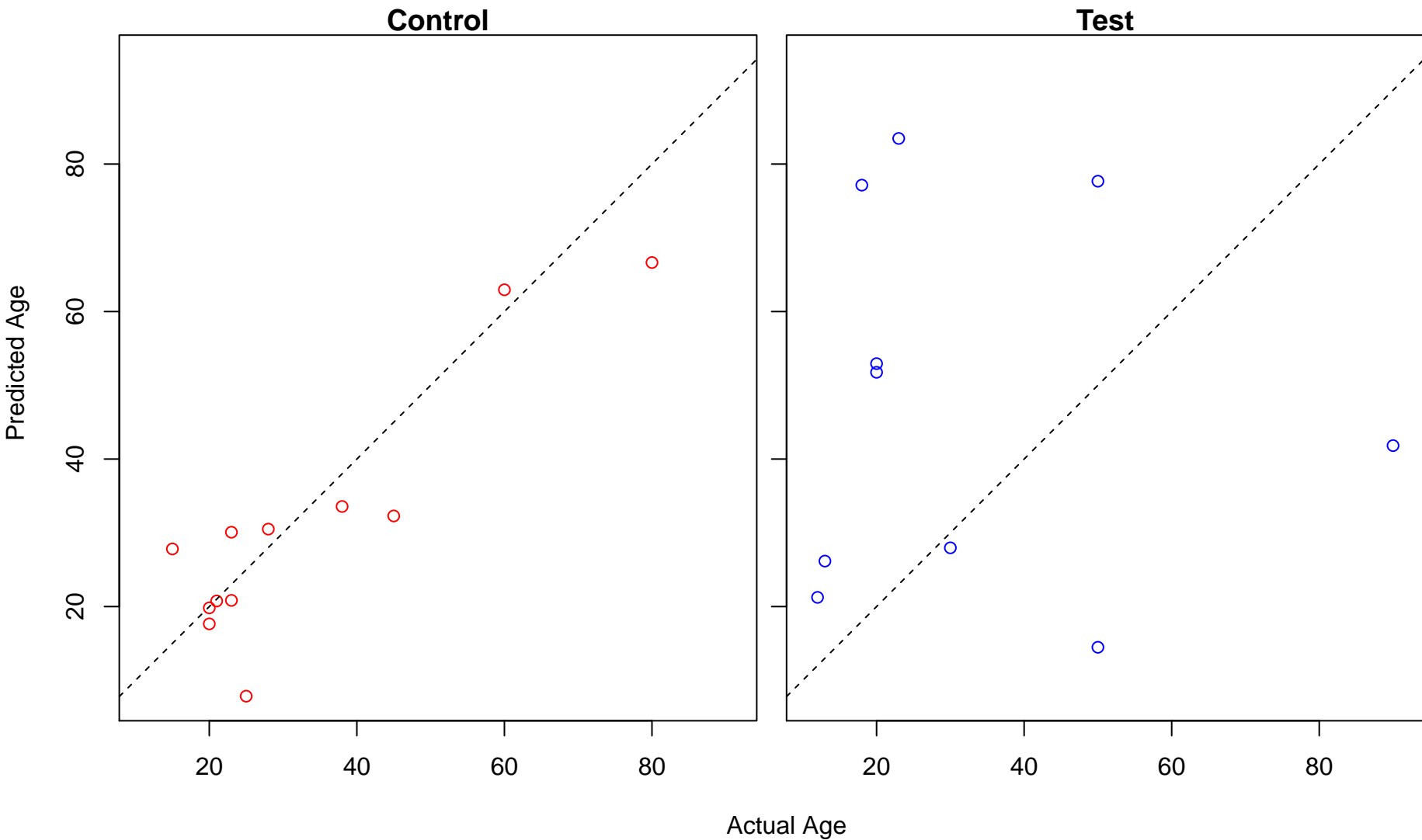
response to ammonium ion (Score: 13.676380)



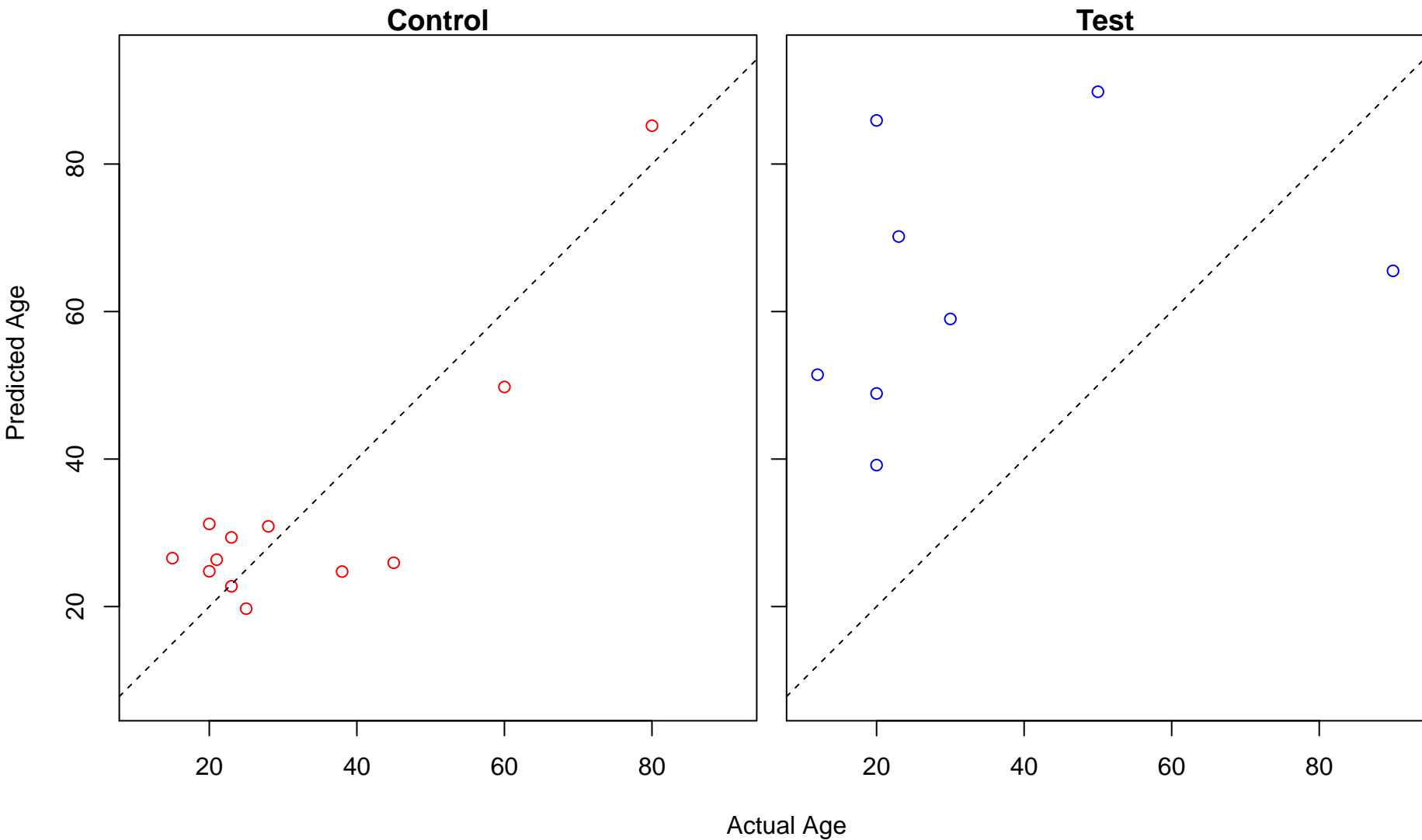
eye development (Score: 13.671129)



positive regulation of osteoblast differentiation (Score: 13.652489)

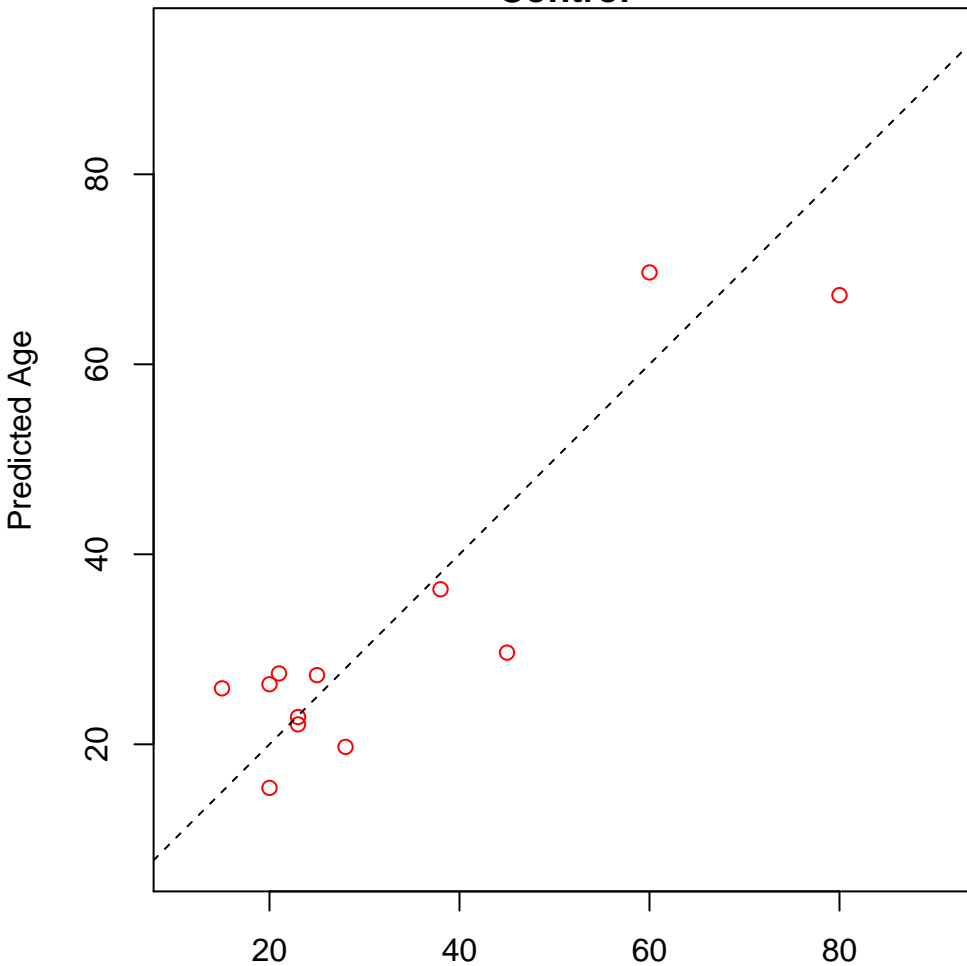


vitamin transport (Score: 13.632027)

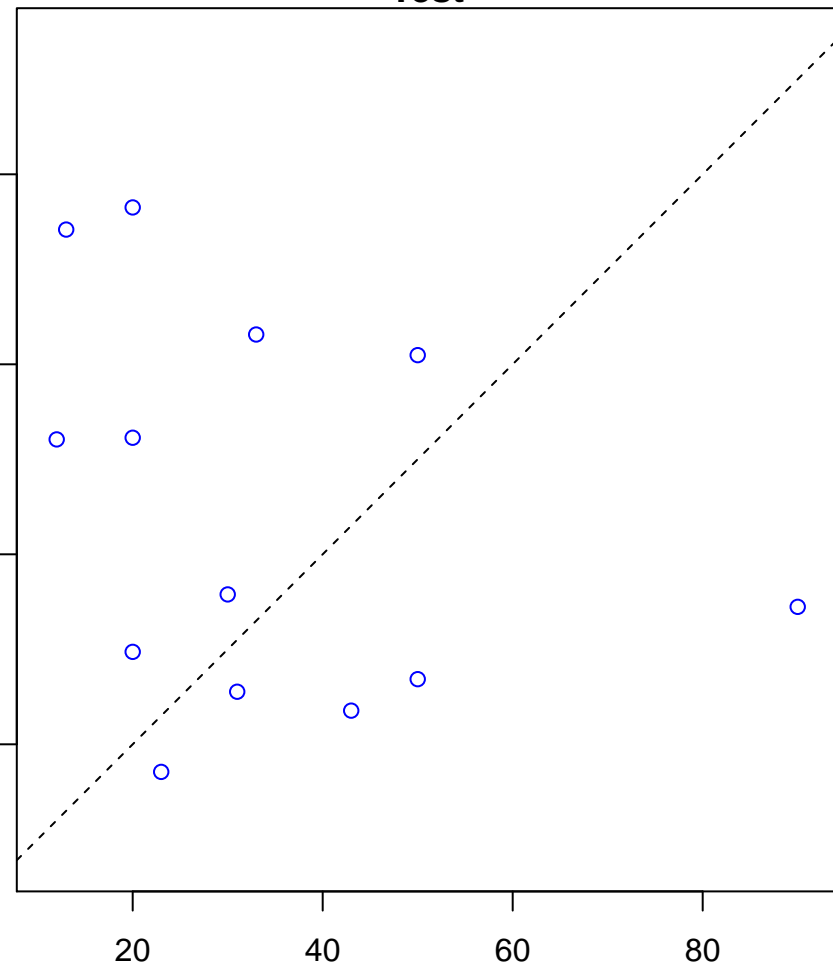


monovalent inorganic cation transport (Score: 13.627718)

Control

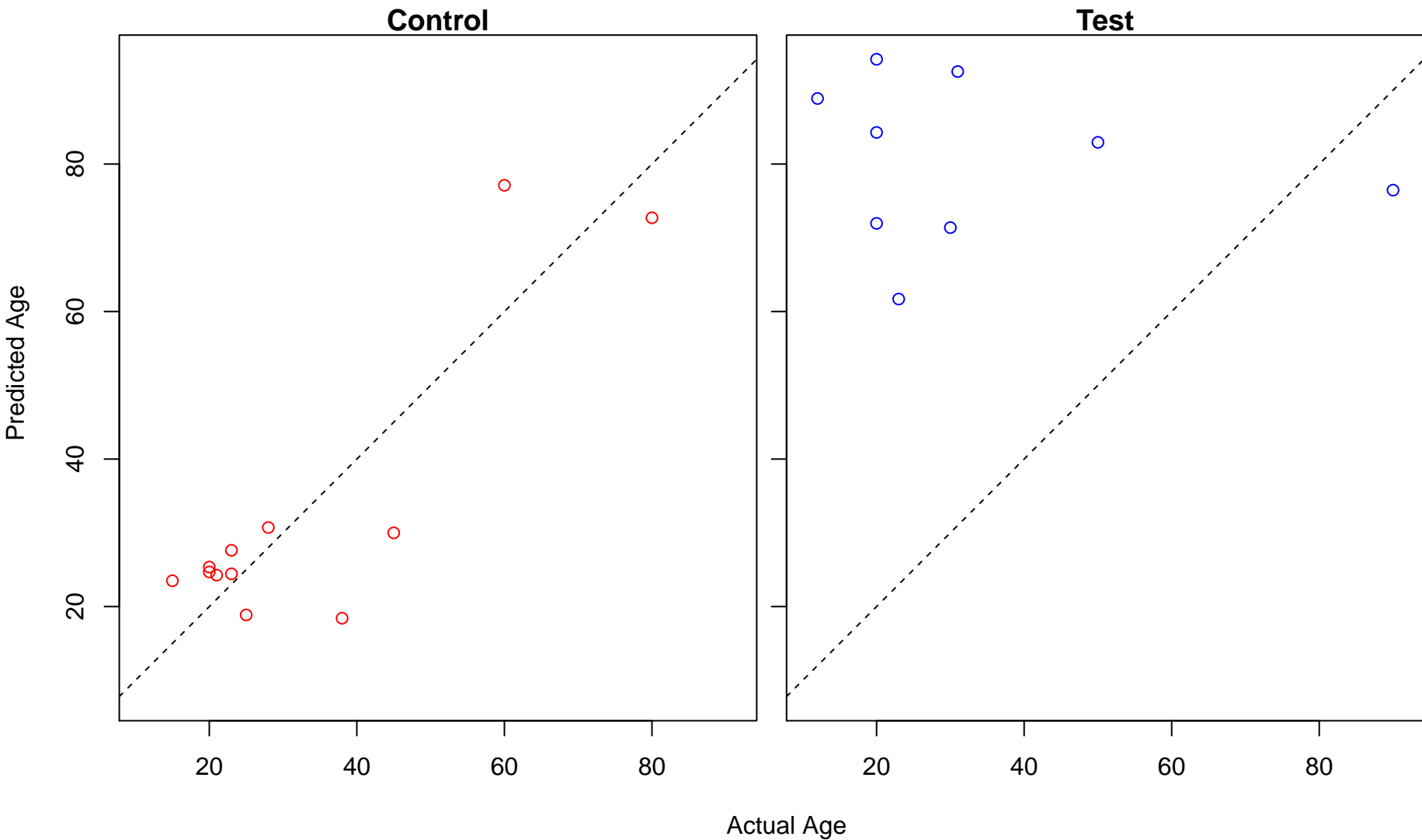


Test

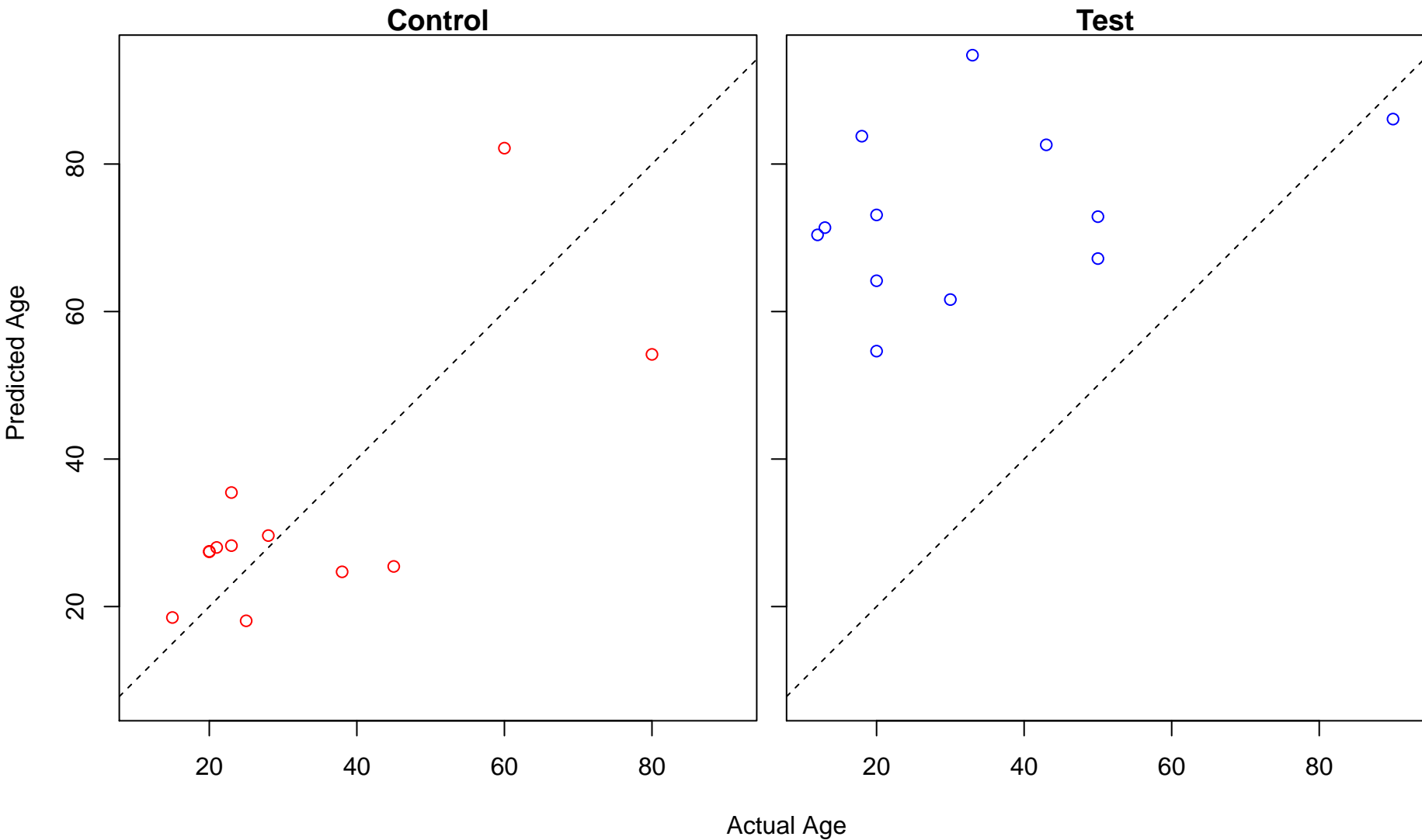


Actual Age

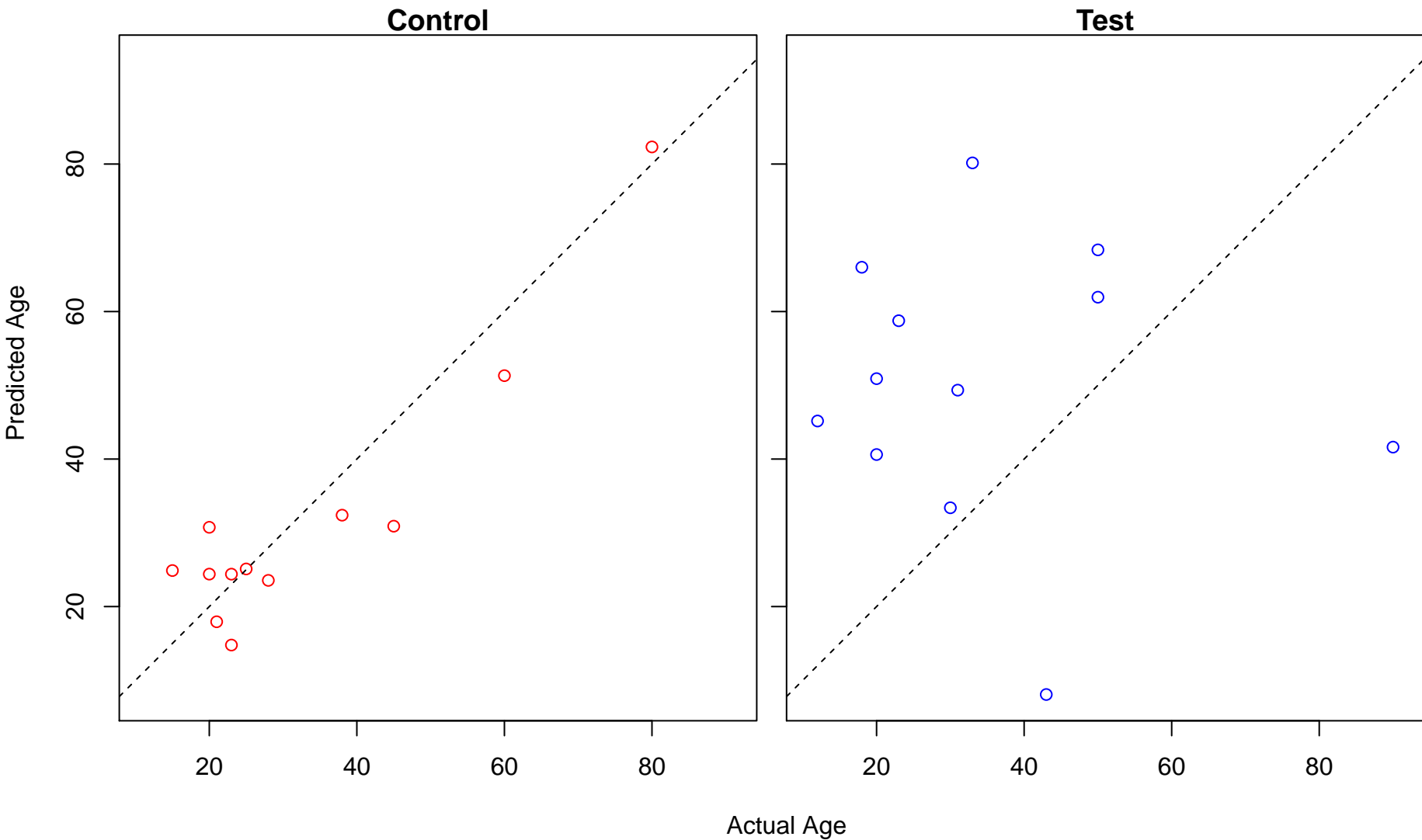
G-protein coupled glutamate receptor signaling pathway (Score: 13.615167)



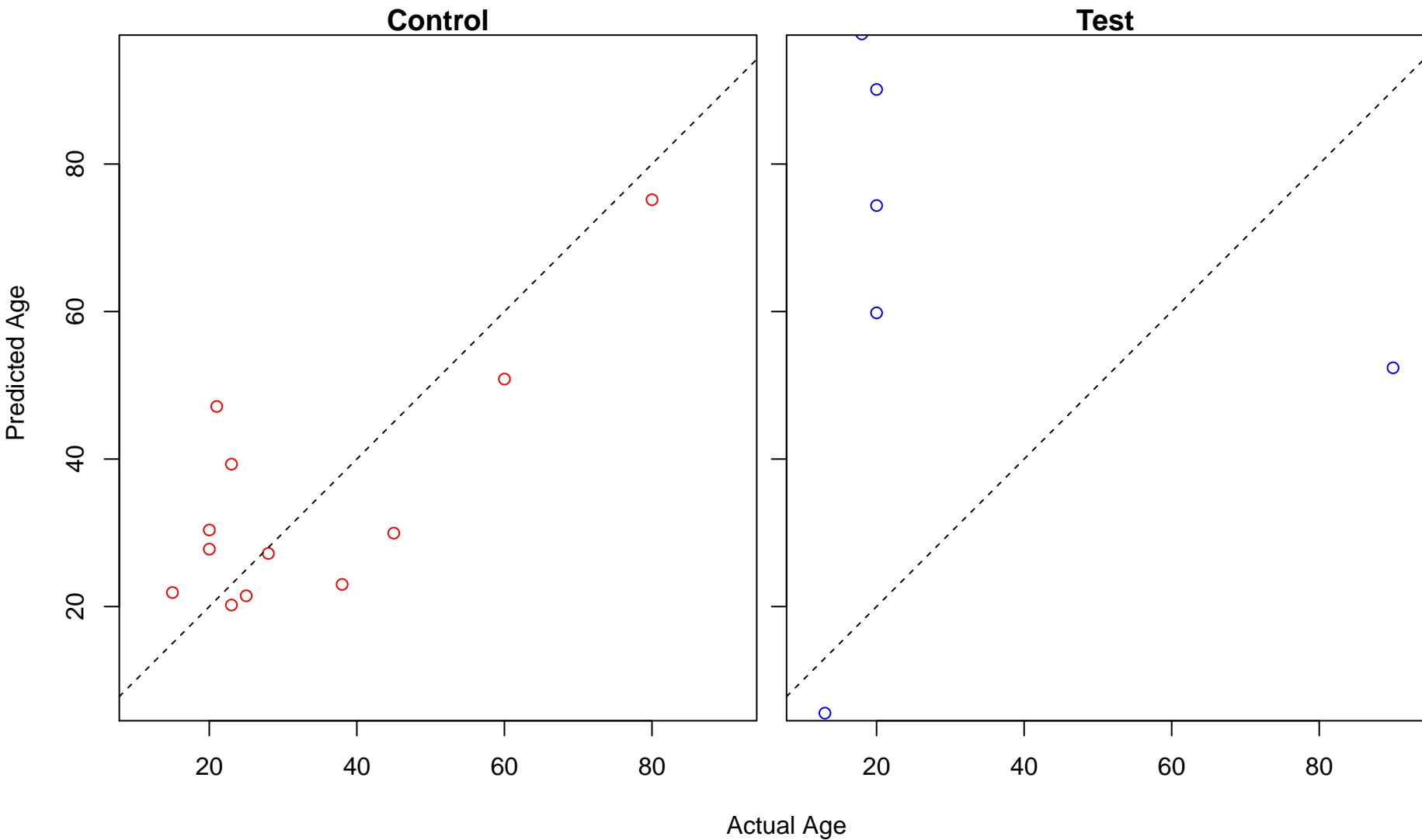
complement receptor mediated signaling pathway (Score: 13.591278)



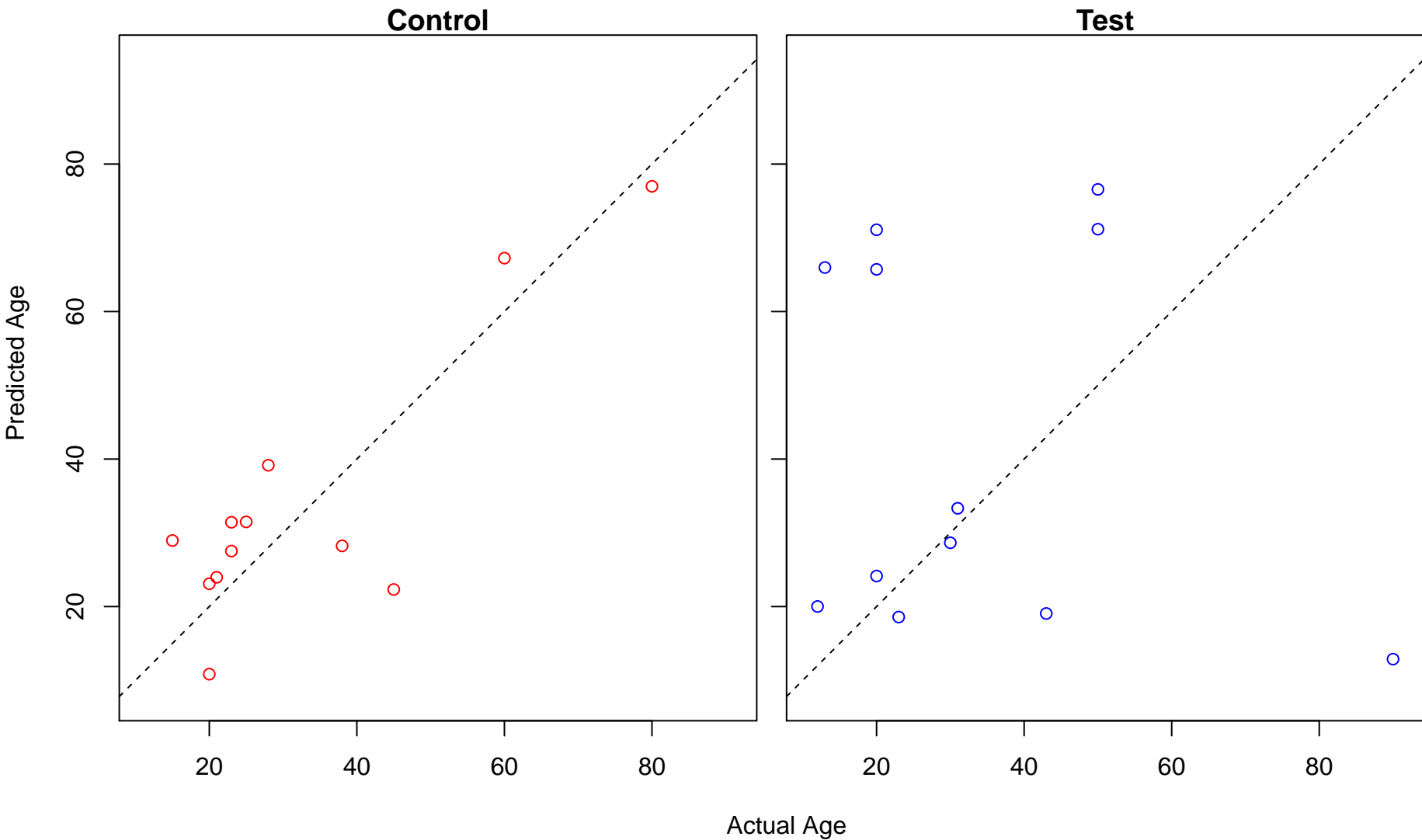
cellular response to heat (Score: 13.590722)



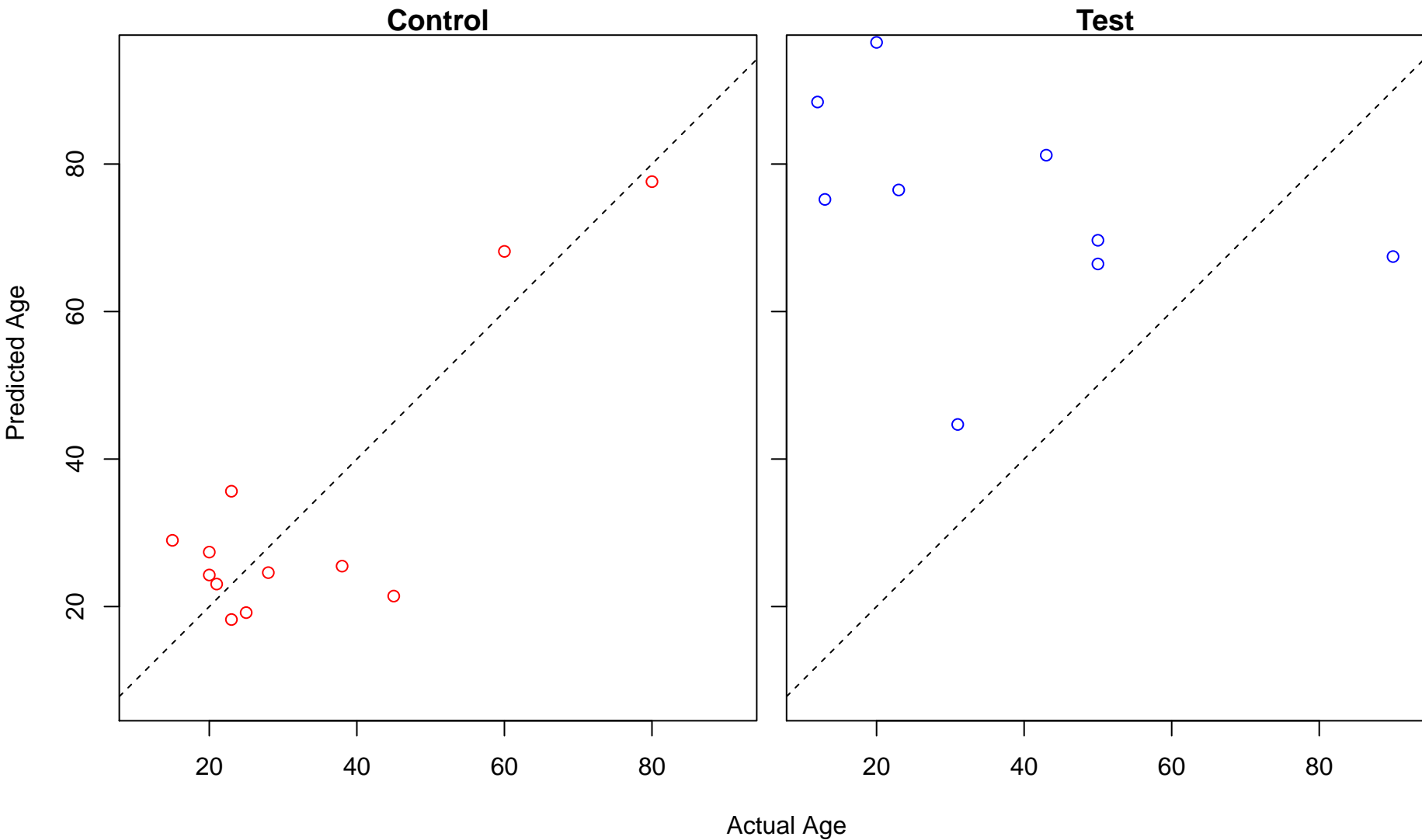
positive regulation of cholesterol esterification (Score: 13.578922)



leukocyte migration (Score: 13.558914)

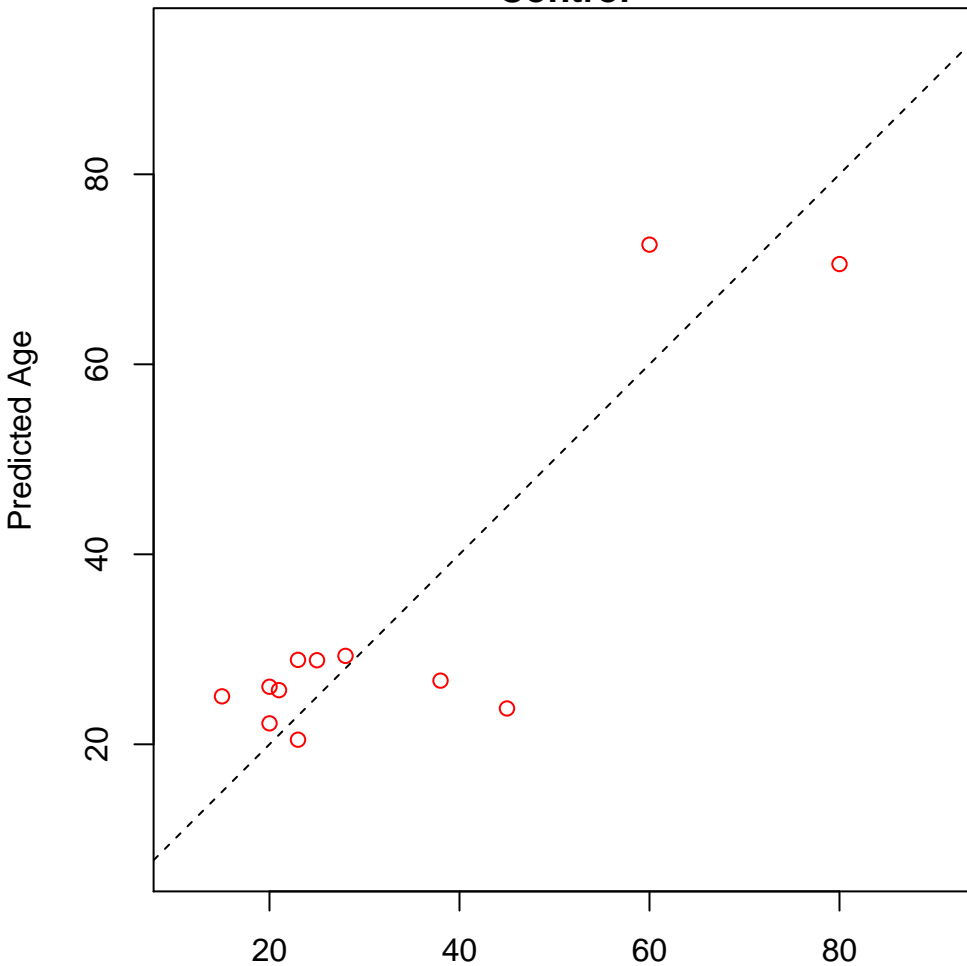


cytoskeletal anchoring at nuclear membrane (Score: 13.535645)

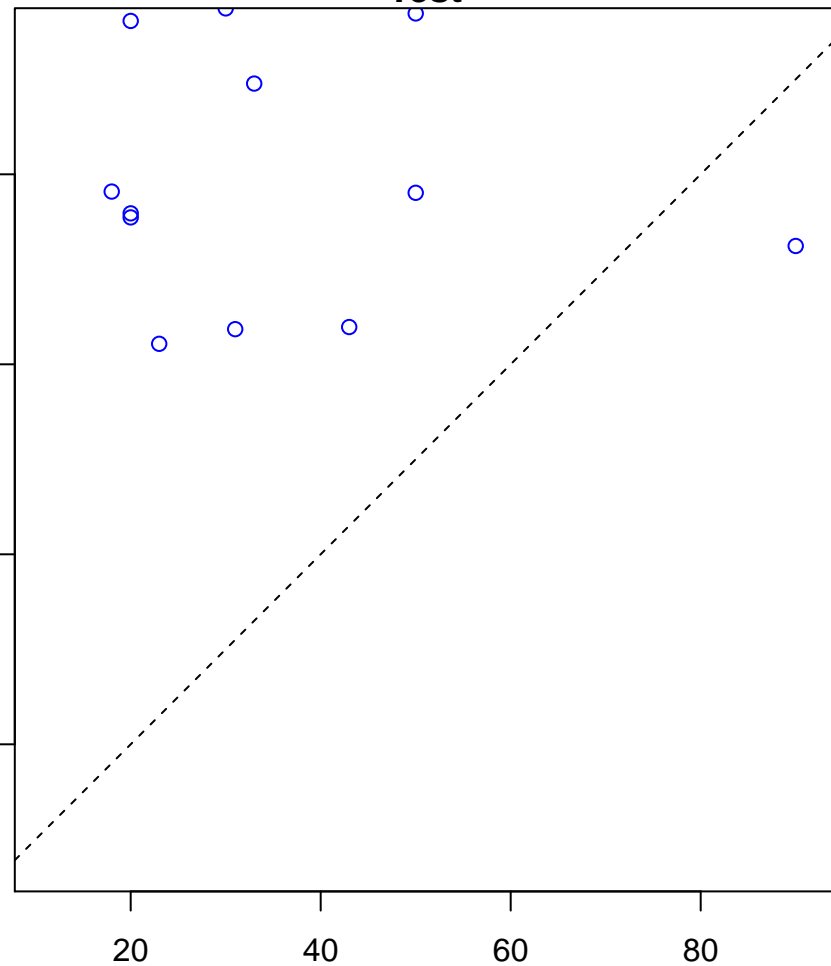


cardiac chamber morphogenesis (Score: 13.527293)

Control

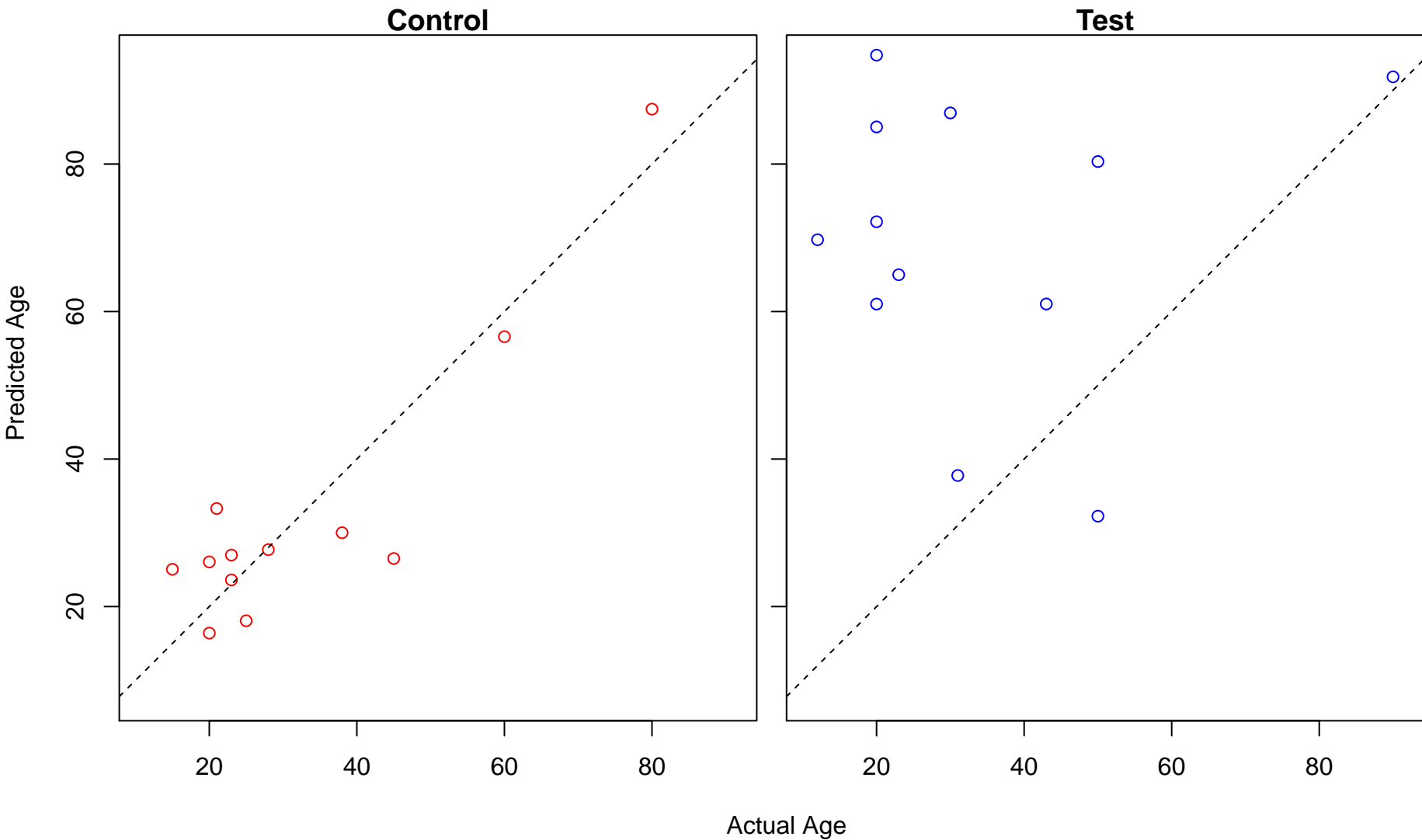


Test

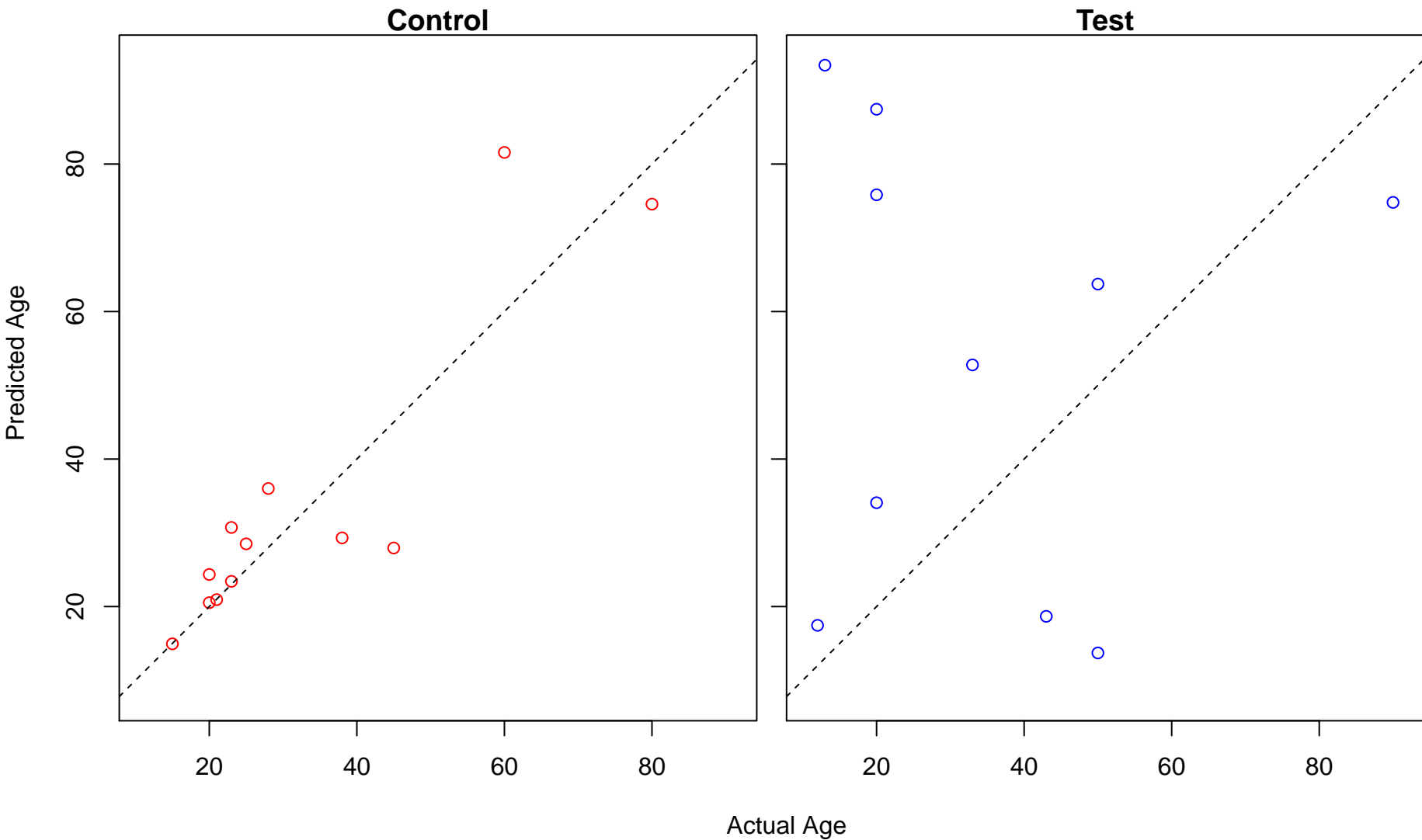


Actual Age

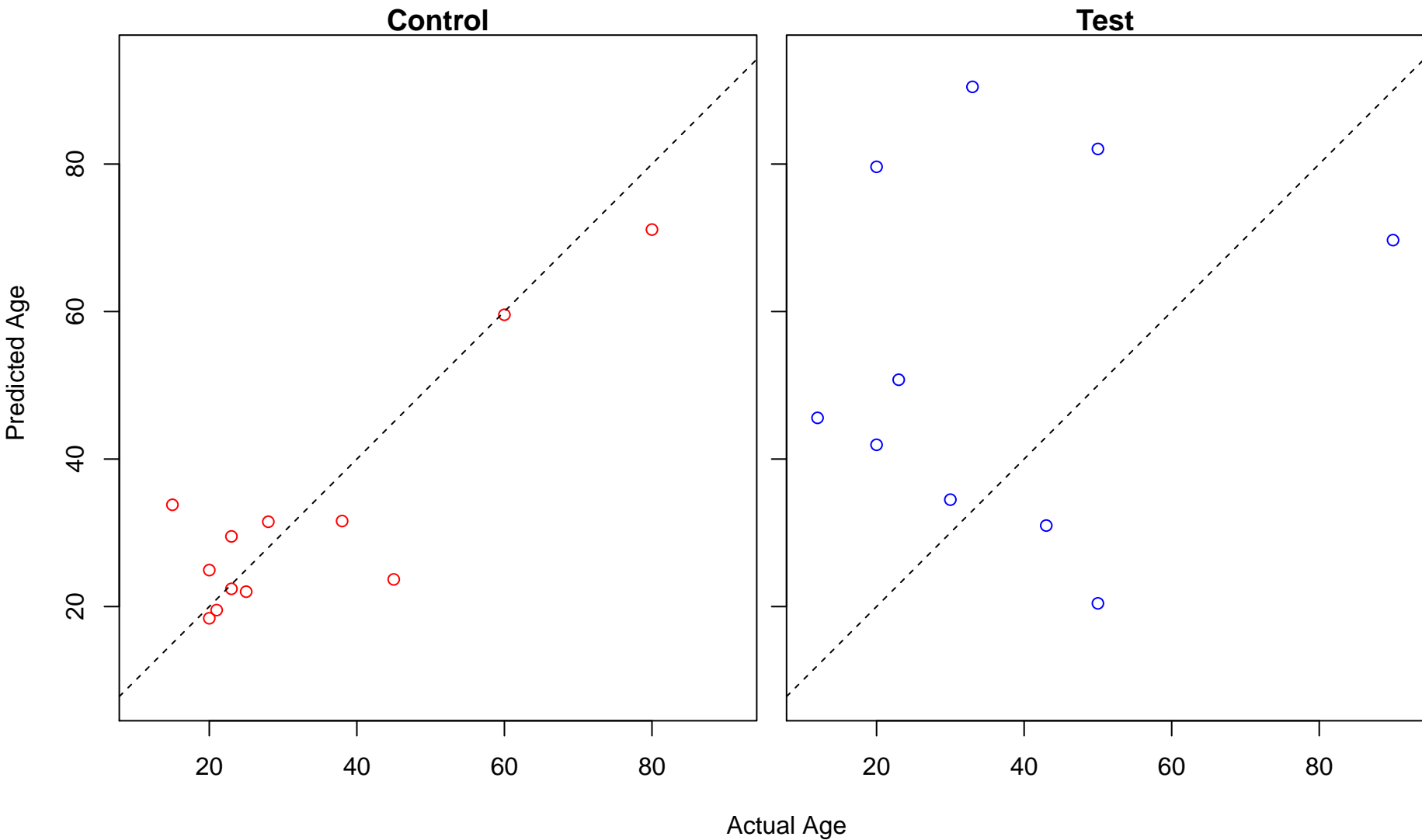
peptidyl-arginine methylation, to asymmetrical-dimethyl arginine (Score: 13.516189)



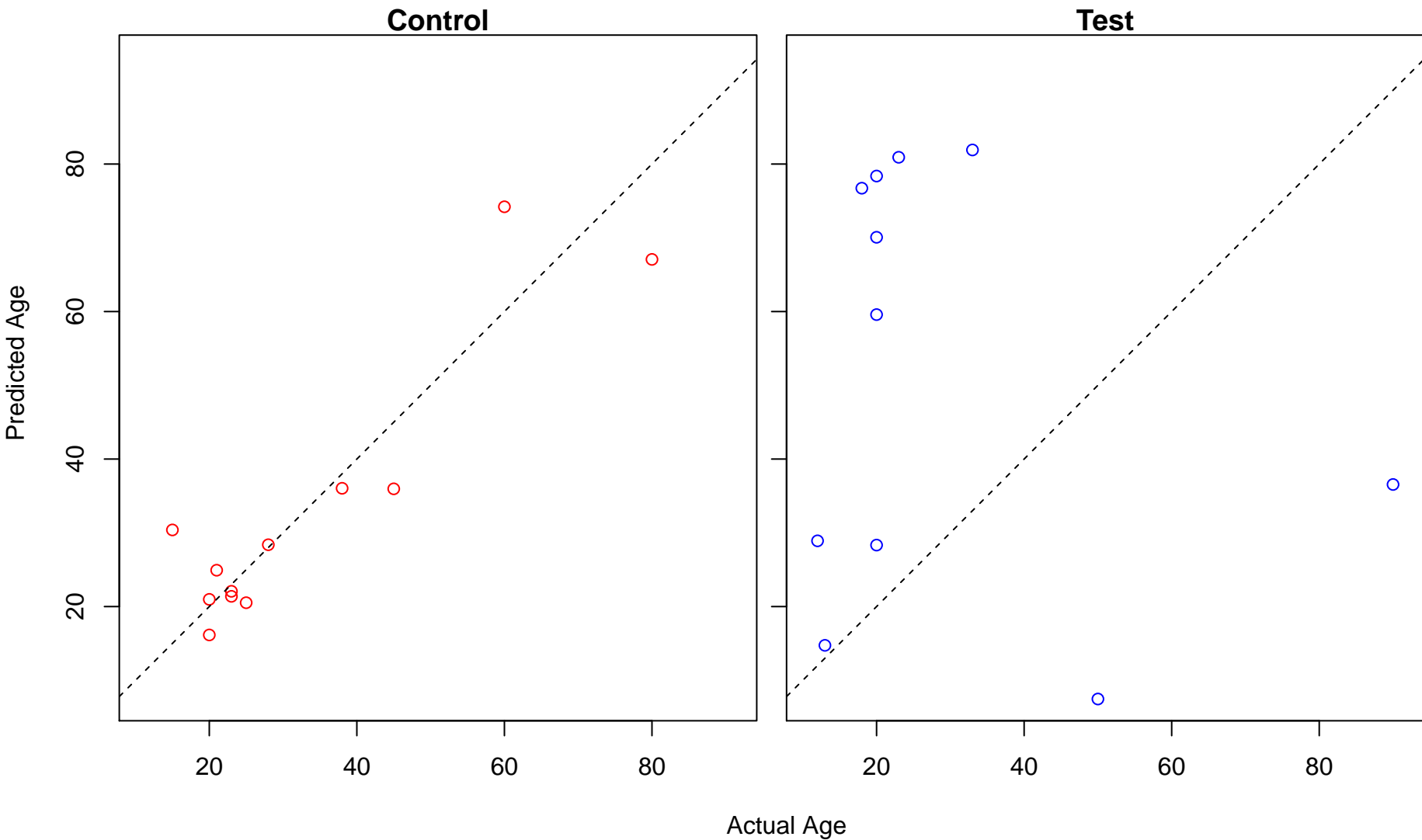
regulation of protein phosphatase type 2A activity (Score: 13.505237)



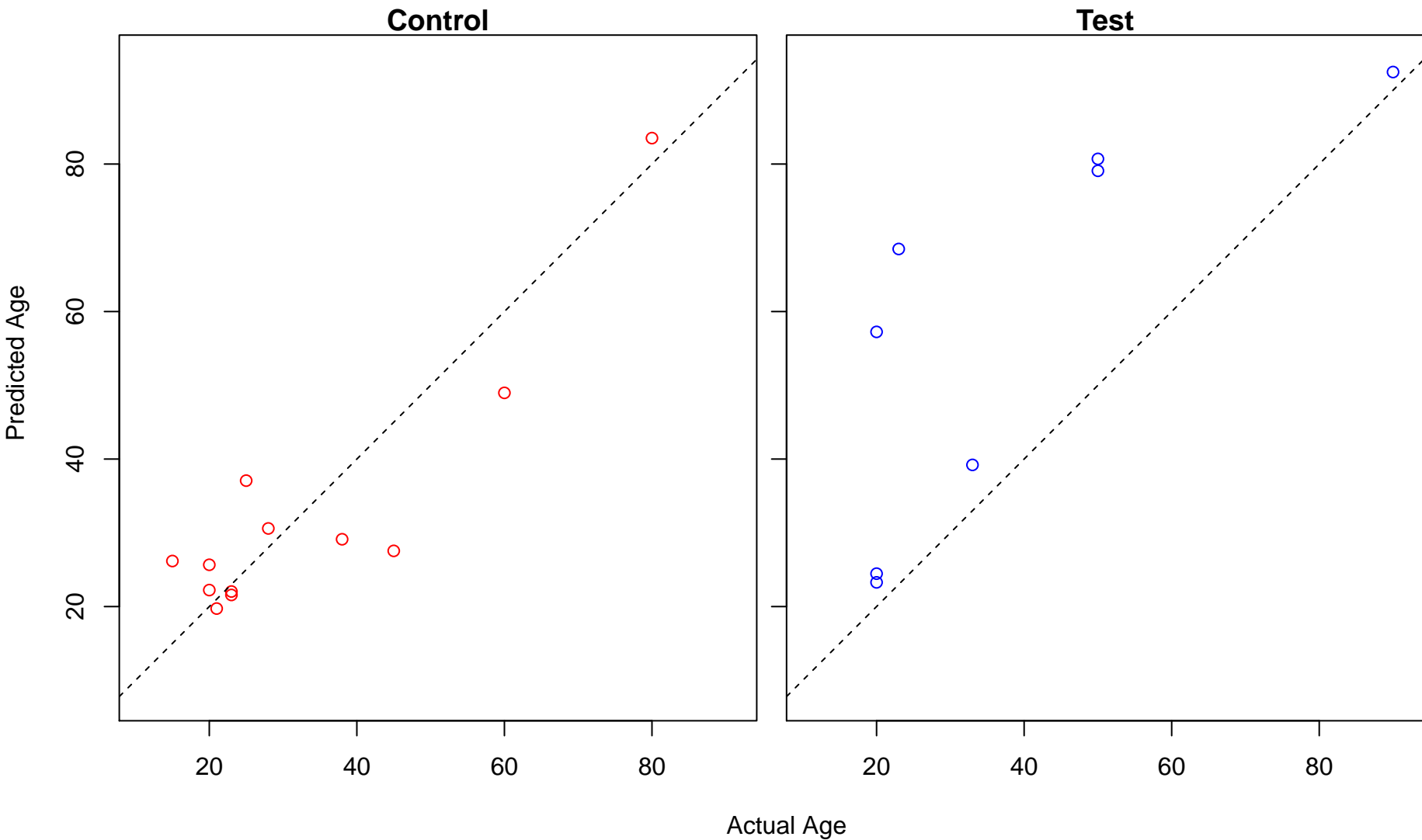
regulation of chromatin modification (Score: 13.489386)



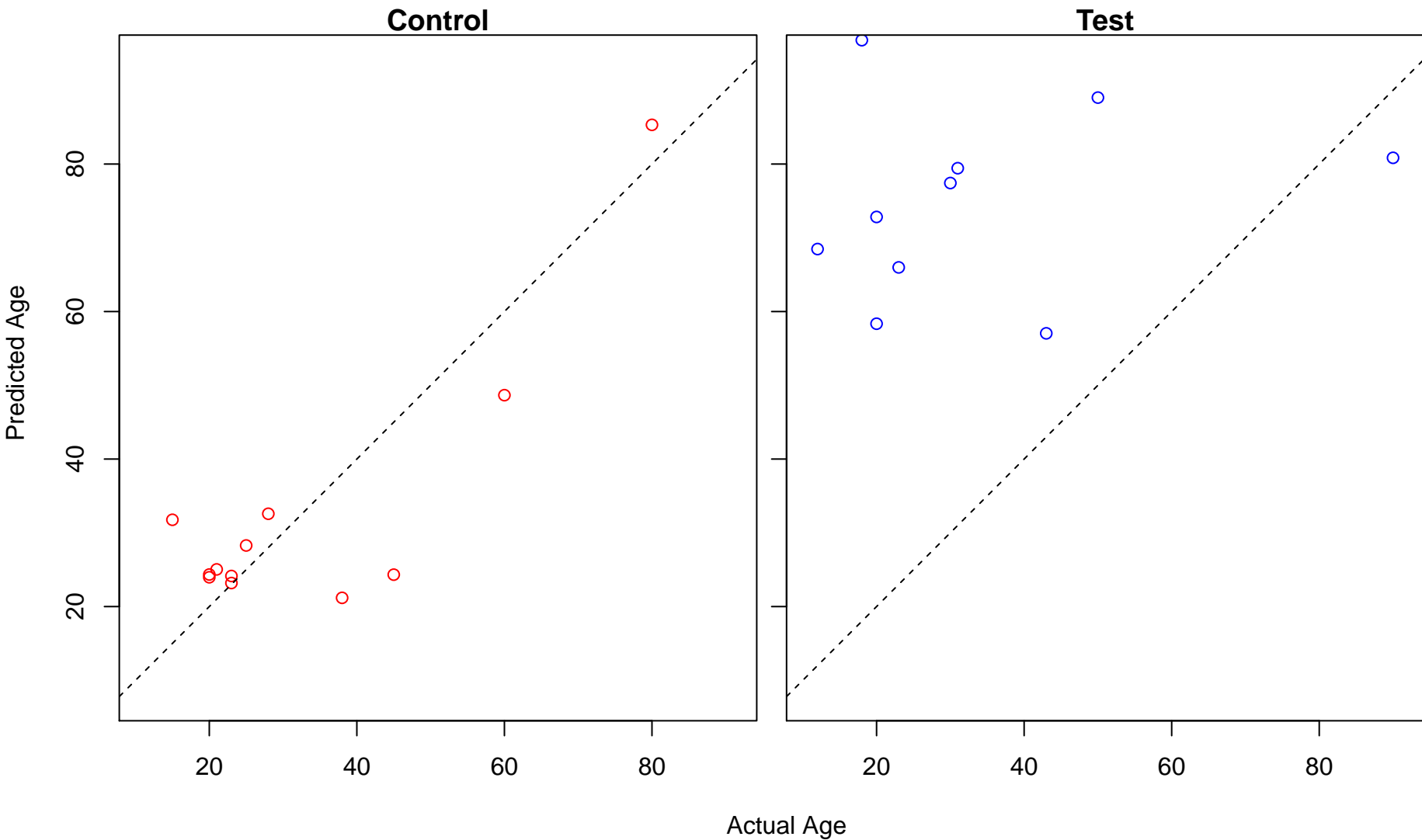
female gamete generation (Score: 13.486607)



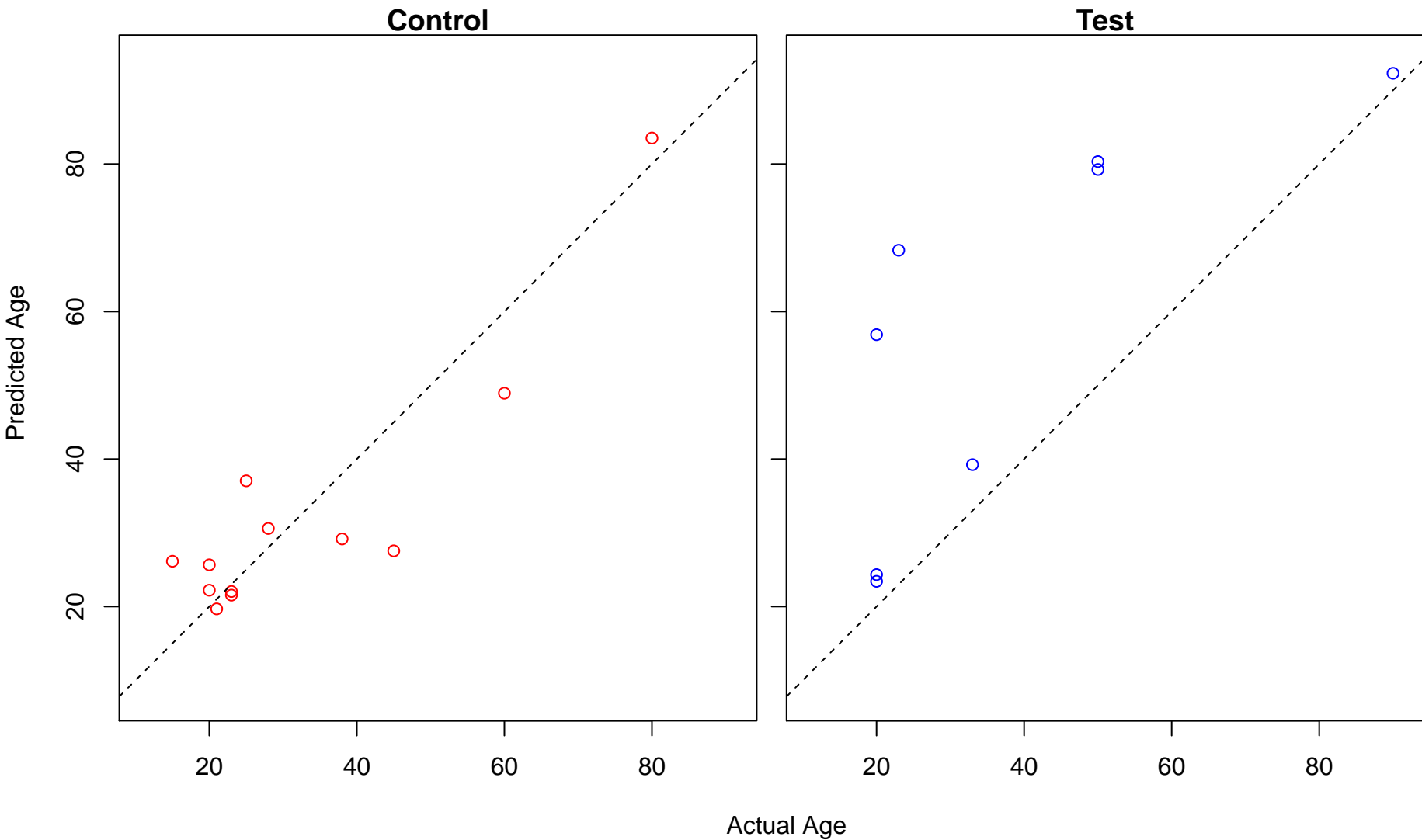
positive regulation of neutrophil migration (Score: 13.484955)



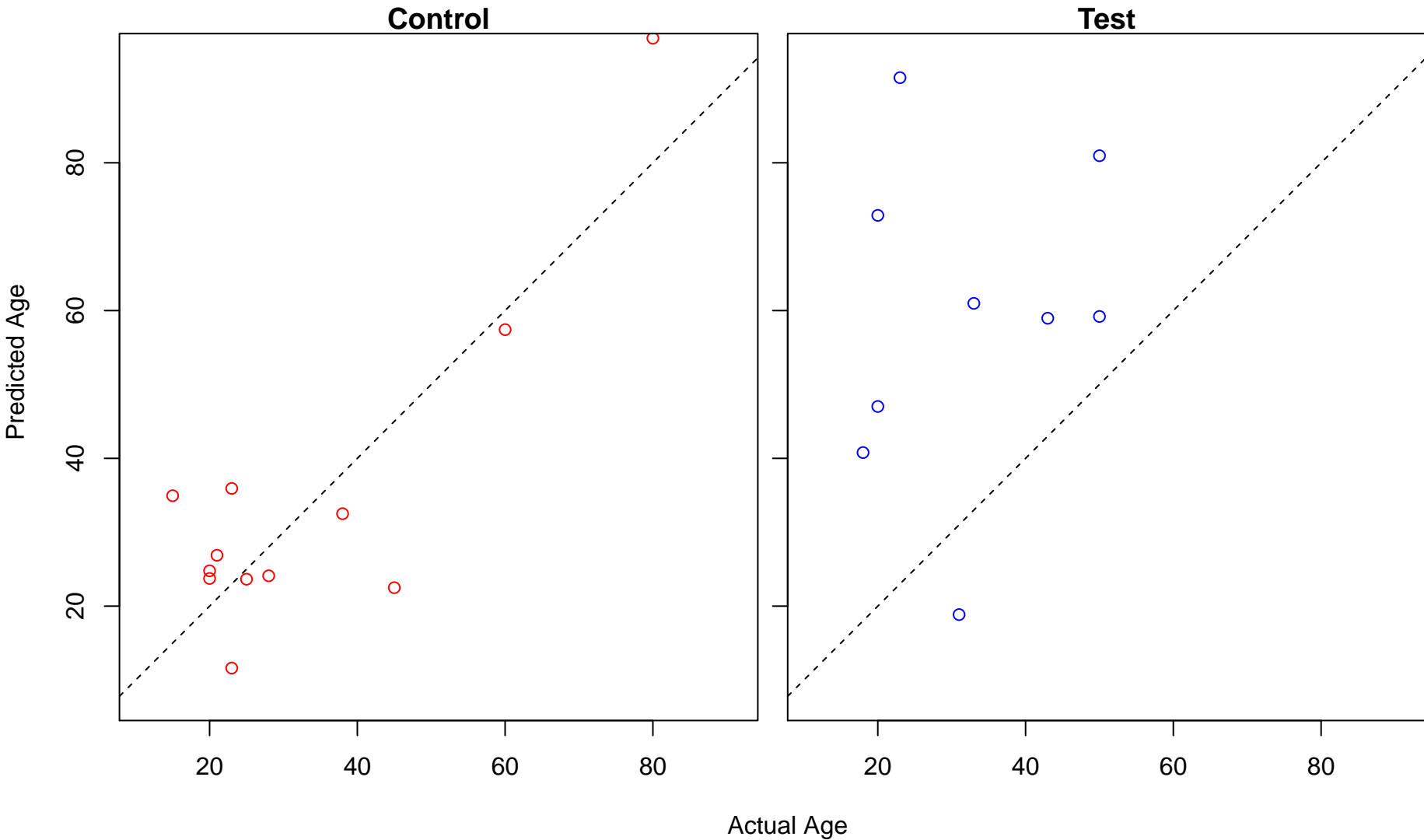
negative regulation of DNA replication (Score: 13.468528)



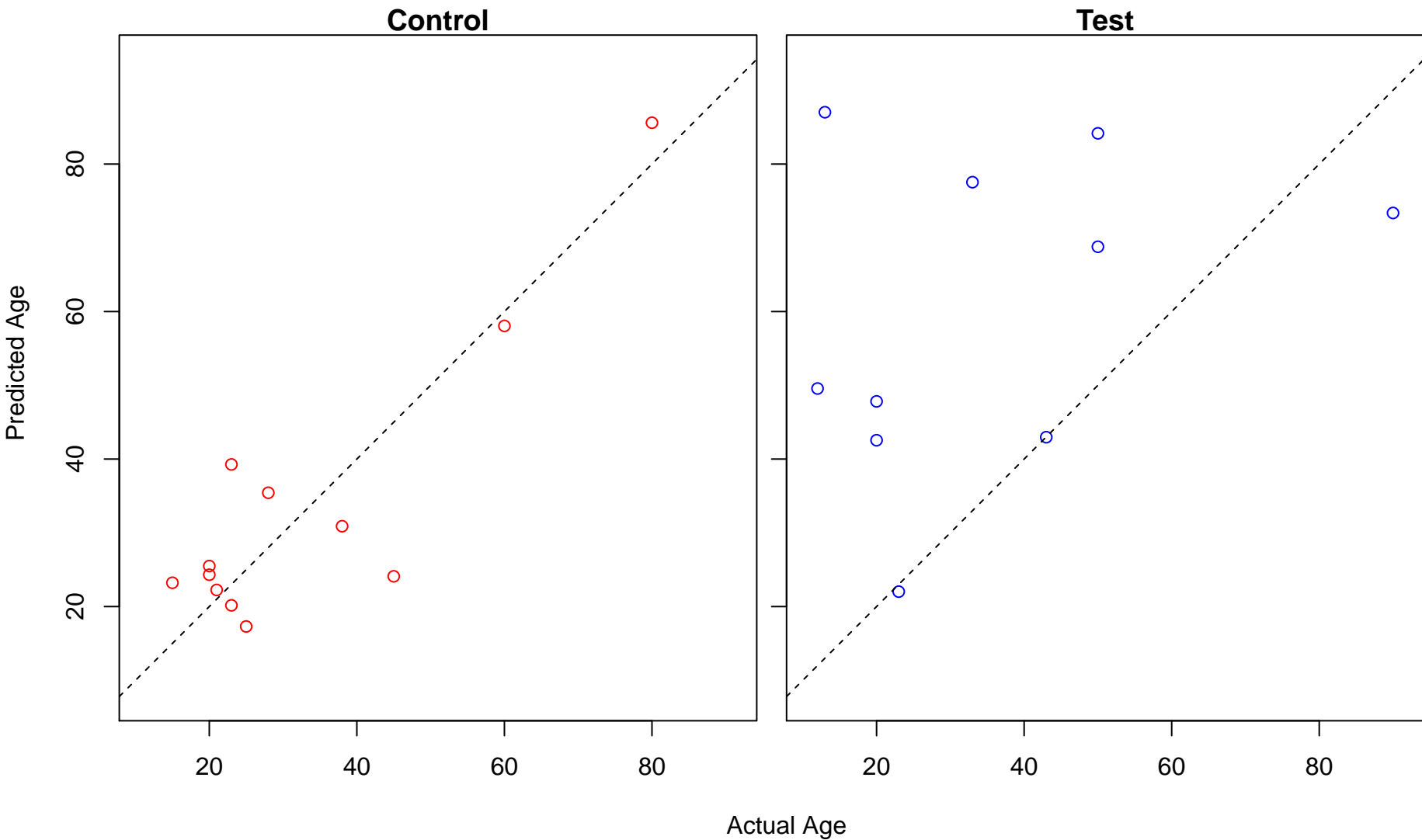
positive regulation of neutrophil chemotaxis (Score: 13.455593)



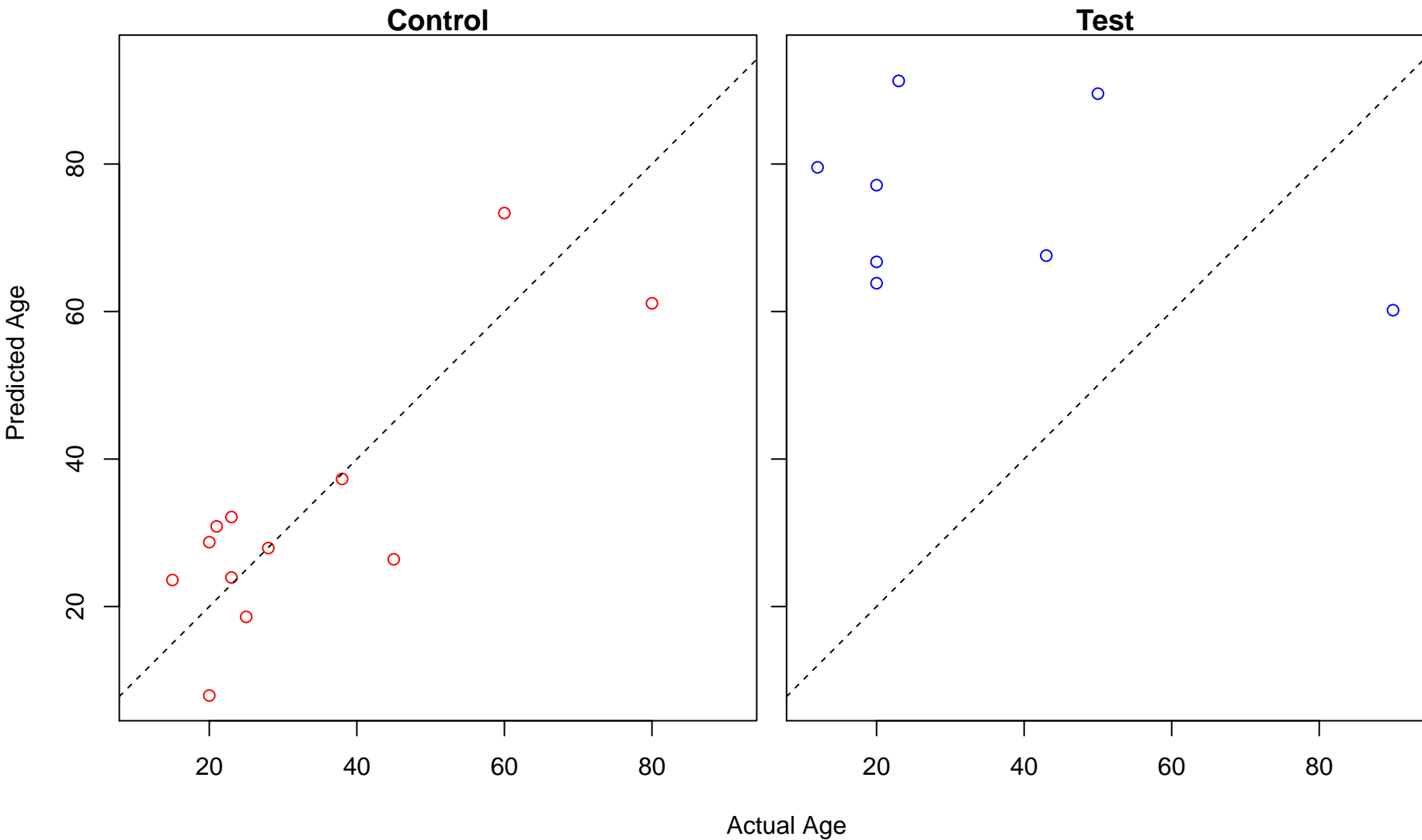
vascular smooth muscle cell development (Score: 13.439960)



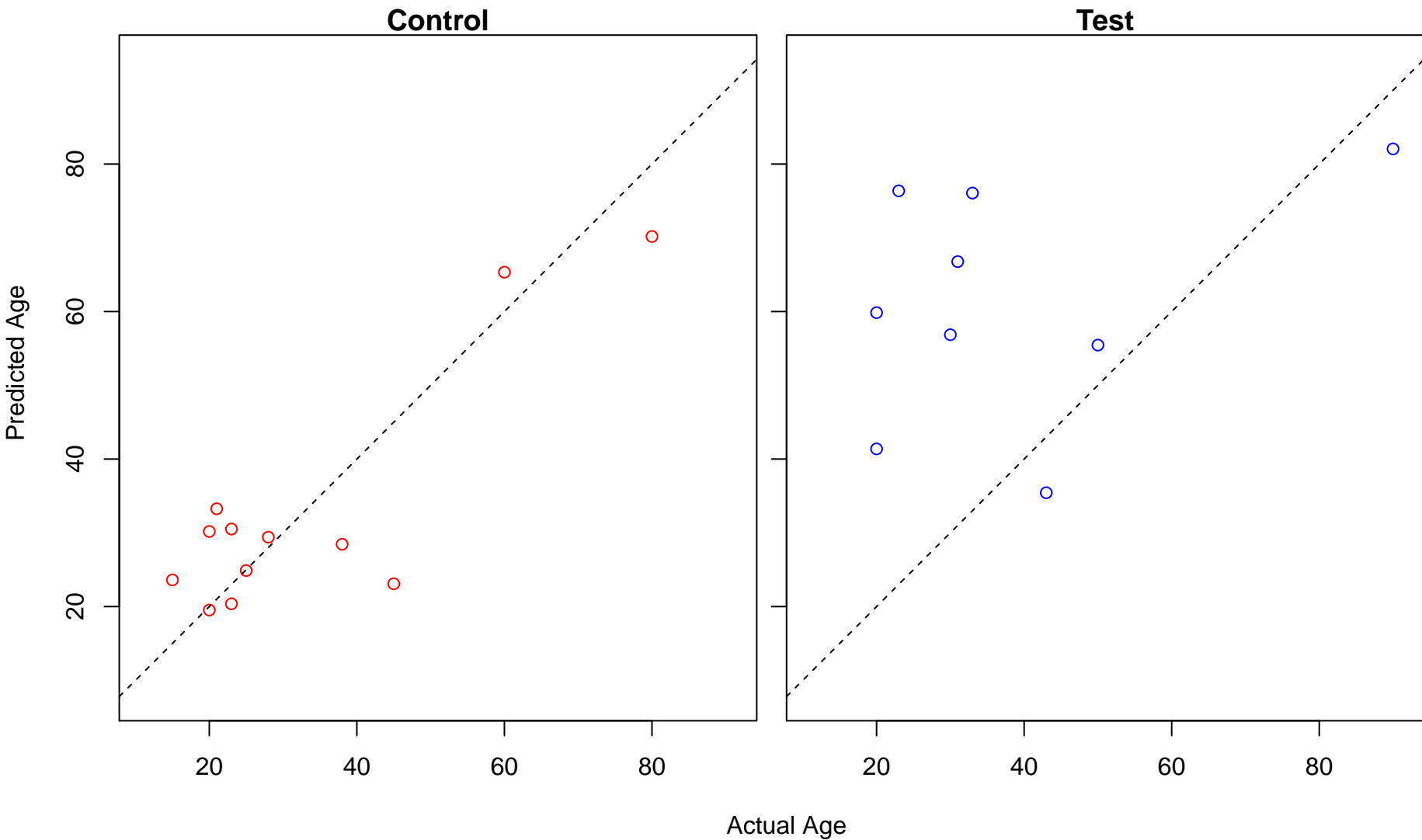
regulation of histone acetylation (Score: 13.429248)



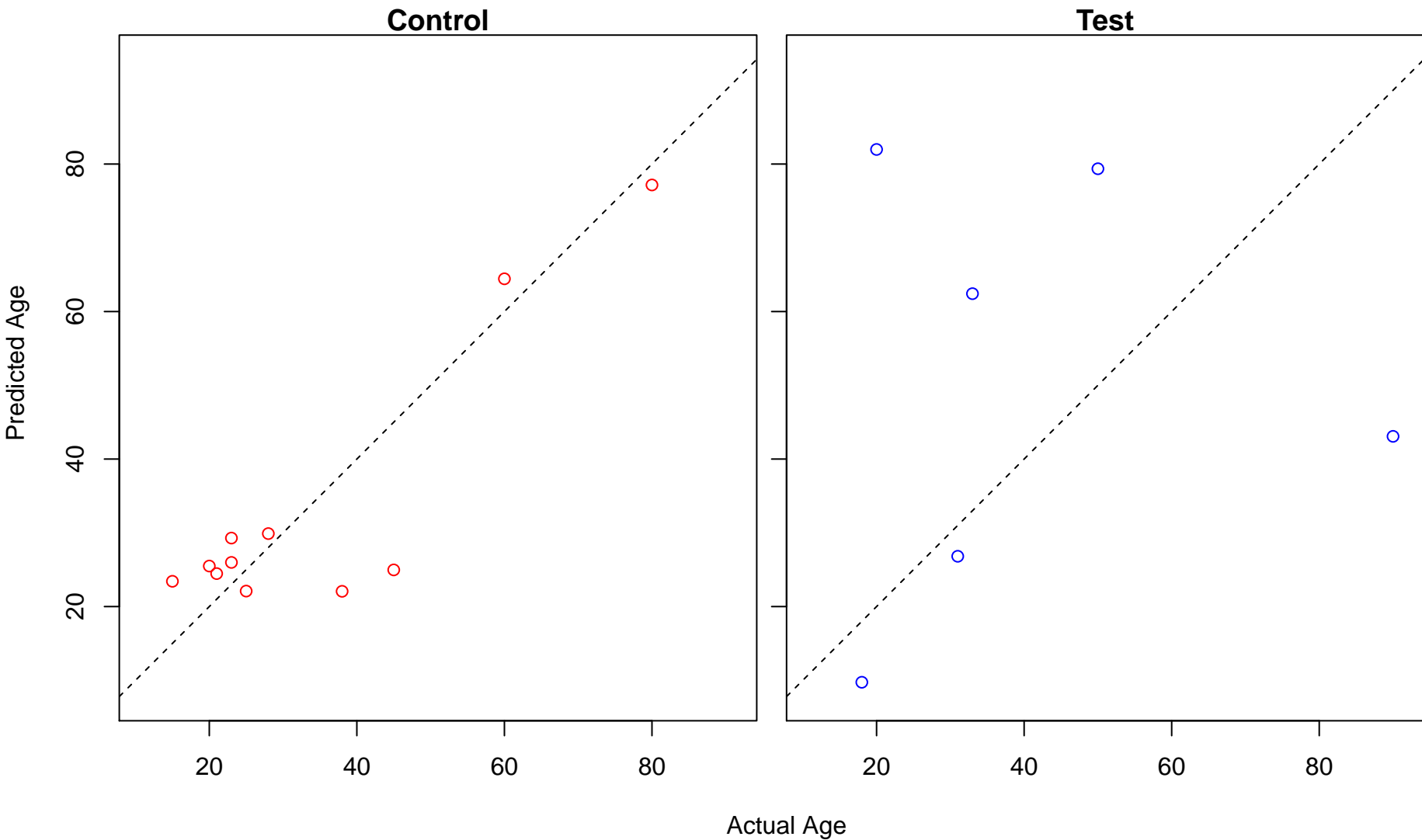
immune response–activating cell surface receptor signaling pathway (Score: 13.396616)



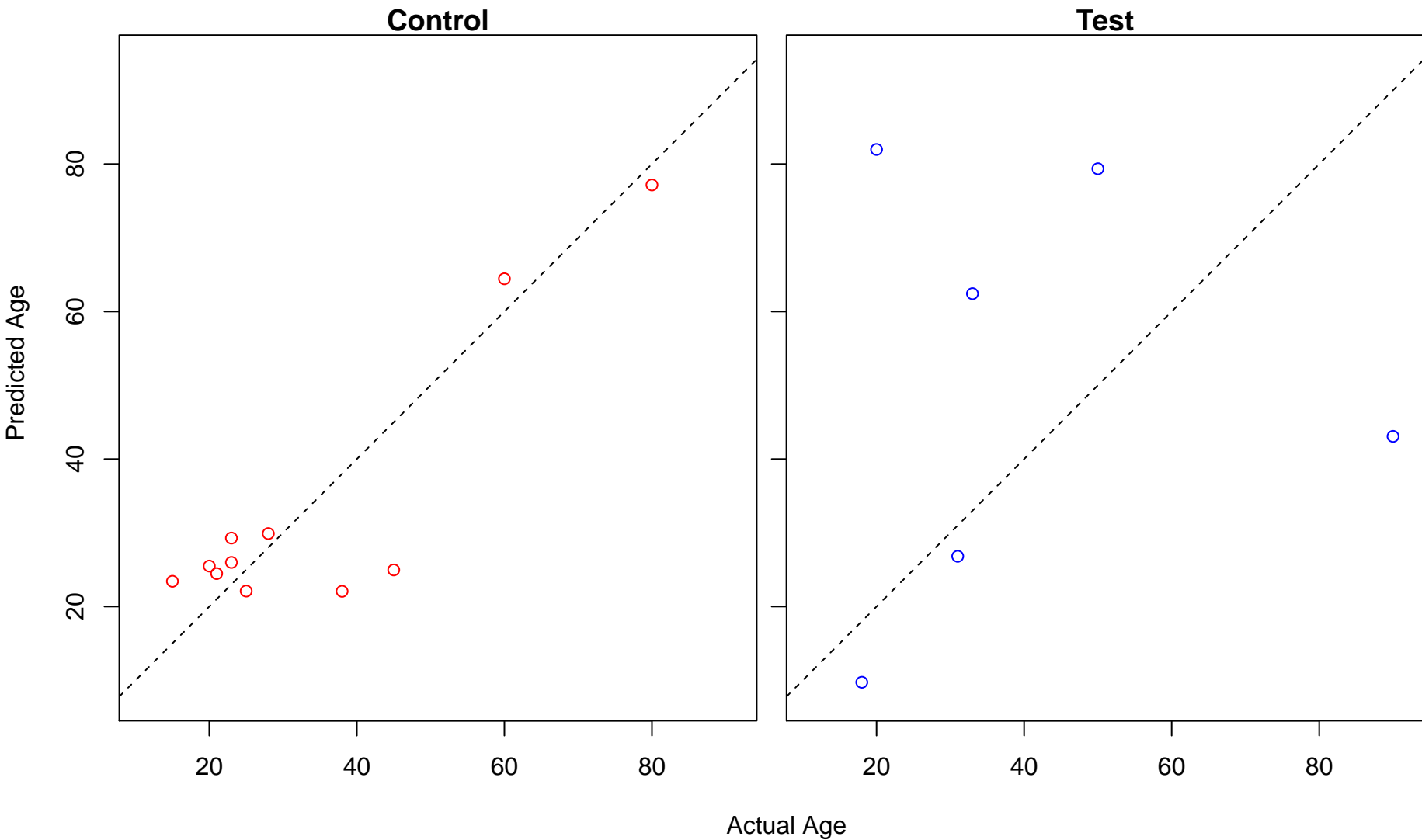
modulation by host of viral process (Score: 13.388809)



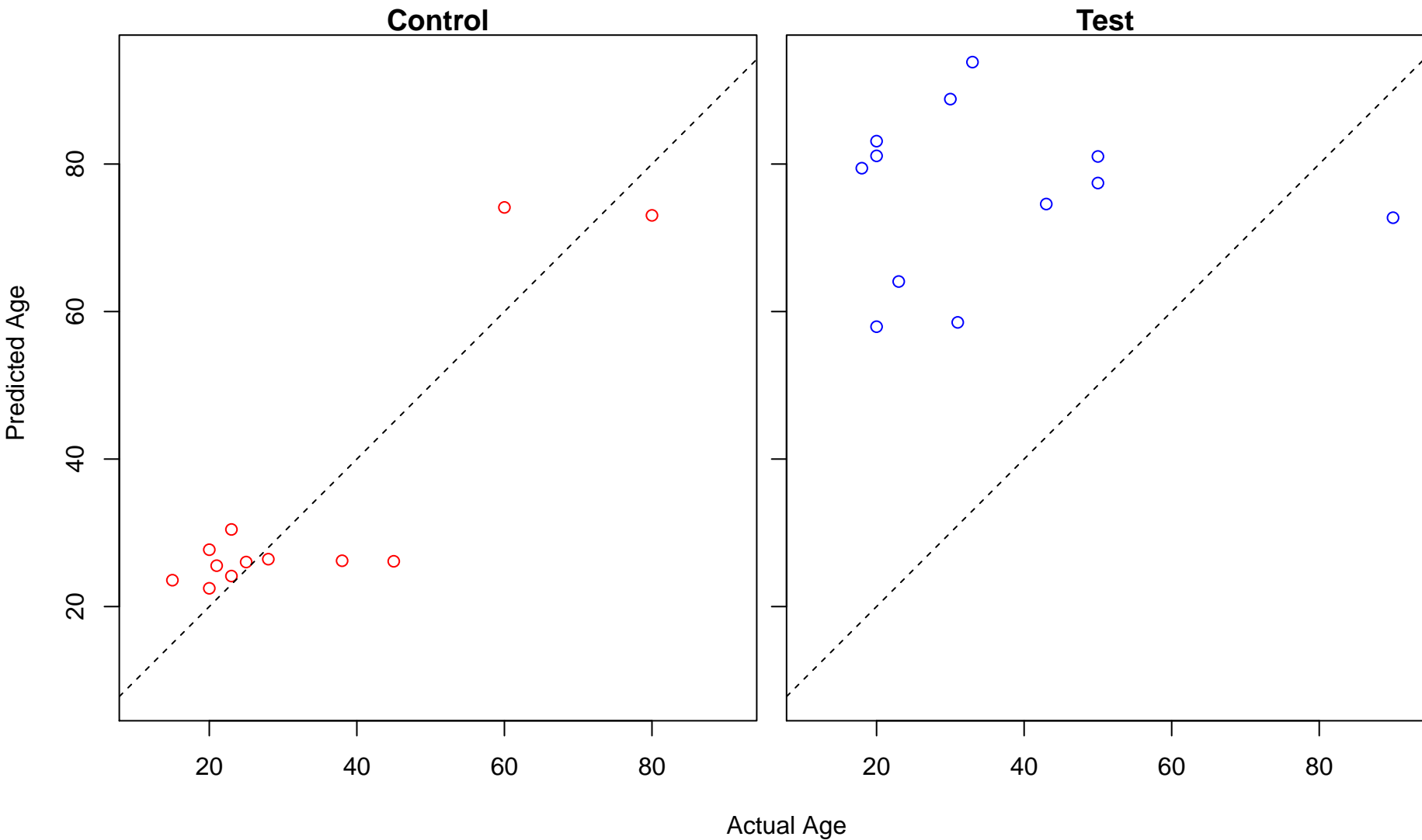
axon extension involved in axon guidance (Score: 13.351685)



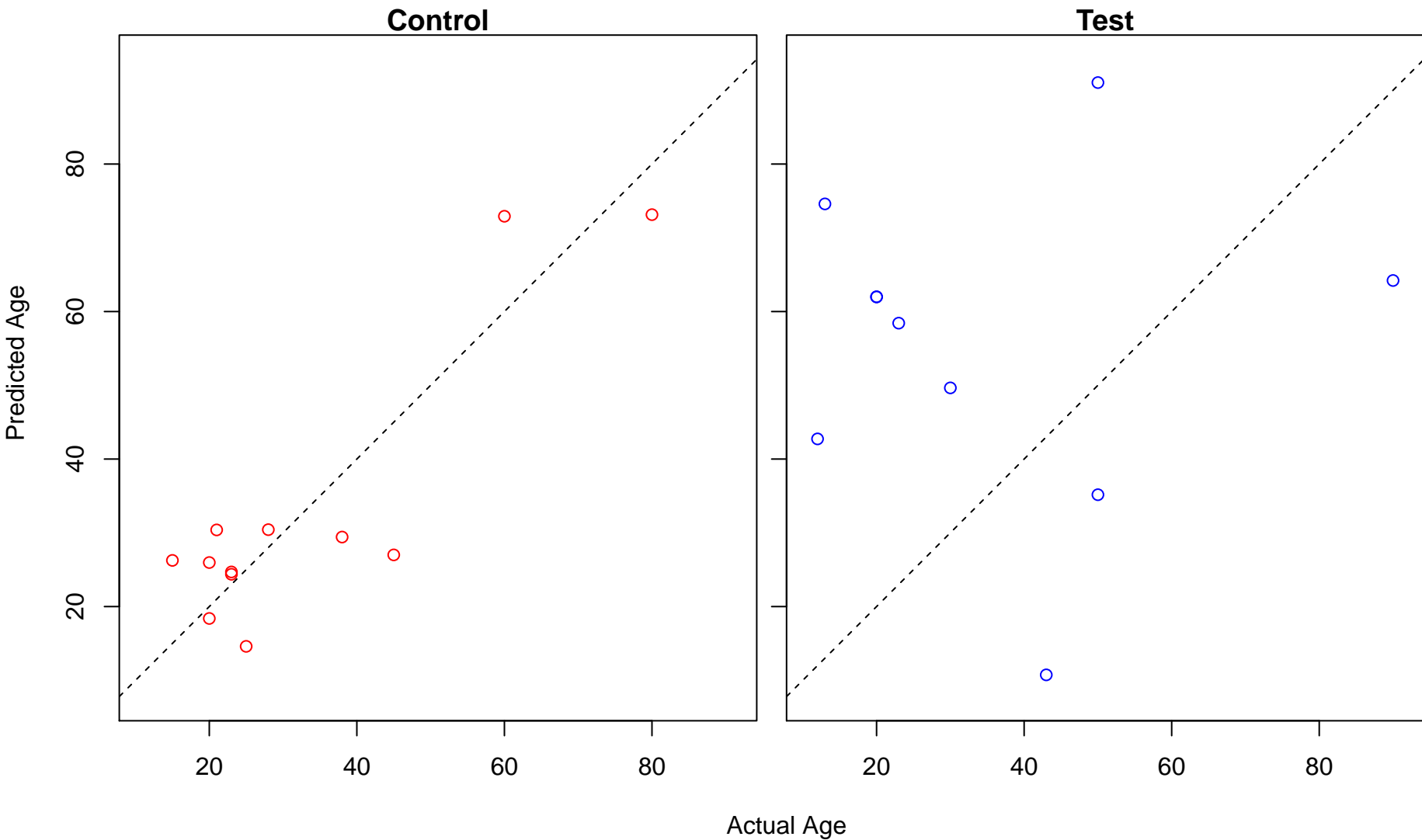
neuron projection extension involved in neuron projection guidance (Score: 13.351685)



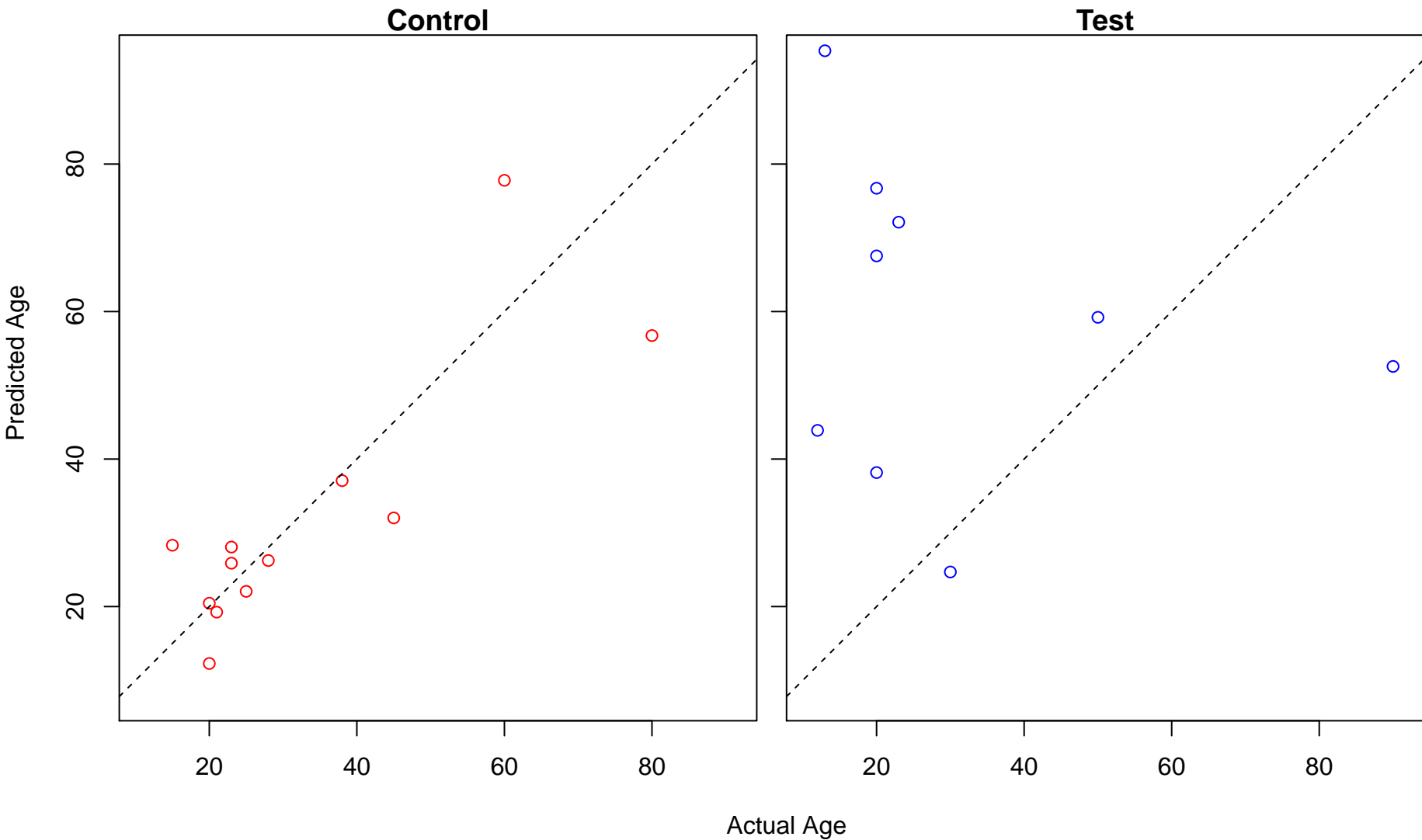
regulation of organ growth (Score: 13.316944)



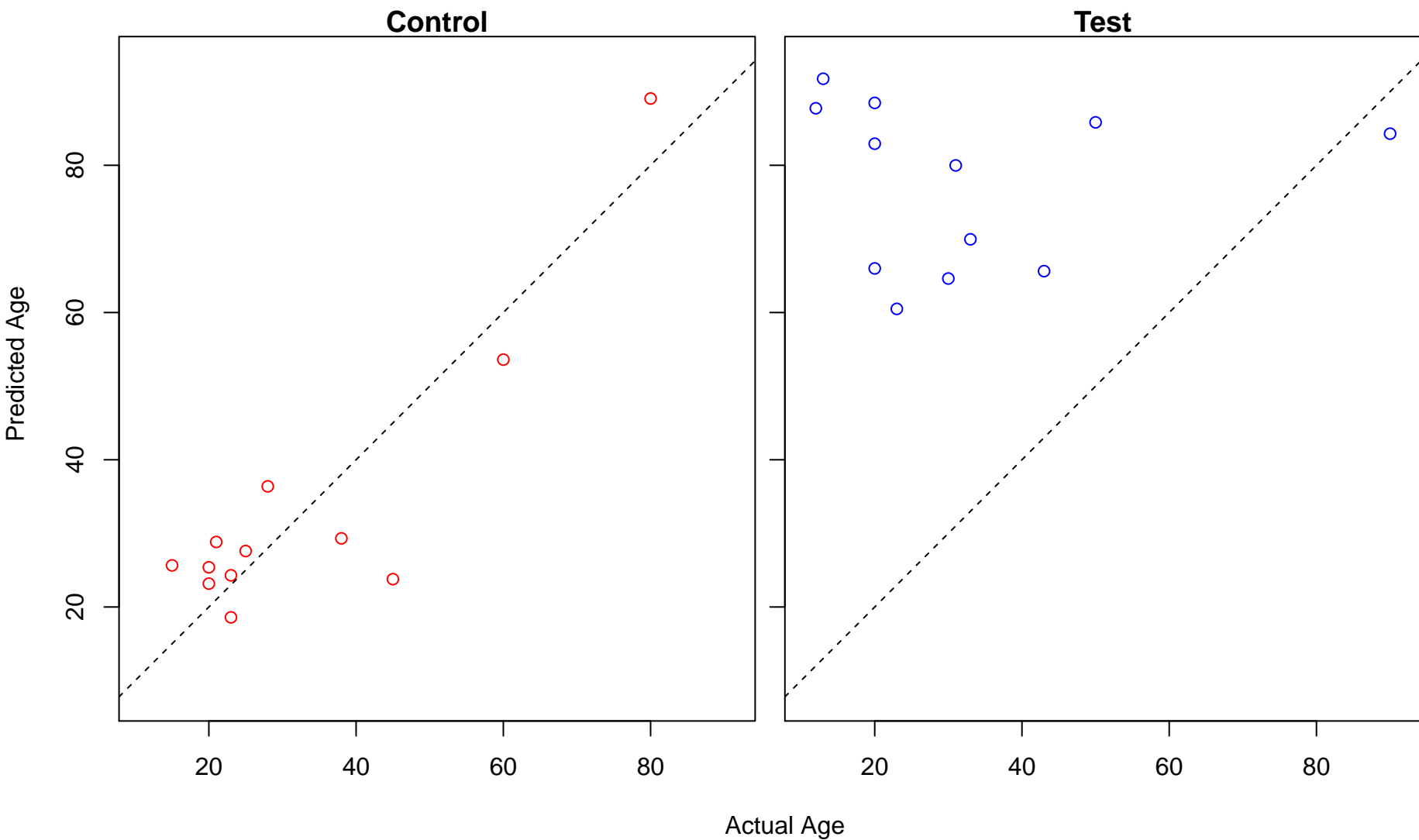
peptidyl-serine modification (Score: 13.303460)



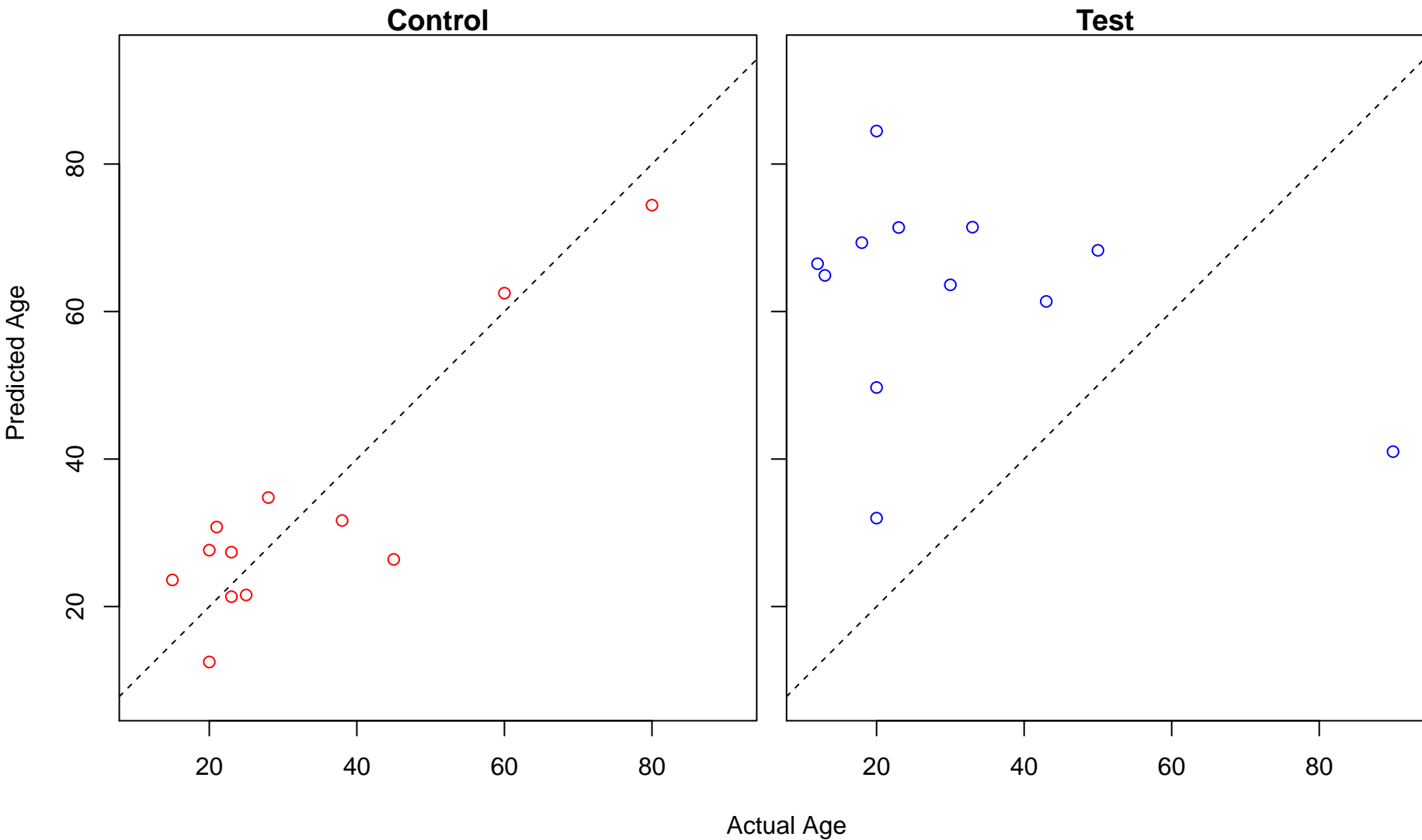
regulation of bone mineralization (Score: 13.266182)



CDP-choline pathway (Score: 13.258587)

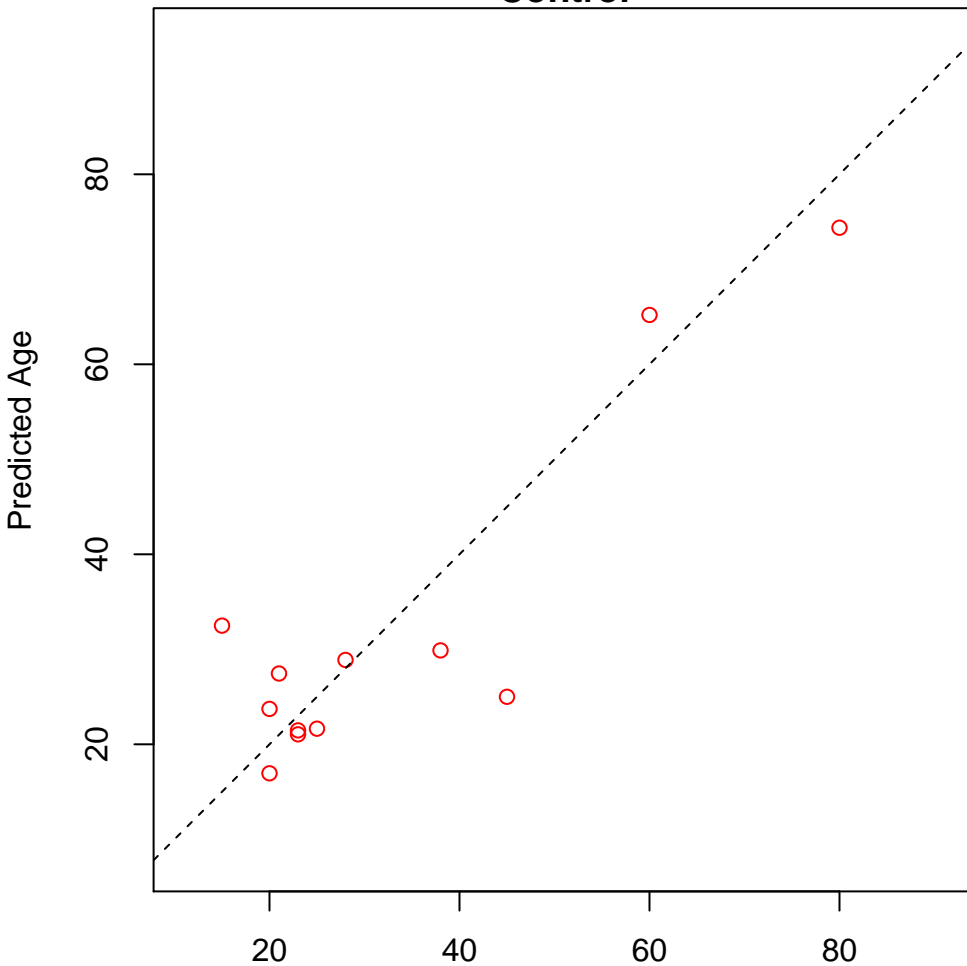


phagocytosis (Score: 13.221666)

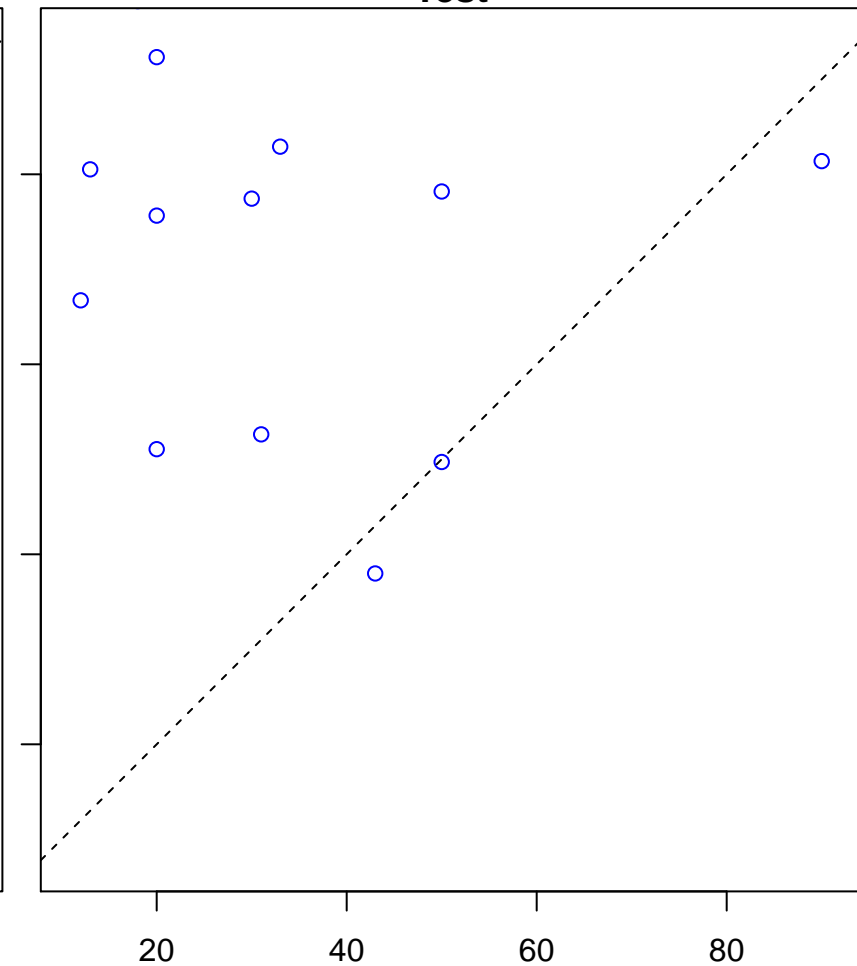


mitotic nuclear envelope disassembly (Score: 13.166662)

Control

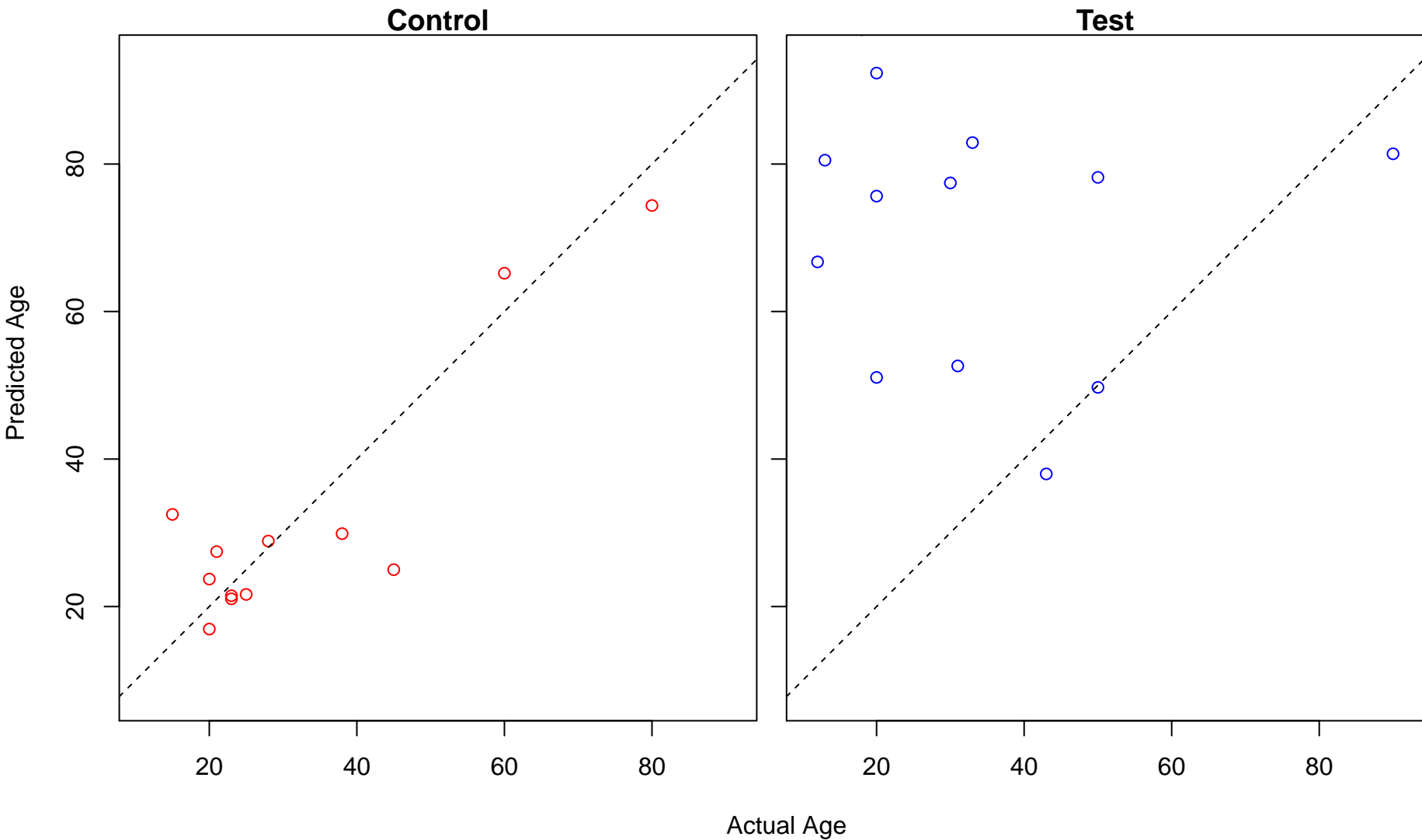


Test

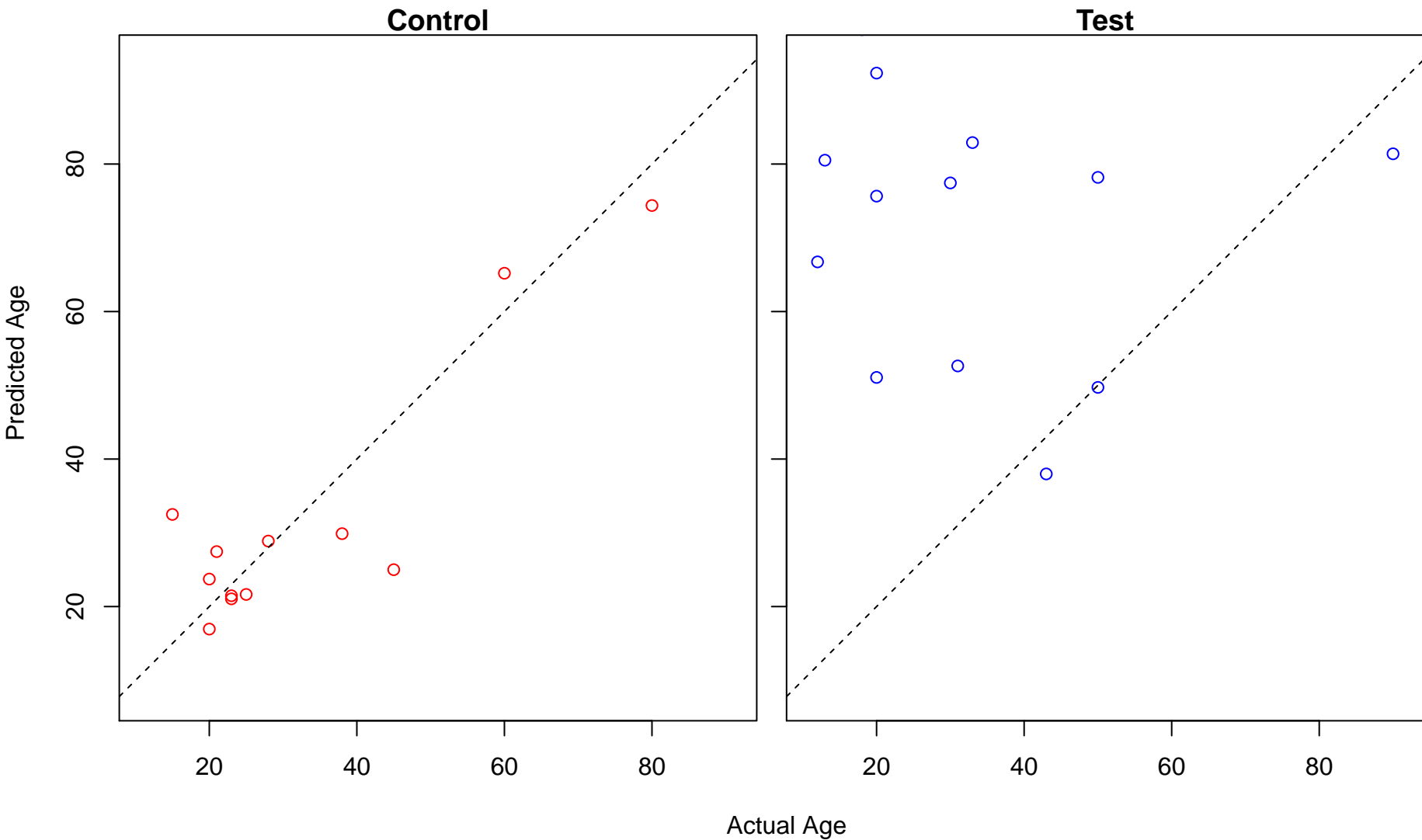


Actual Age

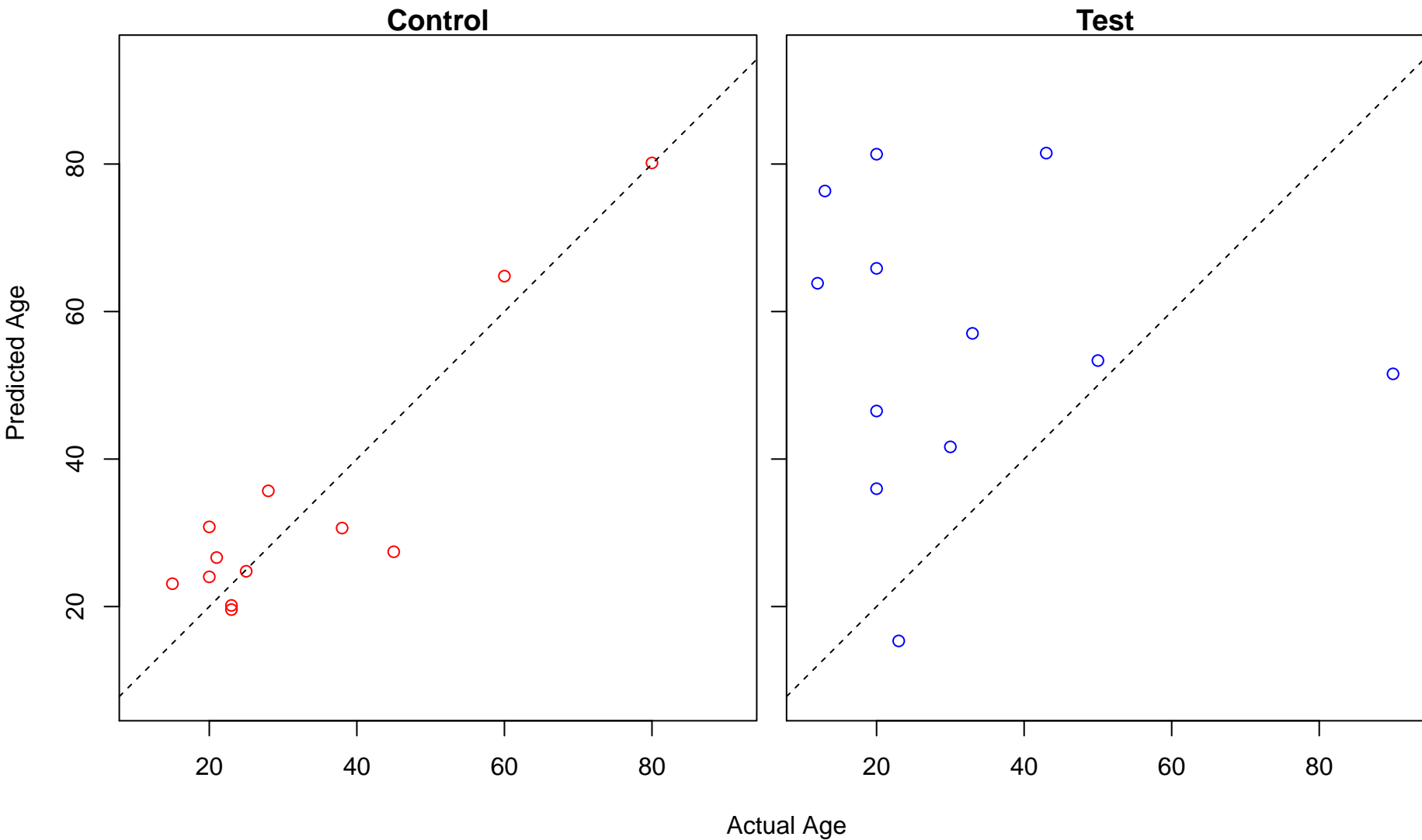
membrane disassembly (Score: 13.166662)



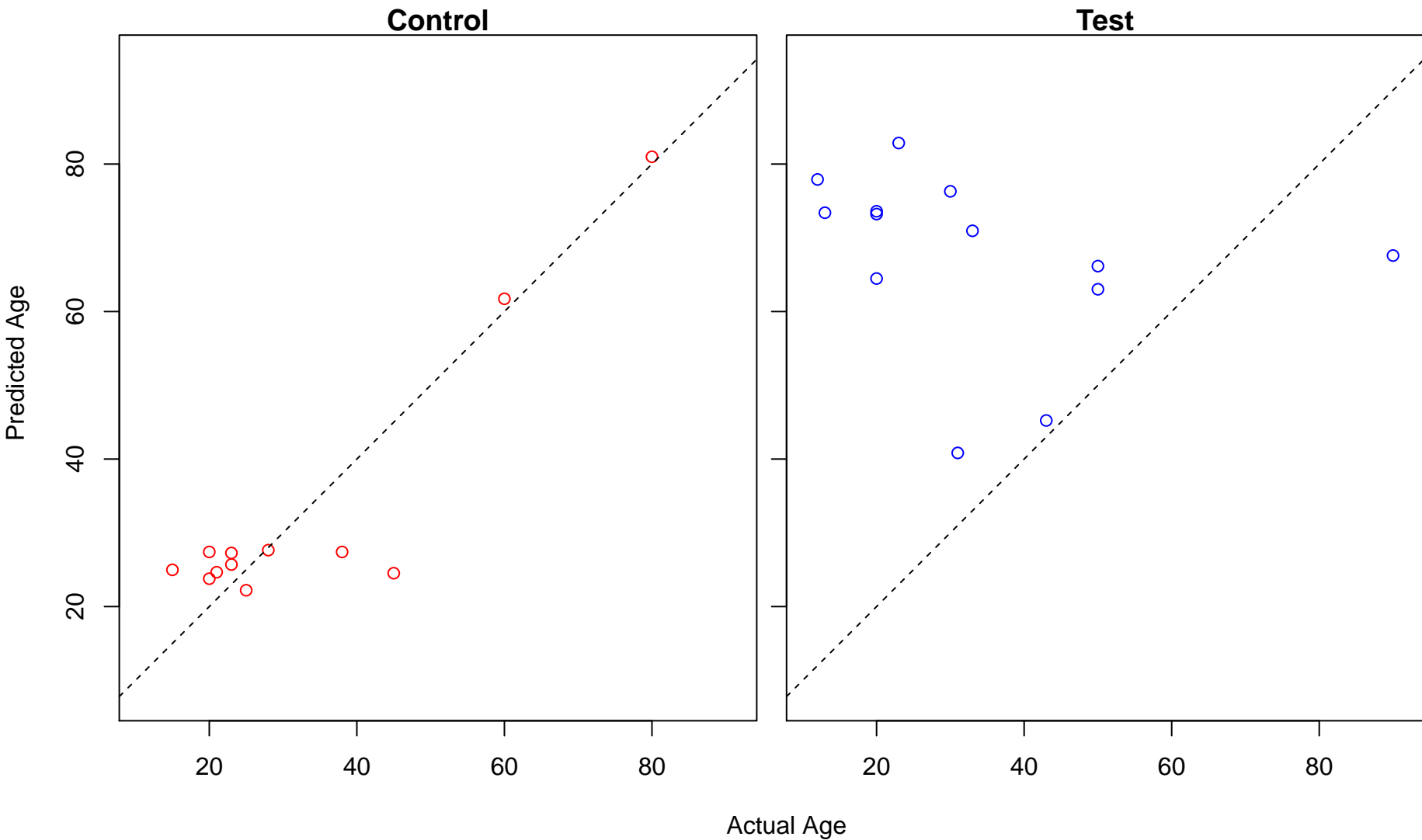
nuclear envelope disassembly (Score: 13.16662)



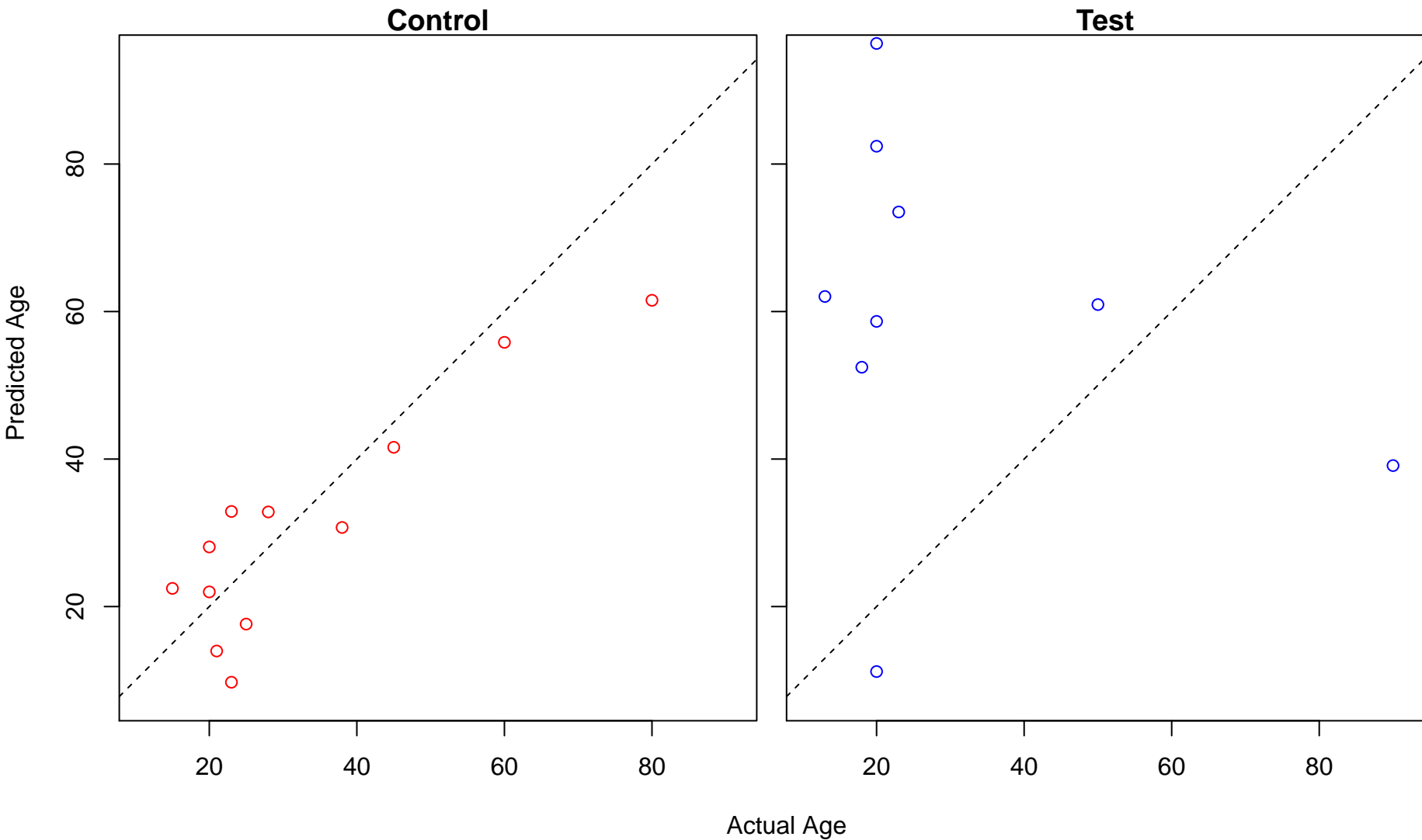
protein export from nucleus (Score: 13.162948)



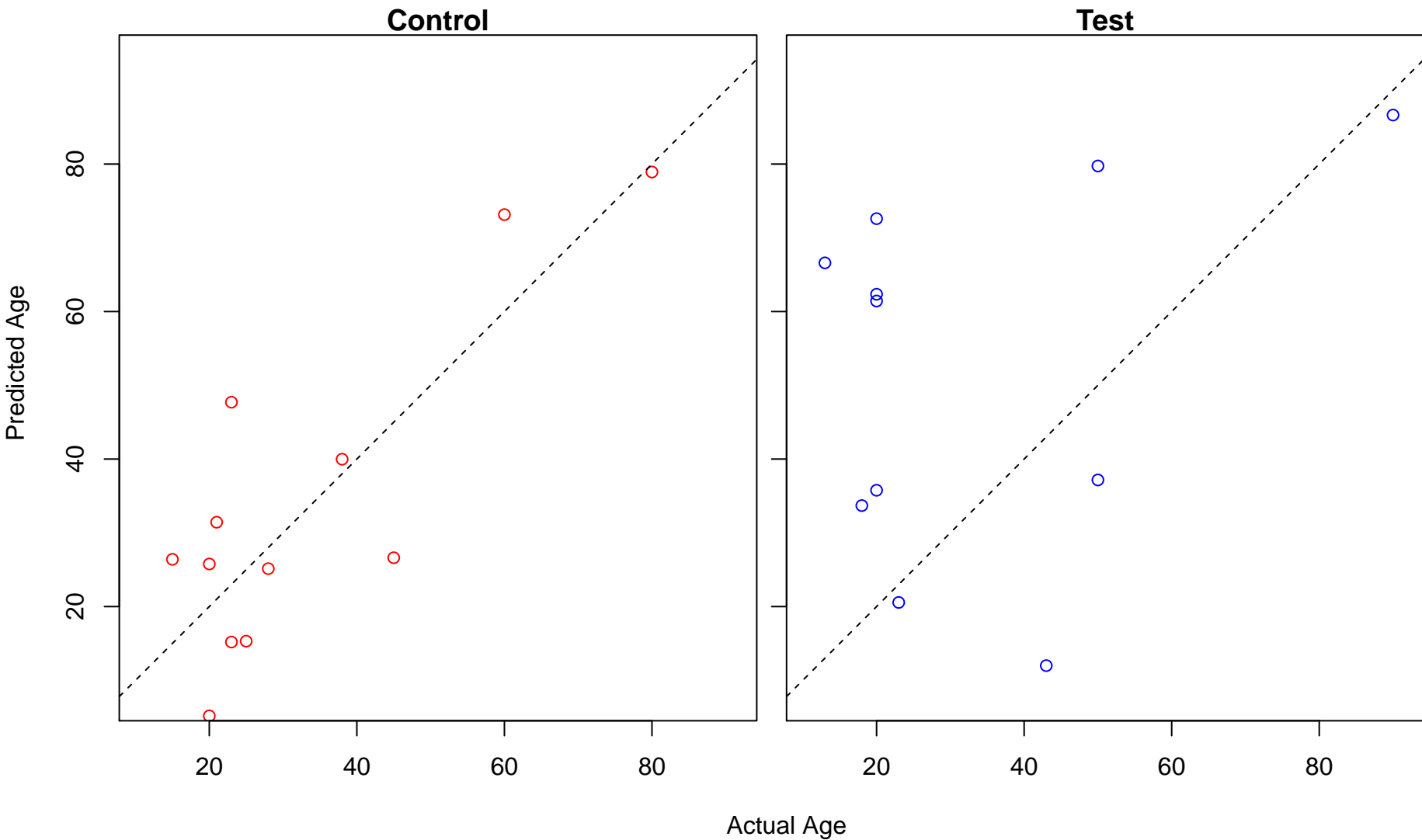
genitalia development (Score: 13.151666)



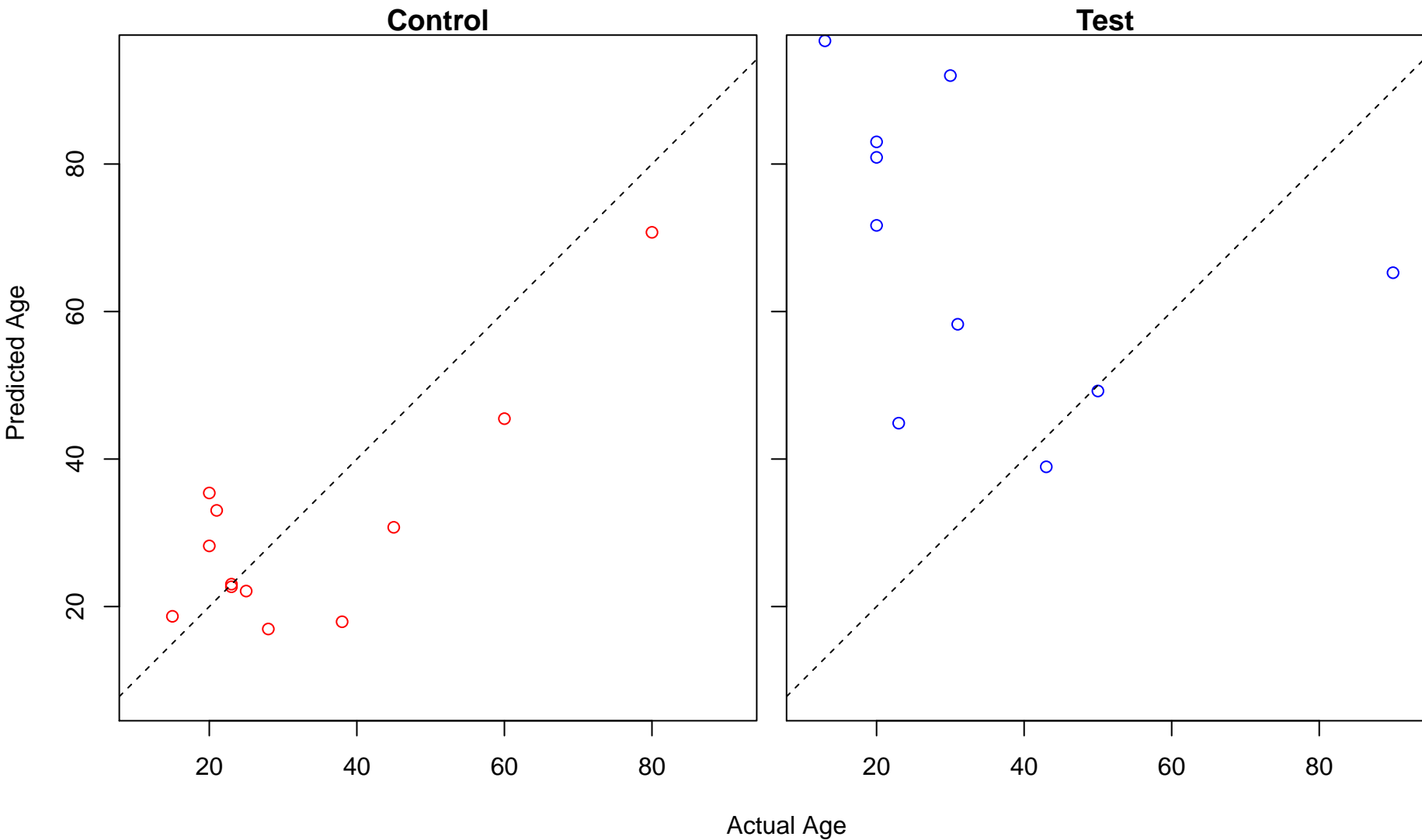
positive regulation of translational initiation (Score: 13.144666)



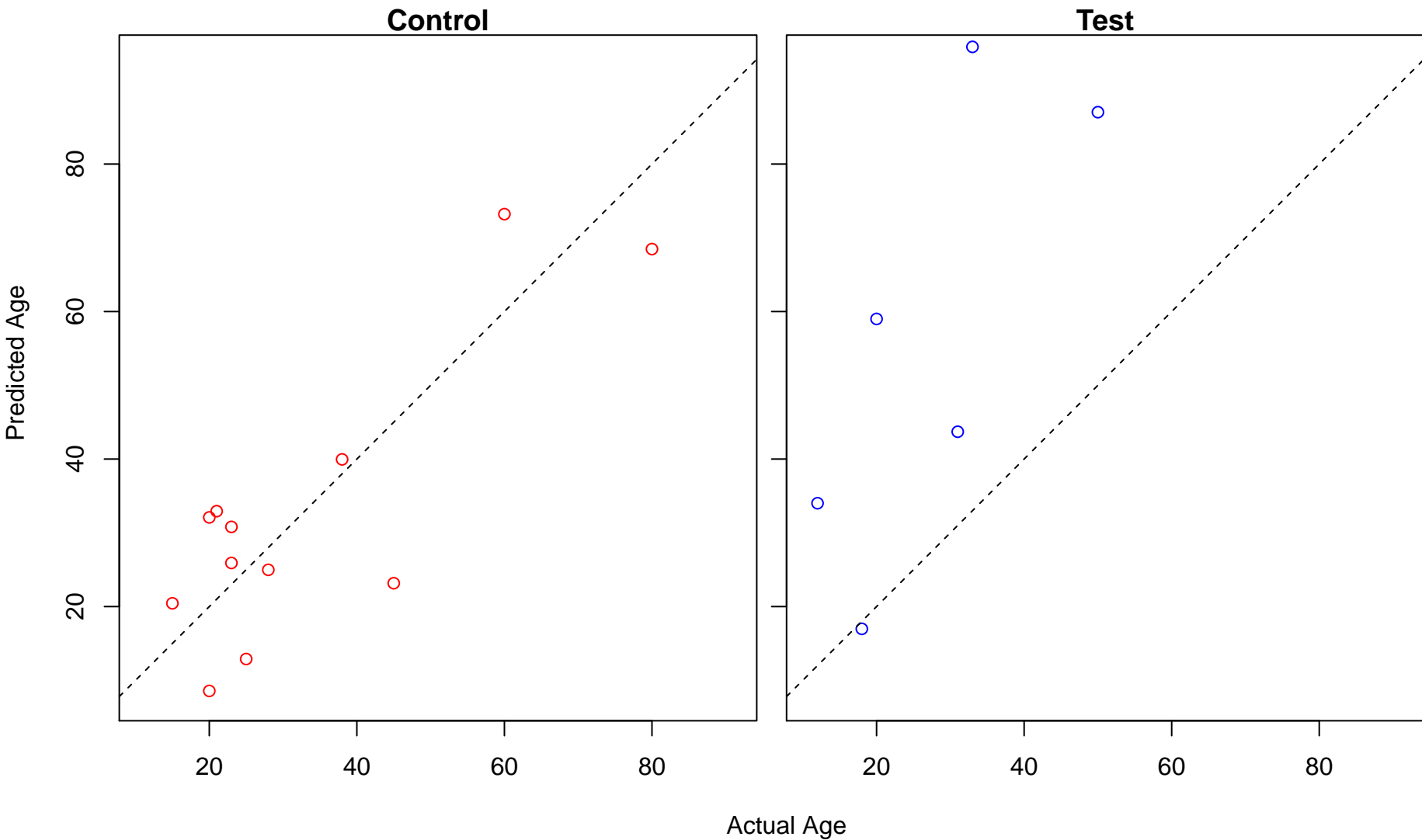
endothelial cell chemotaxis (Score: 13.130623)



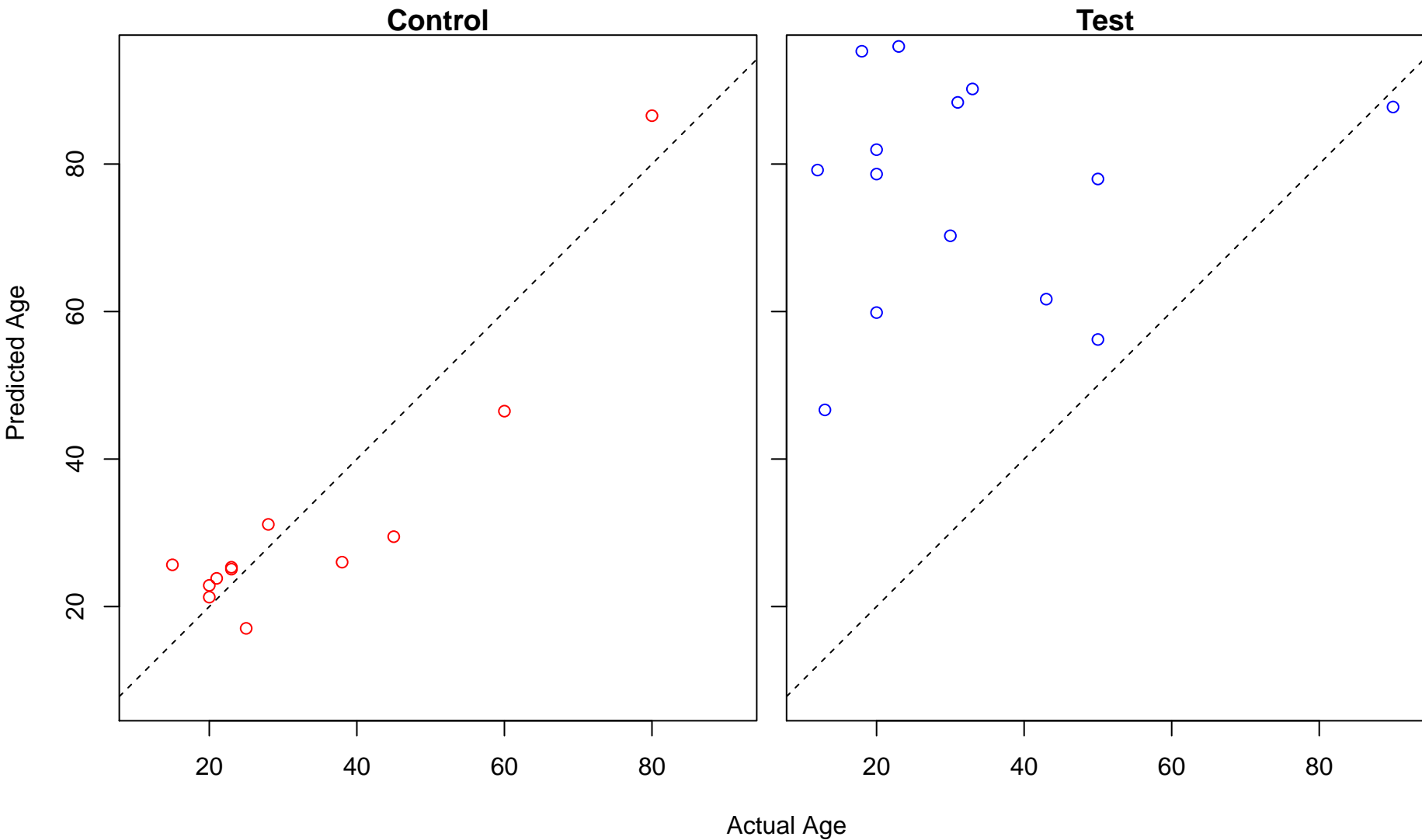
asymmetric stem cell division (Score: 13.126867)



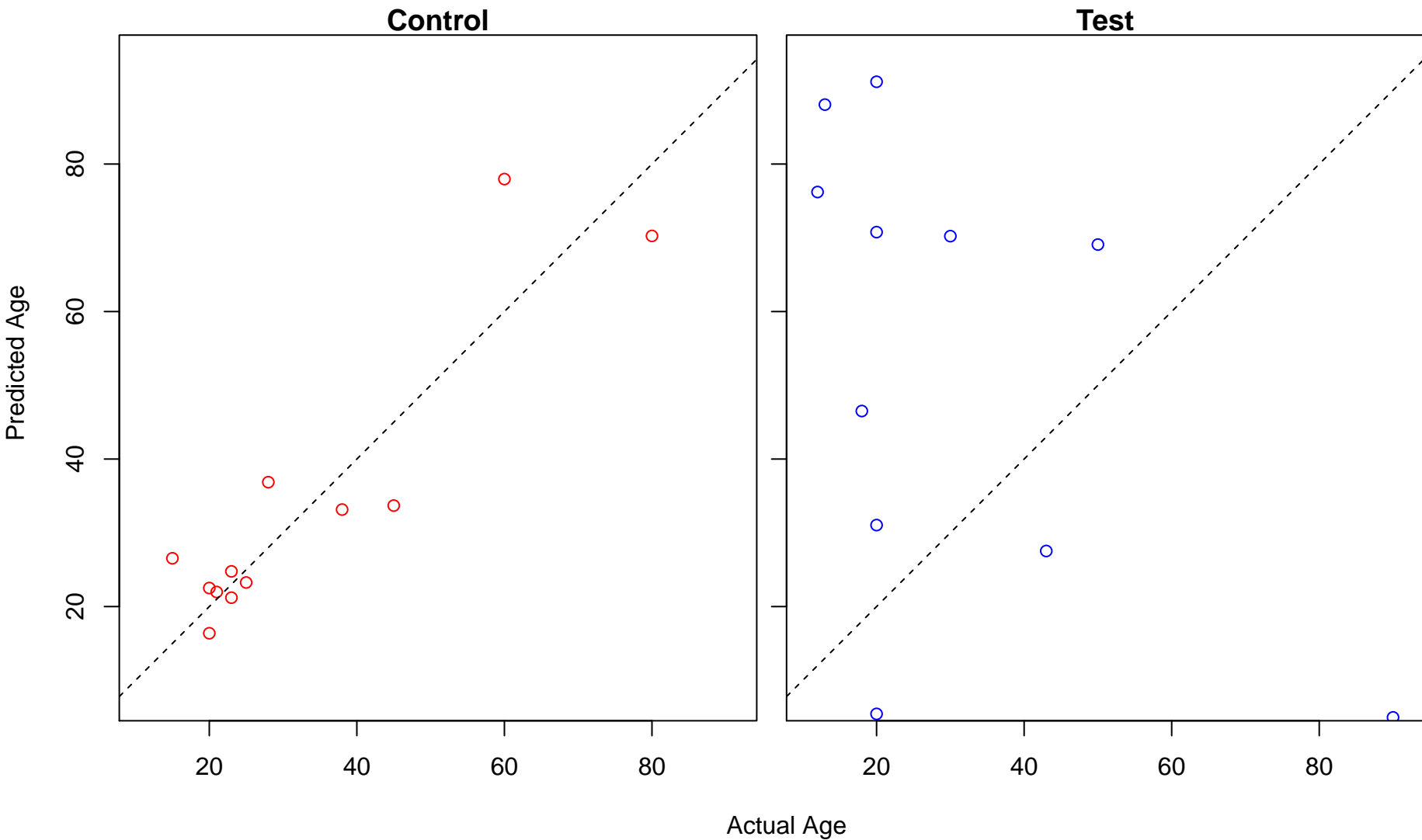
sequestering of actin monomers (Score: 13.107763)



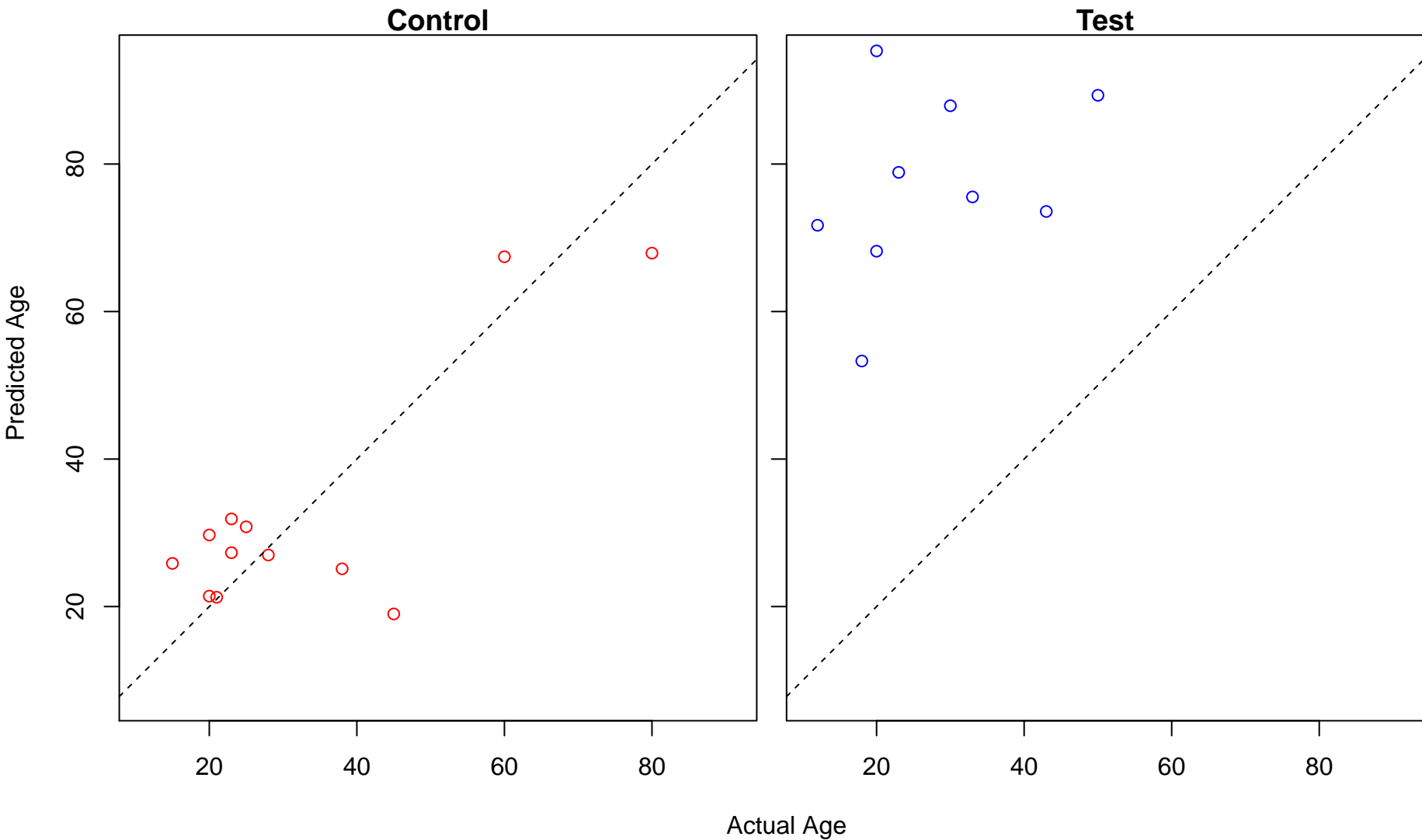
cellular component assembly involved in morphogenesis (Score: 13.105602)



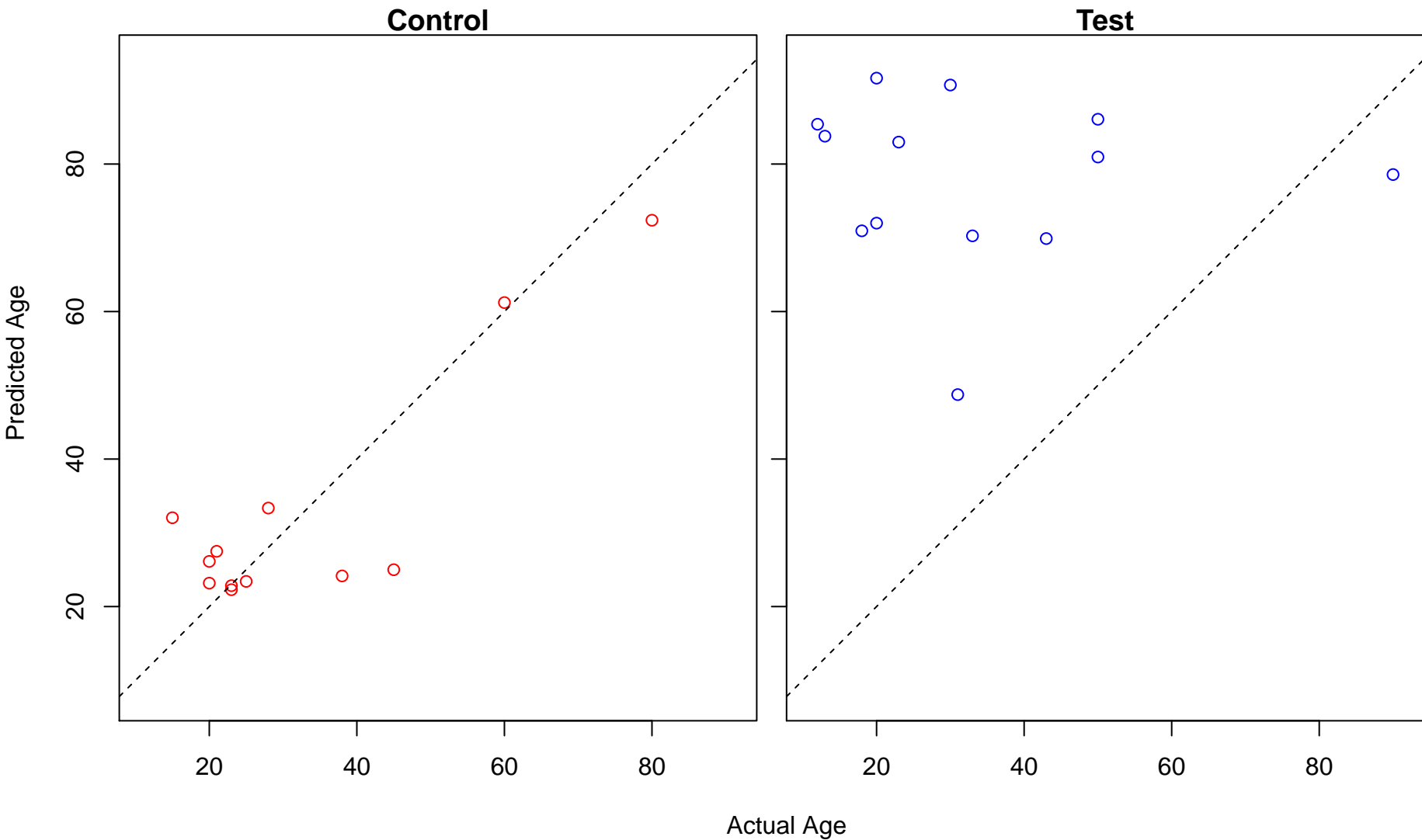
cytokine secretion (Score: 13.103913)



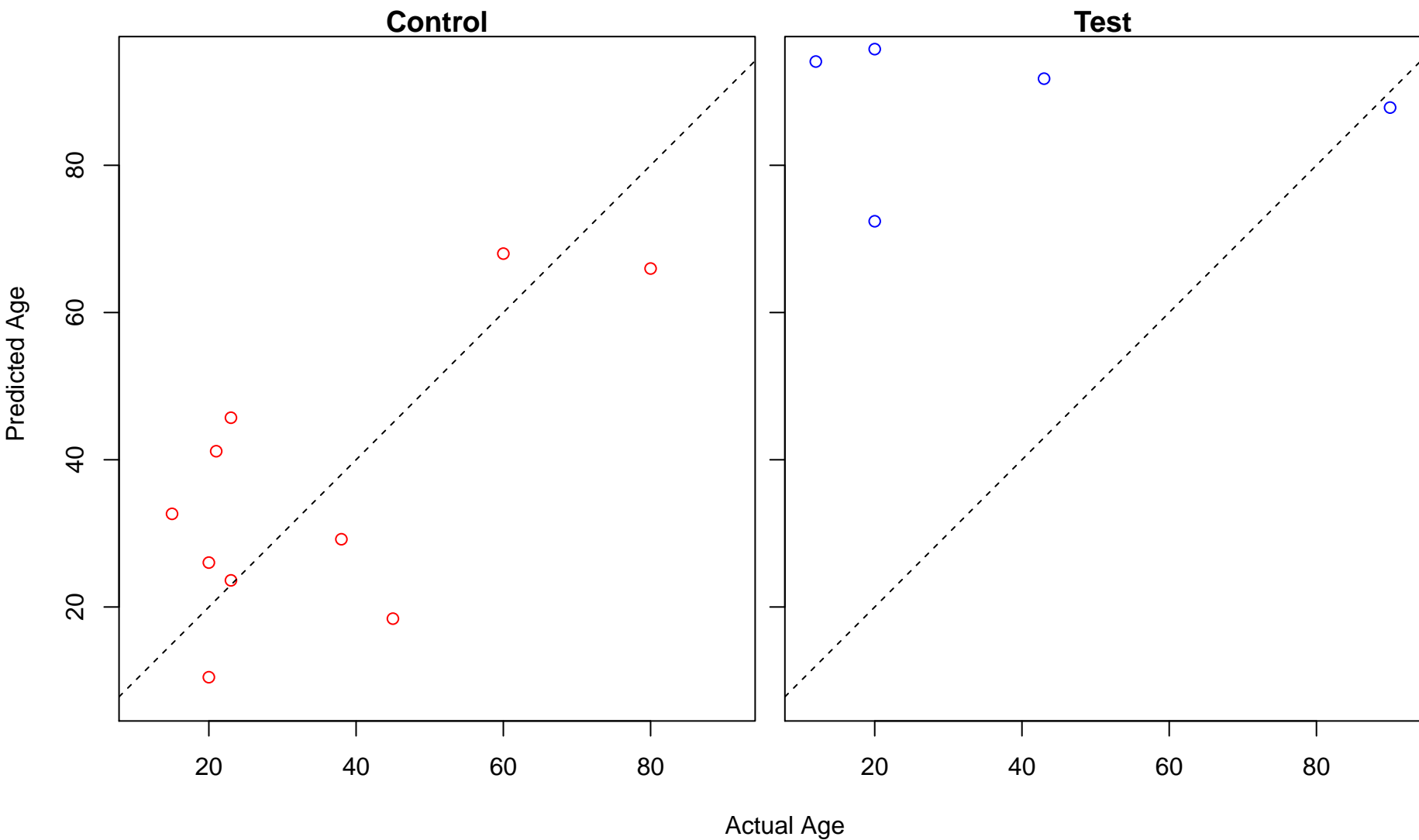
positive regulation of inflammatory response (Score: 13.050725)



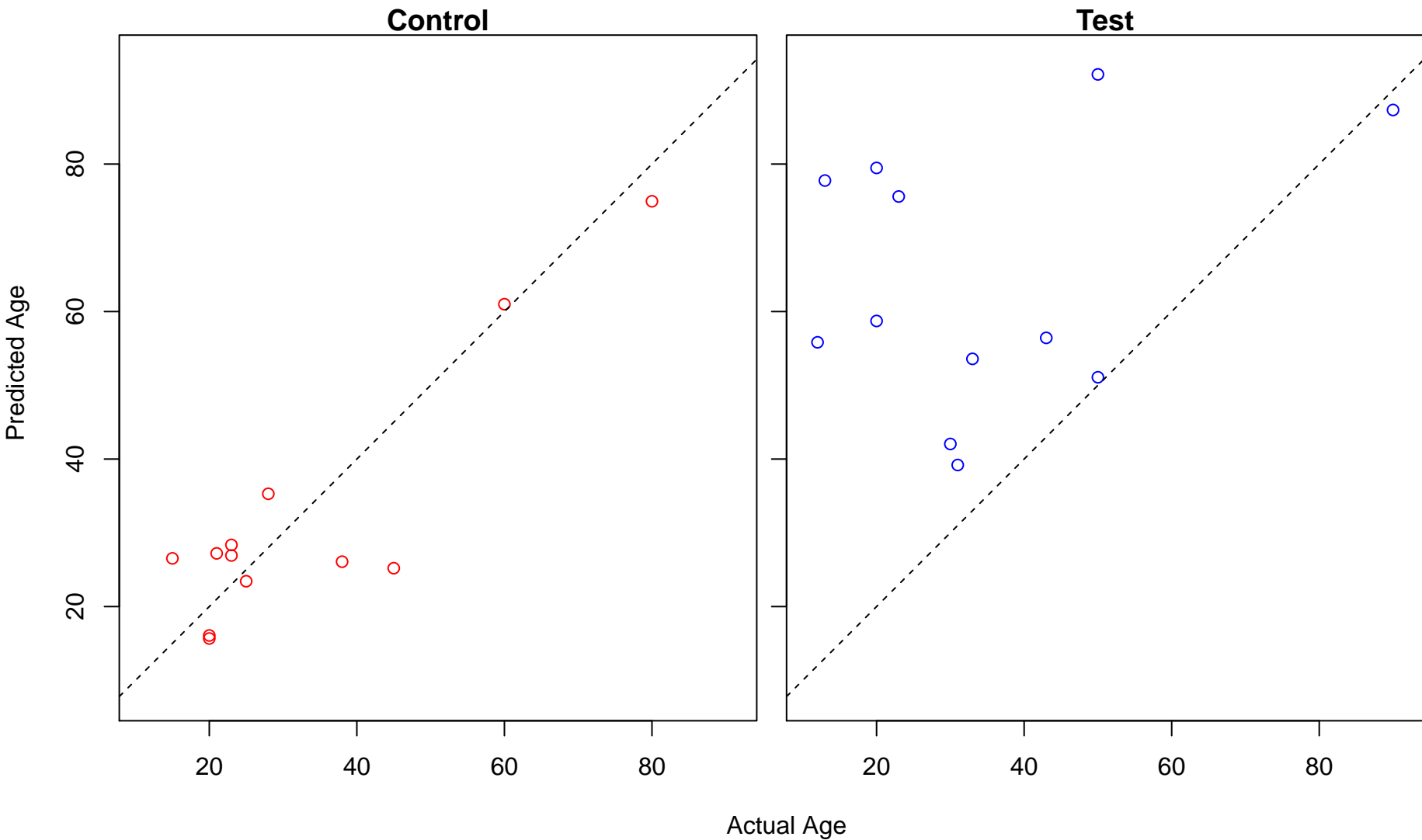
regulation of superoxide anion generation (Score: 13.044805)



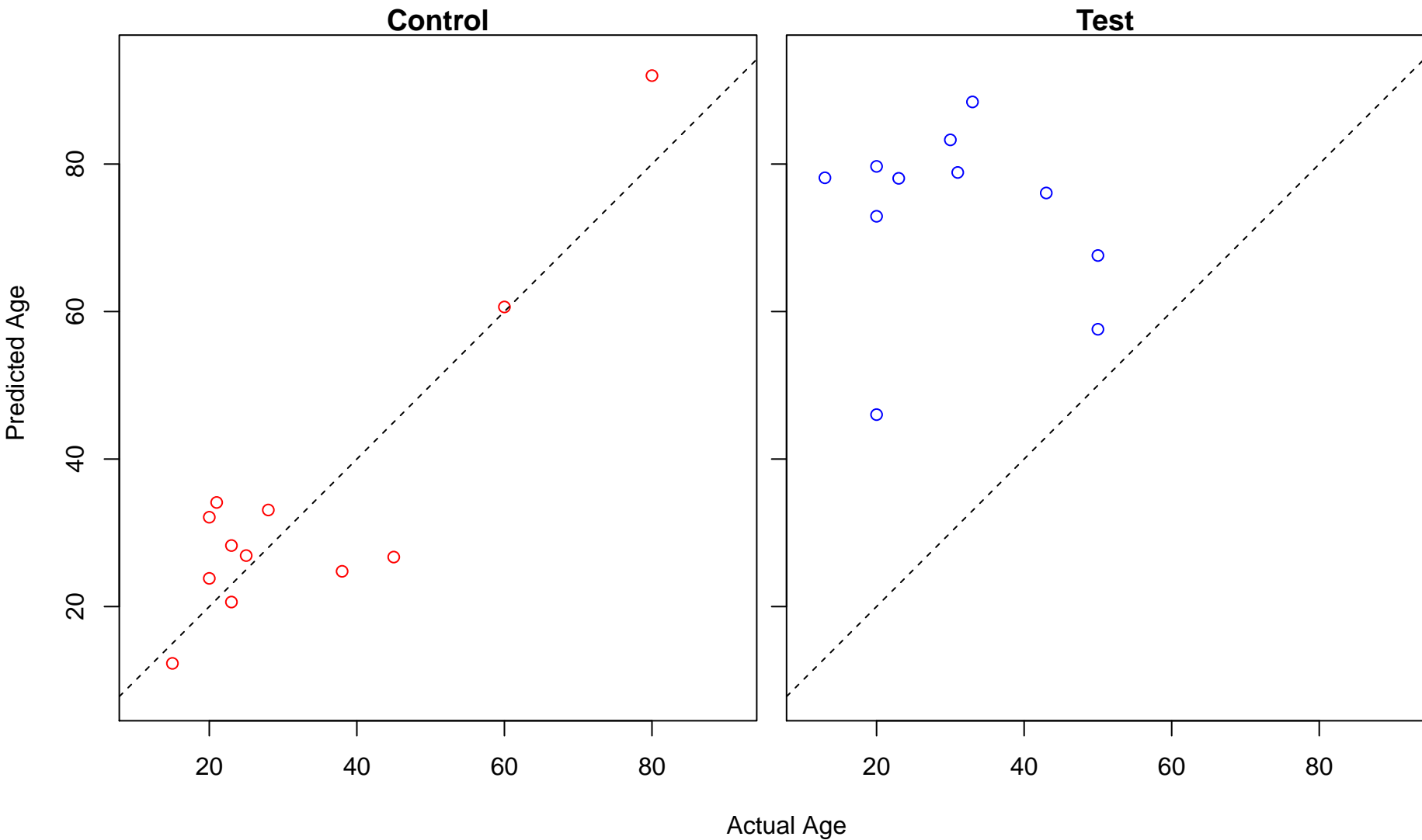
positive regulation of protein processing (Score: 13.012897)



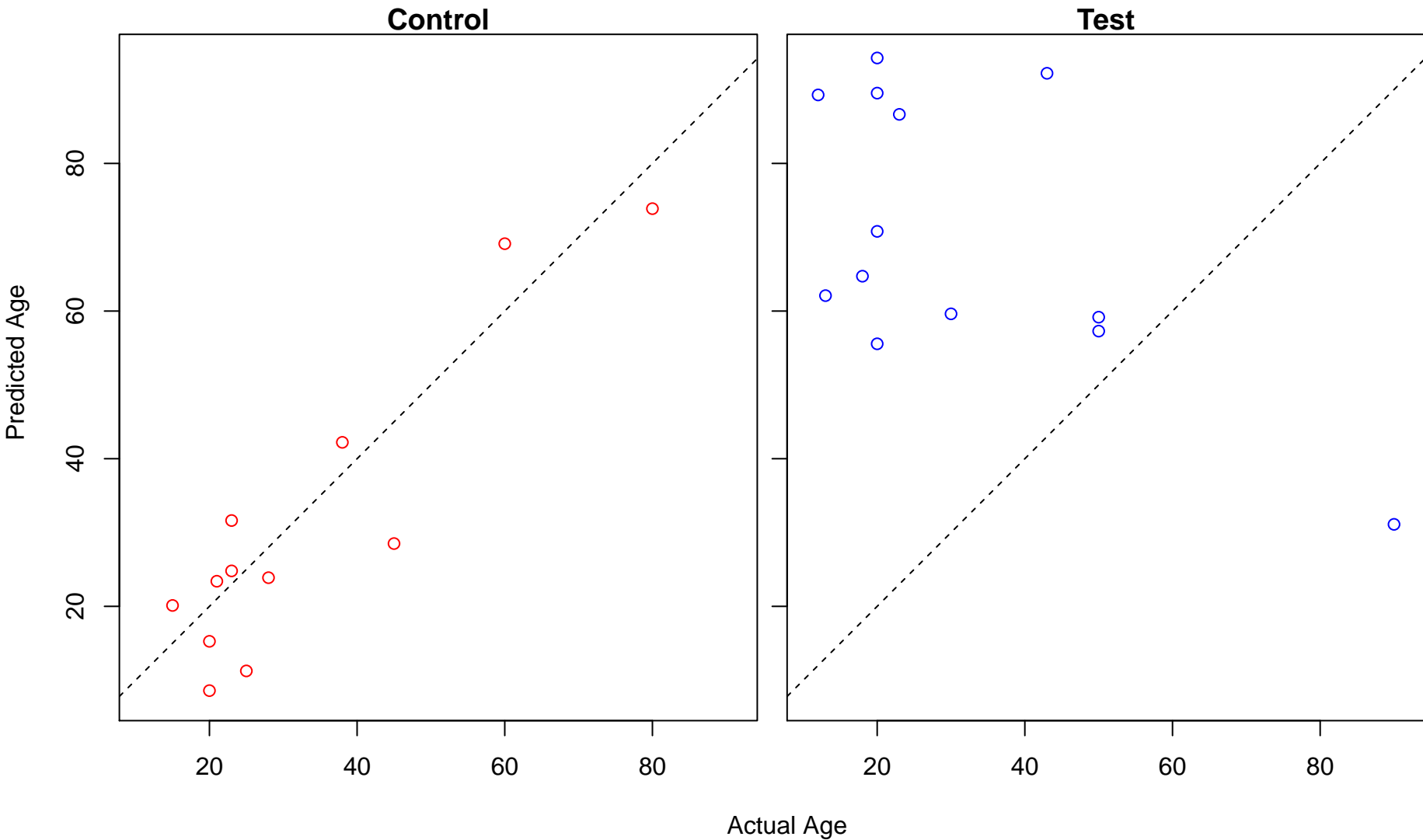
adenylate cyclase-activating G-protein coupled receptor signaling pathway (Score: 13.006964)



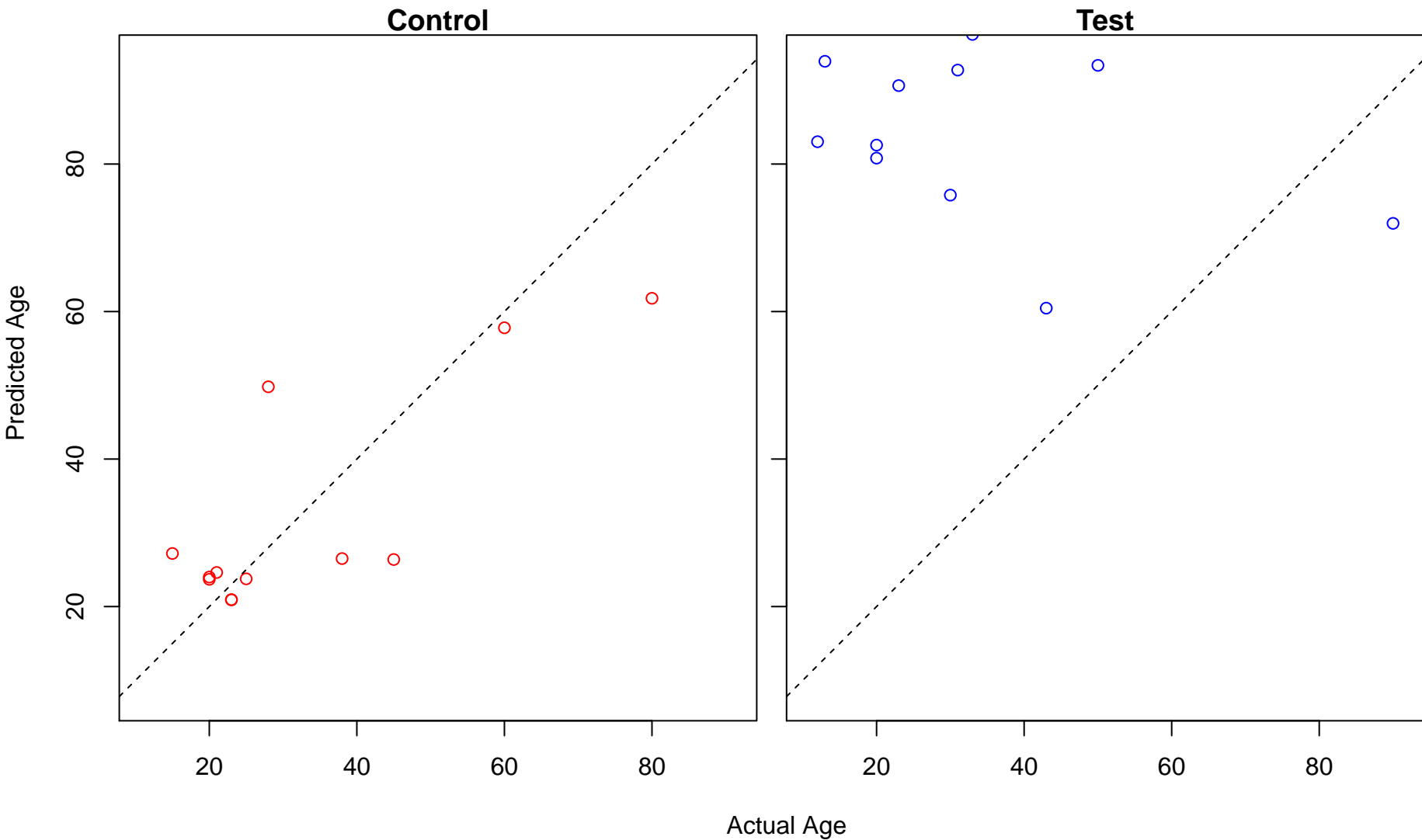
negative regulation of sequestering of triglyceride (Score: 12.997124)



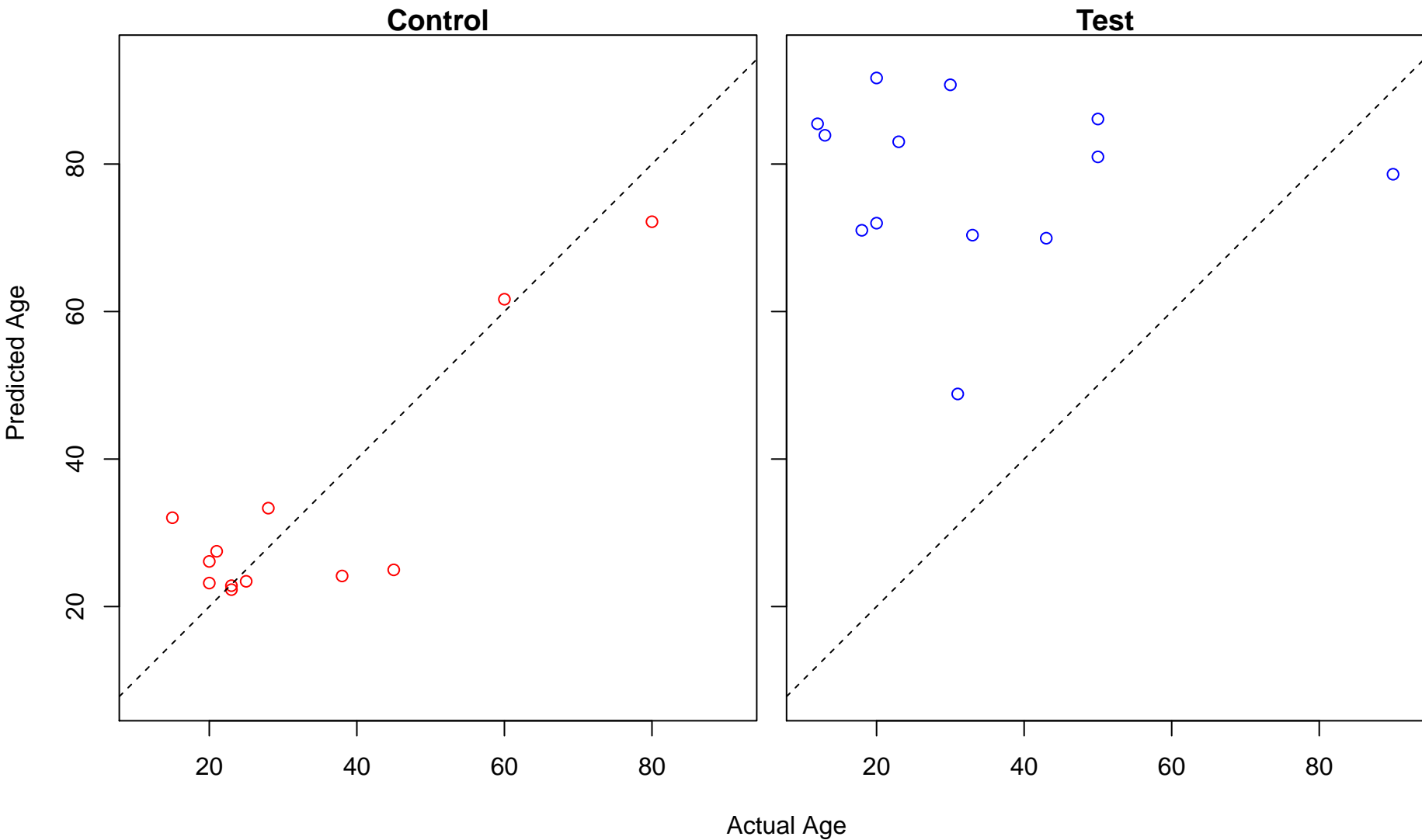
positive regulation of potassium ion transmembrane transport (Score: 12.982091)



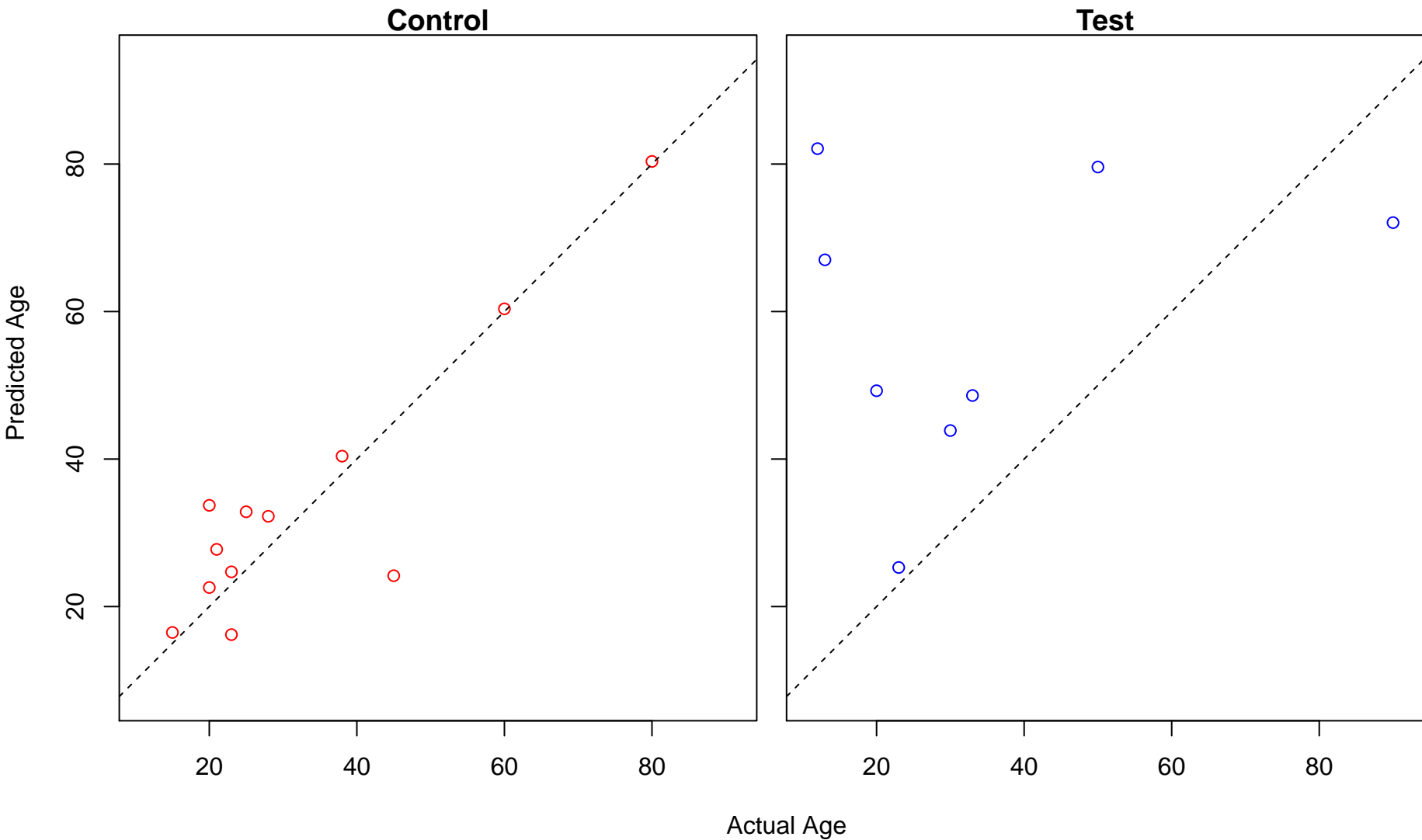
positive regulation of fatty acid biosynthetic process (Score: 12.976828)



positive regulation of superoxide anion generation (Score: 12.972275)

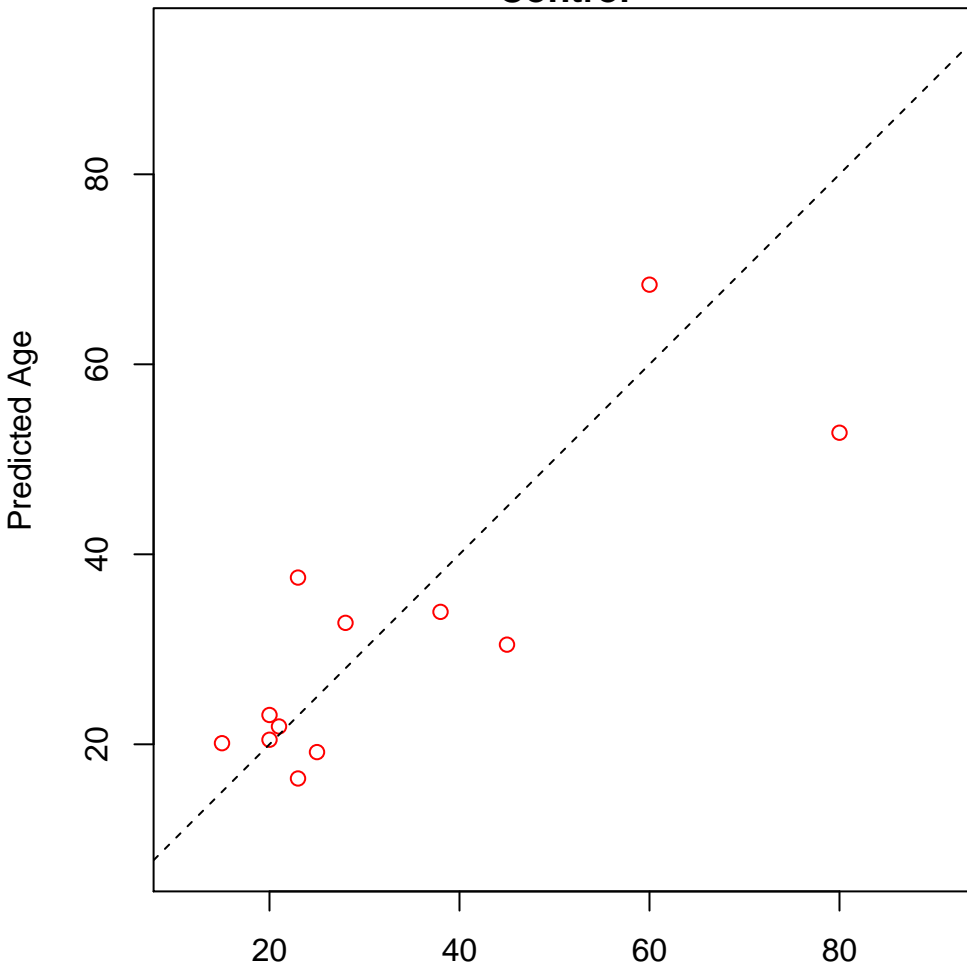


negative regulation of smooth muscle cell migration (Score: 12.960233)

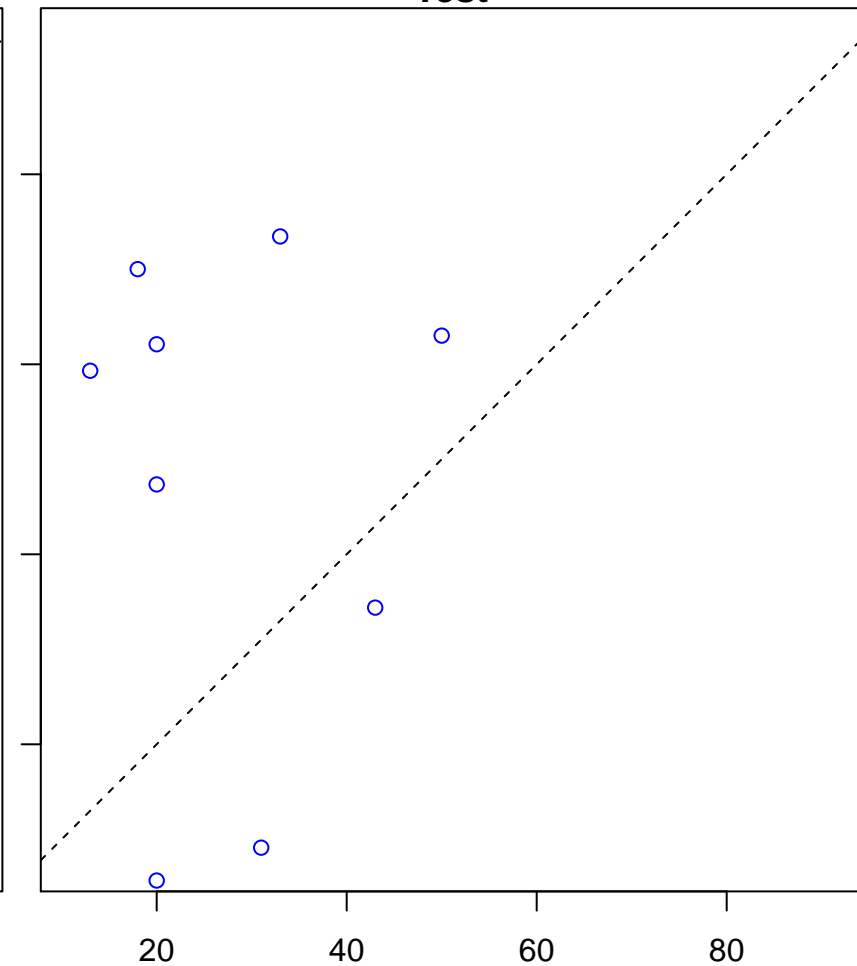


regulation of glial cell differentiation (Score: 12.943993)

Control

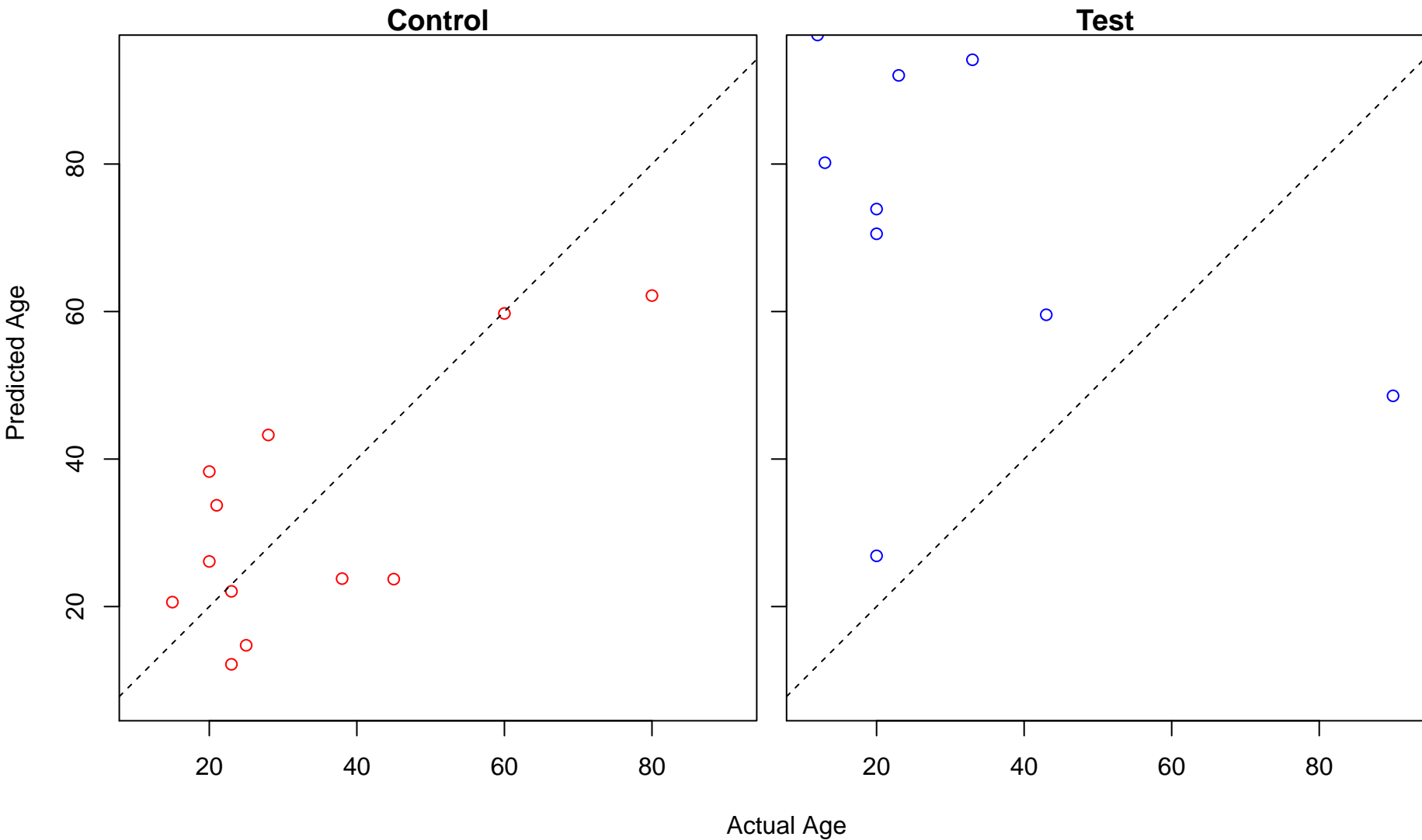


Test

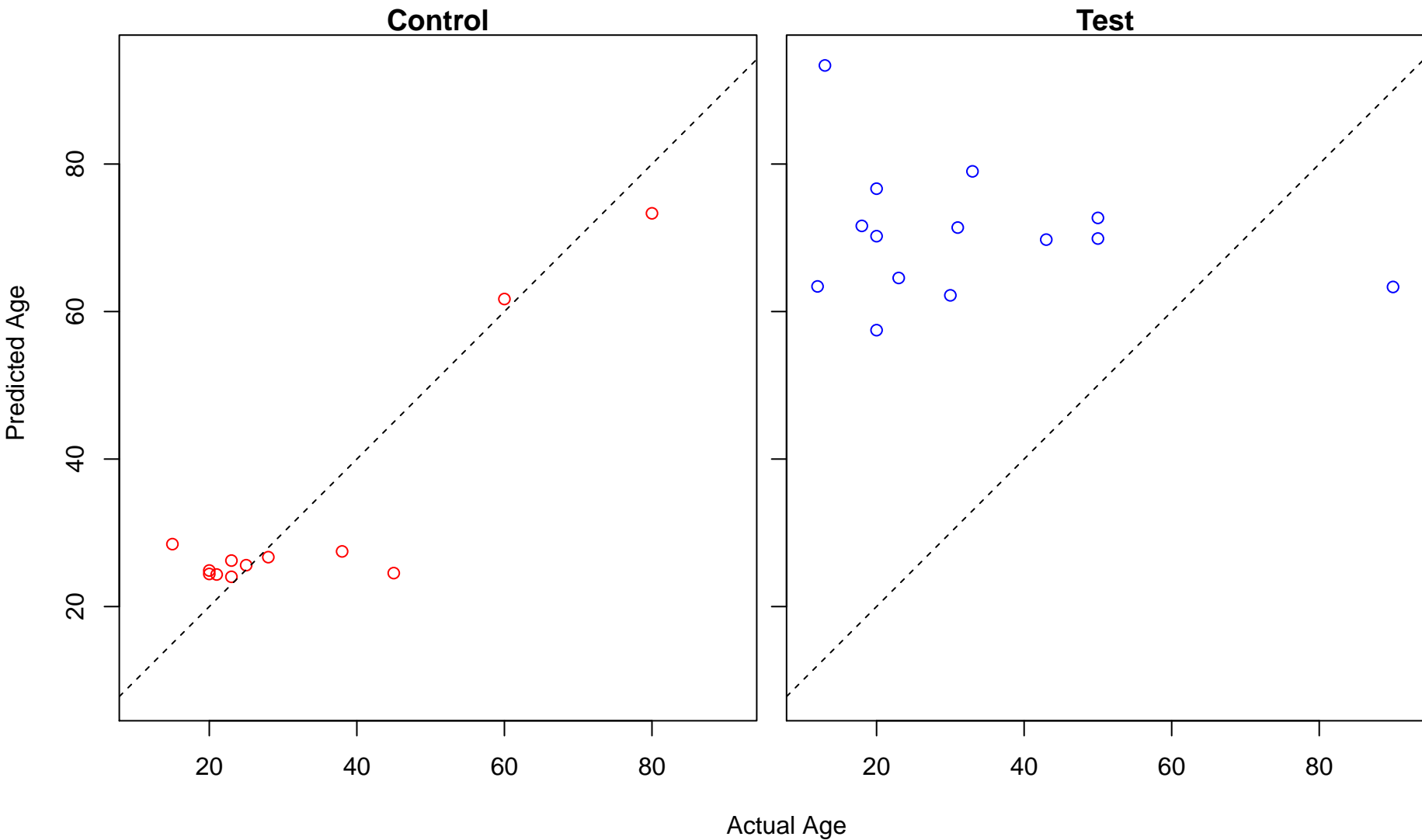


Actual Age

pore complex assembly (Score: 12.931487)

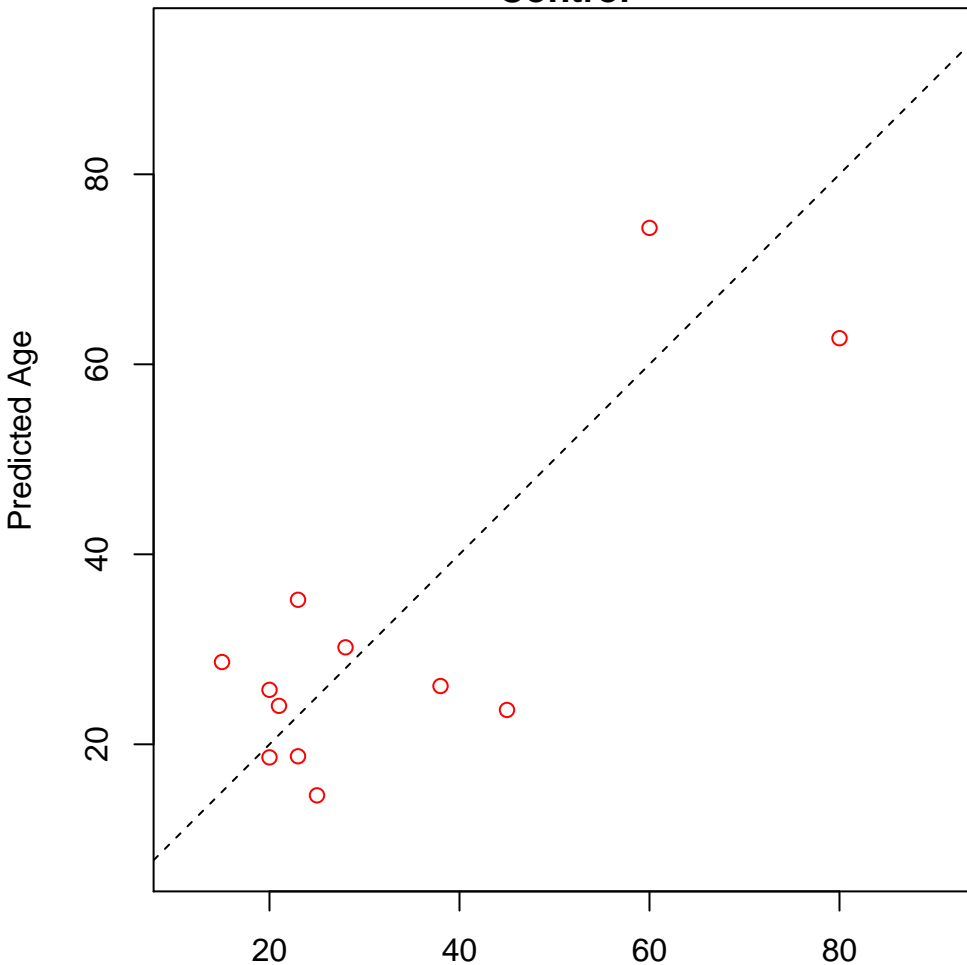


non-canonical Wnt signaling pathway via MAPK cascade (Score: 12.926581)

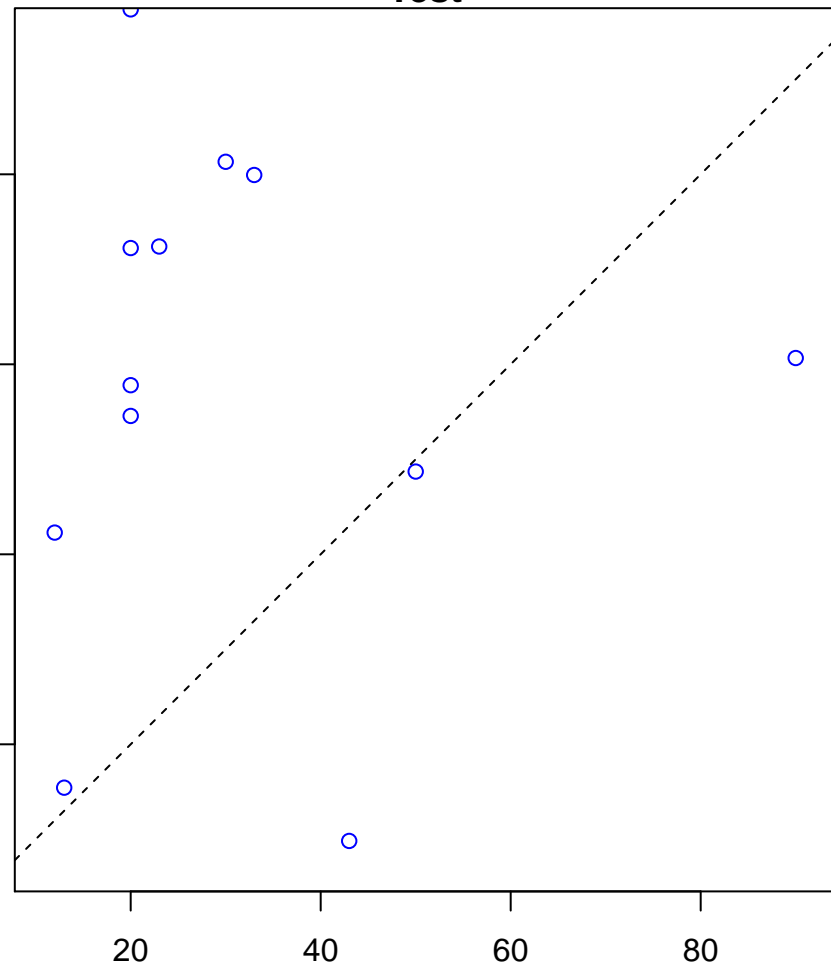


positive regulation of mitotic cell cycle (Score: 12.925659)

Control

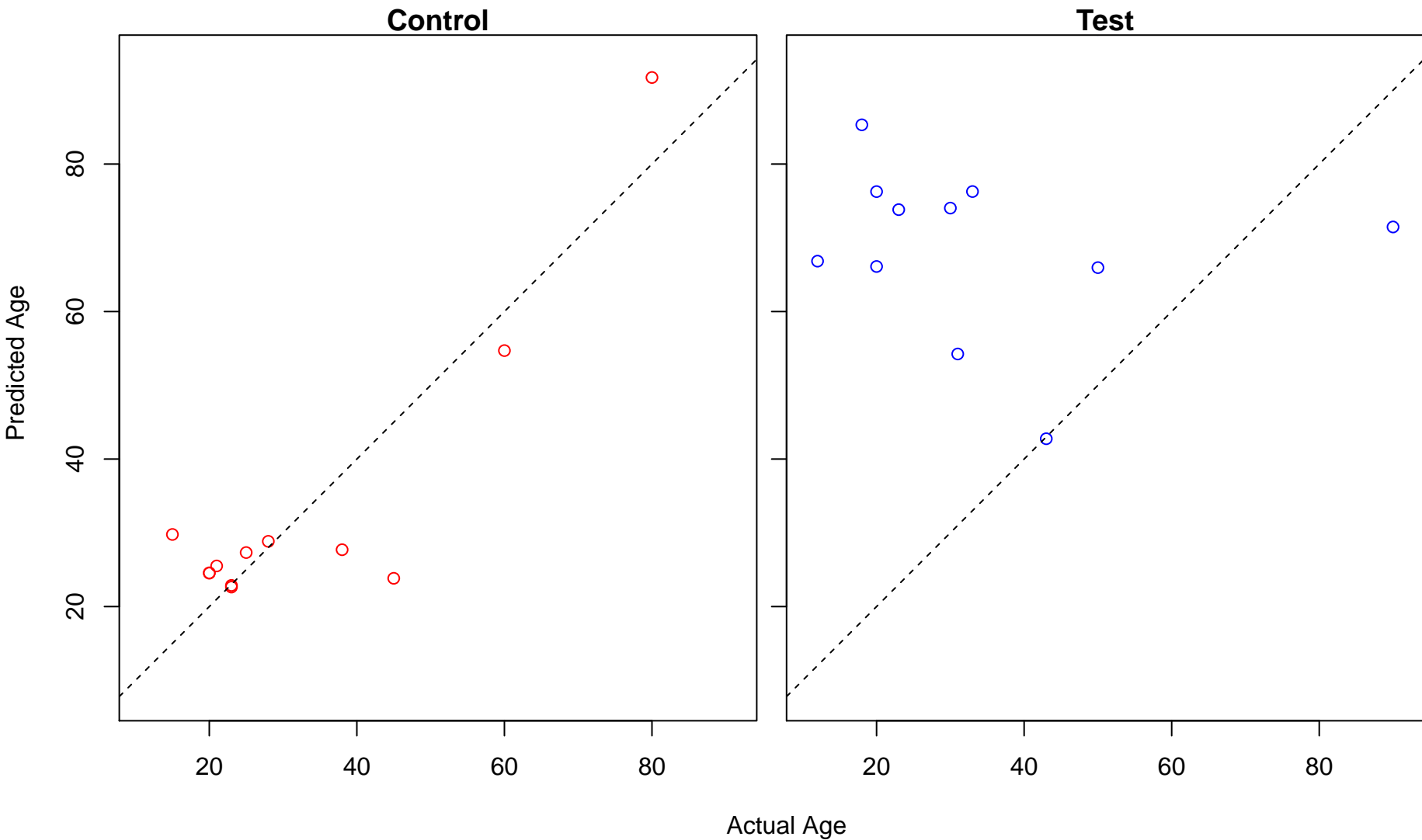


Test

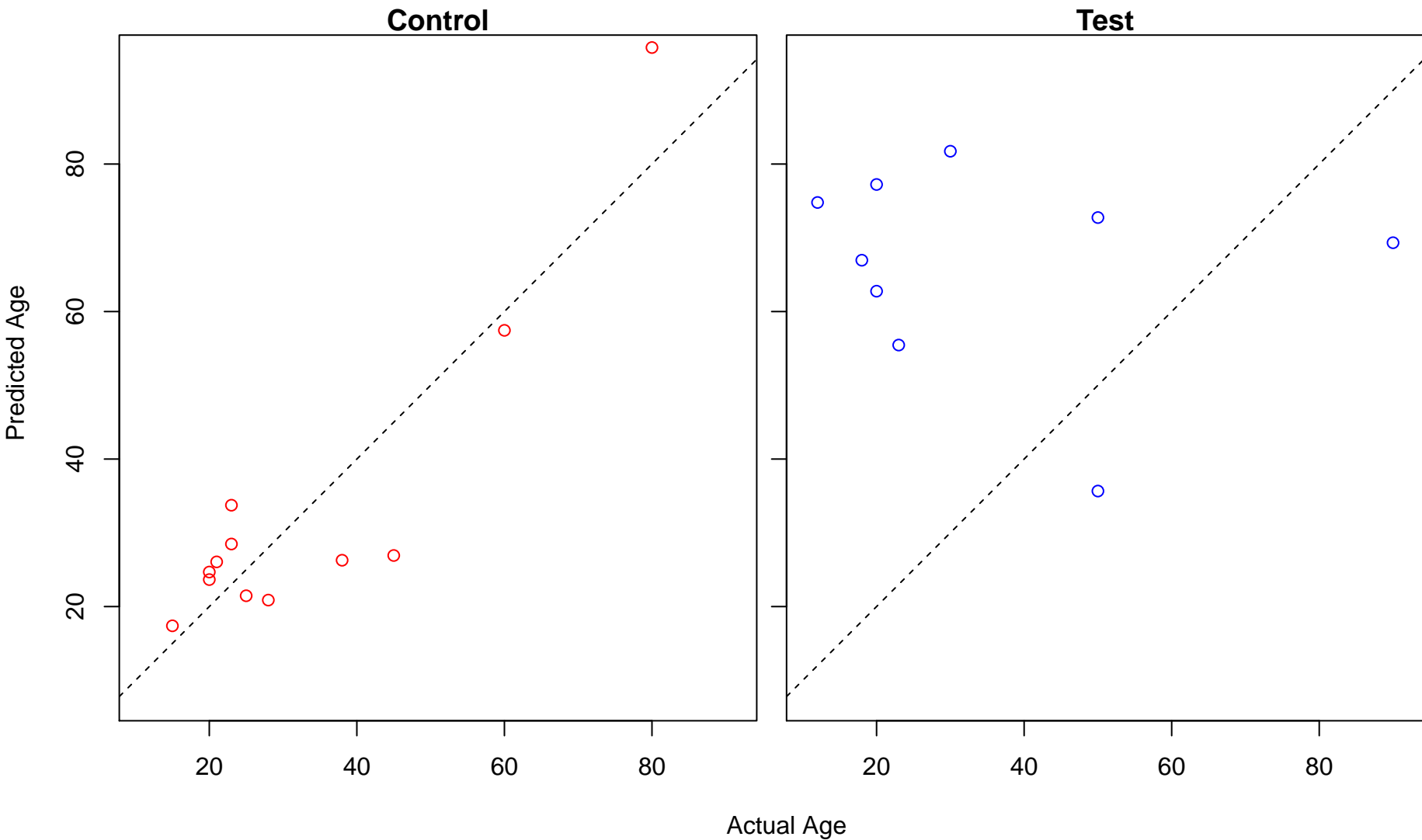


Actual Age

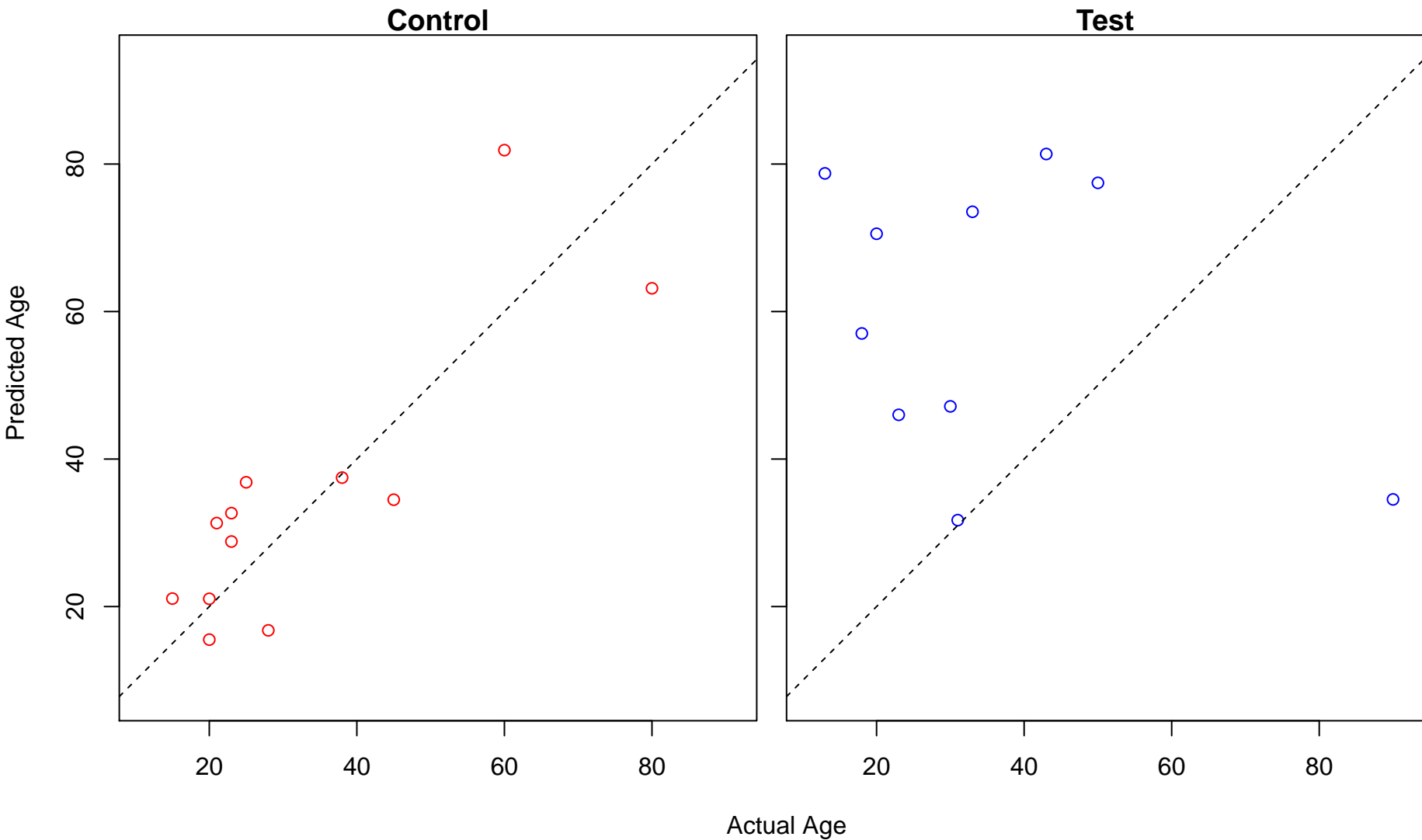
negative regulation of cellular senescence (Score: 12.904629)



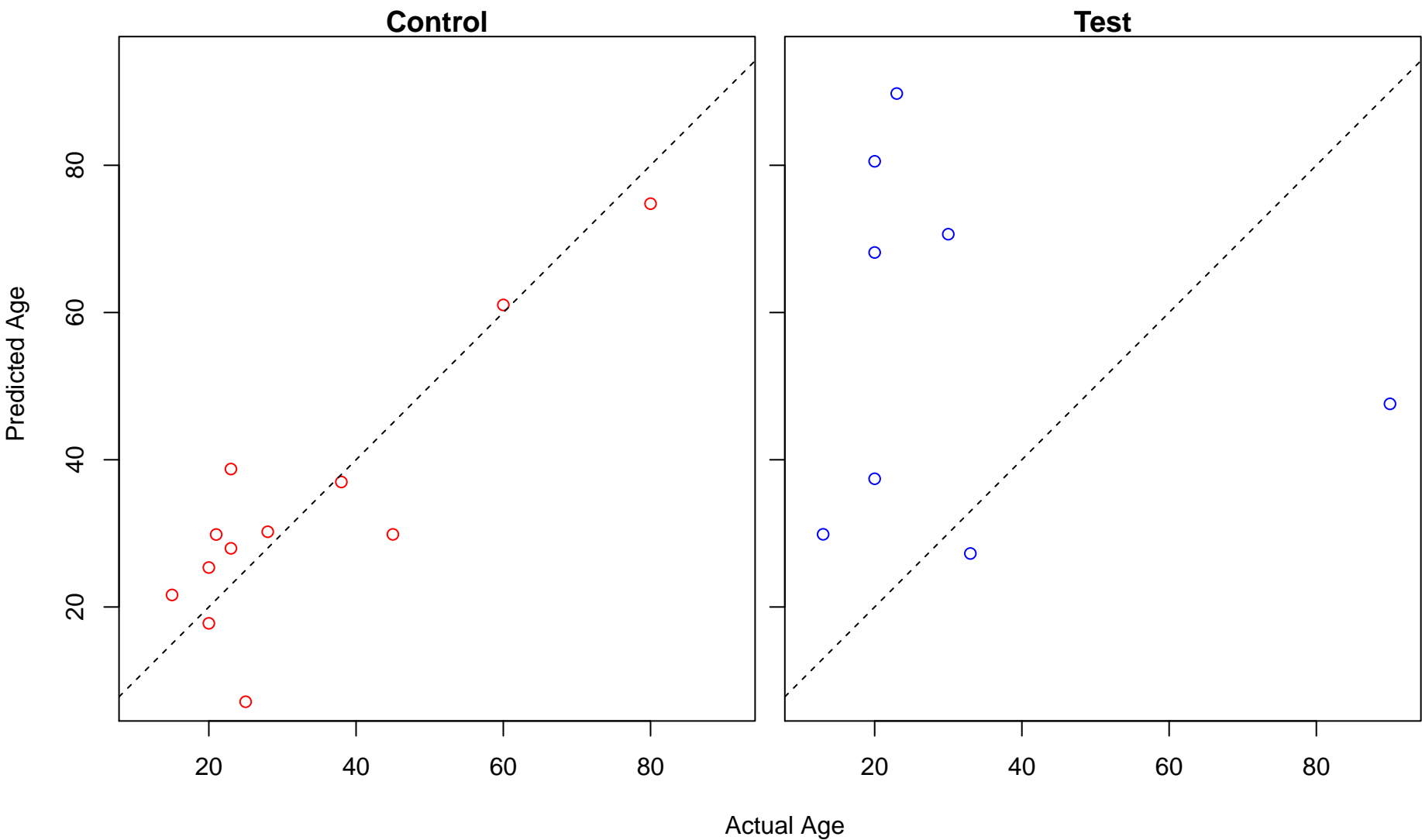
peptidyl-arginine modification (Score: 12.885221)



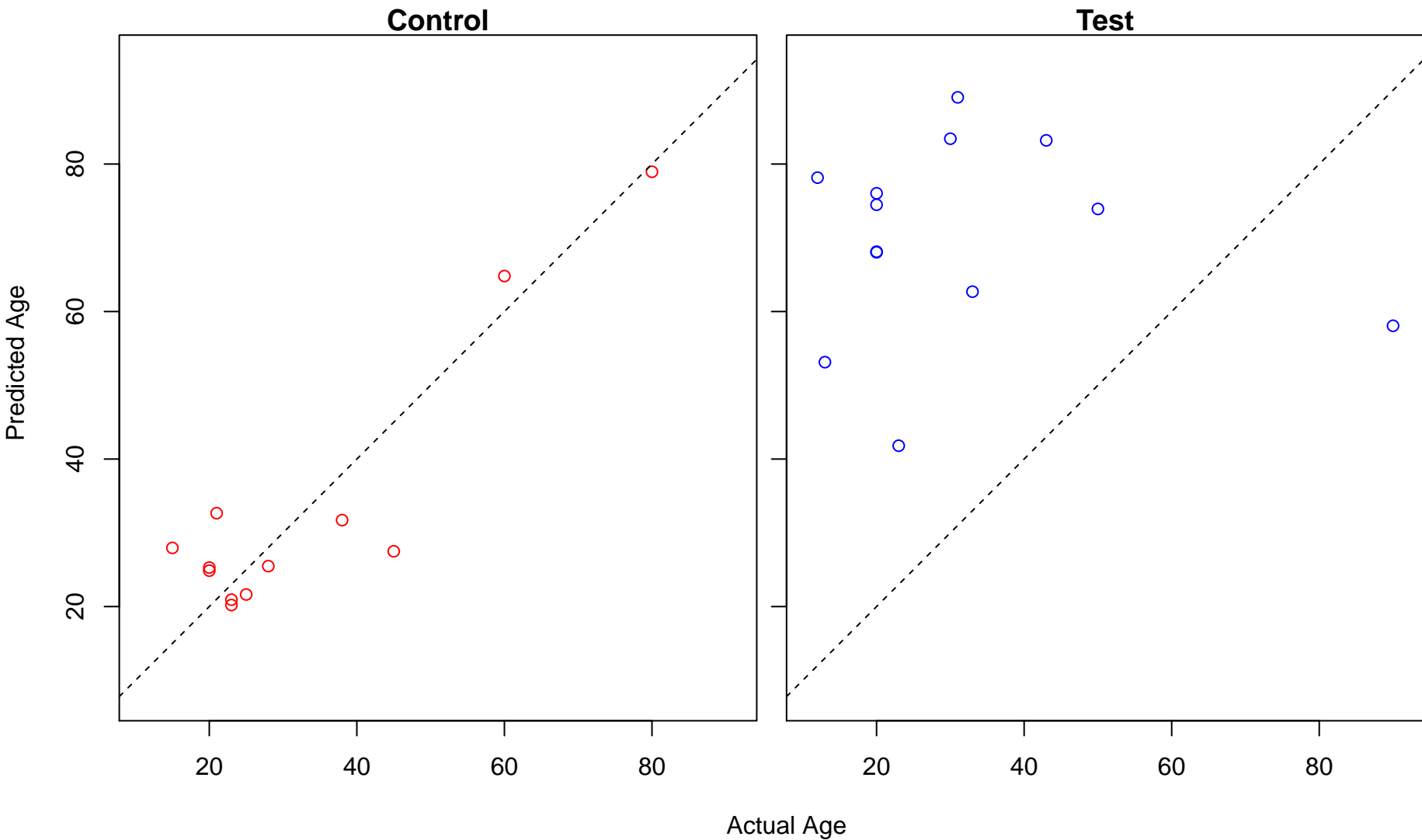
intestinal absorption (Score: 12.881339)



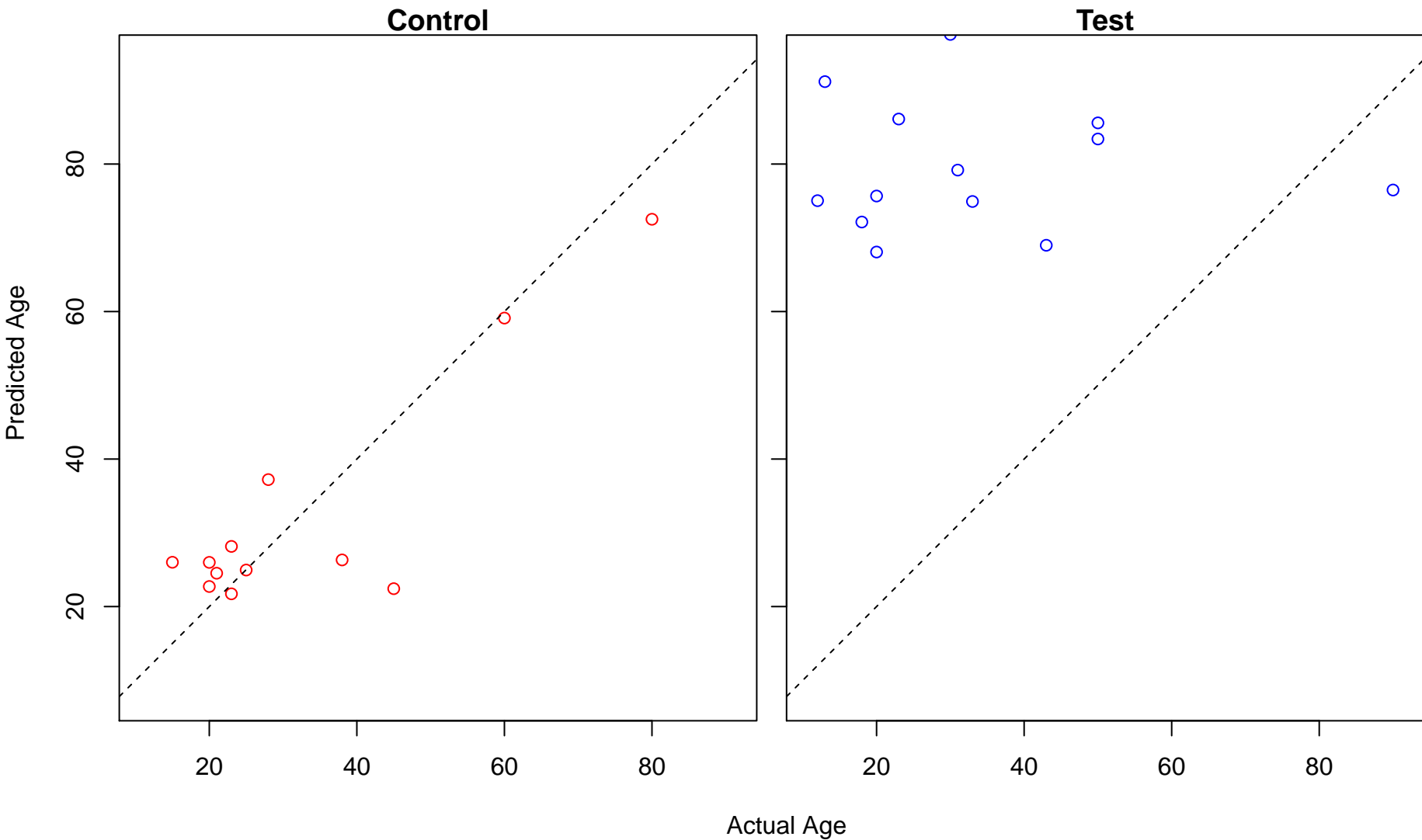
negative regulation of transcription from RNA polymerase II promoter in response to stress (Score: 12.8)



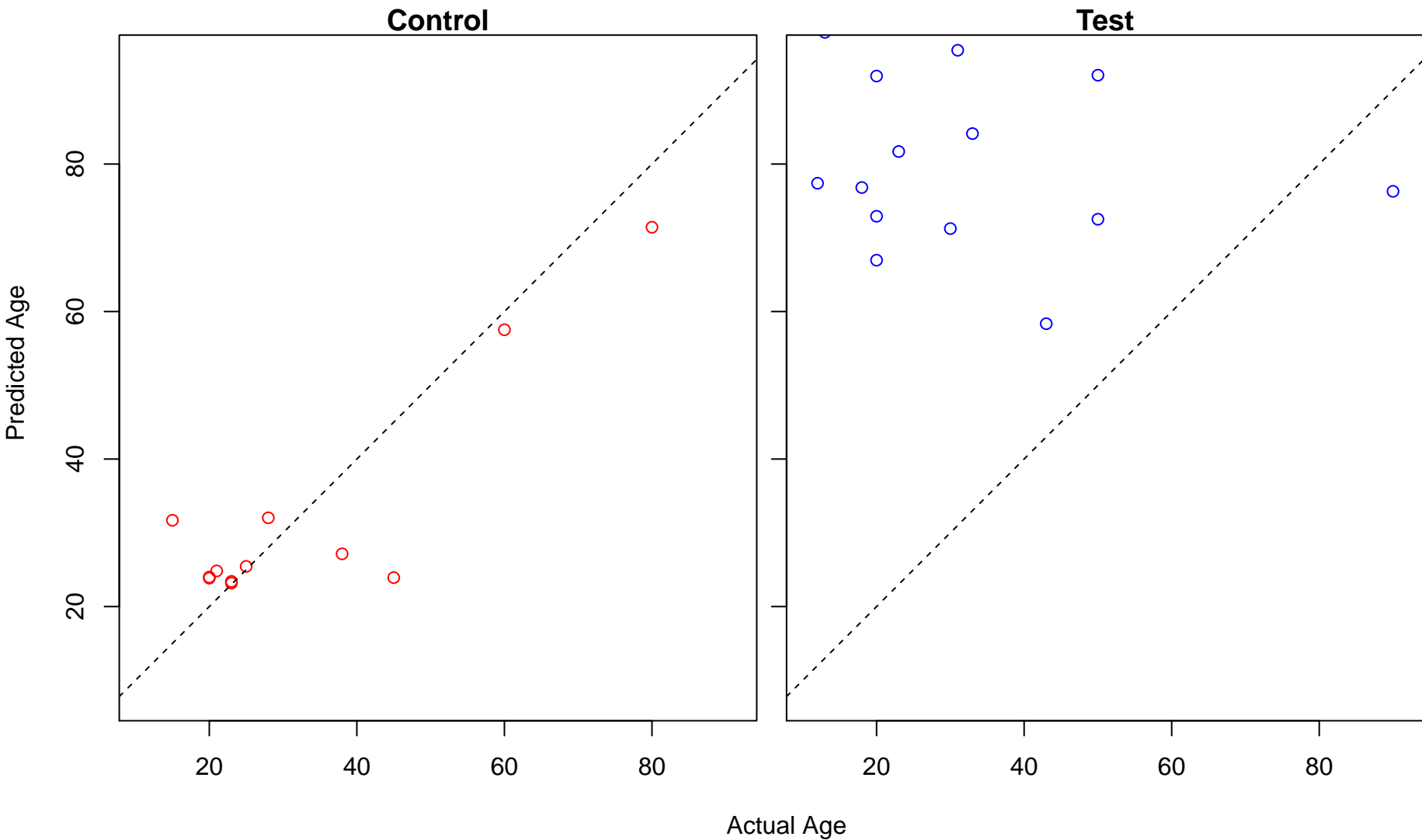
negative regulation of cellular component movement (Score: 12.860622)



regulation of chemokine production (Score: 12.814211)

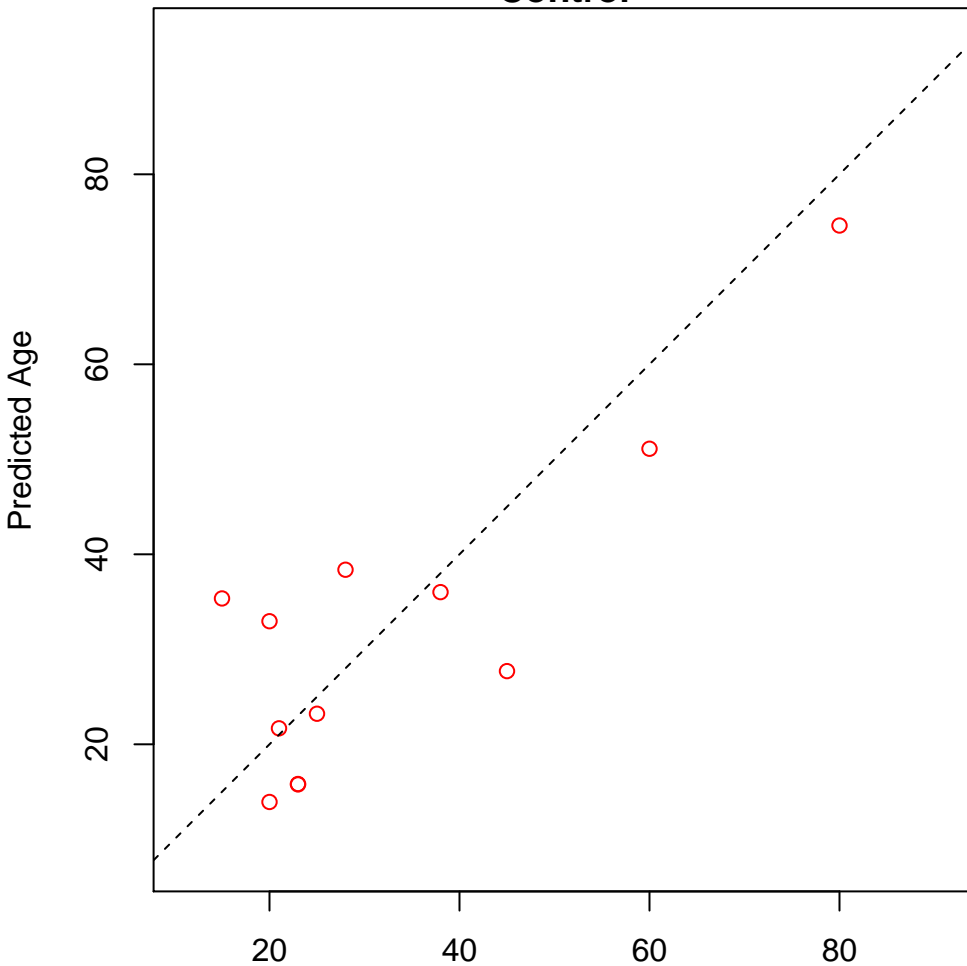


response to nicotine (Score: 12.798721)

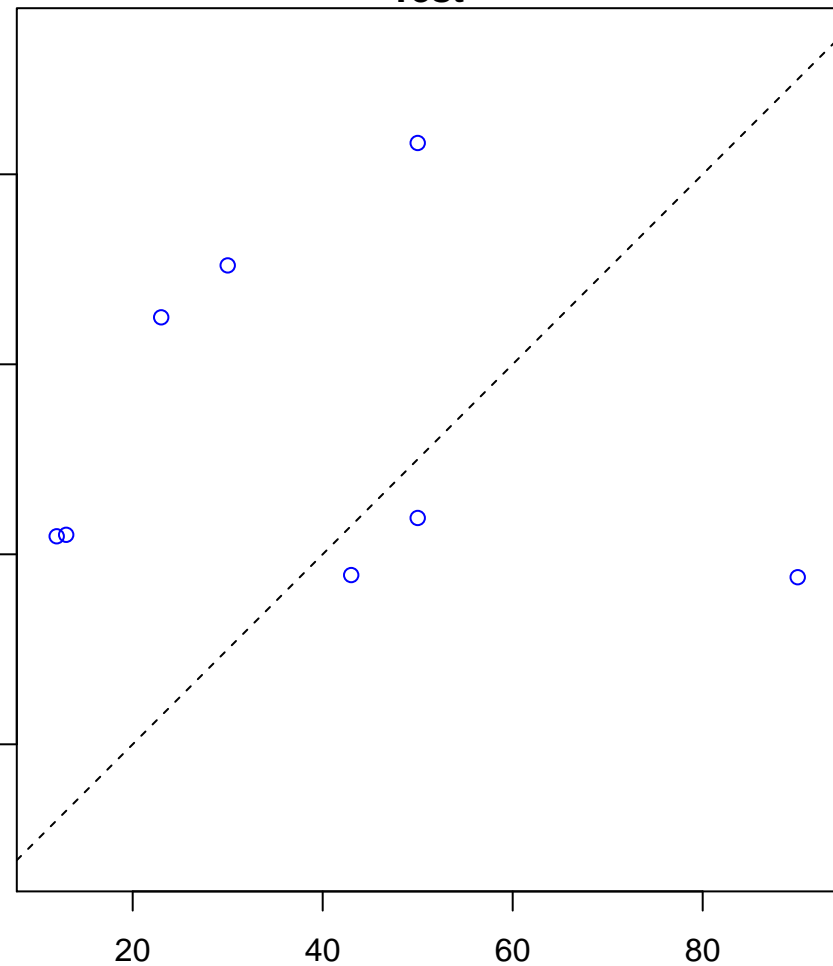


regulation of renal system process (Score: 12.788240)

Control

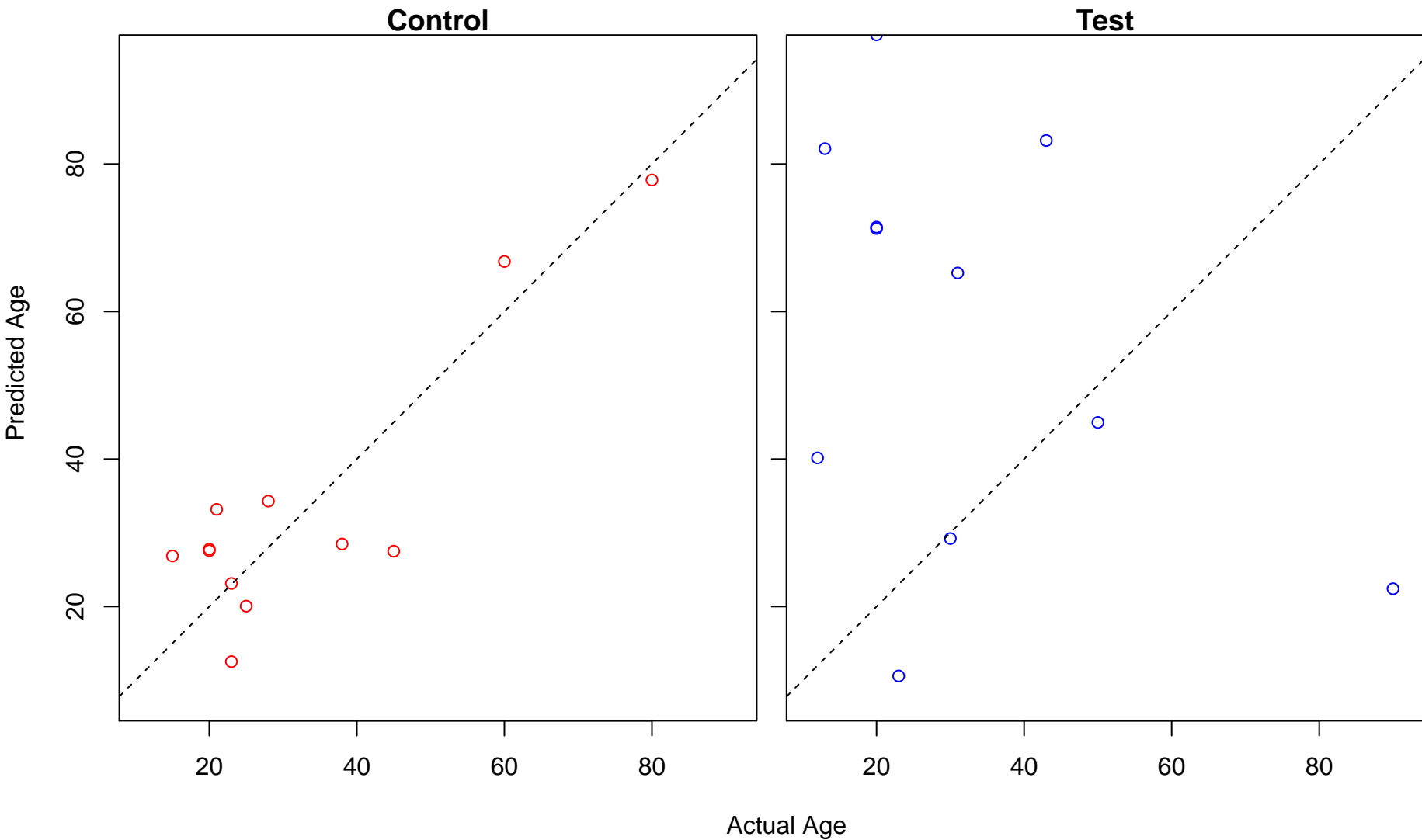


Test

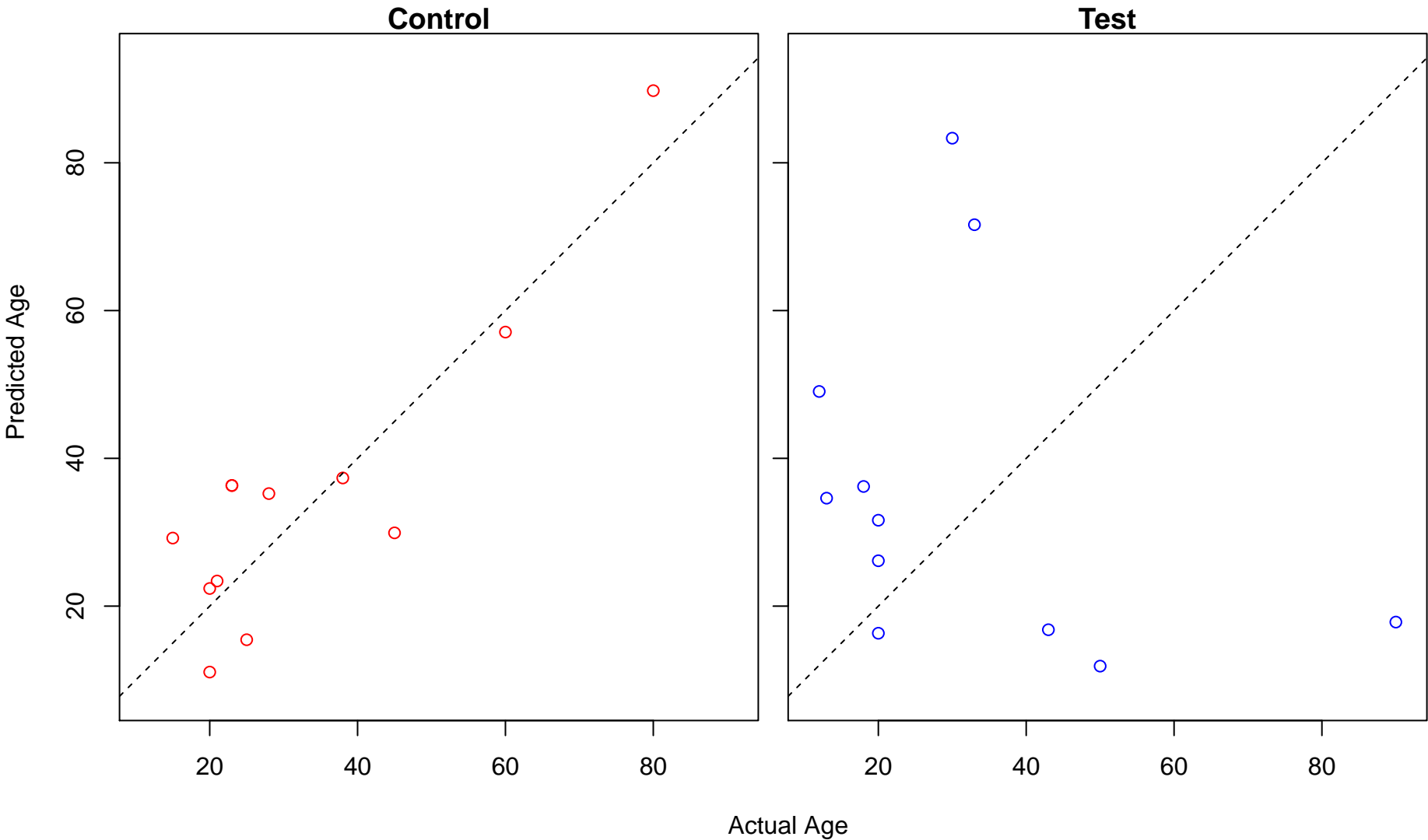


Actual Age

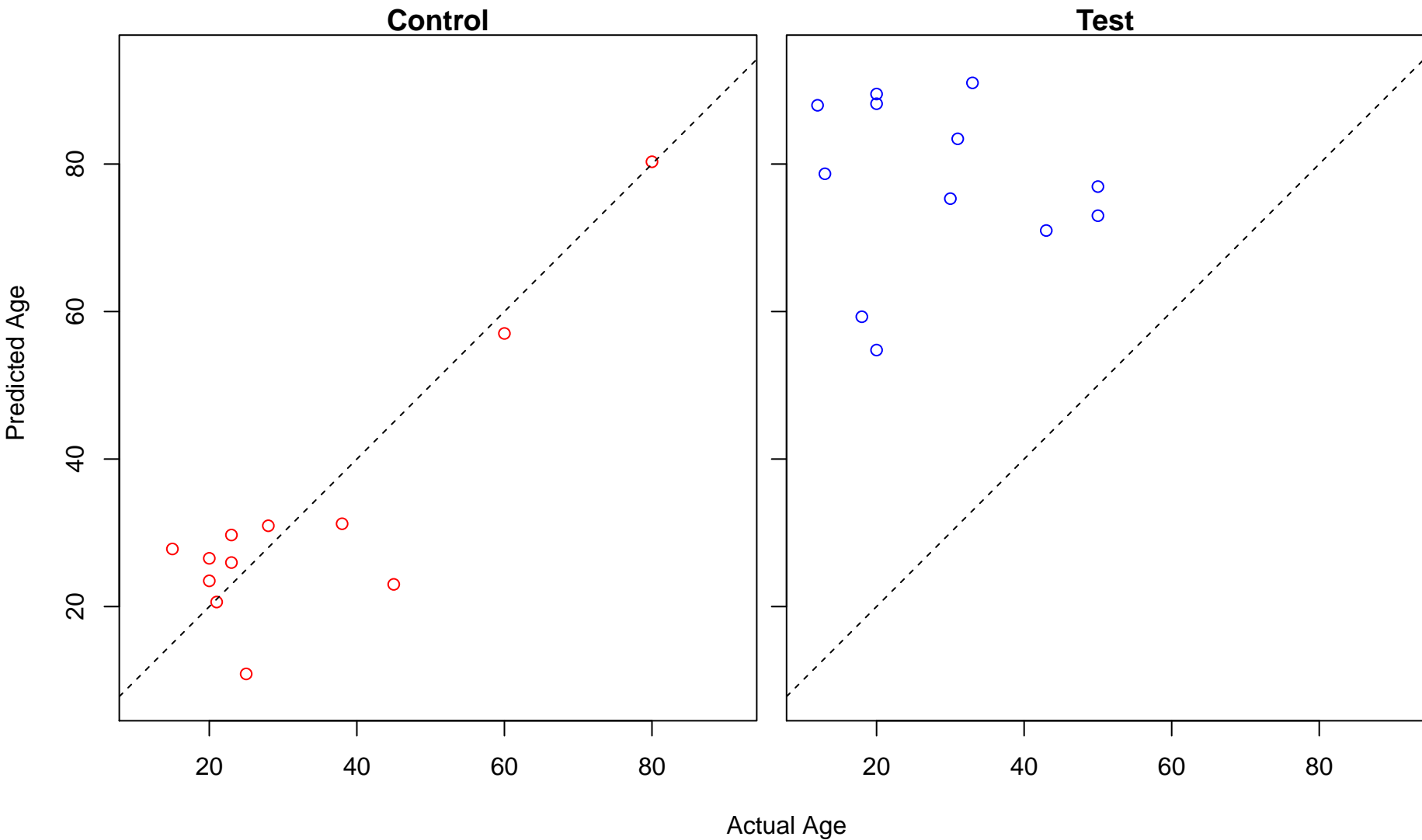
regulation of protein localization to cell surface (Score: 12.775446)



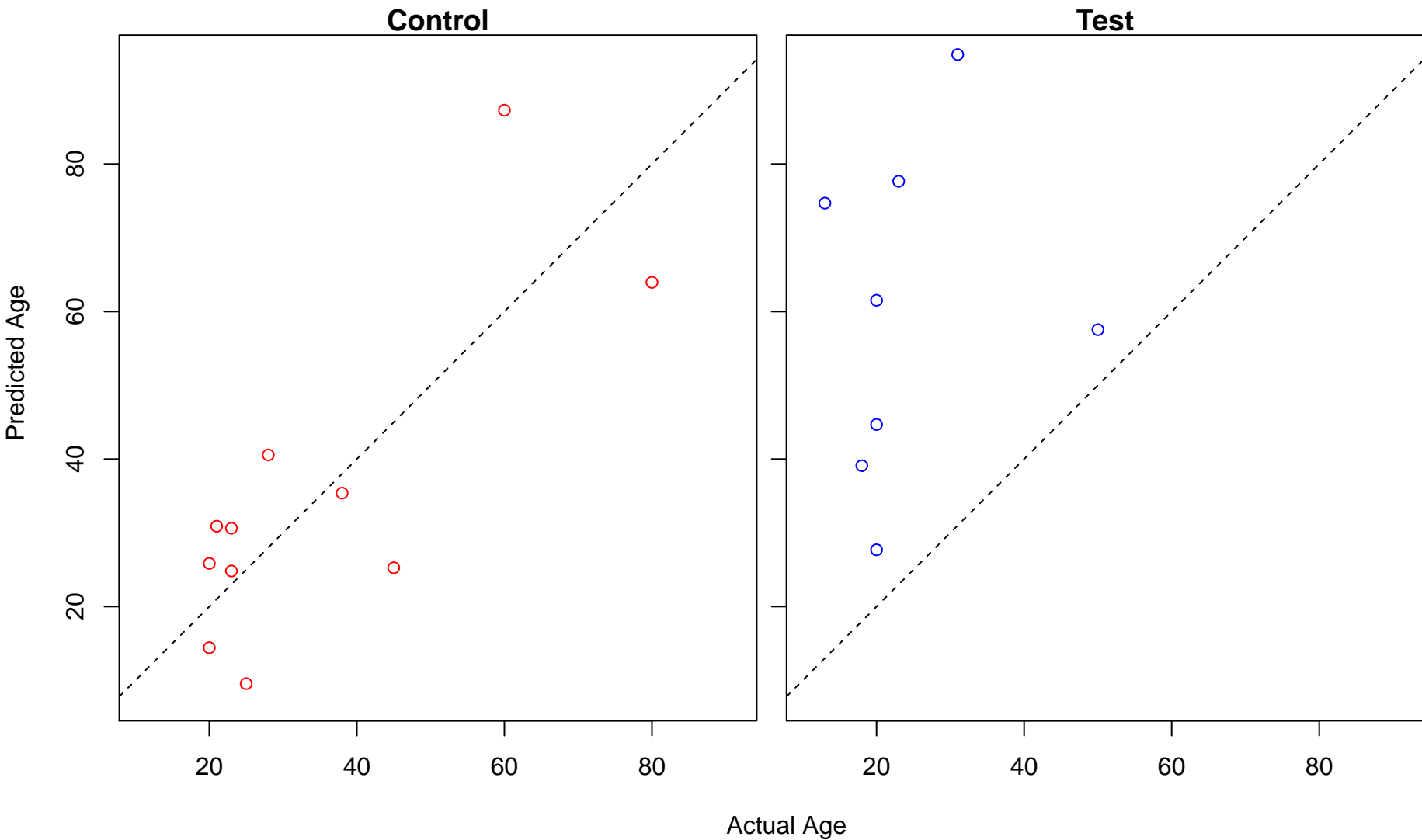
manganese ion transmembrane transport (Score: 12.775011)



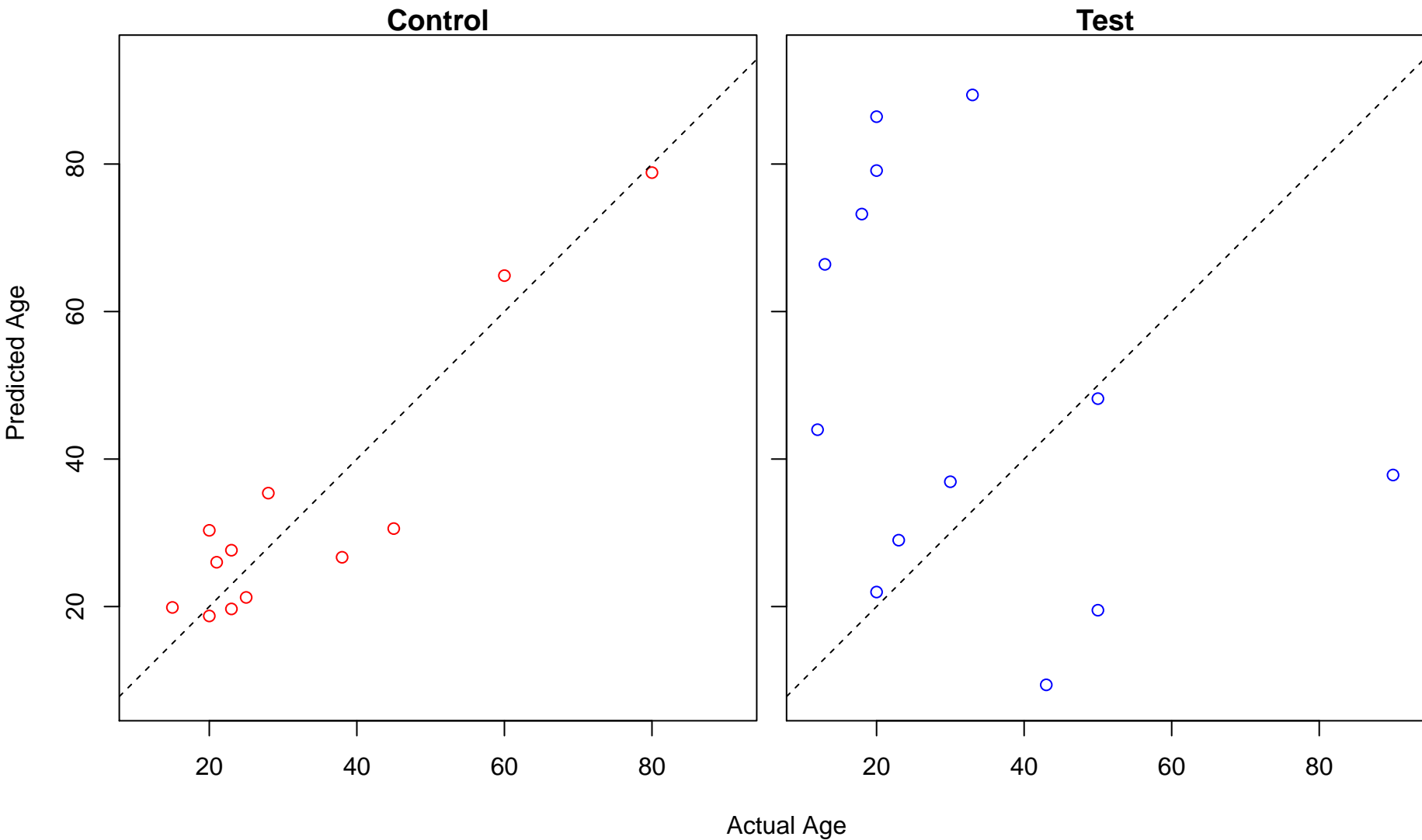
peptidyl-lysine deacetylation (Score: 12.763982)



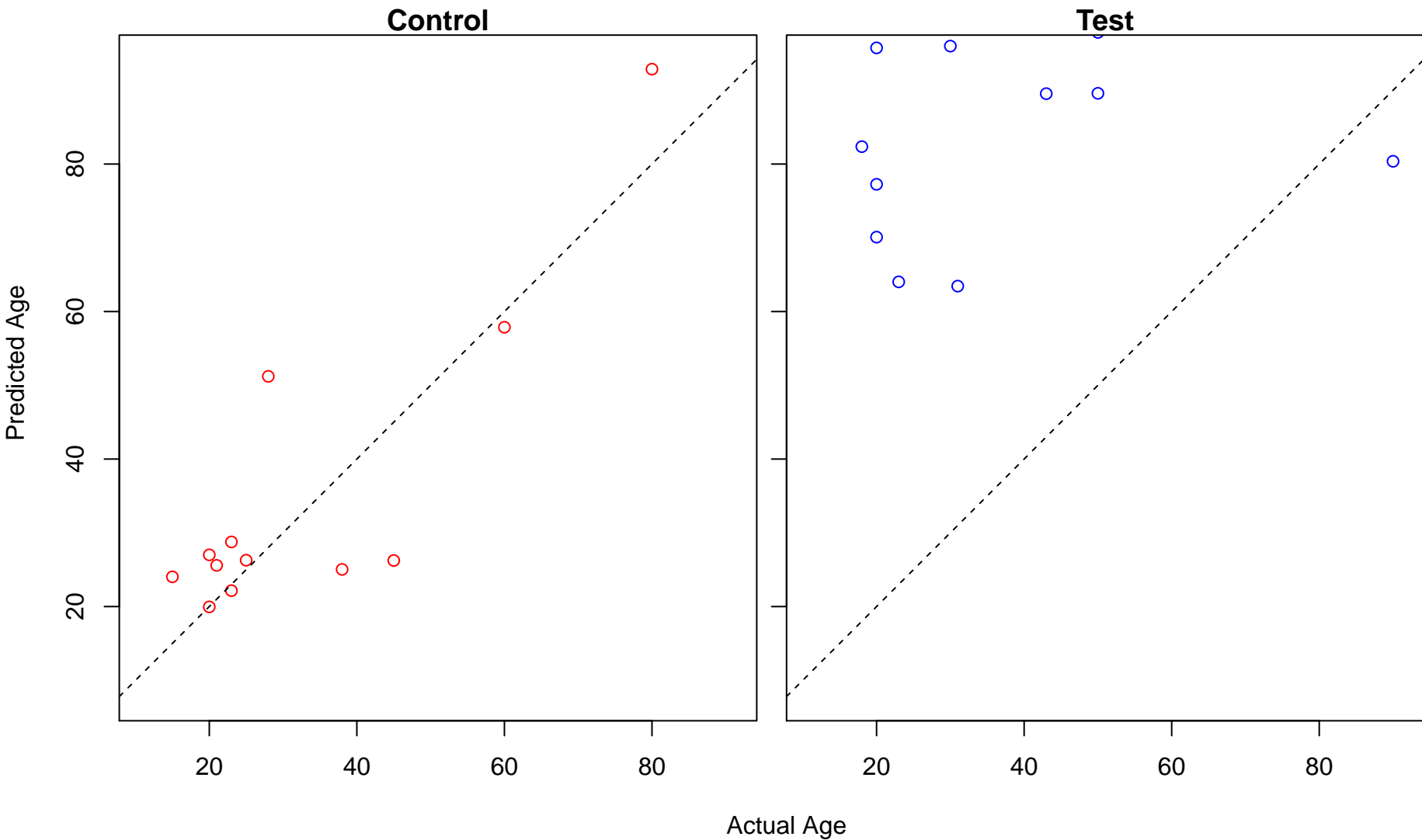
negative regulation of oxidative stress-induced neuron death (Score: 12.726533)



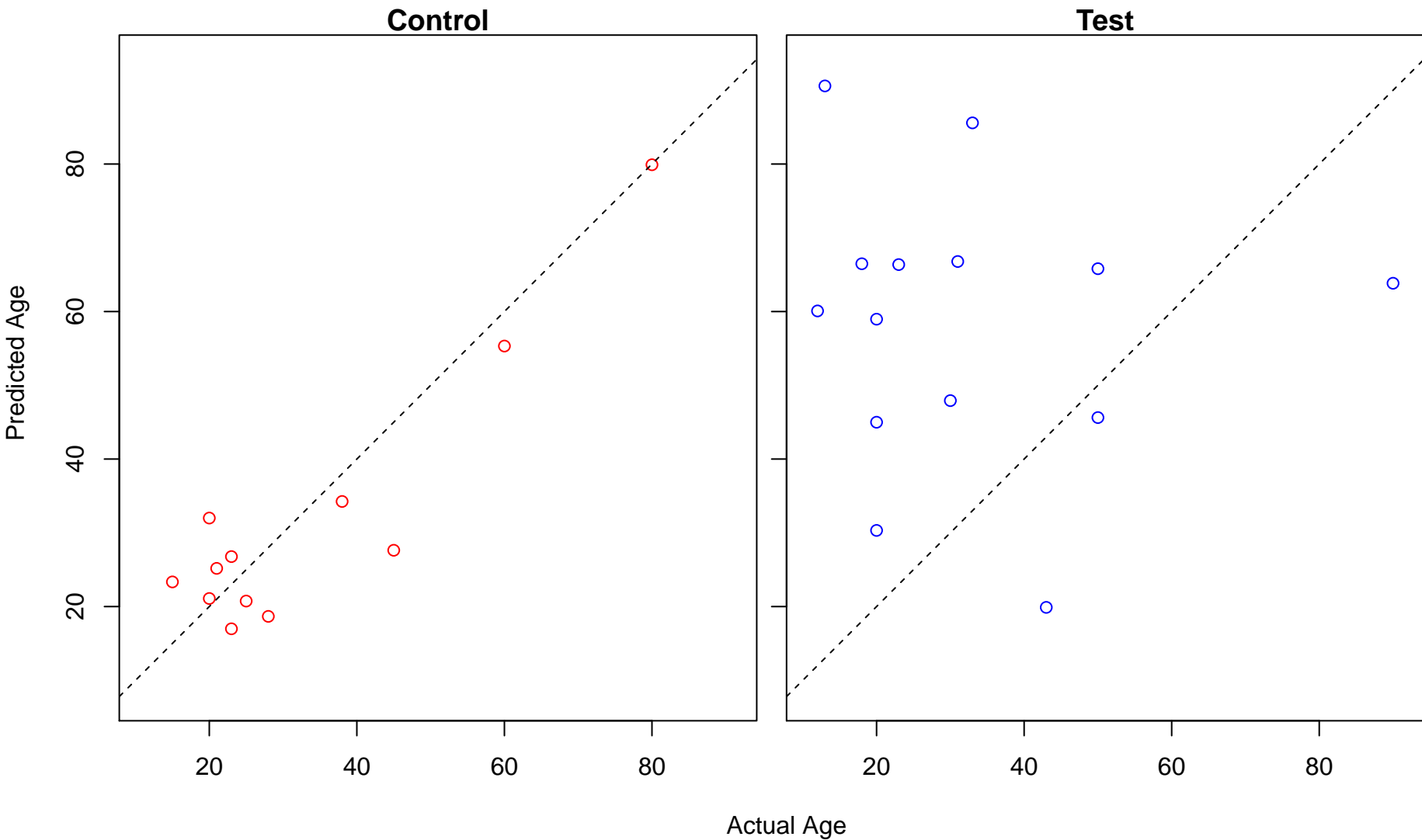
protein autophosphorylation (Score: 12.710049)



placenta development (Score: 12.699219)

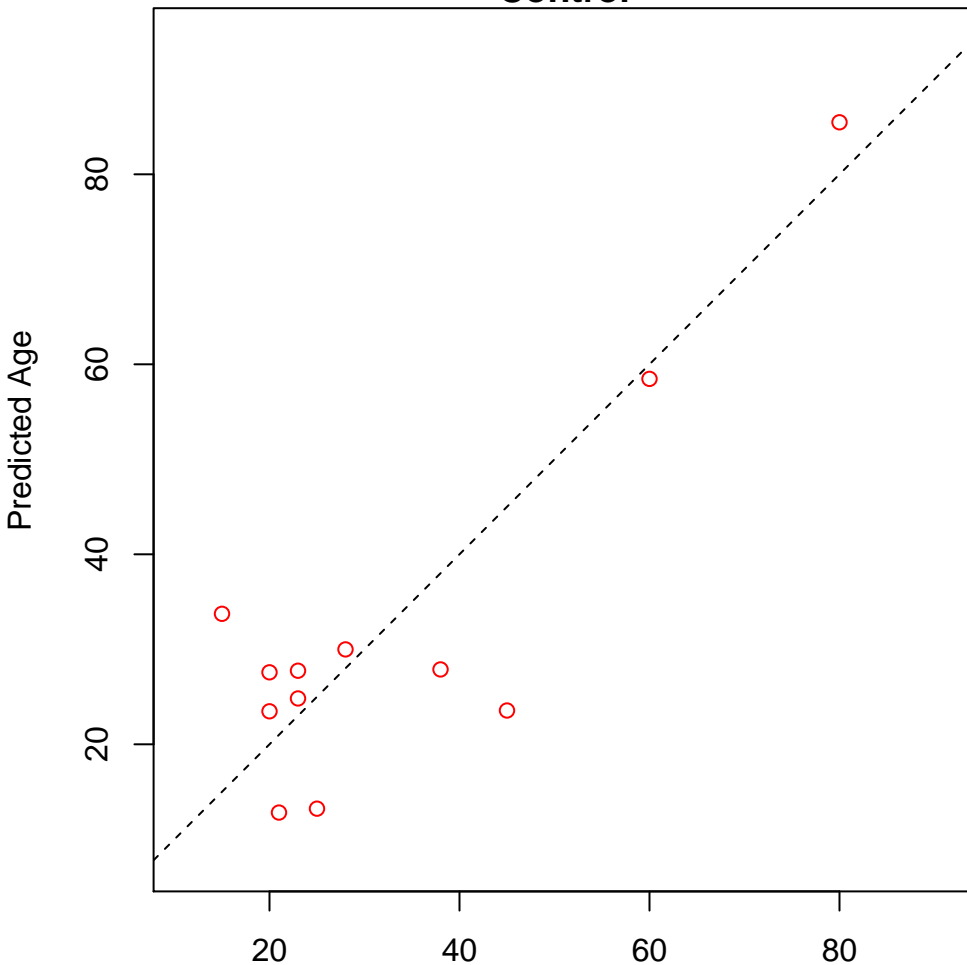


regulation of protein ubiquitination (Score: 12.694337)

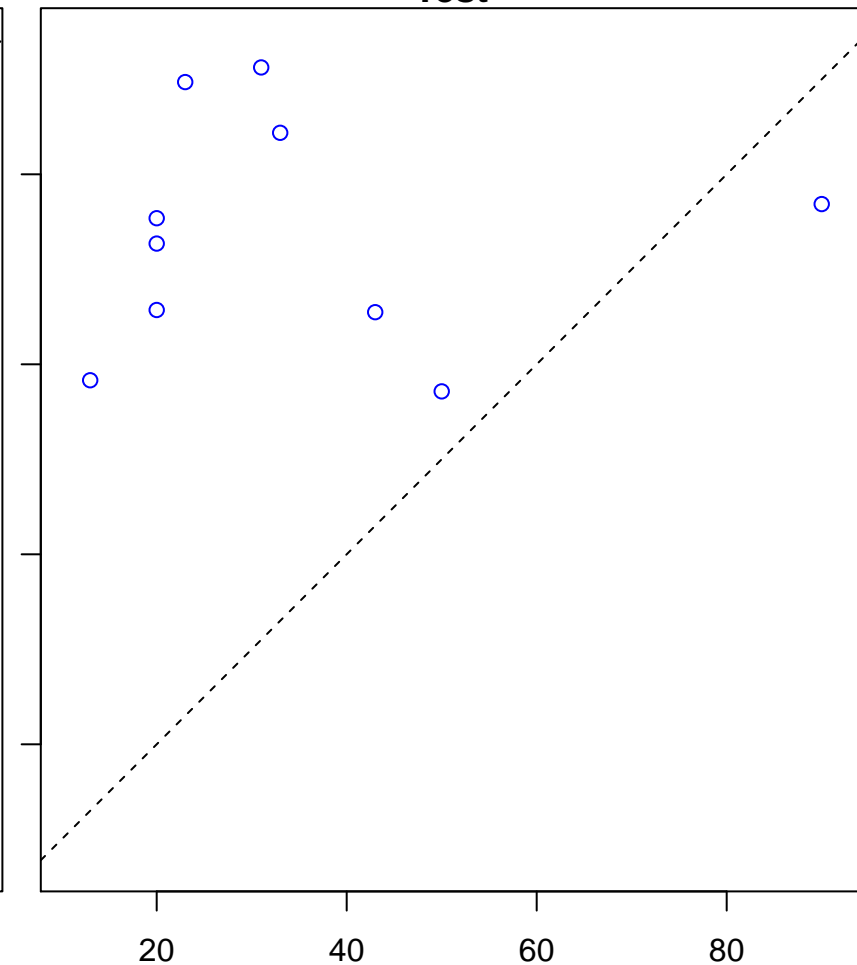


regulation of mesoderm development (Score: 12.669675)

Control

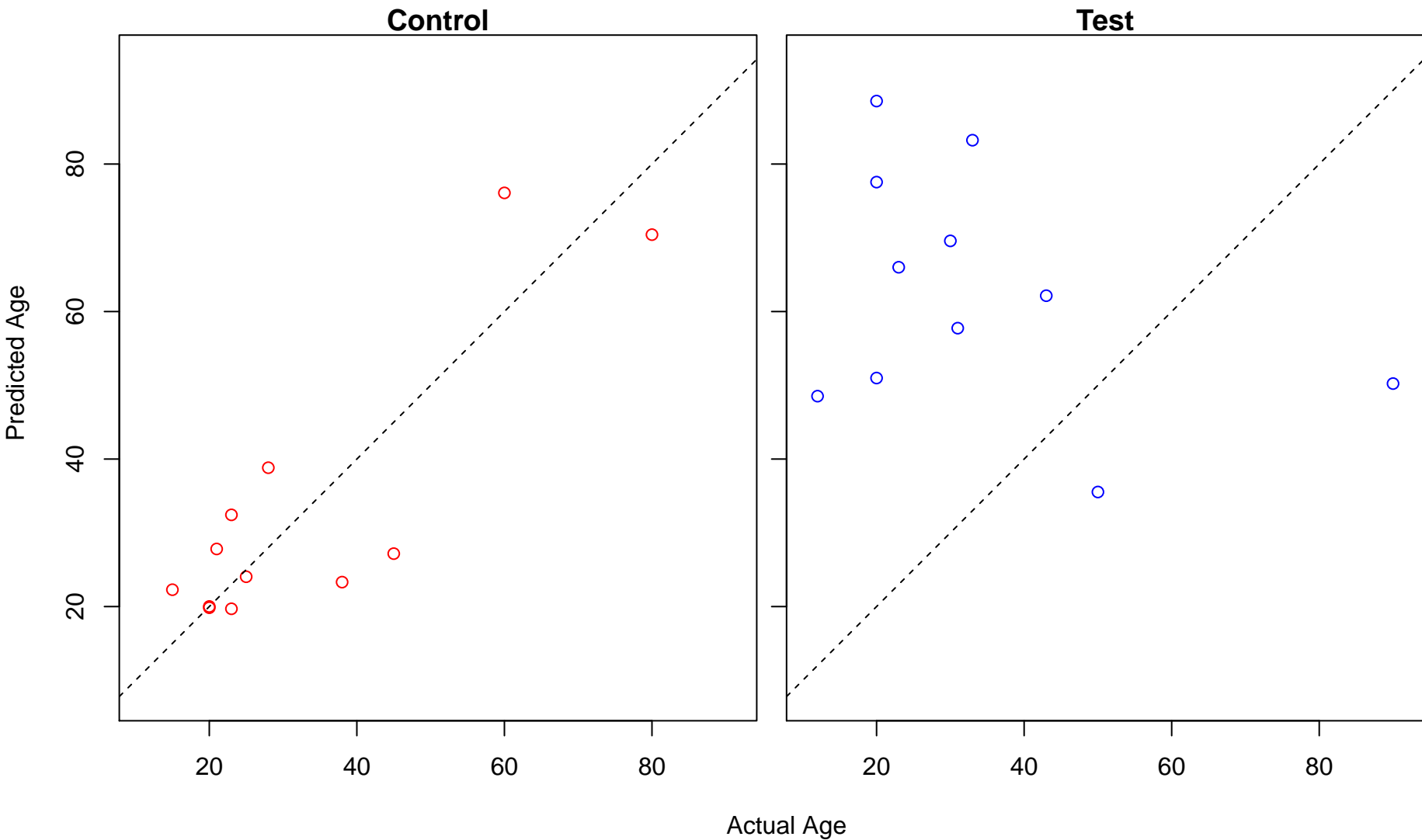


Test



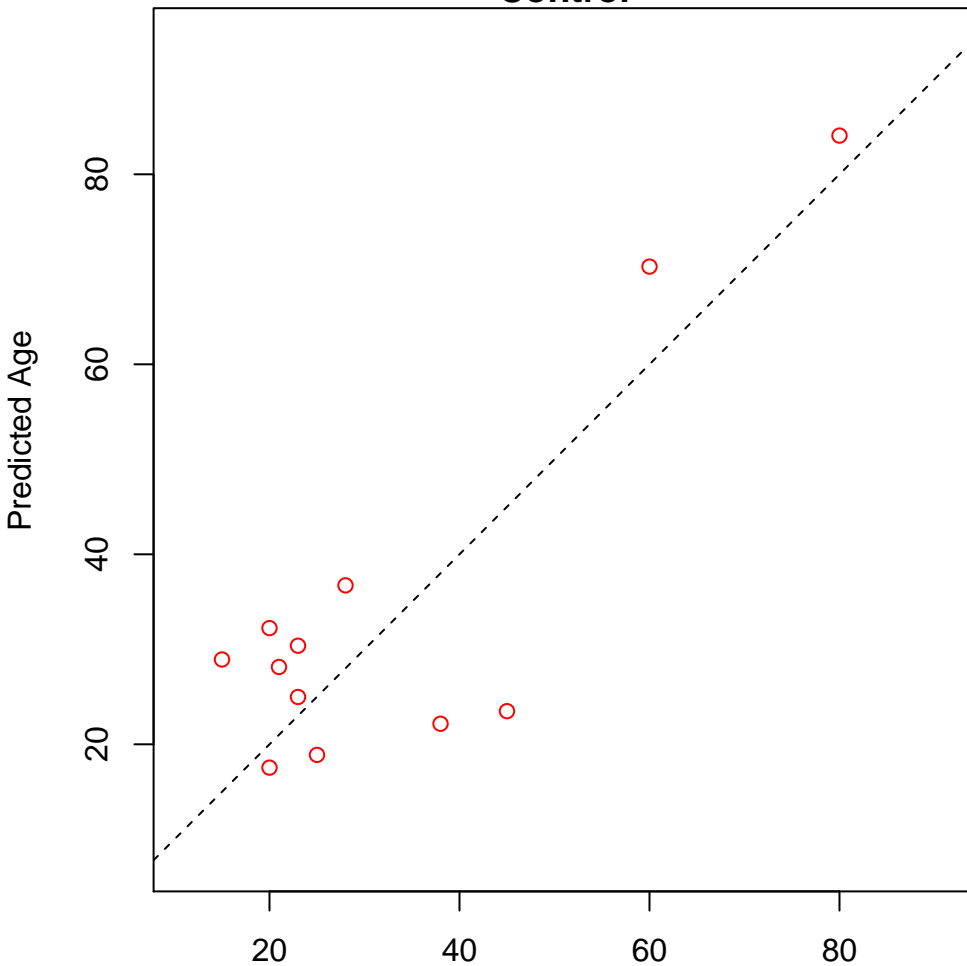
Actual Age

T cell differentiation (Score: 12.662175)

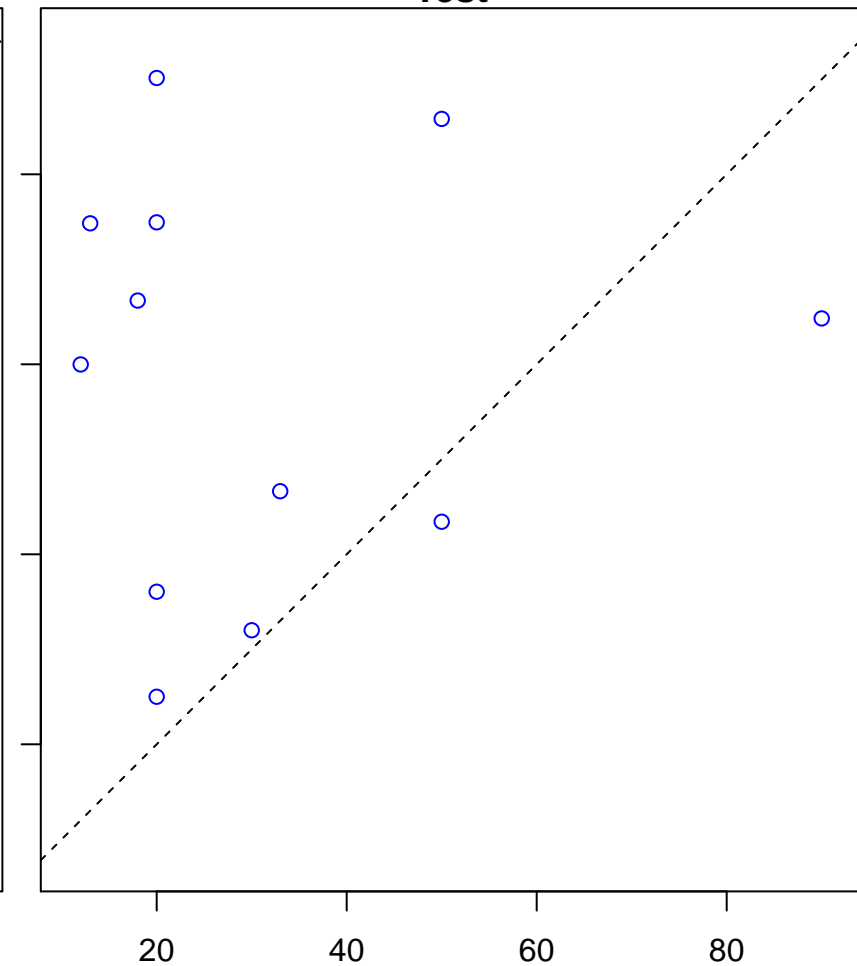


cellular response to external stimulus (Score: 12.661698)

Control



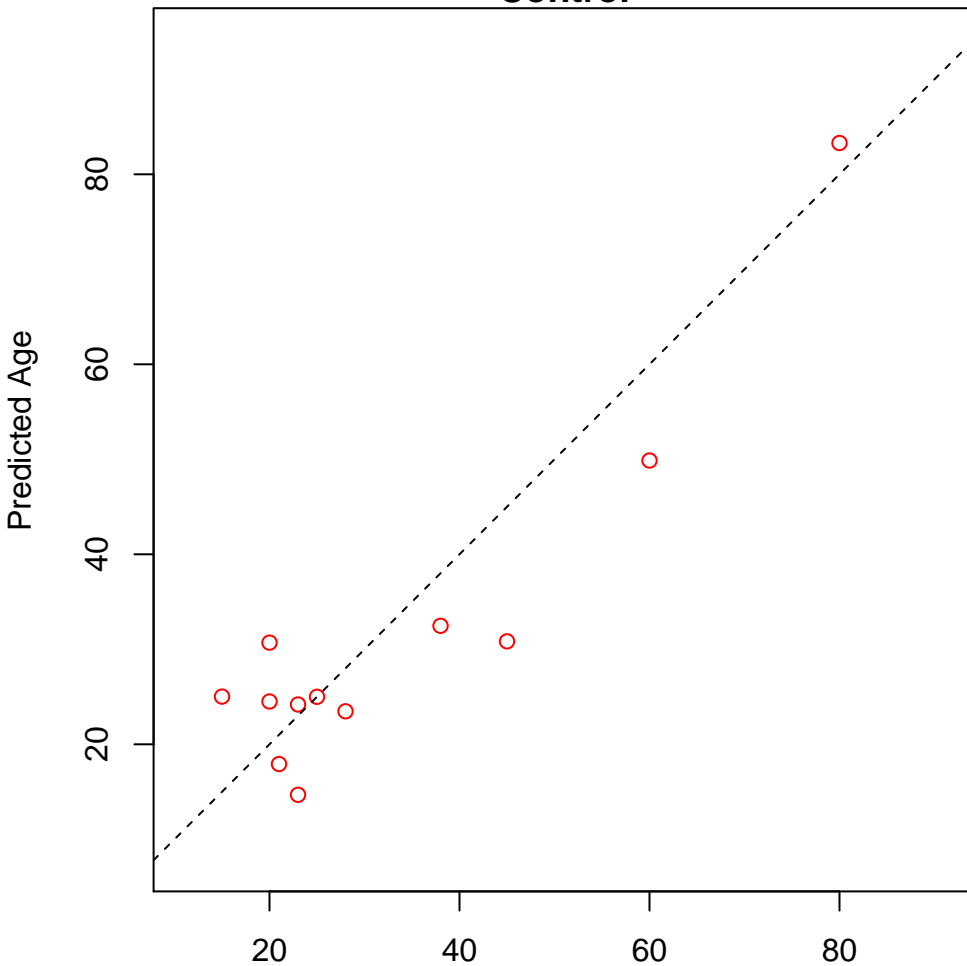
Test



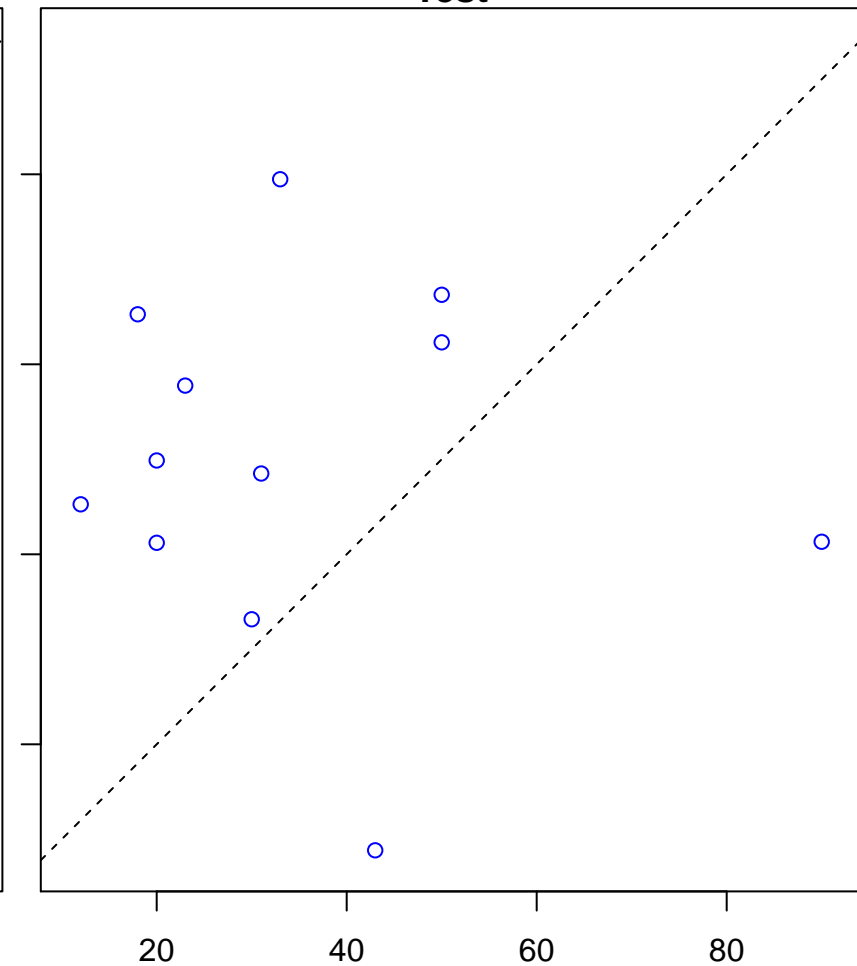
Actual Age

regulation of cellular response to heat (Score: 12.618988)

Control

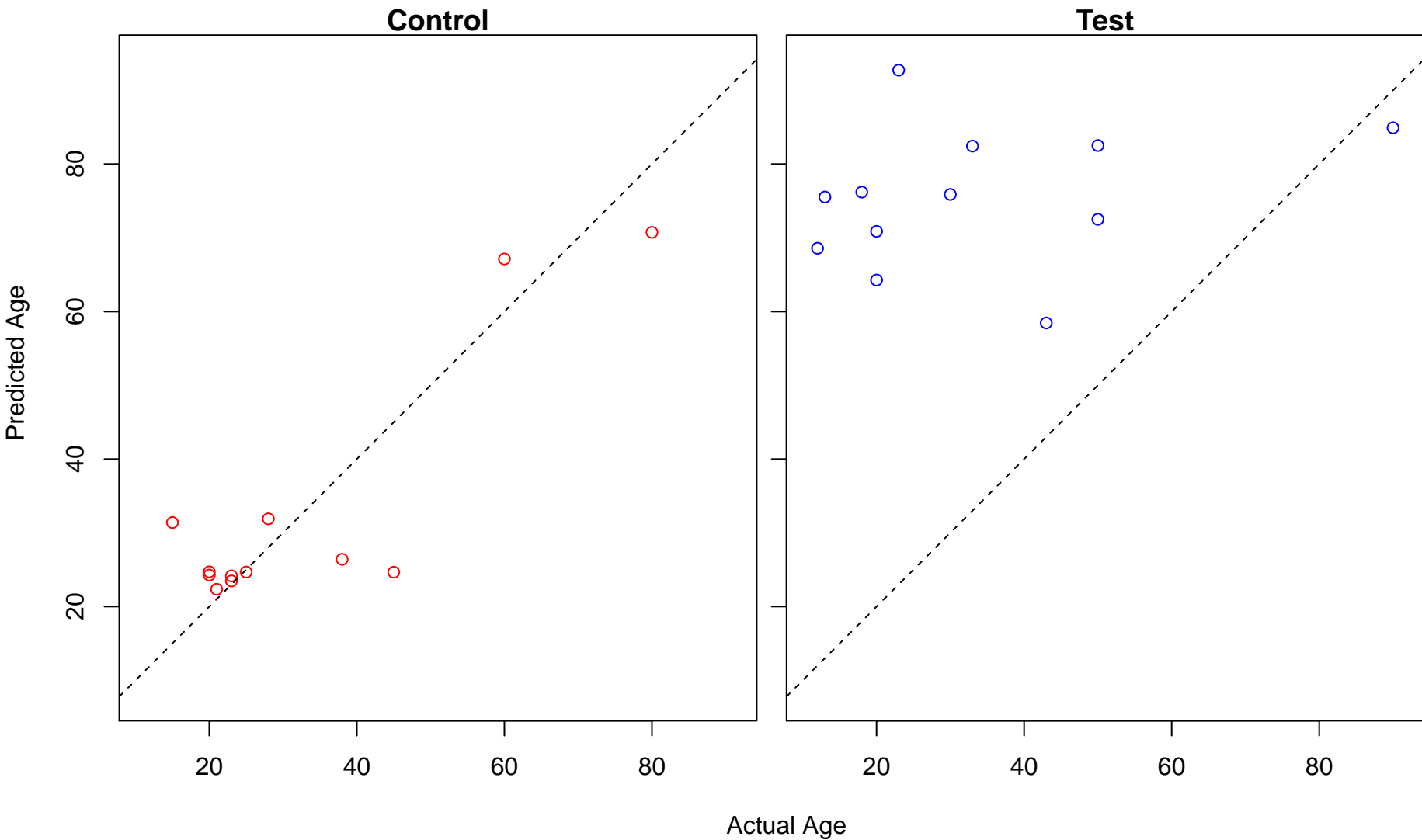


Test

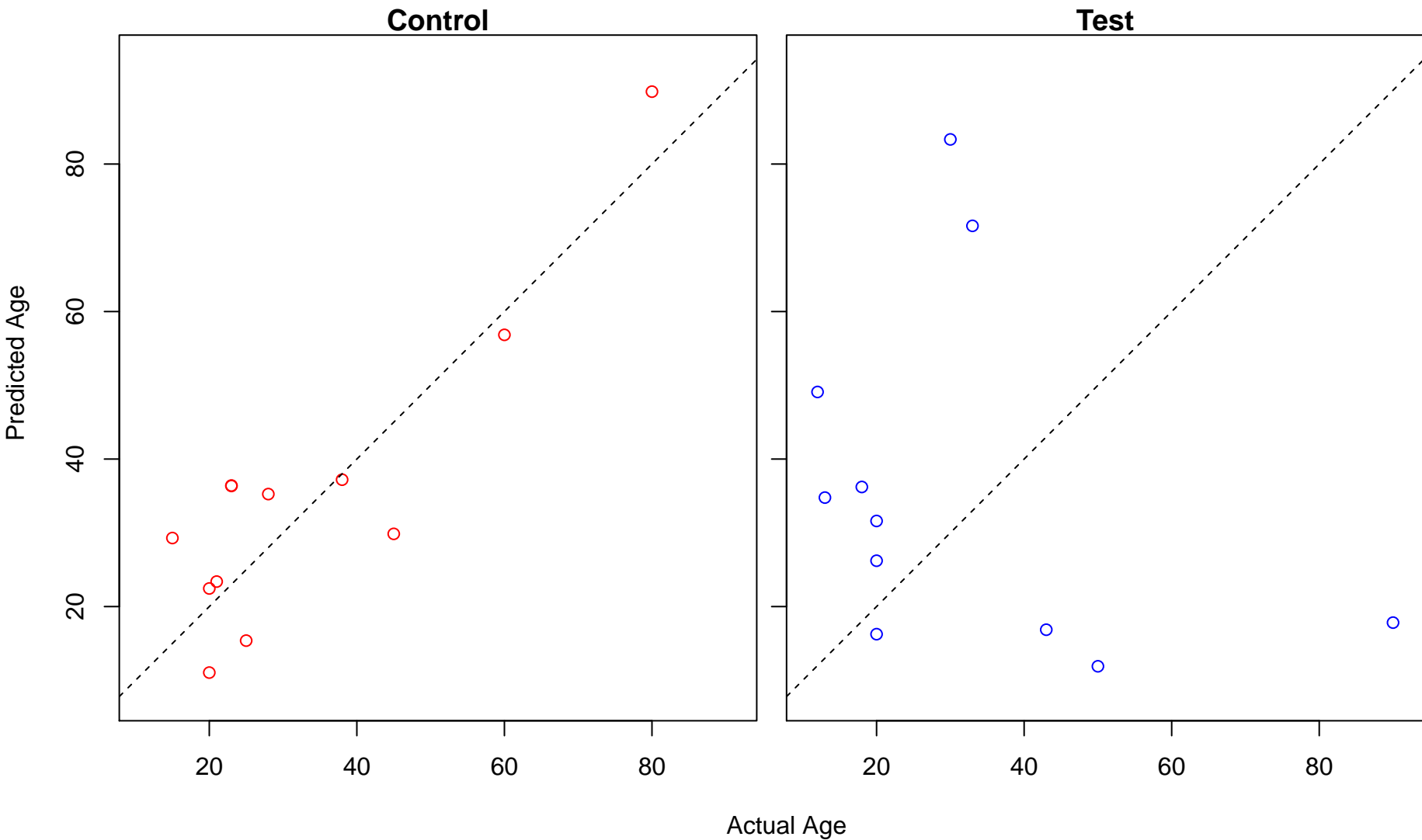


Actual Age

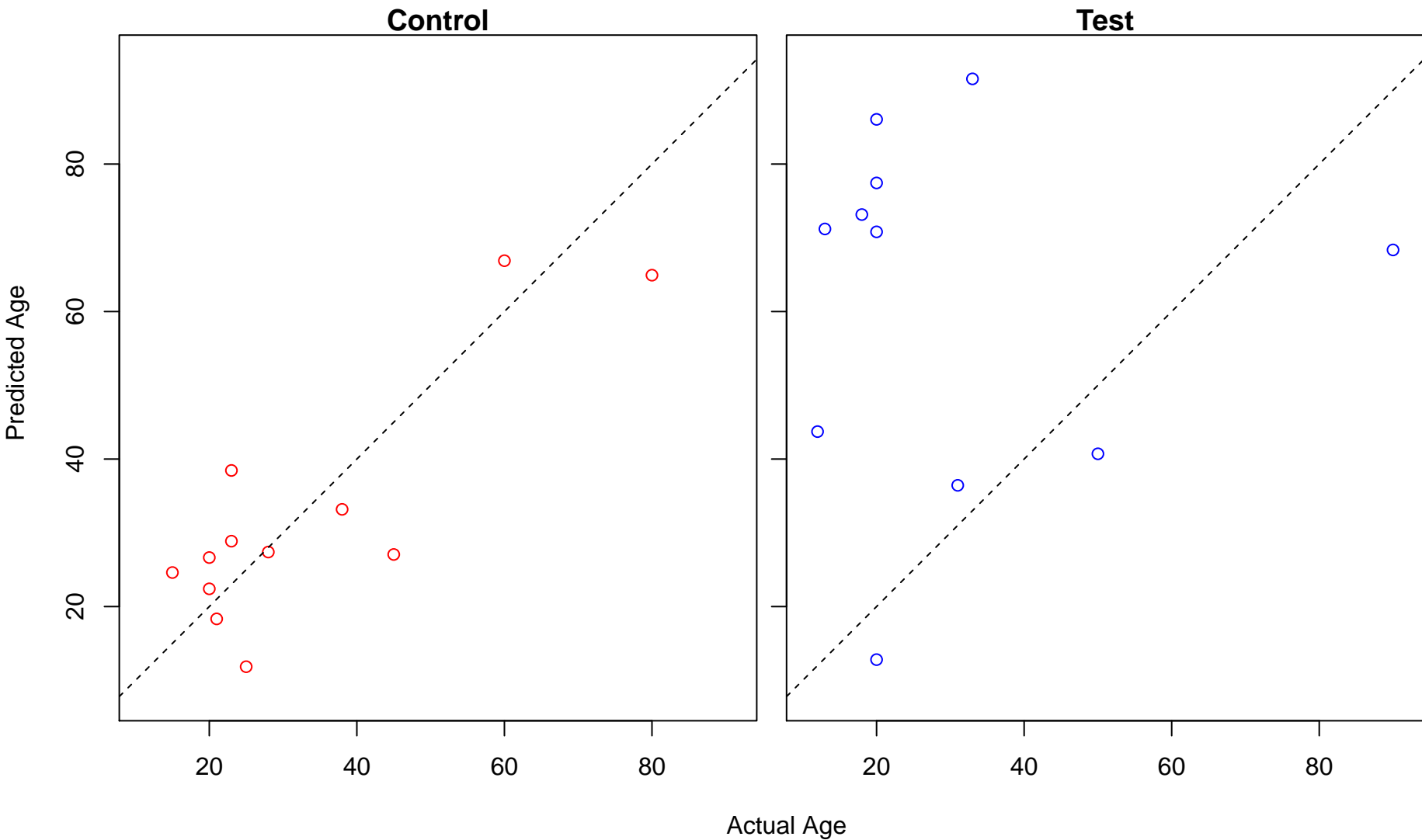
positive regulation of myotube differentiation (Score: 12.611664)



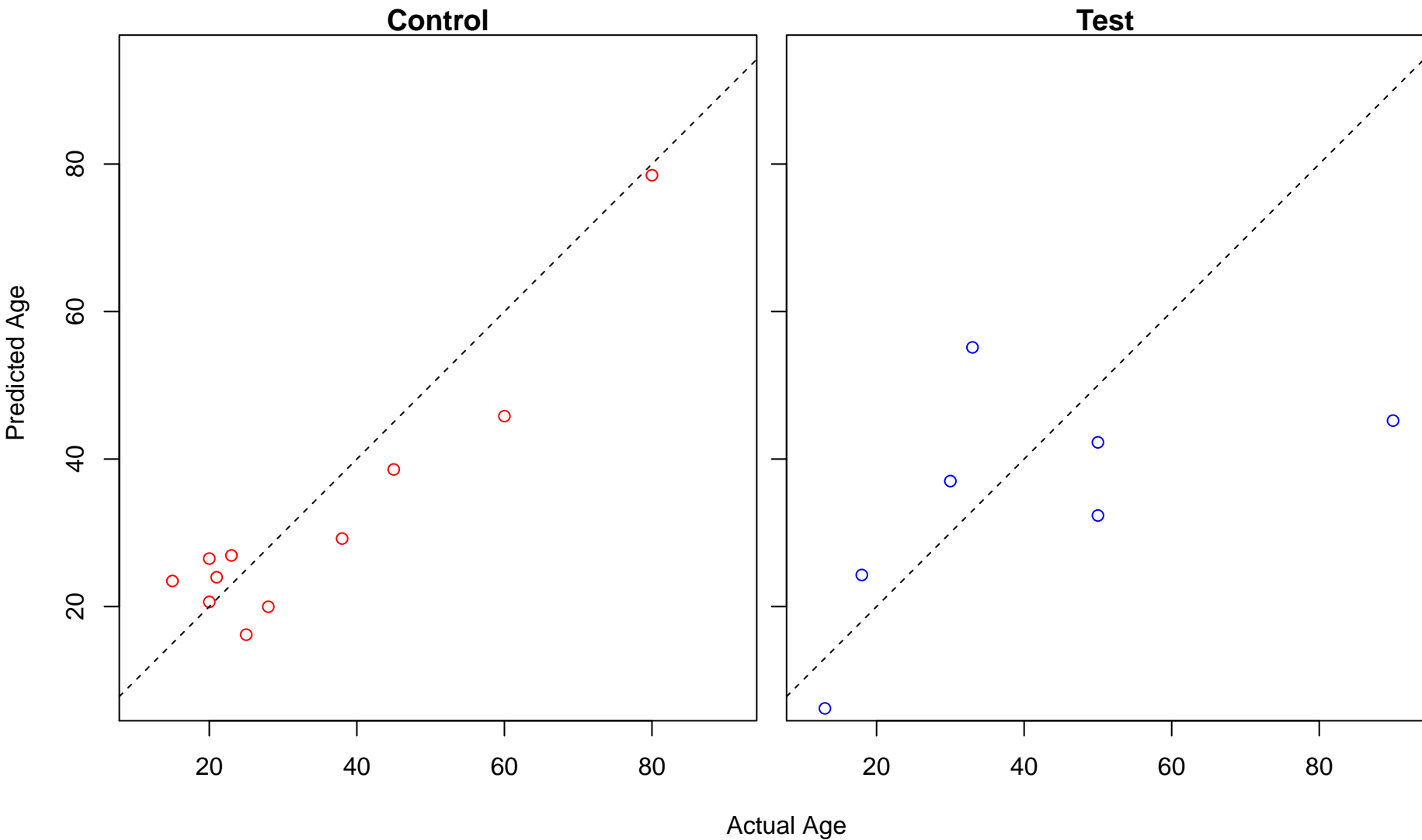
manganese ion transport (Score: 12.609455)



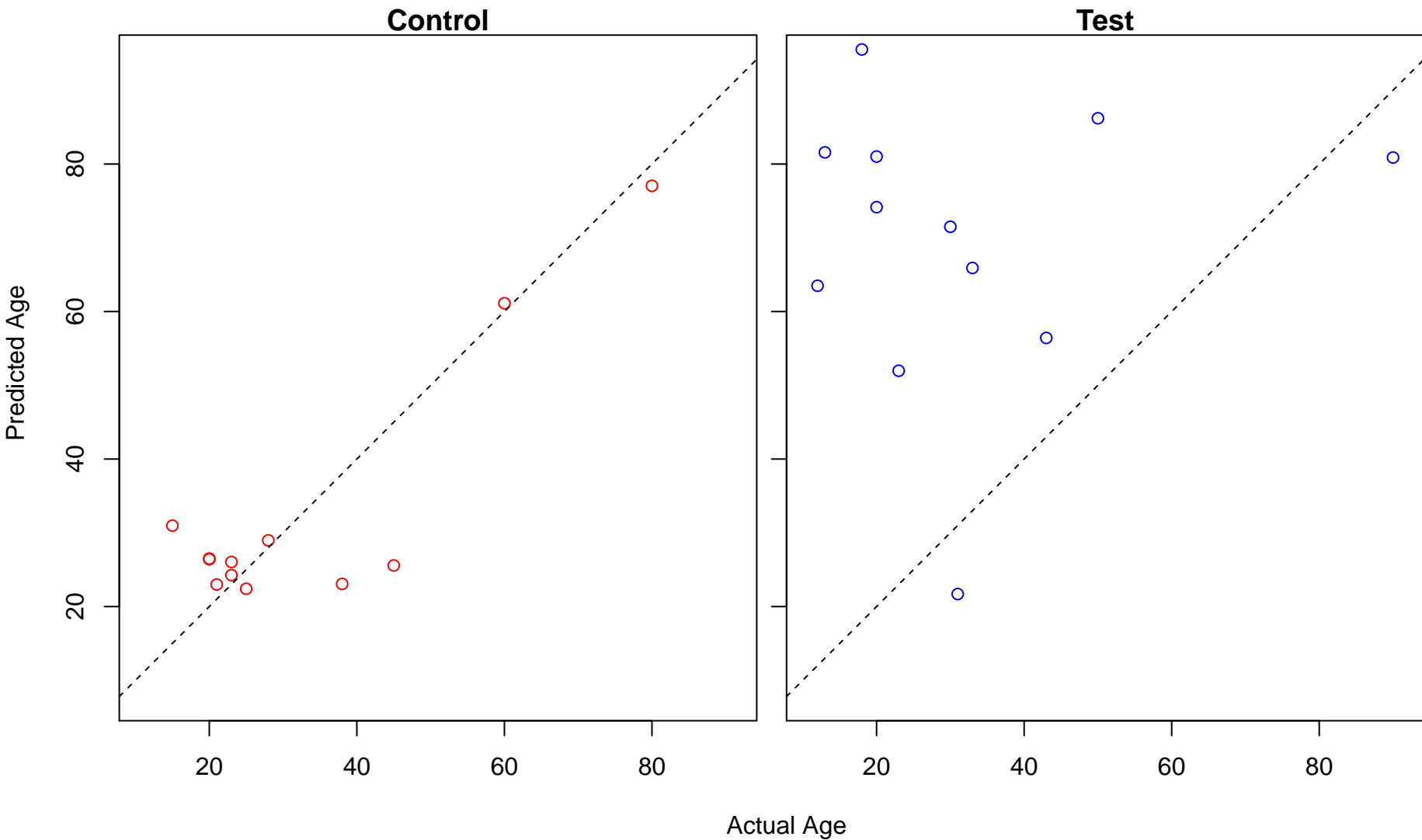
tongue development (Score: 12.592829)



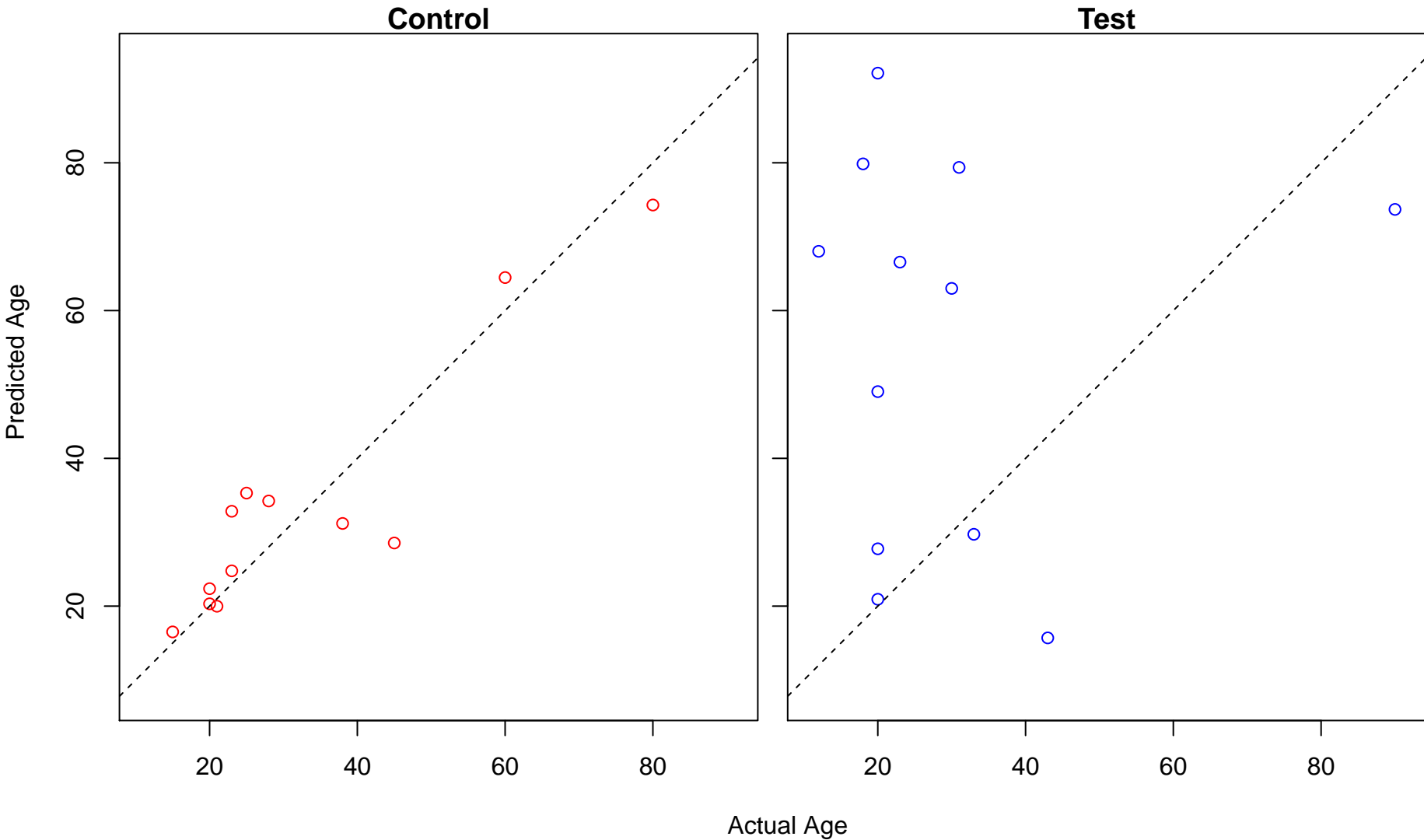
photoreceptor cell differentiation (Score: 12.542432)



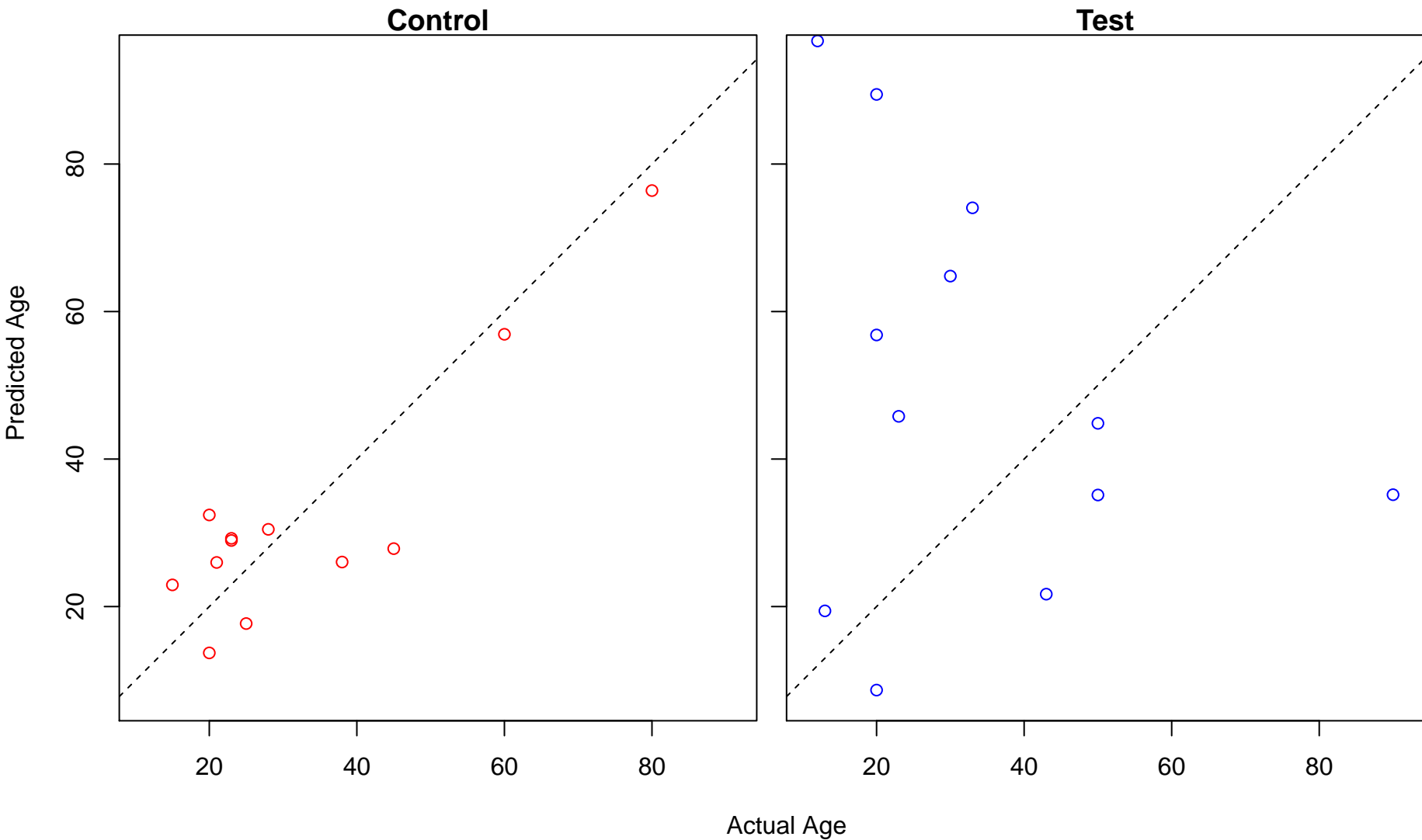
acetyl-CoA biosynthetic process from pyruvate (Score: 12.528143)



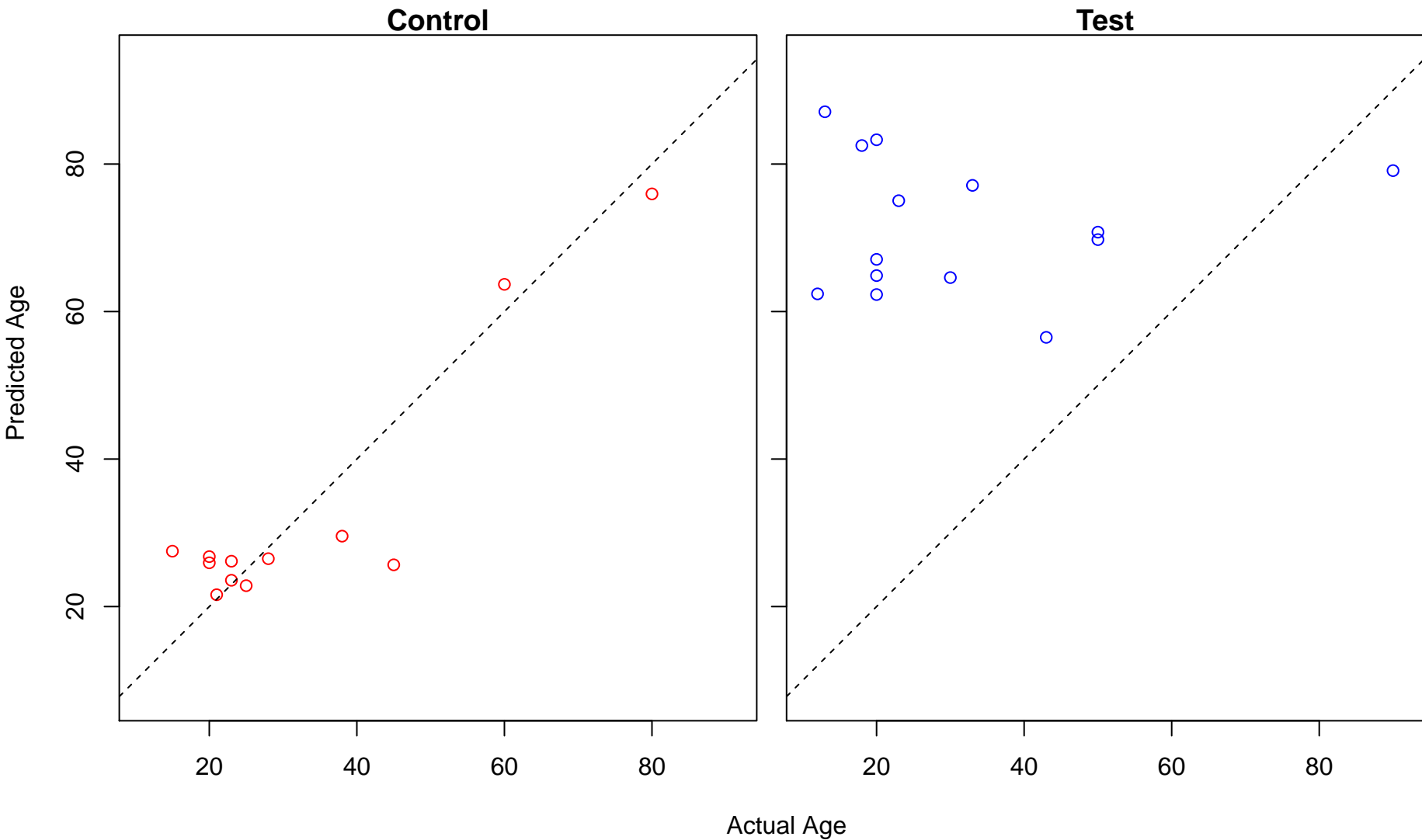
phosphatidylinositol biosynthetic process (Score: 12.527938)



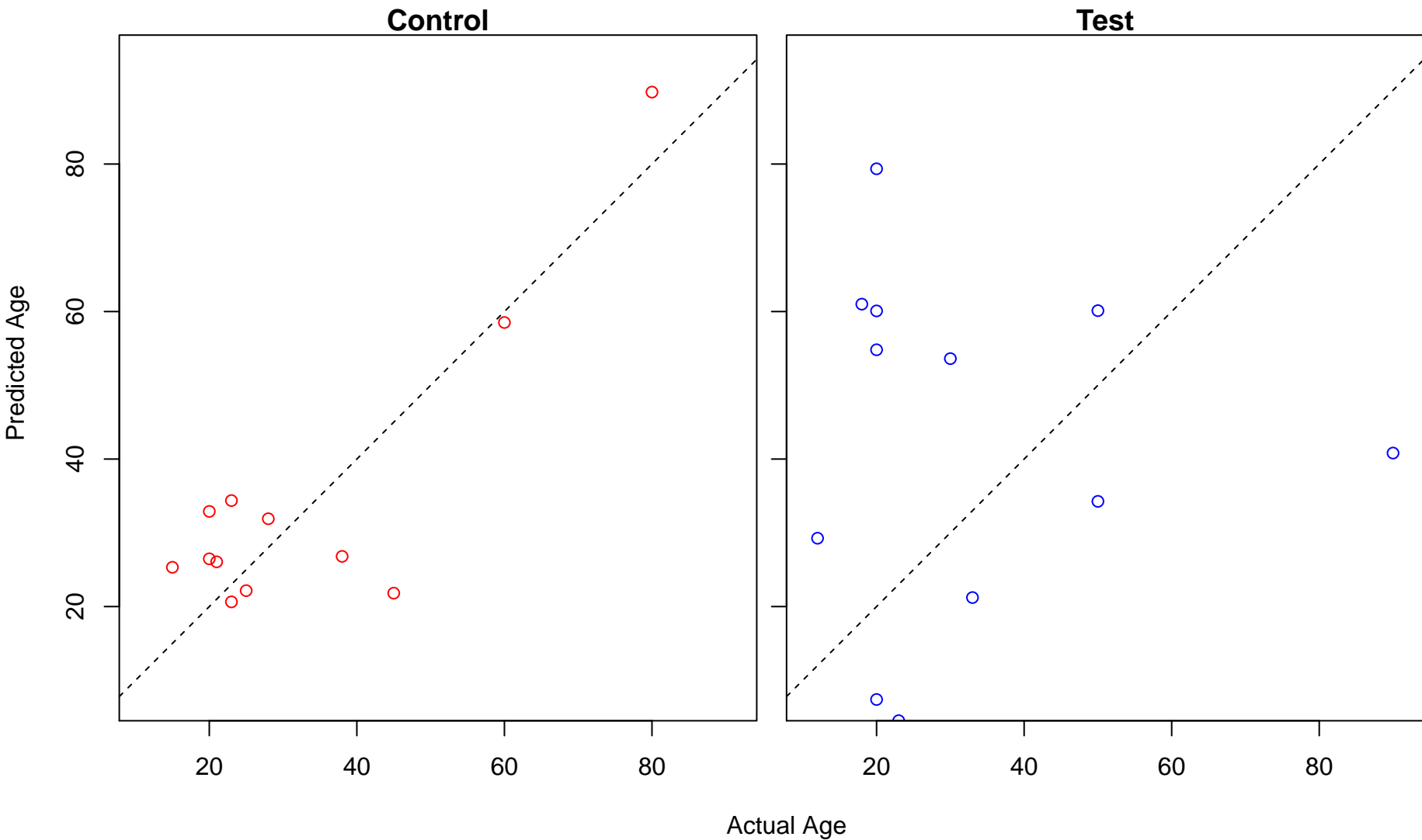
histone monoubiquitination (Score: 12.509350)



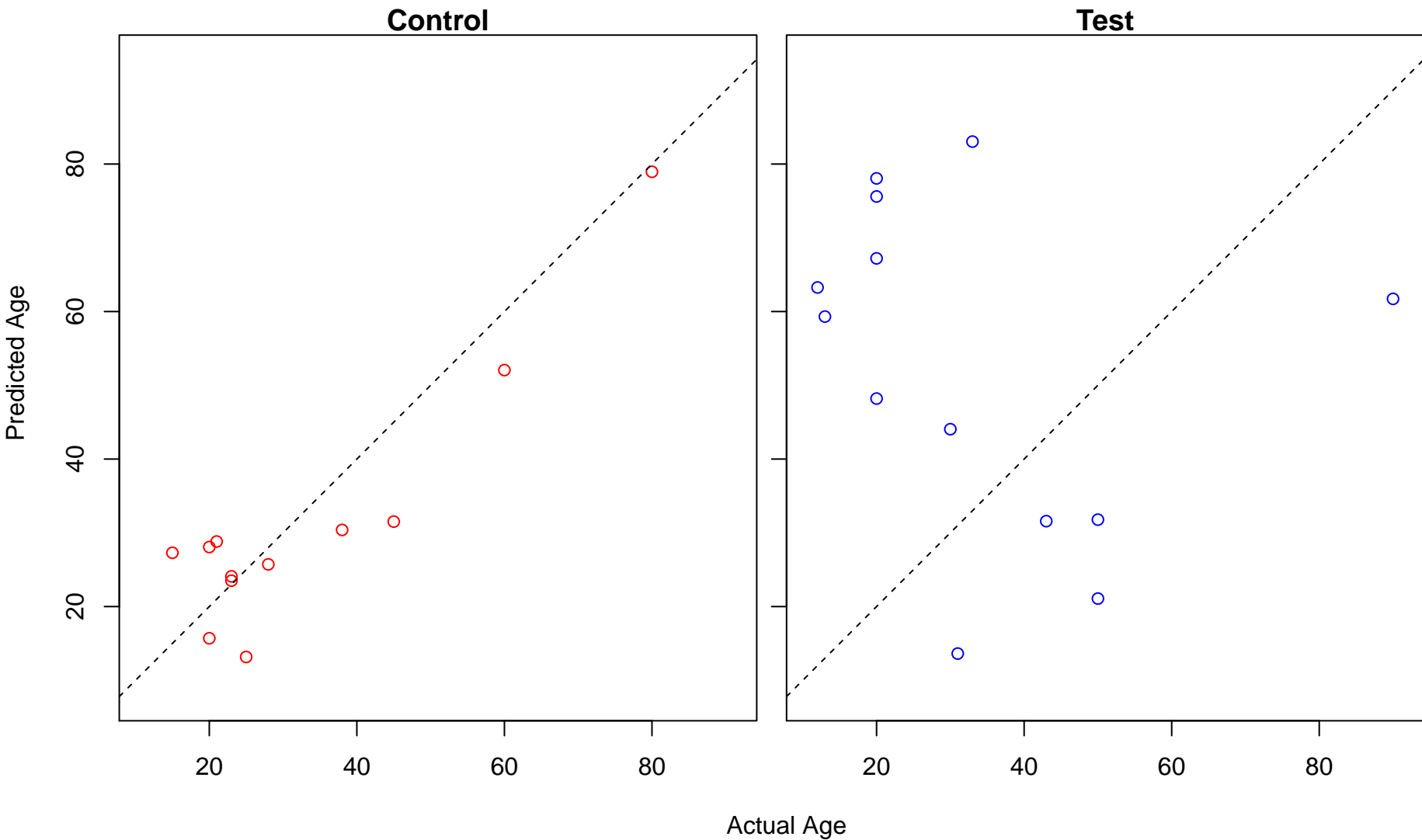
negative regulation of vitamin D biosynthetic process (Score: 12.494757)



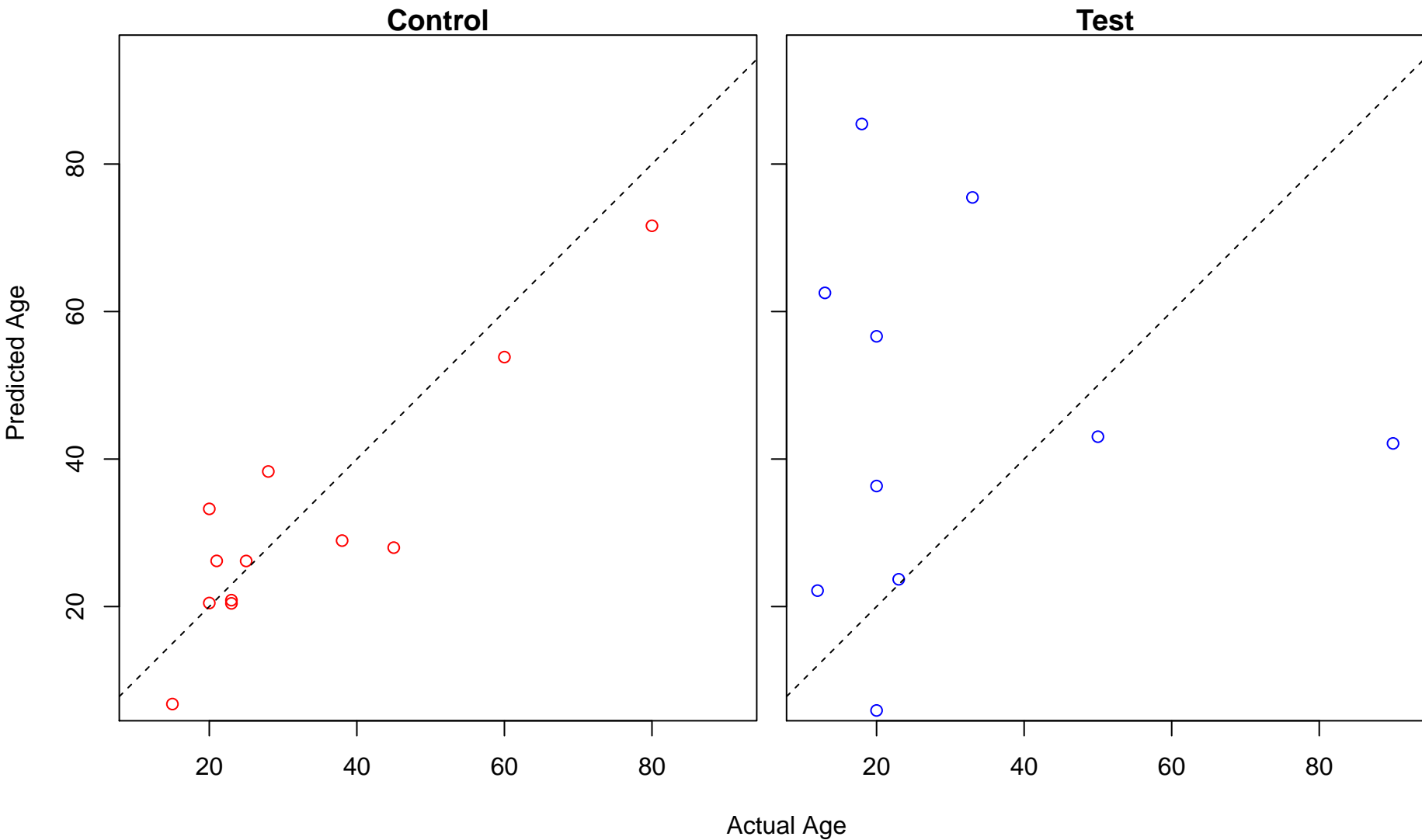
somatic stem cell division (Score: 12.490385)



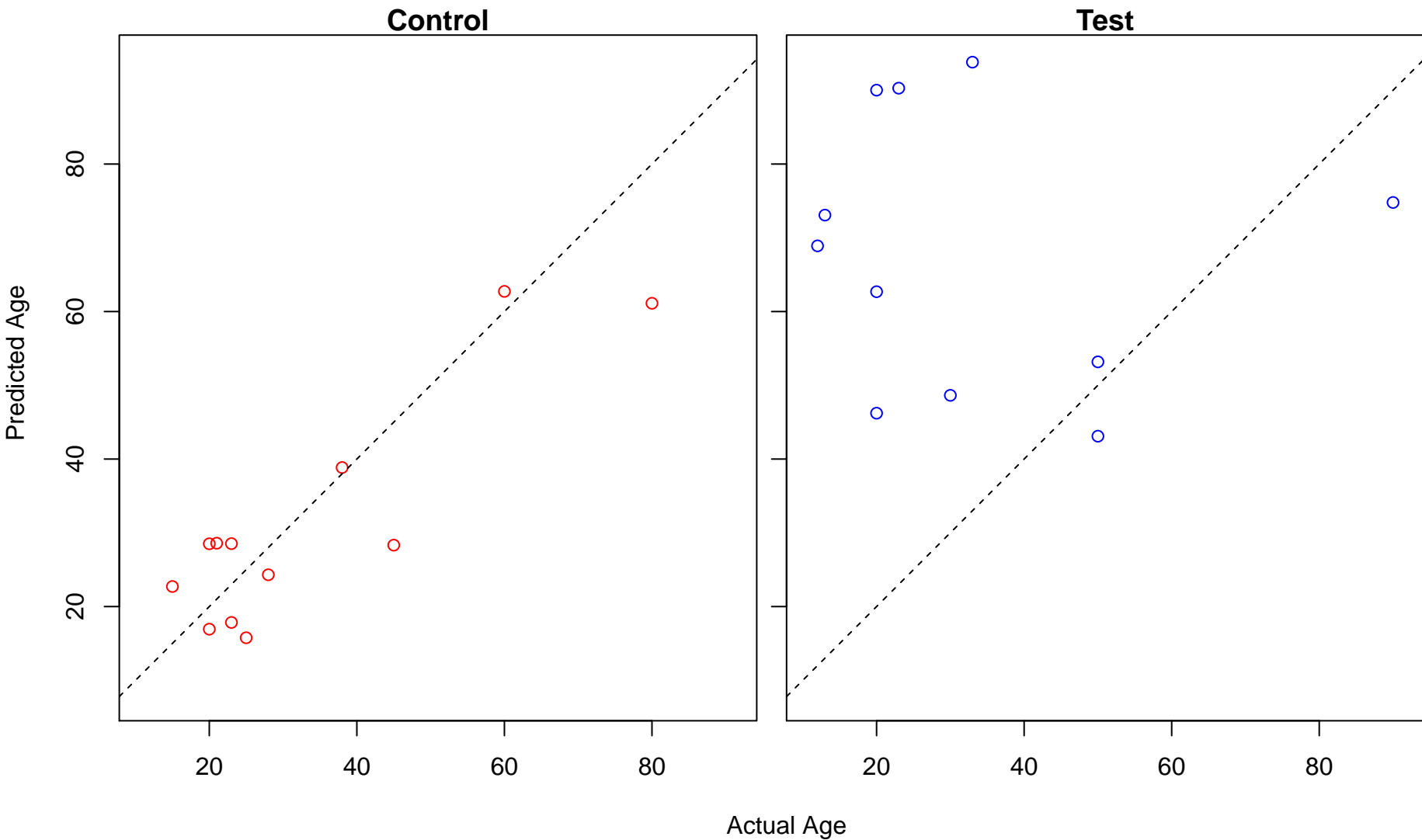
tRNA processing (Score: 12.477383)



regulation of cyclin-dependent protein kinase activity (Score: 12.431658)

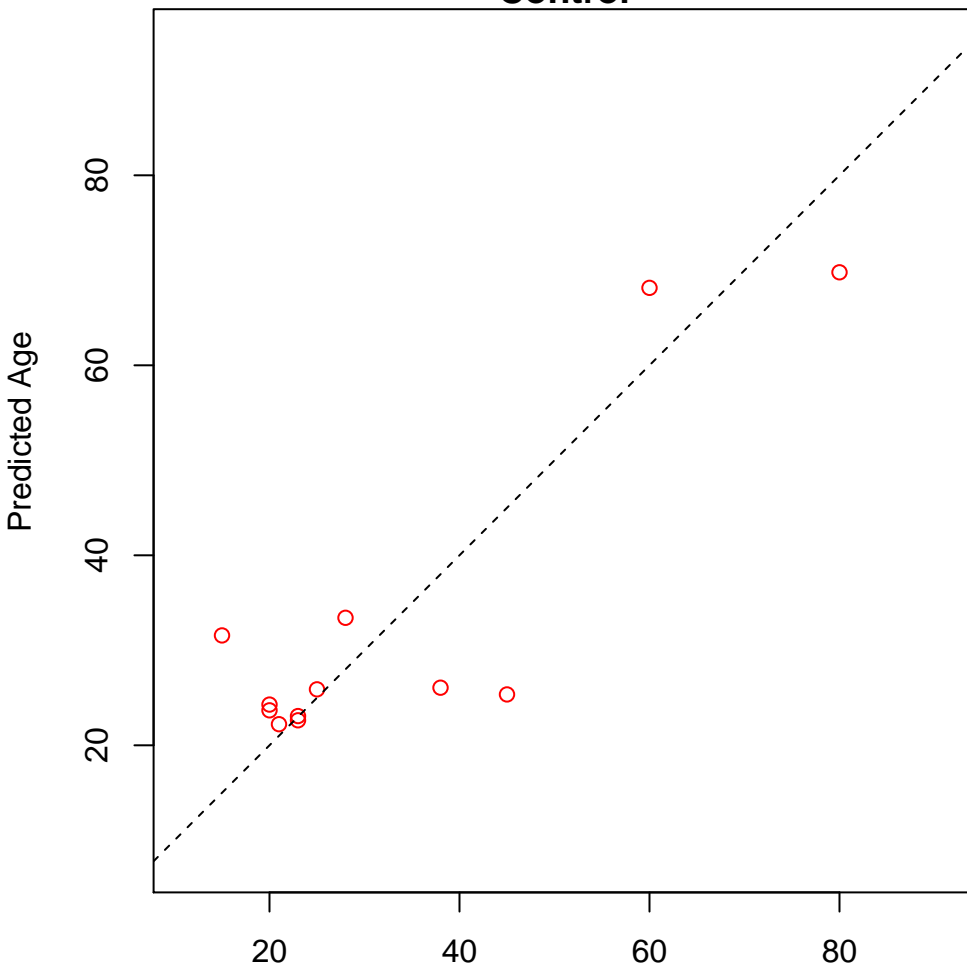


peptidyl-threonine modification (Score: 12.428759)

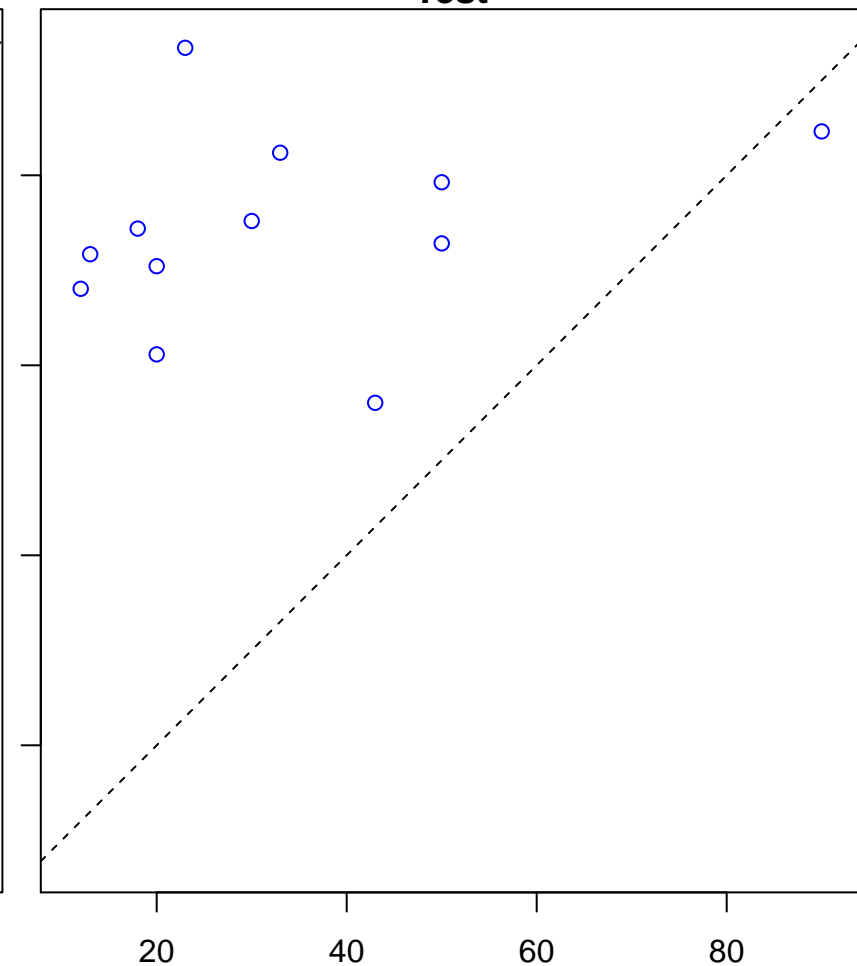


positive regulation of myoblast fusion (Score: 12.427133)

Control

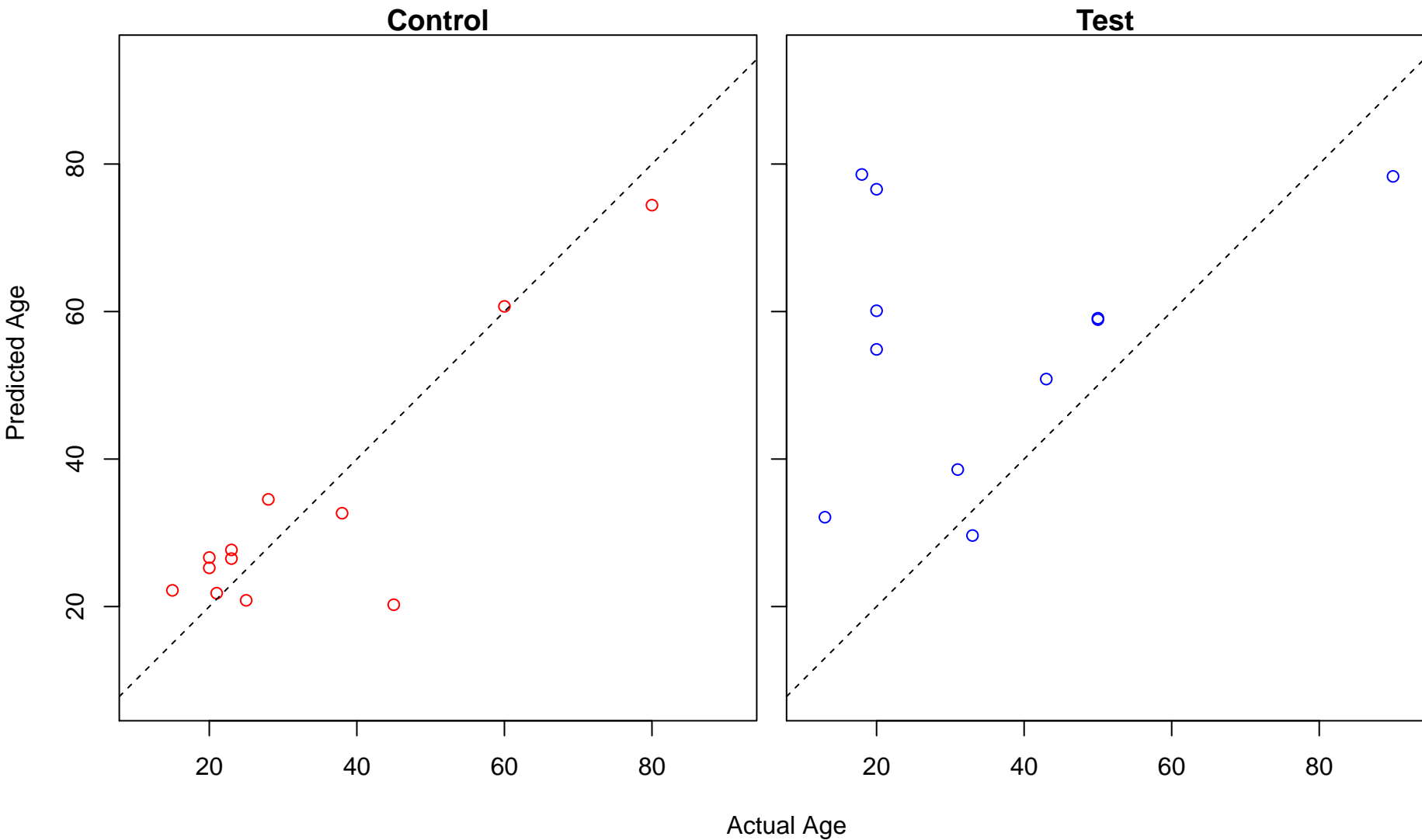


Test

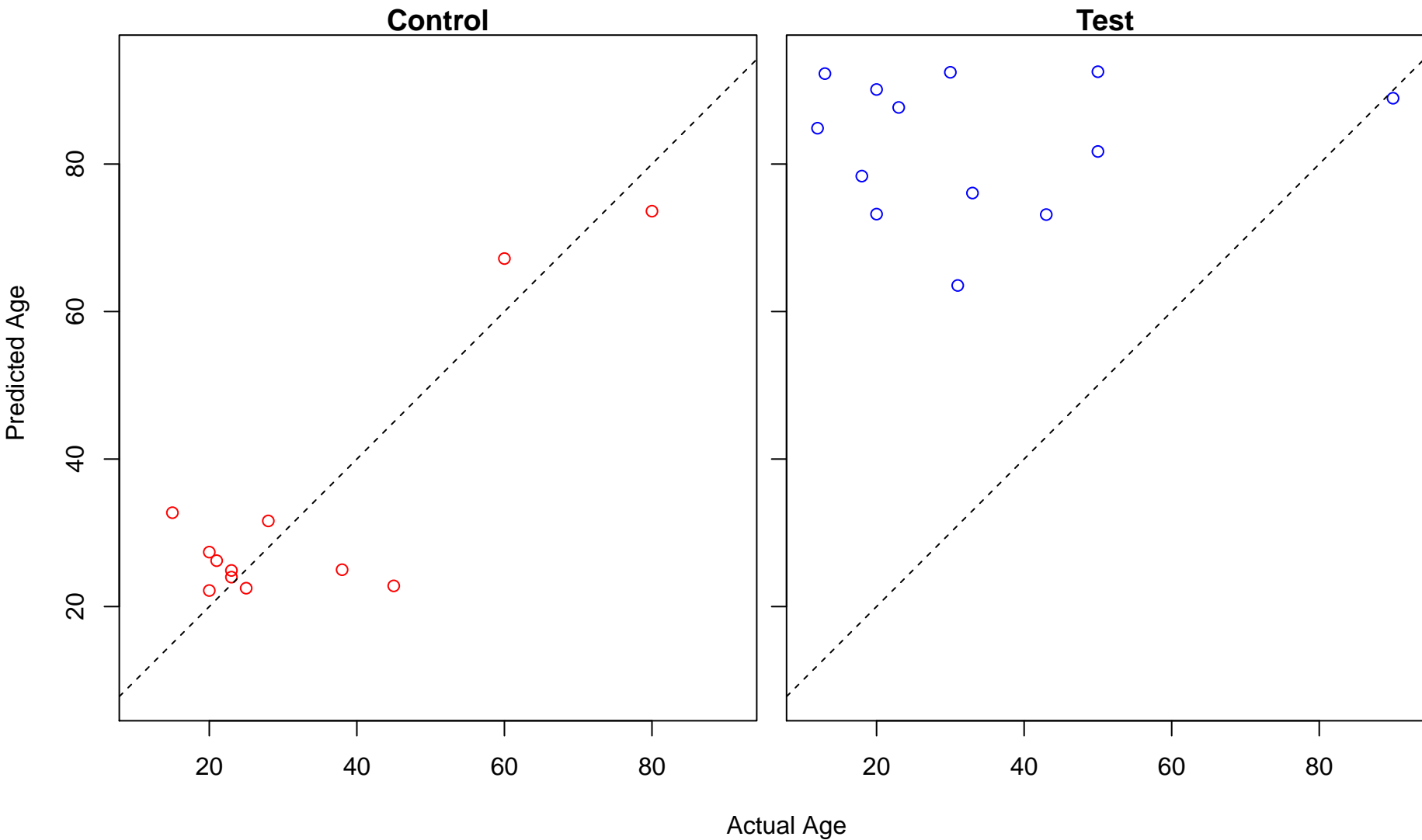


Actual Age

diencephalon development (Score: 12.401852)

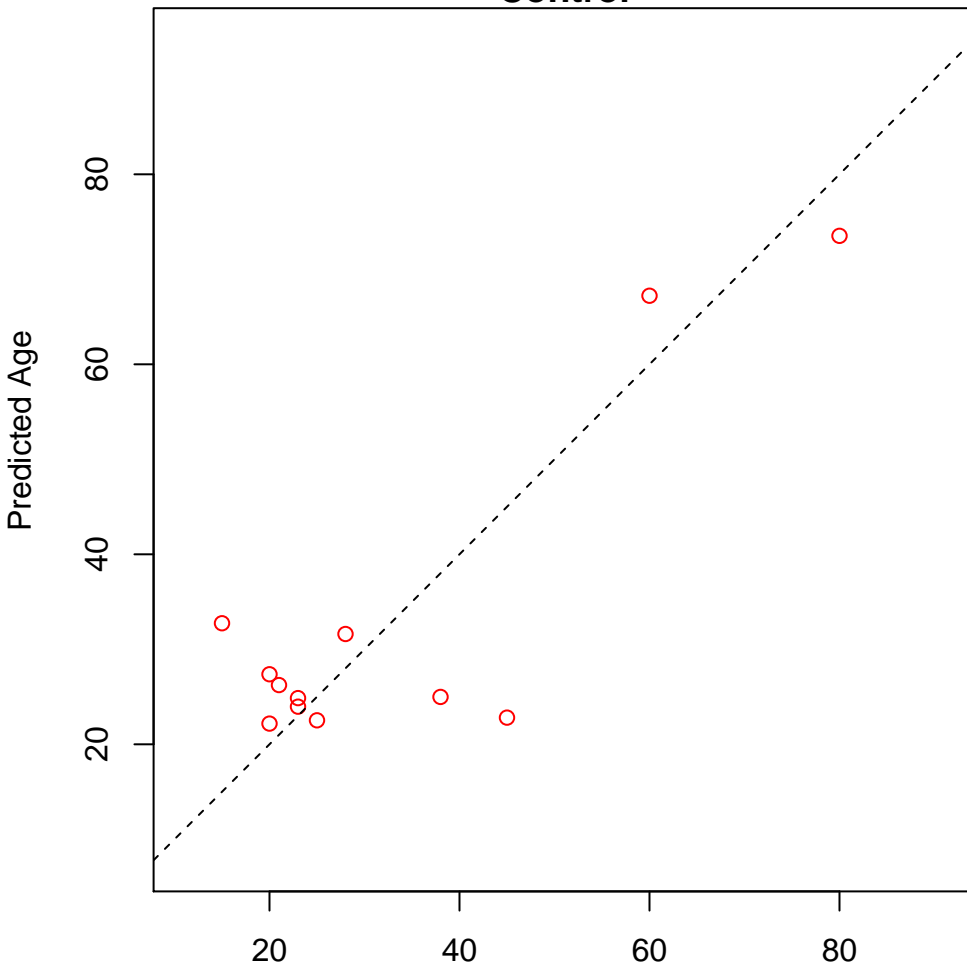


cellular response to molecule of bacterial origin (Score: 12.400708)

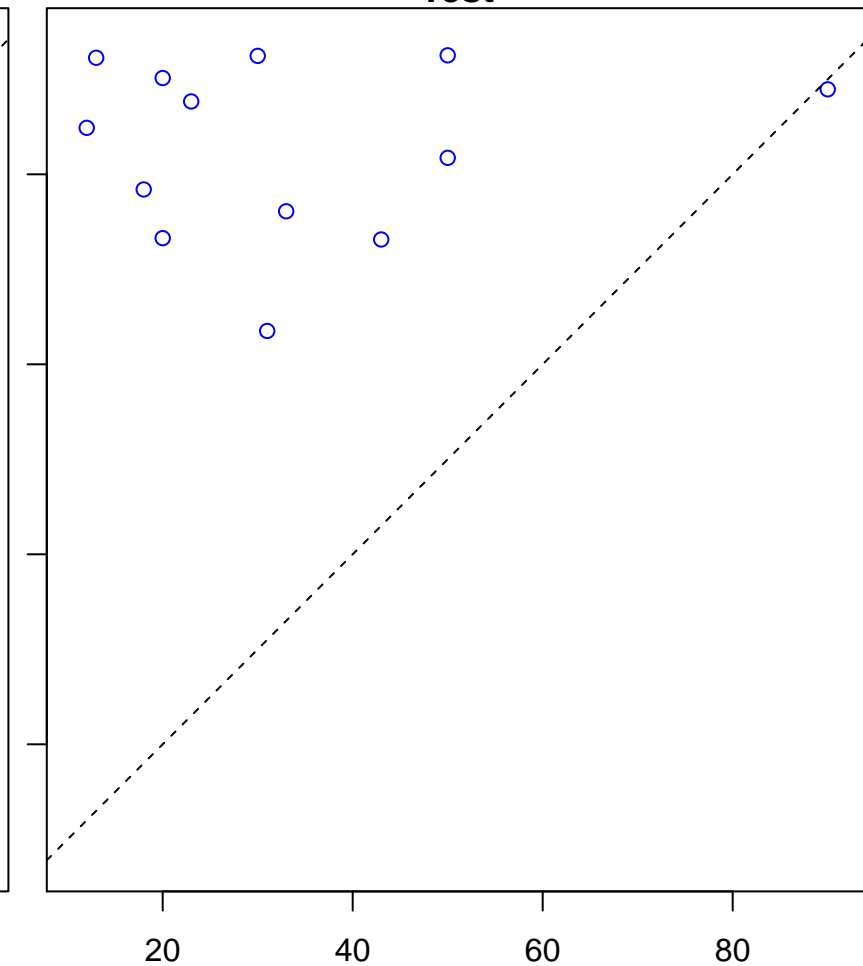


cellular response to lipopolysaccharide (Score: 12.389648)

Control

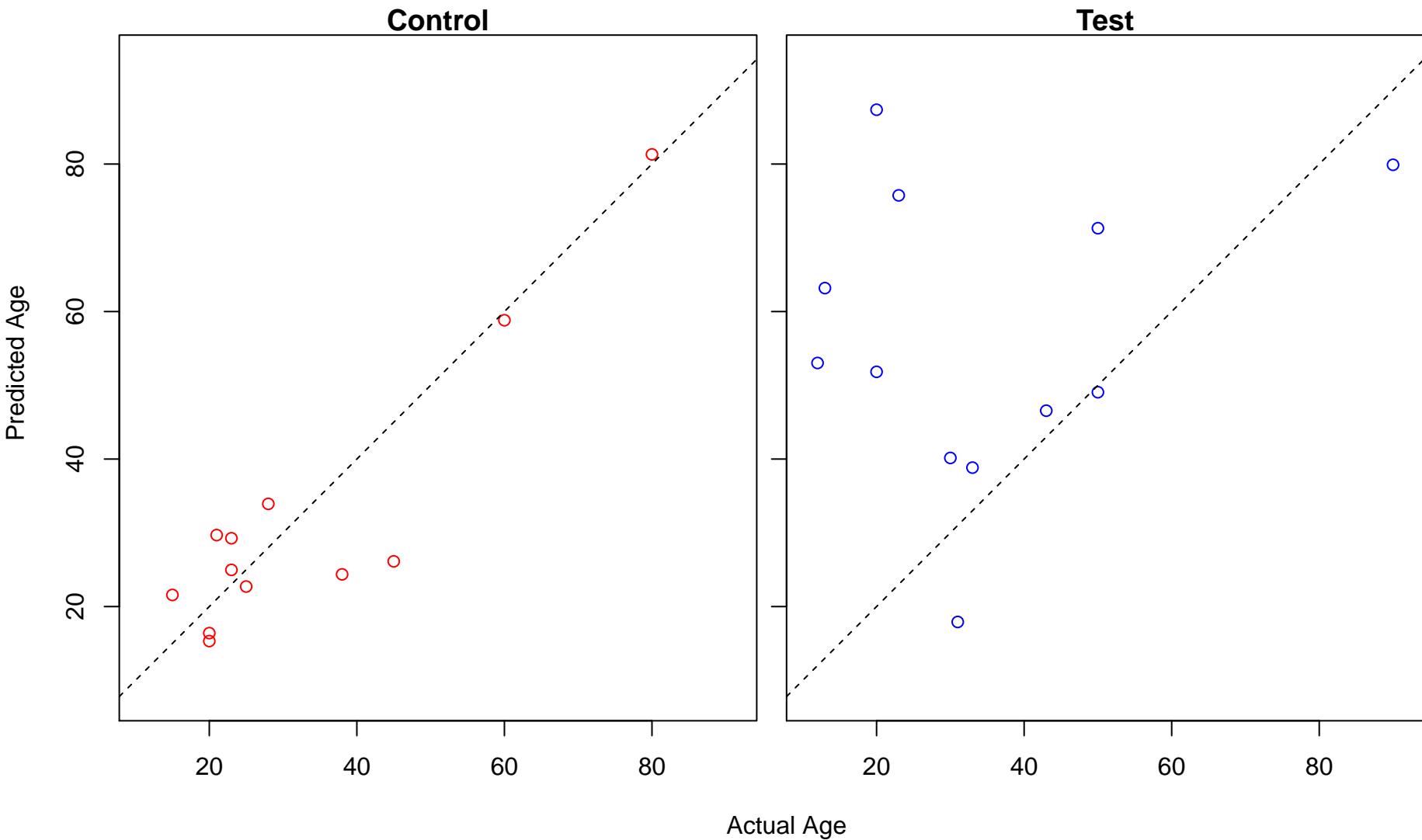


Test

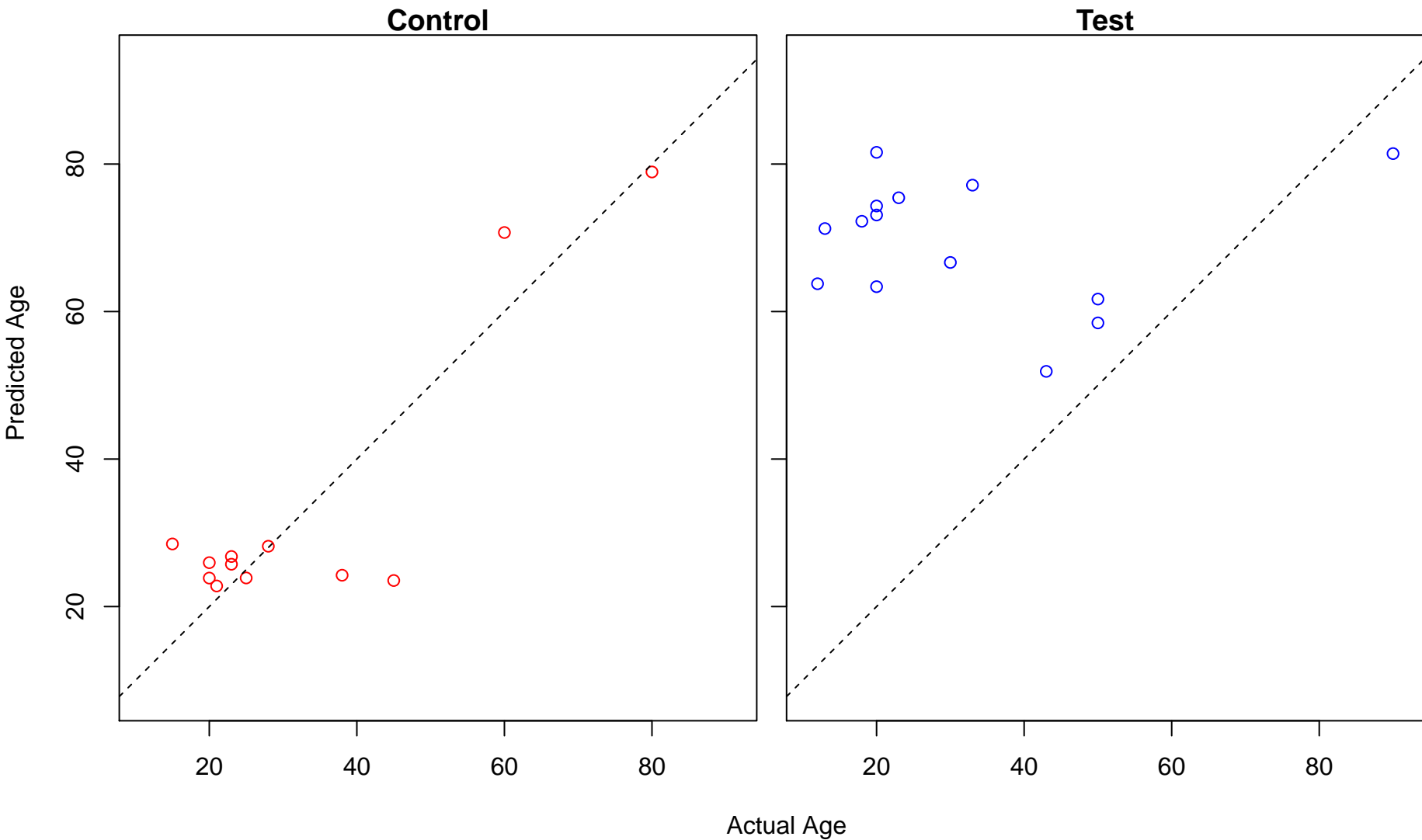


Actual Age

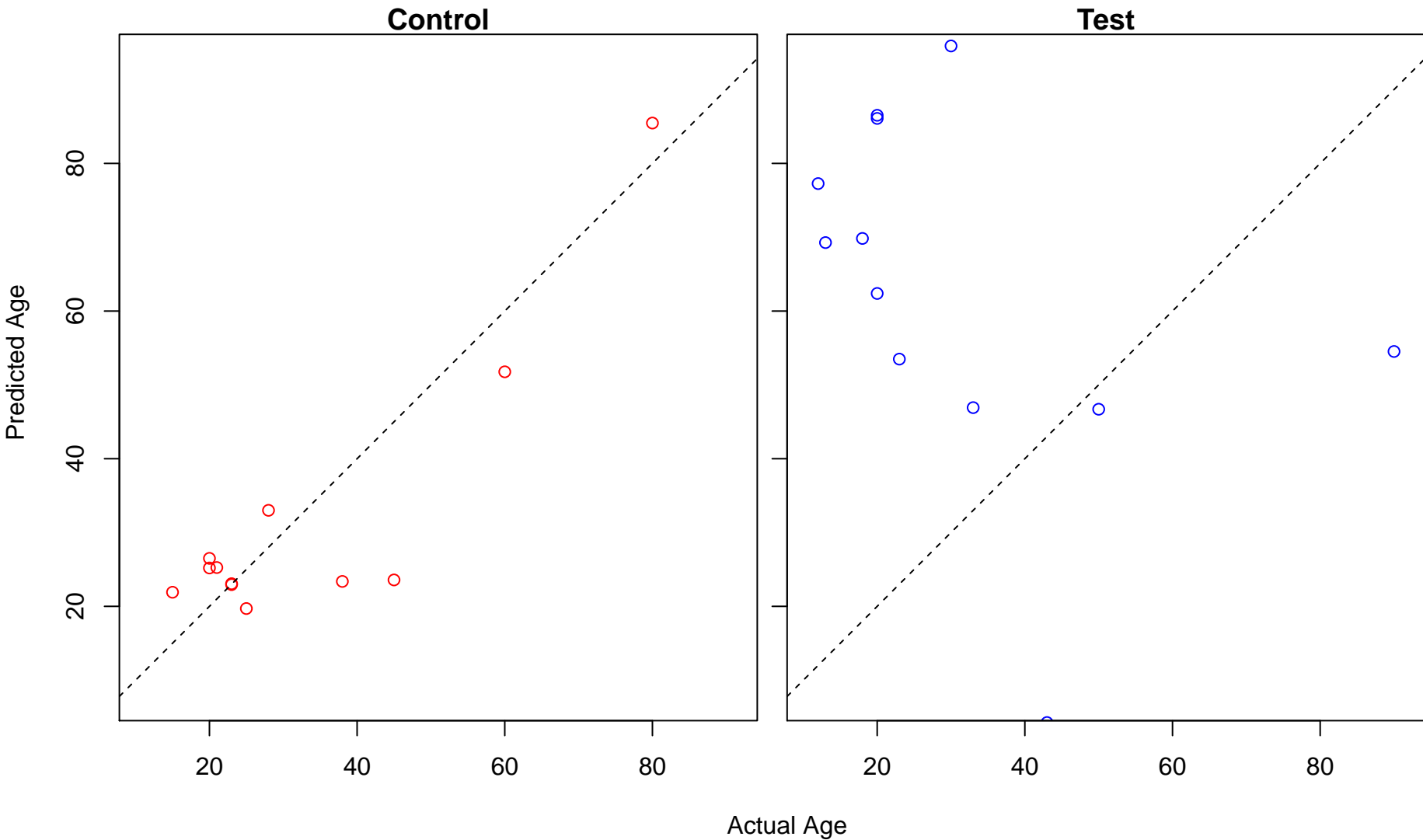
dopamine receptor signaling pathway (Score: 12.389252)



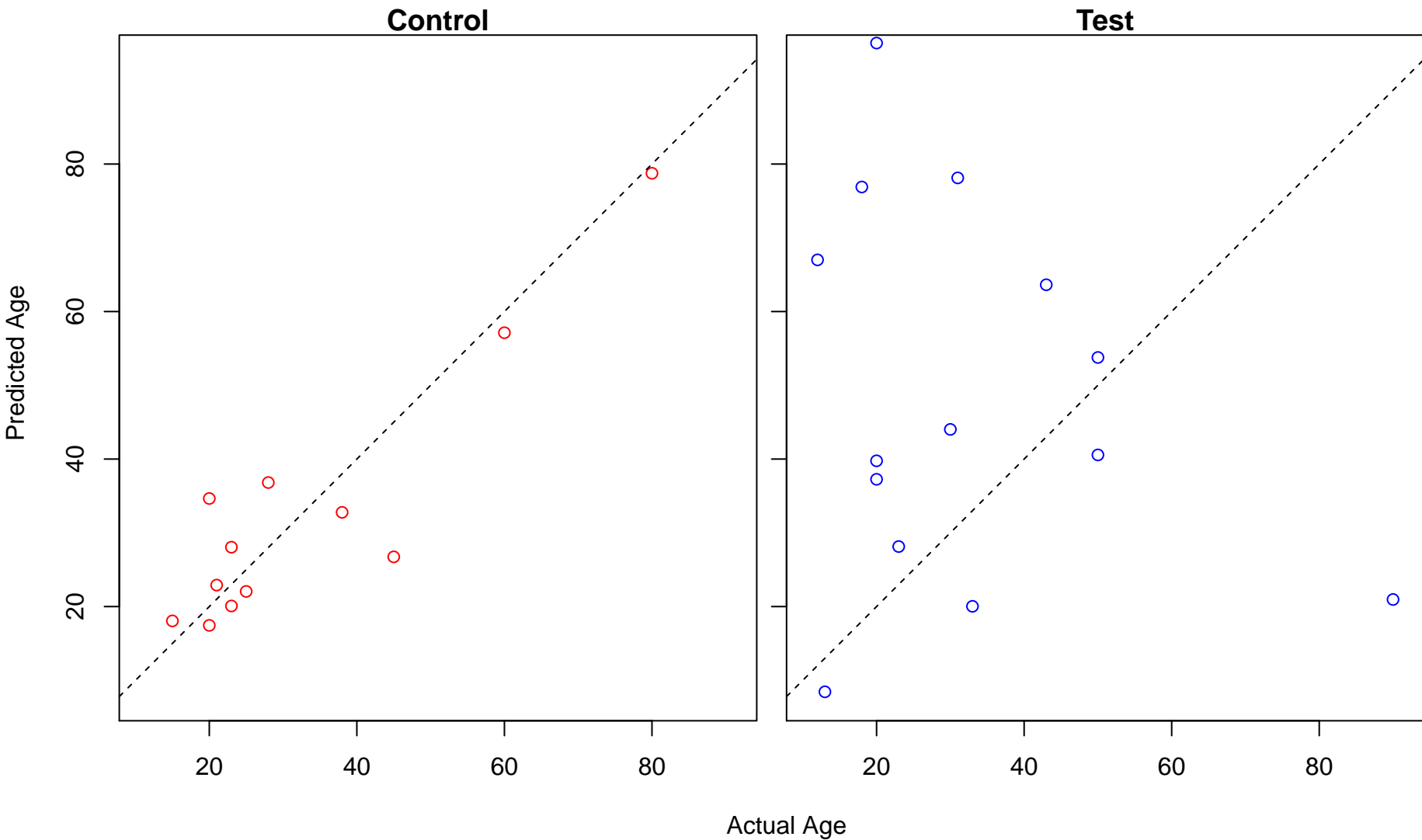
negative regulation of transcription factor import into nucleus (Score: 12.387119)



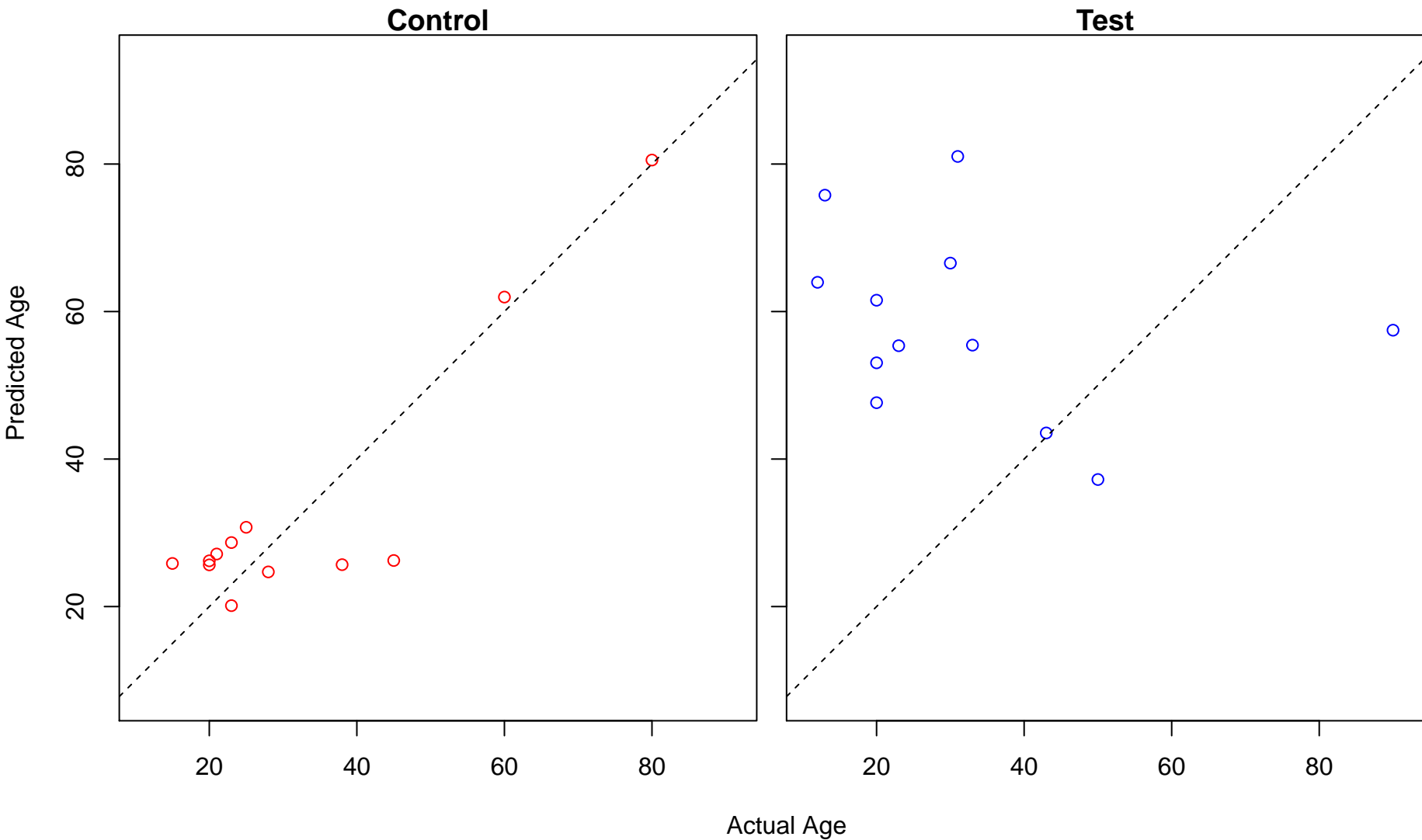
regulation of stress-activated protein kinase signaling cascade (Score: 12.360604)



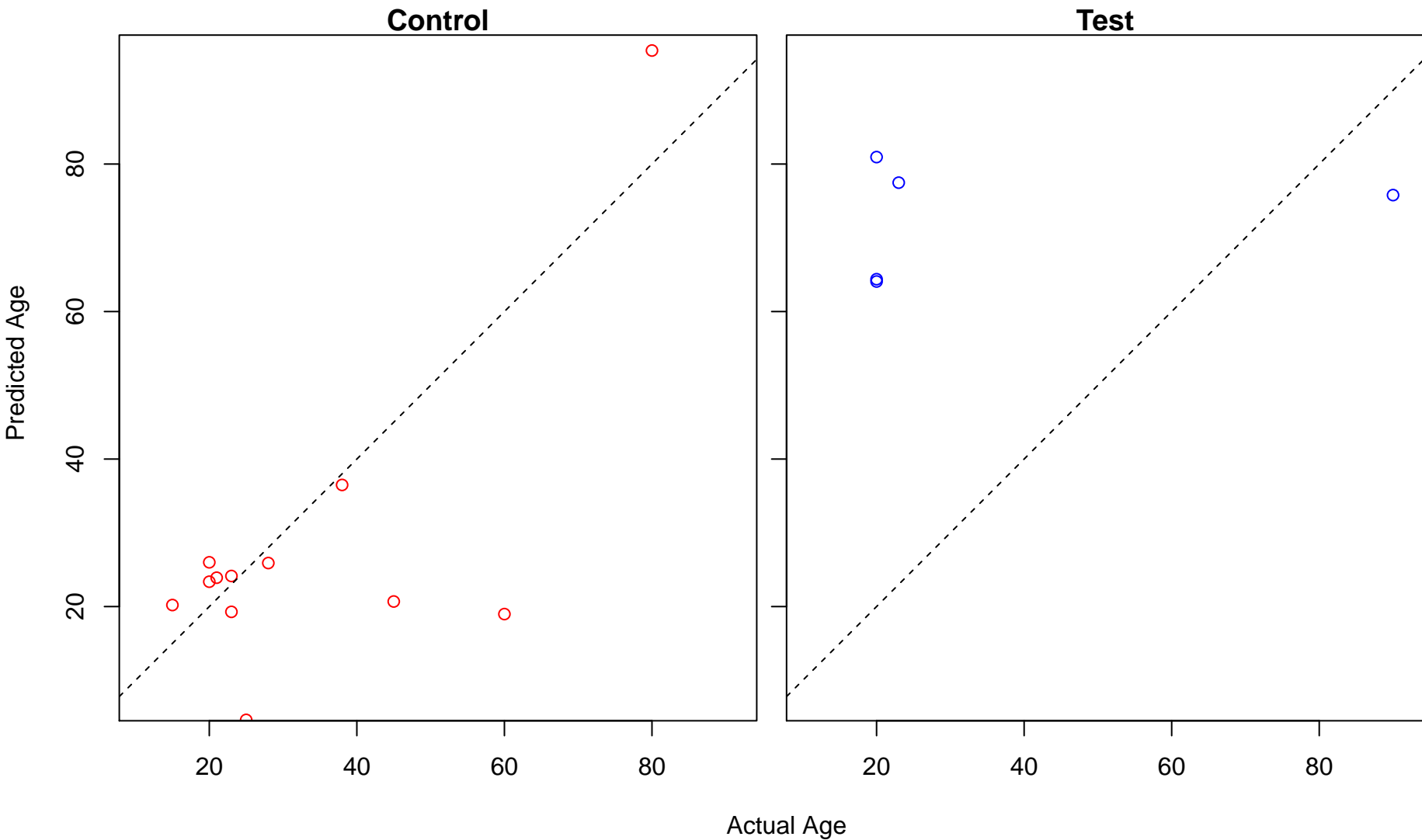
cofactor metabolic process (Score: 12.349806)



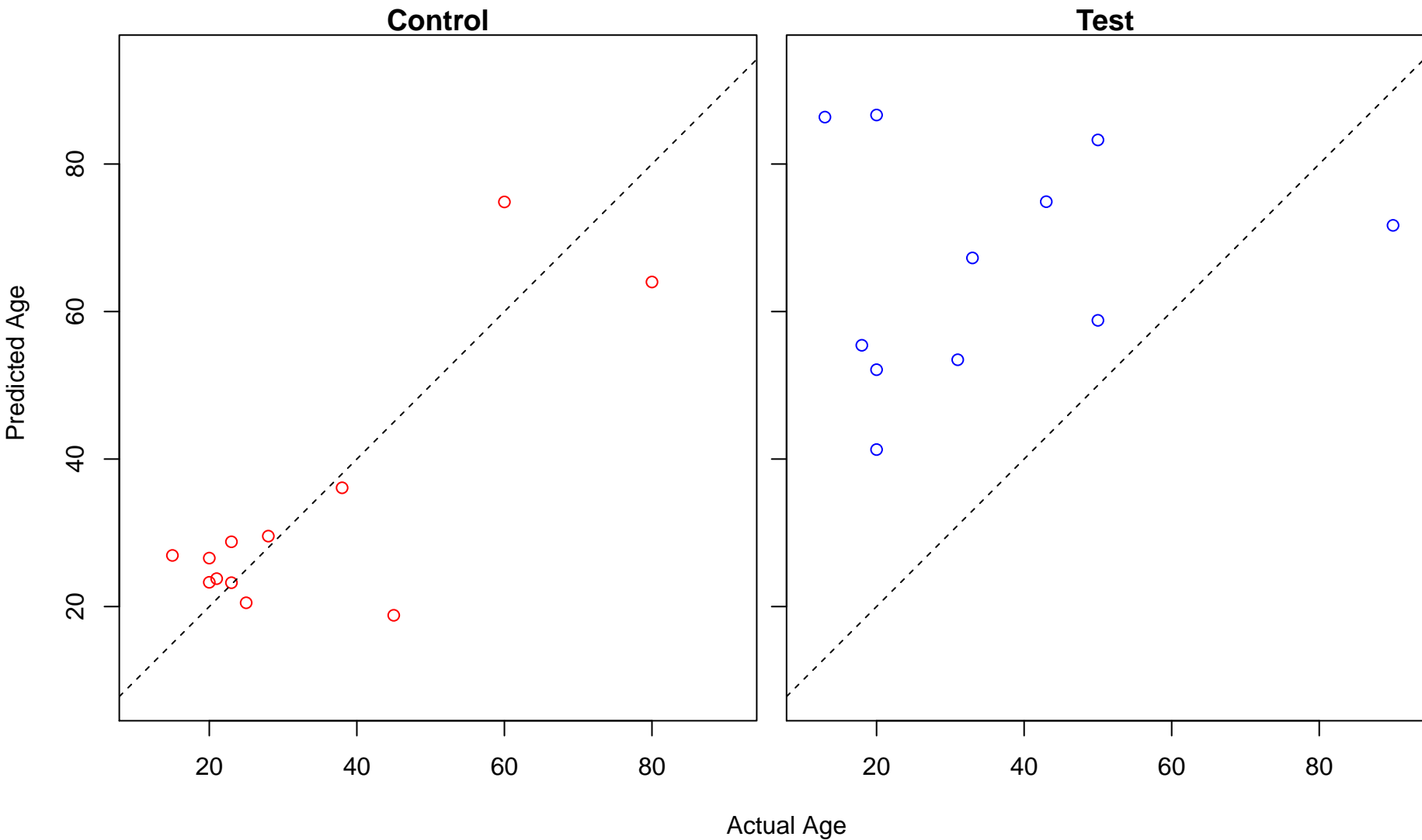
negative regulation of meiotic cell cycle (Score: 12.330912)



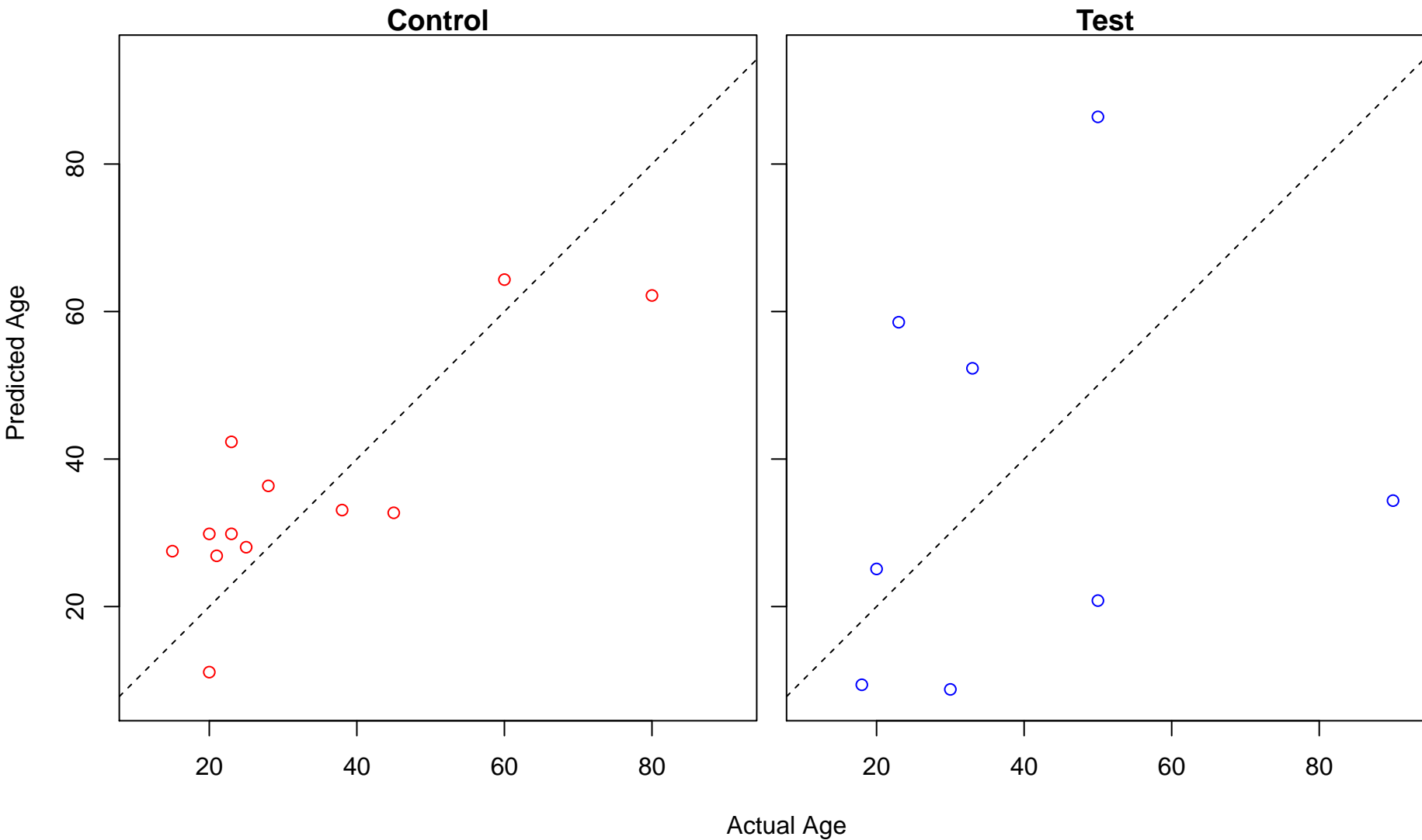
negative regulation of cilium assembly (Score: 12.325533)



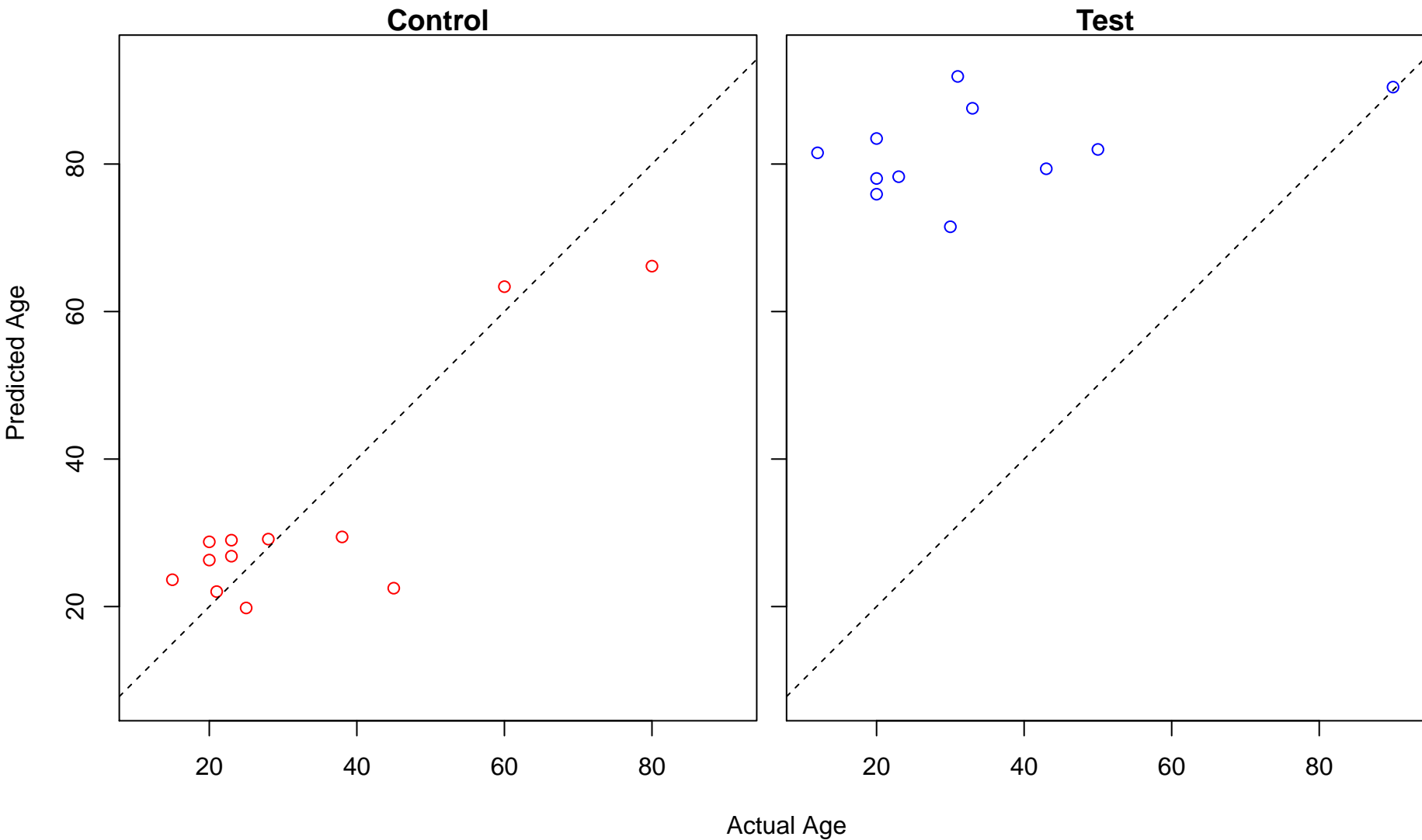
pituitary gland development (Score: 12.316421)



response to estradiol (Score: 12.313817)

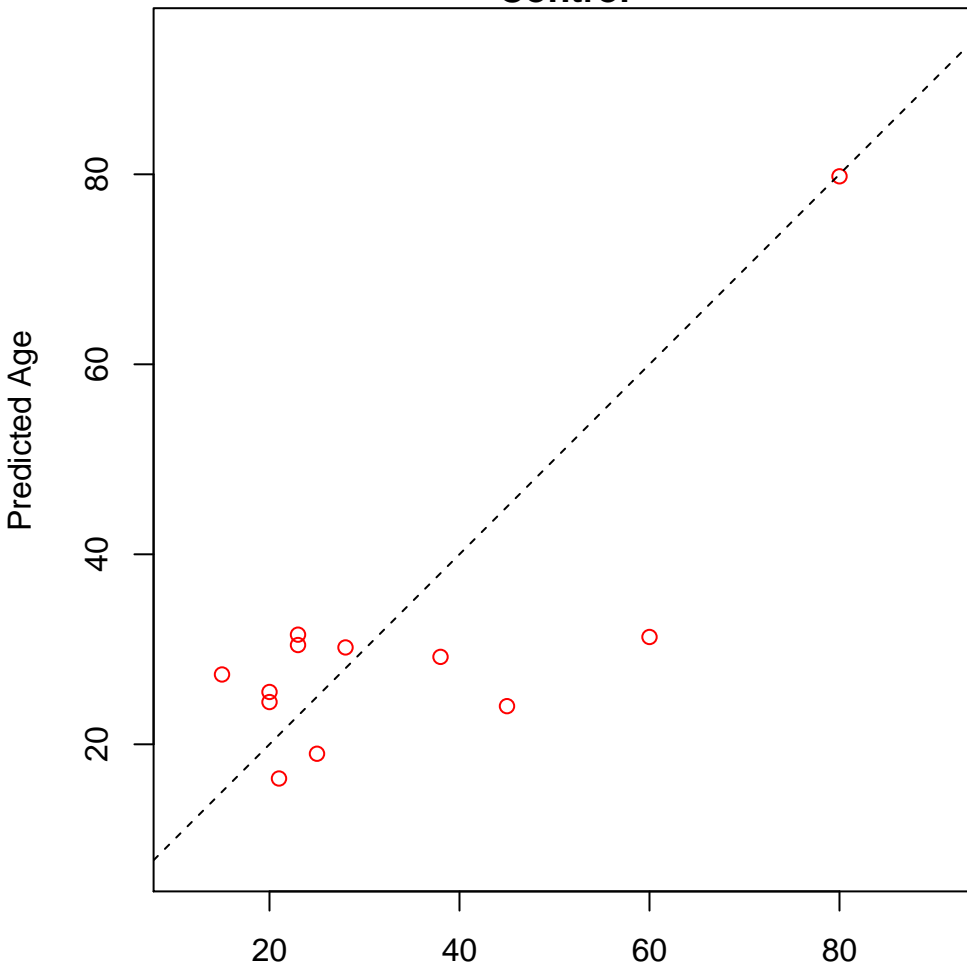


oocyte development (Score: 12.309071)

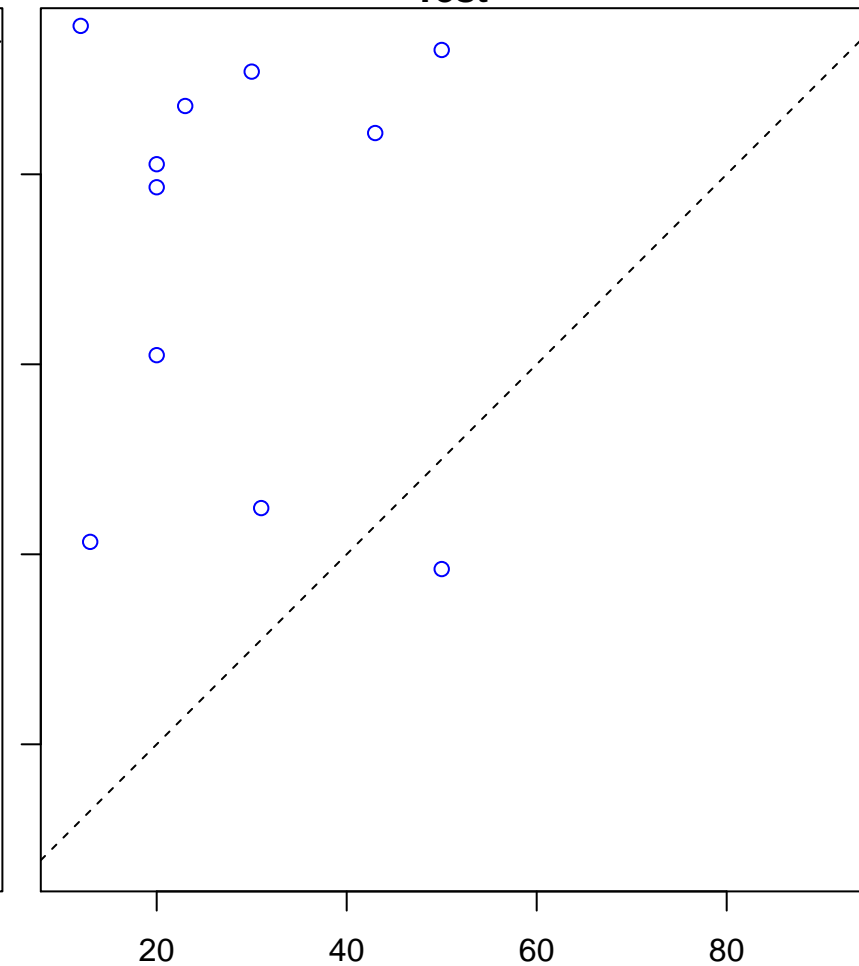


deoxyribonucleotide catabolic process (Score: 12.289421)

Control

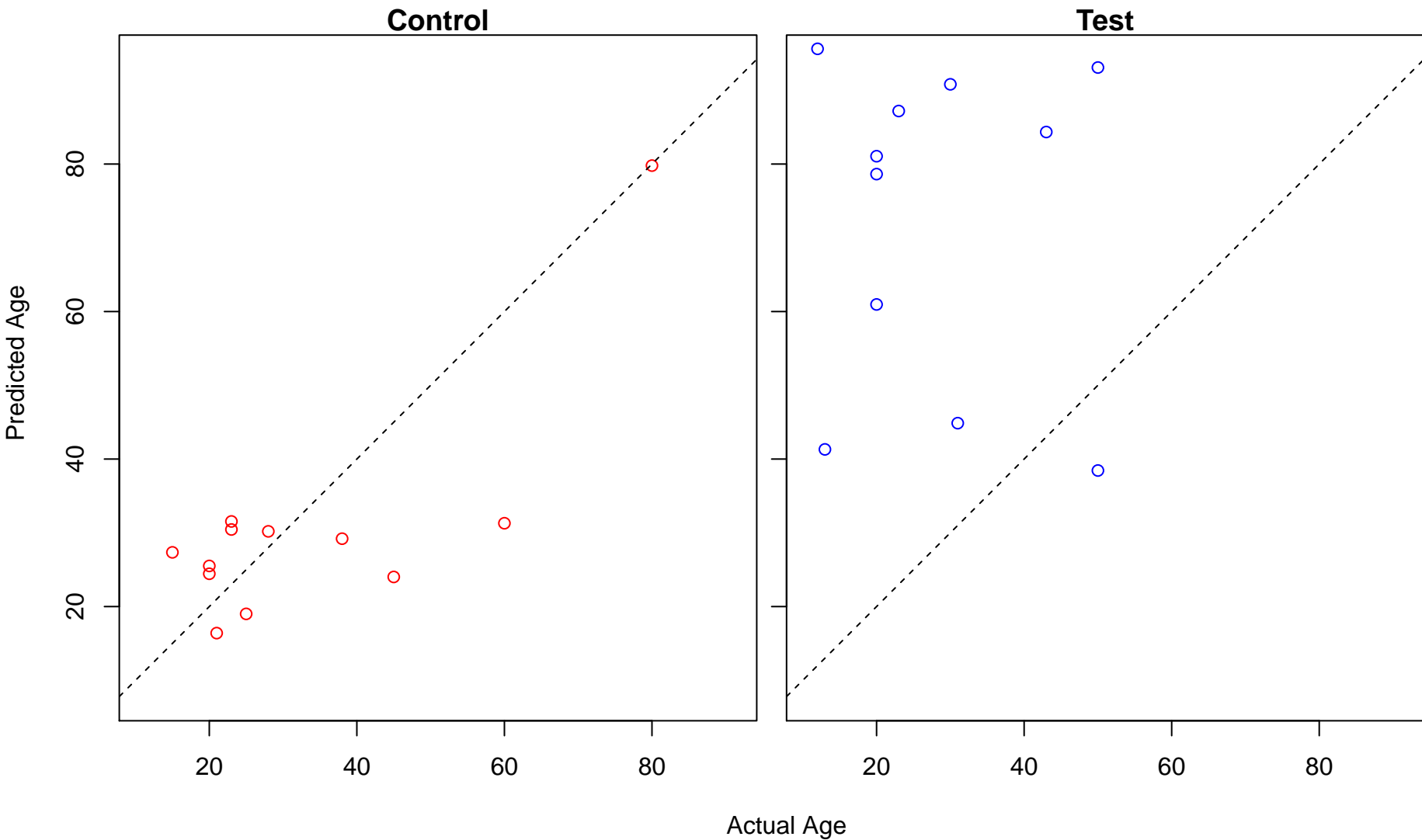


Test

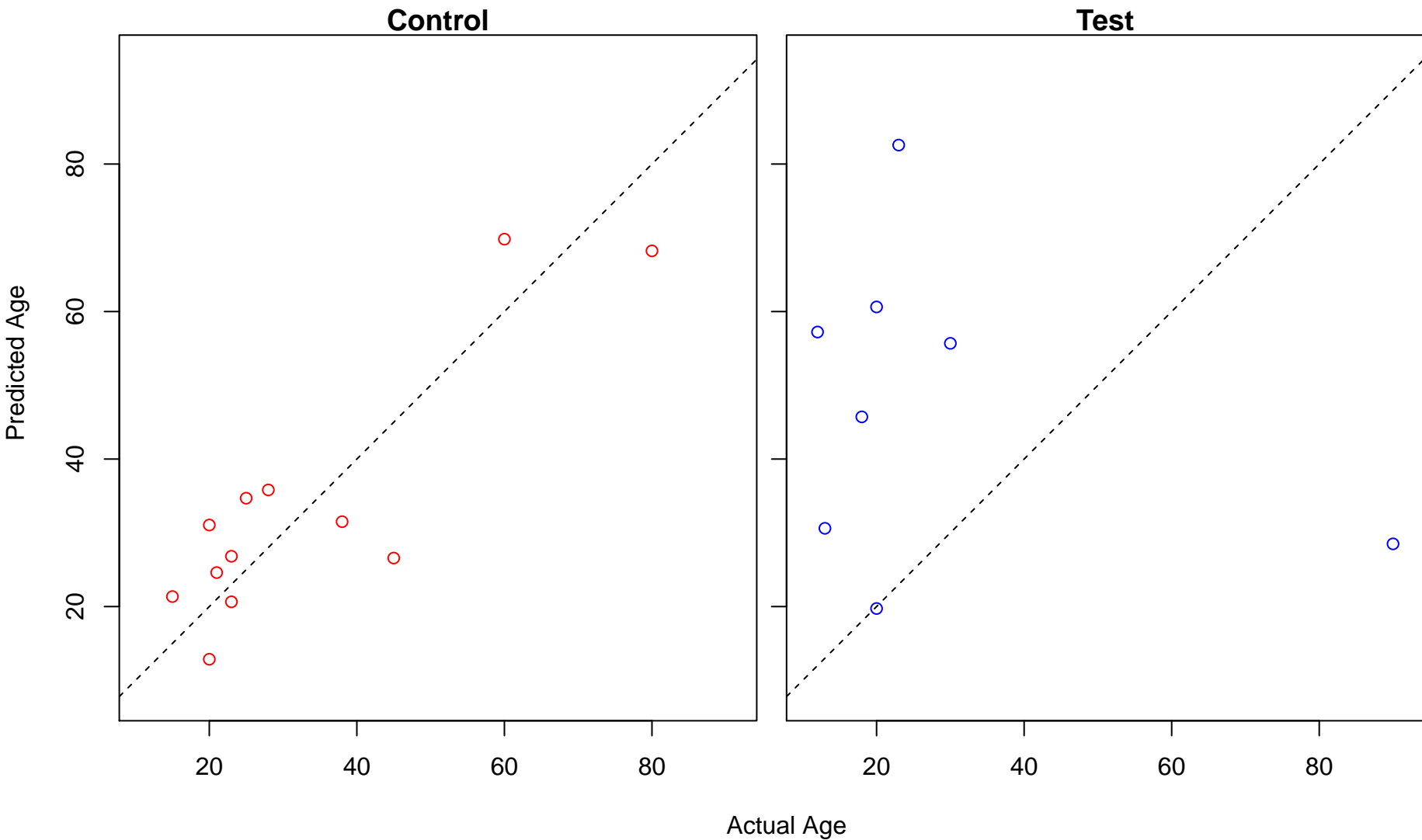


Actual Age

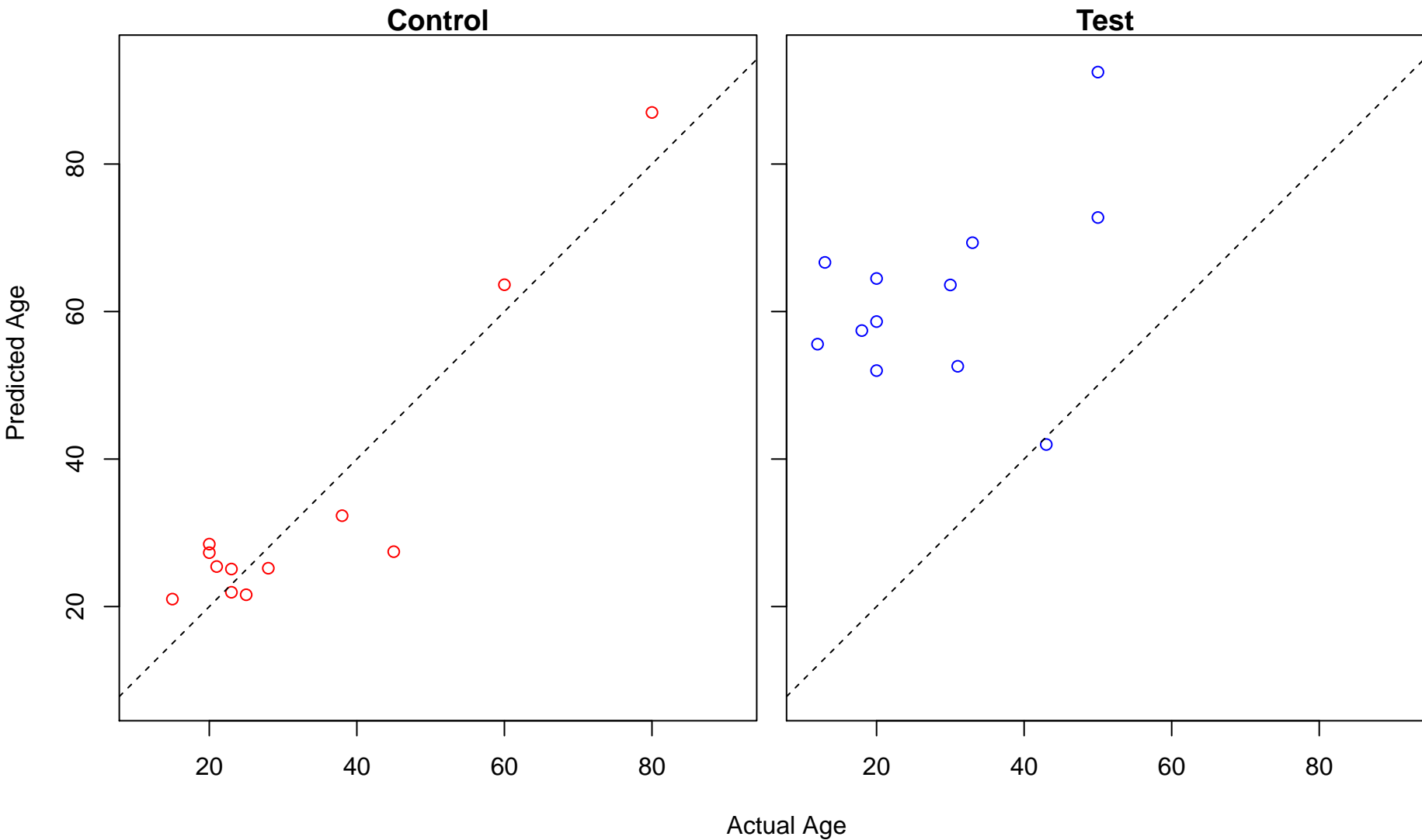
deoxyribose phosphate catabolic process (Score: 12.289421)



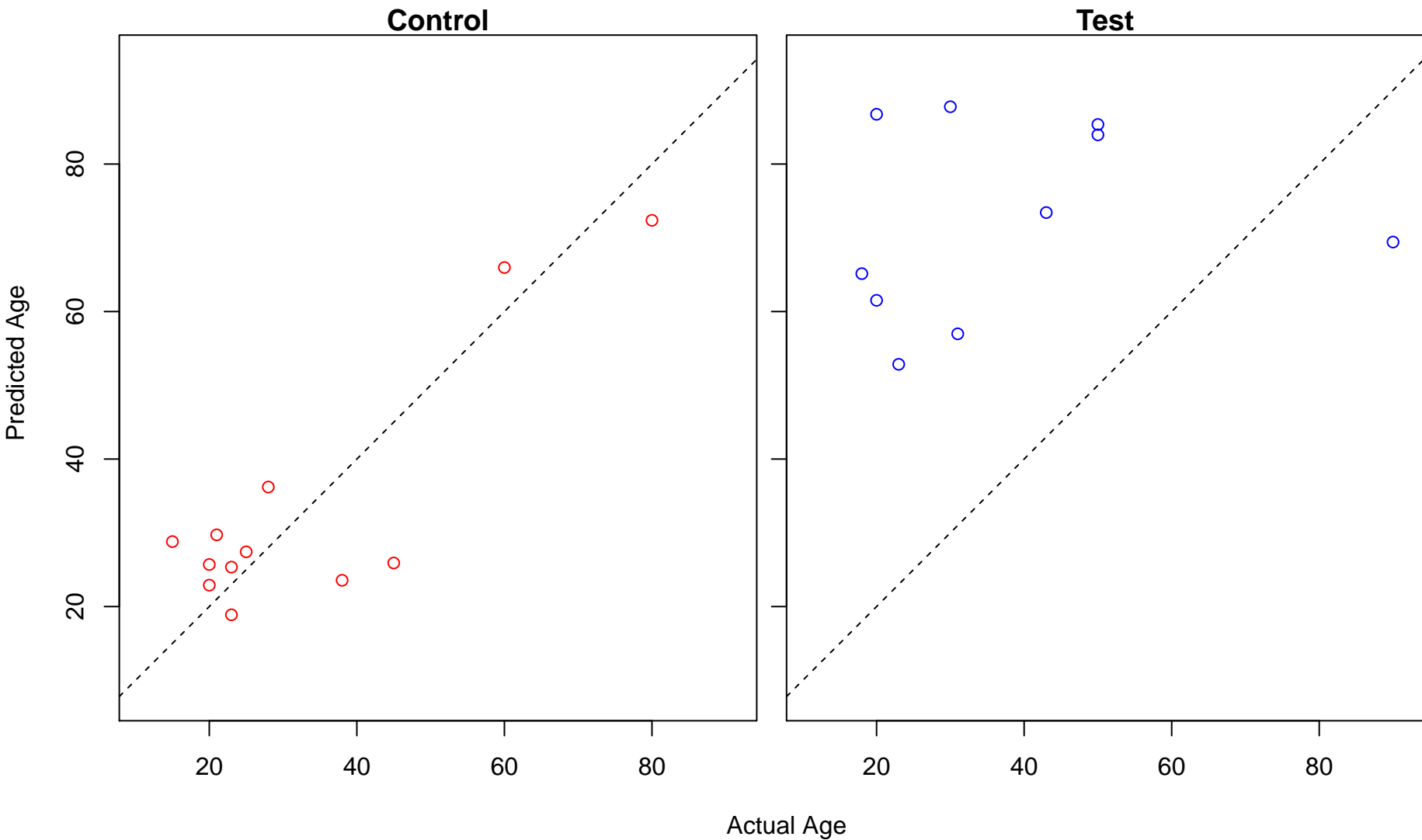
regulation of protein stability (Score: 12.289185)



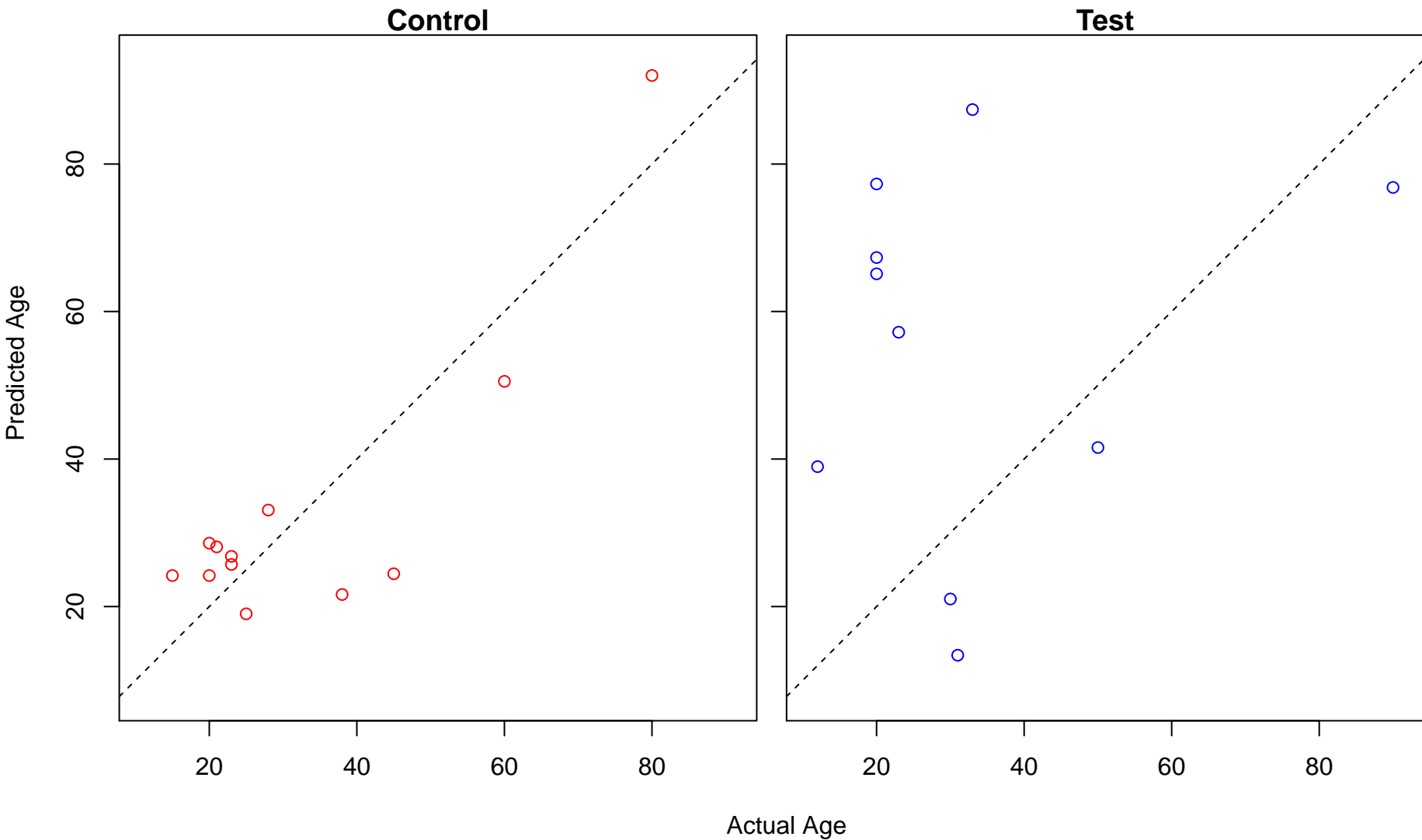
pronephros development (Score: 12.271476)



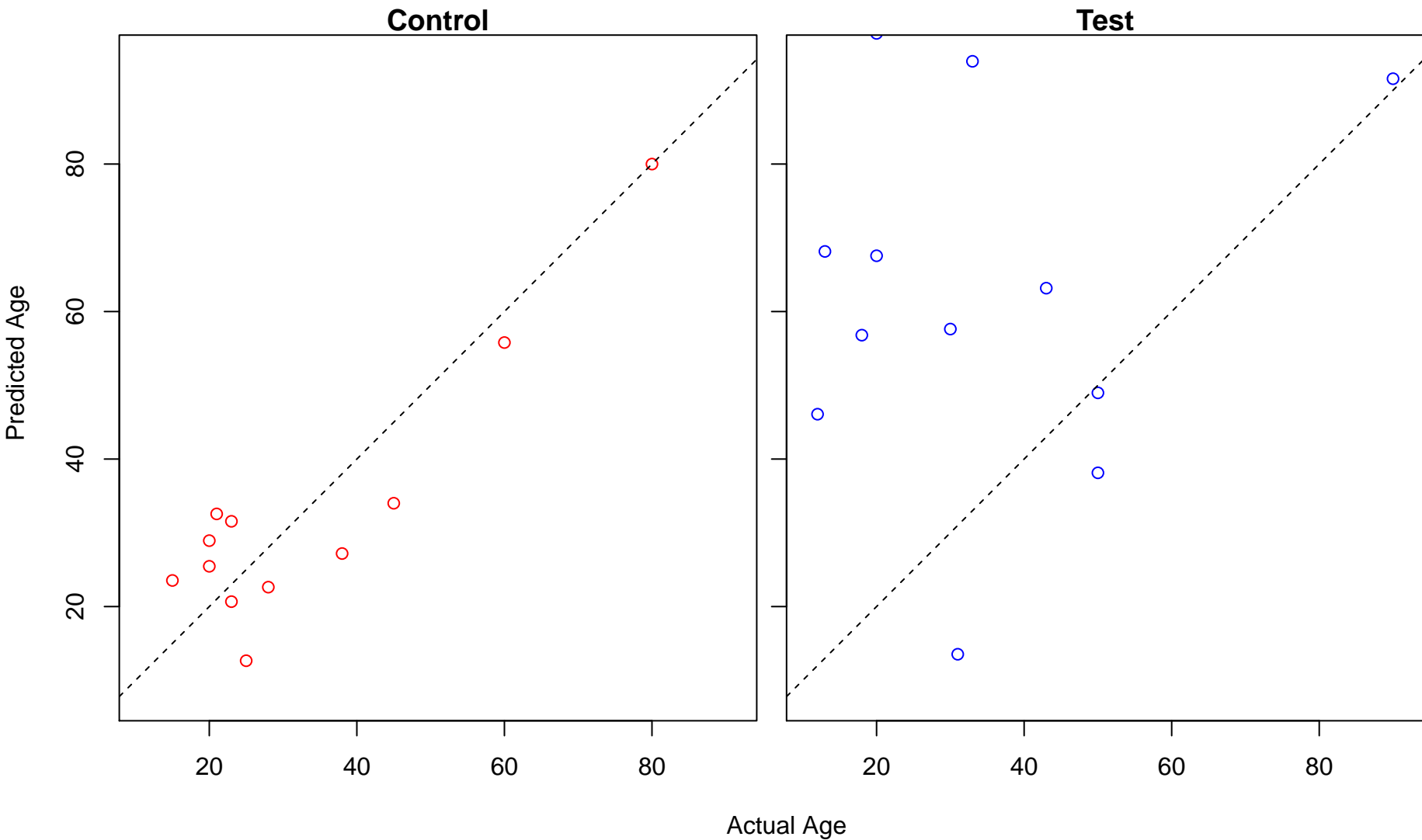
mesenchymal cell differentiation (Score: 12.271307)



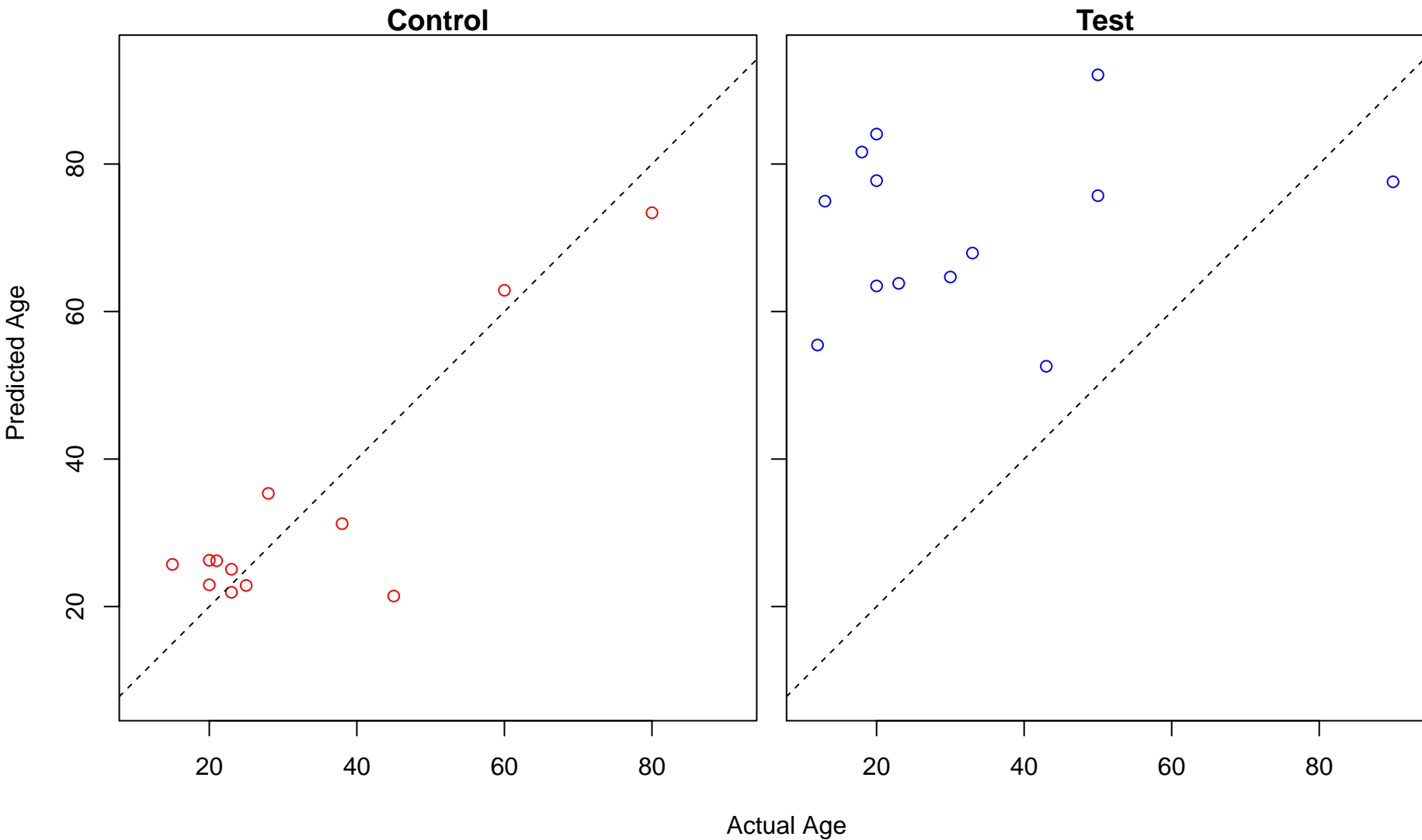
ncRNA processing (Score: 12.269135)



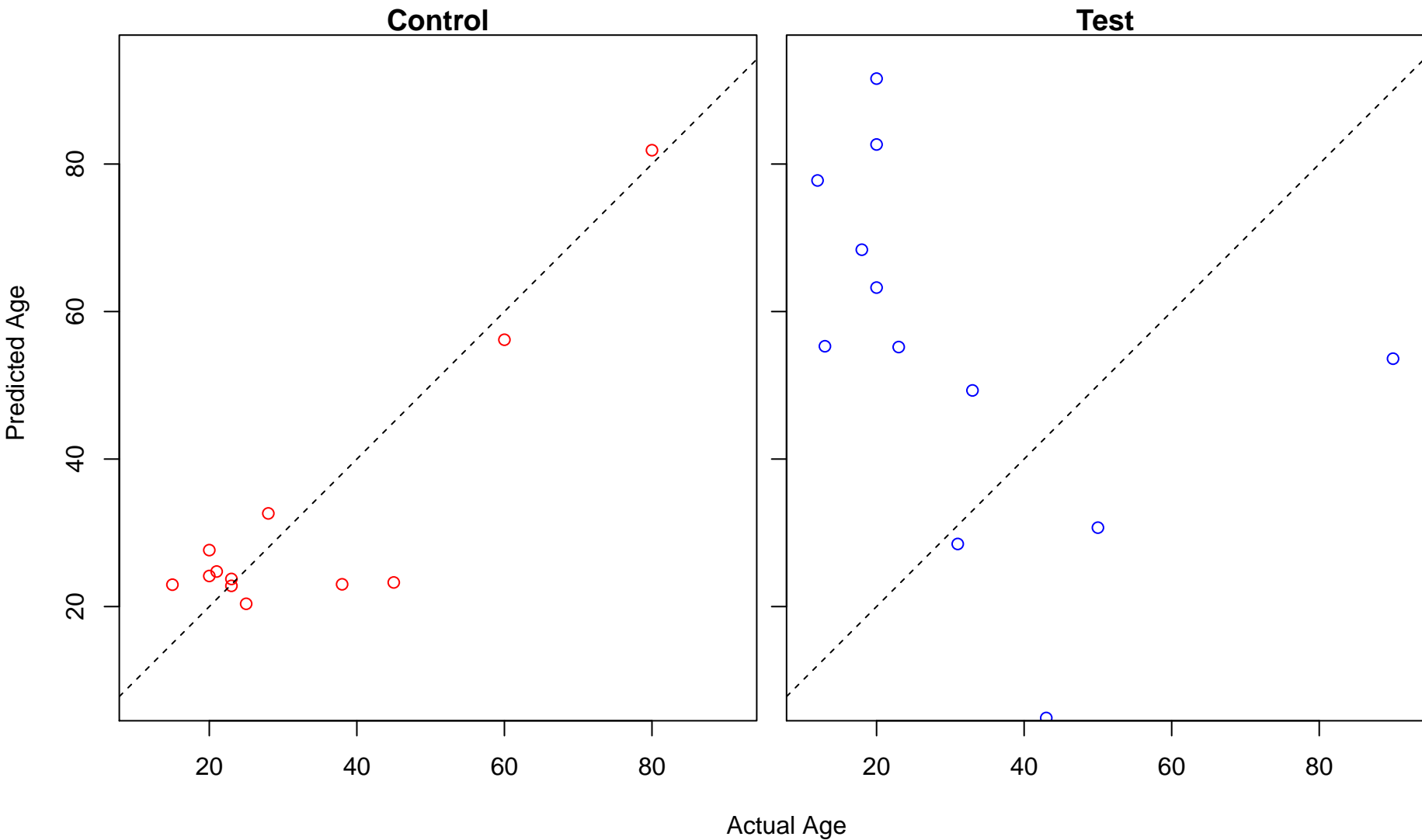
positive regulation of type I interferon-mediated signaling pathway (Score: 12.262588)



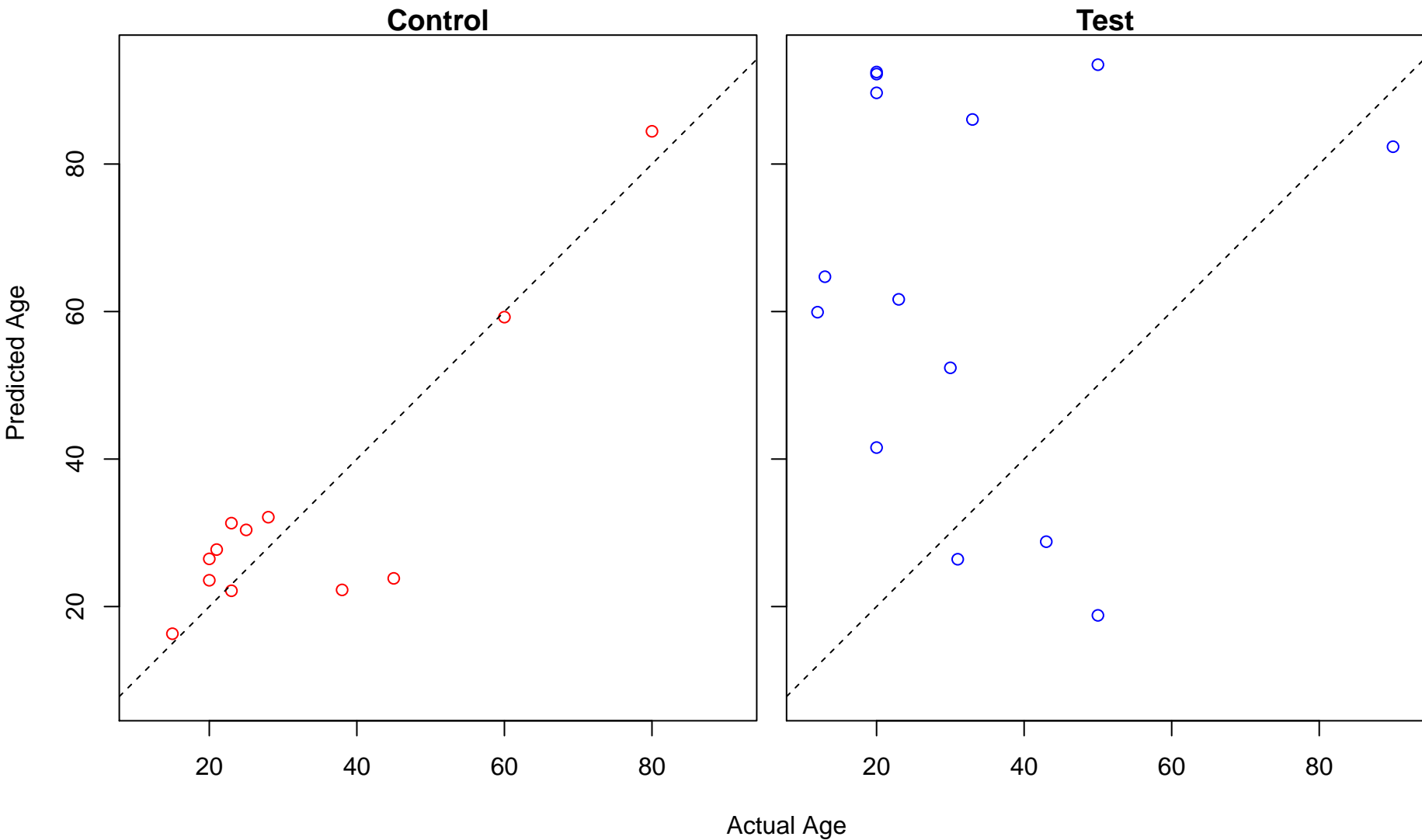
regulation of amyloid precursor protein biosynthetic process (Score: 12.243967)



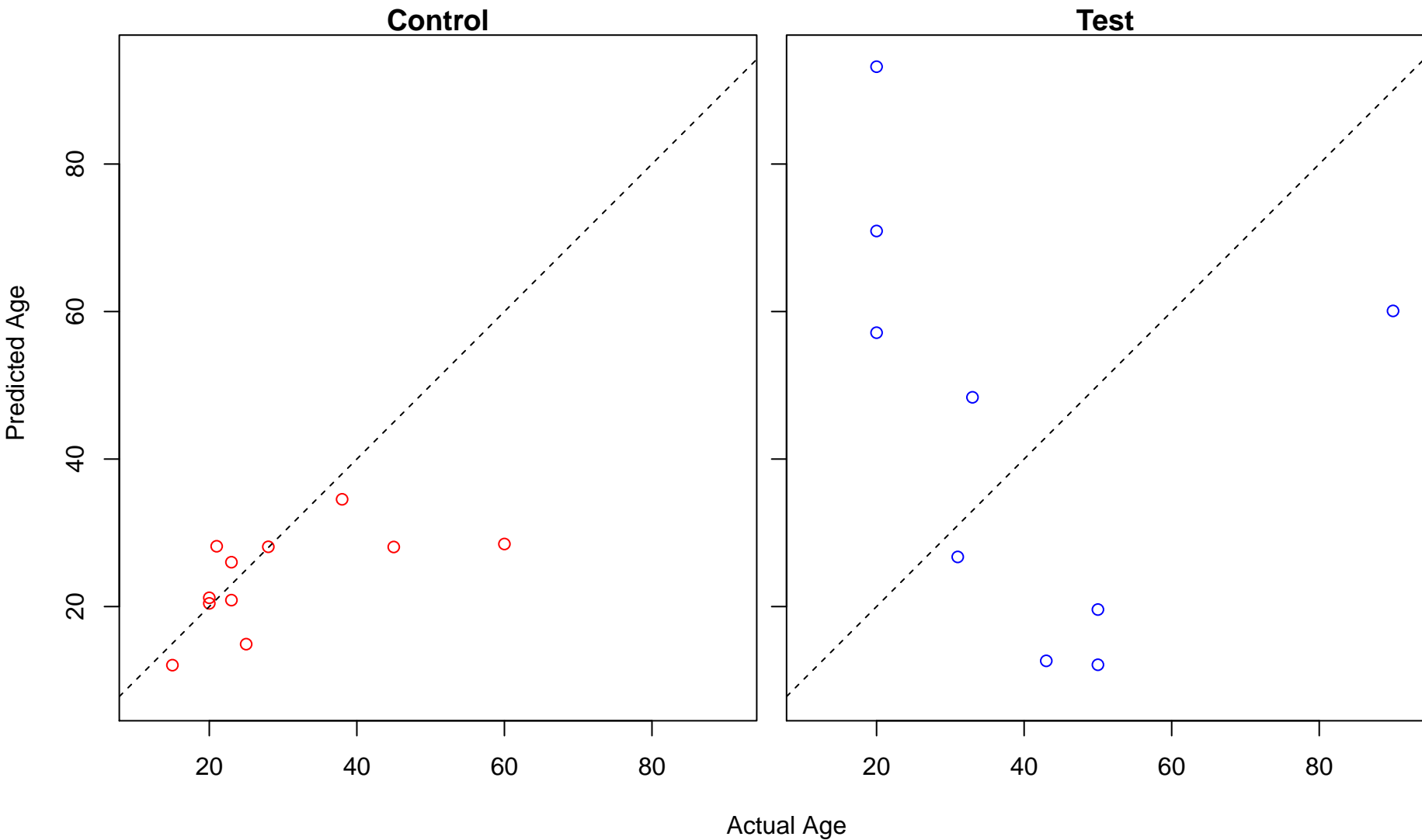
regulation of stress-activated MAPK cascade (Score: 12.207079)



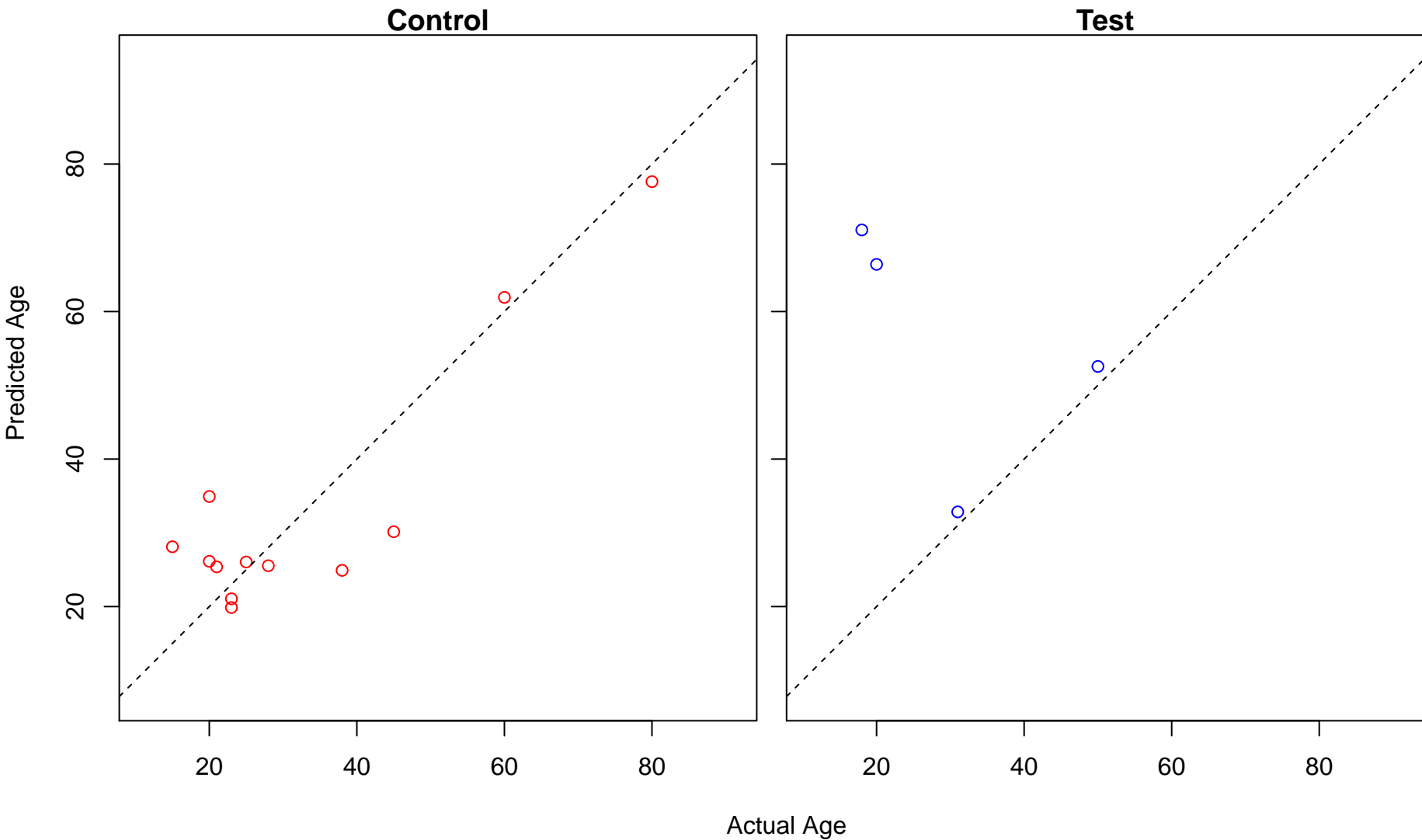
cleavage furrow formation (Score: 12.186111)



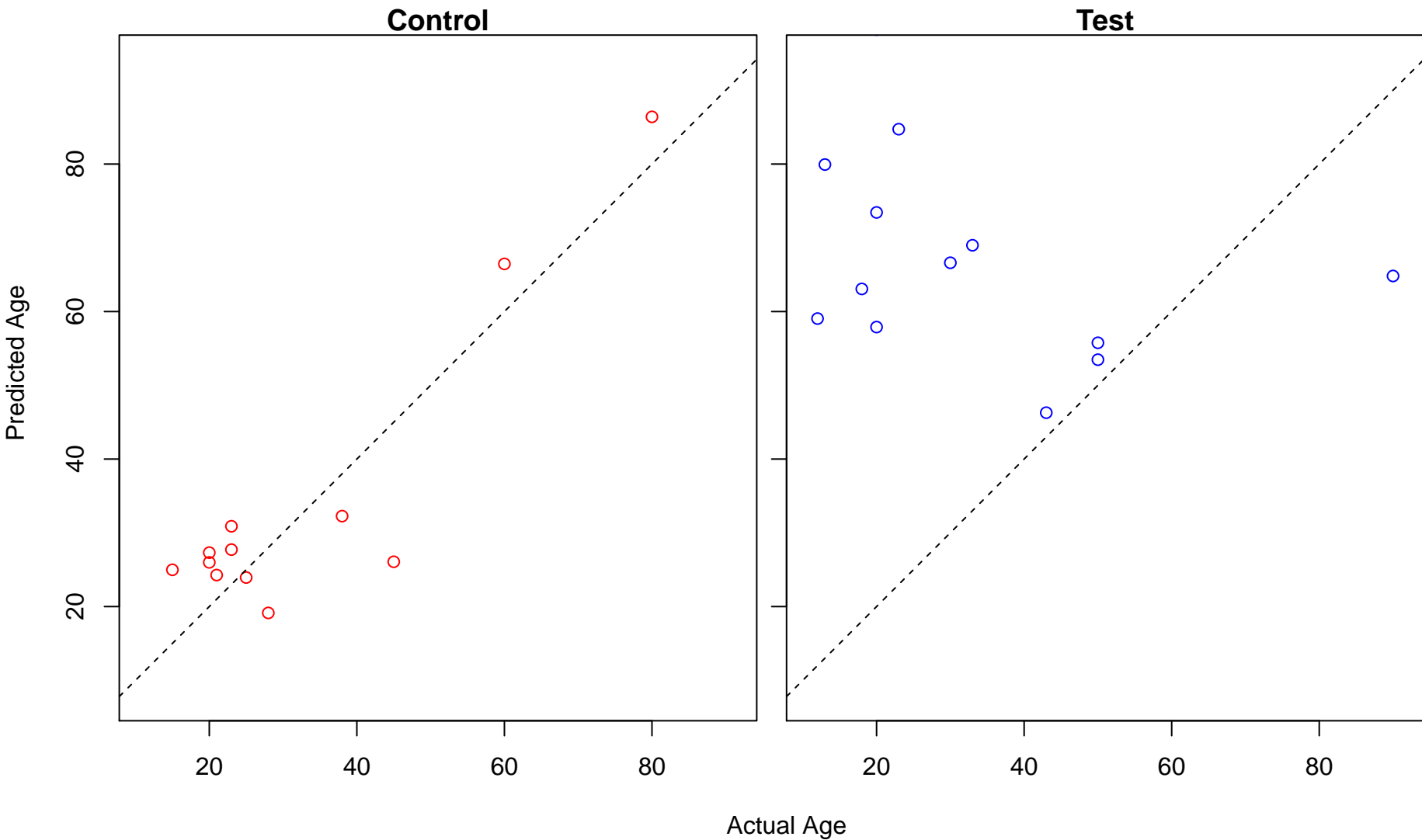
face development (Score: 12.182526)



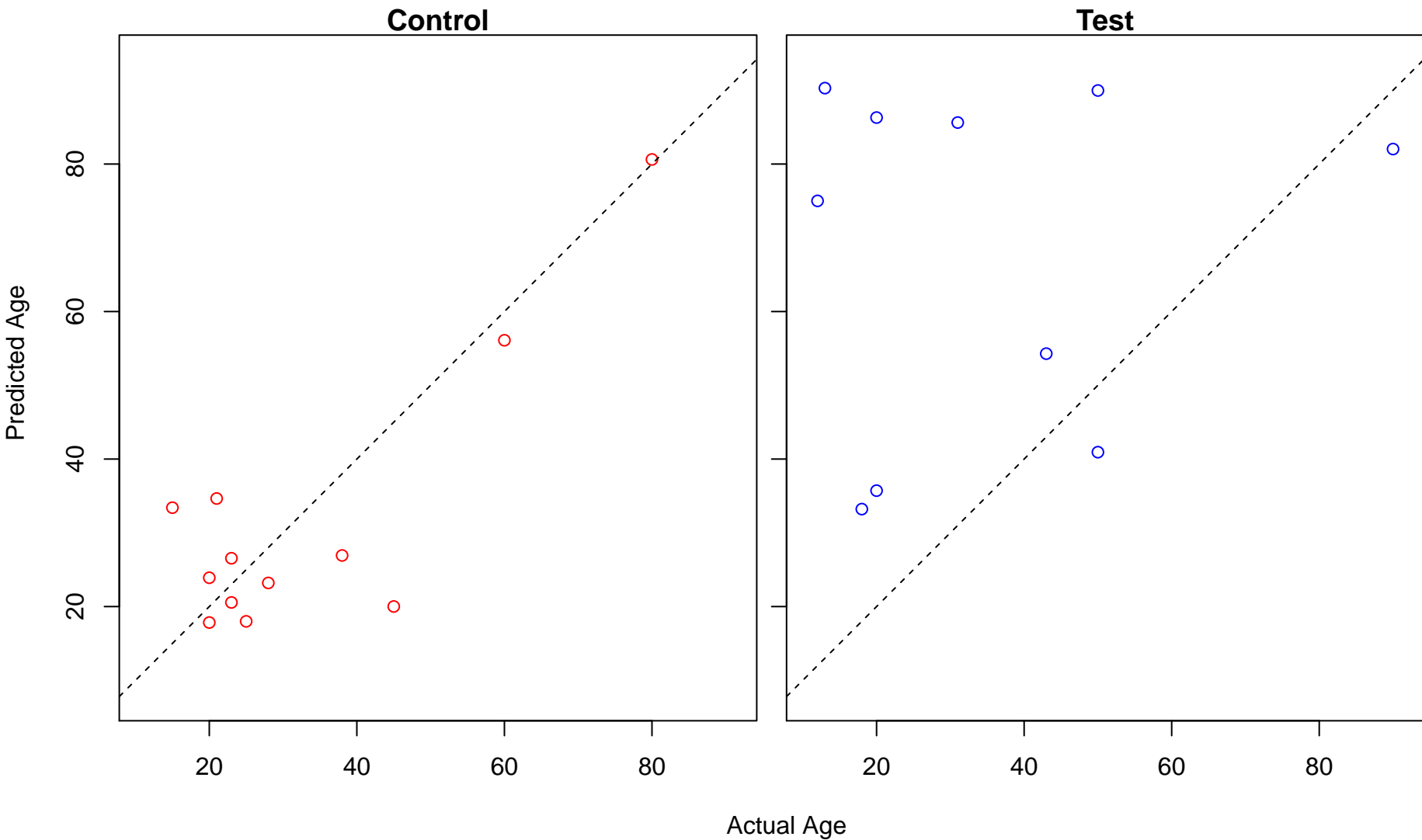
cellular response to alcohol (Score: 12.181581)



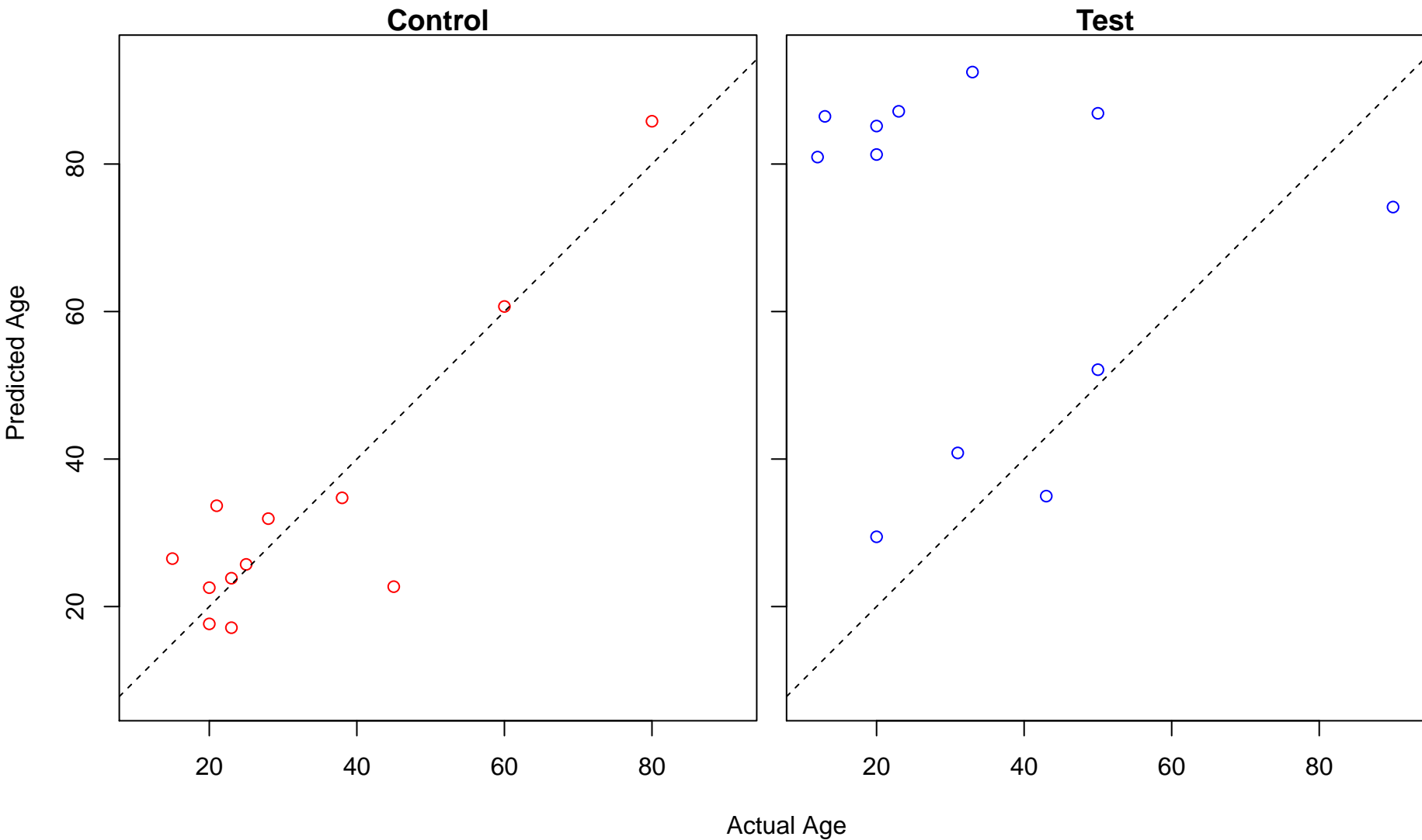
cellular lactam metabolic process (Score: 12.168679)



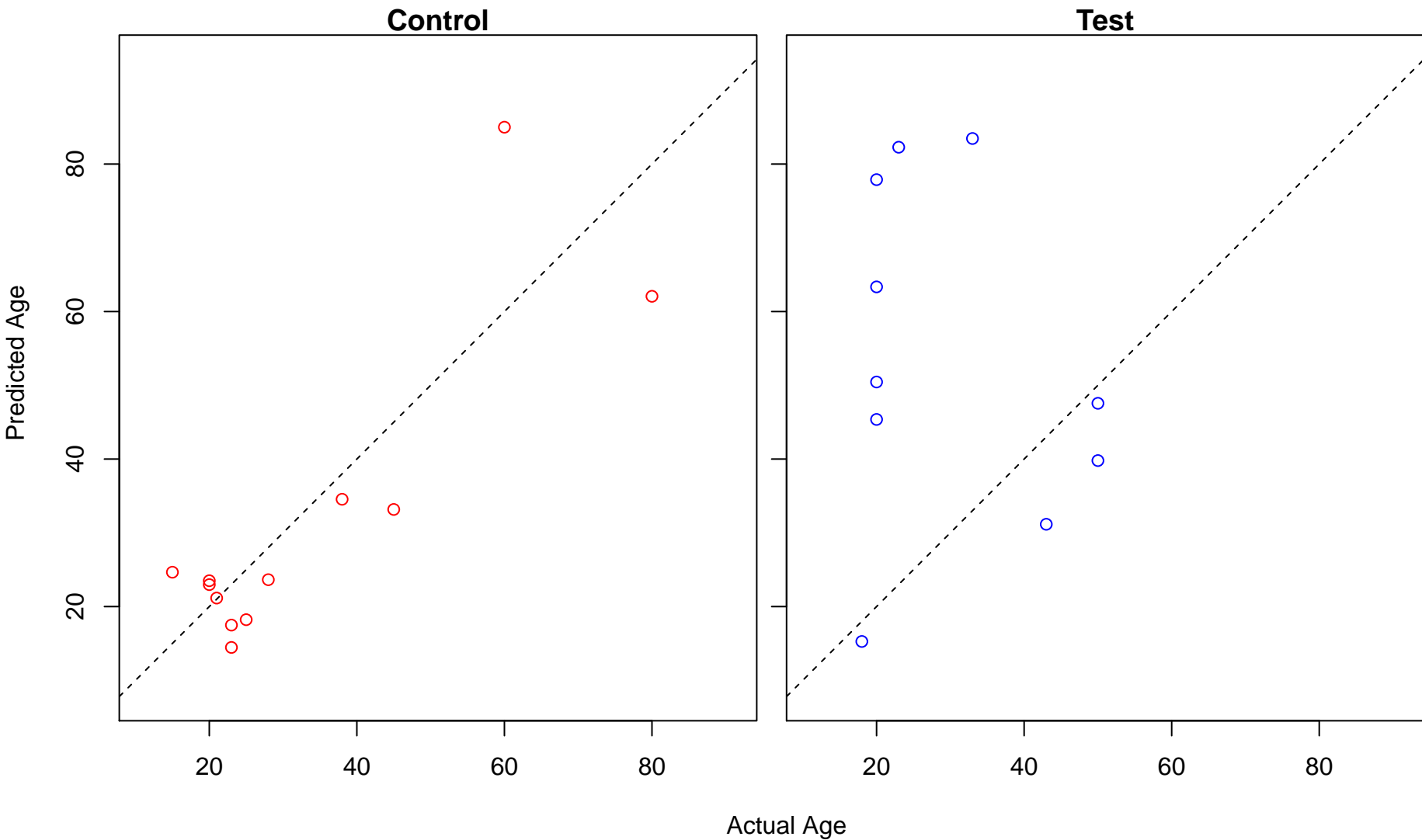
regulation of actin nucleation (Score: 12.168566)



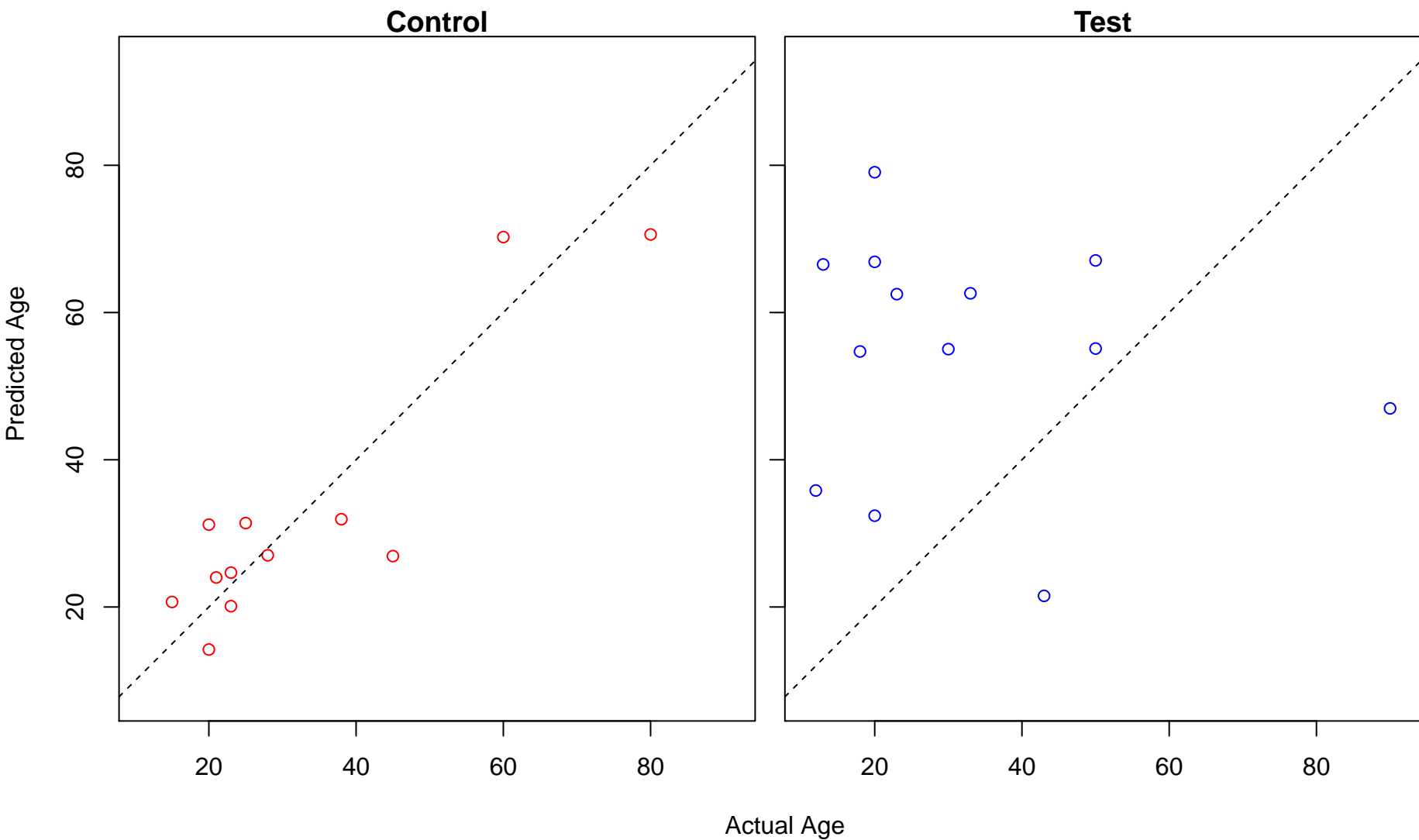
negative regulation of actin filament polymerization (Score: 12.160456)



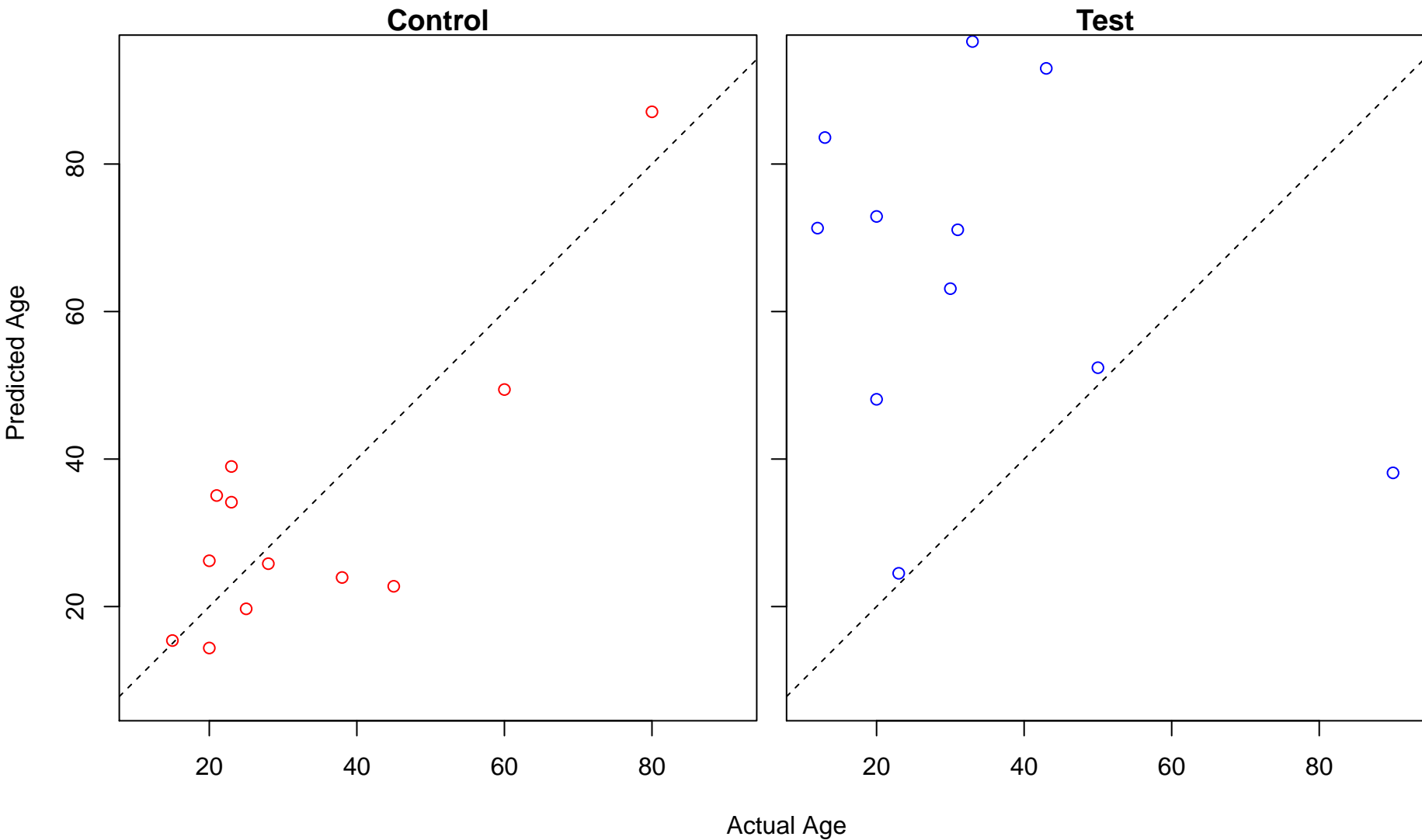
regulation of tyrosine phosphorylation of Stat3 protein (Score: 12.155827)



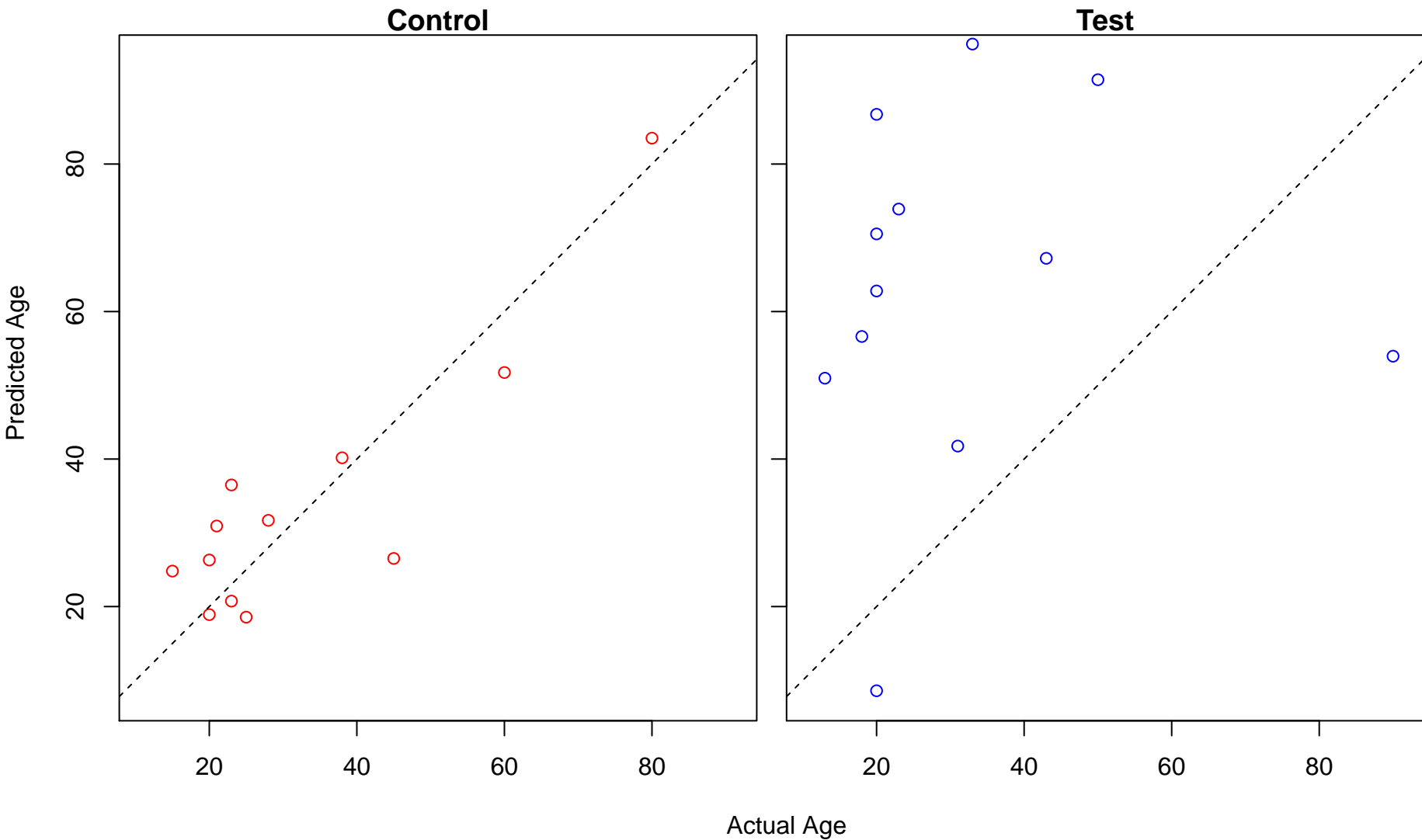
autophagy (Score: 12.152030)



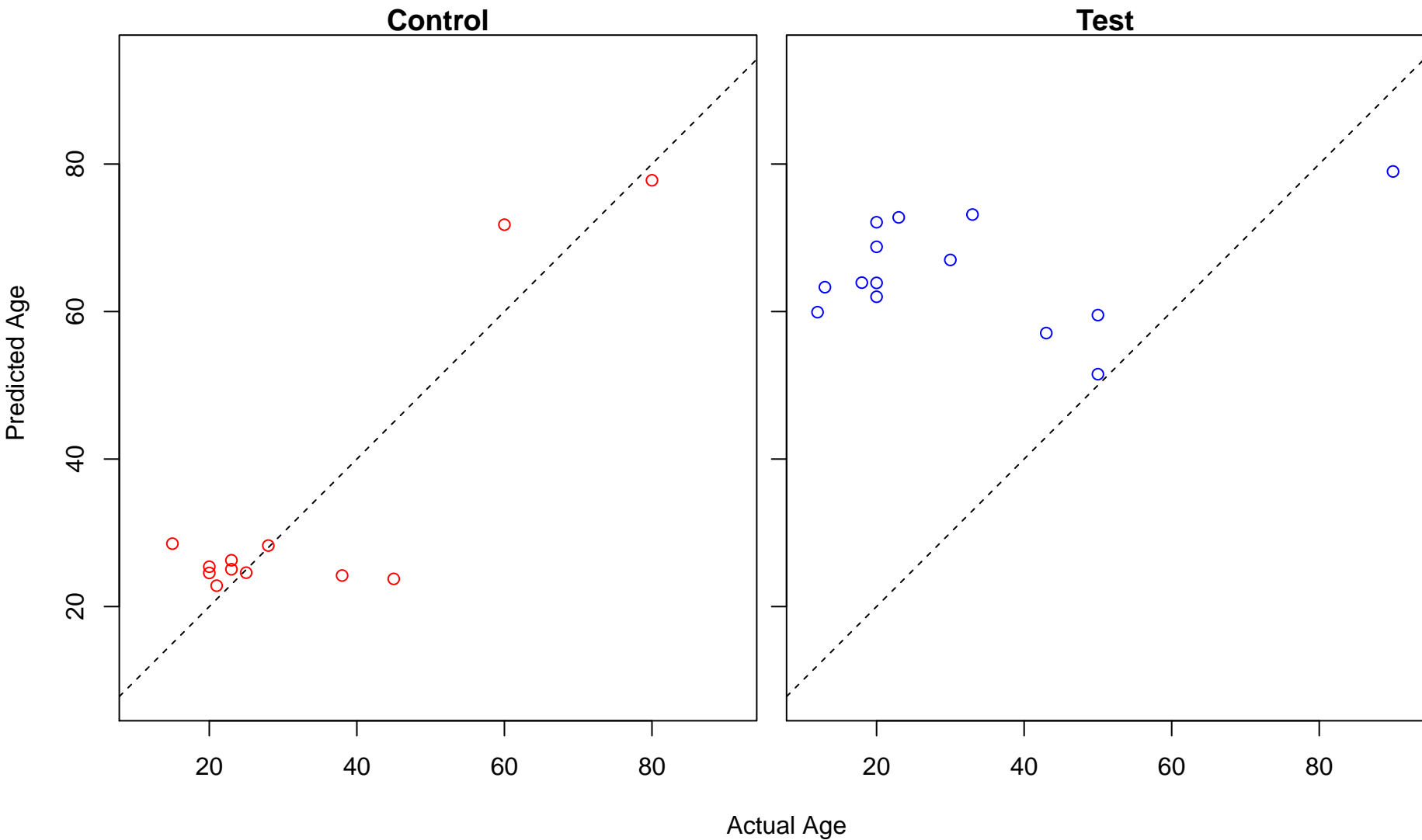
regulation of sprouting angiogenesis (Score: 12.146266)



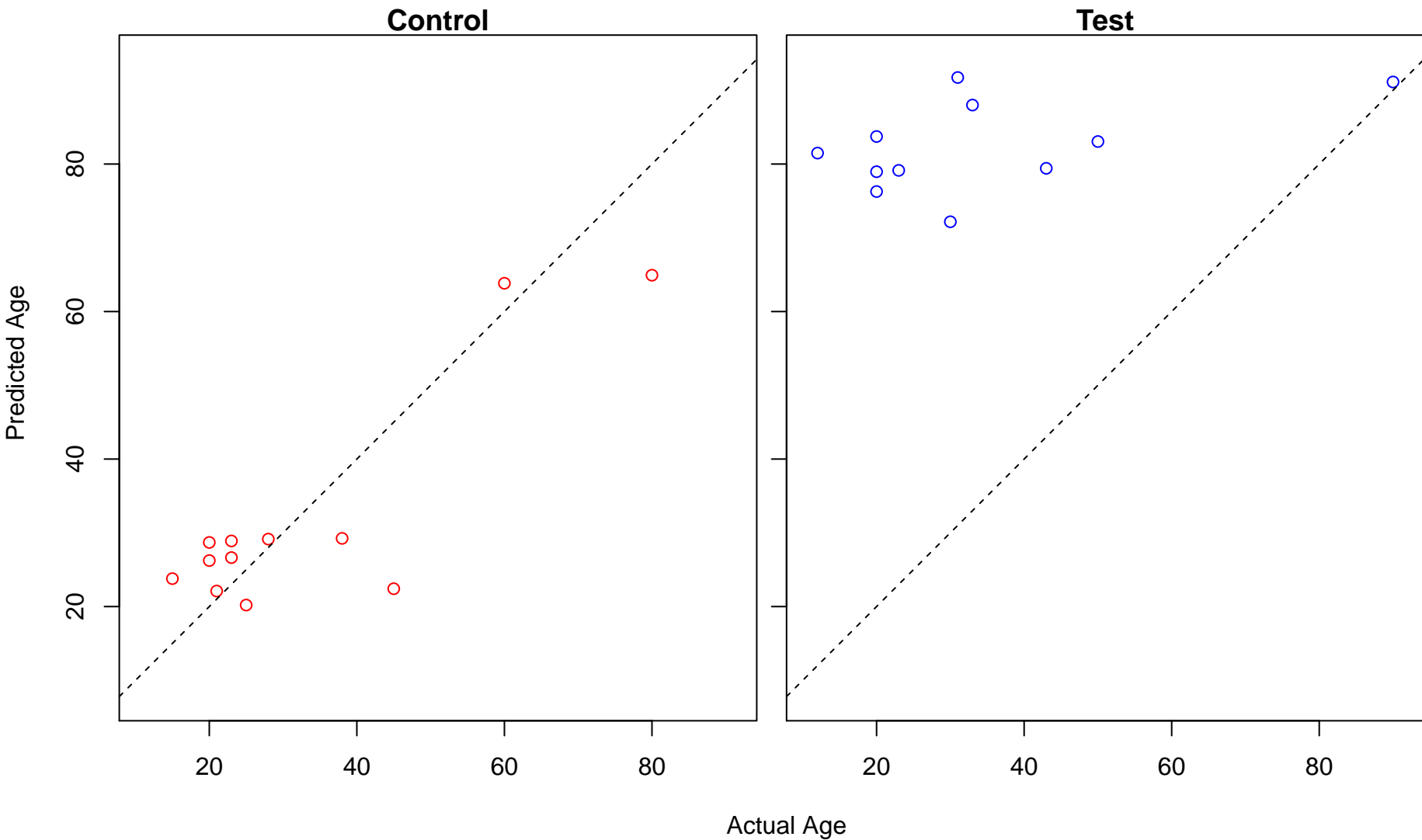
sulfur compound catabolic process (Score: 12.127045)



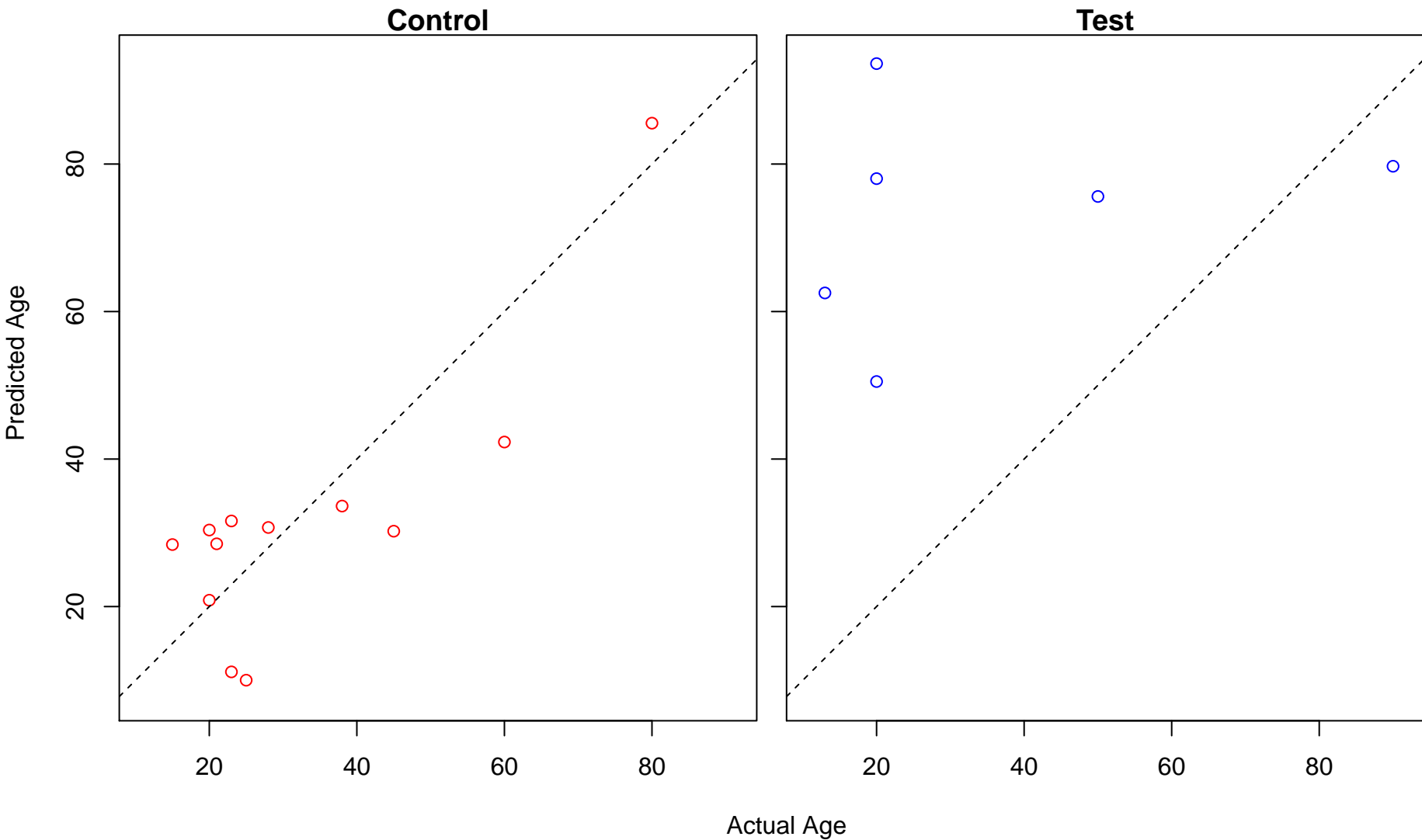
cytoplasmic sequestering of transcription factor (Score: 12.118503)



oocyte differentiation (Score: 12.076069)

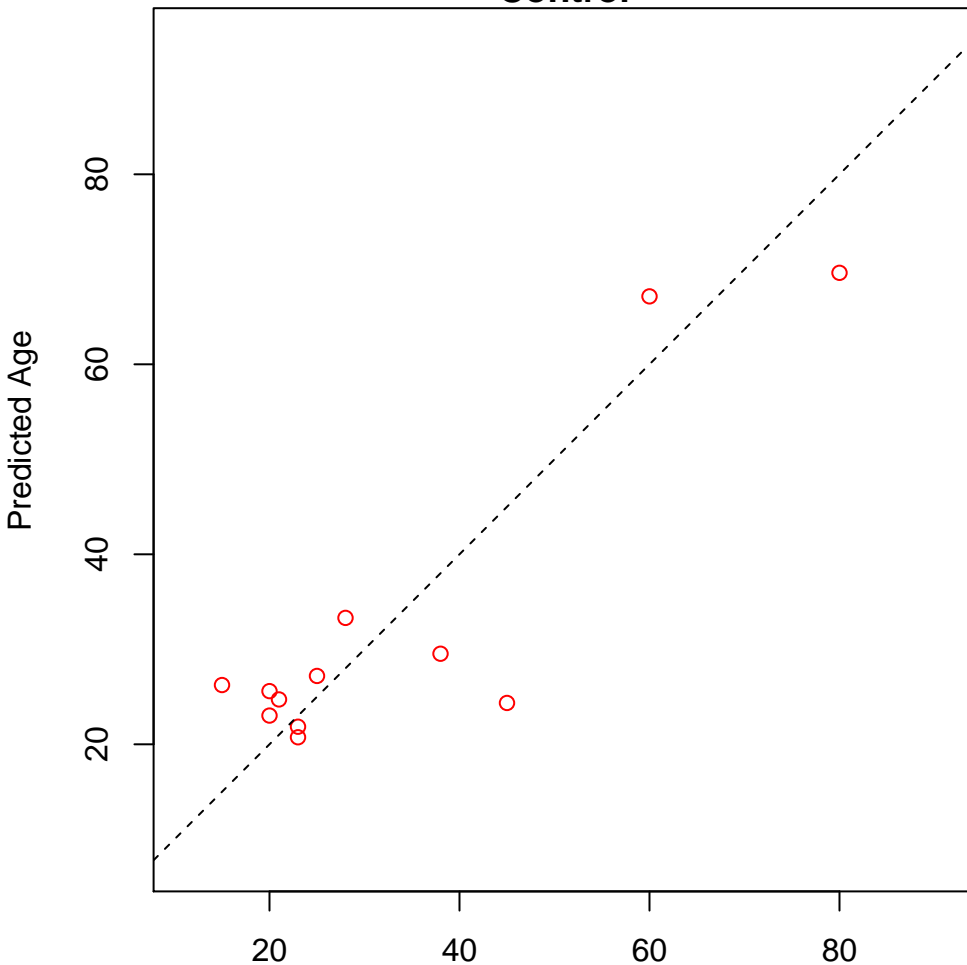


positive regulation of DNA-dependent DNA replication (Score: 12.057202)

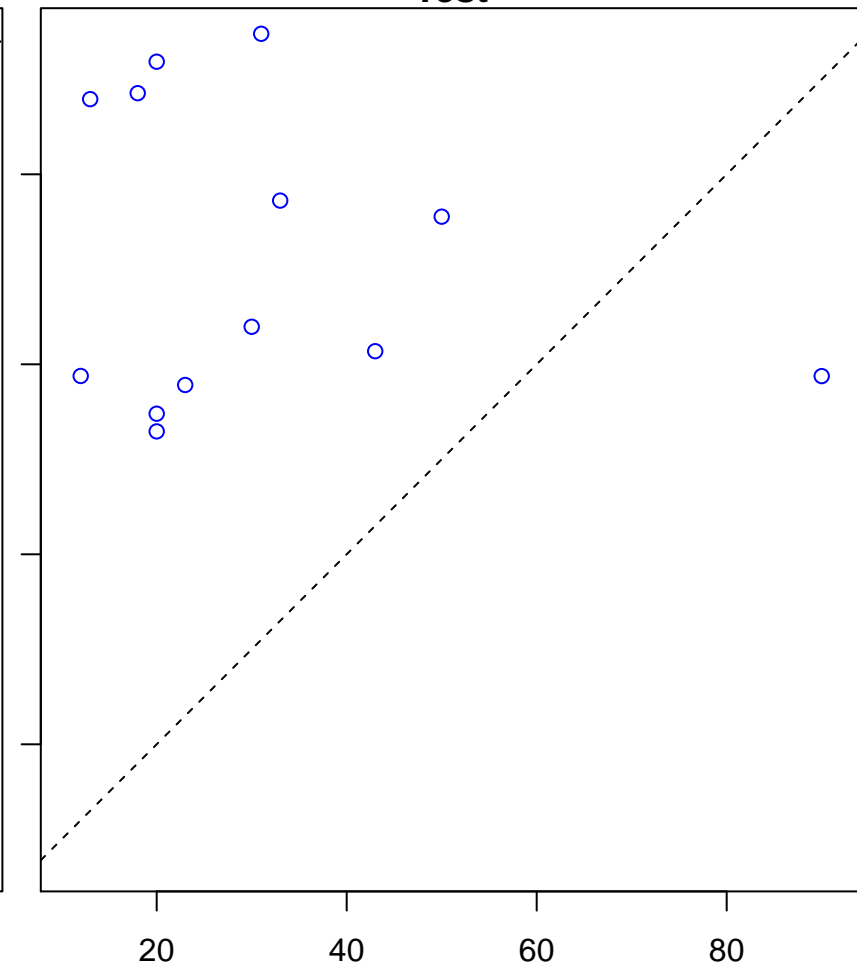


protein maturation by protein folding (Score: 12.038876)

Control

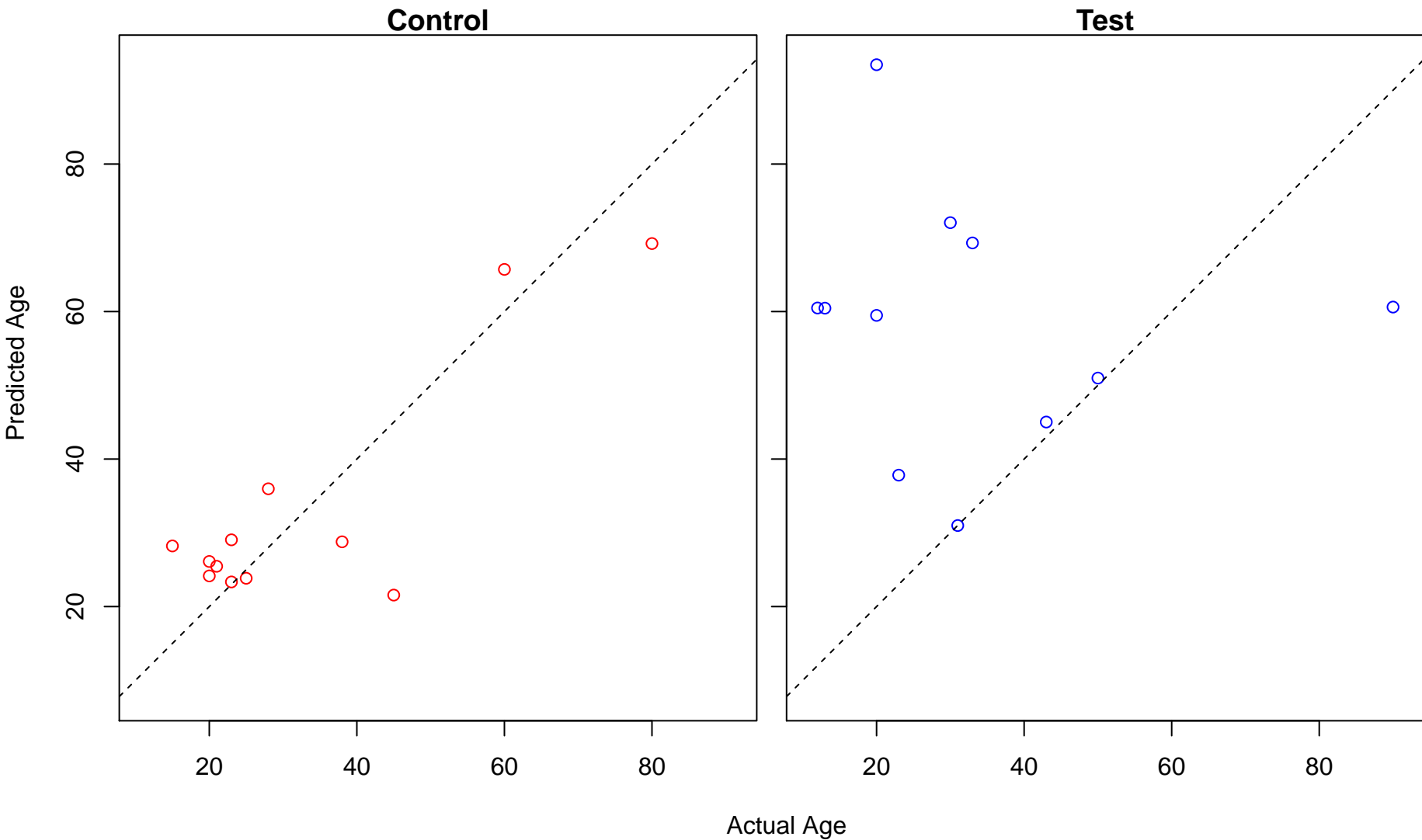


Test



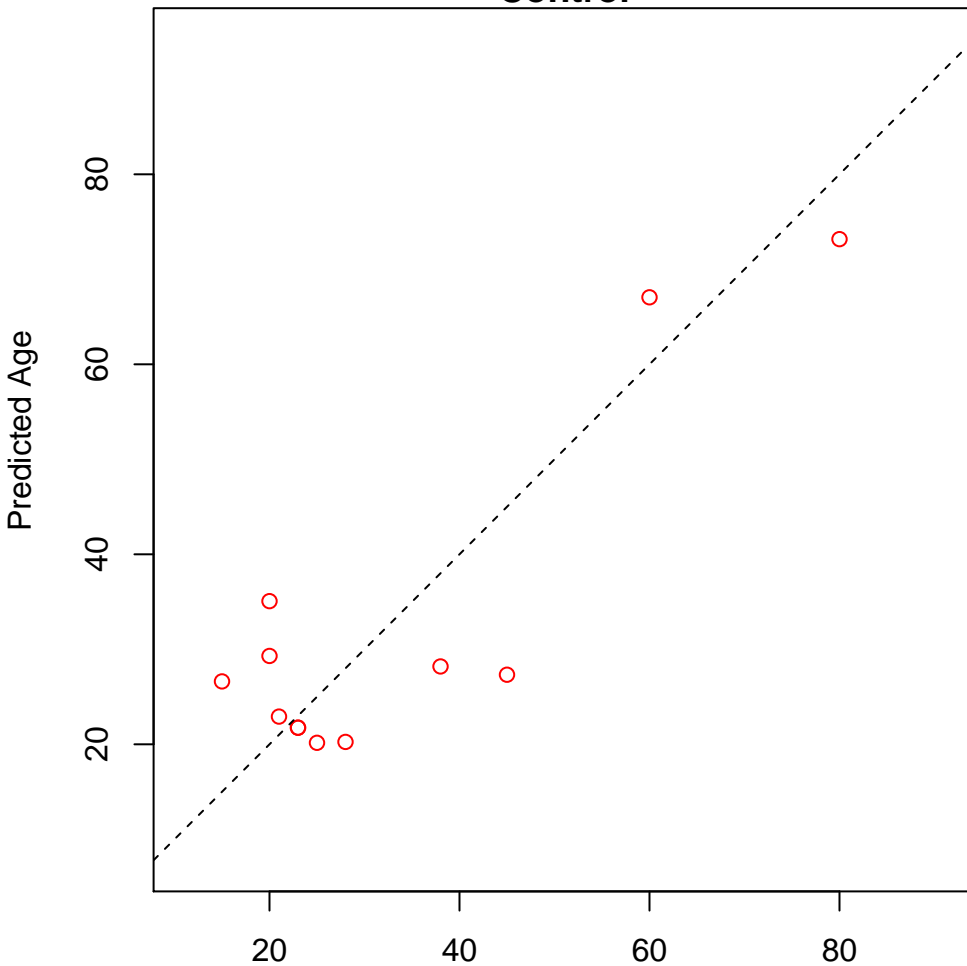
Actual Age

regulation of mammary gland epithelial cell proliferation (Score: 12.029735)

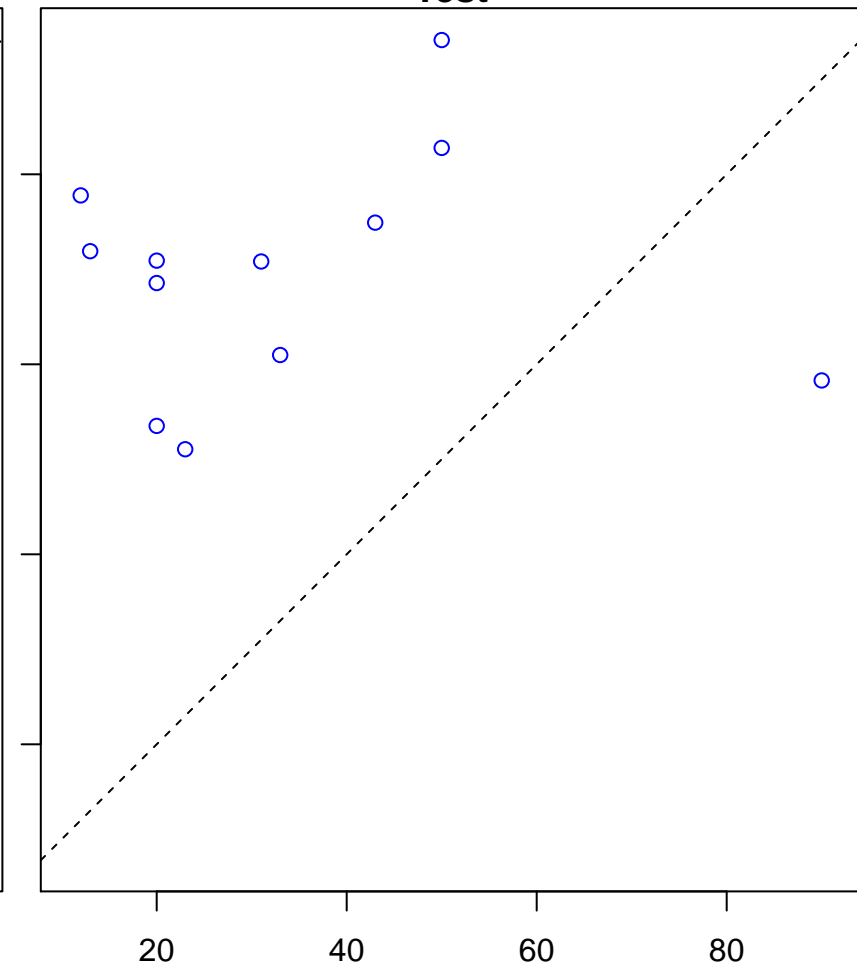


GDP-mannose biosynthetic process (Score: 12.026844)

Control

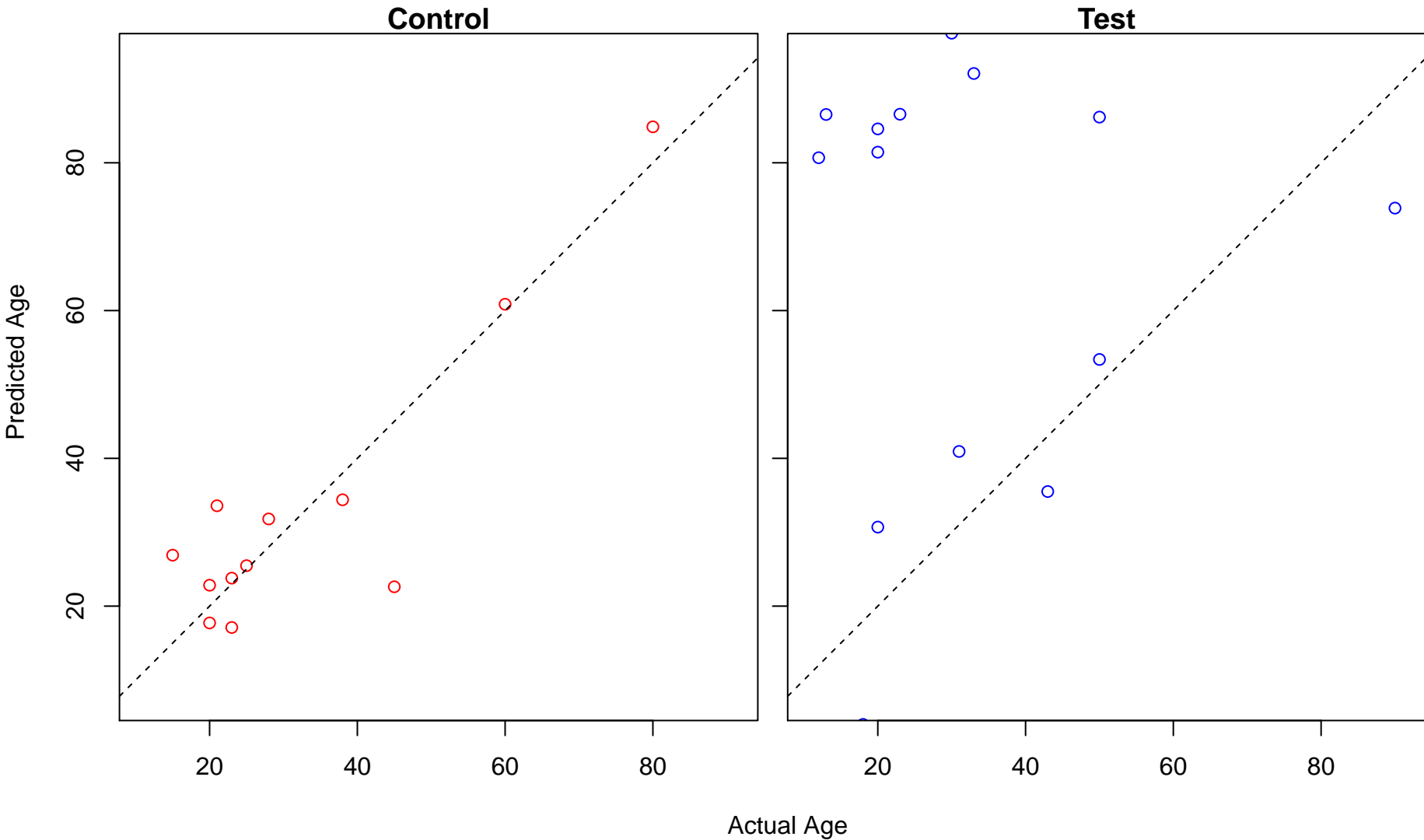


Test



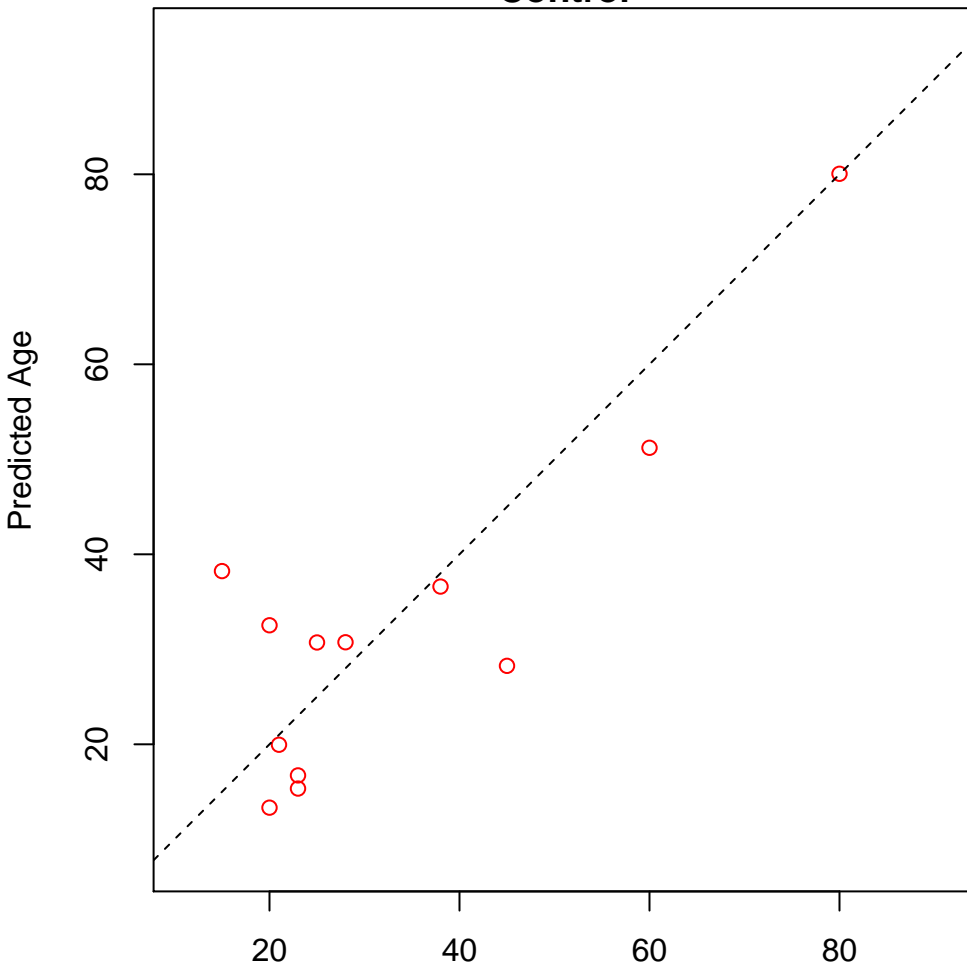
Actual Age

negative regulation of protein polymerization (Score: 12.011285)

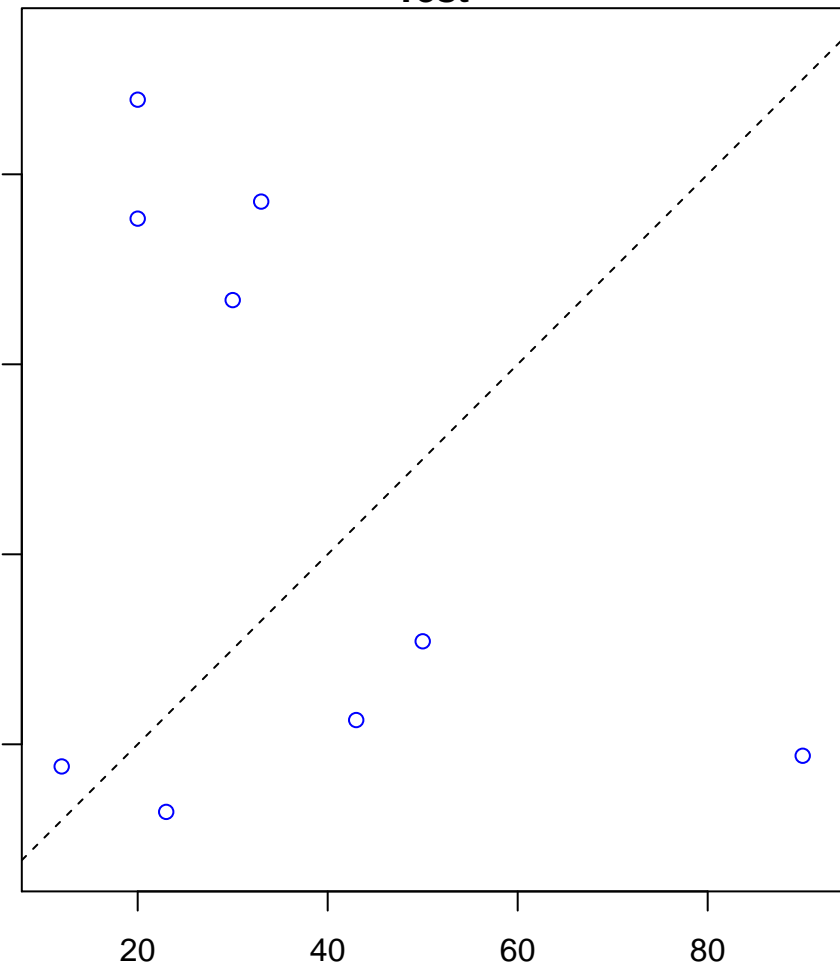


regulation of glomerular filtration (Score: 12.011264)

Control



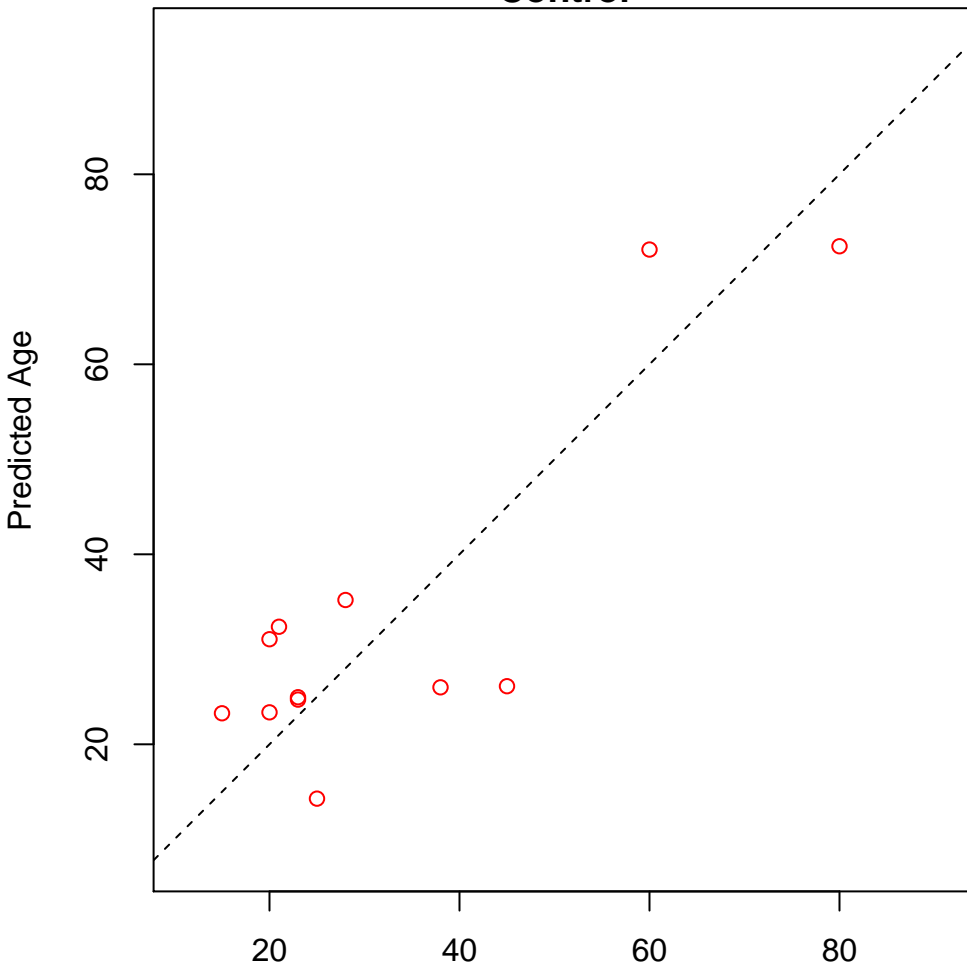
Test



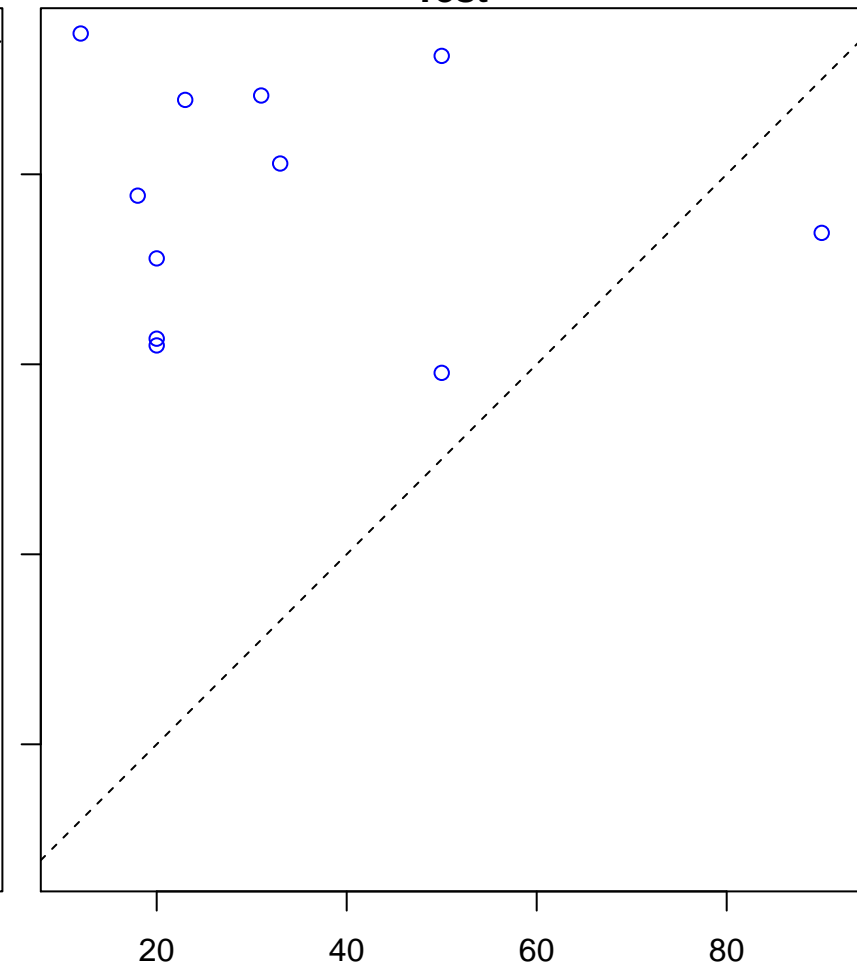
Actual Age

maternal placenta development (Score: 12.011012)

Control

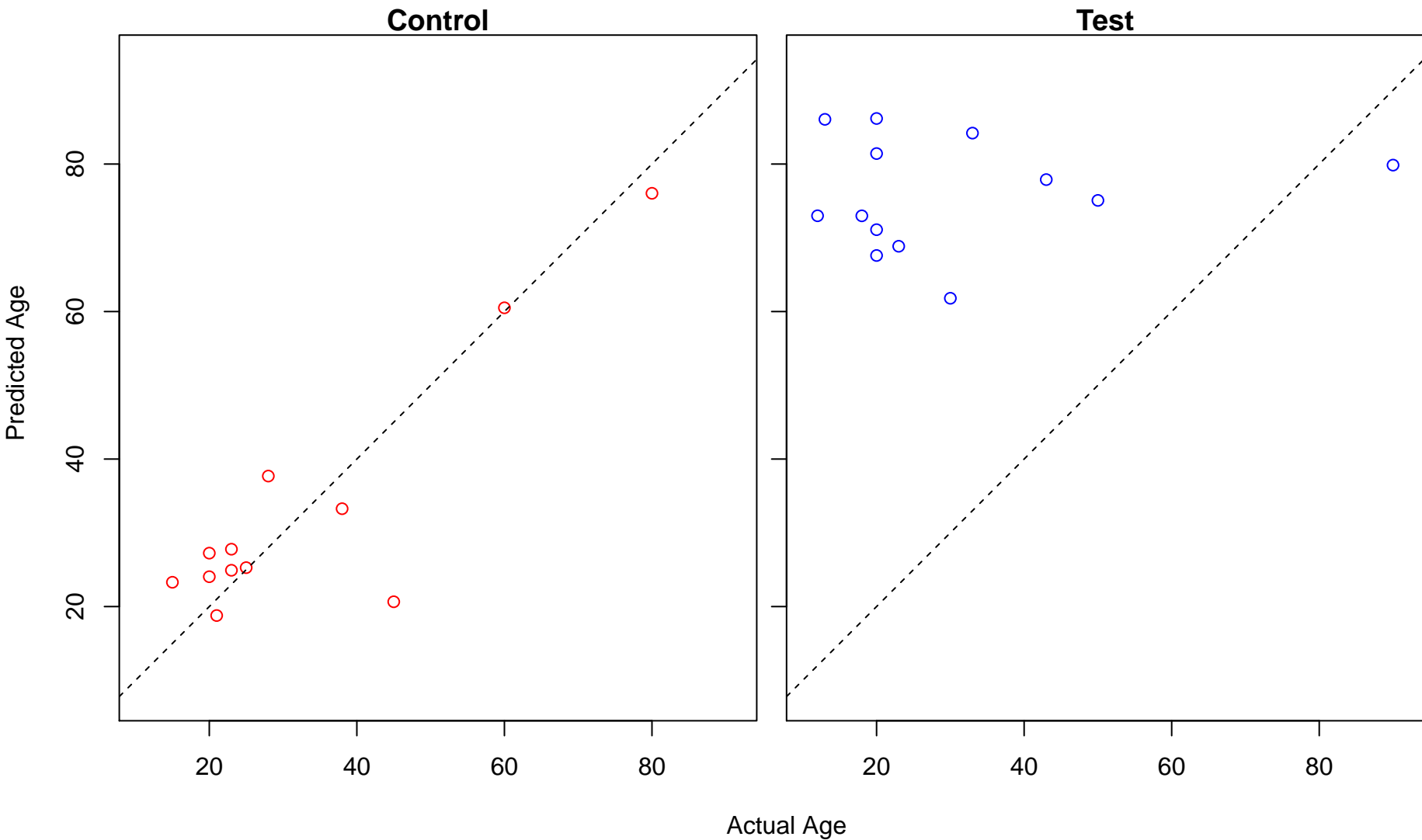


Test

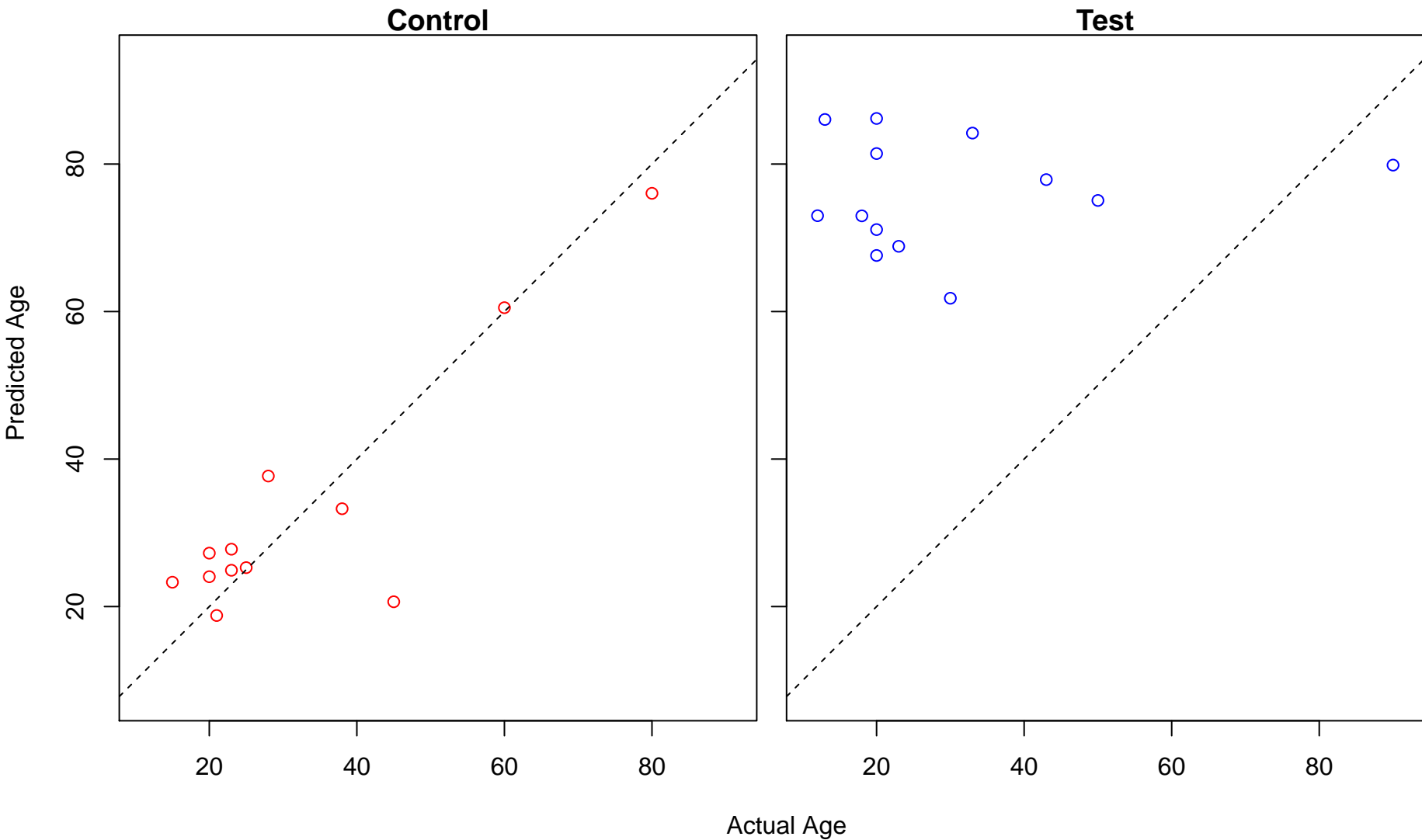


Actual Age

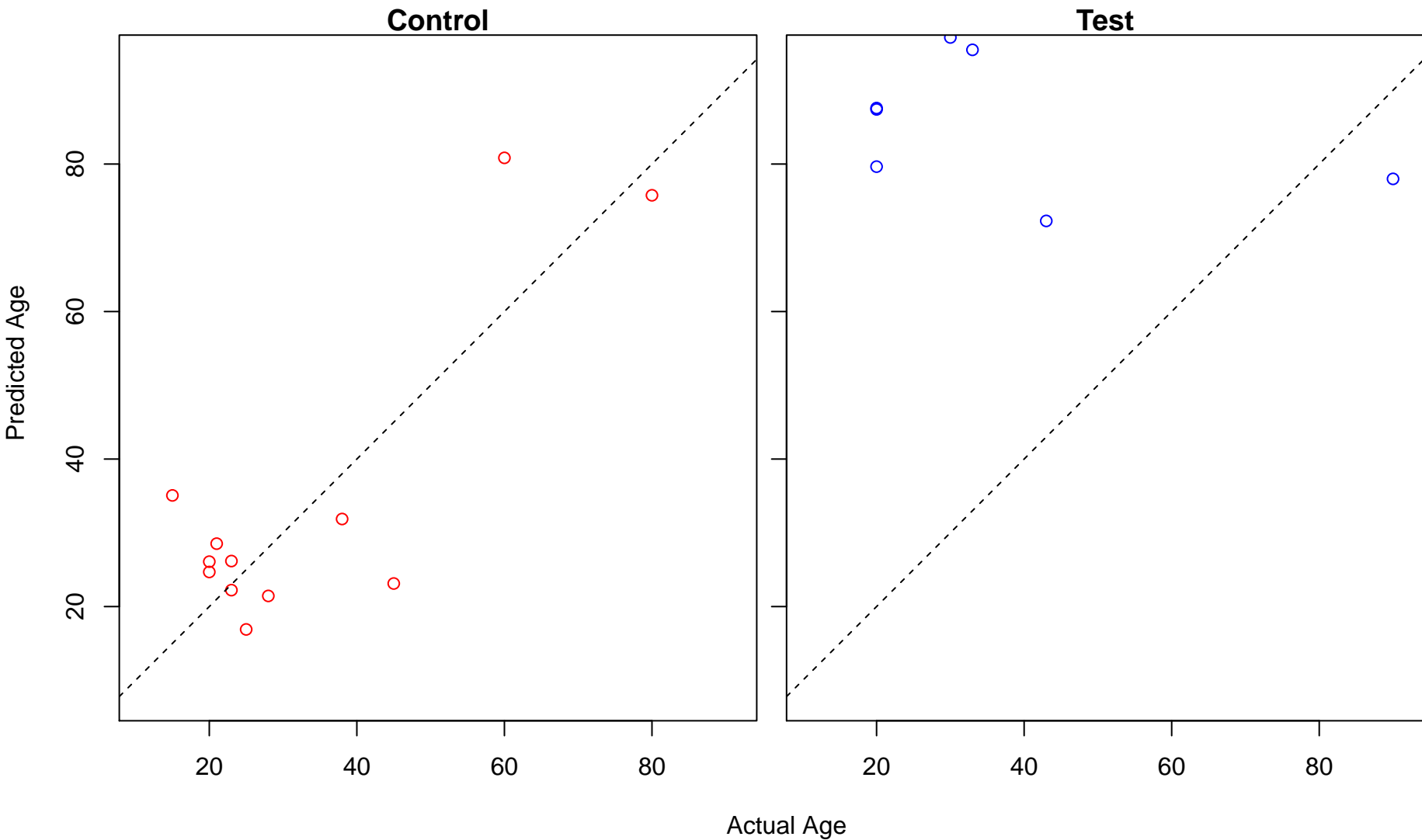
negative regulation of chemotaxis (Score: 12.009810)



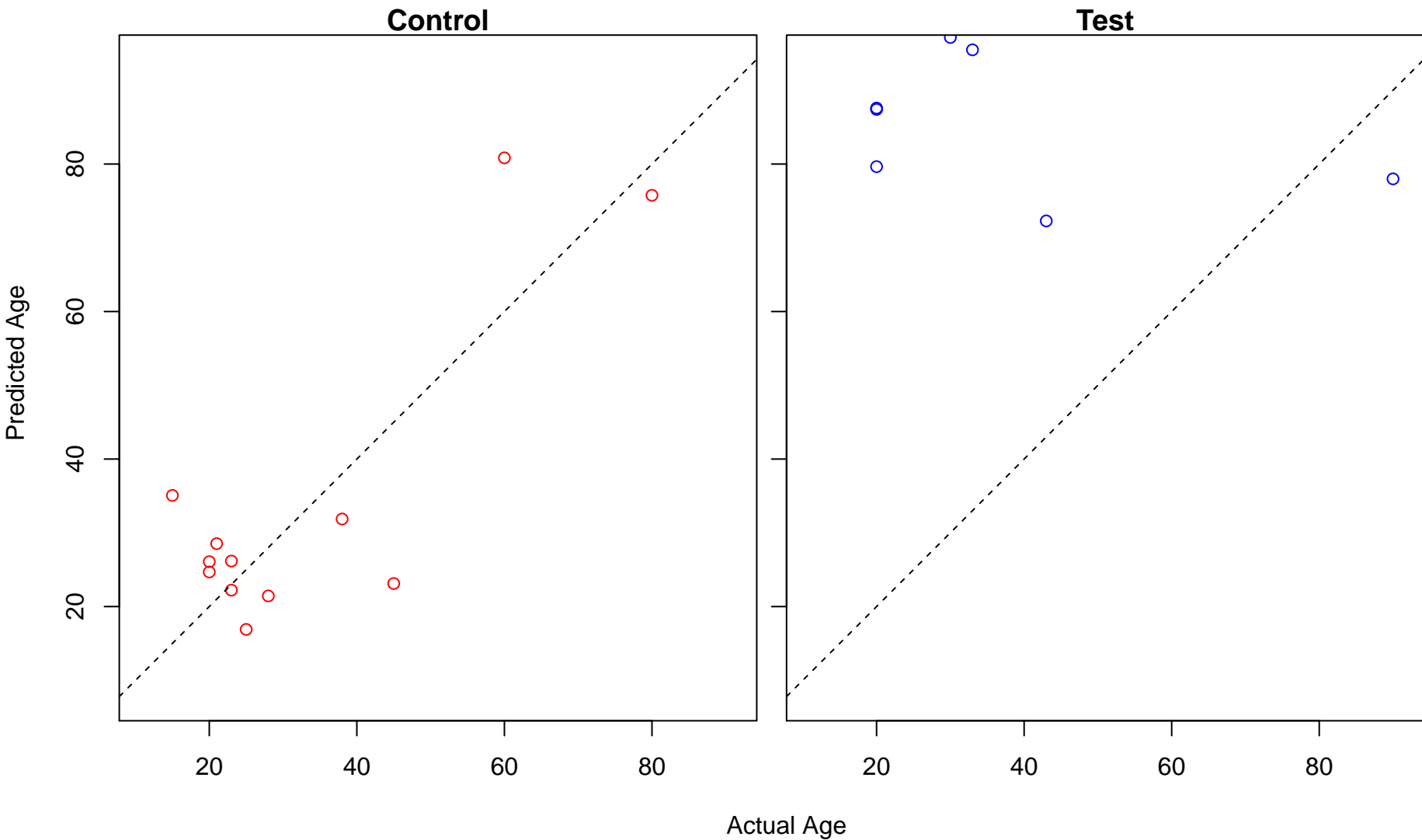
negative regulation of behavior (Score: 12.006619)



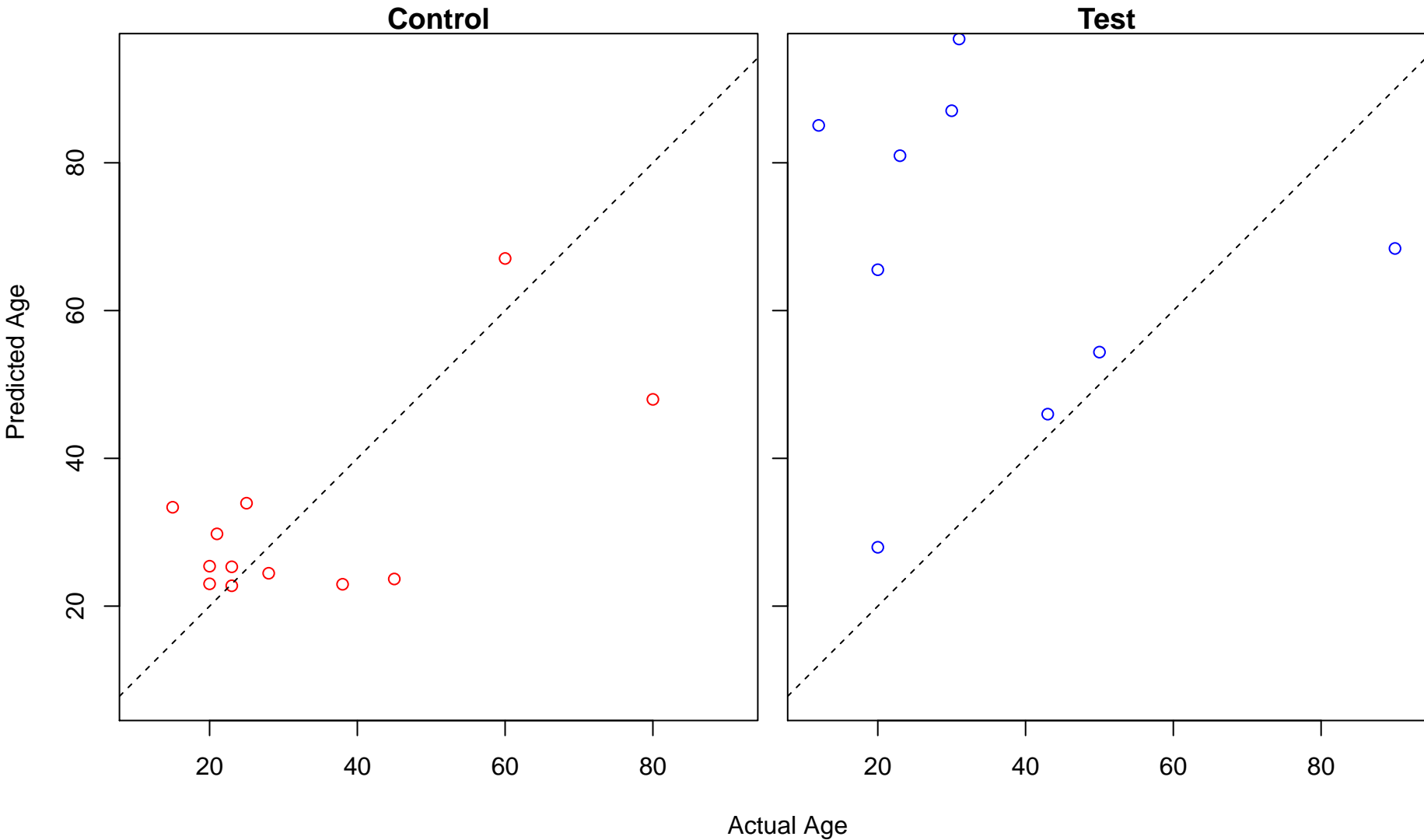
rhythmic behavior (Score: 11.998567)



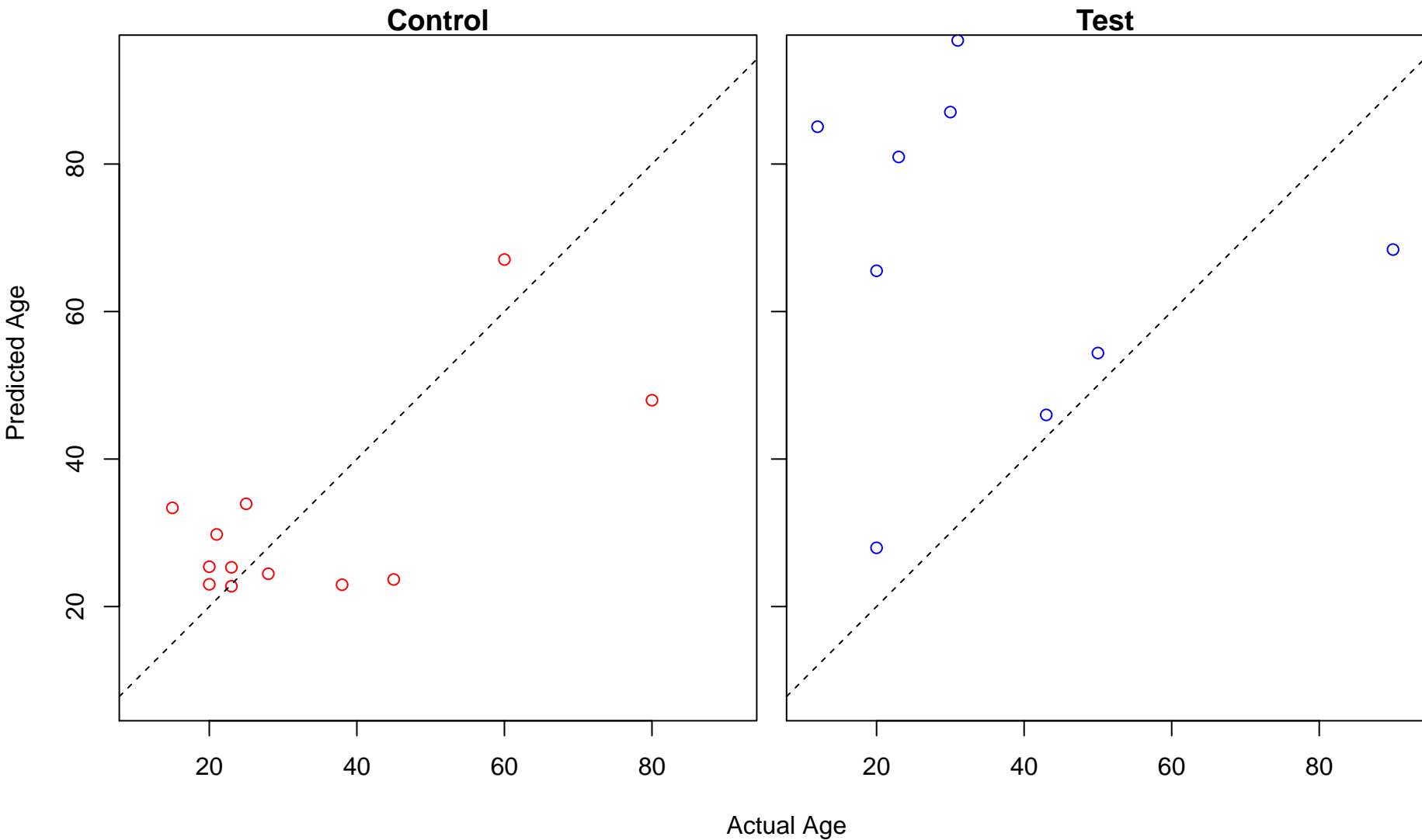
circadian behavior (Score: 11.998567)



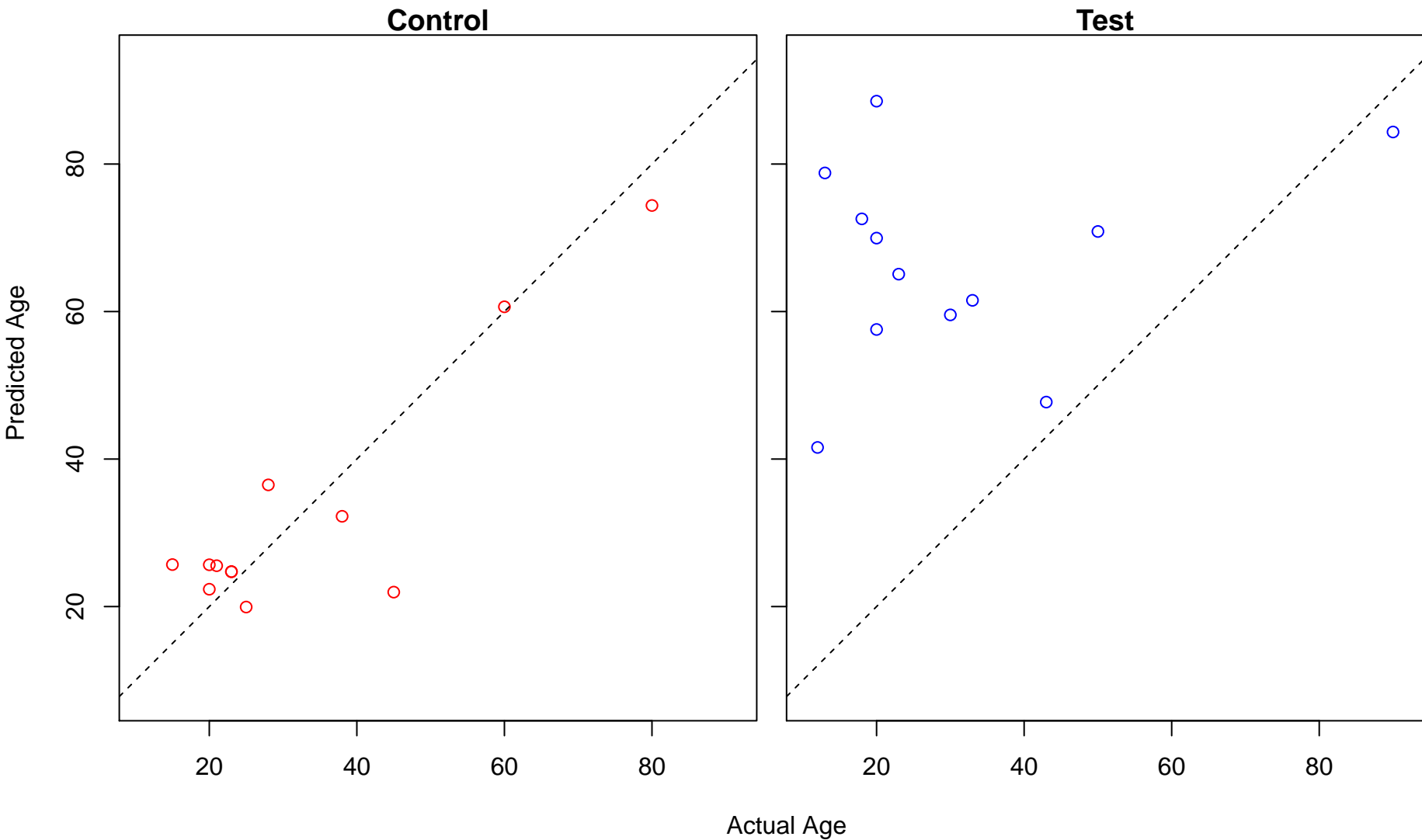
bundle of His cell to Purkinje myocyte signaling (Score: 11.996217)



bundle of His cell action potential (Score: 11.996217)



negative regulation of glycoprotein biosynthetic process (Score: 11.973031)

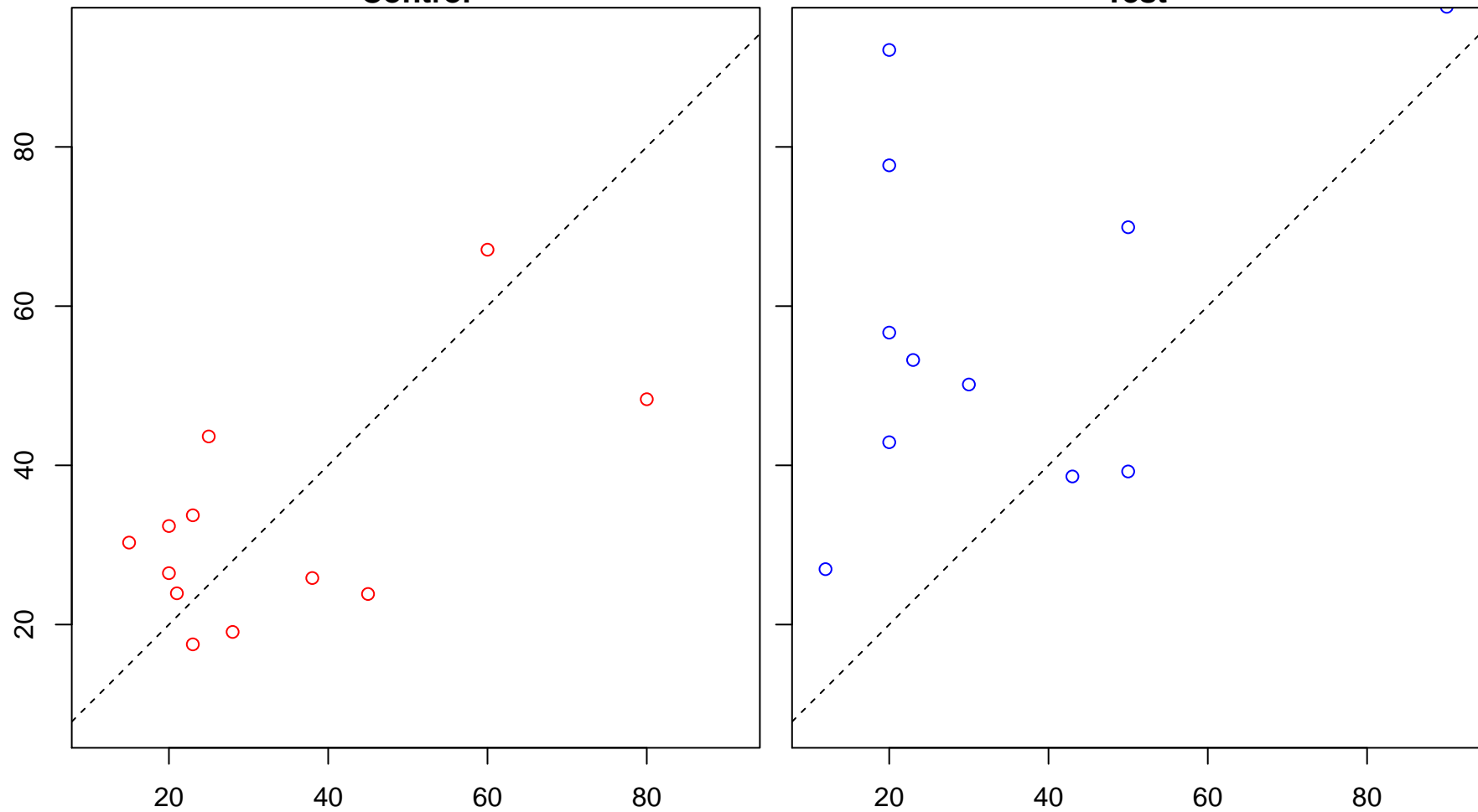


positive regulation of cholesterol efflux (Score: 11.964755)

Control

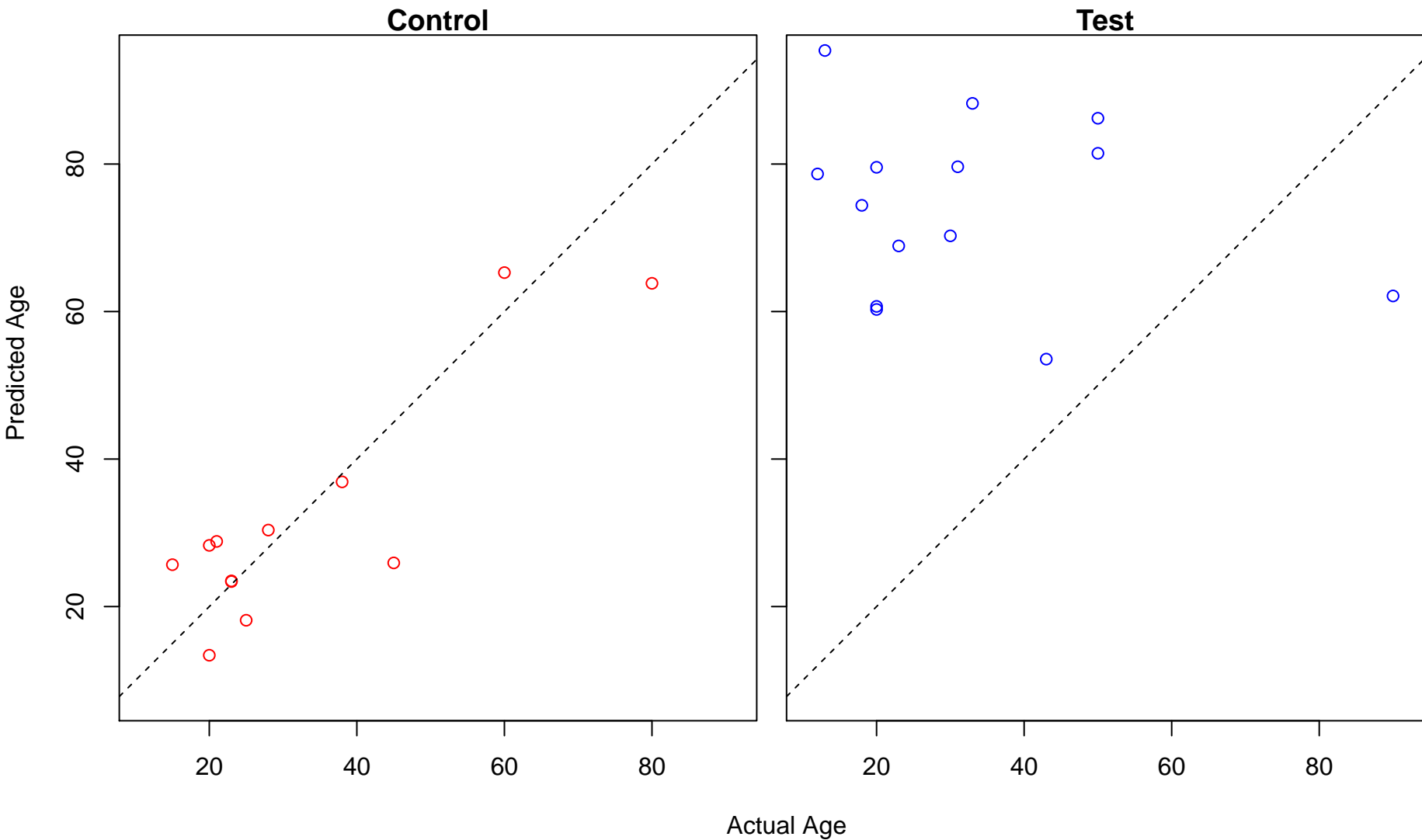
Test

Predicted Age



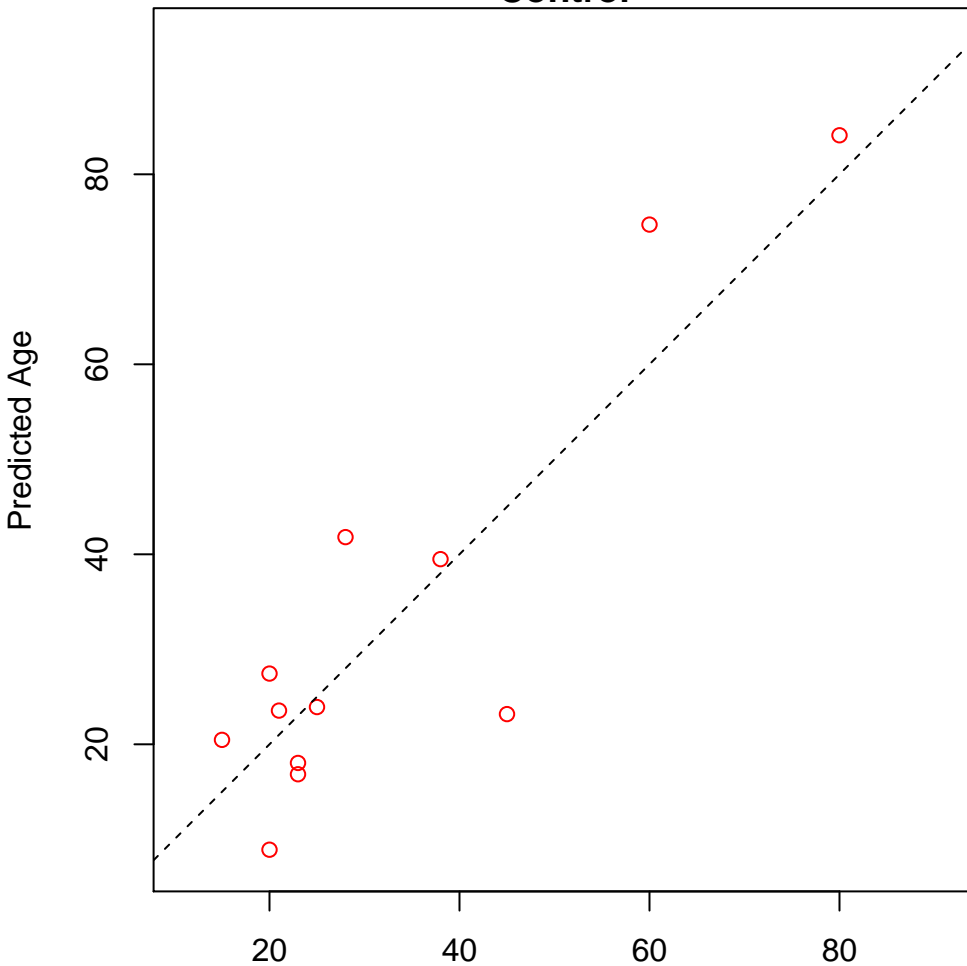
Actual Age

vascular endothelial growth factor receptor signaling pathway (Score: 11.944341)

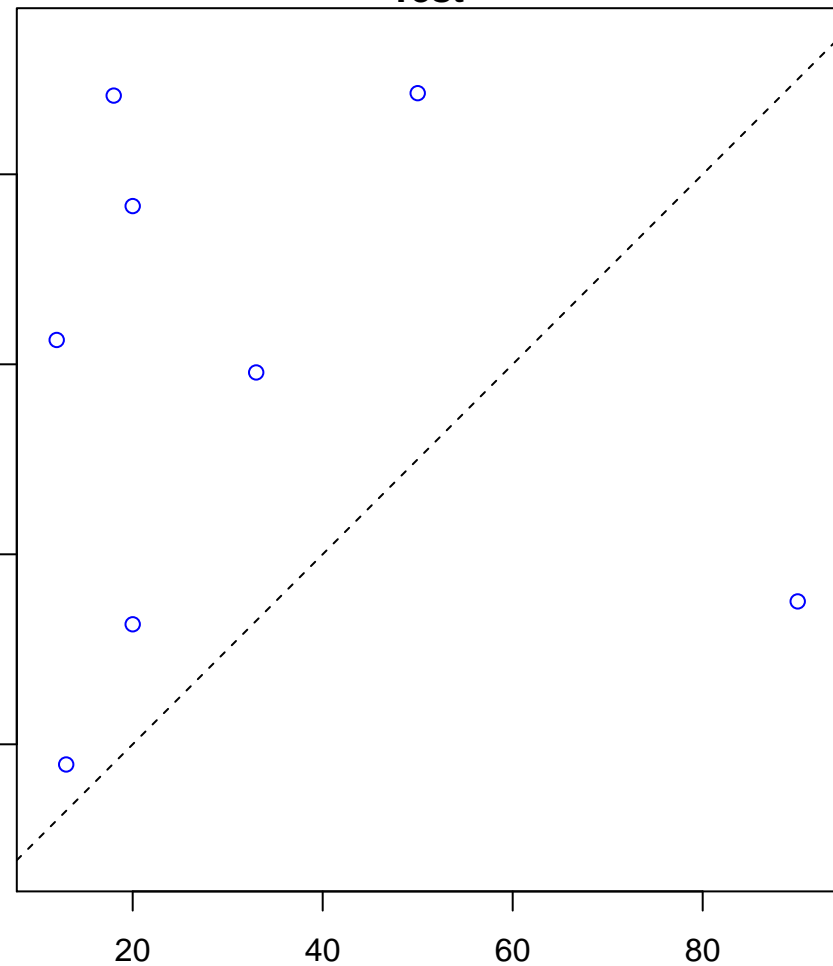


retinal ganglion cell axon guidance (Score: 11.929303)

Control

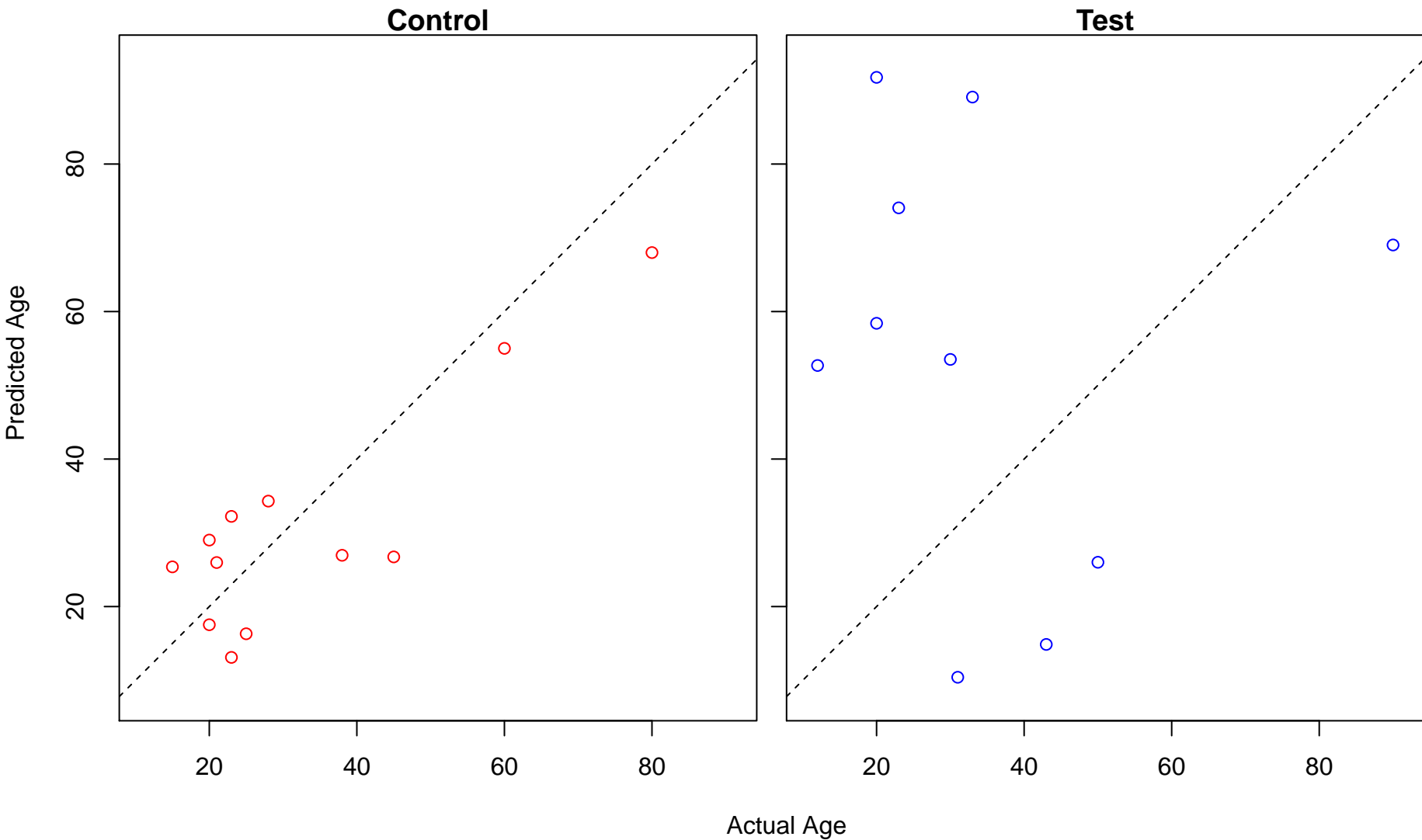


Test

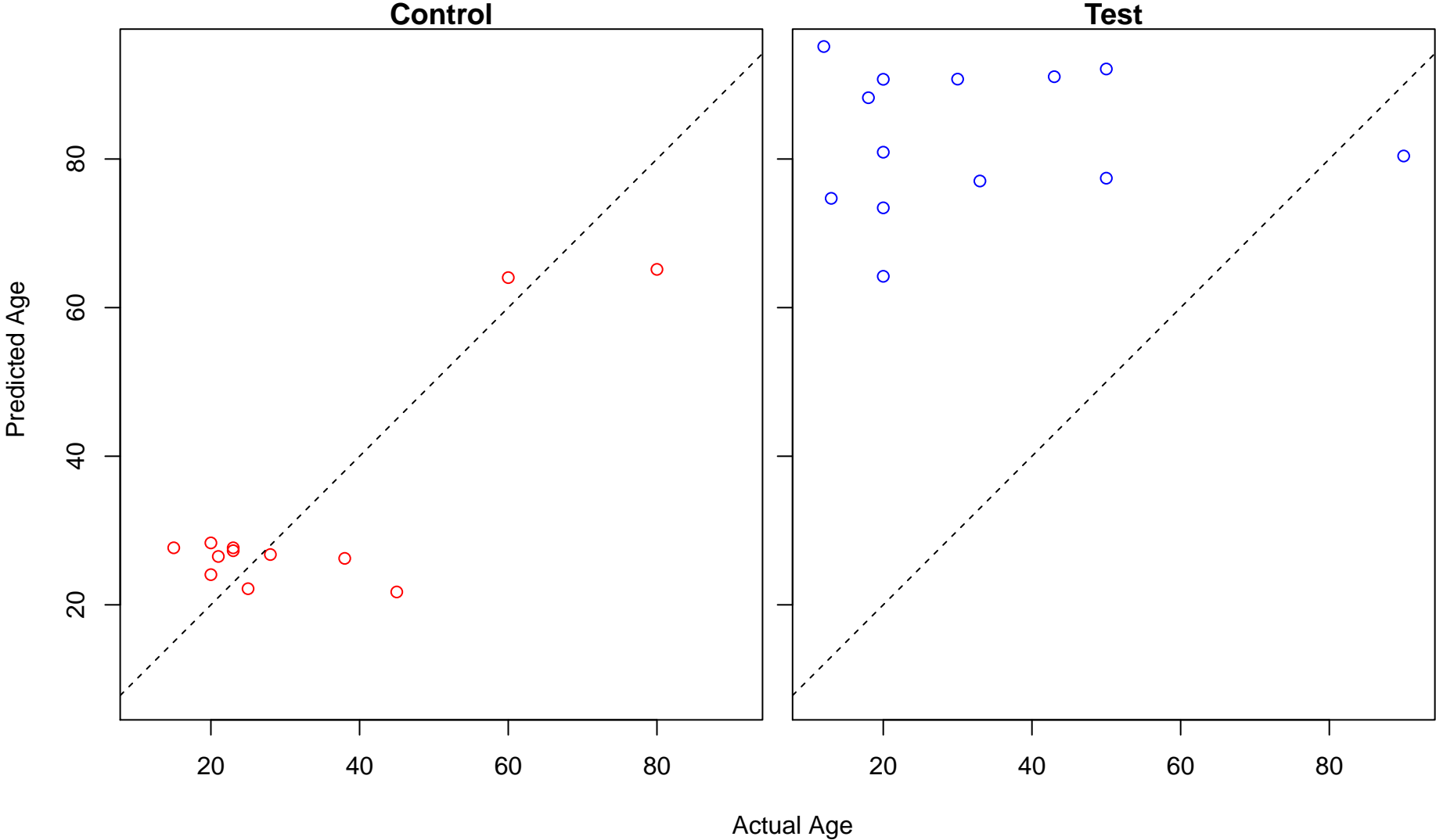


Actual Age

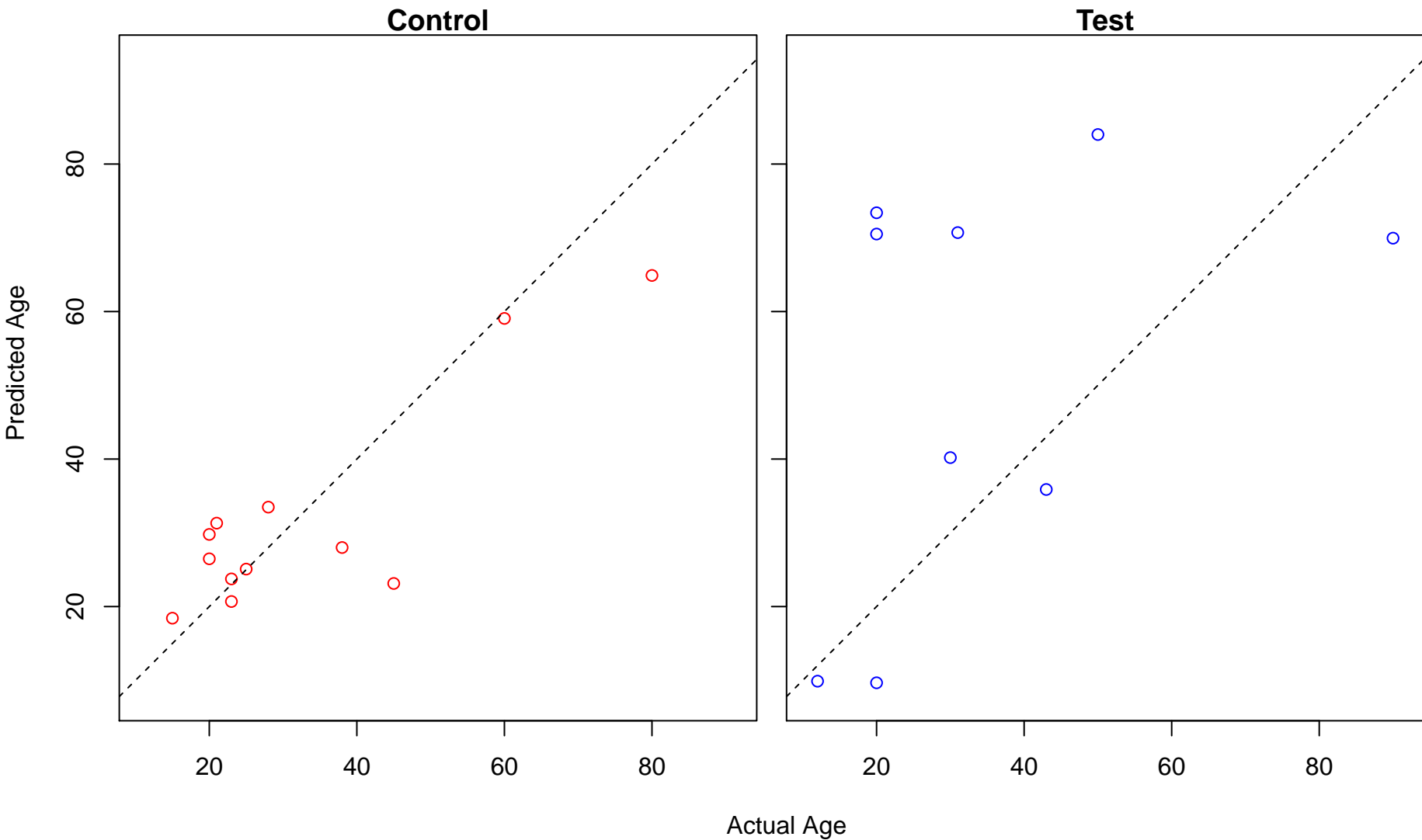
nucleocytoplasmic transport (Score: 11.927566)



regulation of syncytium formation by plasma membrane fusion (Score: 11.924071)

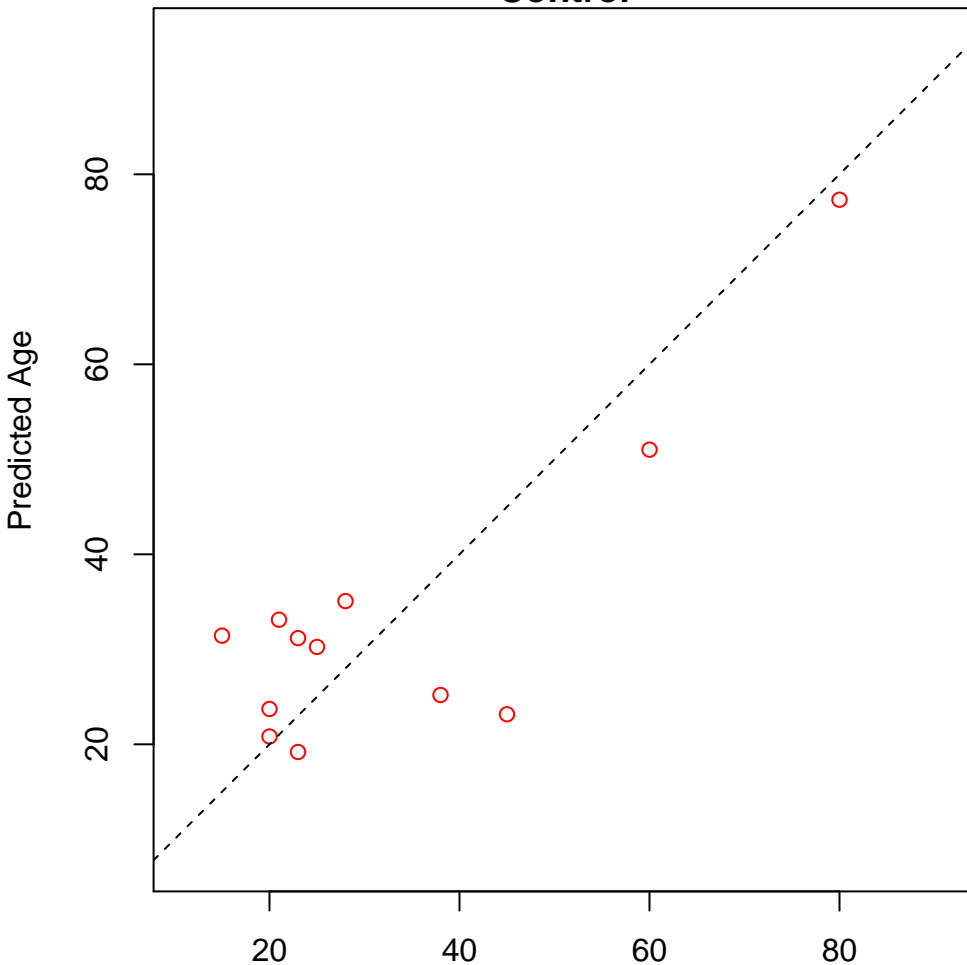


cellular response to platelet-derived growth factor stimulus (Score: 11.922966)

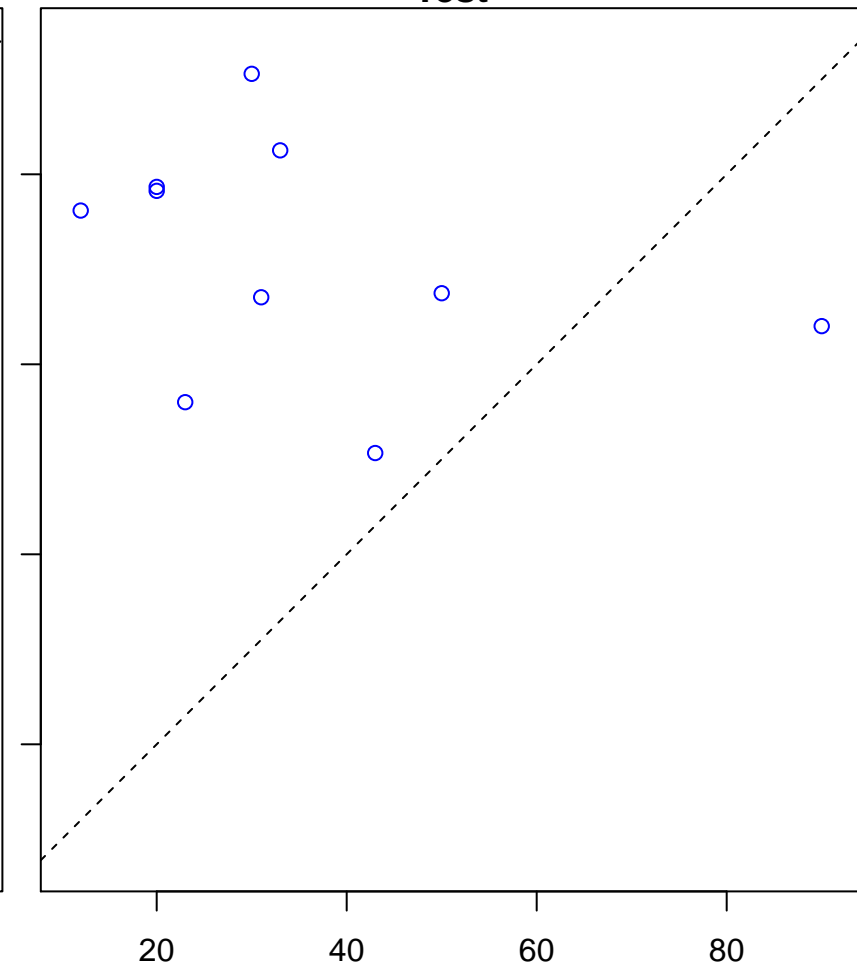


regulation of cholesterol esterification (Score: 11.911027)

Control

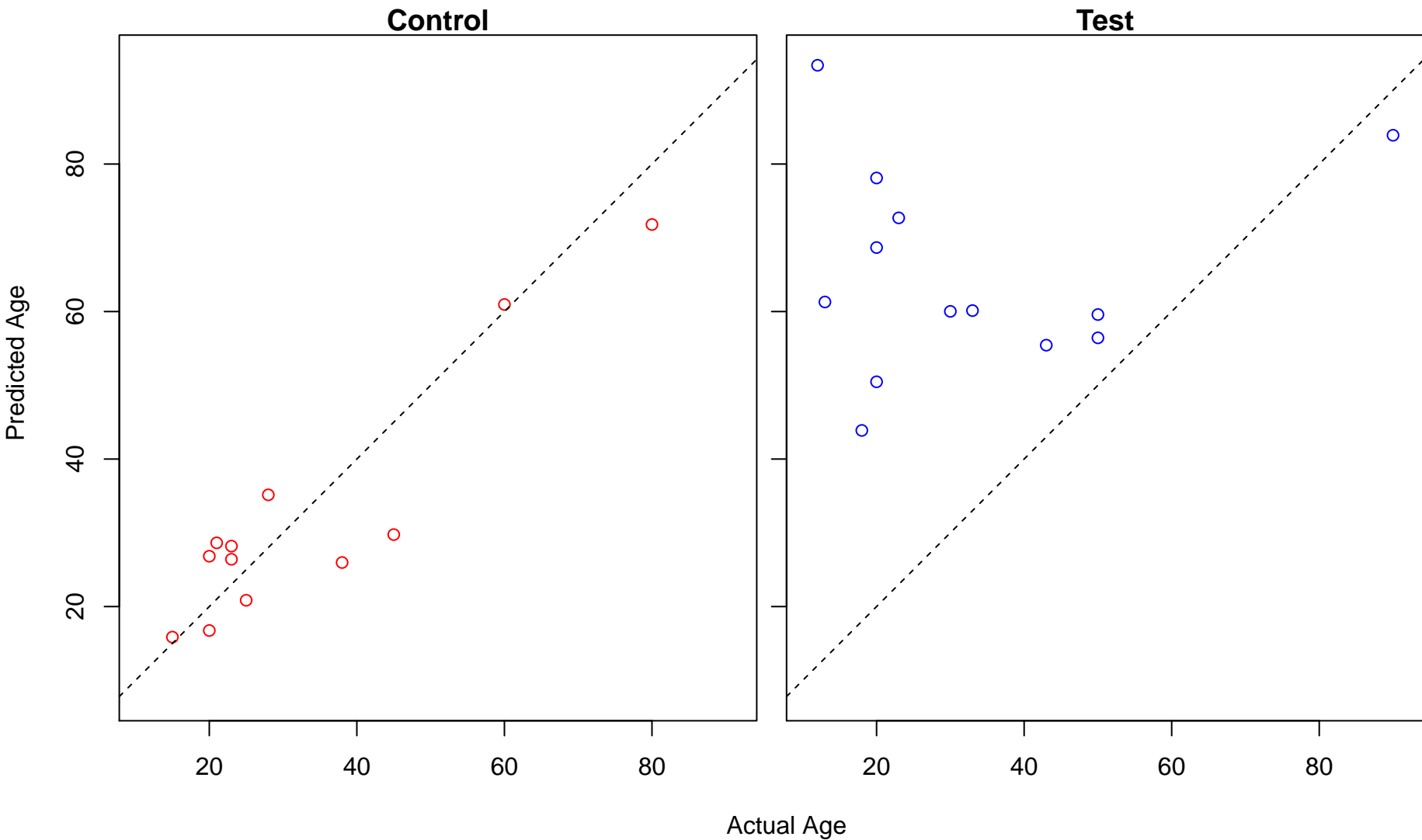


Test

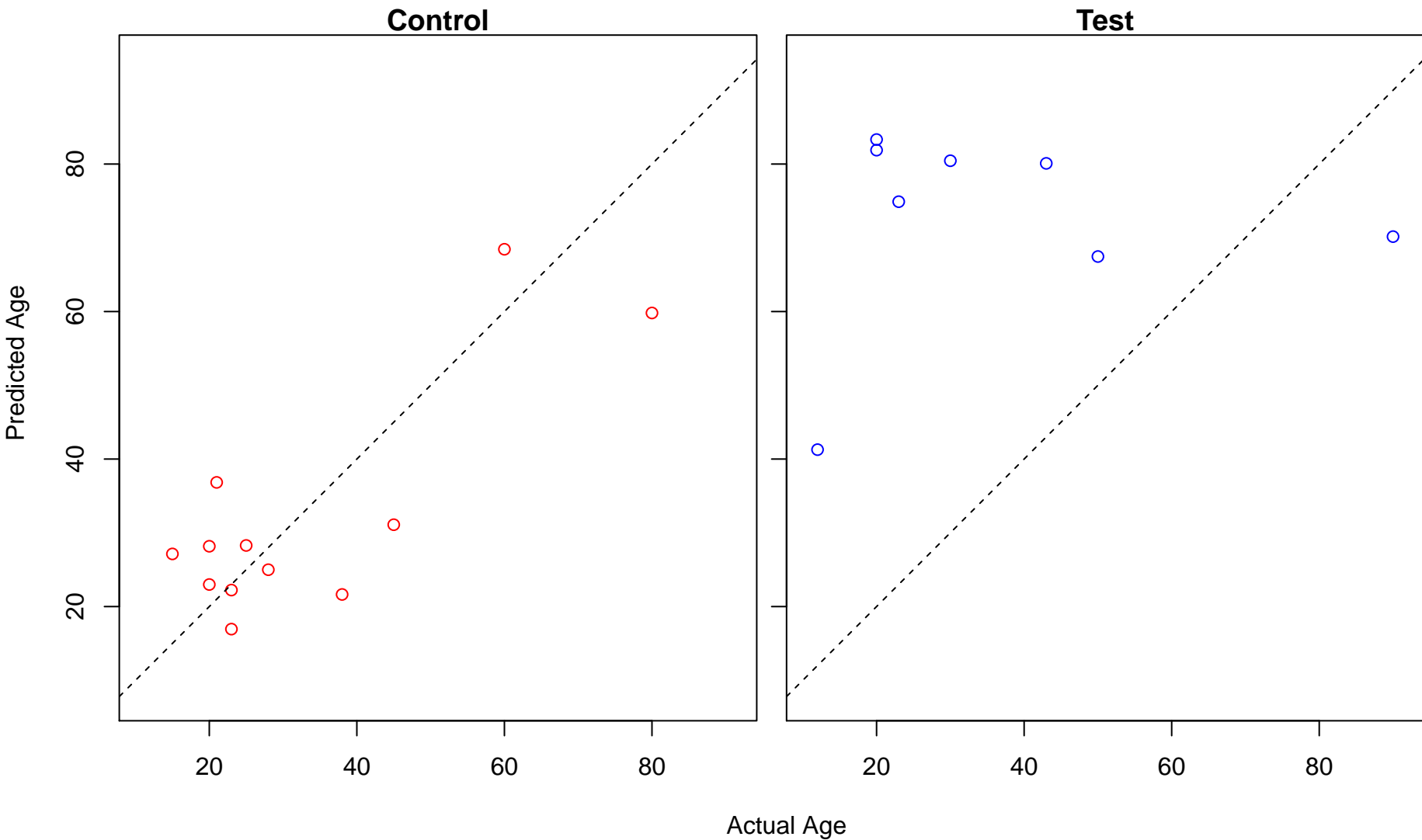


Actual Age

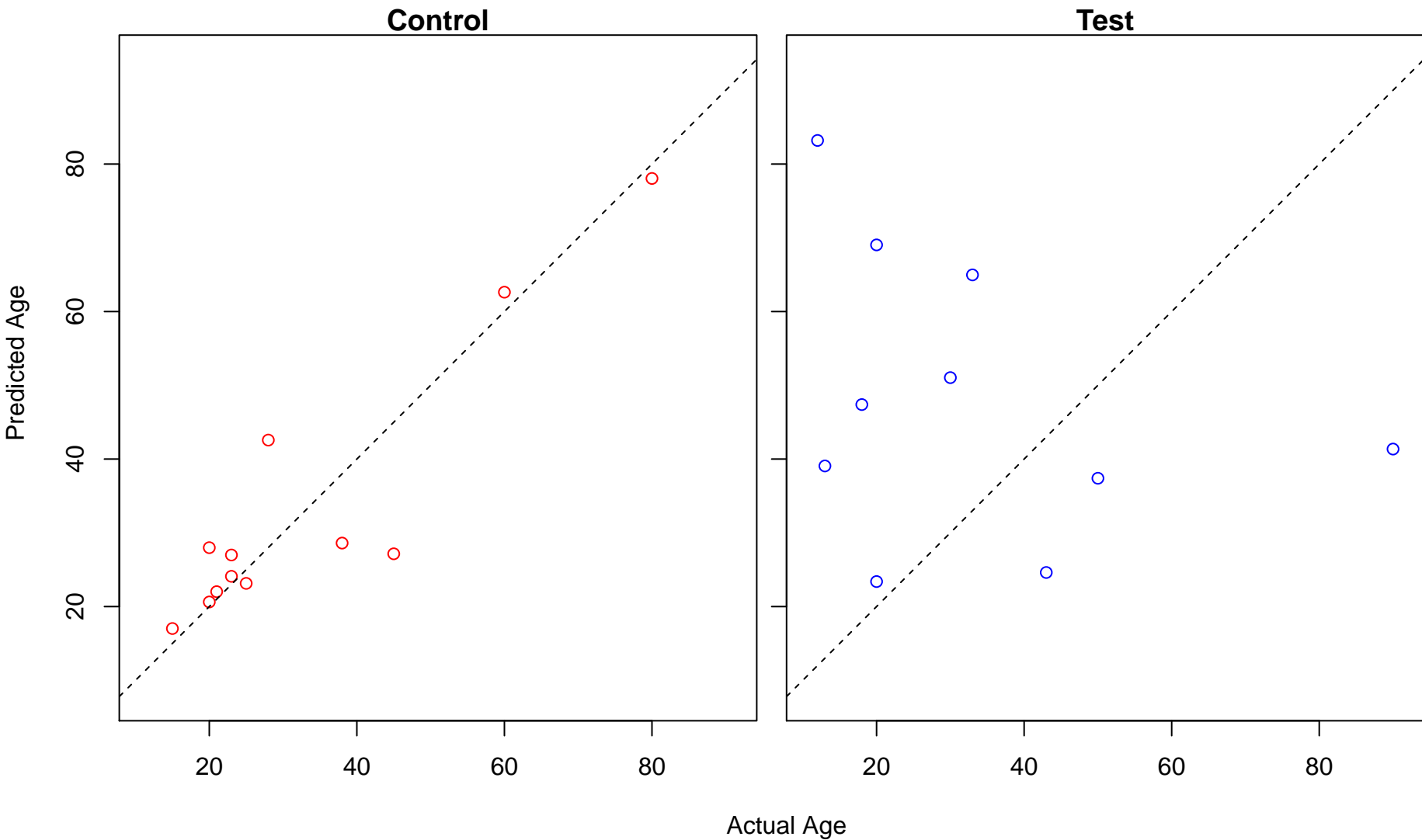
regulation of myeloid leukocyte mediated immunity (Score: 11.877452)



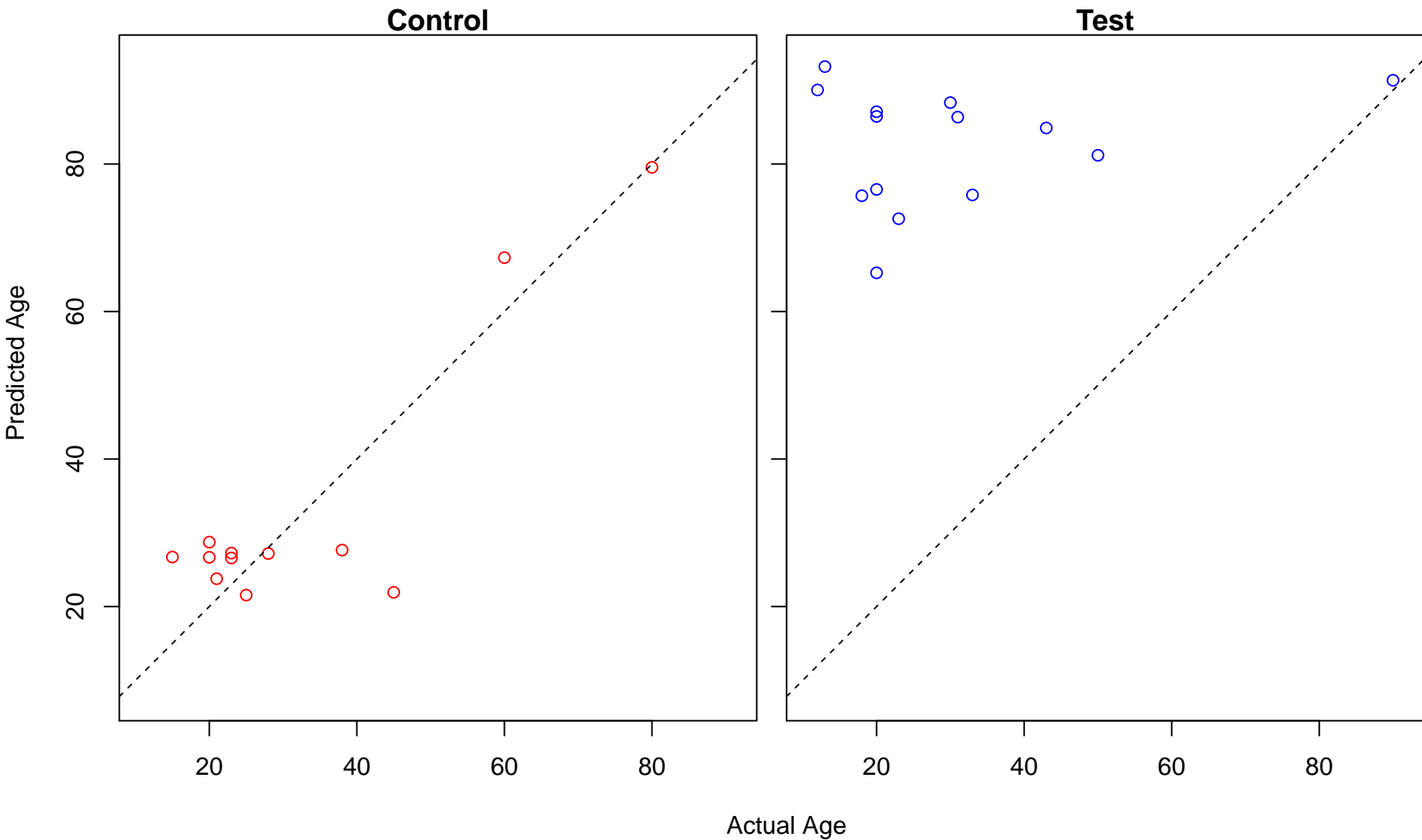
bile acid signaling pathway (Score: 11.871387)



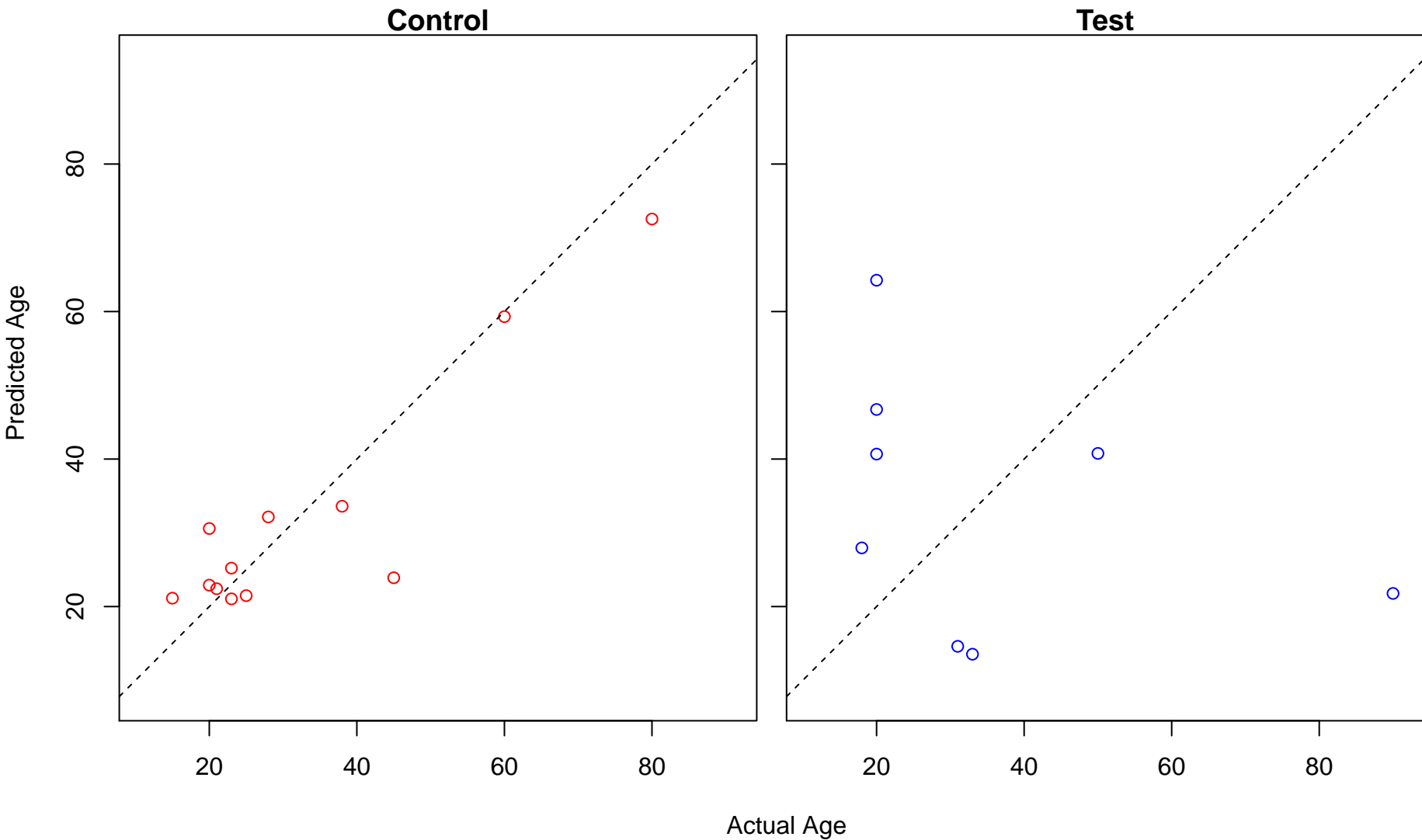
muscle organ development (Score: 11.858047)



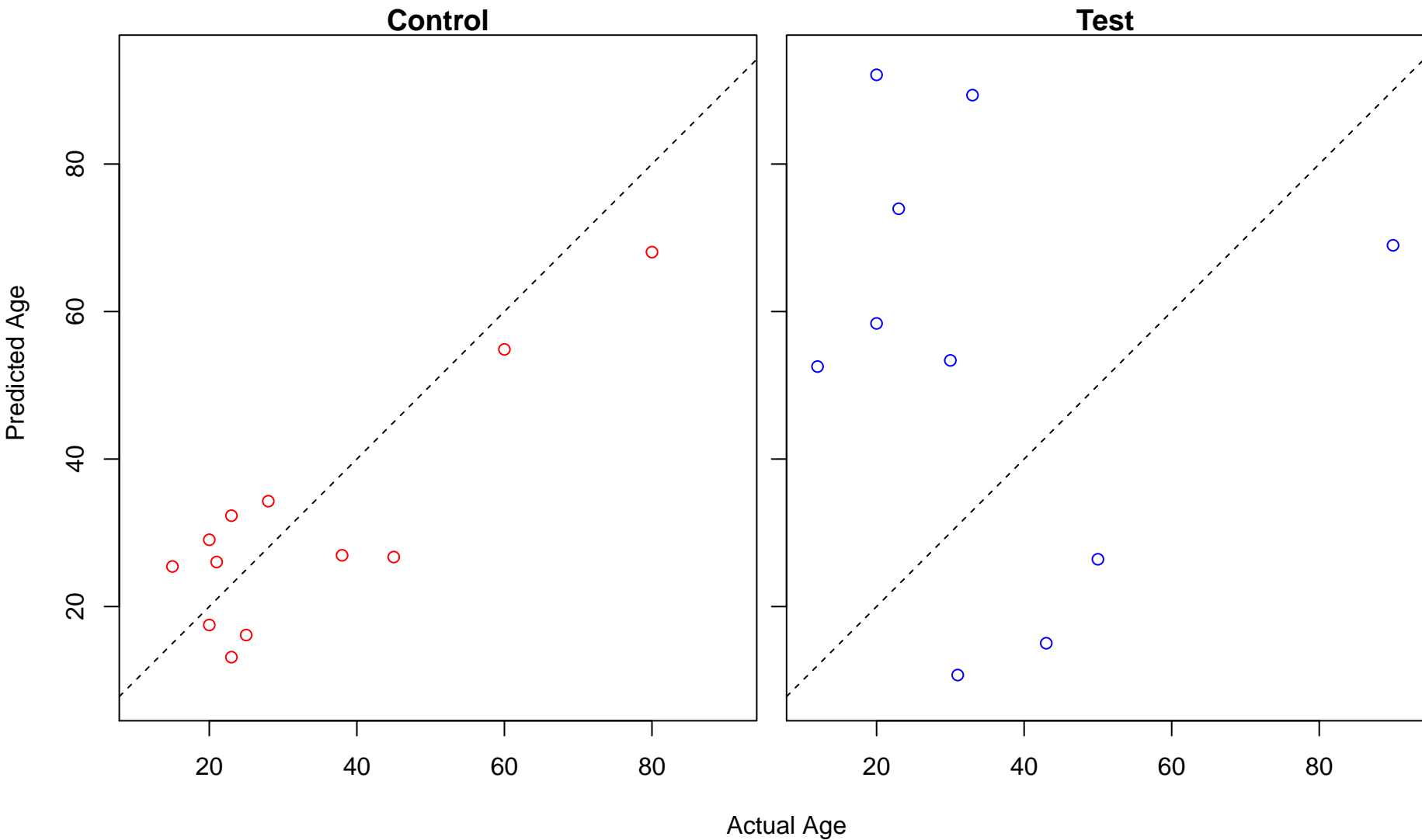
histone H3-K27 methylation (Score: 11.856920)



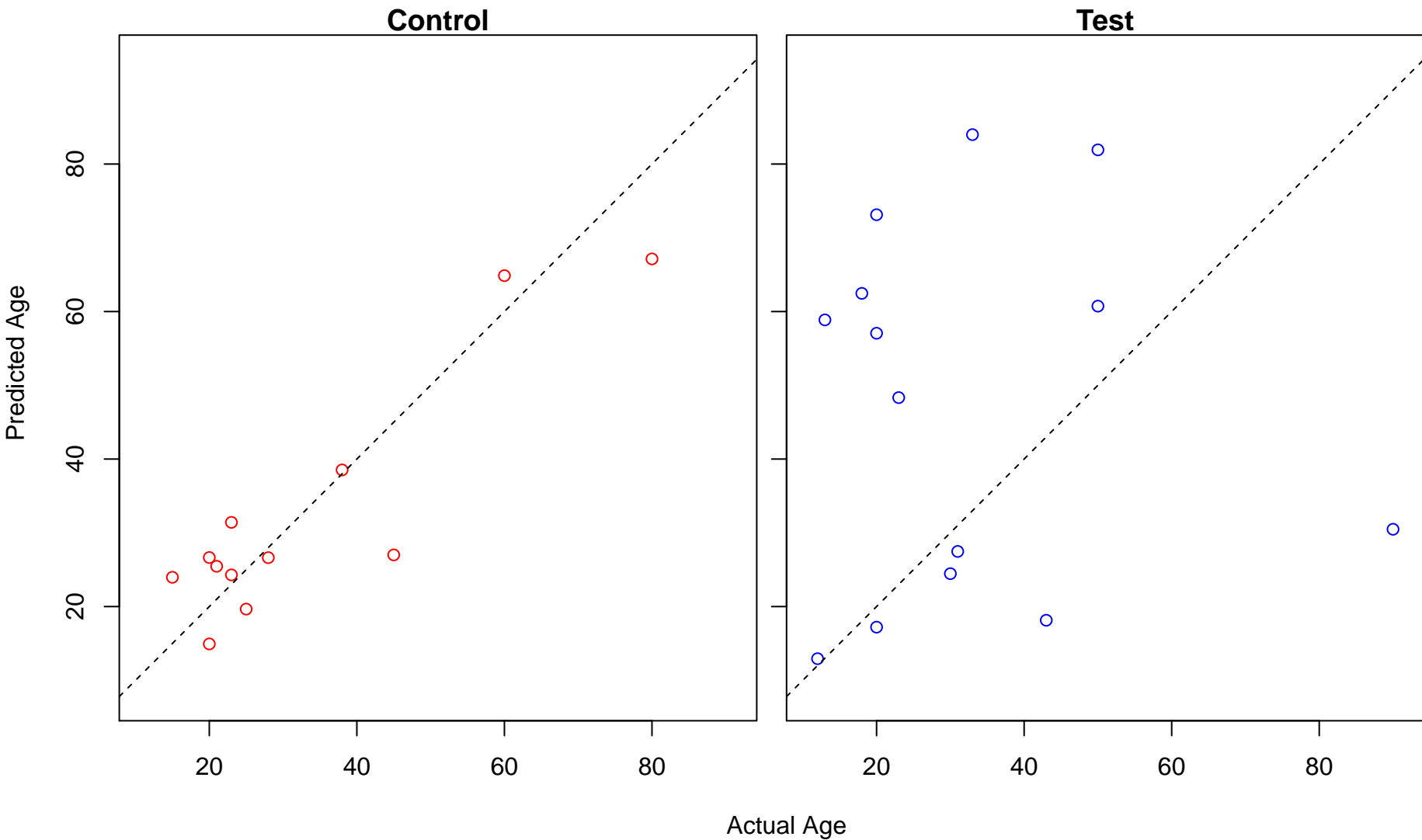
pyrimidine nucleotide–sugar transmembrane transport (Score: 11.856198)



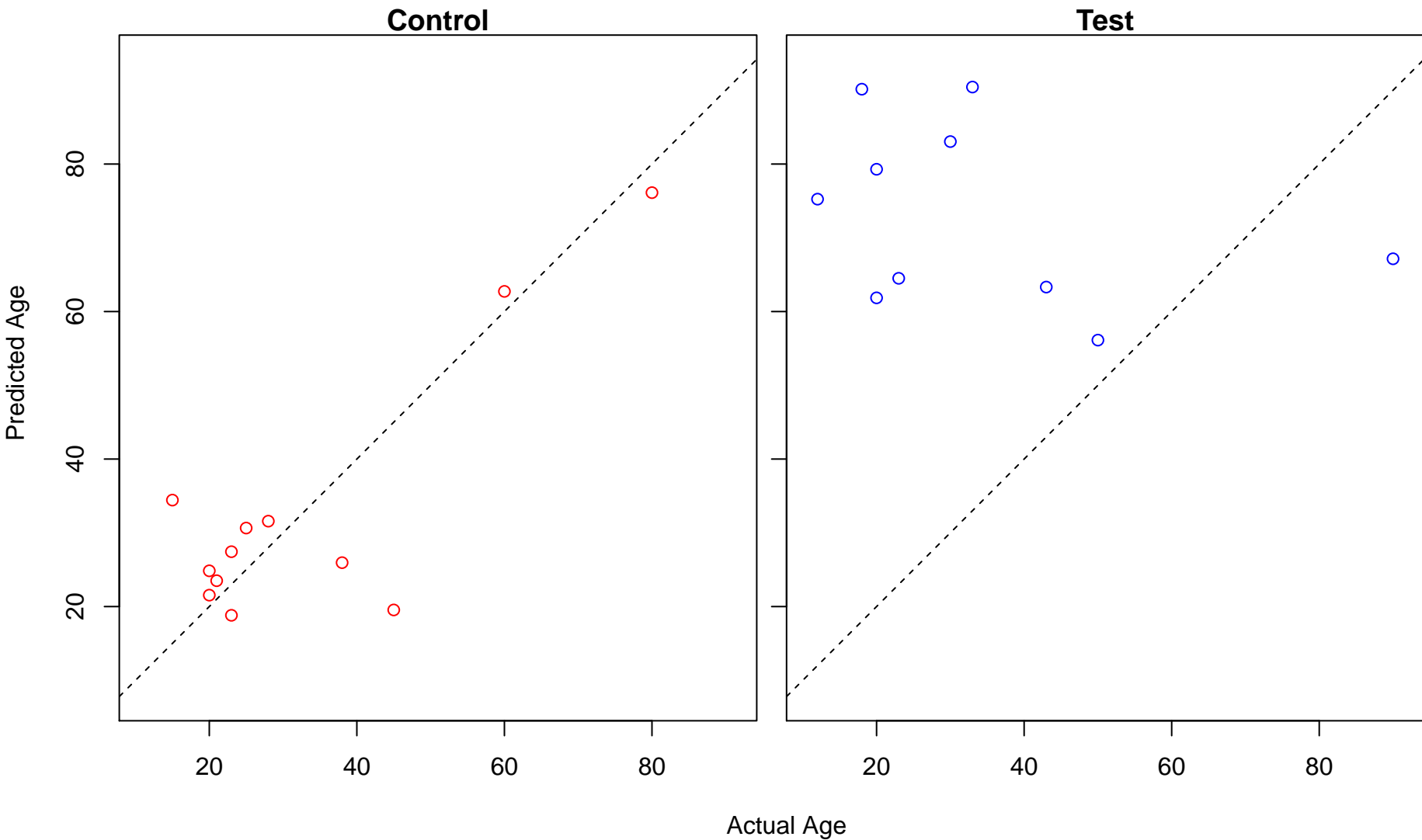
nuclear transport (Score: 11.852837)



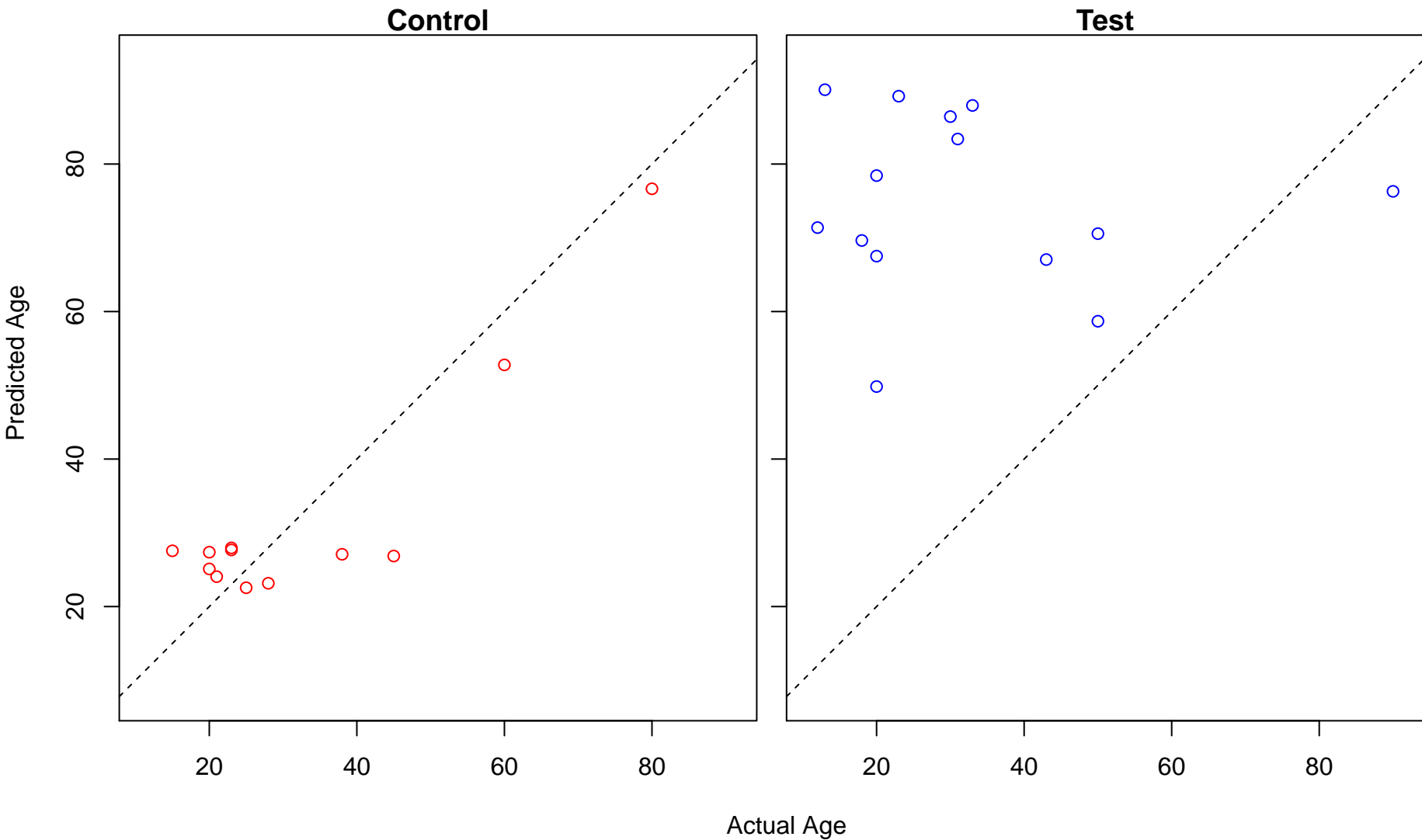
positive regulation of ion transmembrane transport (Score: 11.836775)



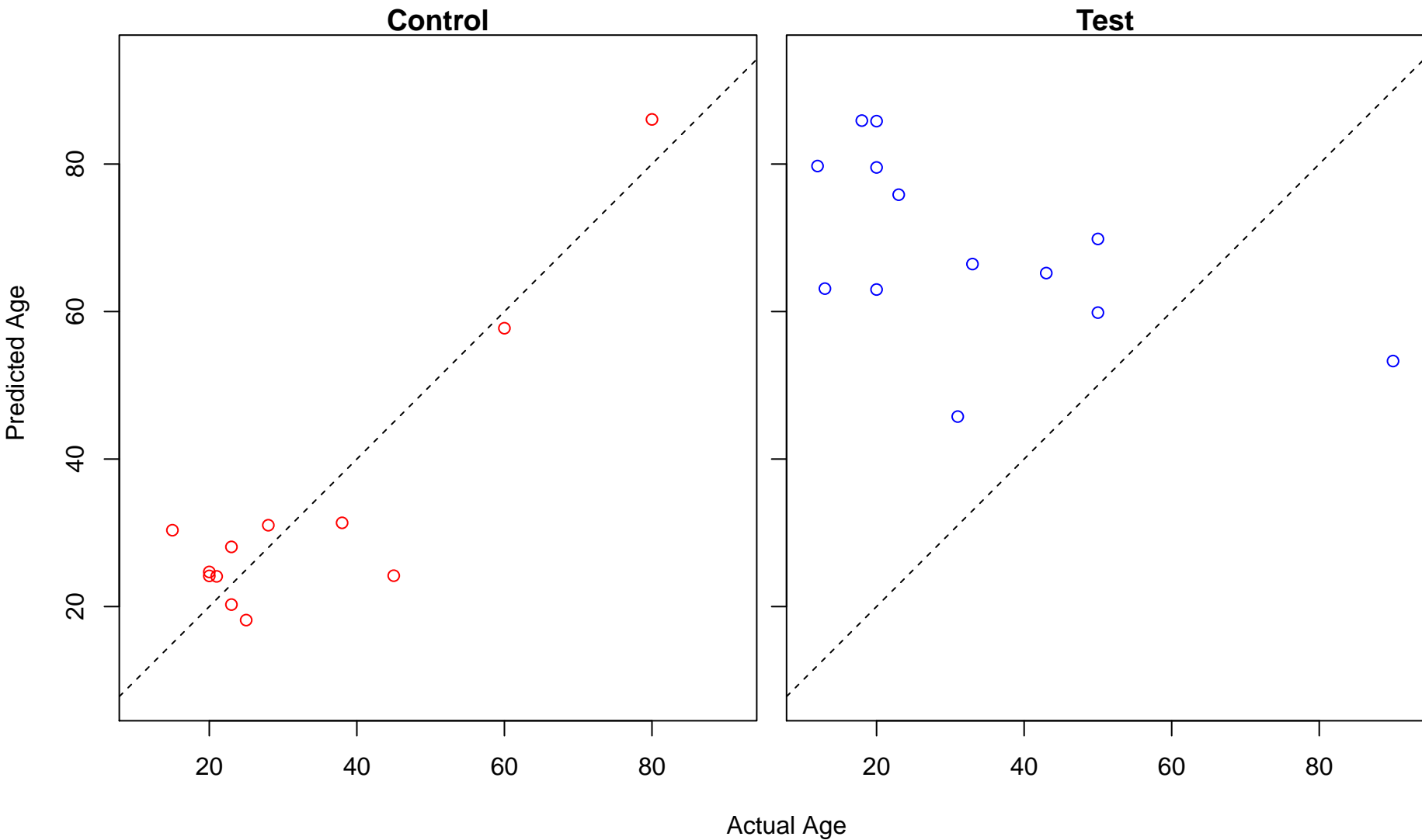
positive regulation of binding (Score: 11.828768)



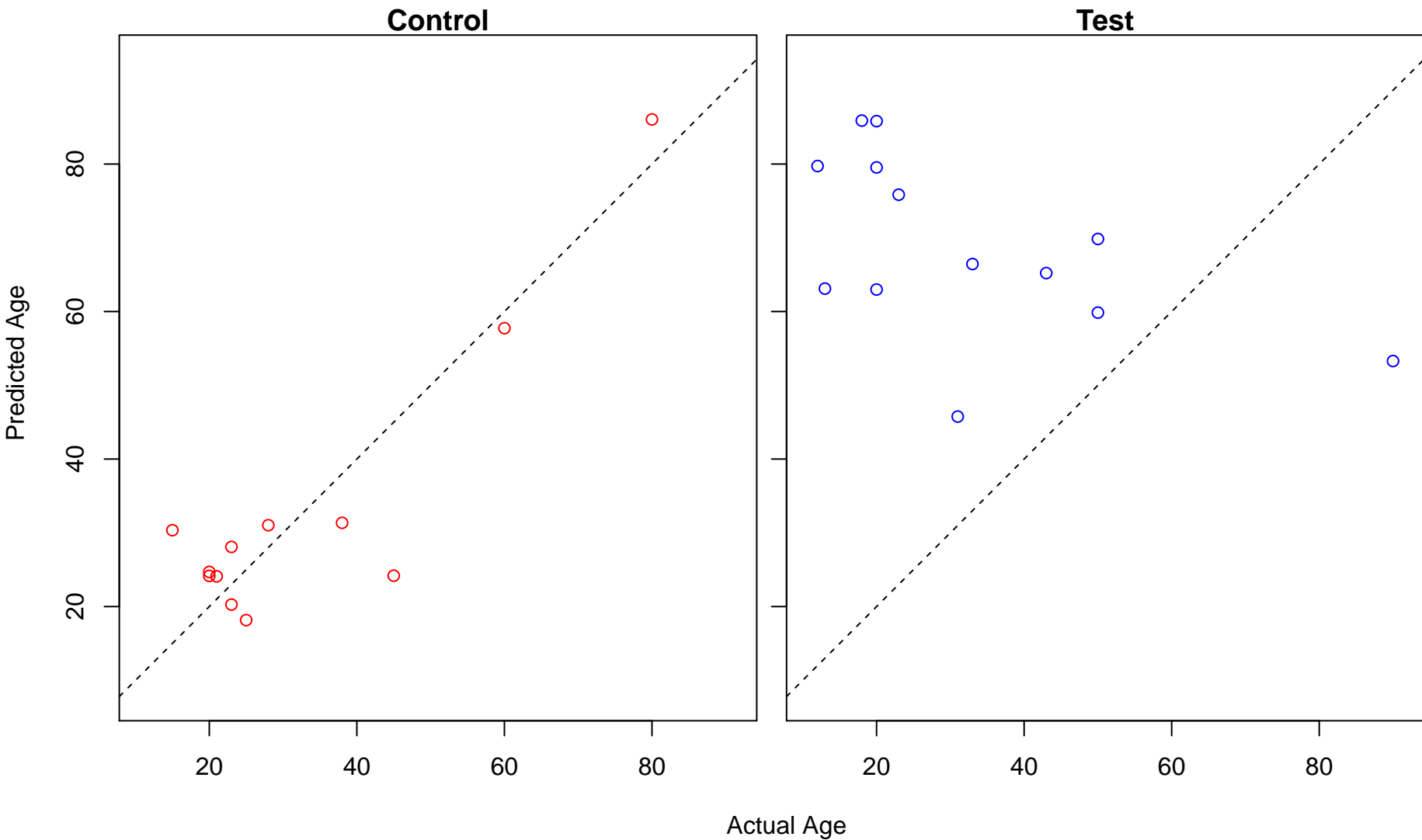
carbon catabolite regulation of transcription (Score: 11.810682)



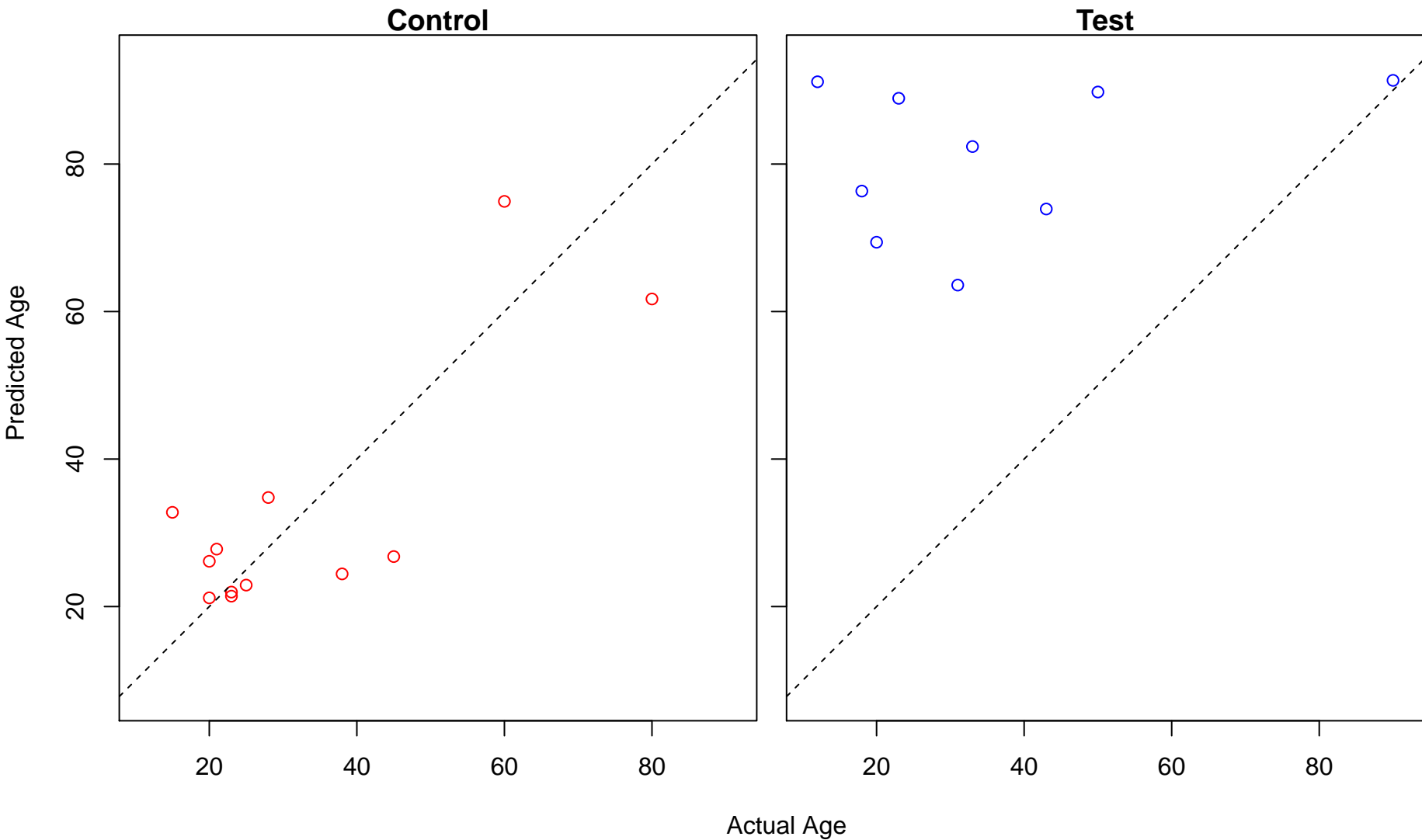
L-serine transport (Score: 11.790713)



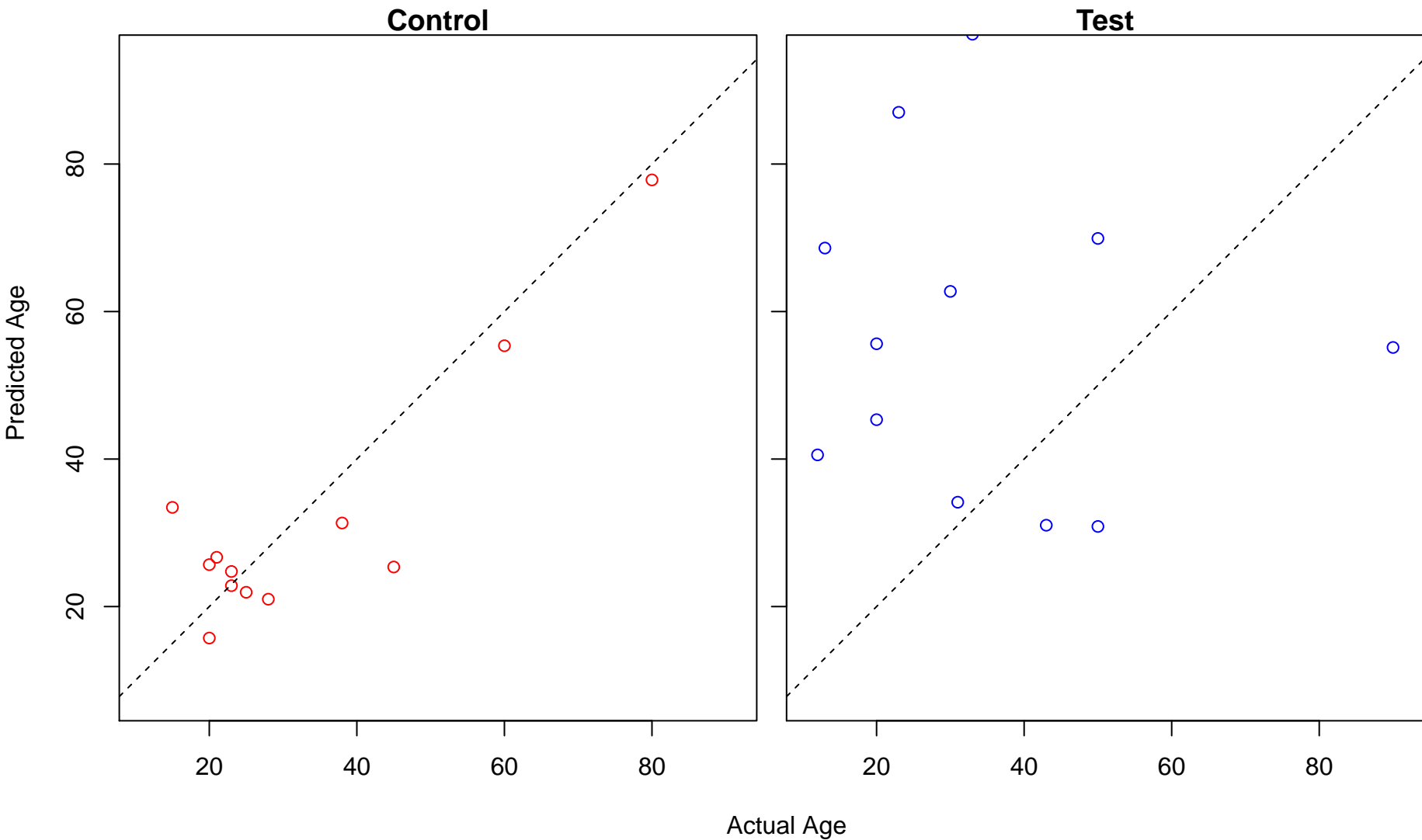
serine transport (Score: 11.790713)



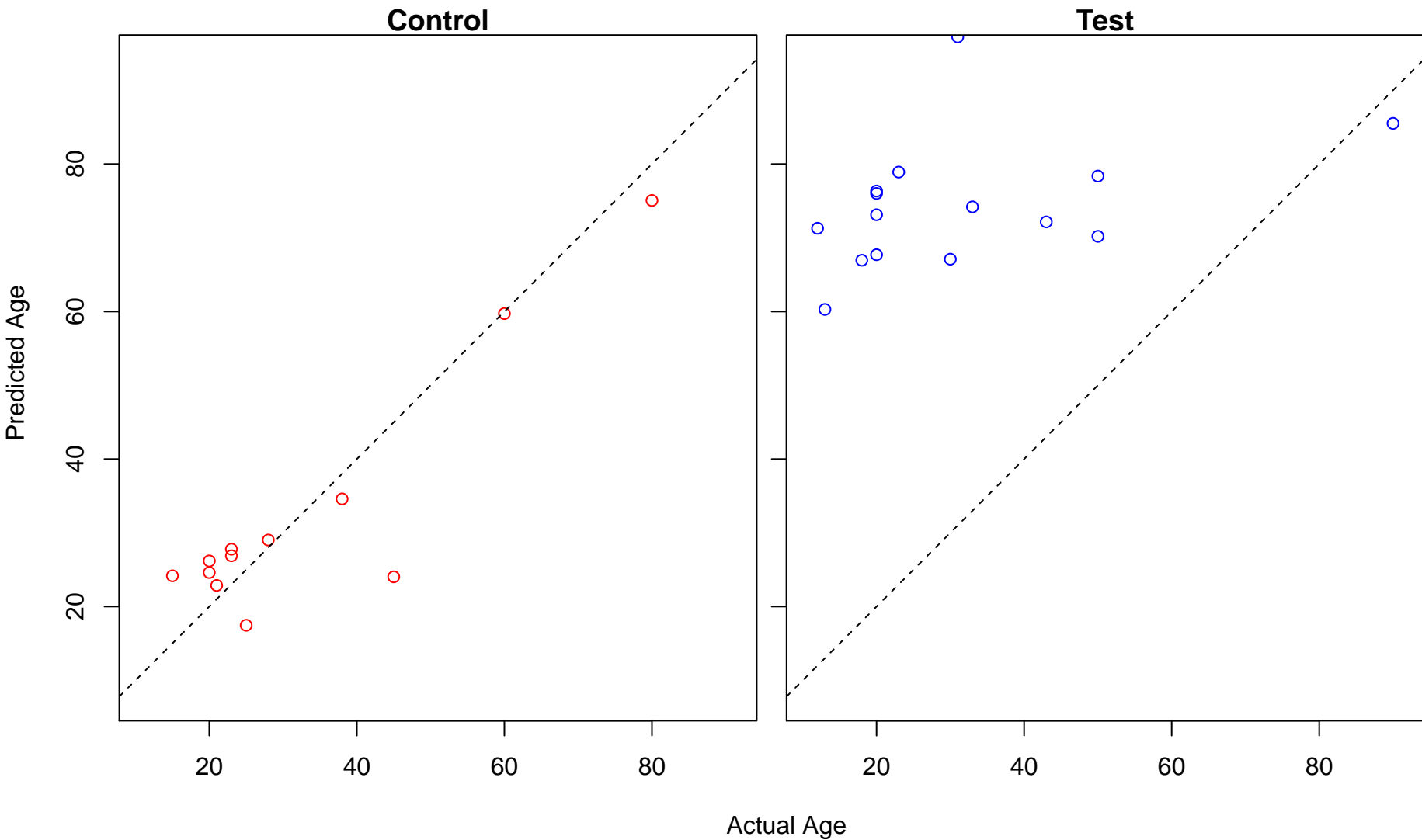
negative regulation of fibroblast proliferation (Score: 11.776451)



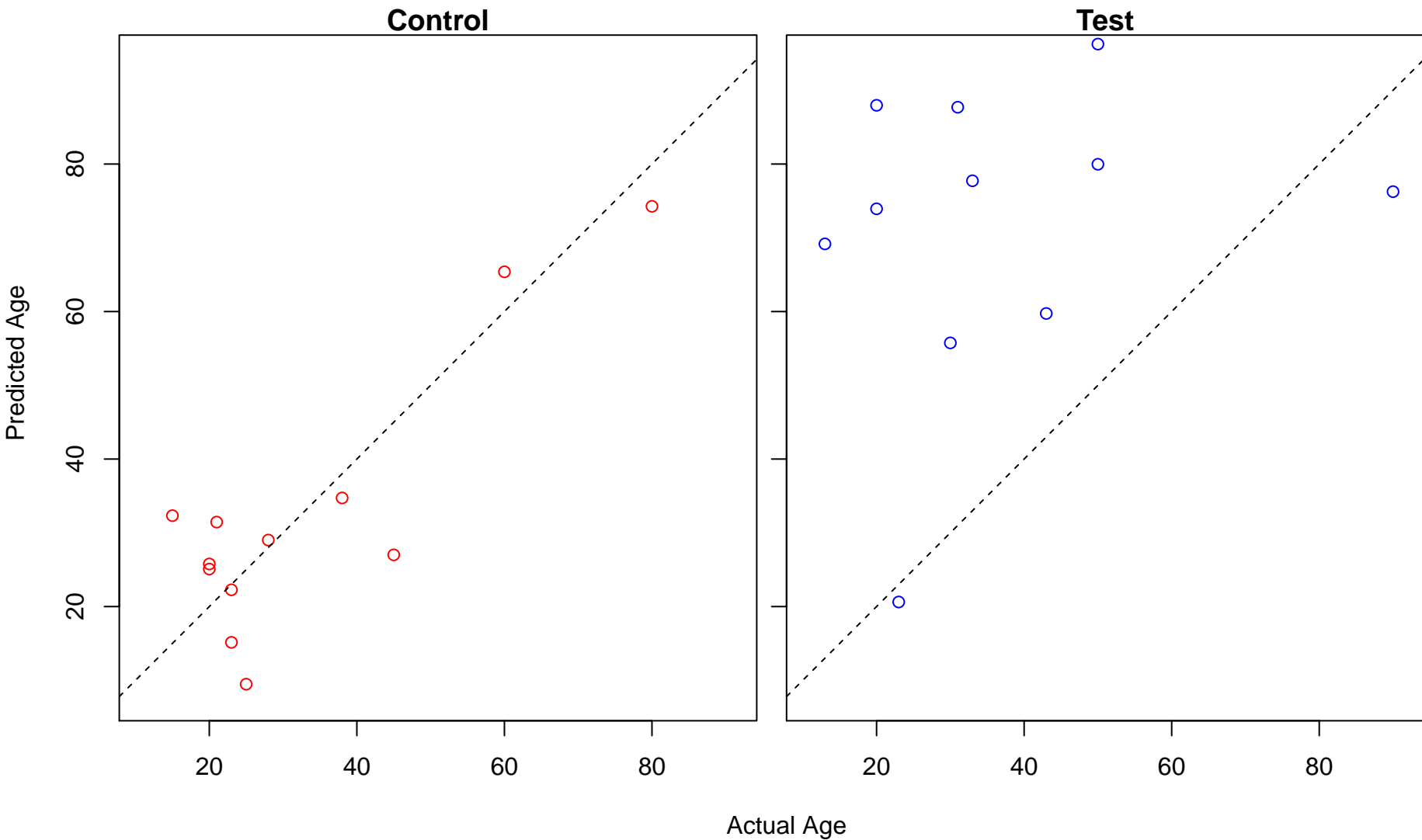
monosaccharide transport (Score: 11.757744)



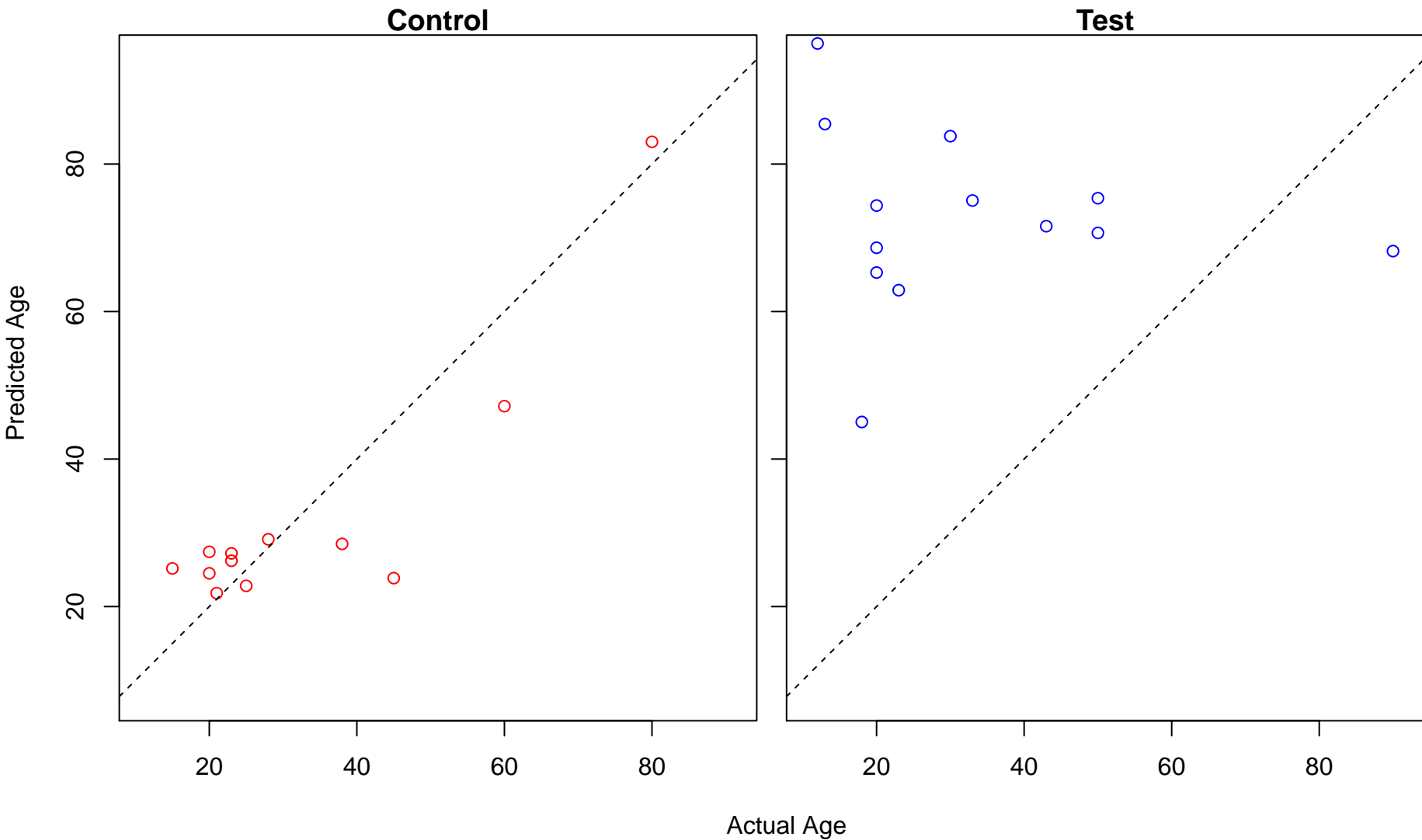
liver development (Score: 11.737356)



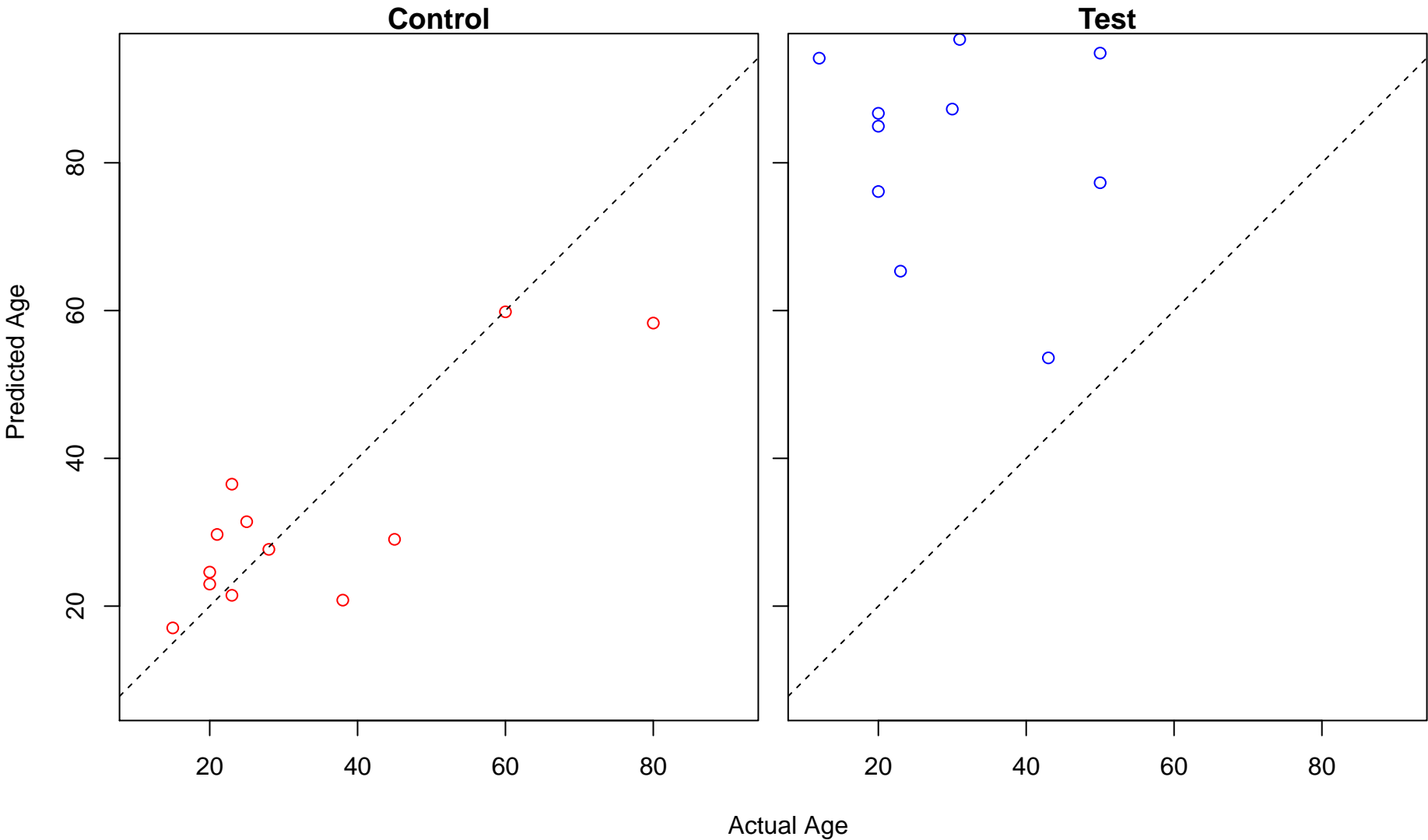
developmental process involved in reproduction (Score: 11.730212)



negative regulation of ossification (Score: 11.698622)

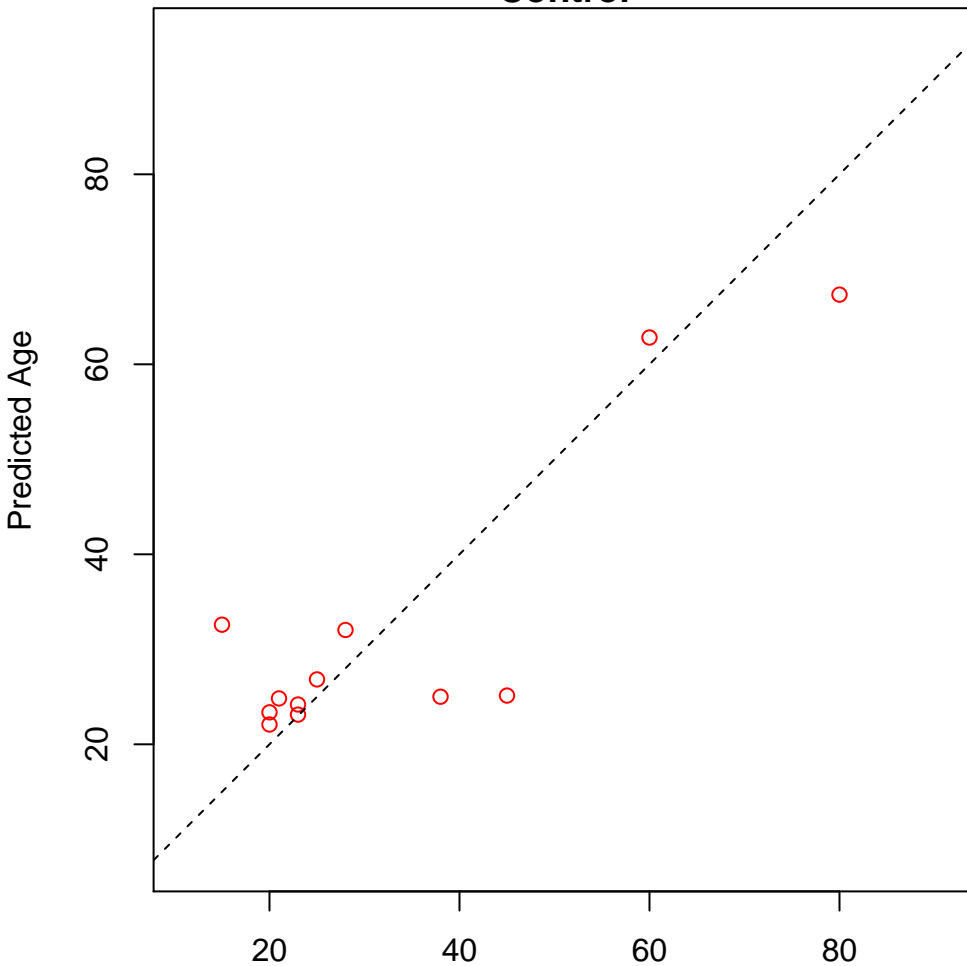


regulation of N-methyl-D-aspartate selective glutamate receptor activity (Score: 11.693528)

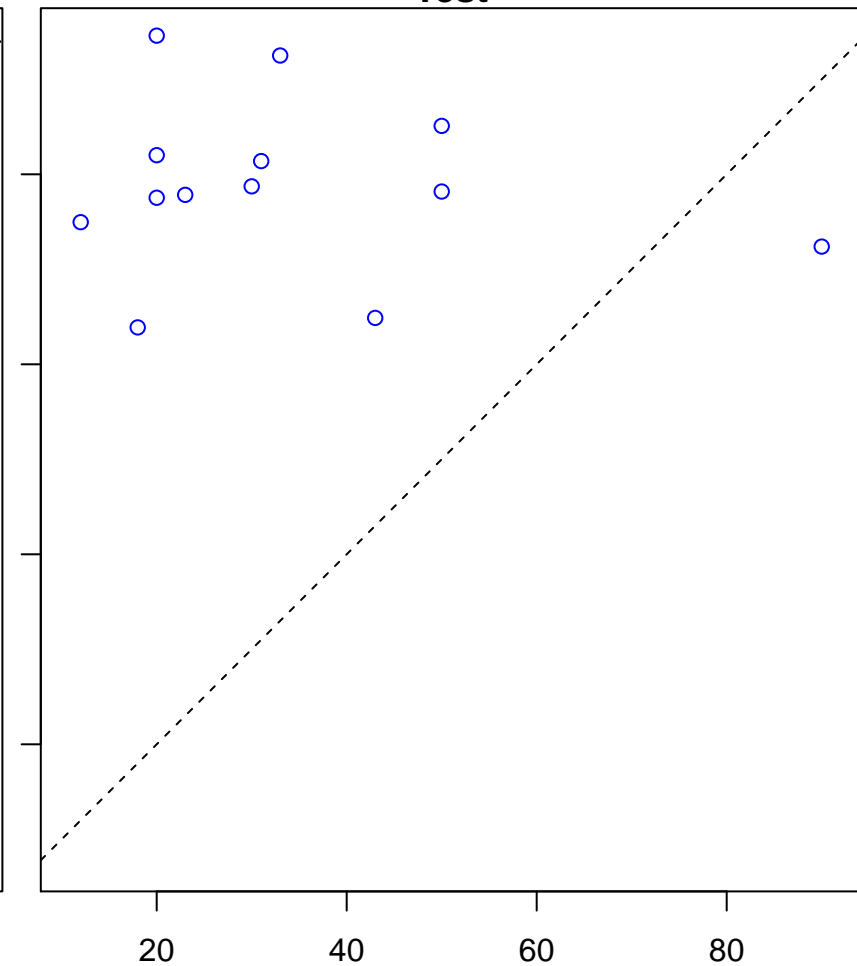


peptidyl-serine autophosphorylation (Score: 11.684260)

Control

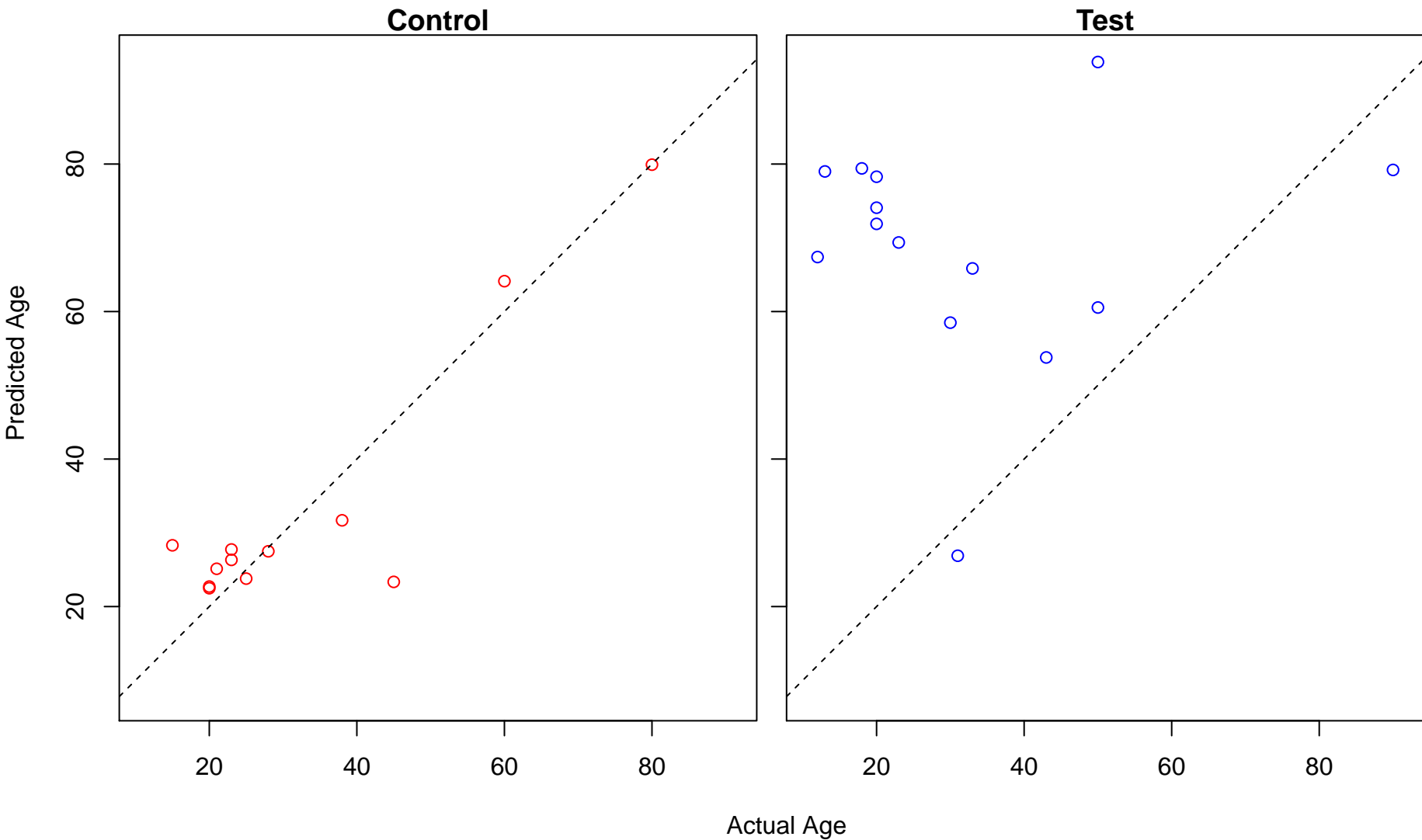


Test

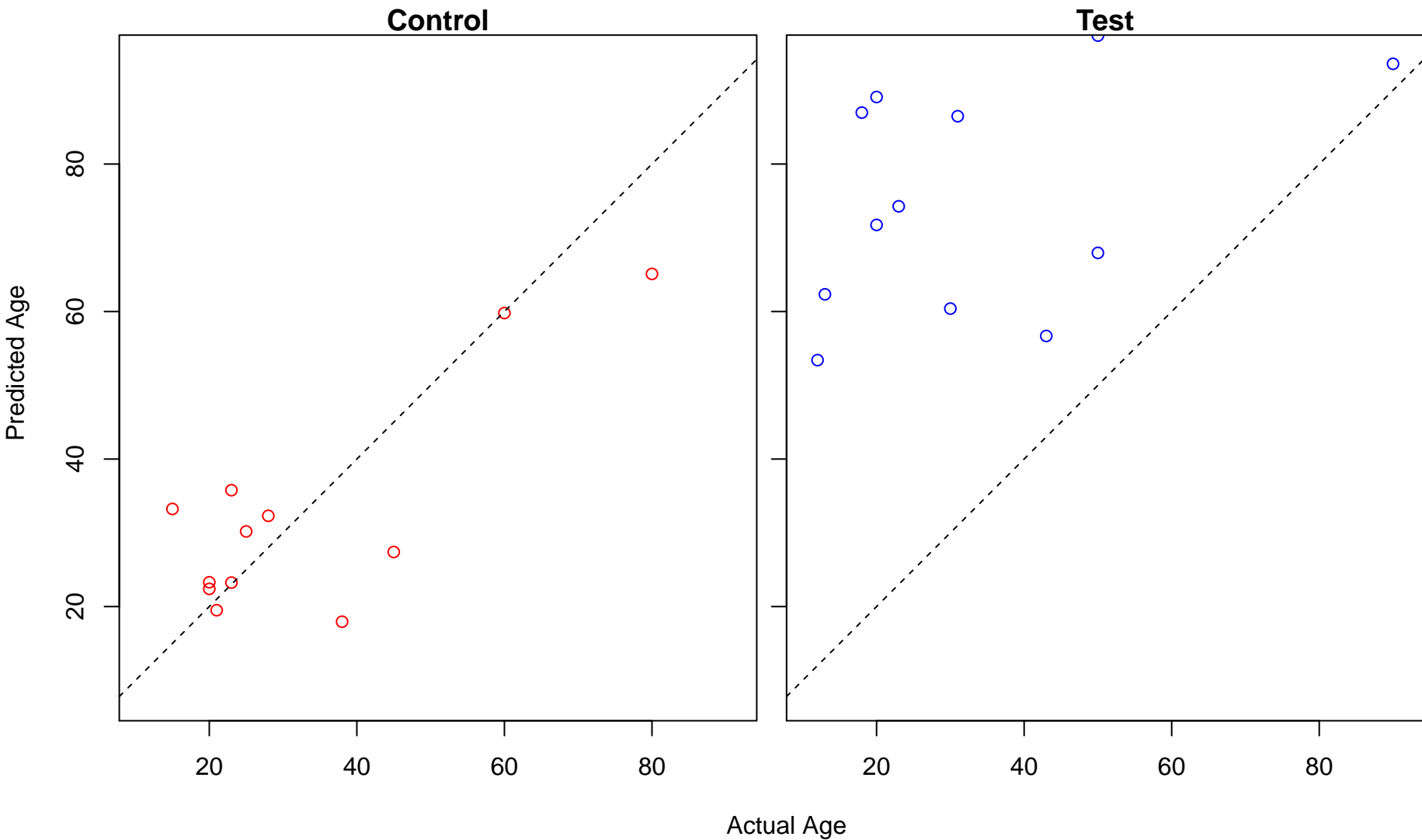


Actual Age

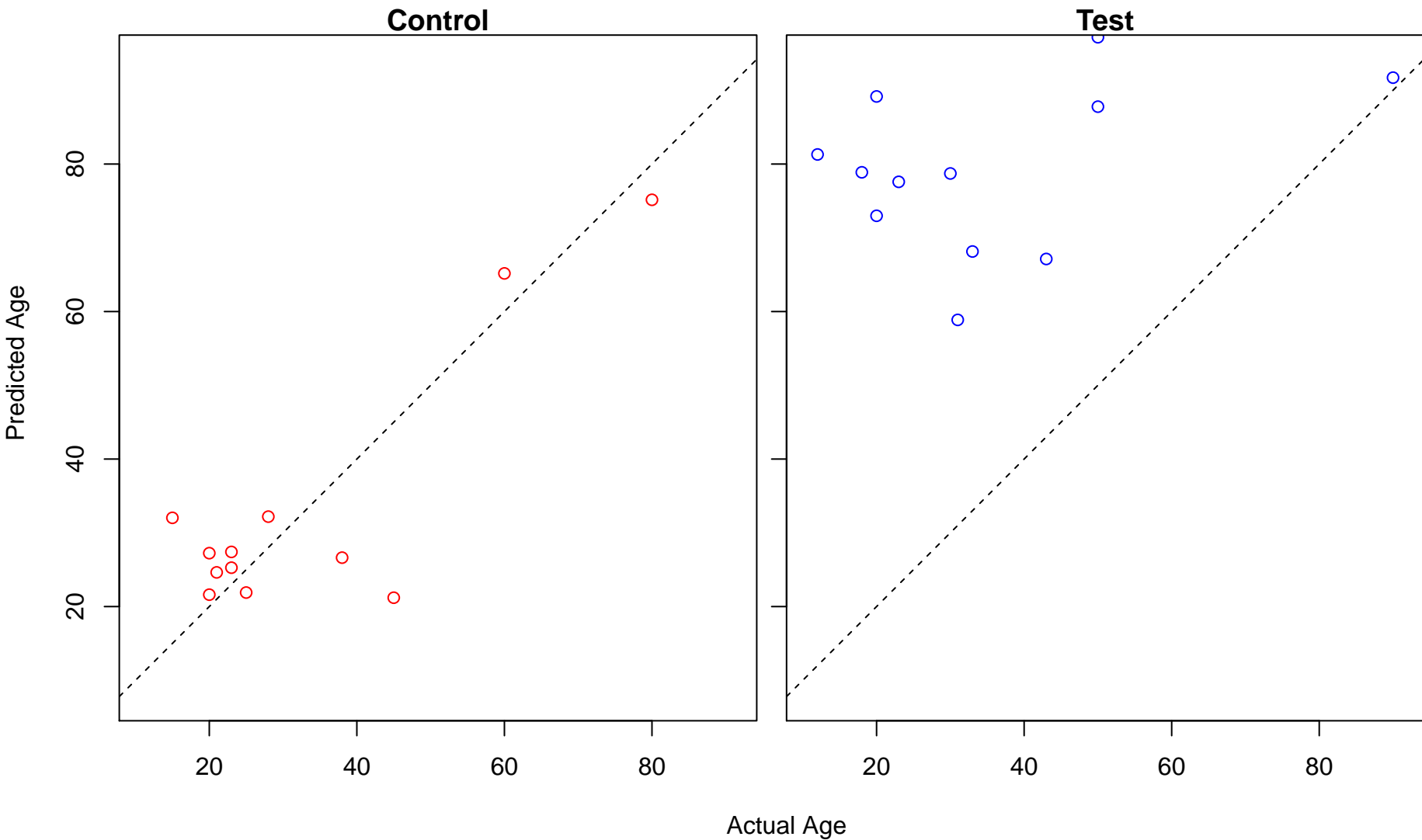
substrate-dependent cell migration (Score: 11.684175)



negative regulation of T cell apoptotic process (Score: 11.675504)

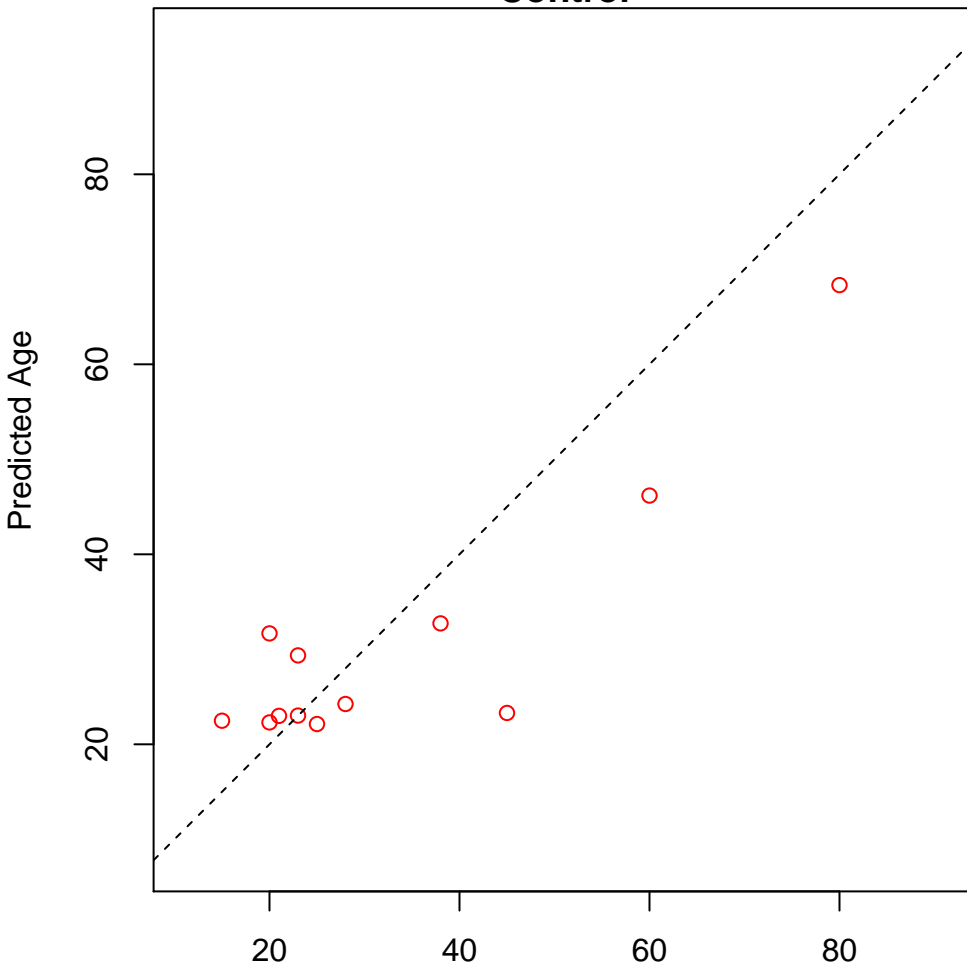


response to lipopolysaccharide (Score: 11.671557)

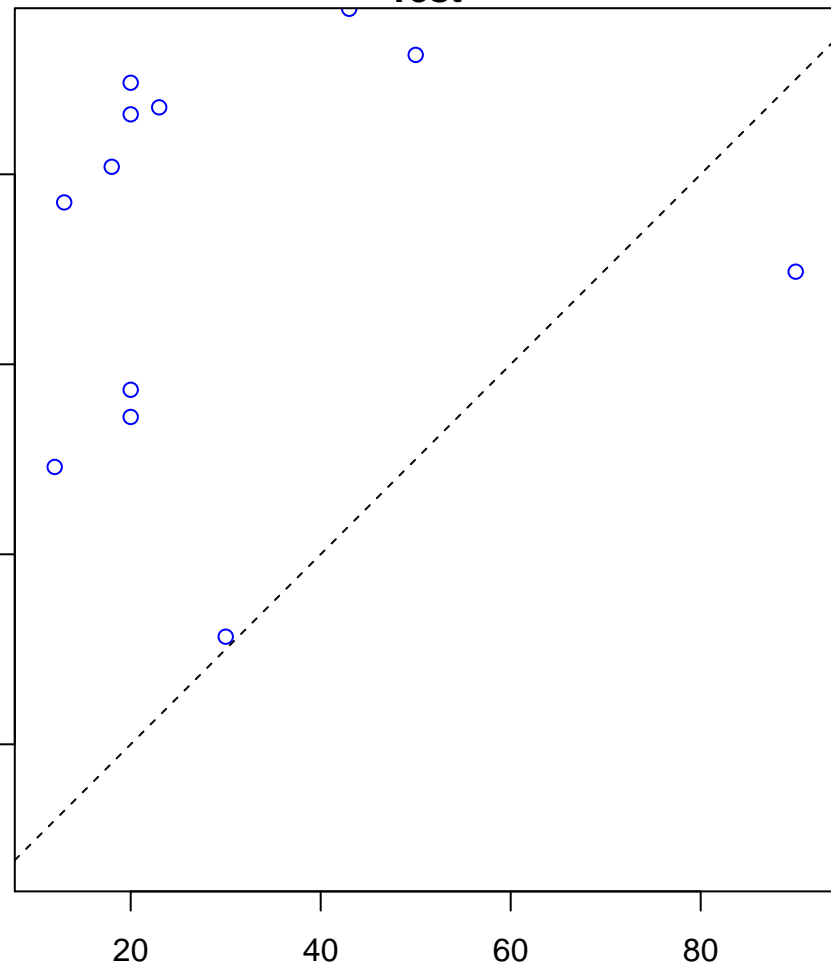


vitamin transmembrane transport (Score: 11.662389)

Control

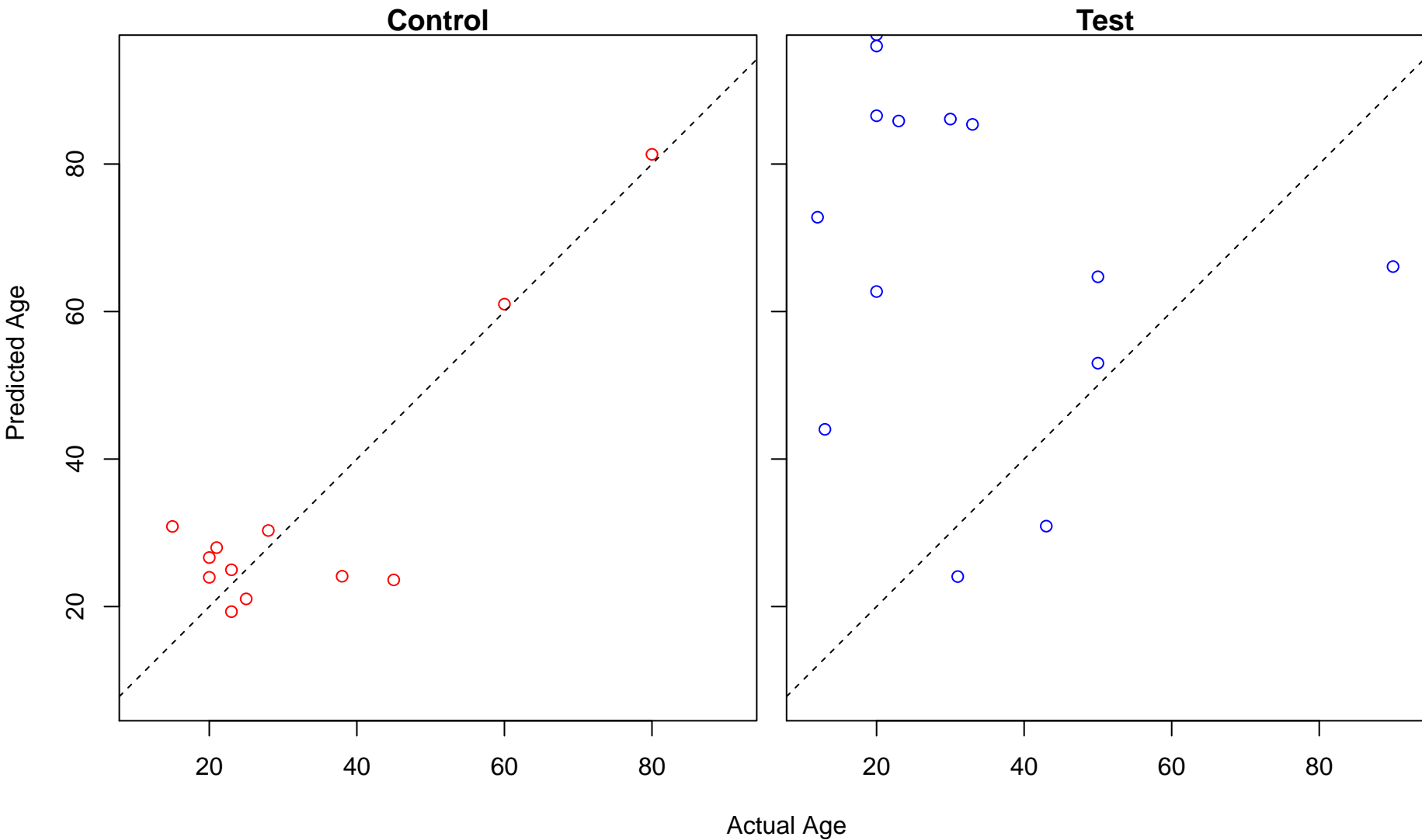


Test

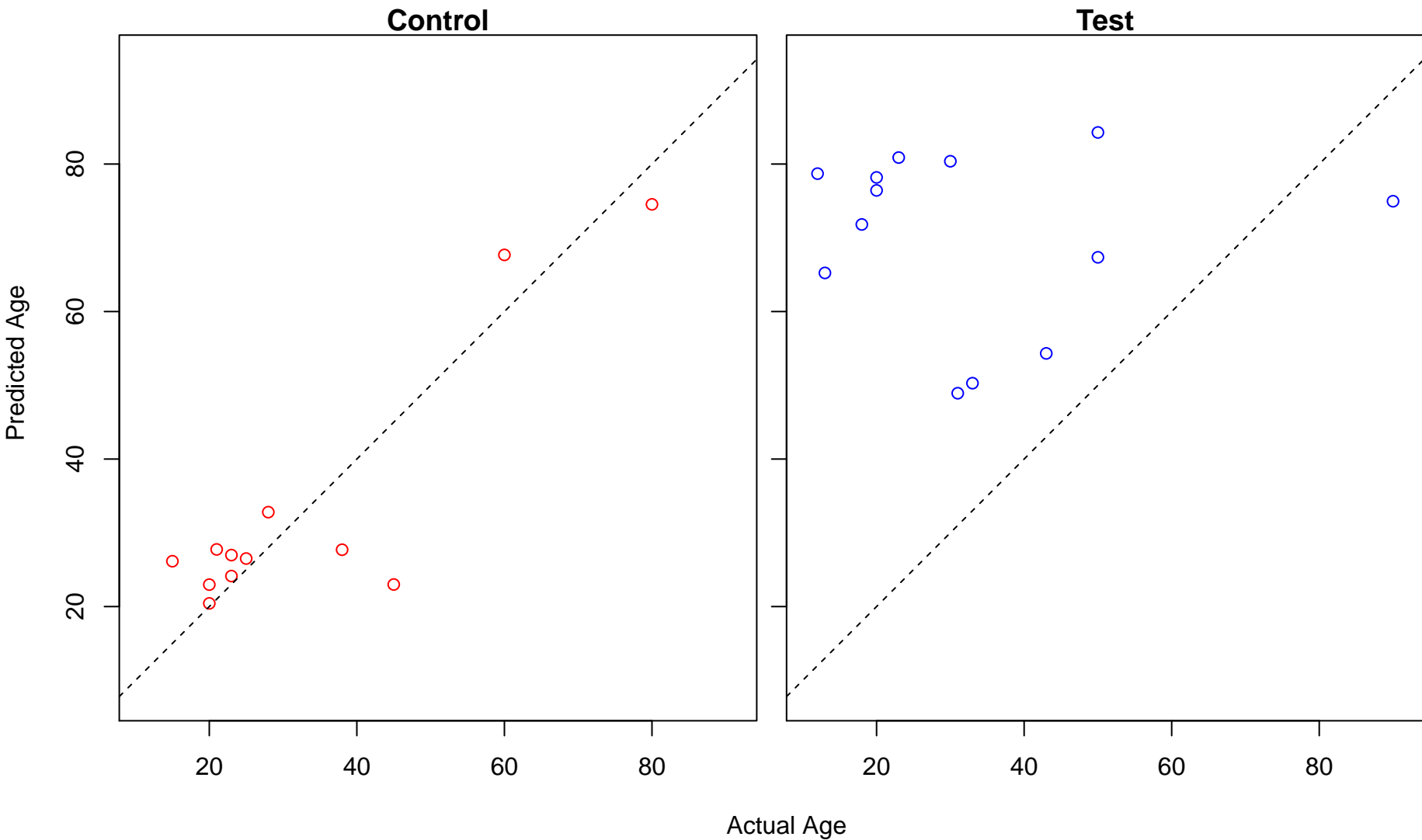


Actual Age

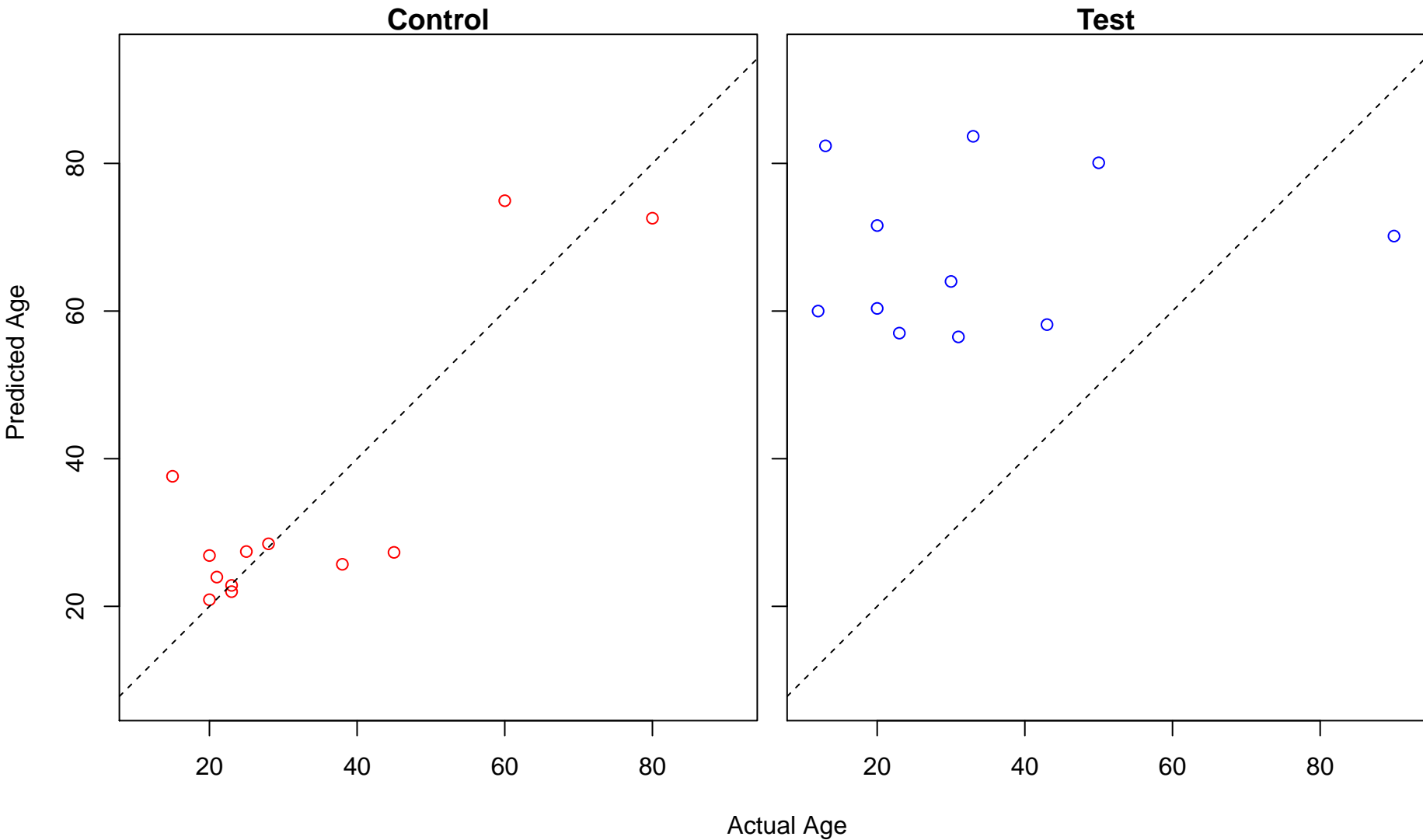
ER-associated ubiquitin-dependent protein catabolic process (Score: 11.656575)



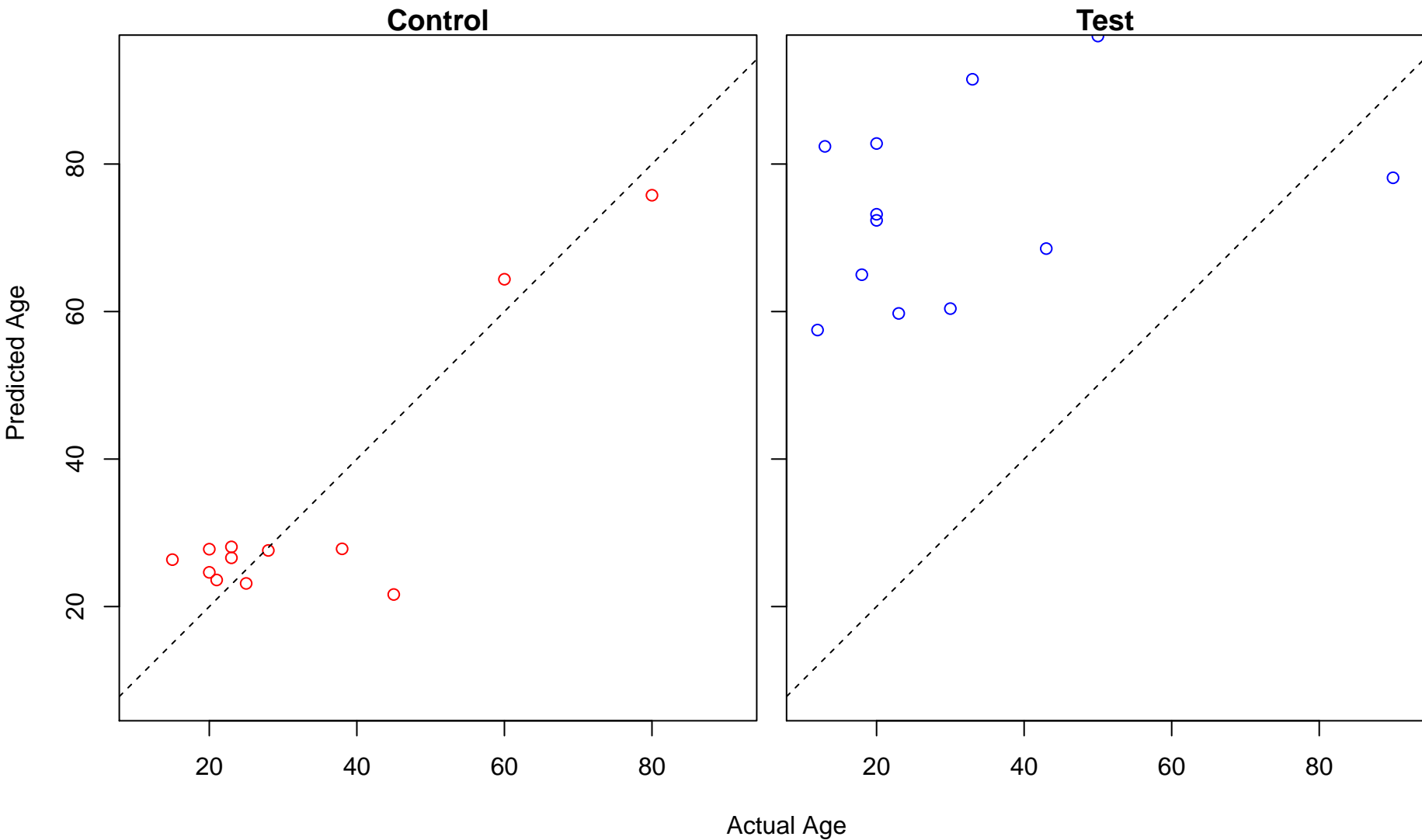
regulation of cellular response to hypoxia (Score: 11.625482)



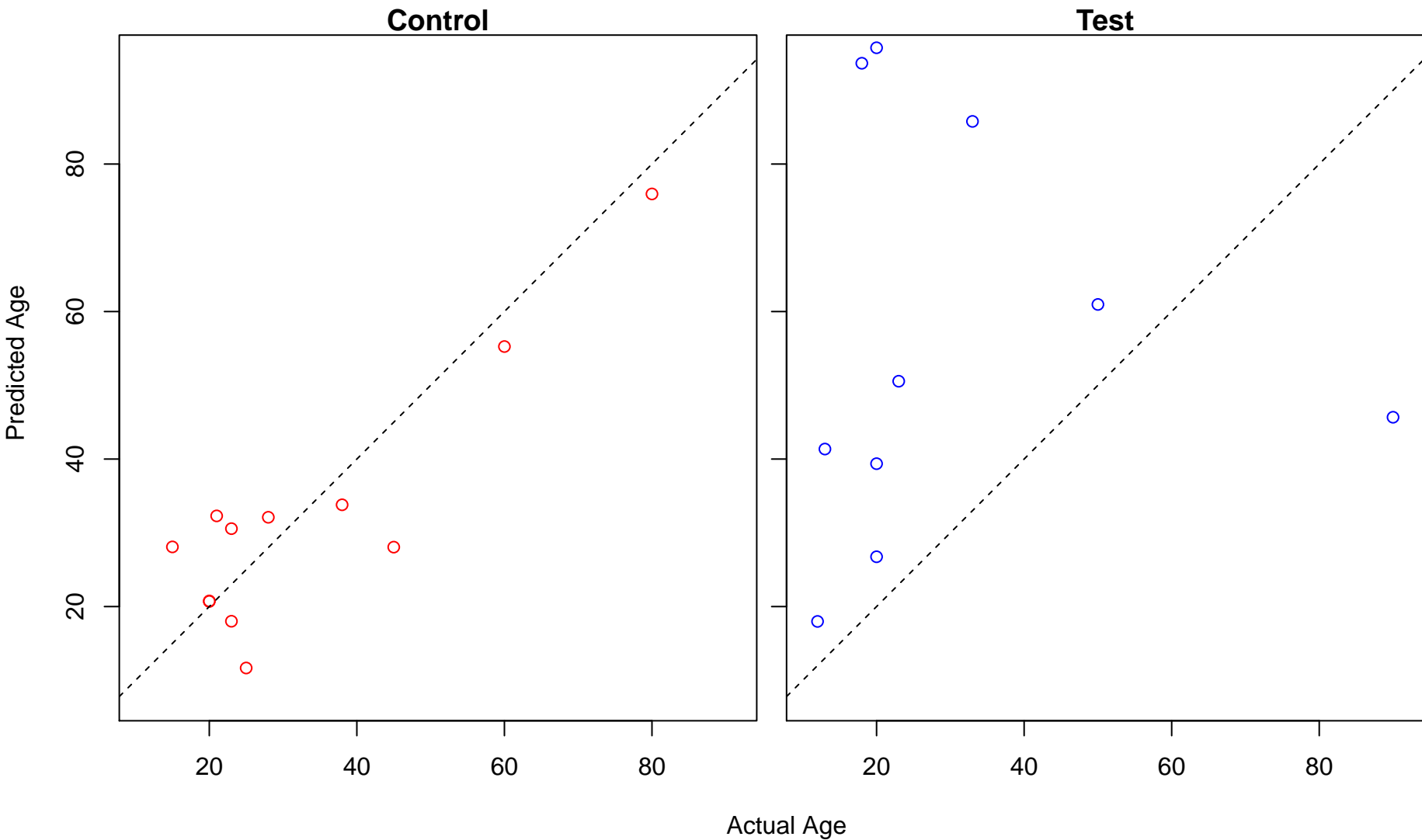
positive regulation of mitochondrial membrane permeability (Score: 11.620998)



neutrophil migration (Score: 11.615920)

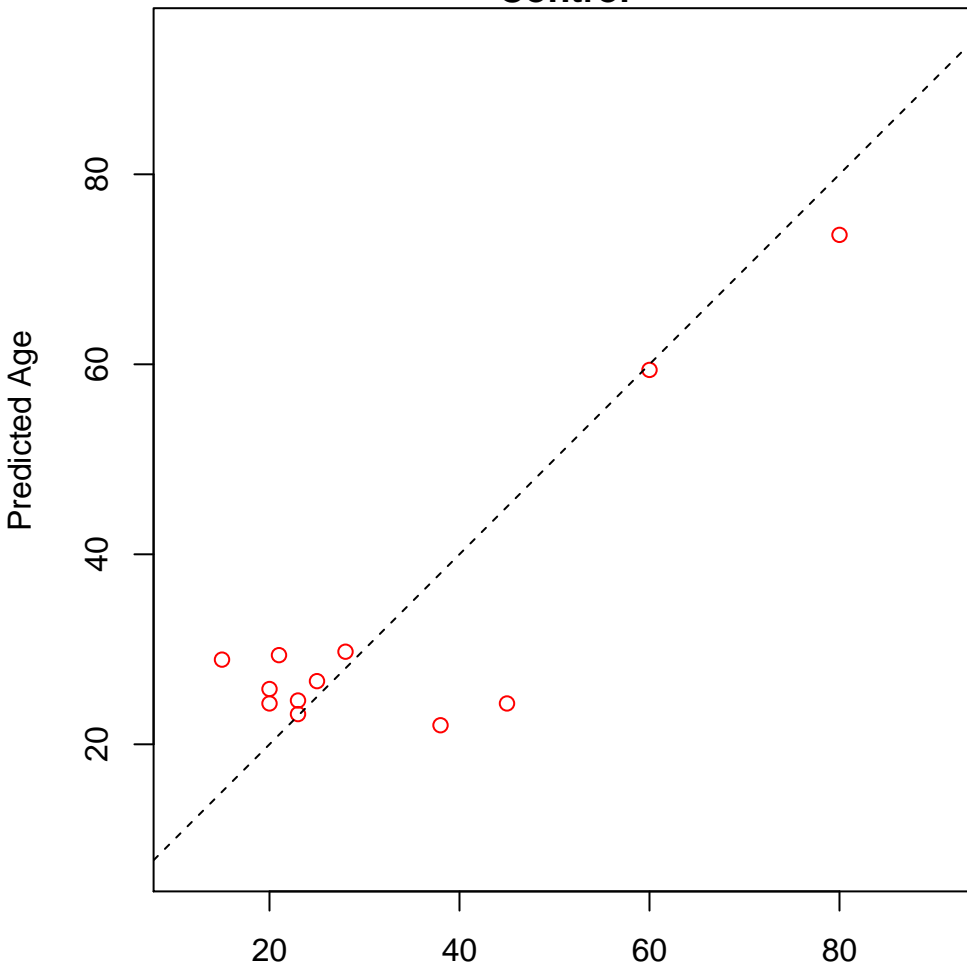


sensory organ development (Score: 11.614567)

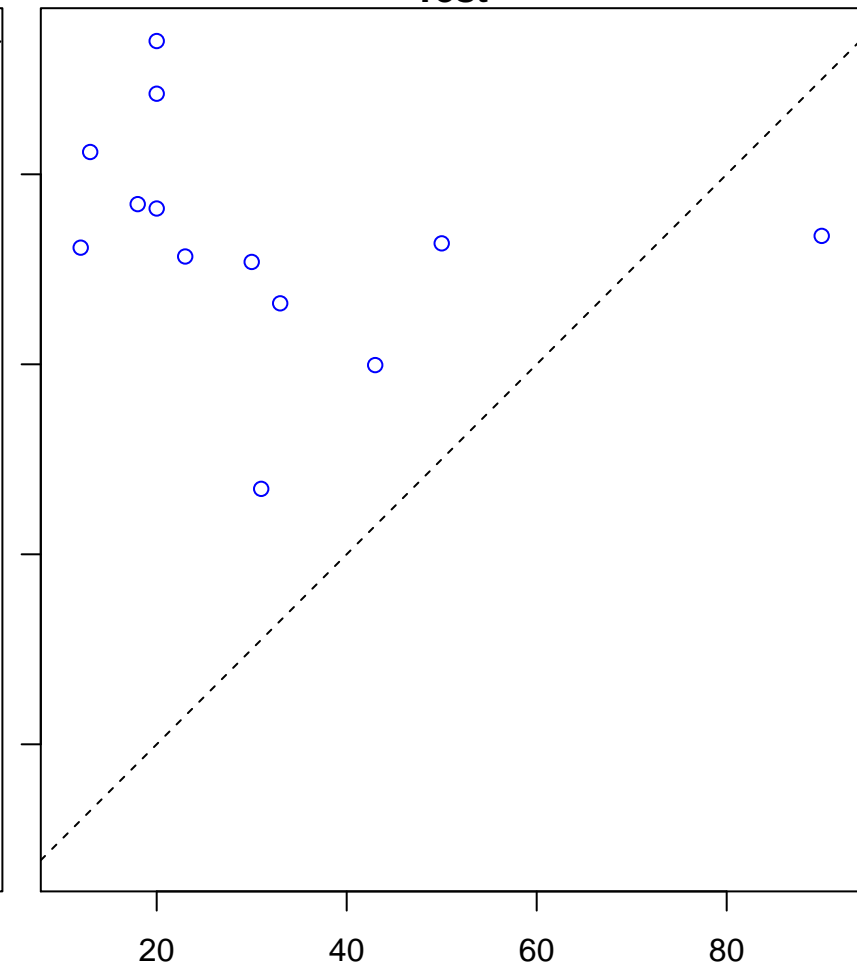


purine ribonucleotide catabolic process (Score: 11.614281)

Control

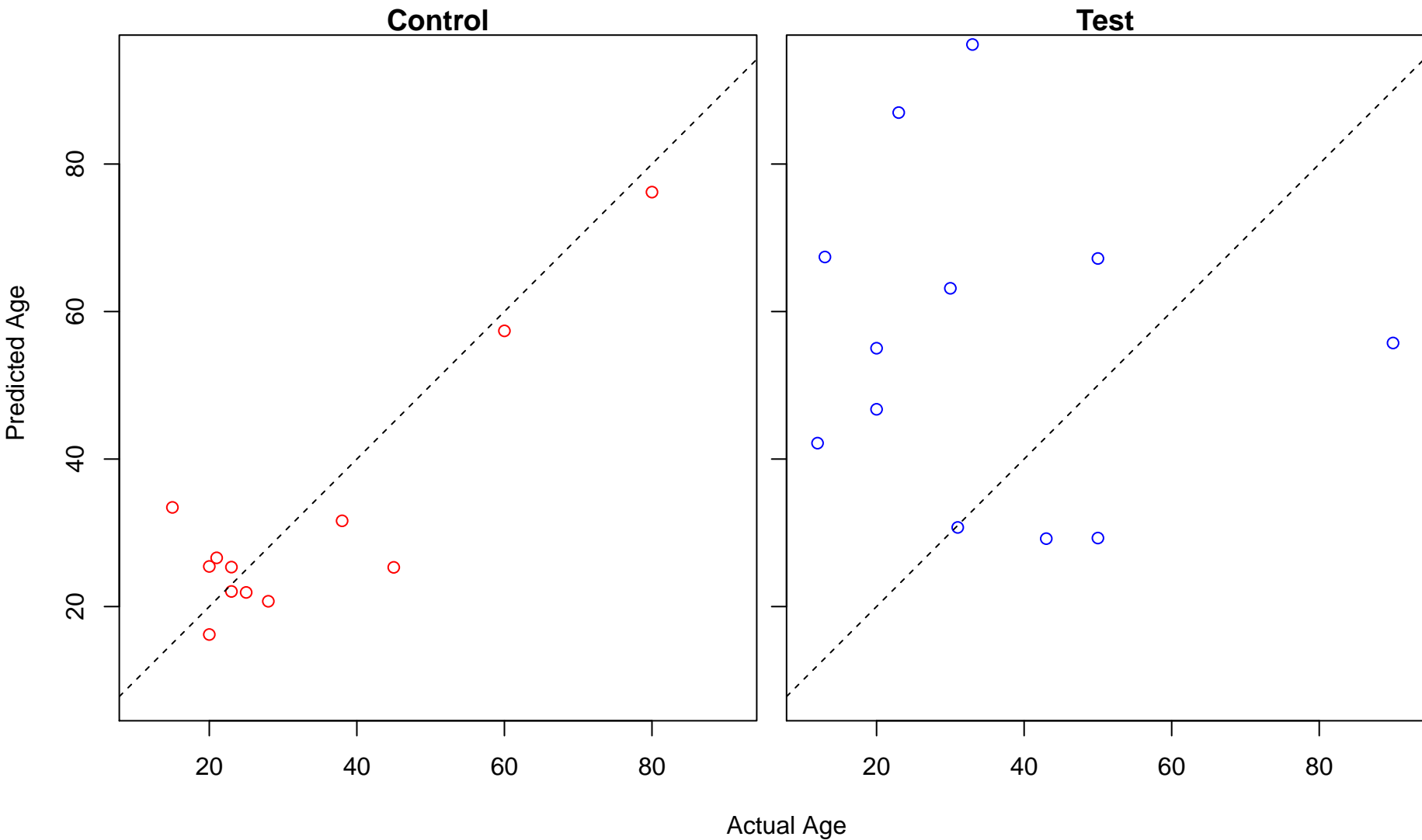


Test

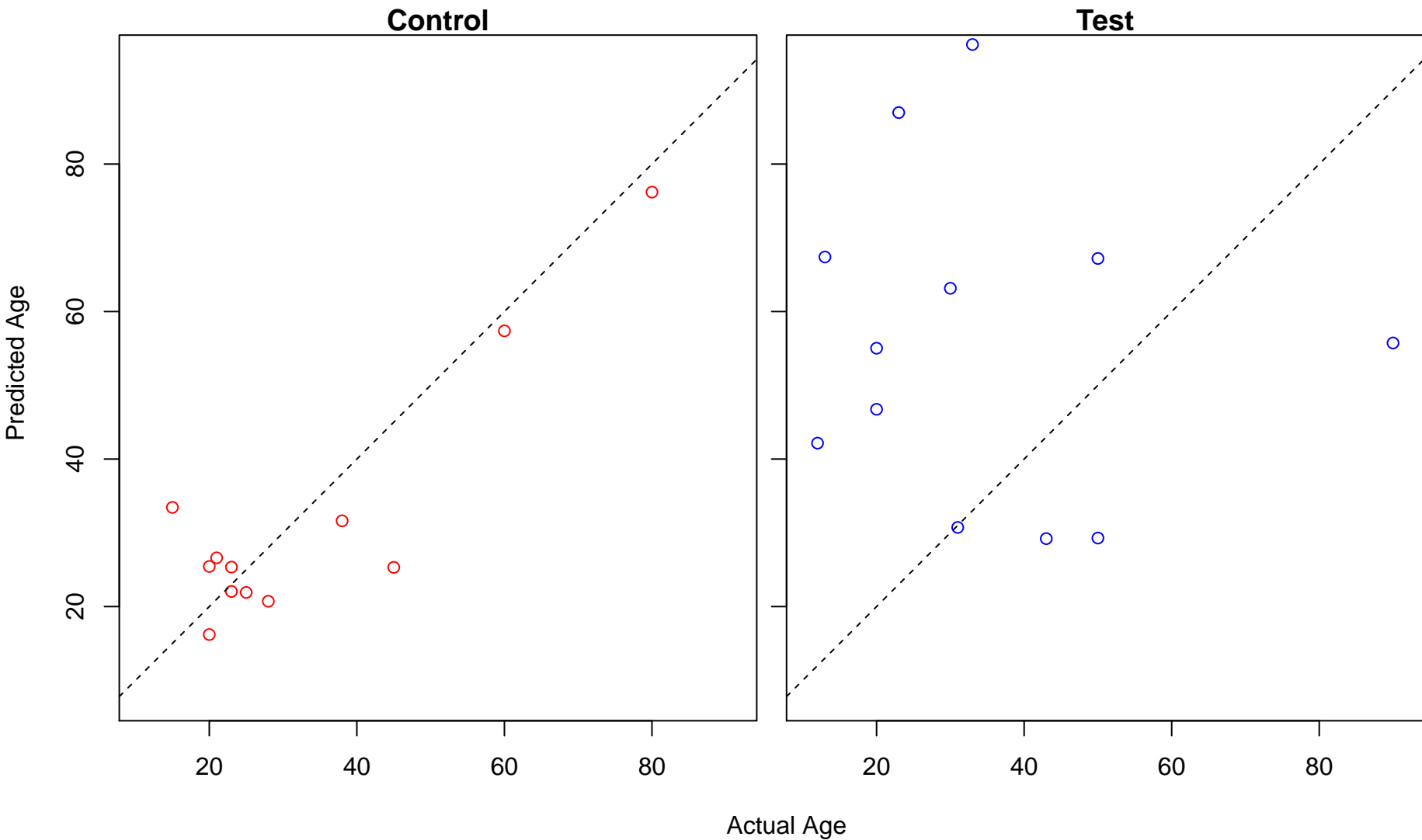


Actual Age

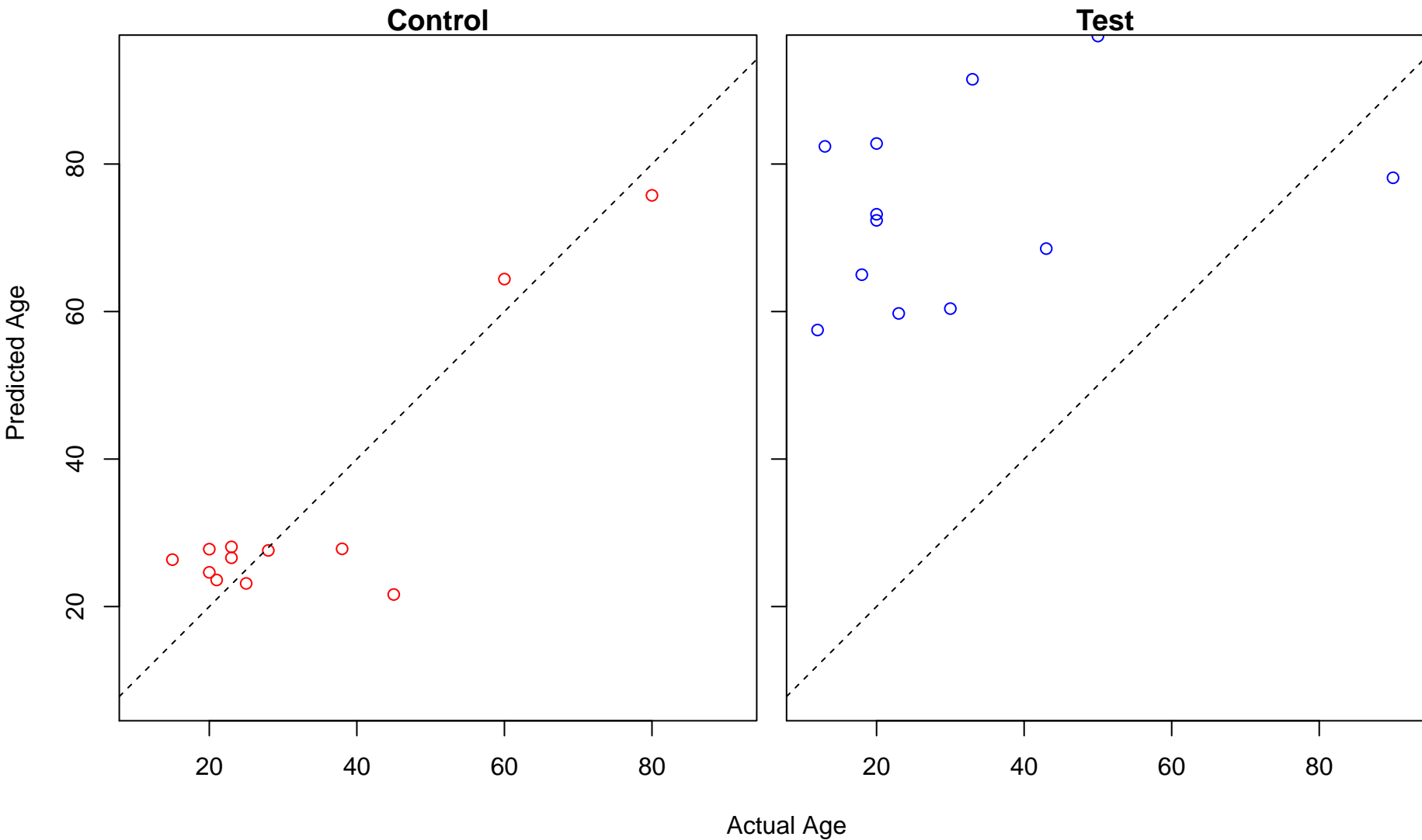
hexose transport (Score: 11.614014)



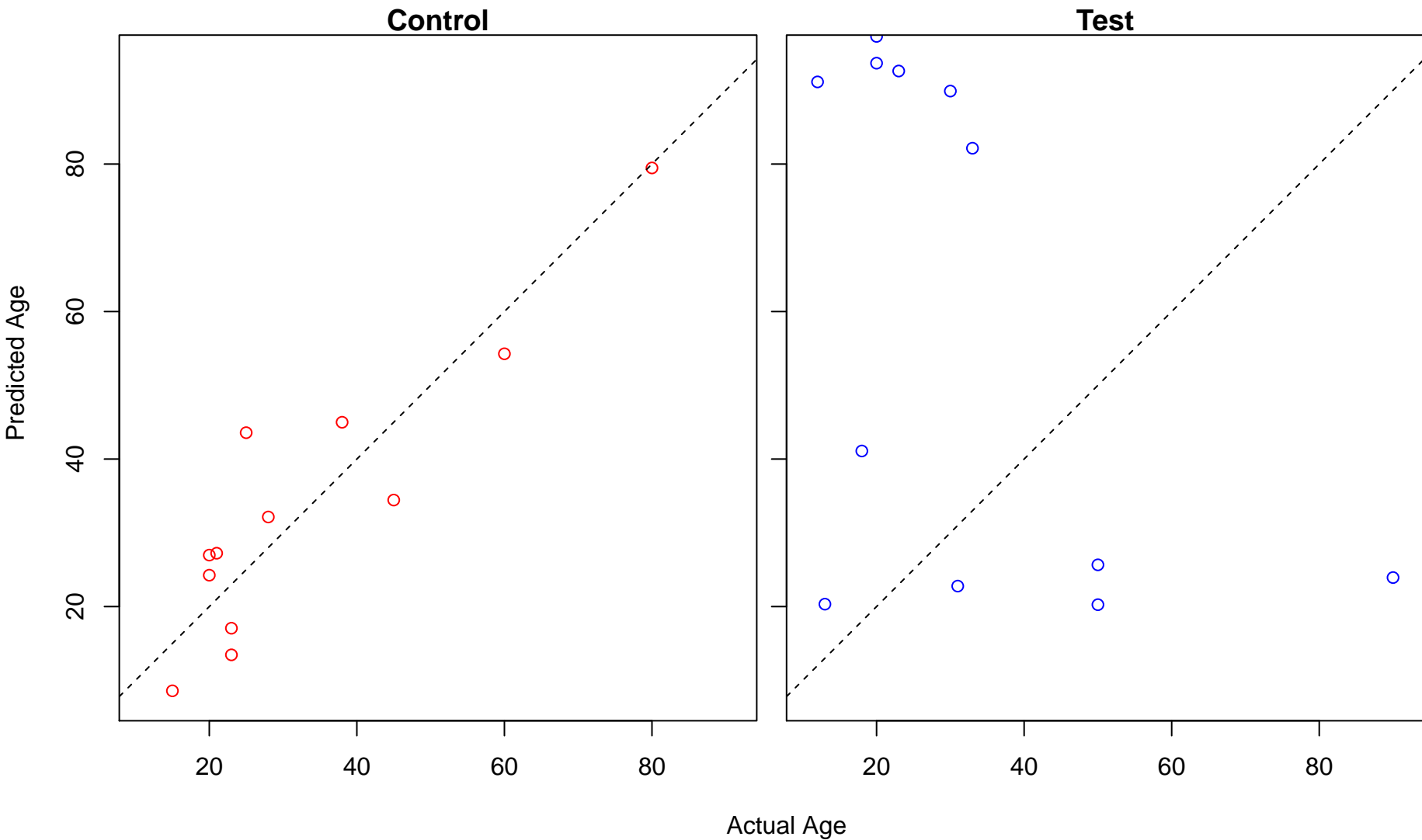
glucose transport (Score: 11.614014)



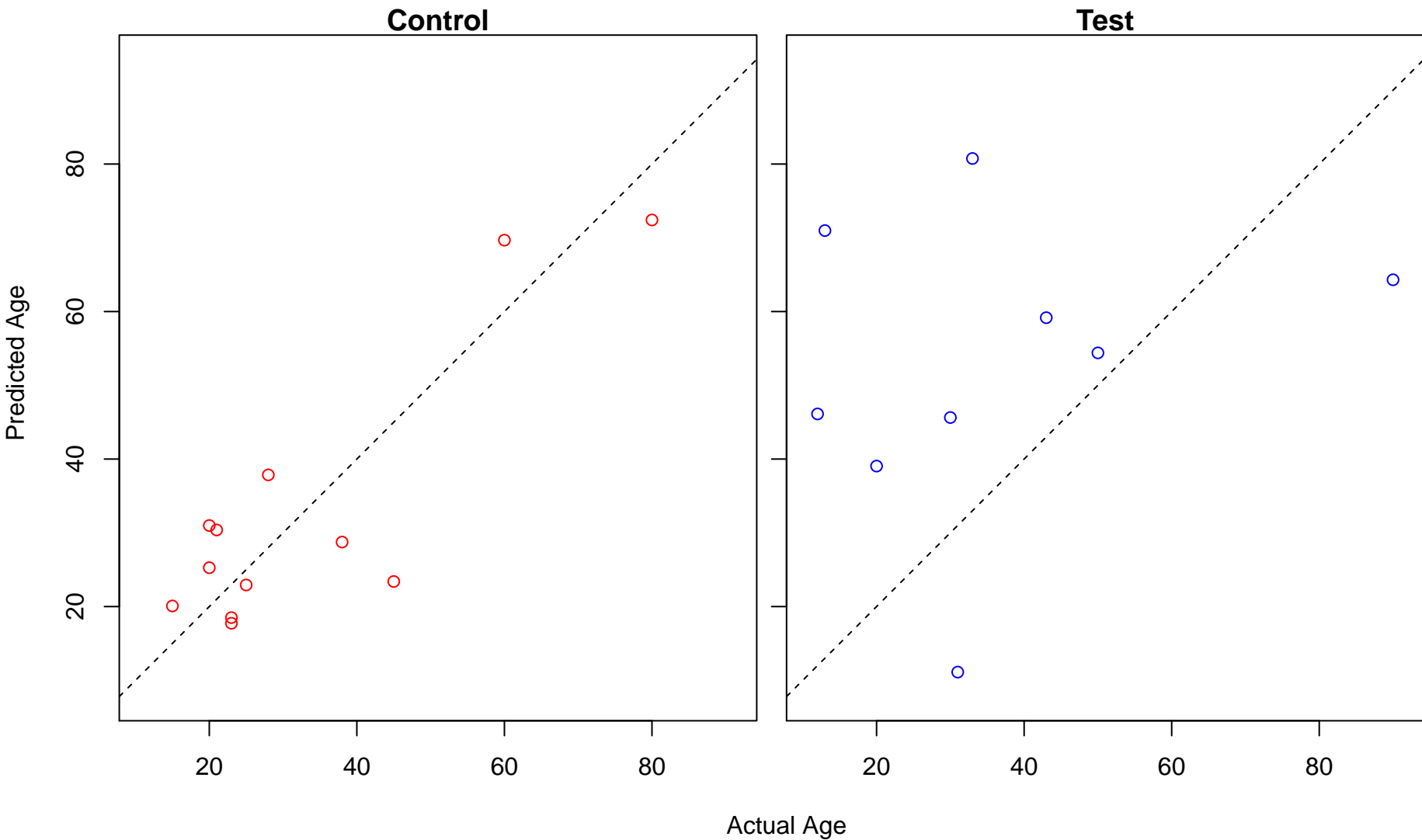
neutrophil chemotaxis (Score: 11.610433)



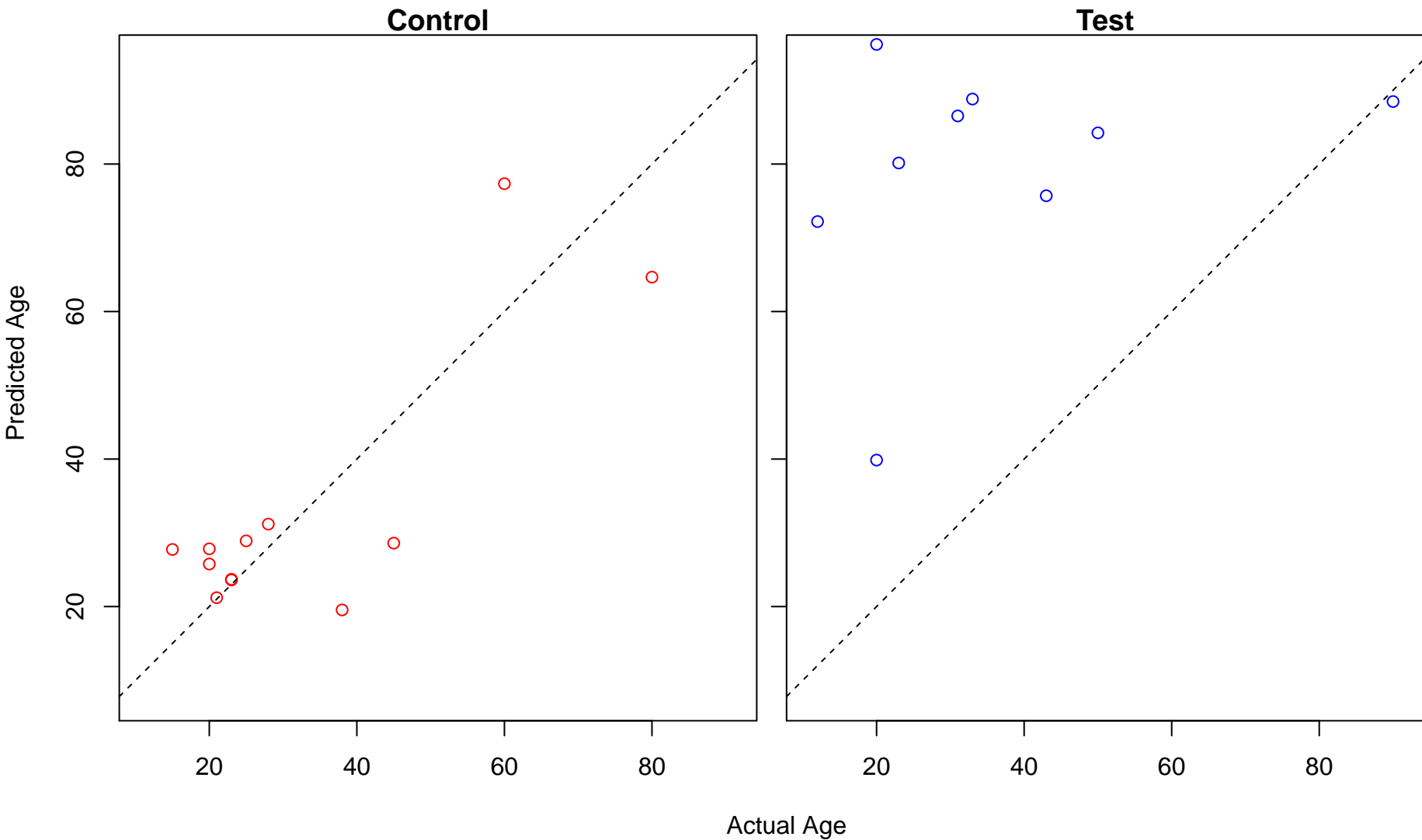
positive regulation of tyrosine phosphorylation of Stat1 protein (Score: 11.589753)



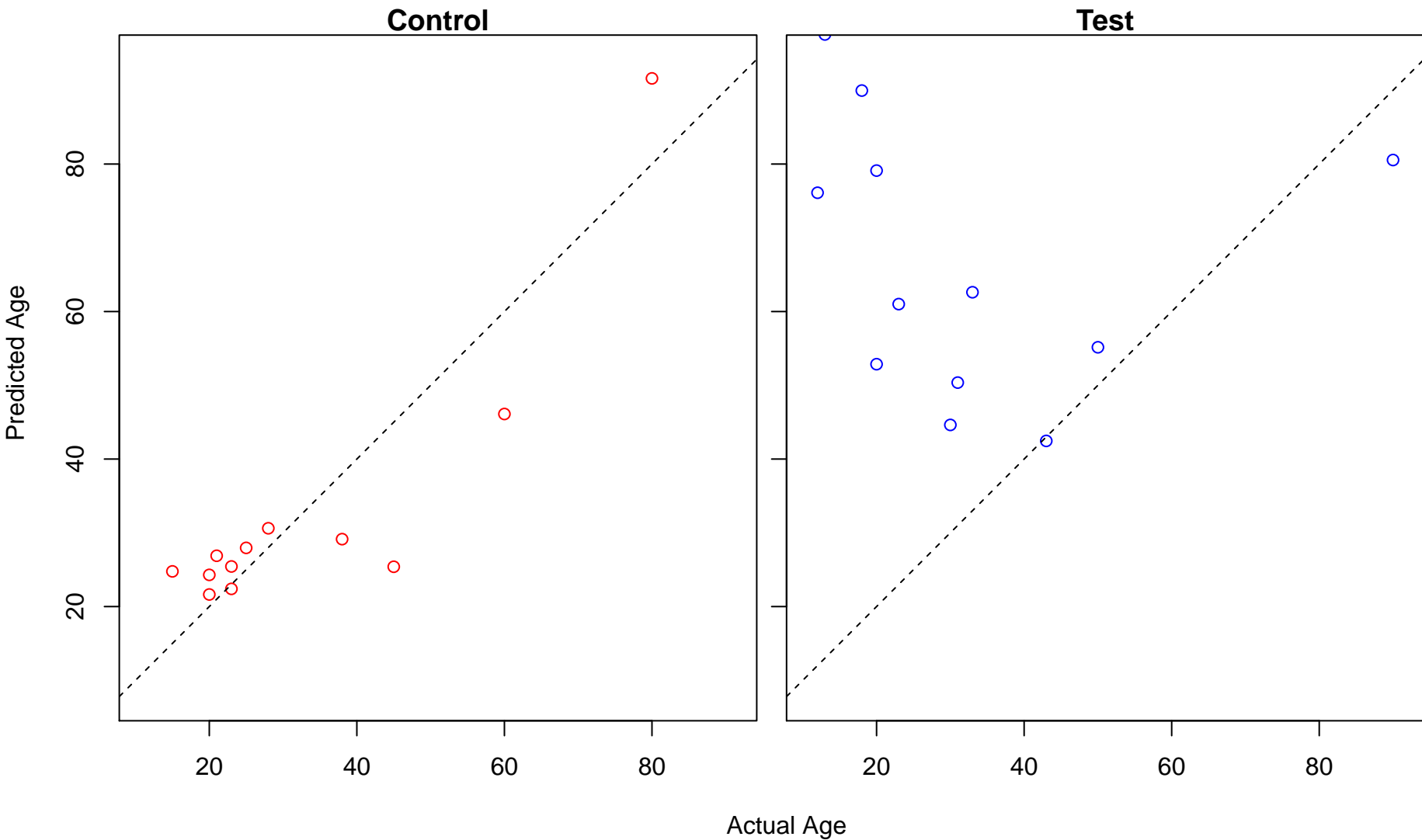
protein maturation (Score: 11.584941)



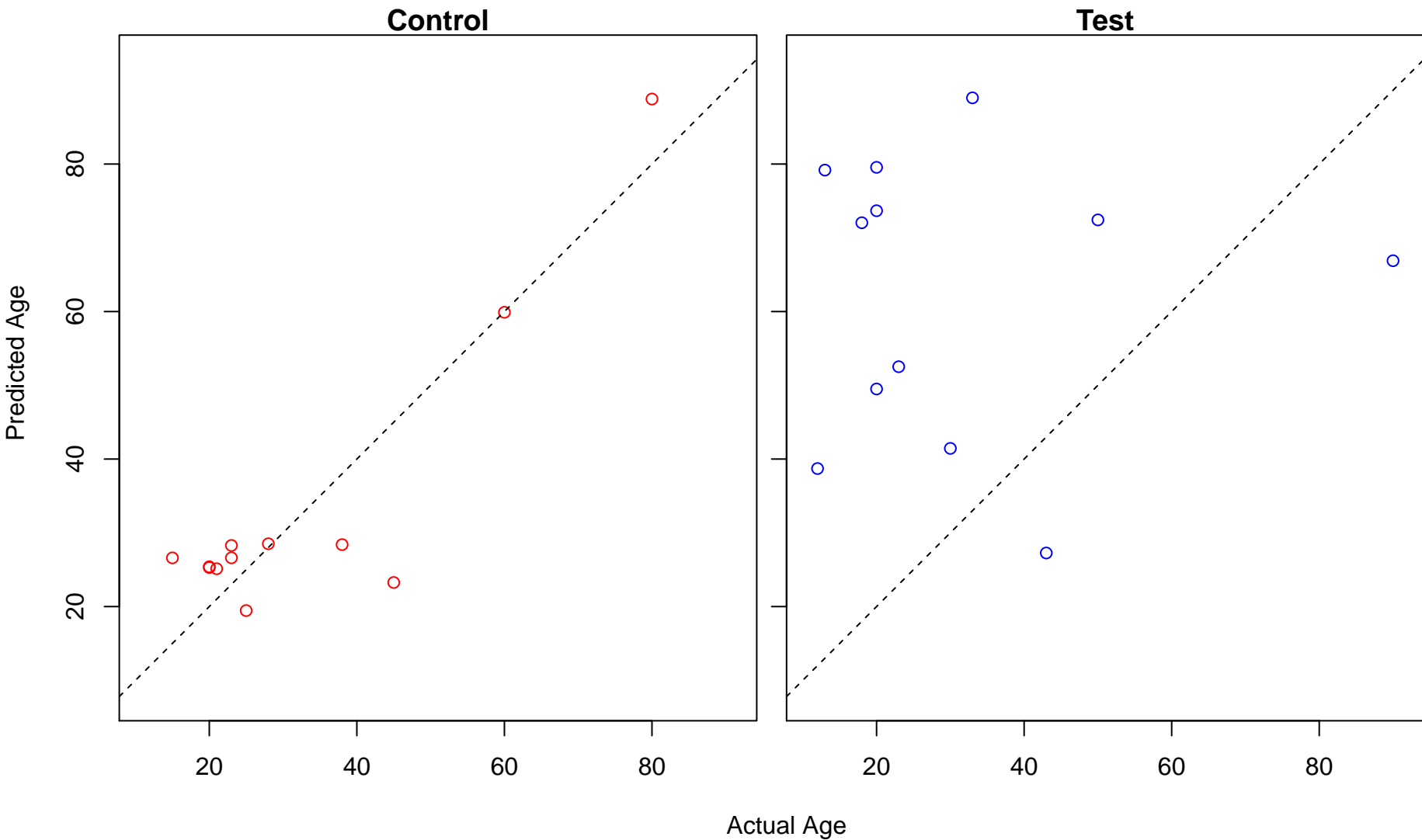
galactose catabolic process (Score: 11.584151)



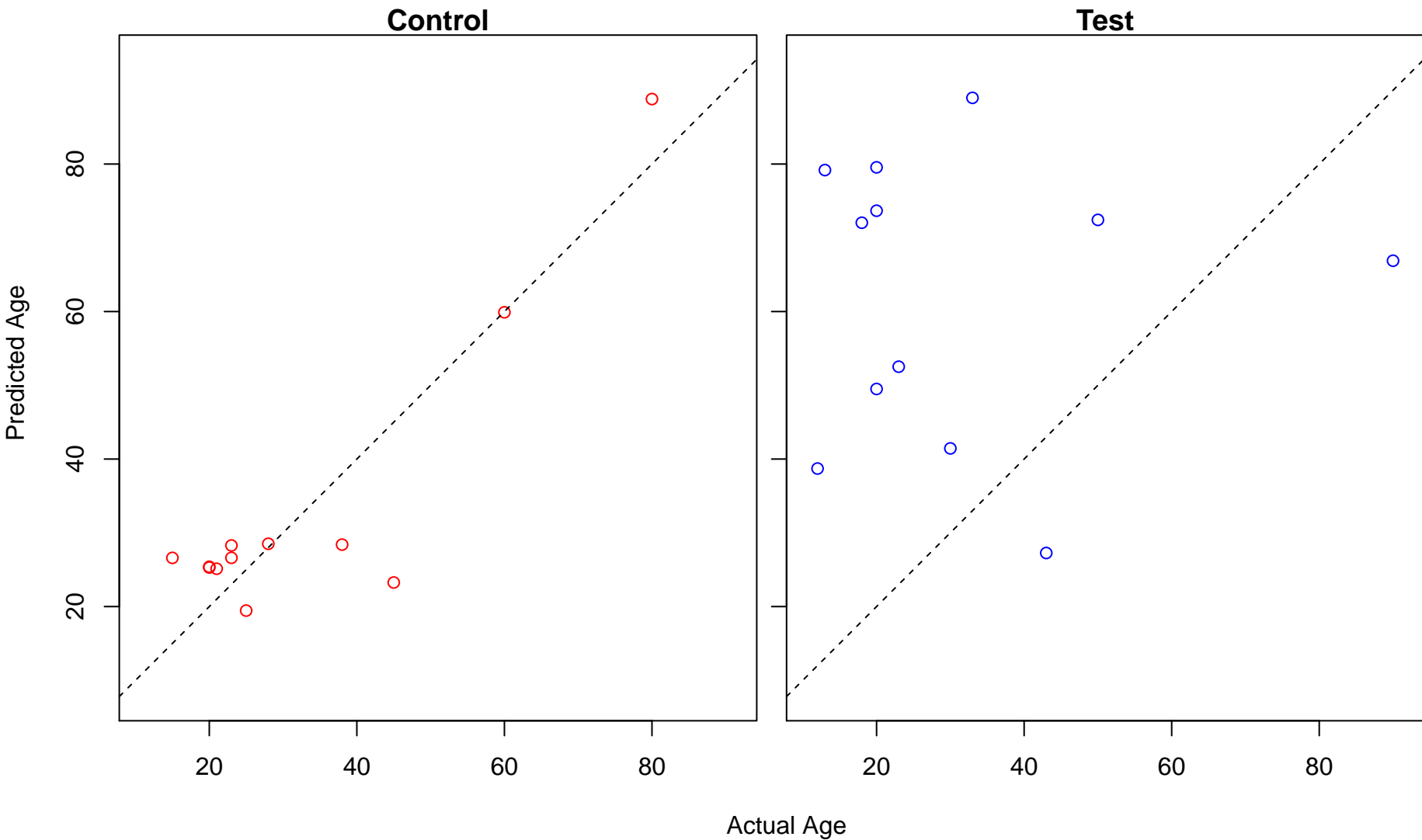
membrane protein proteolysis (Score: 11.561522)



eosinophil chemotaxis (Score: 11.552142)

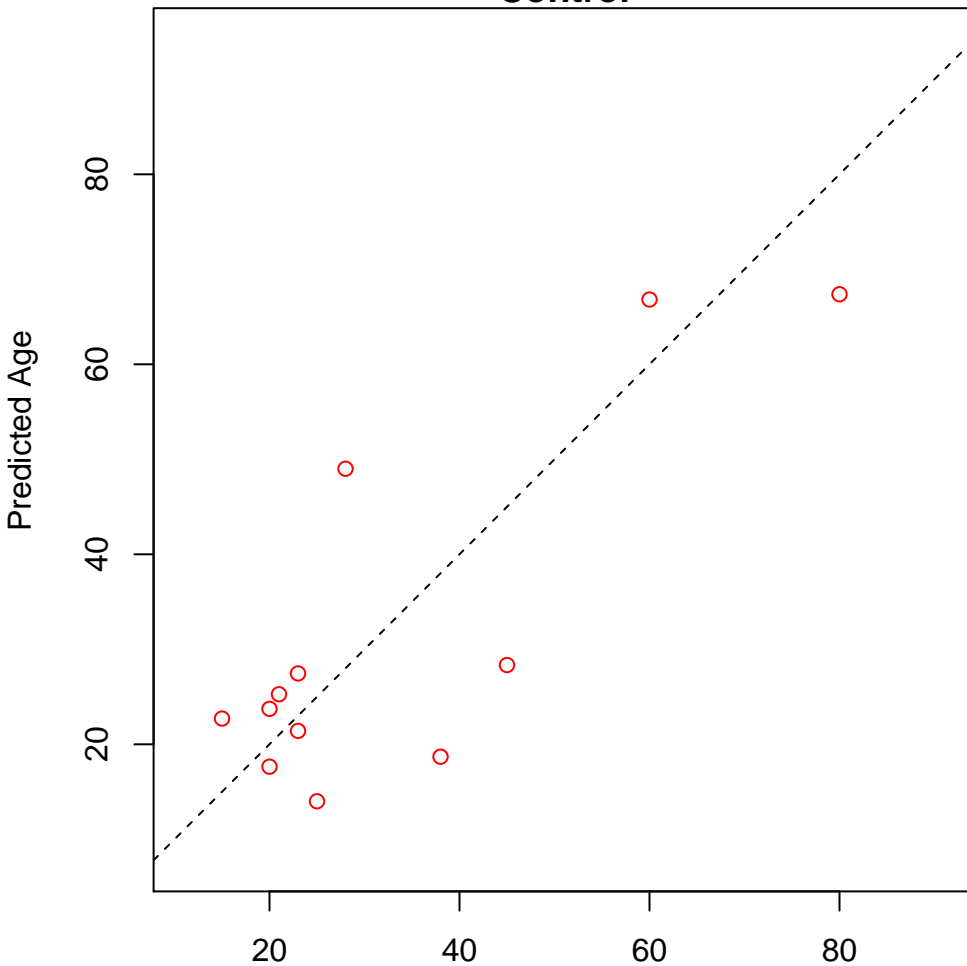


eosinophil migration (Score: 11.552142)

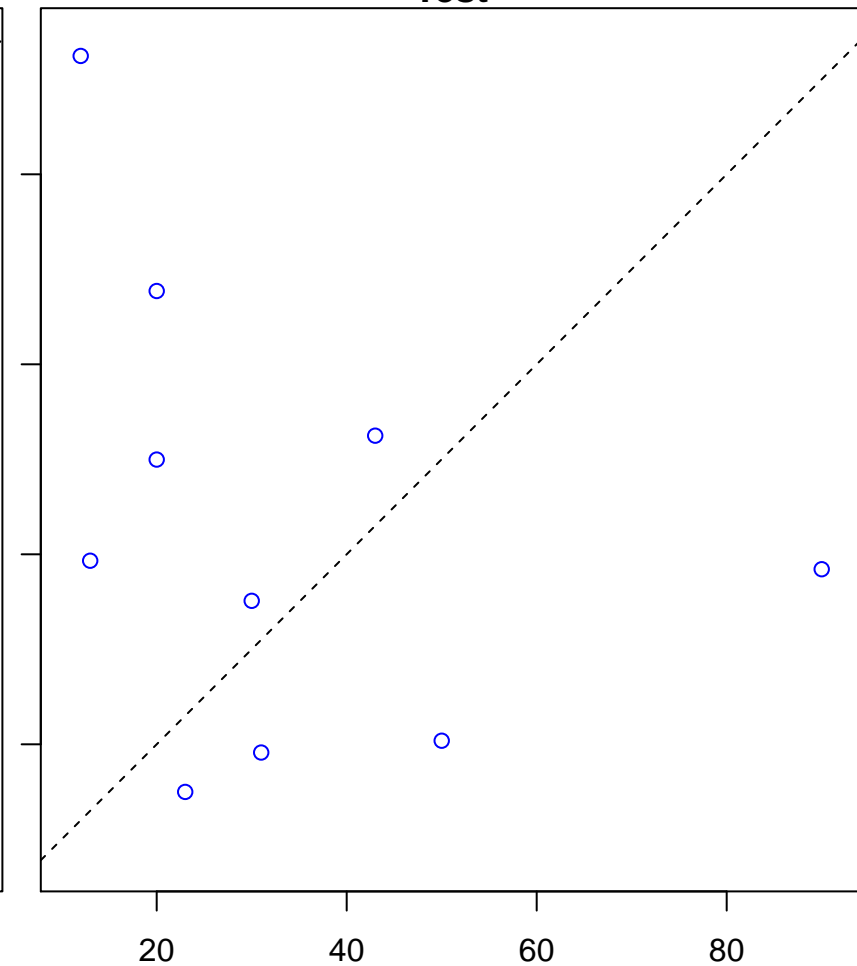


activation of protein kinase B activity (Score: 11.550127)

Control

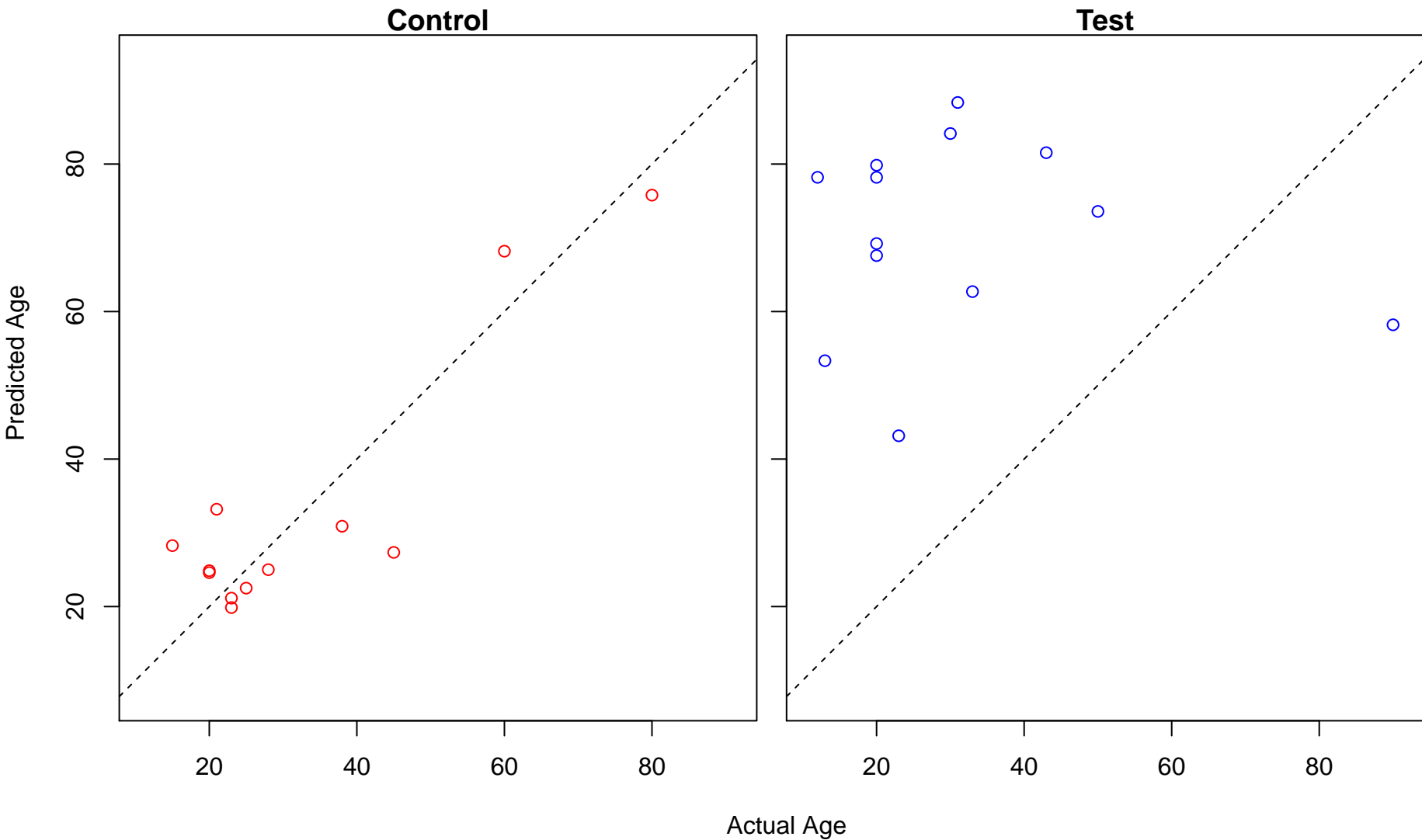


Test

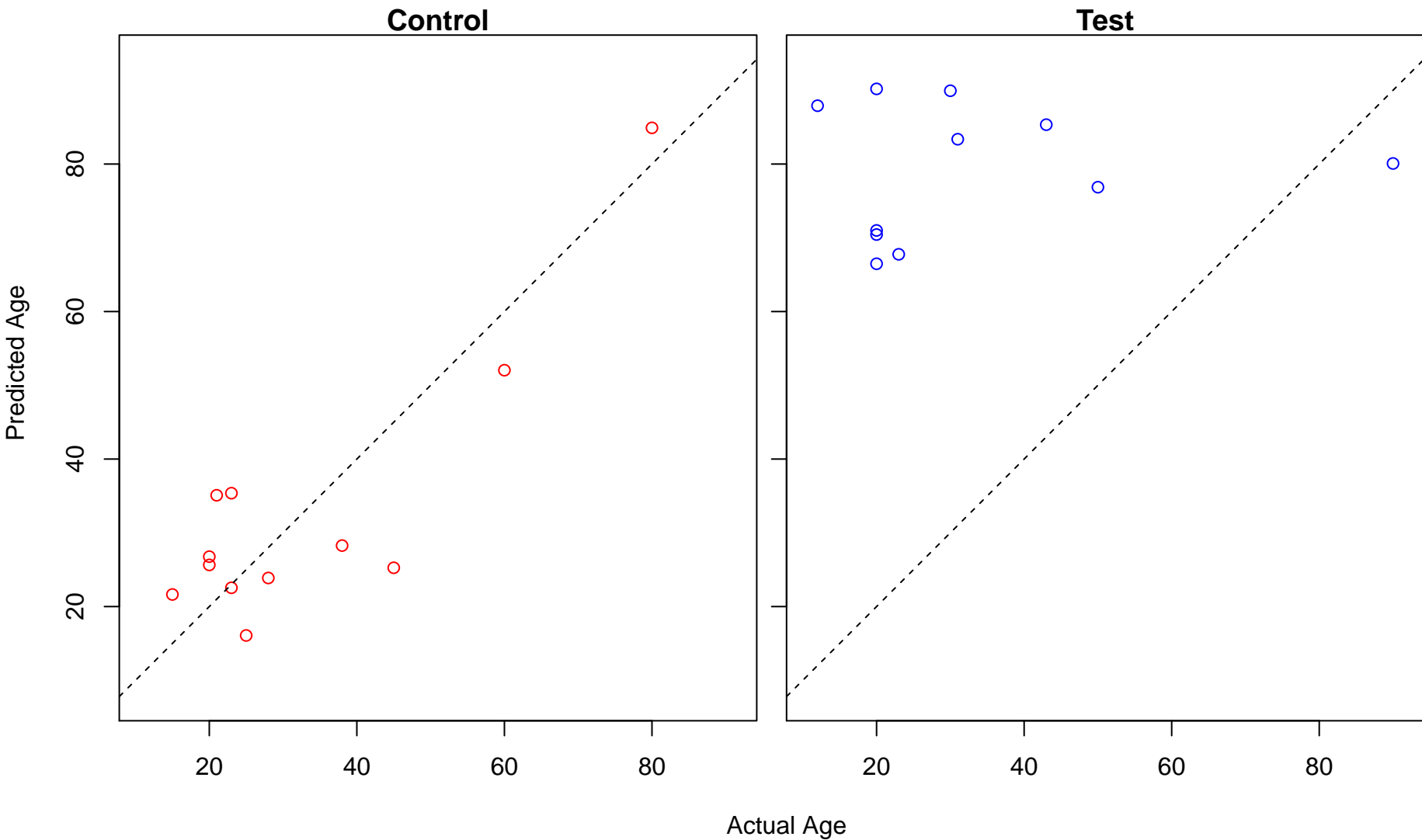


Actual Age

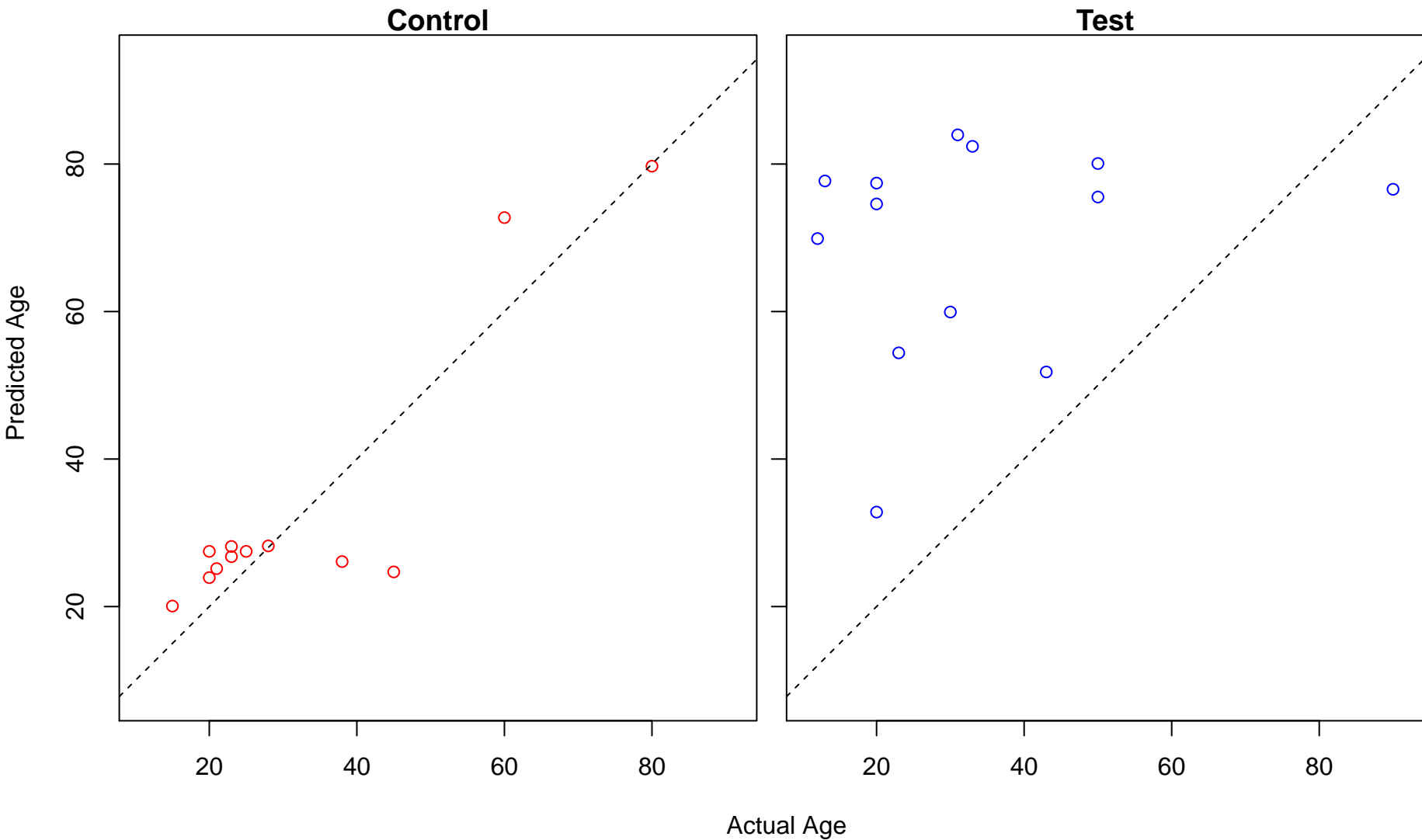
negative regulation of locomotion (Score: 11.528465)



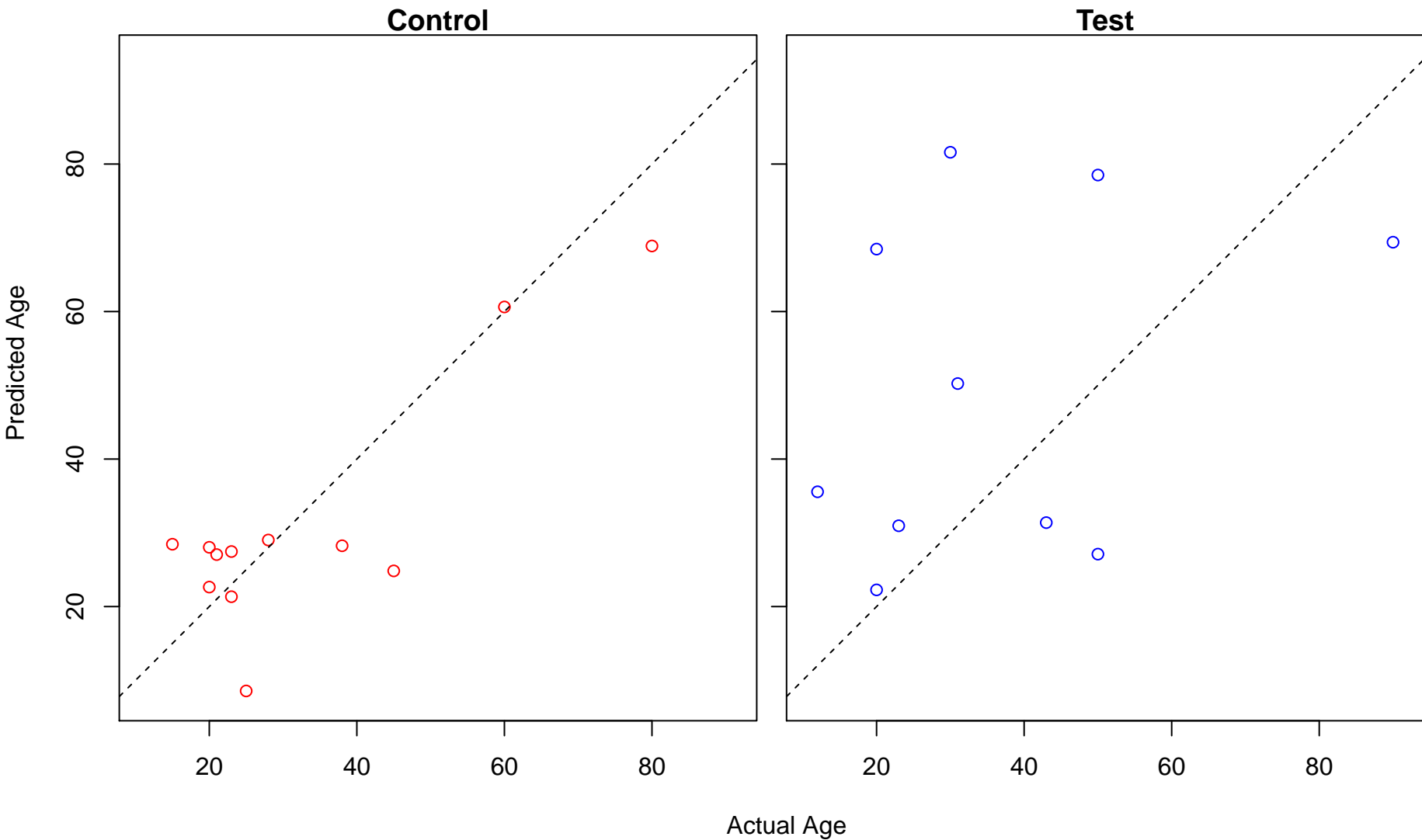
phospholipid homeostasis (Score: 11.510651)



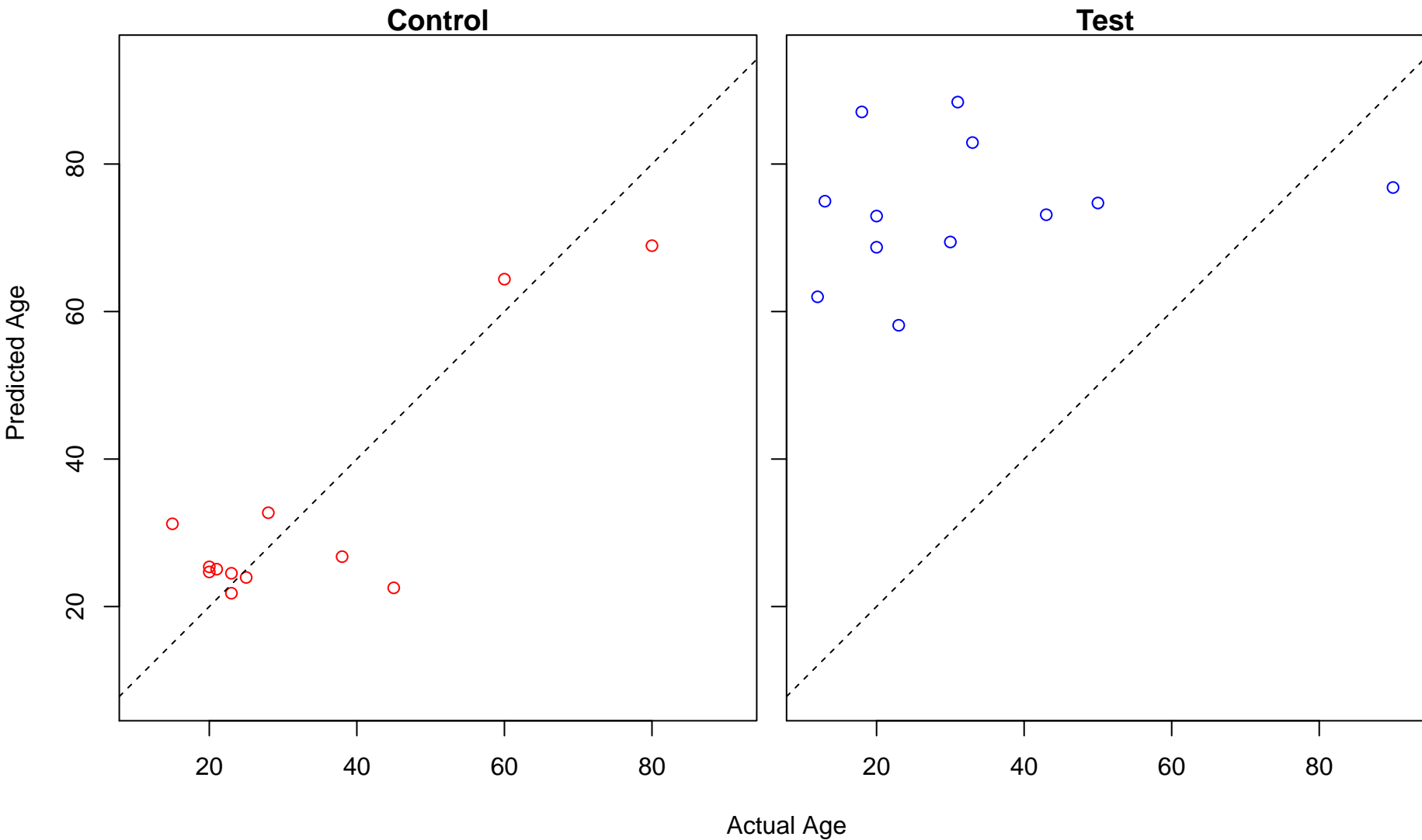
positive regulation of developmental growth (Score: 11.505369)



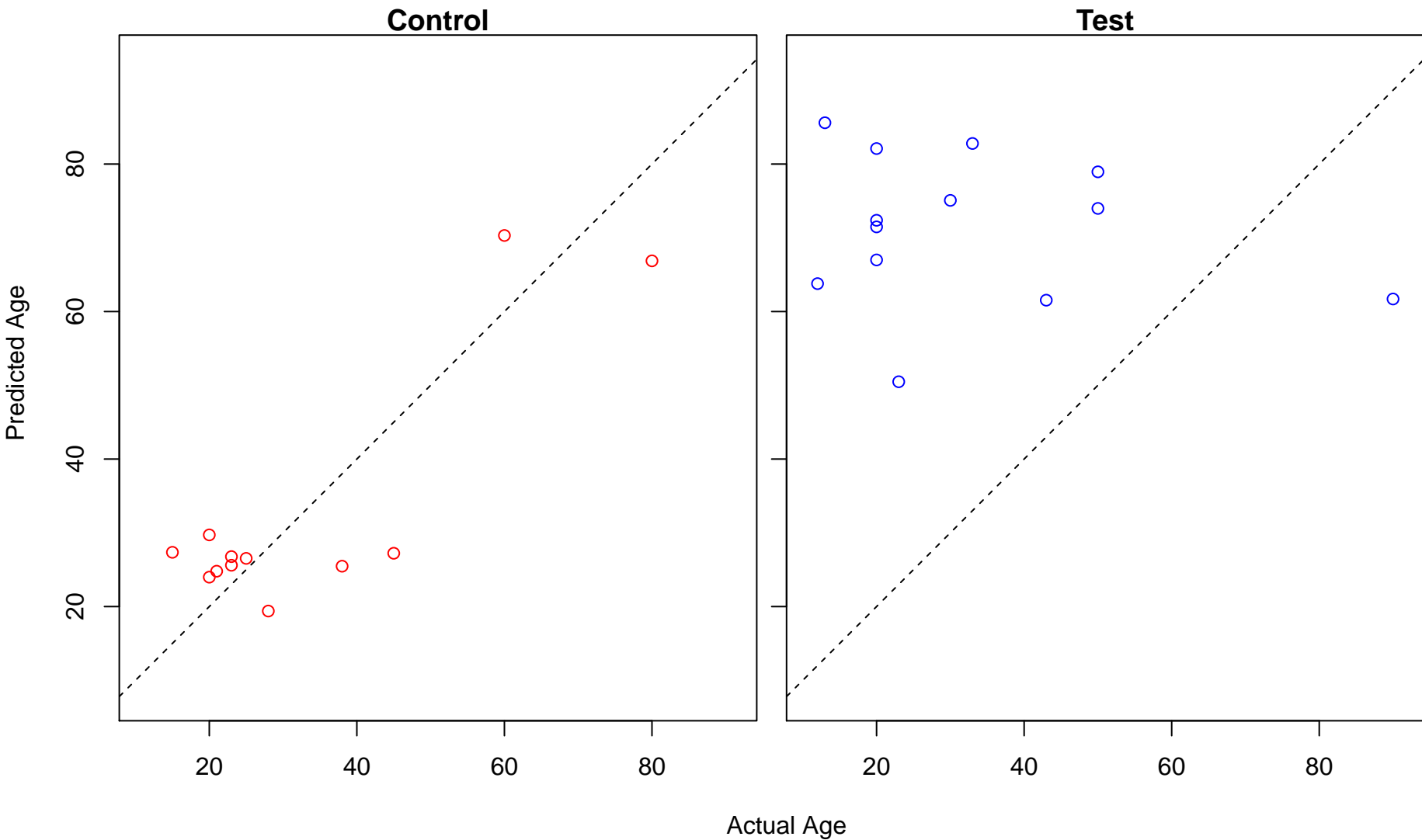
chromosome segregation (Score: 11.486936)



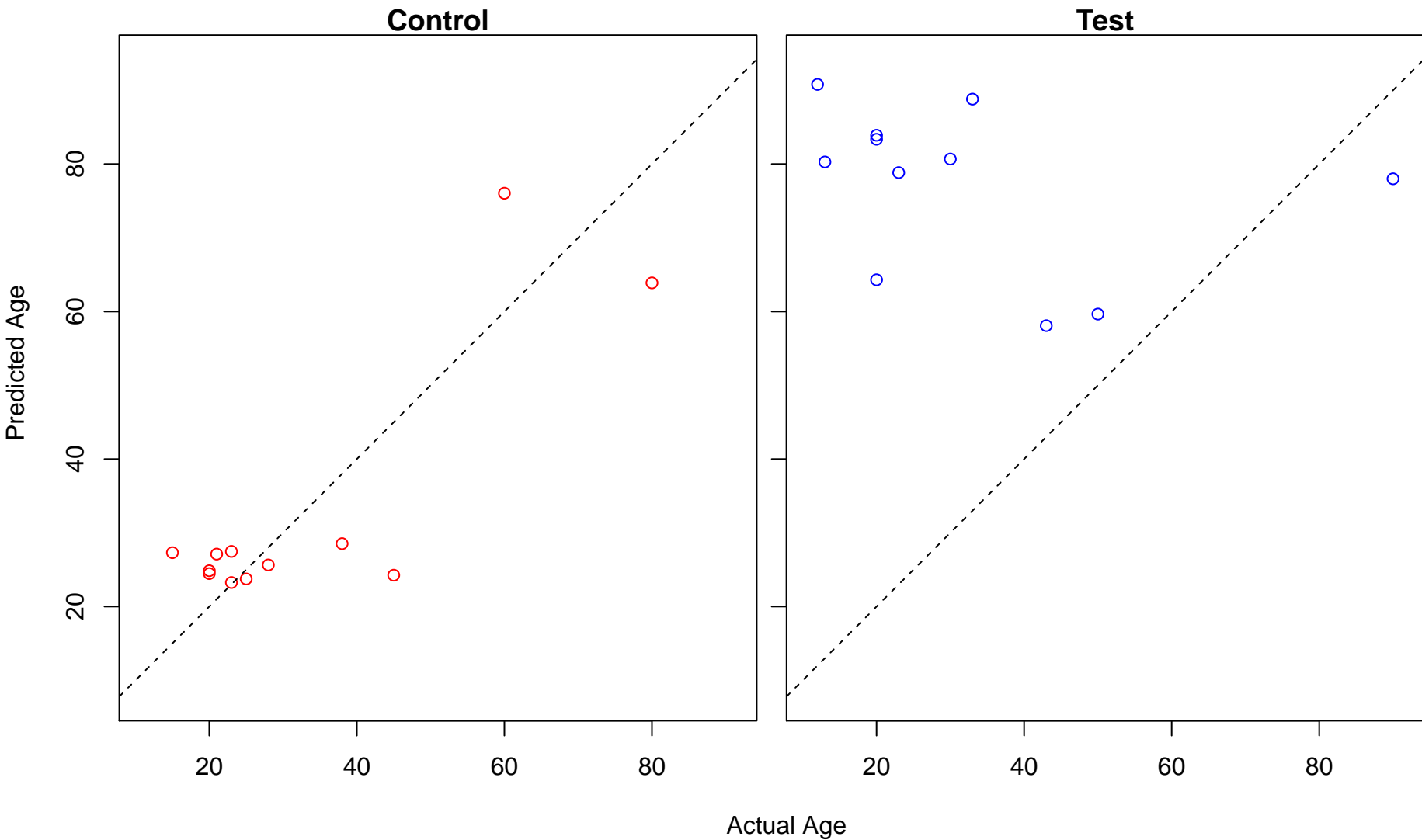
regulation of chromatin binding (Score: 11.480929)



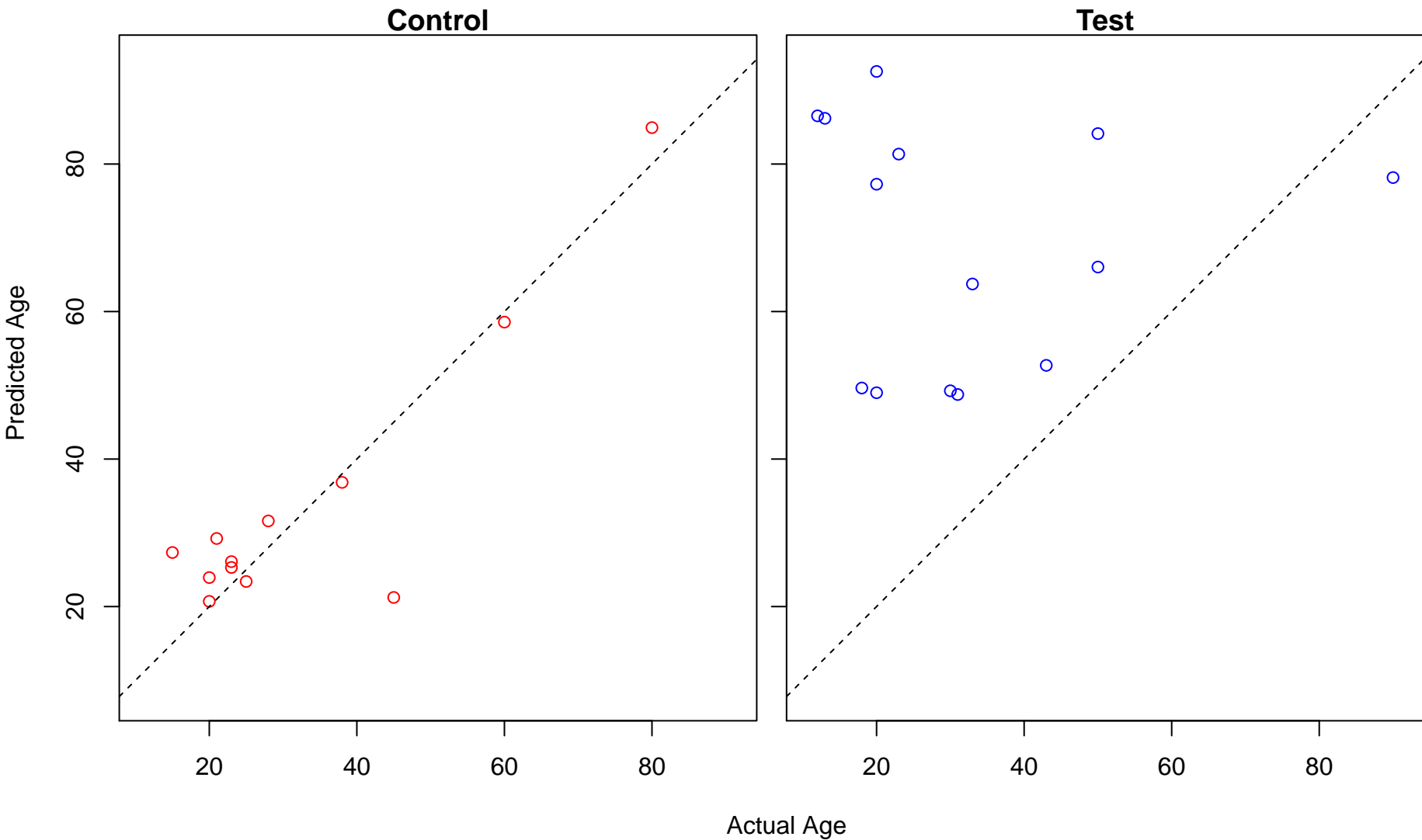
regulation of endocytic recycling (Score: 11.480199)



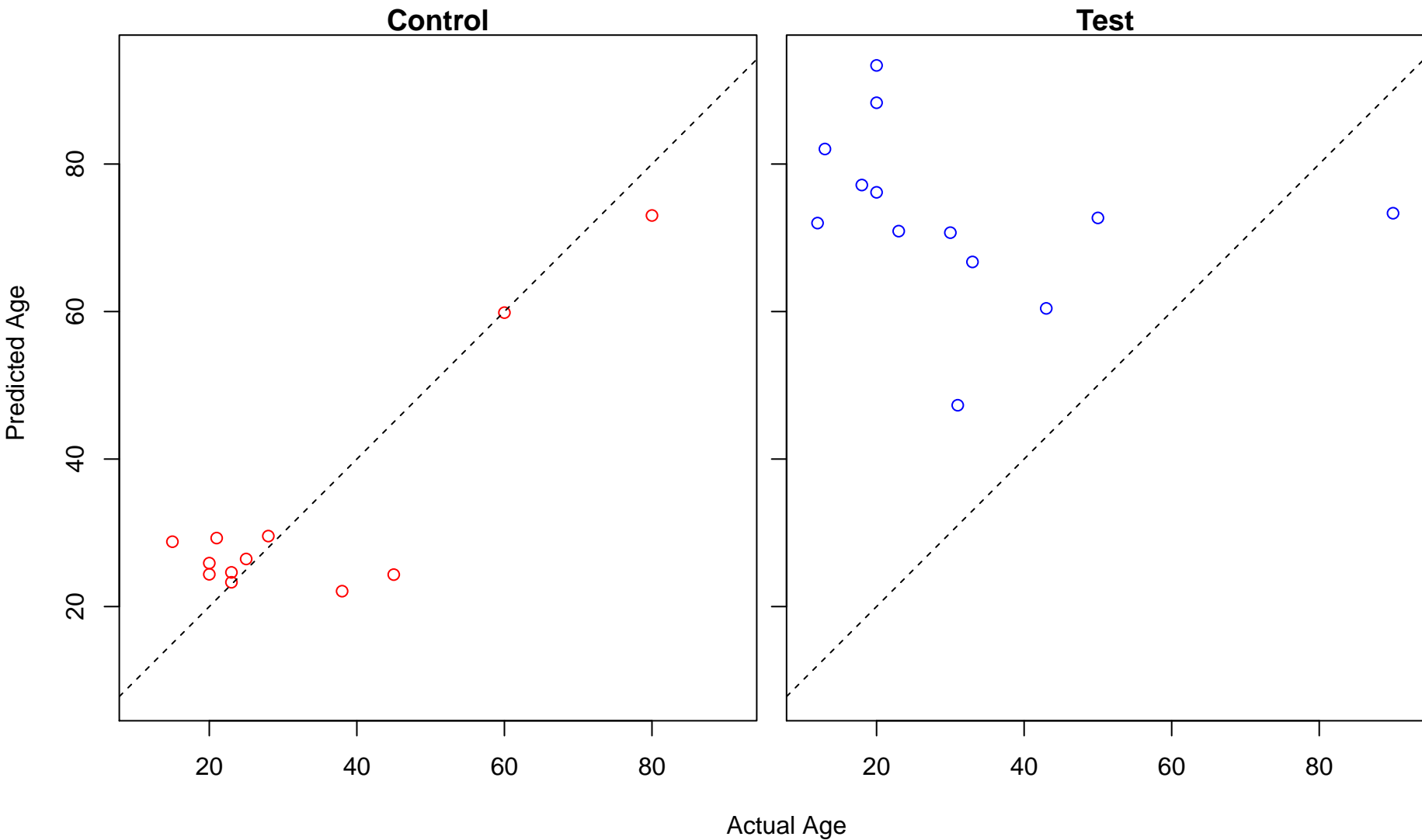
acute inflammatory response (Score: 11.478697)



morphogenesis of a branching structure (Score: 11.478288)

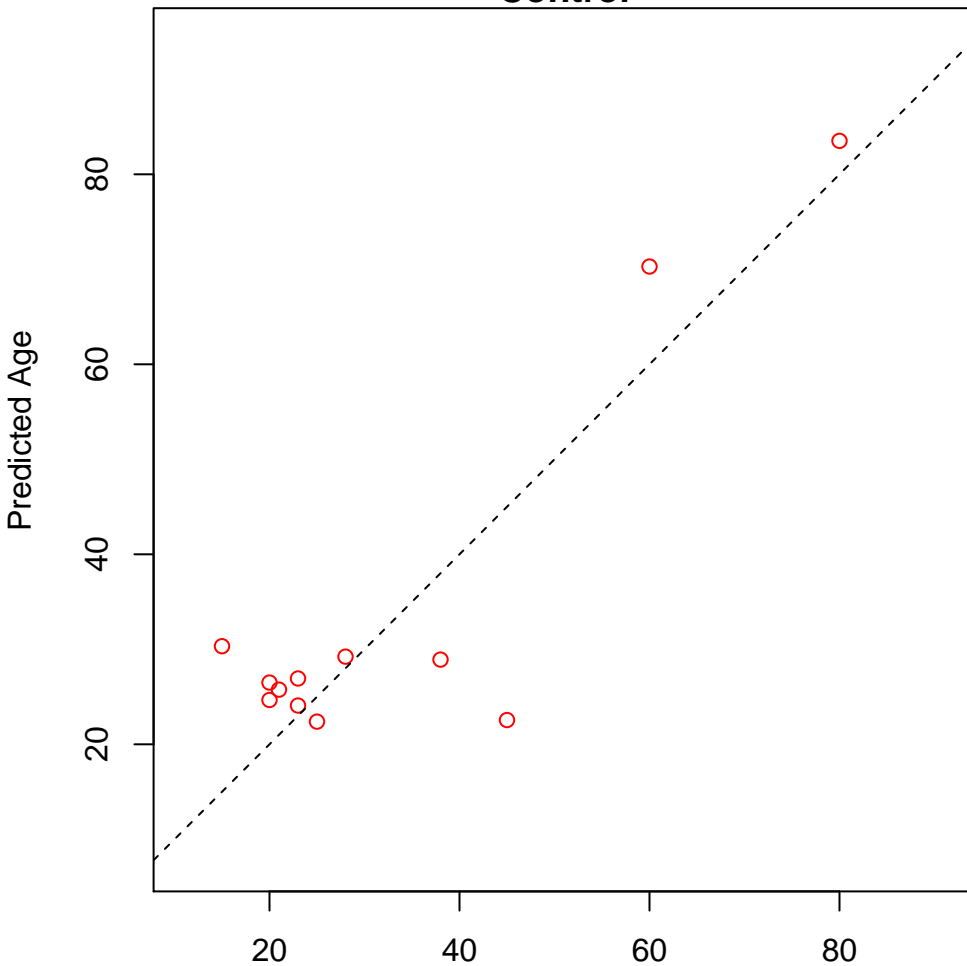


ribonucleotide catabolic process (Score: 11.474645)

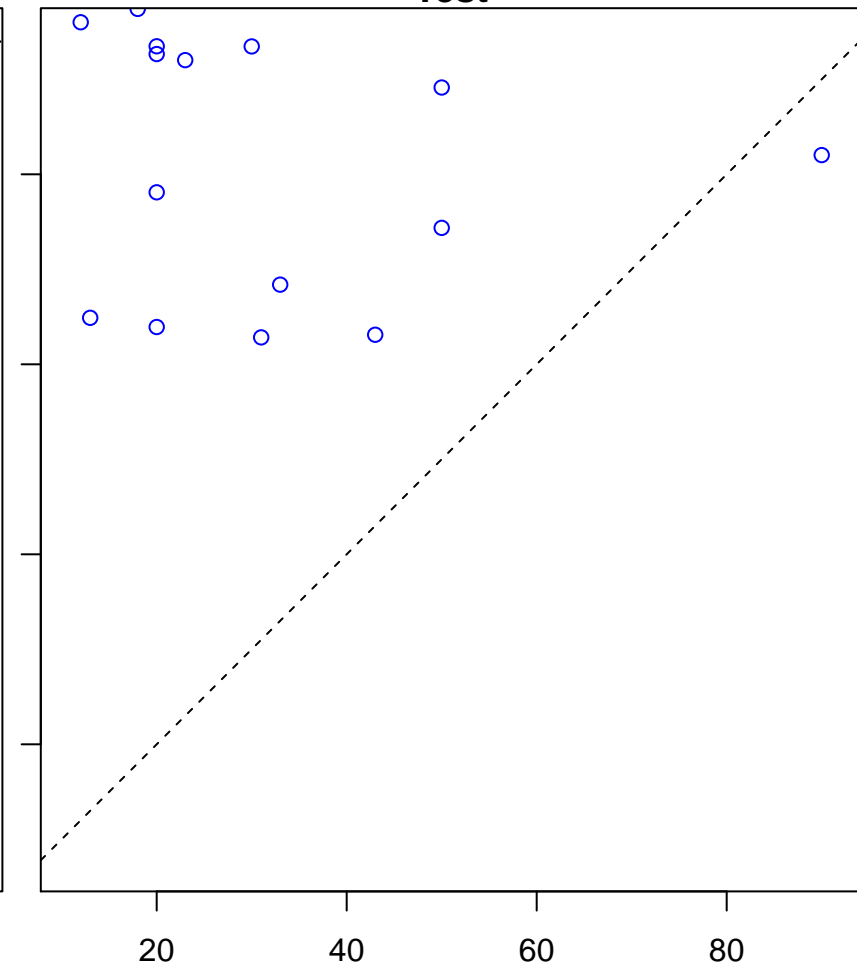


mitotic nuclear envelope reassembly (Score: 11.458390)

Control

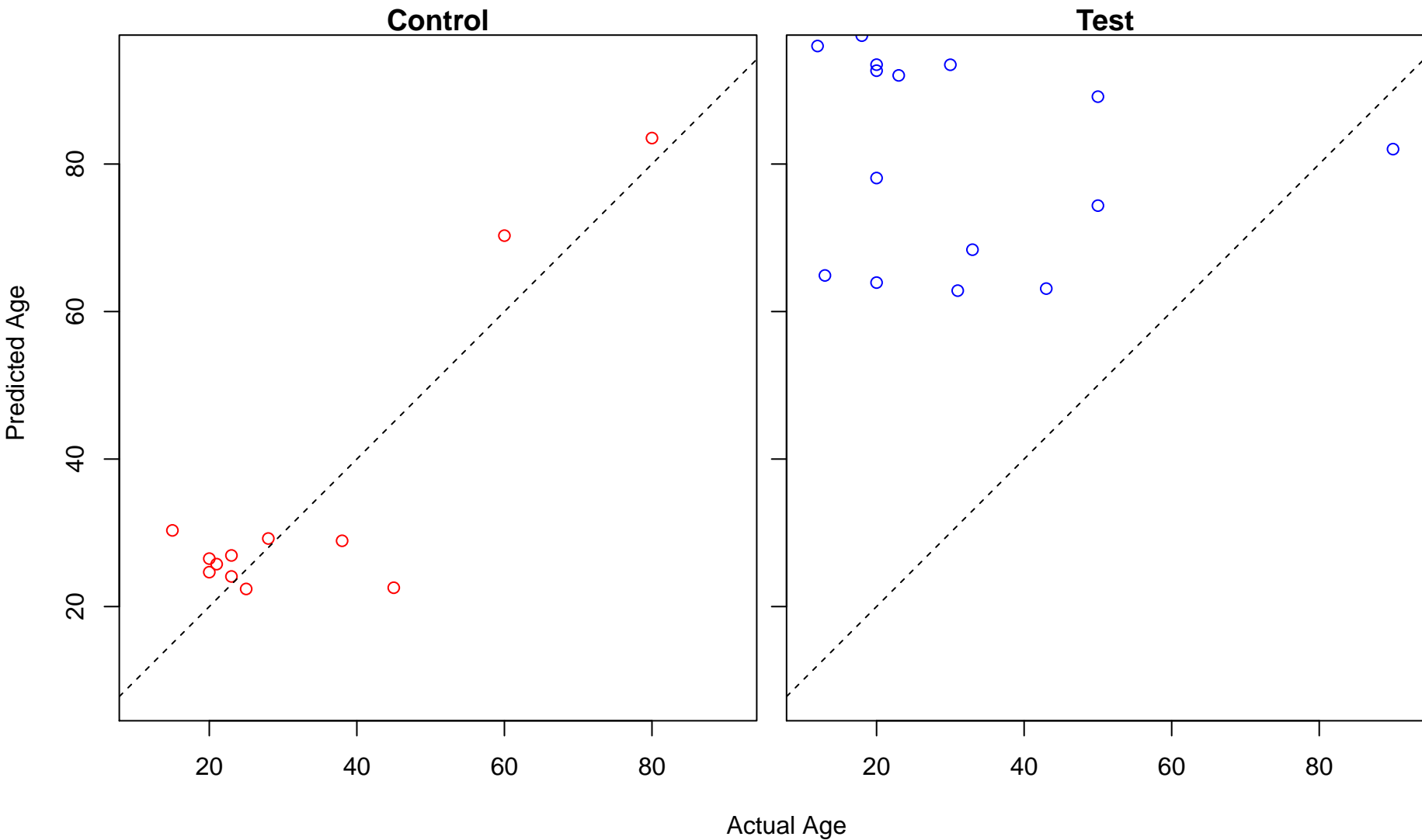


Test

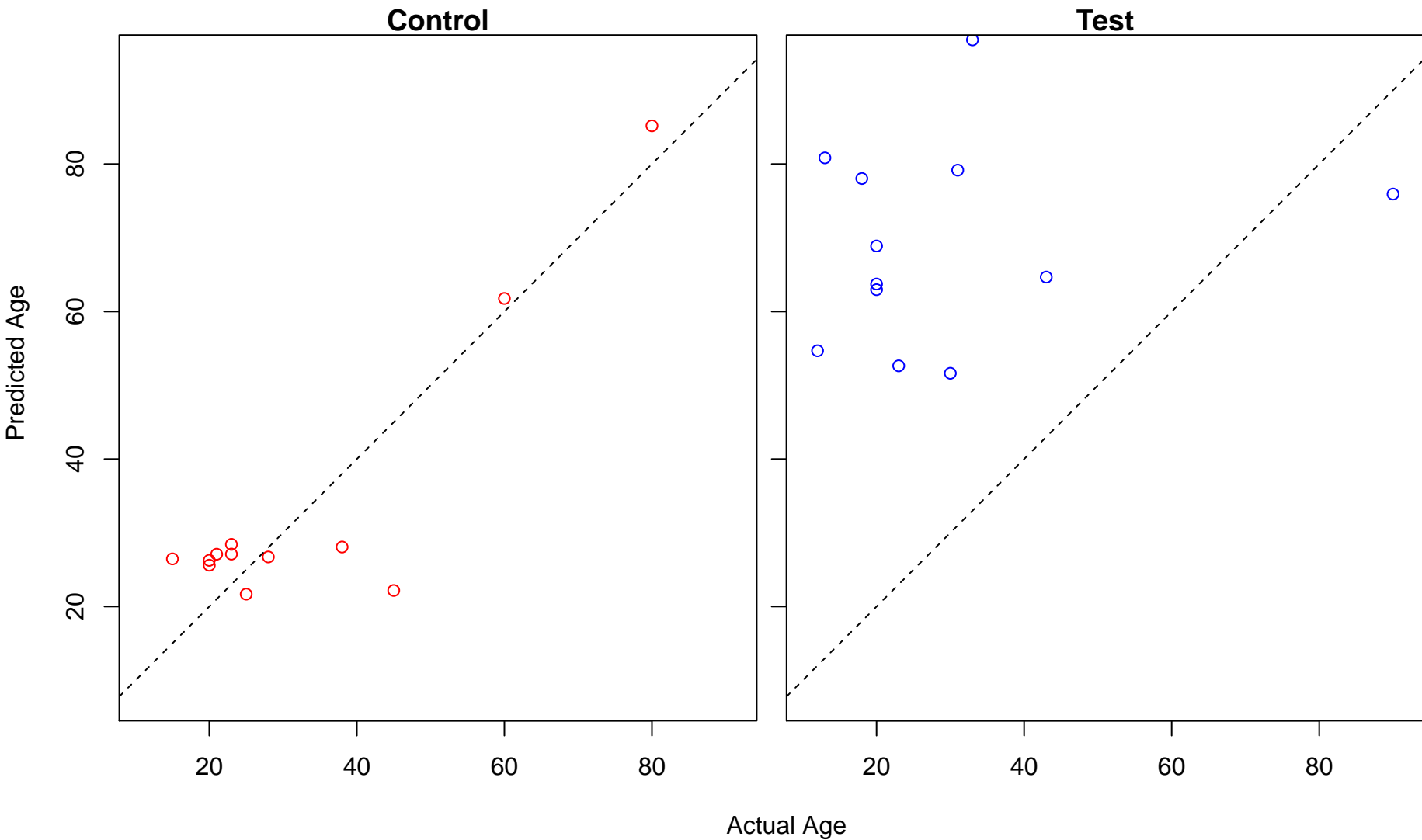


Actual Age

nuclear envelope reassembly (Score: 11.458390)

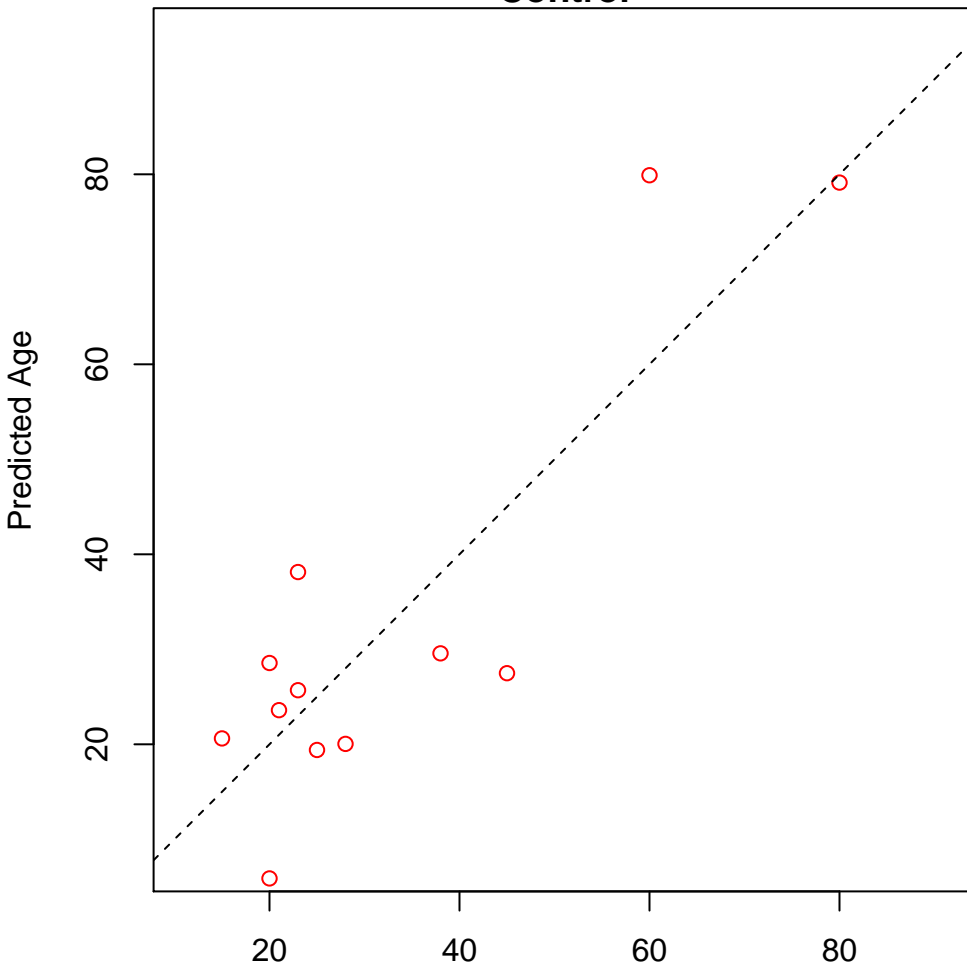


regulation of extrinsic apoptotic signaling pathway via death domain receptors (Score: 11.457981)

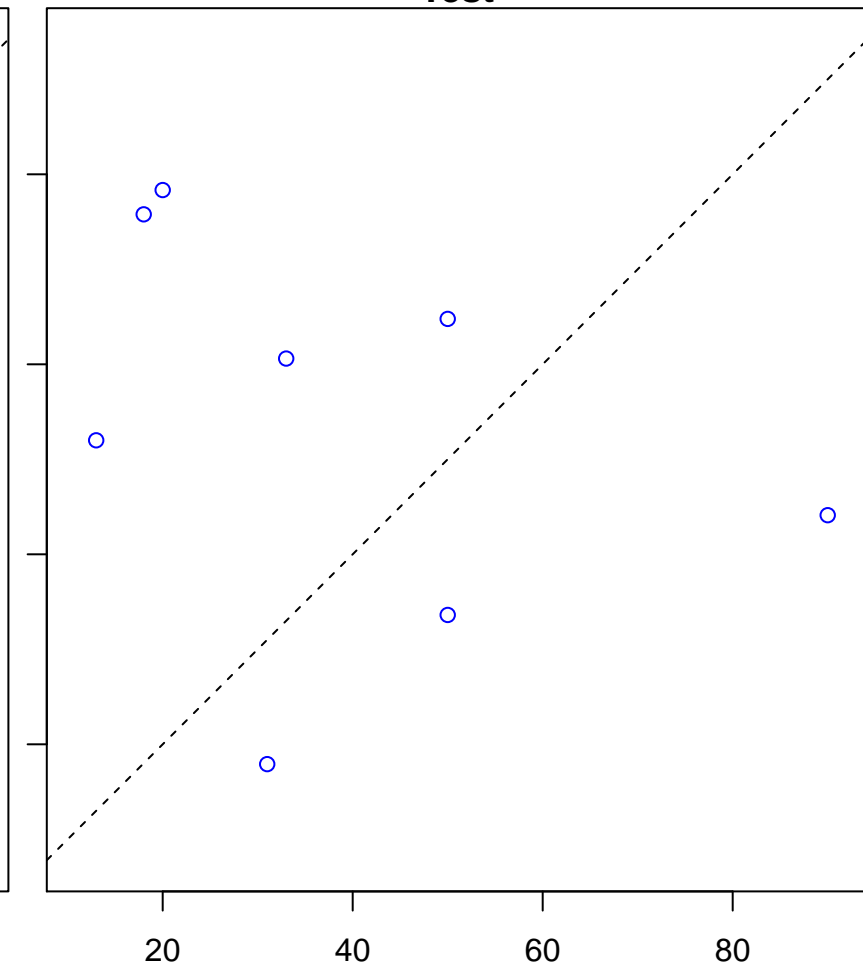


protein localization to membrane raft (Score: 11.449775)

Control

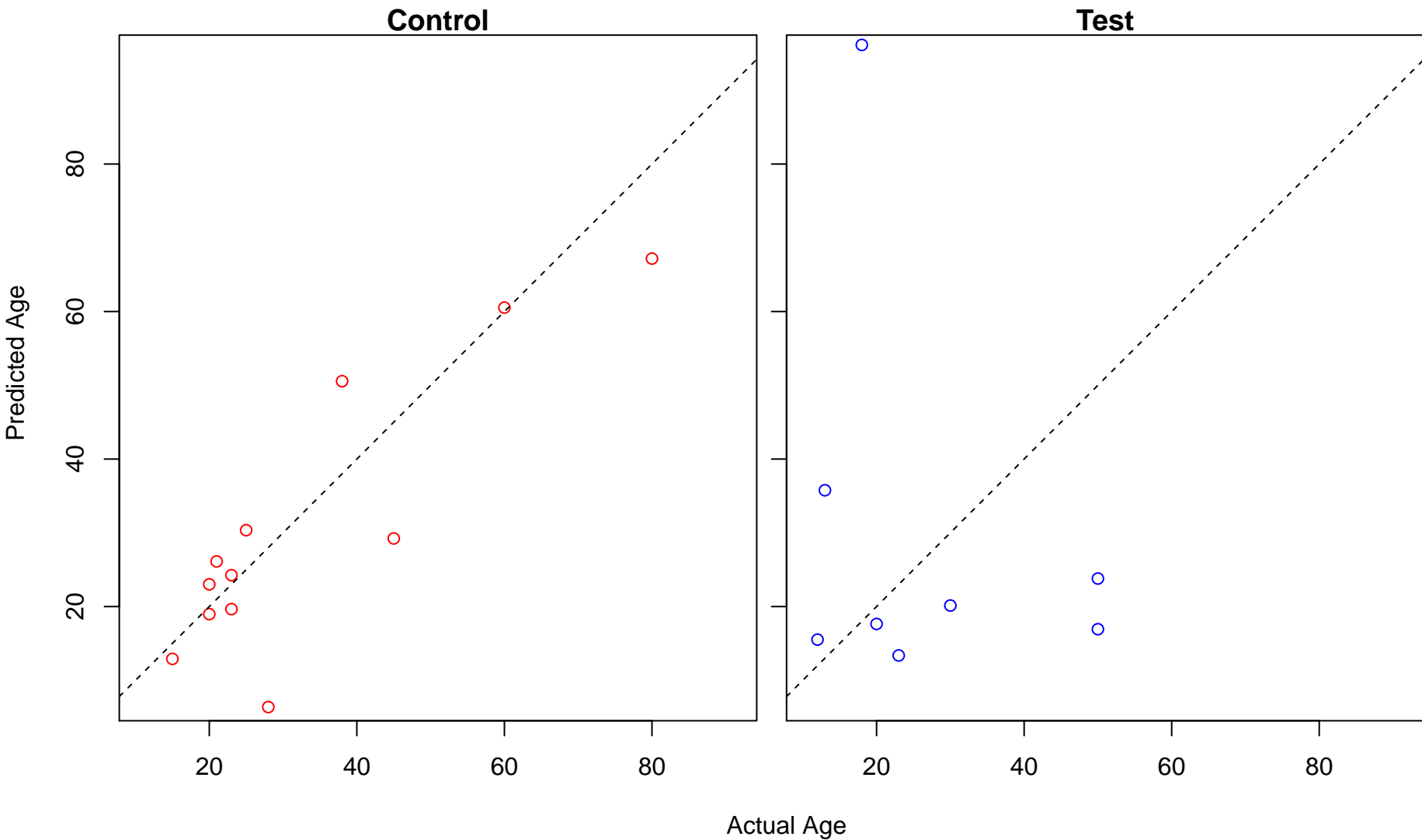


Test

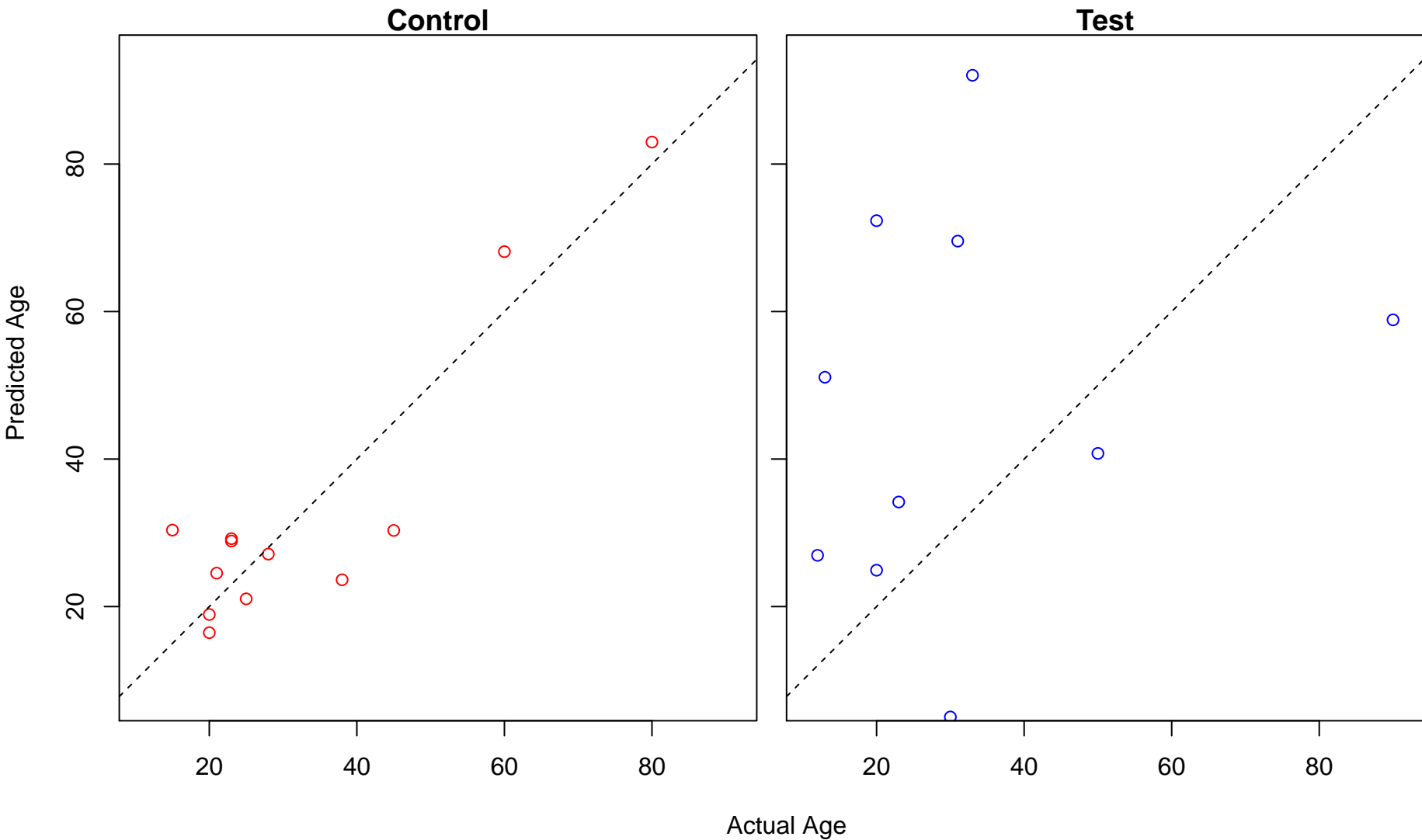


Actual Age

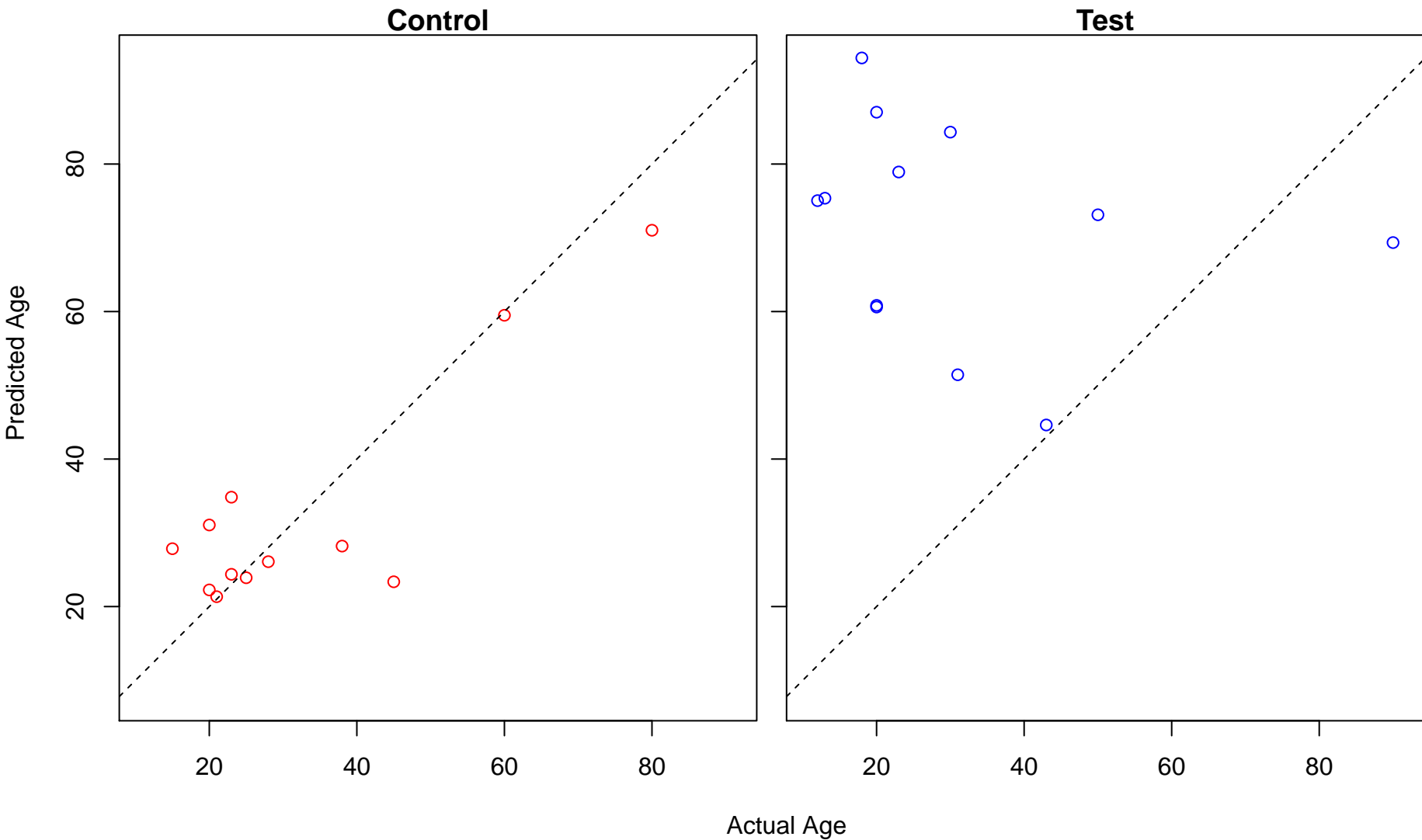
negative regulation of myoblast differentiation (Score: 11.447559)



developmental cell growth (Score: 11.445367)

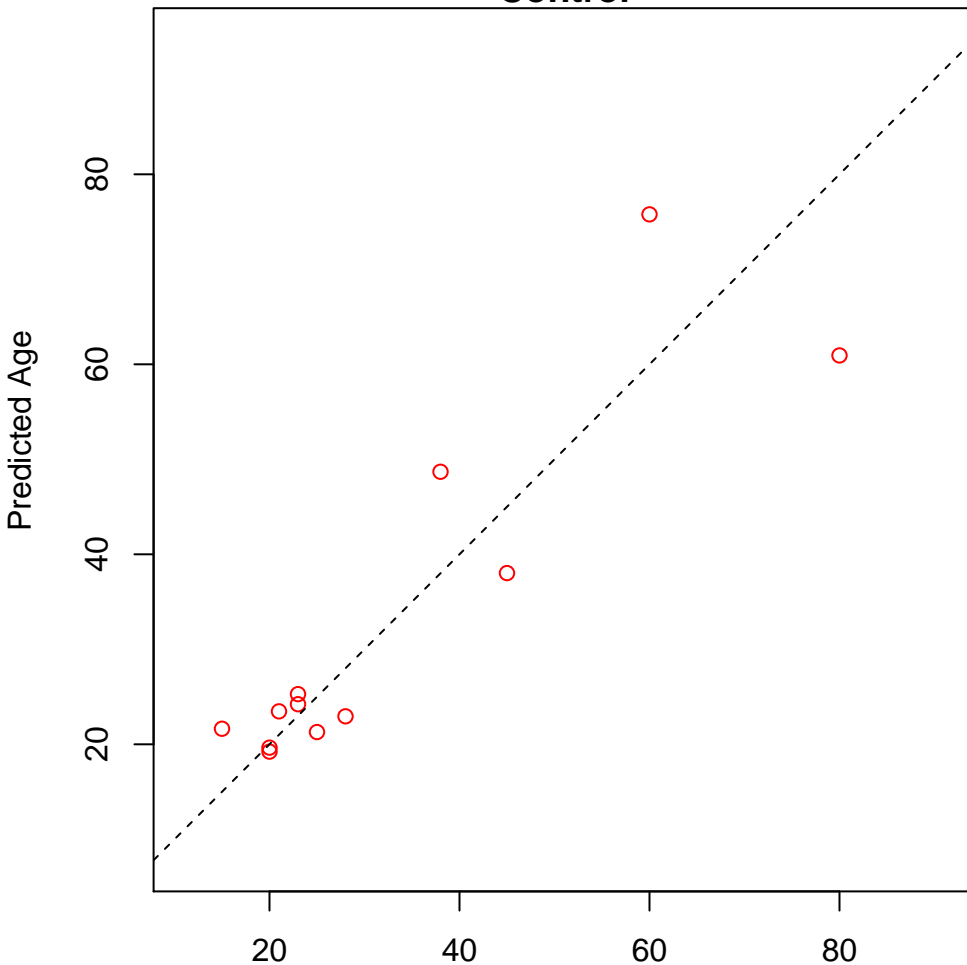


regulation of phospholipid catabolic process (Score: 11.440316)

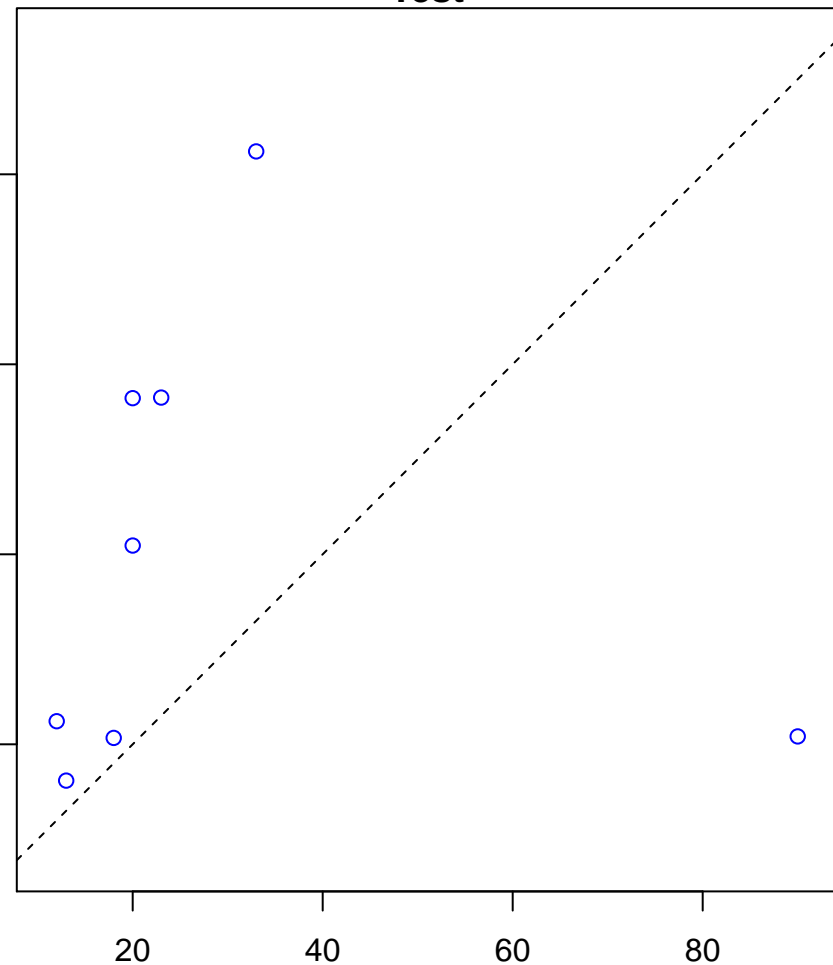


endochondral bone morphogenesis (Score: 11.437347)

Control

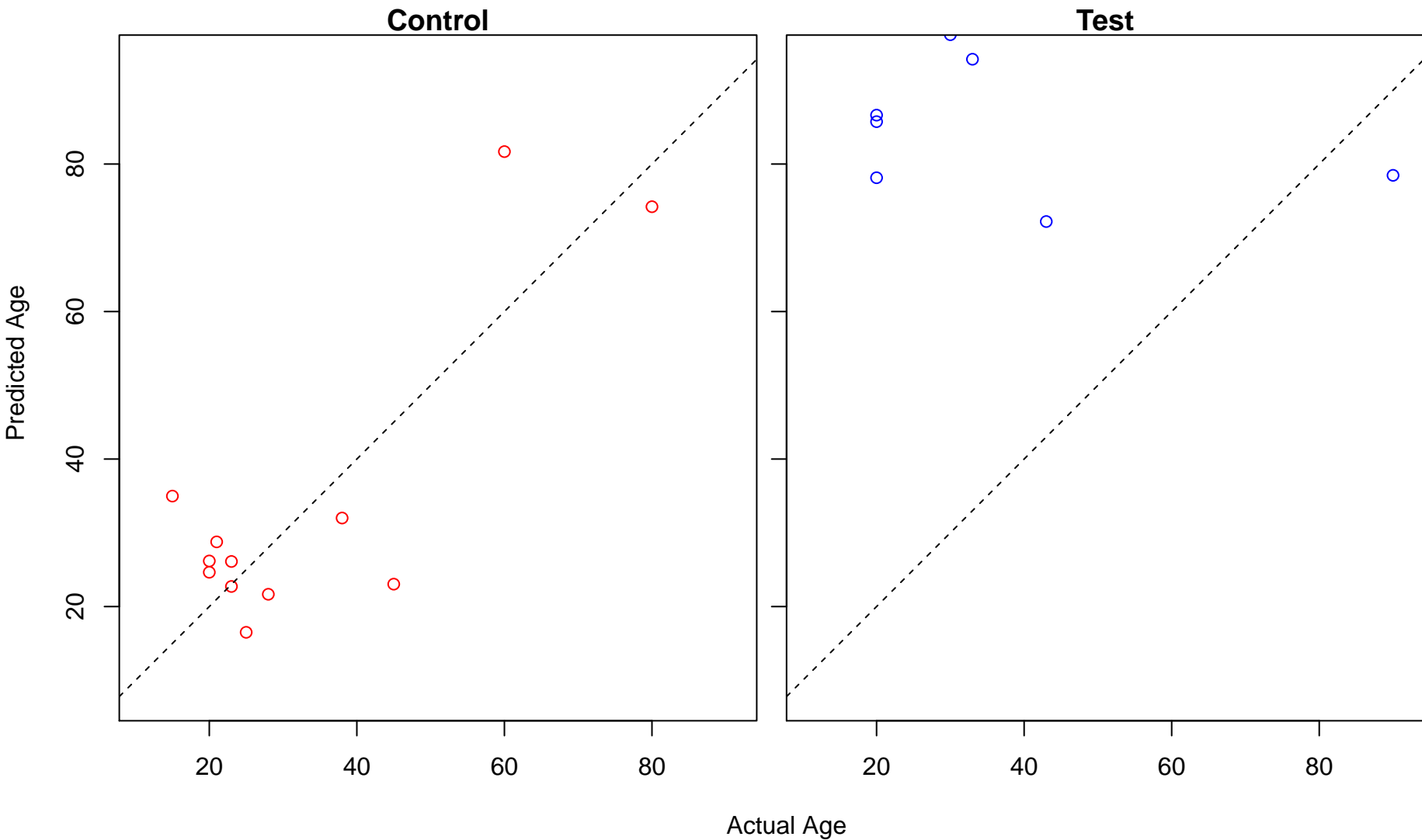


Test

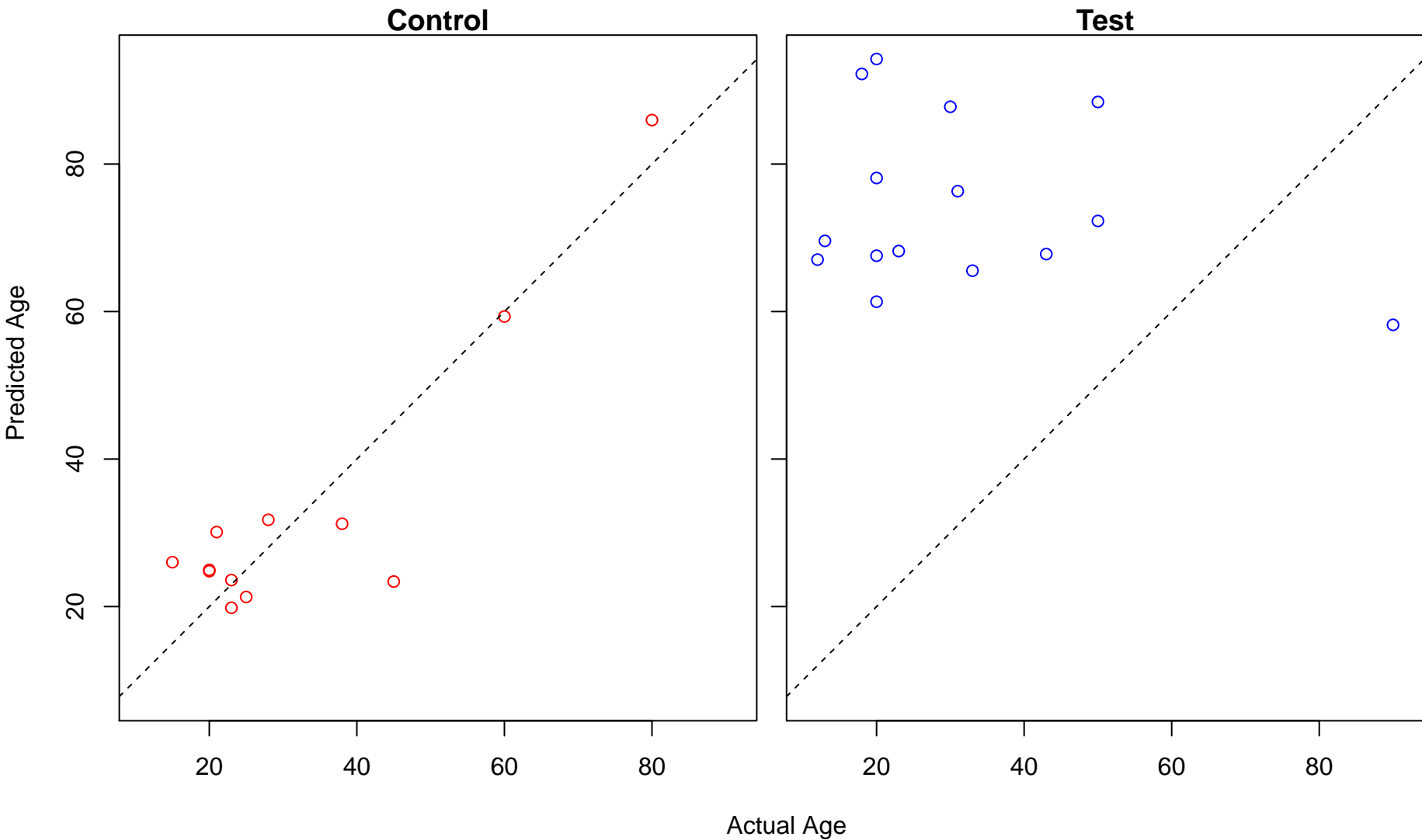


Actual Age

locomotor rhythm (Score: 11.427474)

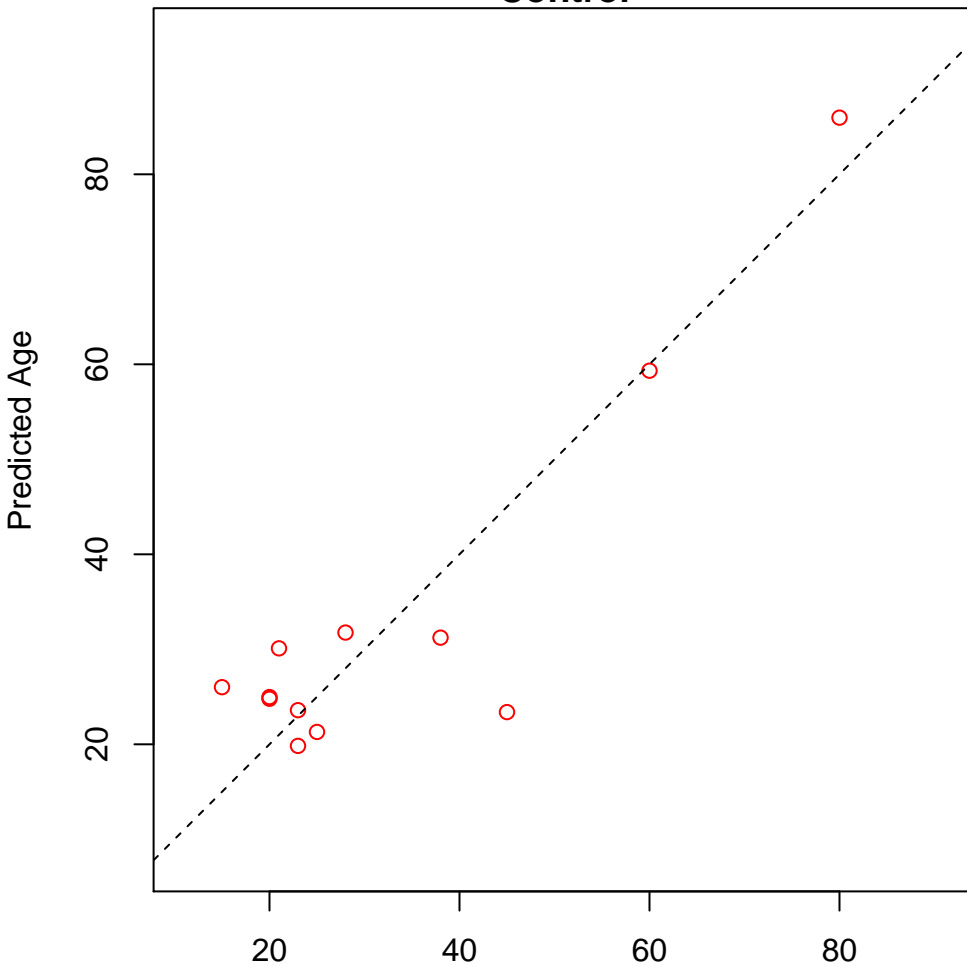


icosanoid metabolic process (Score: 11.426789)

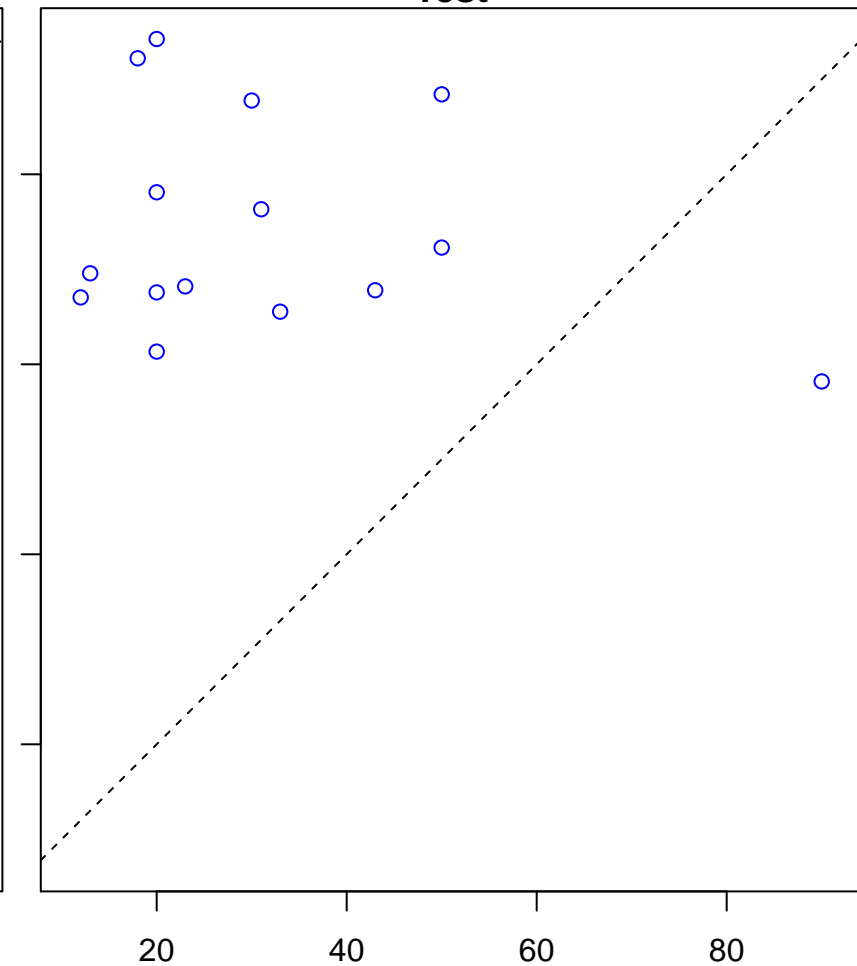


fatty acid derivative metabolic process (Score: 11.426789)

Control

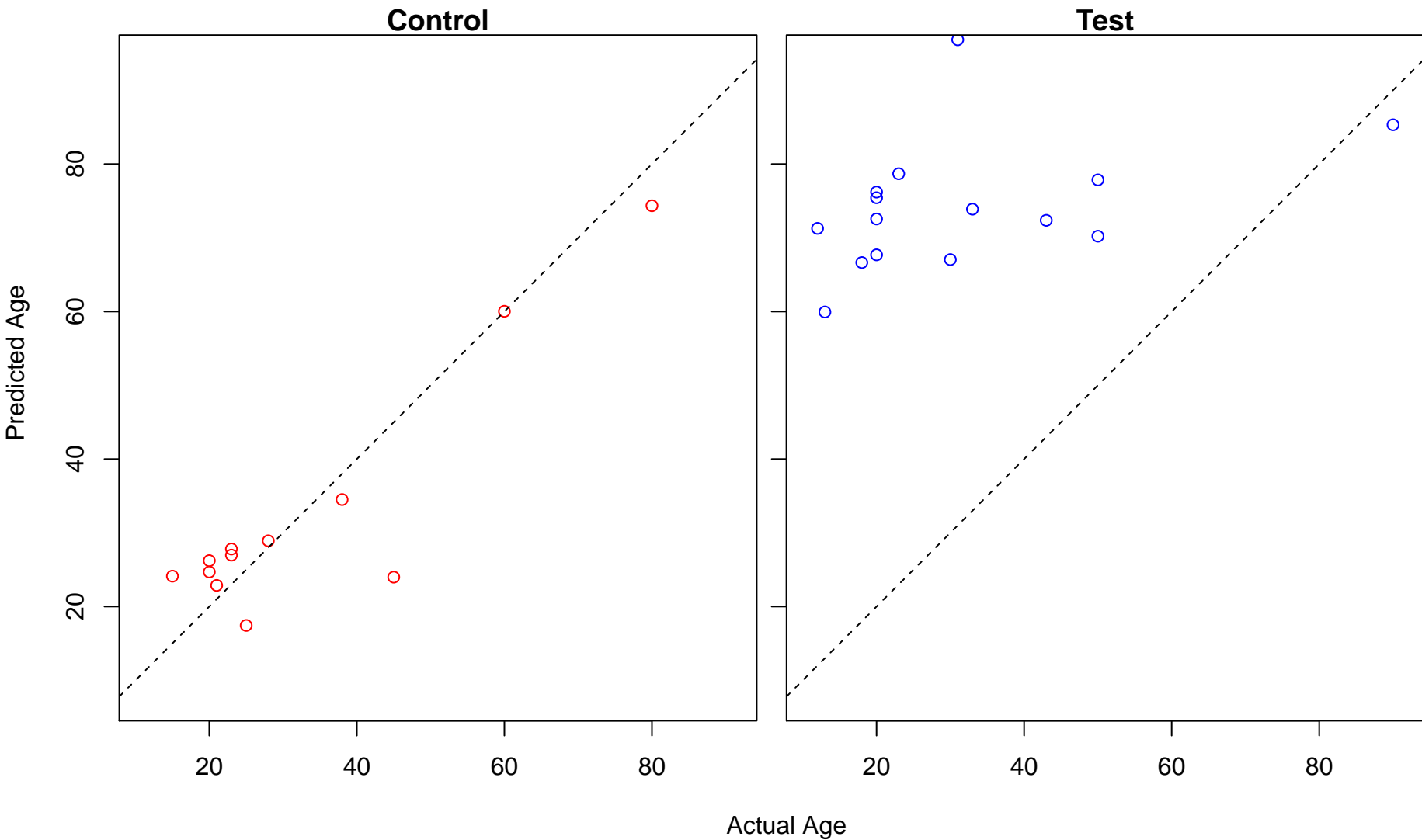


Test

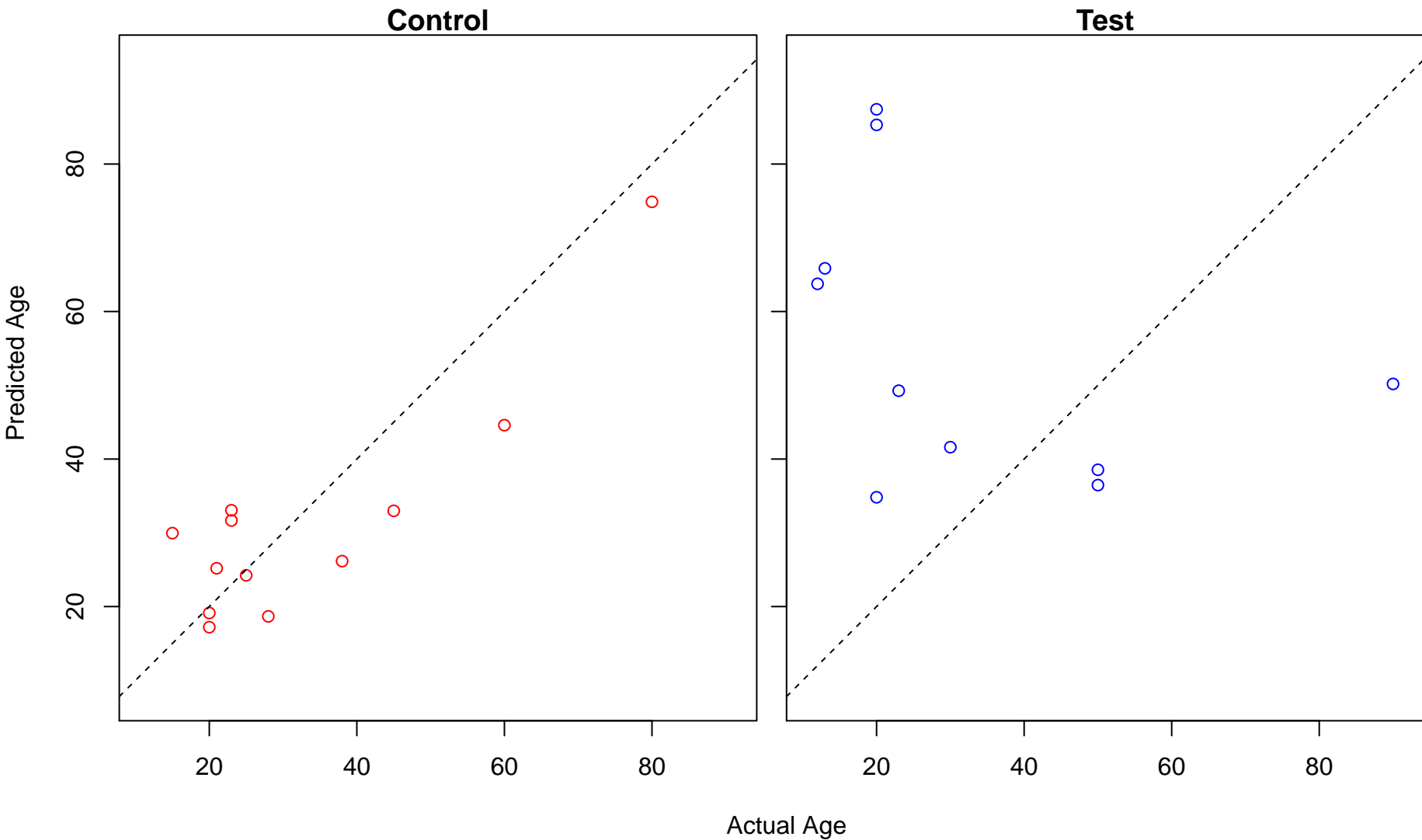


Actual Age

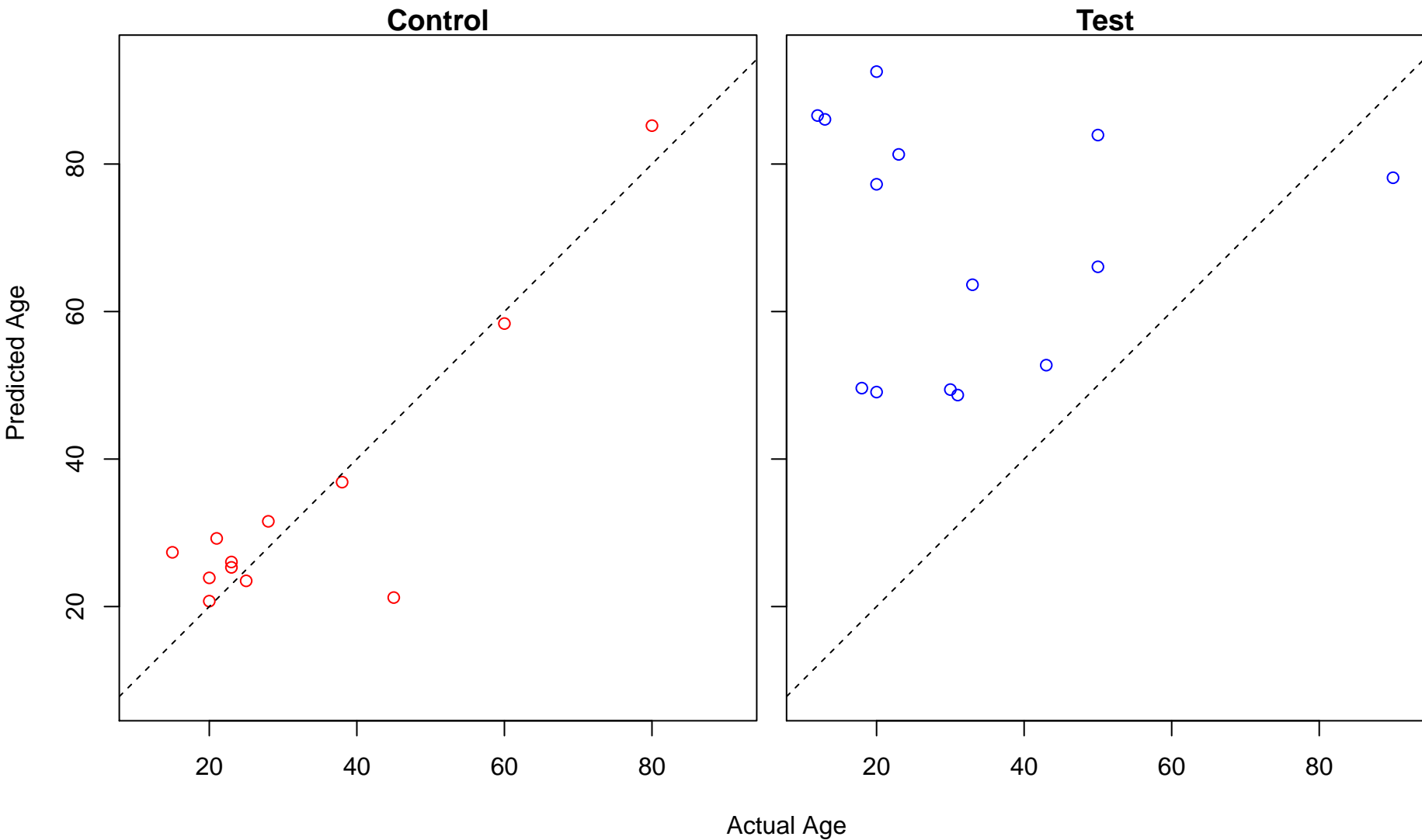
hepaticobiliary system development (Score: 11.424709)



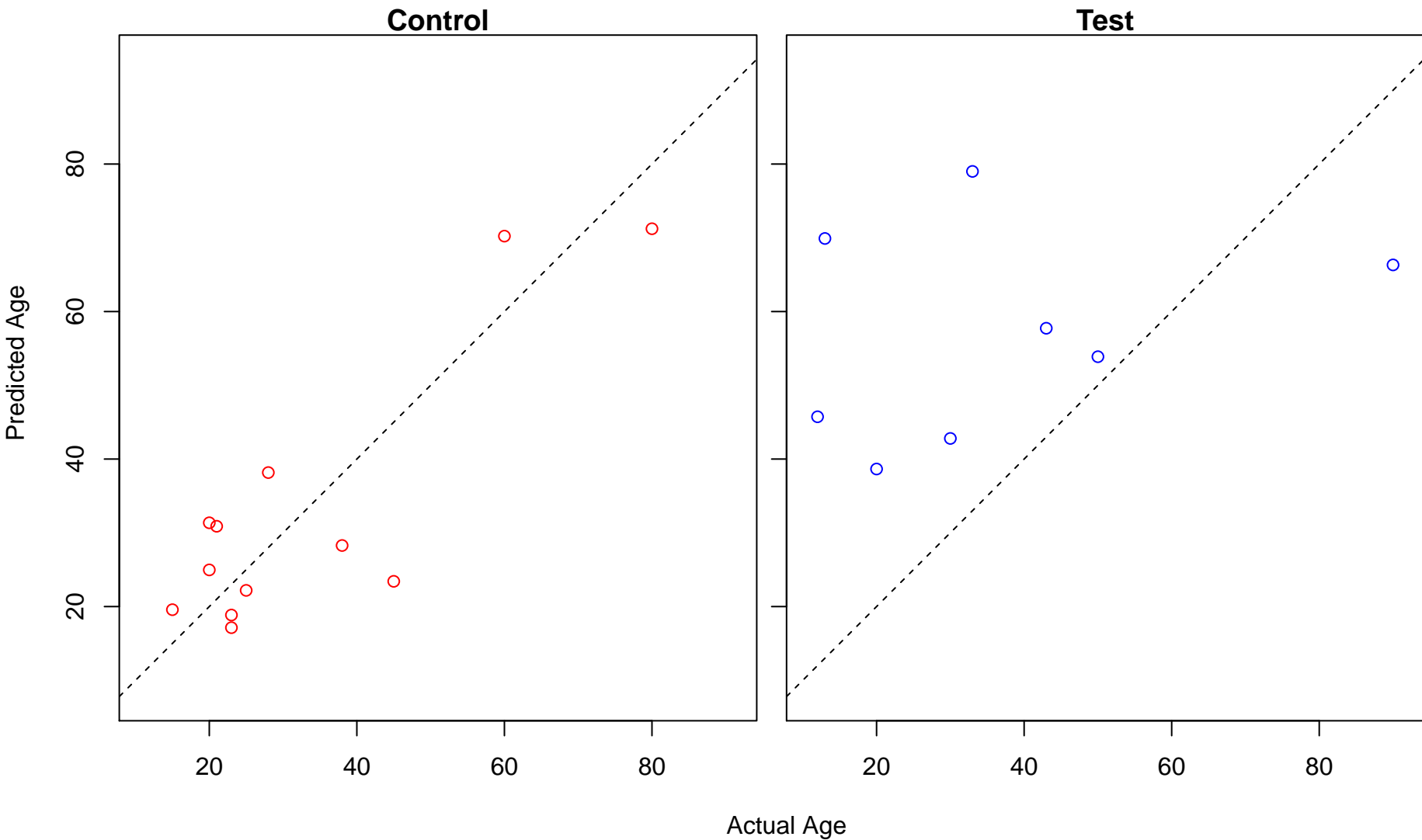
regulation of NFAT protein import into nucleus (Score: 11.418084)



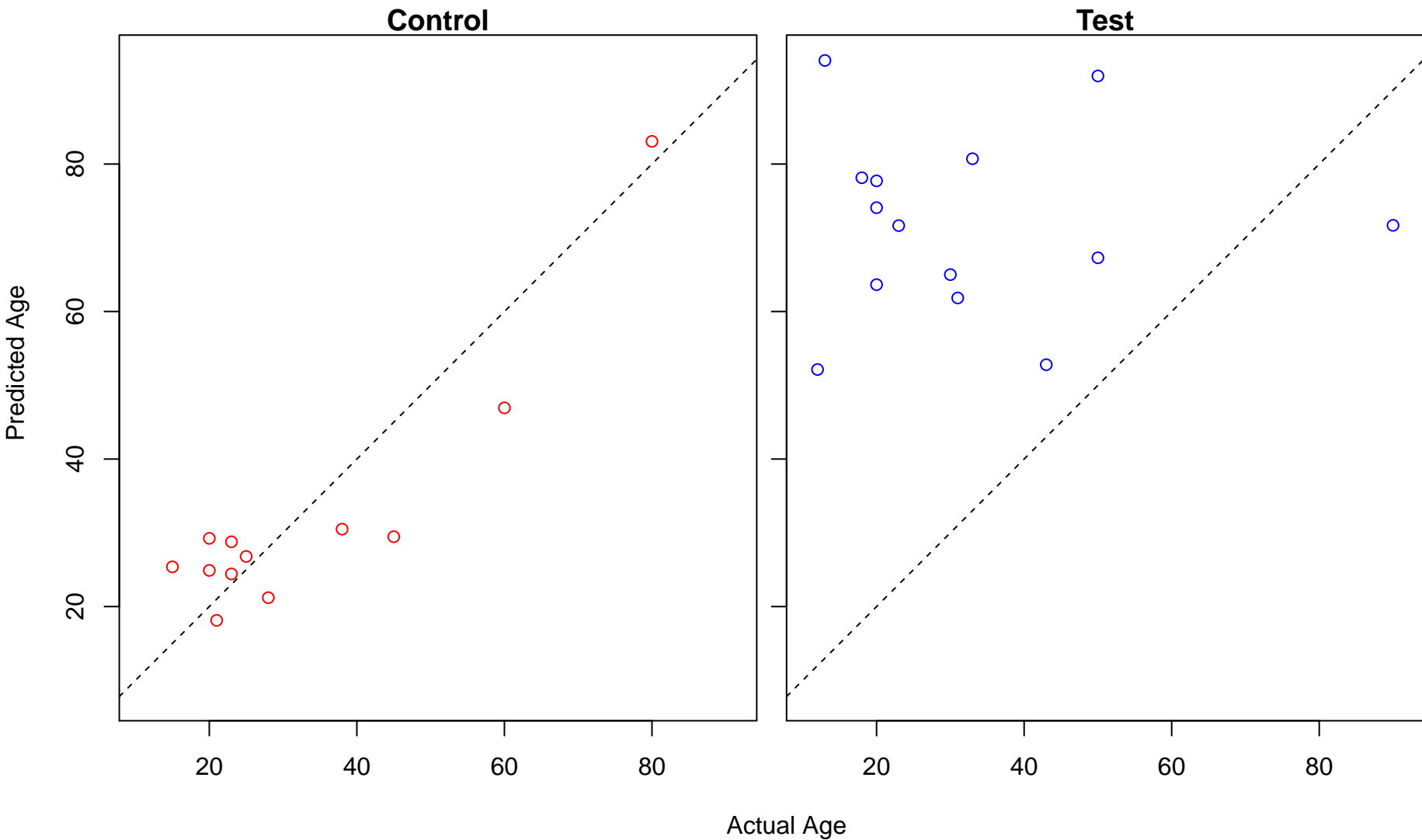
morphogenesis of a branching epithelium (Score: 11.414240)



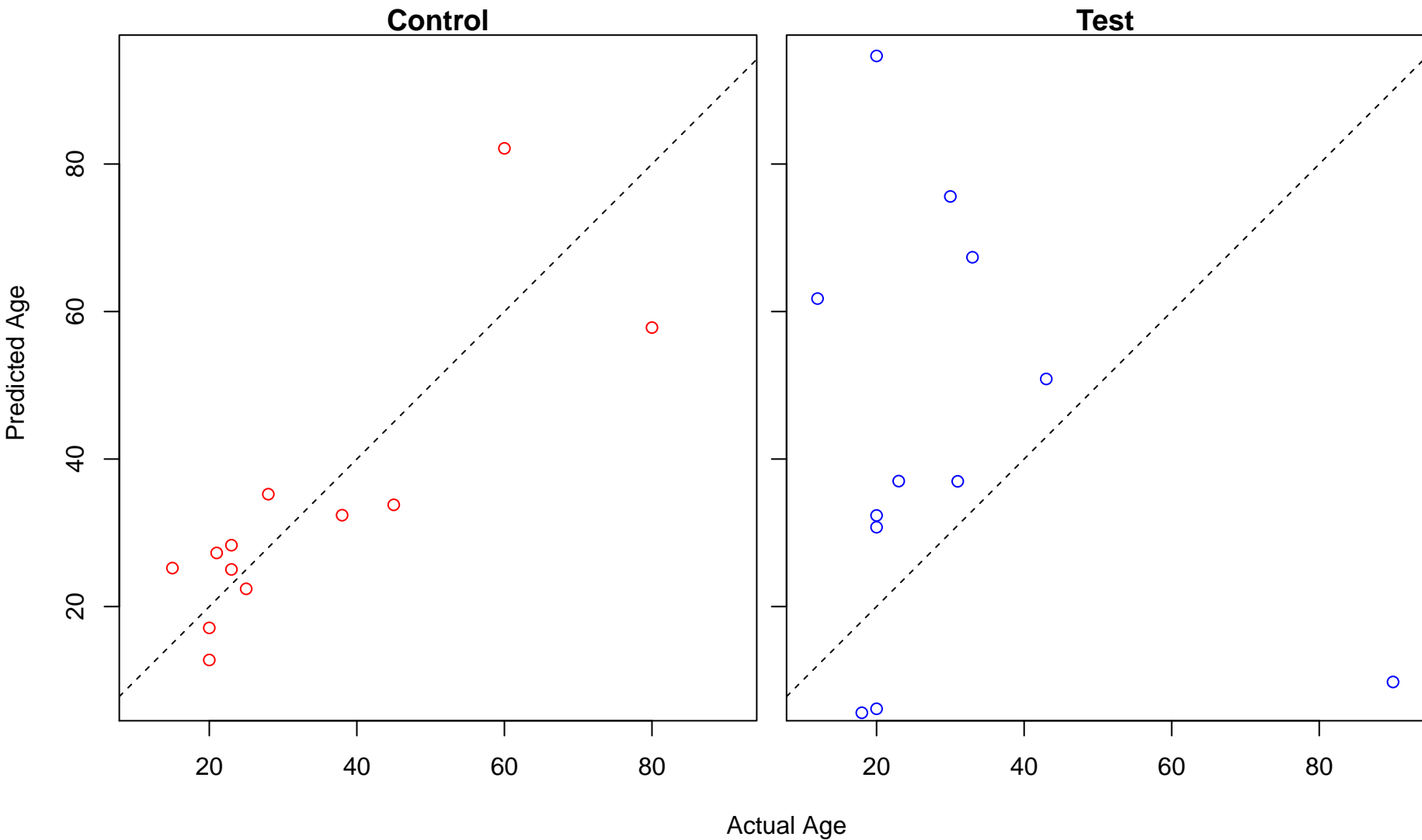
protein processing (Score: 11.403601)



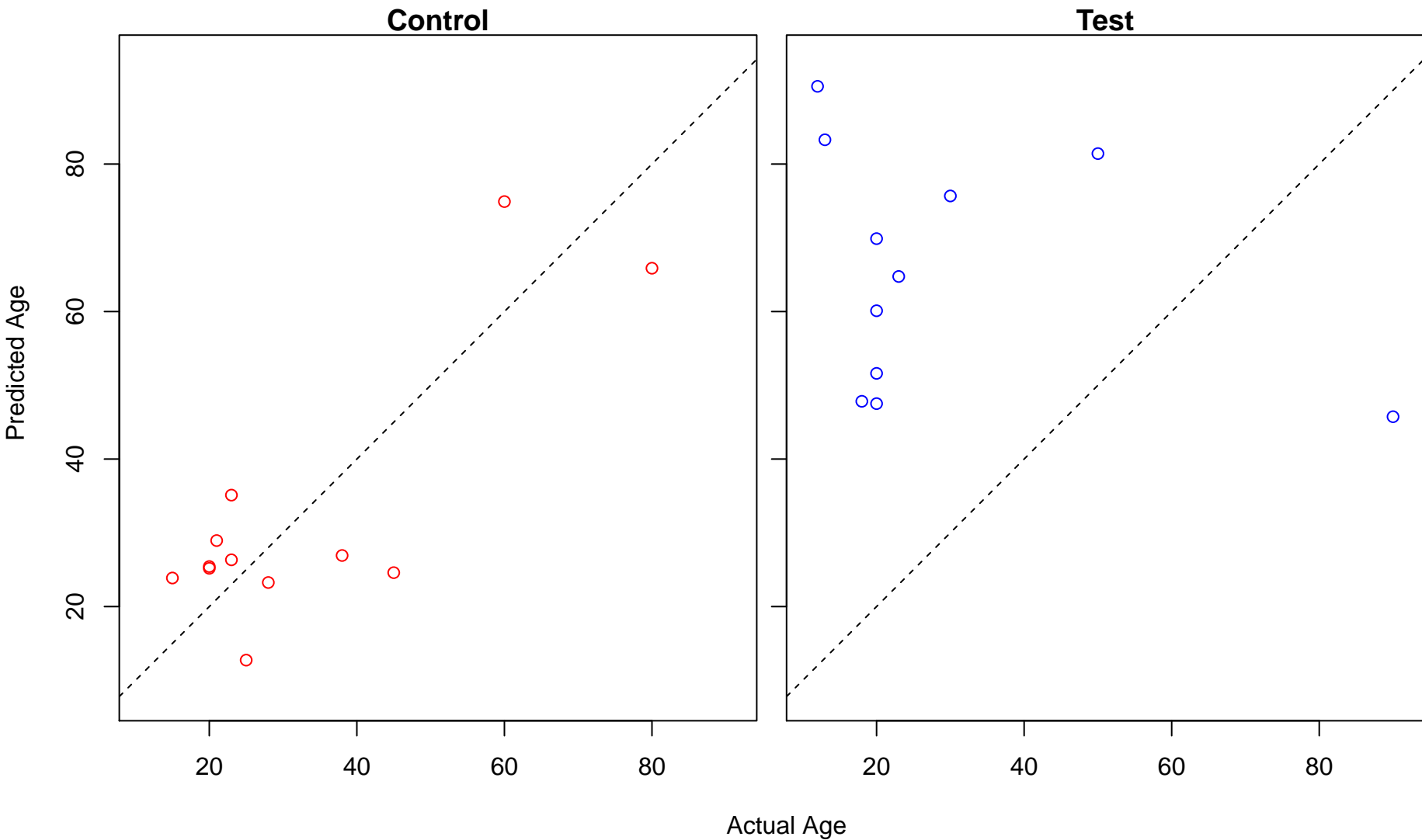
intracellular lipid transport (Score: 11.400837)



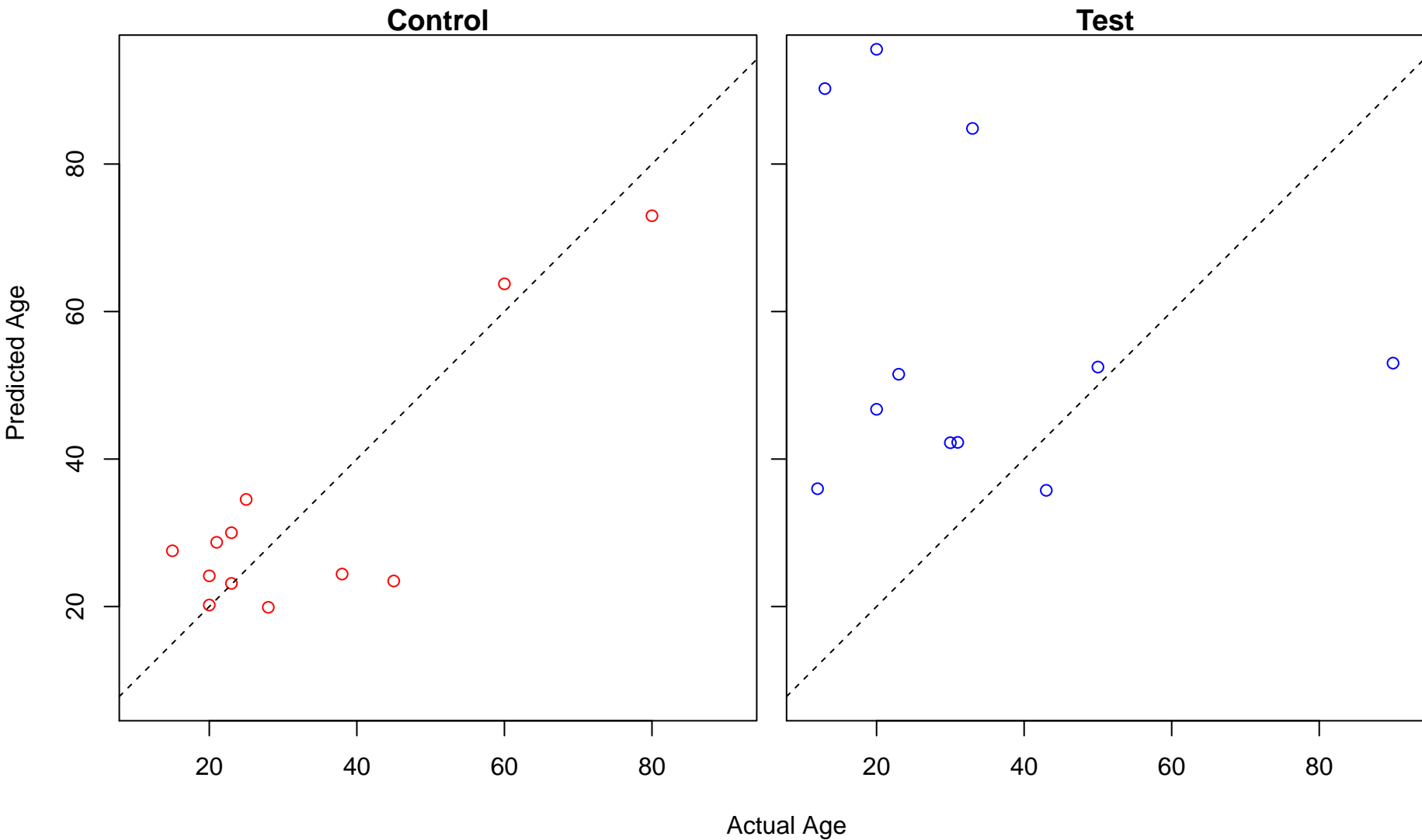
regulation of interleukin-1 secretion (Score: 11.400733)



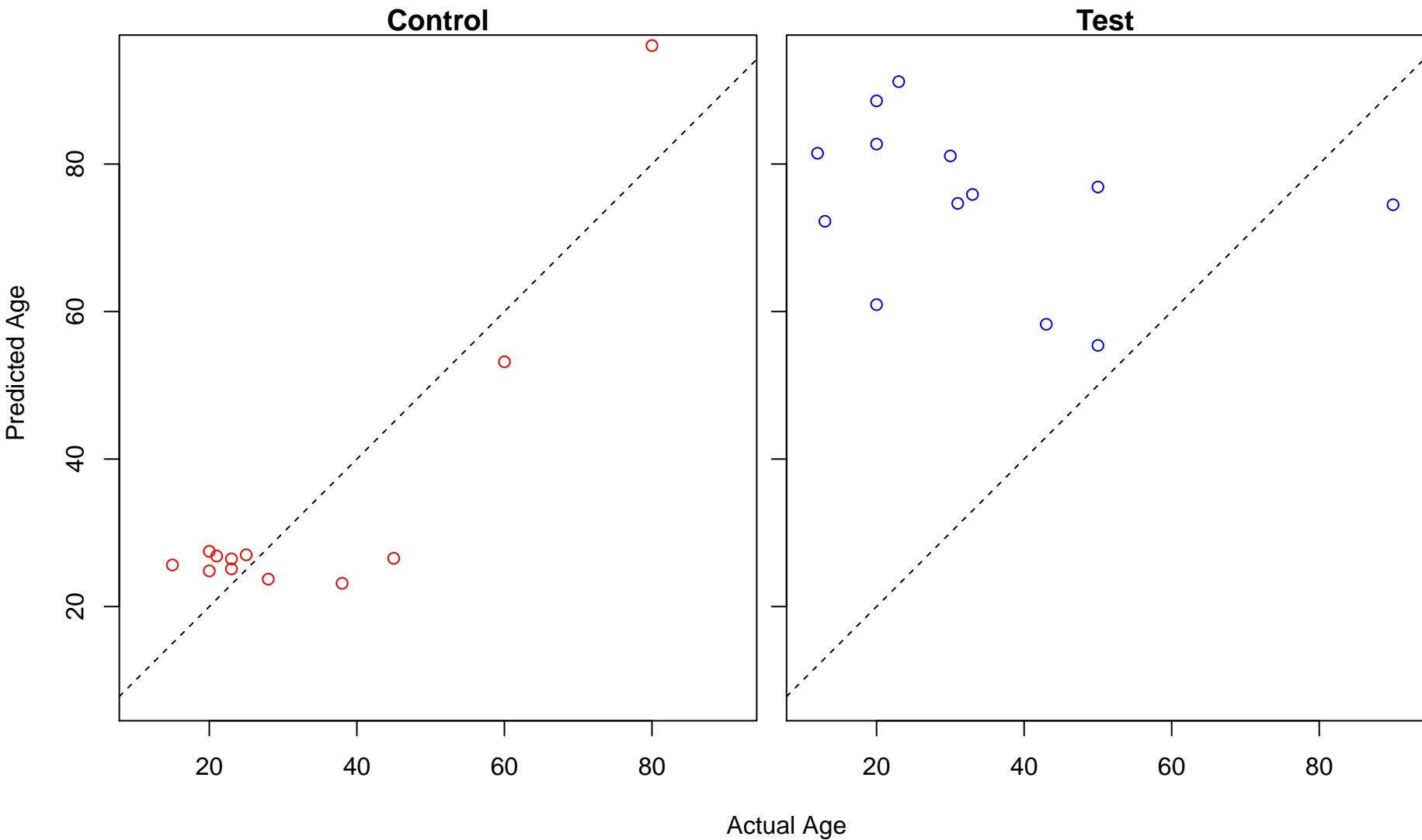
regulation of oocyte development (Score: 11.394764)



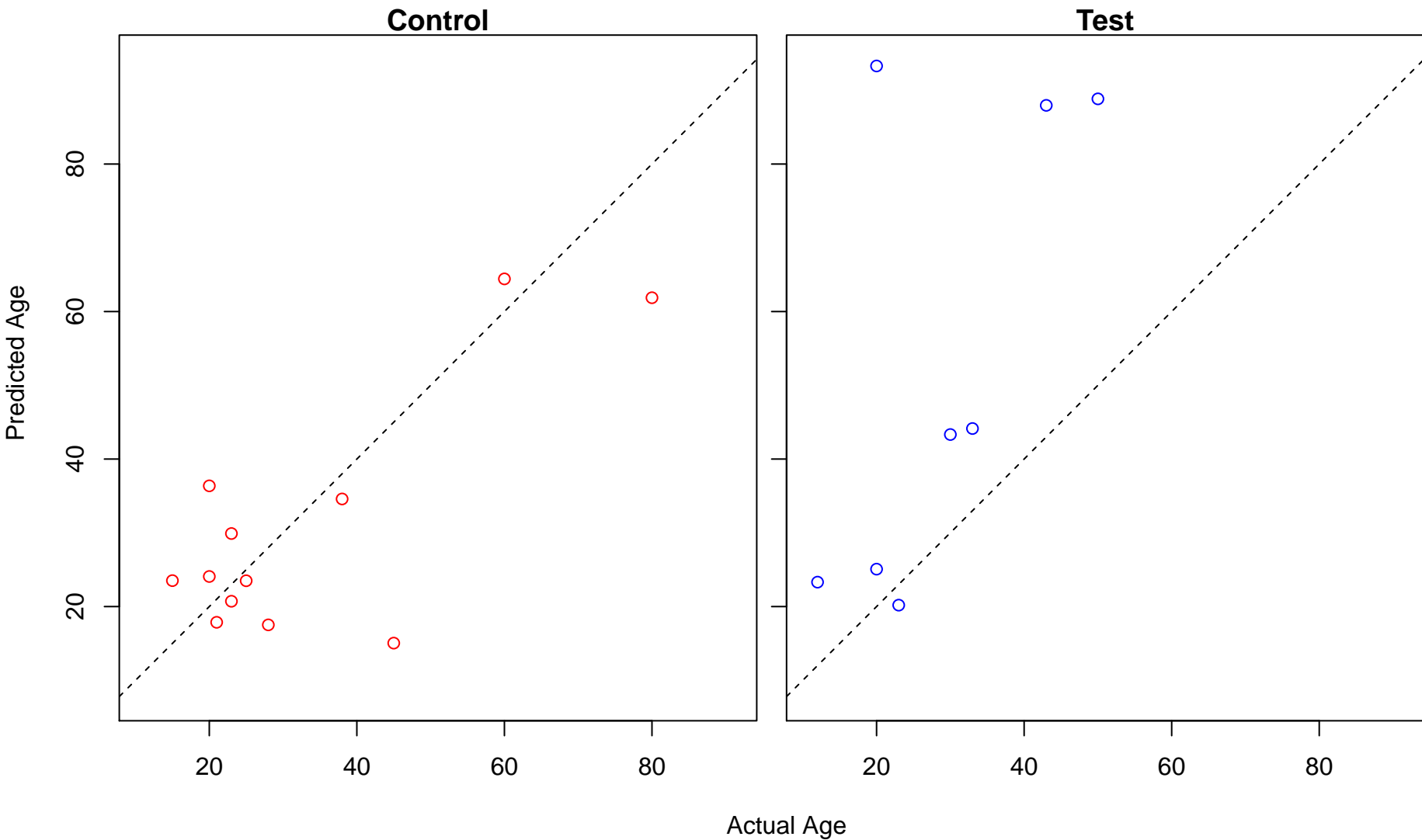
response to tumor cell (Score: 11.387081)



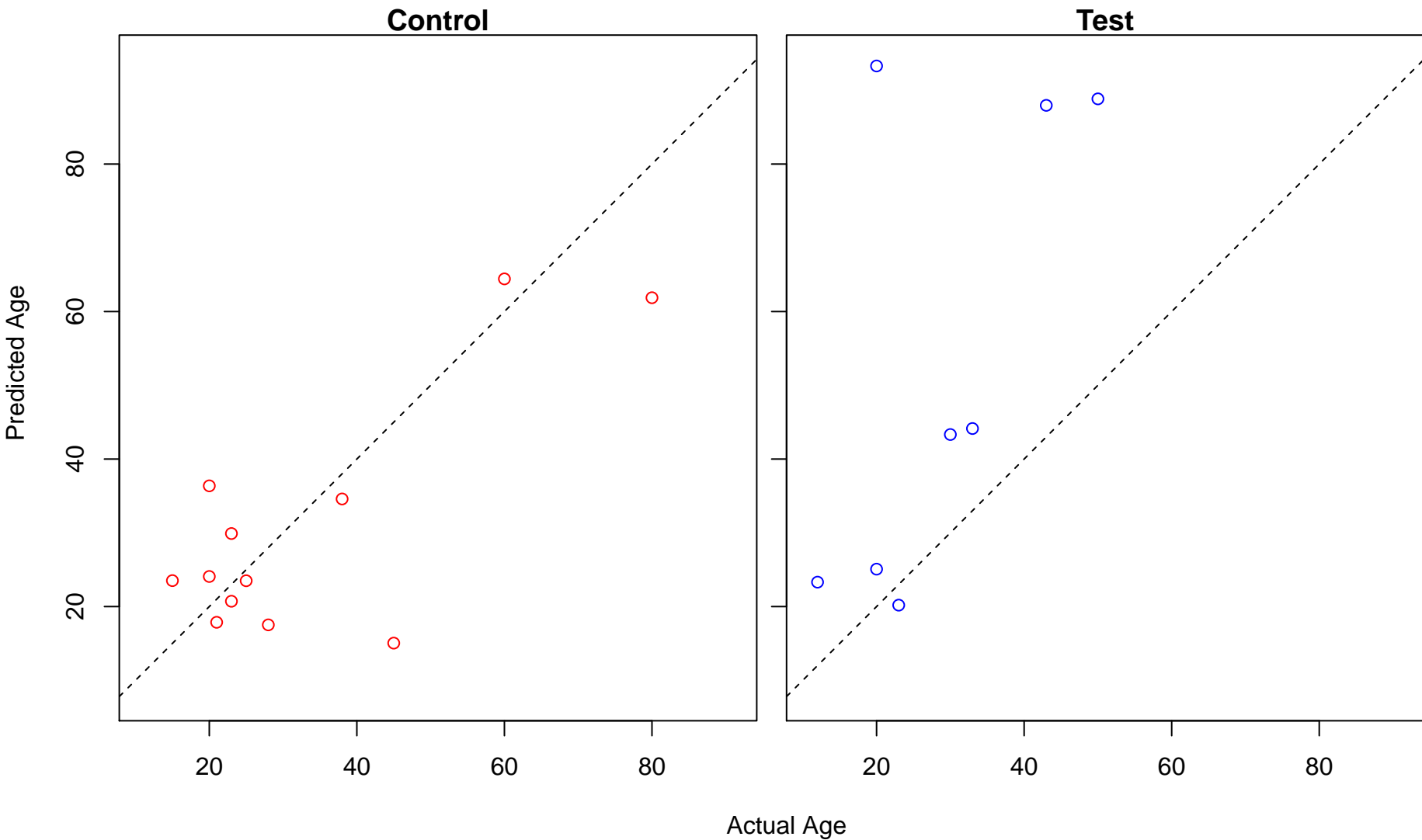
protein myristoylation (Score: 11.381887)



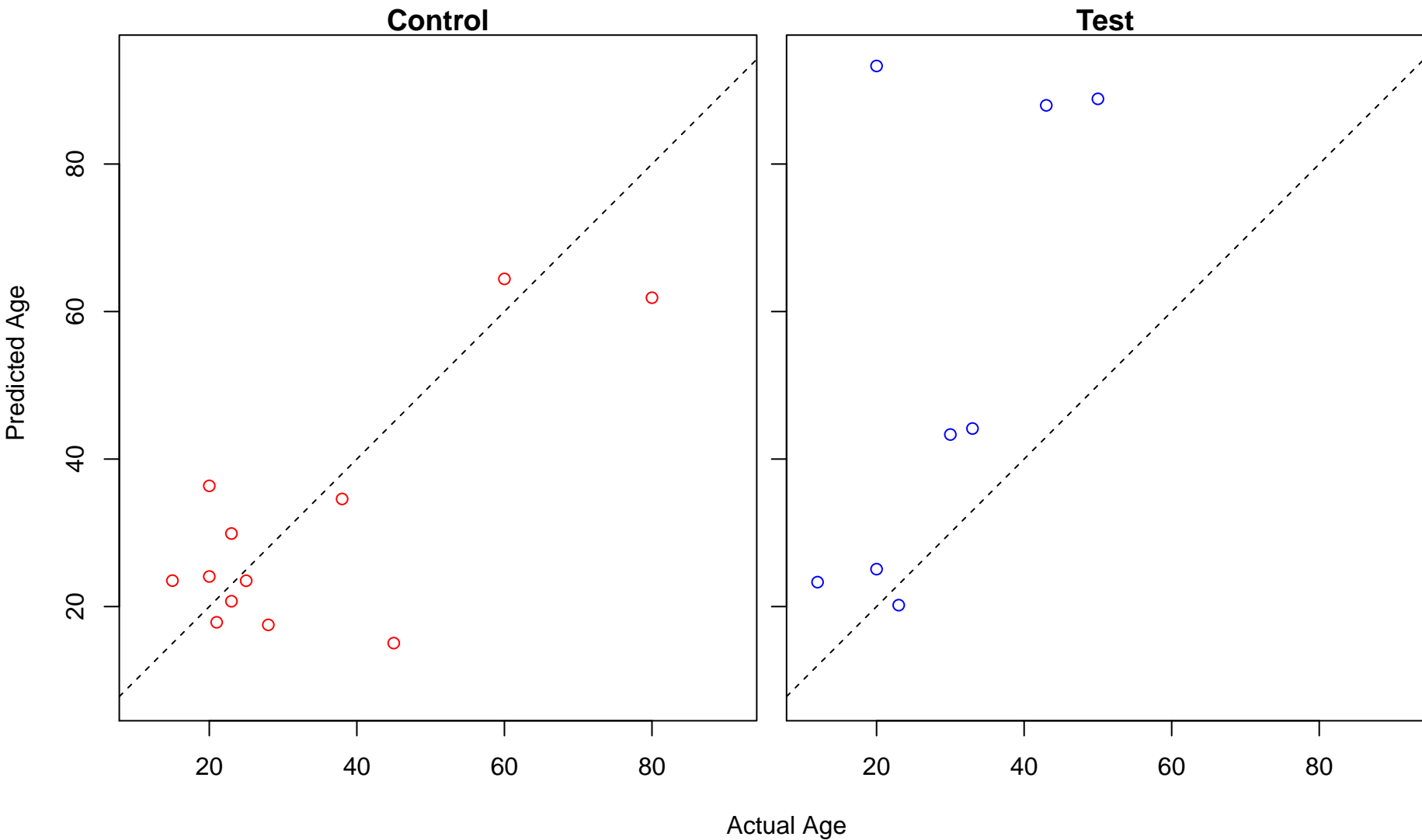
somatic recombination of immunoglobulin genes involved in immune response (Score: 11.380646)



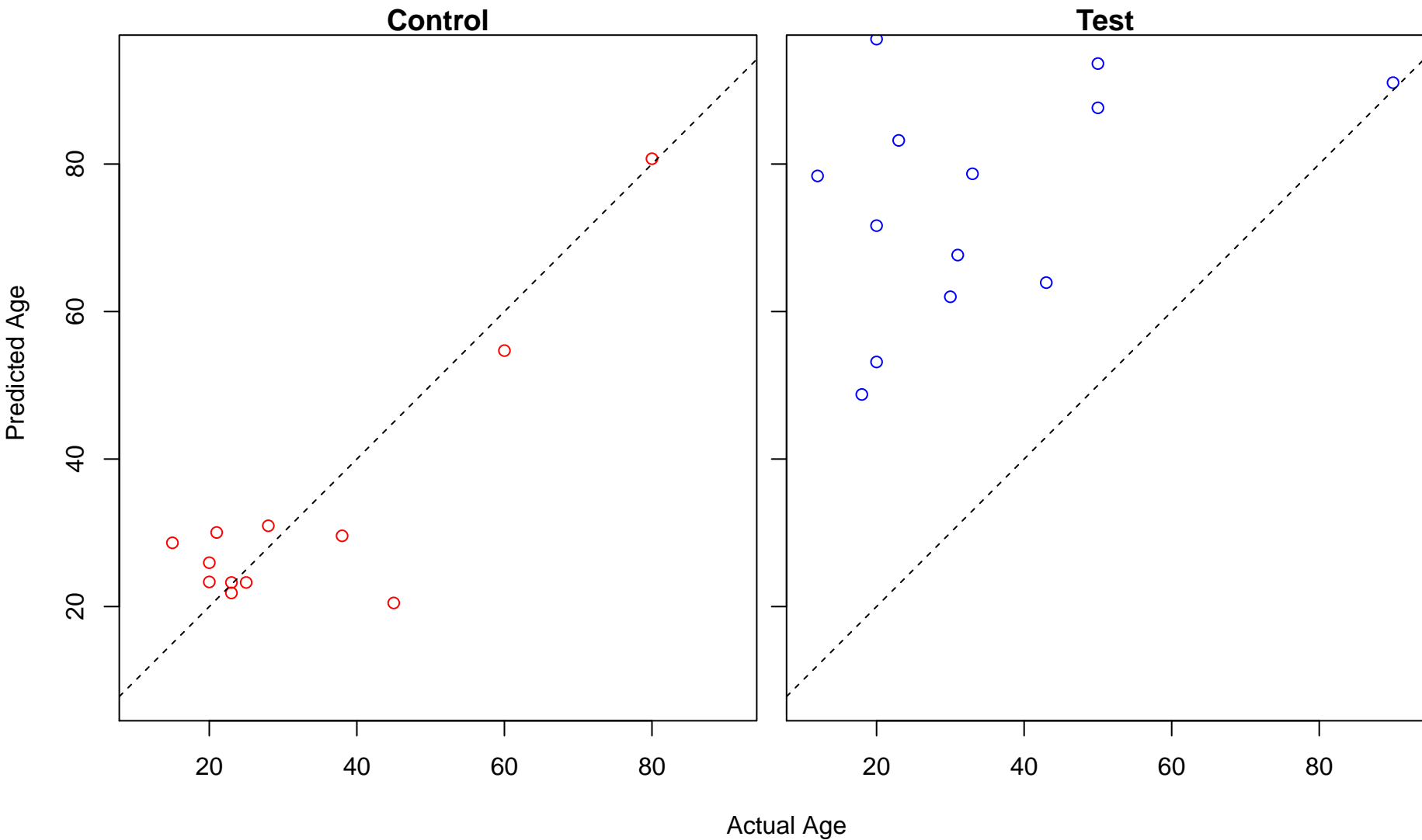
somatic diversification of immunoglobulins involved in immune response (Score: 11.380646)



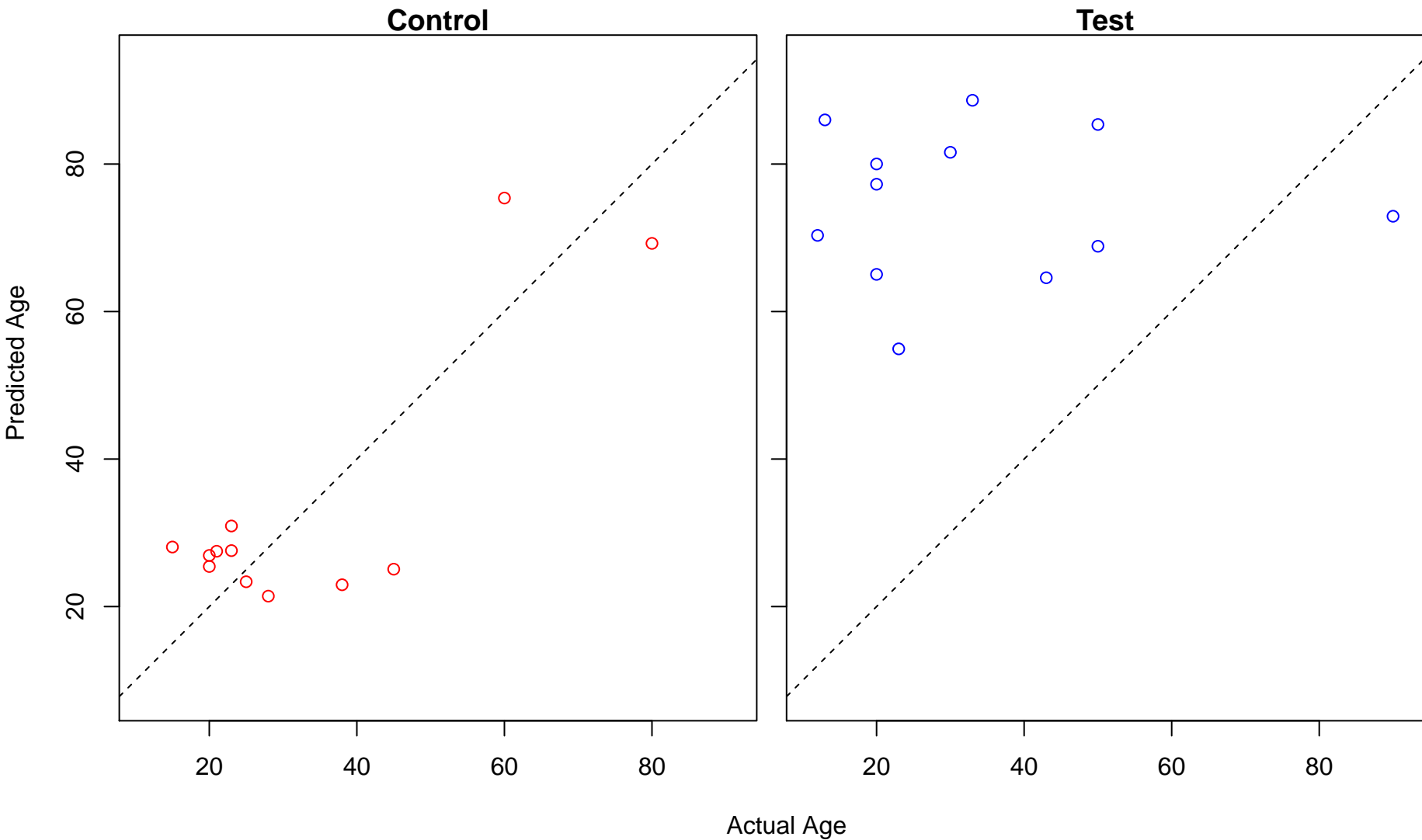
isotype switching (Score: 11.380646)



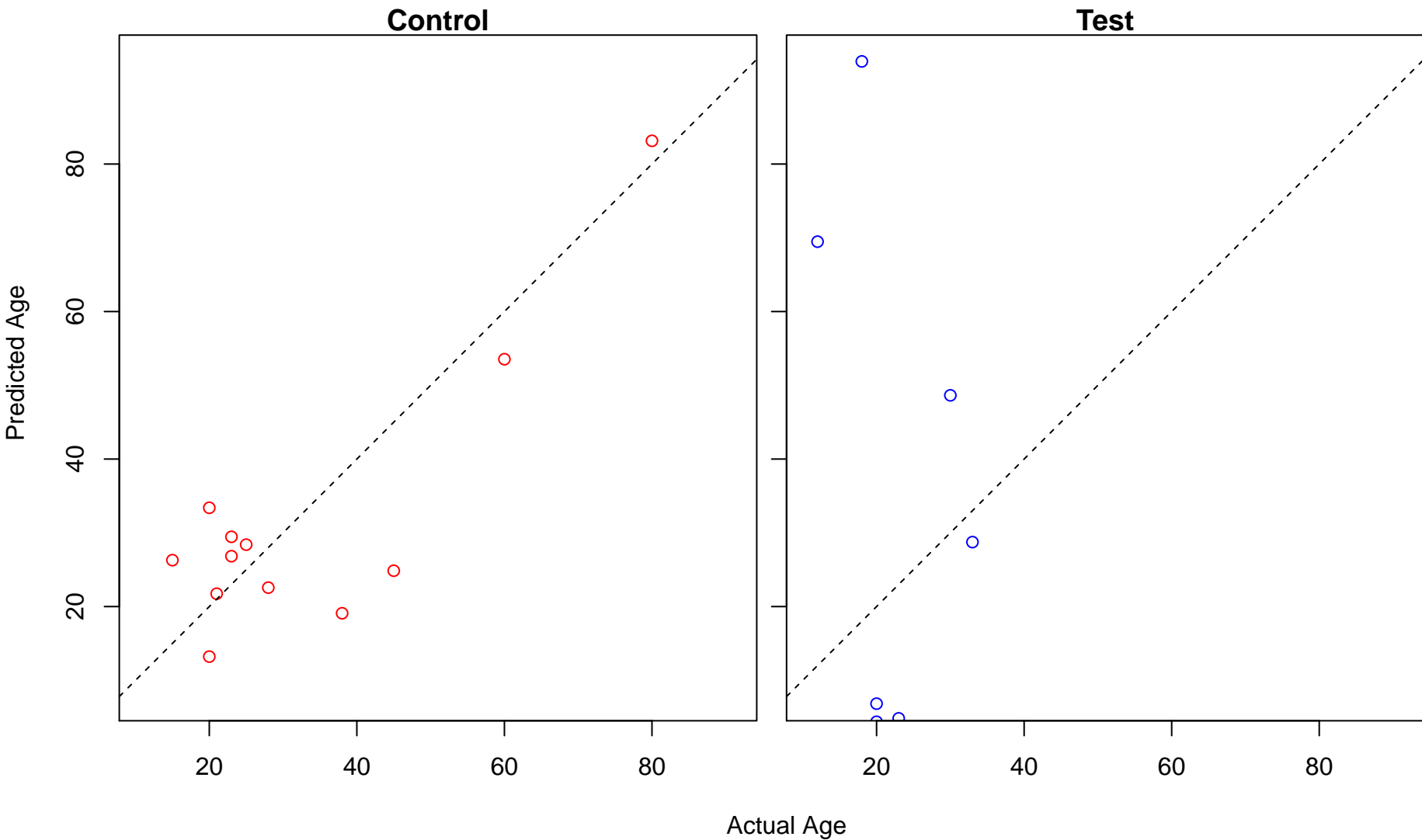
epithelial tube branching involved in lung morphogenesis (Score: 11.364745)



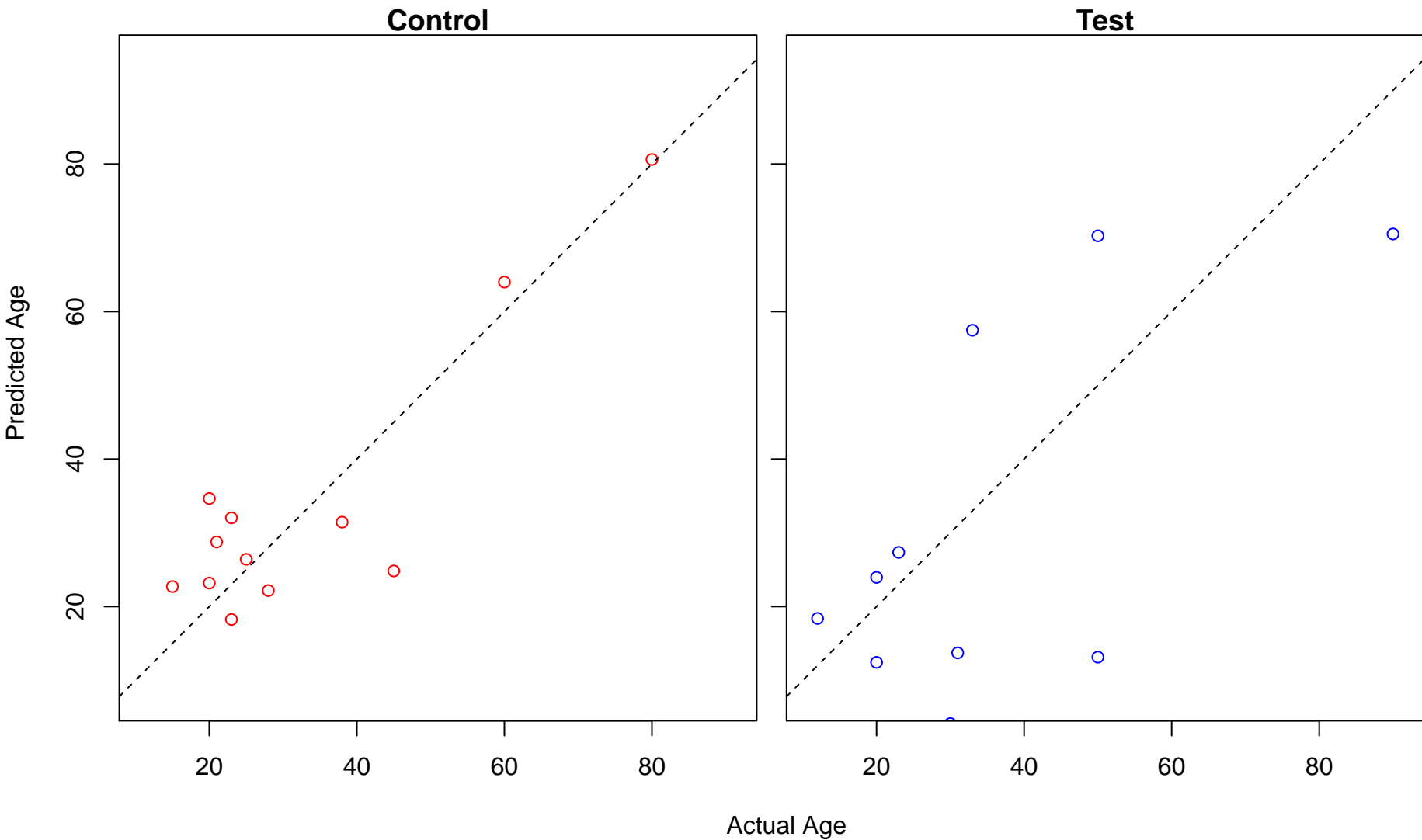
negative regulation of wound healing (Score: 11.360976)



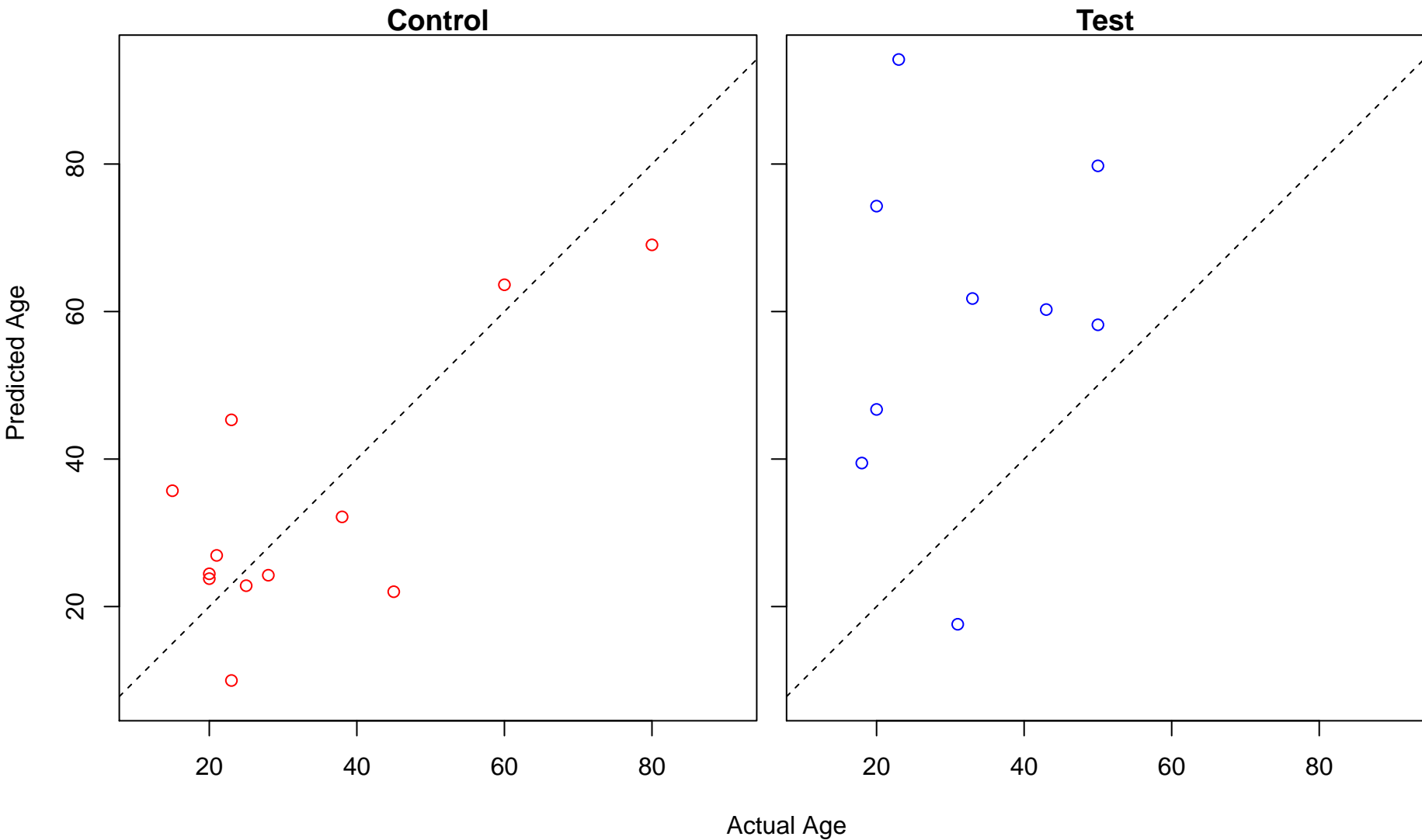
histone H2A ubiquitination (Score: 11.341952)



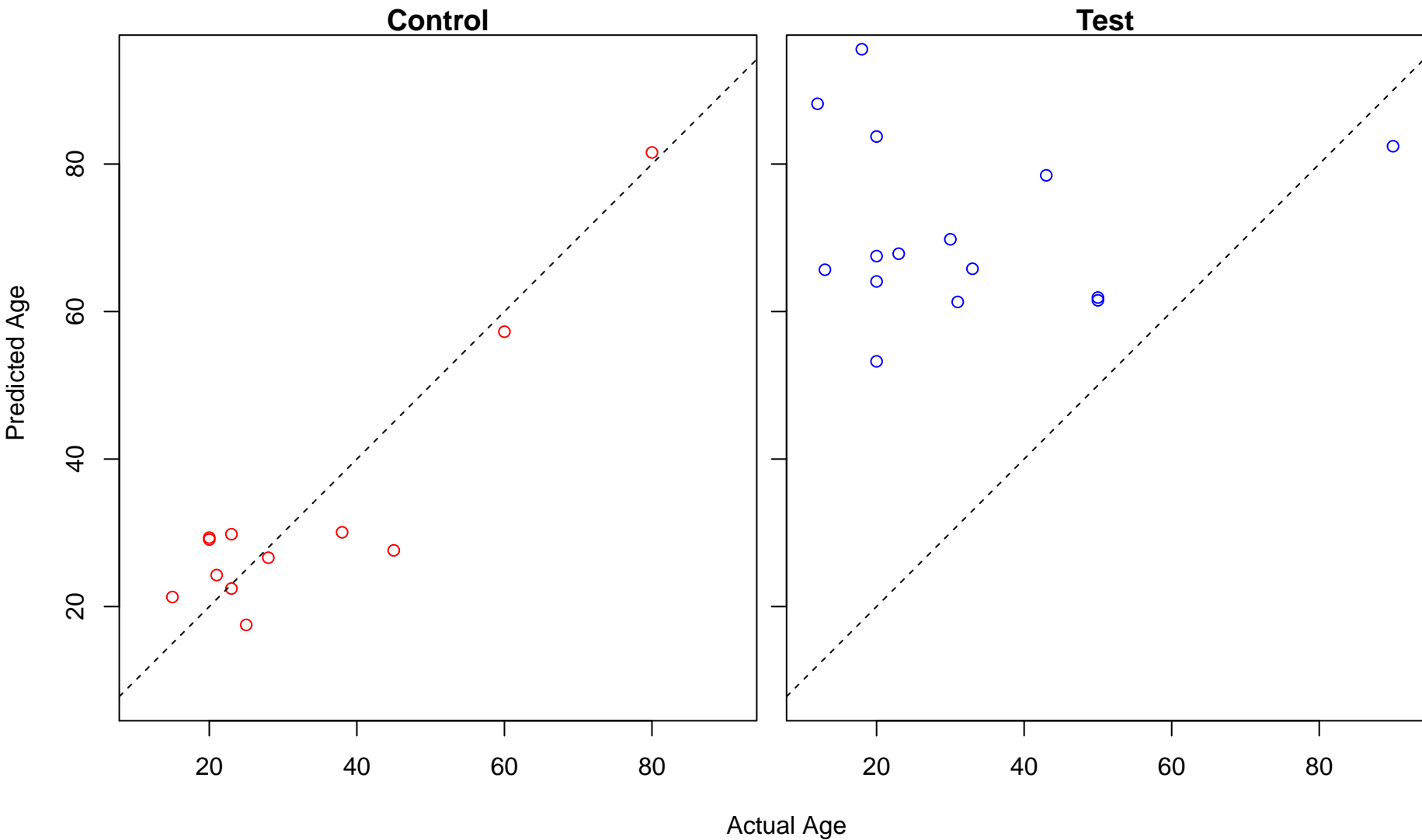
positive regulation of NF-kappaB transcription factor activity (Score: 11.339315)



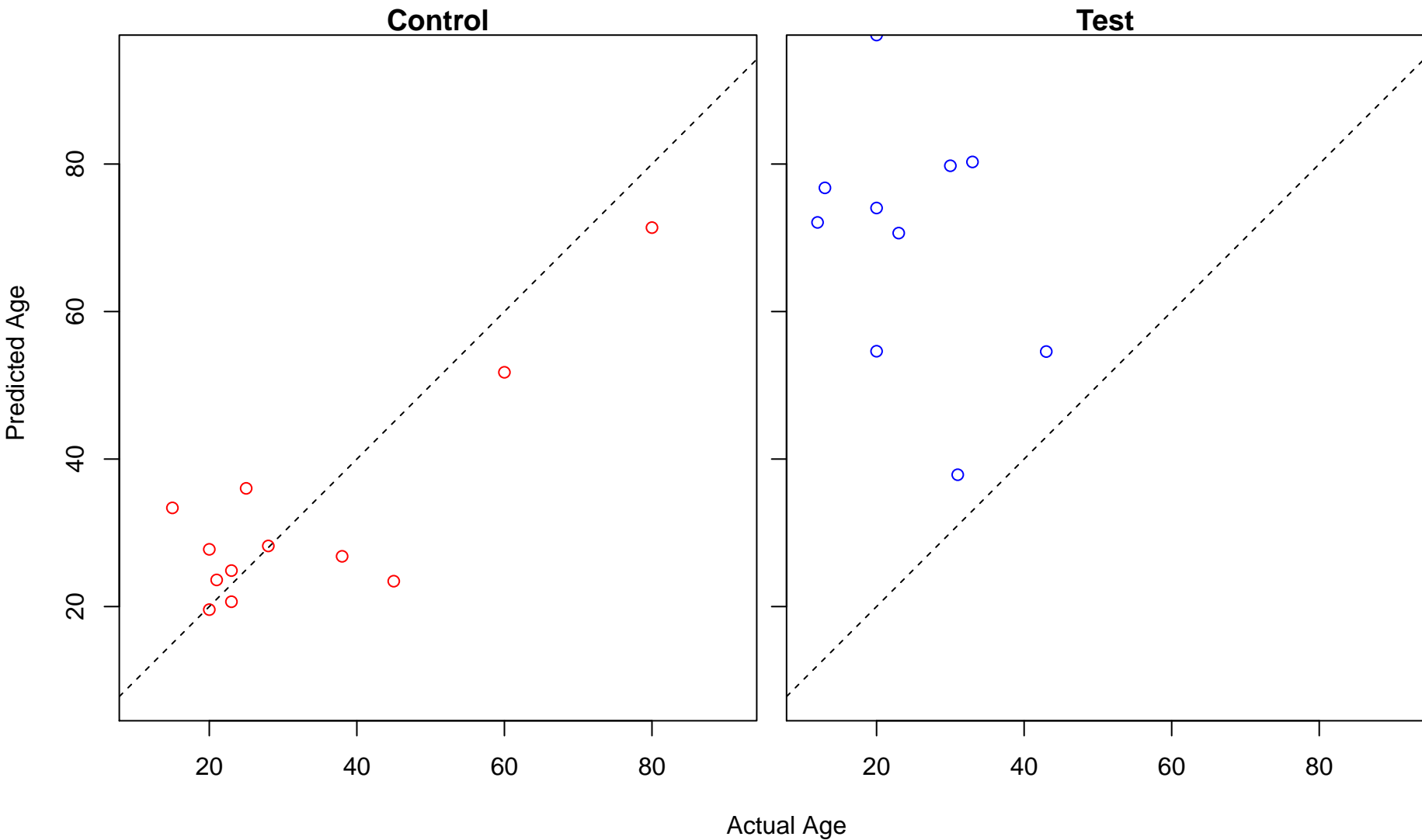
vascular smooth muscle cell differentiation (Score: 11.339010)



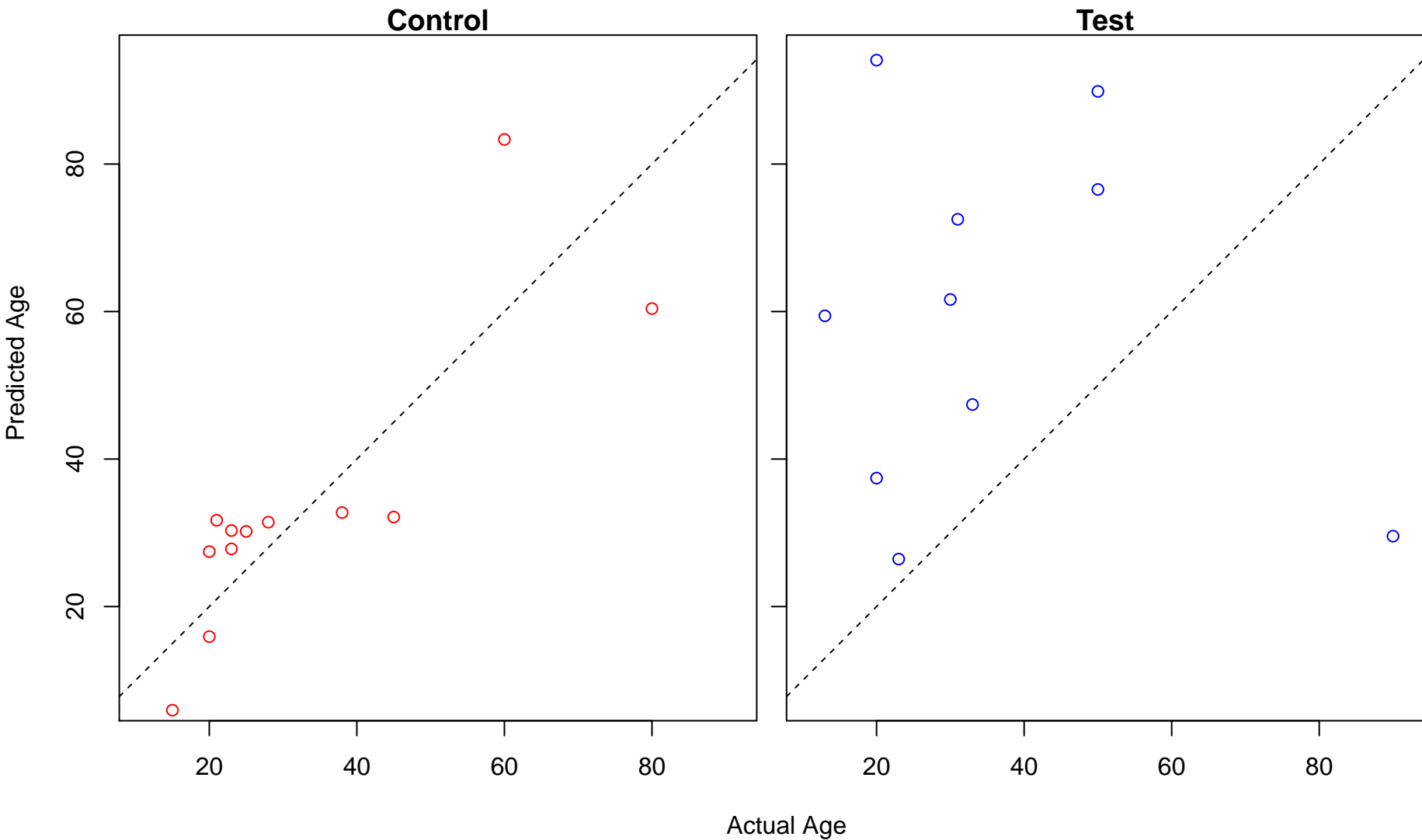
snRNA transcription from RNA polymerase II promoter (Score: 11.330231)



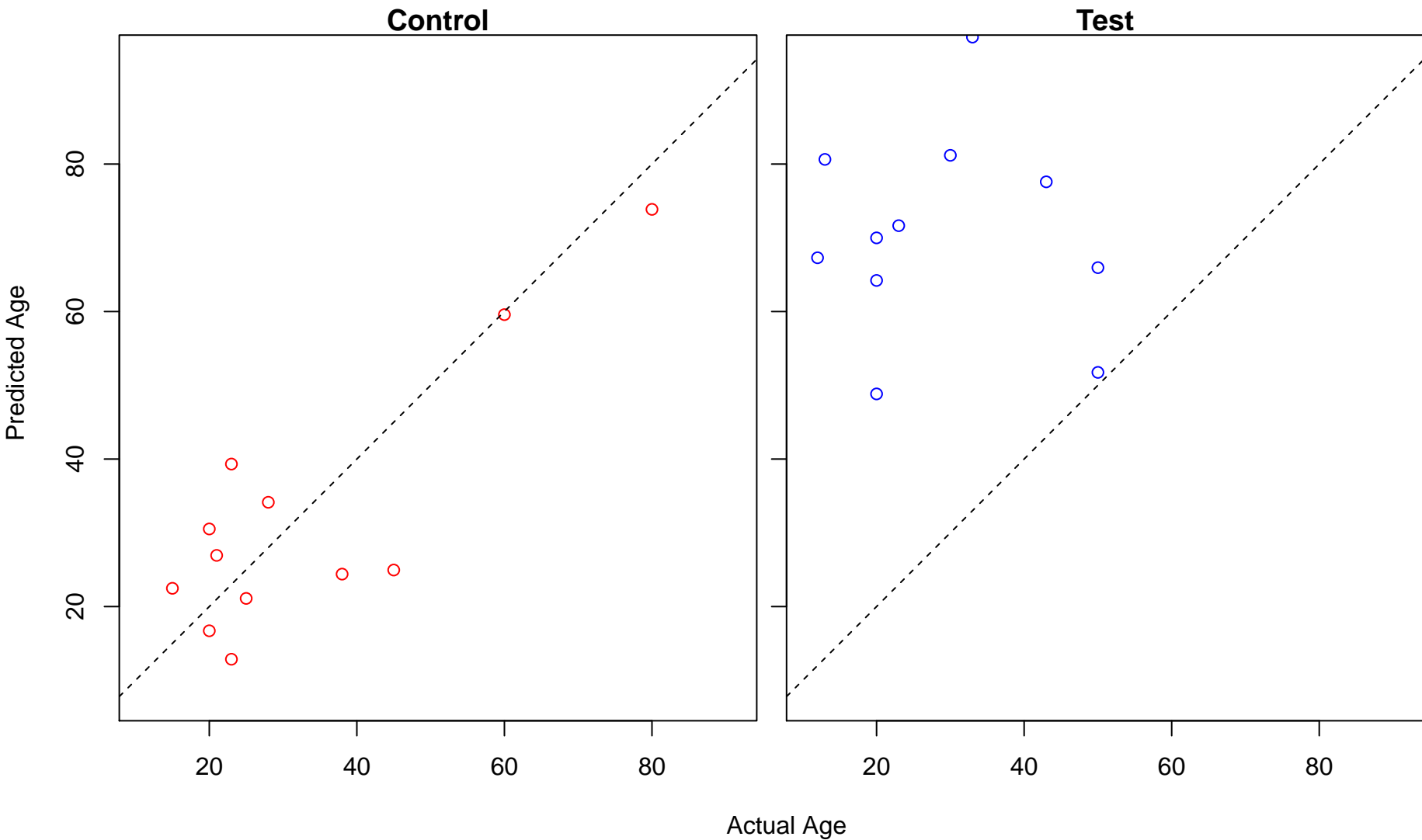
urea metabolic process (Score: 11.326824)



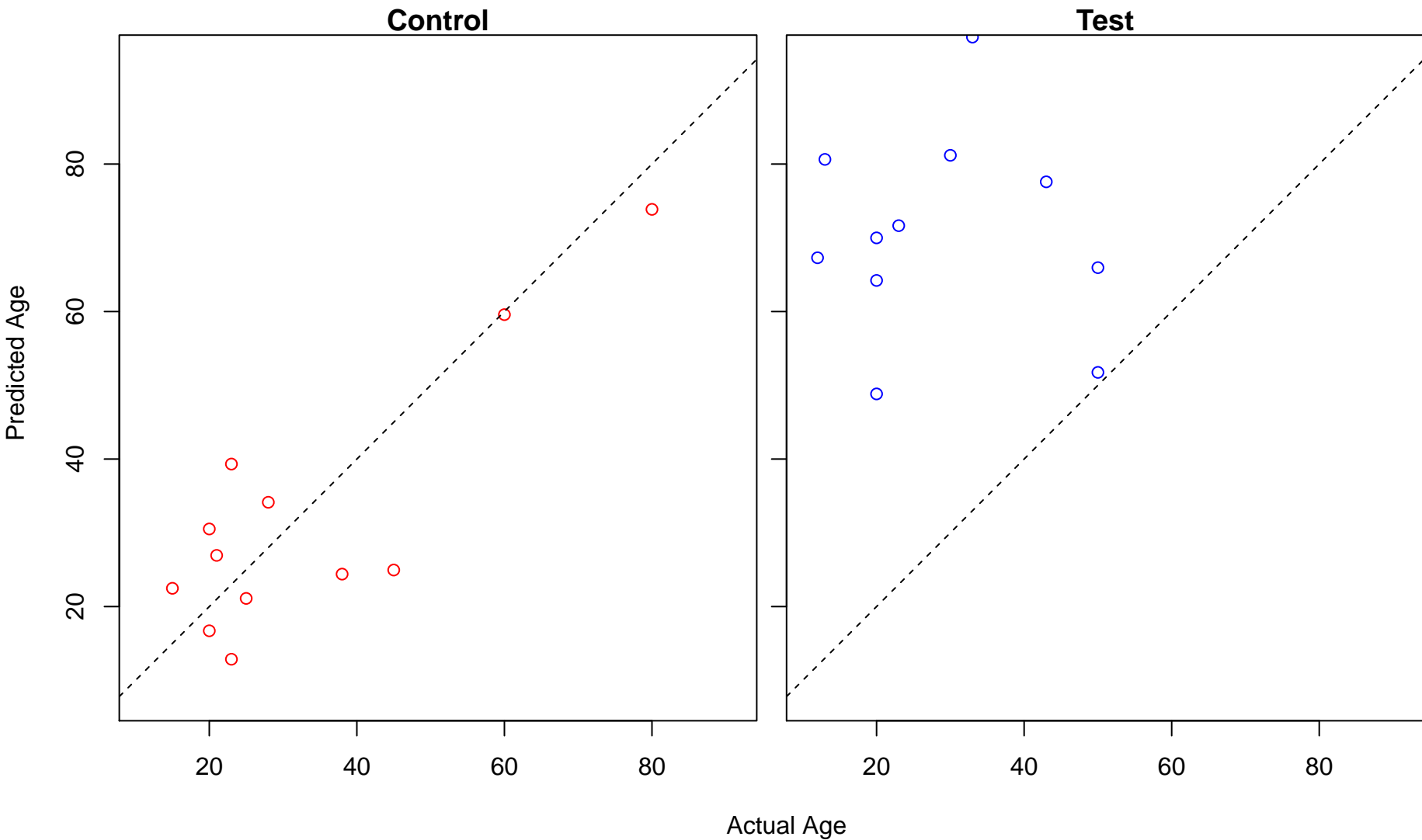
bile acid and bile salt transport (Score: 11.293499)



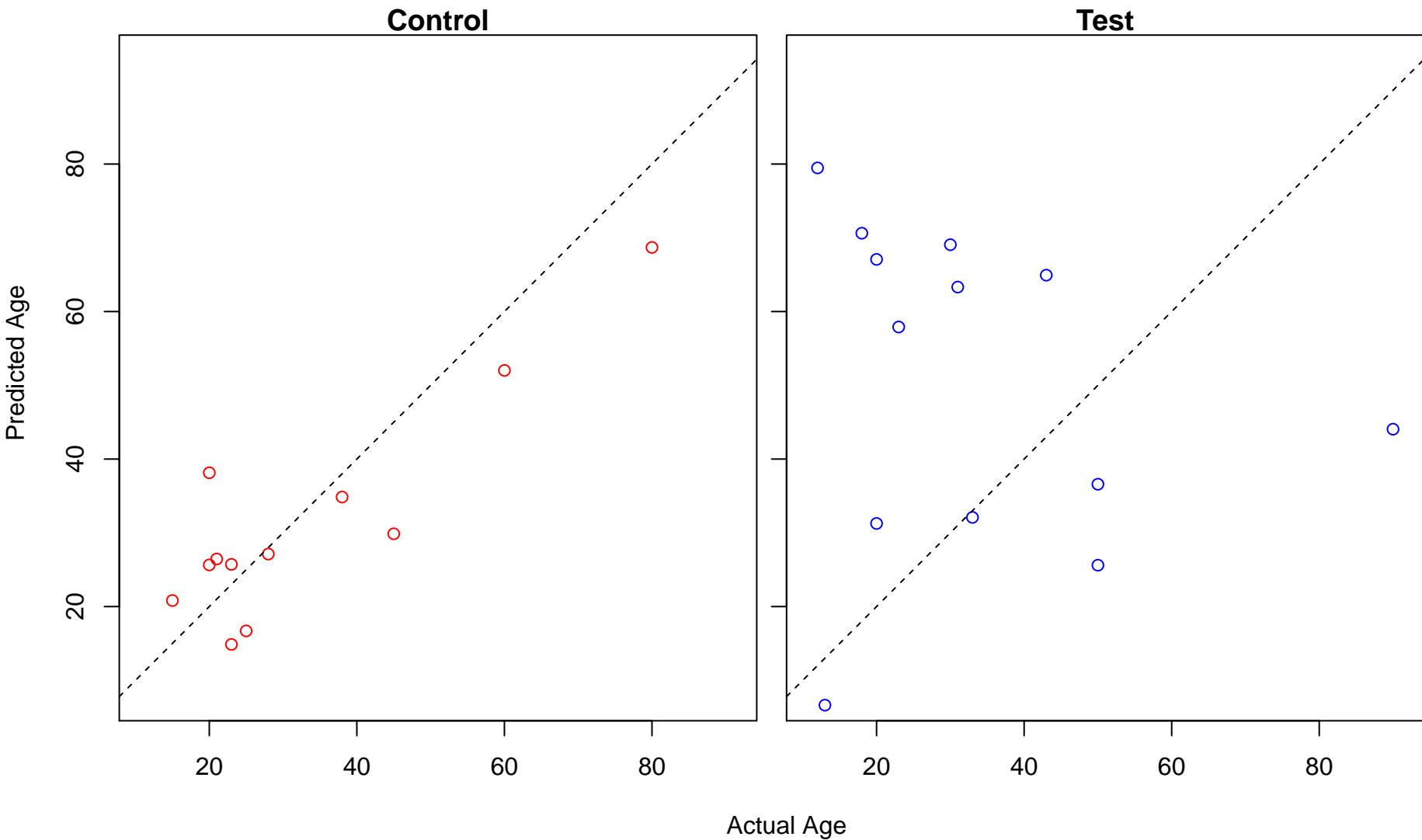
response to nerve growth factor (Score: 11.293005)



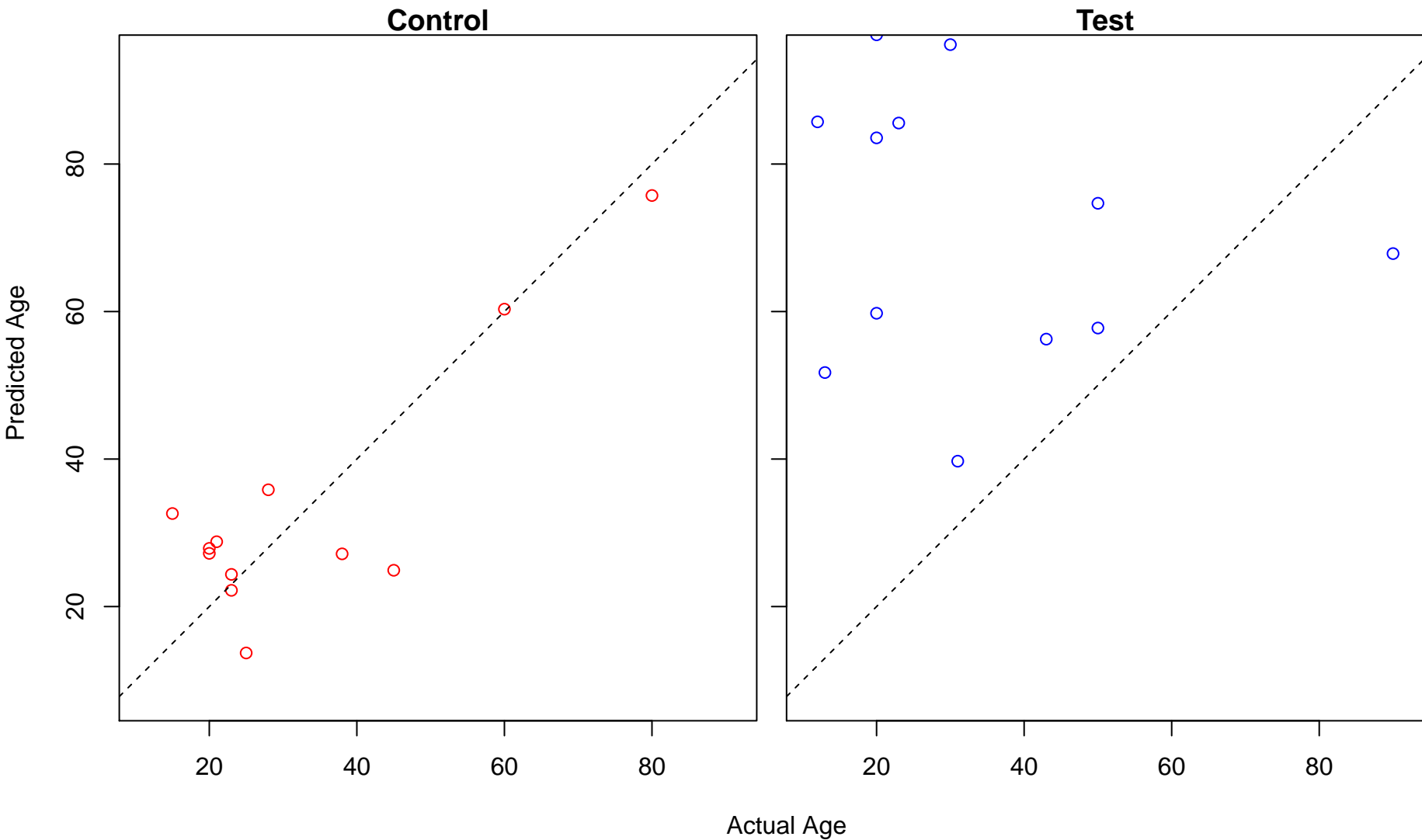
cellular response to nerve growth factor stimulus (Score: 11.293005)



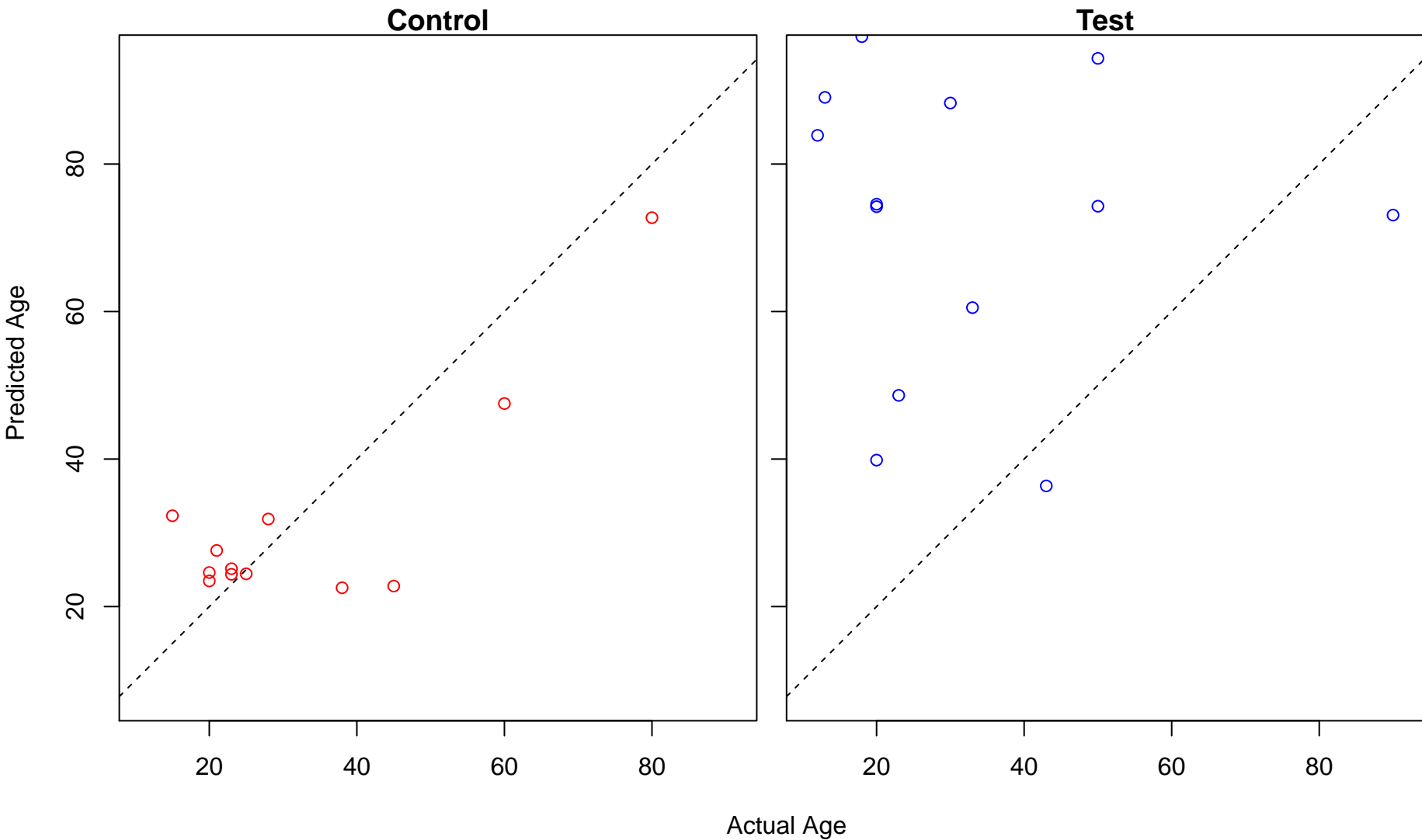
positive regulation of protein kinase B signaling (Score: 11.289379)



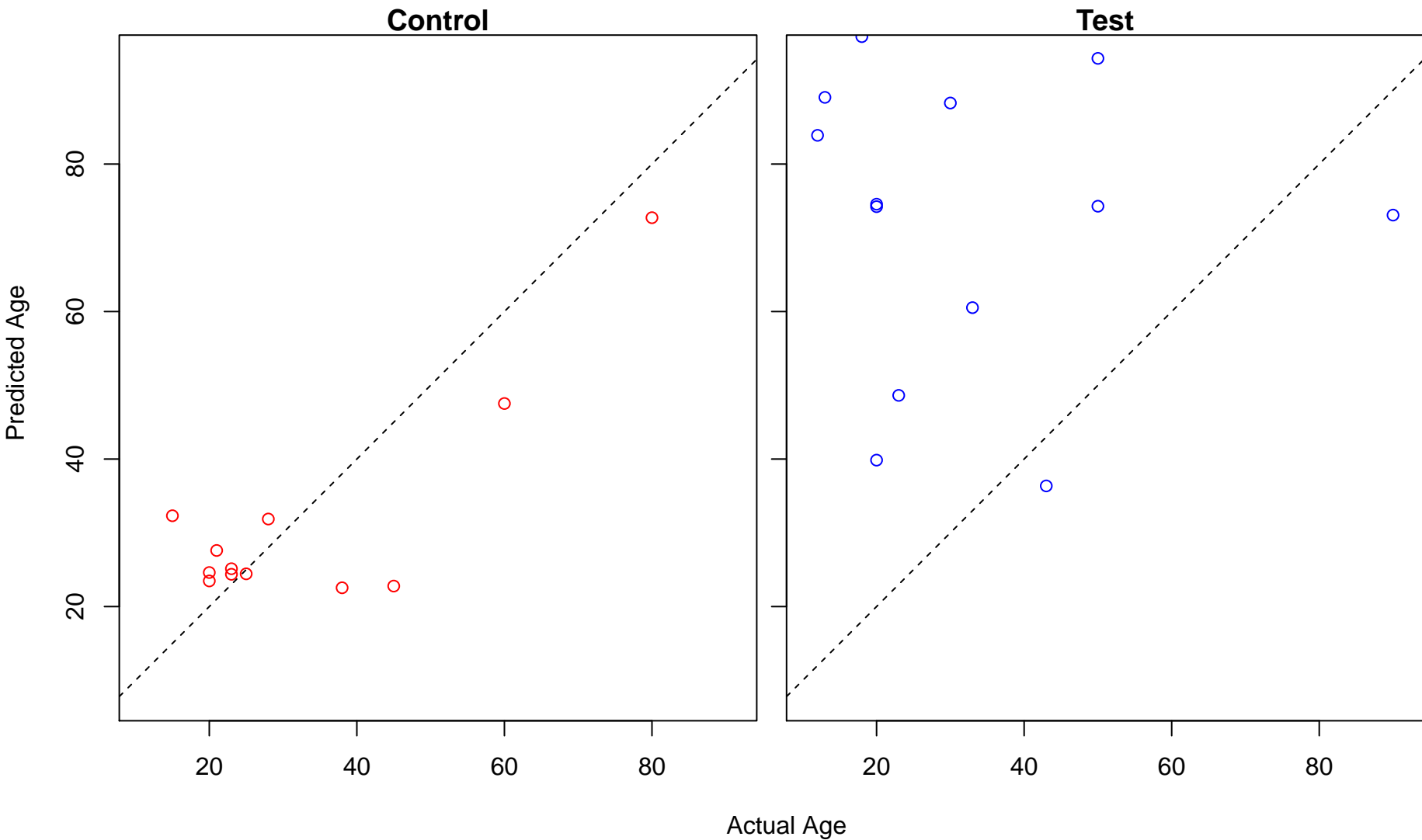
positive regulation of autophagy (Score: 11.275901)



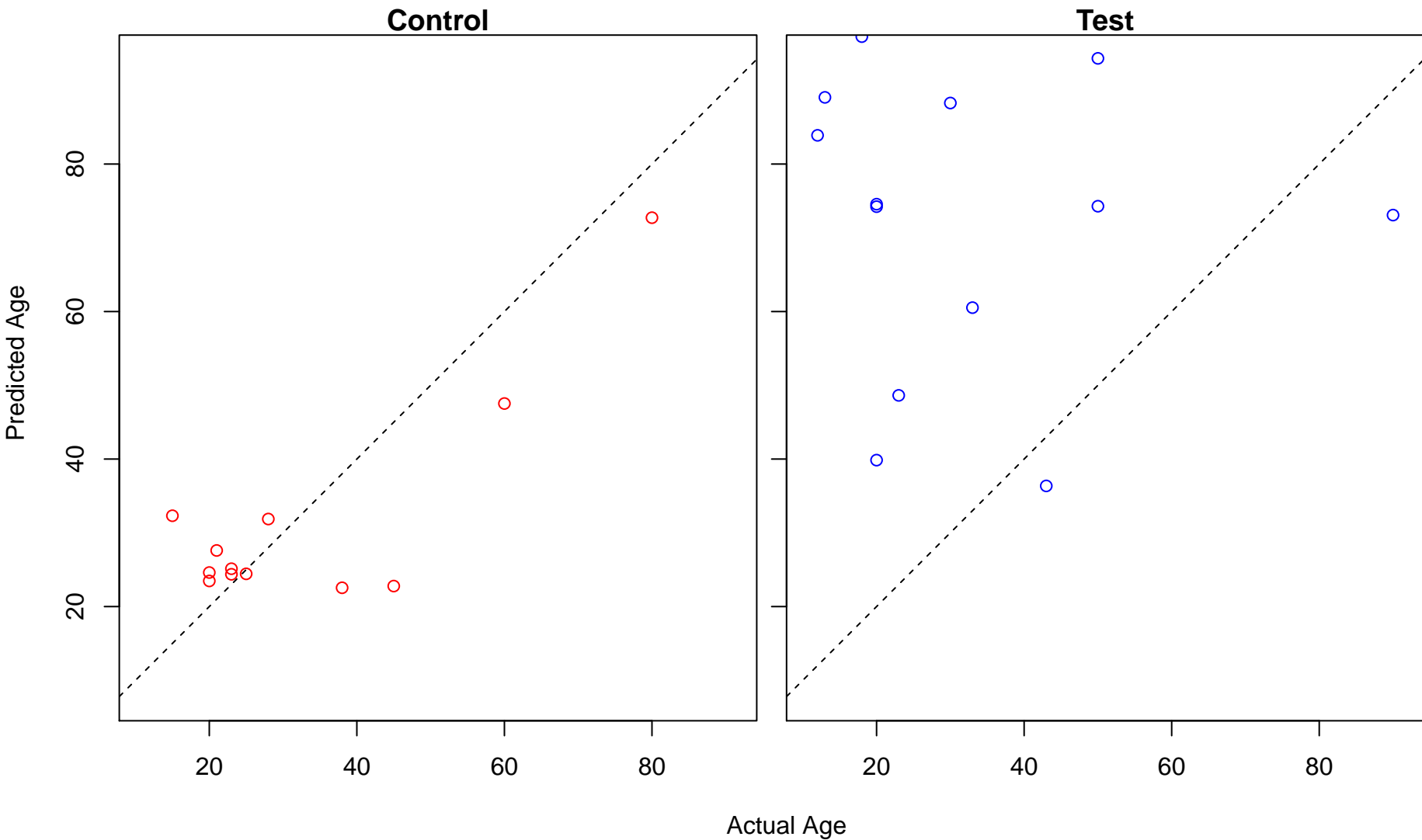
cytidine catabolic process (Score: 11.264202)



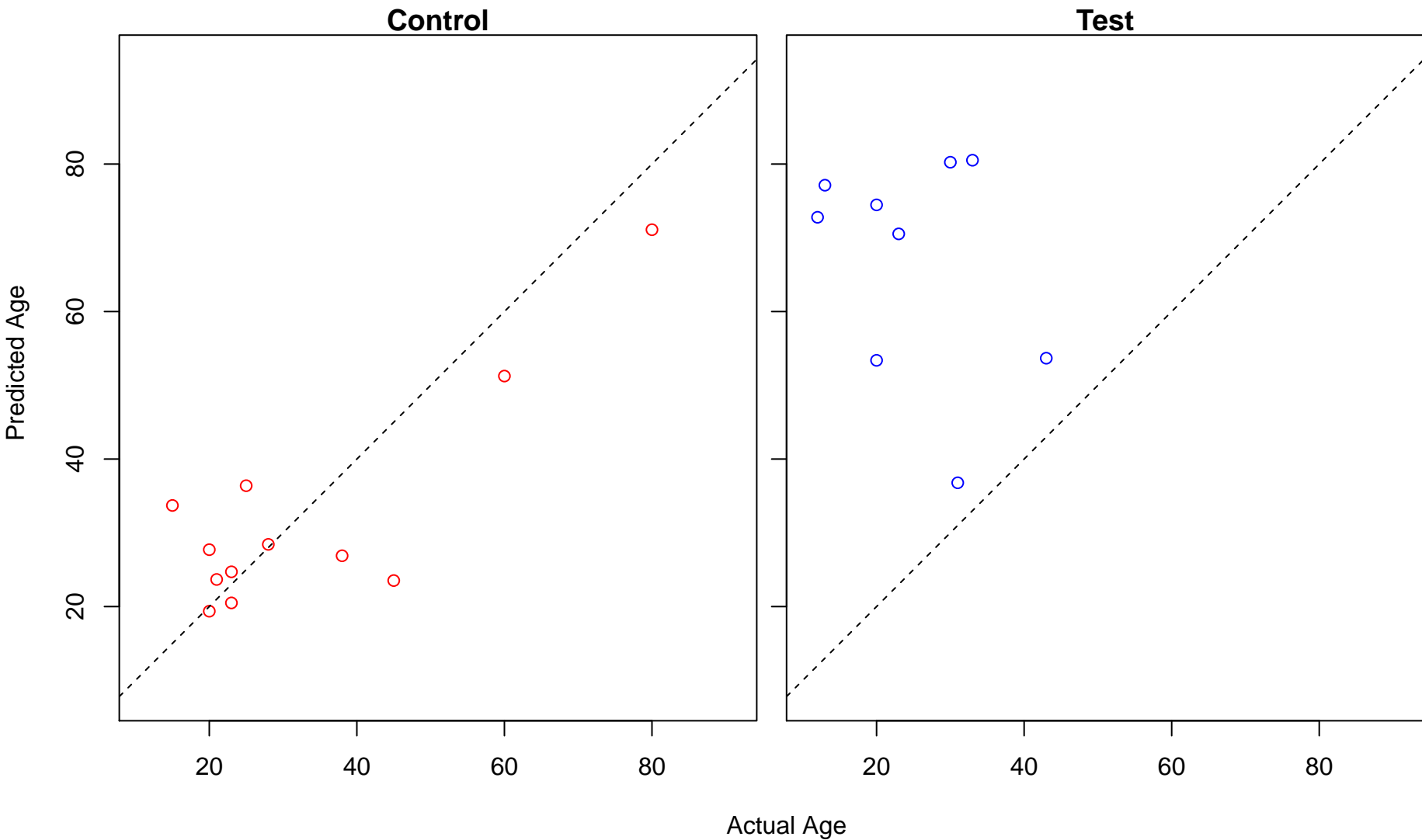
cytidine deamination (Score: 11.264202)



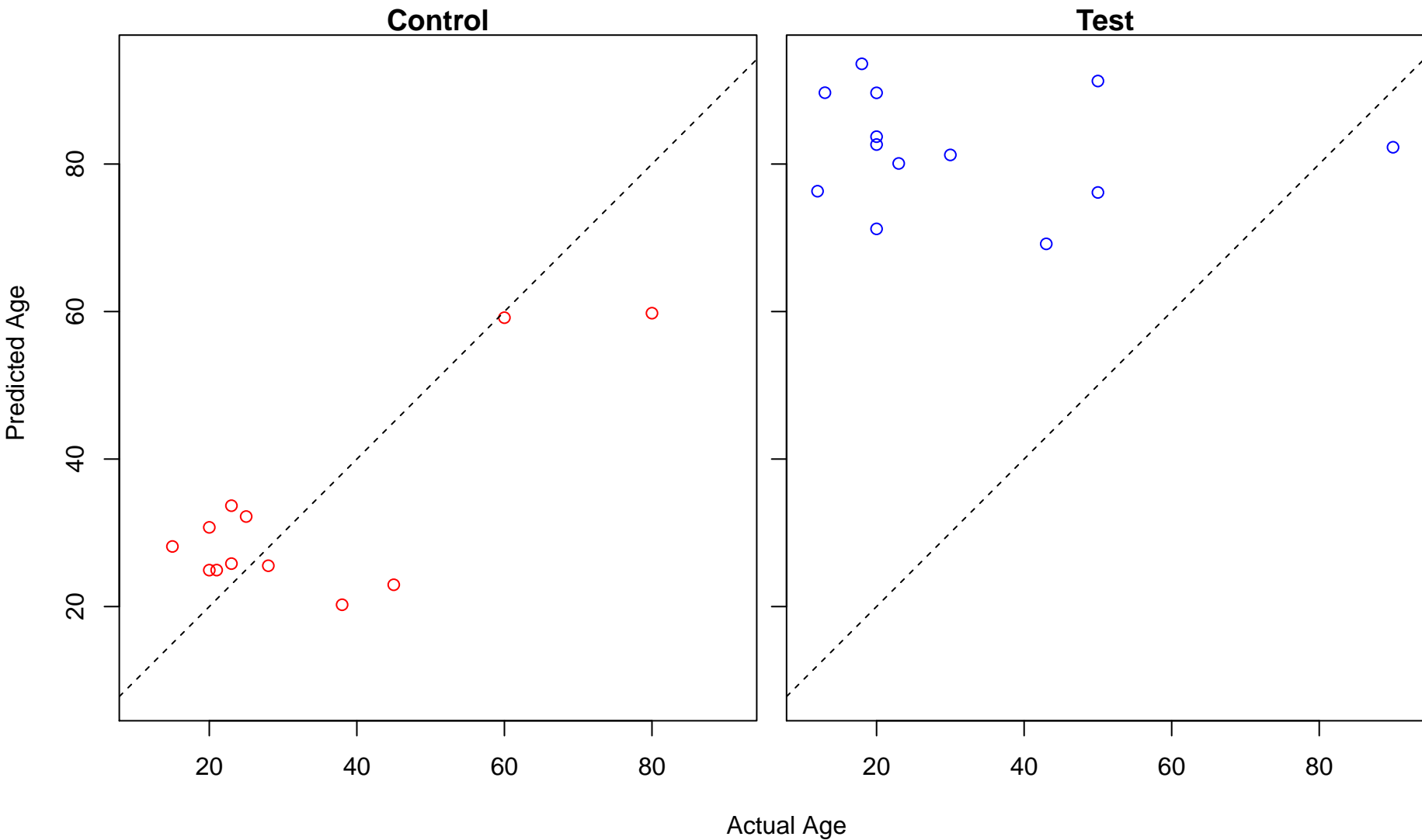
cytidine metabolic process (Score: 11.264202)



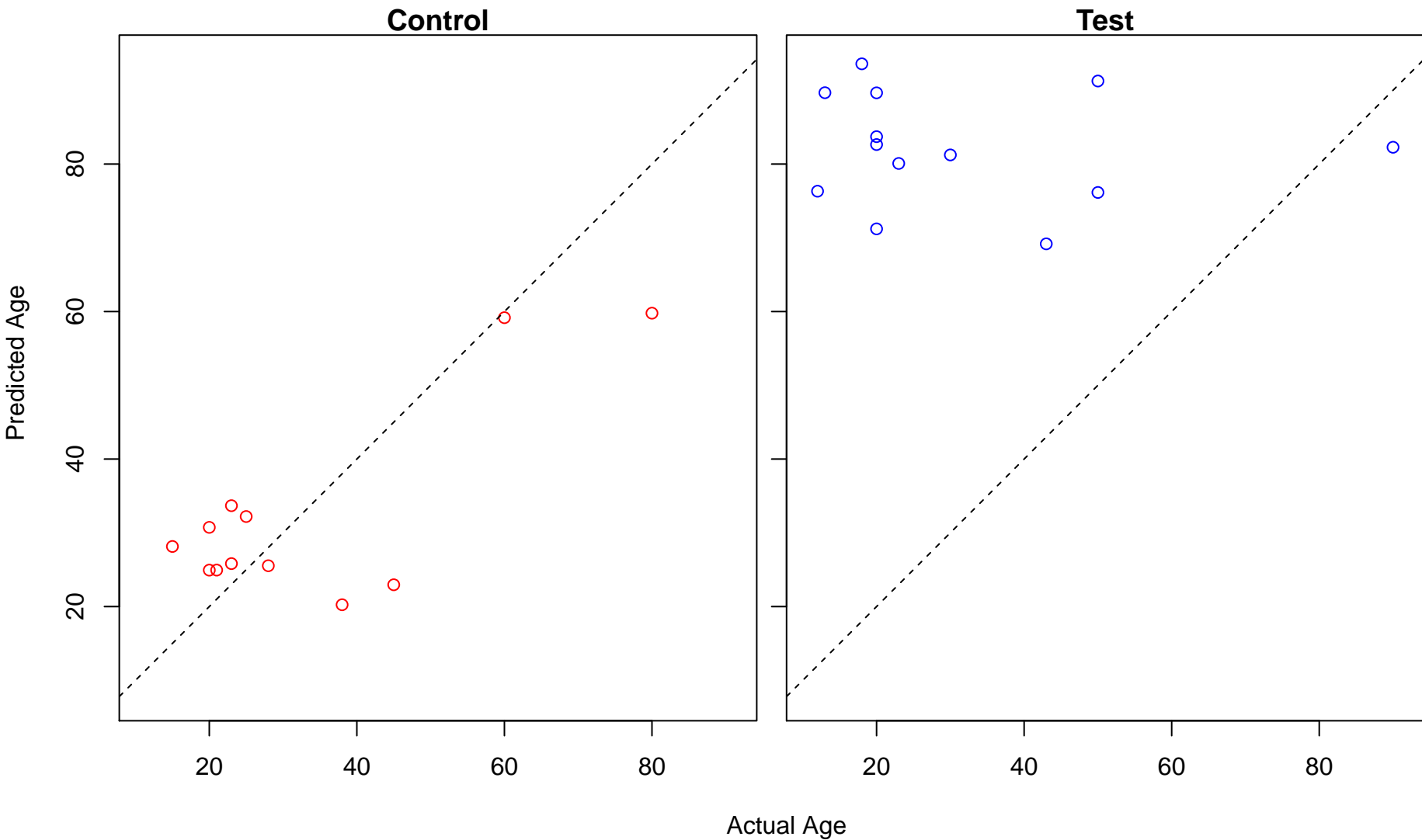
urea cycle (Score: 11.250287)



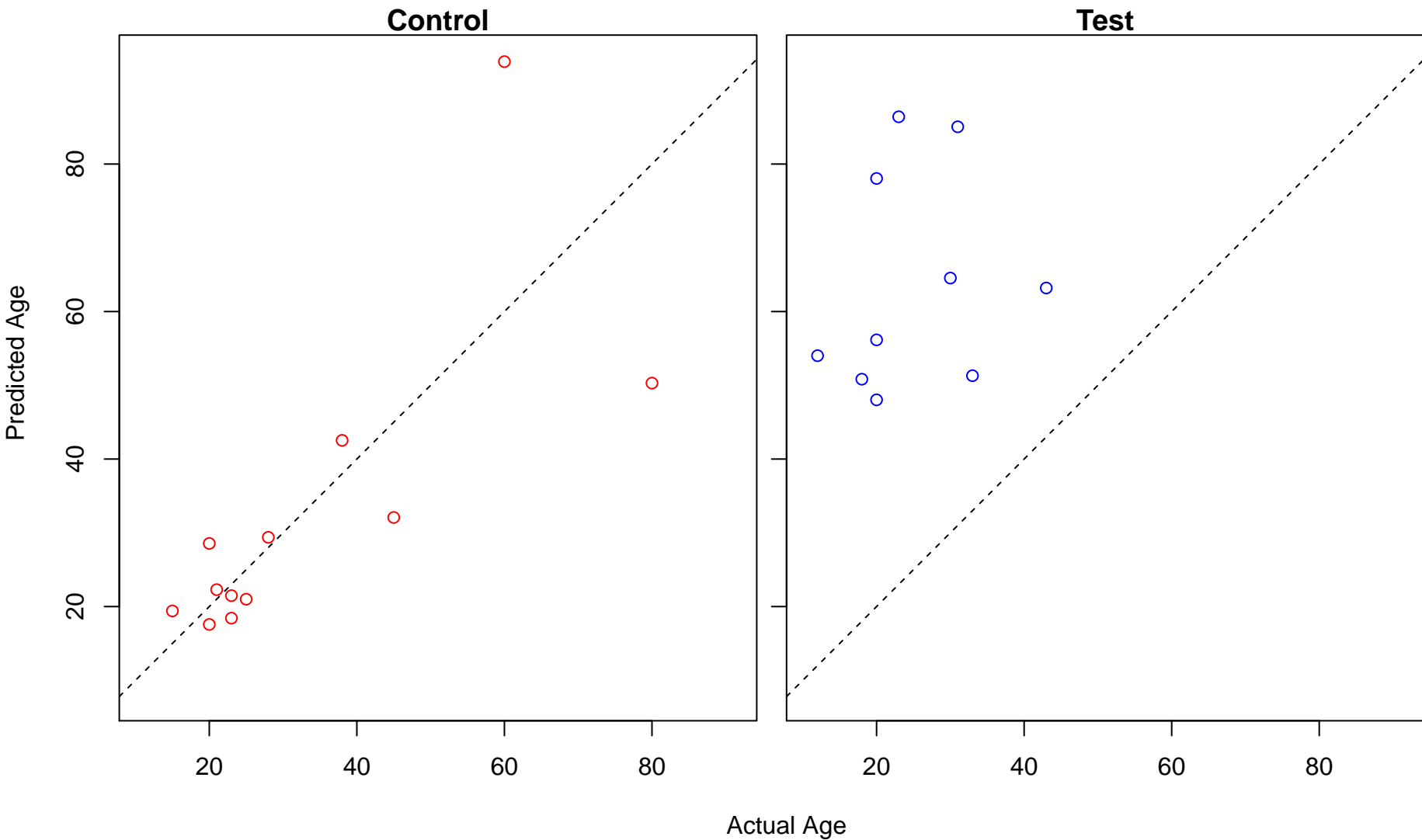
positive regulation of T cell differentiation in thymus (Score: 11.247457)



positive regulation of thymocyte aggregation (Score: 11.247457)

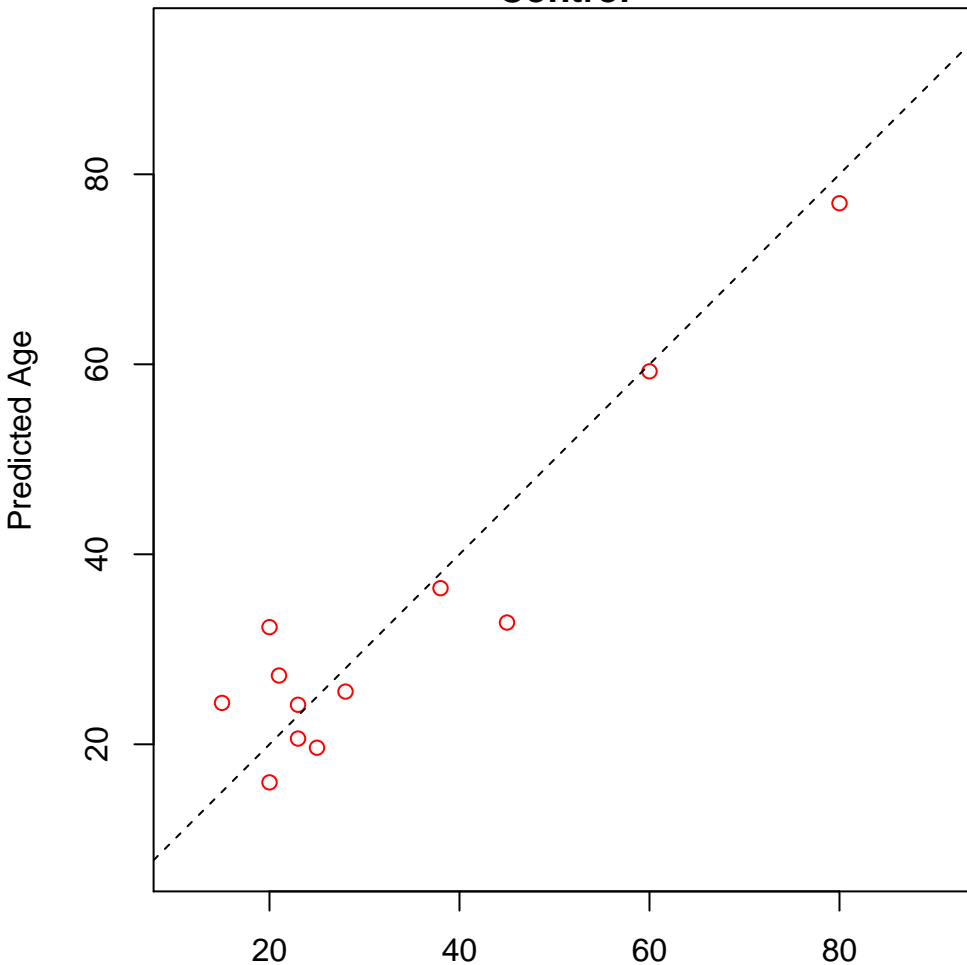


positive regulation of interleukin-10 production (Score: 11.203446)

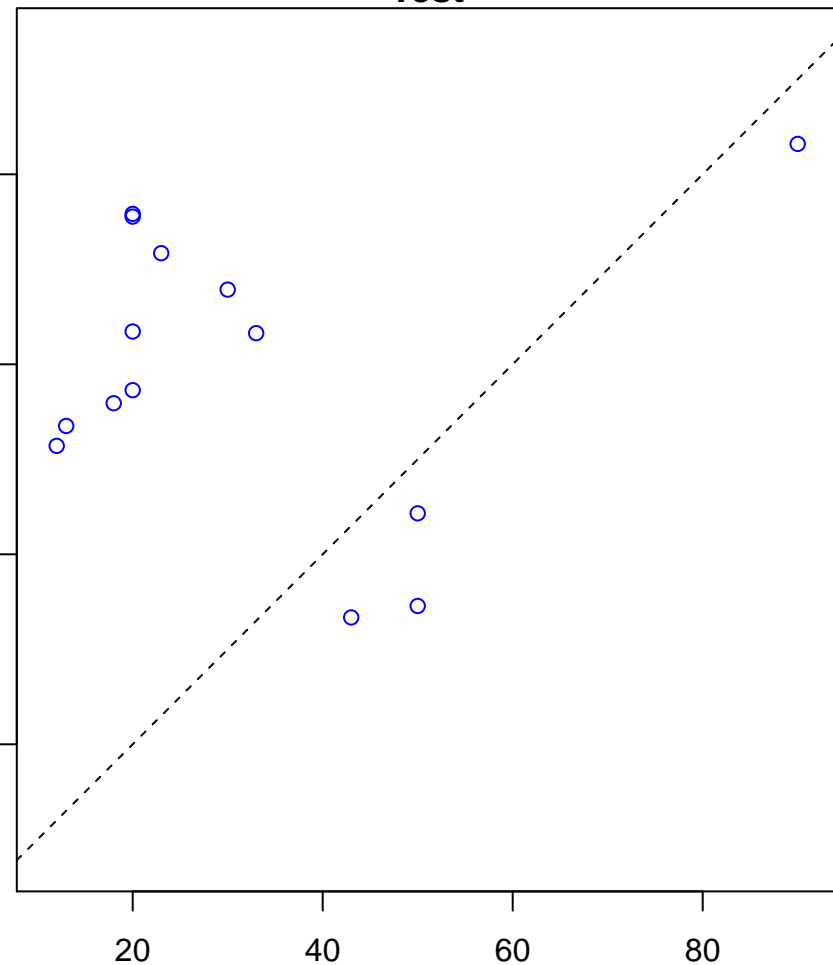


endocrine pancreas development (Score: 11.202074)

Control

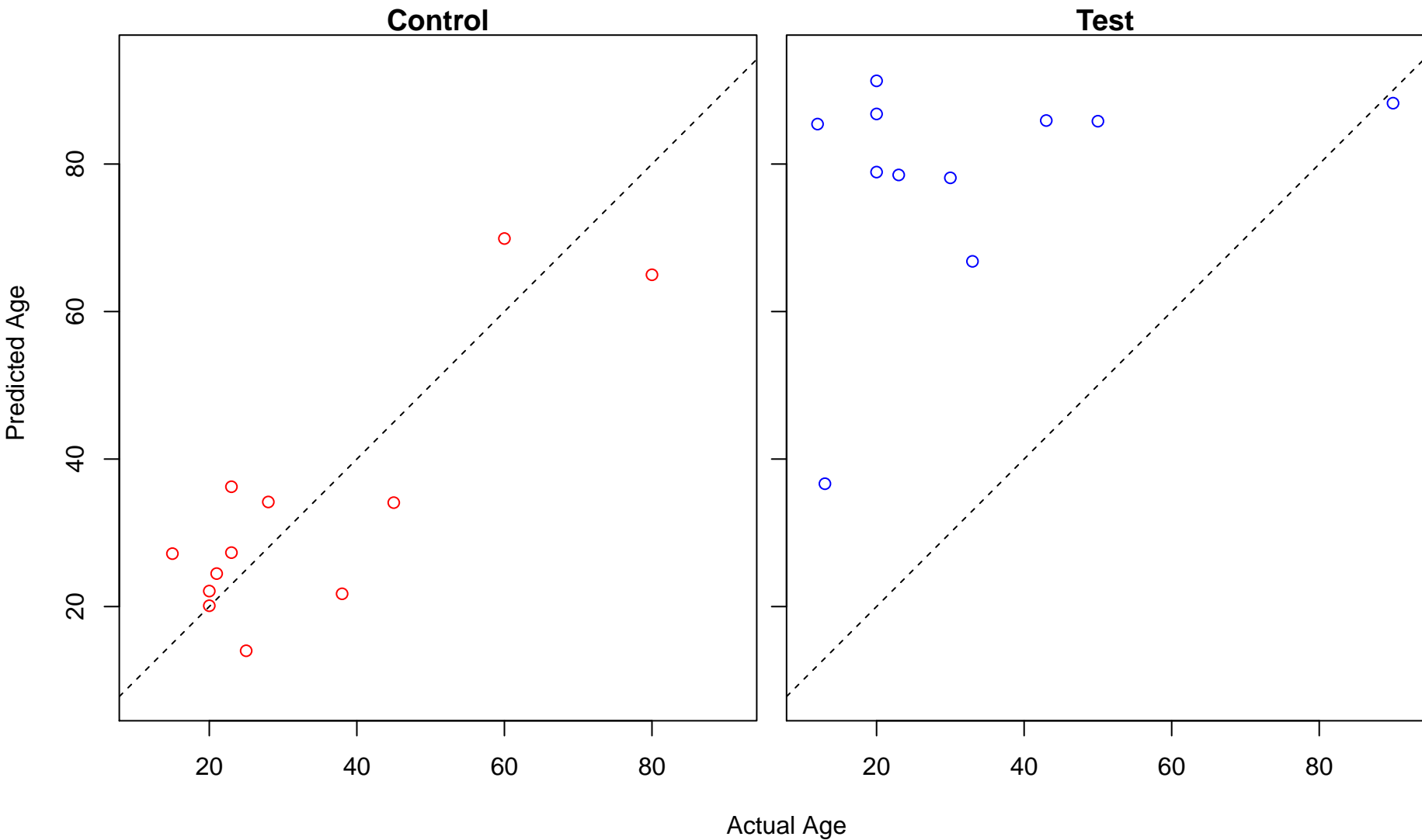


Test

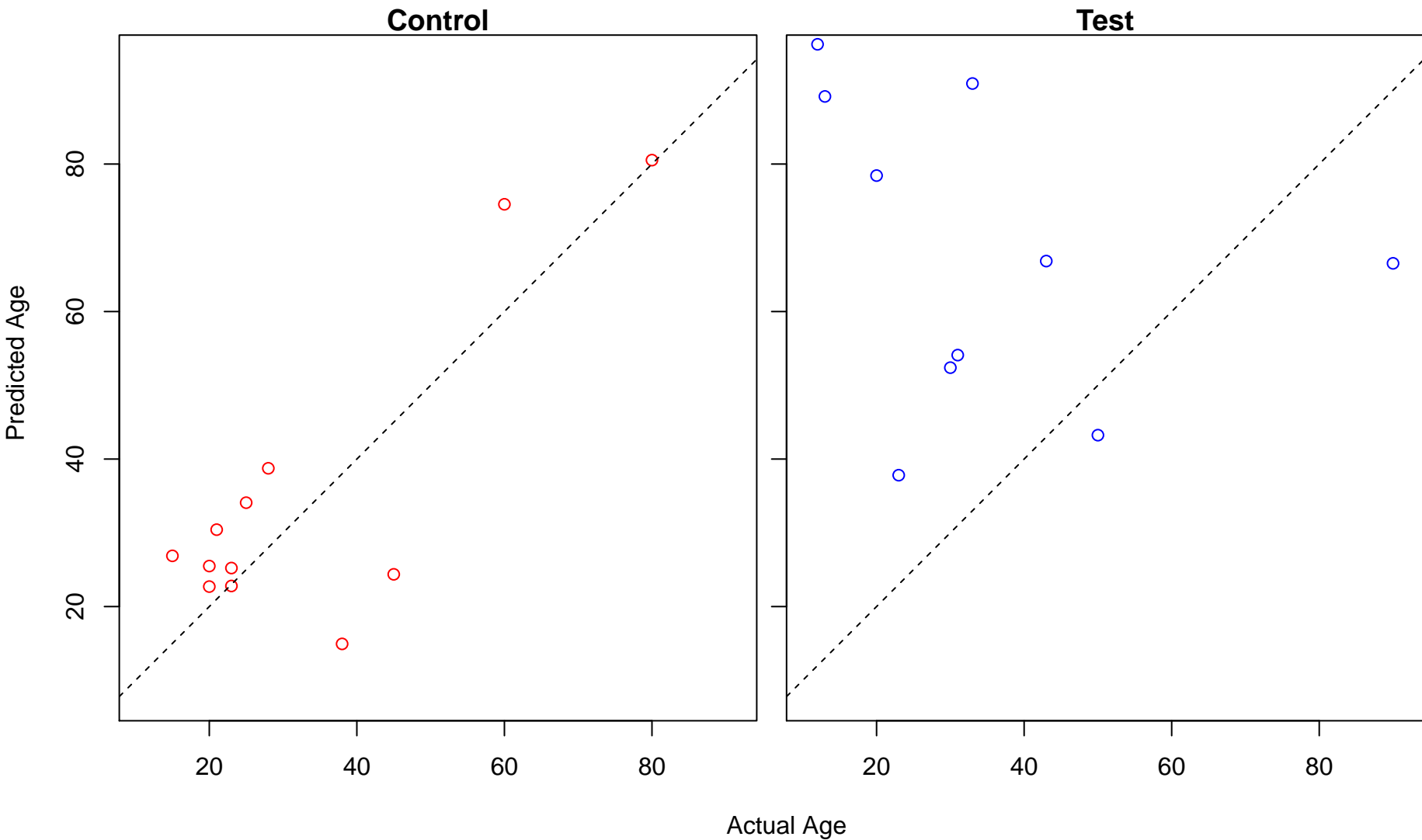


Actual Age

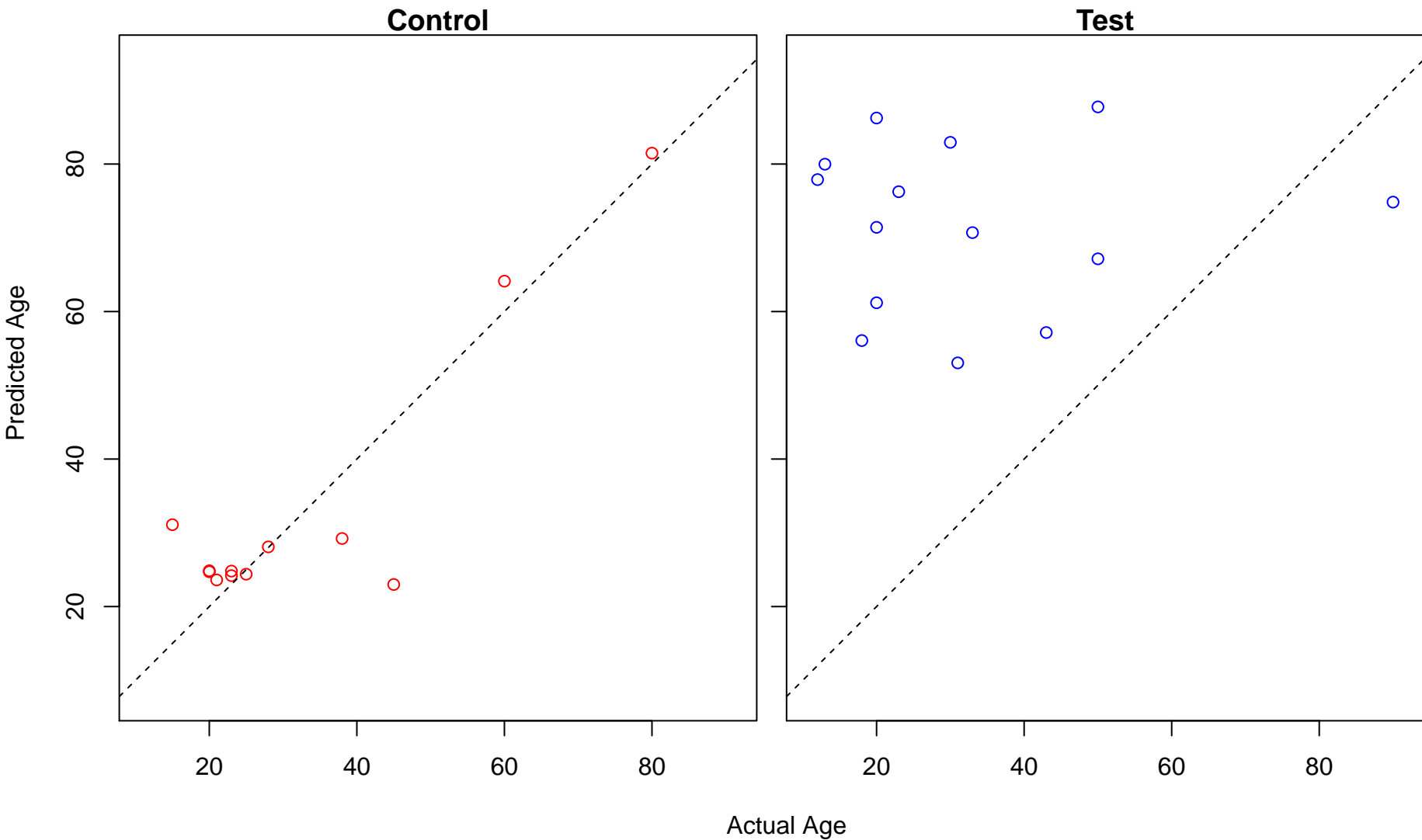
positive regulation of triglyceride catabolic process (Score: 11.199463)



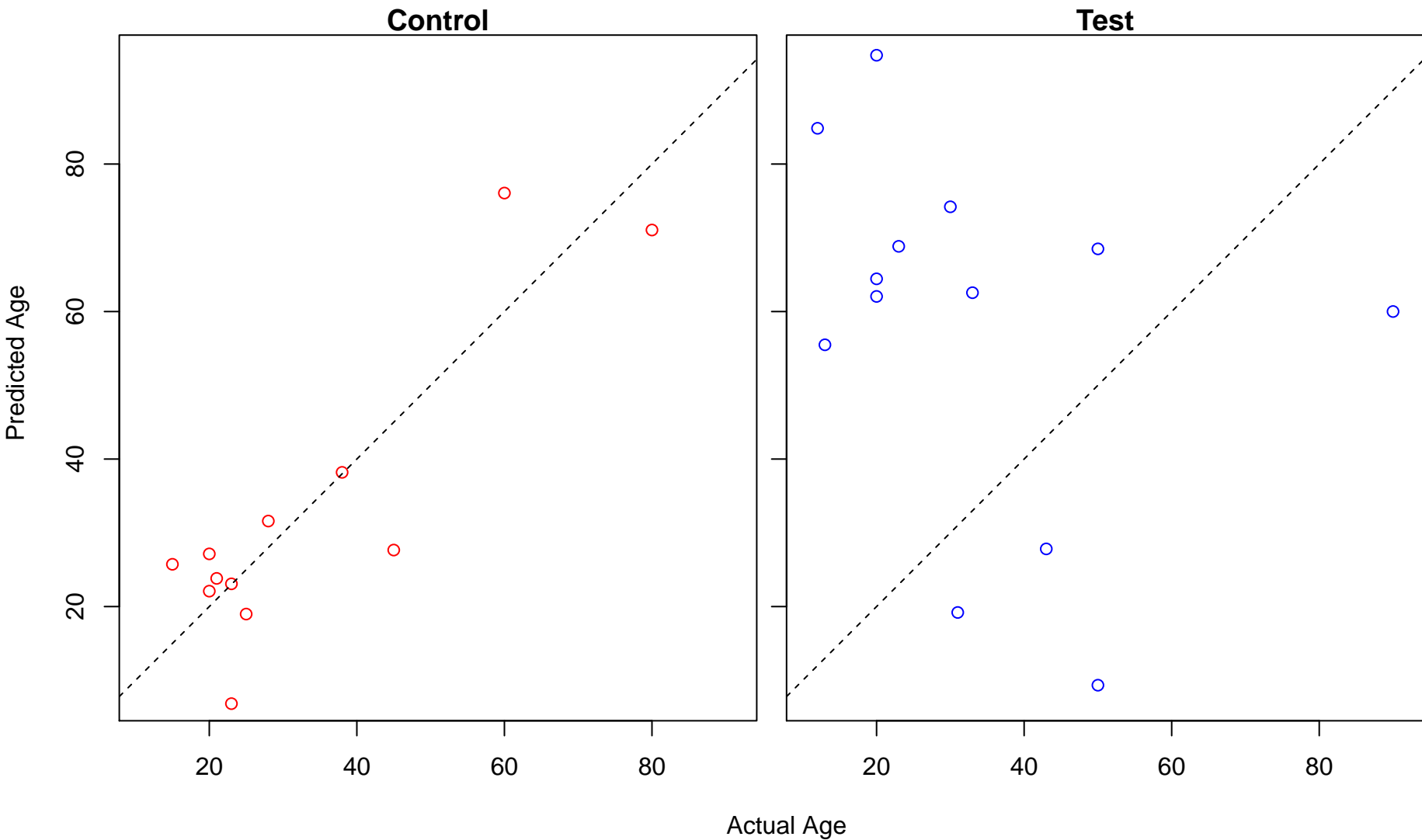
response to vitamin (Score: 11.183022)



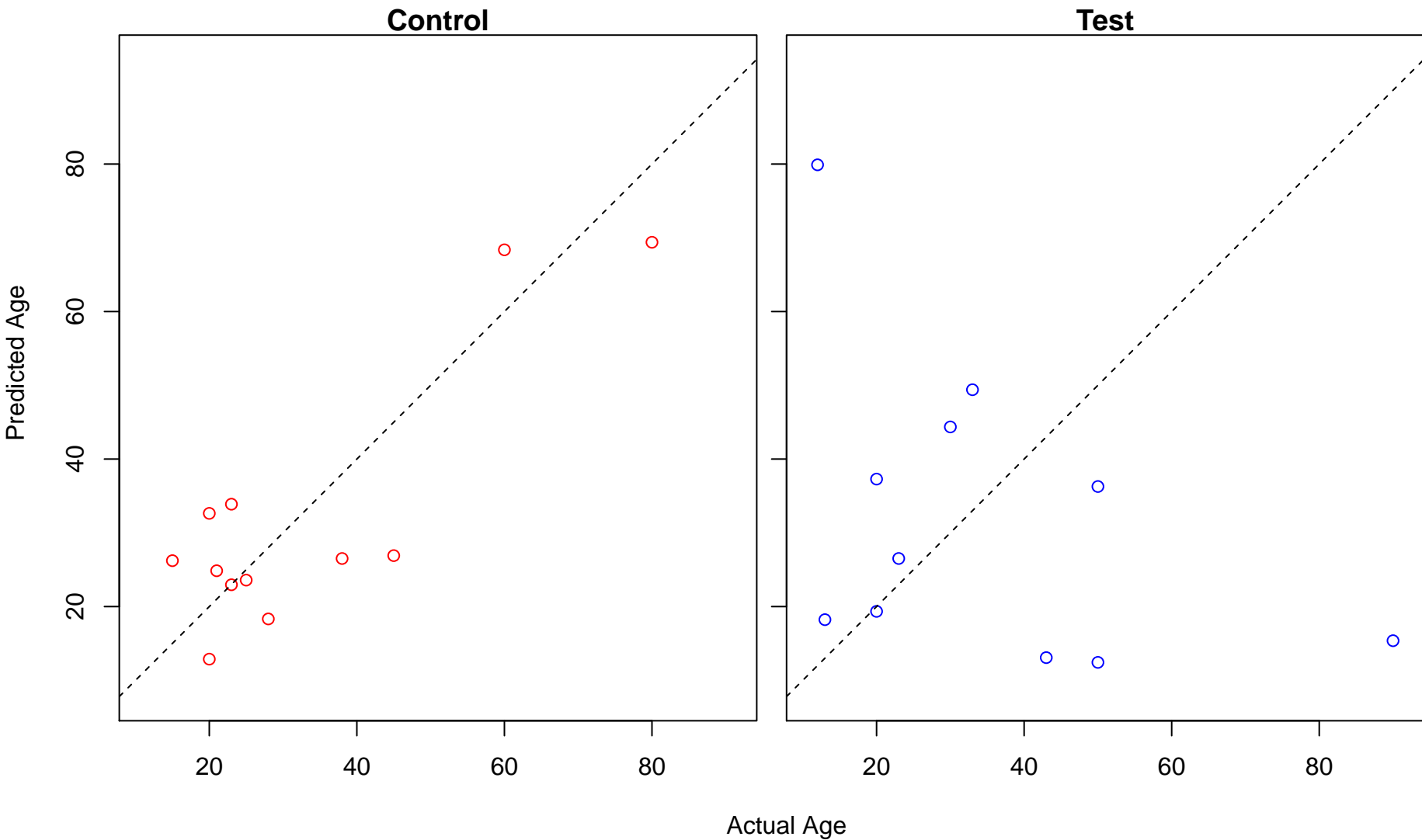
regulation of Golgi organization (Score: 11.155815)



toxin metabolic process (Score: 11.150256)

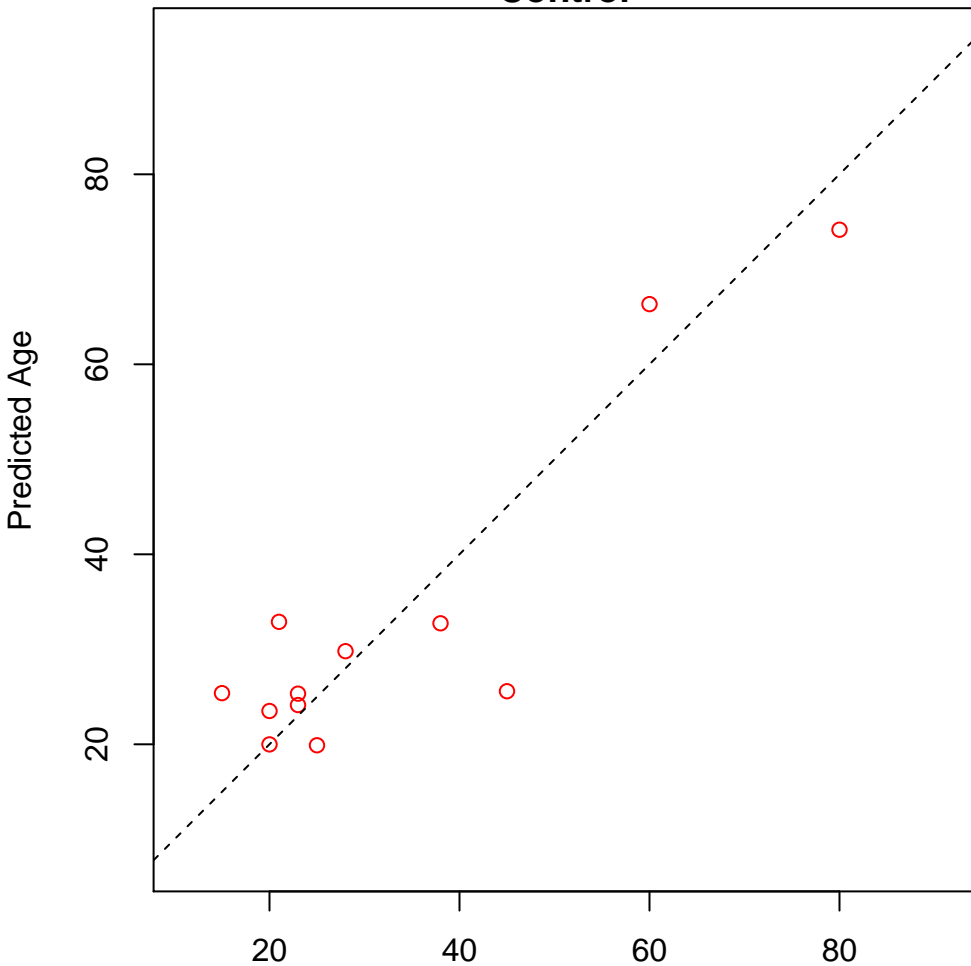


histone H2A monoubiquitination (Score: 11.150167)

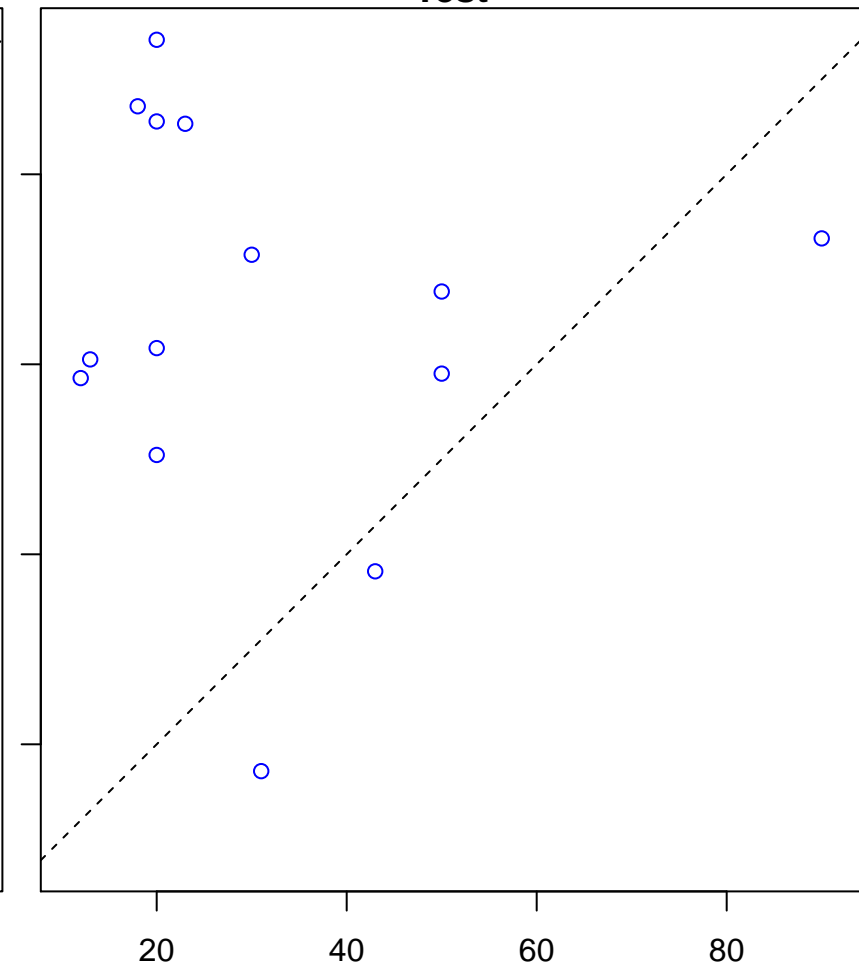


regulation of anatomical structure size (Score: 11.149768)

Control

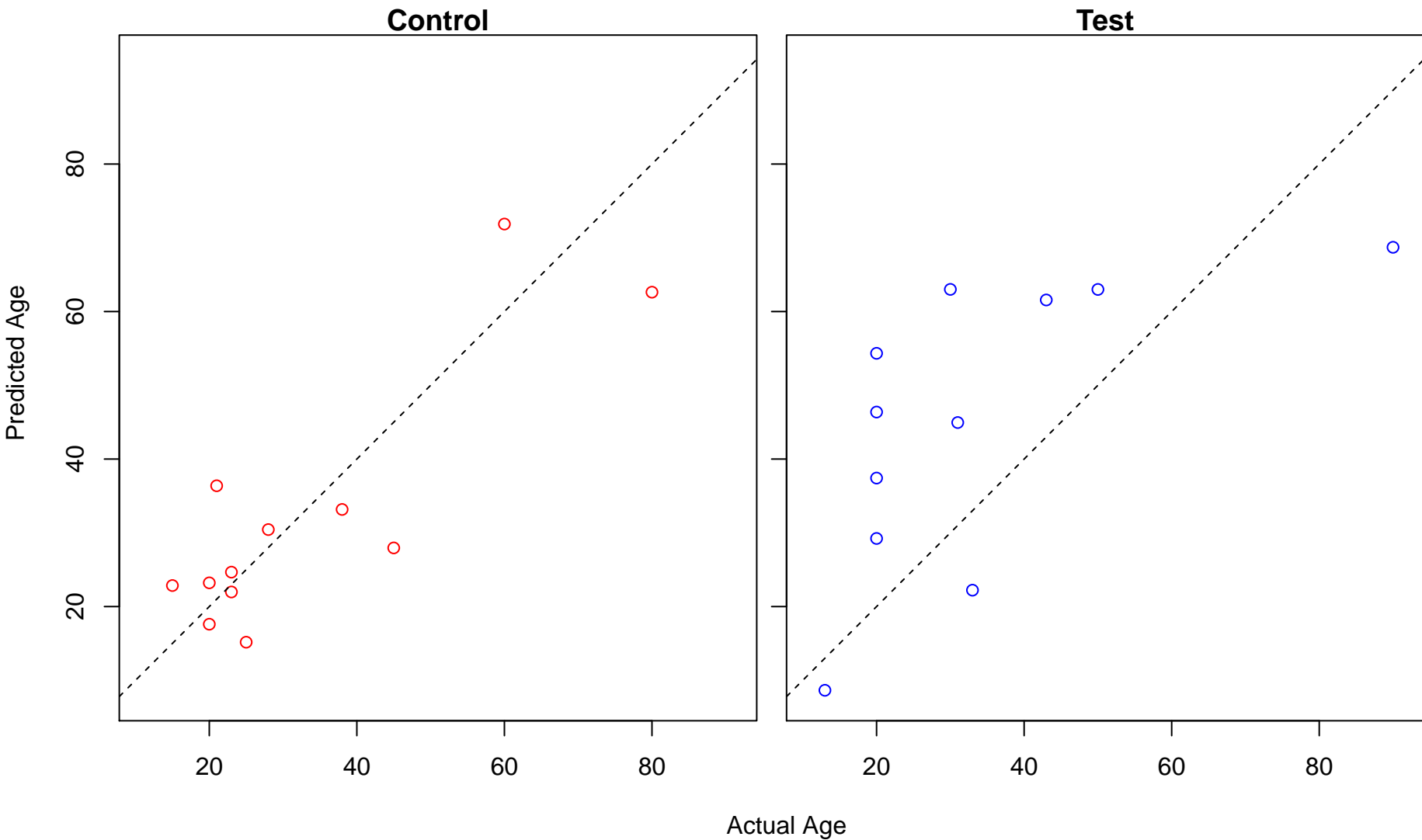


Test

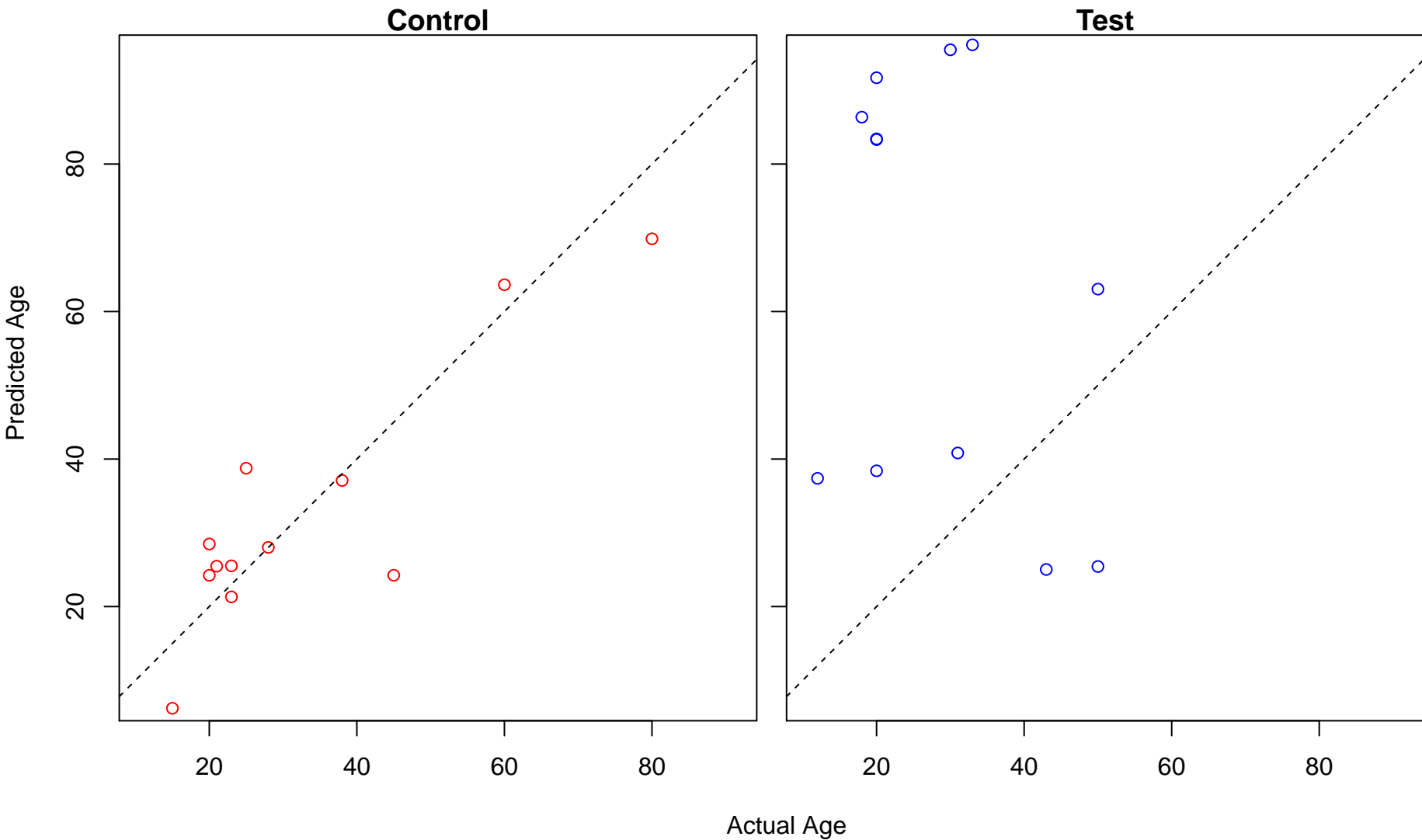


Actual Age

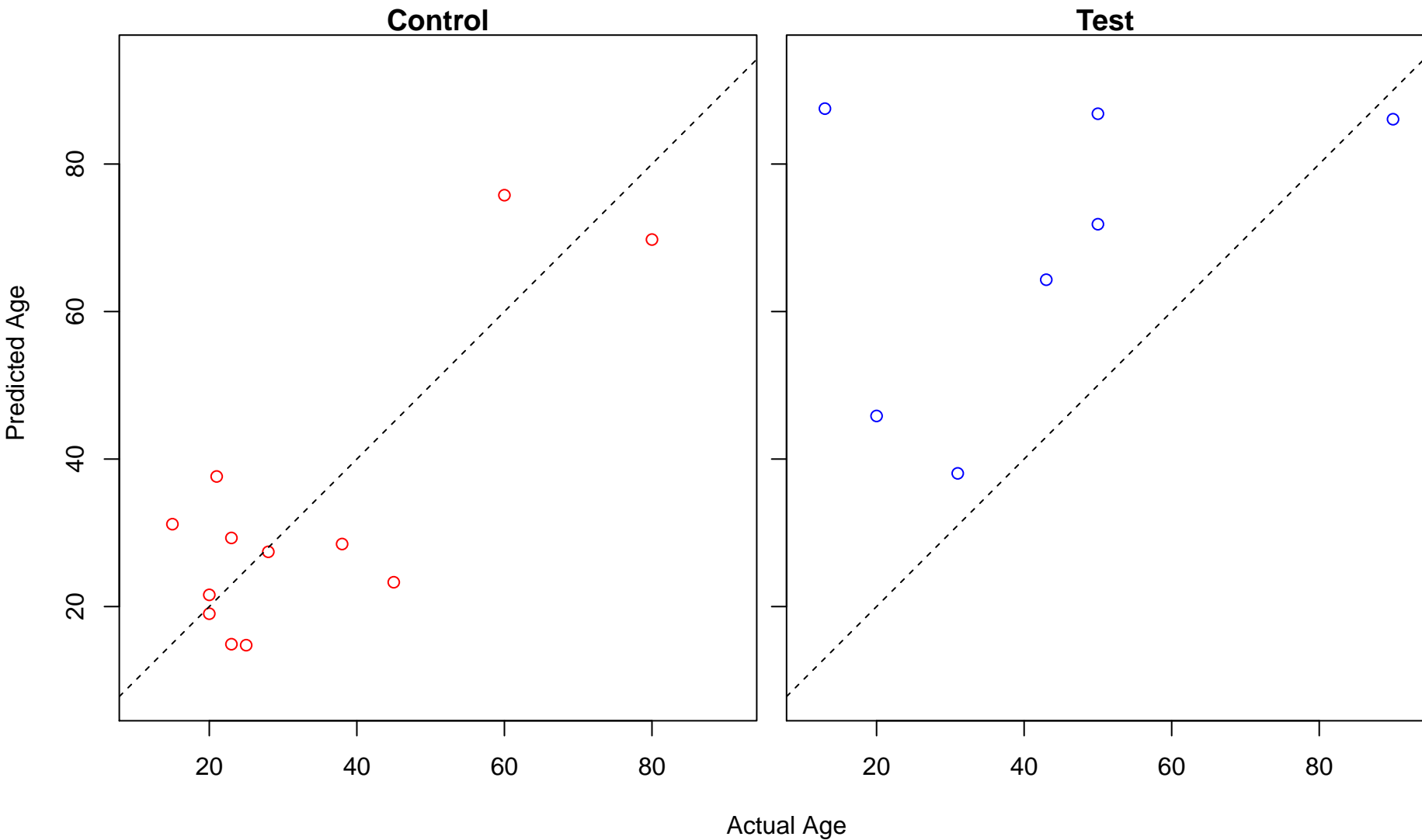
positive regulation of leukocyte degranulation (Score: 11.129790)



positive regulation of glycolytic process (Score: 11.120621)

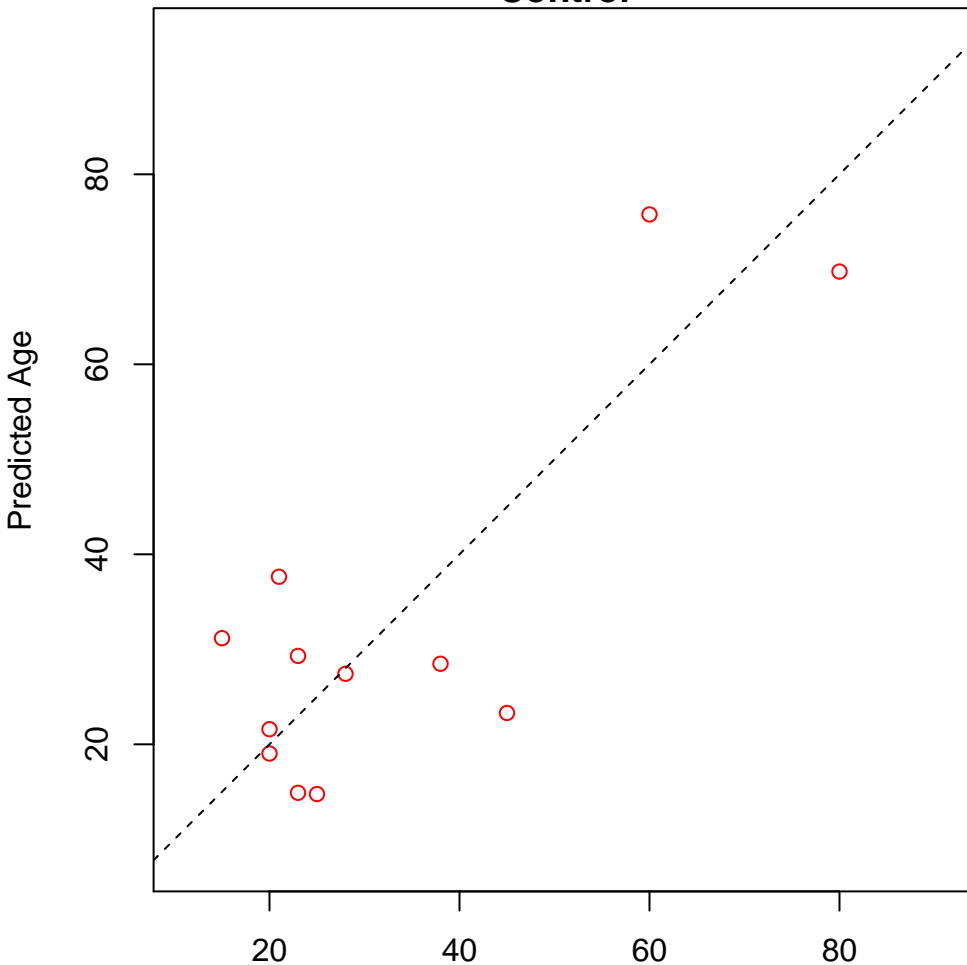


regulation of actin polymerization or depolymerization (Score: 11.082770)

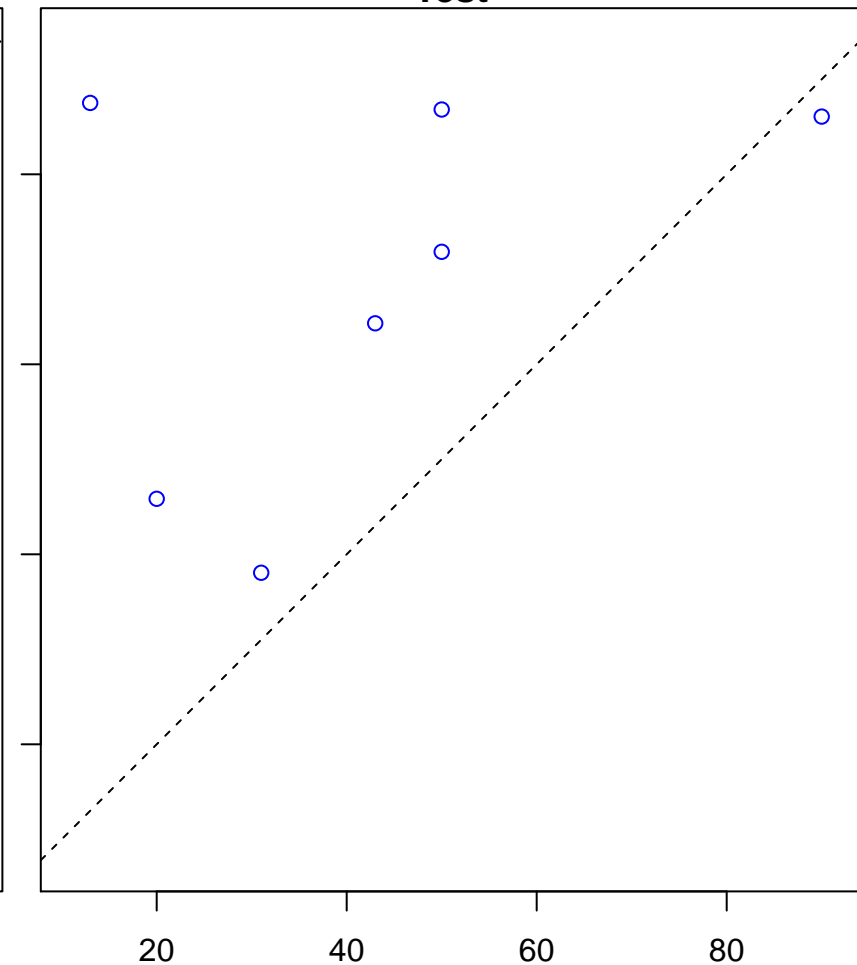


regulation of actin filament length (Score: 11.082770)

Control

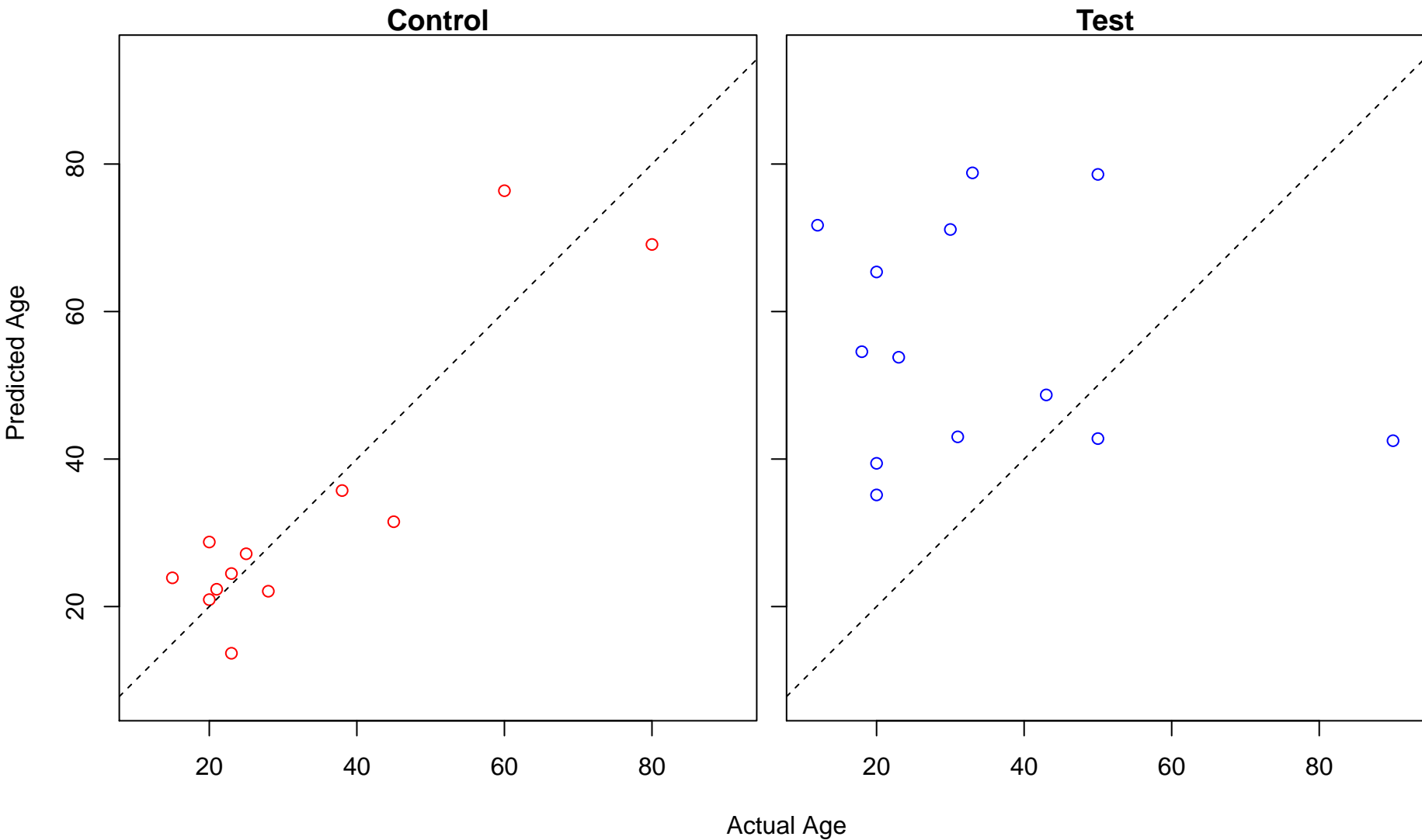


Test

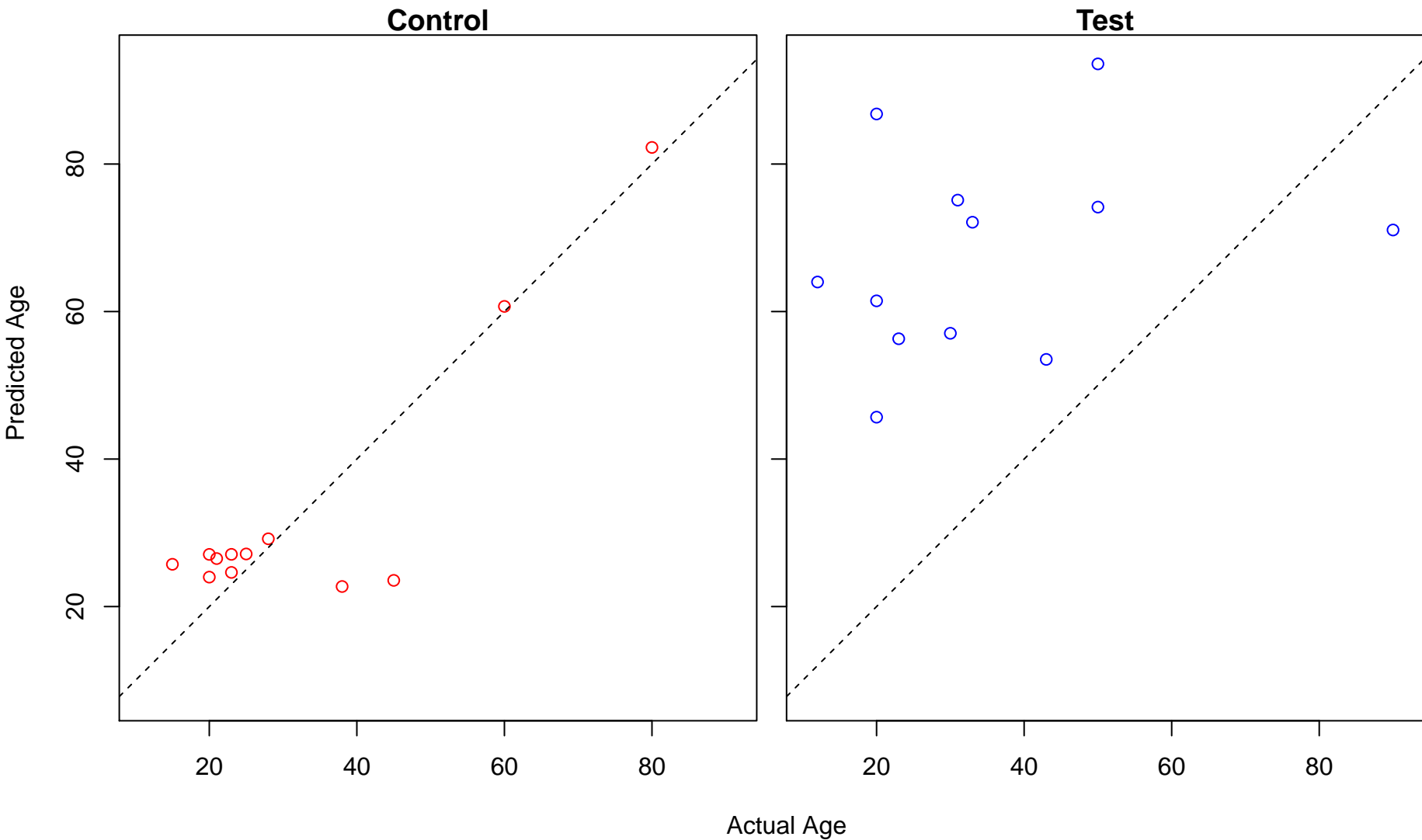


Actual Age

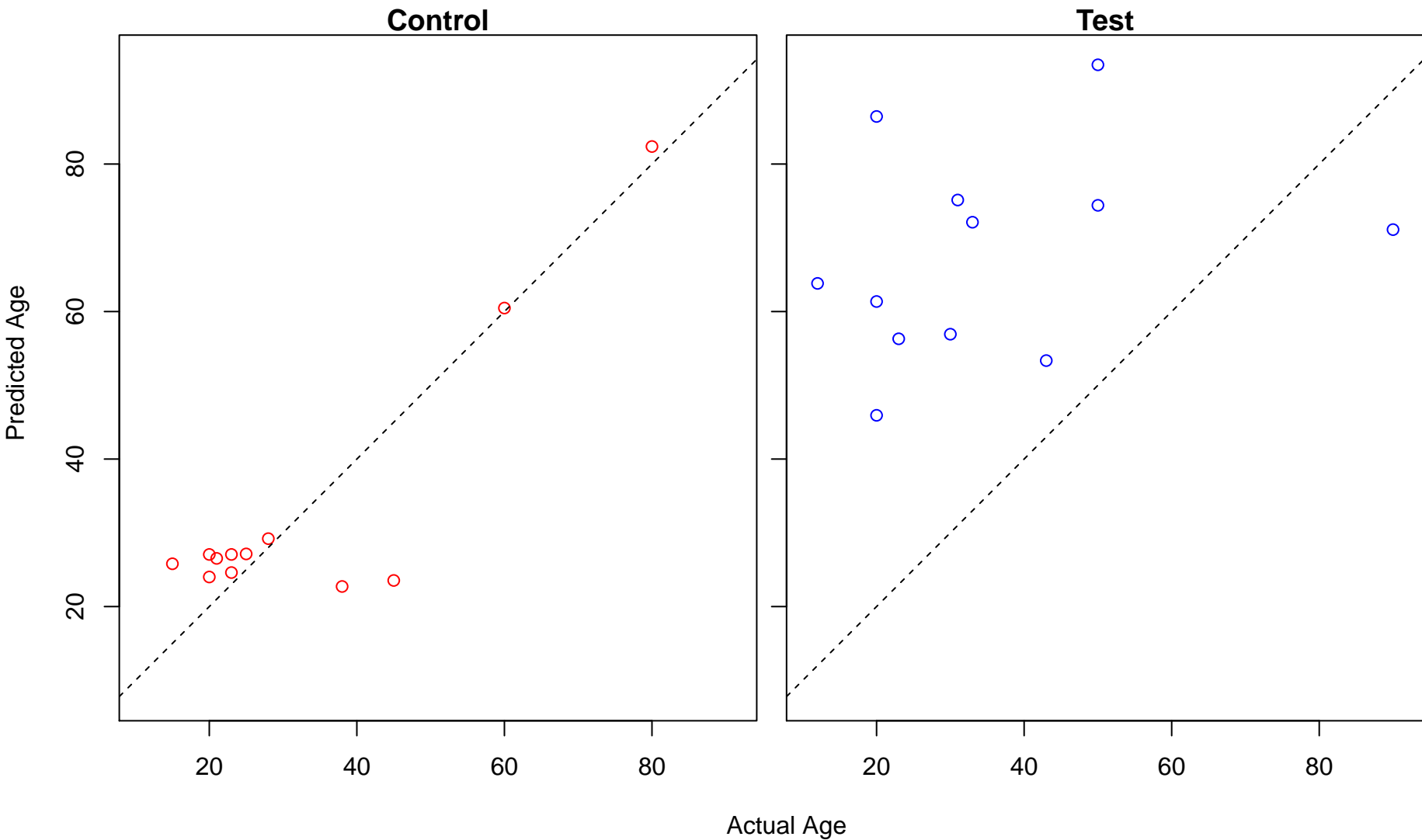
mitochondrial transmembrane transport (Score: 11.075137)



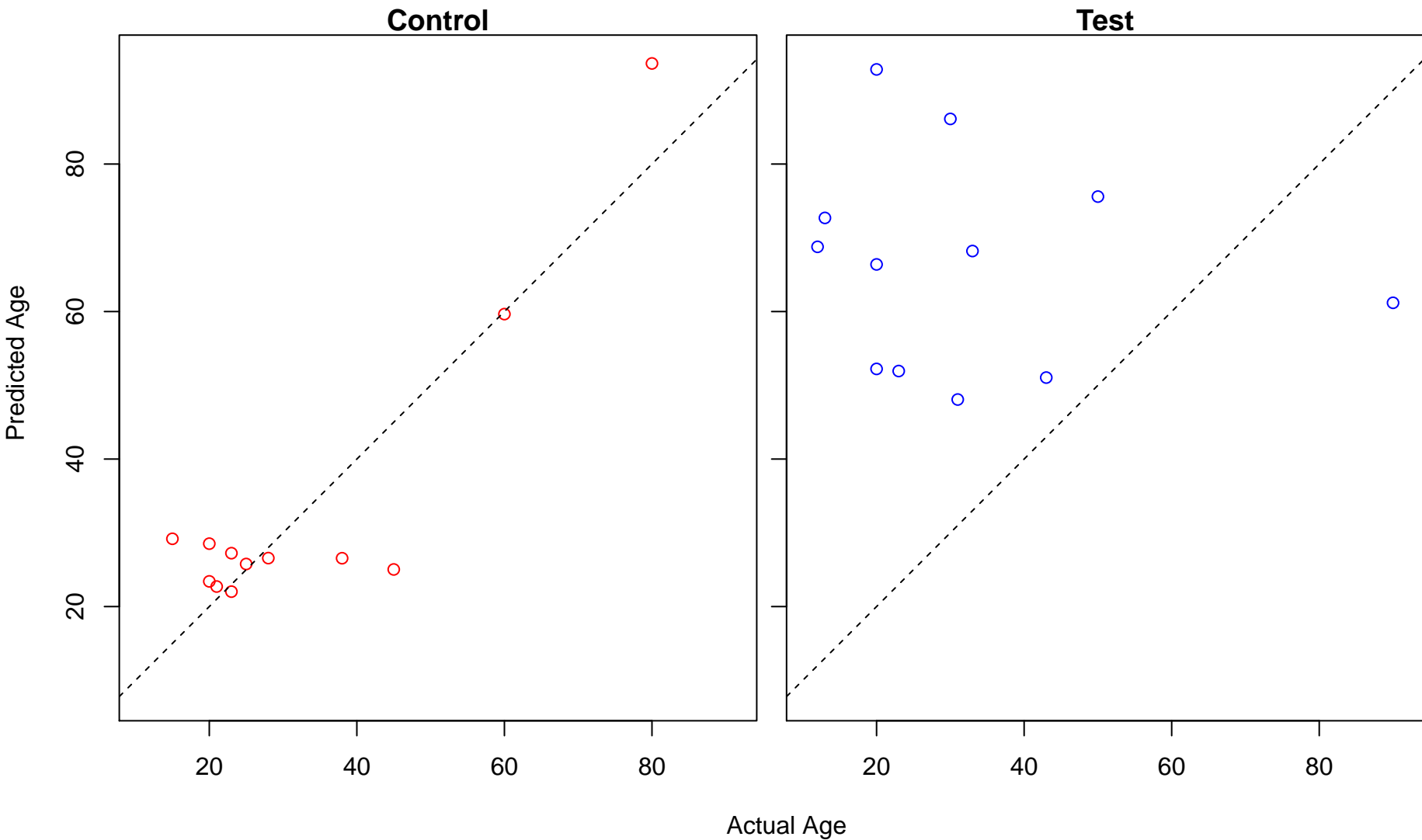
positive regulation of protein targeting to mitochondrion (Score: 11.071463)



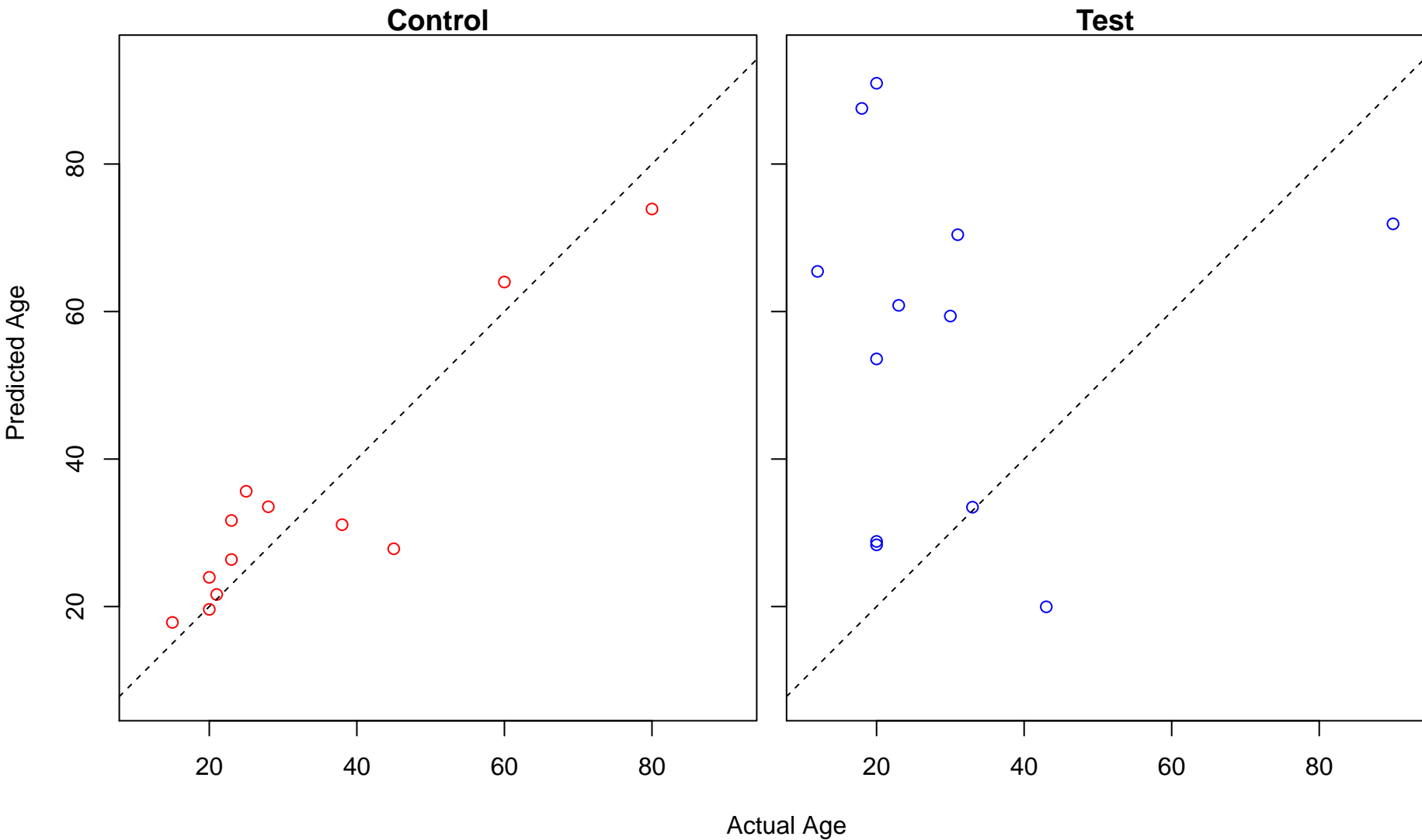
regulation of protein targeting to mitochondrion (Score: 11.013826)



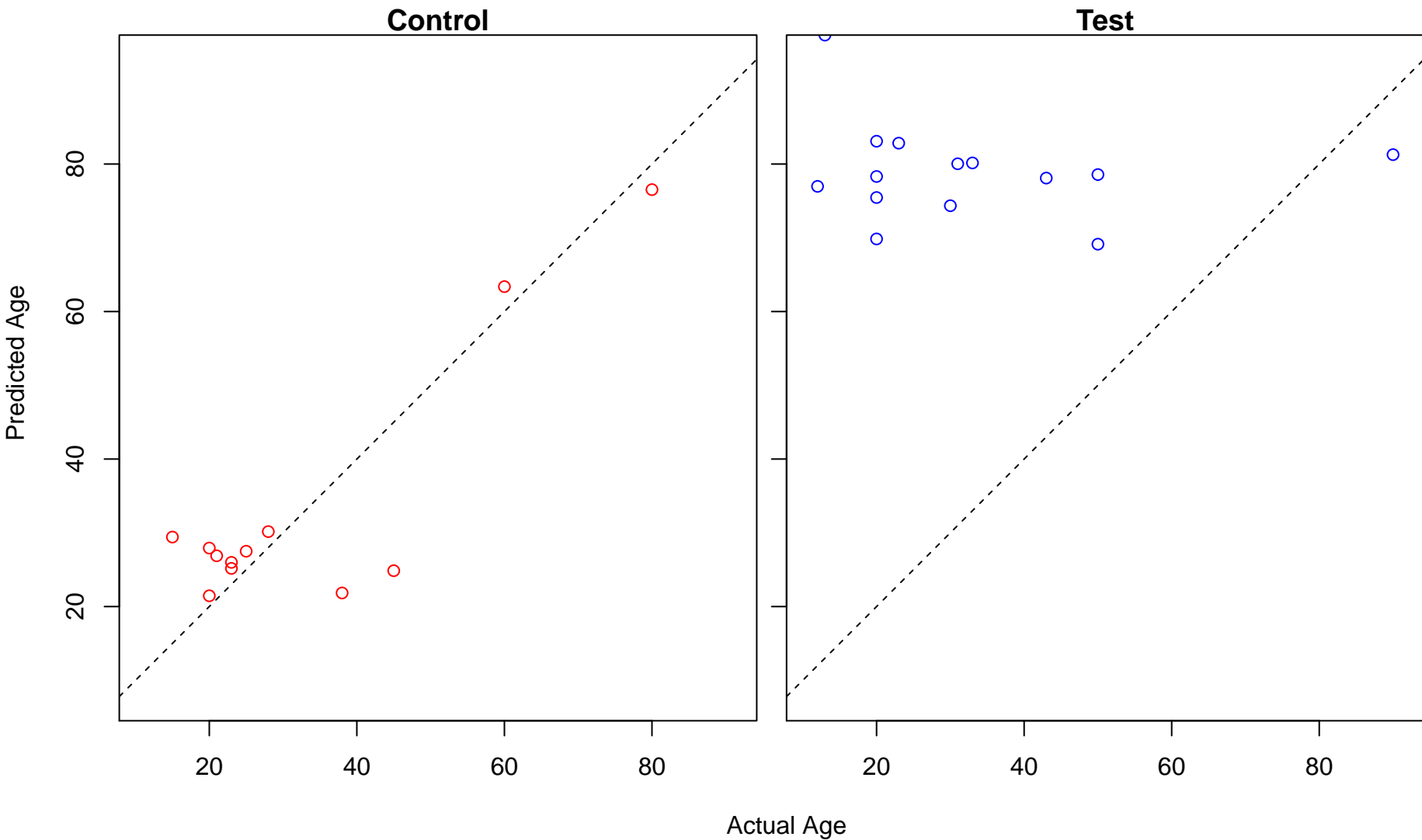
potassium ion export (Score: 11.008511)



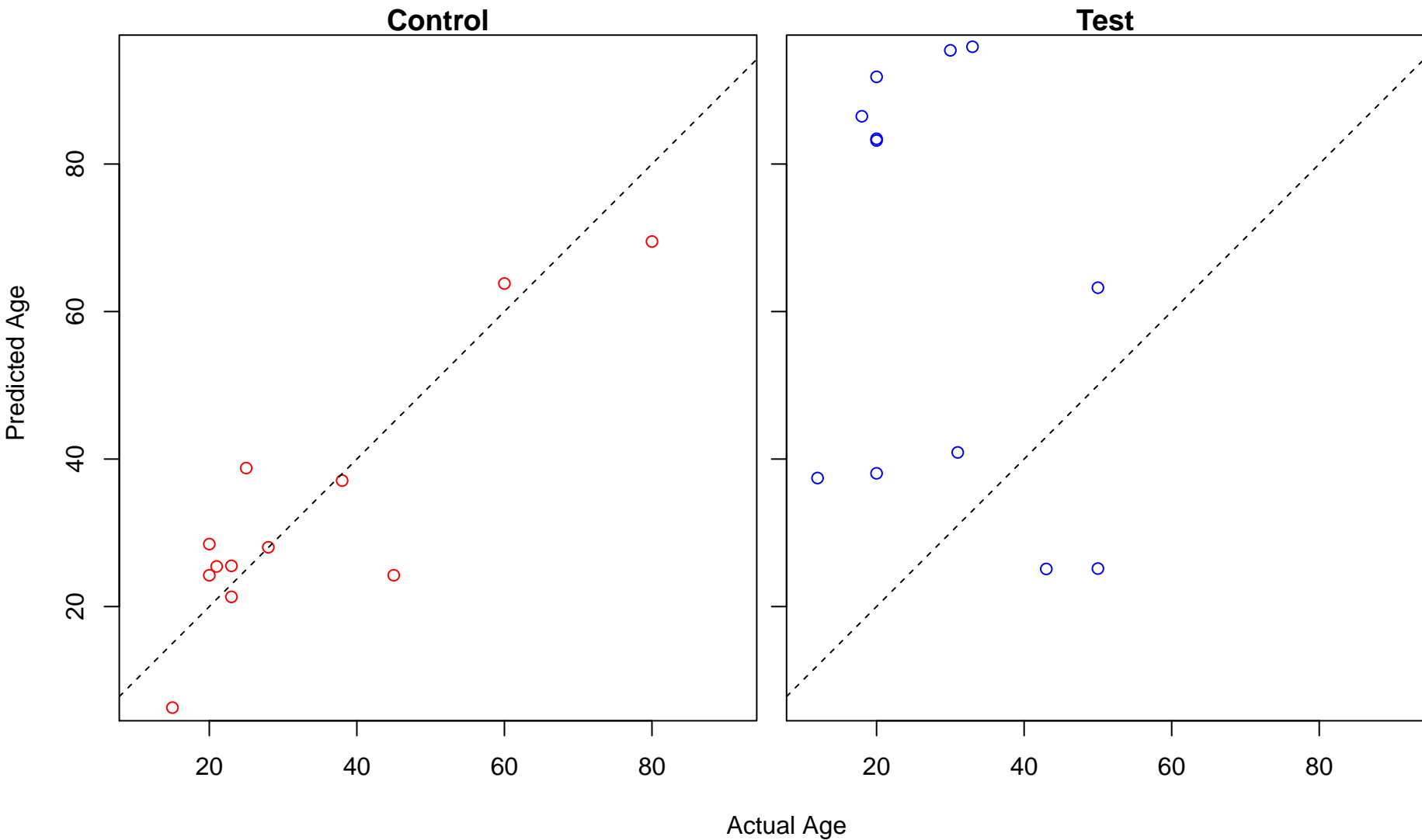
phosphatidylinositol metabolic process (Score: 11.000280)



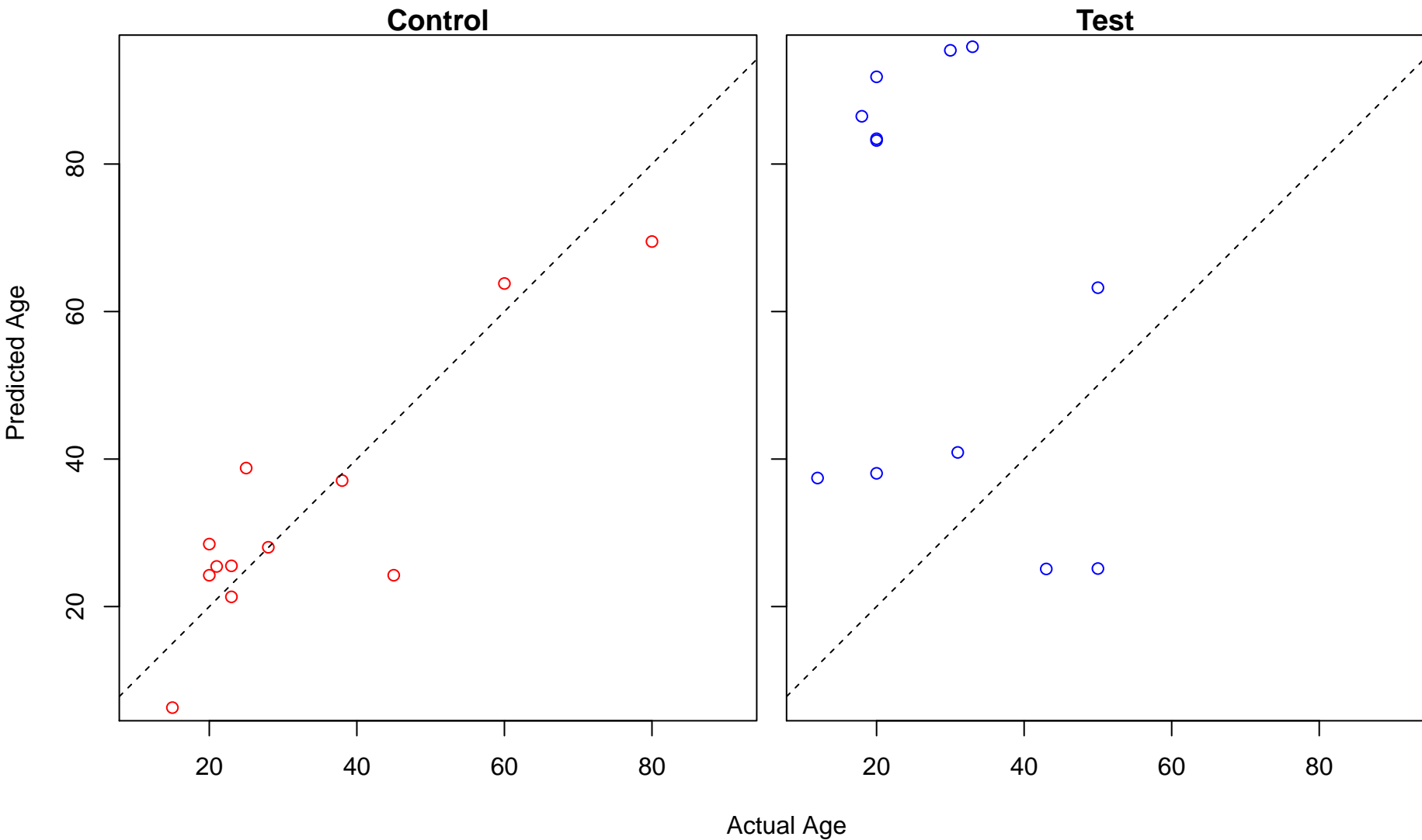
folic acid metabolic process (Score: 10.992891)



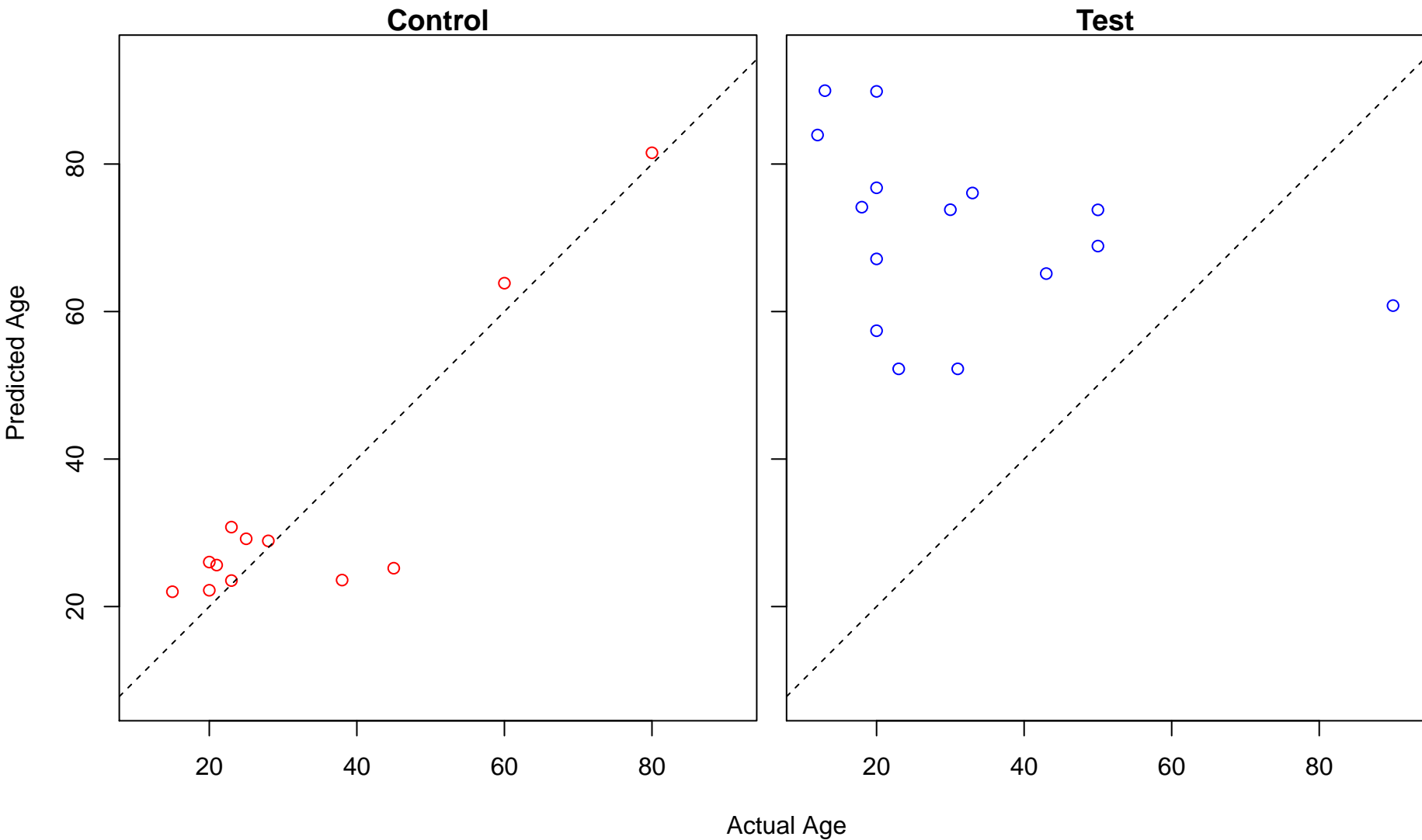
positive regulation of cofactor metabolic process (Score: 10.983371)



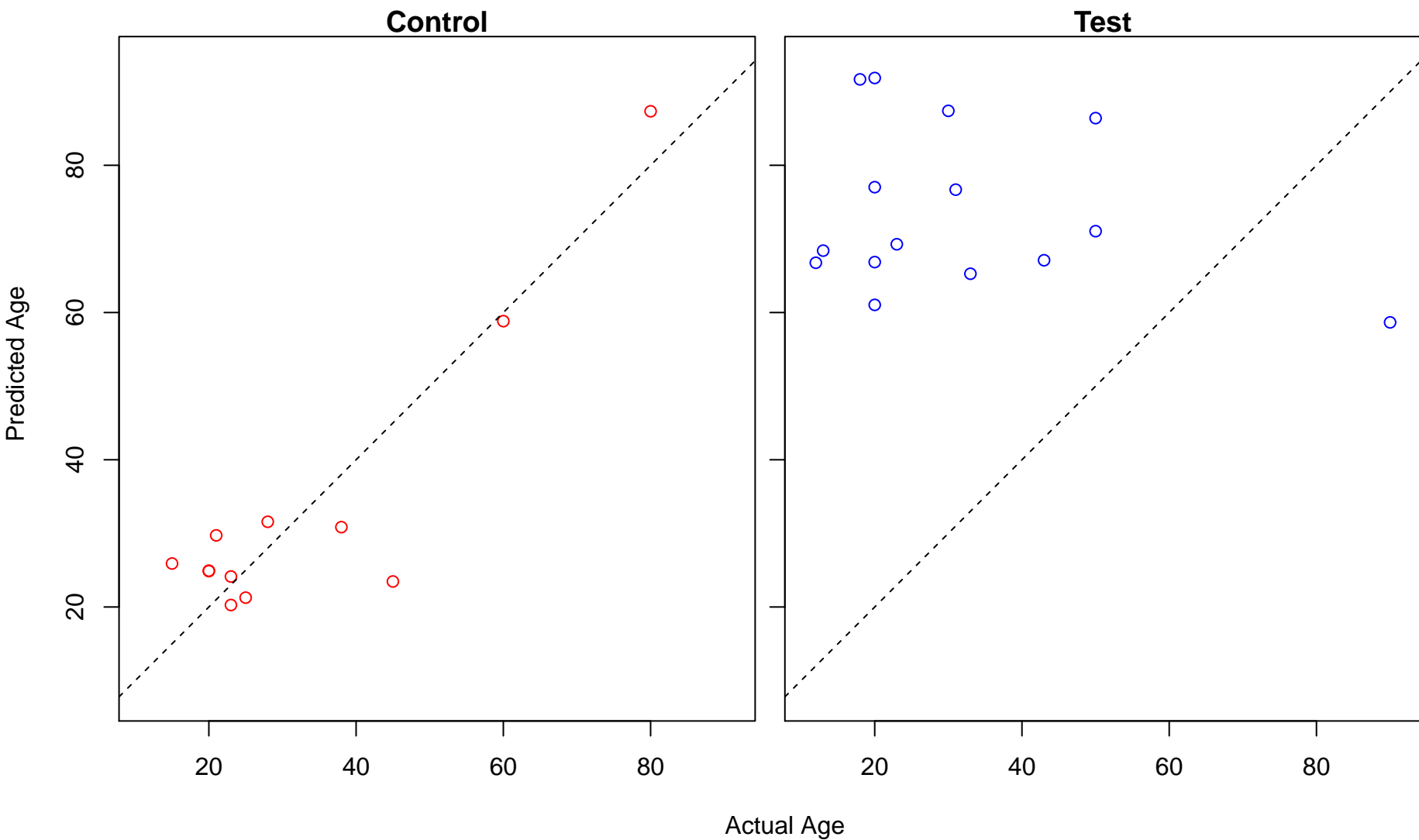
positive regulation of coenzyme metabolic process (Score: 10.983371)



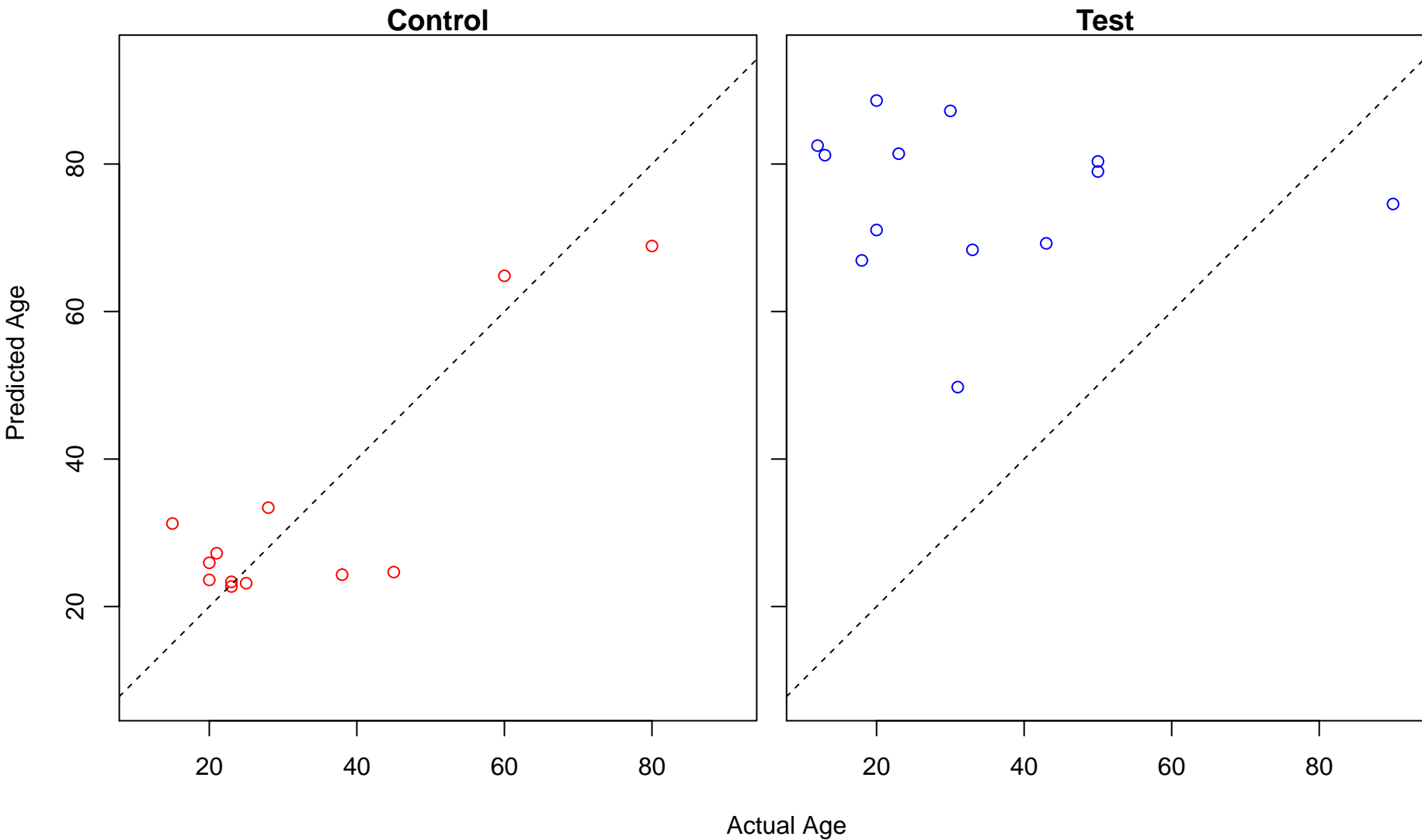
regulation of cell proliferation involved in heart morphogenesis (Score: 10.980628)



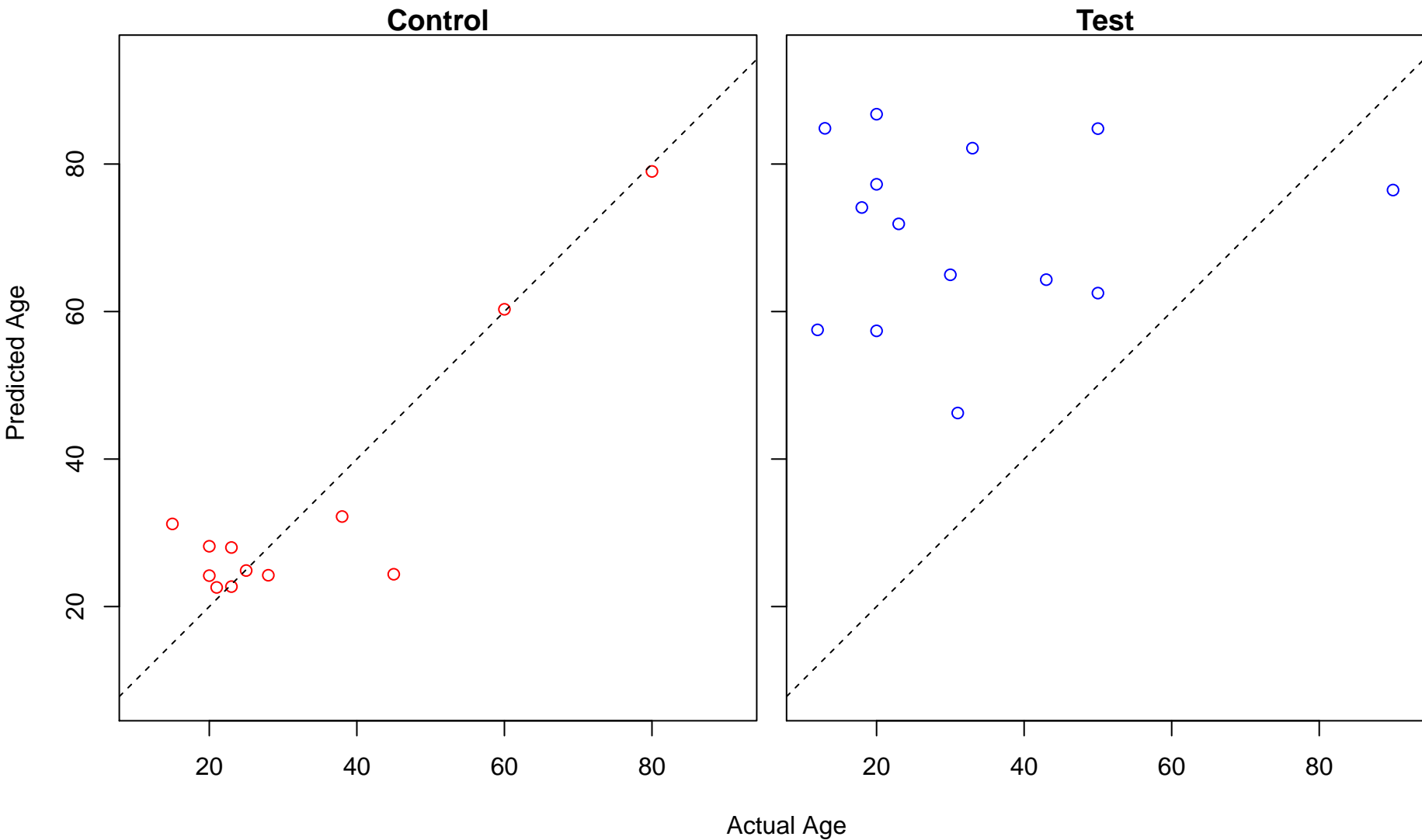
unsaturated fatty acid metabolic process (Score: 10.974058)



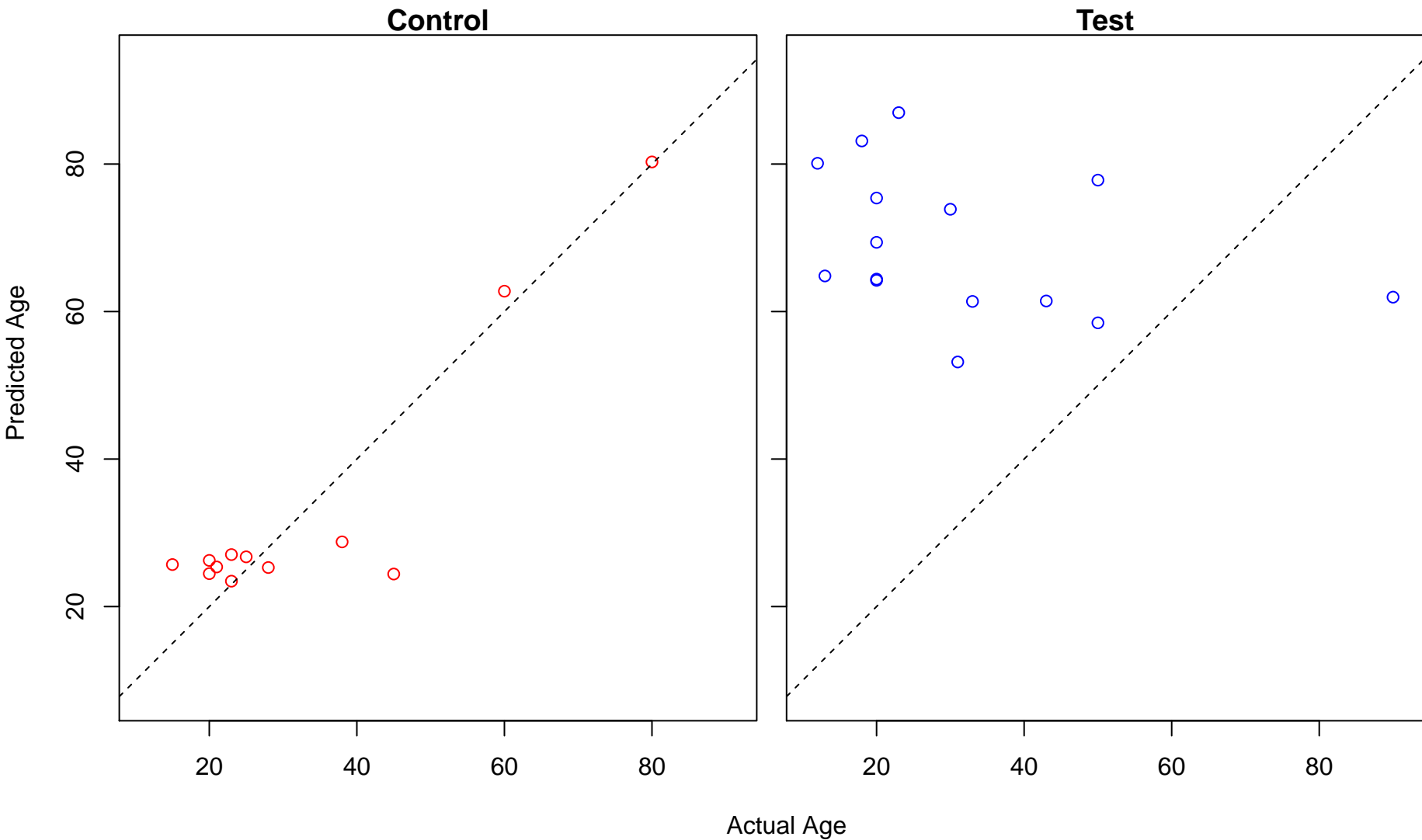
regulation of superoxide metabolic process (Score: 10.973748)



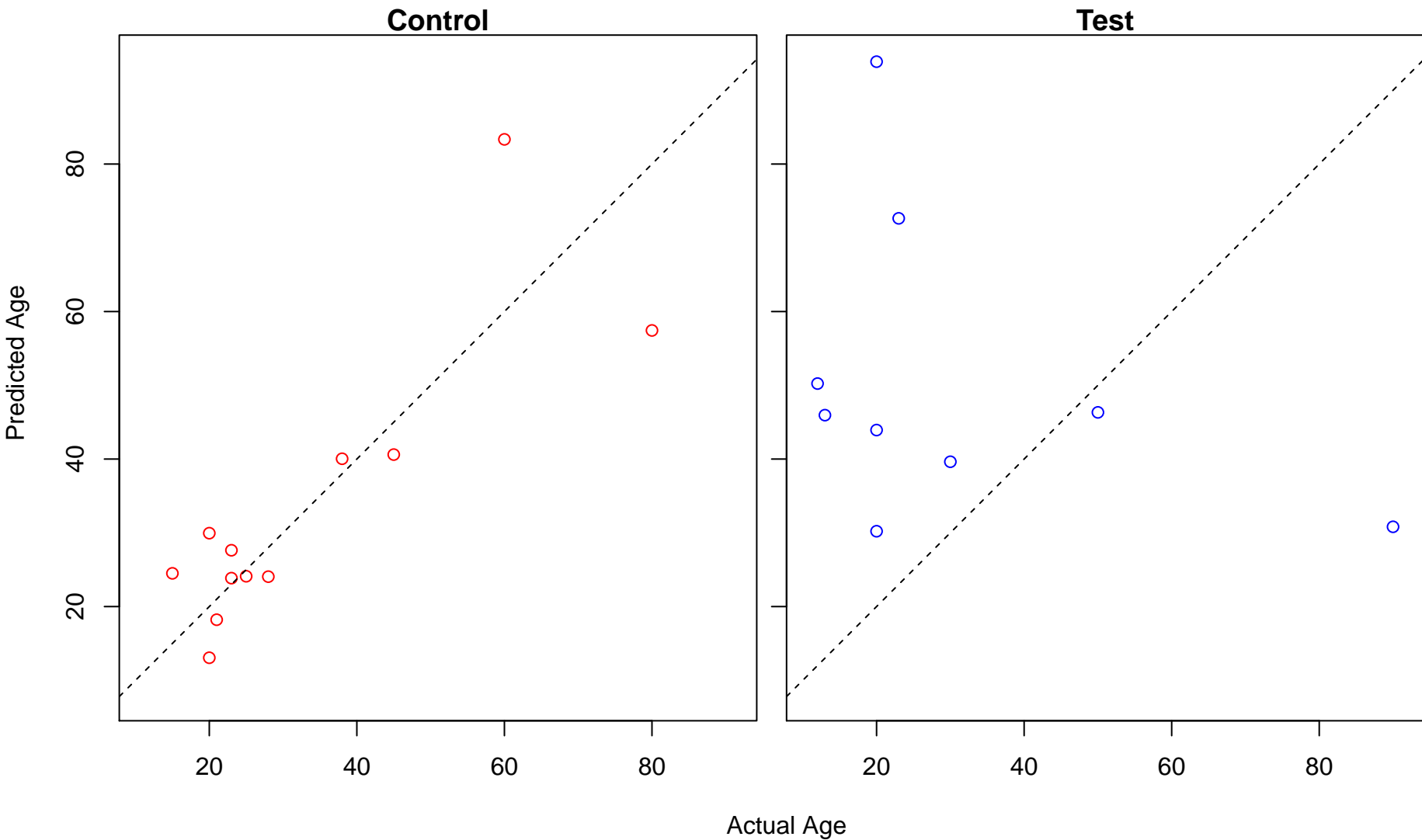
regulation of histone deacetylation (Score: 10.962916)



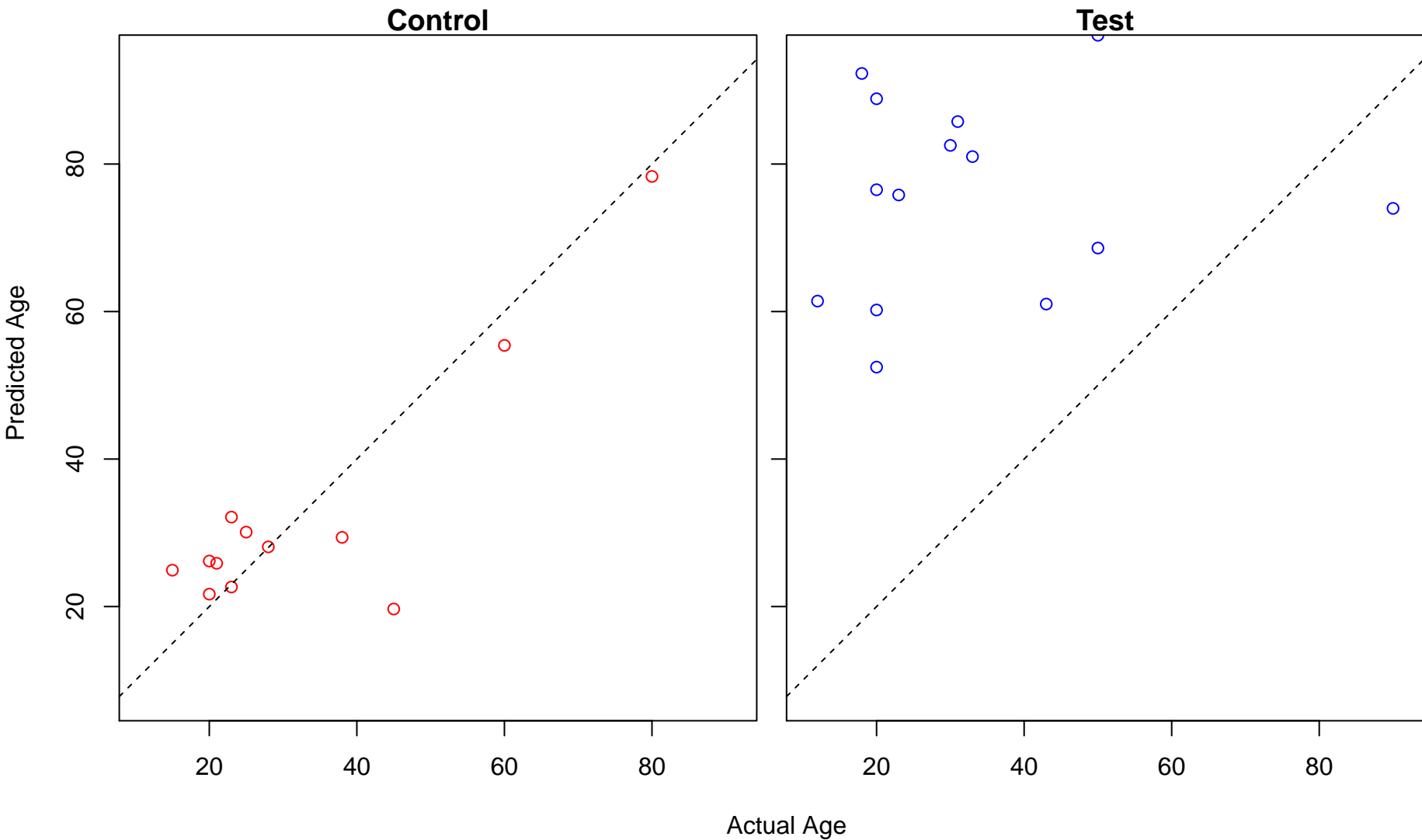
response to muscle stretch (Score: 10.962470)



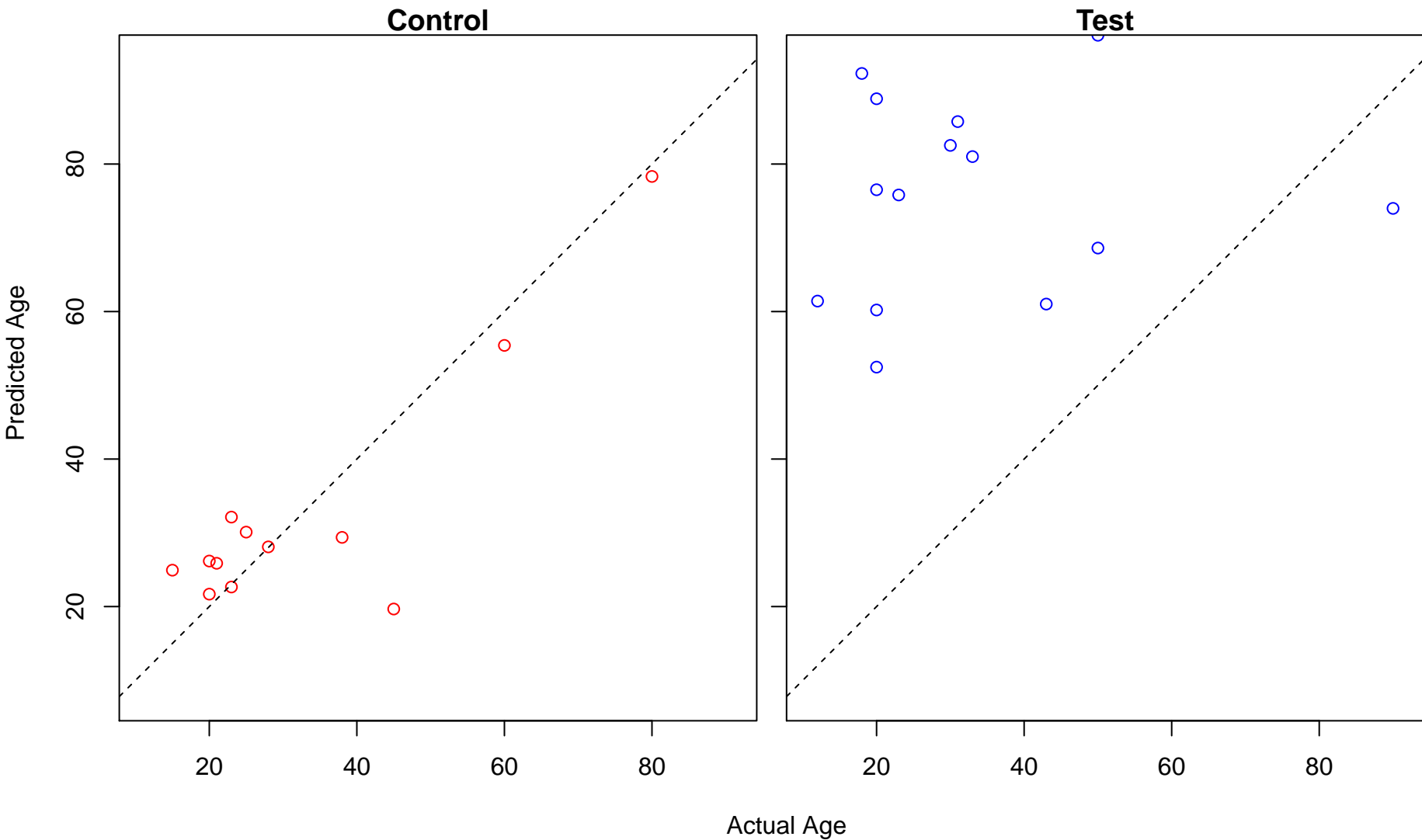
chondrocyte development (Score: 10.958522)



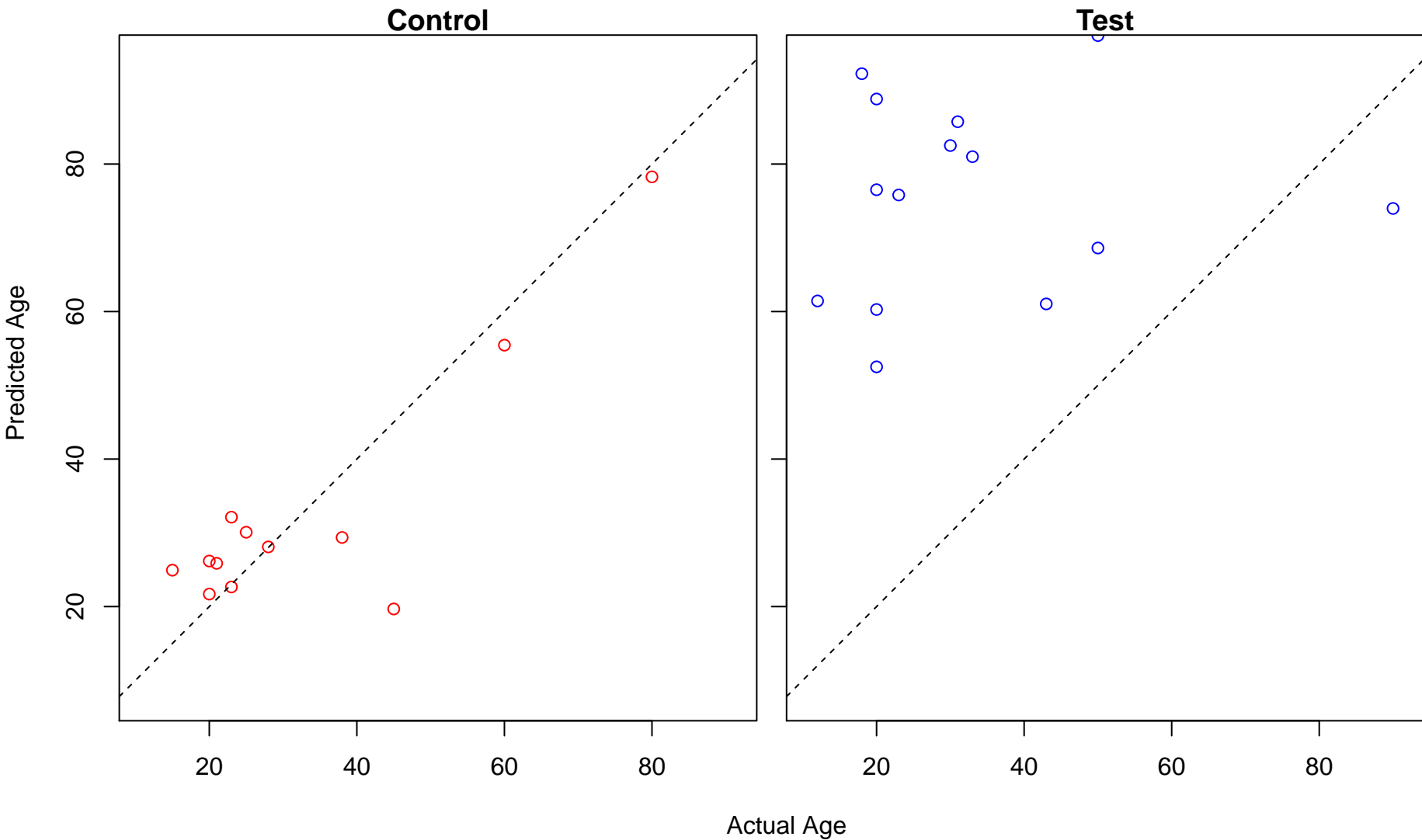
type I interferon signaling pathway (Score: 10.956655)



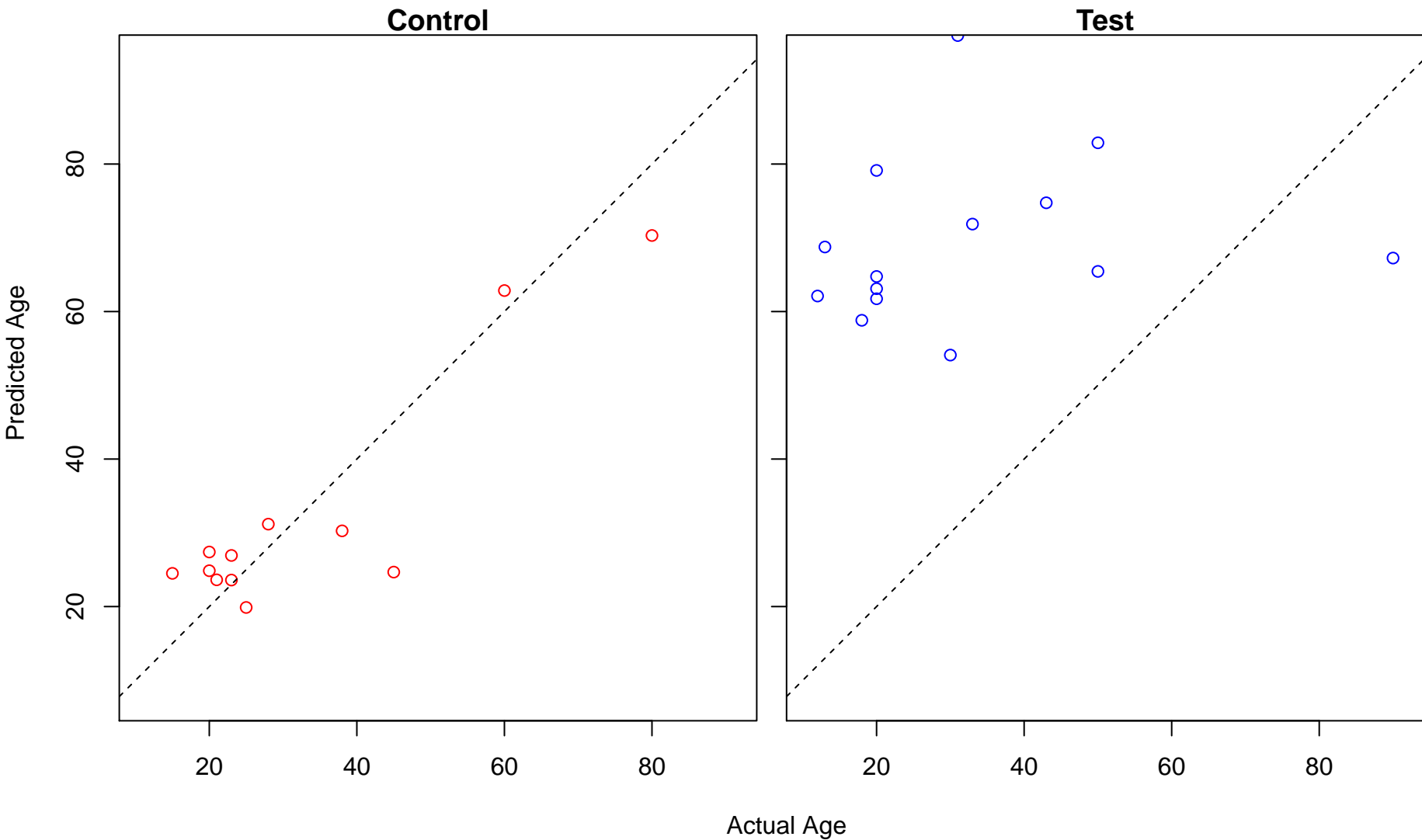
cellular response to type I interferon (Score: 10.956655)



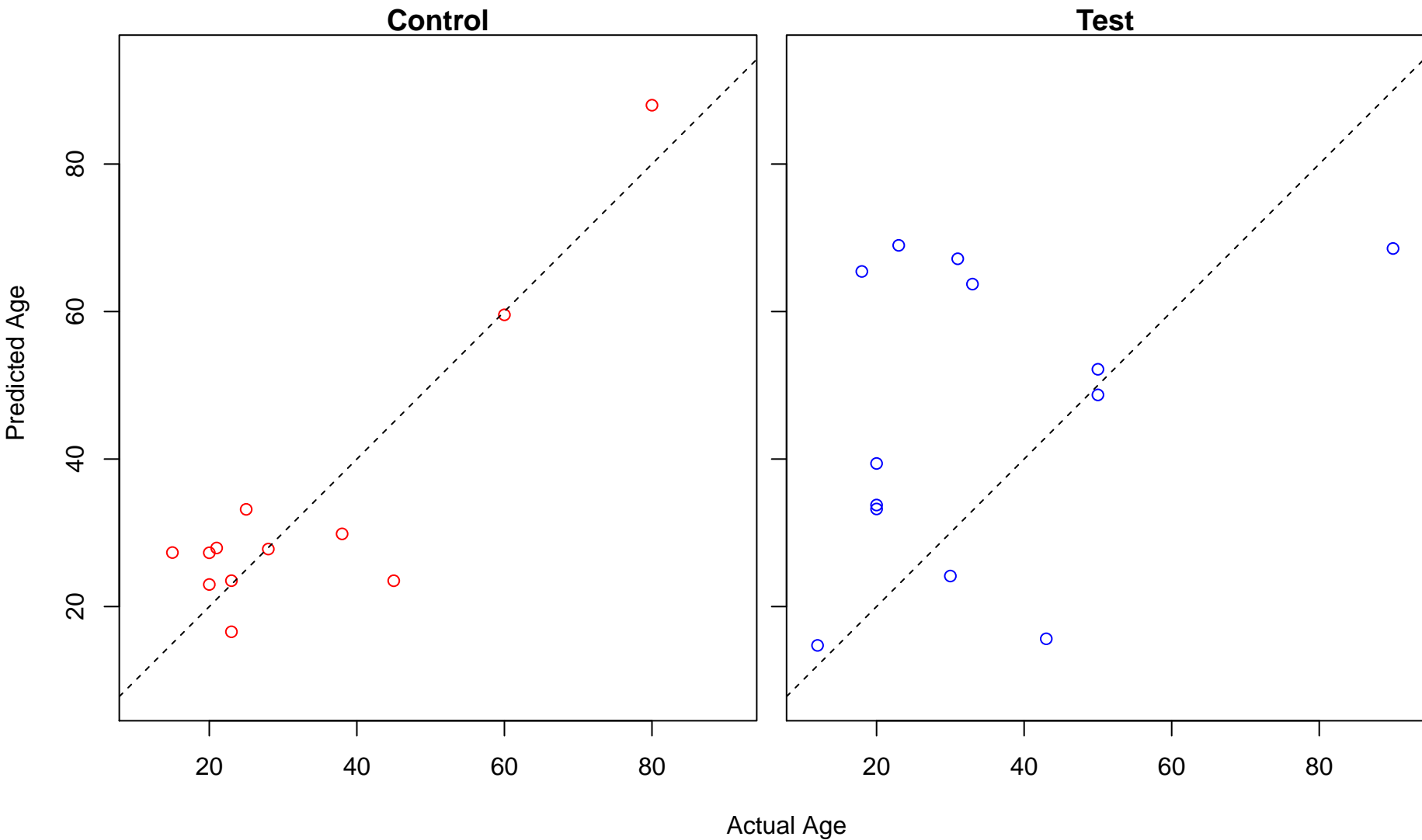
response to type I interferon (Score: 10.956348)



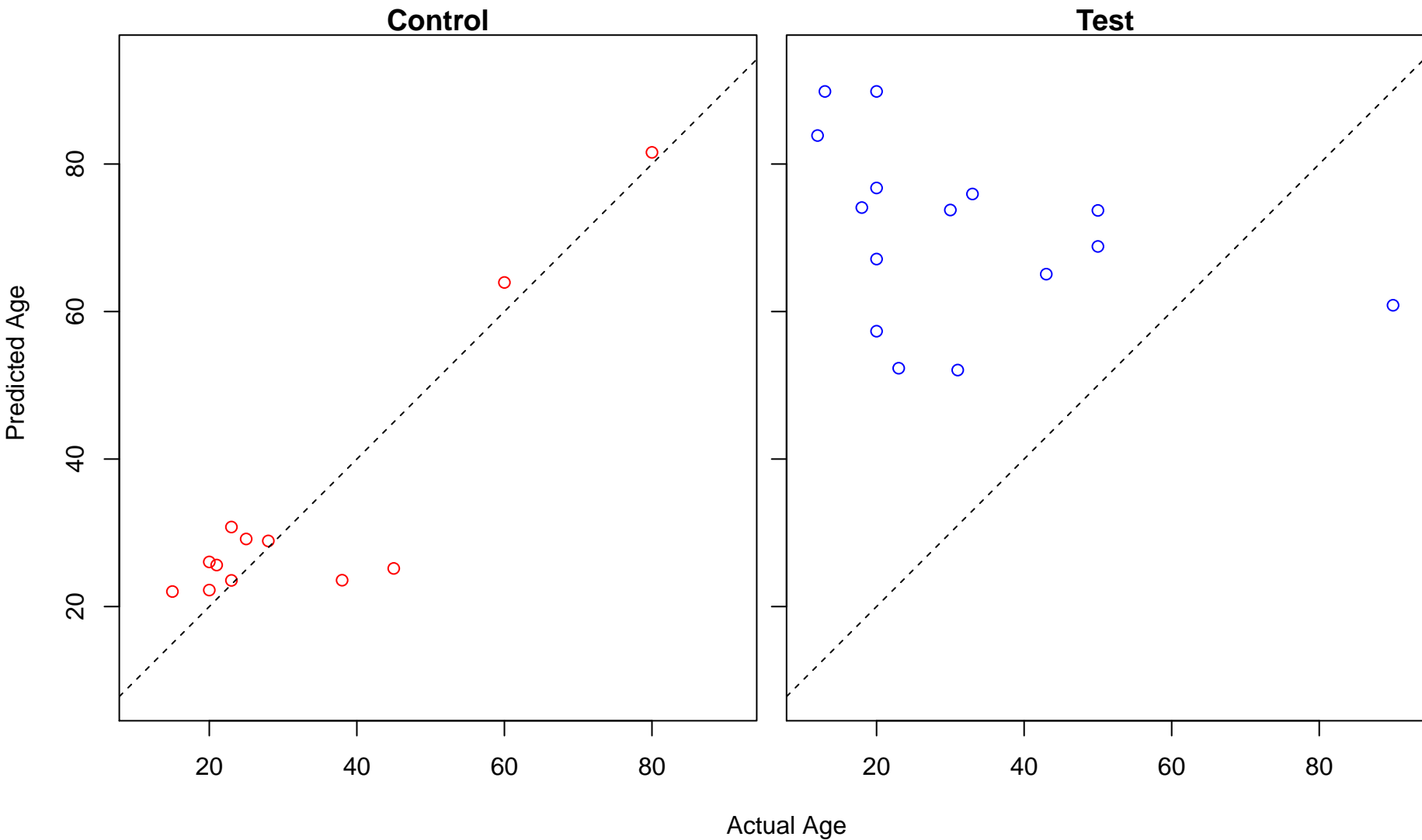
protein O-linked fucosylation (Score: 10.944715)



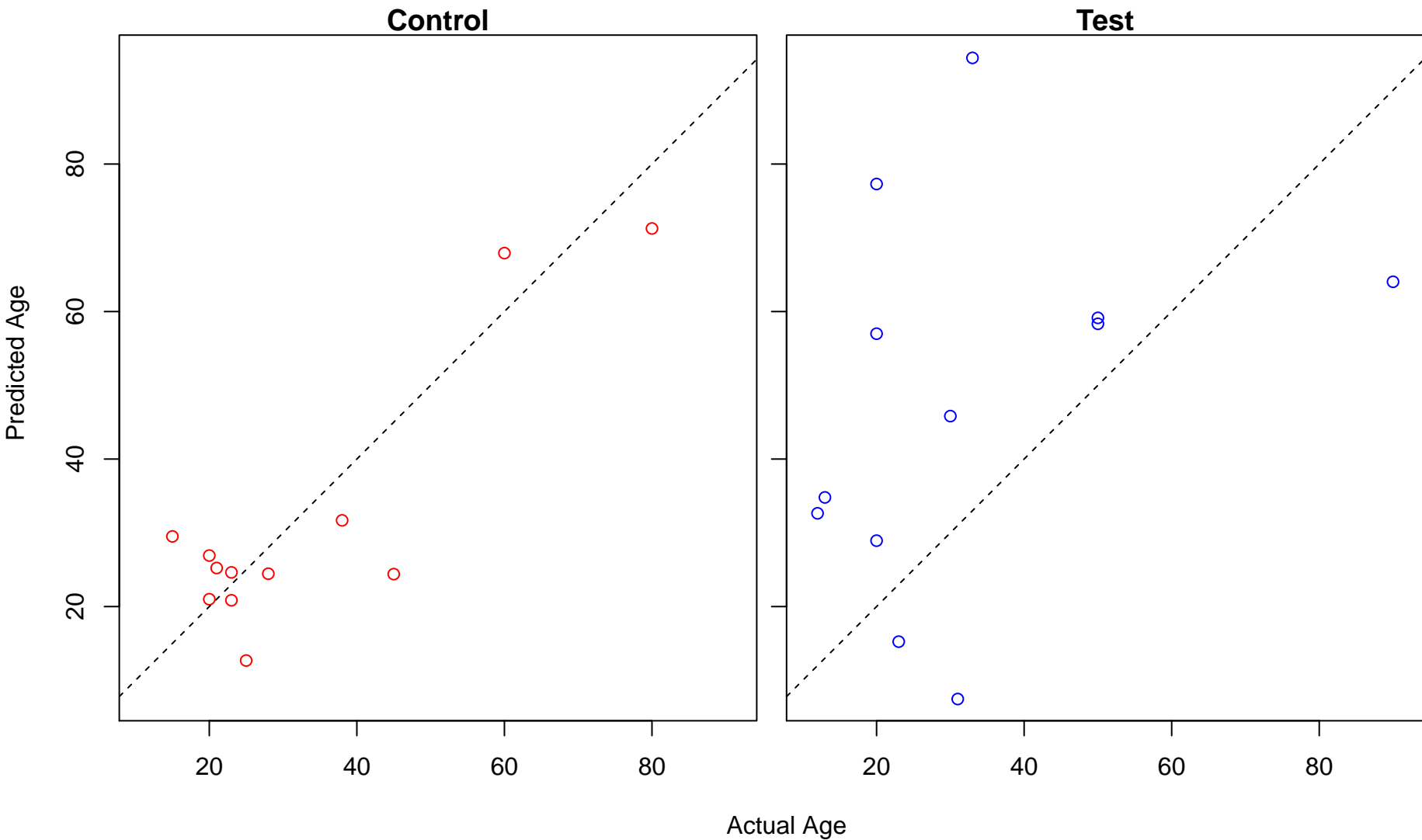
response to biotic stimulus (Score: 10.916849)



regulation of heart morphogenesis (Score: 10.915301)

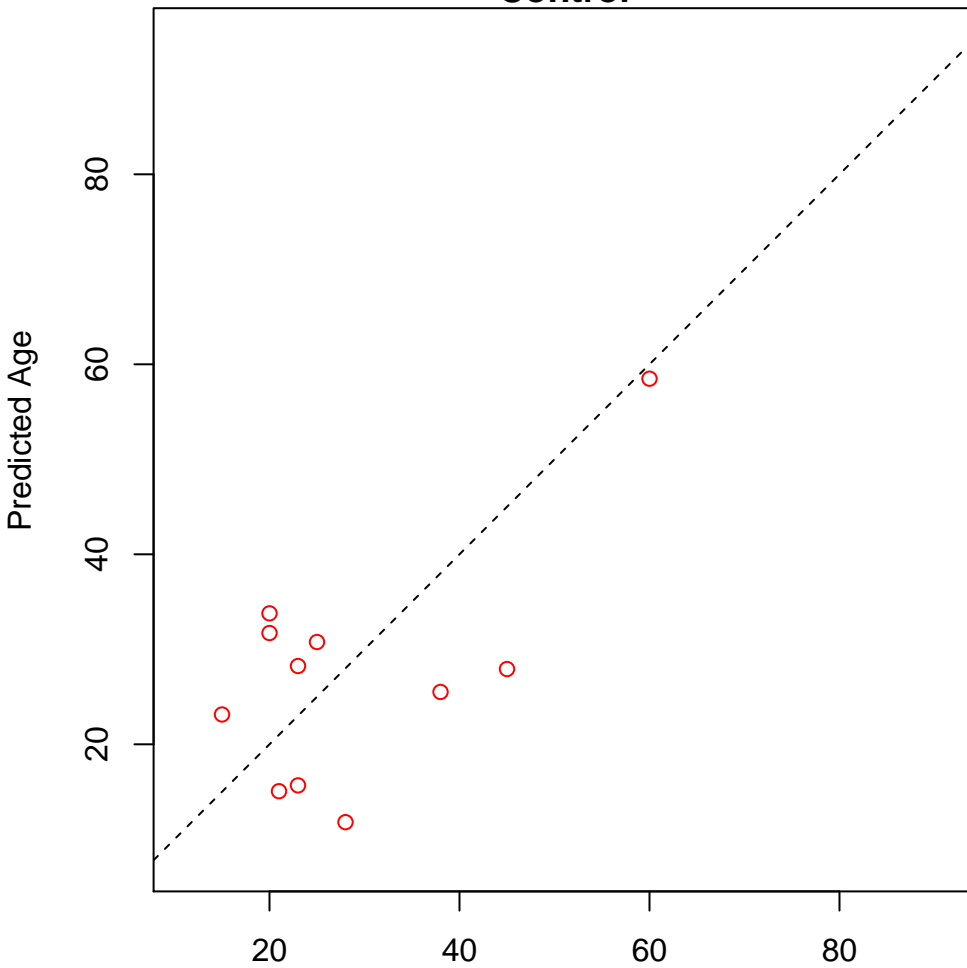


sister chromatid segregation (Score: 10.910134)

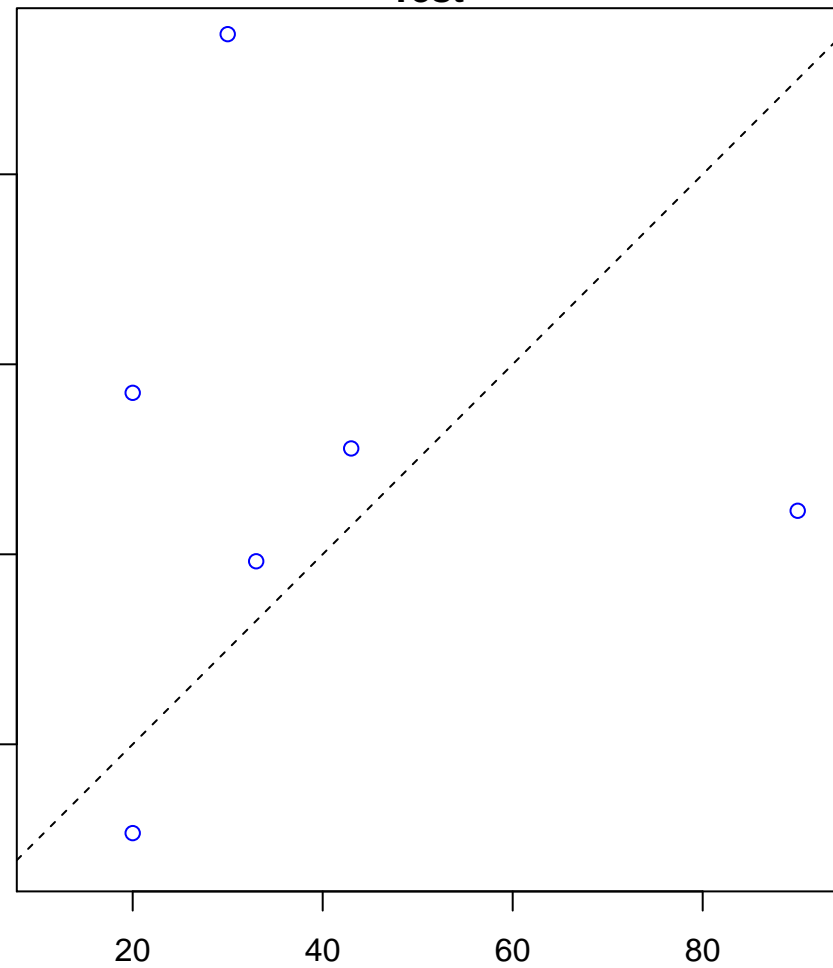


regulation of inclusion body assembly (Score: 10.889302)

Control

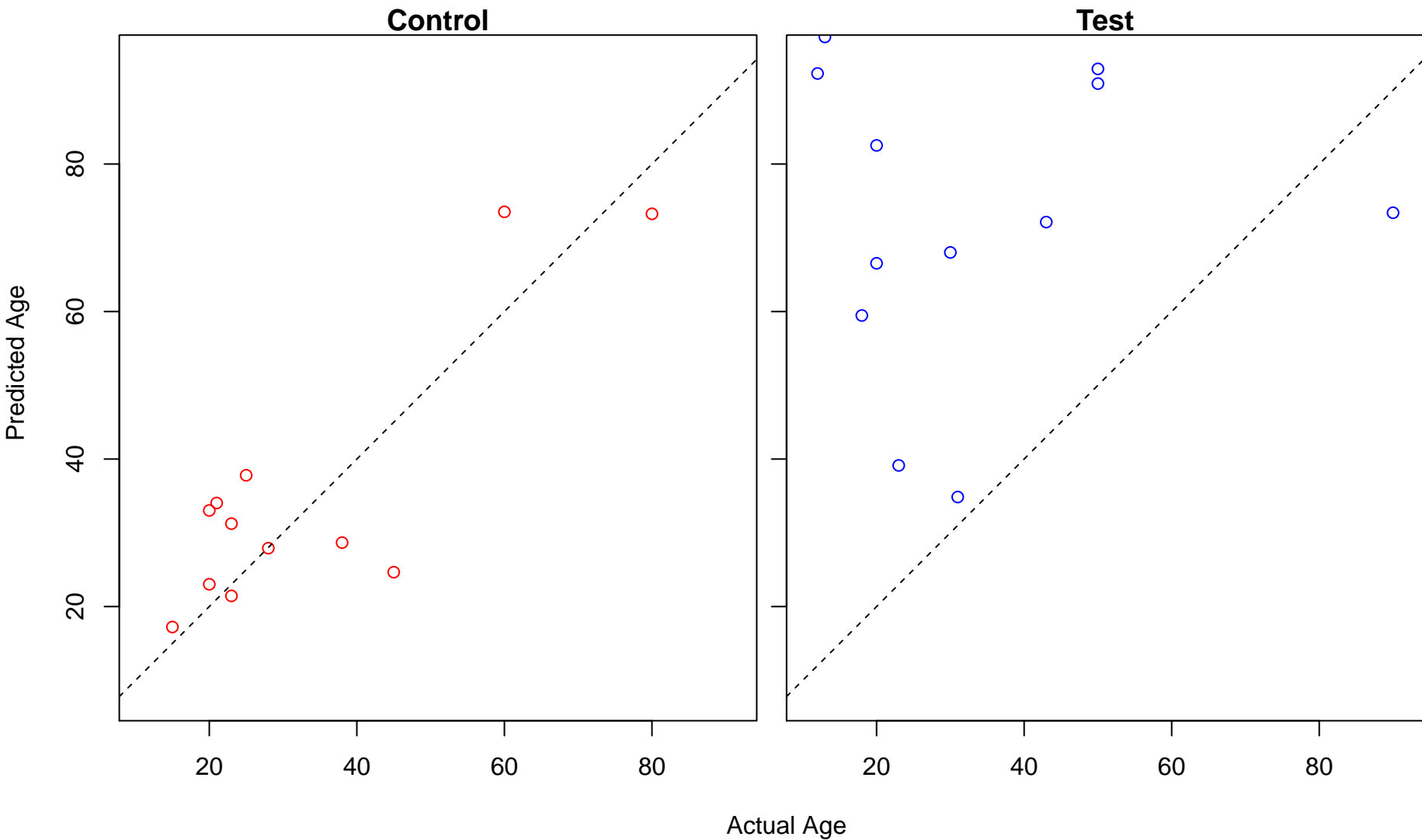


Test



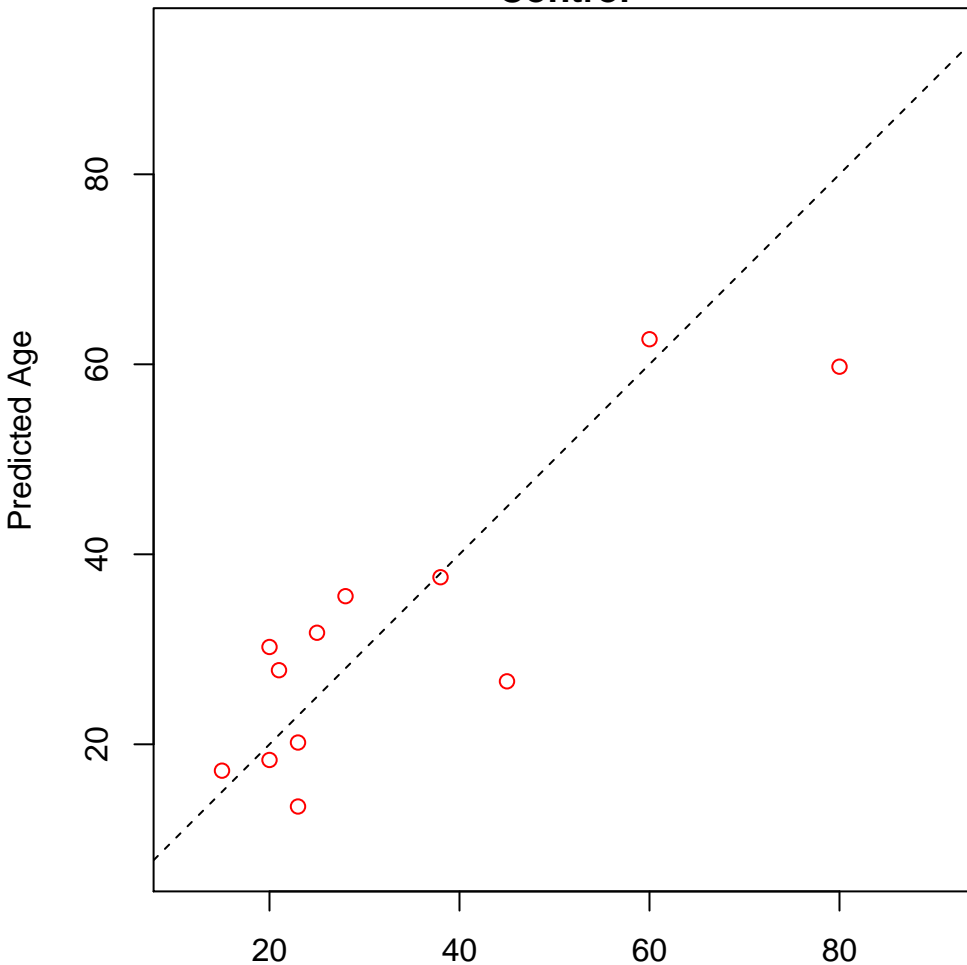
Actual Age

granulocyte differentiation (Score: 10.877212)

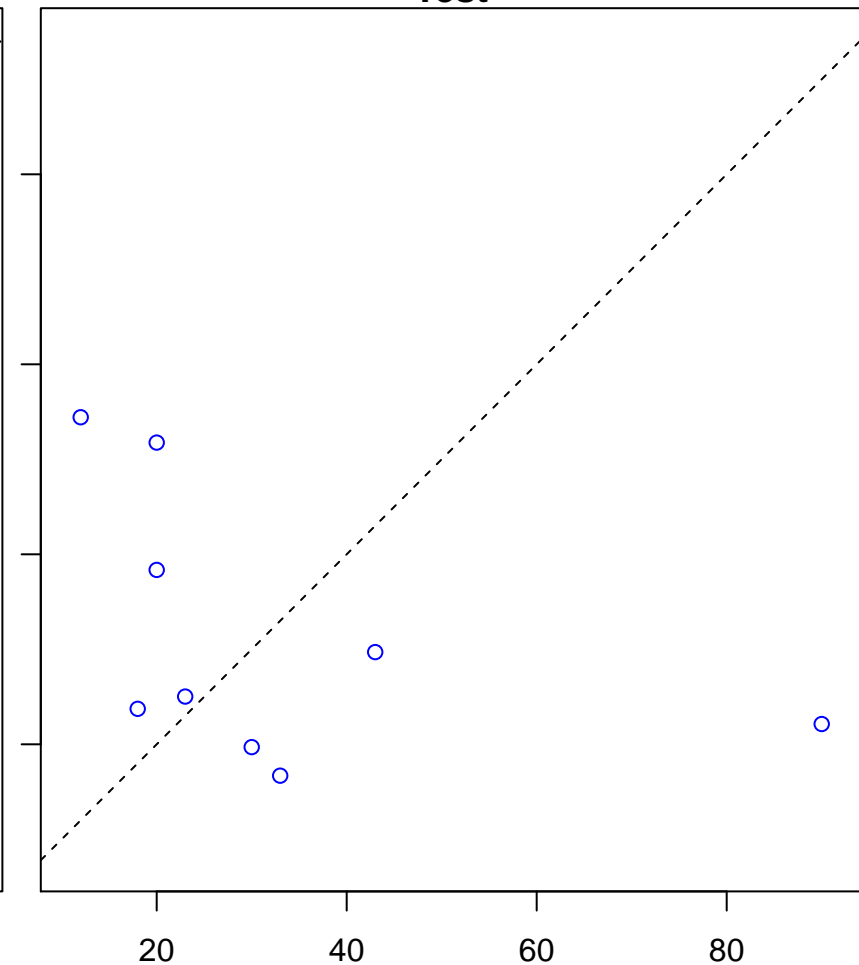


hydrogen peroxide catabolic process (Score: 10.876231)

Control

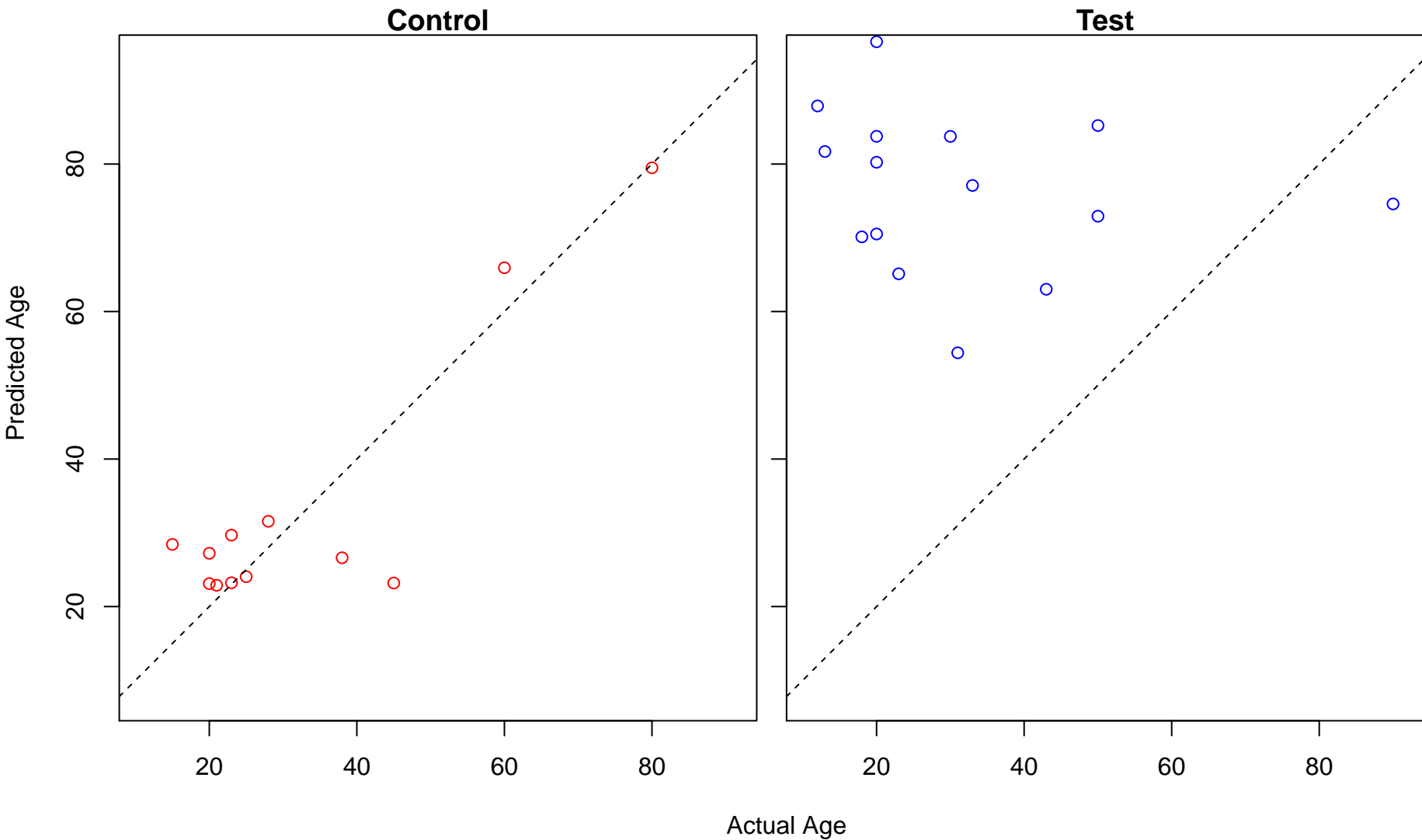


Test

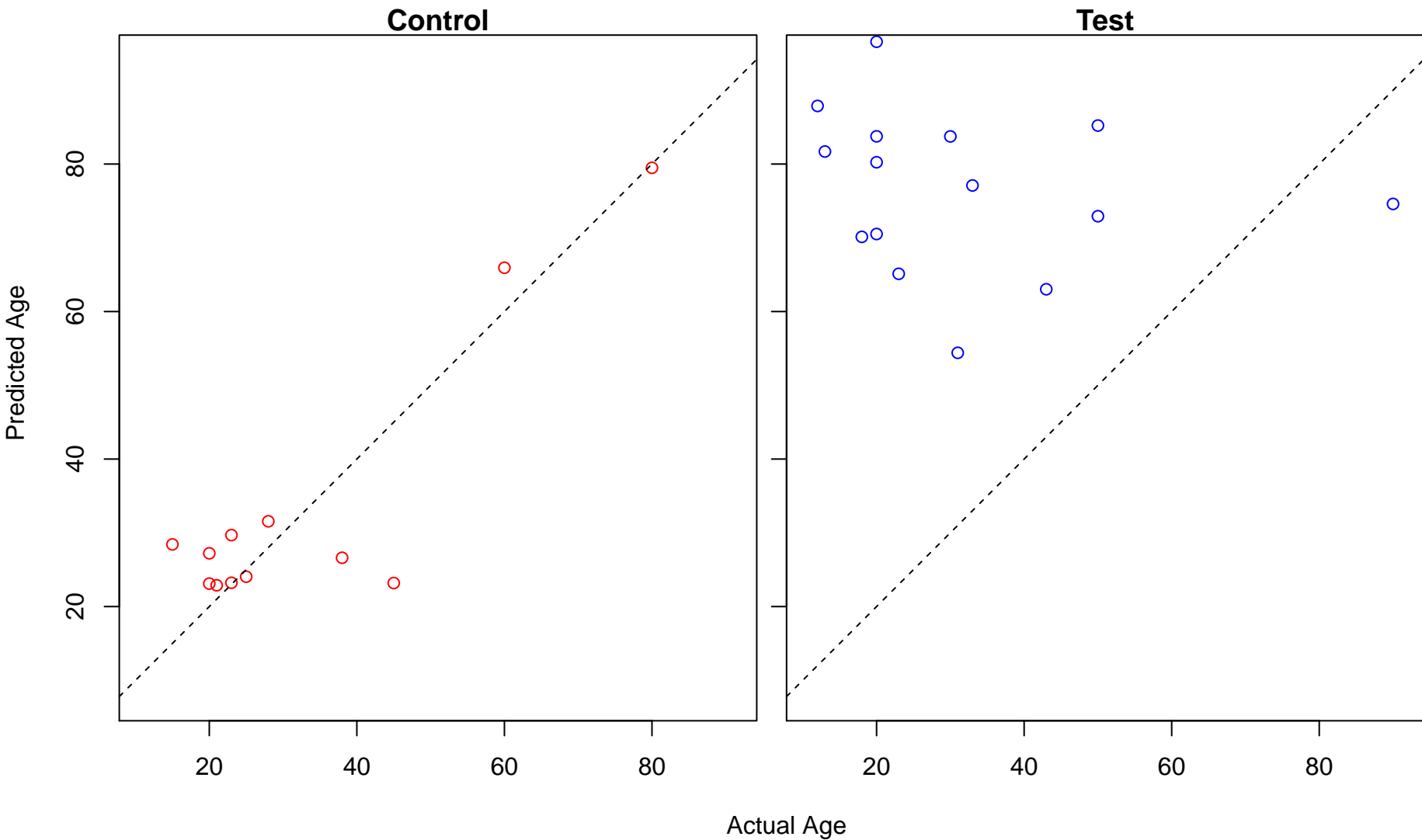


Actual Age

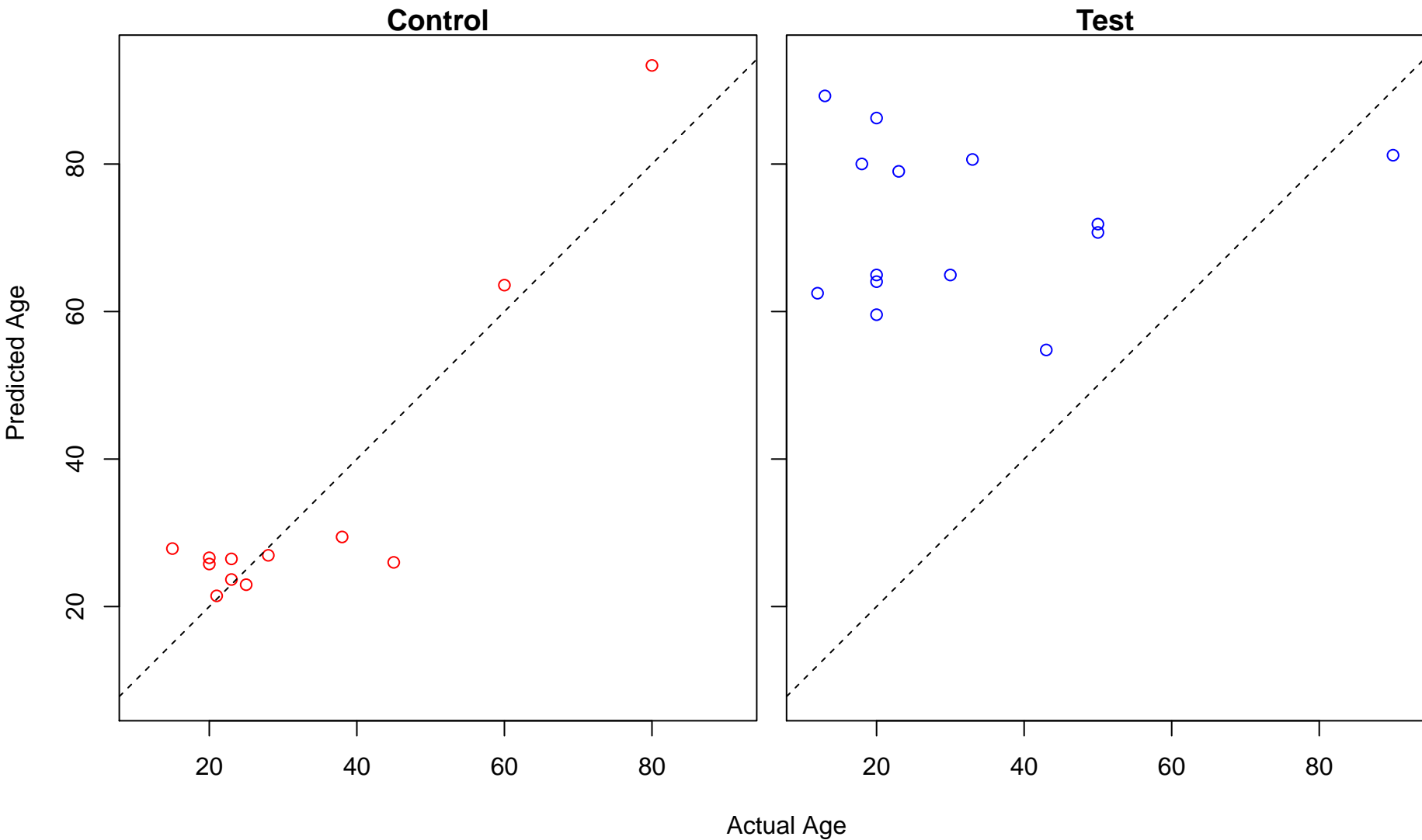
embryo development ending in birth or egg hatching (Score: 10.869794)



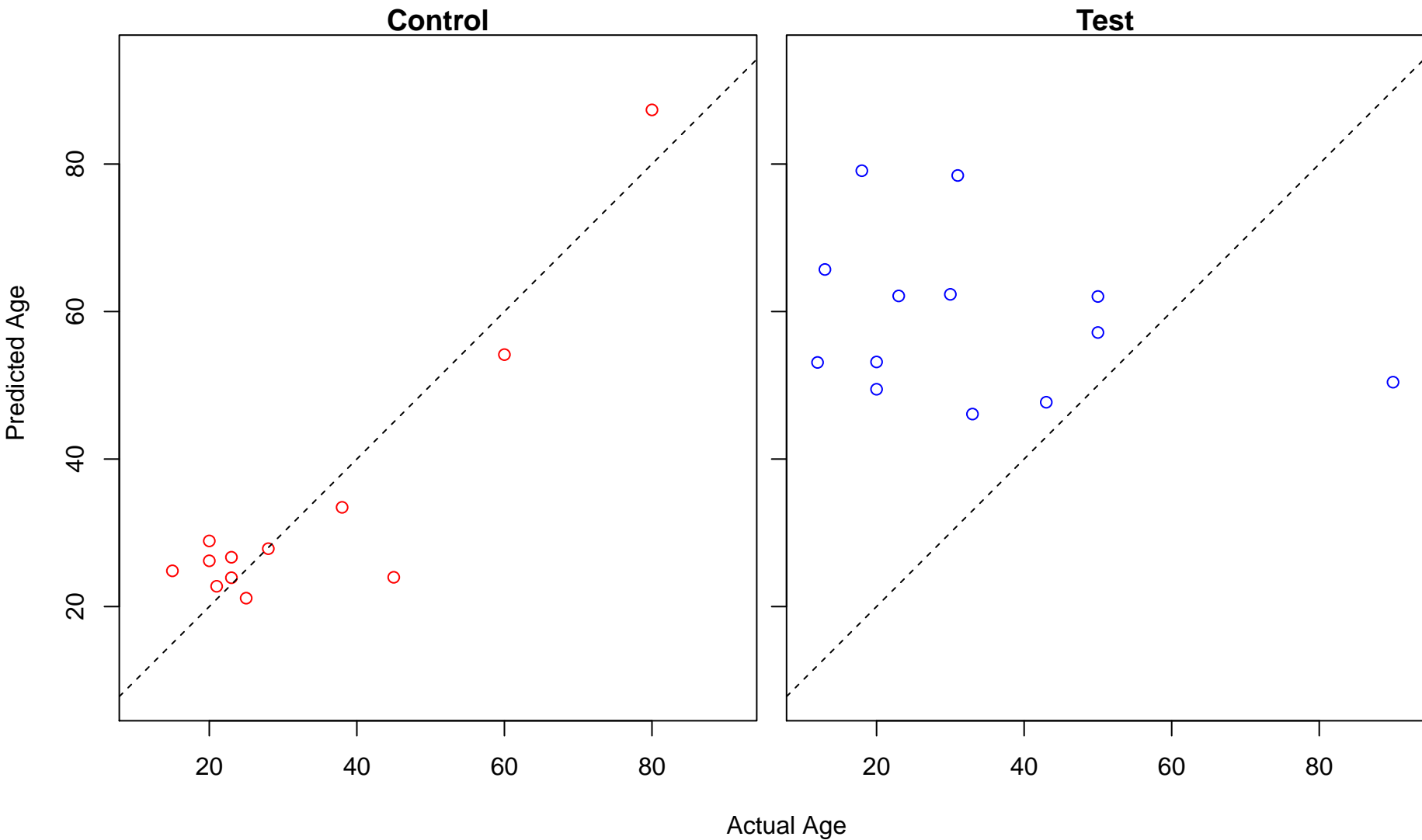
chordate embryonic development (Score: 10.869794)



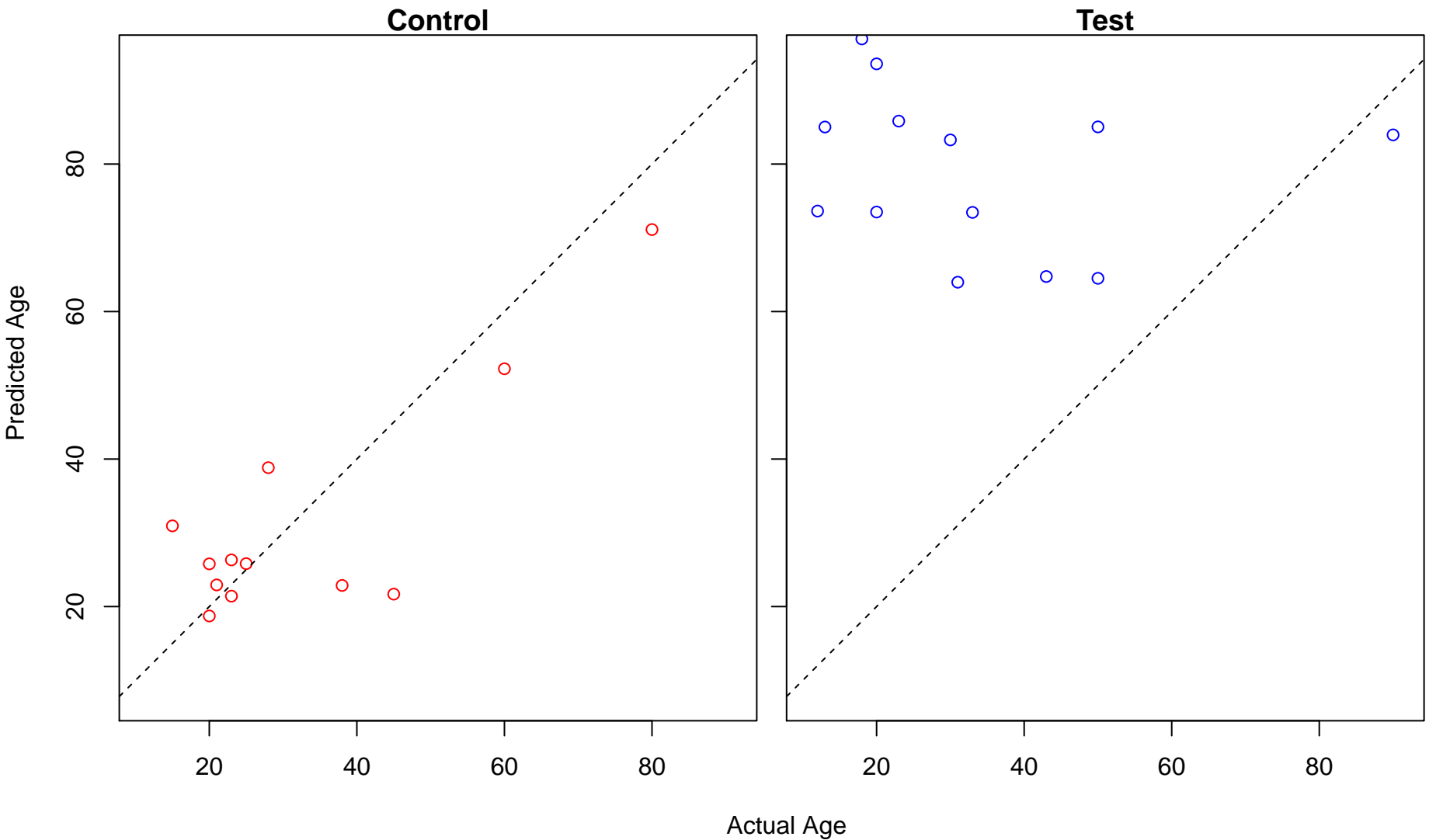
negative regulation of vitamin metabolic process (Score: 10.863579)



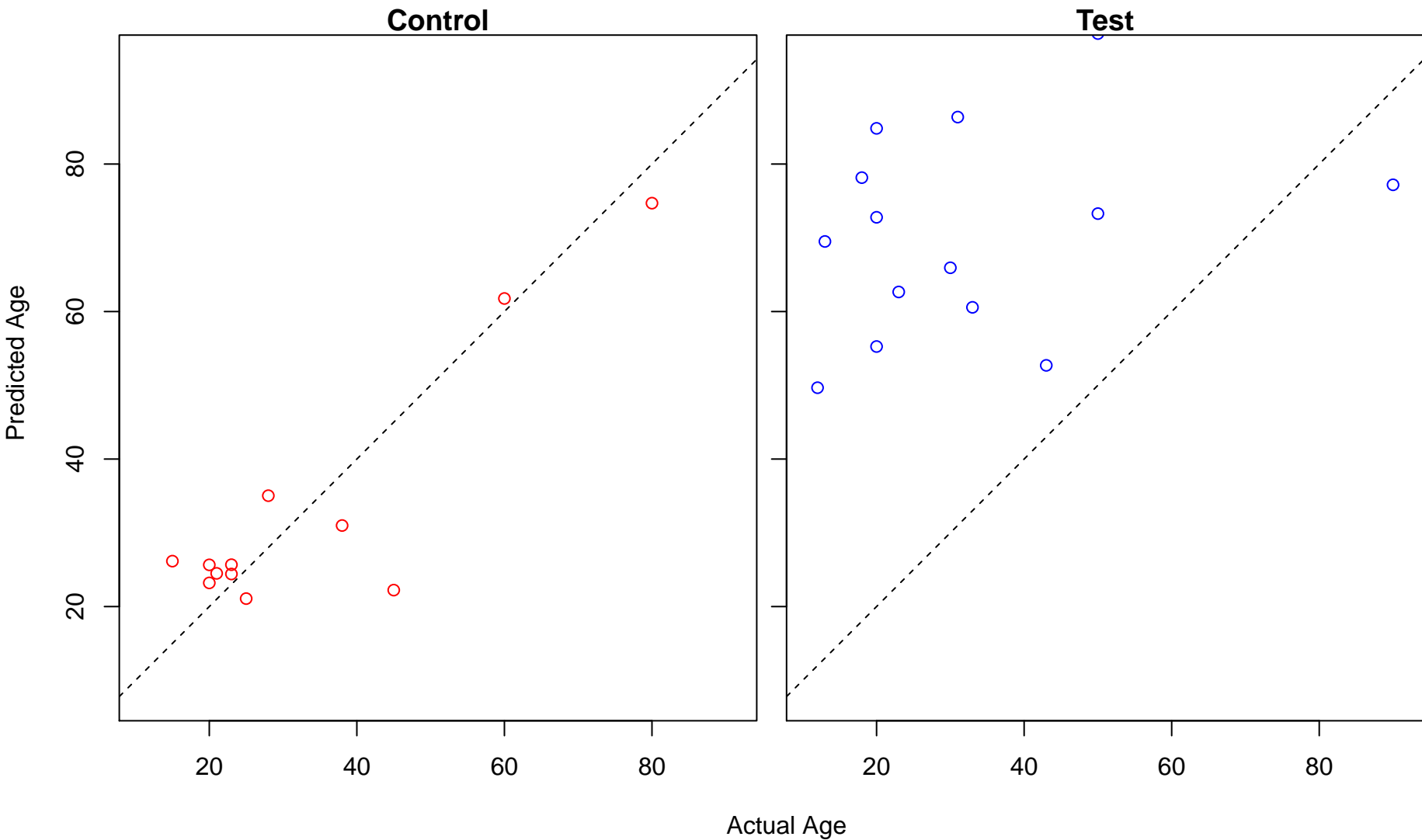
male meiosis (Score: 10.841649)



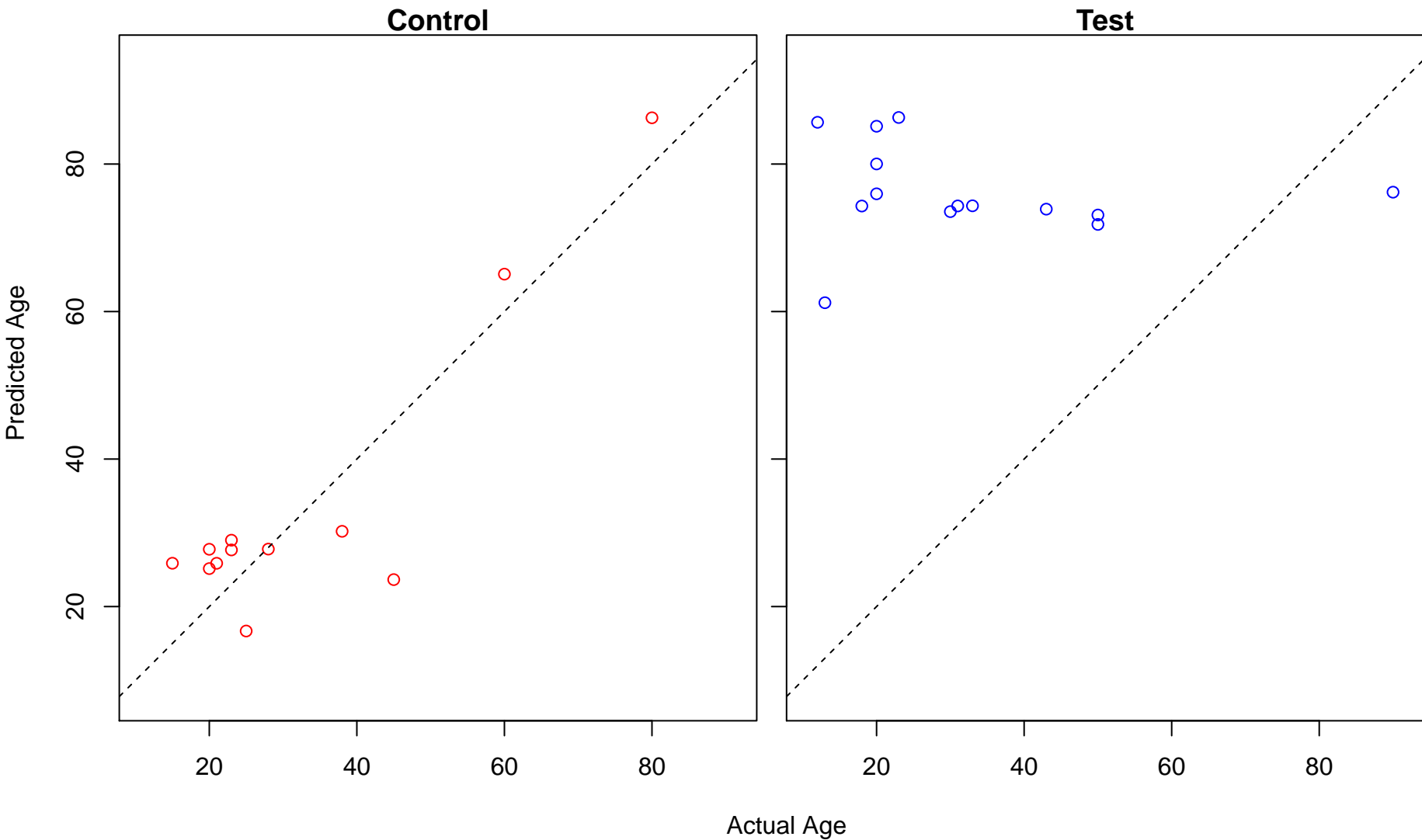
Negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway (Score: 1)



regulation of glycoprotein metabolic process (Score: 10.836440)

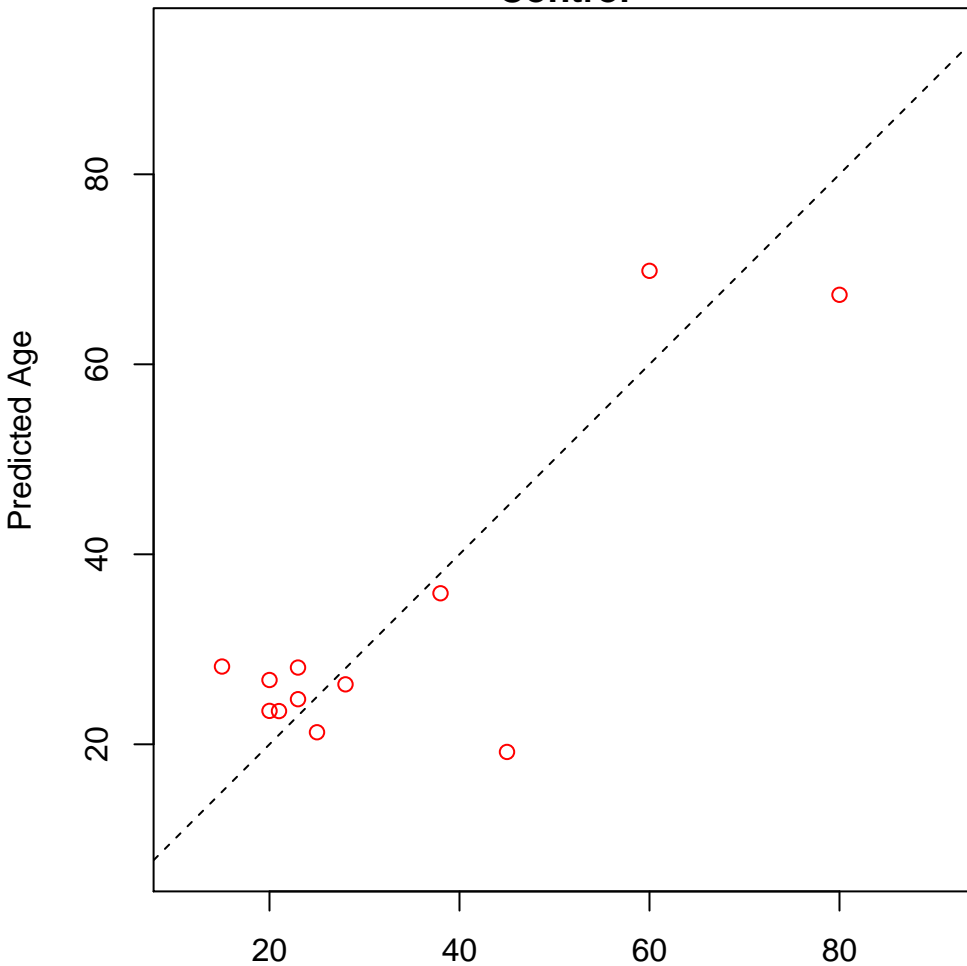


mucopolysaccharide metabolic process (Score: 10.834076)

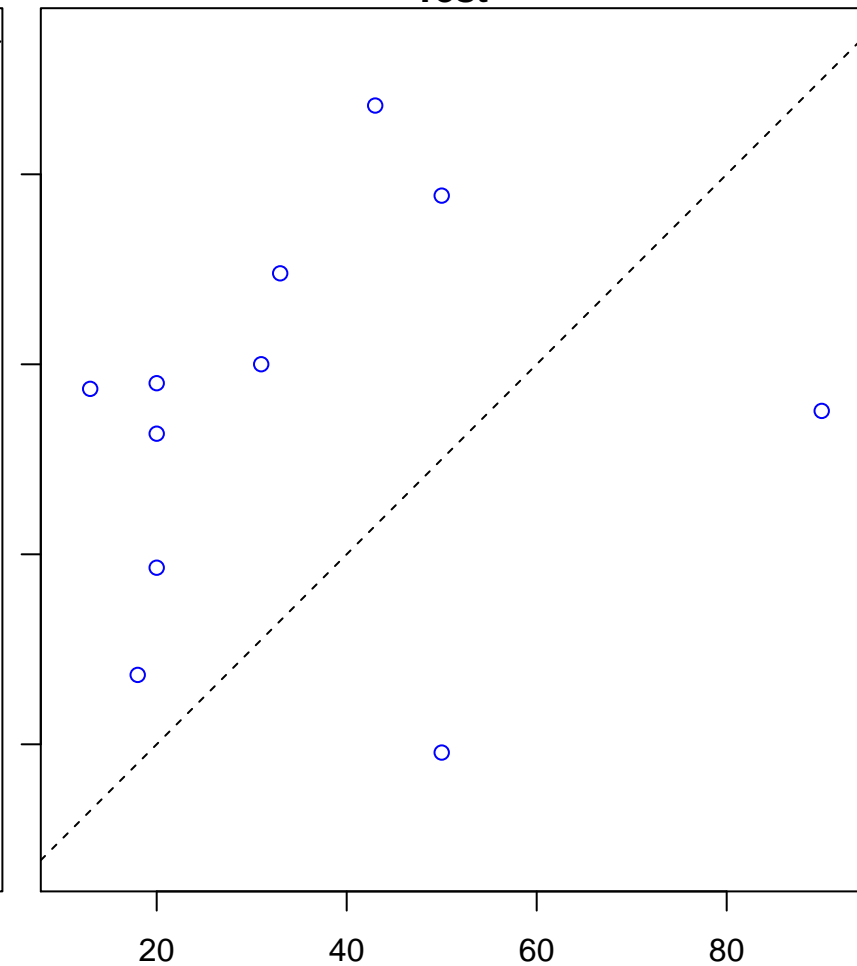


endodermal cell fate commitment (Score: 10.825795)

Control



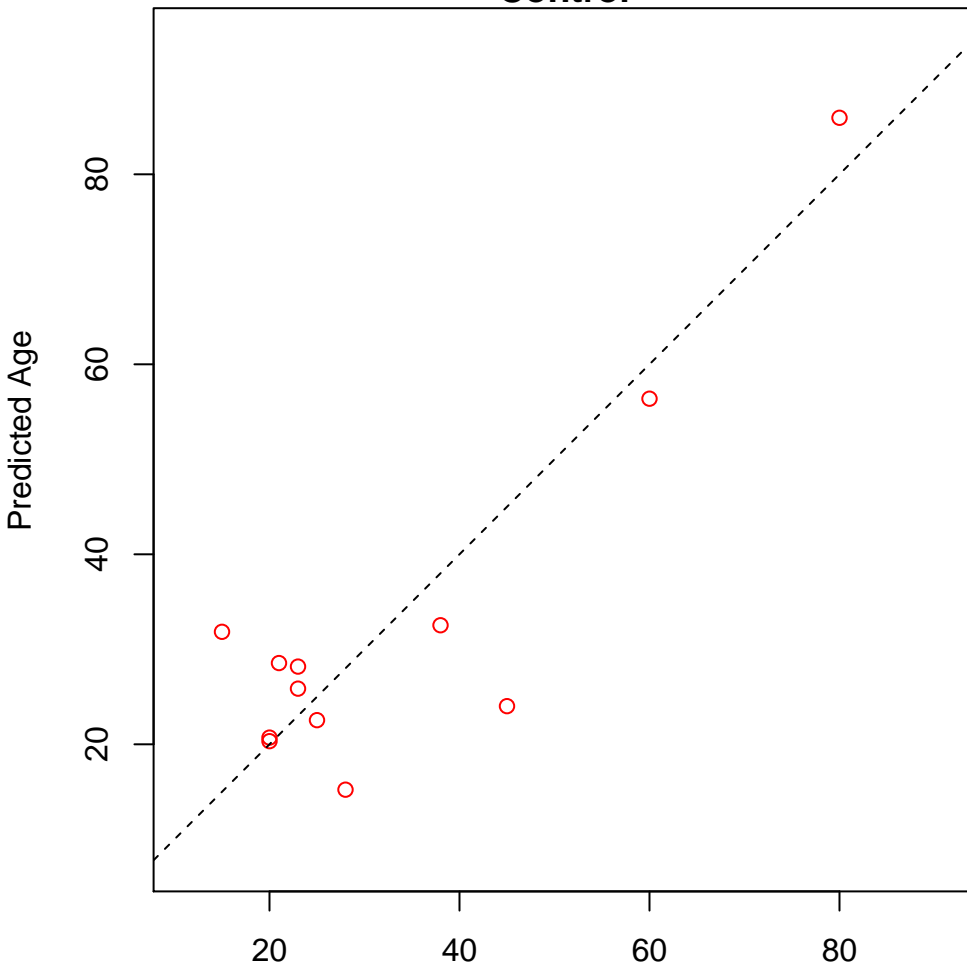
Test



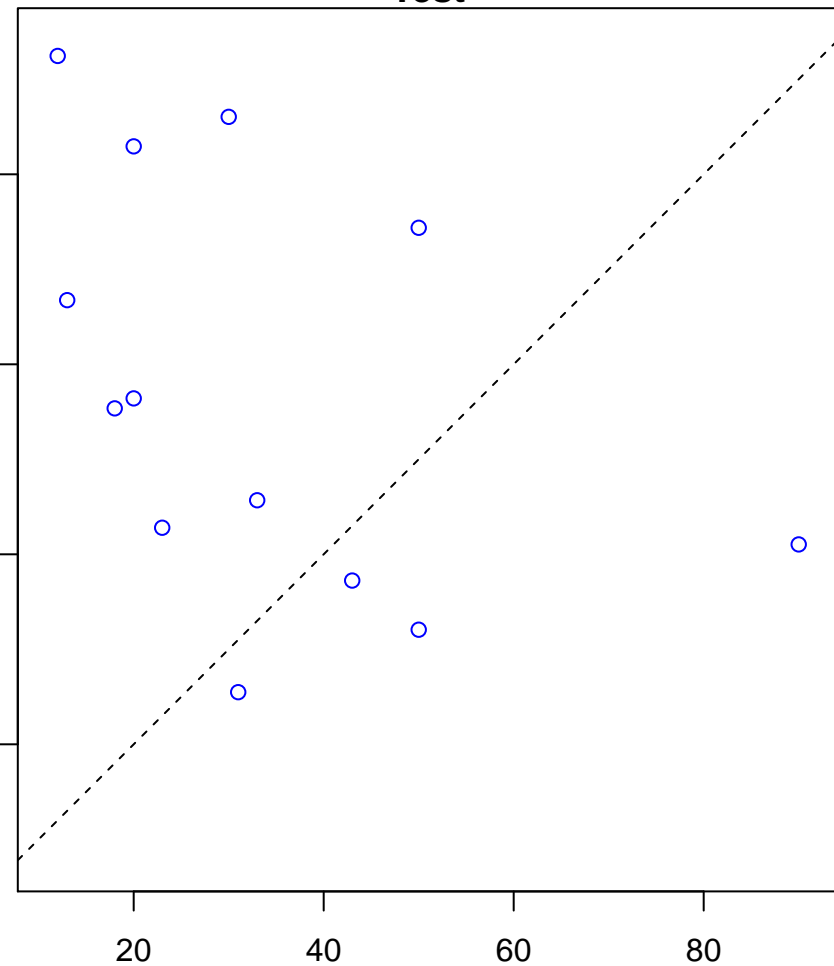
Actual Age

regulation of epithelial cell migration (Score: 10.821413)

Control

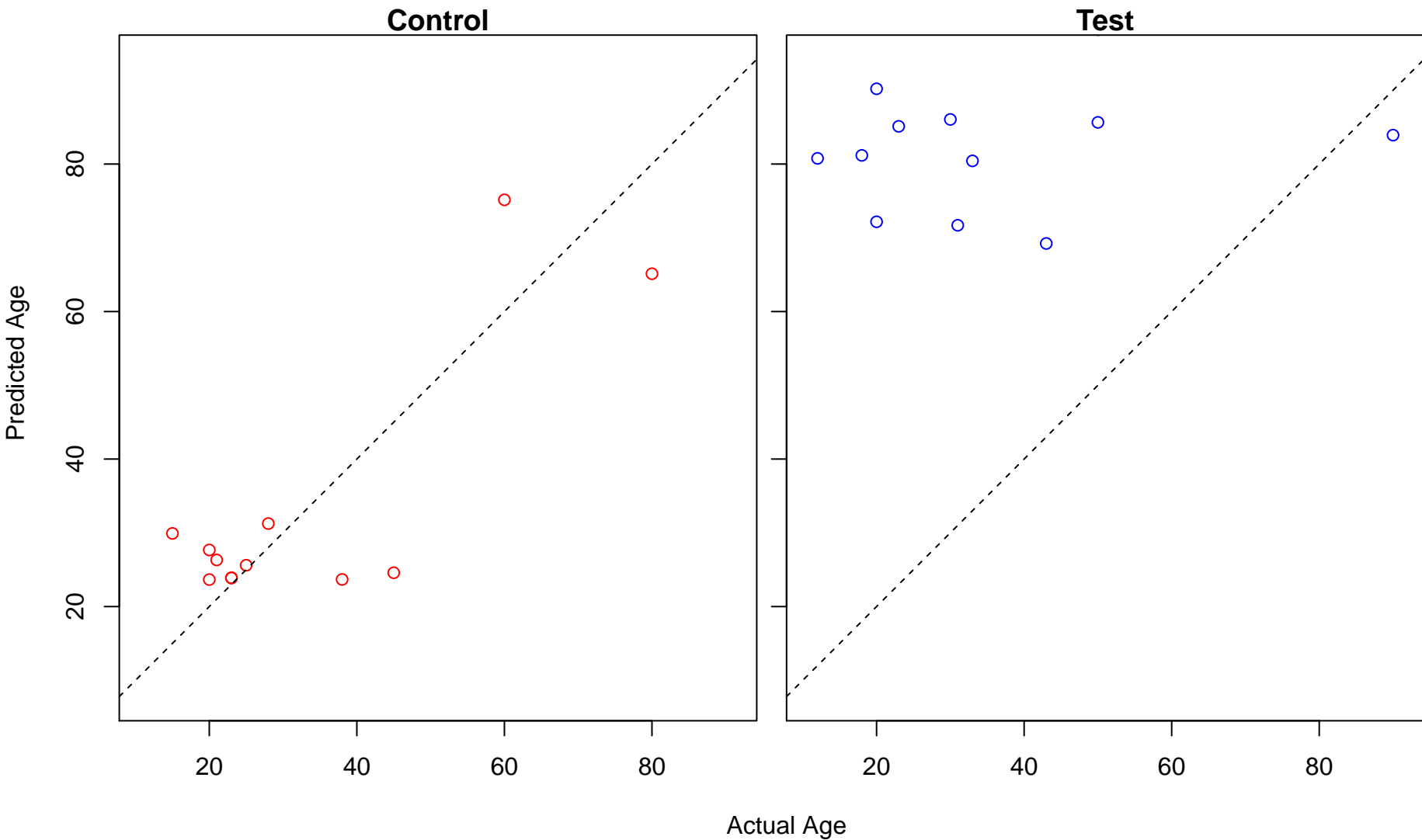


Test



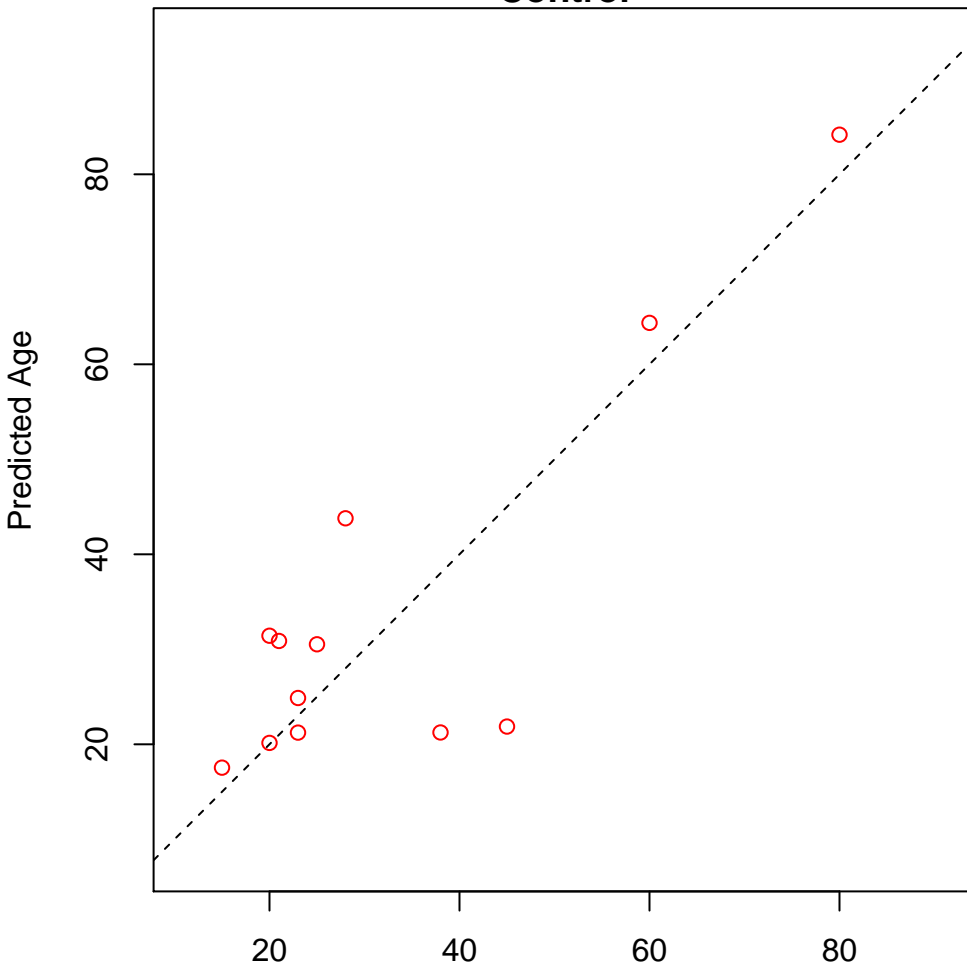
Actual Age

negative regulation of I-kappaB kinase/NF-kappaB signaling (Score: 10.818402)

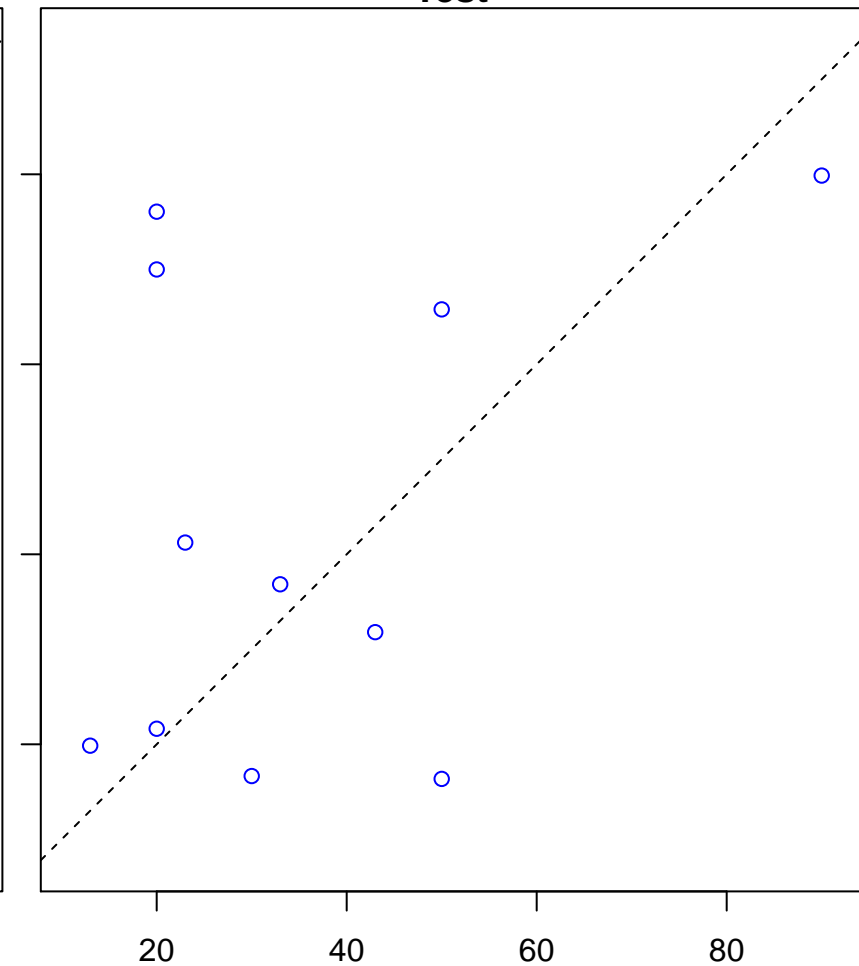


negative regulation of protein transport (Score: 10.805124)

Control

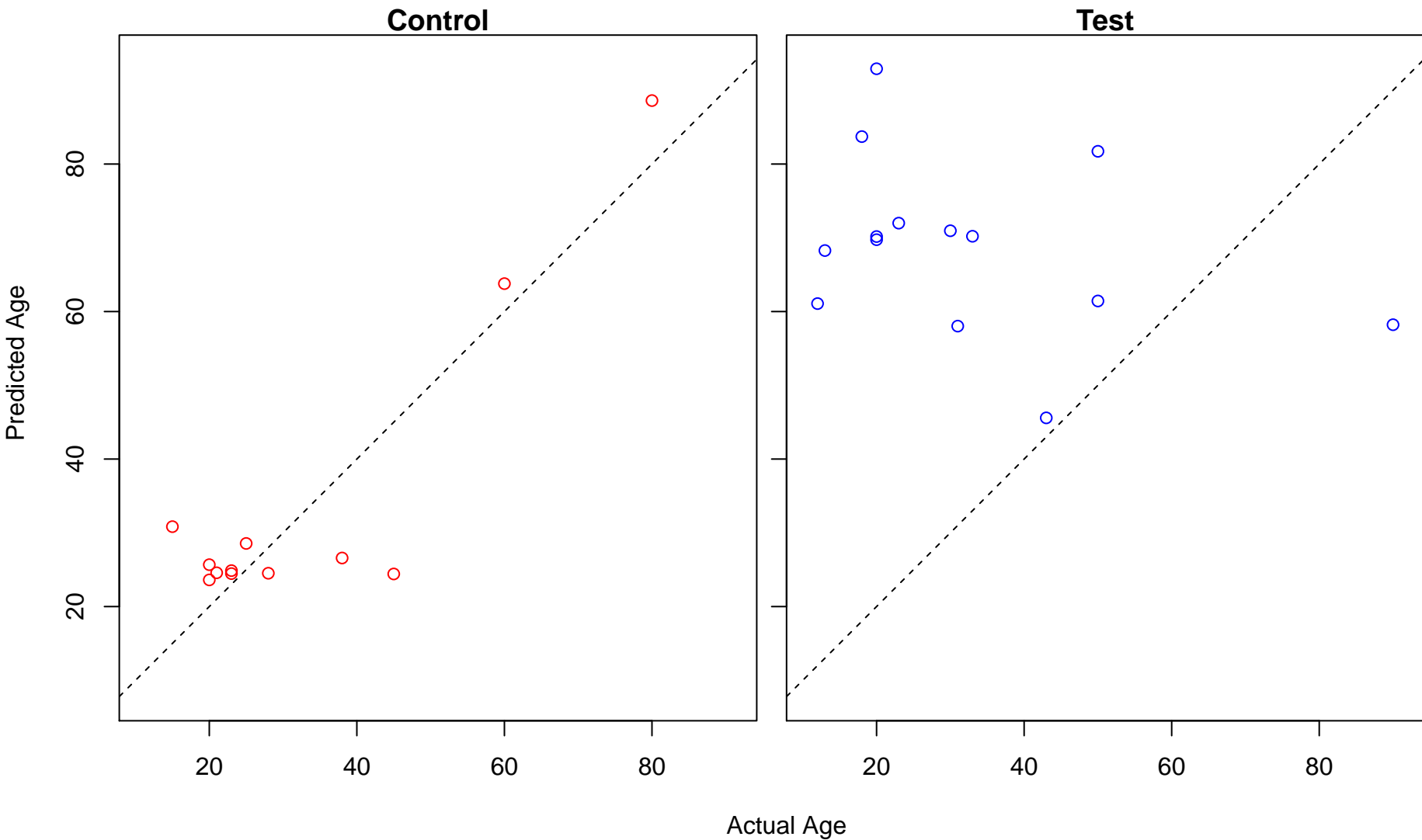


Test

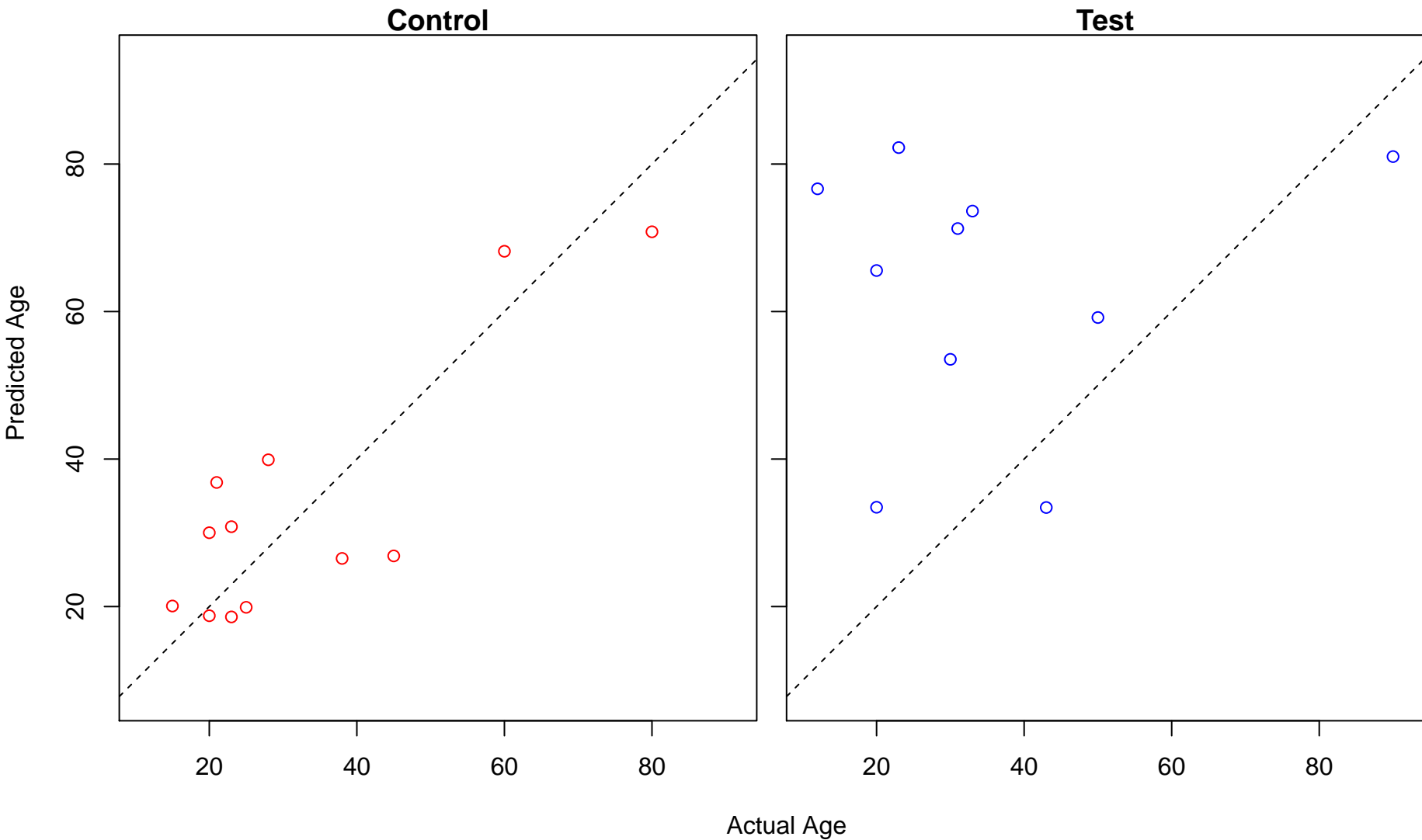


Actual Age

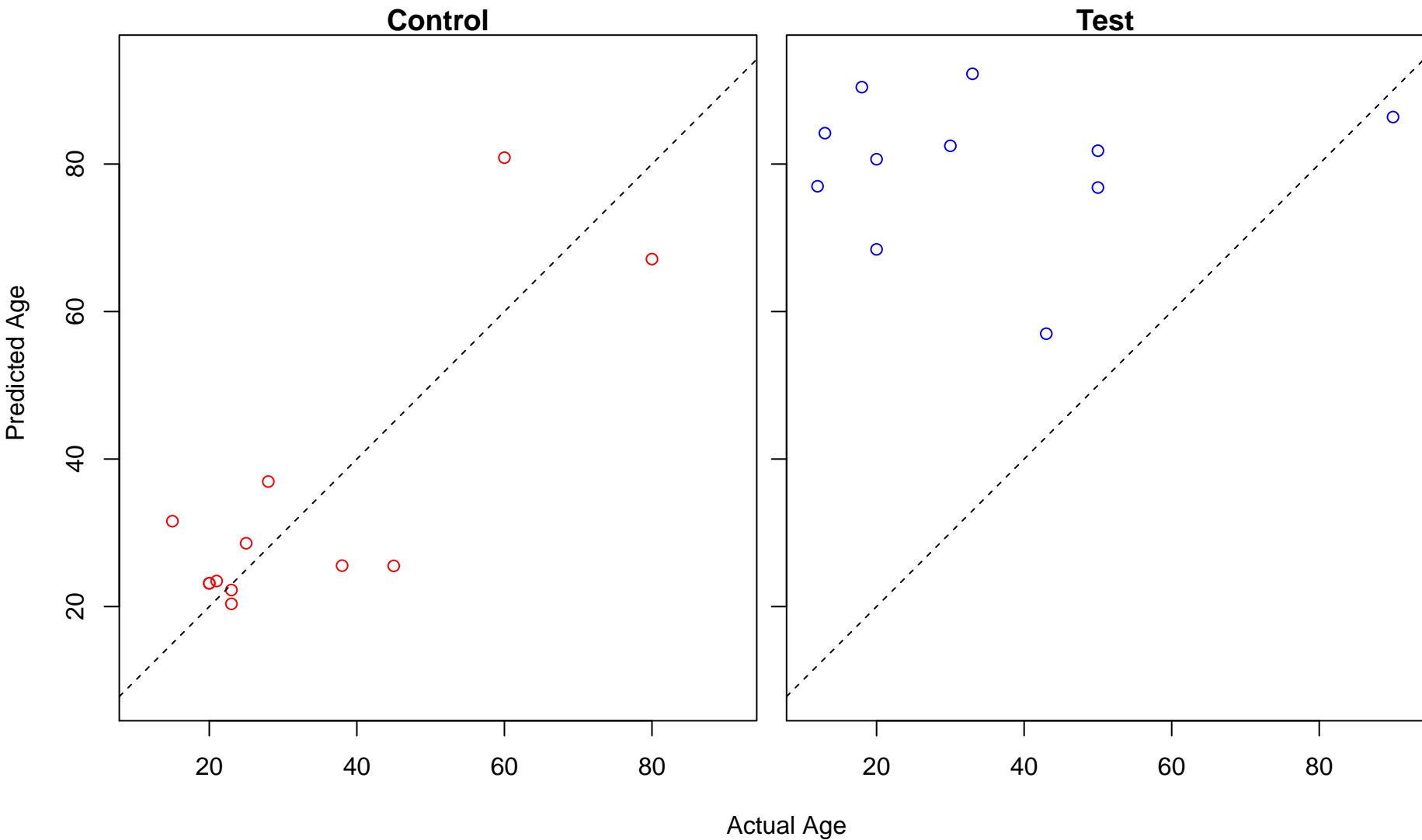
positive regulation of establishment of protein localization to telomere (Score: 10.801549)



positive regulation by host of viral process (Score: 10.792684)

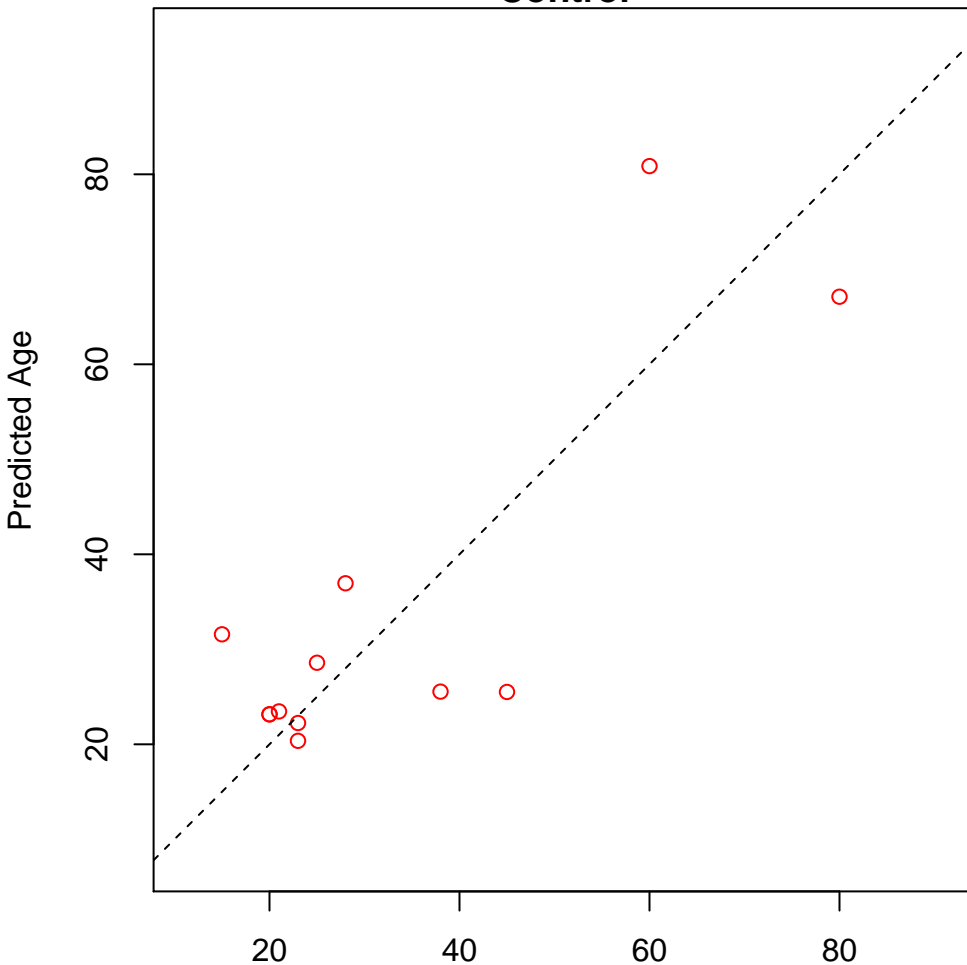


plasma membrane raft assembly (Score: 10.784934)

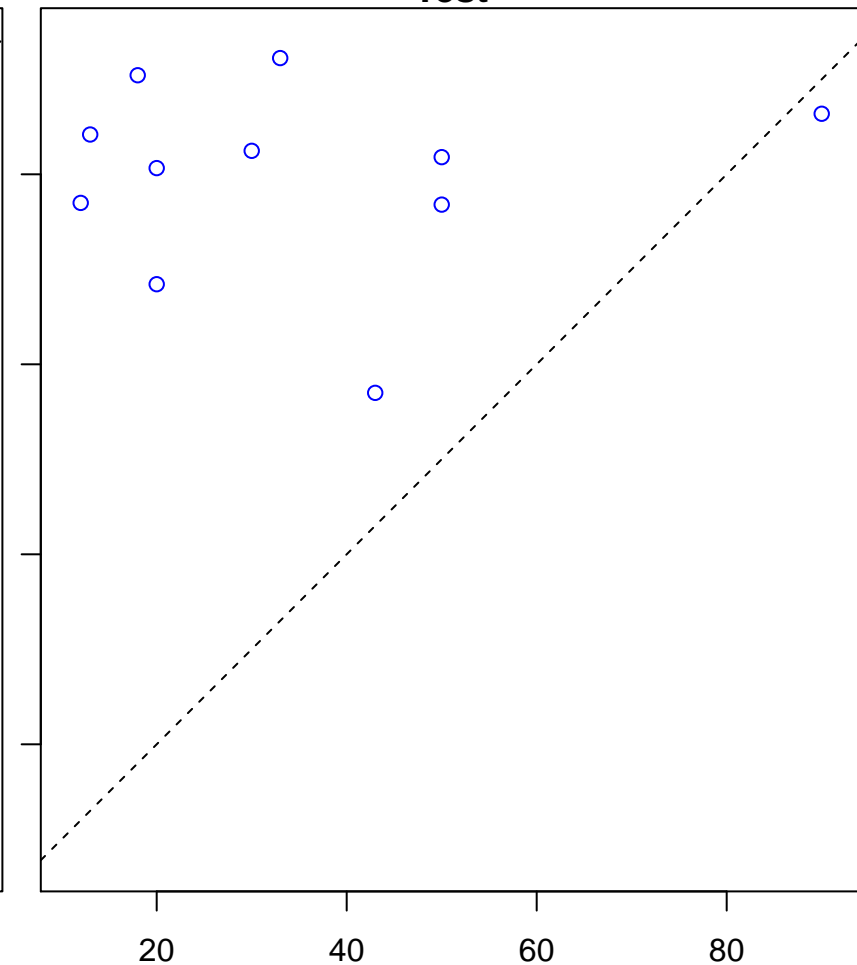


plasma membrane raft organization (Score: 10.784934)

Control

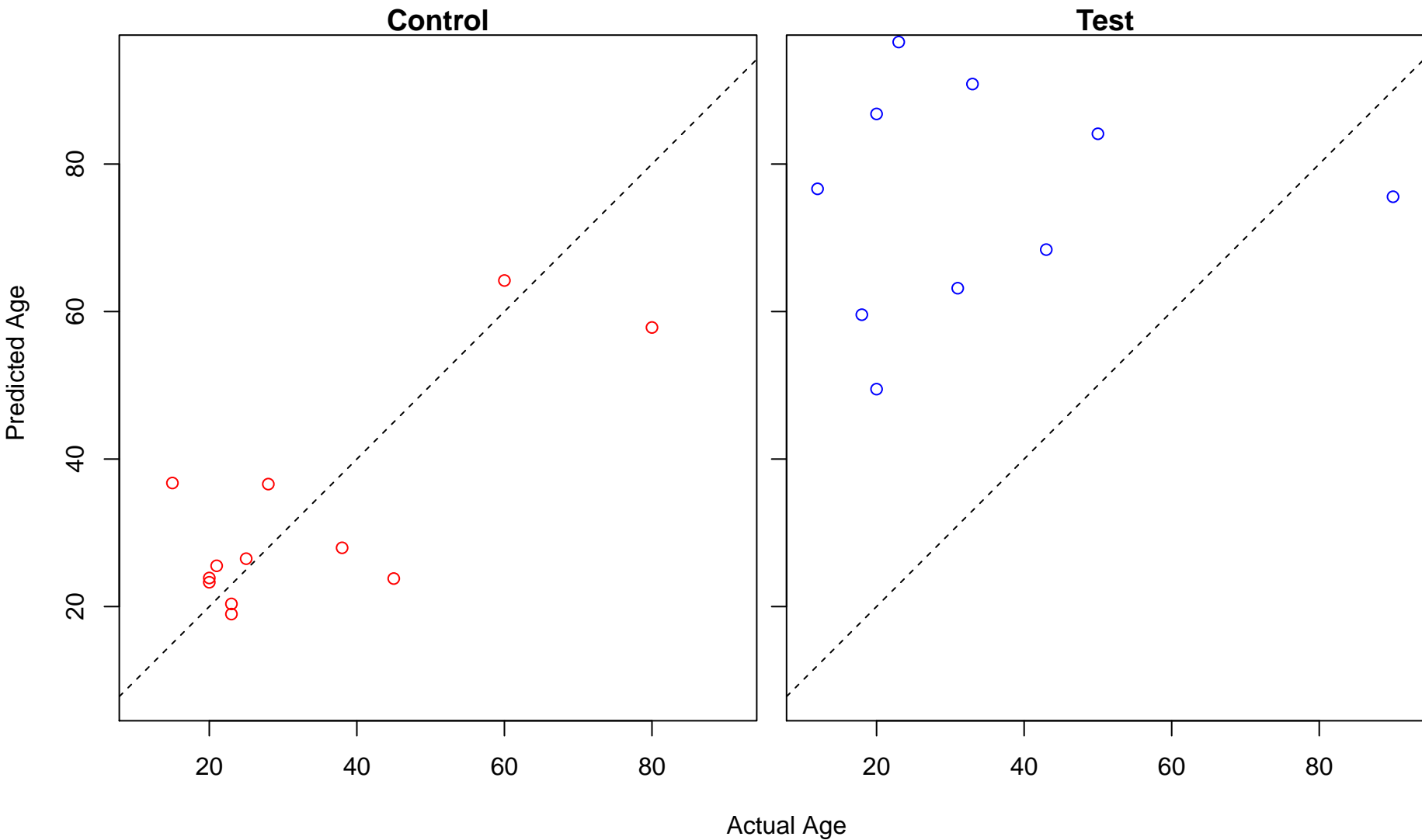


Test

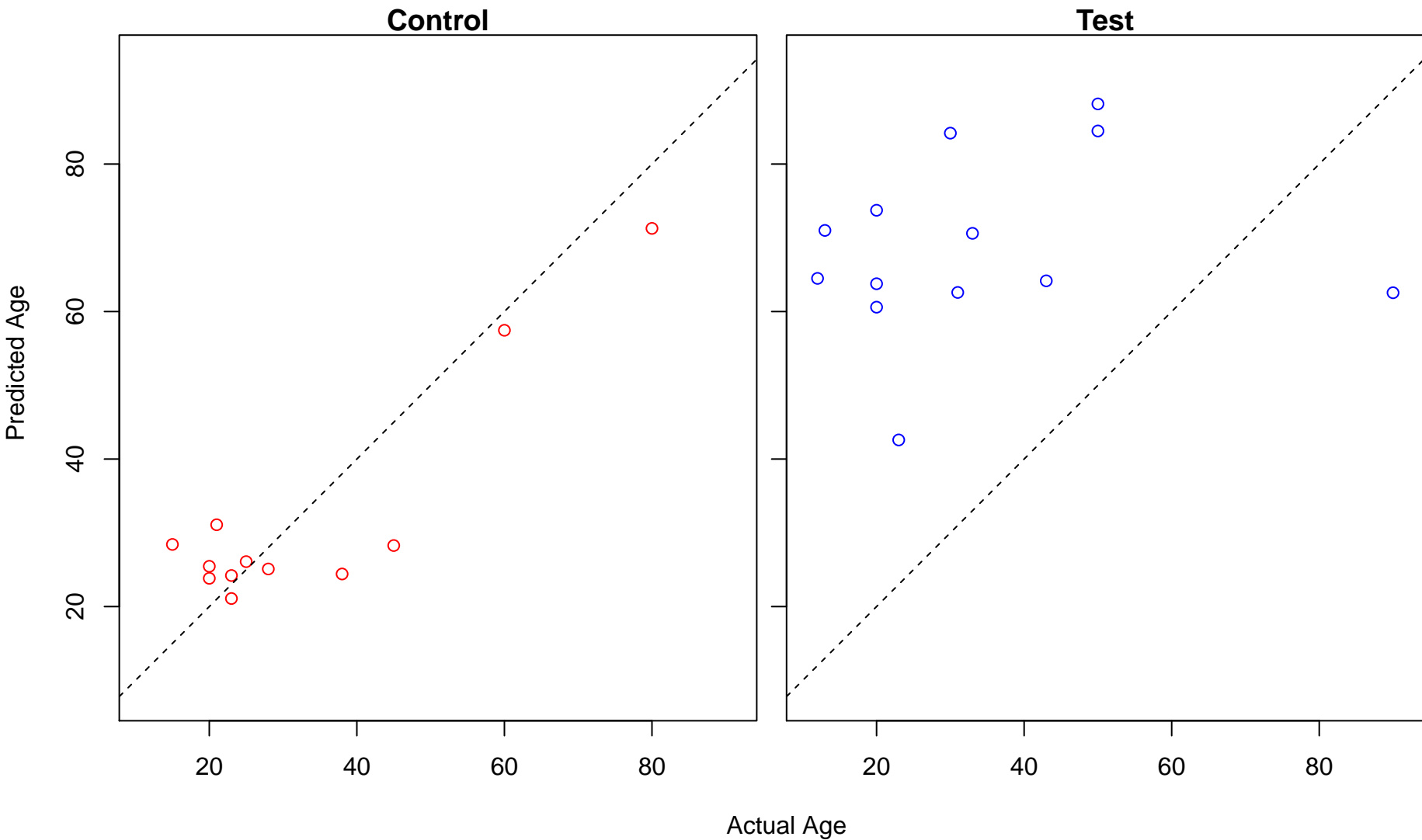


Actual Age

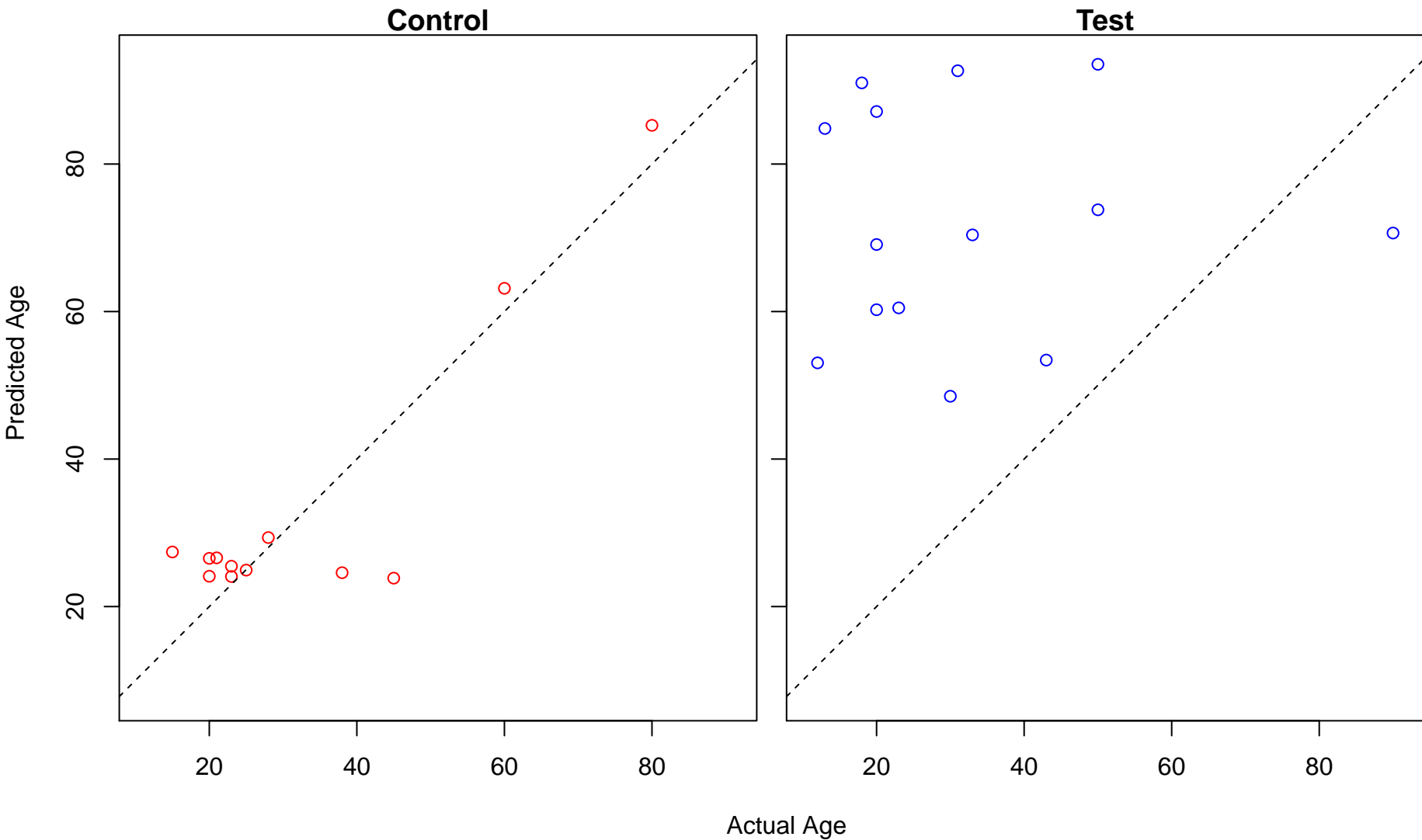
establishment of apical/basal cell polarity (Score: 10.783303)



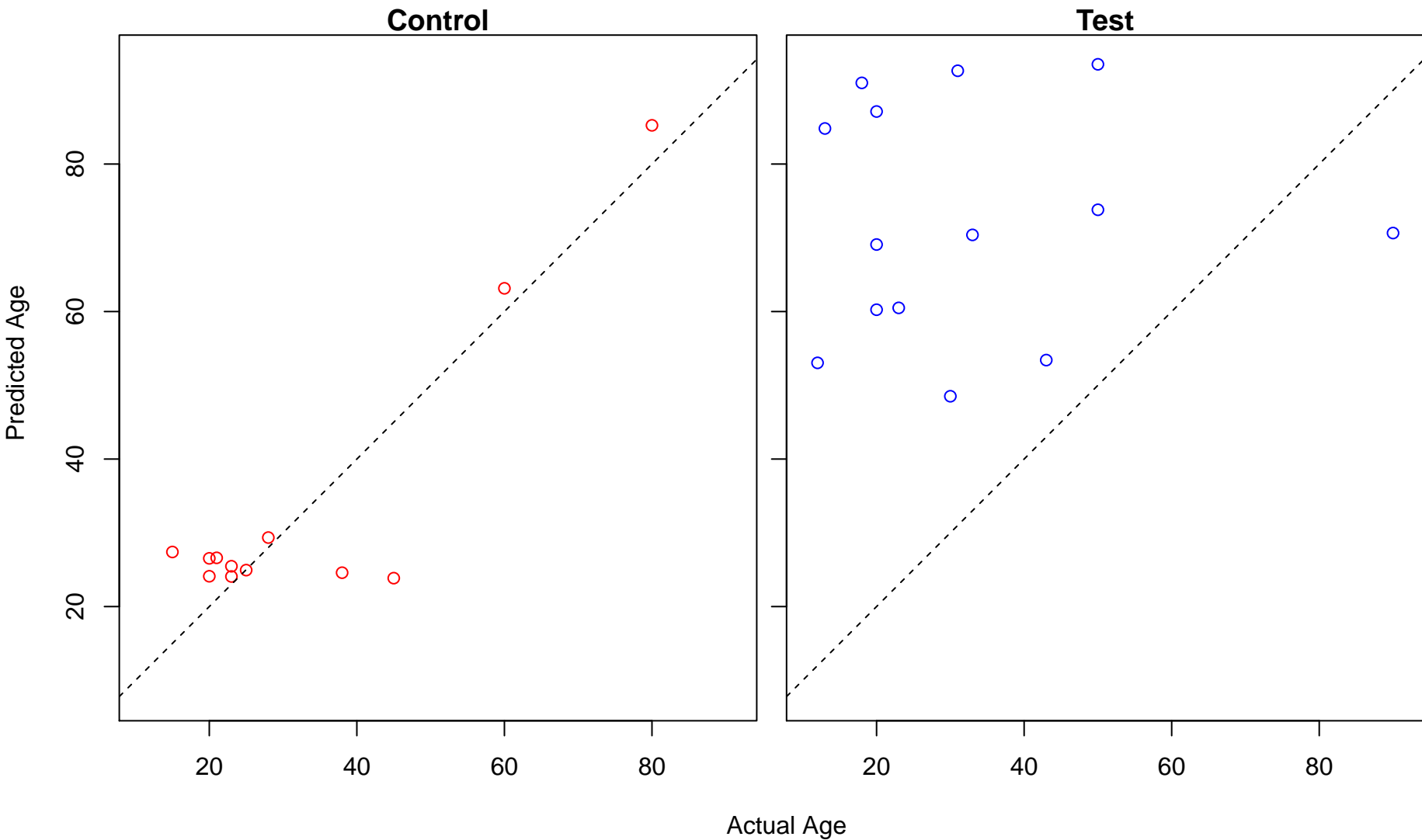
endothelial cell migration (Score: 10.783230)



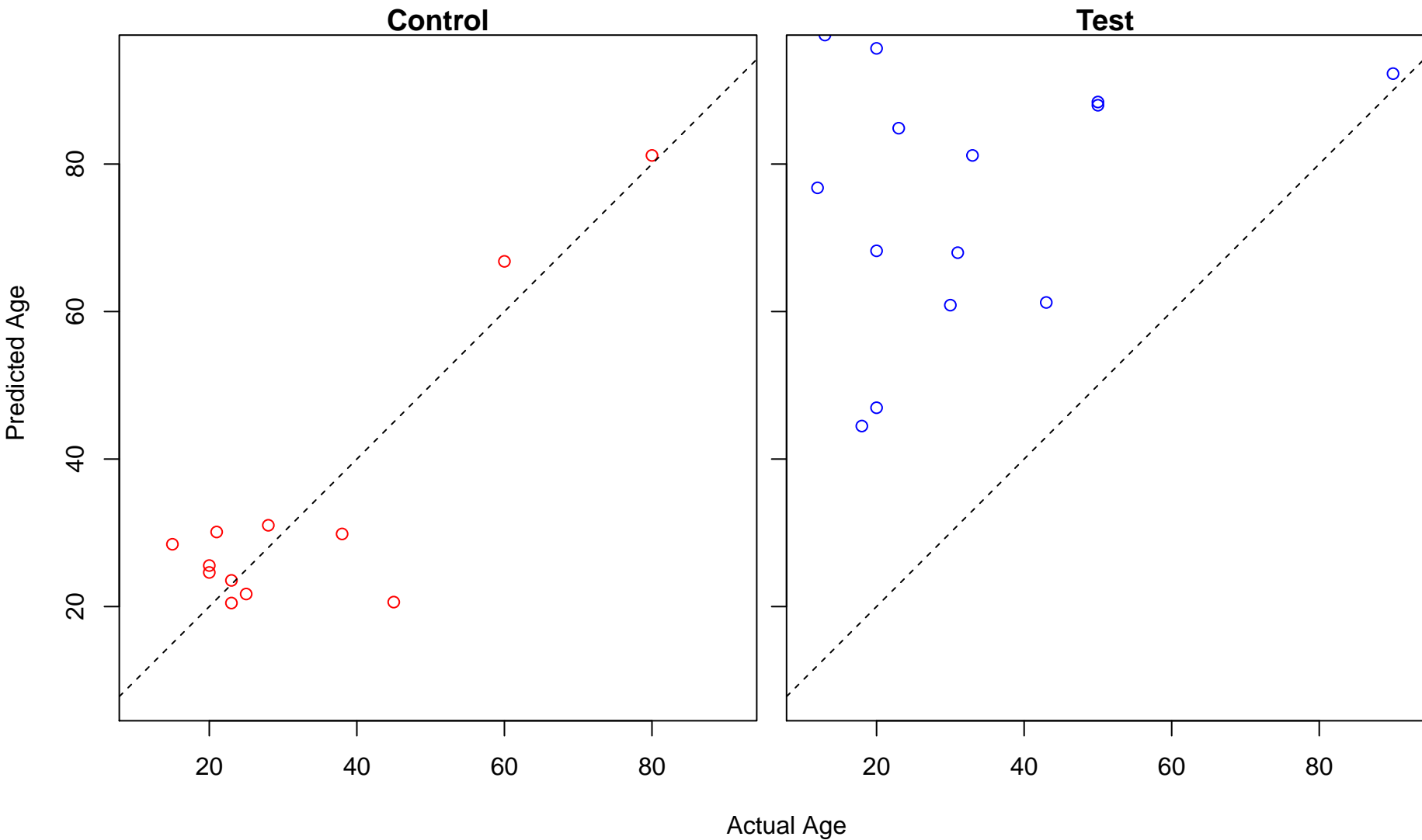
DNA replication-independent nucleosome assembly (Score: 10.775516)



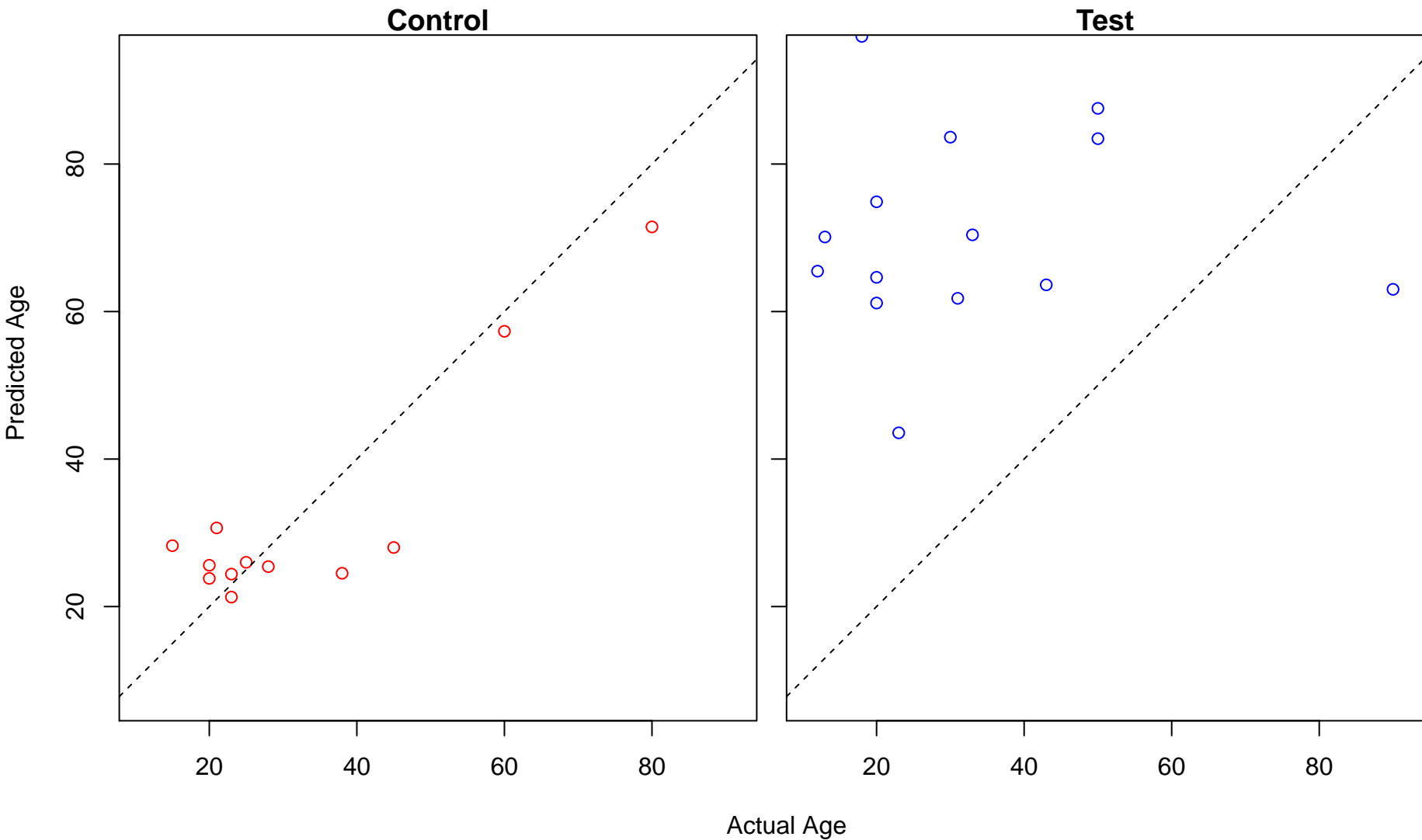
DNA replication-independent nucleosome organization (Score: 10.775516)



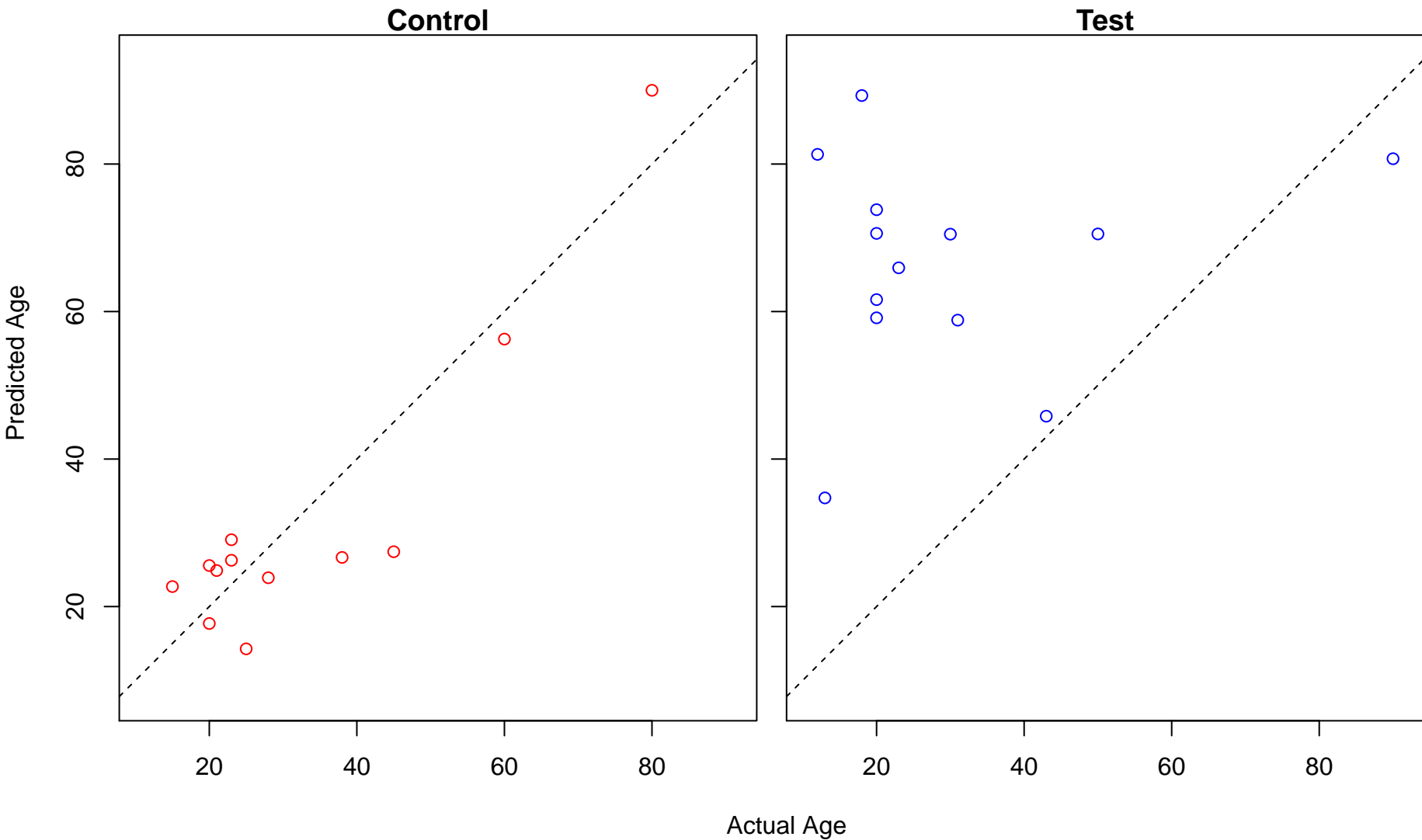
lung morphogenesis (Score: 10.771441)



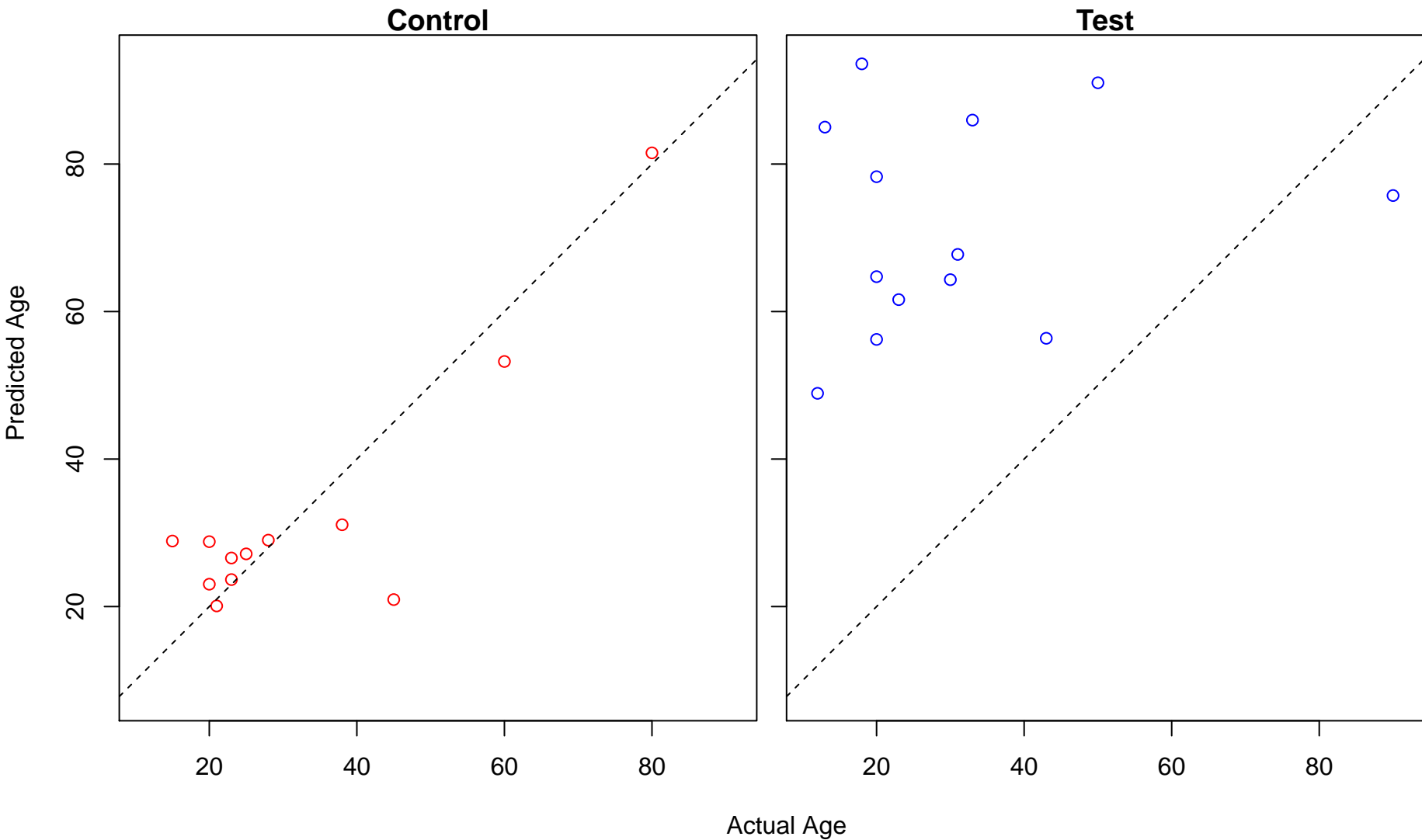
ameboidal-type cell migration (Score: 10.761314)



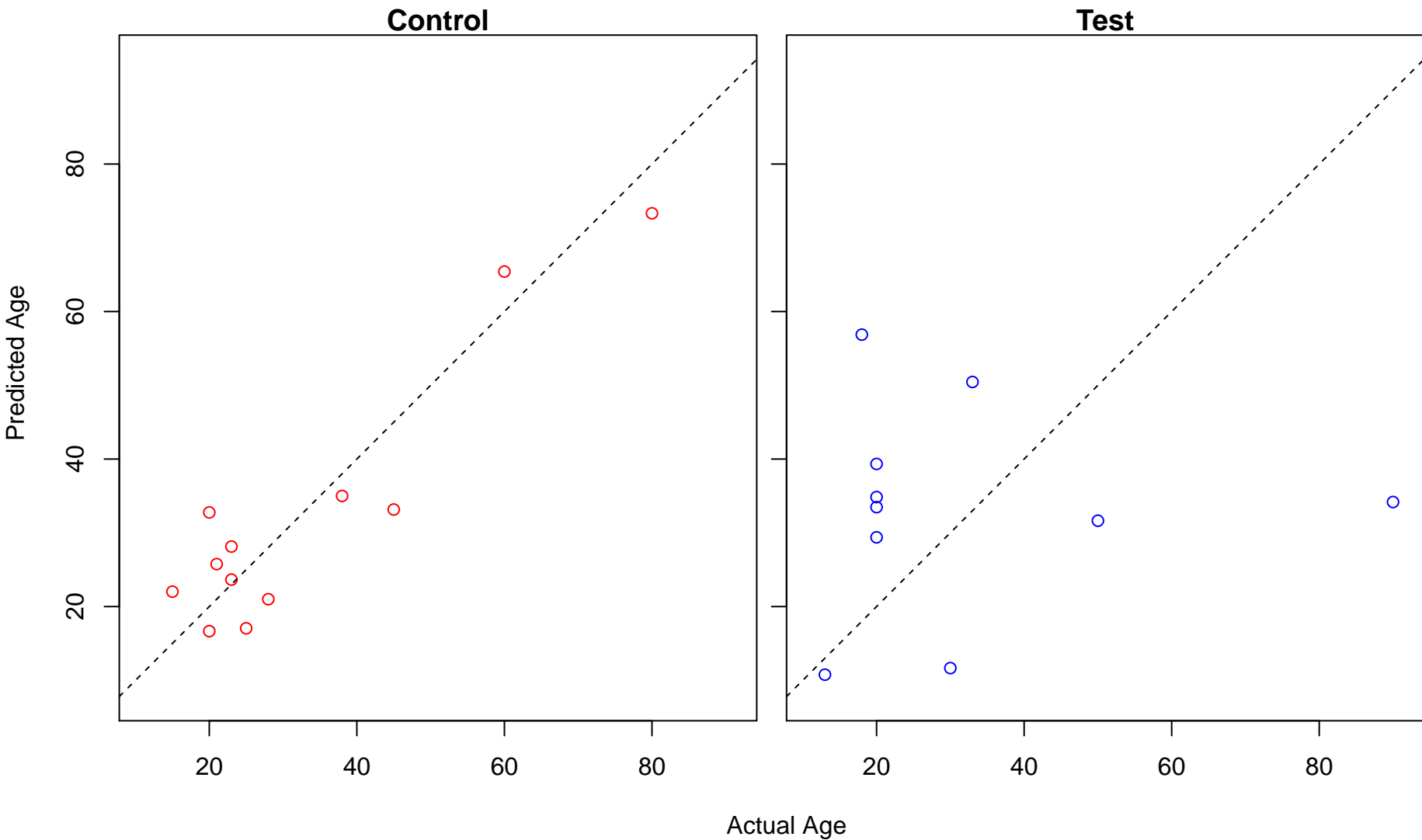
mRNA polyadenylation (Score: 10.759205)



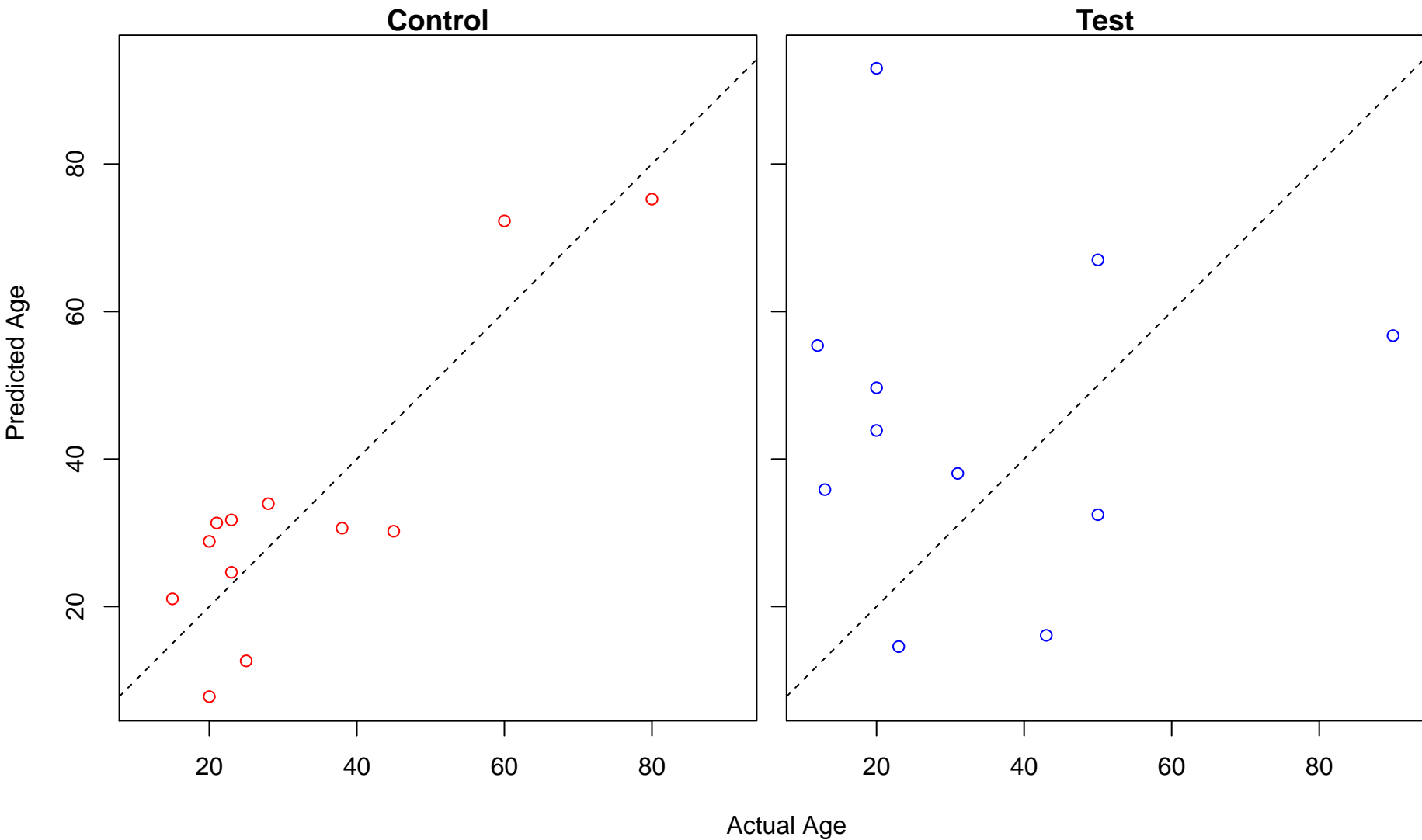
positive regulation of histone H4 acetylation (Score: 10.751757)



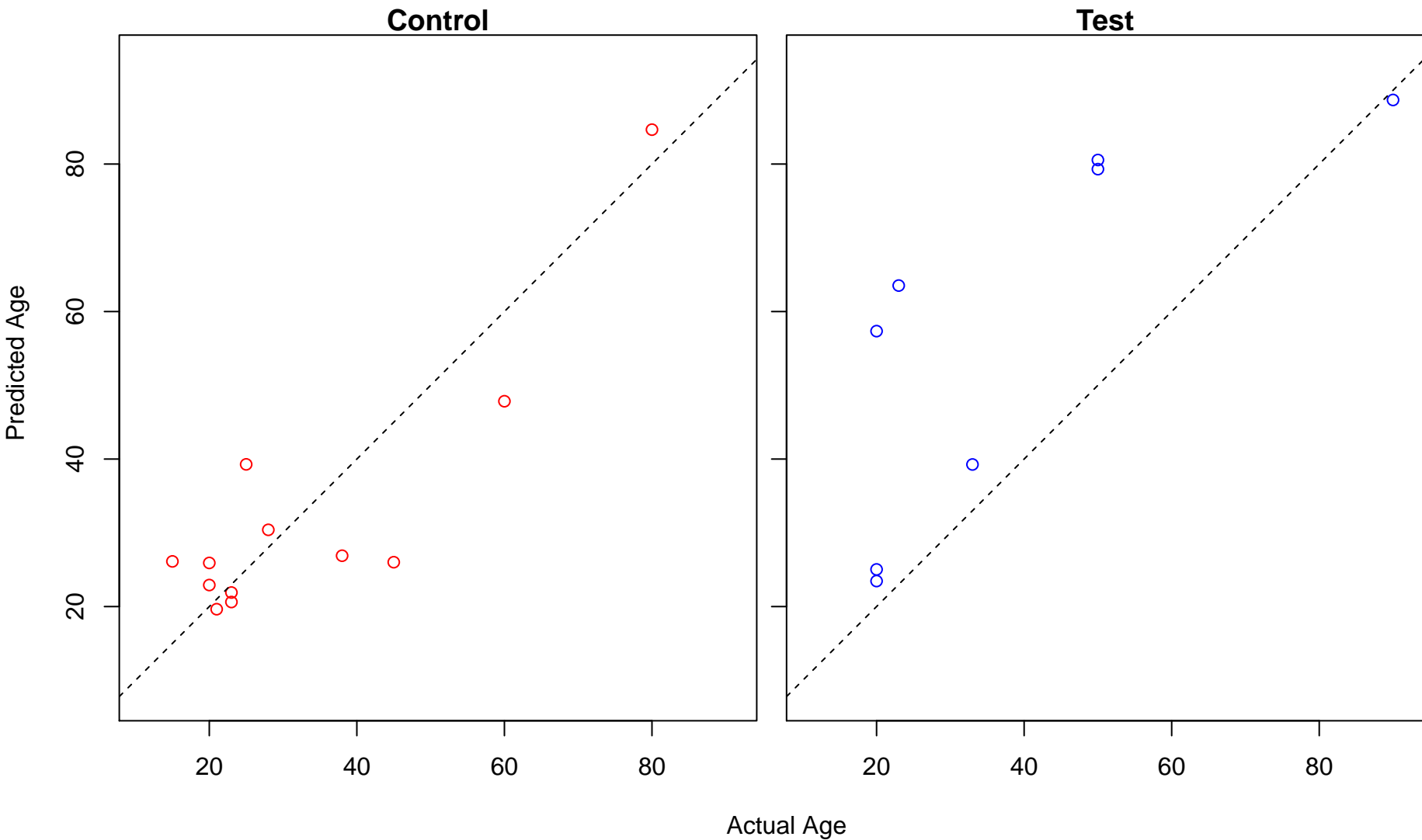
lactate transport (Score: 10.748896)



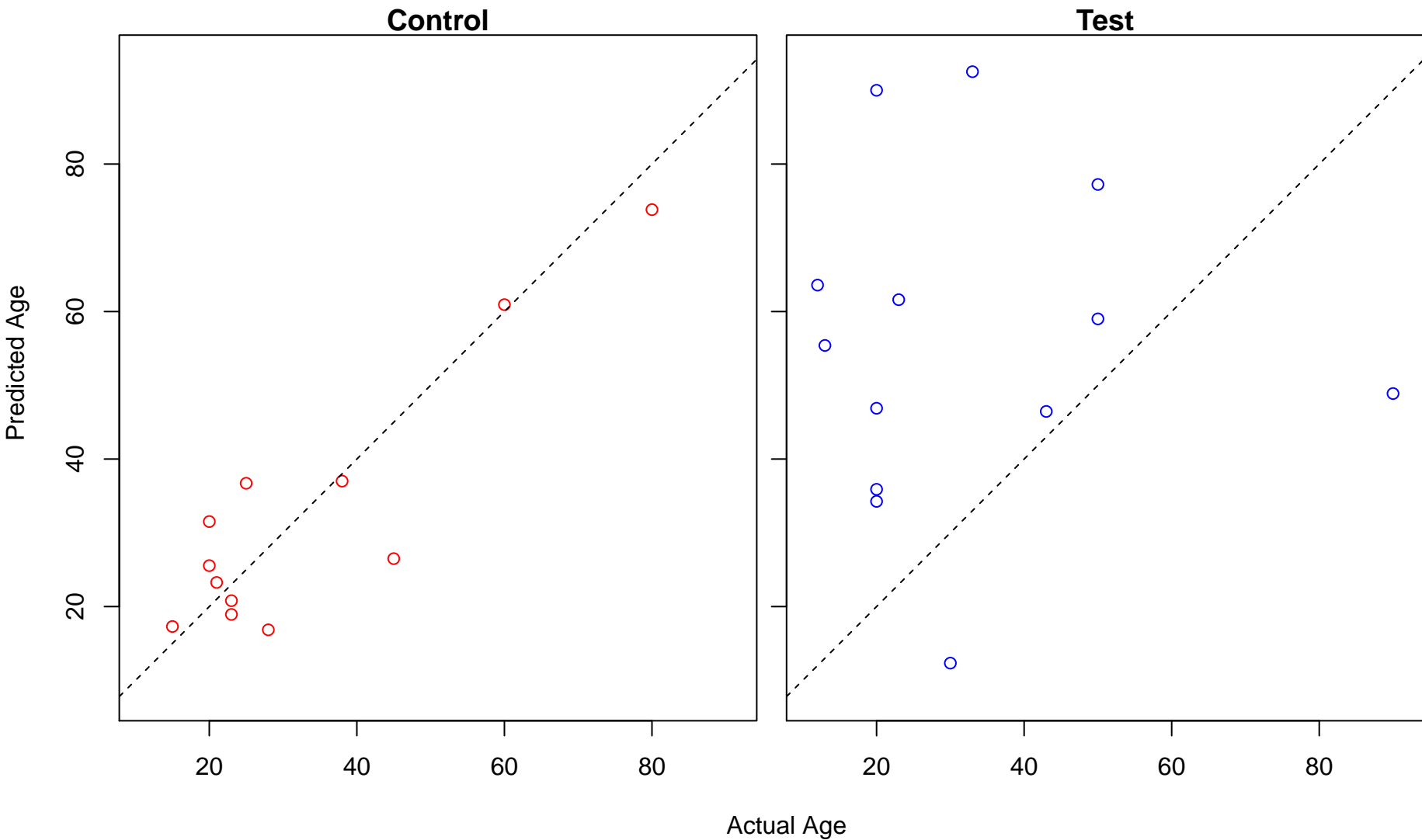
actin filament severing (Score: 10.748301)



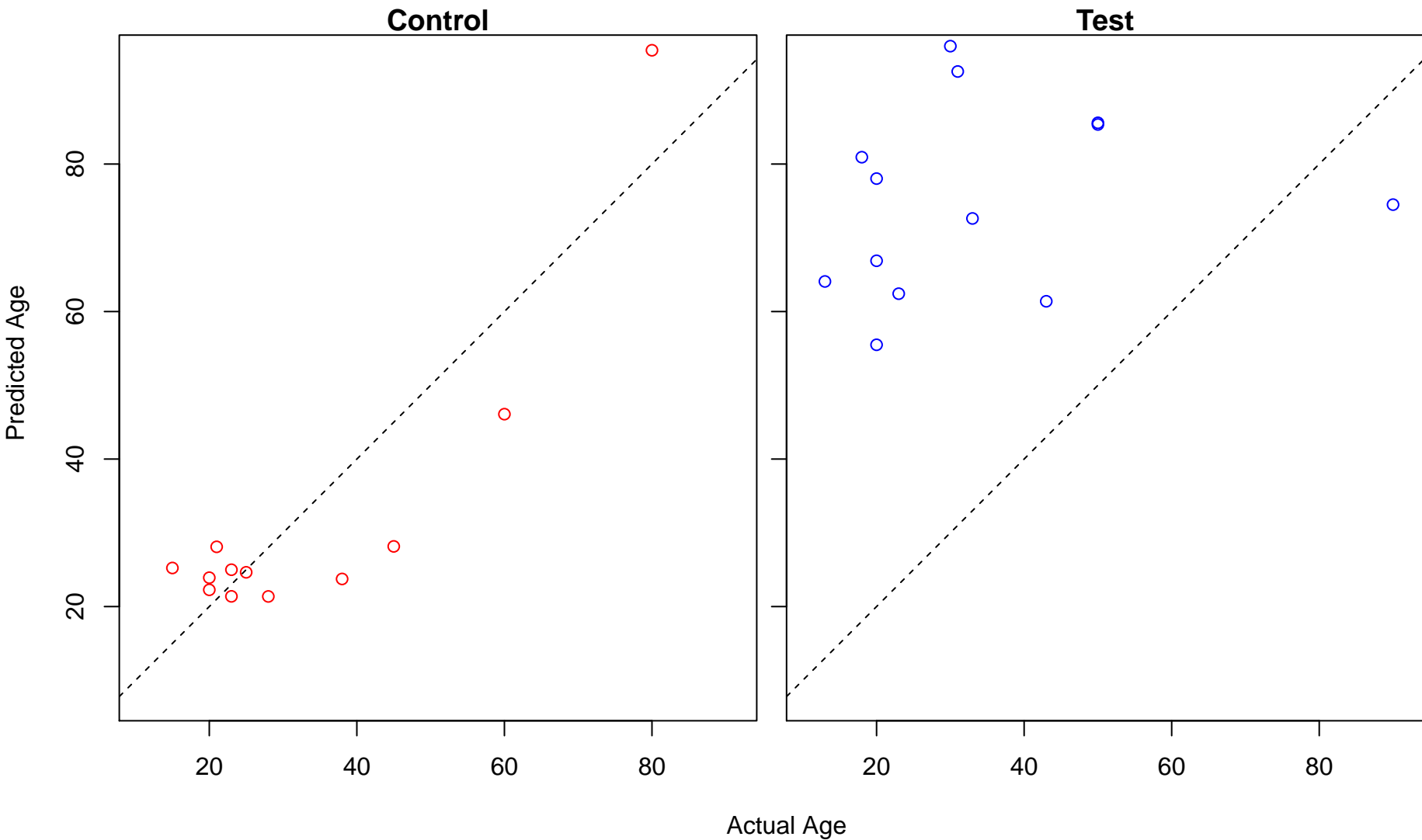
positive regulation of granulocyte chemotaxis (Score: 10.744703)



sulfur compound transport (Score: 10.736242)

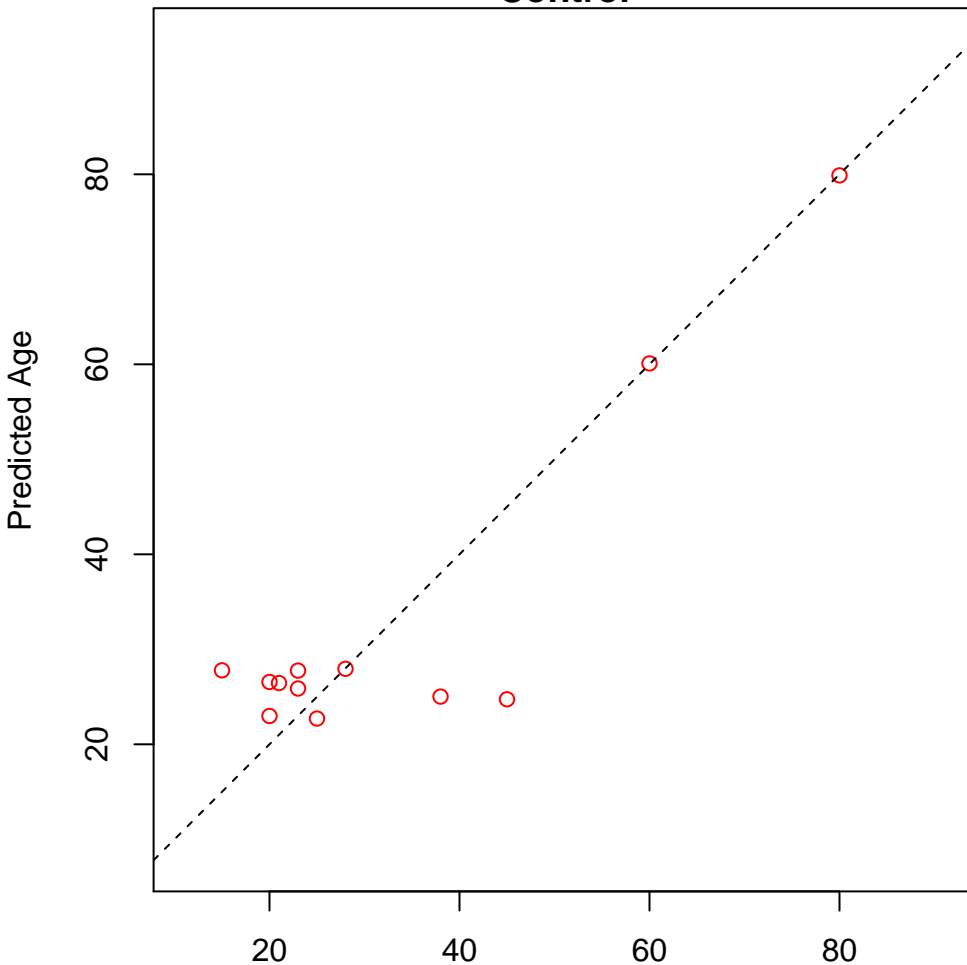


palate development (Score: 10.733966)

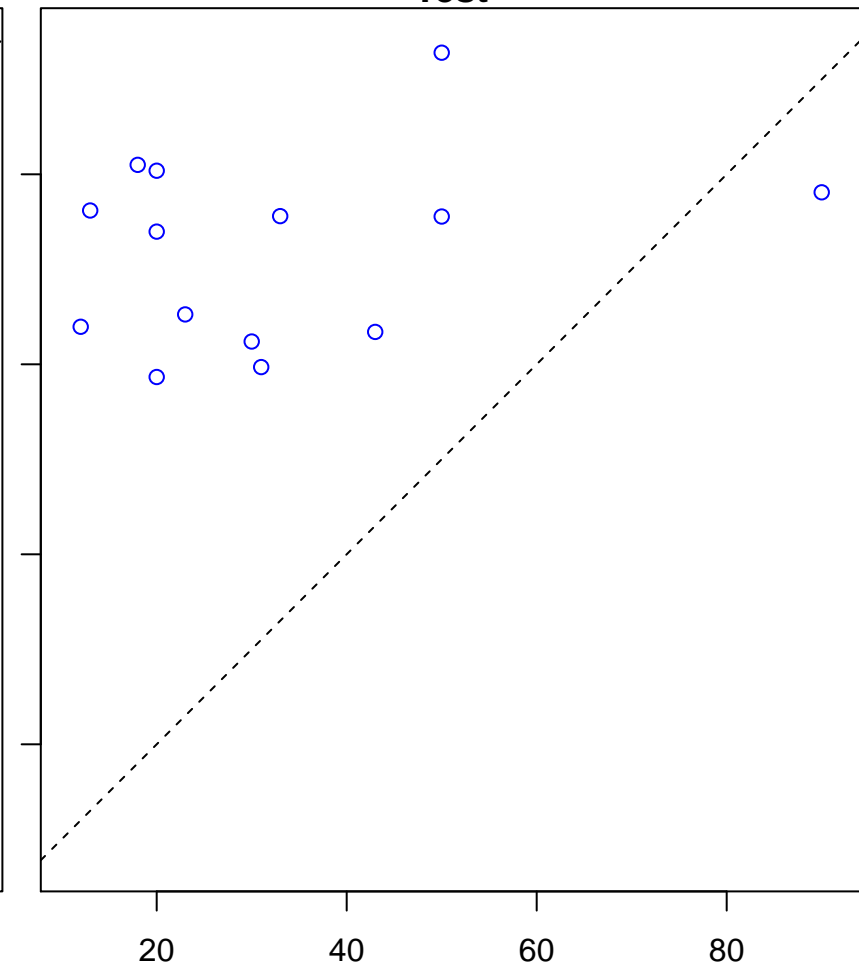


establishment of spindle orientation (Score: 10.721144)

Control

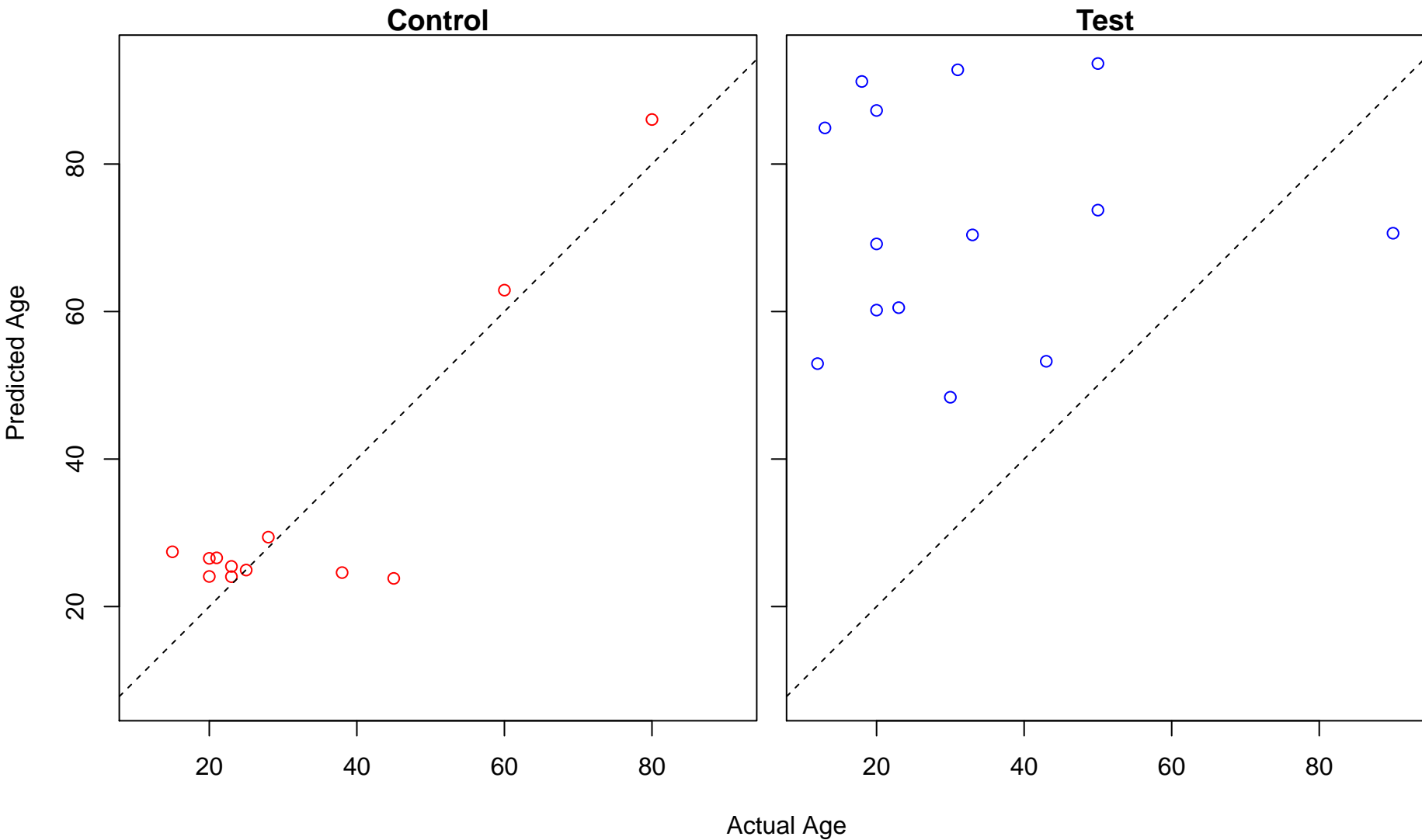


Test

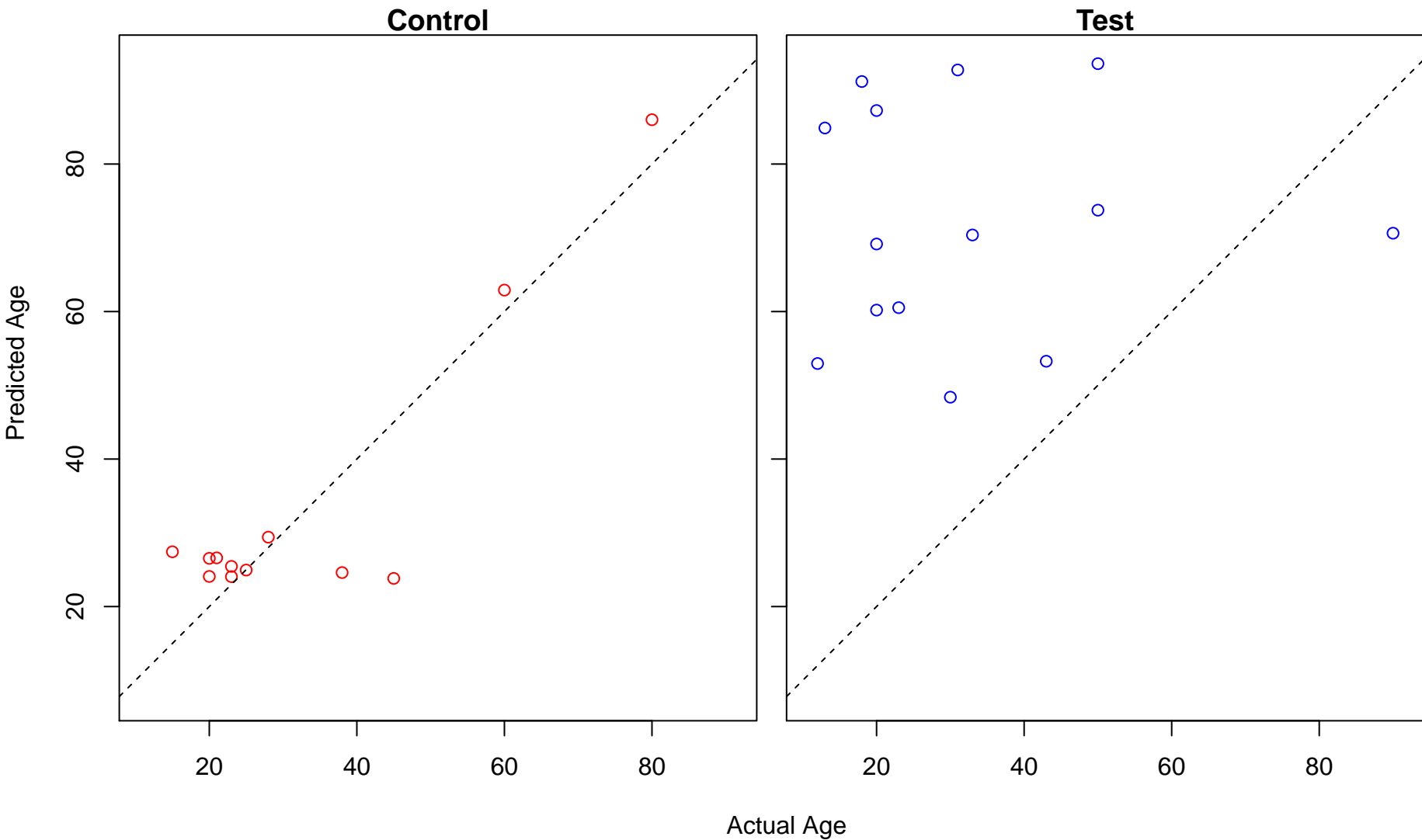


Actual Age

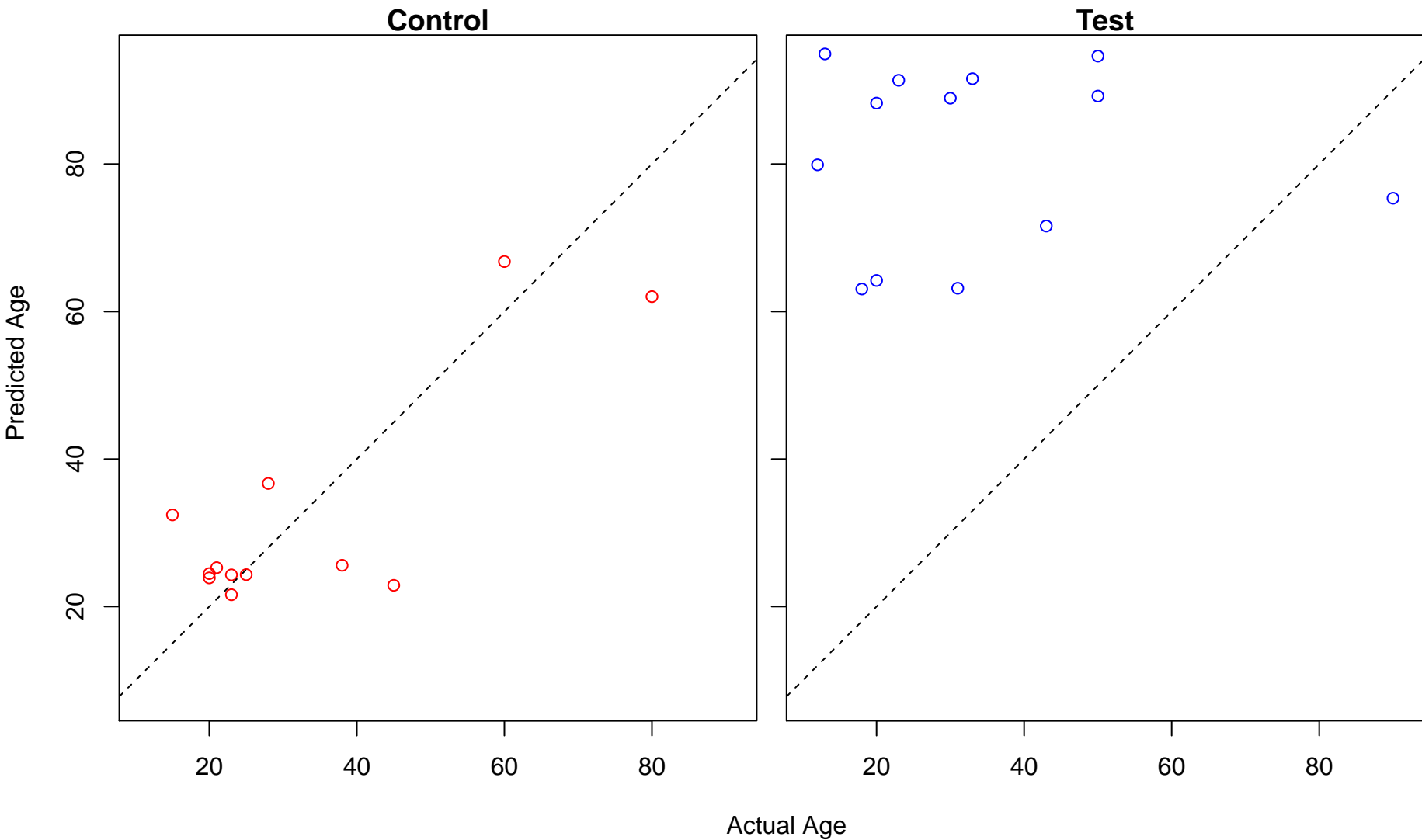
nucleosome assembly (Score: 10.714341)



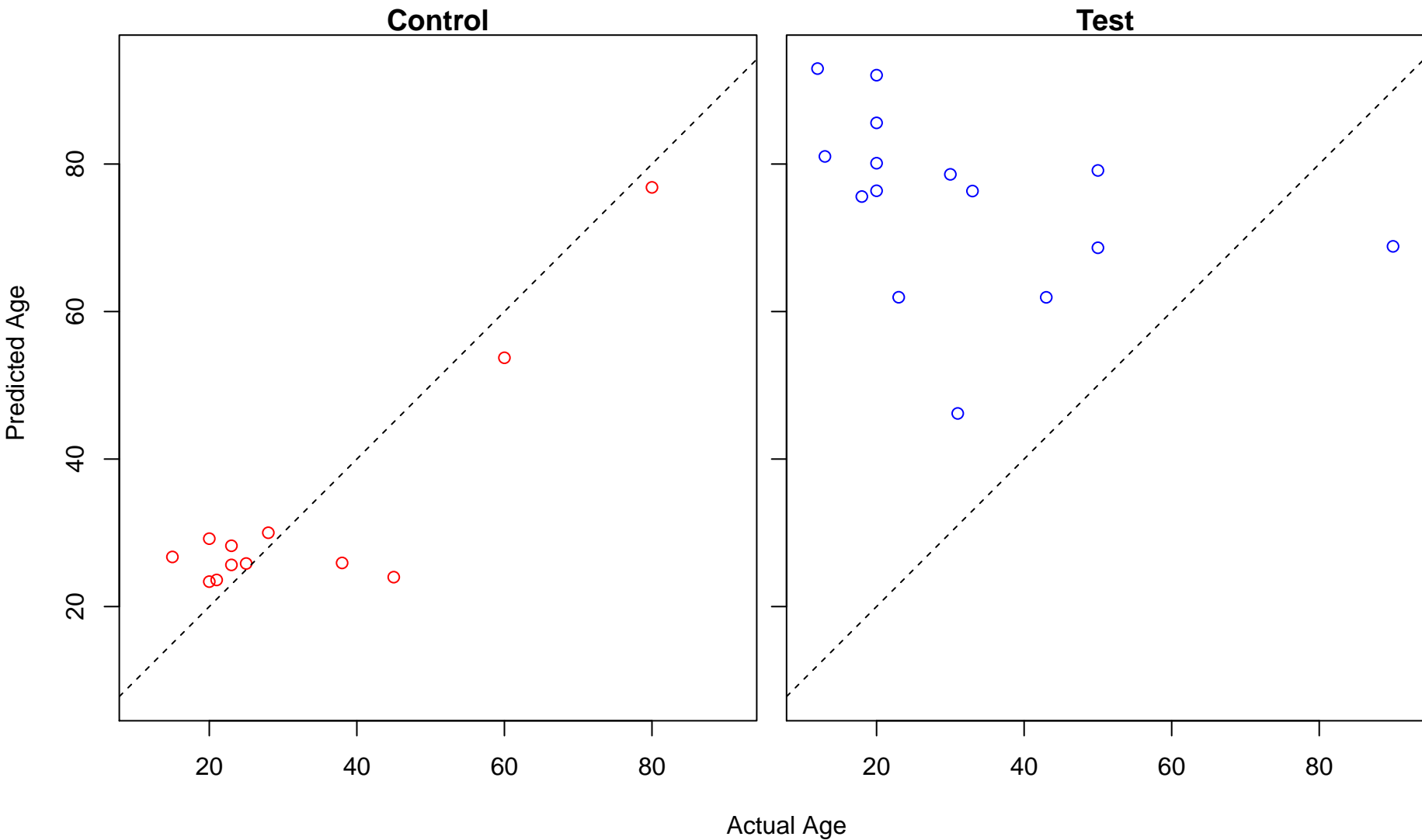
chromatin assembly (Score: 10.712499)



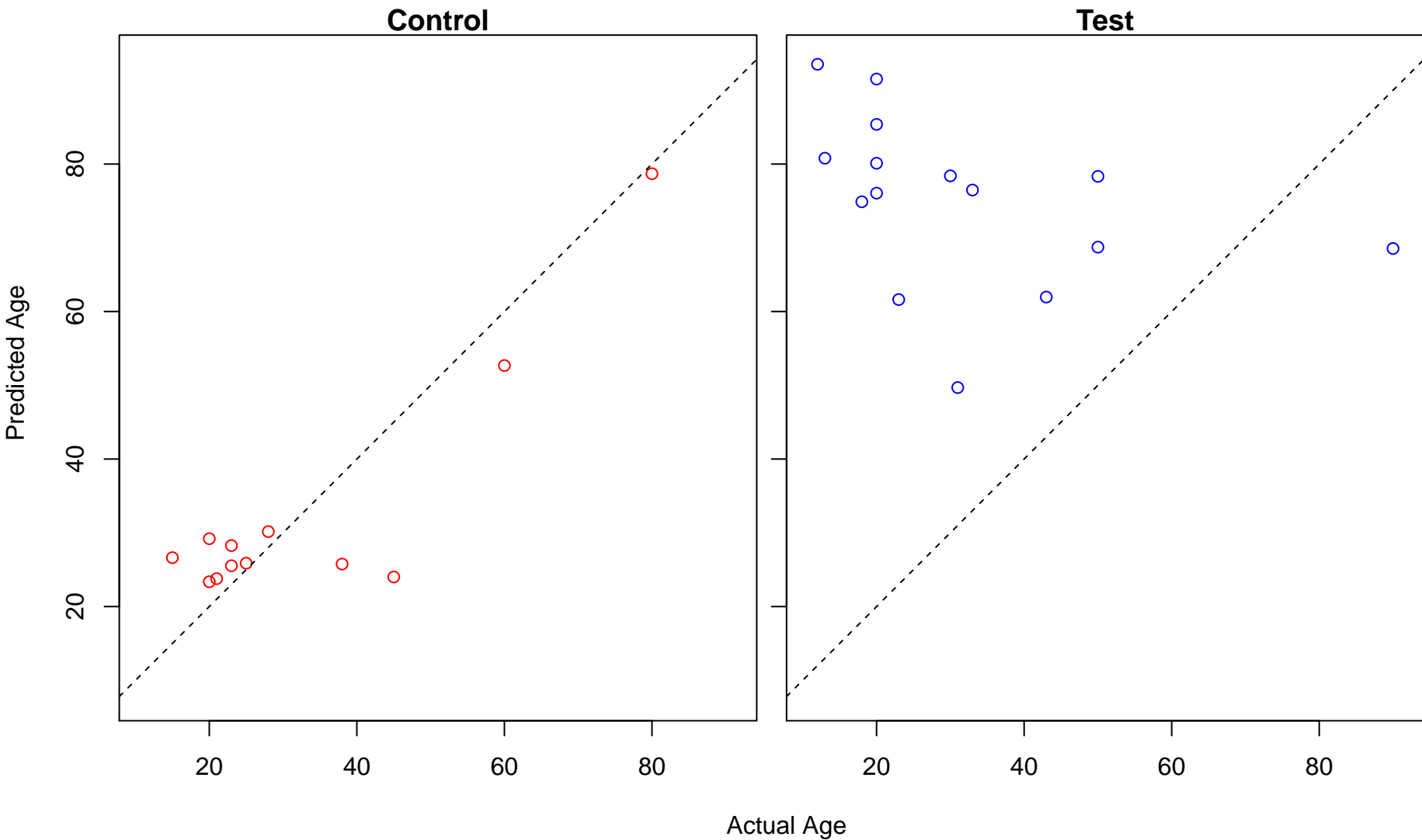
regulation of immunoglobulin mediated immune response (Score: 10.708467)



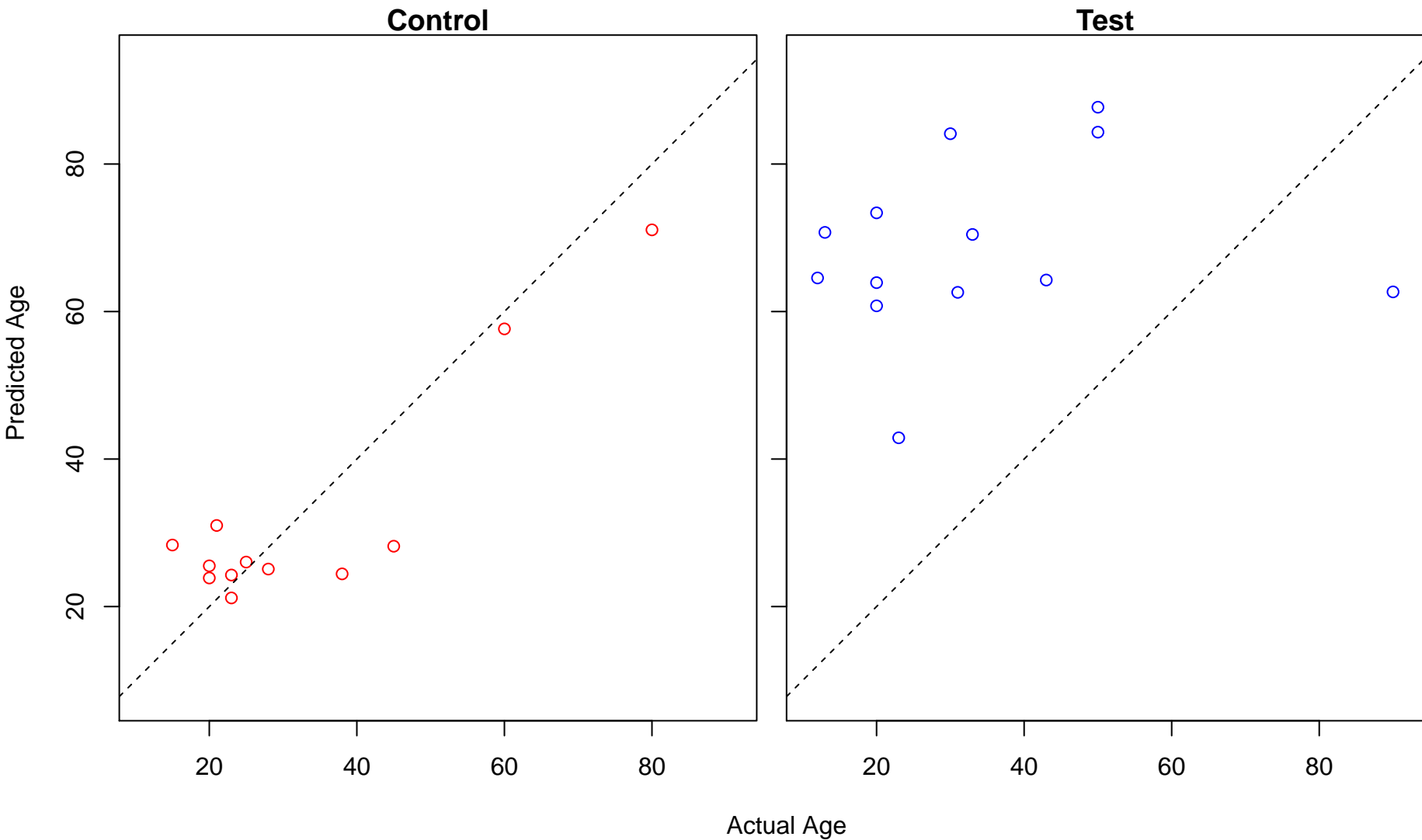
stem cell development (Score: 10.706075)



mesenchymal cell development (Score: 10.694829)

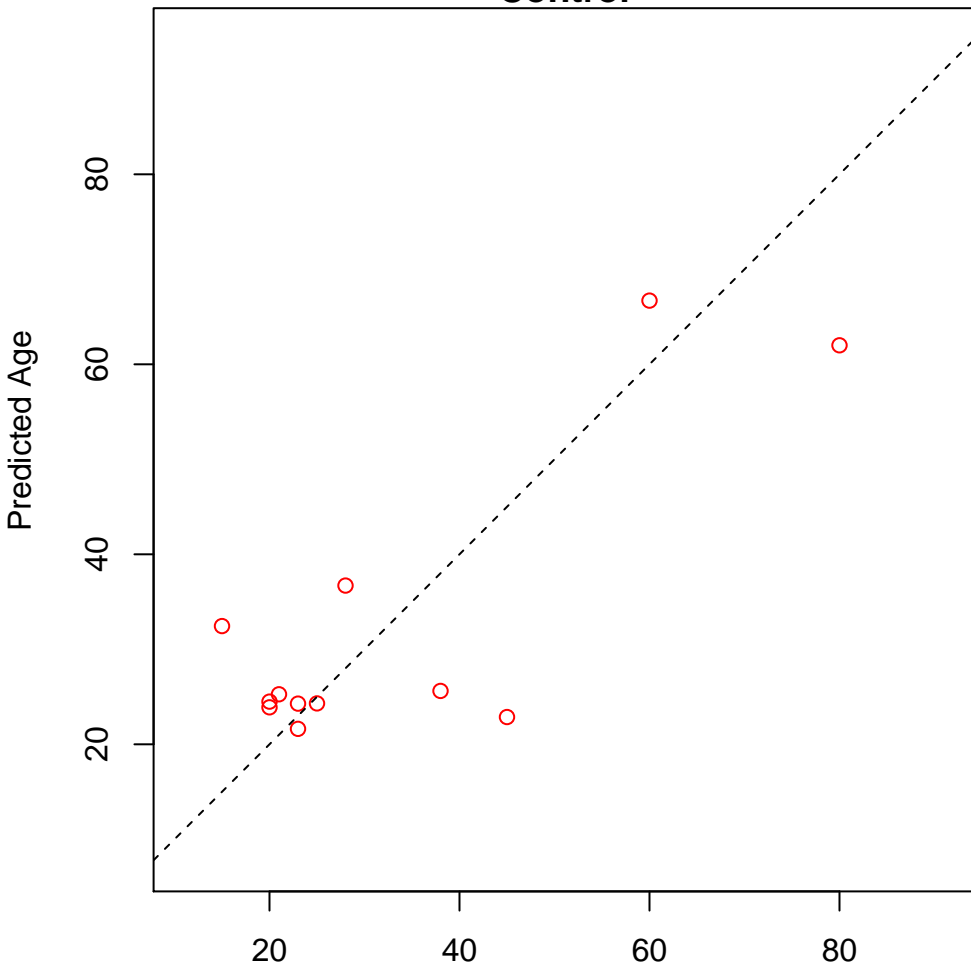


epithelial cell migration (Score: 10.692905)

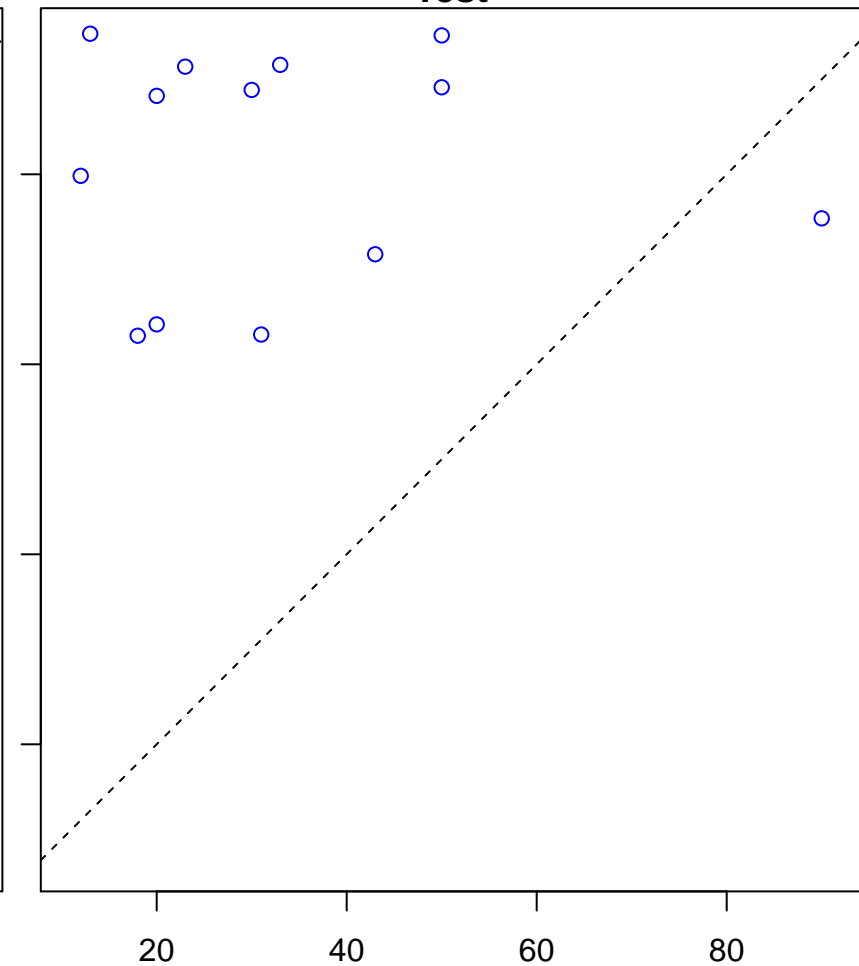


regulation of B cell mediated immunity (Score: 10.690237)

Control

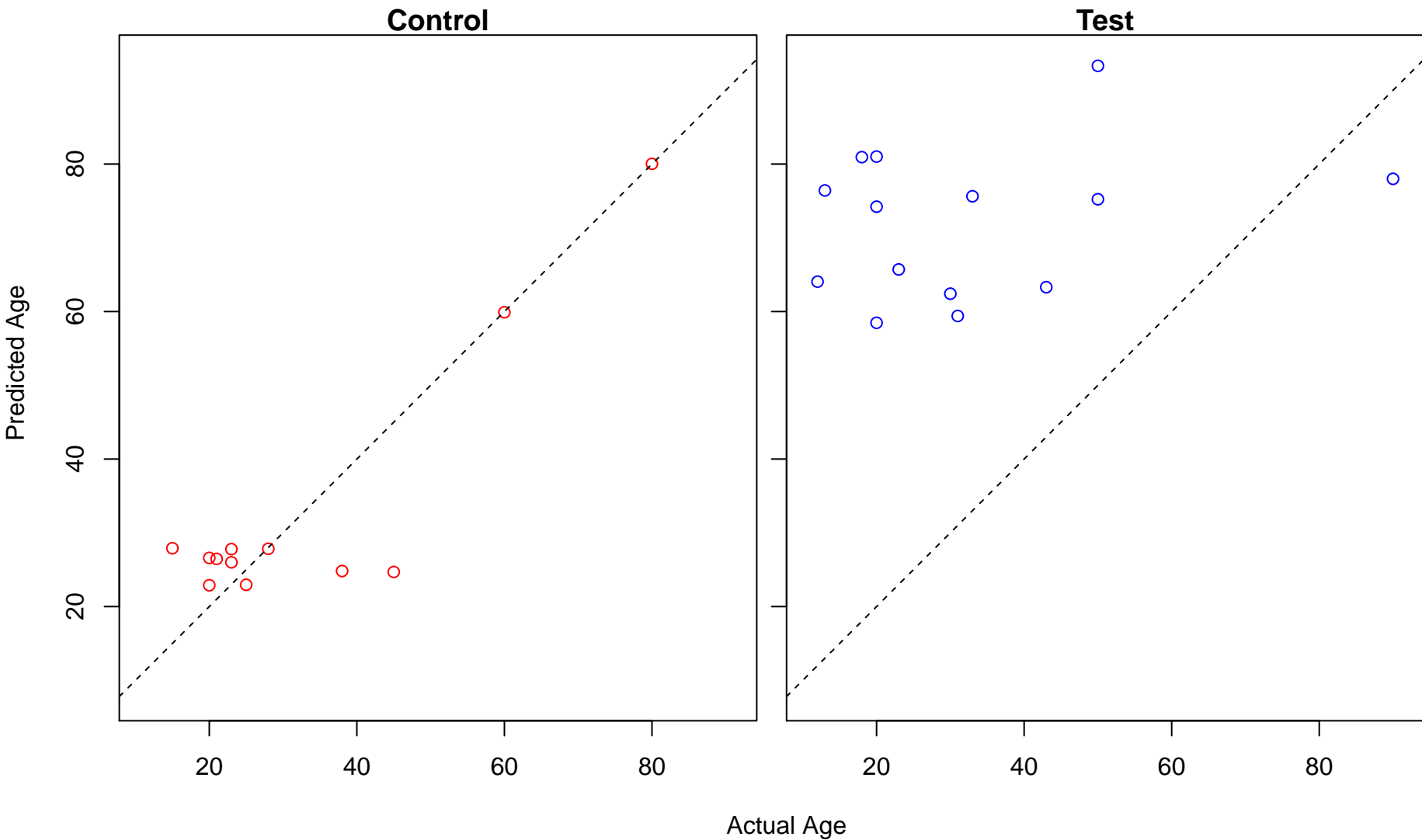


Test

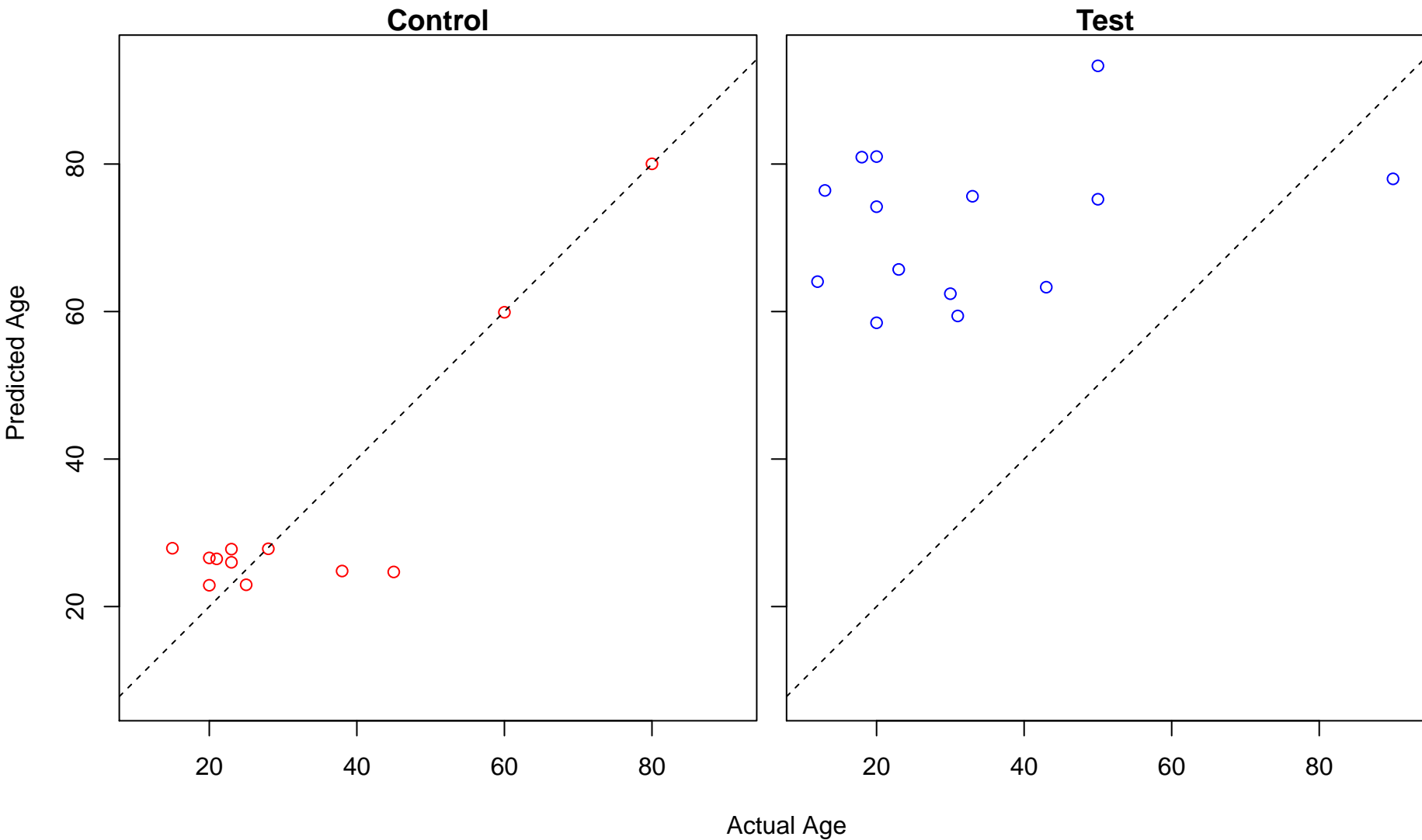


Actual Age

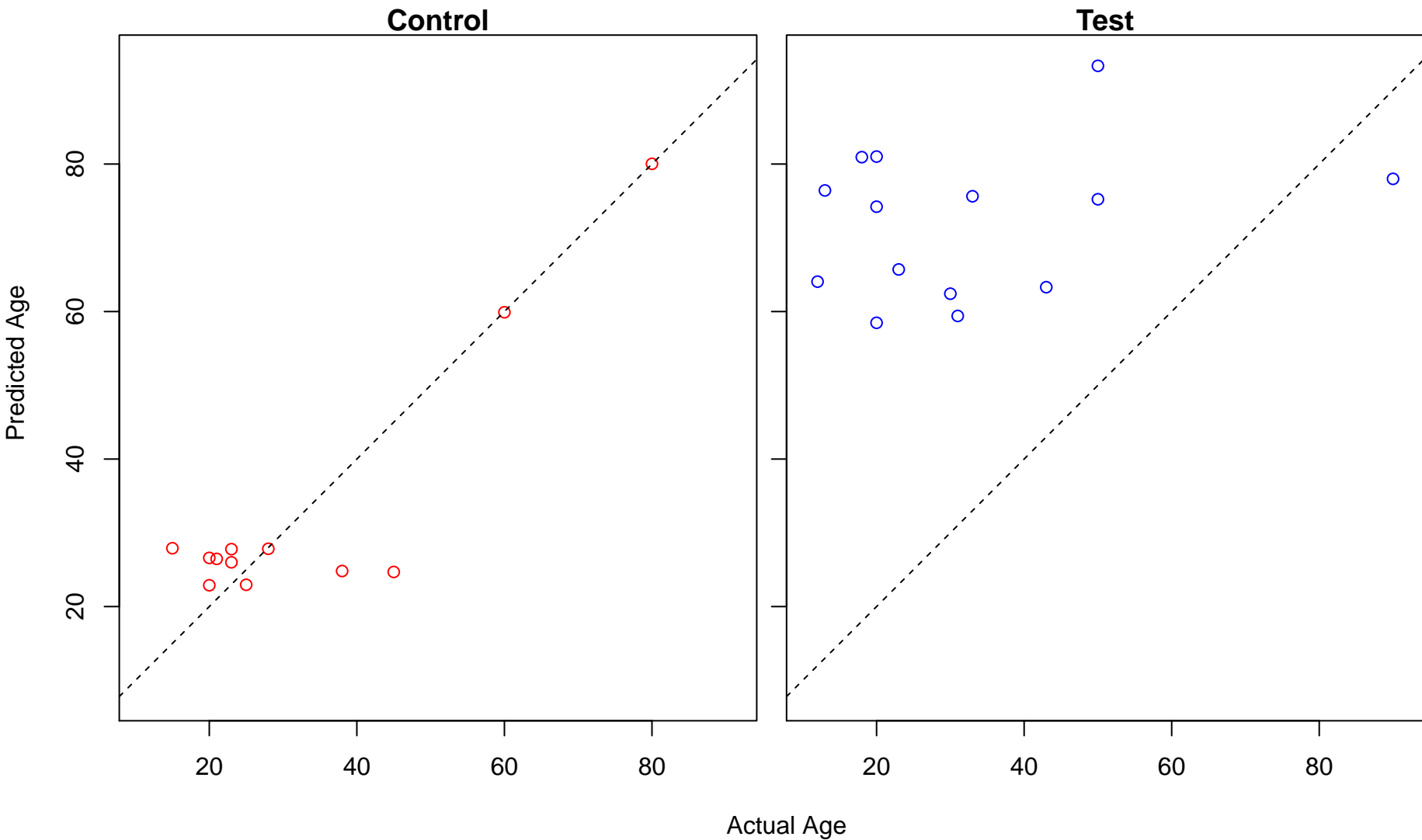
intracellular transport of viral protein in host cell (Score: 10.685911)



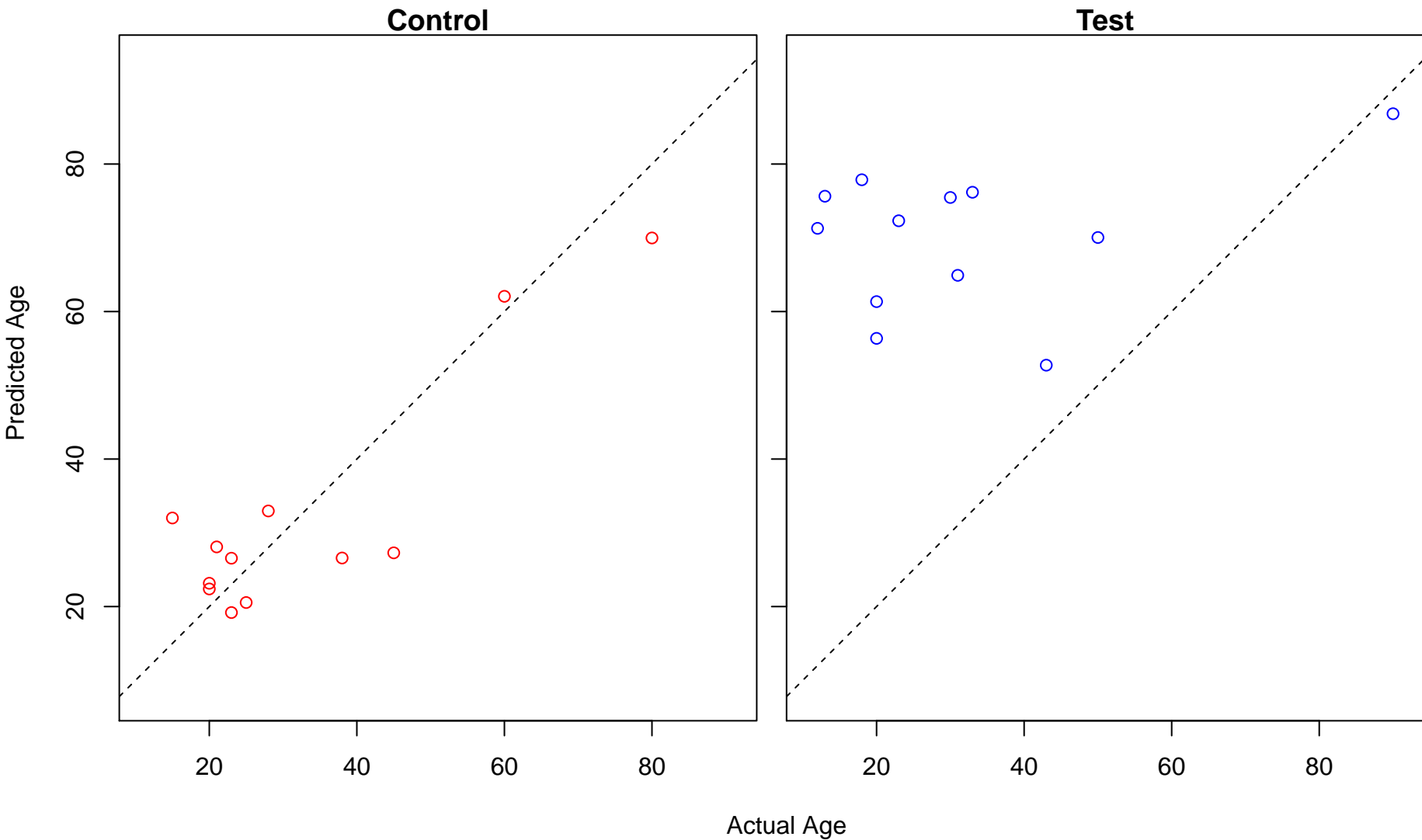
symbiont intracellular protein transport in host (Score: 10.685911)



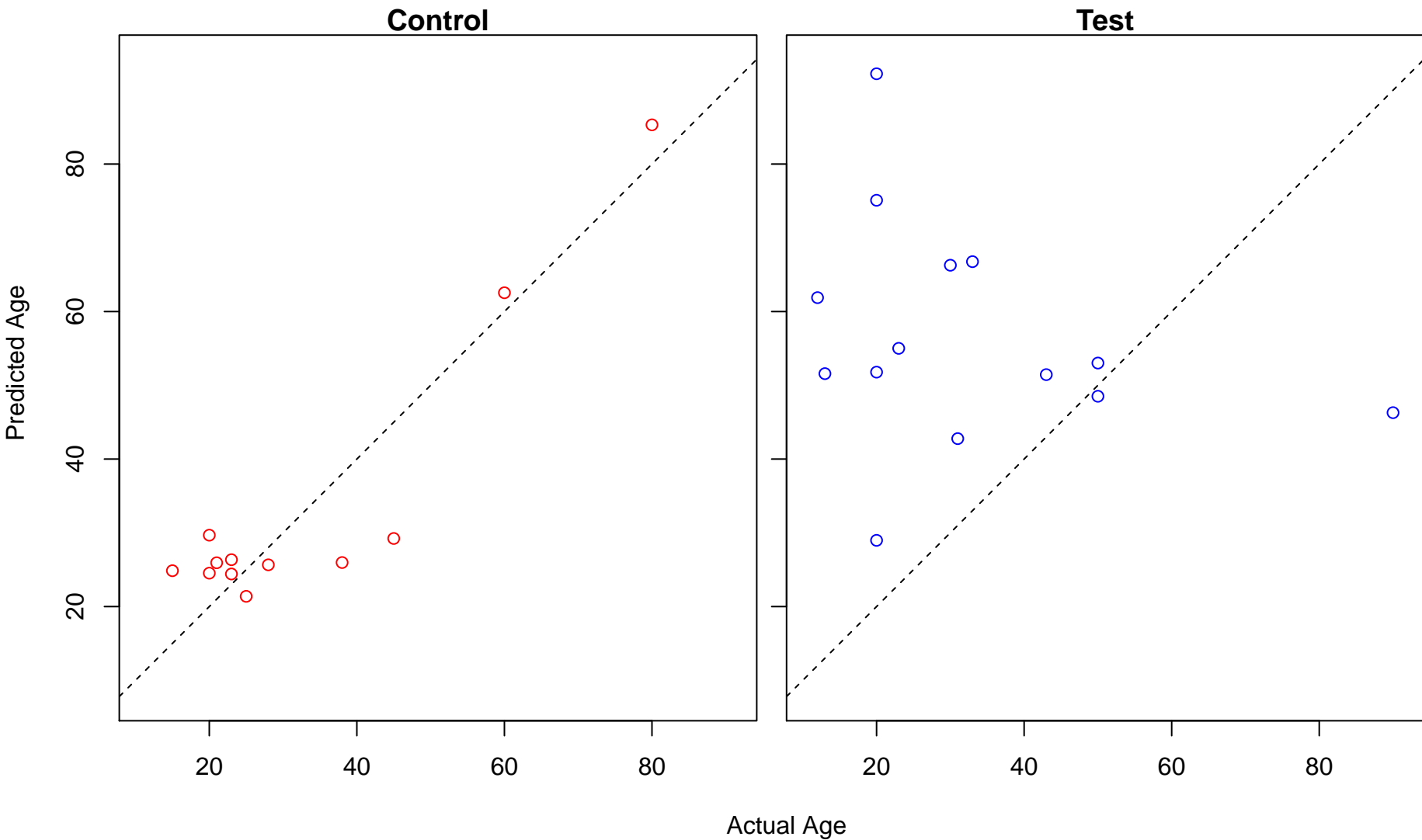
intracellular protein transport in other organism involved in symbiotic interaction (Score: 10.68591)



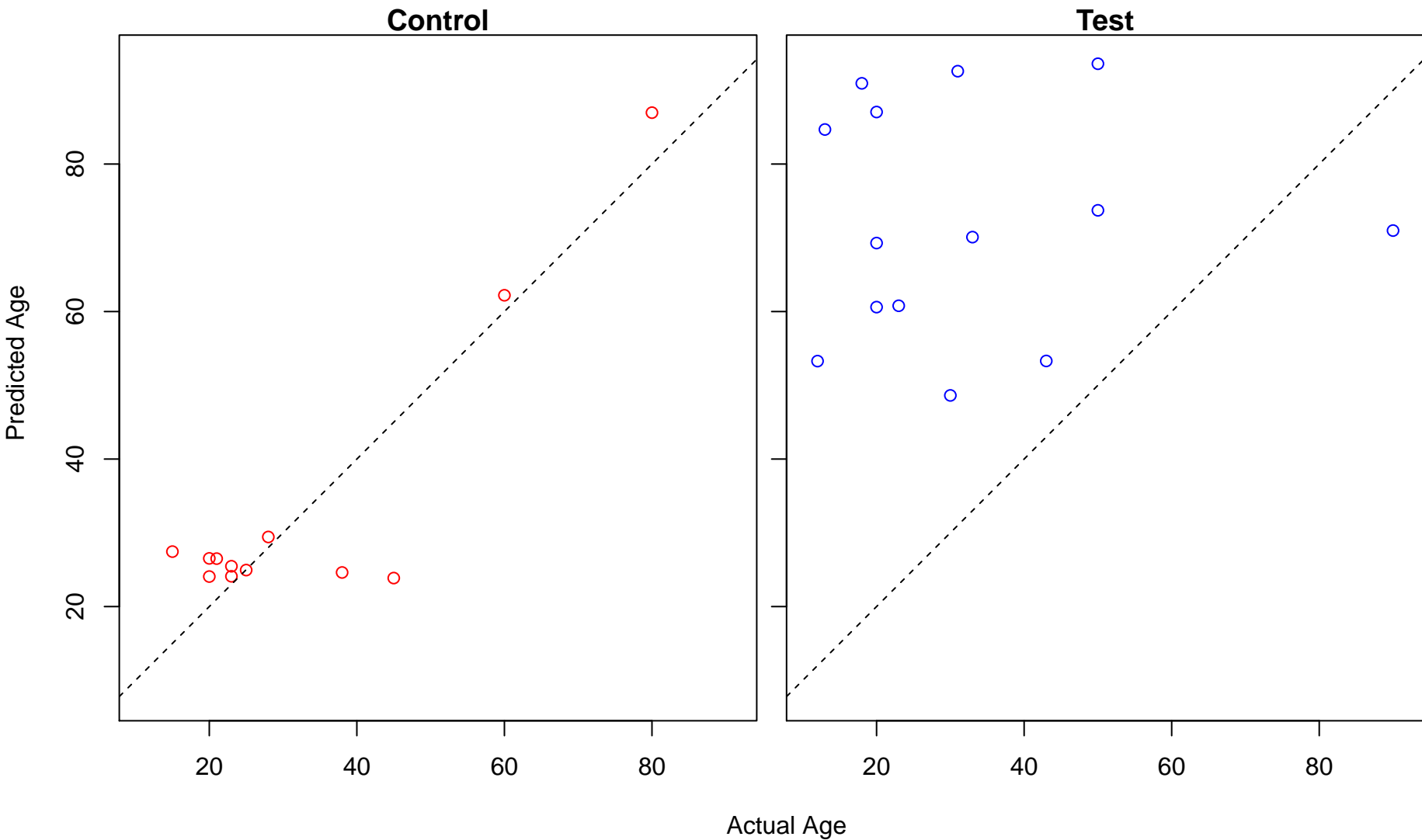
gland morphogenesis (Score: 10.677437)



establishment of protein localization to Golgi (Score: 10.663711)

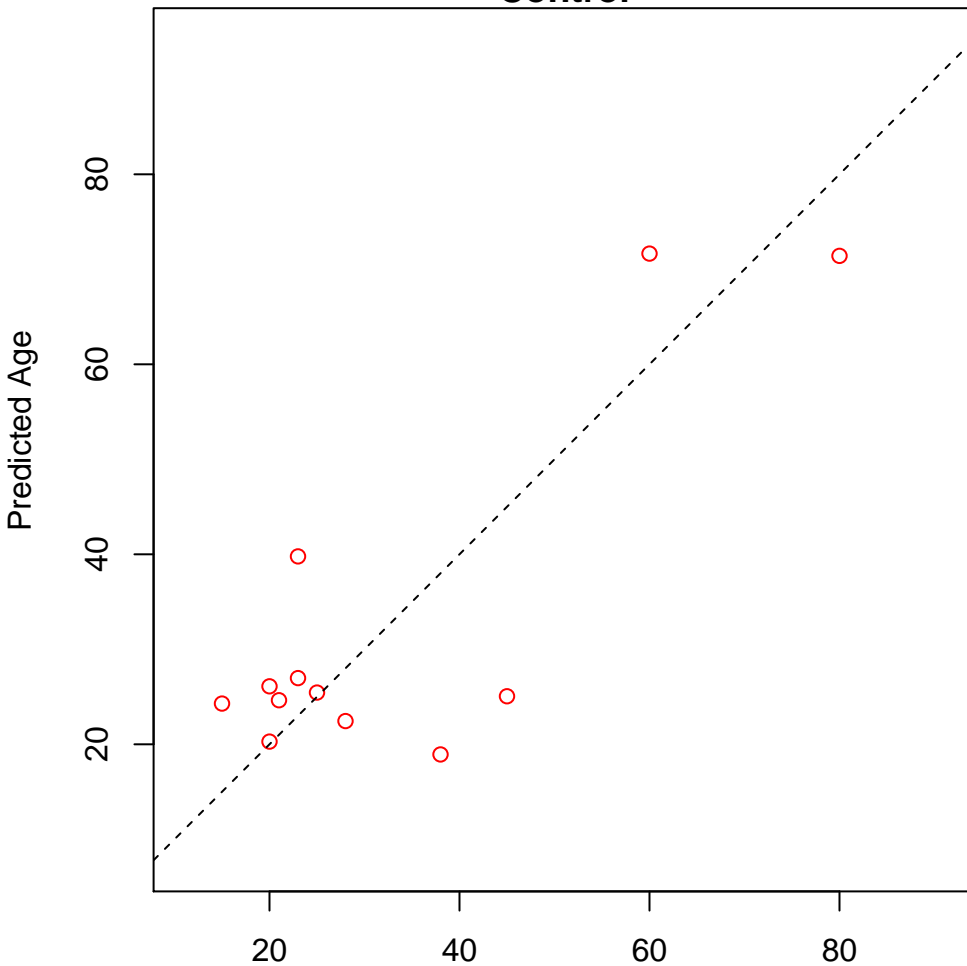


protein-DNA complex assembly (Score: 10.663527)

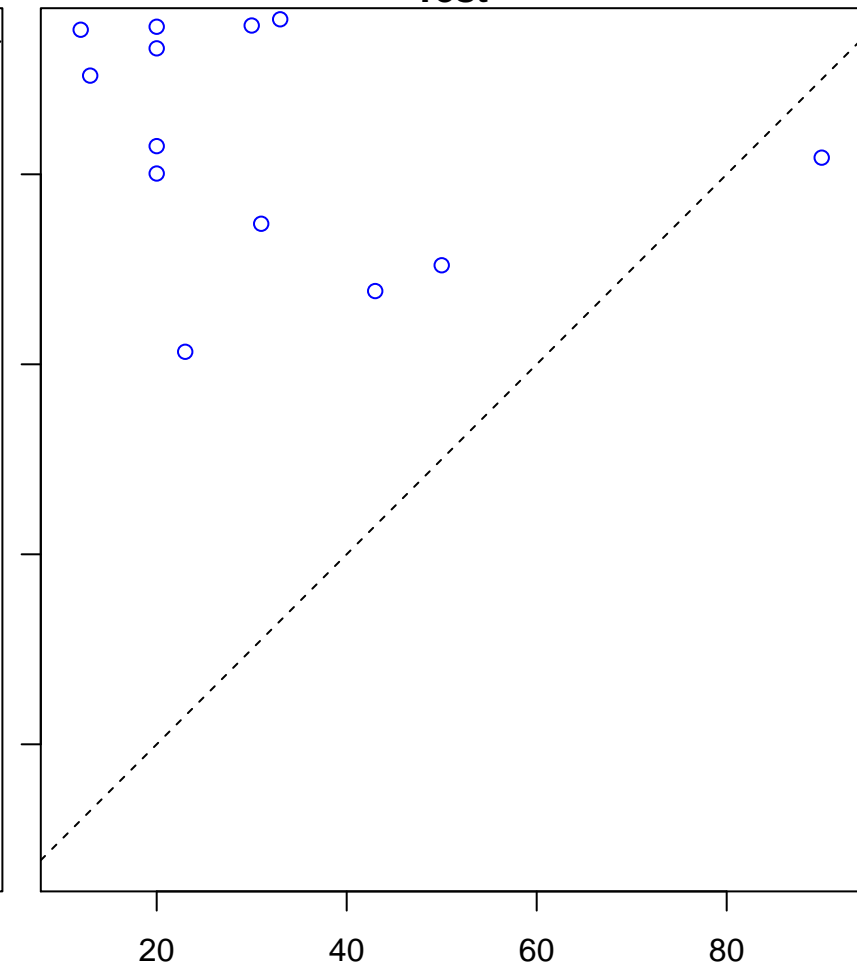


eyelid development in camera-type eye (Score: 10.660866)

Control

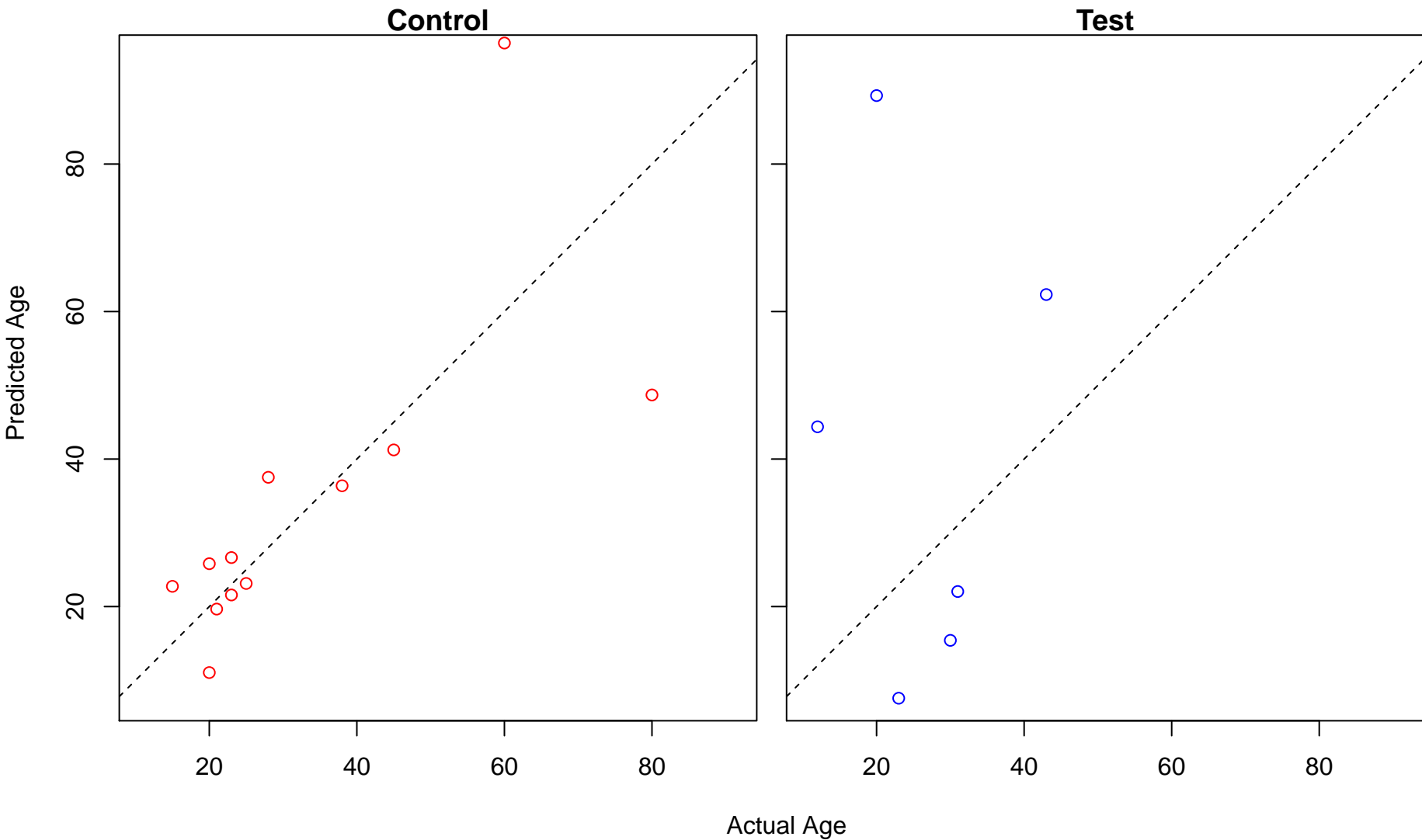


Test

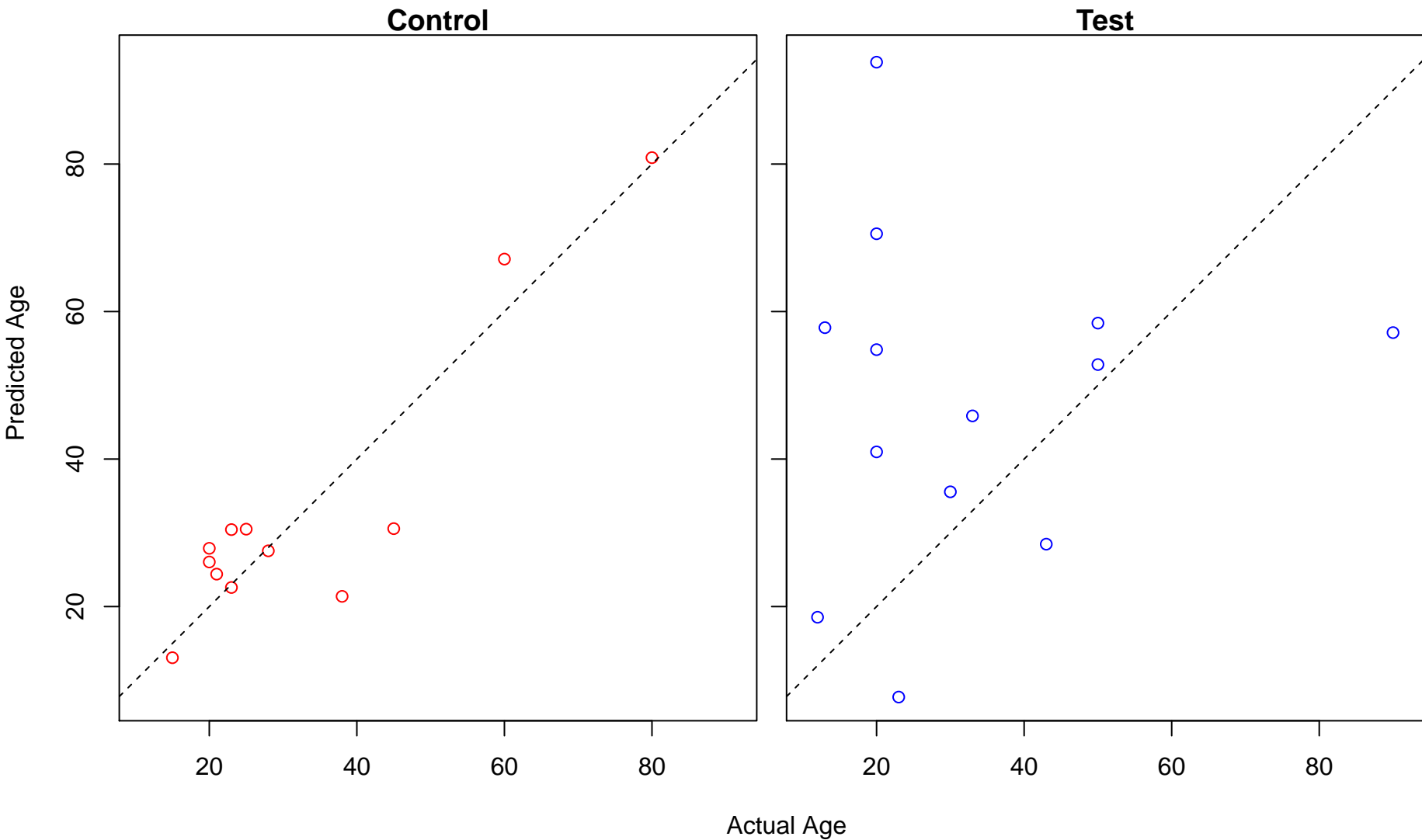


Actual Age

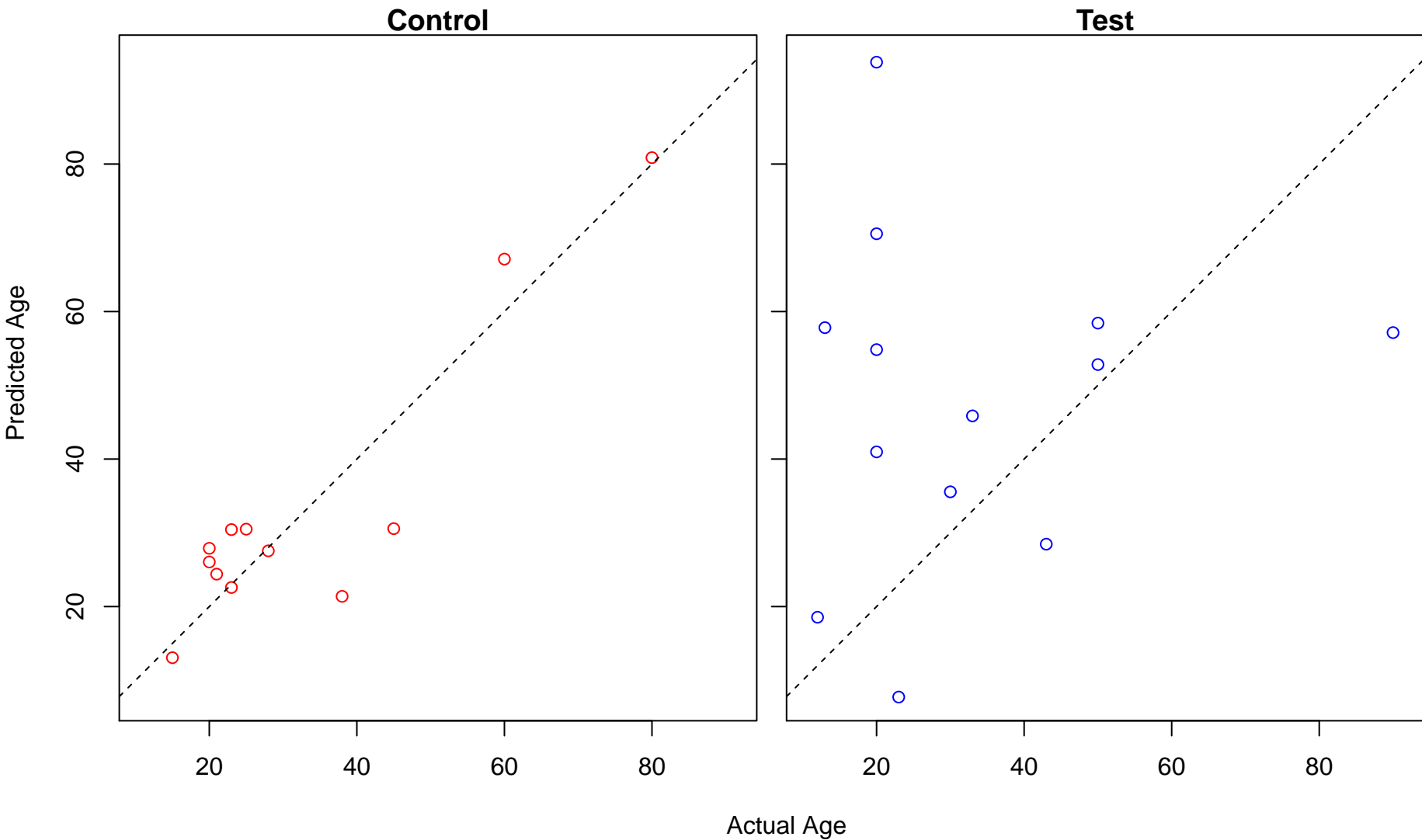
V(D)J recombination (Score: 10.655576)



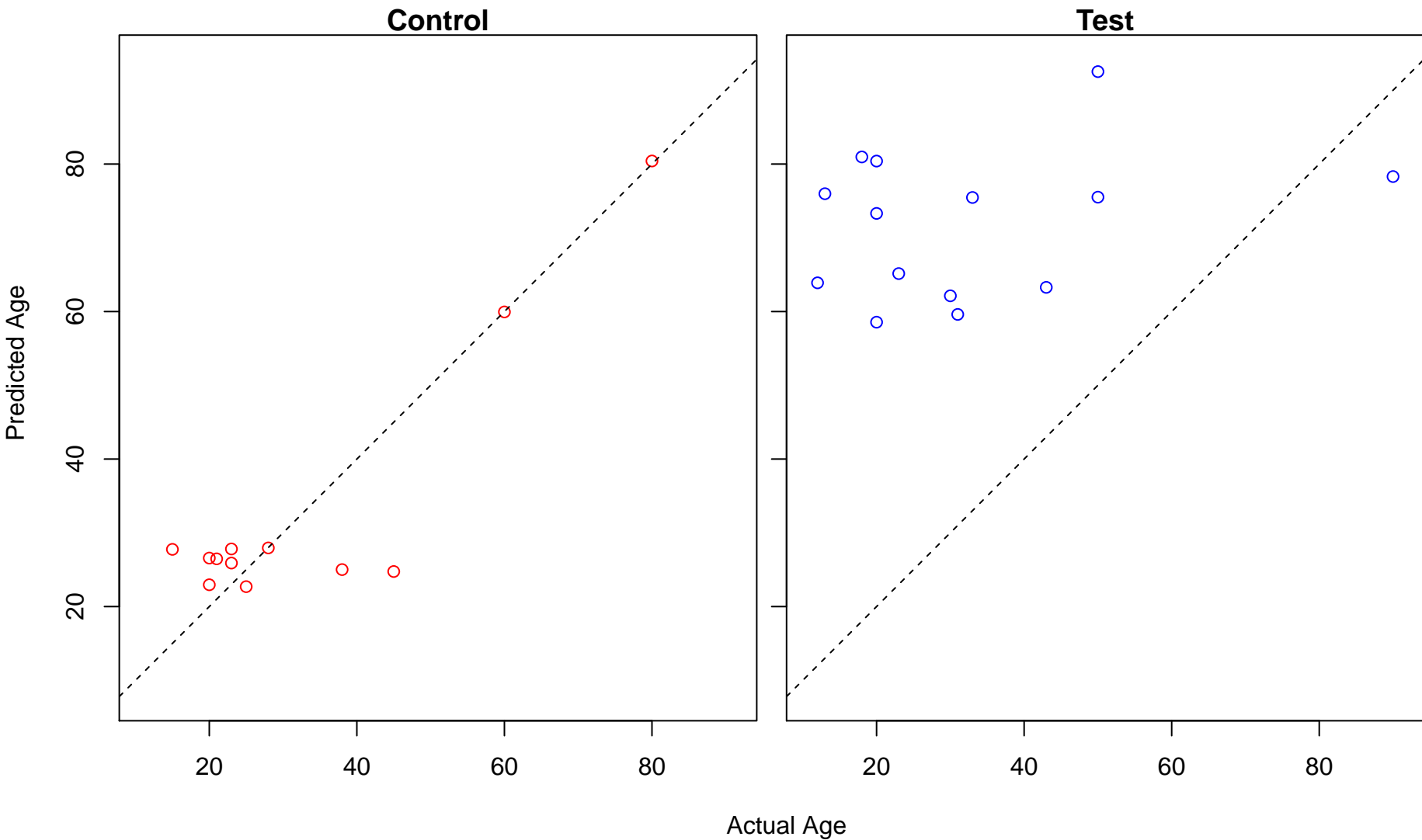
social behavior (Score: 10.649322)



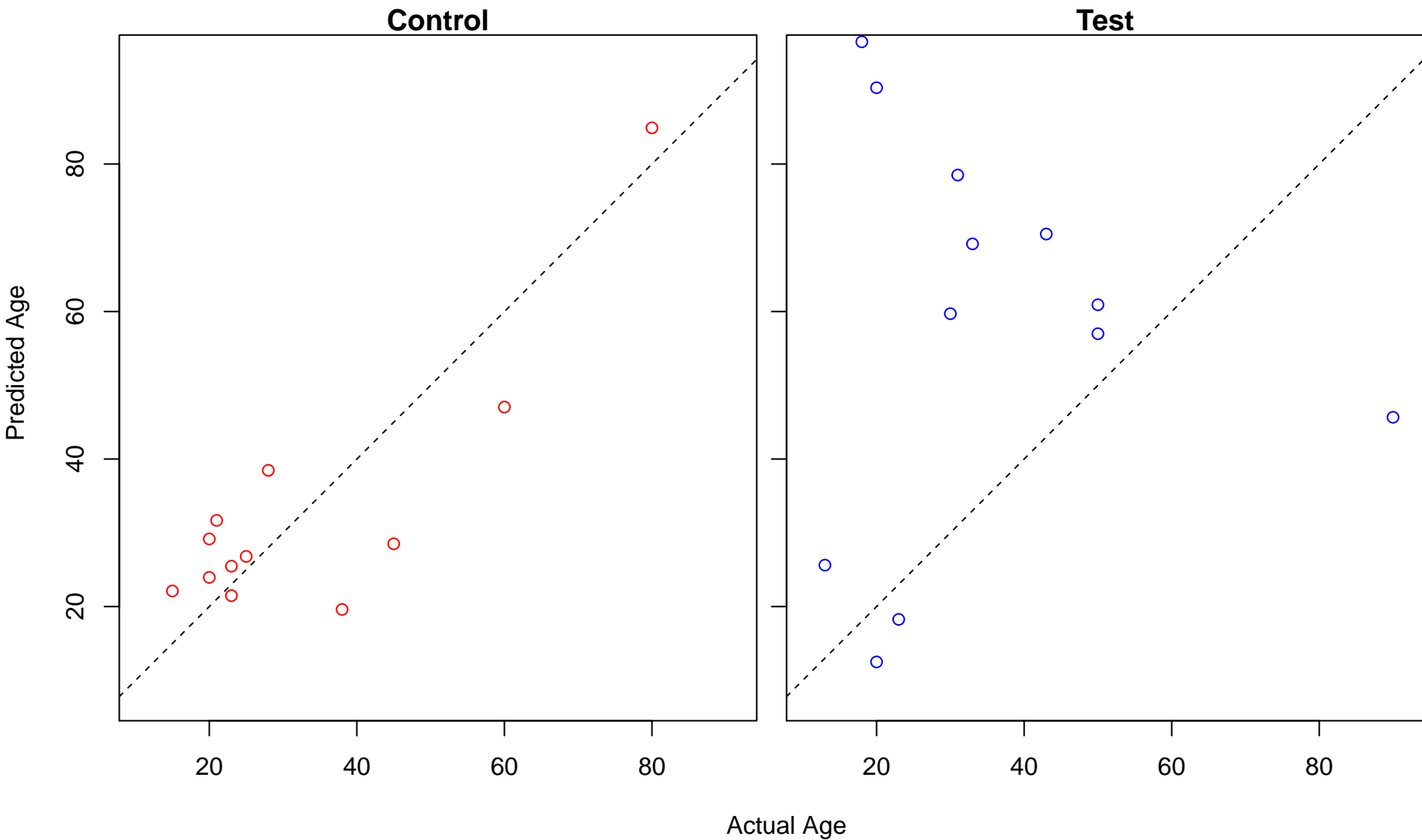
intraspecies interaction between organisms (Score: 10.649322)



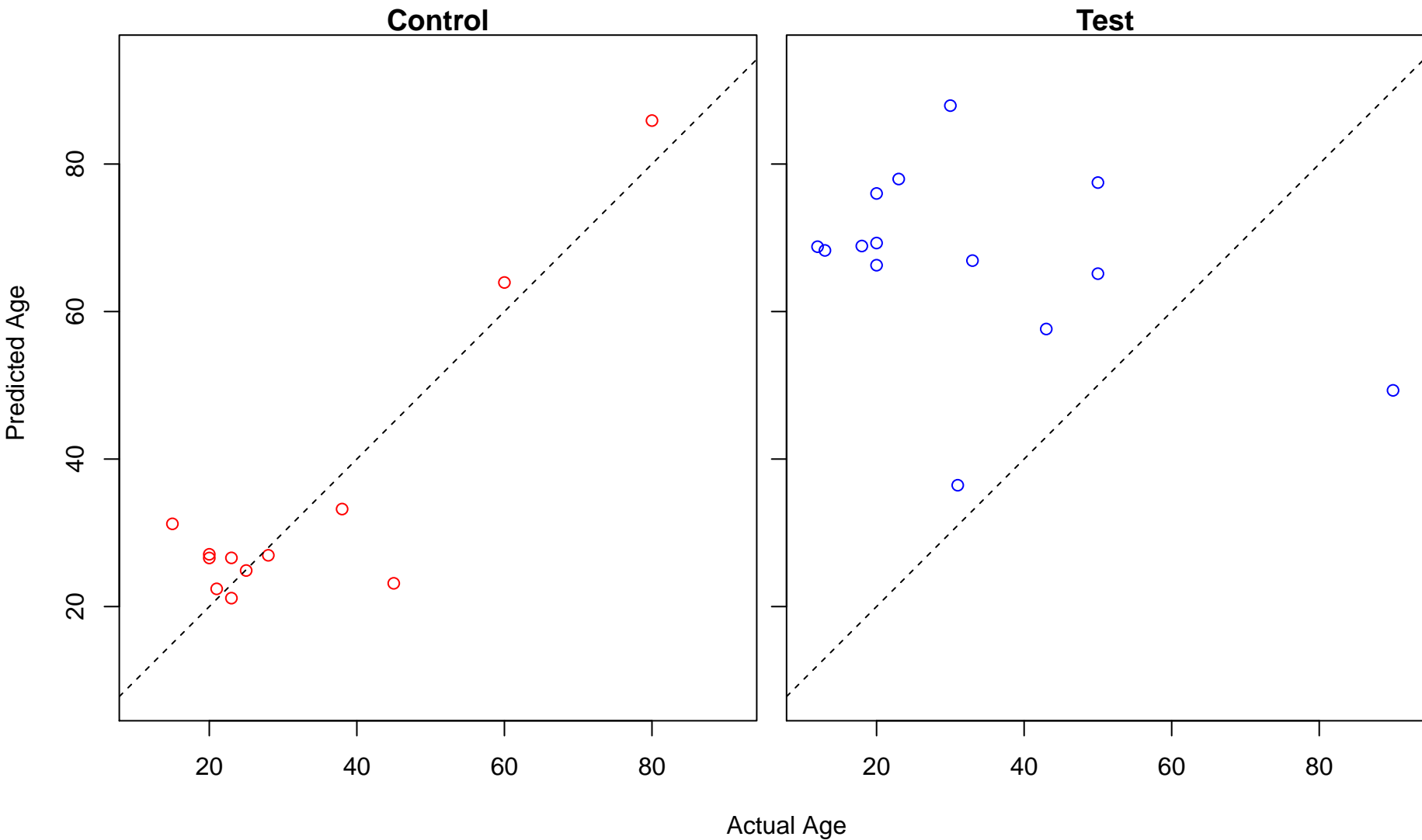
establishment of mitotic spindle orientation (Score: 10.647505)



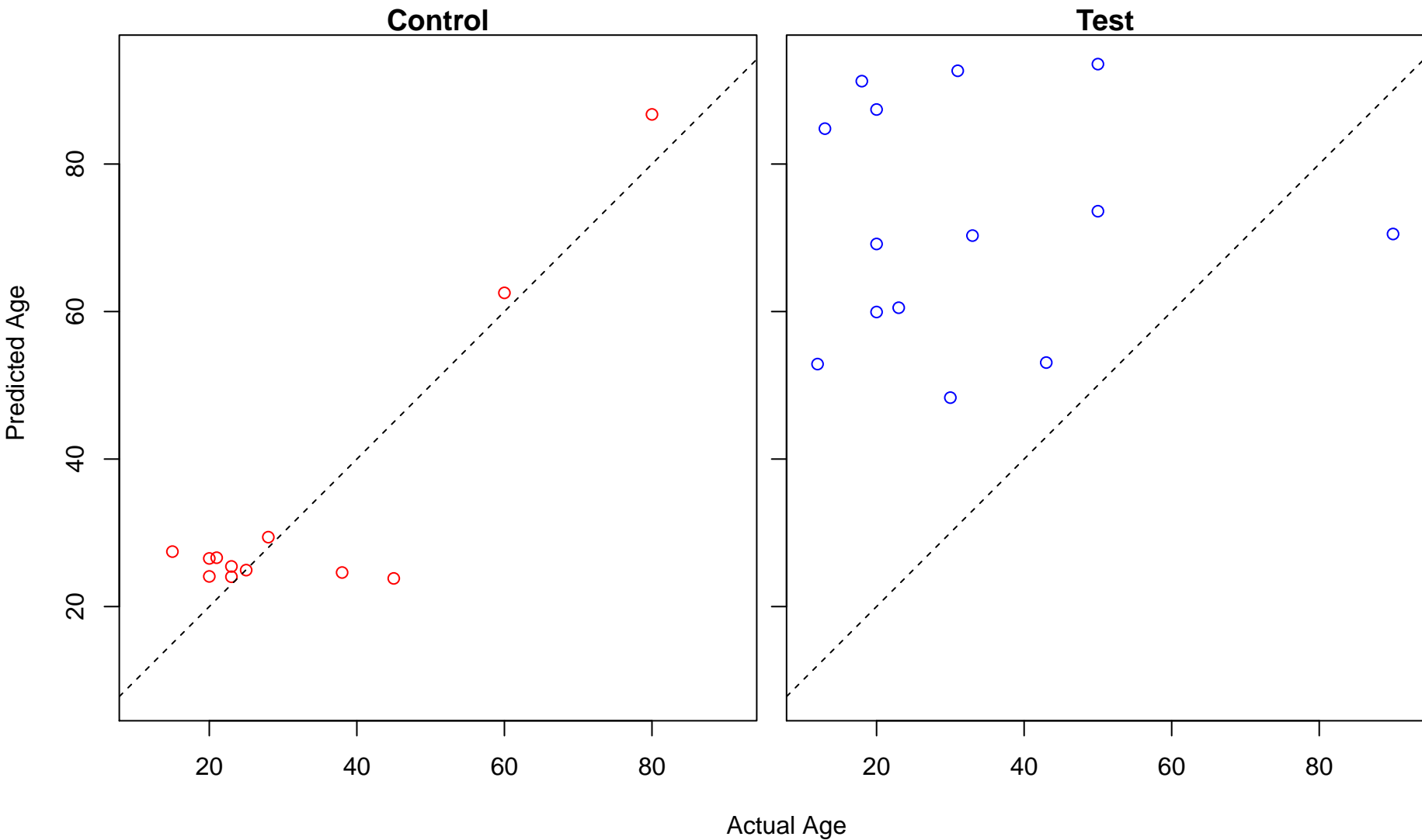
ATP synthesis coupled electron transport (Score: 10.638788)



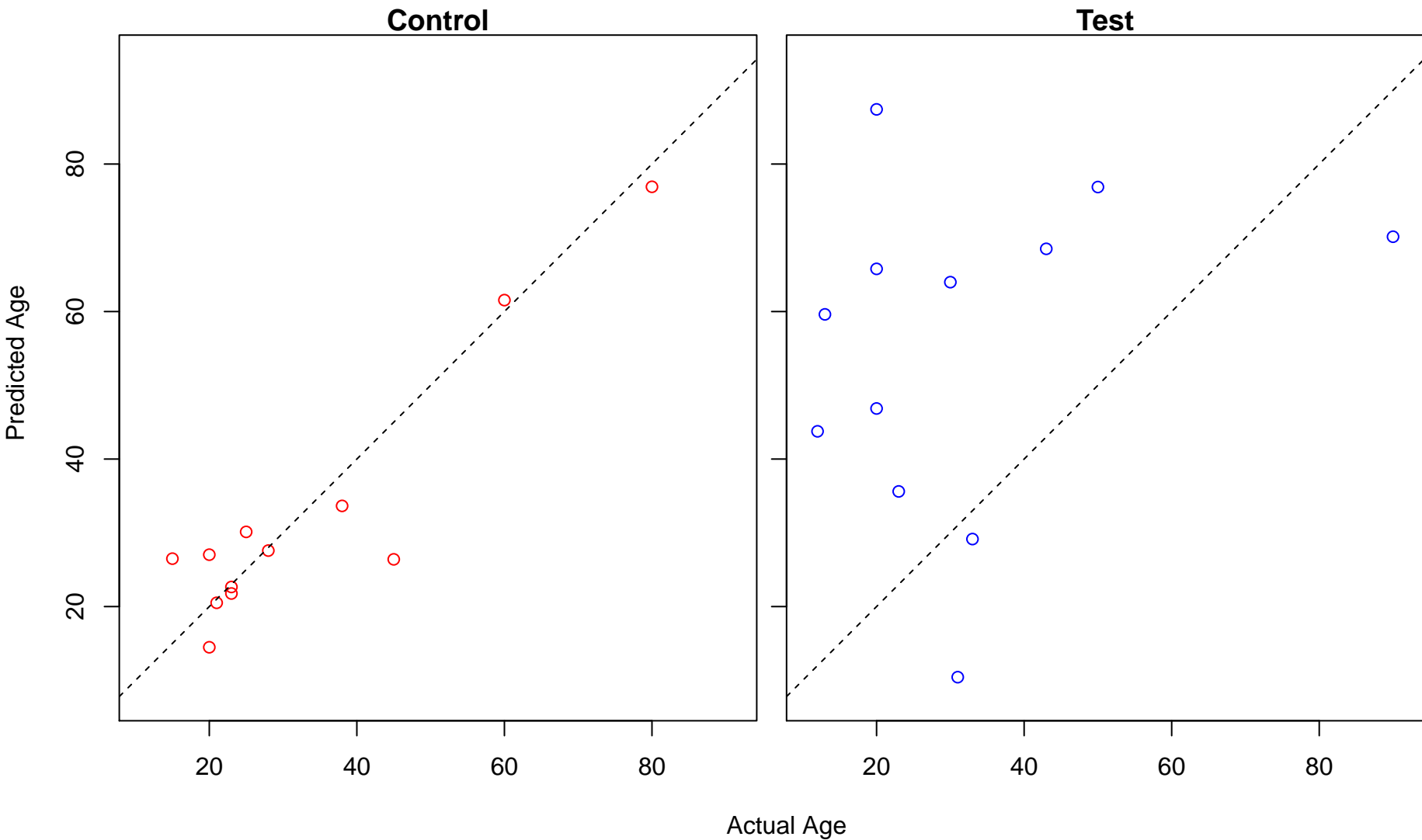
L-alanine transport (Score: 10.637483)



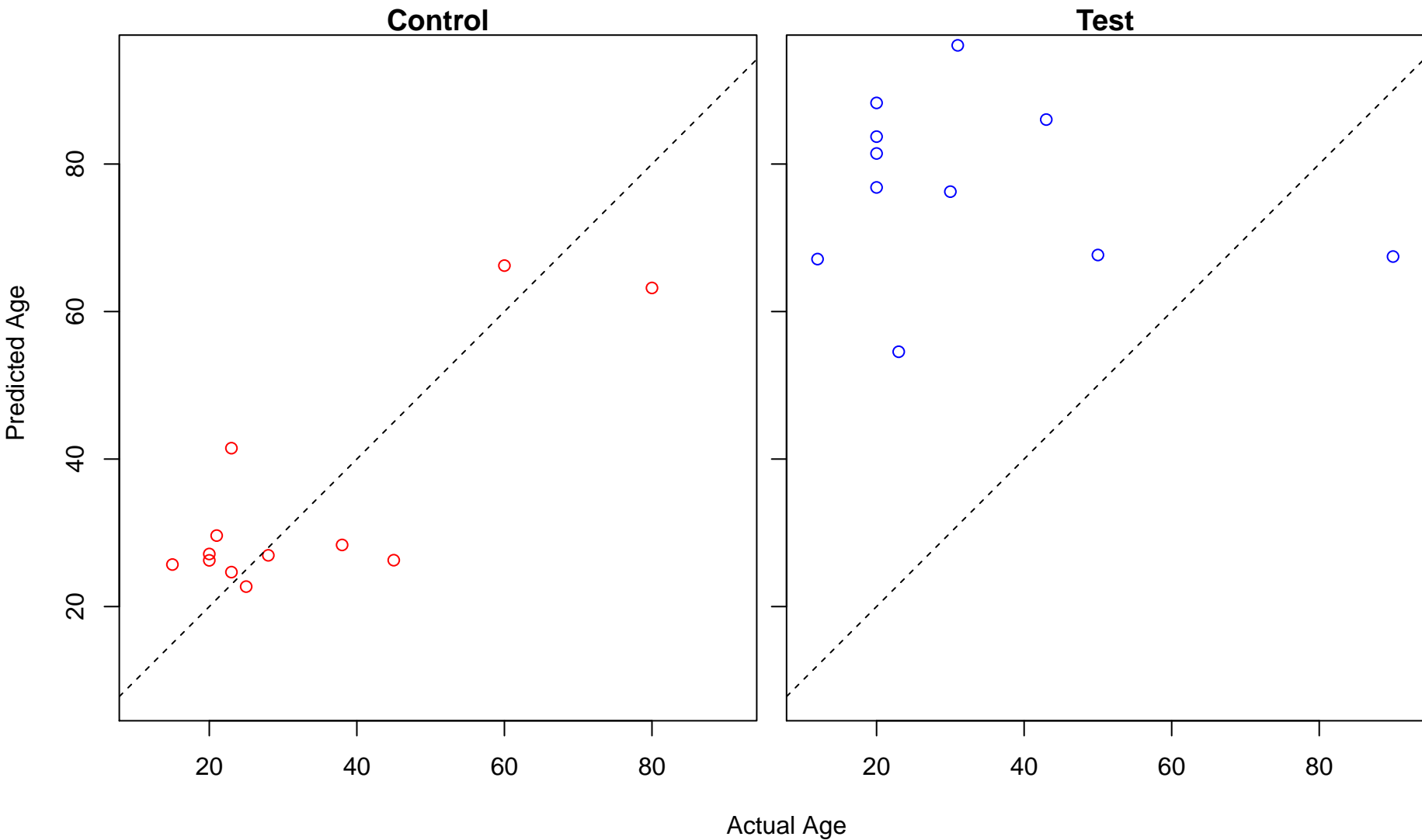
DNA packaging (Score: 10.636932)



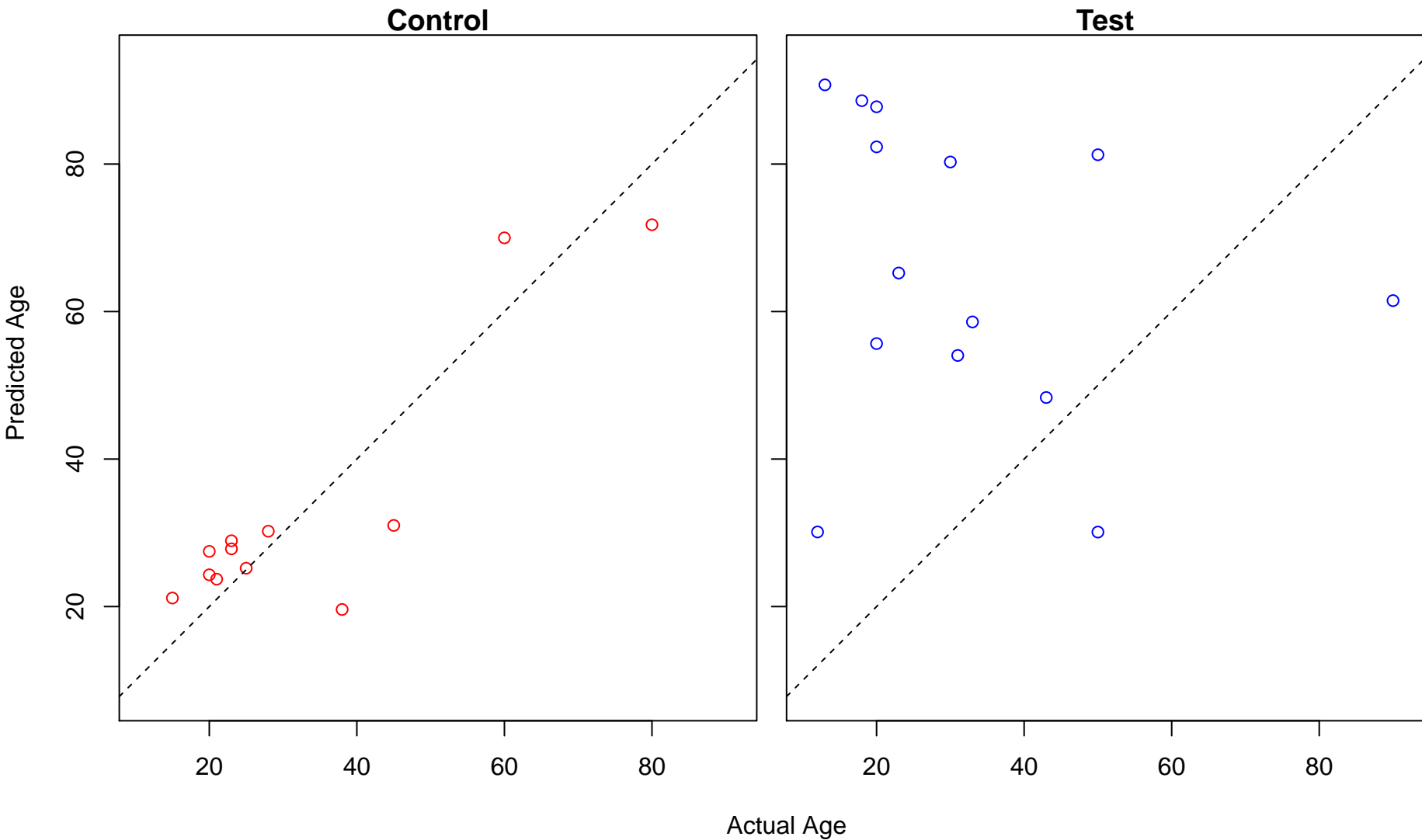
determination of adult lifespan (Score: 10.613934)



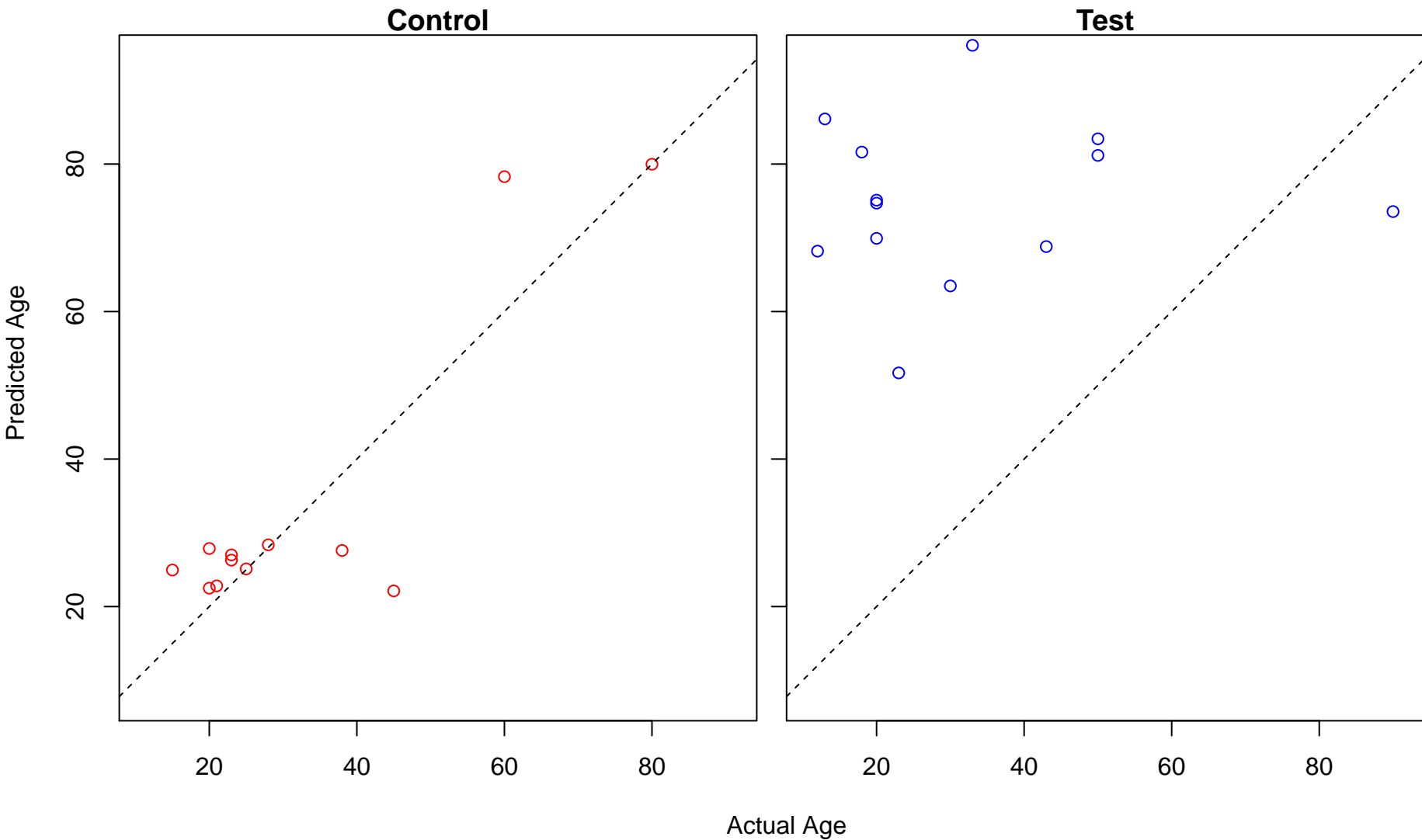
phospholipid efflux (Score: 10.612057)



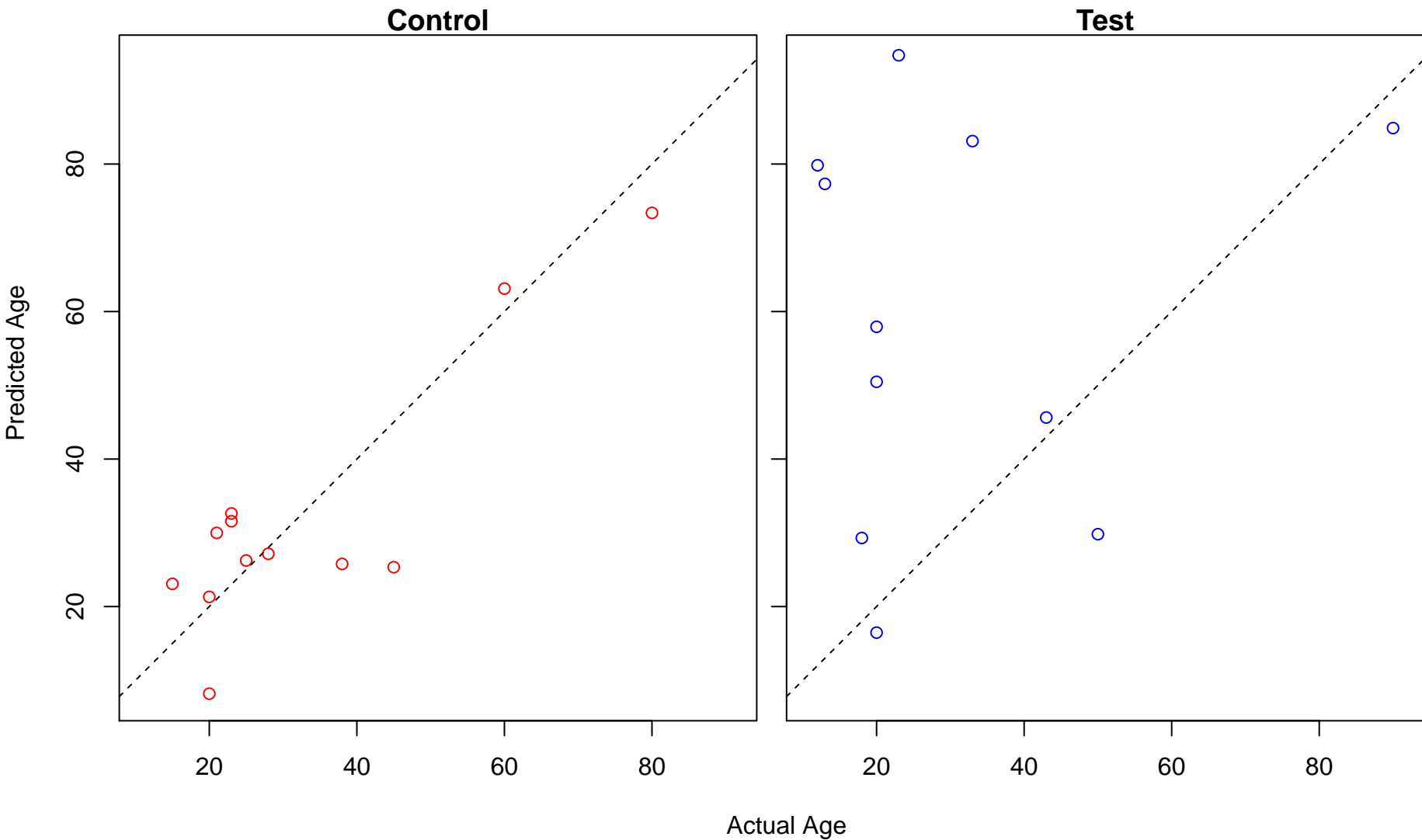
regulation of transcription by glucose (Score: 10.607773)



positive regulation of ERBB signaling pathway (Score: 10.601652)

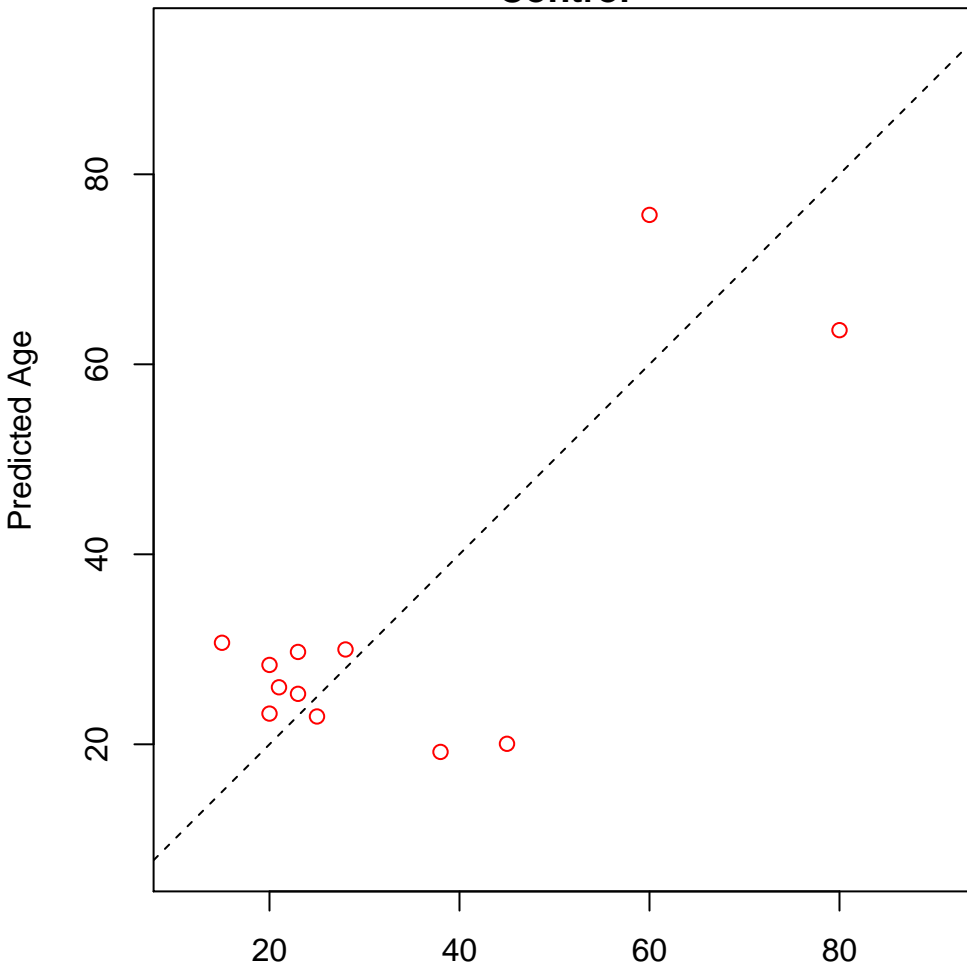


osteoclast differentiation (Score: 10.594968)

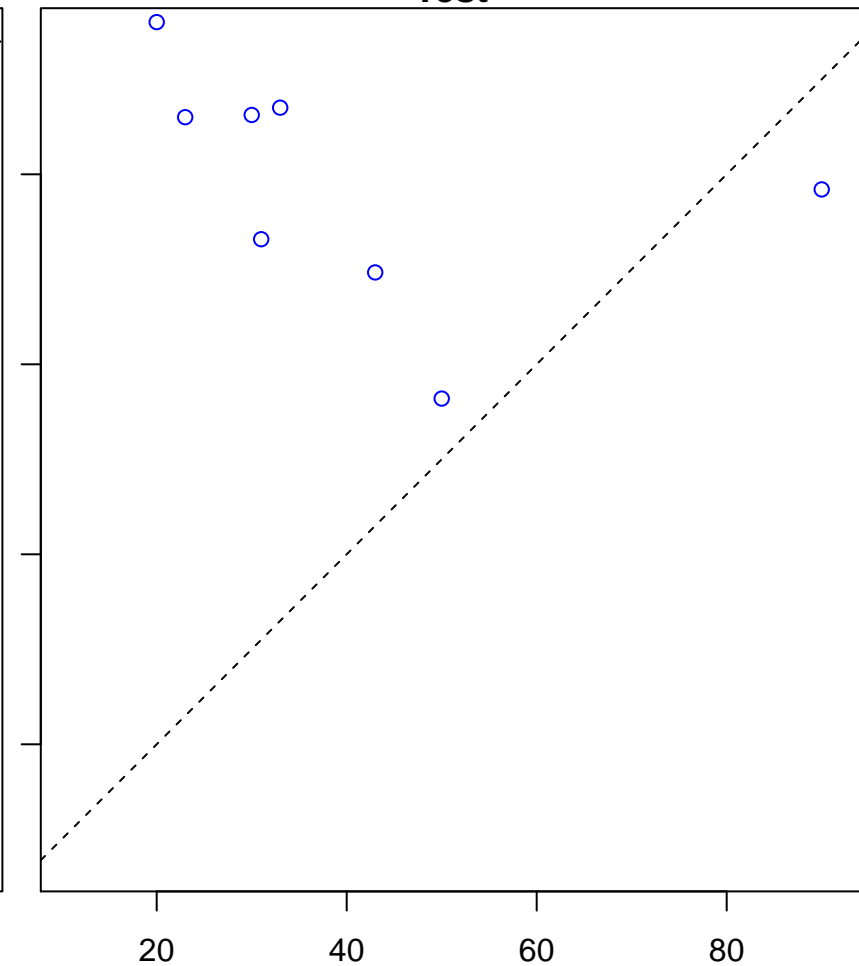


alpha-amino acid biosynthetic process (Score: 10.592871)

Control

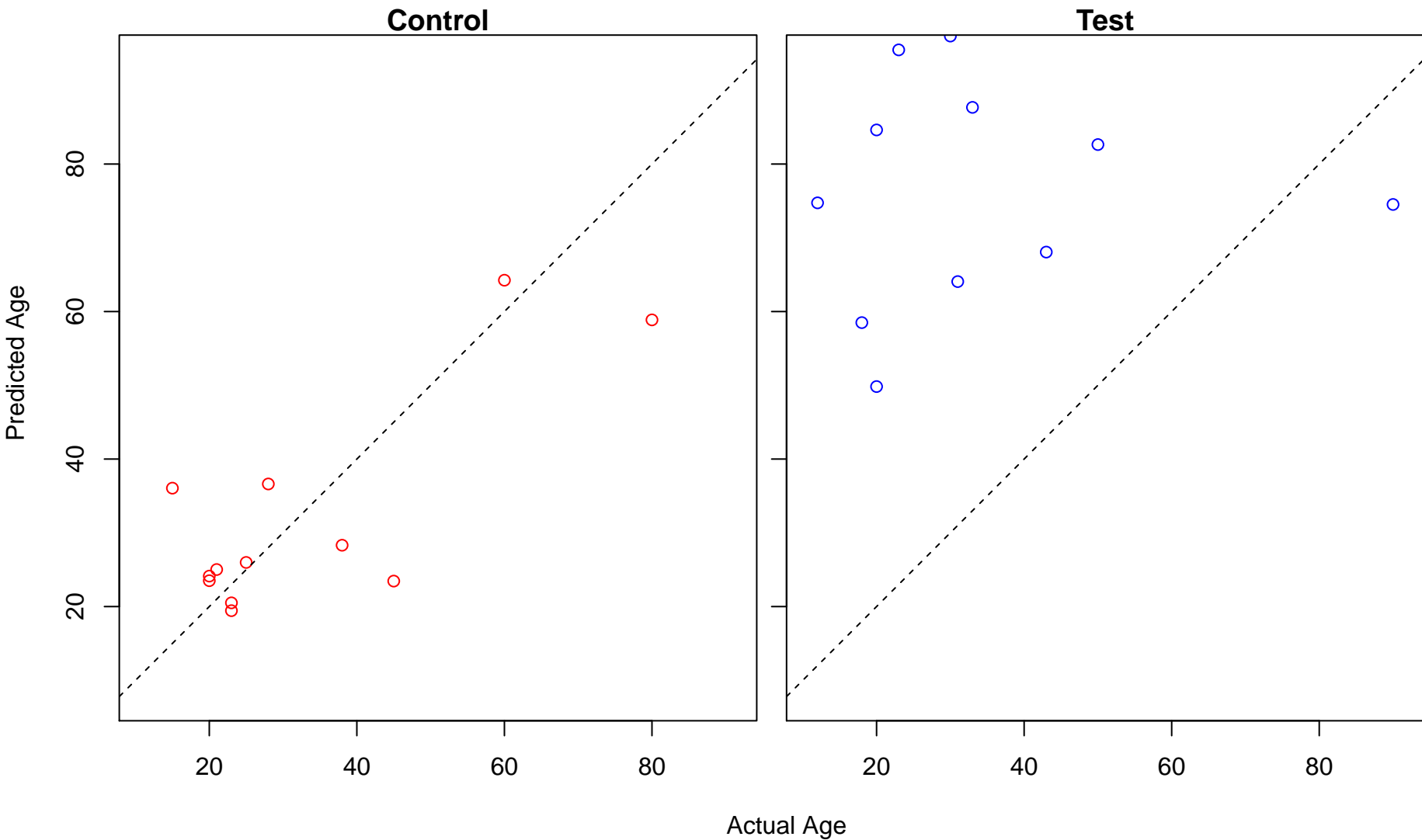


Test

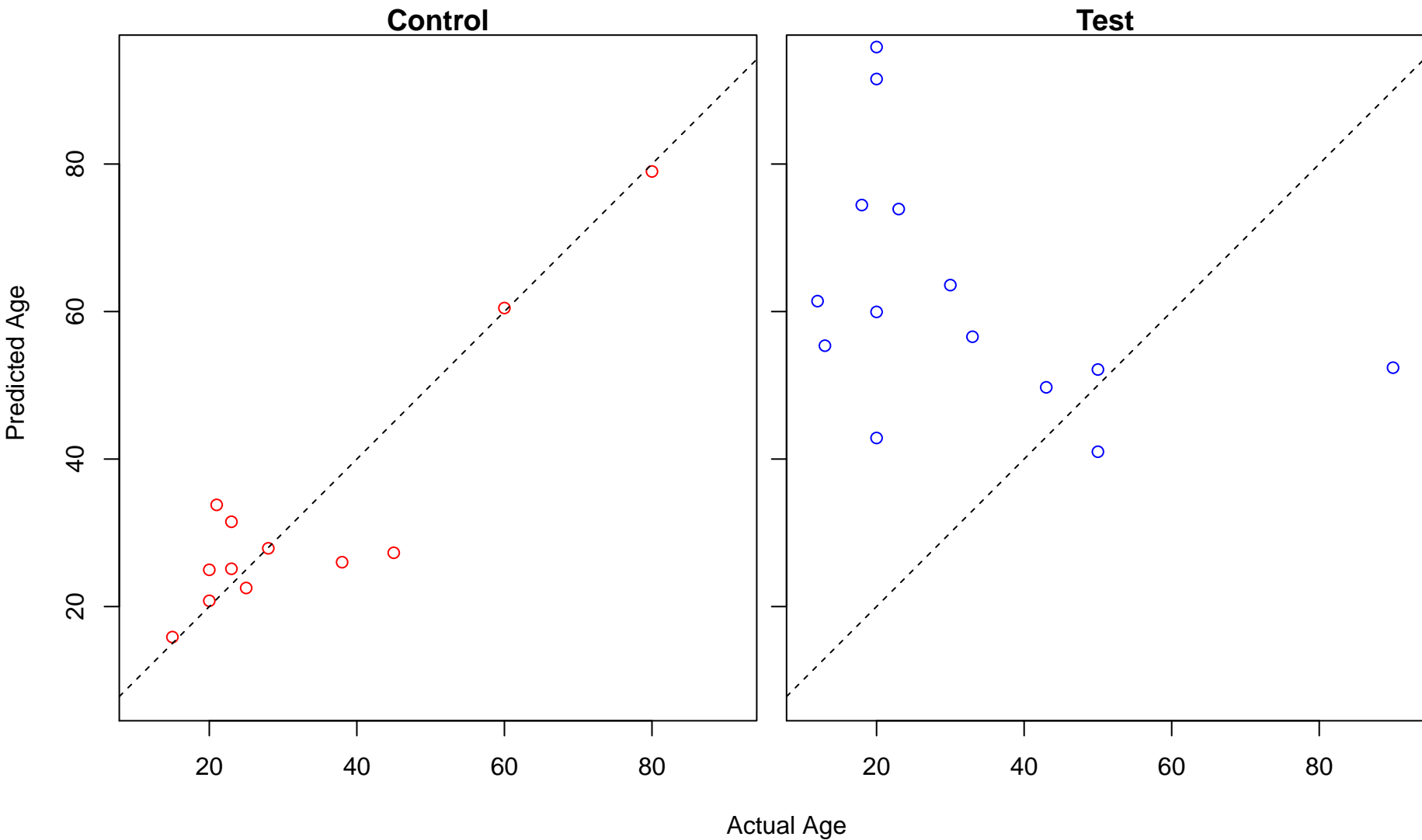


Actual Age

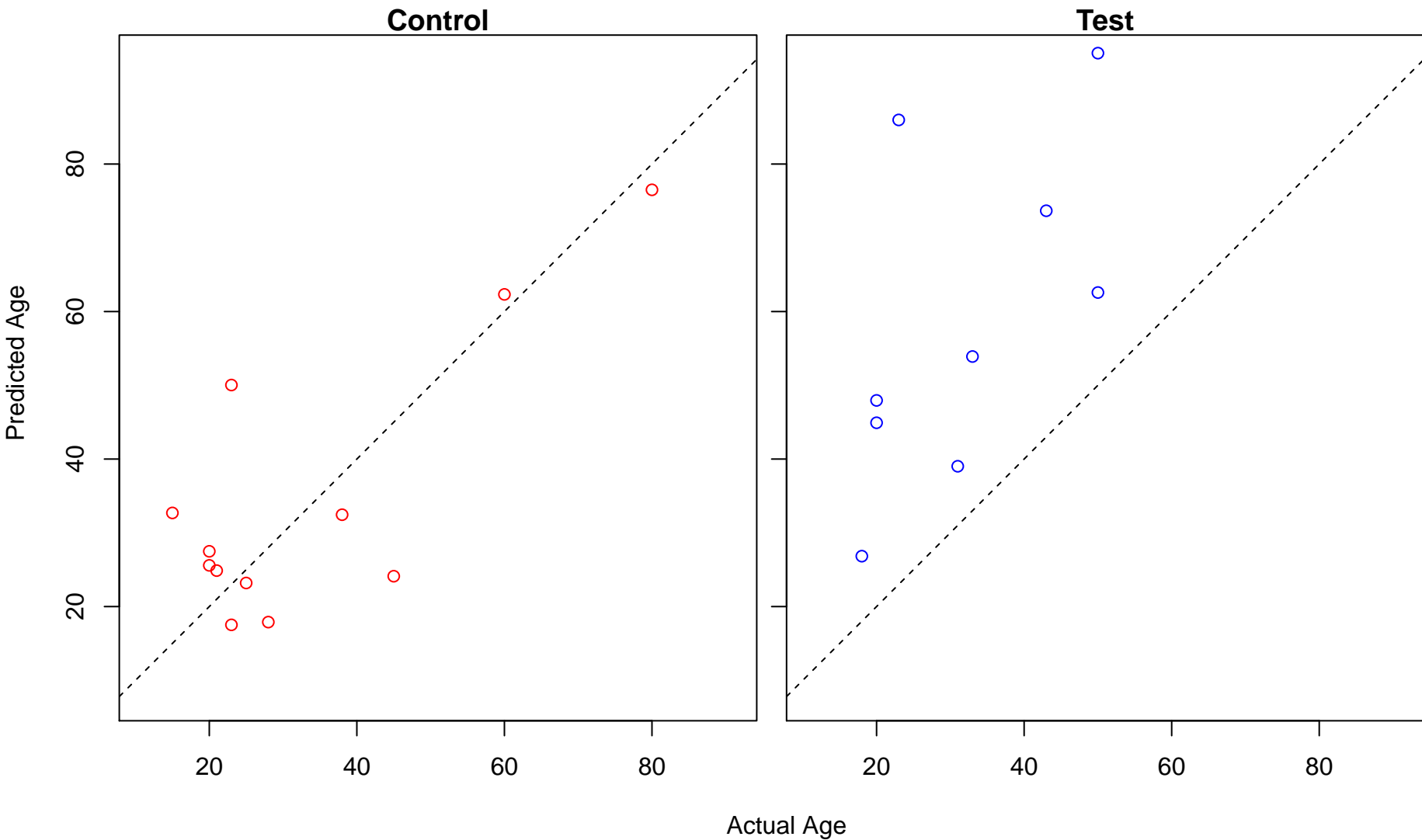
establishment of monopolar cell polarity (Score: 10.589939)



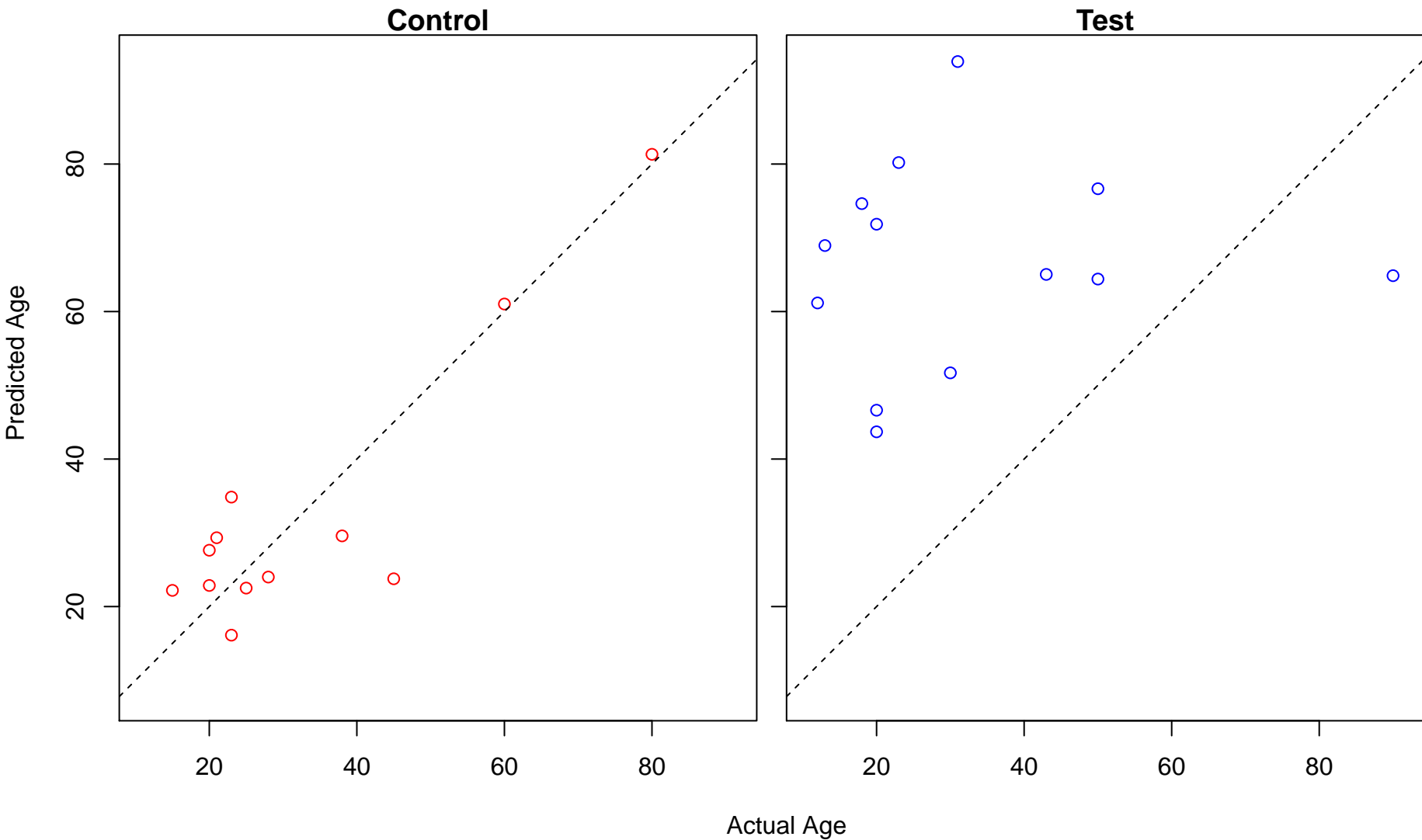
positive regulation of neuron projection development (Score: 10.586702)



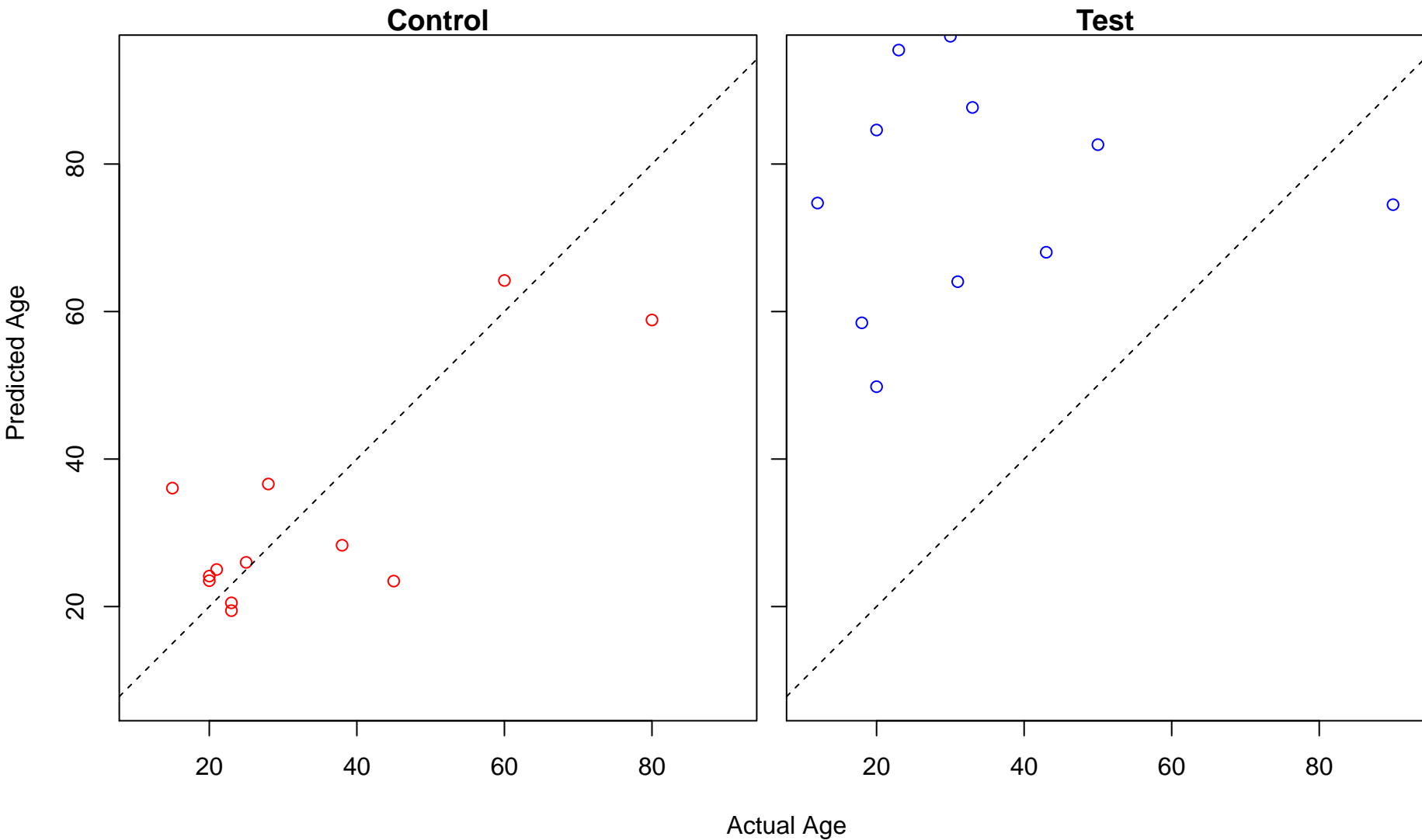
thymus development (Score: 10.584658)



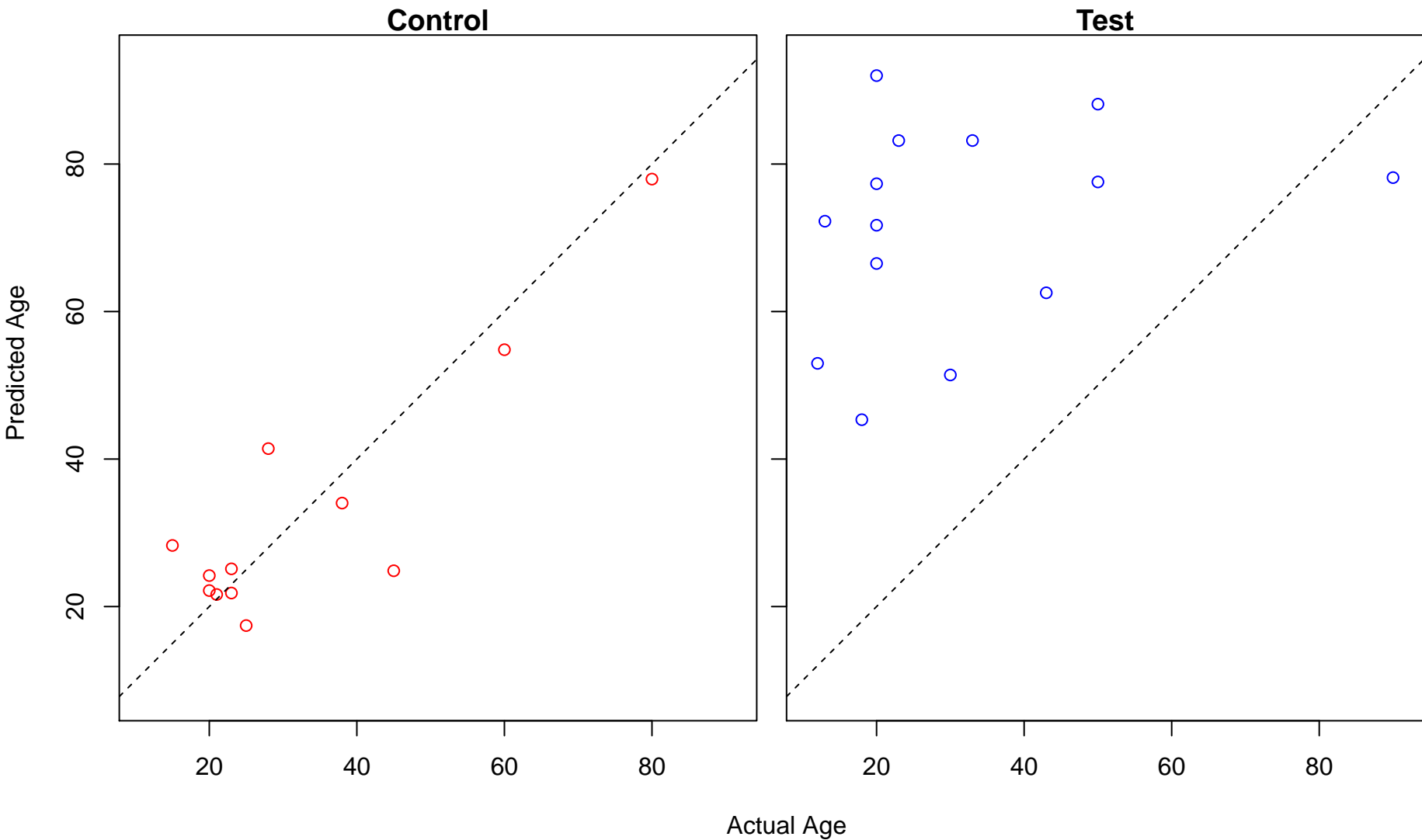
cell cycle arrest (Score: 10.580905)



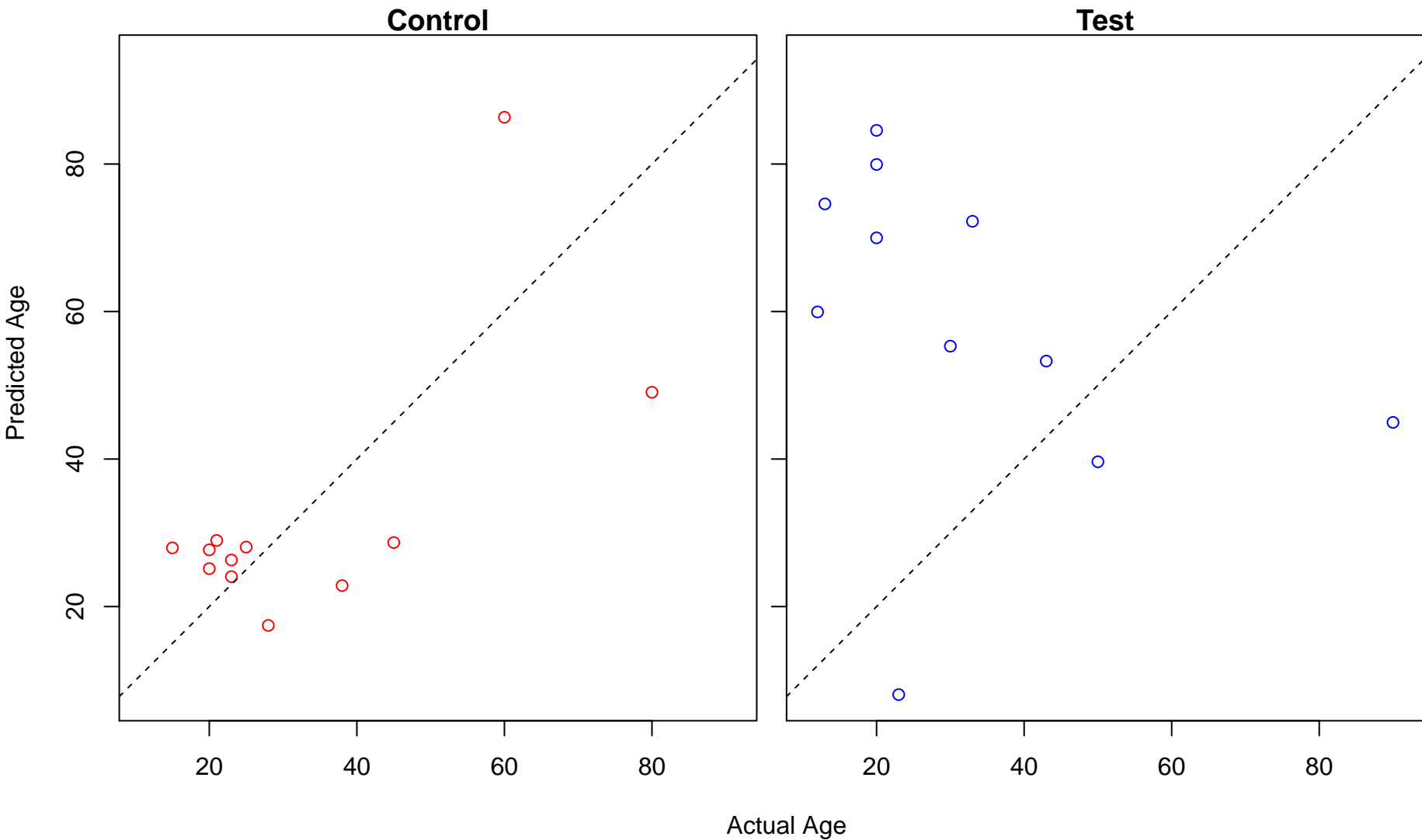
establishment or maintenance of monopolar cell polarity (Score: 10.579007)



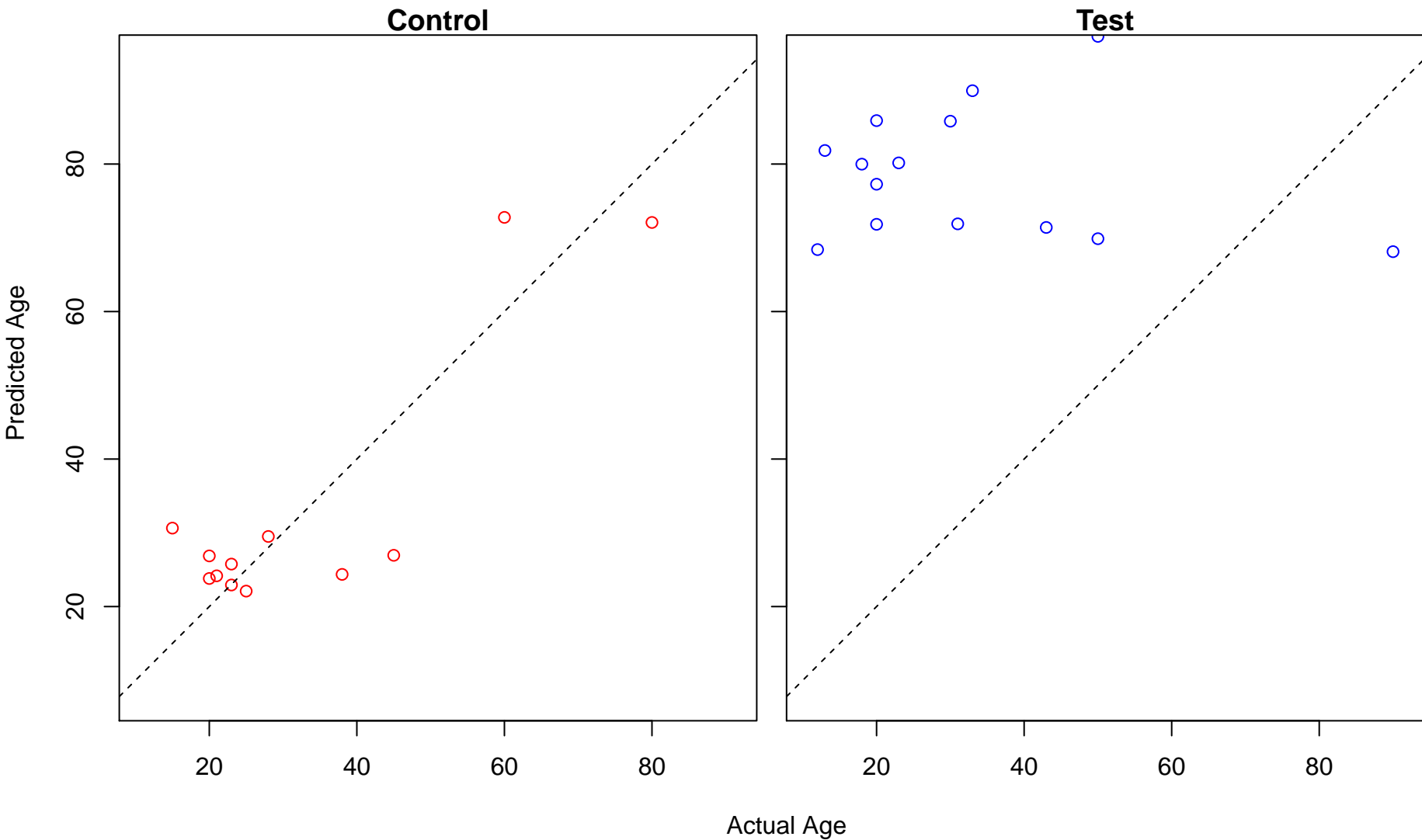
regionalization (Score: 10.576143)



negative regulation of fibrinolysis (Score: 10.574502)

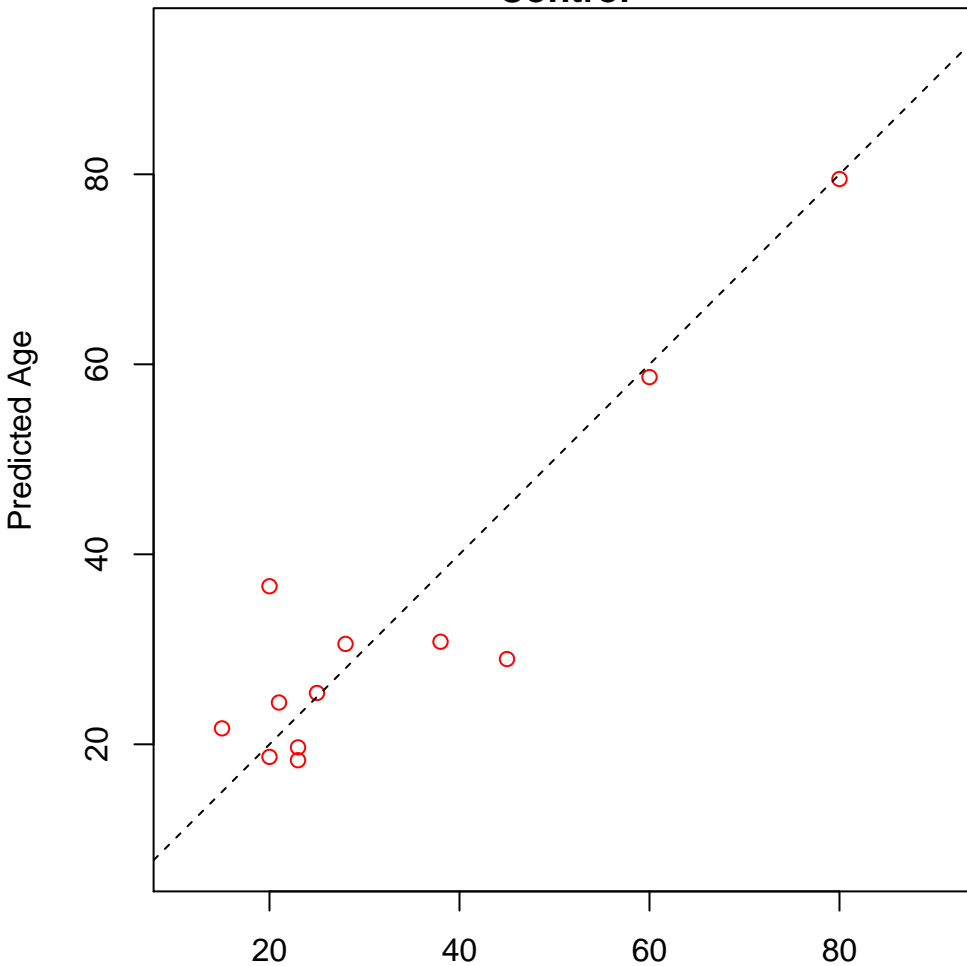


dorsal/ventral pattern formation (Score: 10.564293)

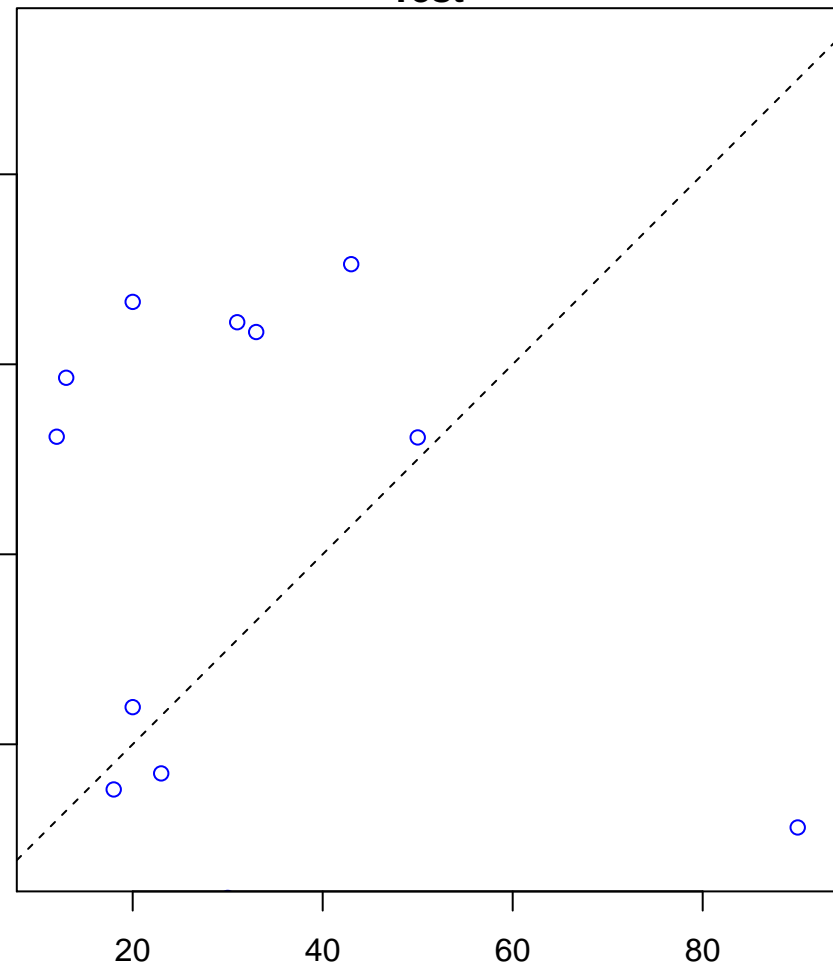


protein insertion into membrane (Score: 10.560136)

Control

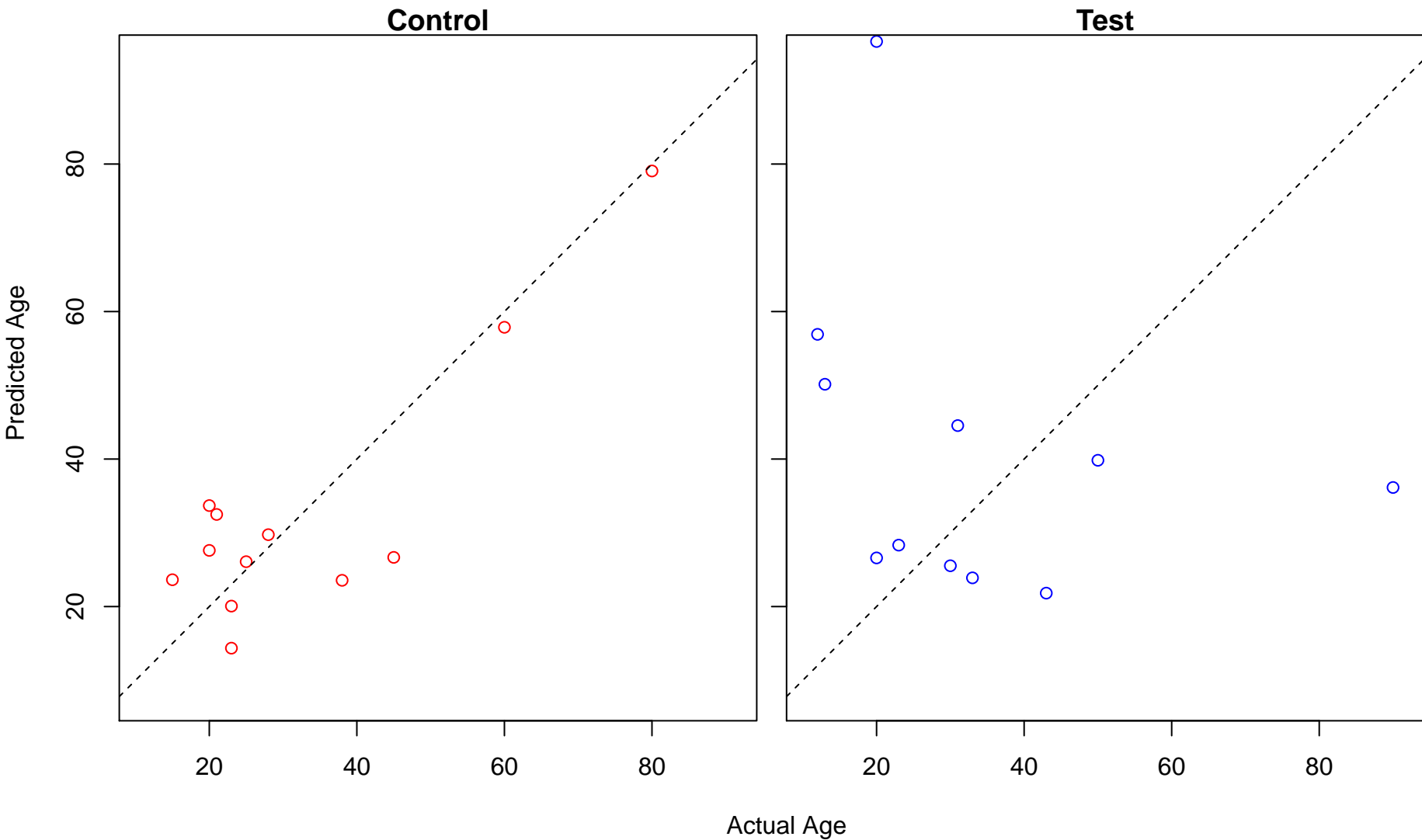


Test

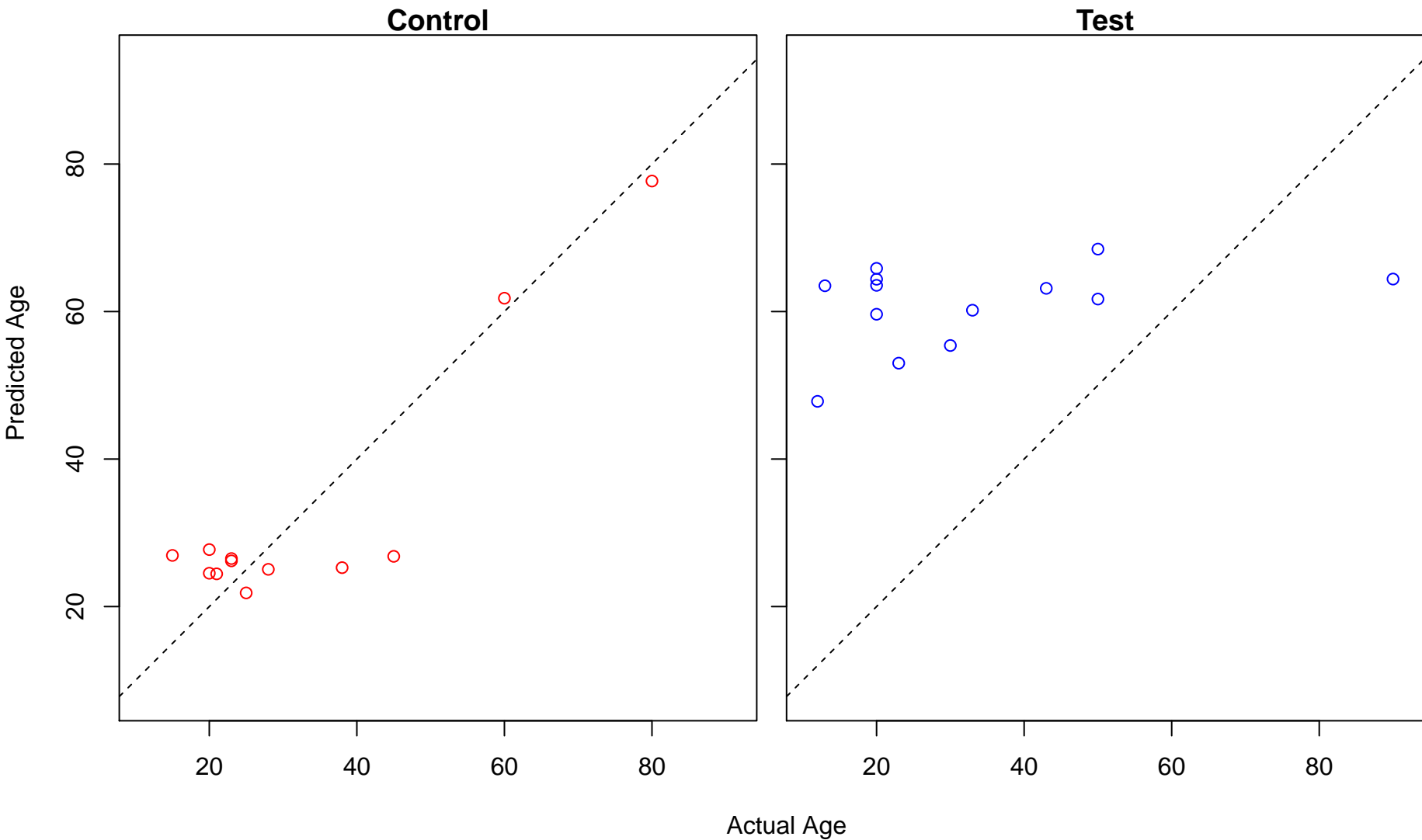


Actual Age

tetrapyrrole metabolic process (Score: 10.557527)

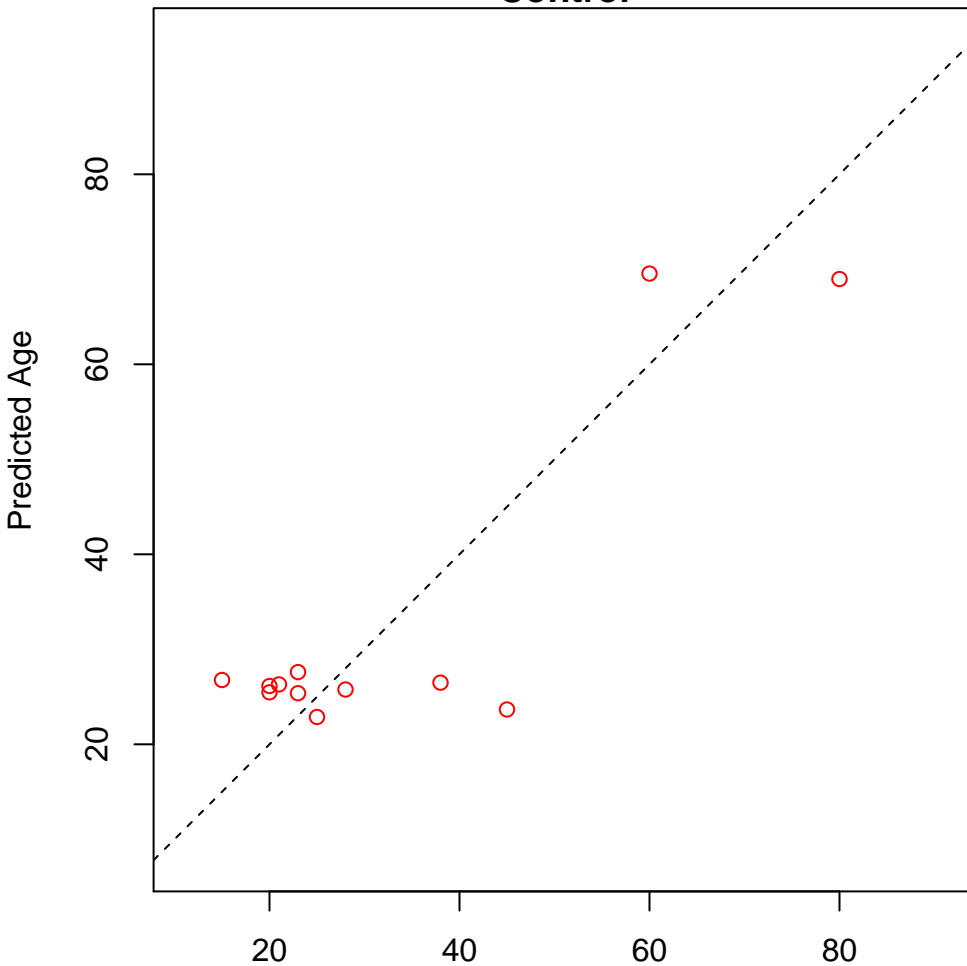


regulation of ER to Golgi vesicle-mediated transport (Score: 10.551348)

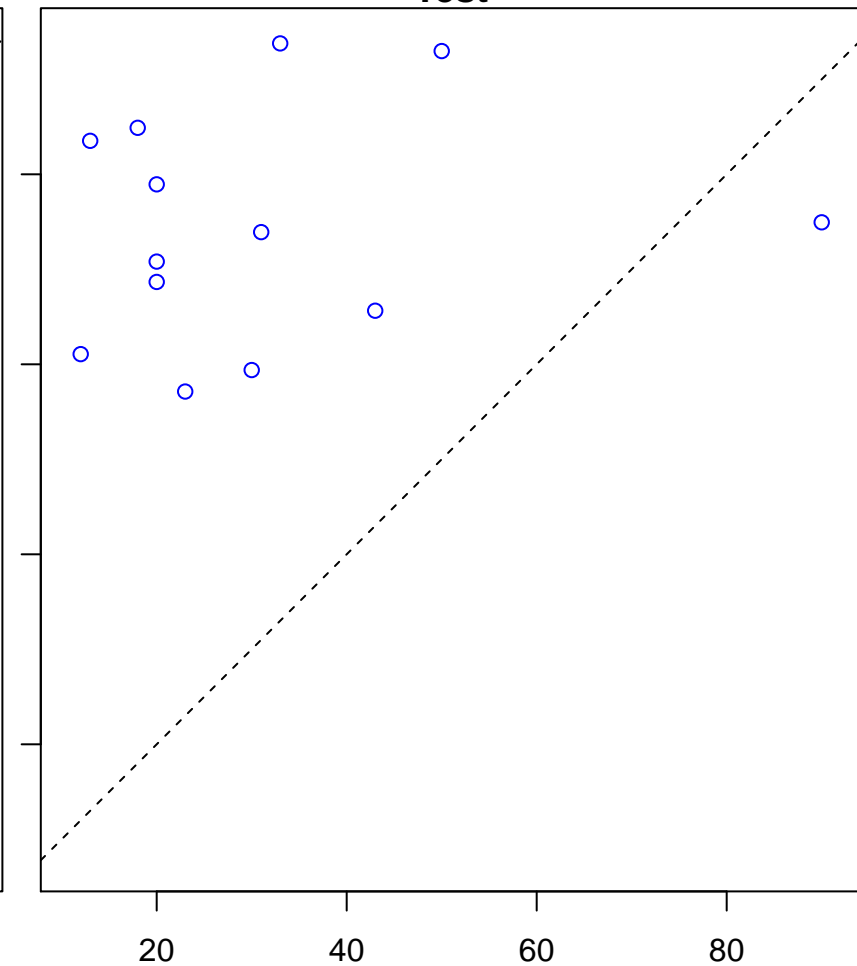


regulation of T cell apoptotic process (Score: 10.545006)

Control

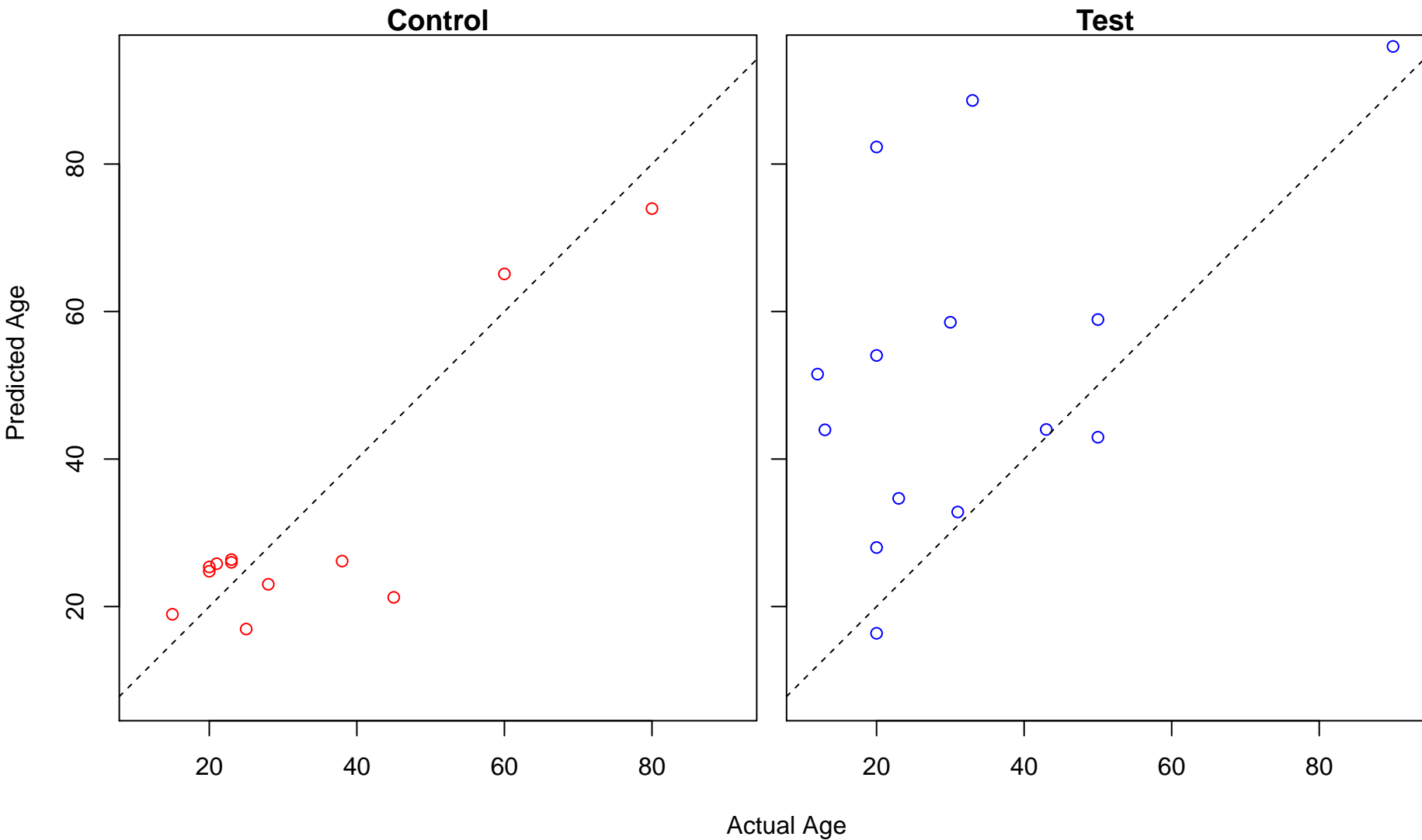


Test

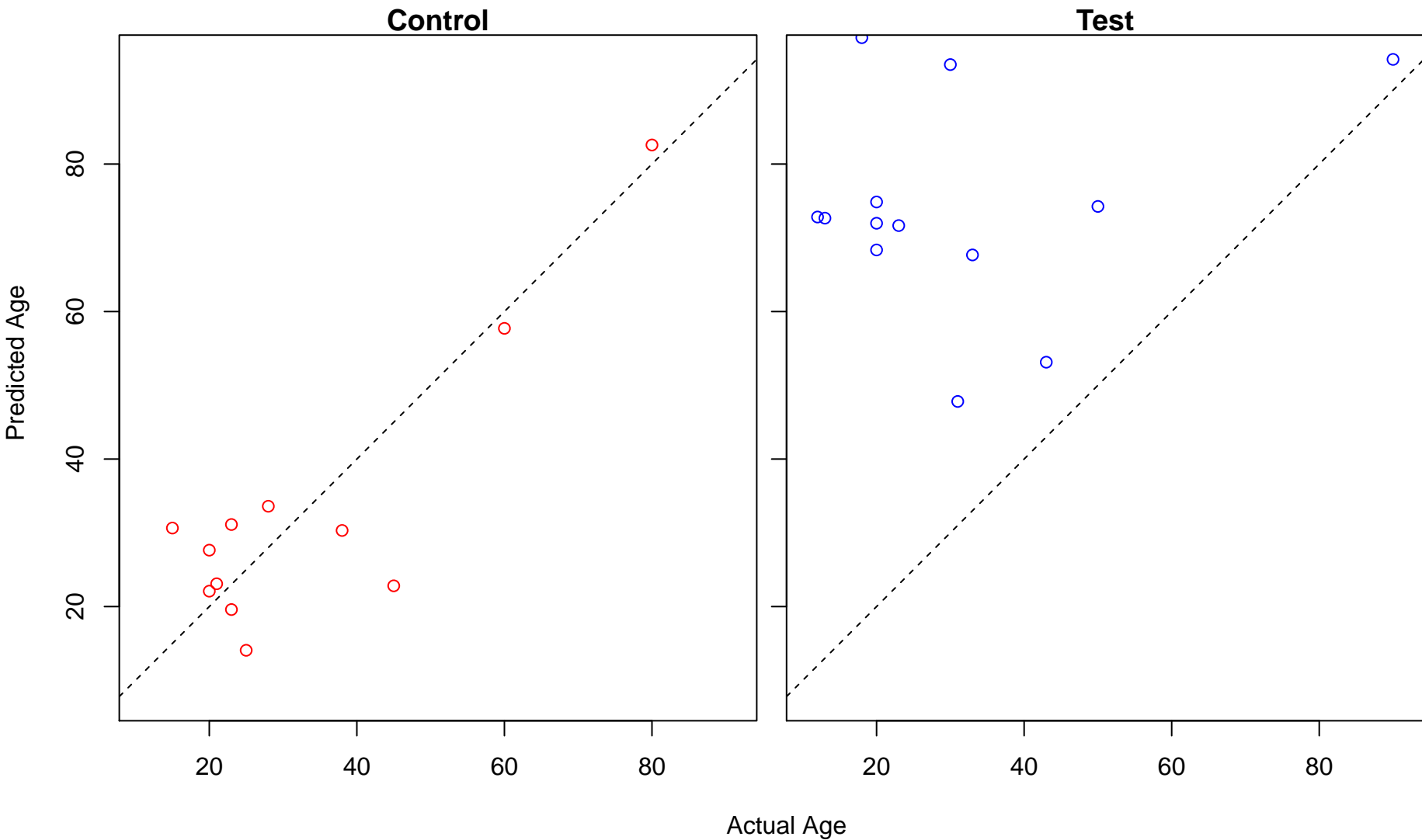


Actual Age

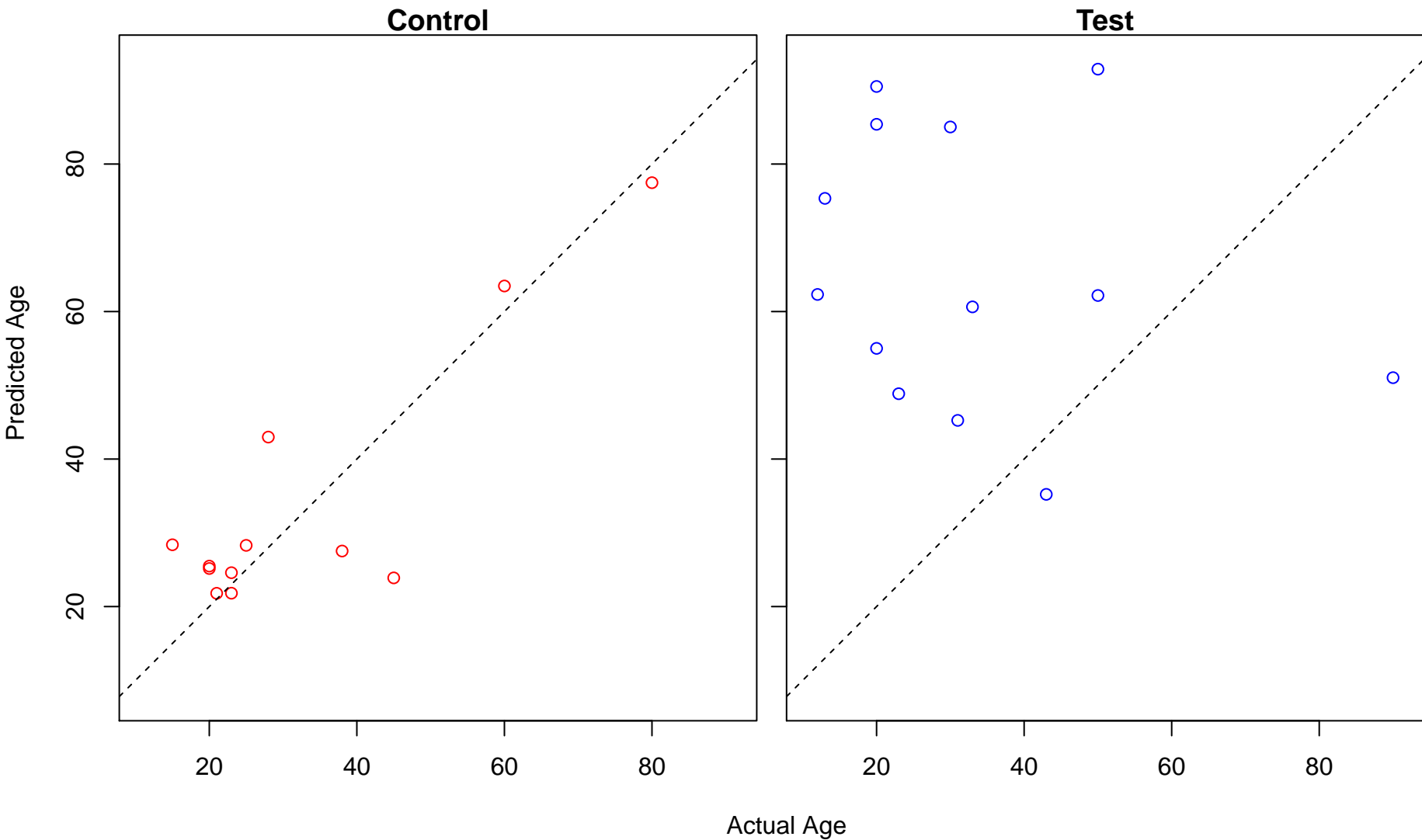
negative regulation of neuron death (Score: 10.537873)



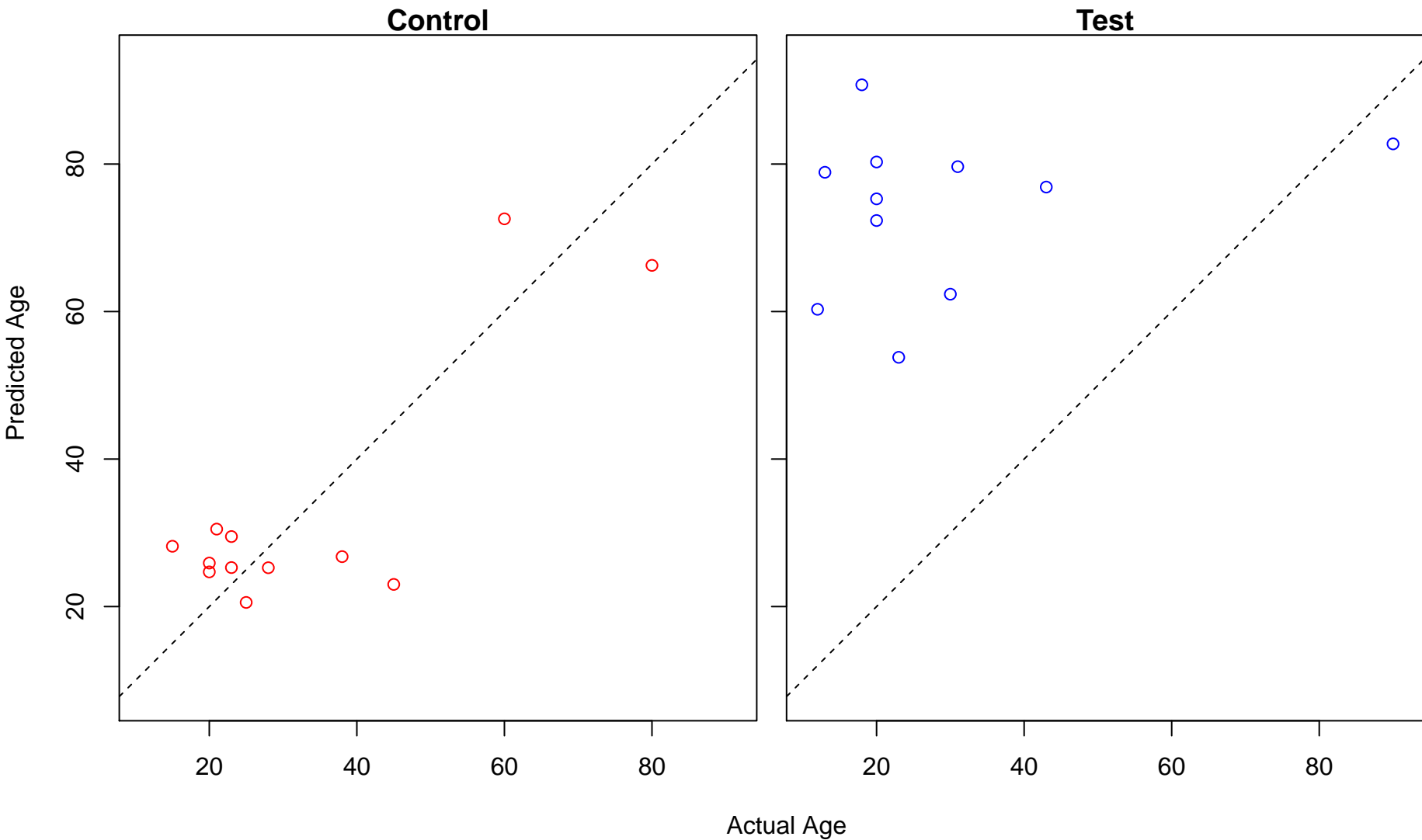
Rho protein signal transduction (Score: 10.536154)



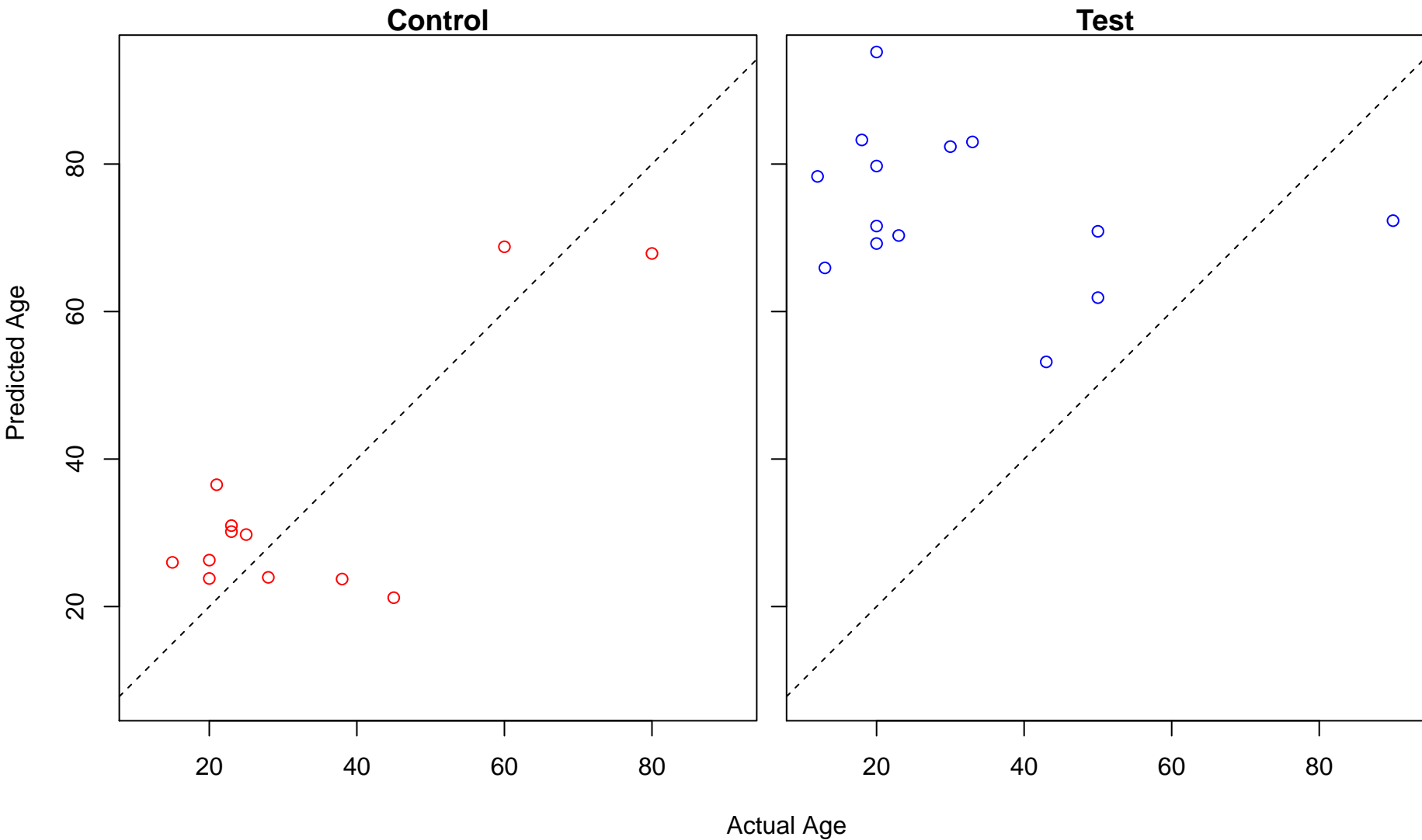
magnesium ion transmembrane transport (Score: 10.534865)



negative regulation of endocytosis (Score: 10.532395)

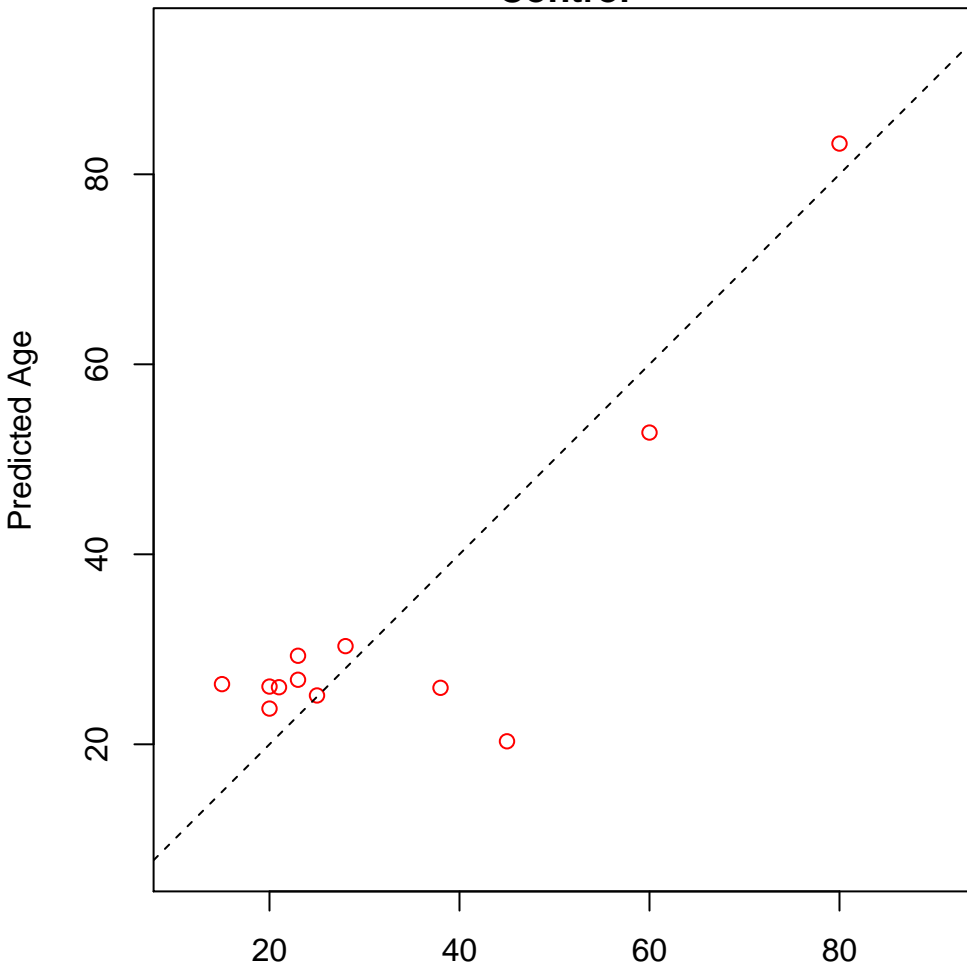


cellular response to drug (Score: 10.507503)

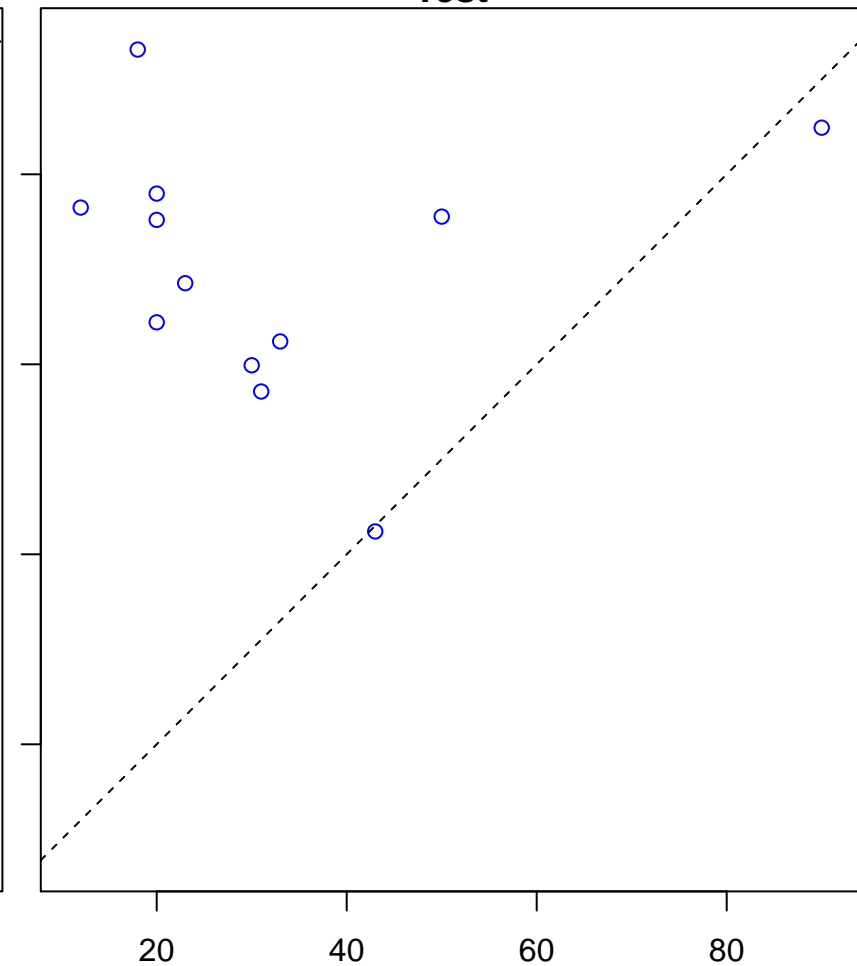


regulation of viral genome replication (Score: 10.497956)

Control

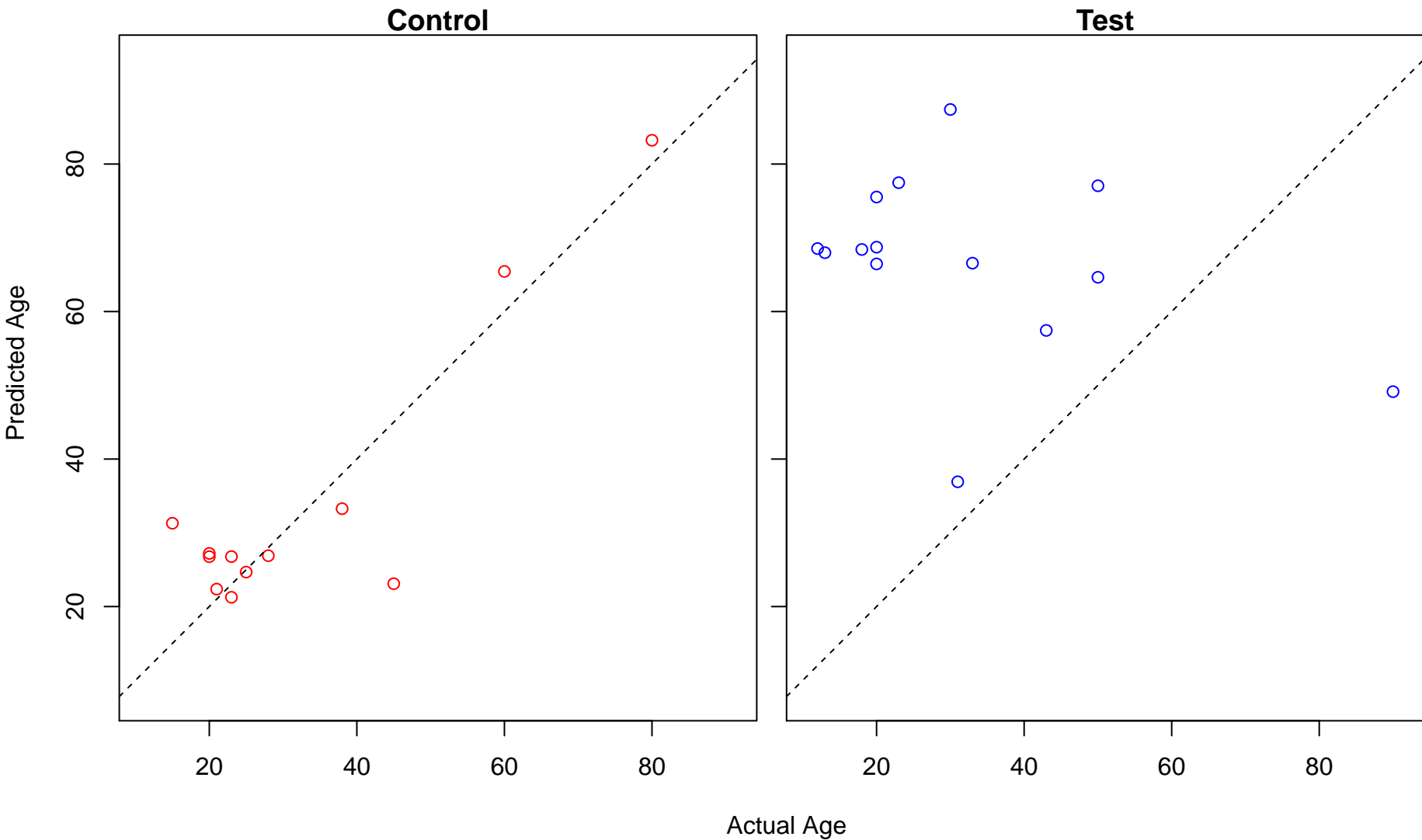


Test



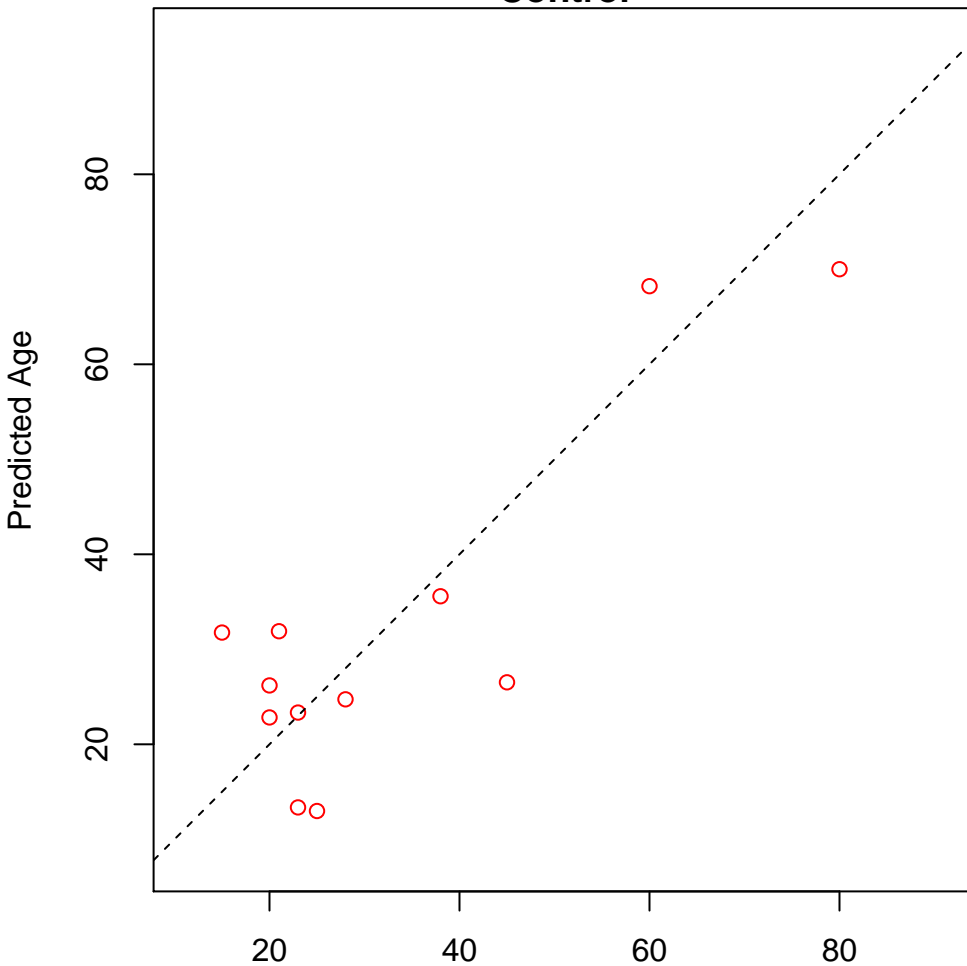
Actual Age

alanine transport (Score: 10.497821)

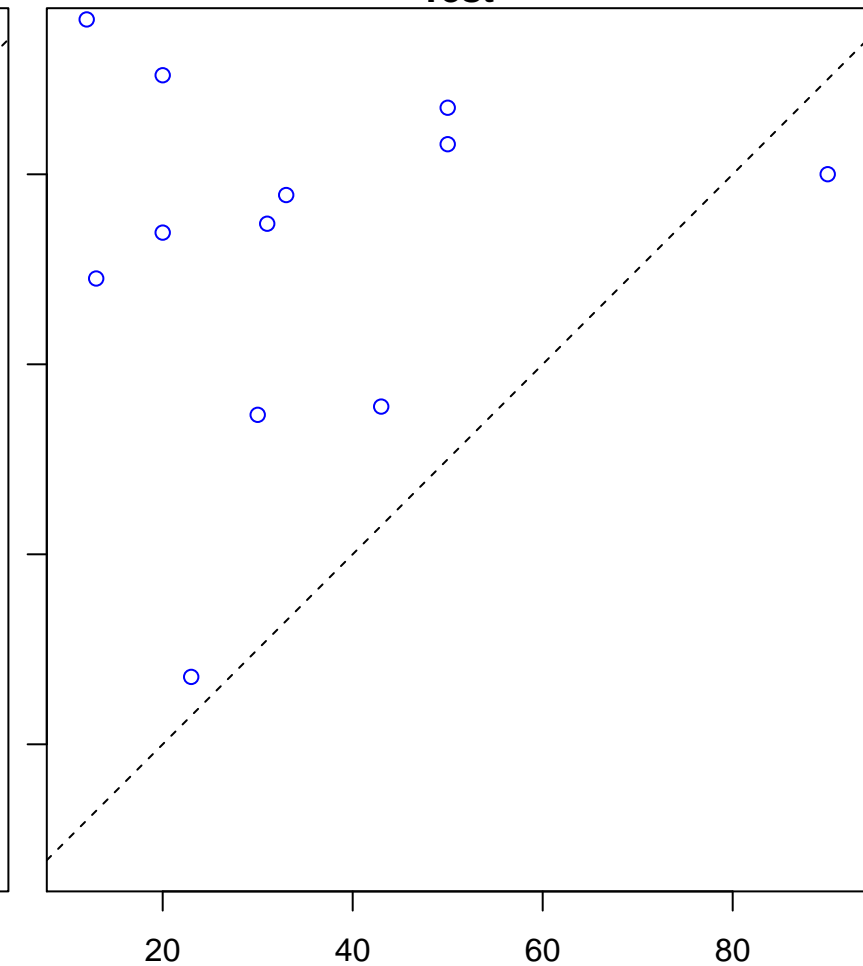


reproductive structure development (Score: 10.490013)

Control



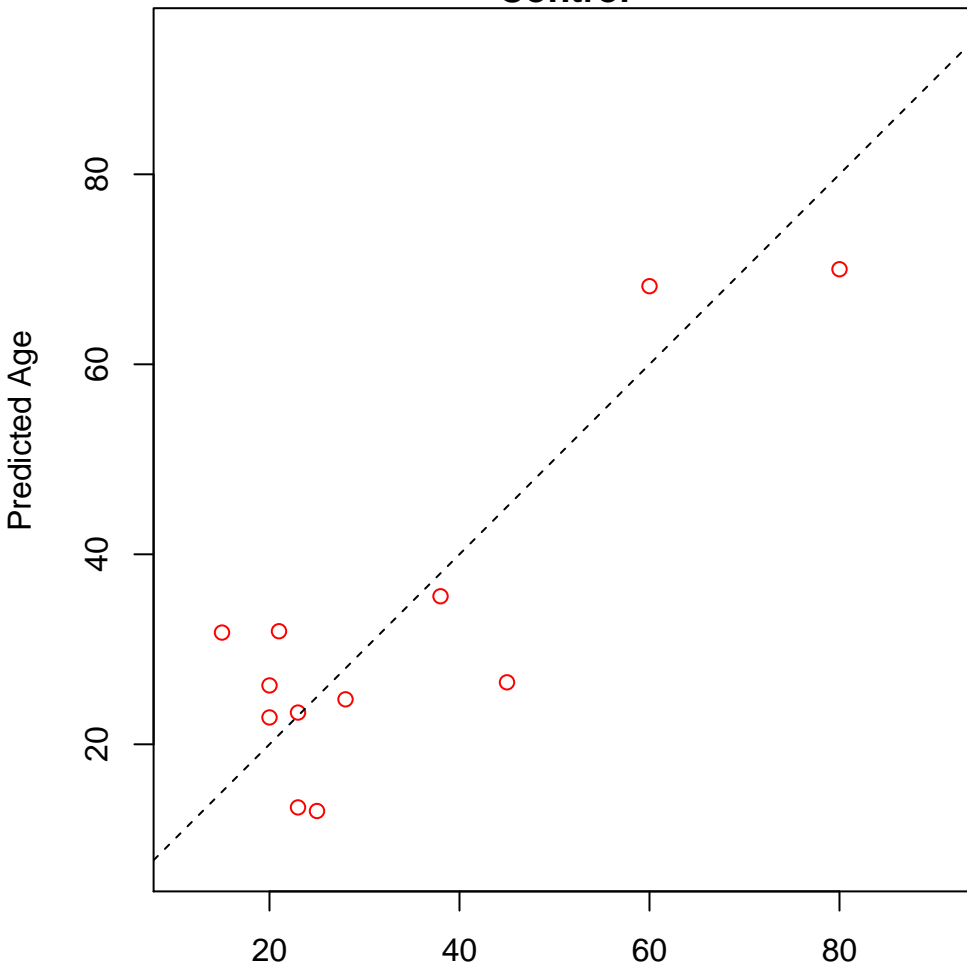
Test



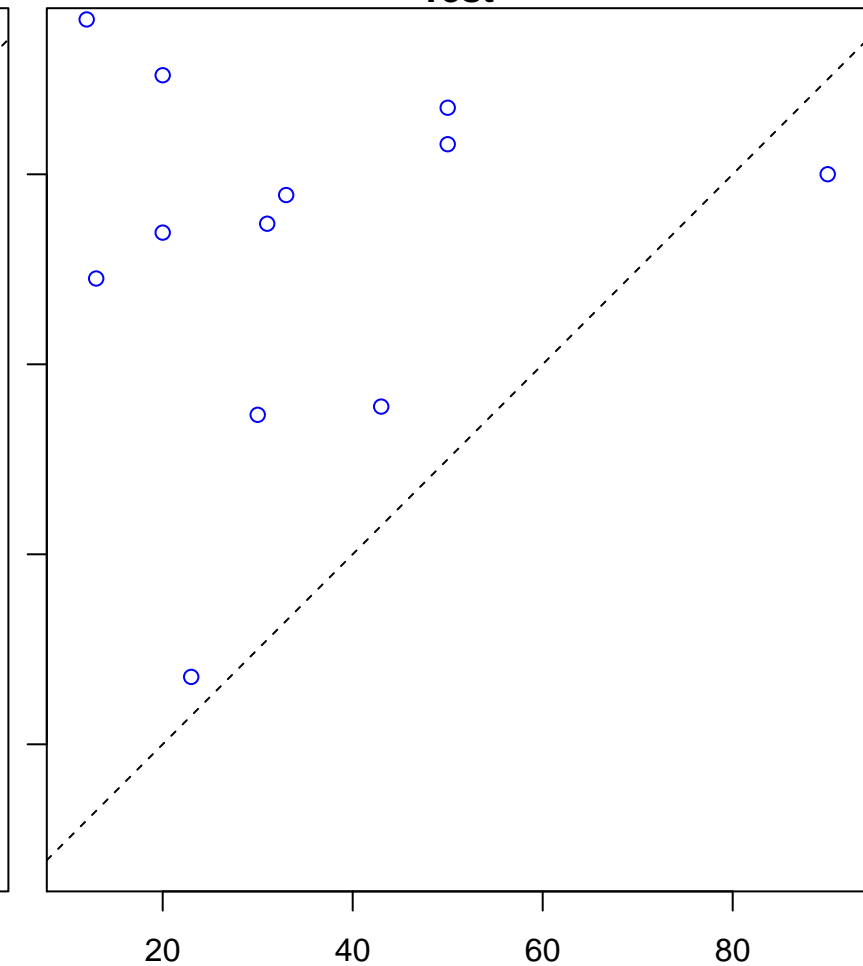
Actual Age

reproductive system development (Score: 10.490013)

Control

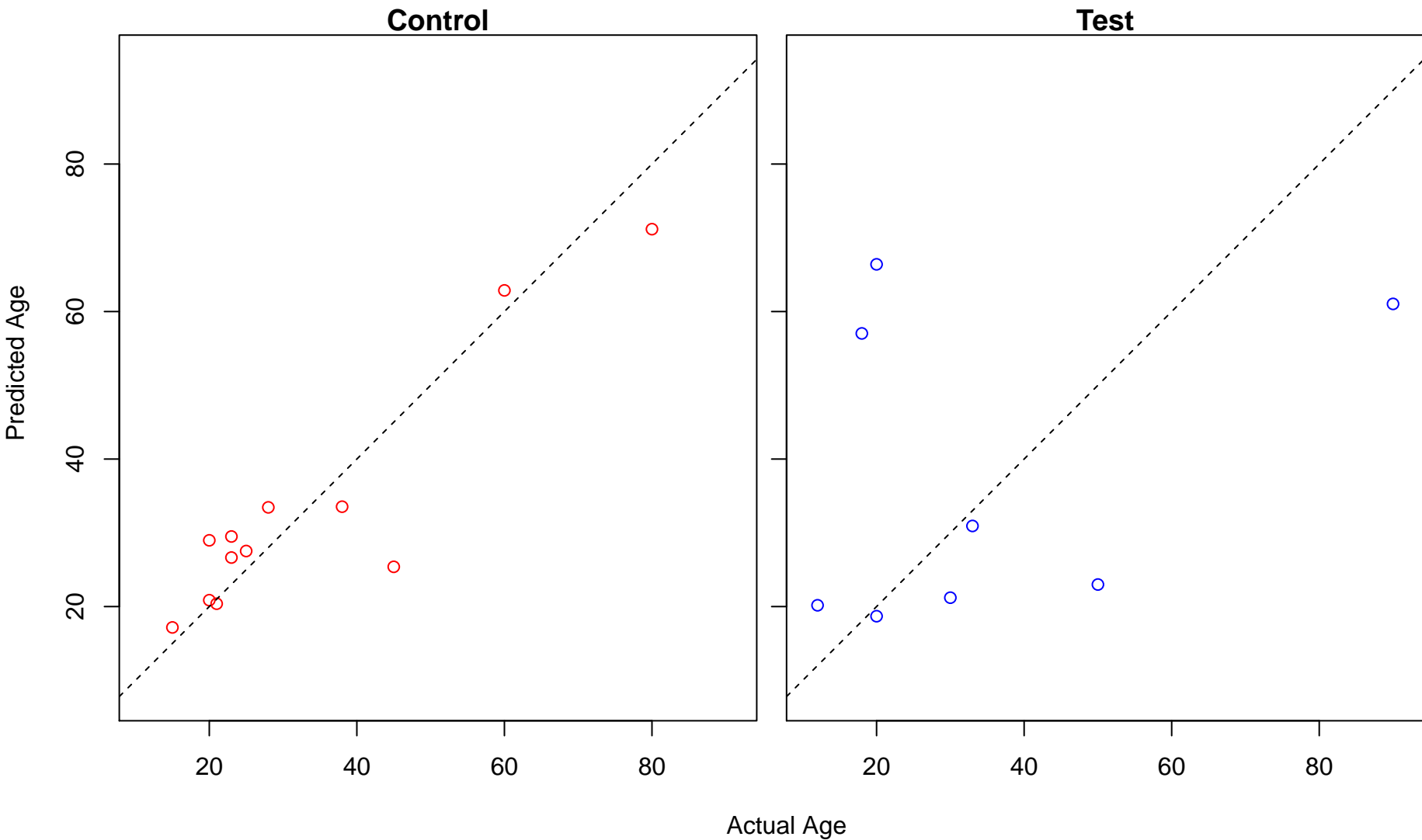


Test

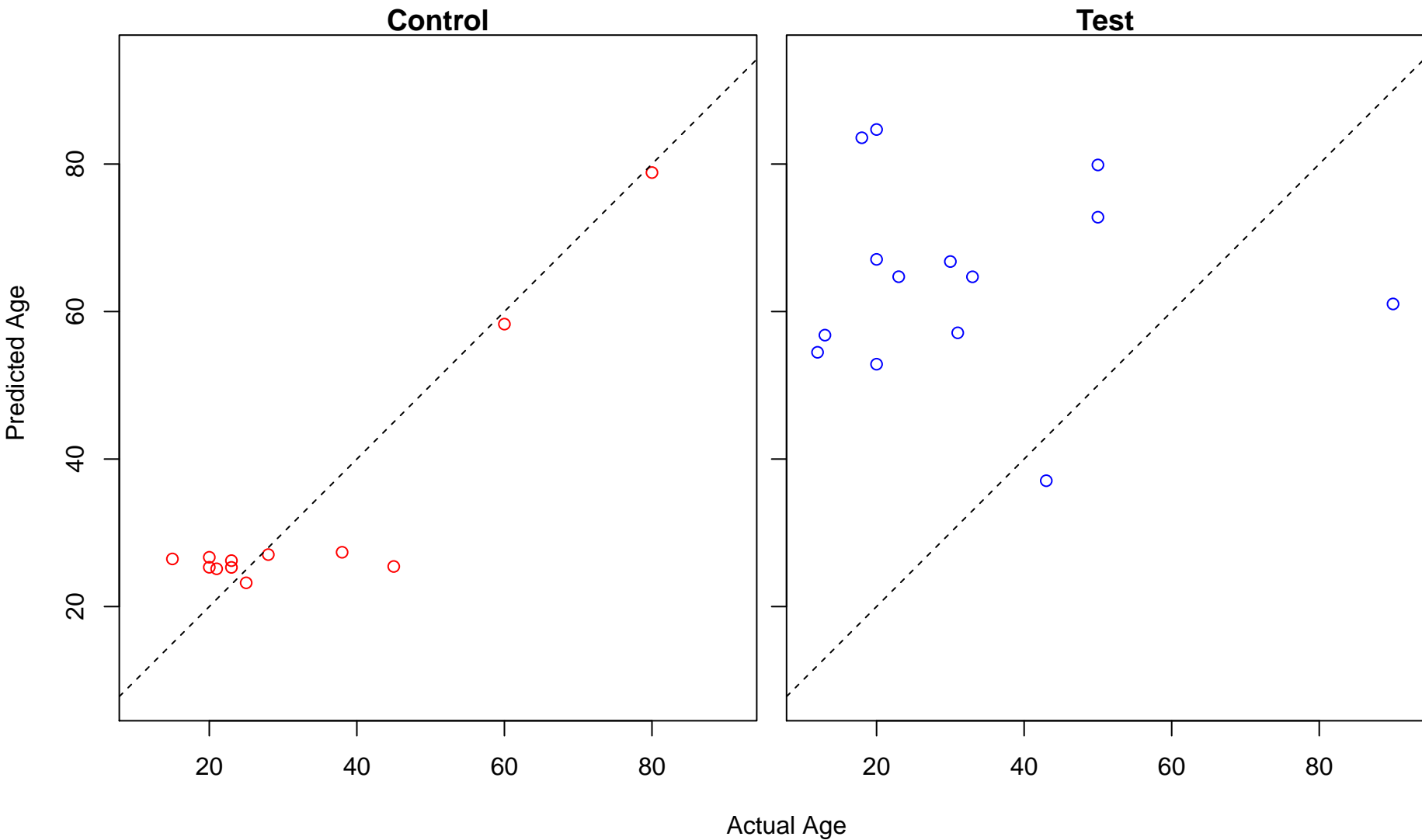


Actual Age

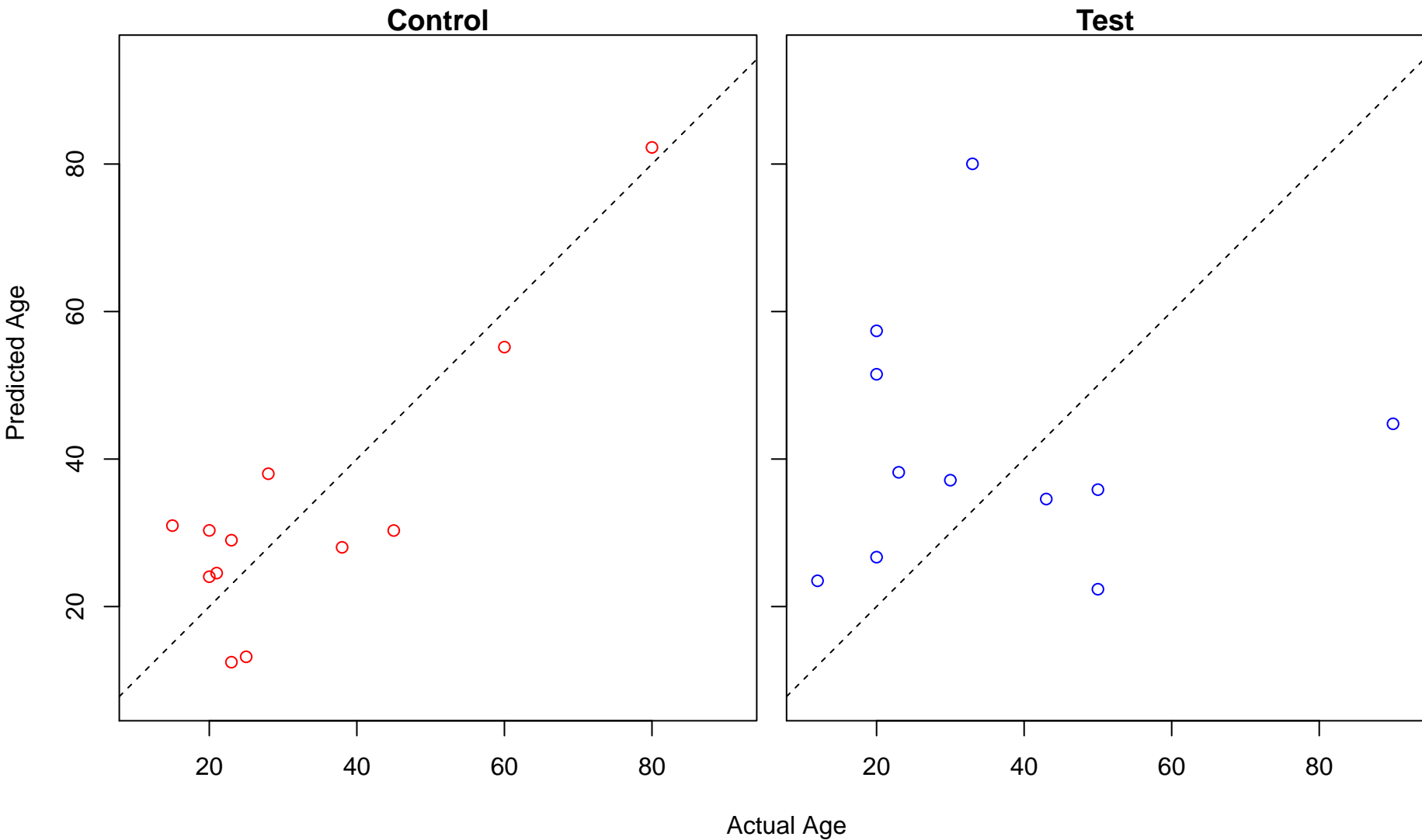
regulation of myoblast fusion (Score: 10.486944)



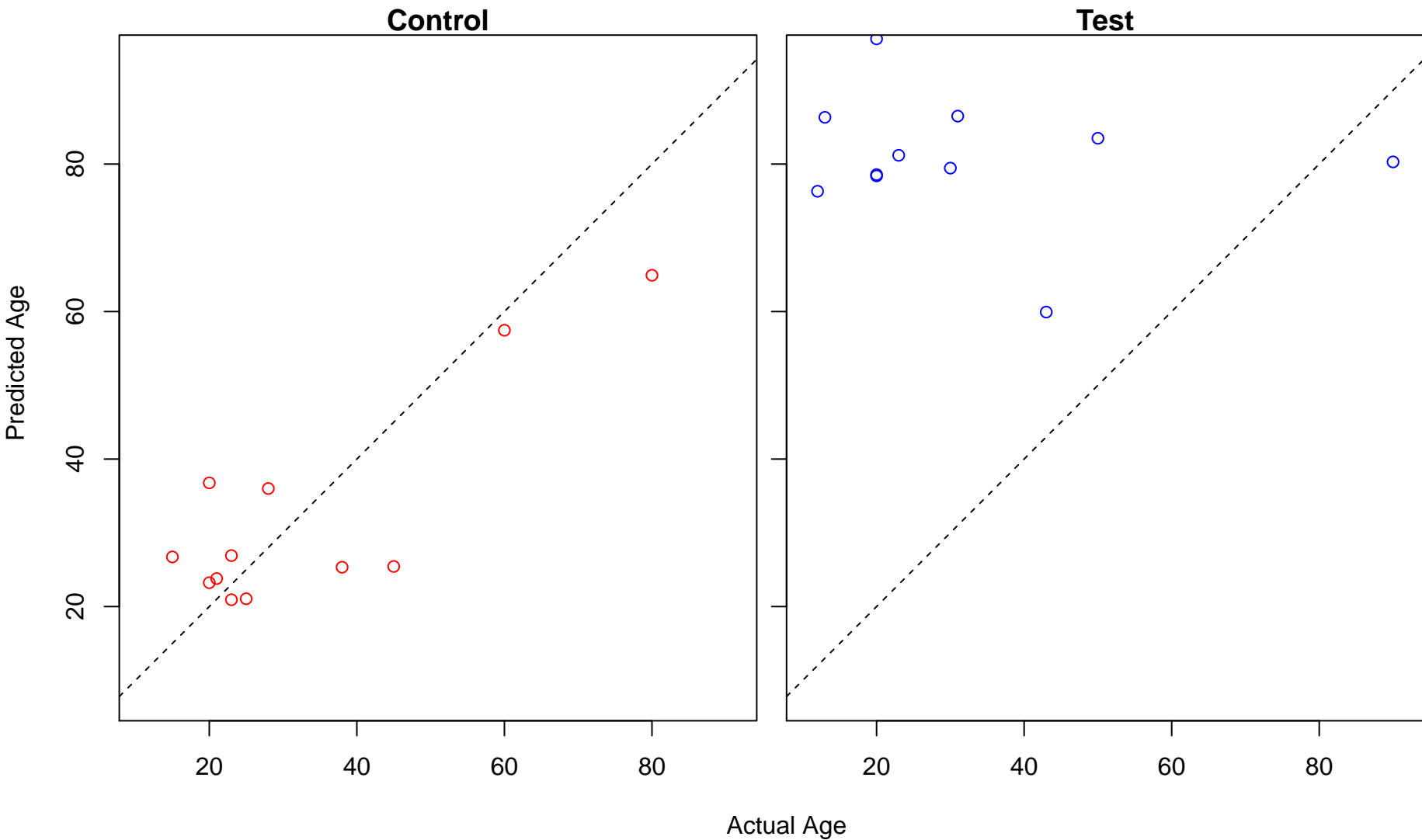
positive regulation of DNA replication (Score: 10.480628)



centrosome organization (Score: 10.471437)

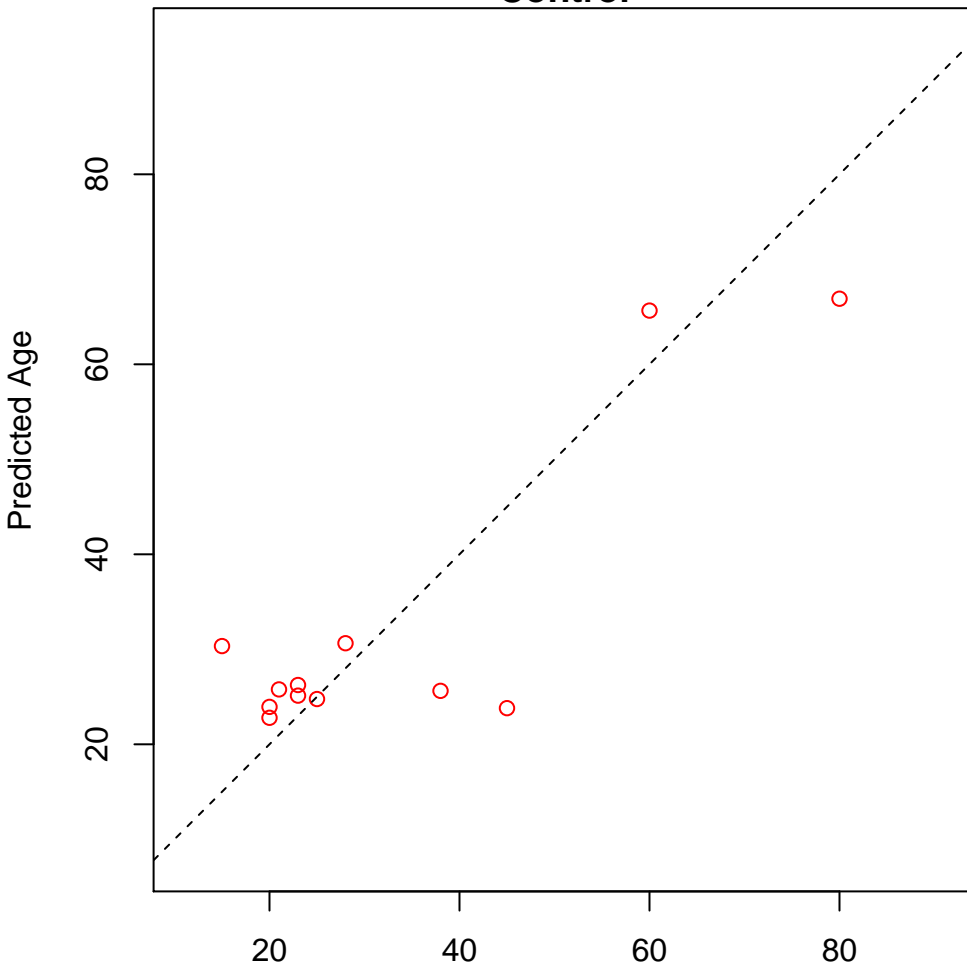


positive regulation of fatty acid metabolic process (Score: 10.468968)

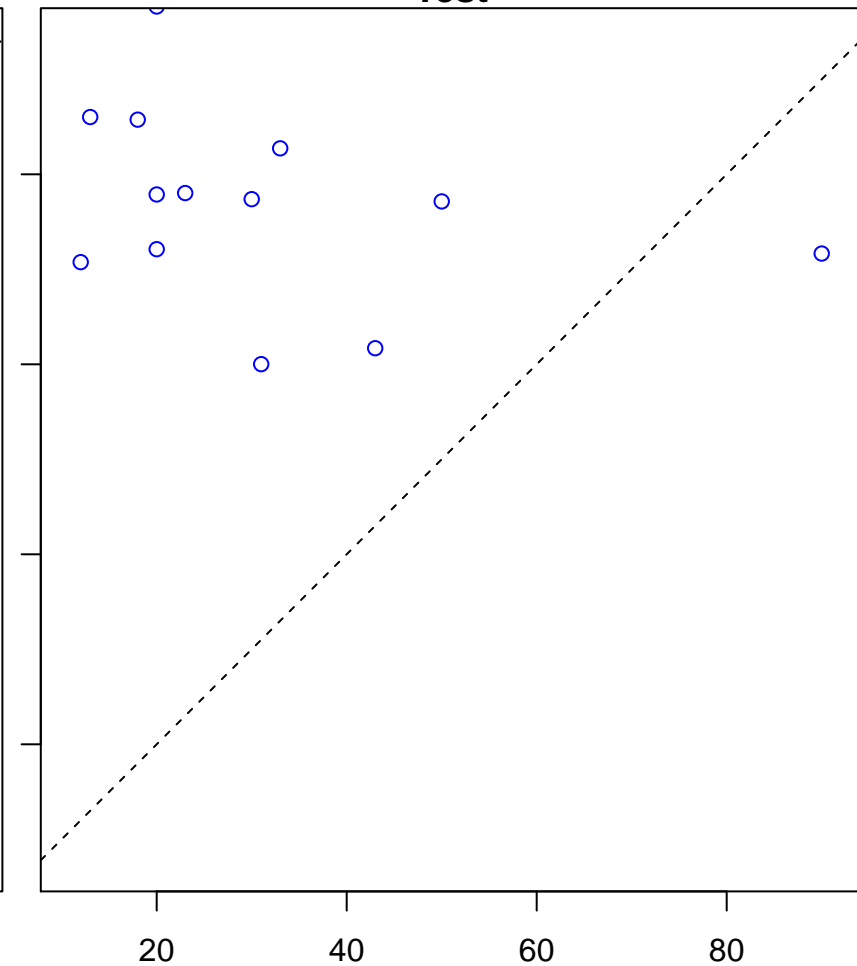


peptidyl-glutamic acid carboxylation (Score: 10.445623)

Control

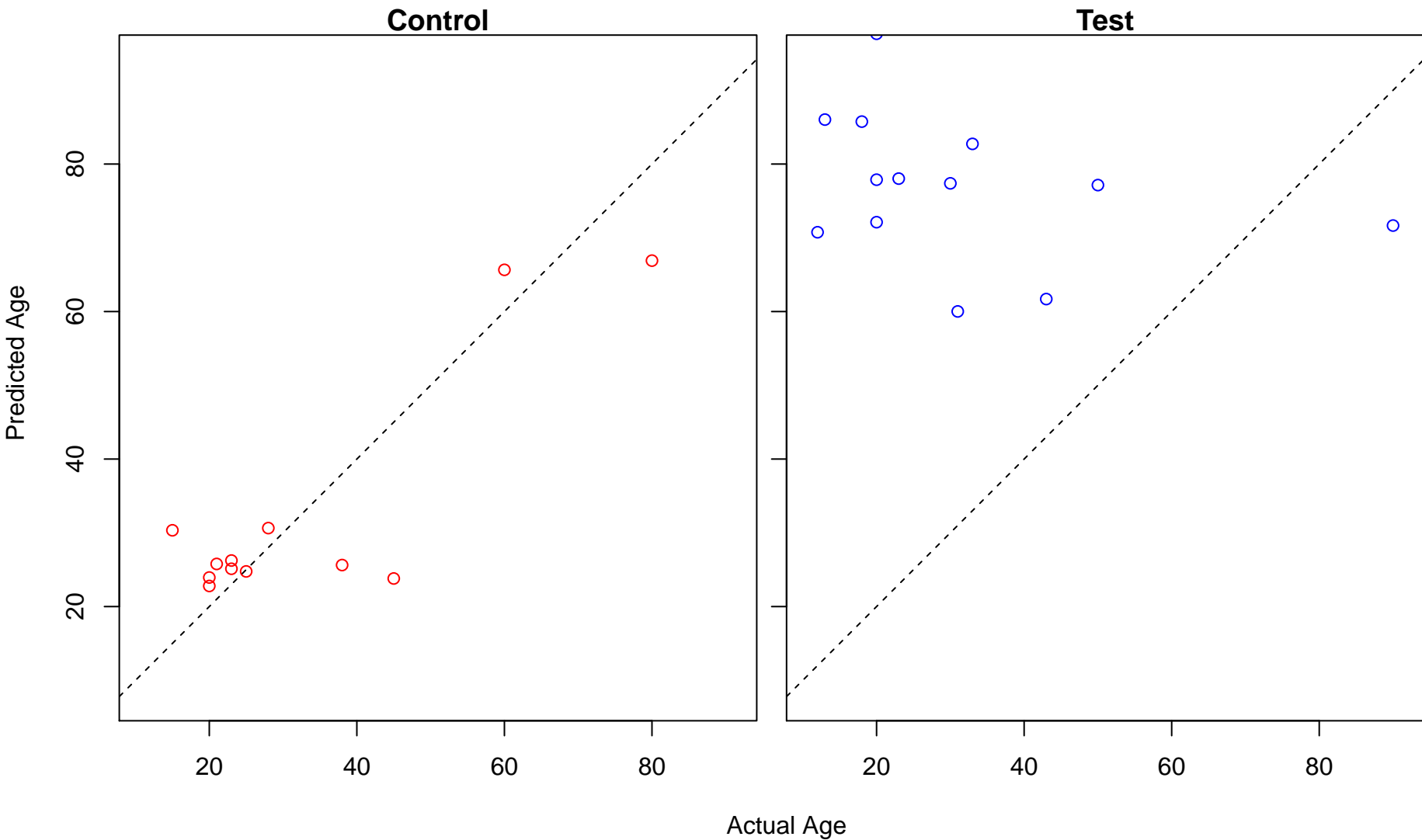


Test

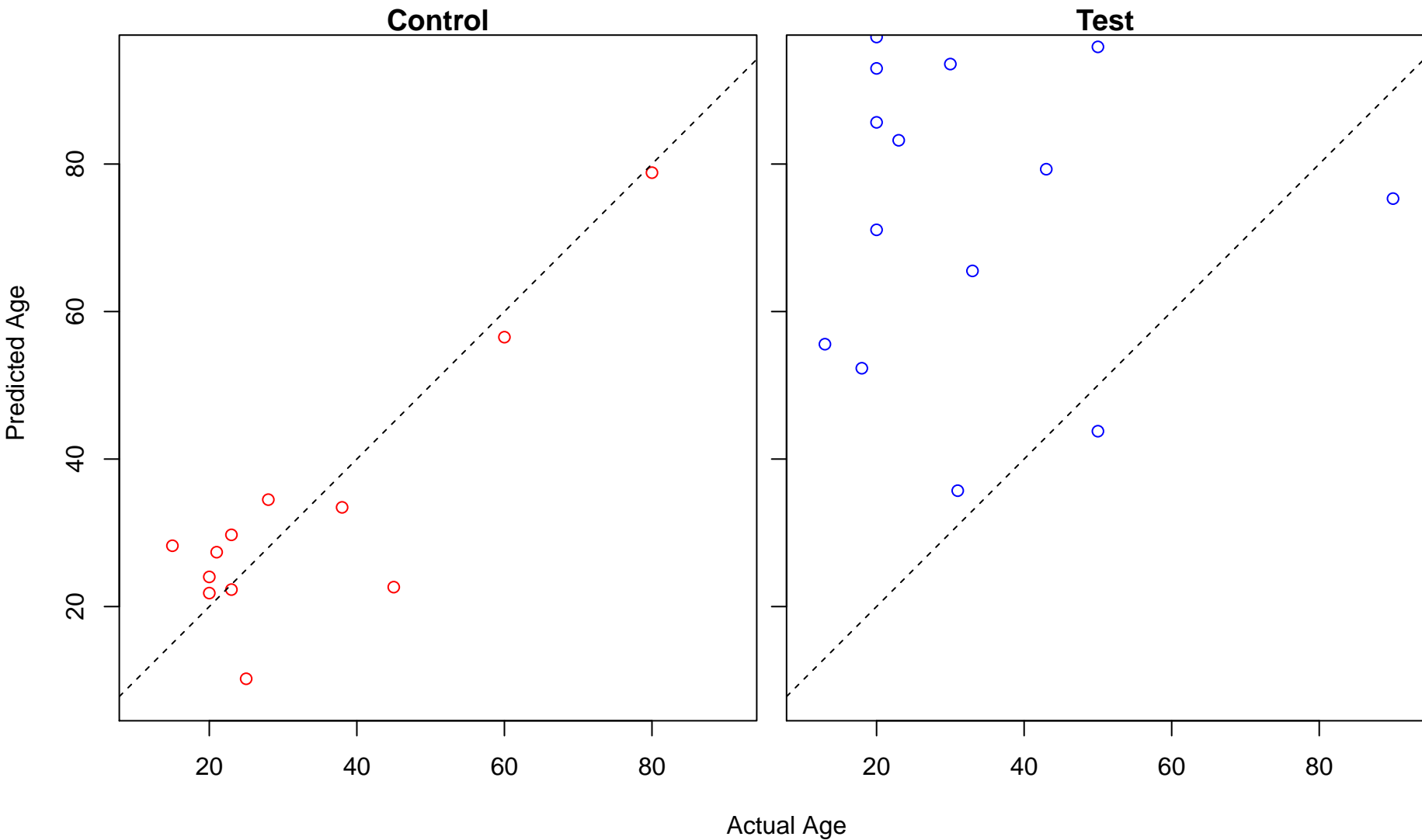


Actual Age

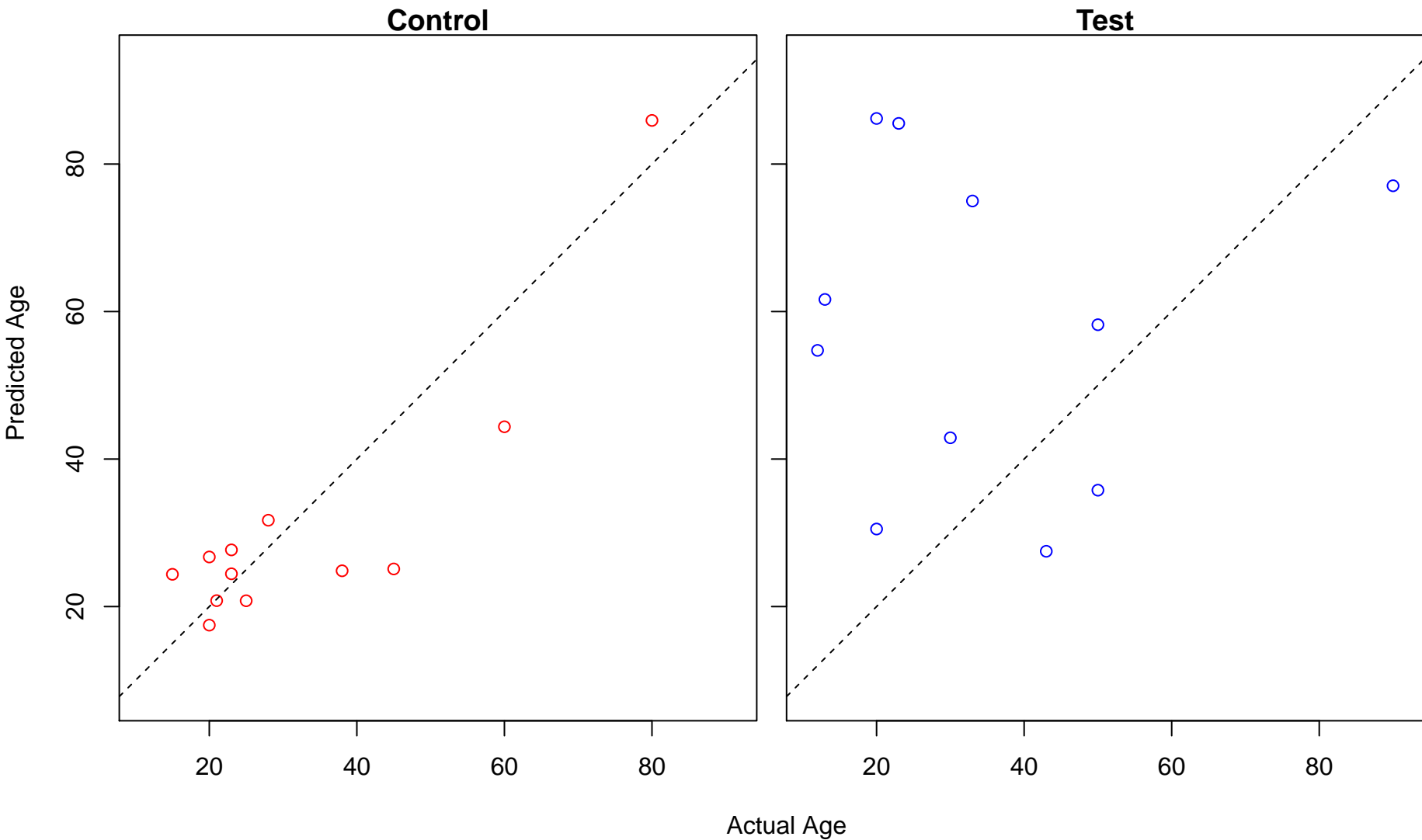
protein carboxylation (Score: 10.445623)



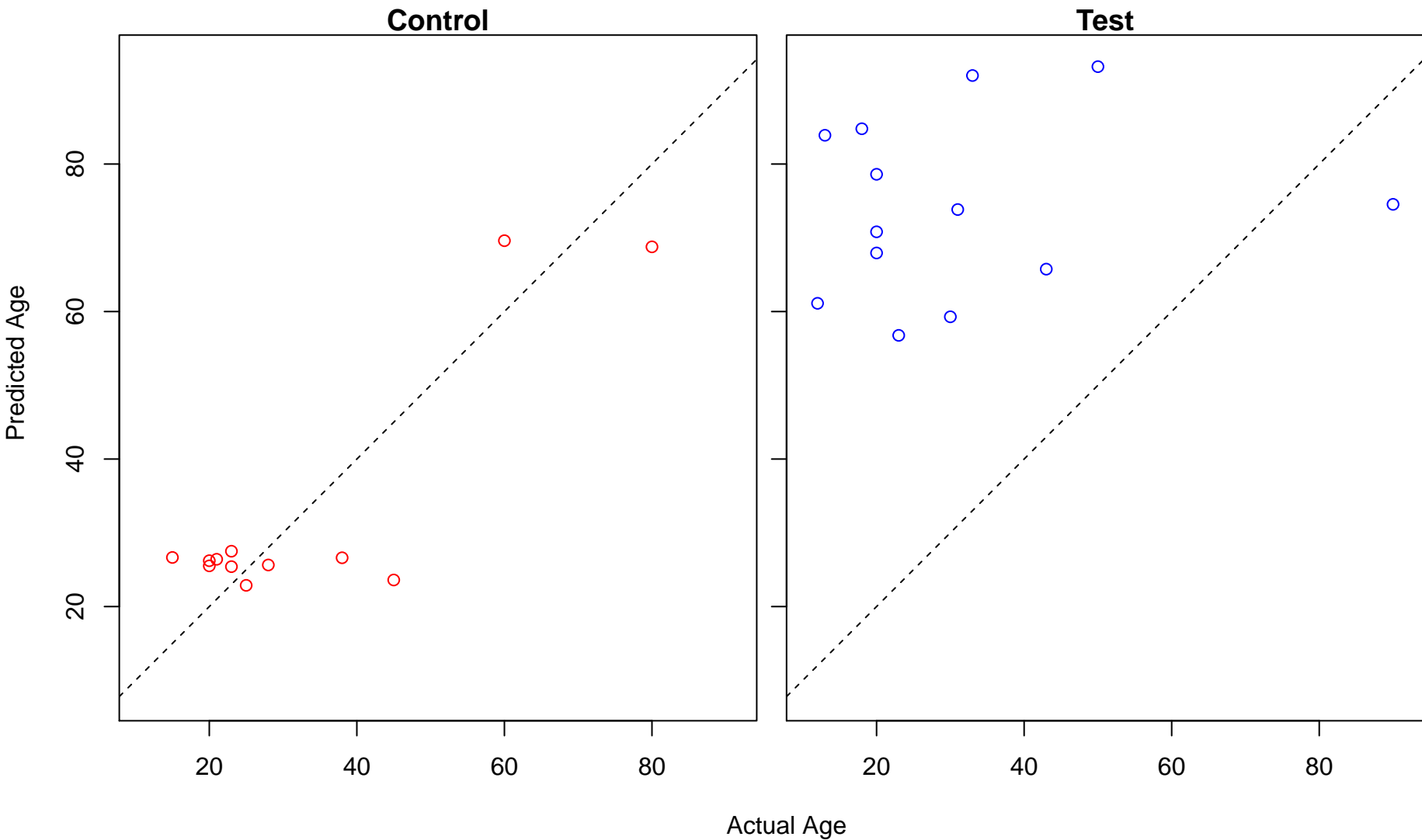
negative regulation of transcription by competitive promoter binding (Score: 10.443665)



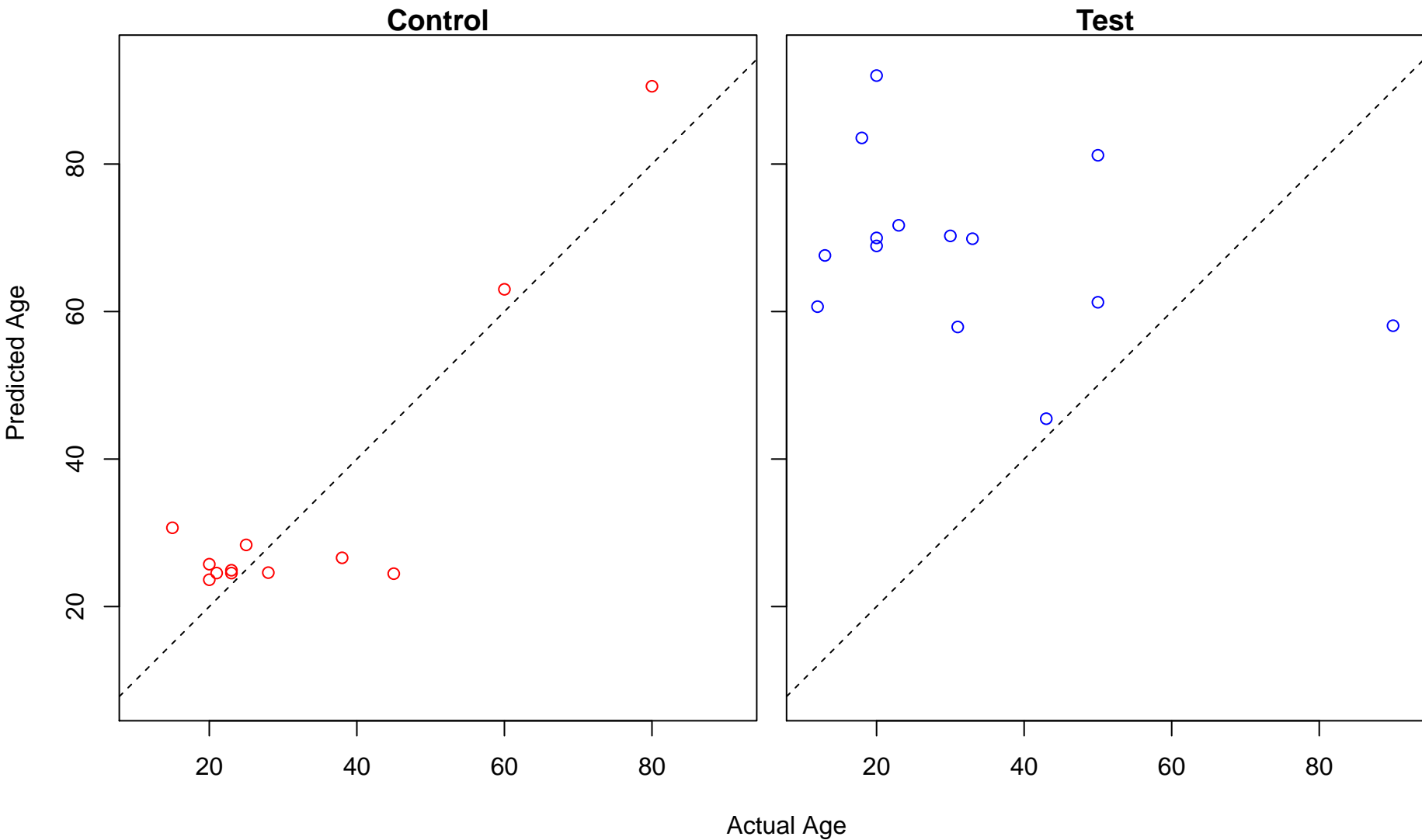
negative regulation of chromosome organization (Score: 10.434282)



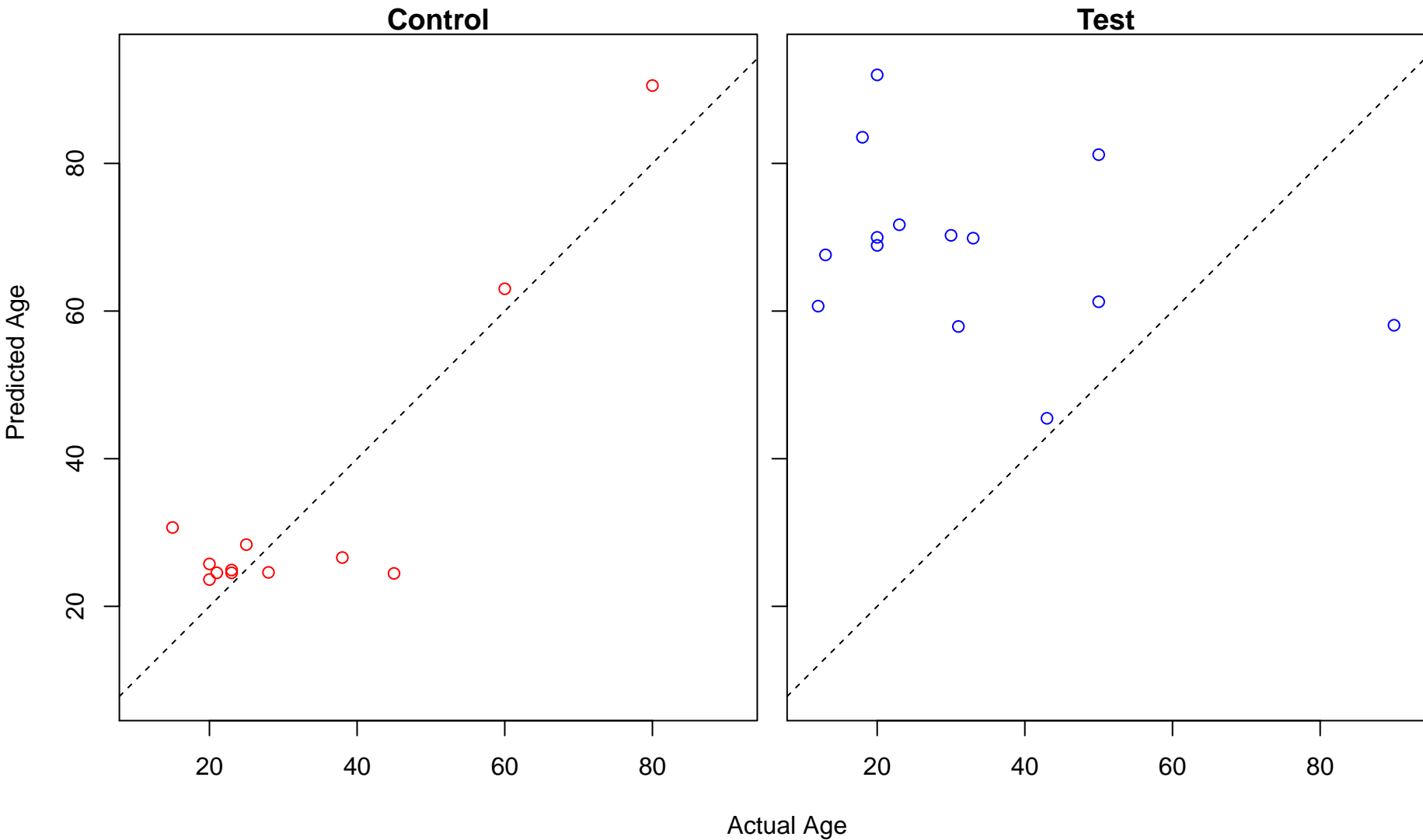
macrophage chemotaxis (Score: 10.427551)



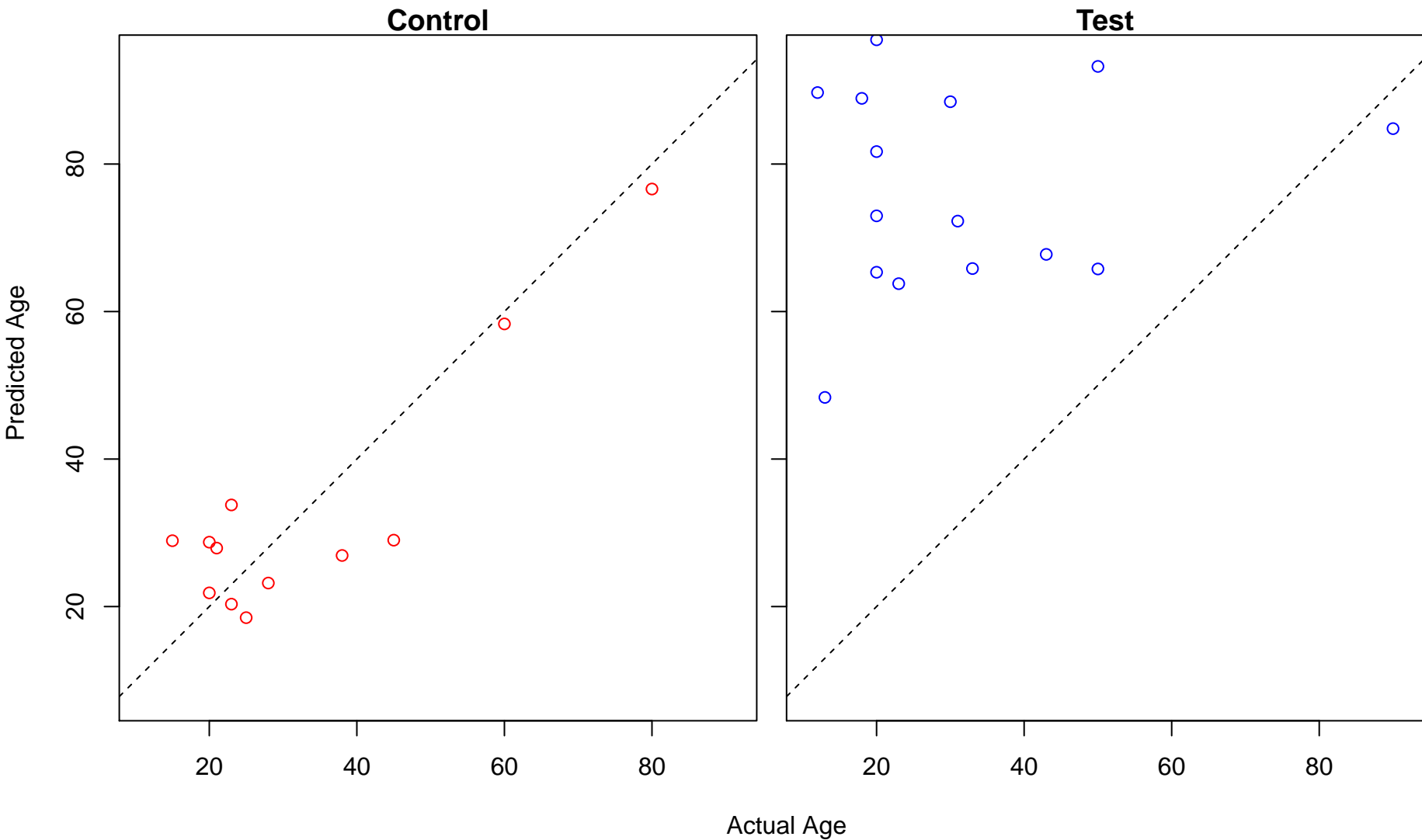
regulation of establishment of protein localization to chromosome (Score: 10.422790)



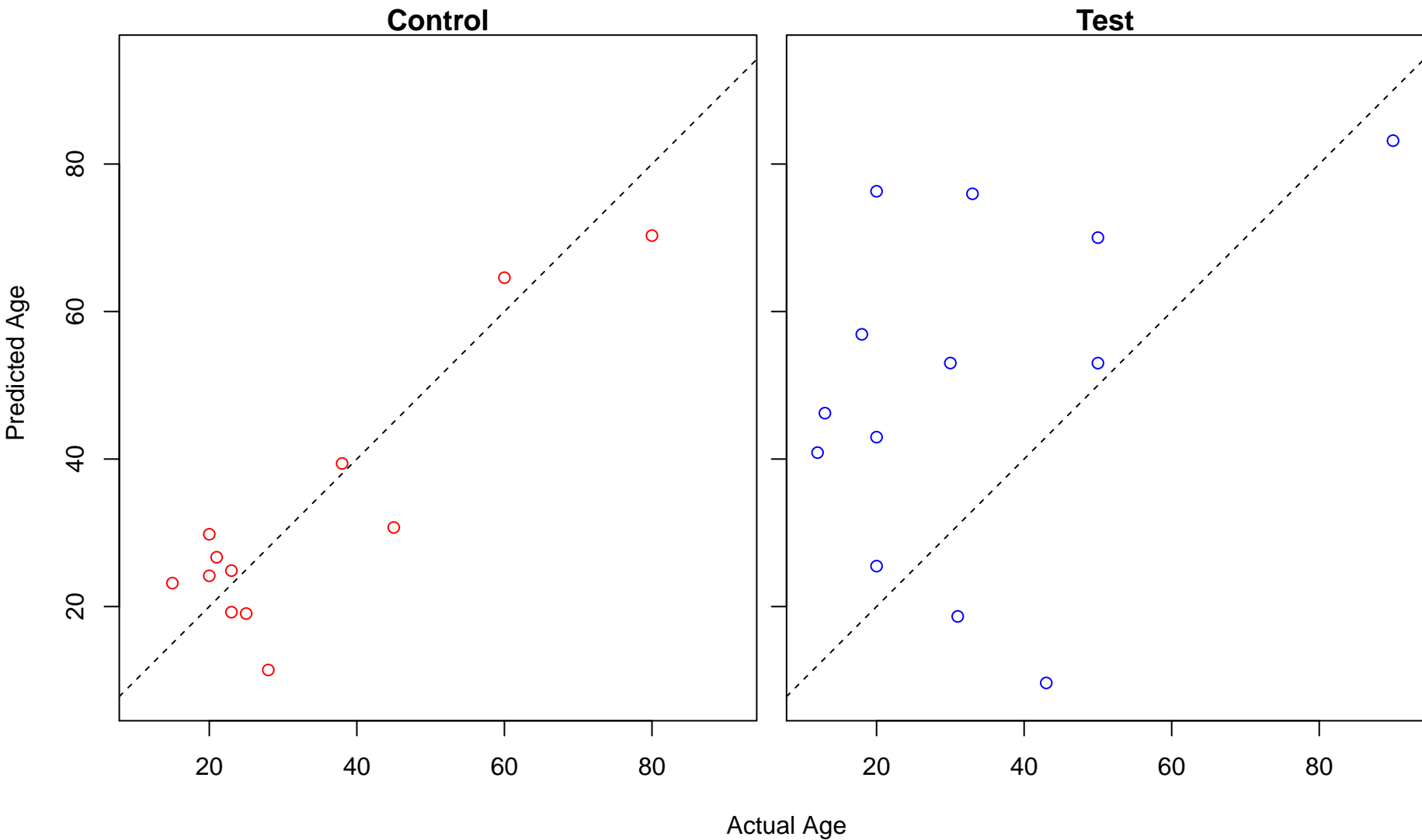
regulation of establishment of protein localization to telomere (Score: 10.422790)



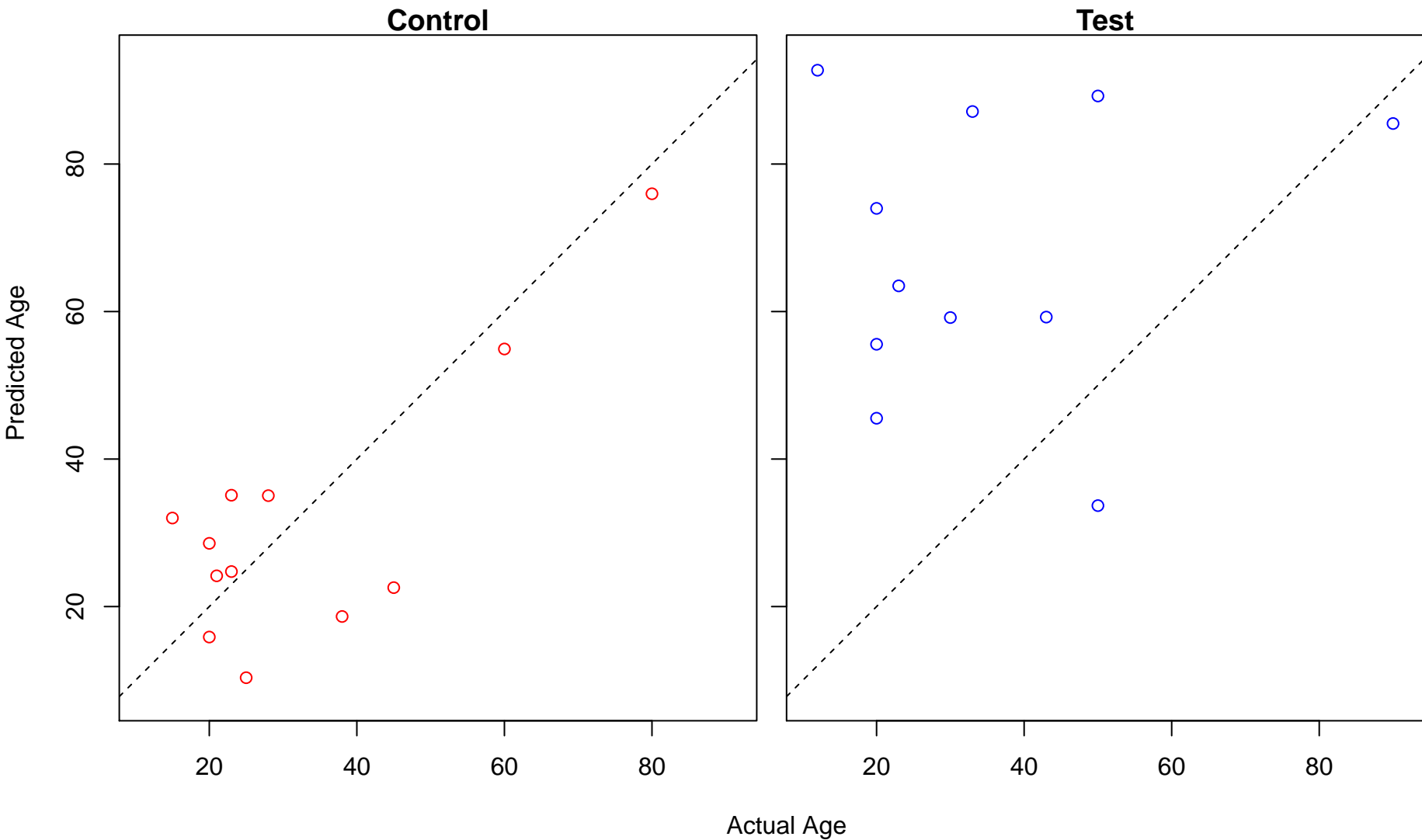
interleukin-1-mediated signaling pathway (Score: 10.419074)



photoreceptor cell development (Score: 10.418190)

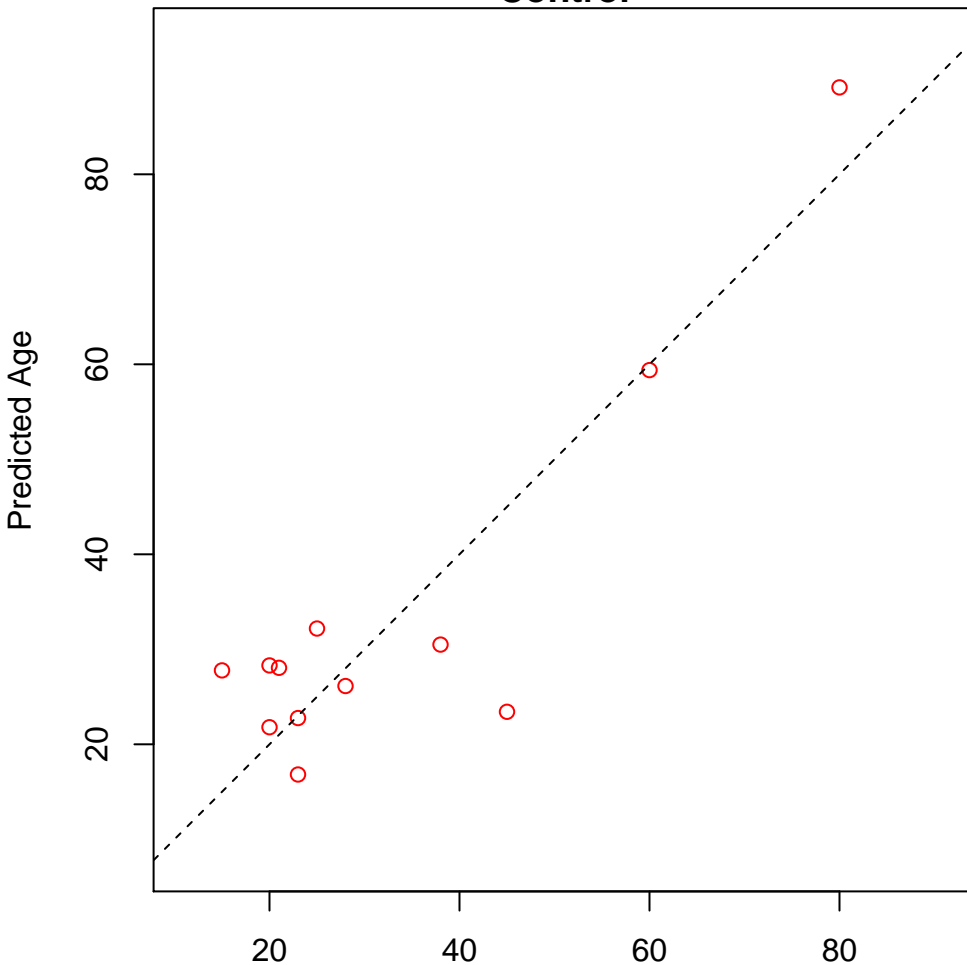


protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score: 10.414232)

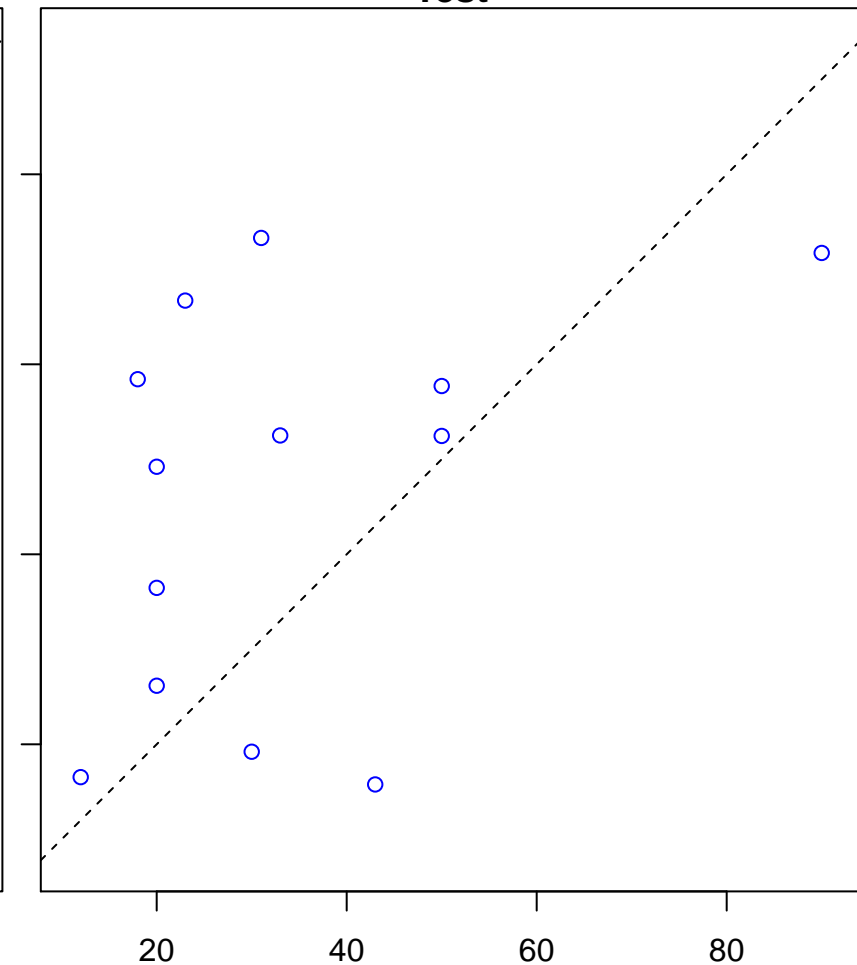


response to external biotic stimulus (Score: 10.412964)

Control

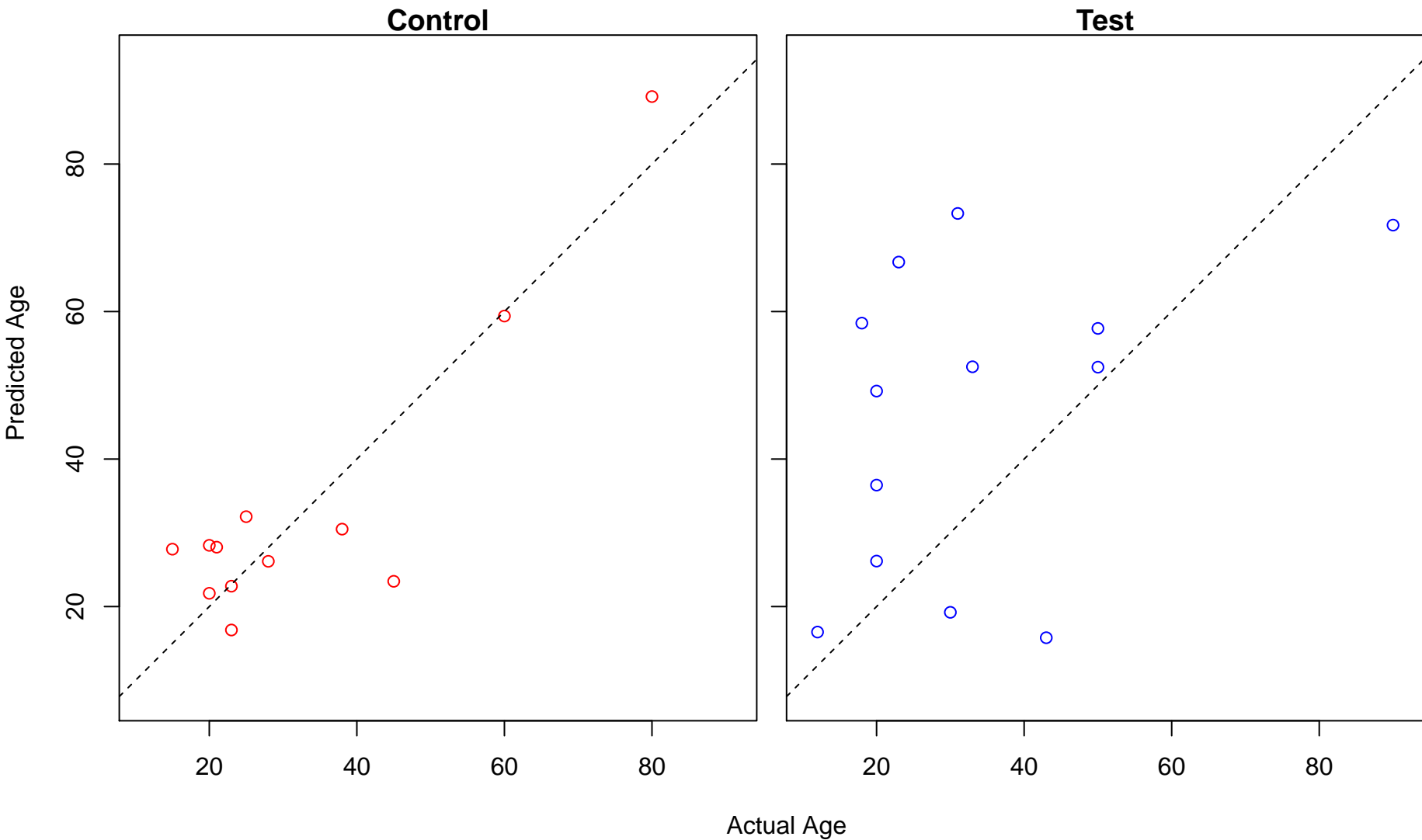


Test

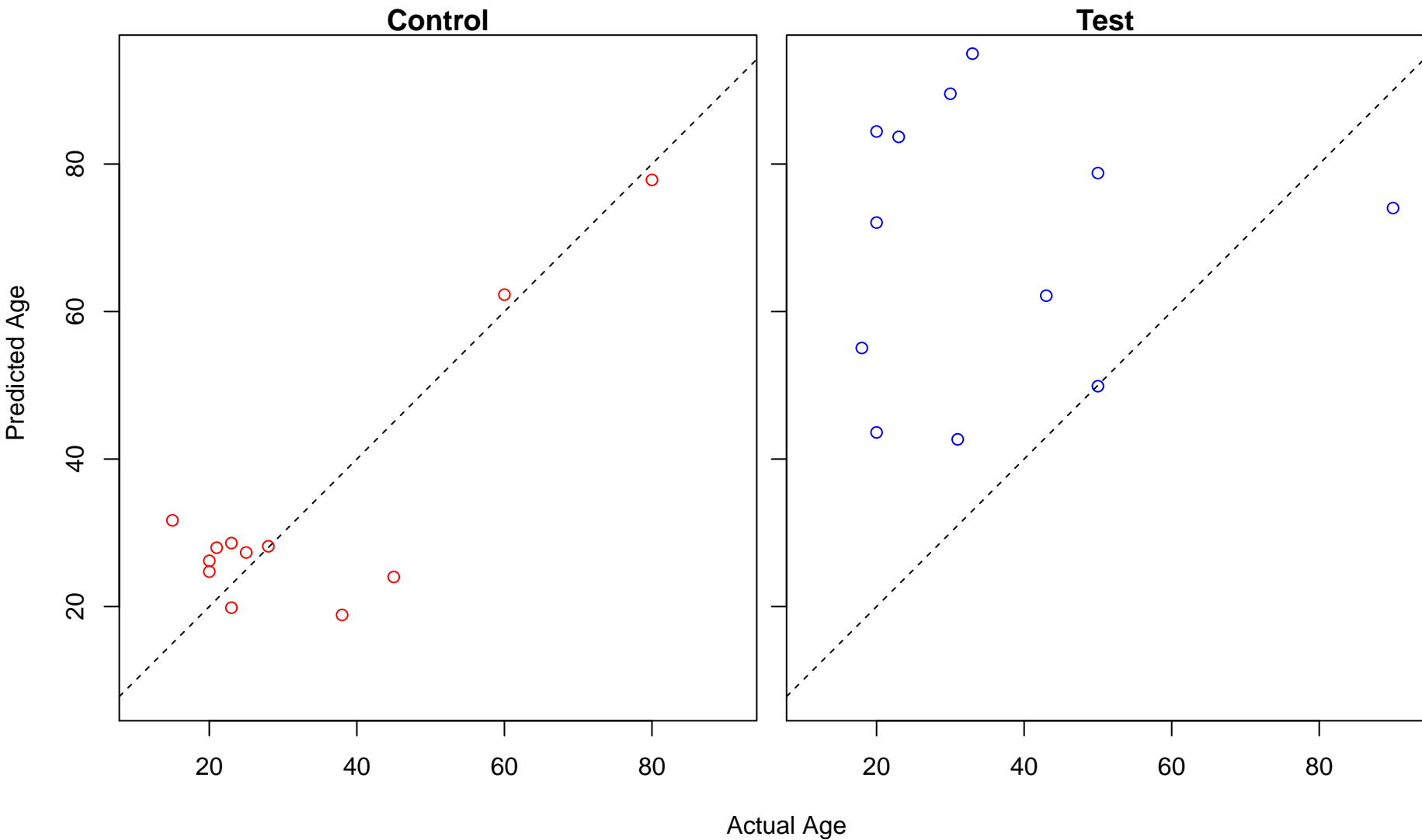


Actual Age

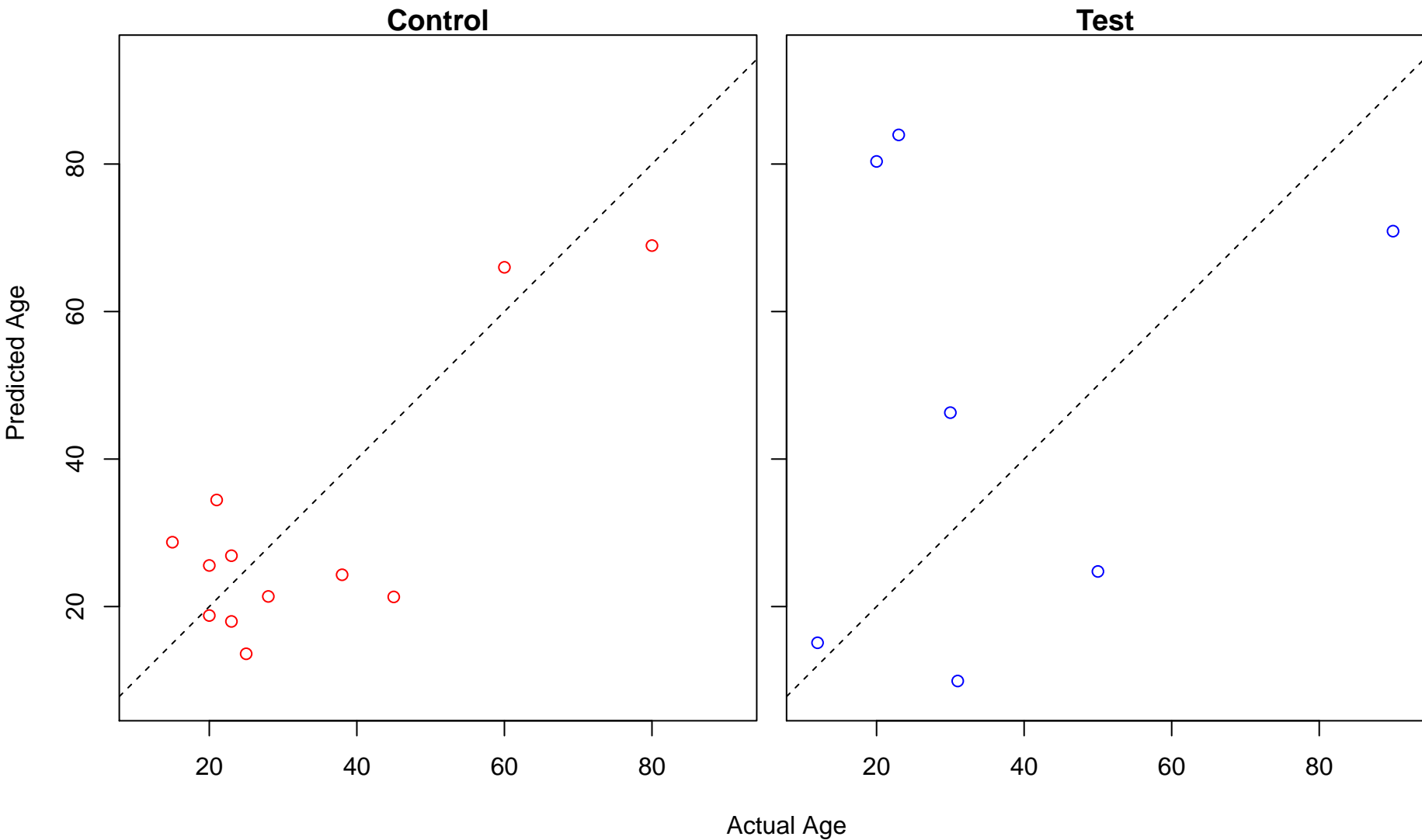
response to other organism (Score: 10.412964)



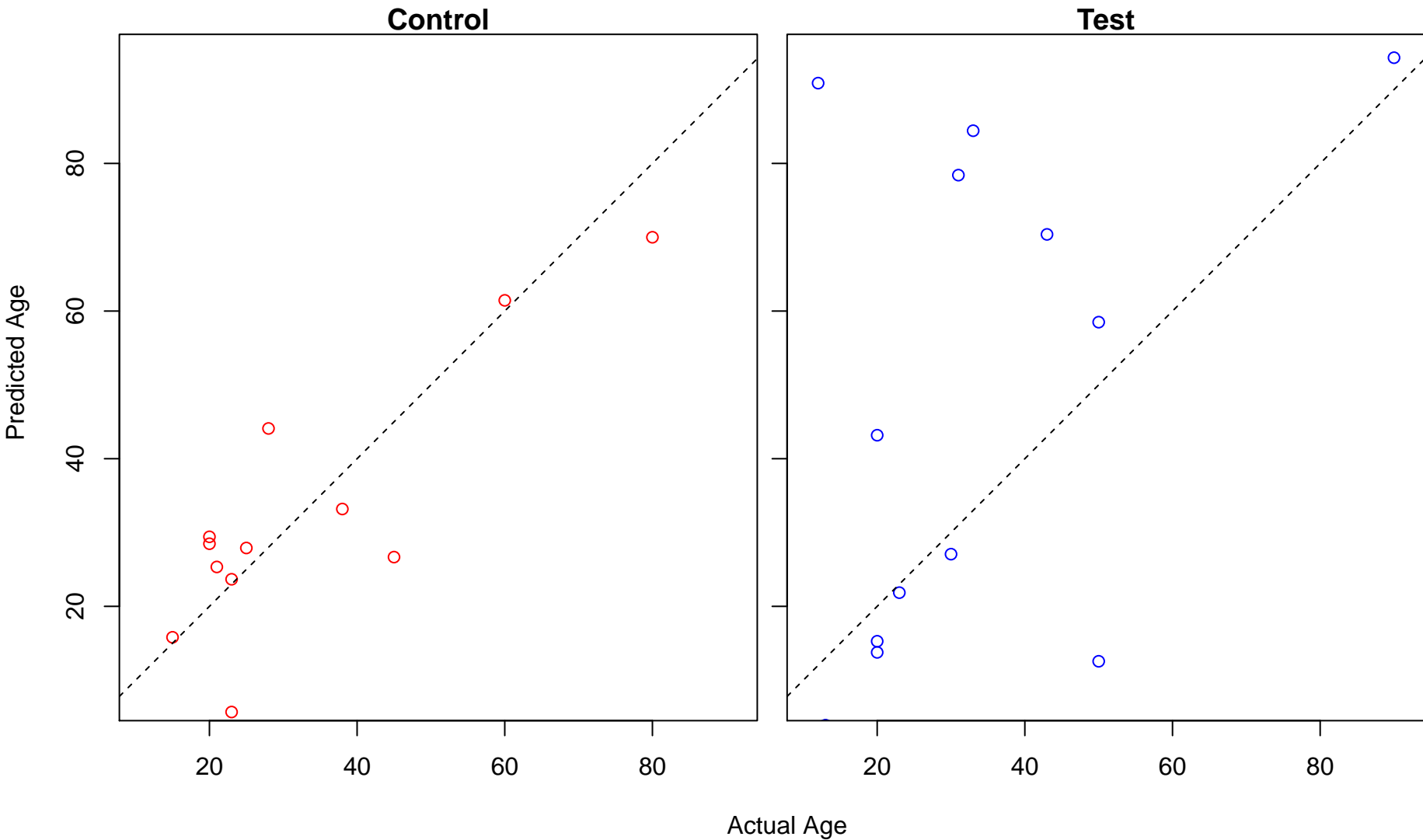
endothelial cell differentiation (Score: 10.406195)



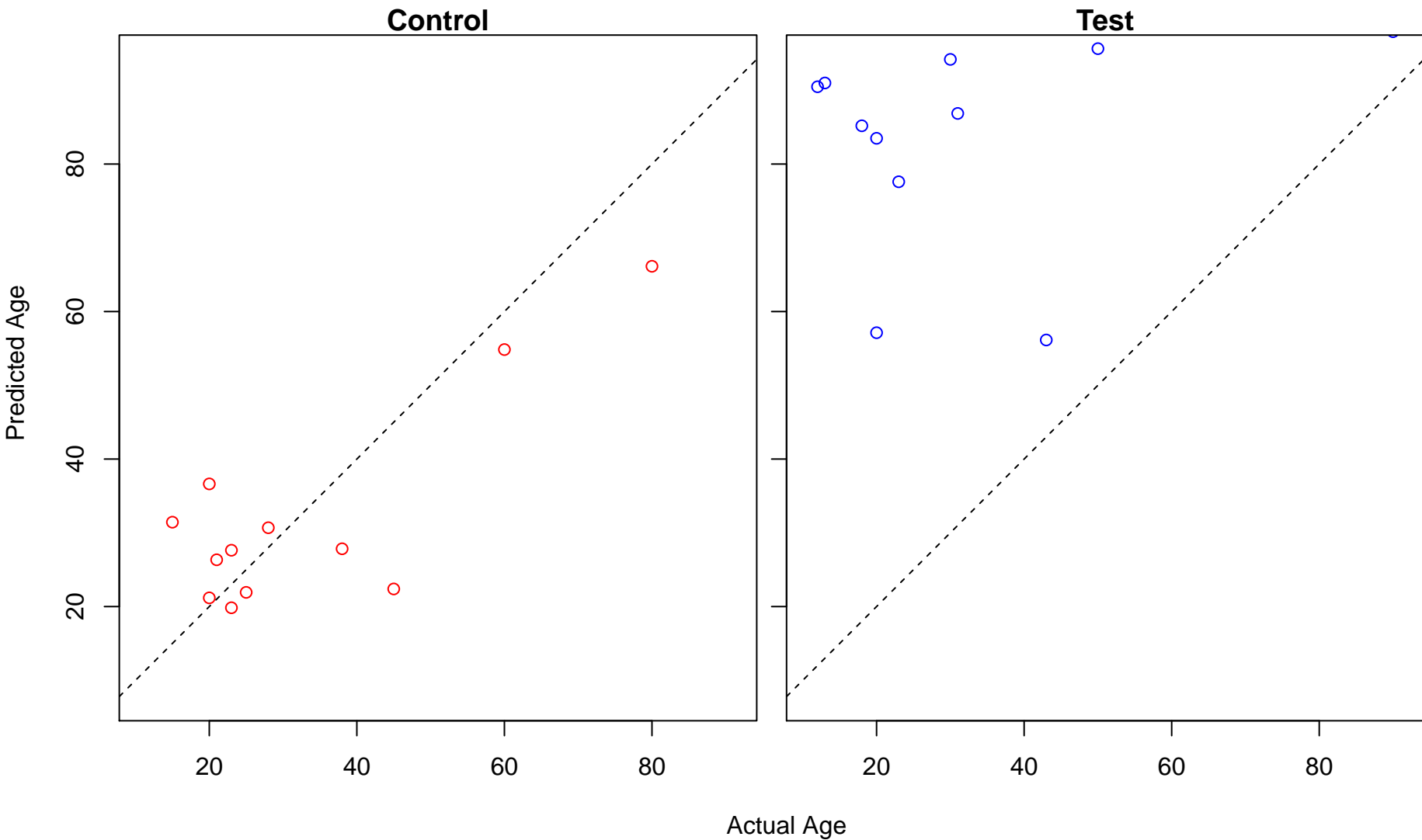
androgen biosynthetic process (Score: 10.405131)



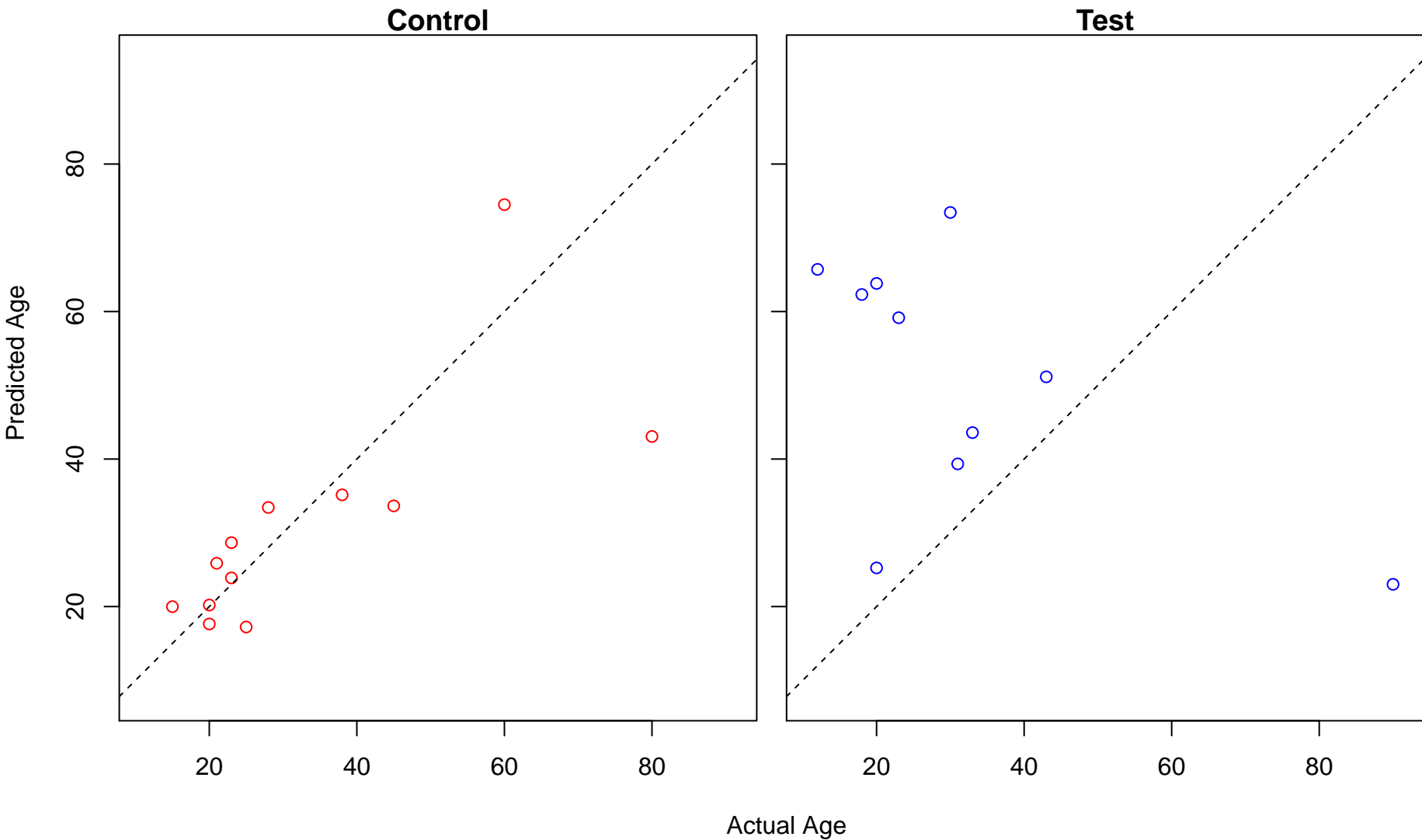
pyrimidine nucleoside metabolic process (Score: 10.400417)



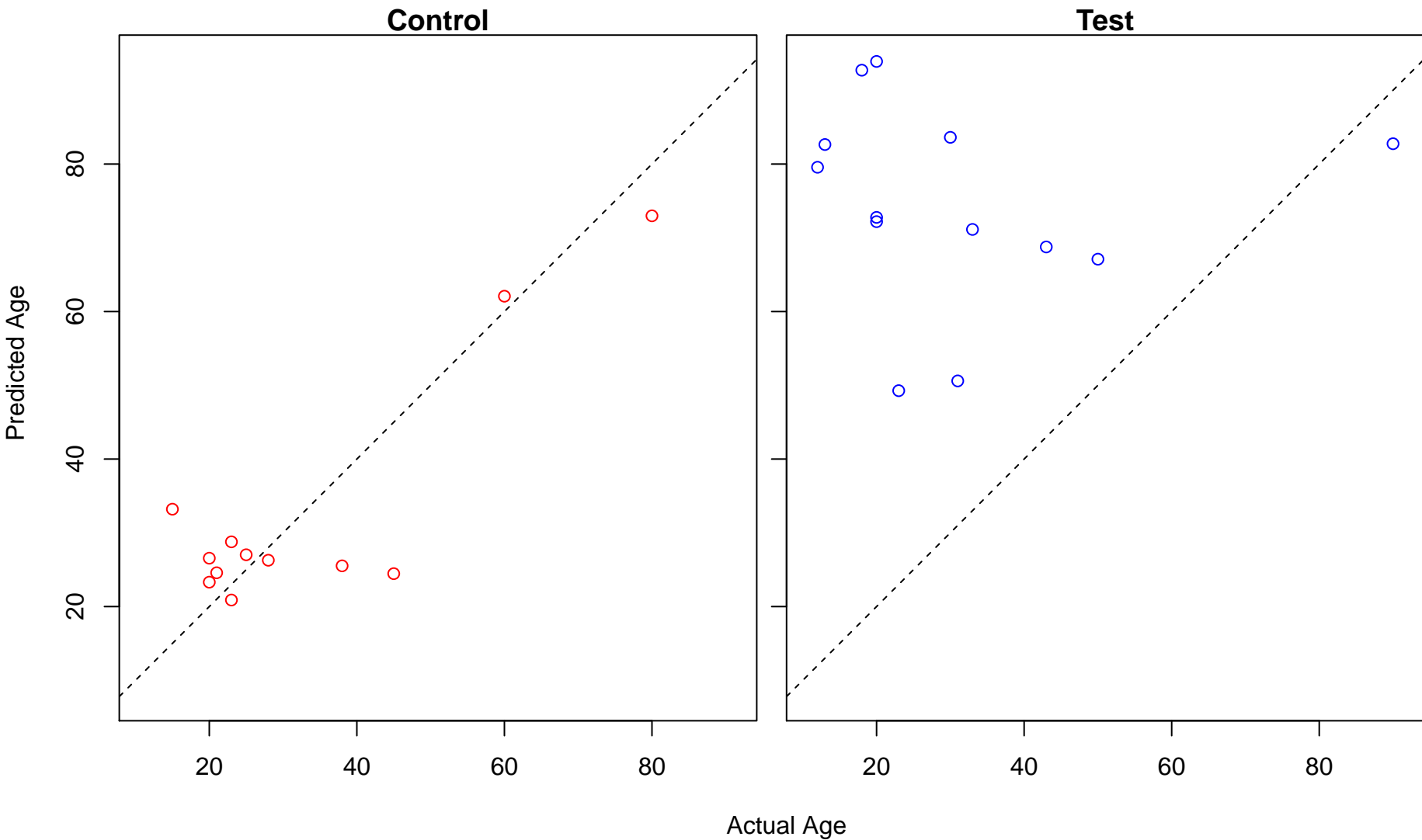
negative regulation of anion transmembrane transport (Score: 10.385135)



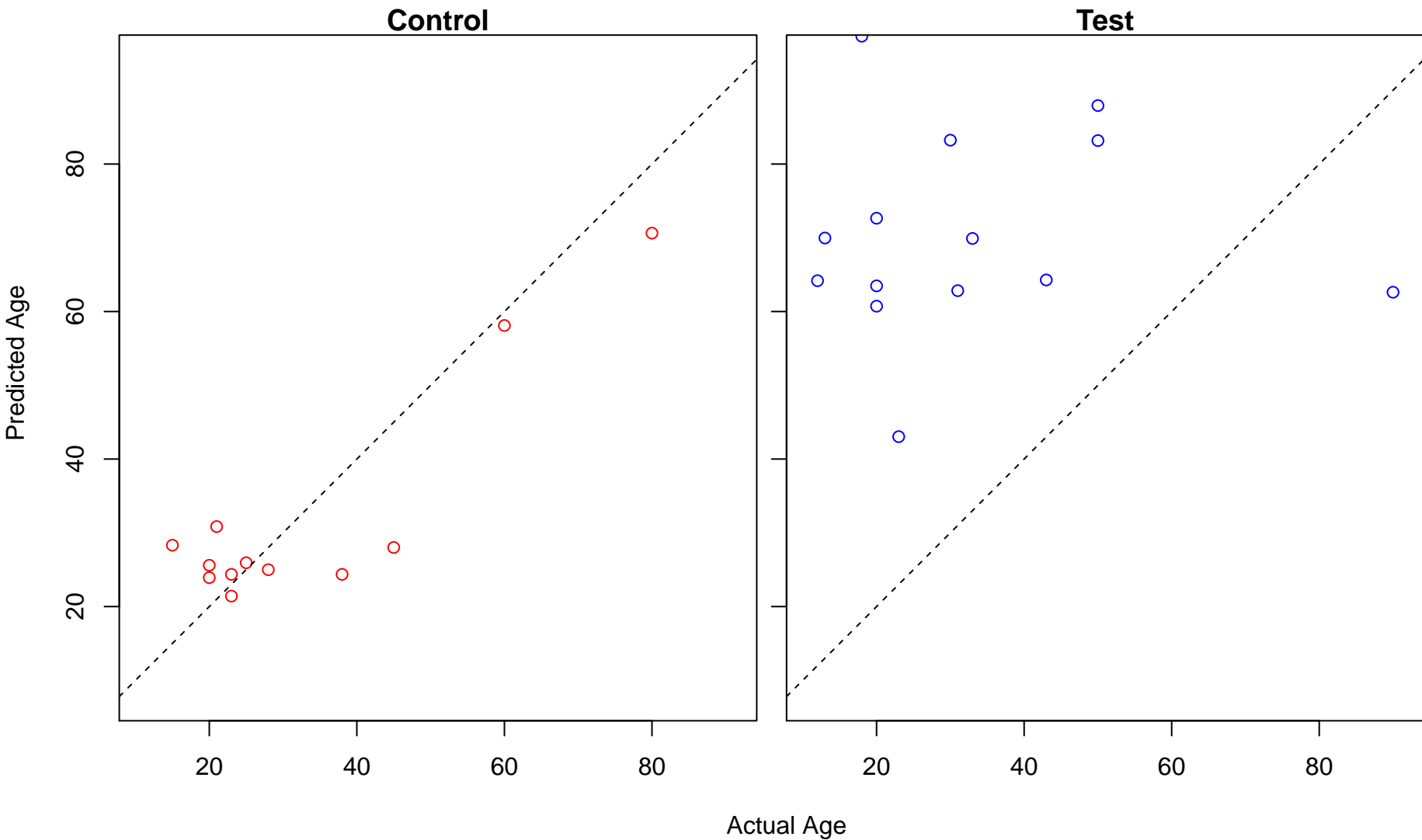
apoptotic nuclear changes (Score: 10.381190)



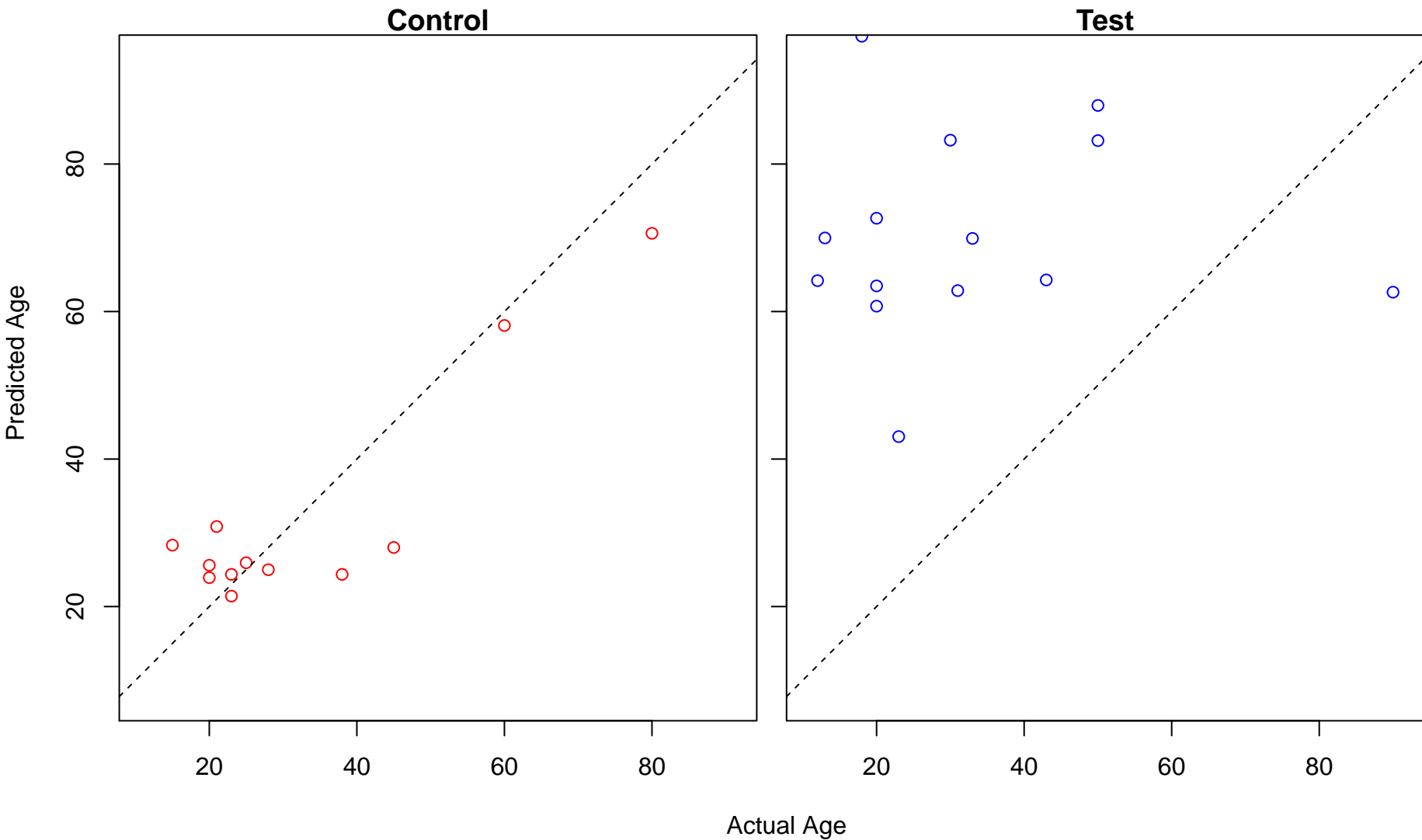
response to fluid shear stress (Score: 10.378282)



epithelium migration (Score: 10.377151)

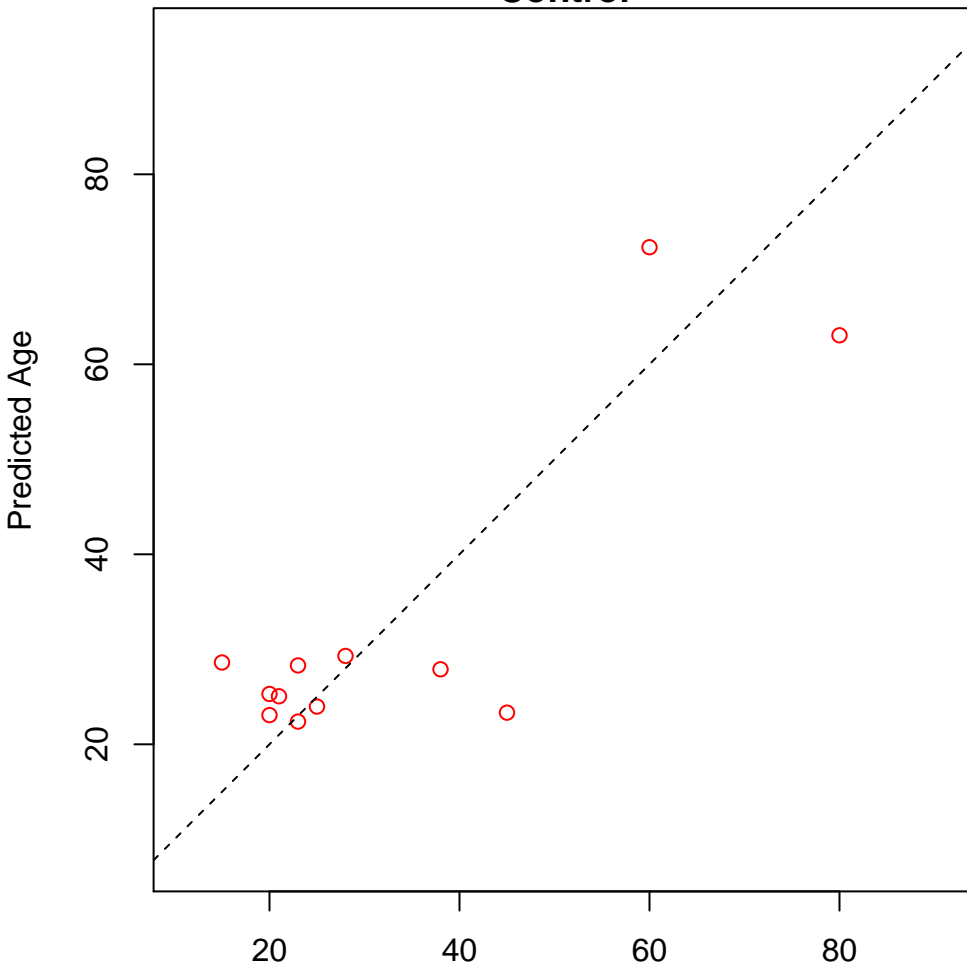


tissue migration (Score: 10.369199)

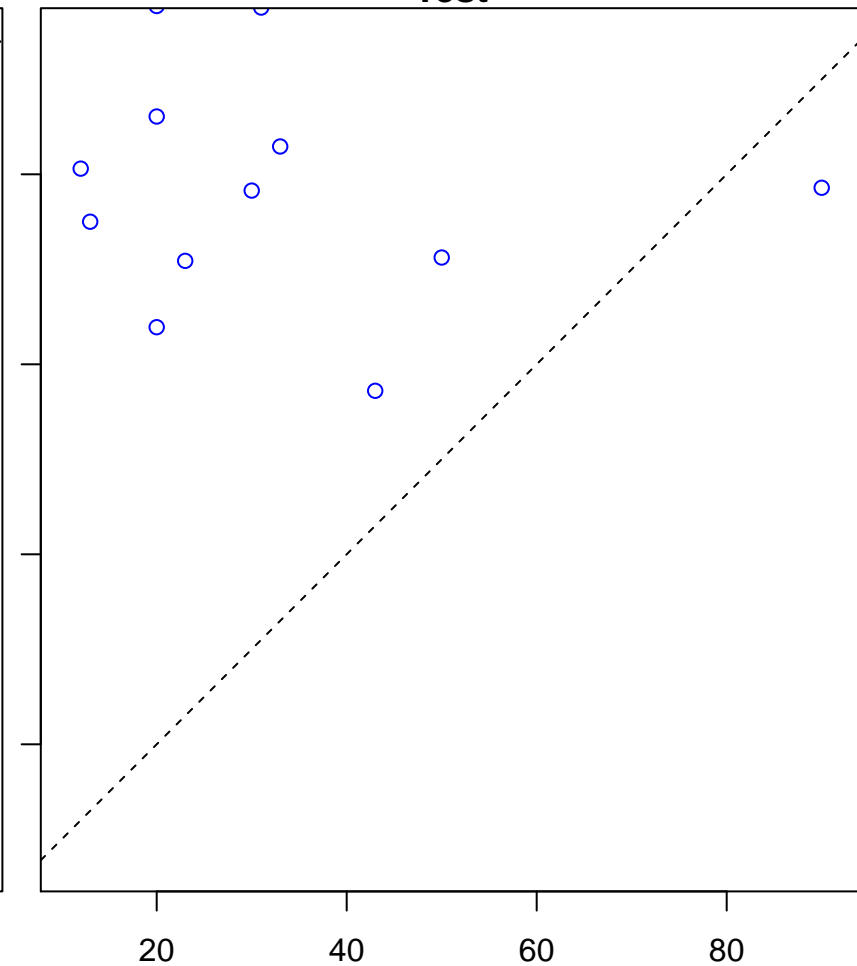


regulation of osteoclast differentiation (Score: 10.361136)

Control

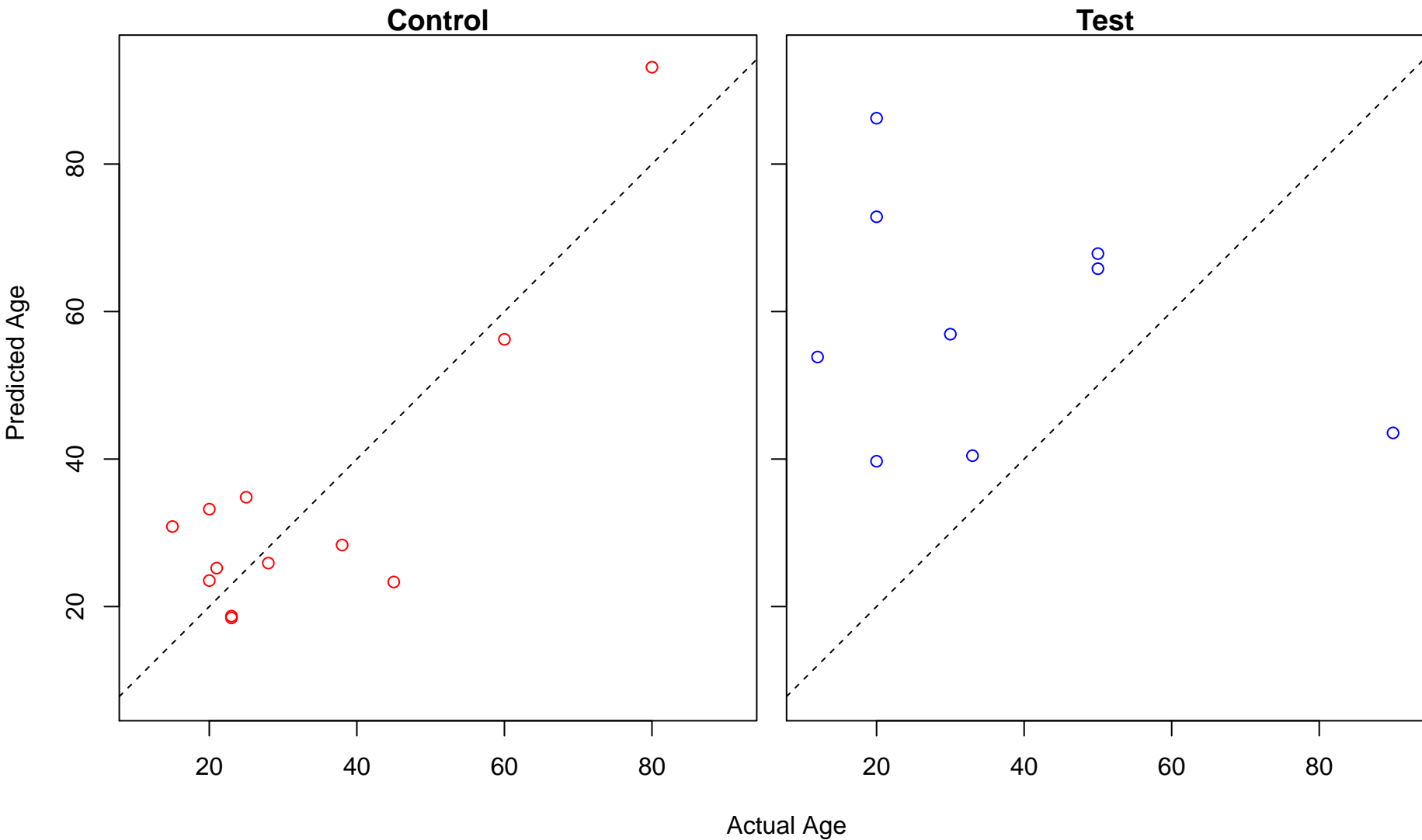


Test

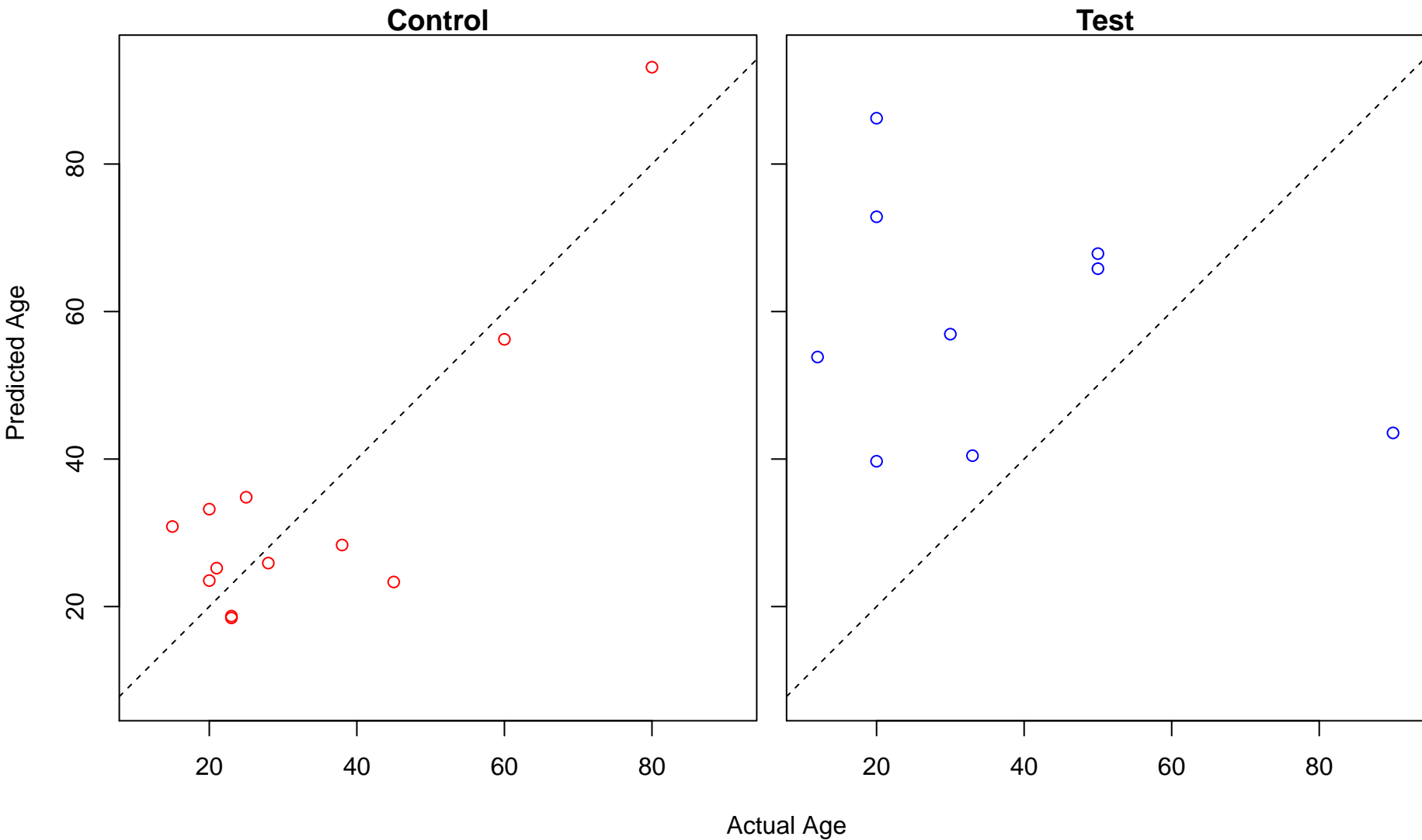


Actual Age

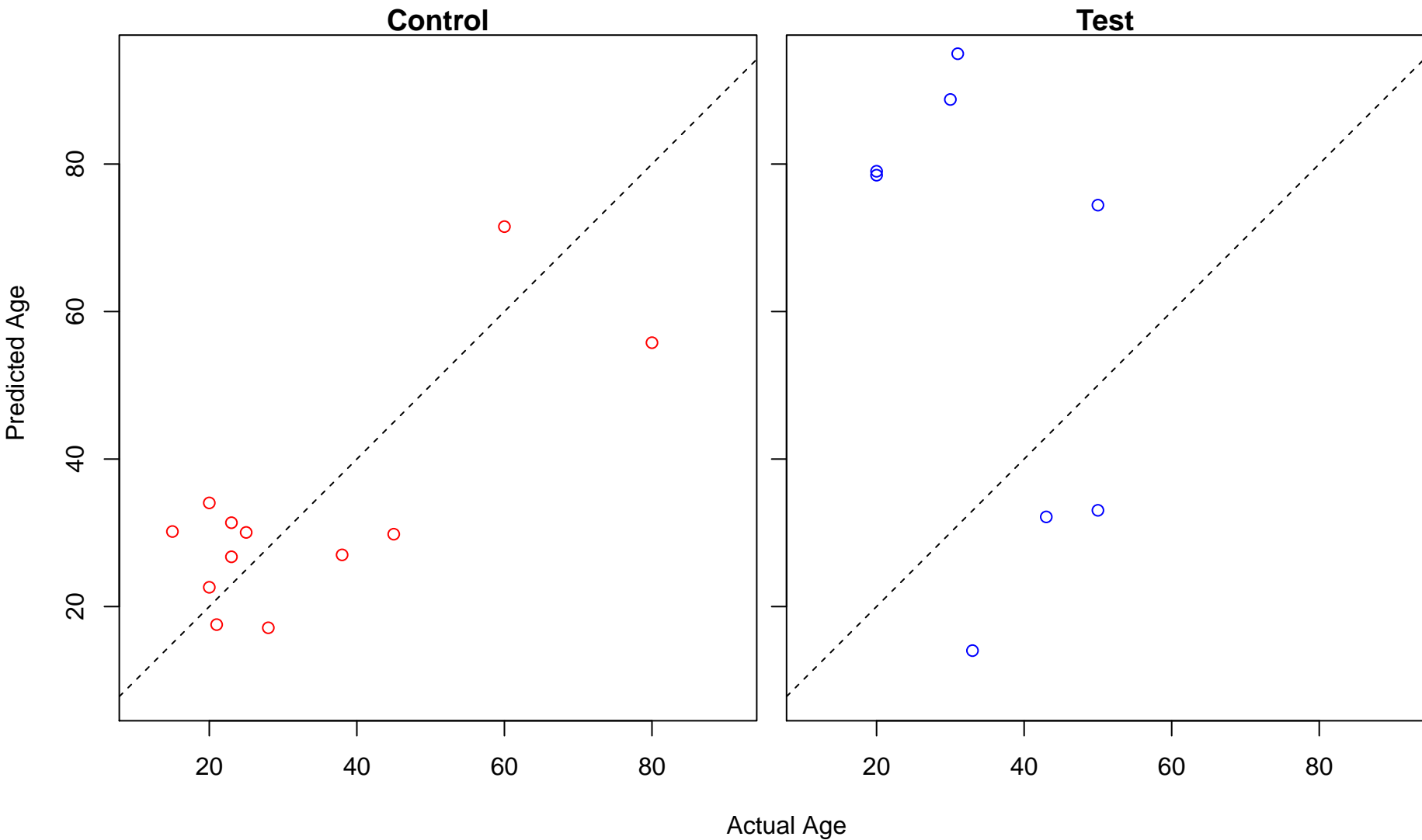
neuronal stem cell division (Score: 10.360674)



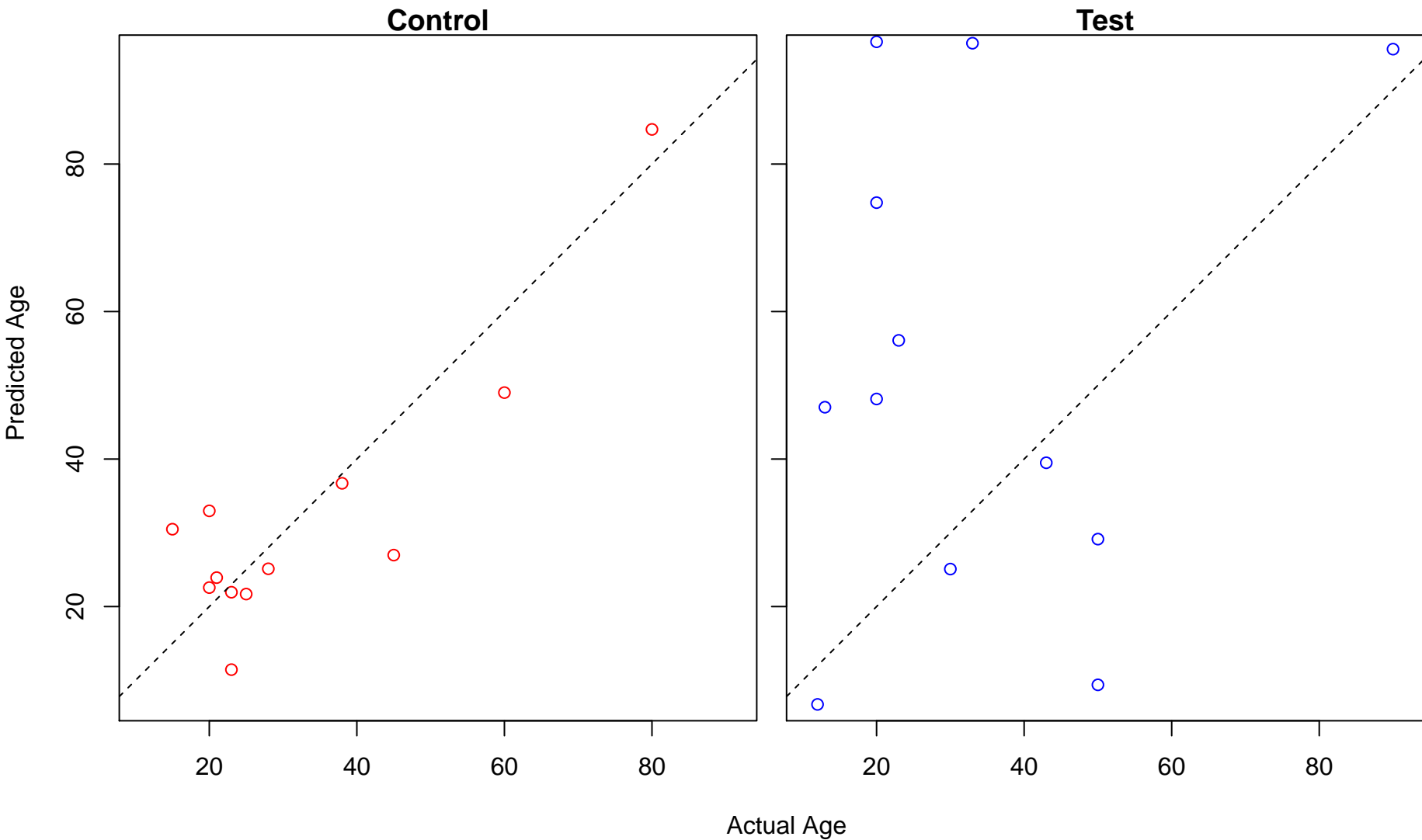
neuroblast division (Score: 10.360674)



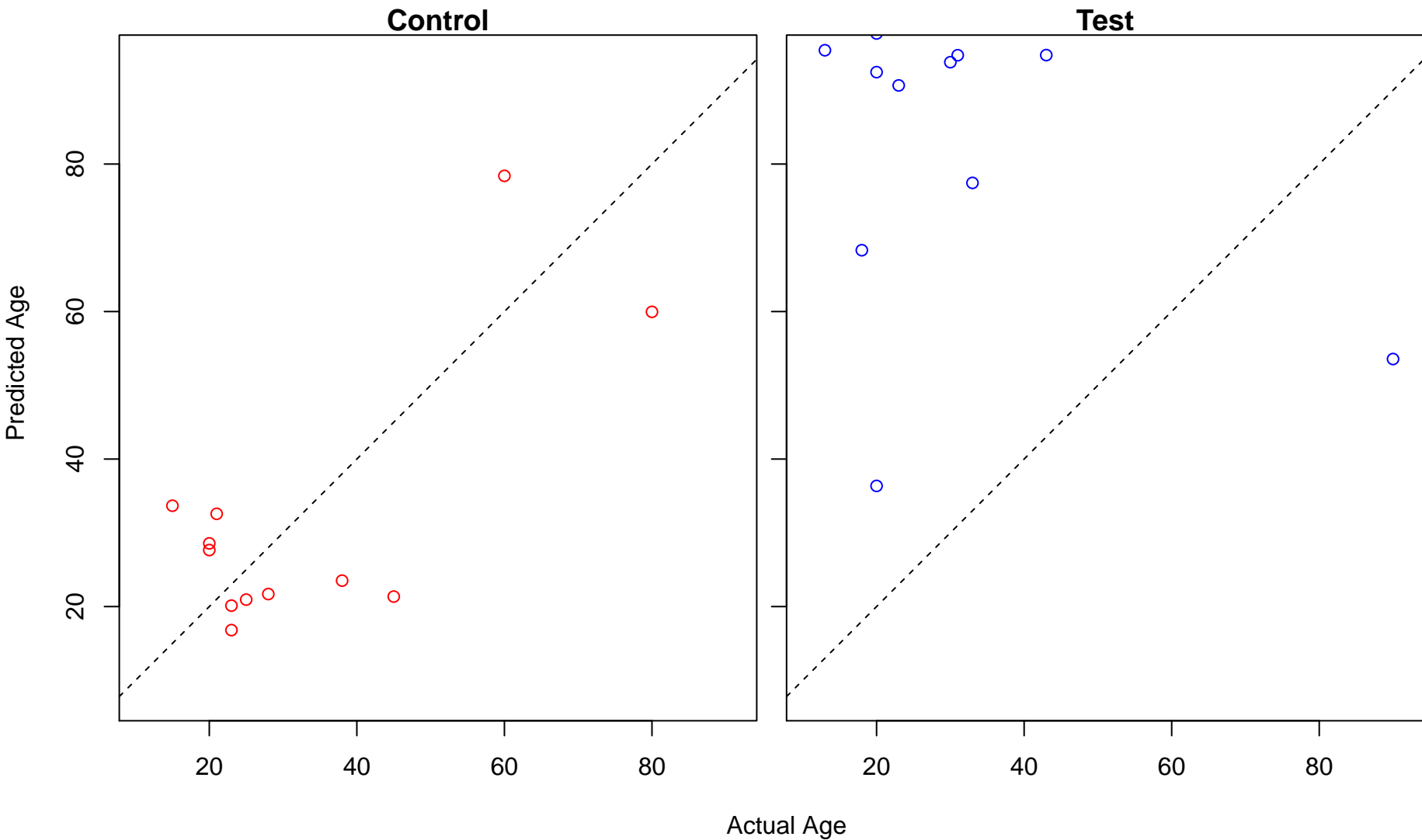
fructose metabolic process (Score: 10.353924)



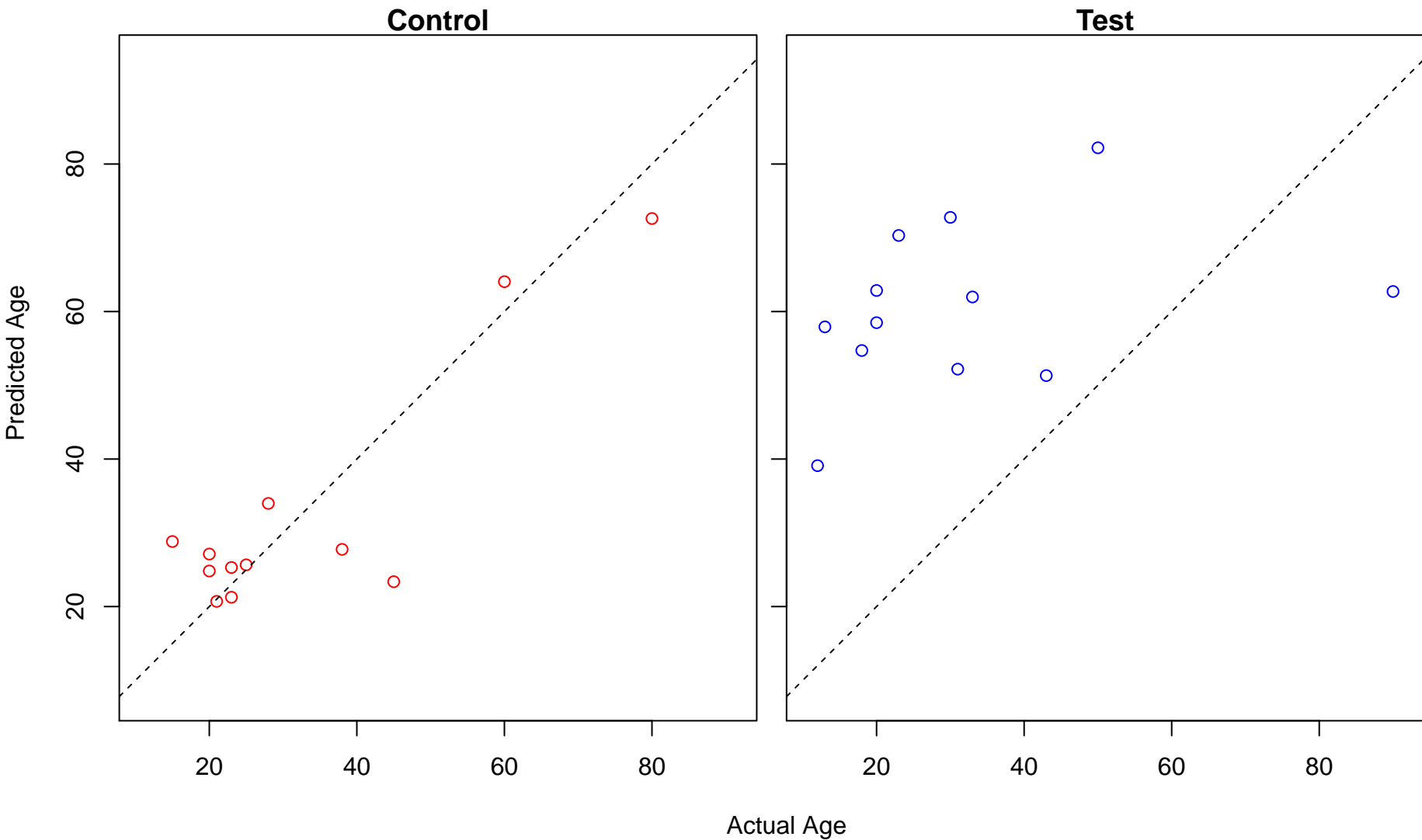
cell maturation (Score: 10.350402)



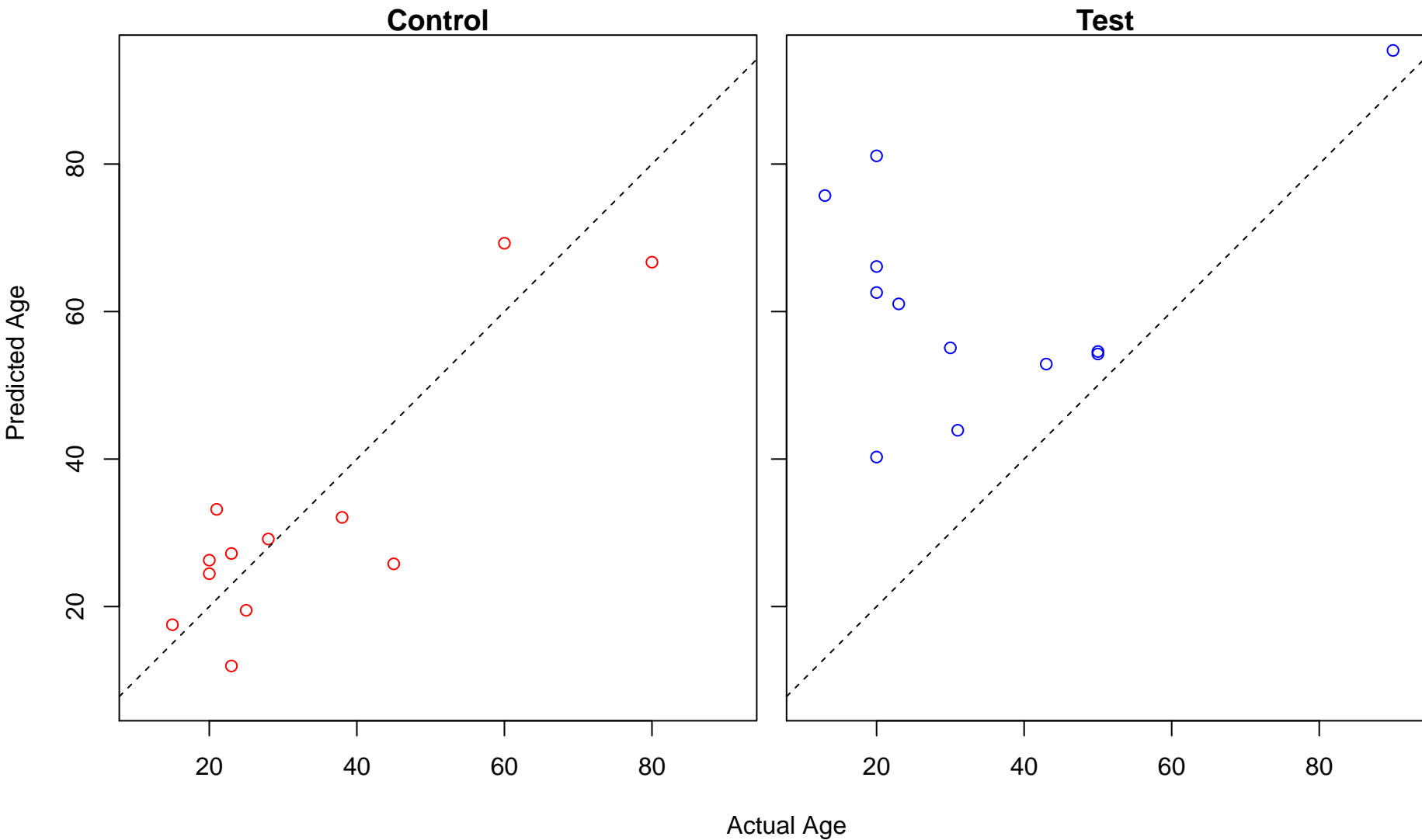
iron coordination entity transport (Score: 10.347646)



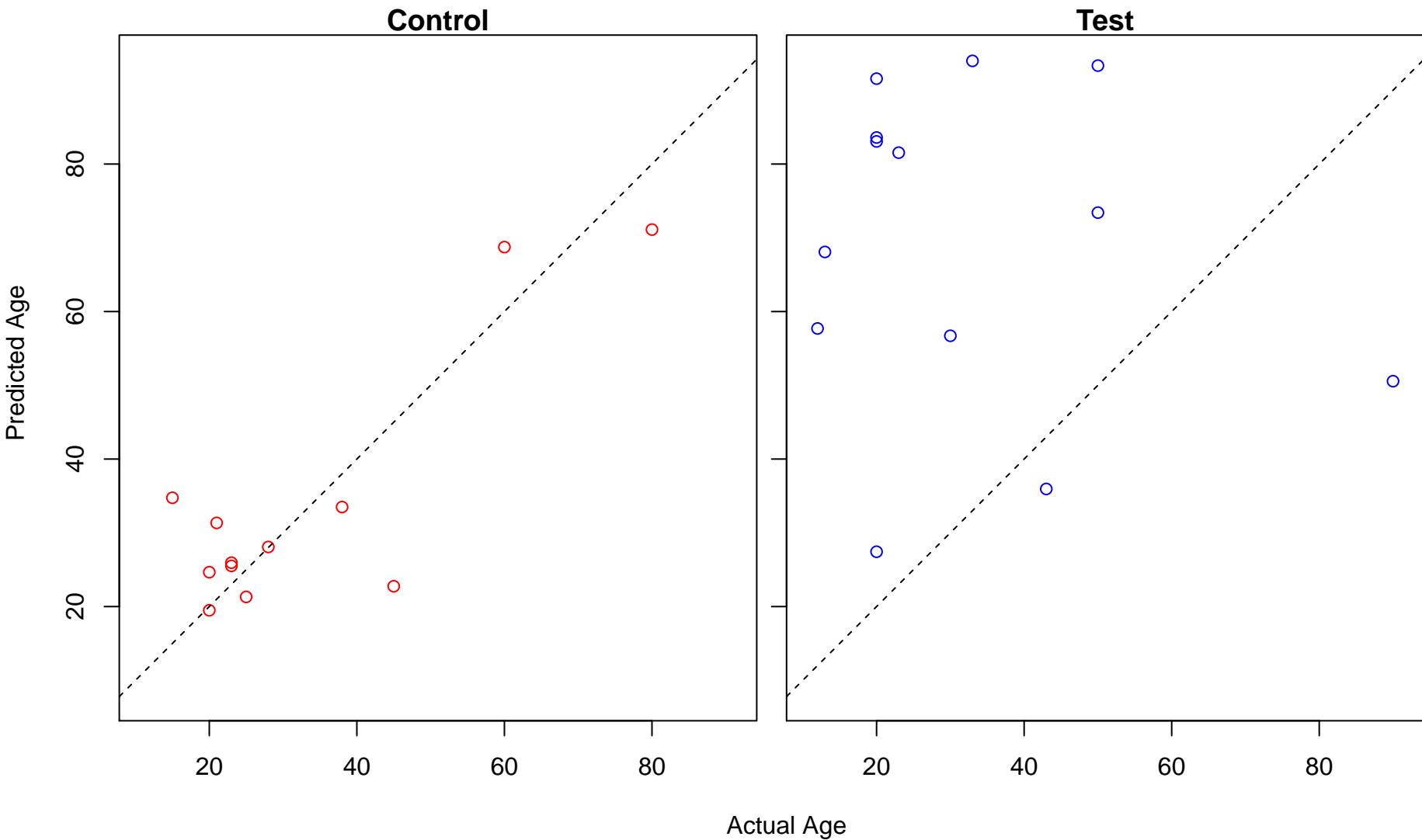
positive regulation of tissue remodeling (Score: 10.344780)



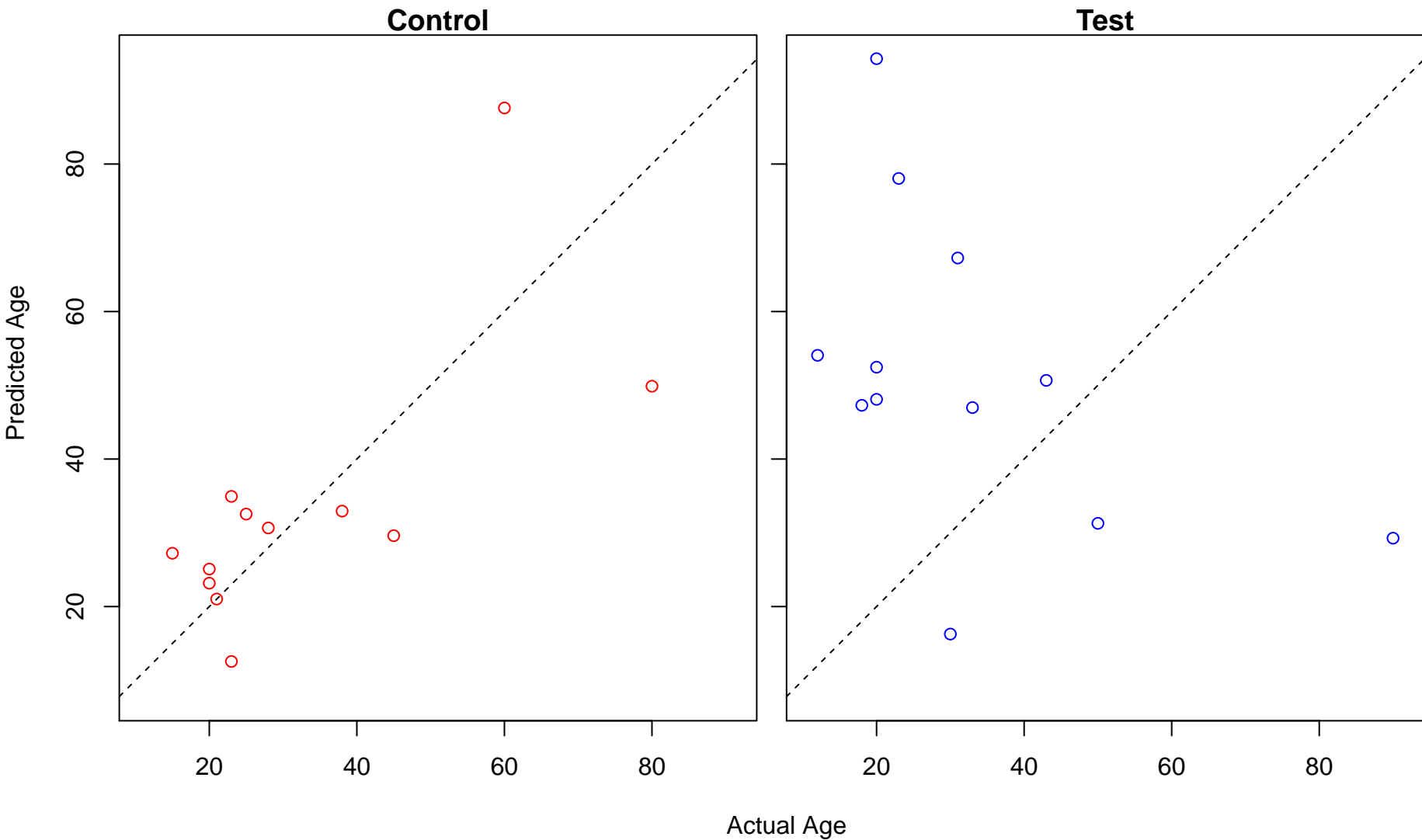
pyrimidine nucleotide metabolic process (Score: 10.344508)



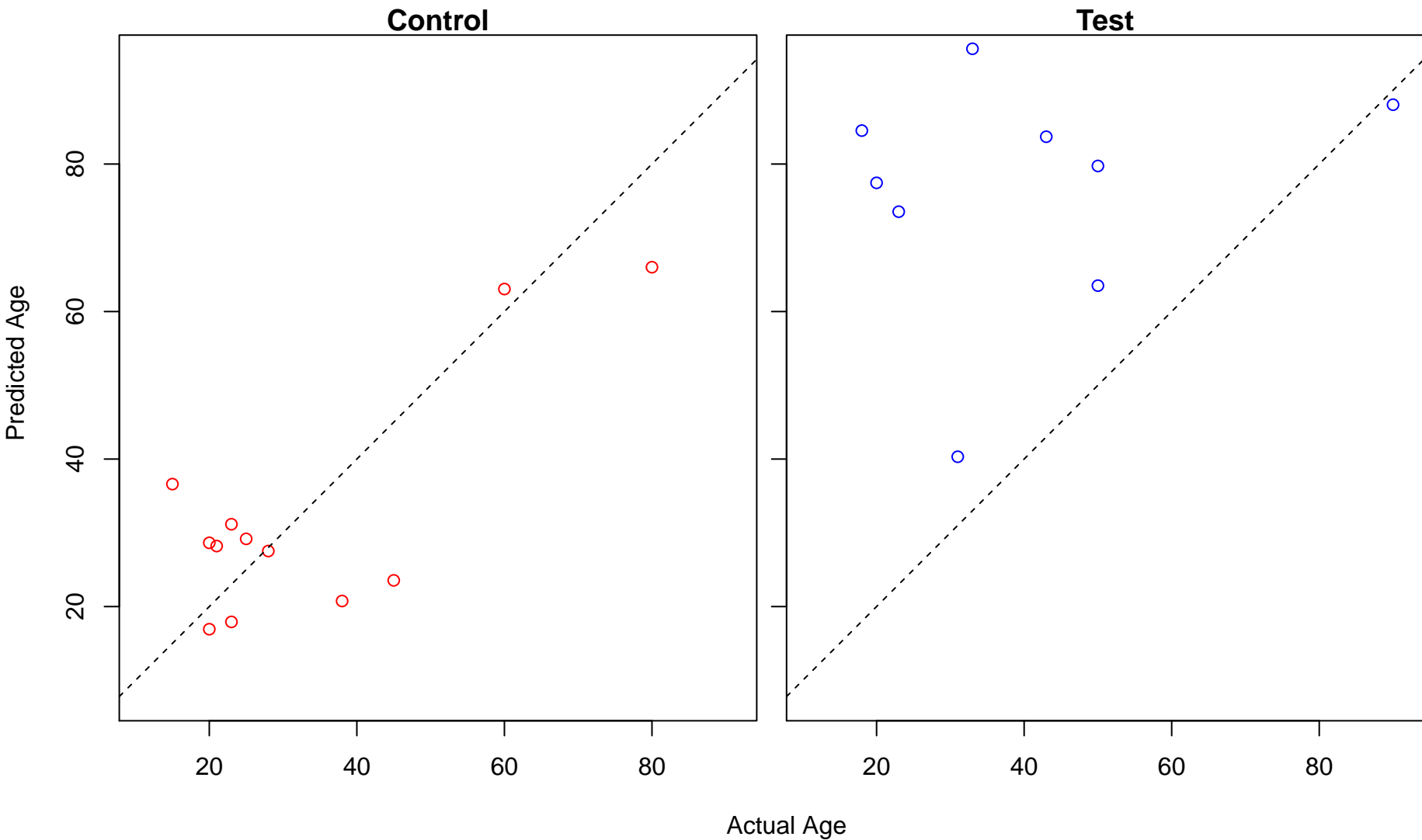
positive regulation of fat cell differentiation (Score: 10.343370)



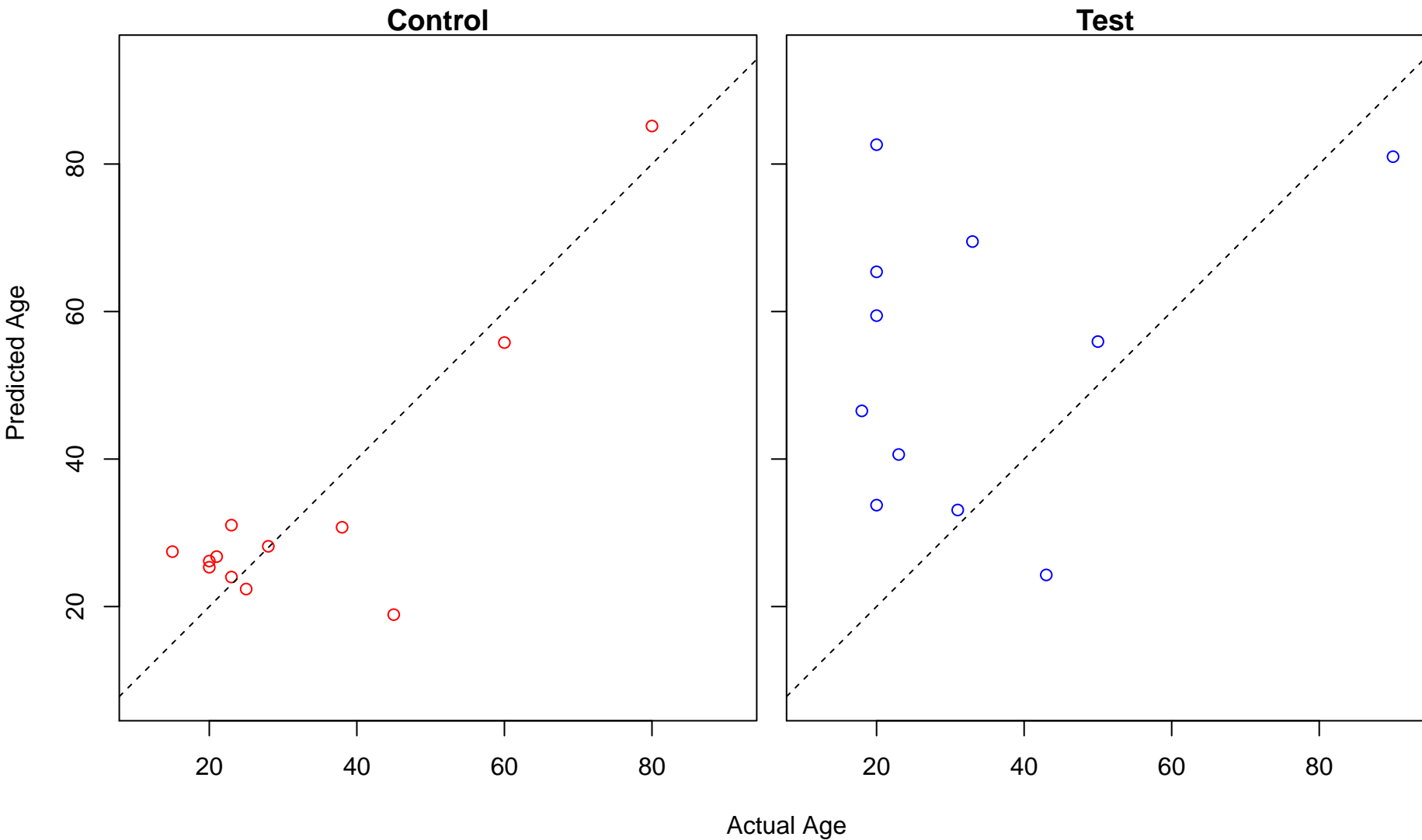
positive regulation of toll-like receptor signaling pathway (Score: 10.339600)



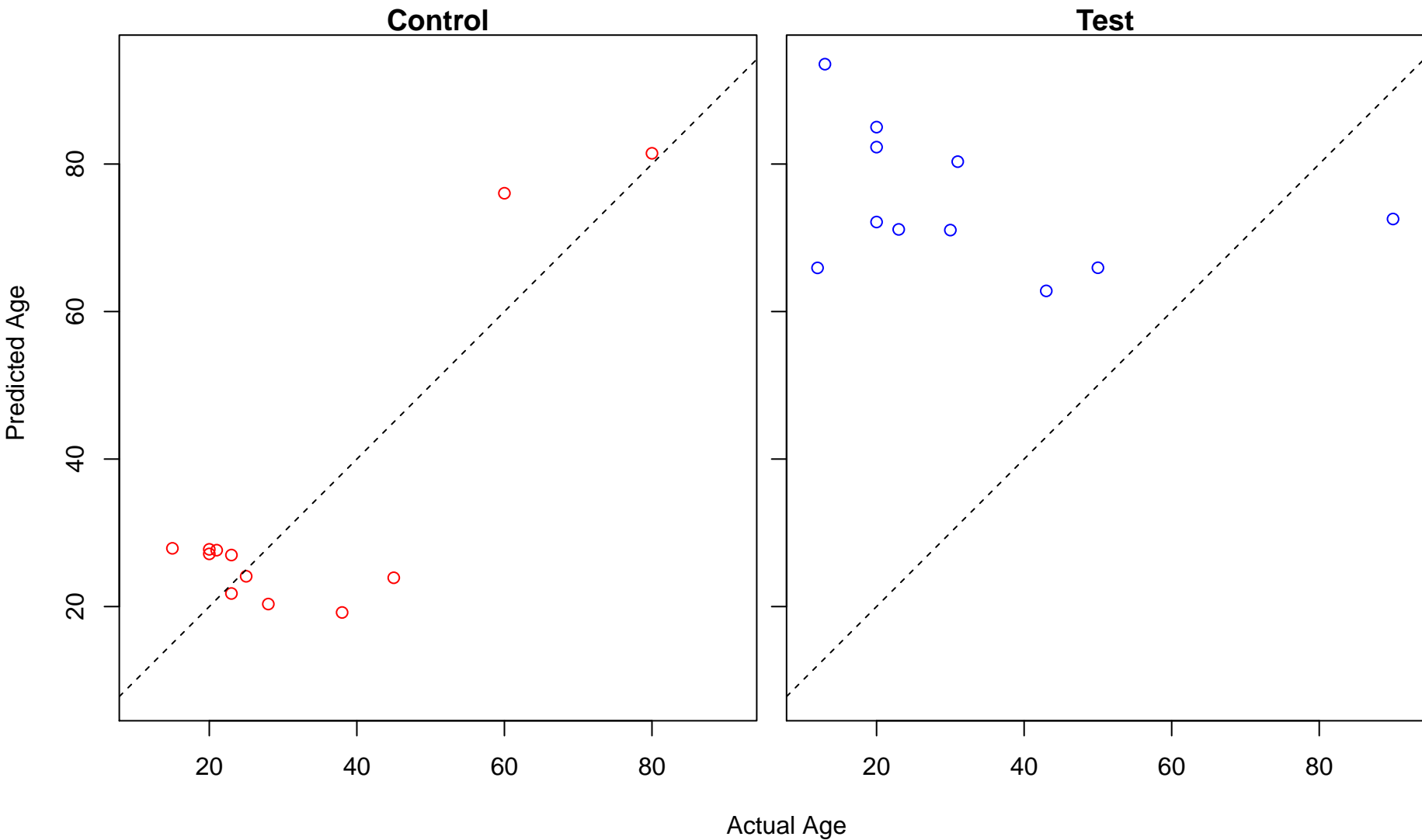
angiogenesis (Score: 10.323949)



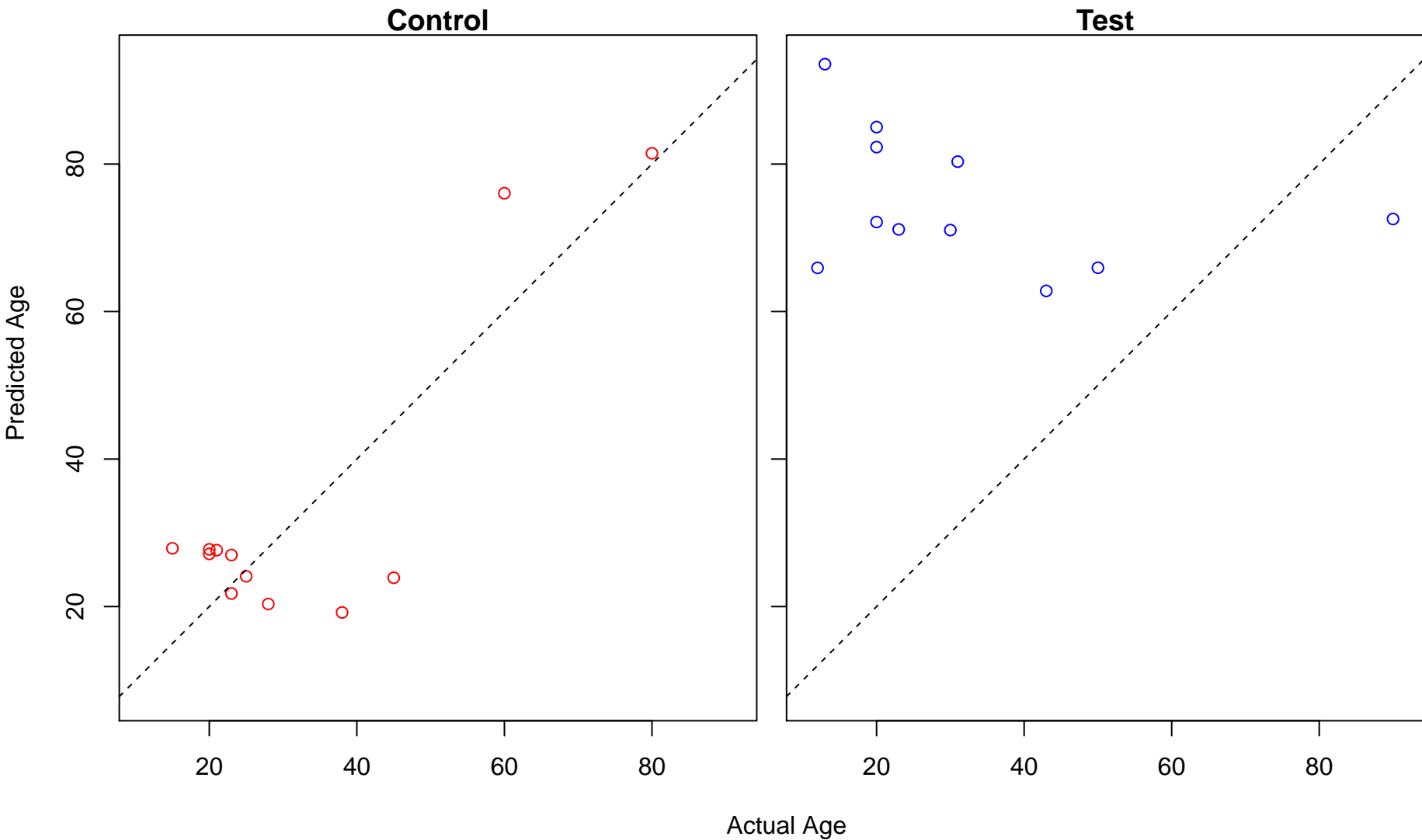
positive regulation of tolerance induction (Score: 10.318981)



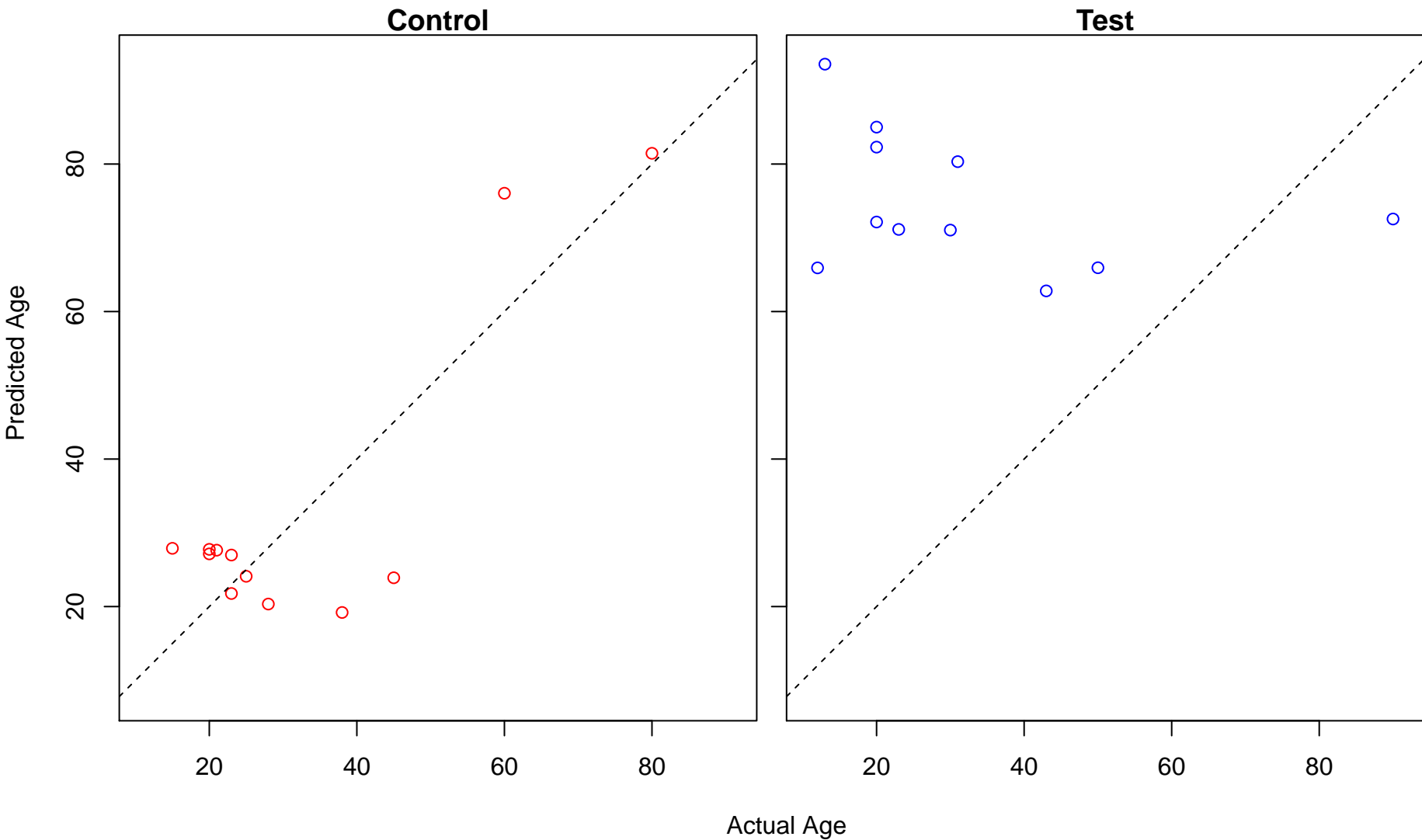
icosanoid secretion (Score: 10.316090)



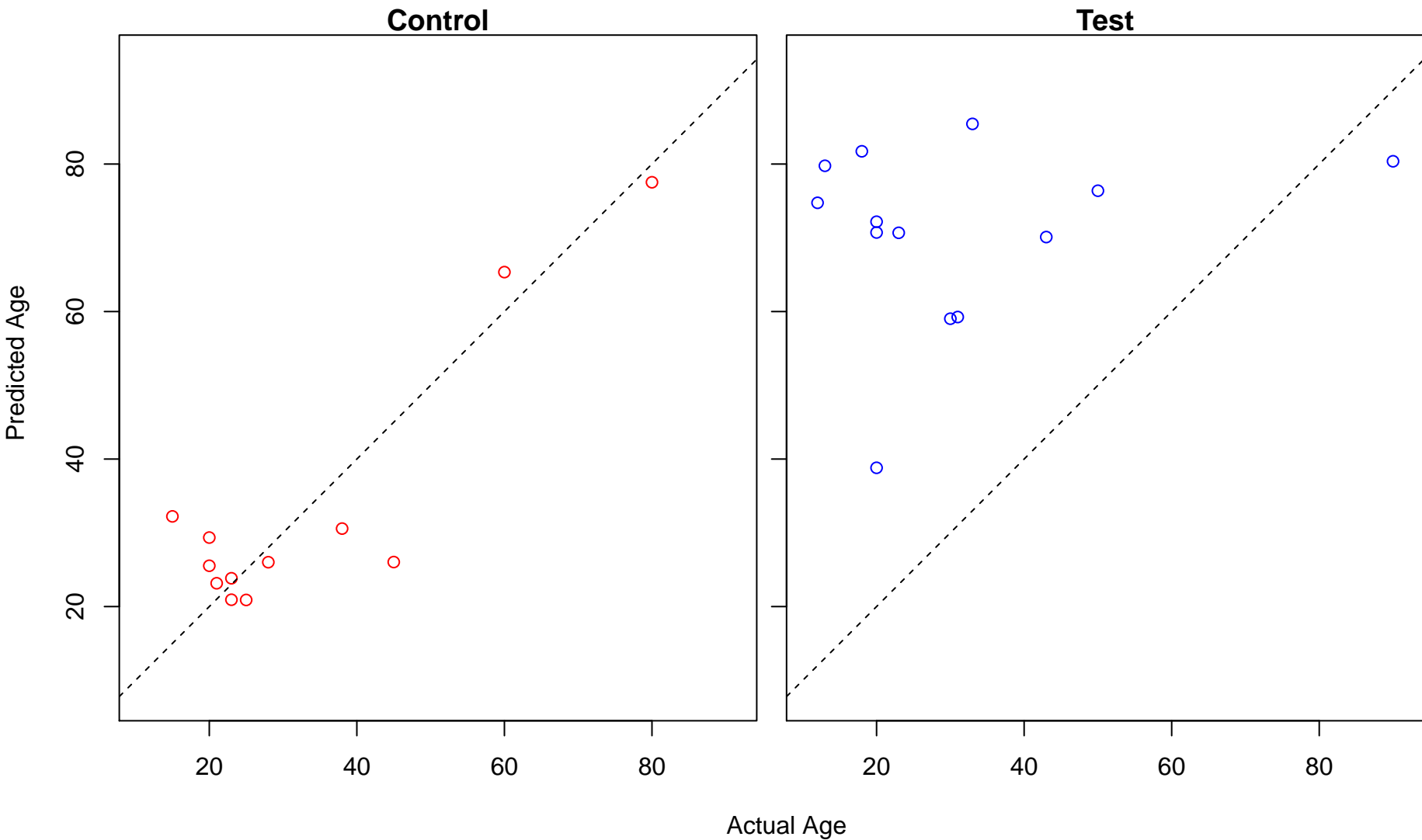
icosanoid transport (Score: 10.316090)



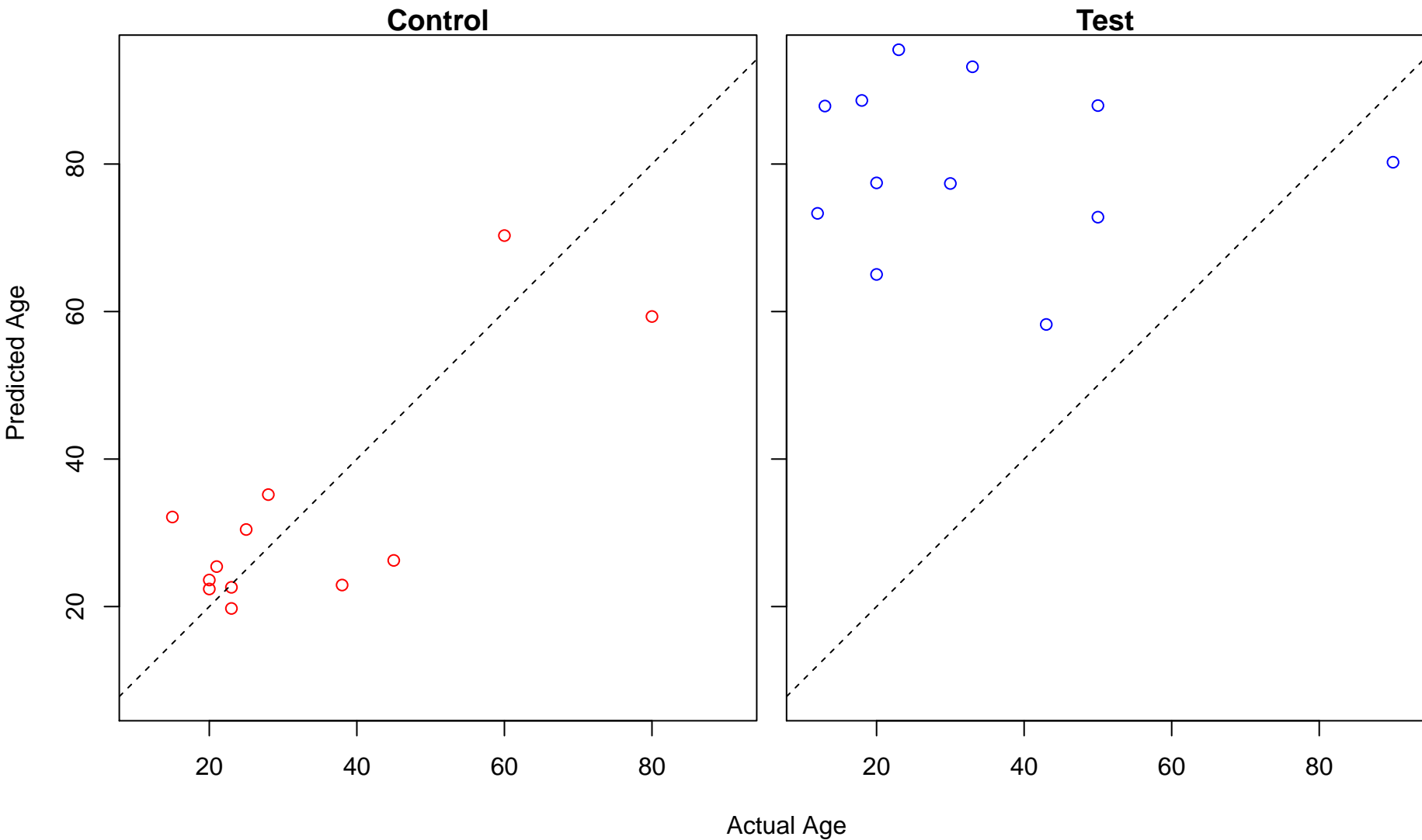
fatty acid derivative transport (Score: 10.316090)



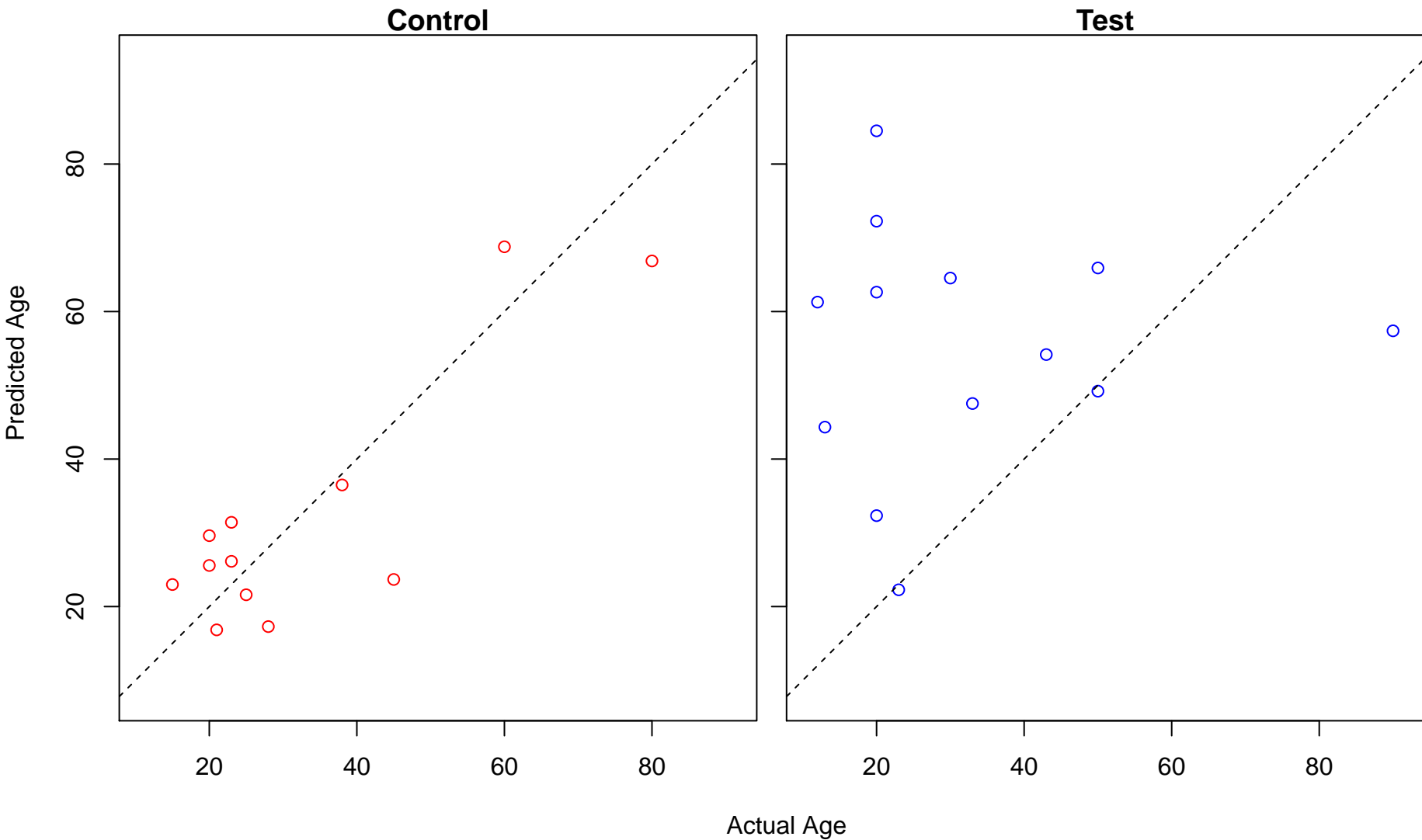
positive regulation of lipopolysaccharide-mediated signaling pathway (Score: 10.309004)



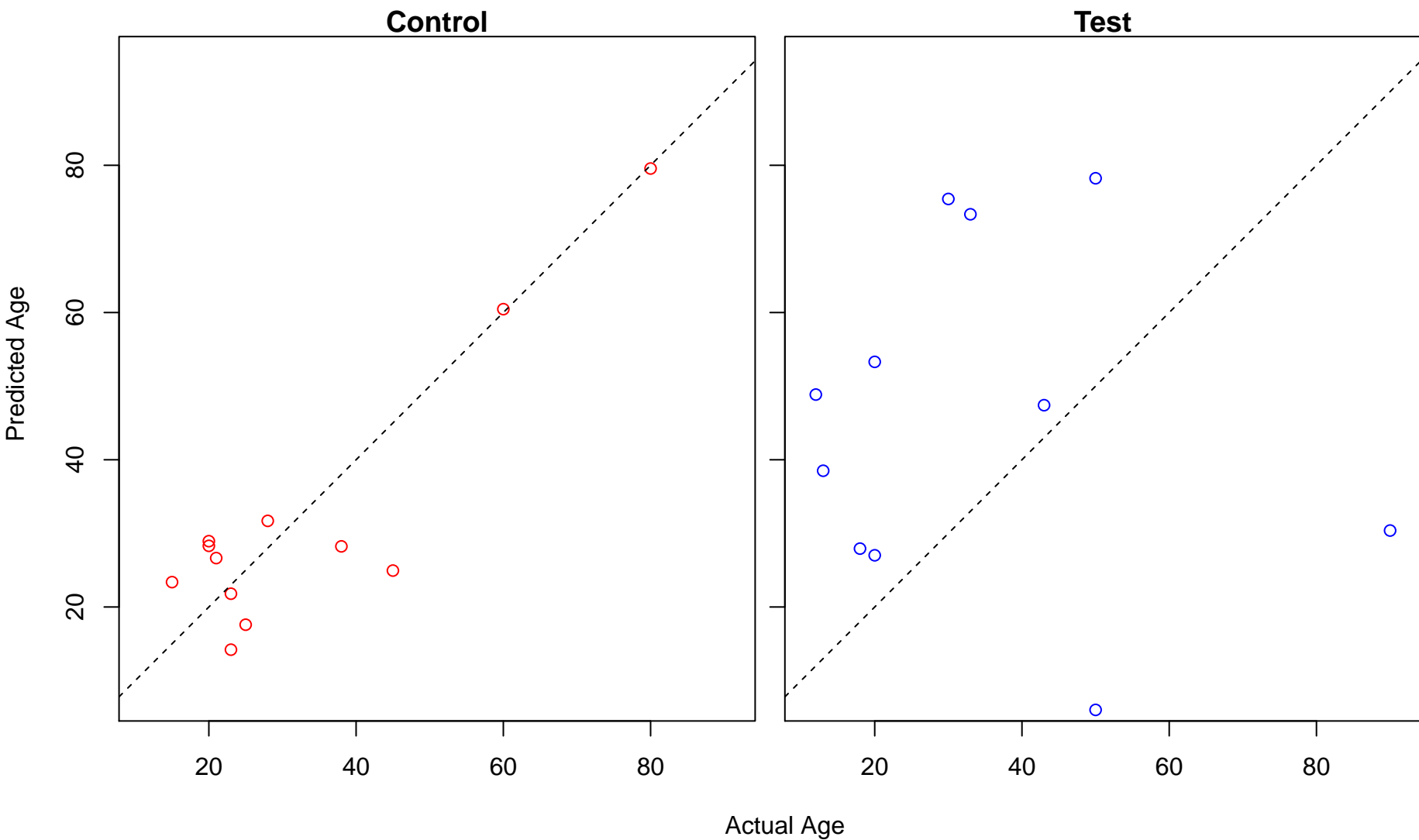
regulation of synaptic transmission, dopaminergic (Score: 10.307403)



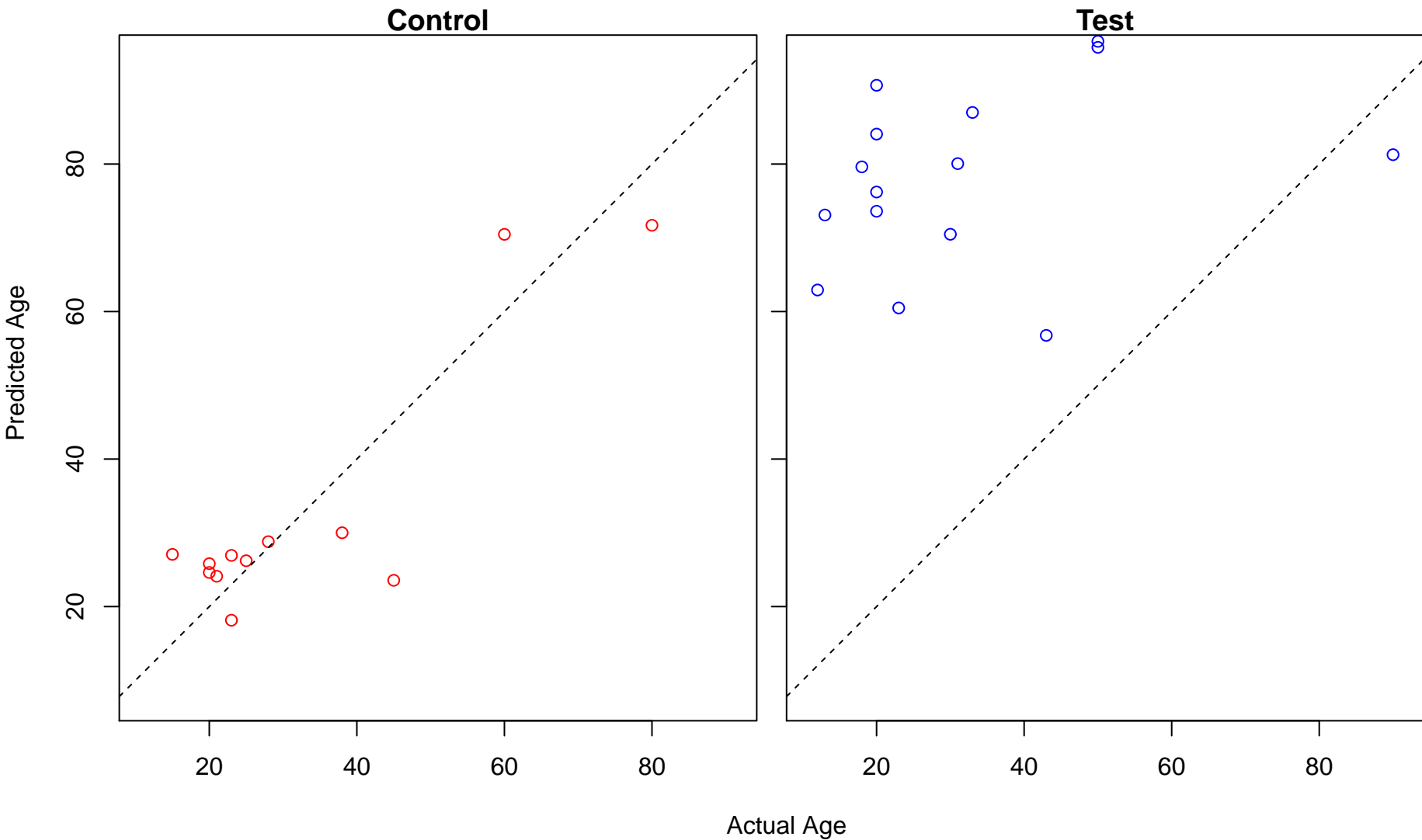
regulation of metalloendopeptidase activity (Score: 10.304799)



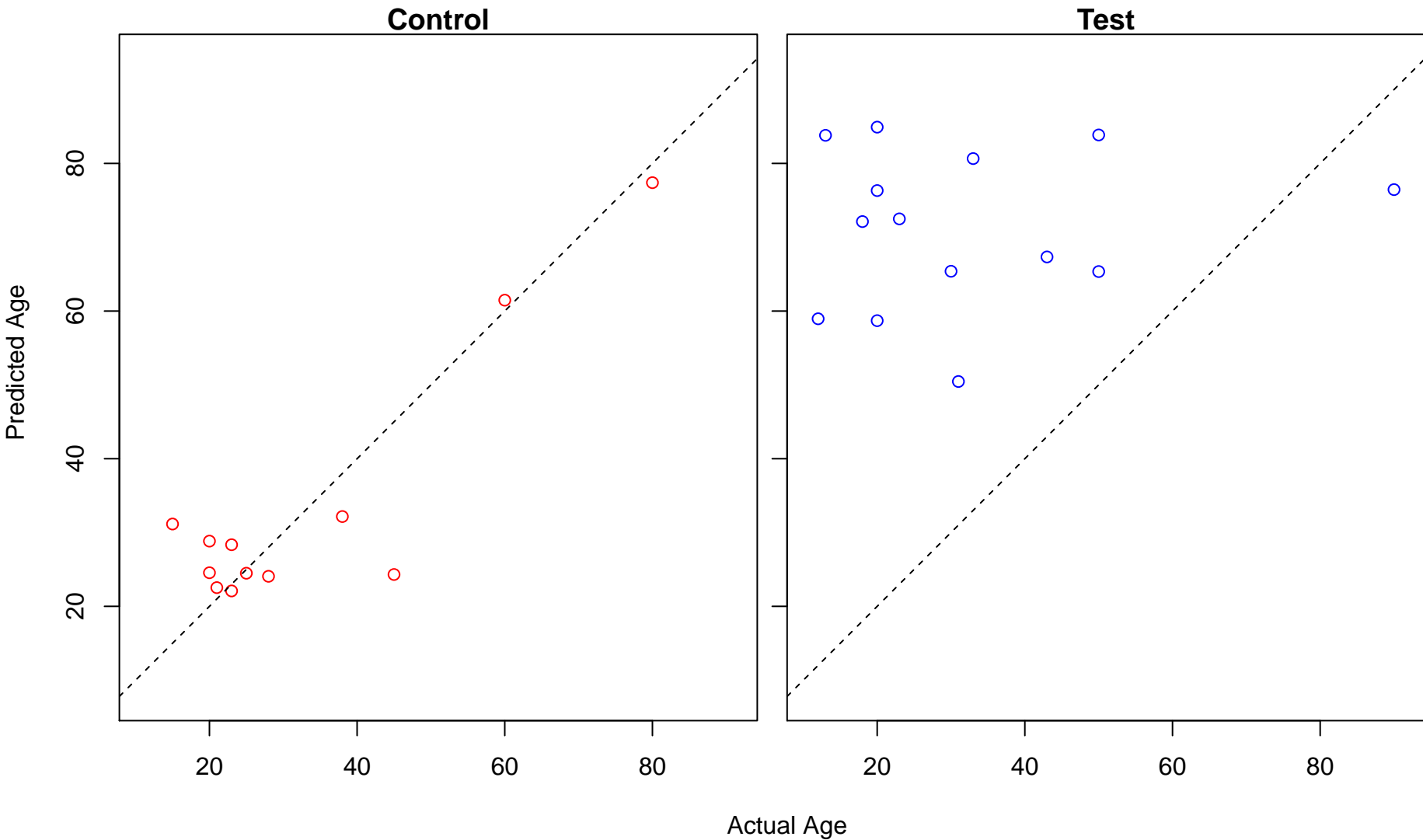
positive regulation of cysteine-type endopeptidase activity (Score: 10.288689)



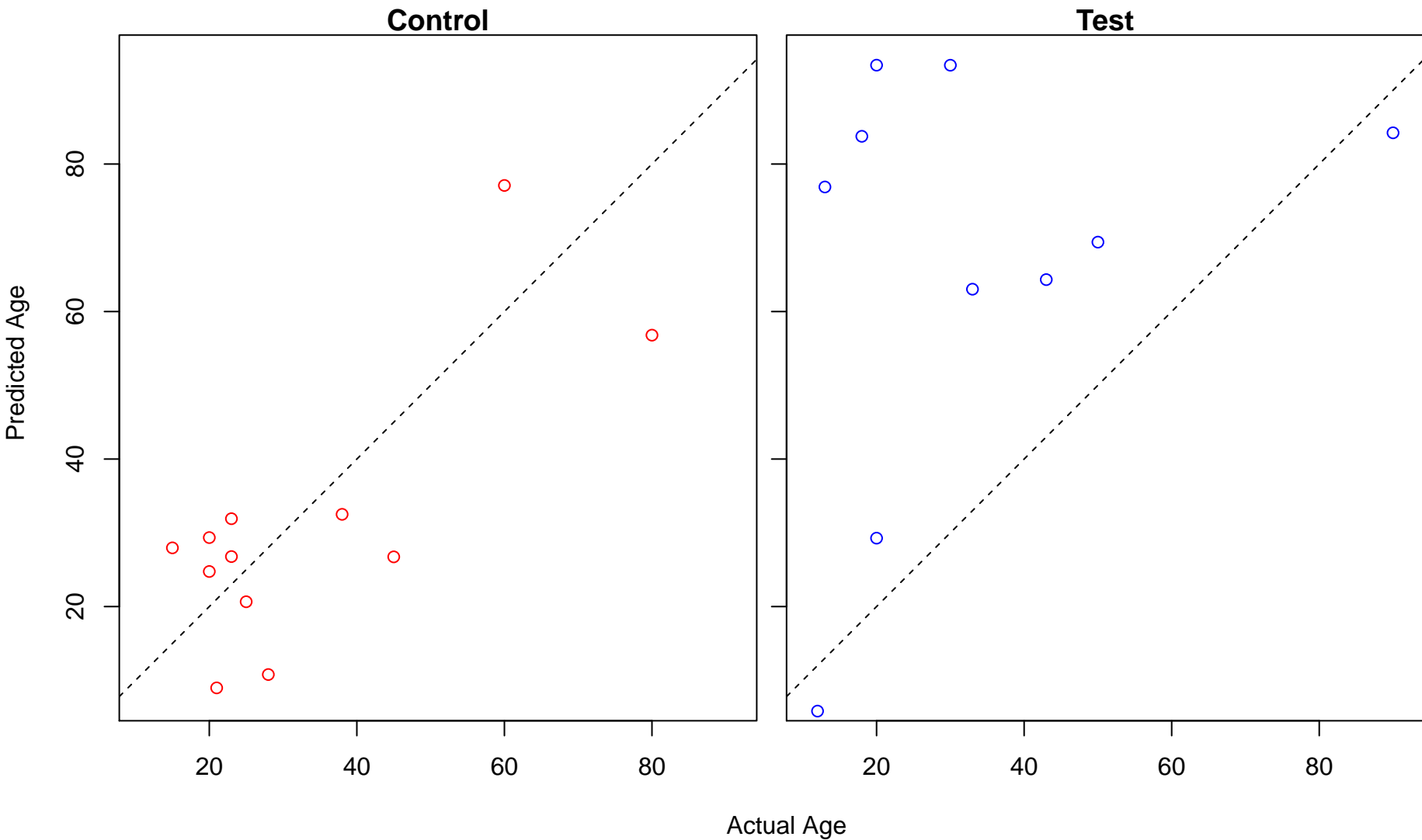
positive regulation of fibroblast migration (Score: 10.282327)



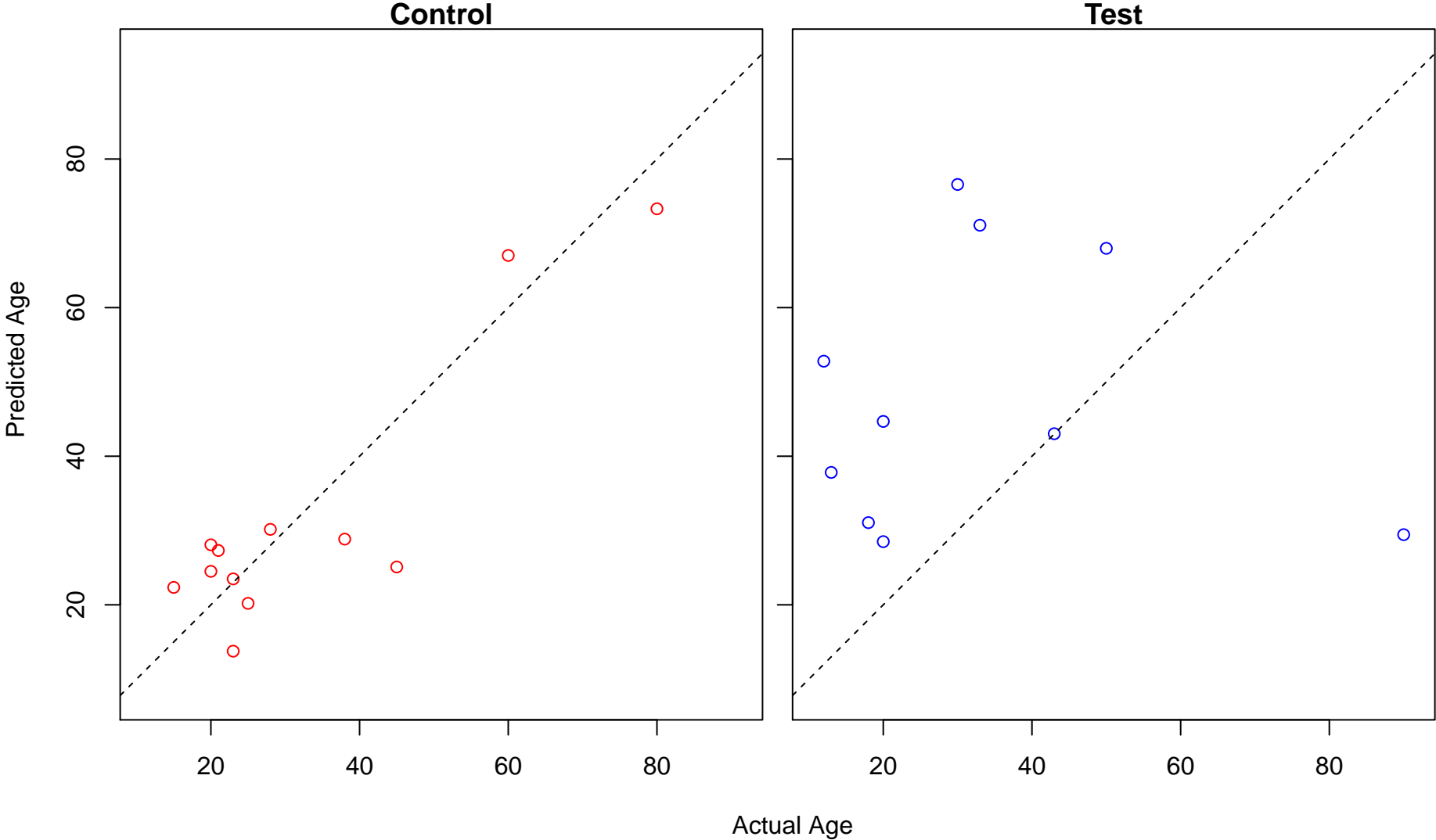
positive regulation of histone deacetylation (Score: 10.269074)



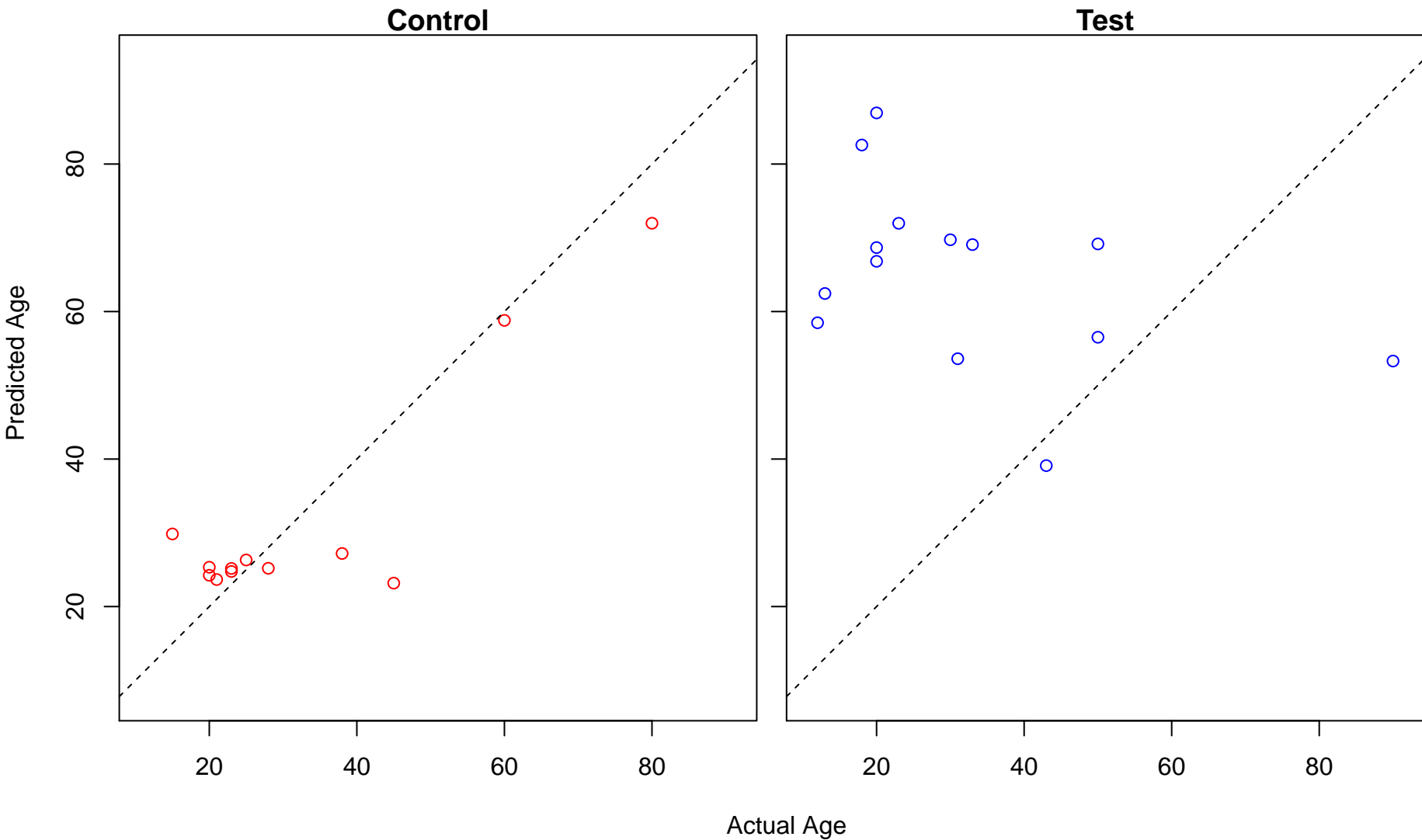
histone H4-K20 demethylation (Score: 10.260038)



positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 10.25)

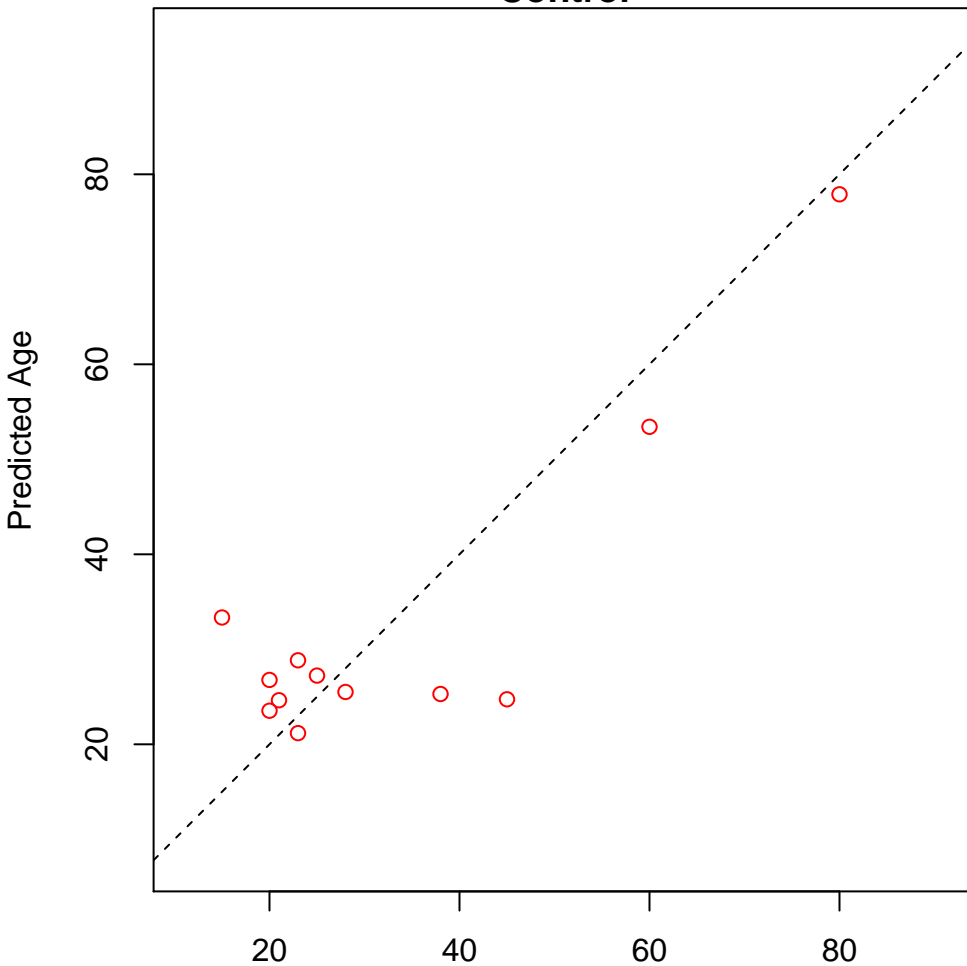


regulation of protein localization to chromosome, telomeric region (Score: 10.250398)

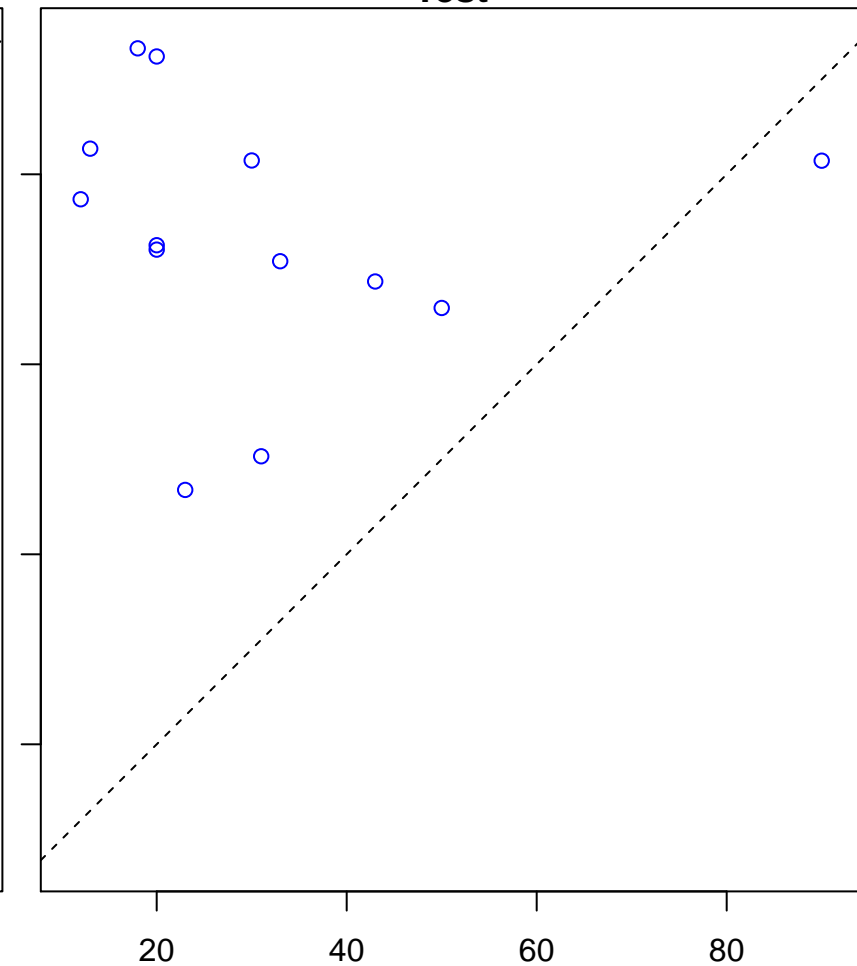


cellular response to fluid shear stress (Score: 10.232827)

Control

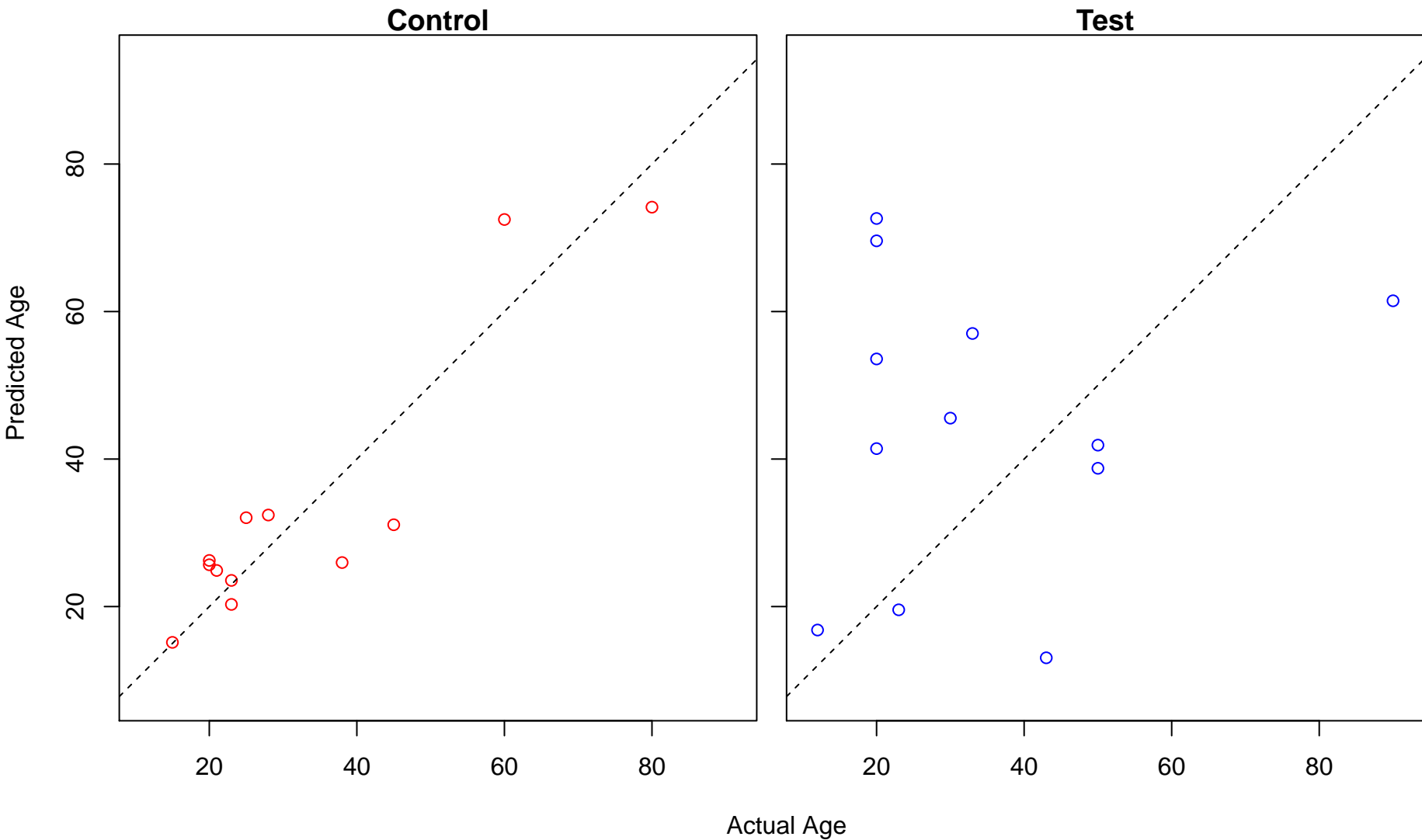


Test

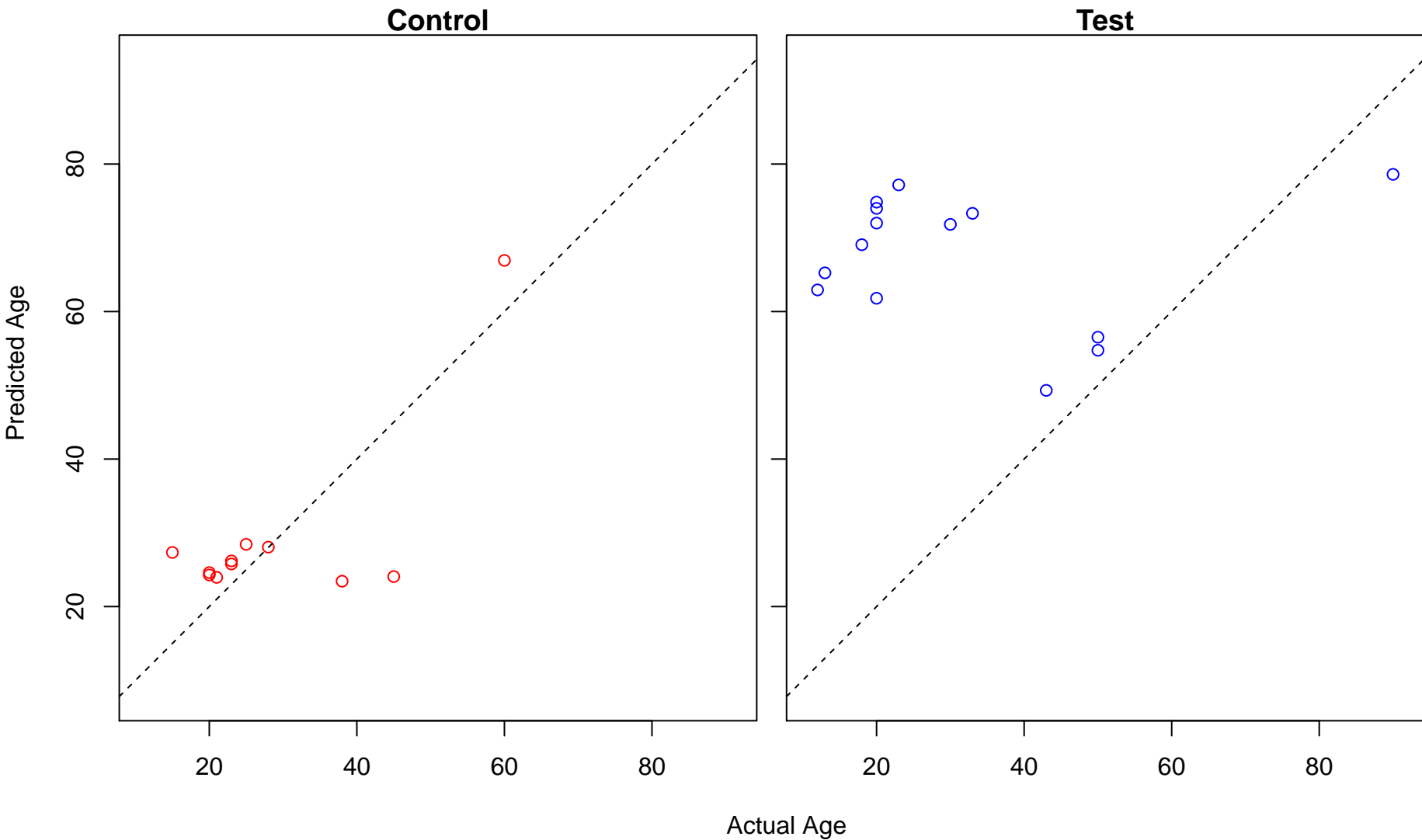


Actual Age

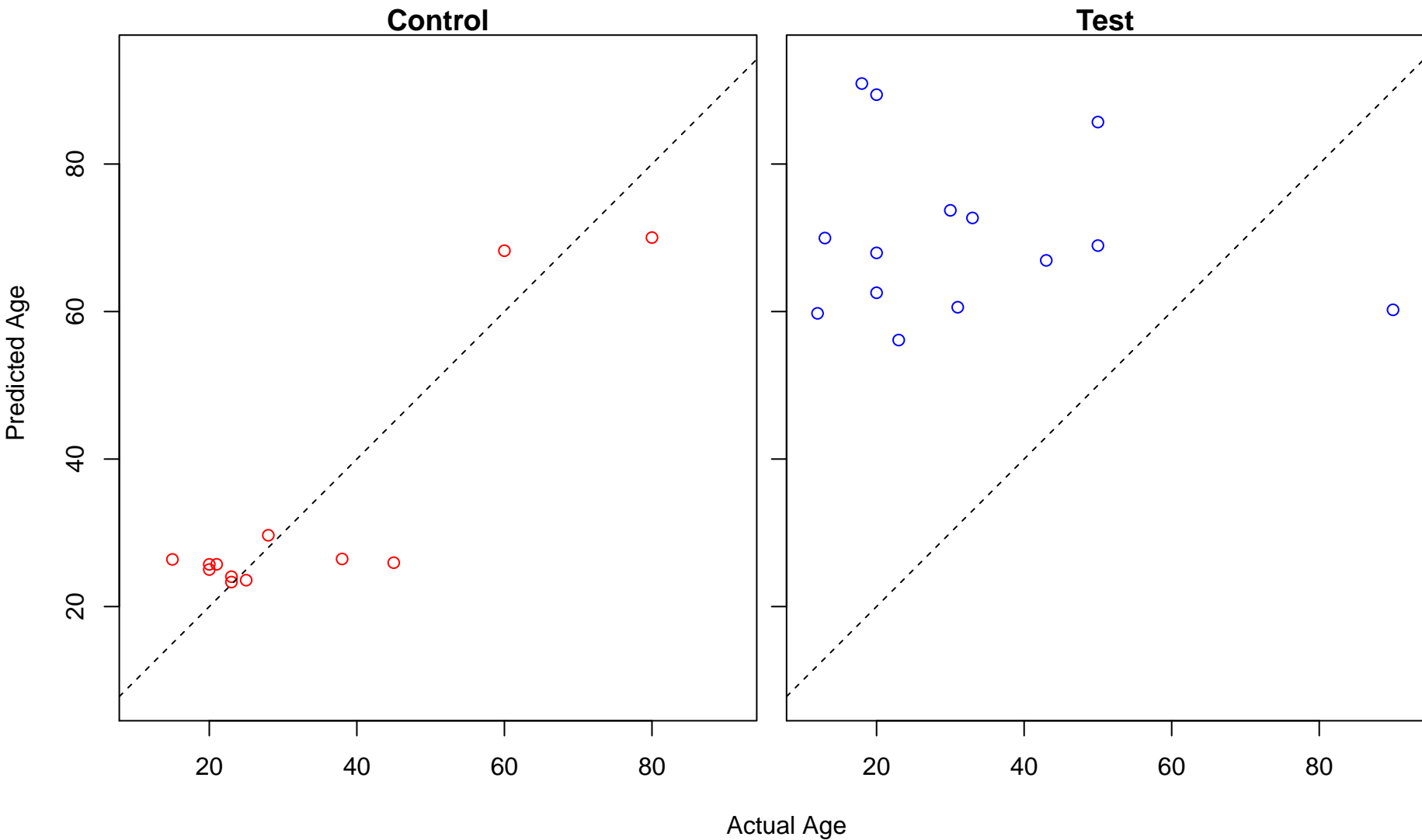
positive regulation of synaptic transmission (Score: 10.230730)



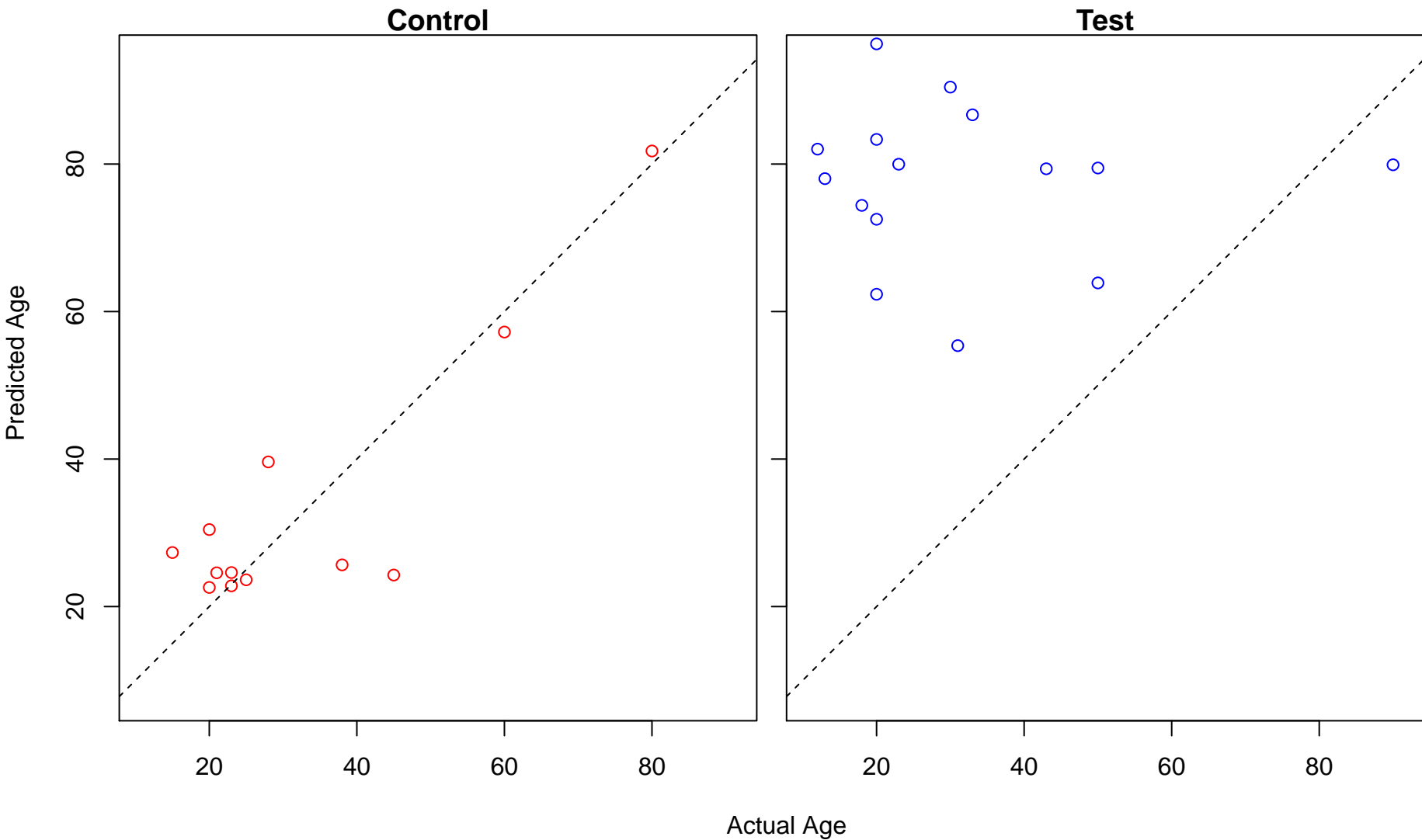
negative regulation of NF-kappaB import into nucleus (Score: 10.227971)



I-kappaB phosphorylation (Score: 10.223130)

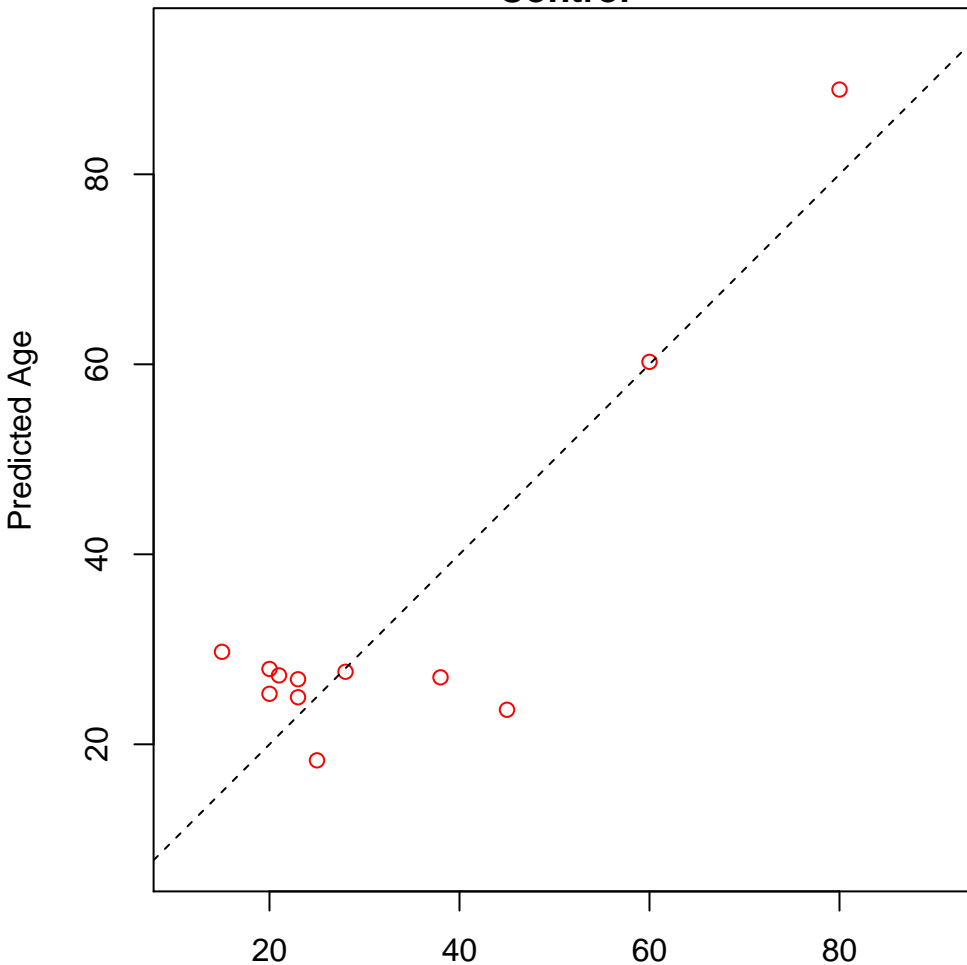


regulation of removal of superoxide radicals (Score: 10.219073)

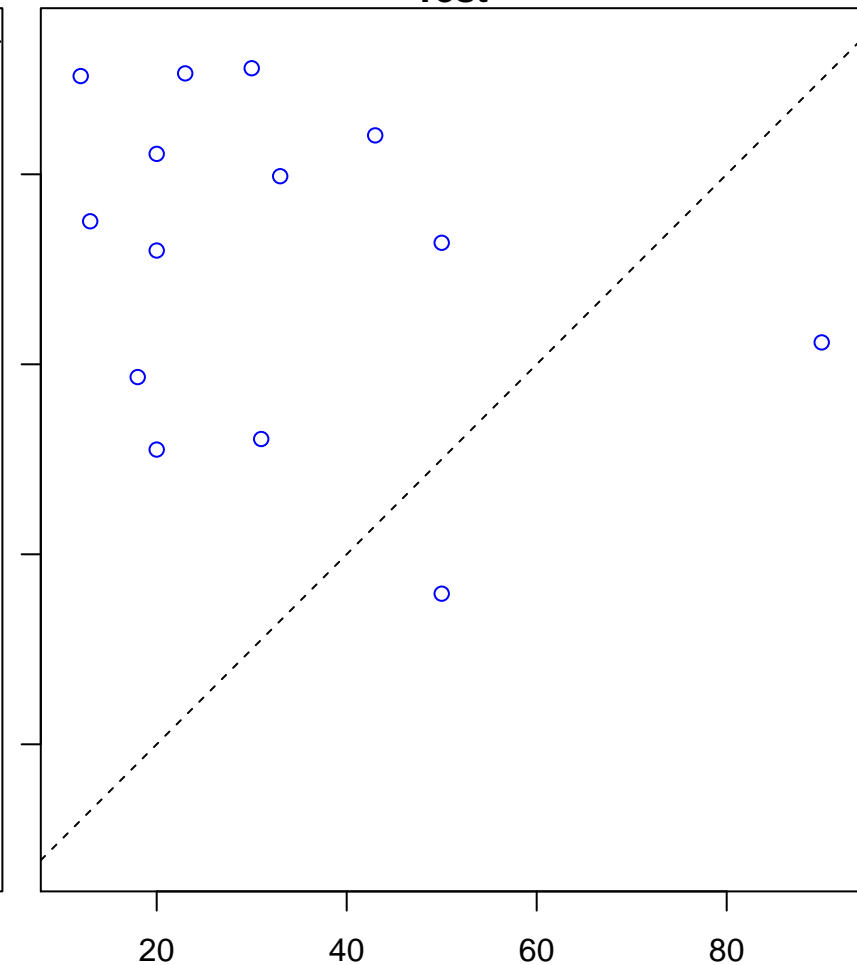


response to electrical stimulus (Score: 10.217363)

Control



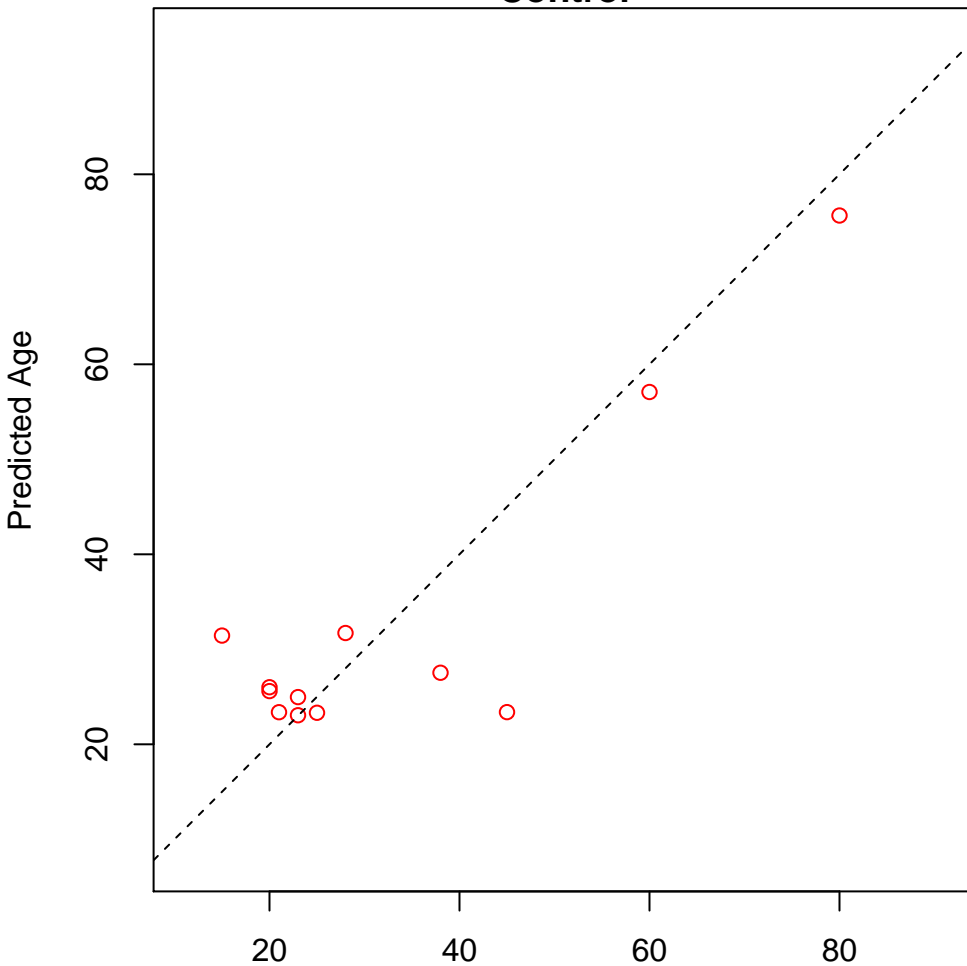
Test



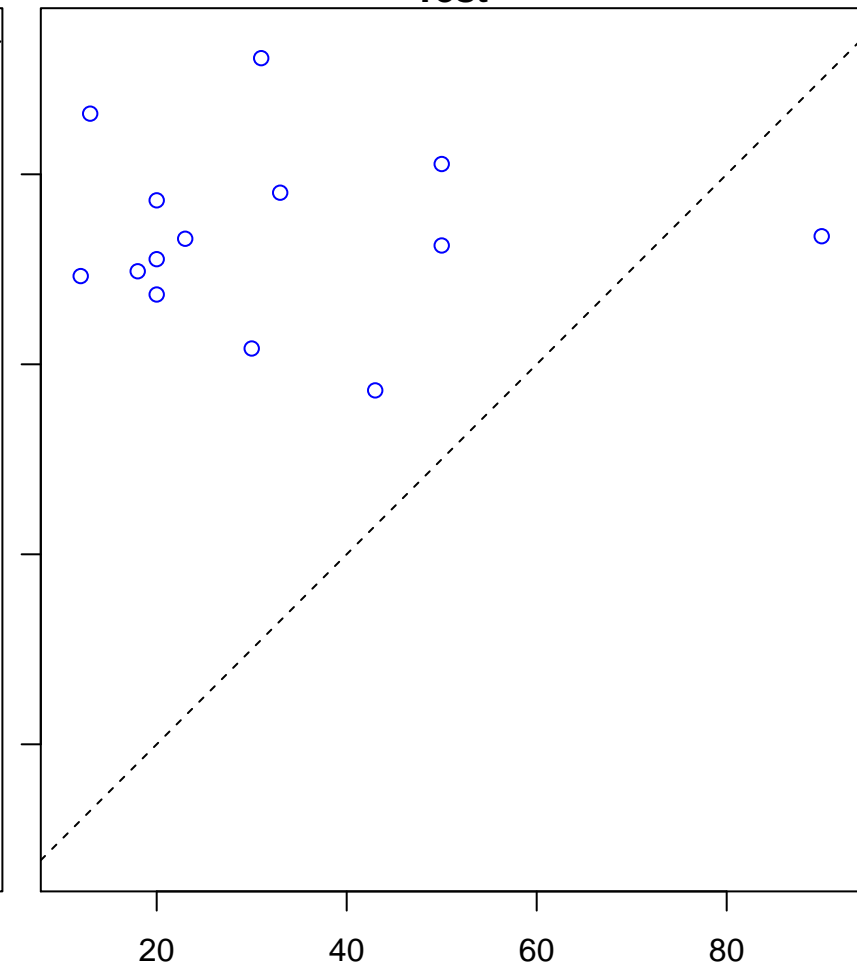
Actual Age

regulation of miRNA metabolic process (Score: 10.215474)

Control

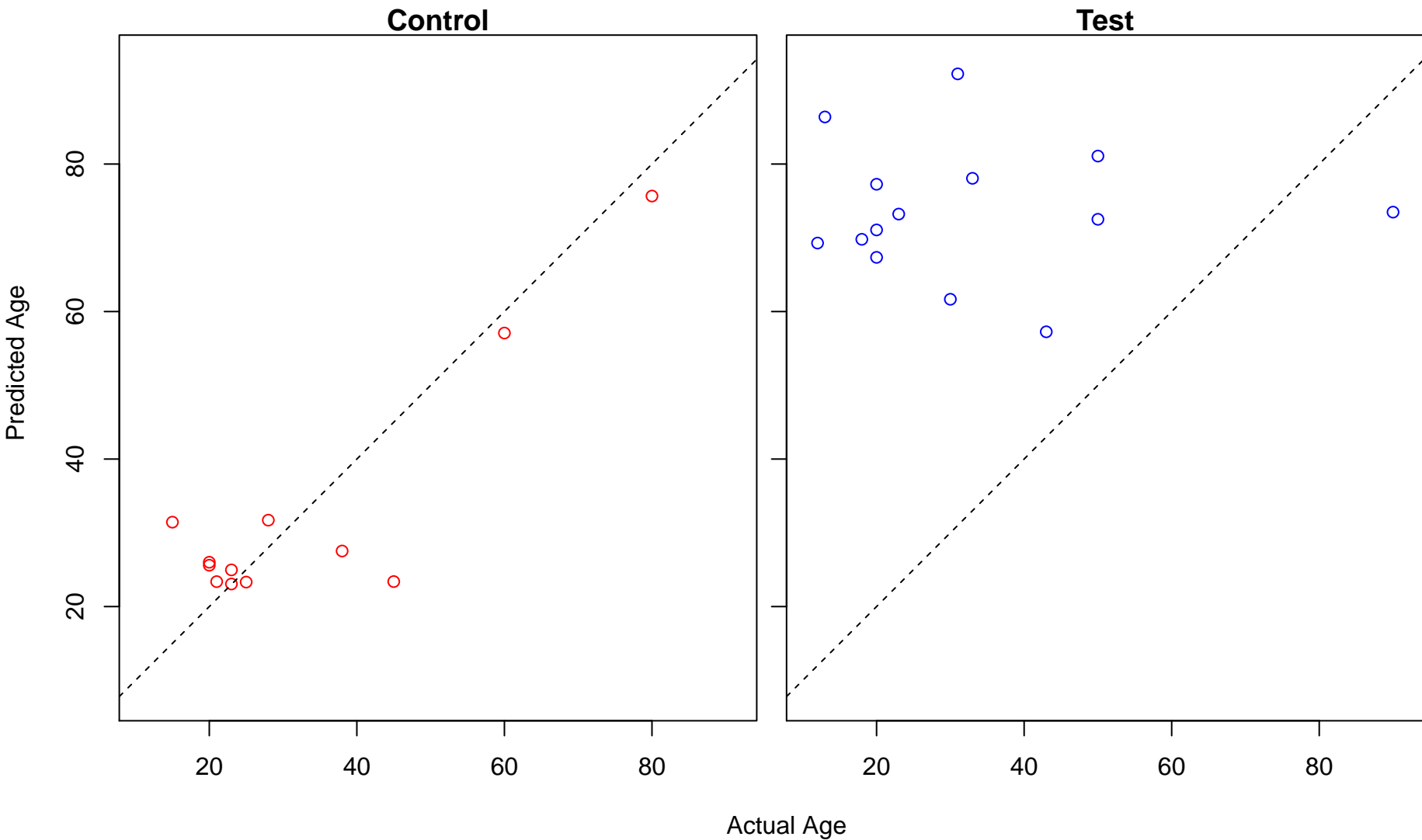


Test

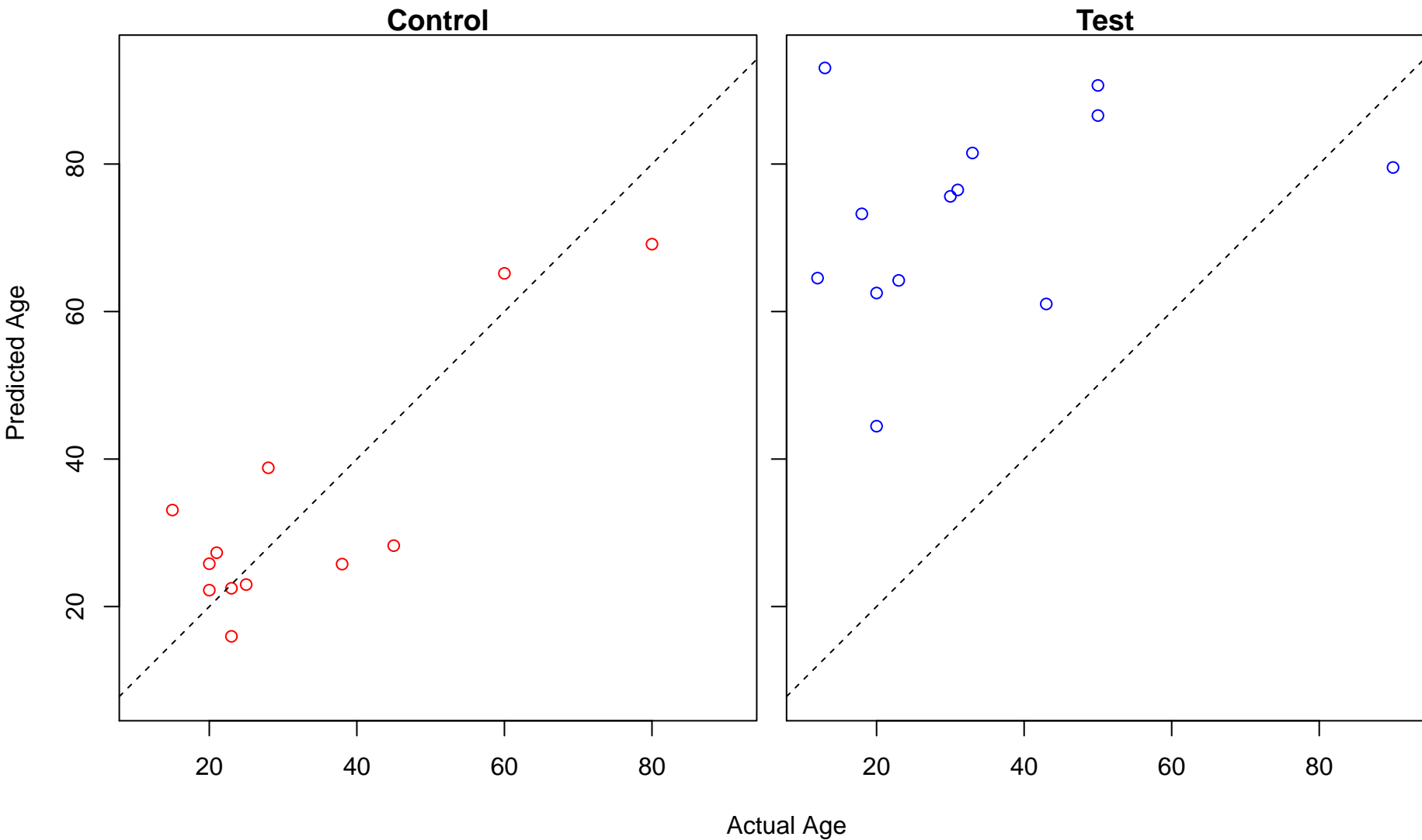


Actual Age

positive regulation of miRNA metabolic process (Score: 10.215474)

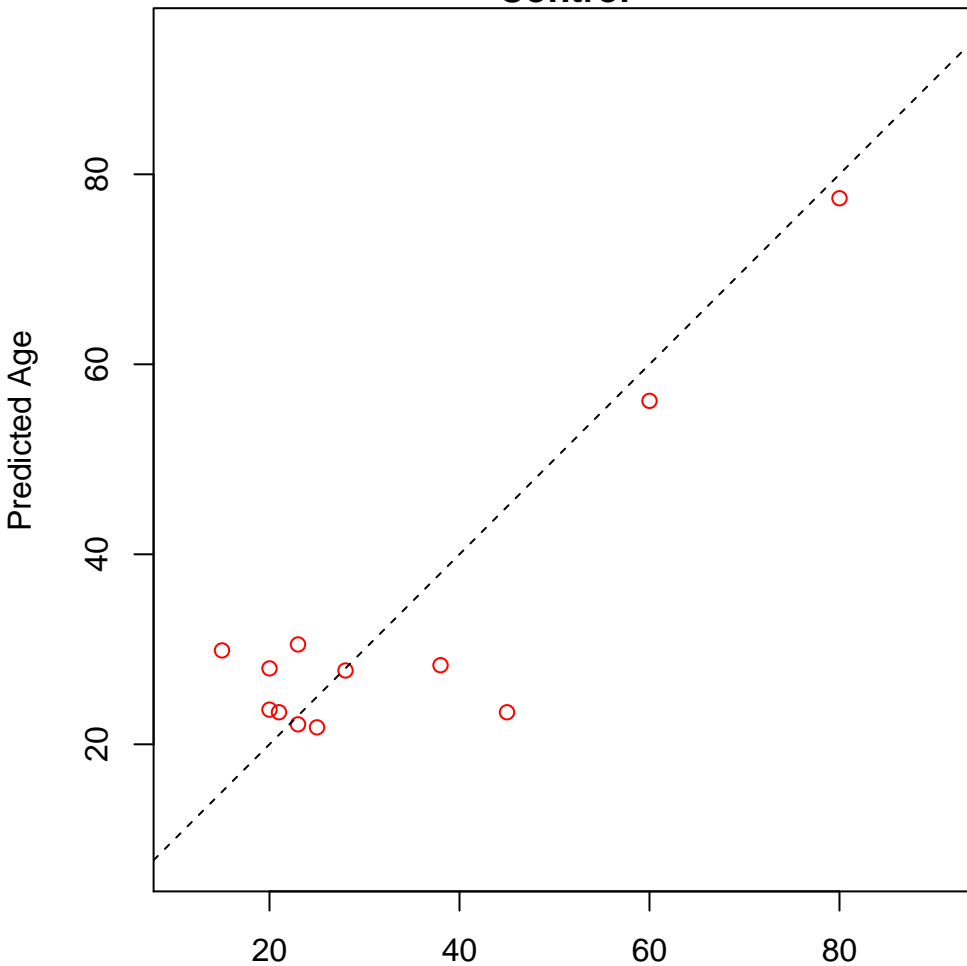


cellular response to UV-B (Score: 10.200565)

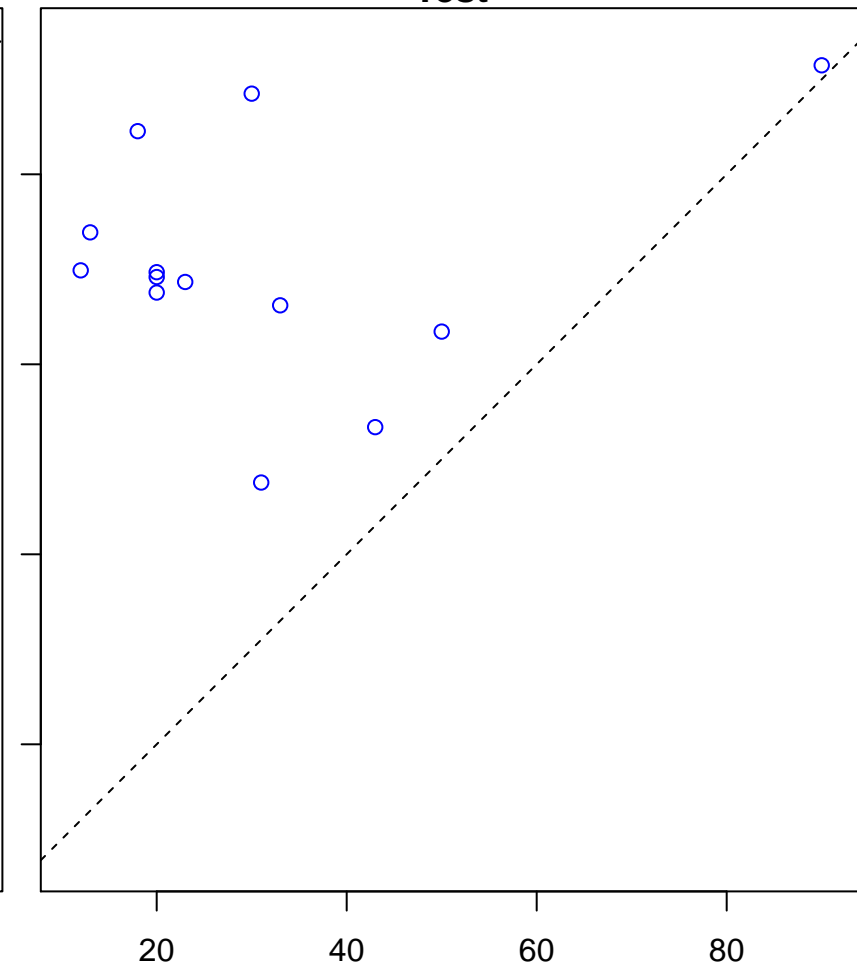


cellular response to ionizing radiation (Score: 10.185914)

Control

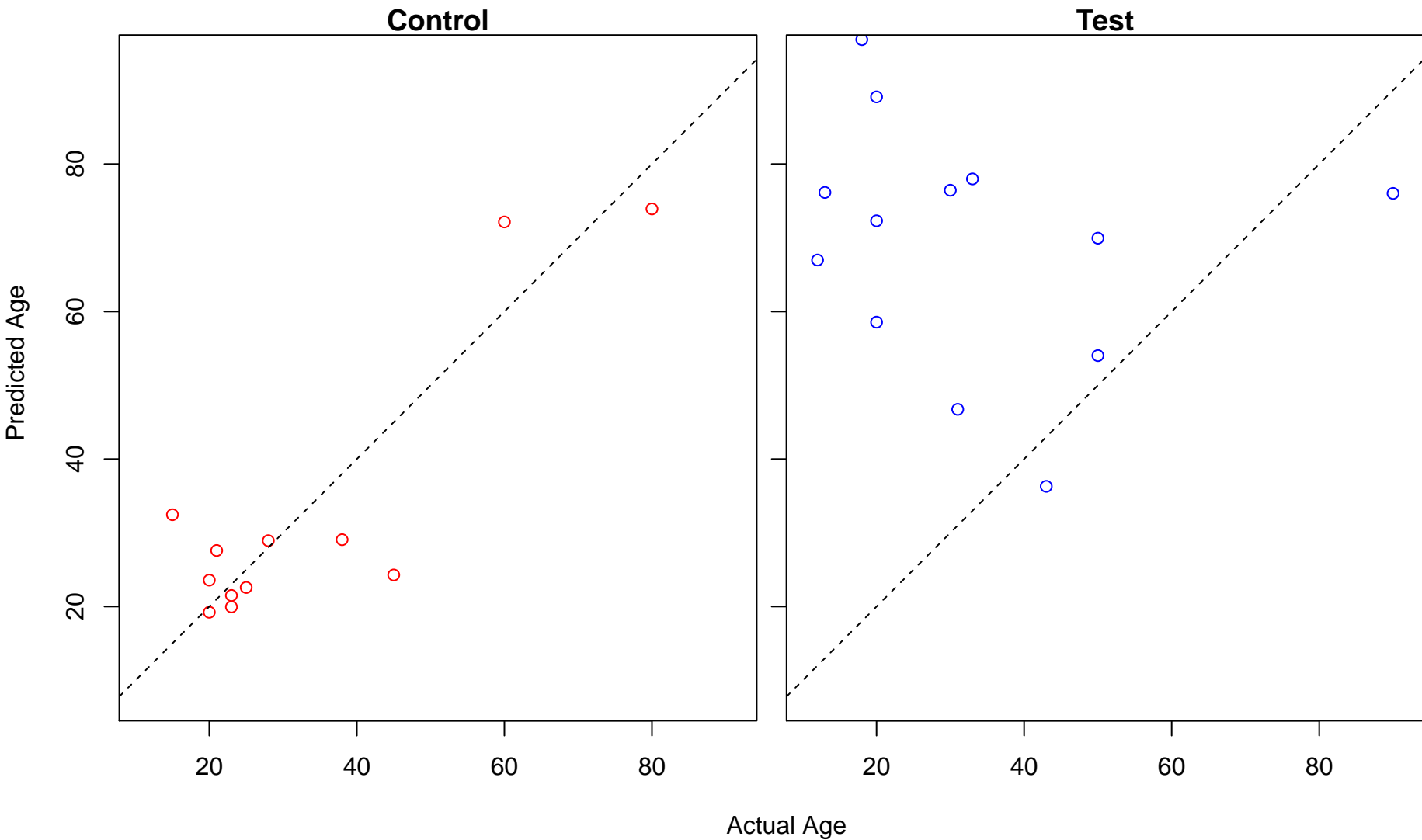


Test

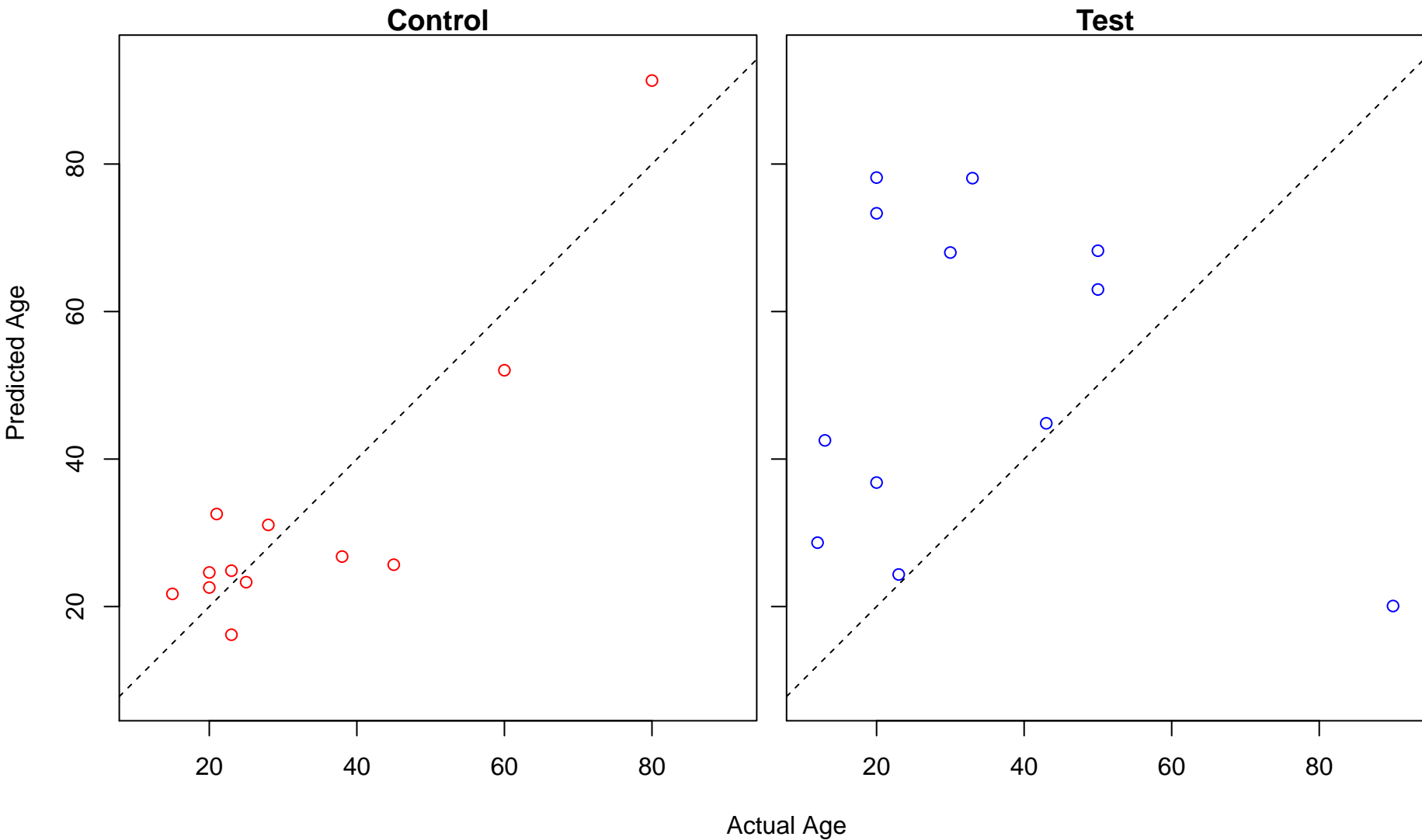


Actual Age

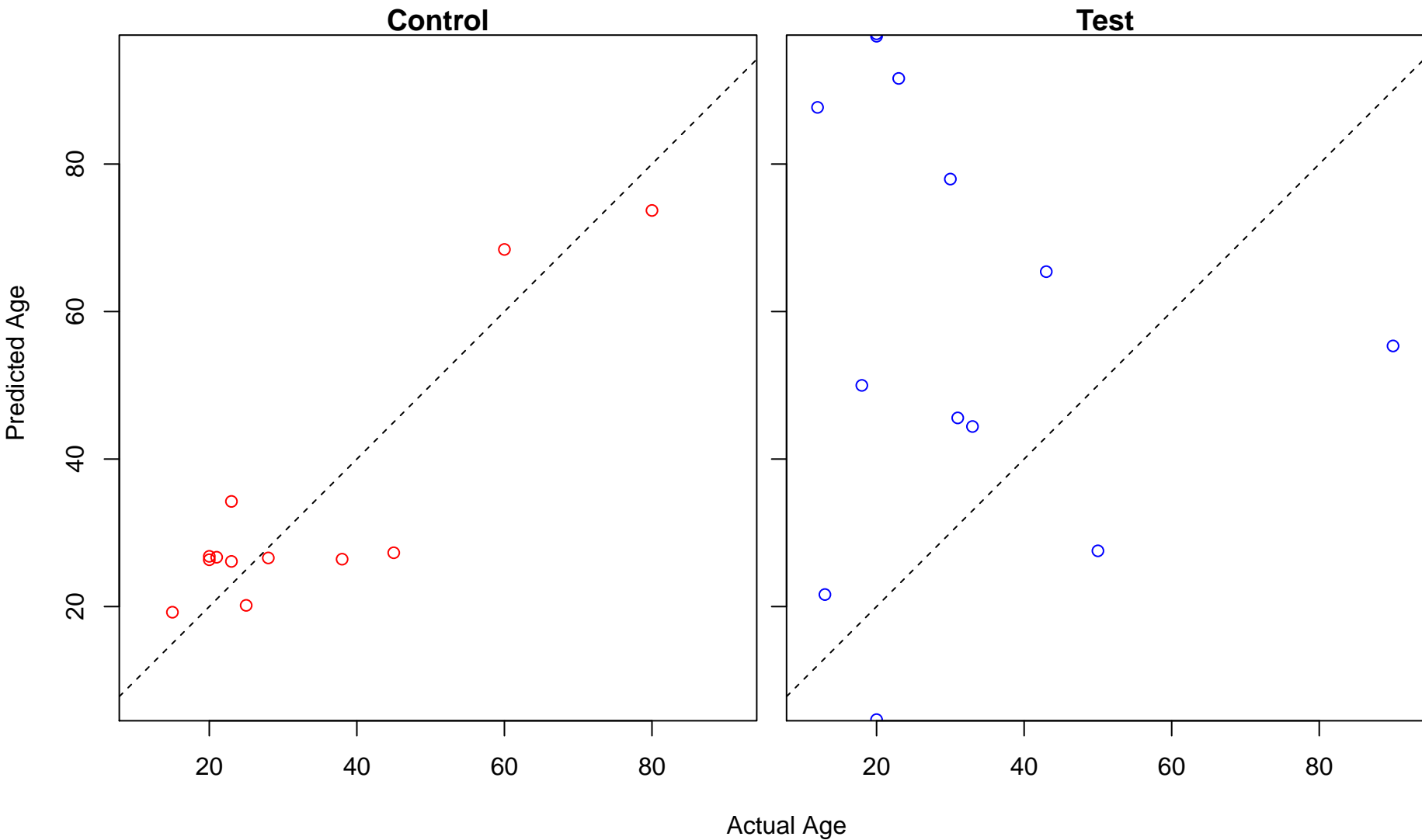
nuclear envelope organization (Score: 10.165935)



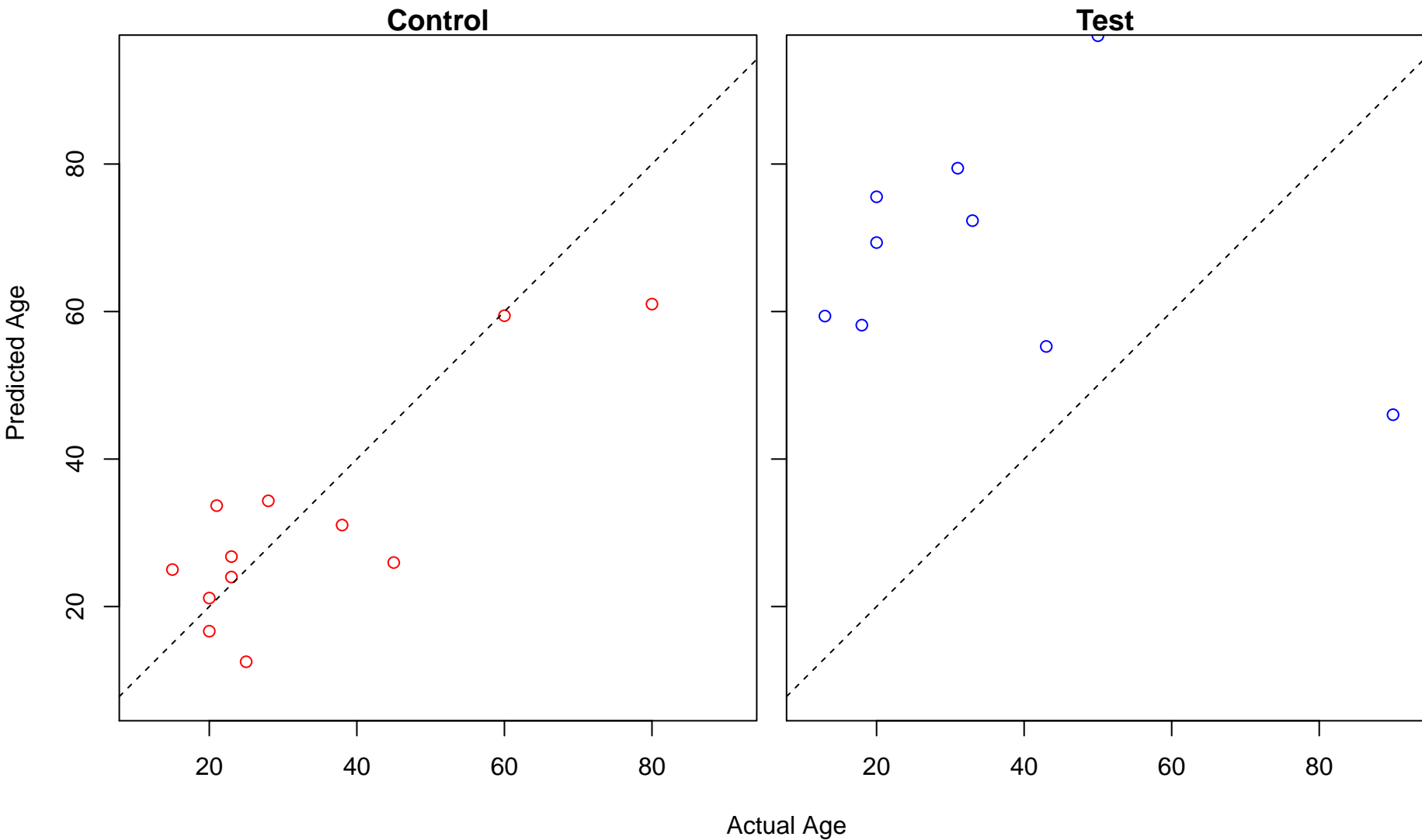
cell migration (Score: 10.154540)



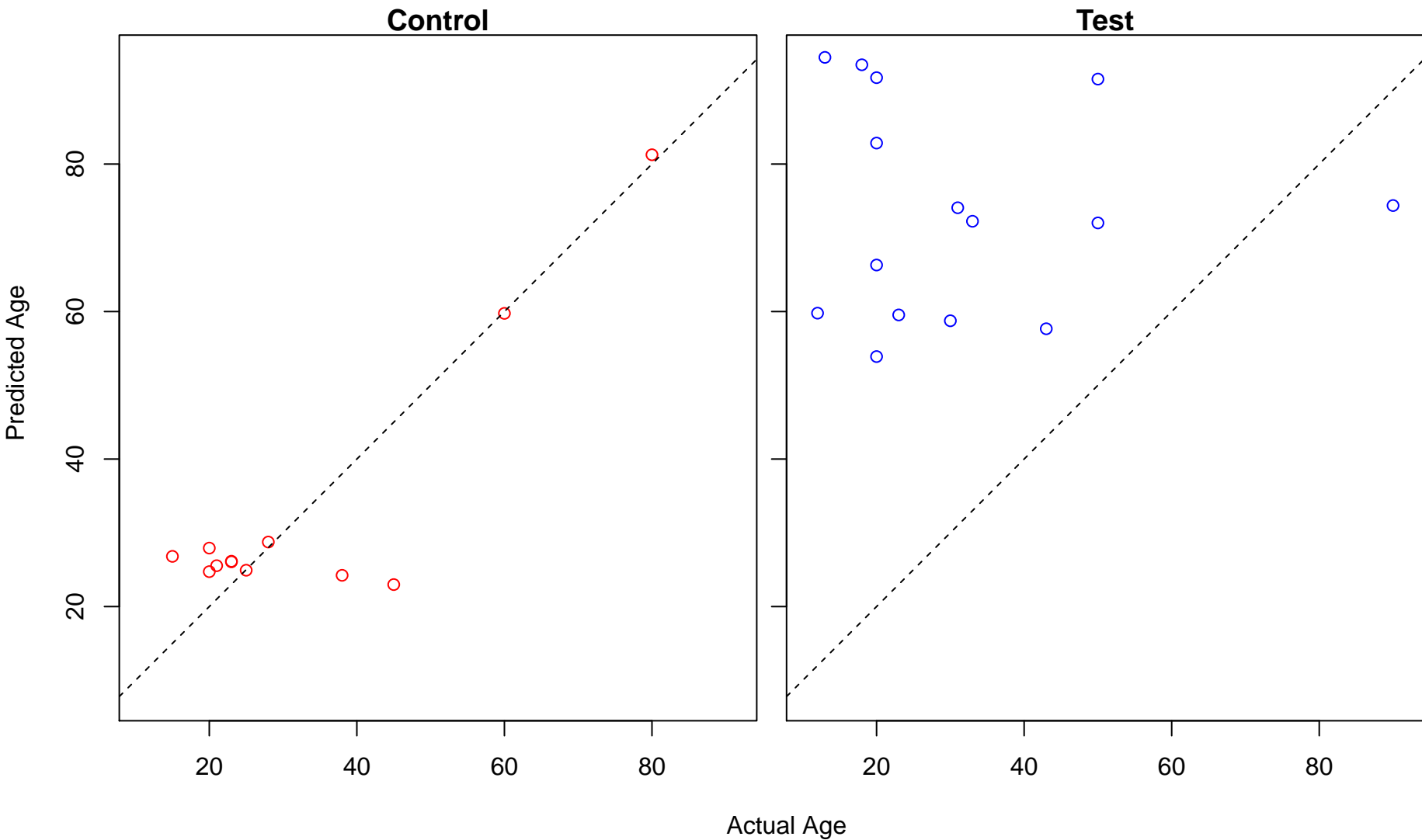
negative regulation of heart rate (Score: 10.153535)



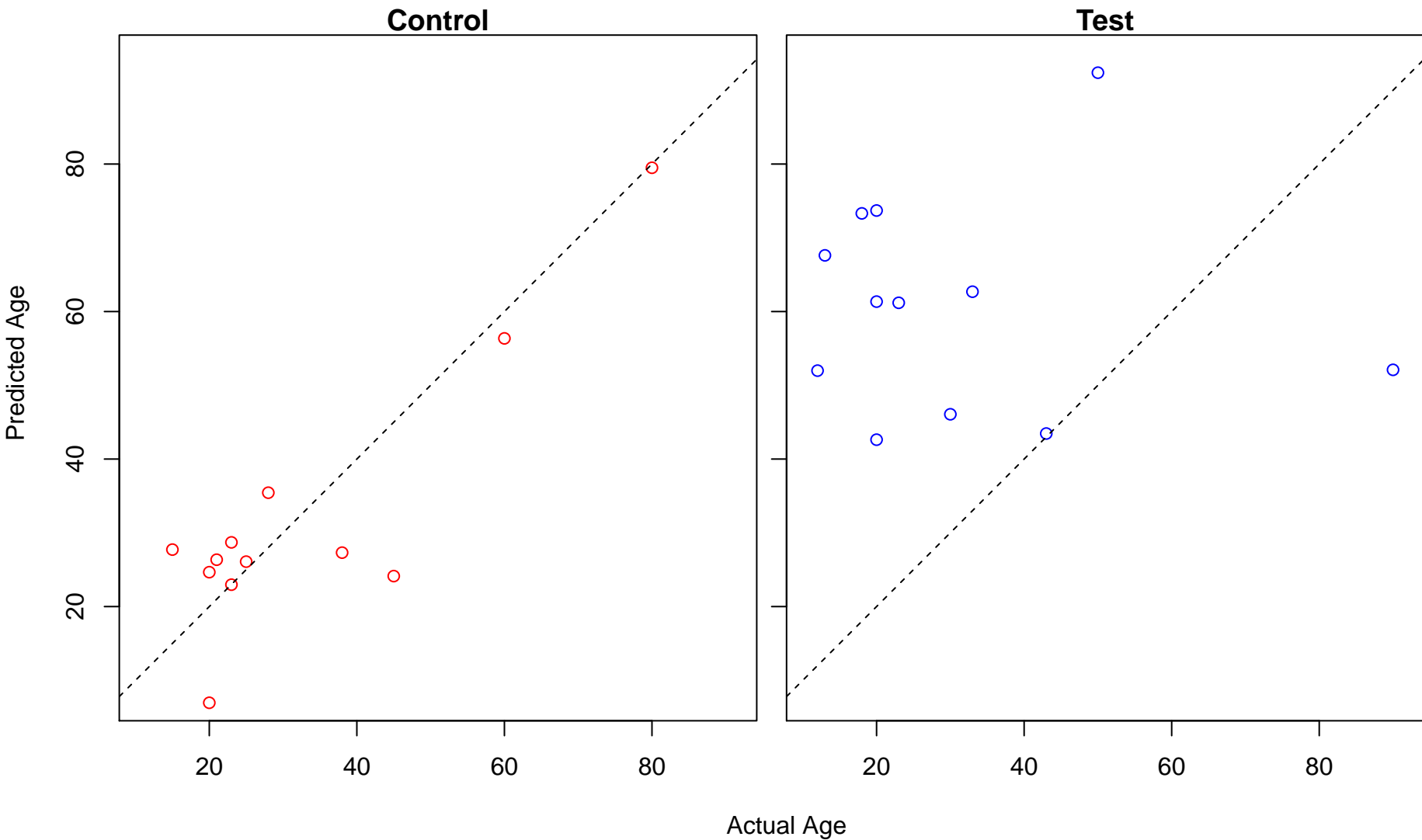
nodal signaling pathway (Score: 10.147252)



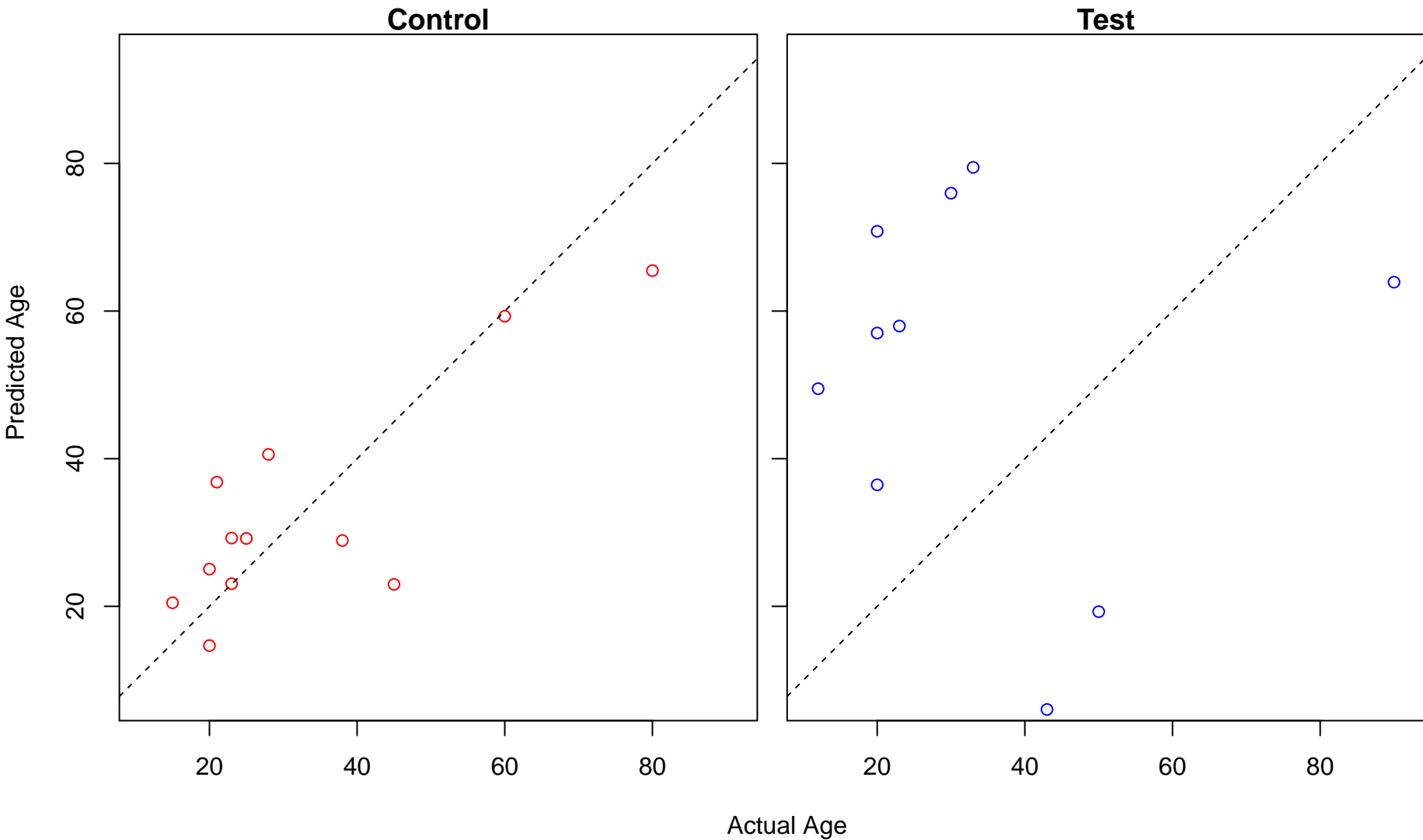
positive regulation of intracellular protein transport (Score: 10.143649)



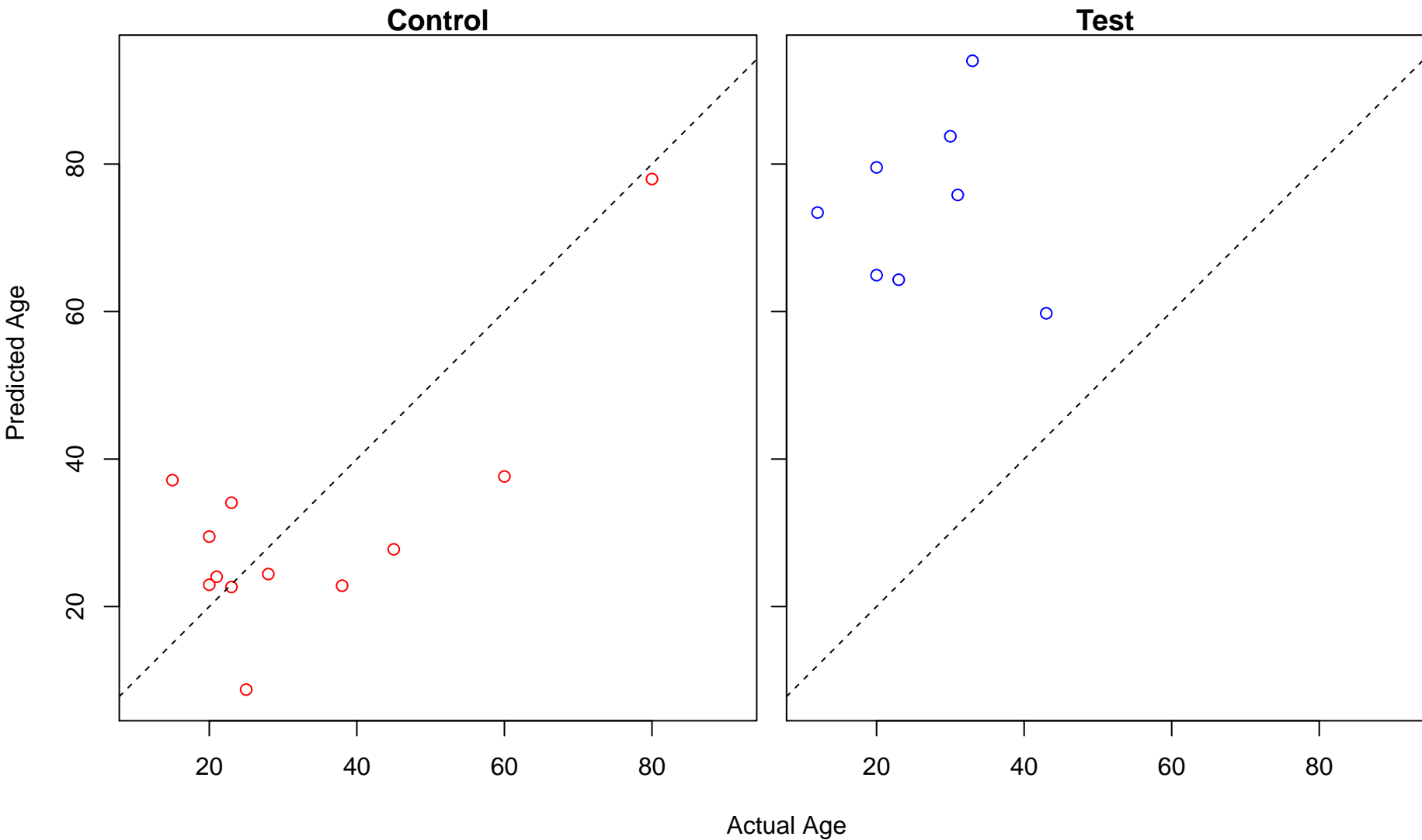
platelet aggregation (Score: 10.138688)



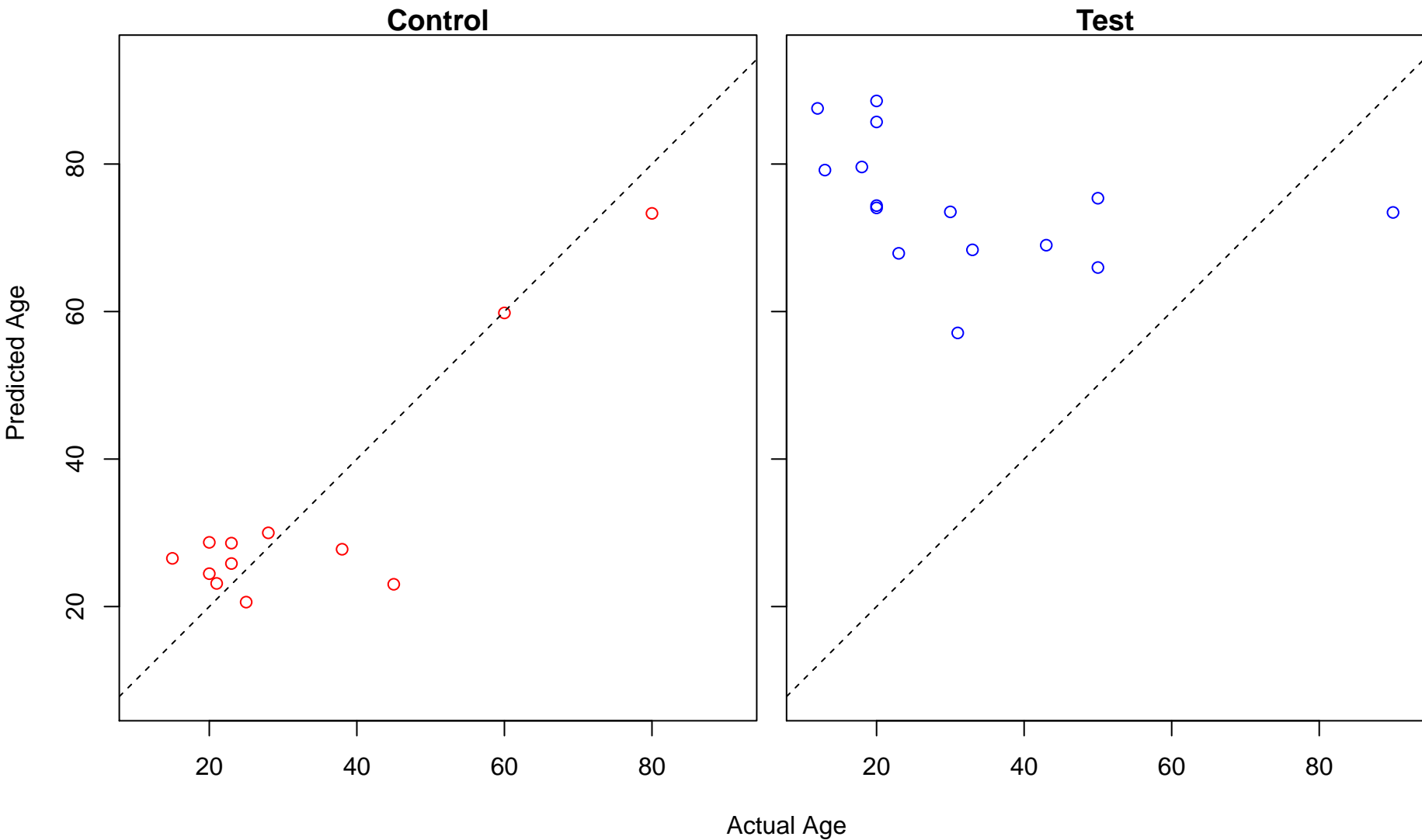
regulation of calcineurin-NFAT signaling cascade (Score: 10.136350)



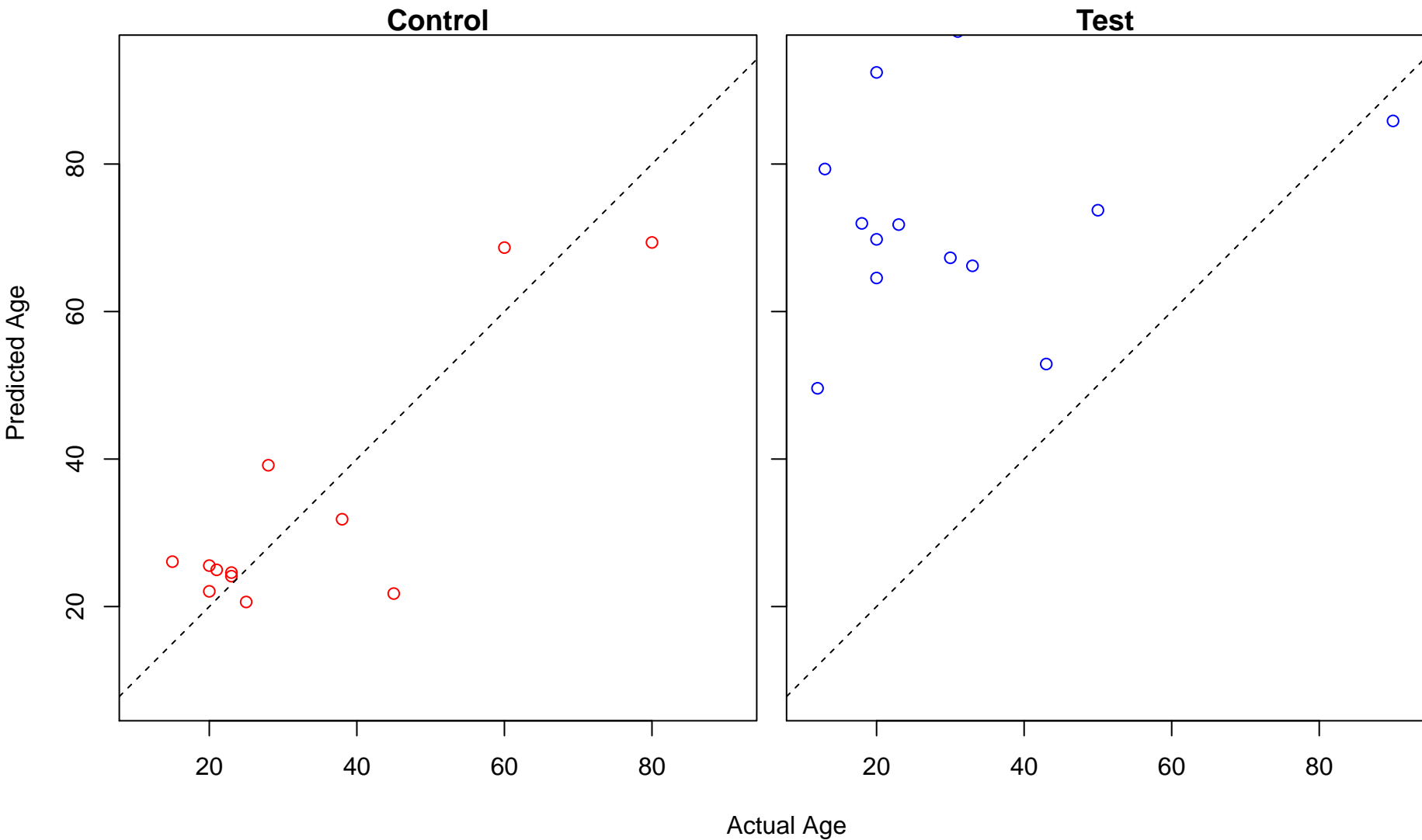
collecting duct development (Score: 10.126813)



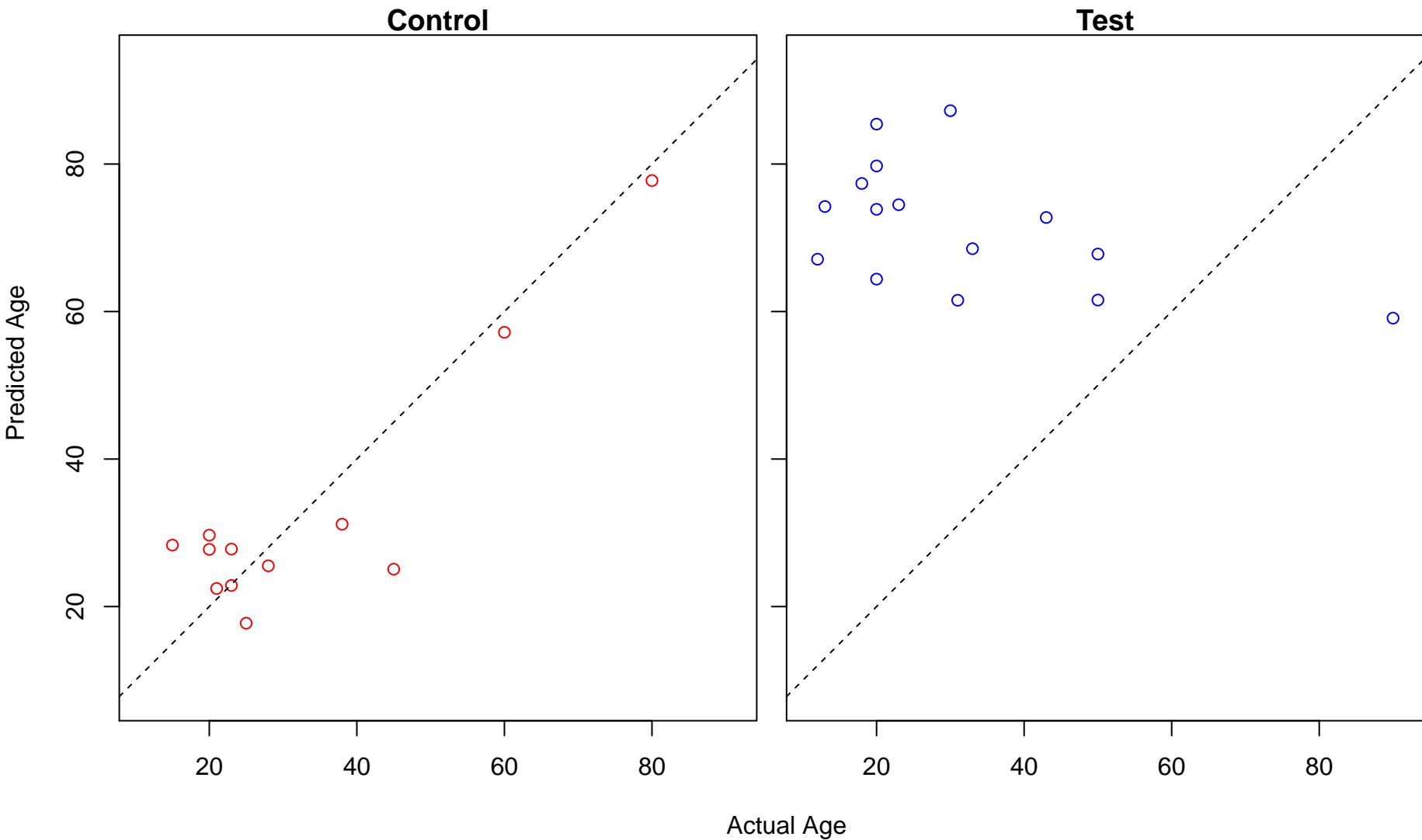
folic acid transport (Score: 10.114327)



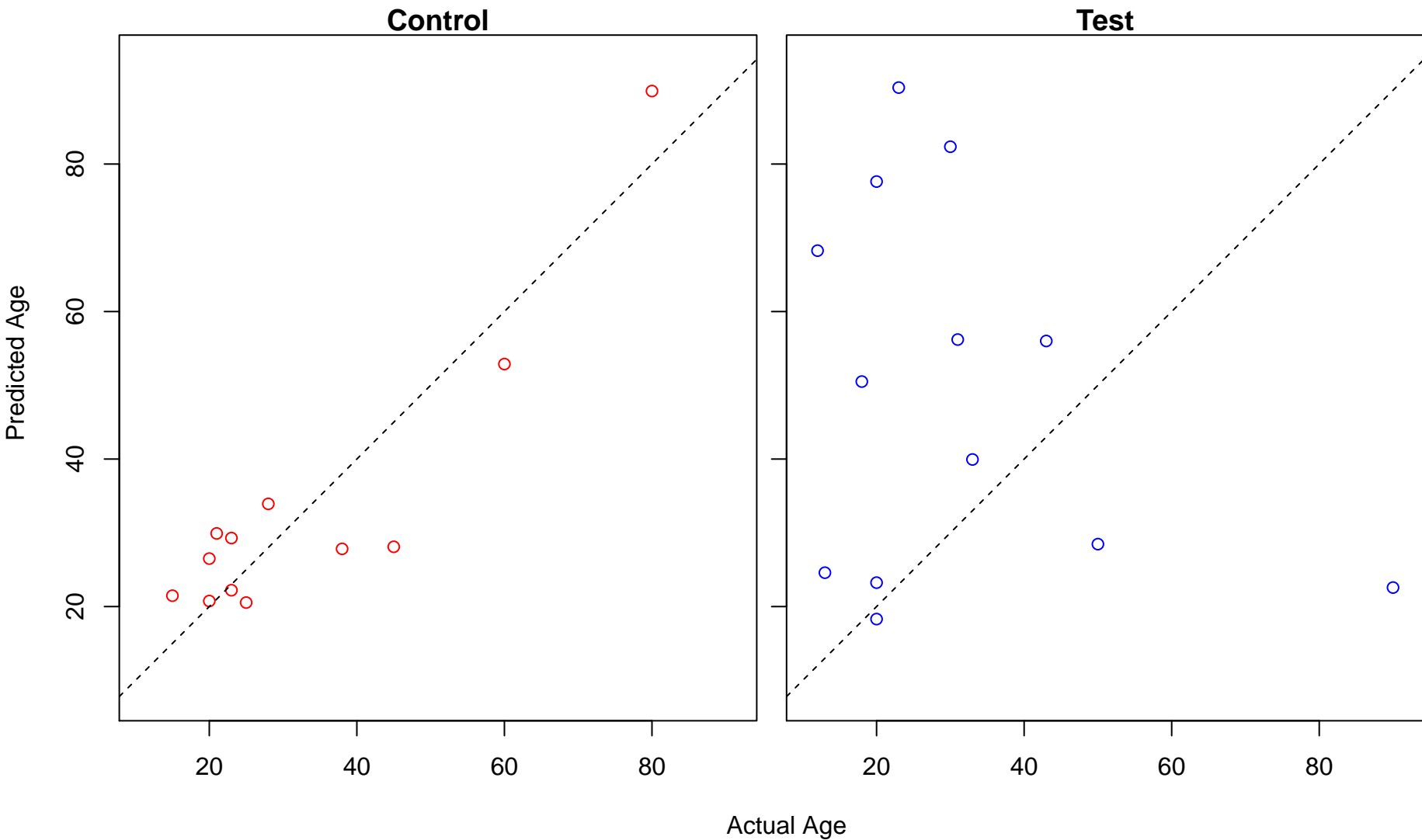
negative regulation of glycoprotein metabolic process (Score: 10.106644)



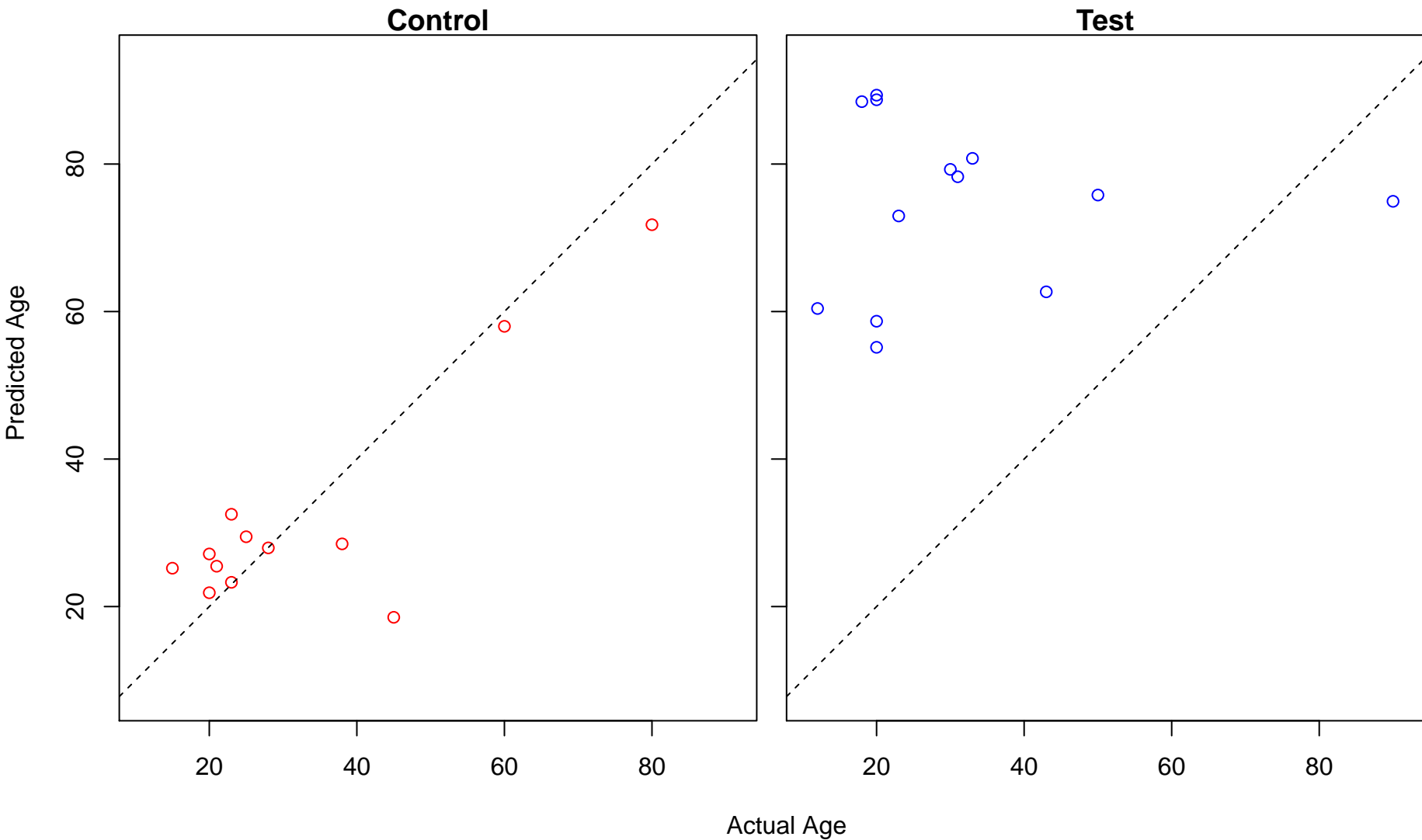
positive regulation of extracellular matrix disassembly (Score: 10.099526)



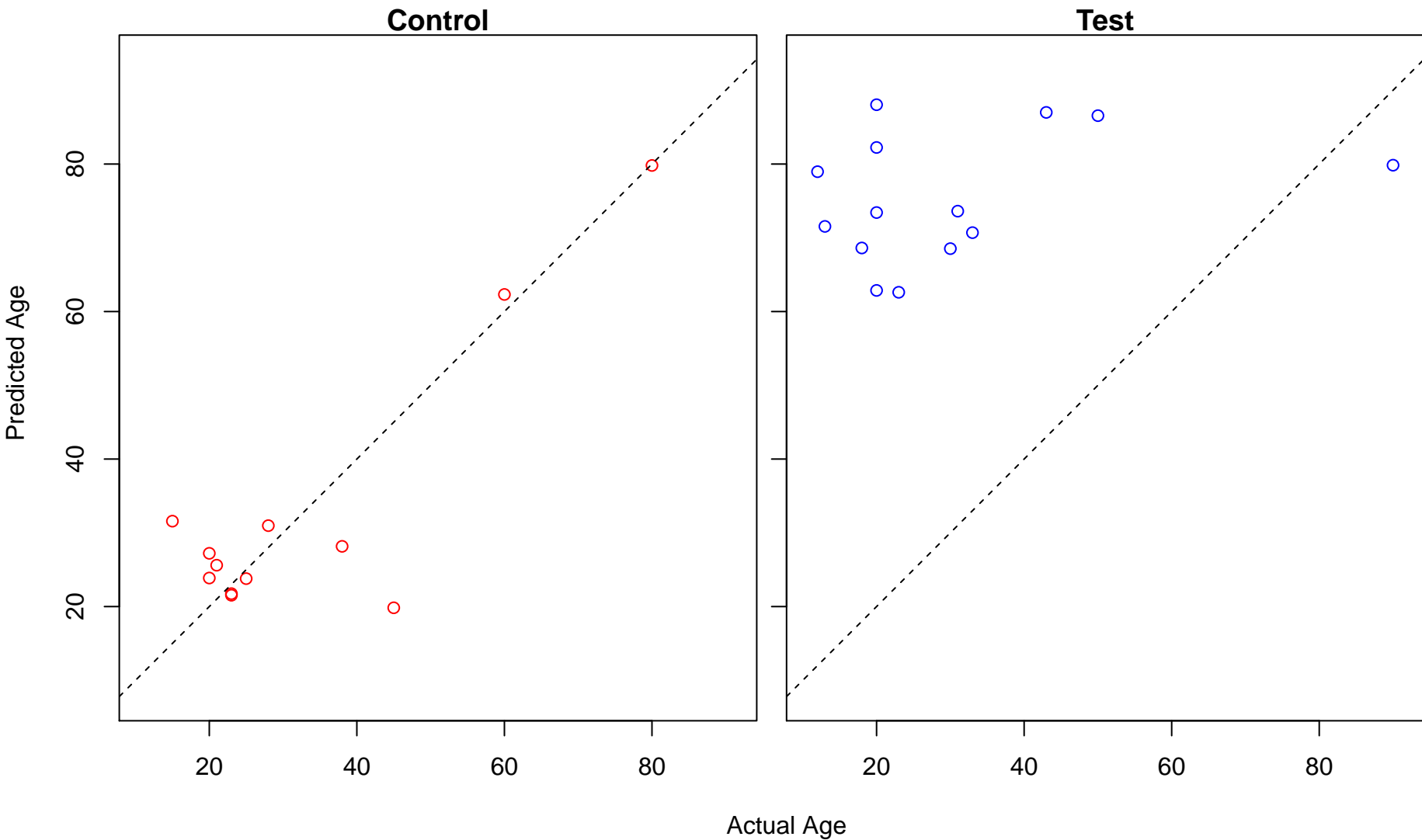
regulation of relaxation of muscle (Score: 10.088688)



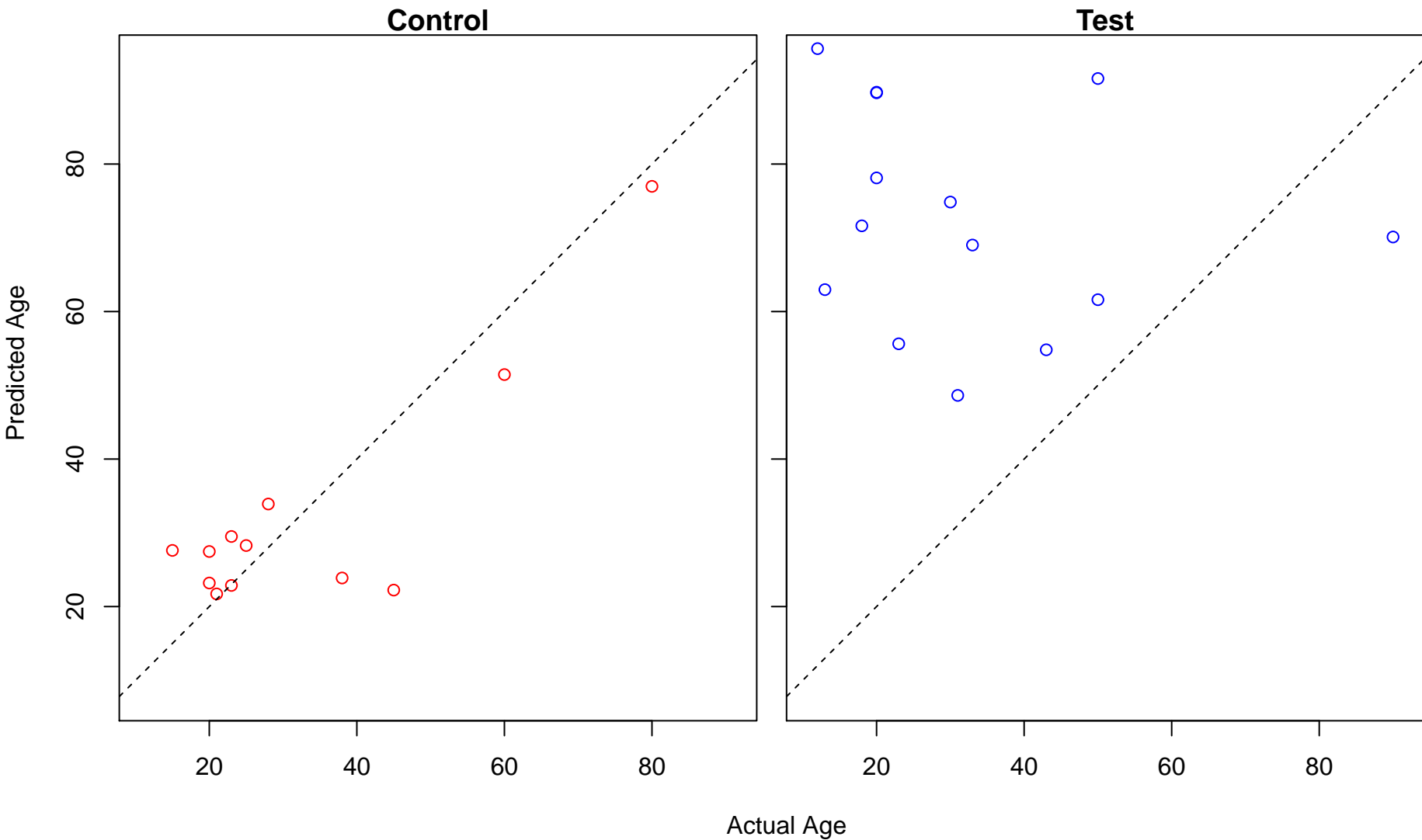
negative regulation of innate immune response (Score: 10.081235)



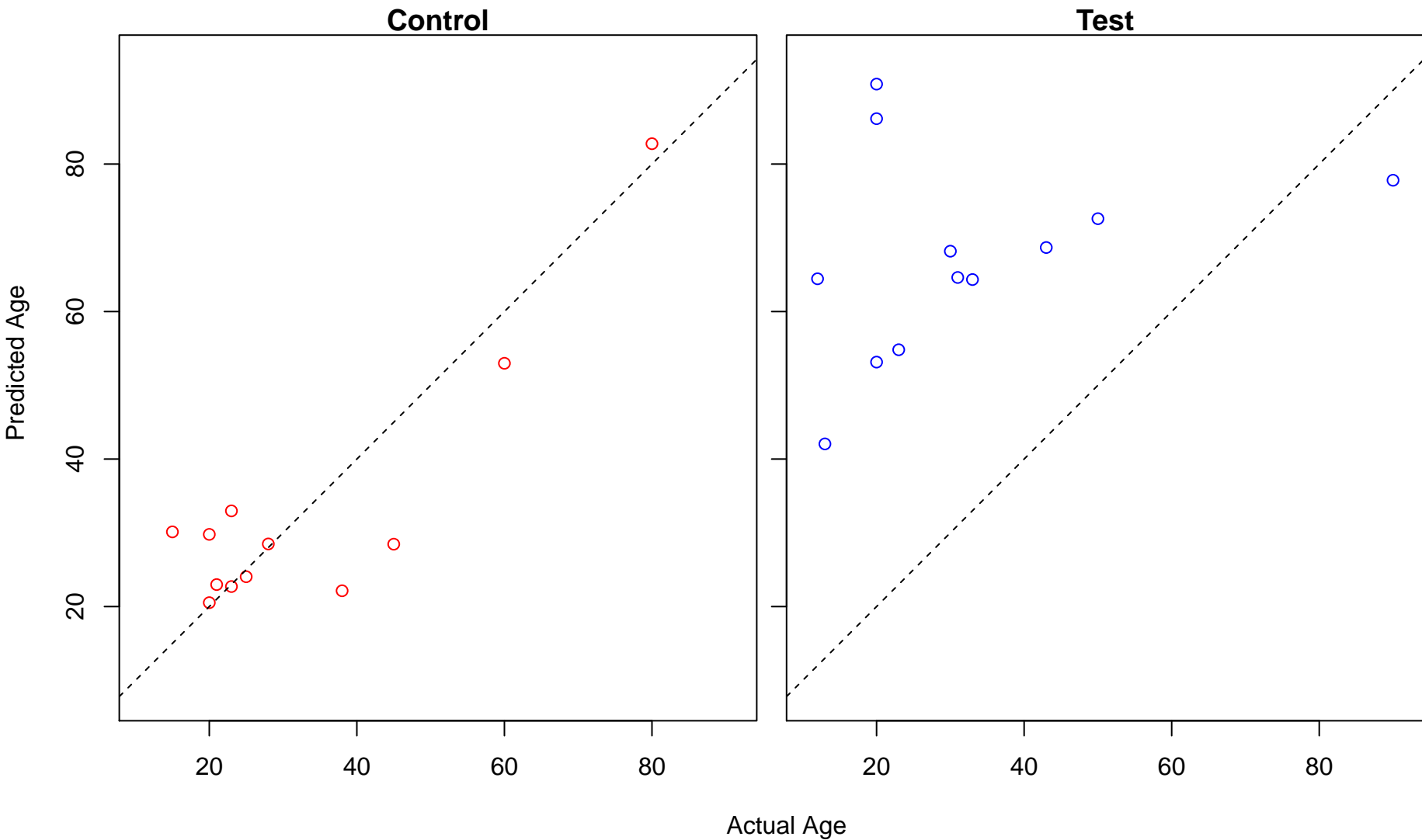
regulation of cell fate commitment (Score: 10.078736)



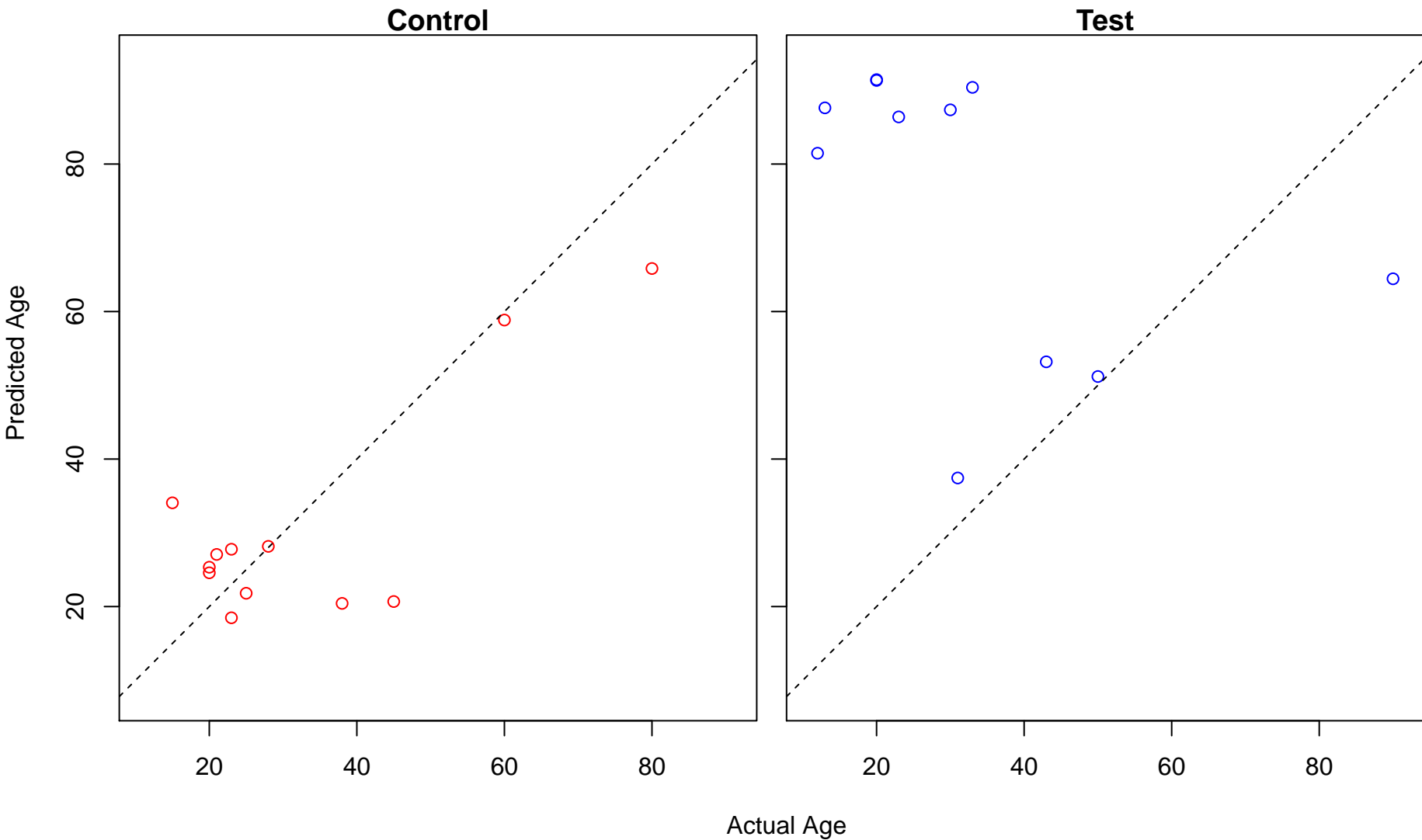
cofactor transport (Score: 10.077740)



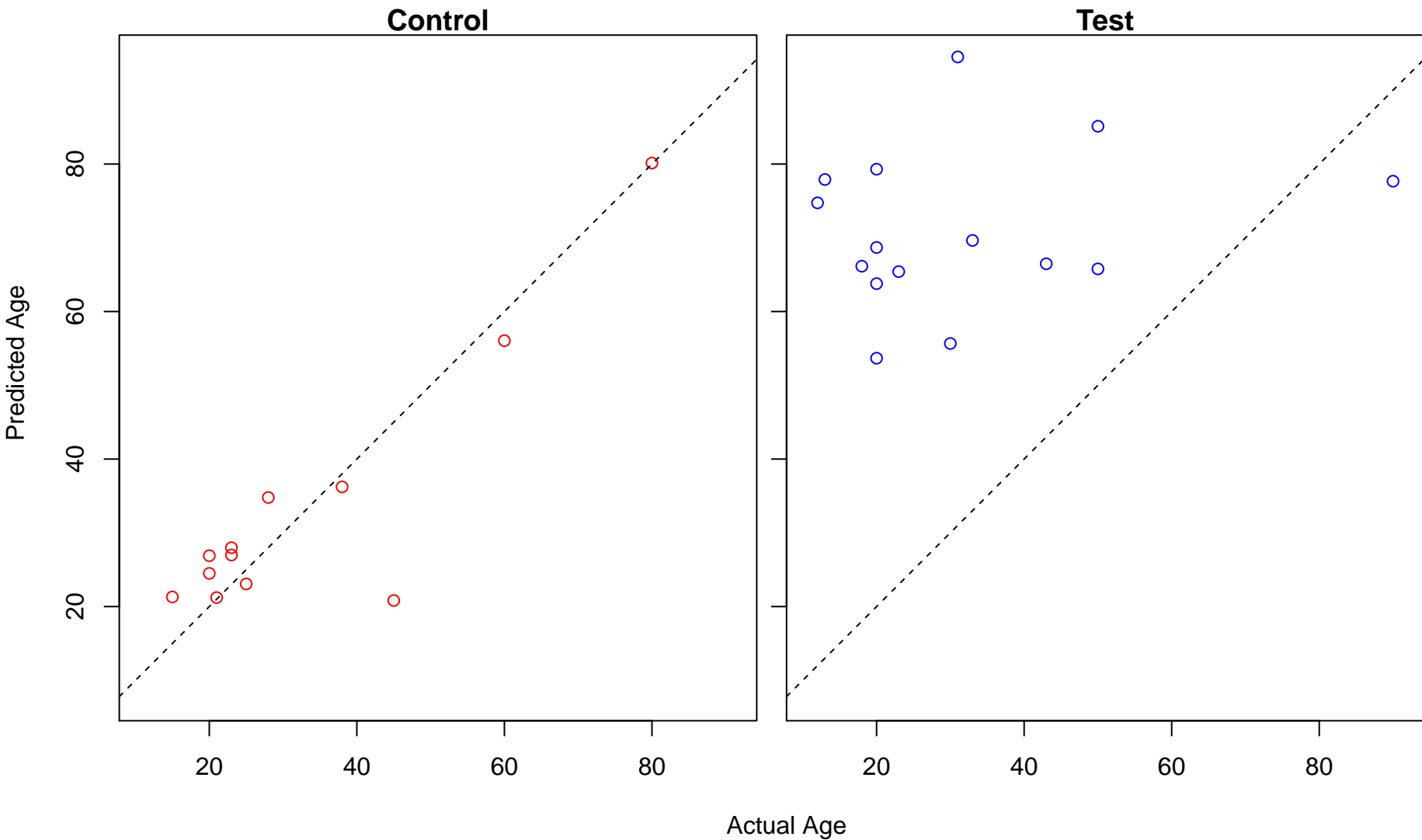
regulation of protein sumoylation (Score: 10.064272)



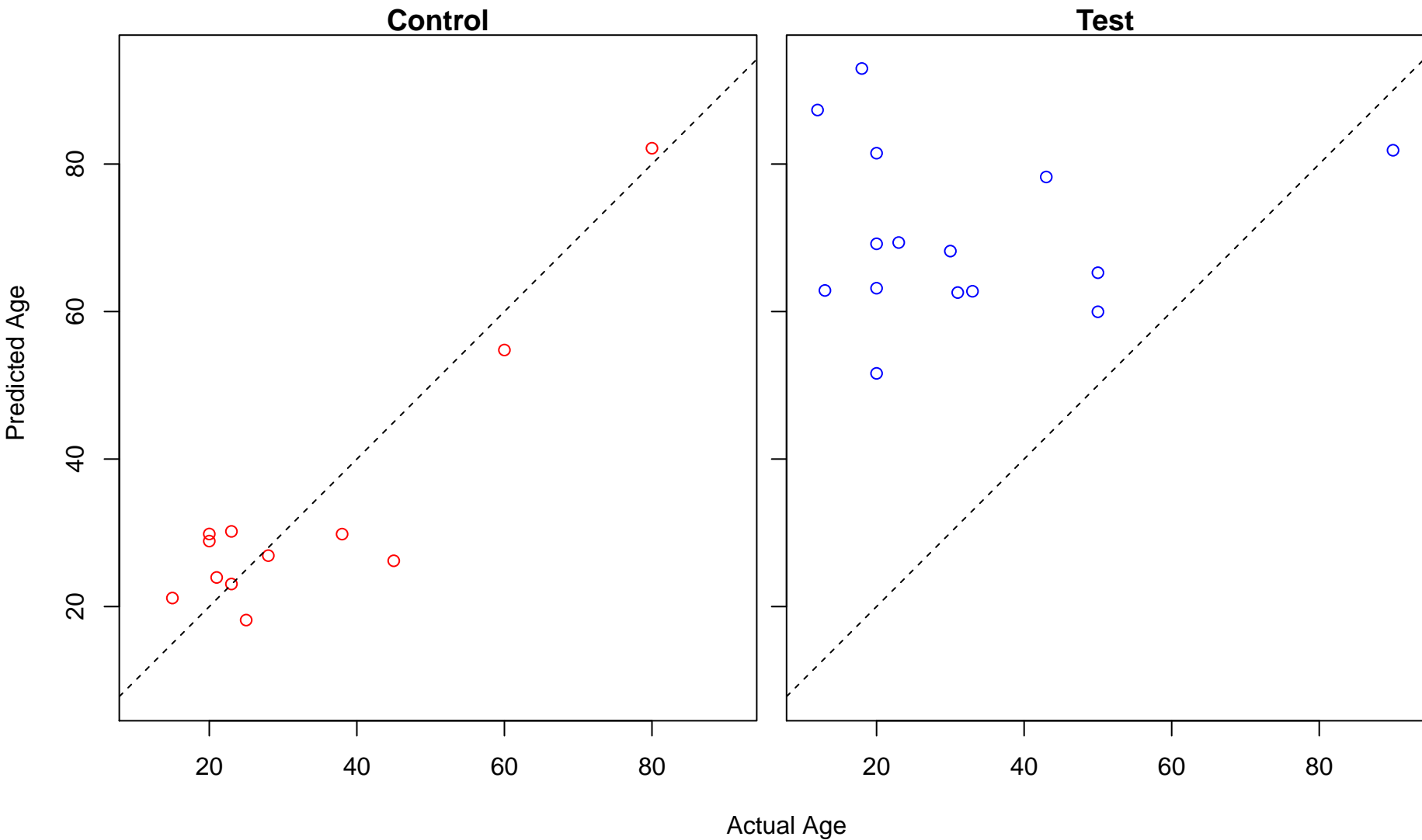
mRNA splice site selection (Score: 10.052498)



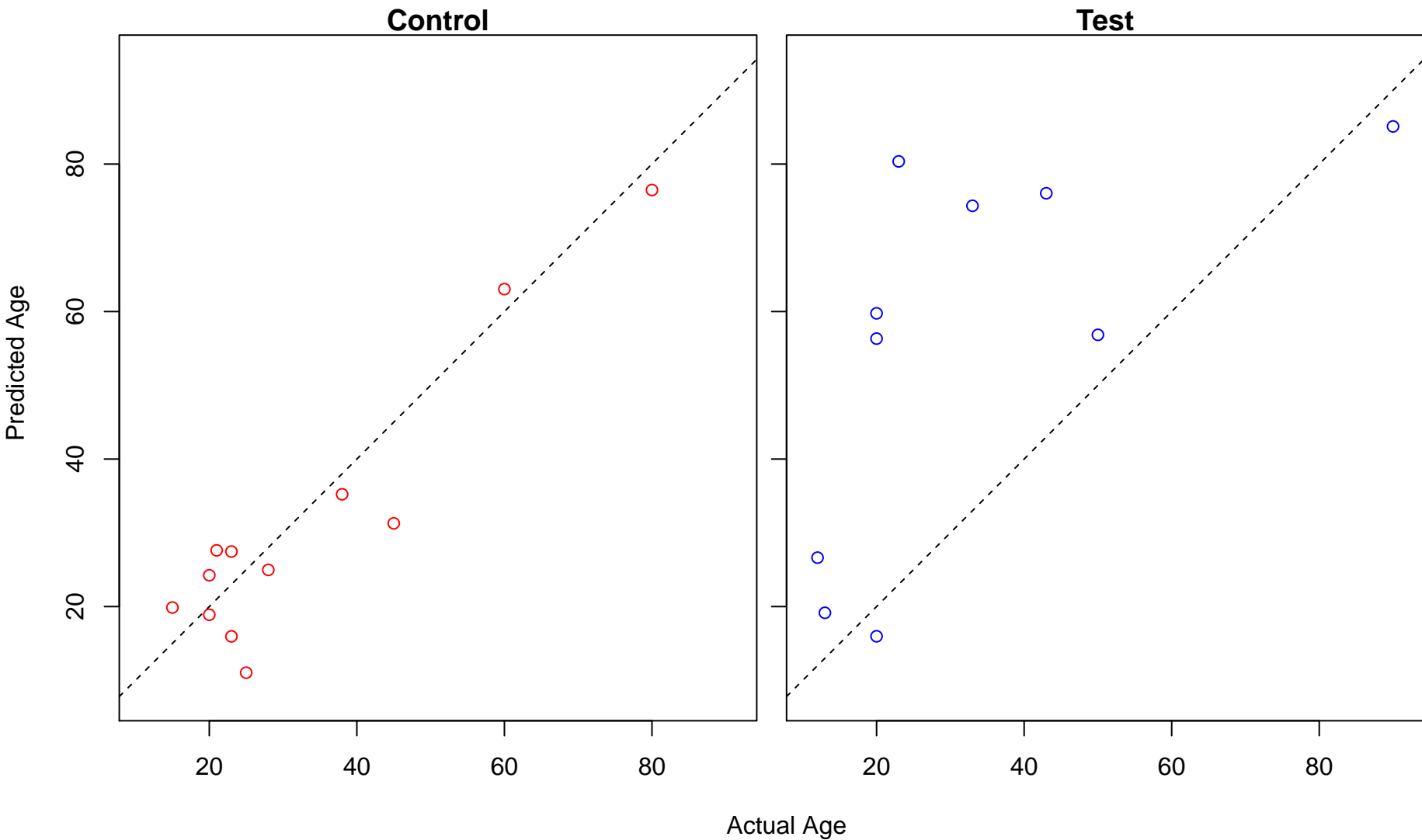
regulation of axon guidance (Score: 10.039877)



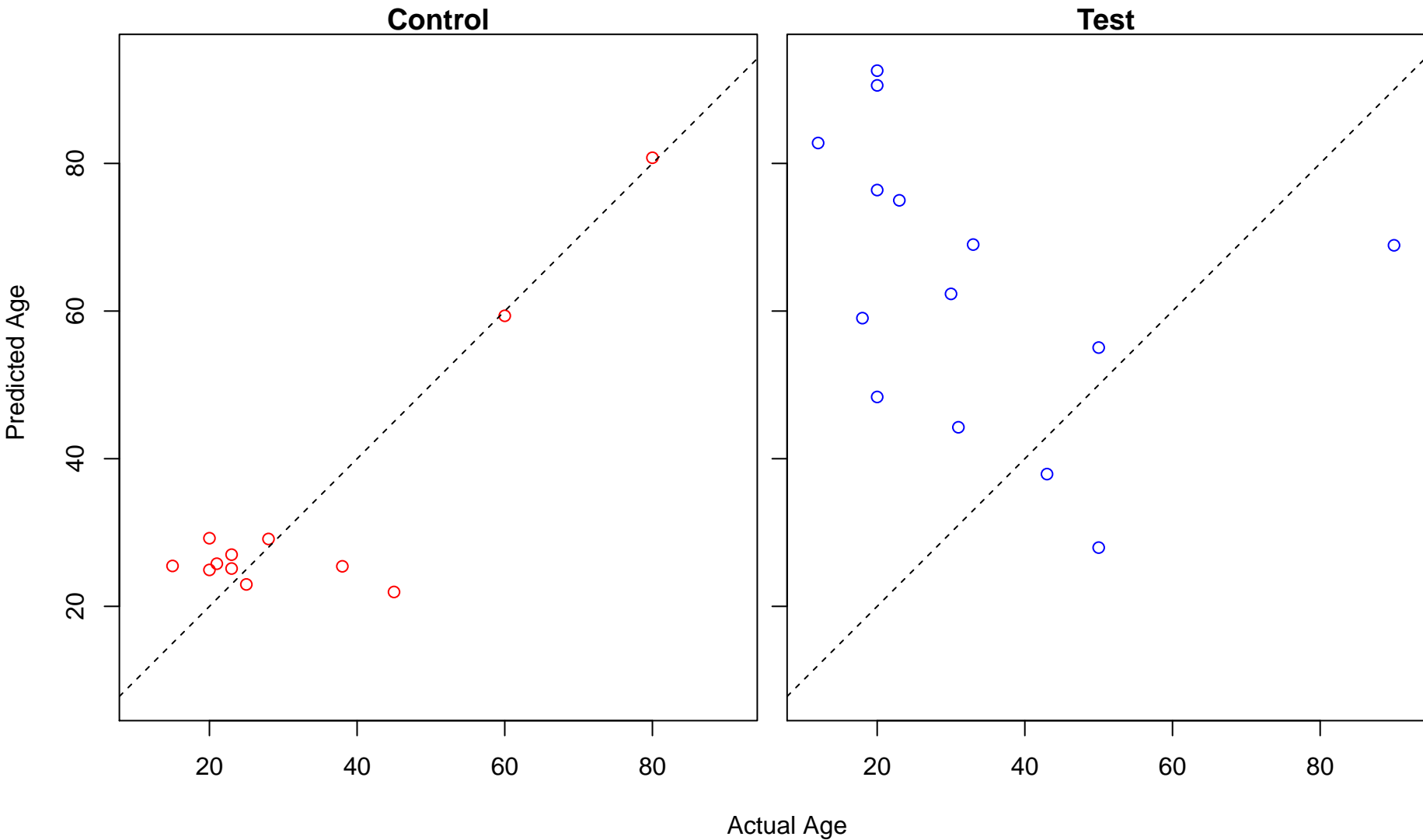
snRNA transcription (Score: 10.038742)



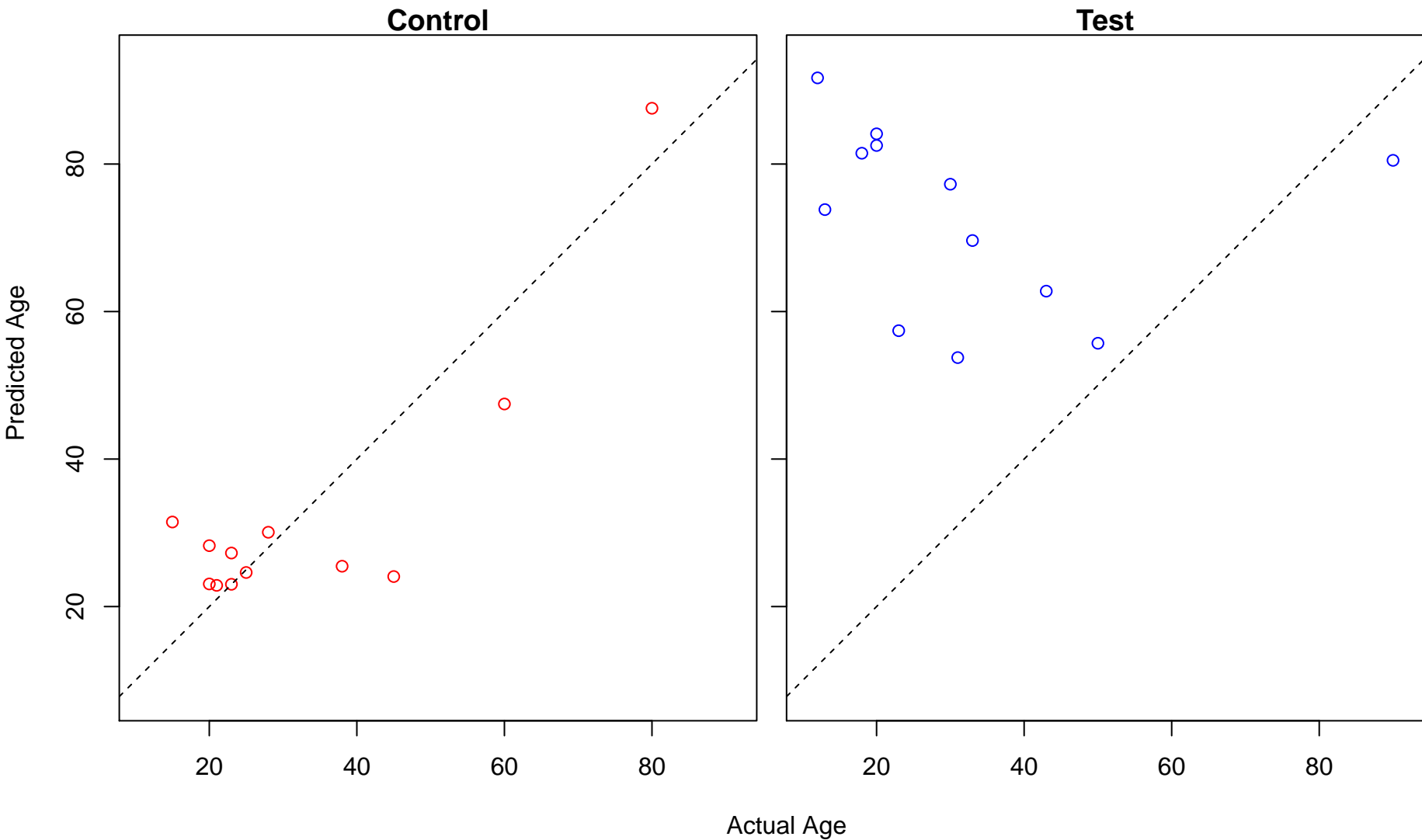
metanephros morphogenesis (Score: 10.021876)



negative regulation of smooth muscle cell differentiation (Score: 10.019774)

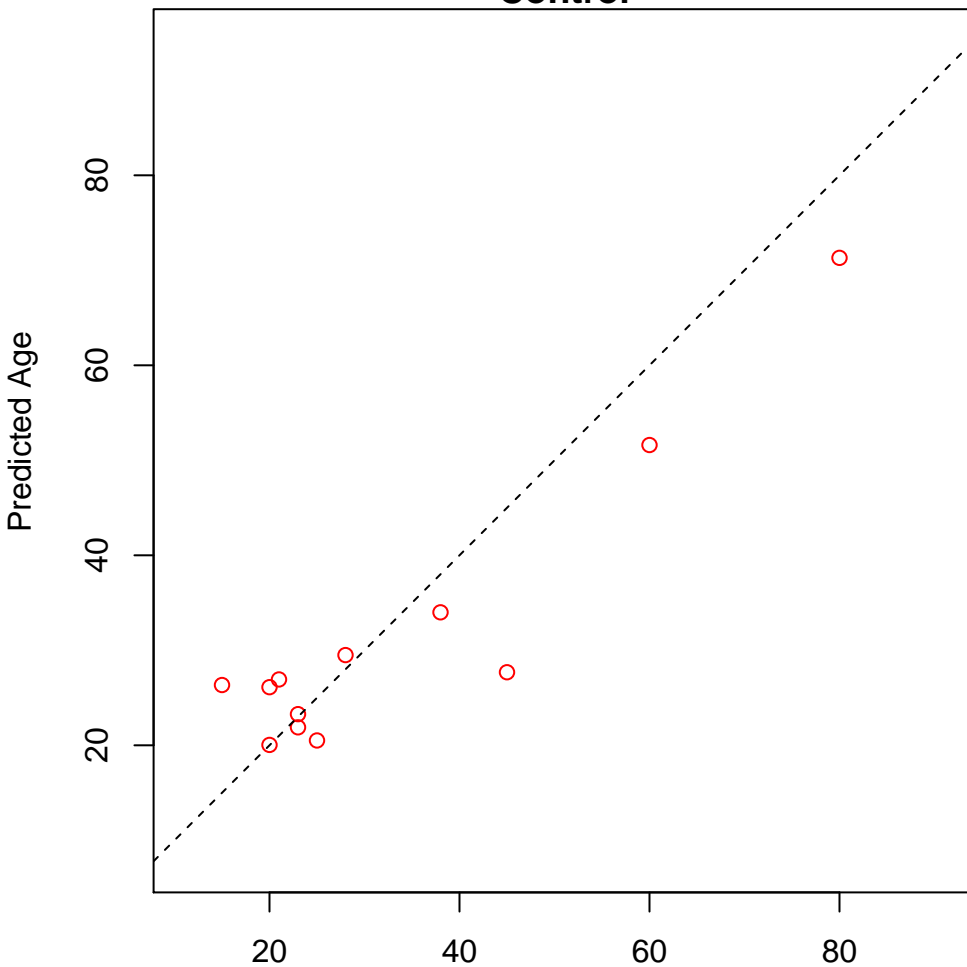


cellular response to nutrient (Score: 10.019190)

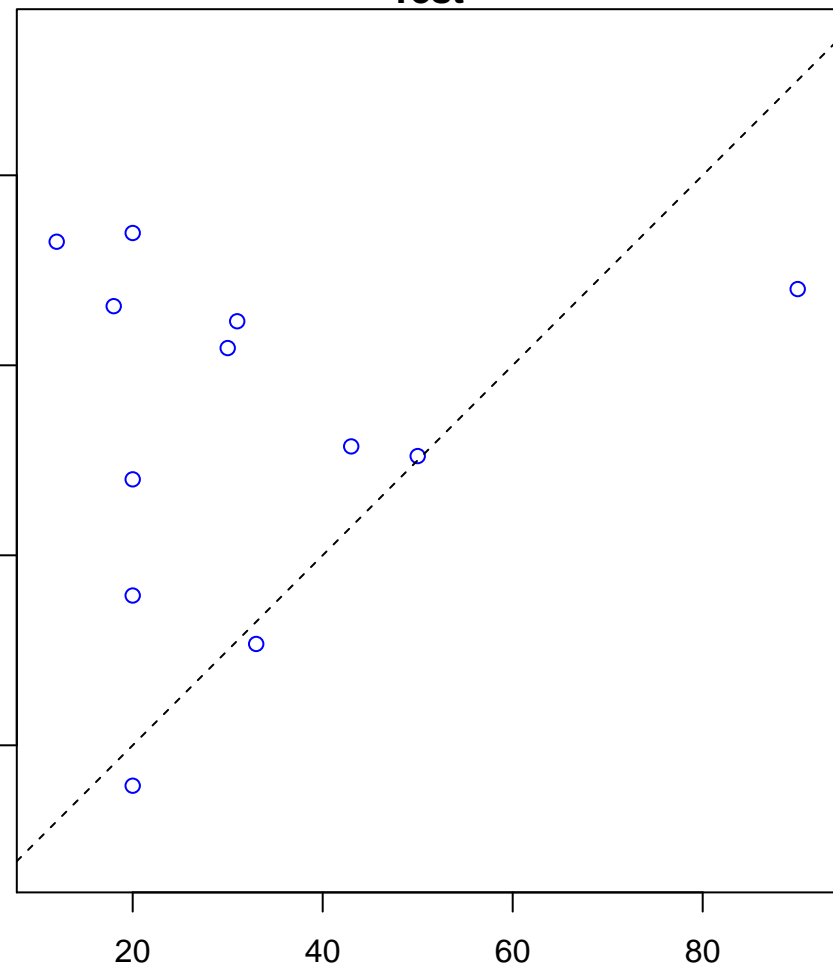


internal protein amino acid acetylation (Score: 10.006727)

Control

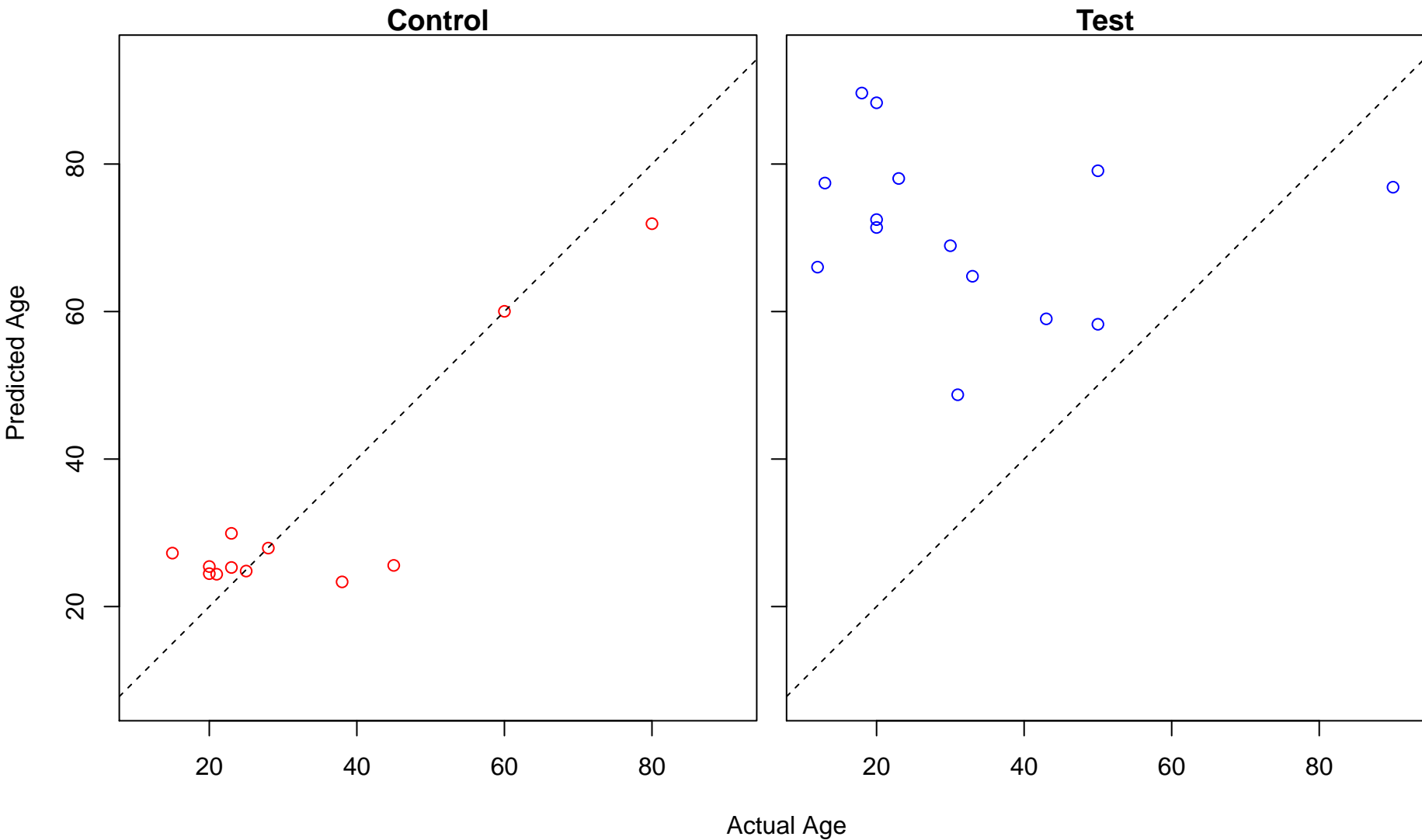


Test

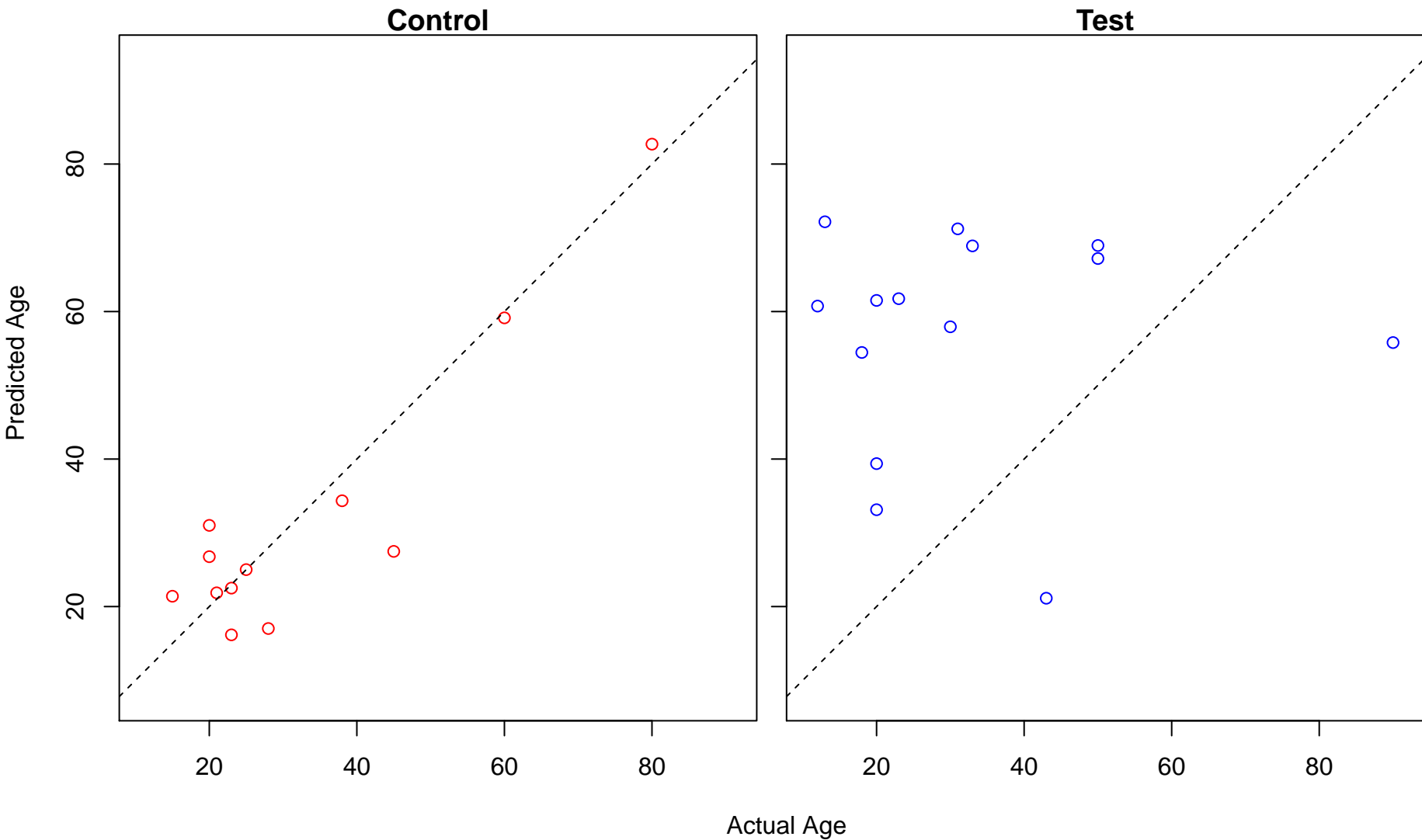


Actual Age

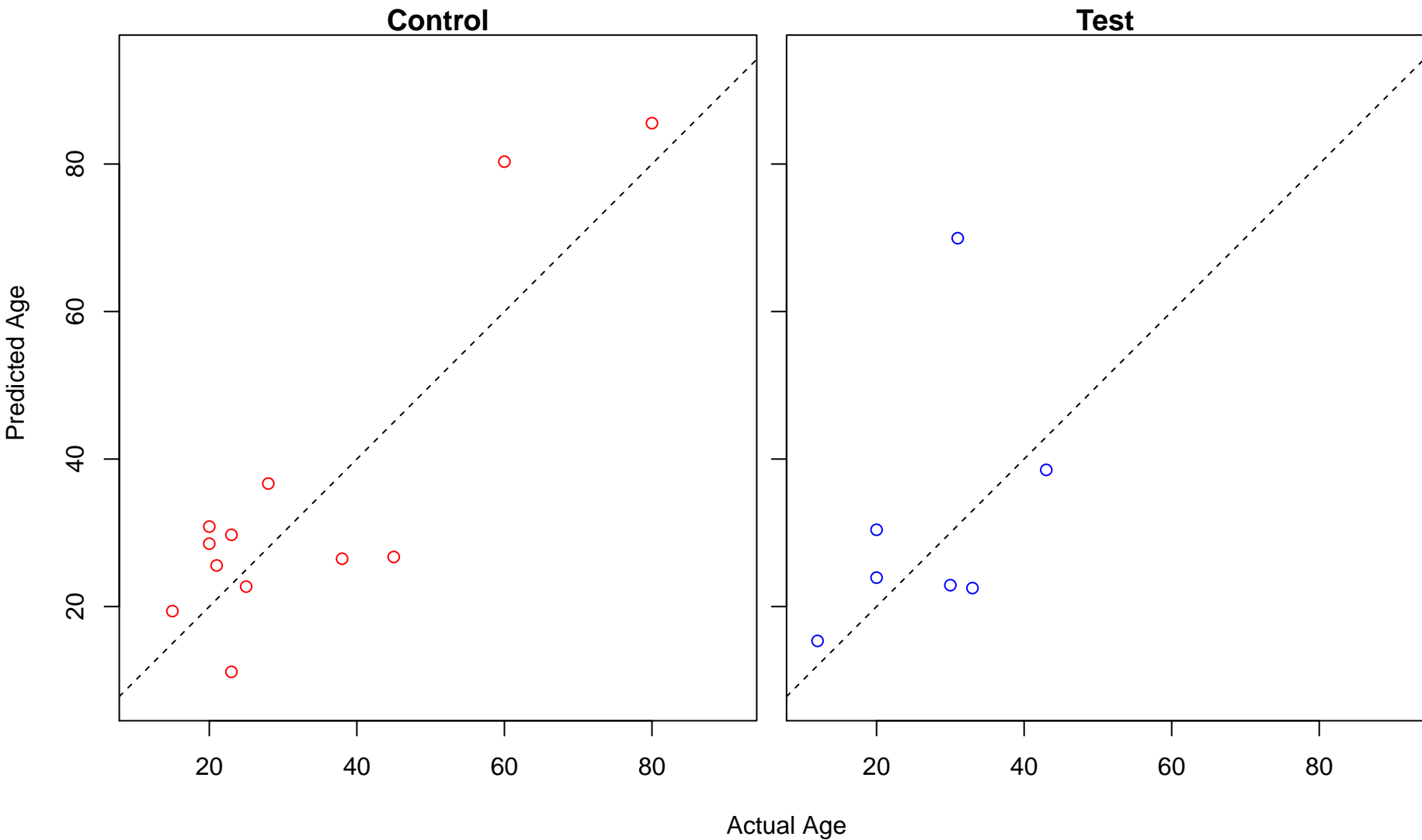
cAMP-mediated signaling (Score: 9.999065)



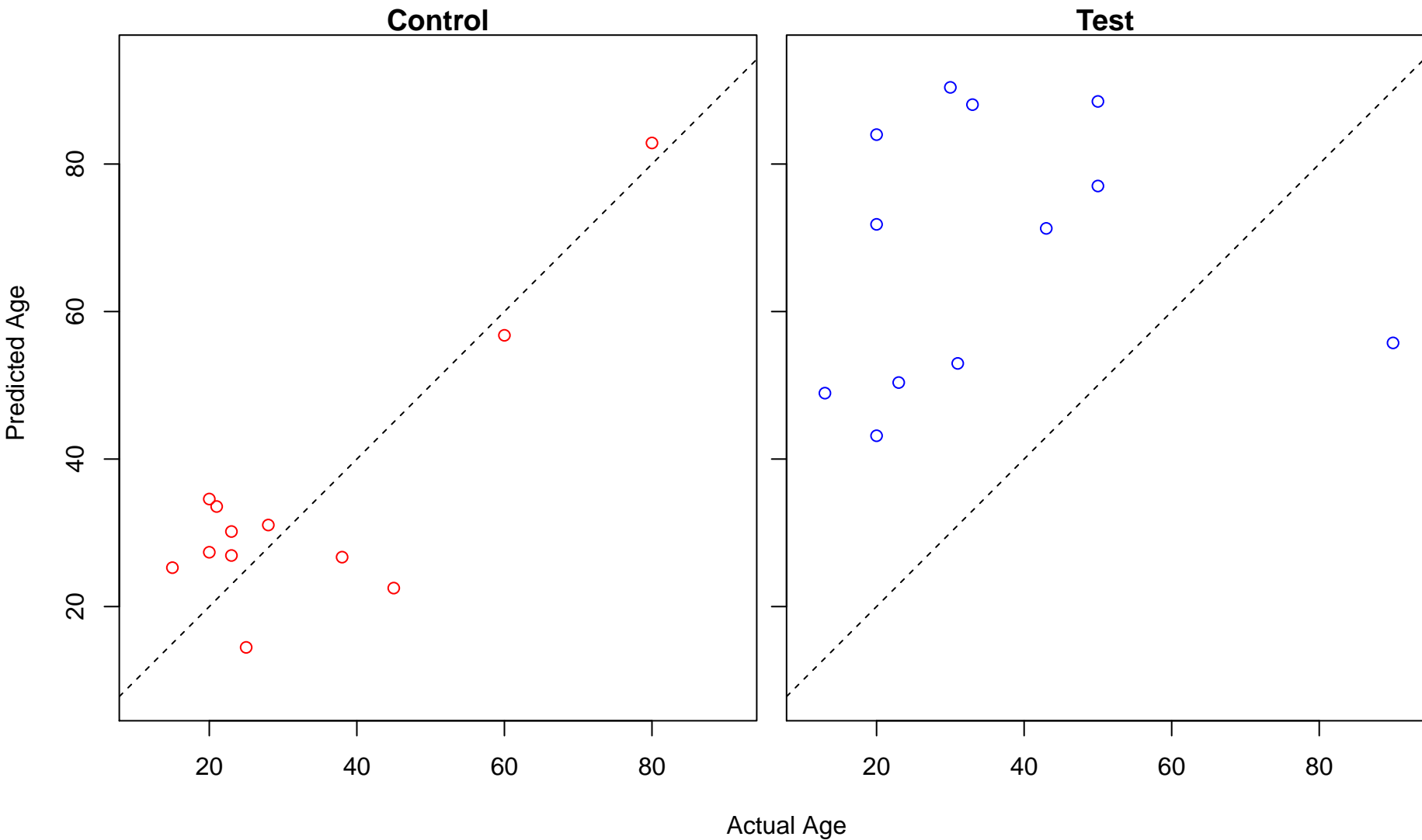
regulation of protein modification by small protein conjugation or removal (Score: 9.984564)



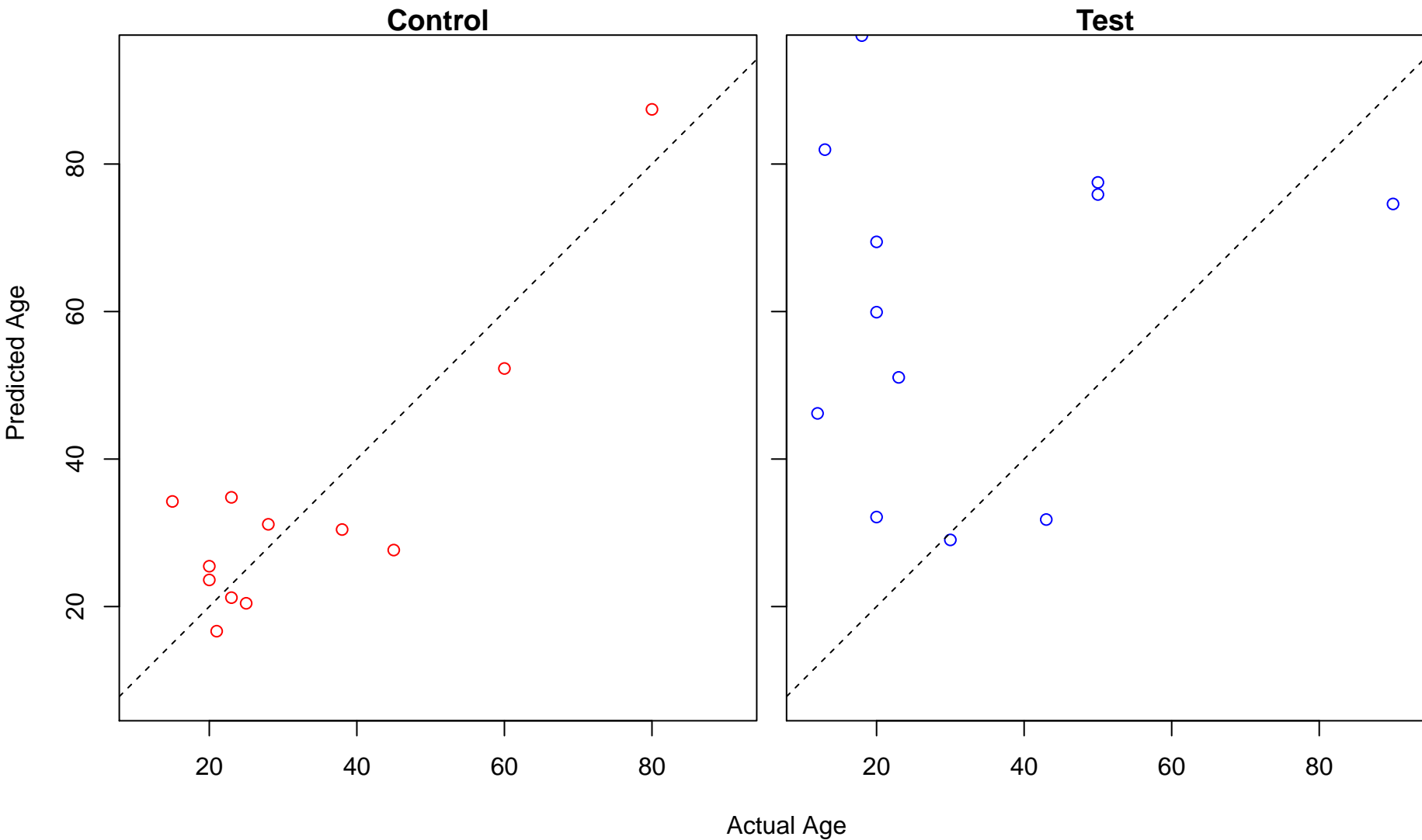
telomere maintenance in response to DNA damage (Score: 9.980733)



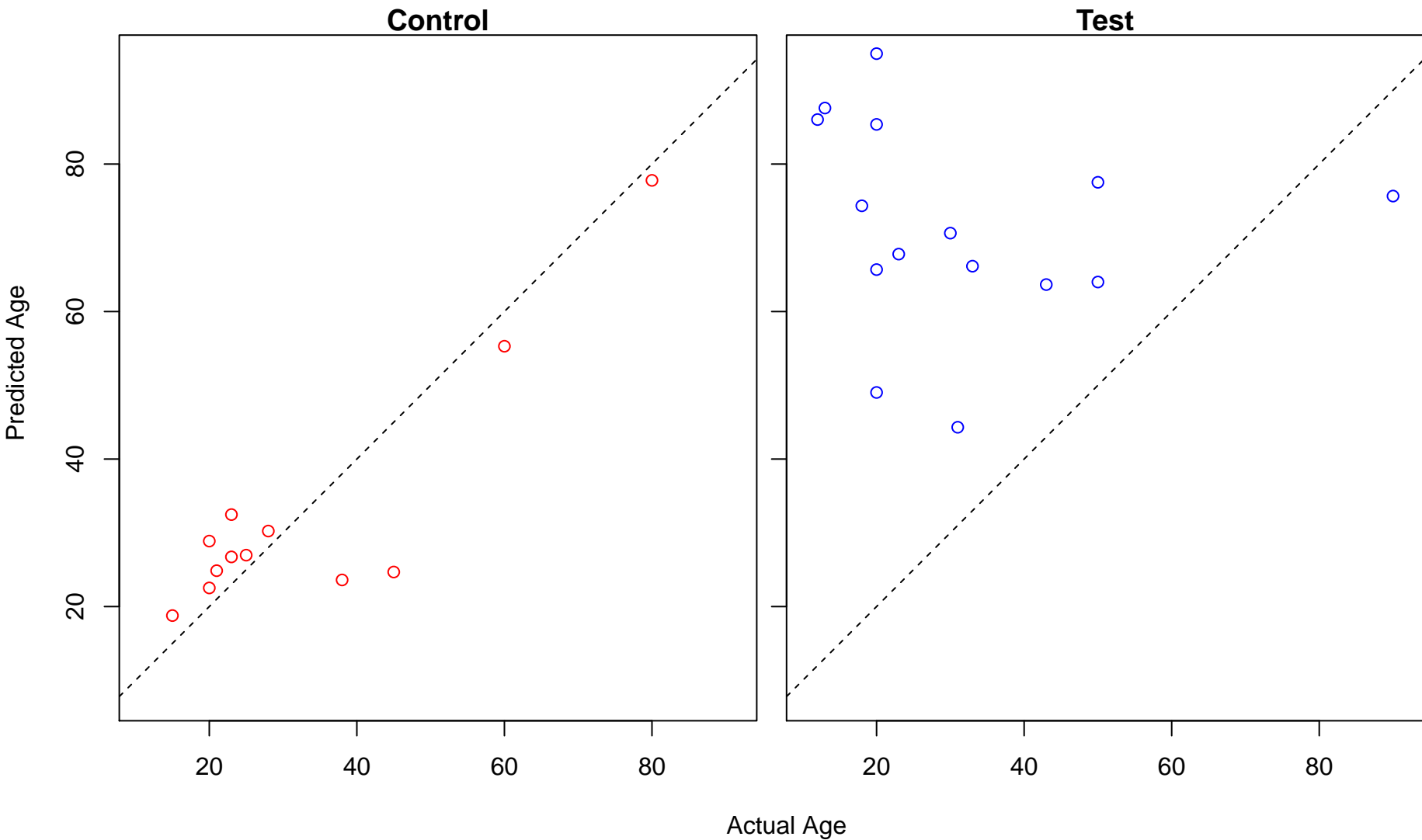
vesicle fusion (Score: 9.980477)



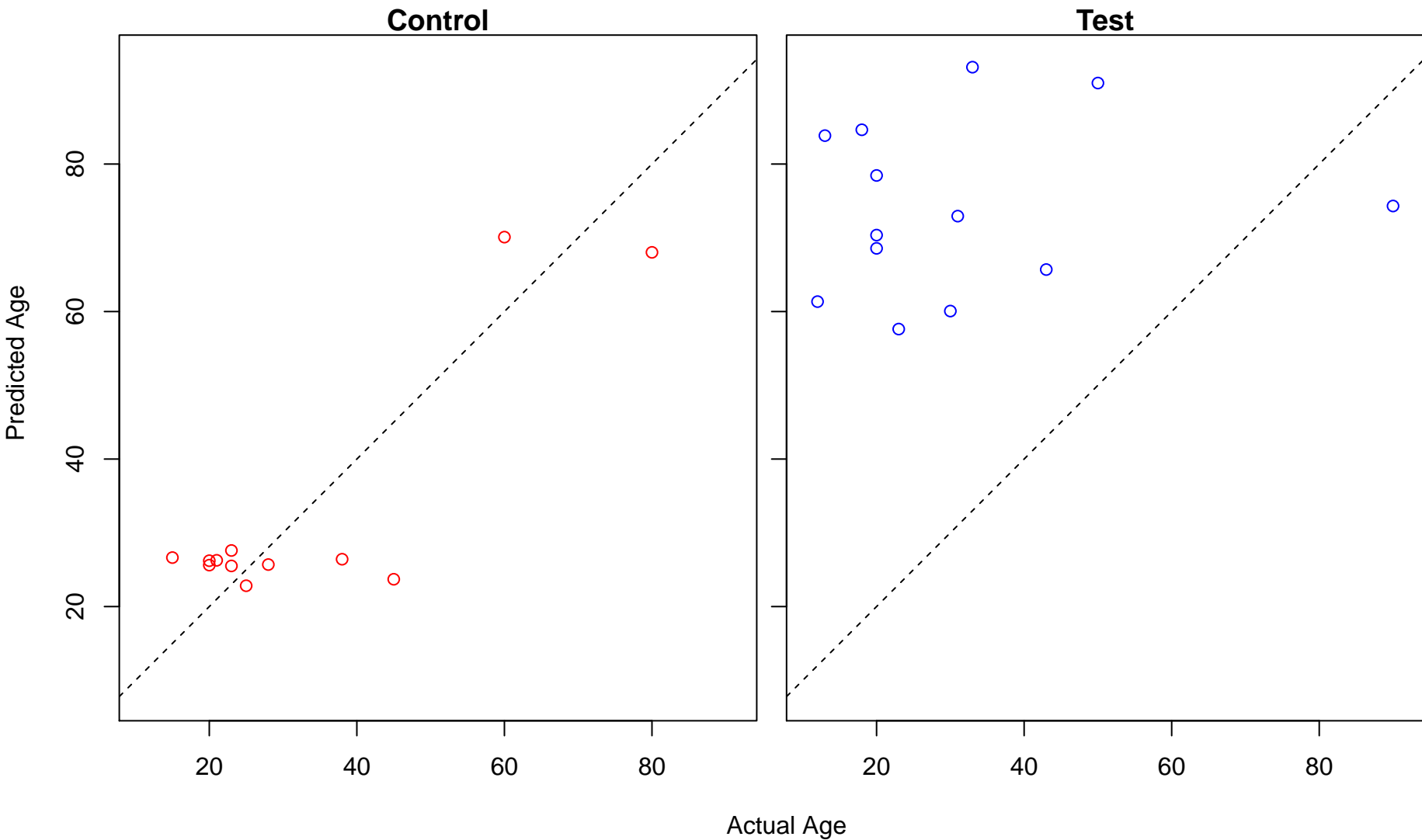
negative regulation of nervous system development (Score: 9.970575)



trabecula morphogenesis (Score: 9.966305)

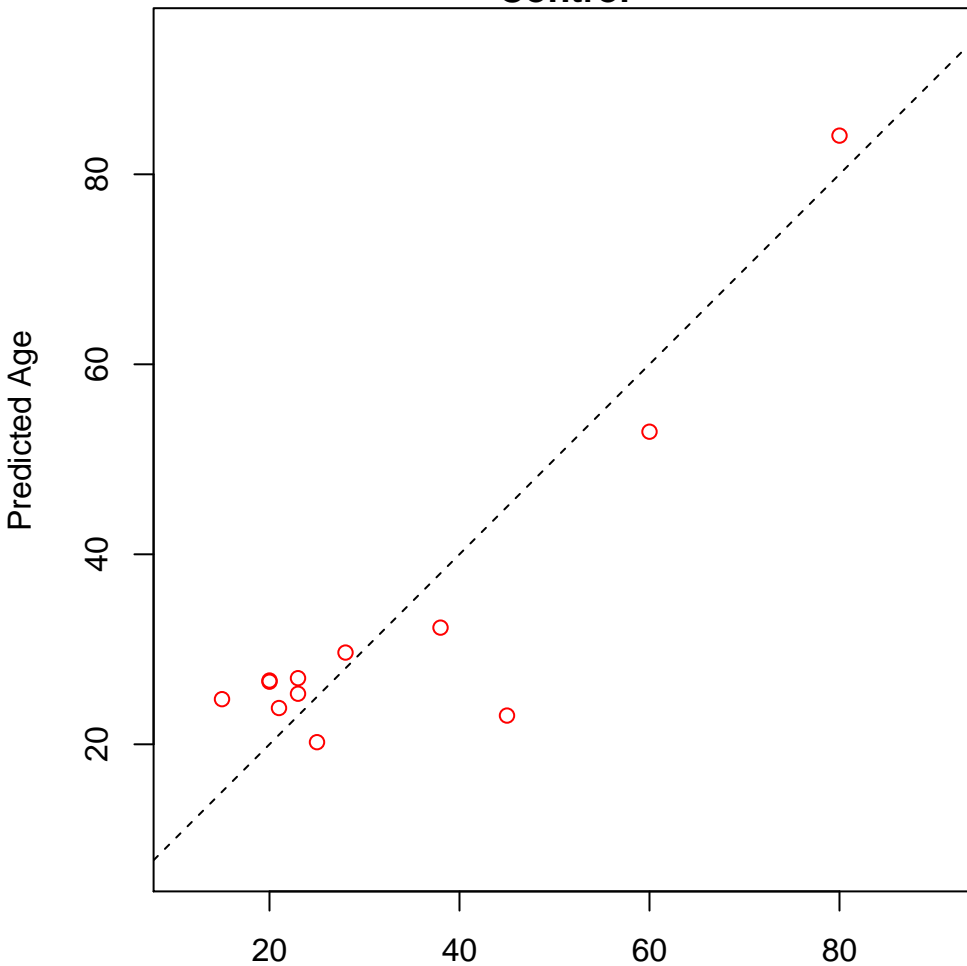


regulation of lymphocyte apoptotic process (Score: 9.963331)

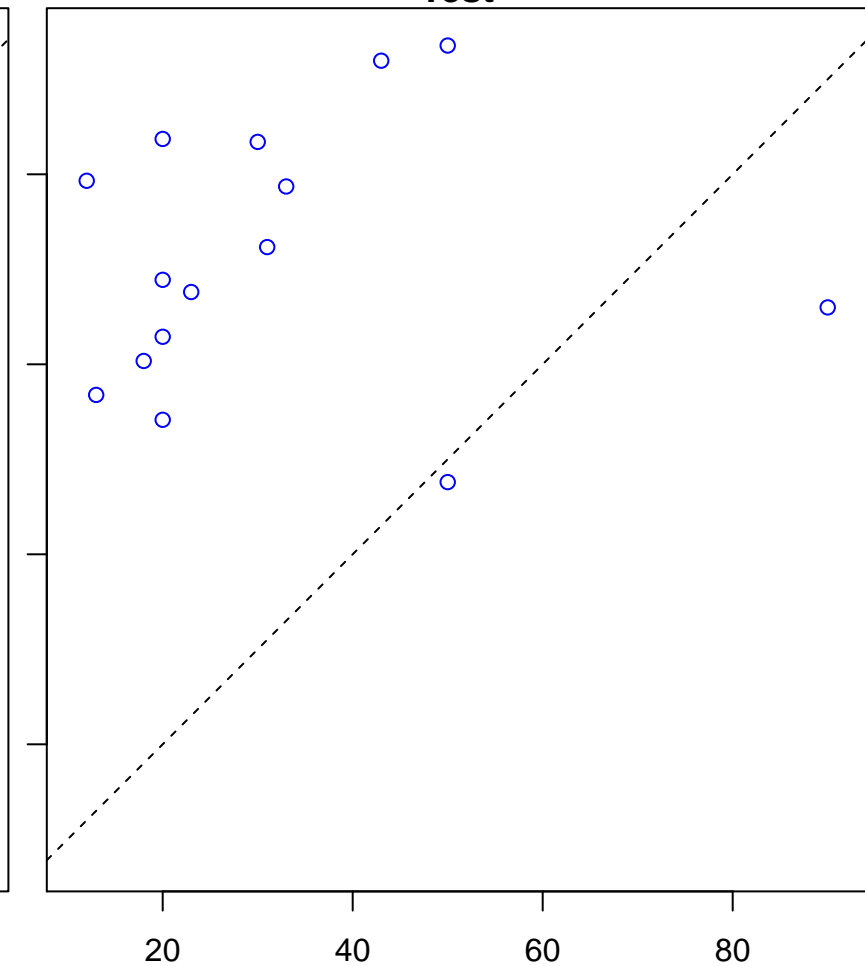


chondroitin sulfate catabolic process (Score: 9.960871)

Control

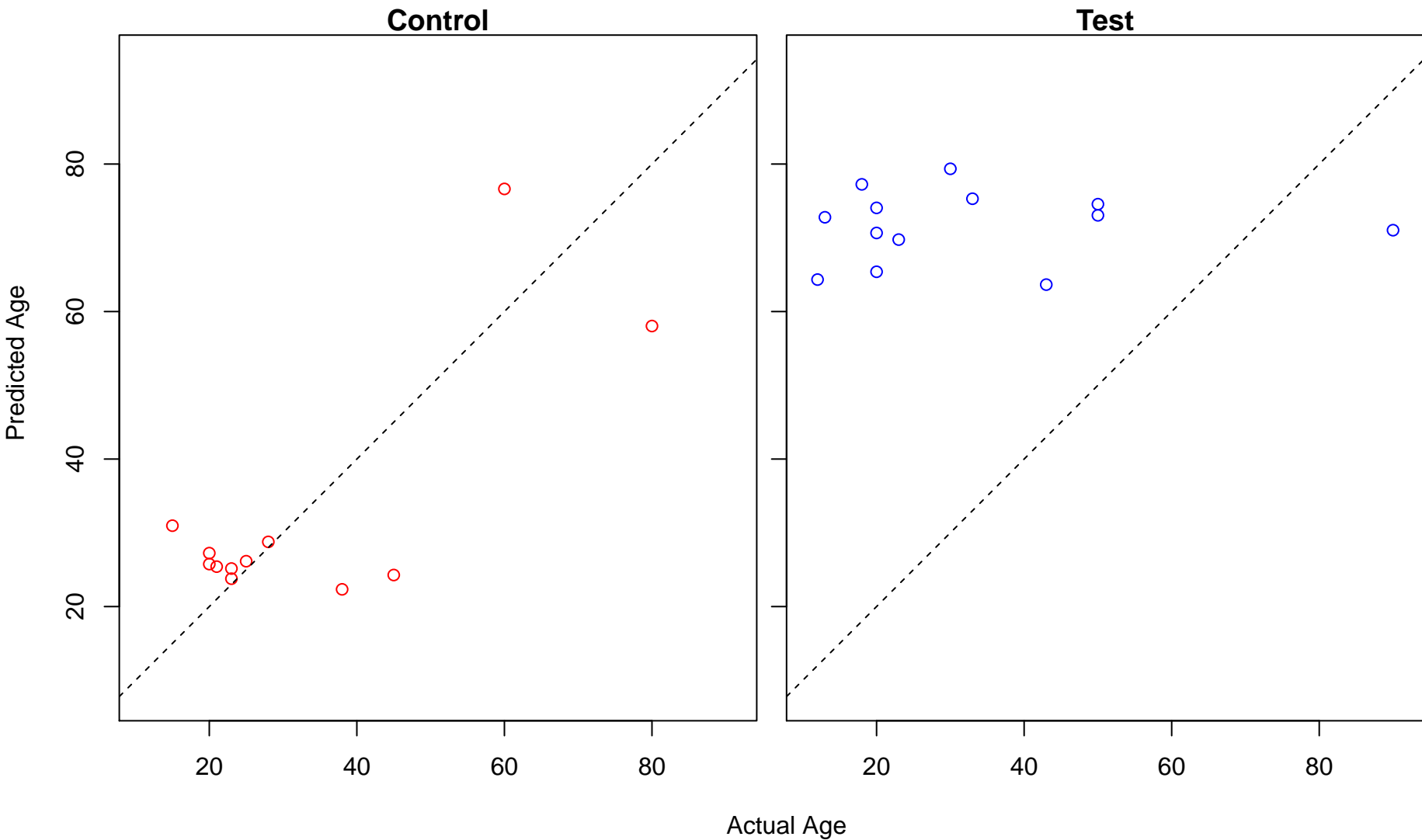


Test

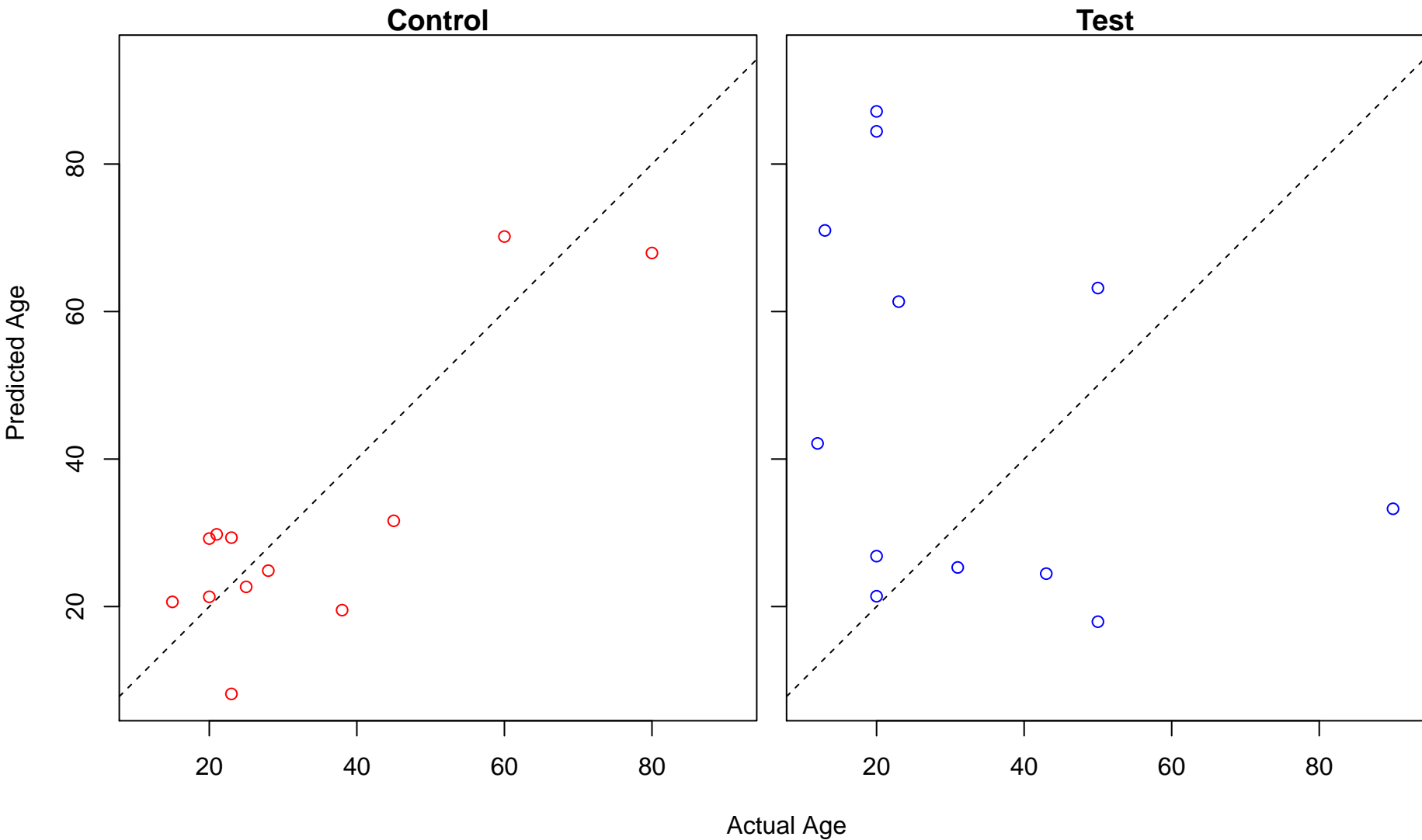


Actual Age

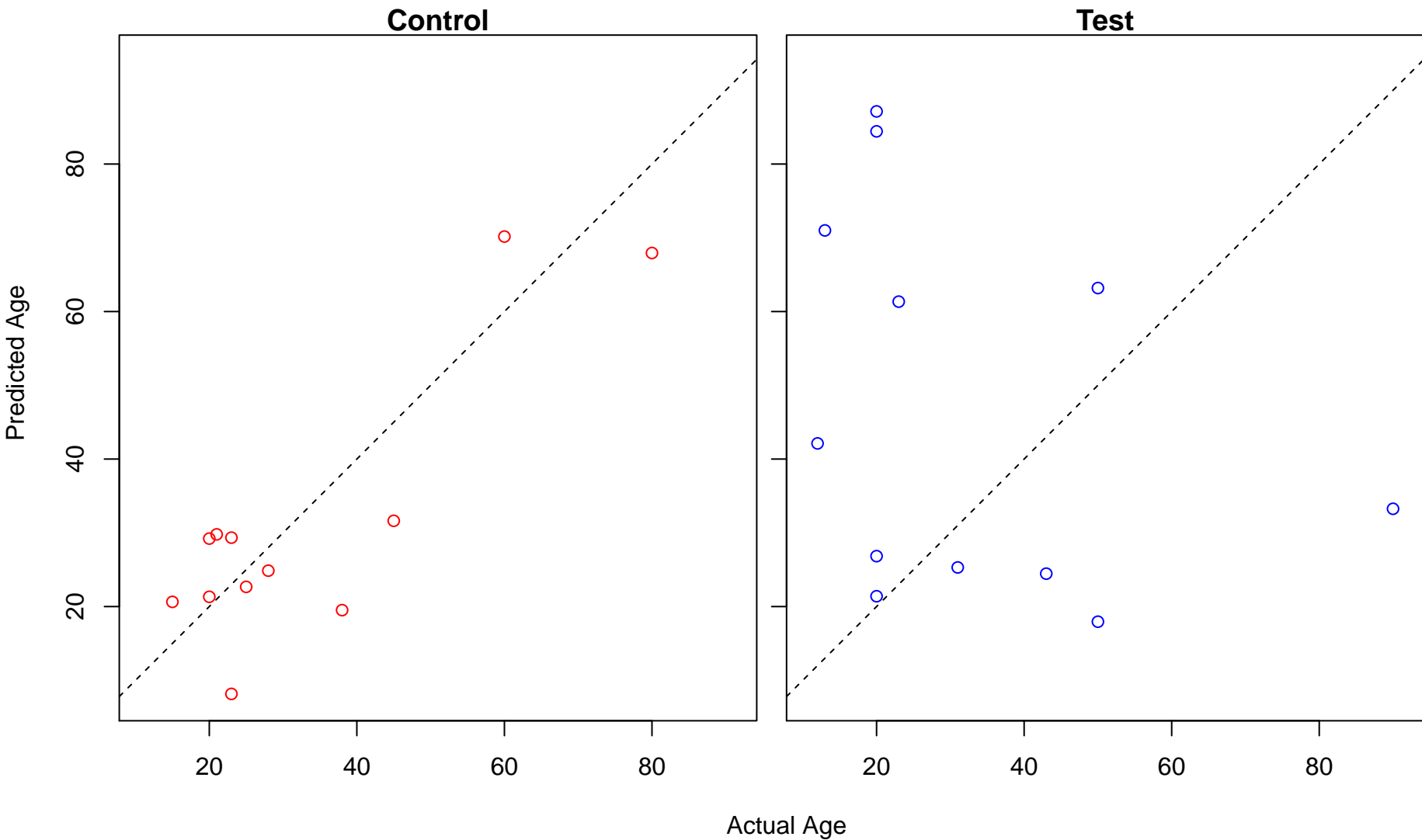
tolerance induction (Score: 9.945045)



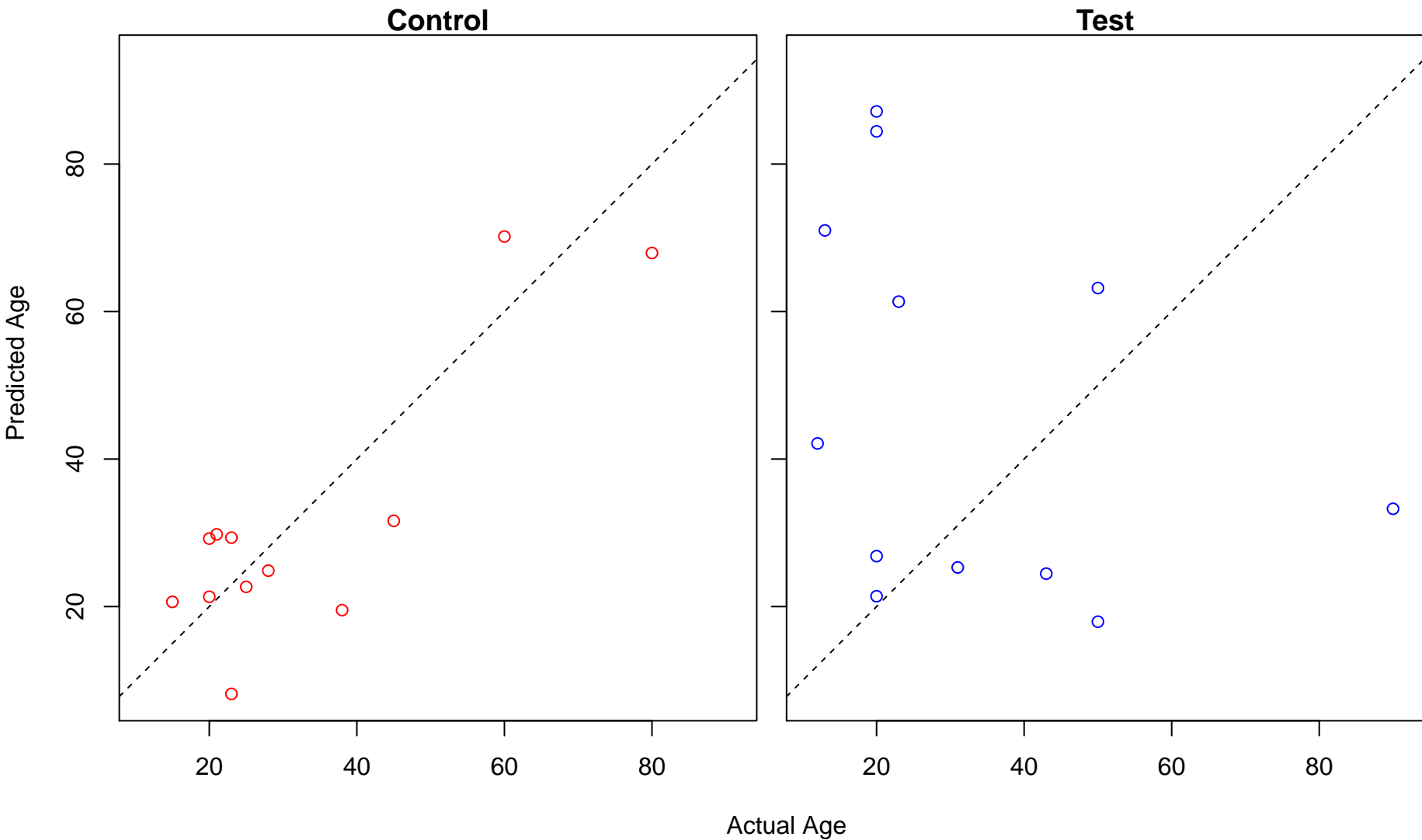
nucleoside bisphosphate biosynthetic process (Score: 9.932424)



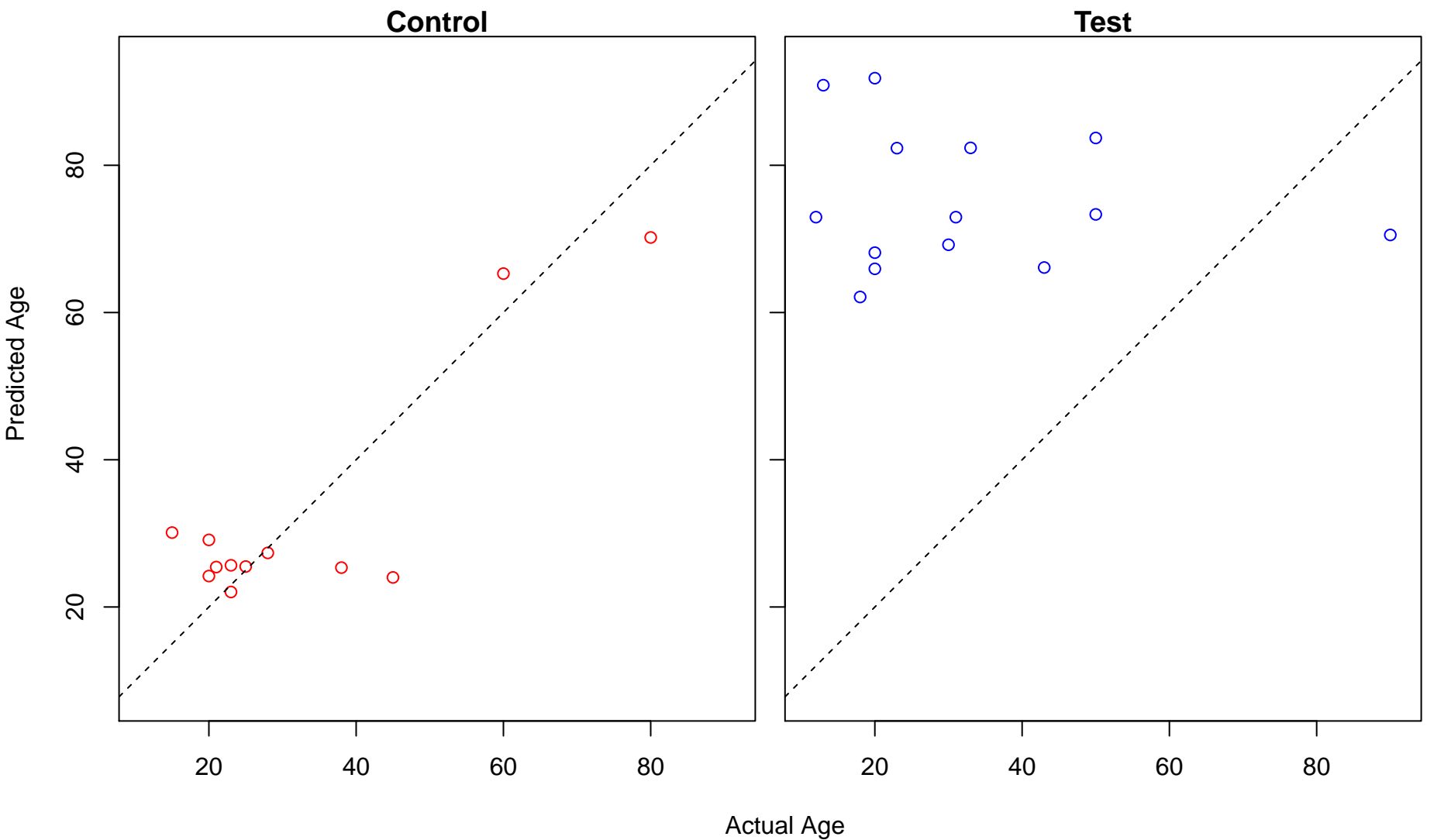
ribonucleoside bisphosphate biosynthetic process (Score: 9.932424)



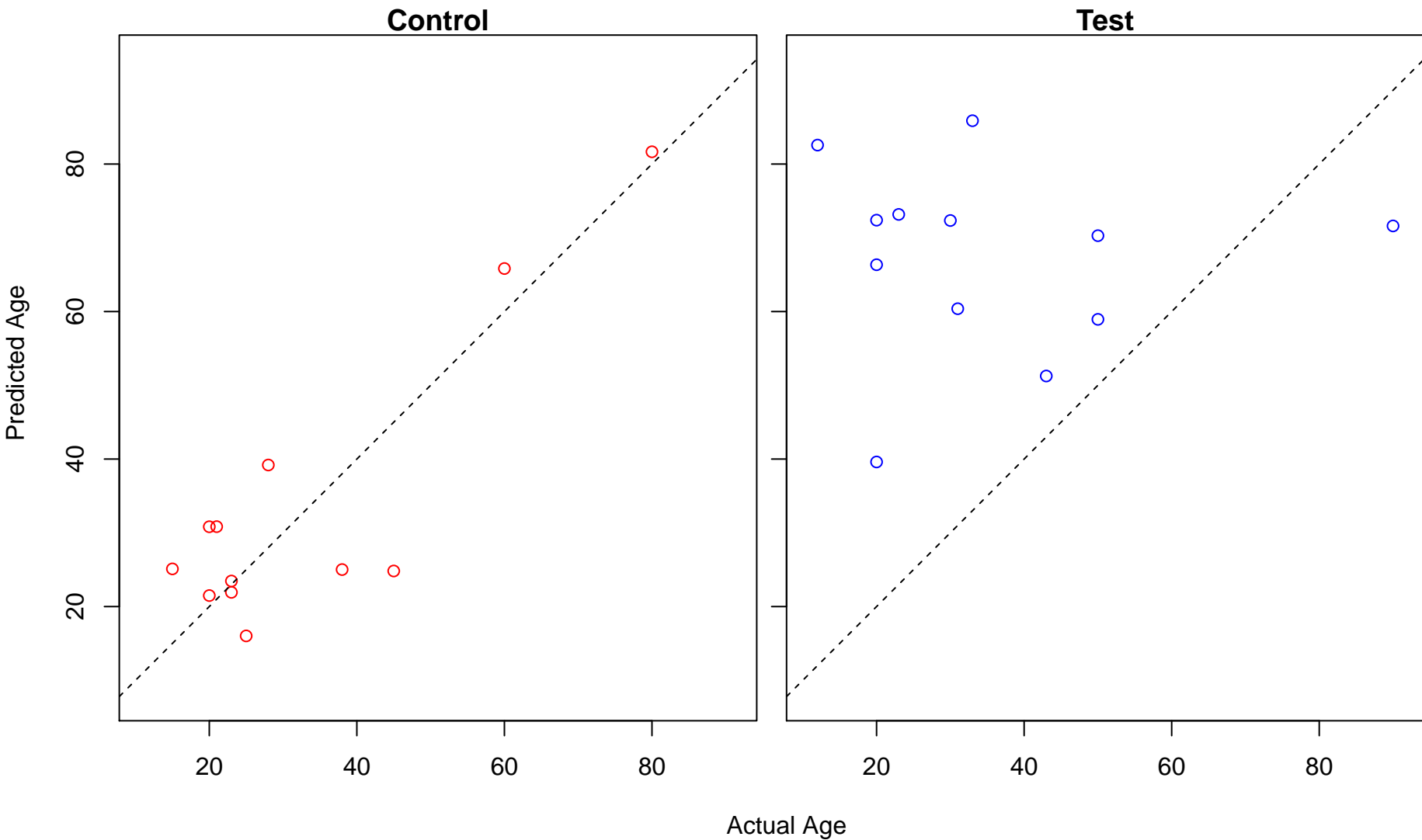
purine nucleoside bisphosphate biosynthetic process (Score: 9.932424)



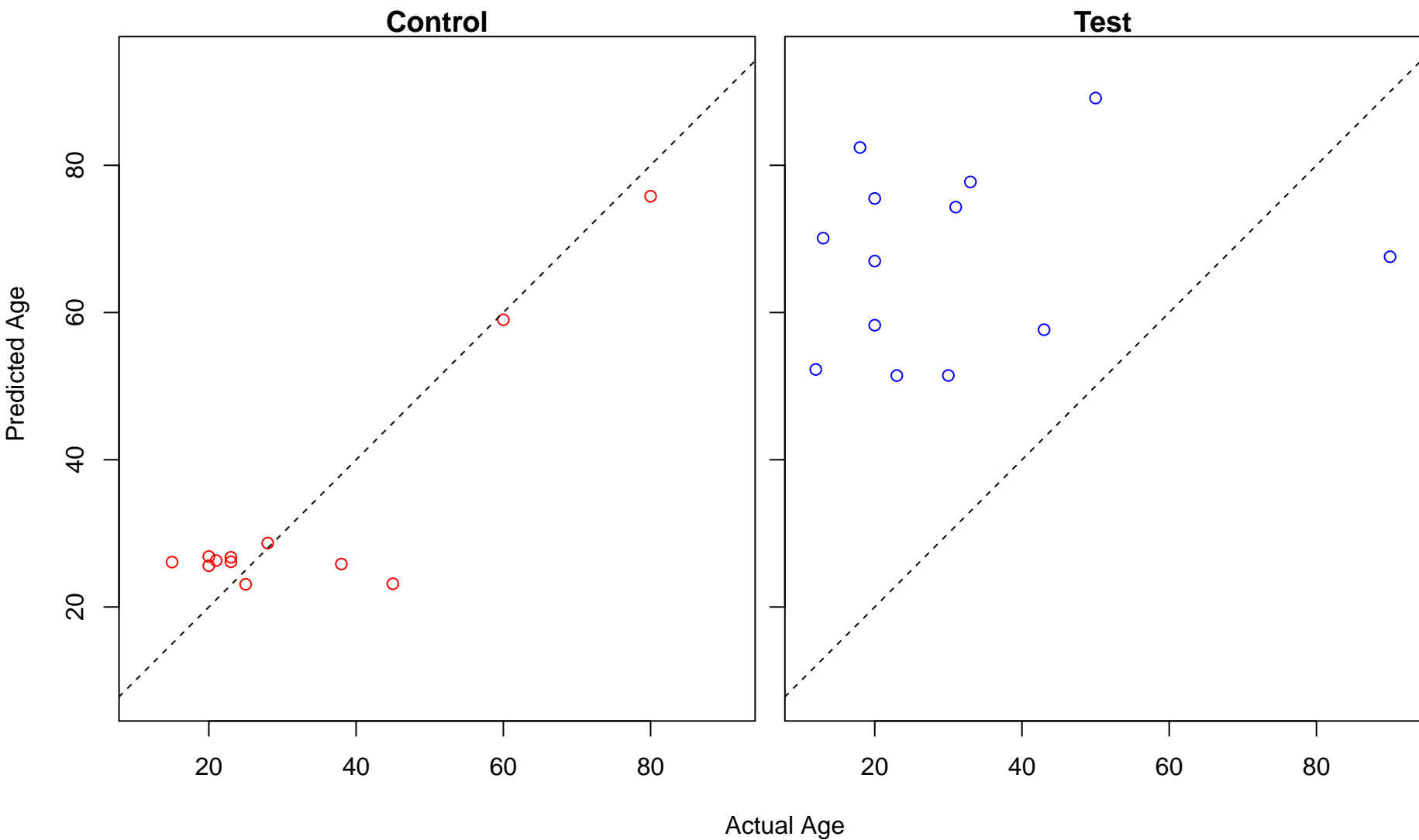
Comparative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score)



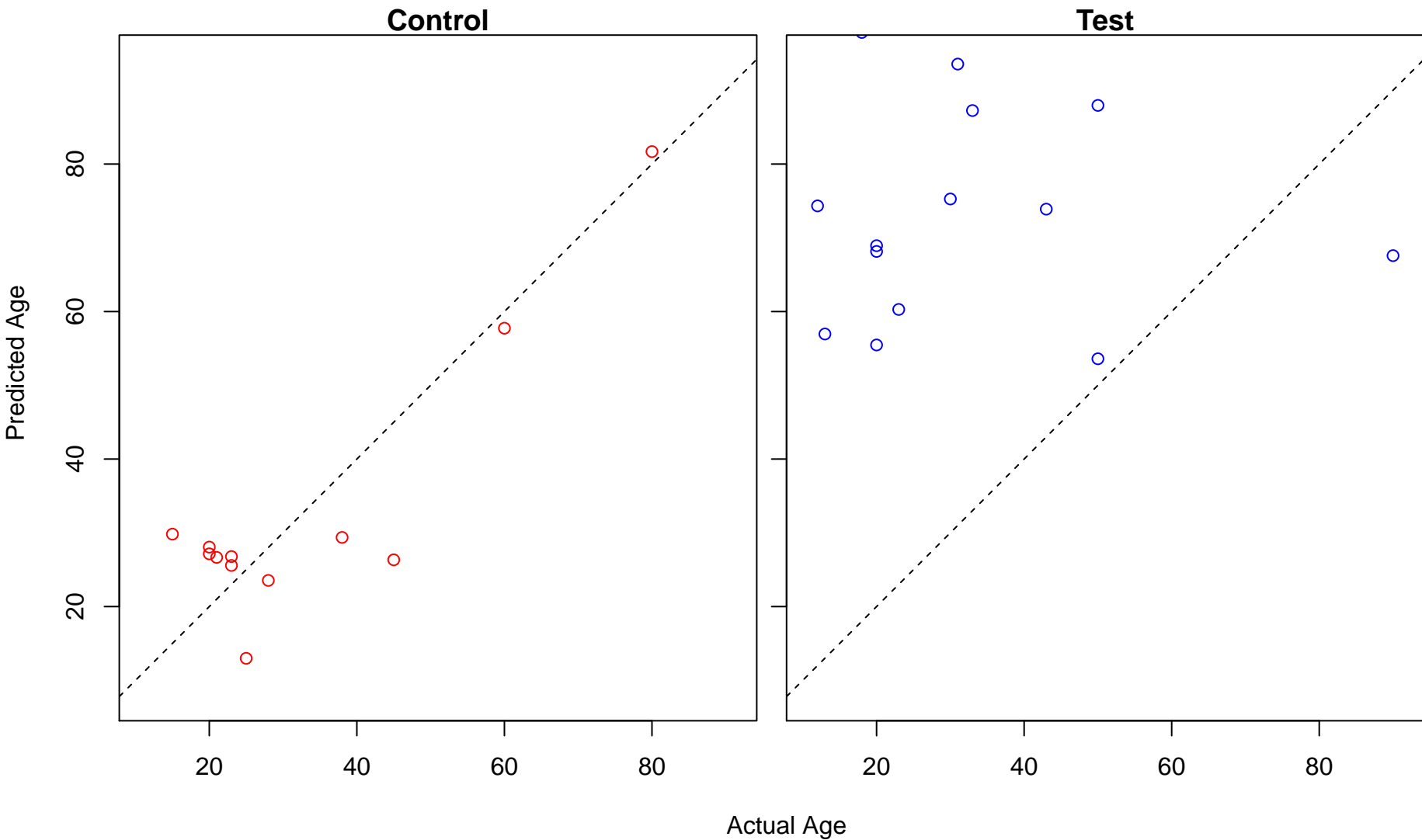
establishment of protein localization to organelle (Score: 9.923615)



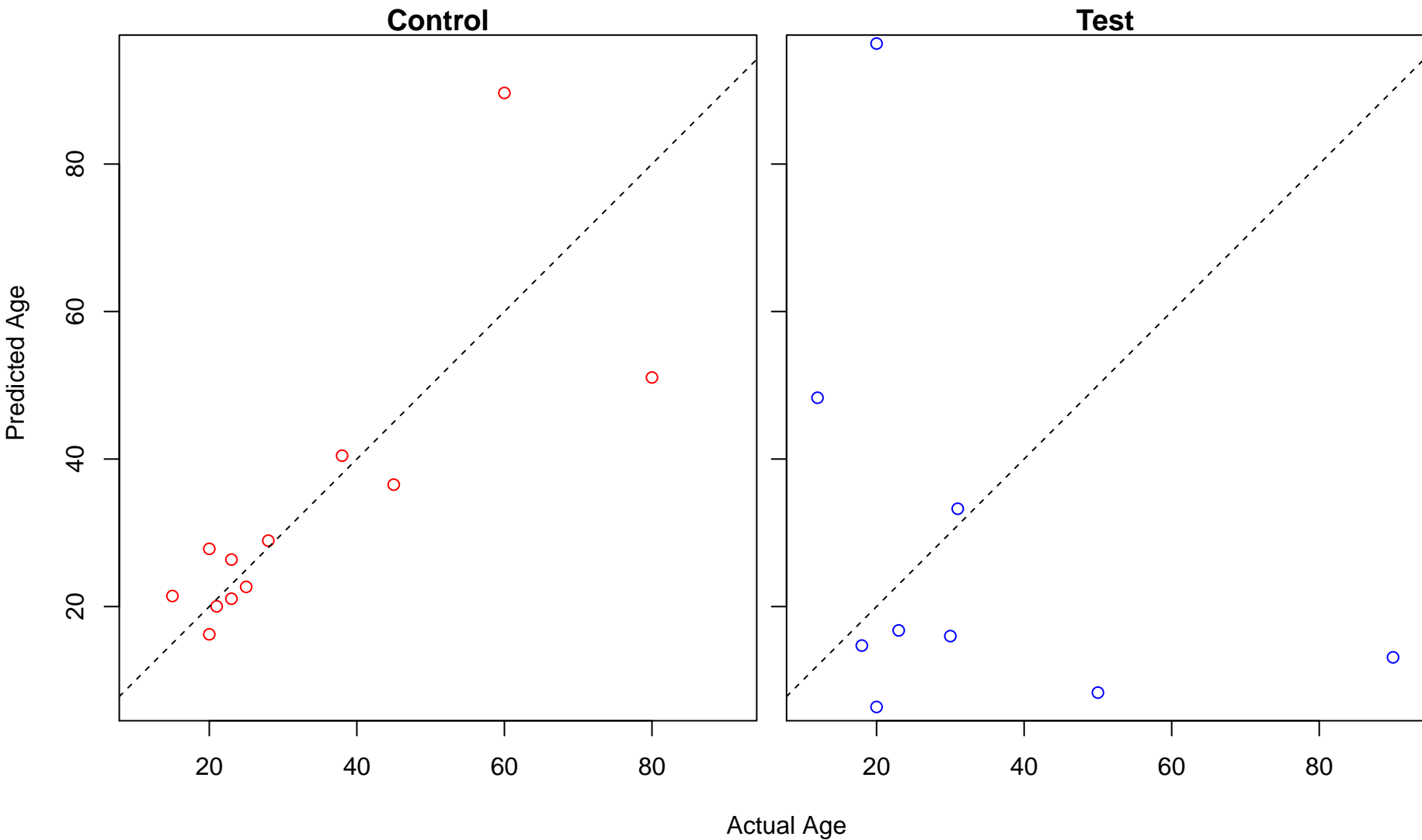
positive regulation of calcium ion import (Score: 9.913787)



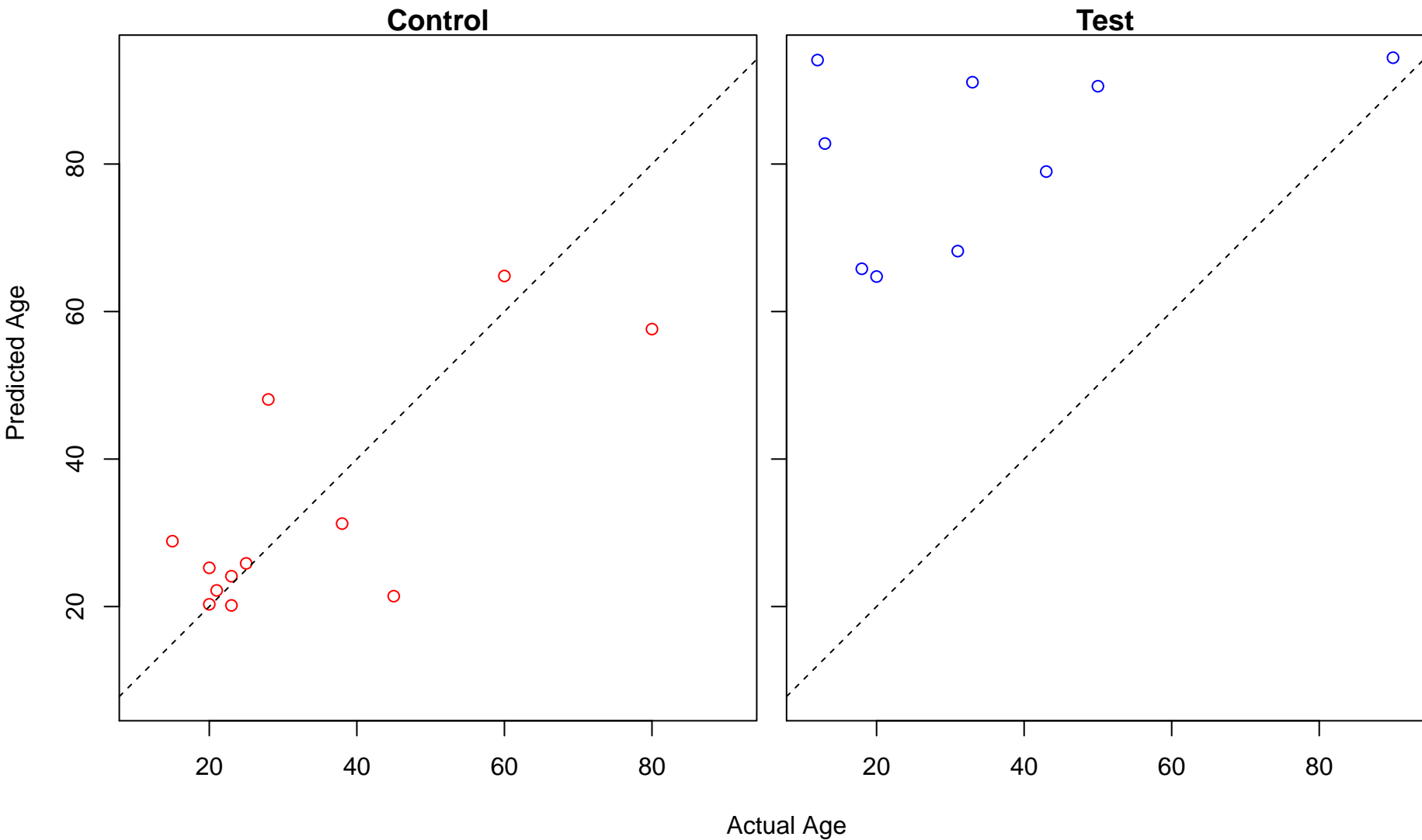
positive regulation of lipid biosynthetic process (Score: 9.911296)



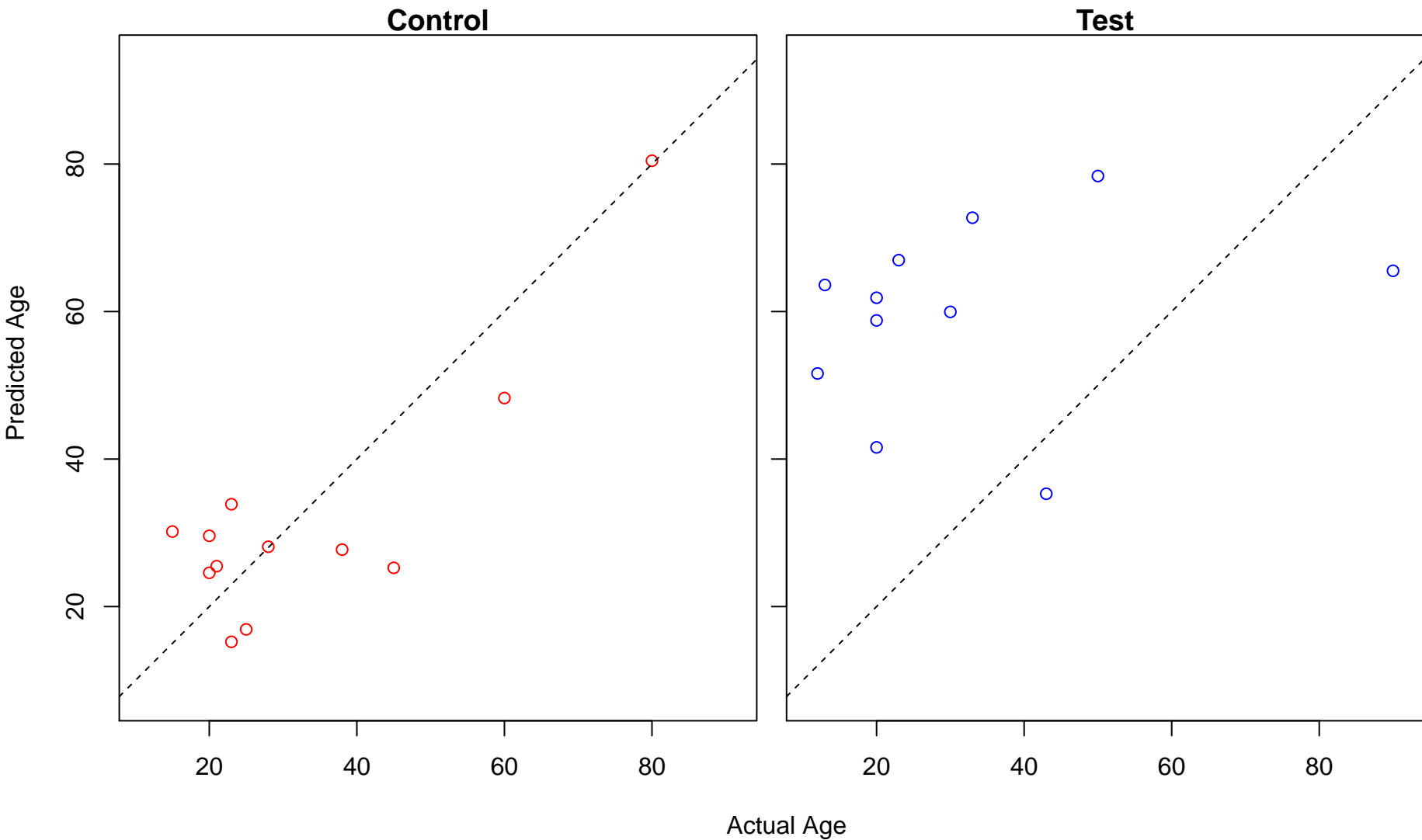
somatic diversification of immune receptors (Score: 9.908521)



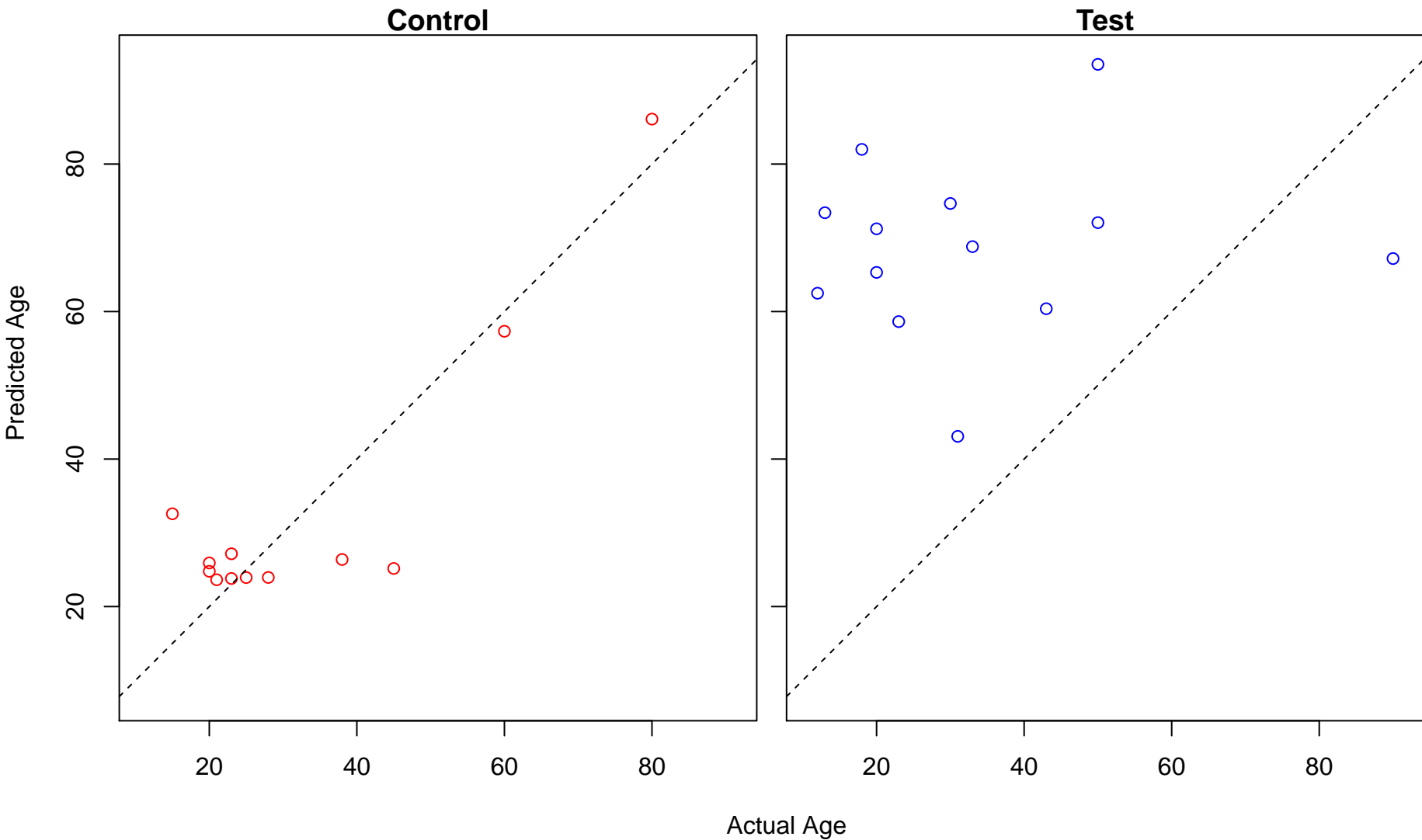
negative regulation of tissue remodeling (Score: 9.907739)



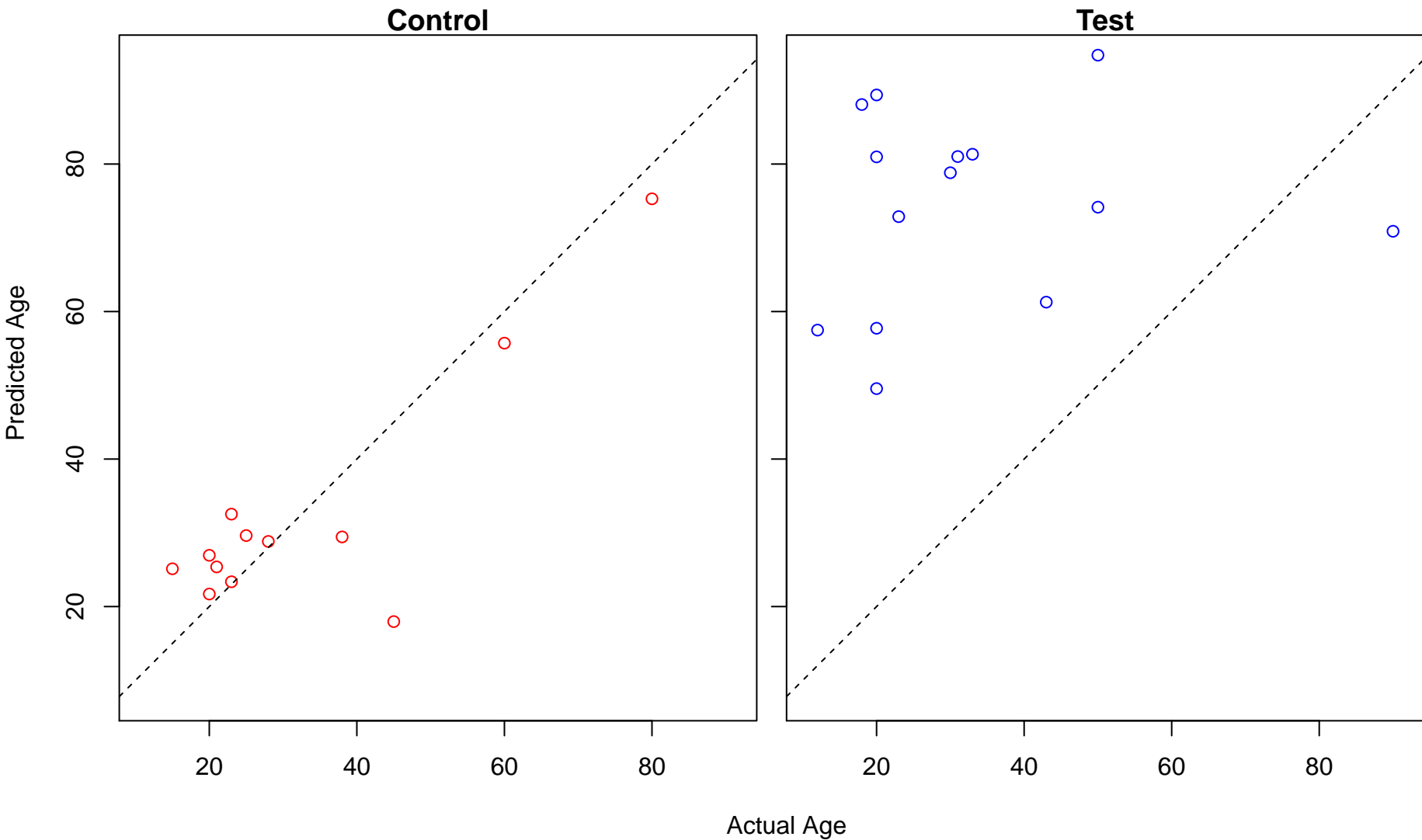
negative regulation of translation (Score: 9.907225)



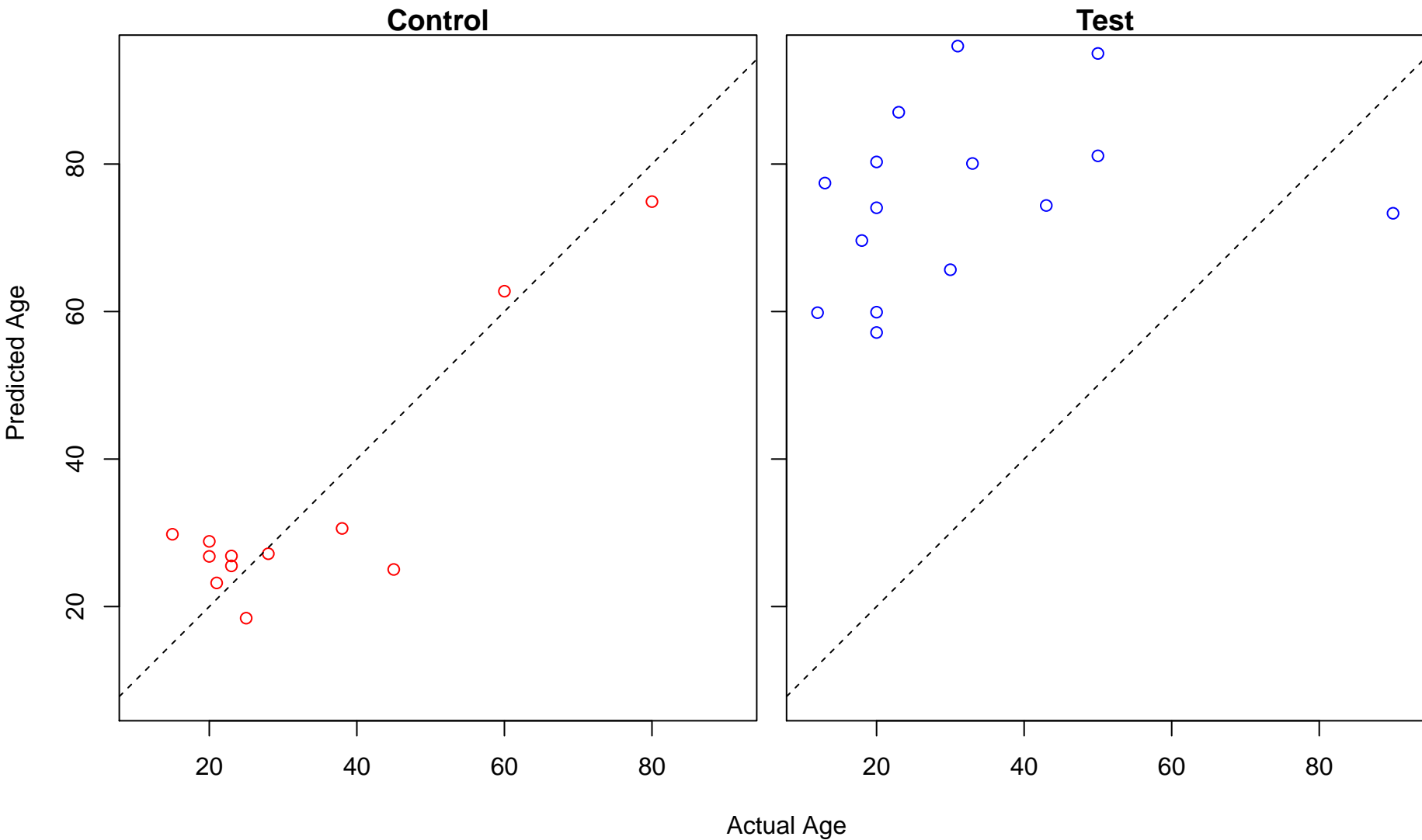
acetyl-CoA biosynthetic process (Score: 9.892588)



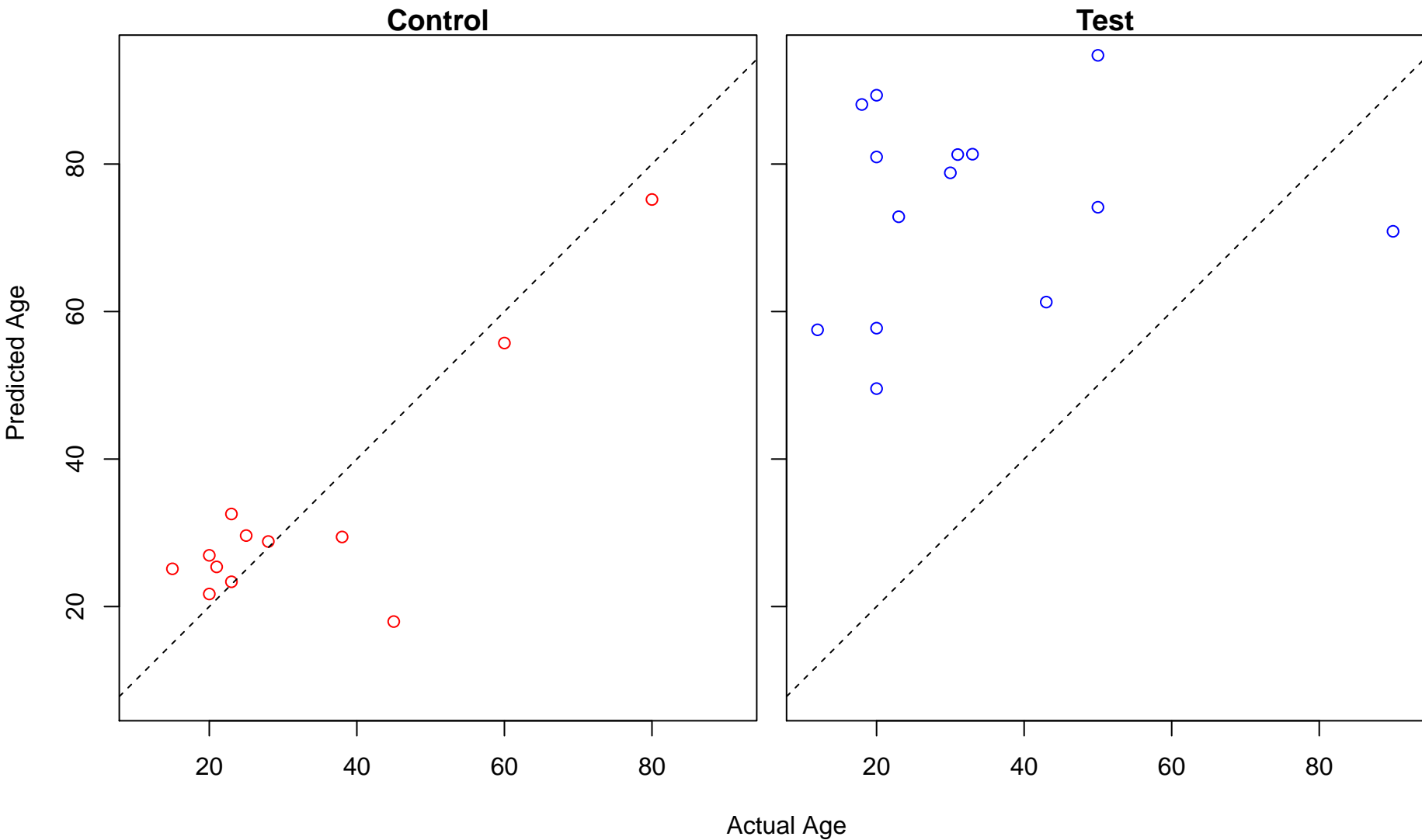
positive regulation of T cell mediated cytotoxicity (Score: 9.889084)



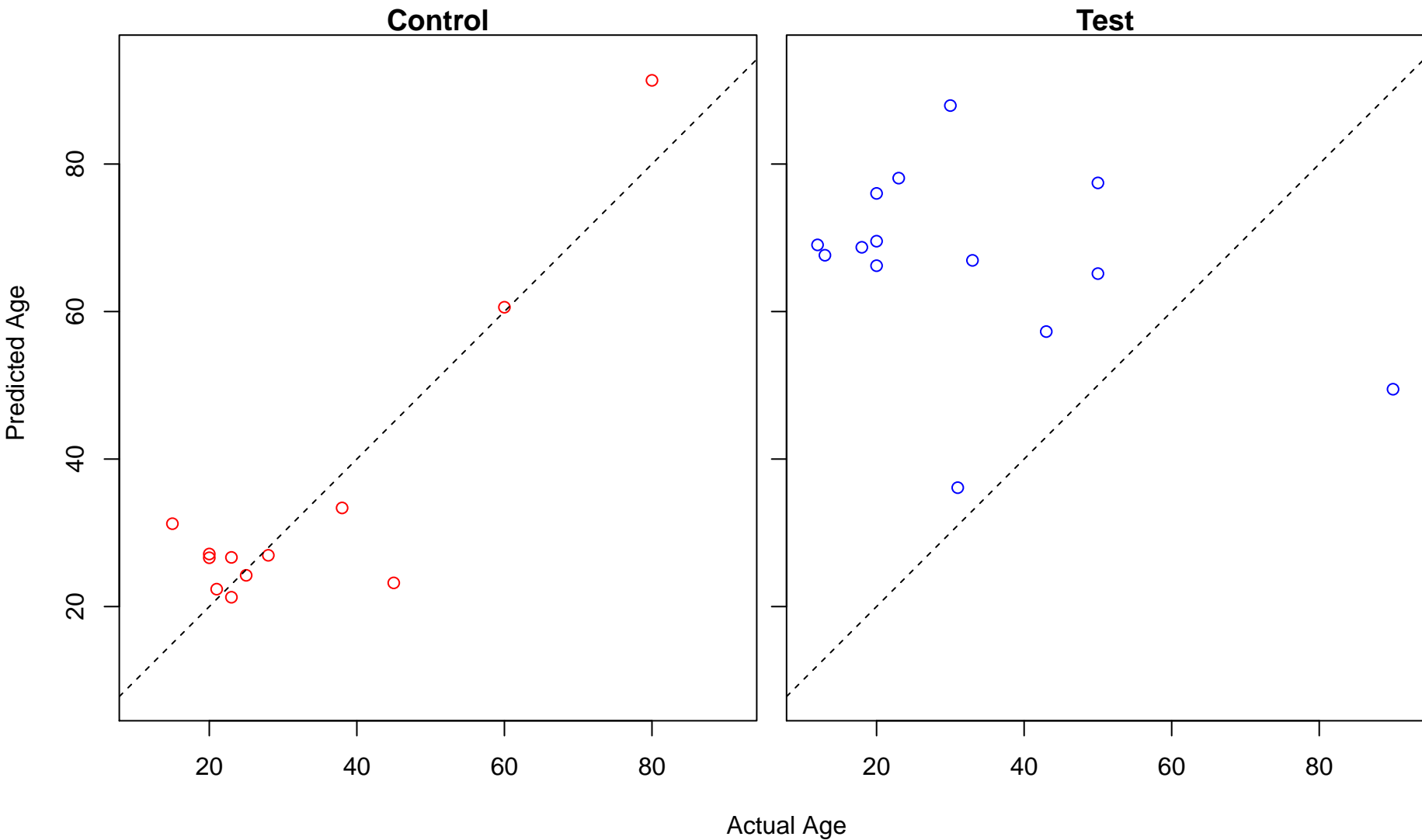
fucosylation (Score: 9.885035)



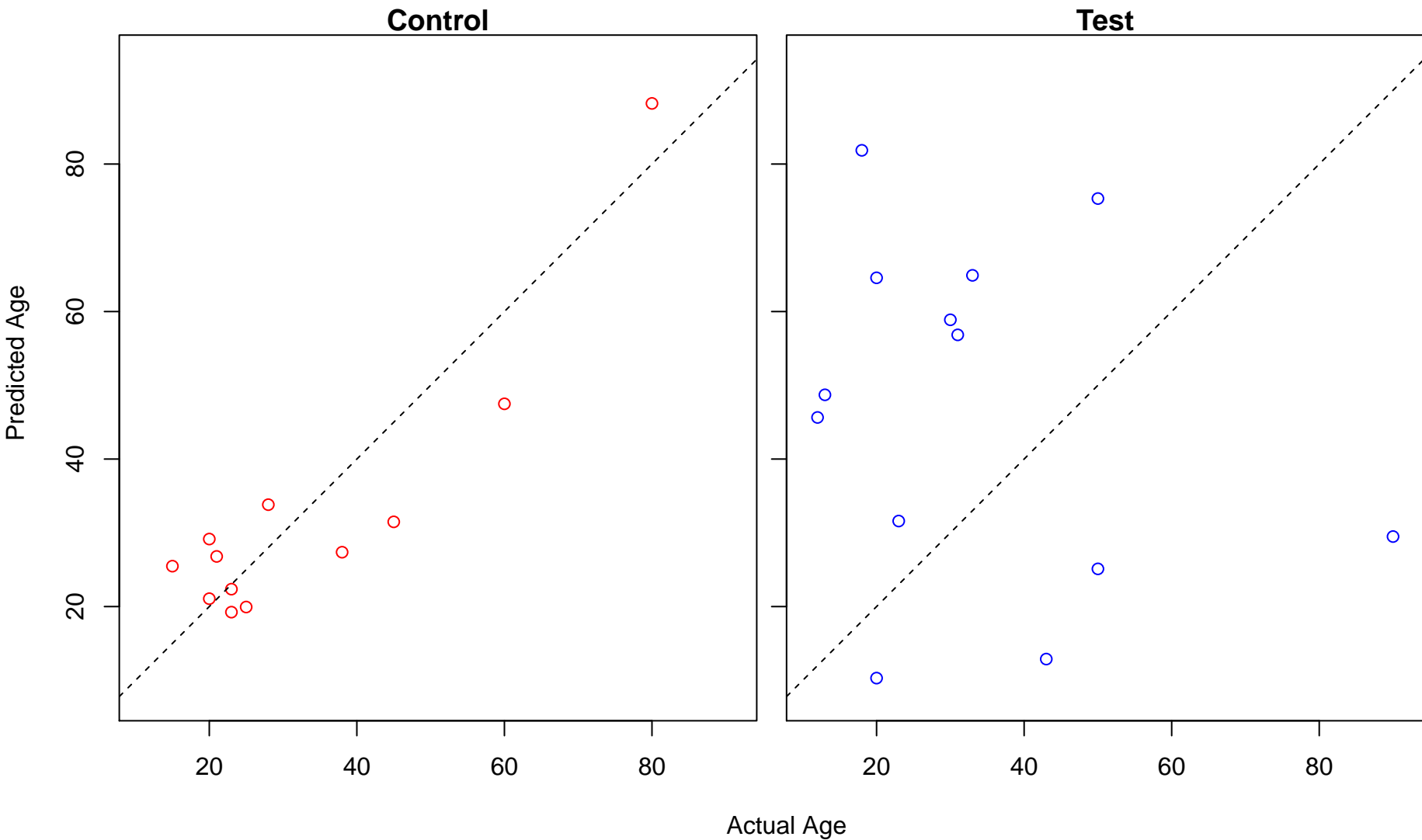
regulation of T cell mediated cytotoxicity (Score: 9.880765)



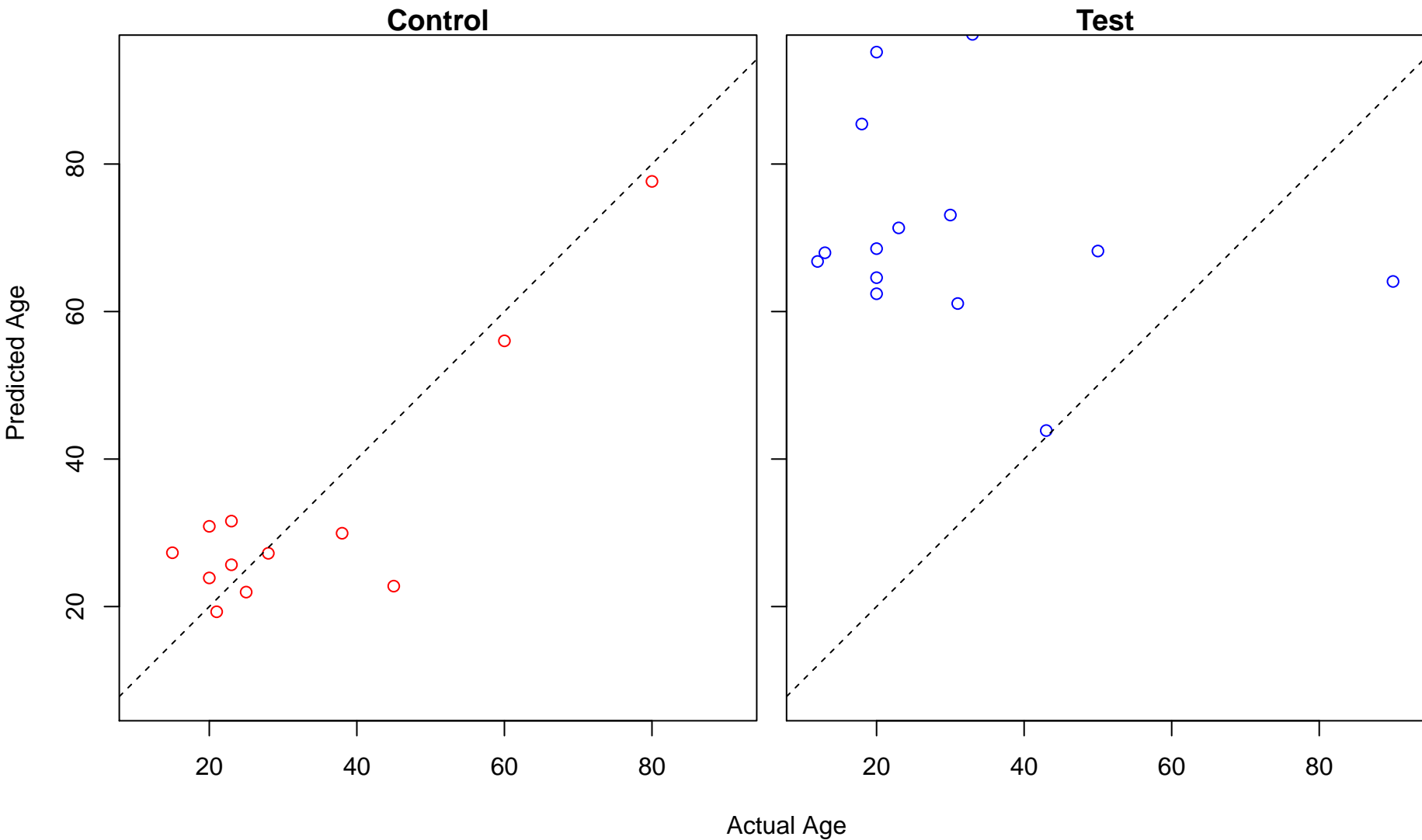
proline transmembrane transport (Score: 9.878915)



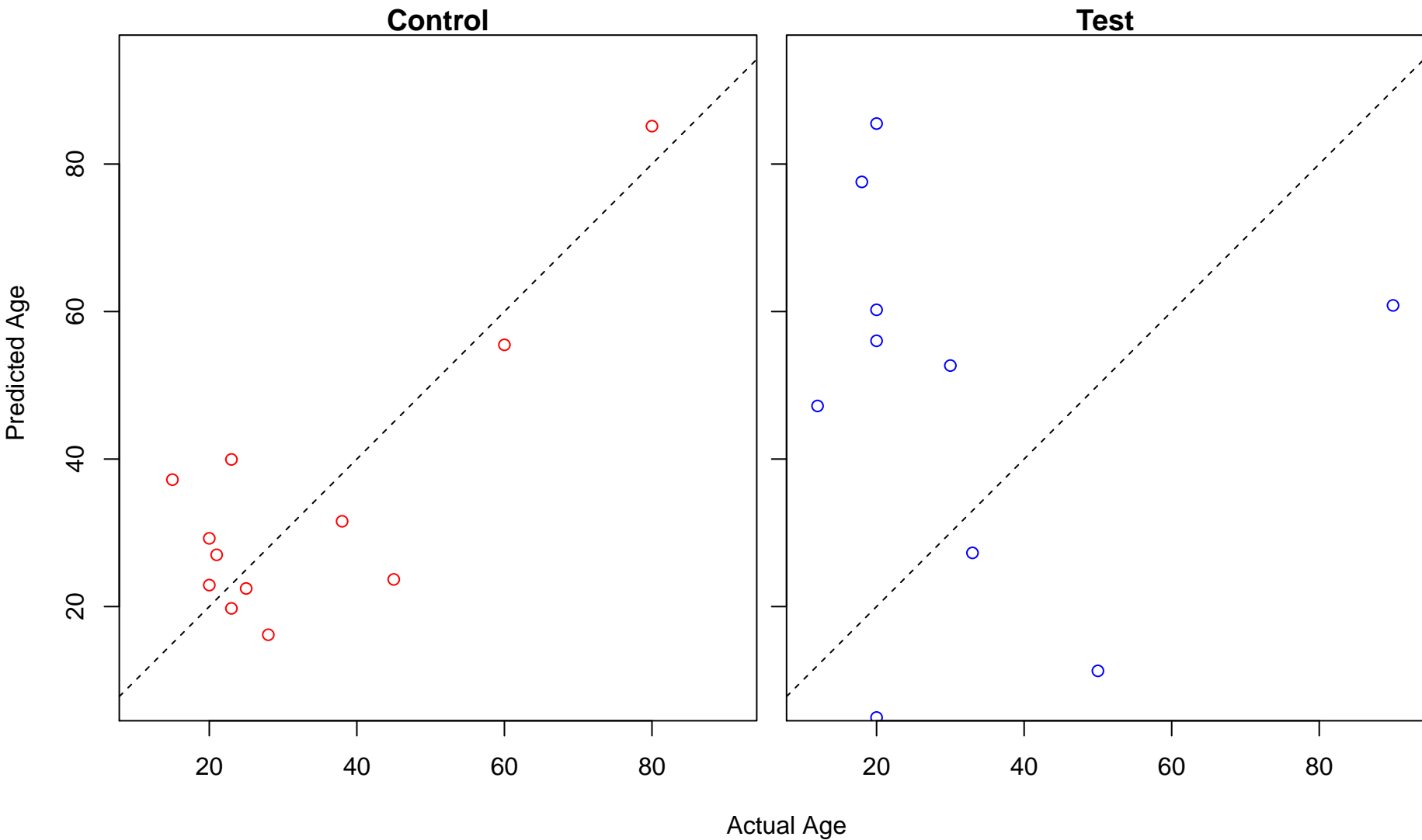
positive regulation of DNA metabolic process (Score: 9.877703)



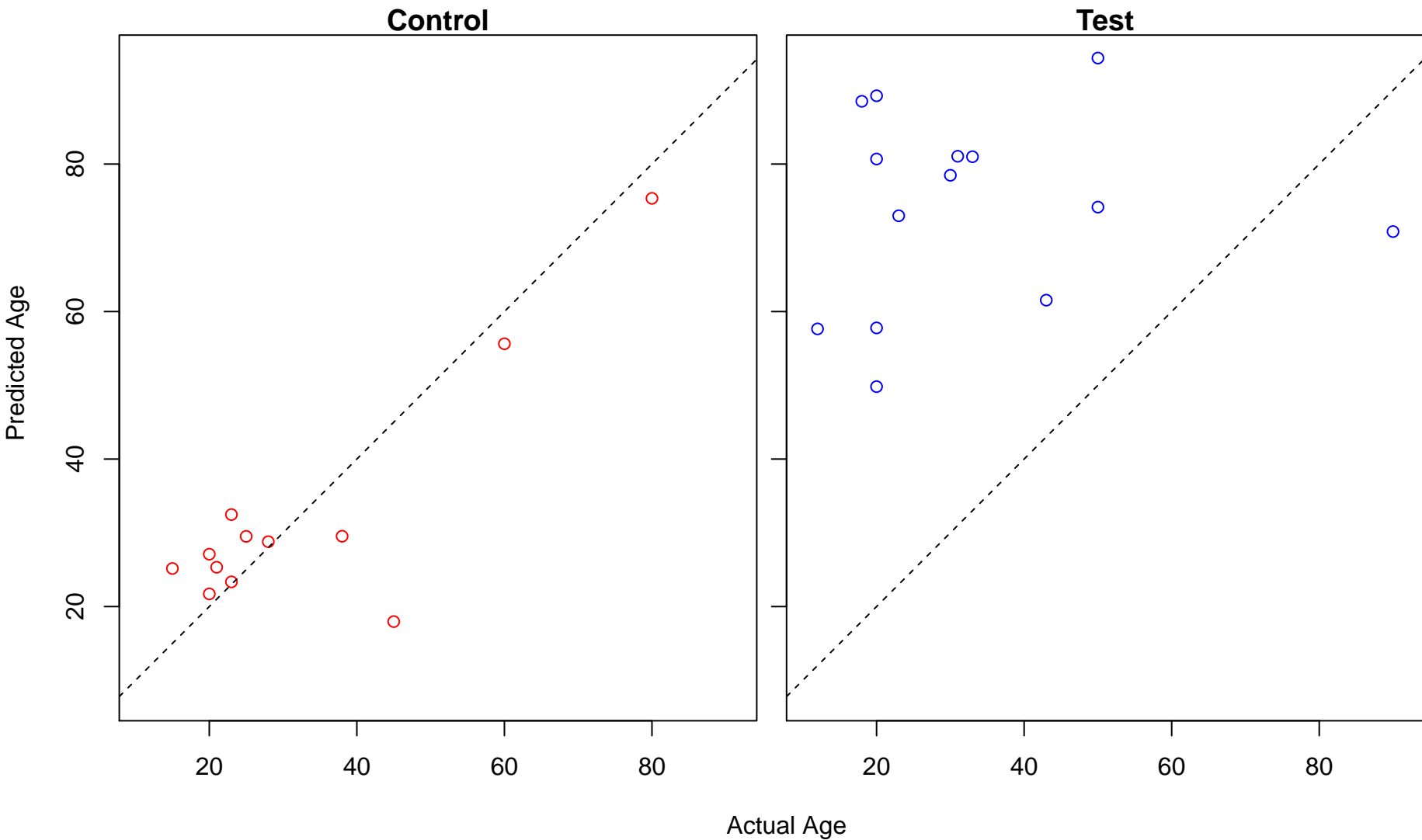
positive regulation of triglyceride biosynthetic process (Score: 9.877447)



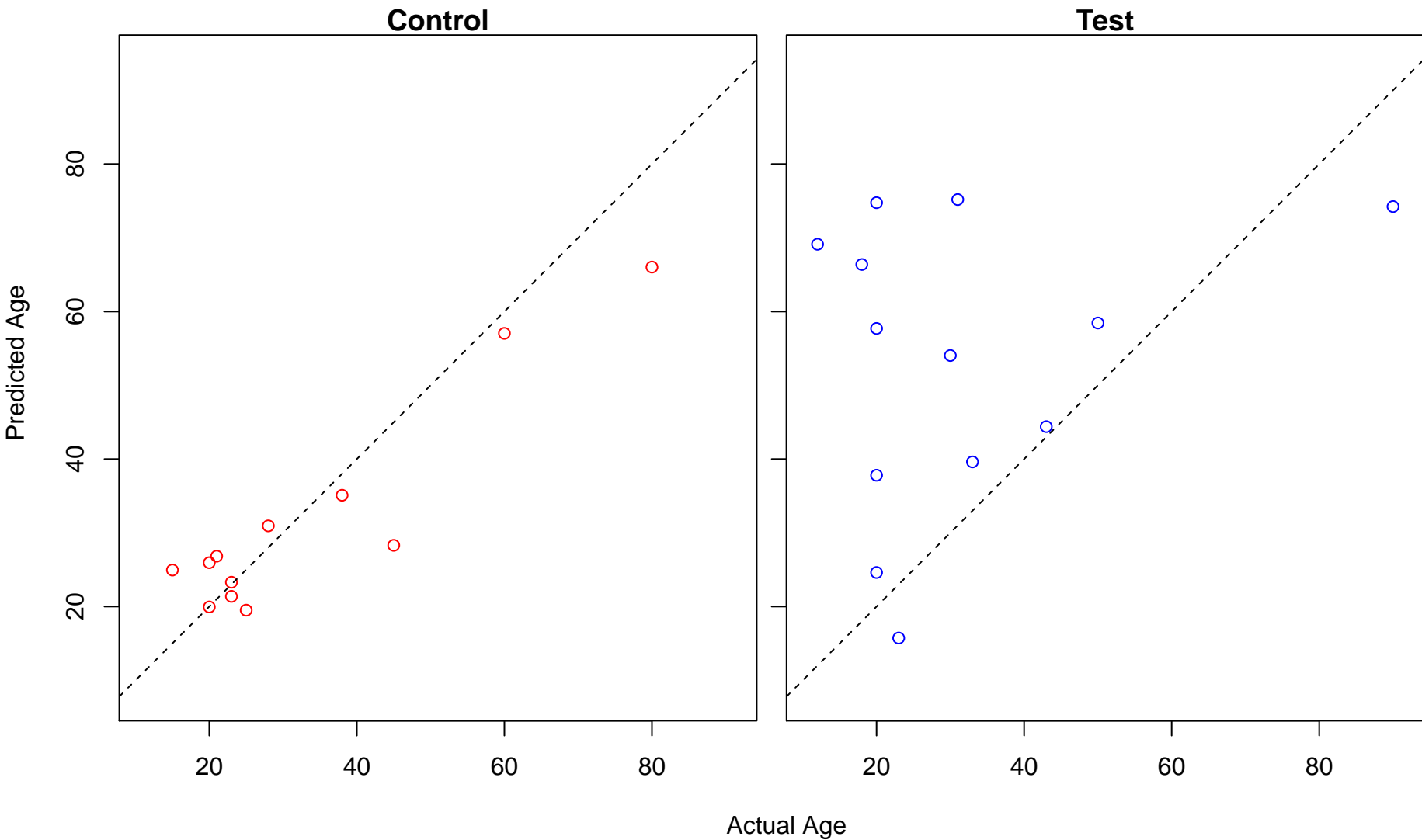
Golgi ribbon formation (Score: 9.876420)



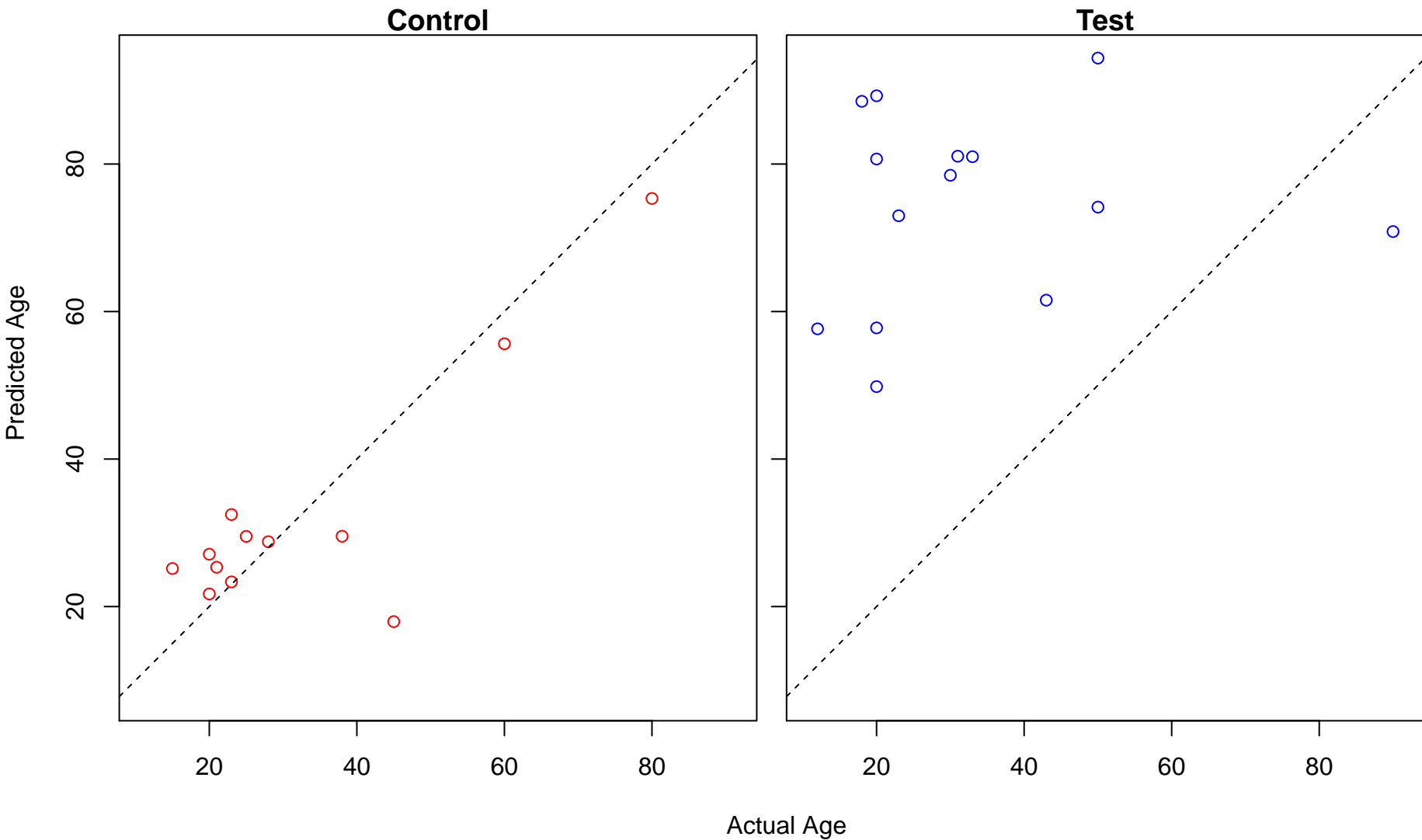
negative regulation of lymphocyte mediated immunity (Score: 9.874105)



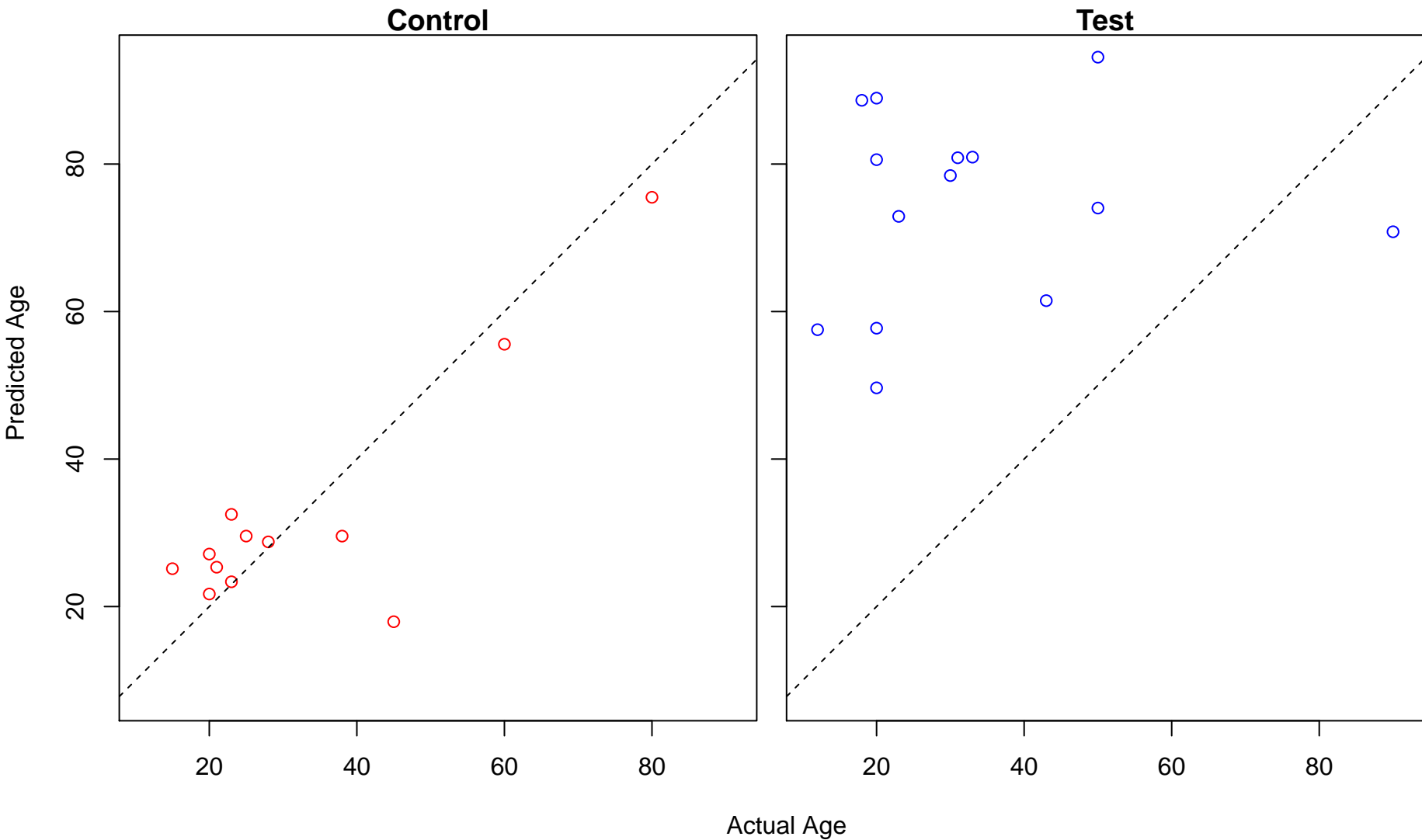
histone acetylation (Score: 9.872637)



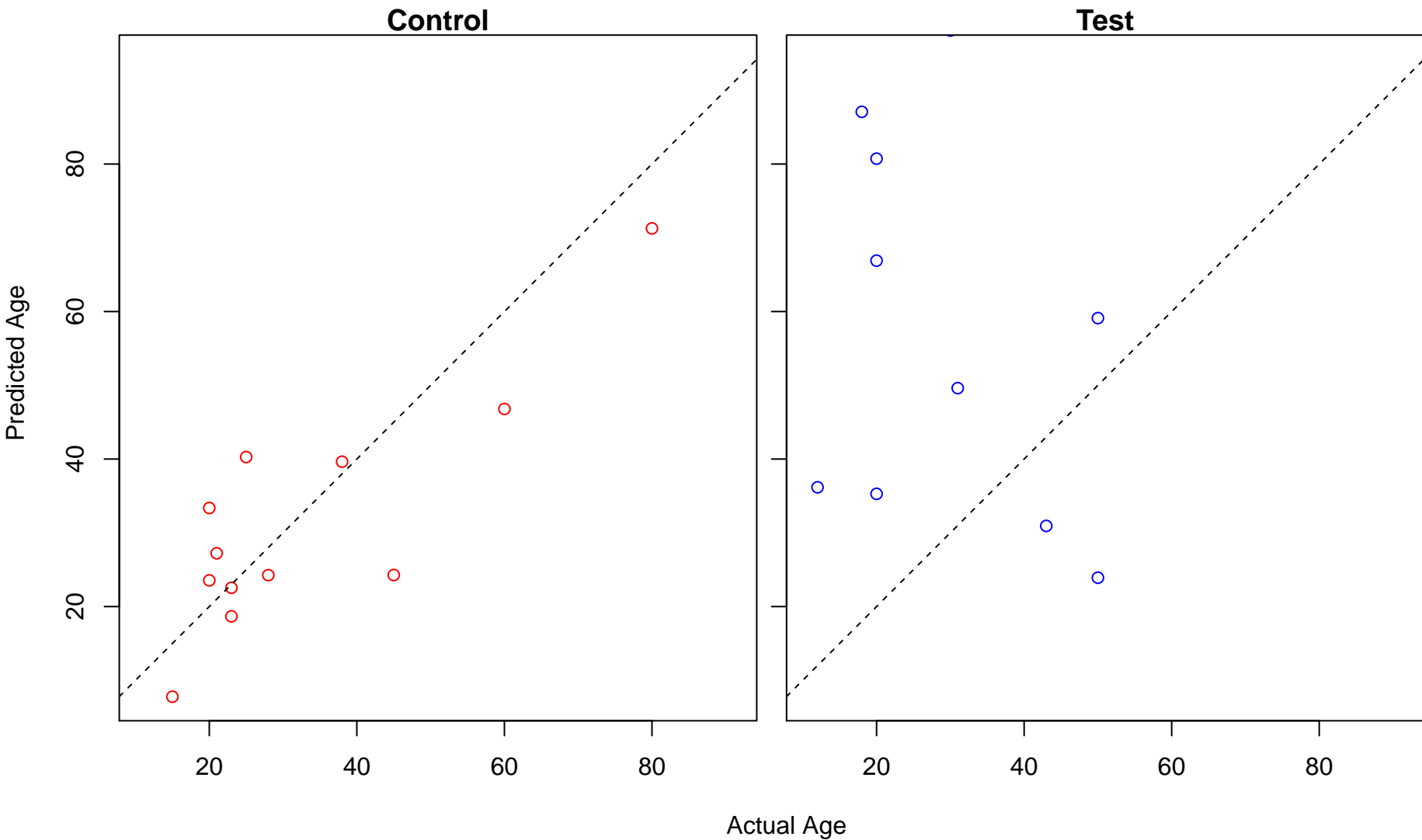
negative regulation of leukocyte mediated immunity (Score: 9.872272)



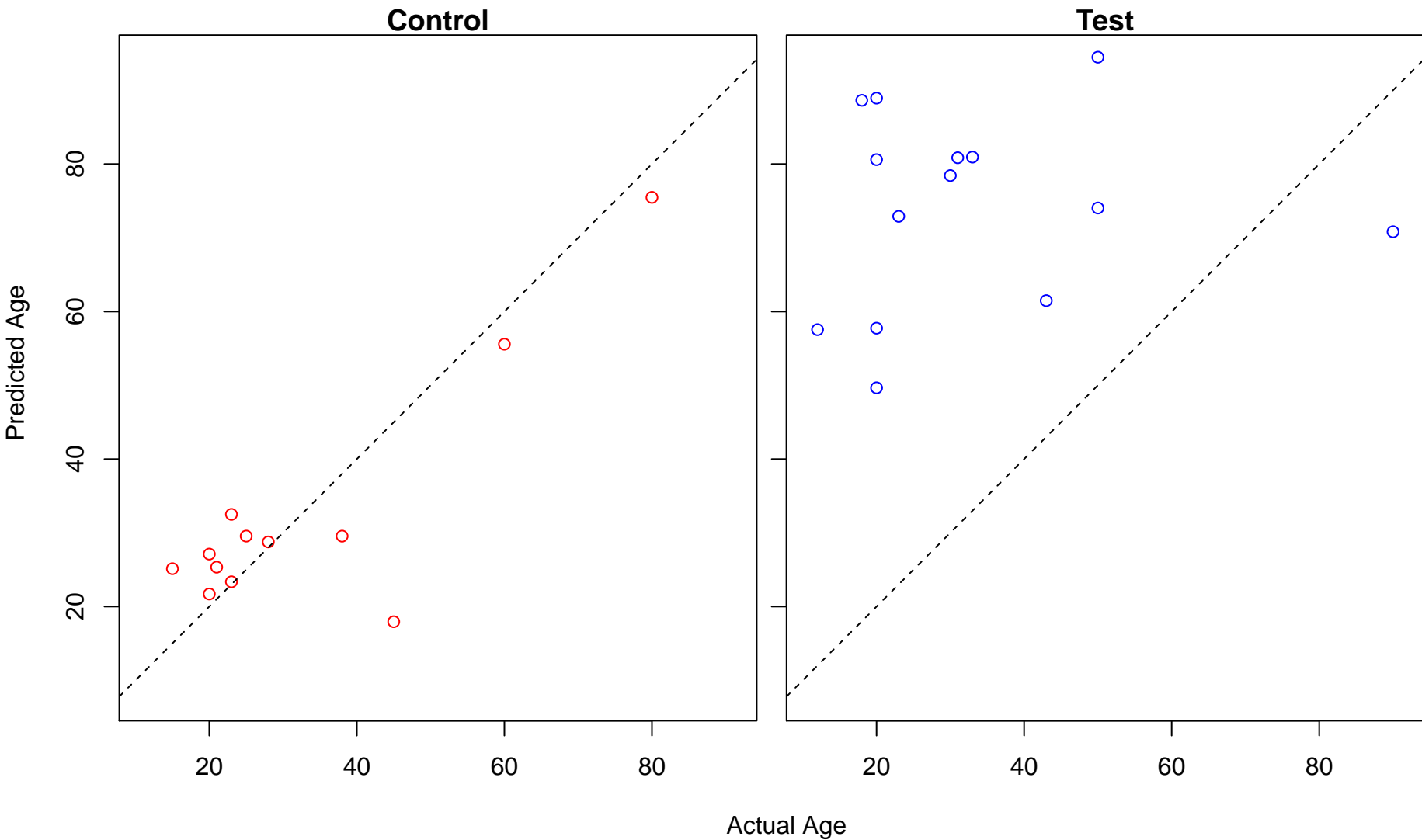
protection from natural killer cell mediated cytotoxicity (Score: 9.863234)



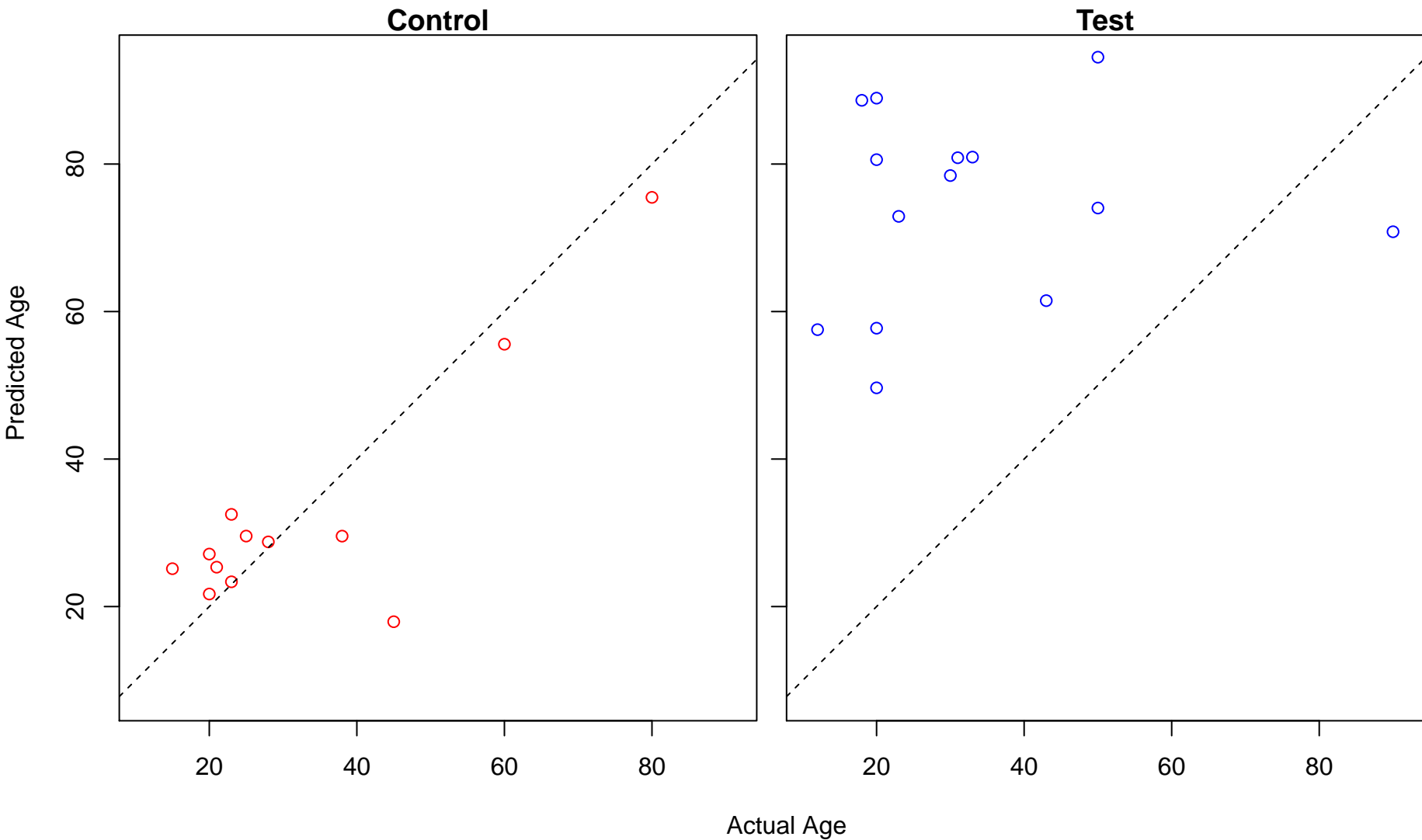
positive regulation of nucleotide catabolic process (Score: 9.862632)



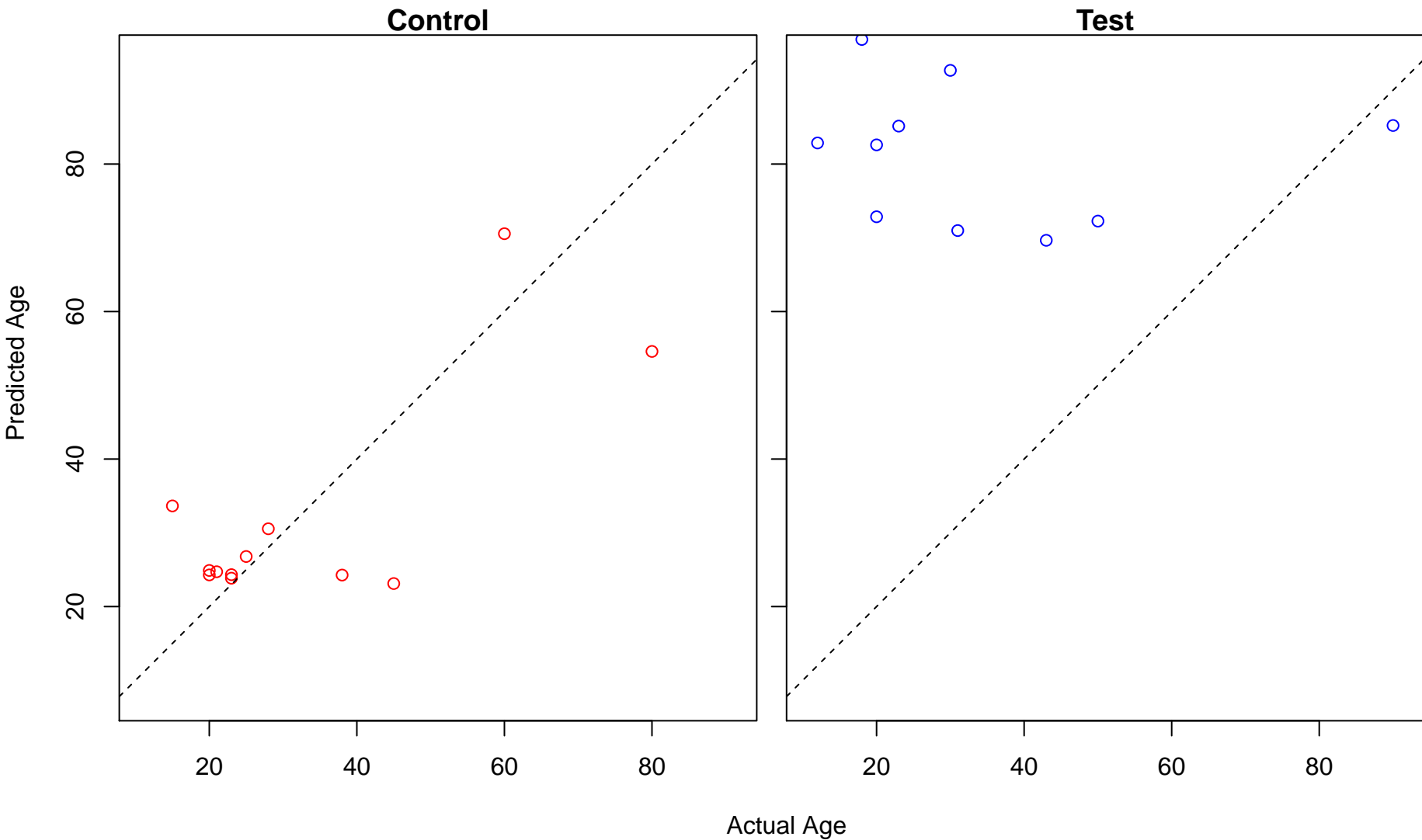
negative regulation of natural killer cell mediated immunity (Score: 9.862376)



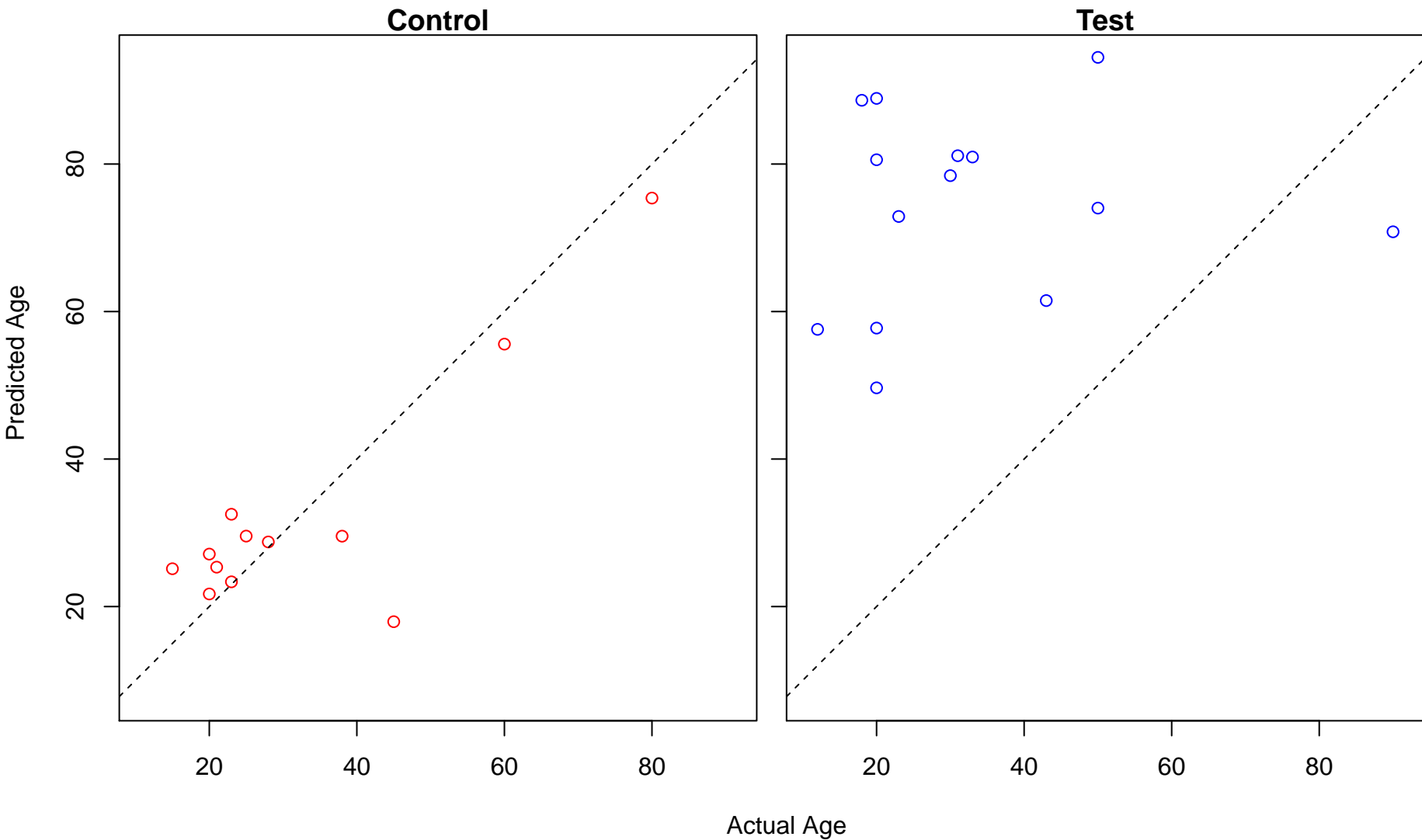
negative regulation of natural killer cell mediated cytotoxicity (Score: 9.862376)



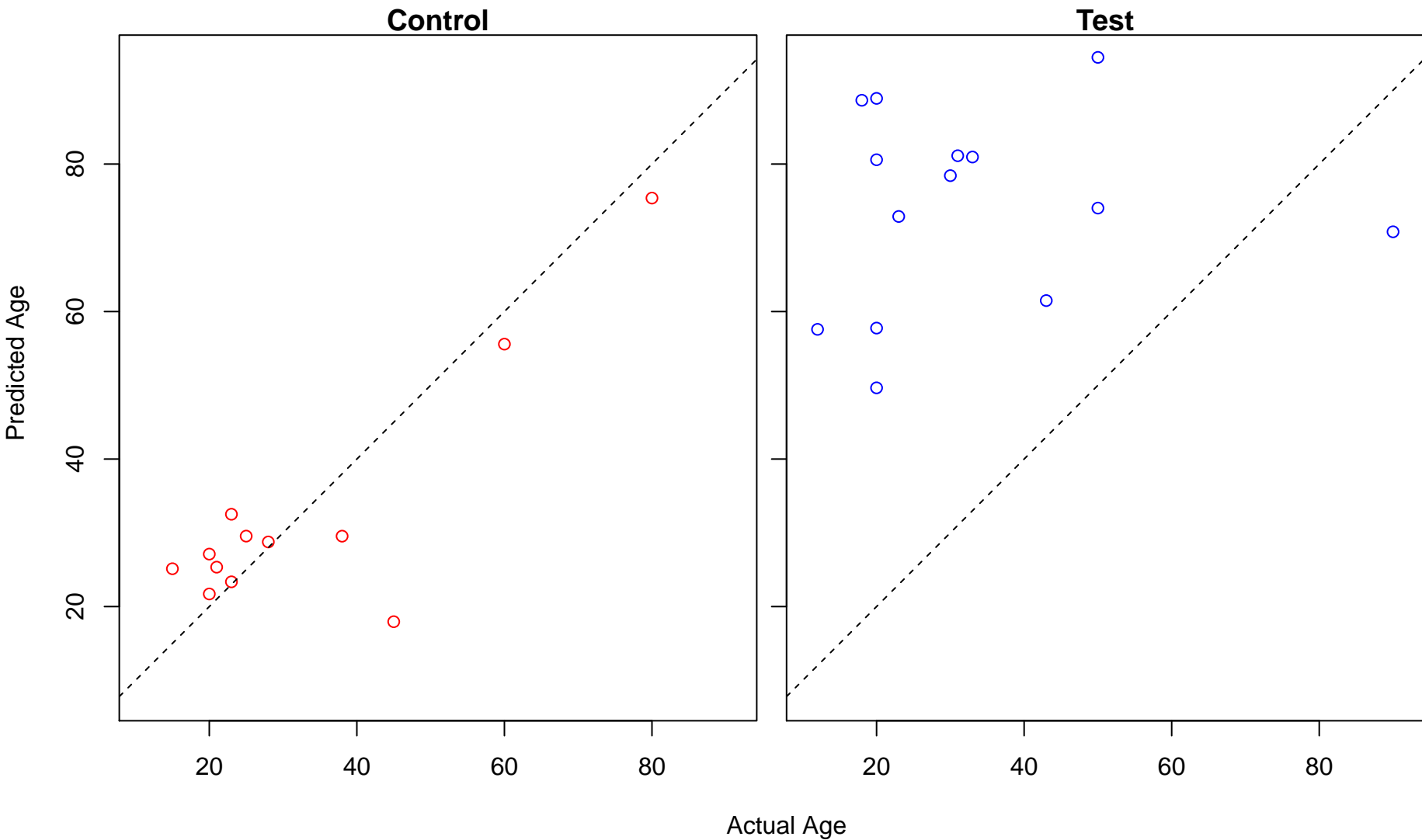
peroxisome proliferator activated receptor signaling pathway (Score: 9.858467)



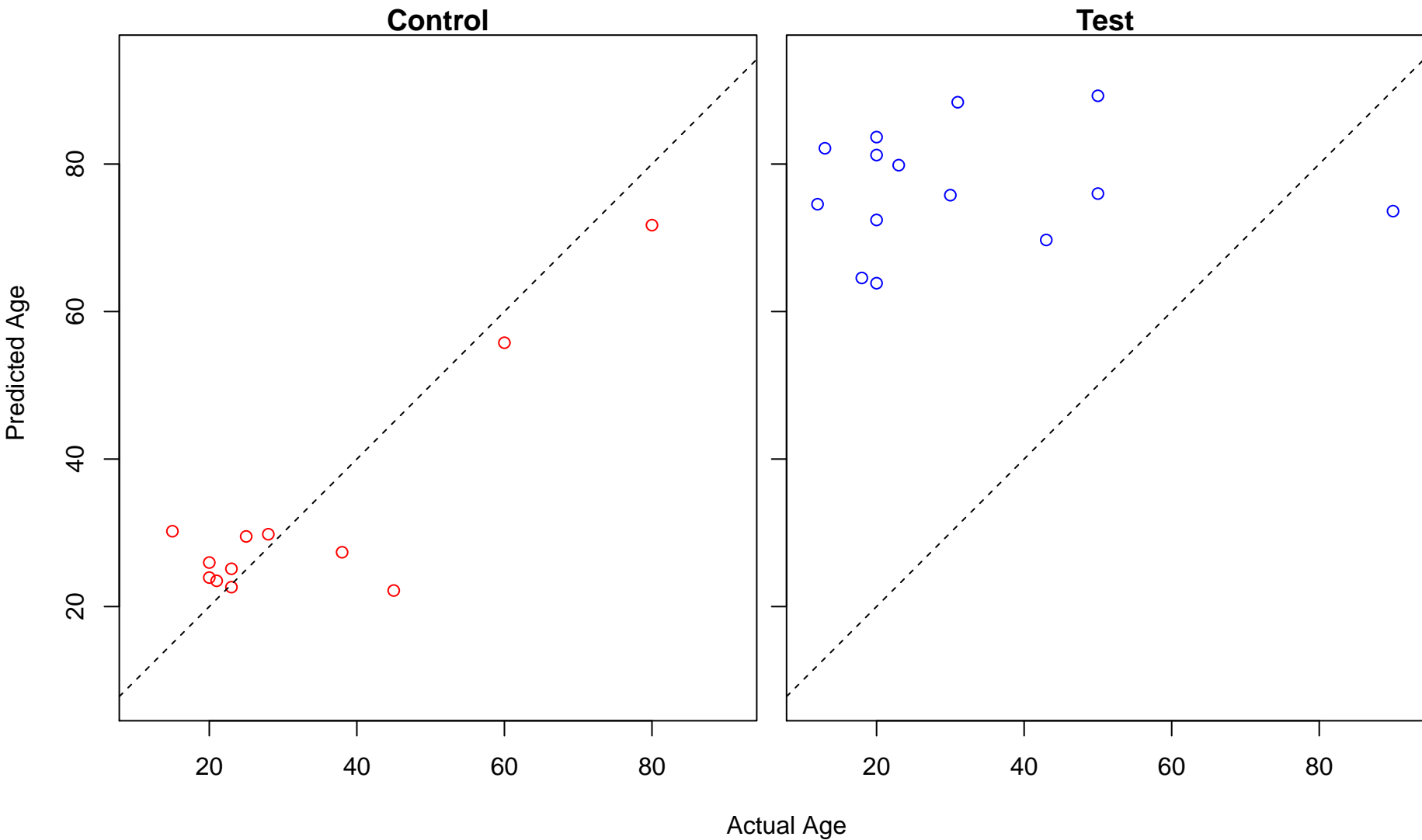
negative regulation of leukocyte mediated cytotoxicity (Score: 9.854374)



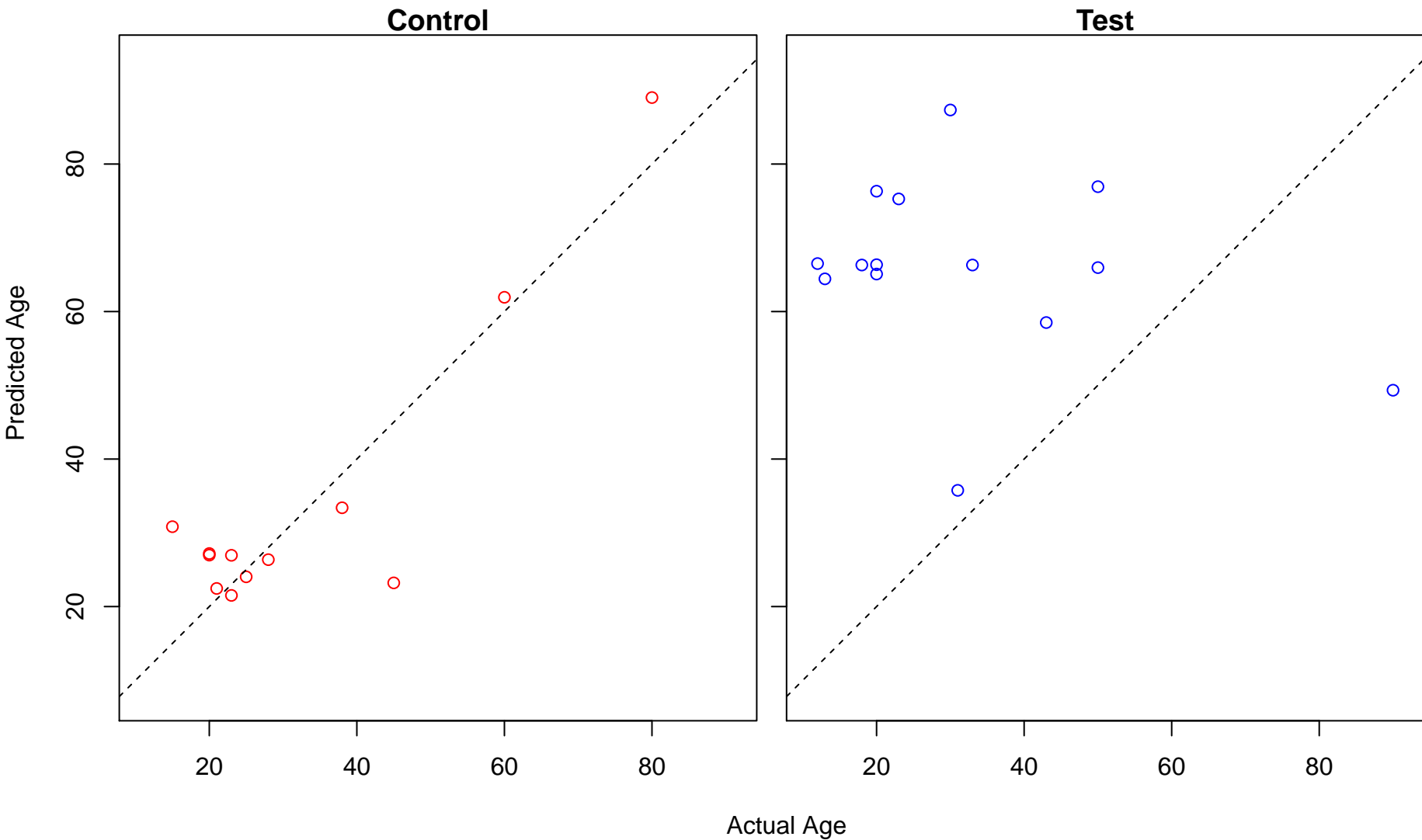
negative regulation of cell killing (Score: 9.854364)



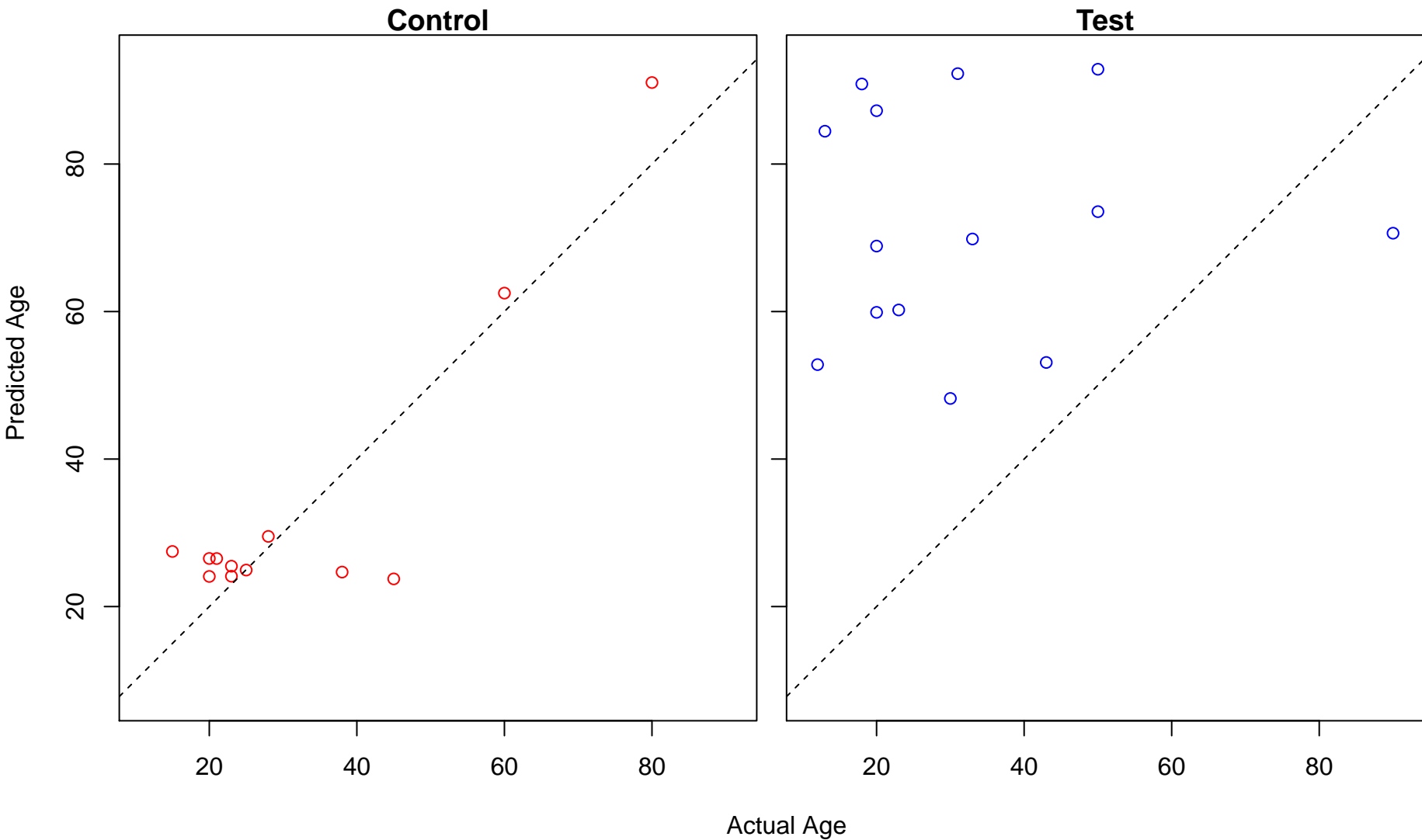
positive regulation of monocyte differentiation (Score: 9.842886)



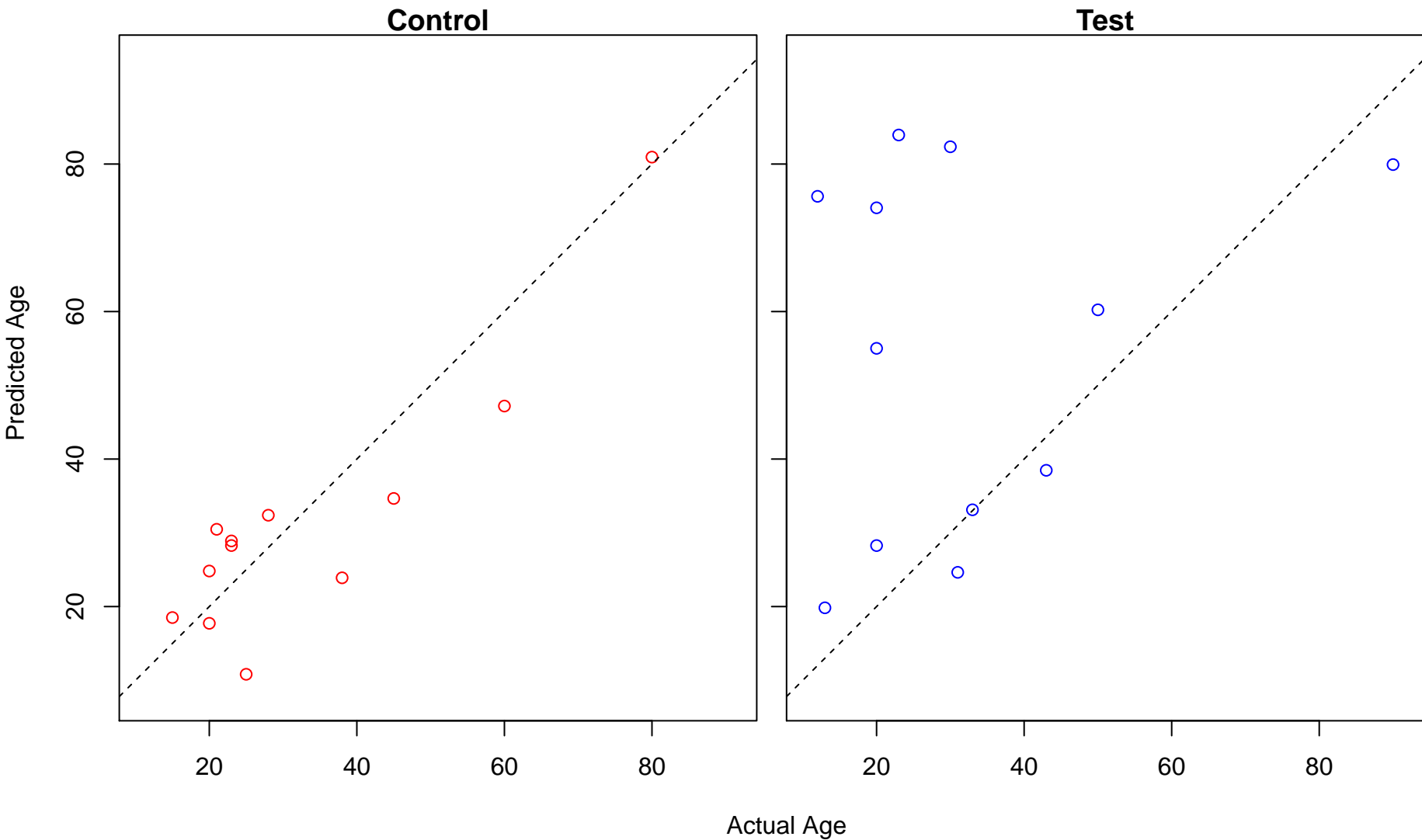
proline transport (Score: 9.836166)



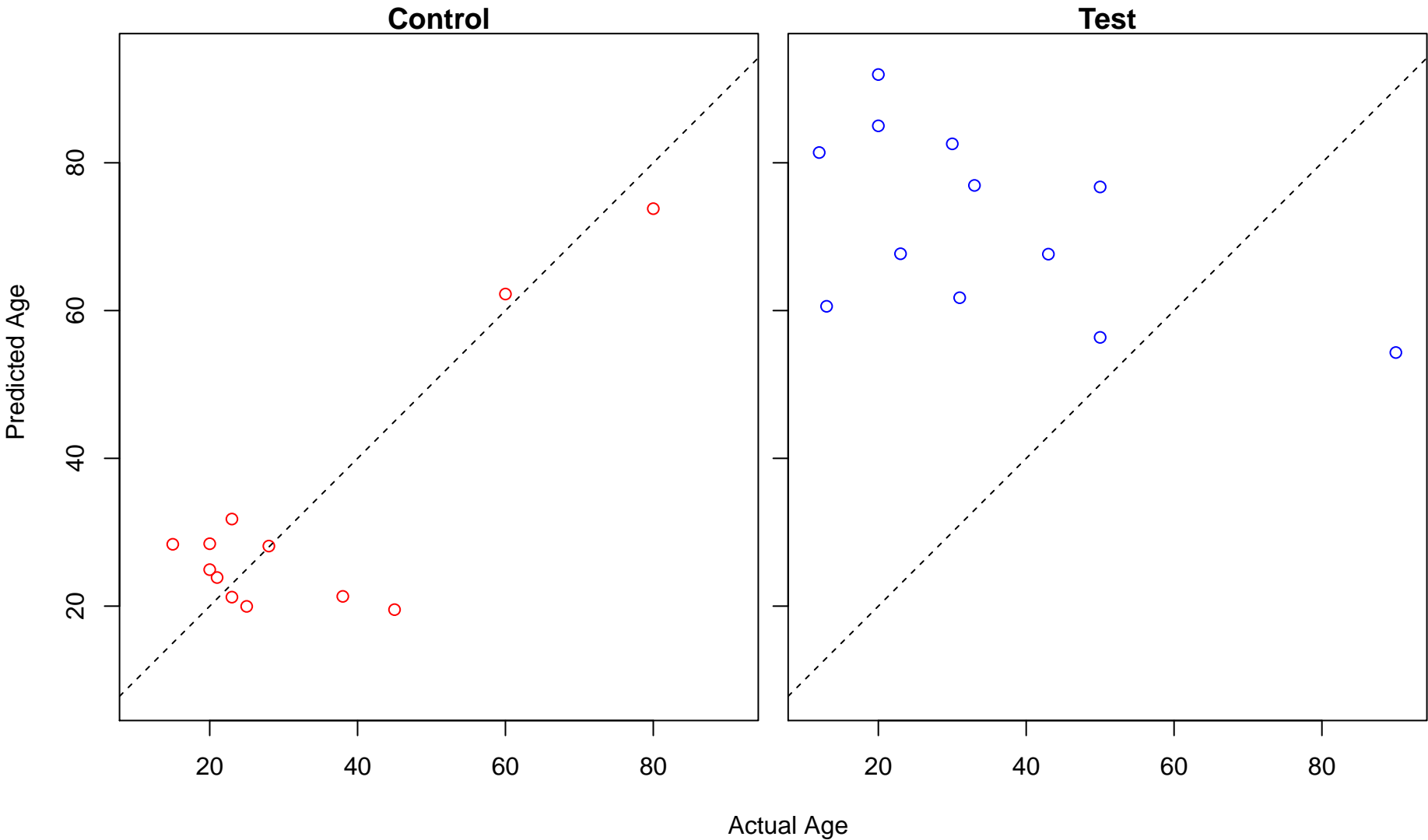
nucleosome organization (Score: 9.833244)



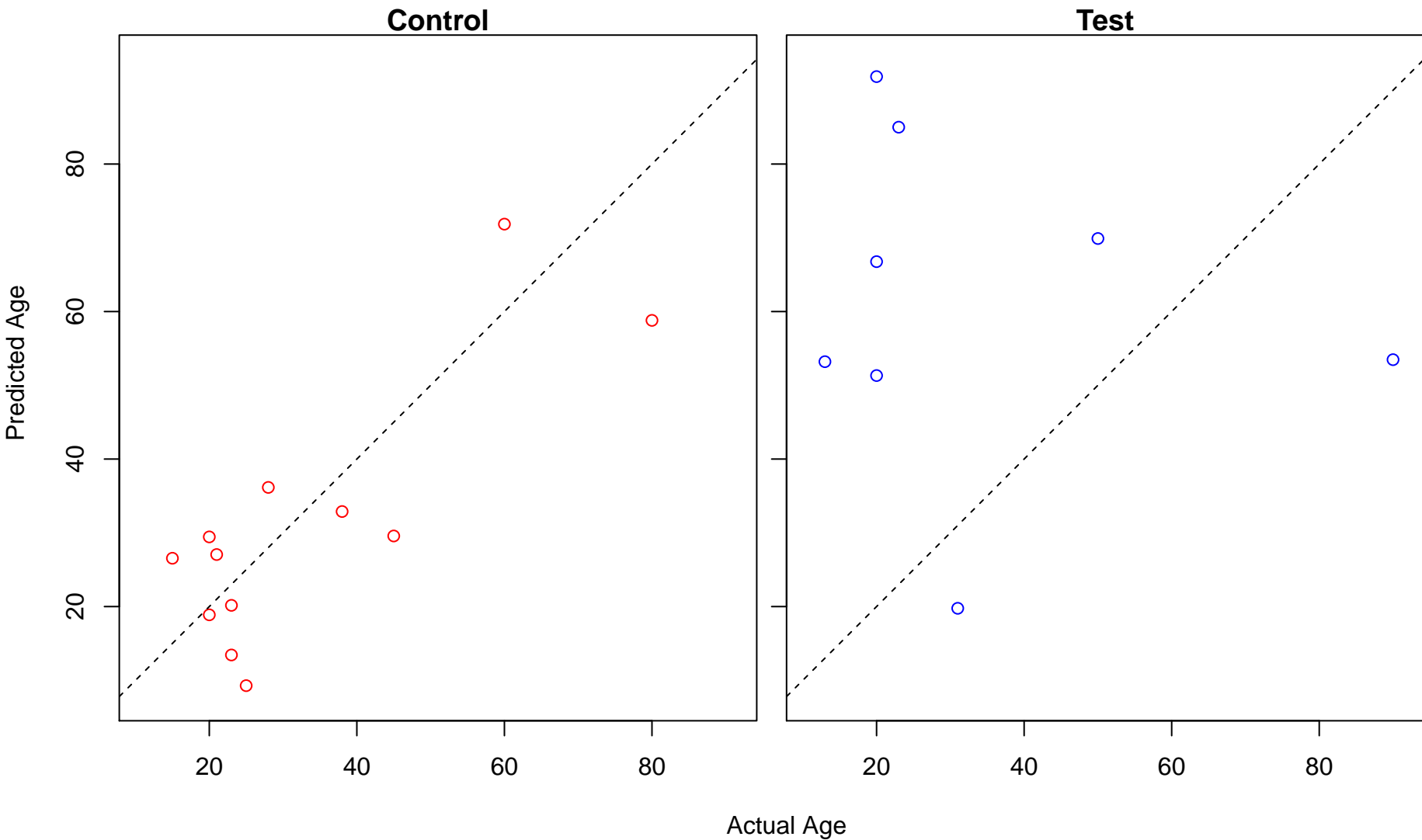
regulation of regulated secretory pathway (Score: 9.831497)



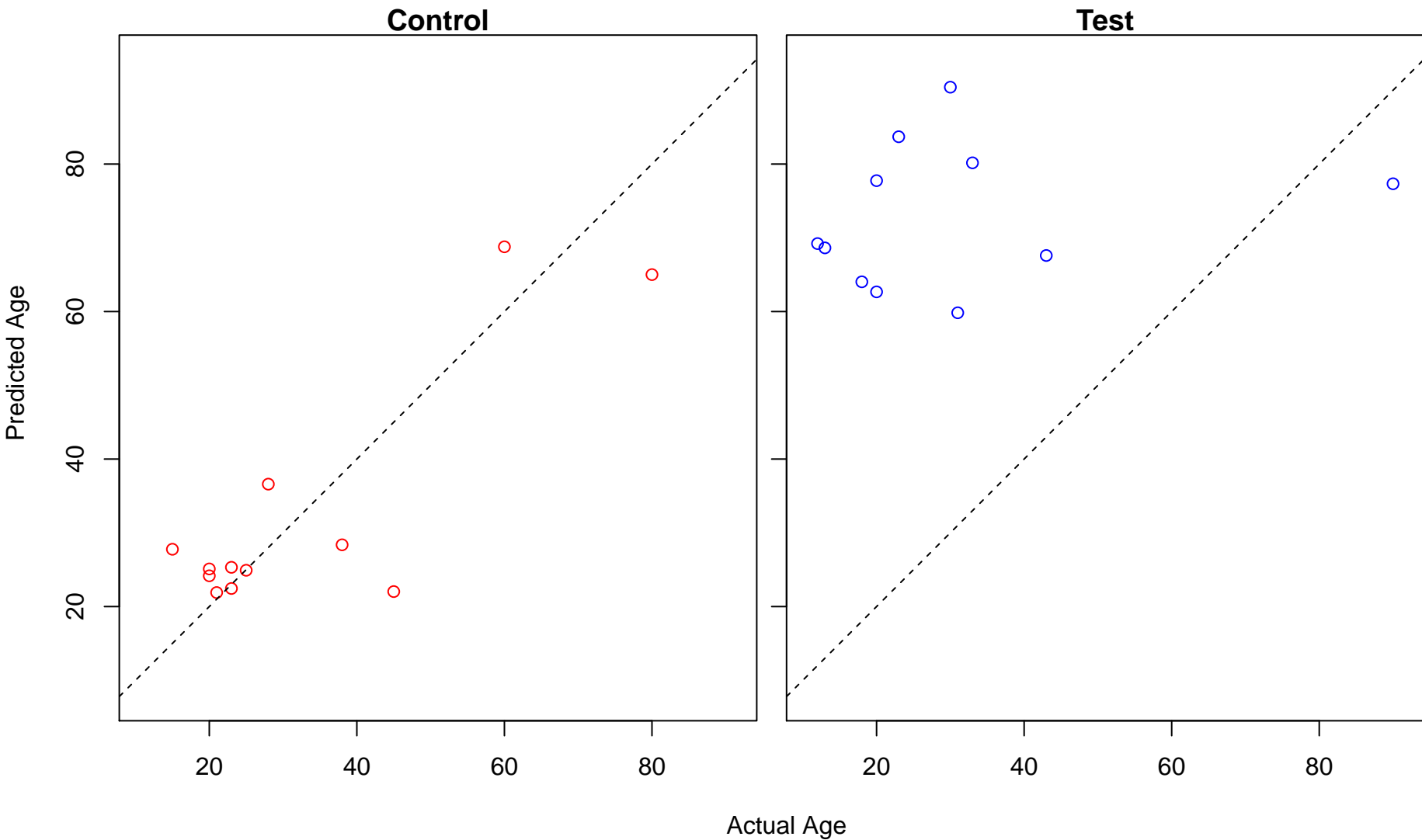
maintenance of protein location in nucleus (Score: 9.829472)



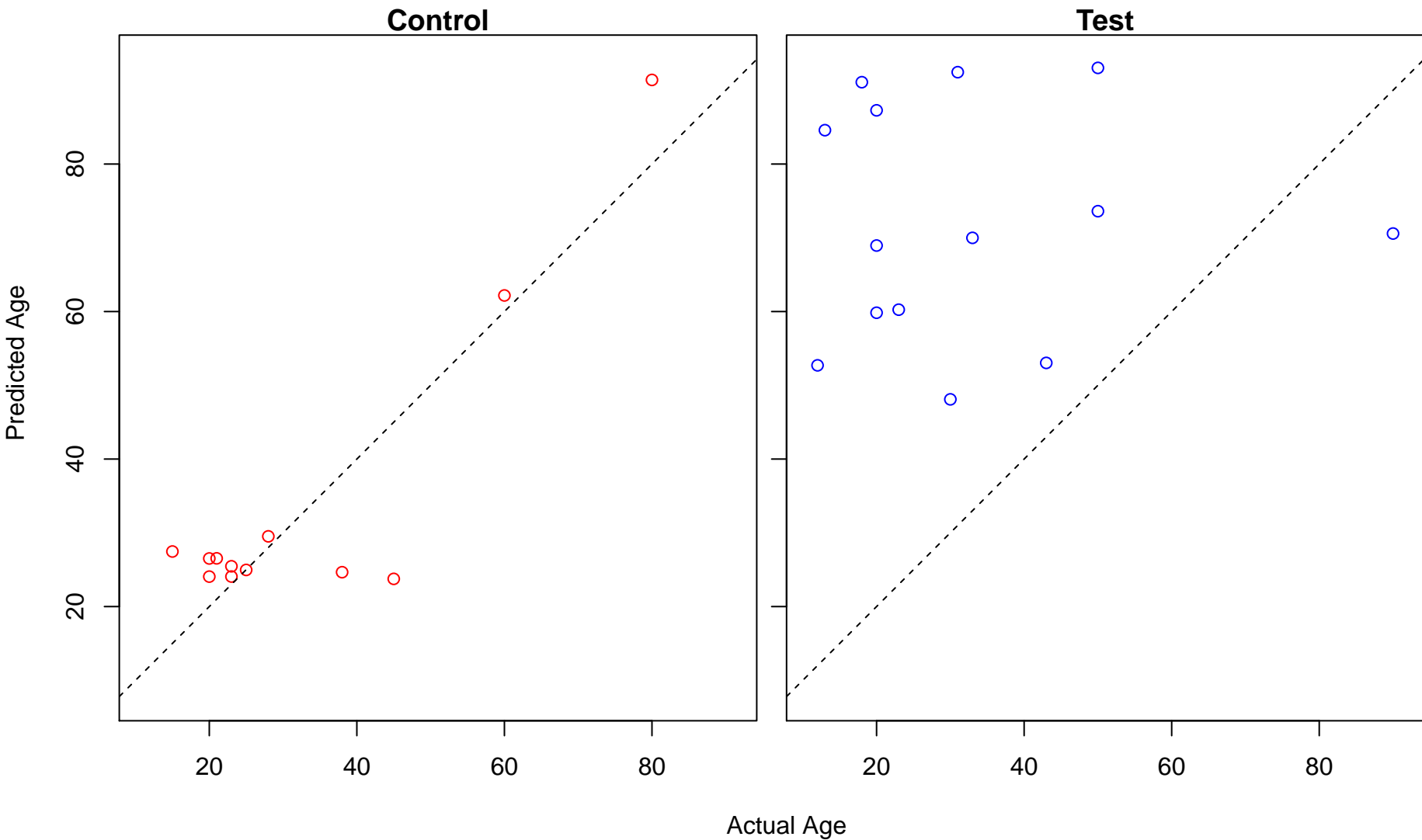
positive regulation of nuclear cell cycle DNA replication (Score: 9.826874)



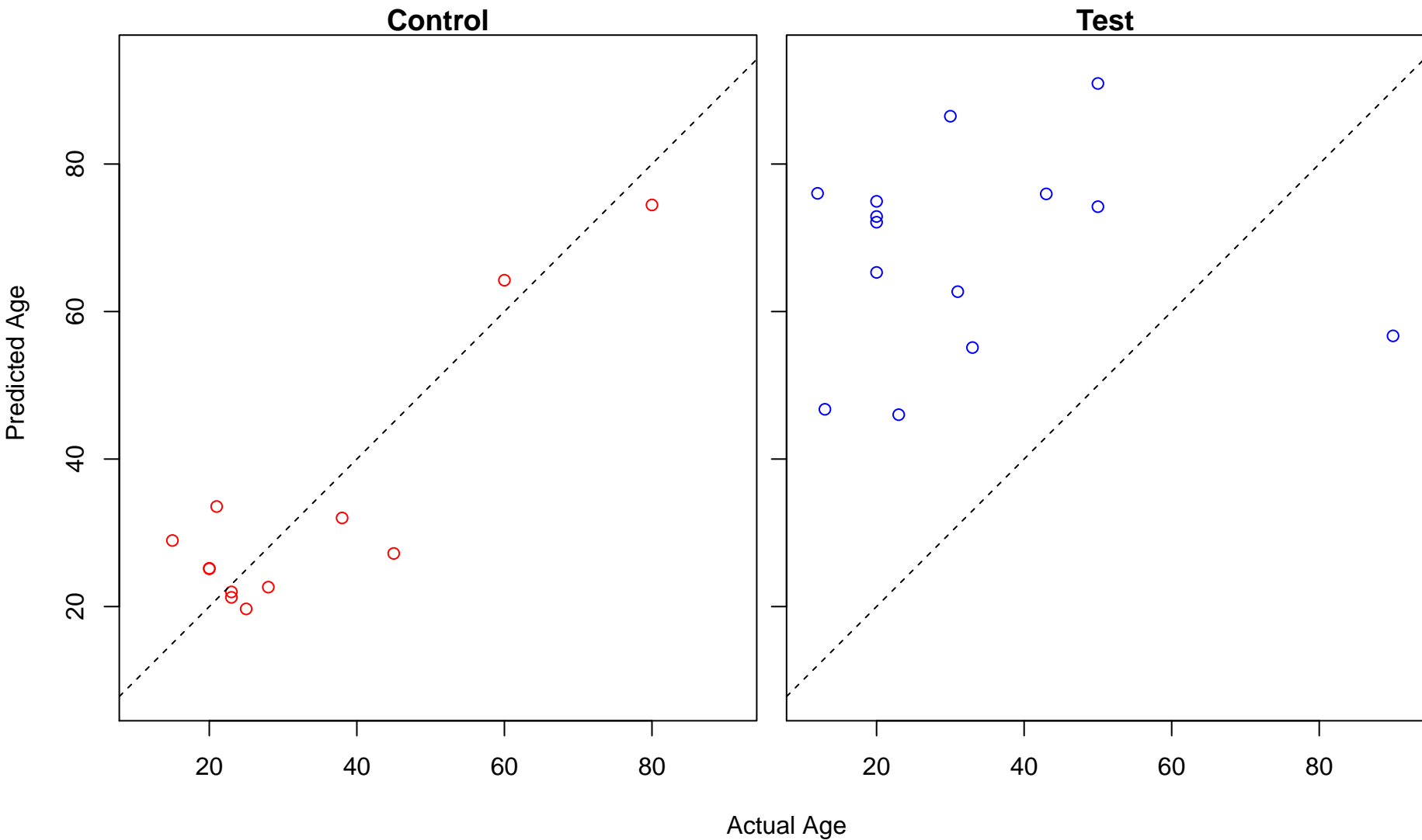
regulation of tissue remodeling (Score: 9.825409)



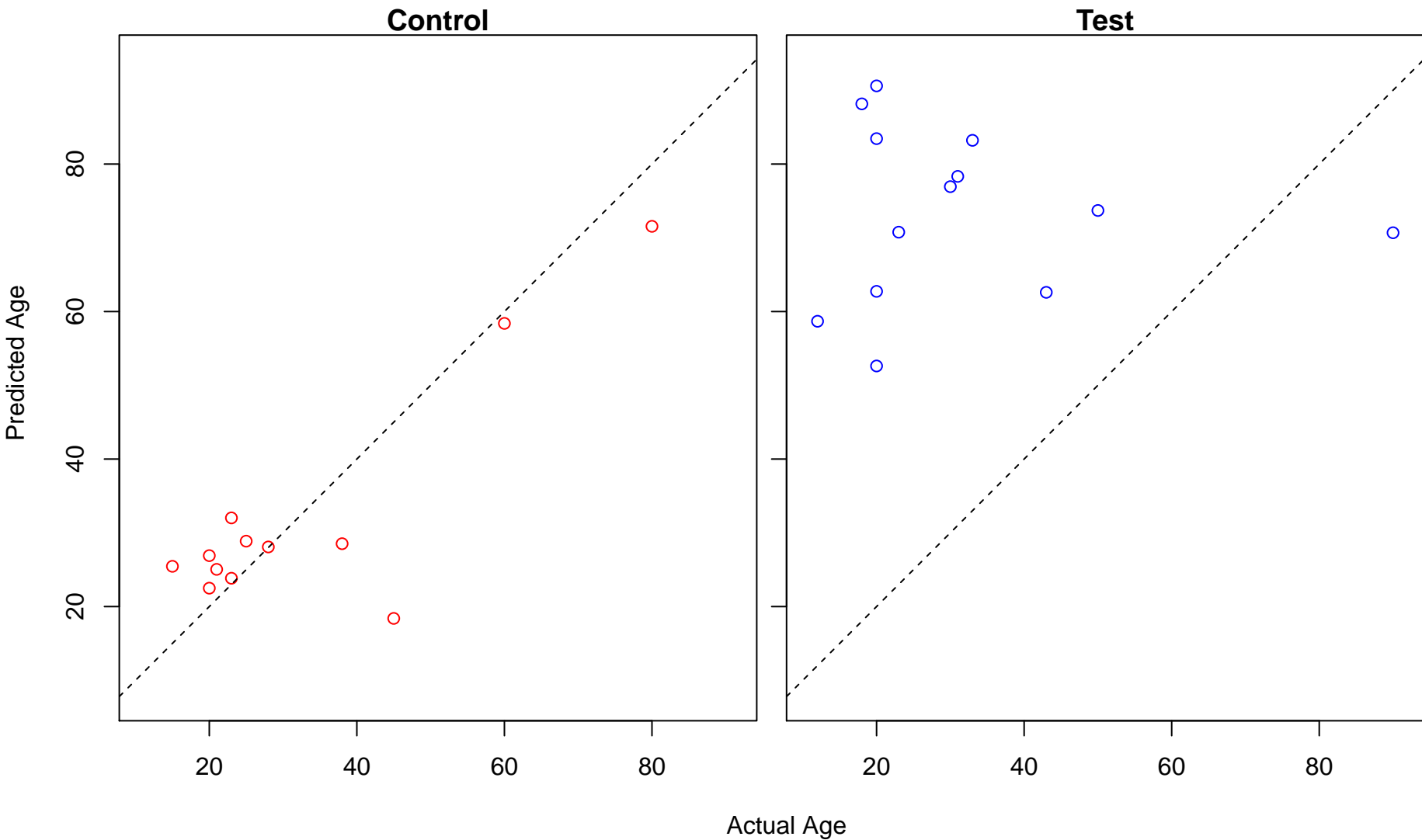
chromatin assembly or disassembly (Score: 9.824106)



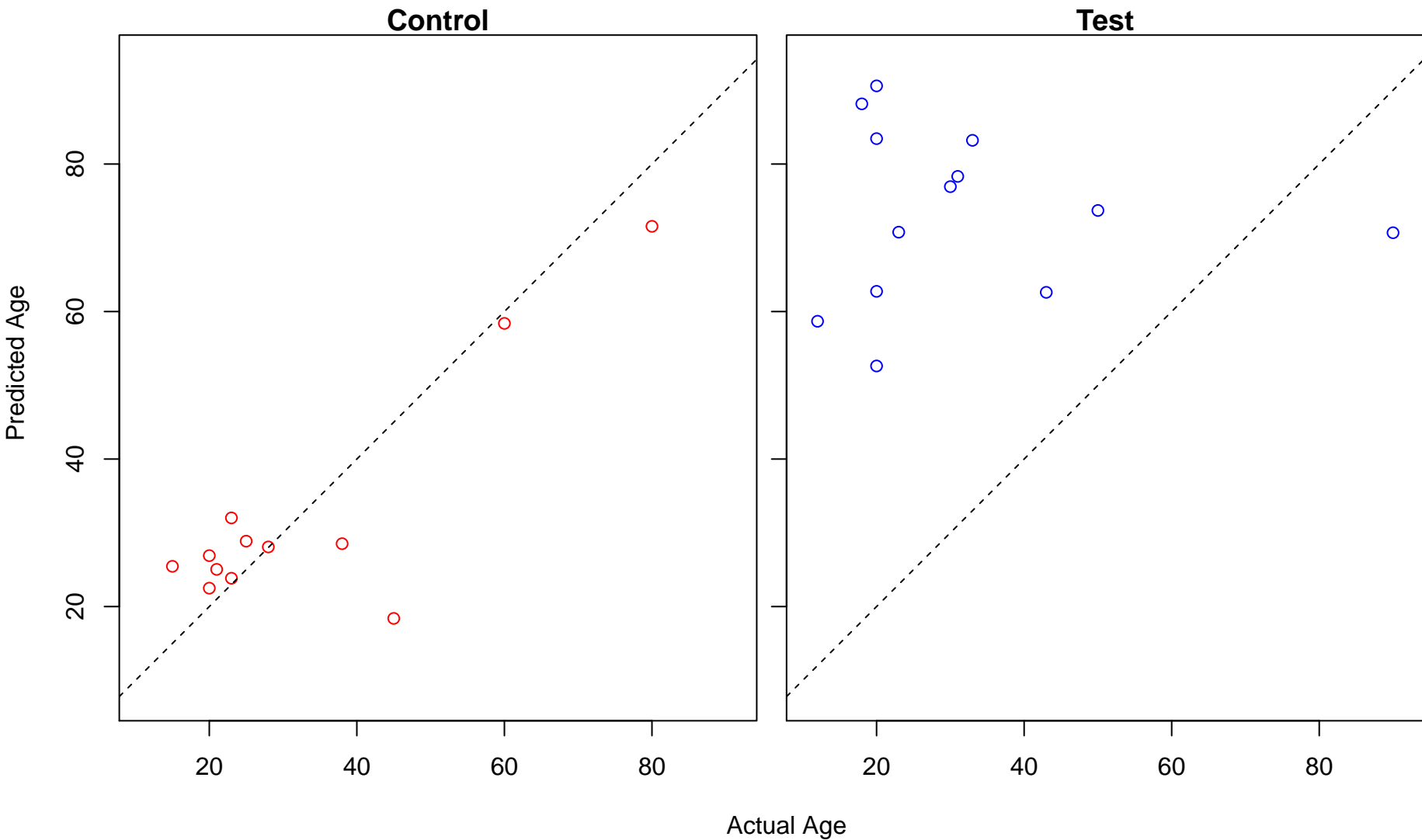
negative regulation of cell motility (Score: 9.823159)



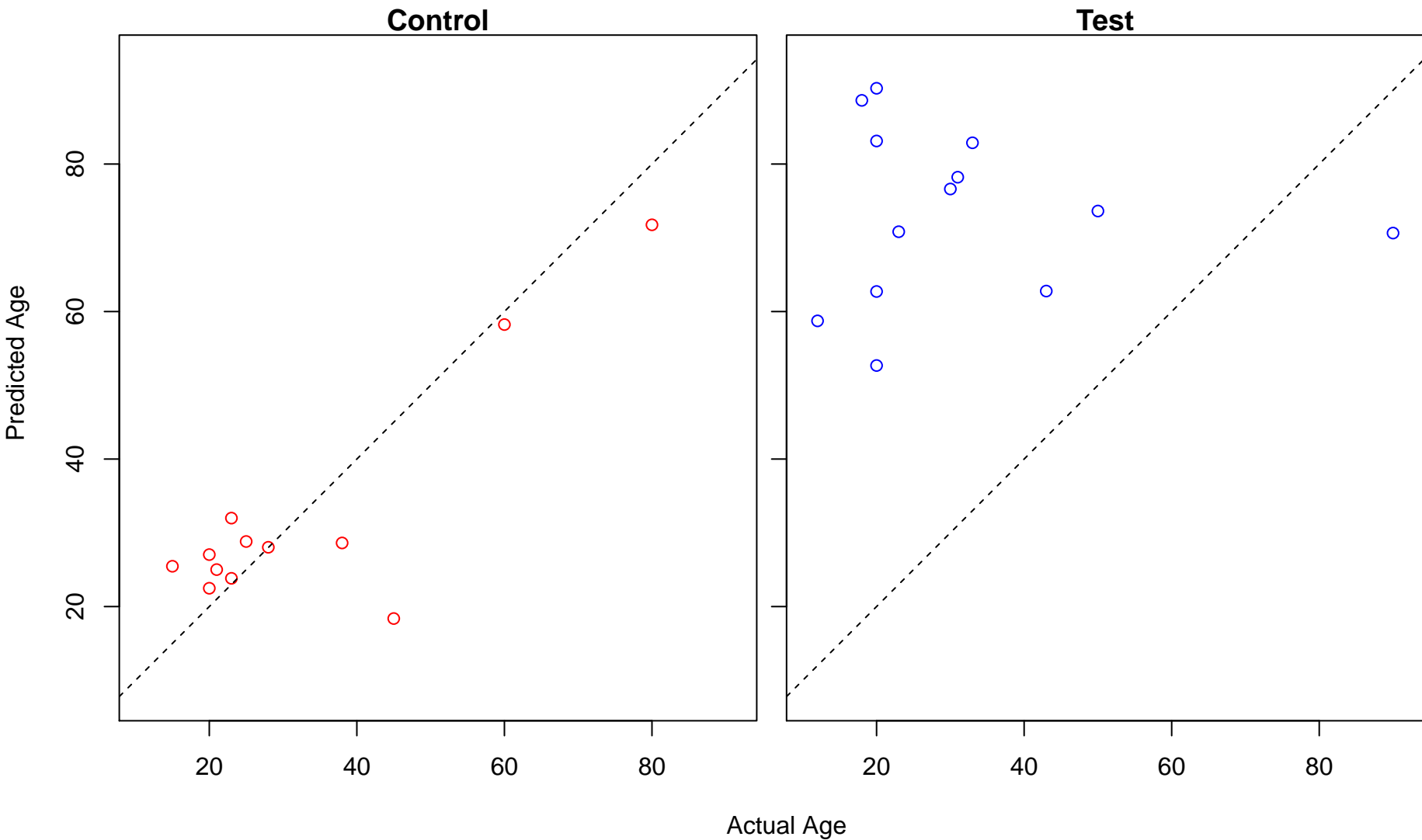
positive regulation of leukocyte mediated cytotoxicity (Score: 9.797563)



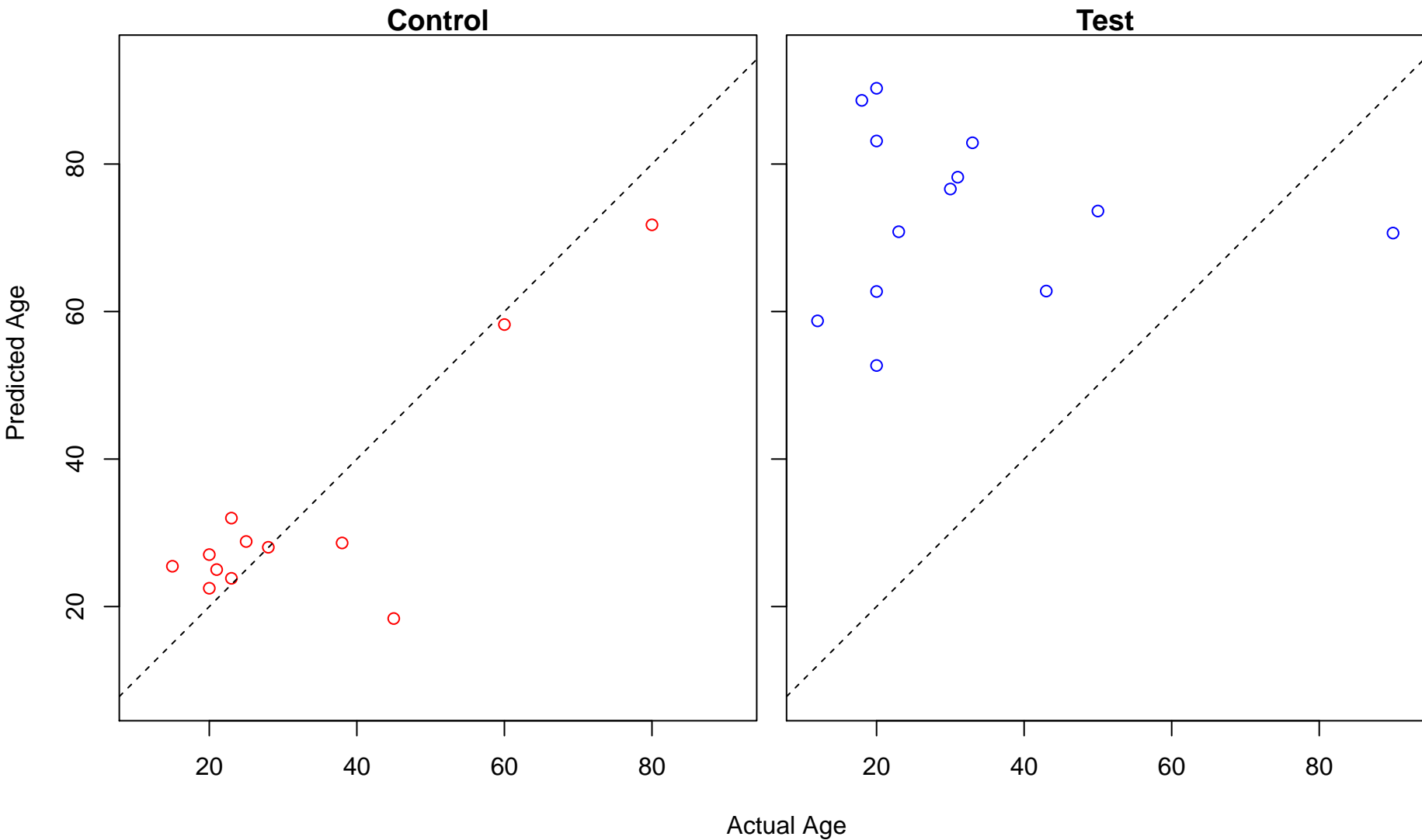
positive regulation of cell killing (Score: 9.797561)



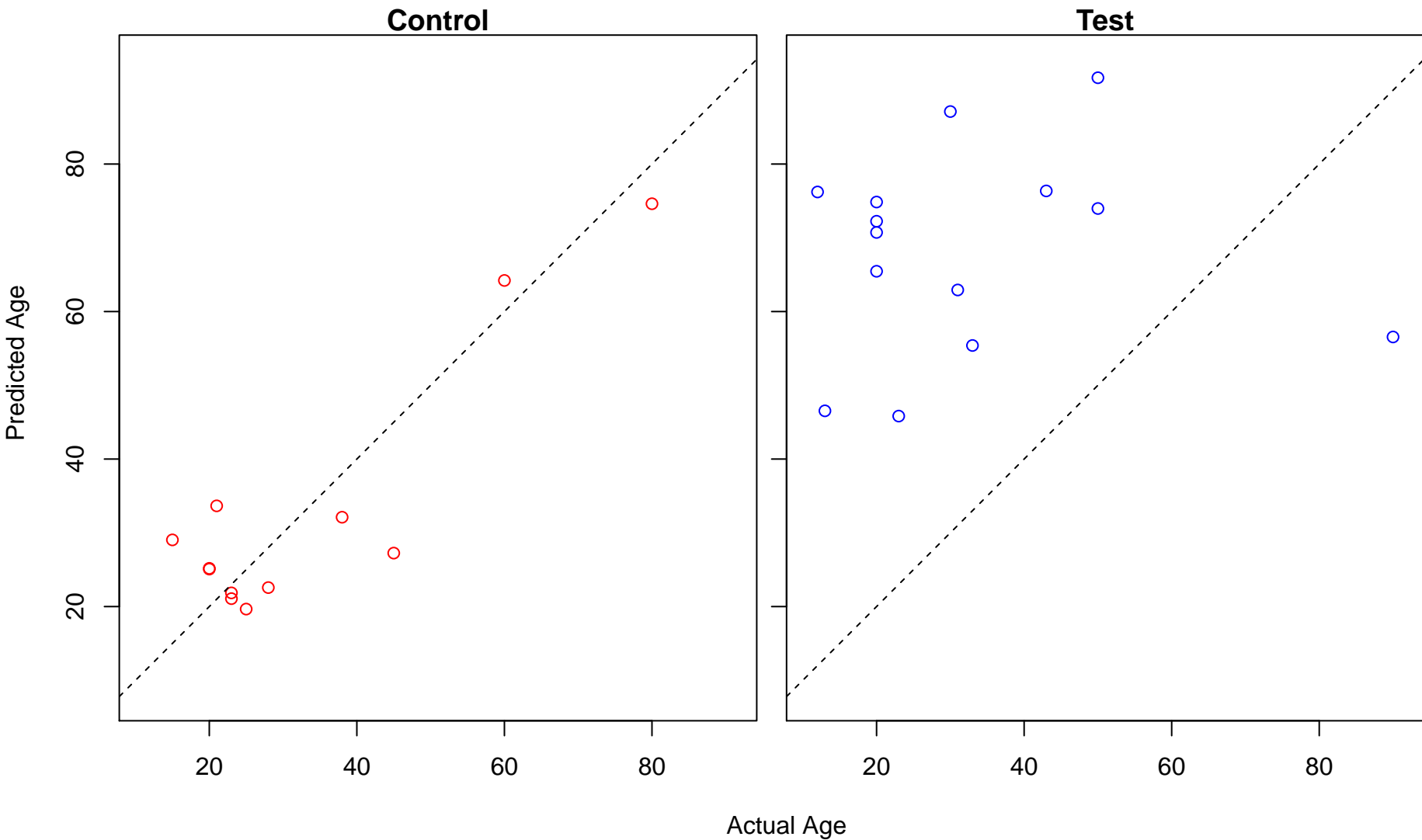
regulation of natural killer cell mediated cytotoxicity (Score: 9.793906)

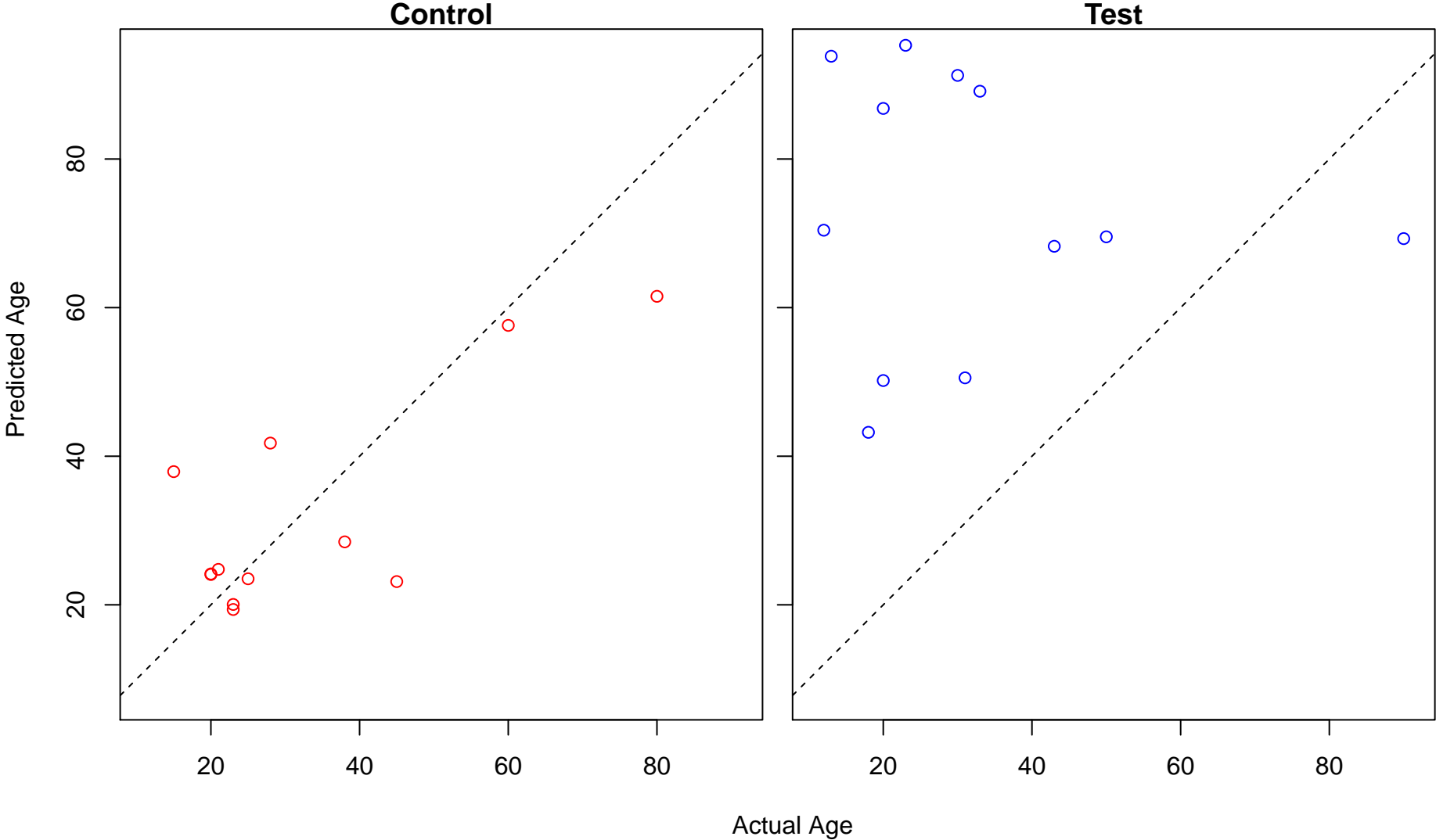


regulation of natural killer cell mediated immunity (Score: 9.793906)

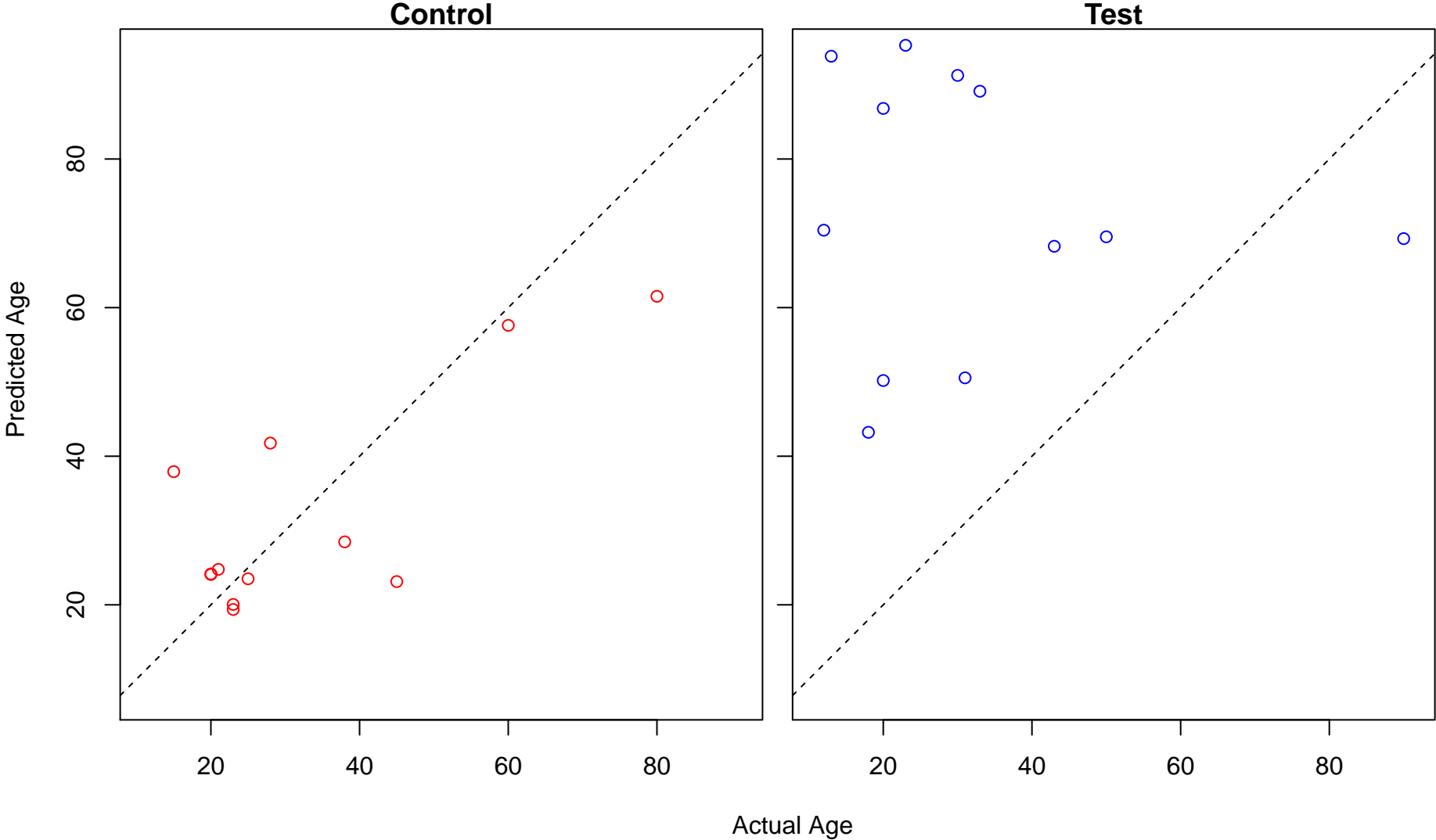


negative regulation of cell migration (Score: 9.791381)



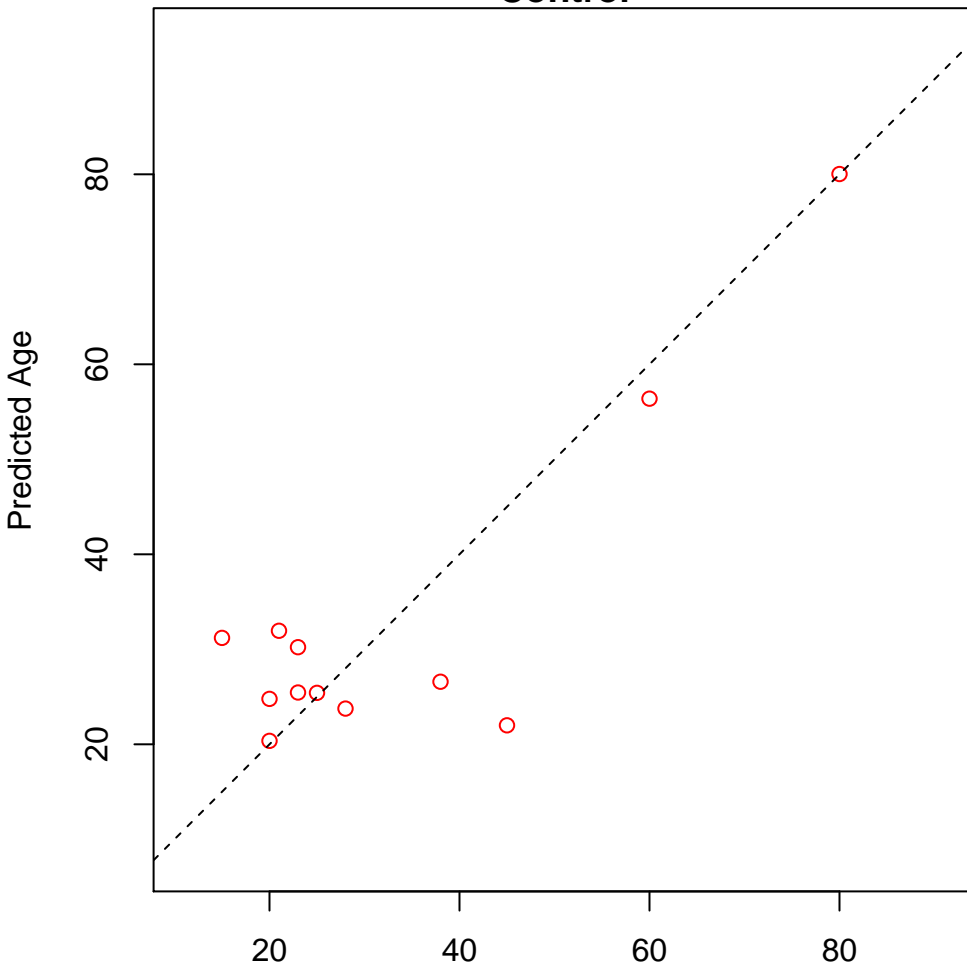


negative regulation of humoral immune response mediated by circulating immunoglobulin (Score: 9.78)

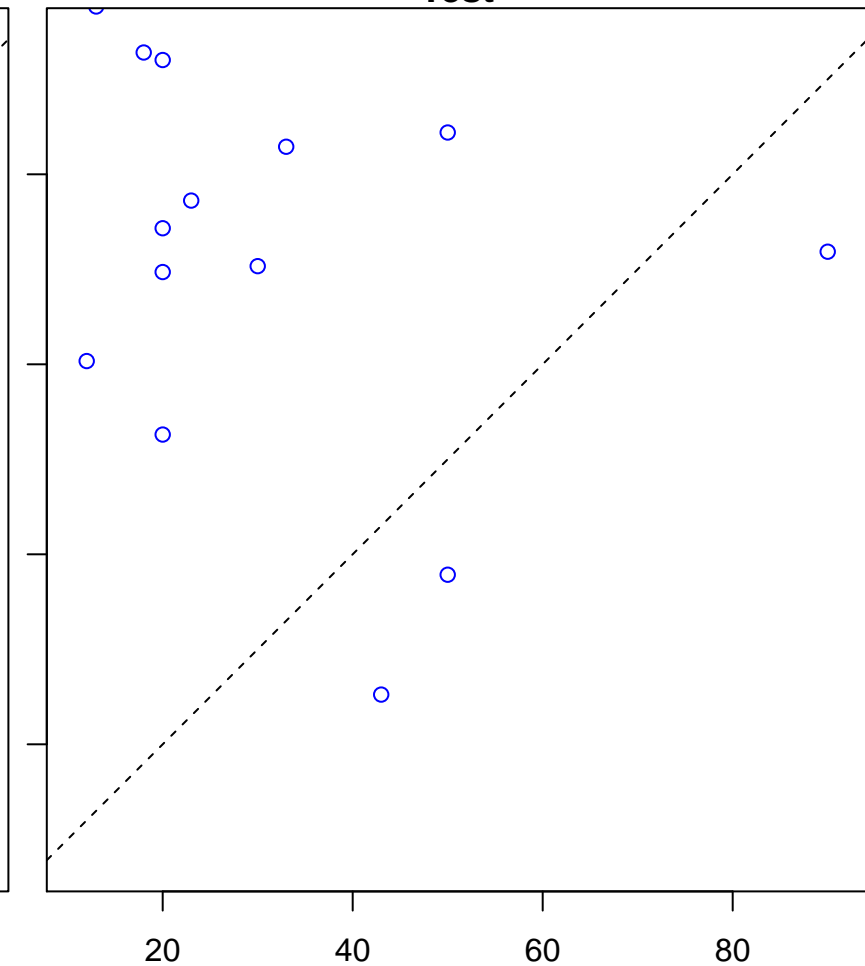


regulation of protein import into nucleus (Score: 9.788974)

Control

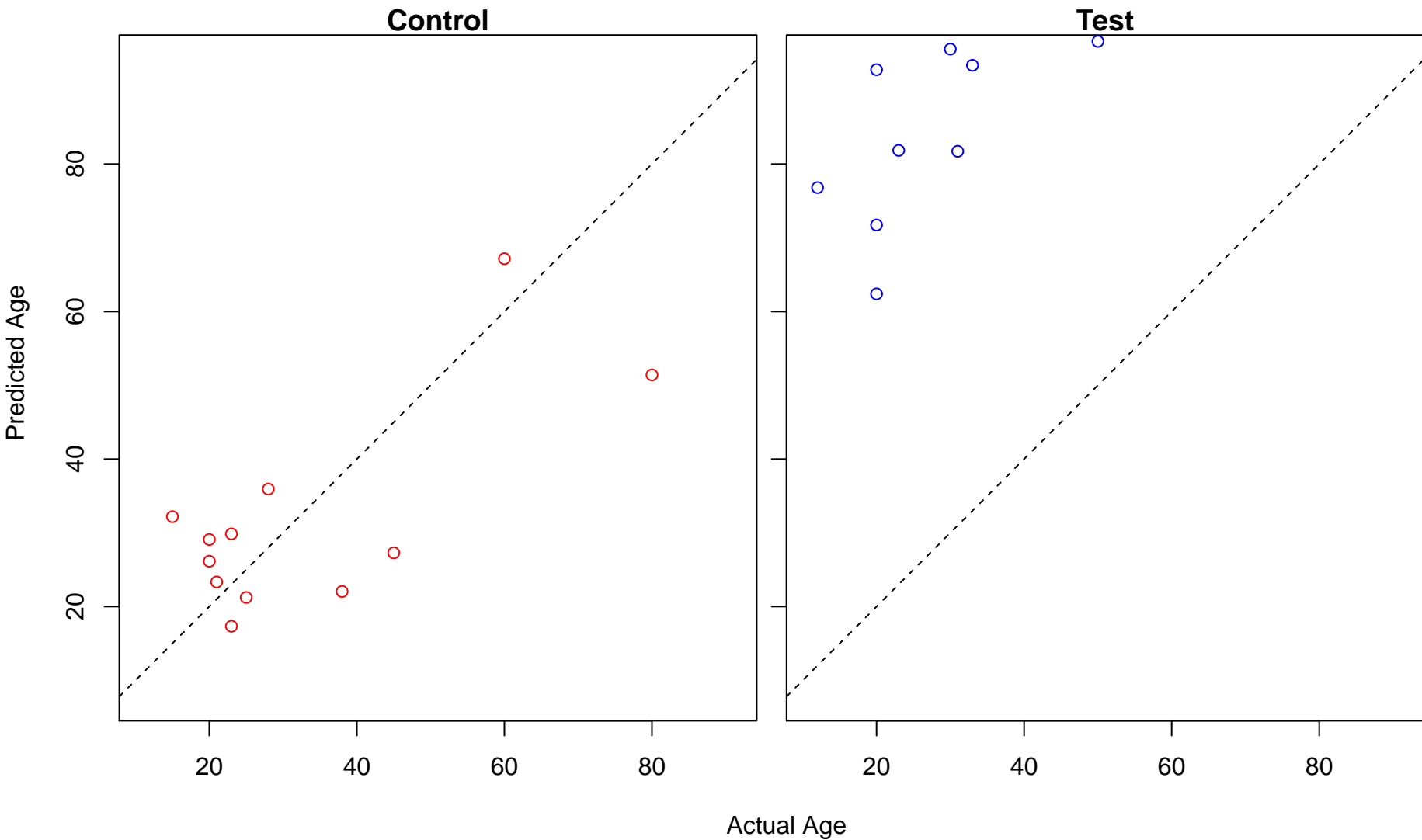


Test

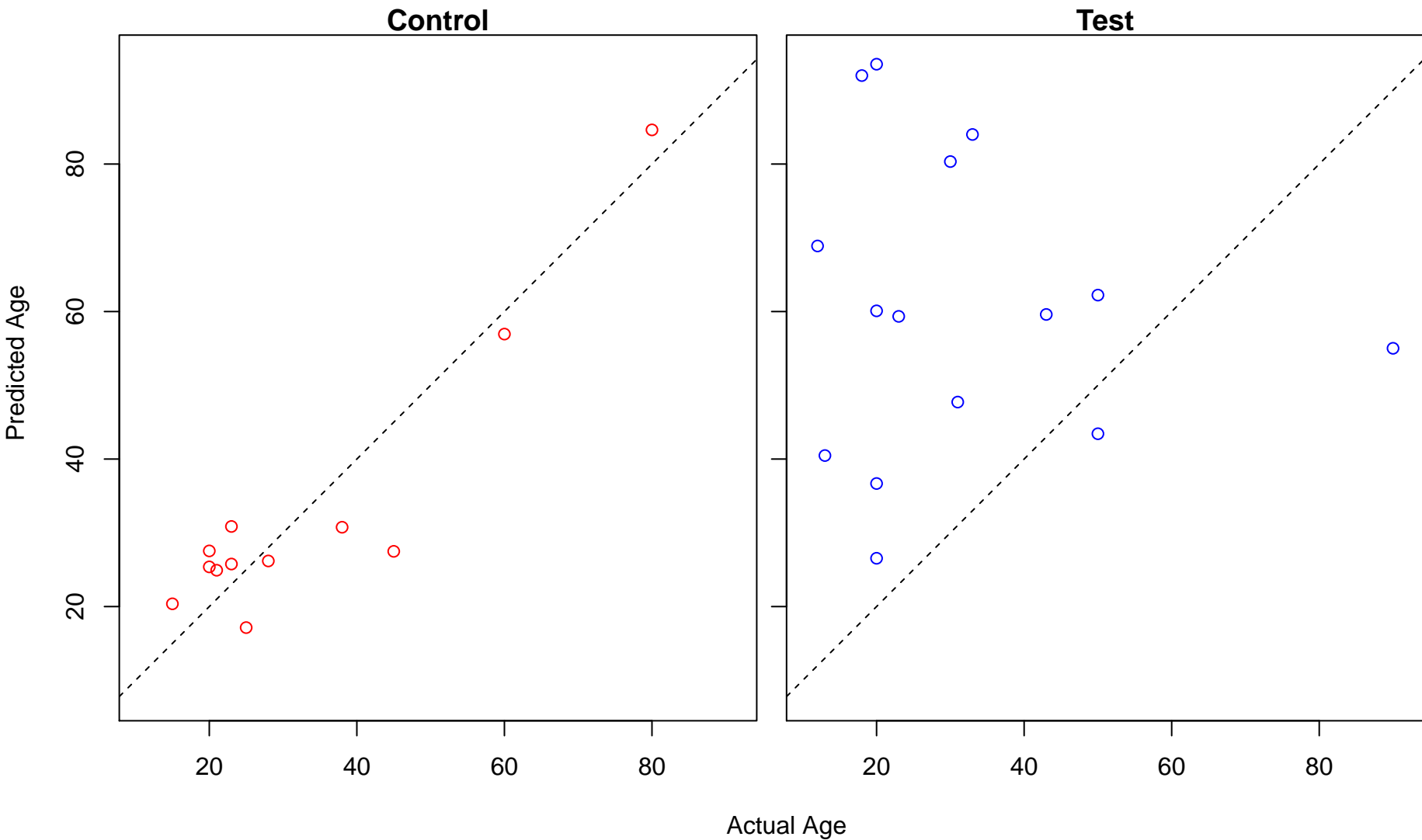


Actual Age

maintenance of cell polarity (Score: 9.771565)

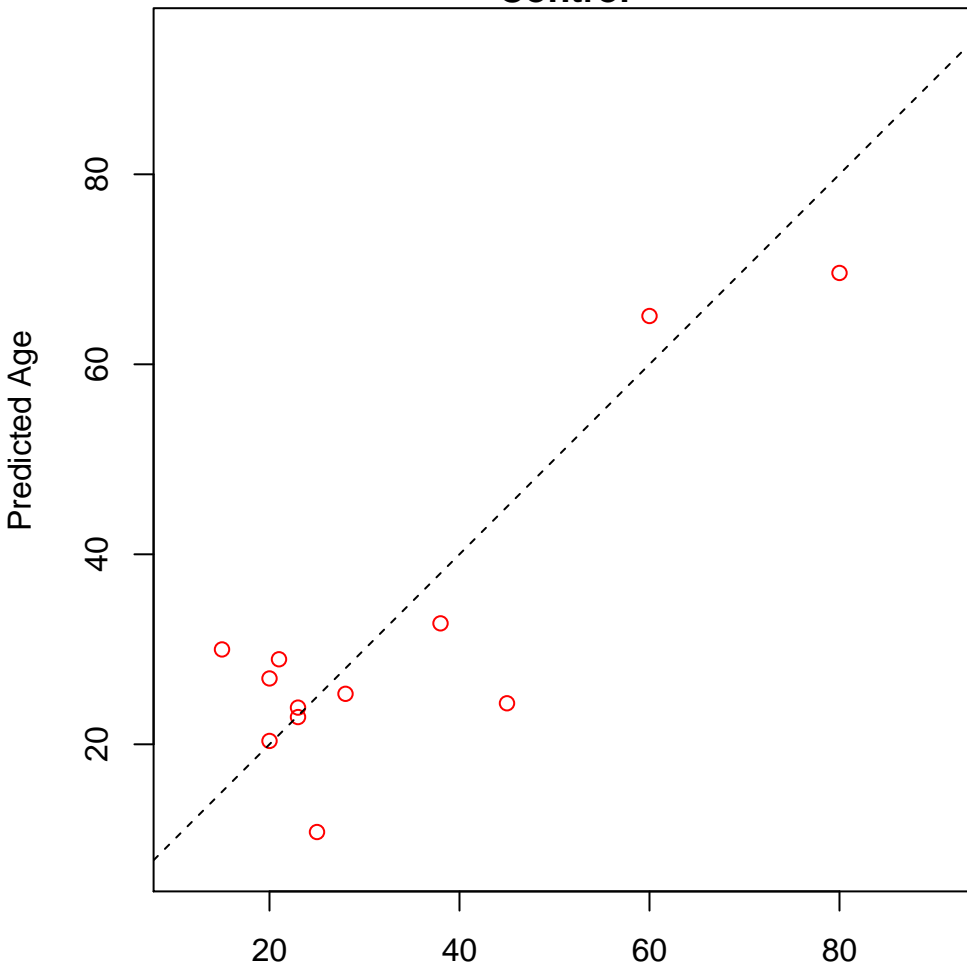


positive regulation of cellular amine metabolic process (Score: 9.771239)

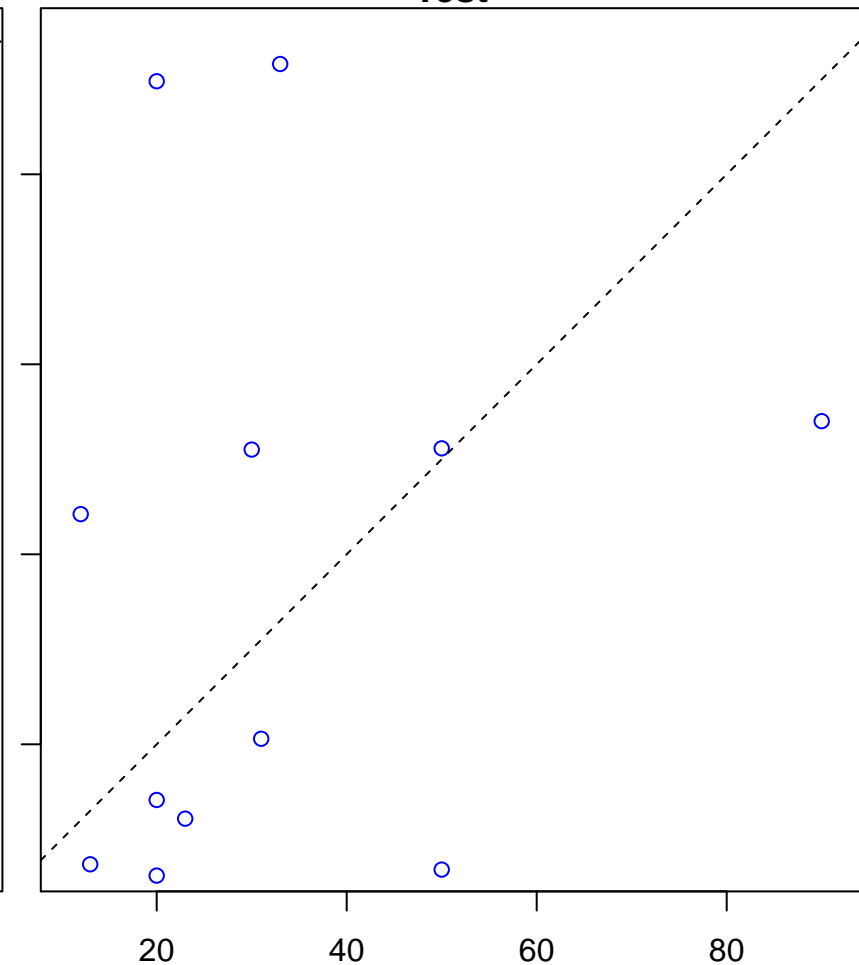


mitotic sister chromatid segregation (Score: 9.770583)

Control

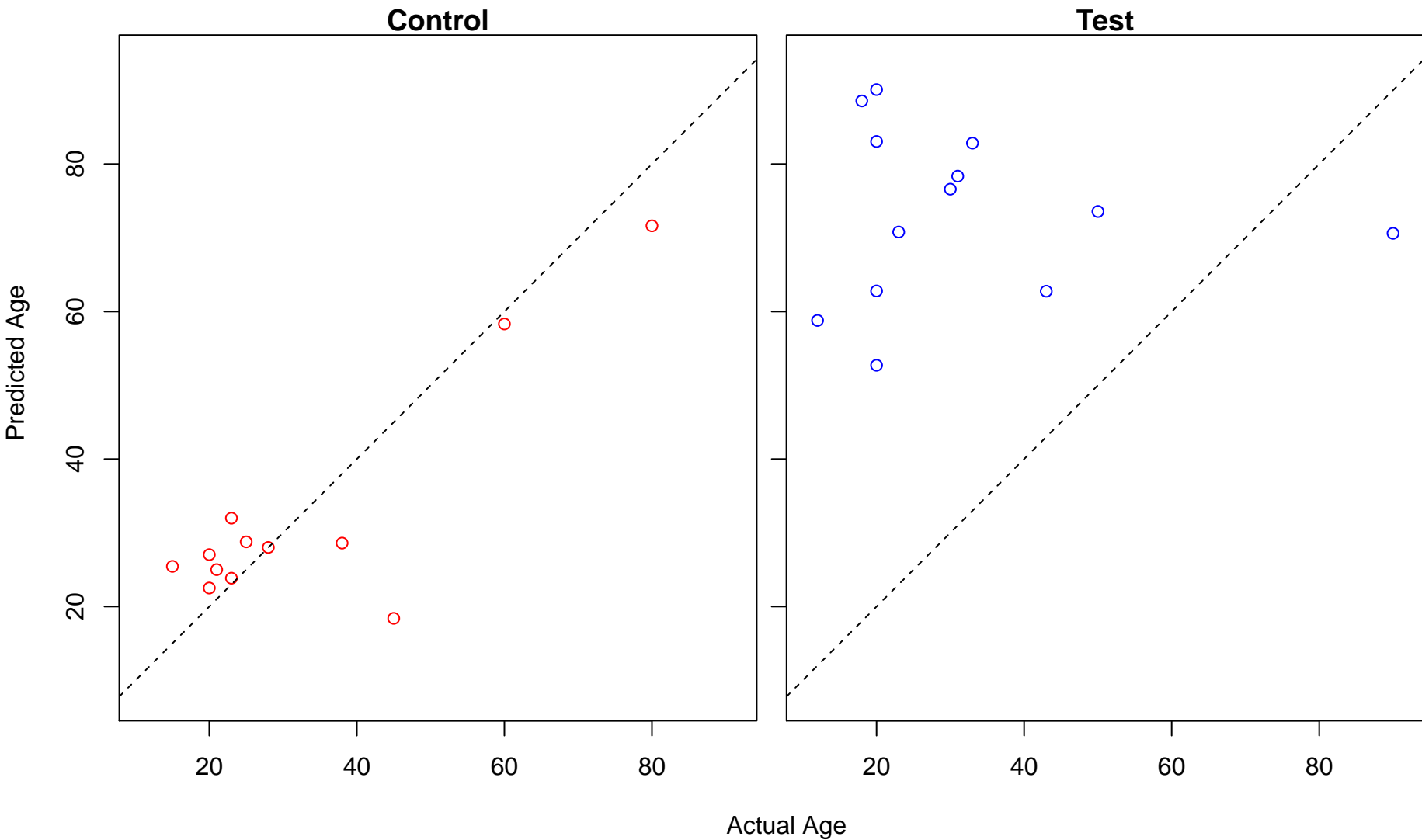


Test

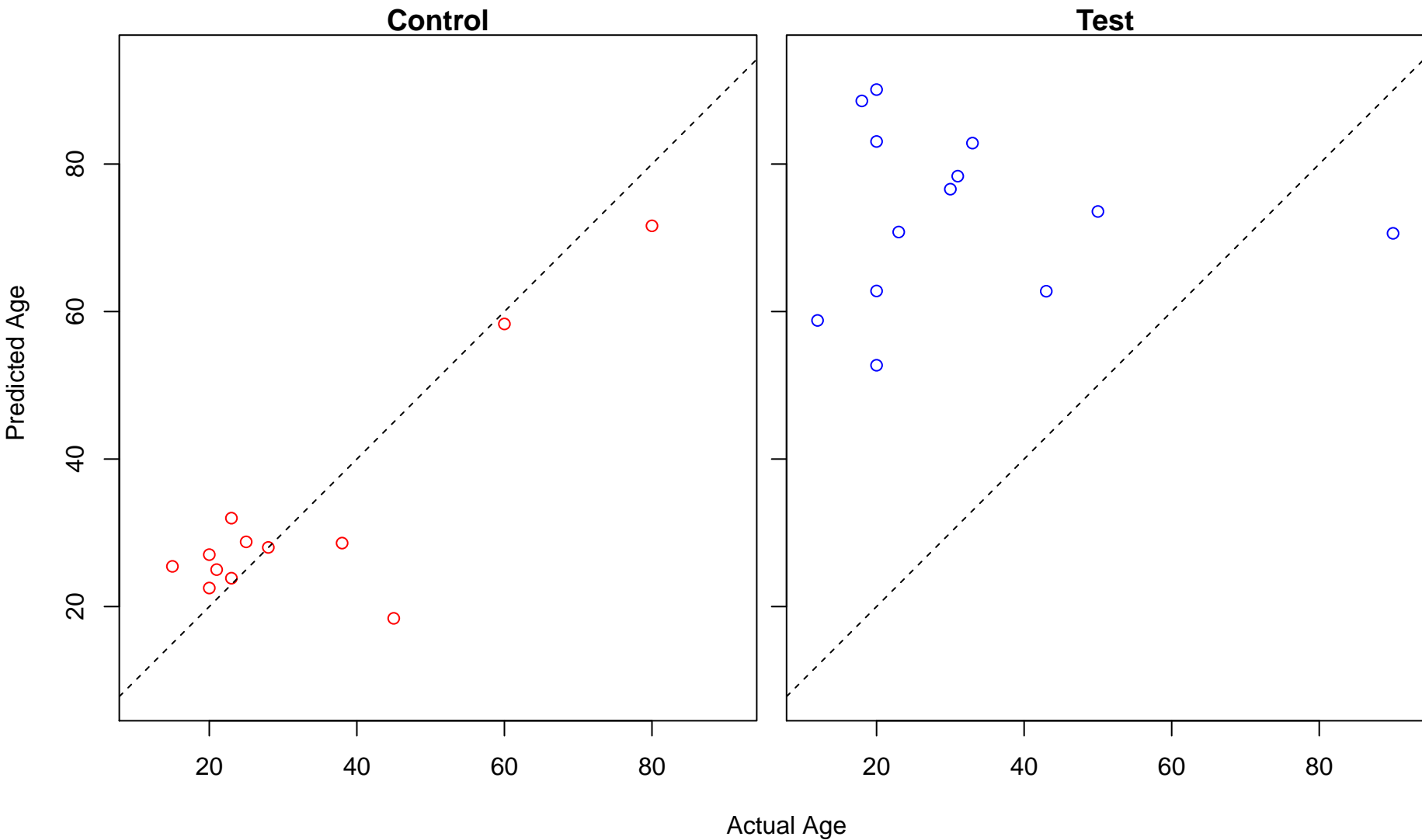


Actual Age

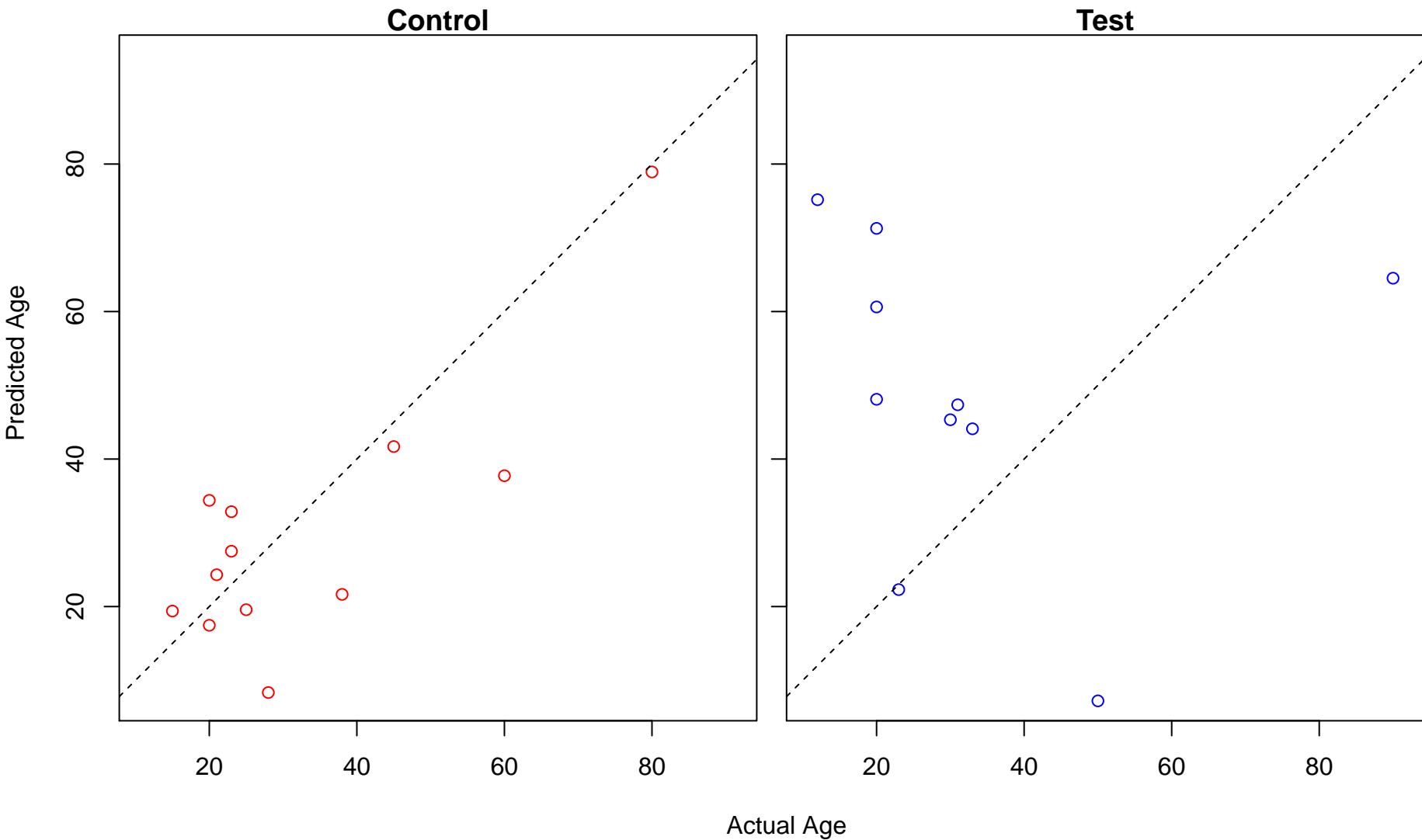
regulation of leukocyte mediated cytotoxicity (Score: 9.769784)



regulation of cell killing (Score: 9.769770)

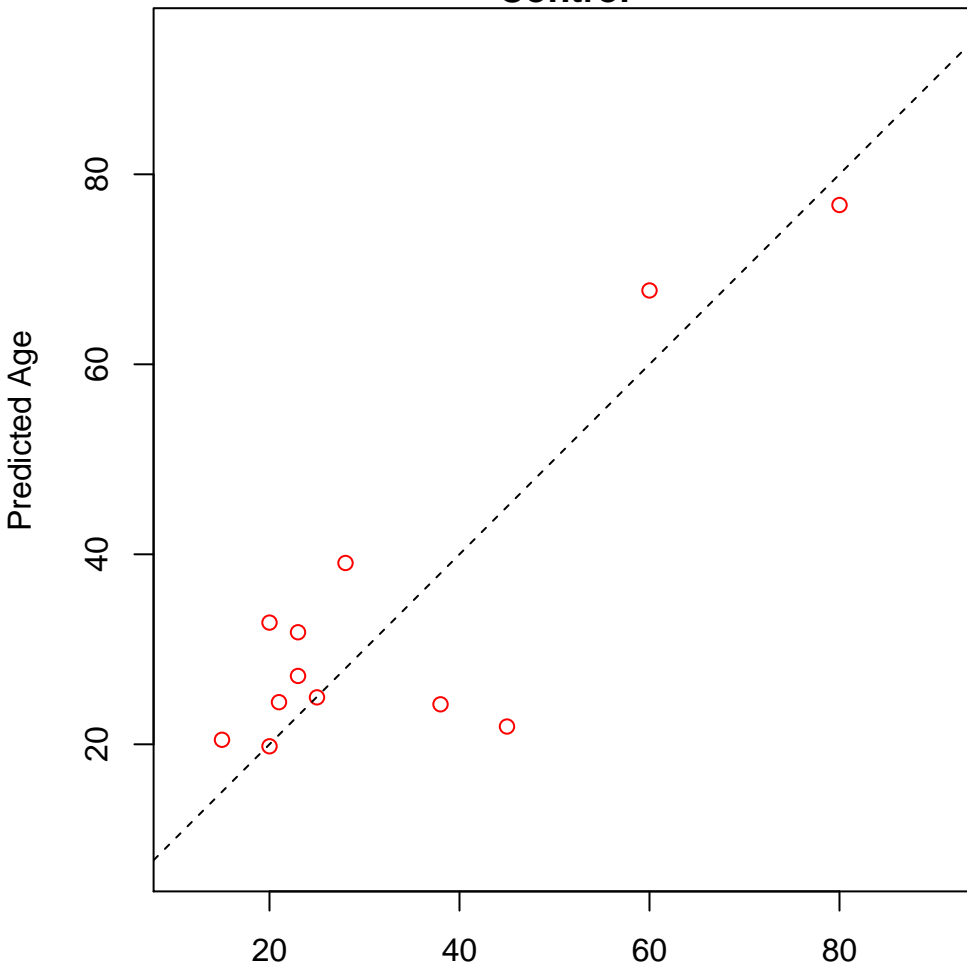


negative regulation of voltage-gated calcium channel activity (Score: 9.766317)

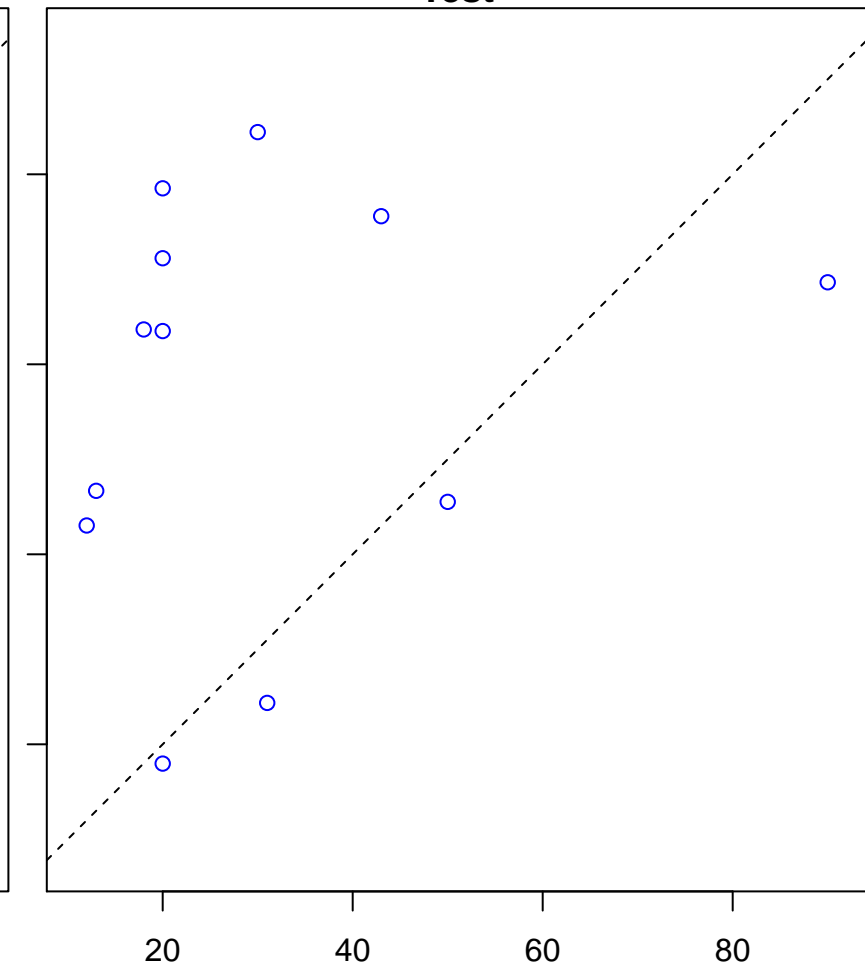


cellular response to muramyl dipeptide (Score: 9.764648)

Control

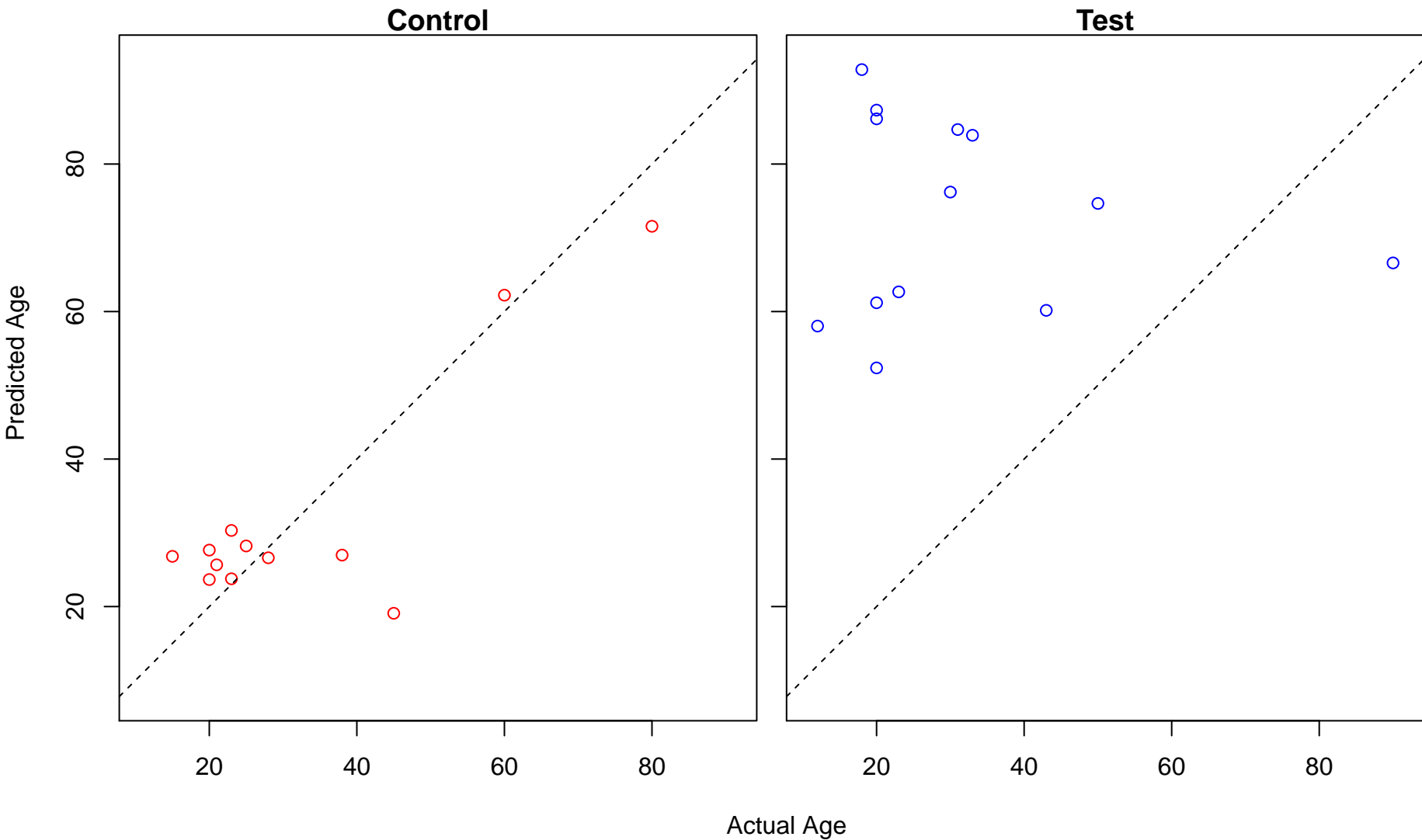


Test

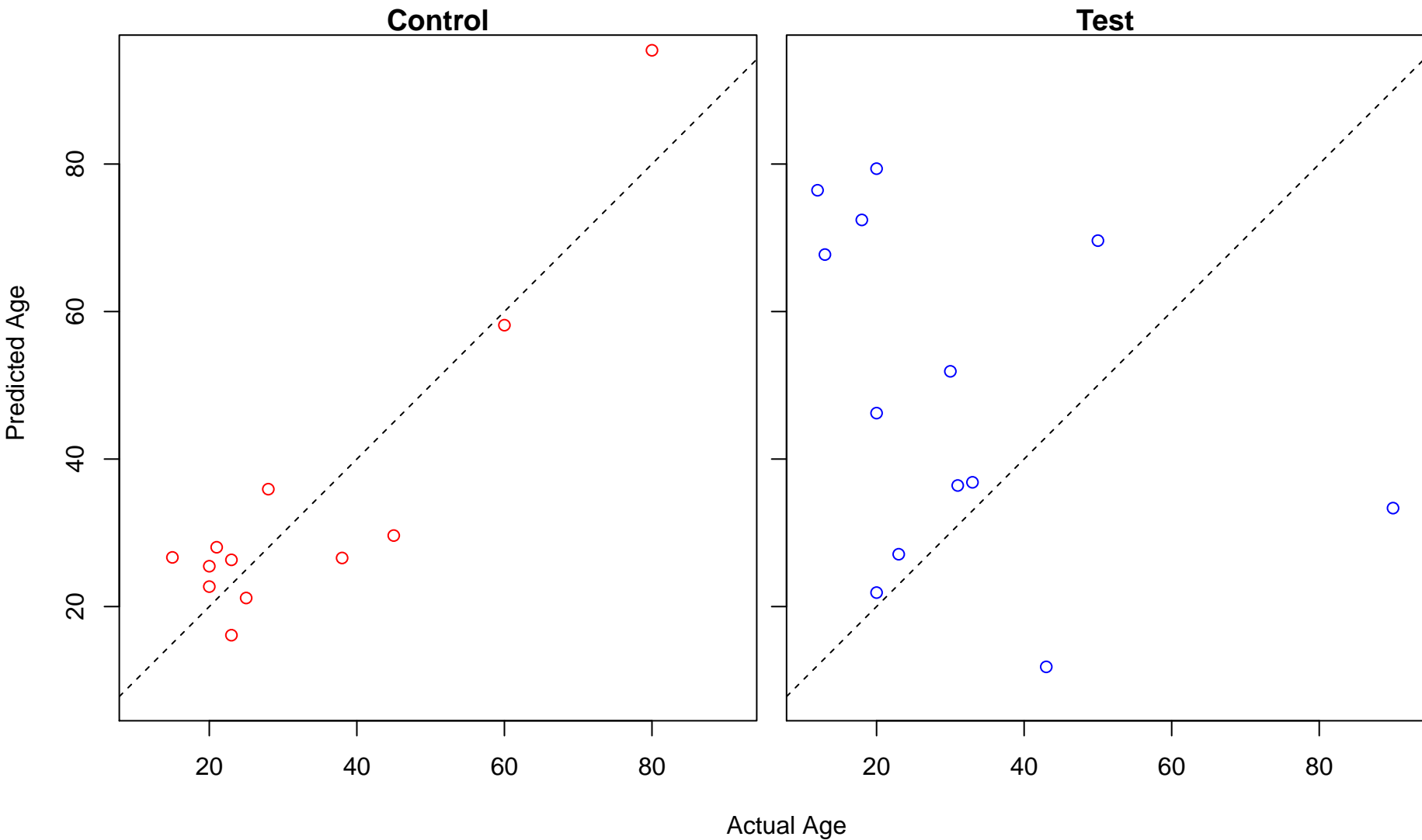


Actual Age

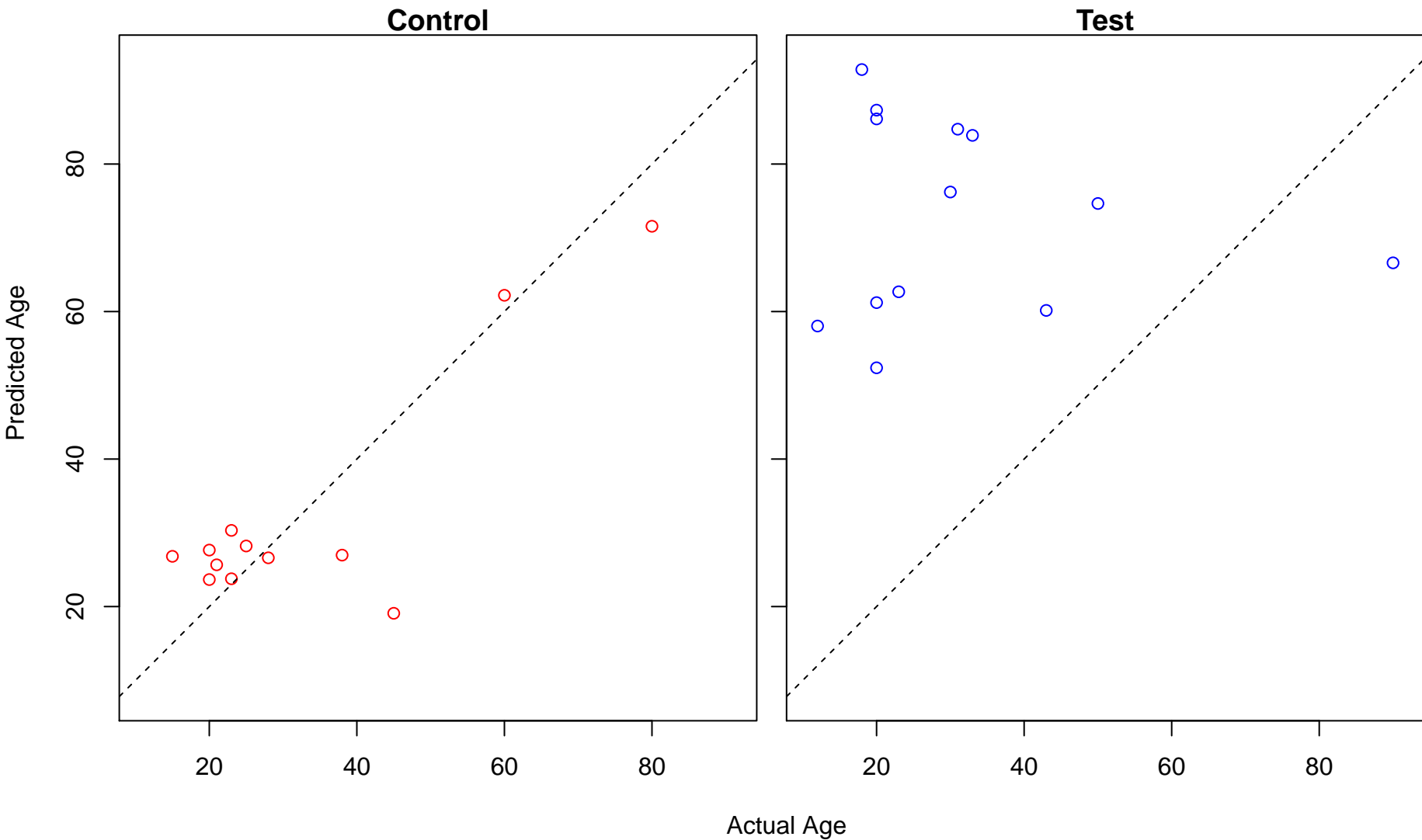
positive regulation of alpha-beta T cell proliferation (Score: 9.763829)



DNA conformation change (Score: 9.763172)

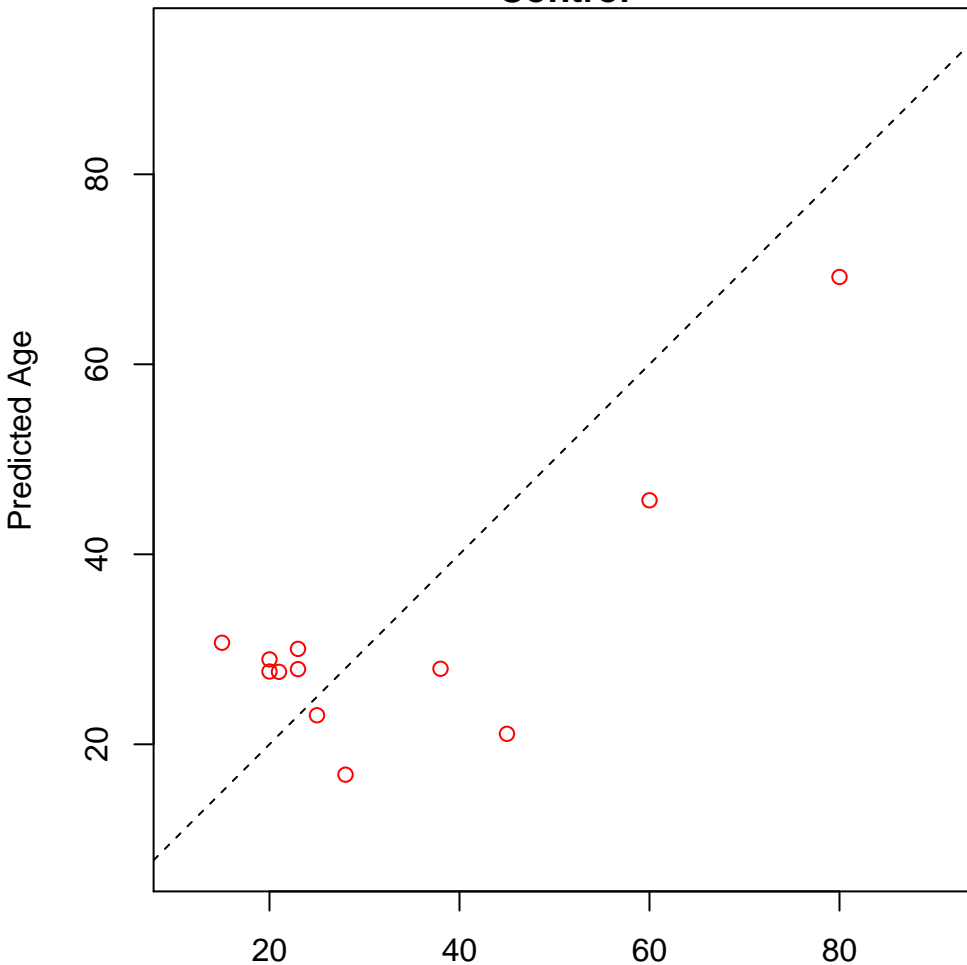


regulation of alpha-beta T cell proliferation (Score: 9.762673)

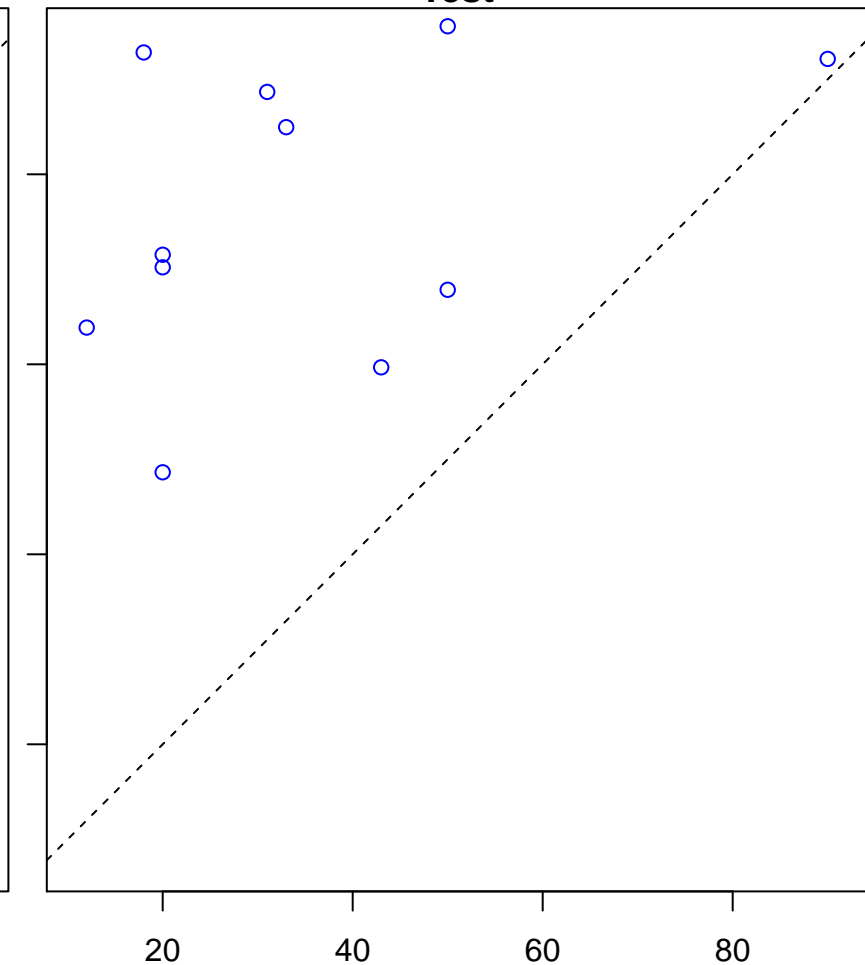


noradrenergic neuron differentiation (Score: 9.757211)

Control

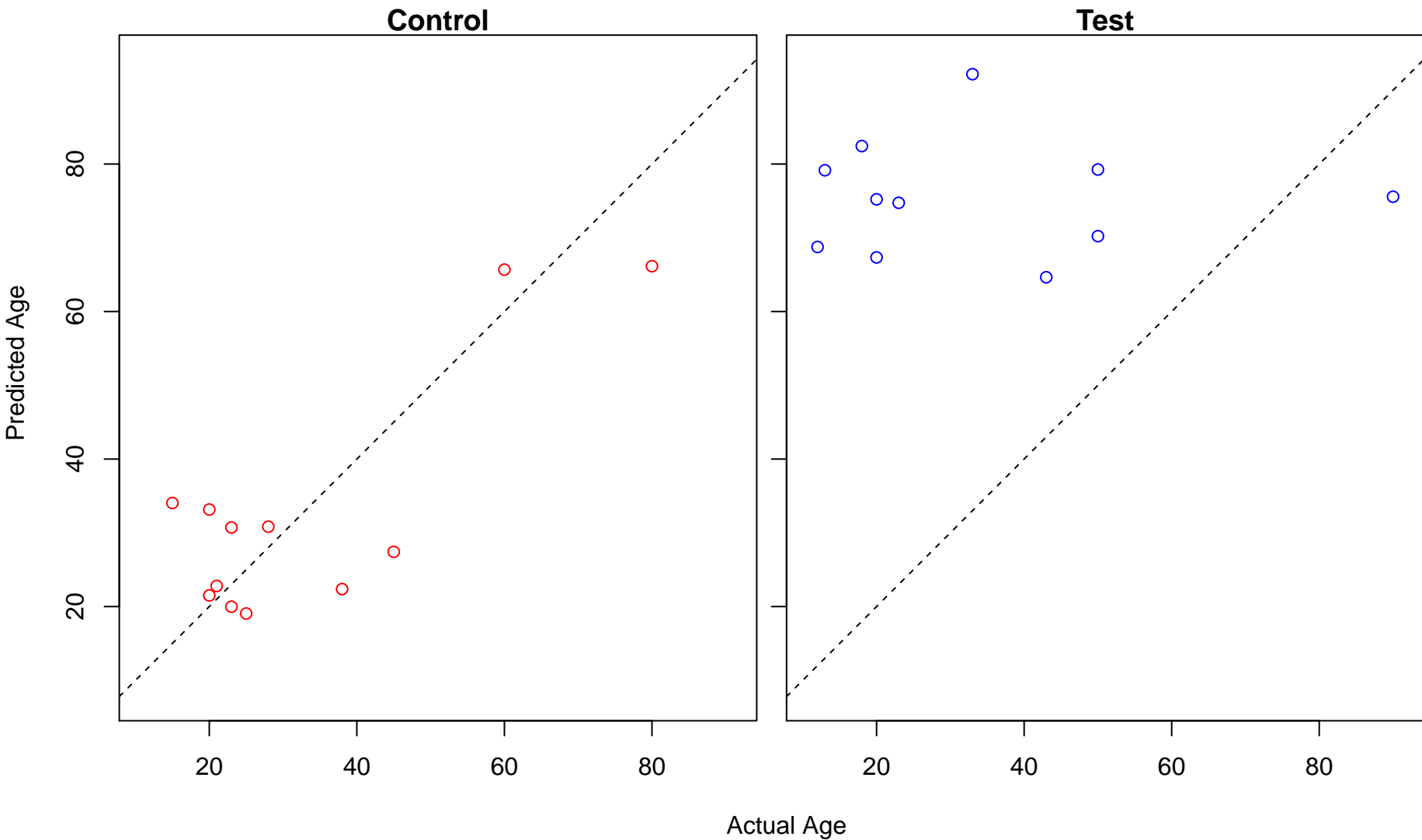


Test

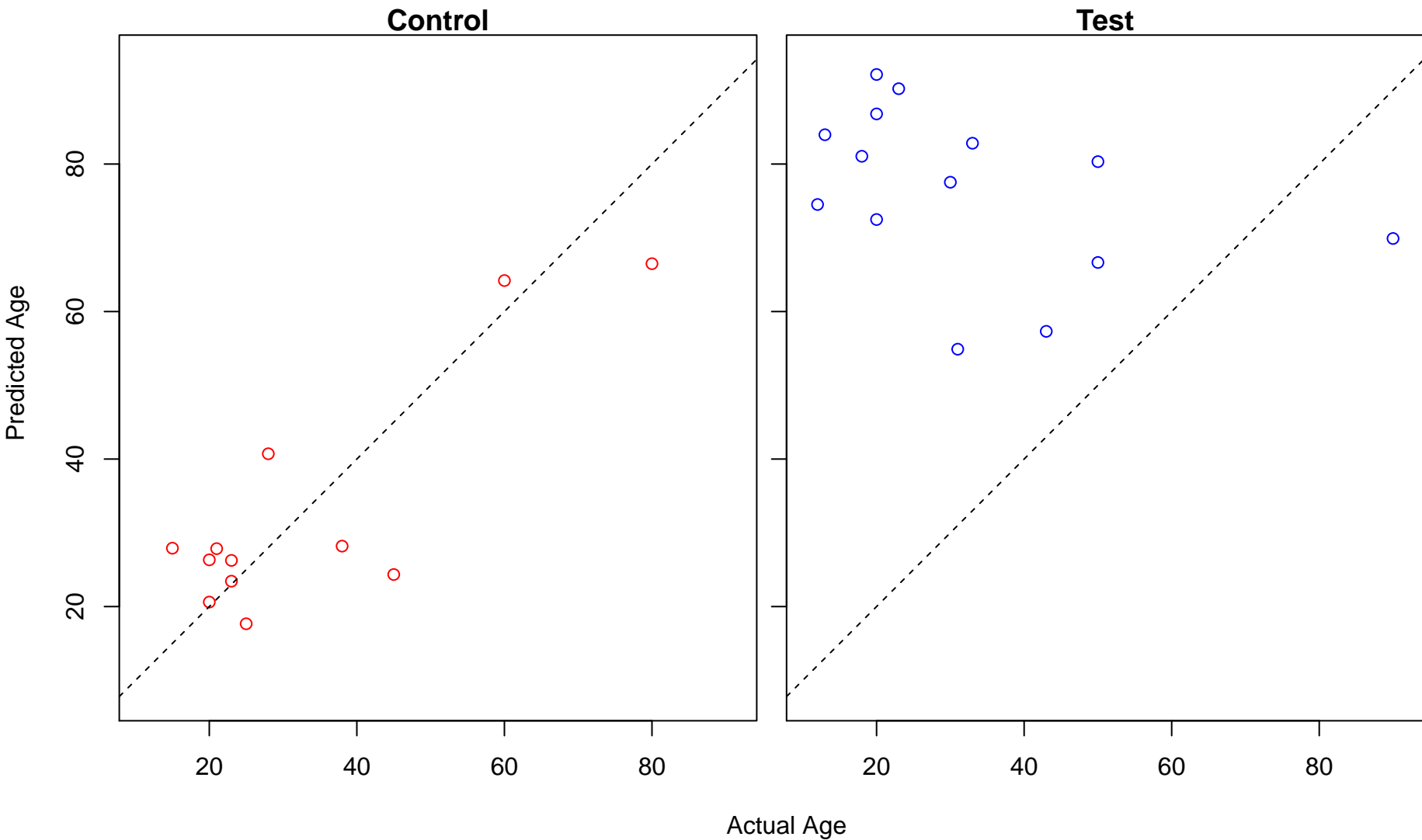


Actual Age

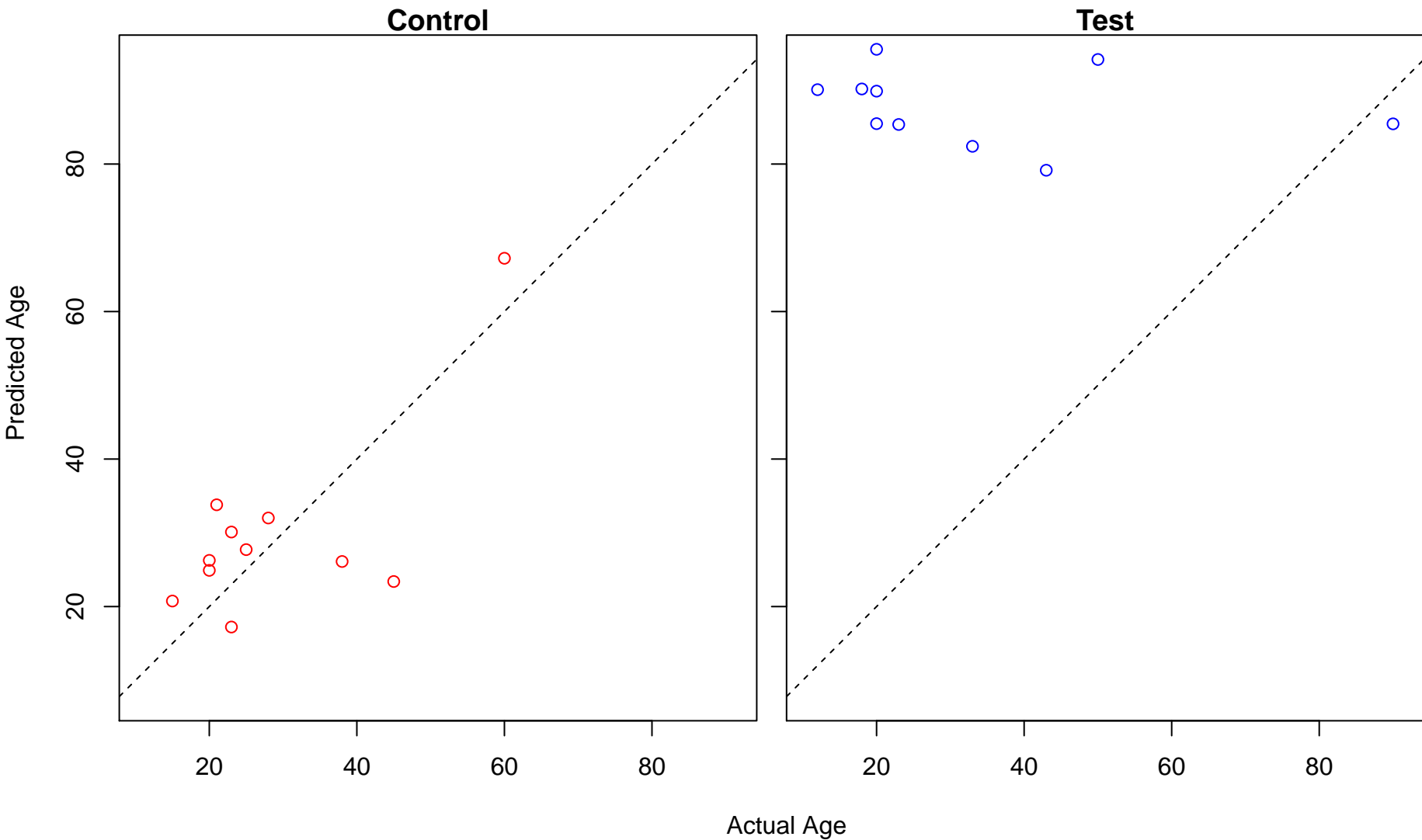
negative regulation of humoral immune response (Score: 9.756472)



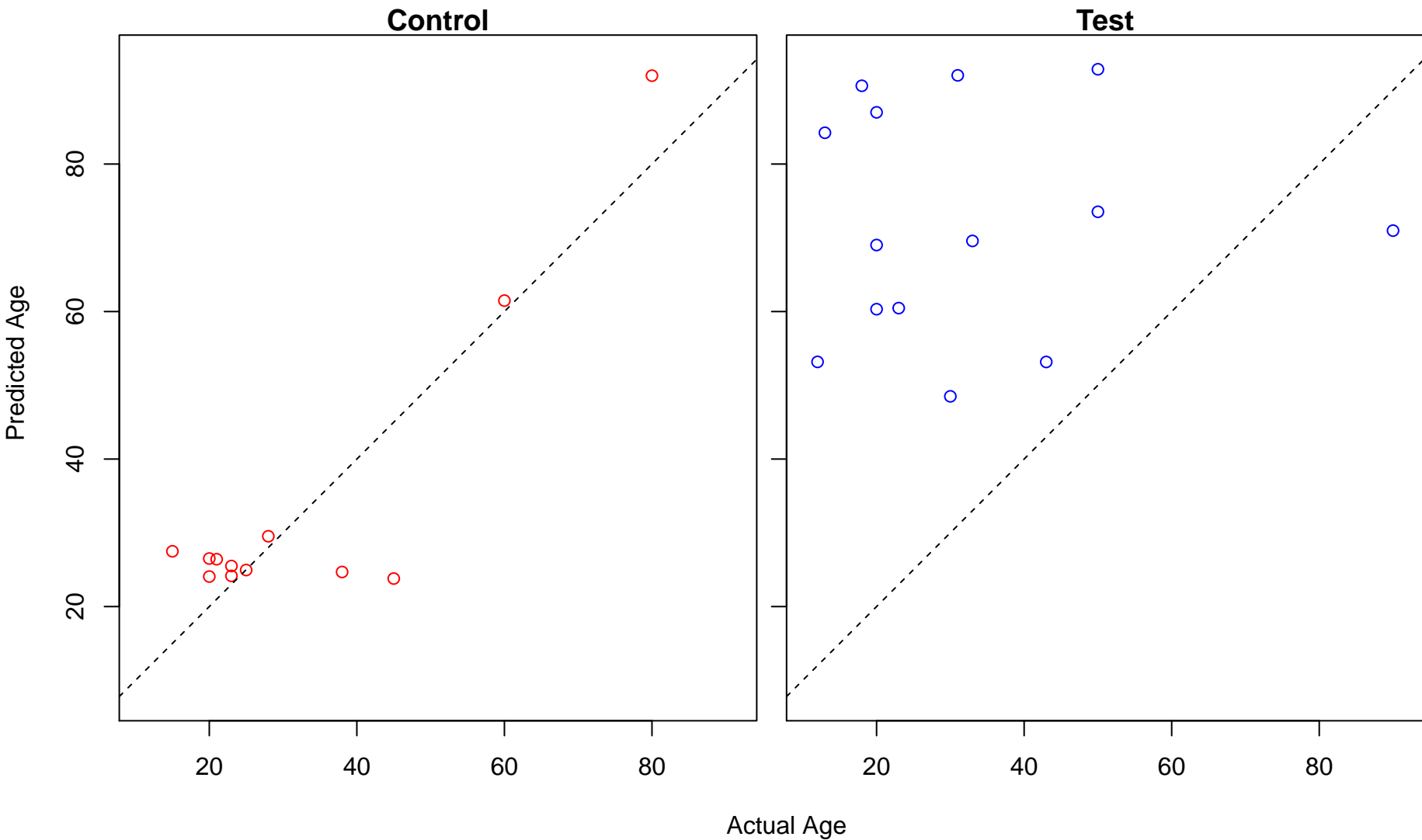
hippo signaling (Score: 9.755233)



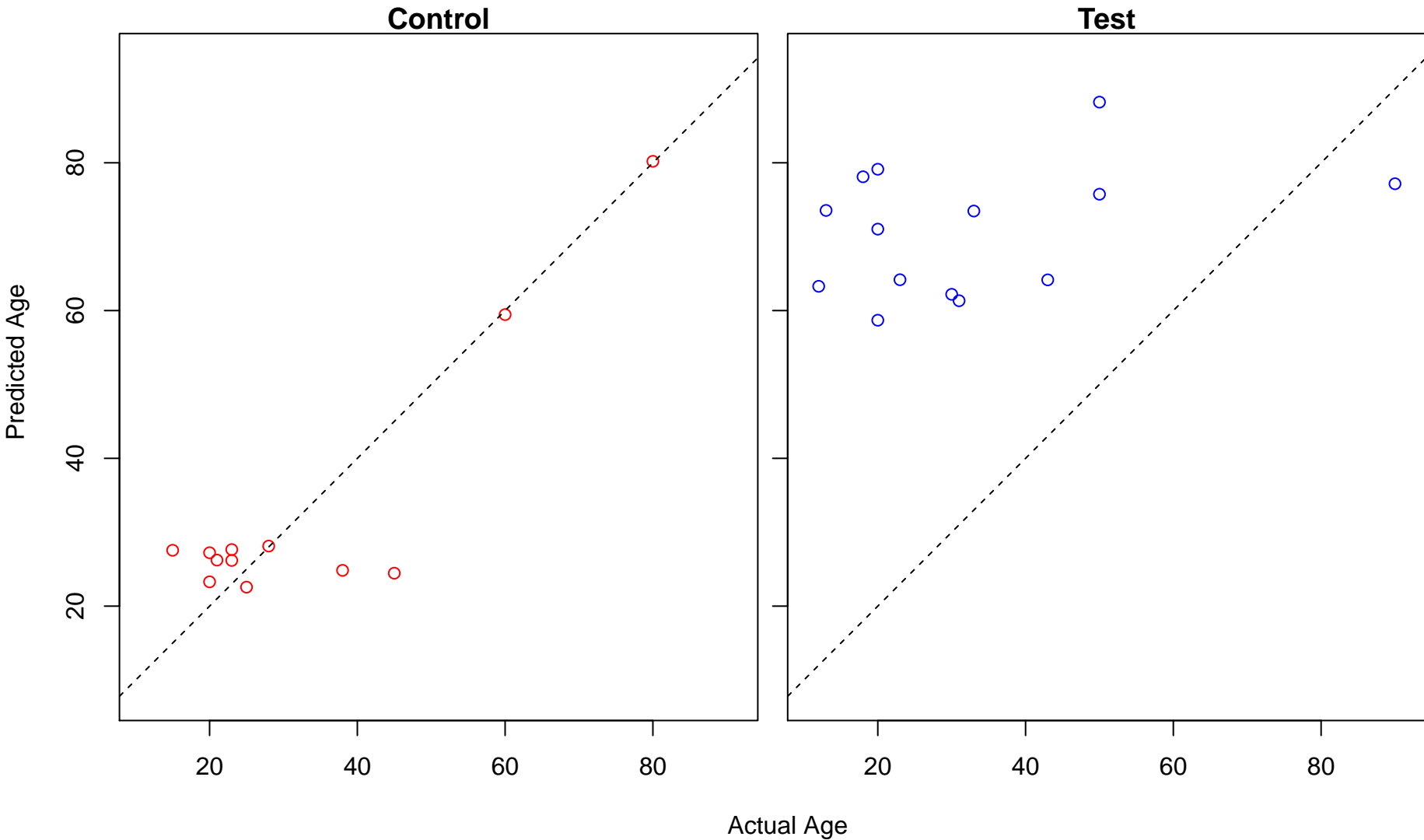
regulation of interleukin-17 production (Score: 9.742279)



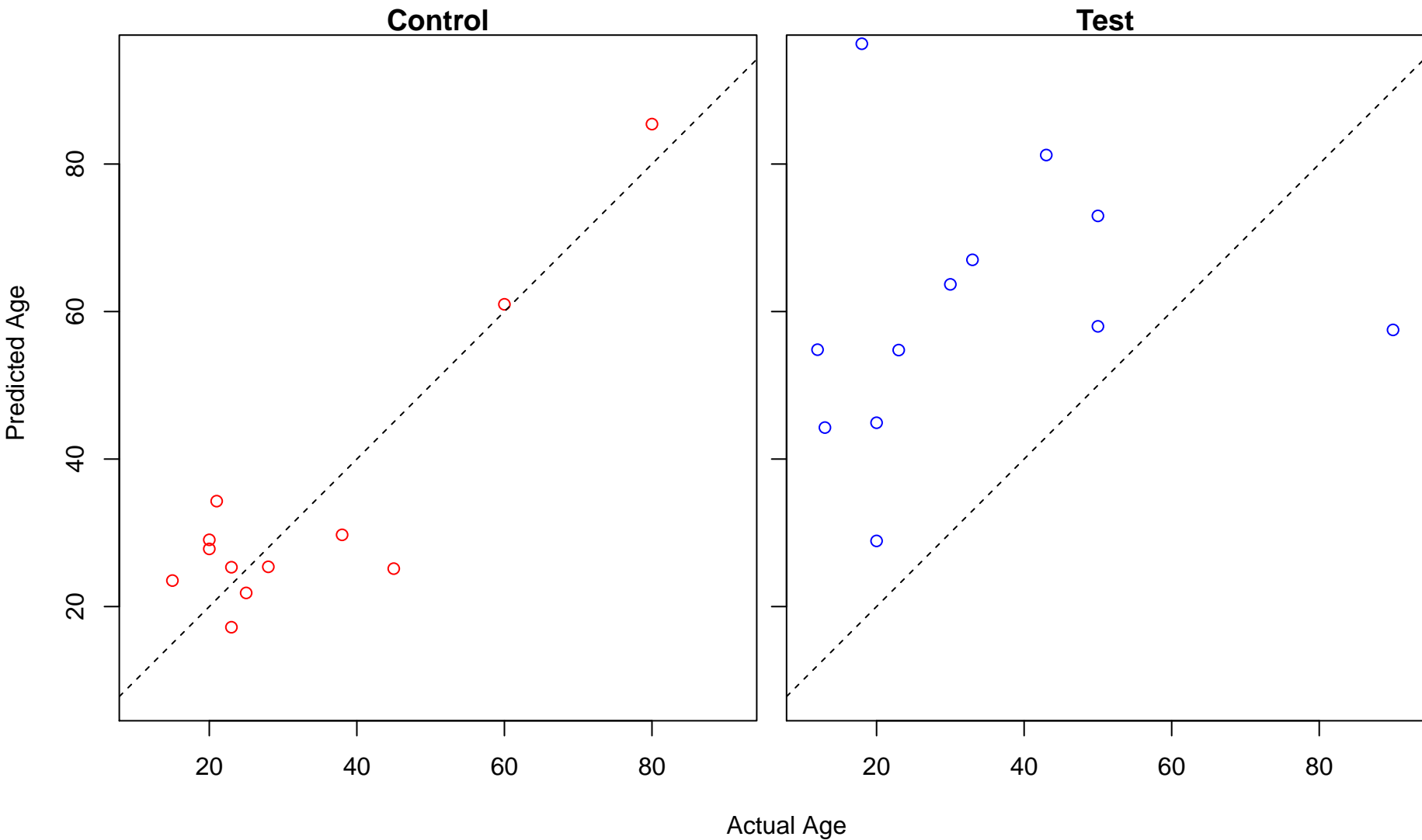
protein-DNA complex subunit organization (Score: 9.736943)



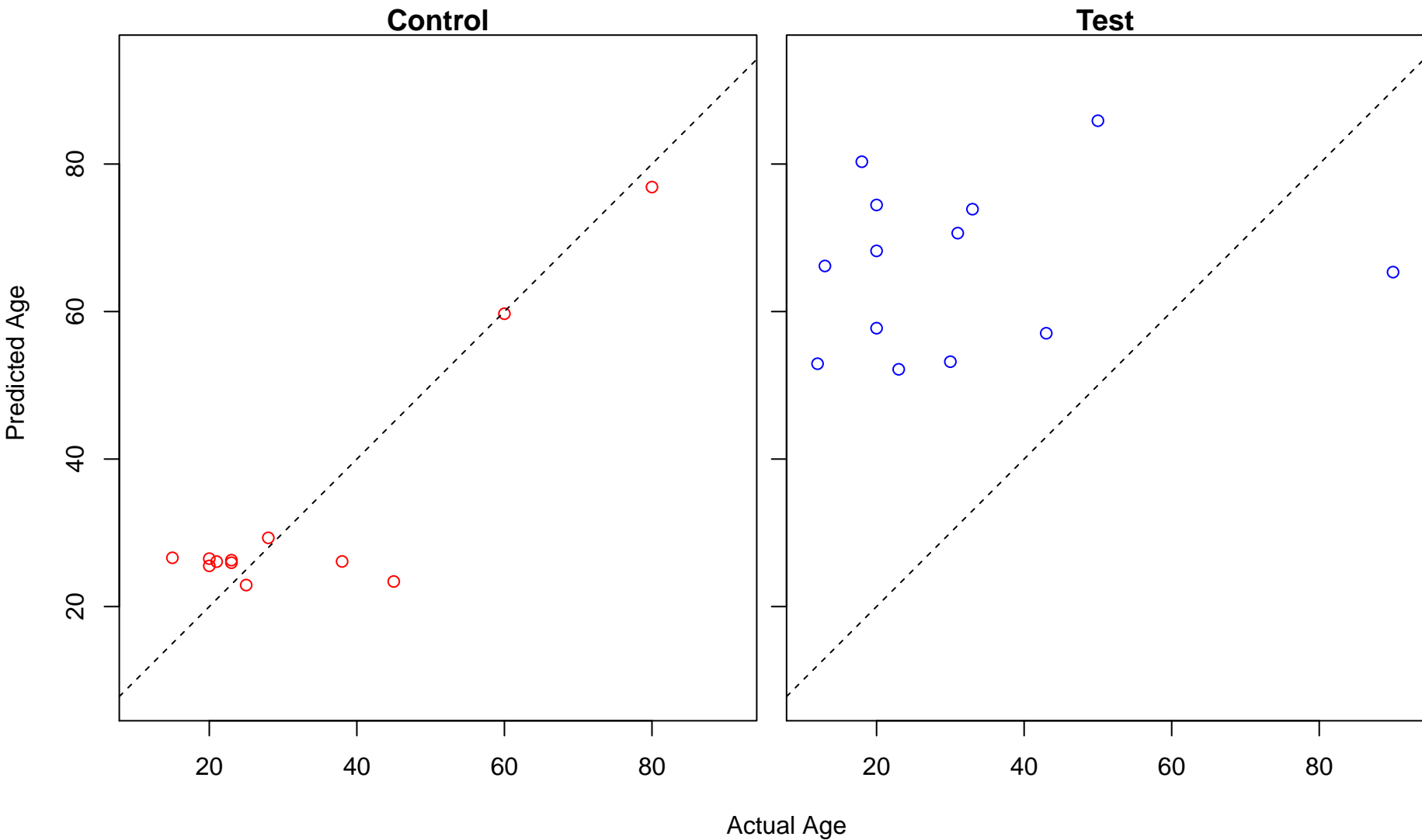
establishment of mitotic spindle localization (Score: 9.726937)



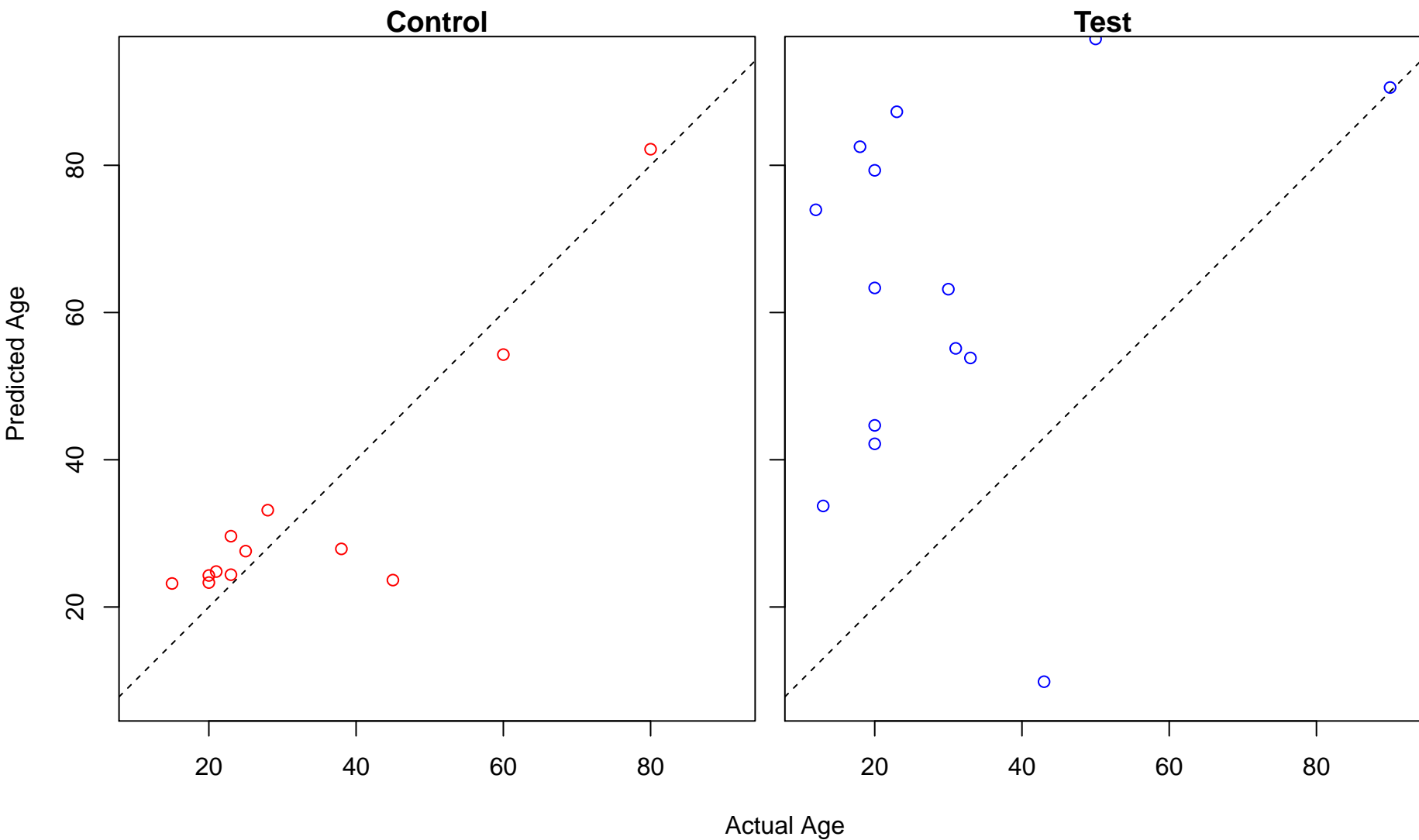
regulation of phagocytosis (Score: 9.719838)



regulation of calcium ion import (Score: 9.713802)

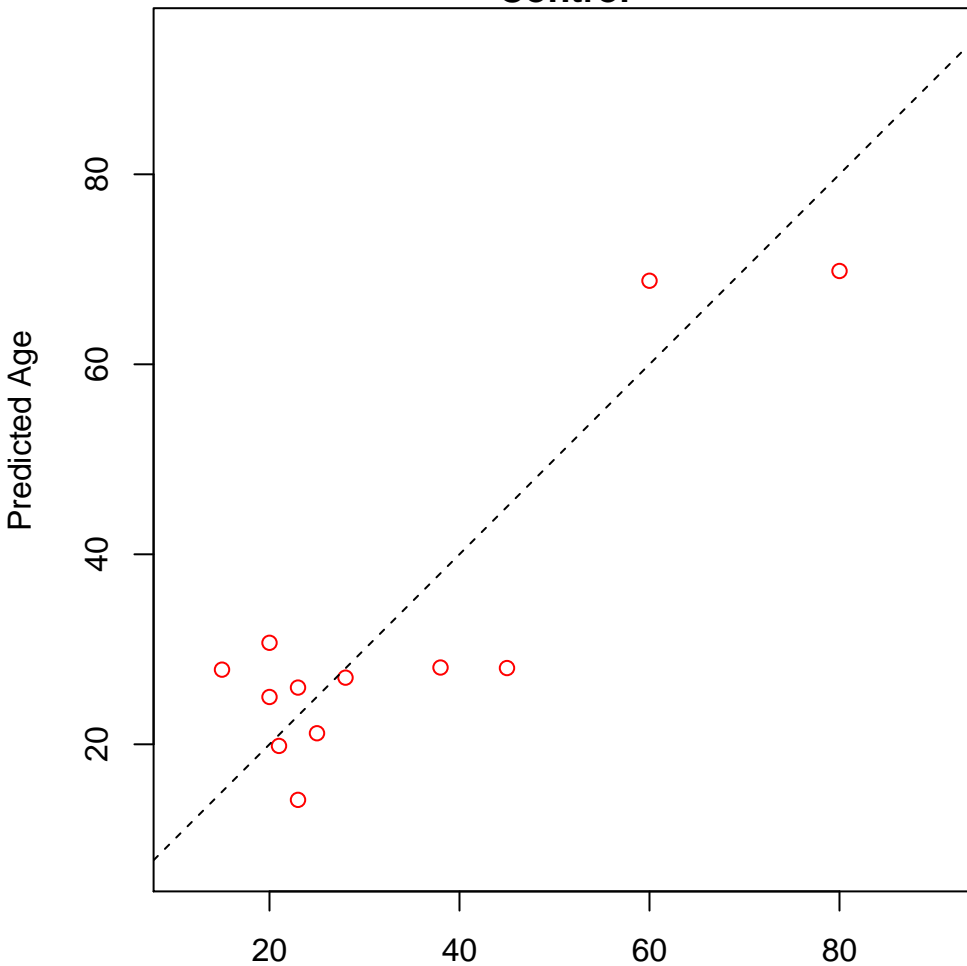


glycerophospholipid biosynthetic process (Score: 9.704975)

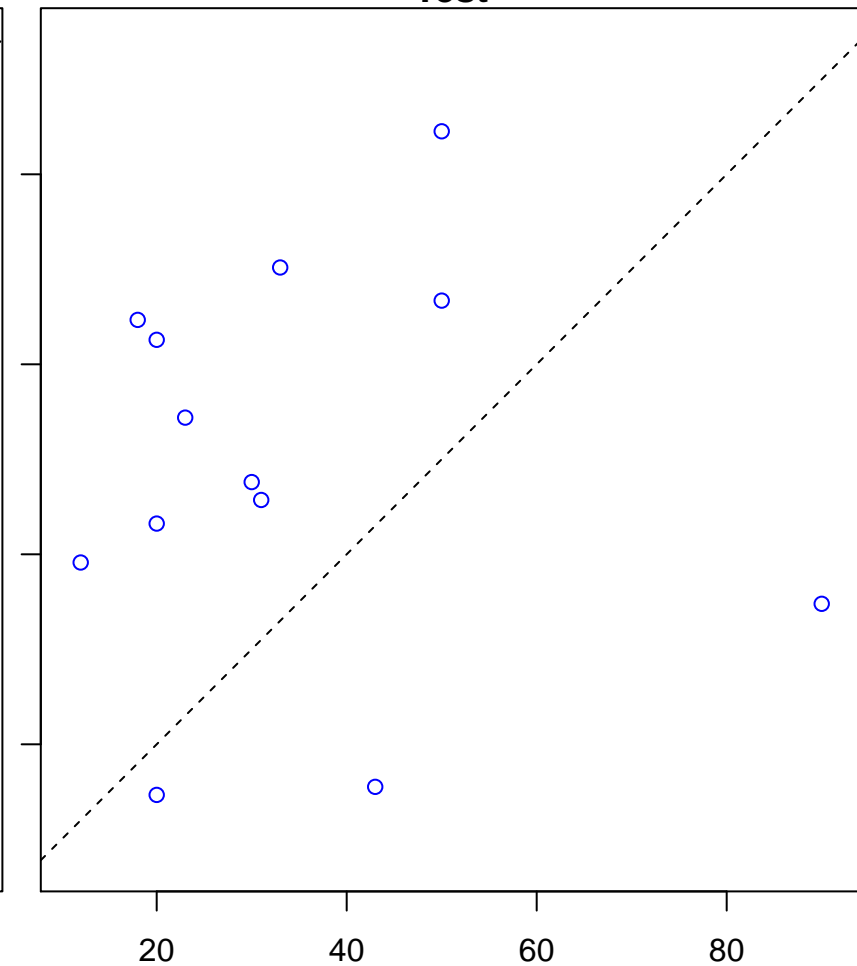


response to temperature stimulus (Score: 9.704735)

Control

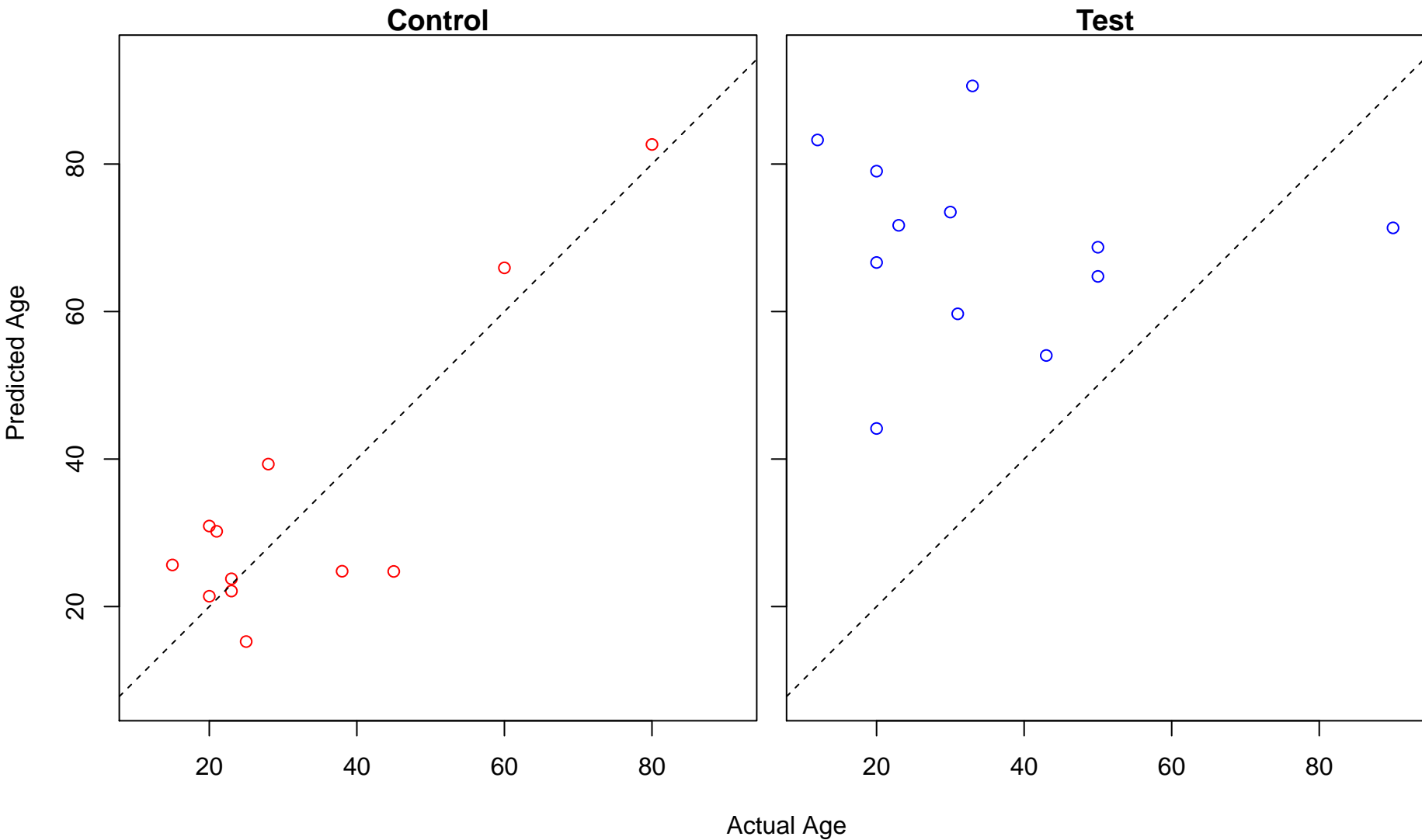


Test

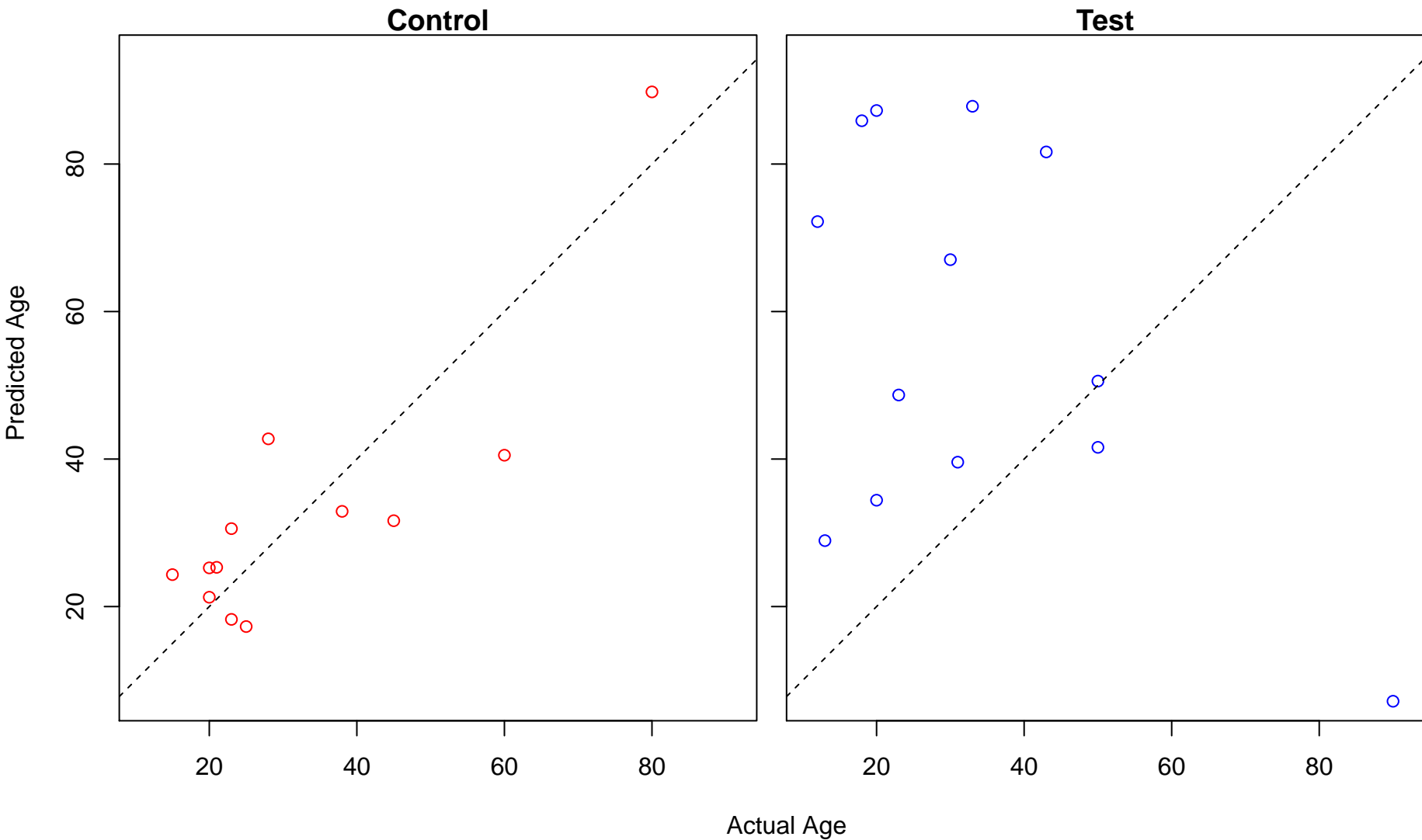


Actual Age

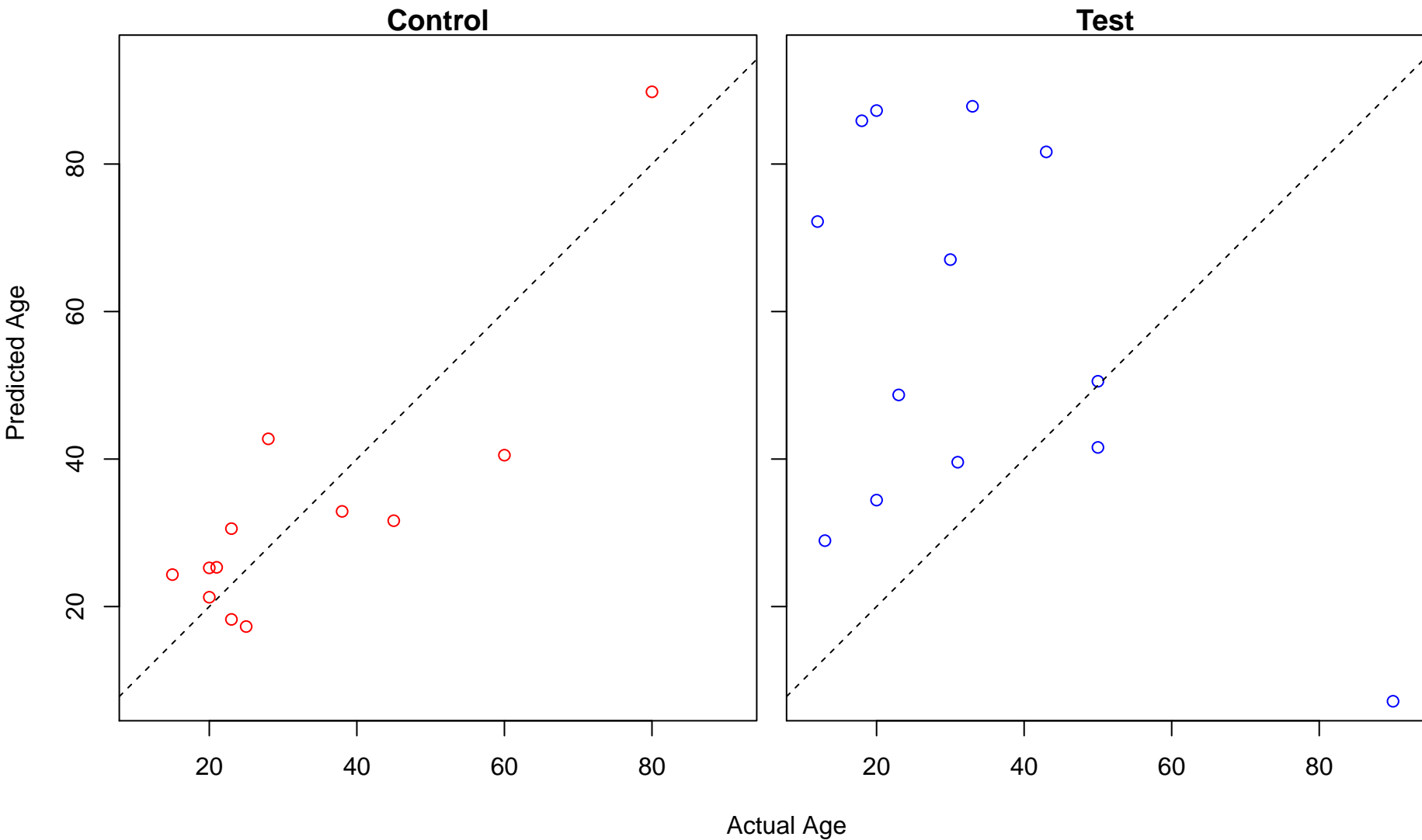
protein targeting (Score: 9.699660)



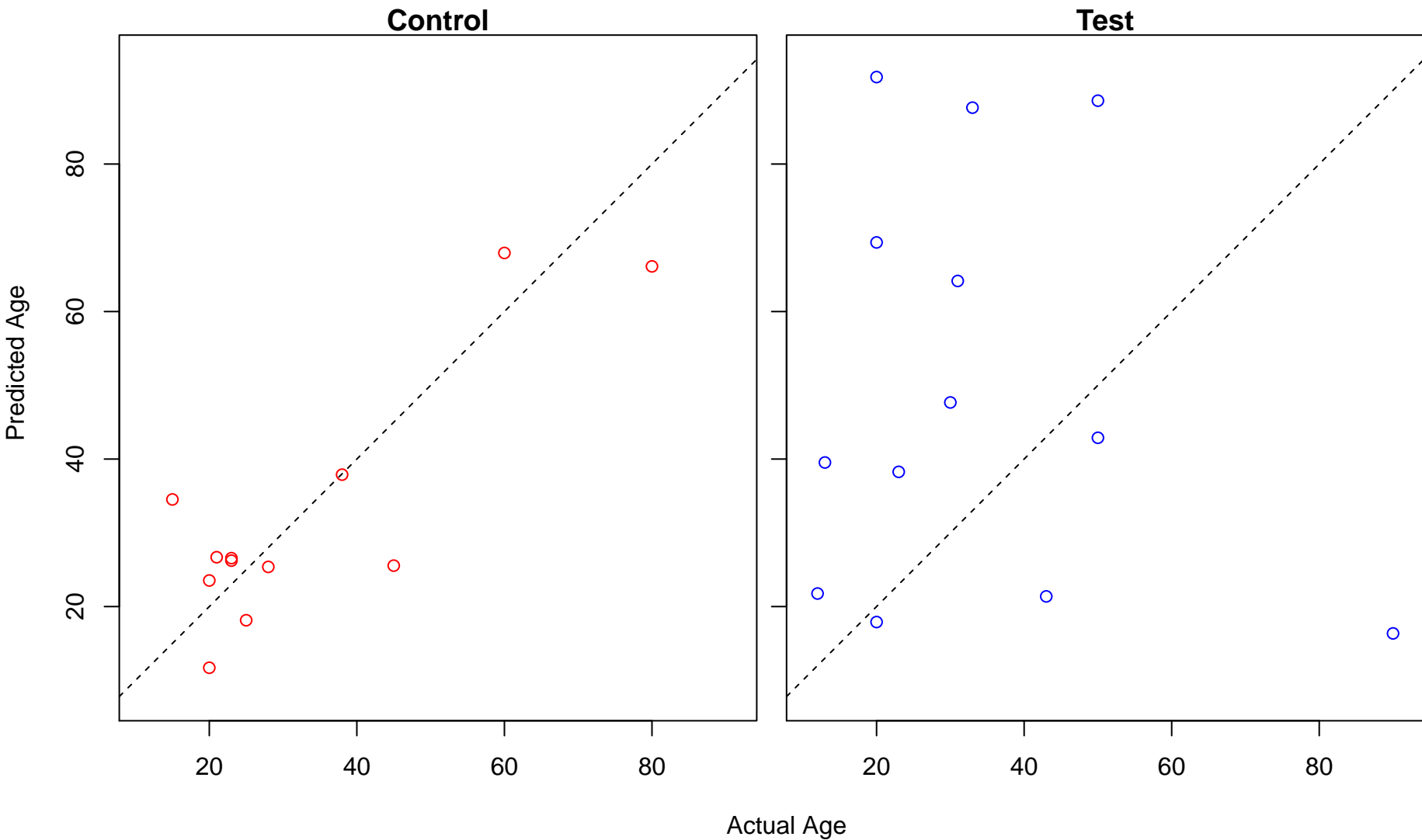
detection of external stimulus (Score: 9.688775)



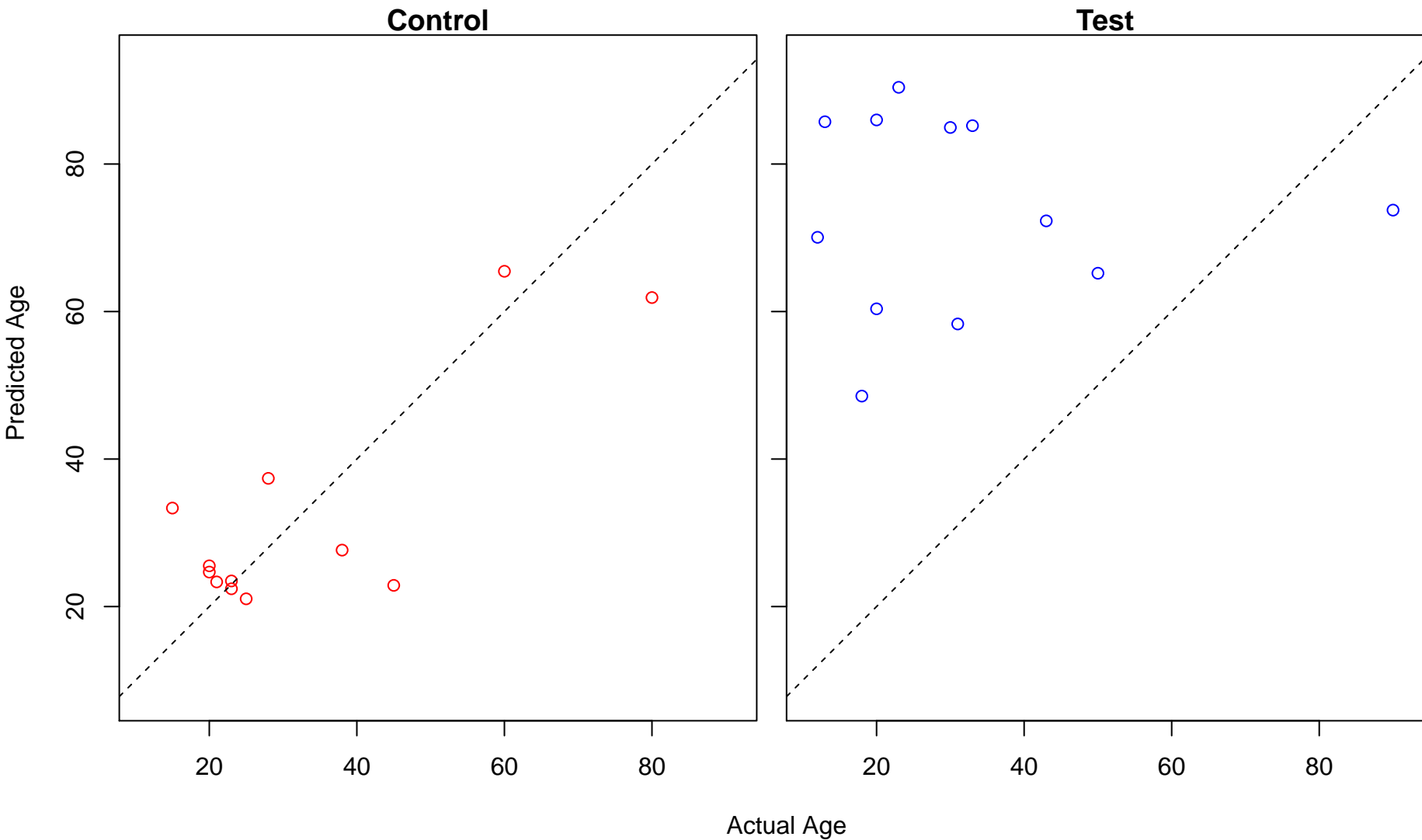
detection of abiotic stimulus (Score: 9.688094)



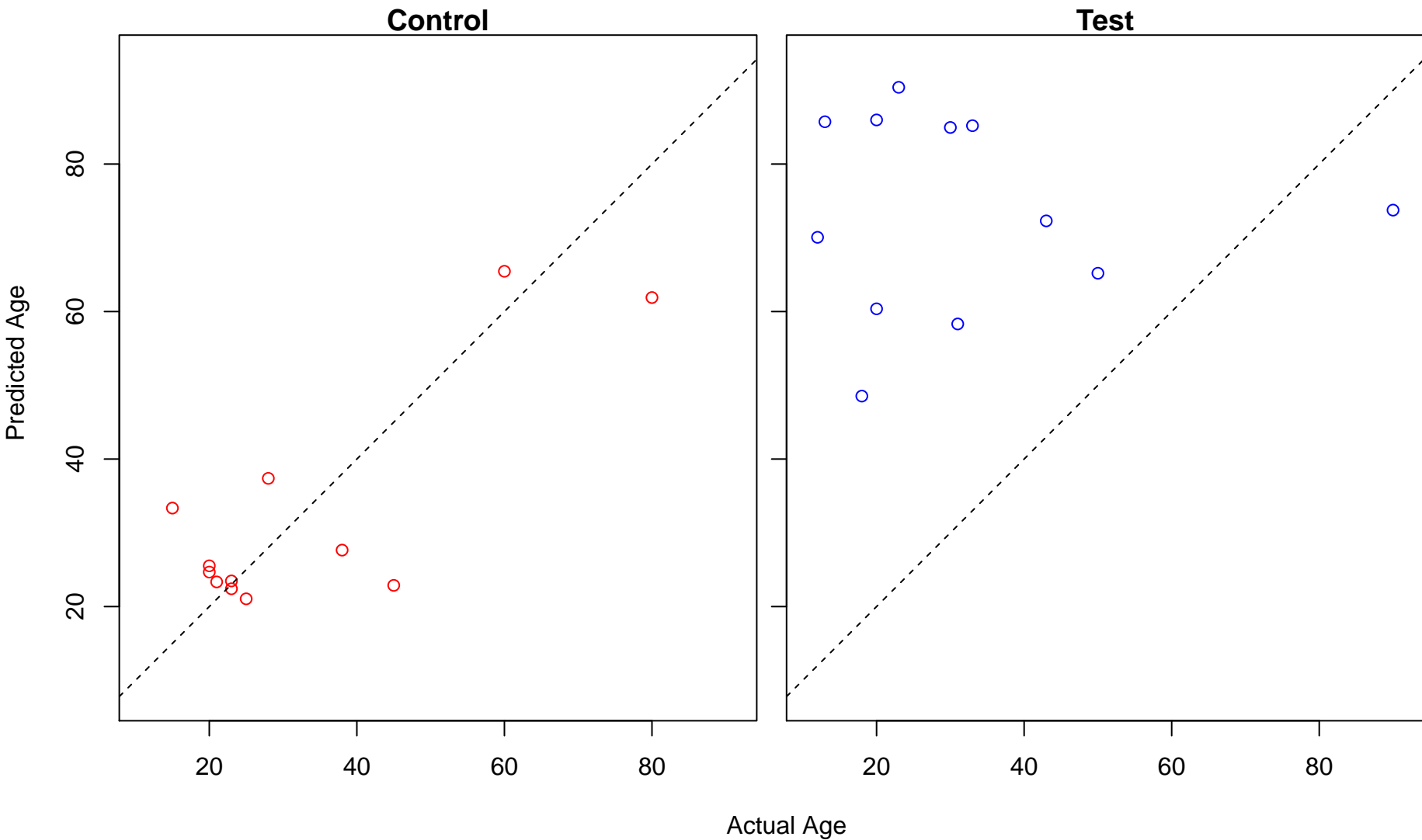
regulation of ion transport (Score: 9.686113)



negative regulation of B cell mediated immunity (Score: 9.686088)

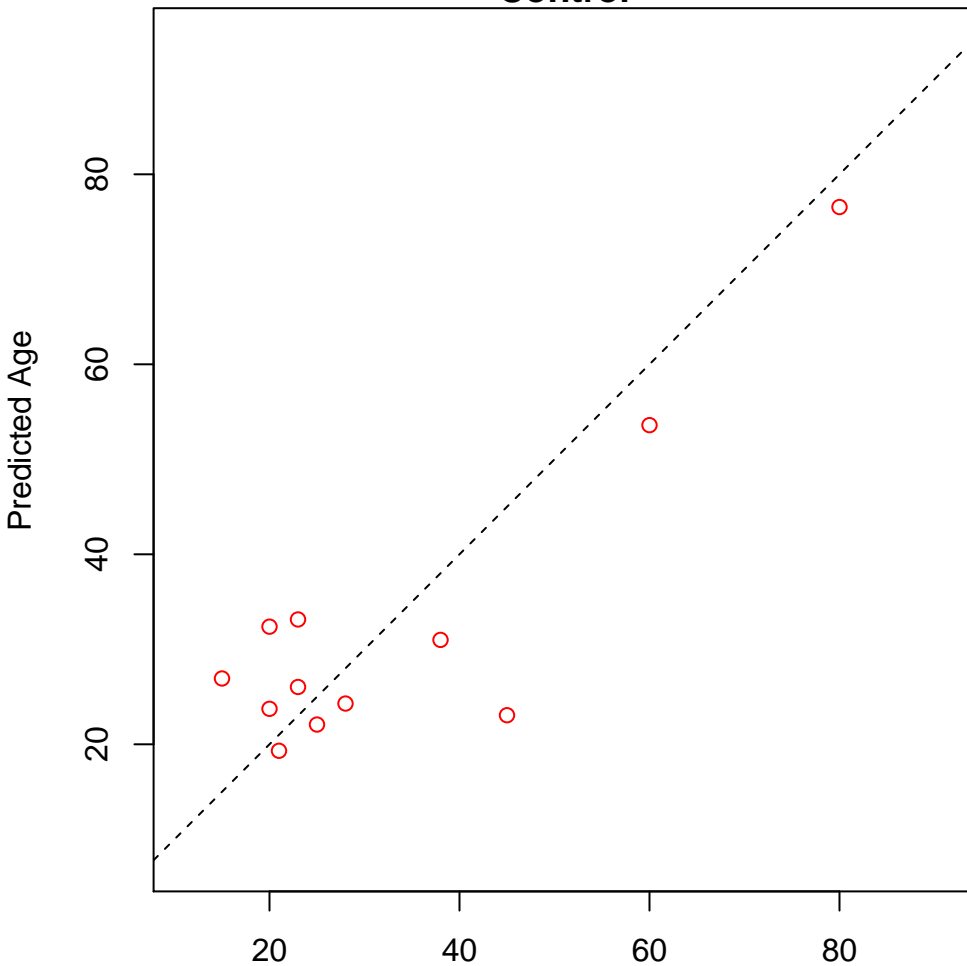


negative regulation of immunoglobulin mediated immune response (Score: 9.686088)

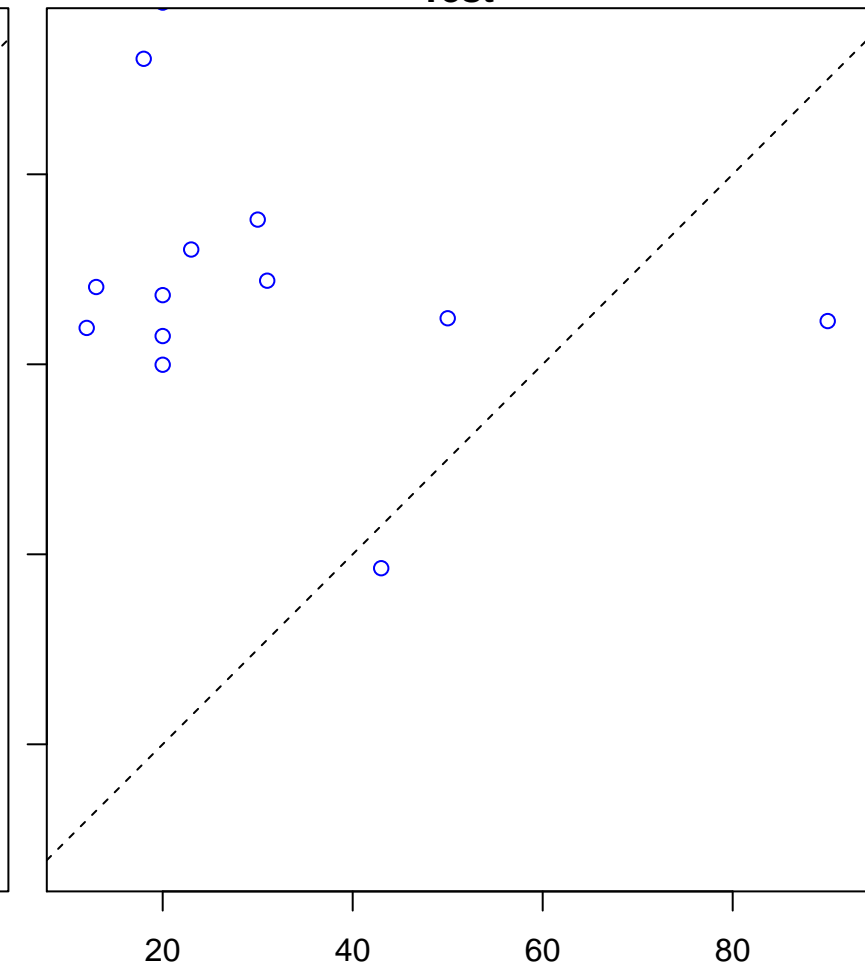


low-density lipoprotein particle clearance (Score: 9.675054)

Control



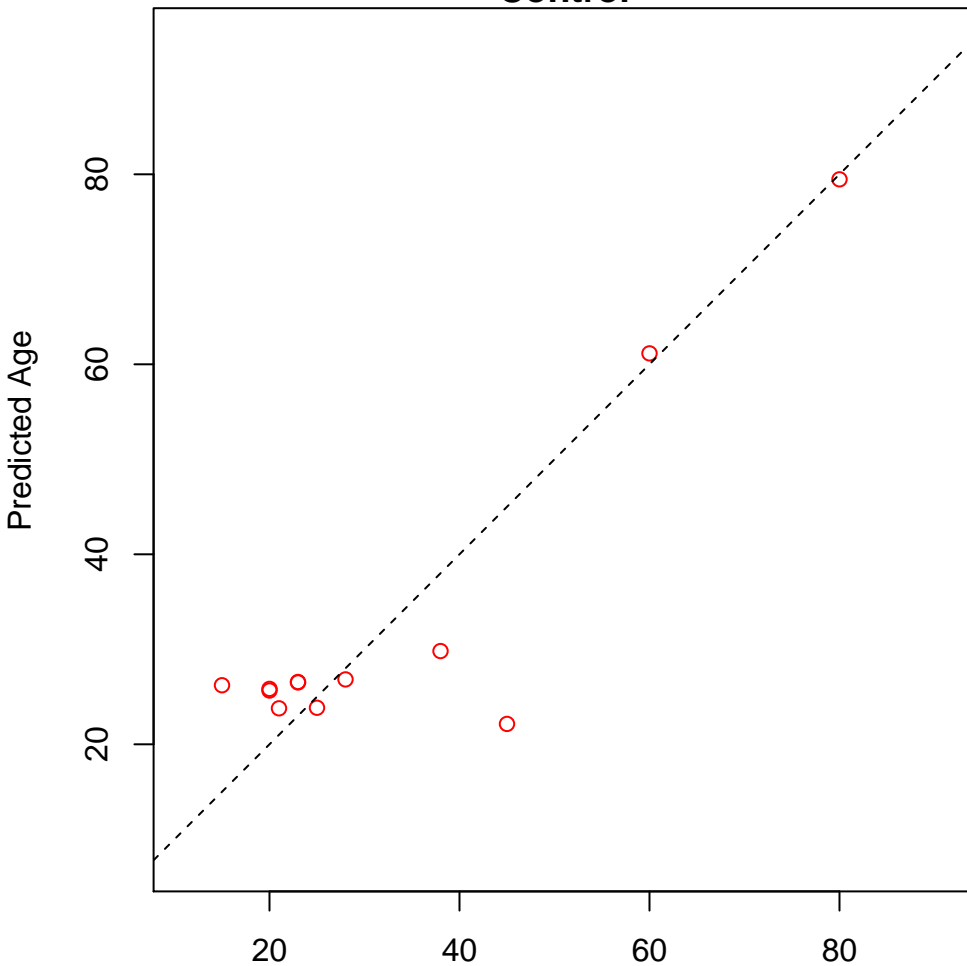
Test



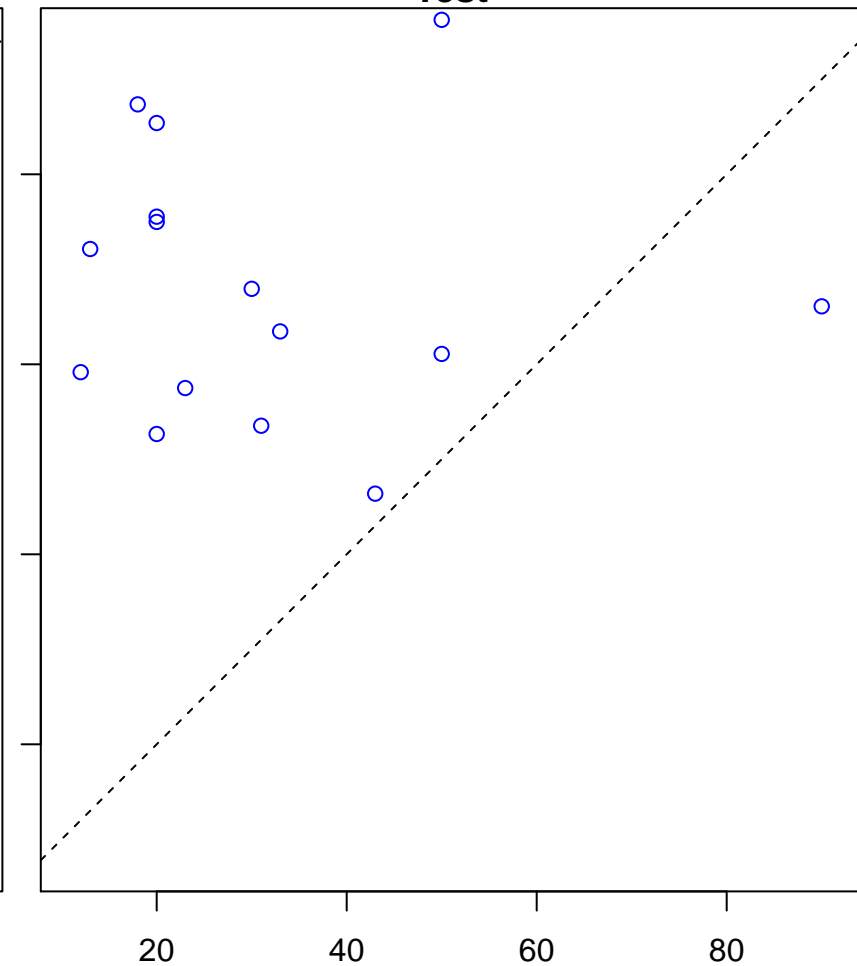
Actual Age

enteric nervous system development (Score: 9.665201)

Control

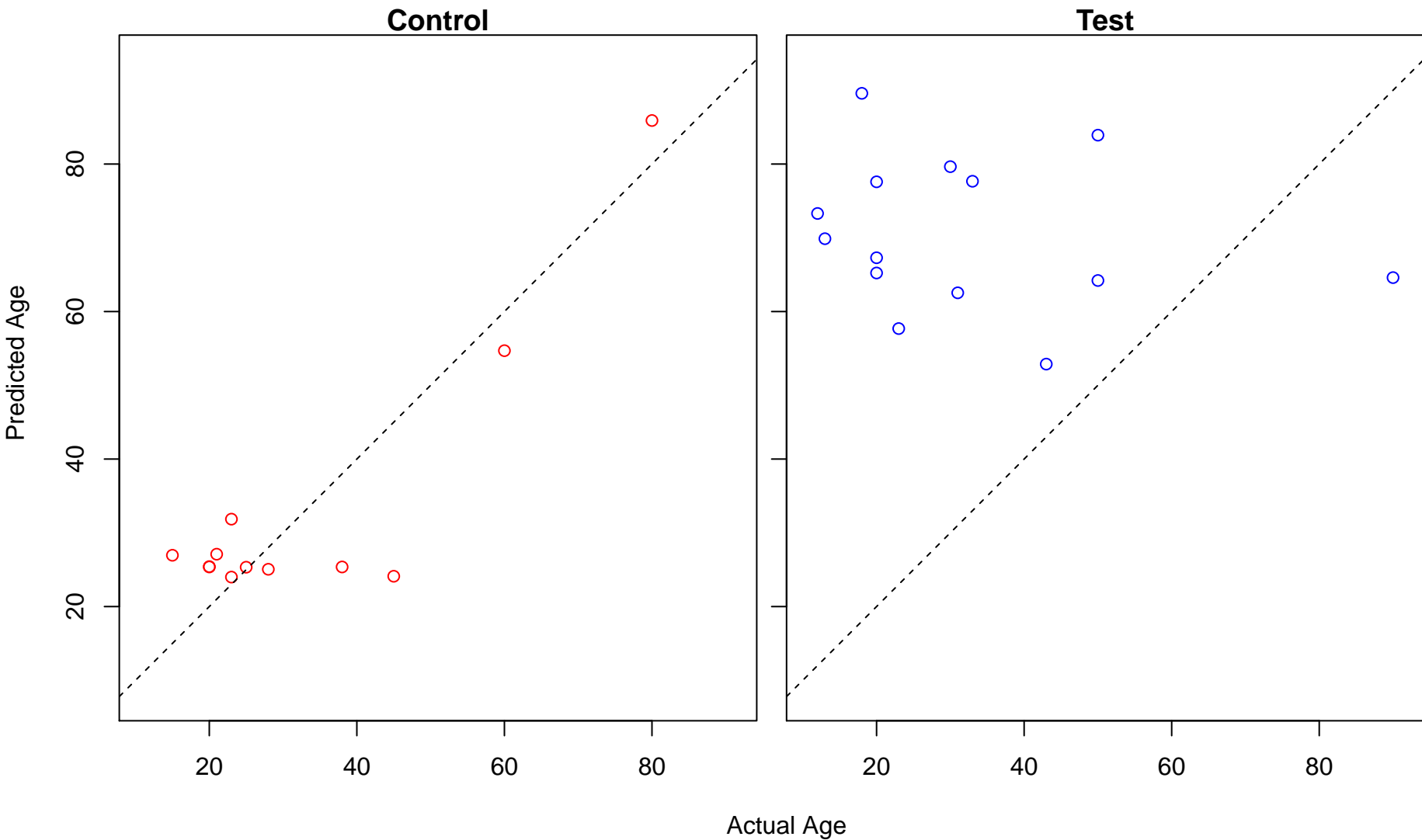


Test

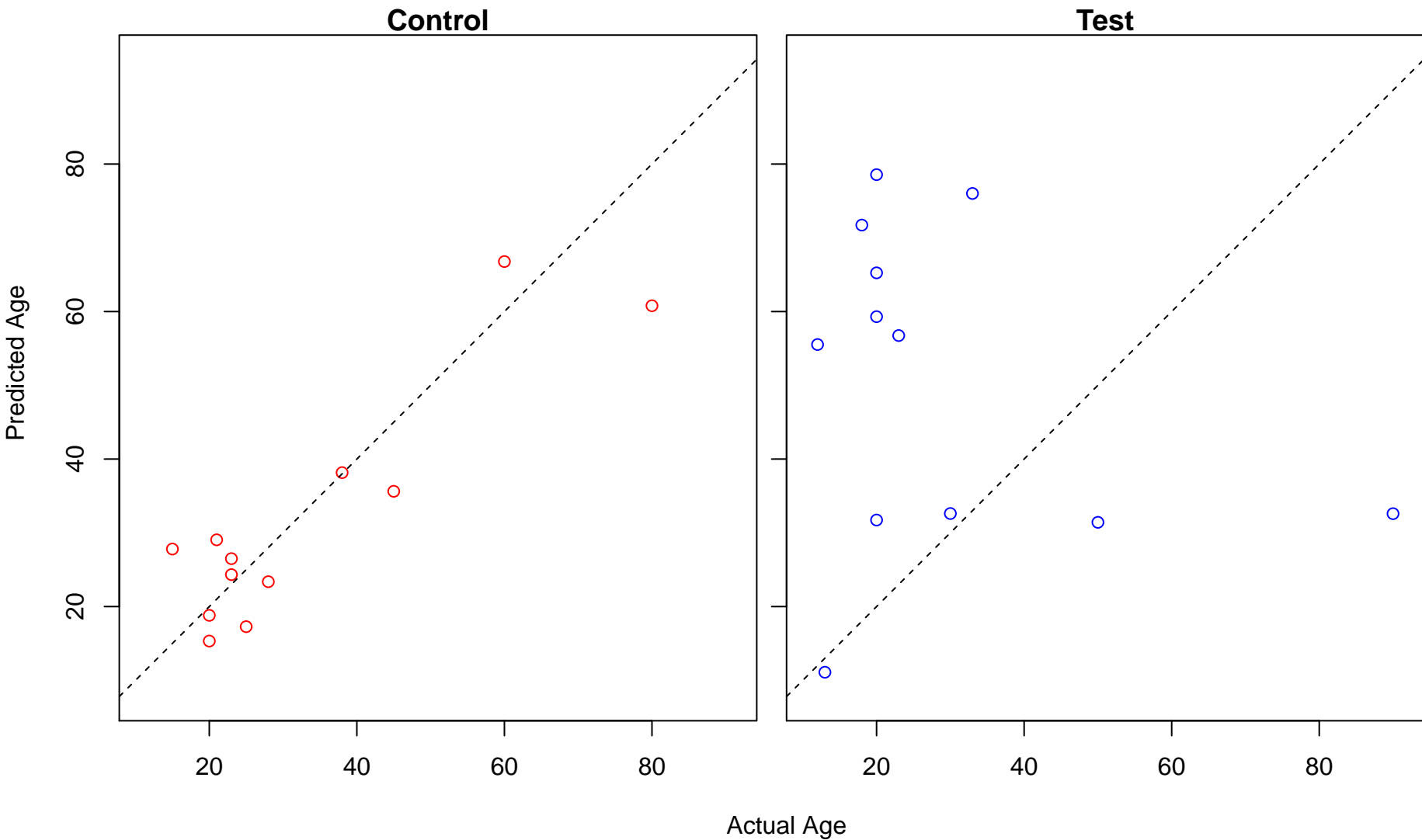


Actual Age

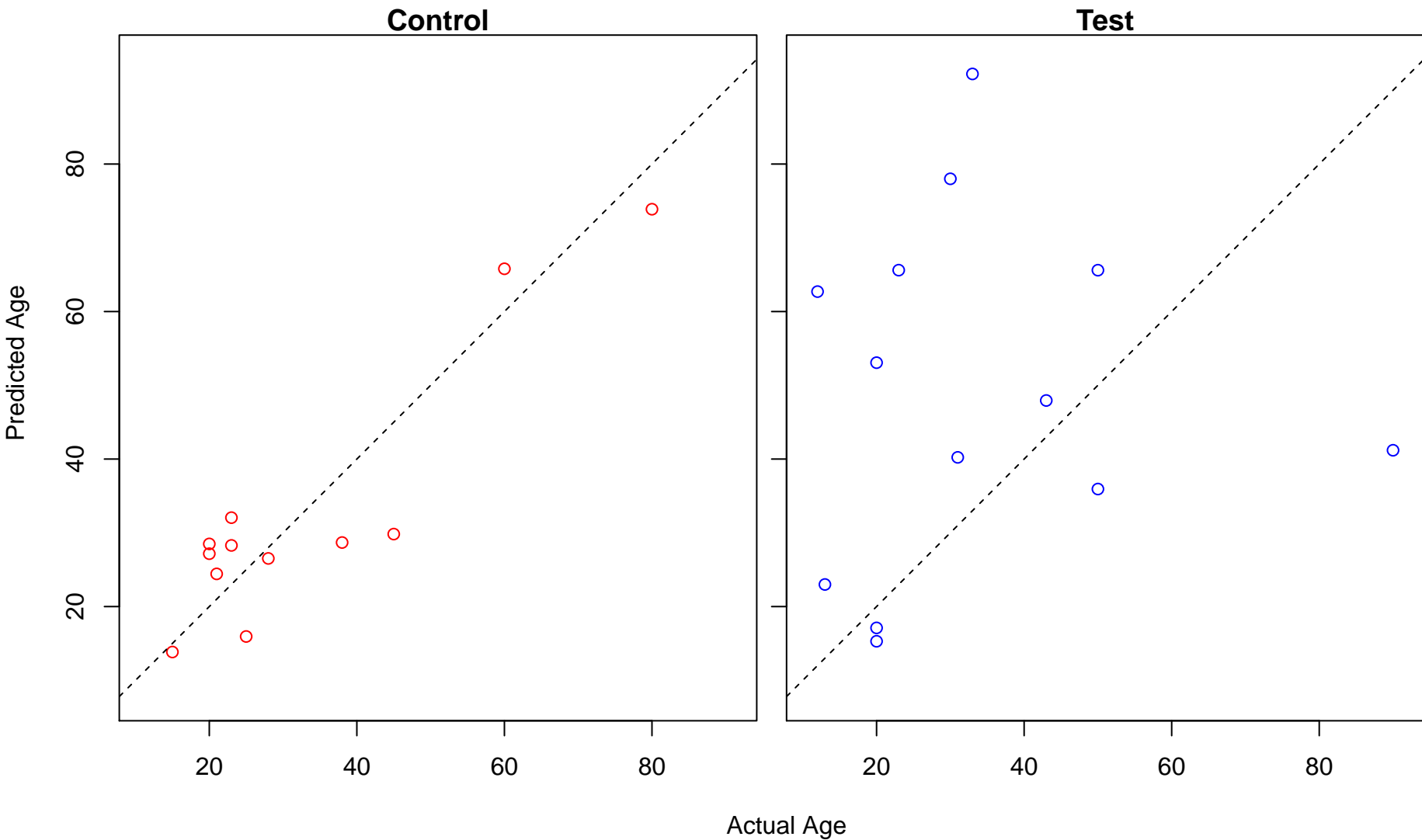
positive regulation of DNA biosynthetic process (Score: 9.656405)



proteoglycan biosynthetic process (Score: 9.640450)

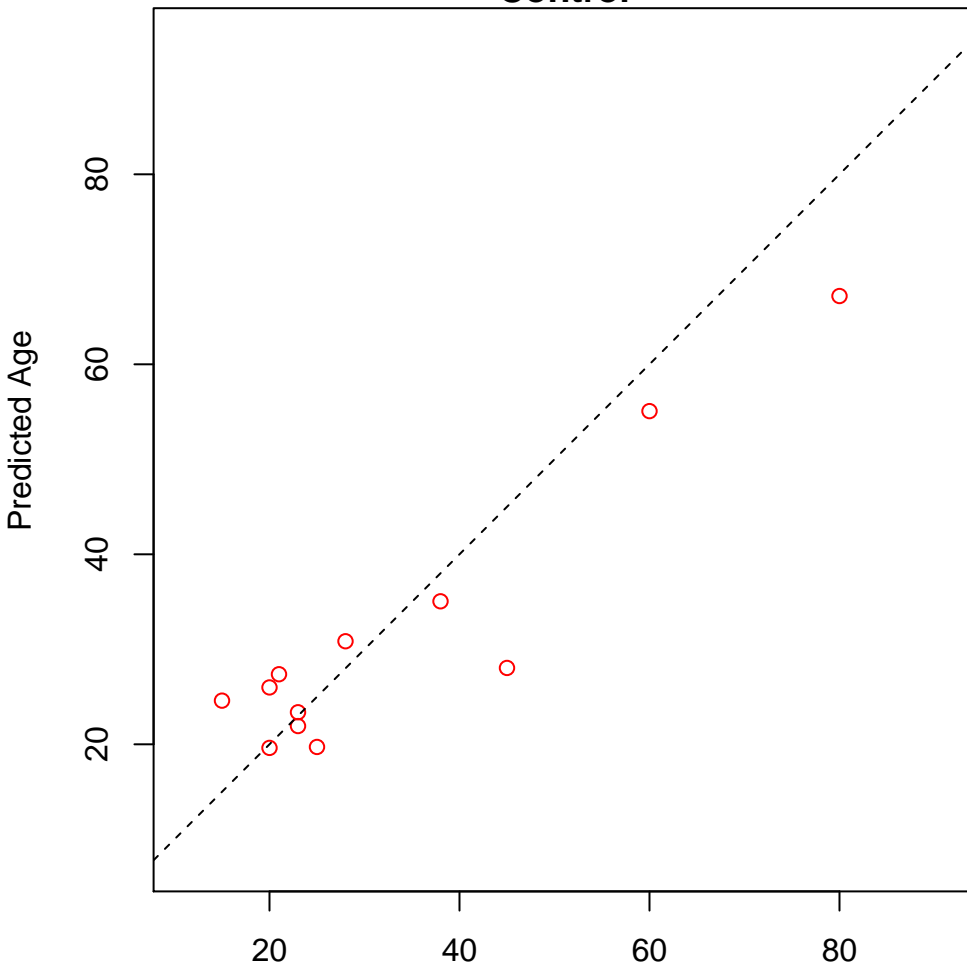


positive regulation of phospholipid biosynthetic process (Score: 9.637767)

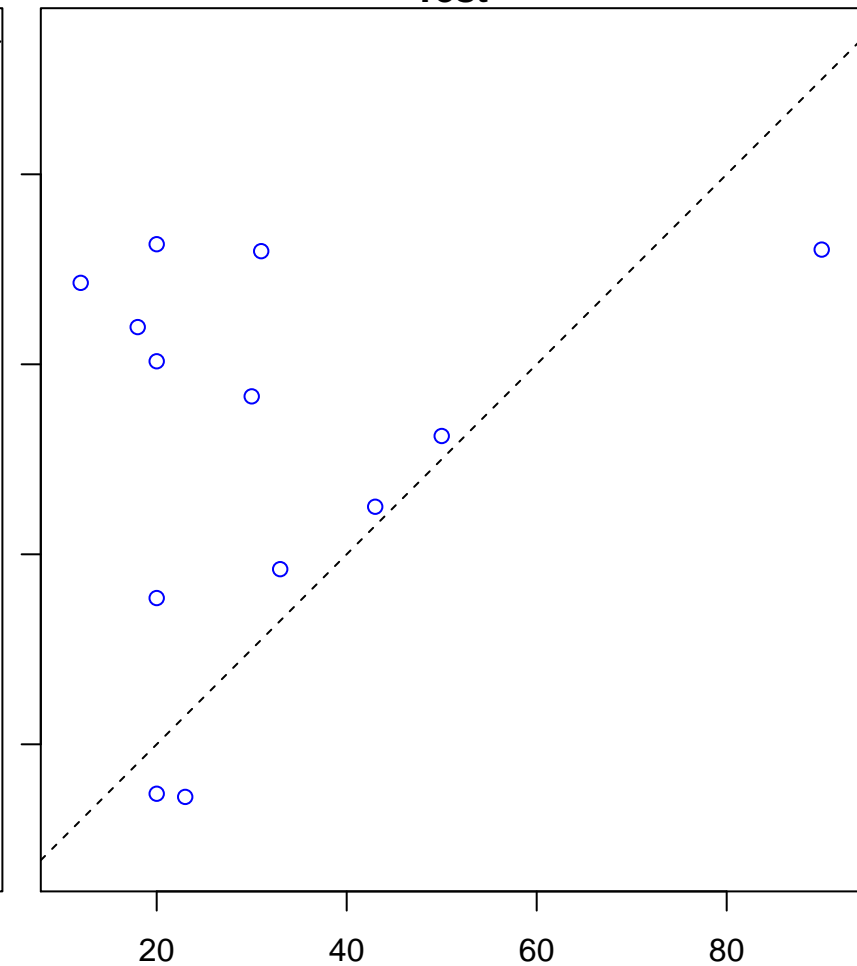


internal peptidyl-lysine acetylation (Score: 9.627653)

Control

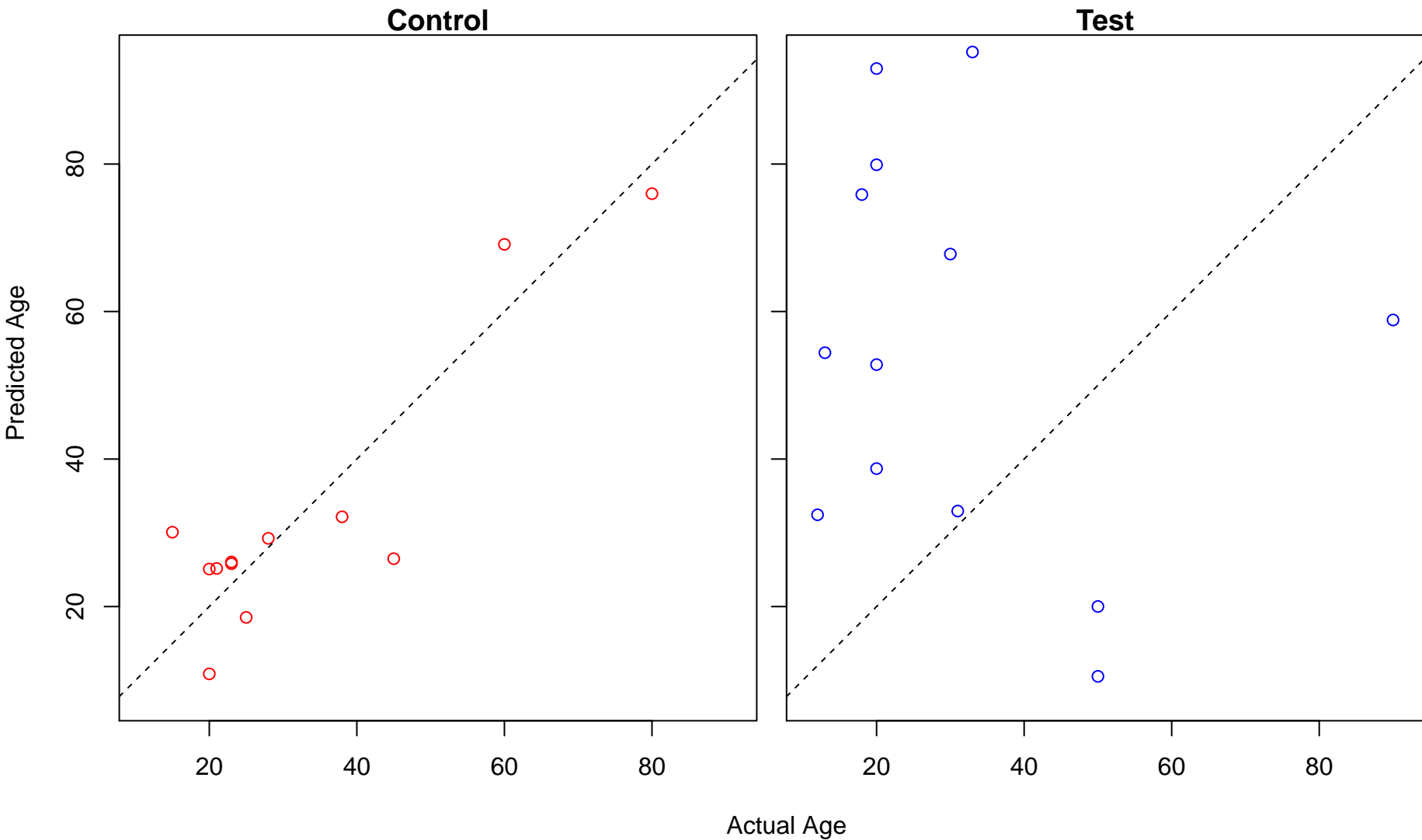


Test

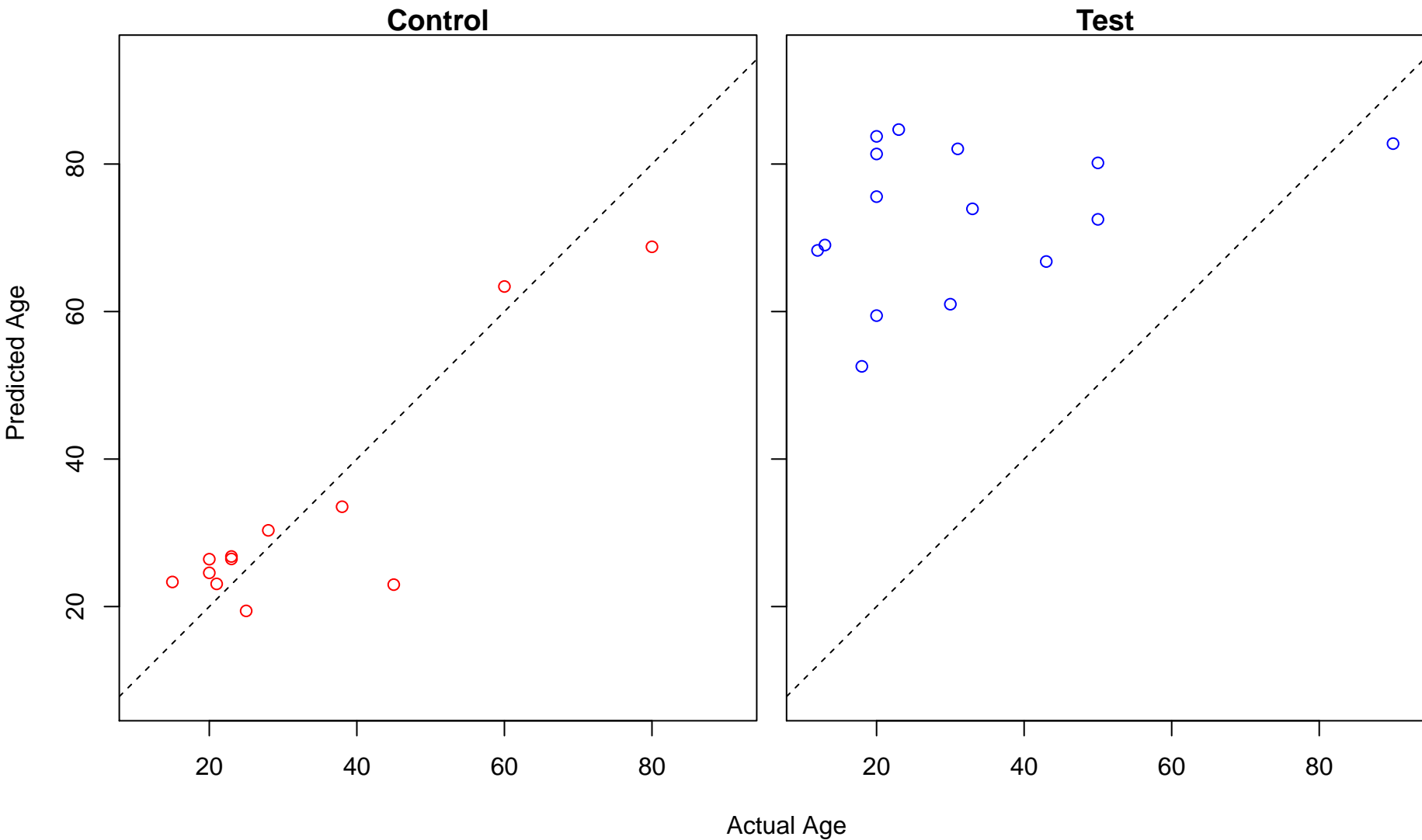


Actual Age

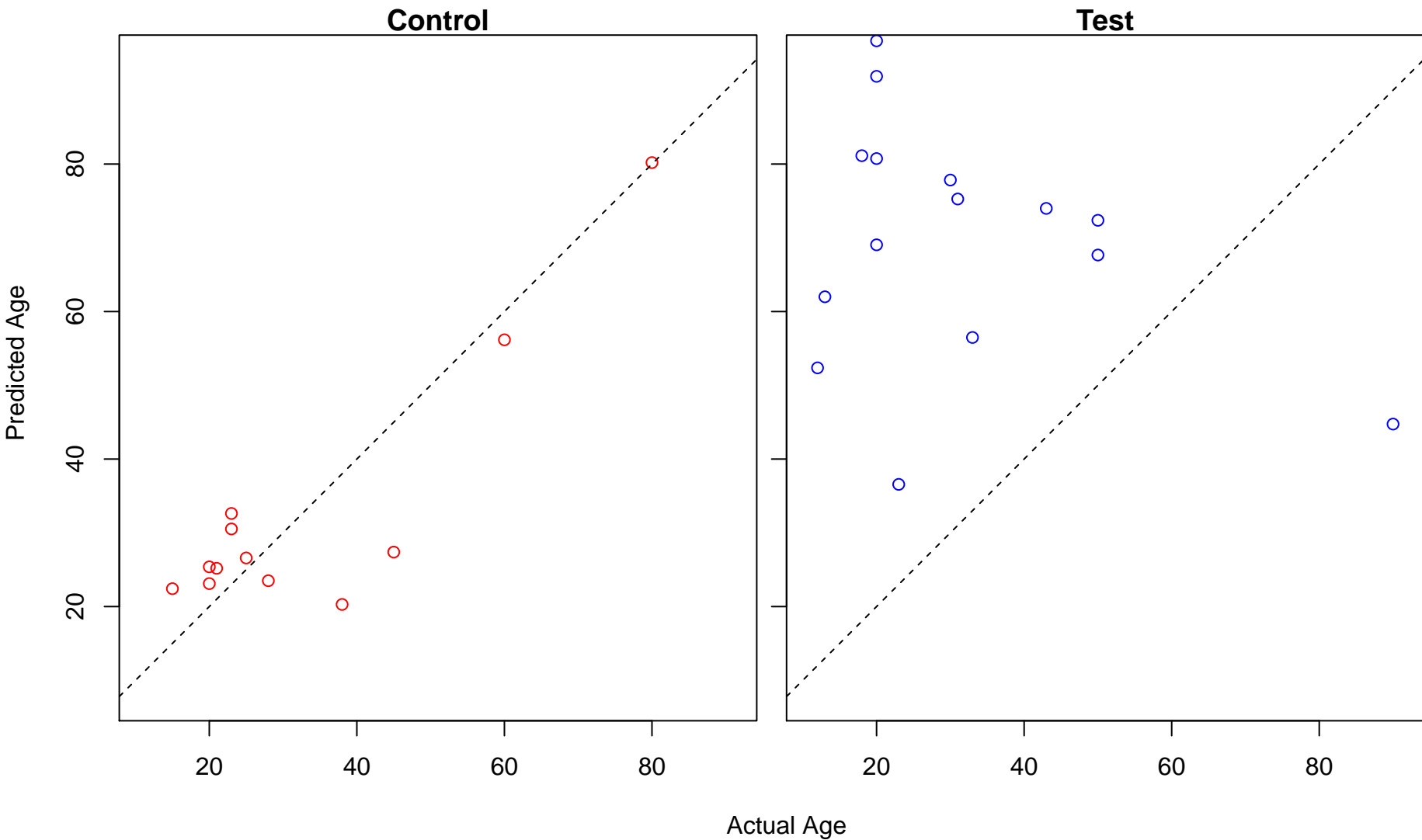
negative regulation of nucleocytoplasmic transport (Score: 9.625319)



lung development (Score: 9.624906)

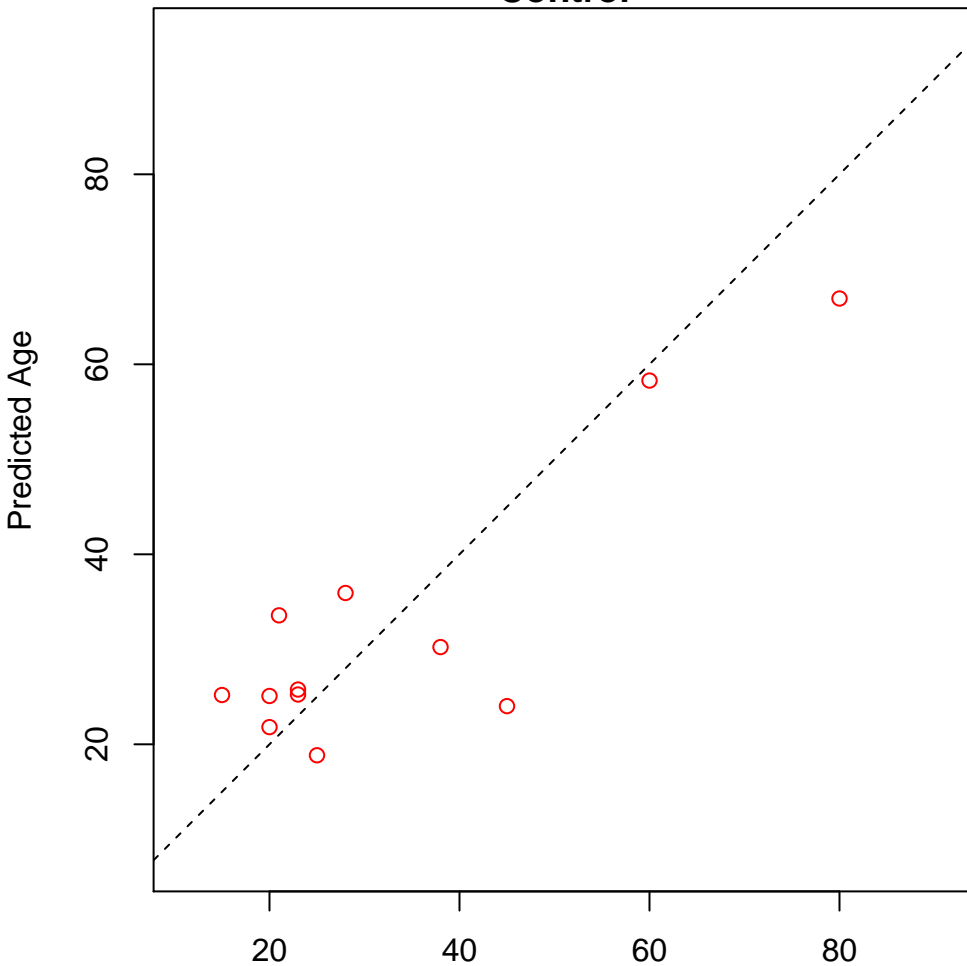


calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules (Score: 9.6220)

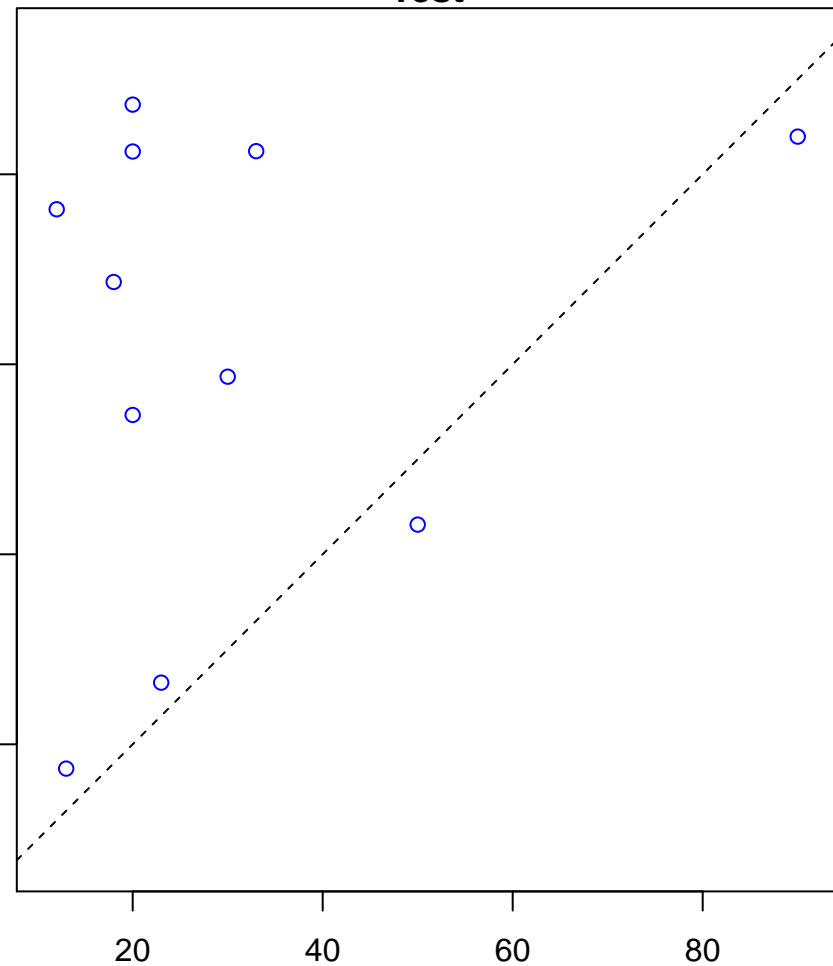


purine nucleobase metabolic process (Score: 9.616413)

Control

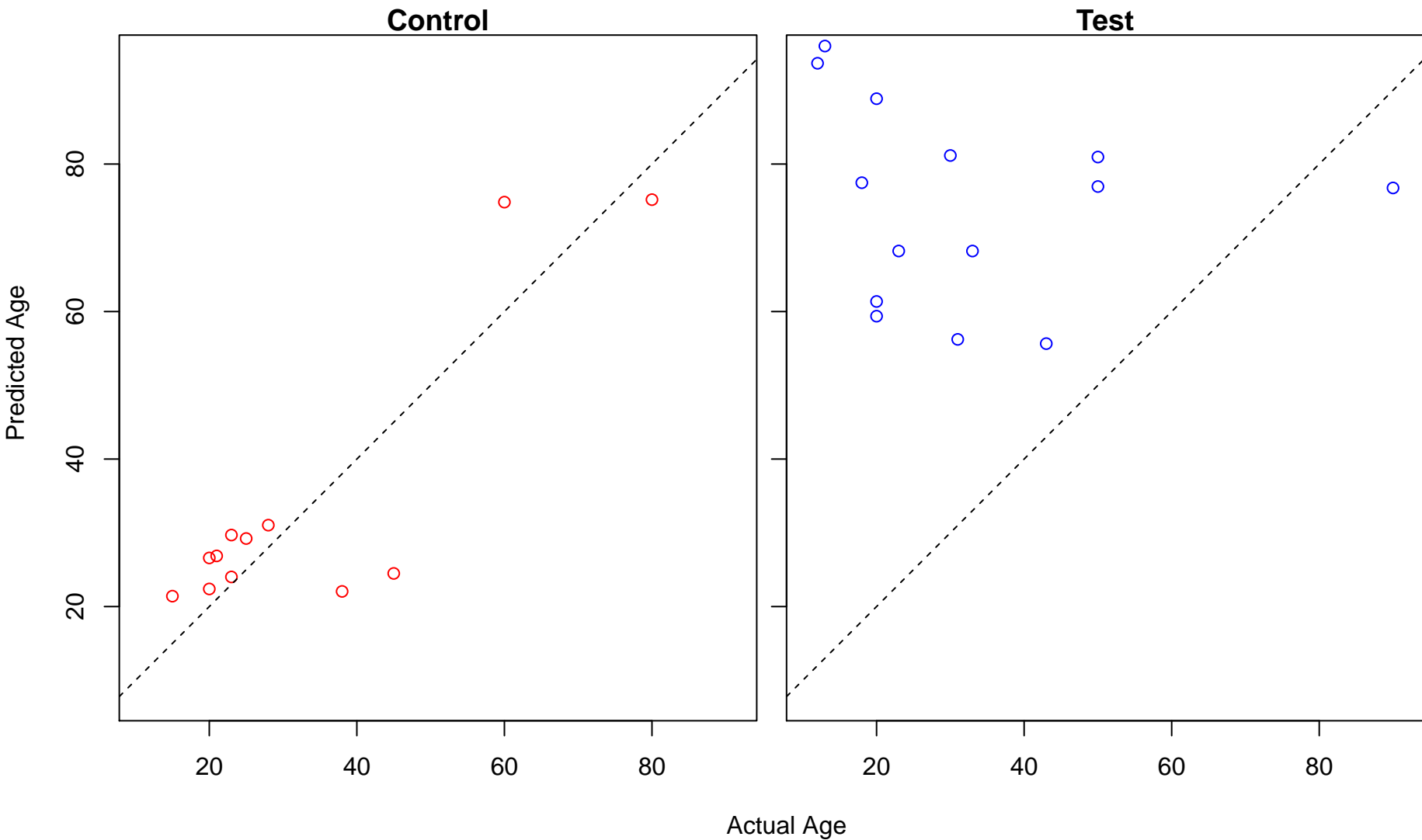


Test

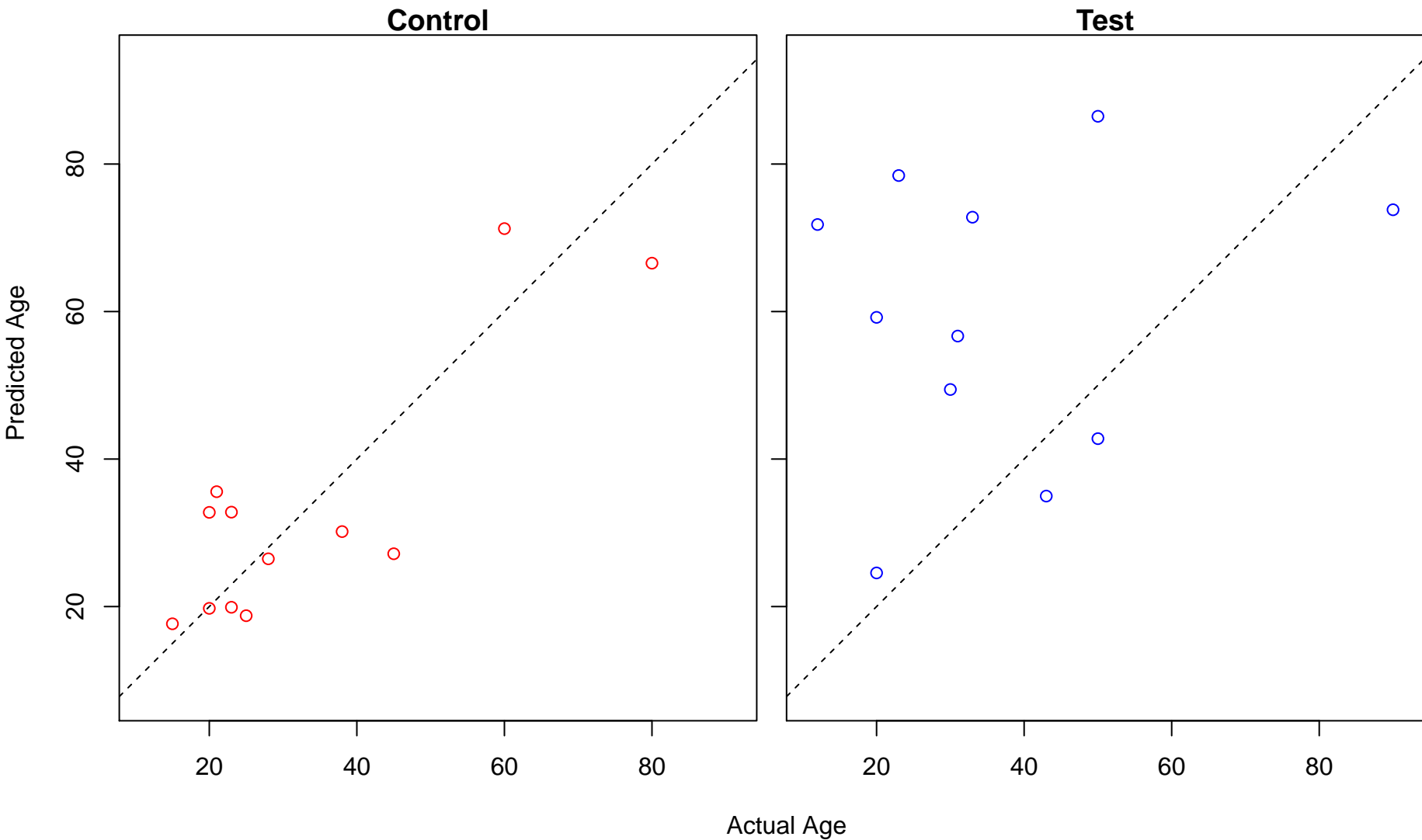


Actual Age

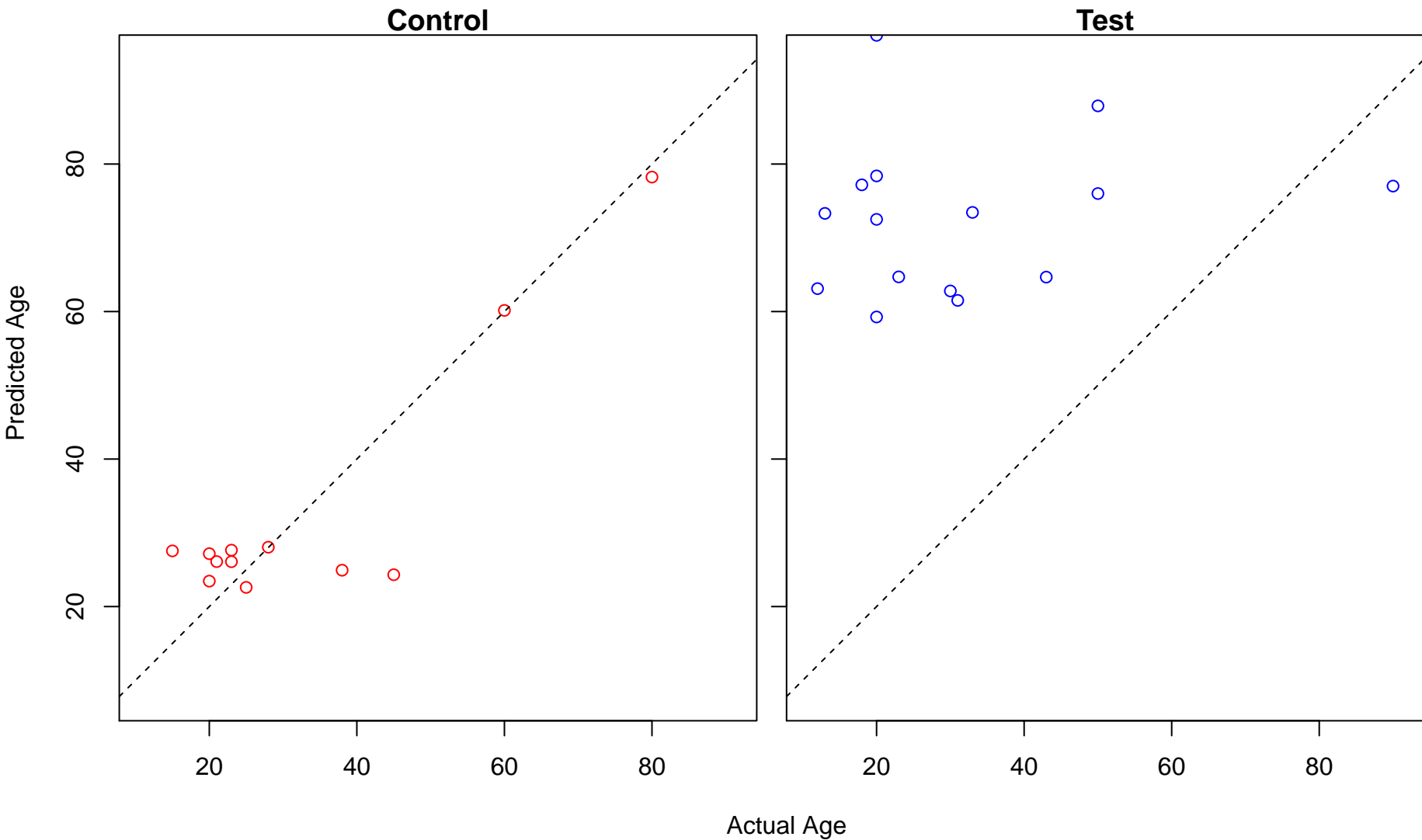
cardiac ventricle development (Score: 9.607802)



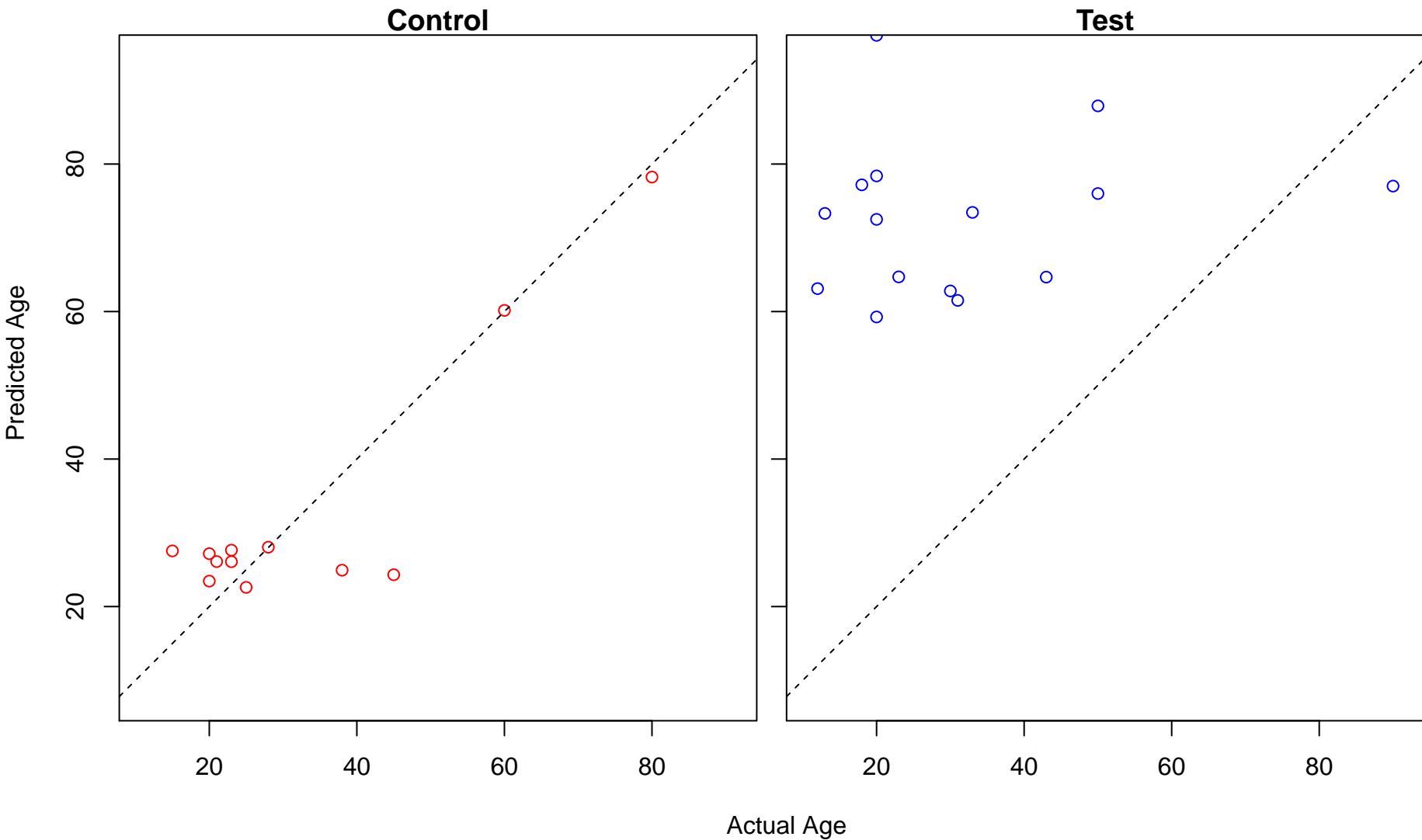
modulation by host of viral genome replication (Score: 9.607660)



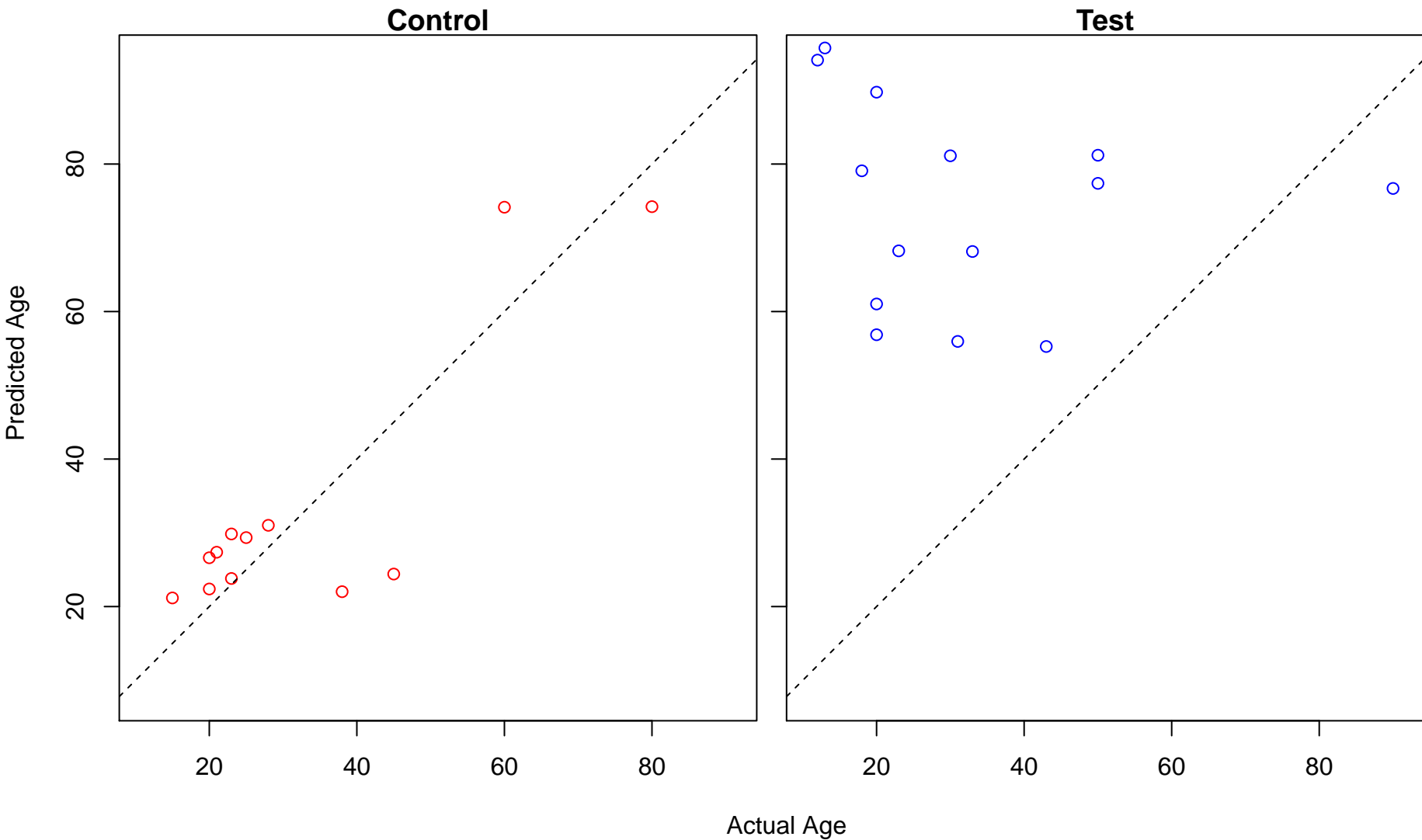
spindle localization (Score: 9.603960)



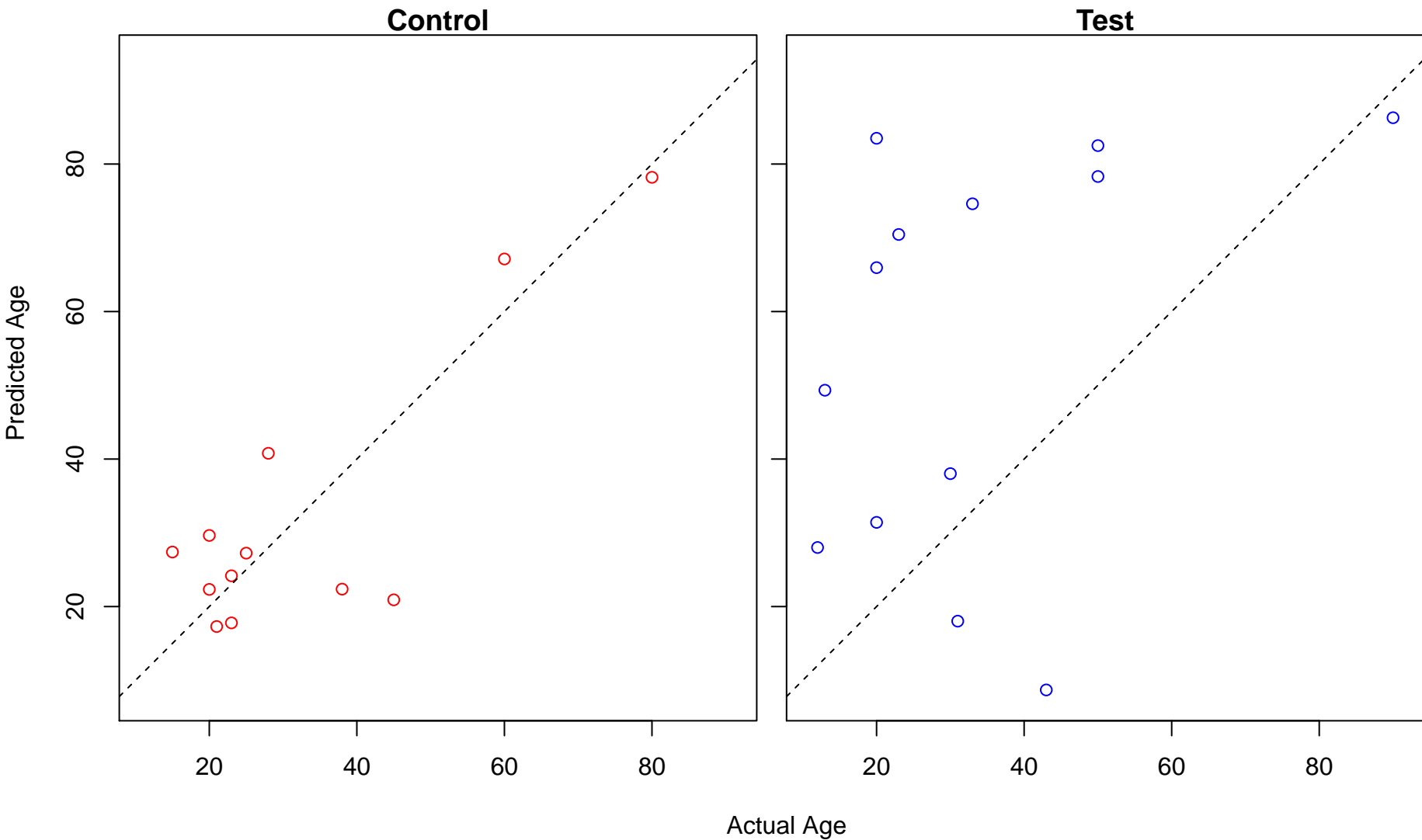
establishment of spindle localization (Score: 9.603943)



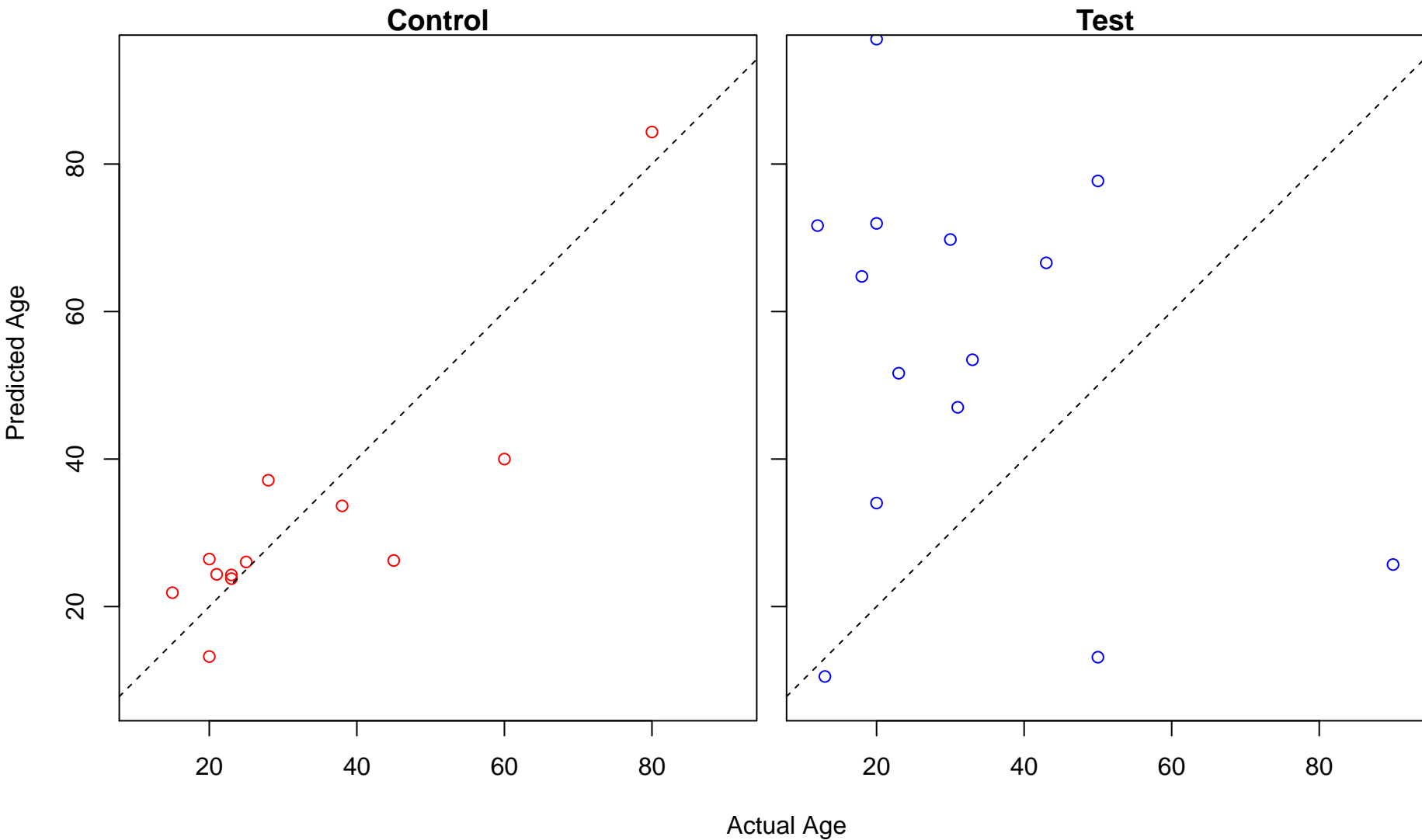
cardiac chamber development (Score: 9.602157)



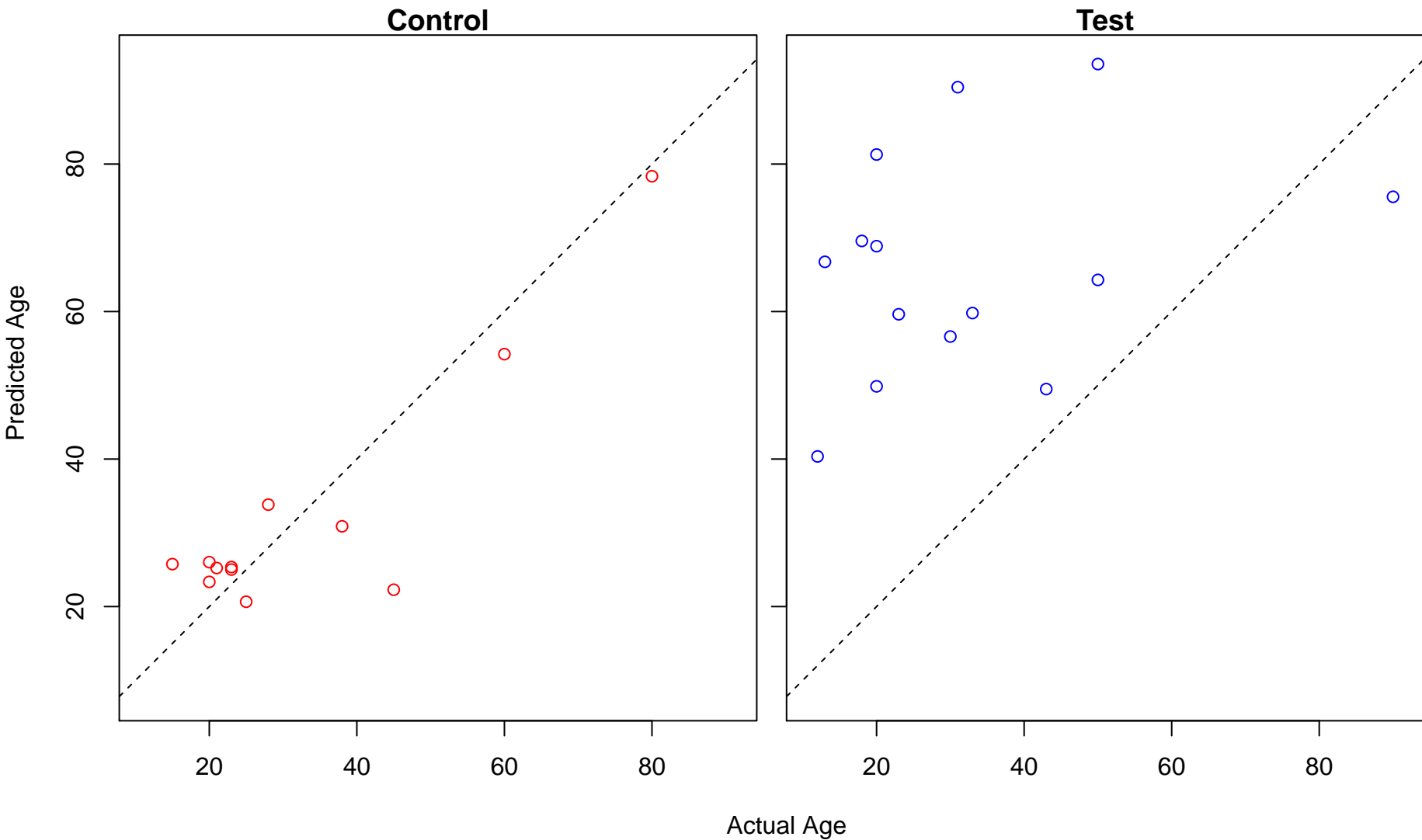
DNA replication (Score: 9.601844)



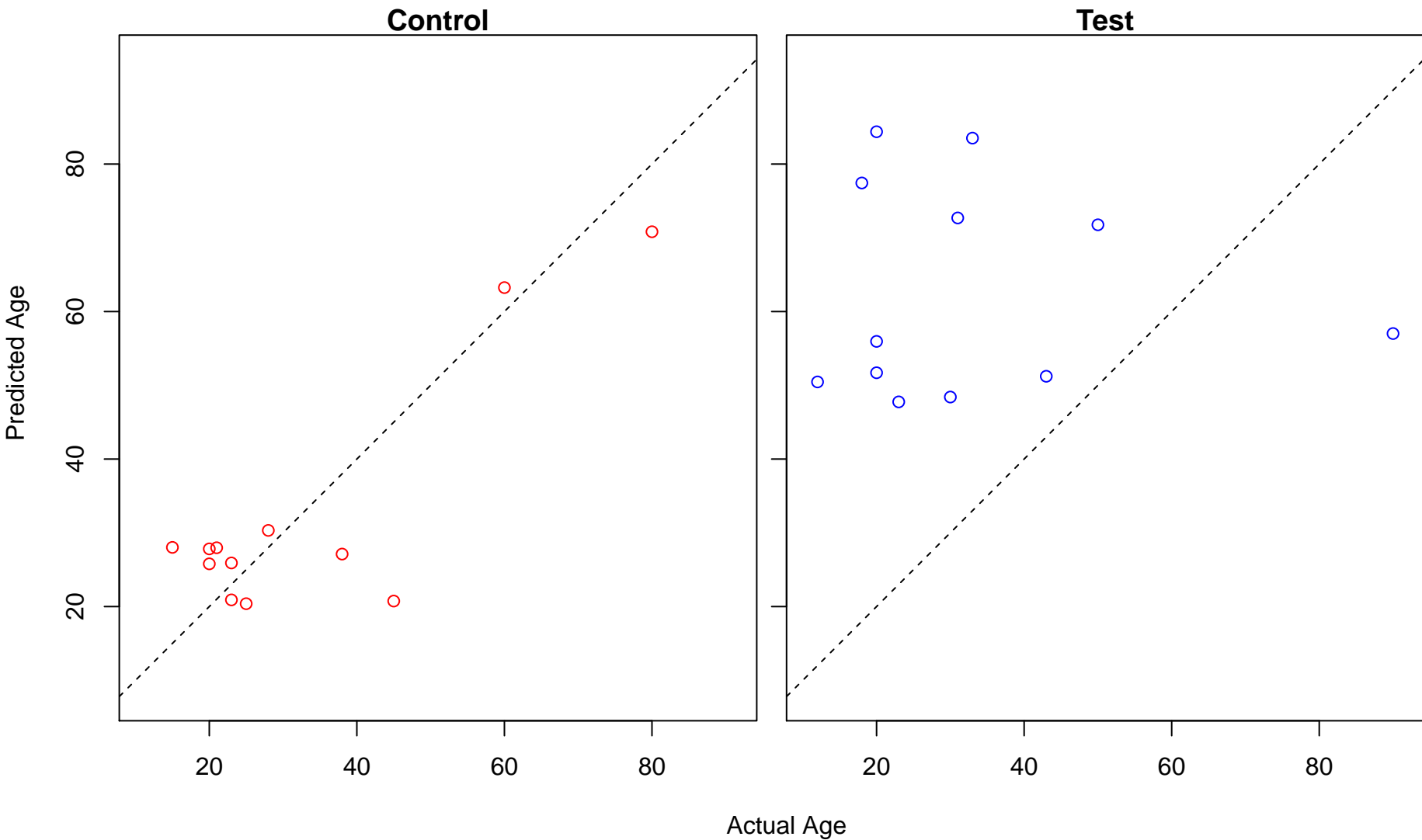
cellular ketone metabolic process (Score: 9.597551)



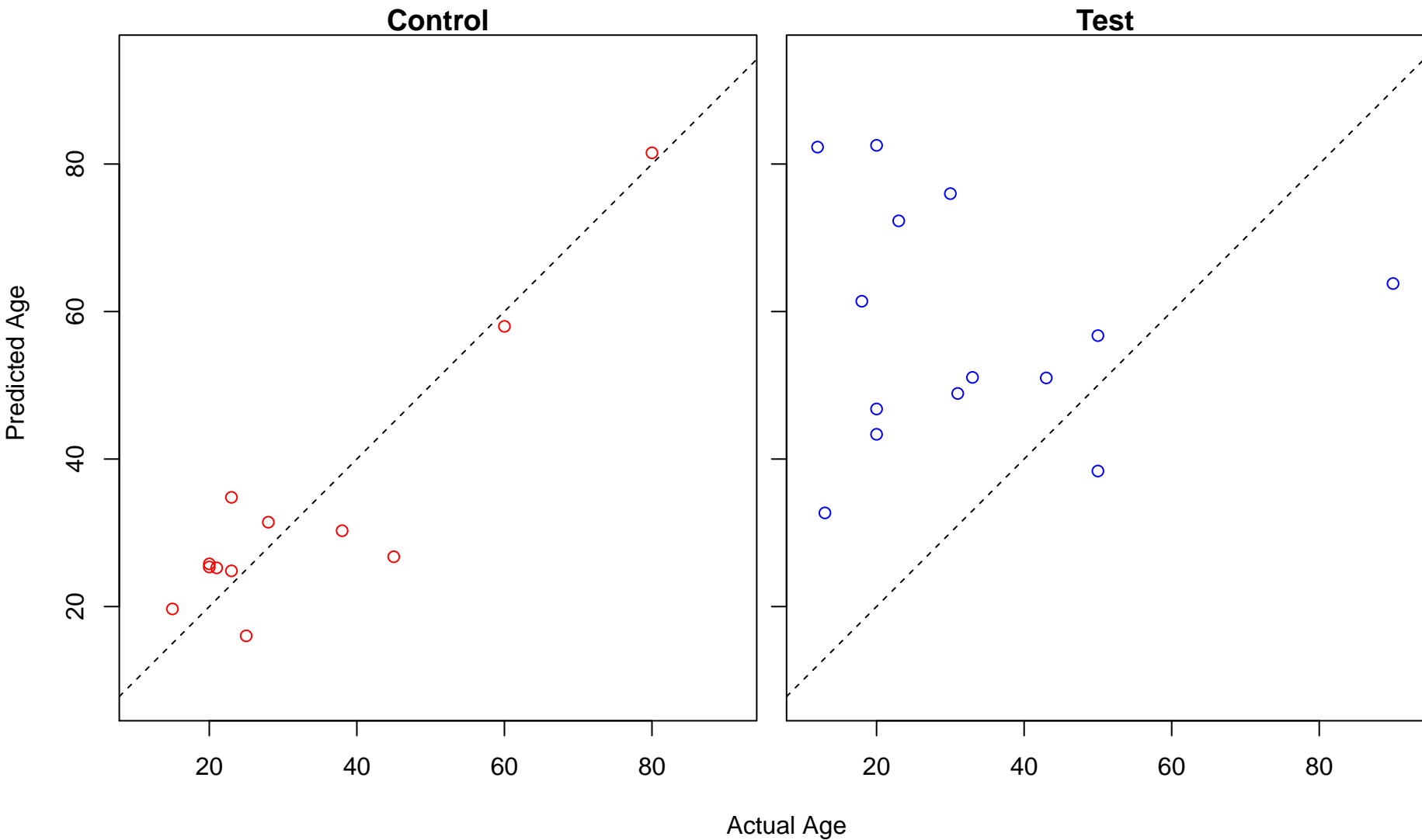
regulation of glycoprotein biosynthetic process (Score: 9.593798)



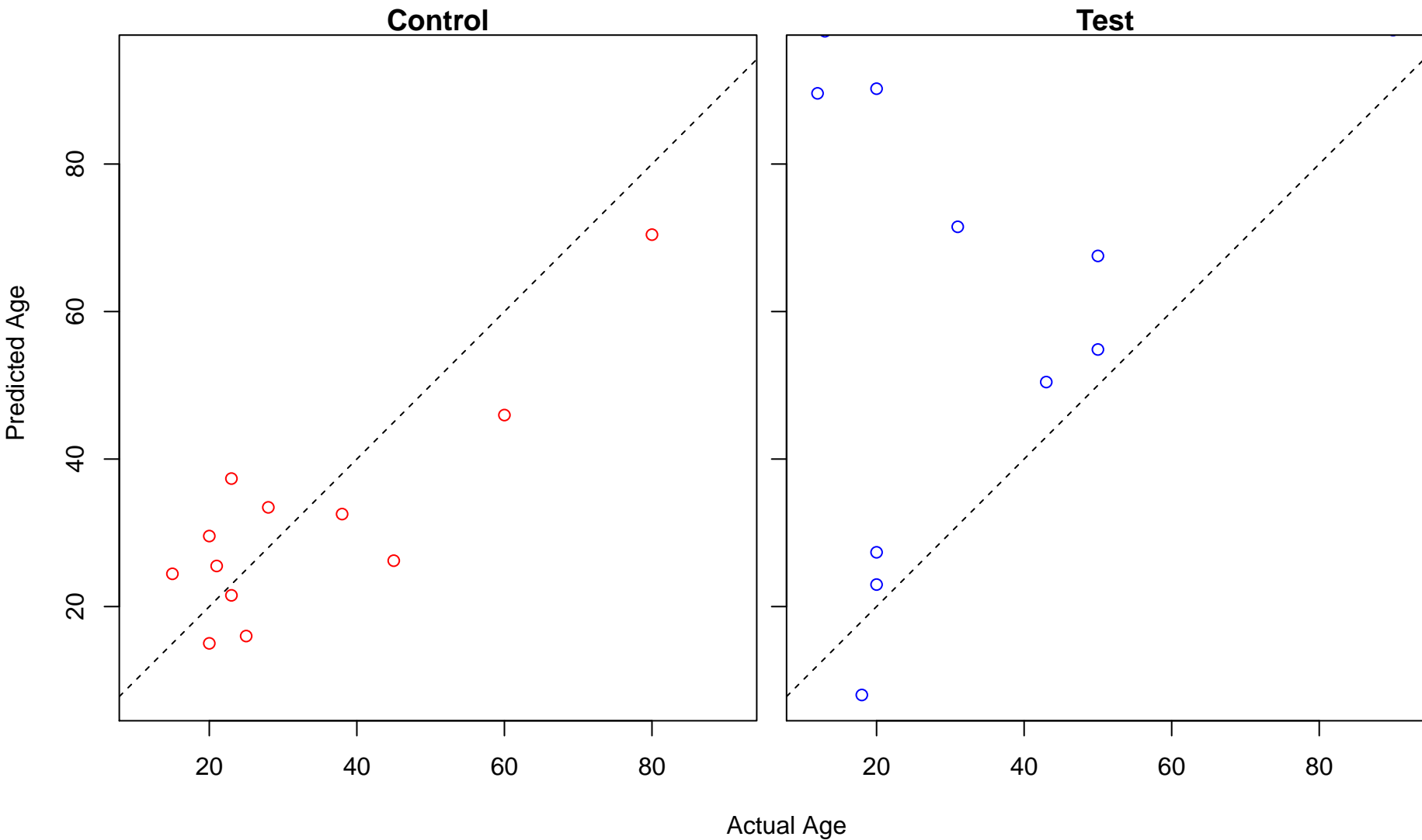
regulation of CD8-positive, alpha-beta T cell activation (Score: 9.592202)



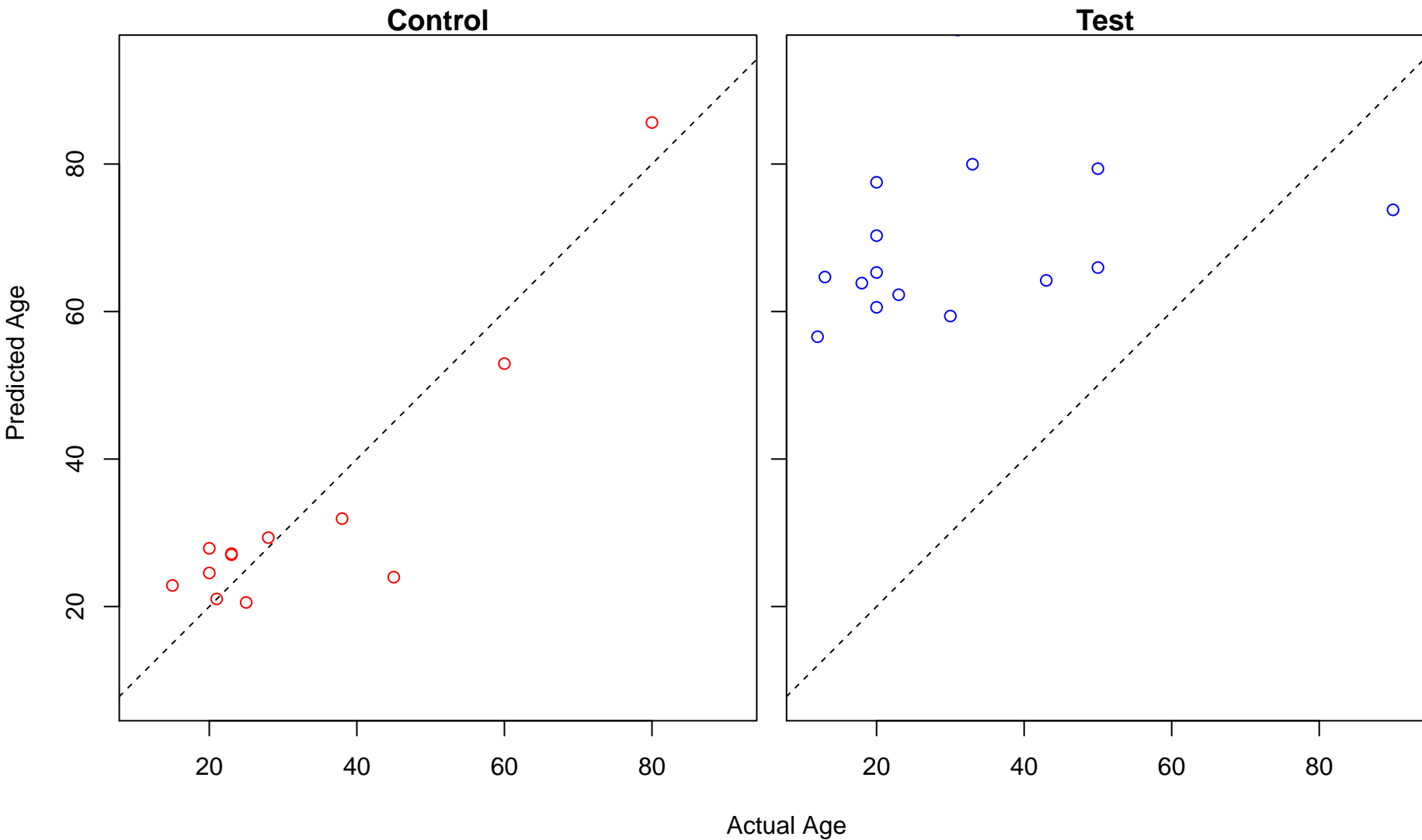
DNA strand renaturation (Score: 9.584499)



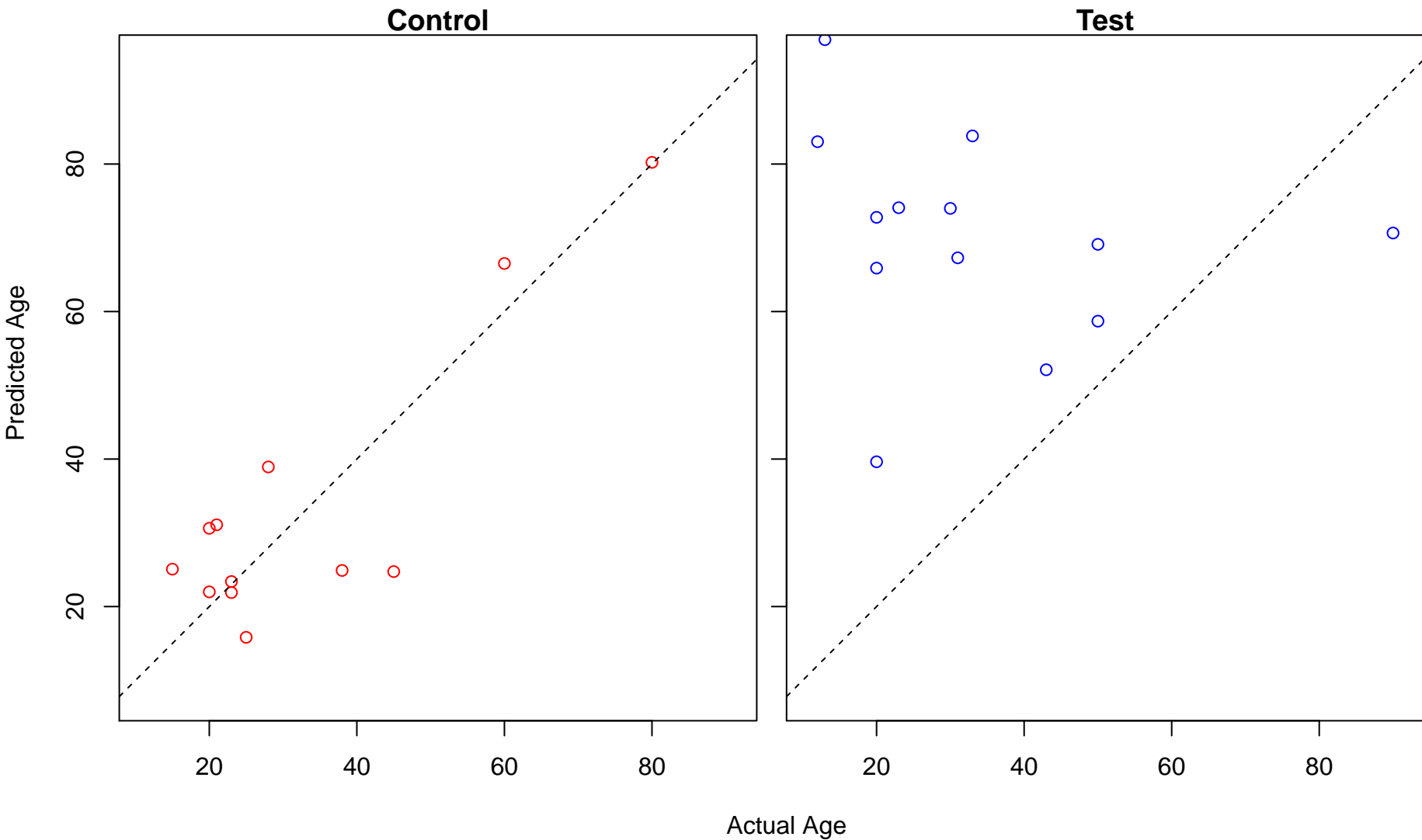
forebrain development (Score: 9.580846)



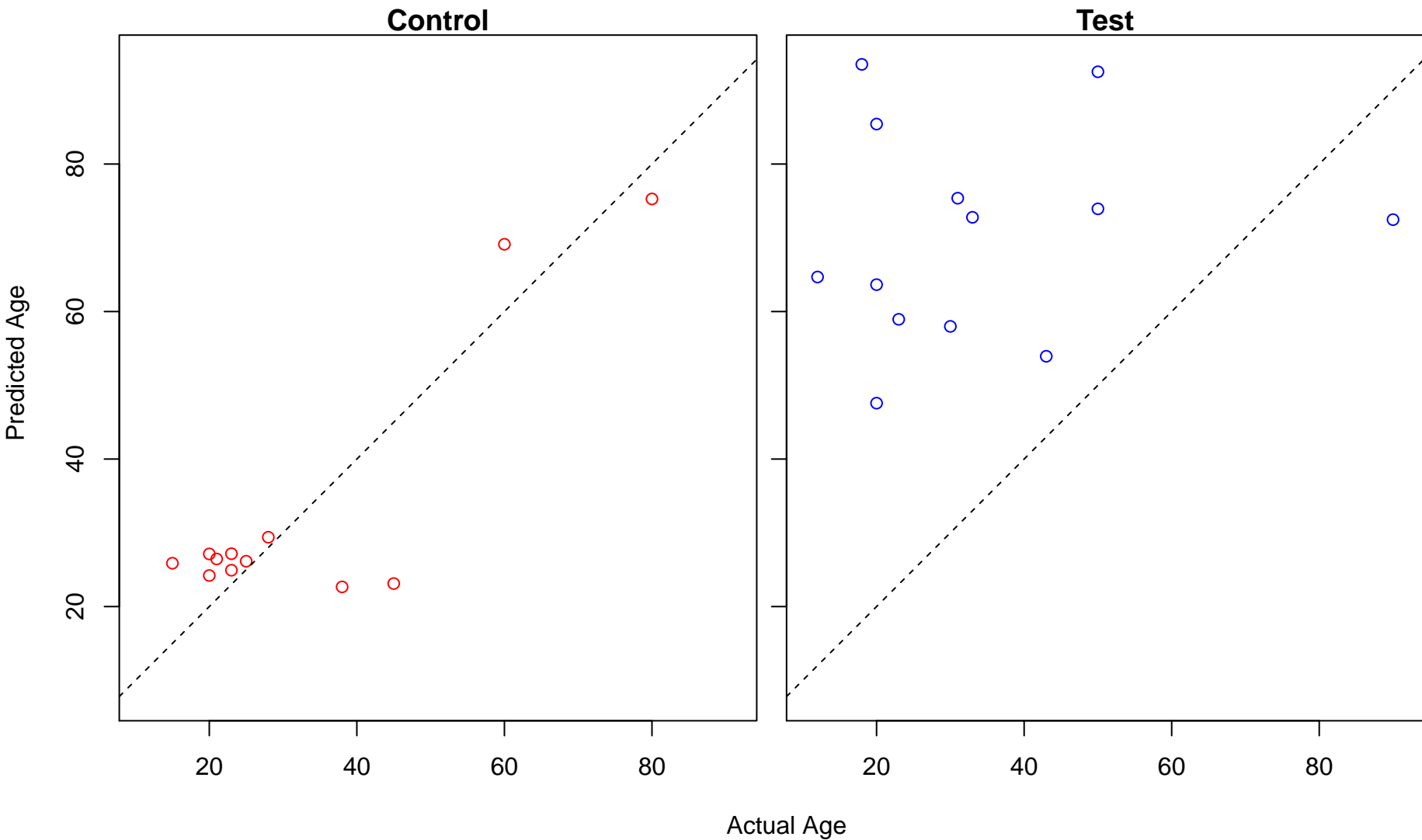
tube morphogenesis (Score: 9.580778)



protein localization to organelle (Score: 9.580402)

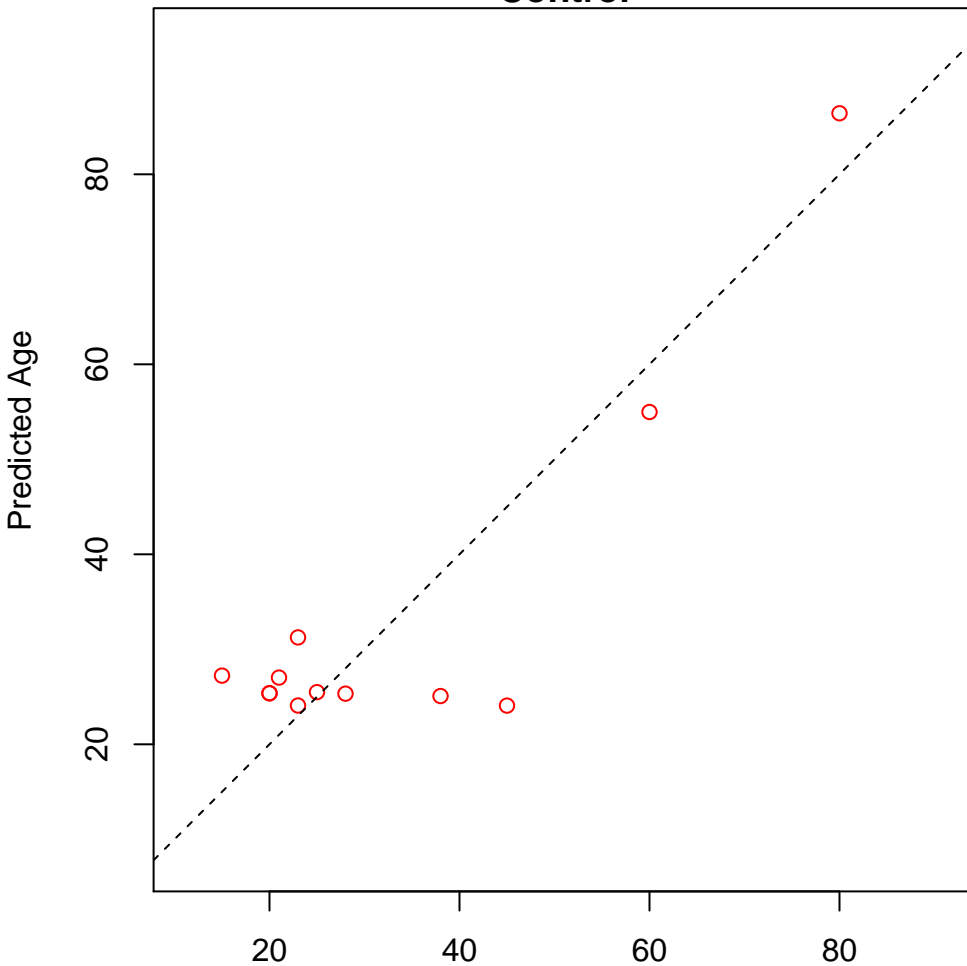


positive regulation of mitochondrion organization (Score: 9.576206)

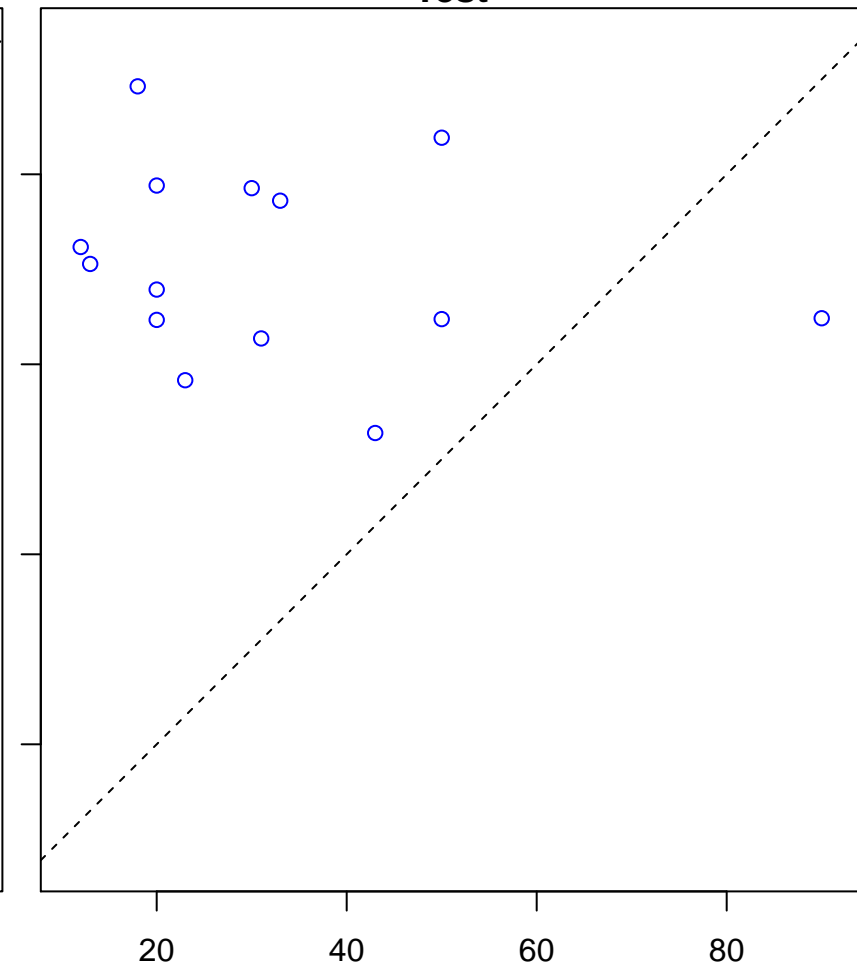


regulation of DNA biosynthetic process (Score: 9.568877)

Control

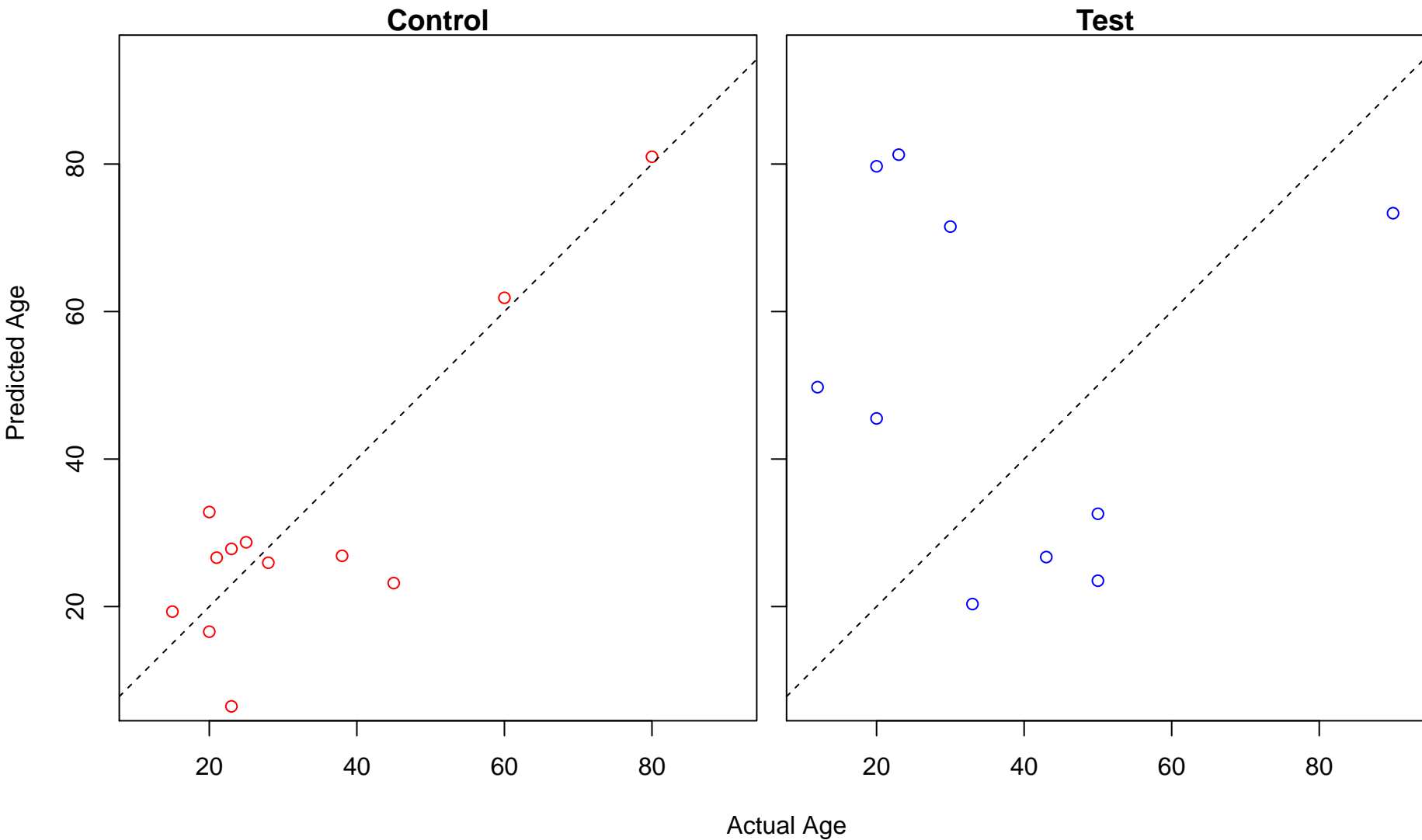


Test

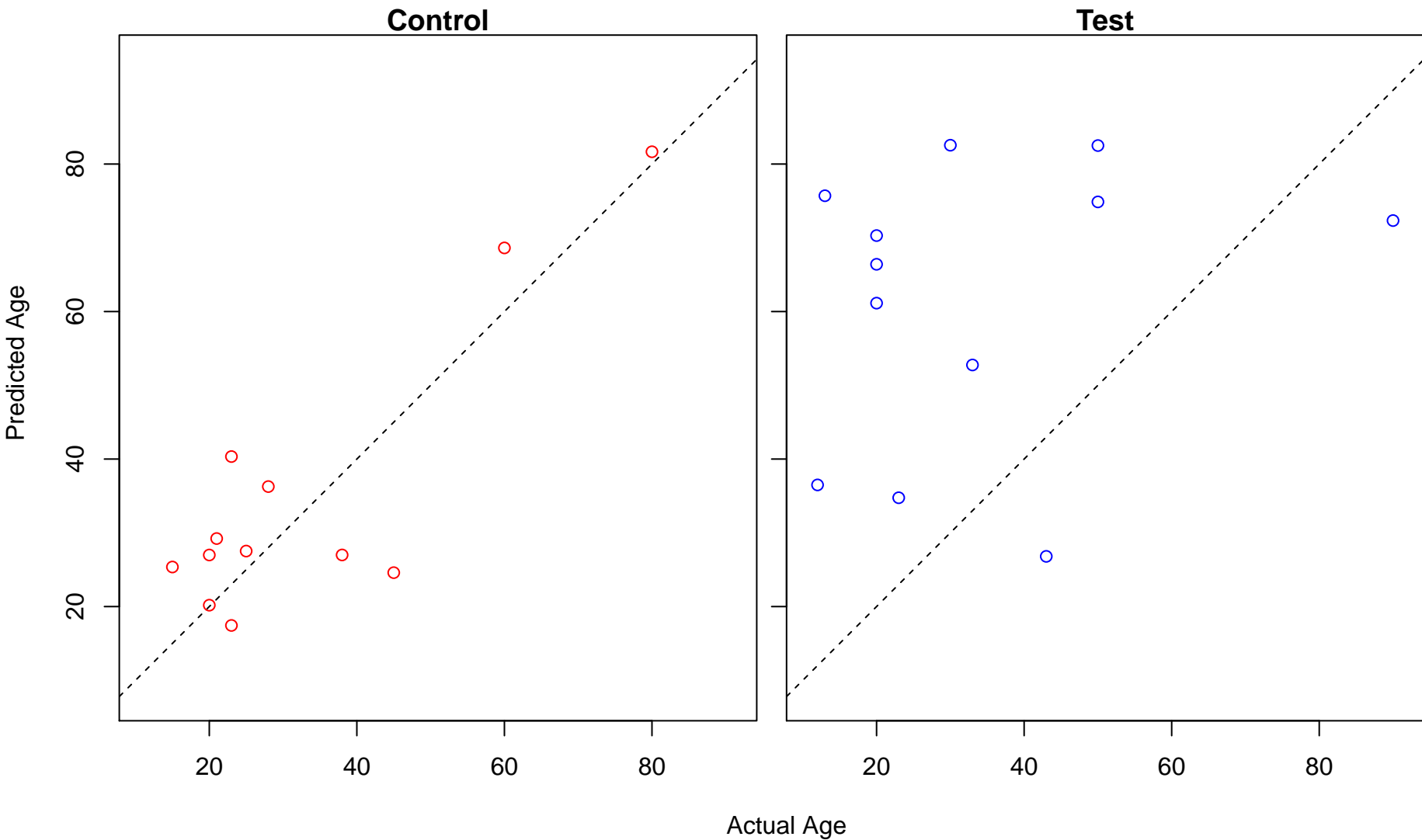


Actual Age

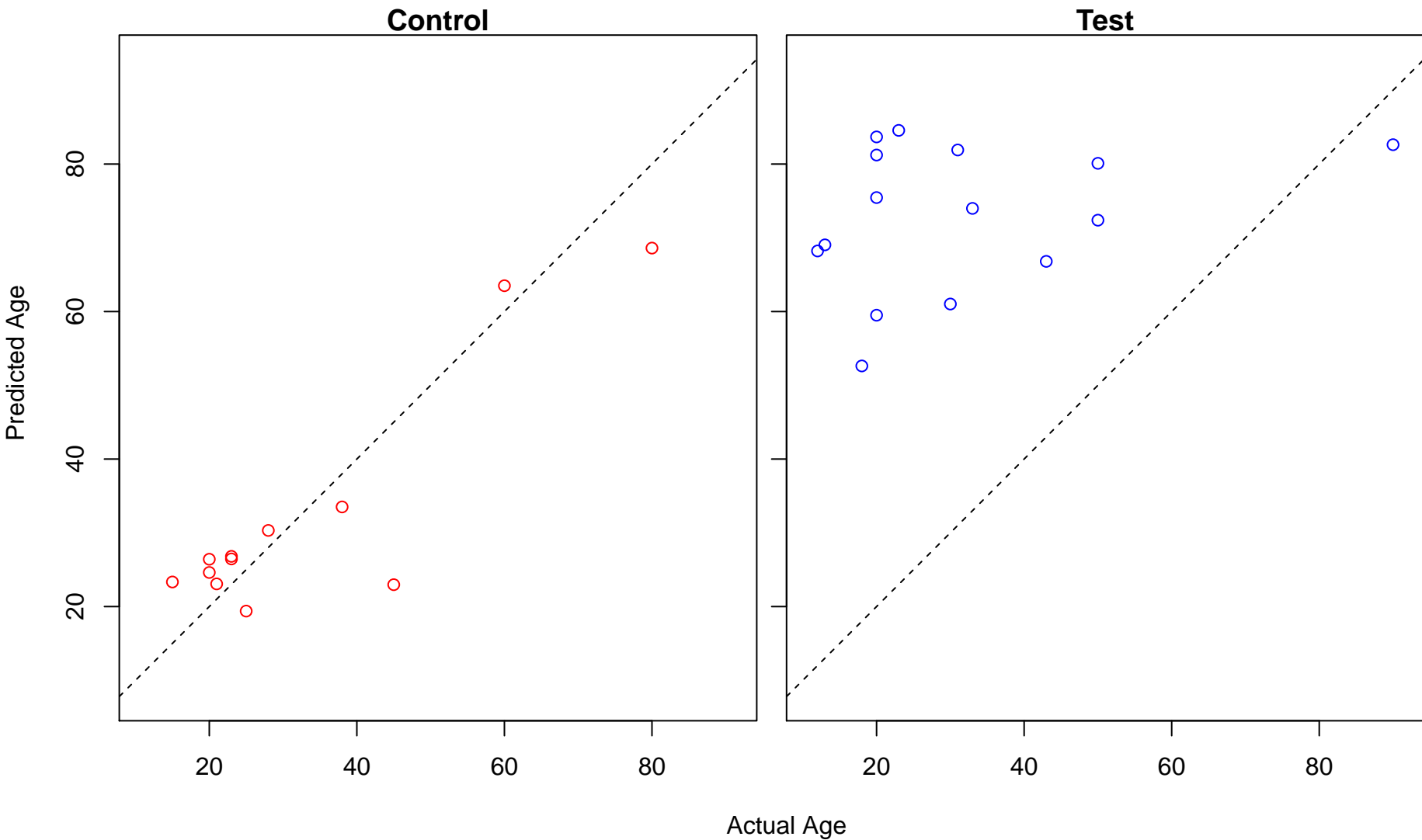
negative regulation of mRNA processing (Score: 9.556712)



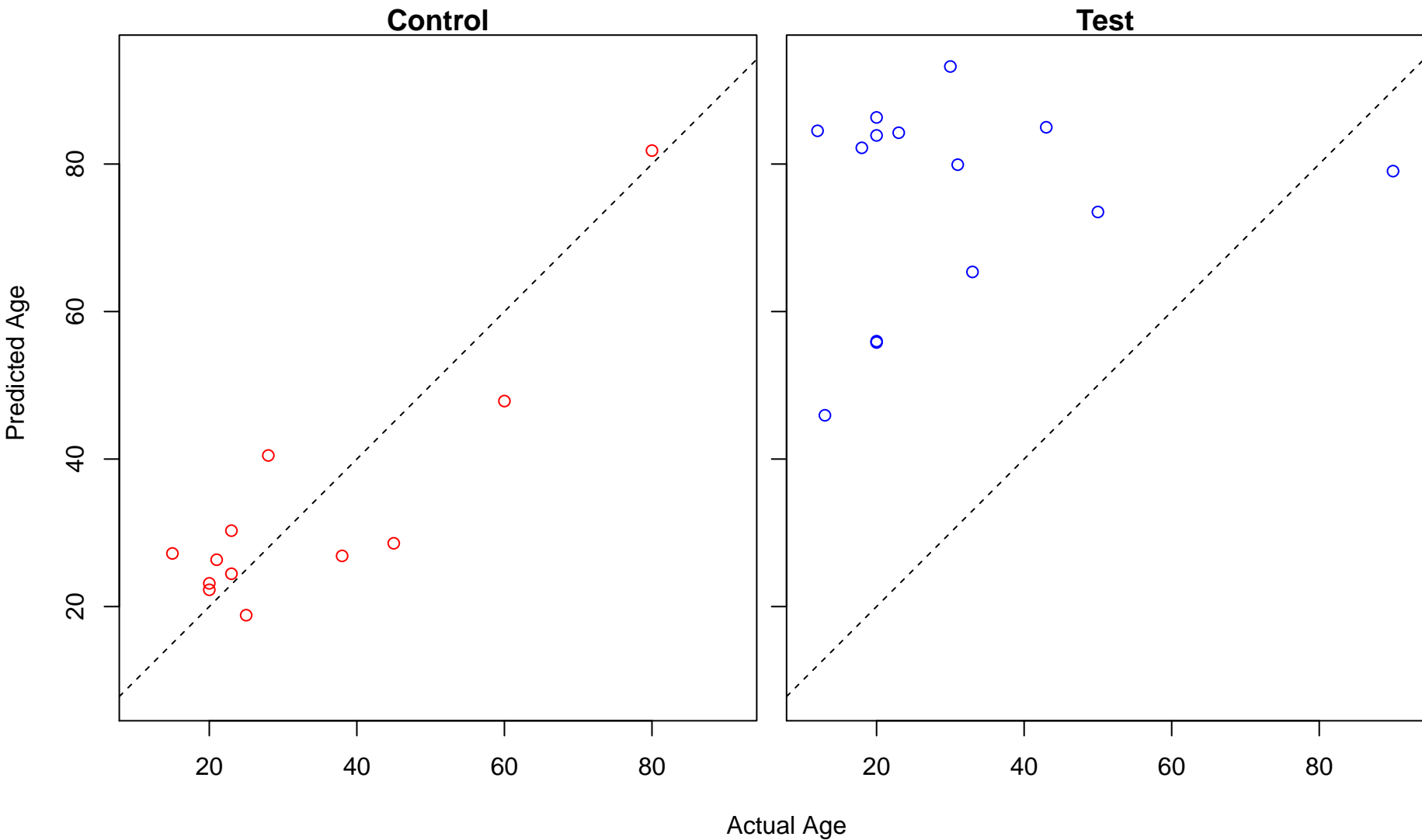
pigmentation (Score: 9.555165)



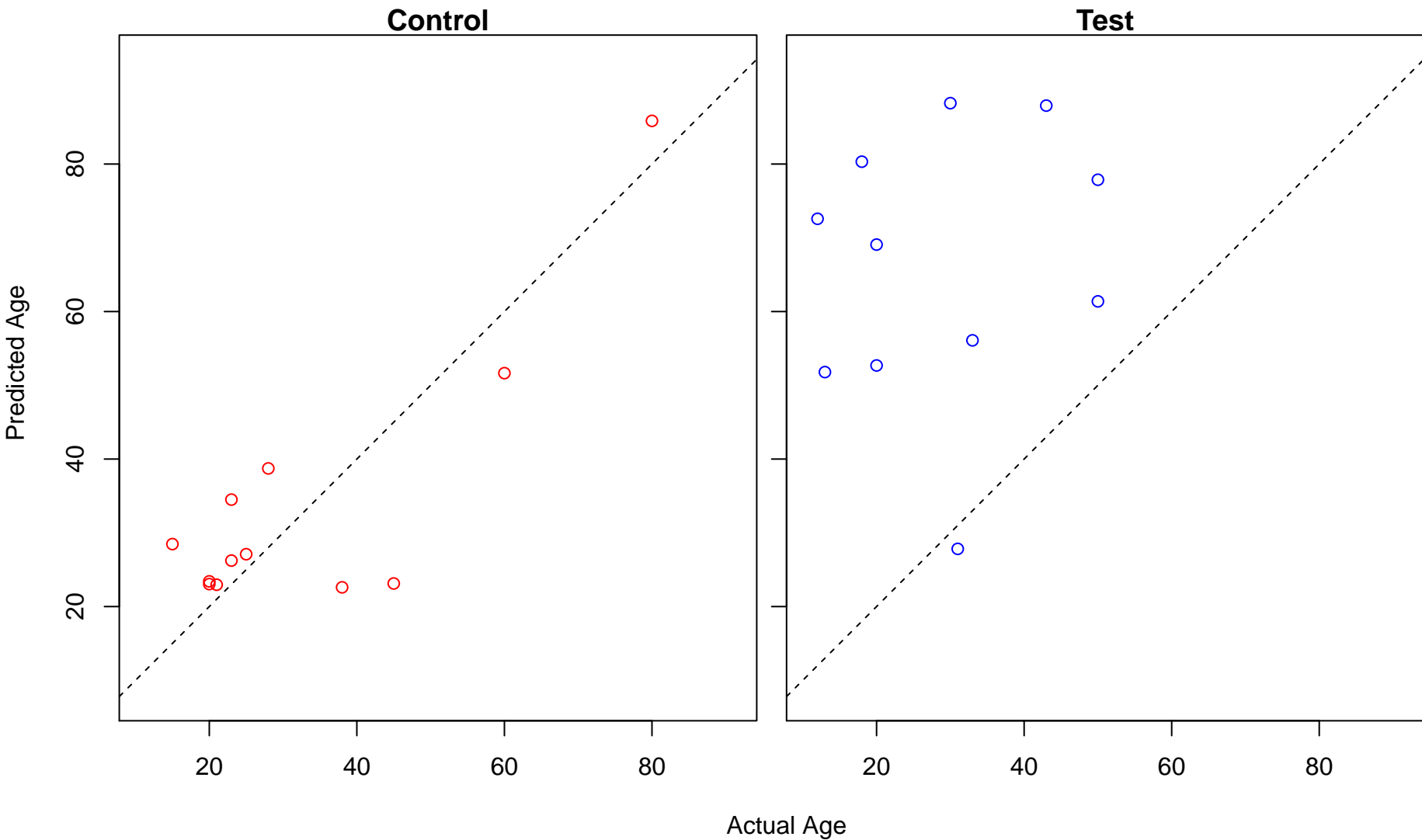
respiratory tube development (Score: 9.542580)



anatomical structure formation involved in morphogenesis (Score: 9.537560)

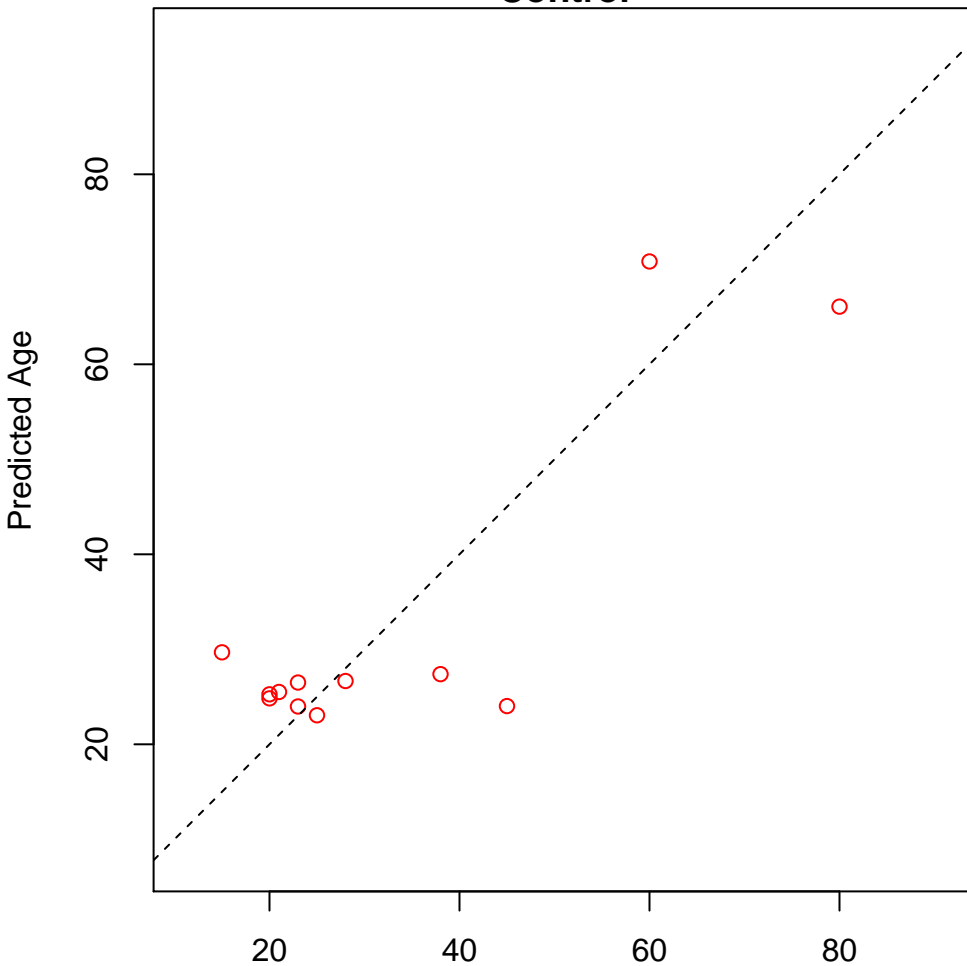


thymic T cell selection (Score: 9.536158)

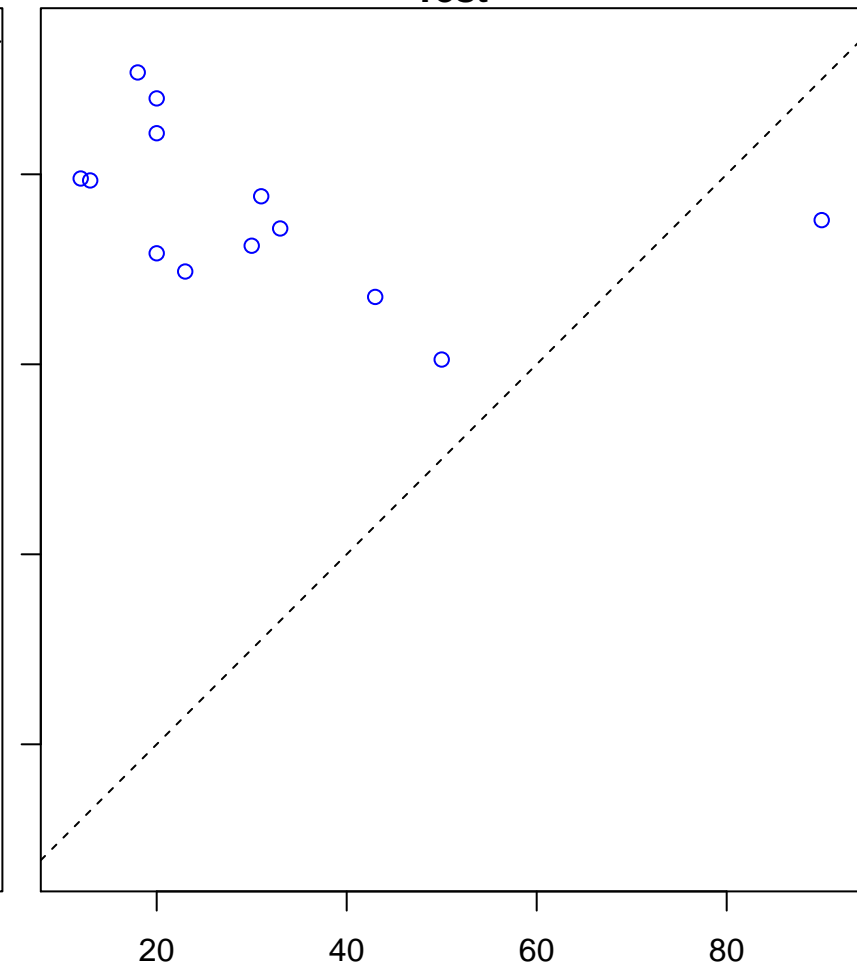


regulation of fat cell differentiation (Score: 9.534567)

Control

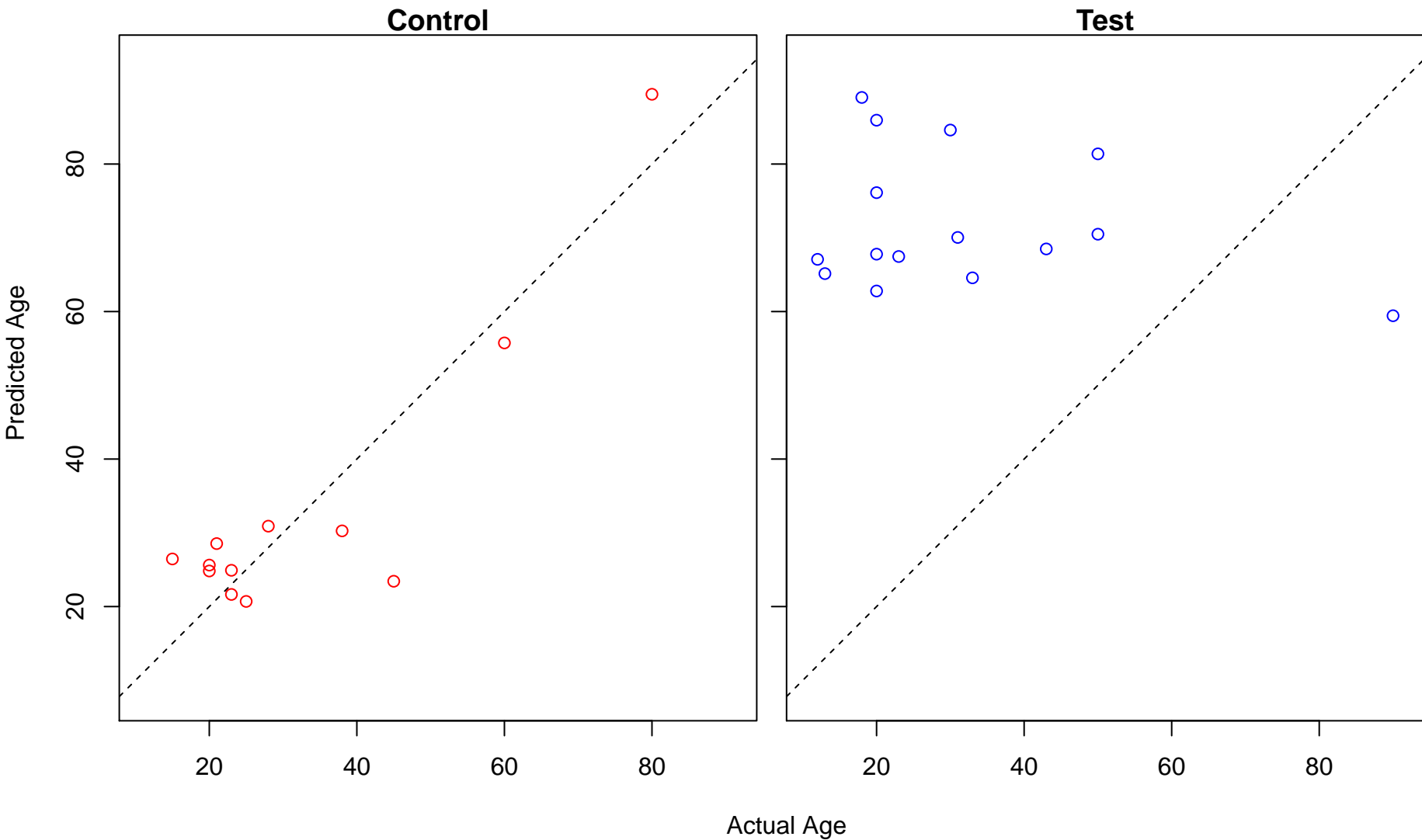


Test

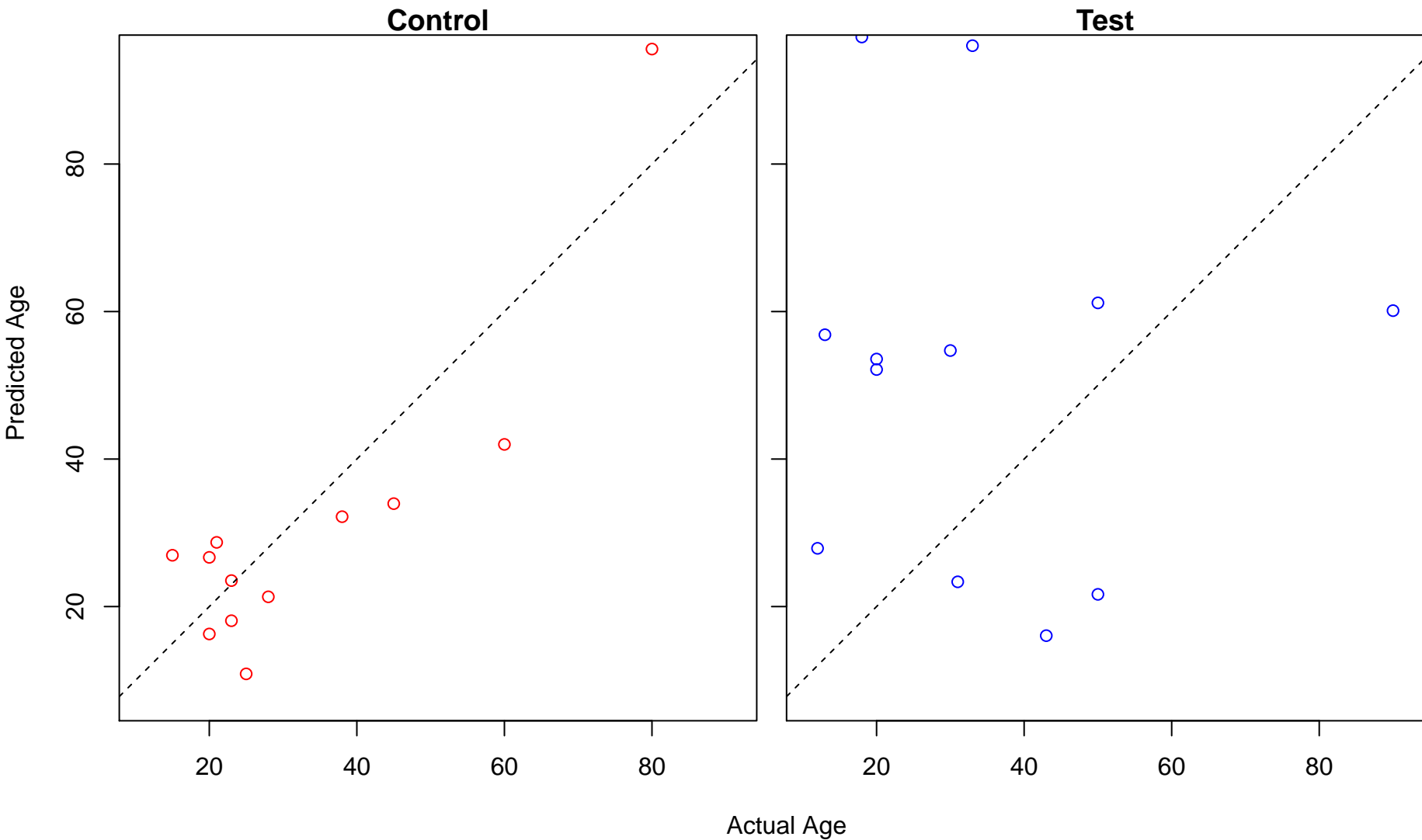


Actual Age

fatty acid metabolic process (Score: 9.533767)

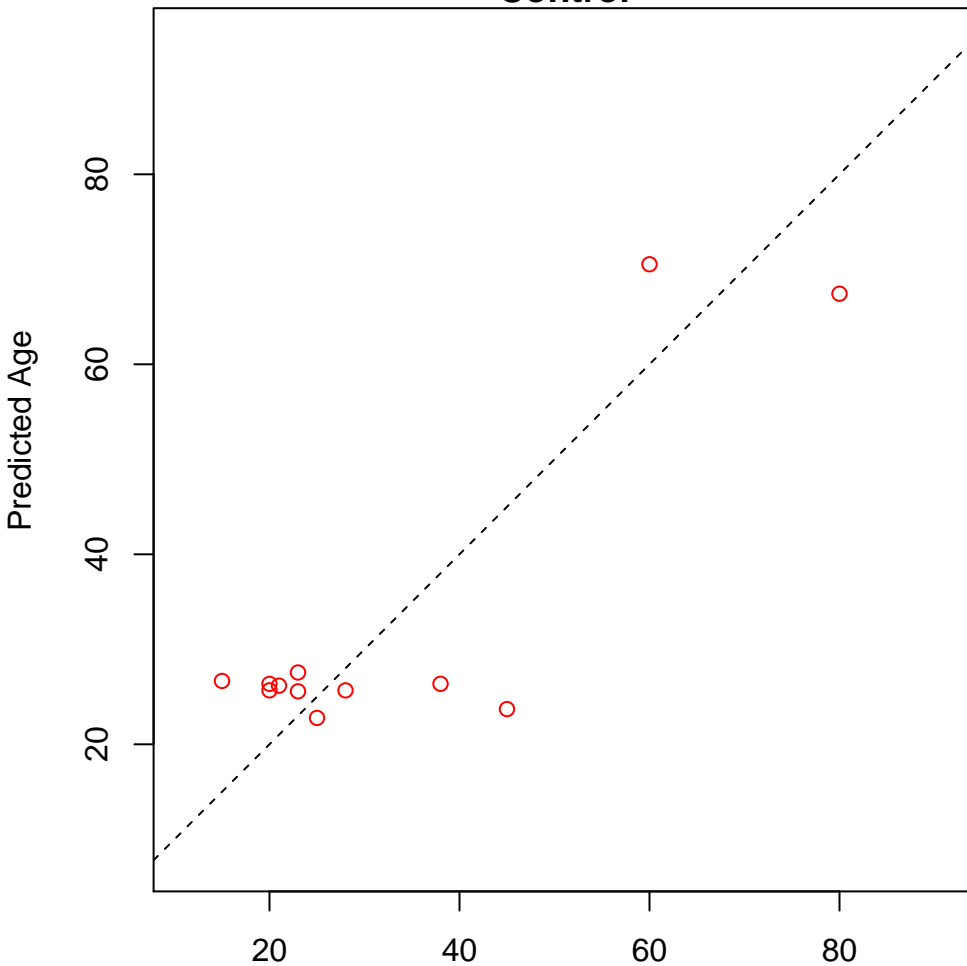


regulation of spindle assembly (Score: 9.519234)

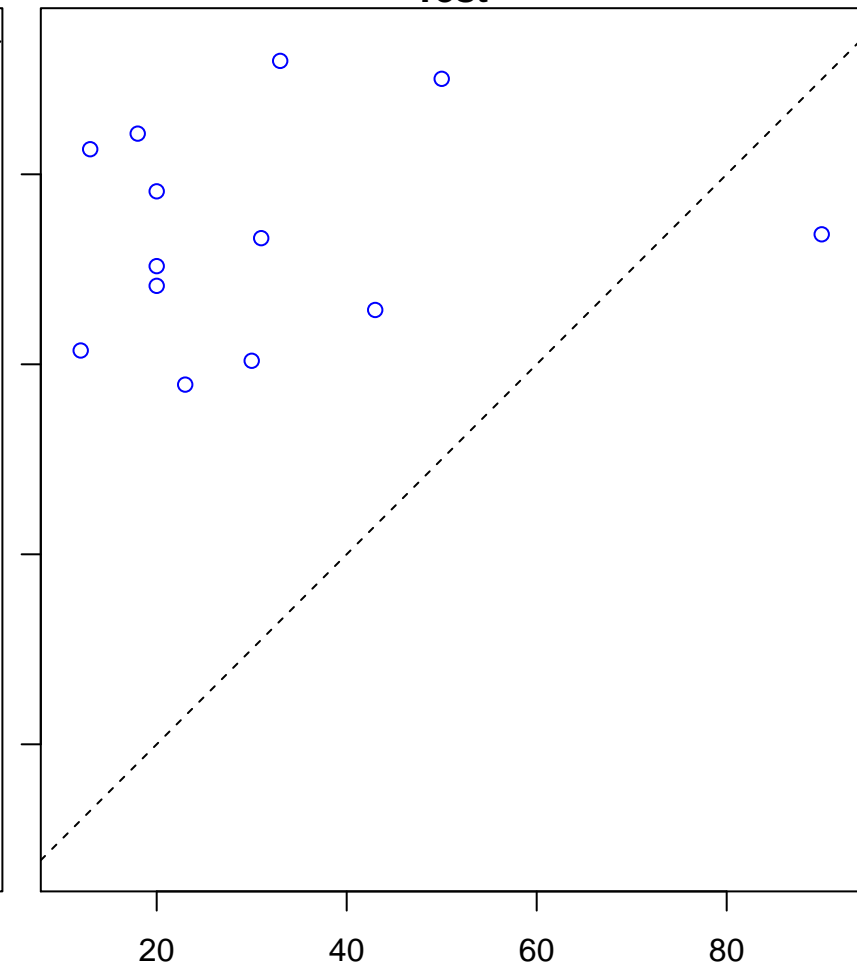


regulation of leukocyte apoptotic process (Score: 9.514136)

Control

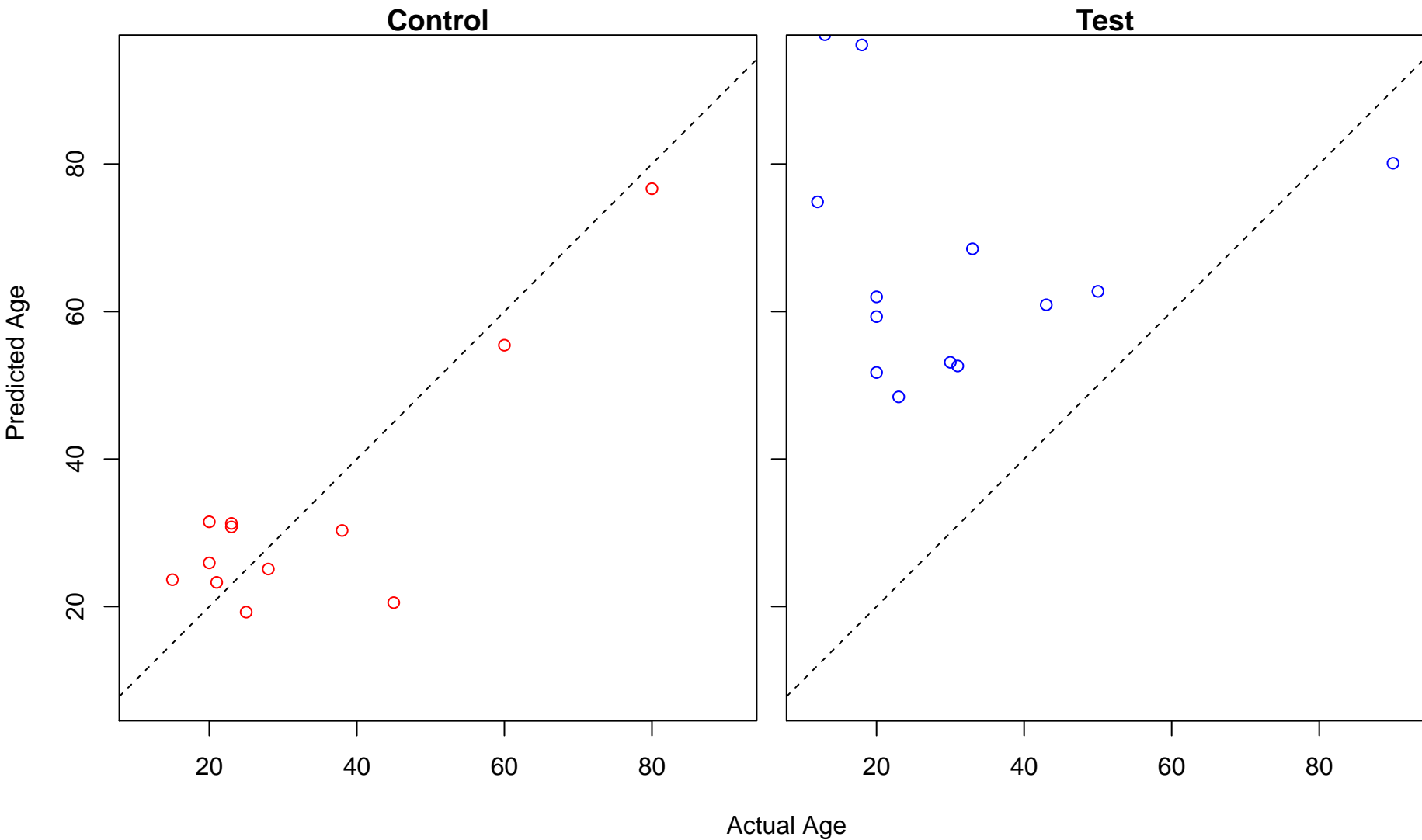


Test

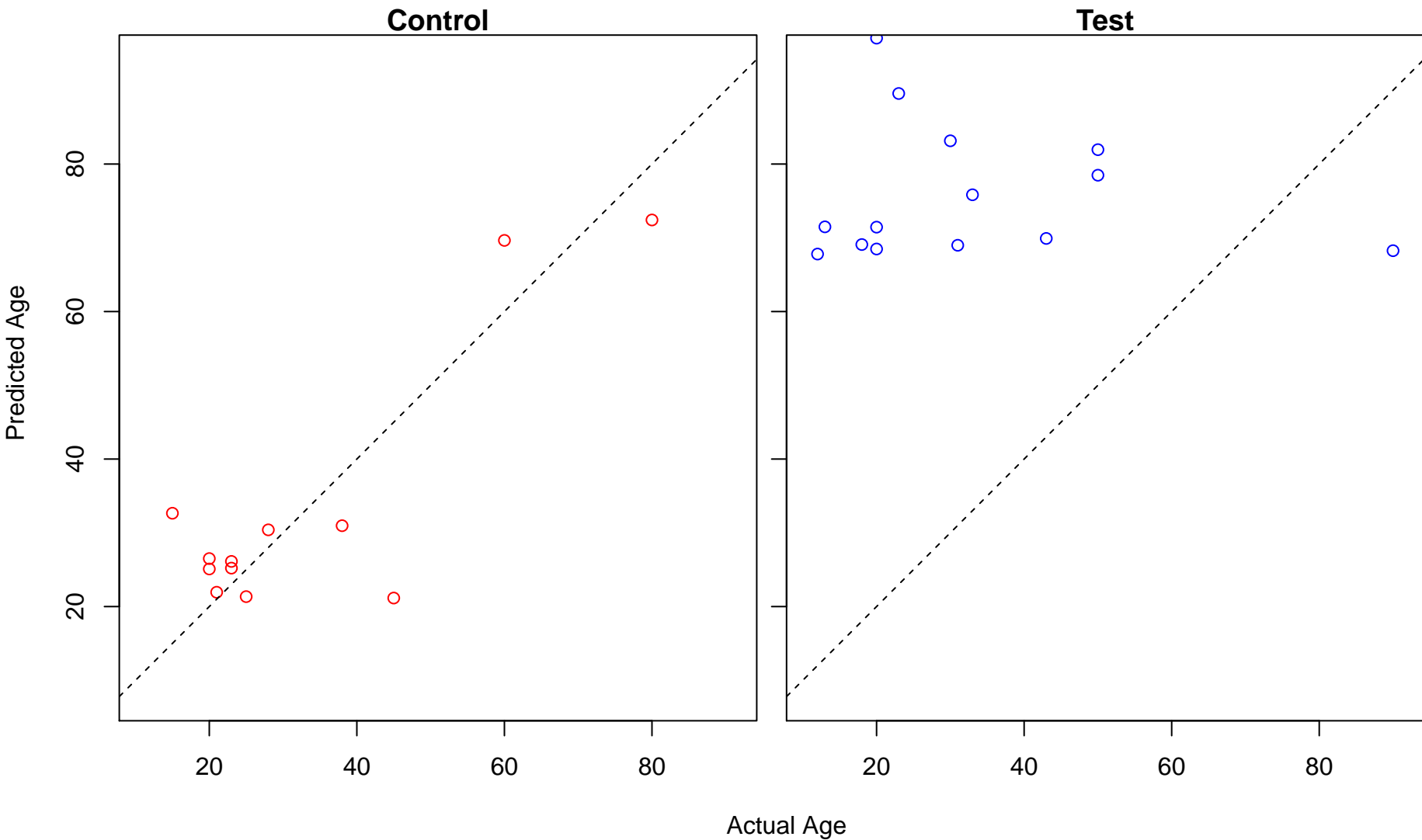


Actual Age

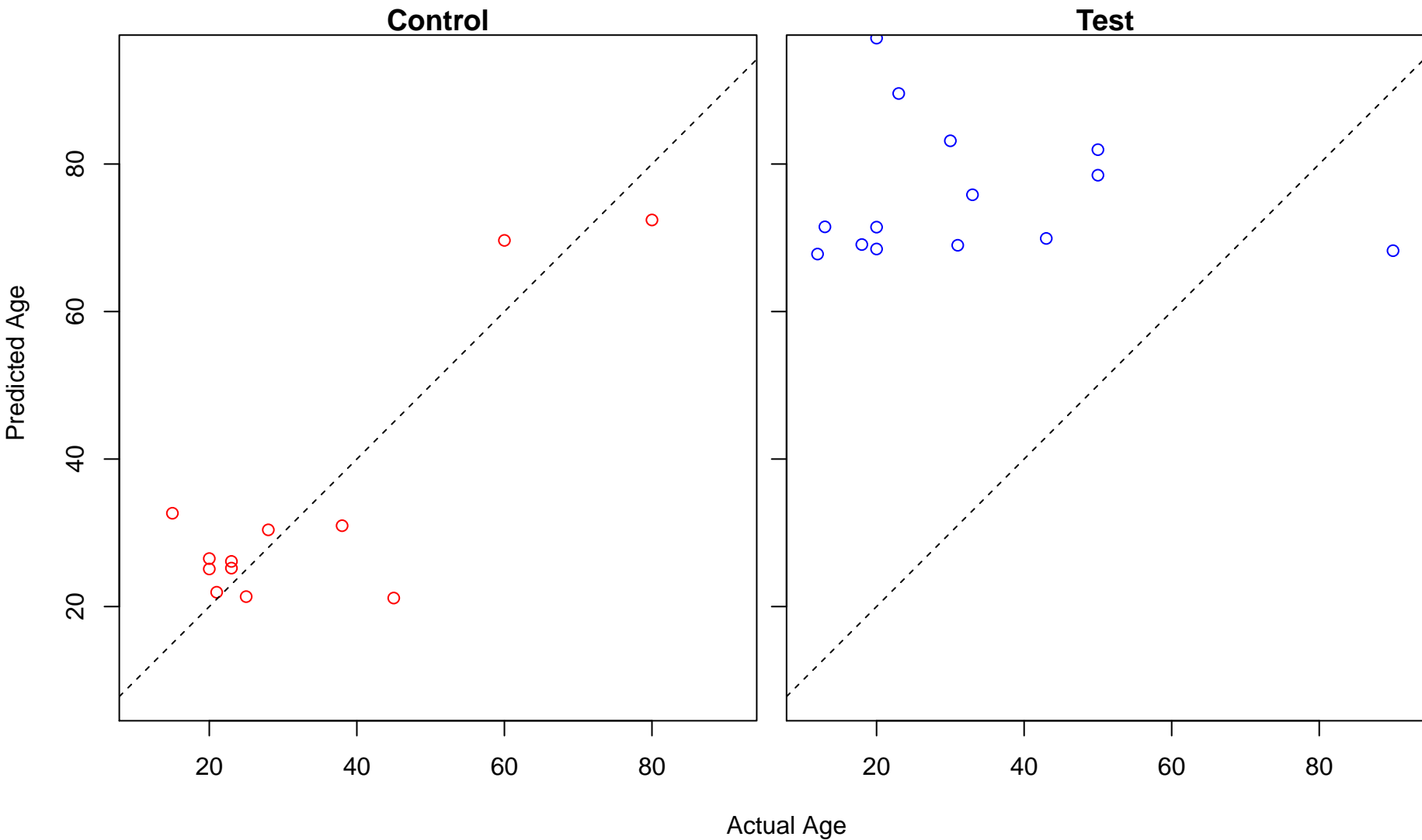
positive regulation of odontogenesis (Score: 9.510917)



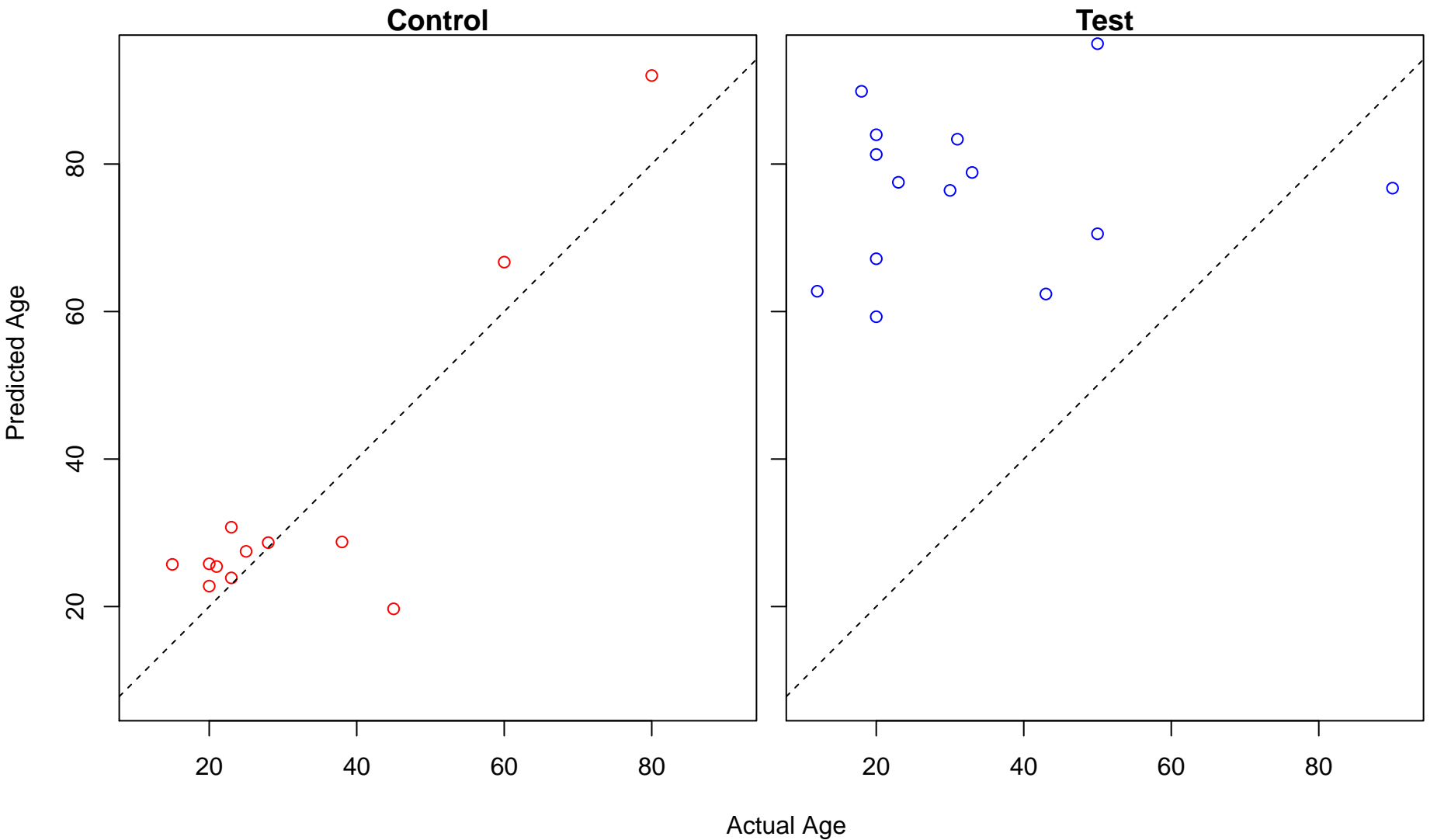
meiotic cell cycle (Score: 9.507391)



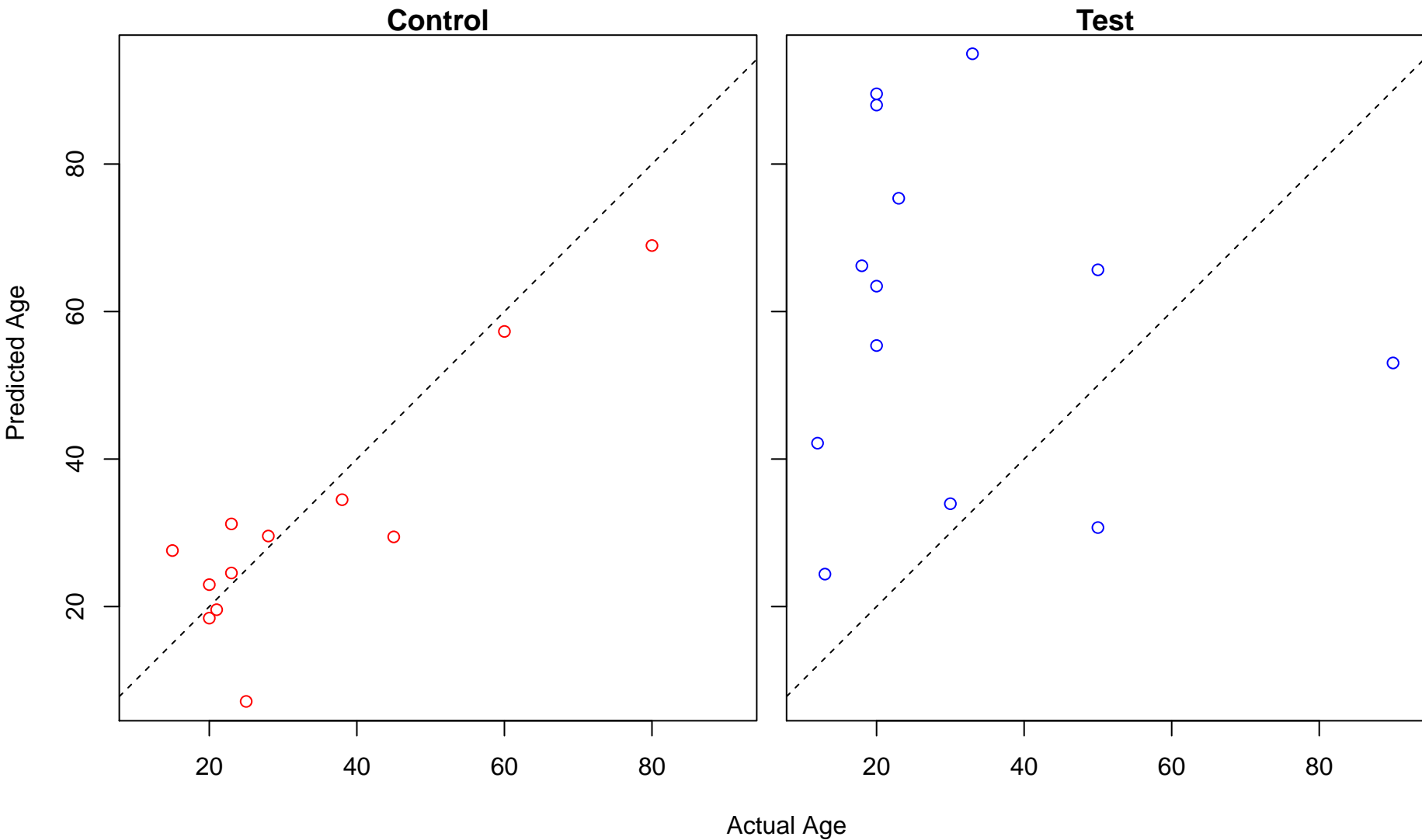
meiotic cell cycle process (Score: 9.507391)



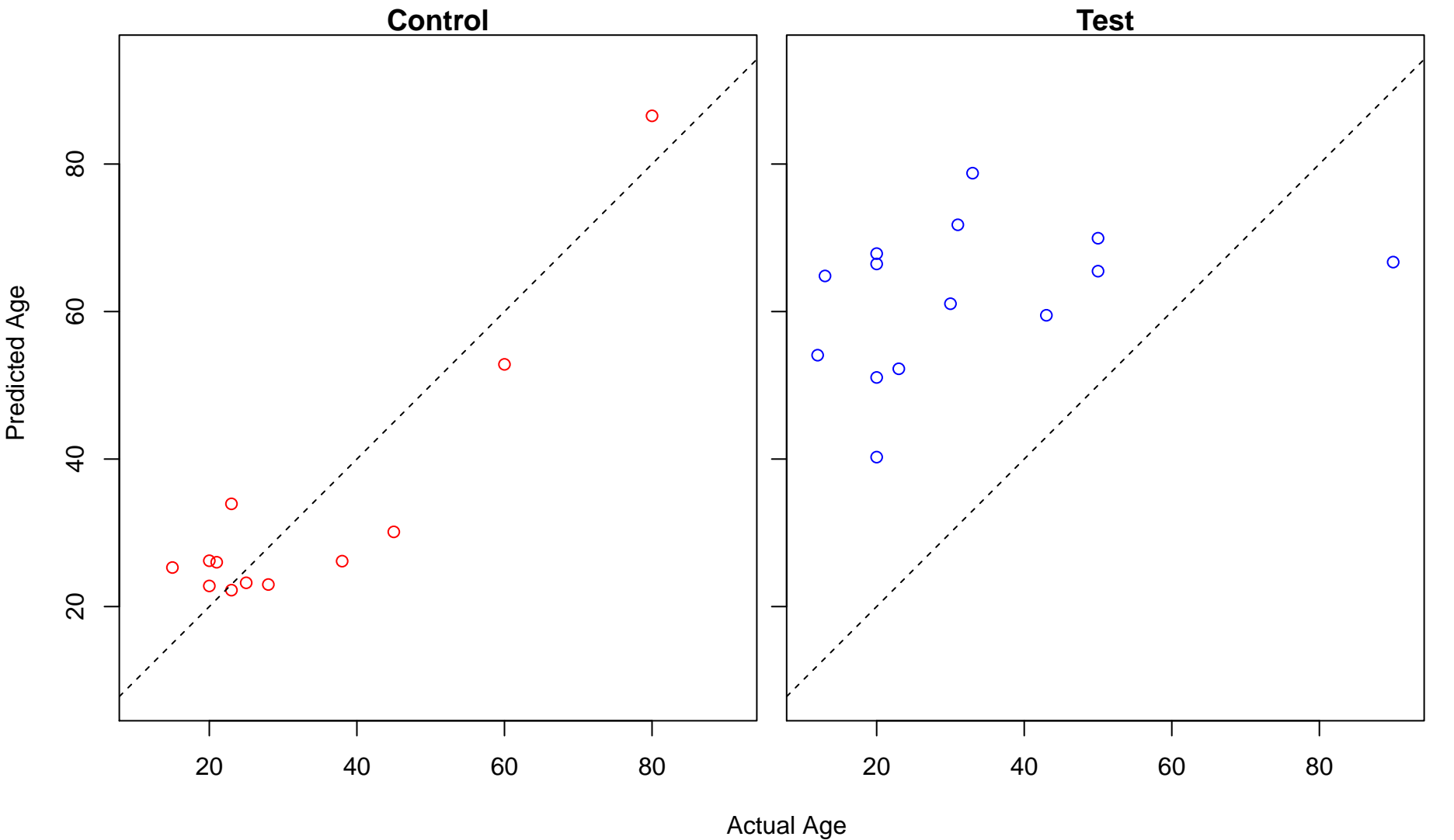
Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (Score



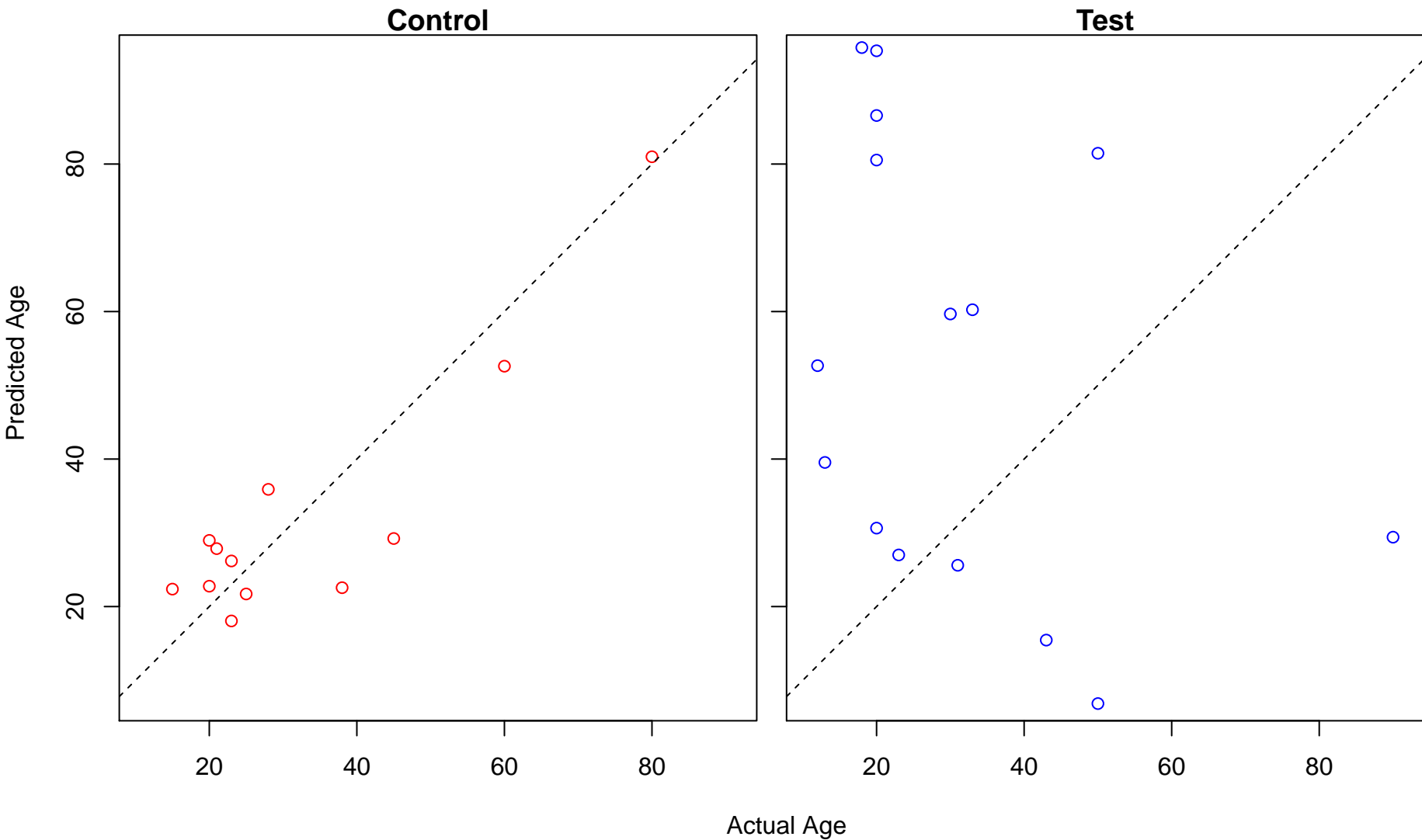
positive regulation of ossification (Score: 9.489492)



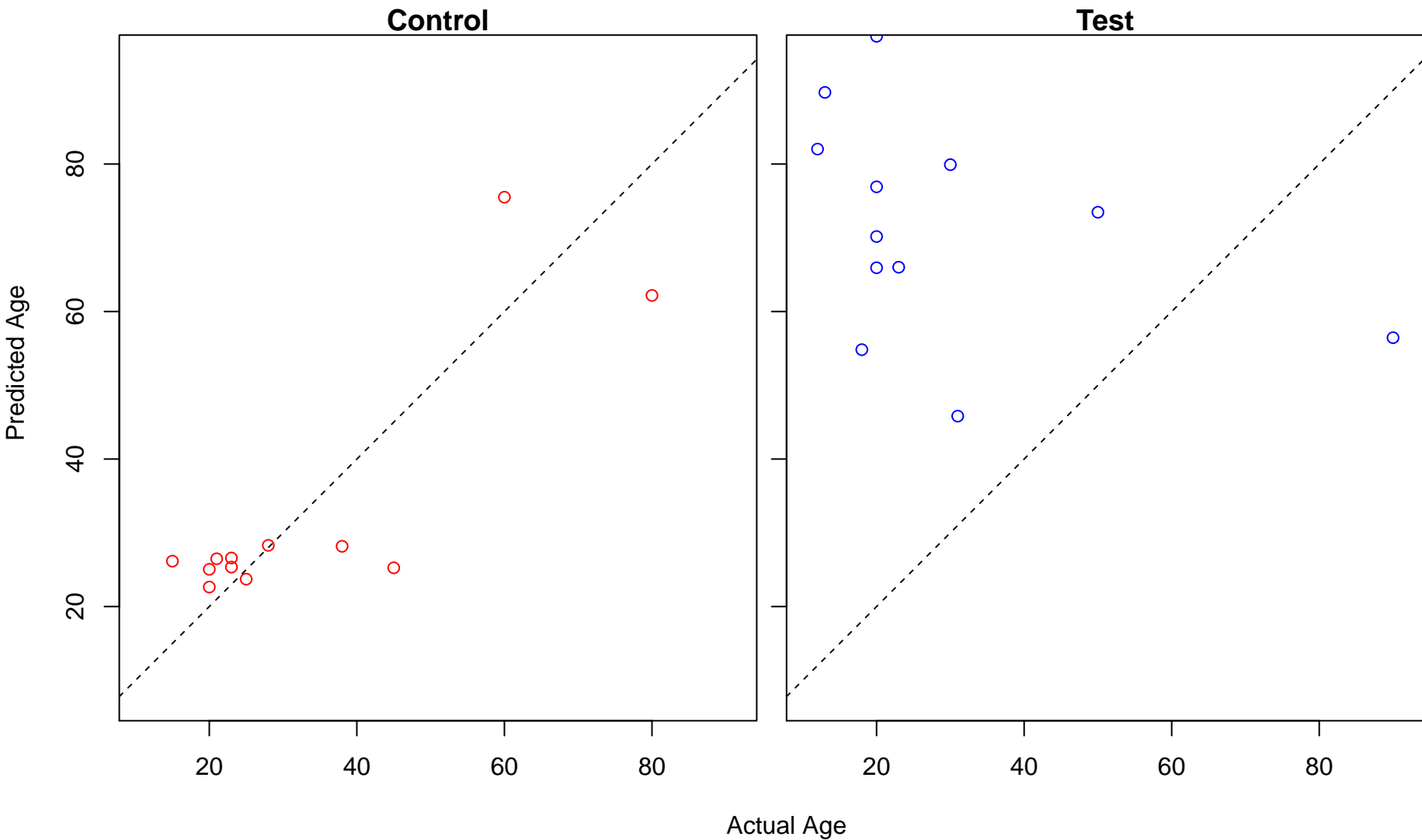
of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling



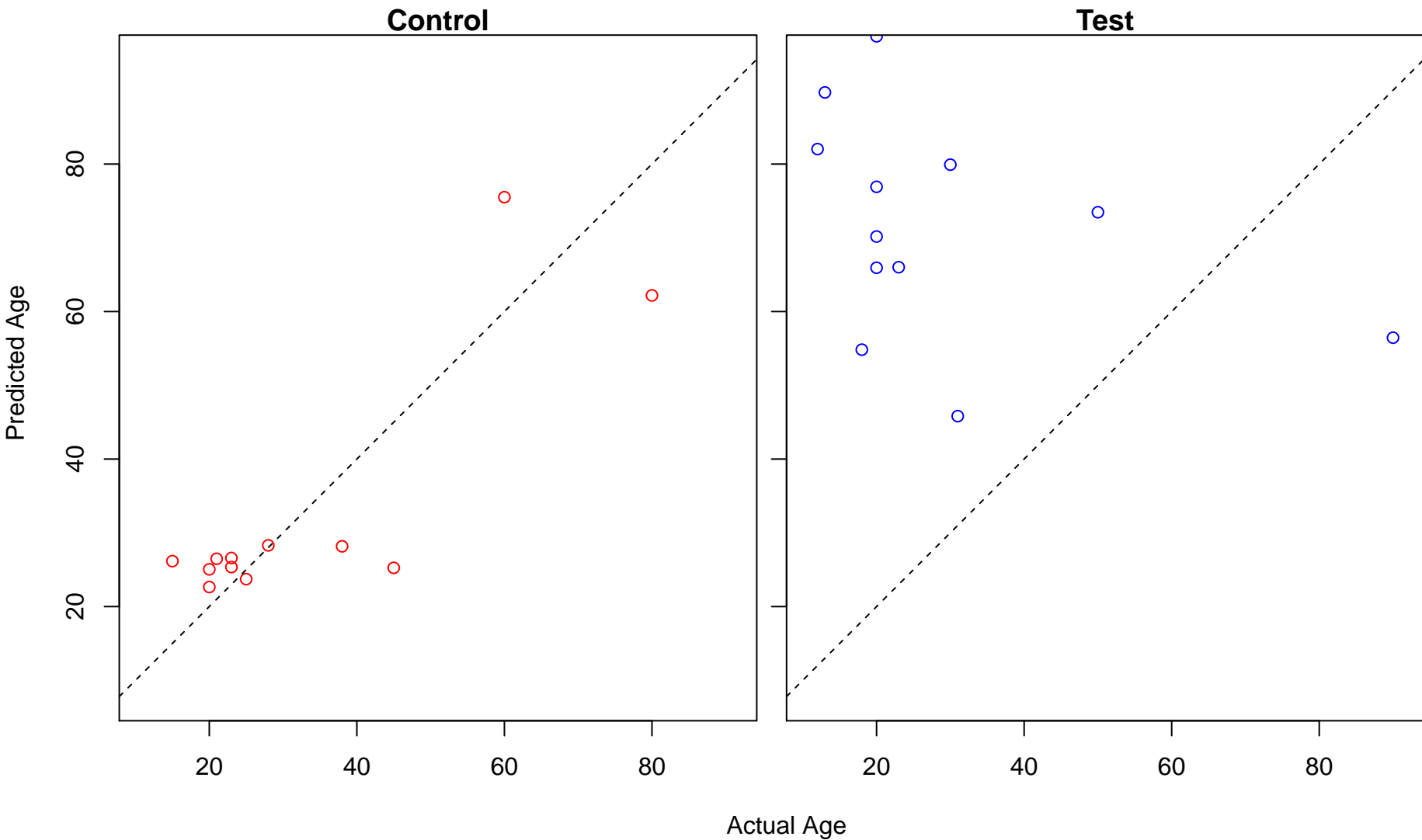
regulation of DNA metabolic process (Score: 9.474233)



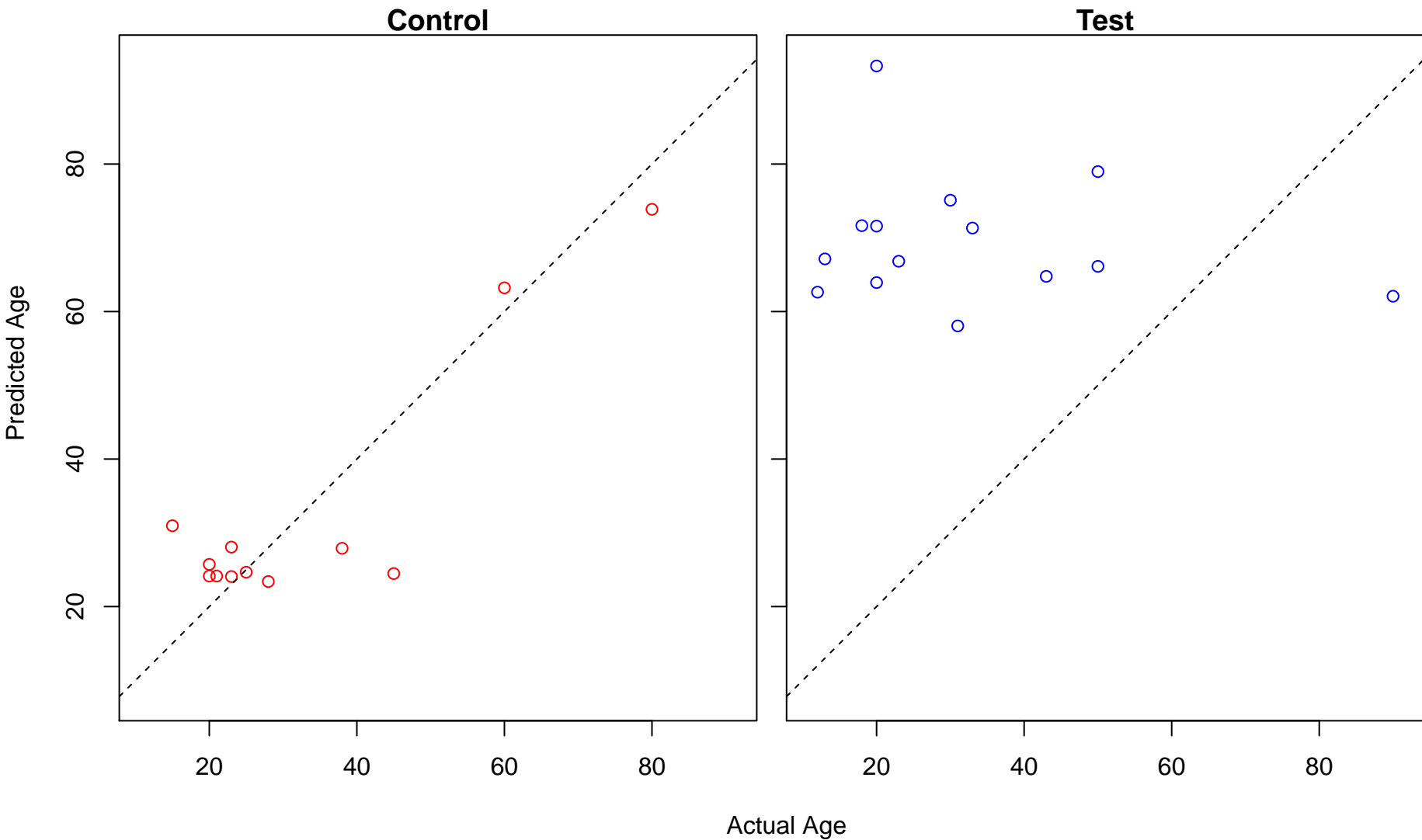
release of sequestered calcium ion into cytosol by sarcoplasmic reticulum (Score: 9.472282)



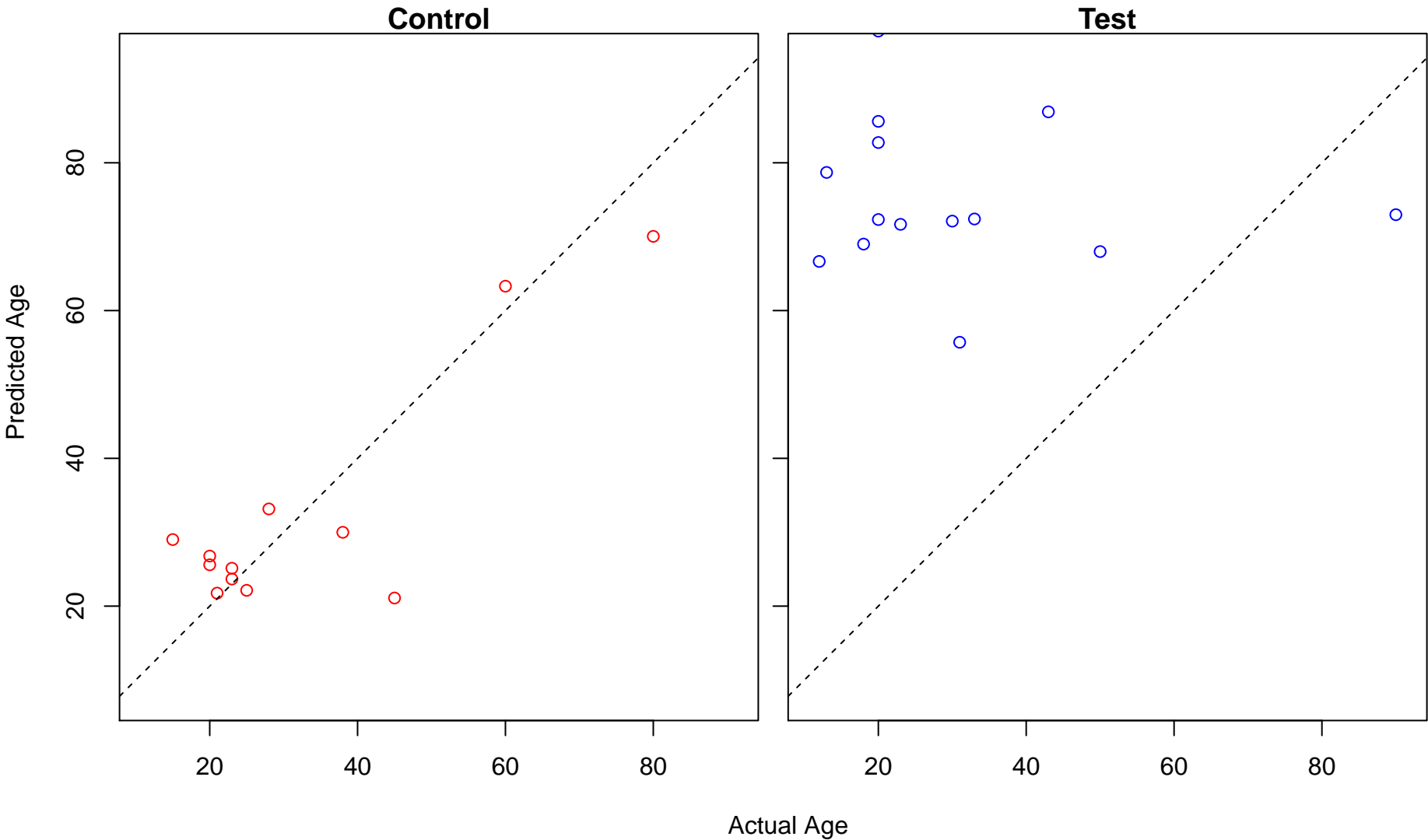
calcium ion transport from endoplasmic reticulum to cytosol (Score: 9.472282)



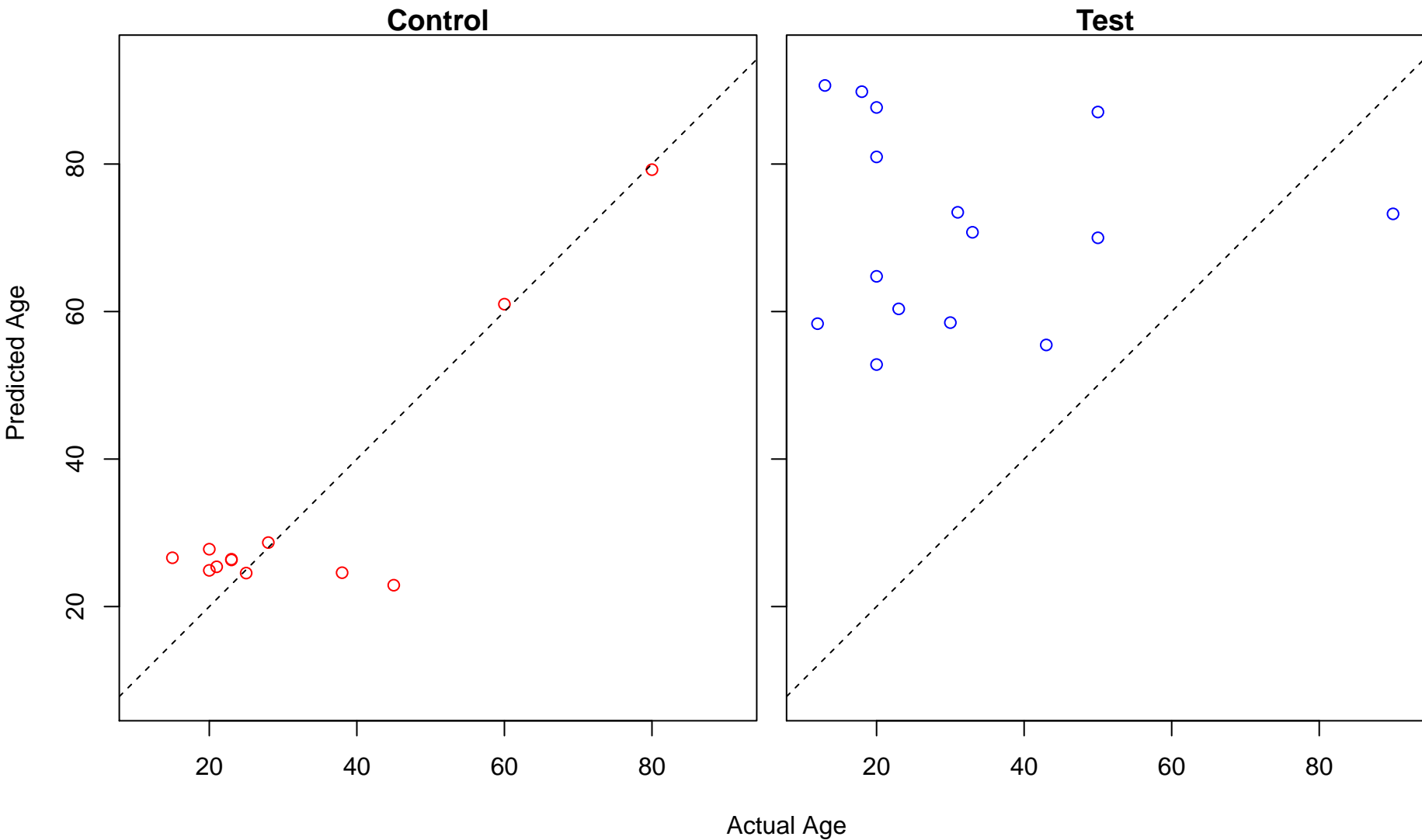
oxaloacetate metabolic process (Score: 9.467676)



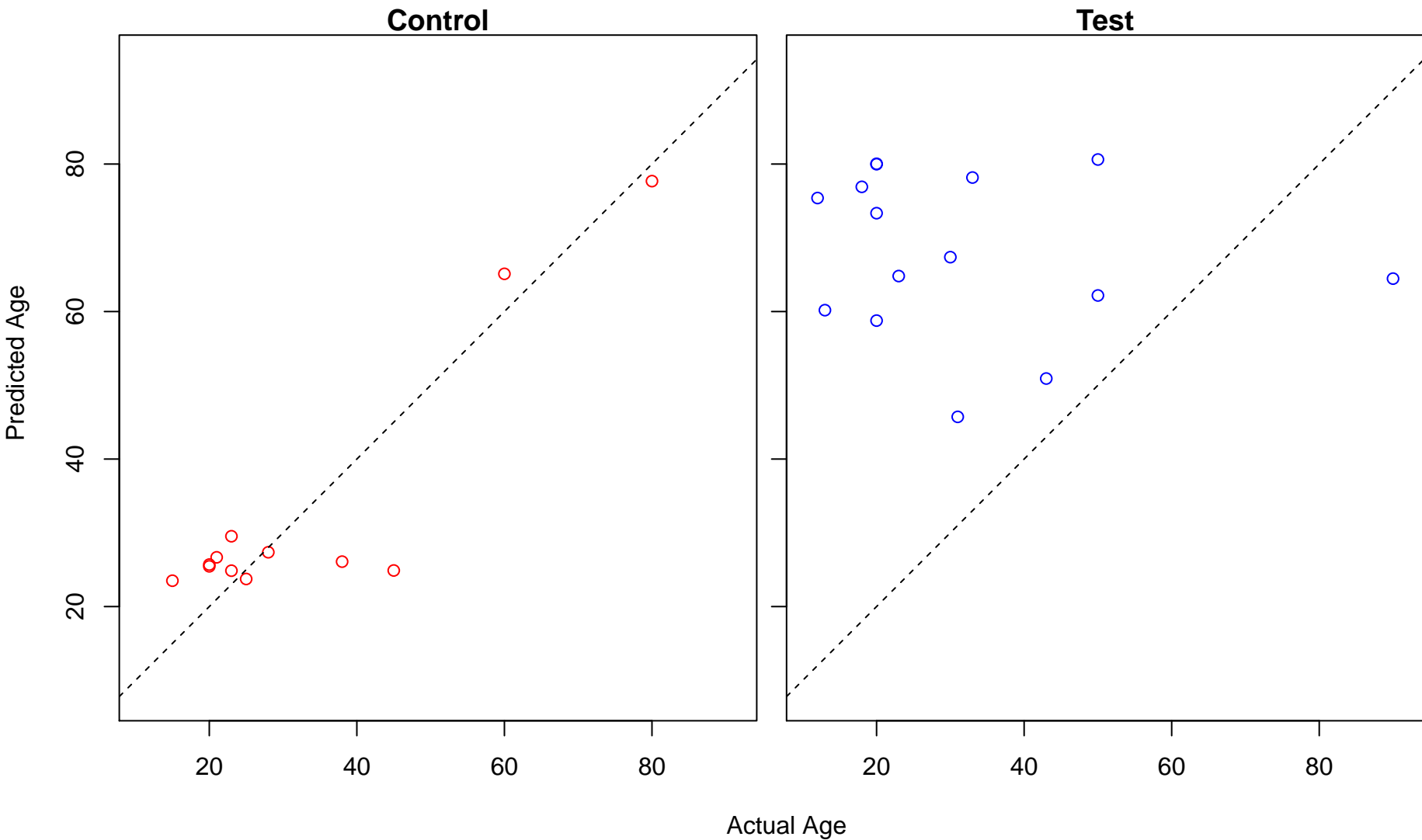
transmembrane receptor protein tyrosine phosphatase signaling pathway (Score: 9.438909)



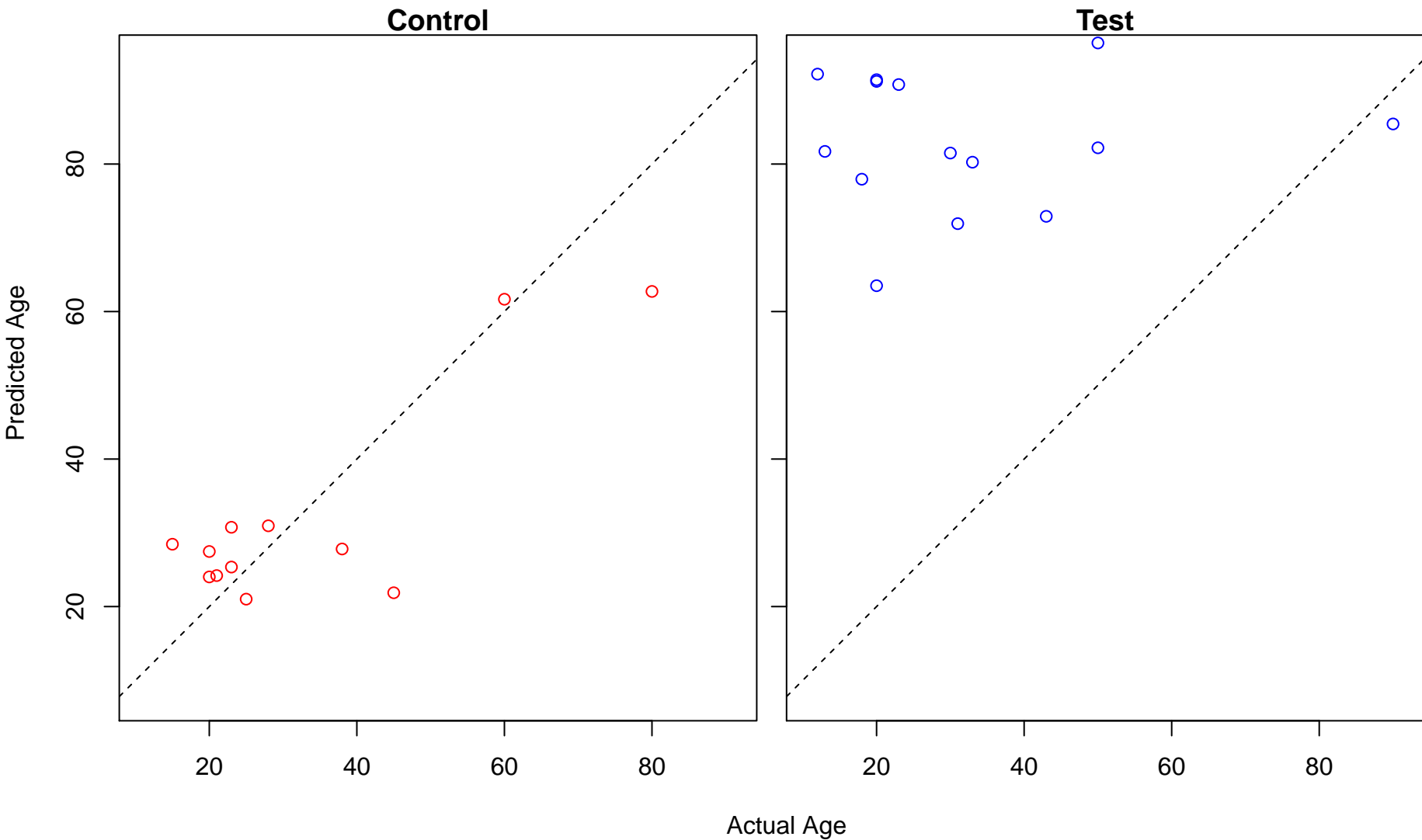
regulation of intracellular protein transport (Score: 9.434096)



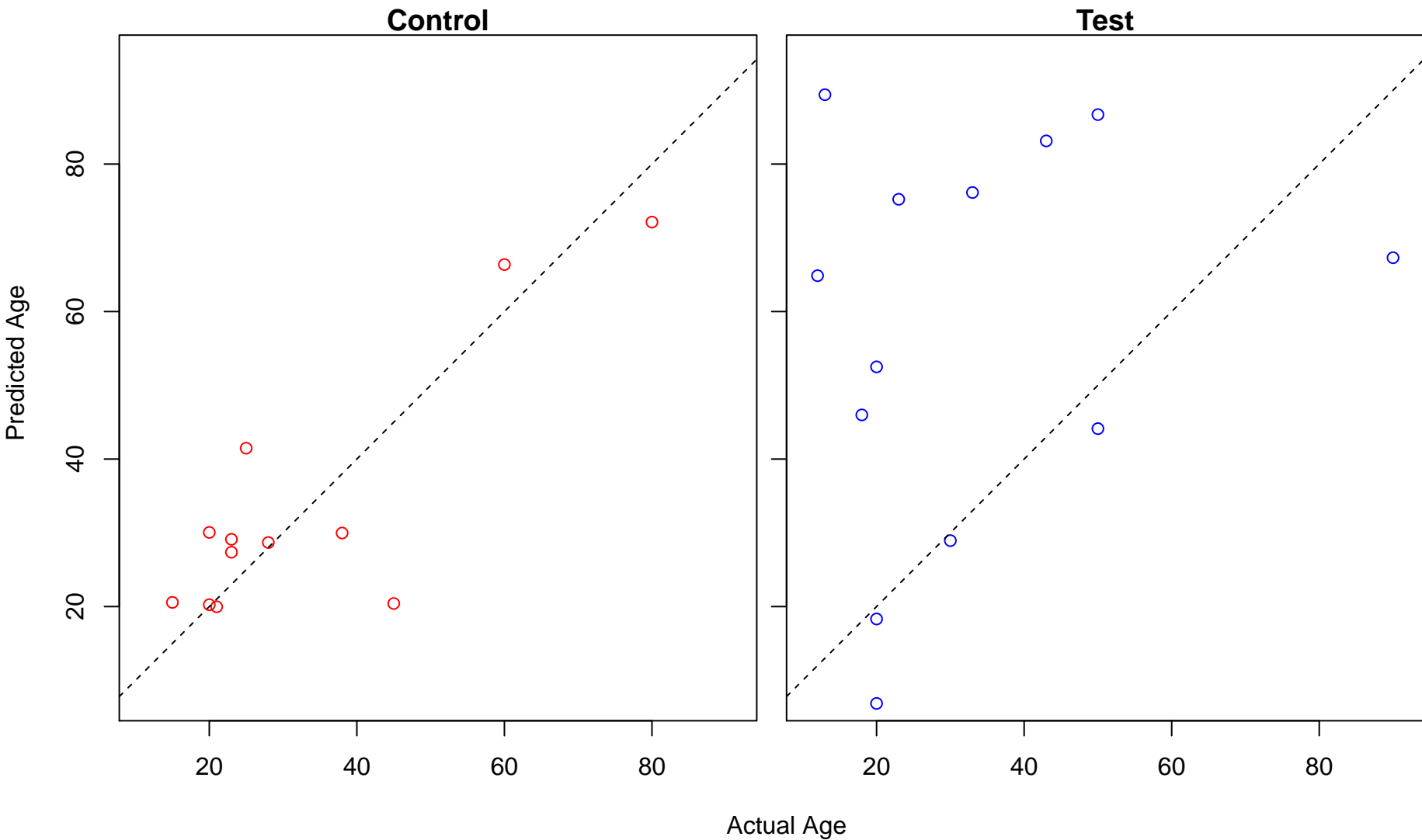
neural crest cell migration (Score: 9.425842)



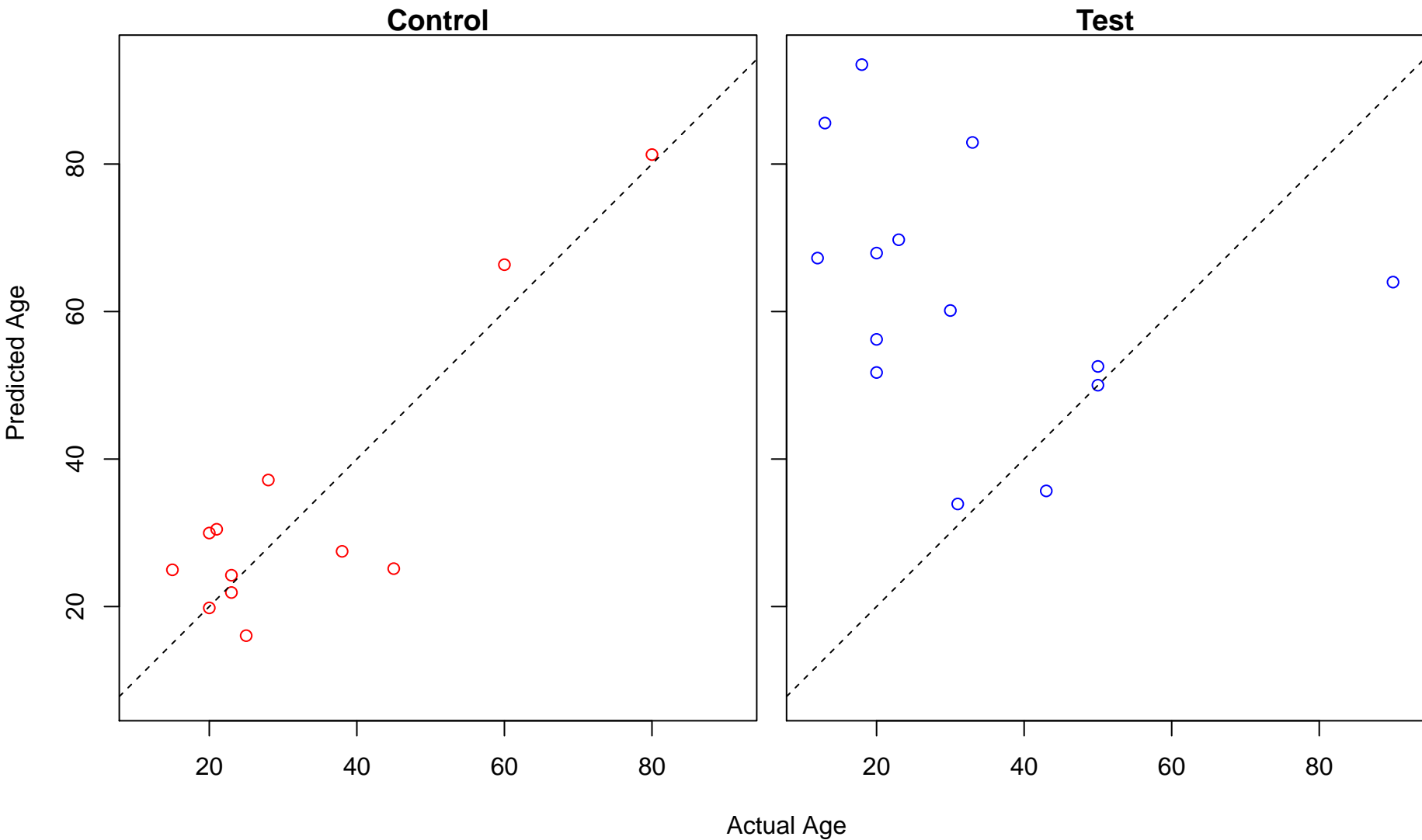
C4-dicarboxylate transport (Score: 9.424862)



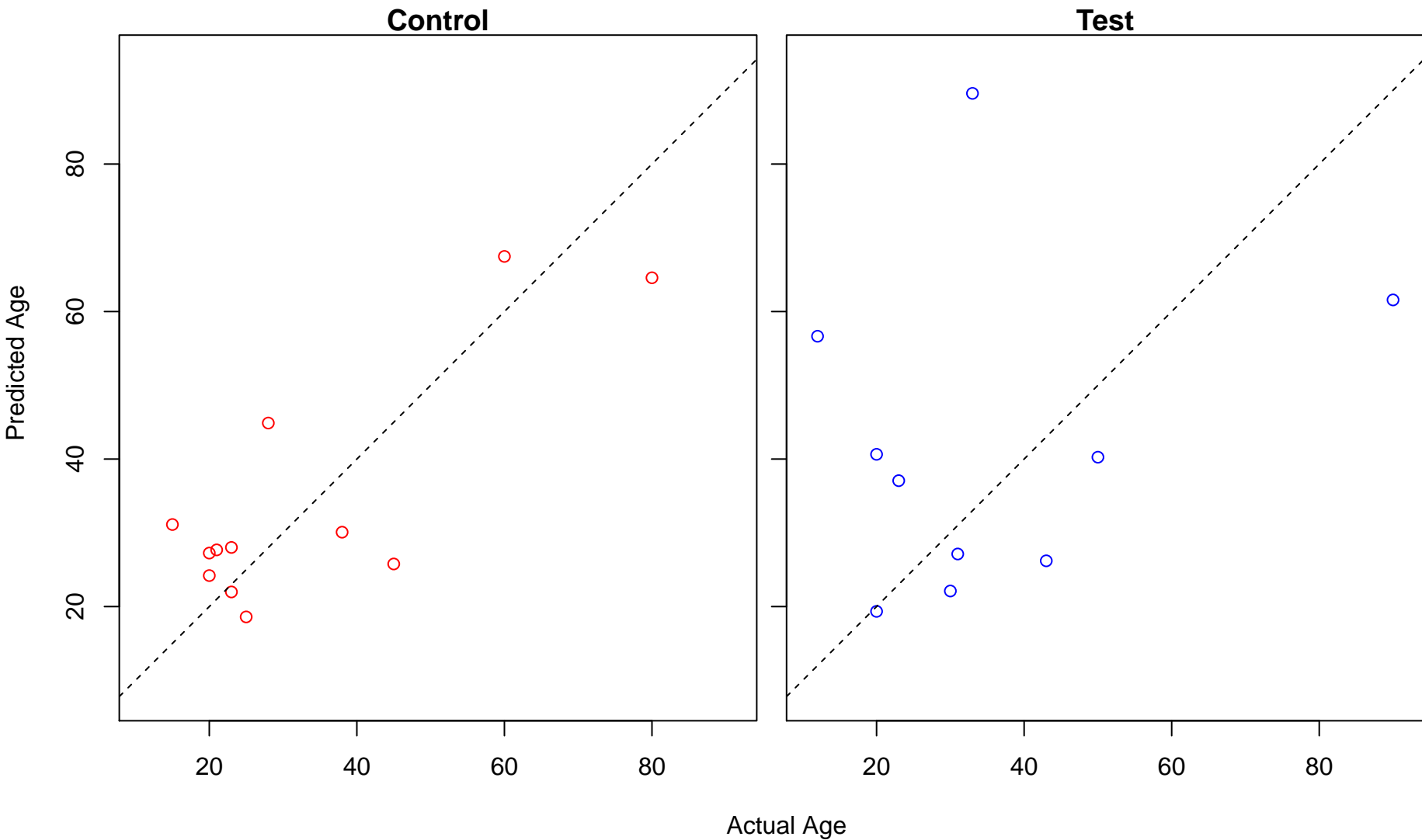
interleukin-1 production (Score: 9.423829)



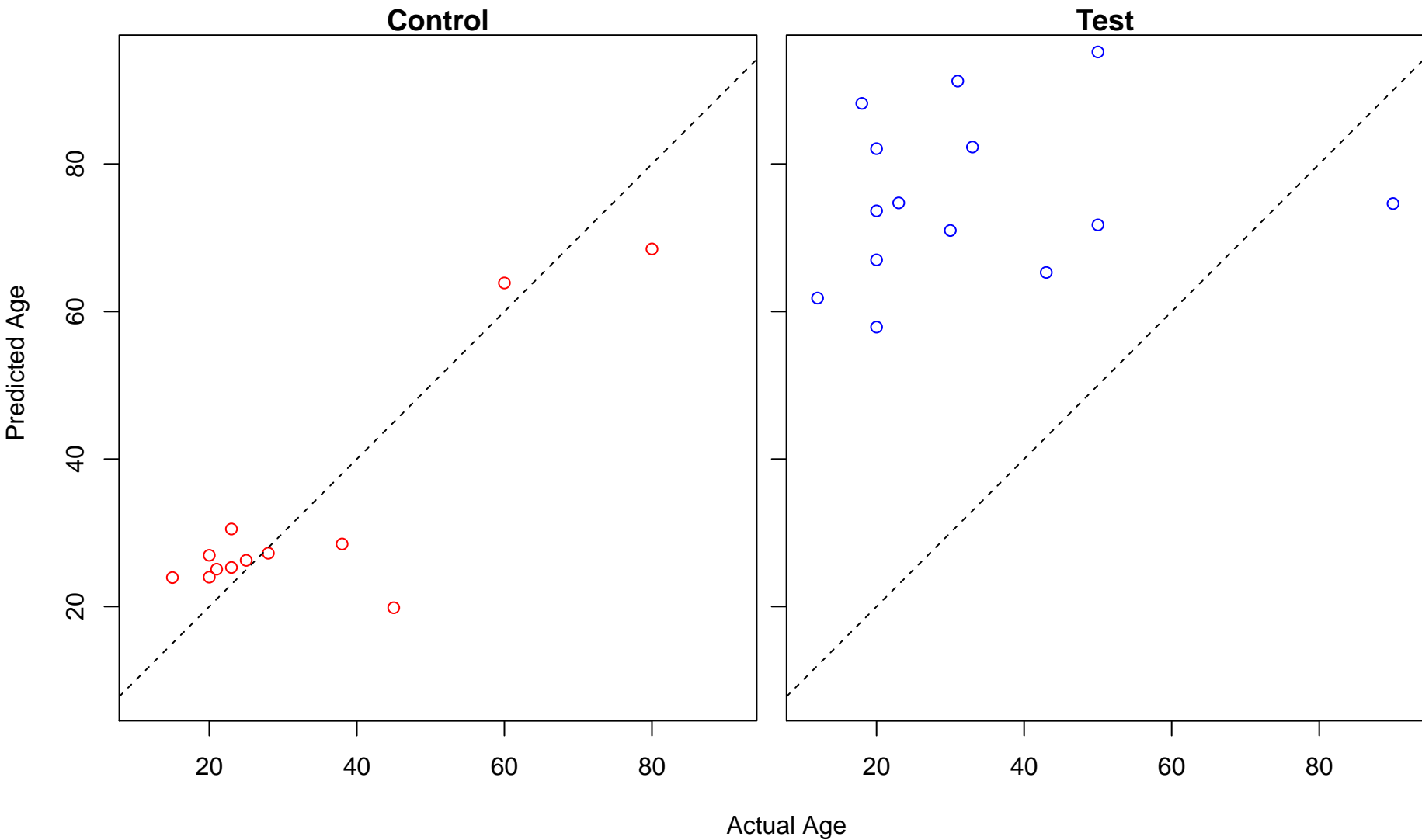
intracellular protein transport (Score: 9.417887)



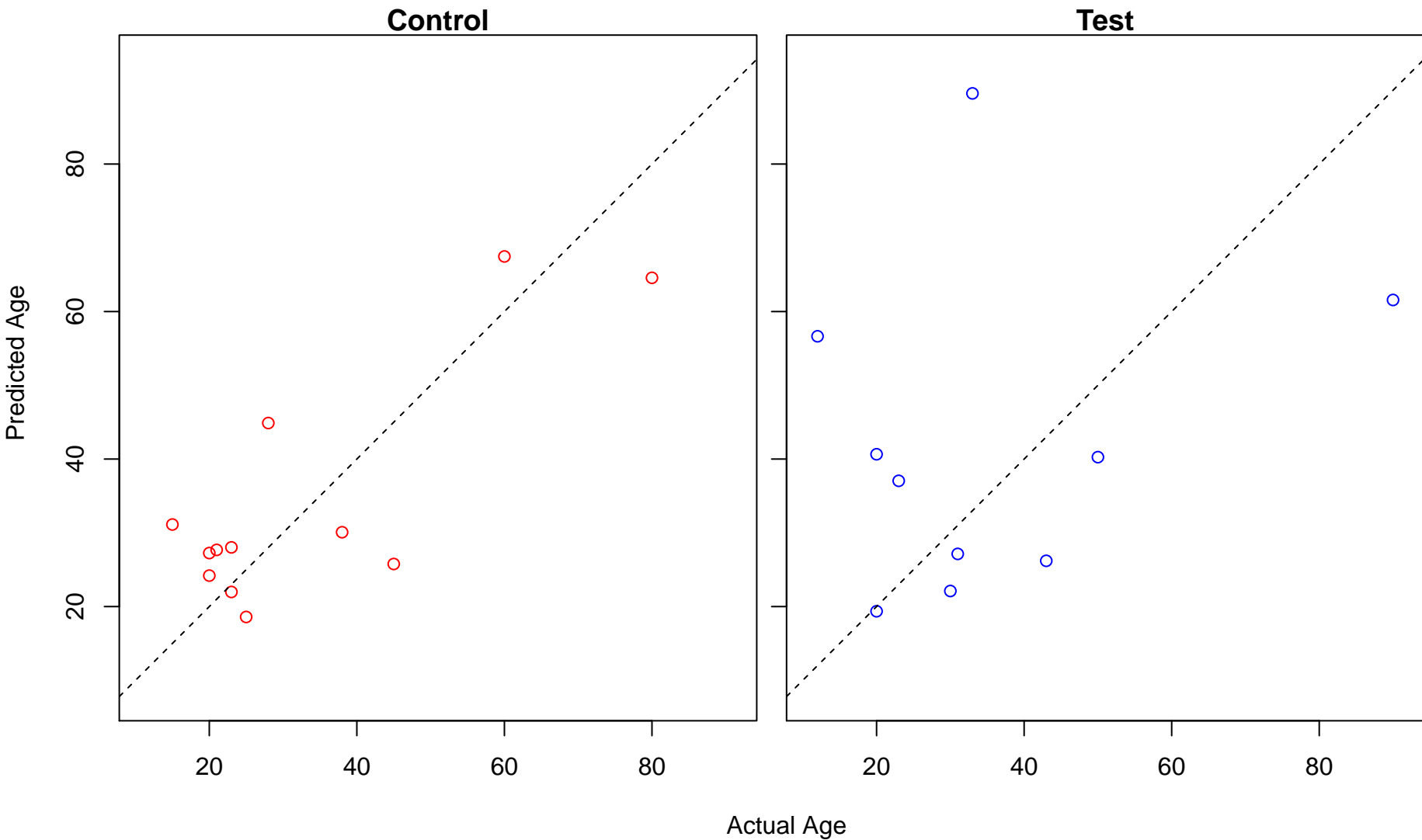
neurotrophin TRK receptor signaling pathway (Score: 9.412980)



antigen processing and presentation of endogenous peptide antigen via MHC class I (Score: 9.41163)

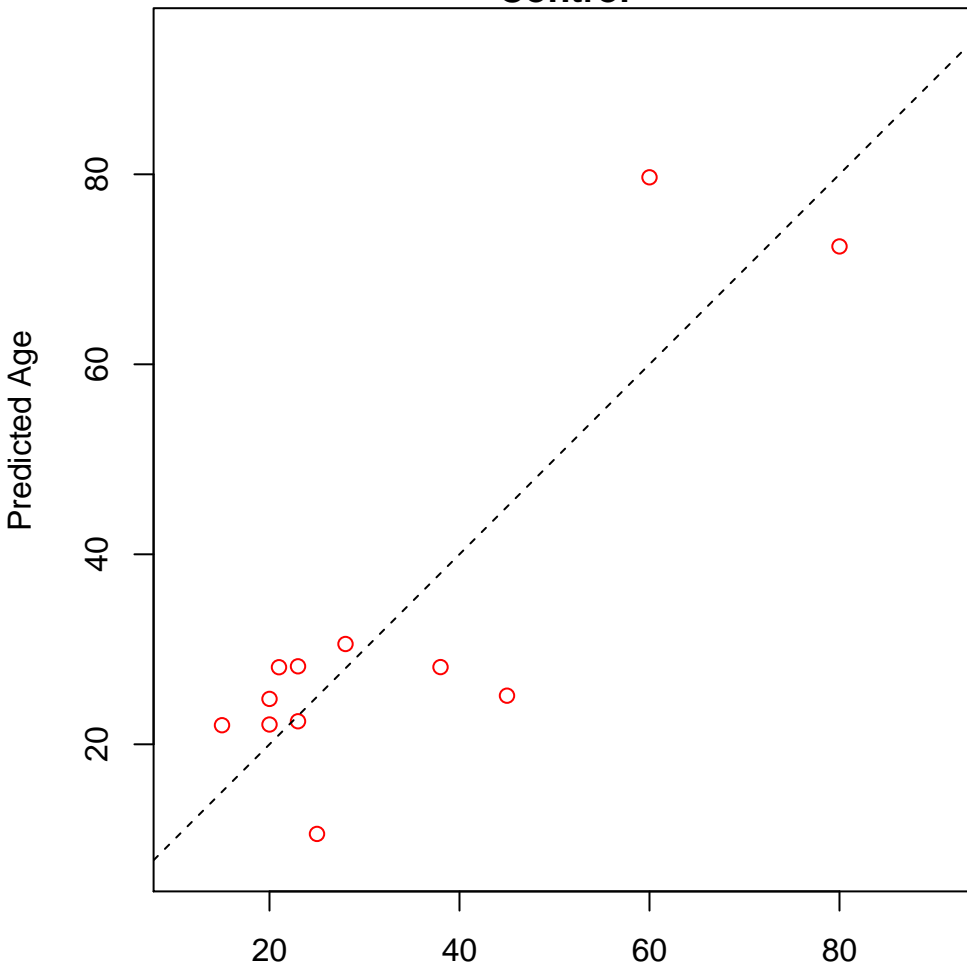


neurotrophin signaling pathway (Score: 9.411232)

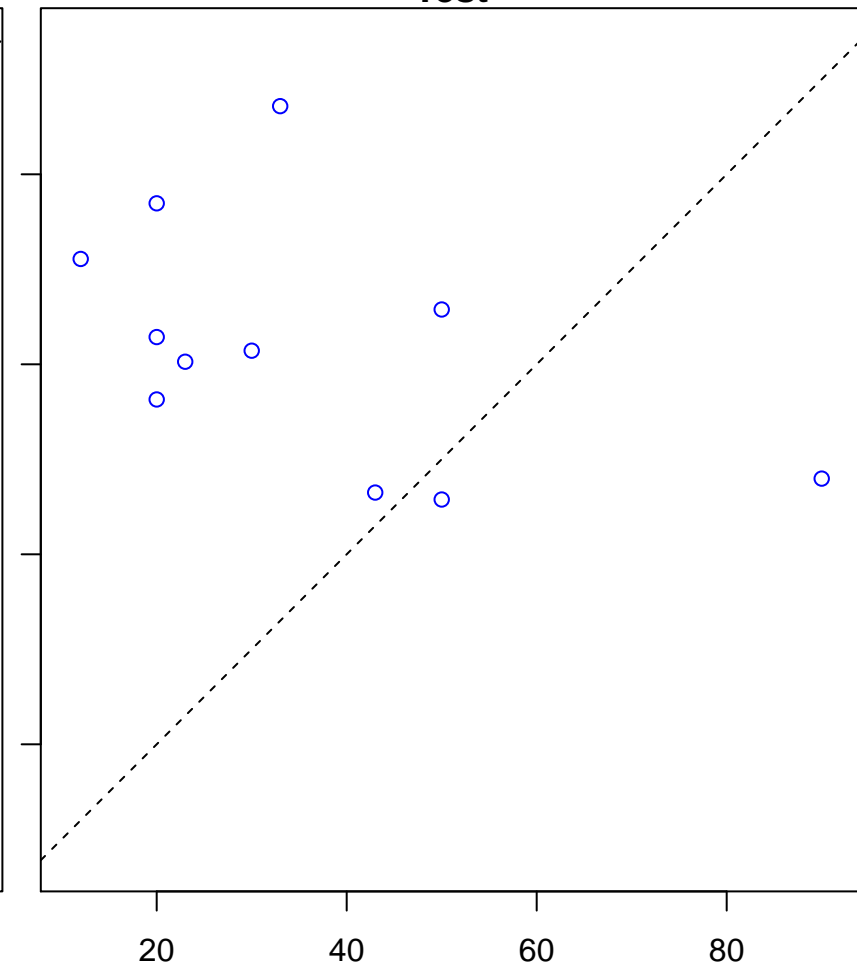


natural killer cell mediated immunity (Score: 9.403518)

Control

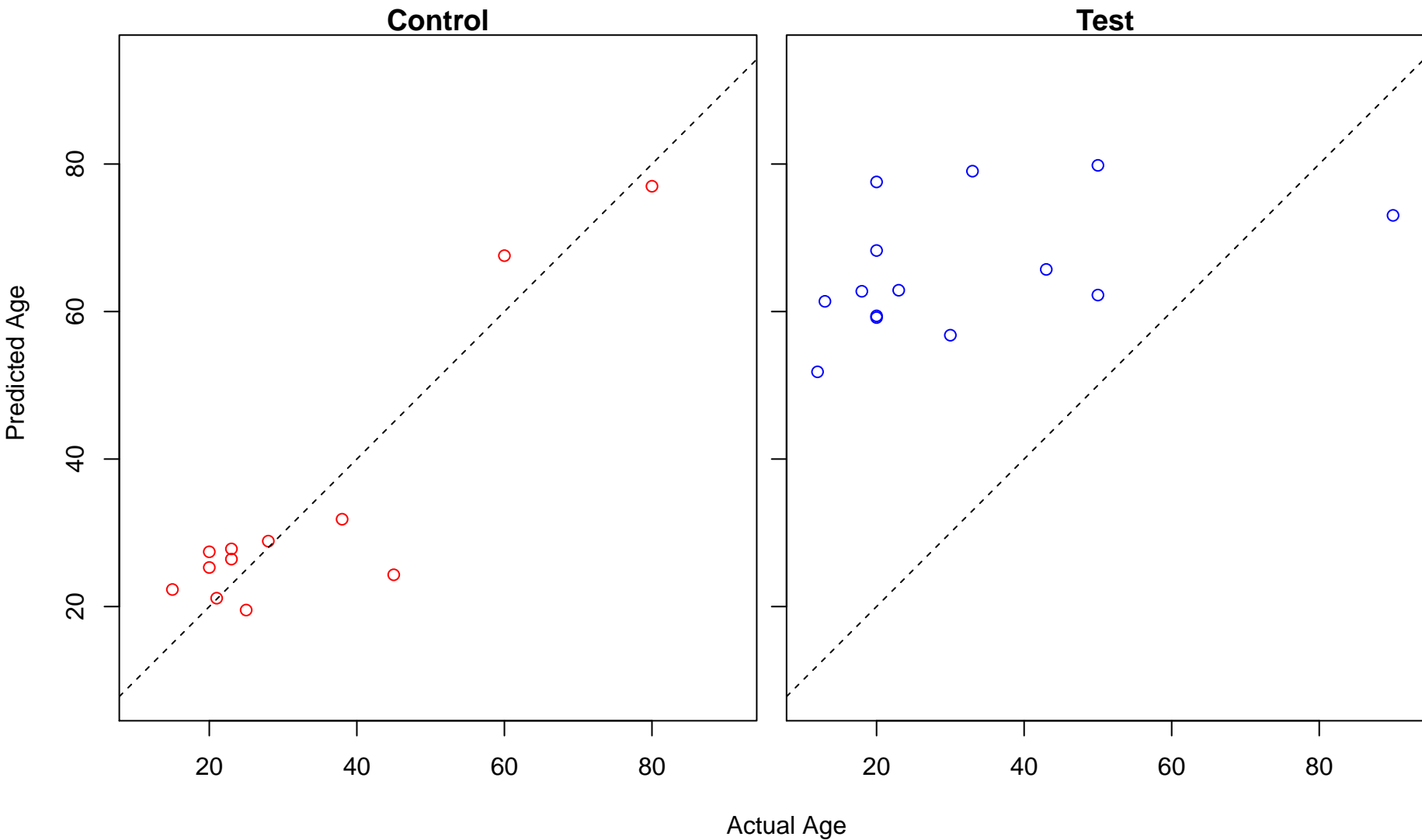


Test

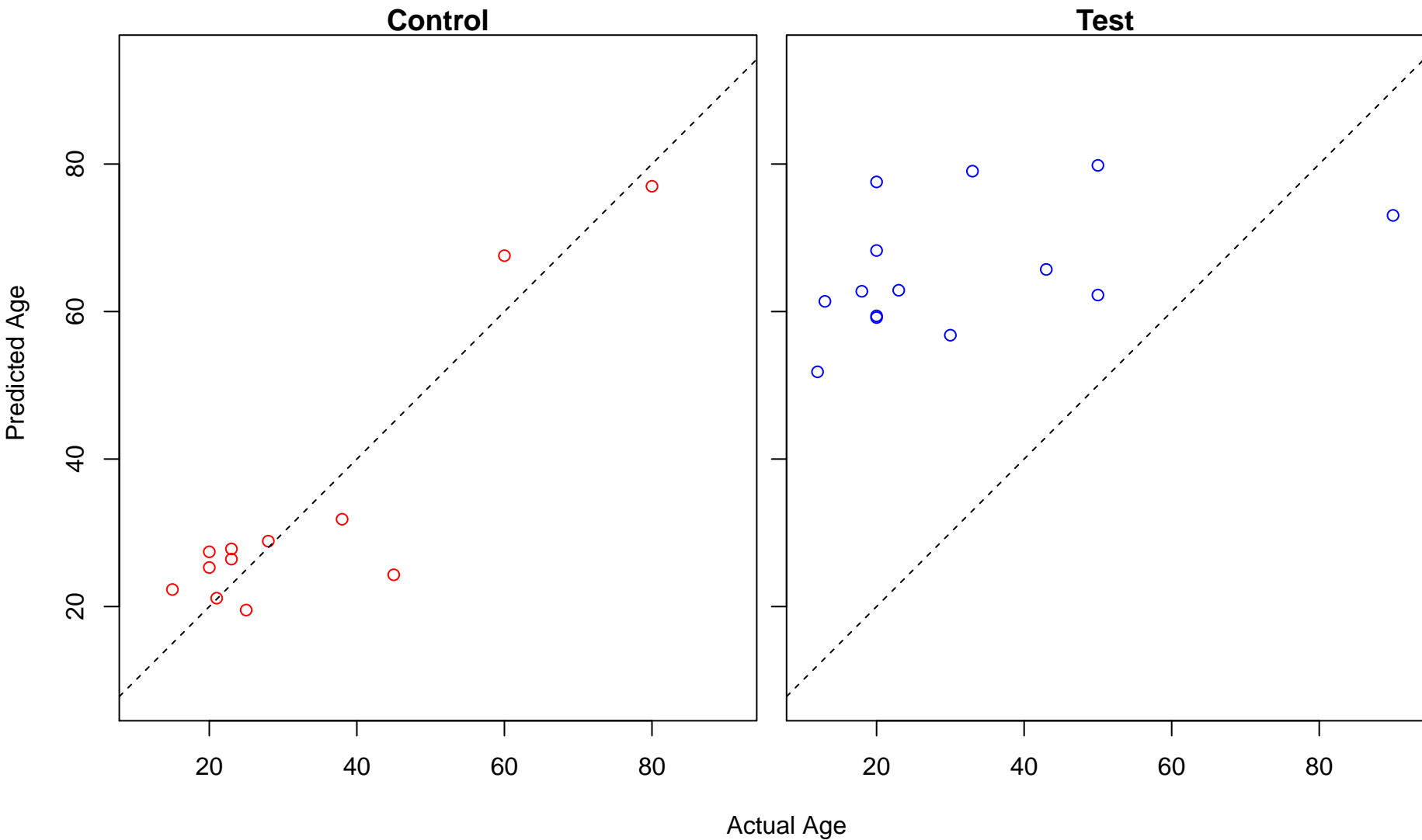


Actual Age

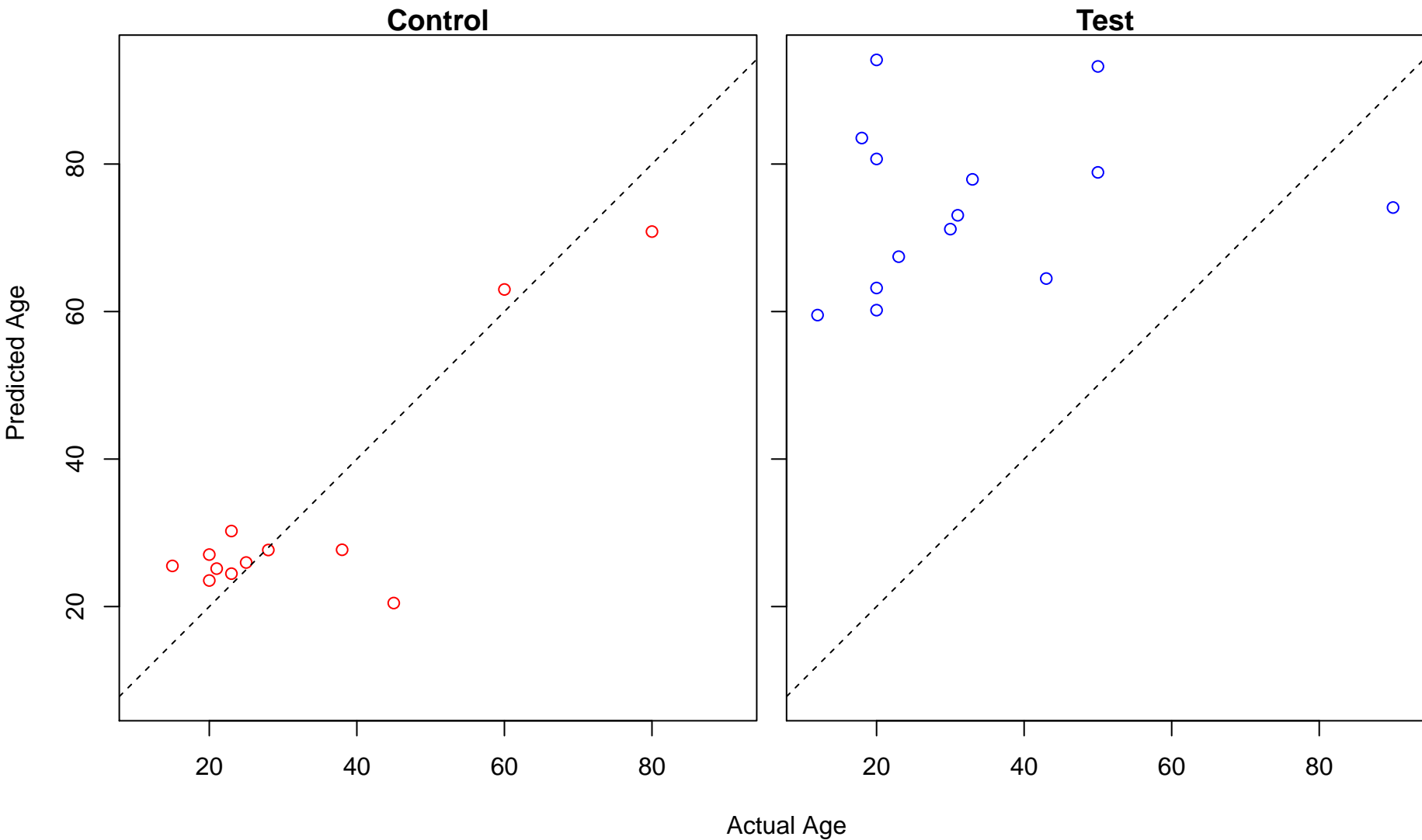
digestive tract development (Score: 9.403008)



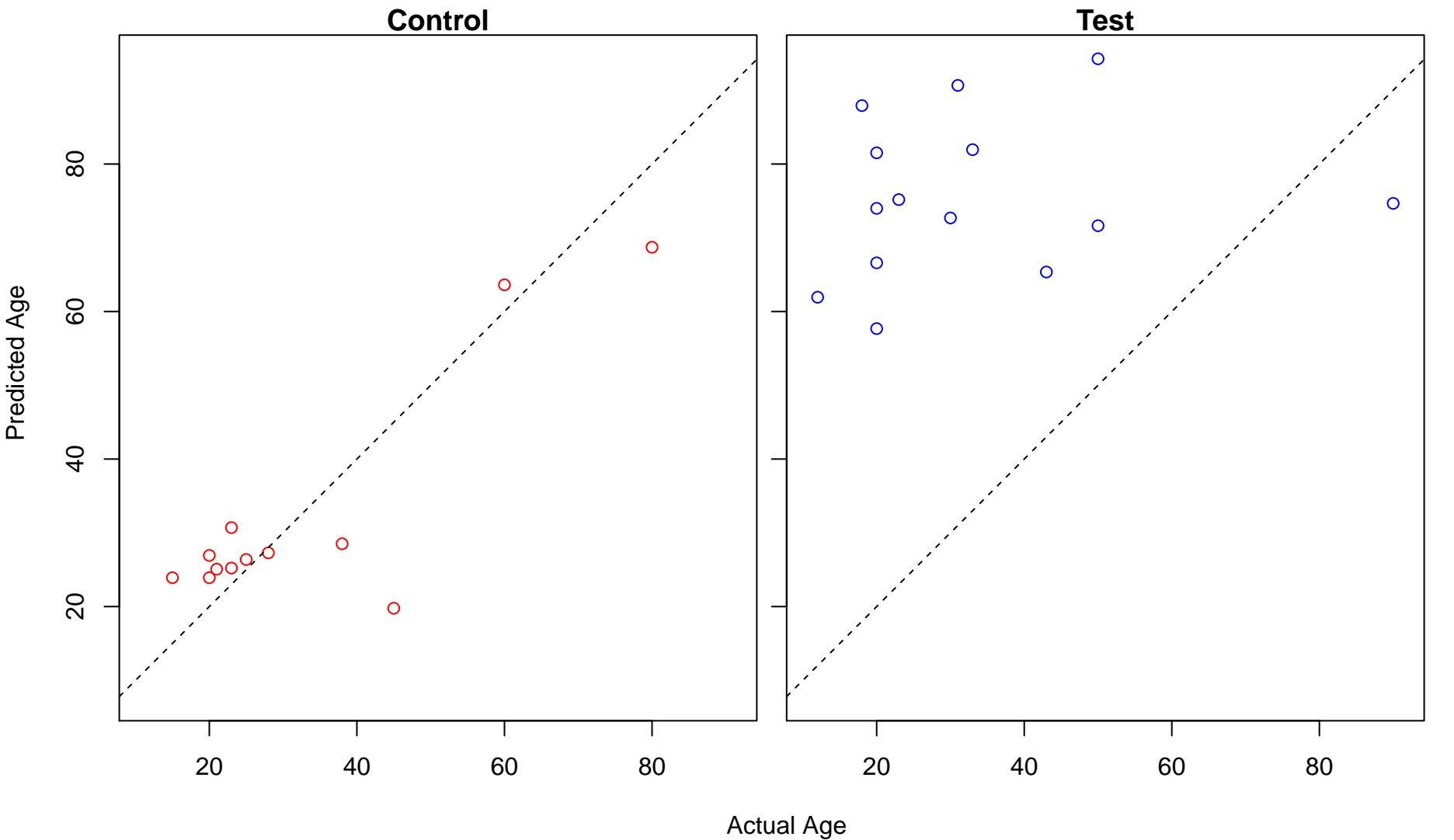
digestive system development (Score: 9.403008)



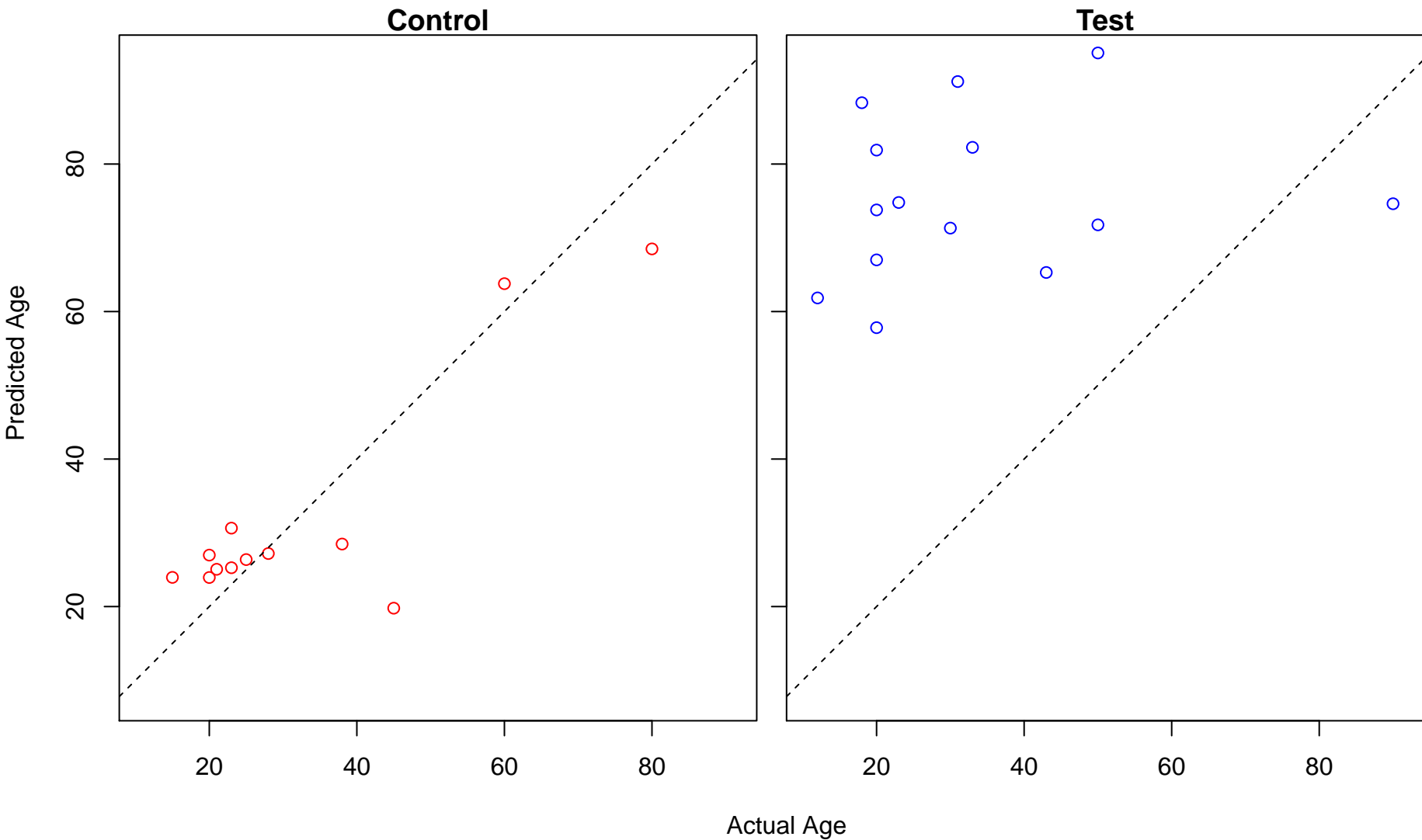
negative regulation of immune effector process (Score: 9.385409)



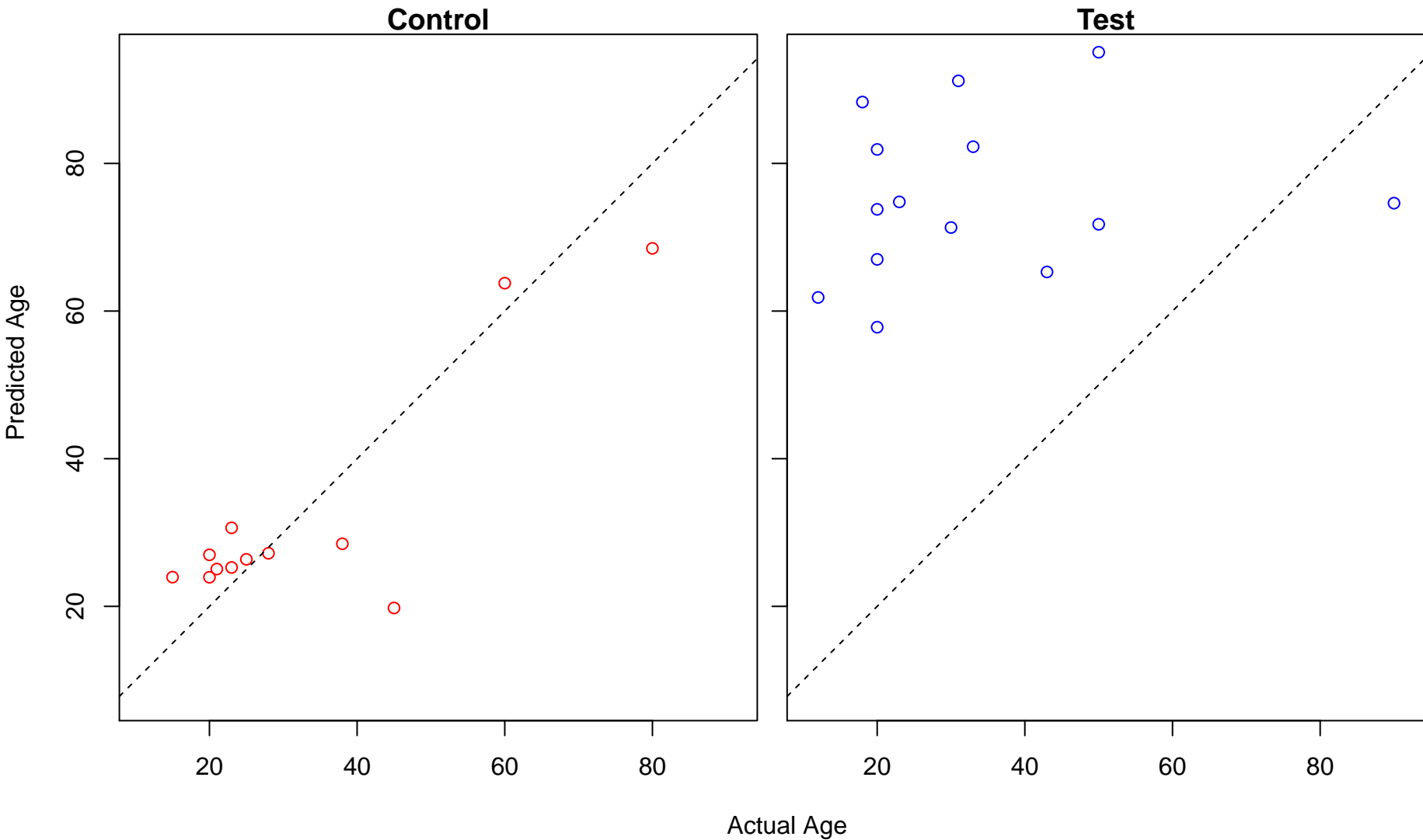
Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent (Score



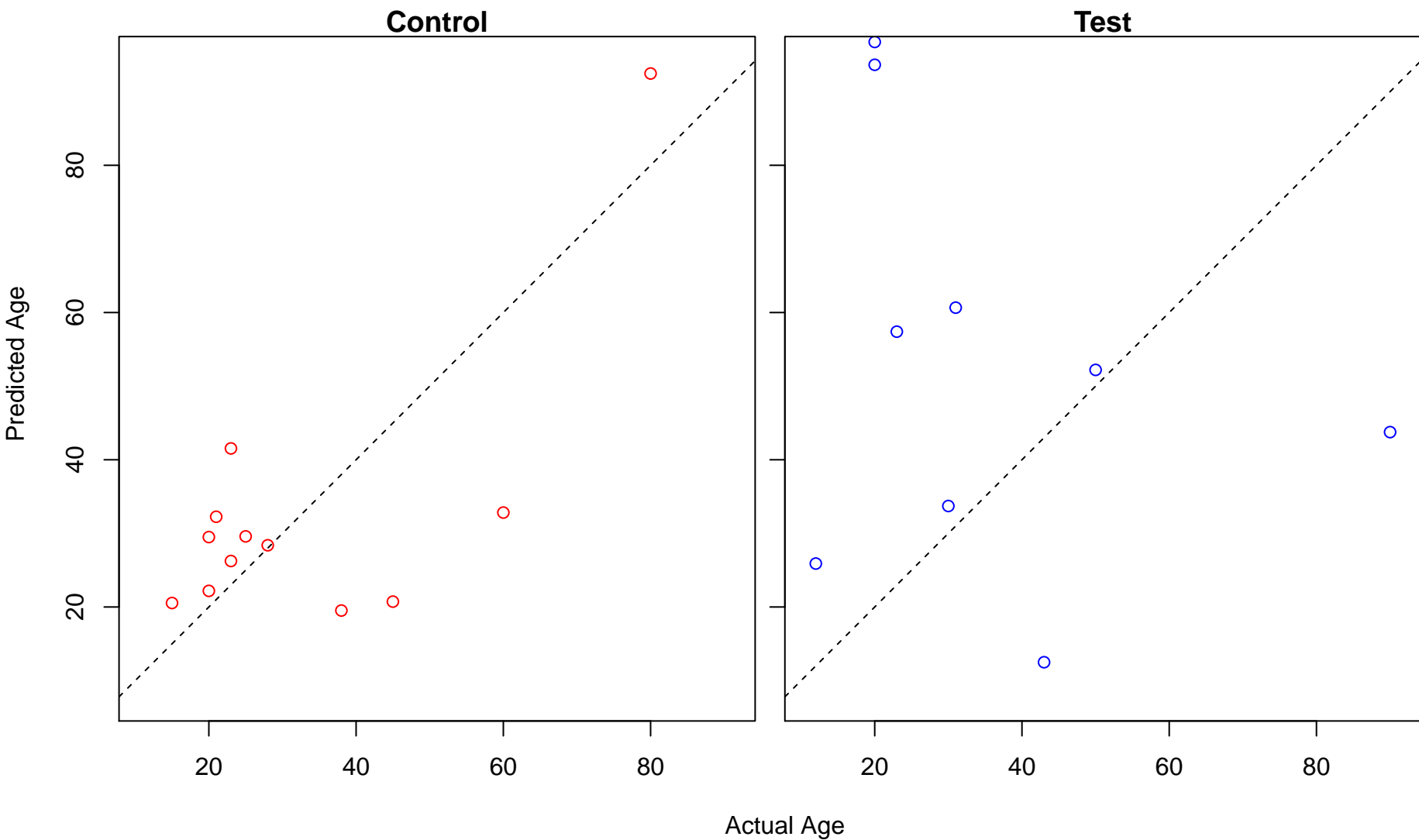
antigen processing and presentation of endogenous peptide antigen (Score: 9.371874)



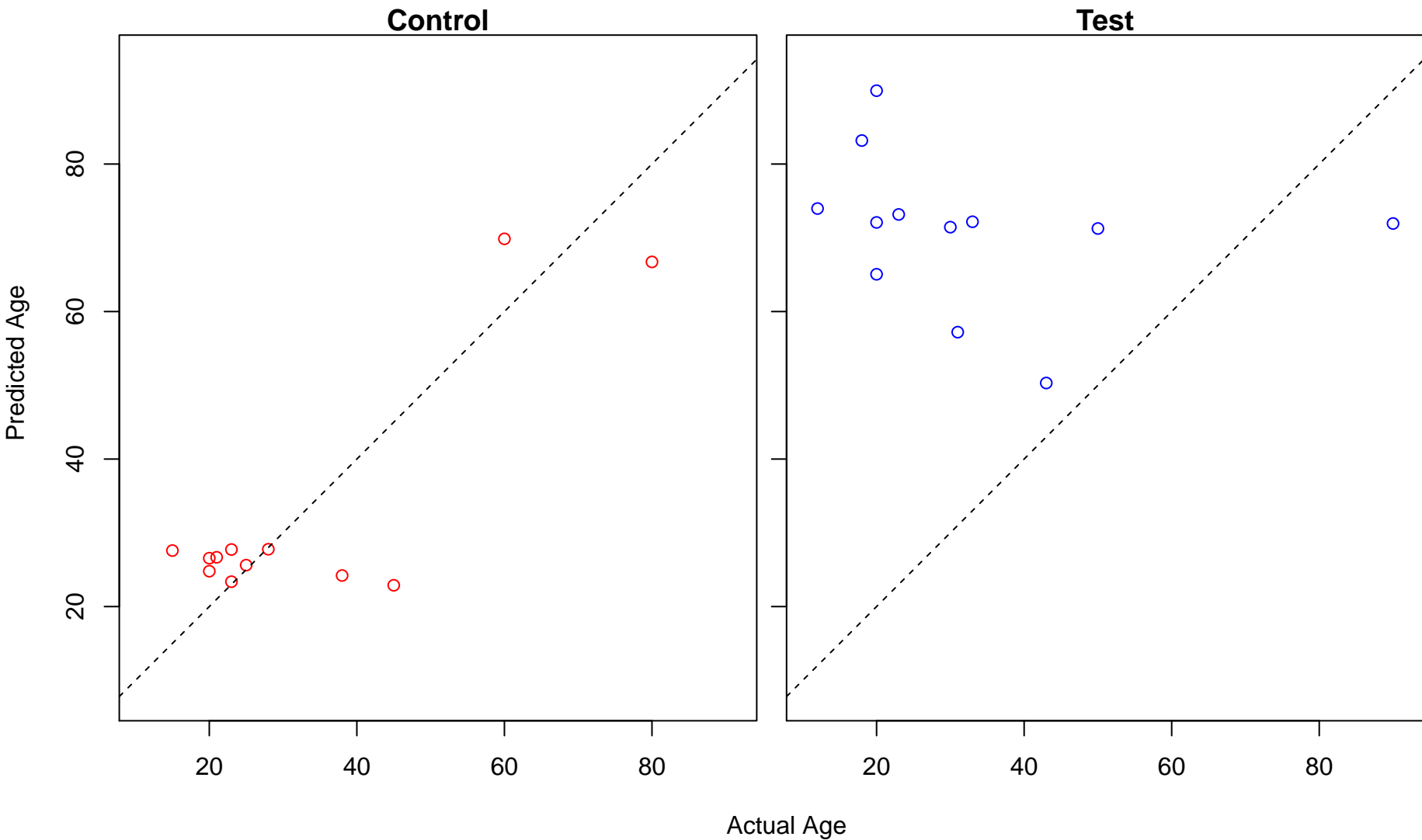
antigen processing and presentation of endogenous antigen (Score: 9.371864)



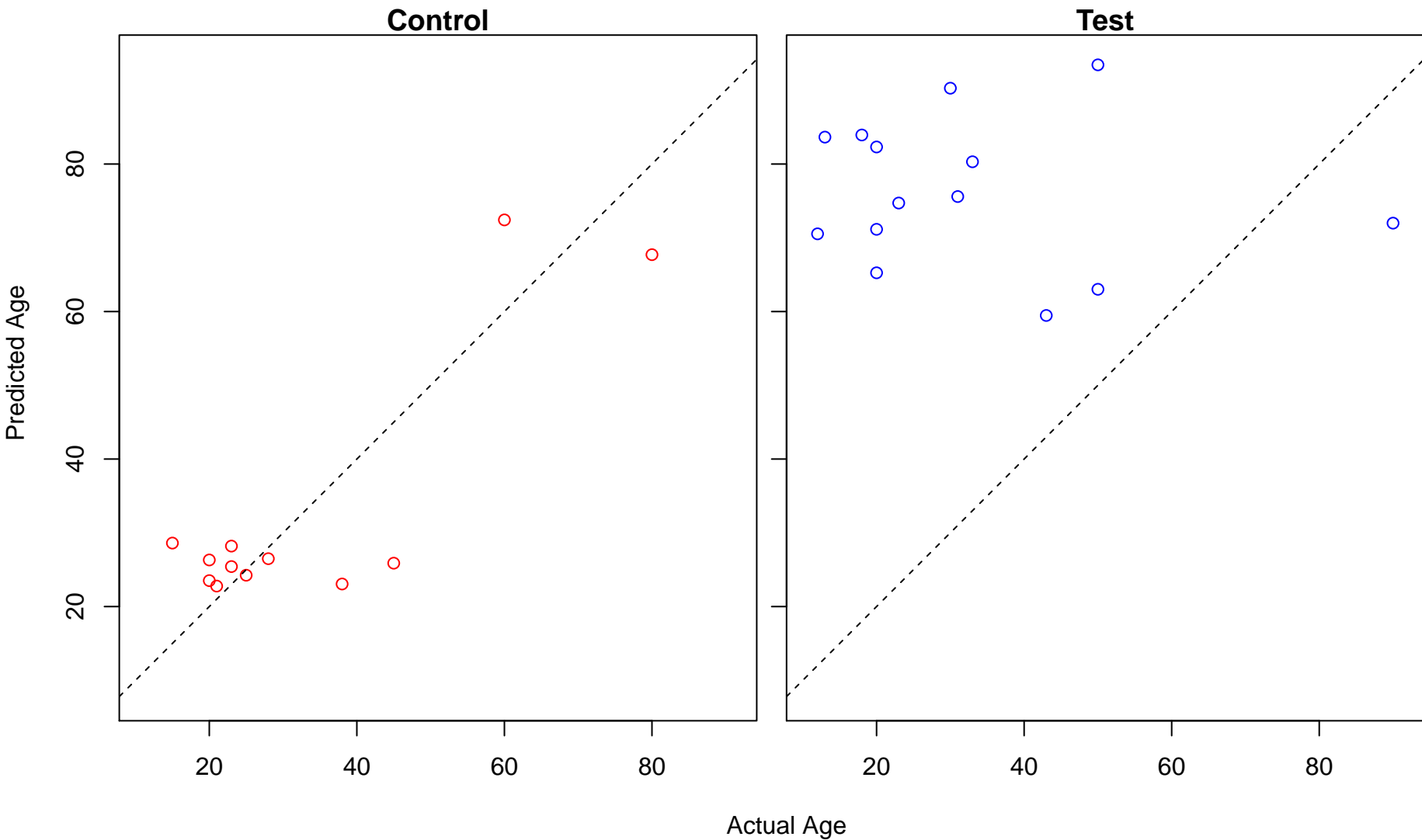
SMAD protein import into nucleus (Score: 9.369852)



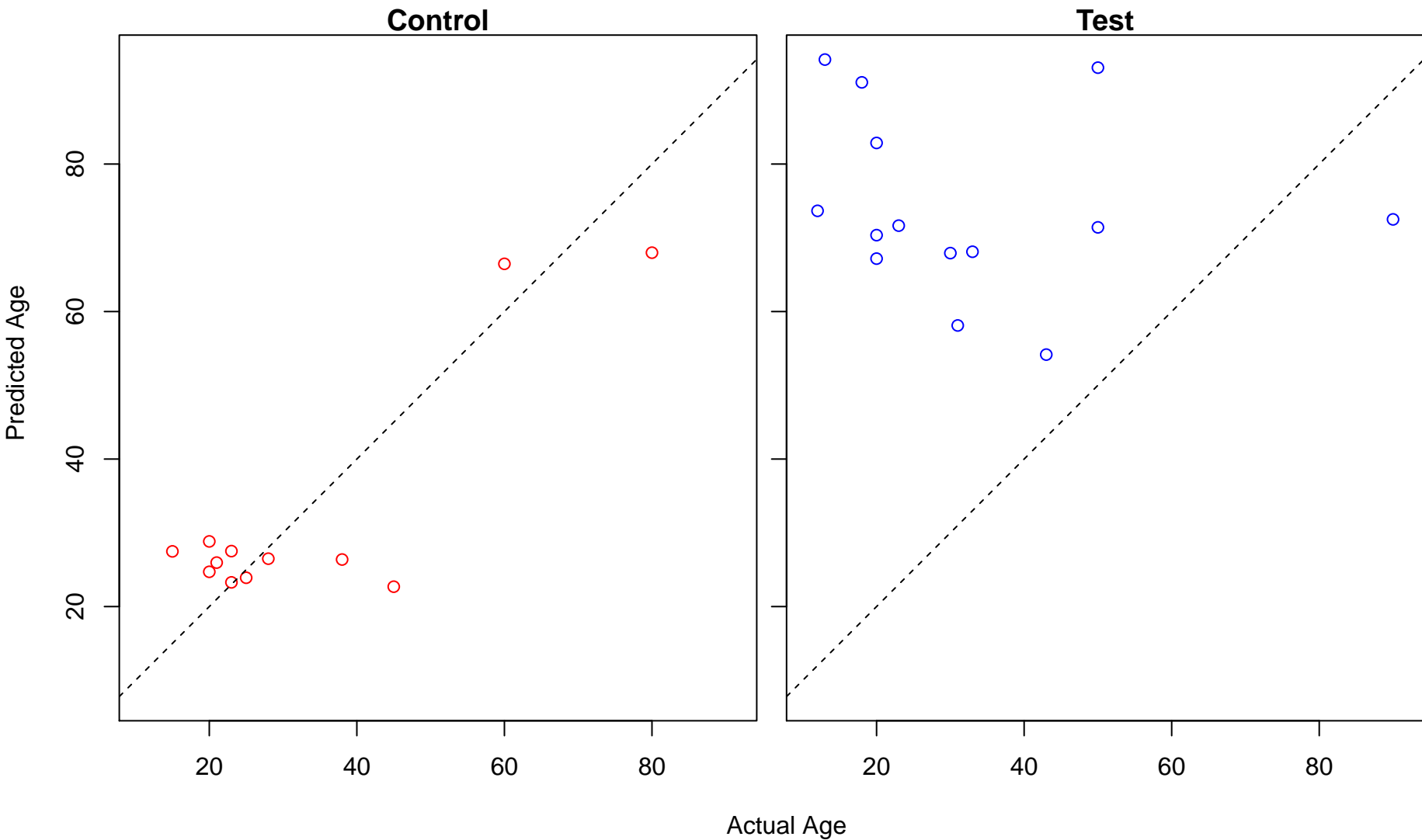
viral release from host cell (Score: 9.357188)



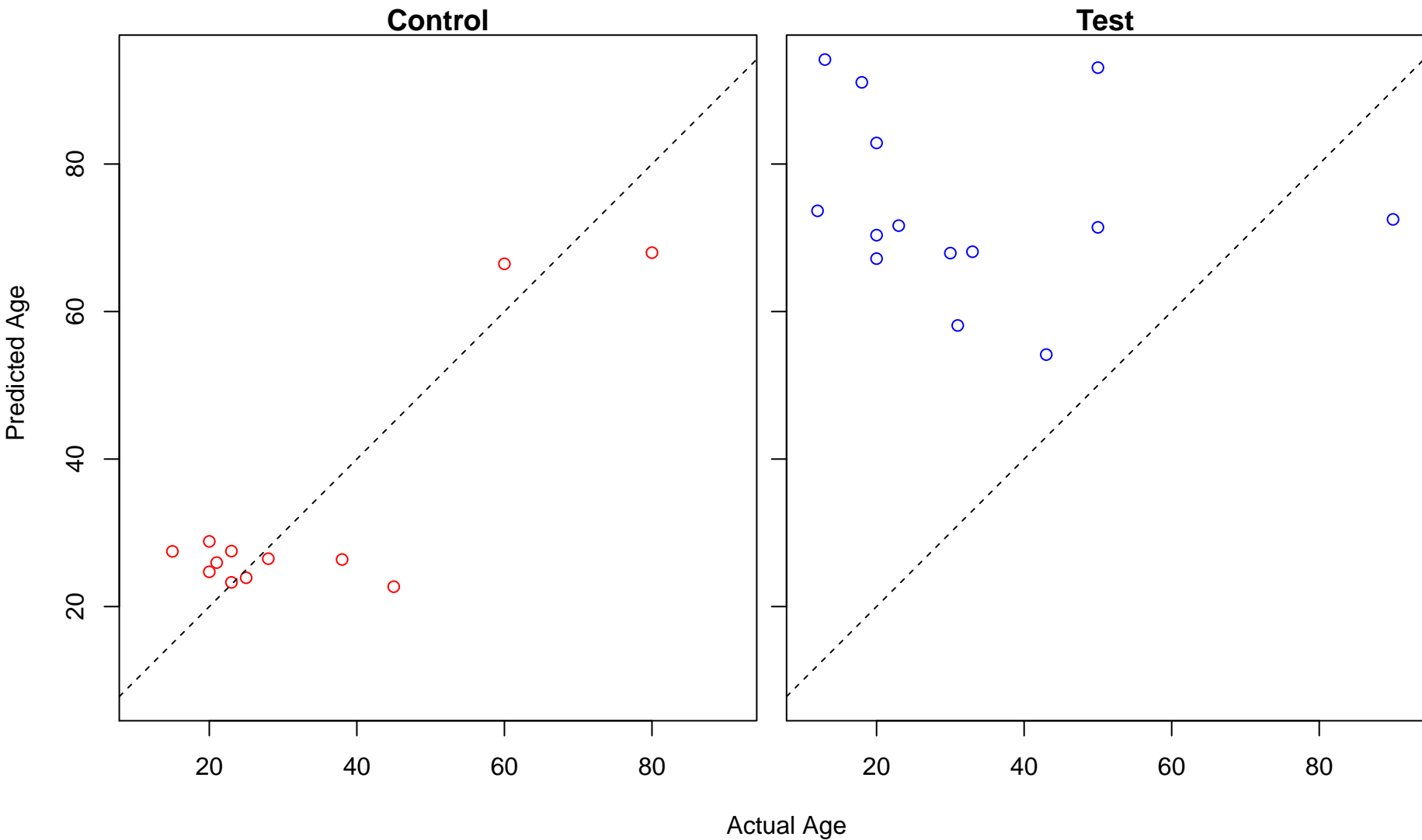
response to alkaloid (Score: 9.356601)



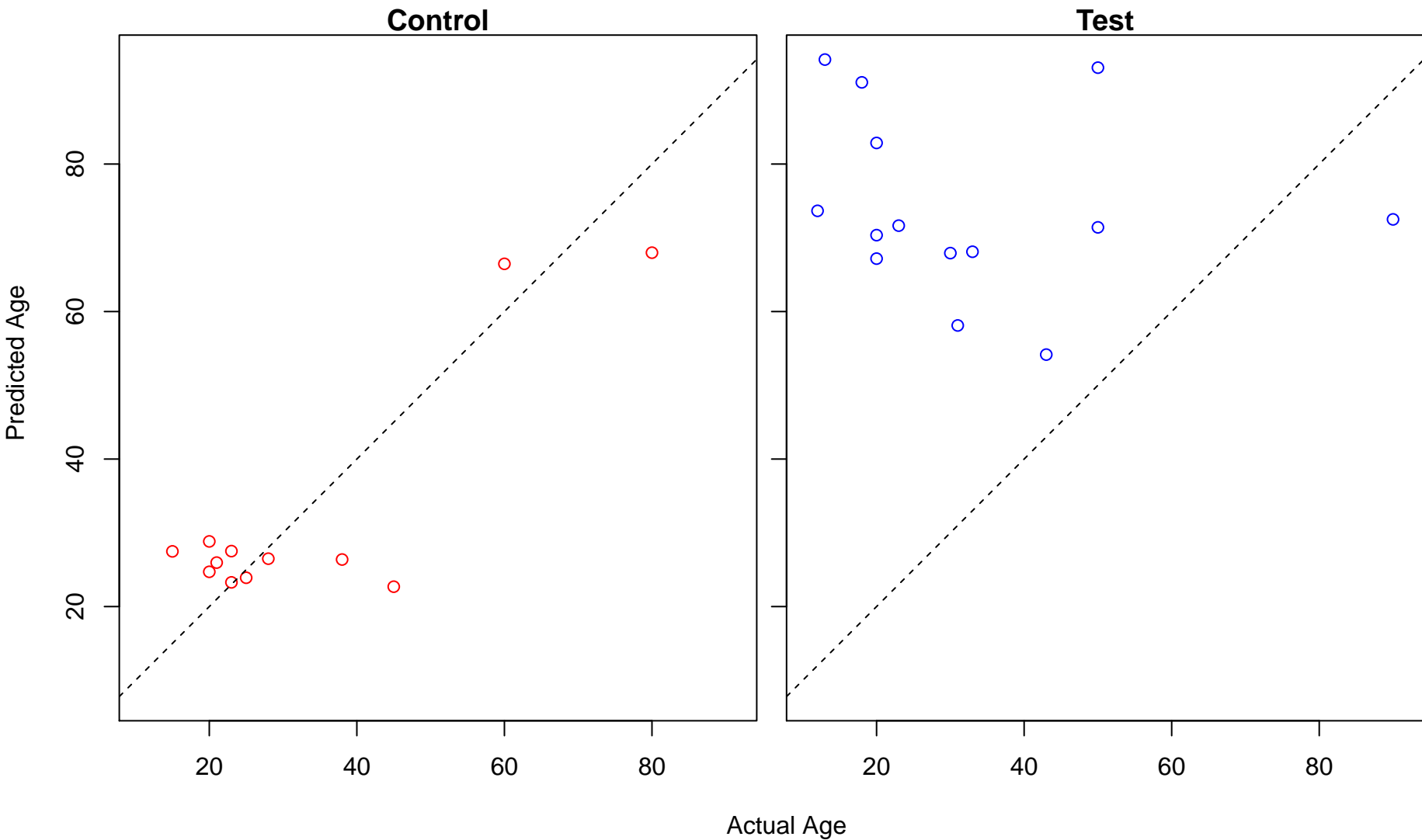
entry into host cell (Score: 9.354903)



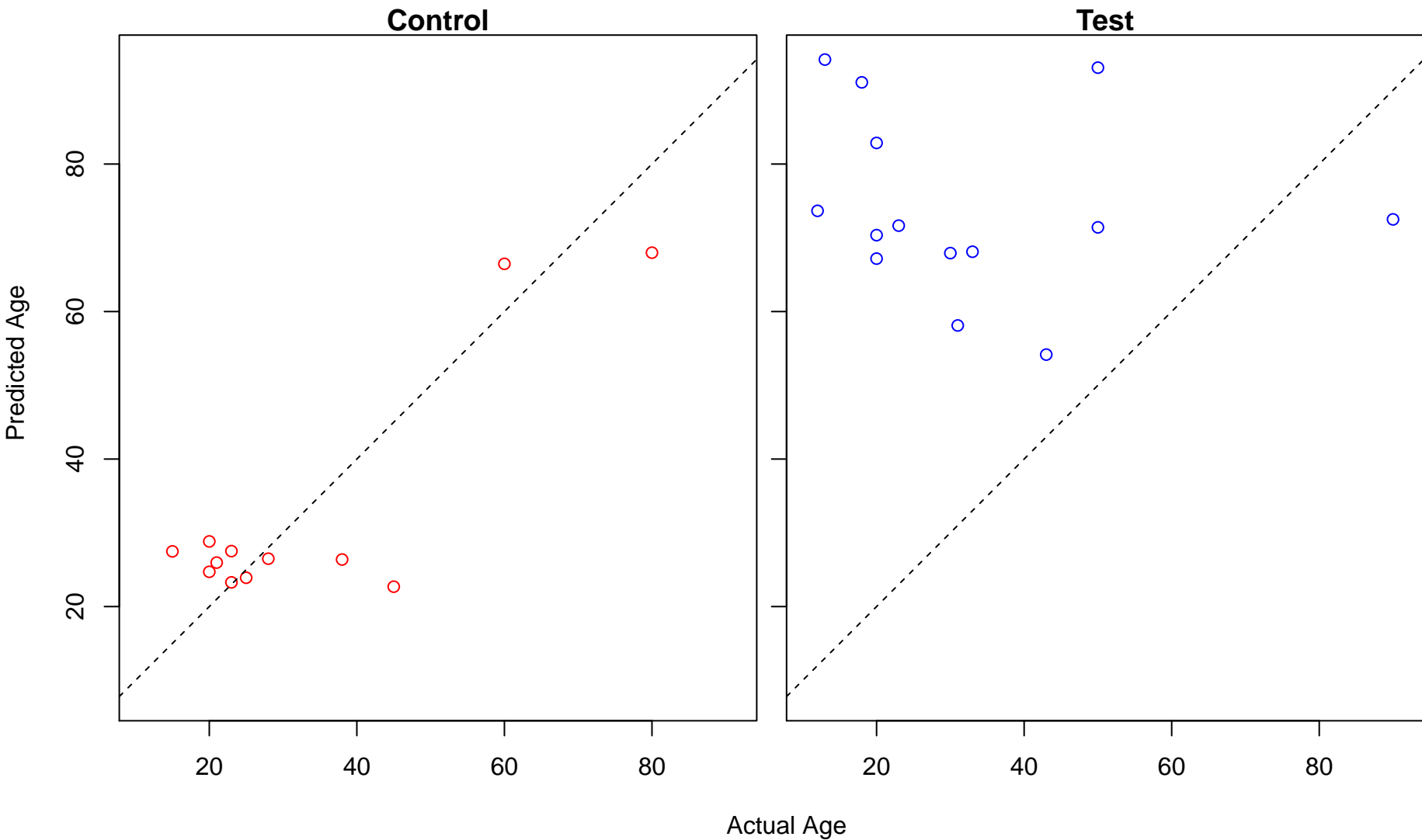
entry into host (Score: 9.354903)



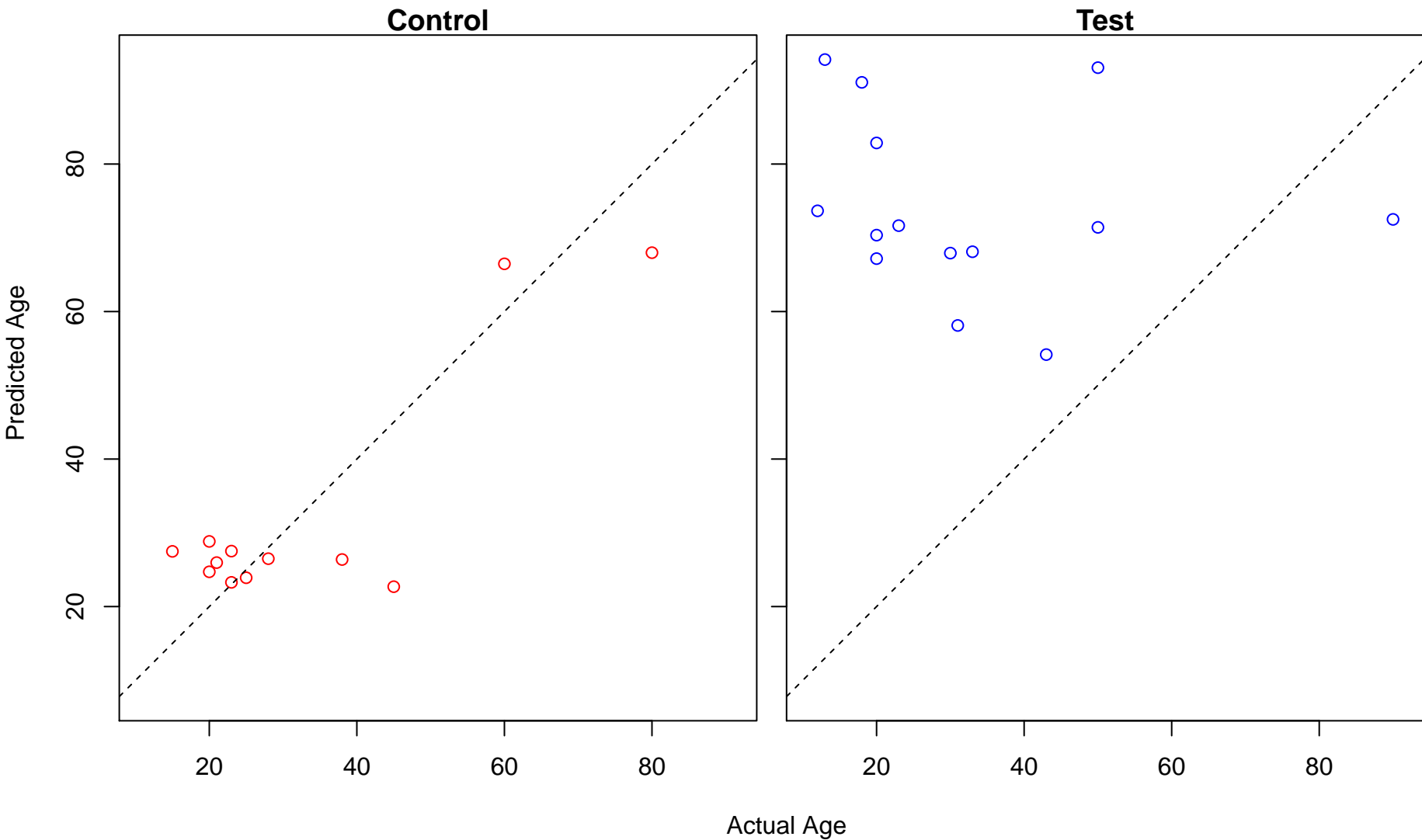
entry into cell of other organism involved in symbiotic interaction (Score: 9.354903)



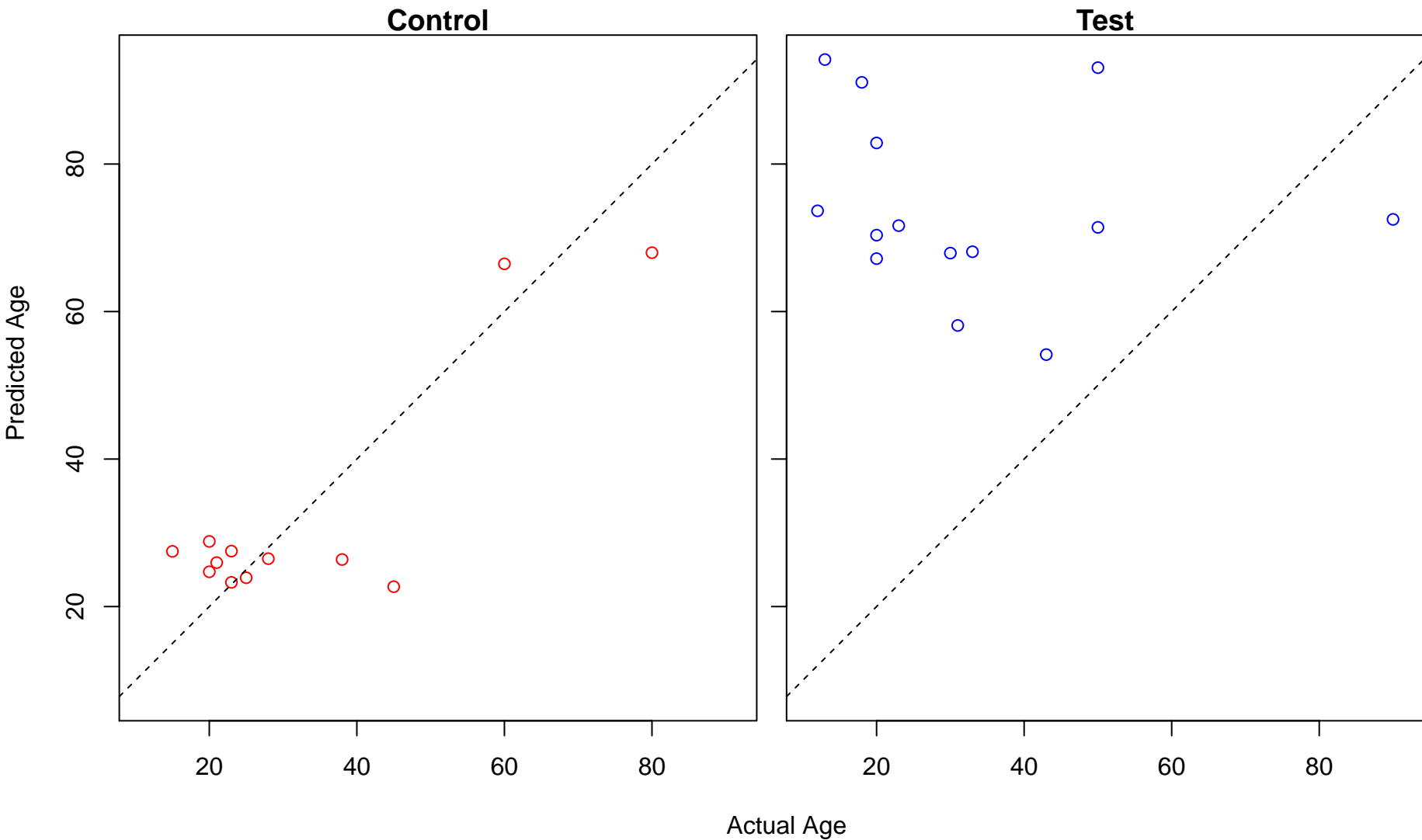
entry into other organism involved in symbiotic interaction (Score: 9.354903)



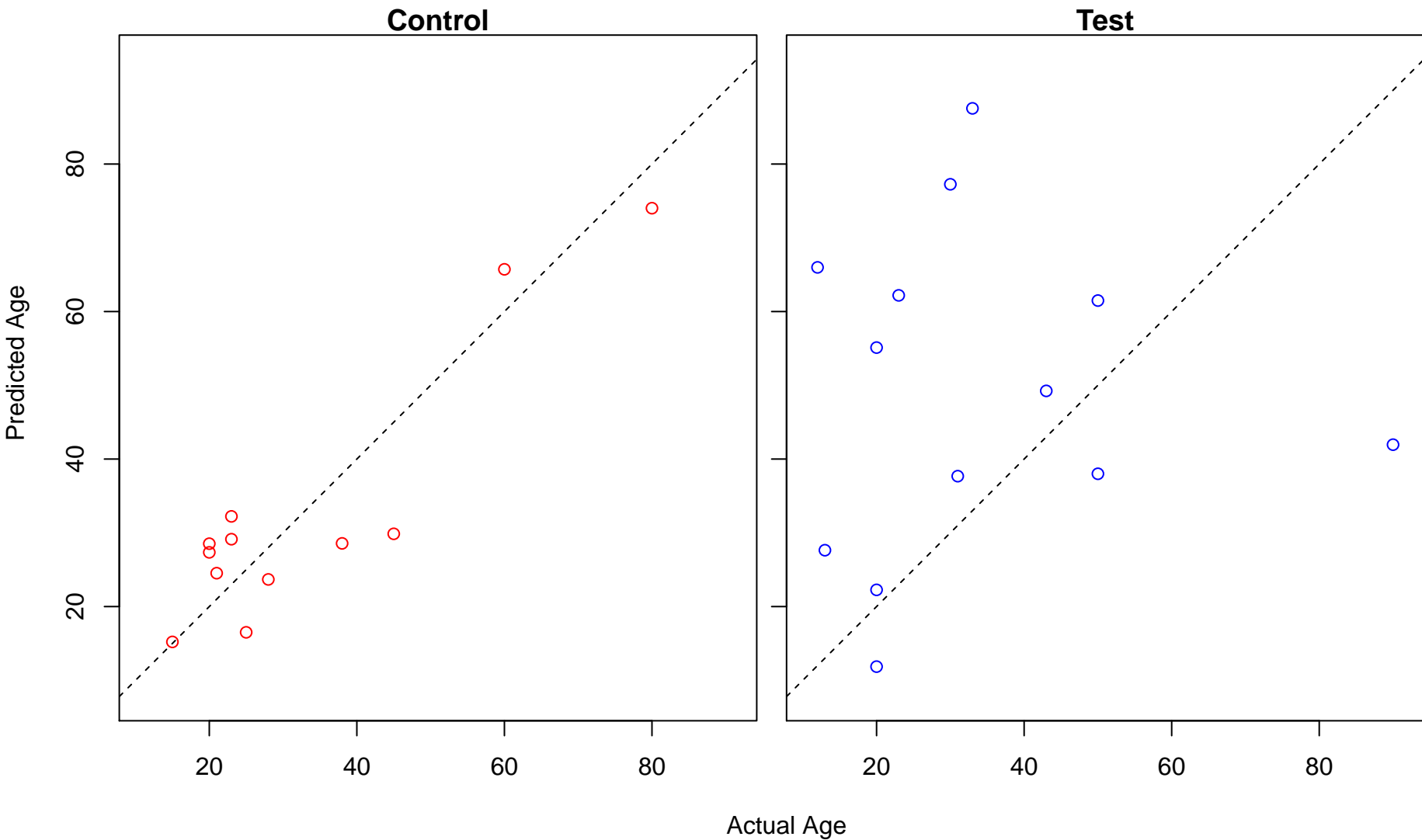
movement in host environment (Score: 9.354903)



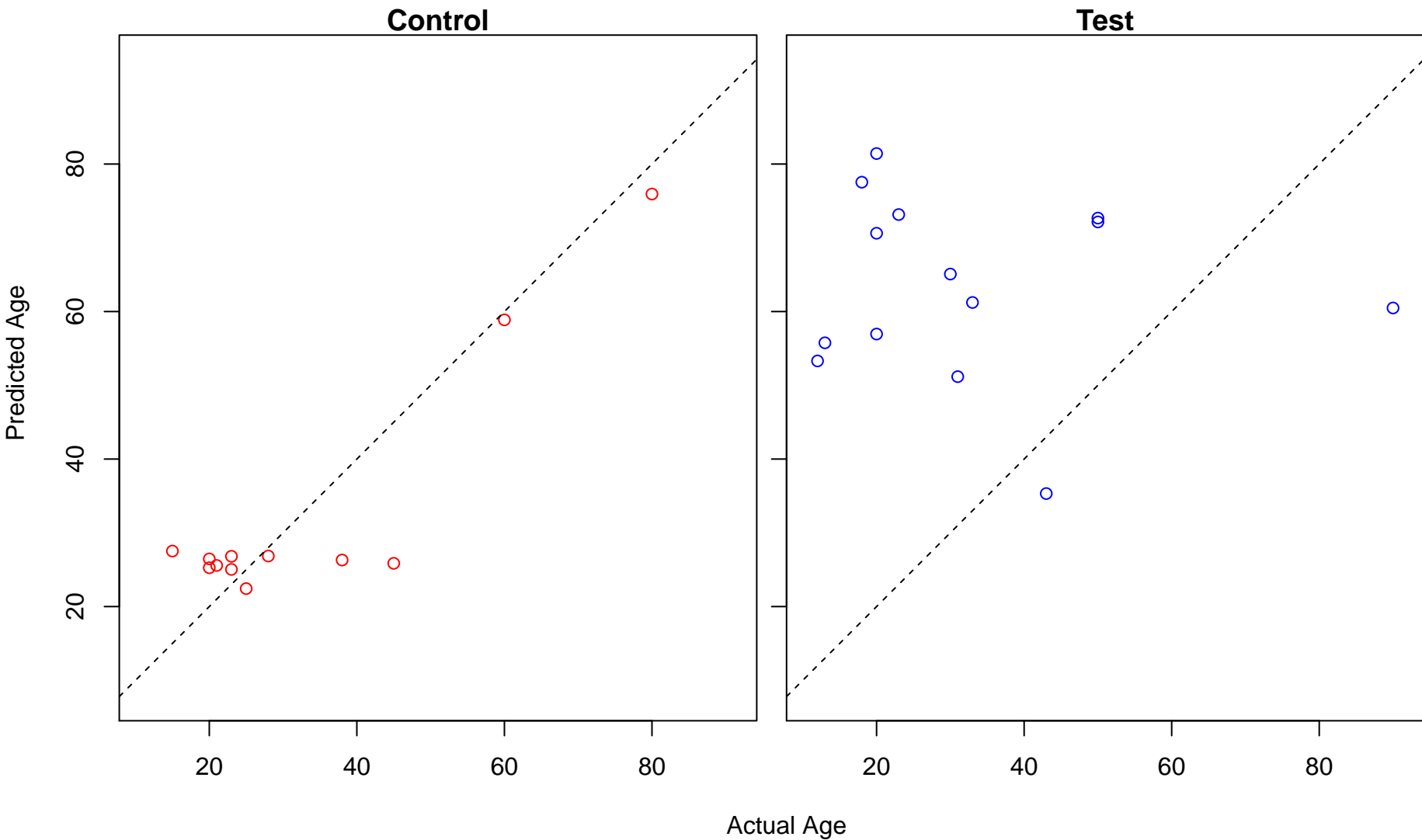
movement in environment of other organism involved in symbiotic interaction (Score: 9.354903)



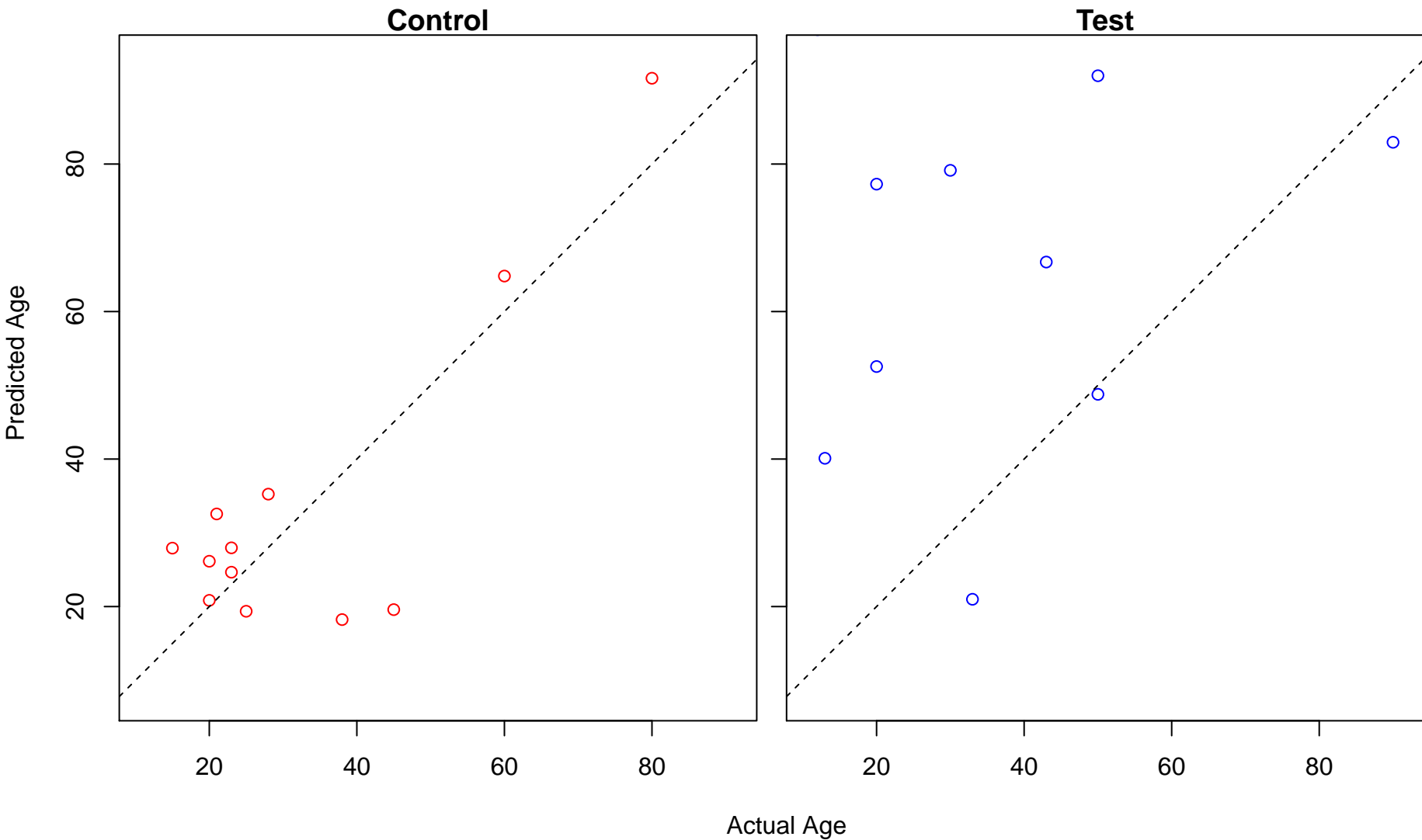
regulation of phospholipid biosynthetic process (Score: 9.346517)



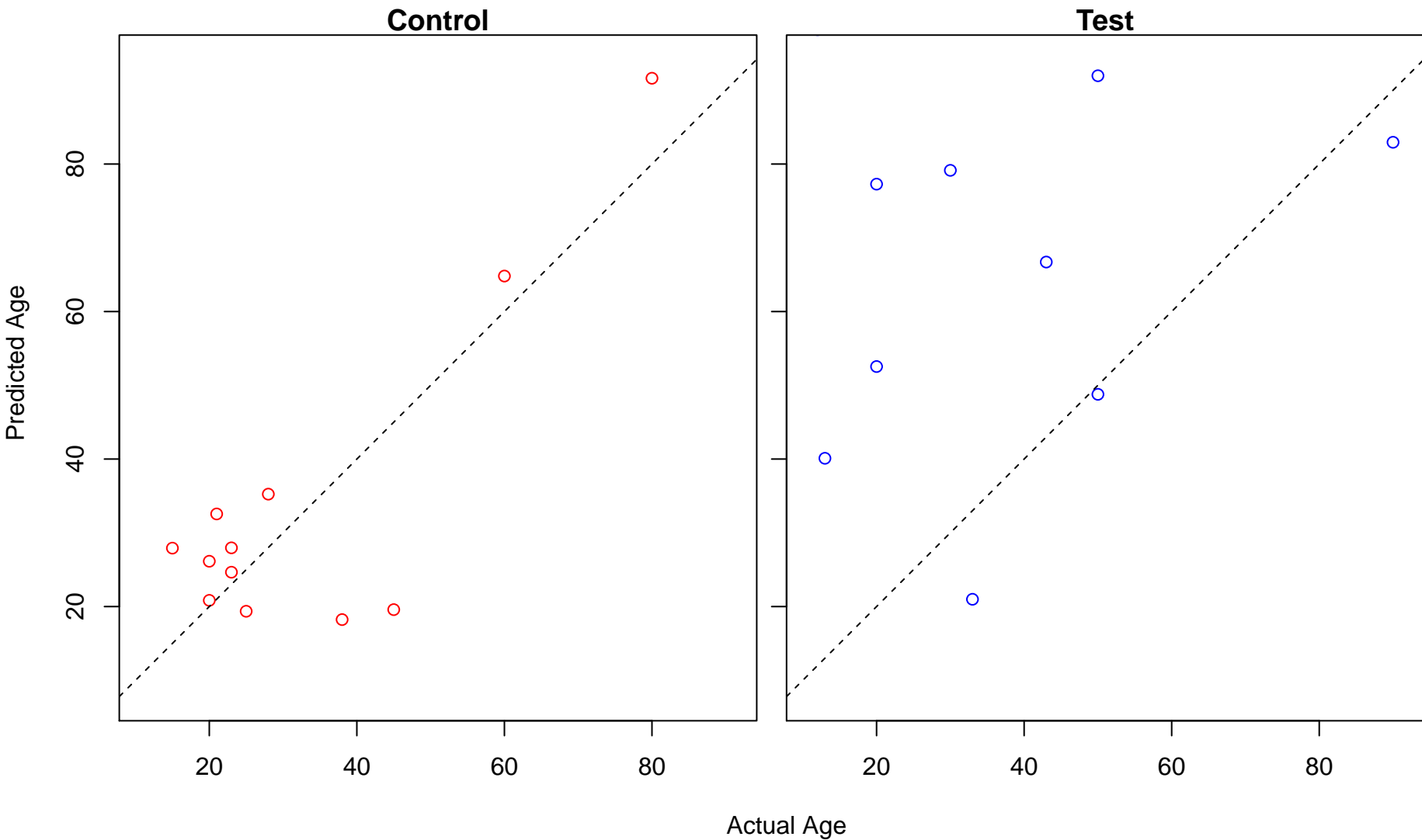
positive regulation of telomere maintenance via telomerase (Score: 9.345989)



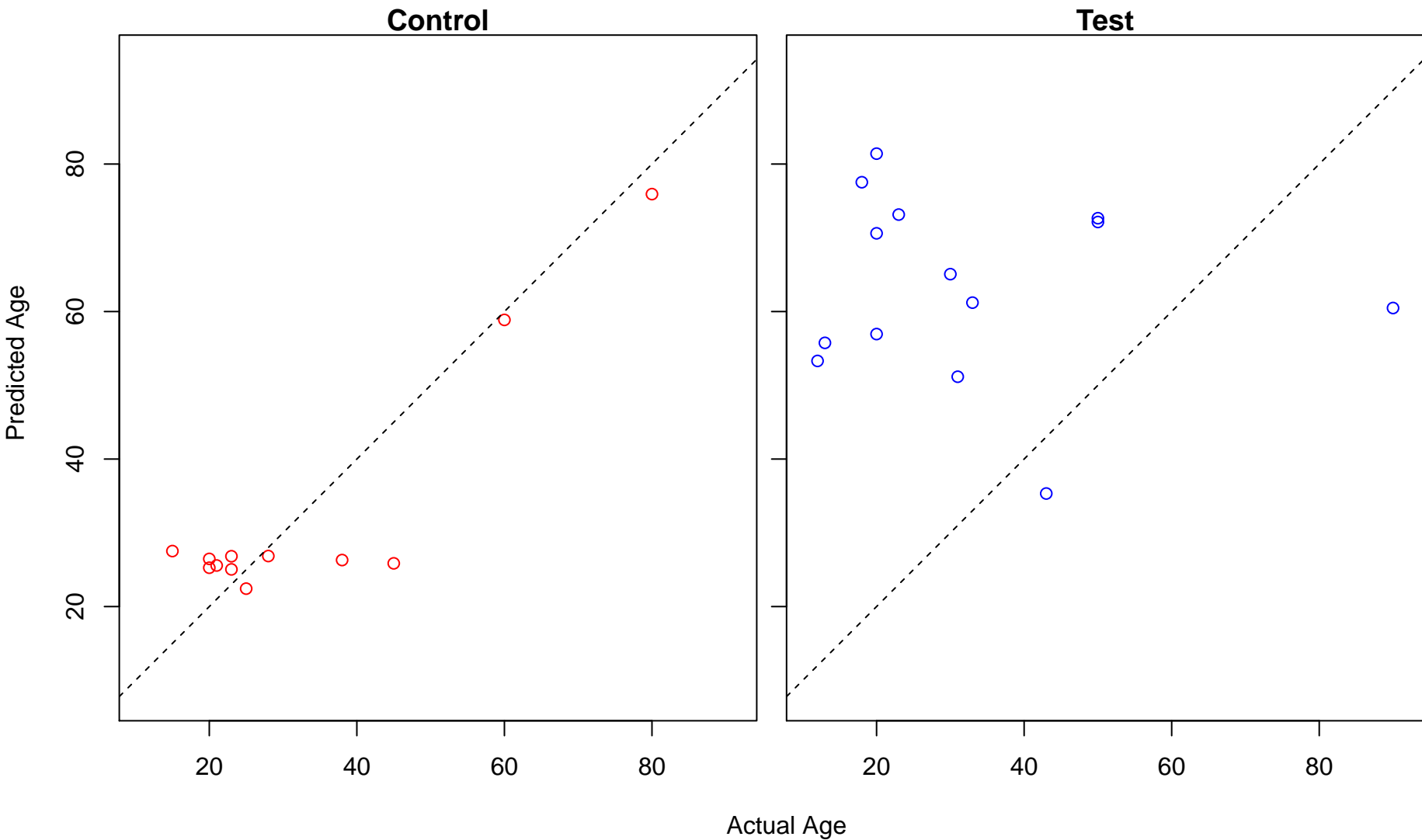
organelle inheritance (Score: 9.340865)



Golgi inheritance (Score: 9.340865)

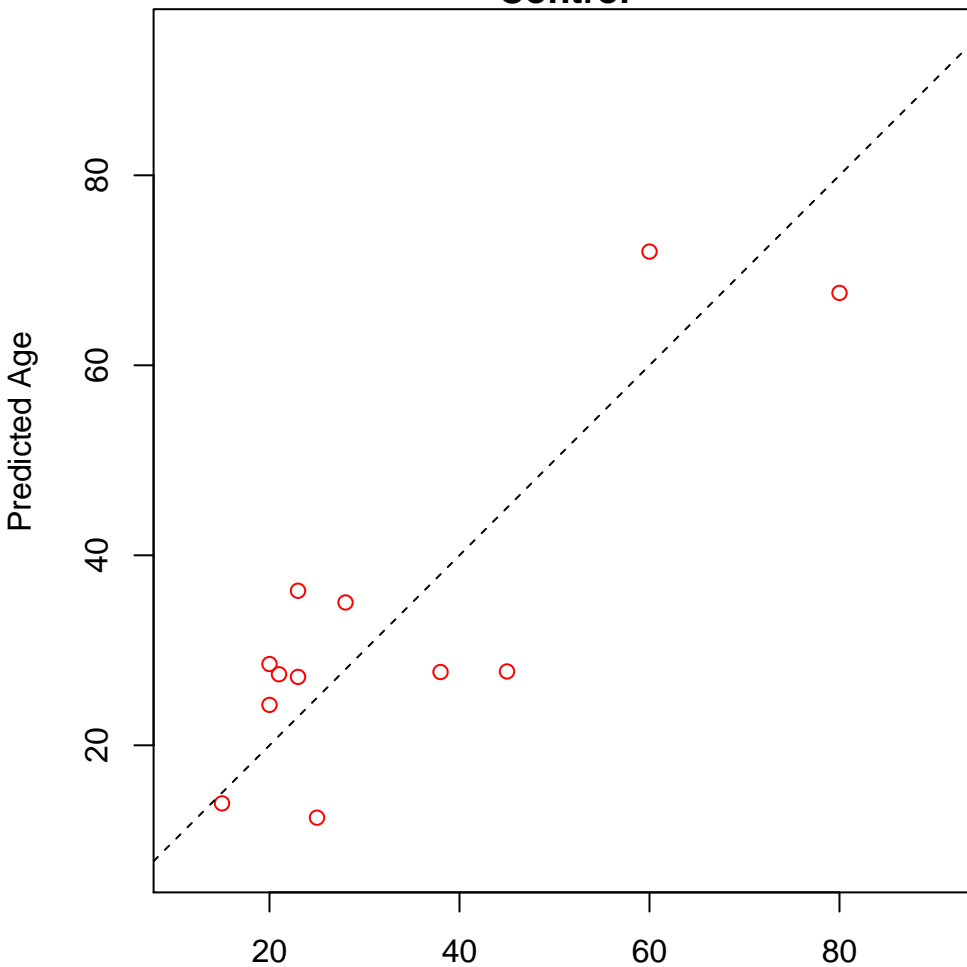


positive regulation of telomere maintenance via telomere lengthening (Score: 9.338028)

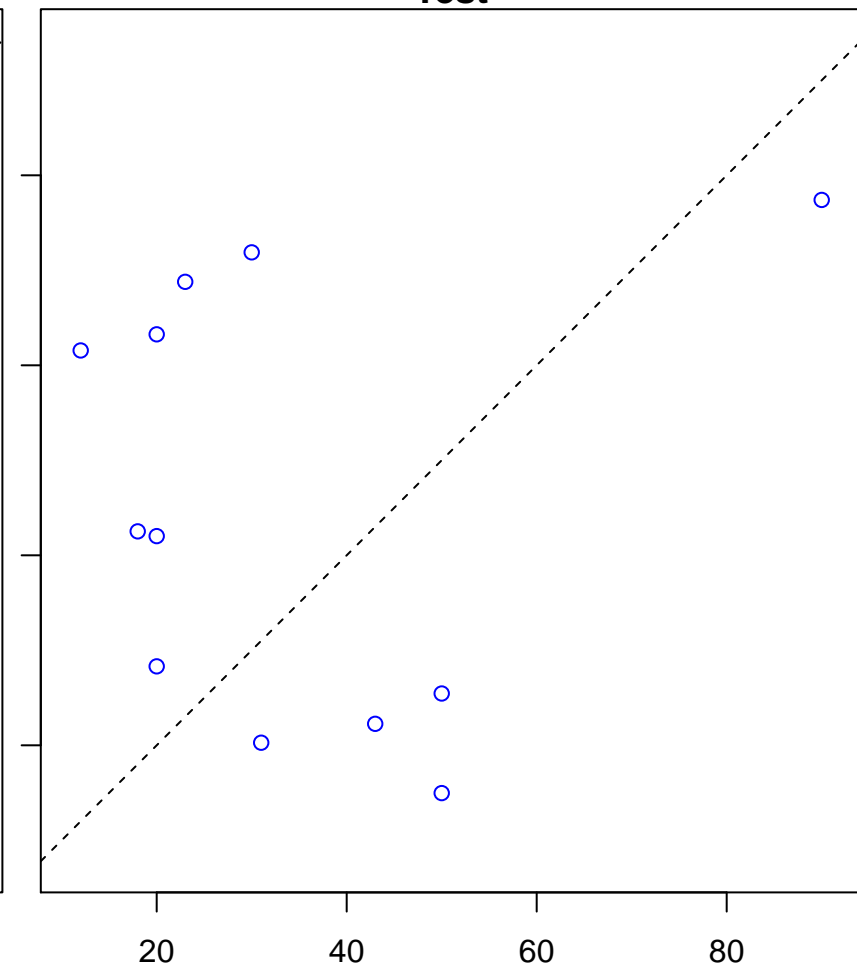


regulation of B cell apoptotic process (Score: 9.337183)

Control



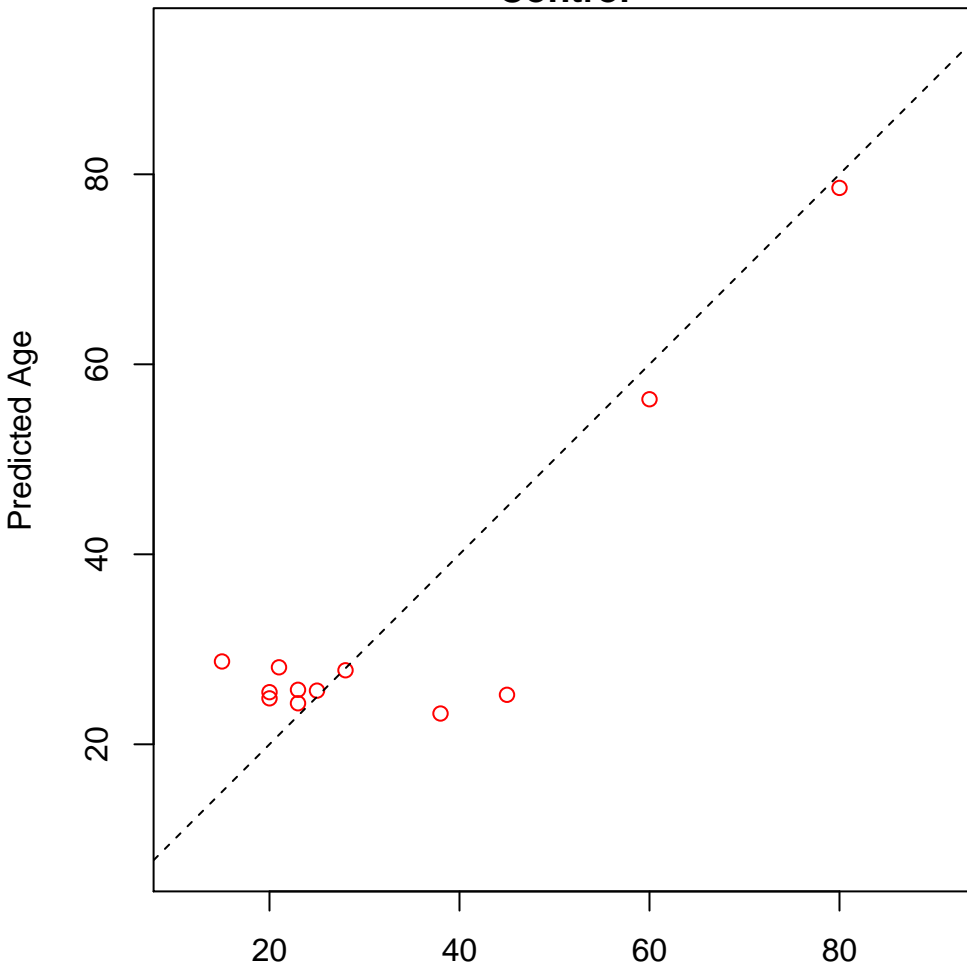
Test



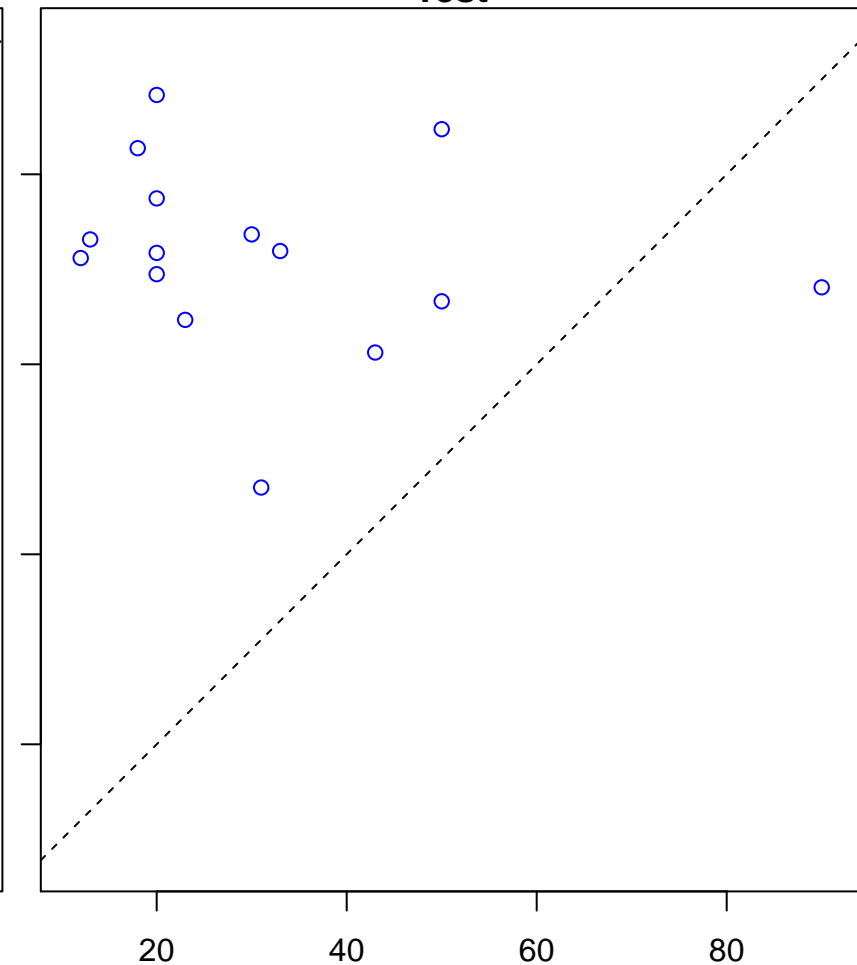
Actual Age

mitochondrial calcium ion transport (Score: 9.334357)

Control



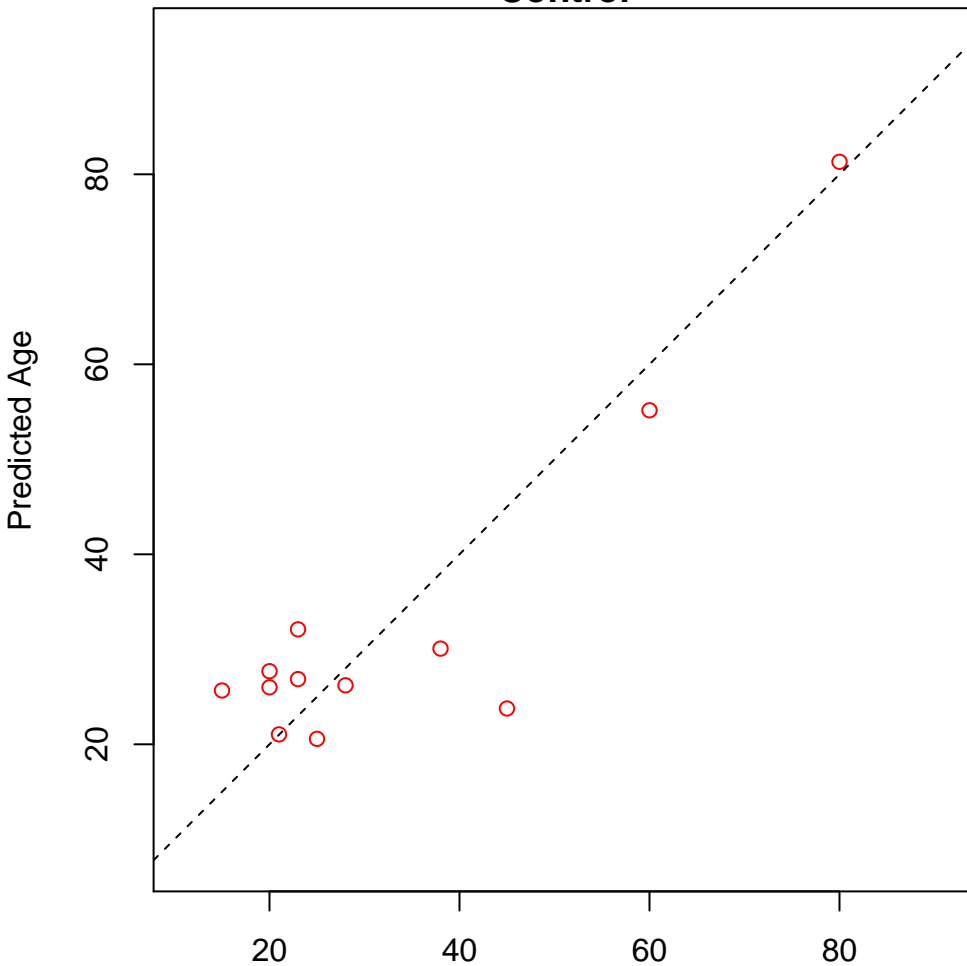
Test



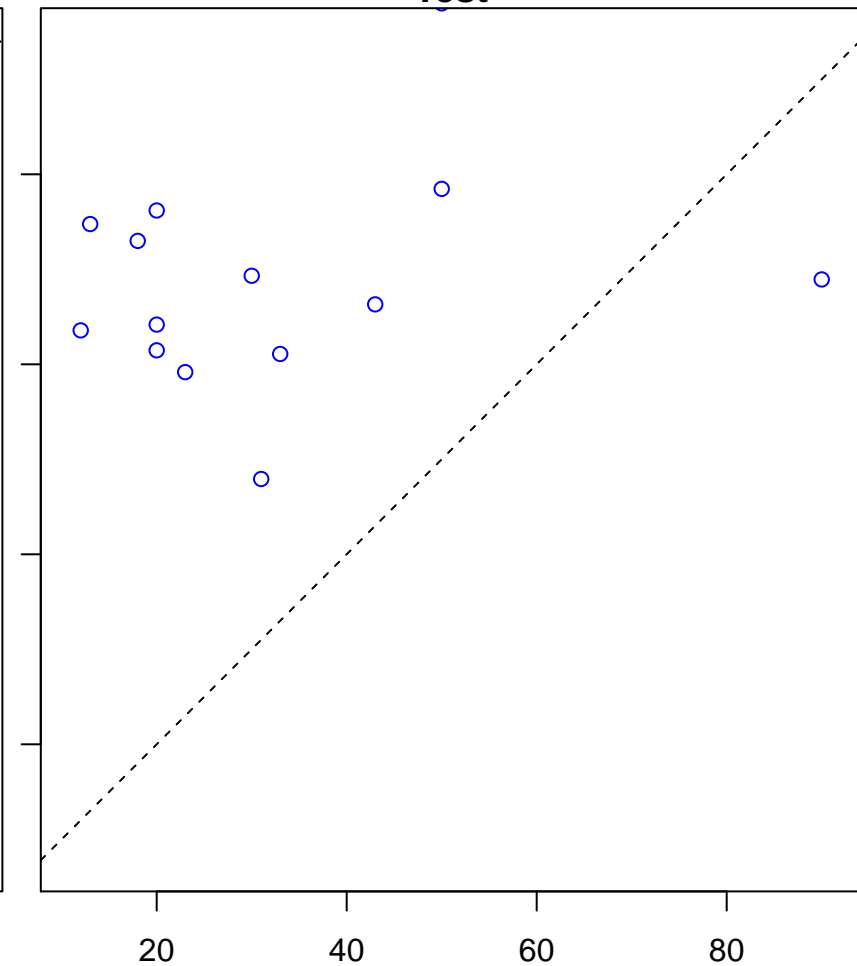
Actual Age

regulation of digestive system process (Score: 9.331403)

Control

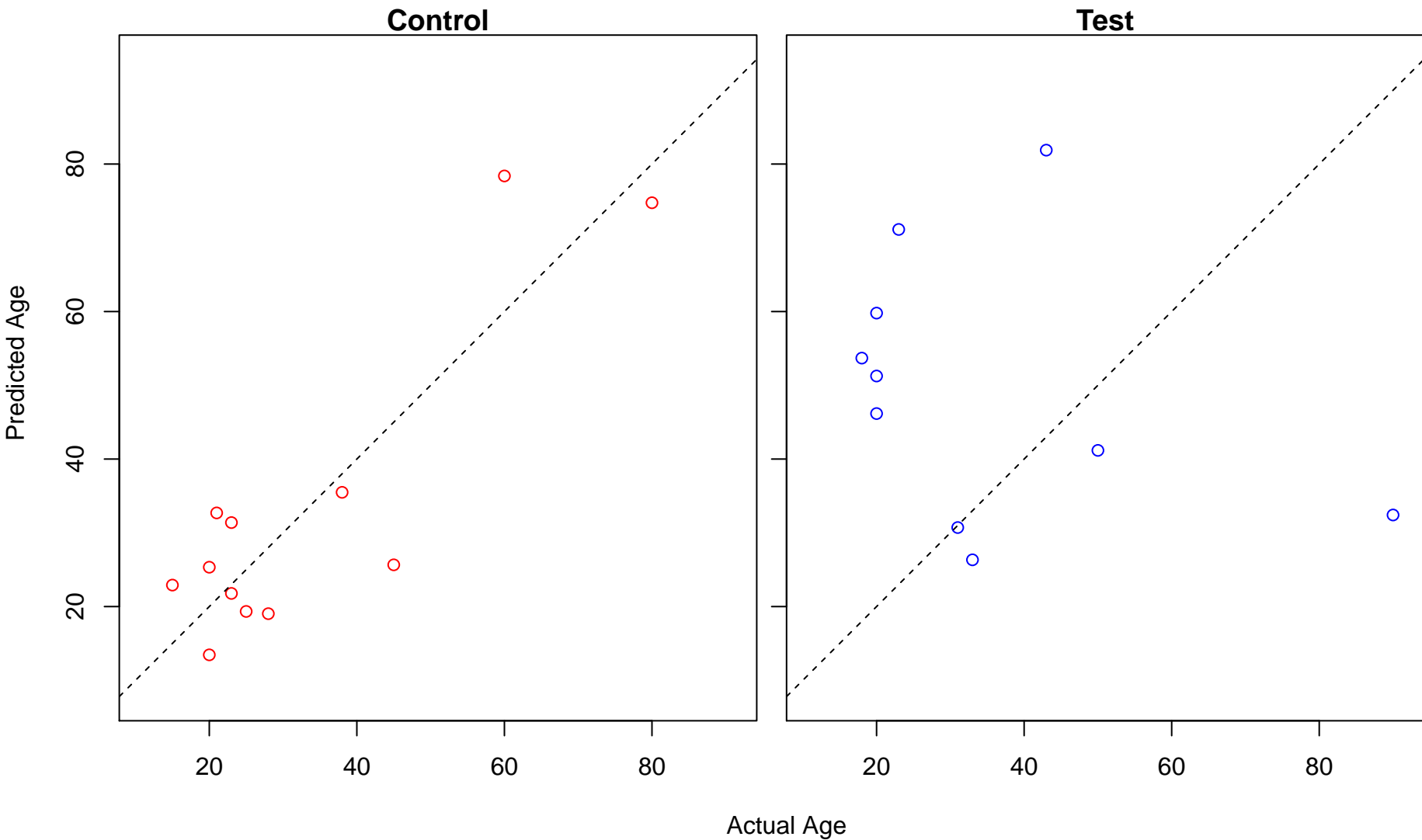


Test

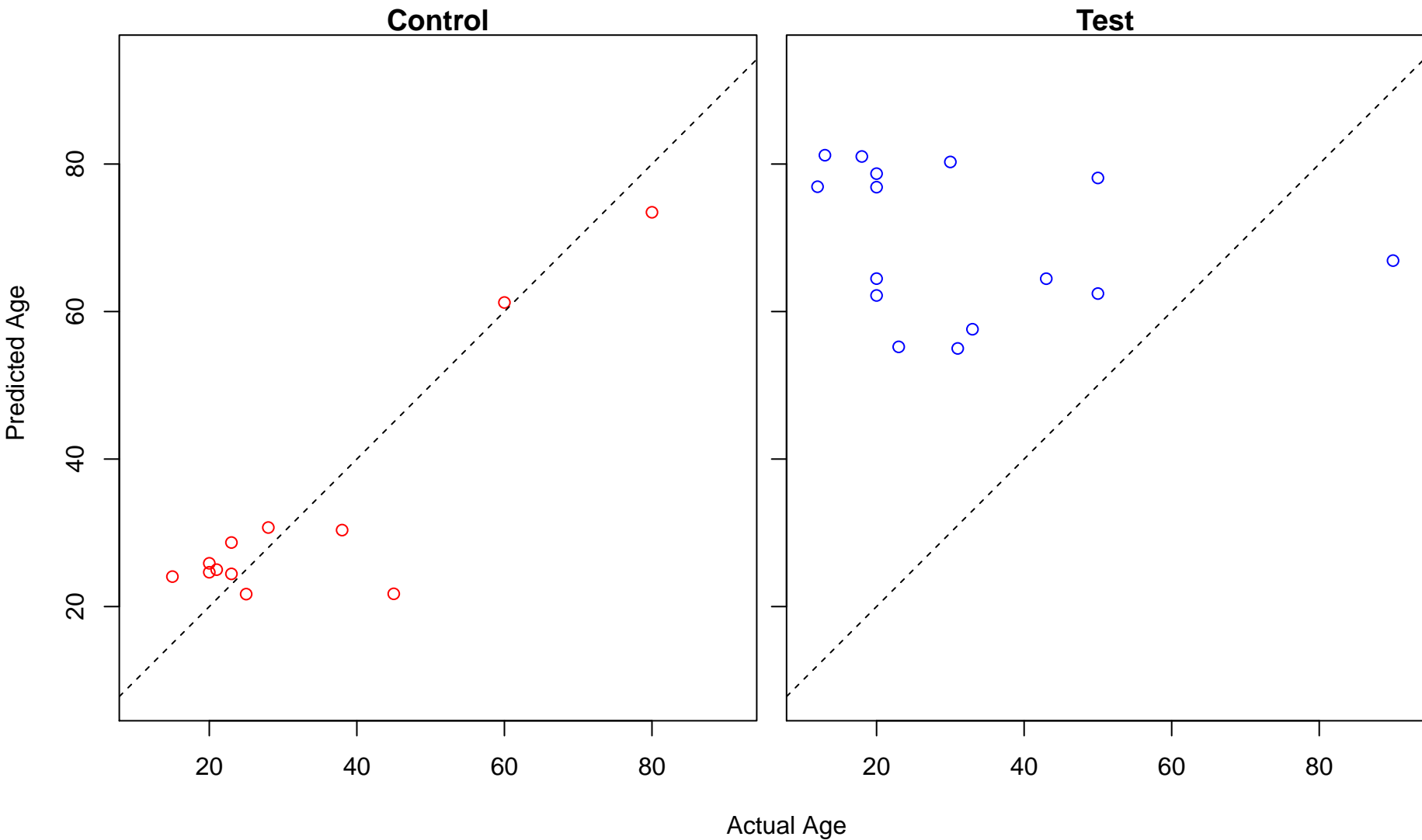


Actual Age

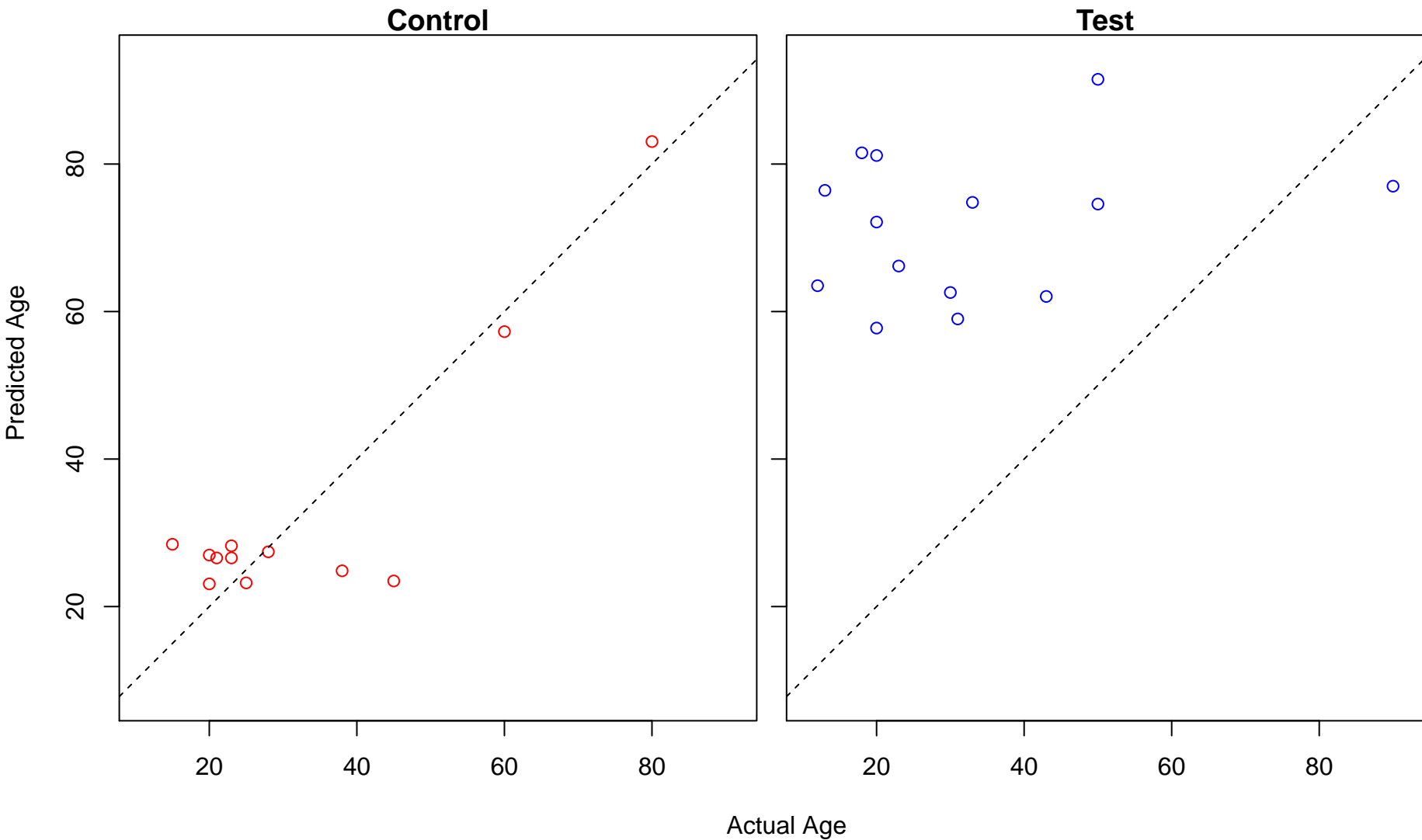
regulation of response to interferon-gamma (Score: 9.327186)



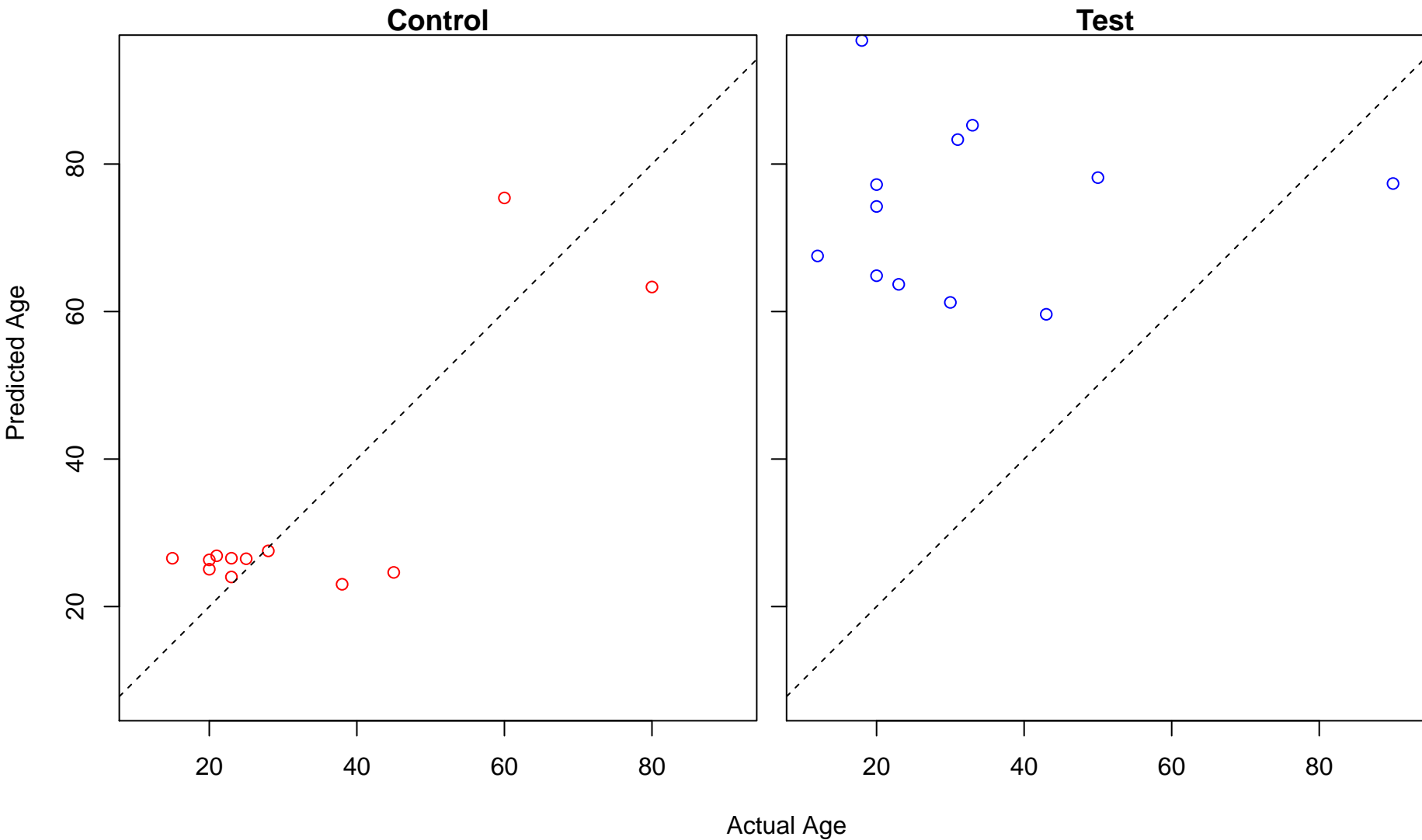
mRNA 3'-end processing by stem-loop binding and cleavage (Score: 9.323236)



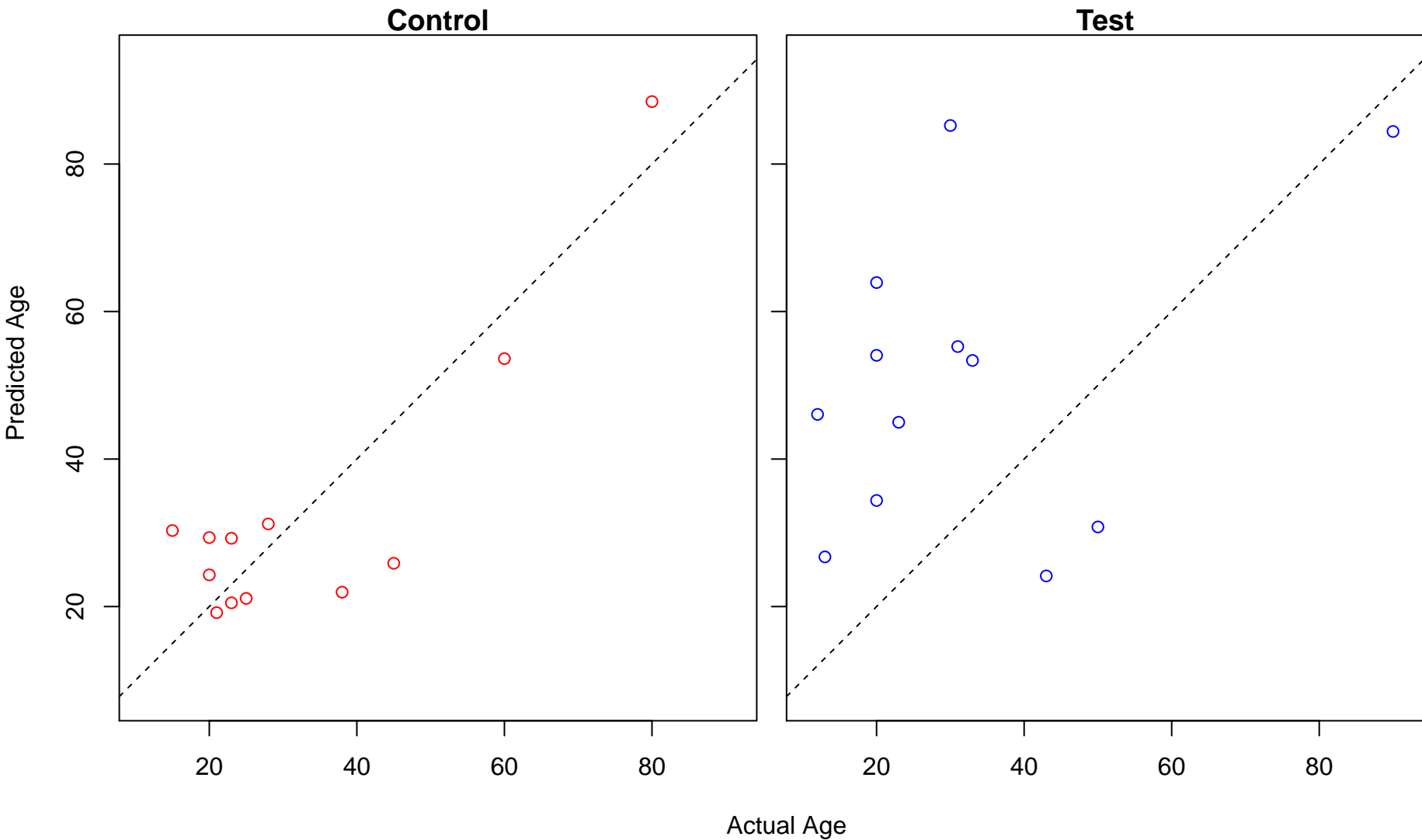
regulation by virus of viral protein levels in host cell (Score: 9.314149)



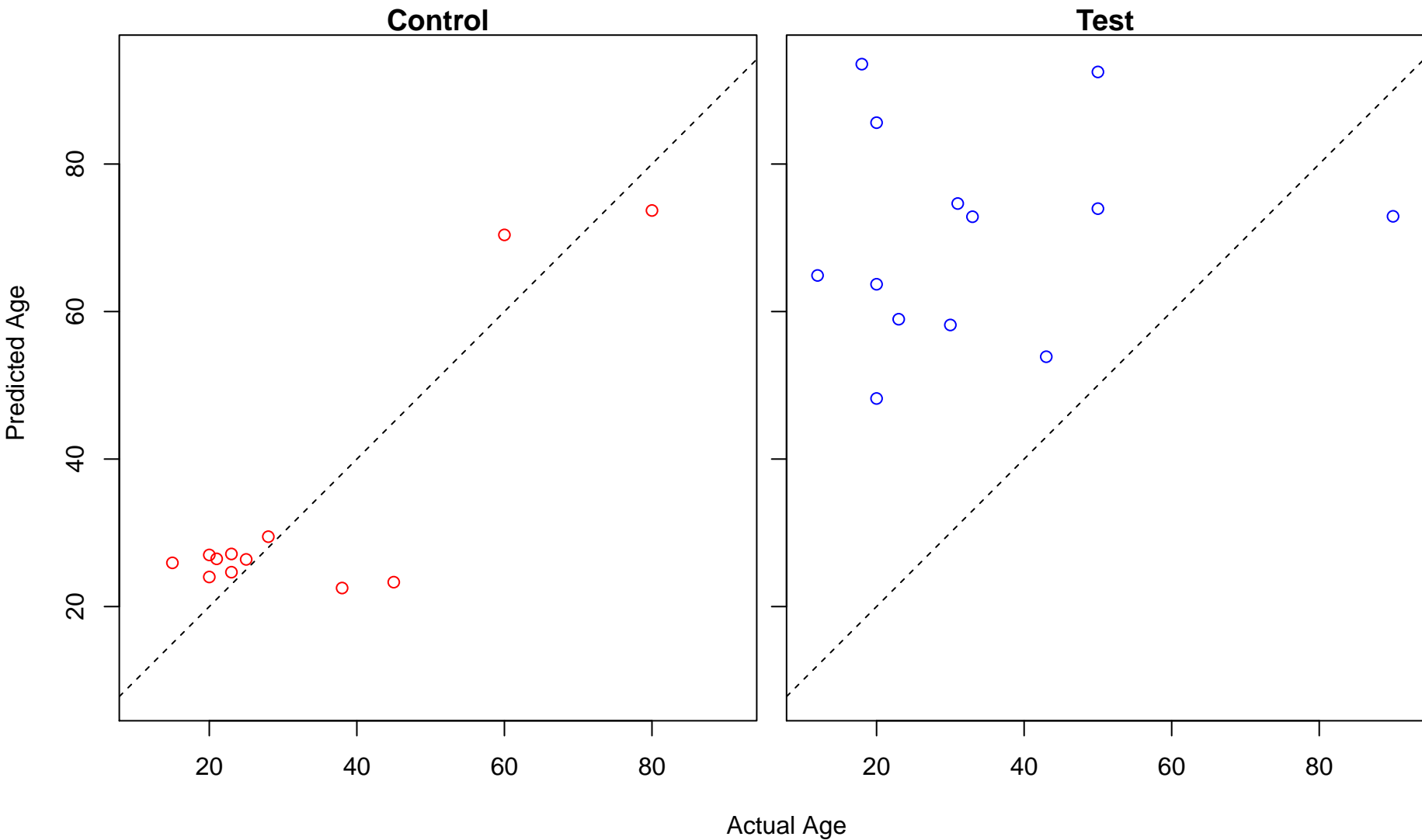
base-excision repair (Score: 9.310990)



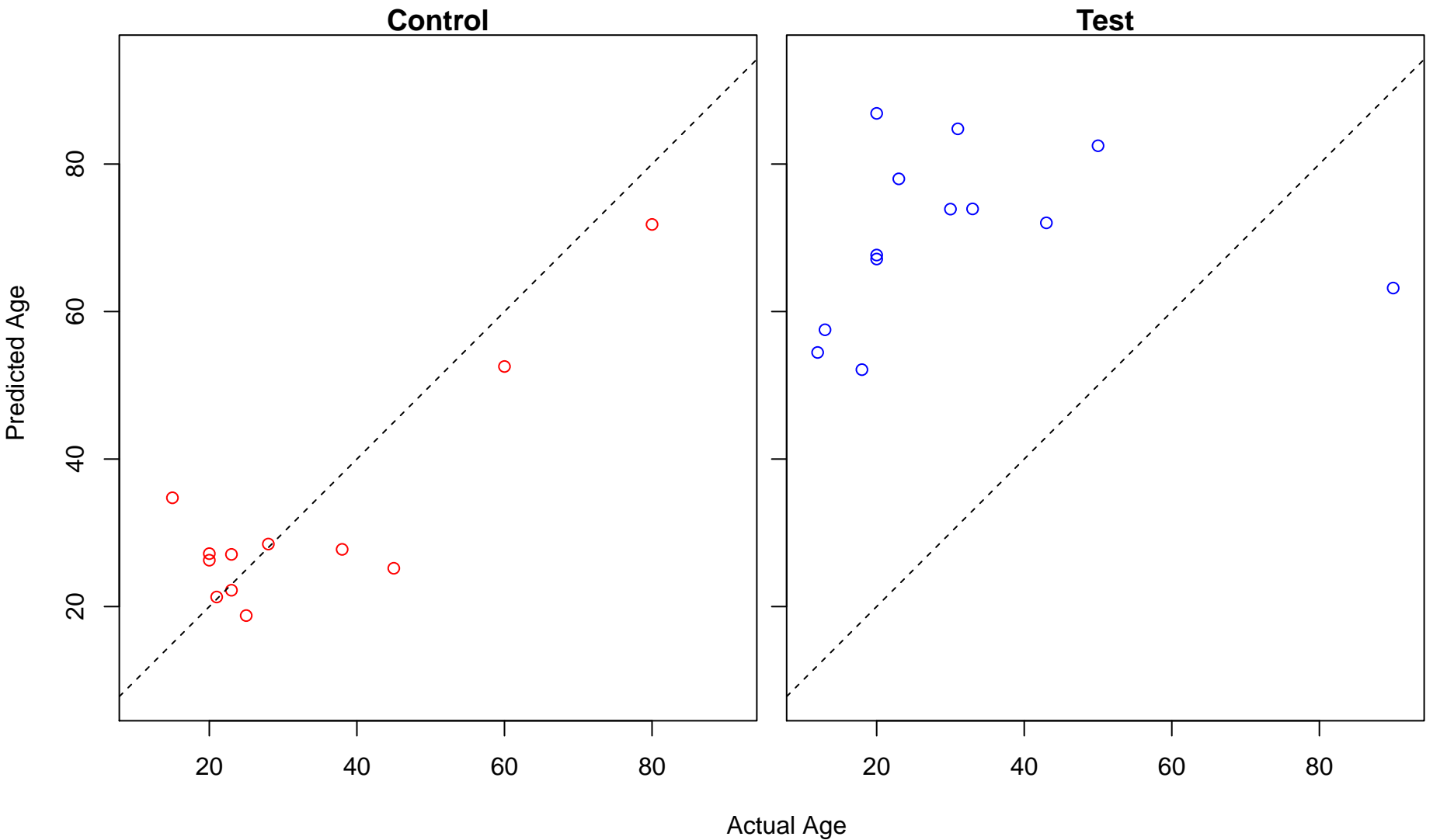
negative regulation of reproductive process (Score: 9.308102)



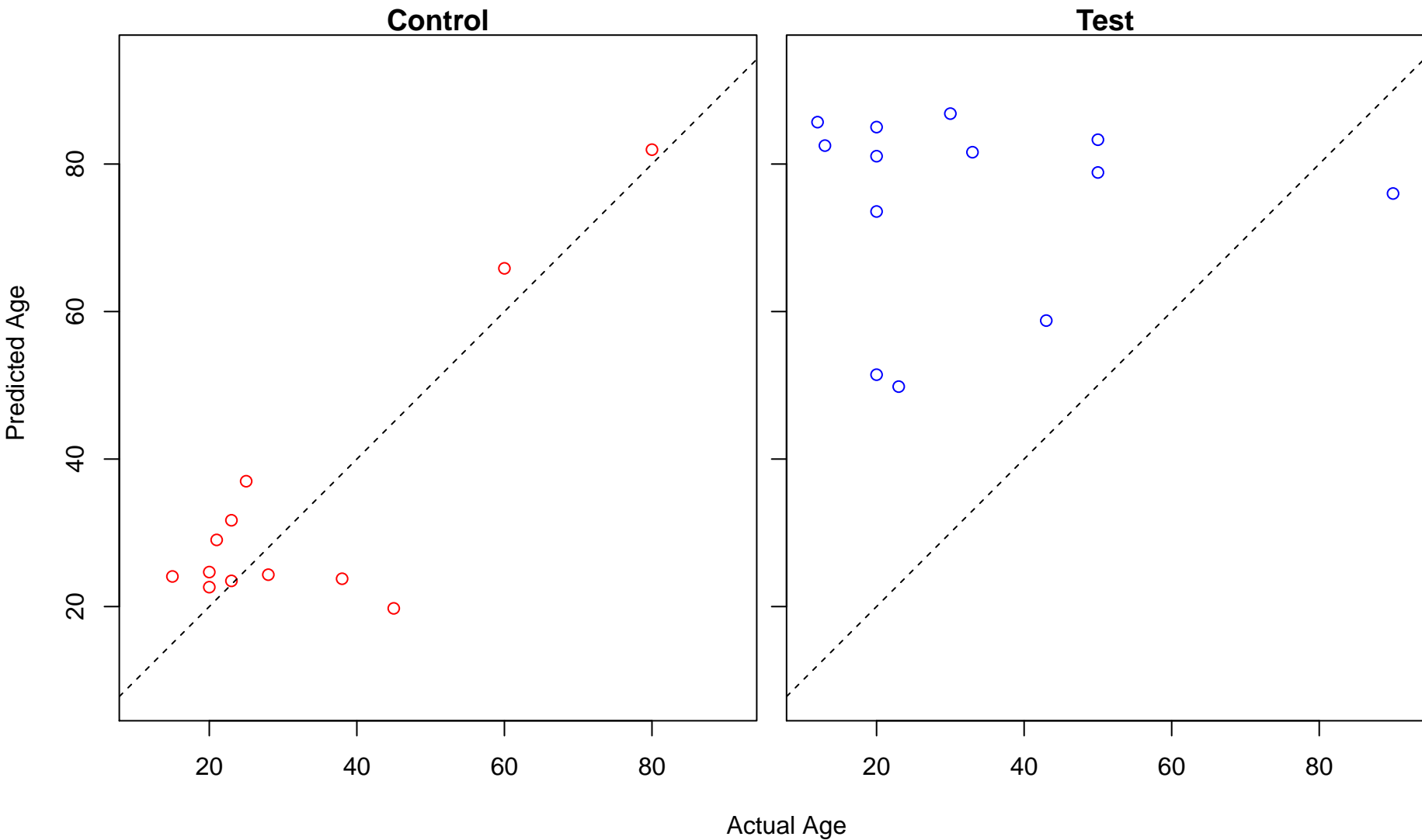
positive regulation of establishment of protein localization to mitochondrion (Score: 9.306360)



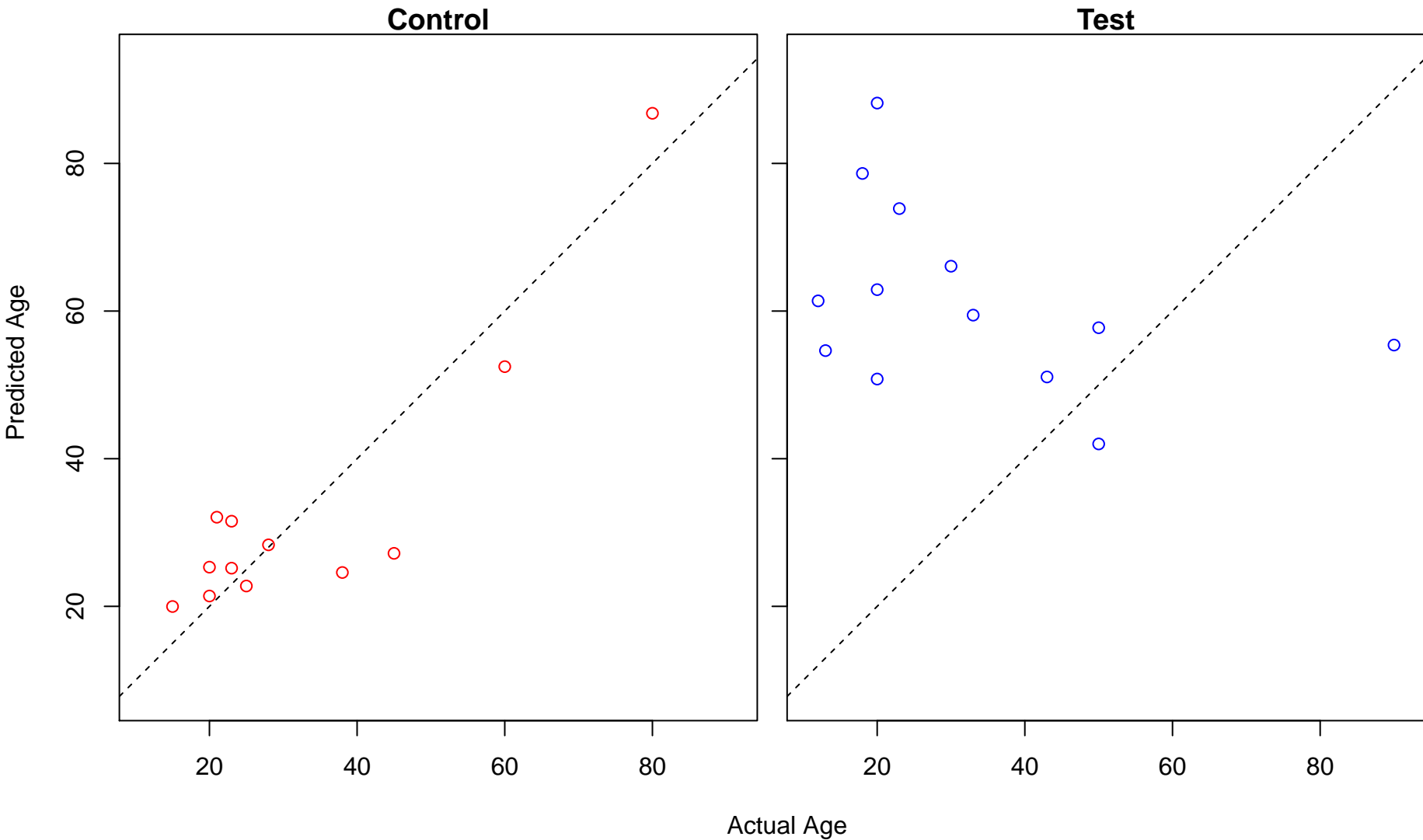
Positive regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter (Score



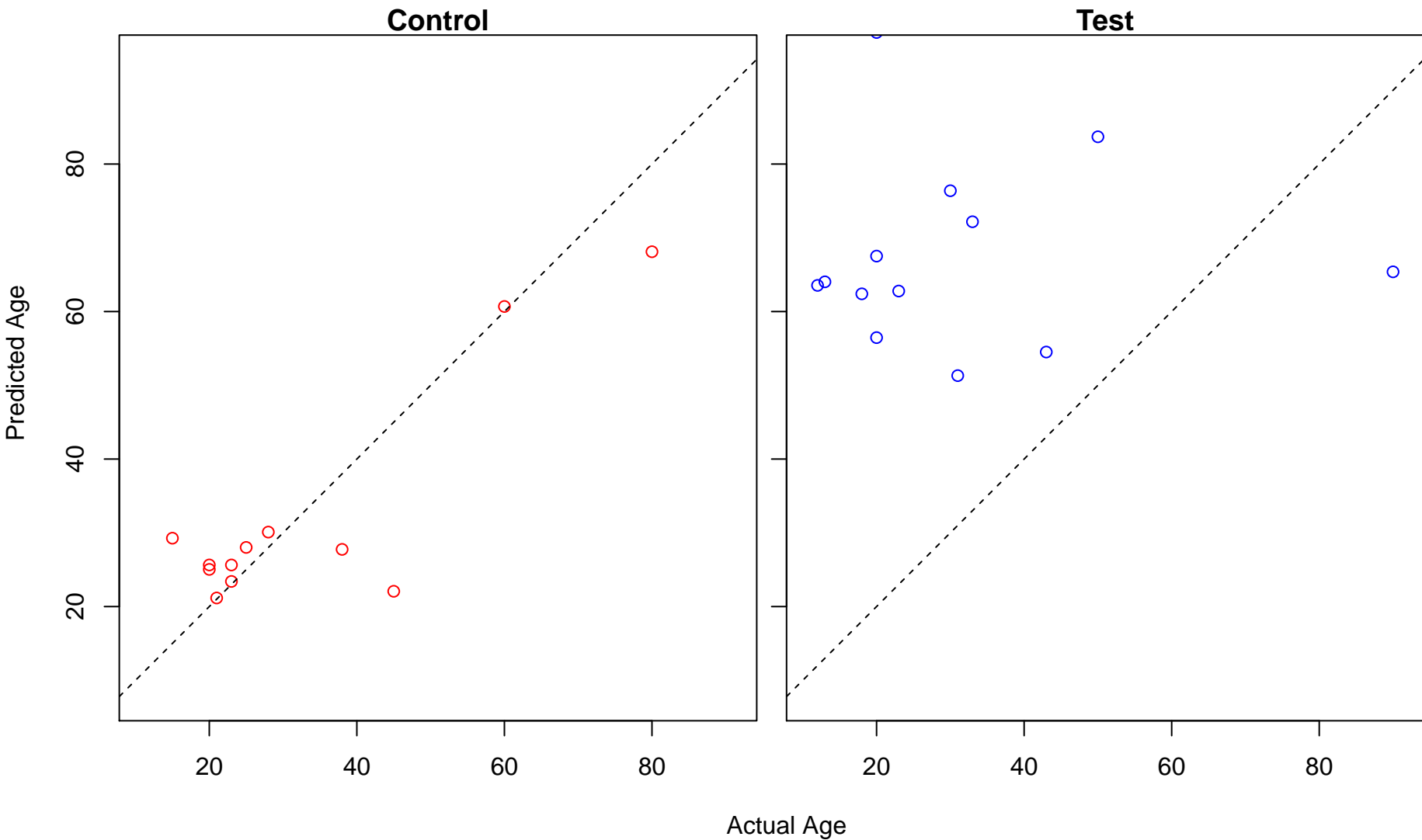
RNA stabilization (Score: 9.298649)



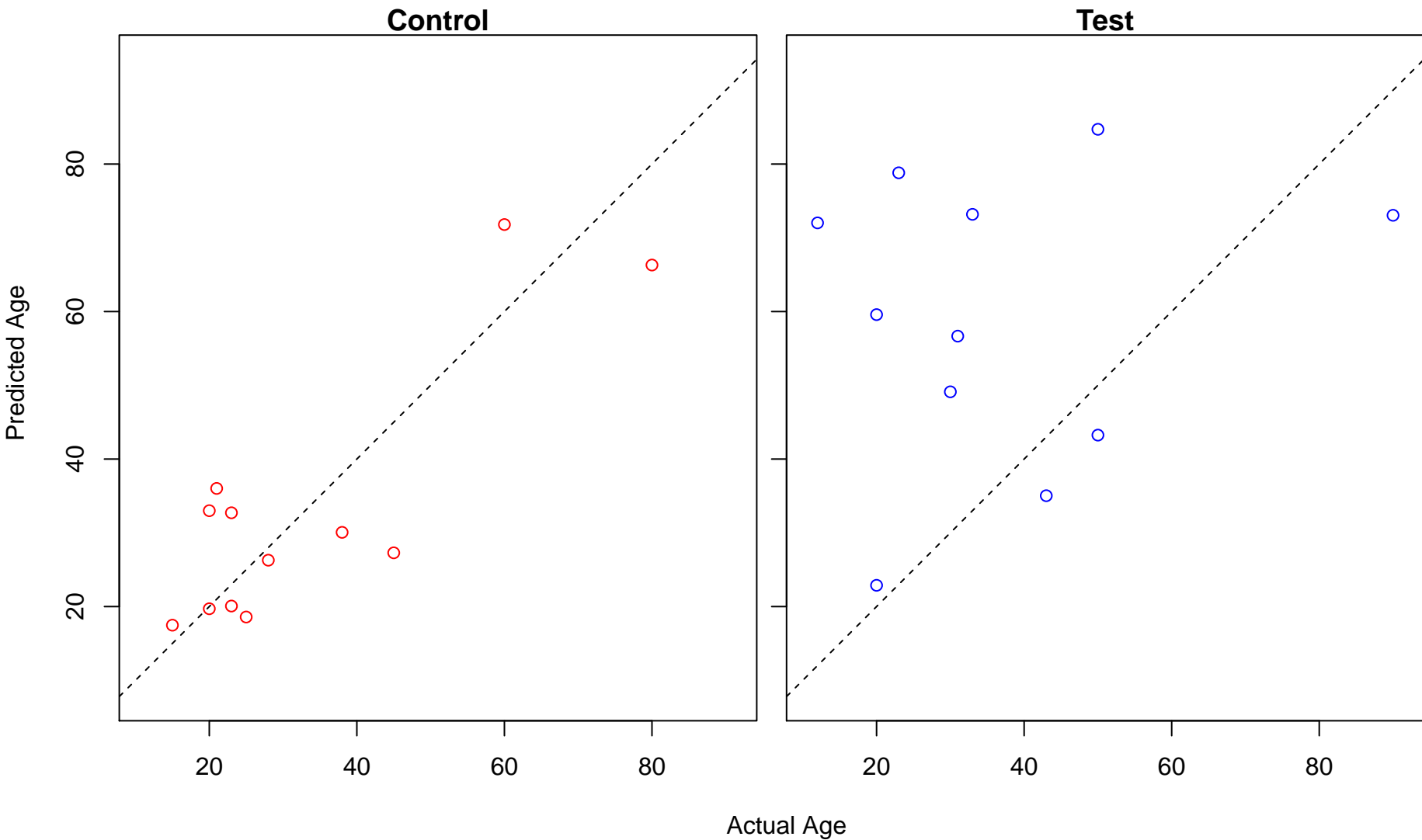
positive regulation of neuron differentiation (Score: 9.293572)



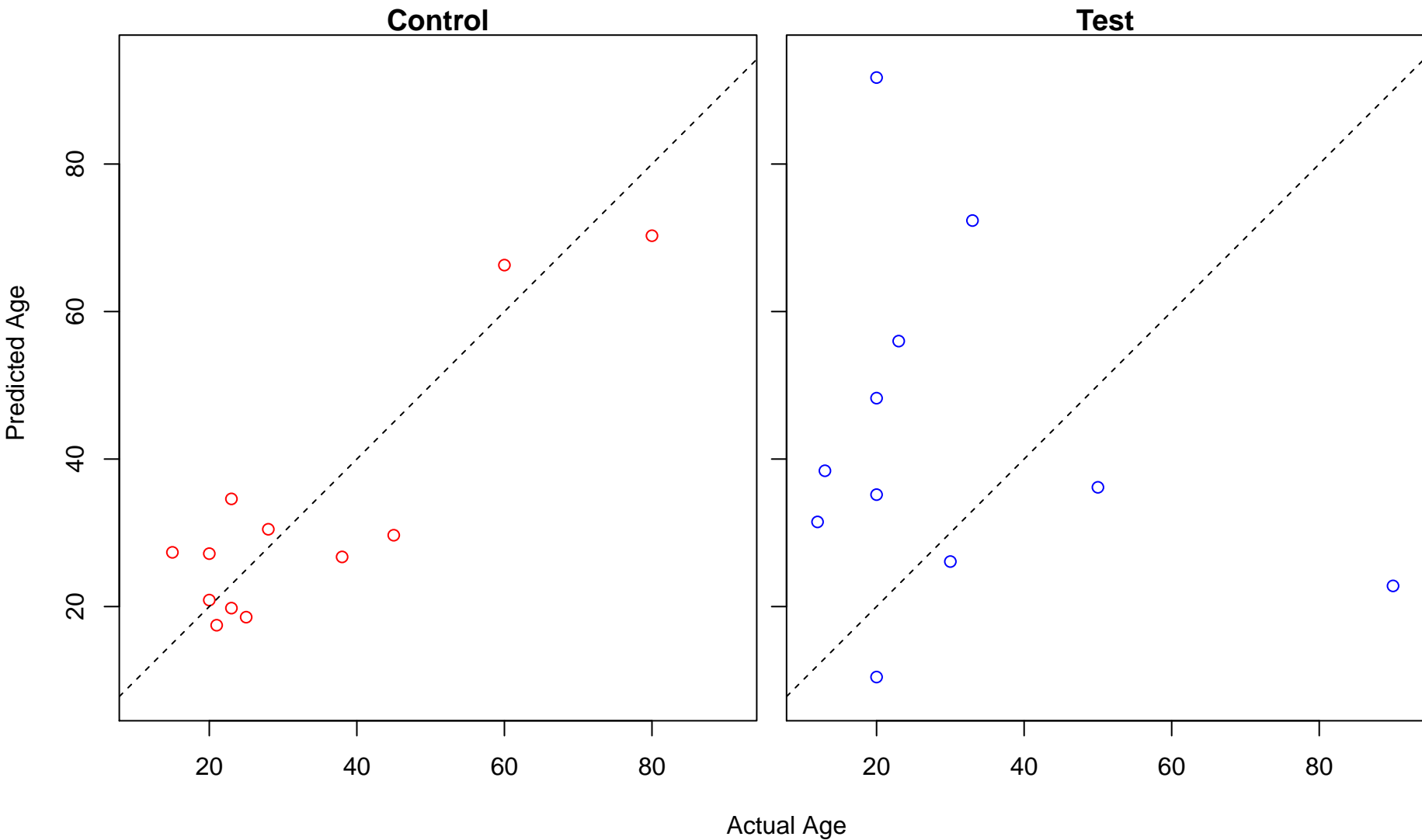
regulation of bone development (Score: 9.293363)



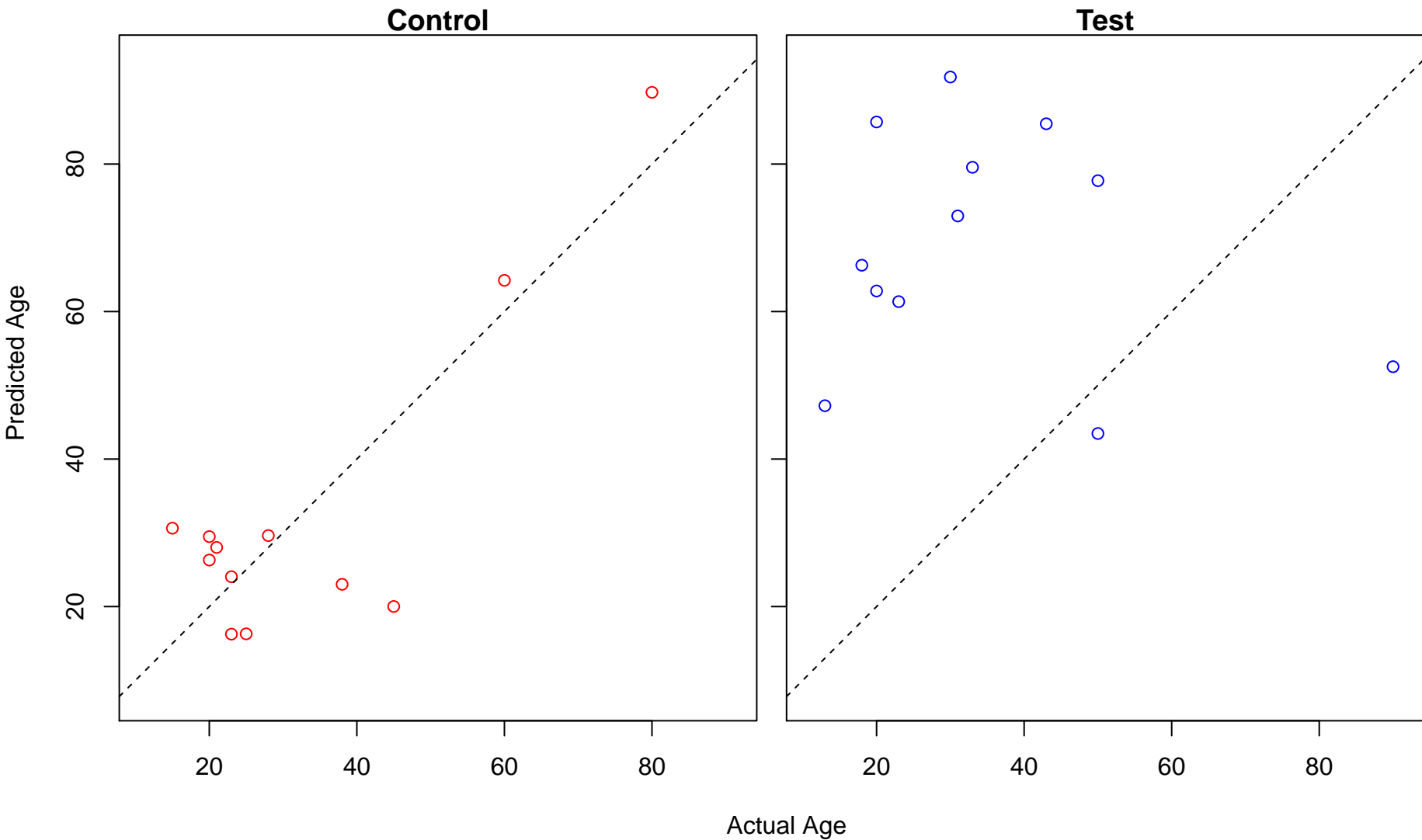
positive regulation by host of viral genome replication (Score: 9.289035)



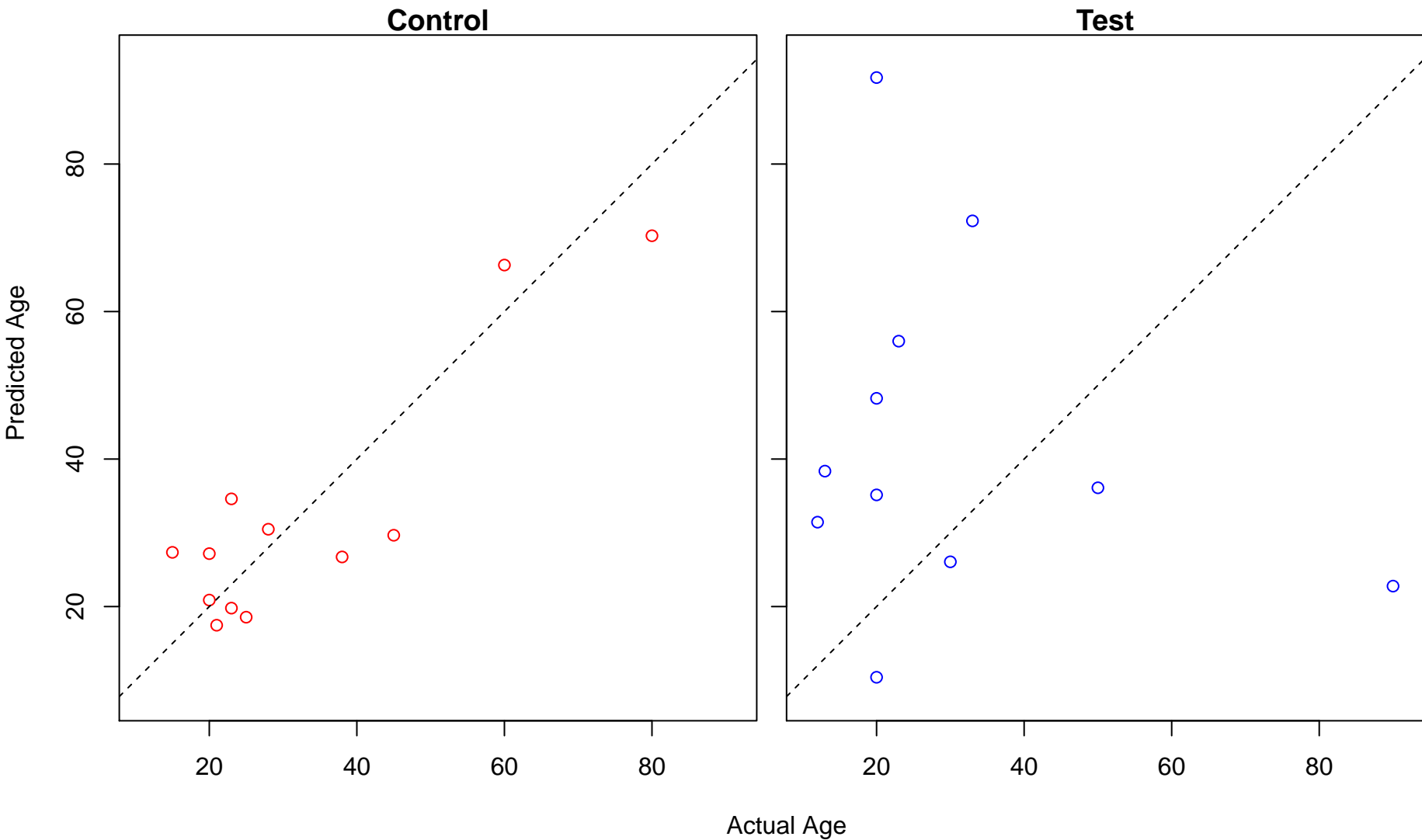
regulation of mitotic sister chromatid separation (Score: 9.287607)



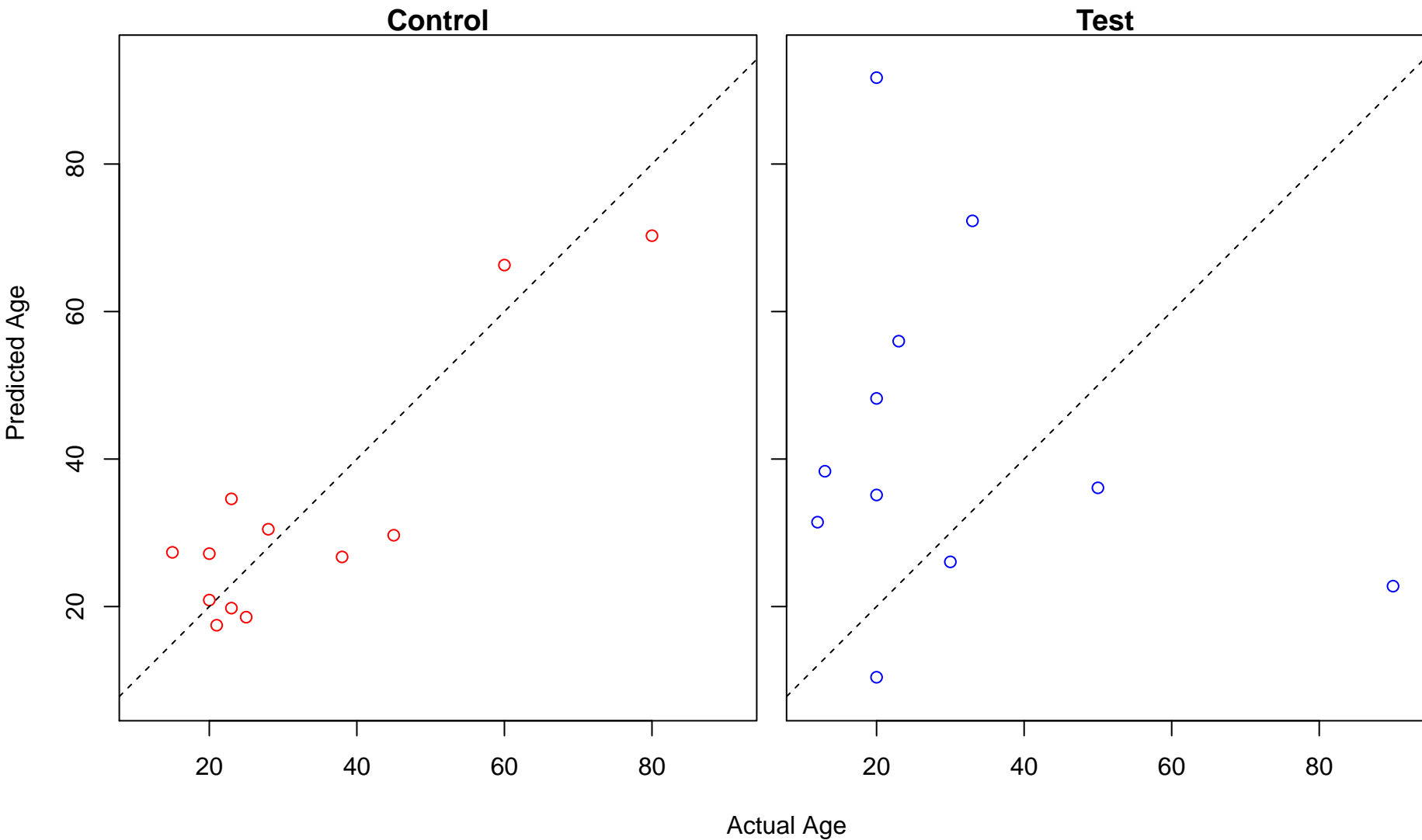
androgen metabolic process (Score: 9.285314)



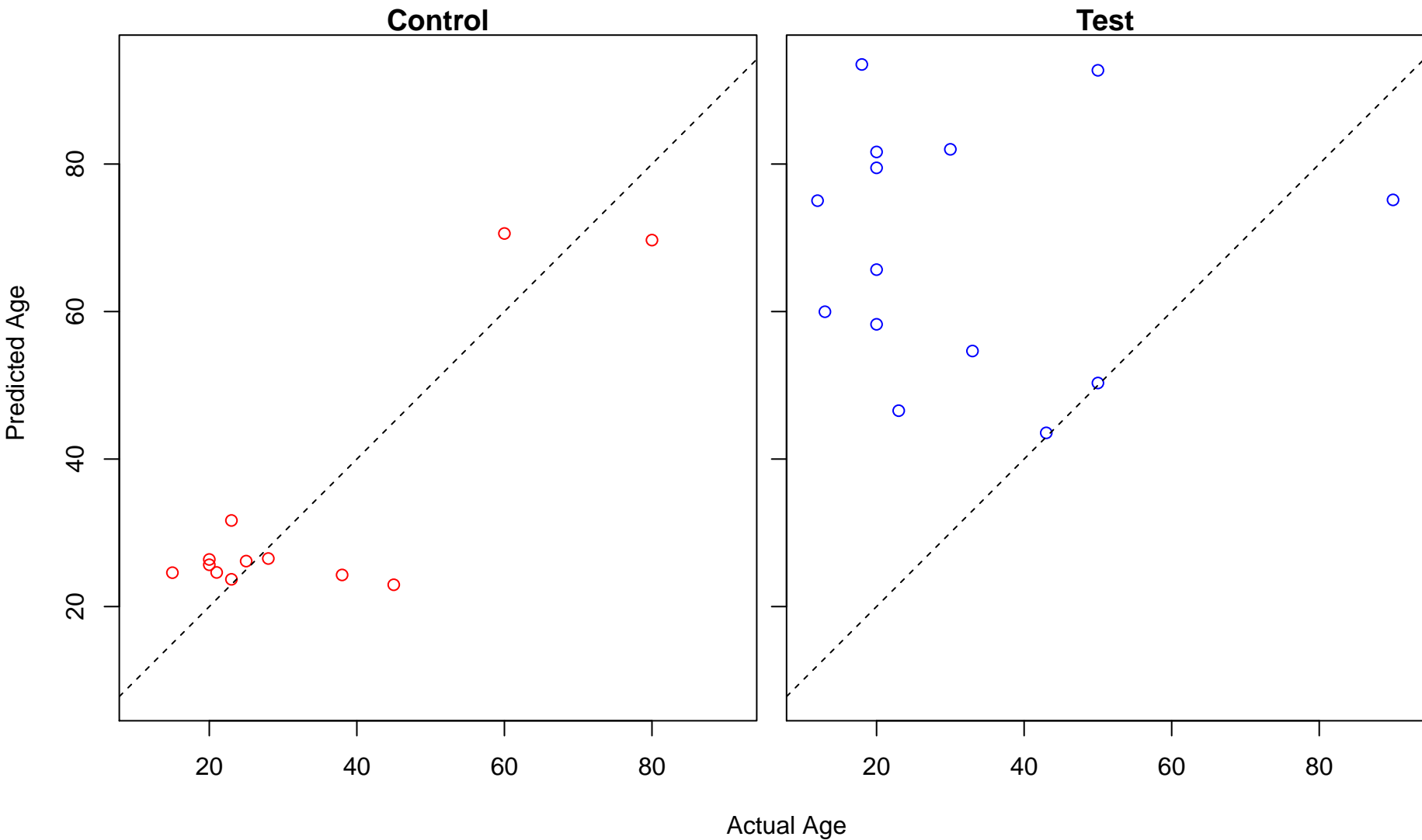
regulation of mitotic metaphase/anaphase transition (Score: 9.285276)



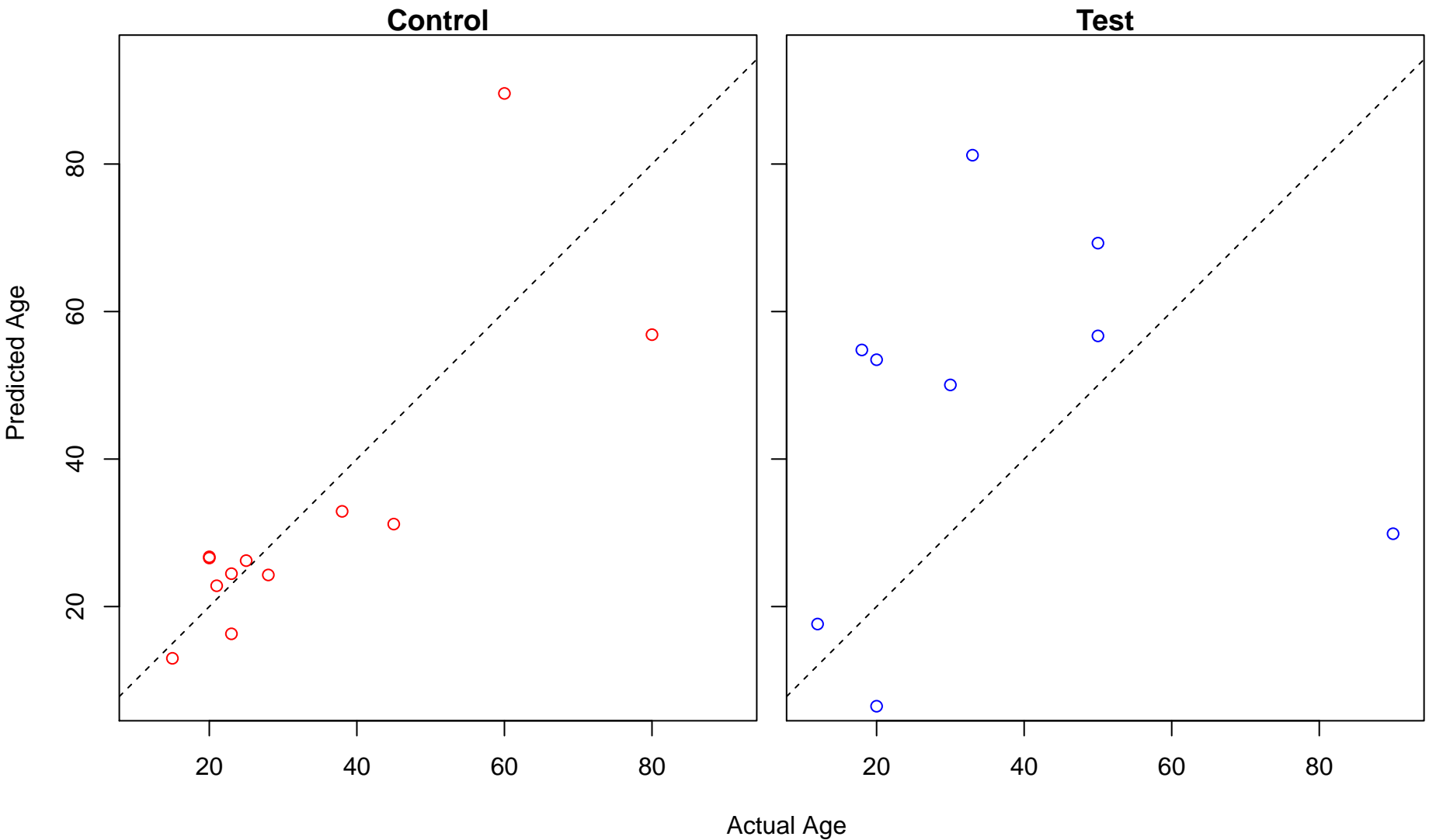
regulation of metaphase/anaphase transition of cell cycle (Score: 9.285075)



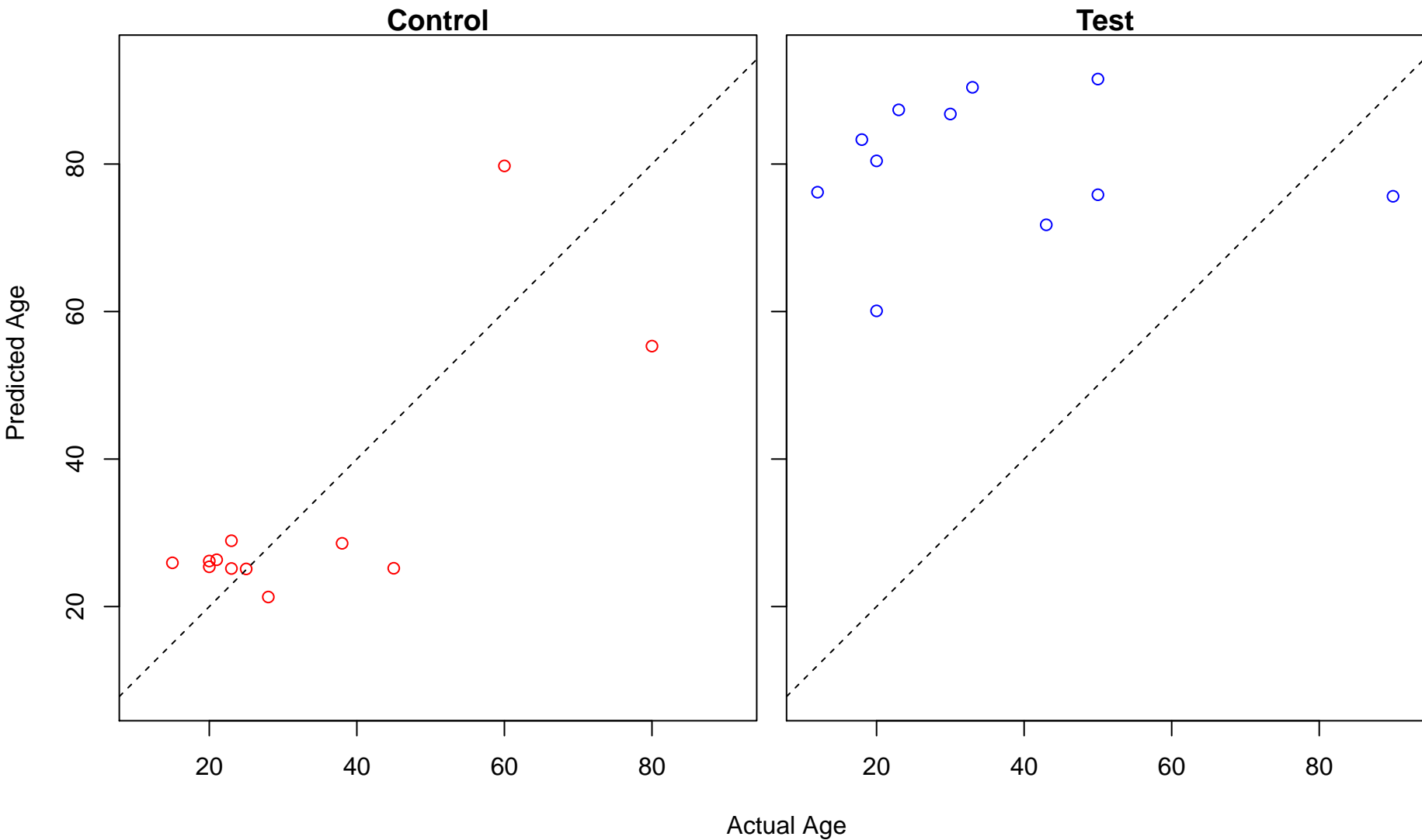
3'-UTR-mediated mRNA stabilization (Score: 9.284094)



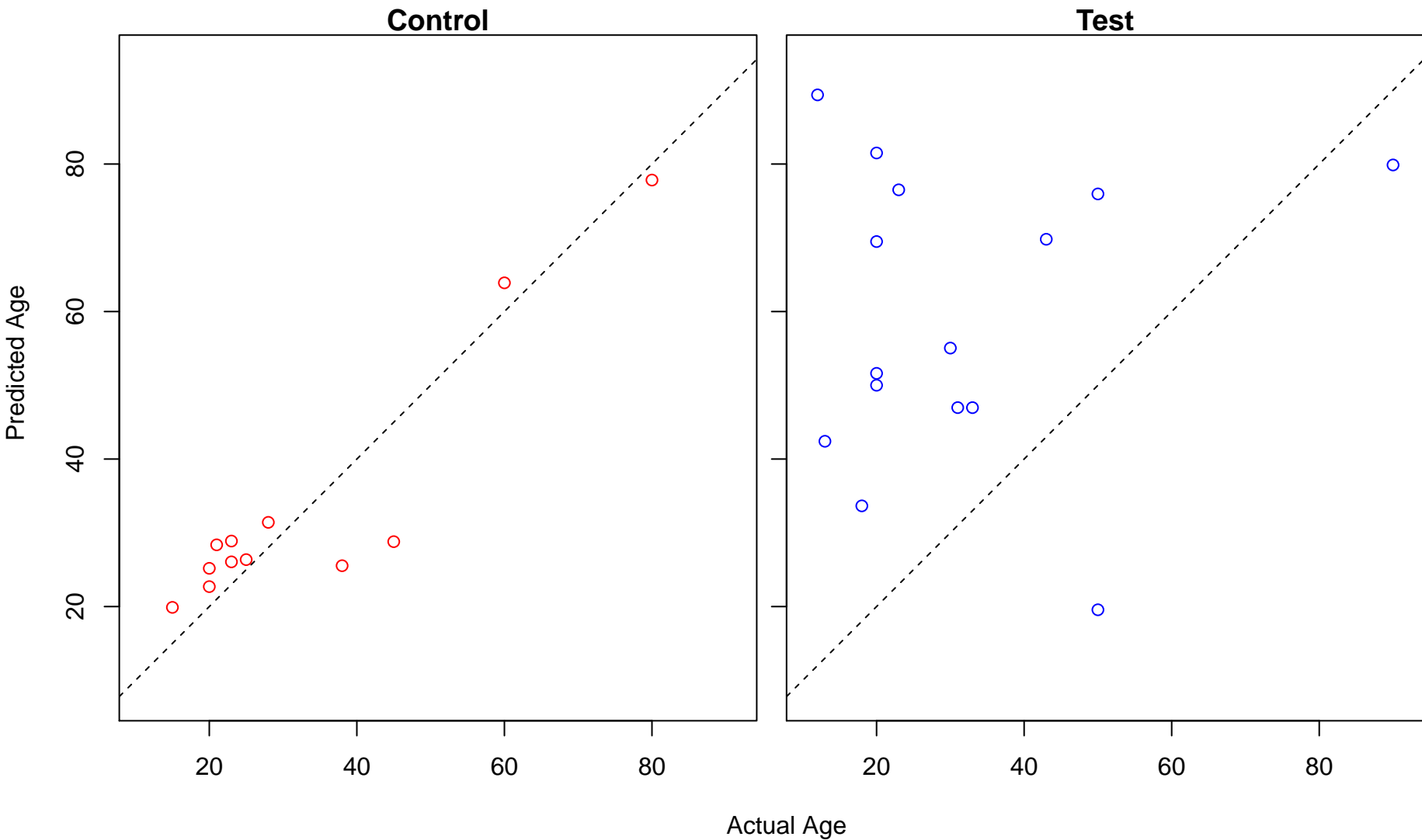
positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 1.0)



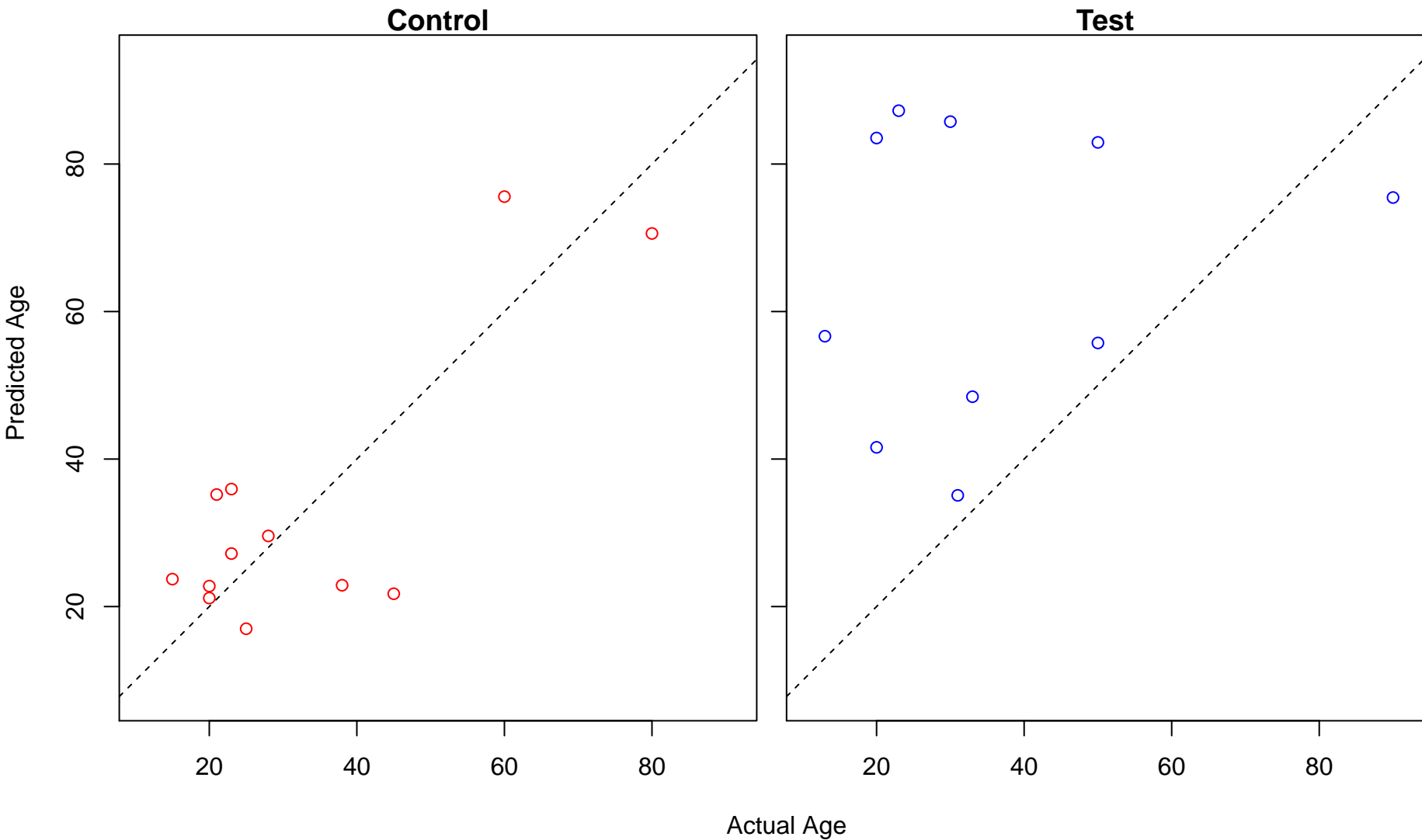
taurine metabolic process (Score: 9.275025)



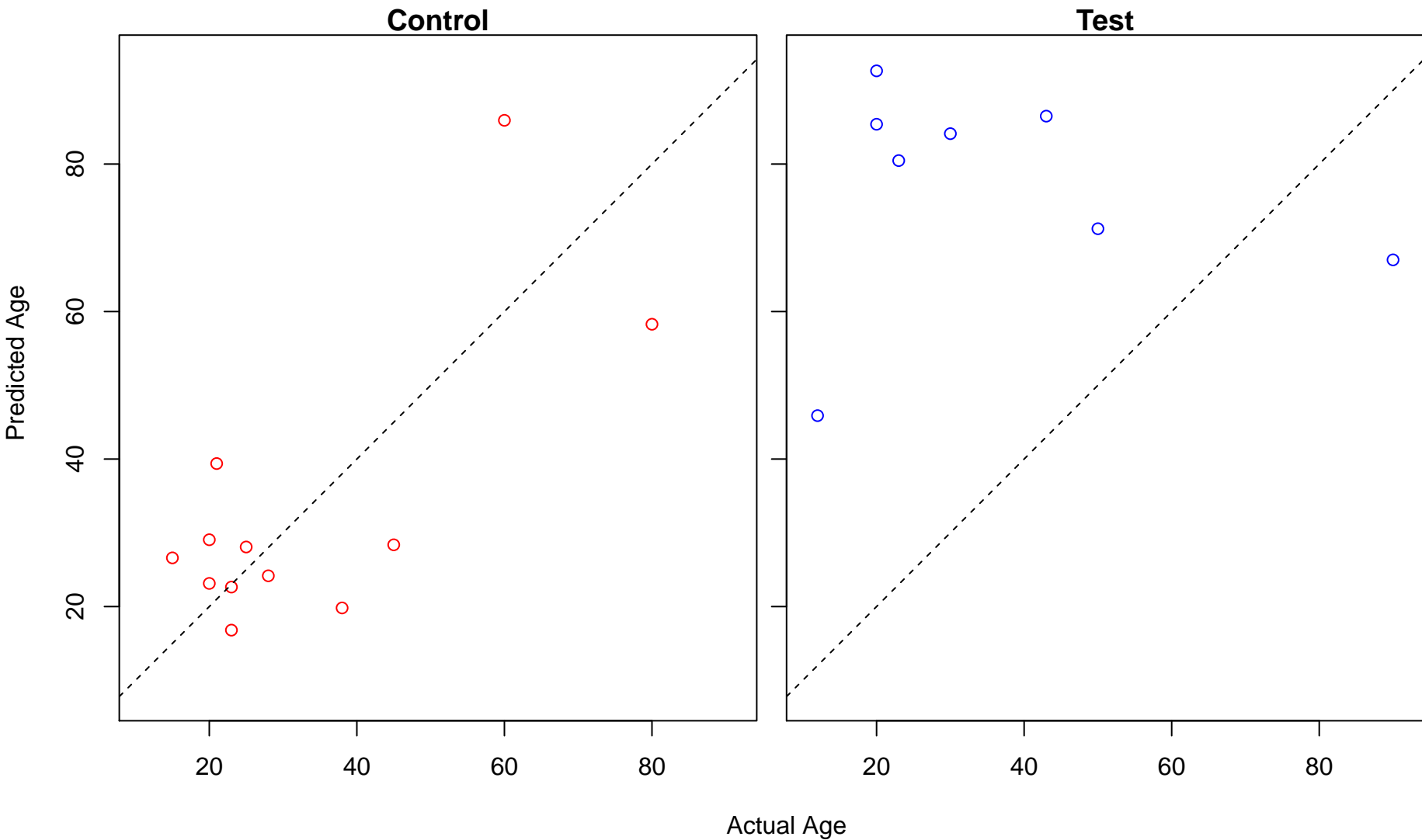
positive regulation of myeloid leukocyte mediated immunity (Score: 9.267666)



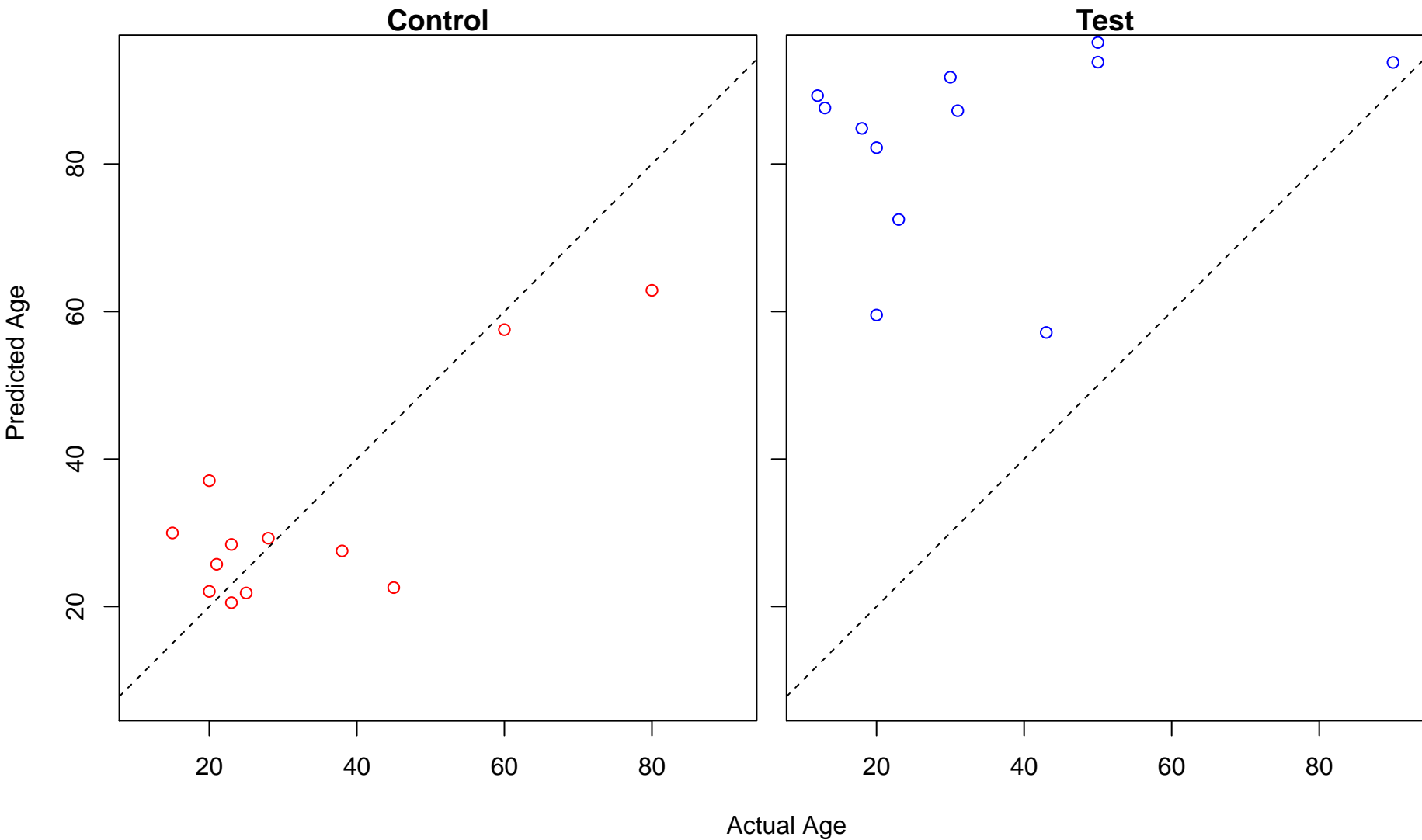
epiboly (Score: 9.266132)



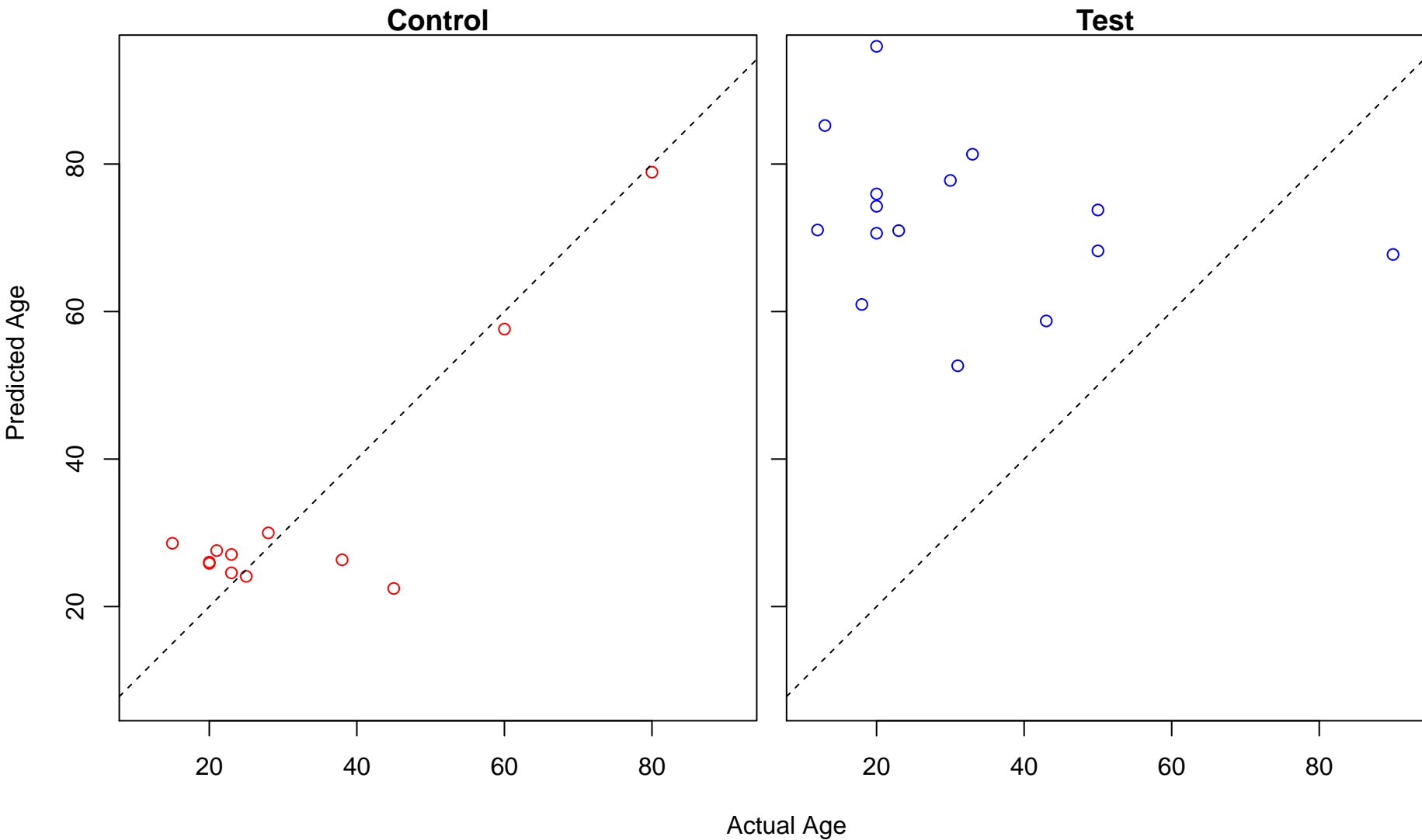
decidualization (Score: 9.261500)



negative regulation of fatty acid transport (Score: 9.260964)

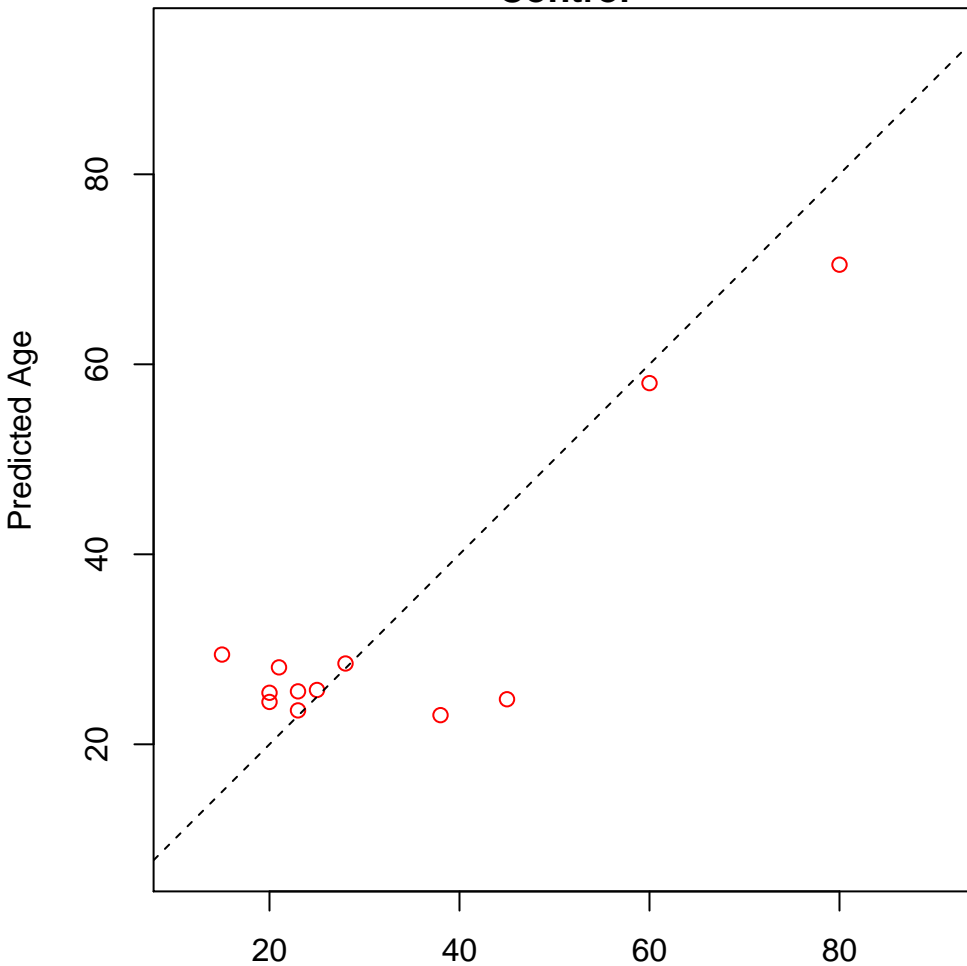


response to platelet-derived growth factor (Score: 9.259567)

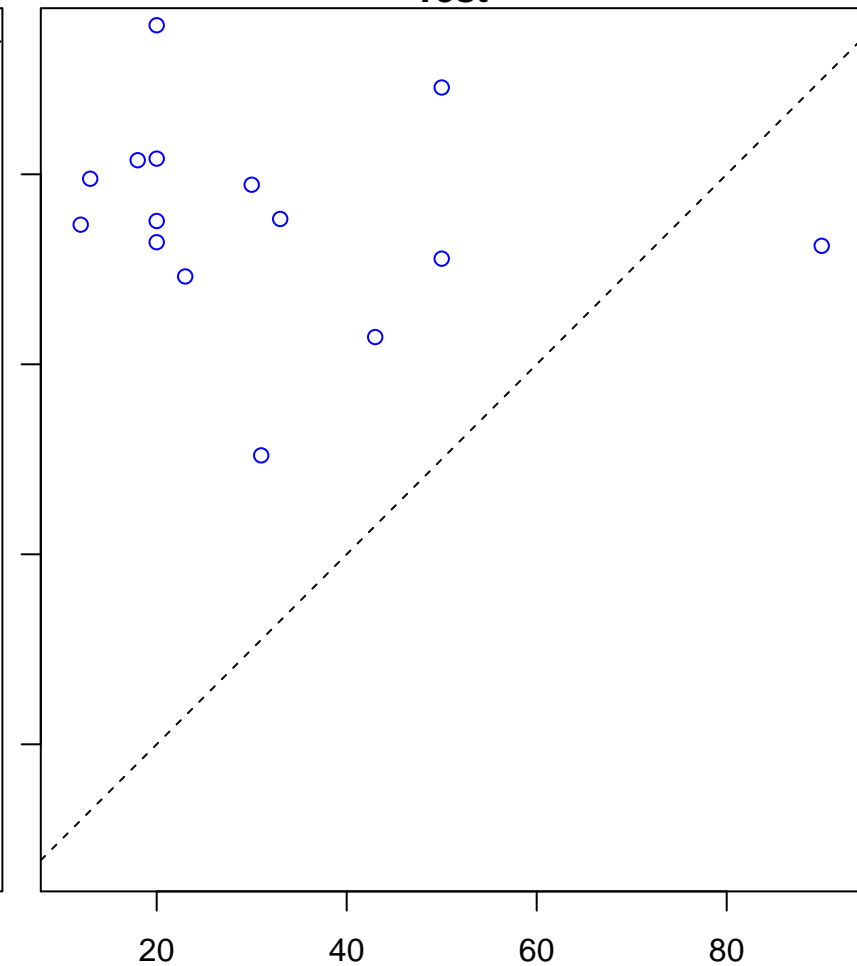


mitochondrial calcium ion homeostasis (Score: 9.253208)

Control

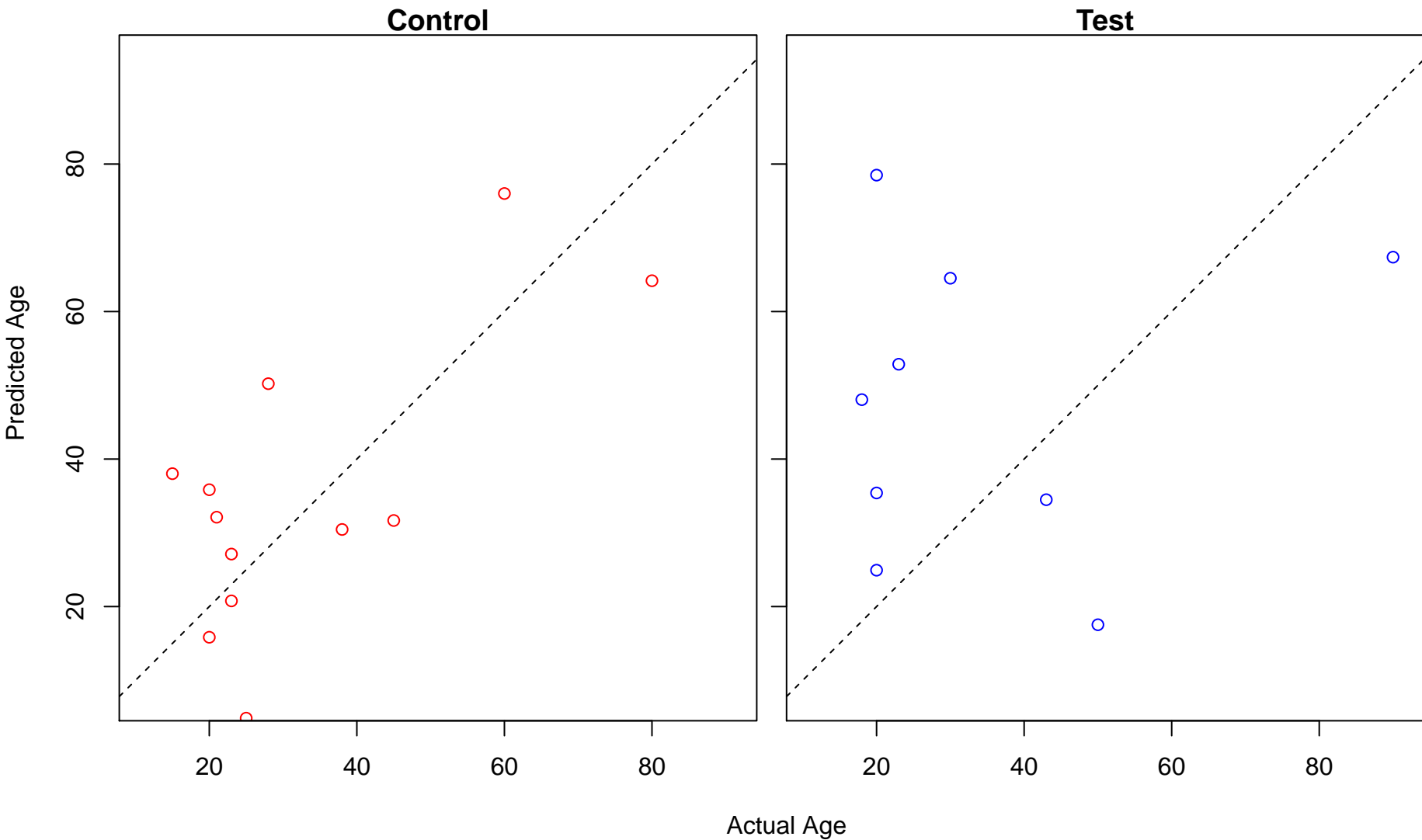


Test

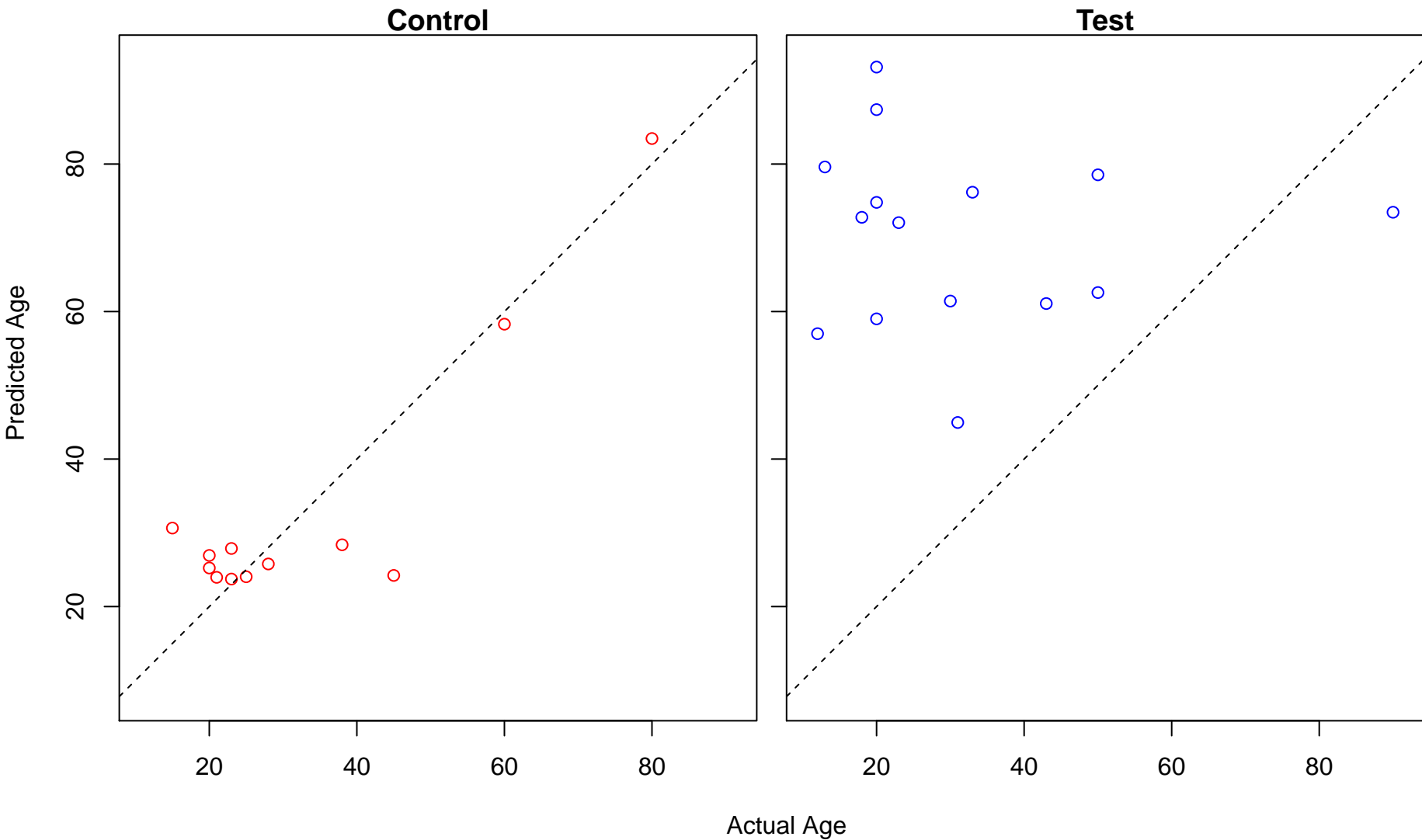


Actual Age

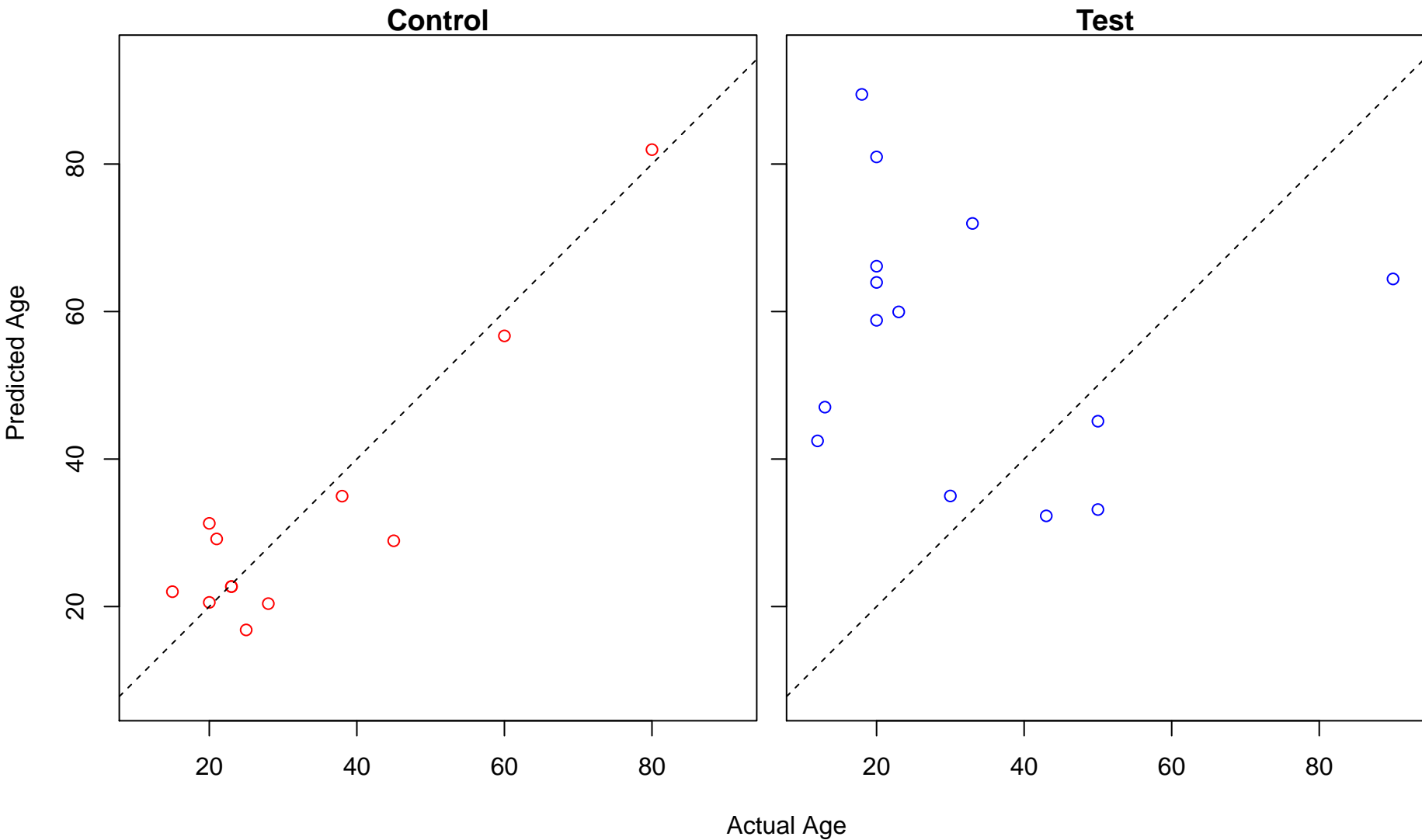
regulation of mast cell activation involved in immune response (Score: 9.239637)



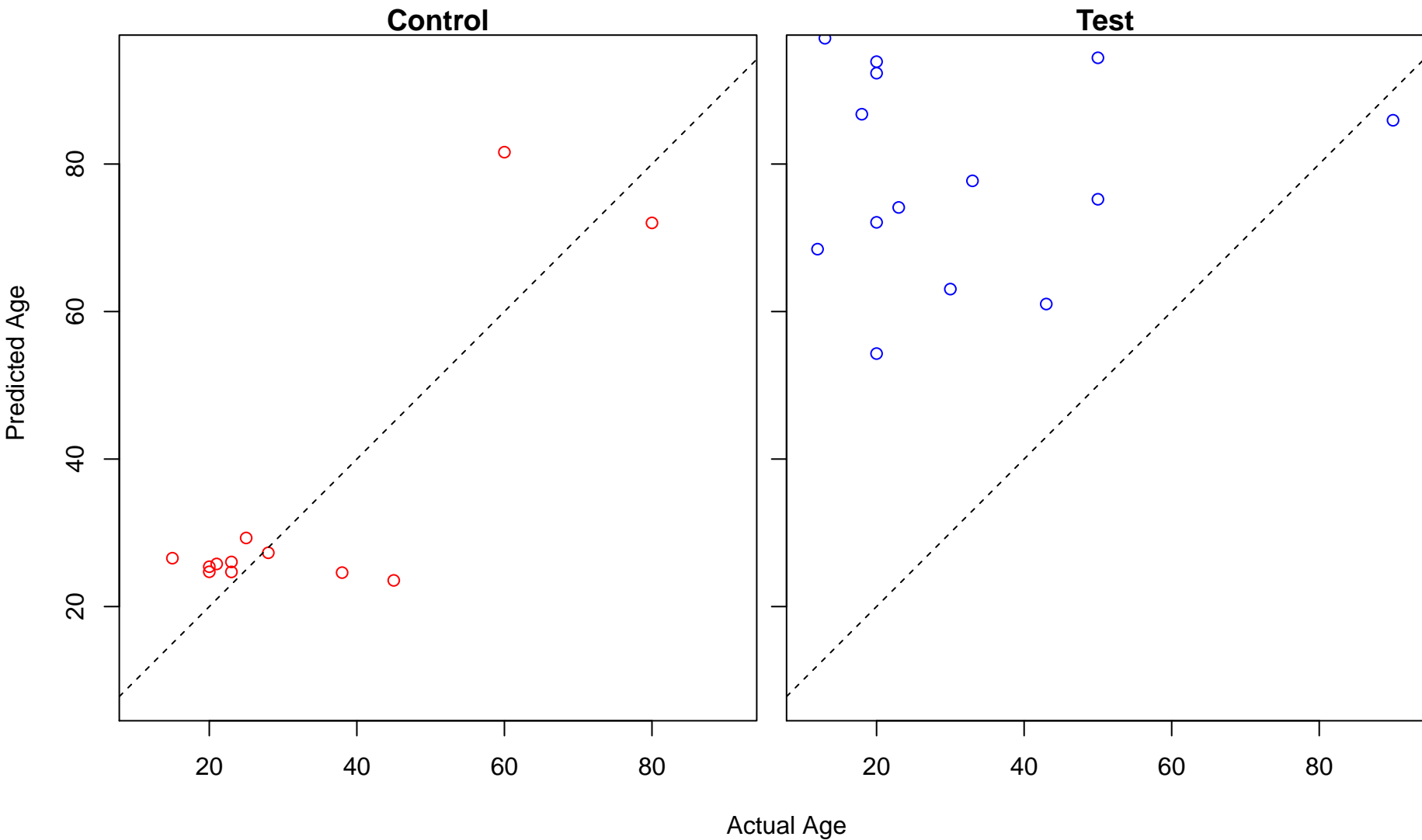
regulation of protein deacetylation (Score: 9.239318)



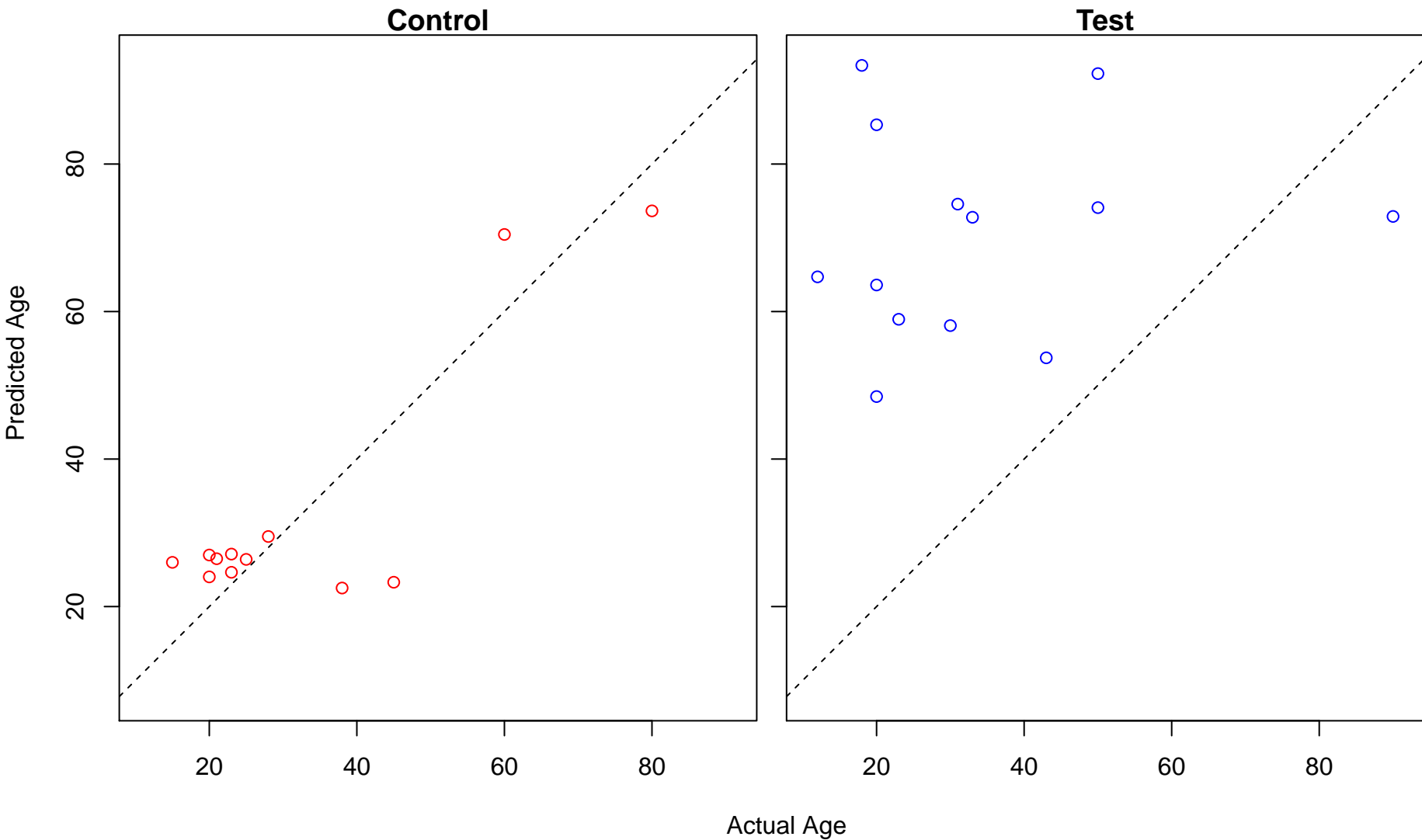
regulation of type B pancreatic cell development (Score: 9.236705)



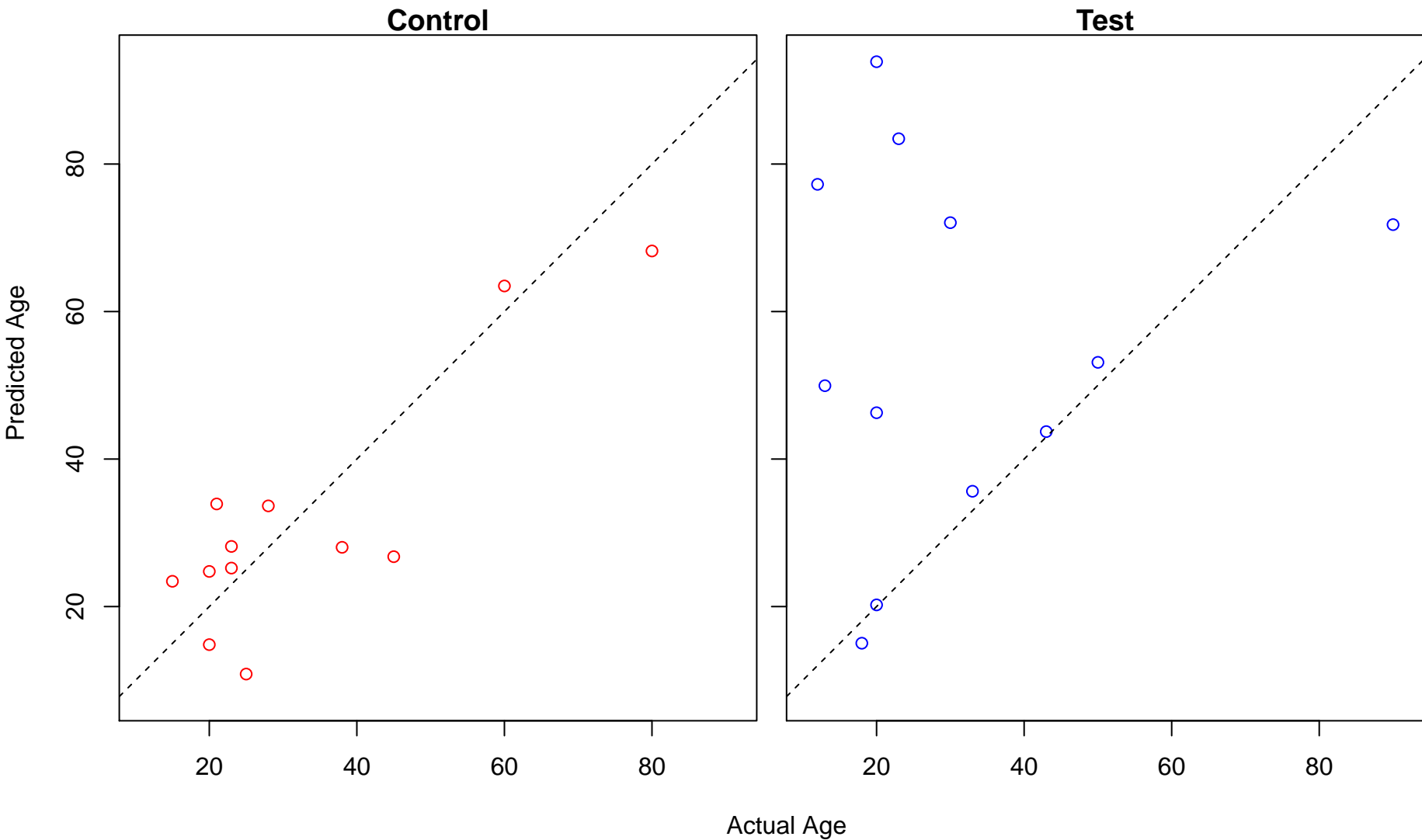
cAMP catabolic process (Score: 9.236130)



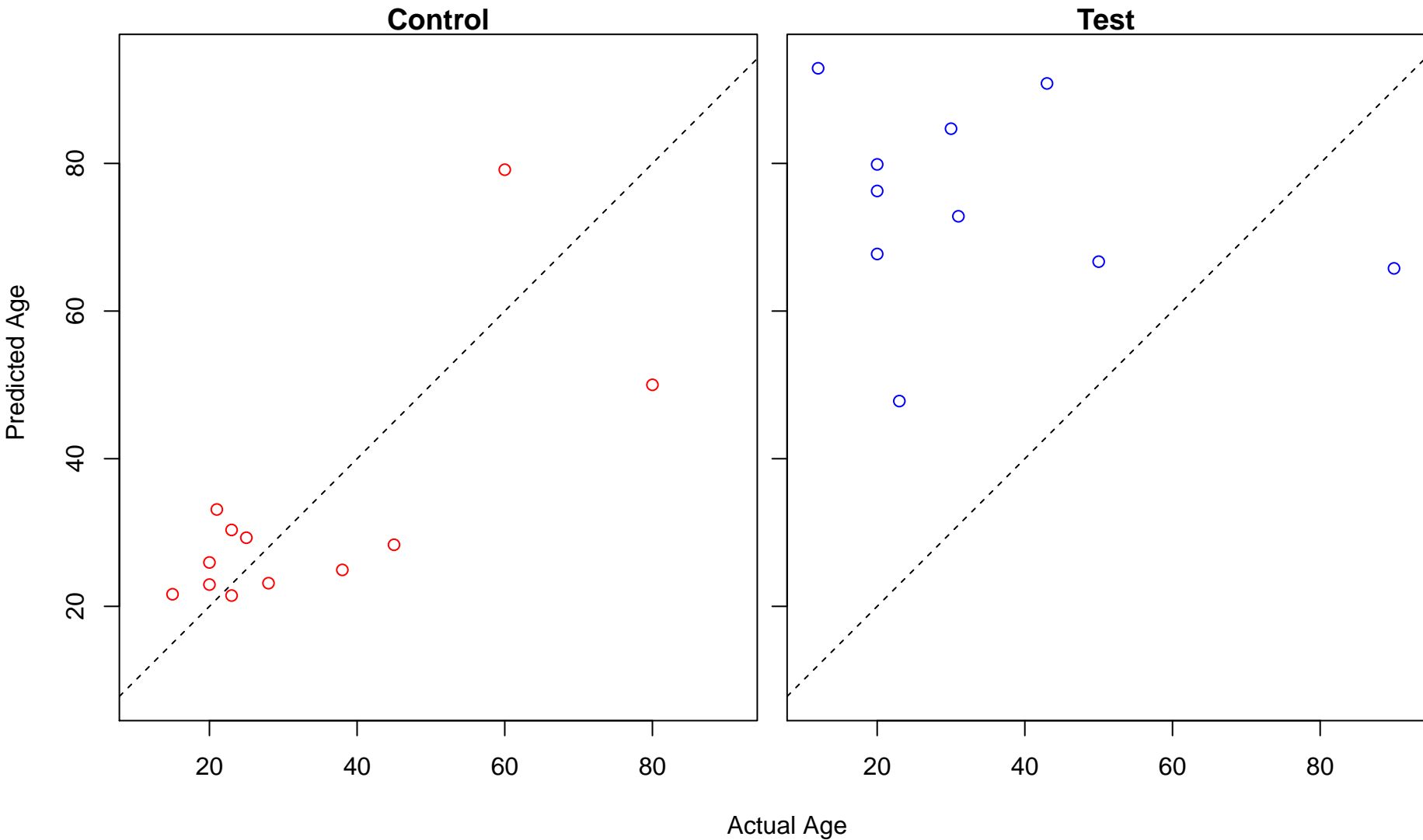
regulation of establishment of protein localization to mitochondrion (Score: 9.234444)



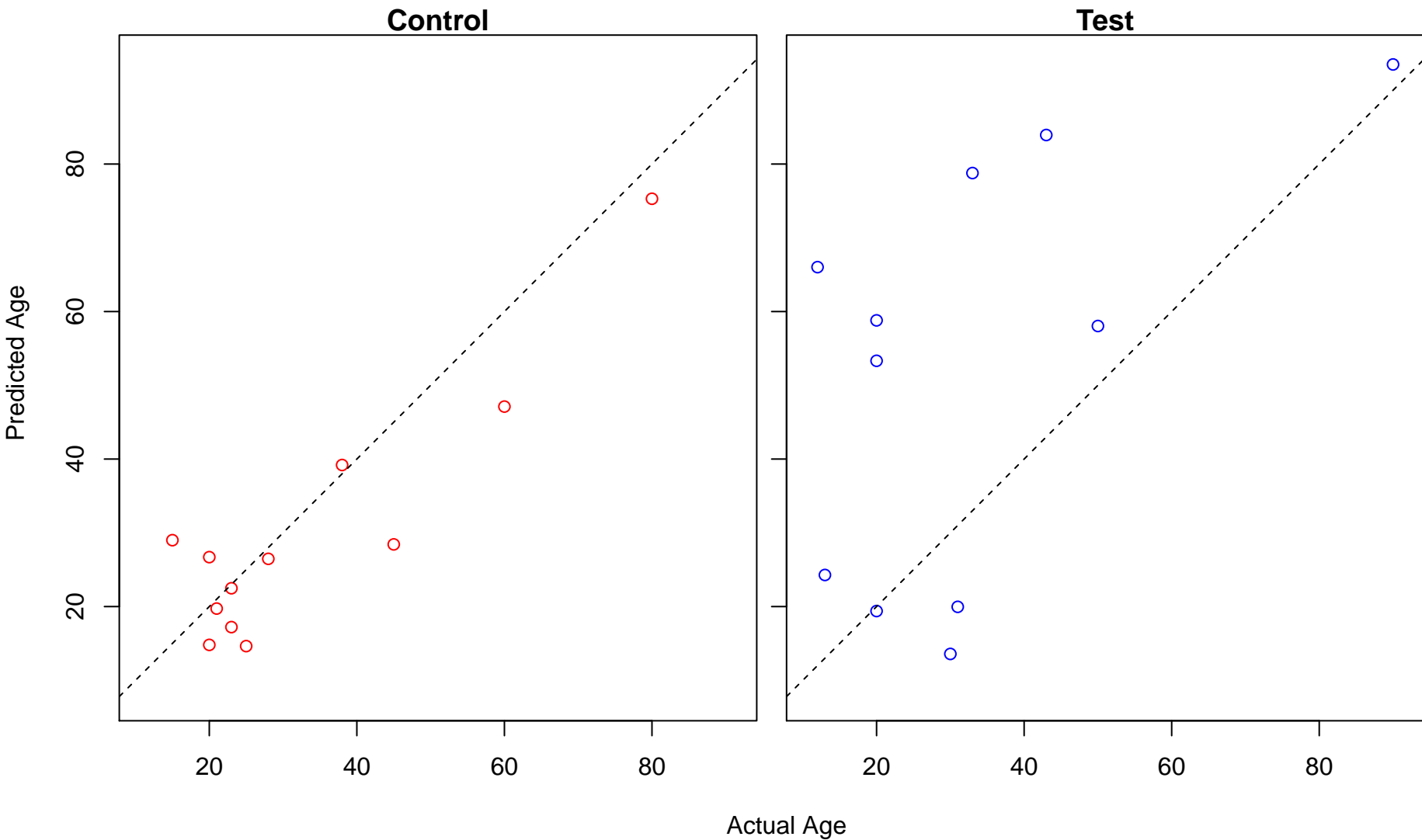
regulation of leukocyte degranulation (Score: 9.229888)



low-density lipoprotein particle remodeling (Score: 9.228191)

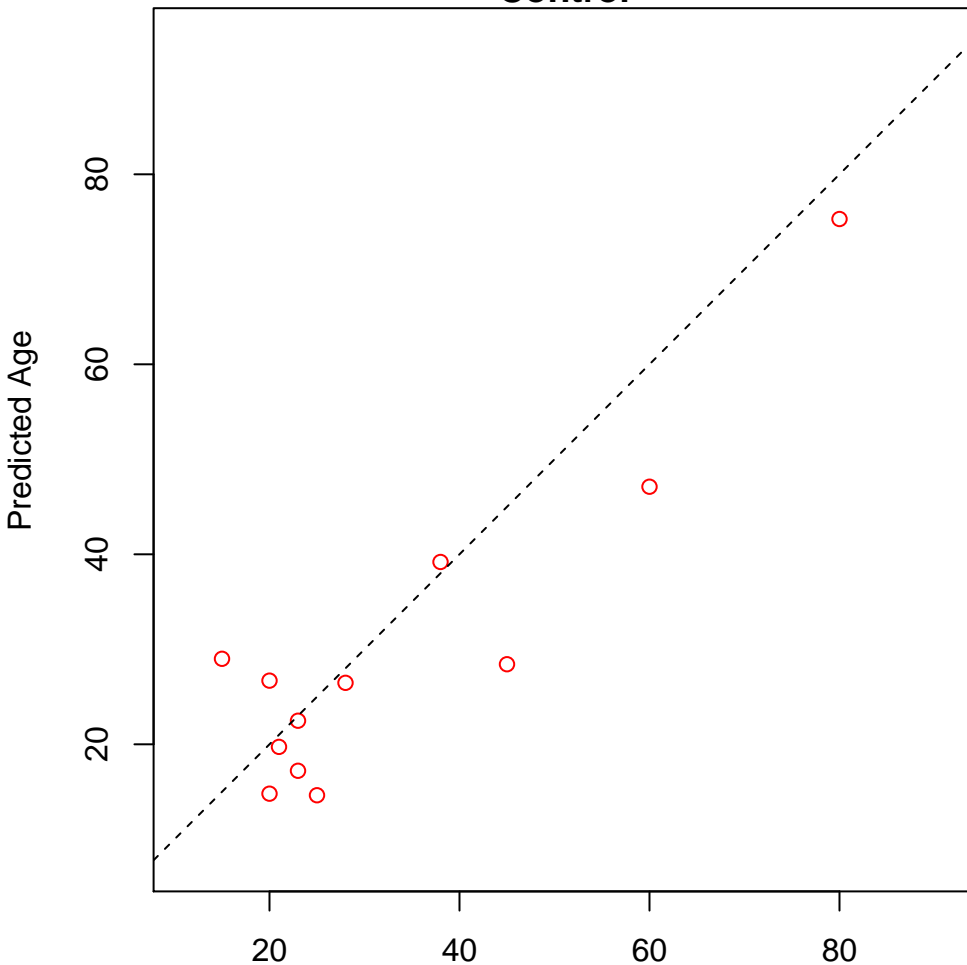


nephron morphogenesis (Score: 9.227810)

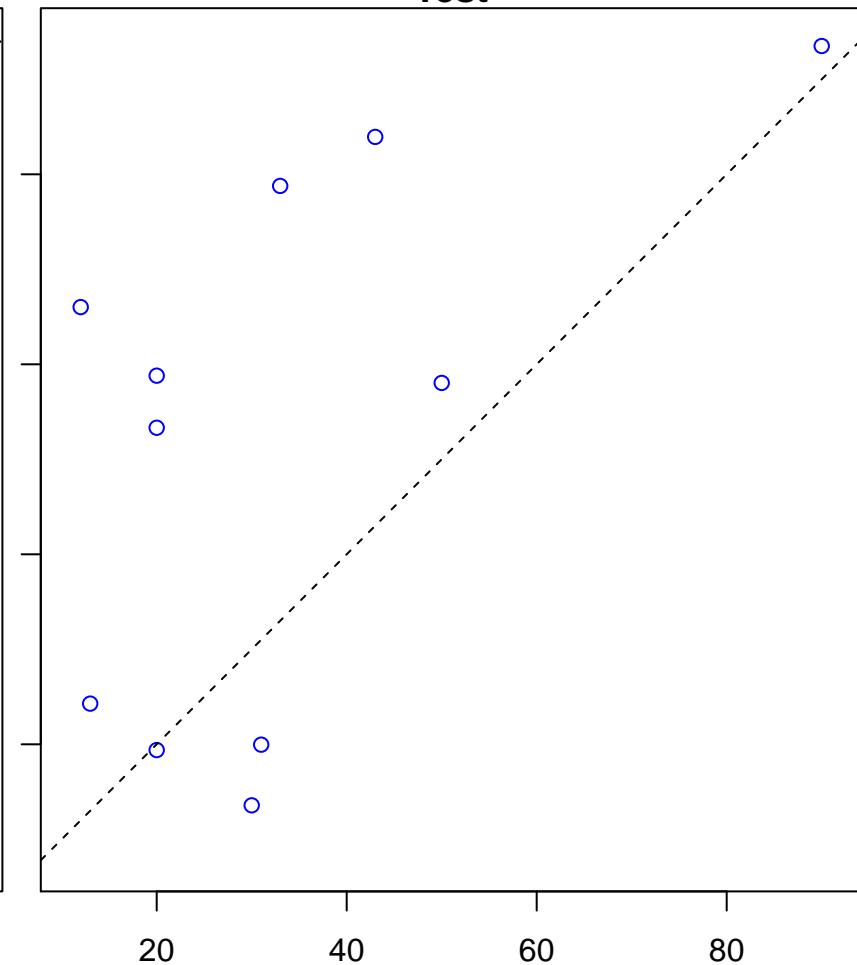


nephron epithelium morphogenesis (Score: 9.227810)

Control

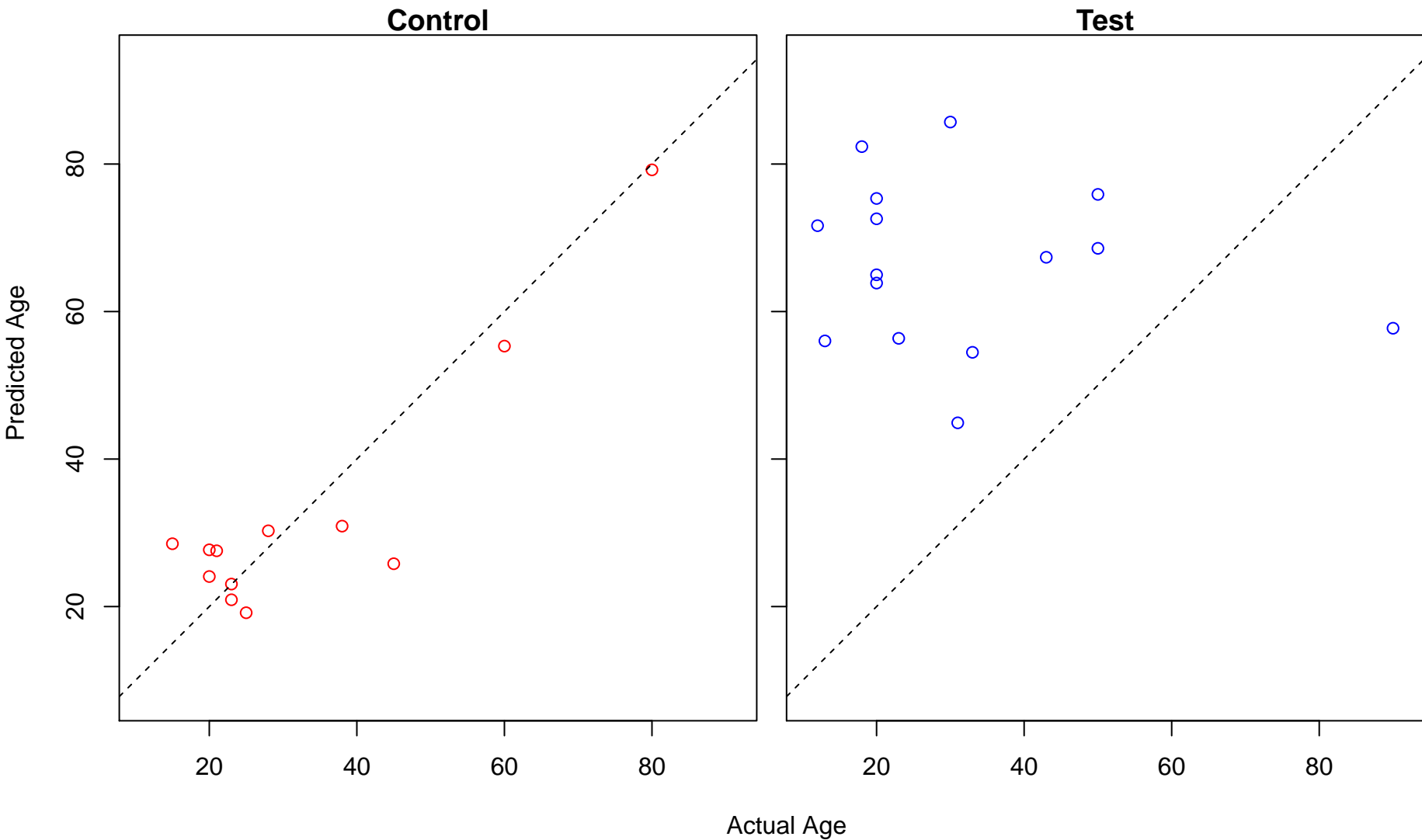


Test

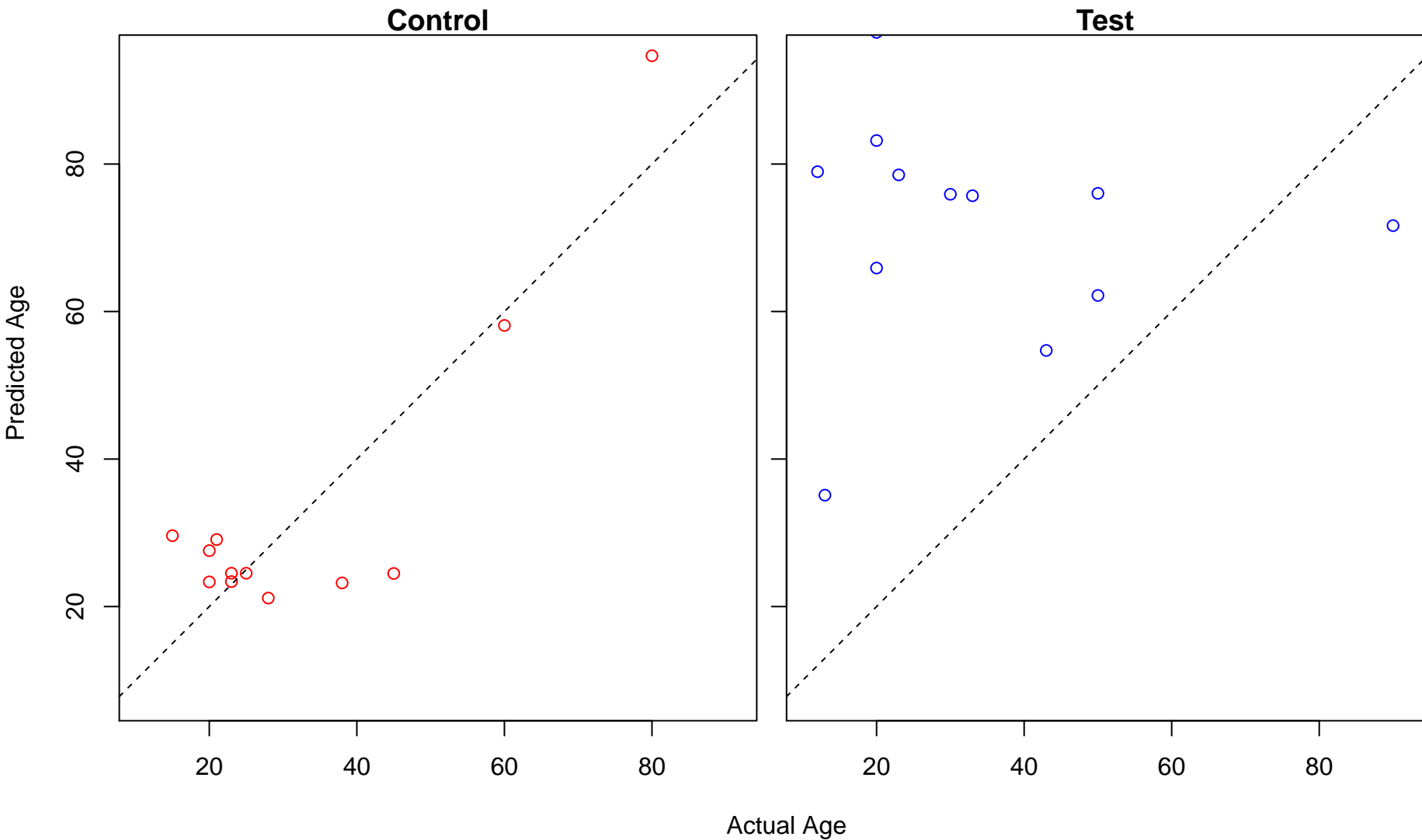


Actual Age

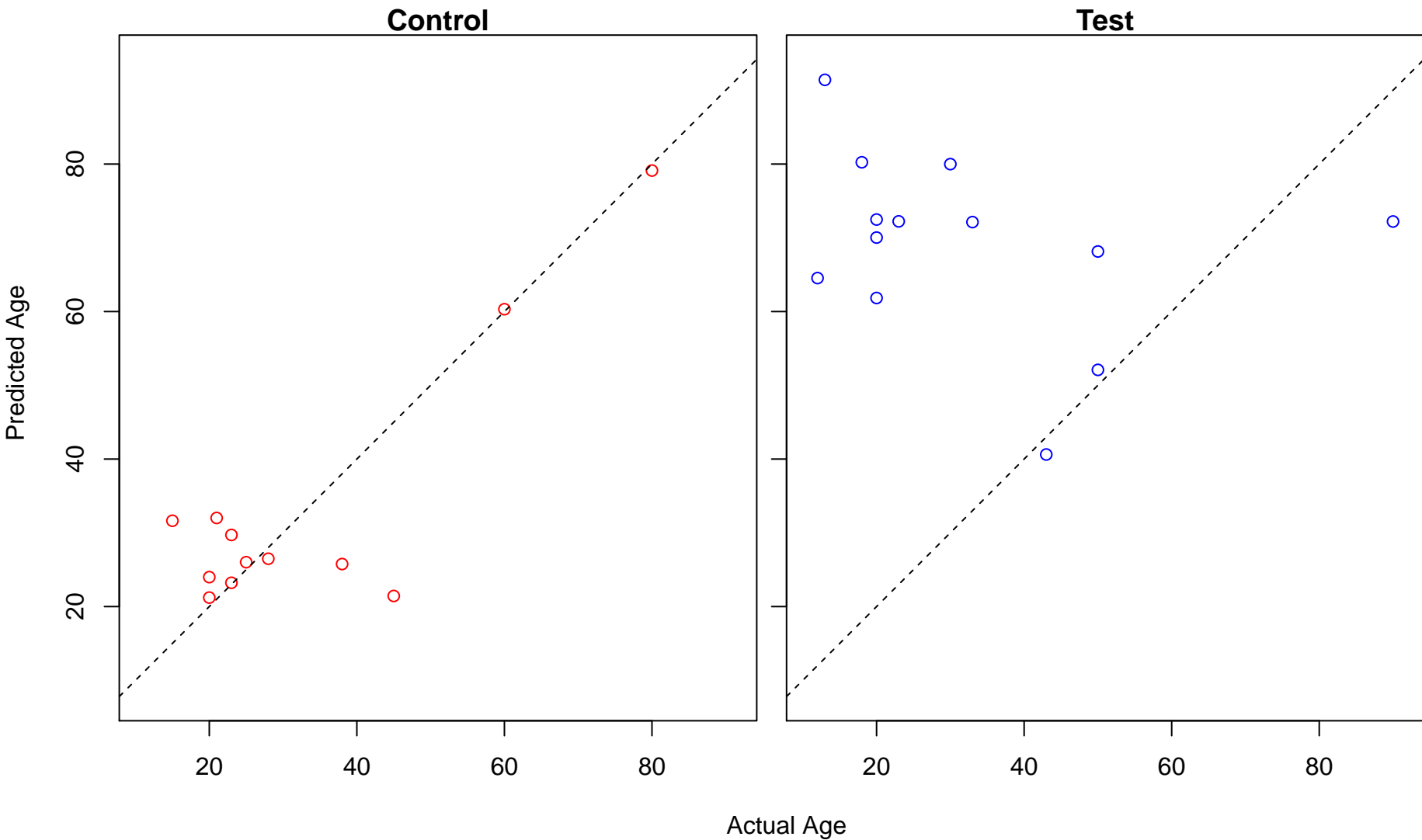
cellular aldehyde metabolic process (Score: 9.225197)



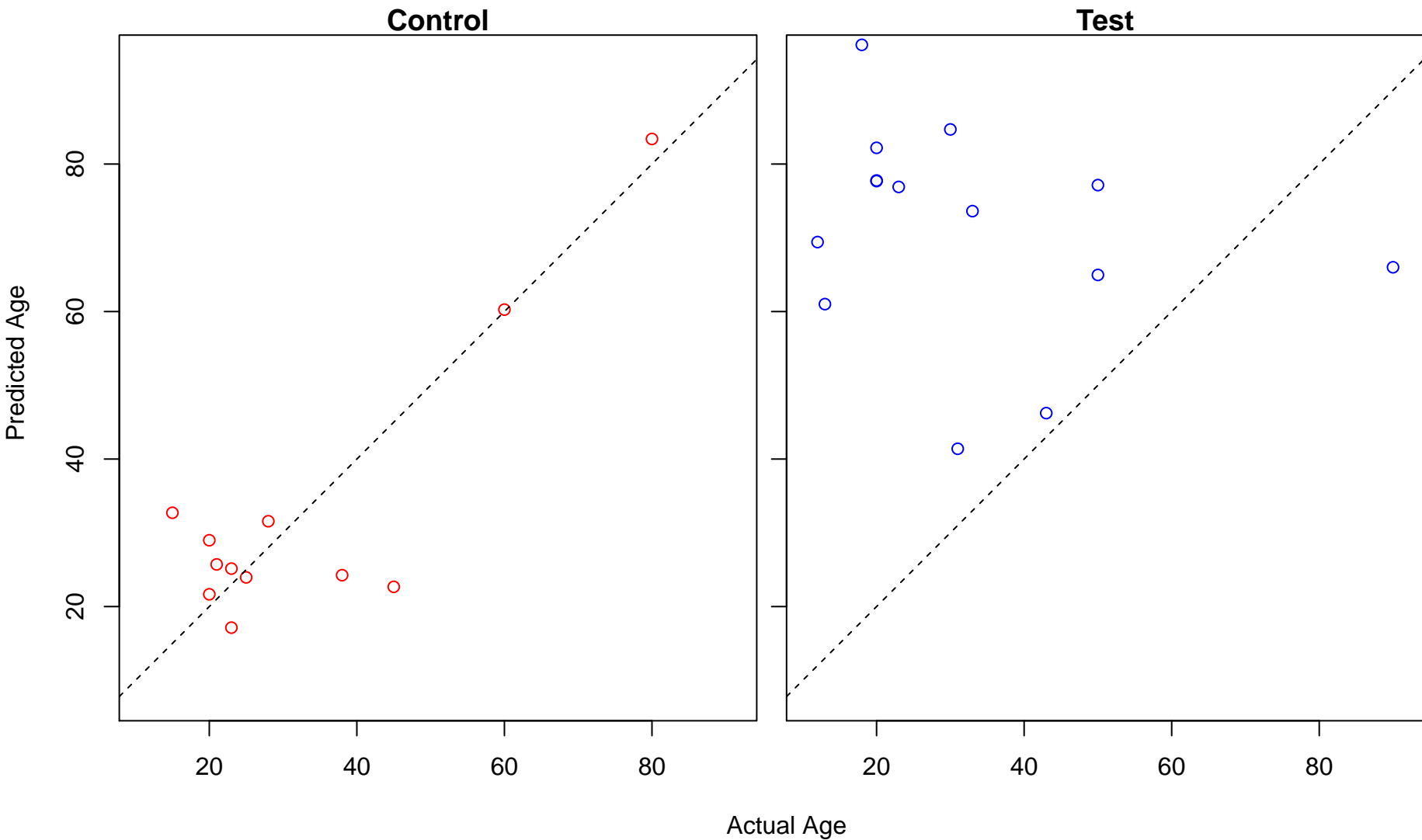
asymmetric cell division (Score: 9.207469)



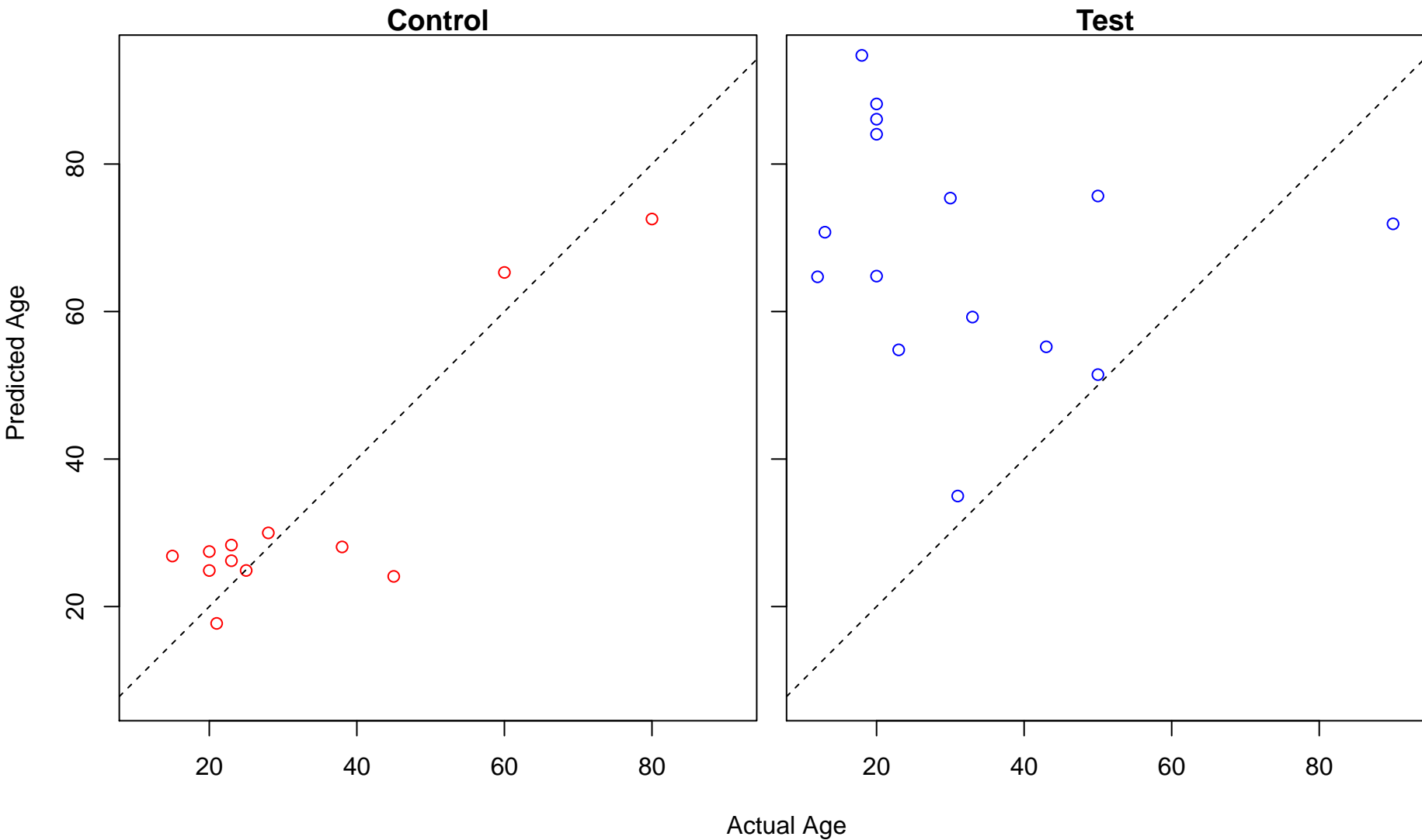
positive regulation of protein localization to nucleus (Score: 9.205107)



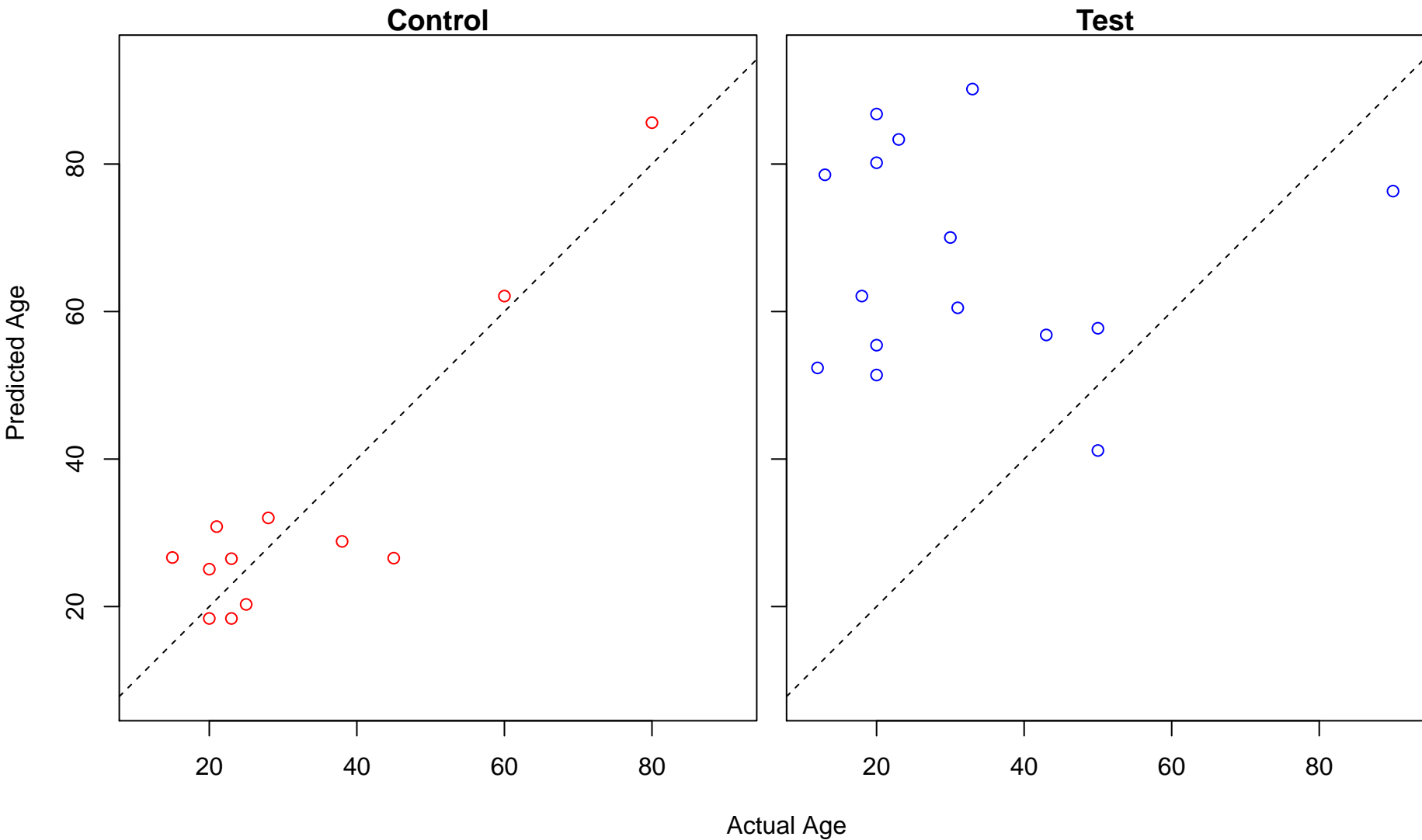
ERAD pathway (Score: 9.202102)



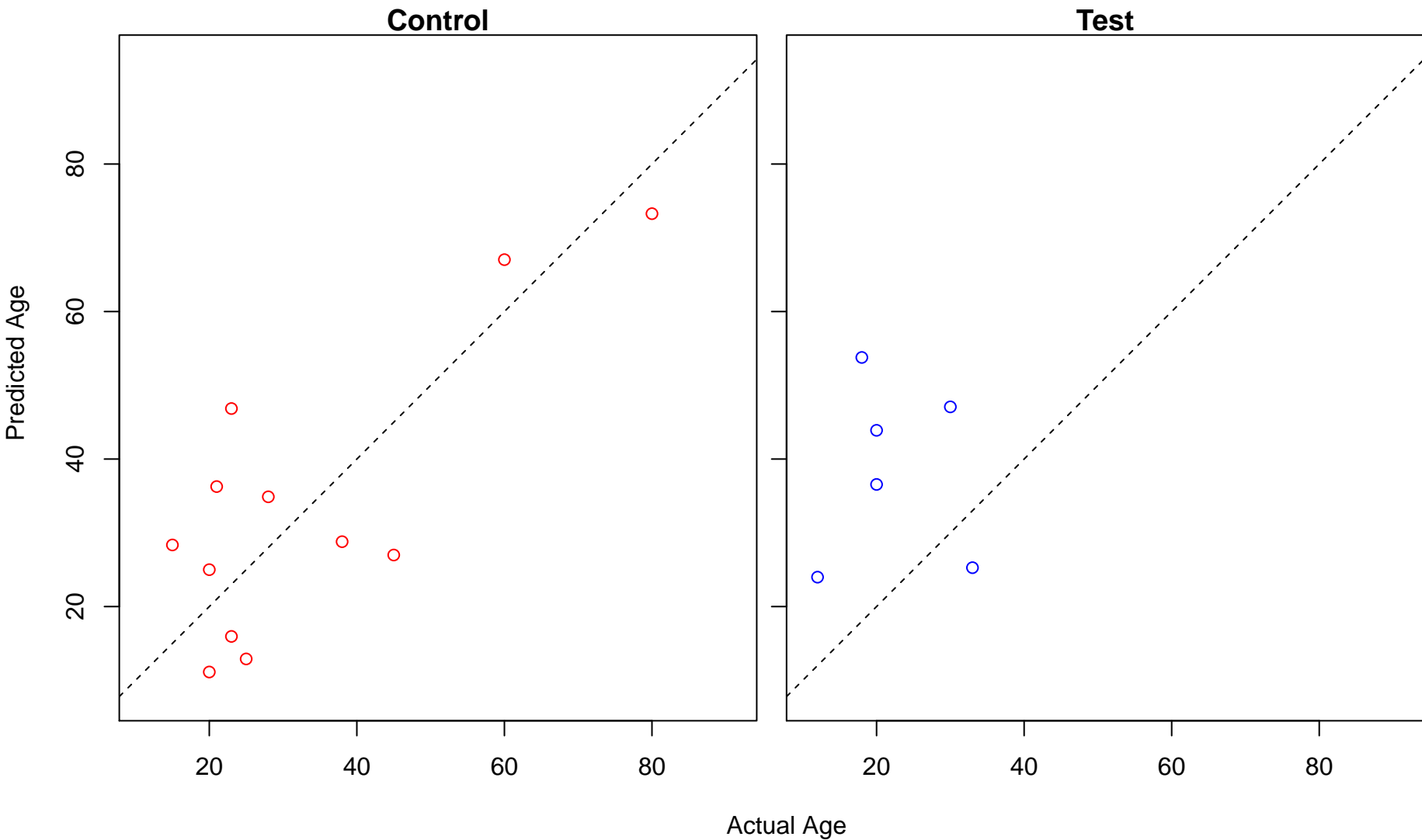
pyrimidine nucleobase metabolic process (Score: 9.199549)



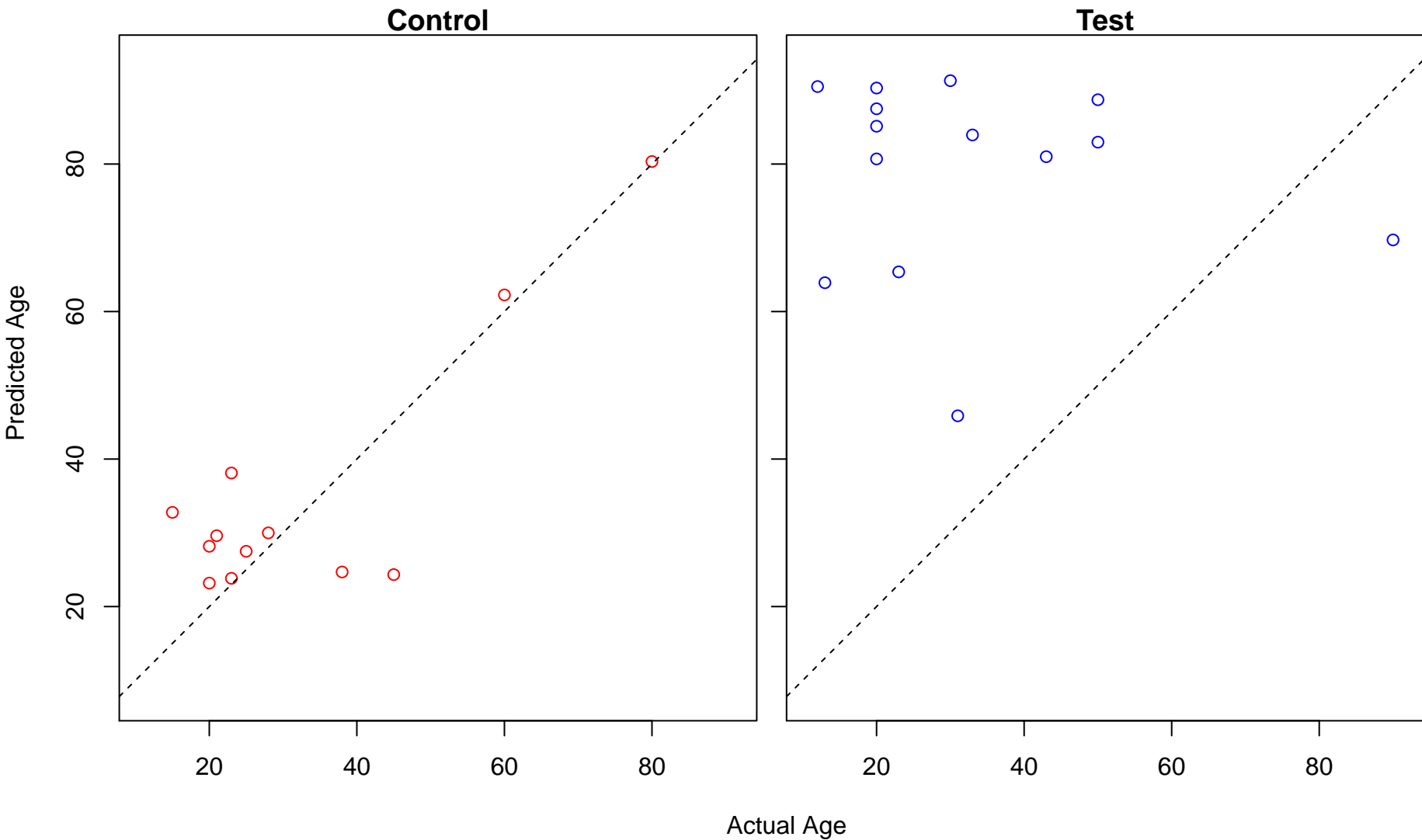
central nervous system neuron development (Score: 9.194917)



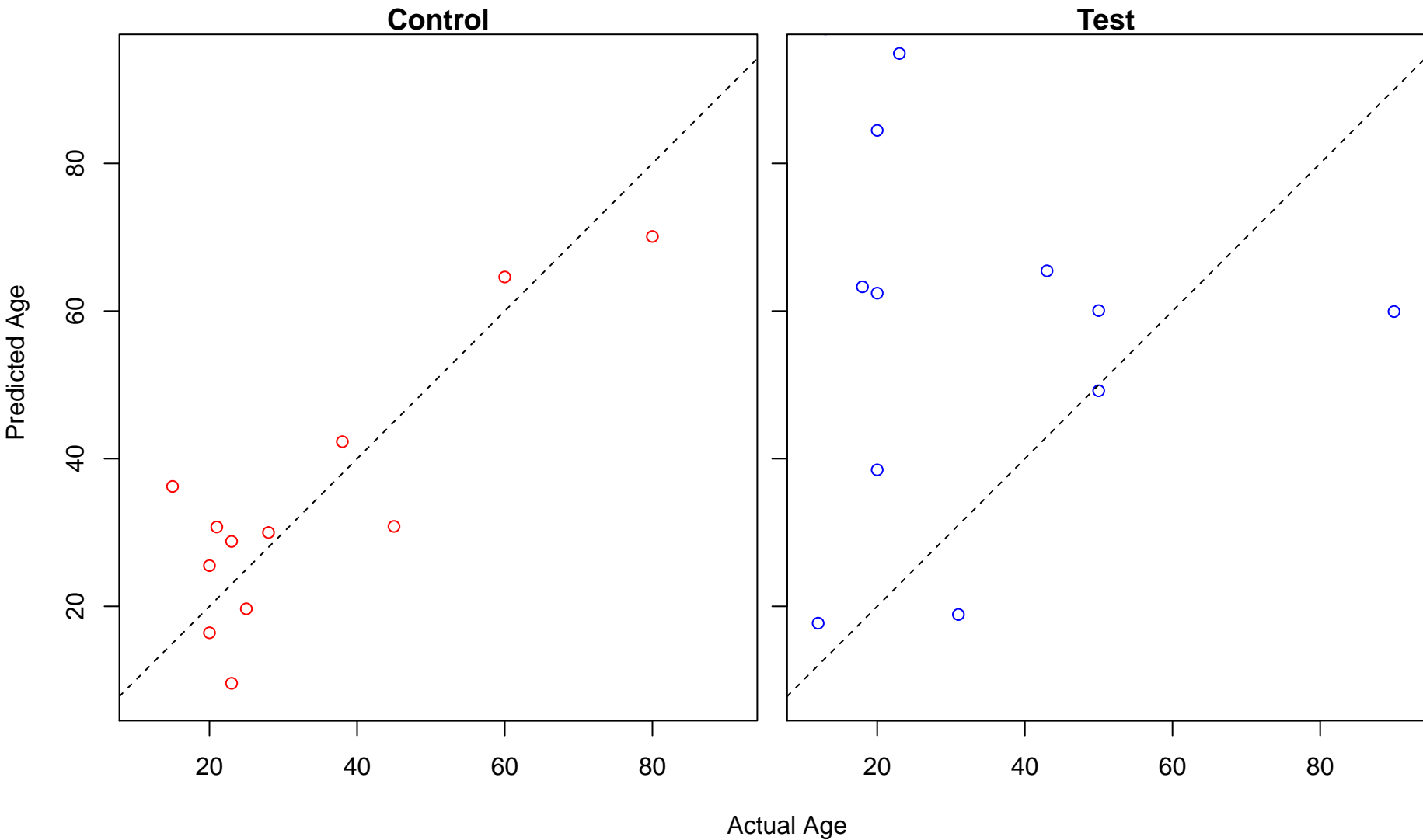
negative regulation of stem cell differentiation (Score: 9.191030)



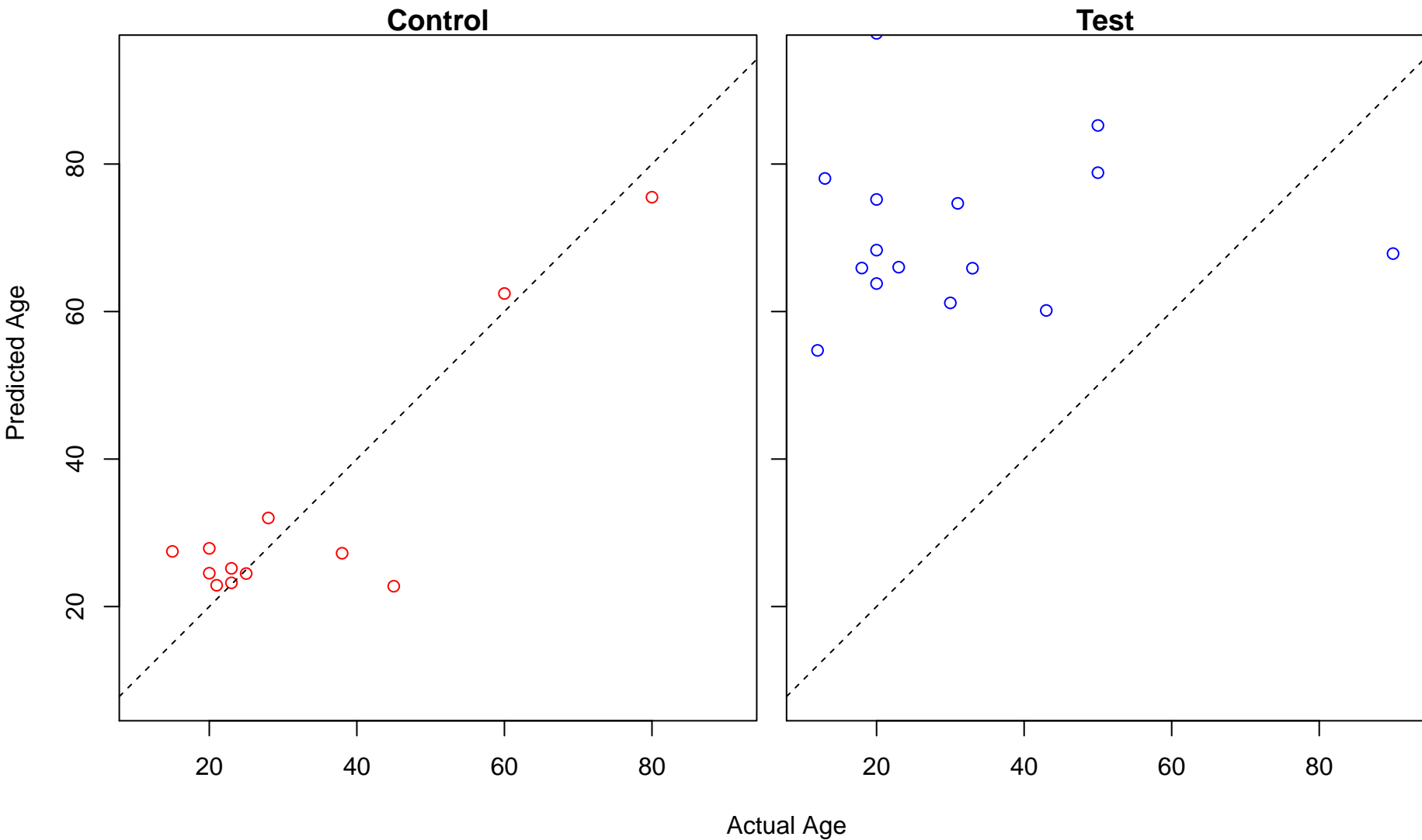
mitochondrial outer membrane permeabilization (Score: 9.188814)



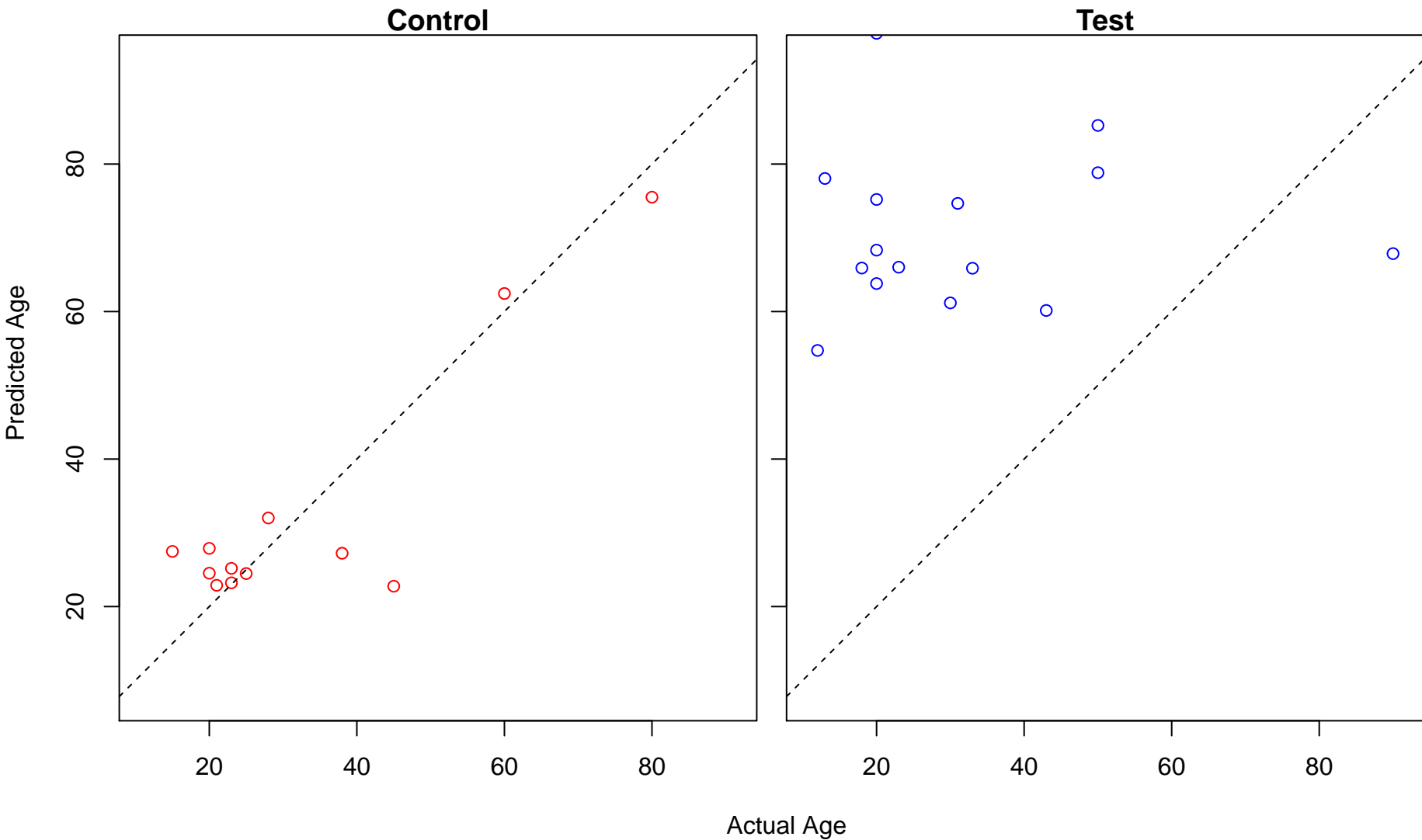
establishment of endothelial intestinal barrier (Score: 9.183187)



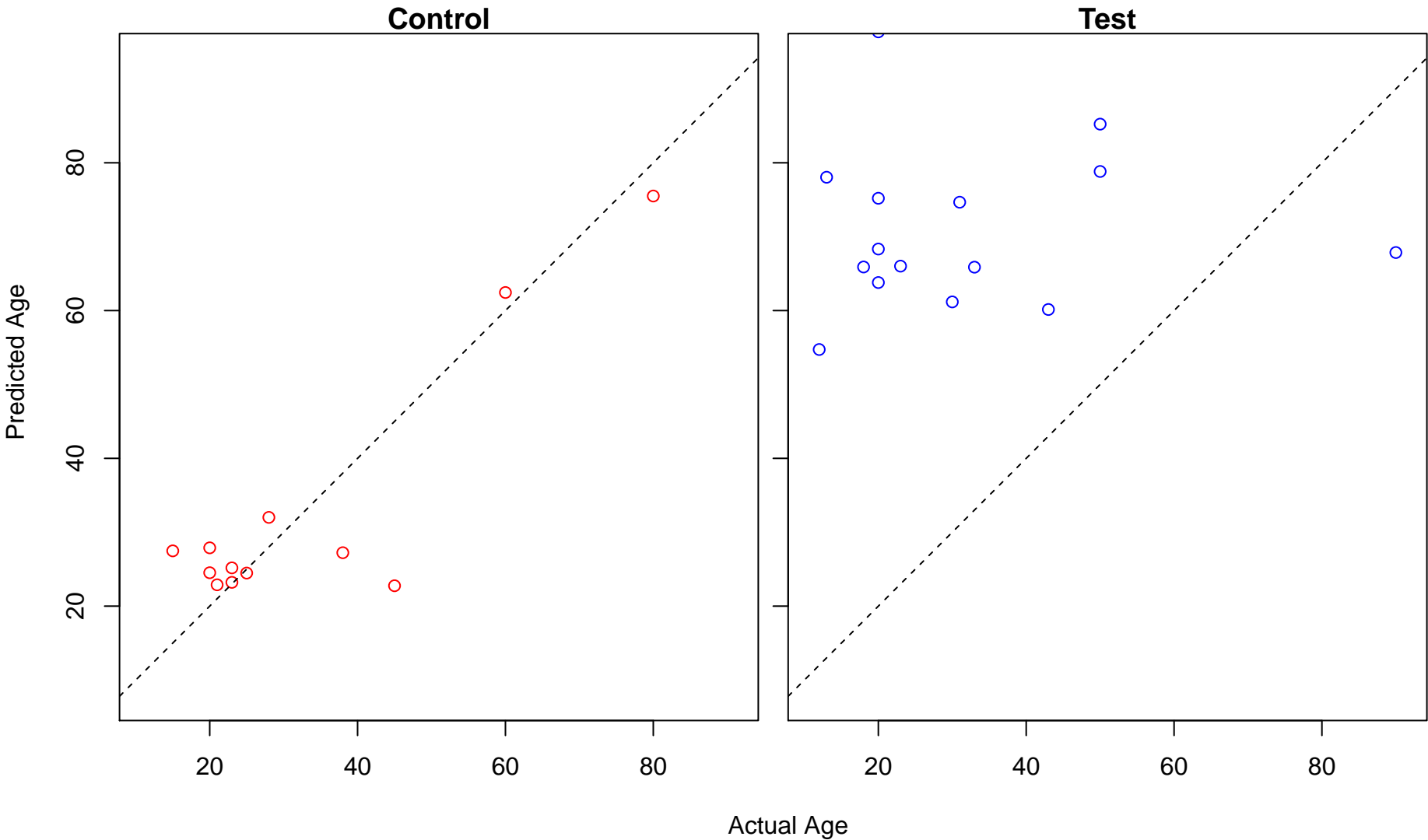
cyclic nucleotide biosynthetic process (Score: 9.180934)



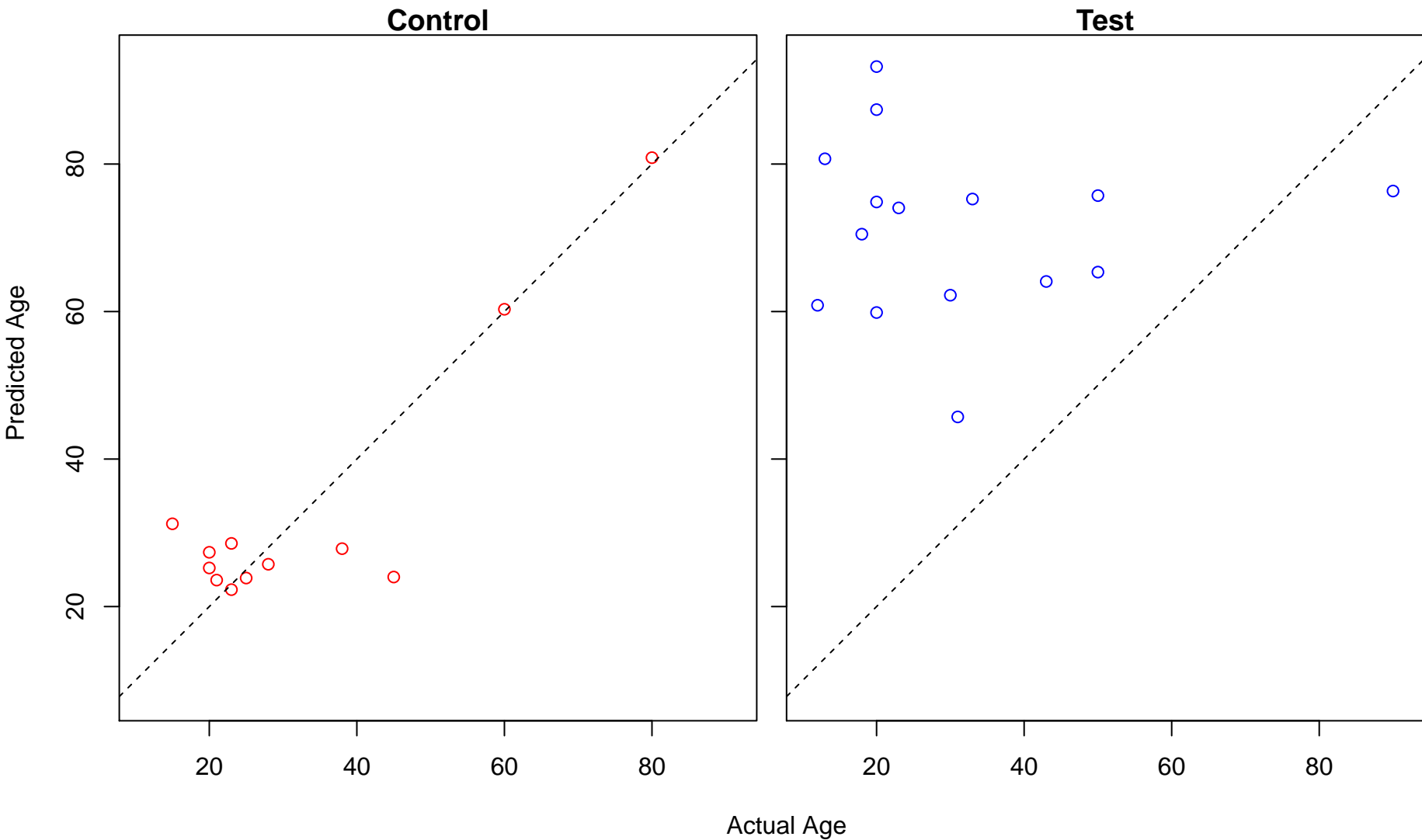
cAMP biosynthetic process (Score: 9.180728)



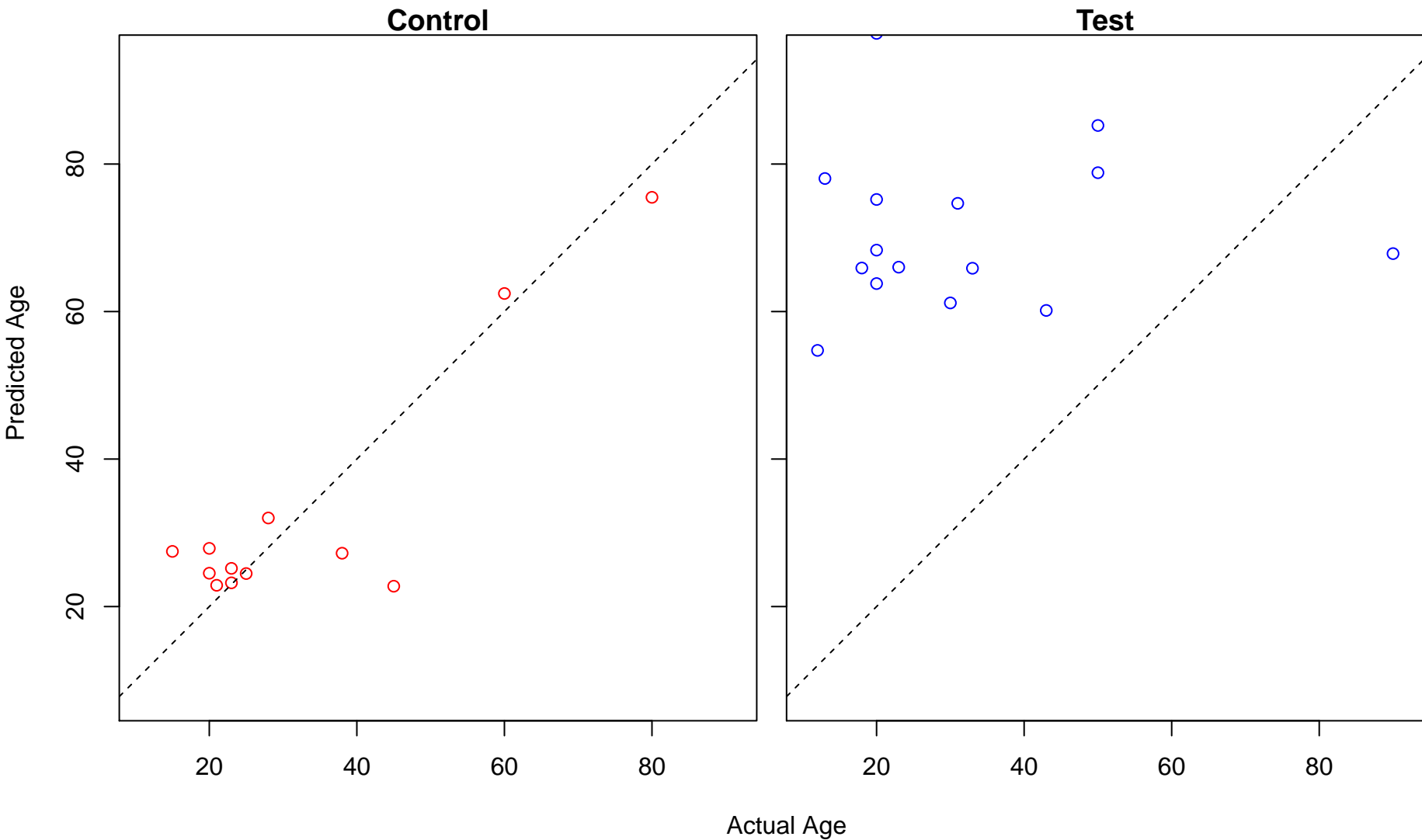
cyclic purine nucleotide metabolic process (Score: 9.180448)



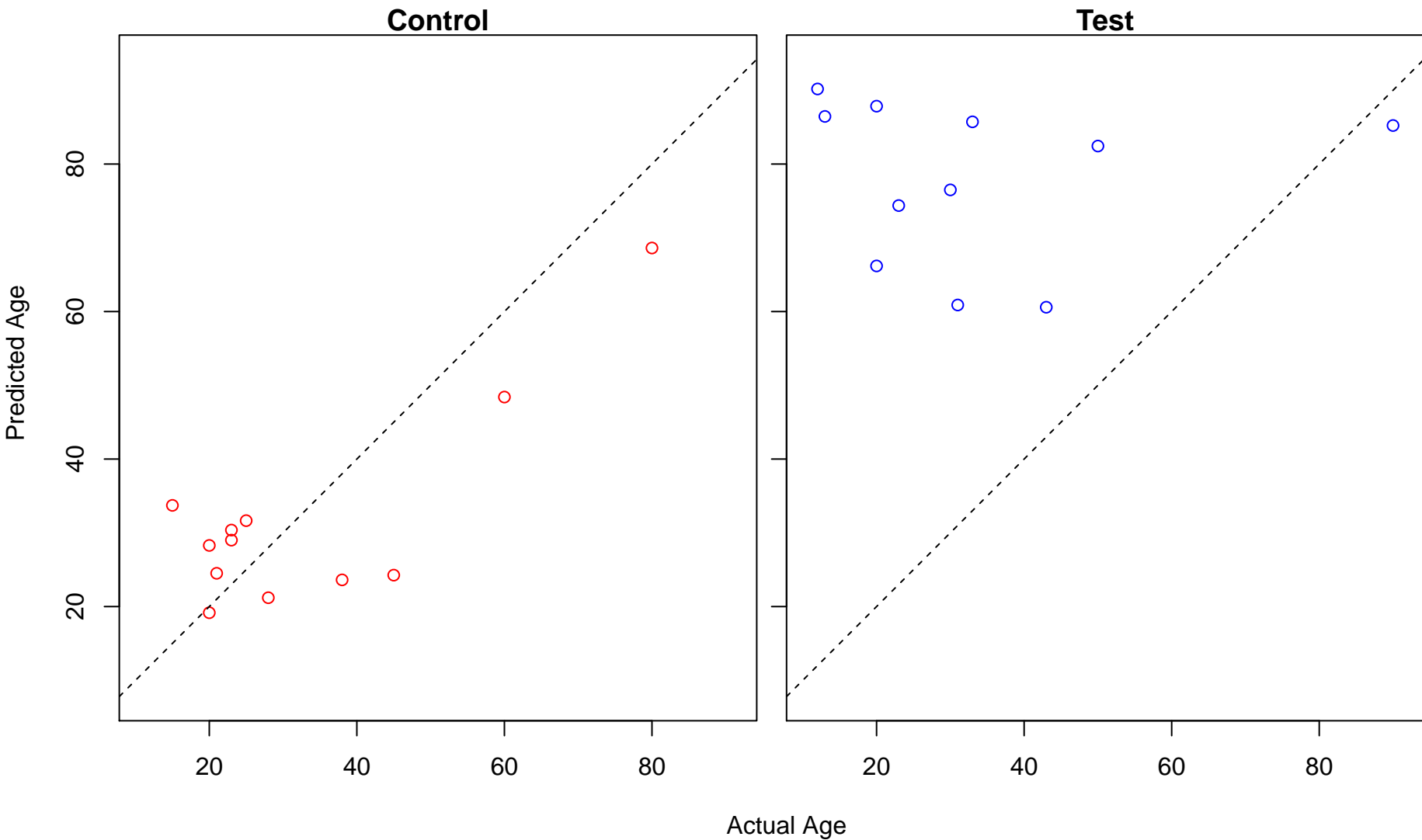
positive regulation of protein deacetylation (Score: 9.180159)



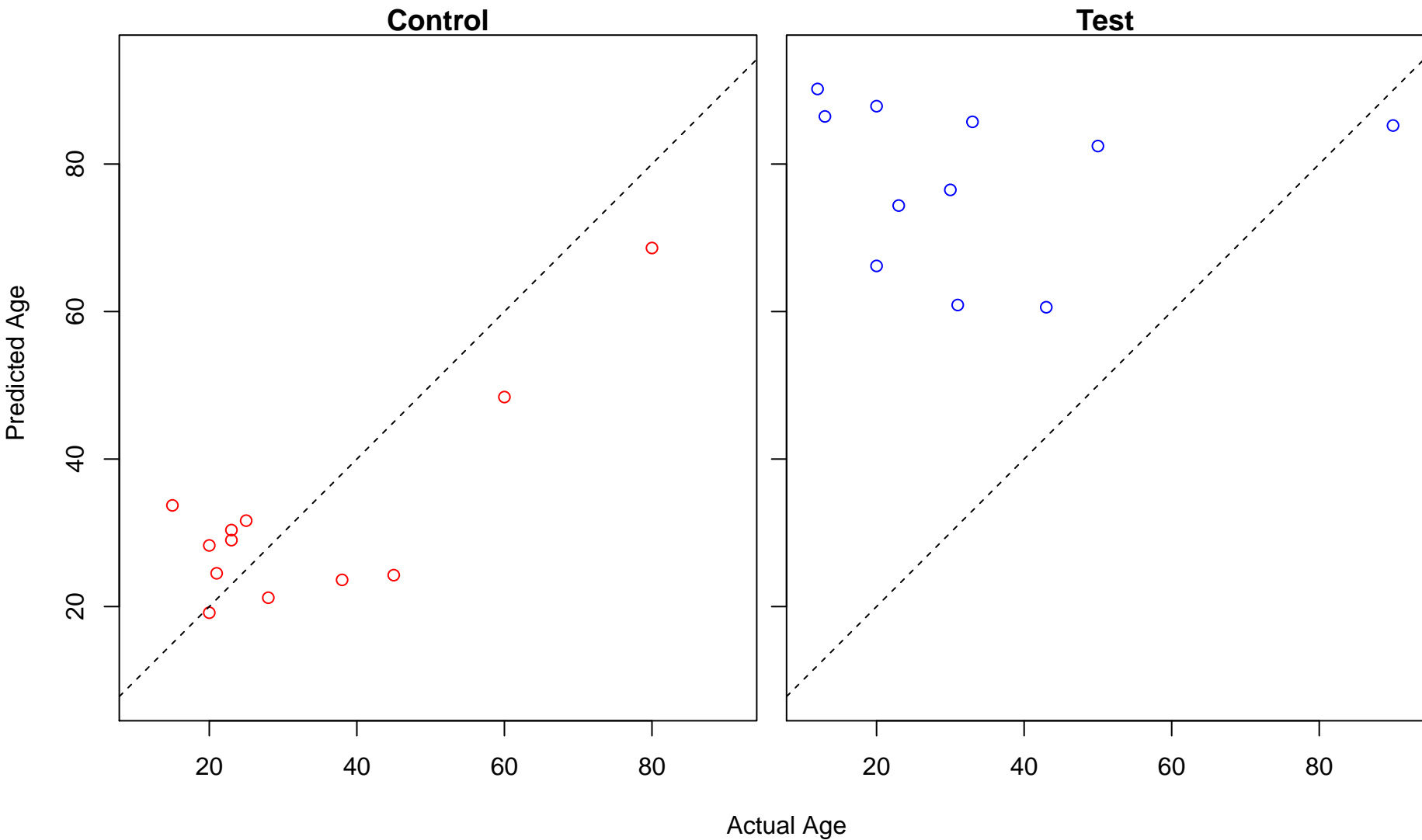
cAMP metabolic process (Score: 9.178314)



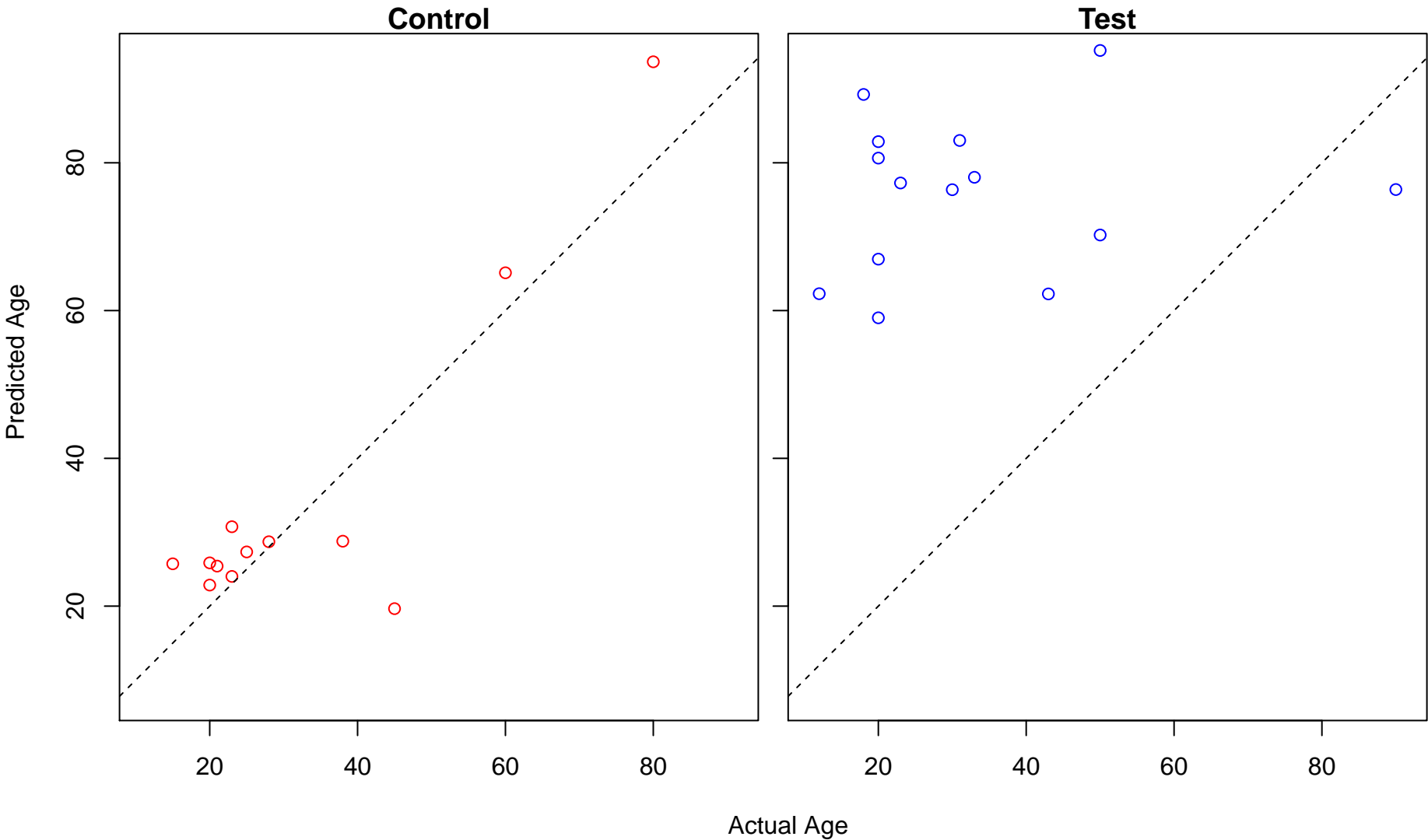
sulfide oxidation (Score: 9.175740)



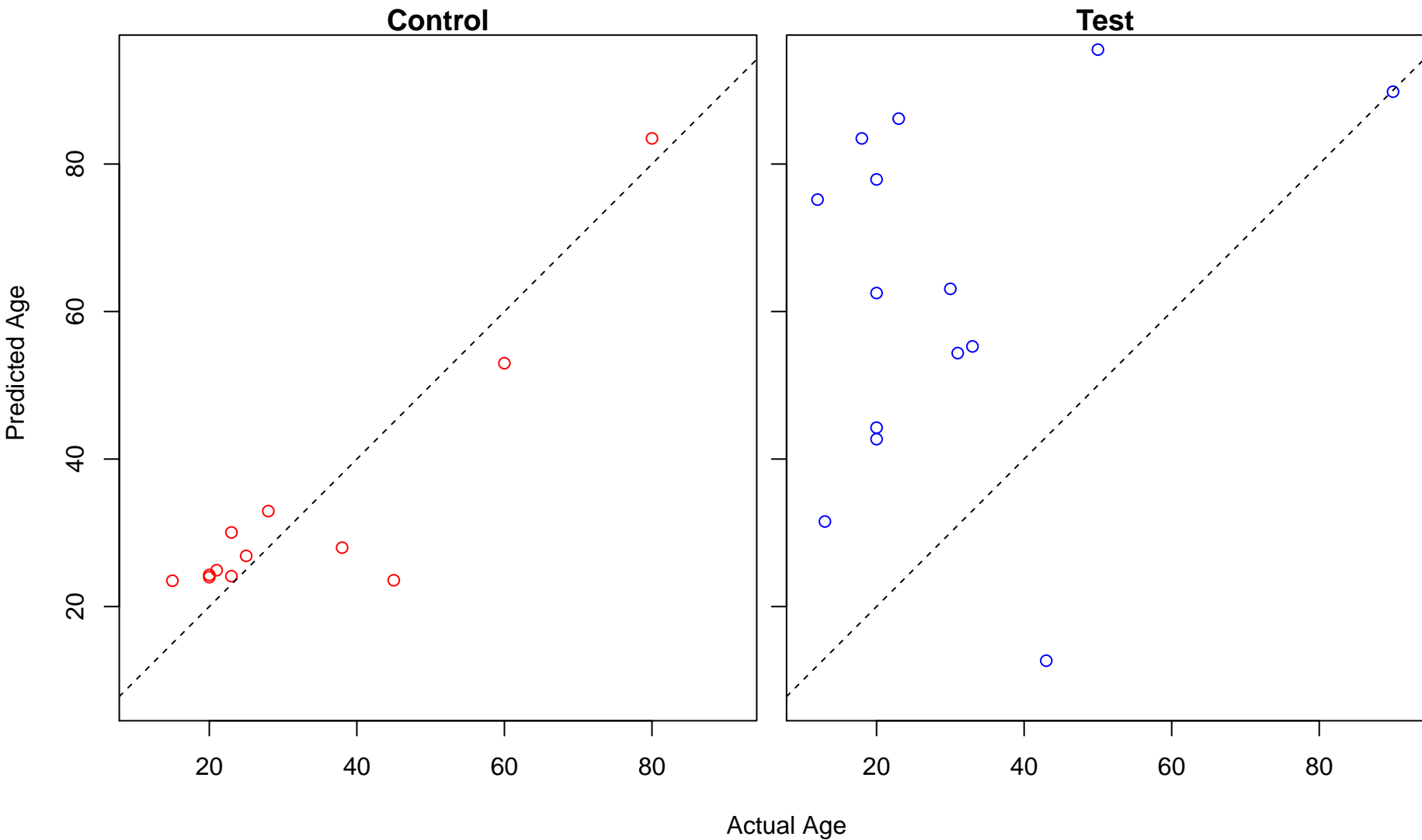
sulfide oxidation, using sulfide:quinone oxidoreductase (Score: 9.175740)



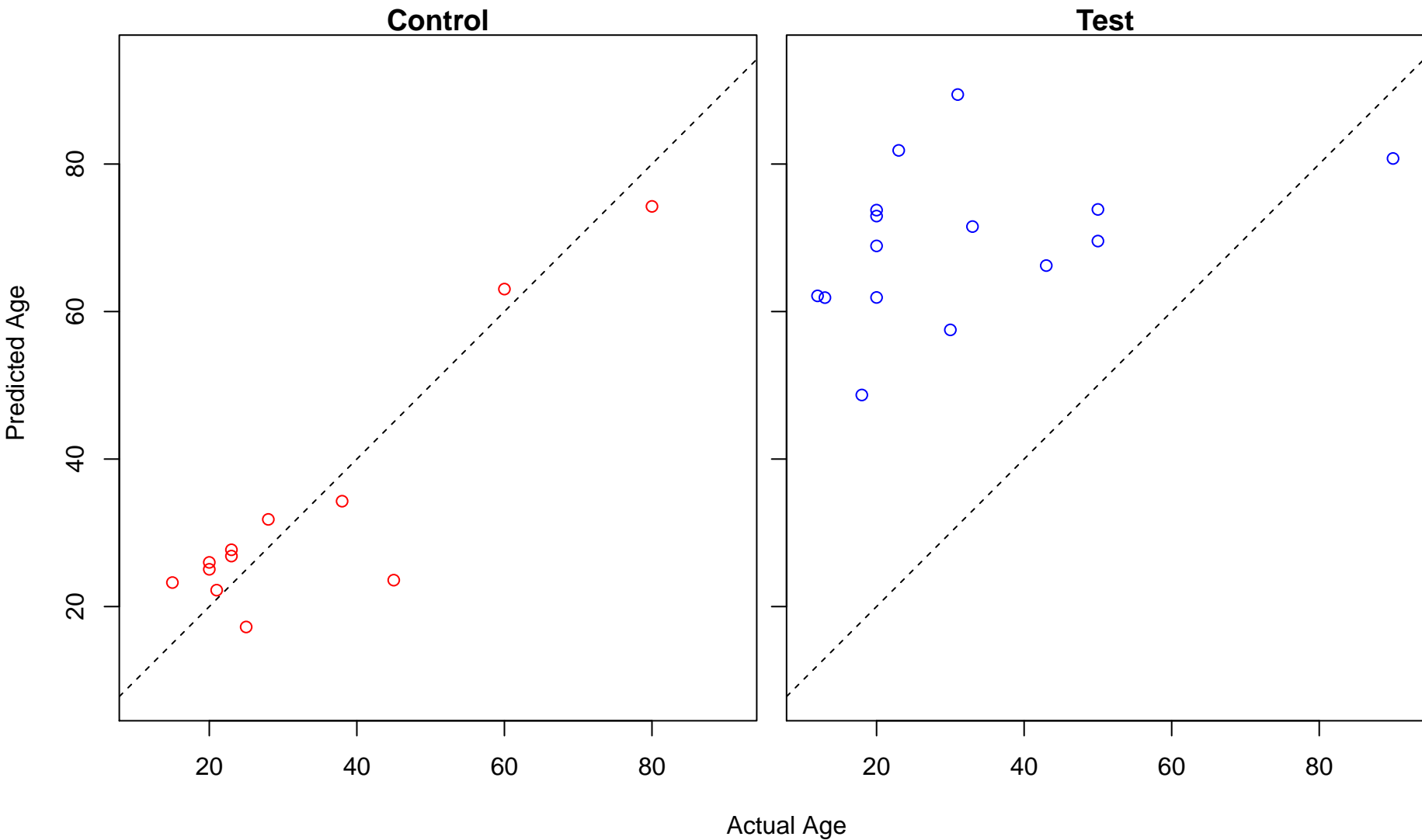
antigen processing and presentation of exogenous peptide antigen via MHC class I (Score: 9.17429)



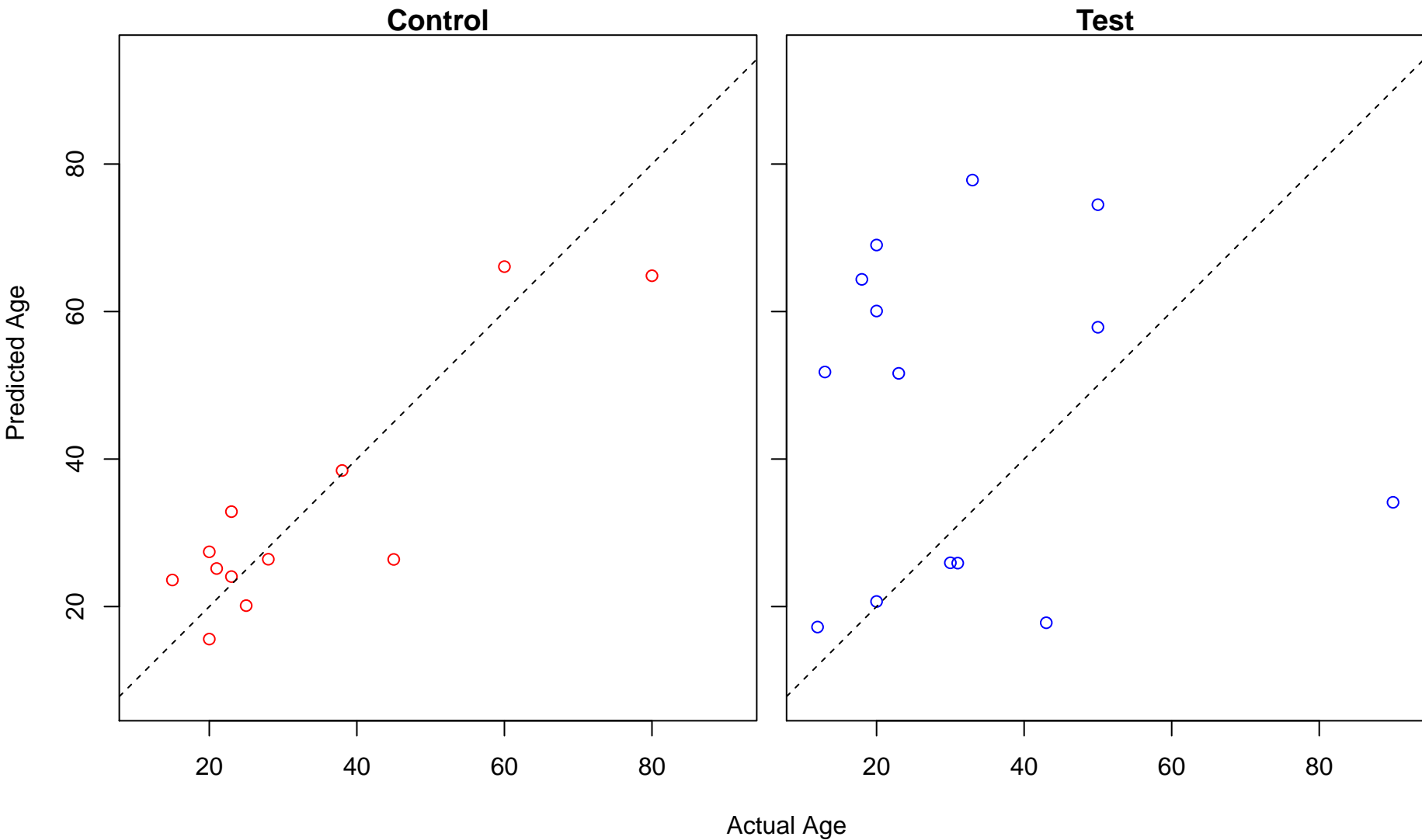
phospholipid biosynthetic process (Score: 9.173818)



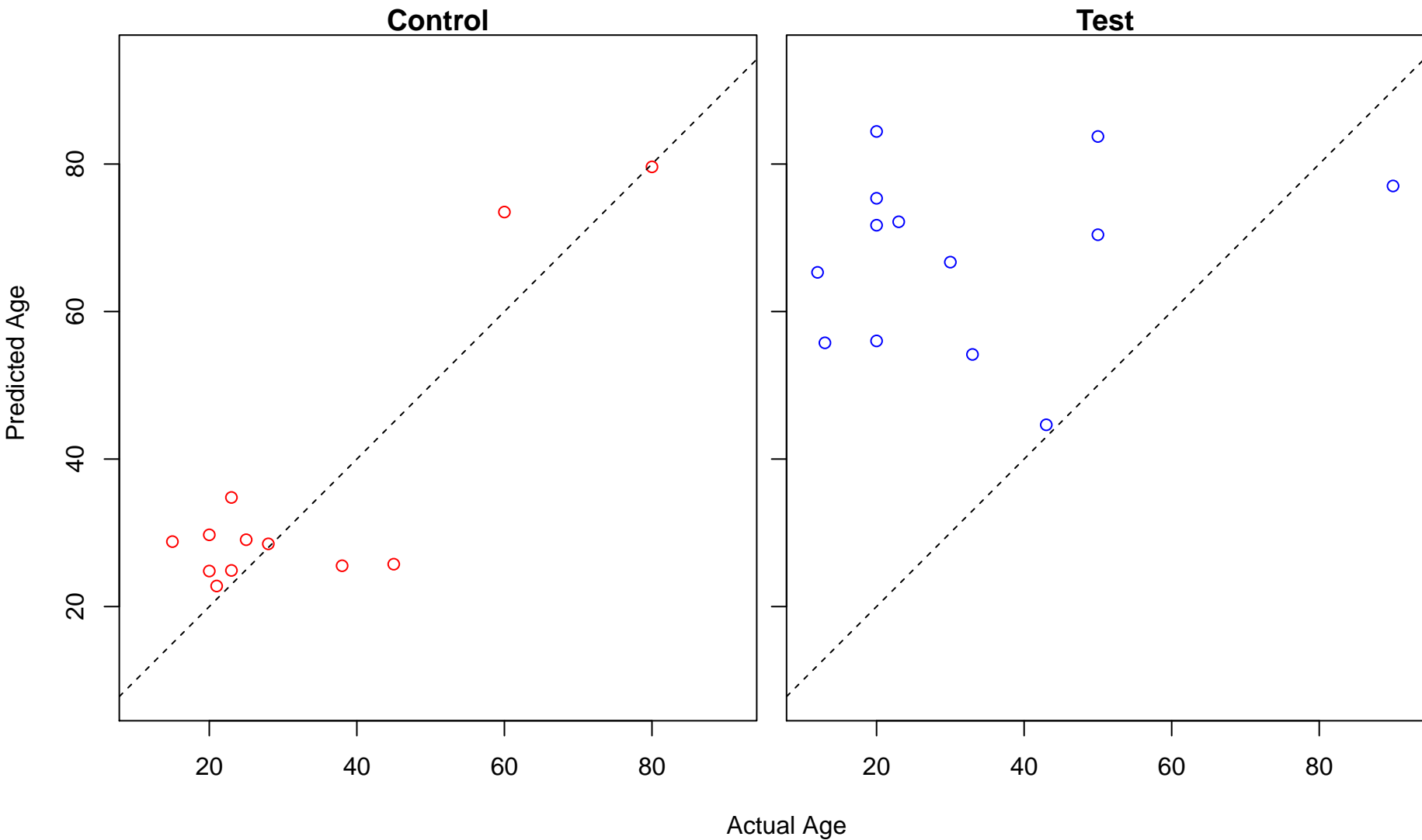
respiratory system development (Score: 9.171855)



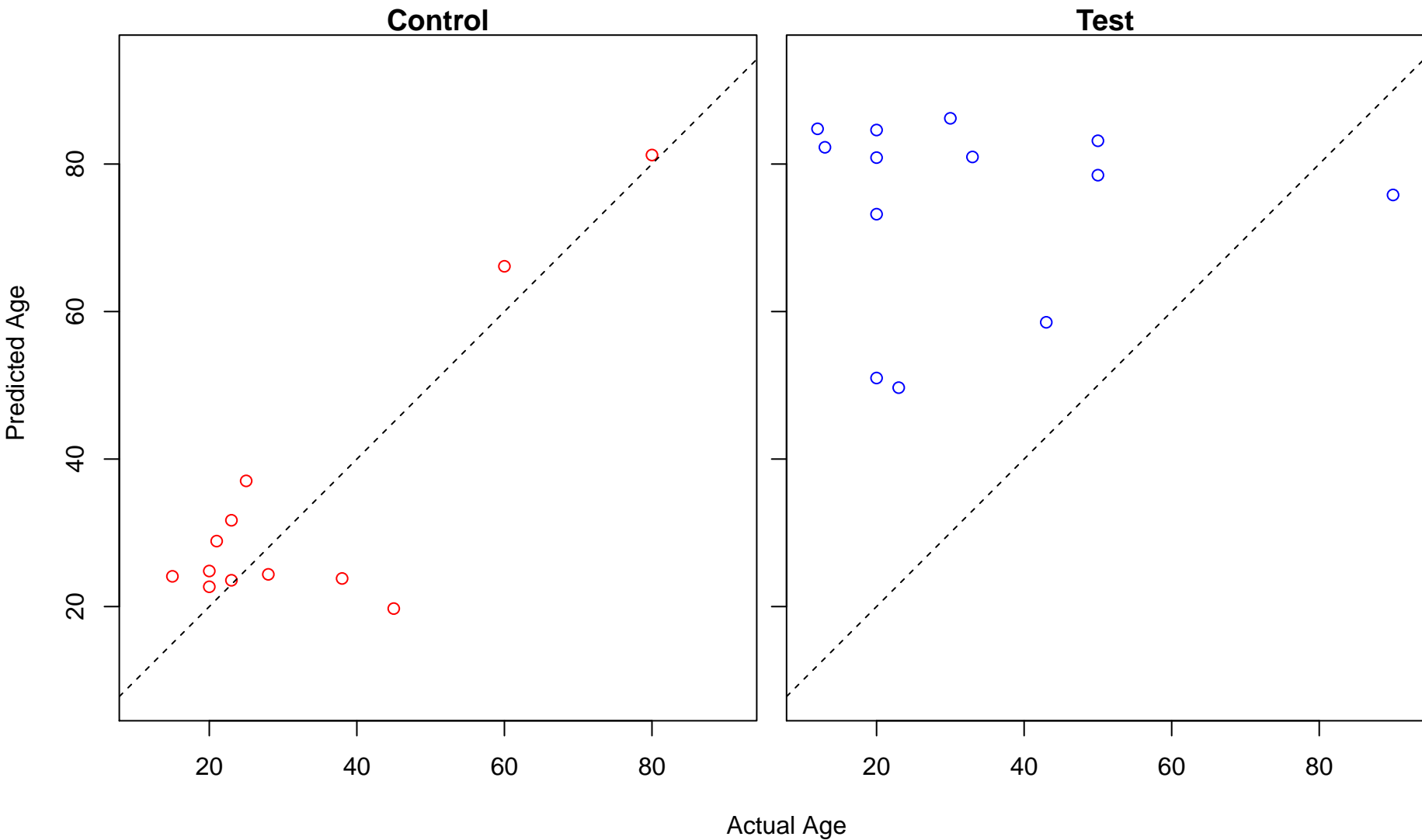
positive regulation of transmembrane transport (Score: 9.168759)



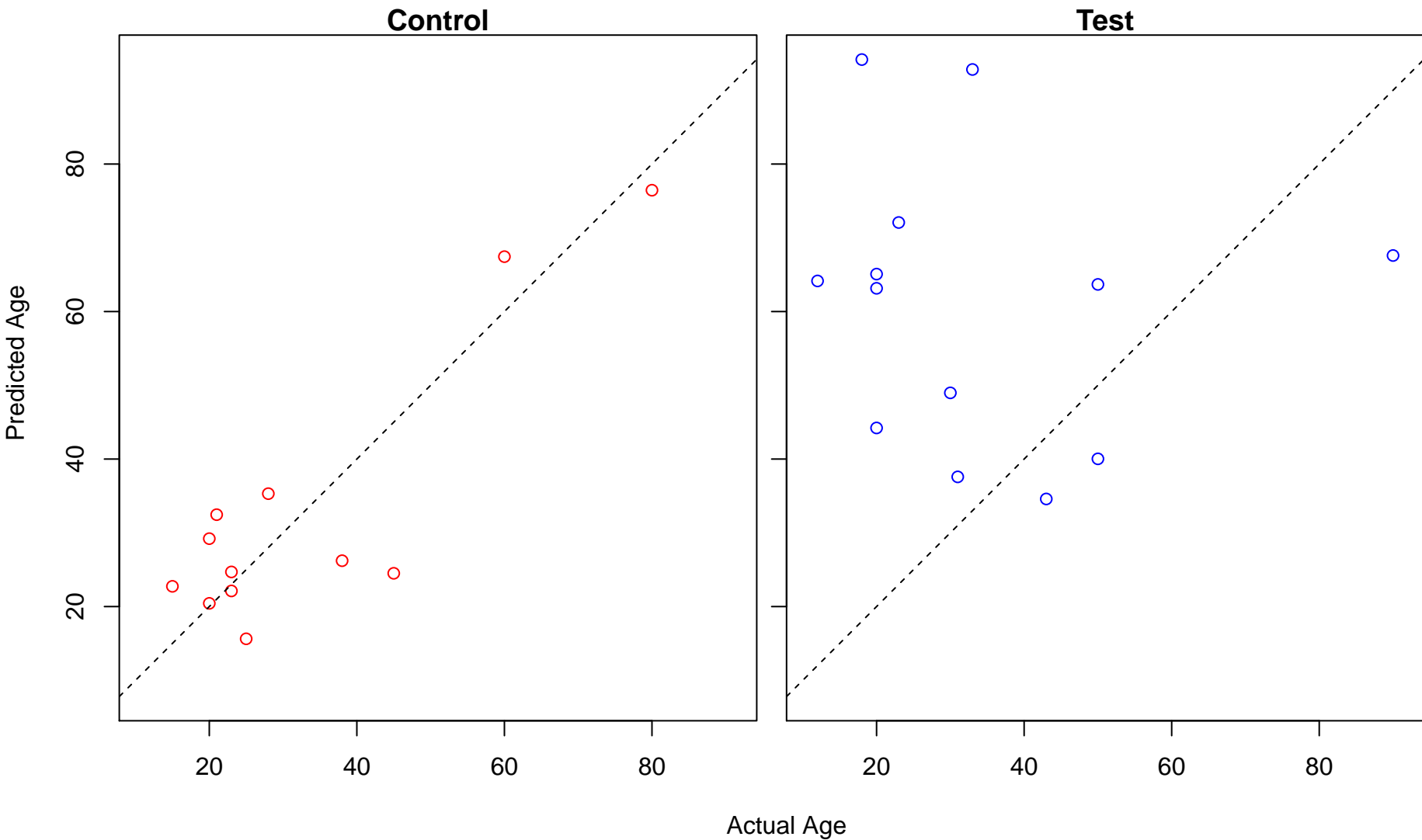
negative regulation of inclusion body assembly (Score: 9.168206)



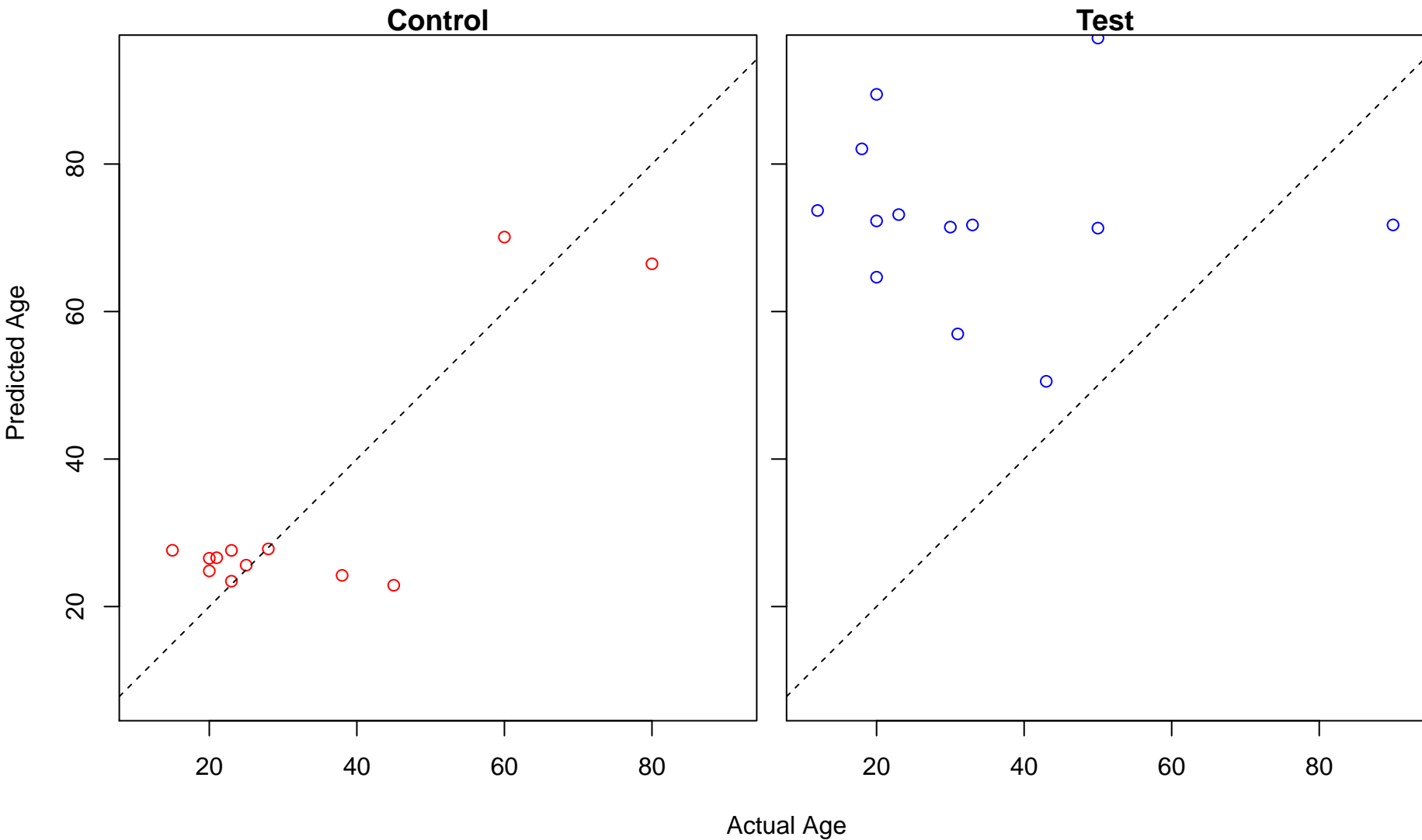
mRNA stabilization (Score: 9.164264)



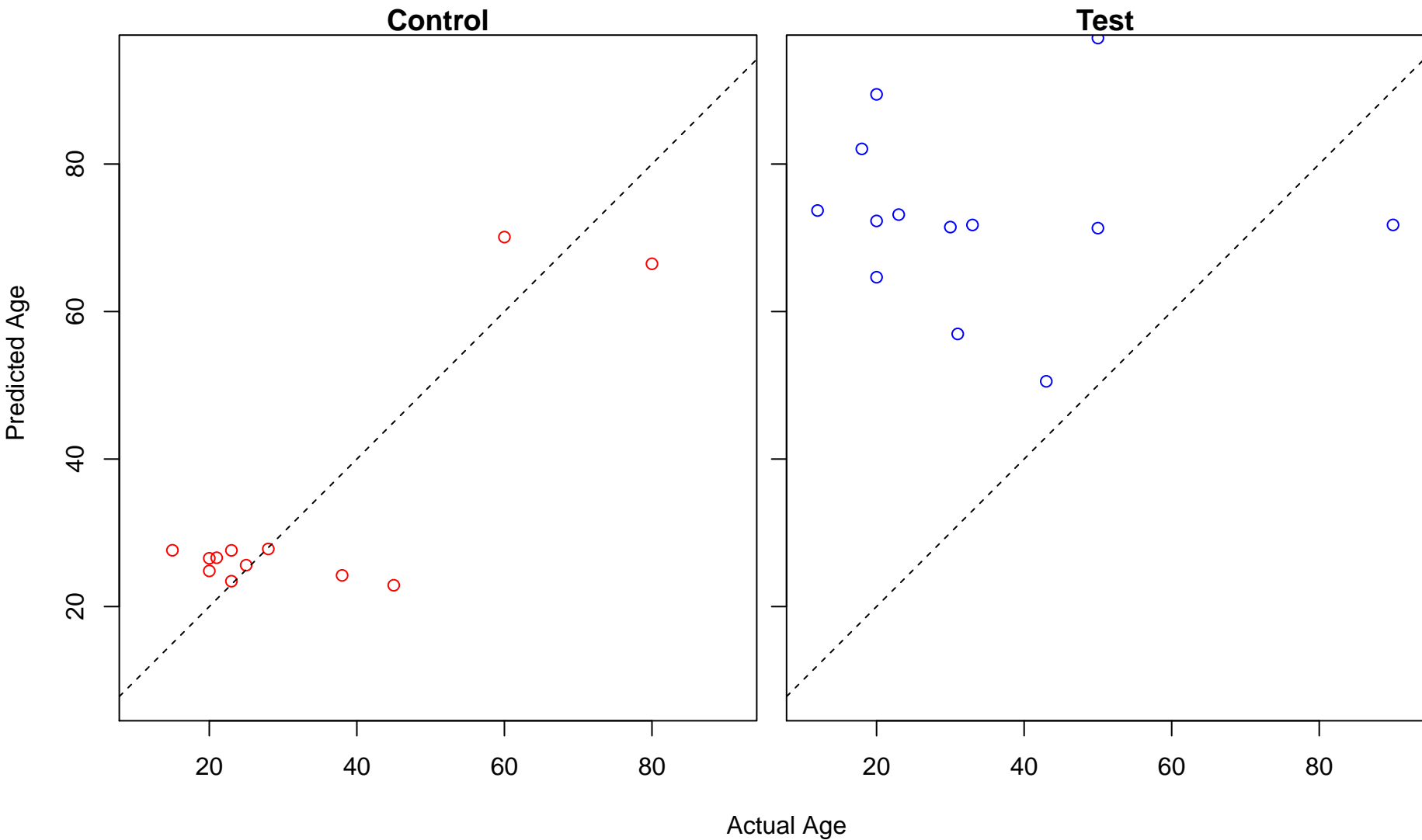
establishment of protein localization to membrane (Score: 9.158033)



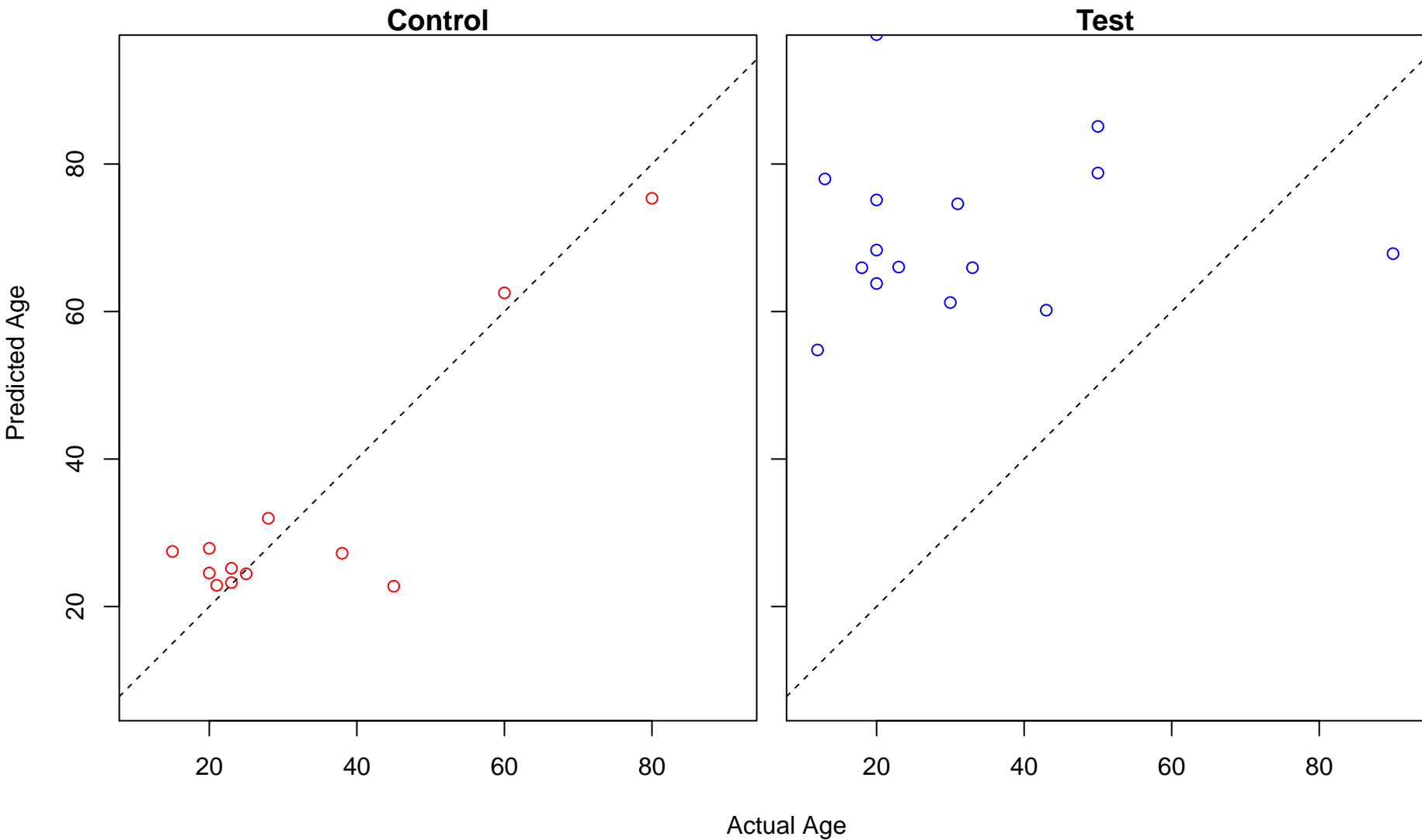
viral latency (Score: 9.145999)



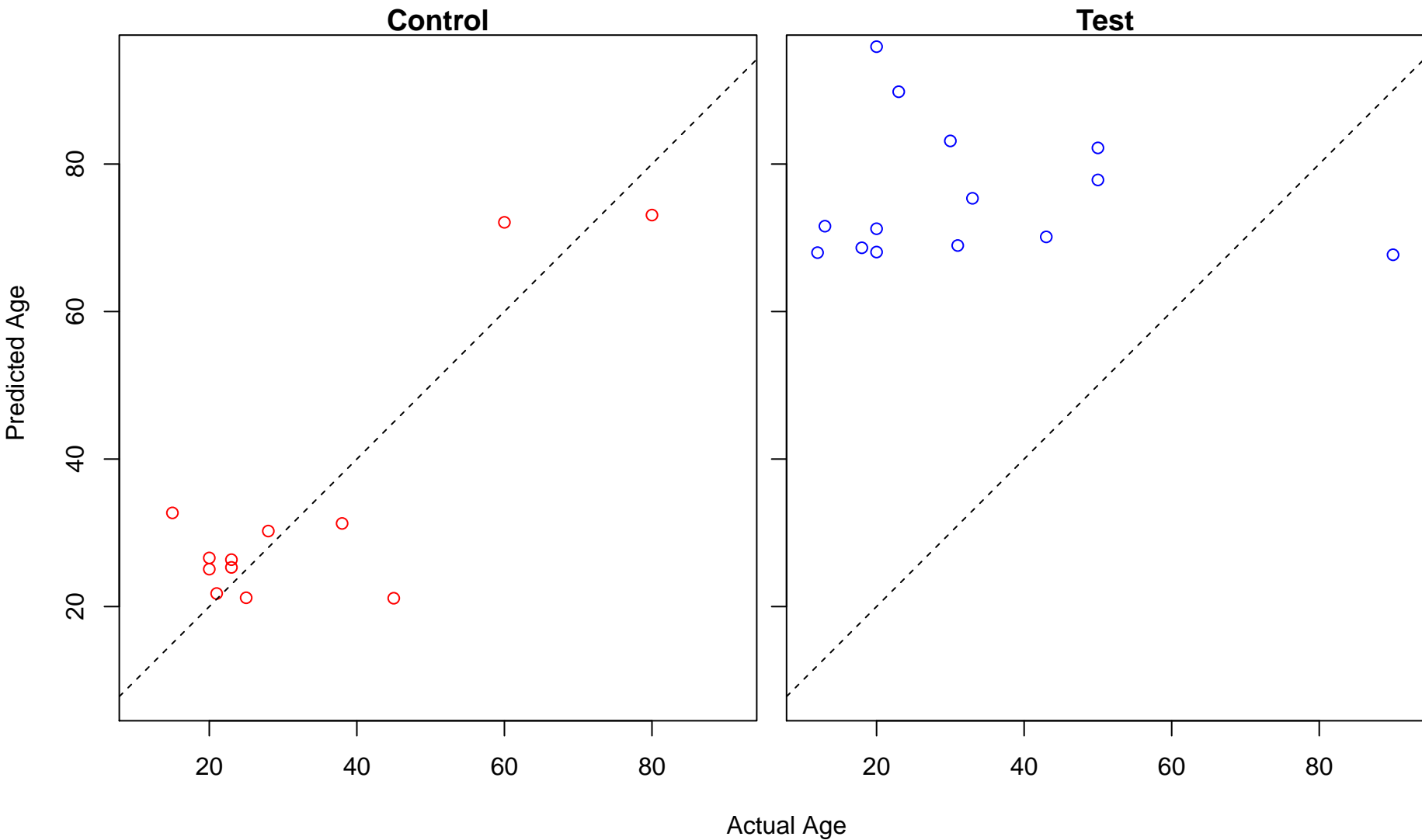
establishment of viral latency (Score: 9.145999)



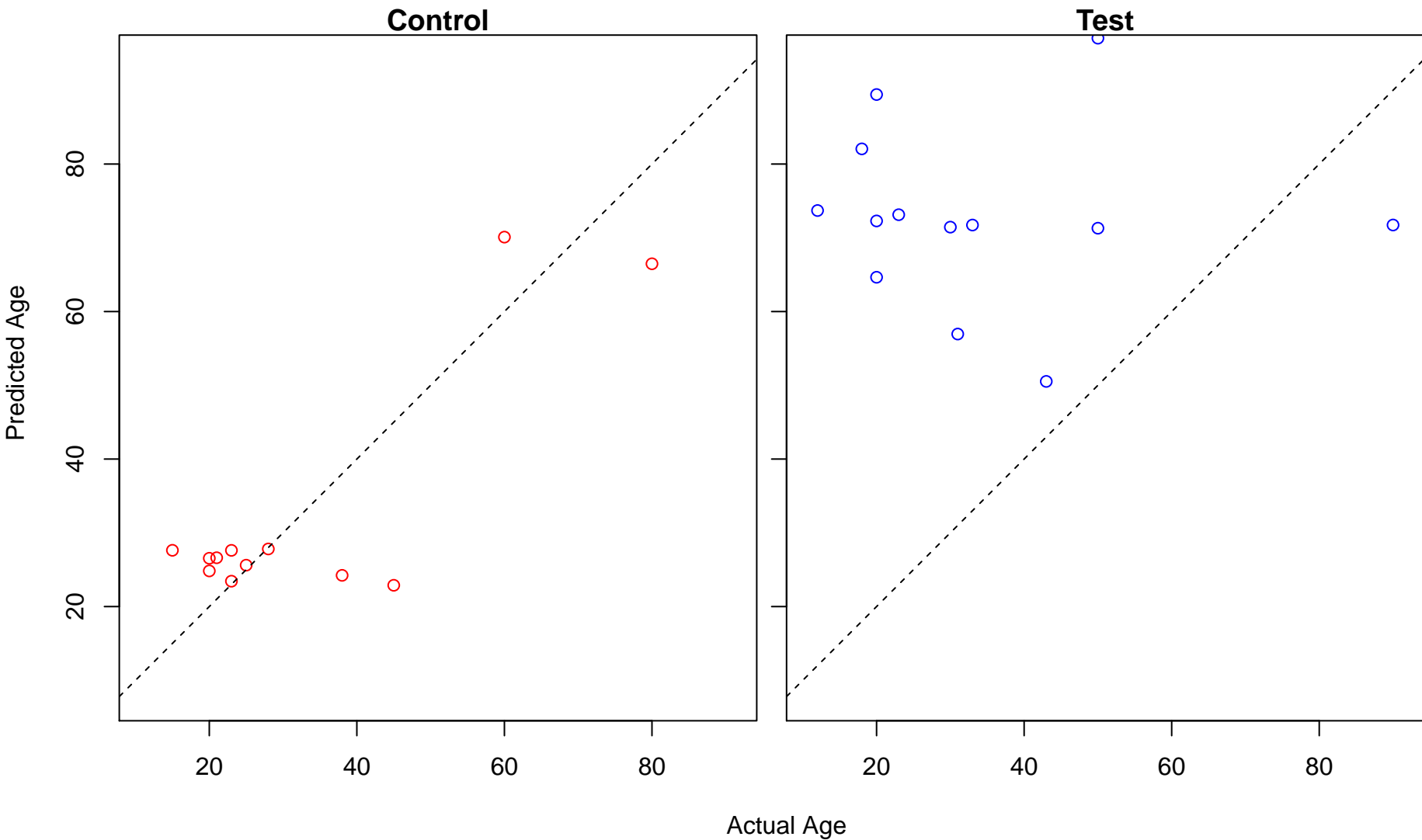
positive regulation of cAMP-mediated signaling (Score: 9.145689)



meiotic nuclear division (Score: 9.145435)

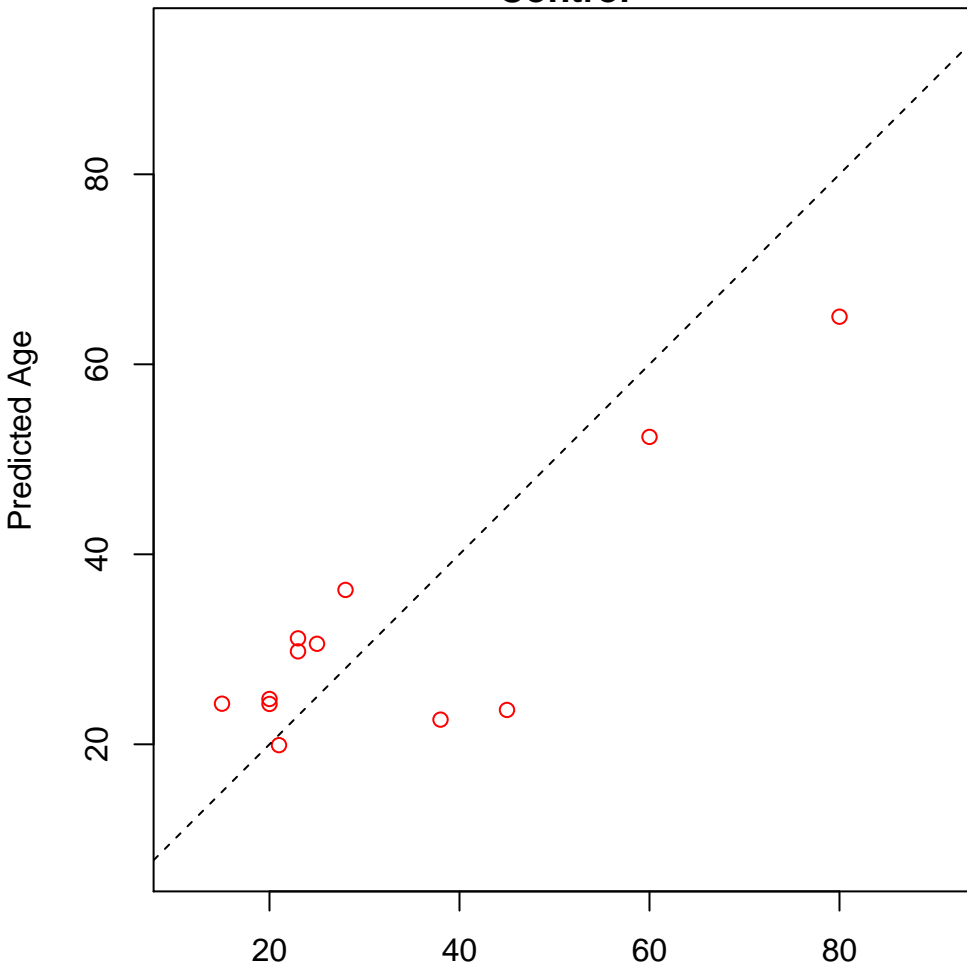


establishment of integrated proviral latency (Score: 9.145140)

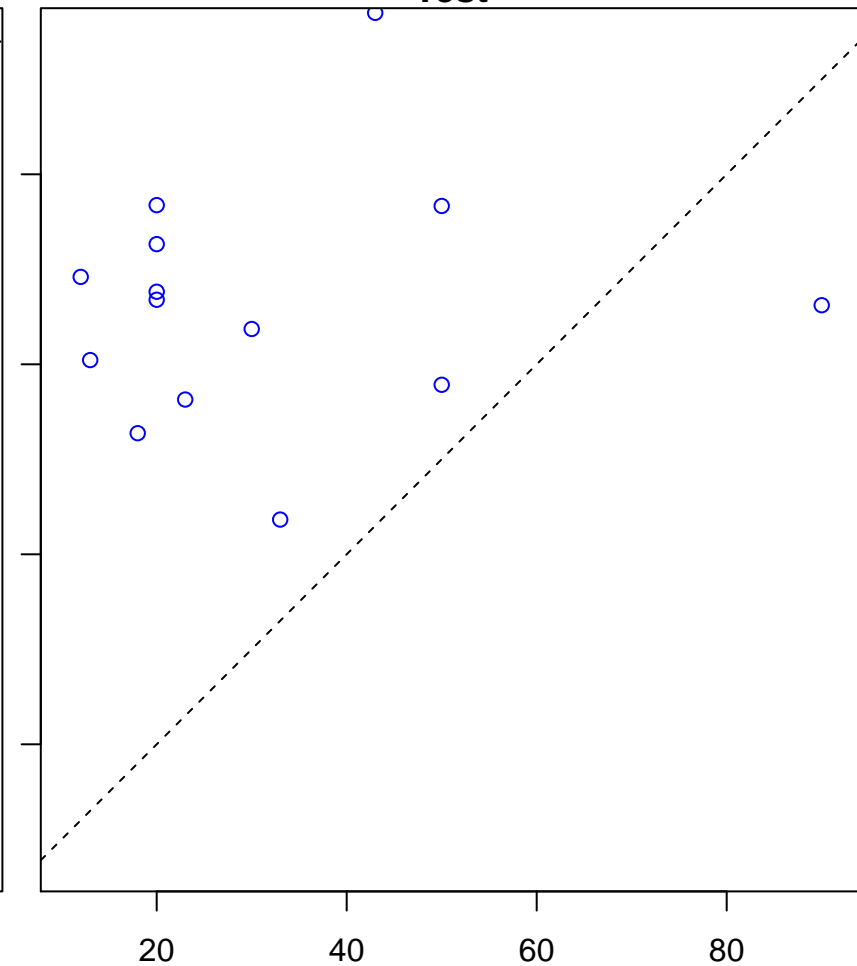


response to bacterial lipoprotein (Score: 9.143446)

Control

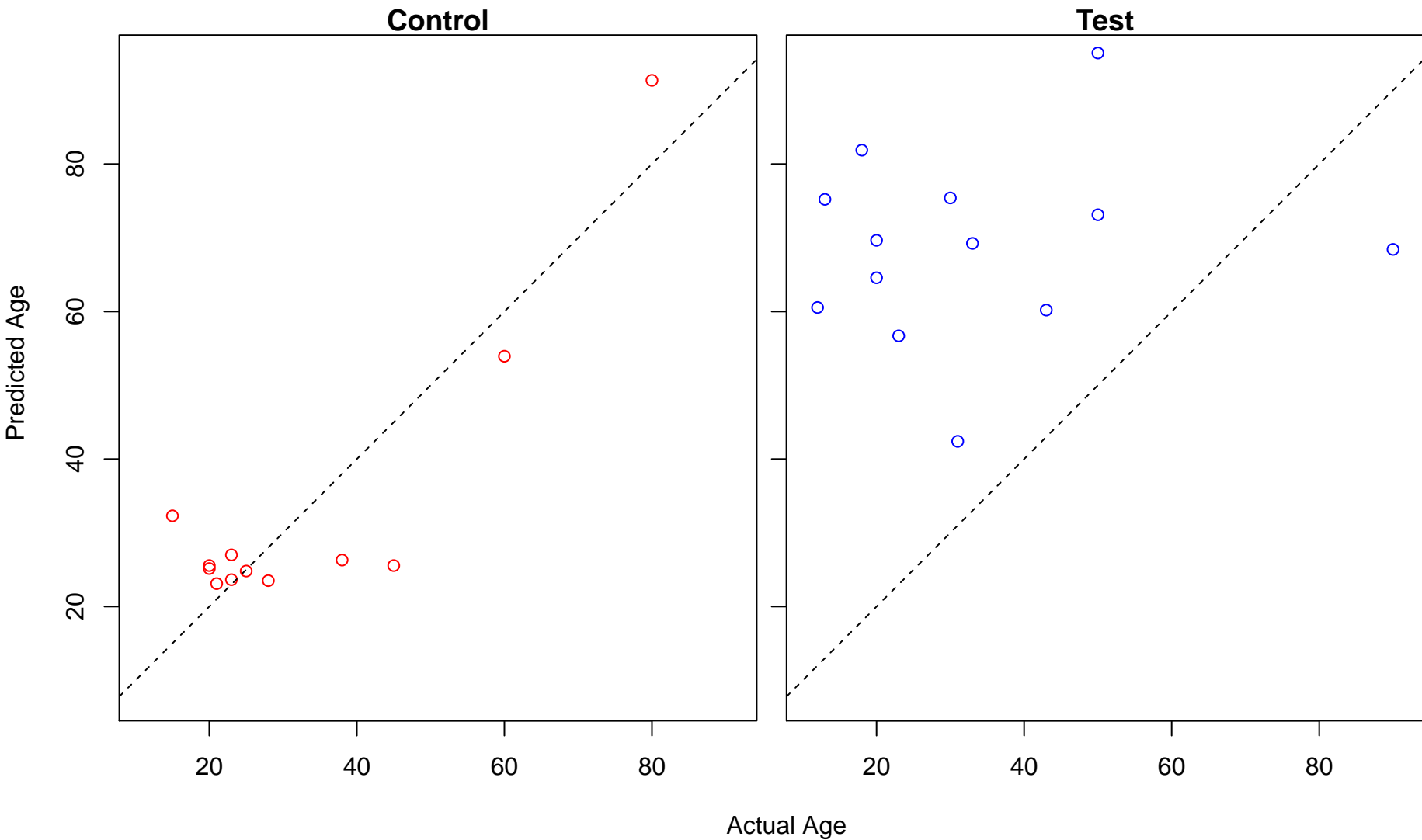


Test

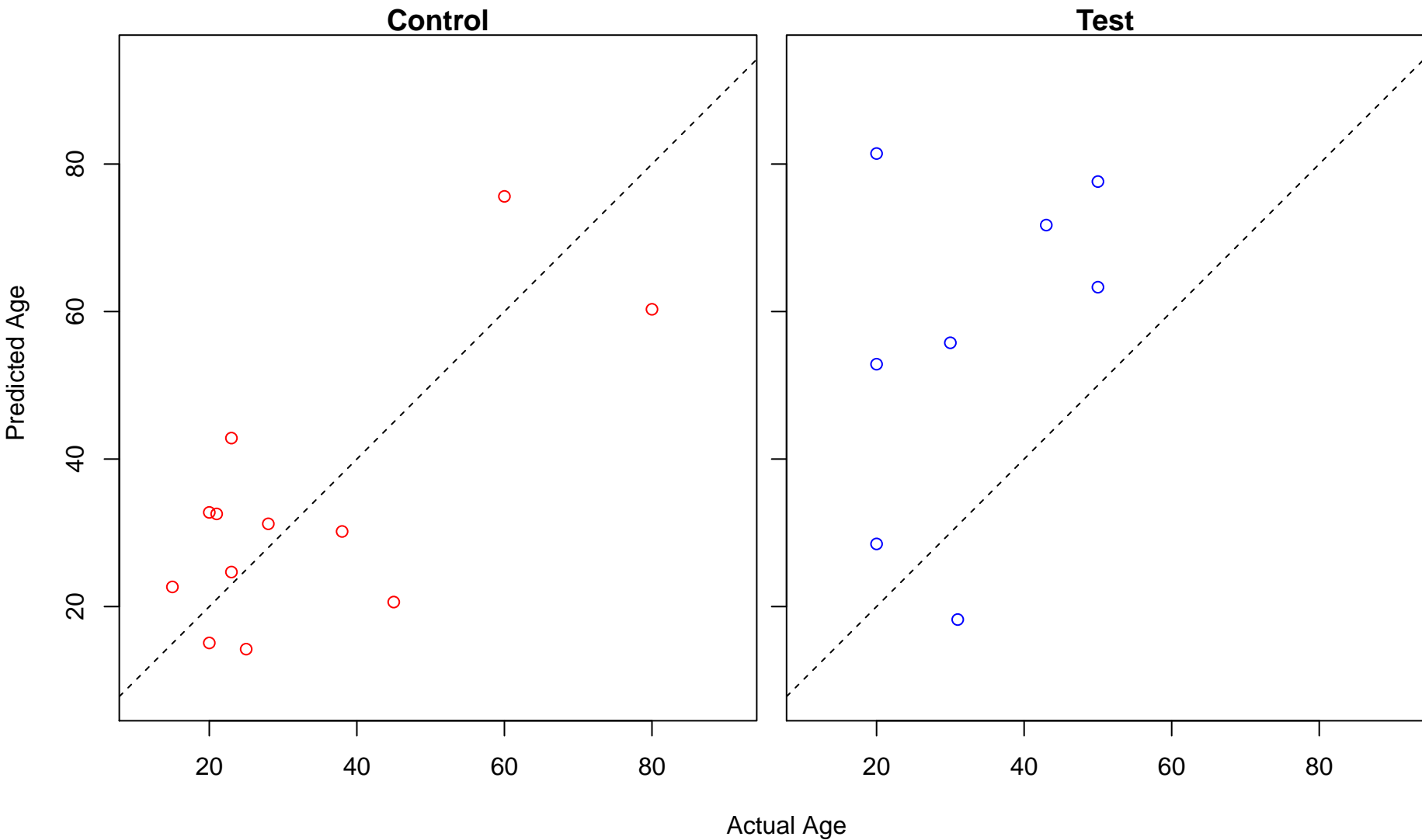


Actual Age

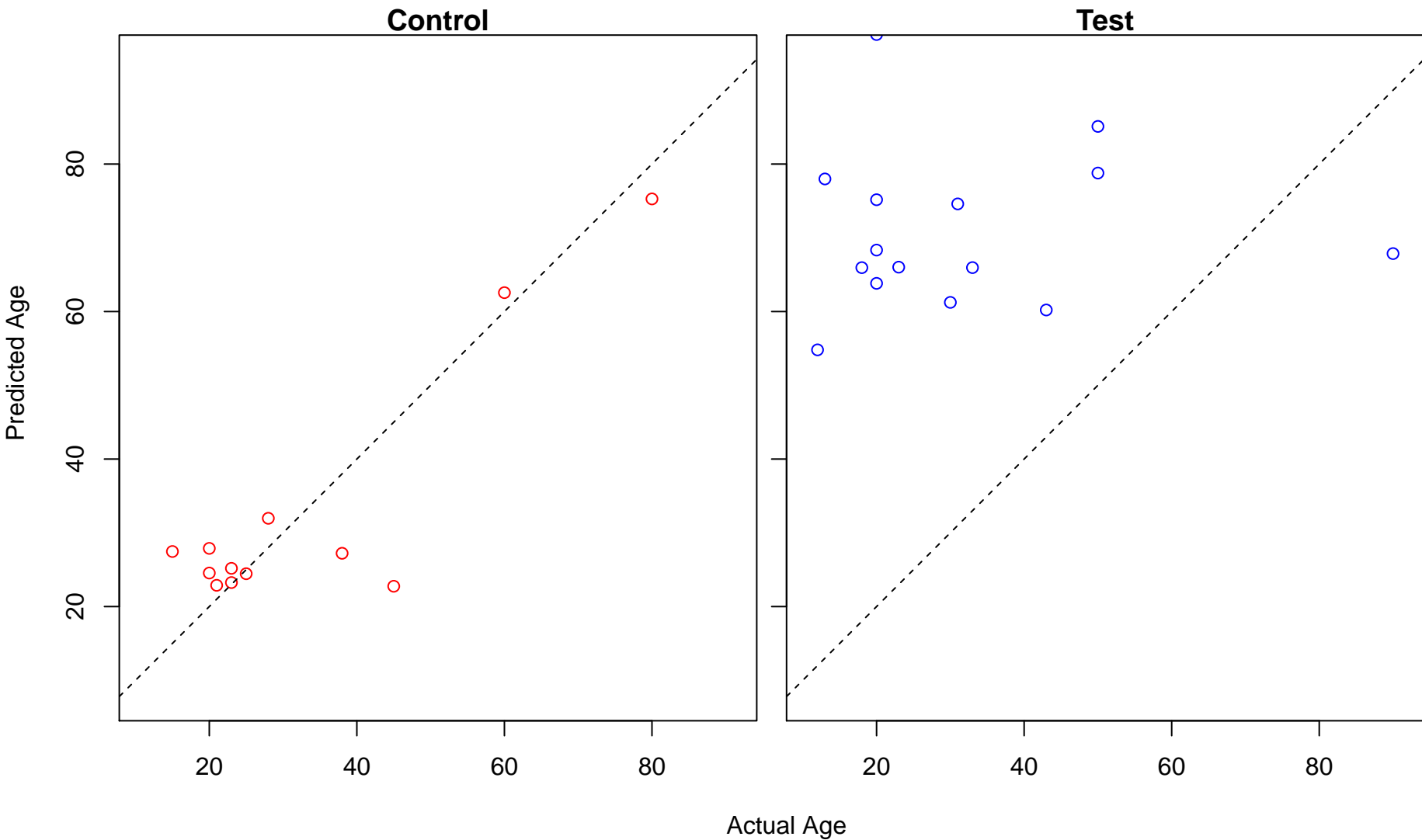
acetyl-CoA metabolic process (Score: 9.140230)



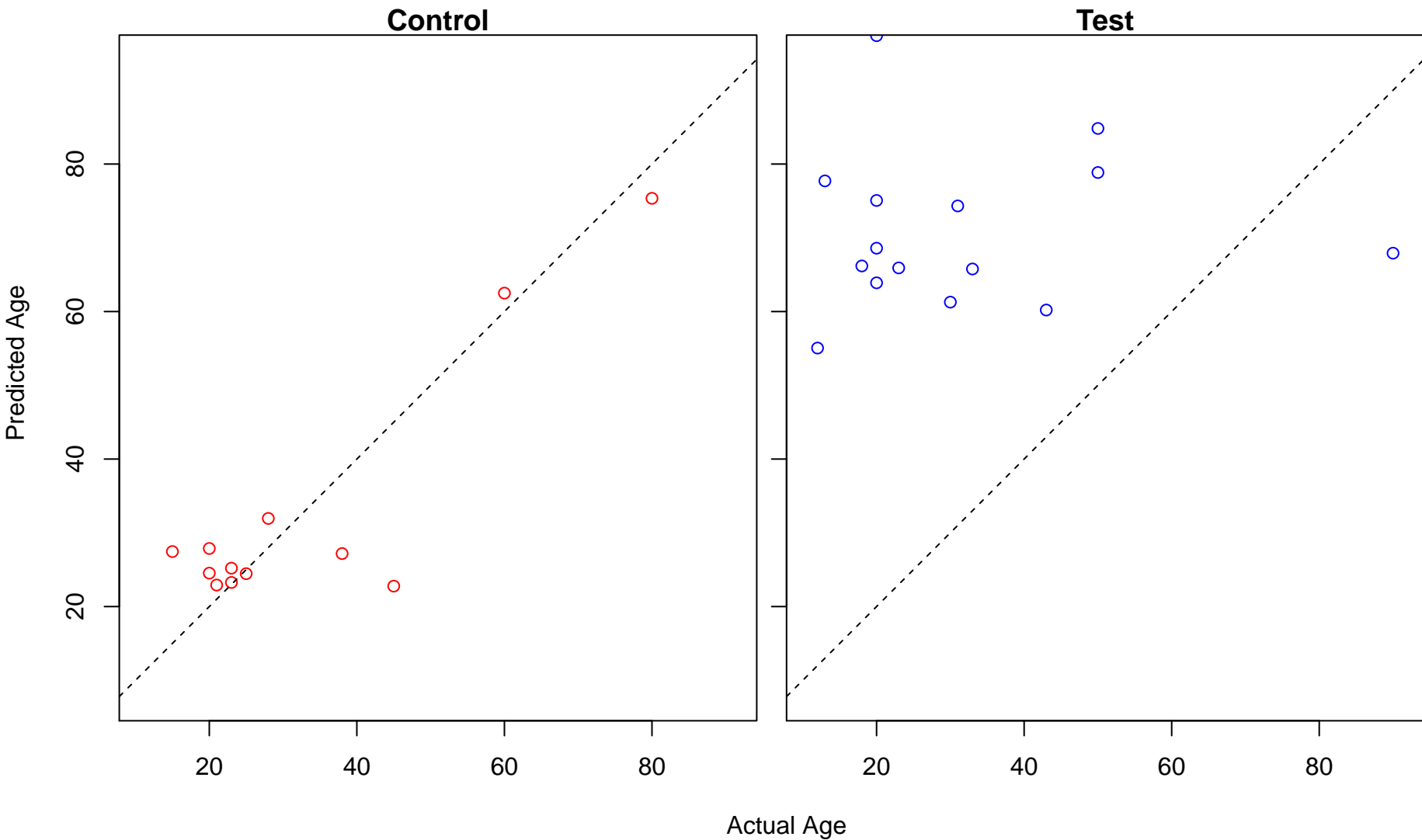
humoral immune response mediated by circulating immunoglobulin (Score: 9.139218)



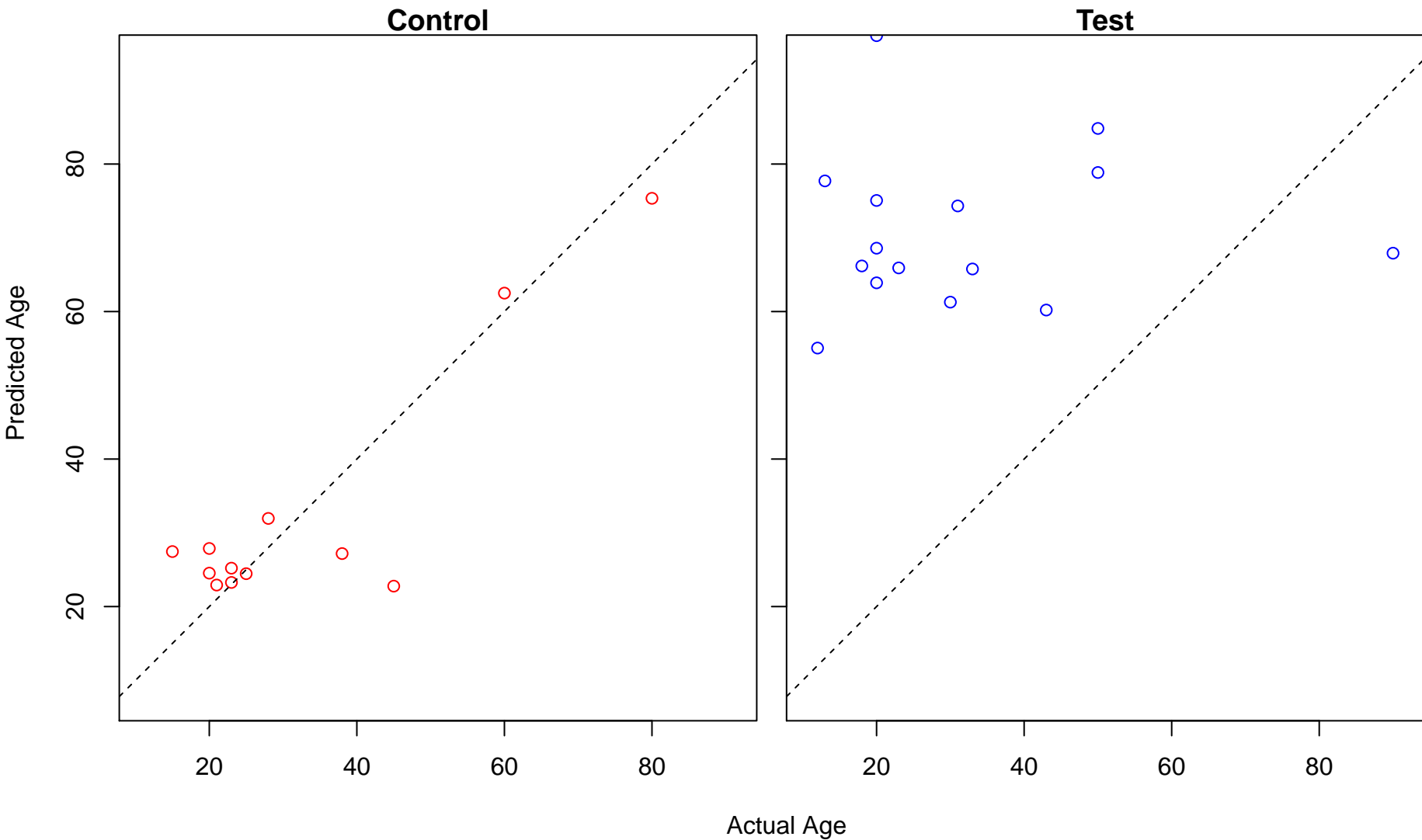
adrenergic receptor signaling pathway (Score: 9.136454)



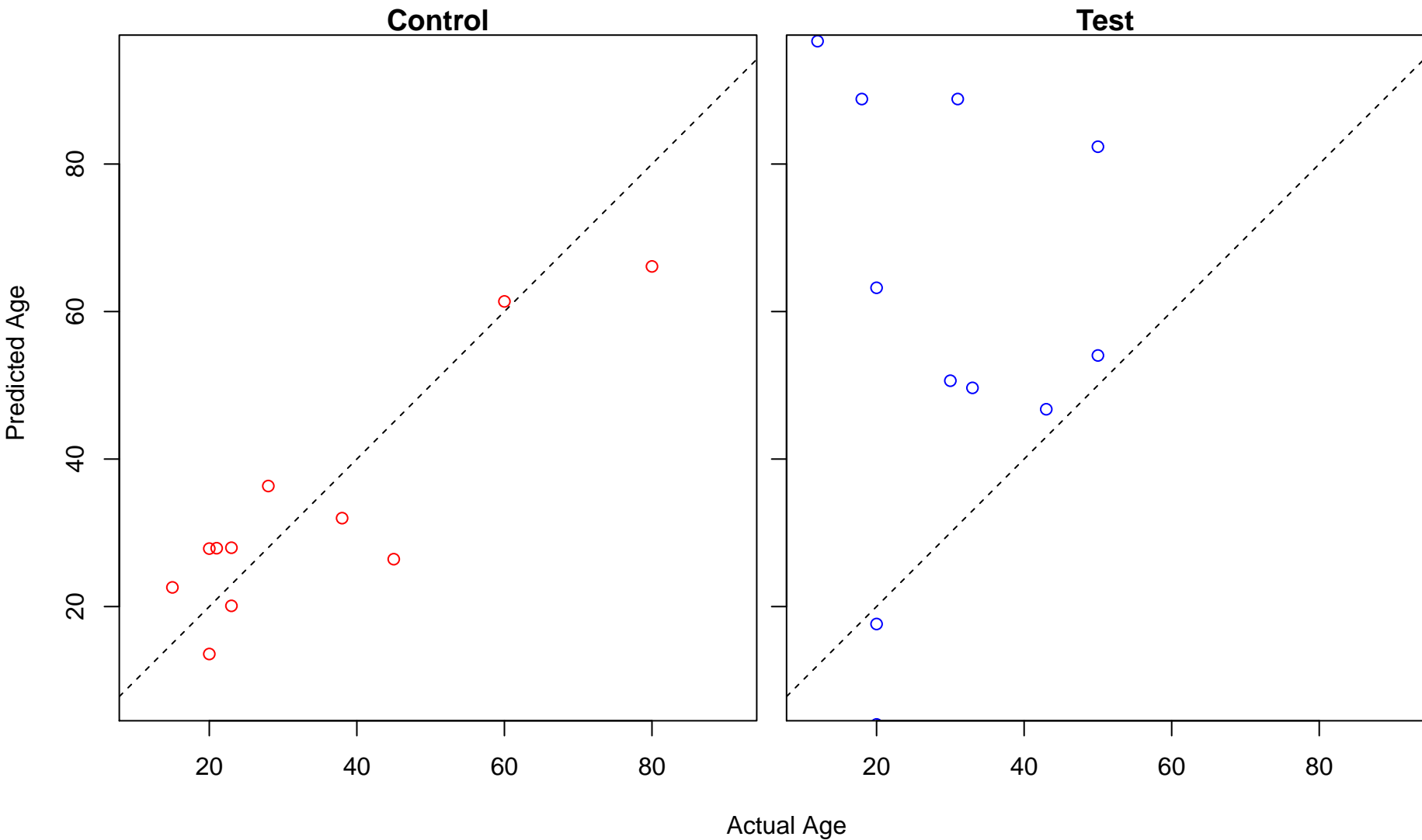
molting cycle (Score: 9.136423)



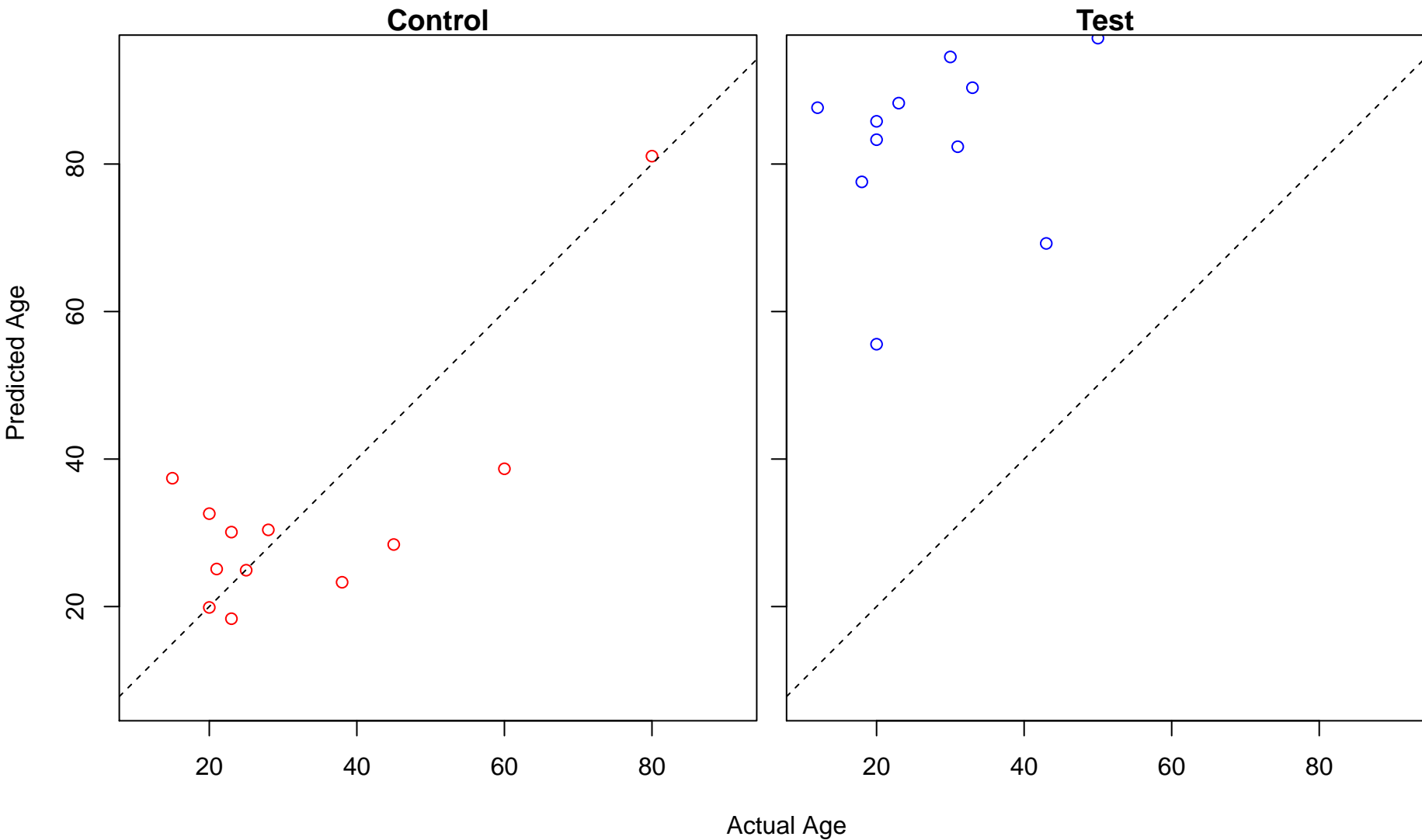
hair cycle (Score: 9.136423)



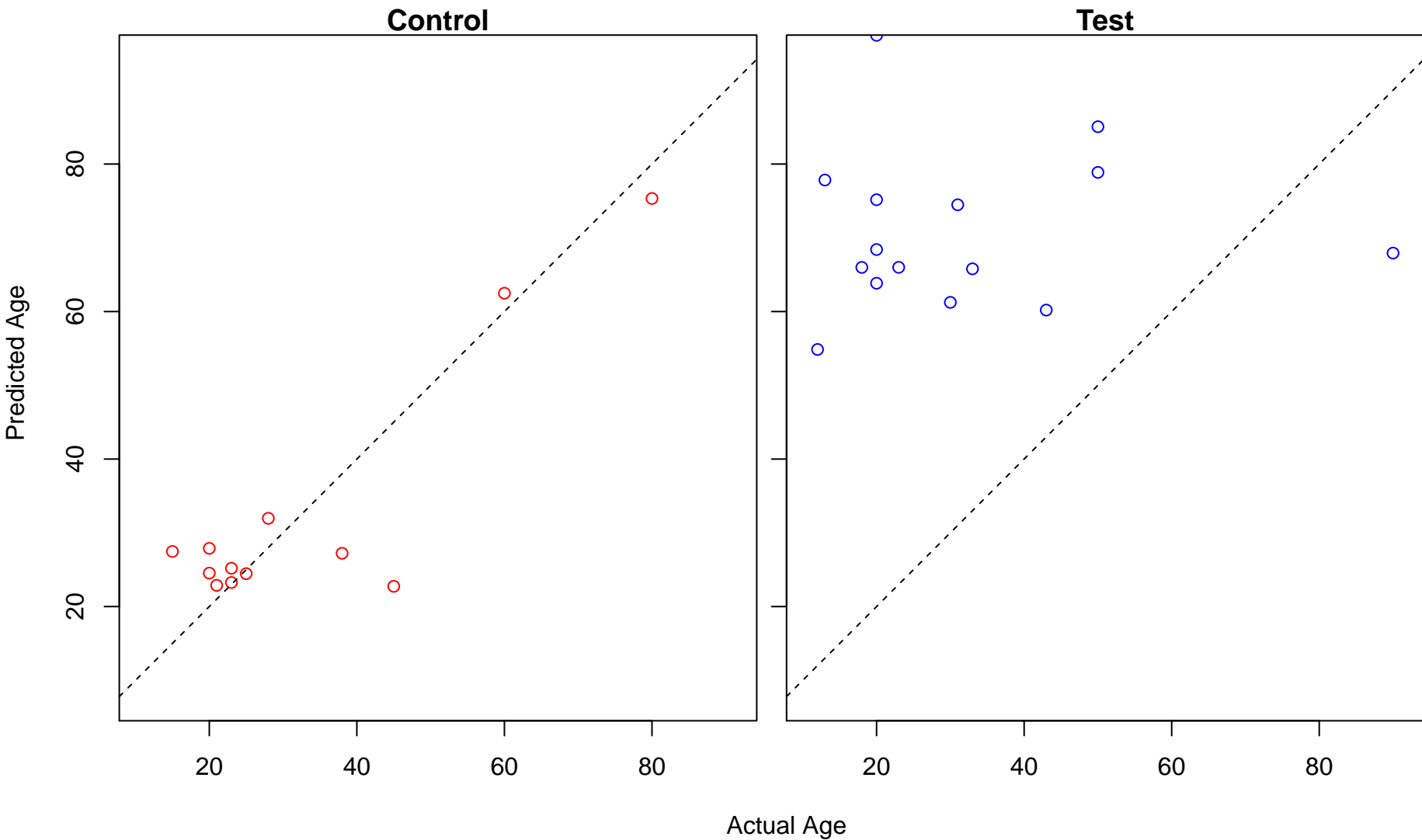
cardiolipin biosynthetic process (Score: 9.134779)



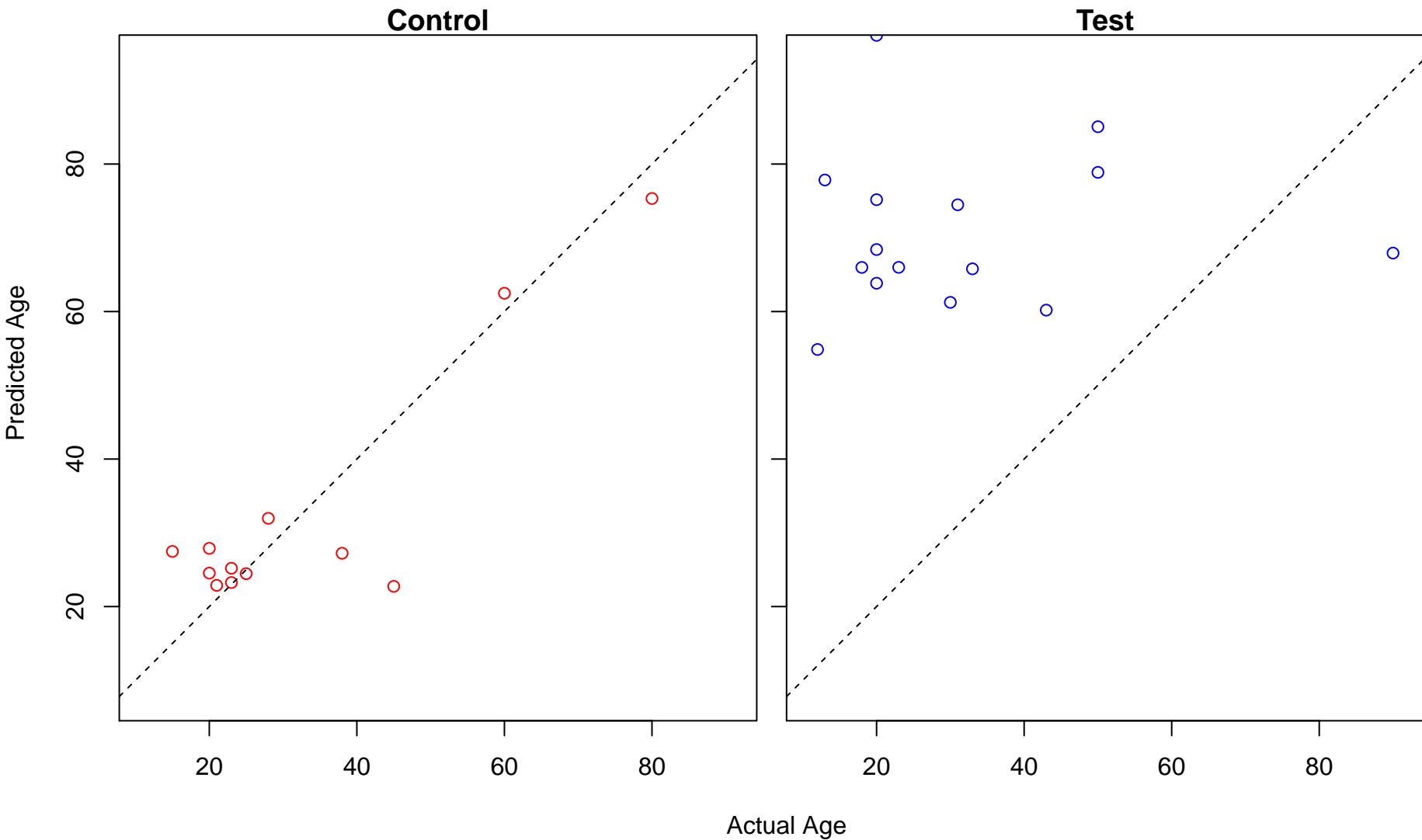
induction of positive chemotaxis (Score: 9.133954)



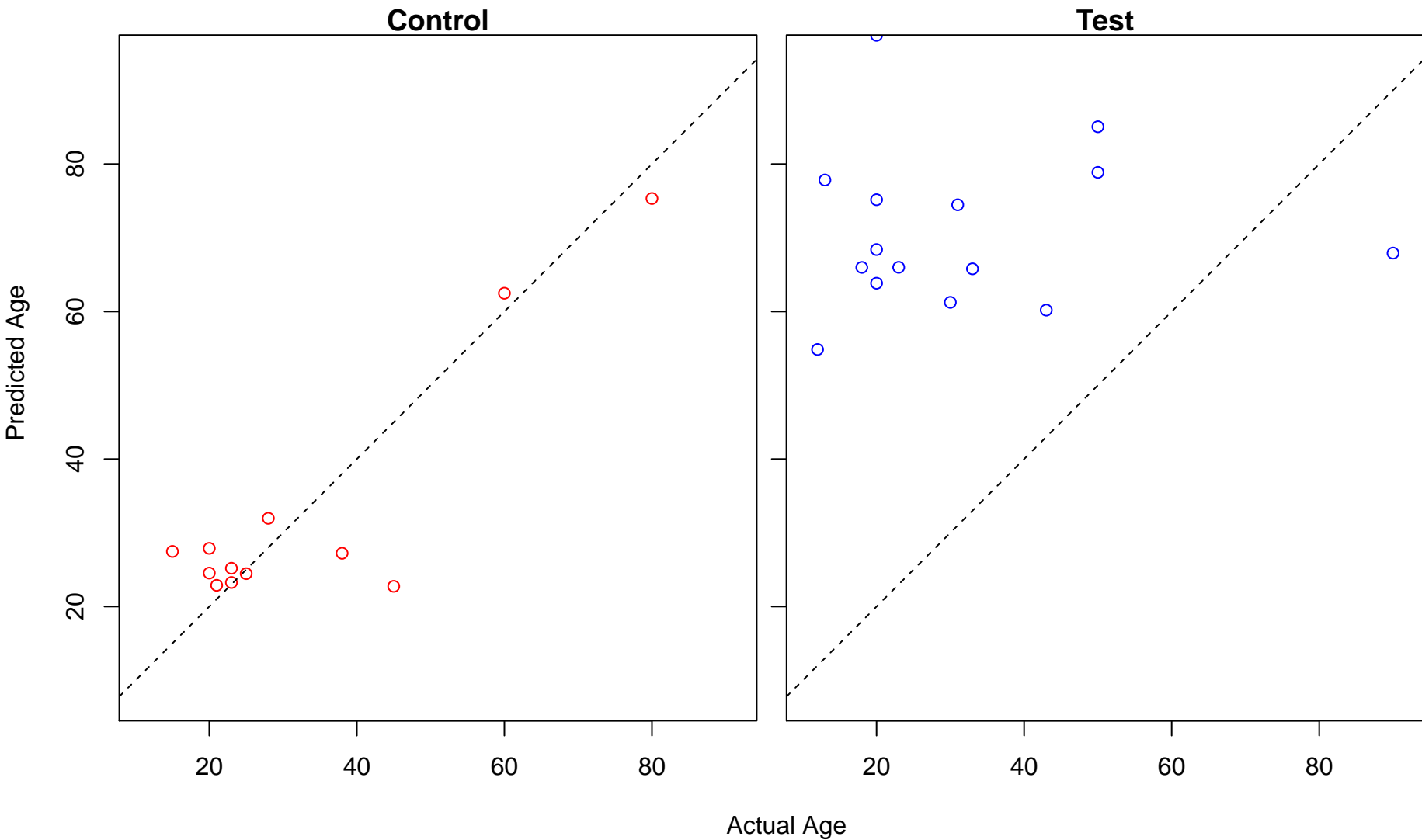
hair follicle development (Score: 9.131842)



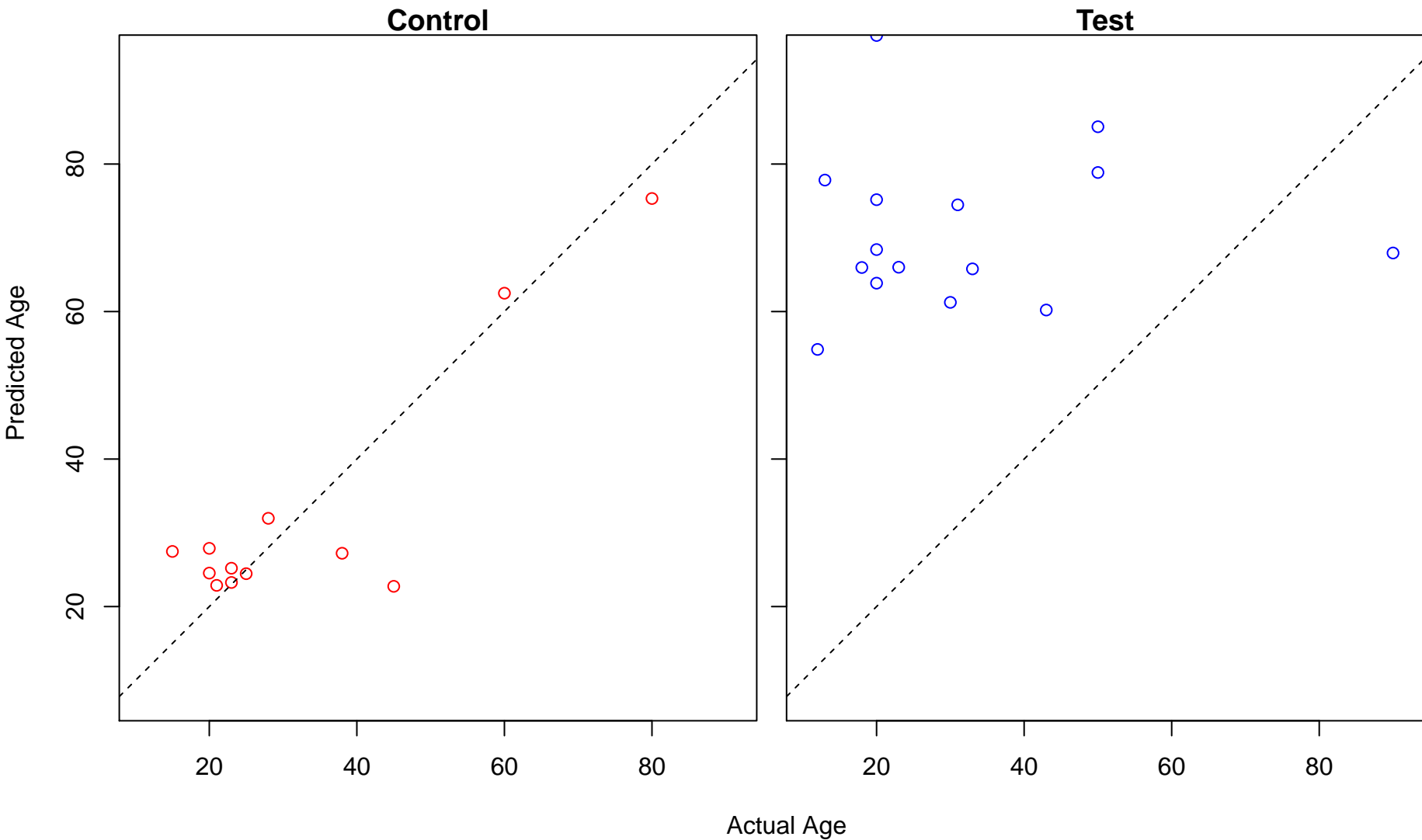
molting cycle process (Score: 9.131763)



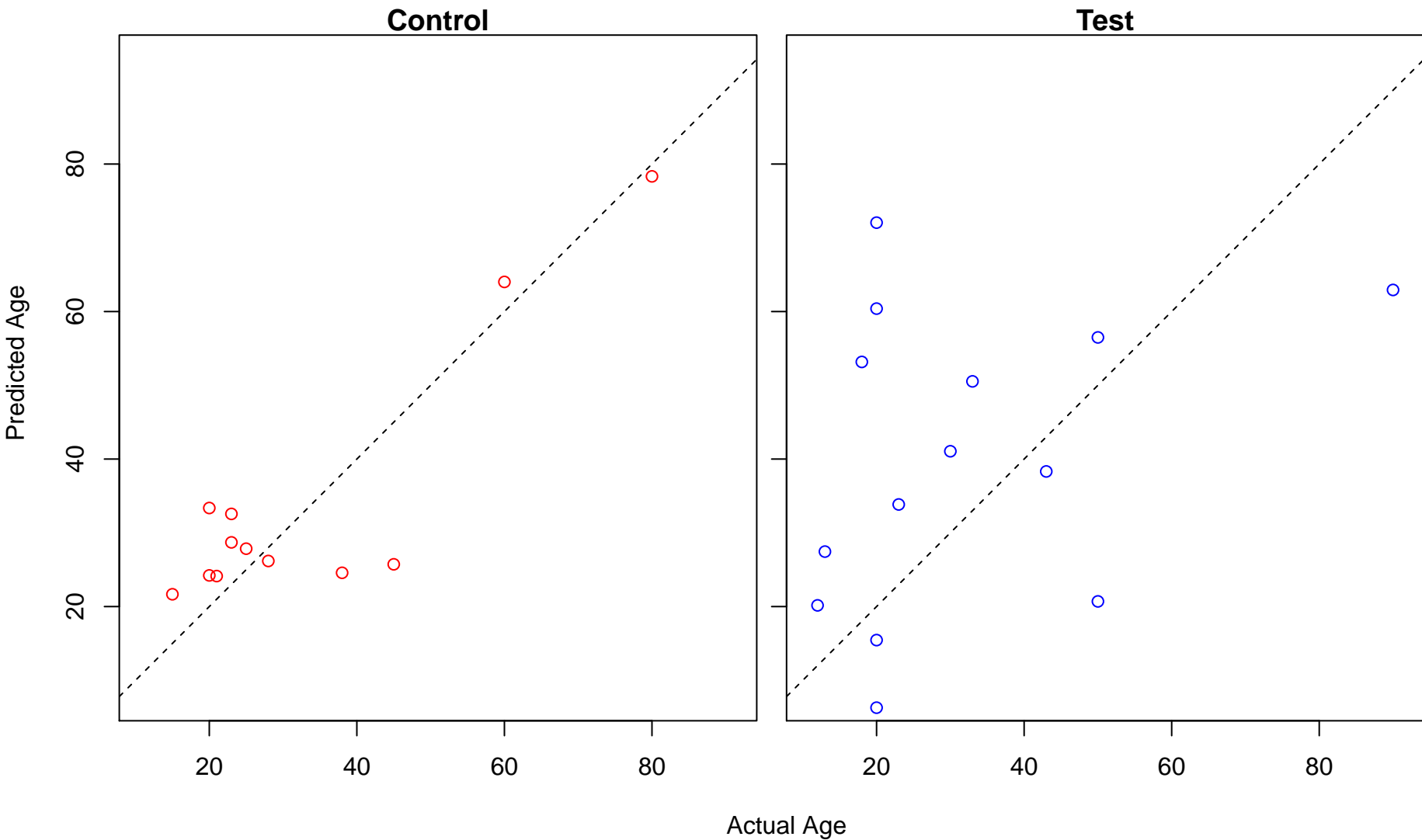
hair cycle process (Score: 9.131763)



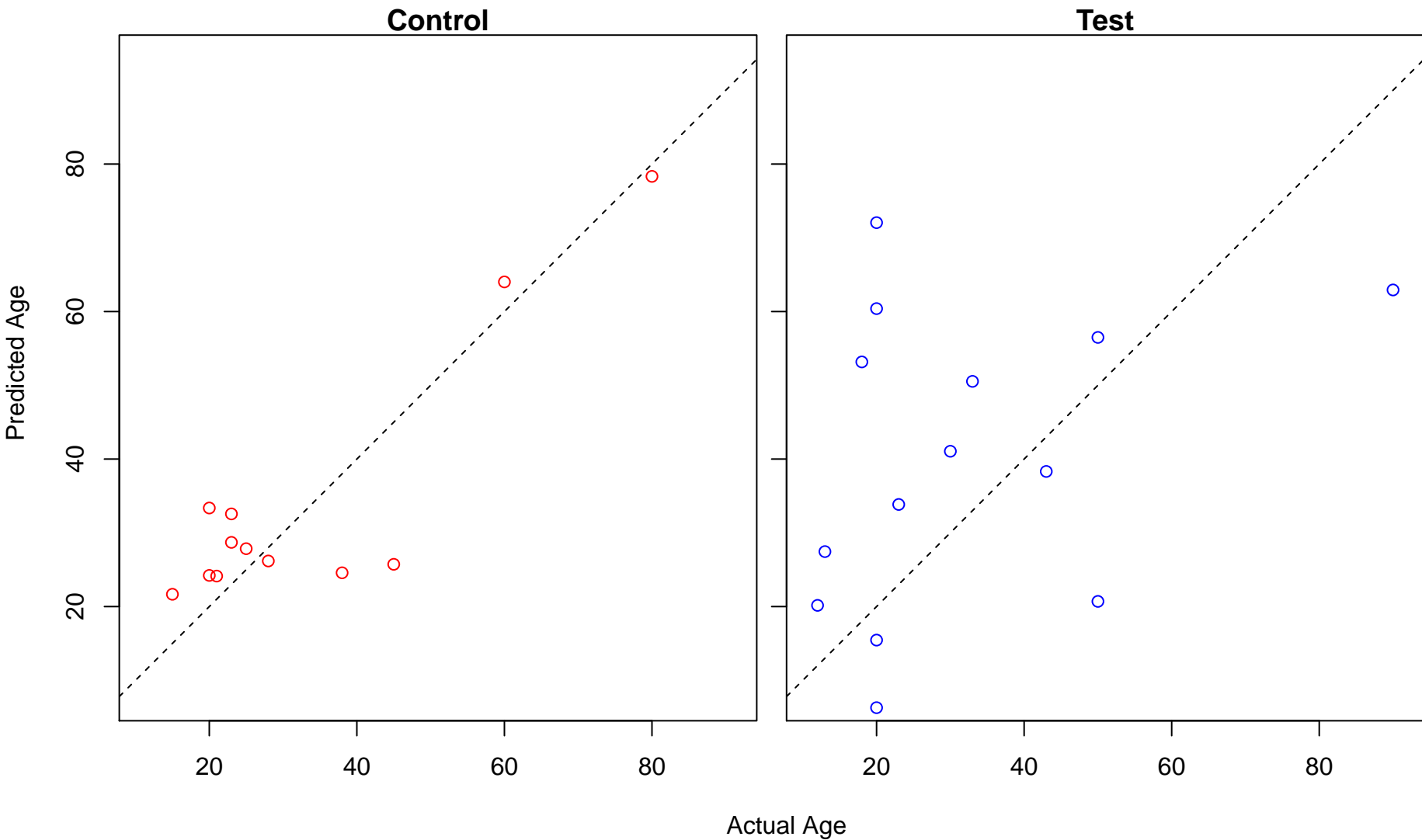
skin epidermis development (Score: 9.129804)



positive regulation of sterol transport (Score: 9.127152)

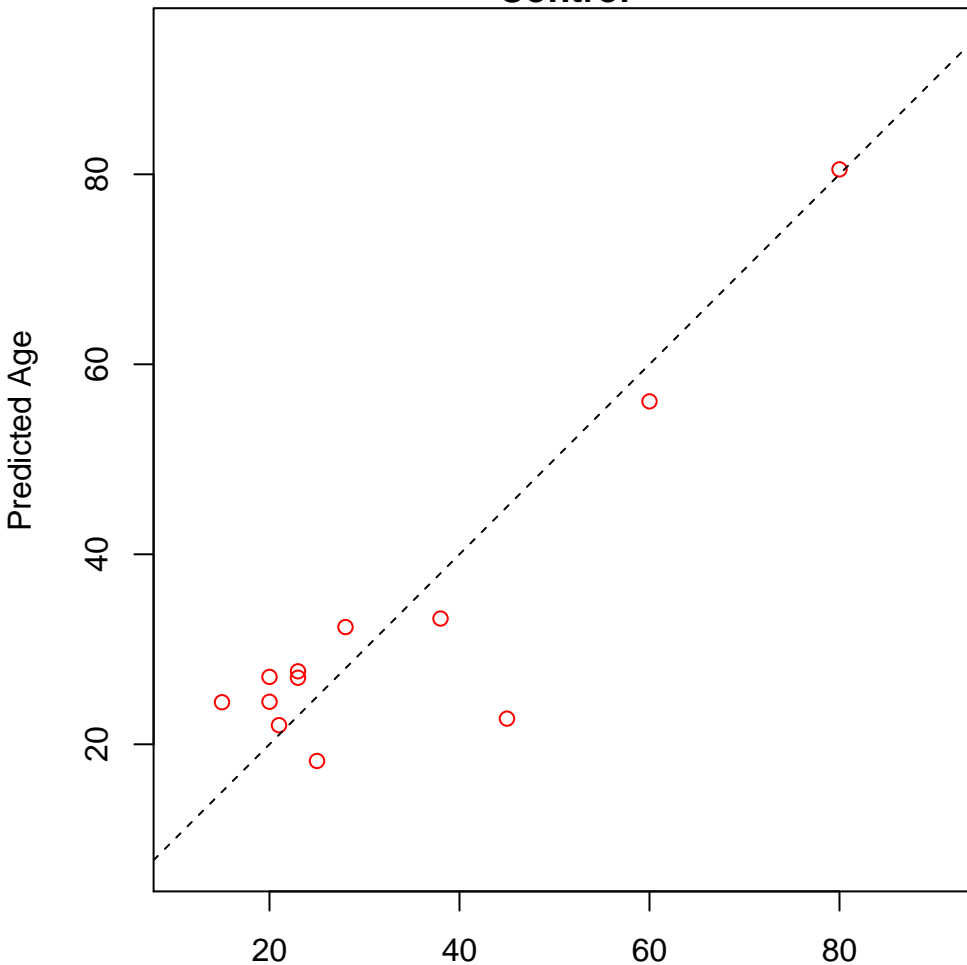


positive regulation of cholesterol transport (Score: 9.127152)

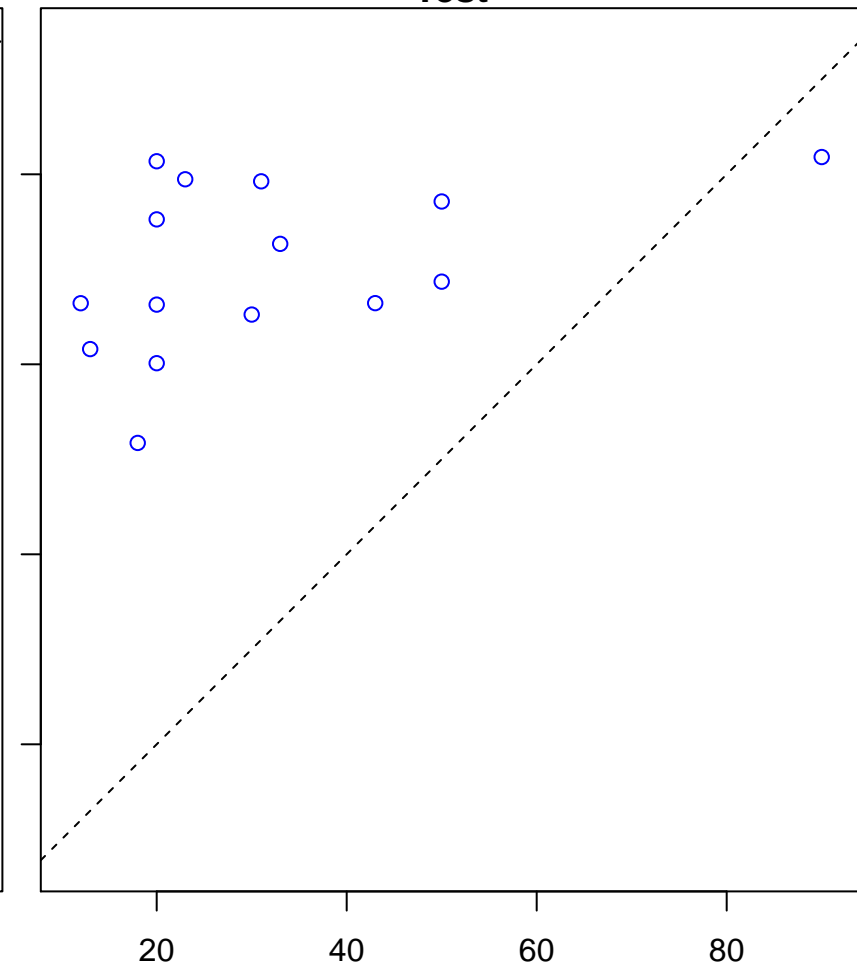


morphogenesis of an epithelium (Score: 9.125082)

Control

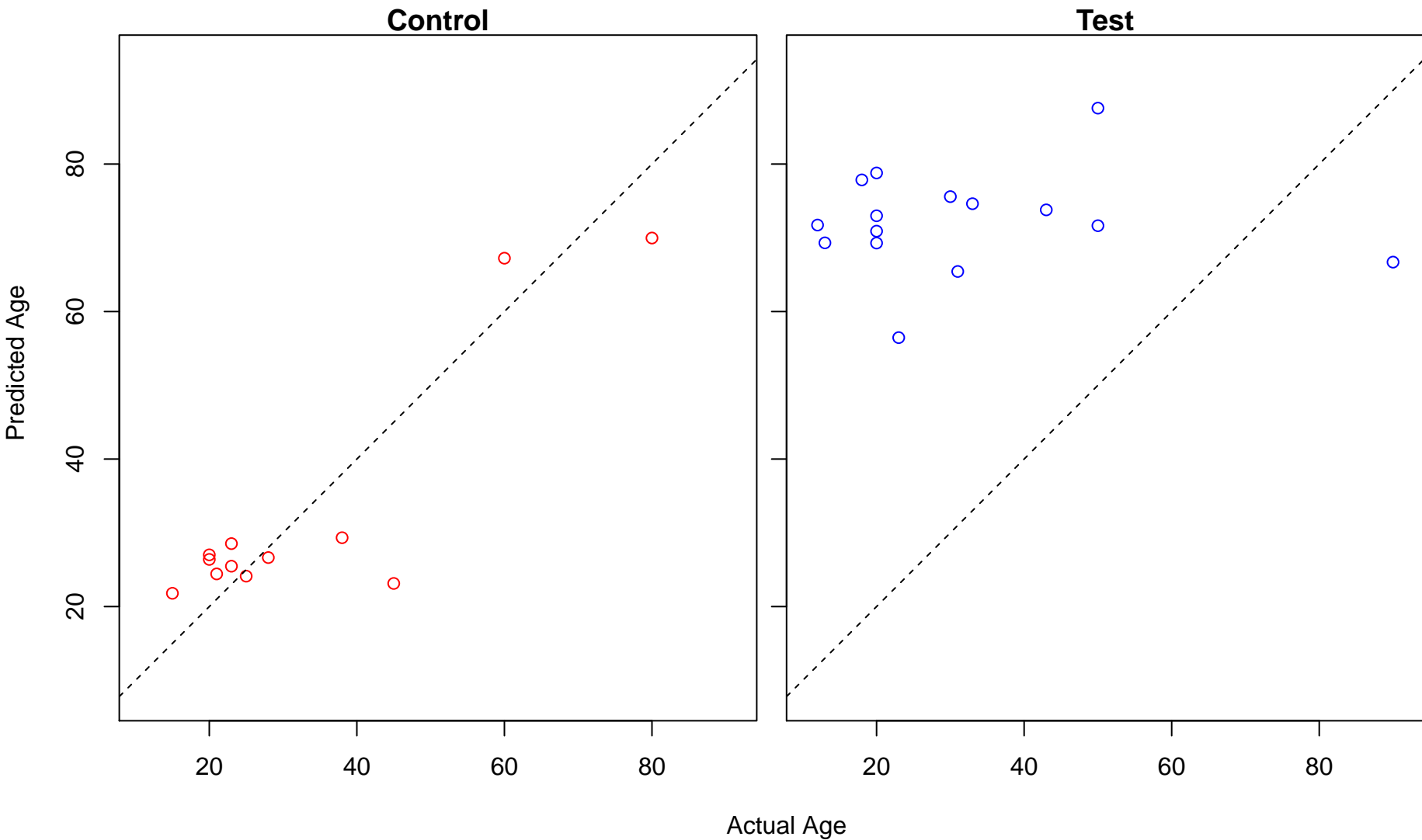


Test

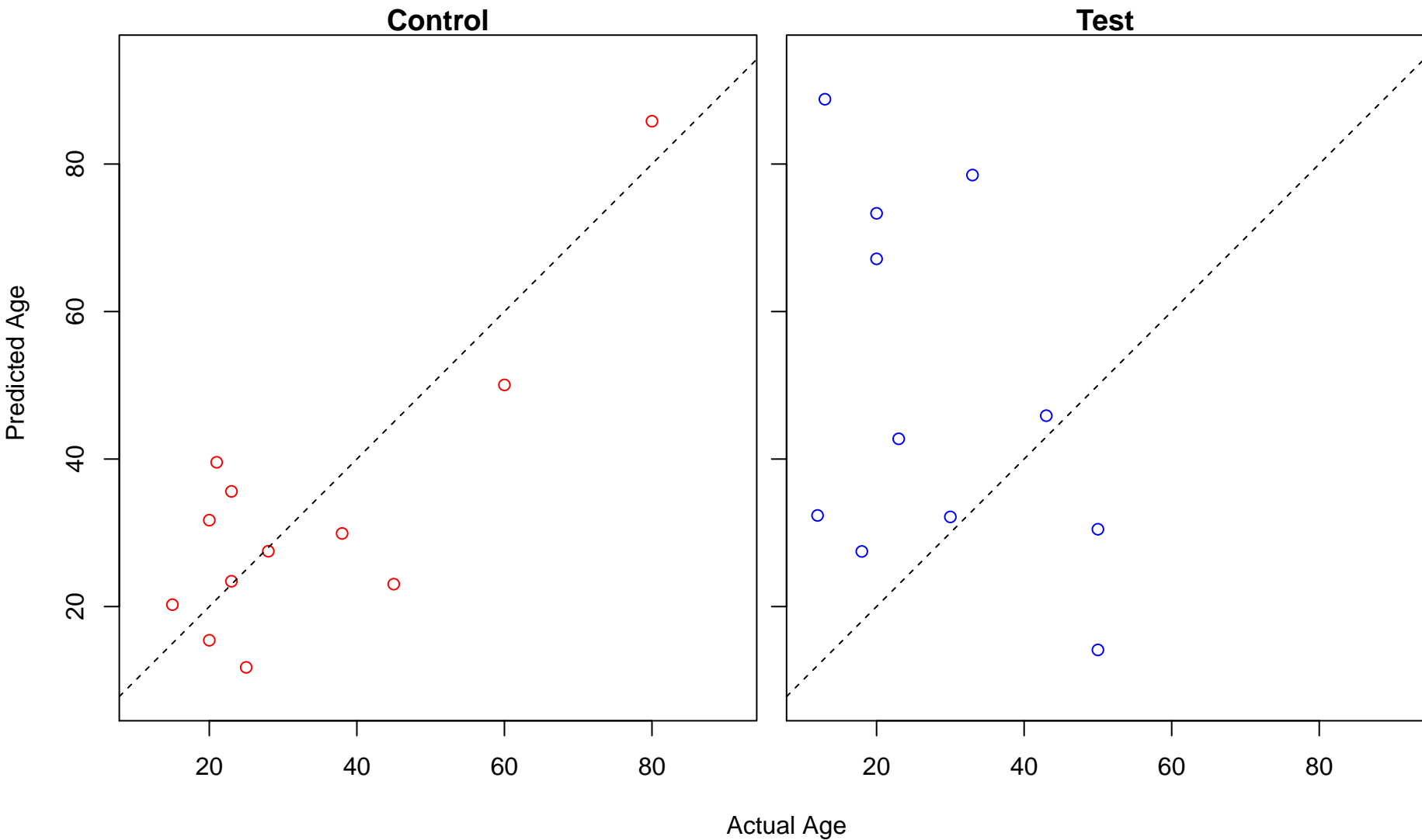


Actual Age

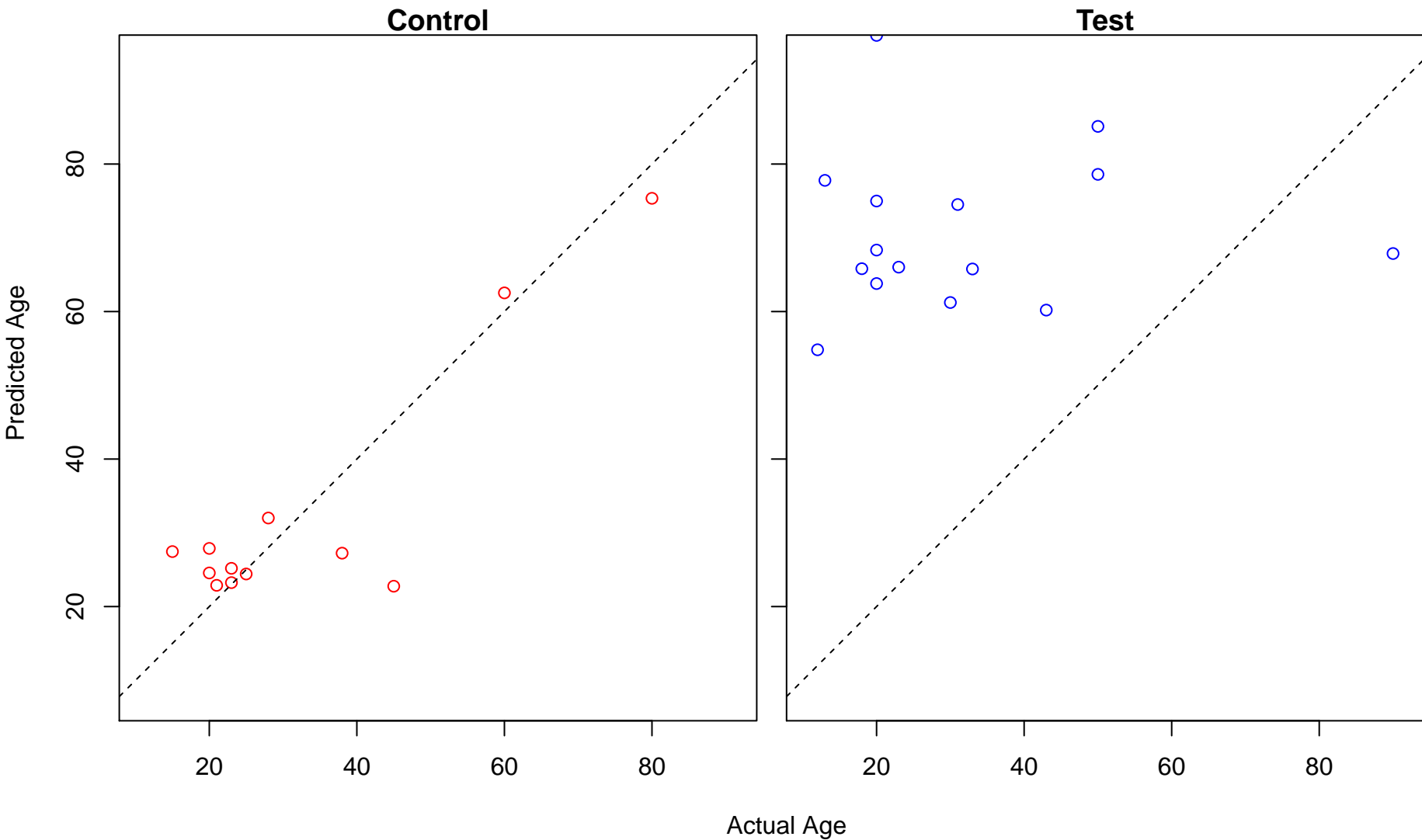
toxin transport (Score: 9.124136)



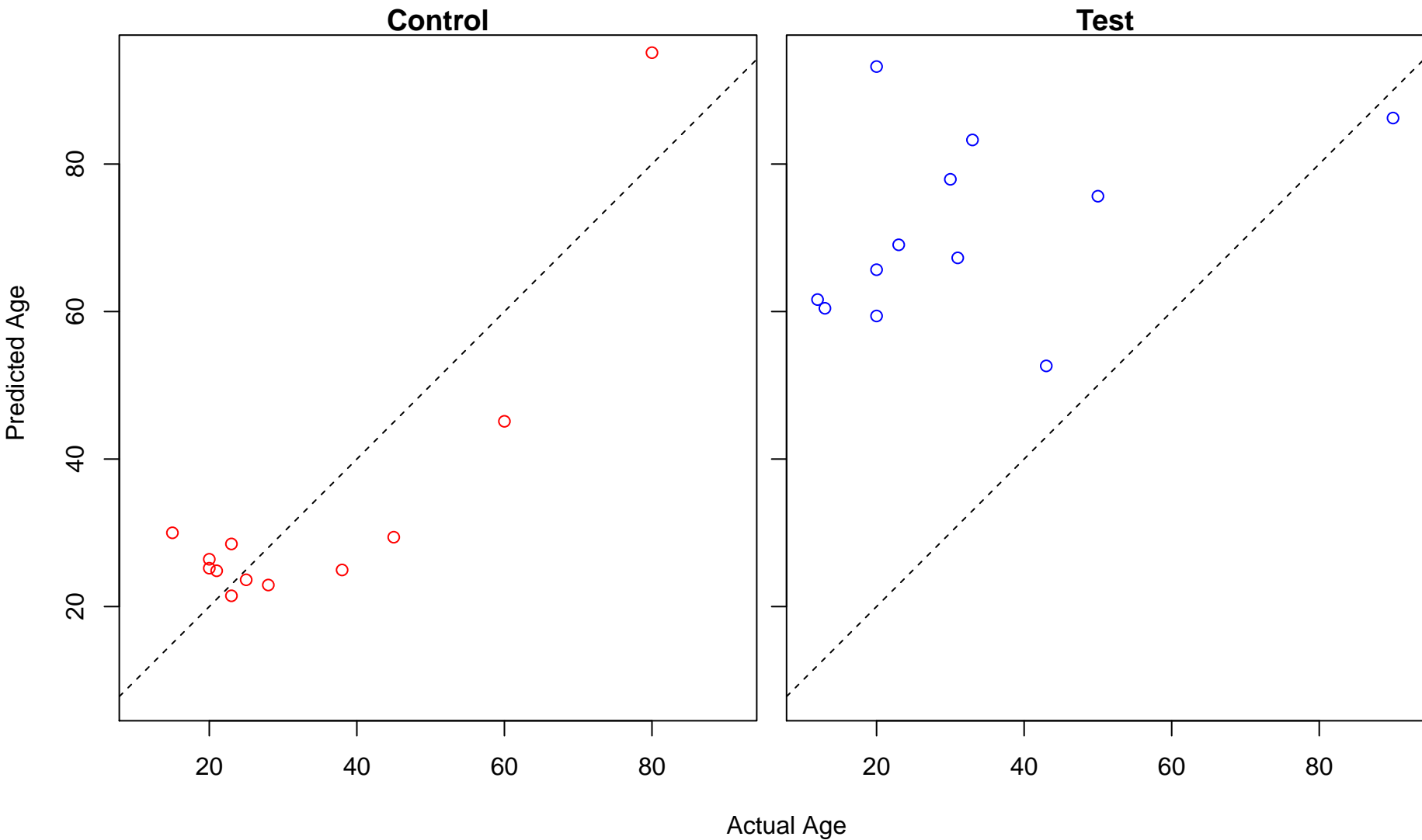
protein localization to synapse (Score: 9.122258)



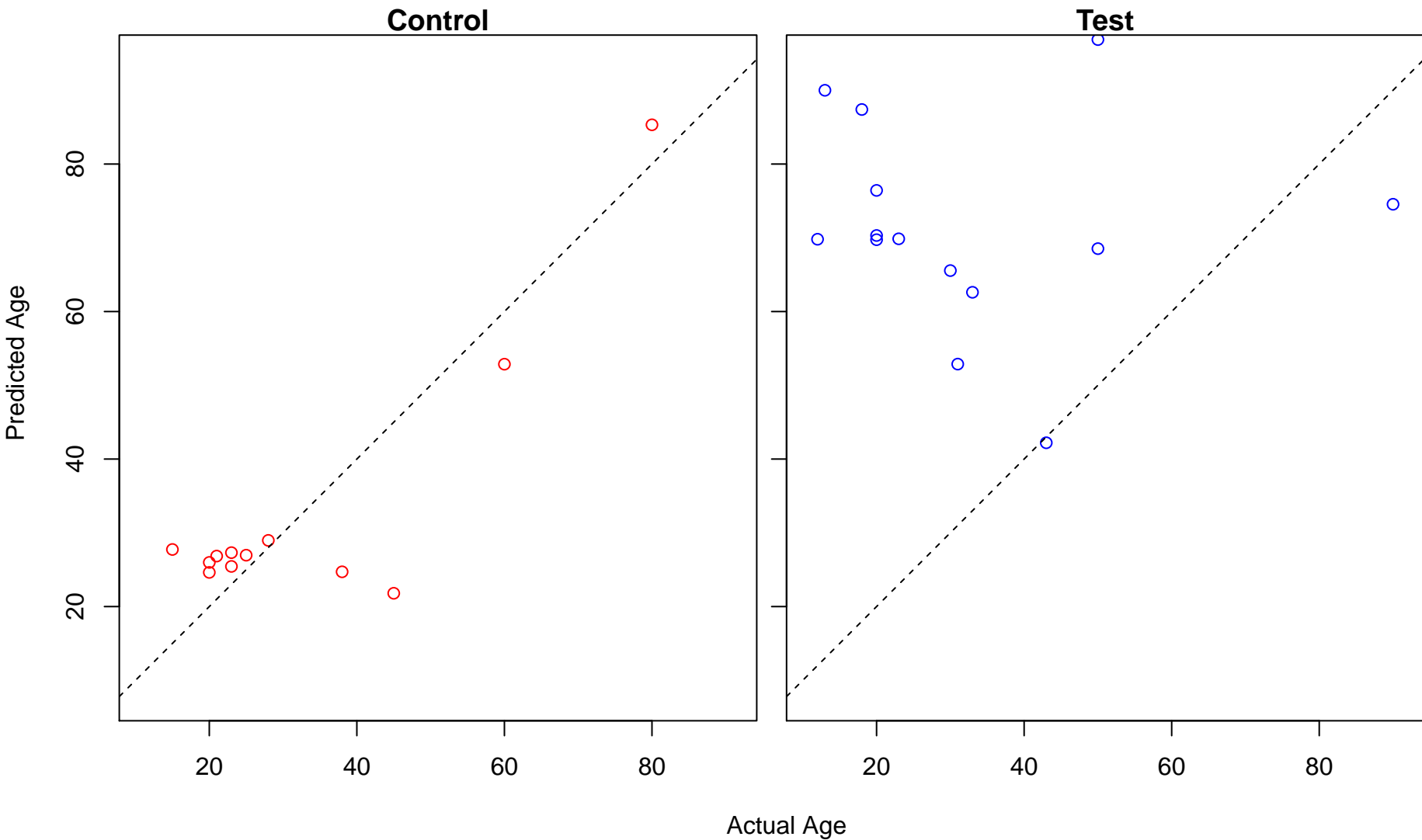
sensory perception of smell (Score: 9.121650)



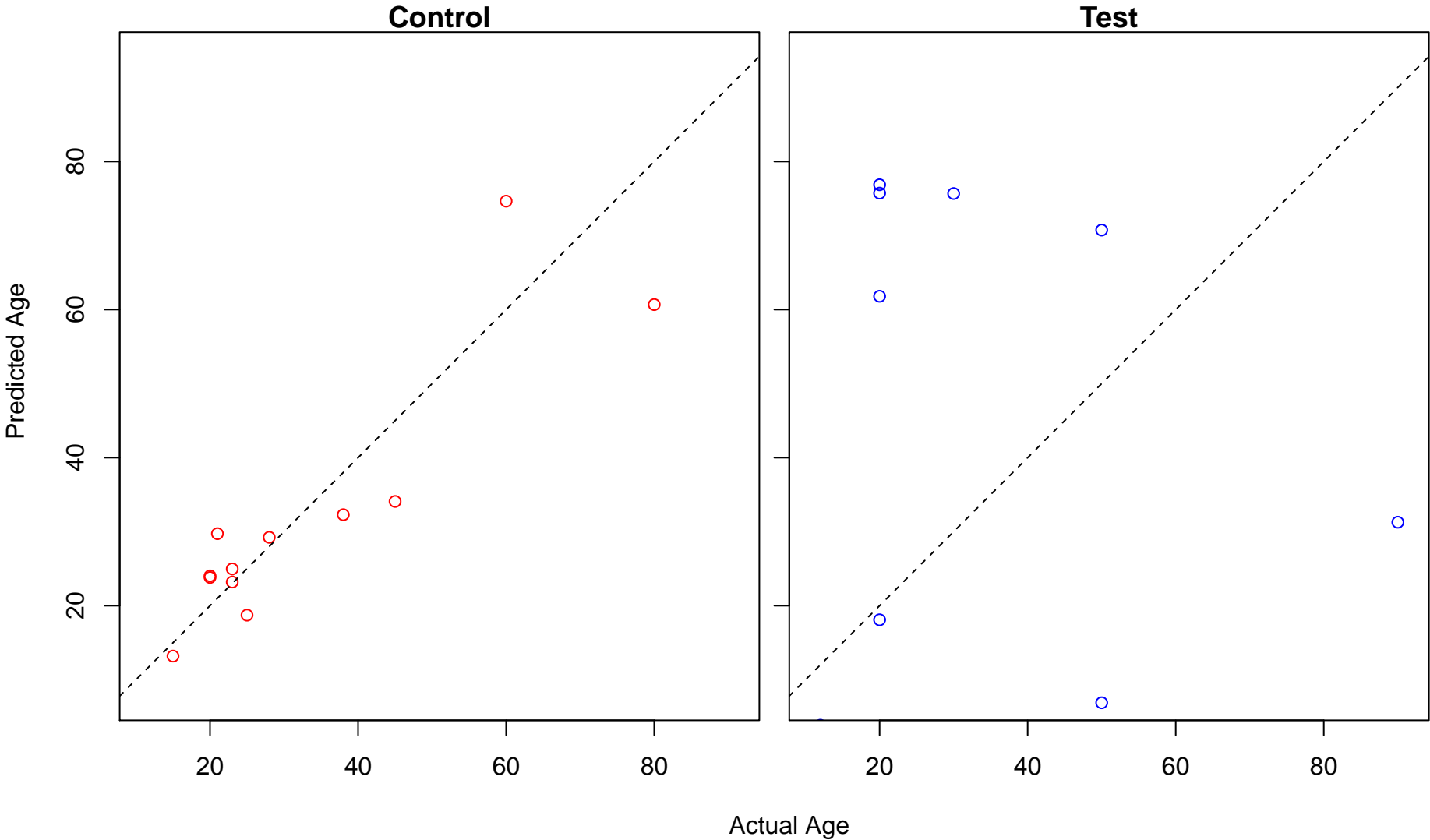
positive regulation of calcium ion-dependent exocytosis (Score: 9.121027)



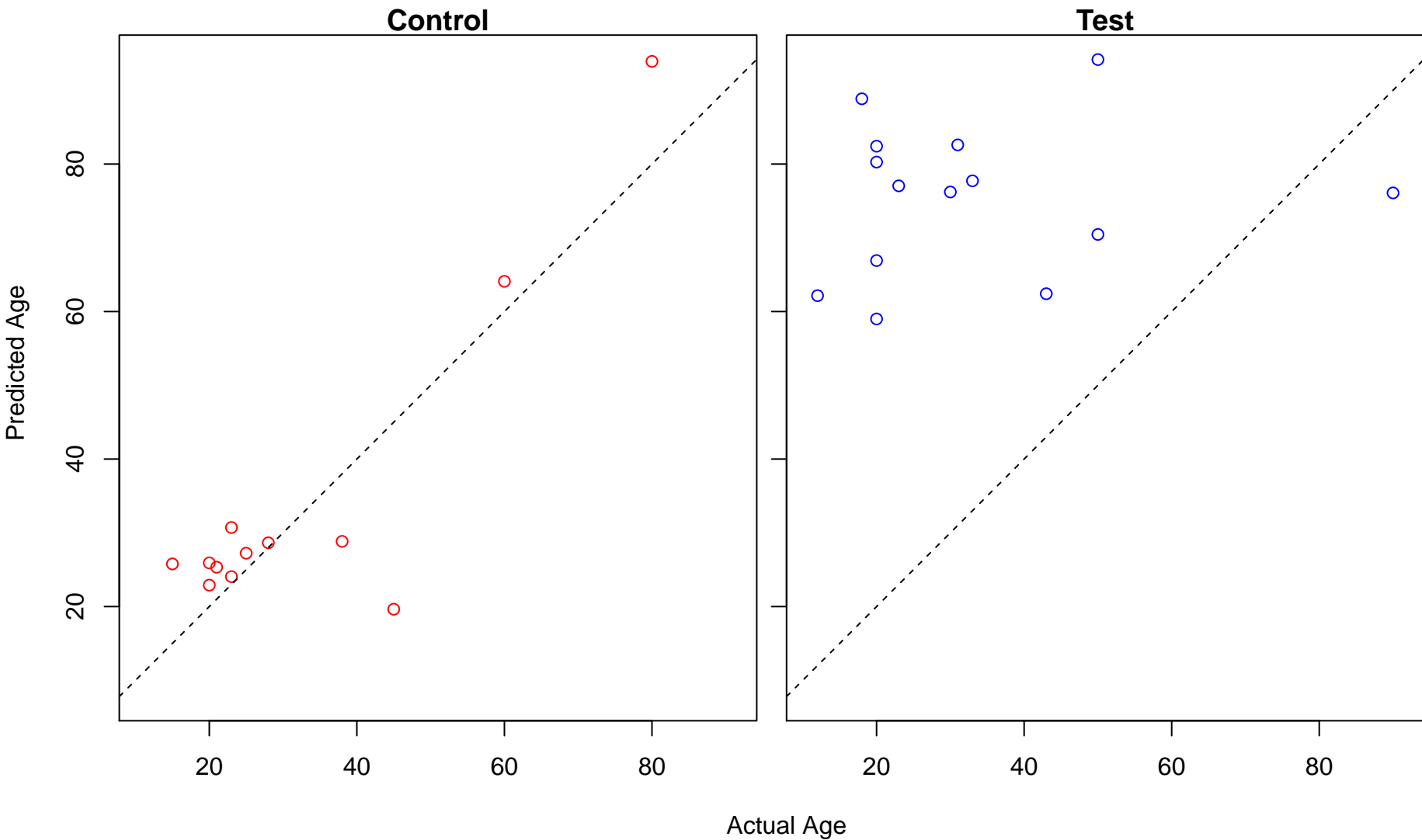
positive regulation of viral life cycle (Score: 9.118933)



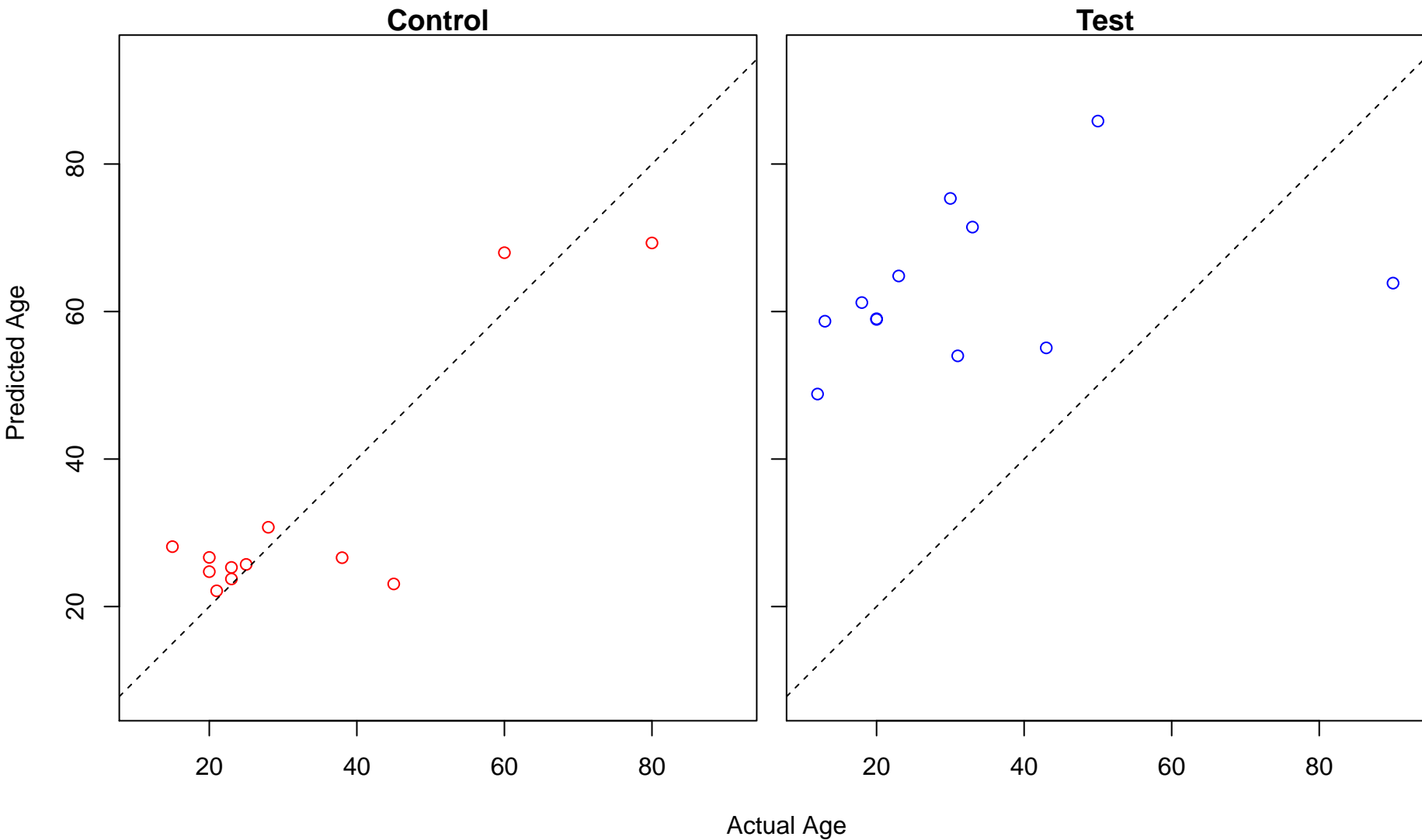
regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 9.11)



antigen processing and presentation of peptide antigen via MHC class I (Score: 9.106529)

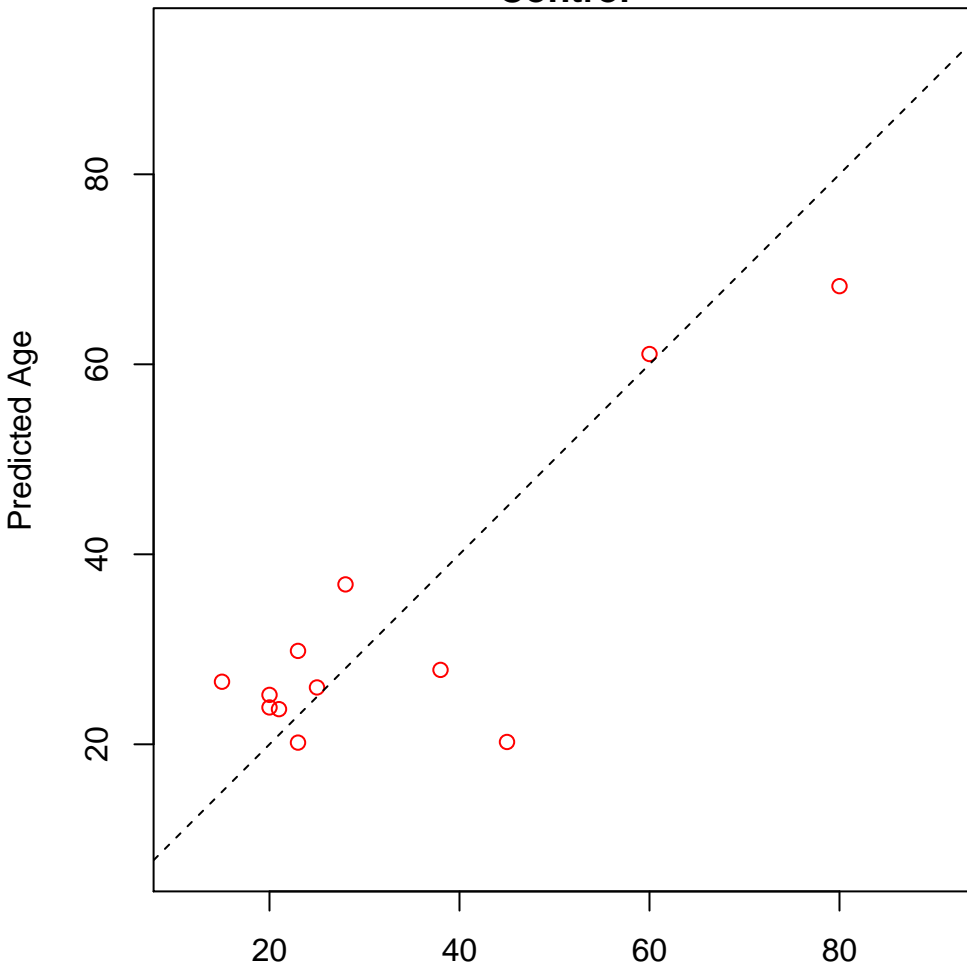


positive regulation of osteoclast differentiation (Score: 9.105062)

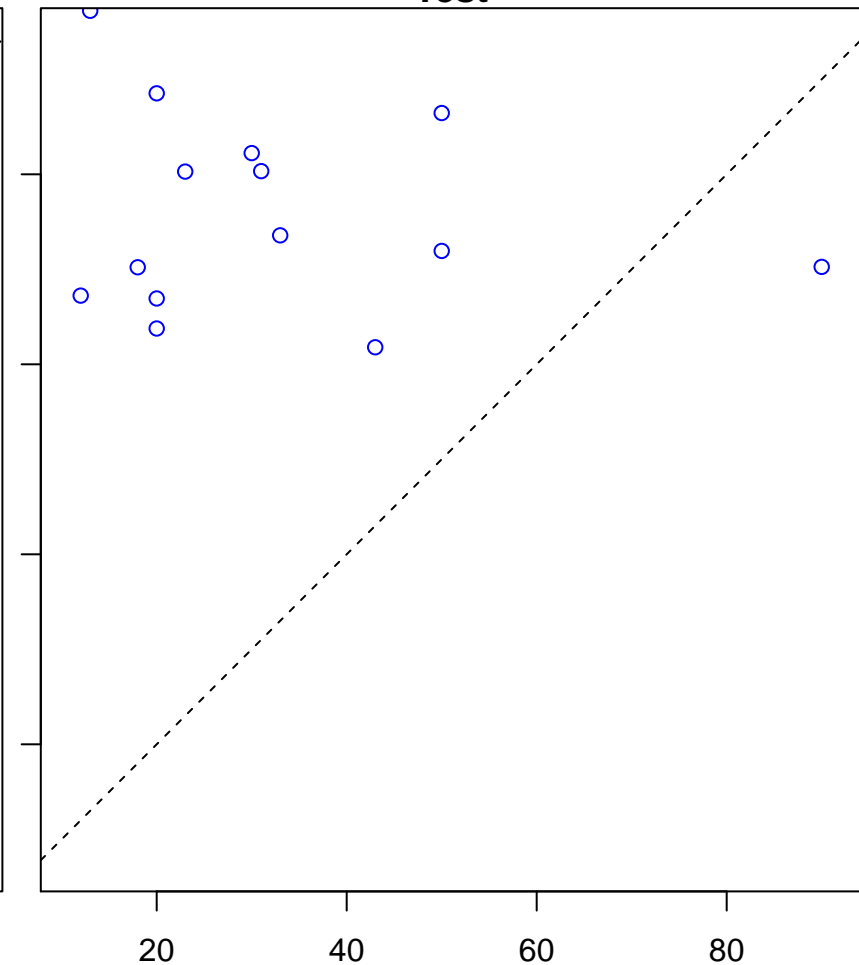


positive regulation of B cell activation (Score: 9.101558)

Control

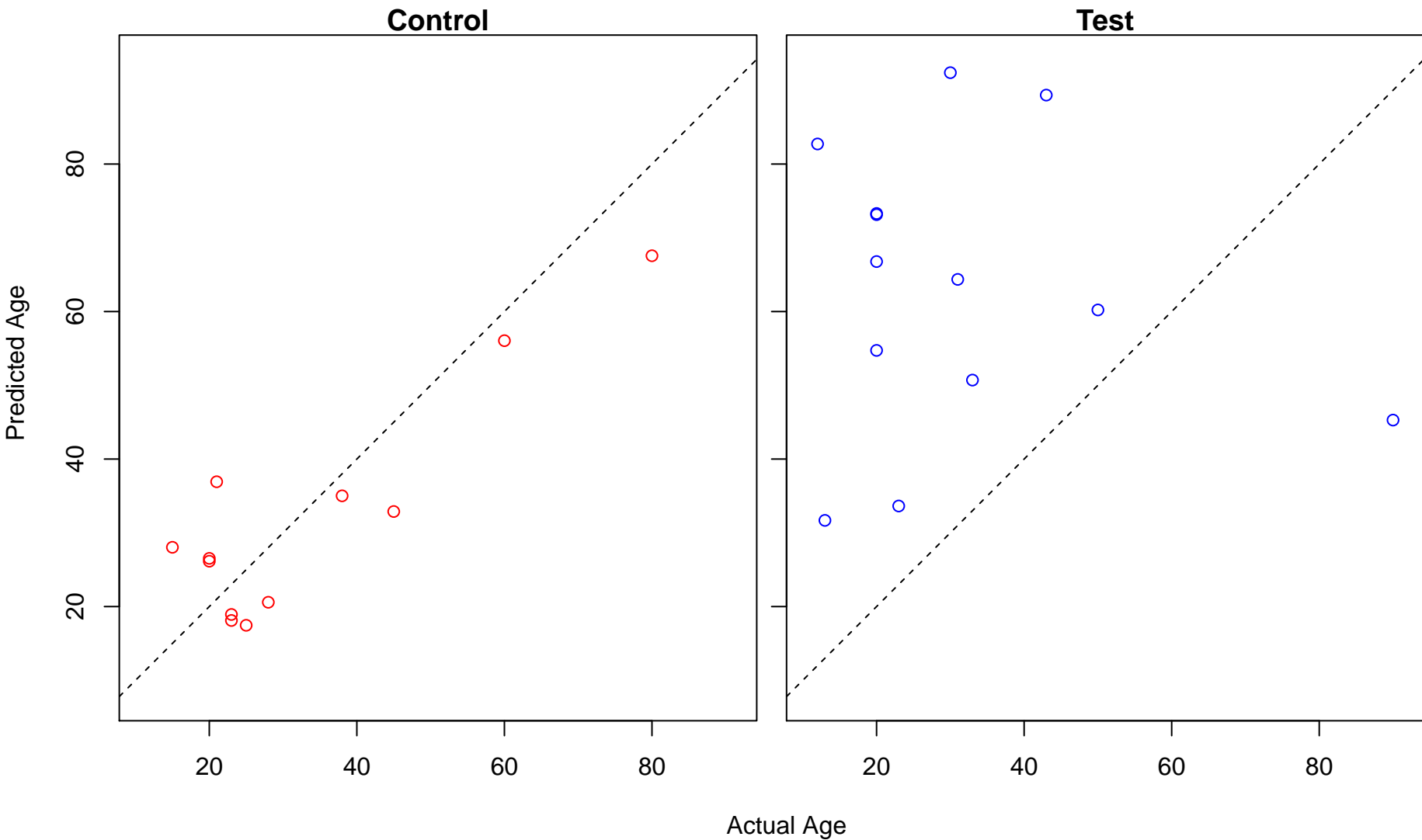


Test

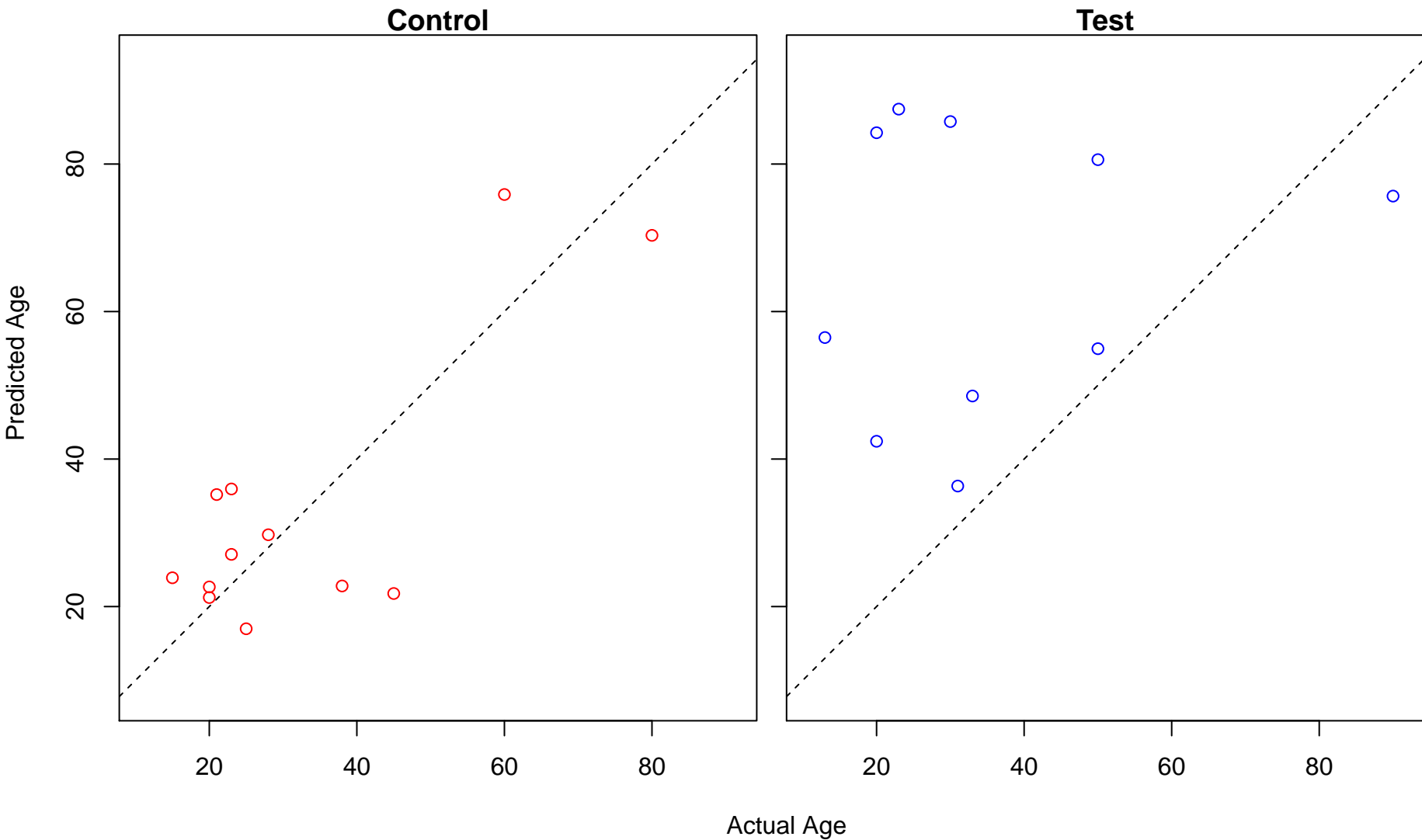


Actual Age

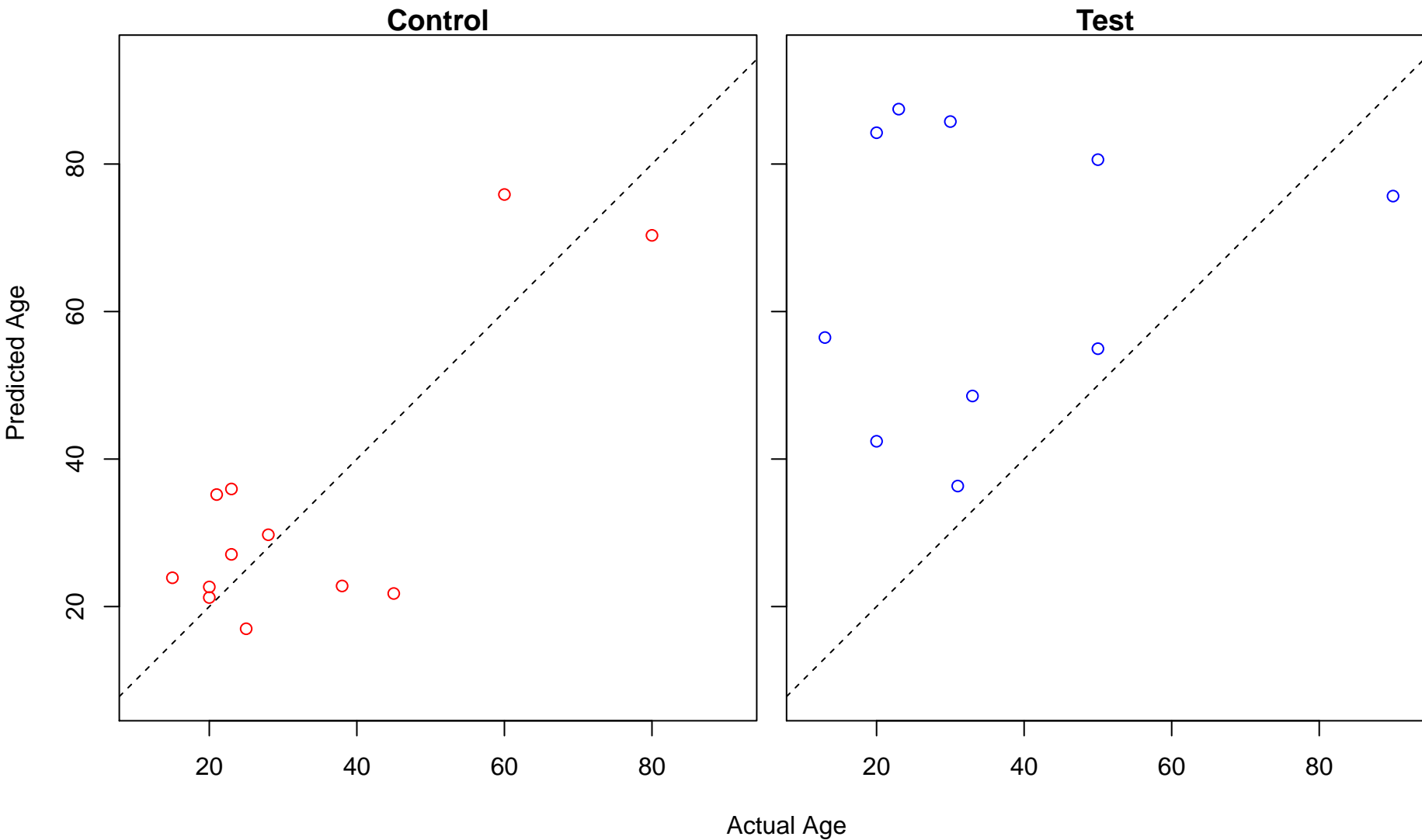
estrogen metabolic process (Score: 9.100492)



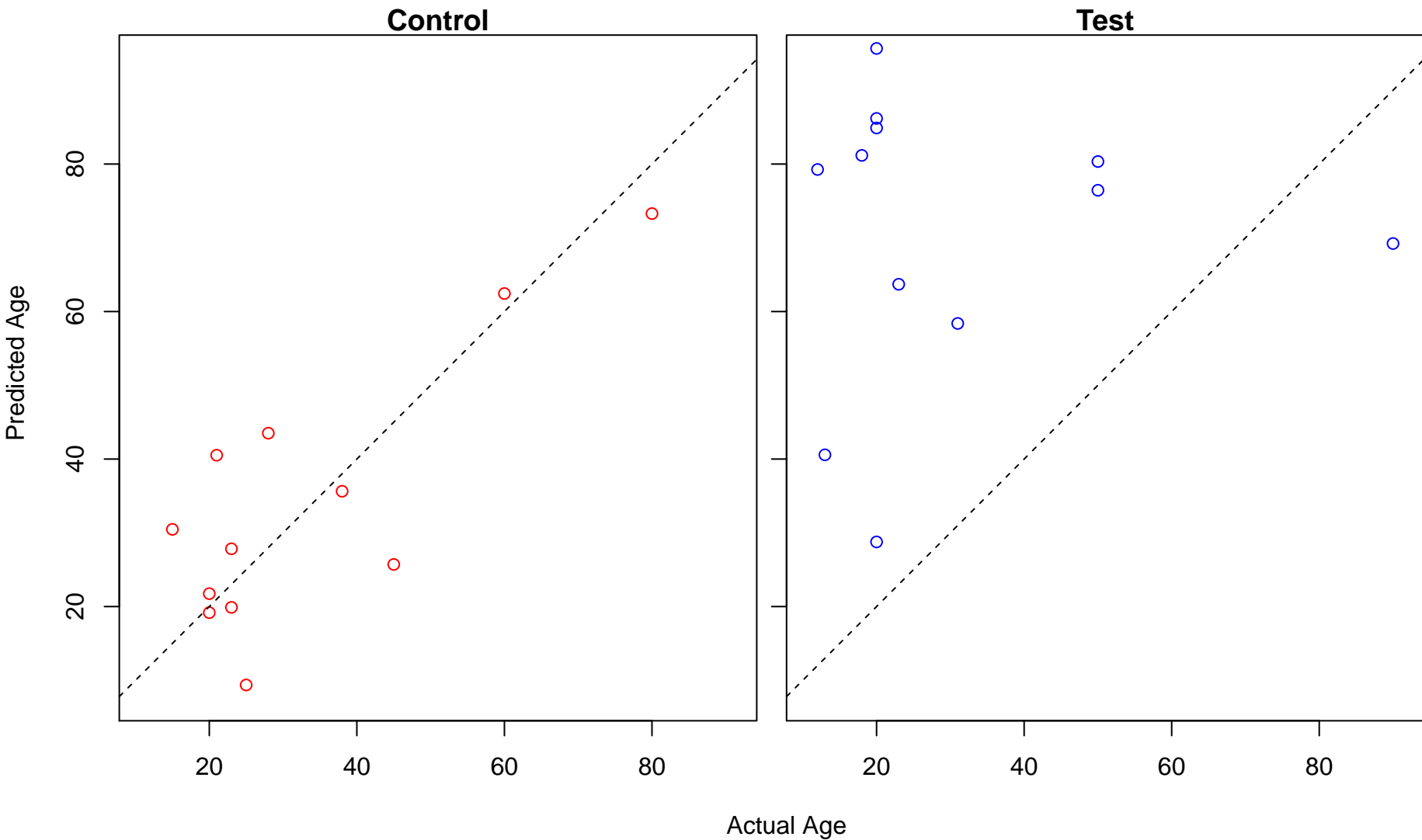
wound healing, spreading of cells (Score: 9.099984)



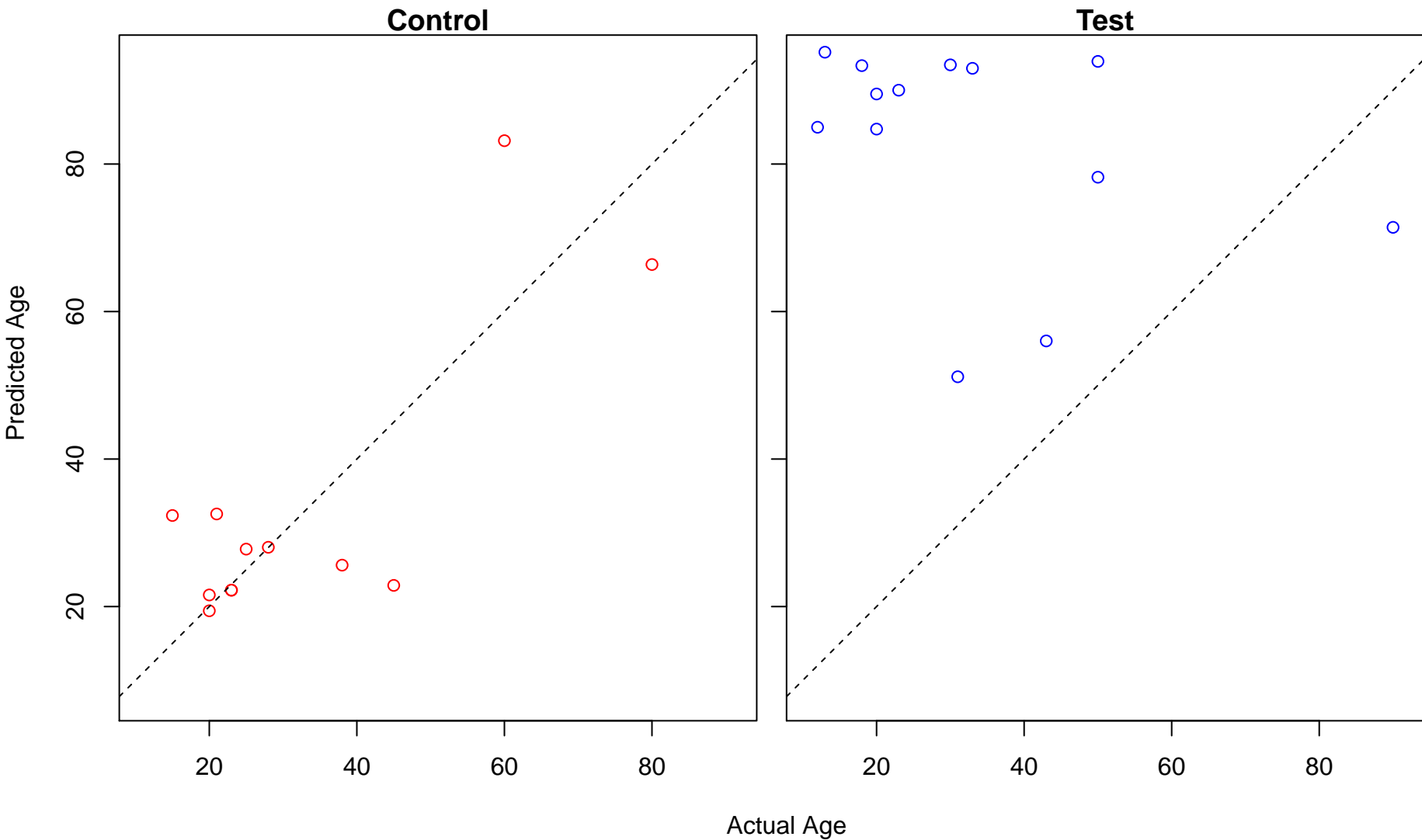
epiboly involved in wound healing (Score: 9.099984)



negative regulation of actin filament depolymerization (Score: 9.099965)

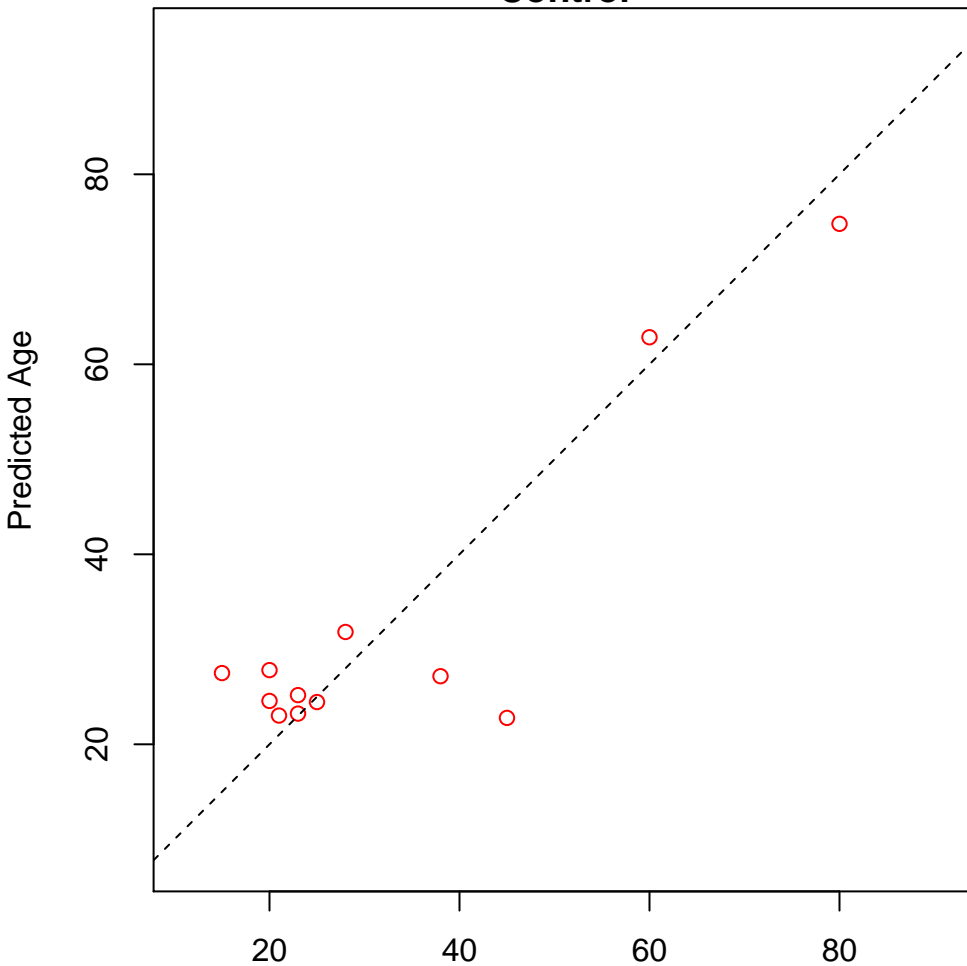


regulation of actin filament polymerization (Score: 9.097705)

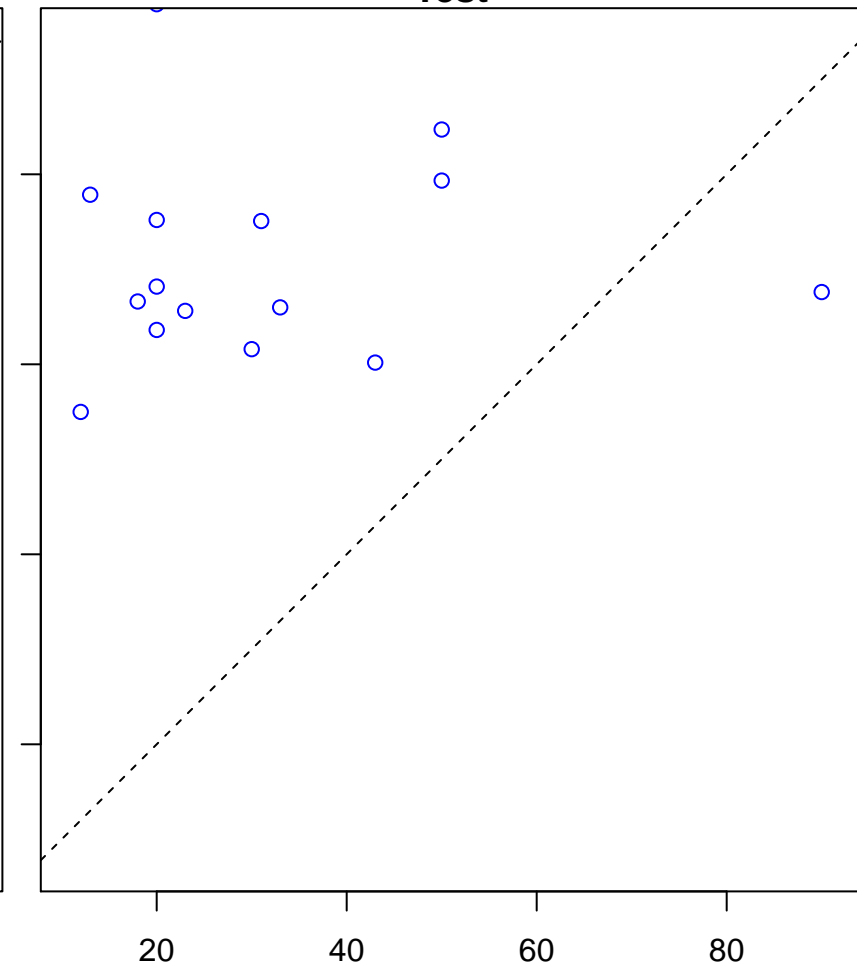


activation of adenylate cyclase activity (Score: 9.096211)

Control

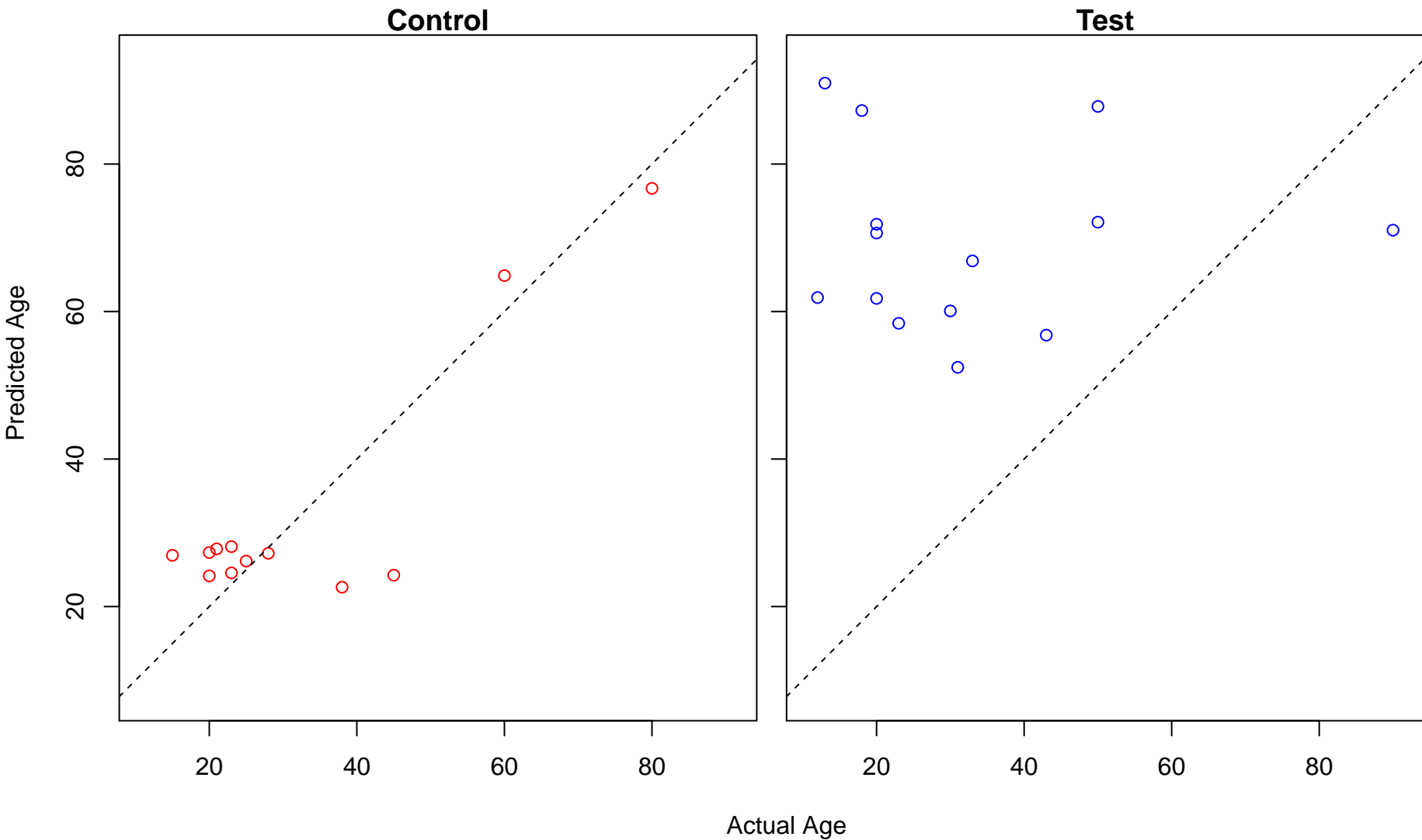


Test

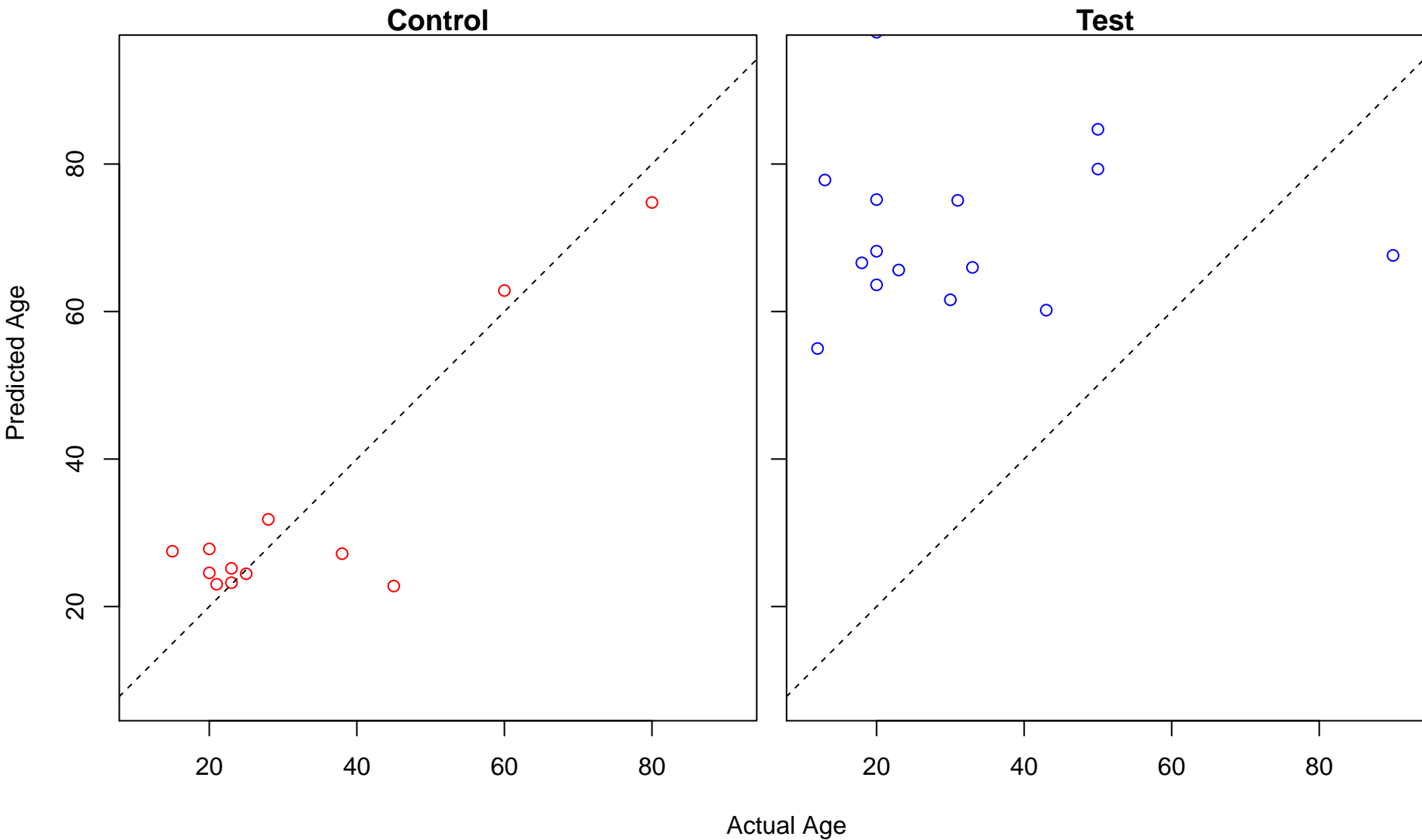


Actual Age

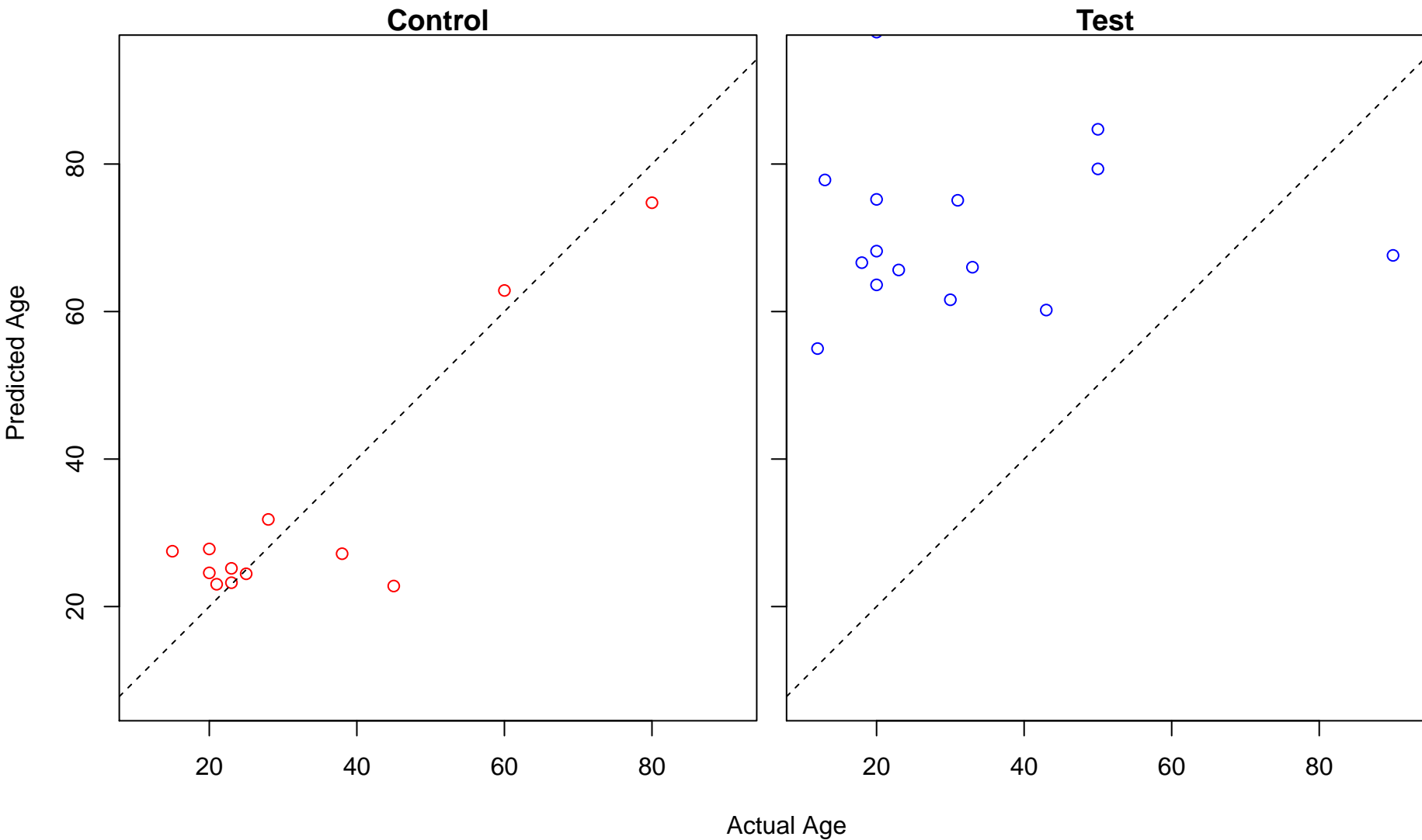
homeostasis of number of cells (Score: 9.095046)



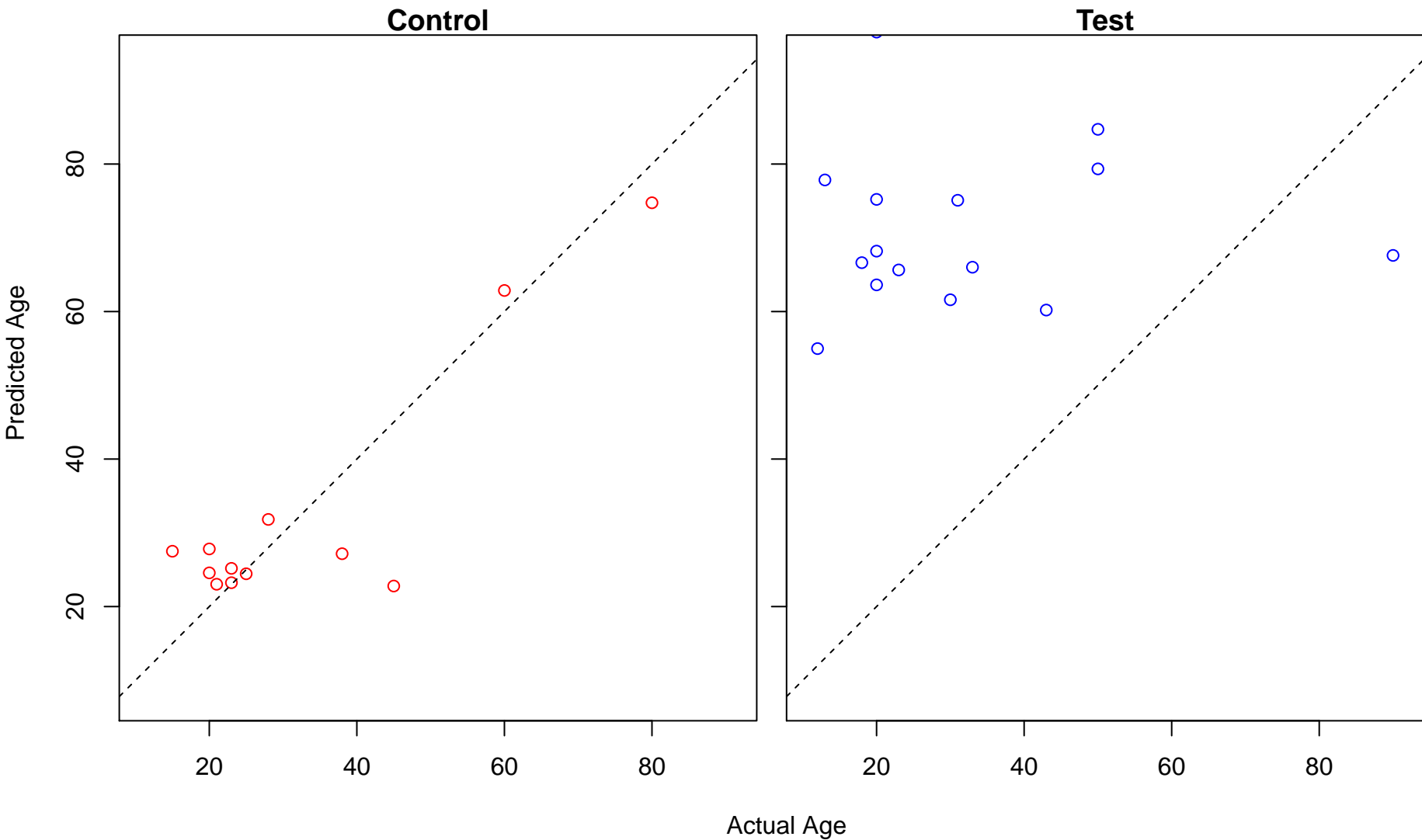
positive regulation of adenylate cyclase activity (Score: 9.094275)



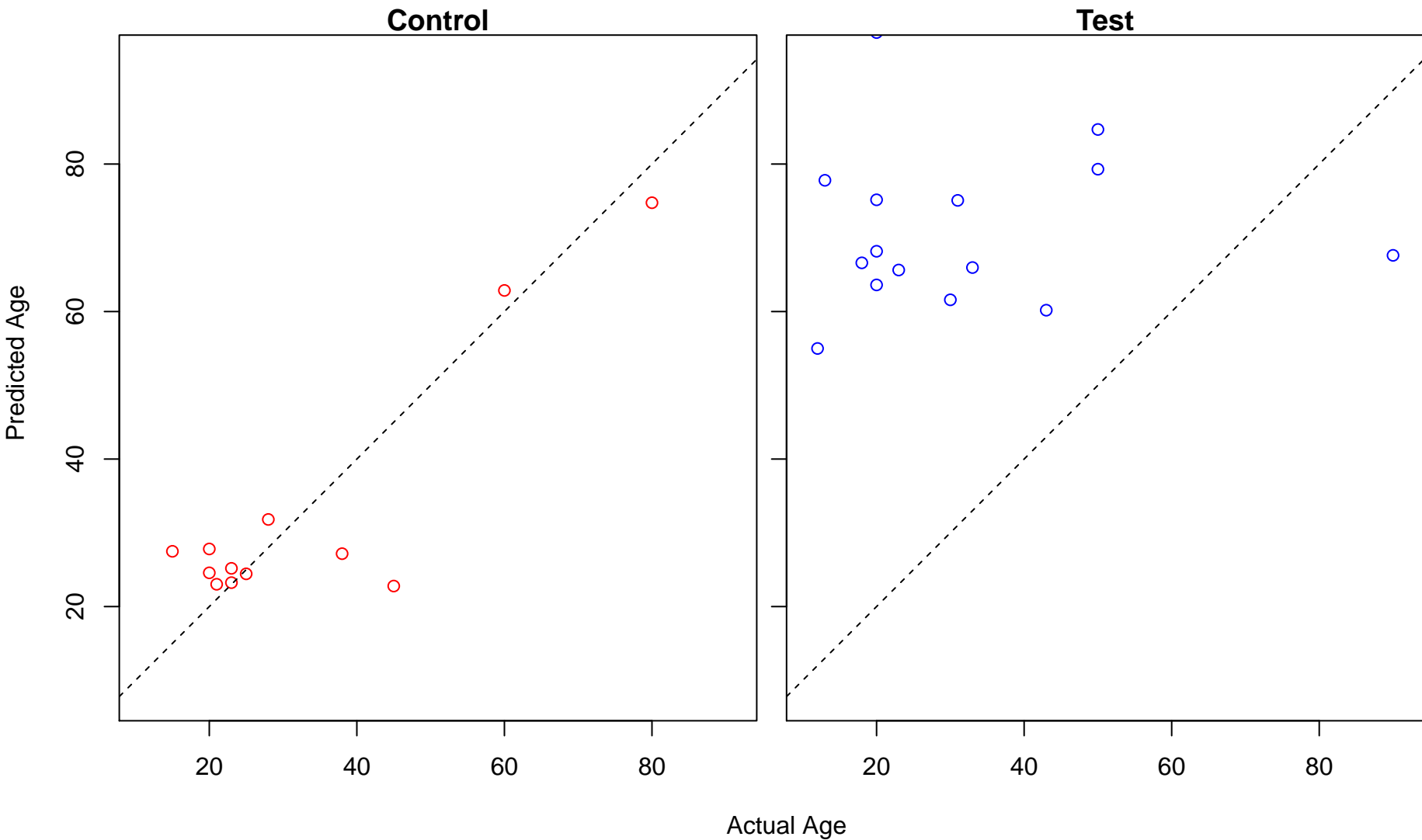
positive regulation of cAMP biosynthetic process (Score: 9.092115)



positive regulation of cyclic nucleotide biosynthetic process (Score: 9.091293)

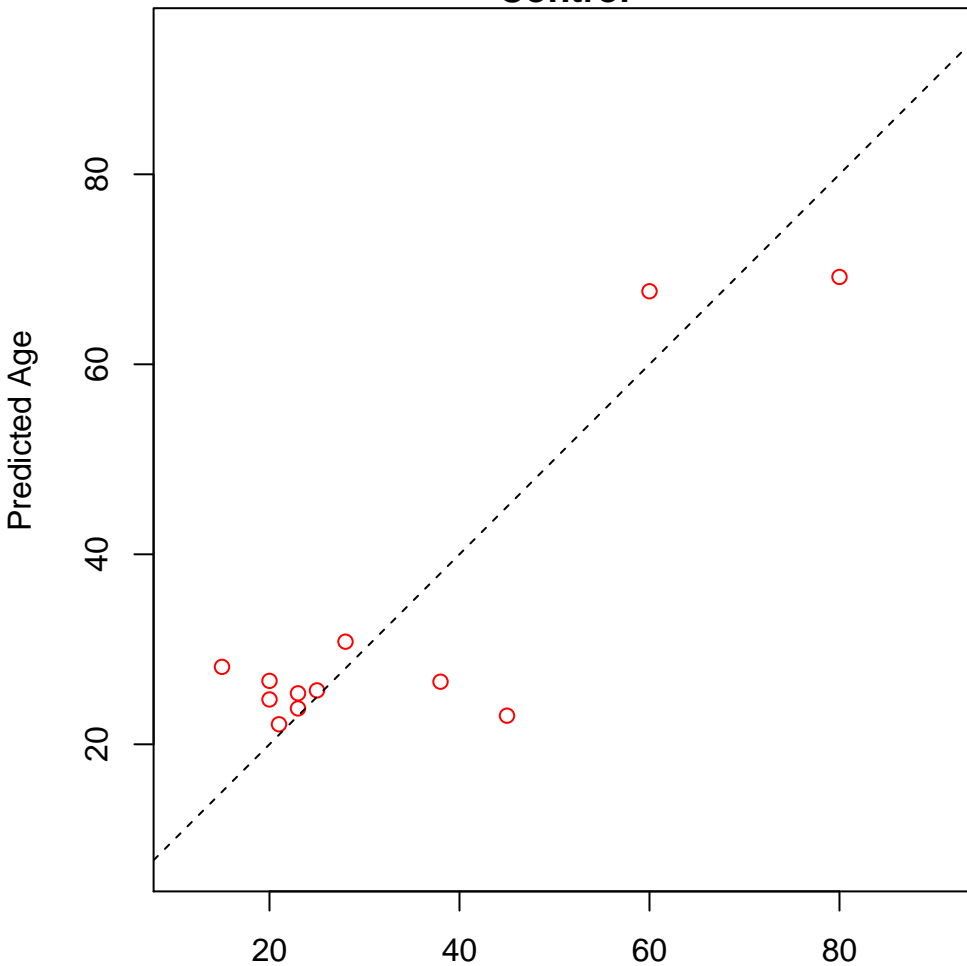


positive regulation of cyclase activity (Score: 9.084292)

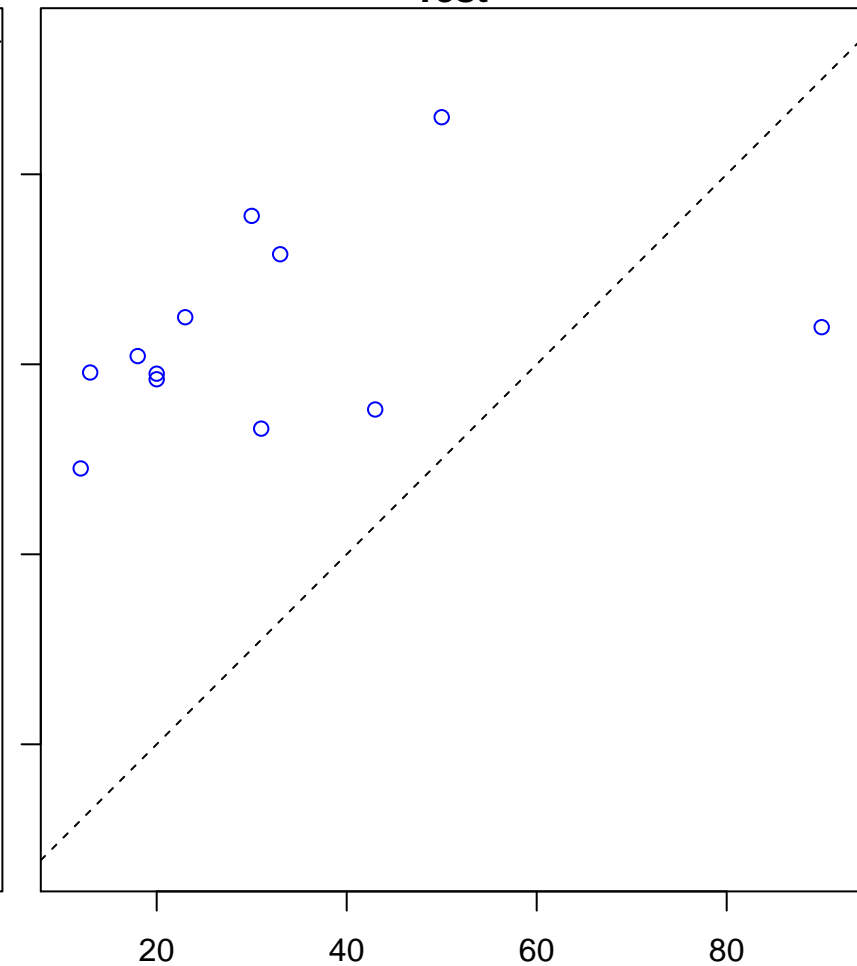


positive regulation of bone resorption (Score: 9.084201)

Control



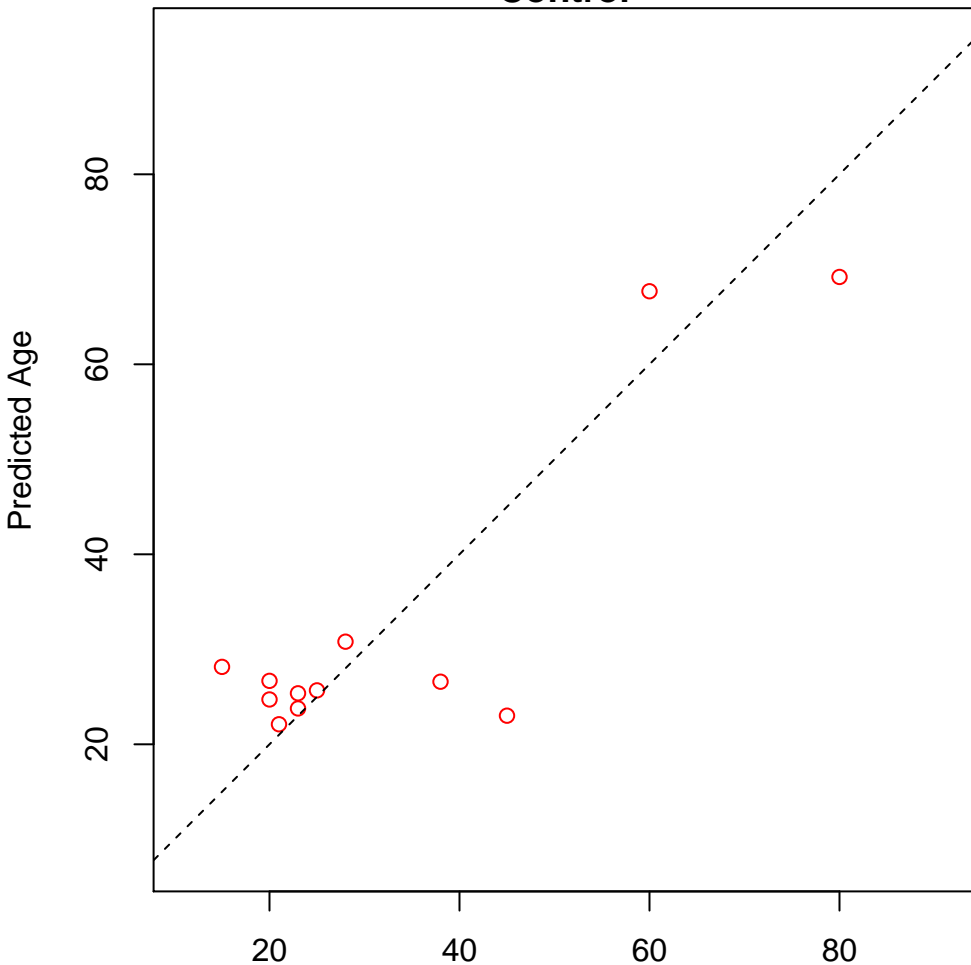
Test



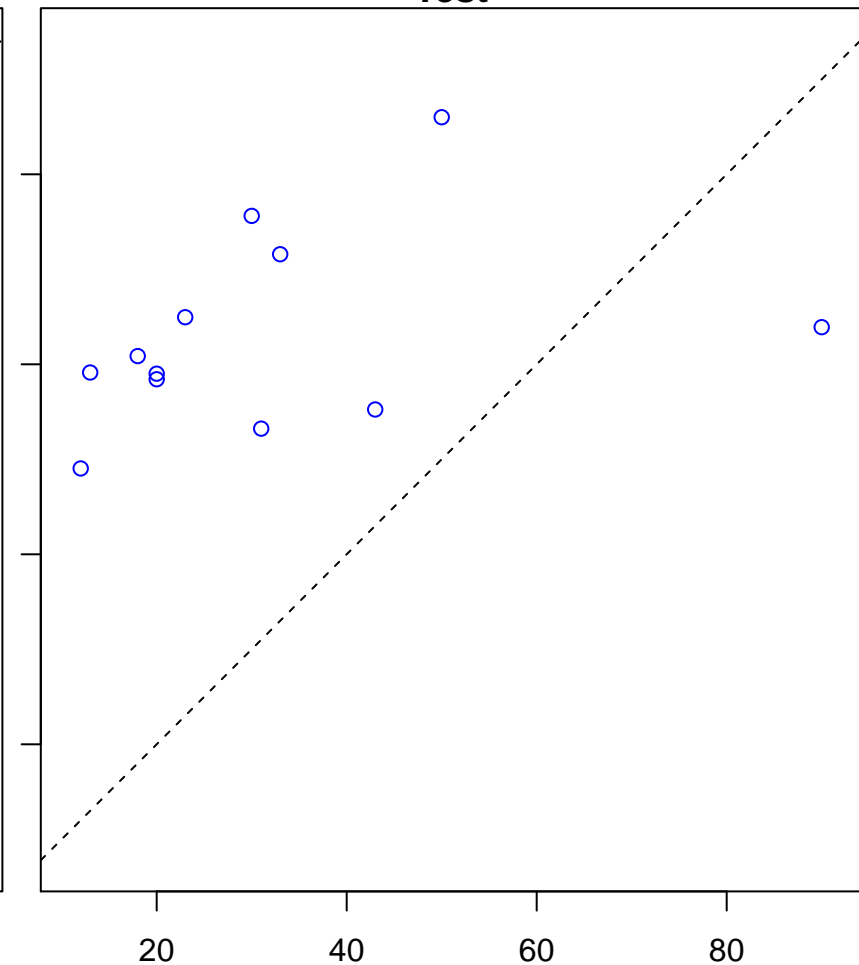
Actual Age

positive regulation of bone remodeling (Score: 9.084201)

Control



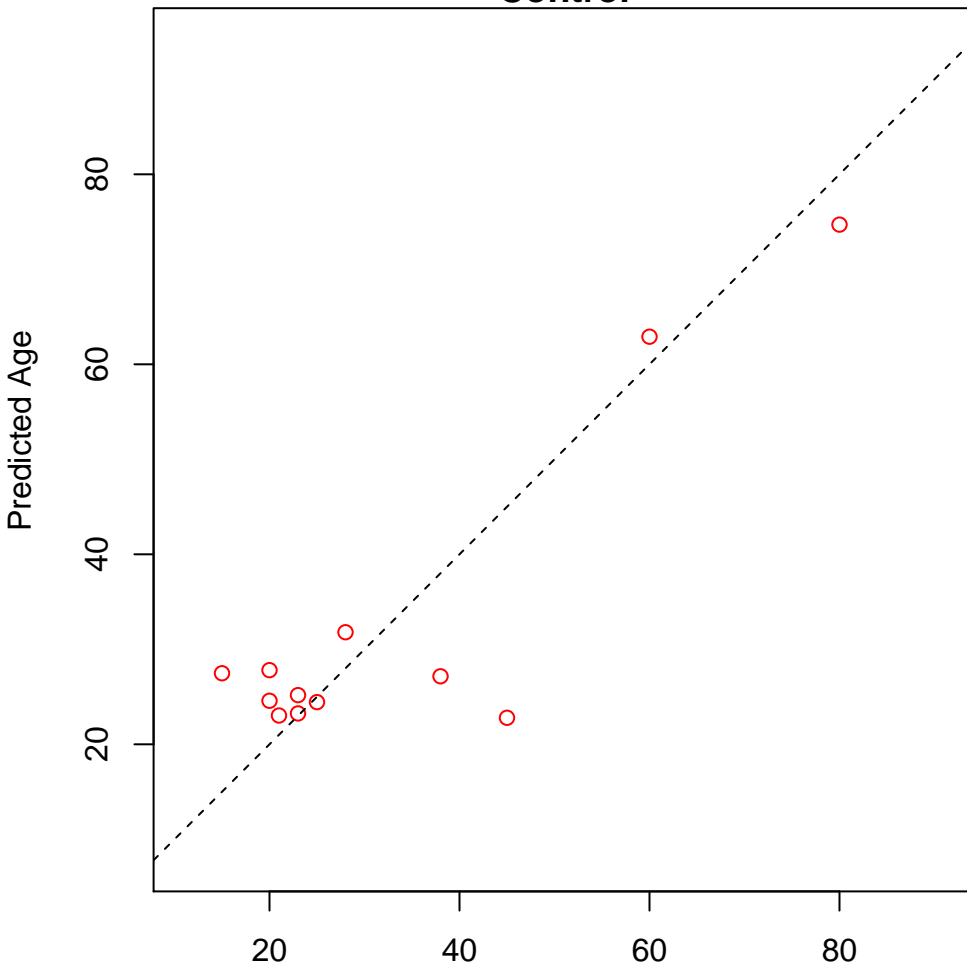
Test



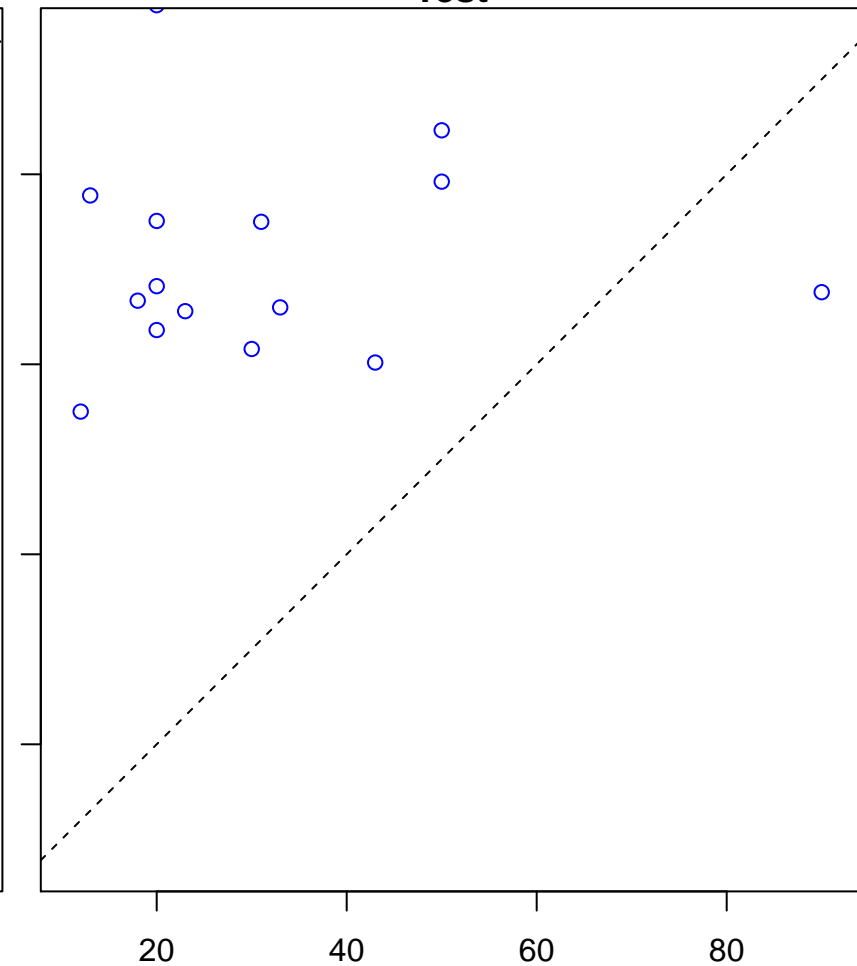
Actual Age

regulation of adenylate cyclase activity (Score: 9.077403)

Control

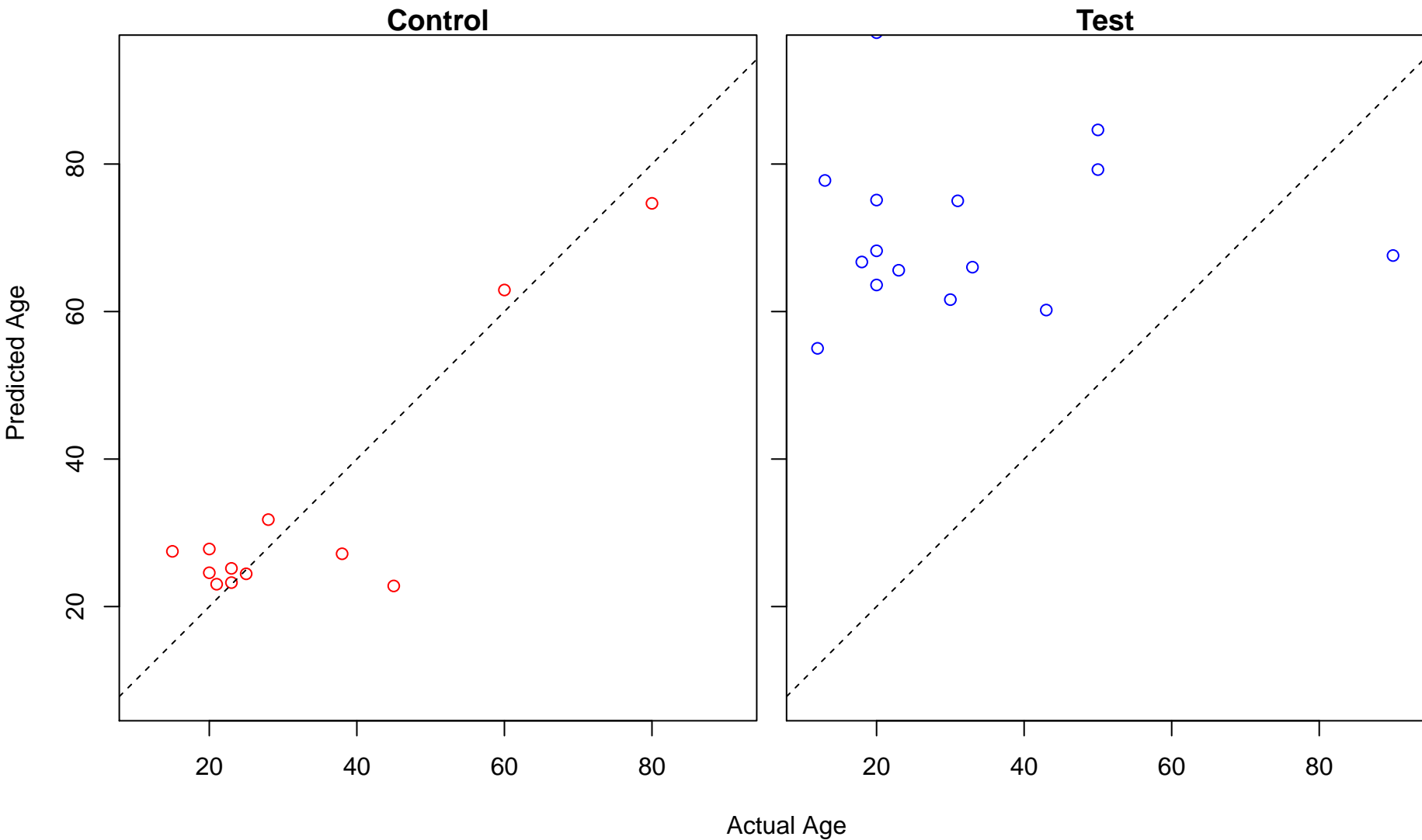


Test

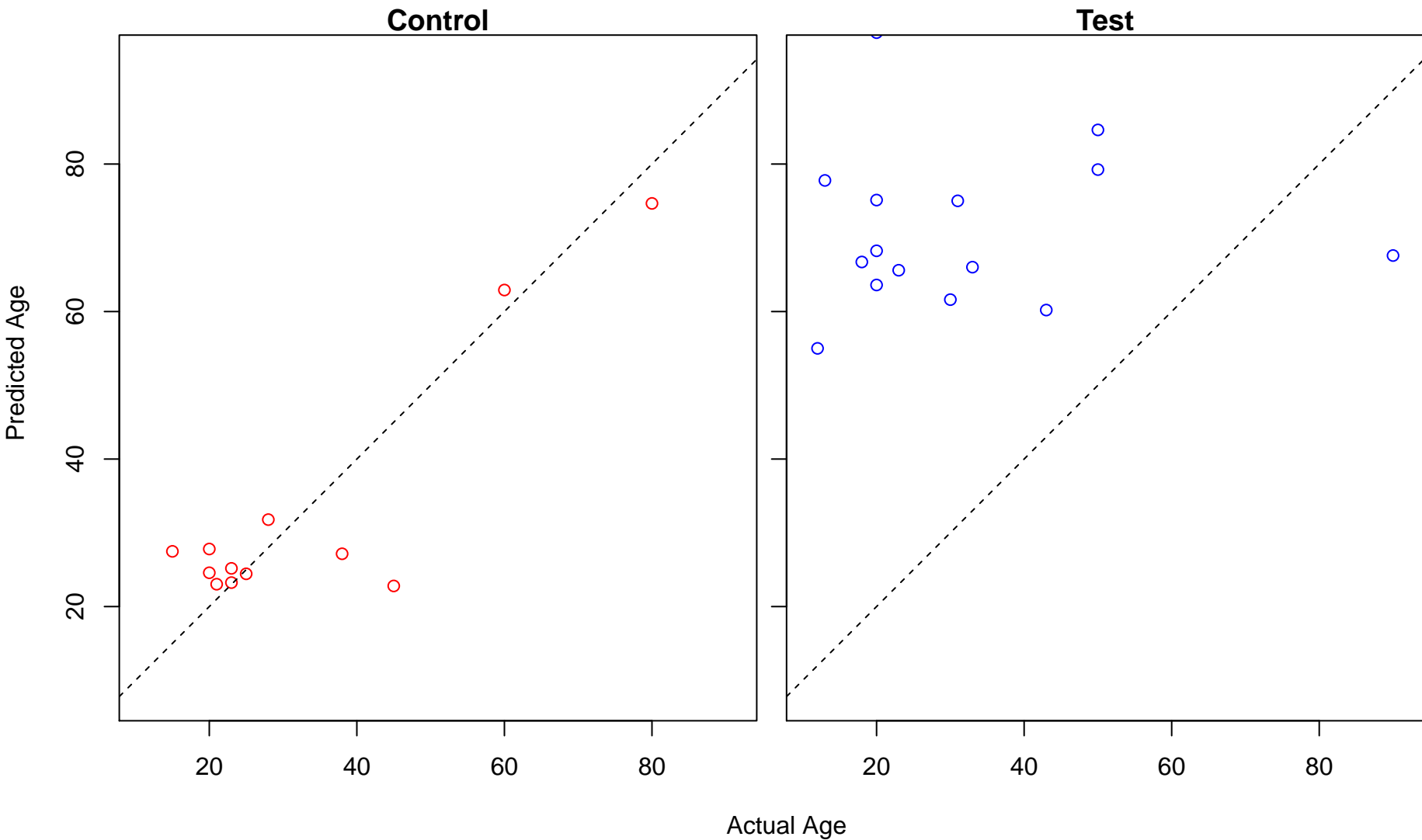


Actual Age

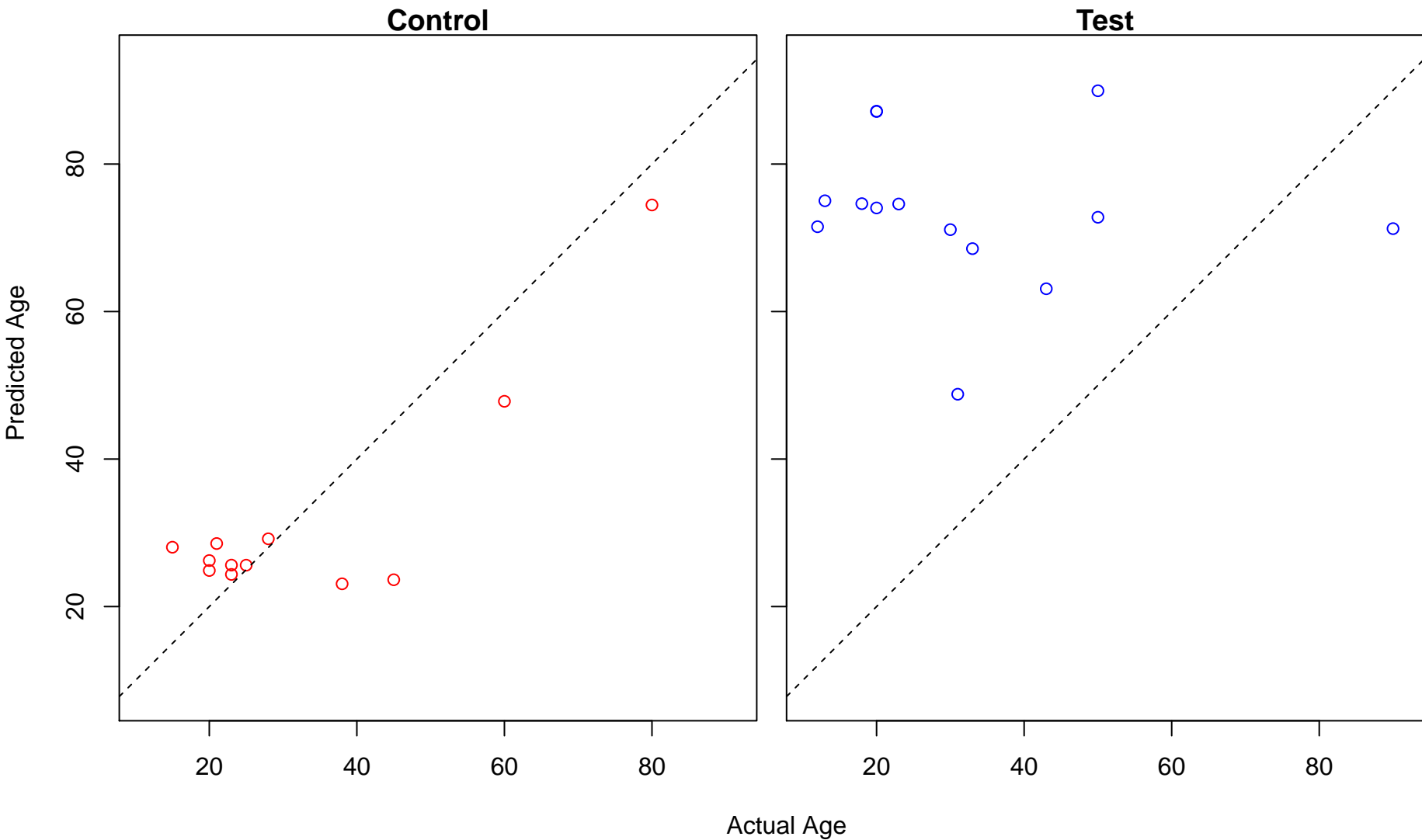
regulation of cAMP biosynthetic process (Score: 9.075036)



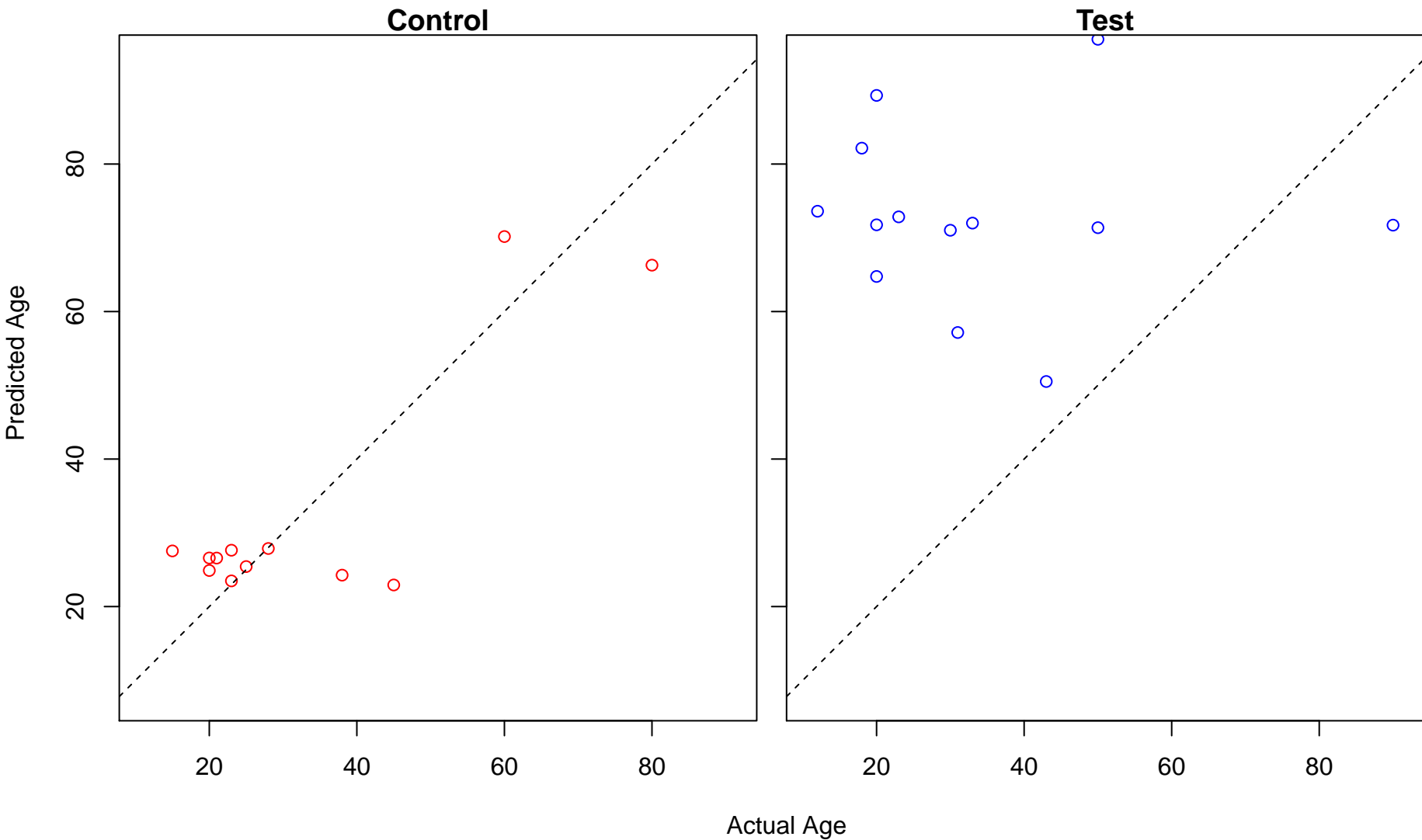
regulation of cyclic nucleotide biosynthetic process (Score: 9.074200)



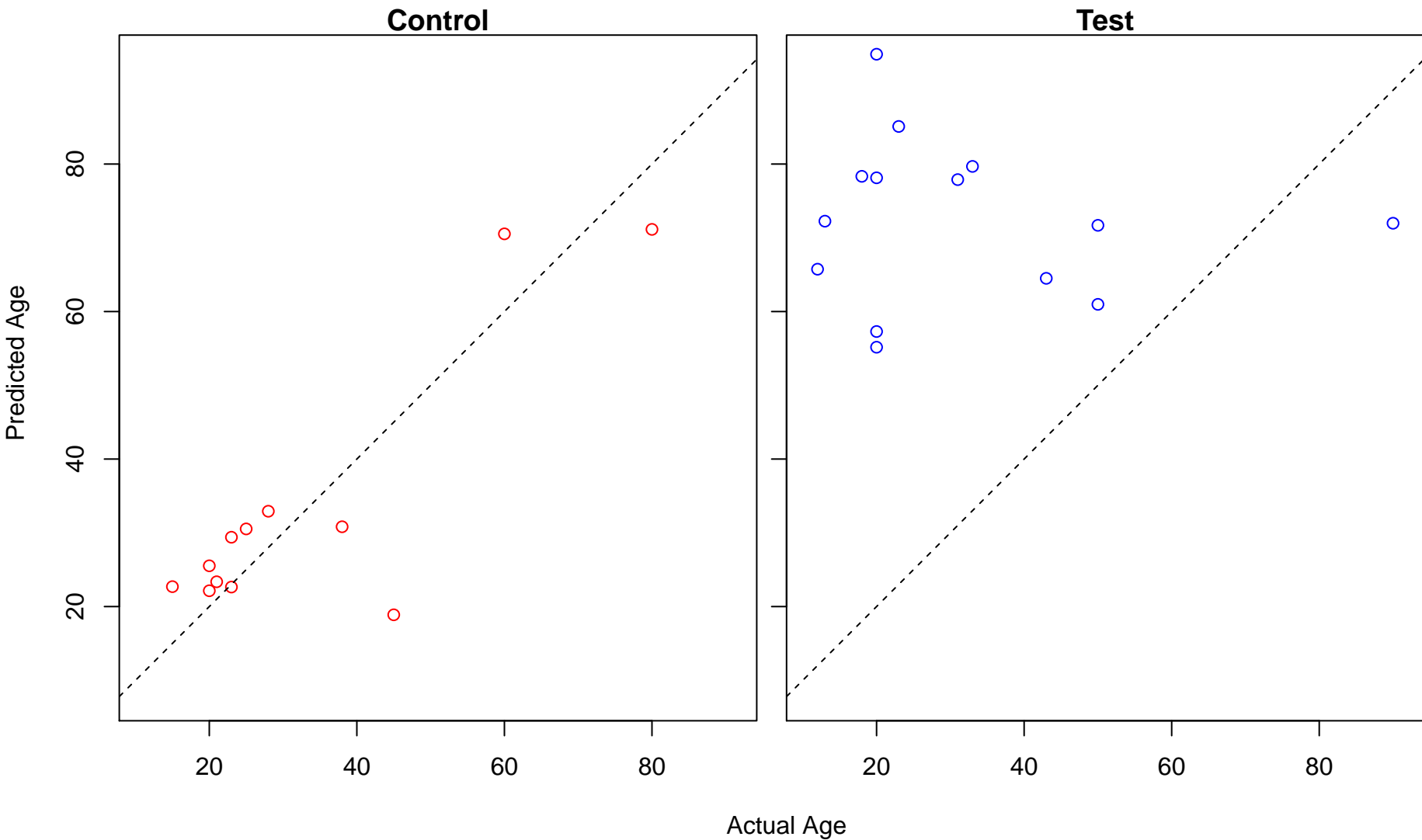
carbohydrate derivative catabolic process (Score: 9.073756)



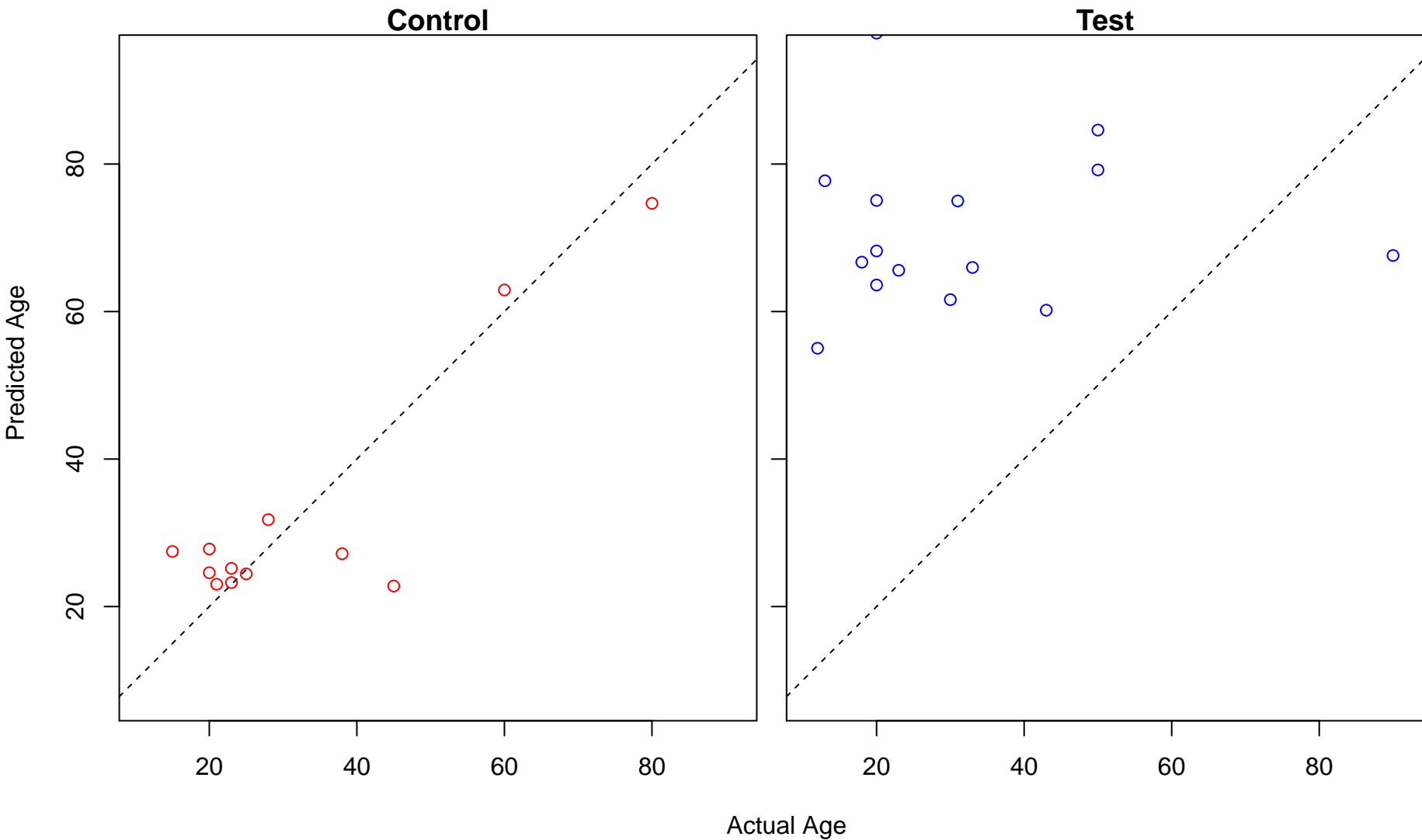
lipid particle organization (Score: 9.070730)



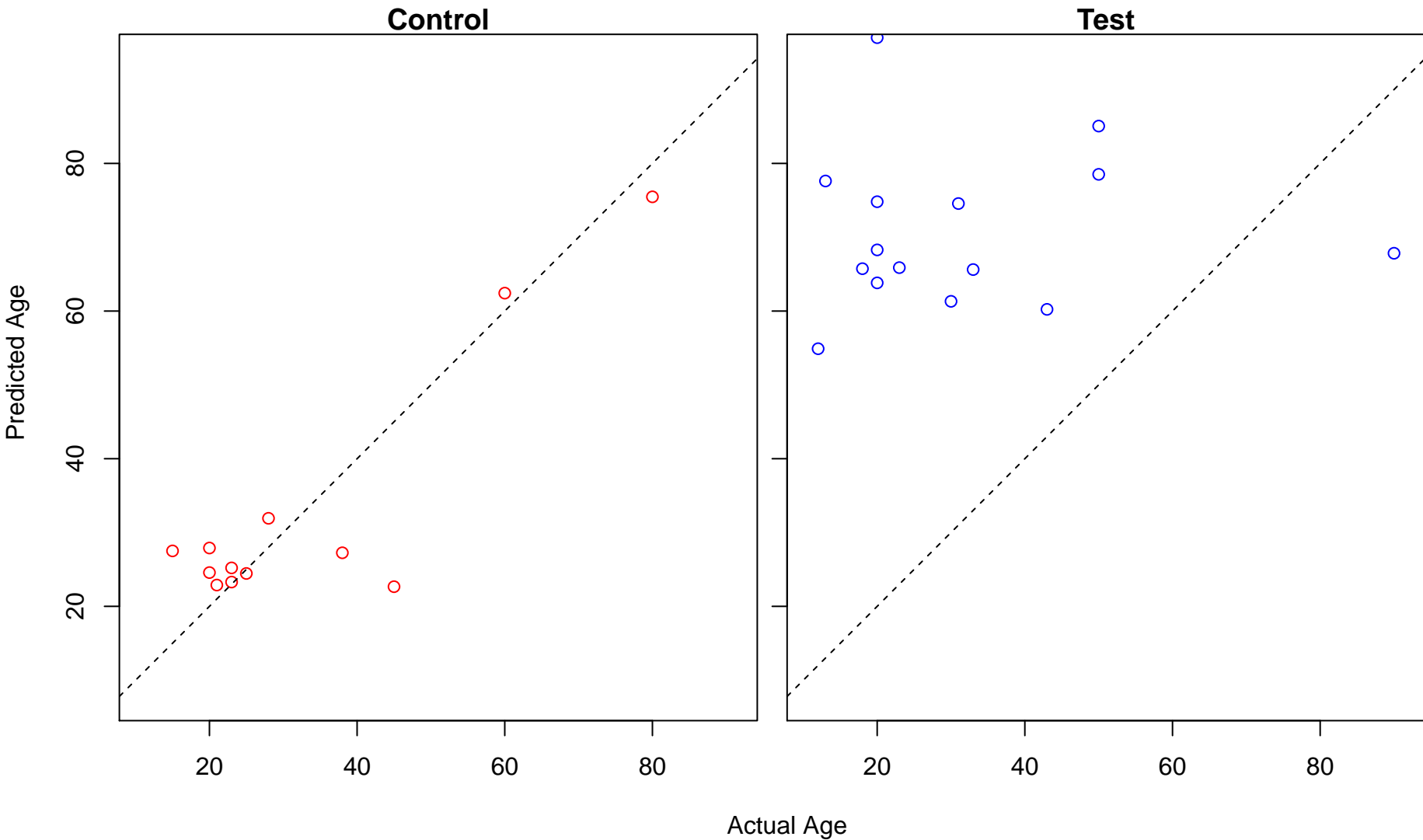
positive regulation of interleukin-12 production (Score: 9.068882)



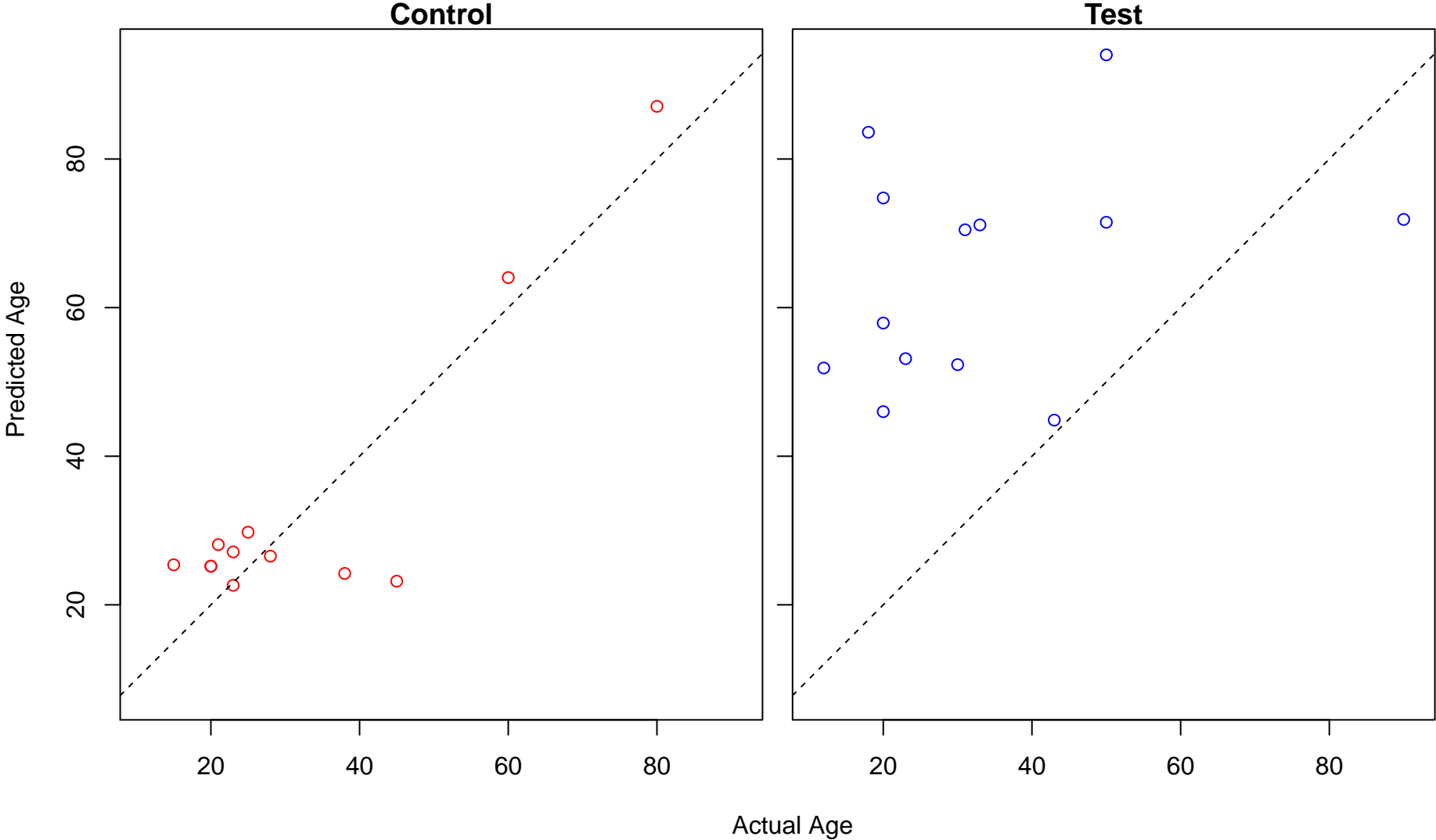
regulation of cyclase activity (Score: 9.067425)



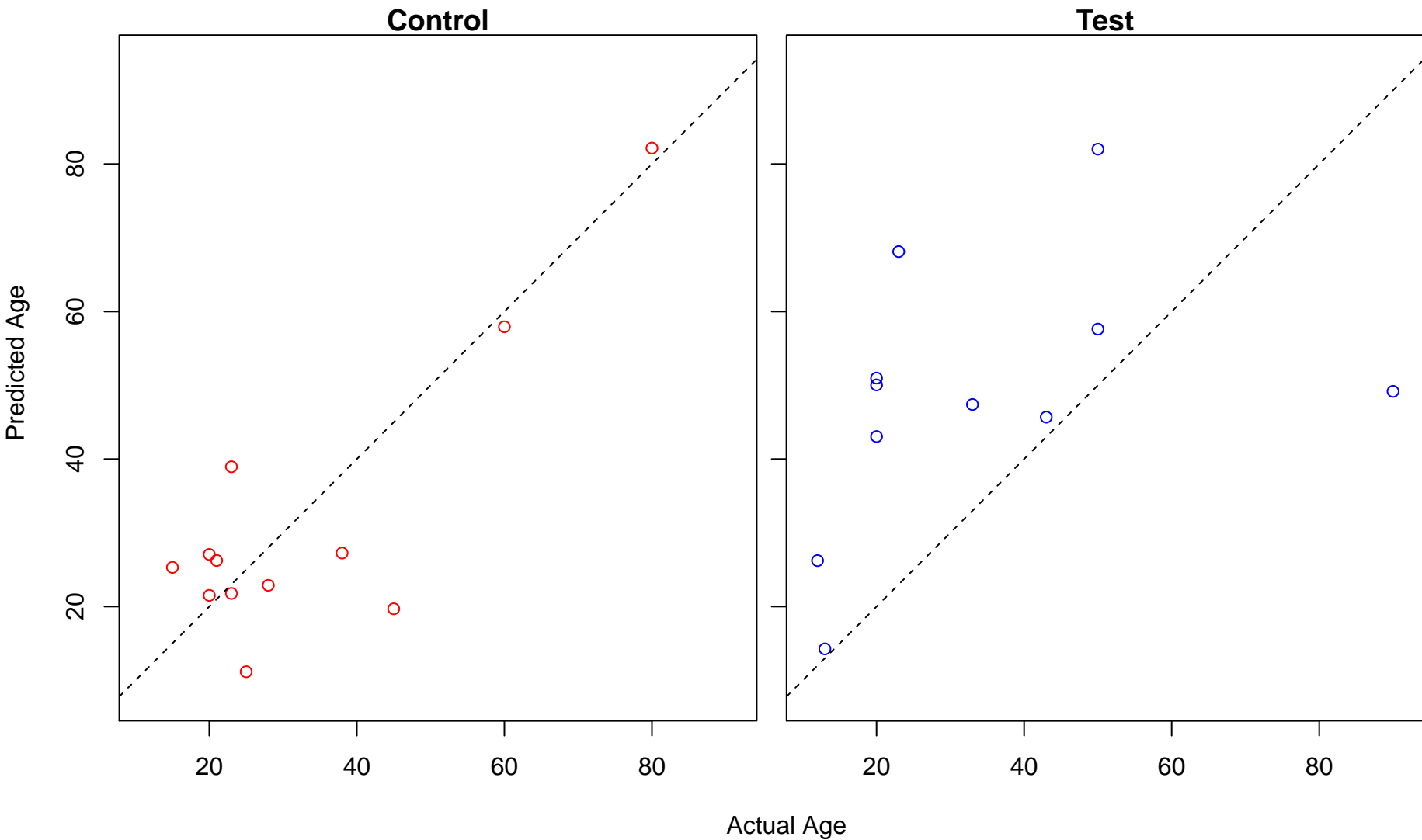
adenylate cyclase-activating dopamine receptor signaling pathway (Score: 9.066611)



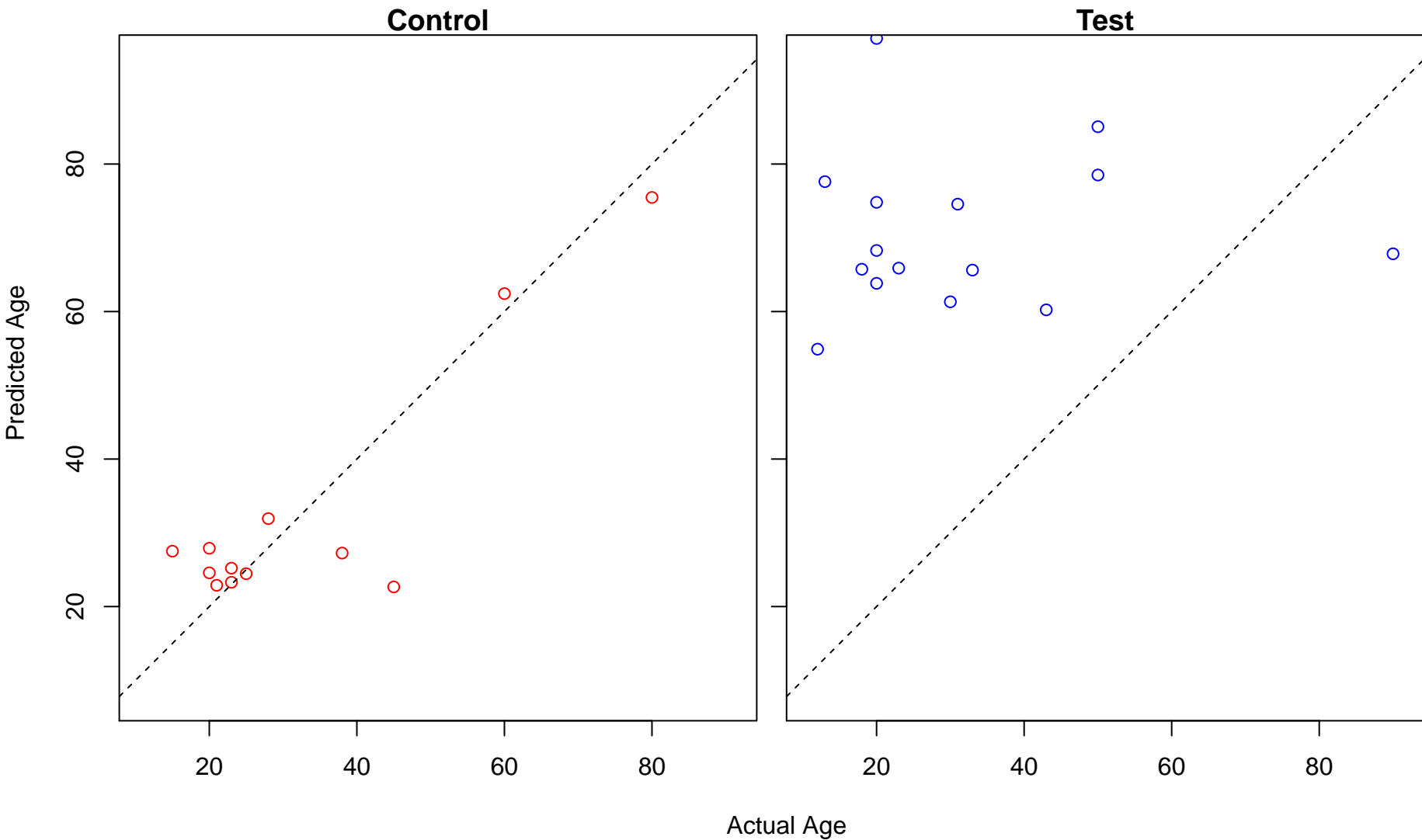
negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage (Score: 9.066)



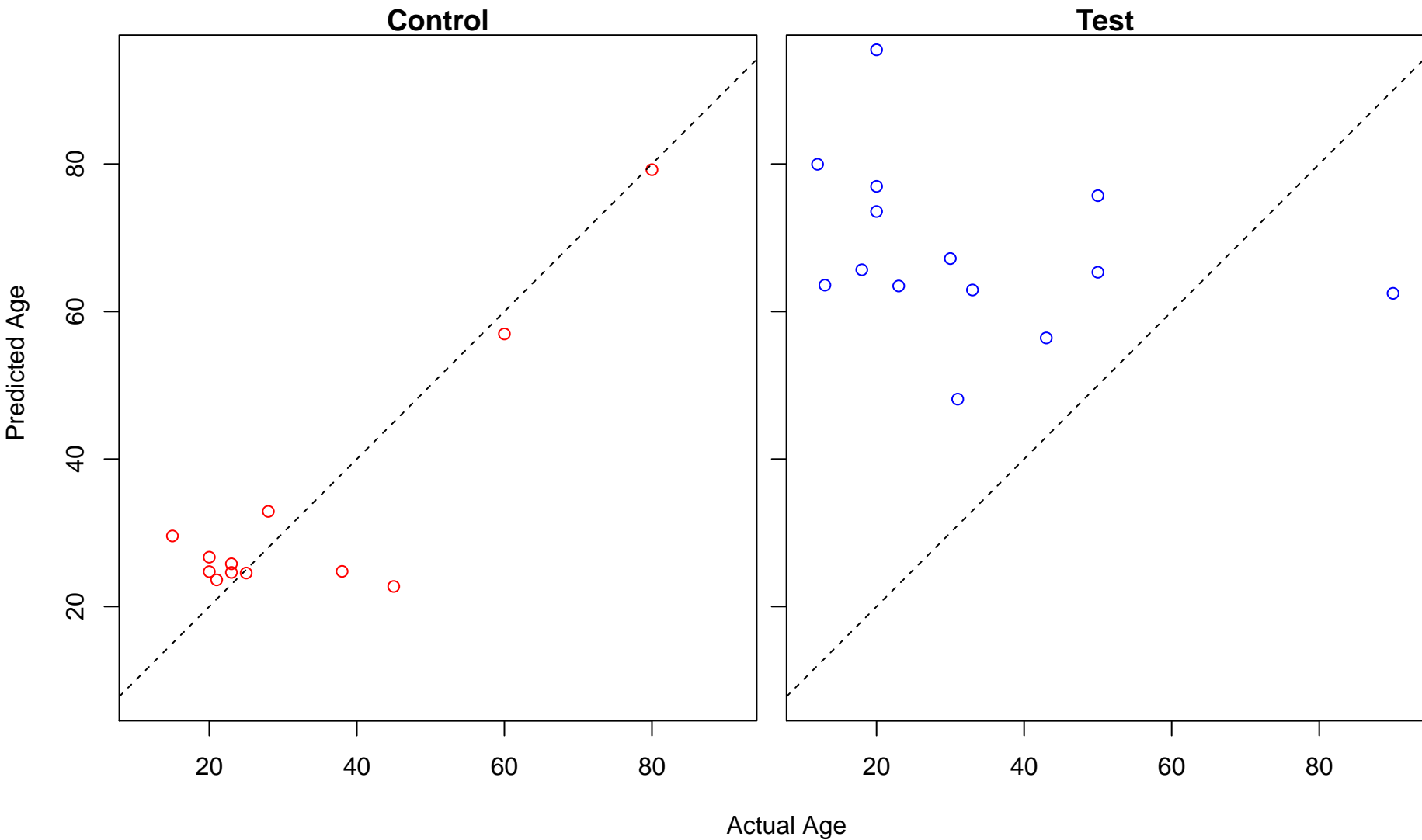
regulation of T cell activation (Score: 9.066481)



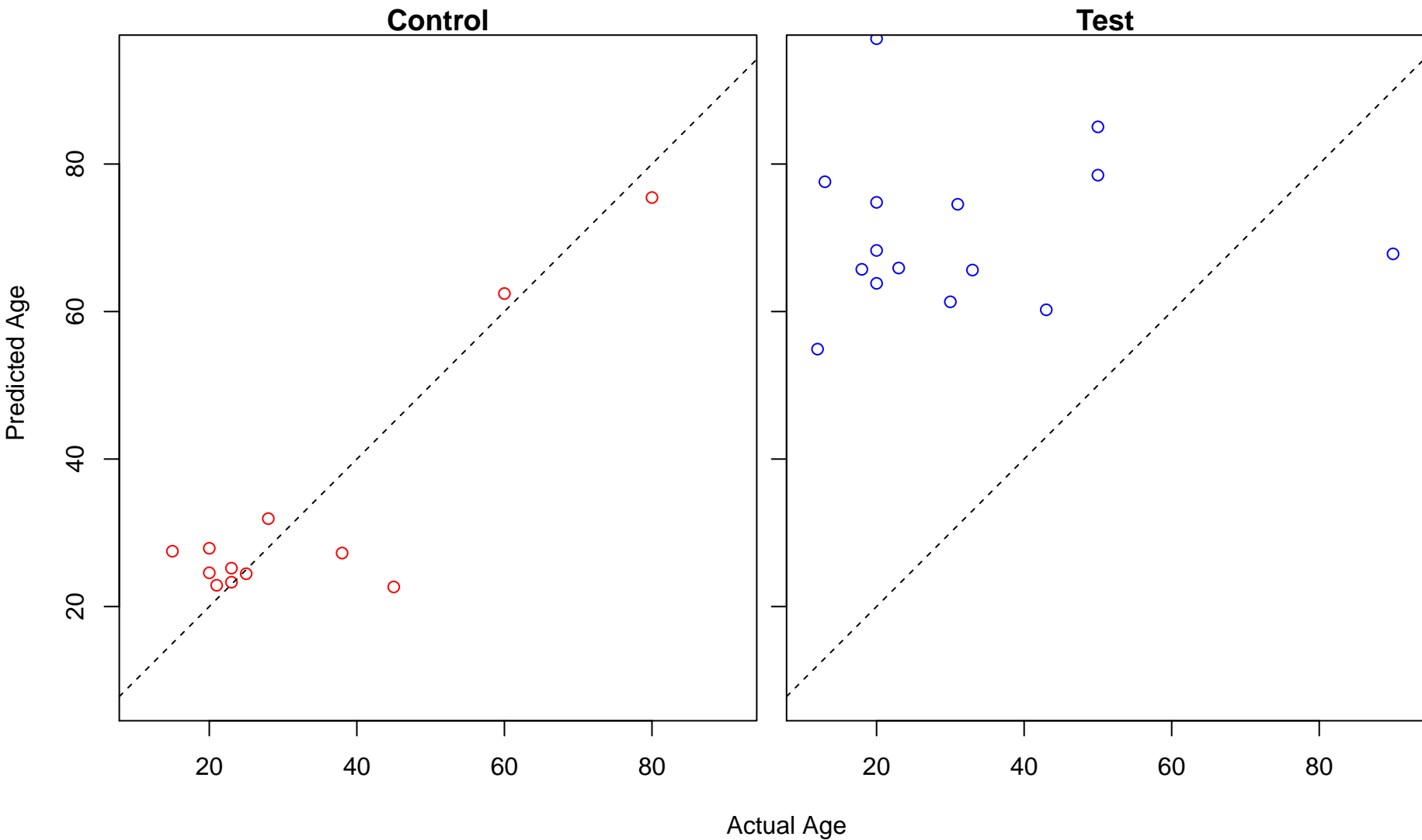
cellular response to prostaglandin E stimulus (Score: 9.065590)



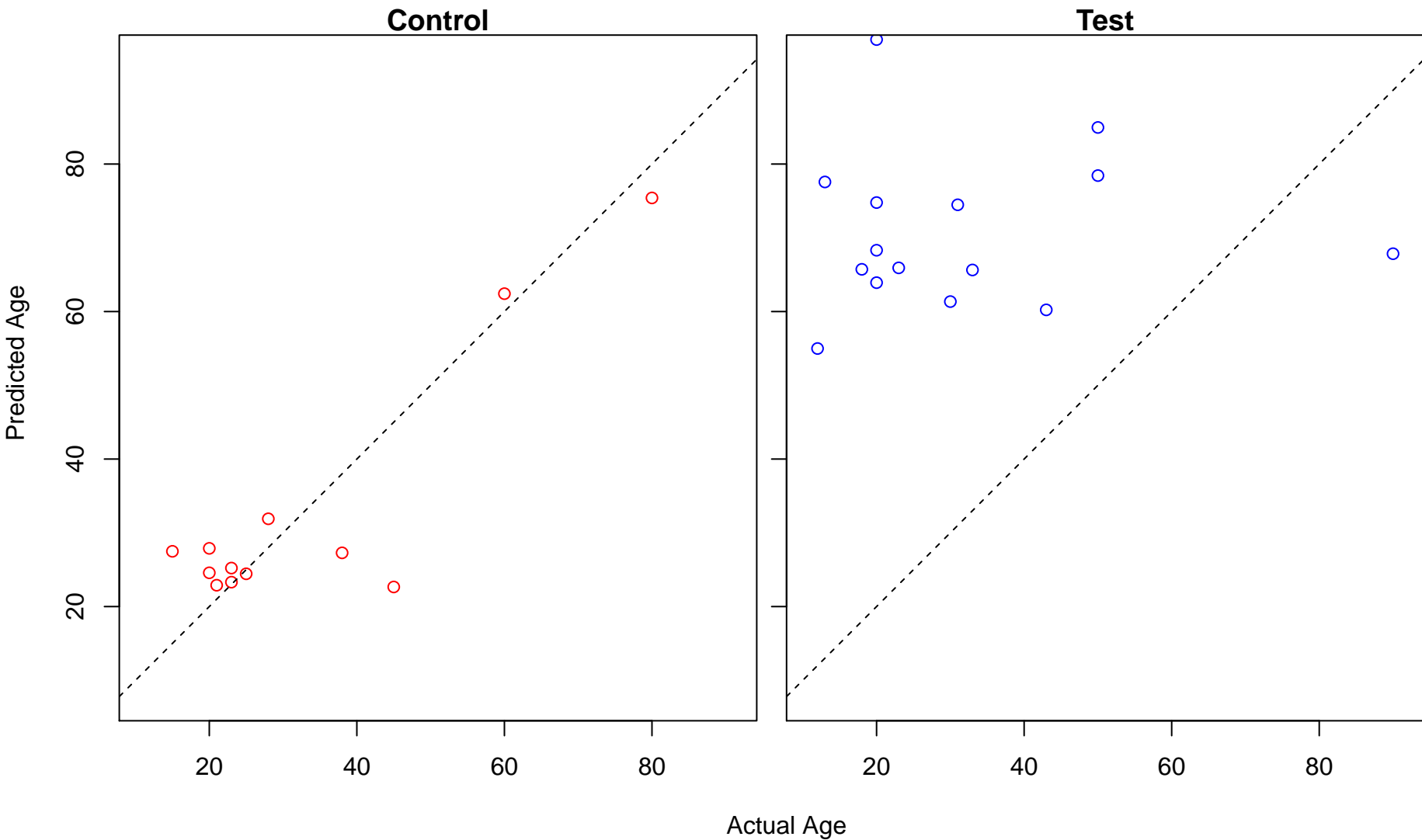
response to axon injury (Score: 9.062842)



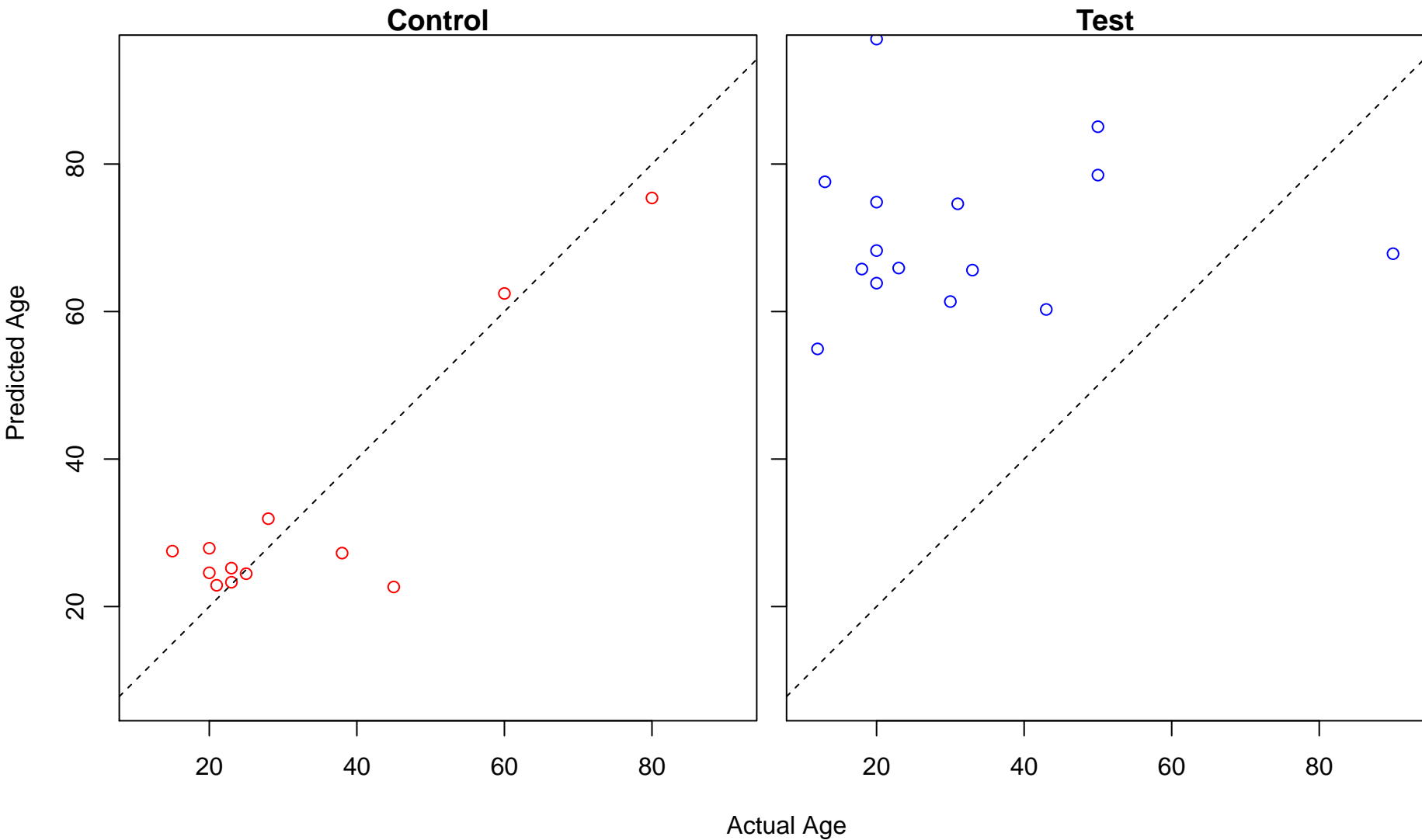
response to prostaglandin E (Score: 9.060546)



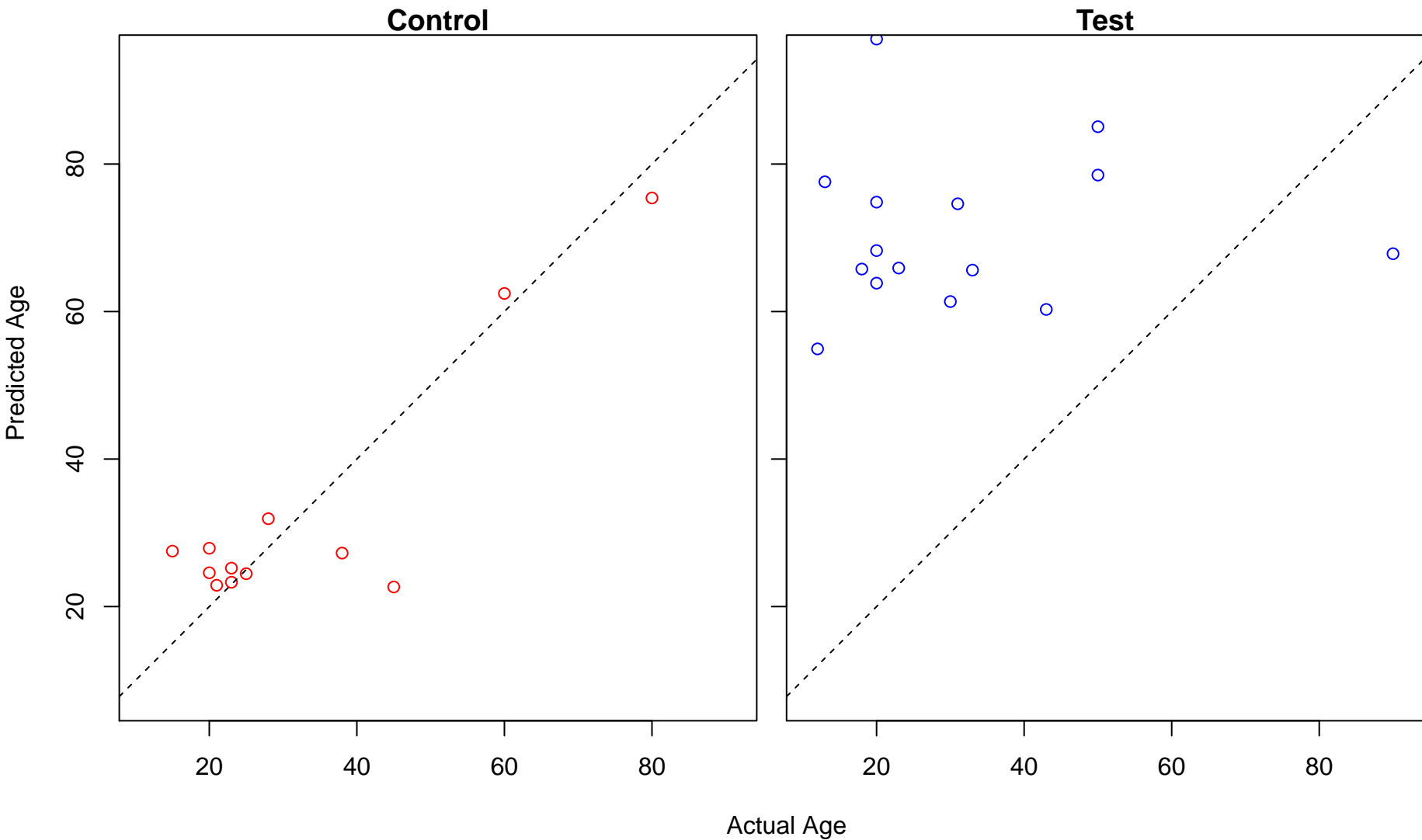
response to ketone (Score: 9.059925)



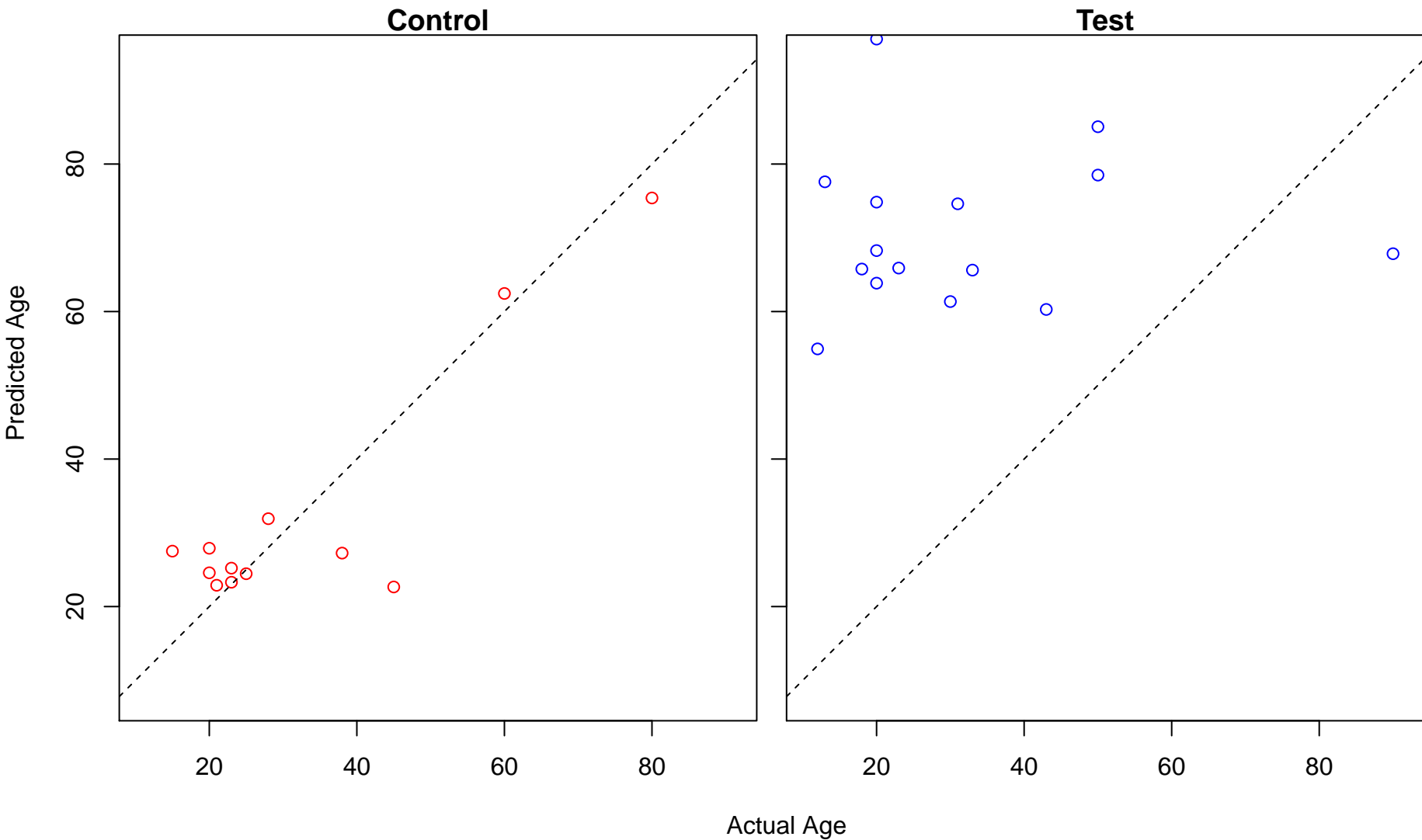
response to monoamine (Score: 9.050651)



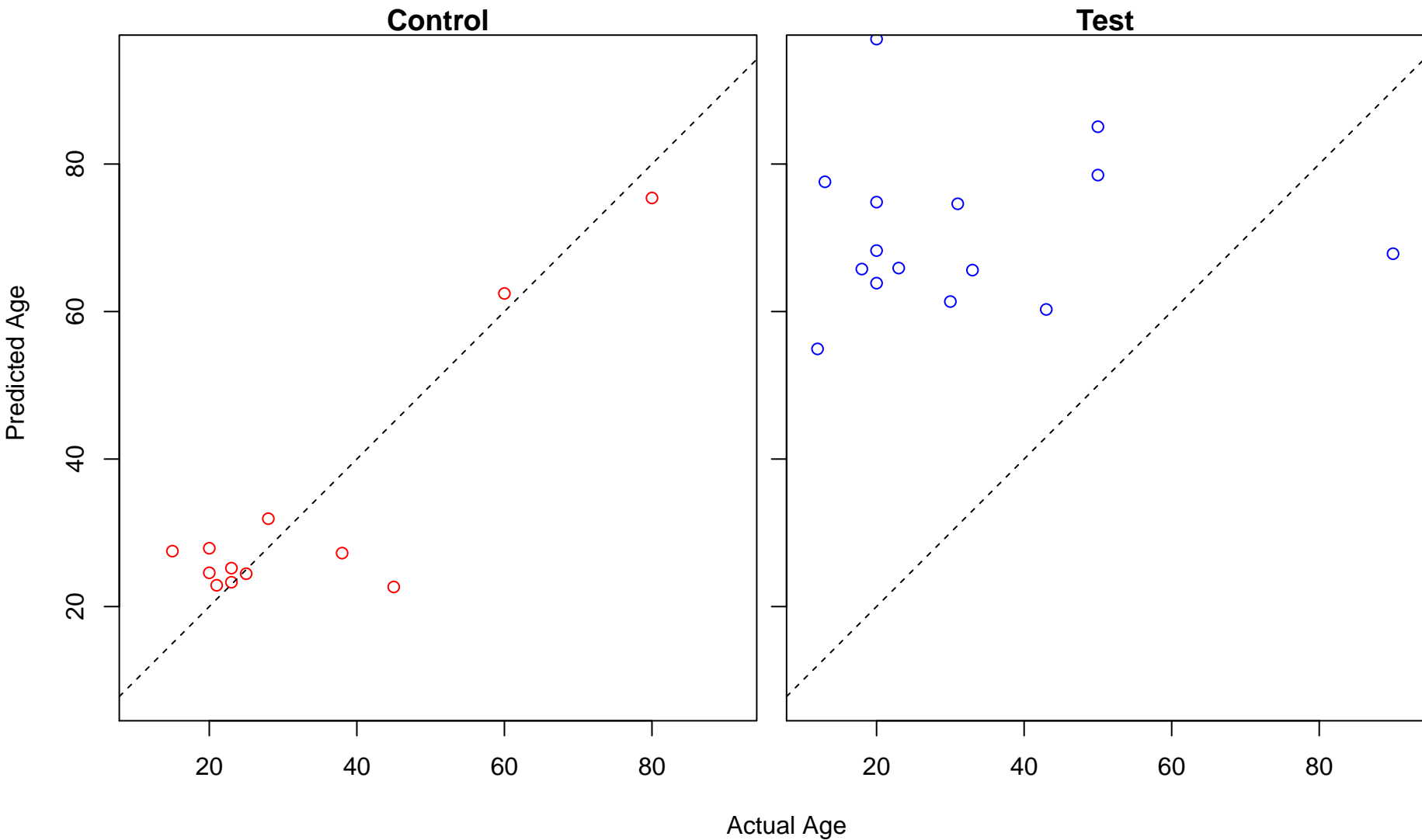
cellular response to monoamine stimulus (Score: 9.050651)



response to catecholamine (Score: 9.050651)

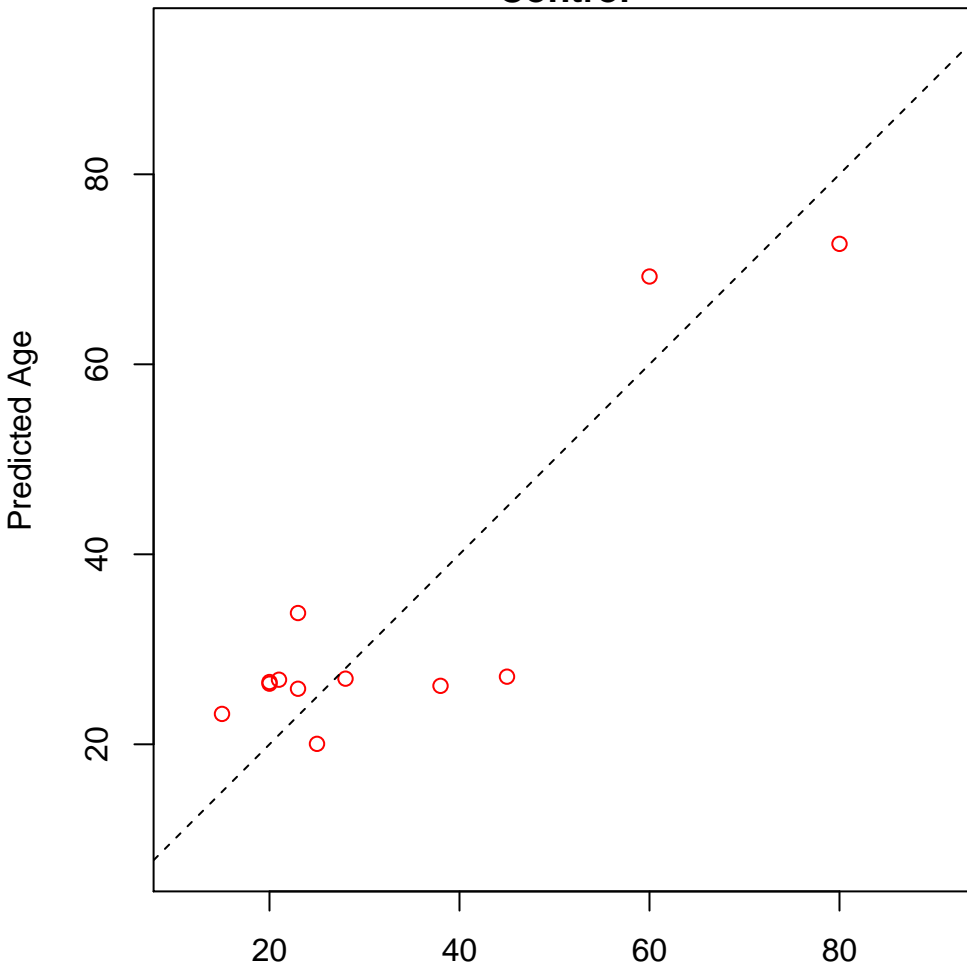


cellular response to catecholamine stimulus (Score: 9.050651)

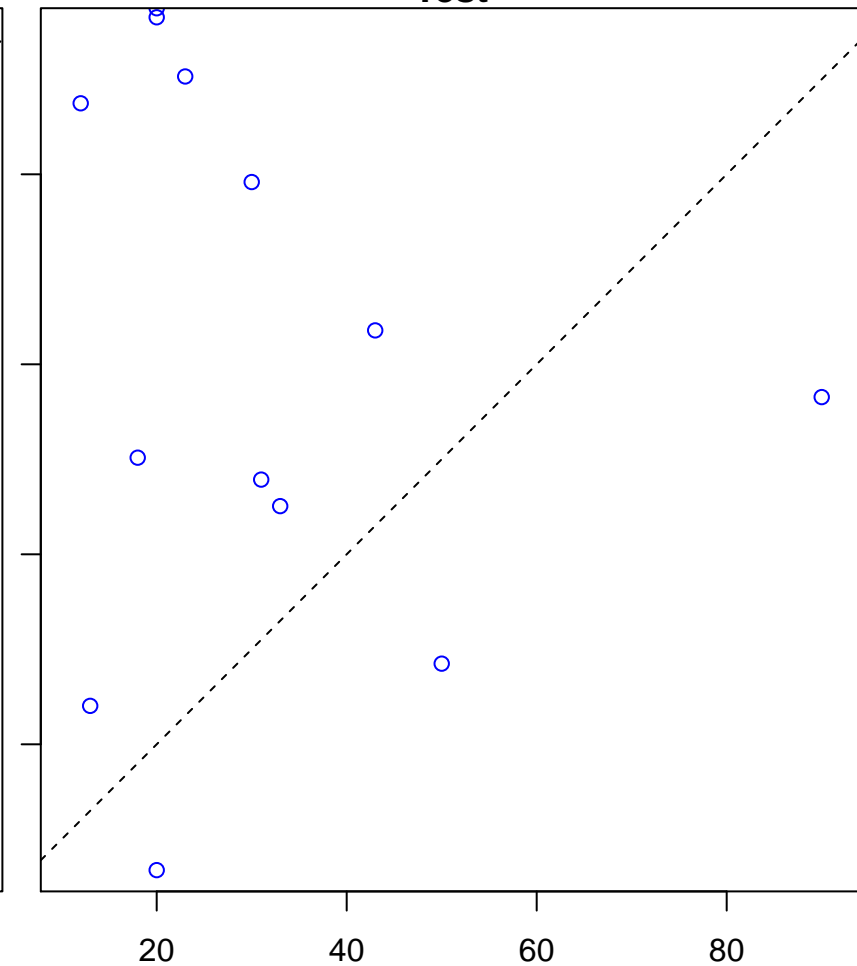


negative regulation of heart contraction (Score: 9.048797)

Control

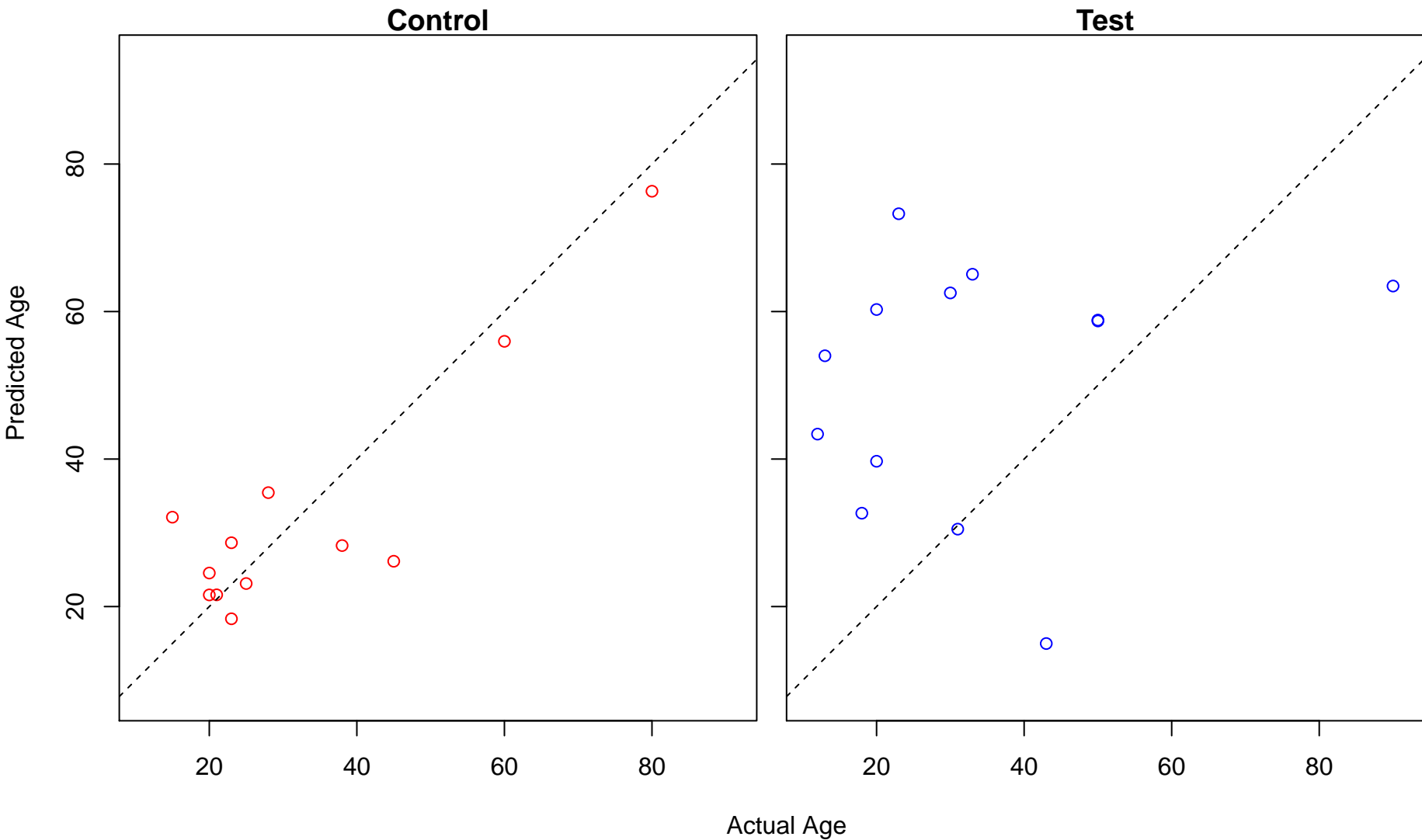


Test

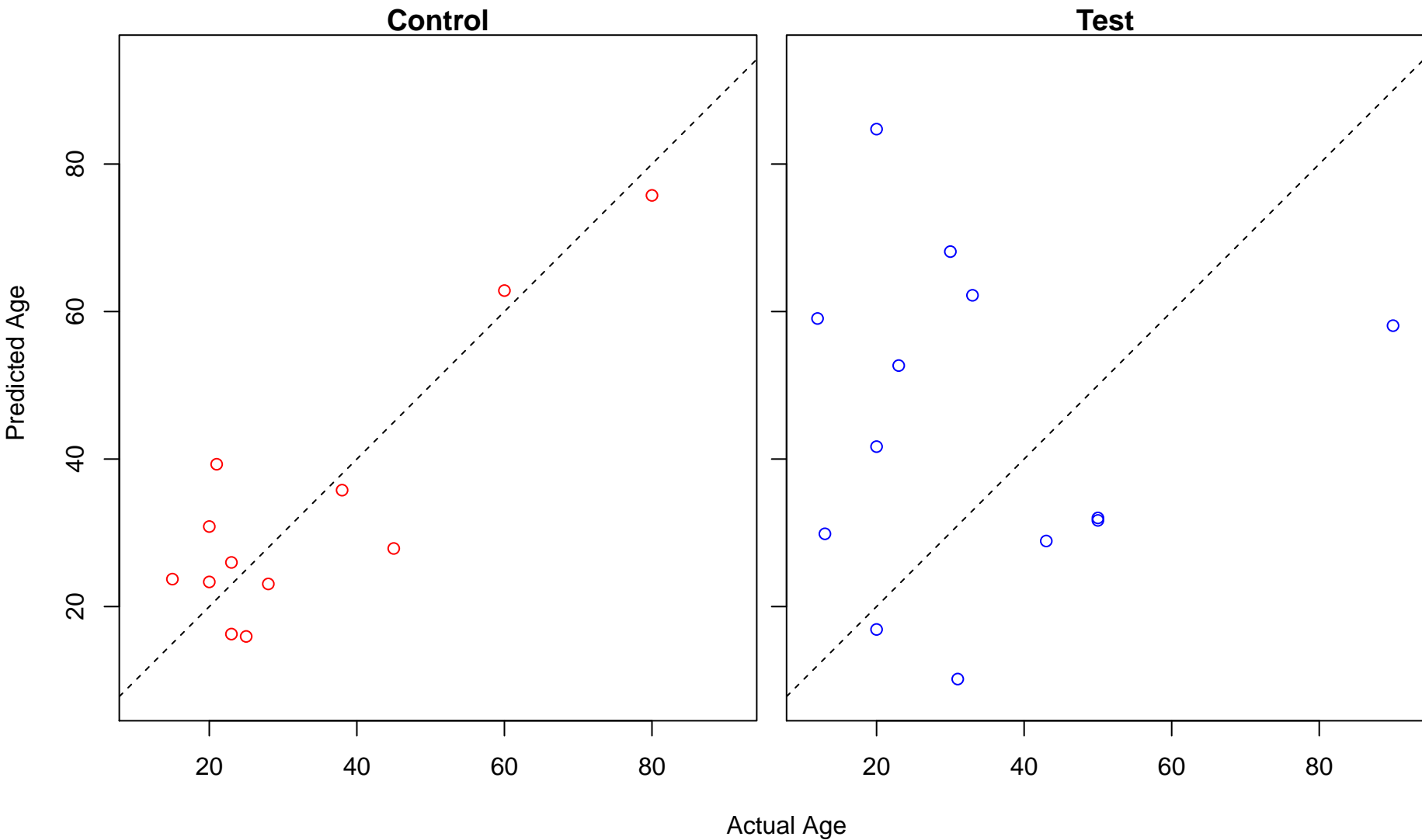


Actual Age

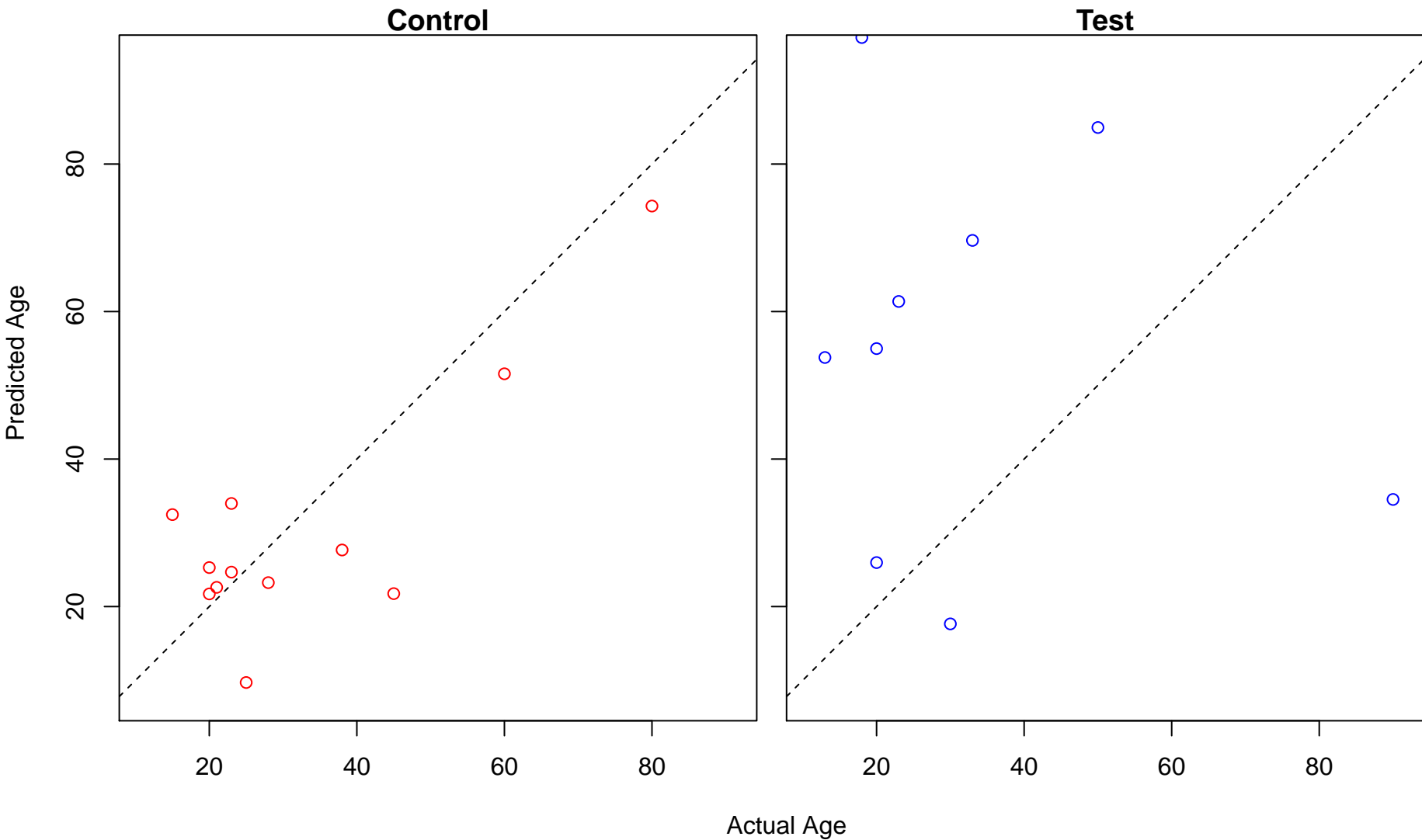
RNA phosphodiester bond hydrolysis, endonucleolytic (Score: 9.048303)



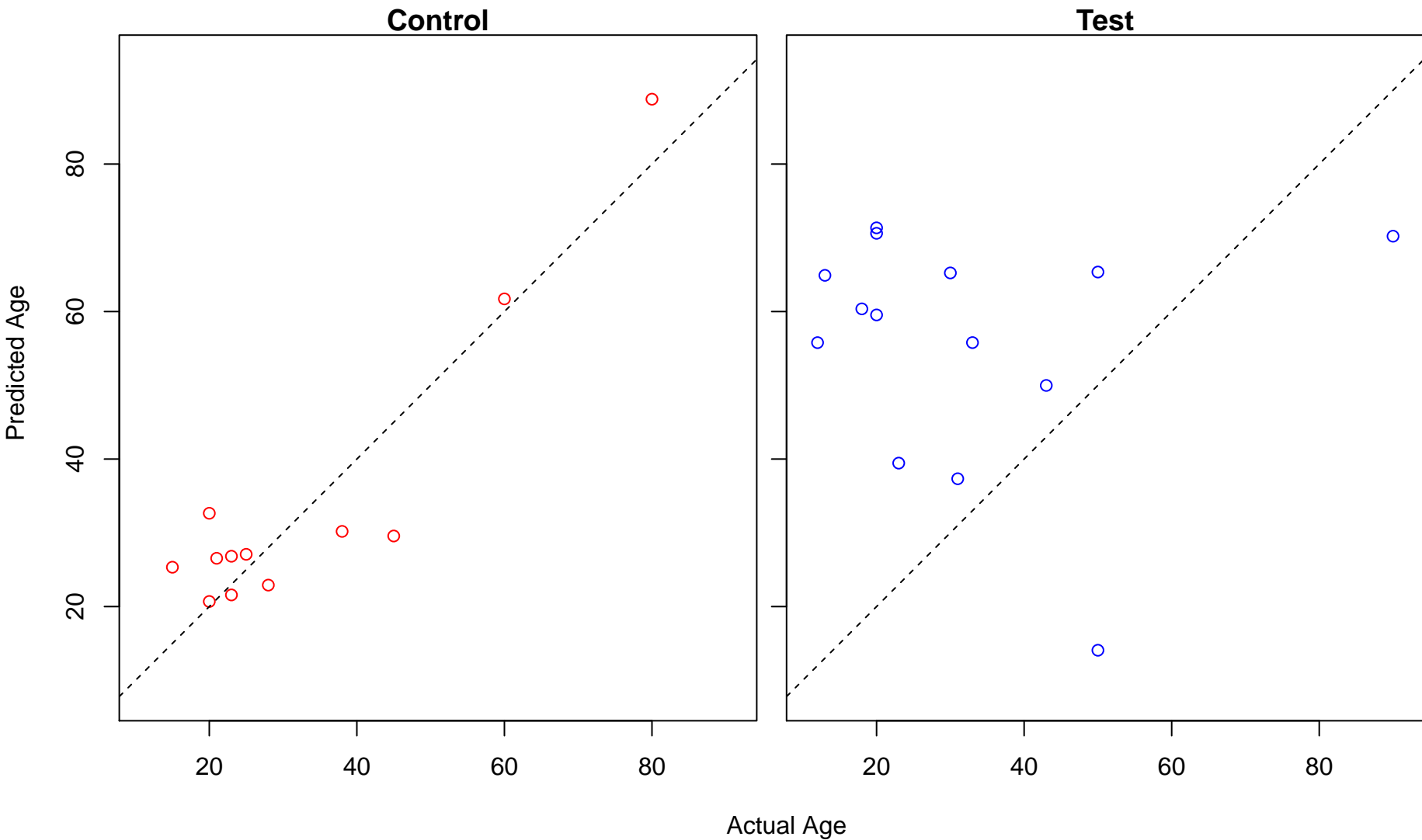
positive regulation of glucose import in response to insulin stimulus (Score: 9.044667)



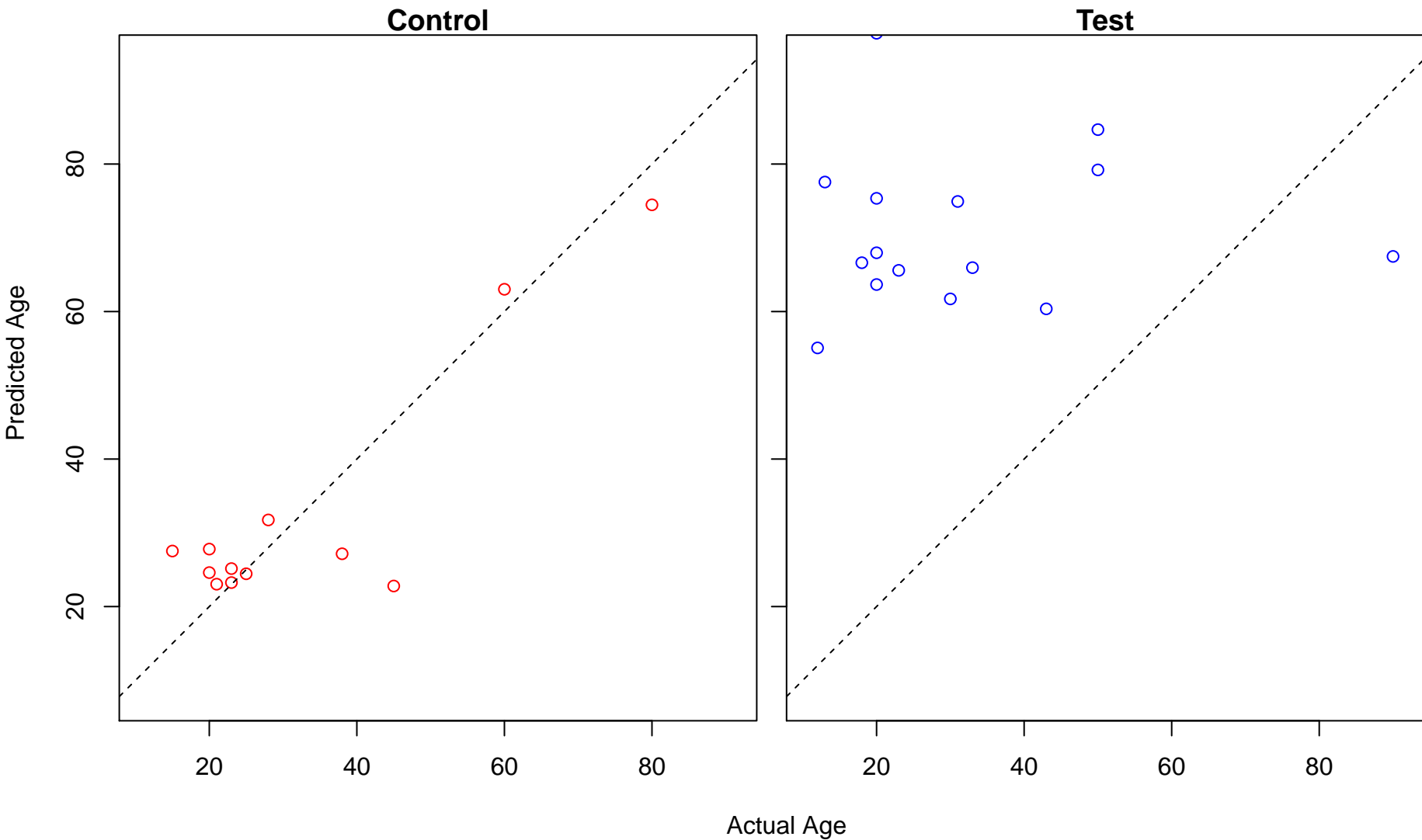
cellular ion homeostasis (Score: 9.034700)



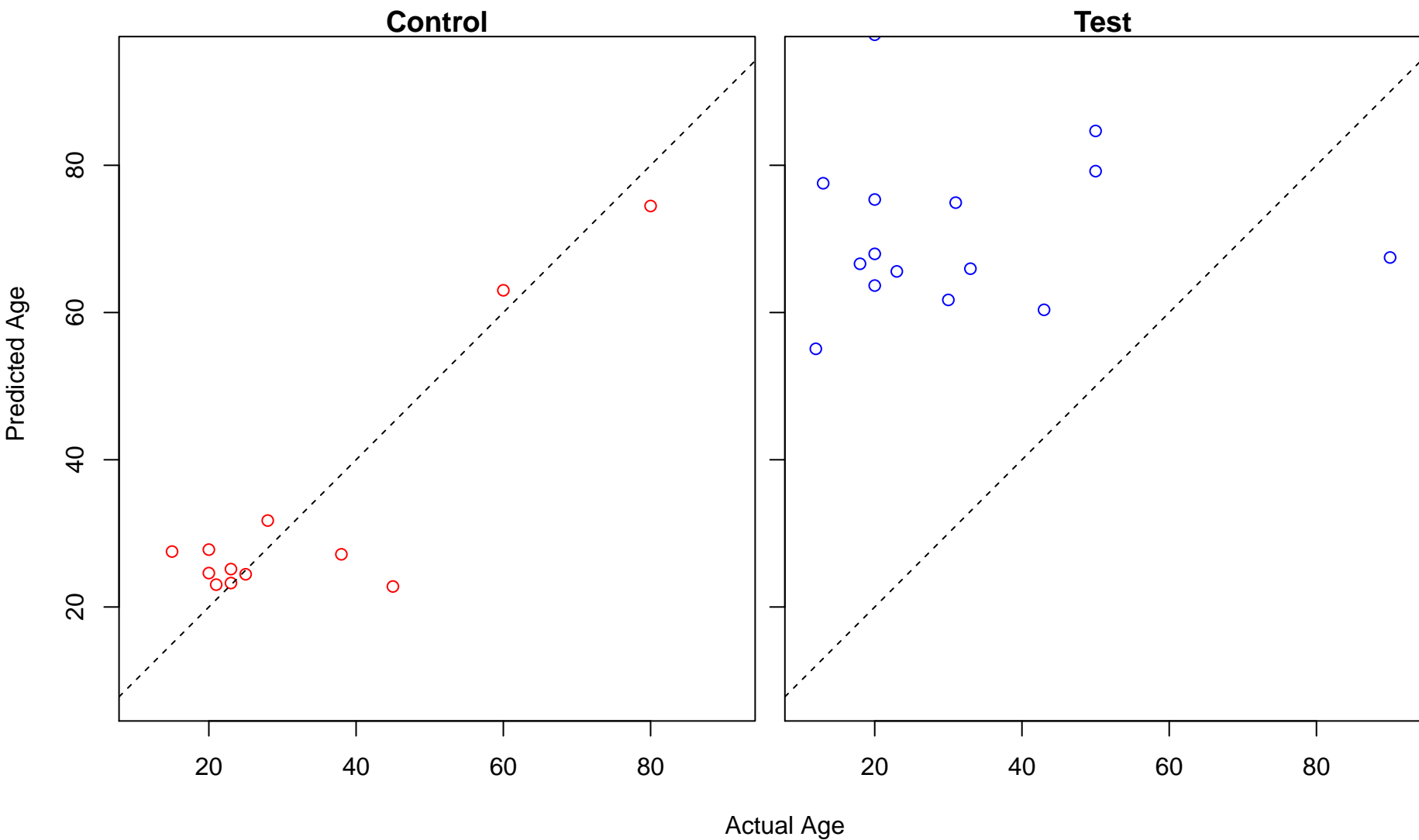
histone H4-K12 acetylation (Score: 9.026841)



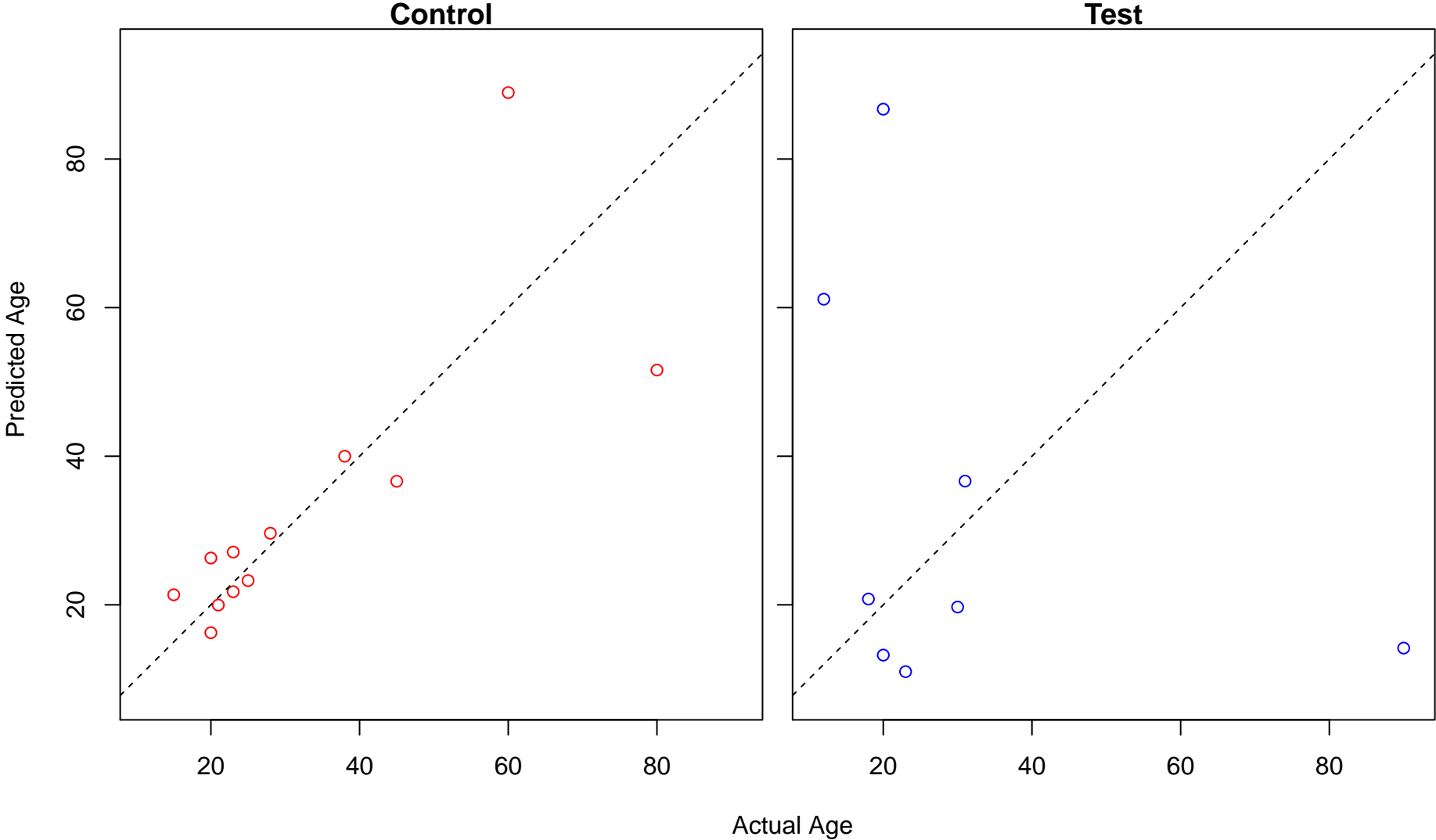
positive regulation of nucleotide biosynthetic process (Score: 9.026027)



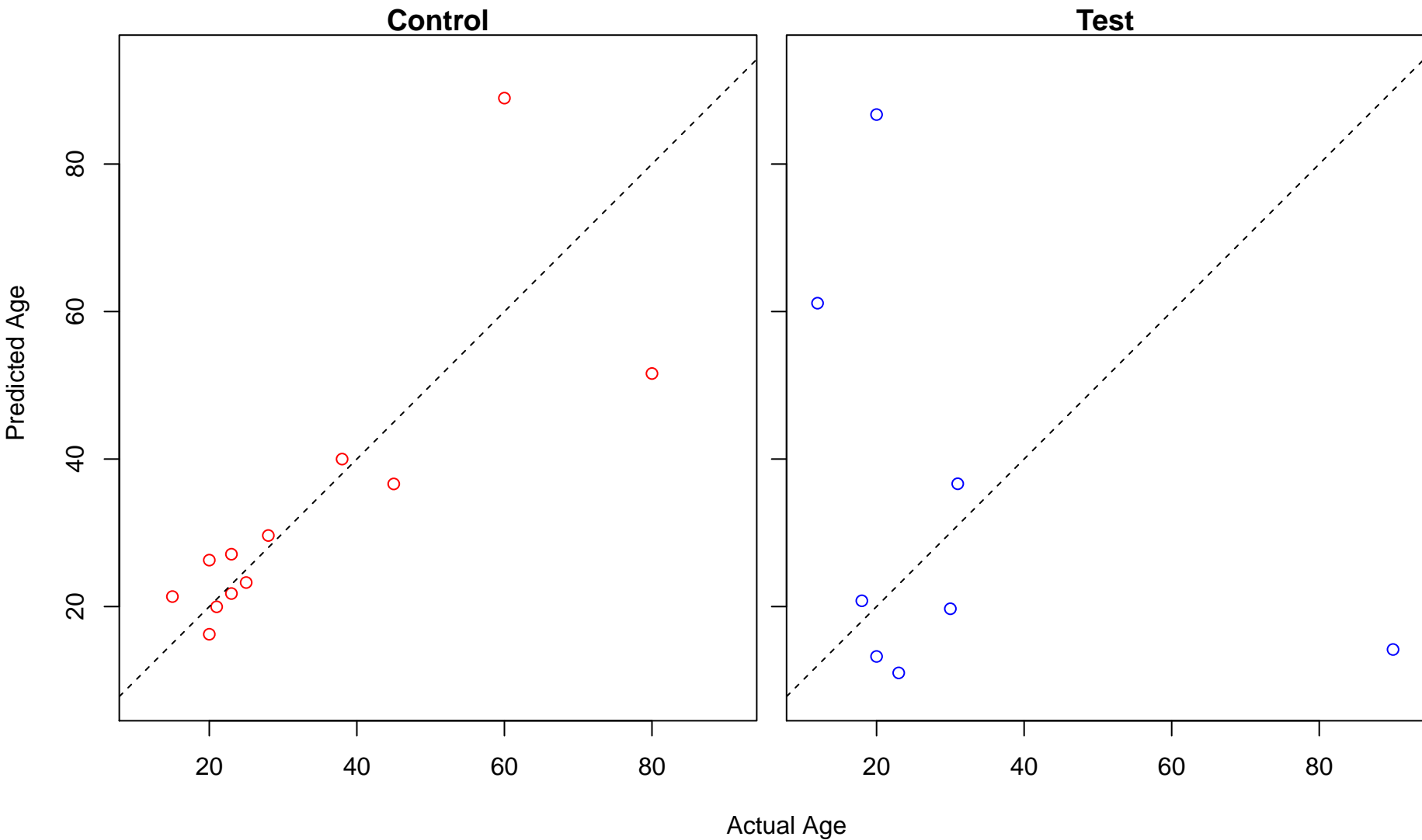
positive regulation of purine nucleotide biosynthetic process (Score: 9.026027)



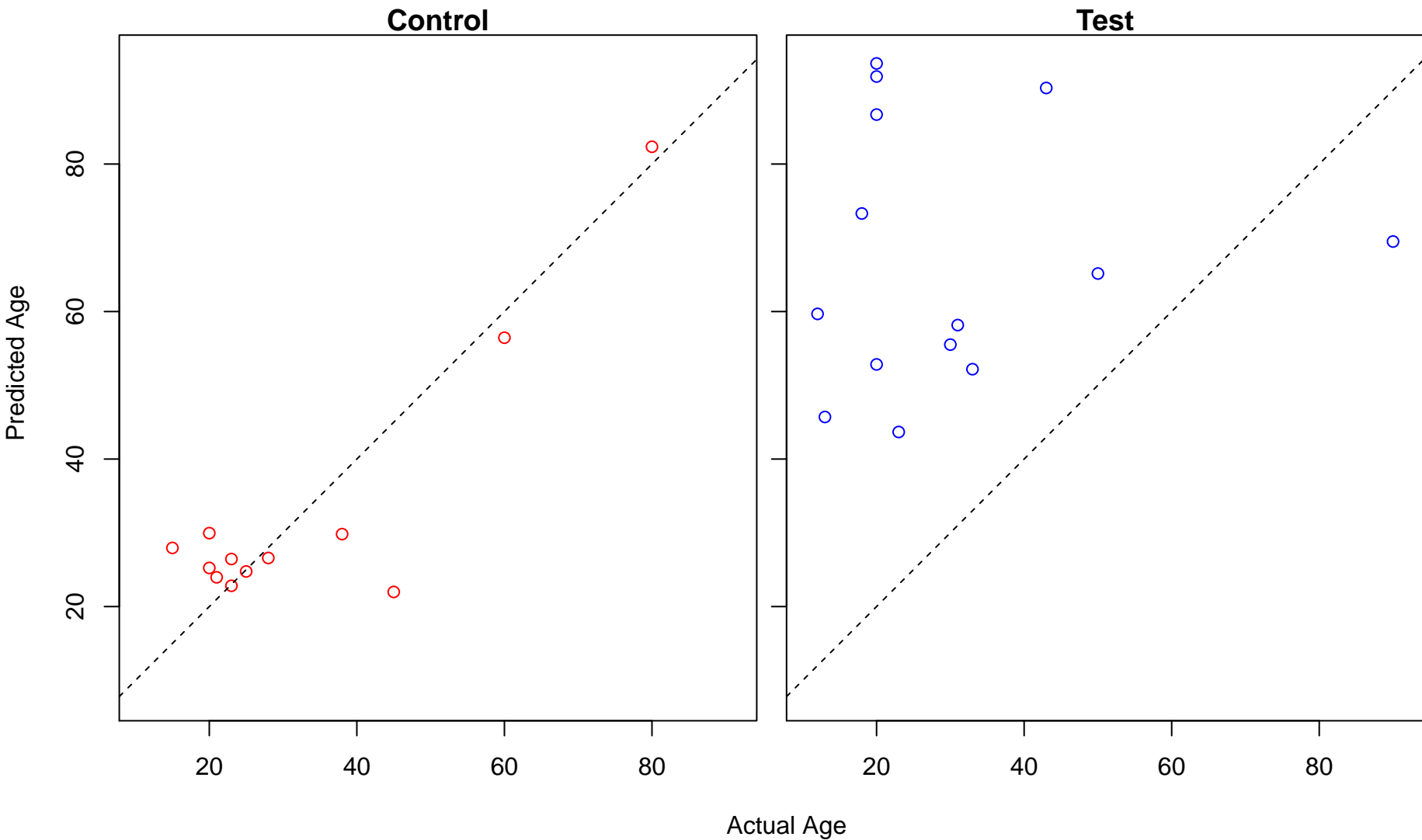
somatic diversification of immune receptors via germline recombination within a single locus (Score: 9.0



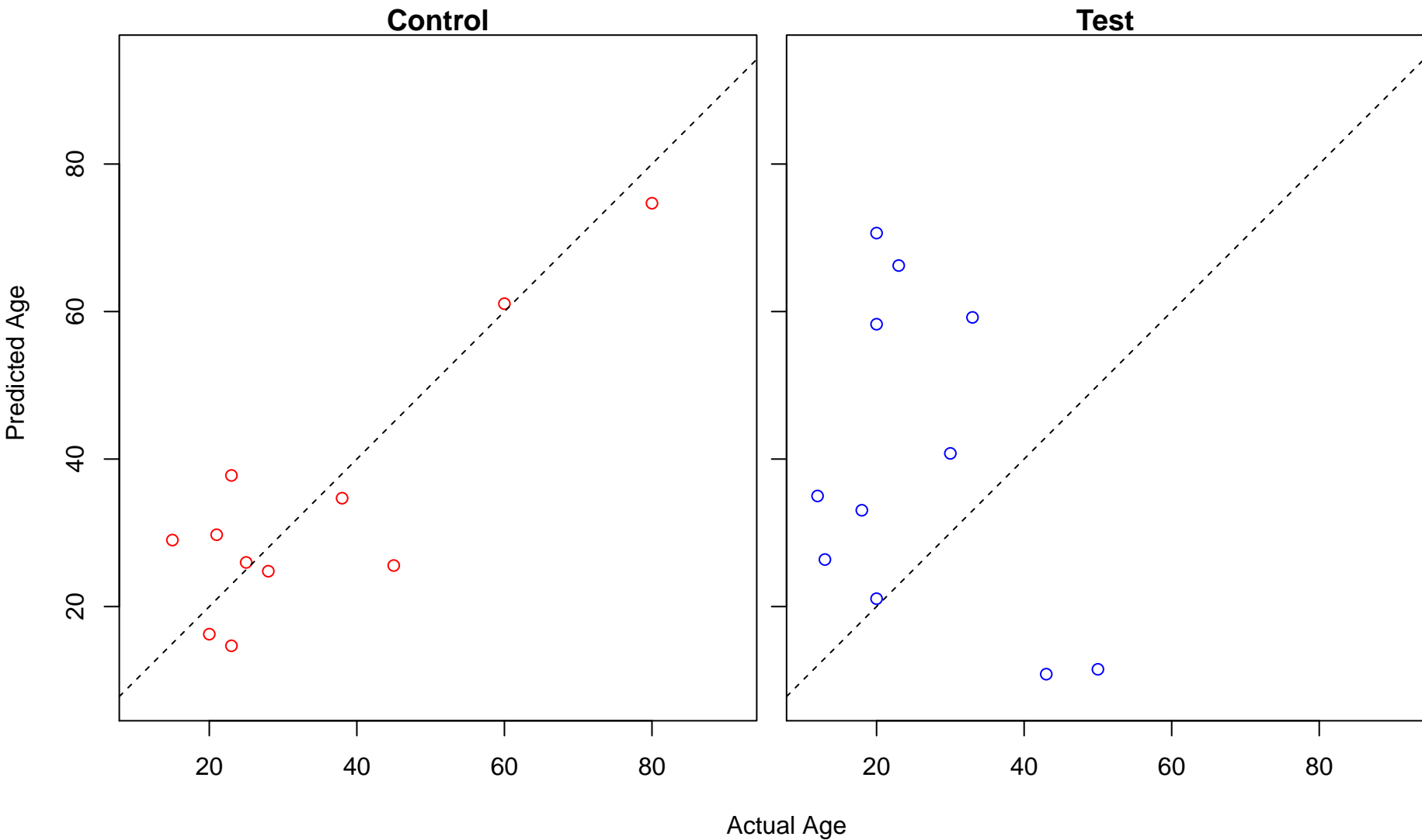
somatic cell DNA recombination (Score: 9.023421)



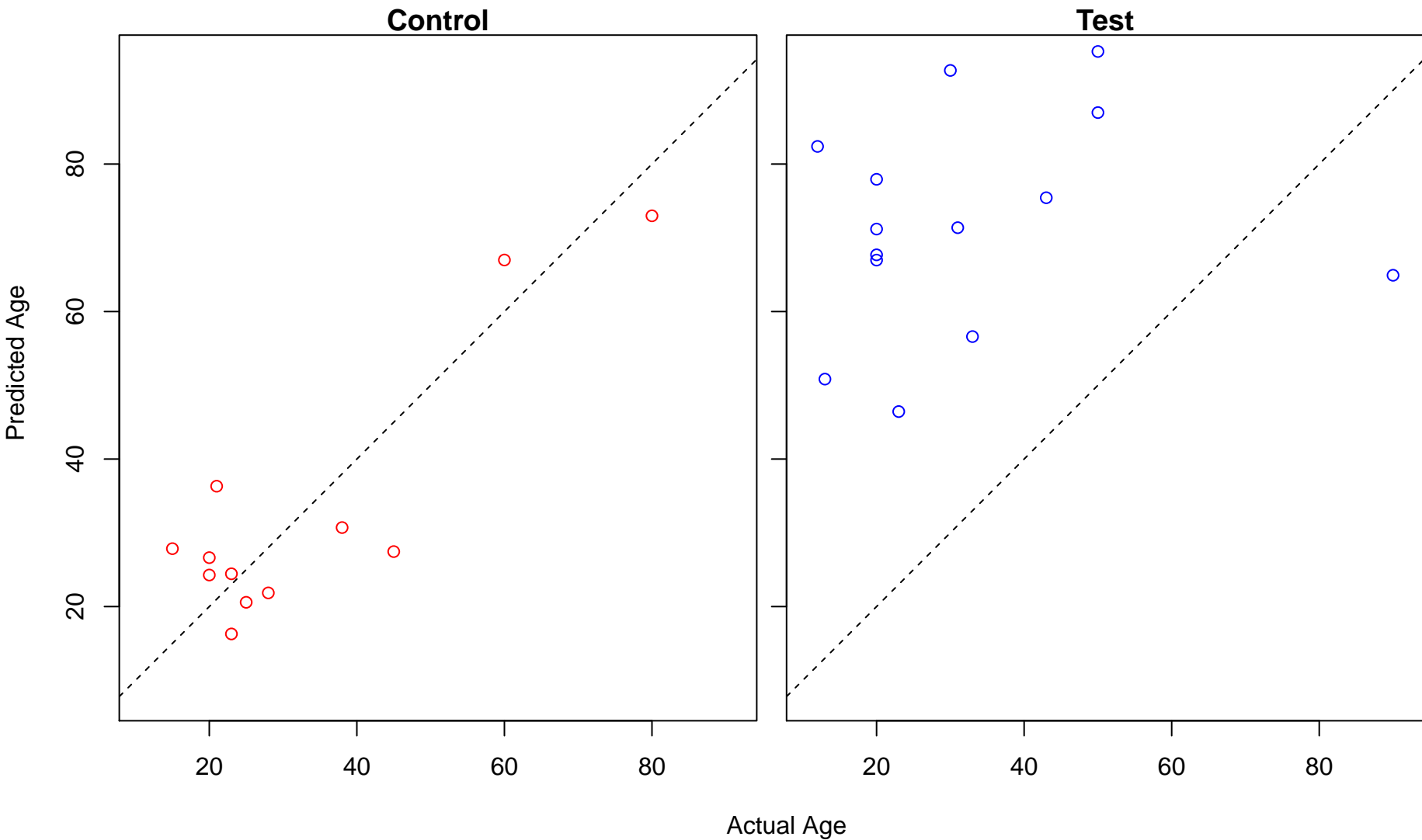
response to hydroperoxide (Score: 9.022992)



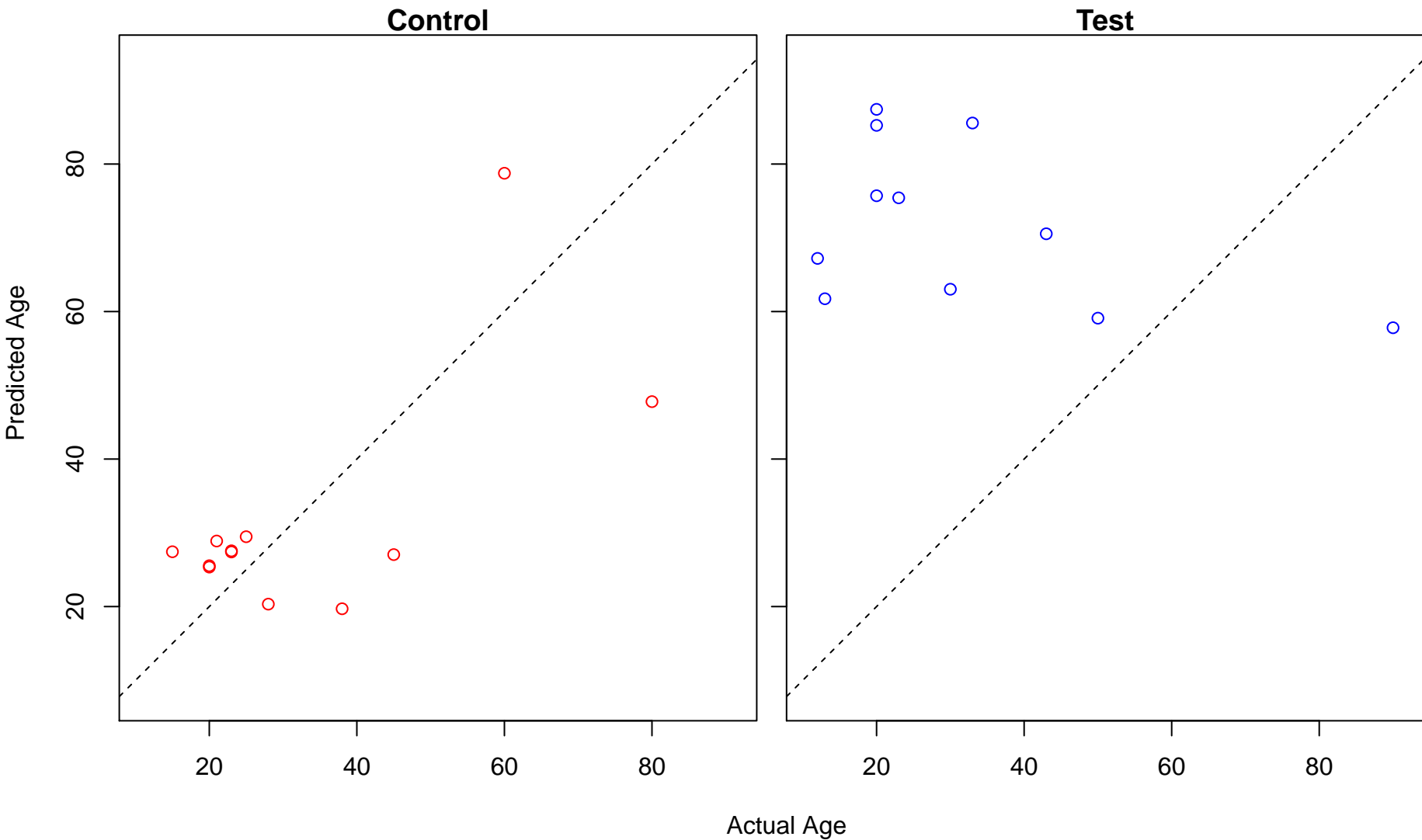
regulation of calcium ion transmembrane transporter activity (Score: 9.020247)



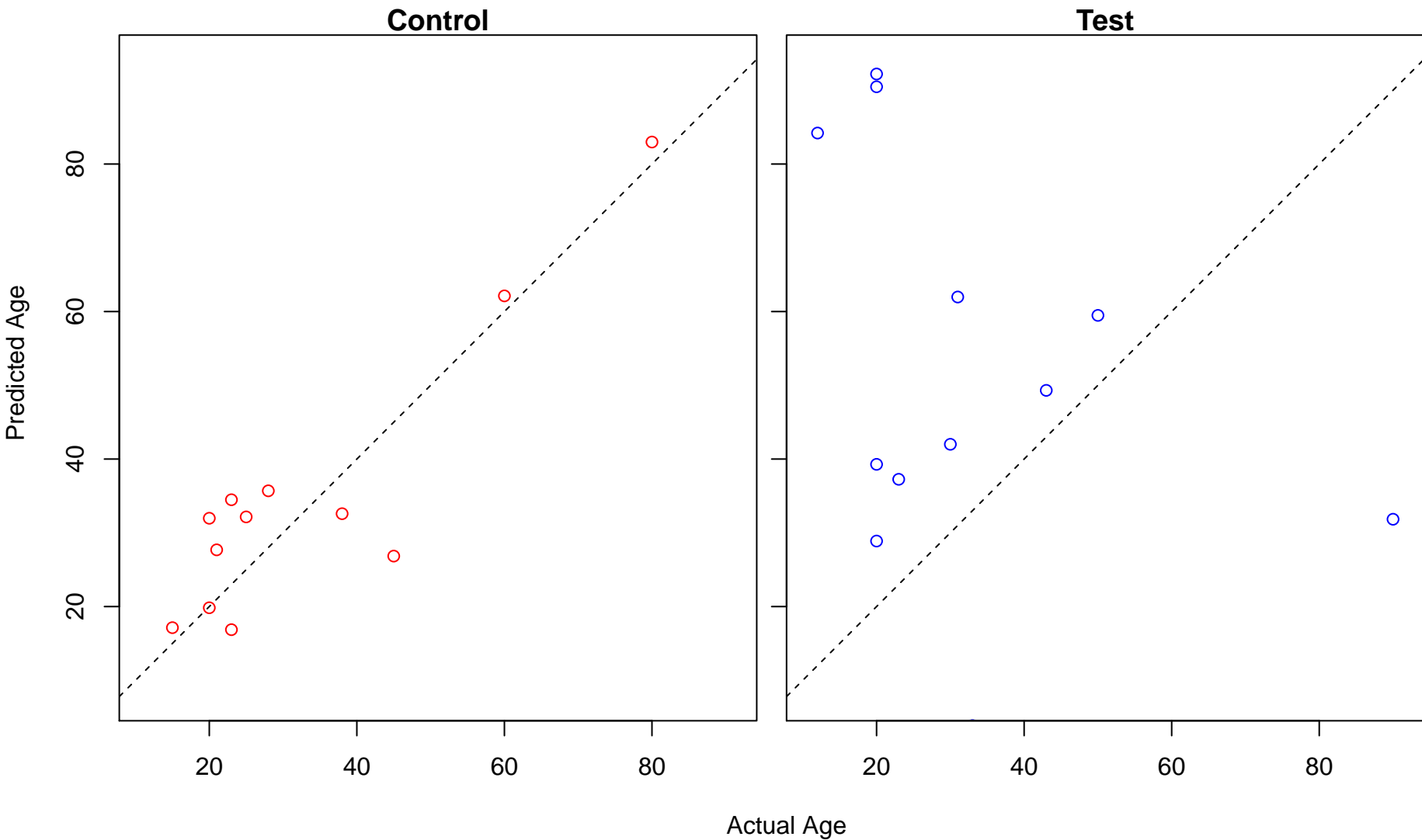
positive regulation of vasculature development (Score: 9.018103)



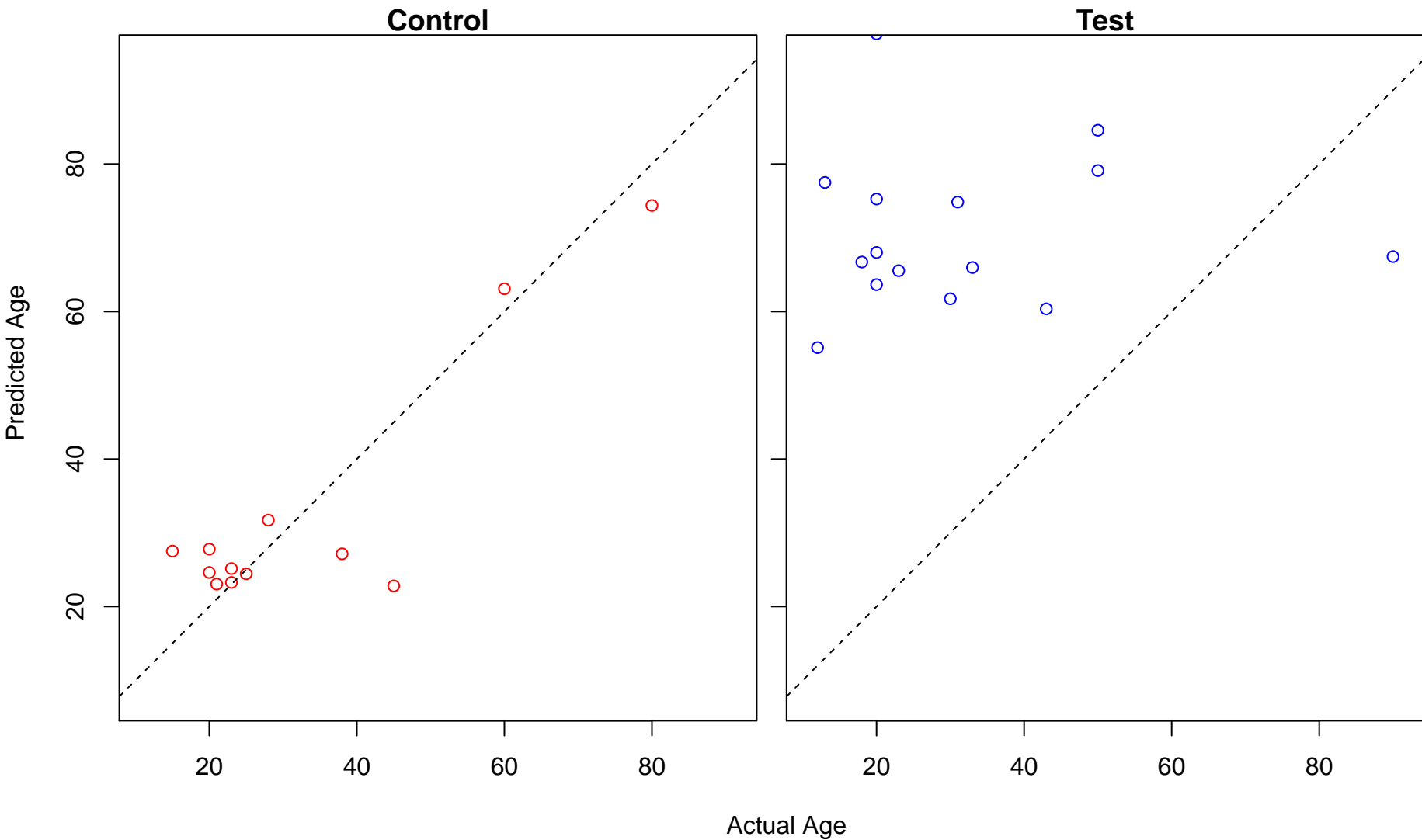
regulation of fibrinolysis (Score: 9.017236)



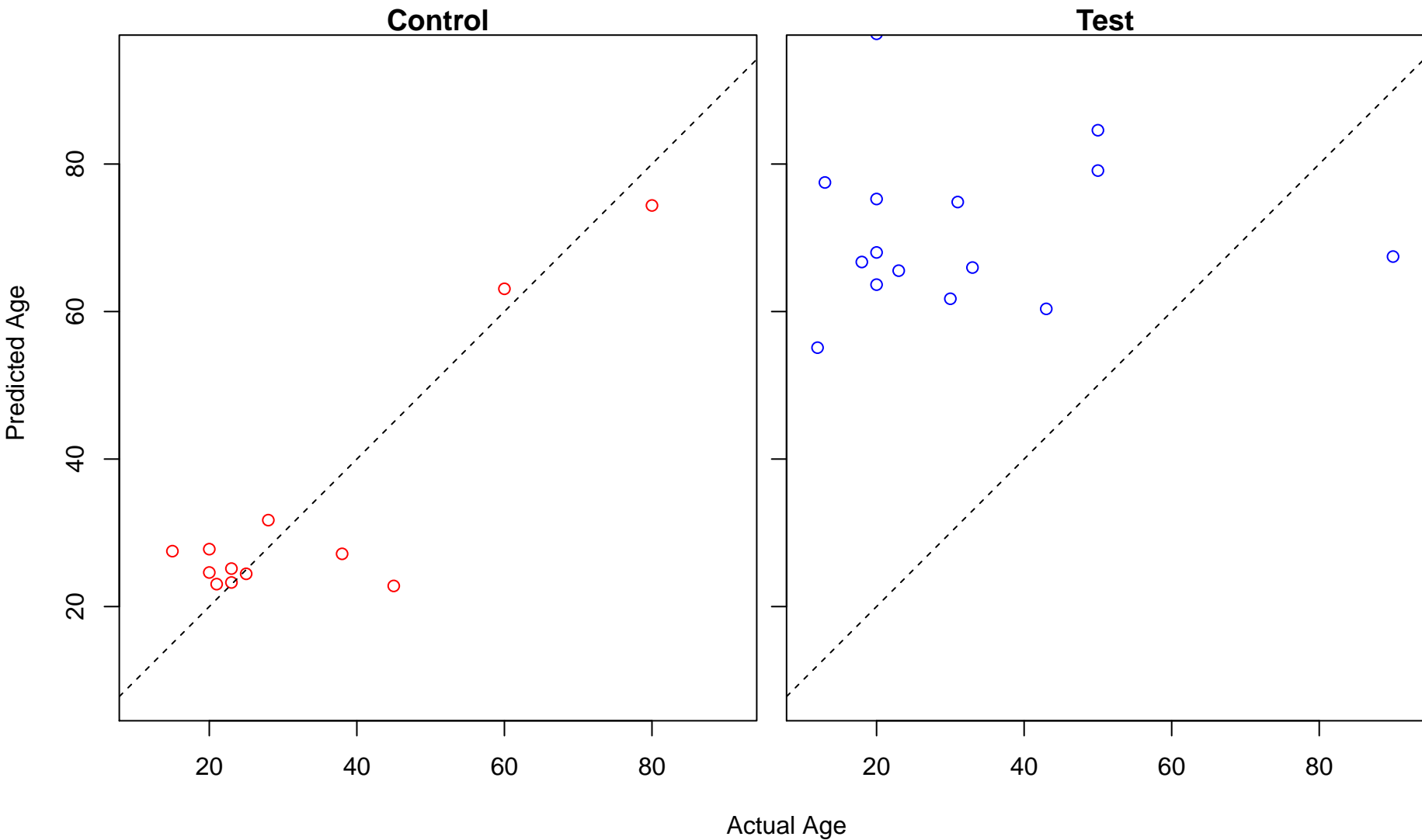
response to acid chemical (Score: 9.013636)



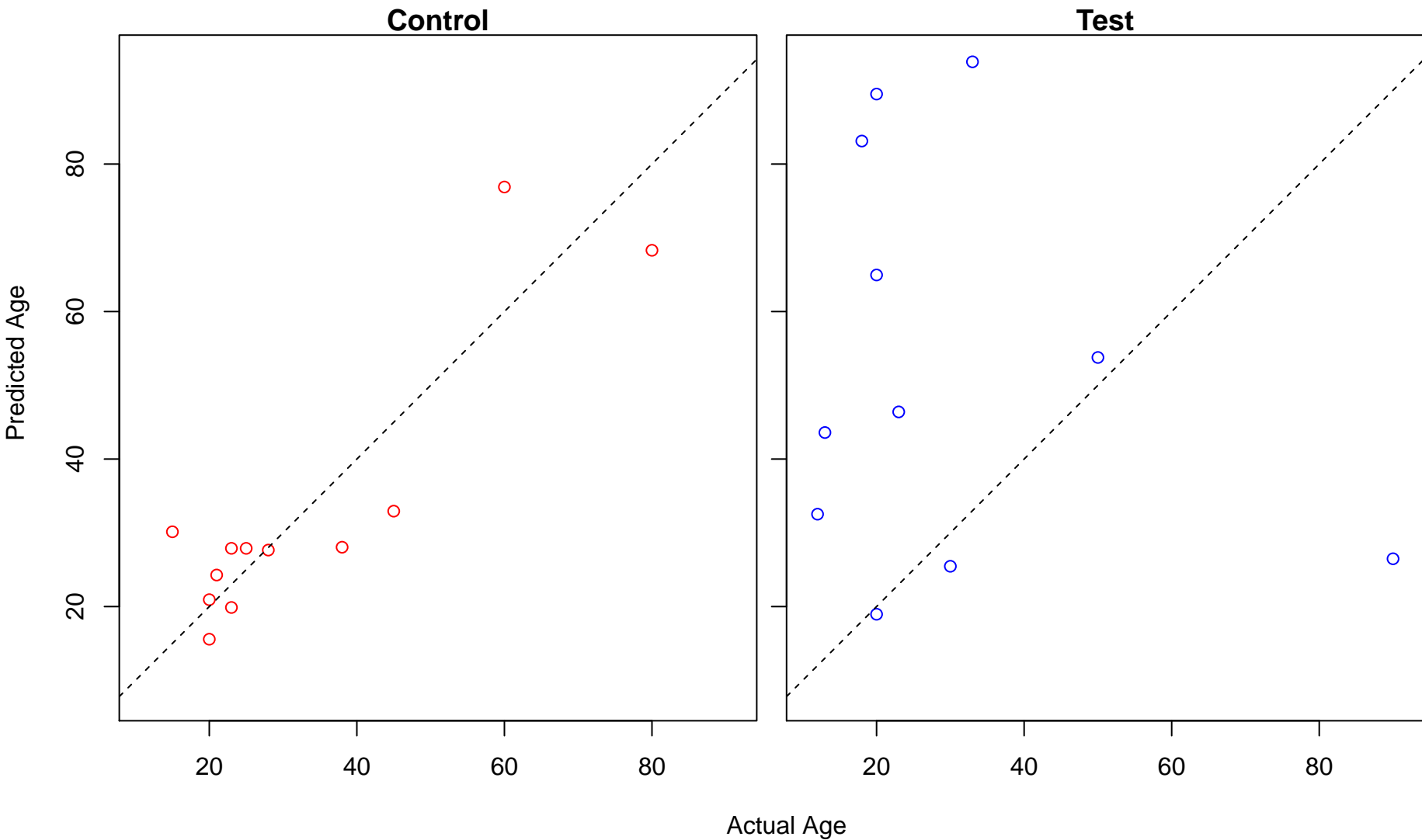
regulation of nucleotide biosynthetic process (Score: 9.008712)



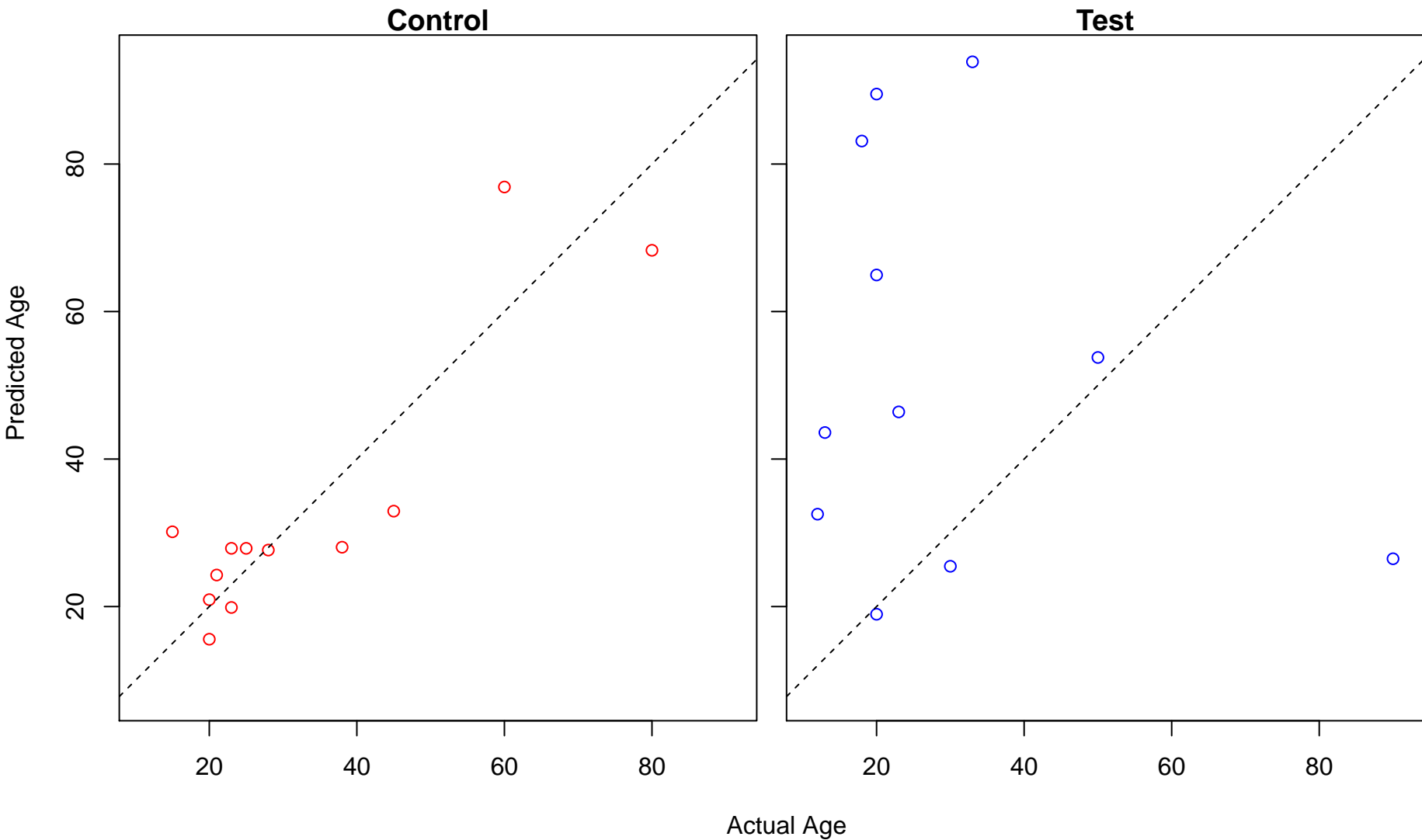
regulation of purine nucleotide biosynthetic process (Score: 9.008712)



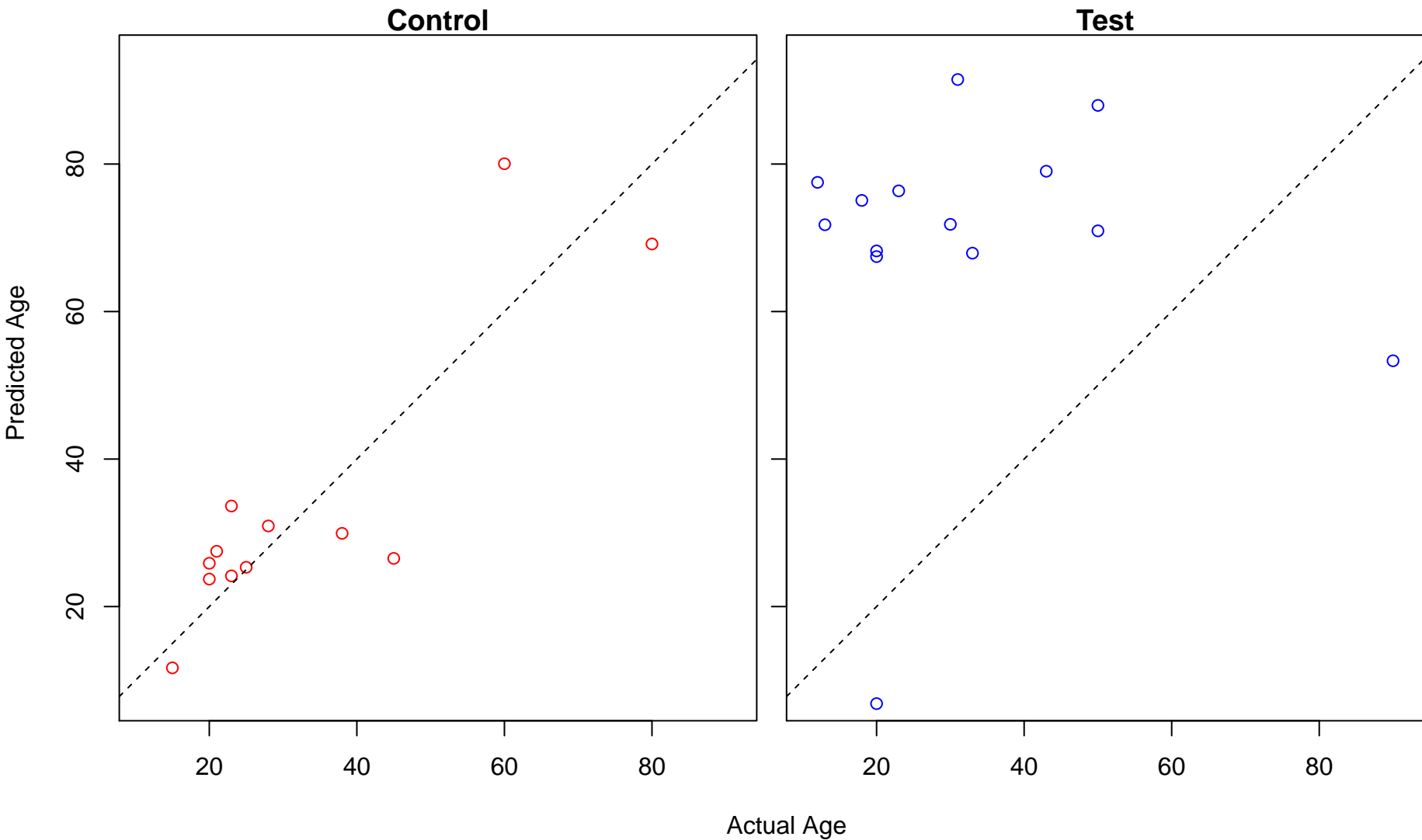
appendage morphogenesis (Score: 9.006167)



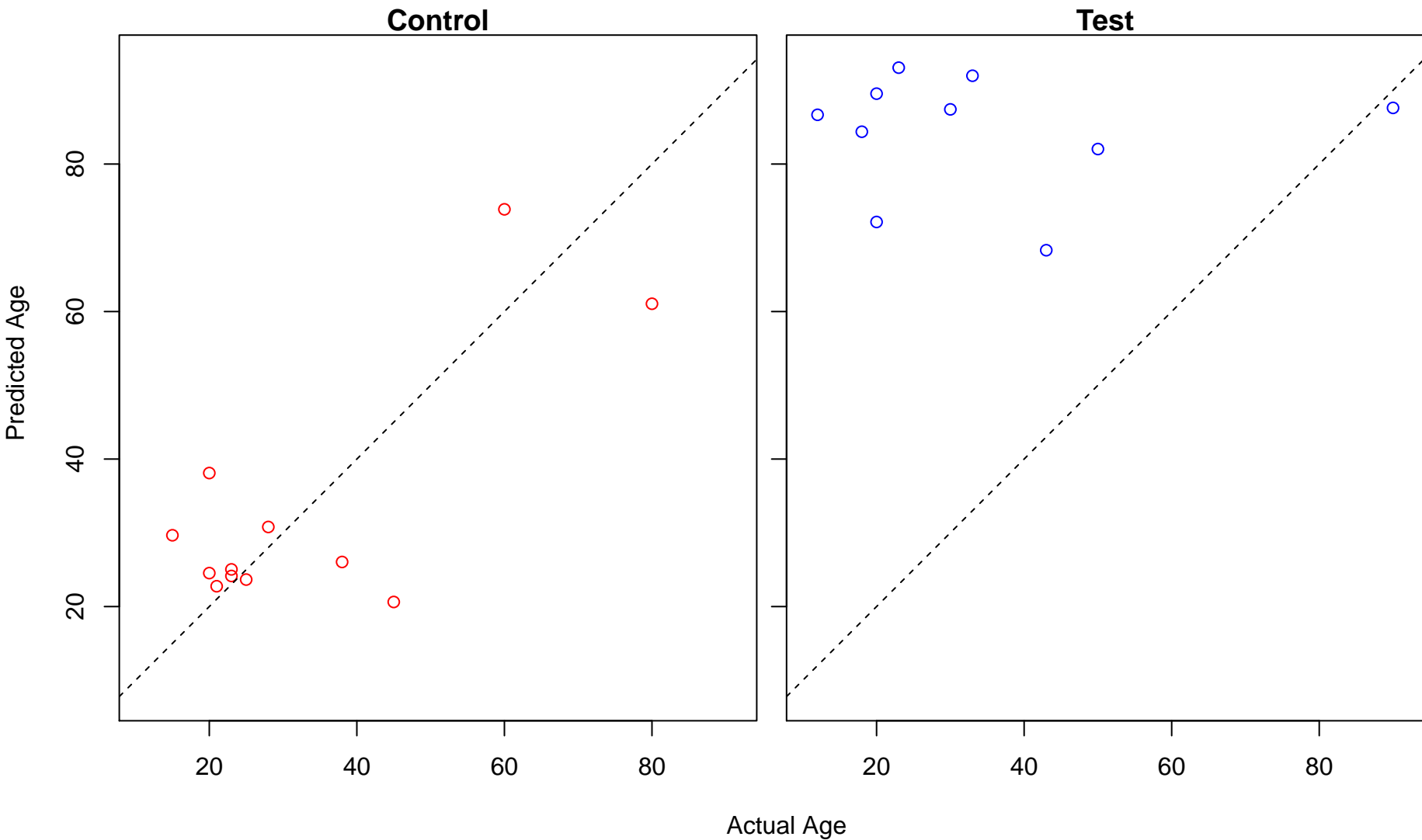
limb morphogenesis (Score: 9.006167)



negative regulation of skeletal muscle tissue development (Score: 9.003758)

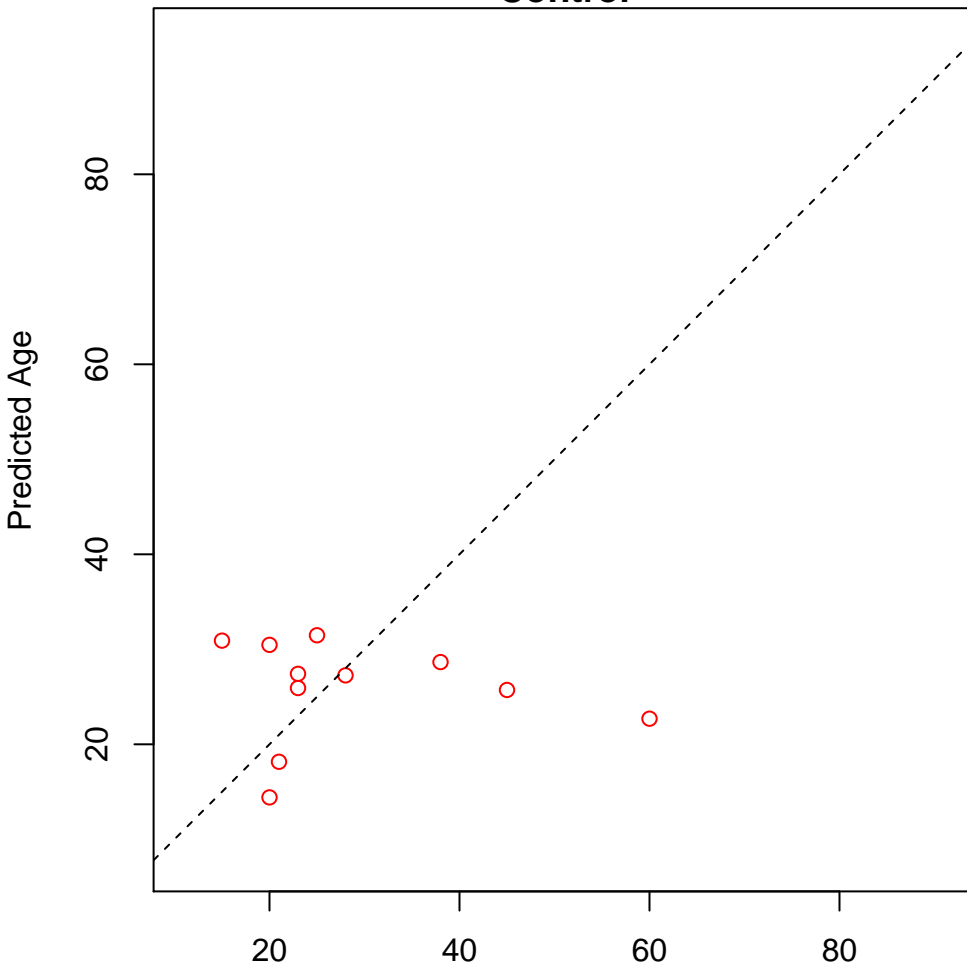


negative regulation of gene silencing by miRNA (Score: 9.002818)

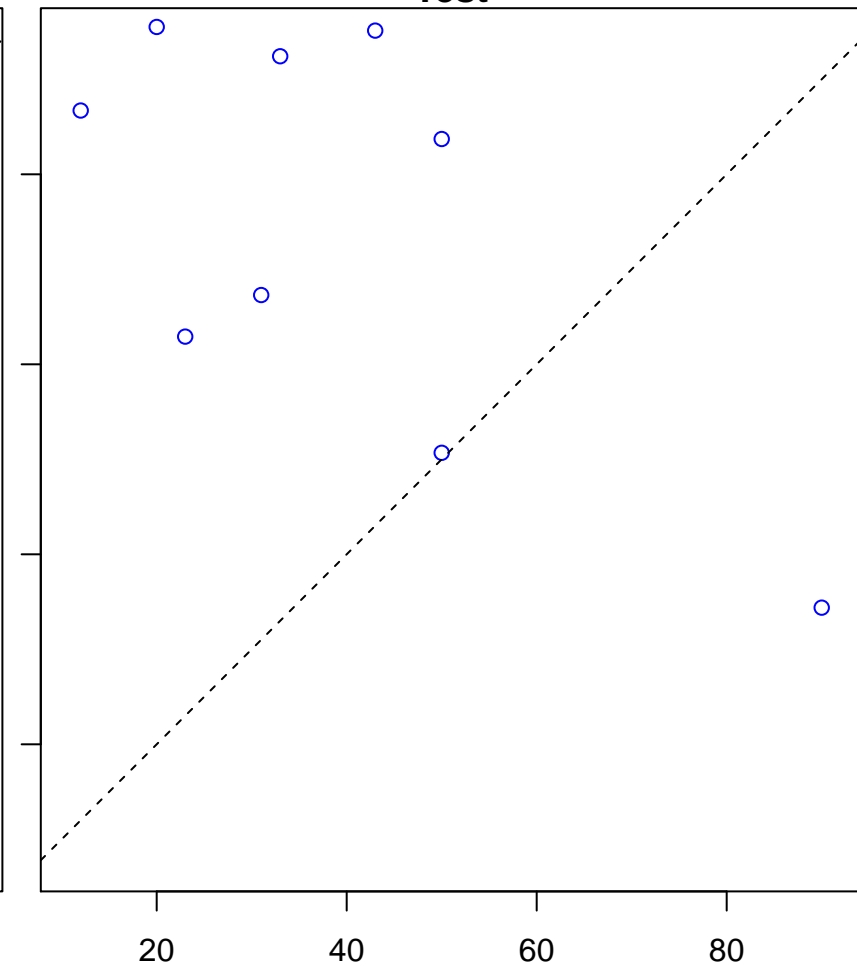


cerebellar granular layer development (Score: 8.998550)

Control

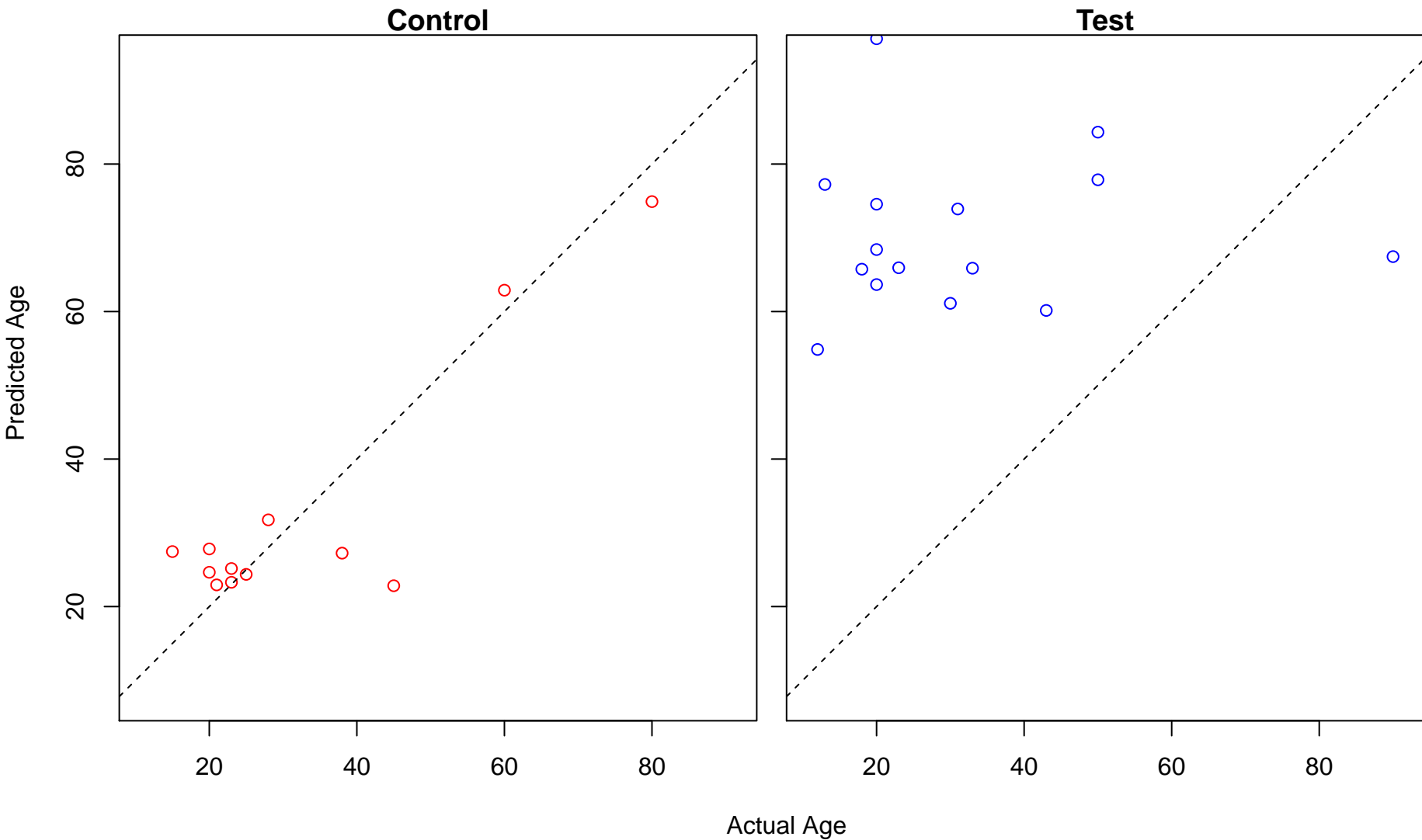


Test

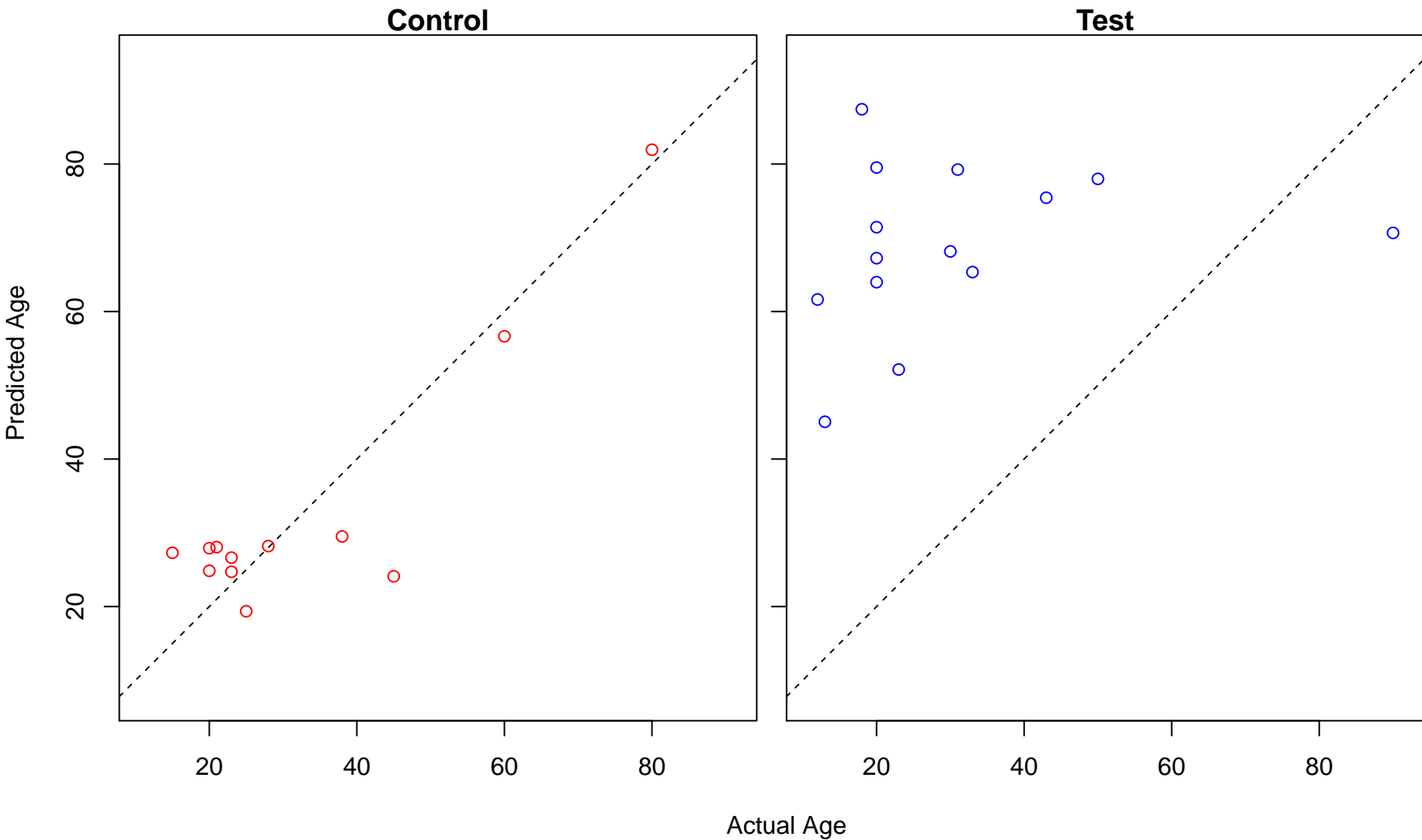


Actual Age

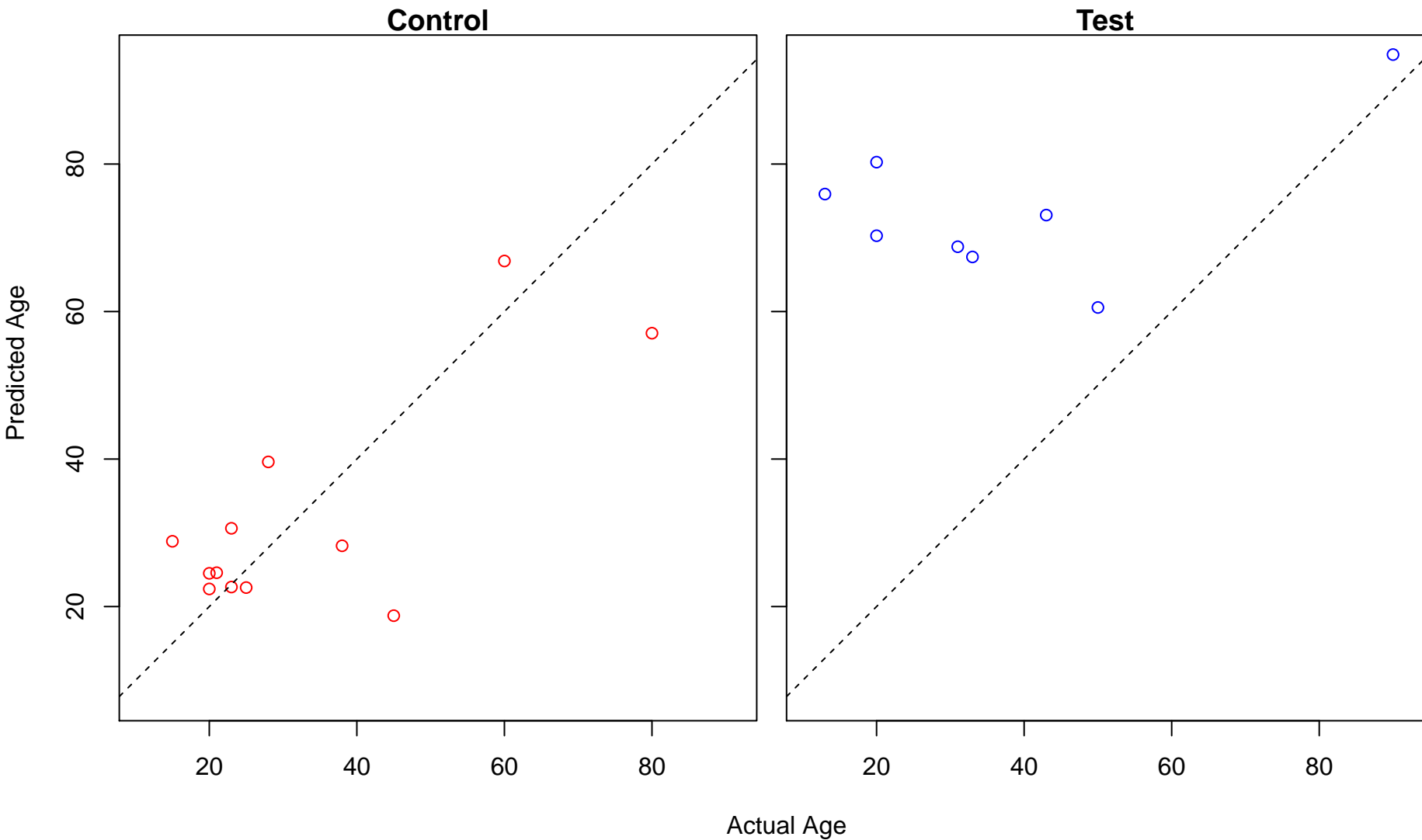
cyclic nucleotide metabolic process (Score: 8.996671)



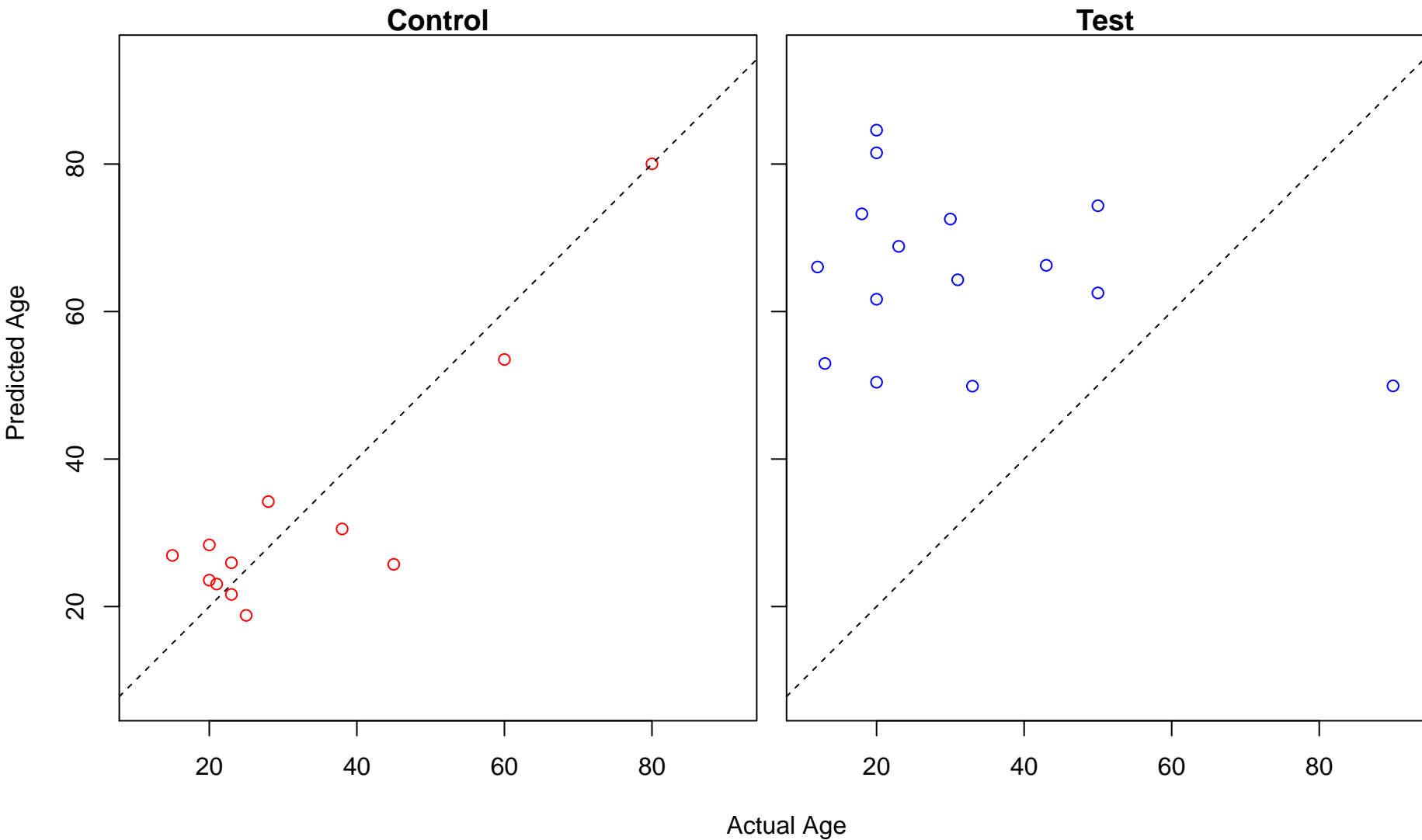
negative regulation of cell adhesion (Score: 8.985934)



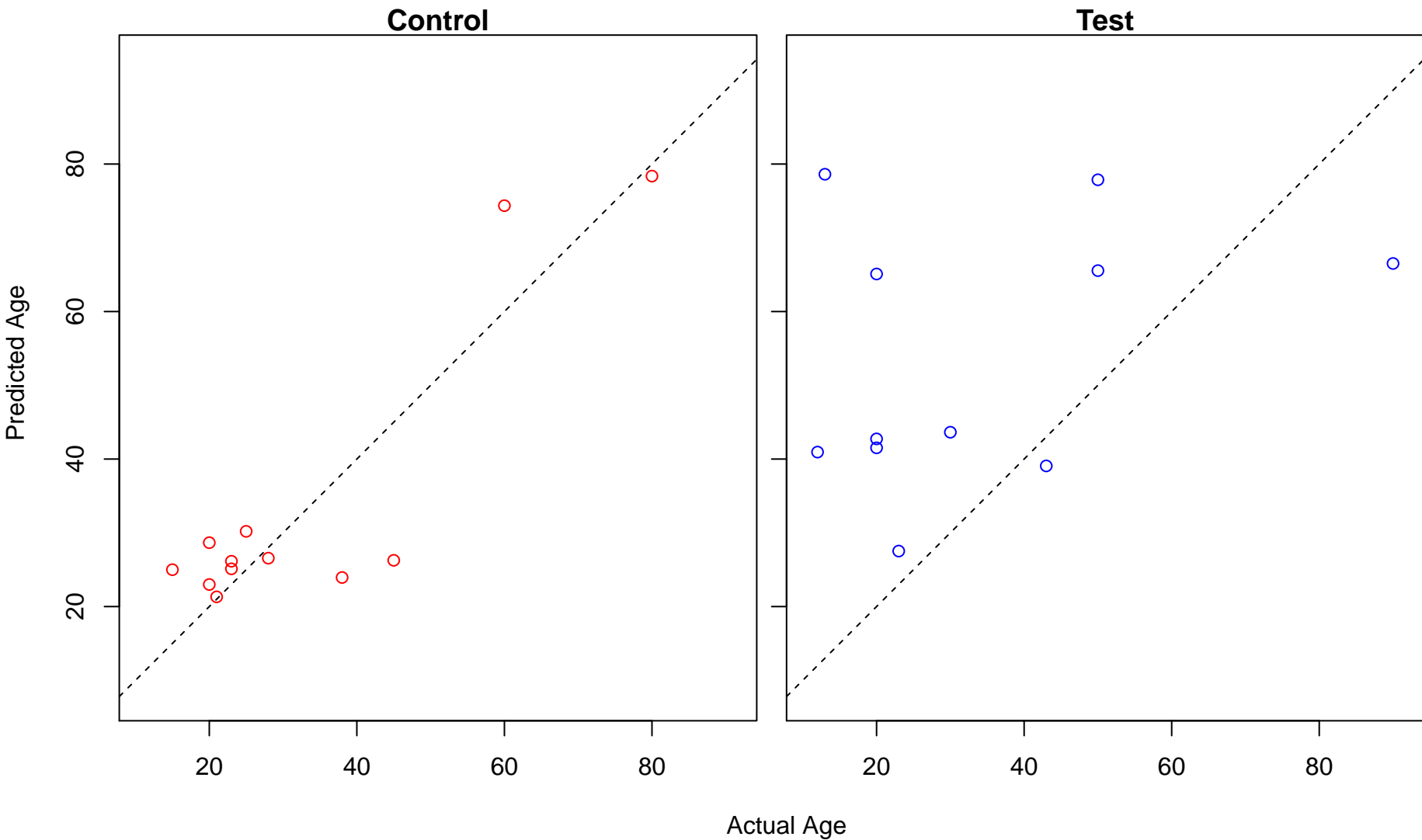
positive regulation of male gonad development (Score: 8.983227)



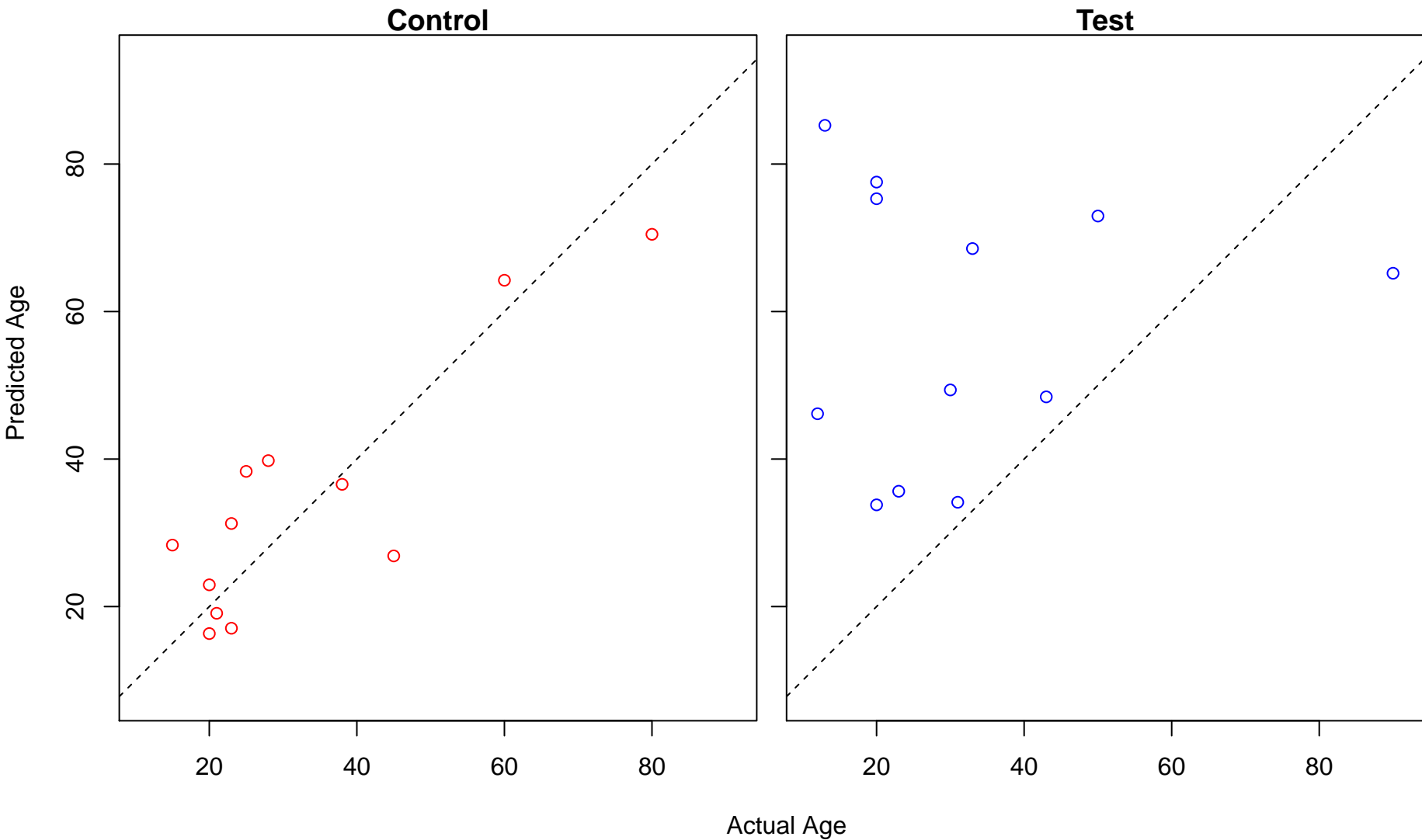
floor plate development (Score: 8.976522)



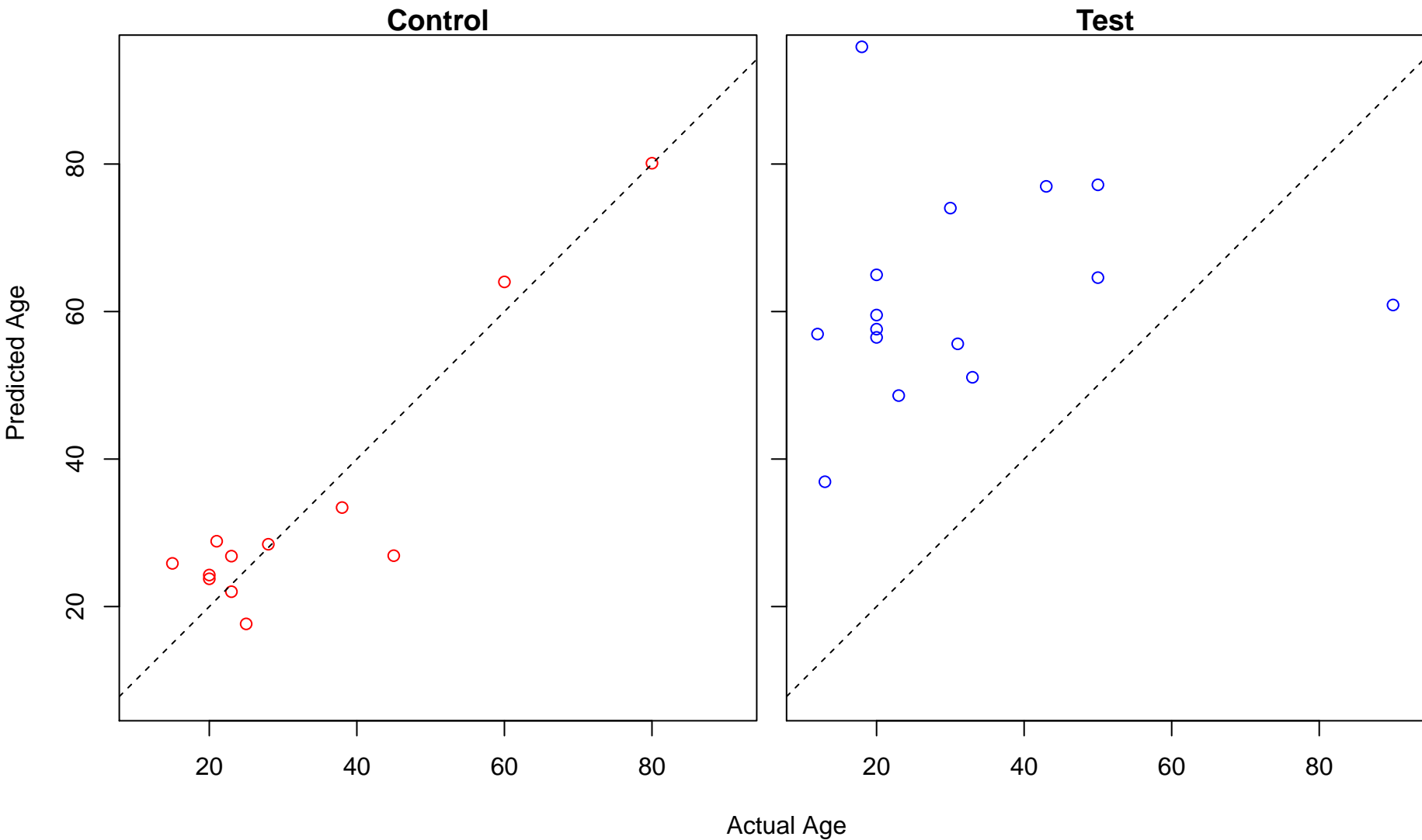
positive regulation of IRE1-mediated unfolded protein response (Score: 8.976257)



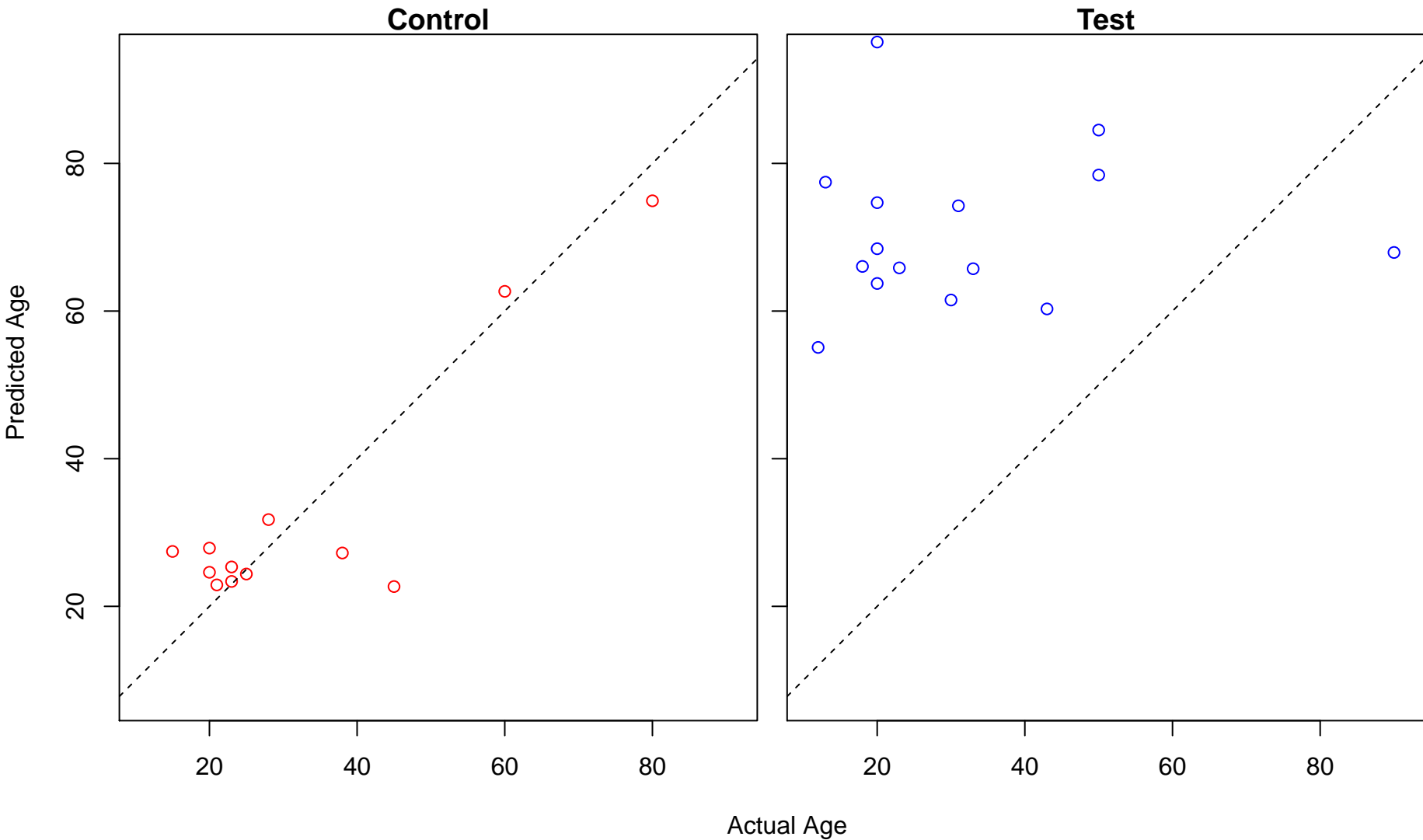
positive regulation of respiratory burst (Score: 8.976107)



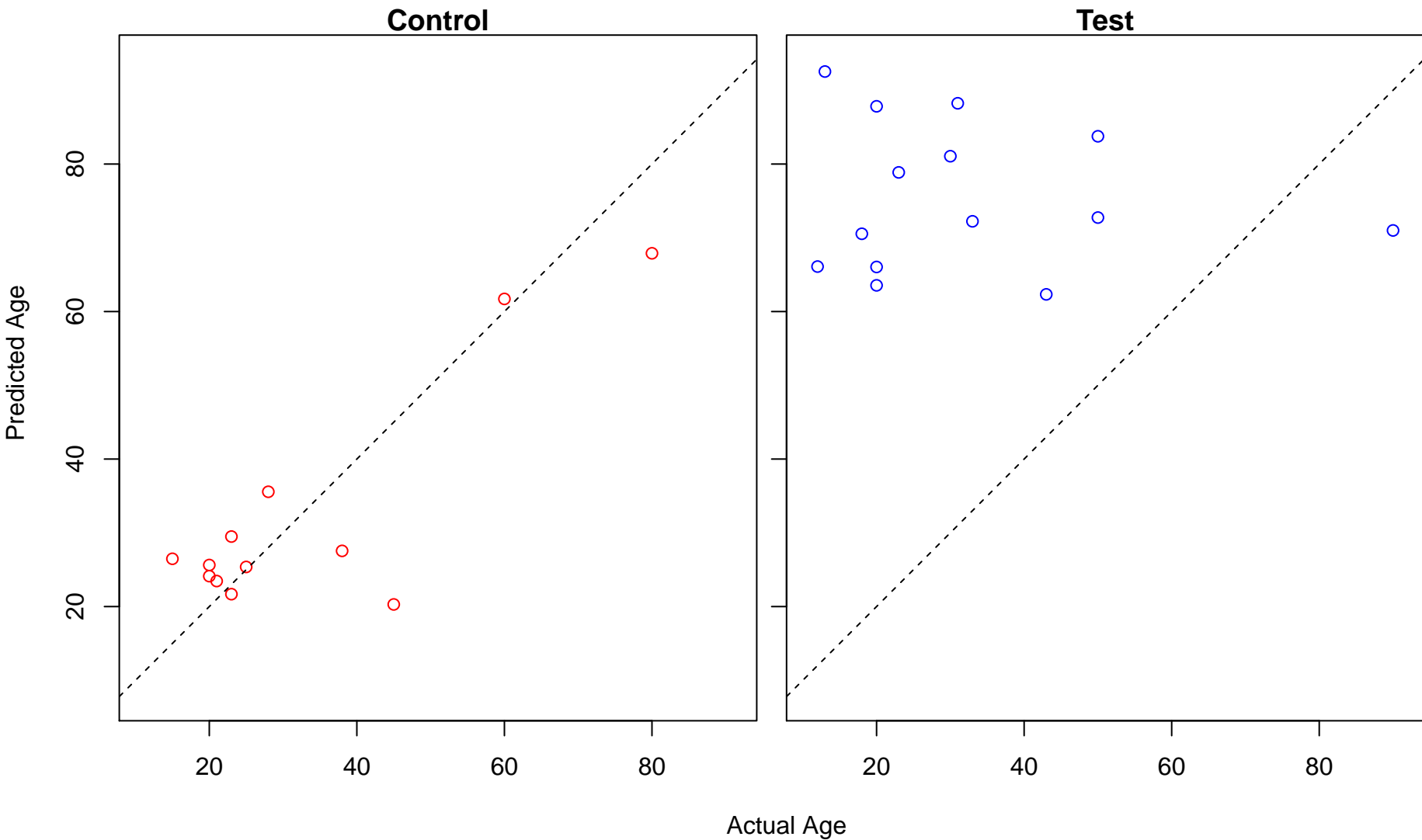
hormone metabolic process (Score: 8.970466)



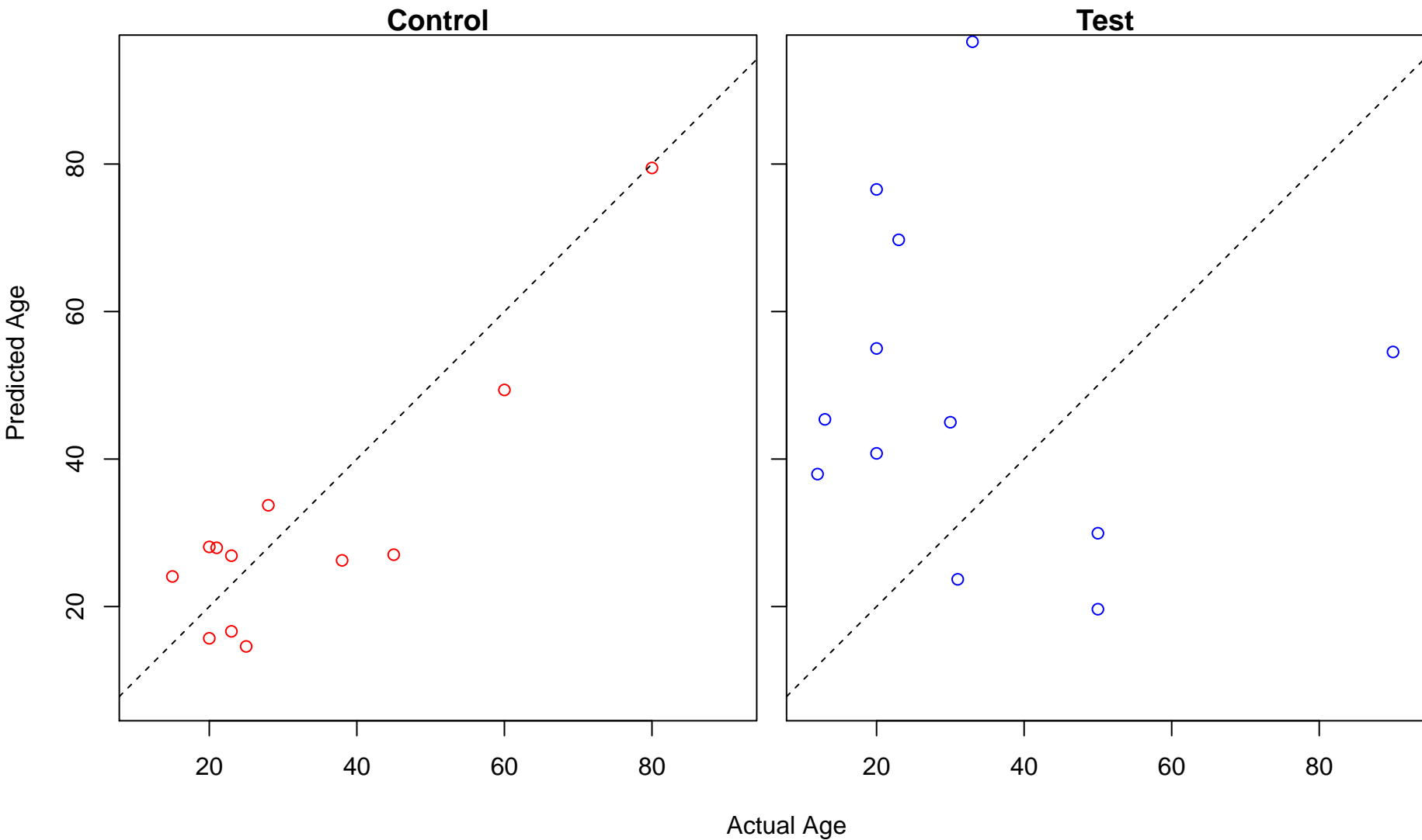
adenylate cyclase–modulating G–protein coupled receptor signaling pathway (Score: 8.965202)



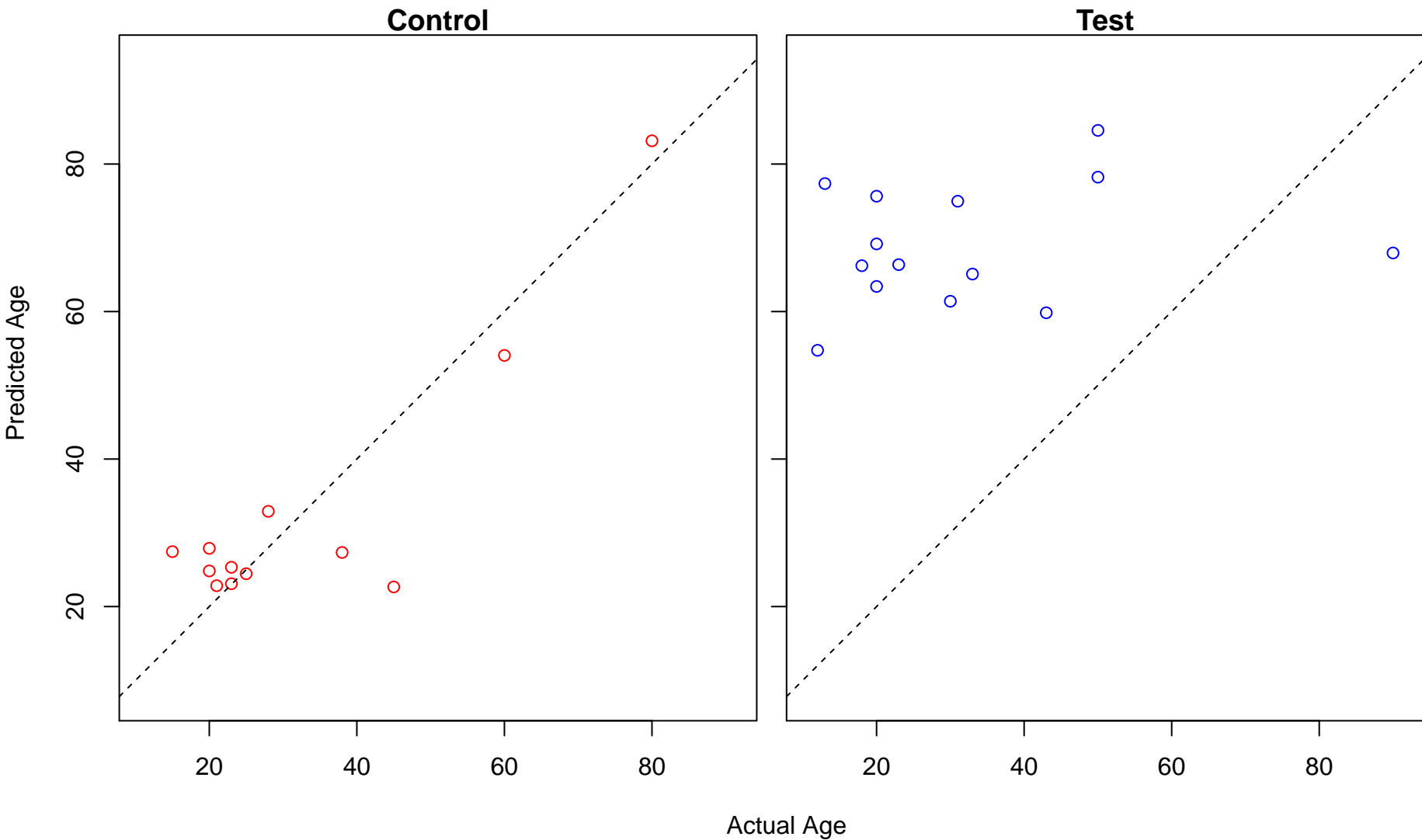
regulation of B cell activation (Score: 8.962959)



nucleobase-containing compound transport (Score: 8.960346)

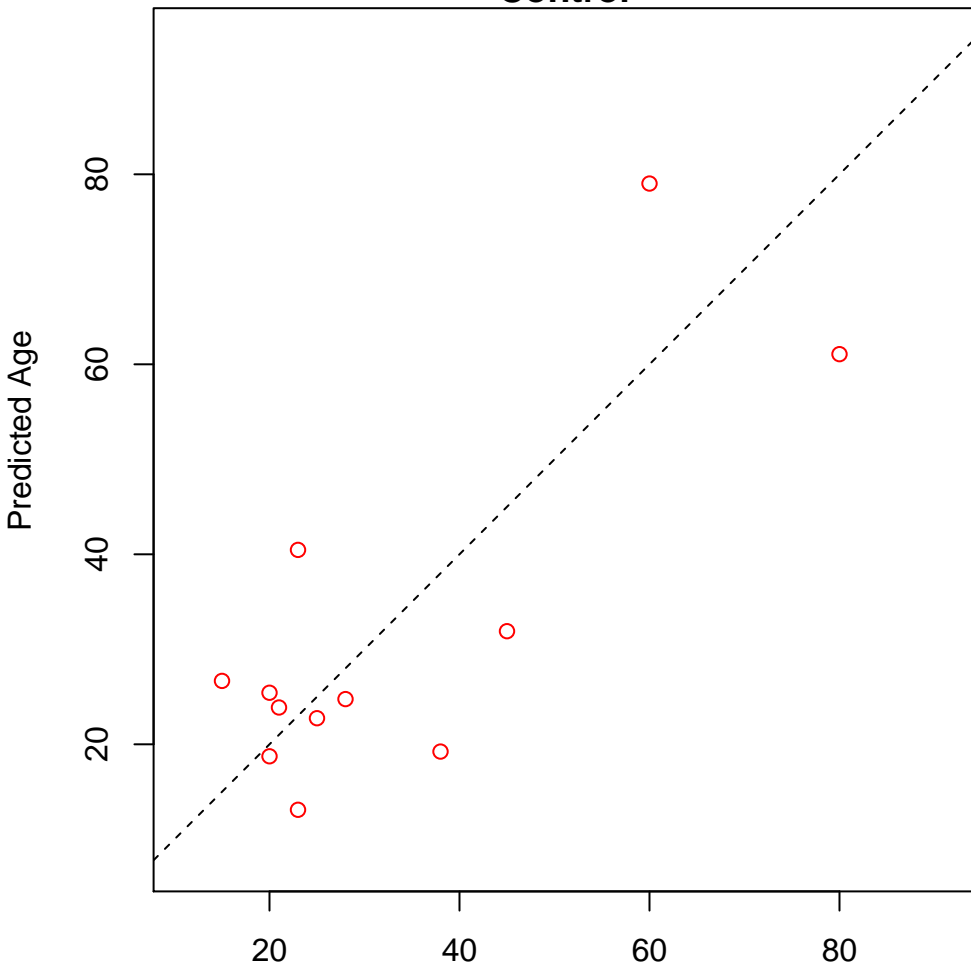


cellular response to prostaglandin stimulus (Score: 8.953321)

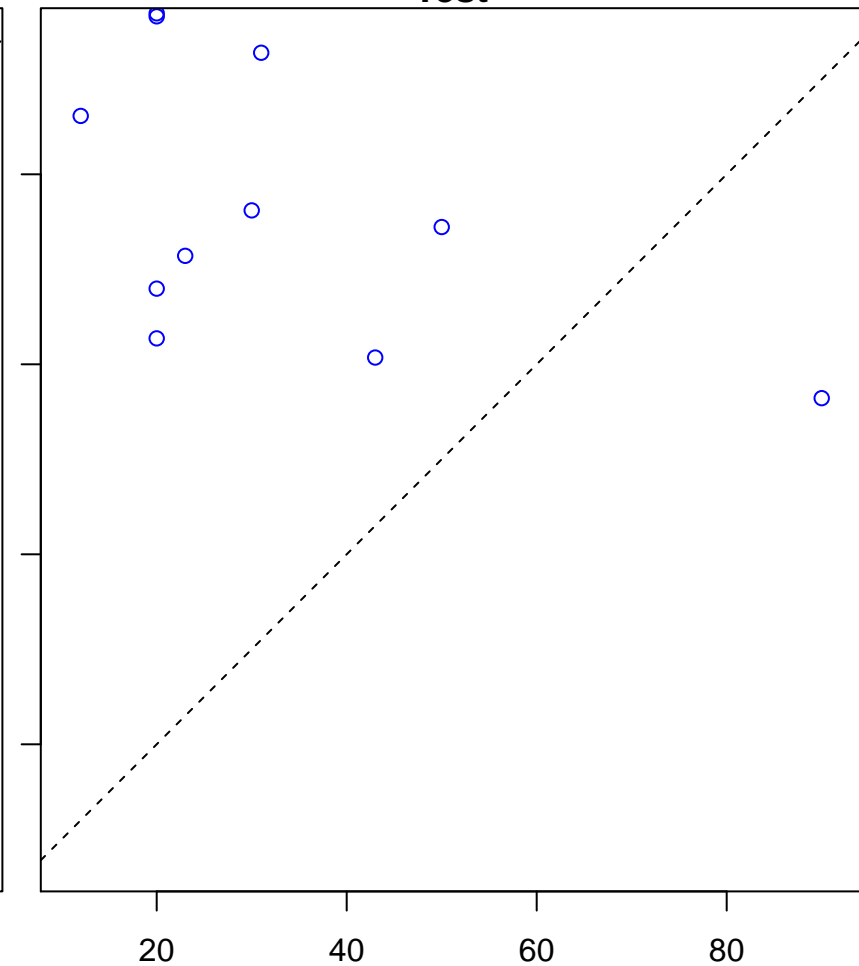


negative regulation of platelet activation (Score: 8.952992)

Control

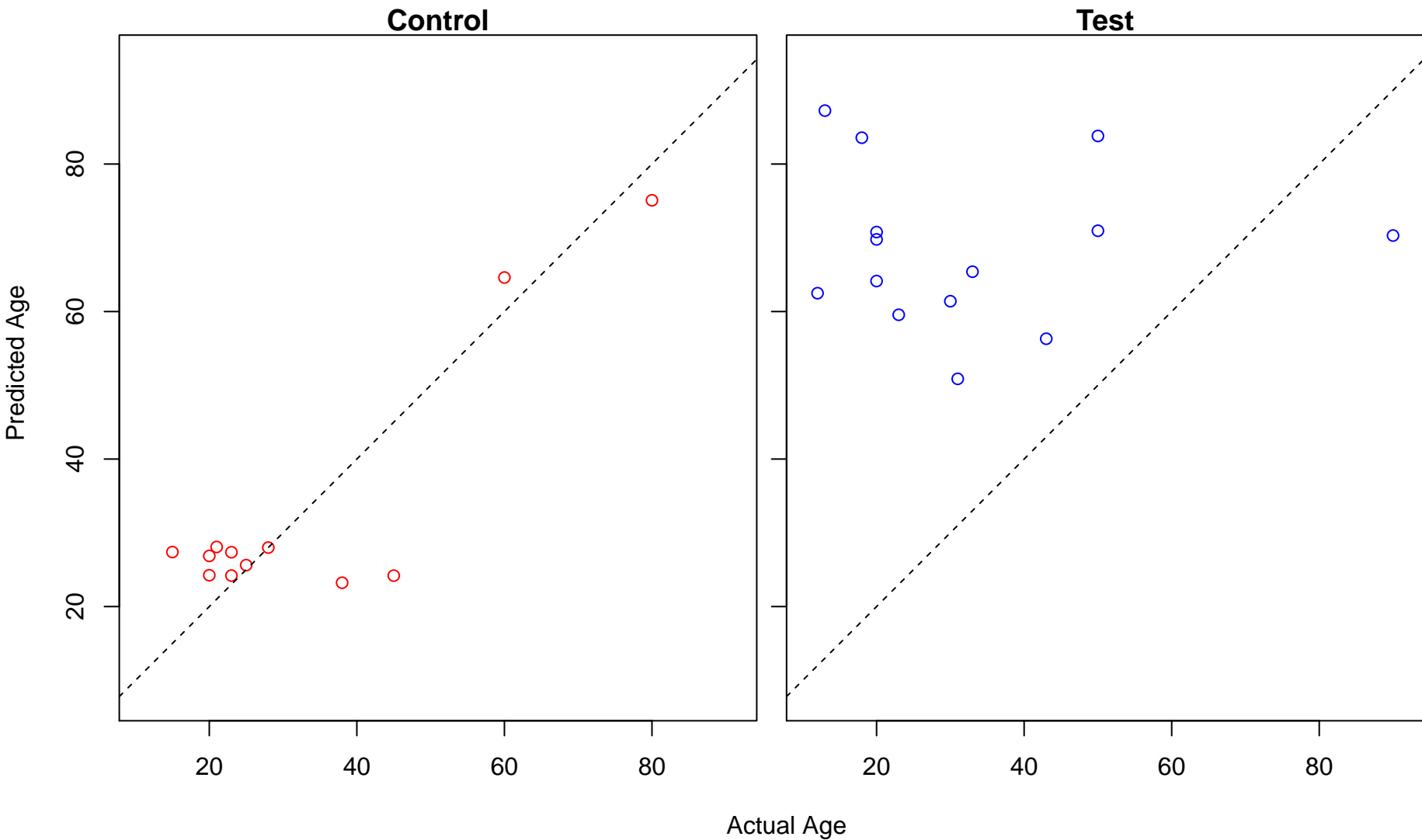


Test

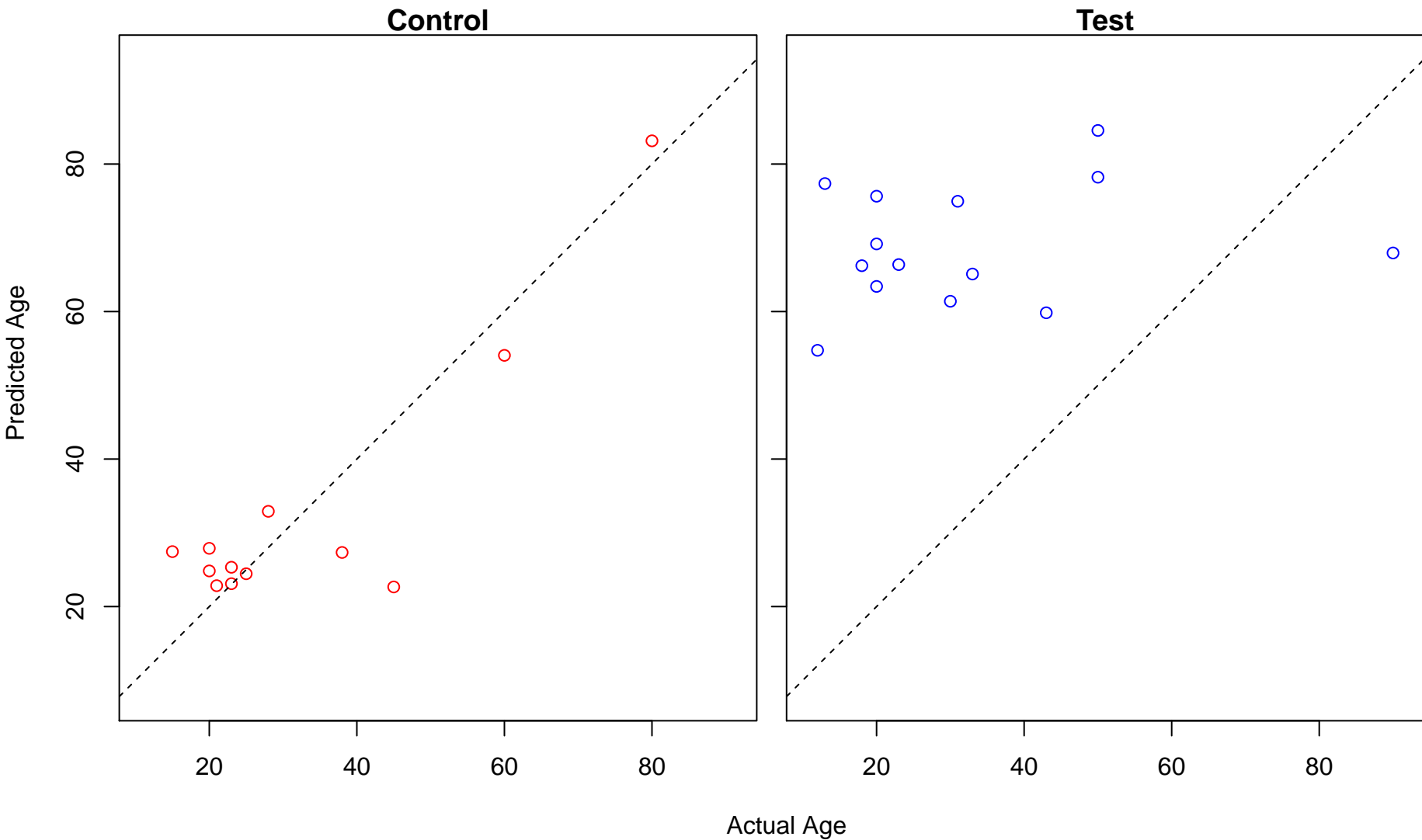


Actual Age

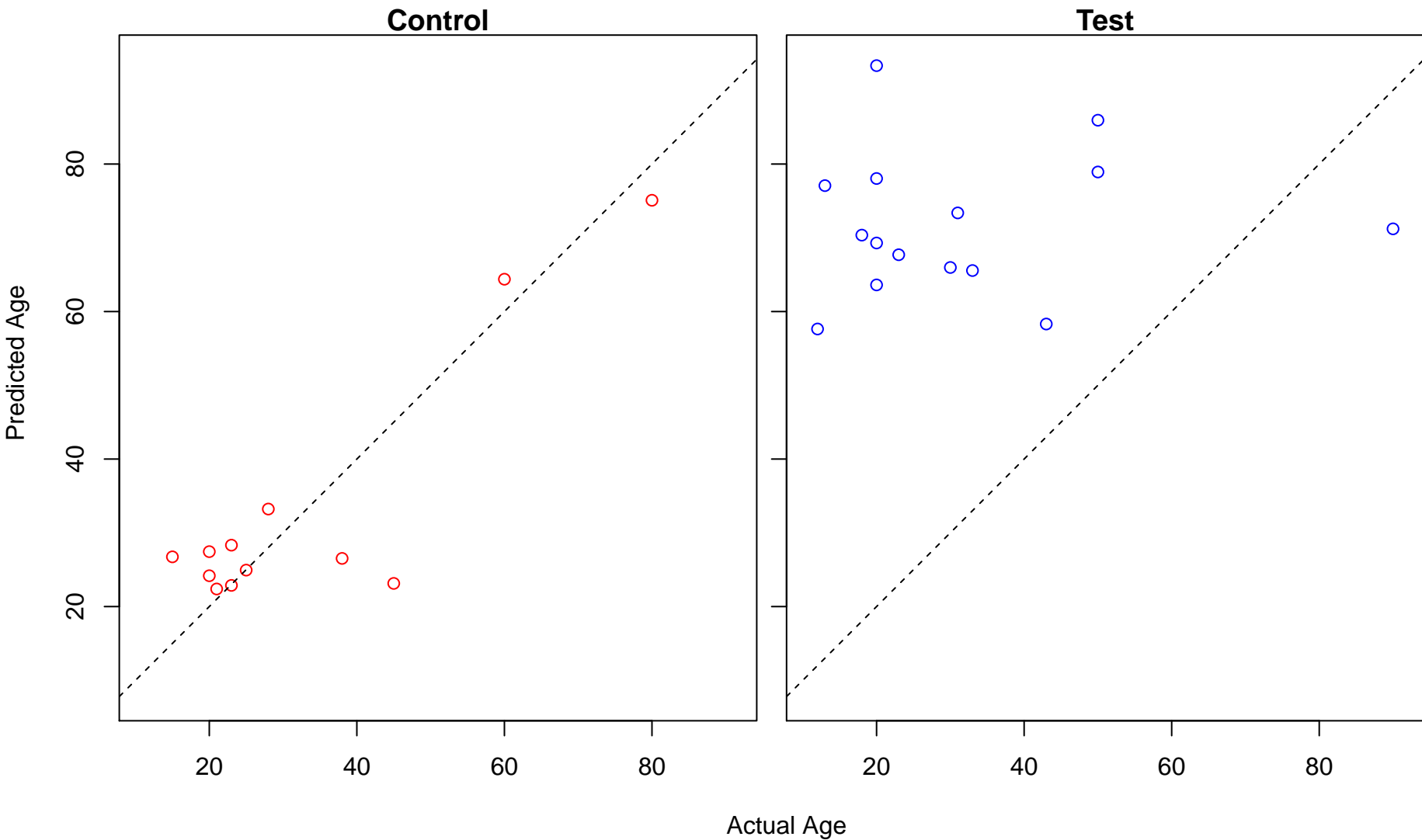
myeloid cell homeostasis (Score: 8.952970)



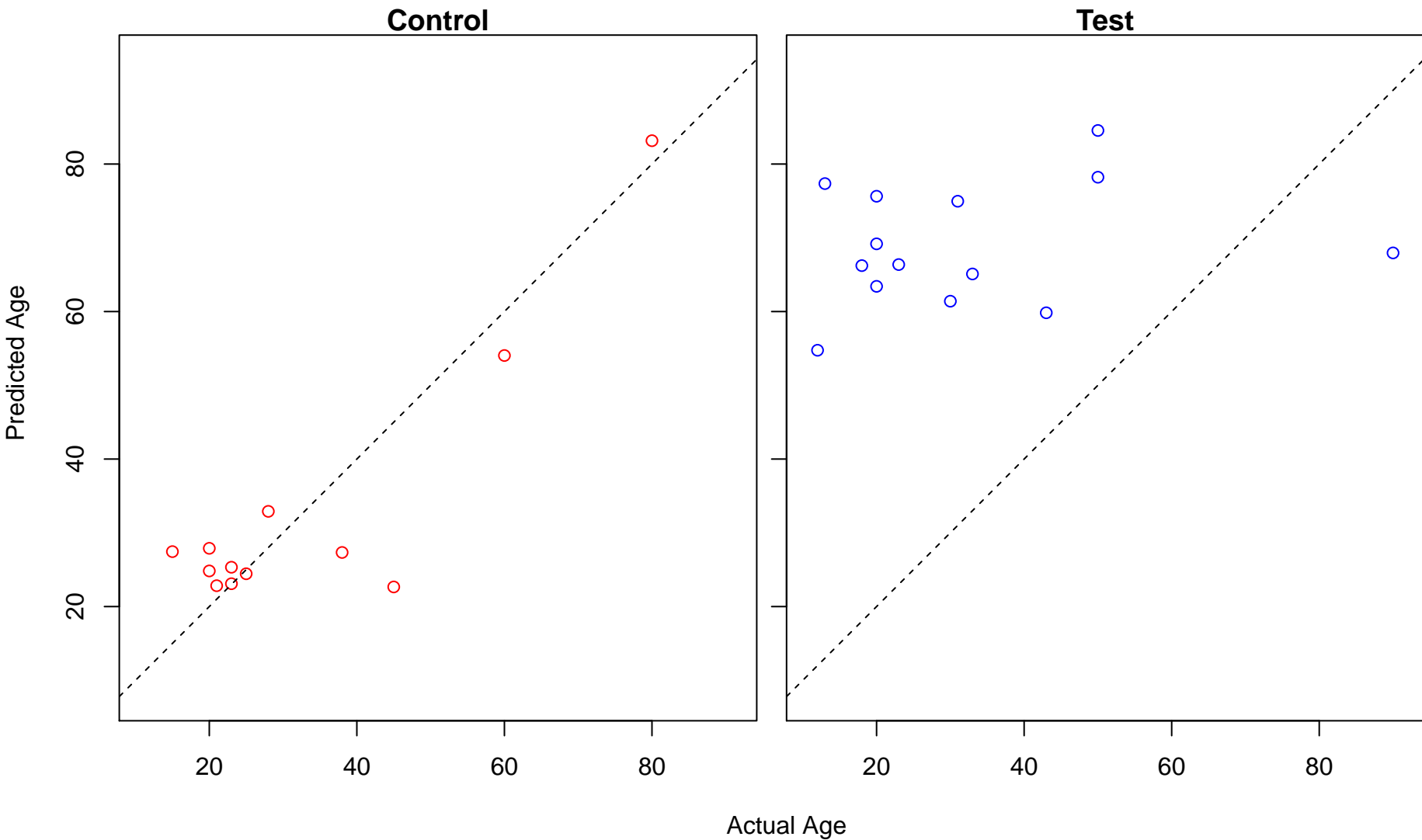
response to prostaglandin (Score: 8.952376)



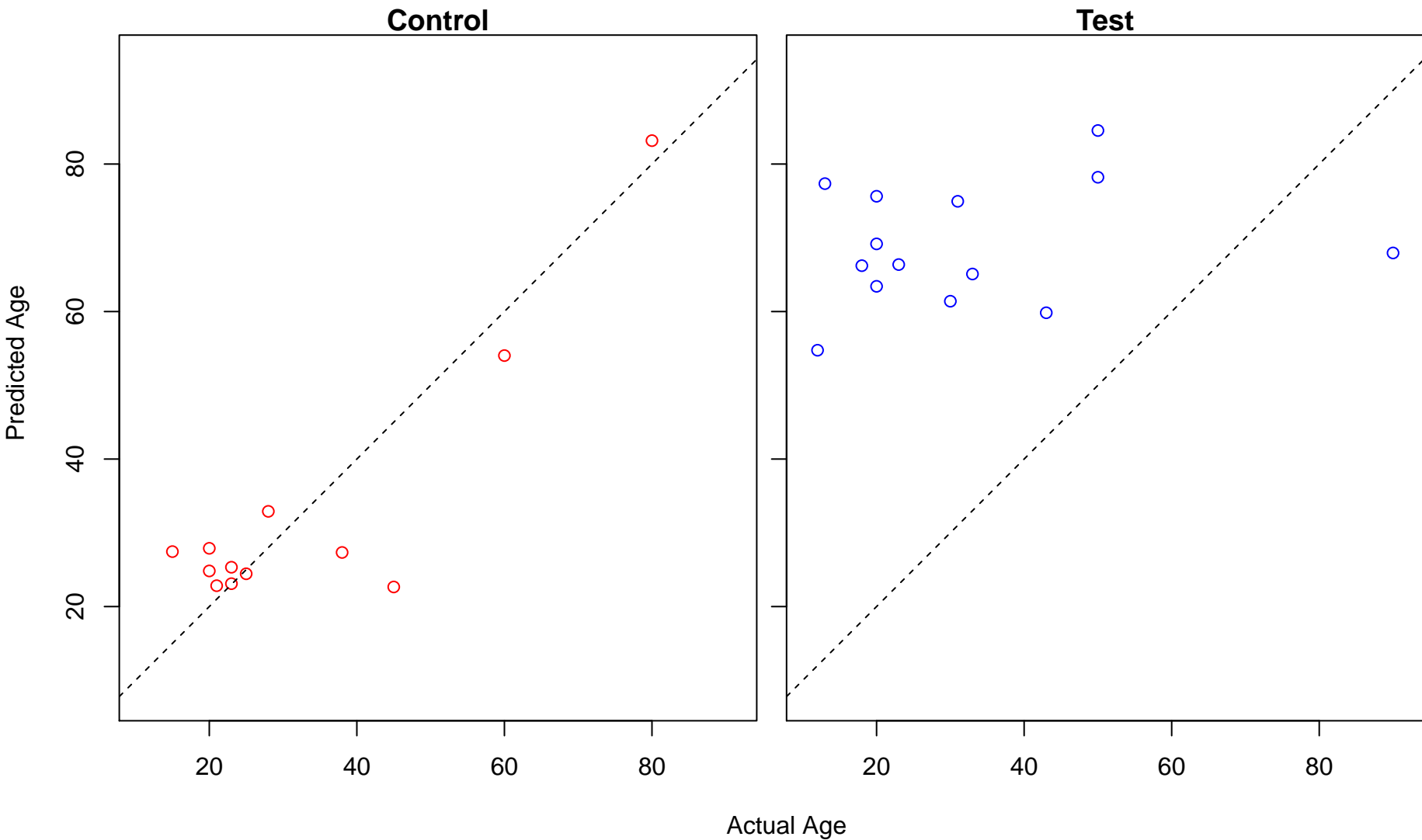
cellular response to acid chemical (Score: 8.951737)



cellular response to fatty acid (Score: 8.949708)

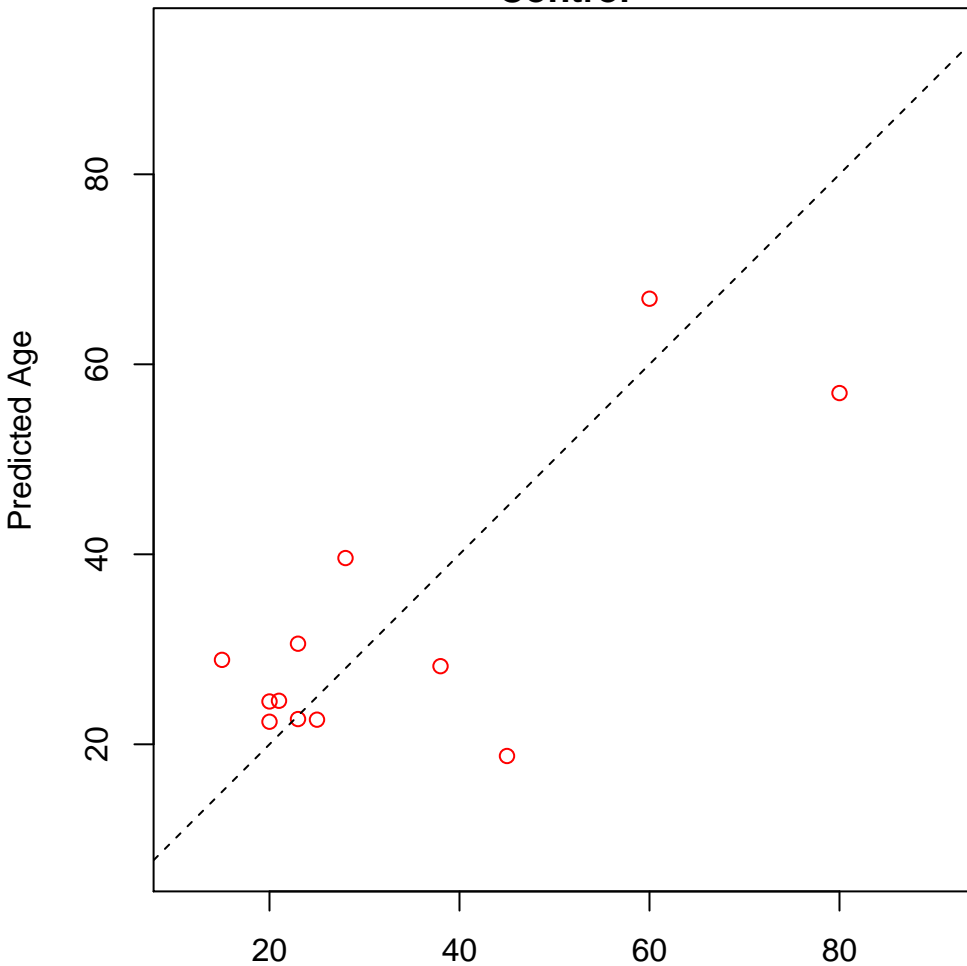


response to fatty acid (Score: 8.945988)

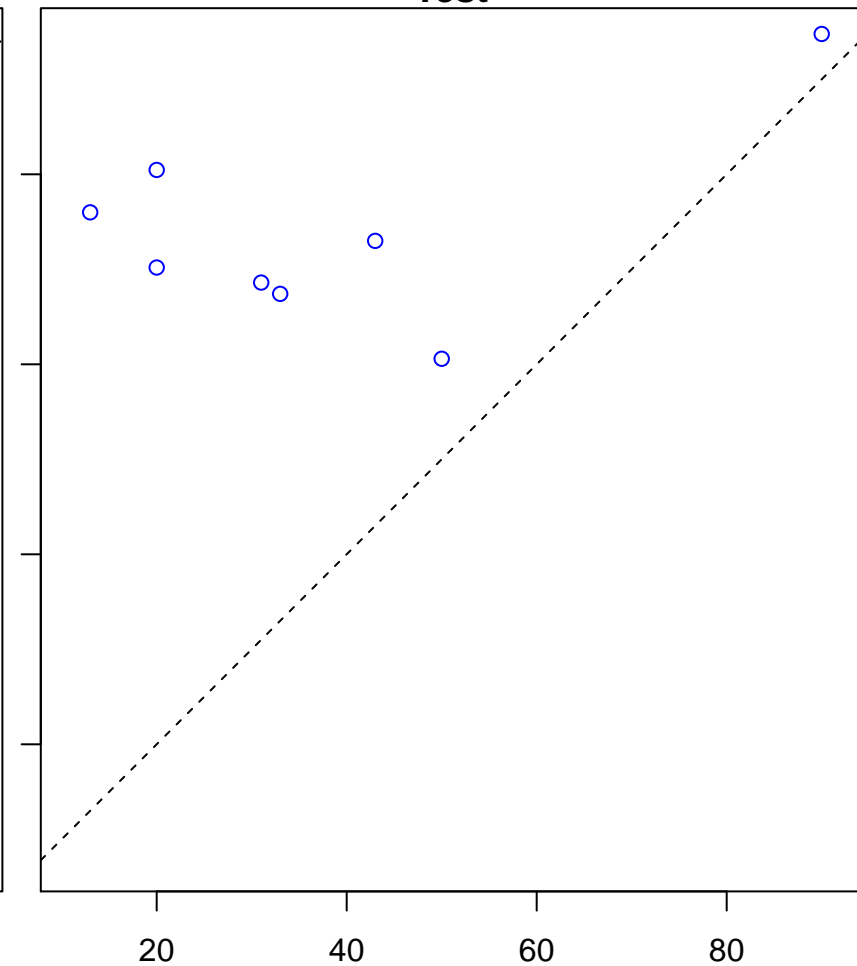


regulation of male gonad development (Score: 8.943693)

Control

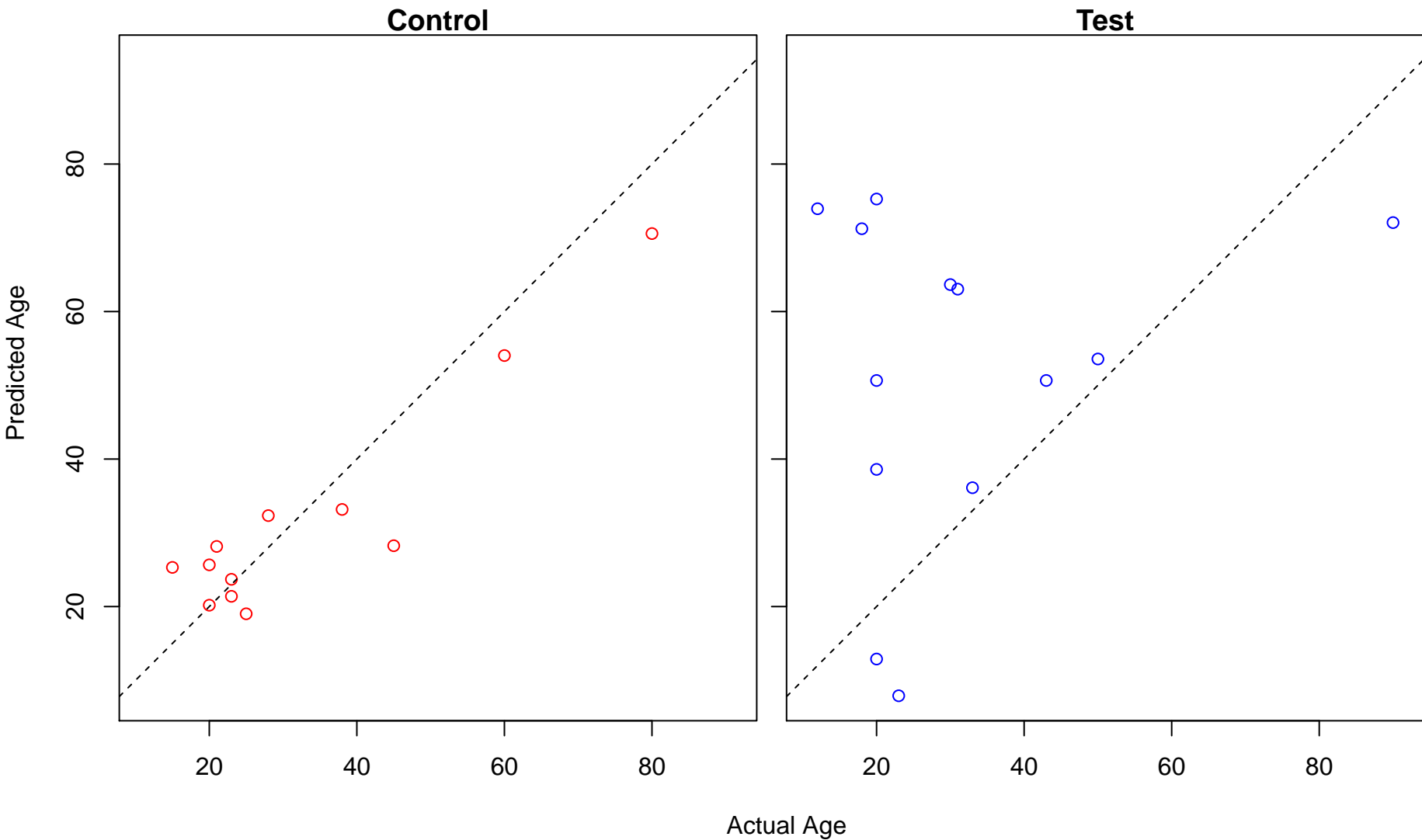


Test

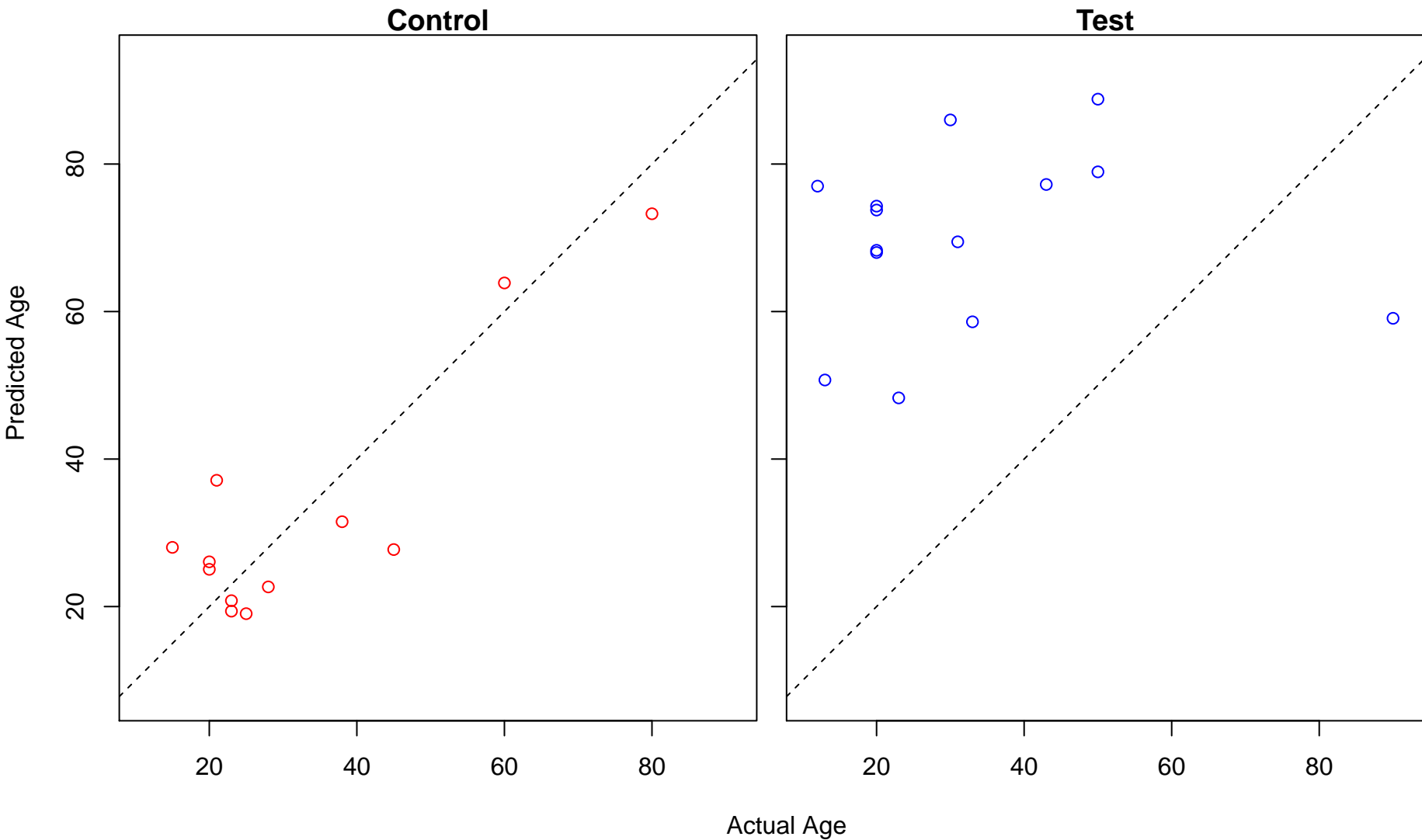


Actual Age

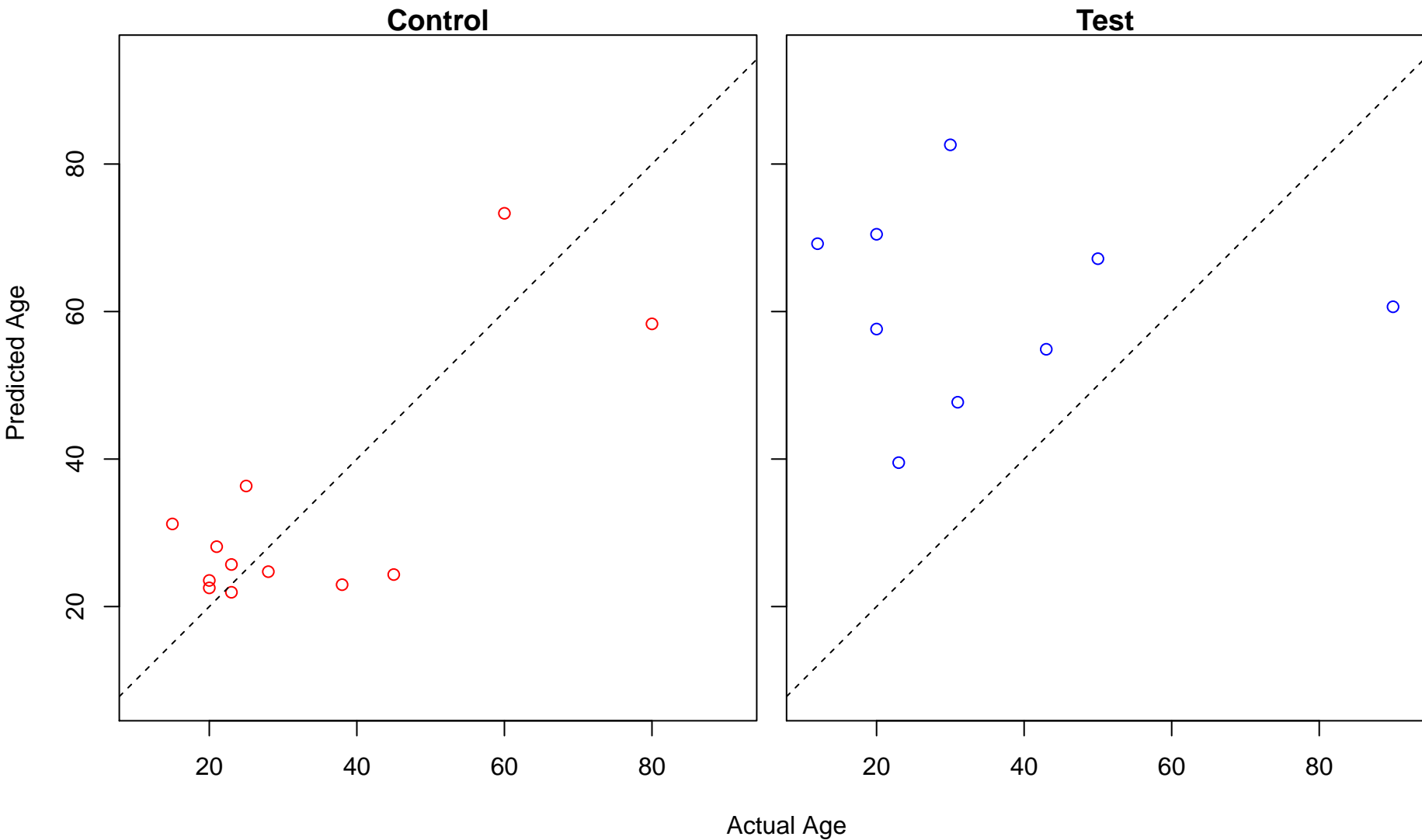
protein acetylation (Score: 8.938791)



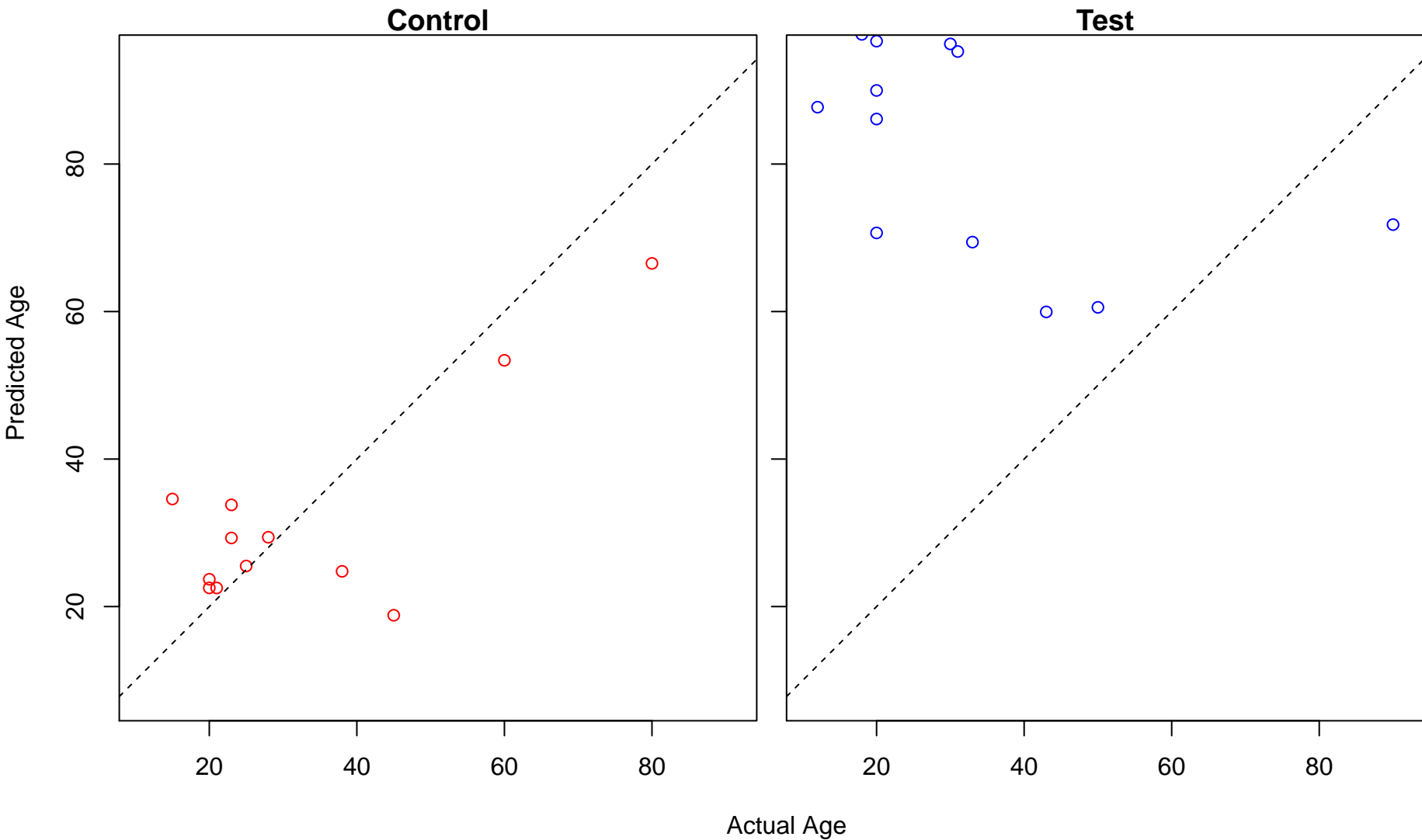
positive regulation of angiogenesis (Score: 8.931768)



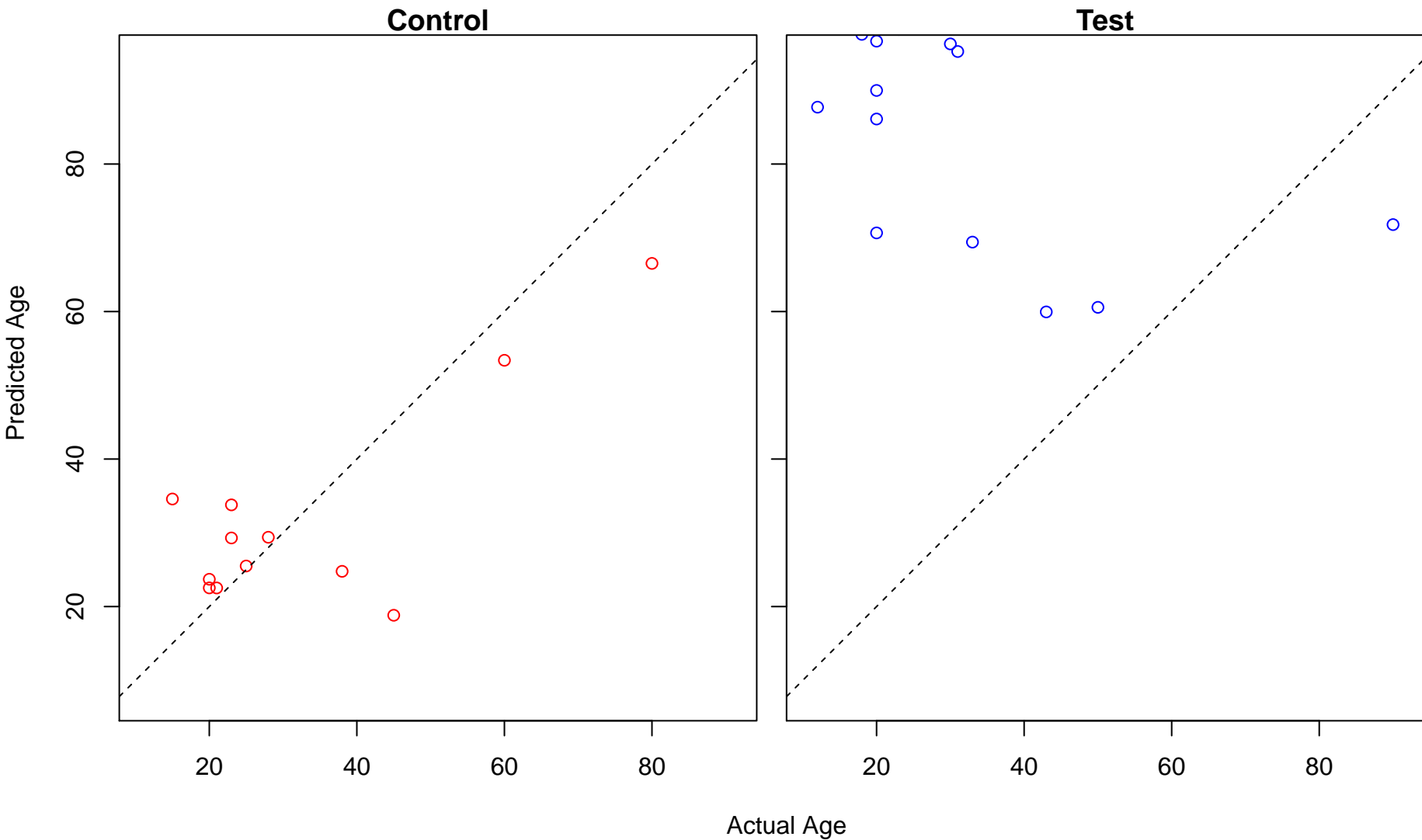
cellular response to acidic pH (Score: 8.927986)



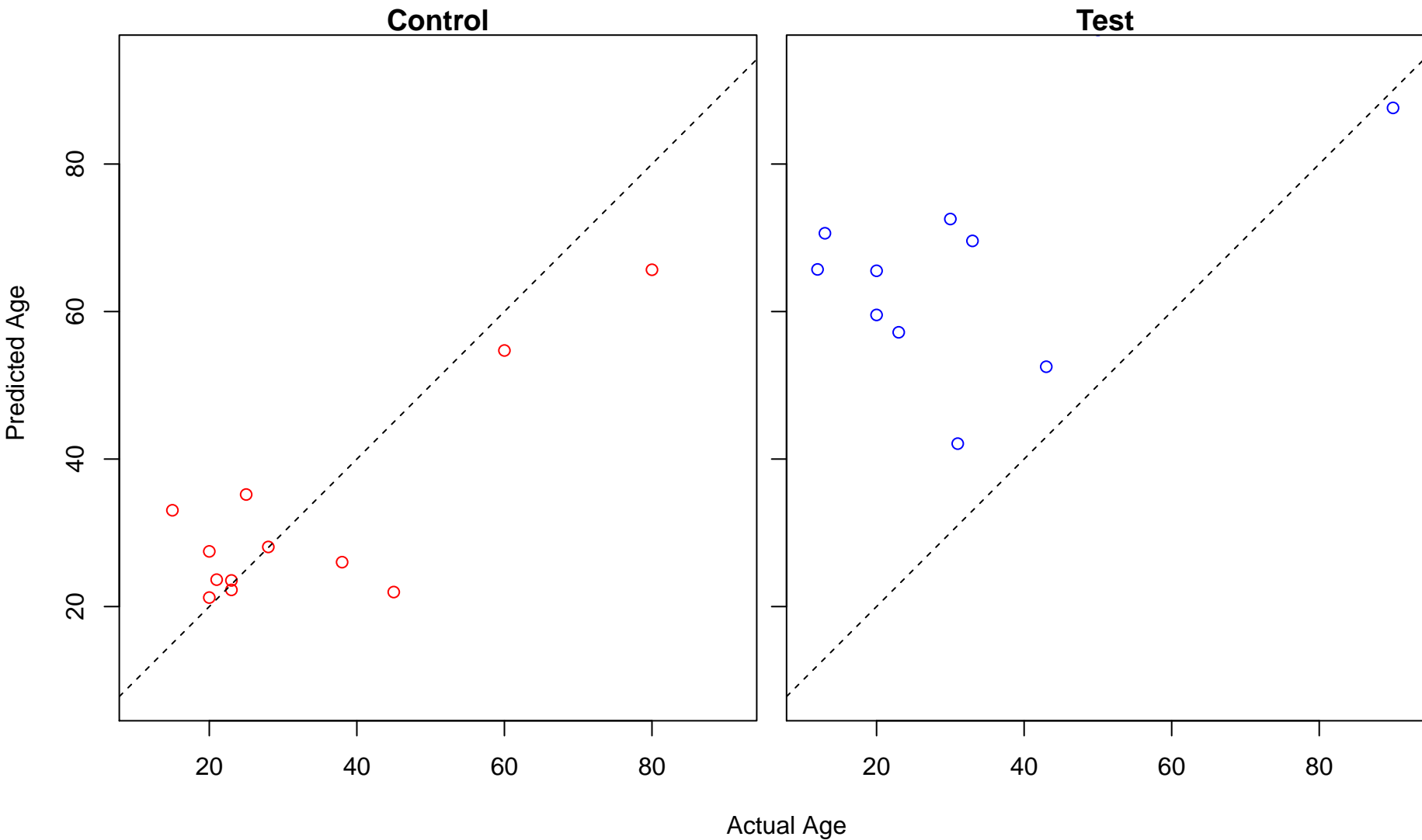
metanephric tubule morphogenesis (Score: 8.927817)



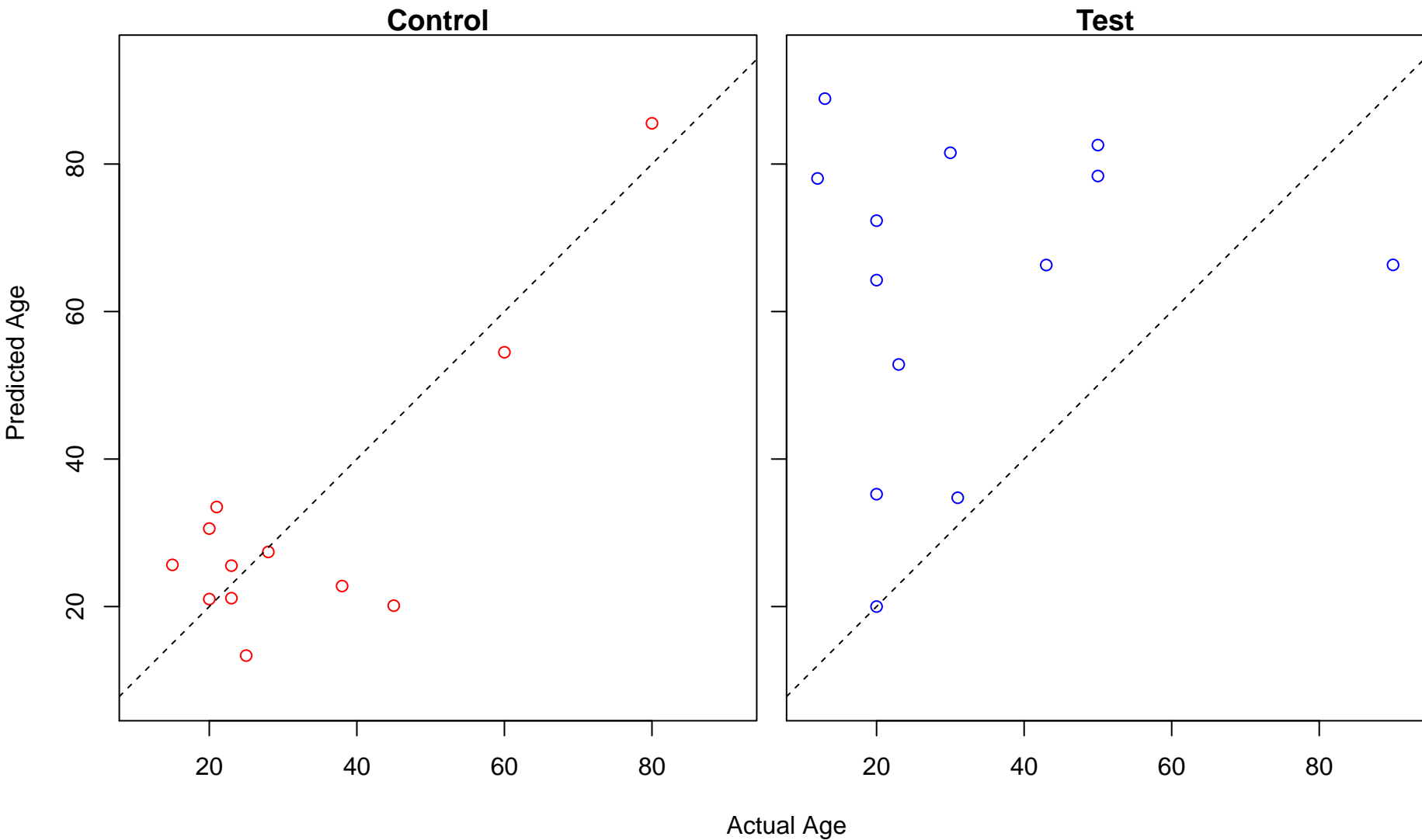
metanephric nephron tubule morphogenesis (Score: 8.927817)



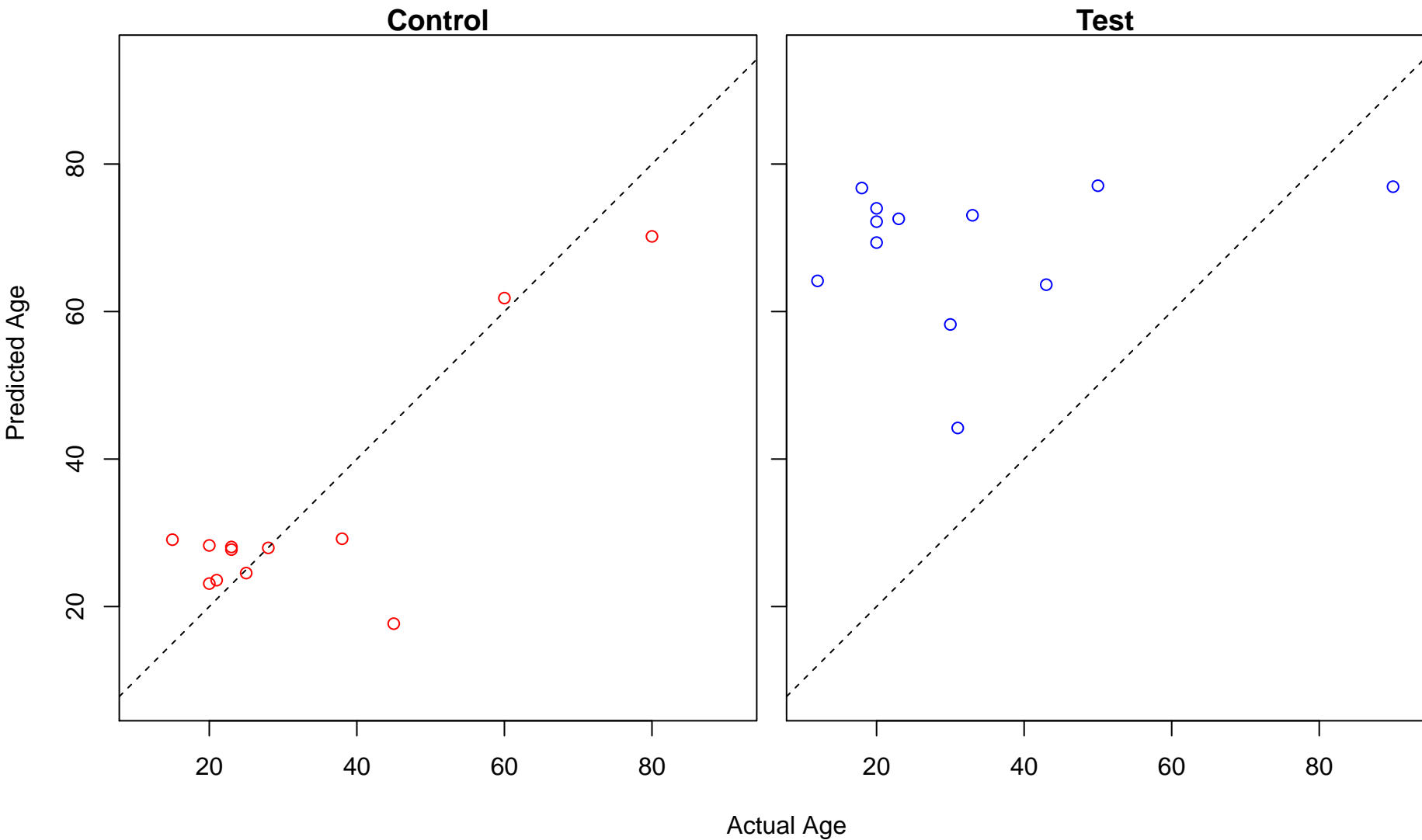
aspartate metabolic process (Score: 8.927148)



multivesicular body organization (Score: 8.922831)

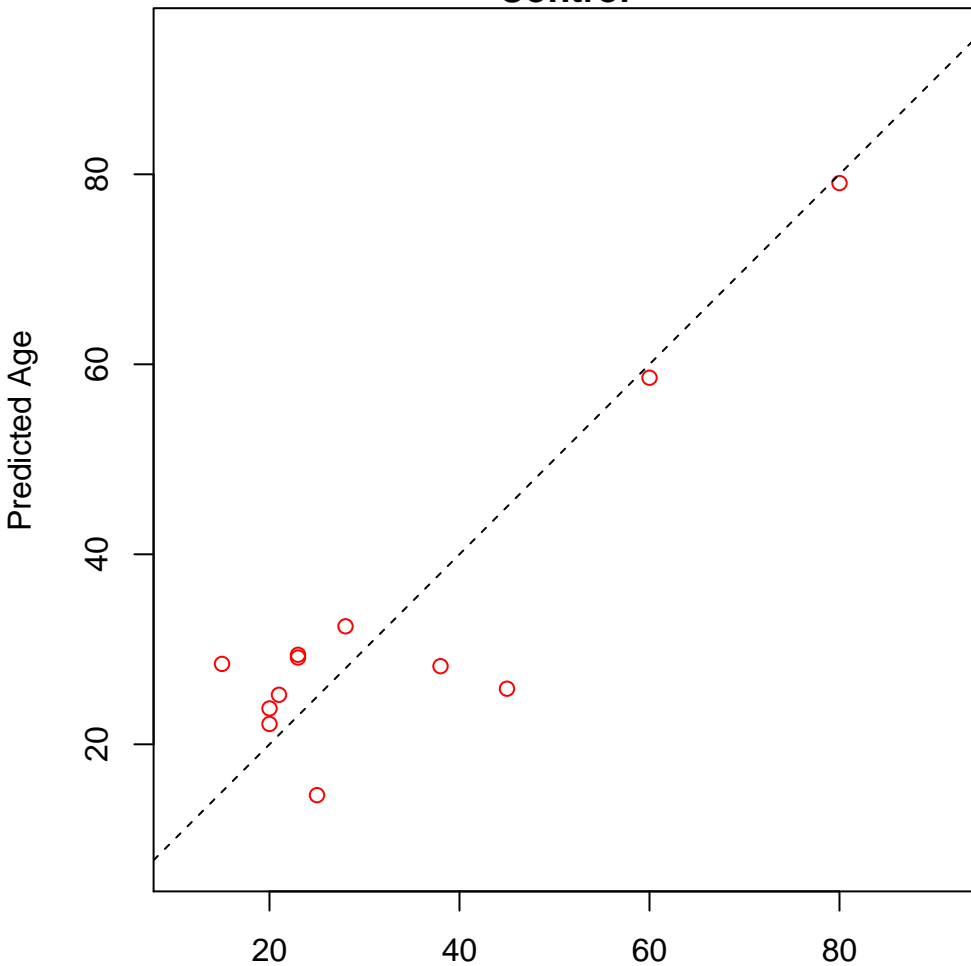


embryo implantation (Score: 8.919045)

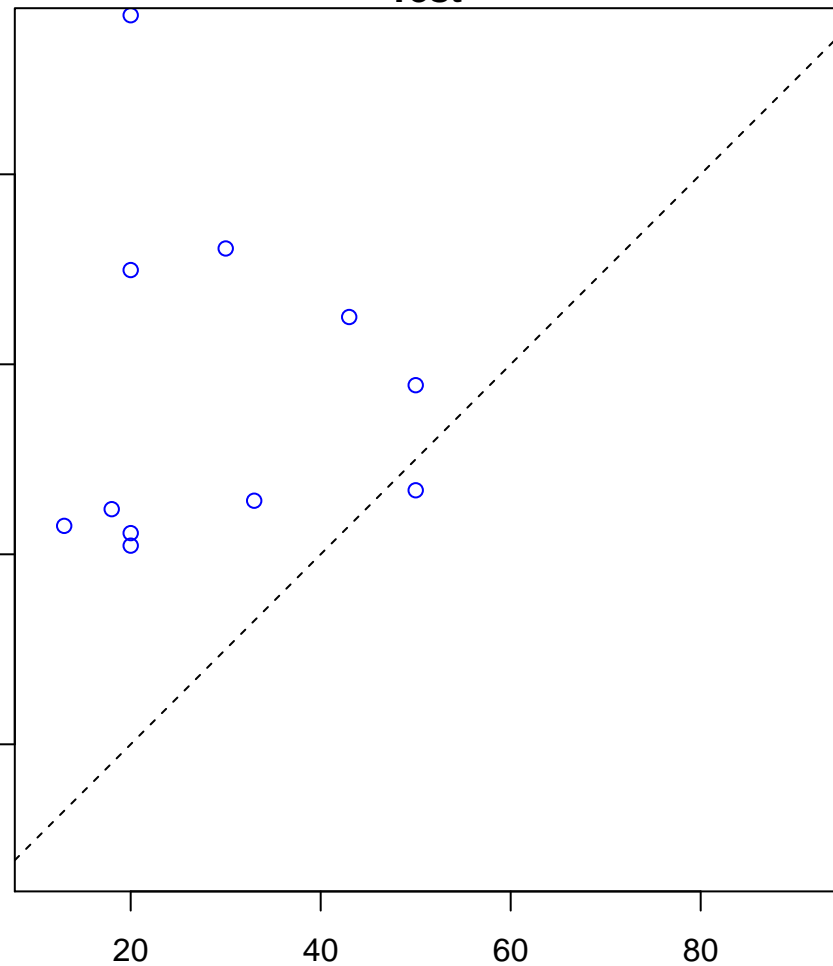


chondroitin sulfate biosynthetic process (Score: 8.918108)

Control

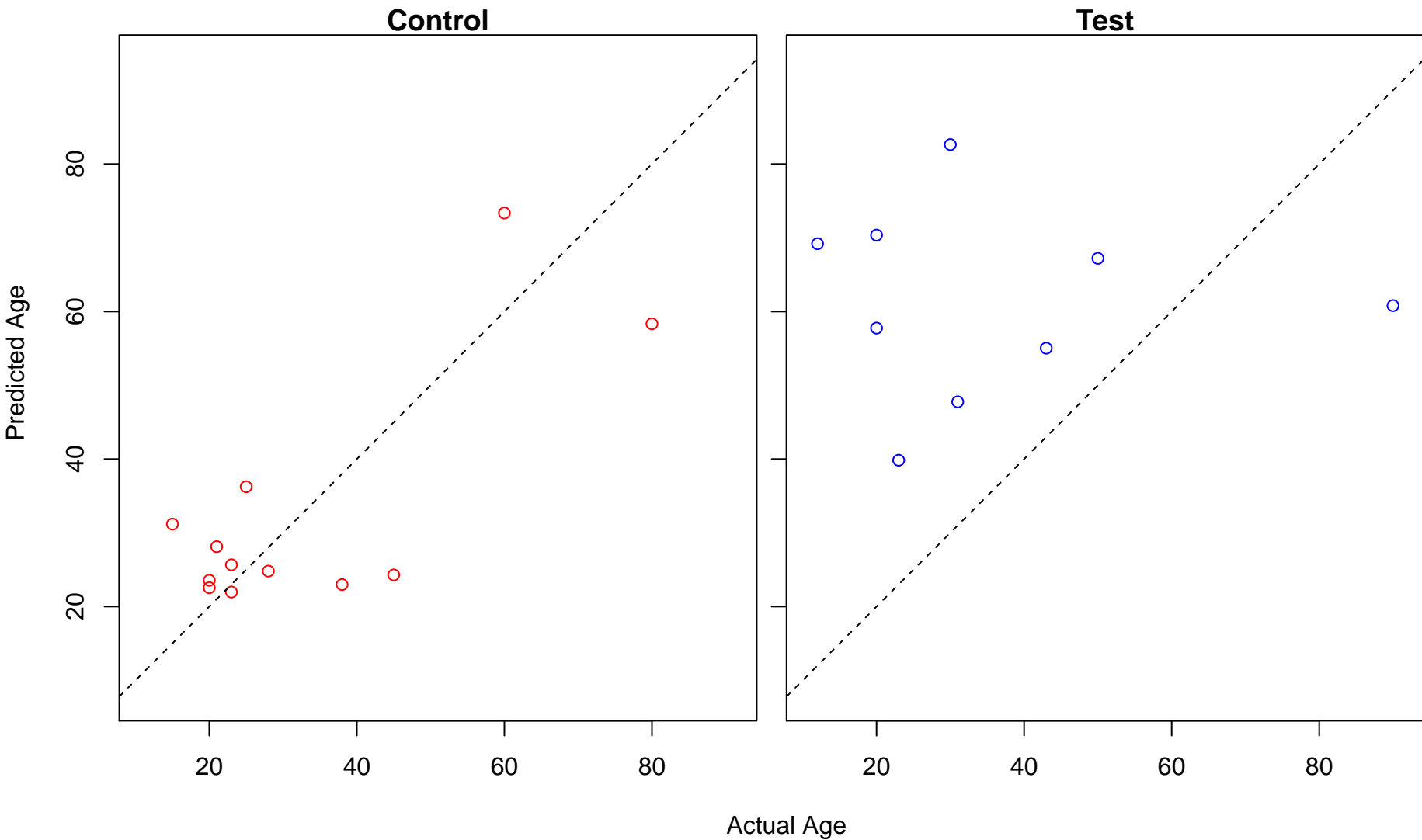


Test



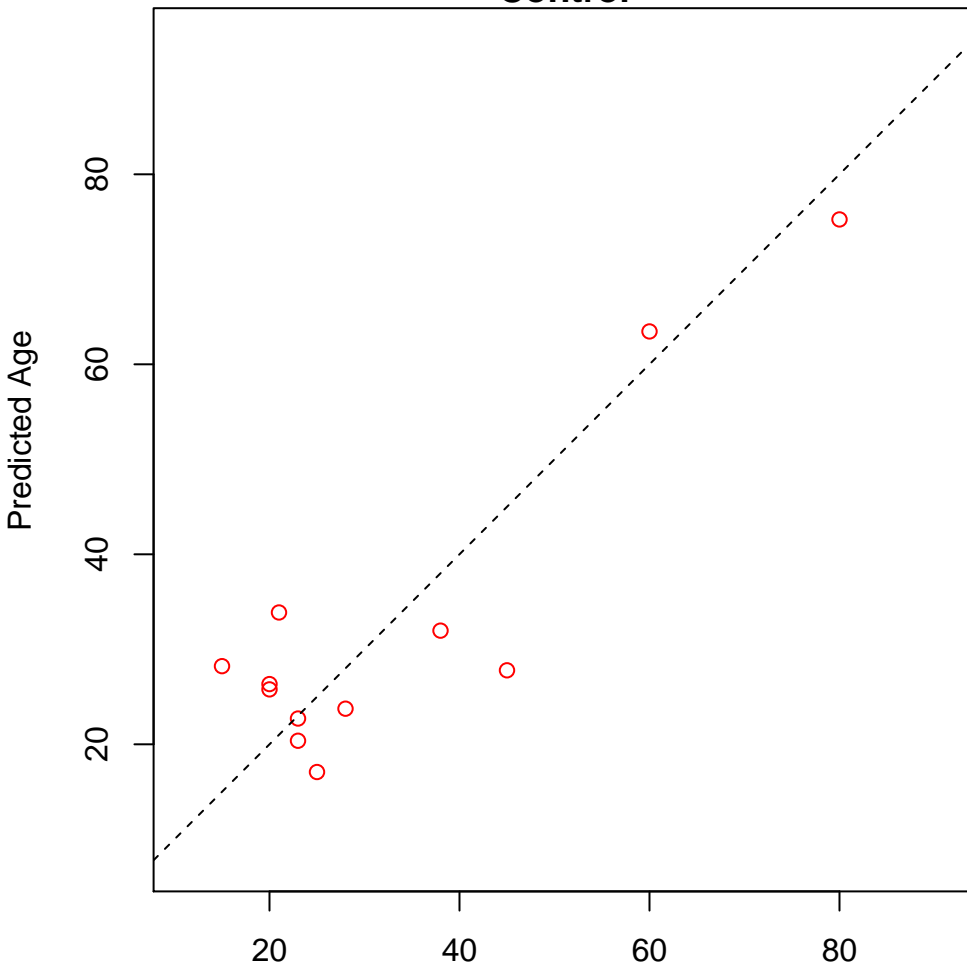
Actual Age

cellular response to pH (Score: 8.916926)

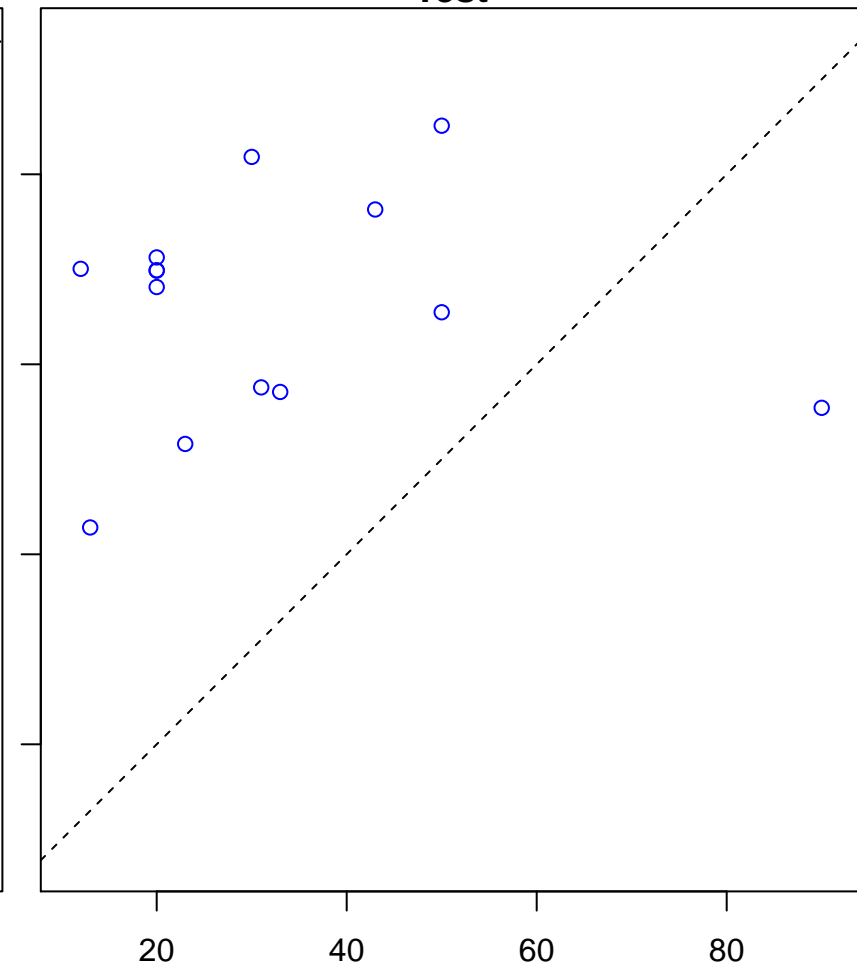


long-chain fatty acid metabolic process (Score: 8.916128)

Control

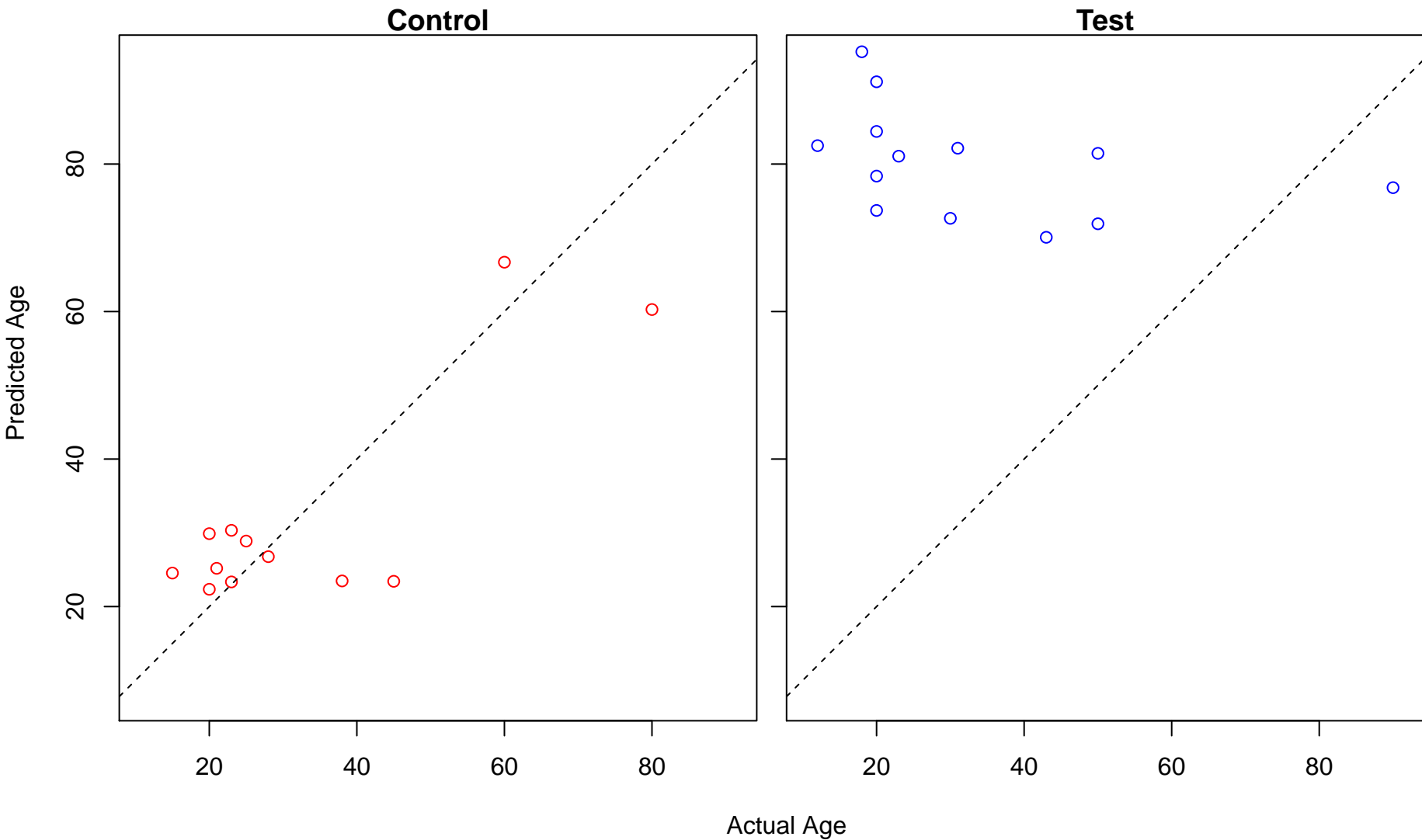


Test



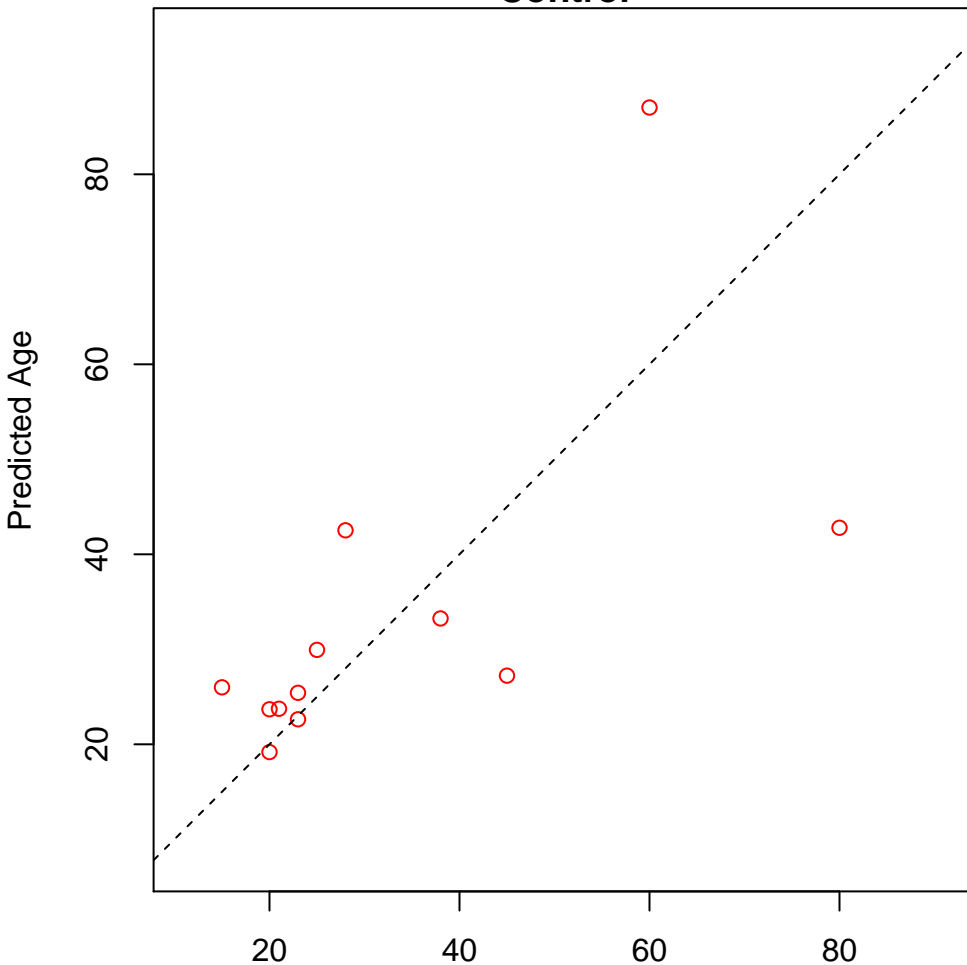
Actual Age

benzene-containing compound metabolic process (Score: 8.915713)

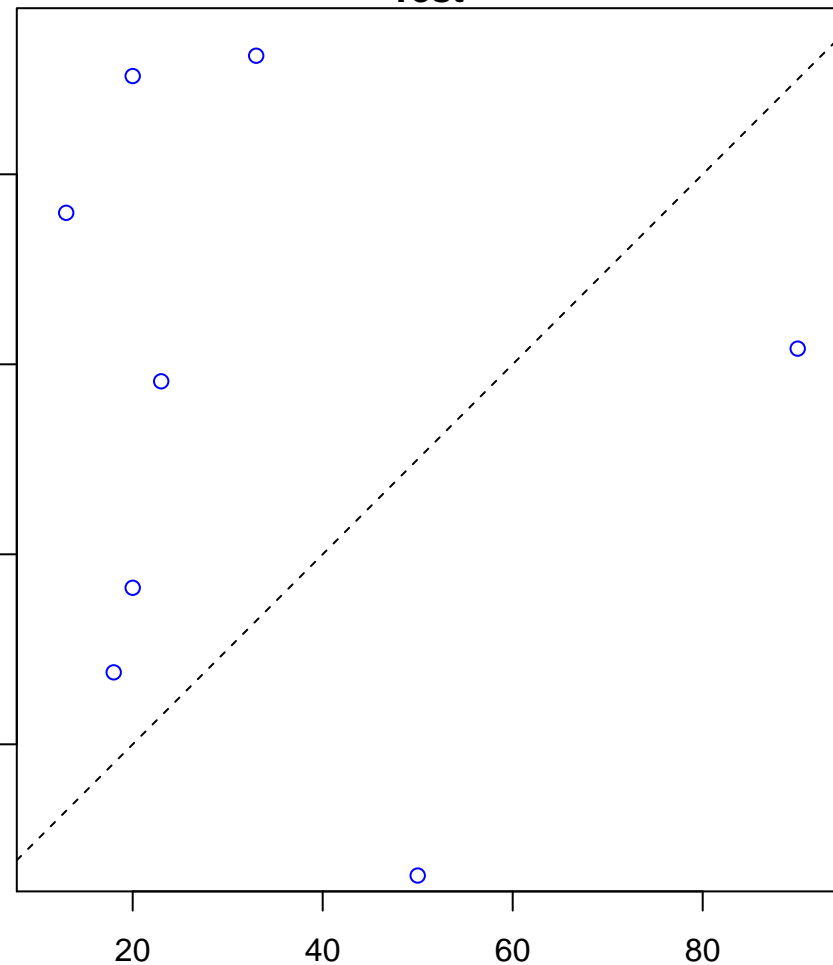


myeloid leukocyte mediated immunity (Score: 8.913189)

Control

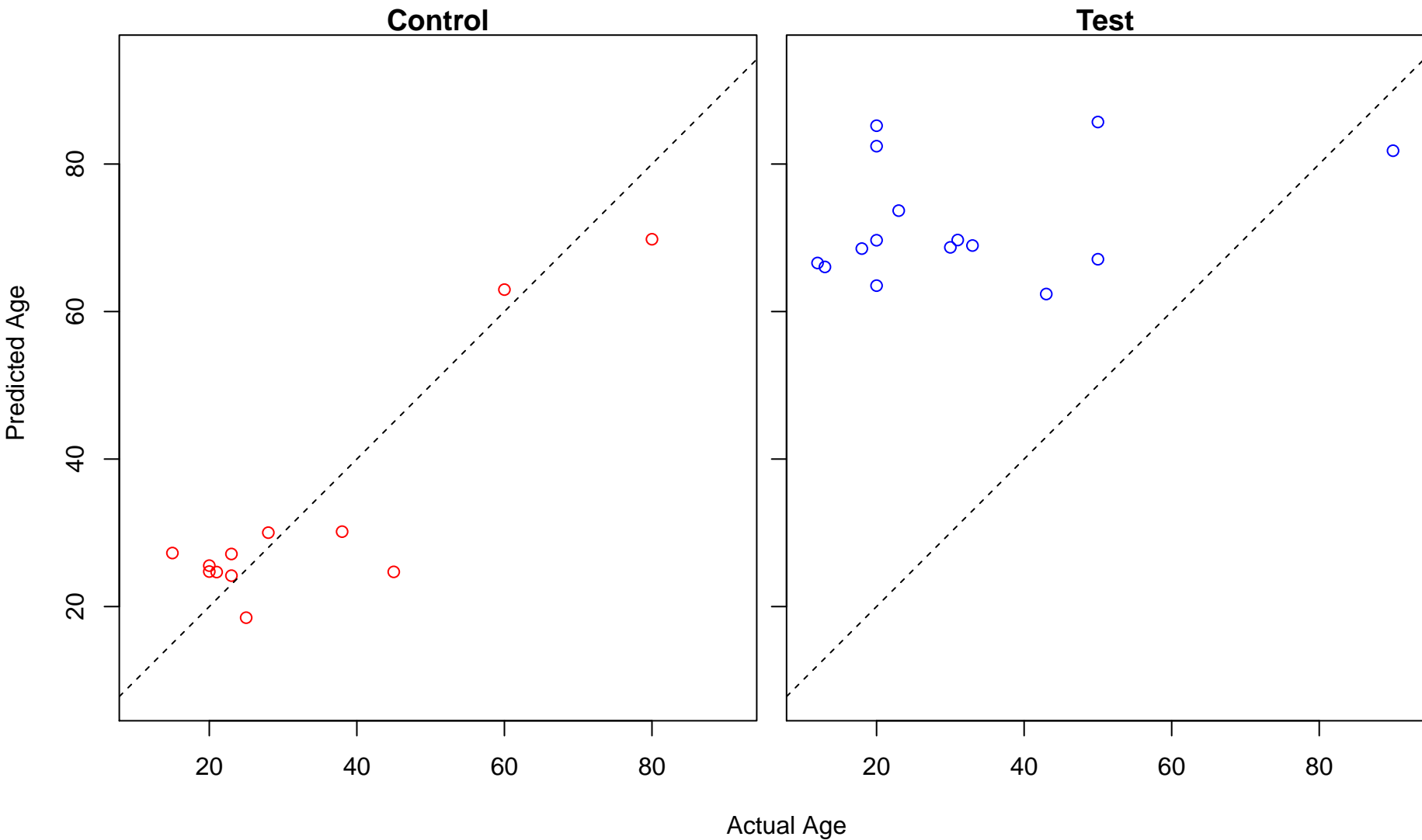


Test

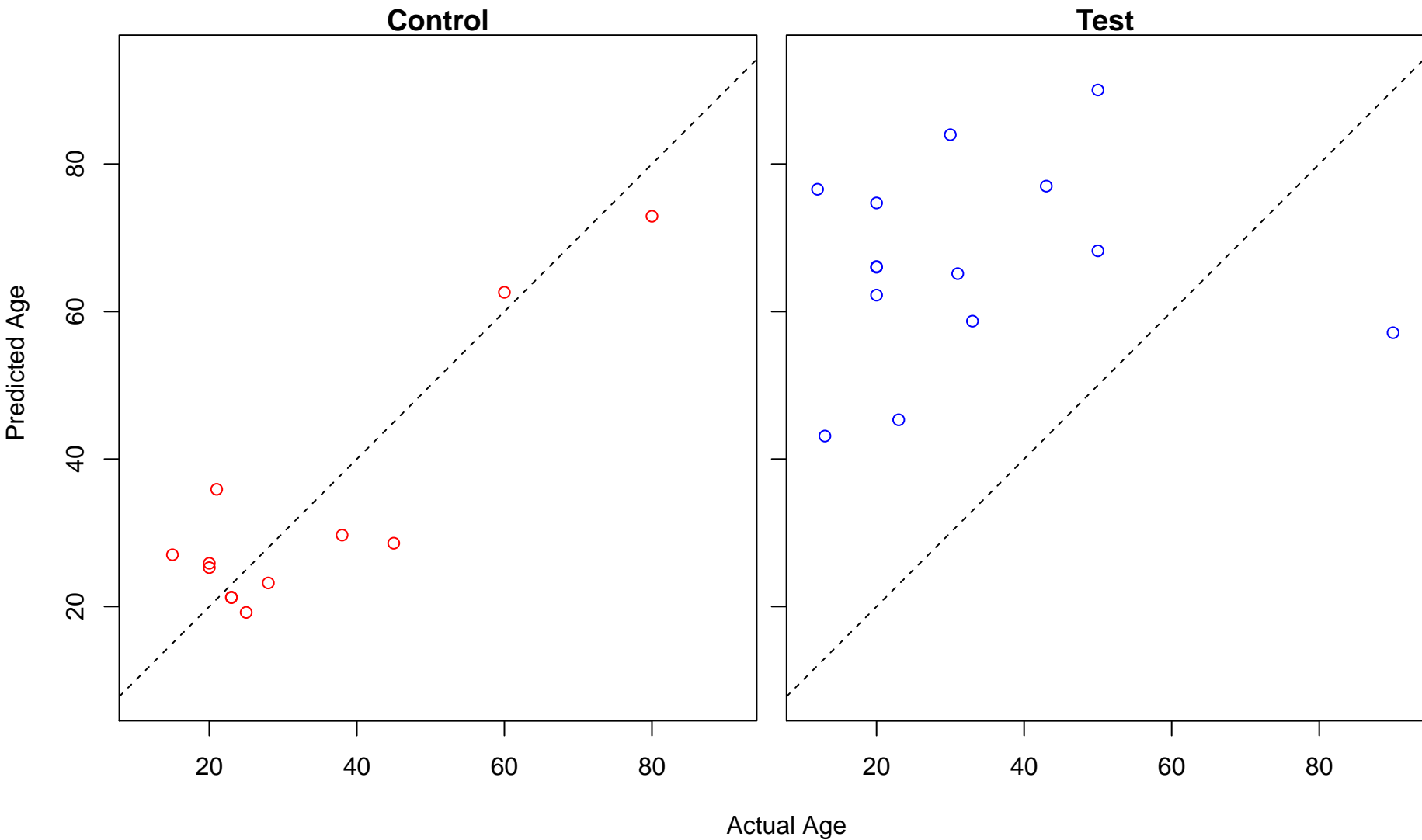


Actual Age

gland development (Score: 8.911363)

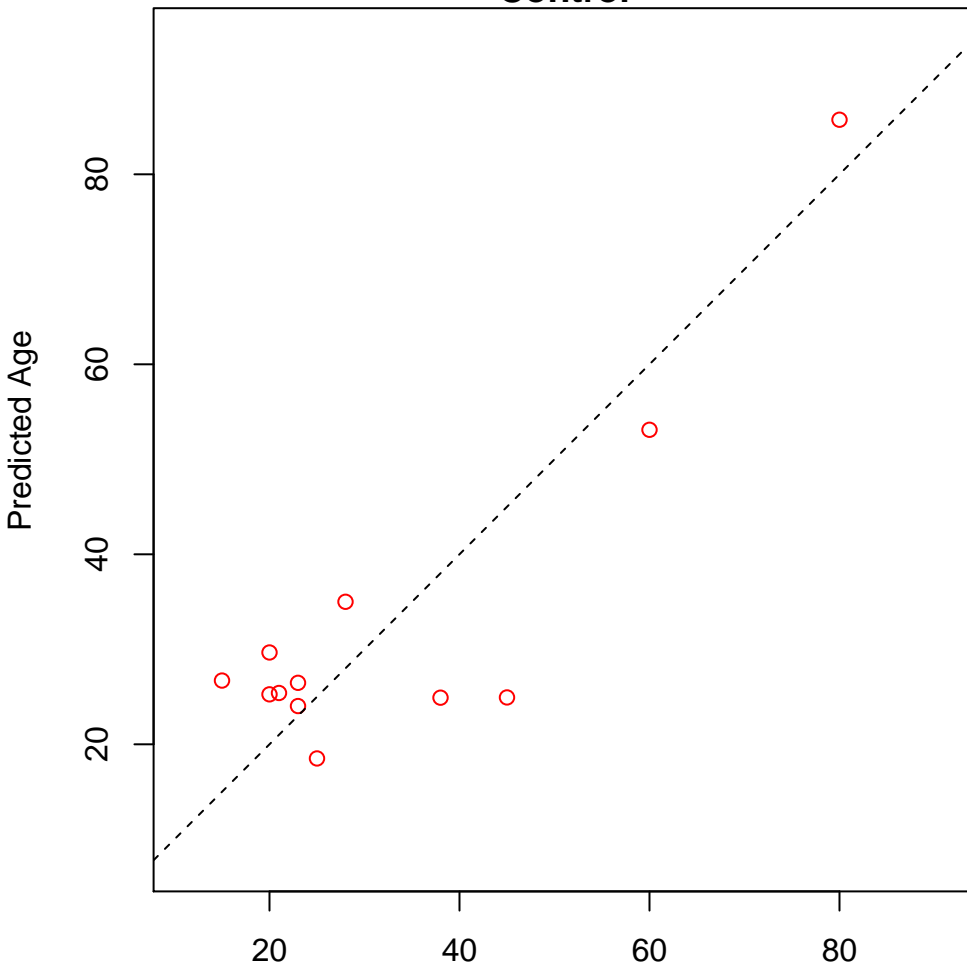


negative regulation of sequence-specific DNA binding transcription factor activity (Score: 8.90951)

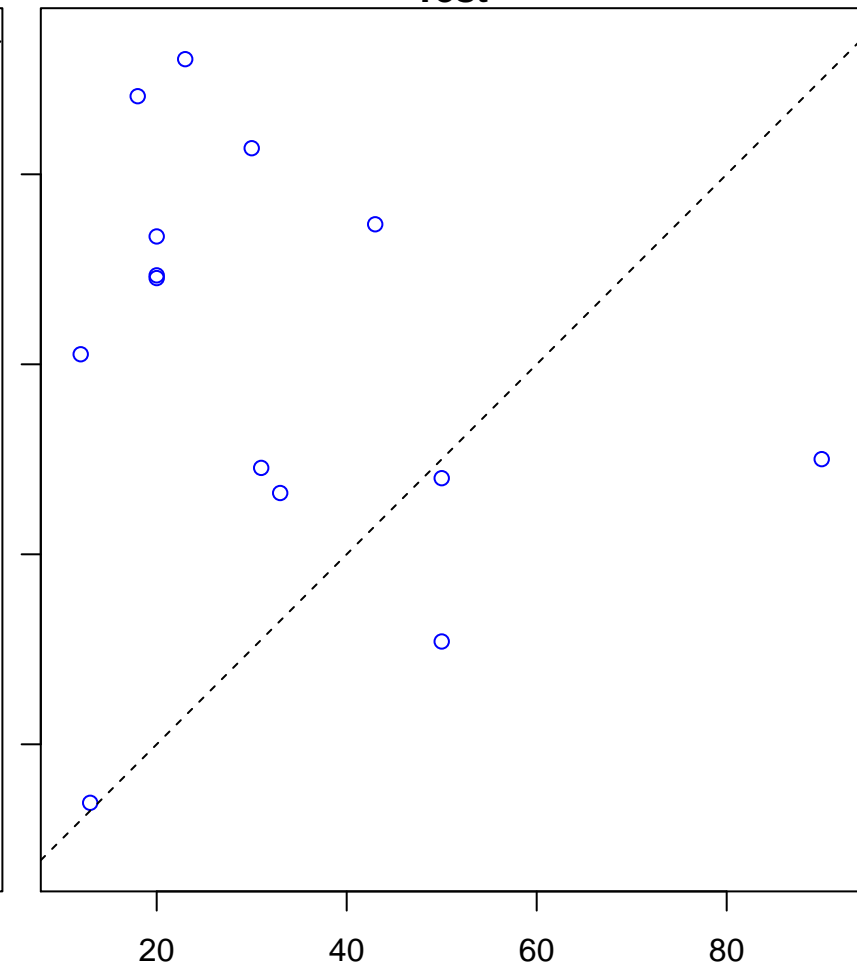


cytoplasmic sequestering of protein (Score: 8.907572)

Control

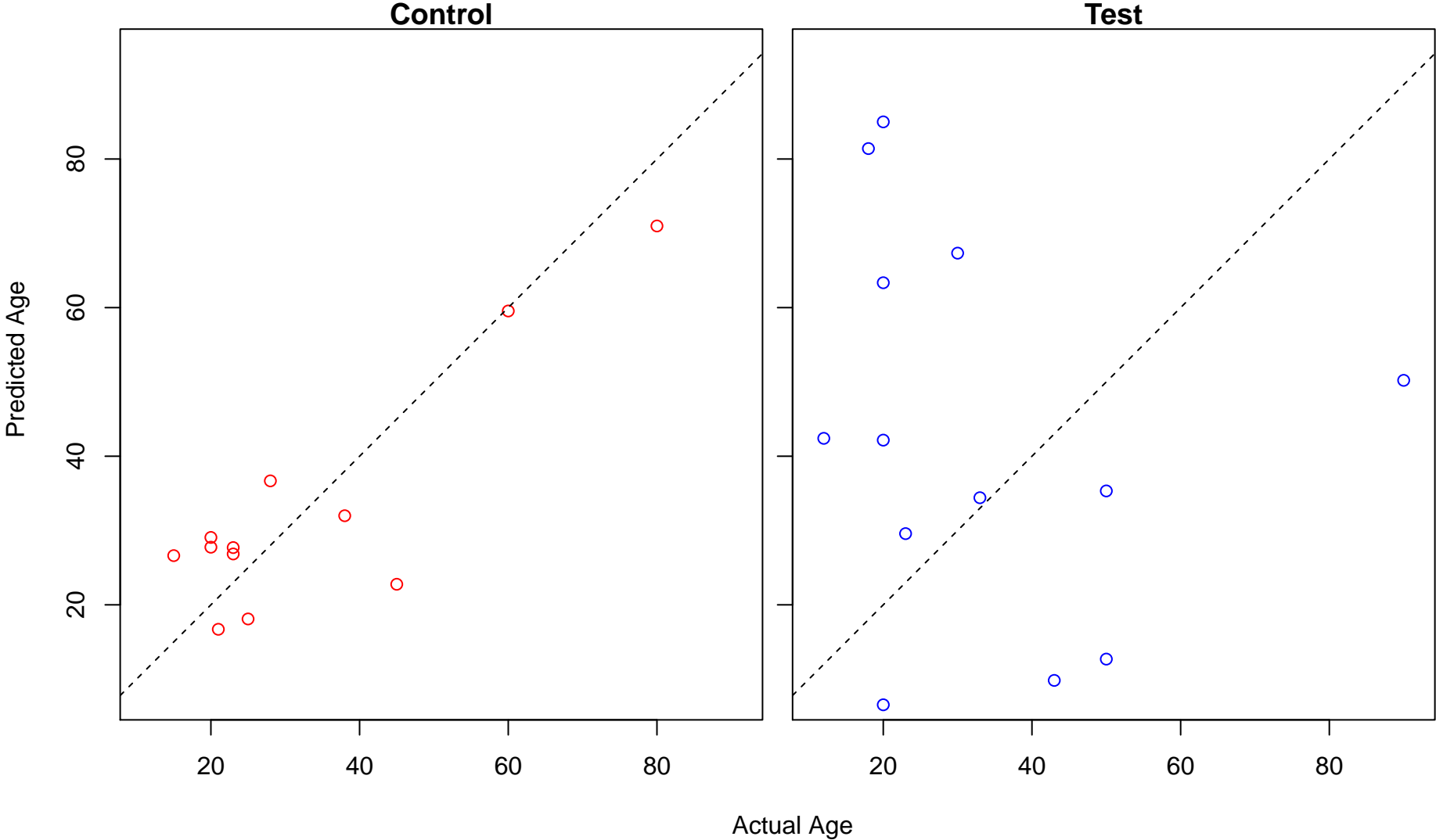


Test

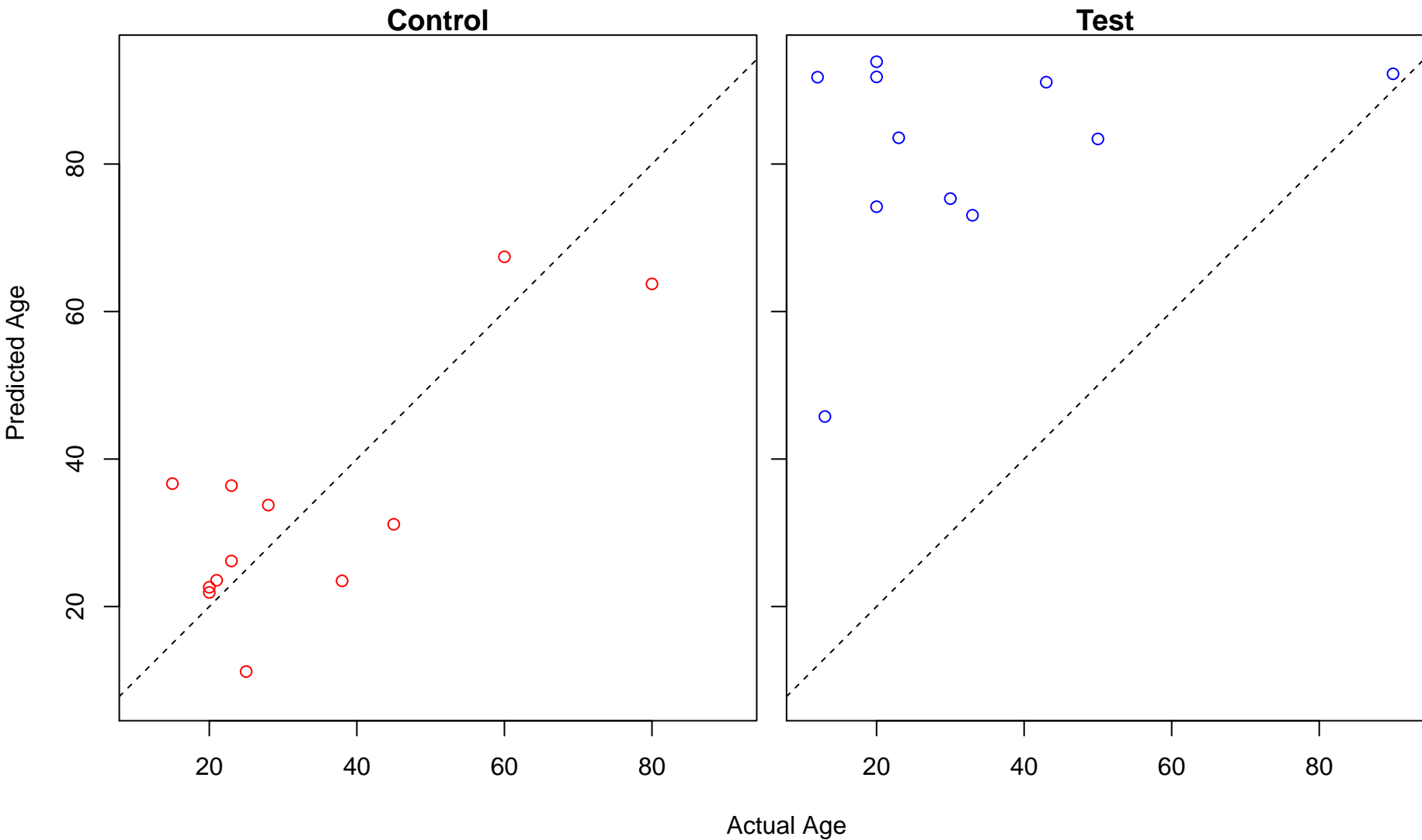


Actual Age

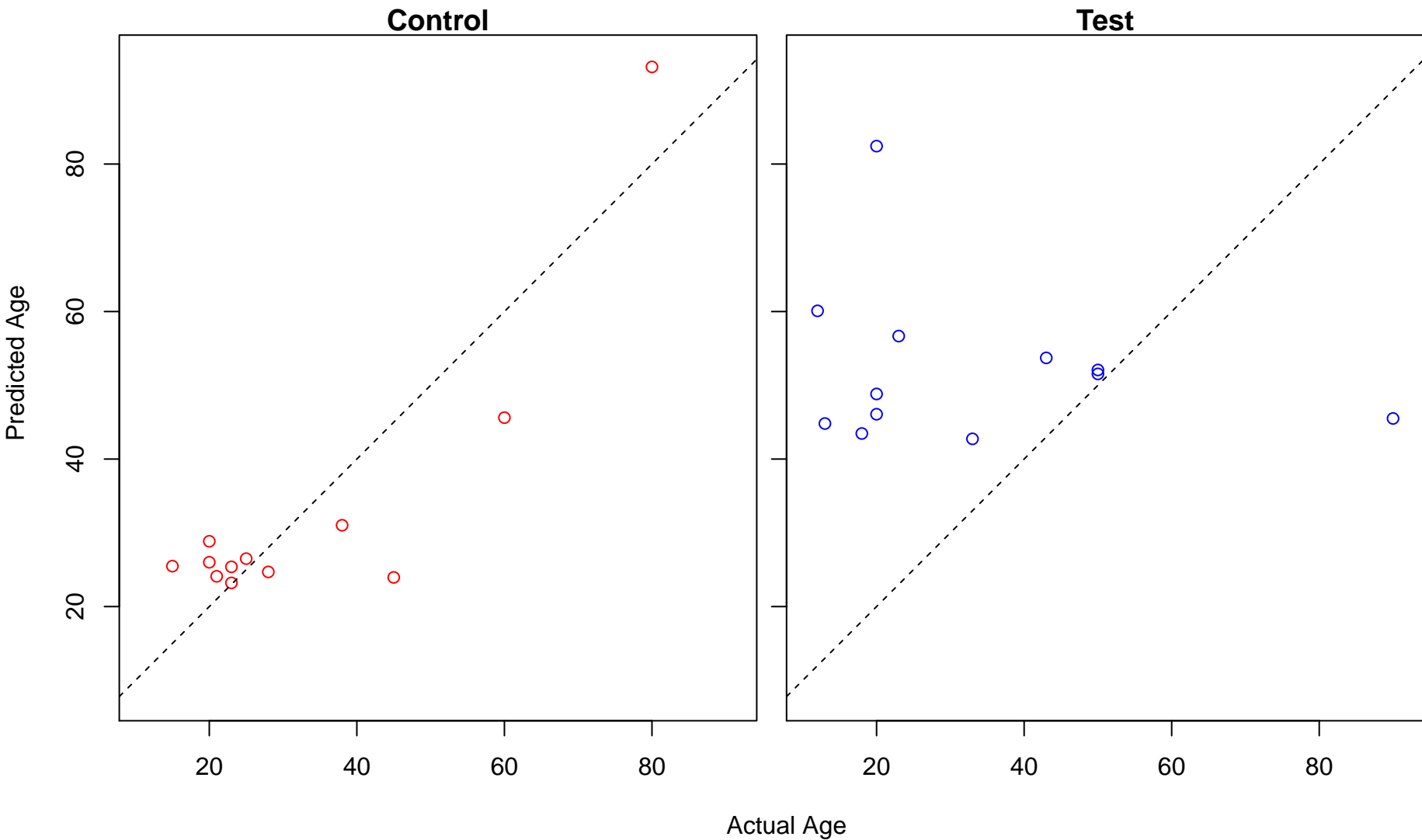
branched-chain amino acid metabolic process (Score: 8.901492)



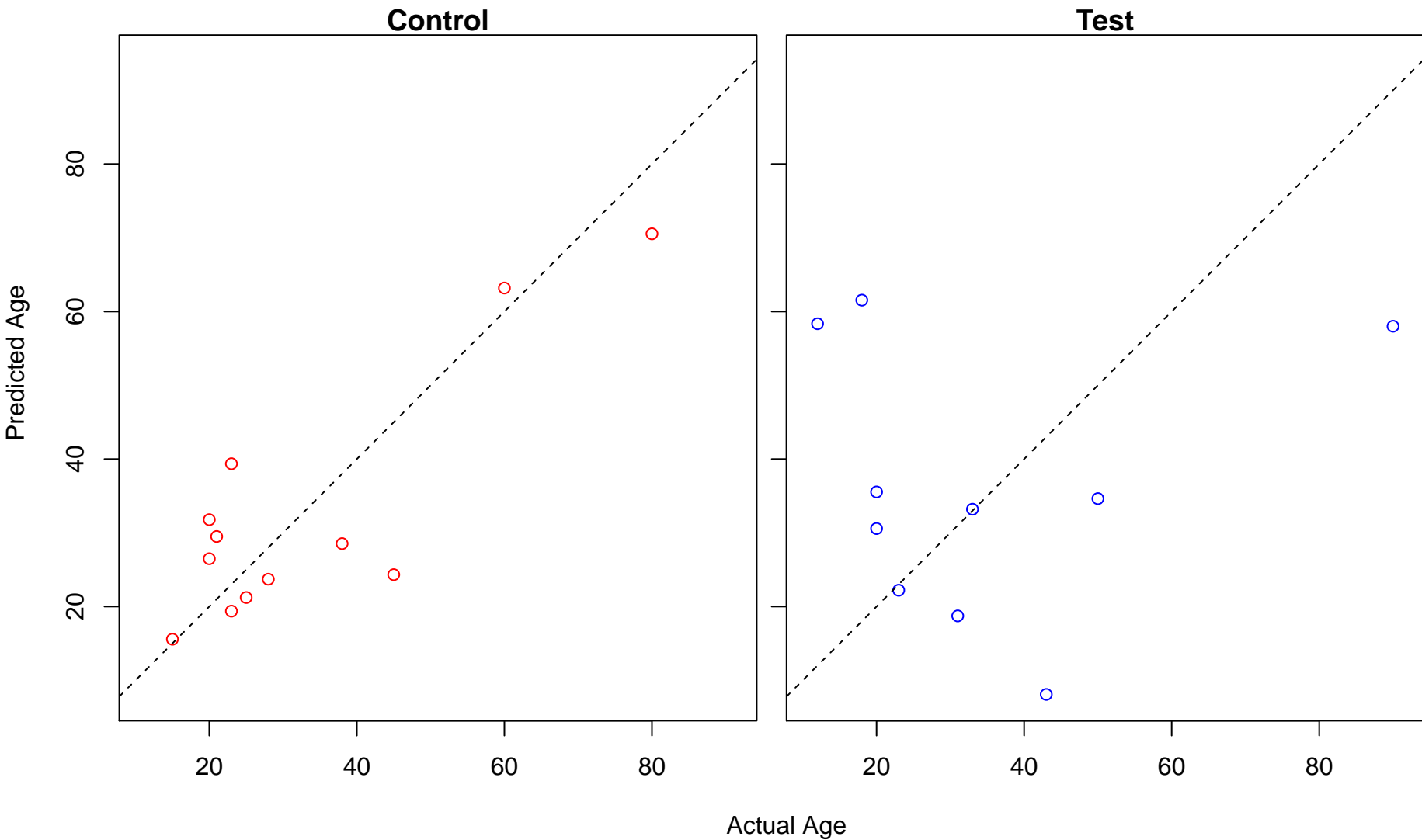
regulation of triglyceride catabolic process (Score: 8.900924)



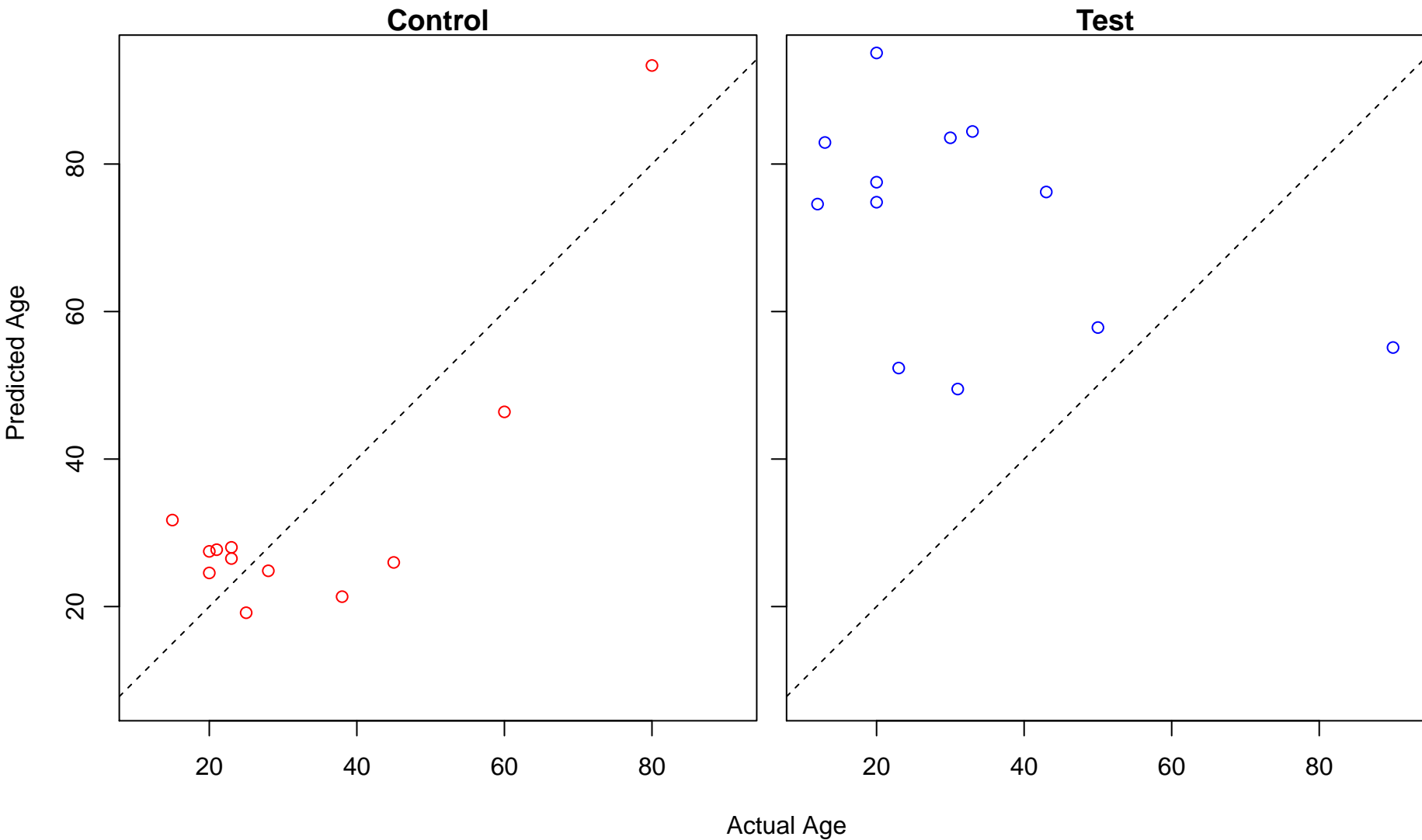
regulation of sarcomere organization (Score: 8.896096)



deoxyribonucleoside monophosphate biosynthetic process (Score: 8.890684)

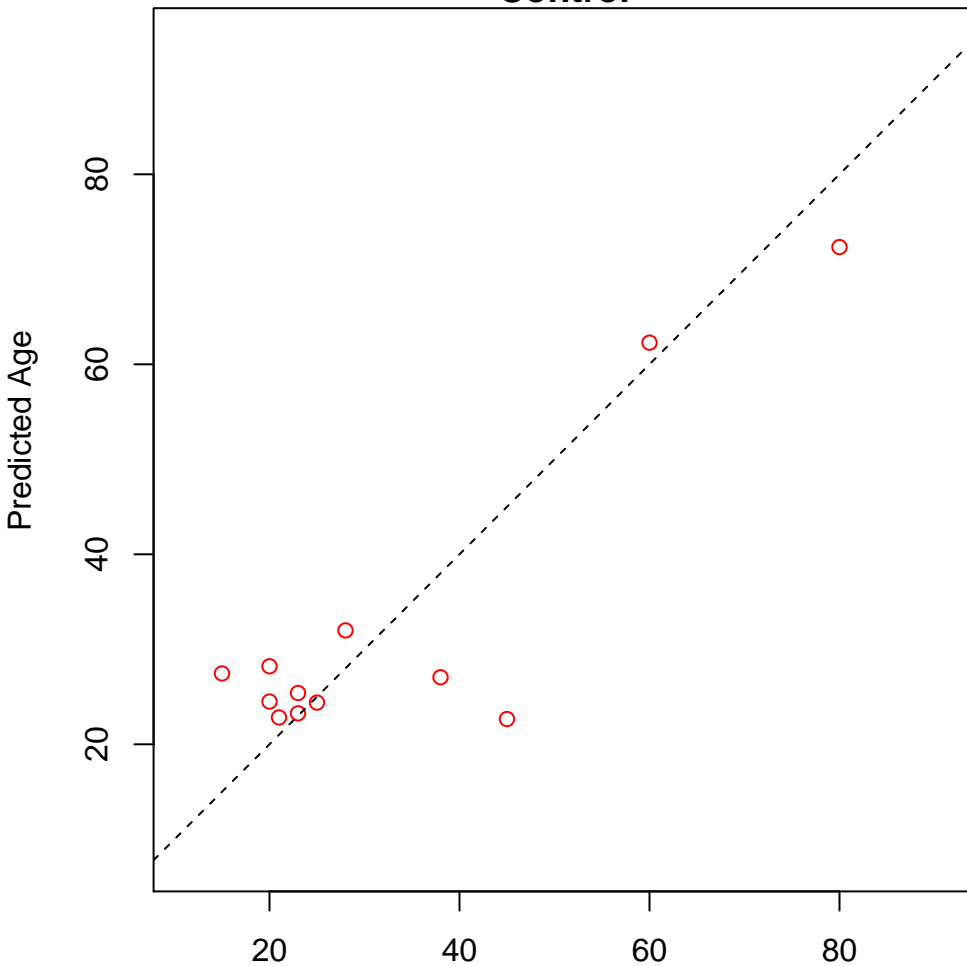


negative regulation of double-strand break repair (Score: 8.890556)

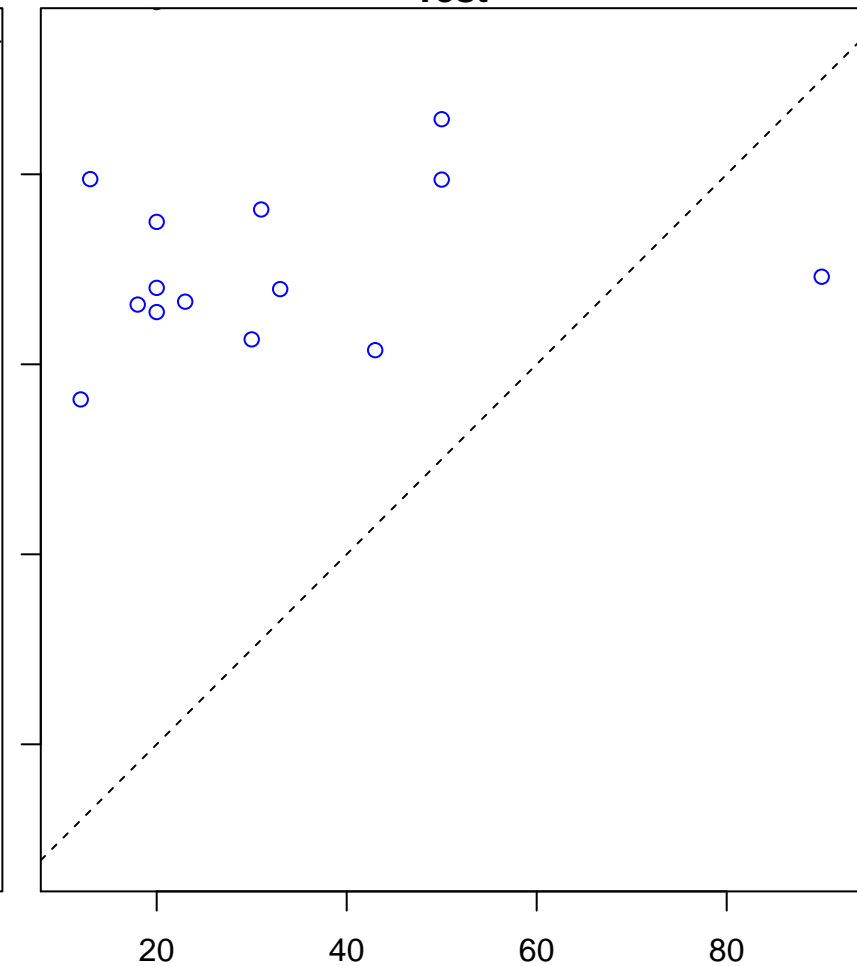


sensory perception of chemical stimulus (Score: 8.882757)

Control

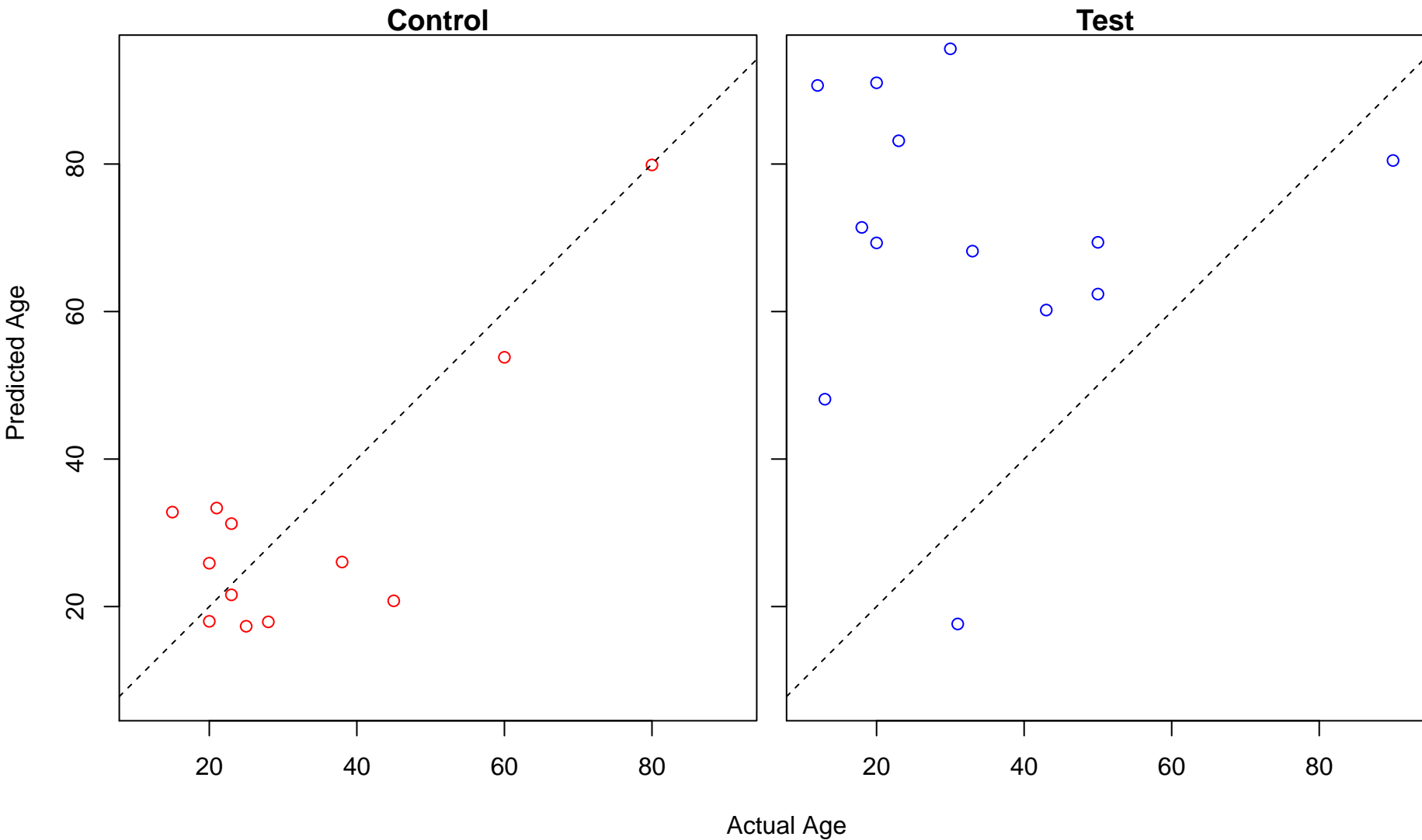


Test

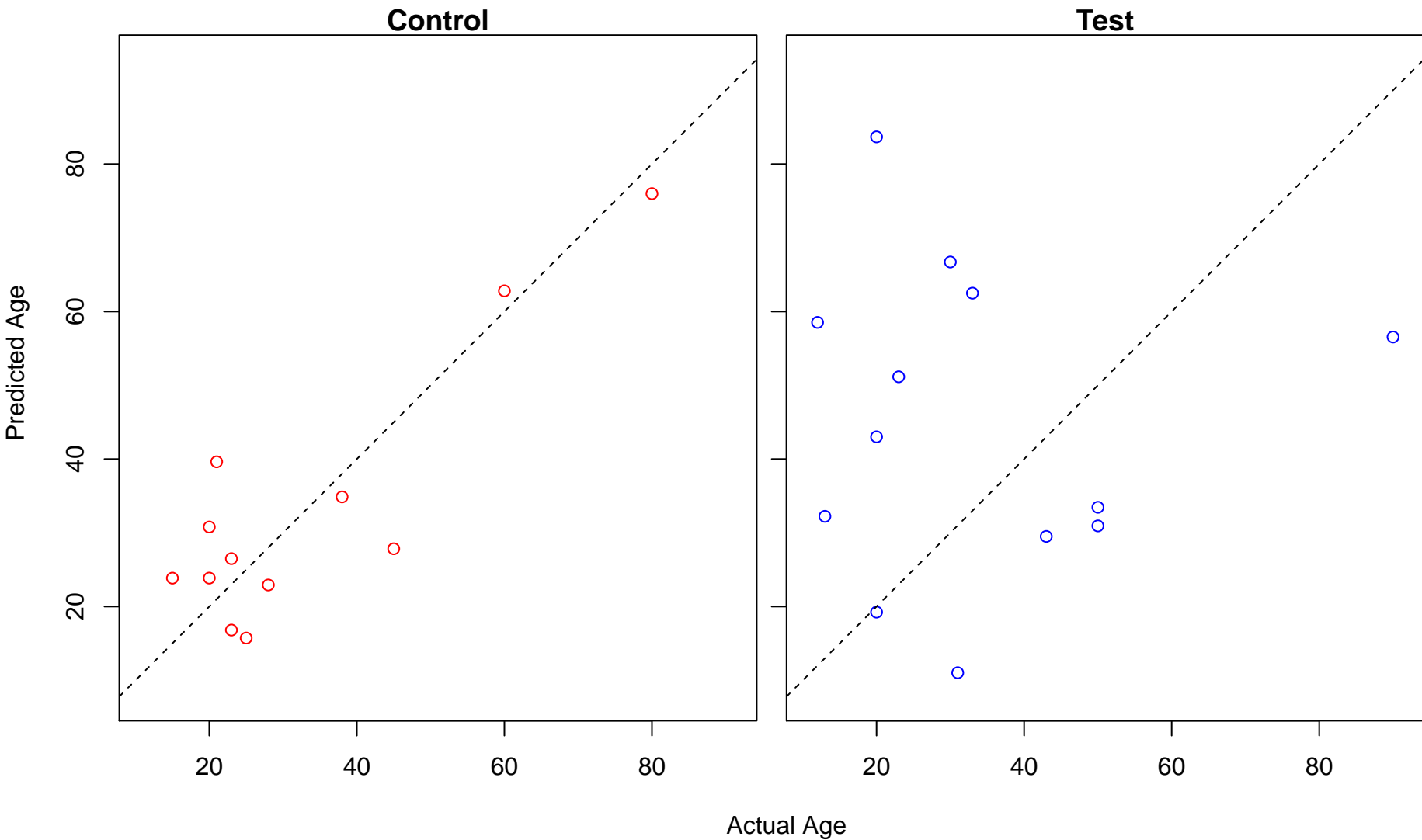


Actual Age

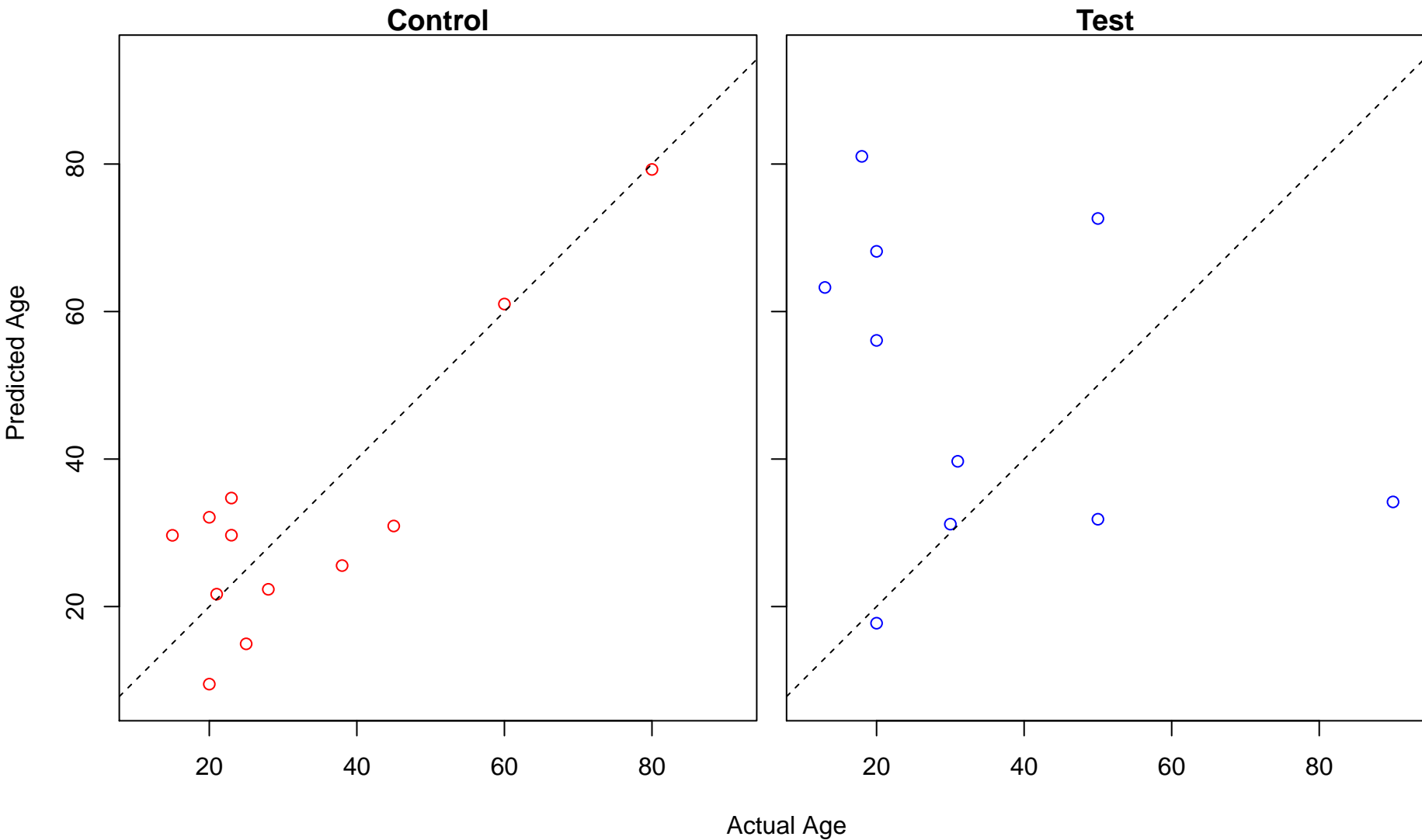
regulation of actin cytoskeleton organization (Score: 8.881051)



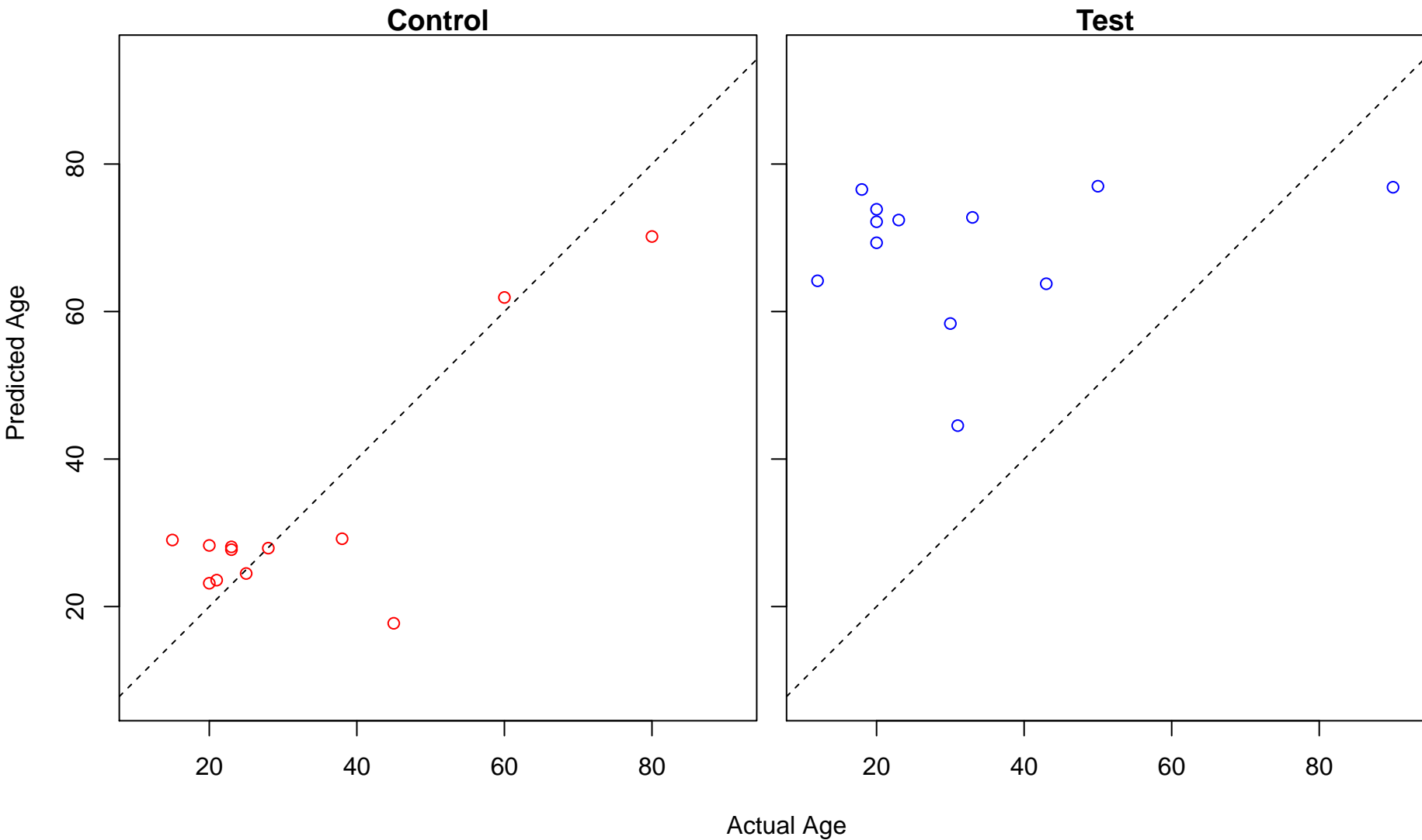
regulation of glucose import in response to insulin stimulus (Score: 8.871541)



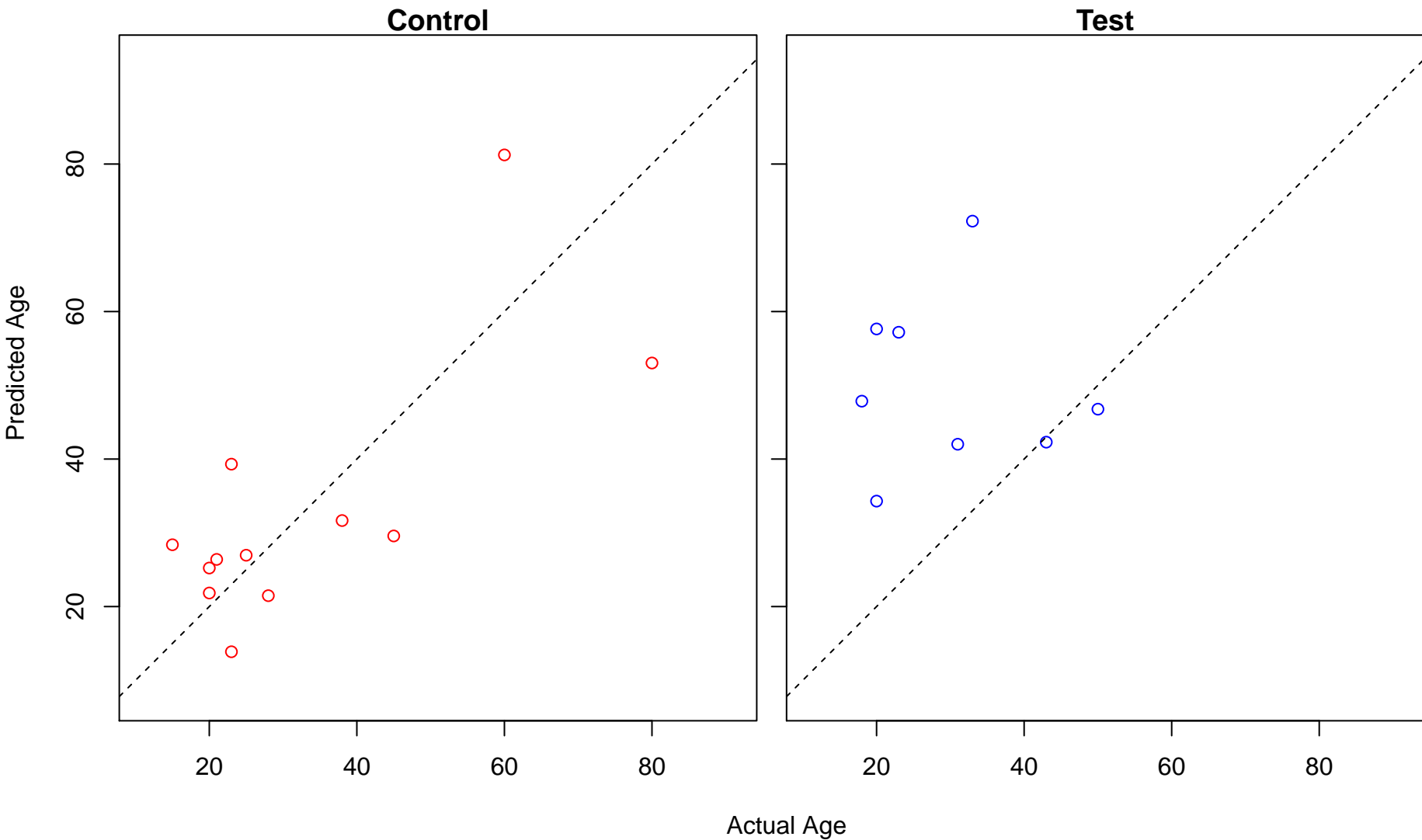
AMP metabolic process (Score: 8.869431)



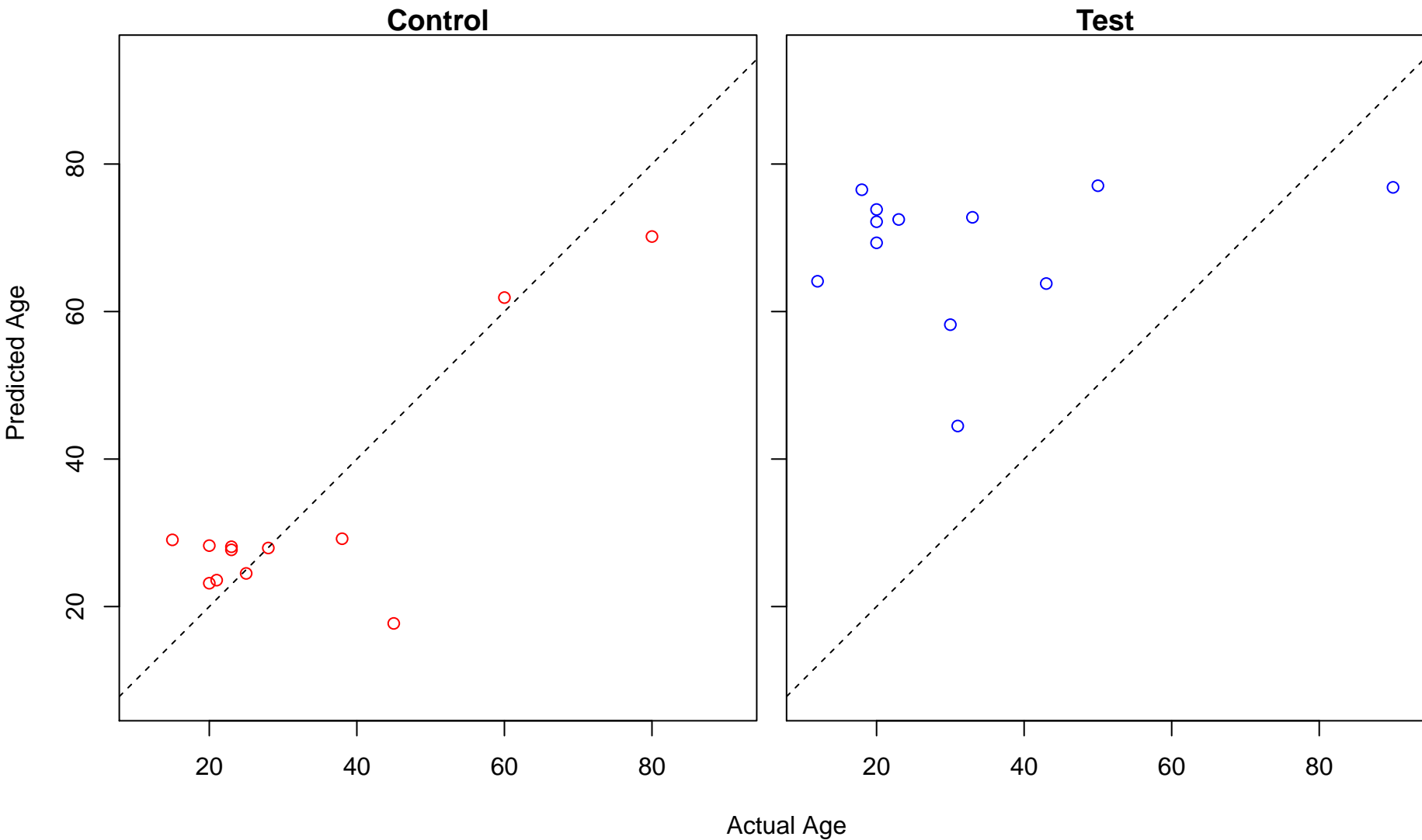
multi-multicellular organism process (Score: 8.864494)



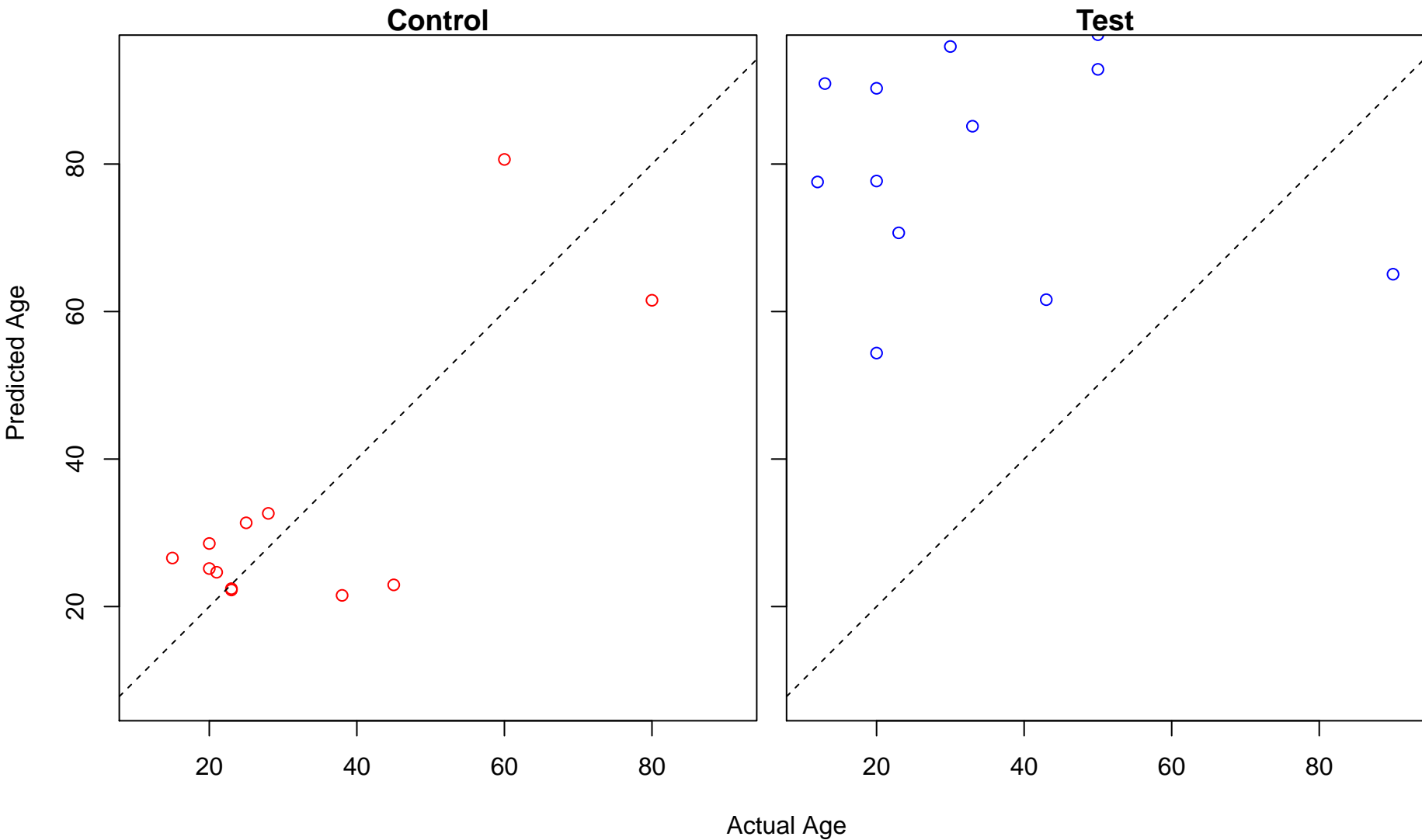
positive regulation of astrocyte differentiation (Score: 8.864480)



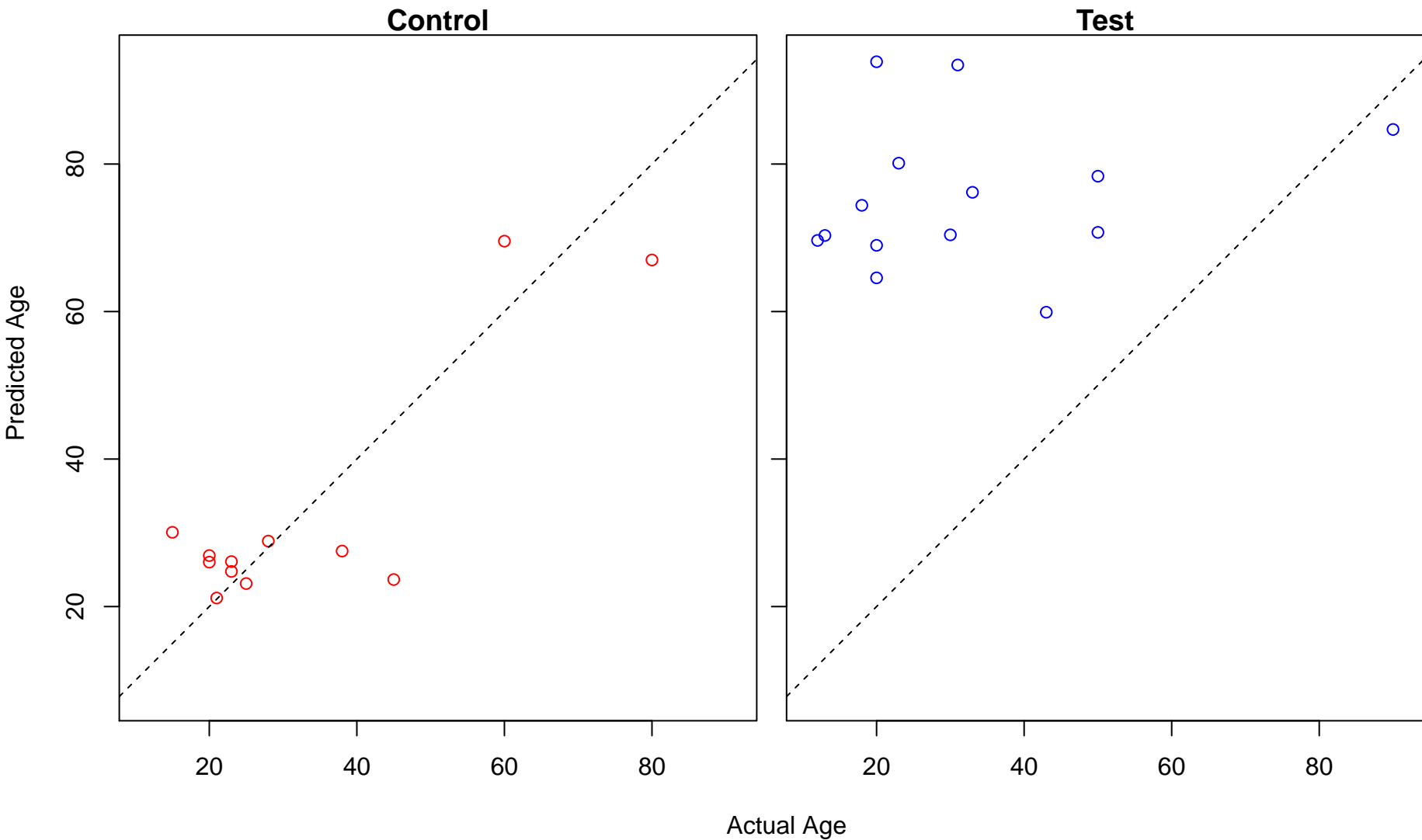
female pregnancy (Score: 8.862769)



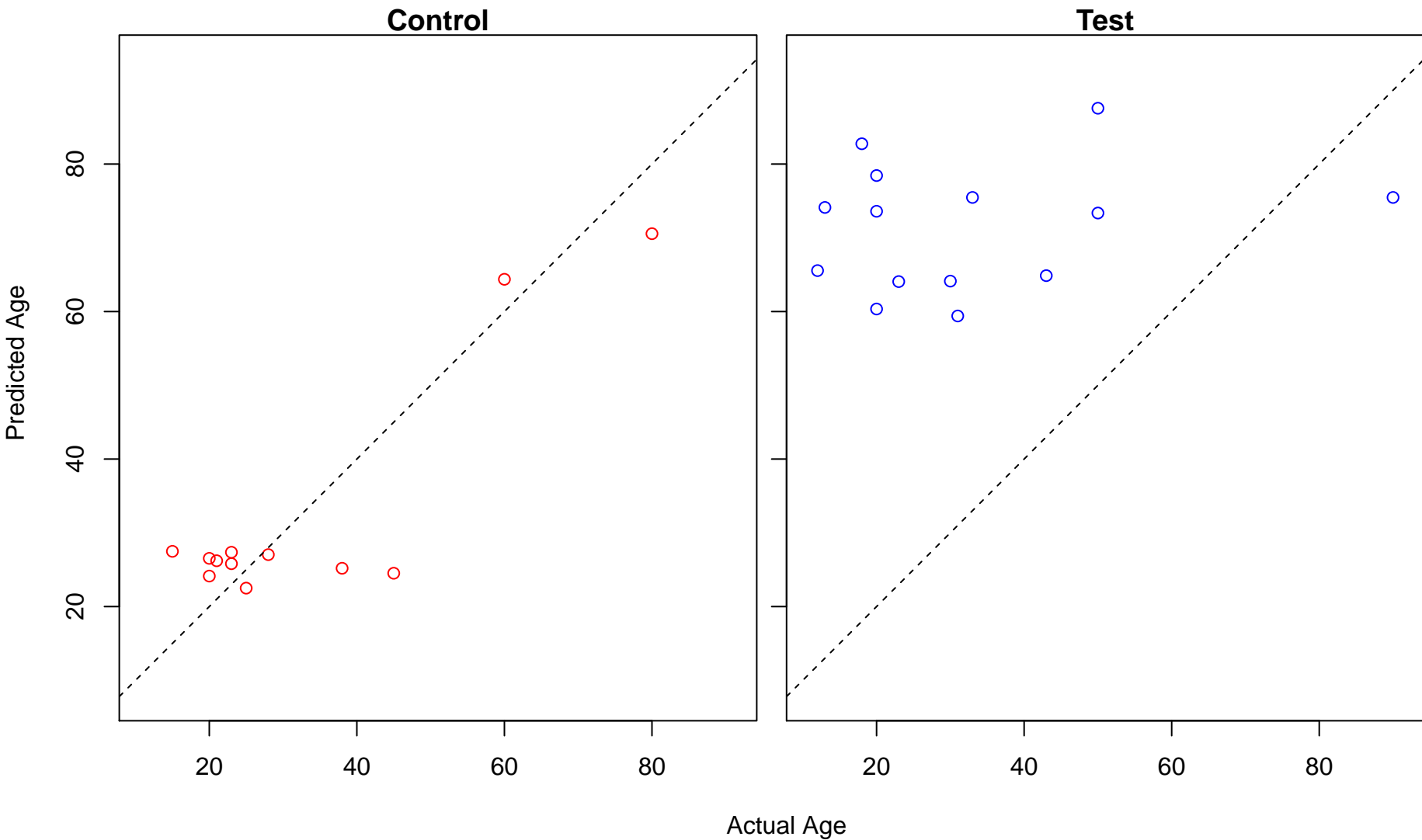
heterochromatin organization (Score: 8.856278)



positive regulation of striated muscle cell differentiation (Score: 8.848349)

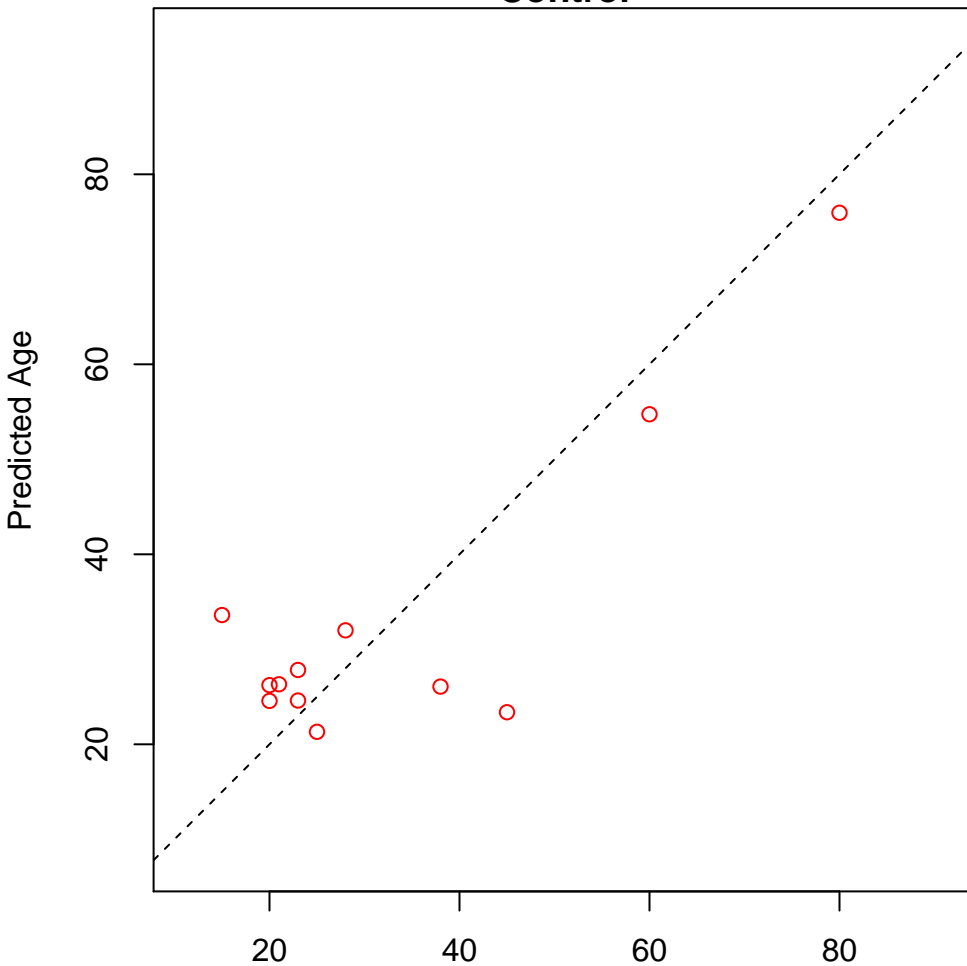


establishment of cell polarity (Score: 8.845929)

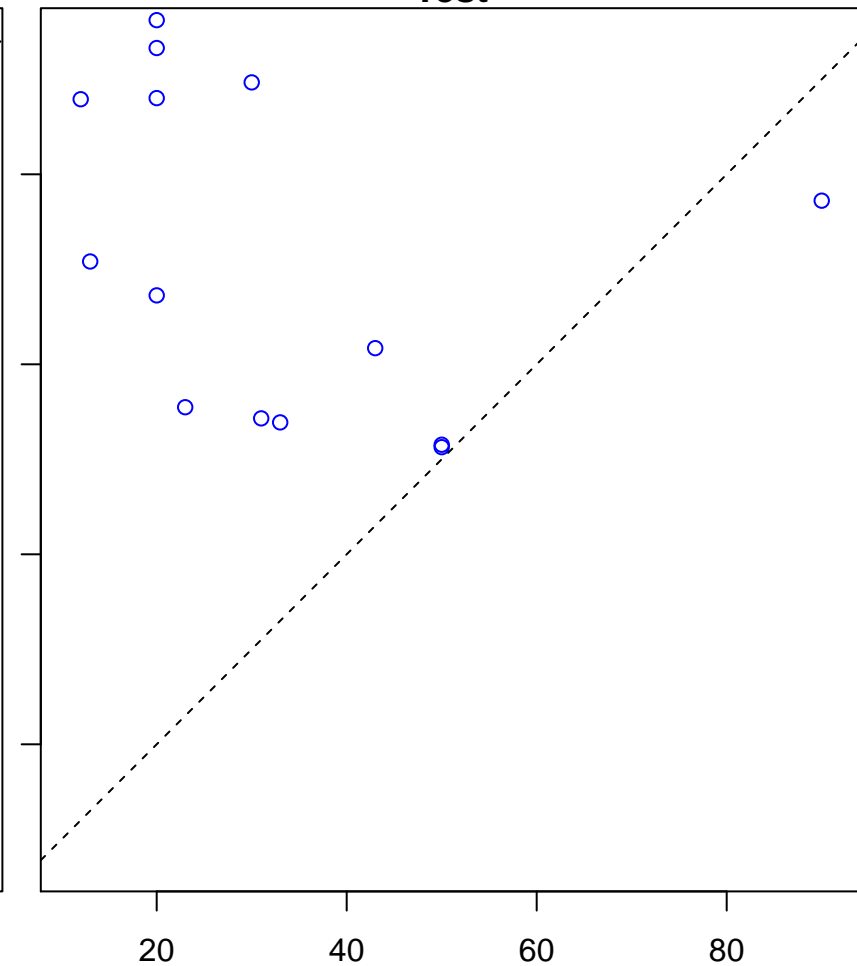


polynucleotide dephosphorylation (Score: 8.838904)

Control



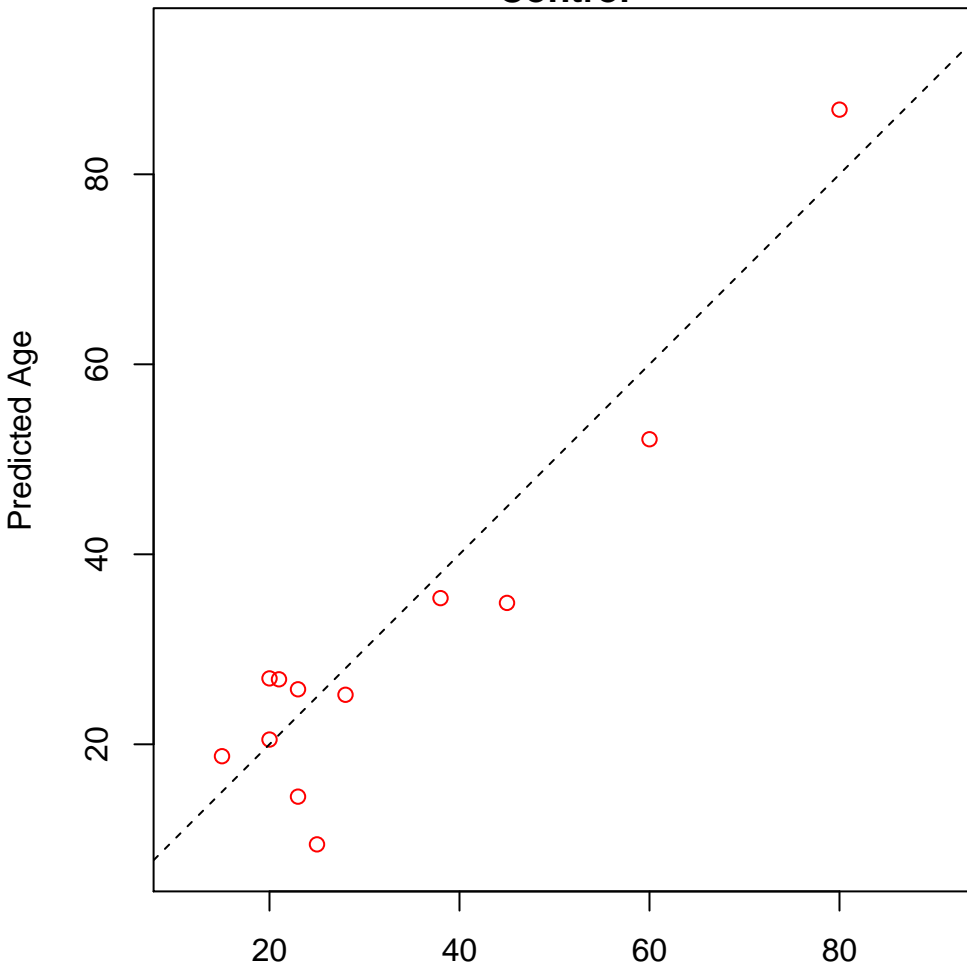
Test



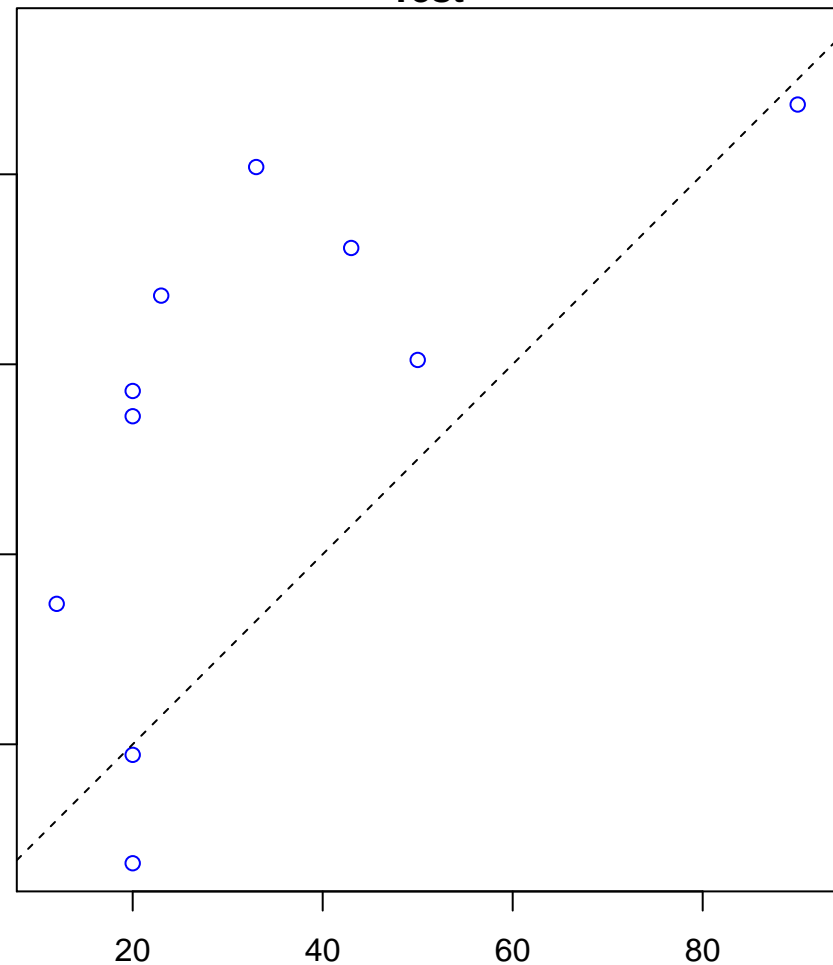
Actual Age

metanephric nephron morphogenesis (Score: 8.832000)

Control

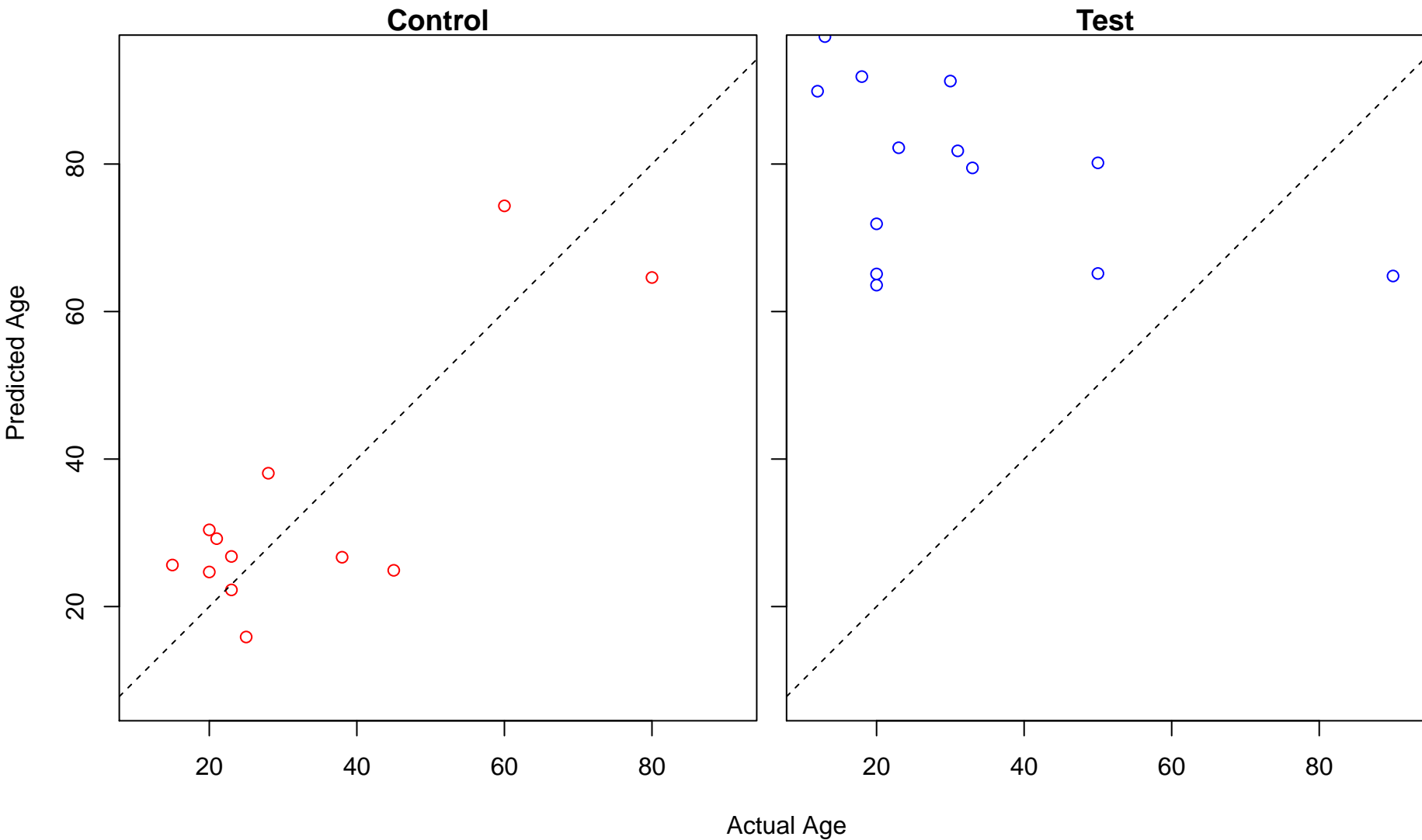


Test



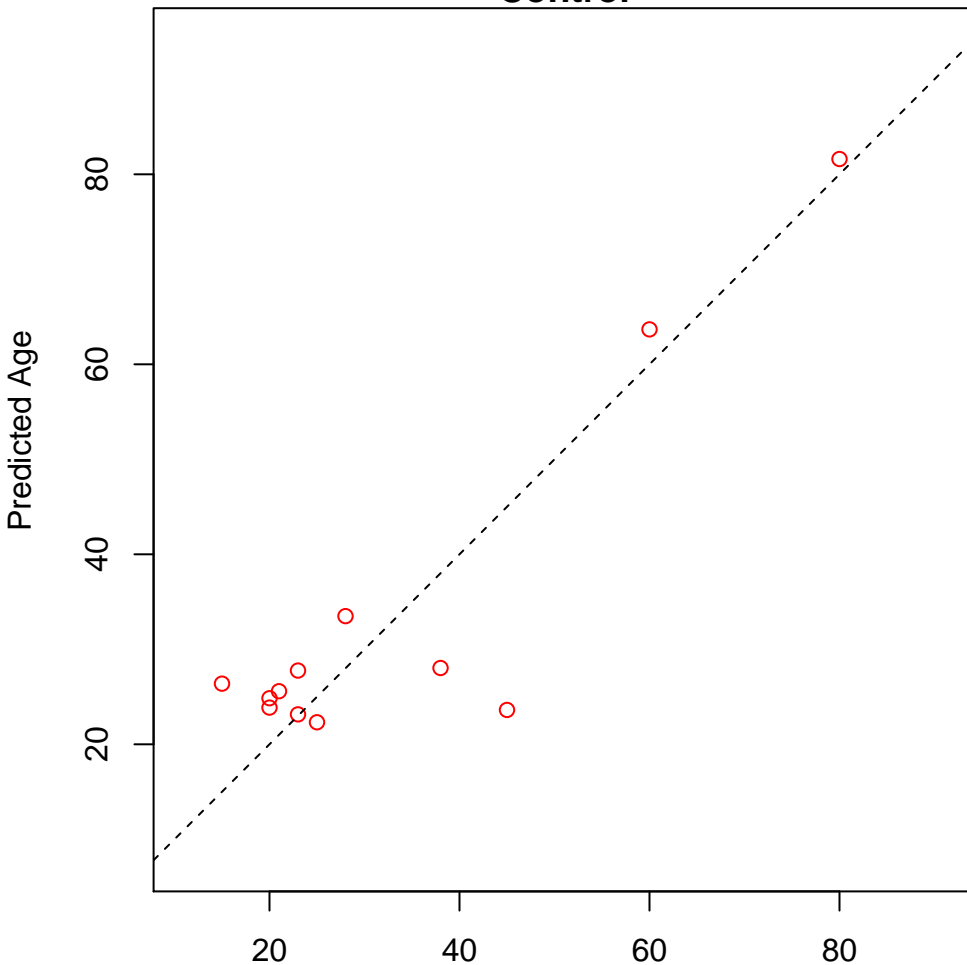
Actual Age

maternal process involved in female pregnancy (Score: 8.830955)

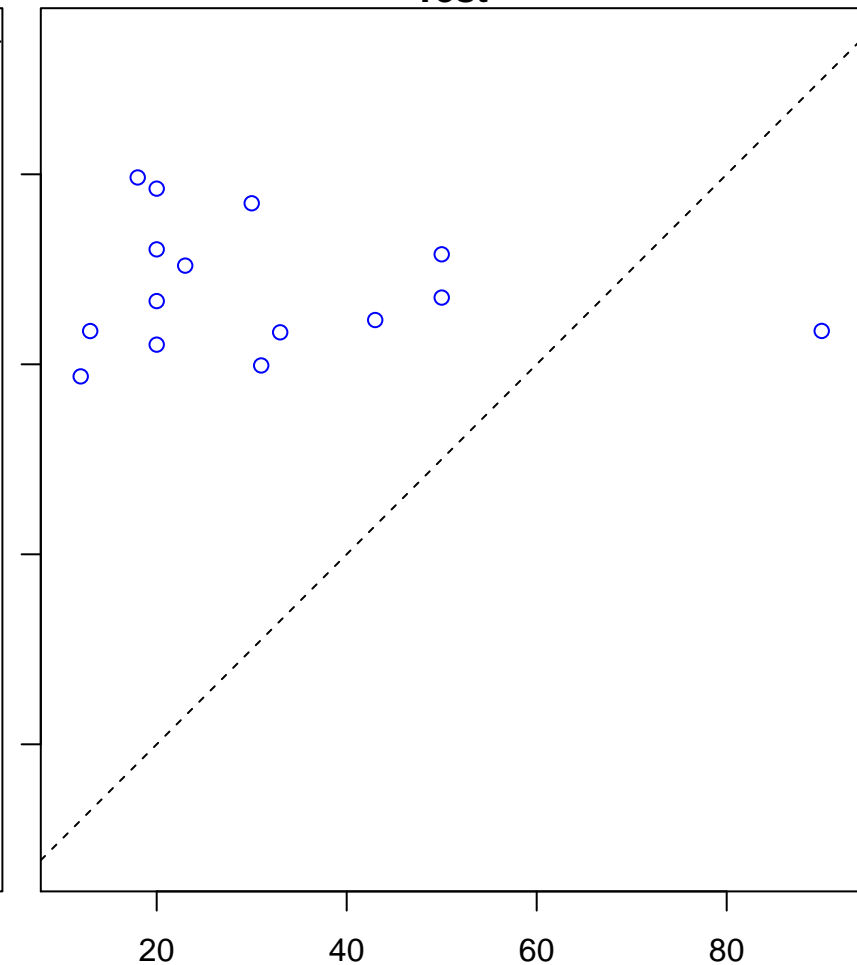


monocarboxylic acid metabolic process (Score: 8.830633)

Control

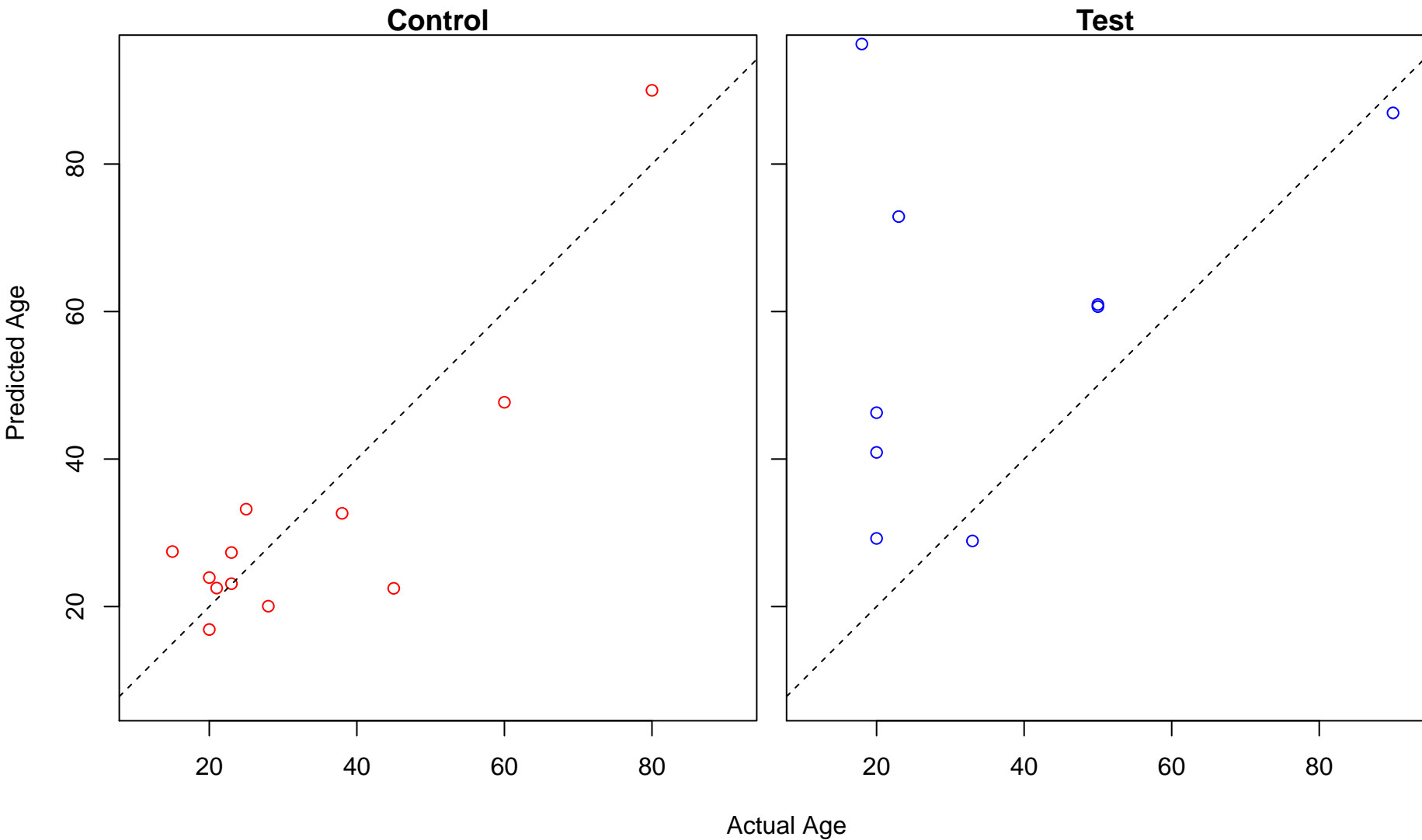


Test

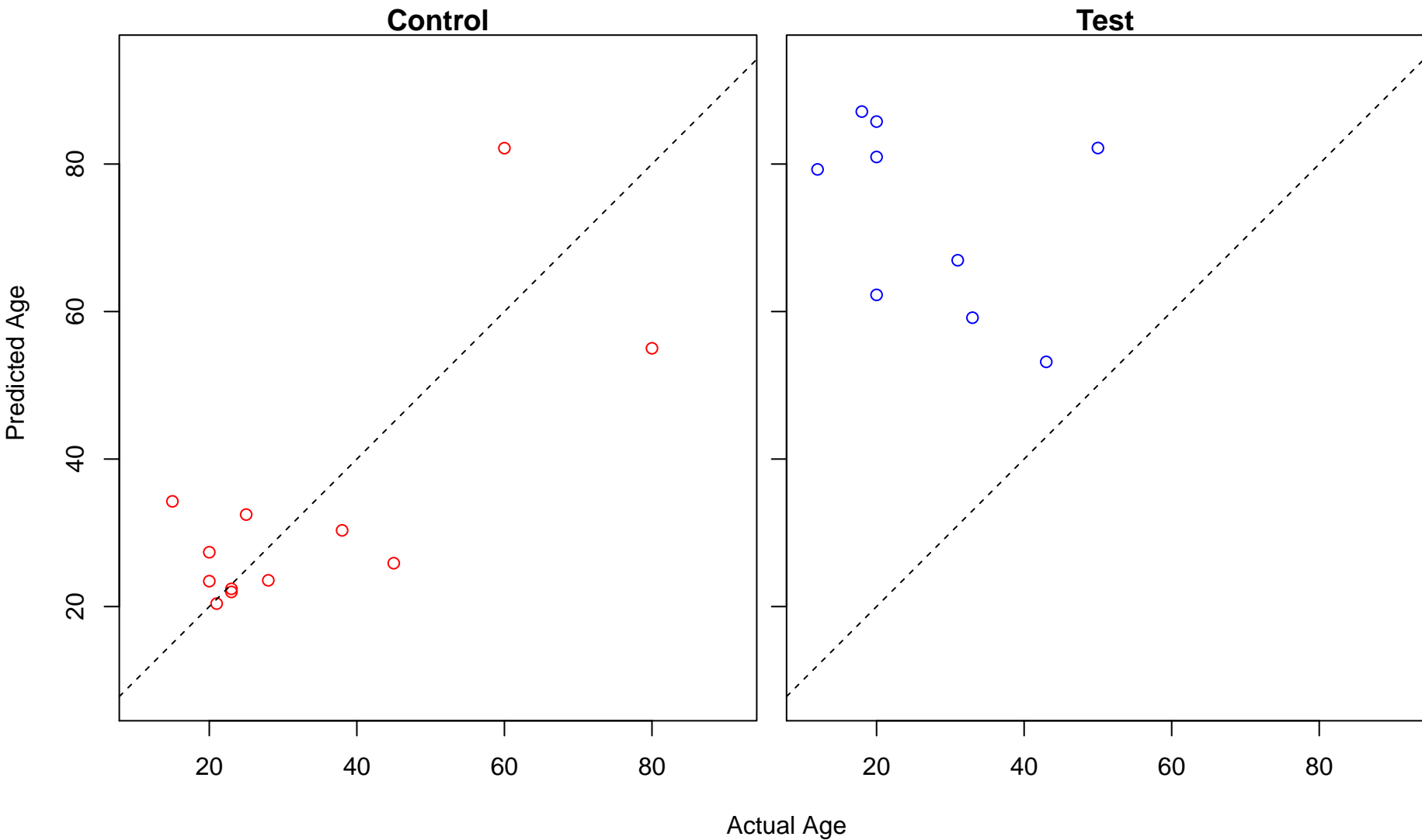


Actual Age

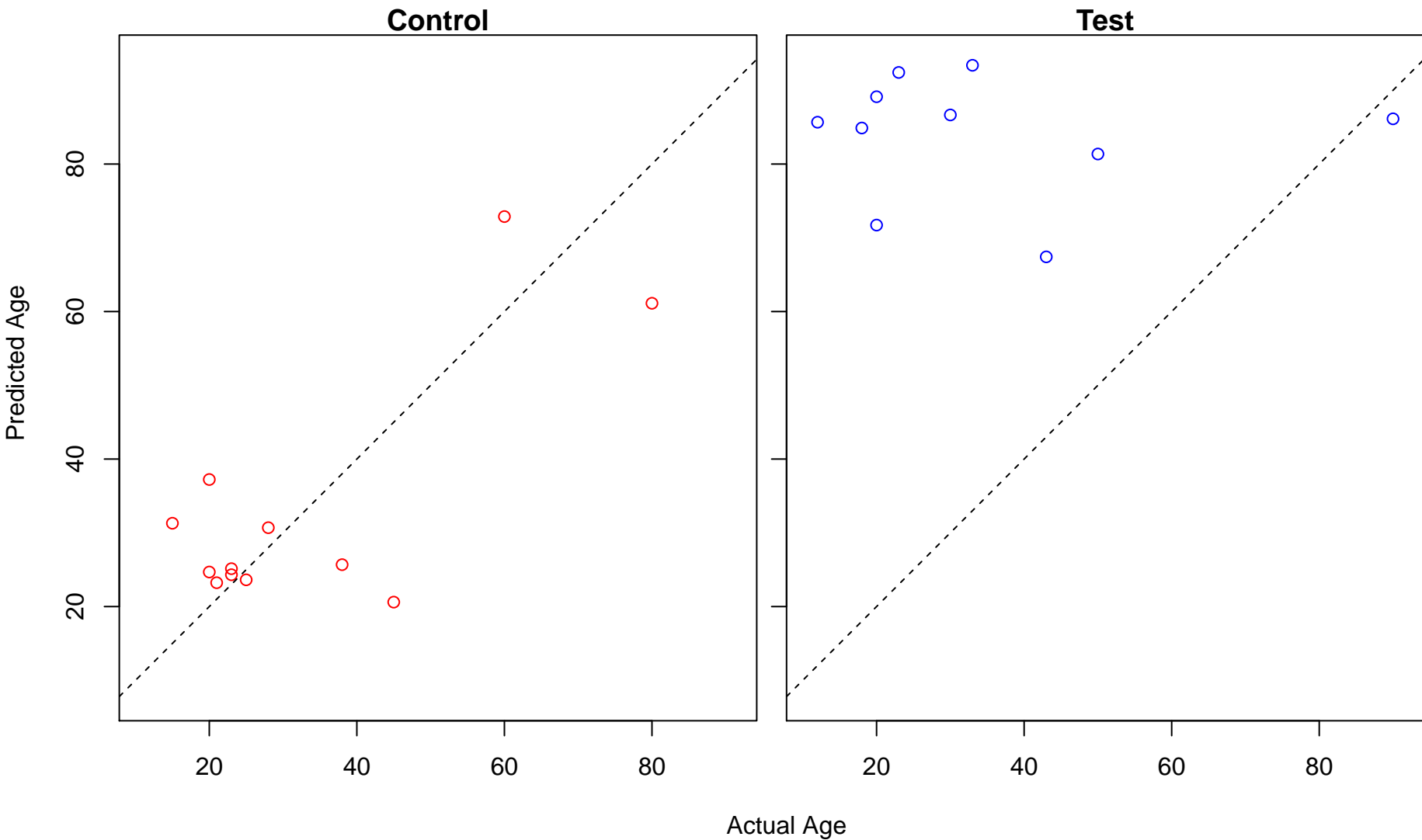
regulation of neutrophil chemotaxis (Score: 8.824883)



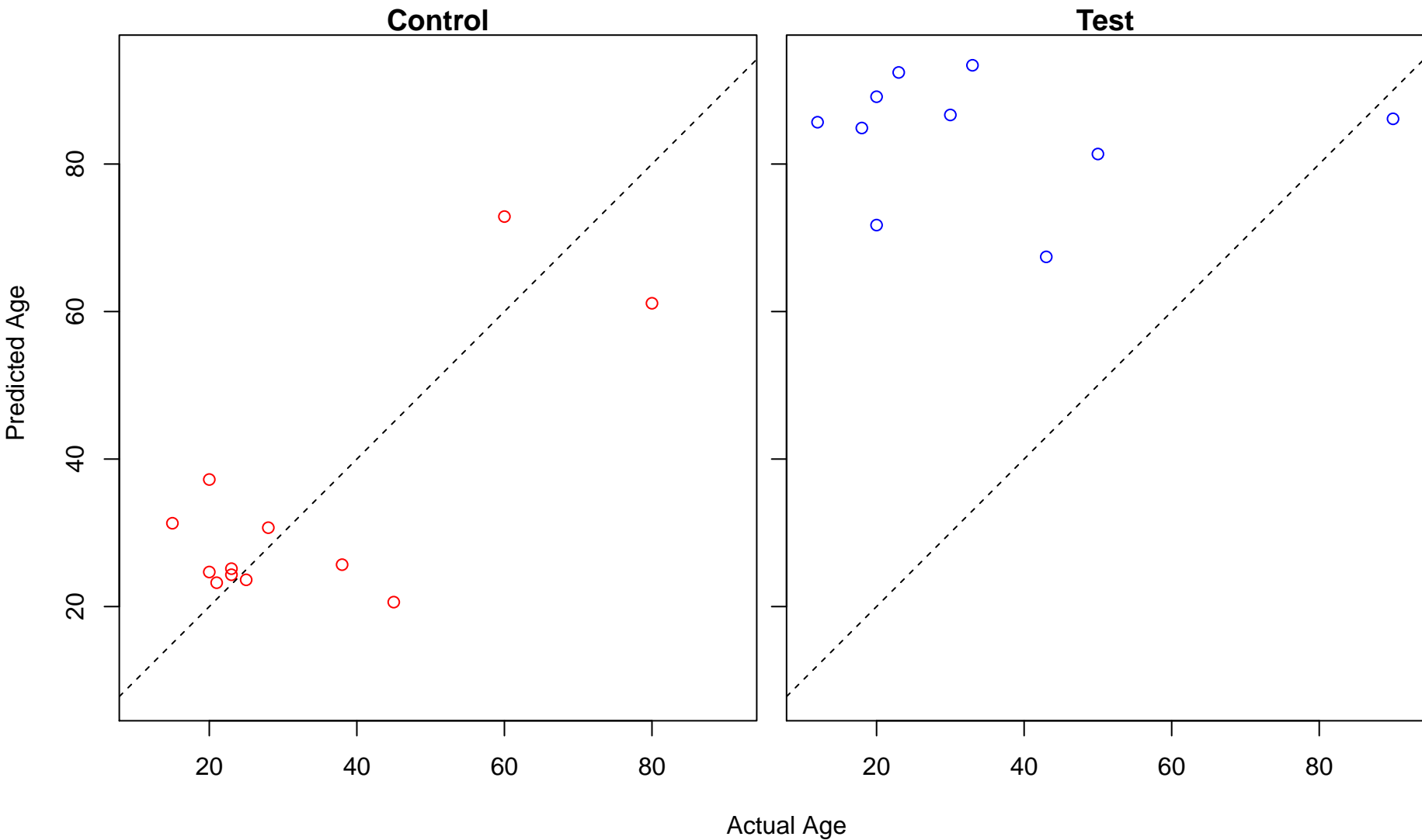
oligopeptide transport (Score: 8.821438)



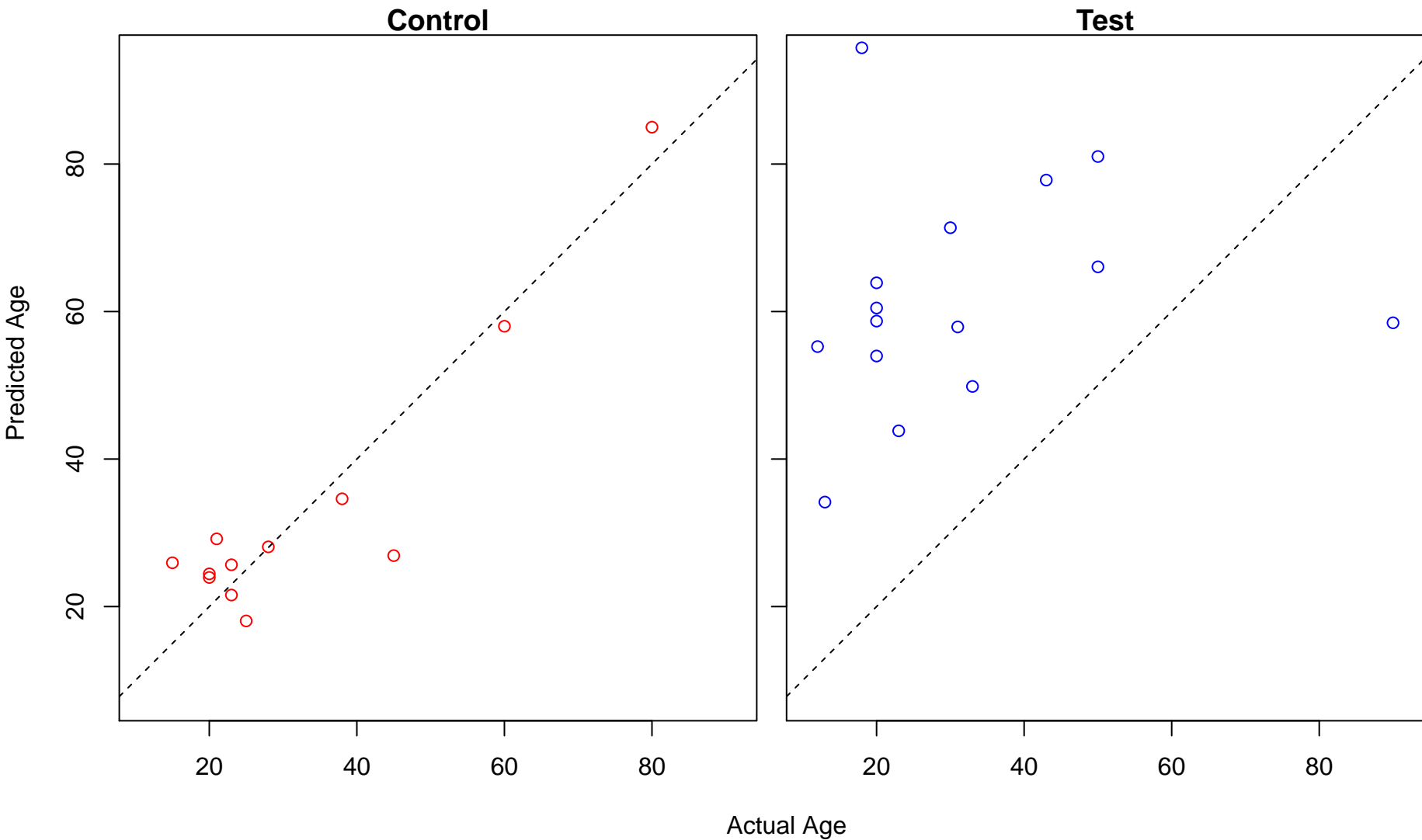
negative regulation of posttranscriptional gene silencing (Score: 8.819750)



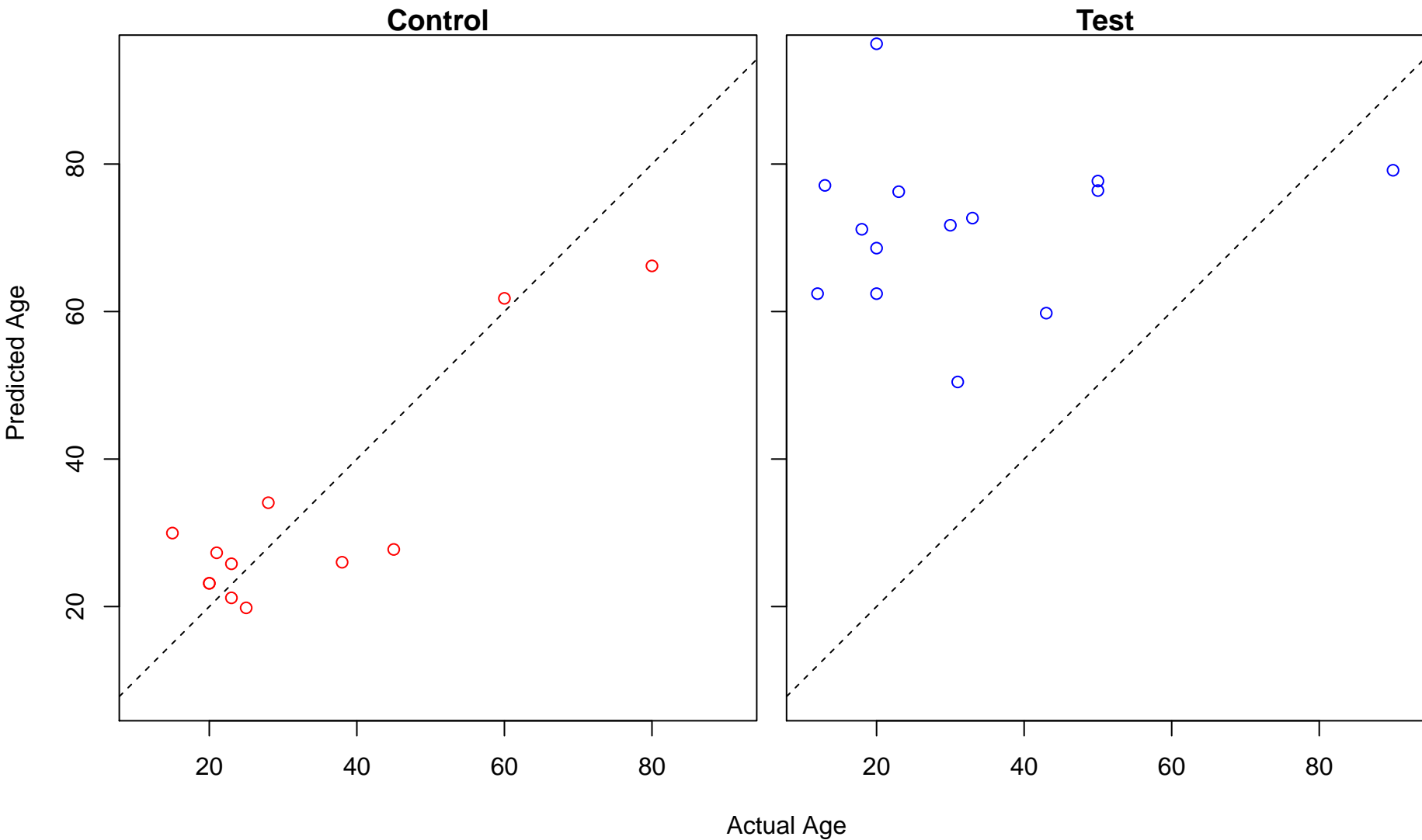
negative regulation of gene silencing by RNA (Score: 8.819750)



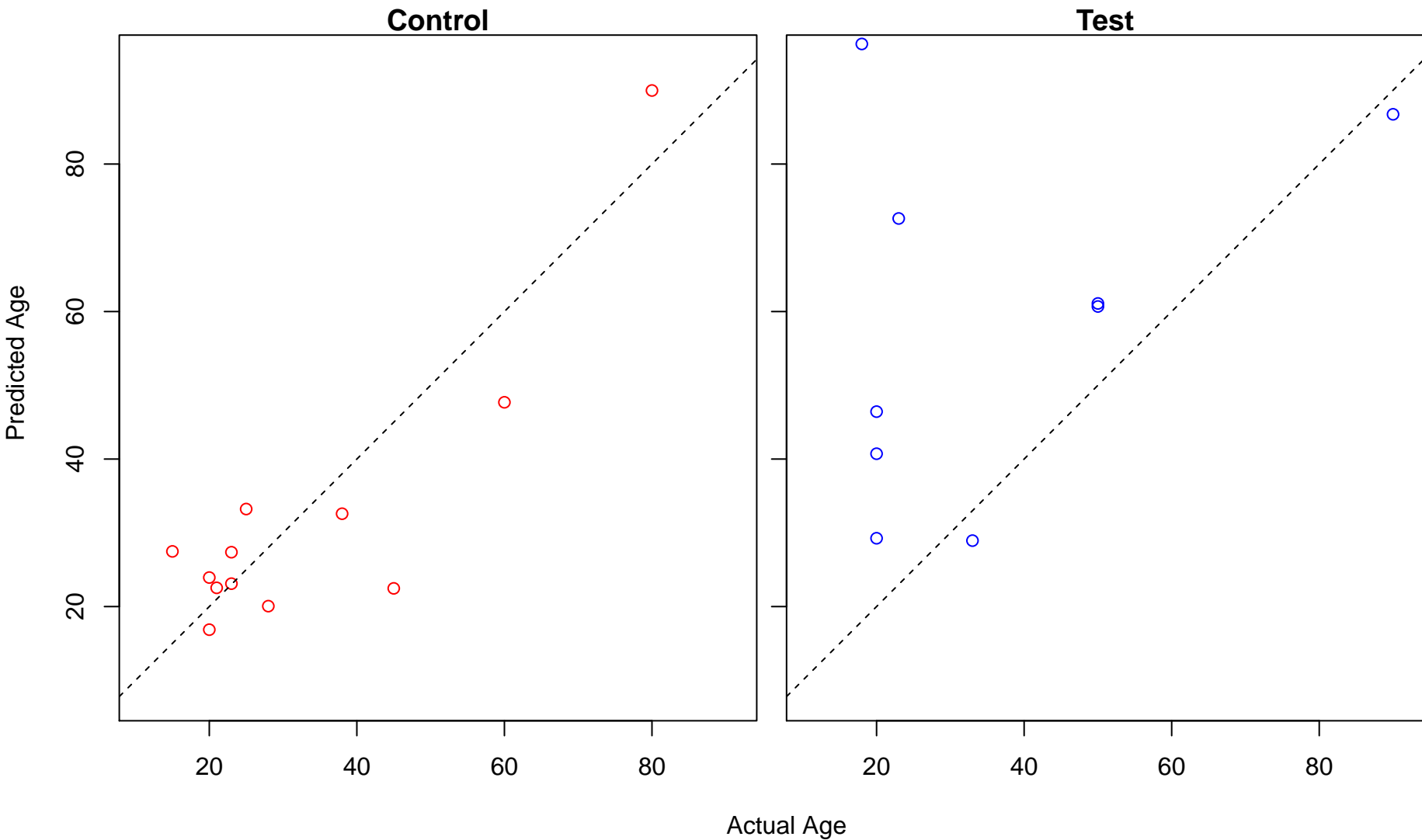
cellular hormone metabolic process (Score: 8.815393)



intrinsic apoptotic signaling pathway in response to DNA damage (Score: 8.814662)

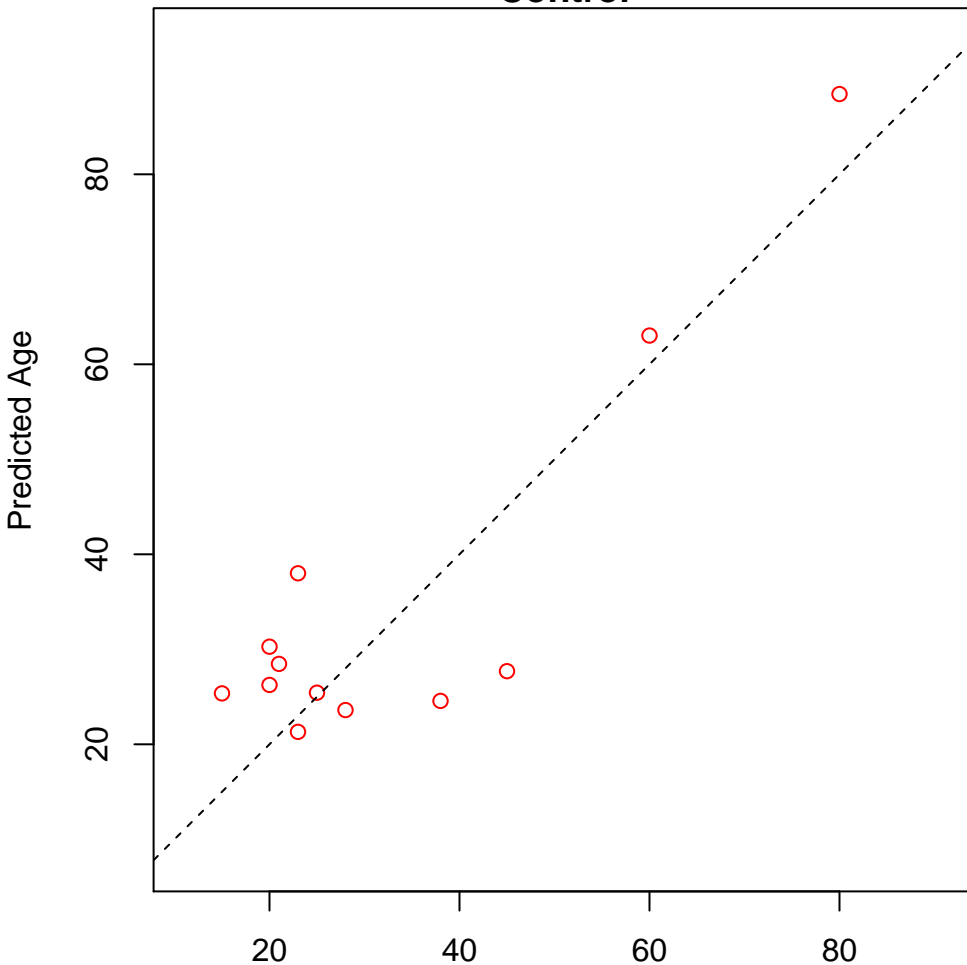


regulation of neutrophil migration (Score: 8.810506)

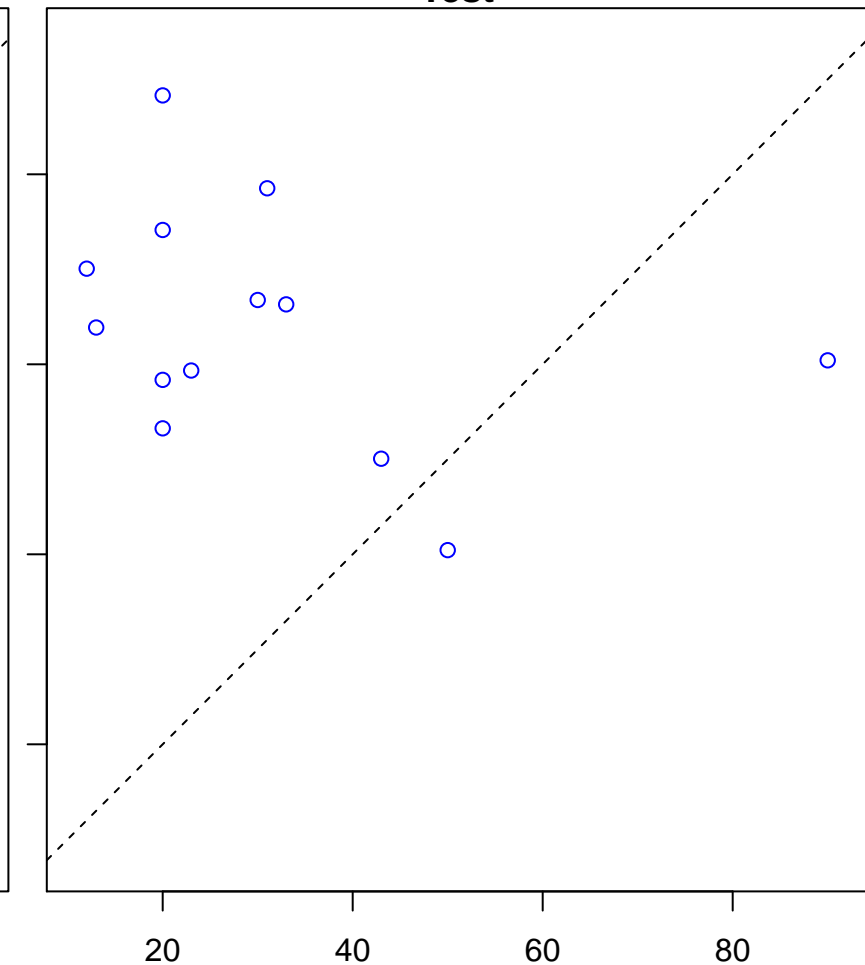


peptidyl-threonine dephosphorylation (Score: 8.808844)

Control

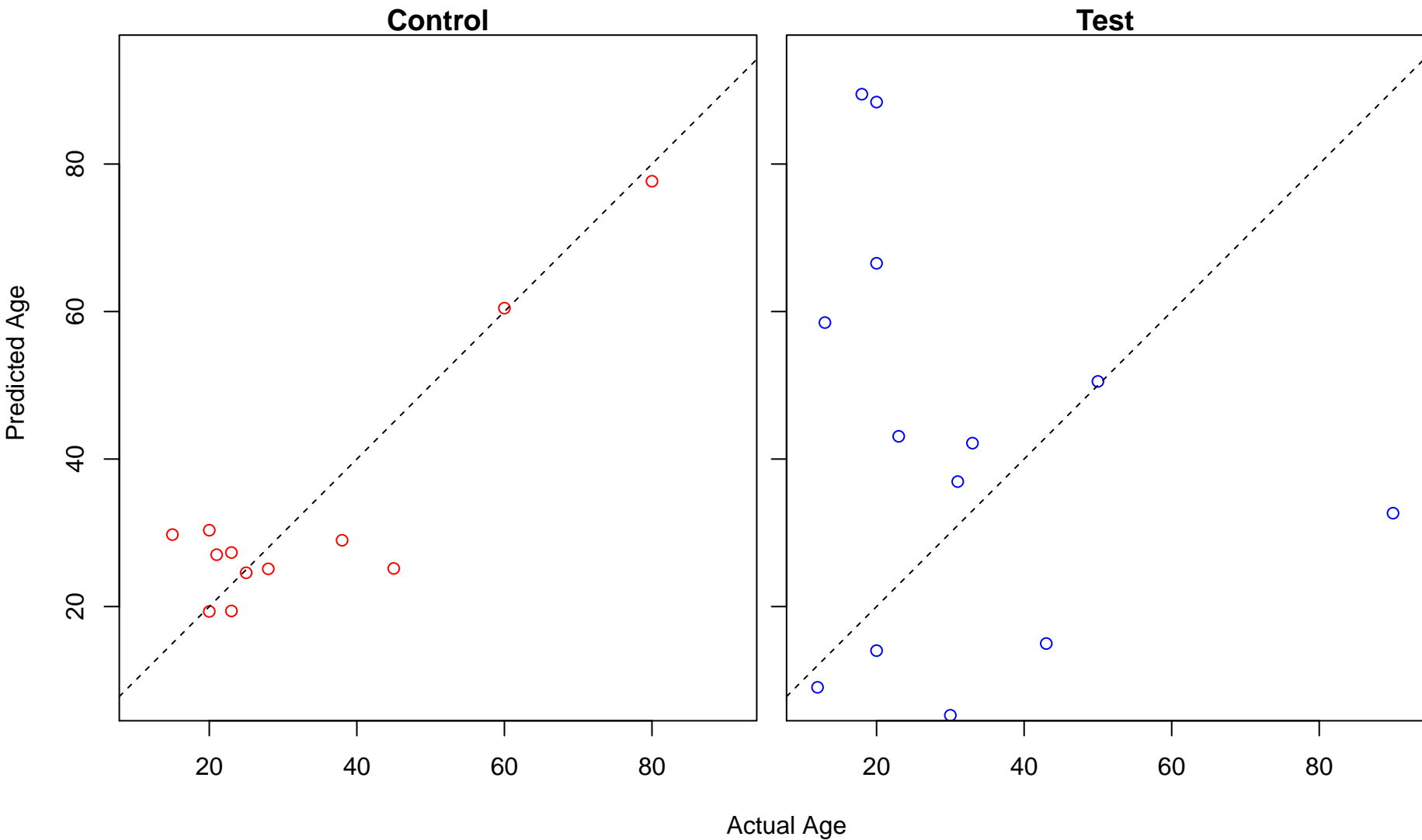


Test

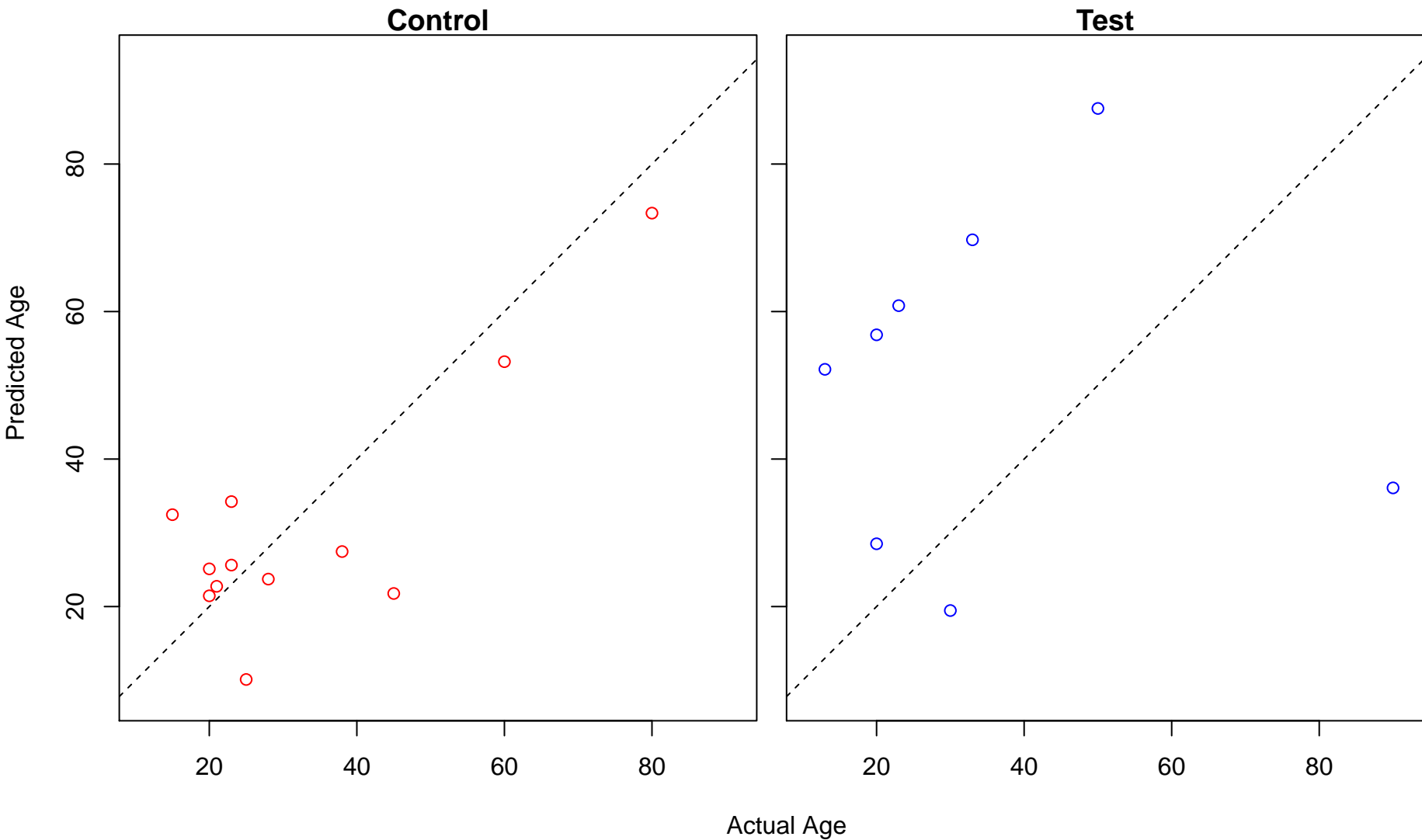


Actual Age

mucosal immune response (Score: 8.804527)

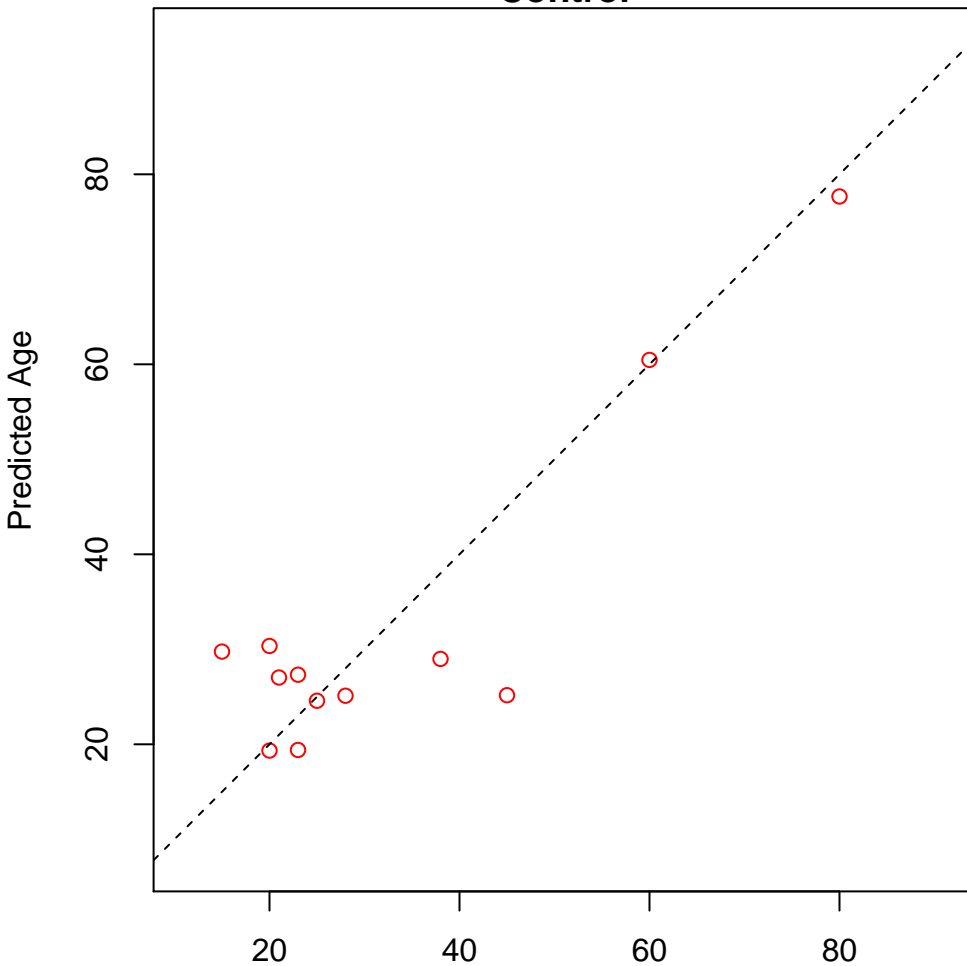


inorganic ion homeostasis (Score: 8.804482)

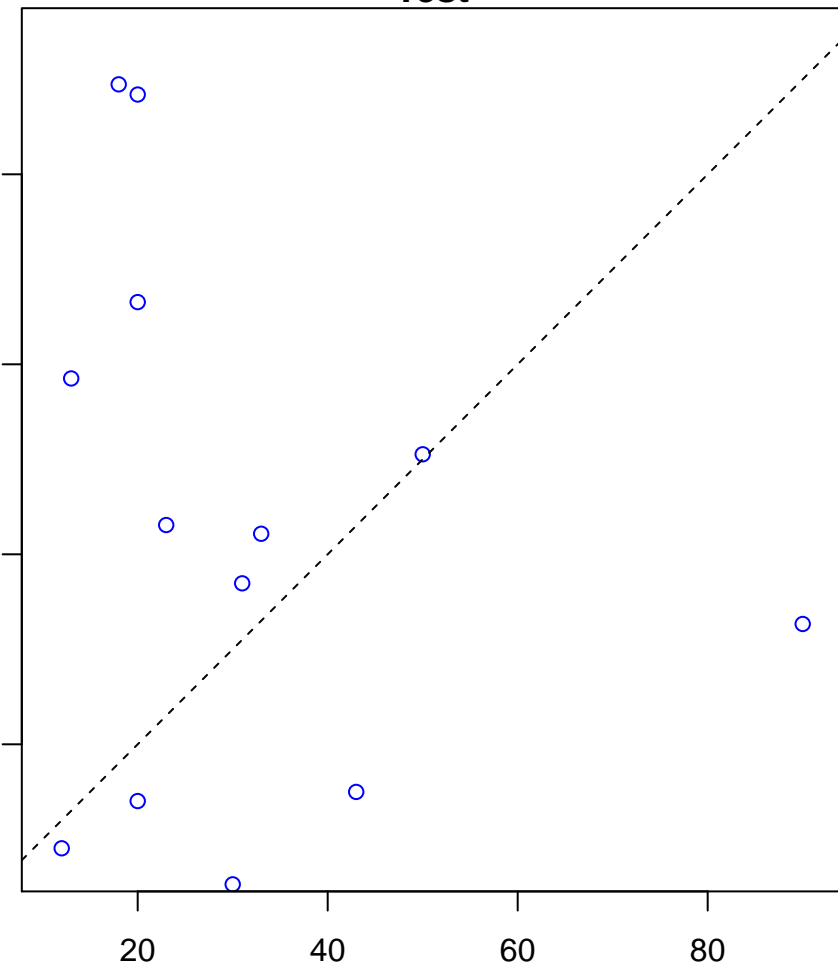


organ or tissue specific immune response (Score: 8.804027)

Control

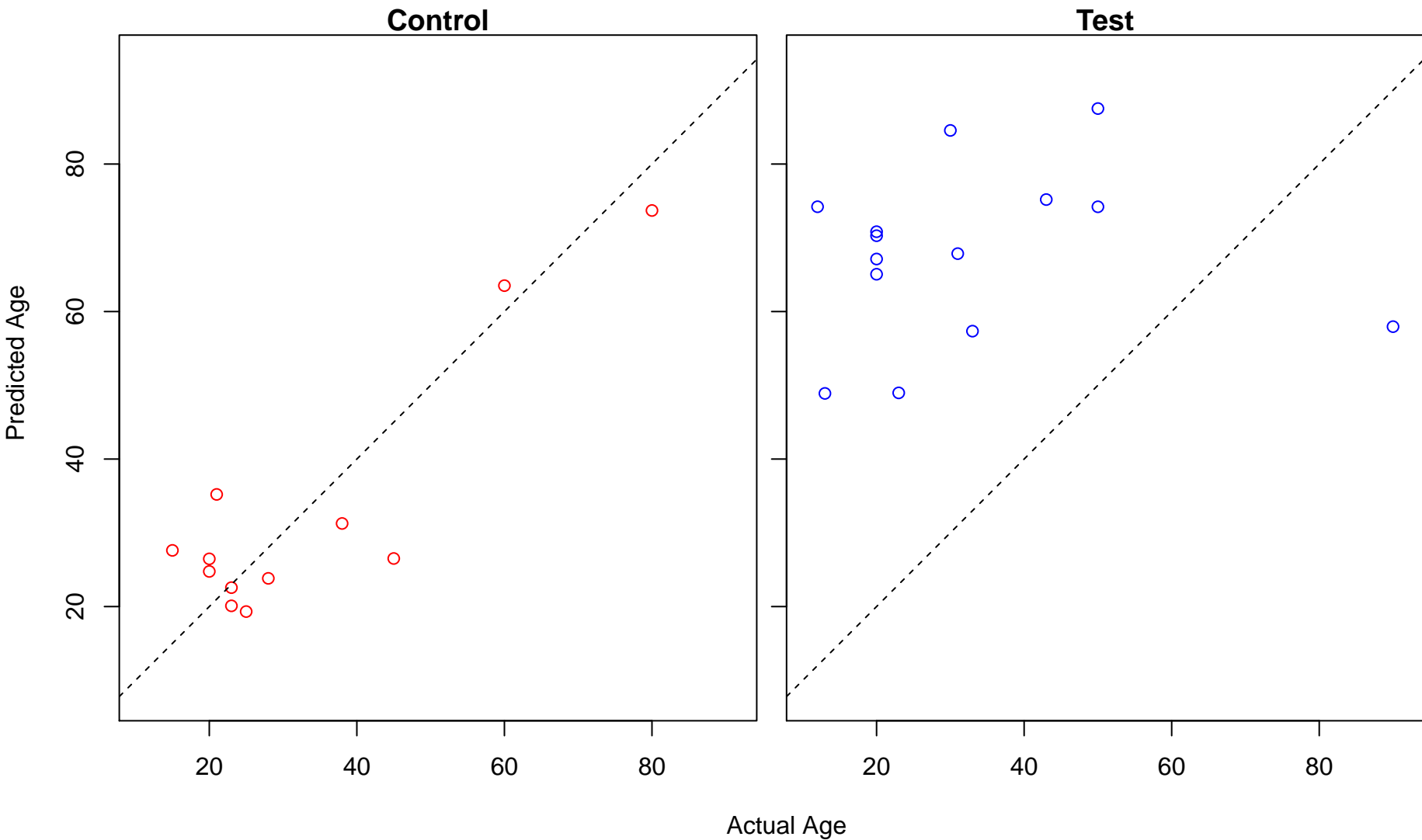


Test

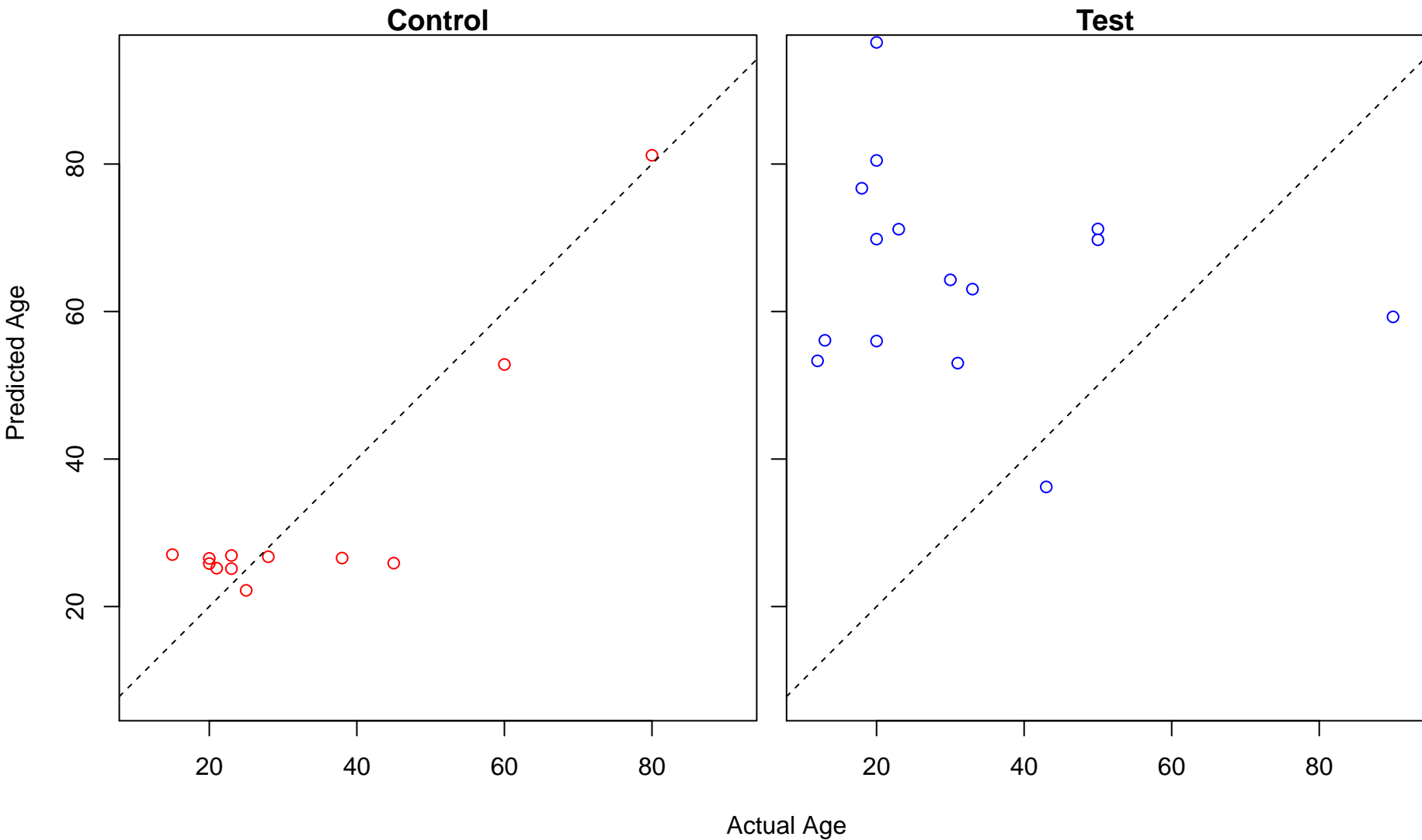


Actual Age

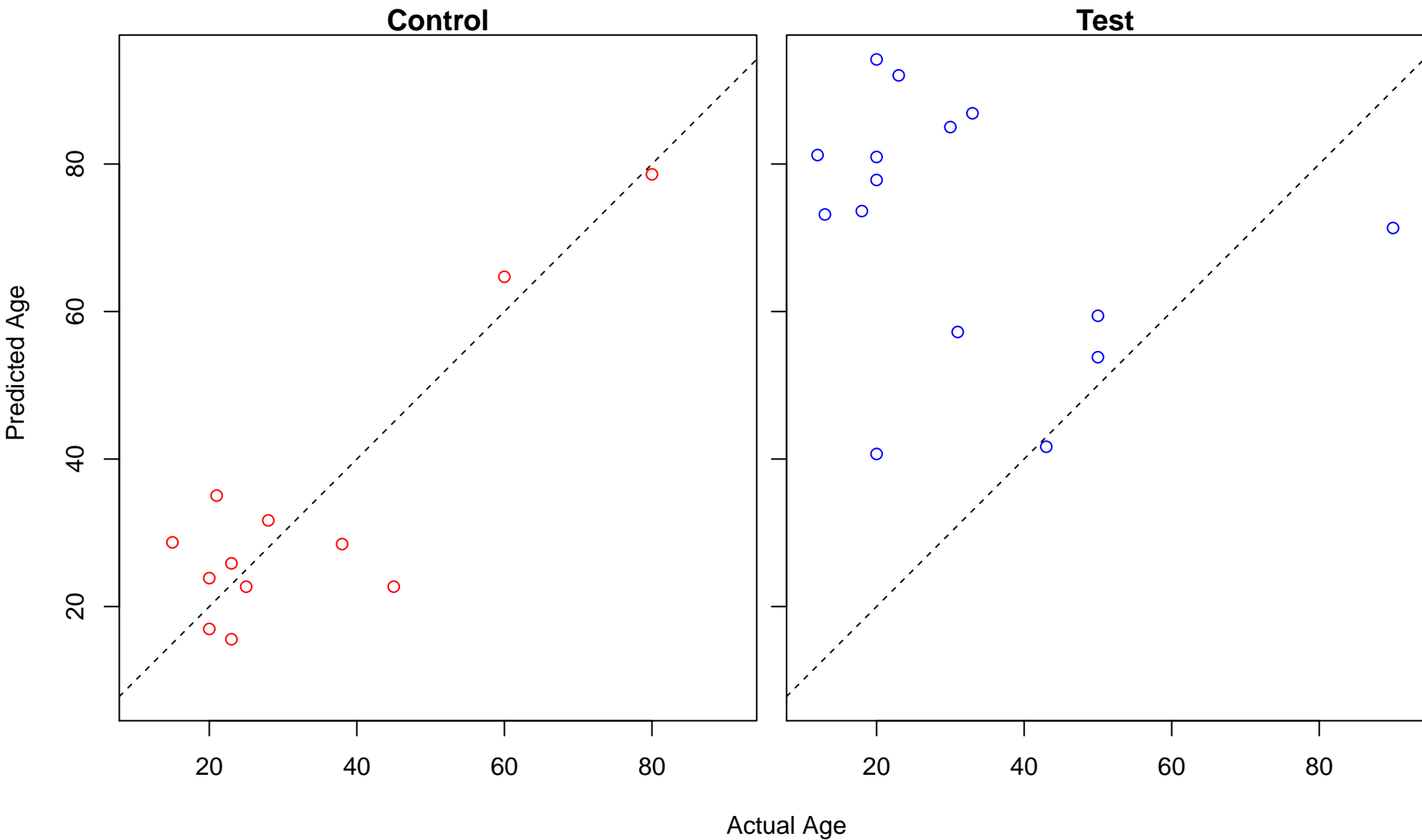
regulation of angiogenesis (Score: 8.798806)



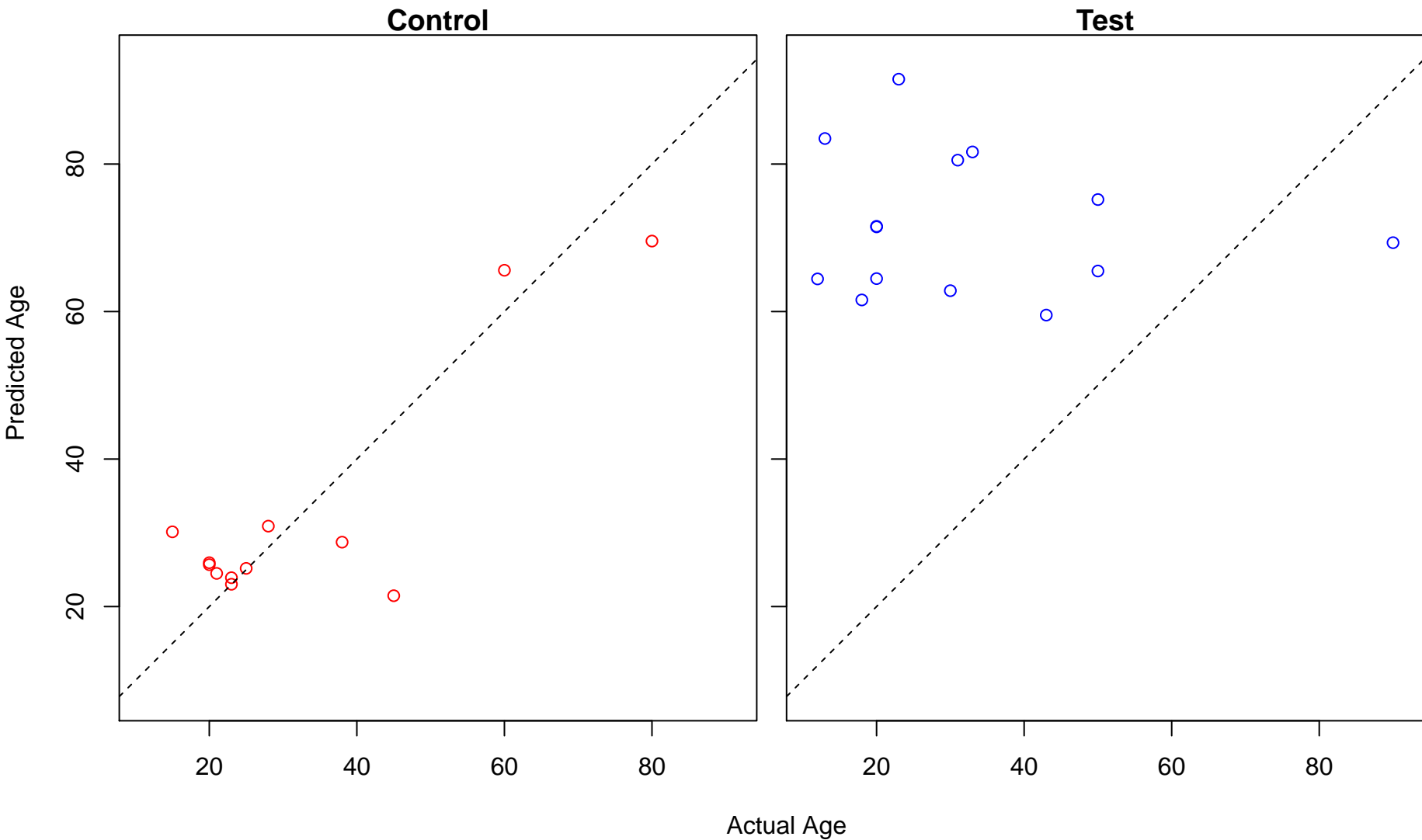
positive regulation of telomere maintenance (Score: 8.795578)



GMP metabolic process (Score: 8.793965)

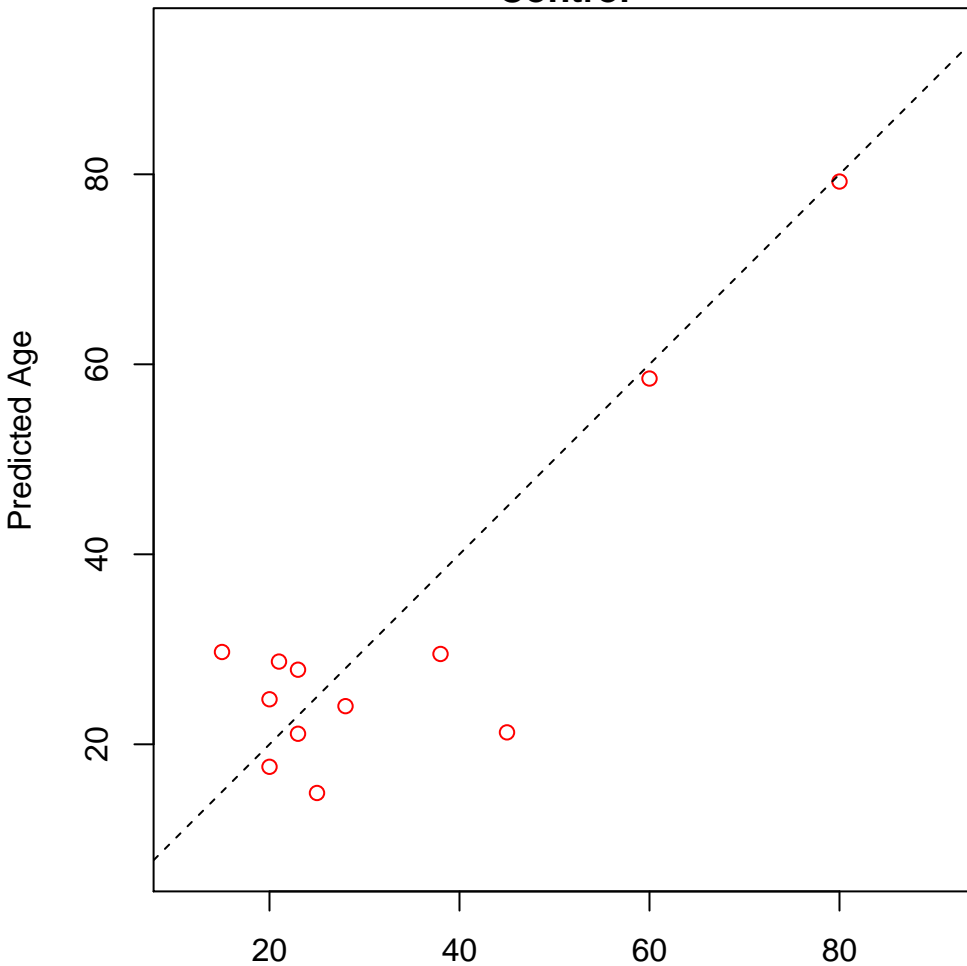


cellular response to alkaloid (Score: 8.792183)

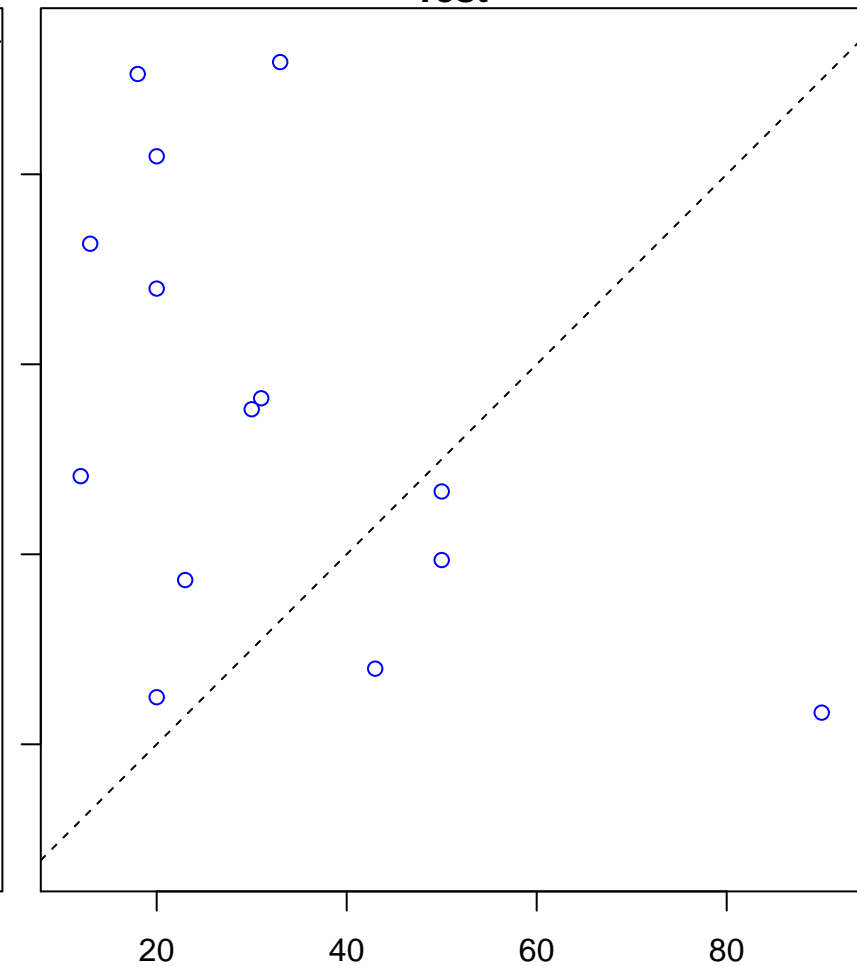


phosphatidylinositol phosphorylation (Score: 8.780993)

Control

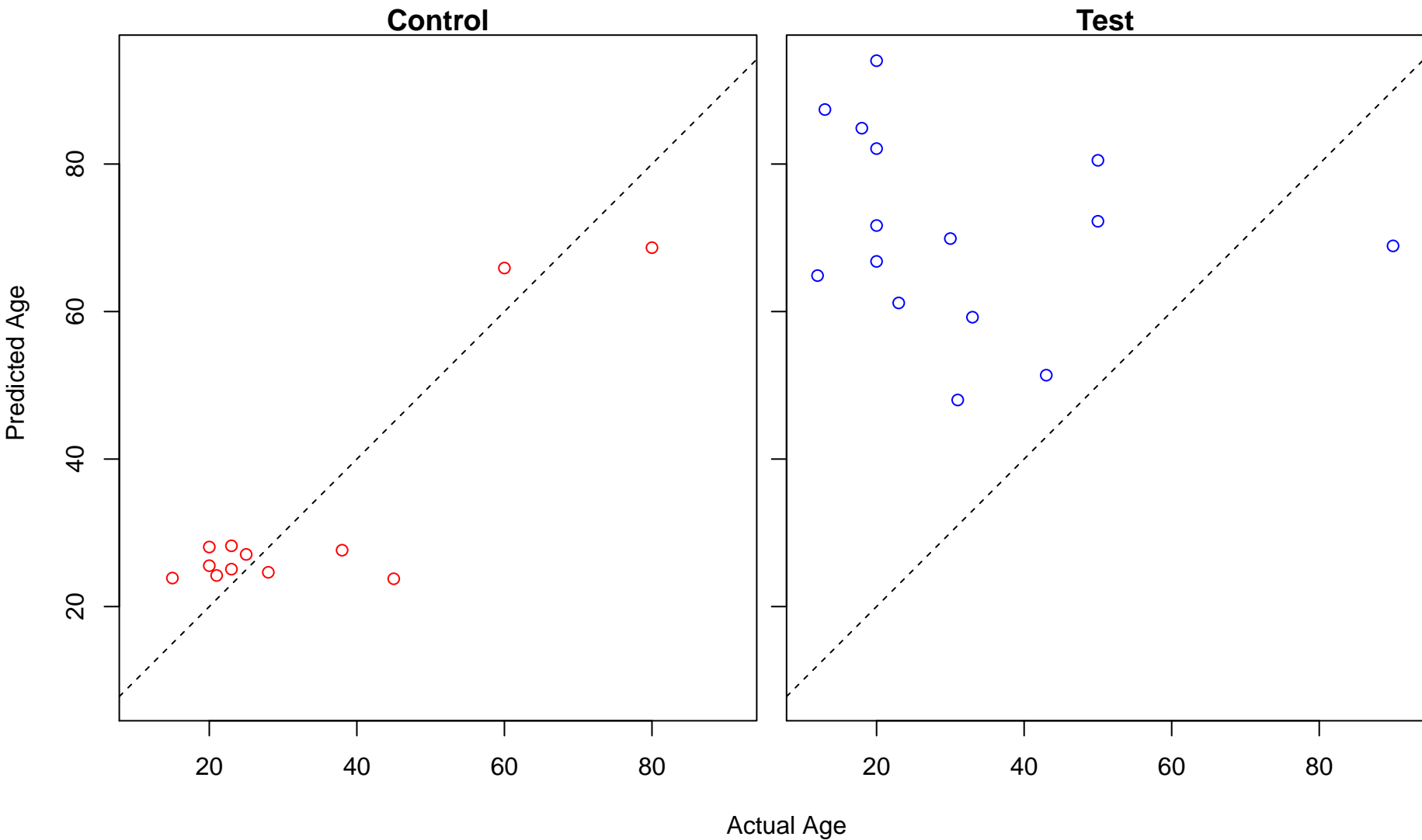


Test

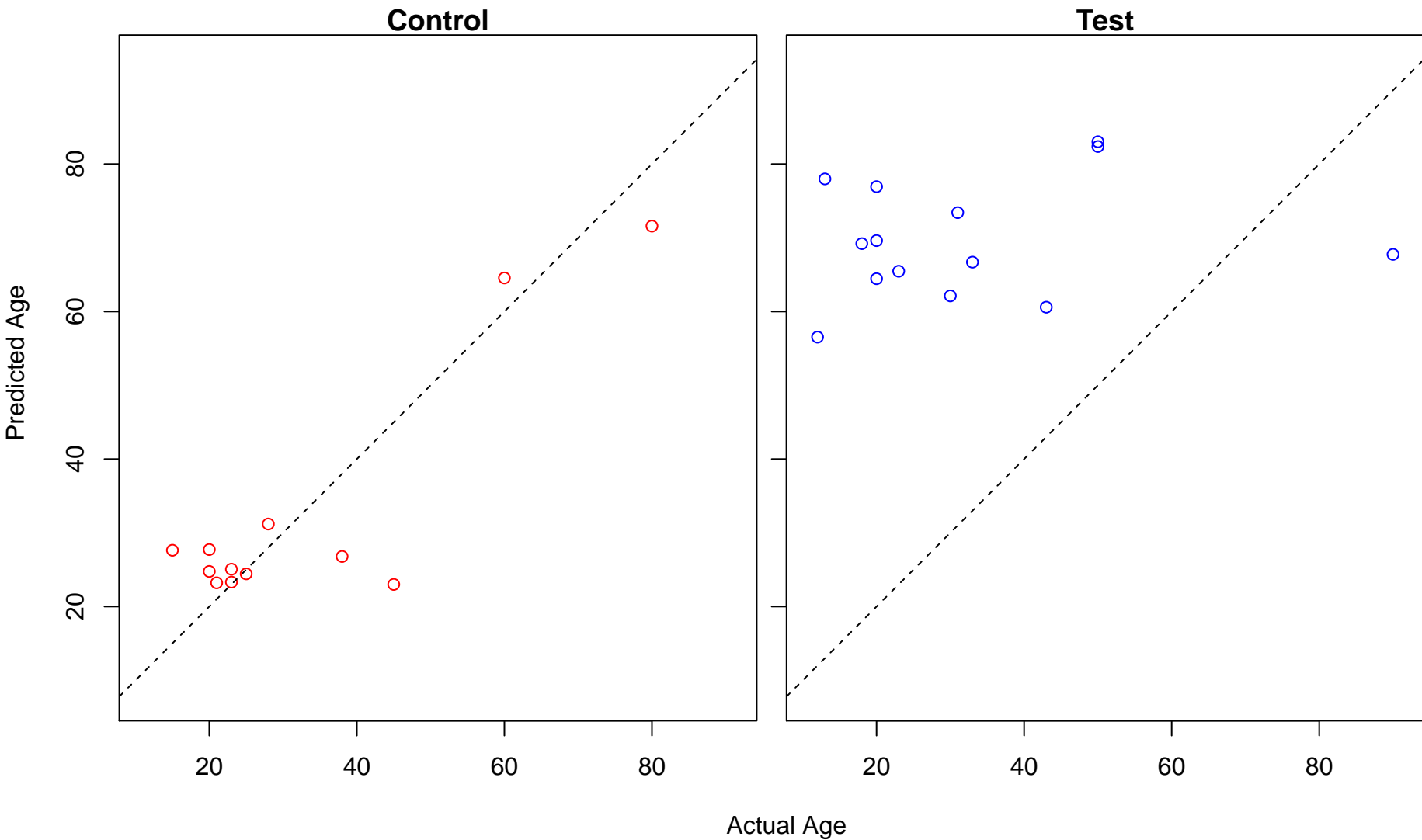


Actual Age

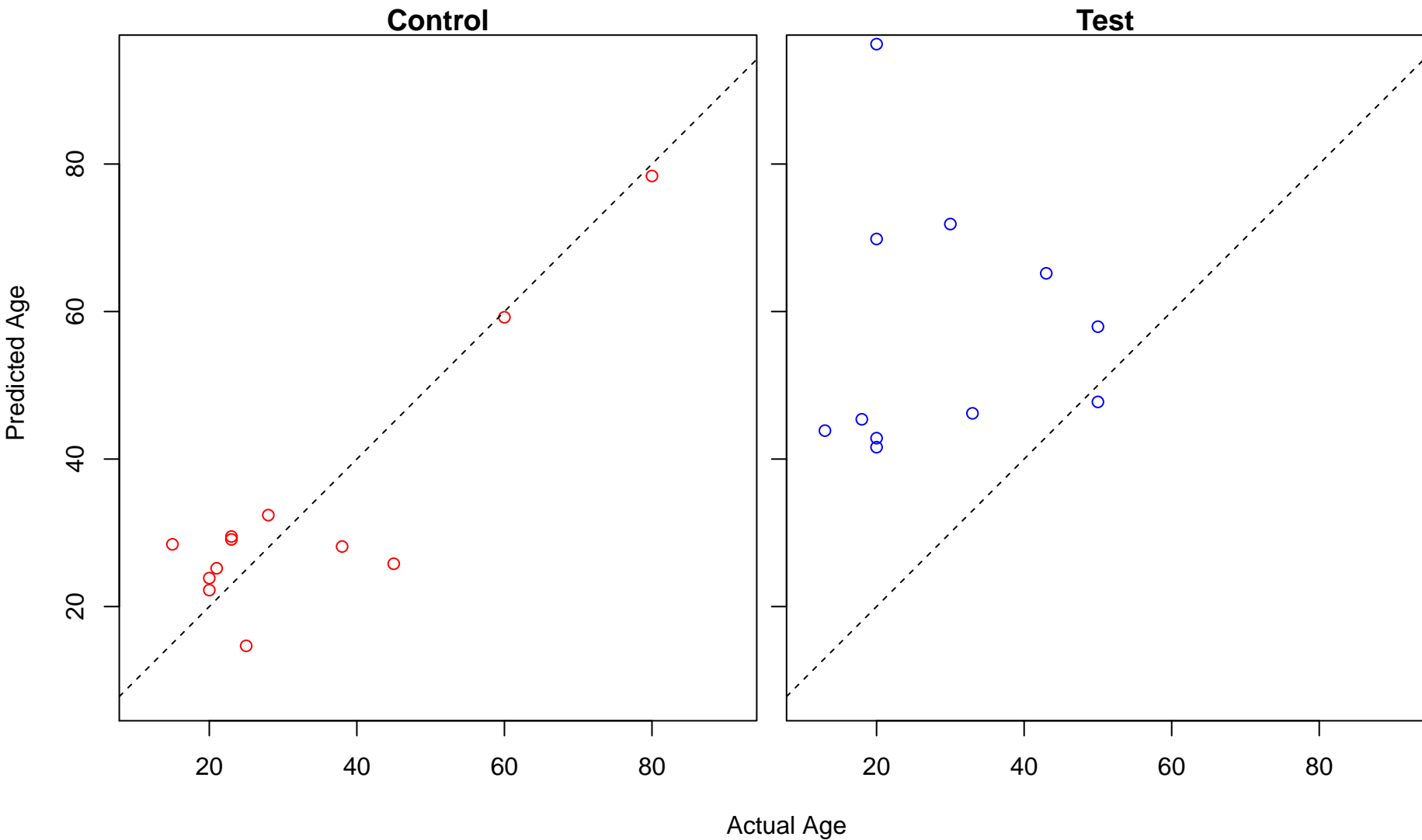
regulation of G0 to G1 transition (Score: 8.770665)



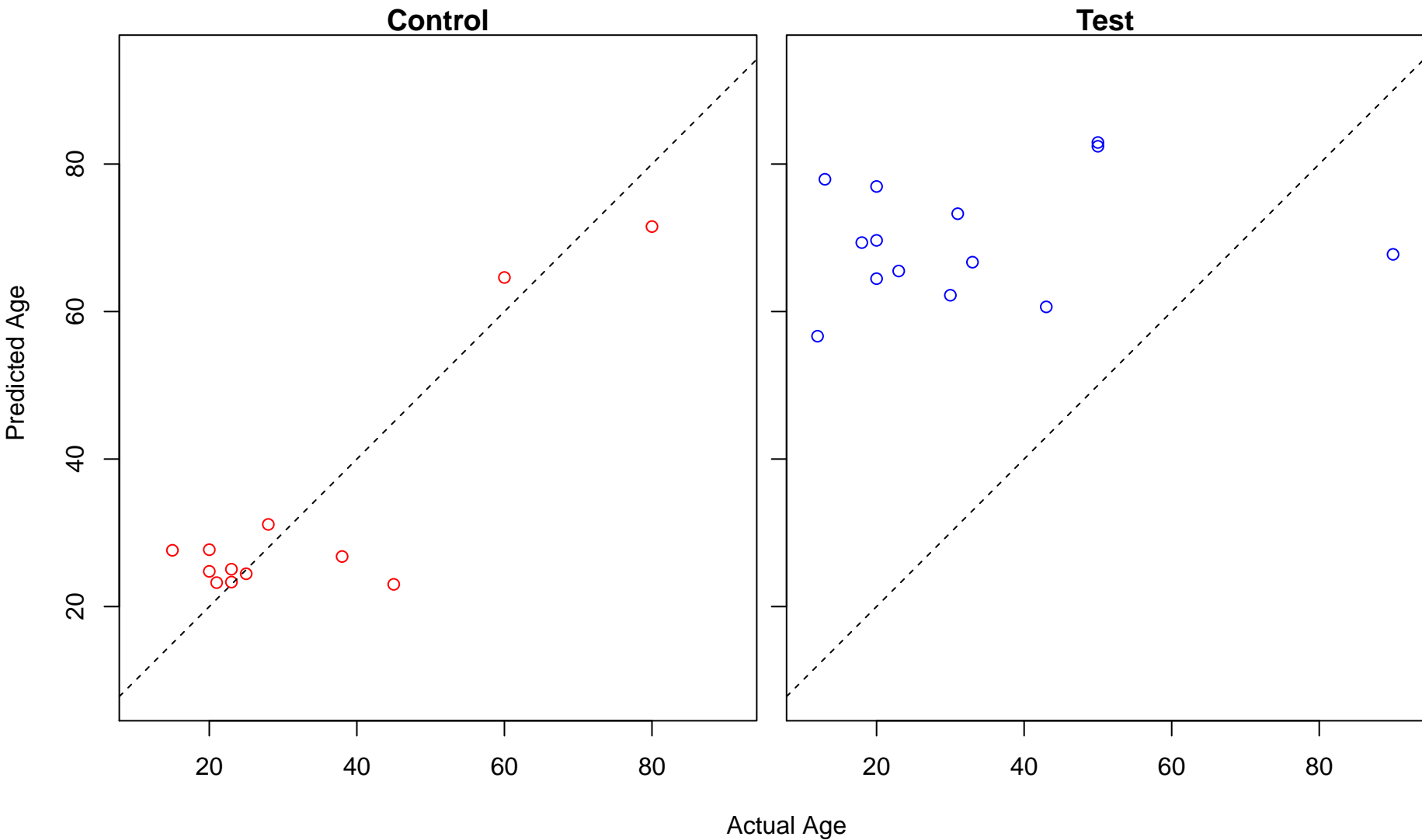
positive regulation of lyase activity (Score: 8.768080)



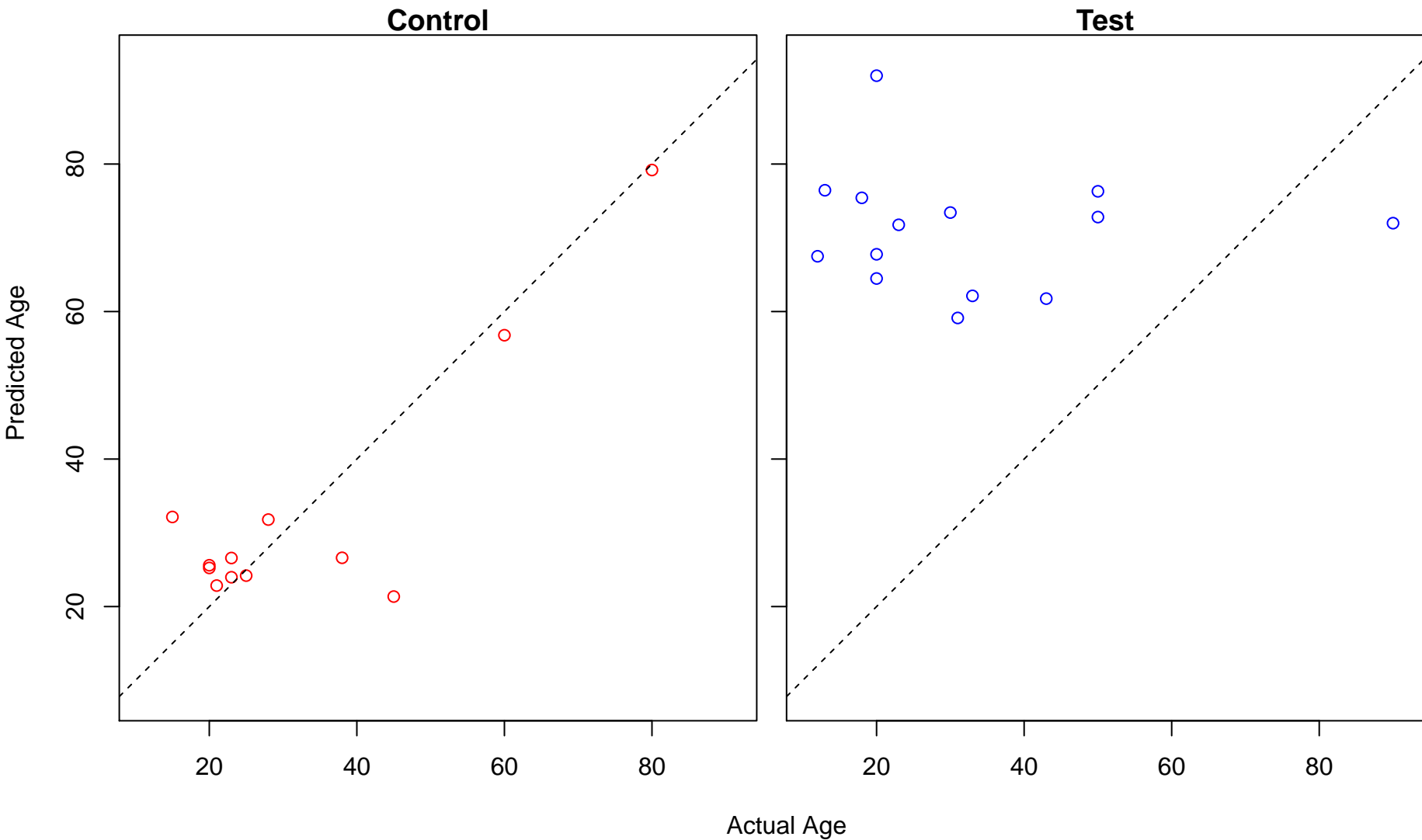
chondroitin sulfate proteoglycan biosynthetic process (Score: 8.766558)



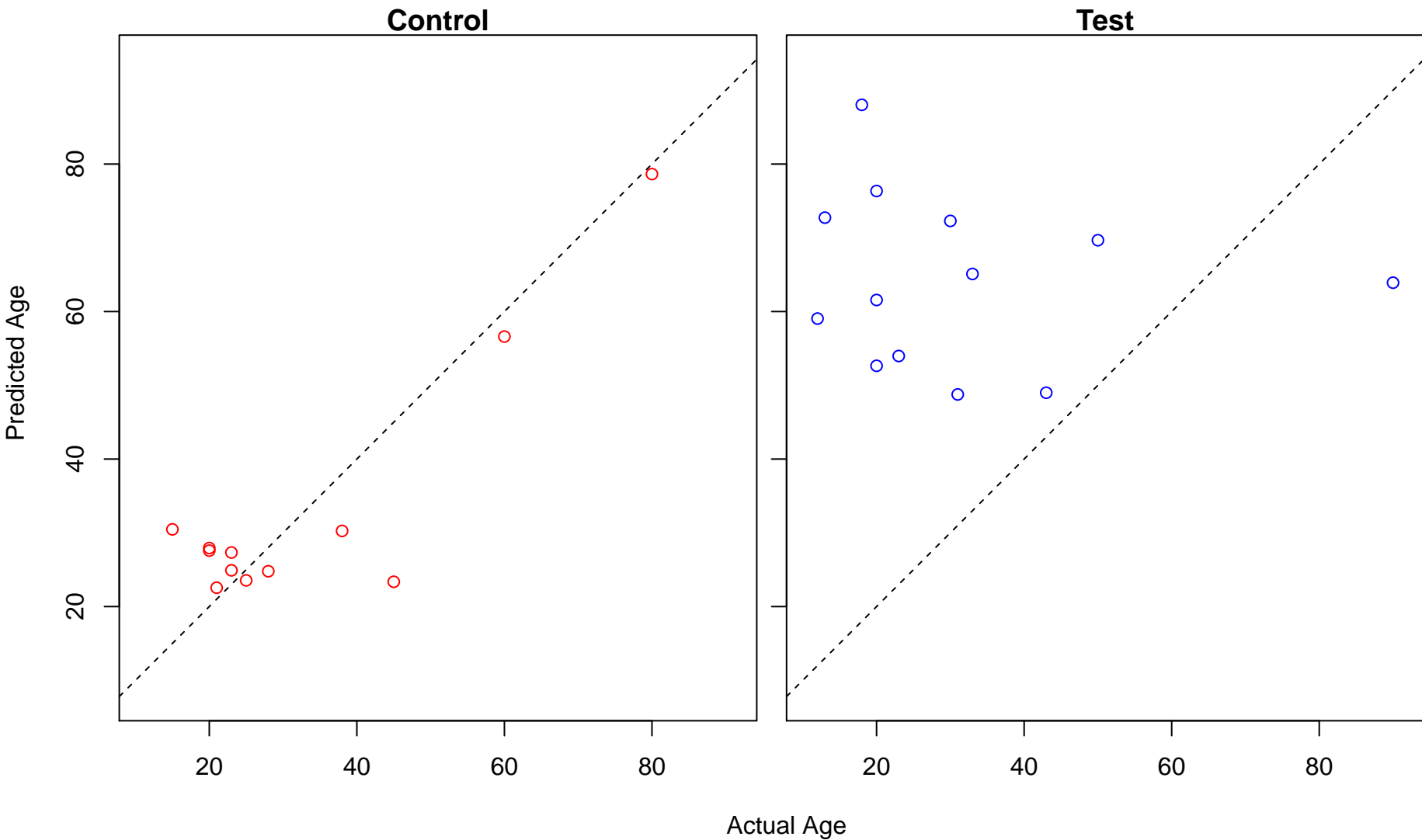
regulation of lyase activity (Score: 8.764869)



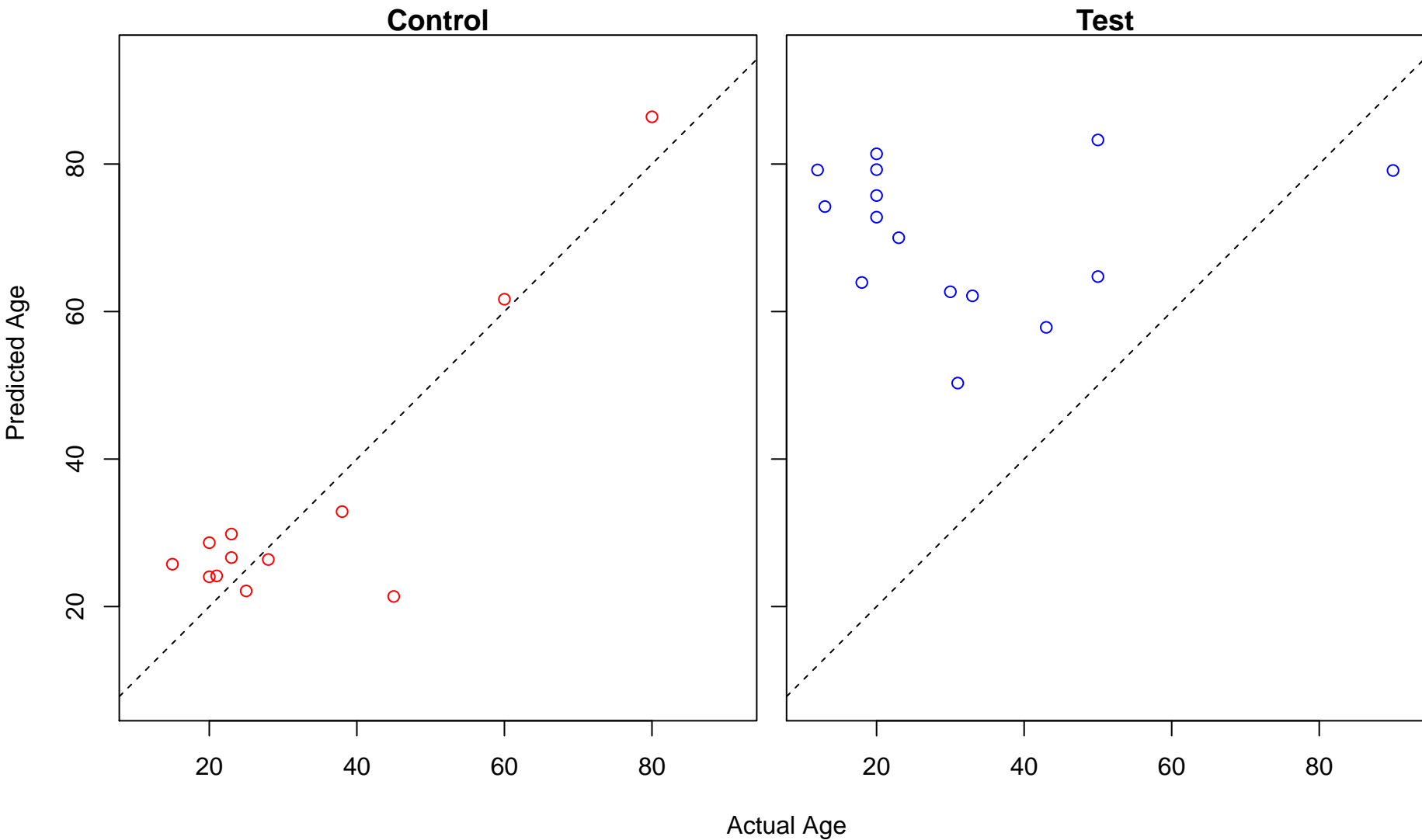
positive regulation of pathway-restricted SMAD protein phosphorylation (Score: 8.758861)



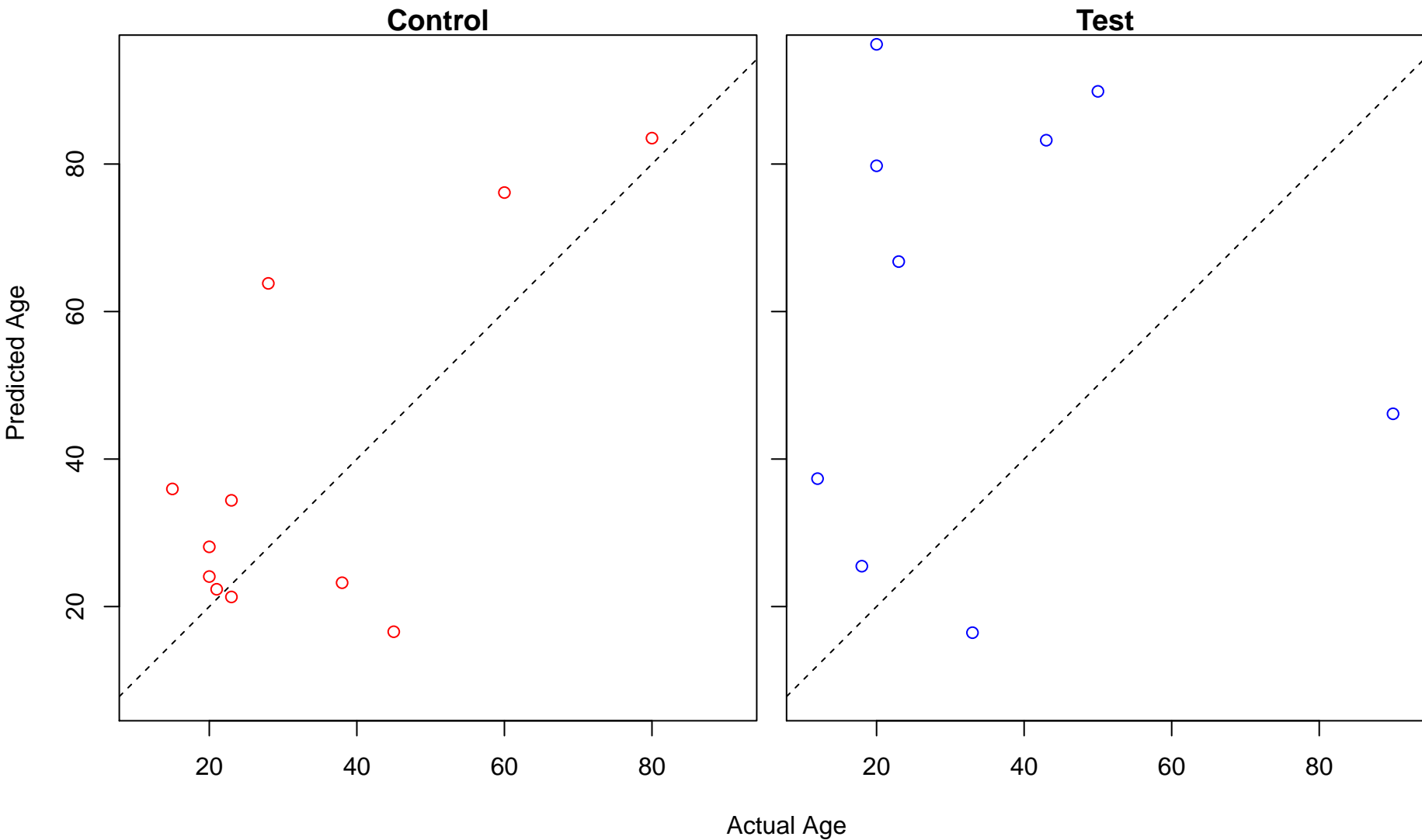
cell-cell signaling involved in cardiac conduction (Score: 8.758584)



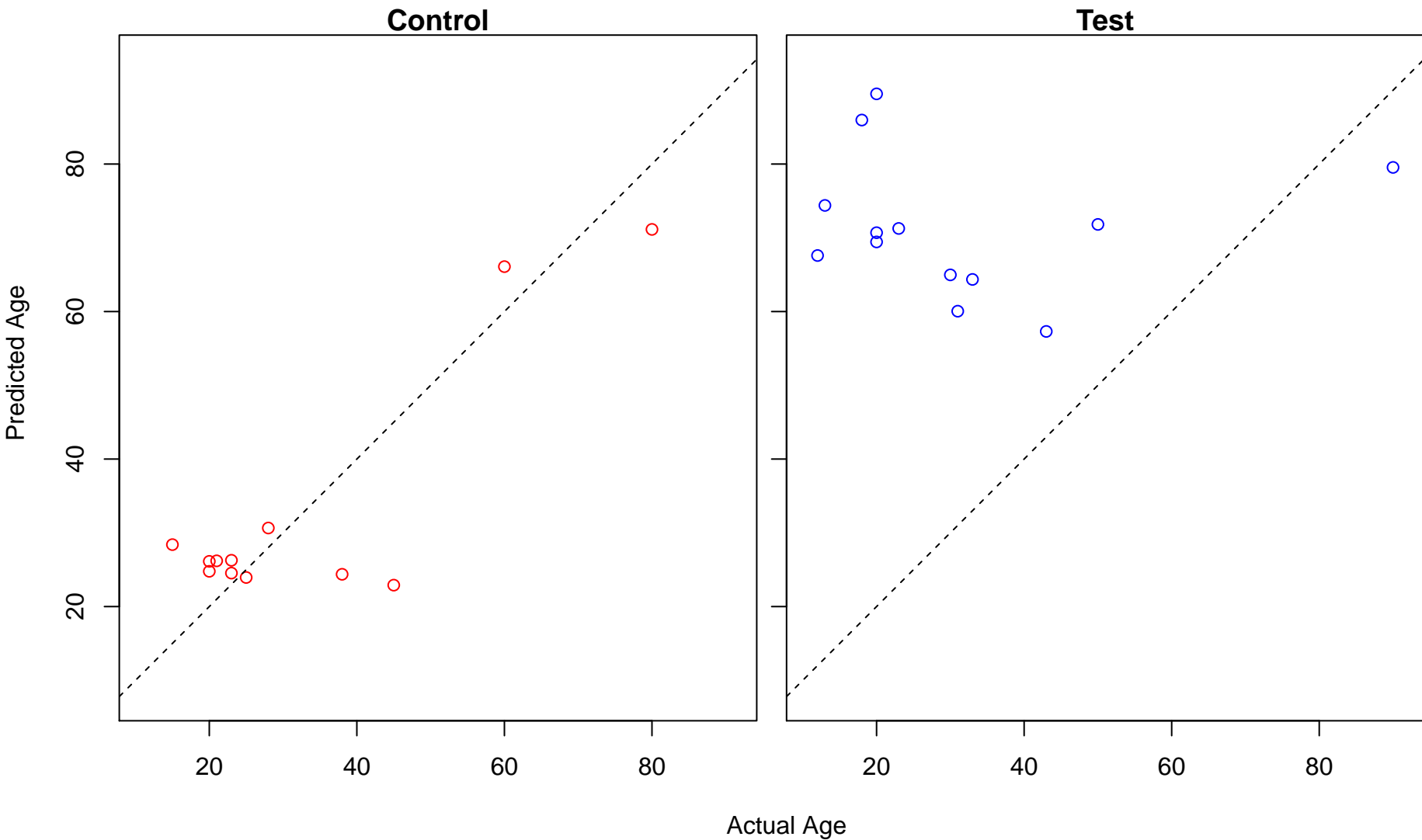
branching morphogenesis of an epithelial tube (Score: 8.755499)



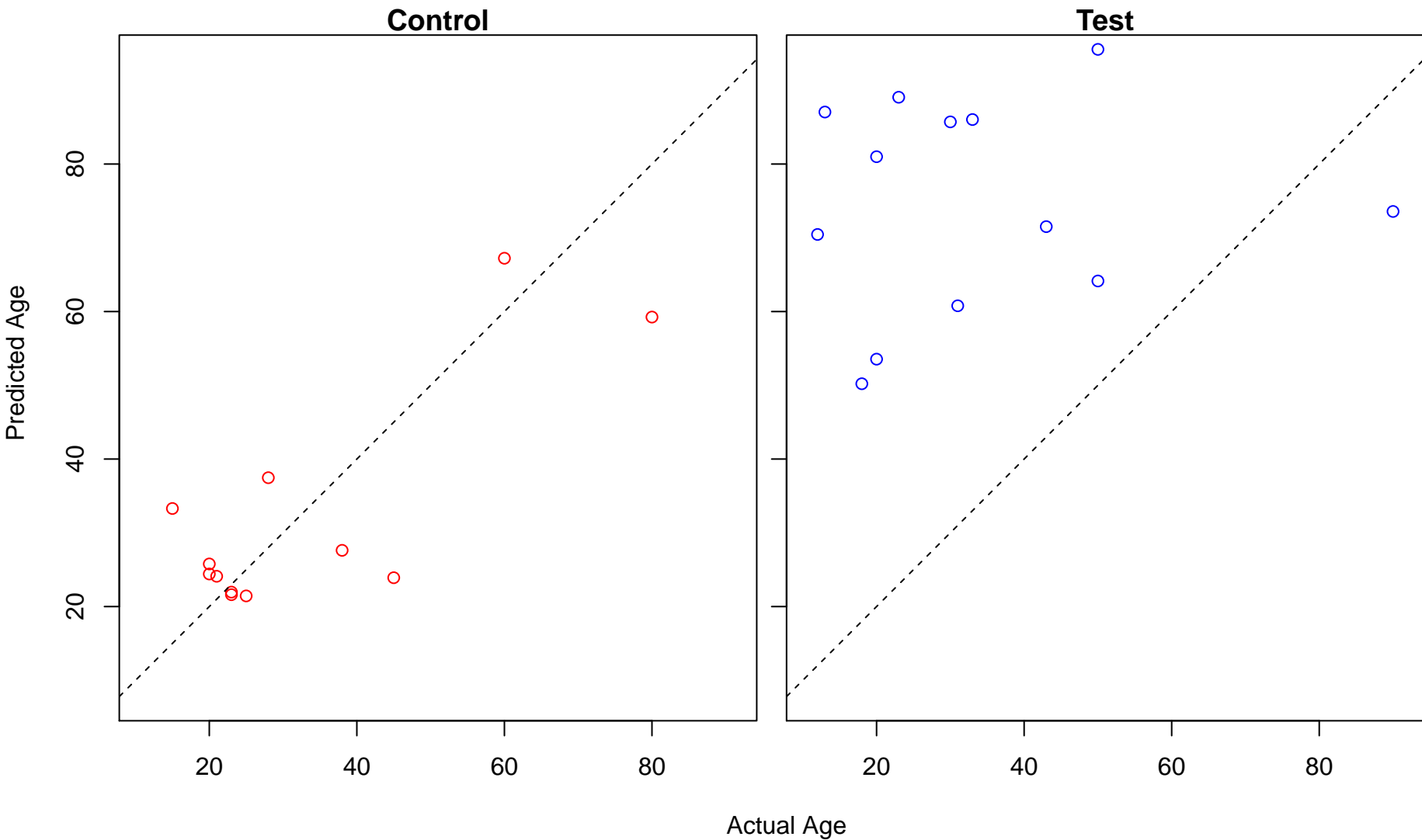
negative regulation of regulated secretory pathway (Score: 8.753894)



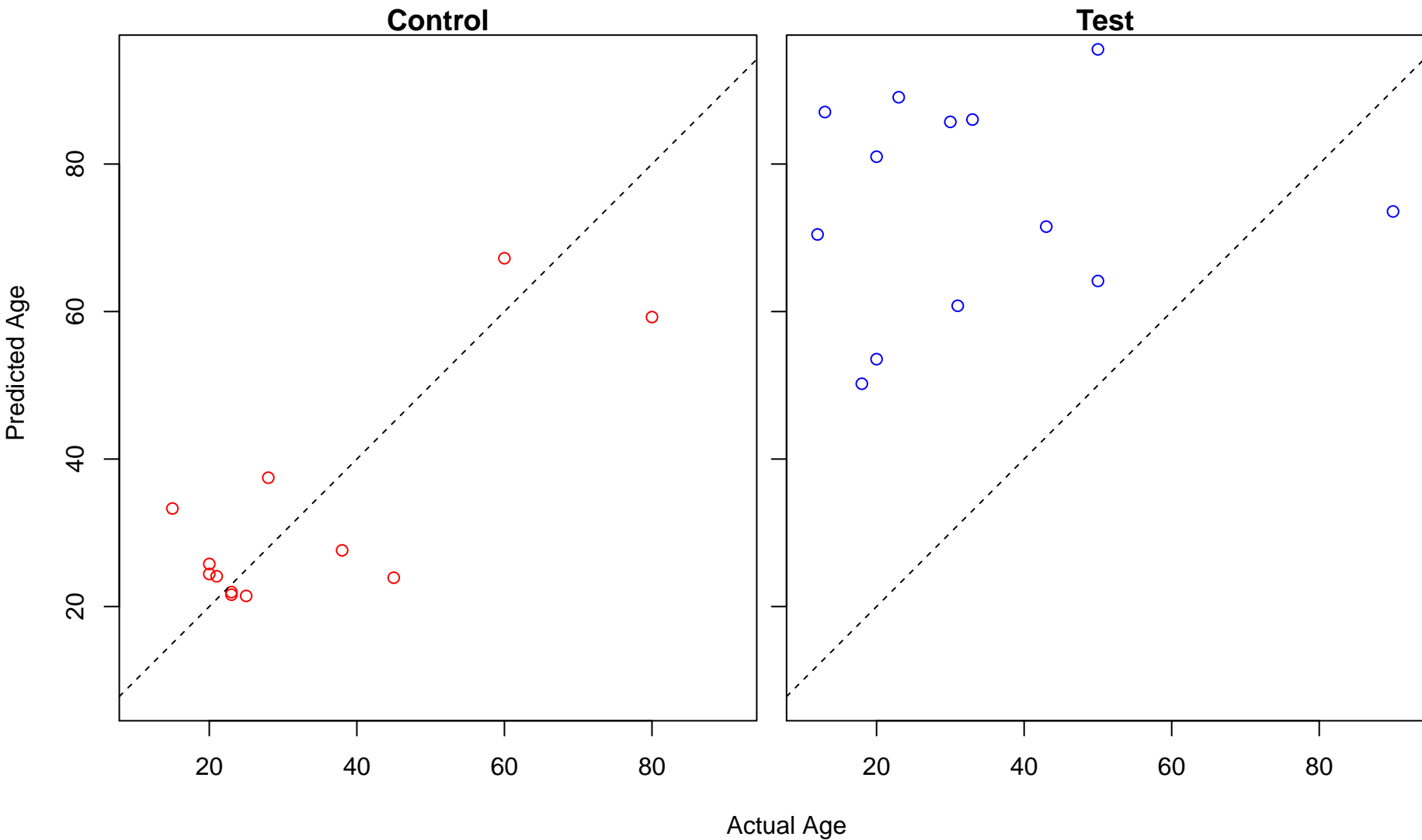
transcription initiation from RNA polymerase II promoter (Score: 8.744058)



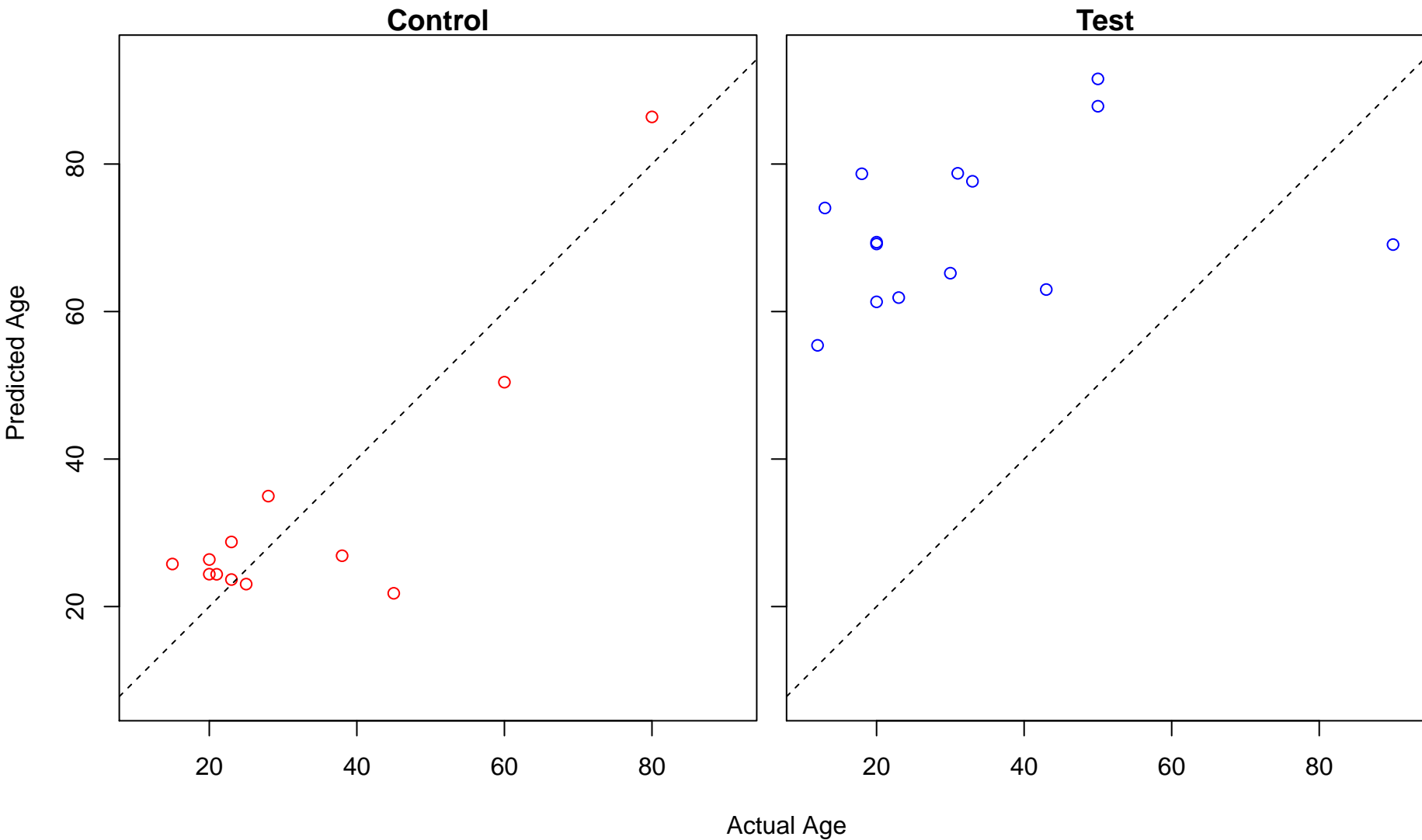
negative regulation of T cell differentiation in thymus (Score: 8.739231)



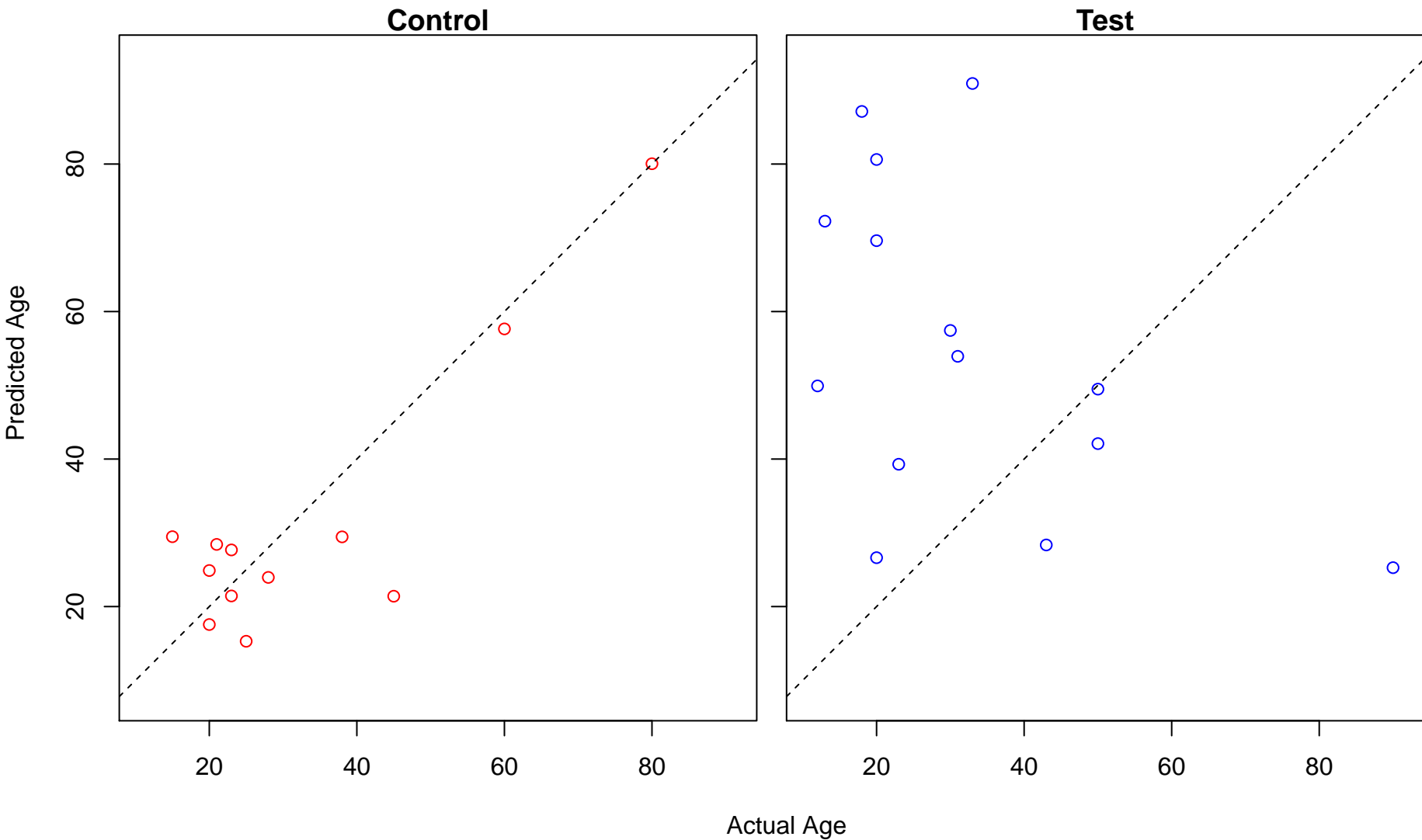
negative regulation of thymocyte aggregation (Score: 8.739231)



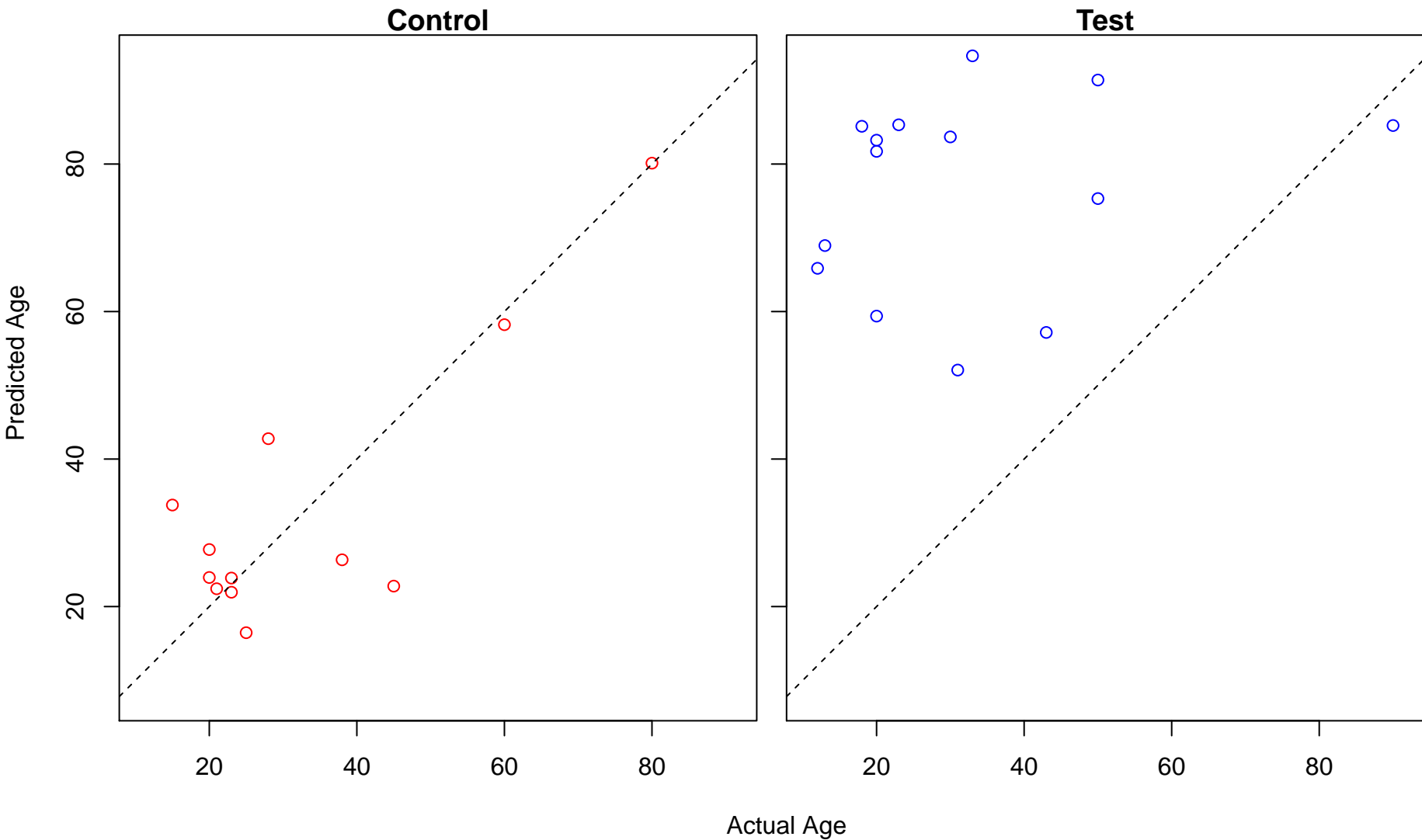
regulation of leukocyte migration (Score: 8.733975)



lipid phosphorylation (Score: 8.731518)

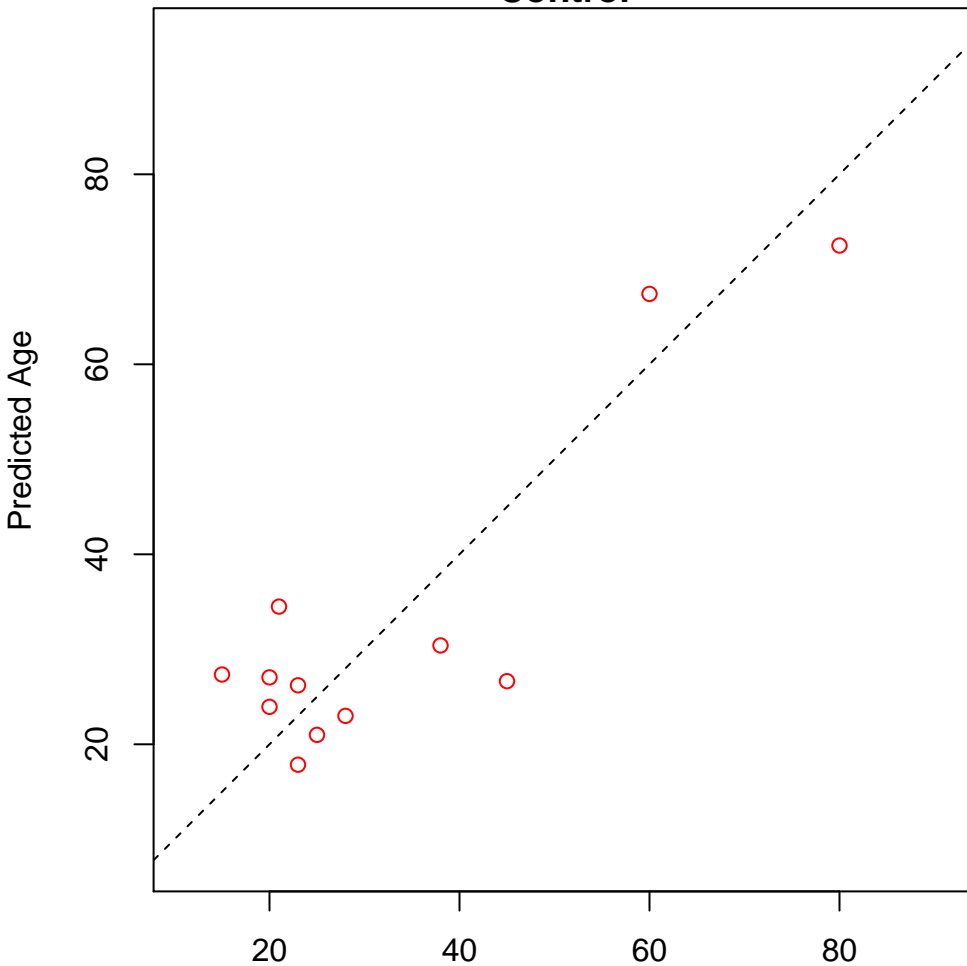


positive regulation of NIK/NF-kappaB signaling (Score: 8.725785)

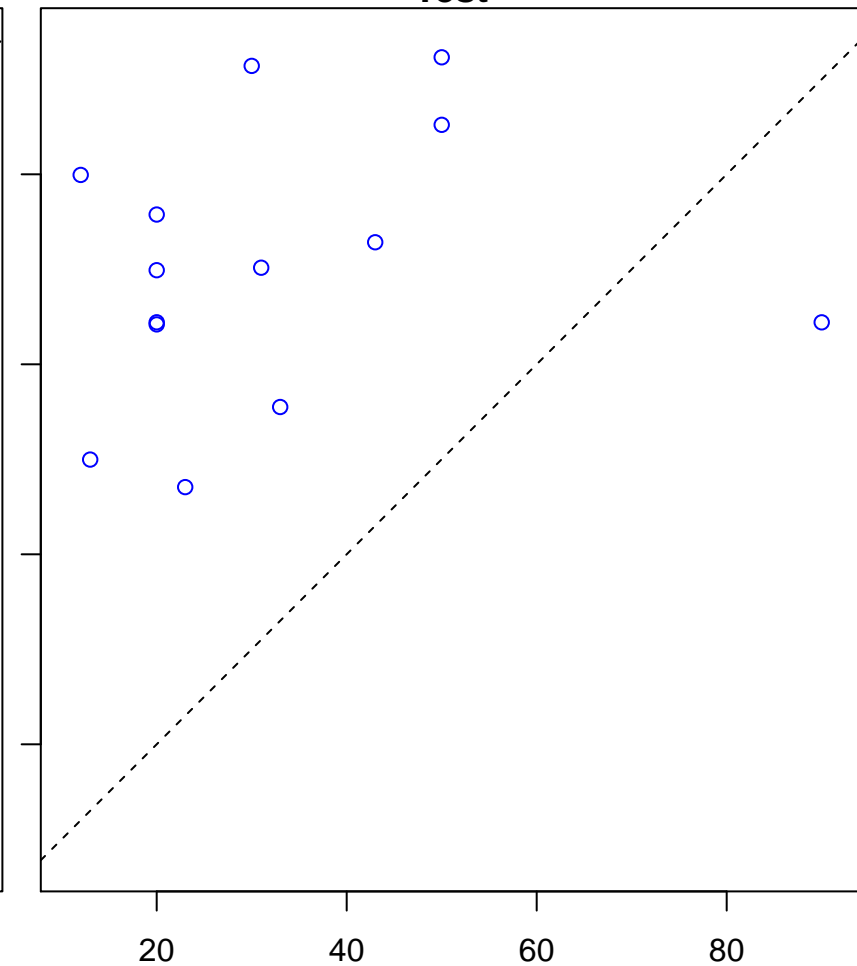


regulation of vasculature development (Score: 8.711103)

Control

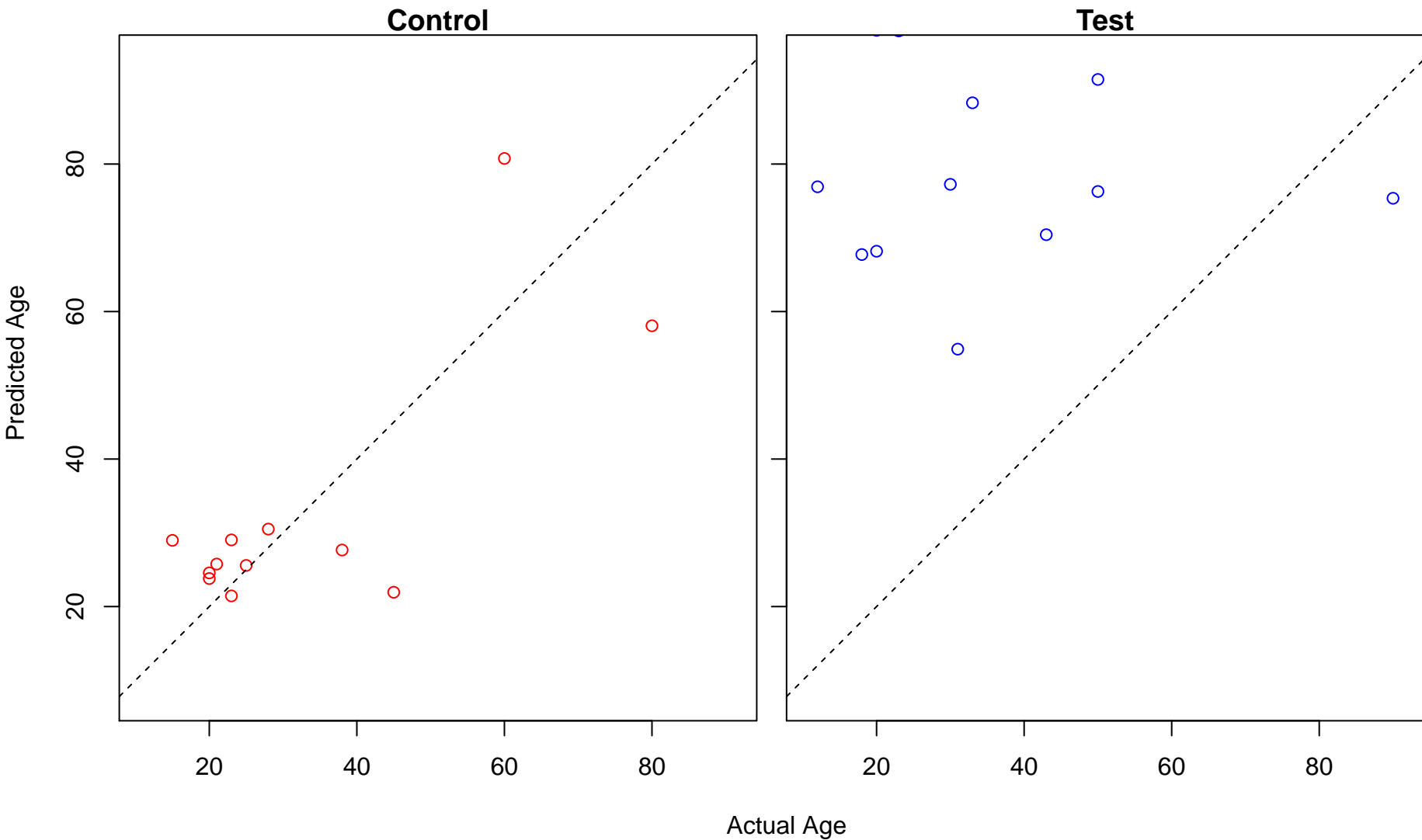


Test

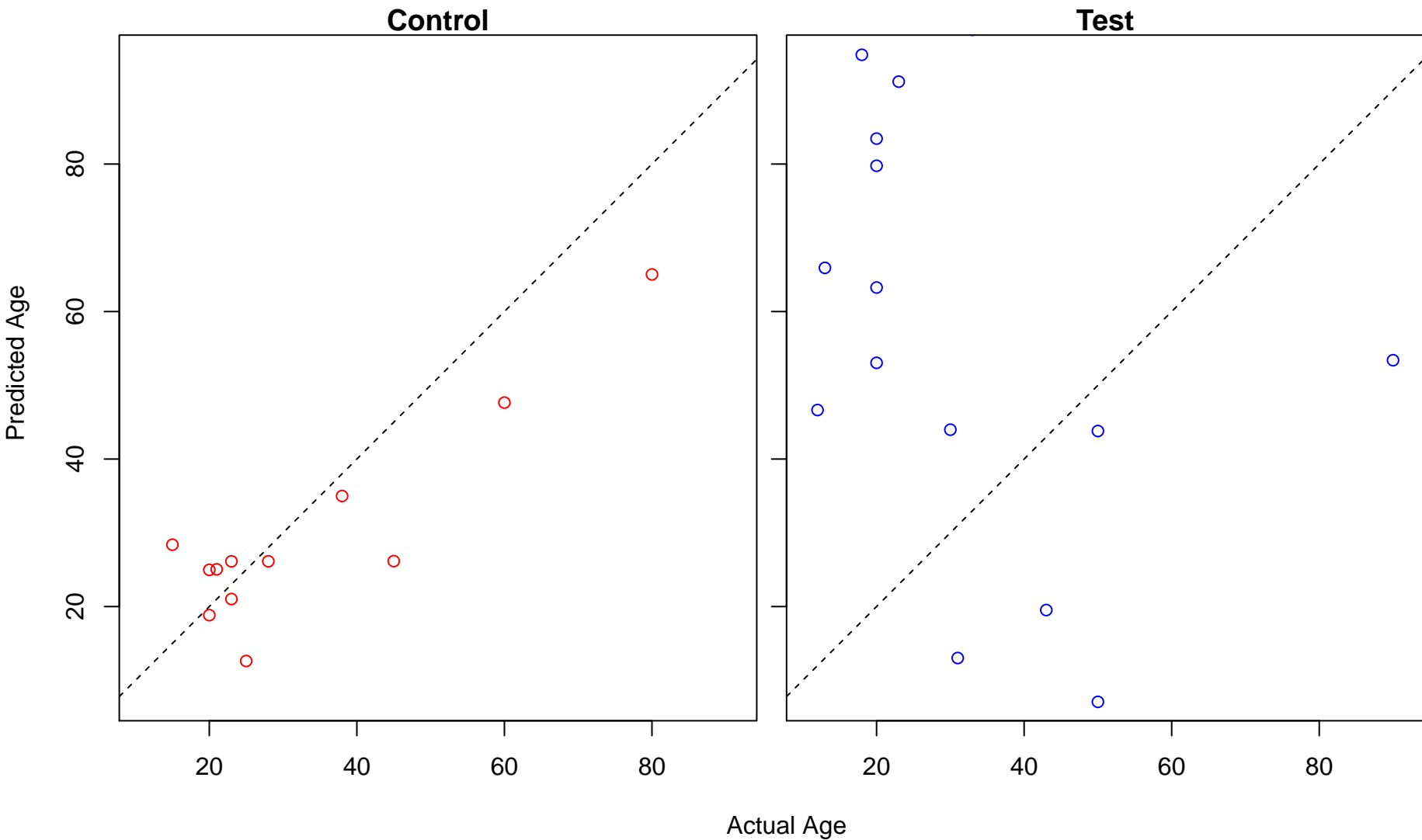


Actual Age

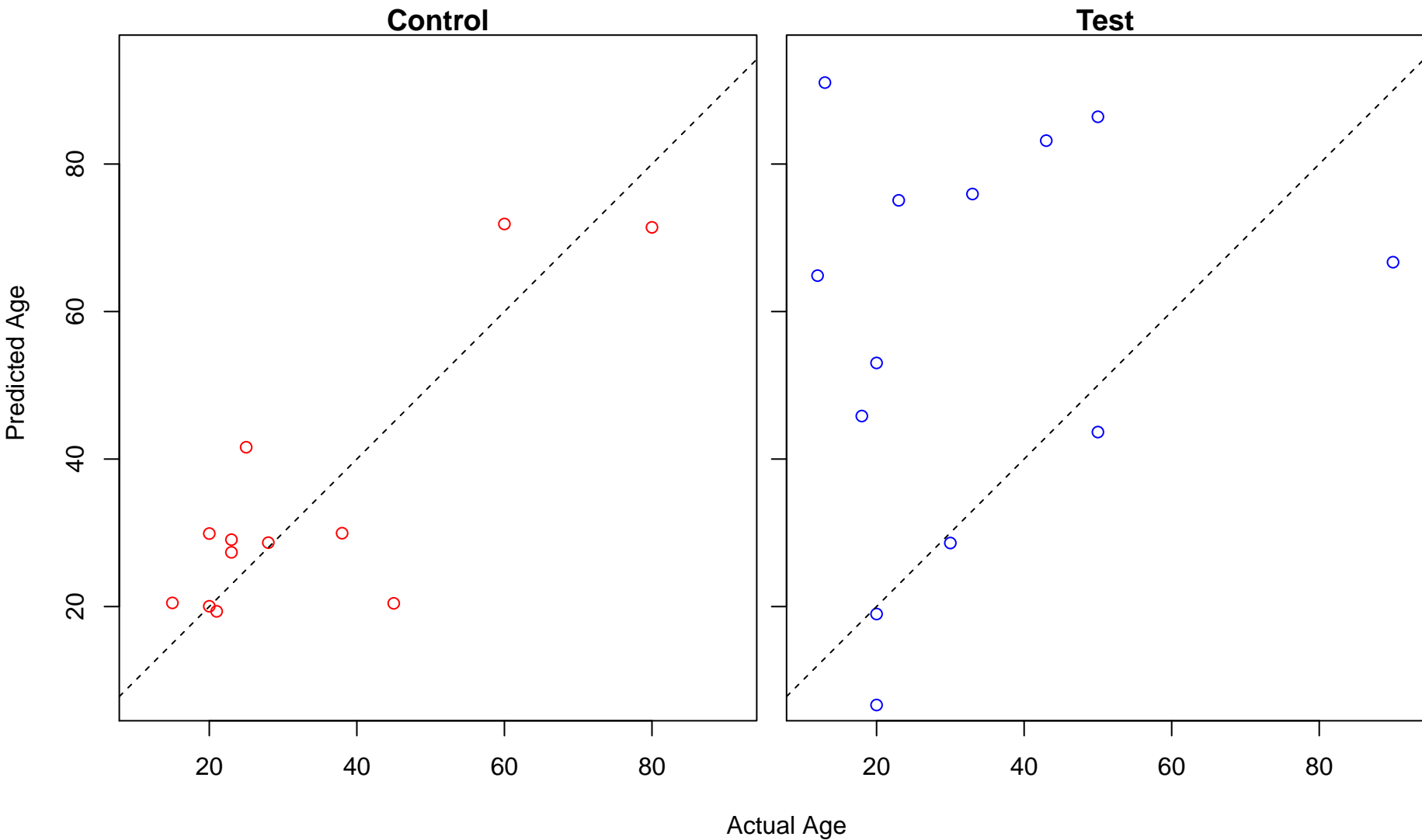
receptor-mediated virion attachment to host cell (Score: 8.706780)



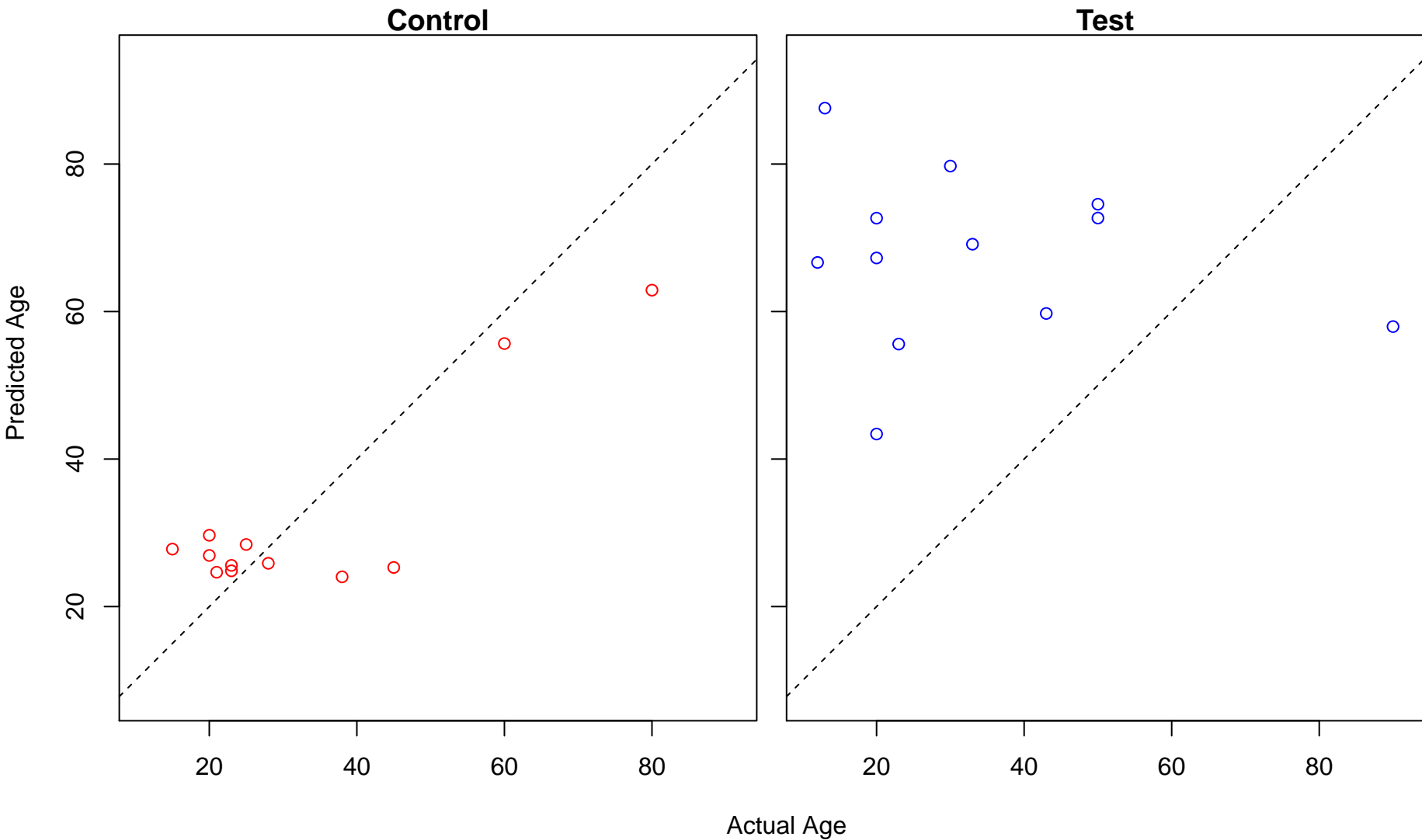
modulation by symbiont of host cellular process (Score: 8.706331)



interleukin-1 secretion (Score: 8.706065)

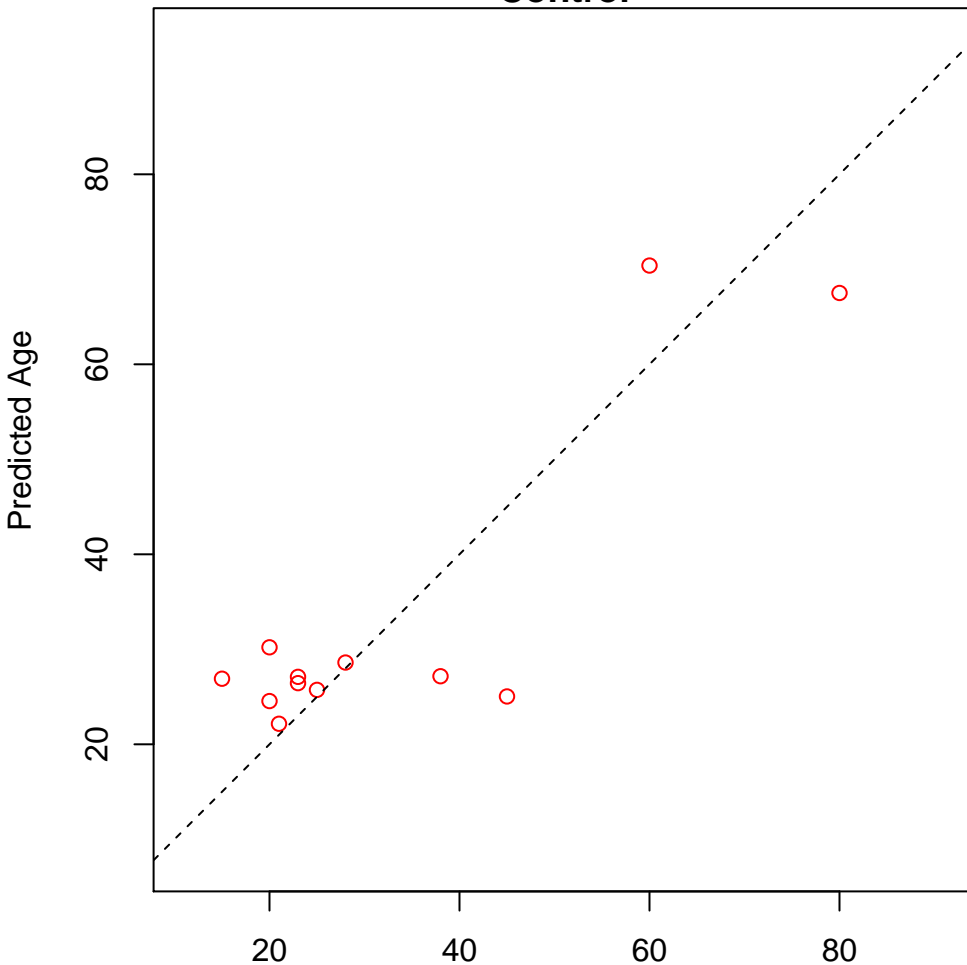


regulation of plasminogen activation (Score: 8.702375)

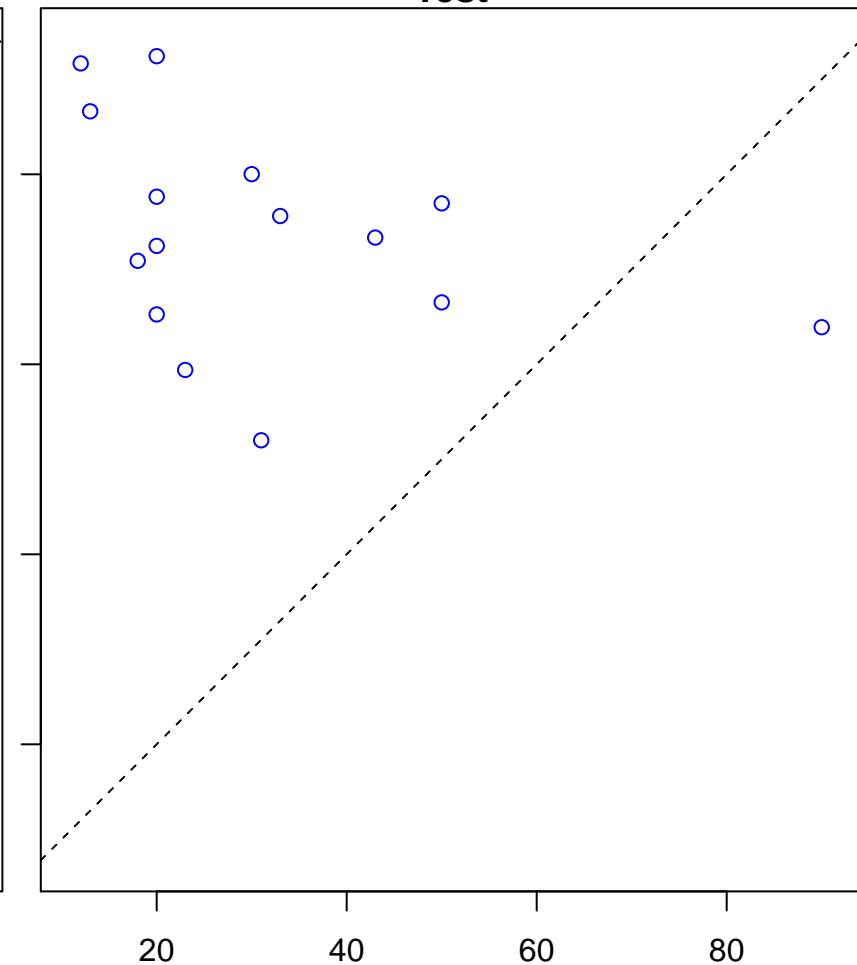


epithelial to mesenchymal transition (Score: 8.700564)

Control



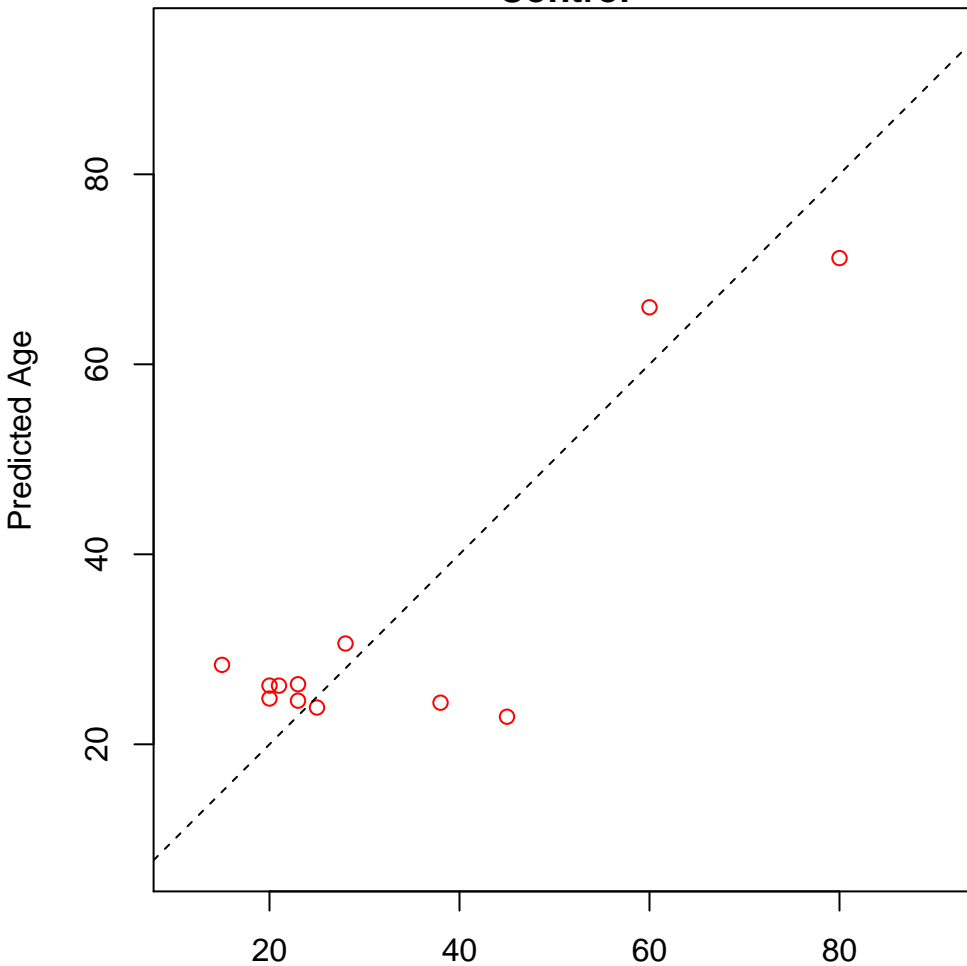
Test



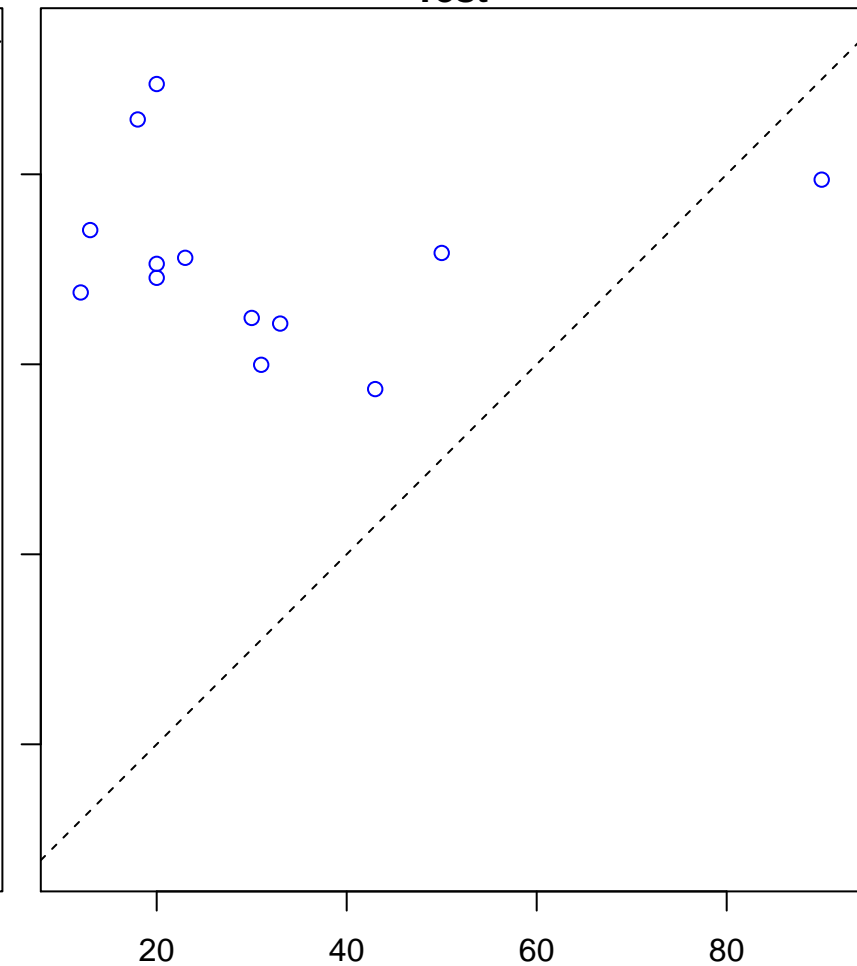
Actual Age

DNA-templated transcription, initiation (Score: 8.695322)

Control

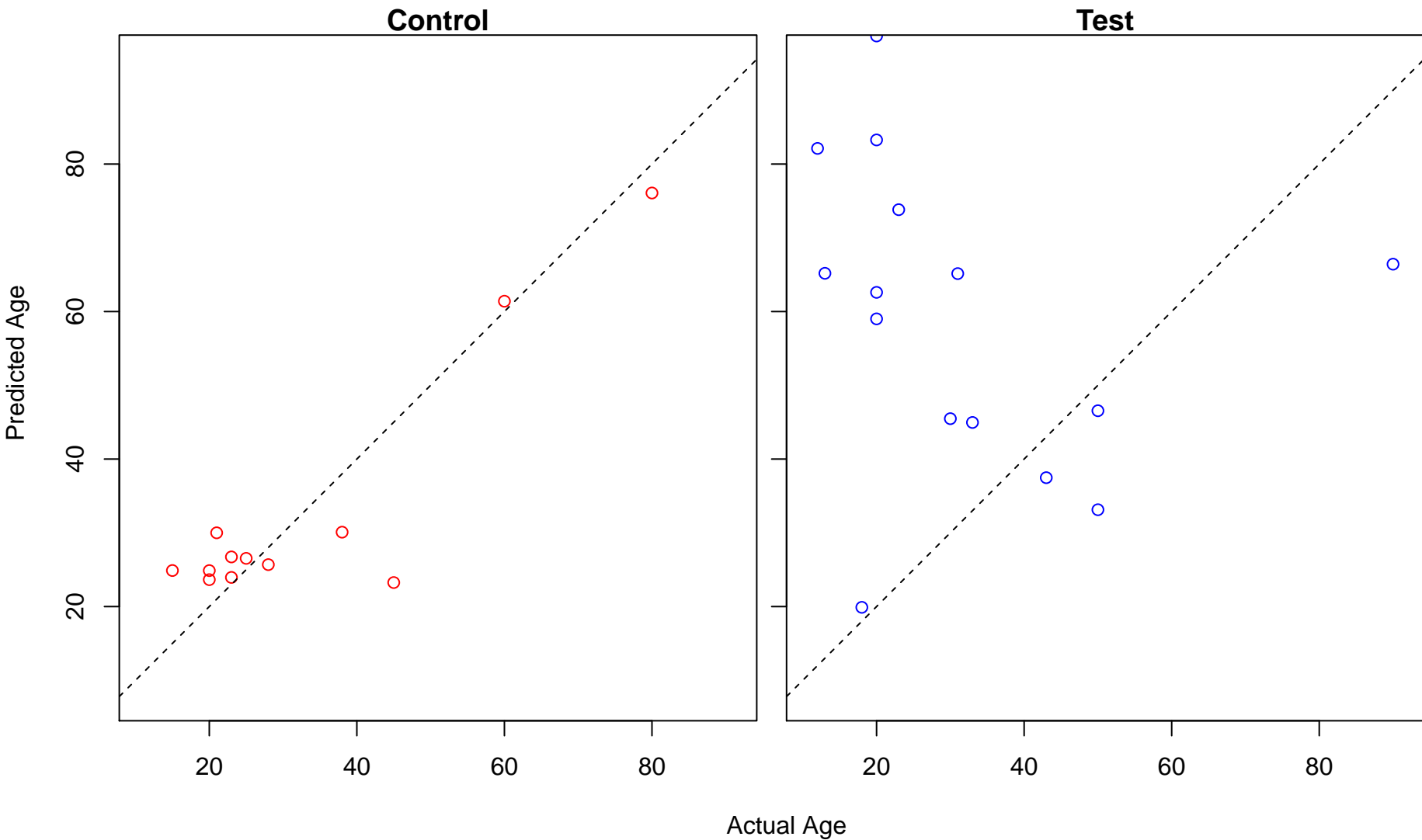


Test

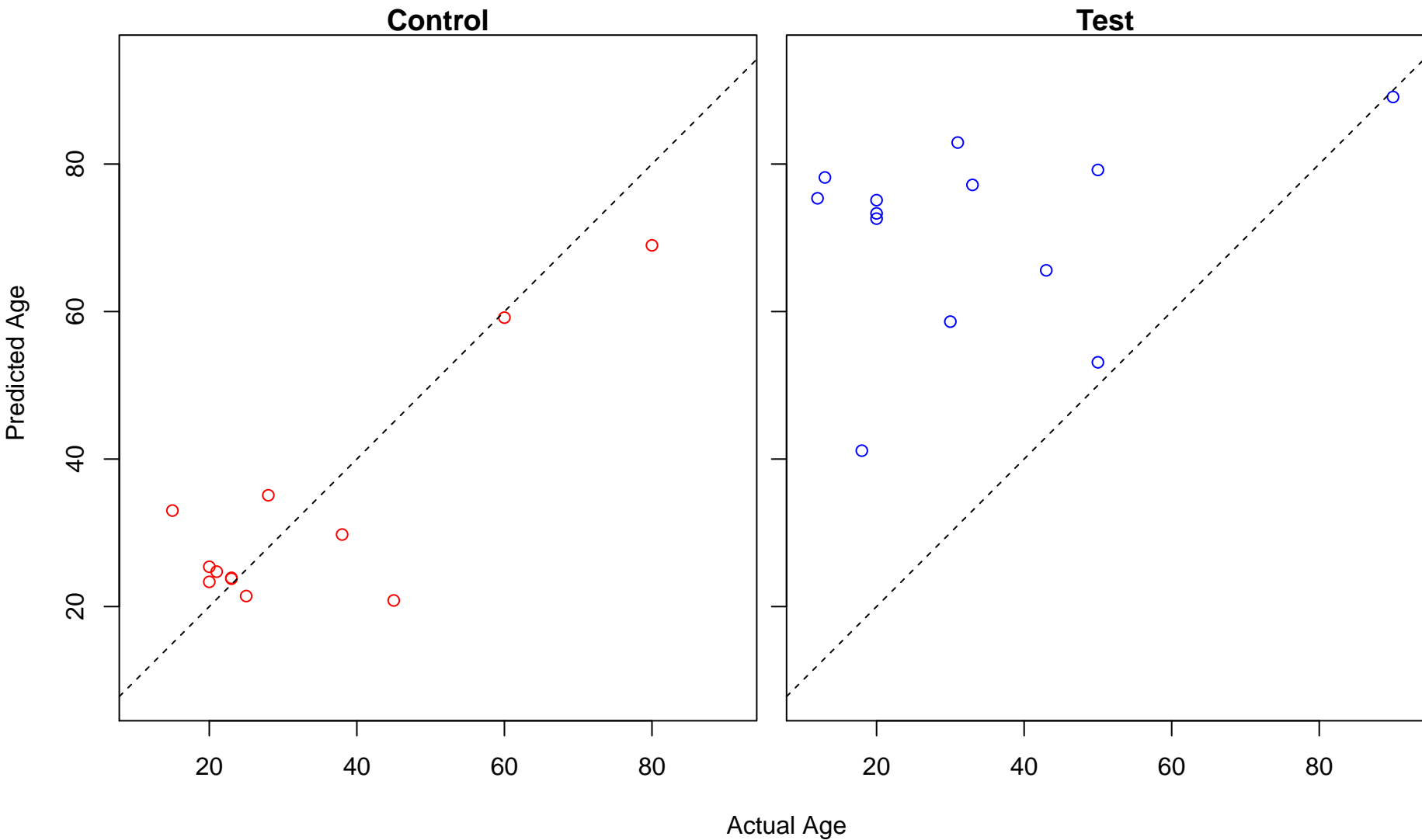


Actual Age

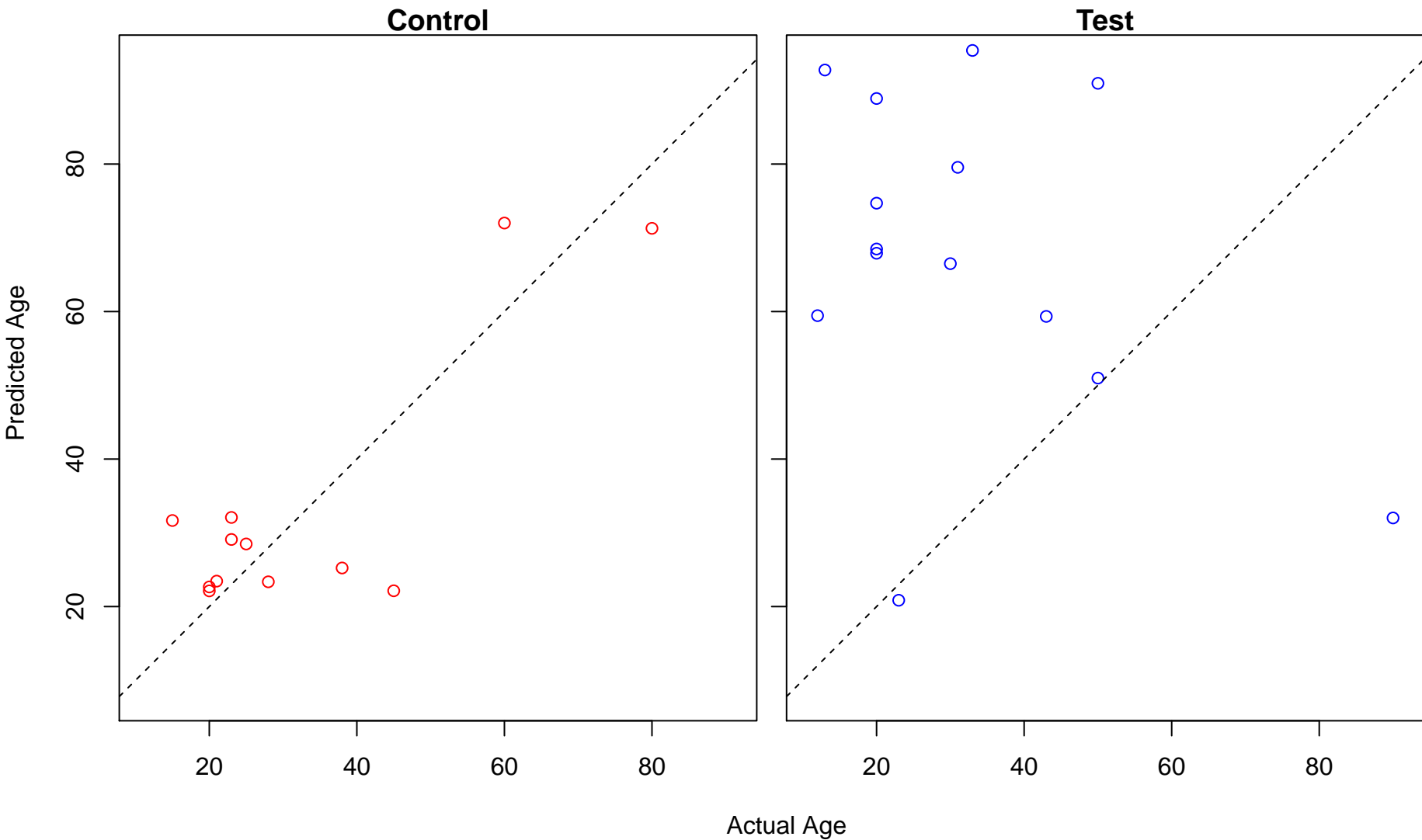
response to retinoic acid (Score: 8.690684)



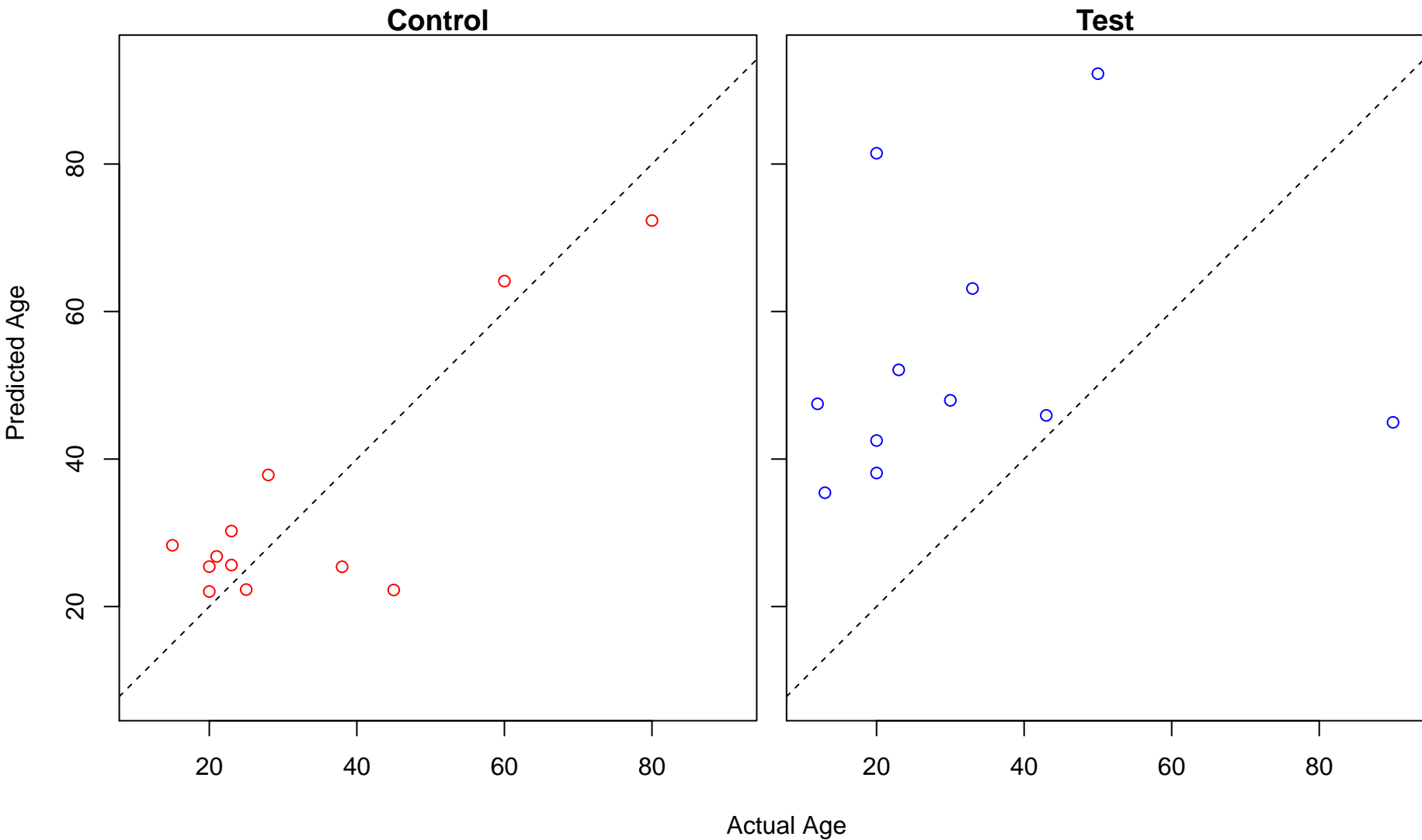
negative regulation of interleukin-1 secretion (Score: 8.690616)



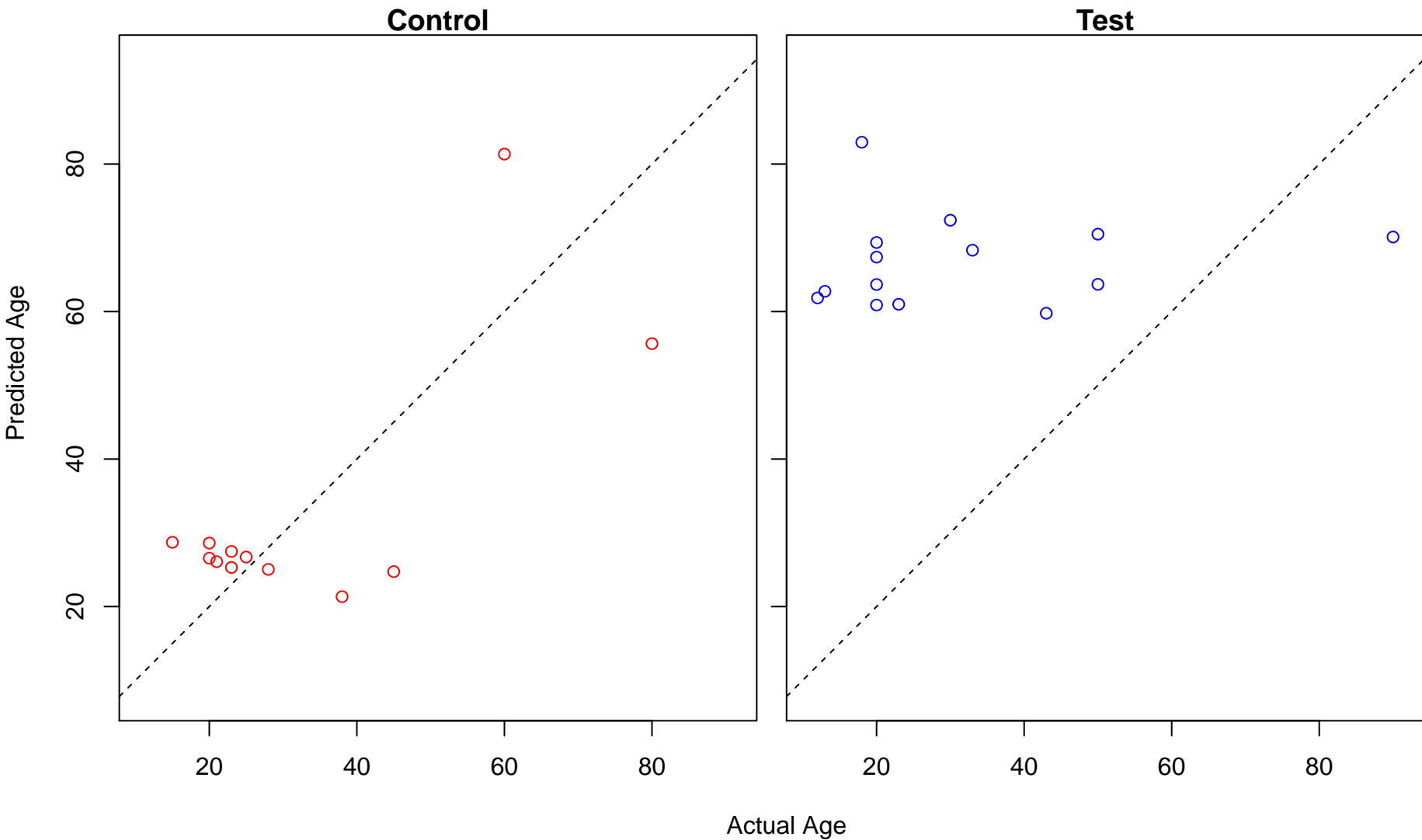
mitochondrion morphogenesis (Score: 8.689056)



homotypic cell-cell adhesion (Score: 8.687376)

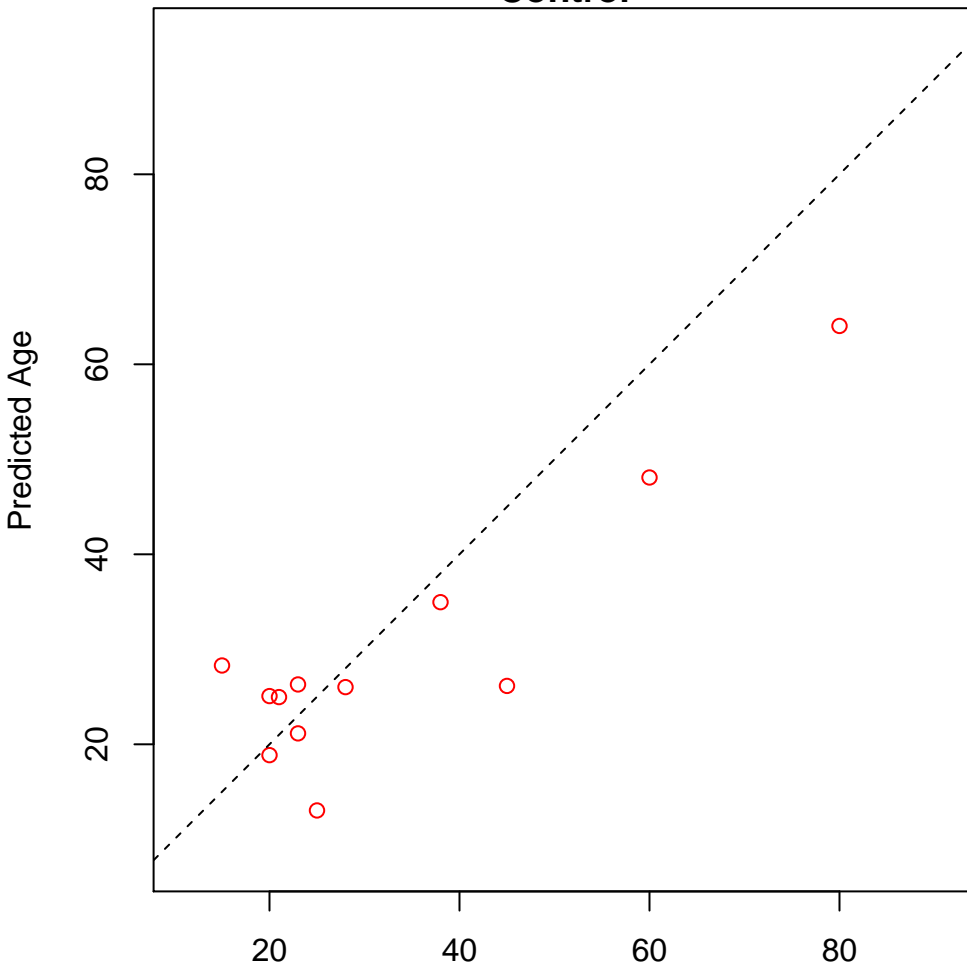


lymphocyte homeostasis (Score: 8.686636)

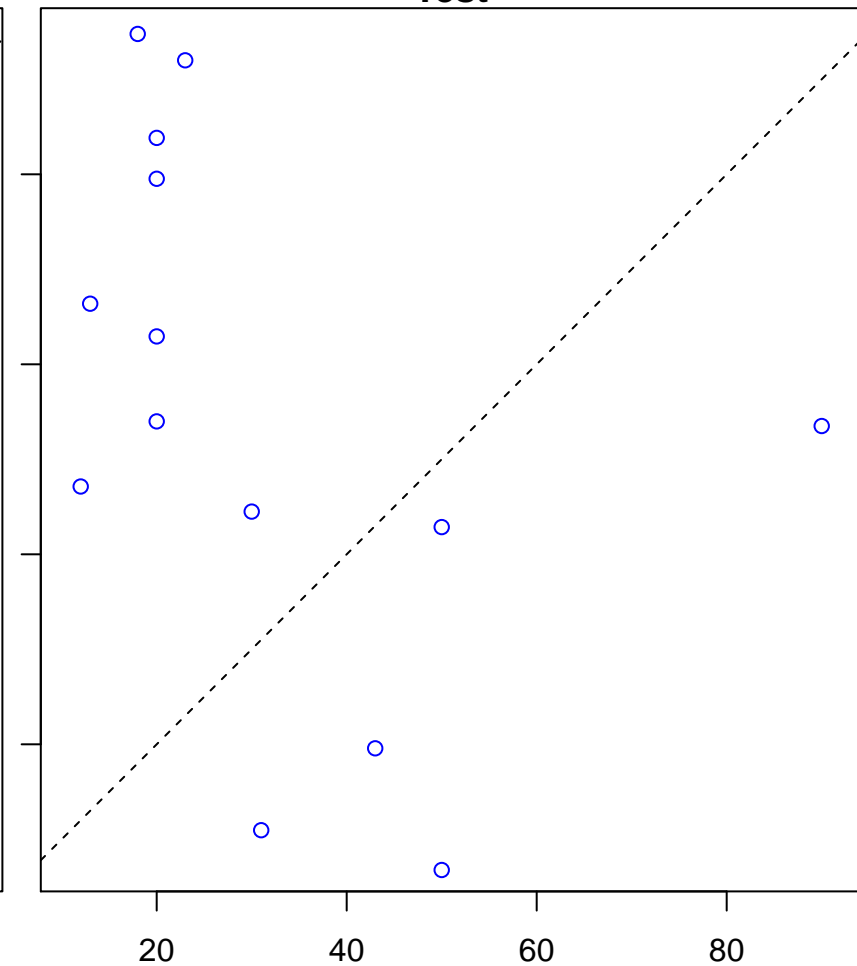


modulation by virus of host process (Score: 8.685886)

Control



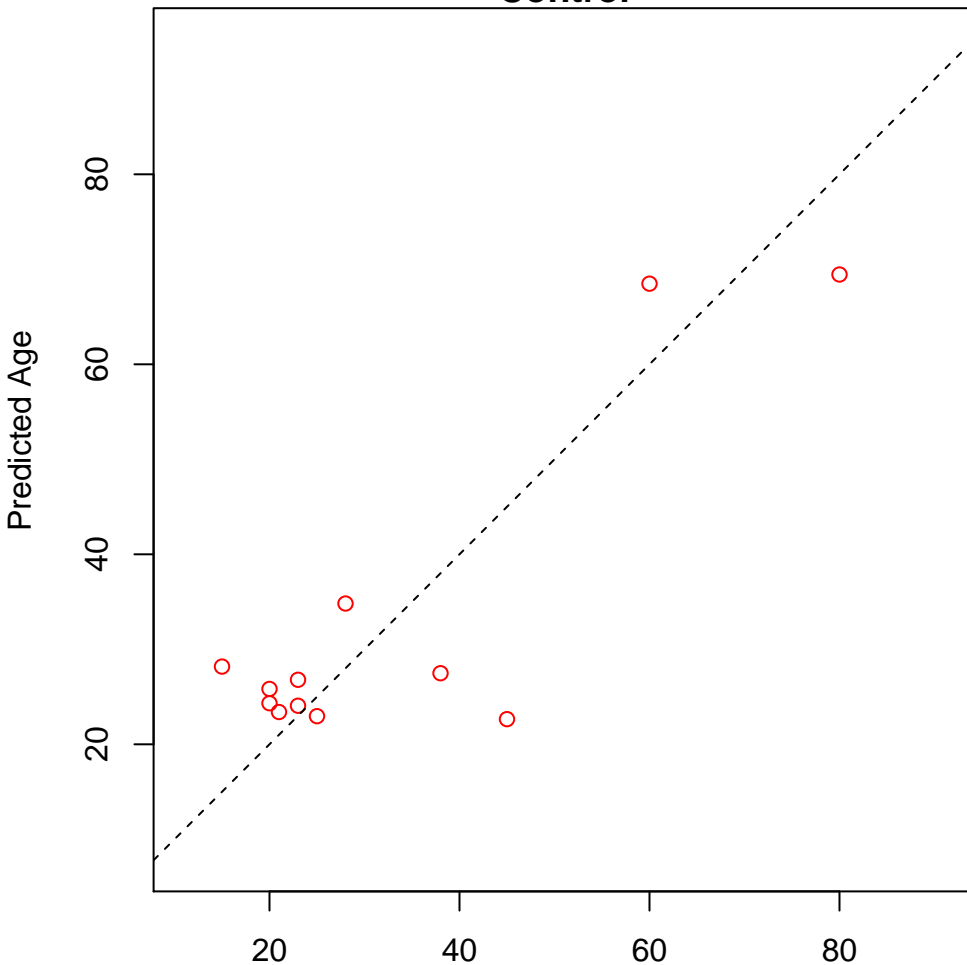
Test



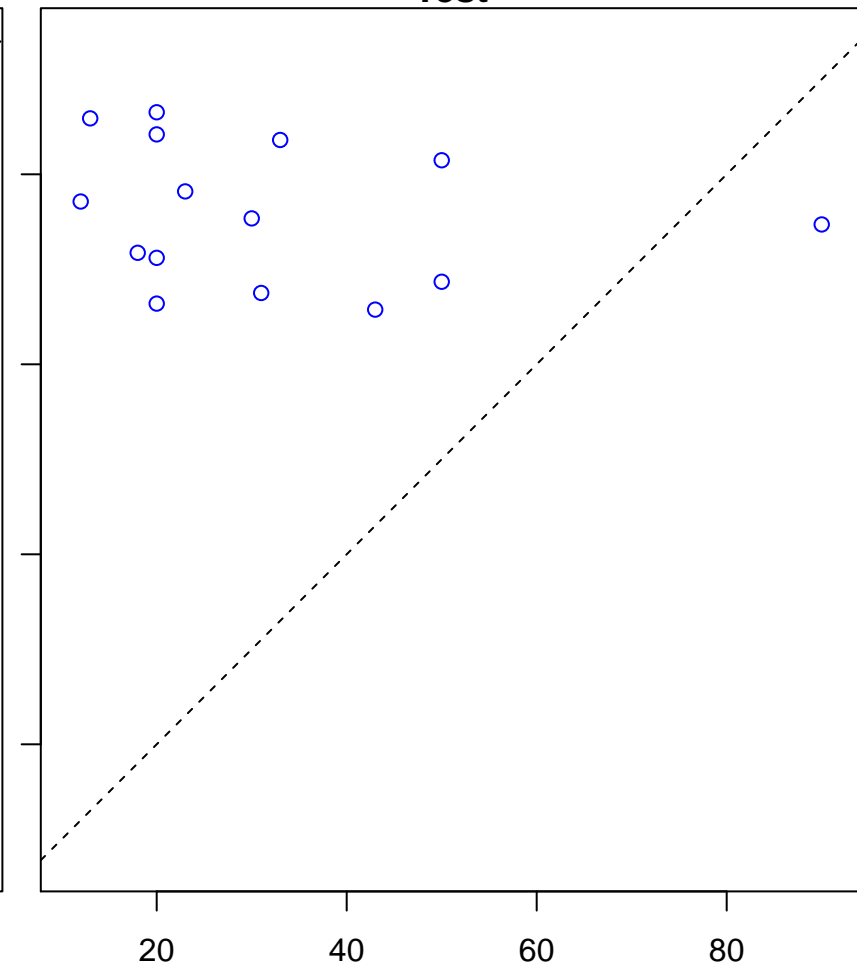
Actual Age

poly(A)+ mRNA export from nucleus (Score: 8.684662)

Control

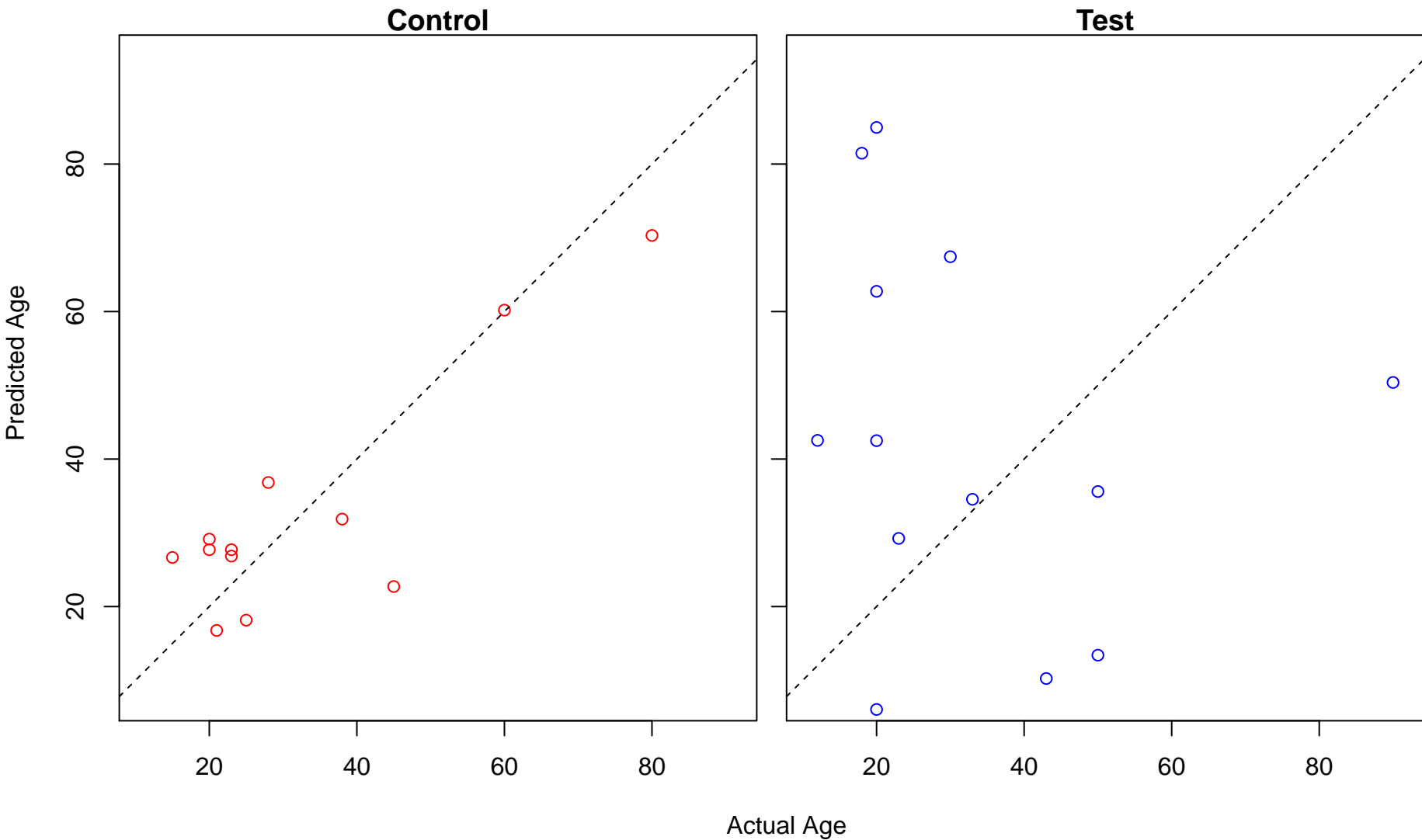


Test

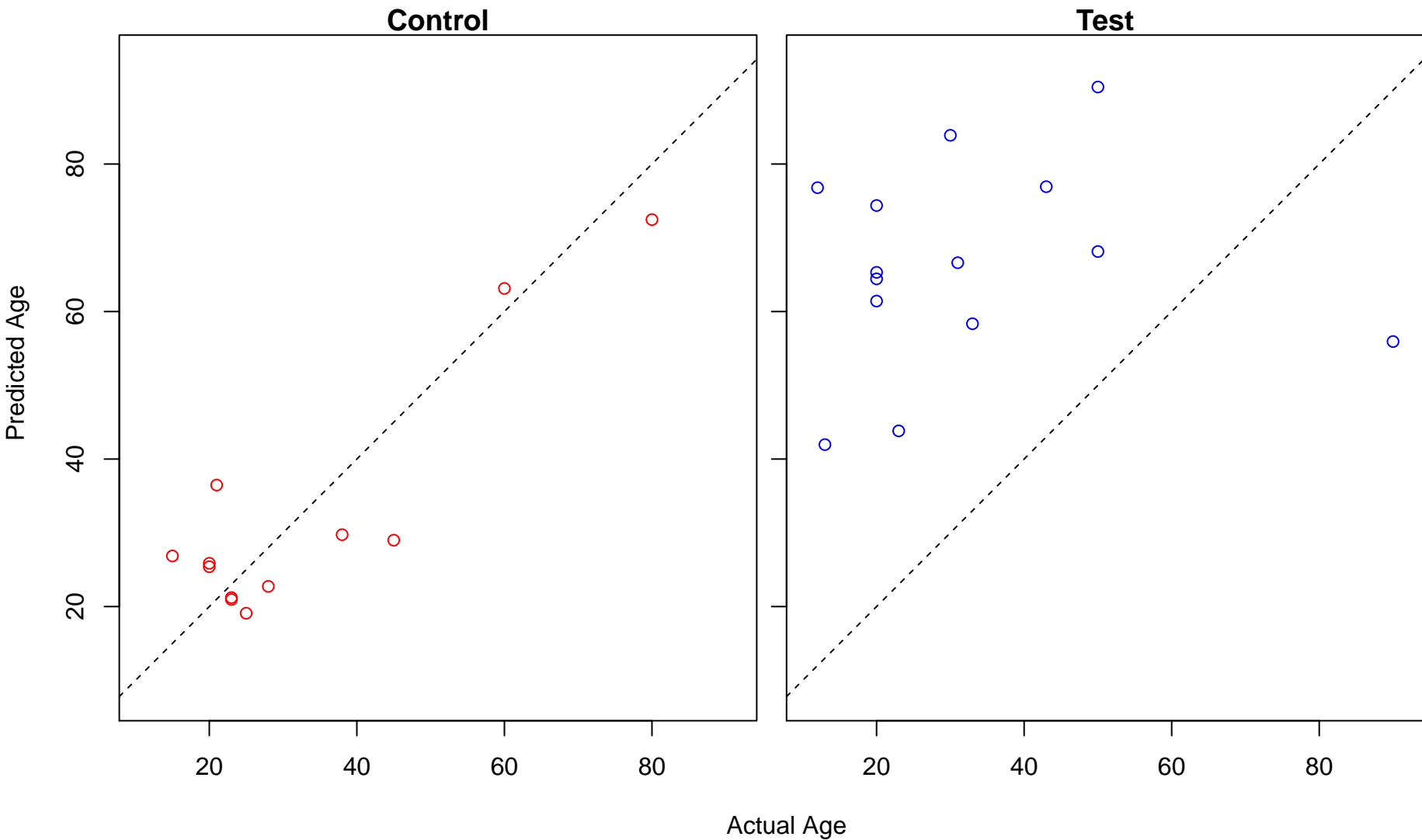


Actual Age

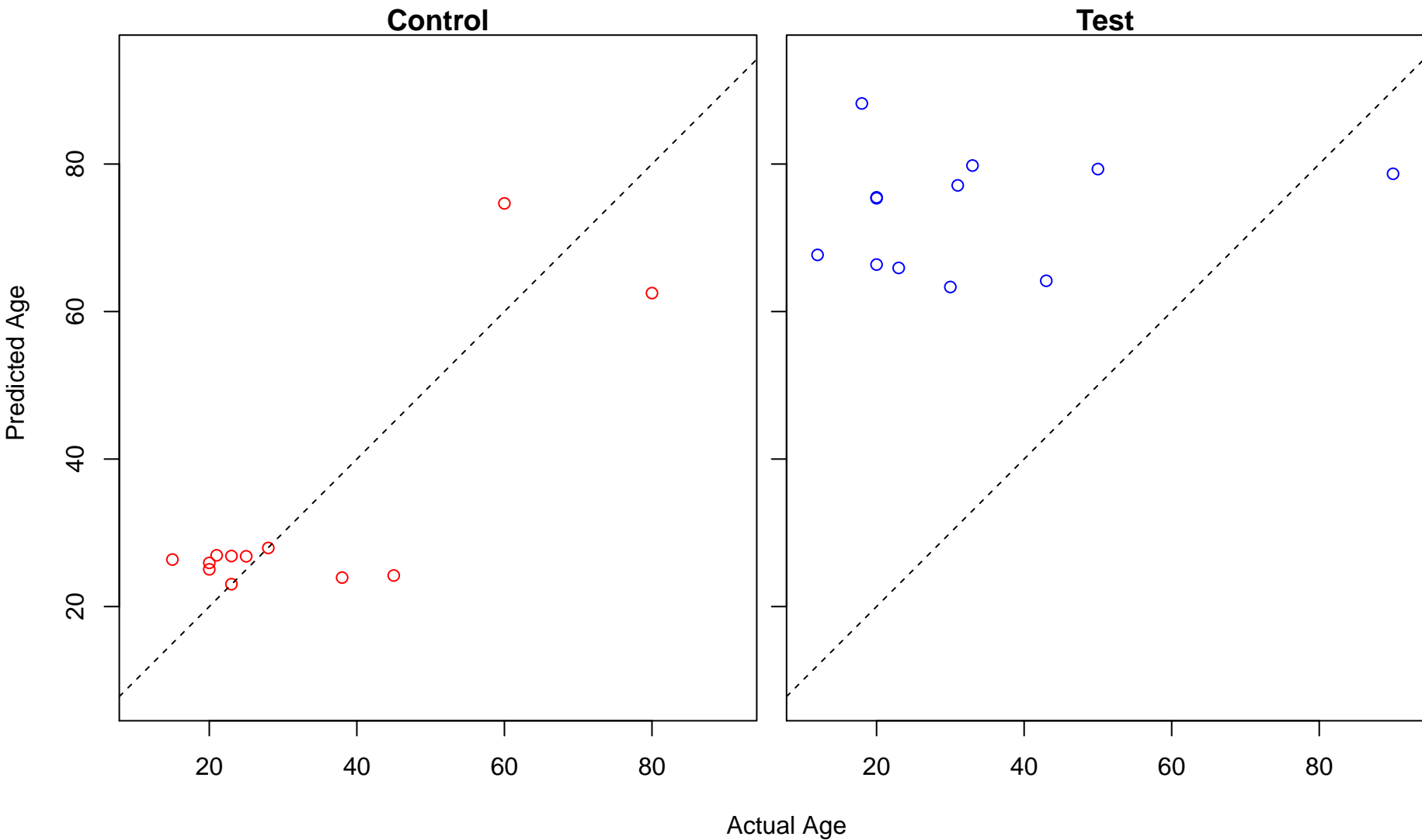
branched-chain amino acid catabolic process (Score: 8.682267)



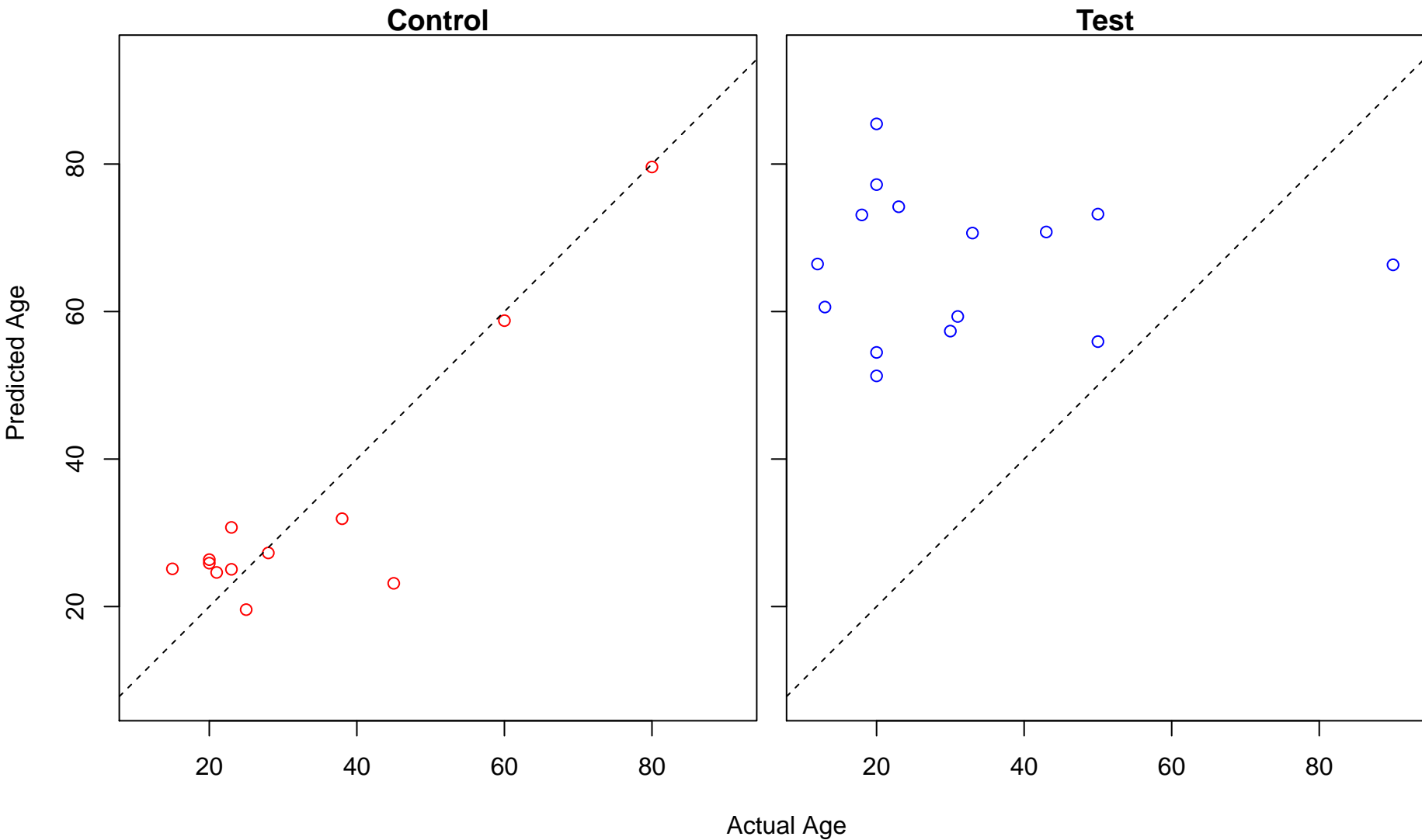
negative regulation of NF-kappaB transcription factor activity (Score: 8.679066)



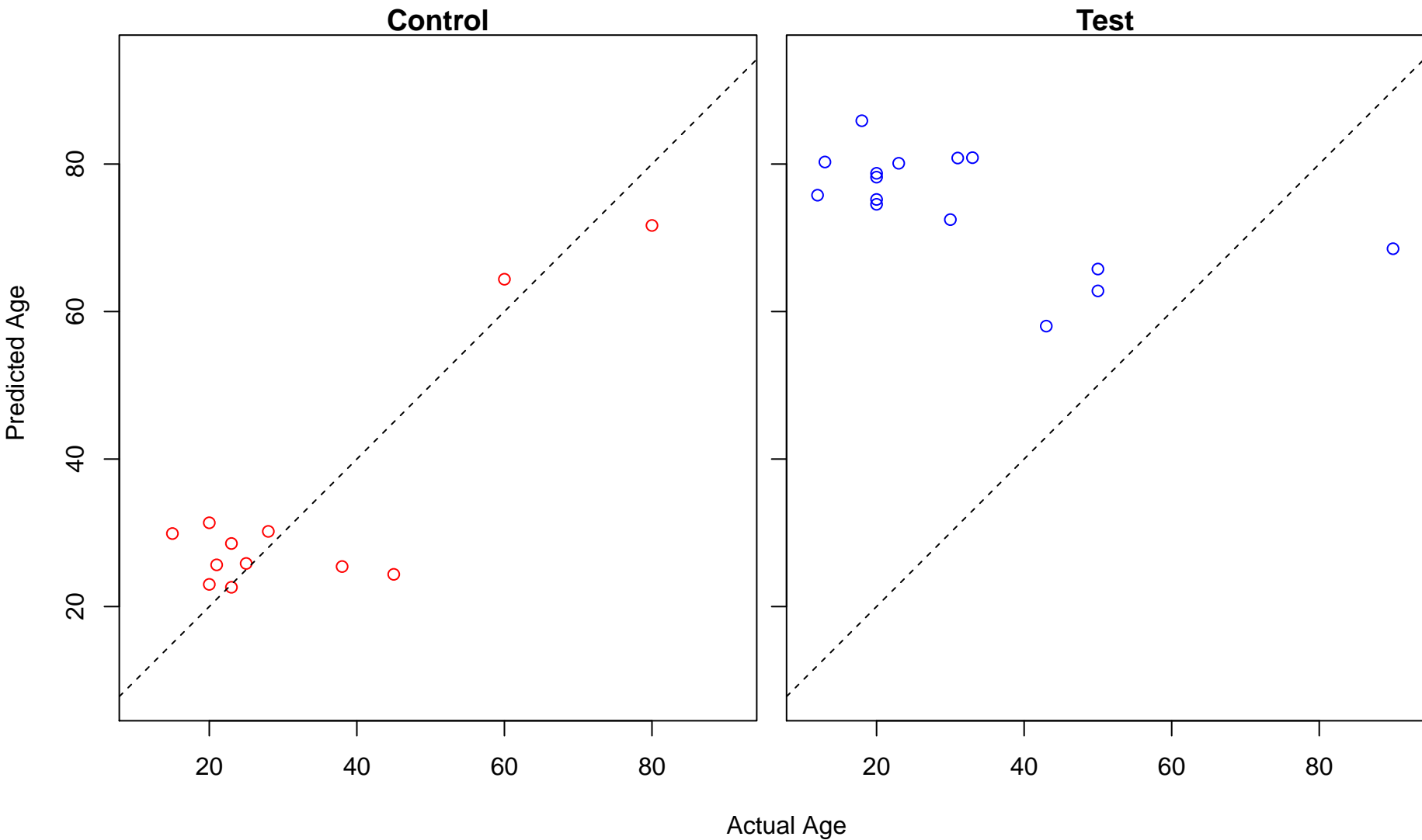
negative regulation of response to DNA damage stimulus (Score: 8.674893)



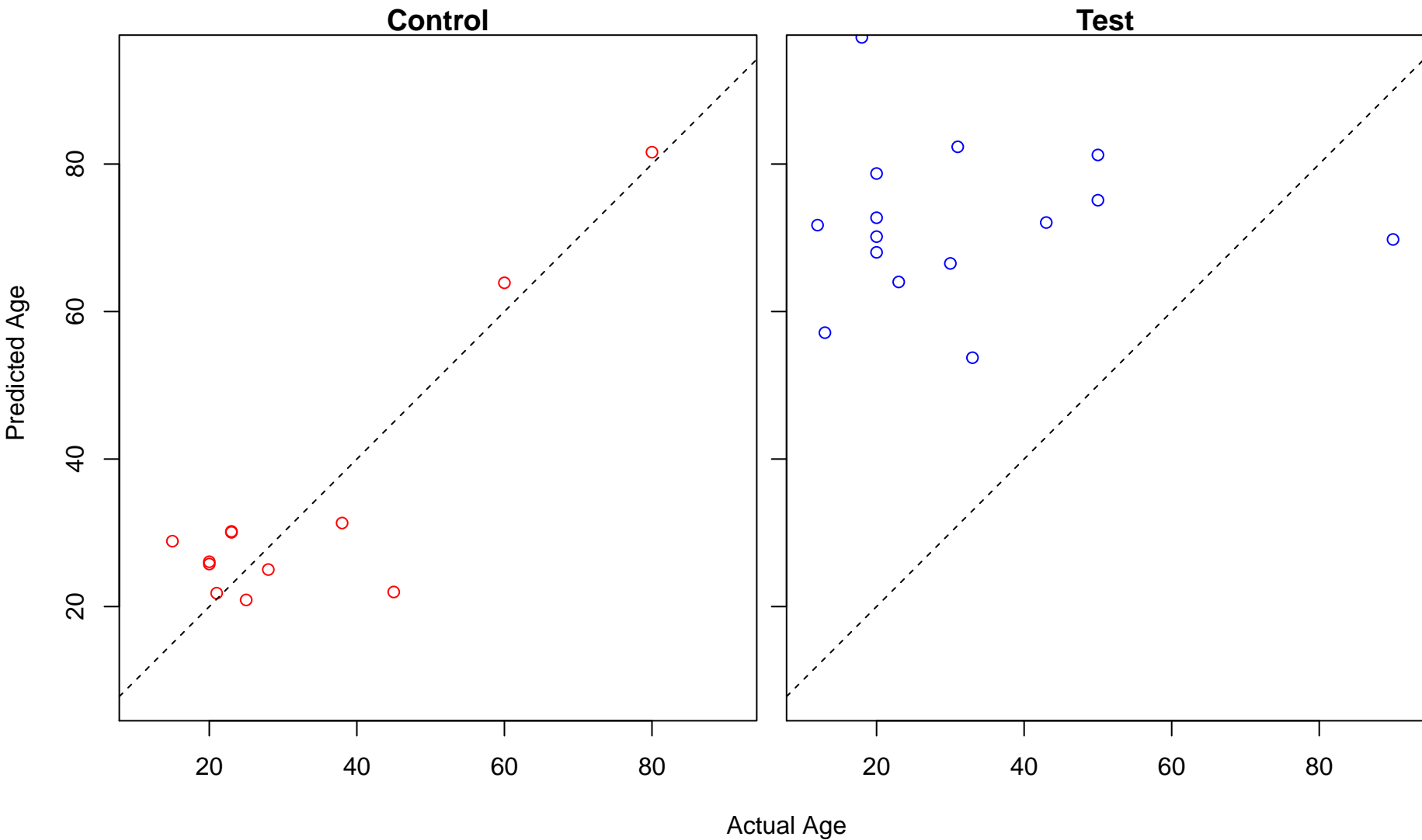
central nervous system neuron differentiation (Score: 8.663008)



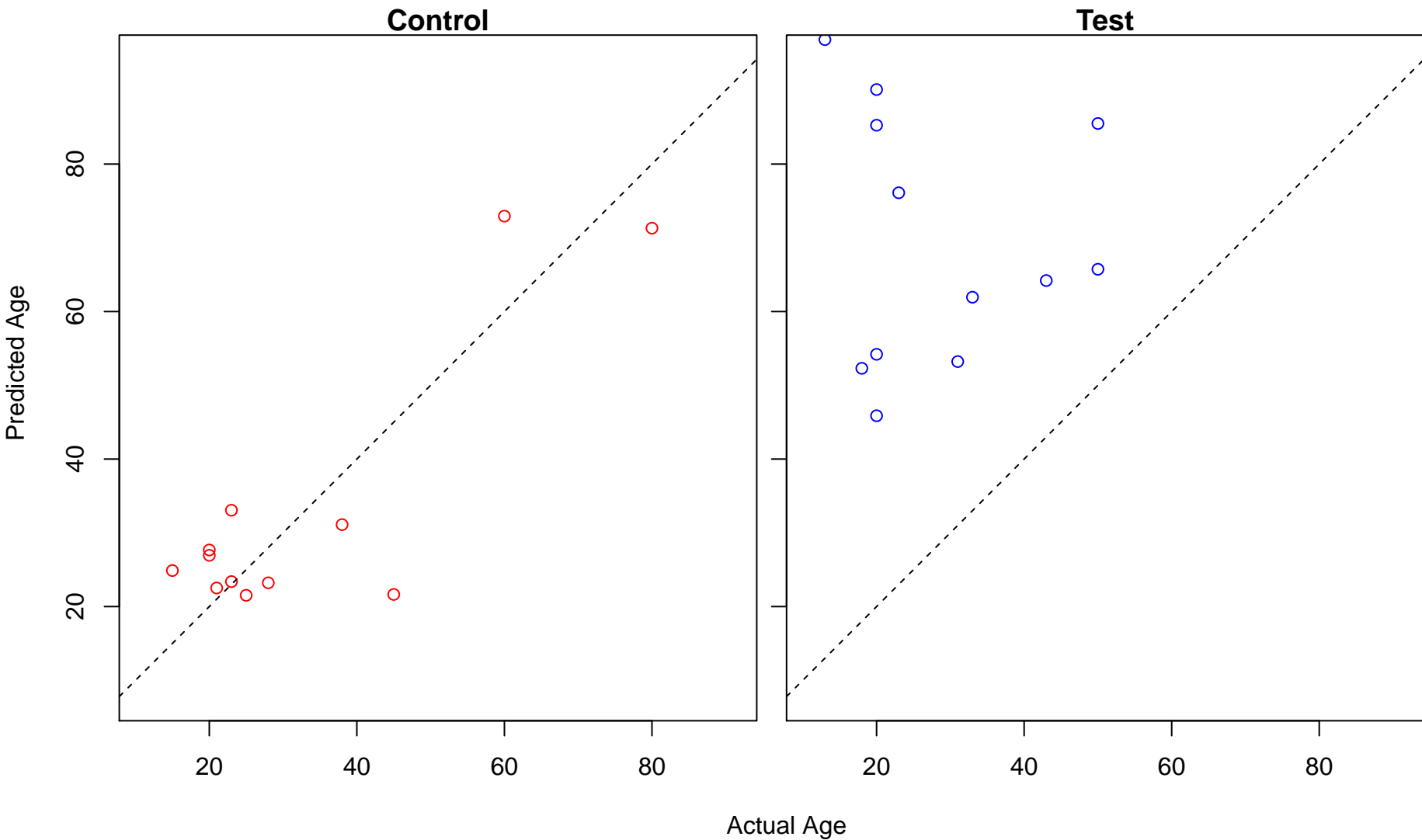
pteridine-containing compound biosynthetic process (Score: 8.661199)



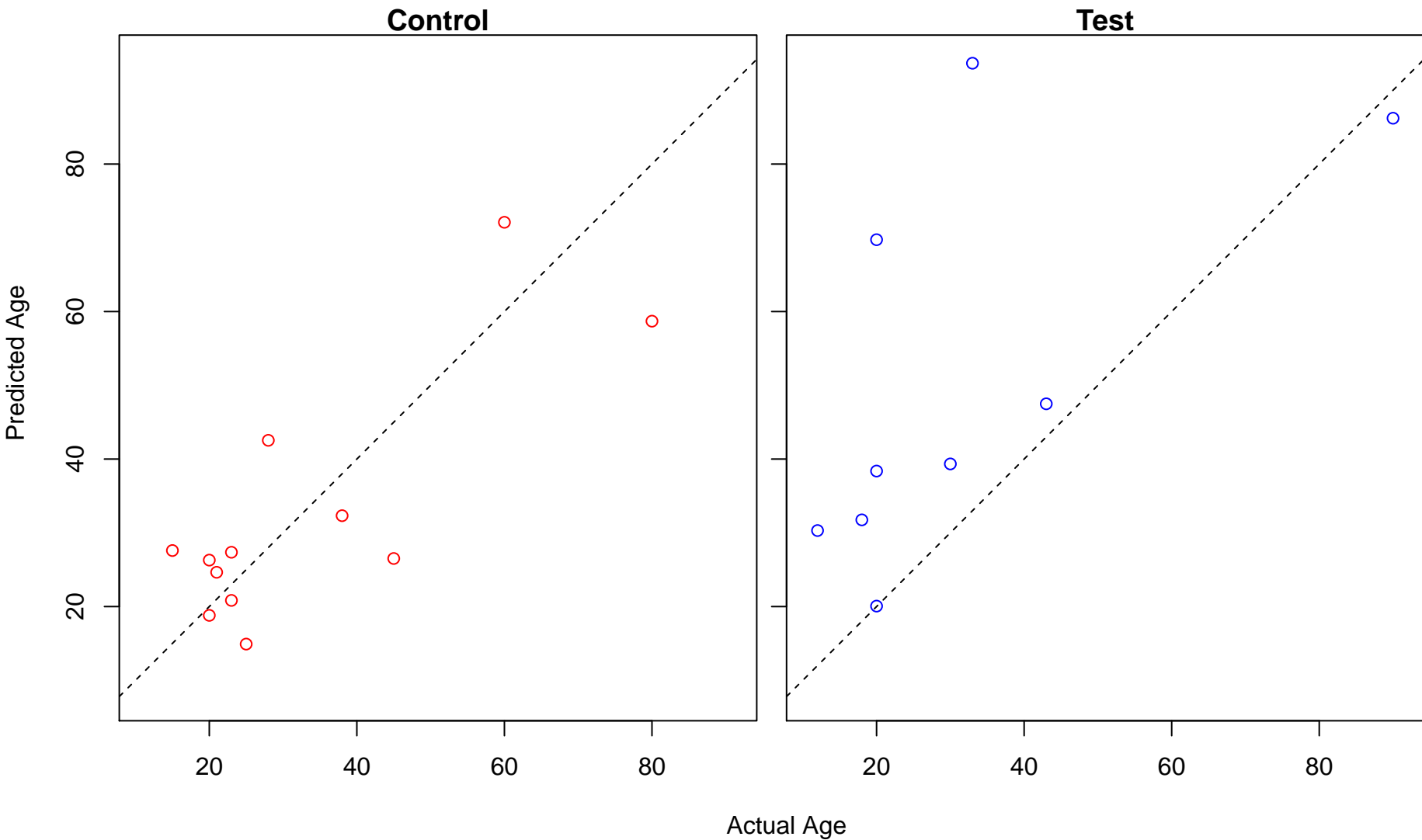
negative regulation of smooth muscle cell proliferation (Score: 8.657875)



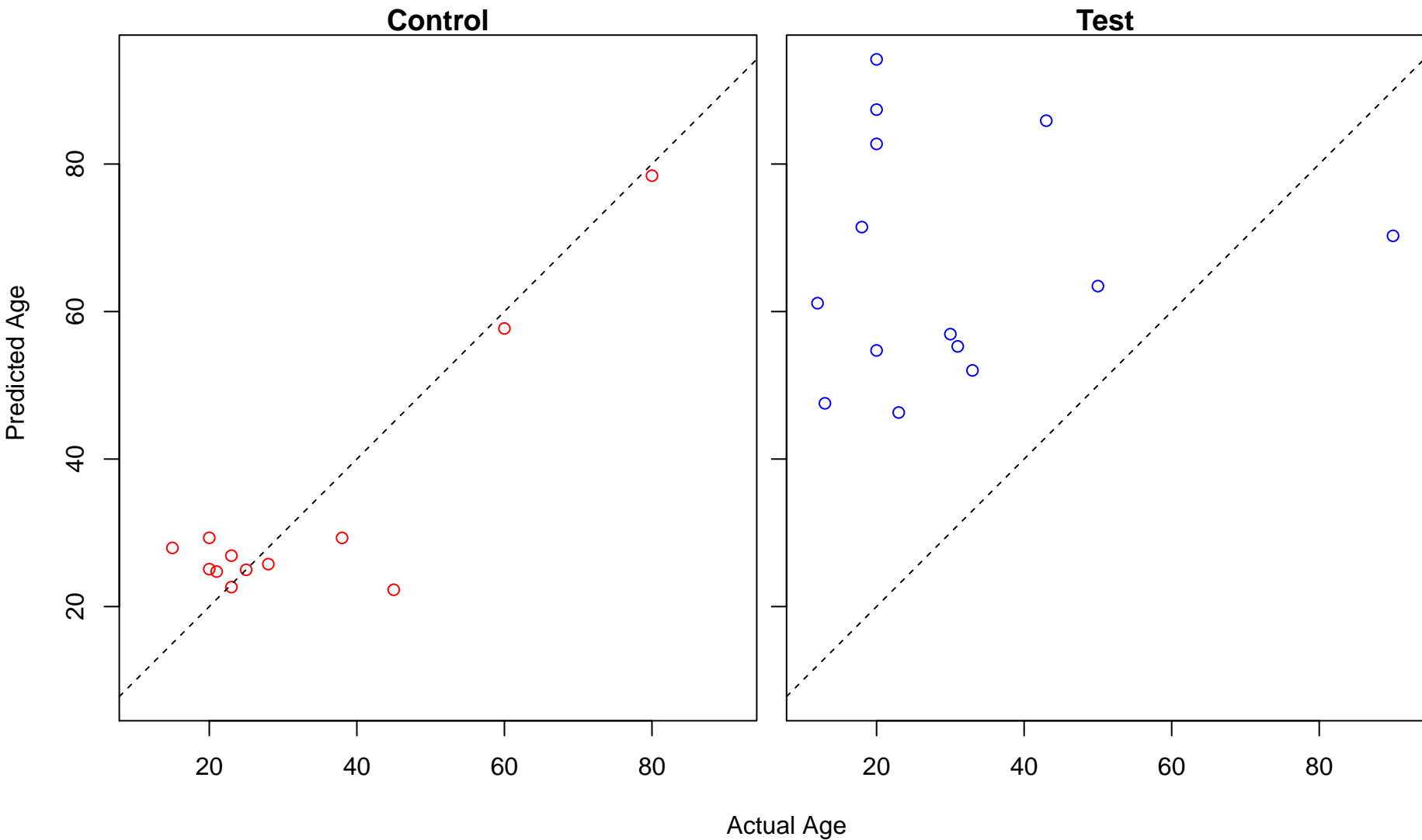
negative regulation of glial cell differentiation (Score: 8.657674)



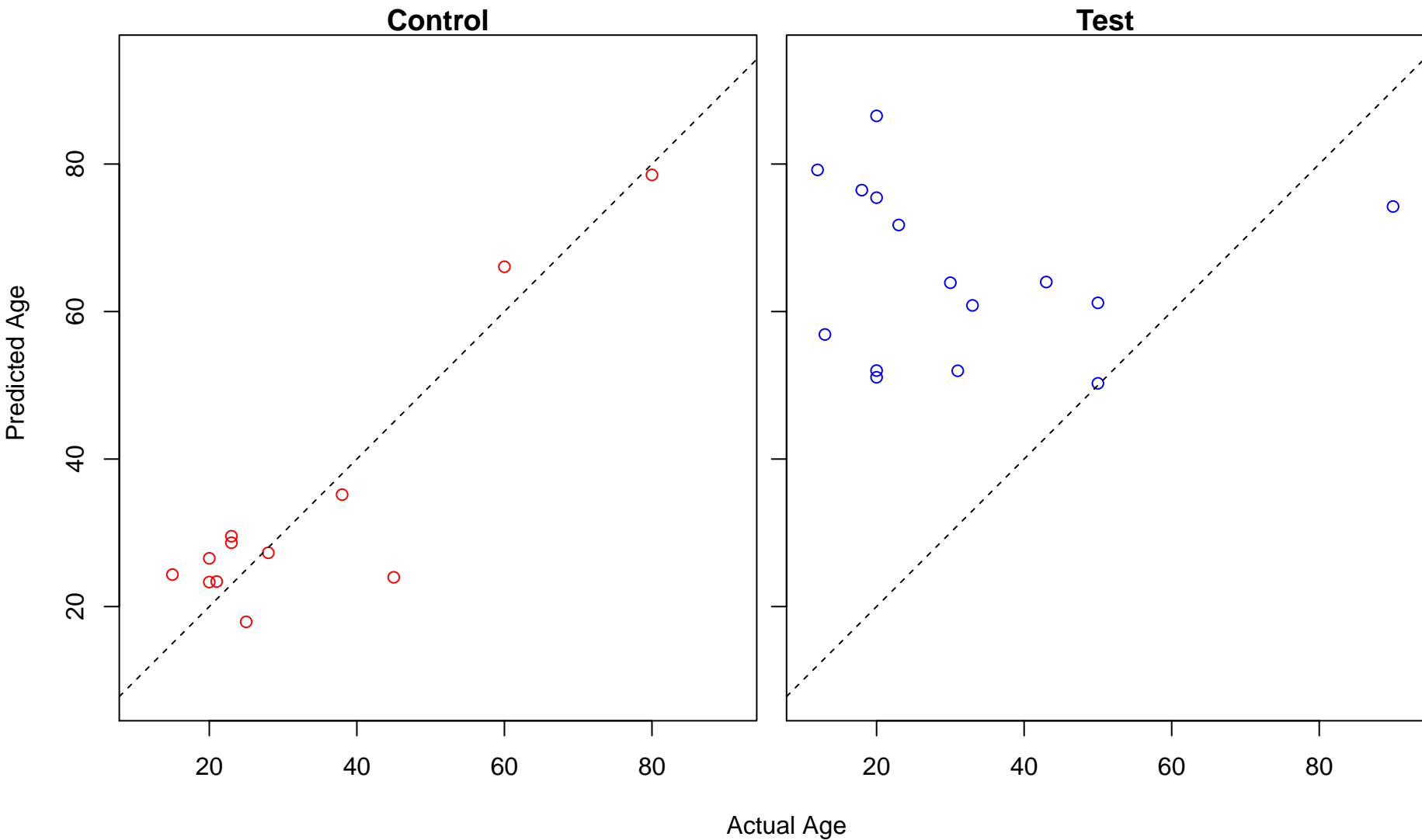
axis specification (Score: 8.656851)



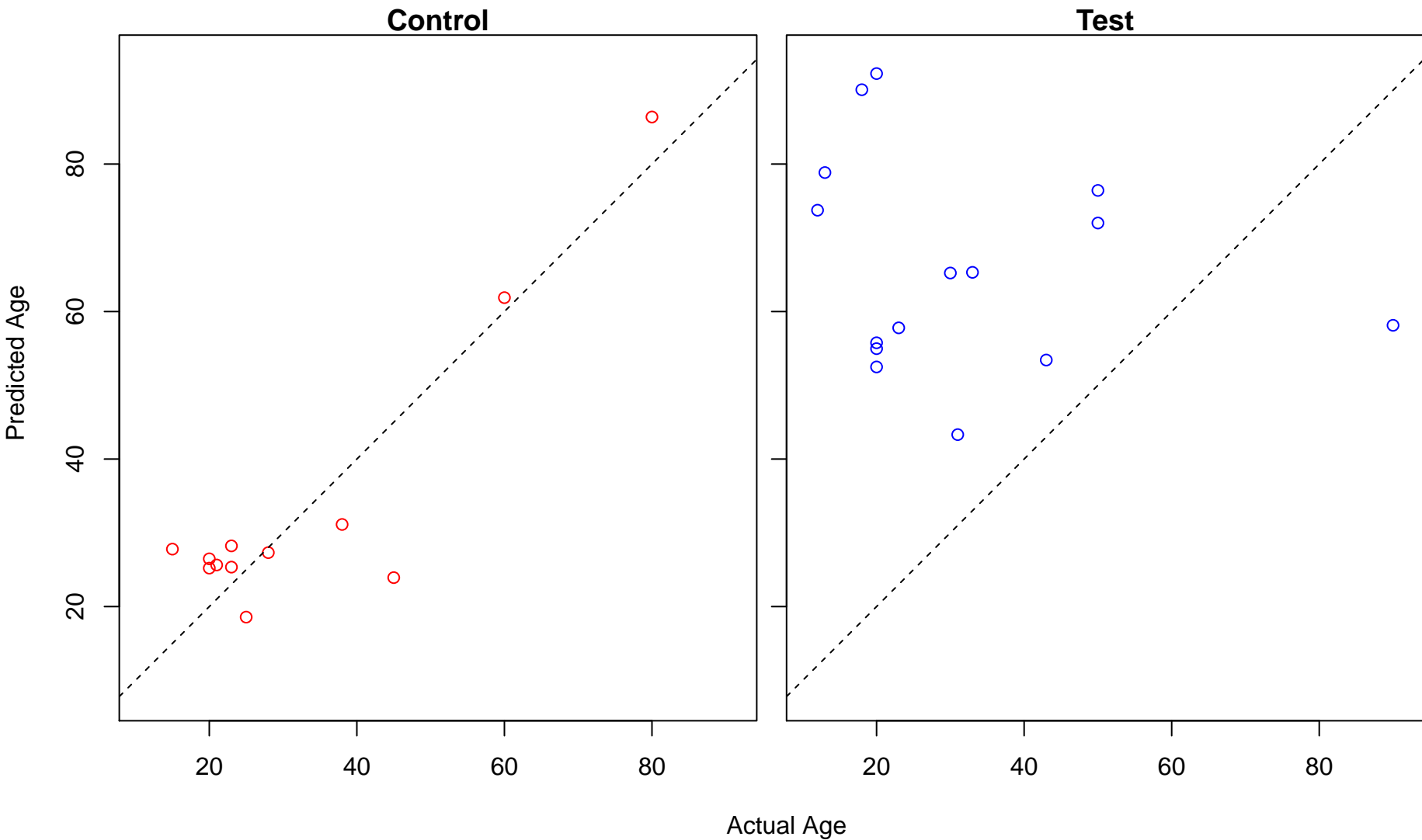
protein homotrimerization (Score: 8.656755)



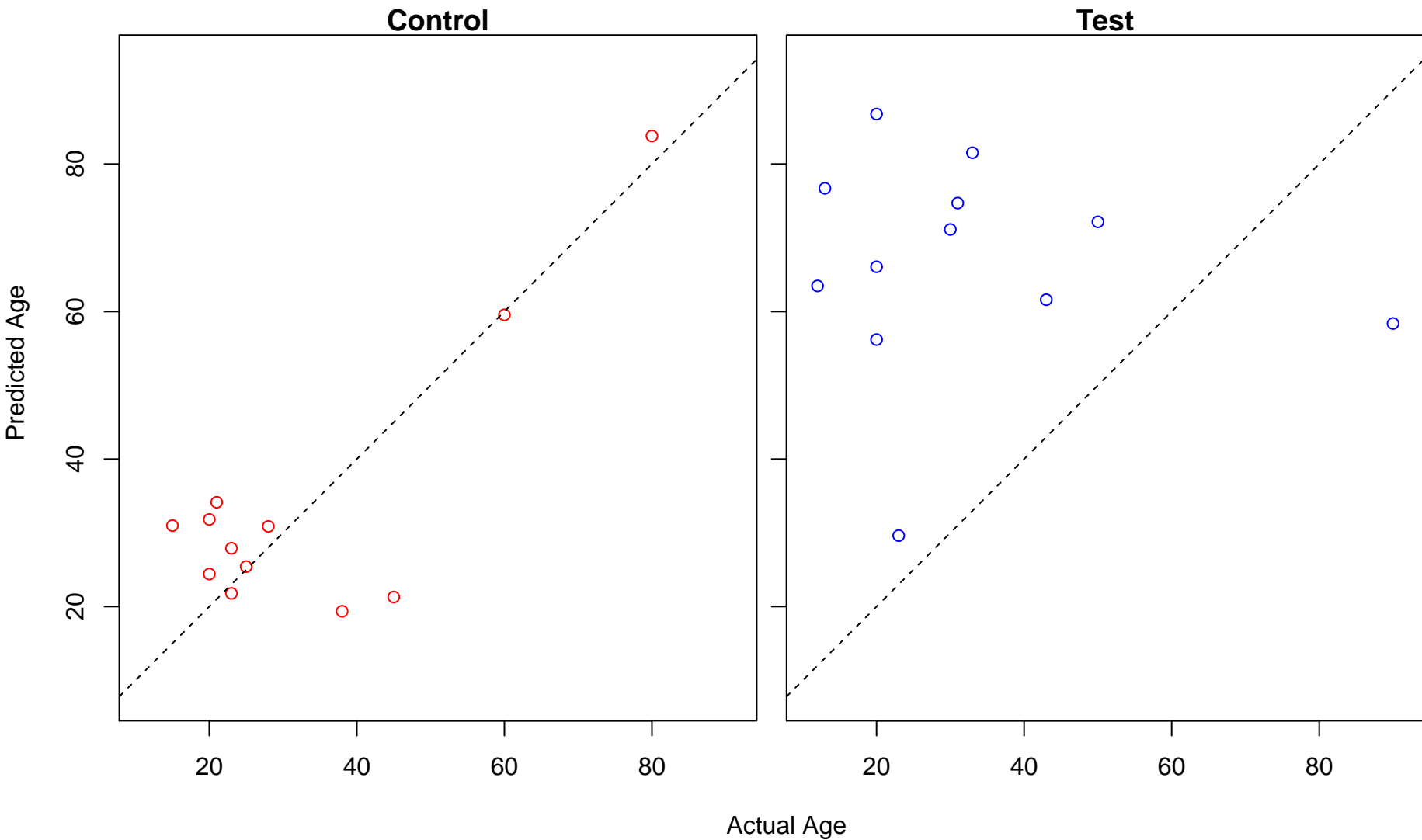
regulation of vascular permeability (Score: 8.656342)



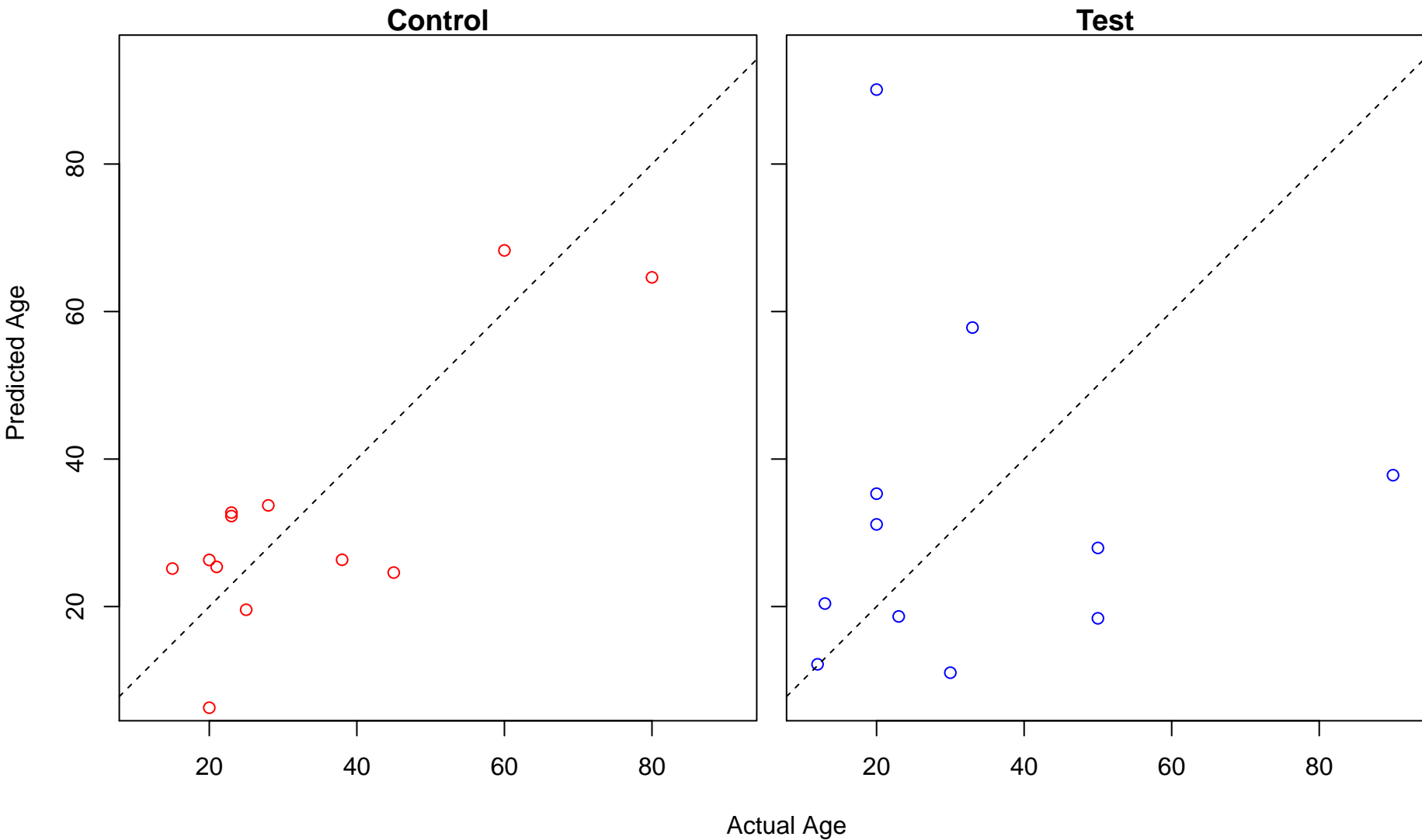
nucleoside transmembrane transport (Score: 8.655892)



regulation of endopeptidase activity (Score: 8.653928)

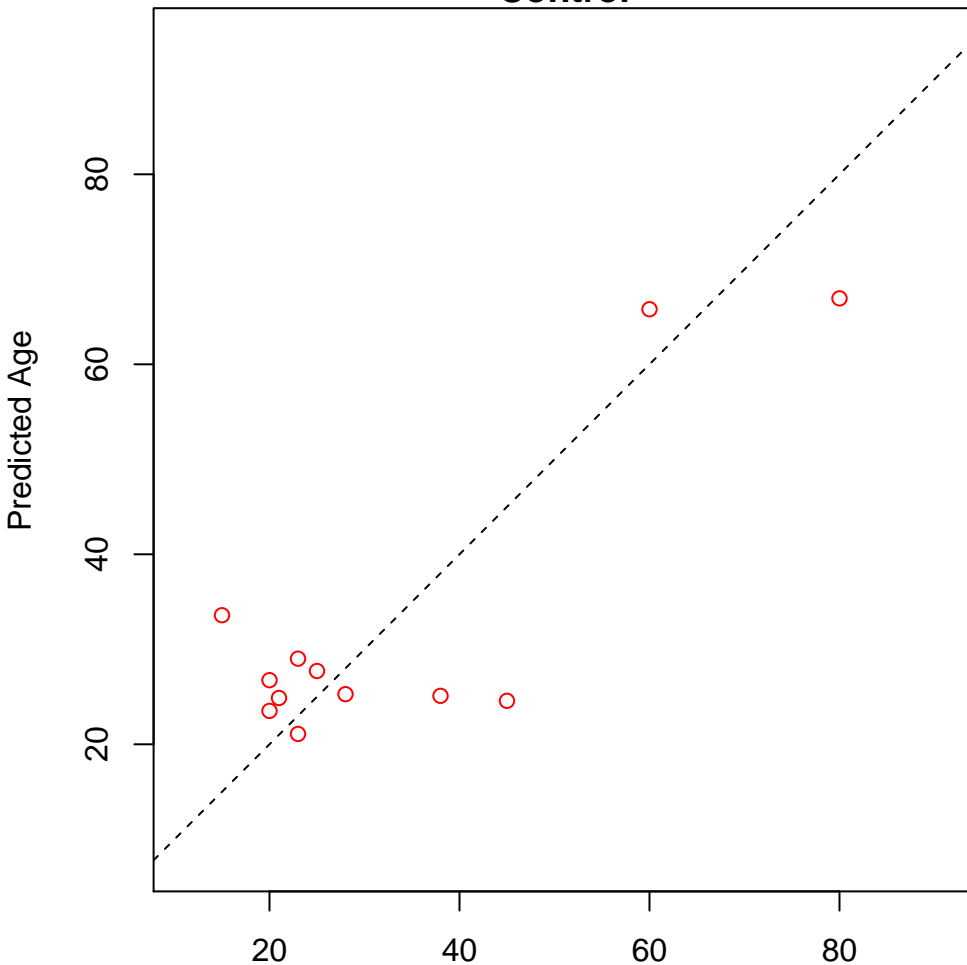


organelle disassembly (Score: 8.650003)

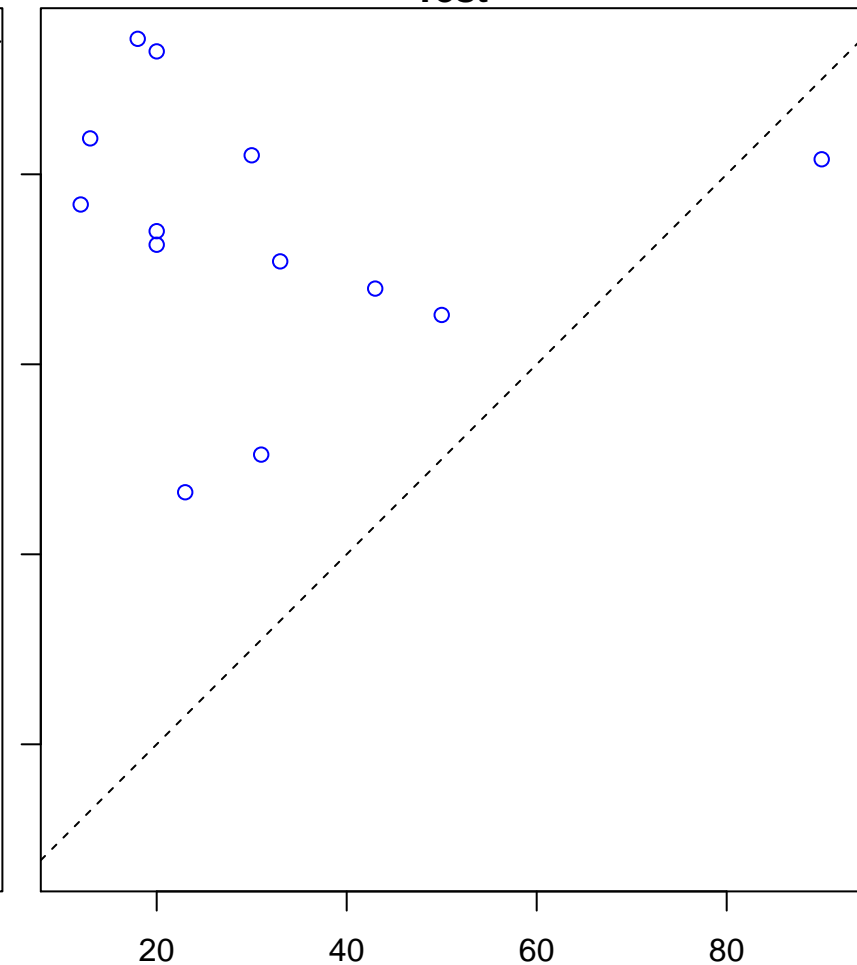


response to laminar fluid shear stress (Score: 8.649549)

Control



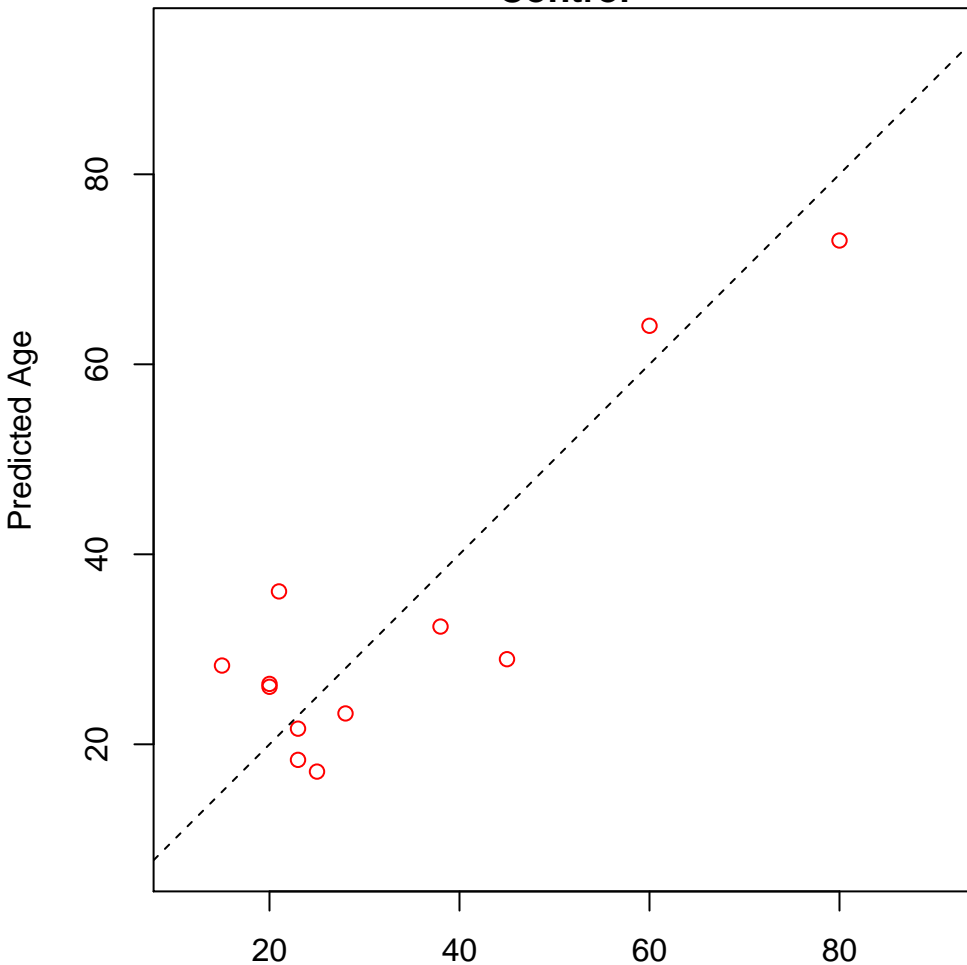
Test



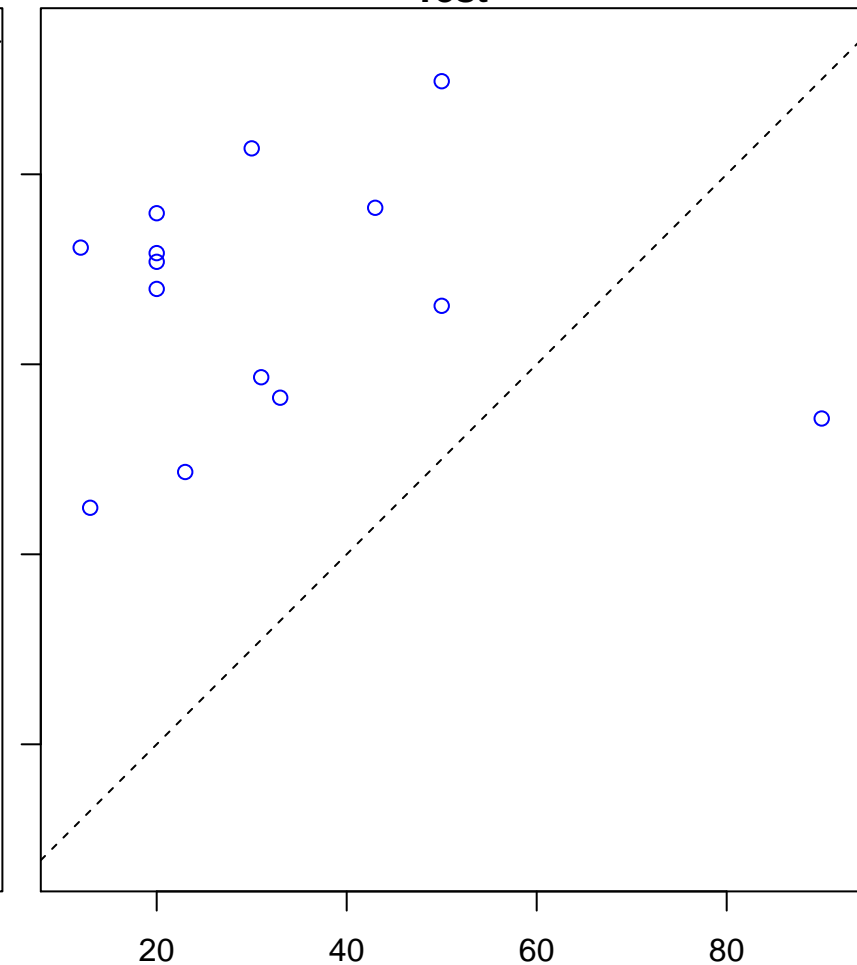
Actual Age

arachidonic acid metabolic process (Score: 8.649483)

Control

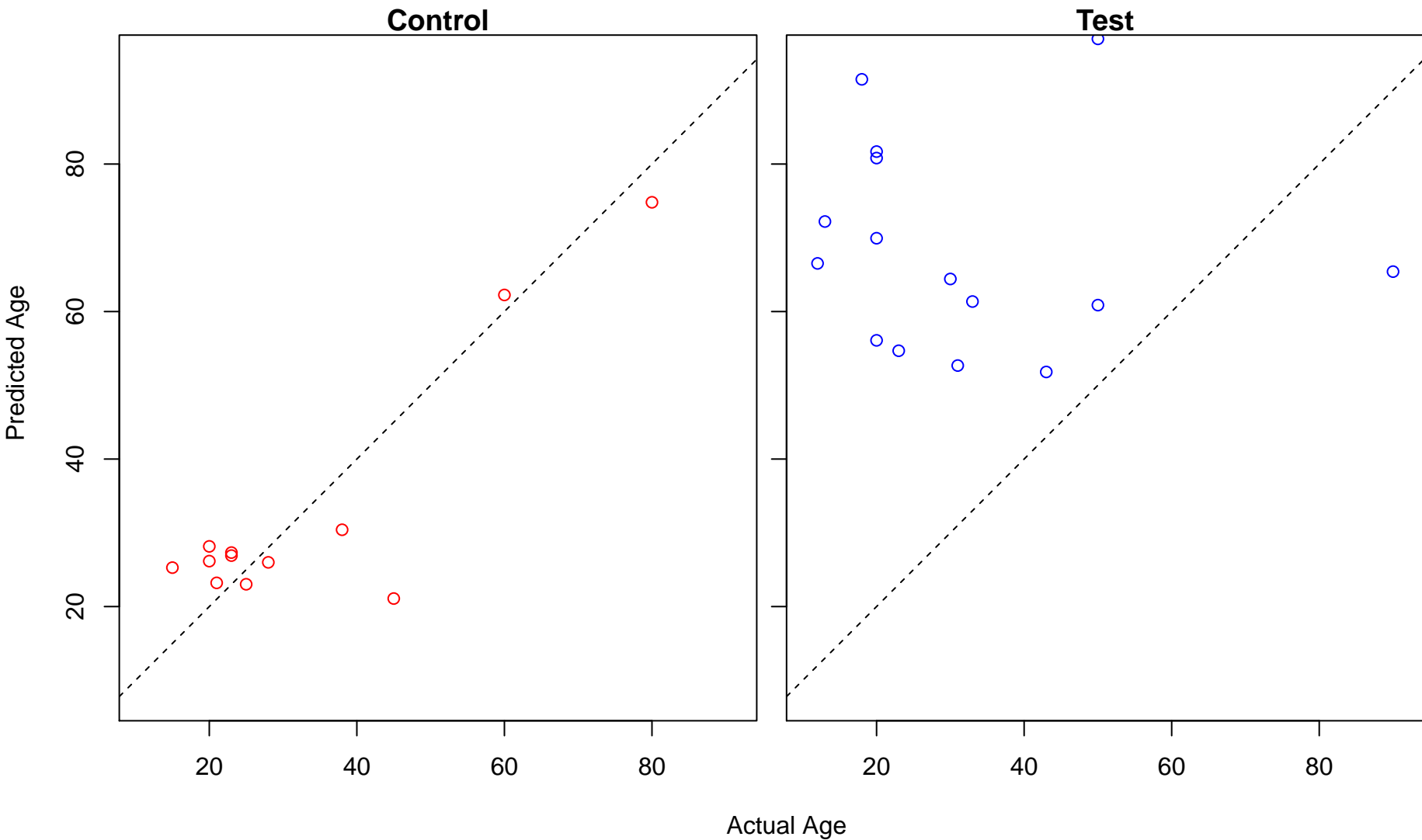


Test

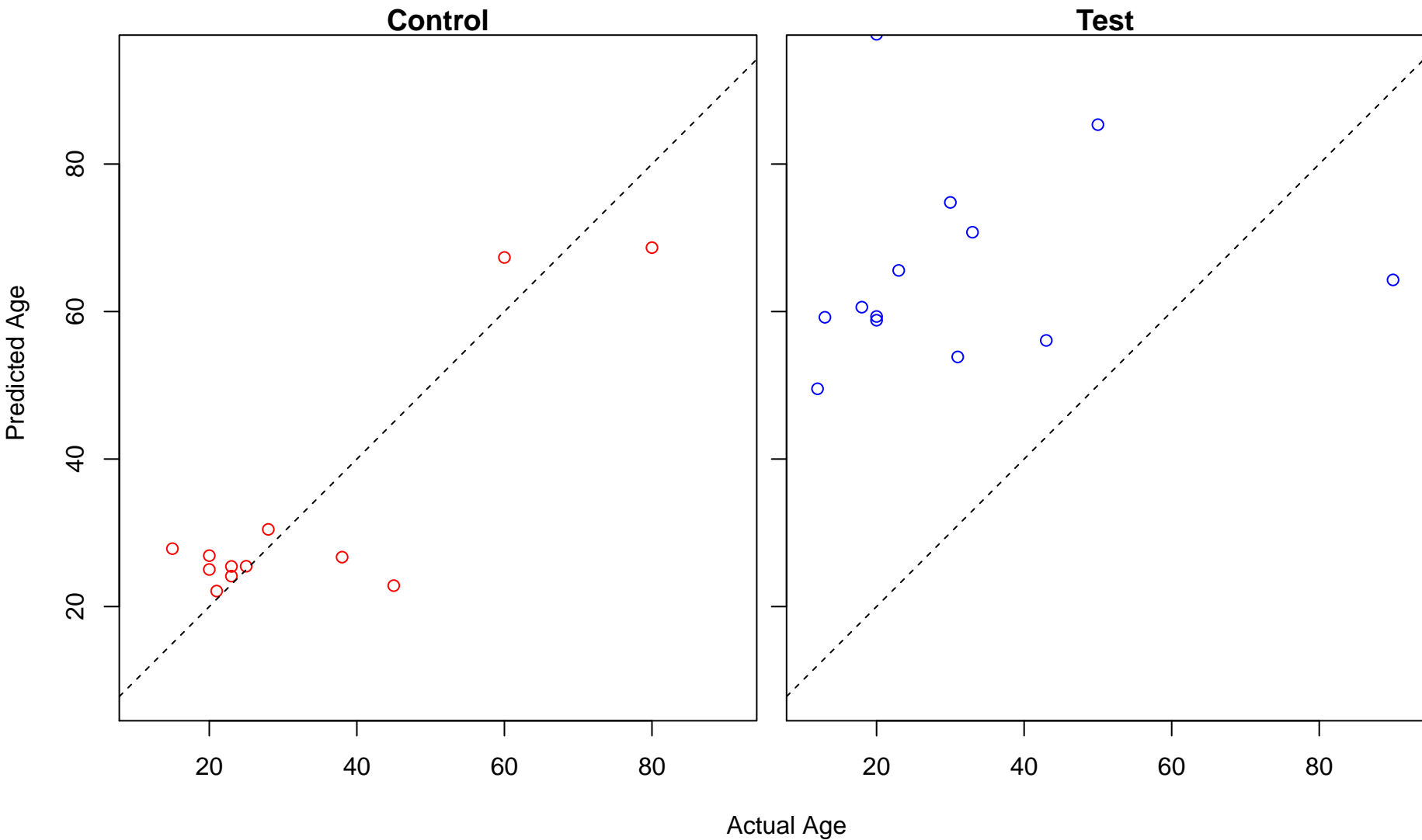


Actual Age

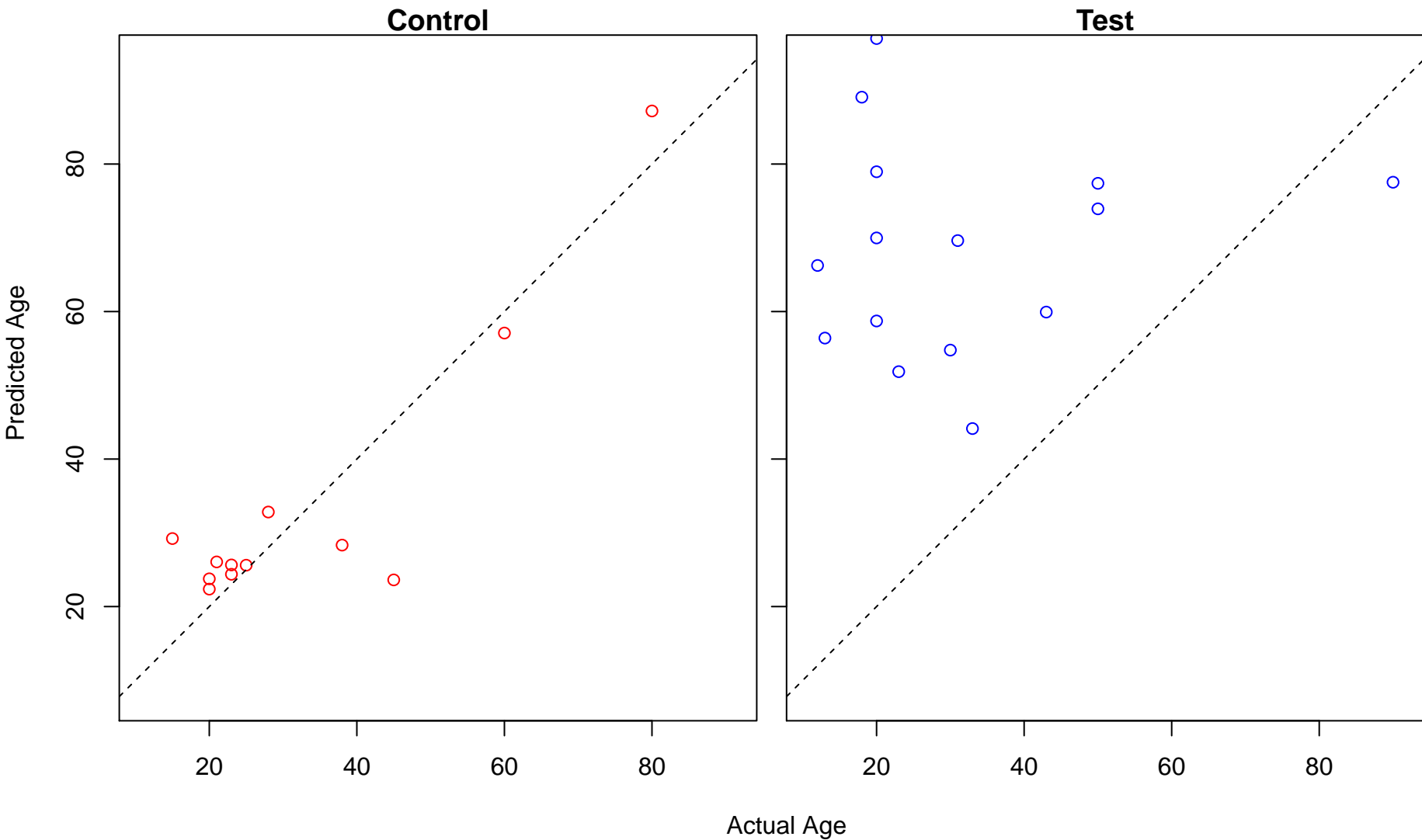
optic cup morphogenesis involved in camera-type eye development (Score: 8.643757)



regulation of bone resorption (Score: 8.642431)

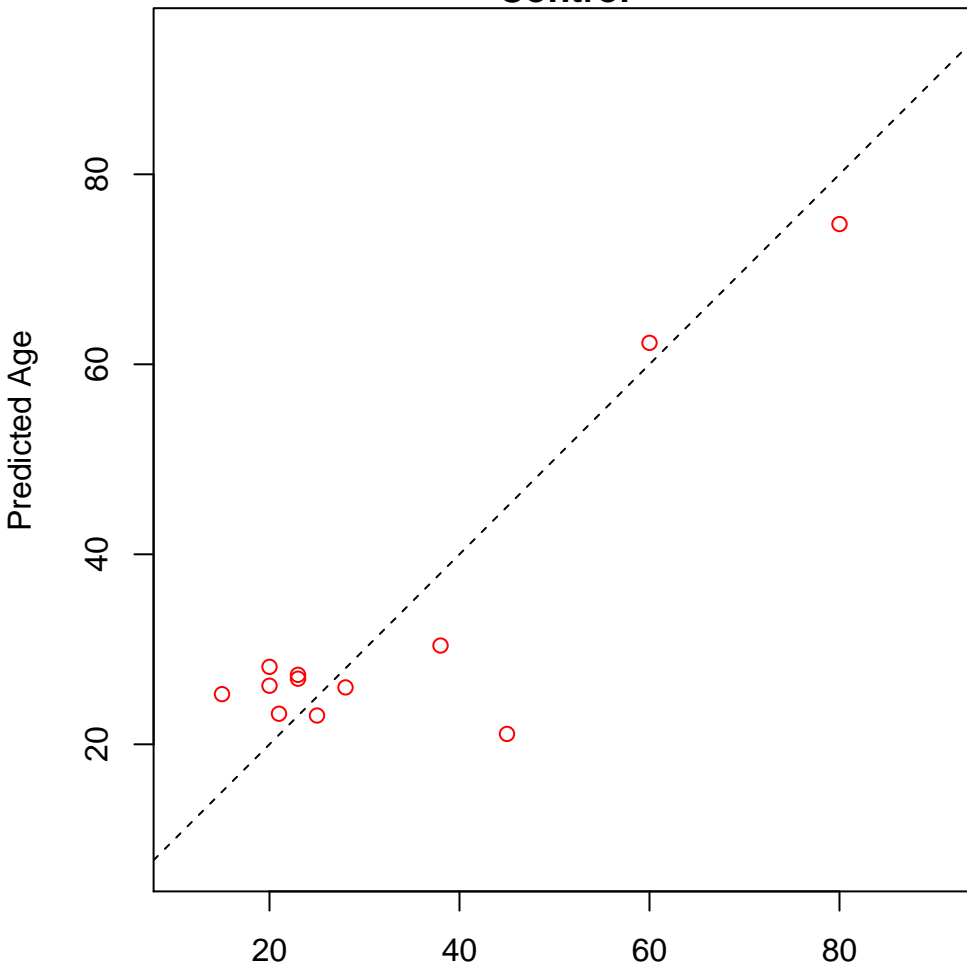


regulation of cAMP-mediated signaling (Score: 8.634982)

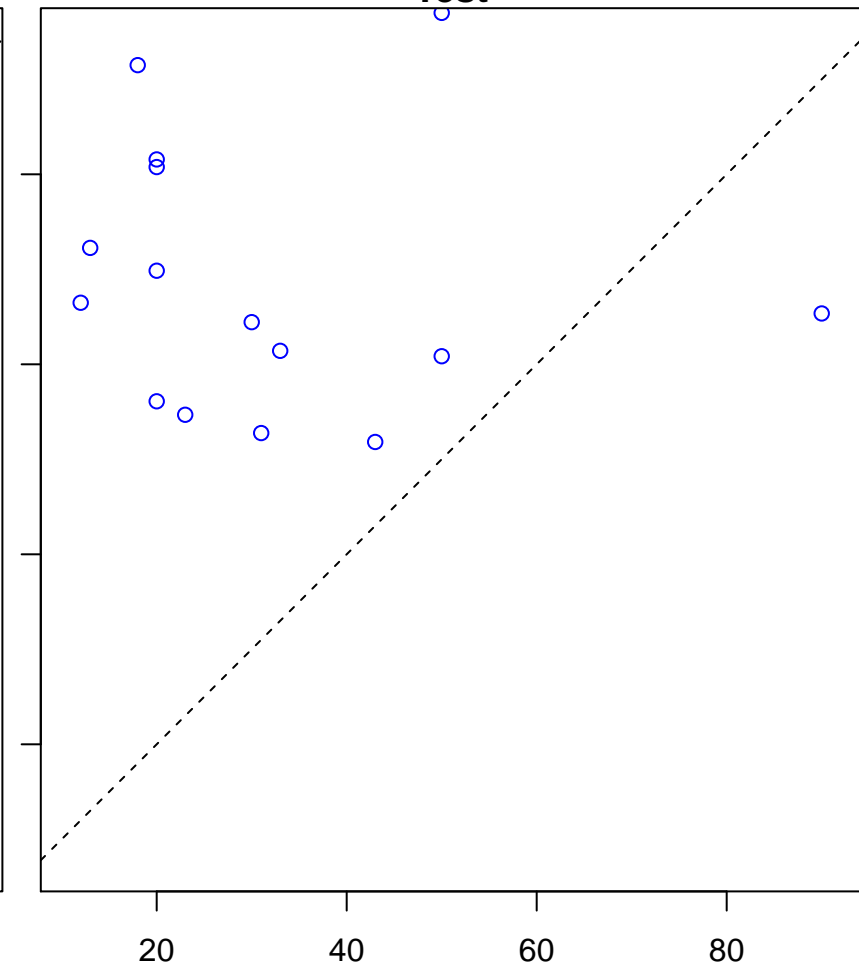


embryonic camera-type eye formation (Score: 8.633280)

Control

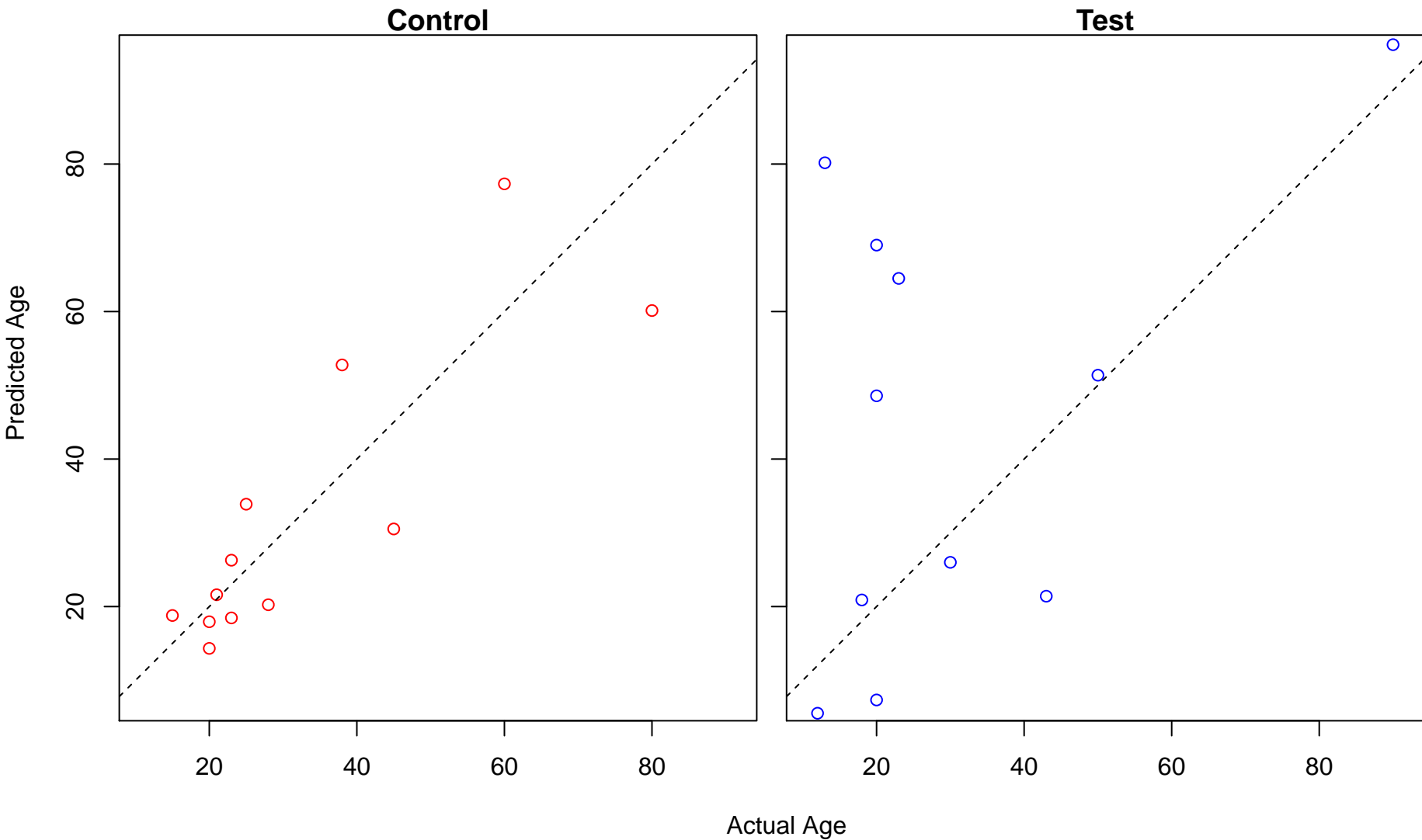


Test

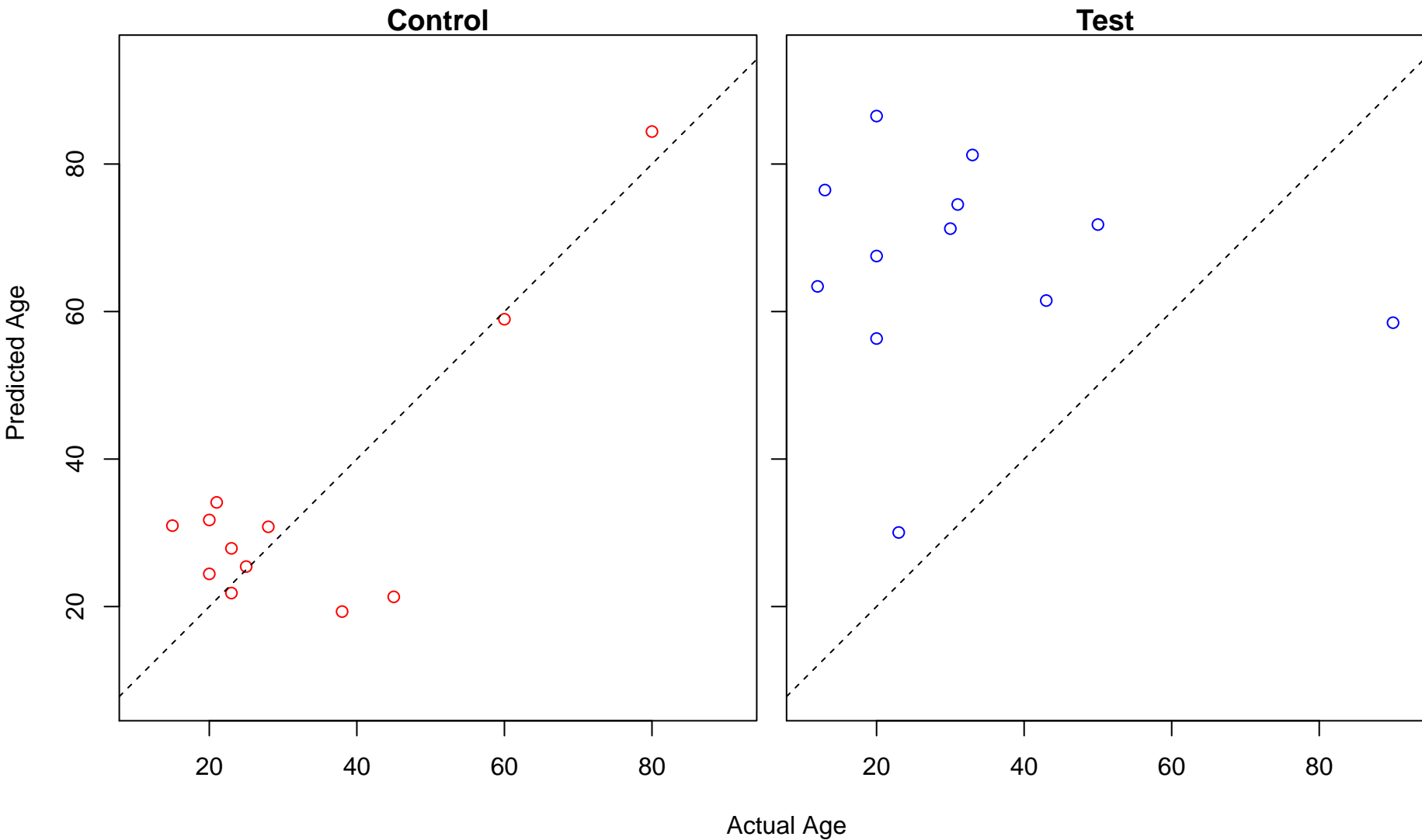


Actual Age

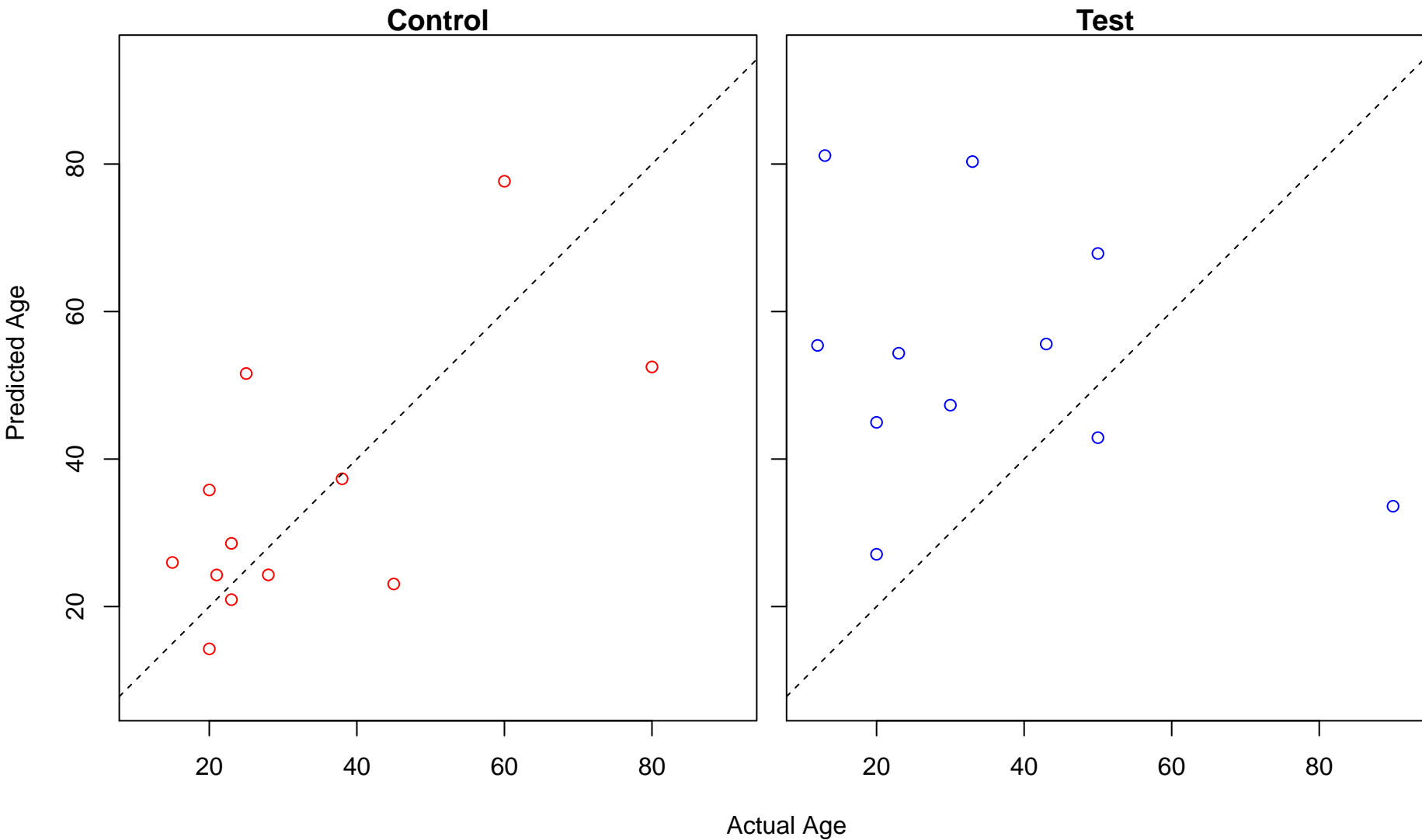
developmental induction (Score: 8.627549)



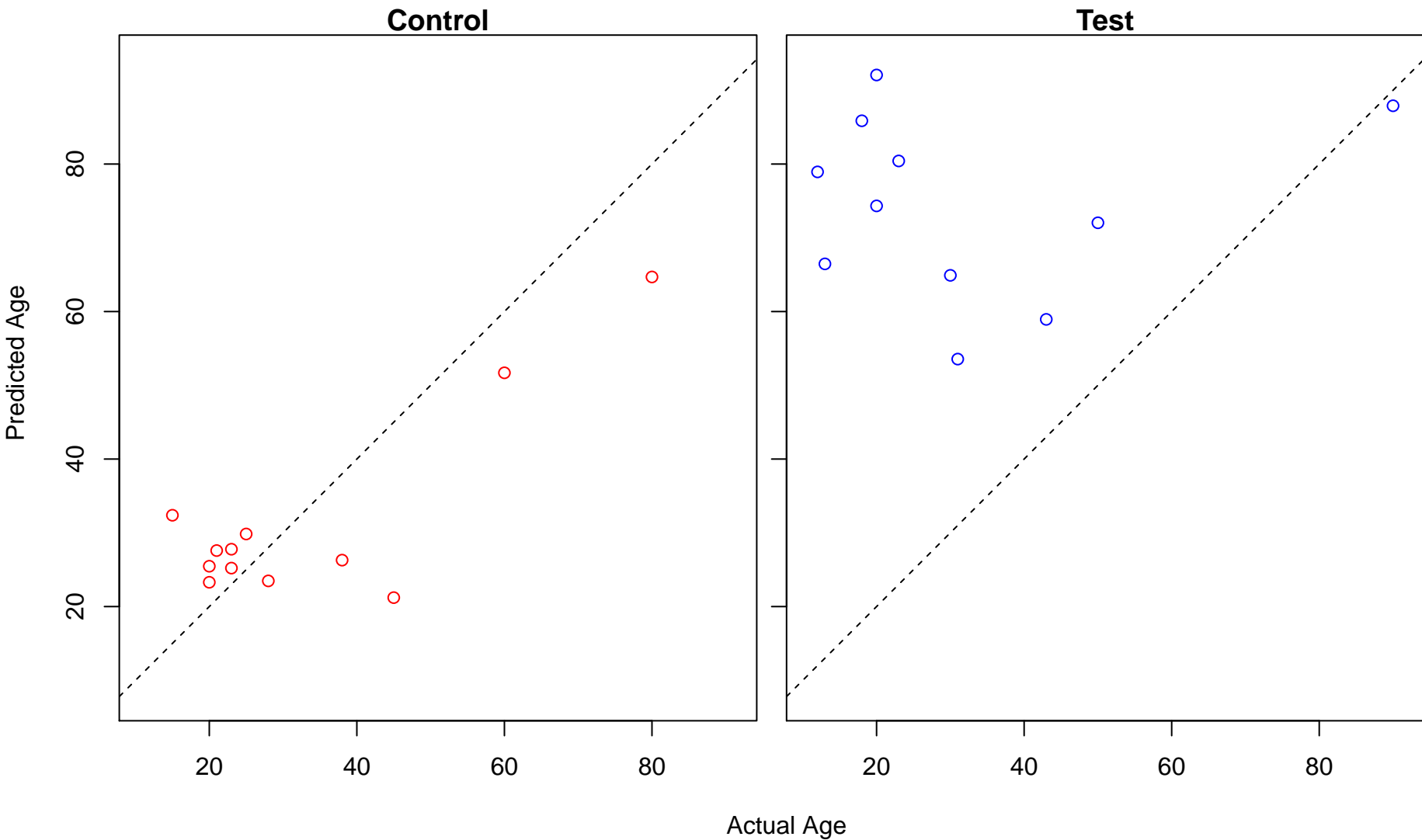
regulation of peptidase activity (Score: 8.626692)



negative regulation of G-protein coupled receptor protein signaling pathway (Score: 8.623766)

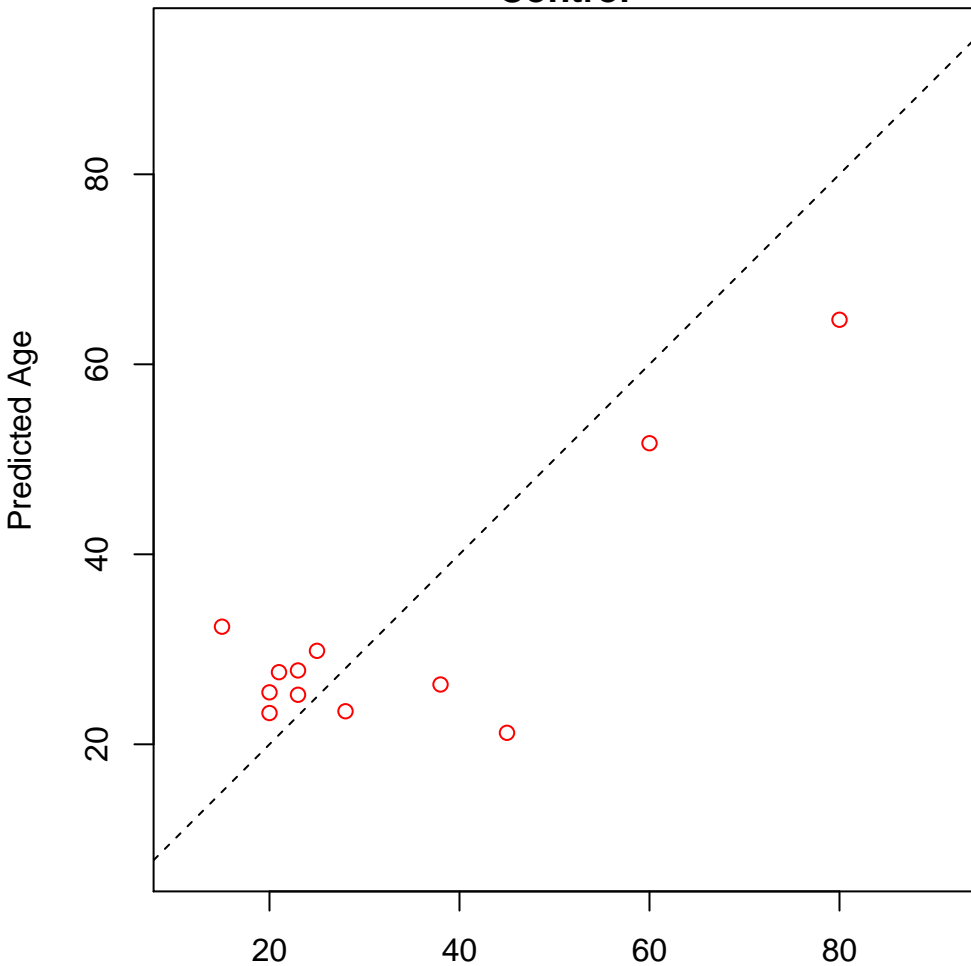


vitamin biosynthetic process (Score: 8.622196)

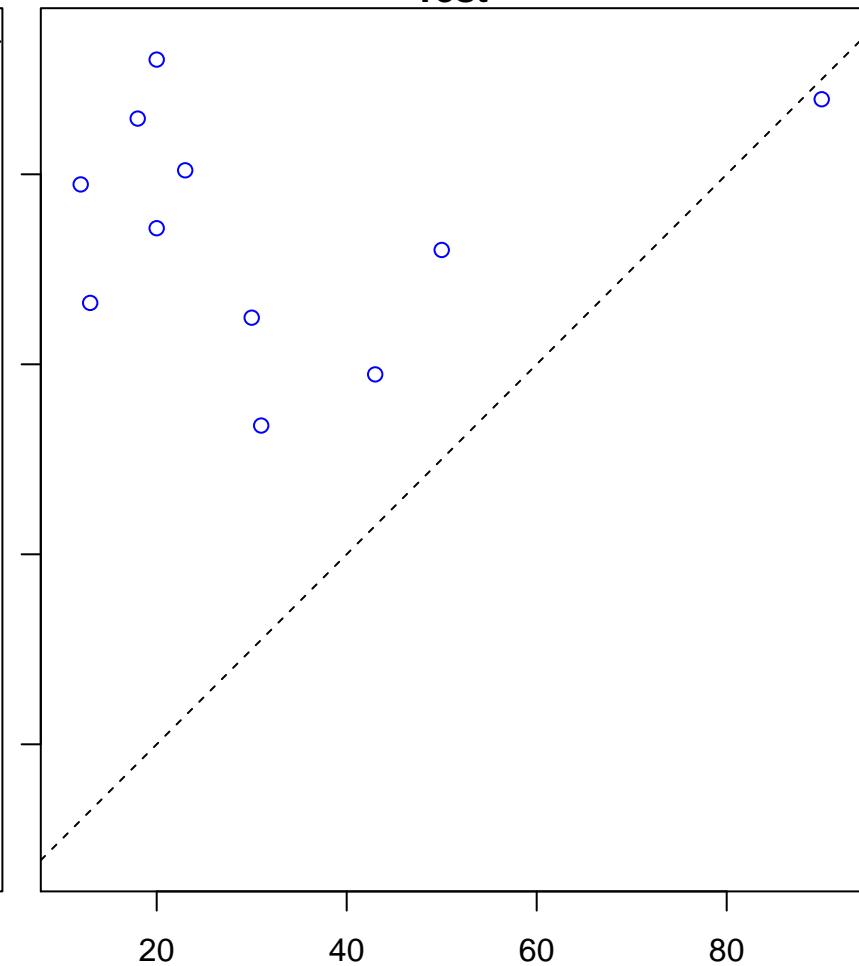


fat-soluble vitamin biosynthetic process (Score: 8.622196)

Control

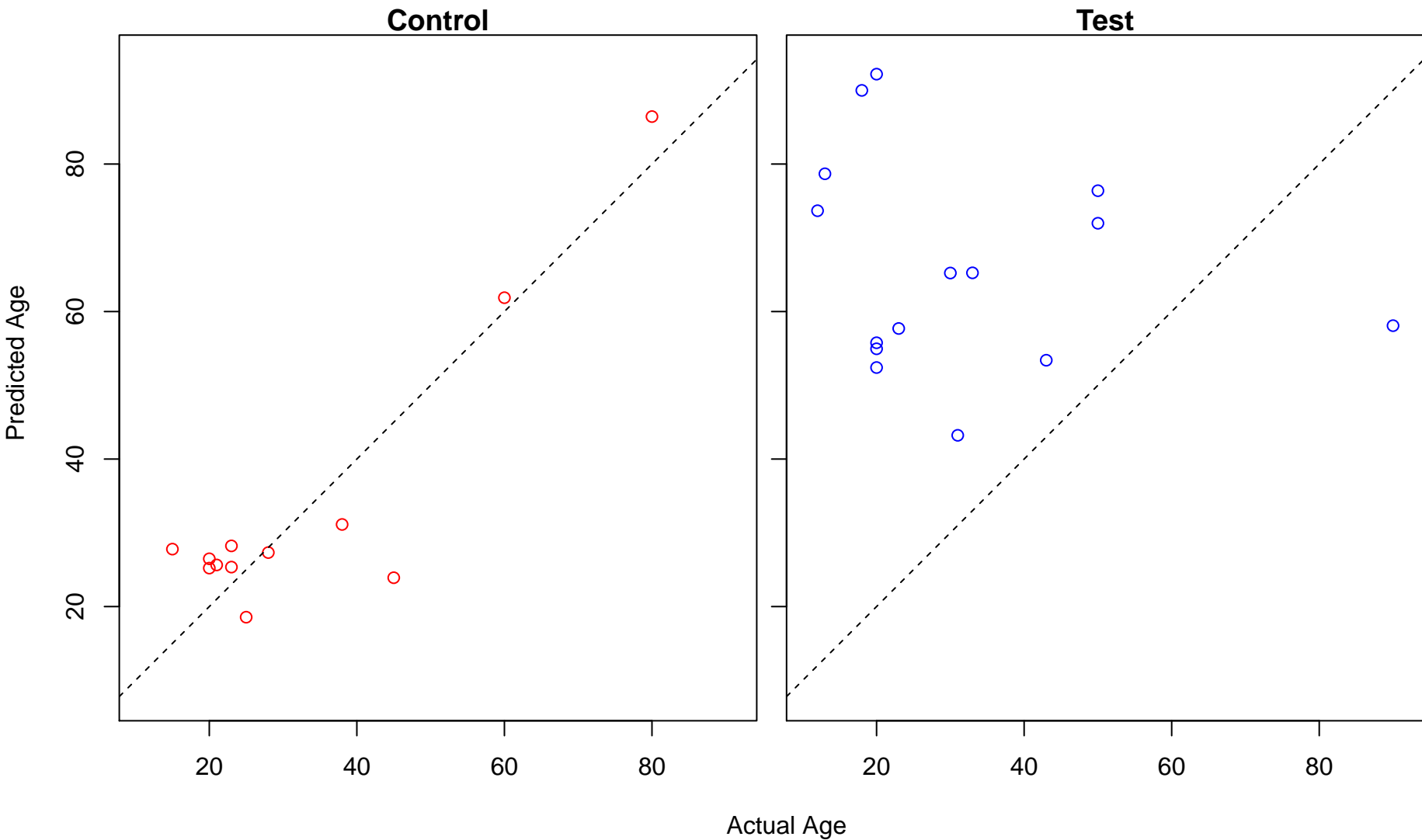


Test

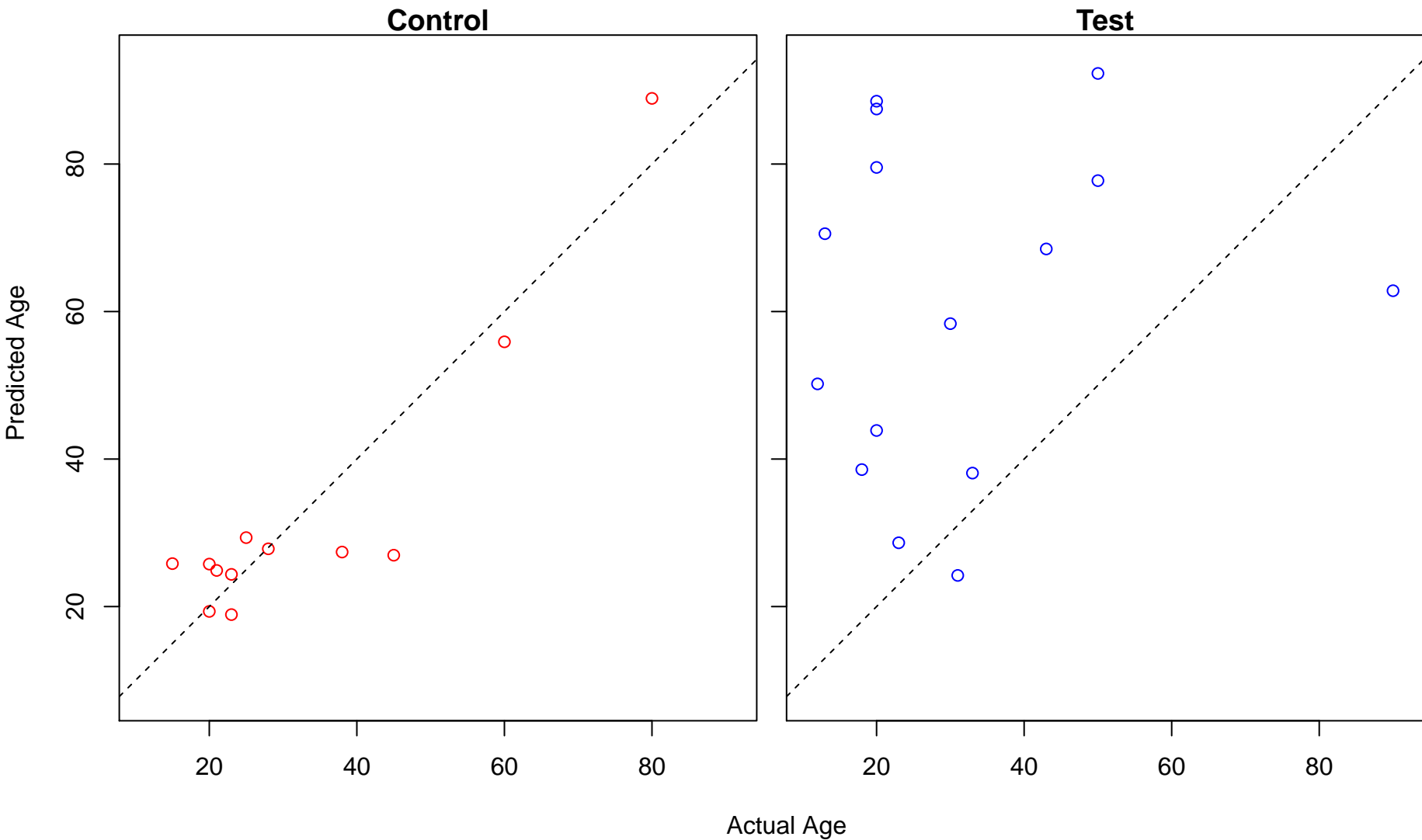


Actual Age

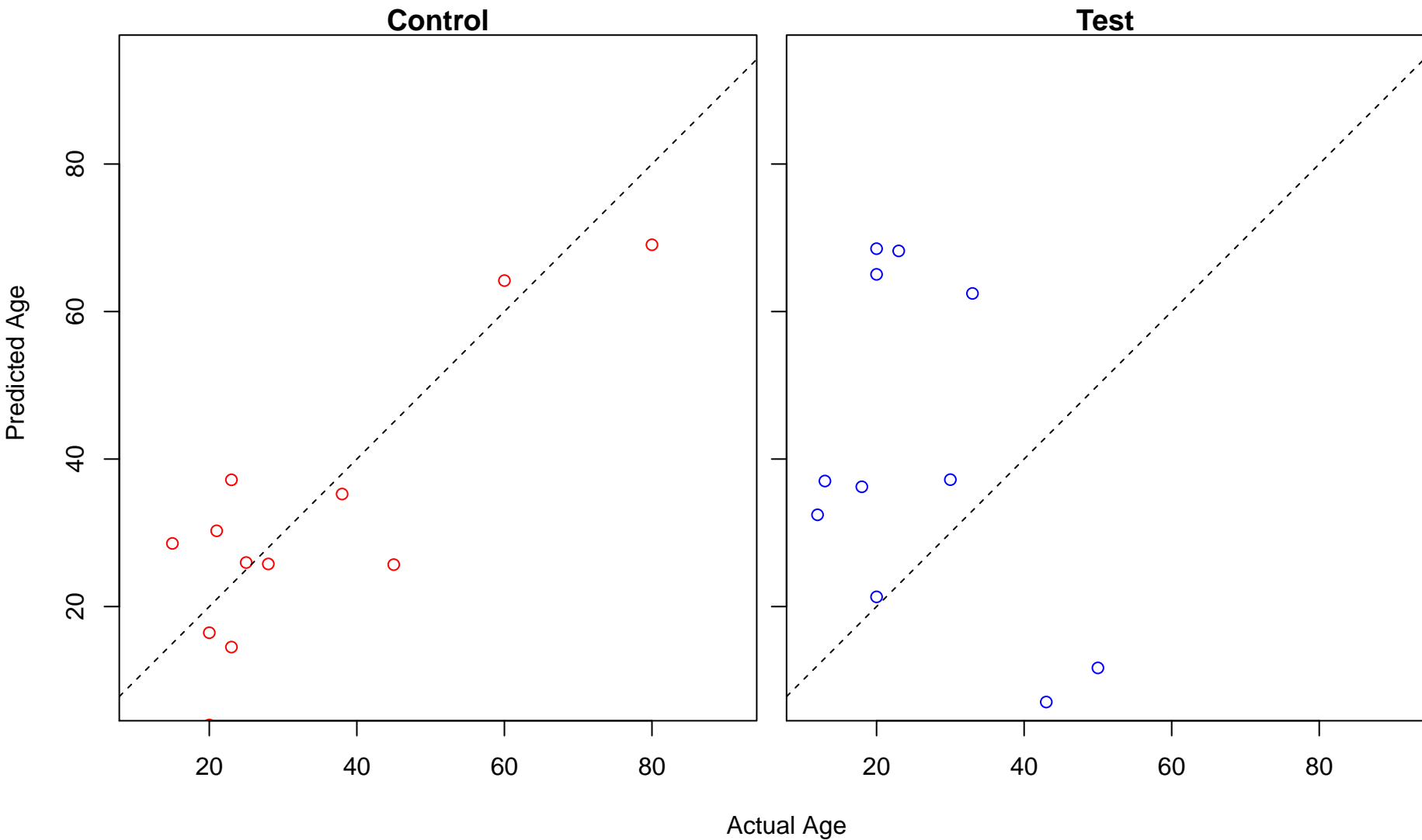
nucleoside transport (Score: 8.622187)



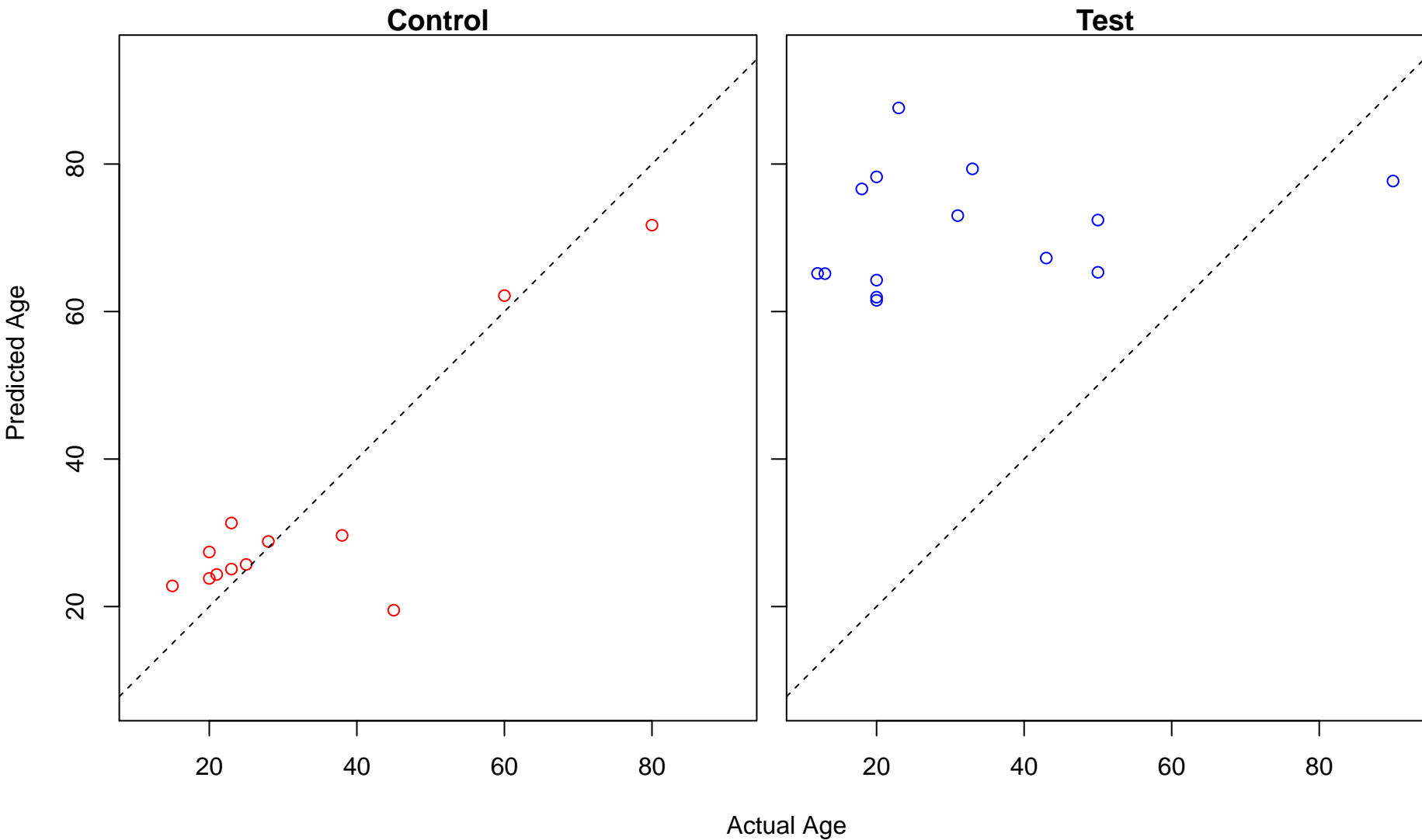
multicellular organismal aging (Score: 8.617392)



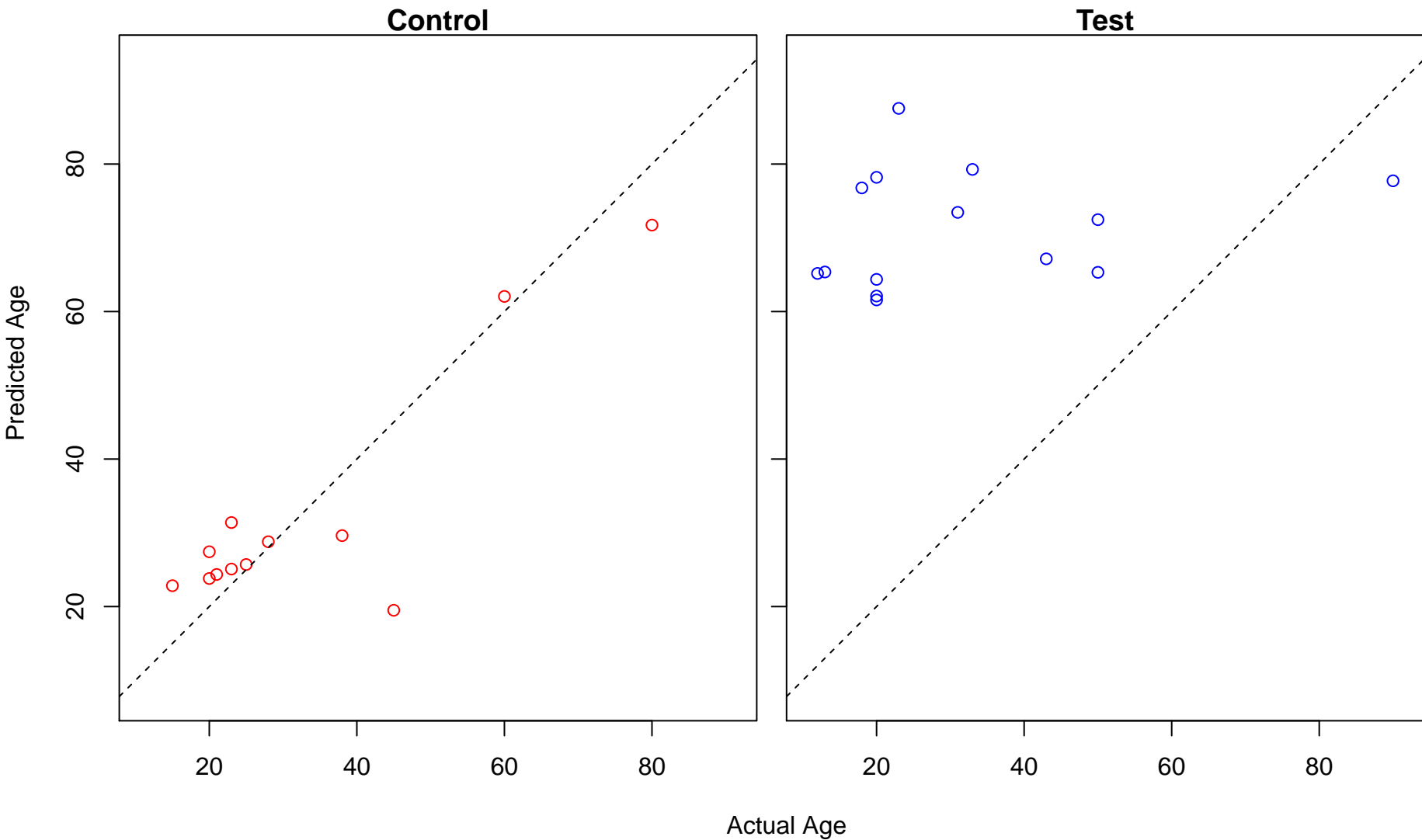
regulation of calcium ion transmembrane transport (Score: 8.613533)



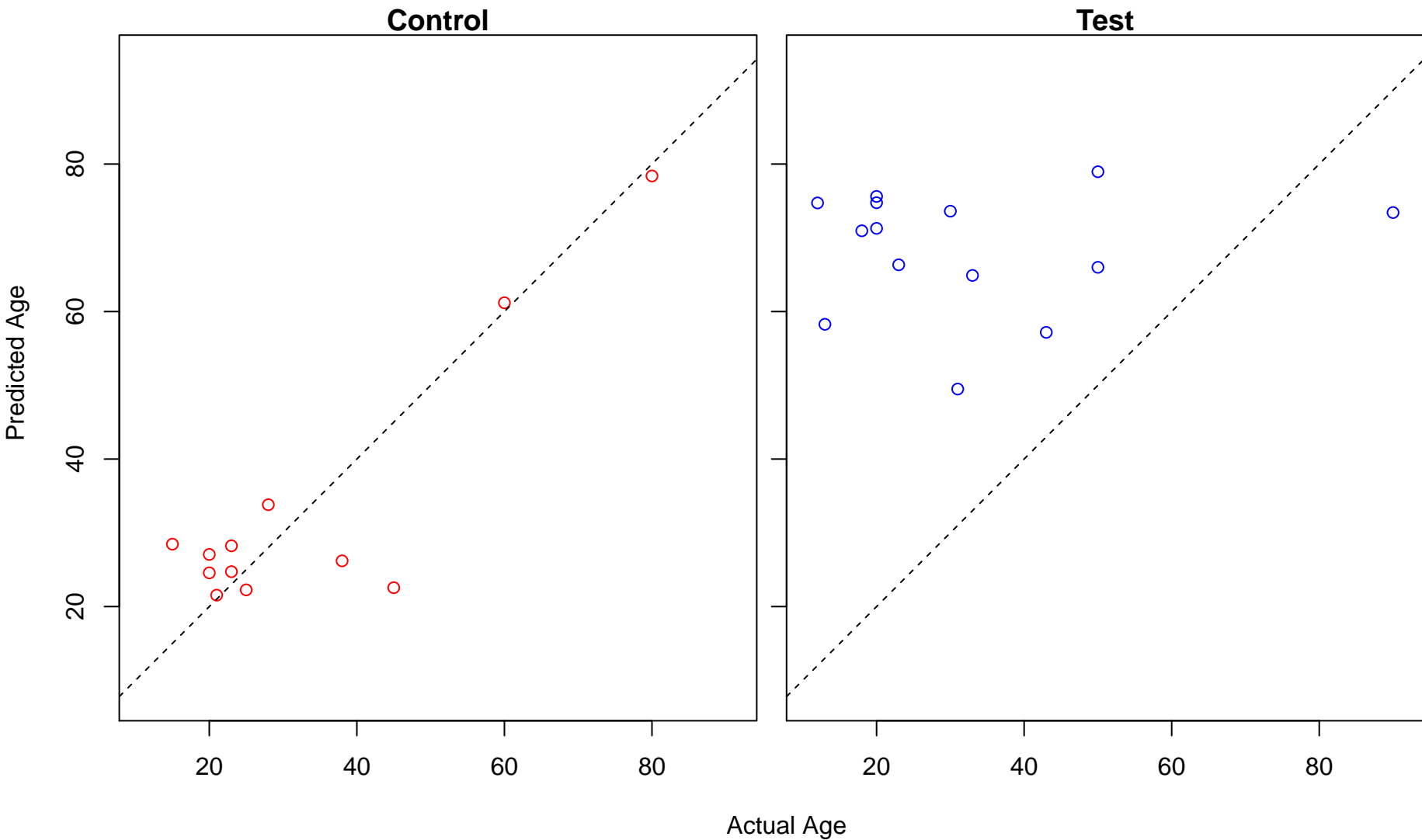
positive regulation of regulatory T cell differentiation (Score: 8.607840)



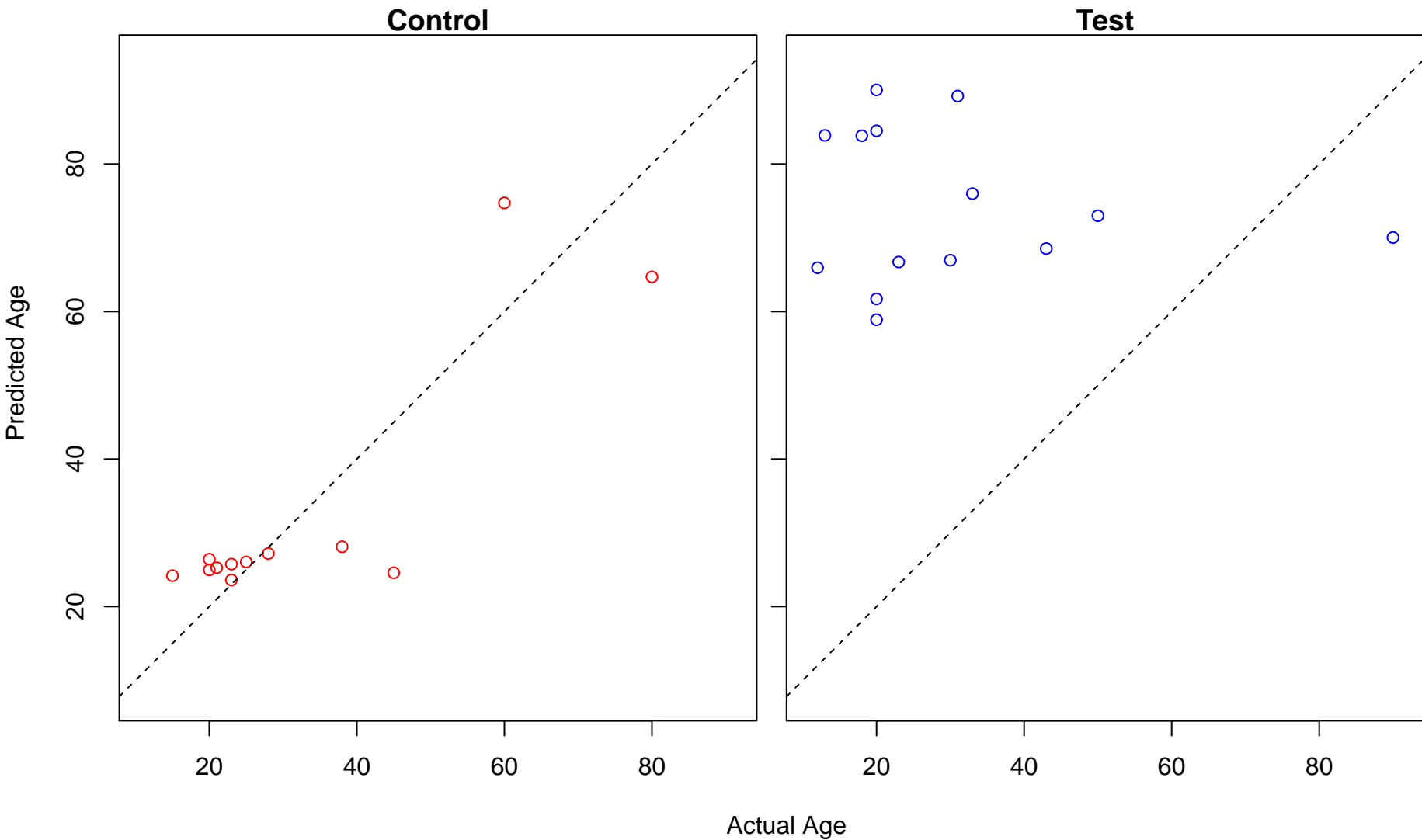
regulation of regulatory T cell differentiation (Score: 8.606978)



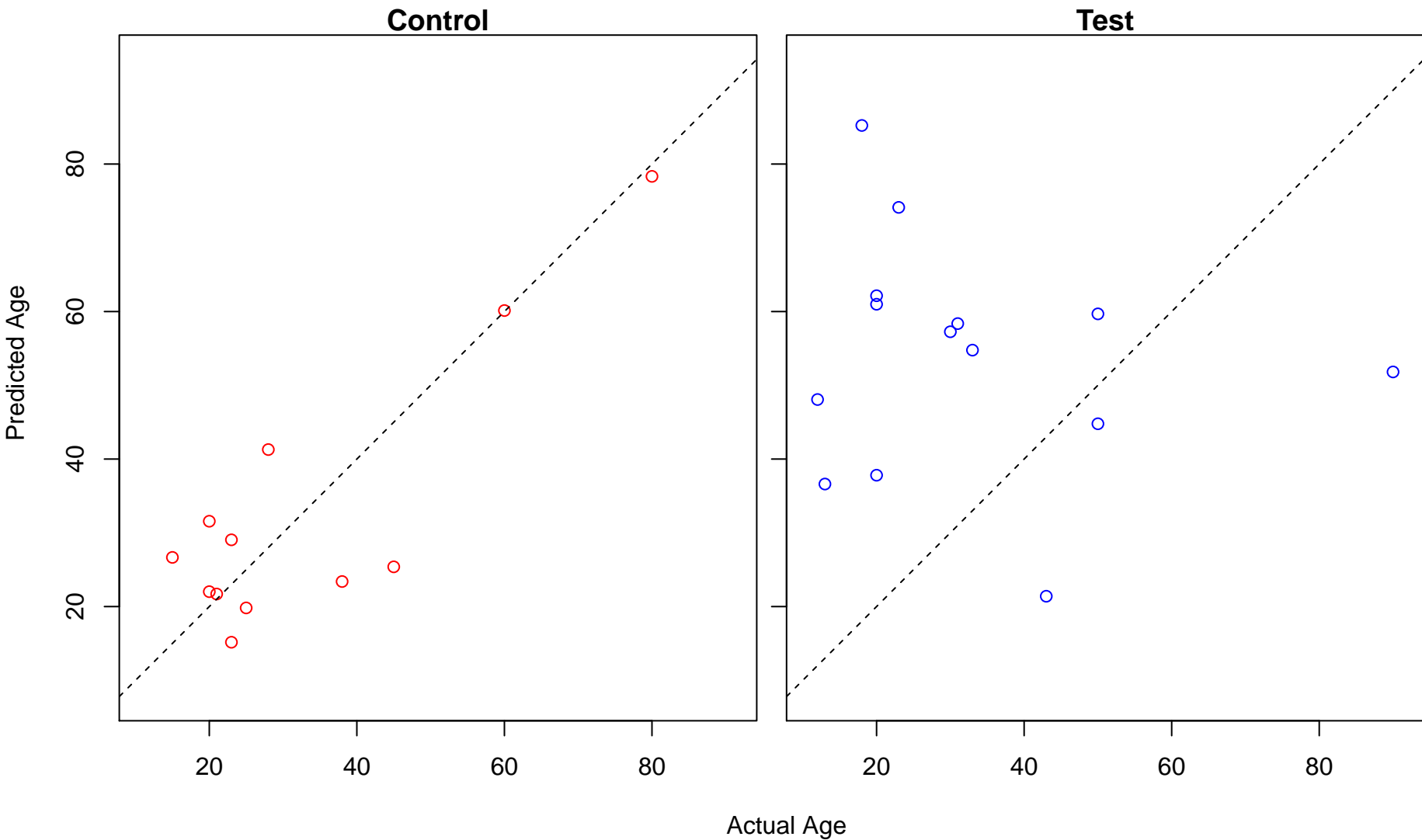
neural tube development (Score: 8.603473)



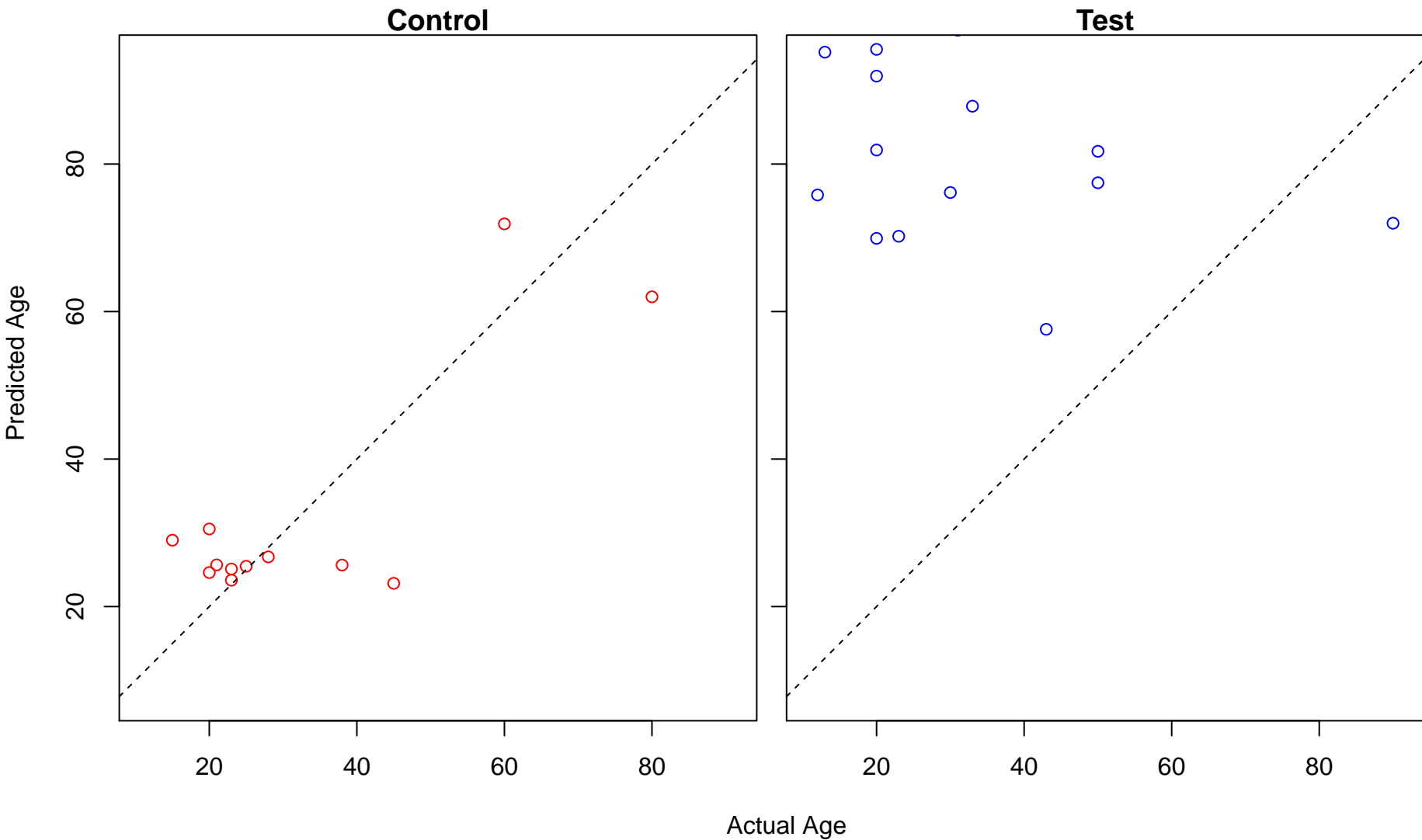
cellular senescence (Score: 8.603156)



posttranscriptional regulation of gene expression (Score: 8.597592)

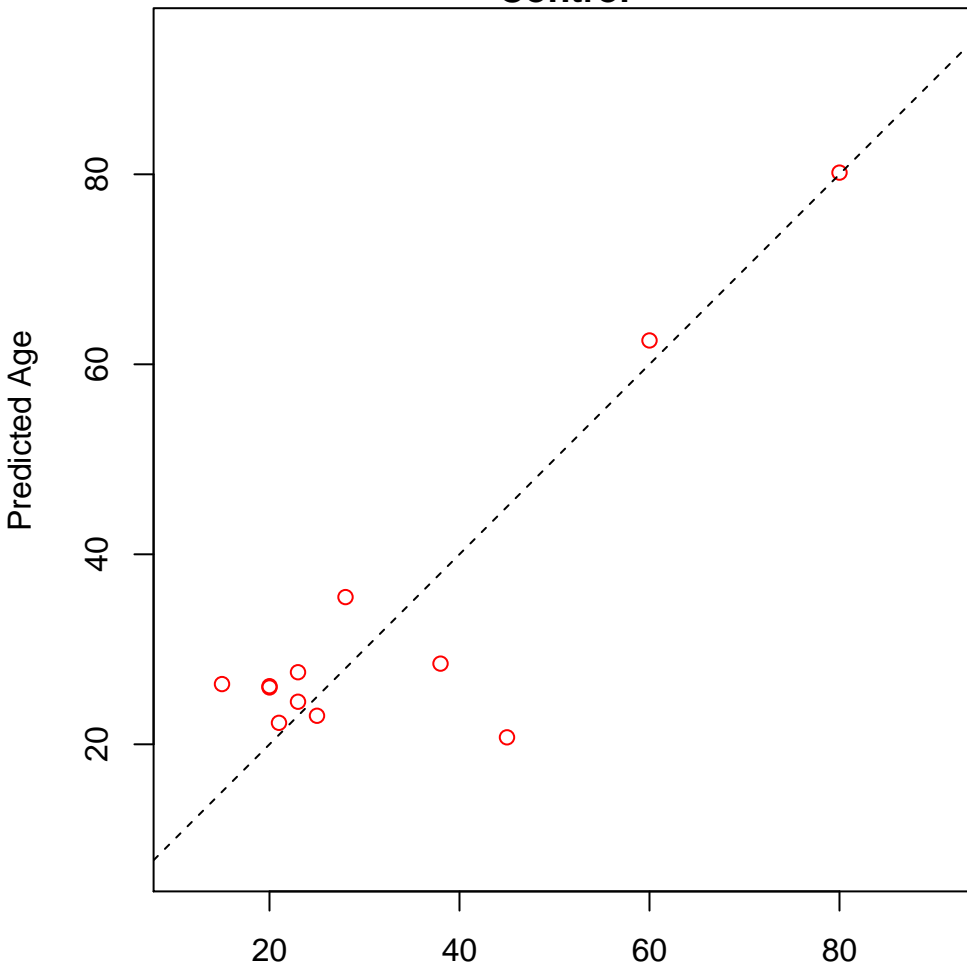


positive regulation of nitric-oxide synthase activity (Score: 8.596985)

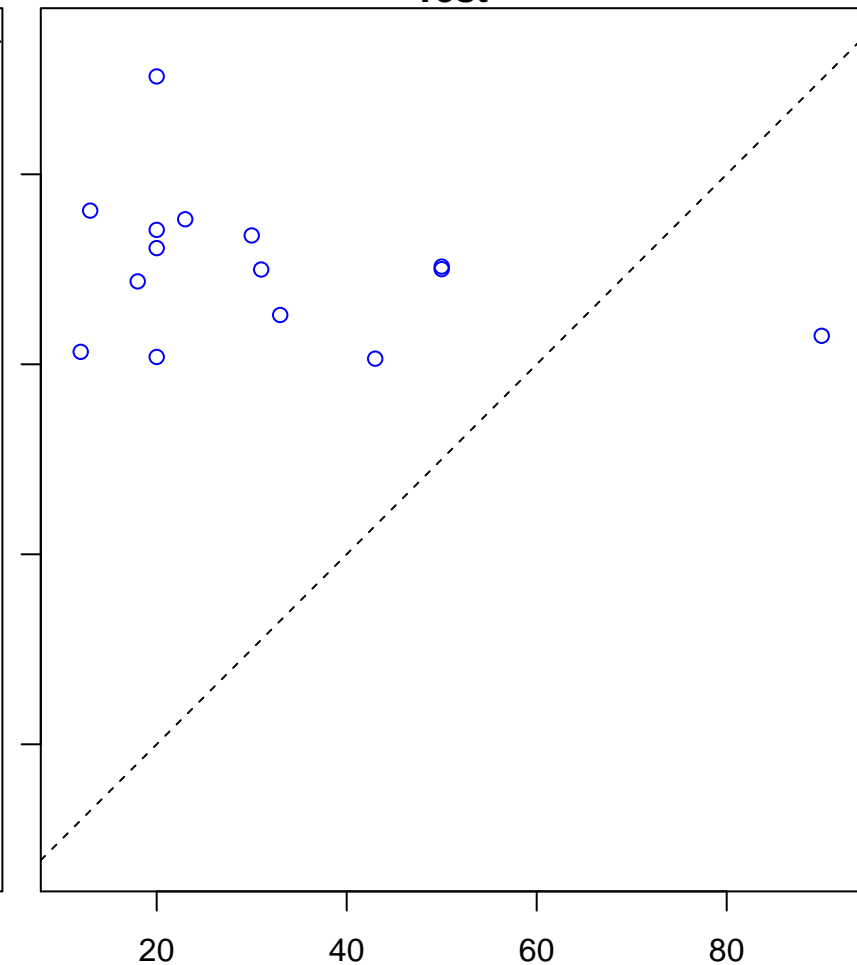


organic acid biosynthetic process (Score: 8.592371)

Control



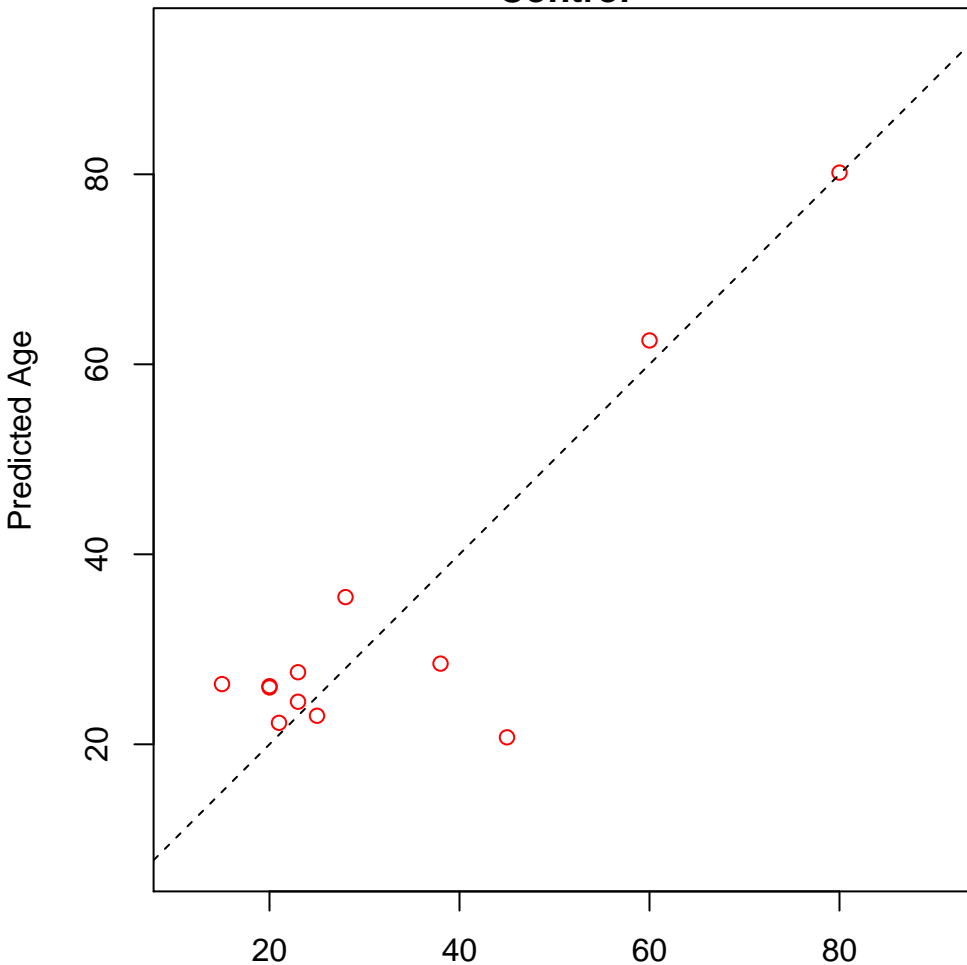
Test



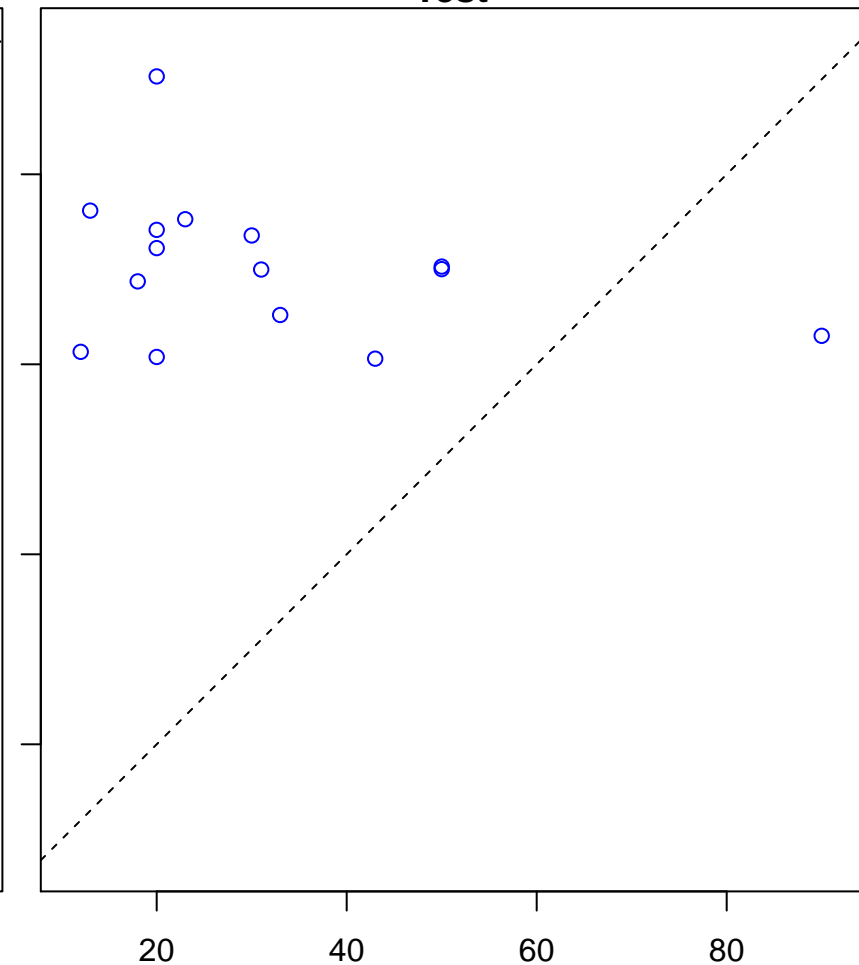
Actual Age

carboxylic acid biosynthetic process (Score: 8.592371)

Control

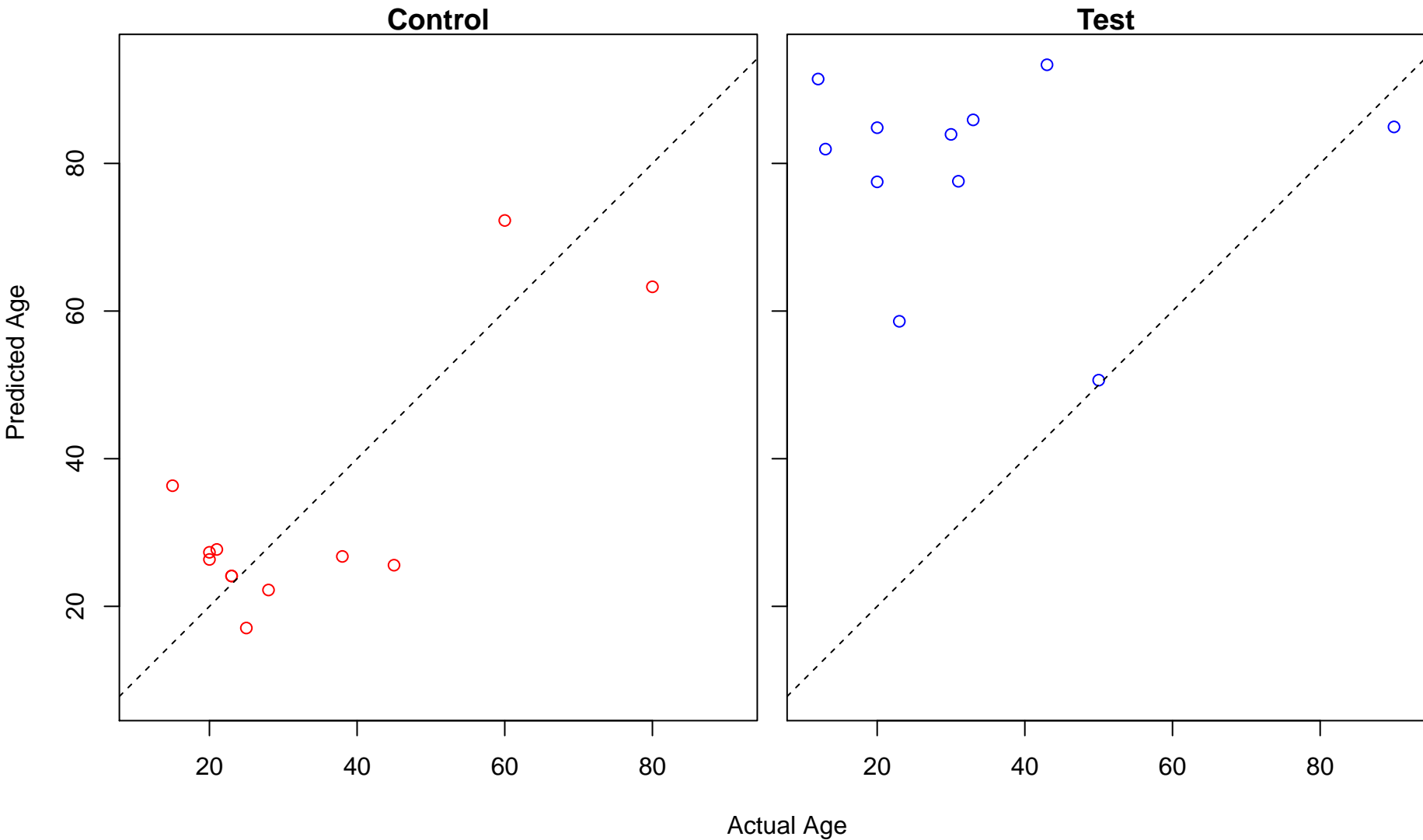


Test



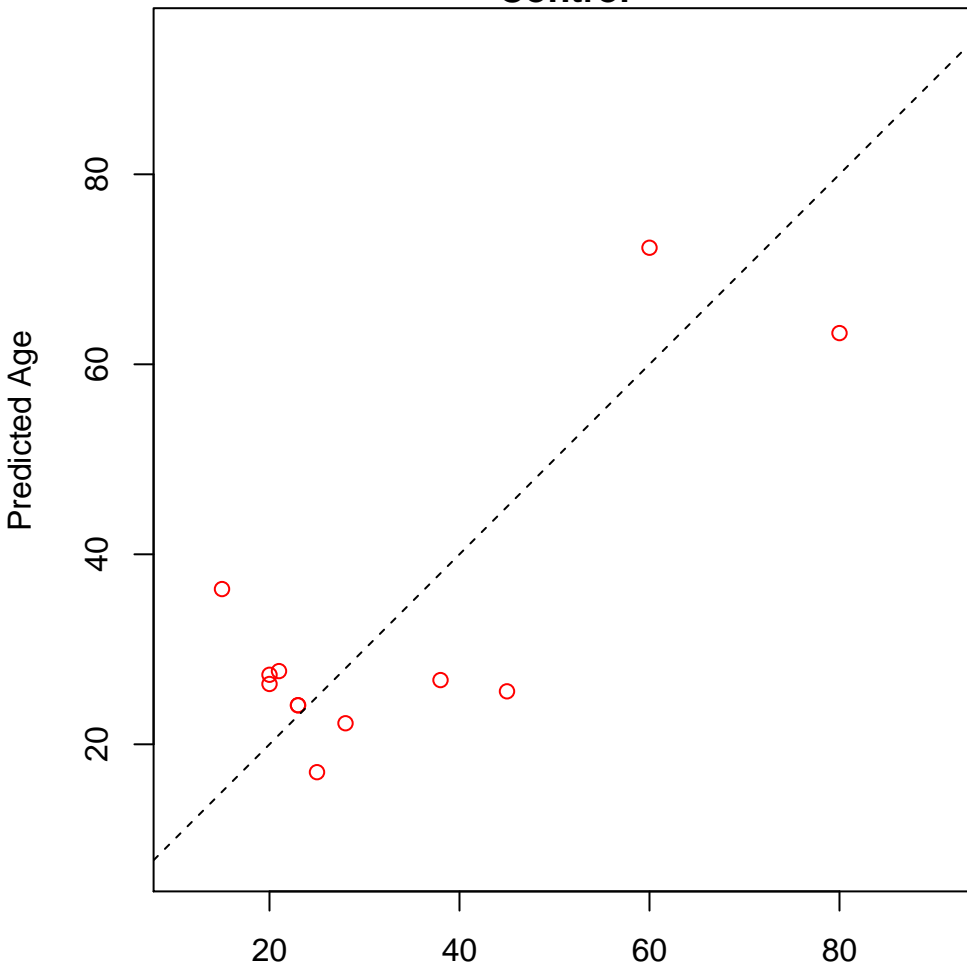
Actual Age

cellular response to monosaccharide stimulus (Score: 8.589209)

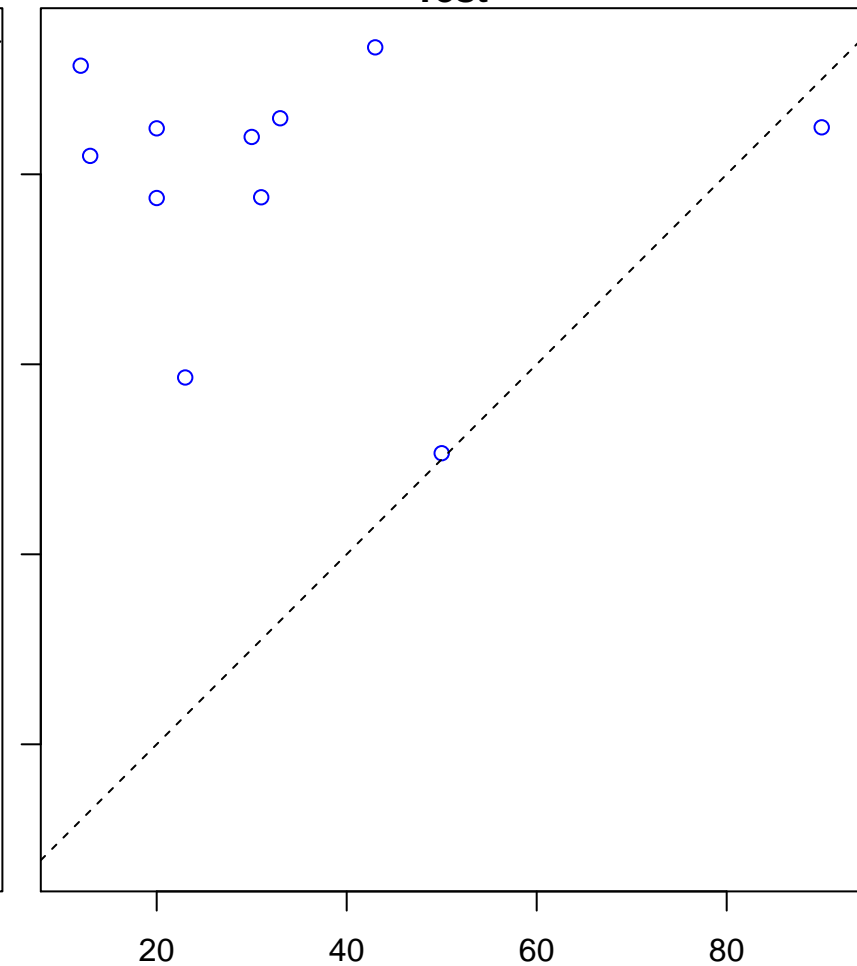


cellular response to hexose stimulus (Score: 8.589209)

Control



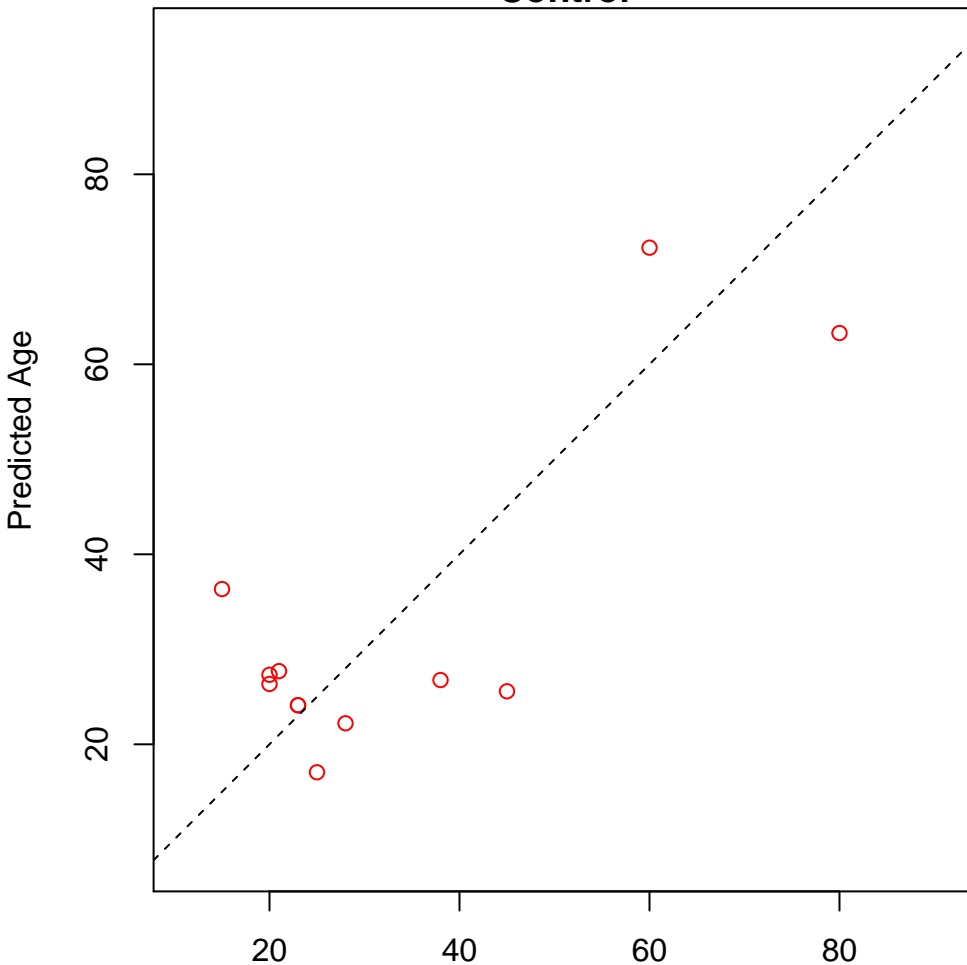
Test



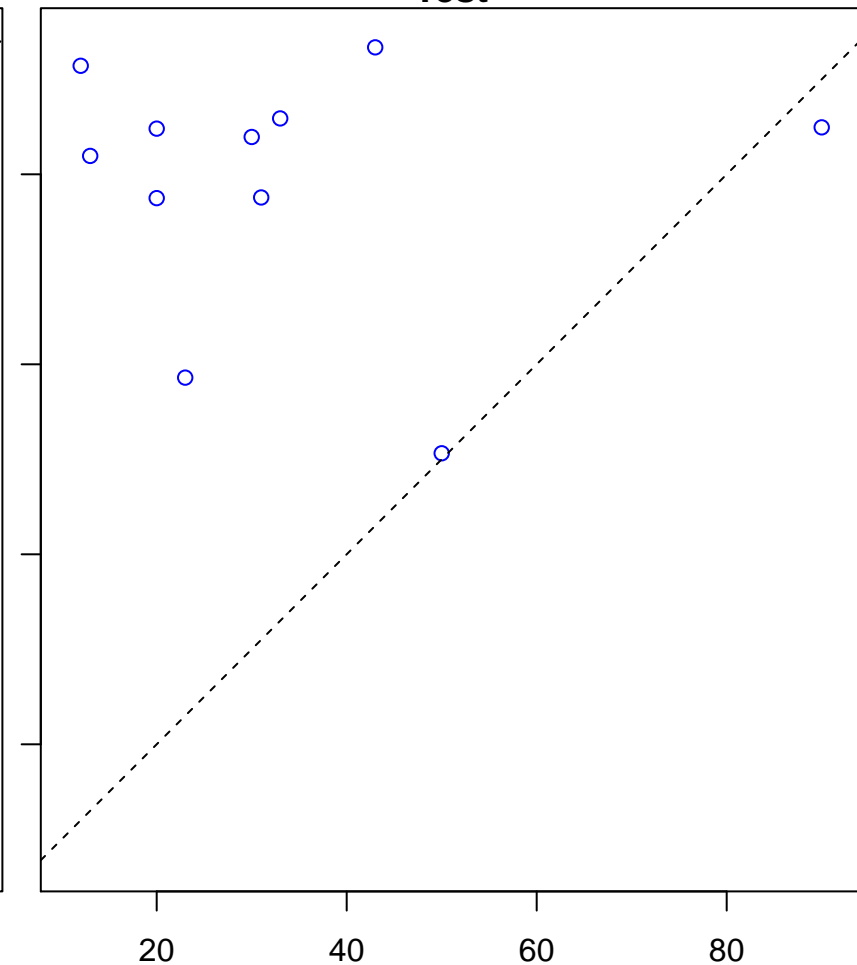
Actual Age

cellular response to glucose stimulus (Score: 8.588051)

Control

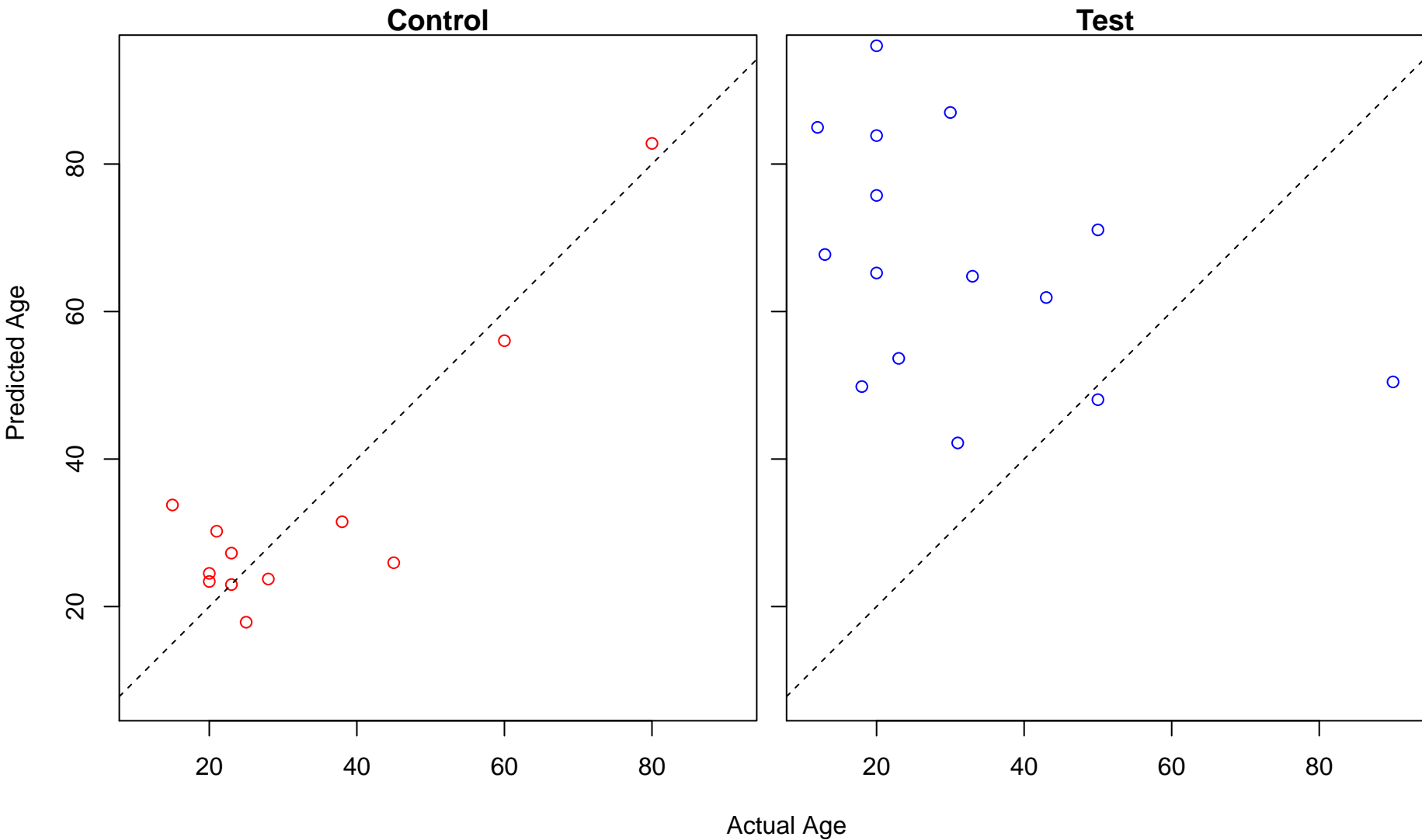


Test

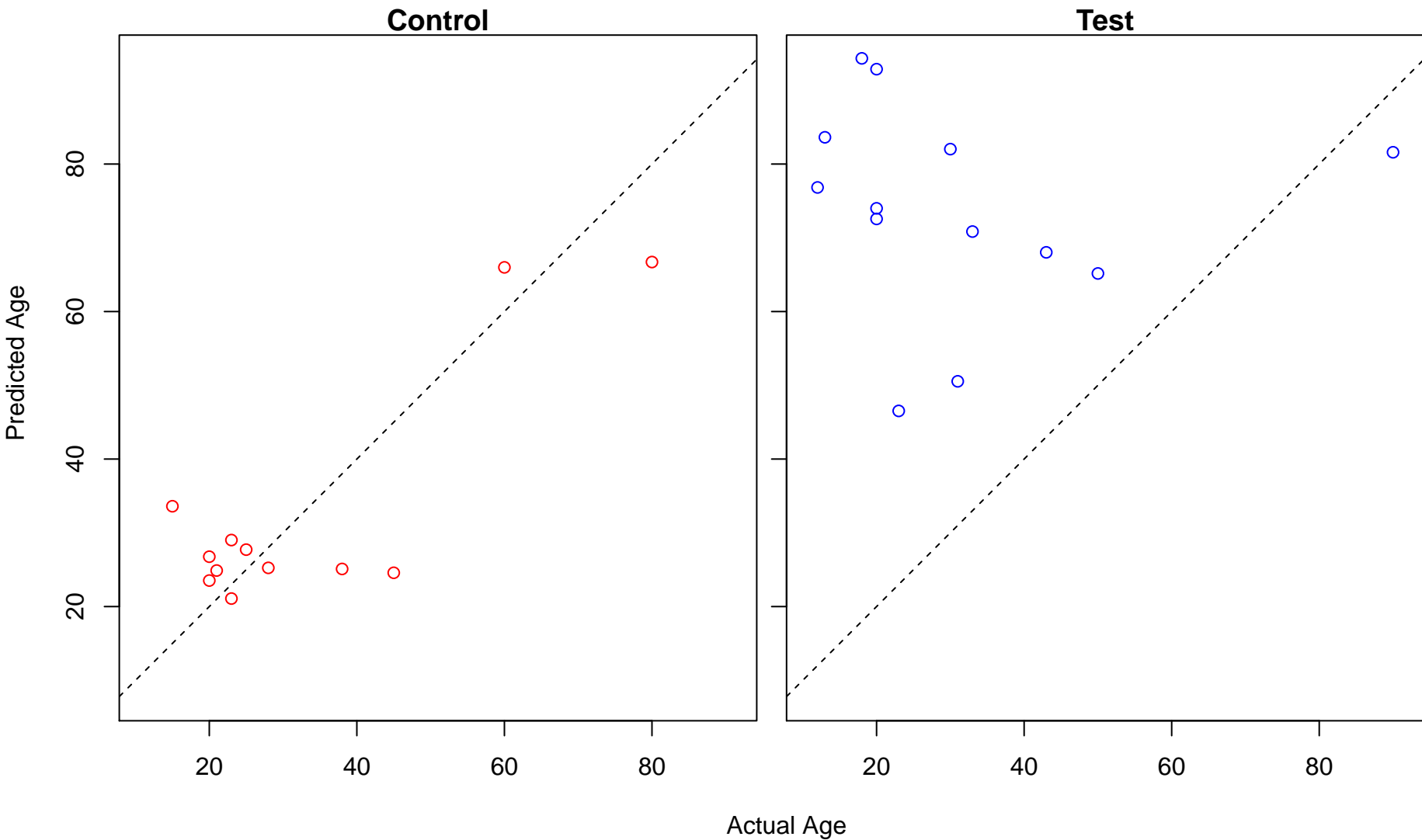


Actual Age

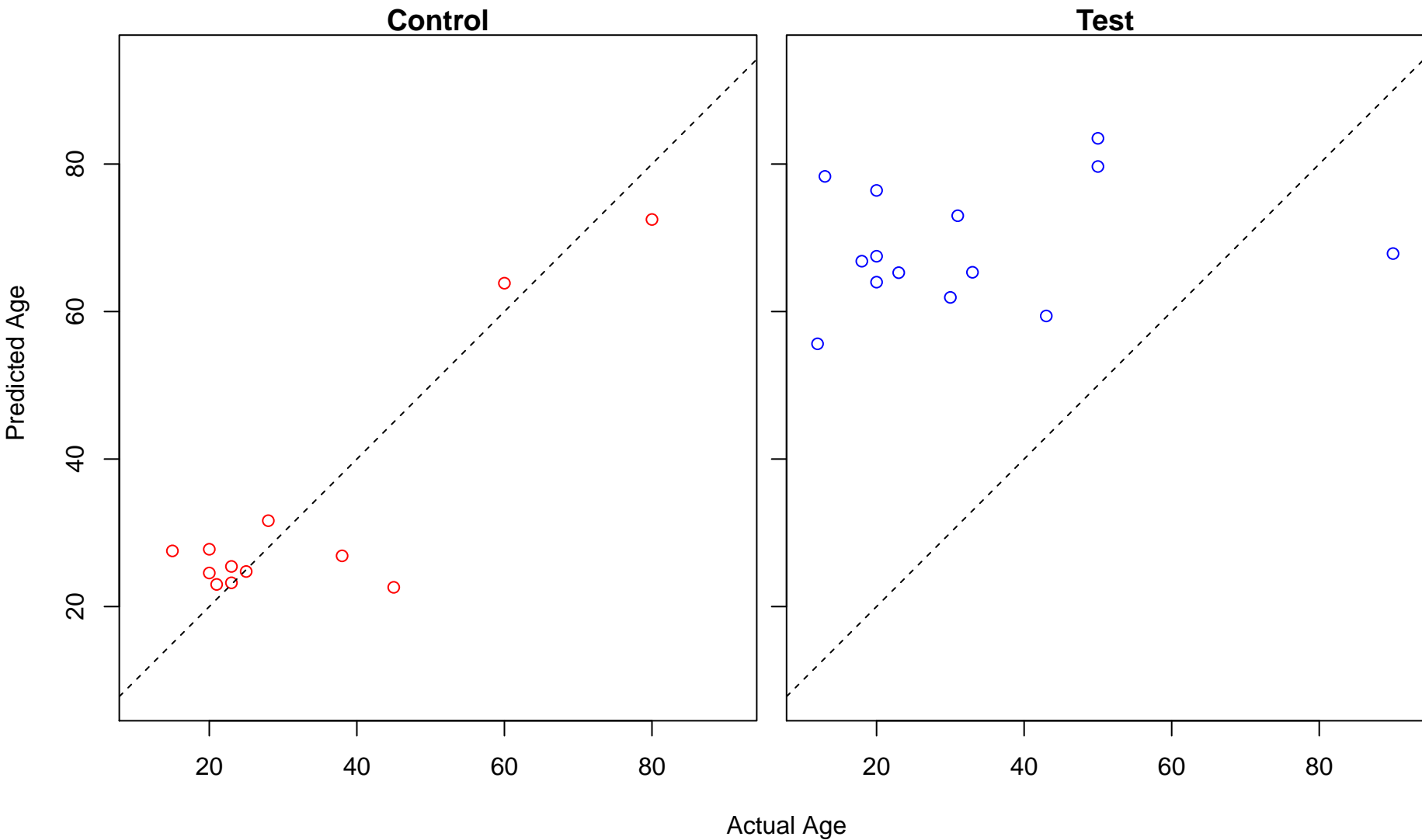
regulation of interleukin-1 beta secretion (Score: 8.587843)



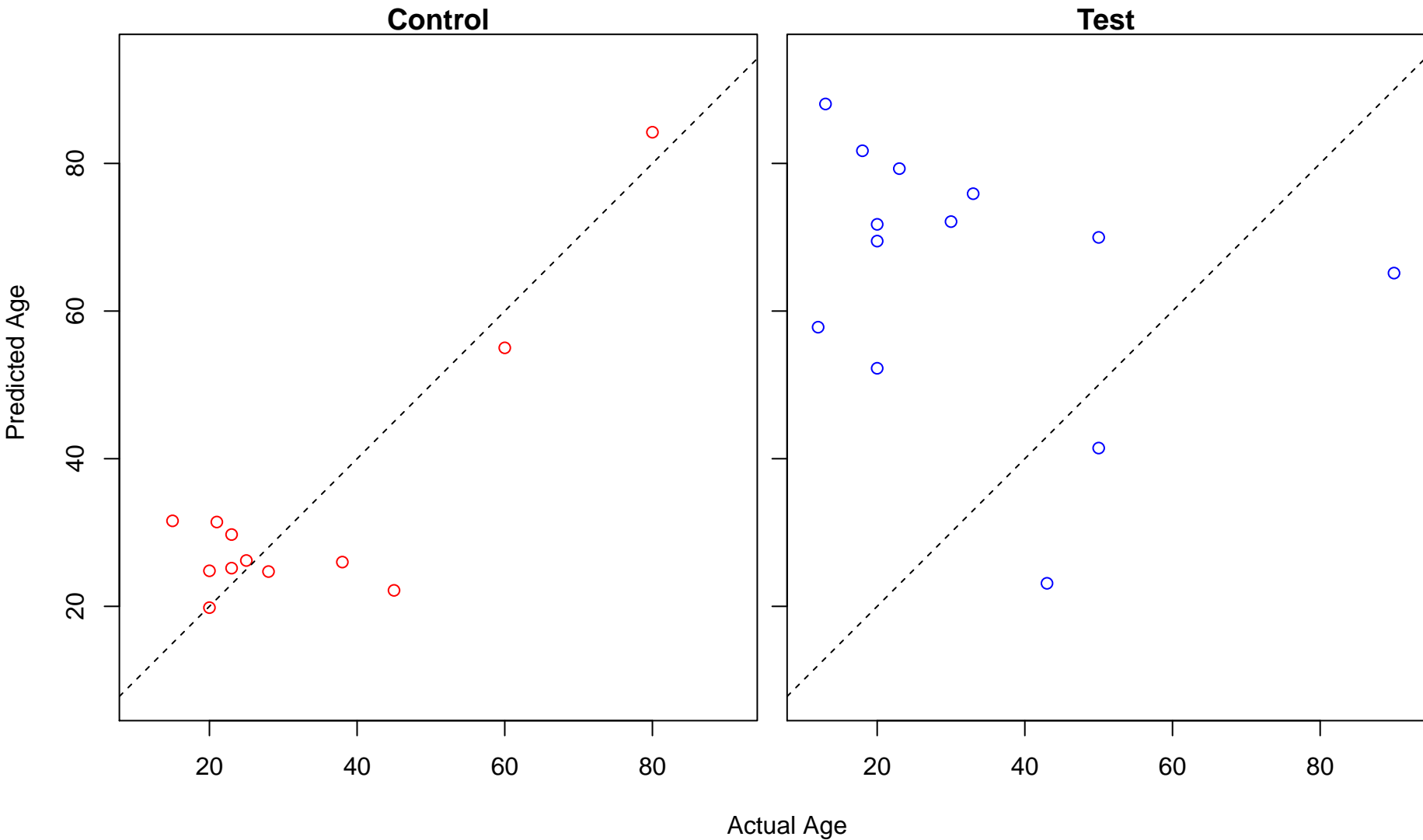
cellular response to laminar fluid shear stress (Score: 8.585338)



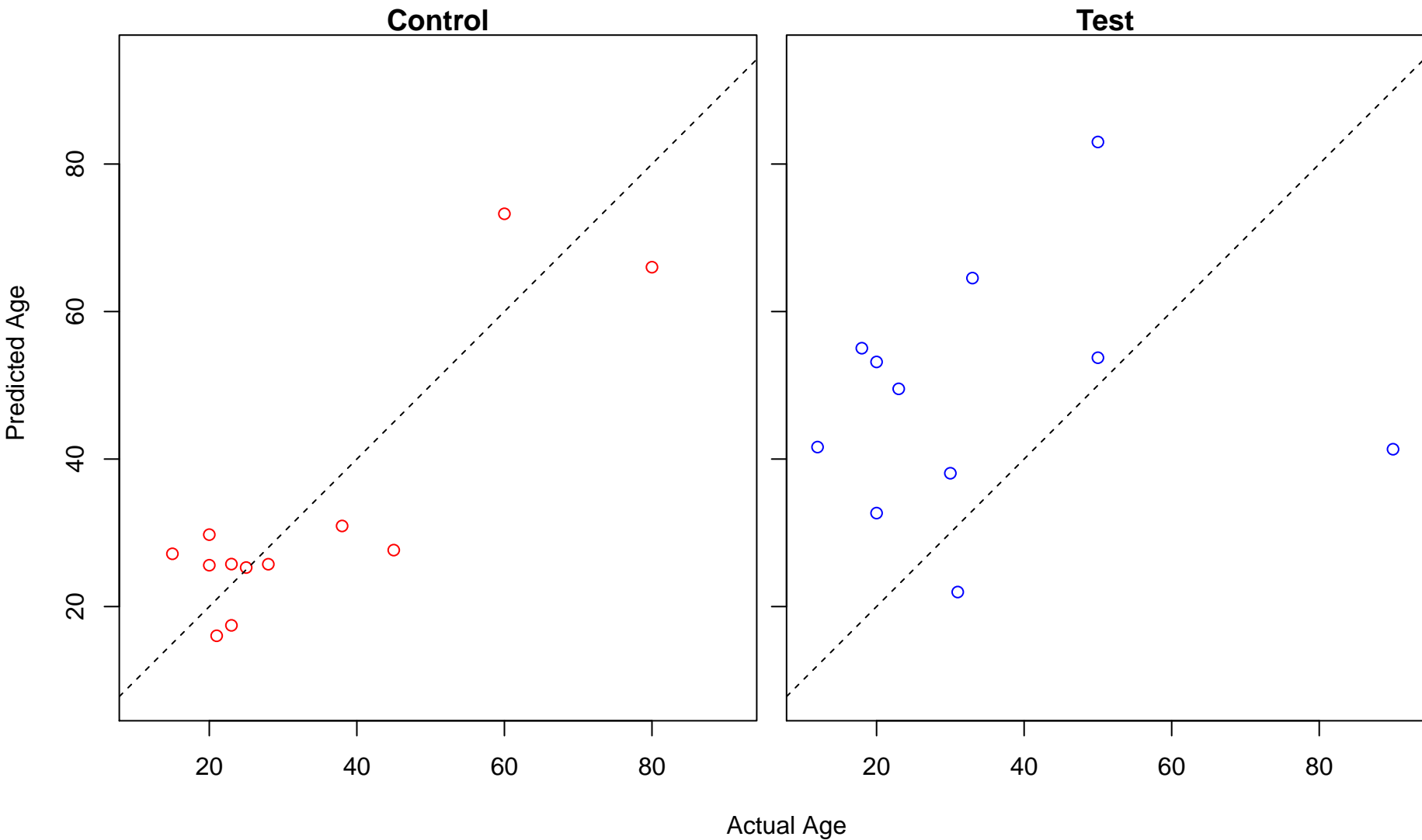
positive regulation of cAMP metabolic process (Score: 8.584440)



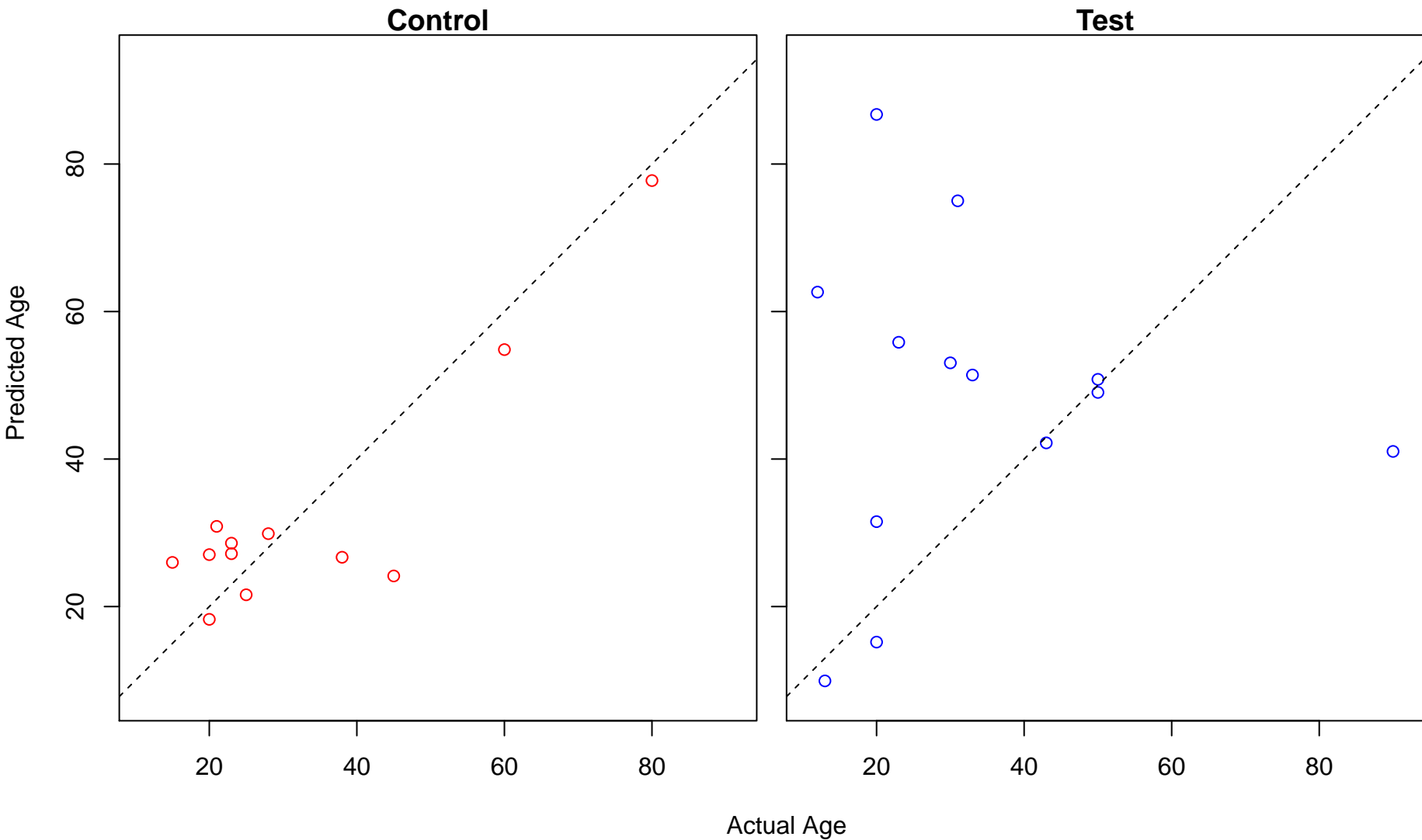
regulation of protein localization to nucleus (Score: 8.579869)



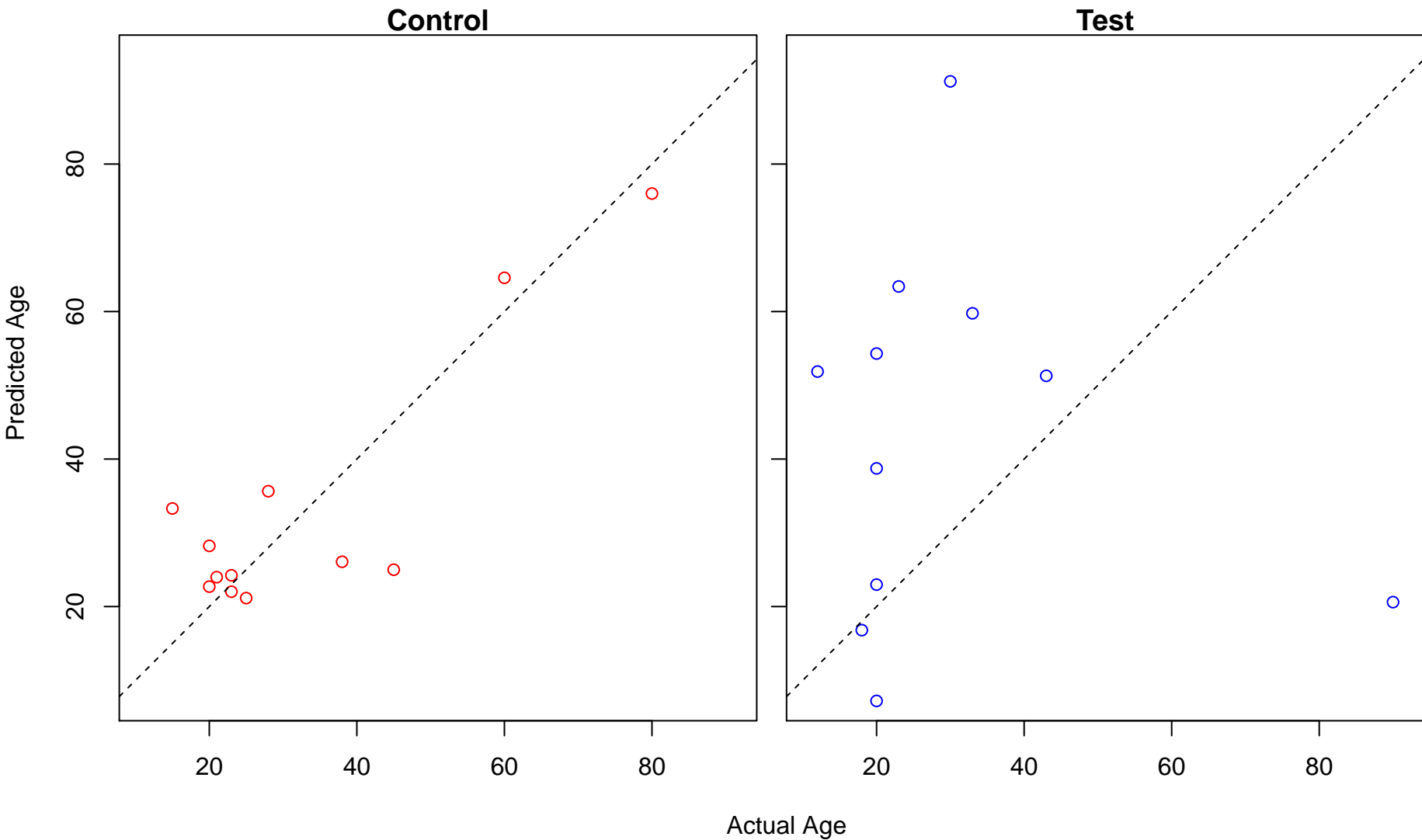
protein refolding (Score: 8.578632)



ephrin receptor signaling pathway (Score: 8.574641)

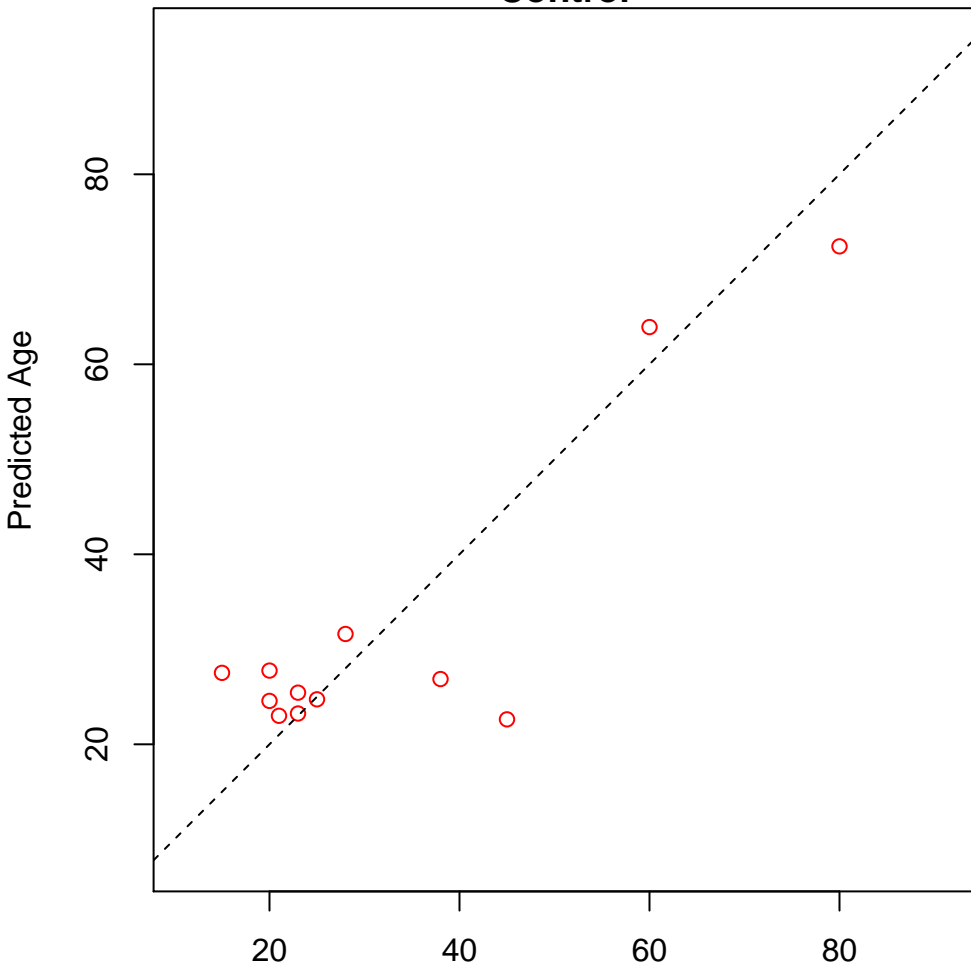


negative regulation of cytoplasmic transport (Score: 8.572068)

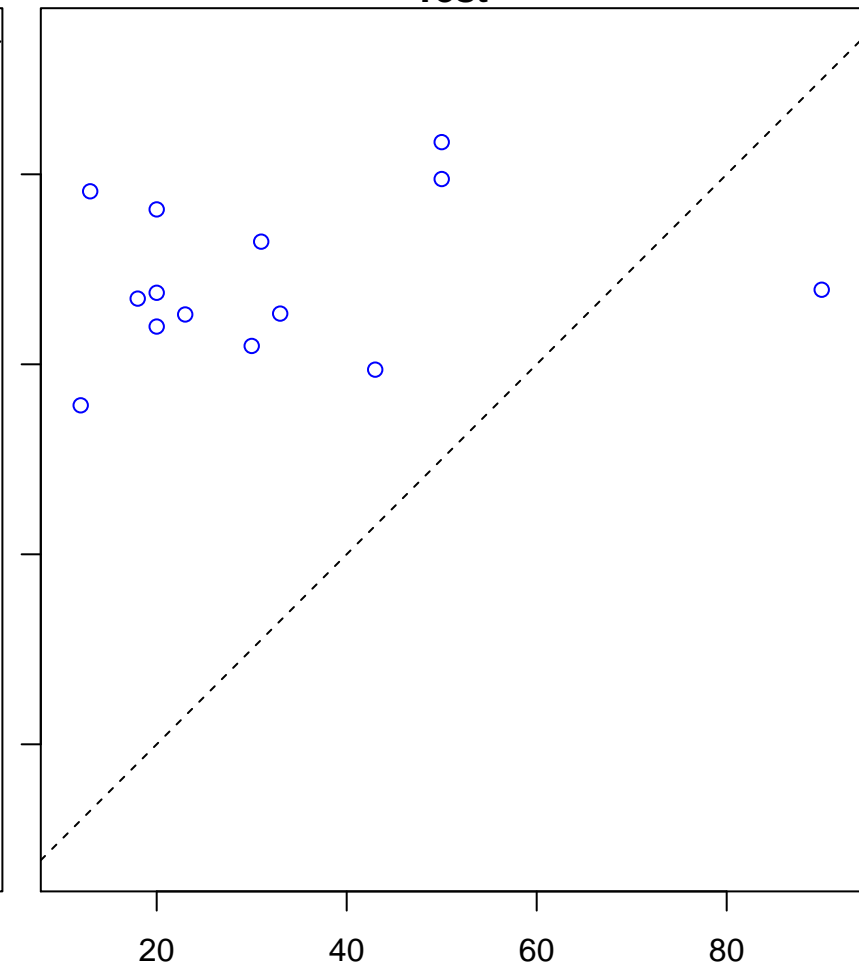


regulation of cAMP metabolic process (Score: 8.567591)

Control

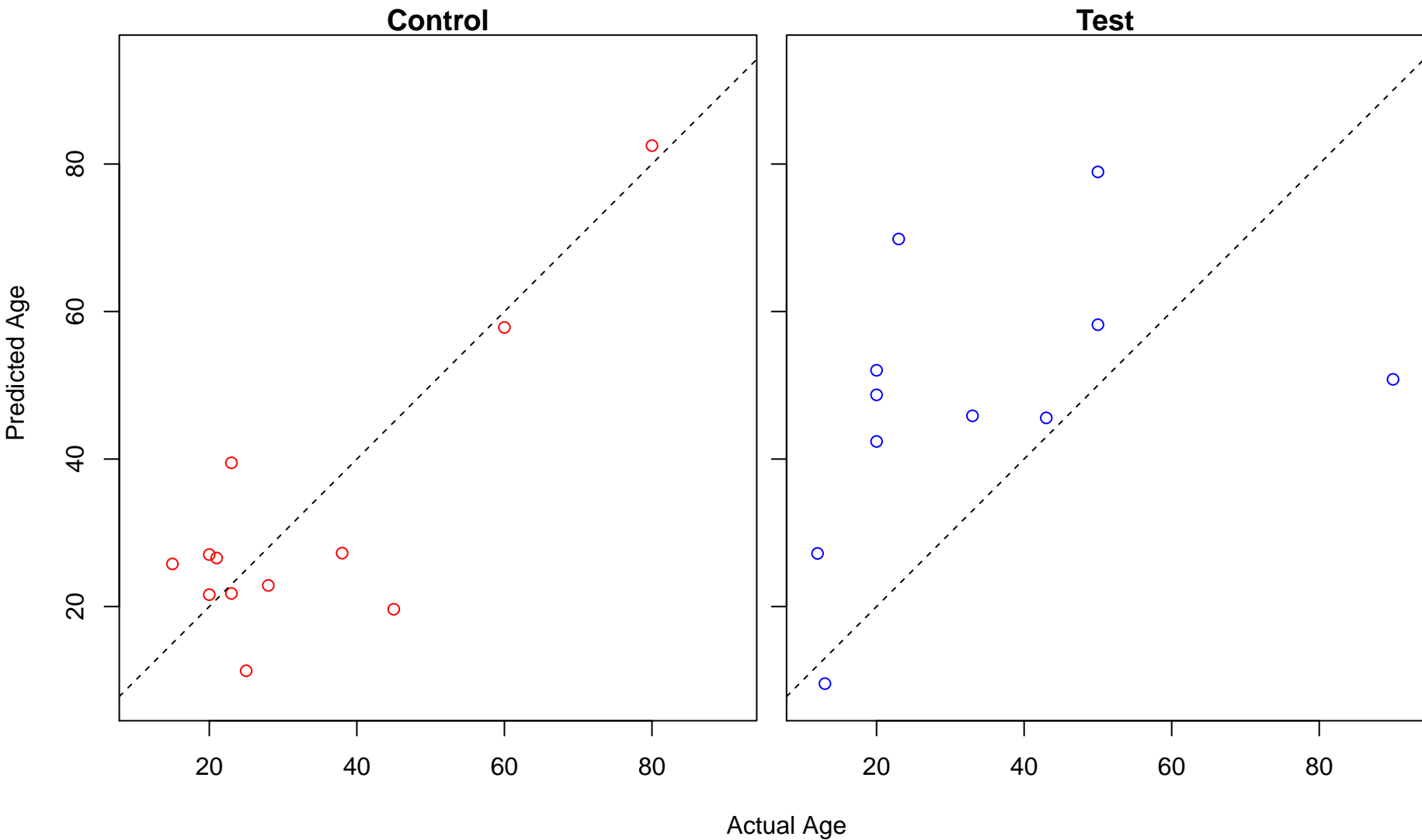


Test

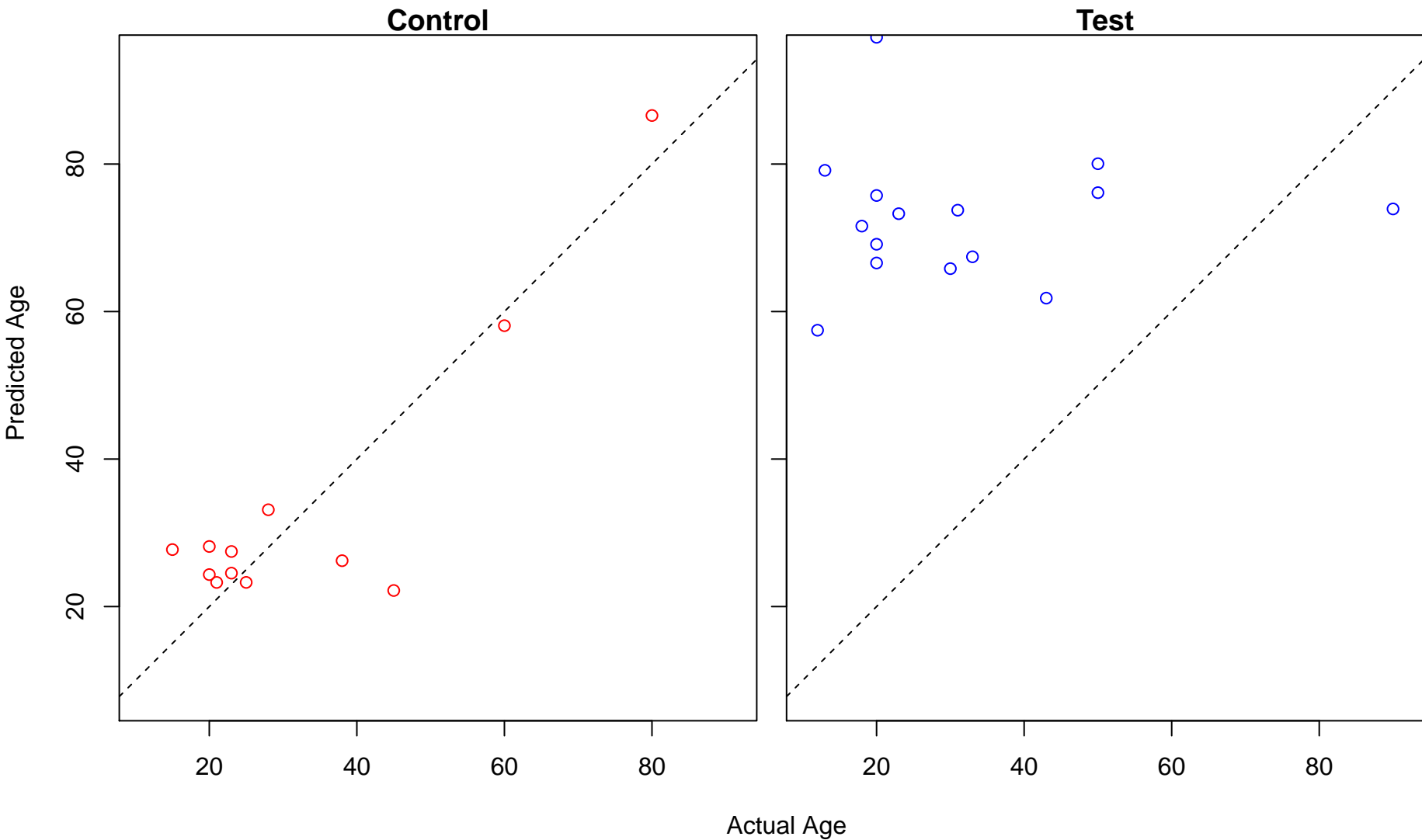


Actual Age

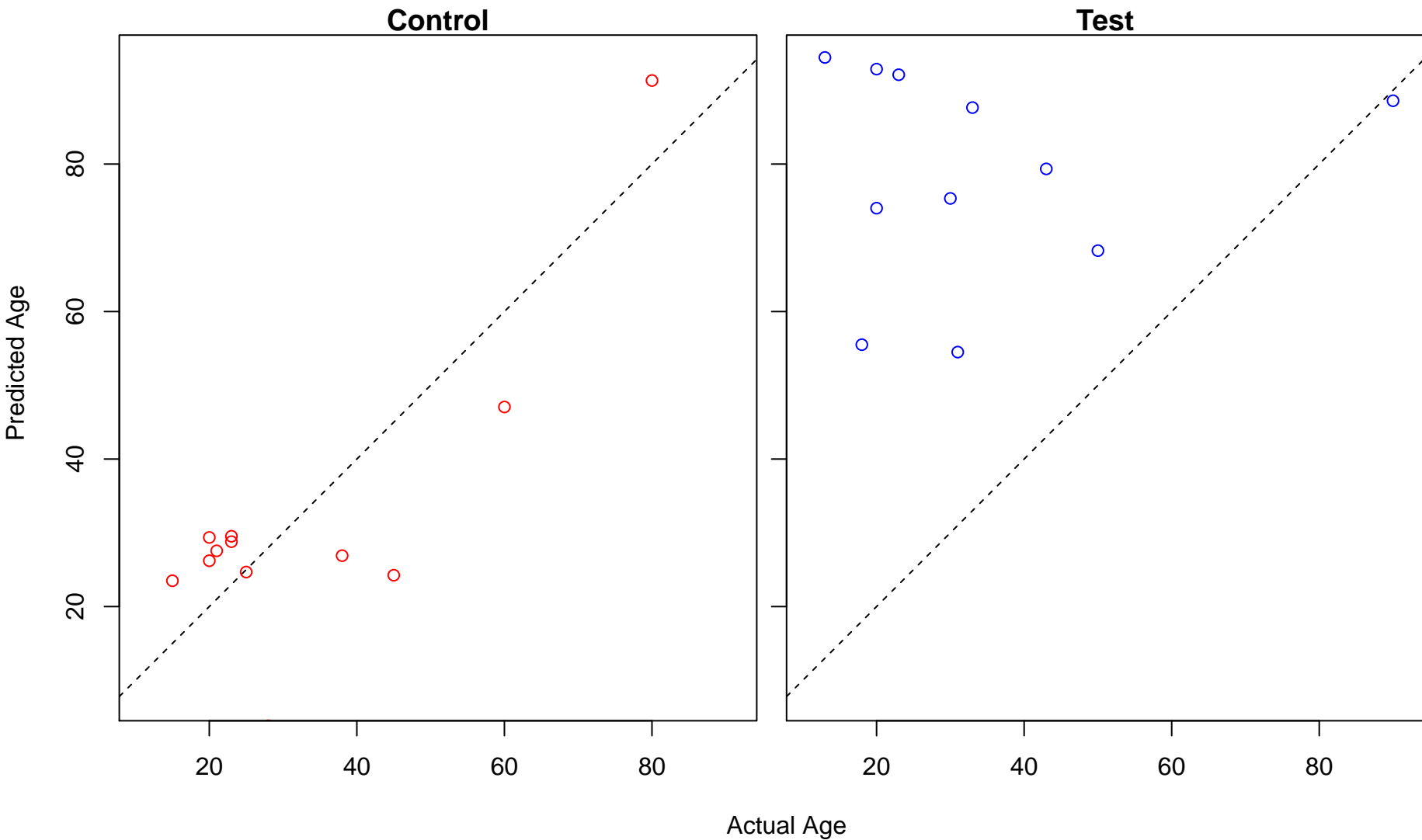
regulation of leukocyte cell-cell adhesion (Score: 8.564888)



cellular response to lipid (Score: 8.562549)

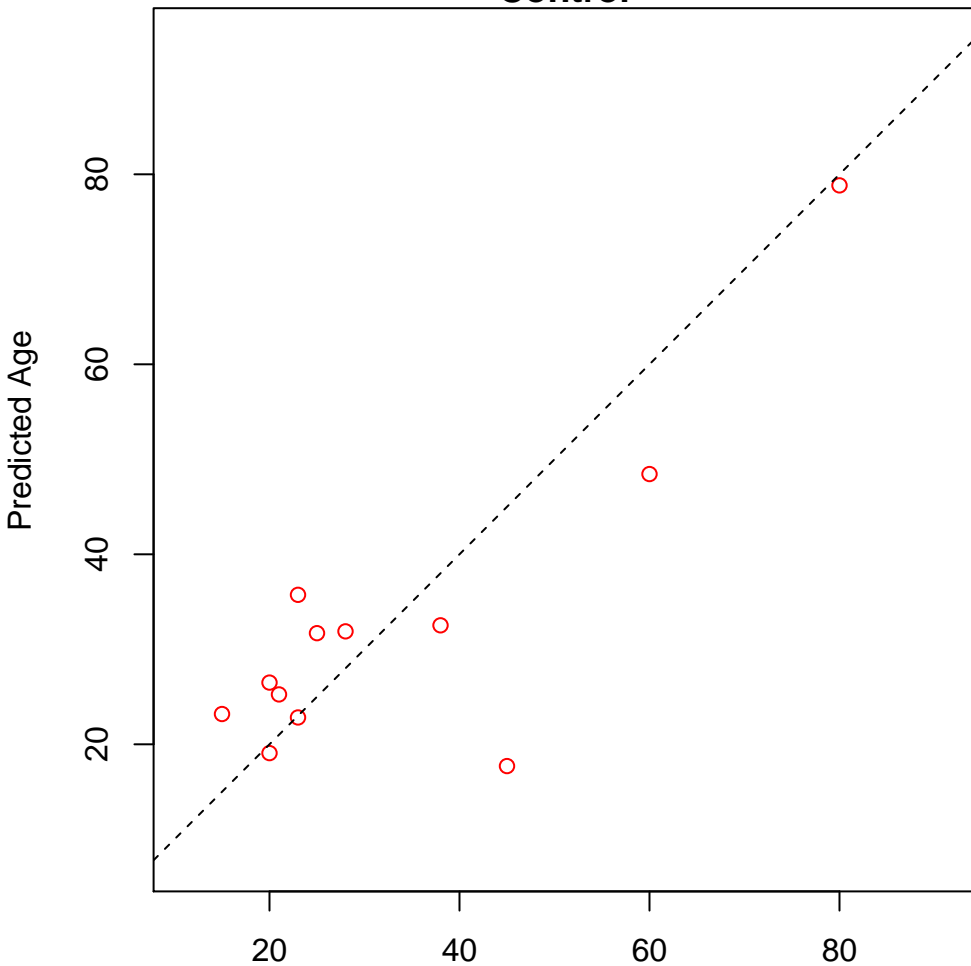


aspartate transport (Score: 8.558561)

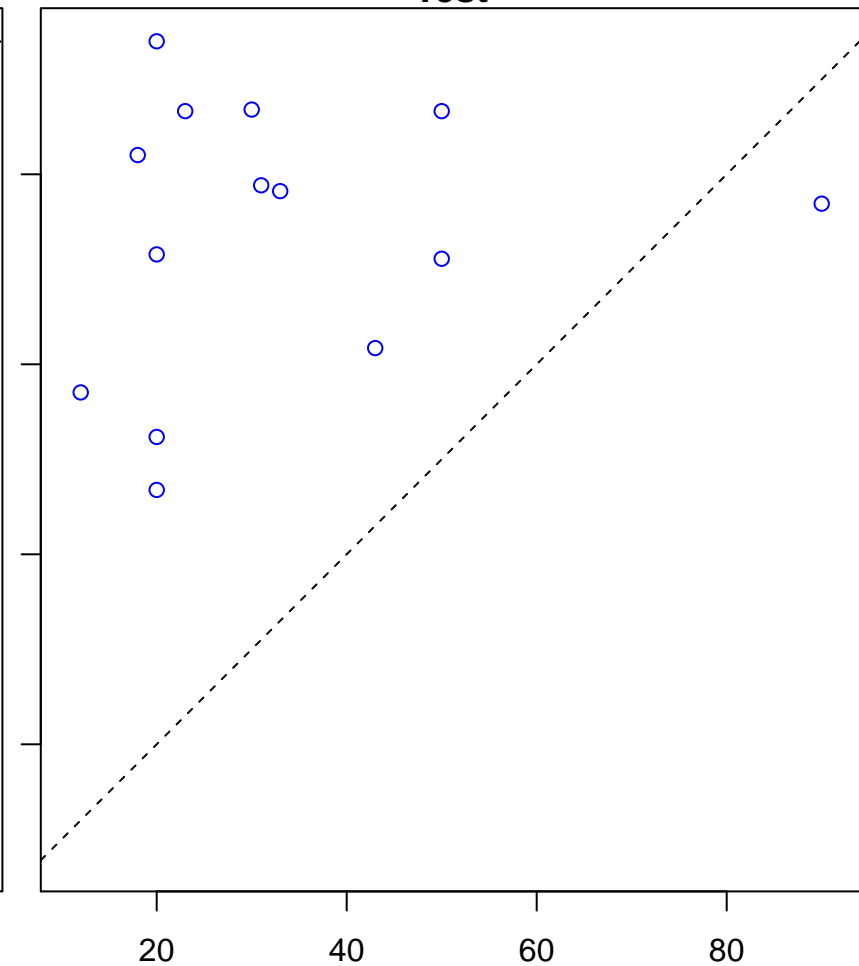


regulation of T cell tolerance induction (Score: 8.558286)

Control

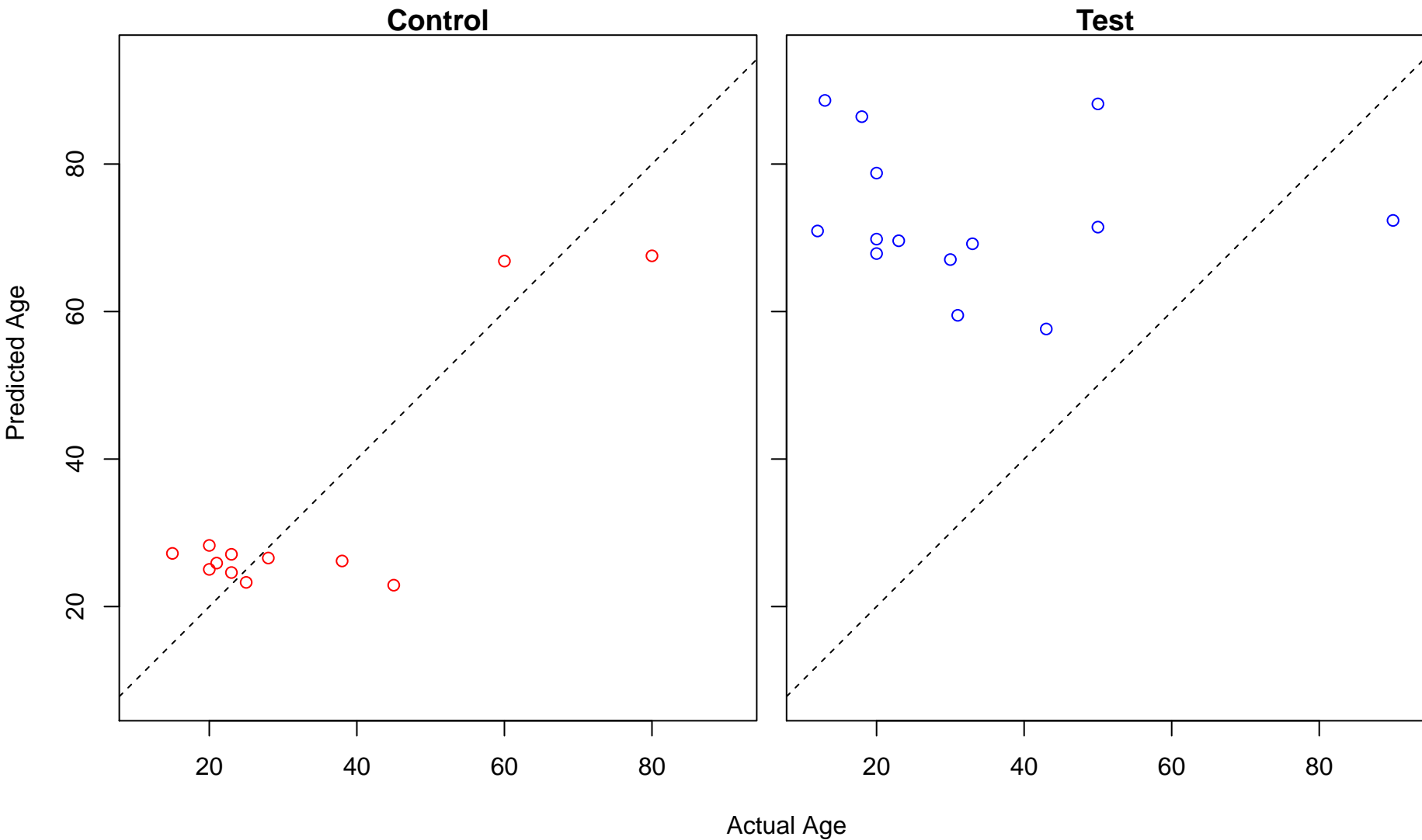


Test



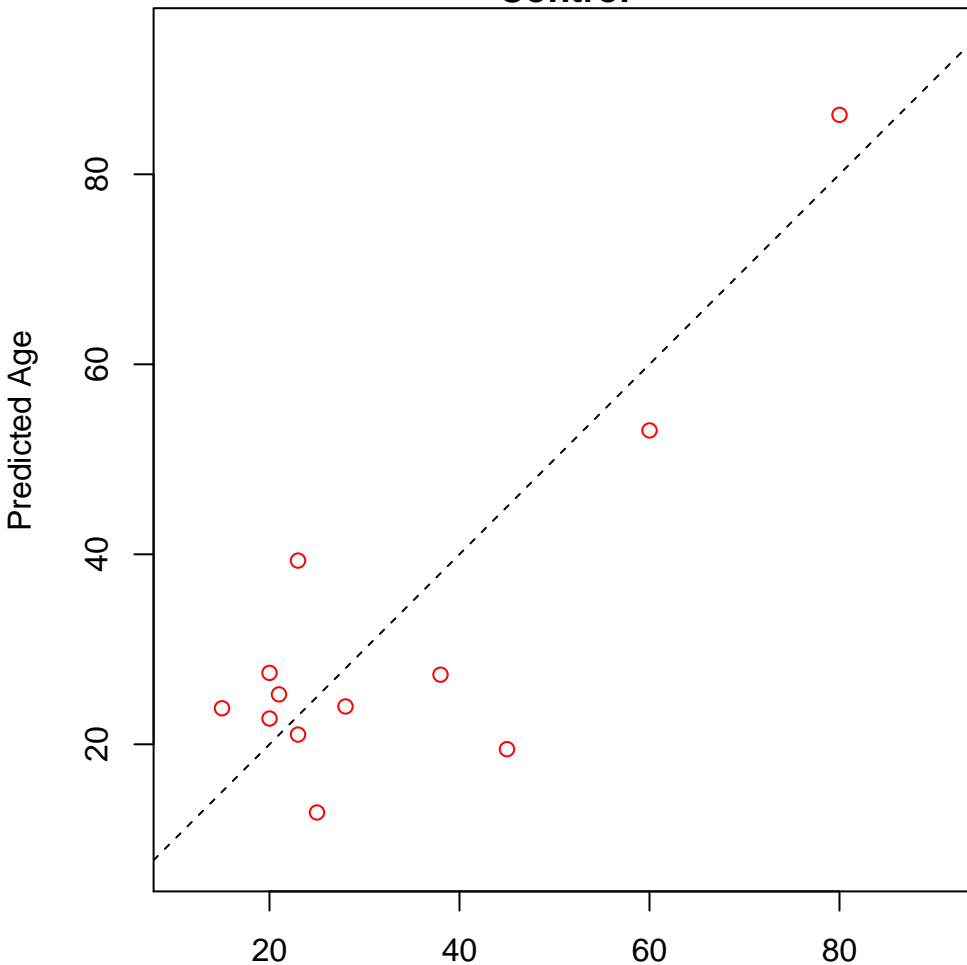
Actual Age

interaction with host (Score: 8.557625)

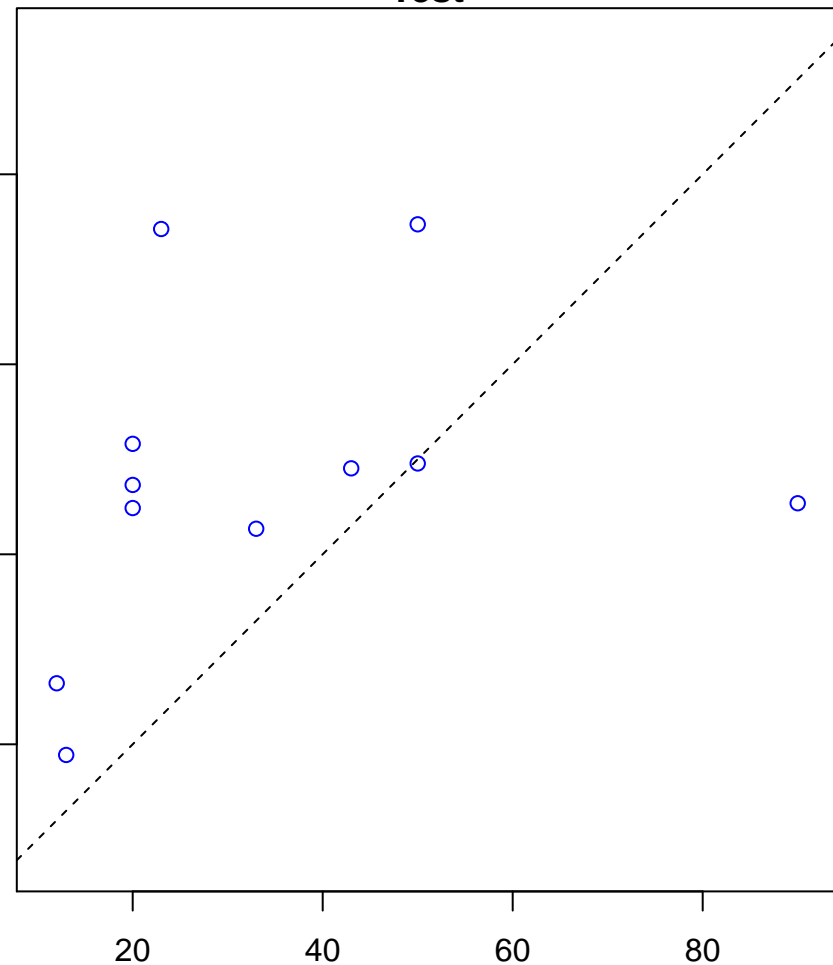


positive regulation of T cell activation (Score: 8.554105)

Control

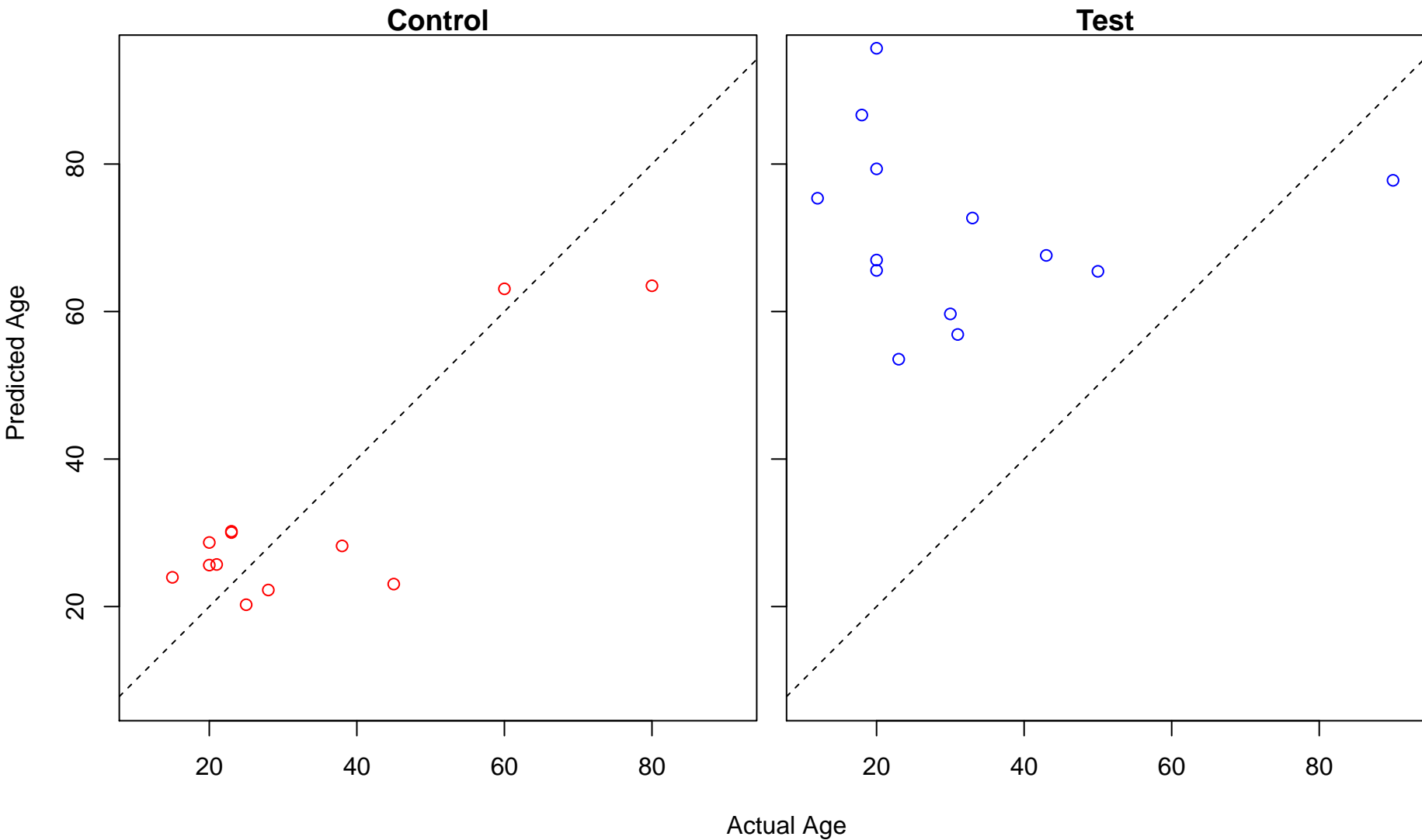


Test

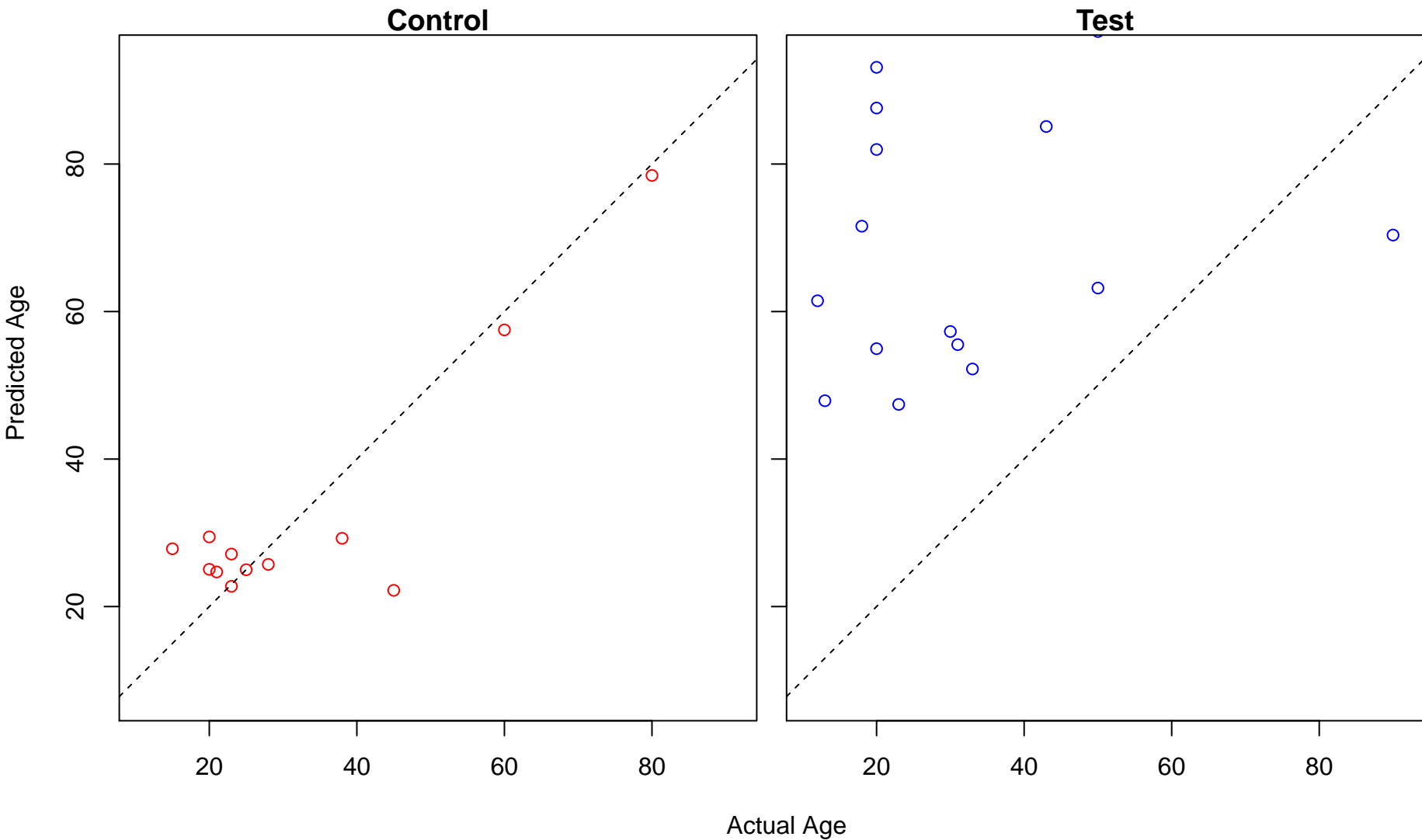


Actual Age

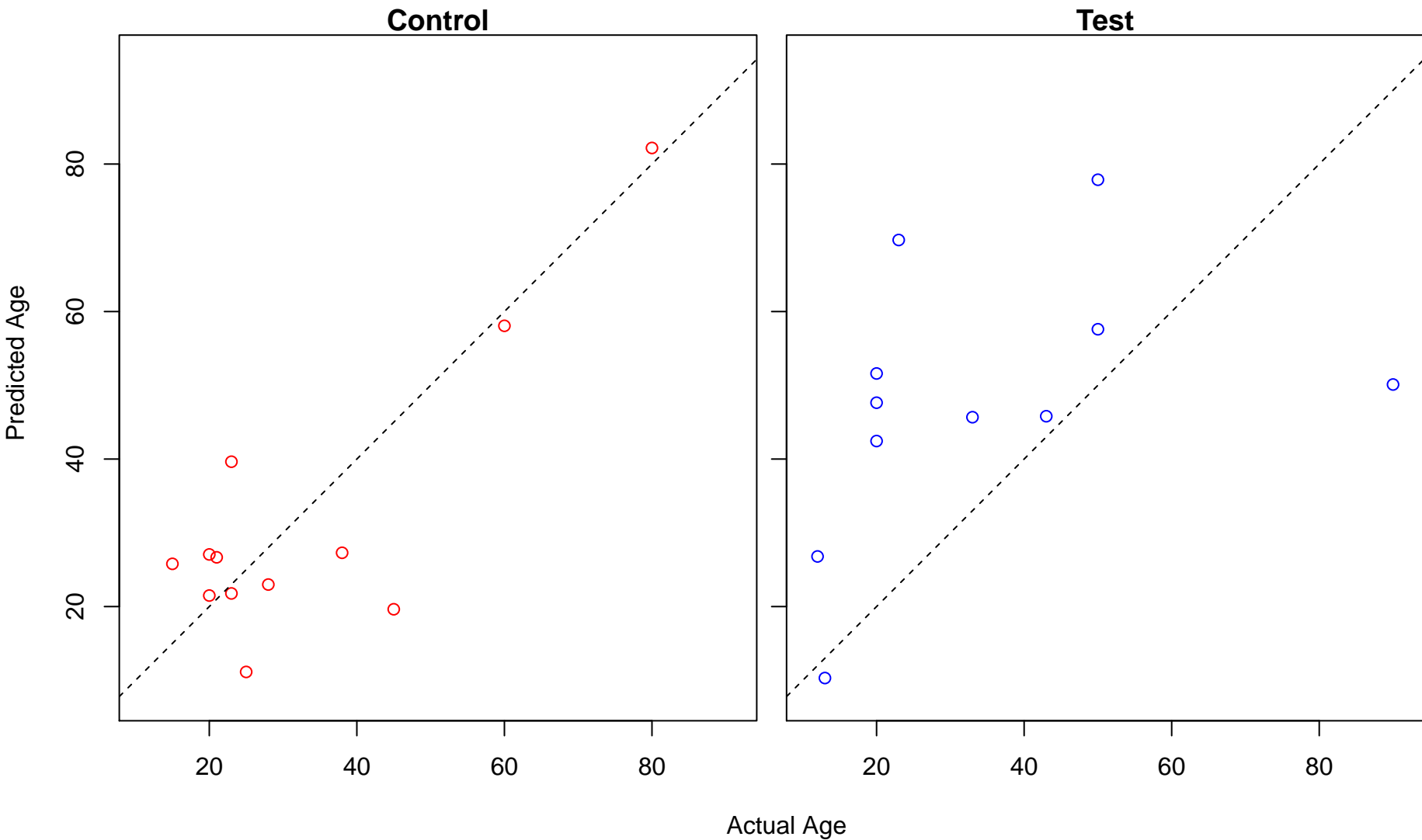
regulation of odontogenesis (Score: 8.550418)



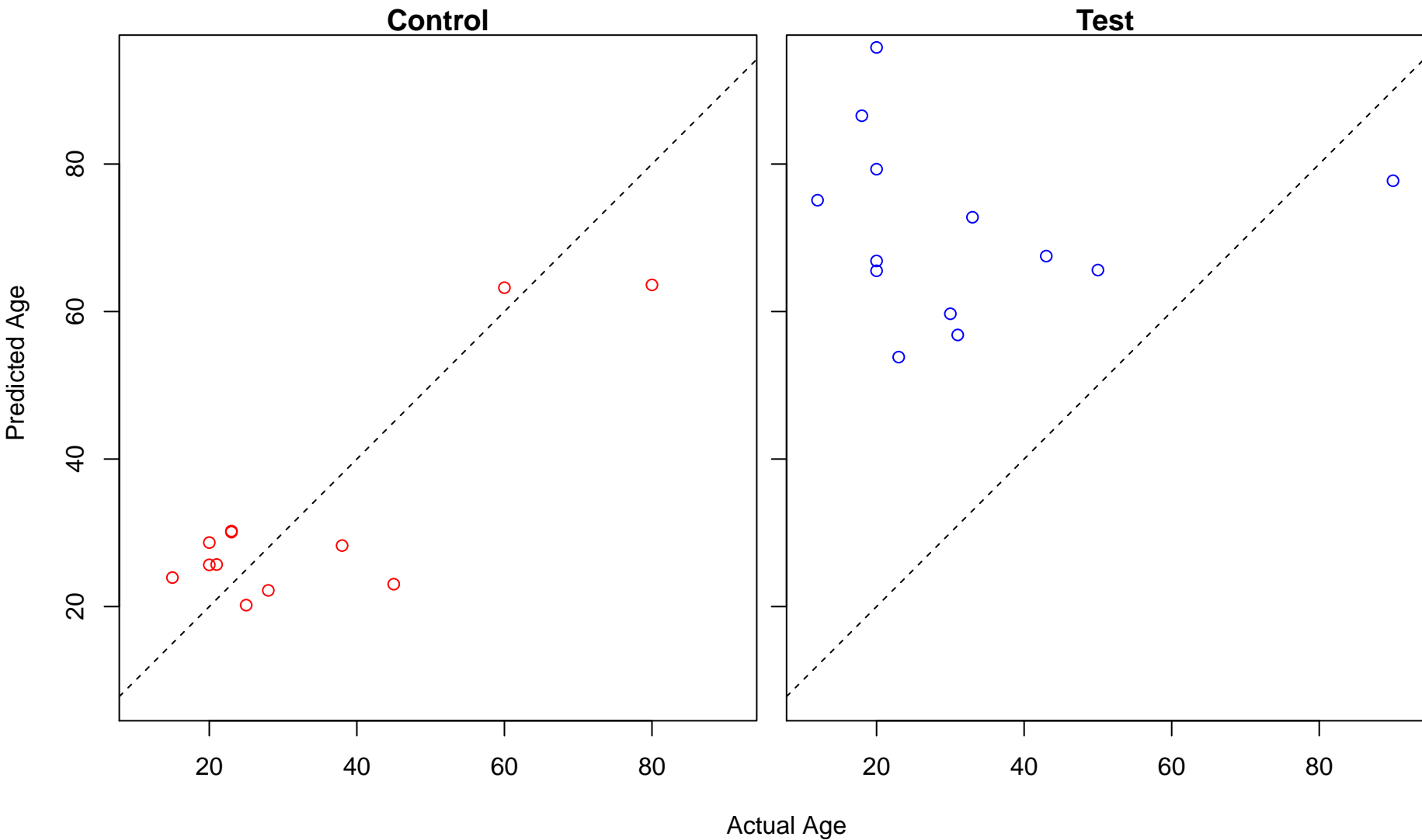
protein trimerization (Score: 8.548487)



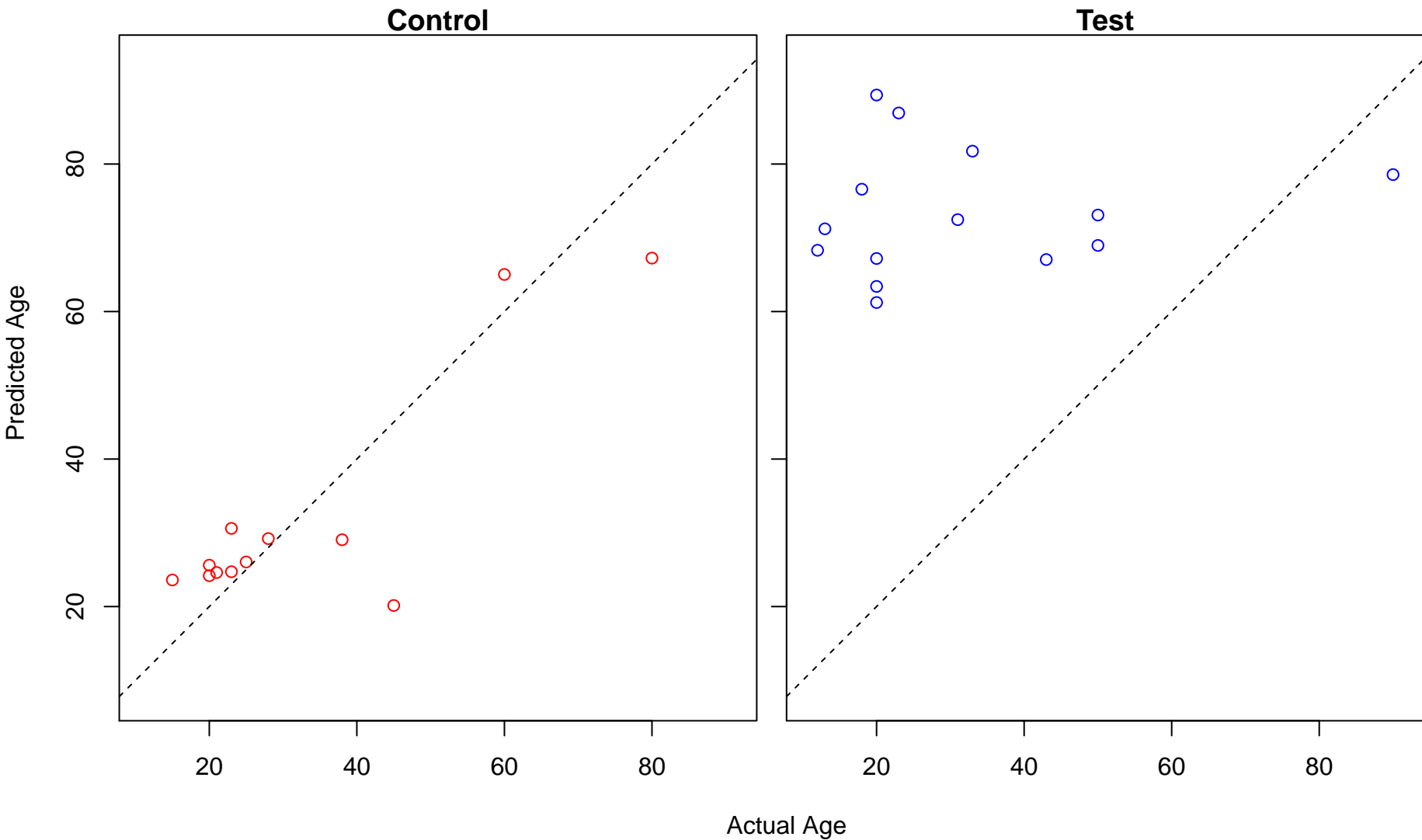
regulation of homotypic cell-cell adhesion (Score: 8.547599)



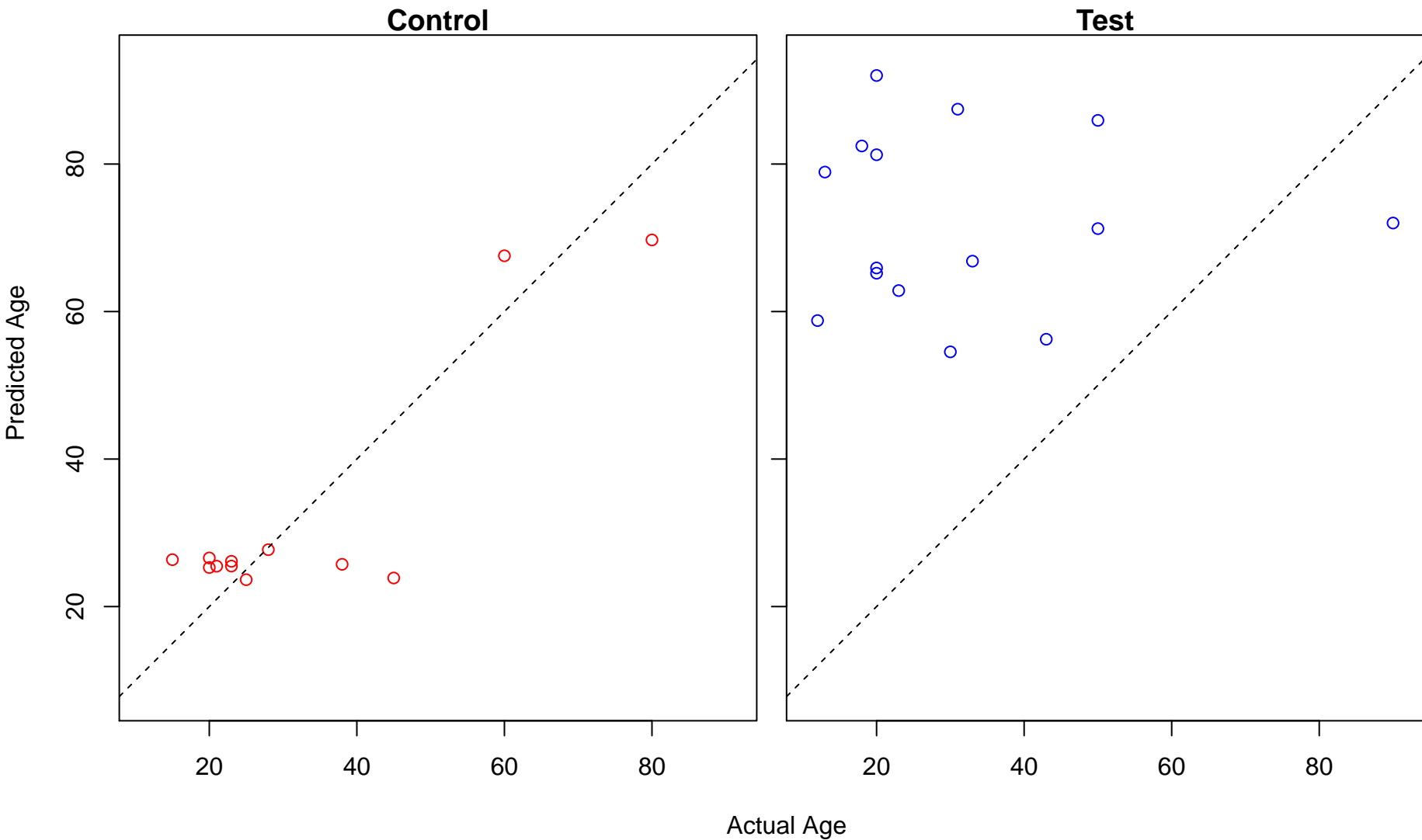
regulation of tooth mineralization (Score: 8.546945)



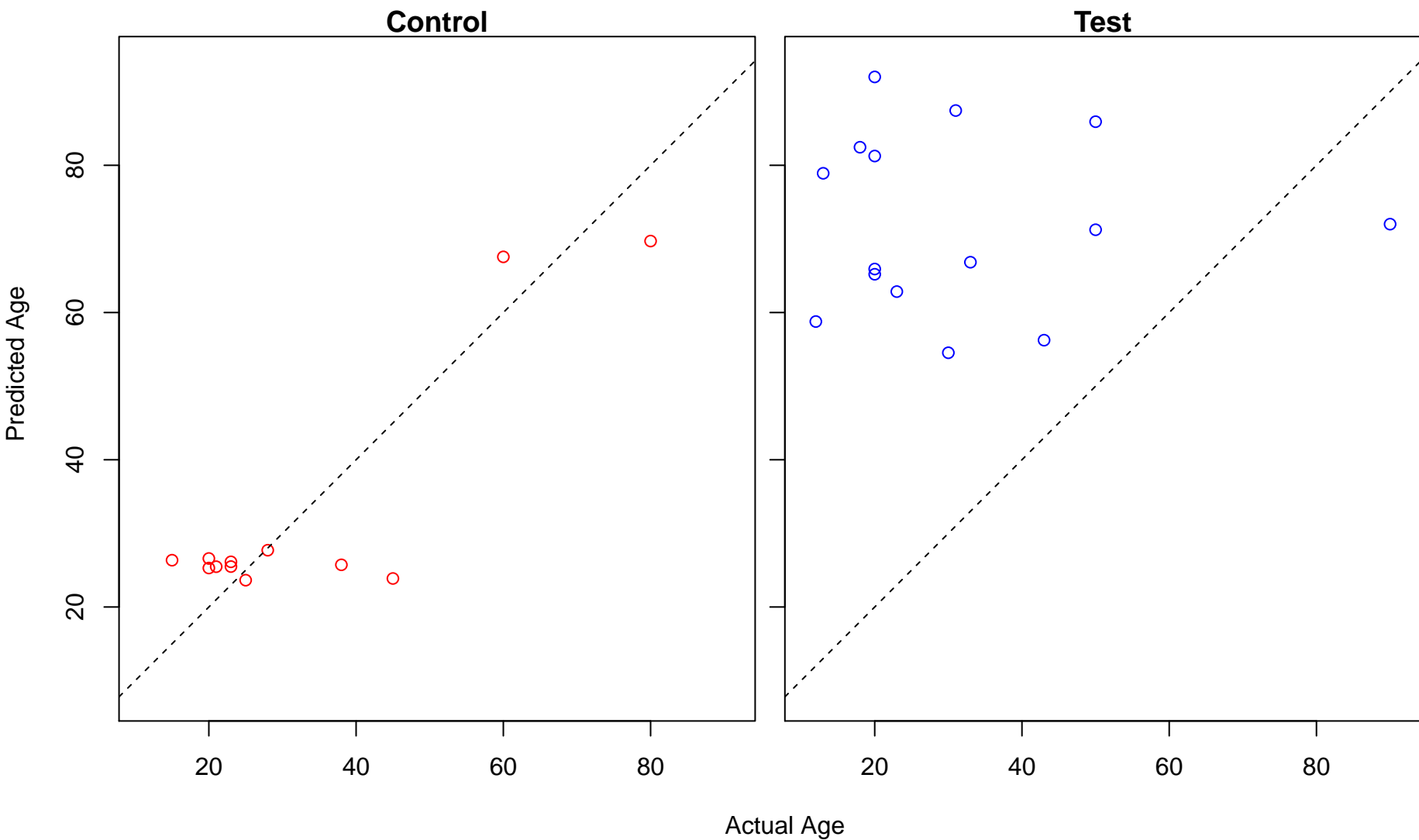
cellular defense response (Score: 8.545785)



DNA alkylation (Score: 8.540220)

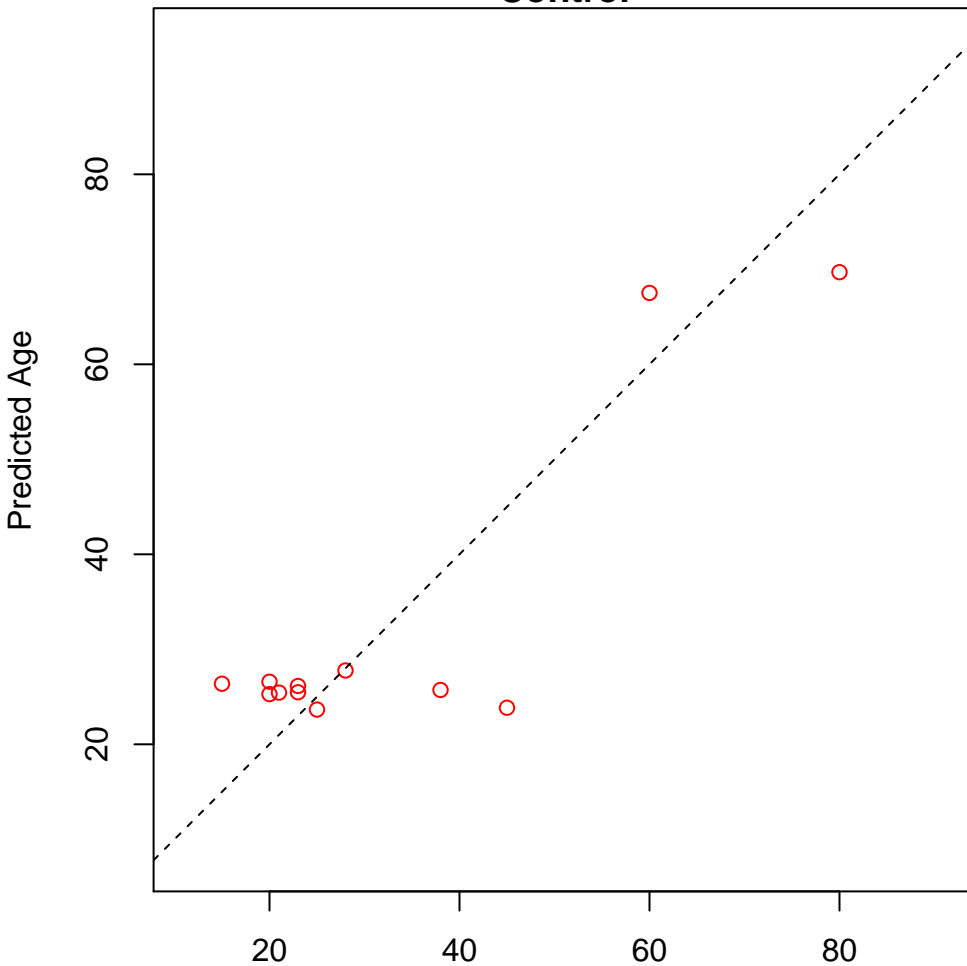


DNA methylation (Score: 8.540220)

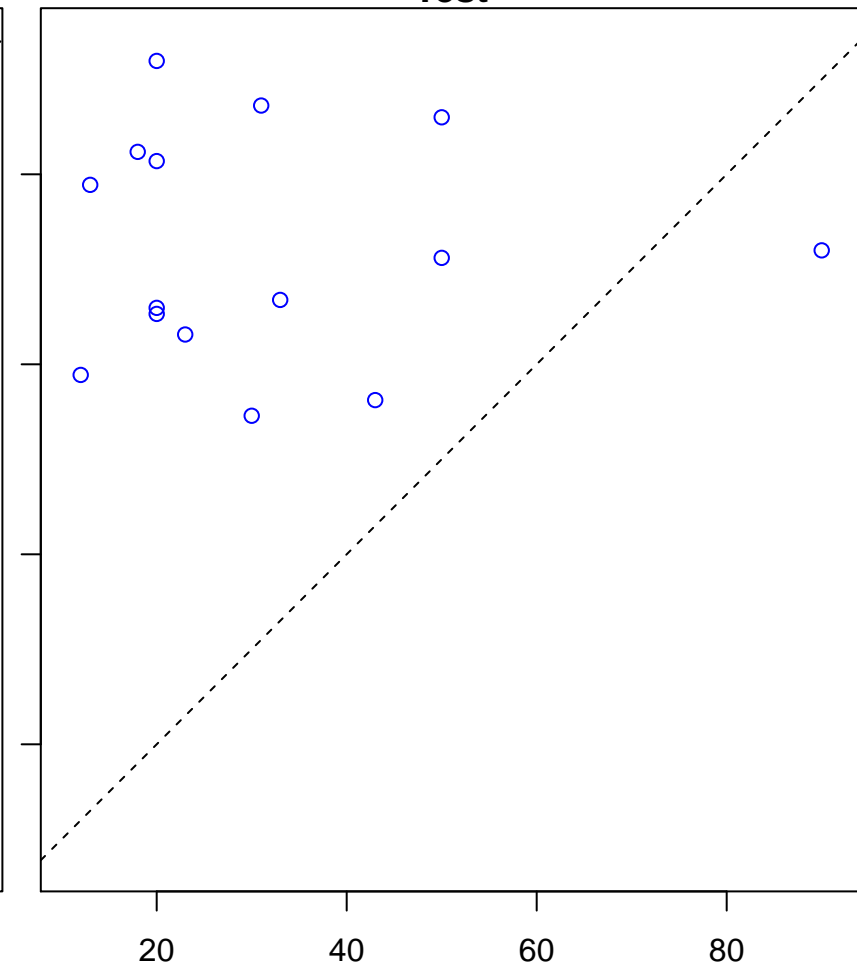


DNA methylation or demethylation (Score: 8.539451)

Control

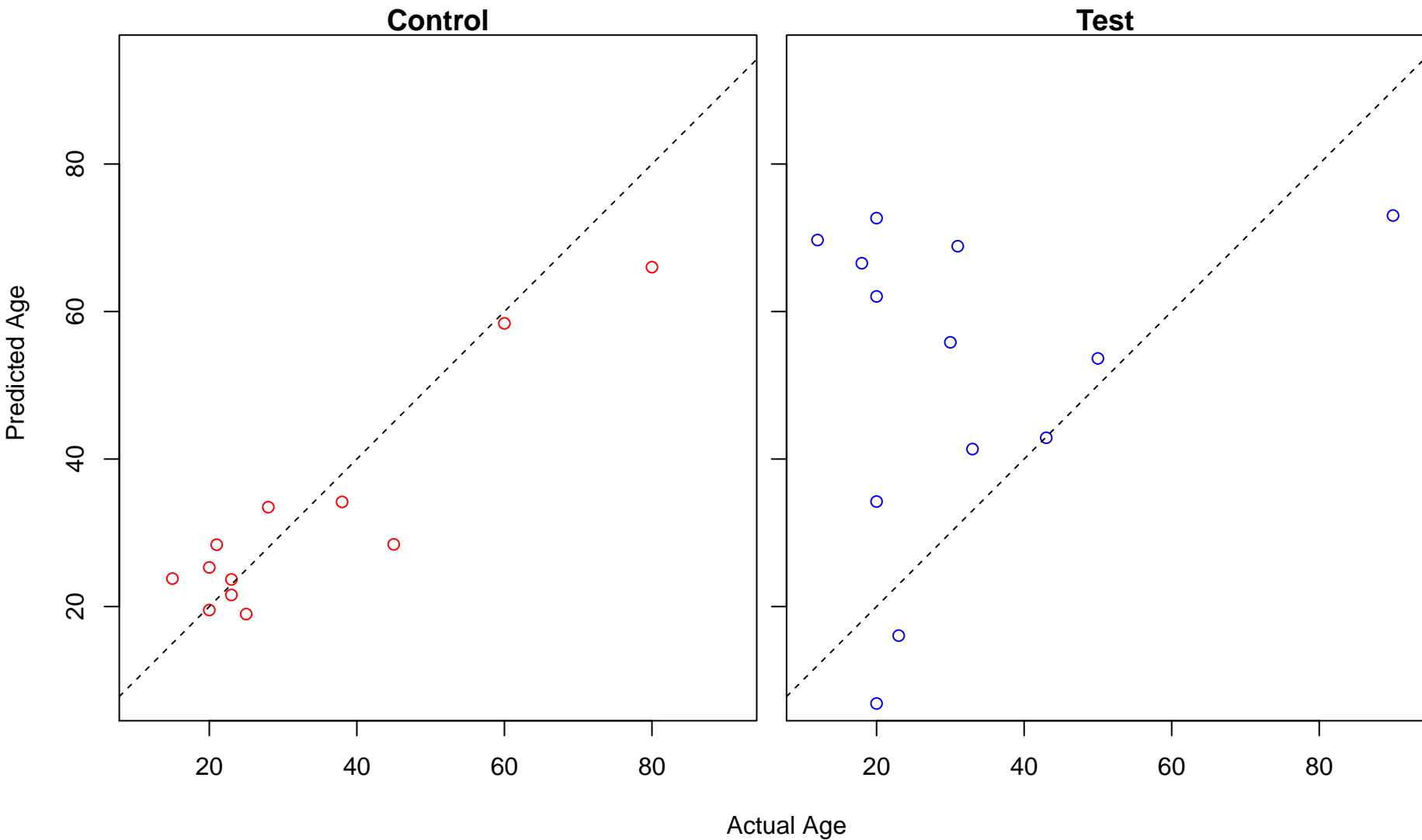


Test



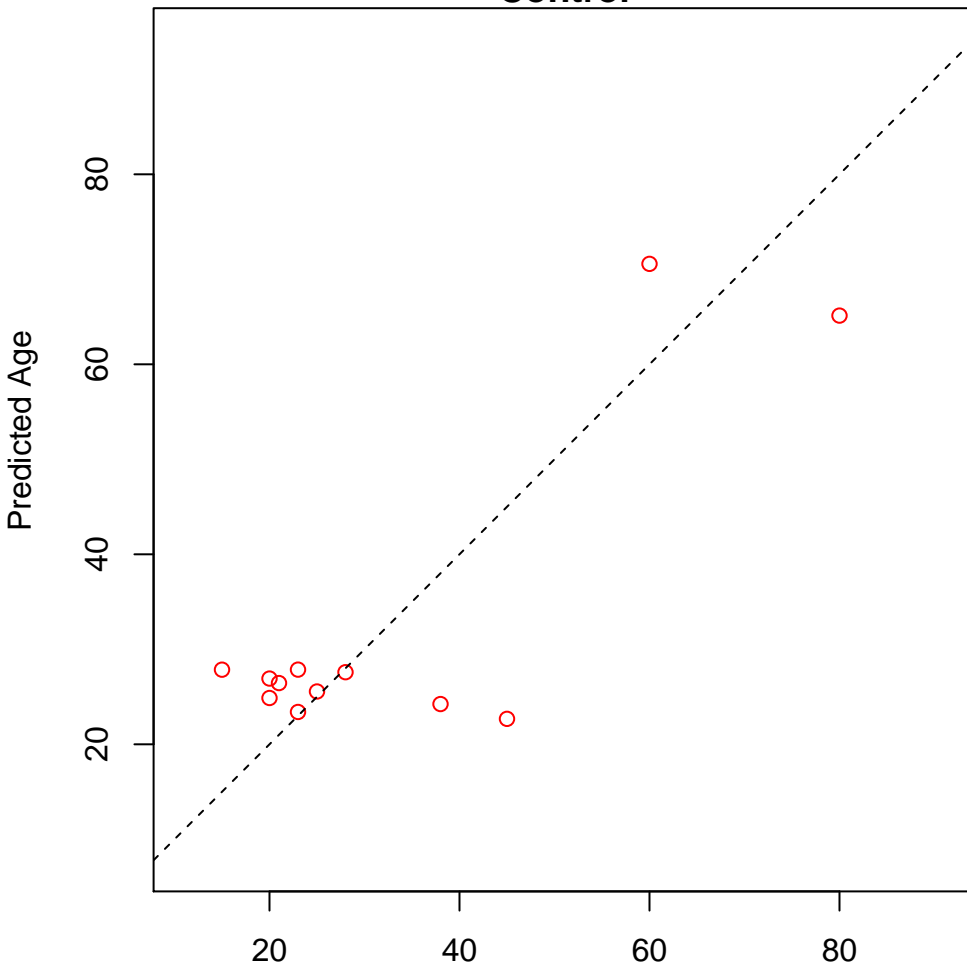
Actual Age

peptidyl-lysine acetylation (Score: 8.536948)

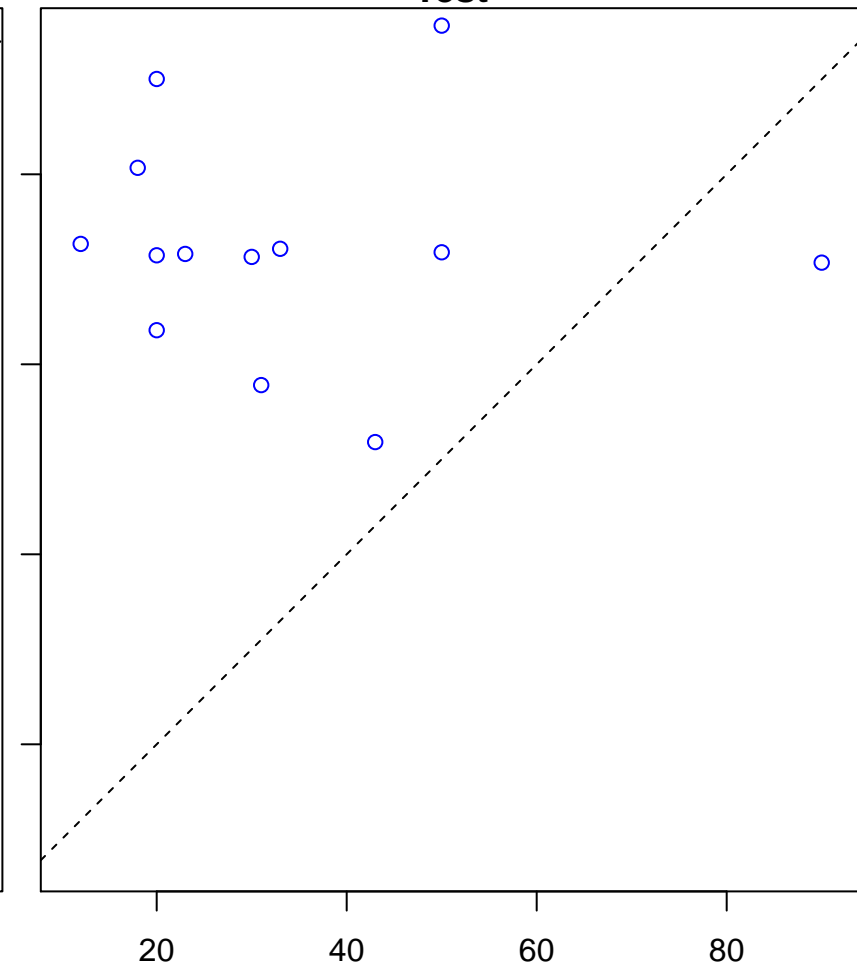


protein peptidyl–prolyl isomerization (Score: 8.528821)

Control

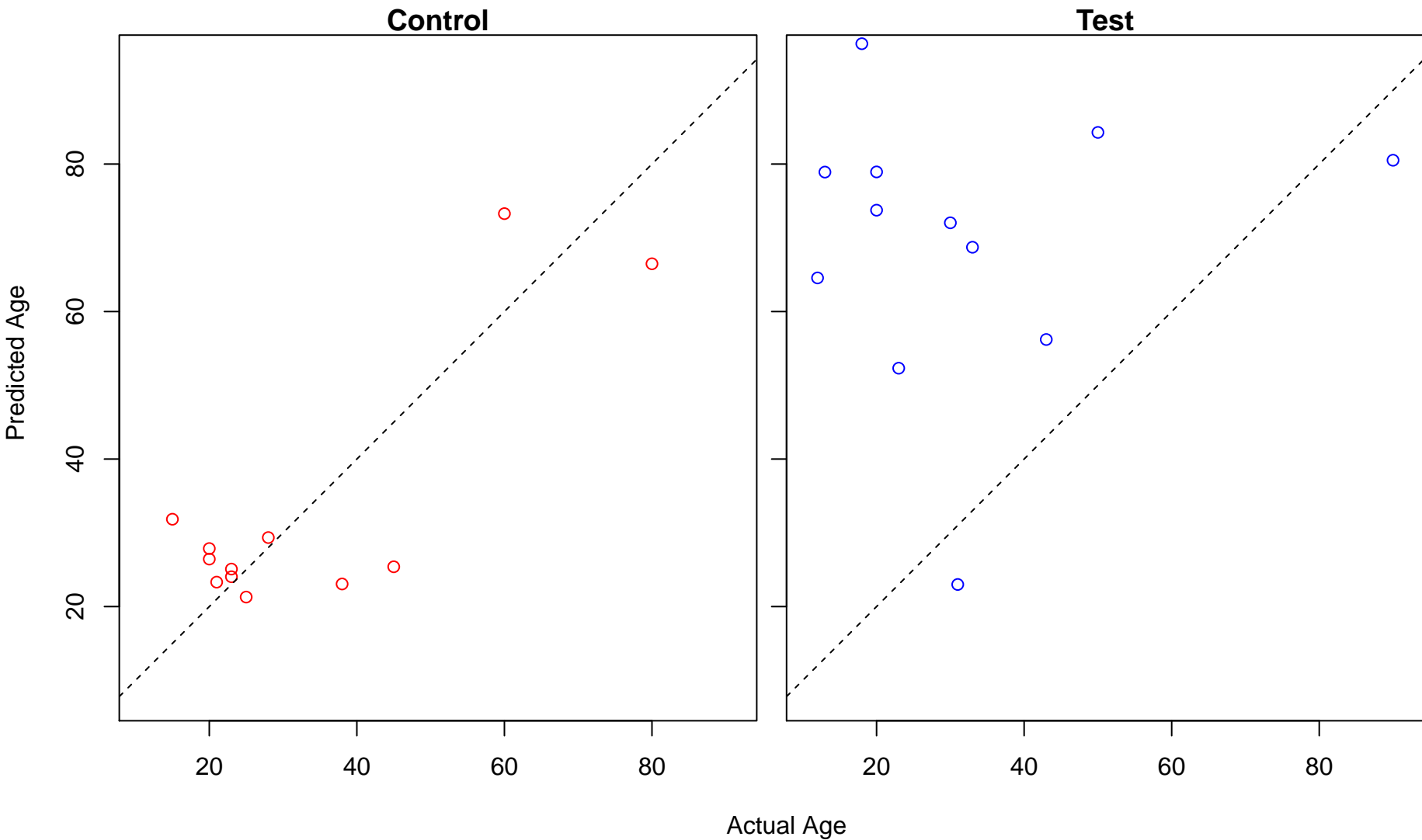


Test

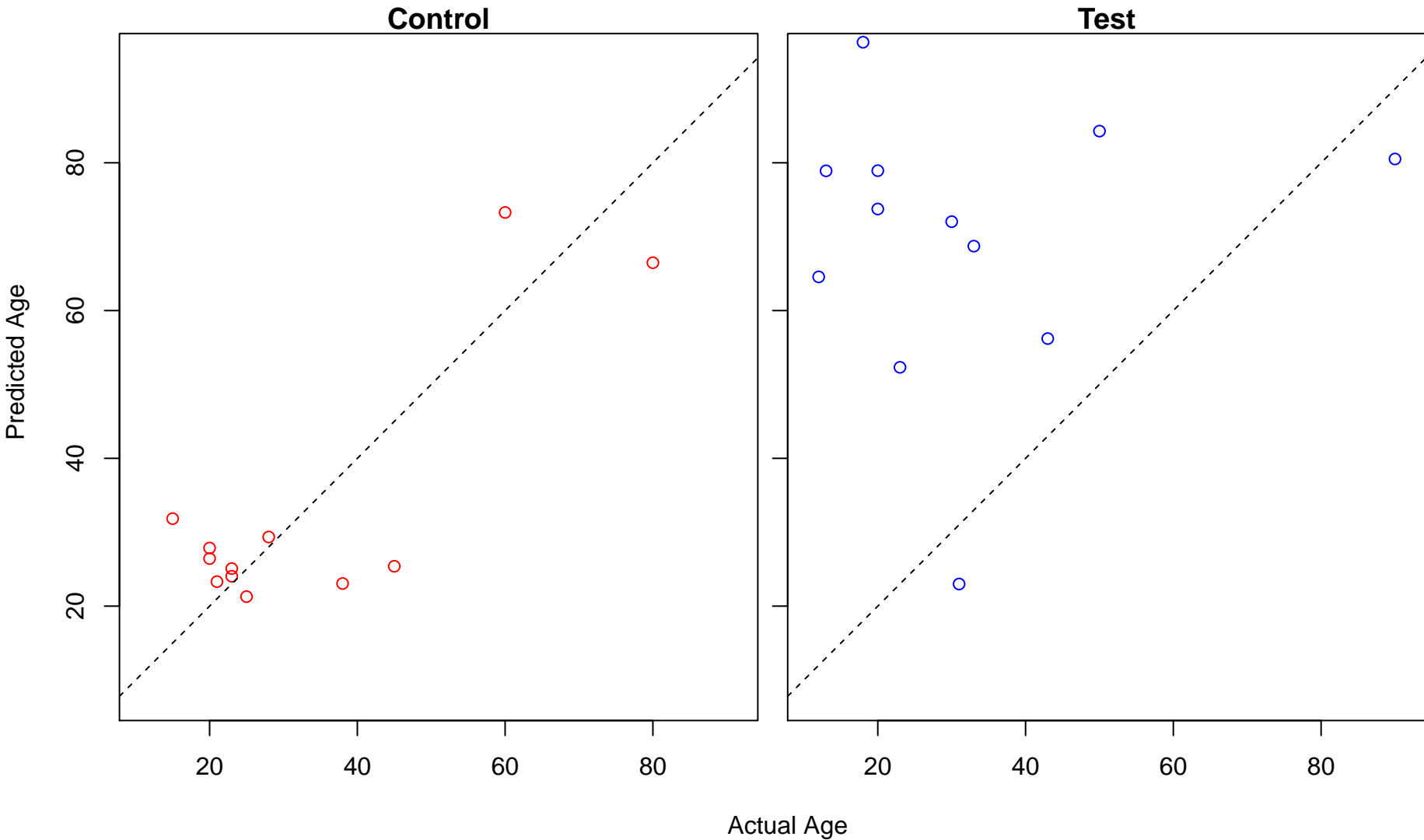


Actual Age

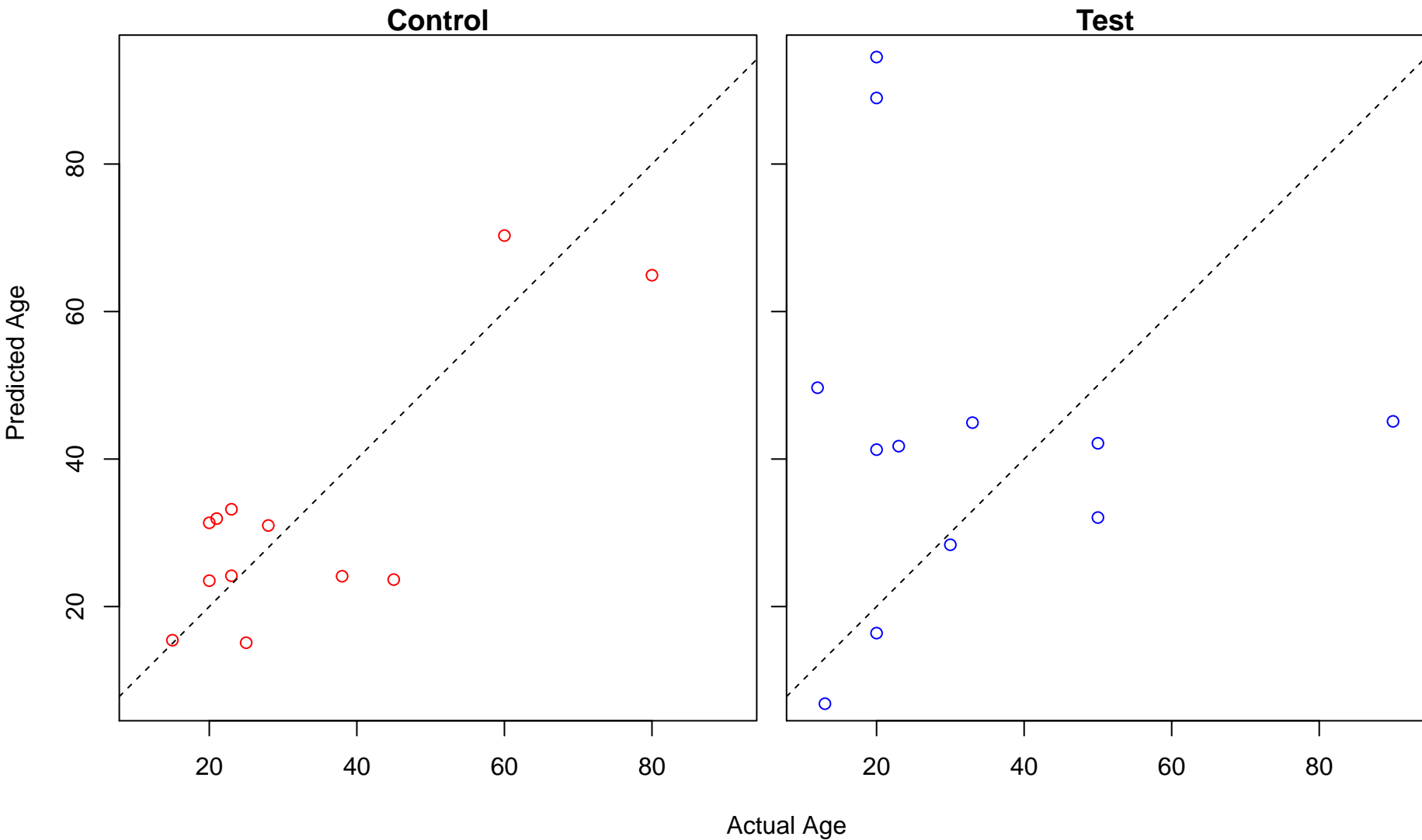
regulation of acetyl-CoA biosynthetic process from pyruvate (Score: 8.516957)



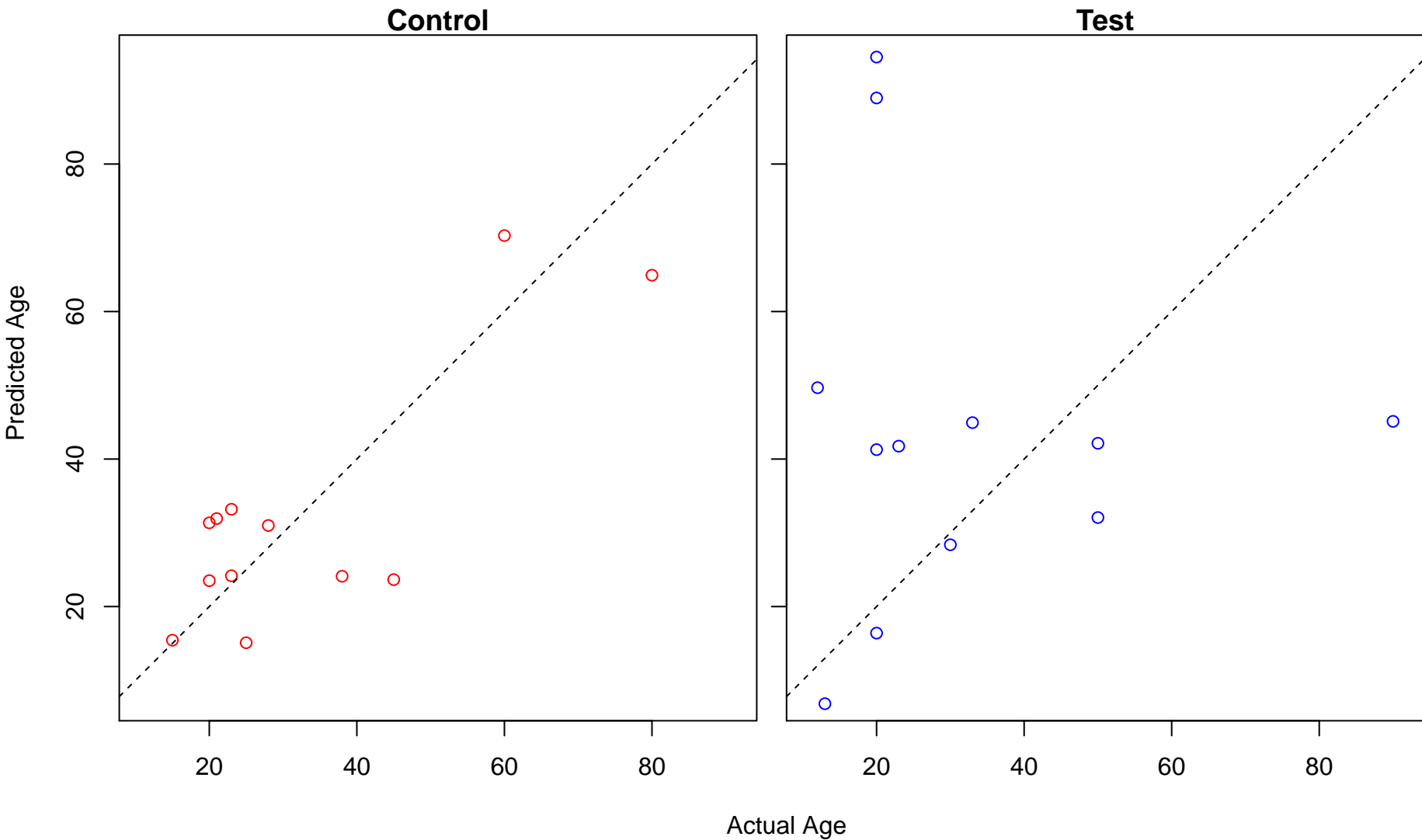
regulation of acyl-CoA biosynthetic process (Score: 8.516957)



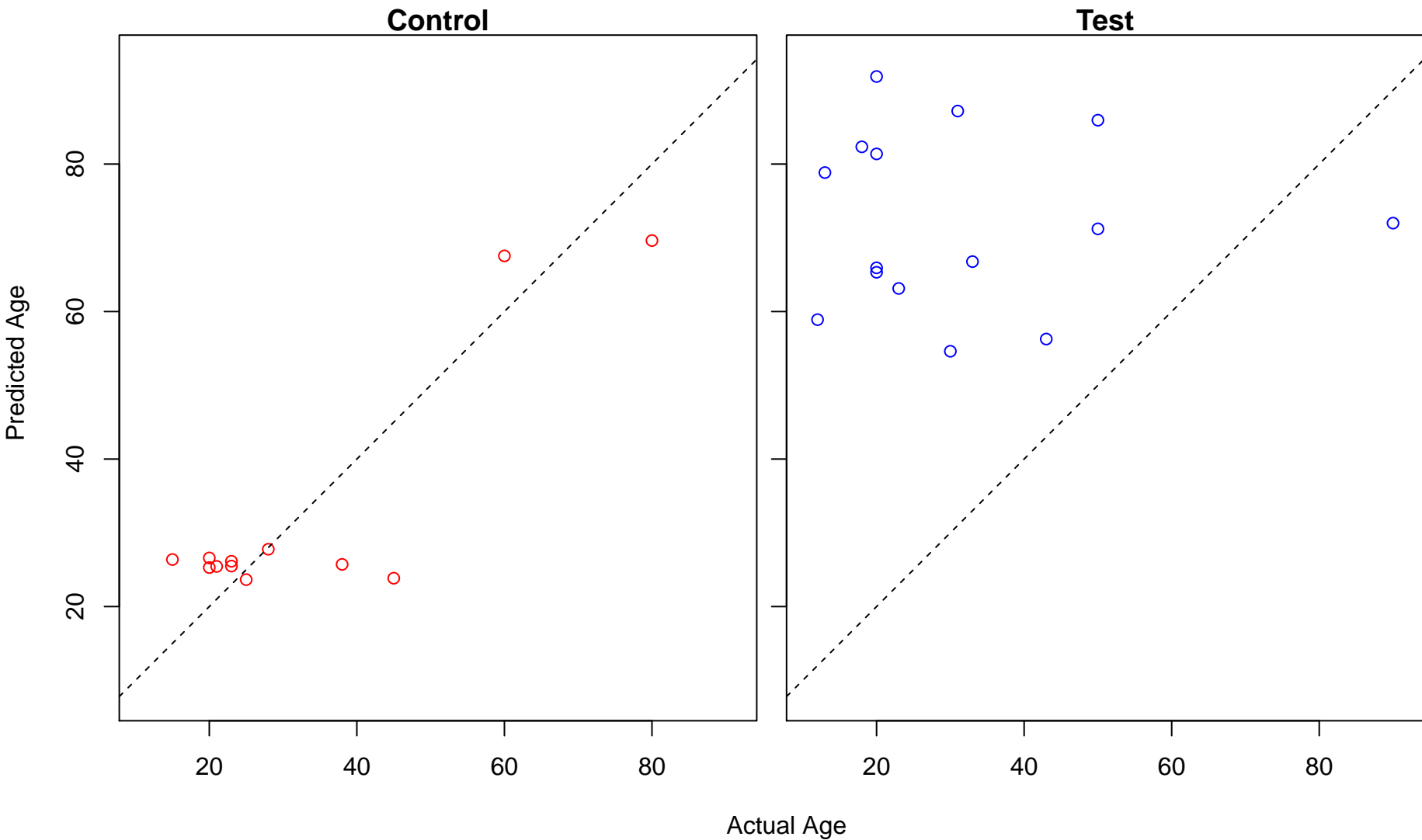
regulation of cardiac muscle hypertrophy (Score: 8.513867)



regulation of muscle hypertrophy (Score: 8.513867)

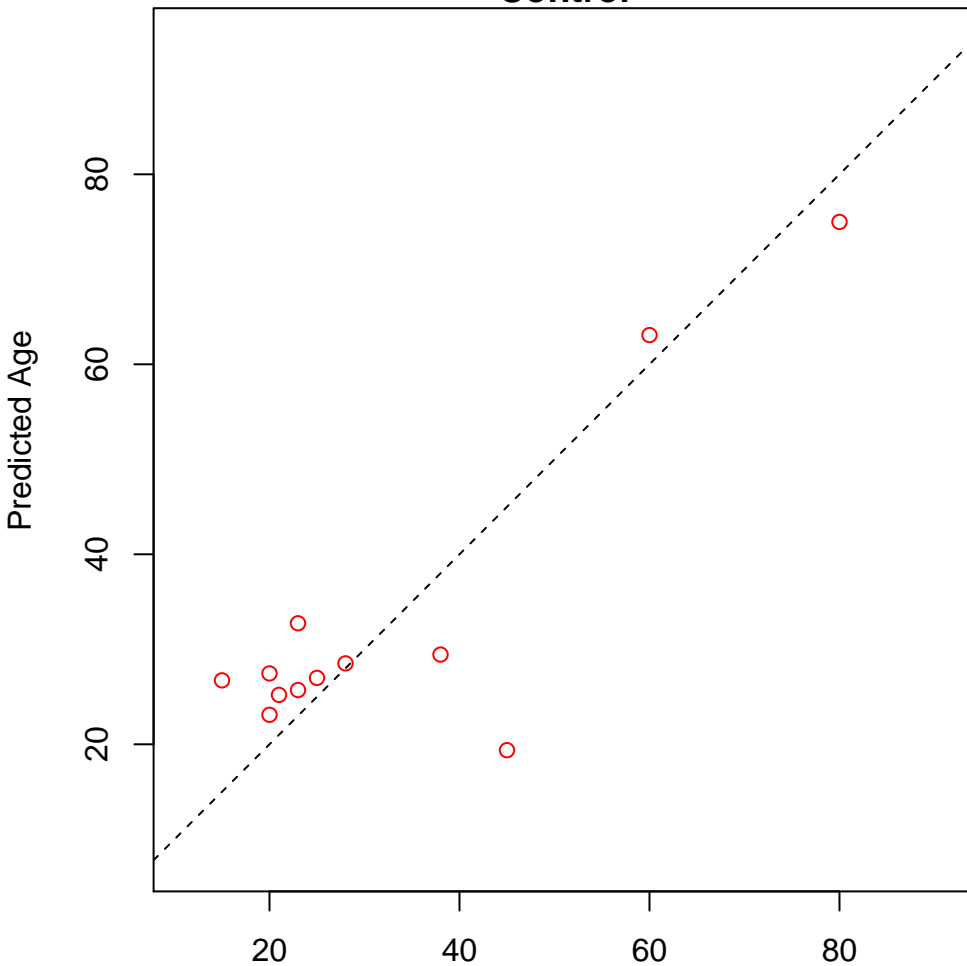


DNA modification (Score: 8.513172)

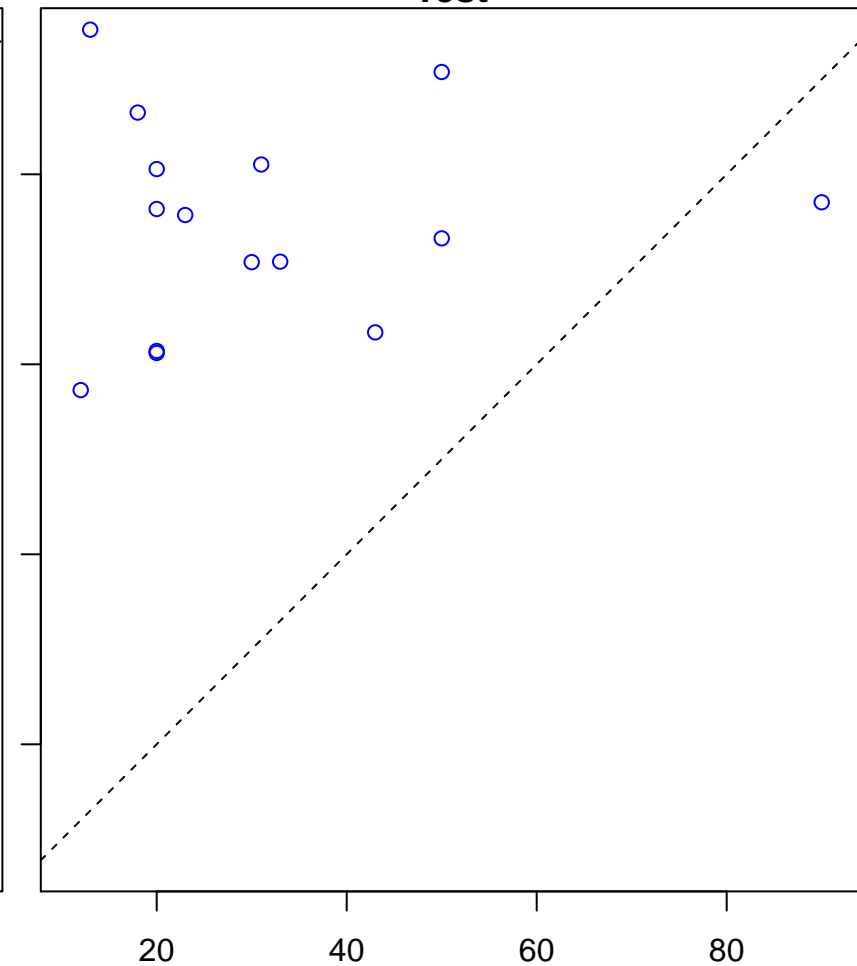


cellular response to interferon-gamma (Score: 8.513155)

Control

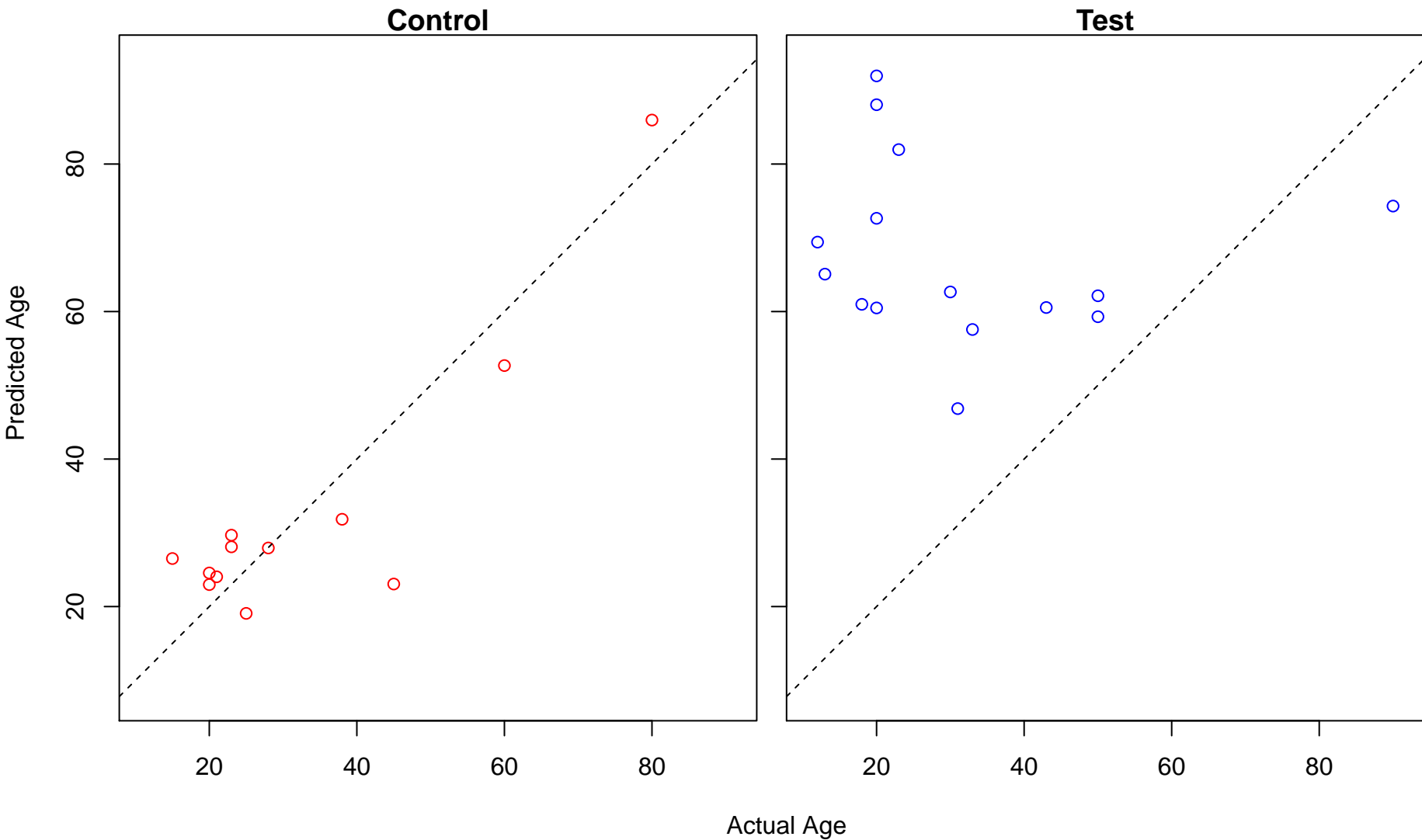


Test

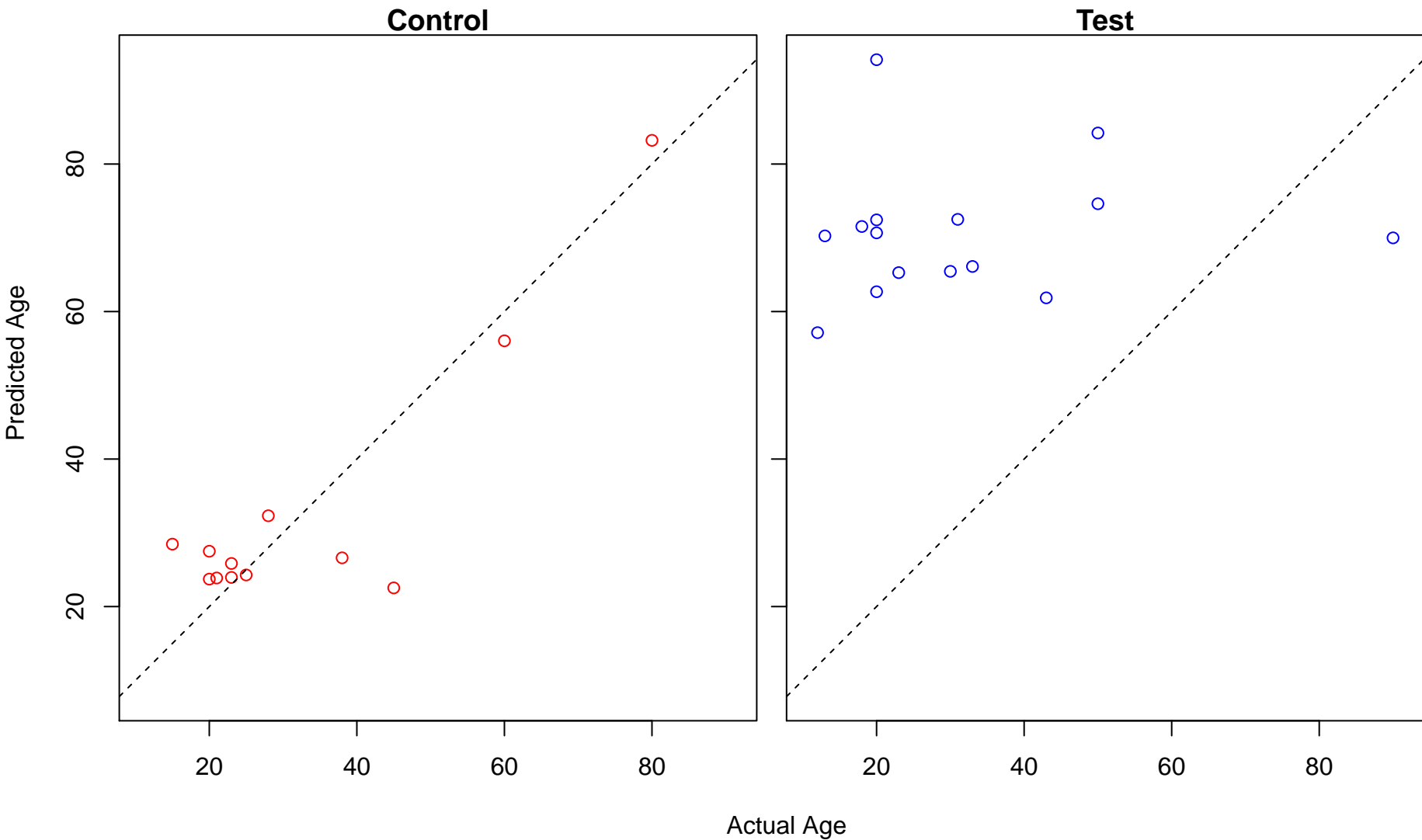


Actual Age

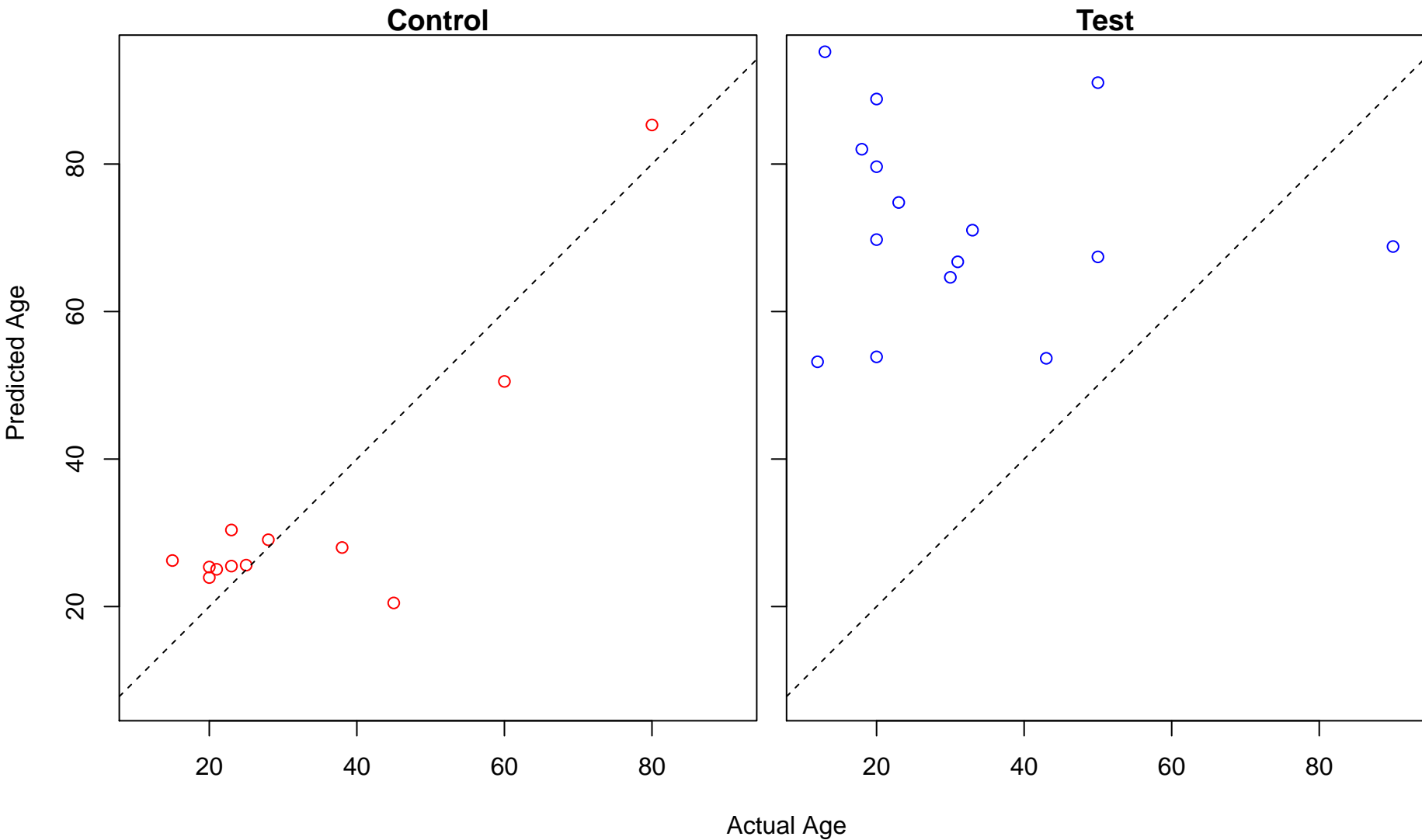
motor neuron axon guidance (Score: 8.494151)



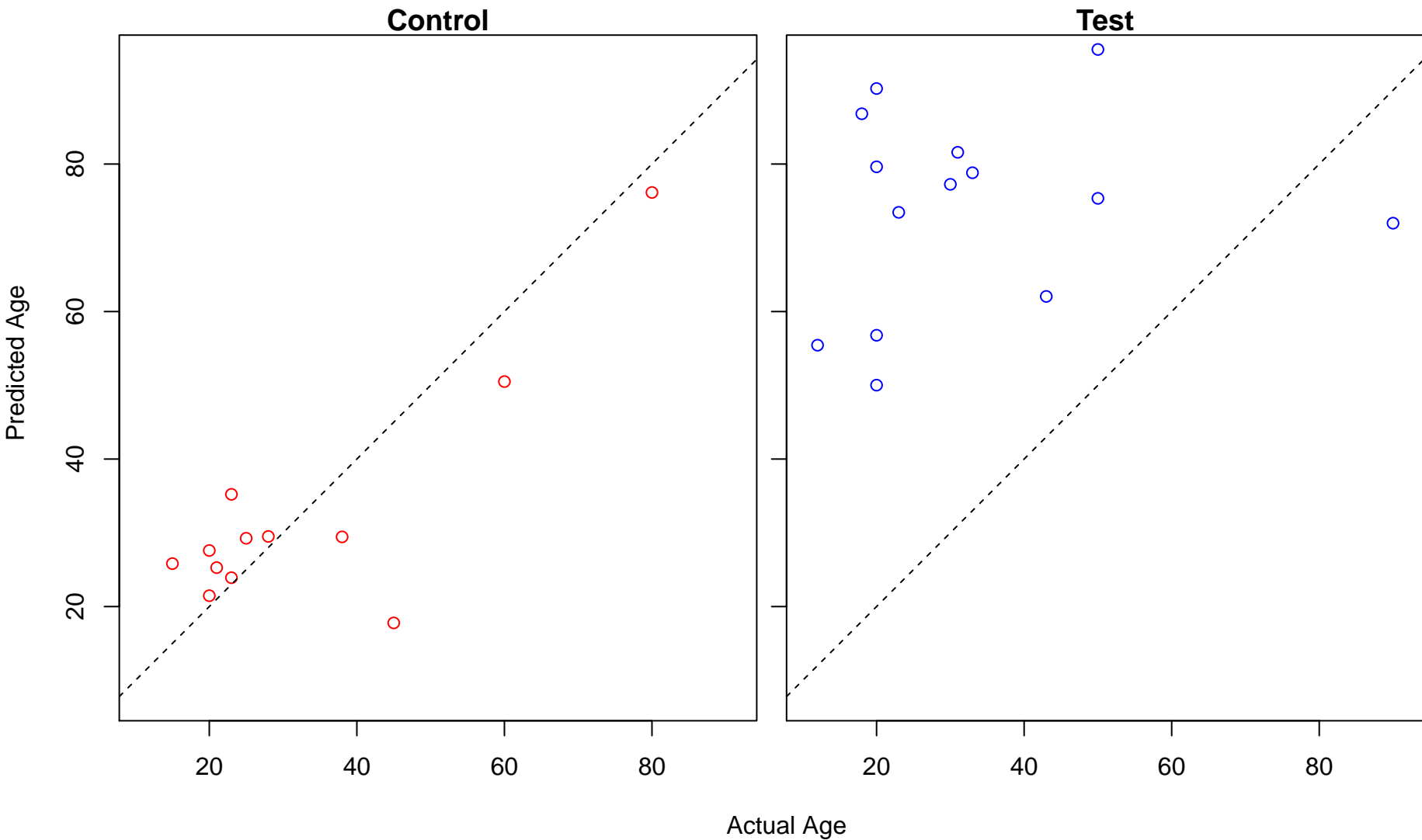
negative regulation of developmental process (Score: 8.476545)



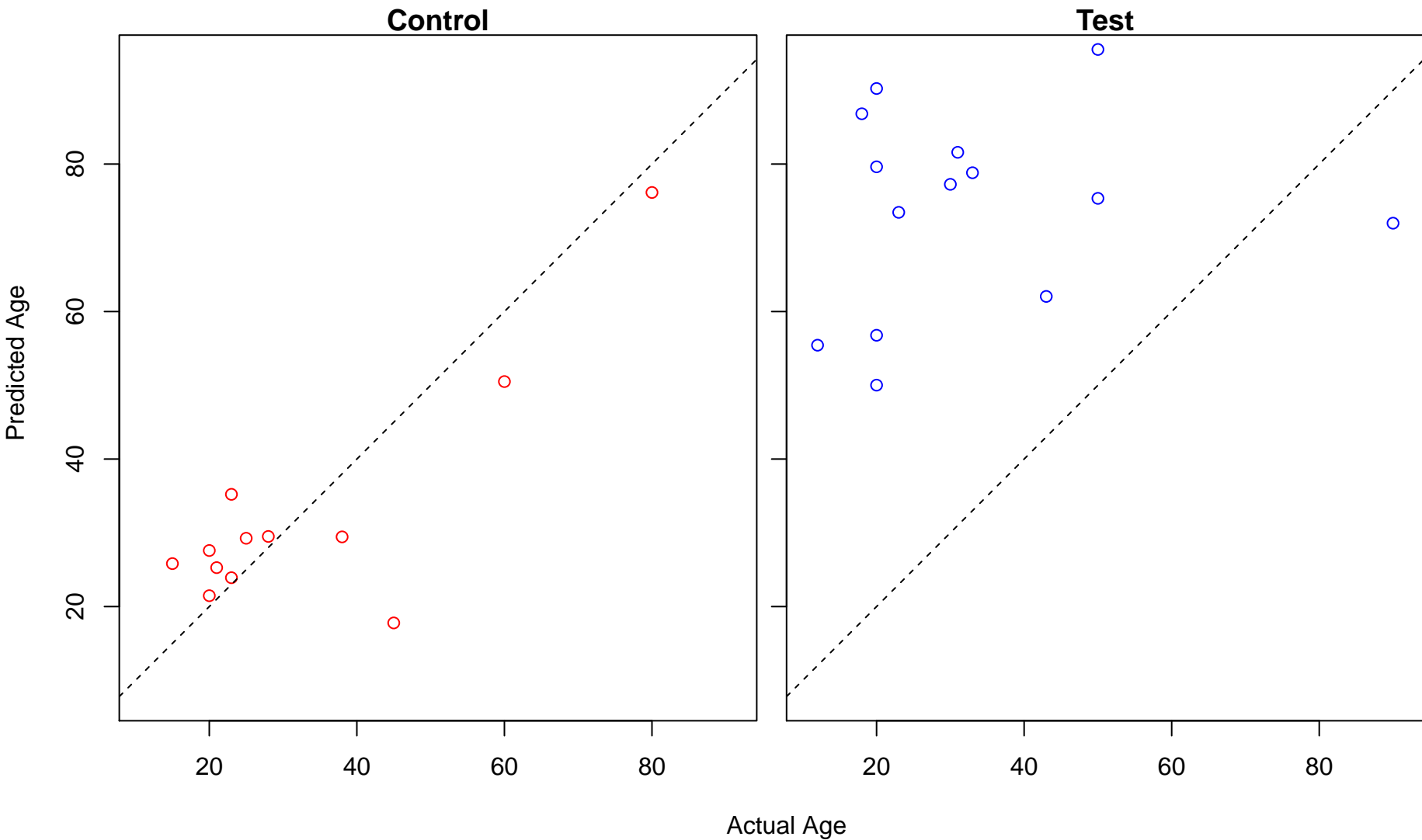
detection of stimulus (Score: 8.470247)



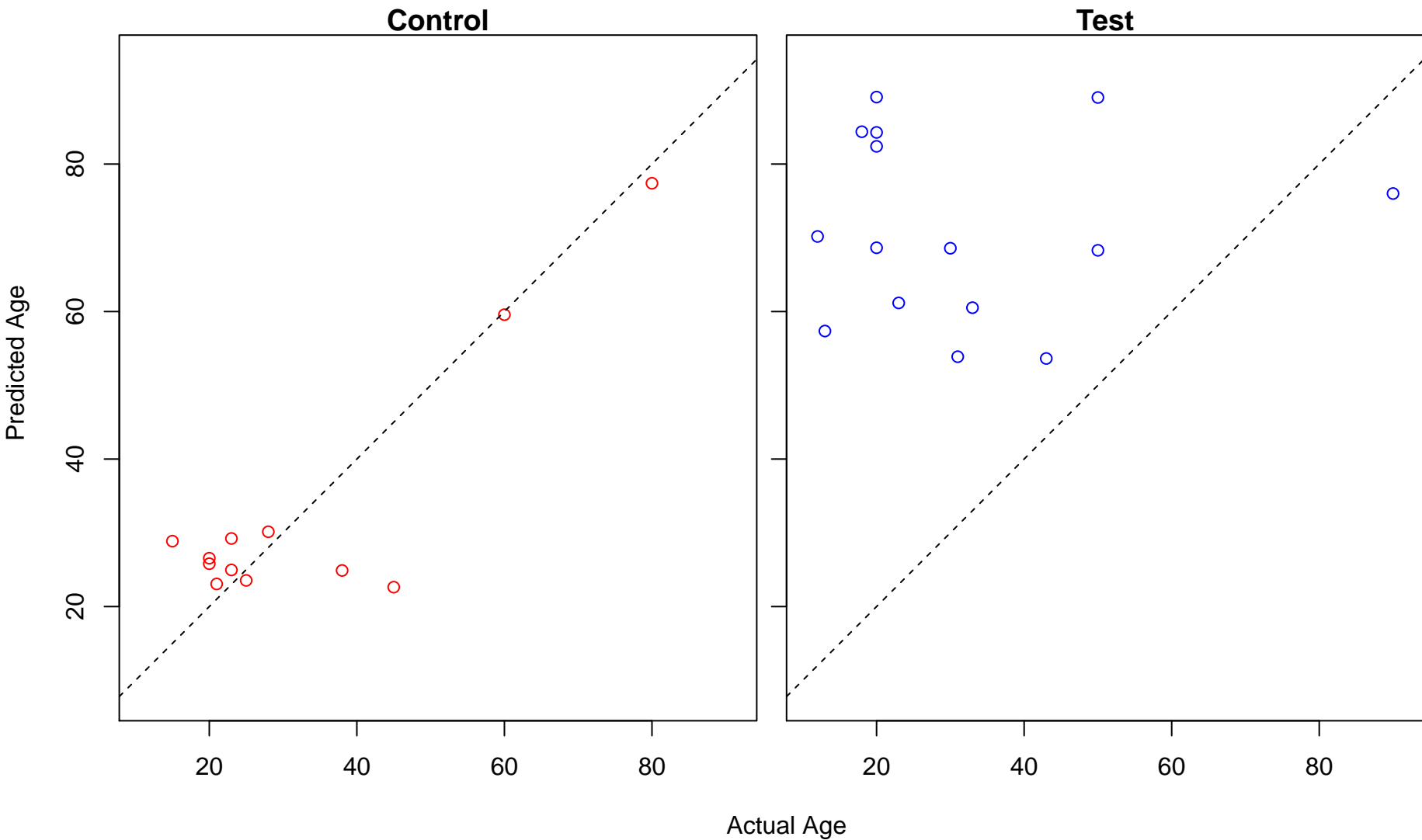
detection of bacterium (Score: 8.469688)



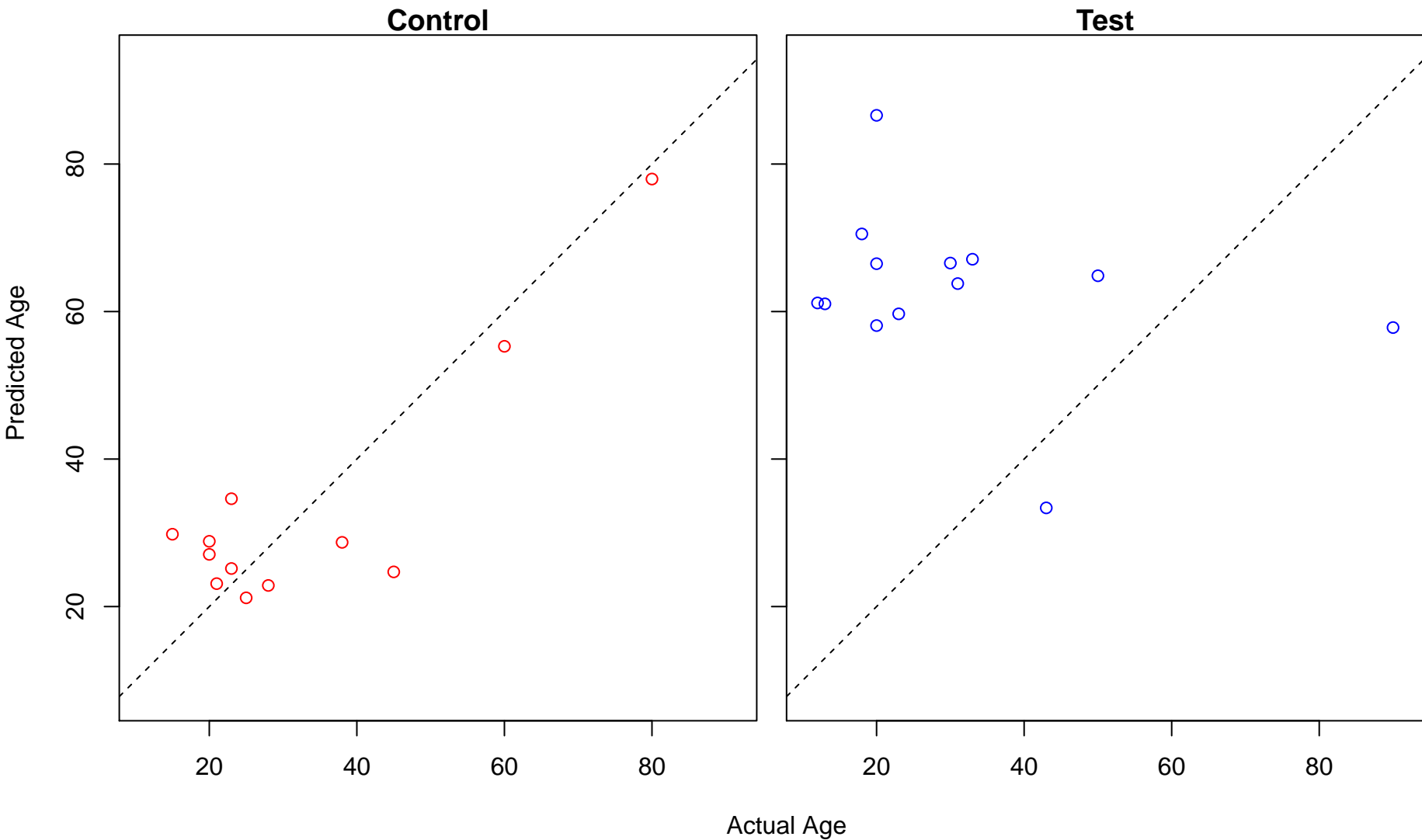
detection of other organism (Score: 8.469688)



response to amino acid (Score: 8.469413)

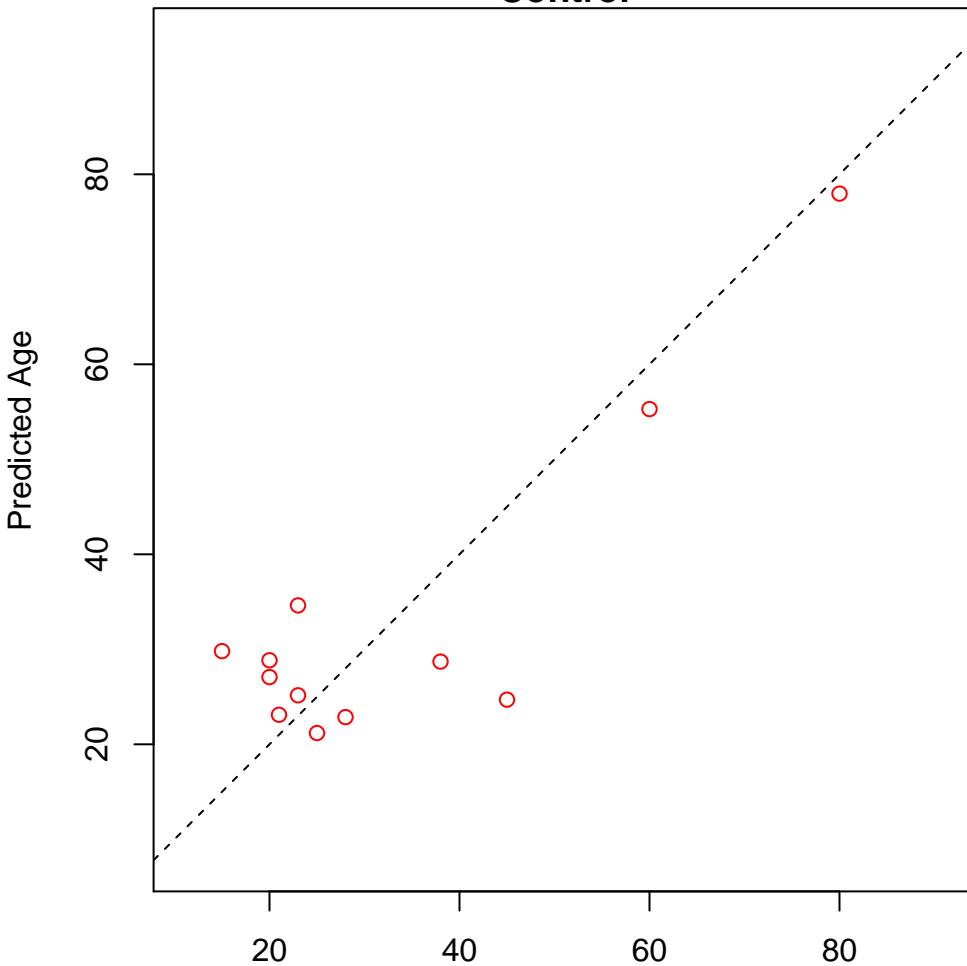


icosanoid biosynthetic process (Score: 8.468863)

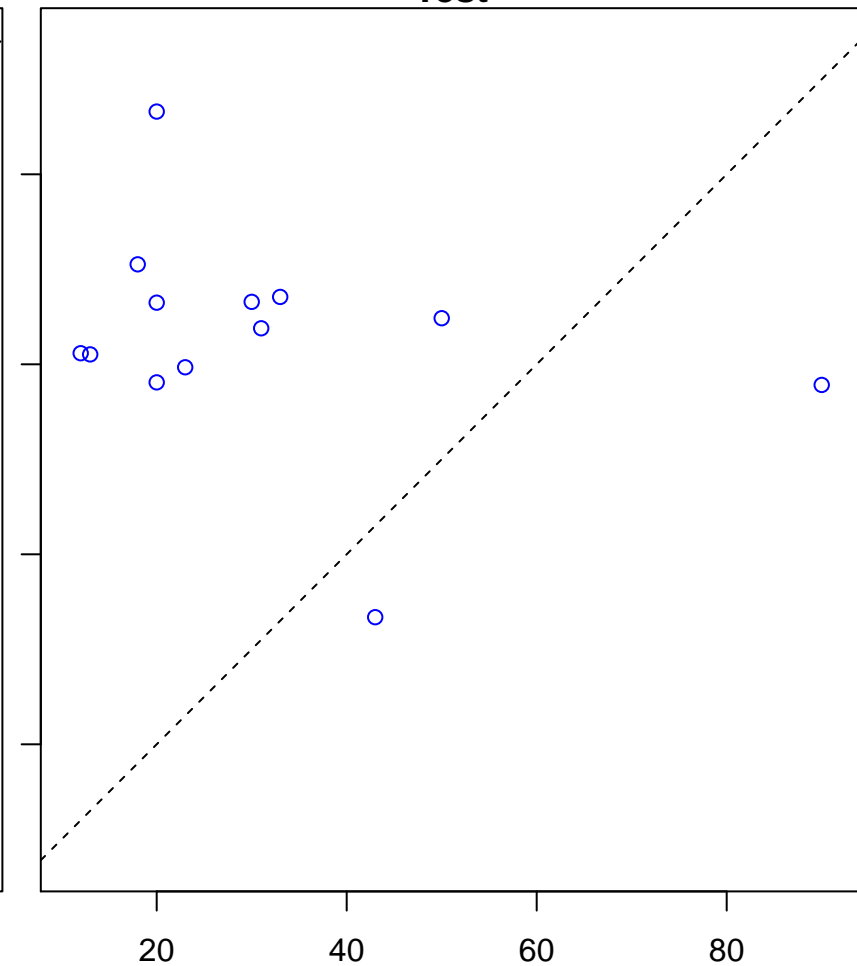


fatty acid derivative biosynthetic process (Score: 8.468863)

Control

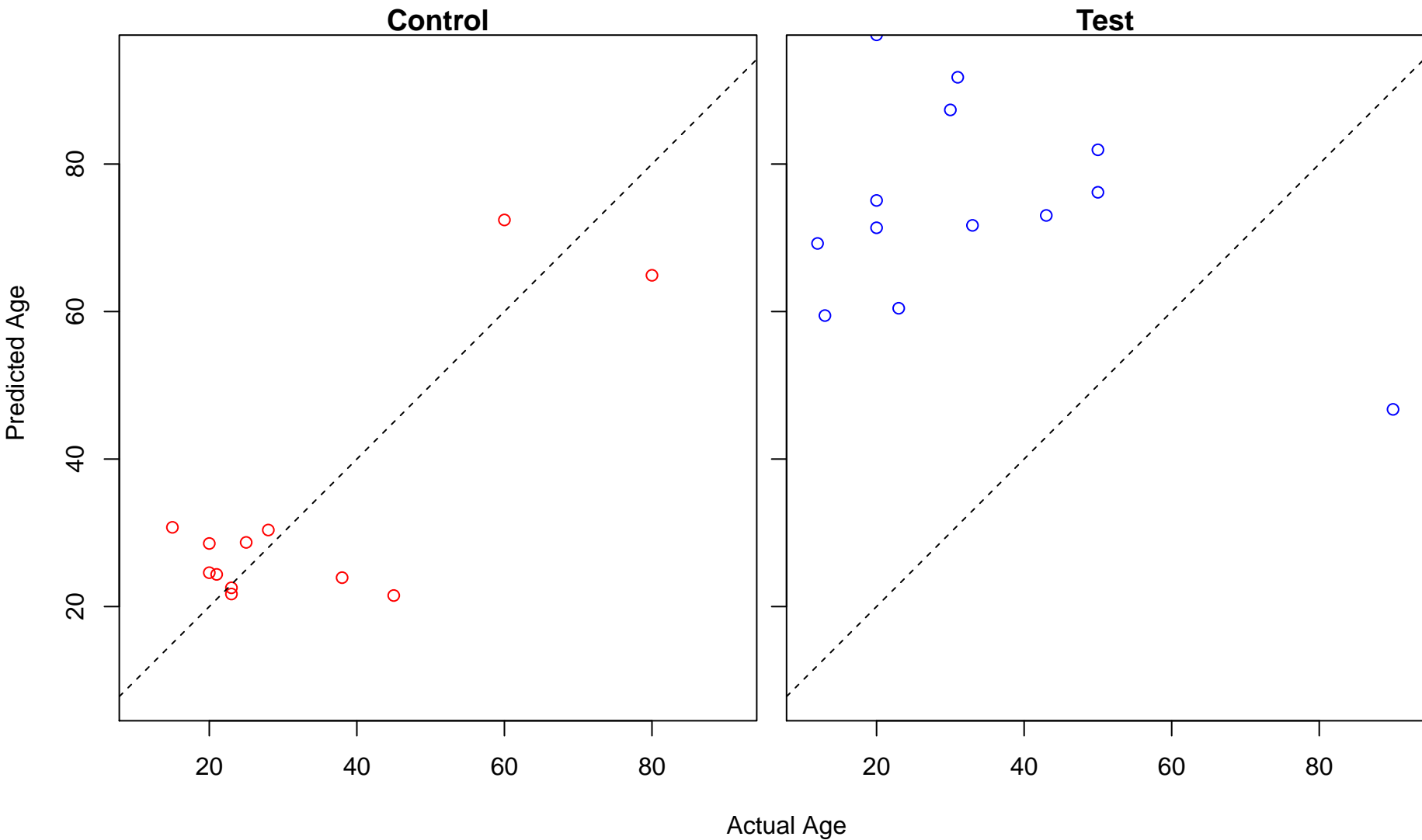


Test

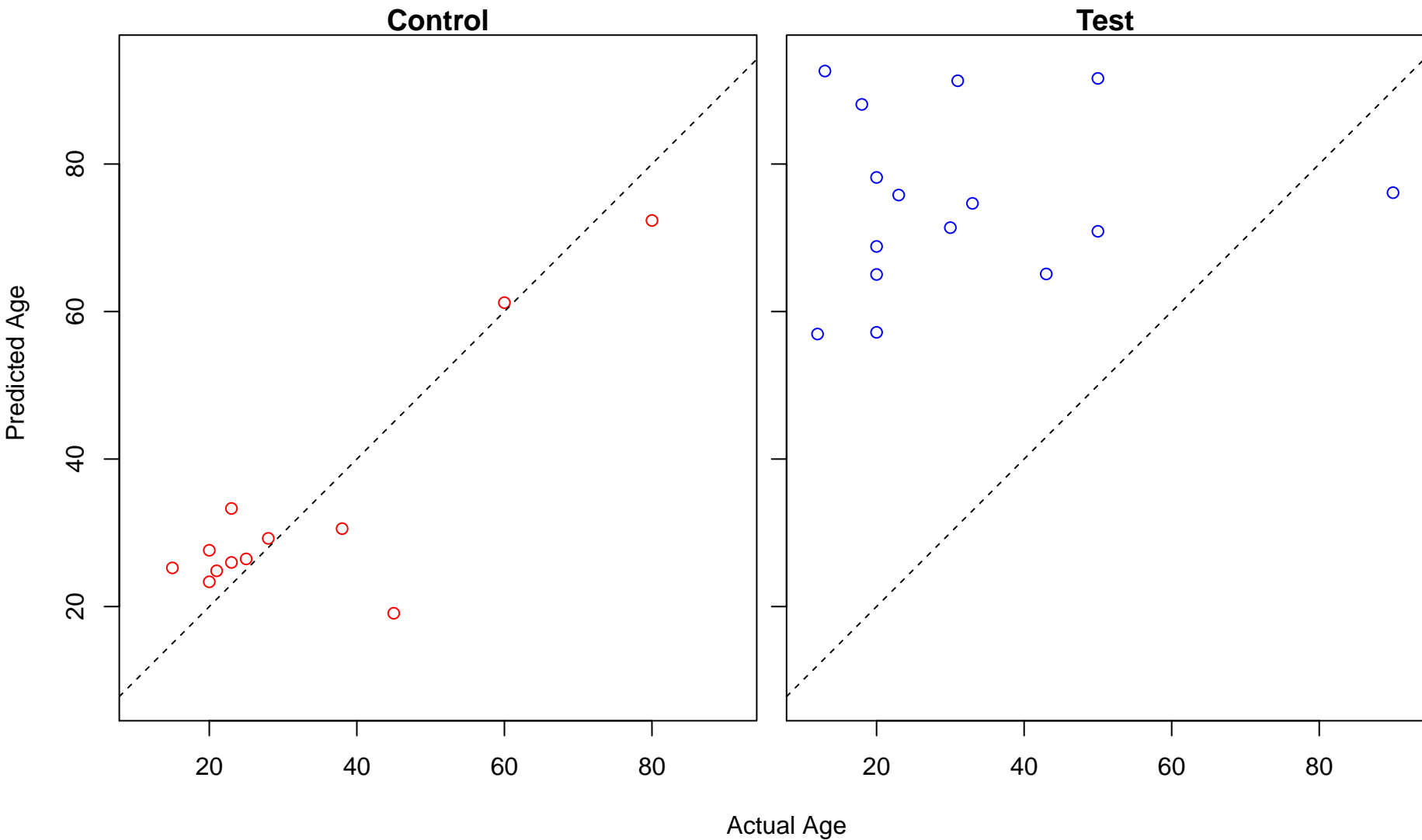


Actual Age

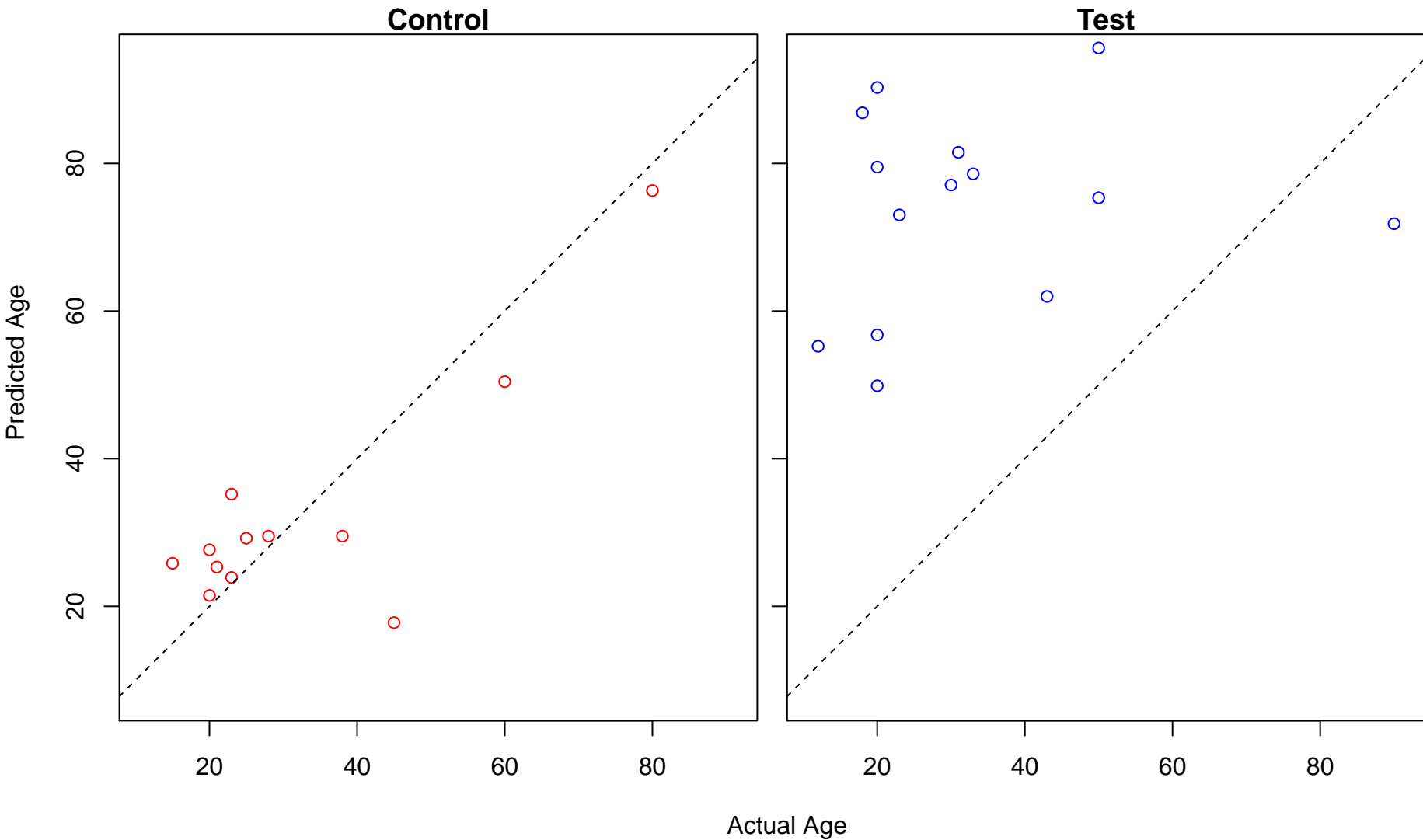
maintenance of protein localization in organelle (Score: 8.455619)



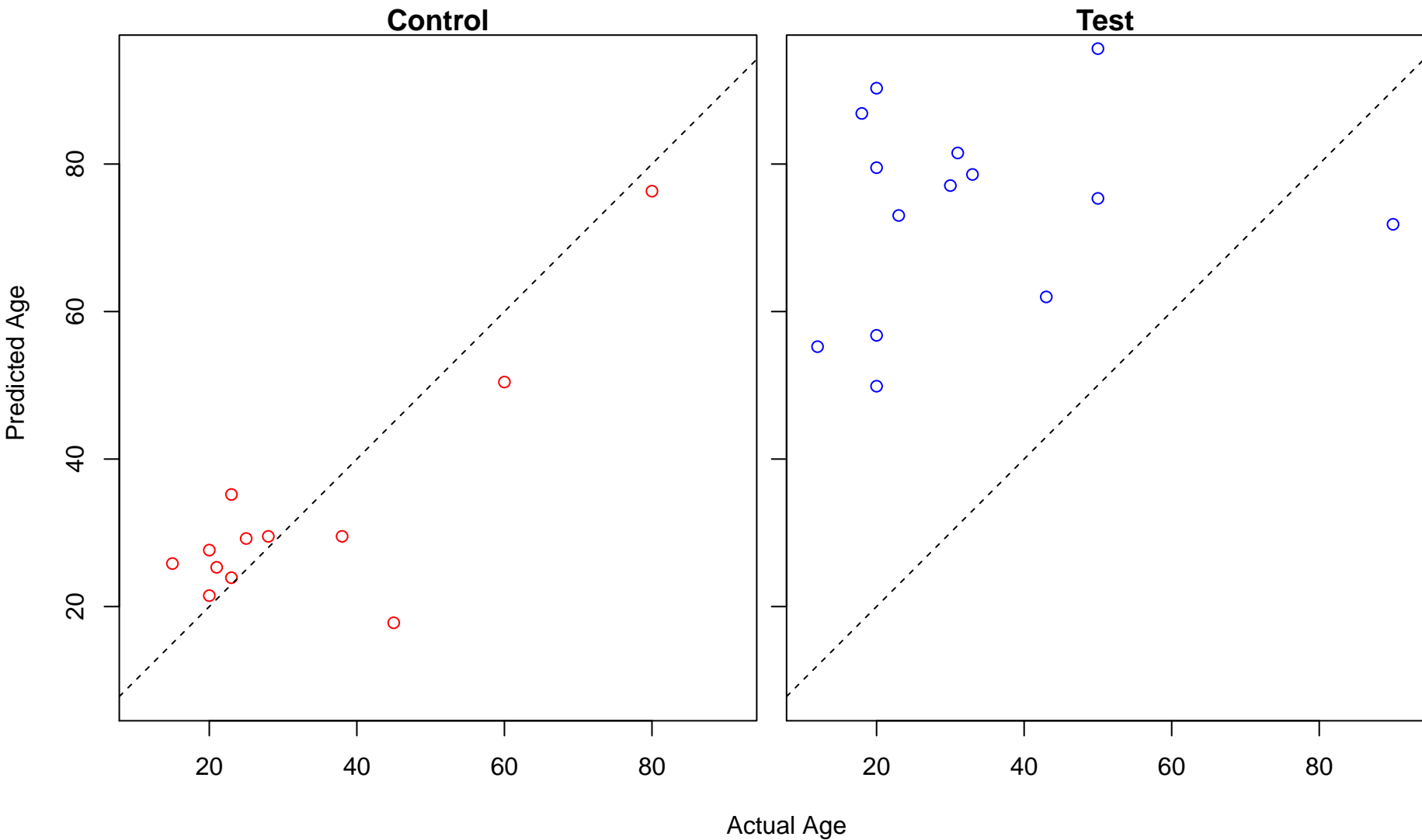
interferon-gamma-mediated signaling pathway (Score: 8.451469)



detection of external biotic stimulus (Score: 8.447320)

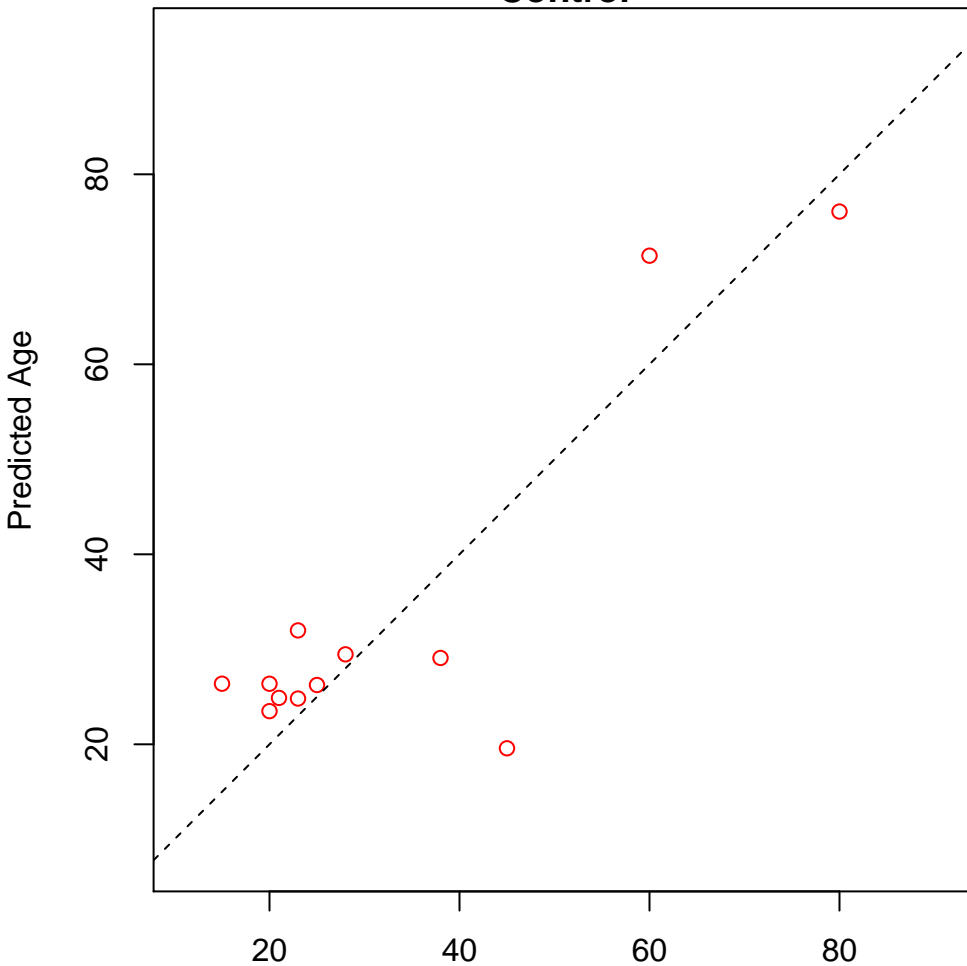


detection of biotic stimulus (Score: 8.447238)

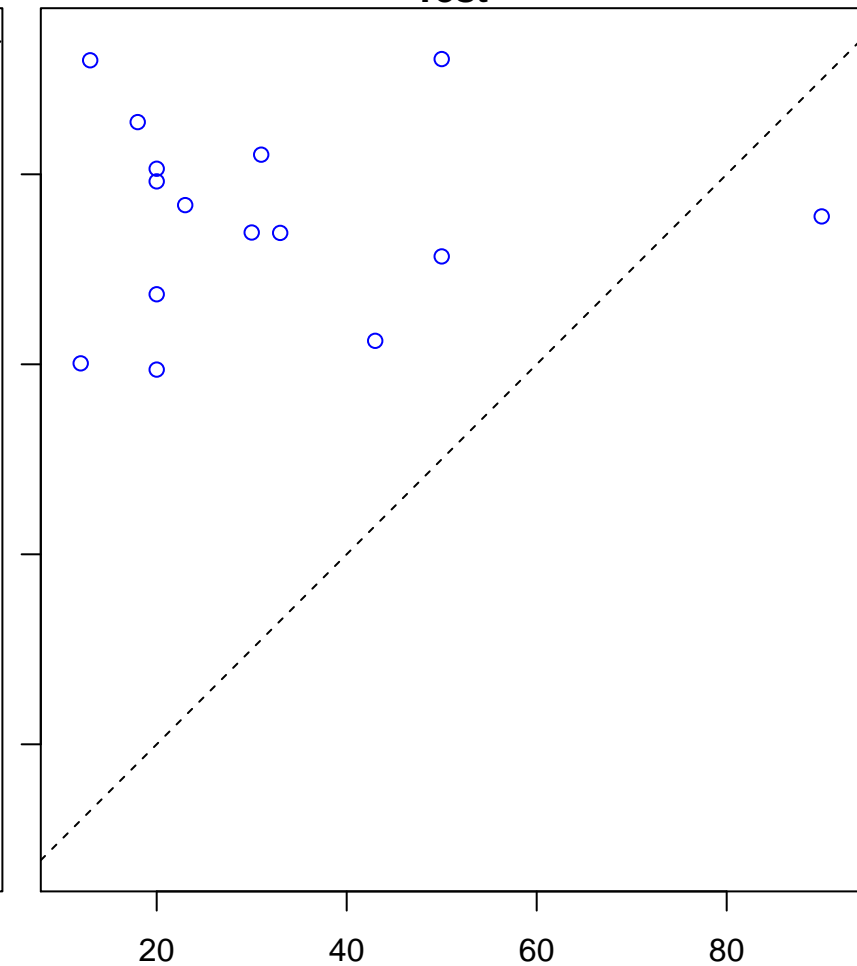


antigen processing and presentation (Score: 8.445689)

Control



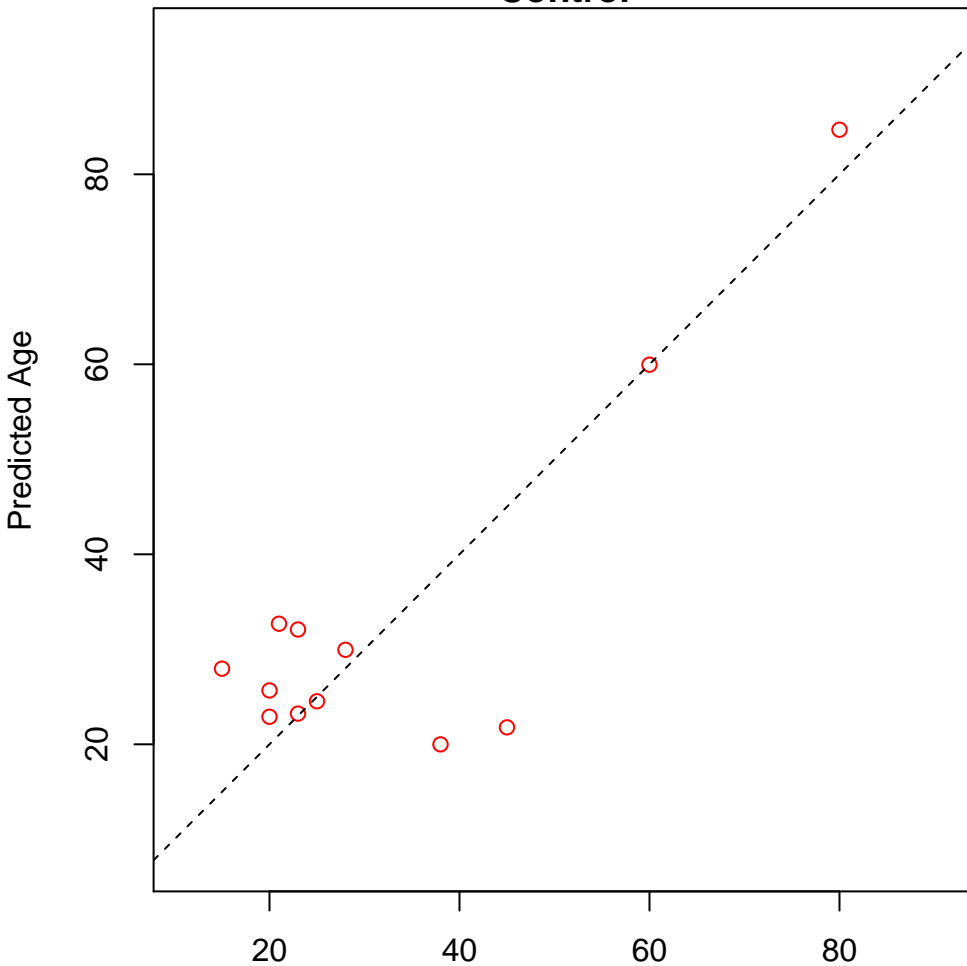
Test



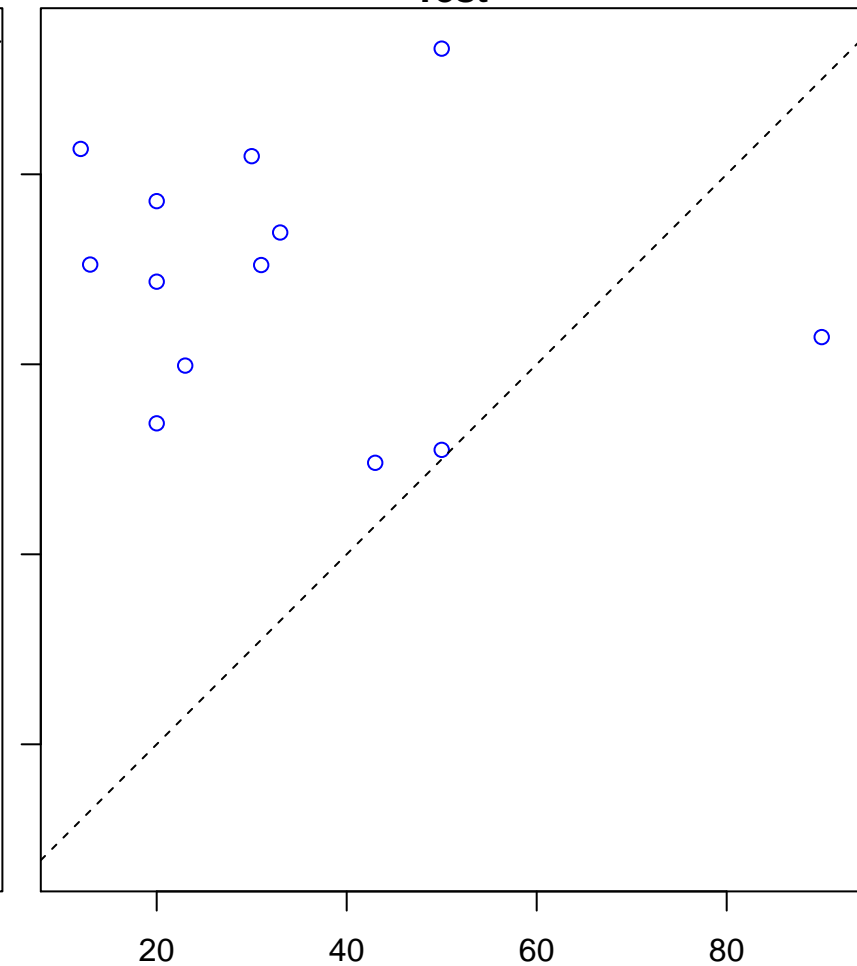
Actual Age

vesicle targeting, rough ER to cis-Golgi (Score: 8.445580)

Control

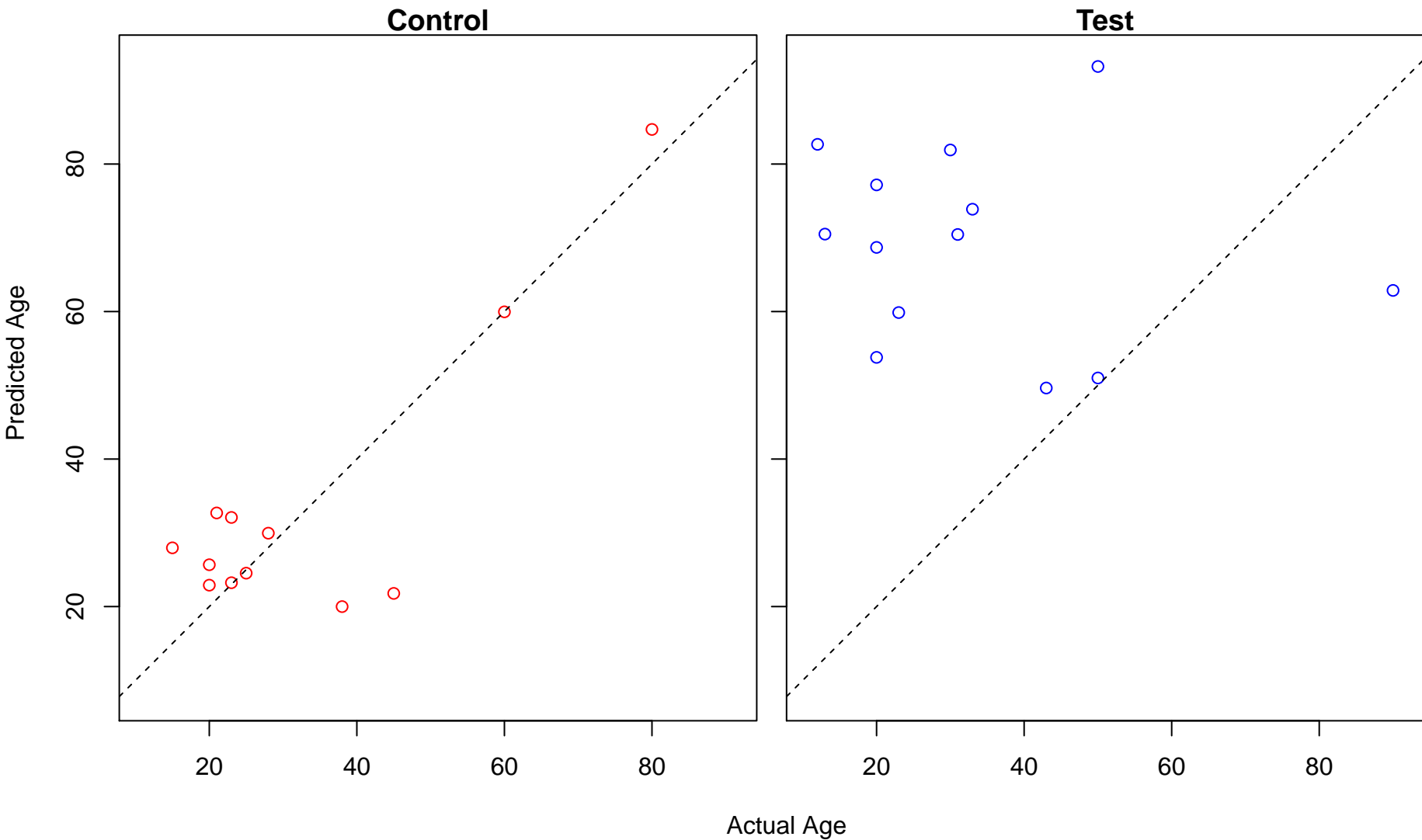


Test

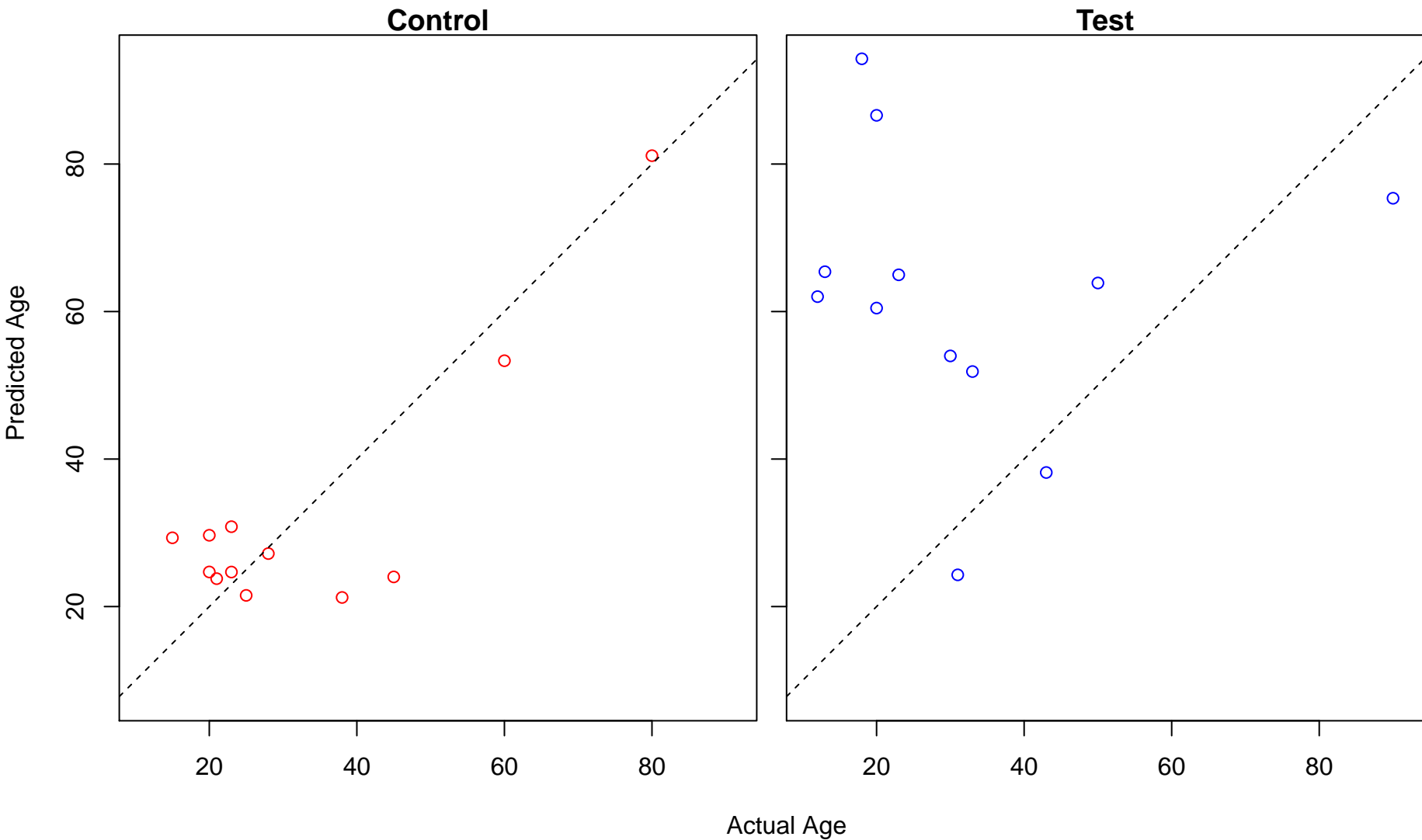


Actual Age

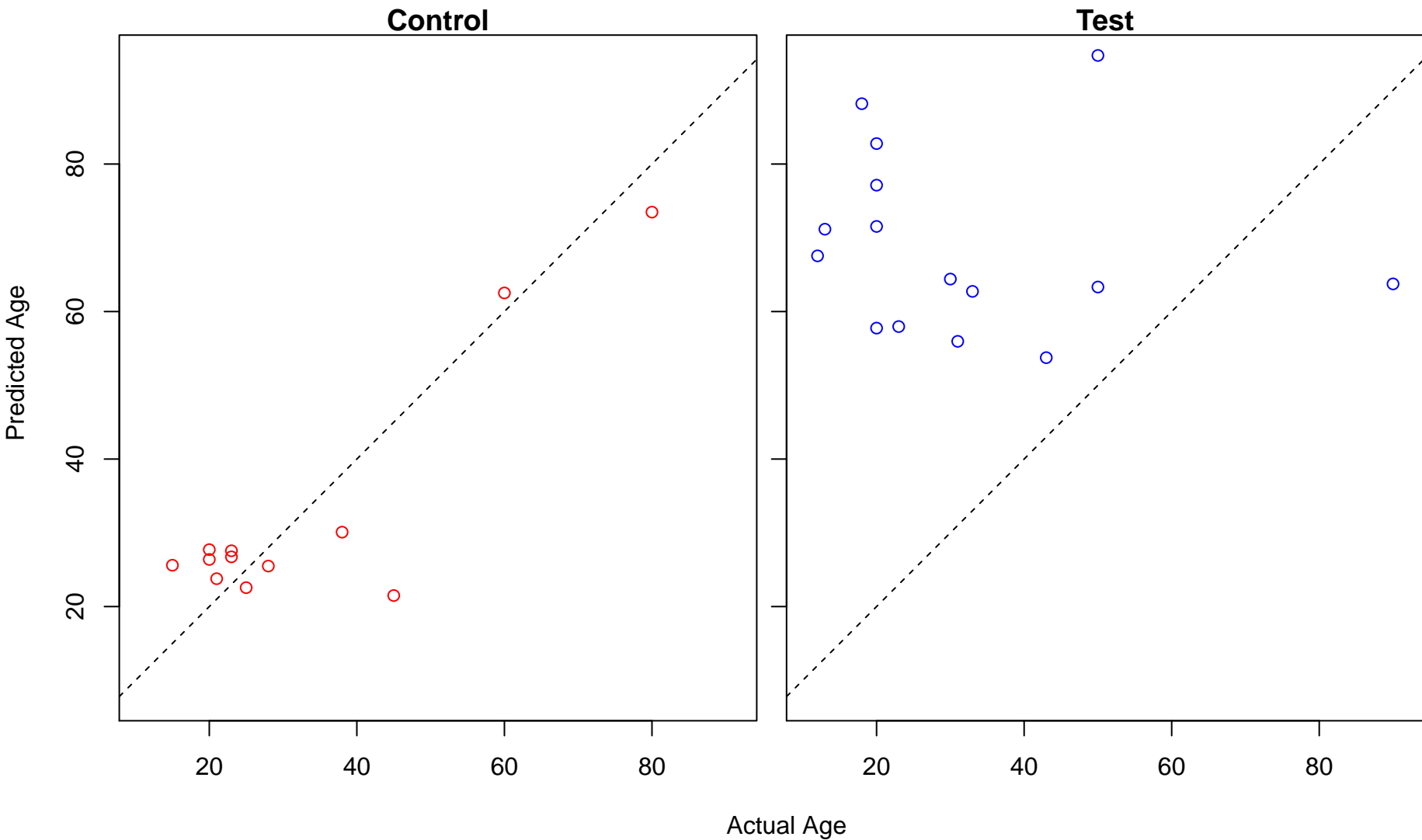
COP2 vesicle coating (Score: 8.445580)



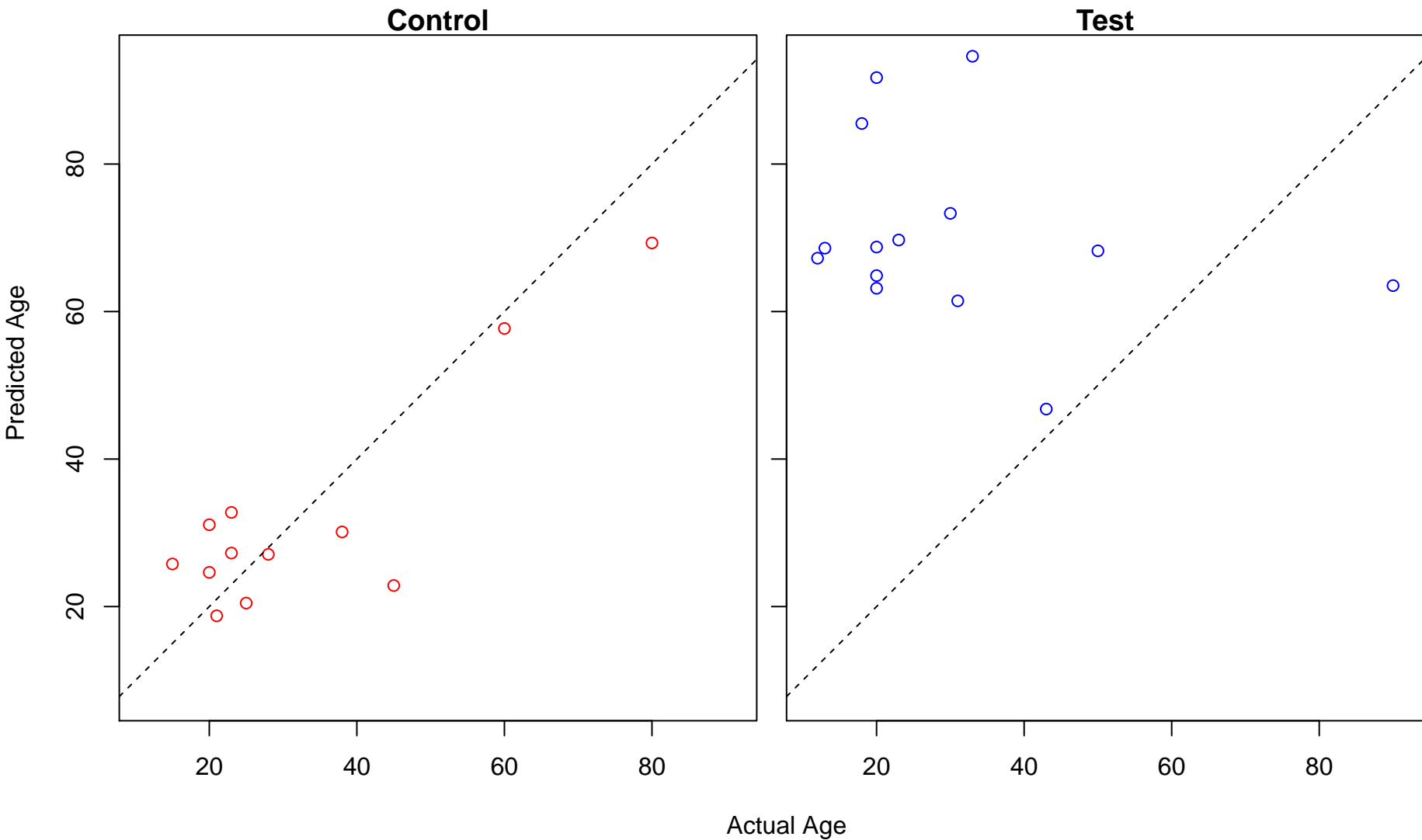
protein deglycosylation (Score: 8.437465)



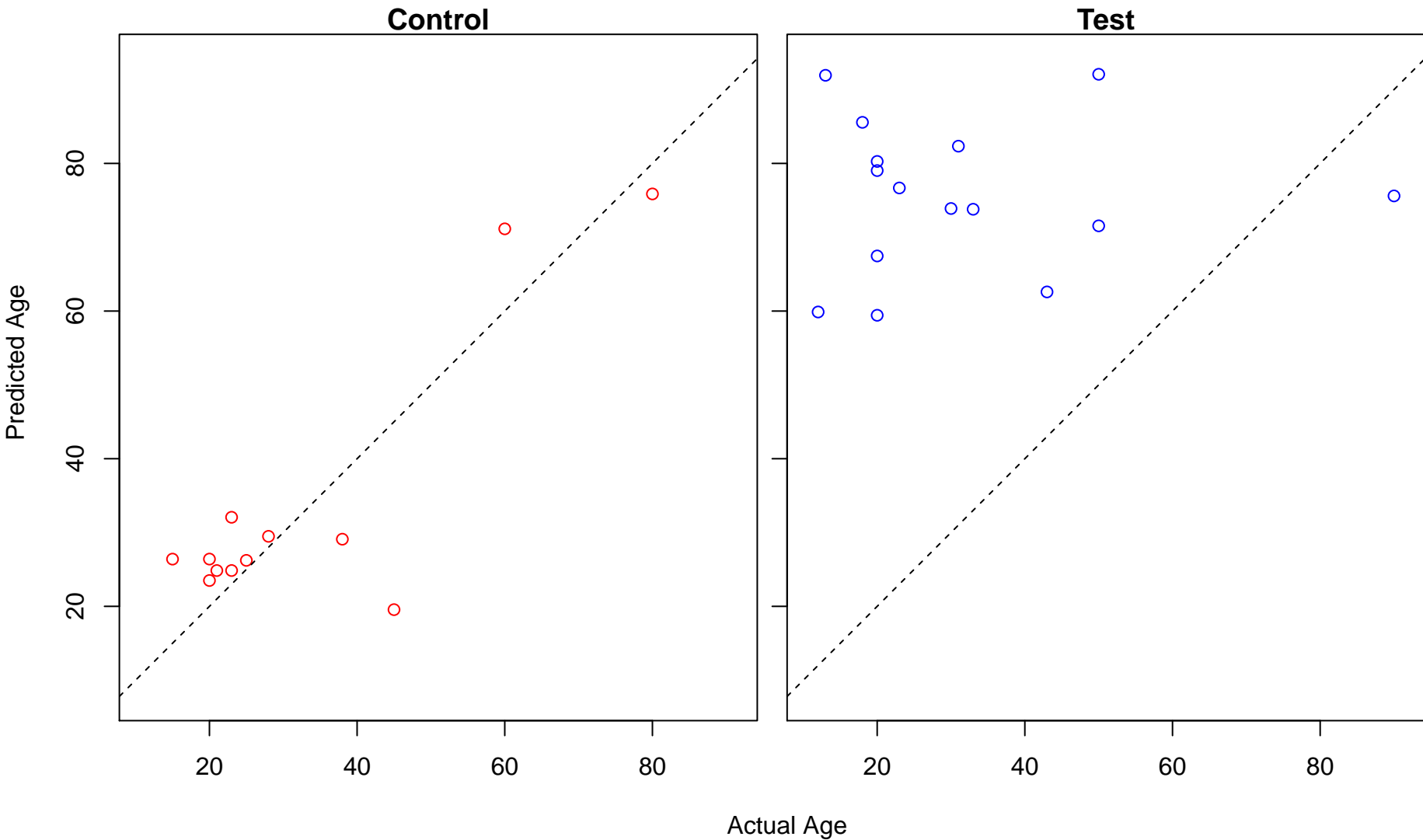
embryonic camera-type eye morphogenesis (Score: 8.434157)



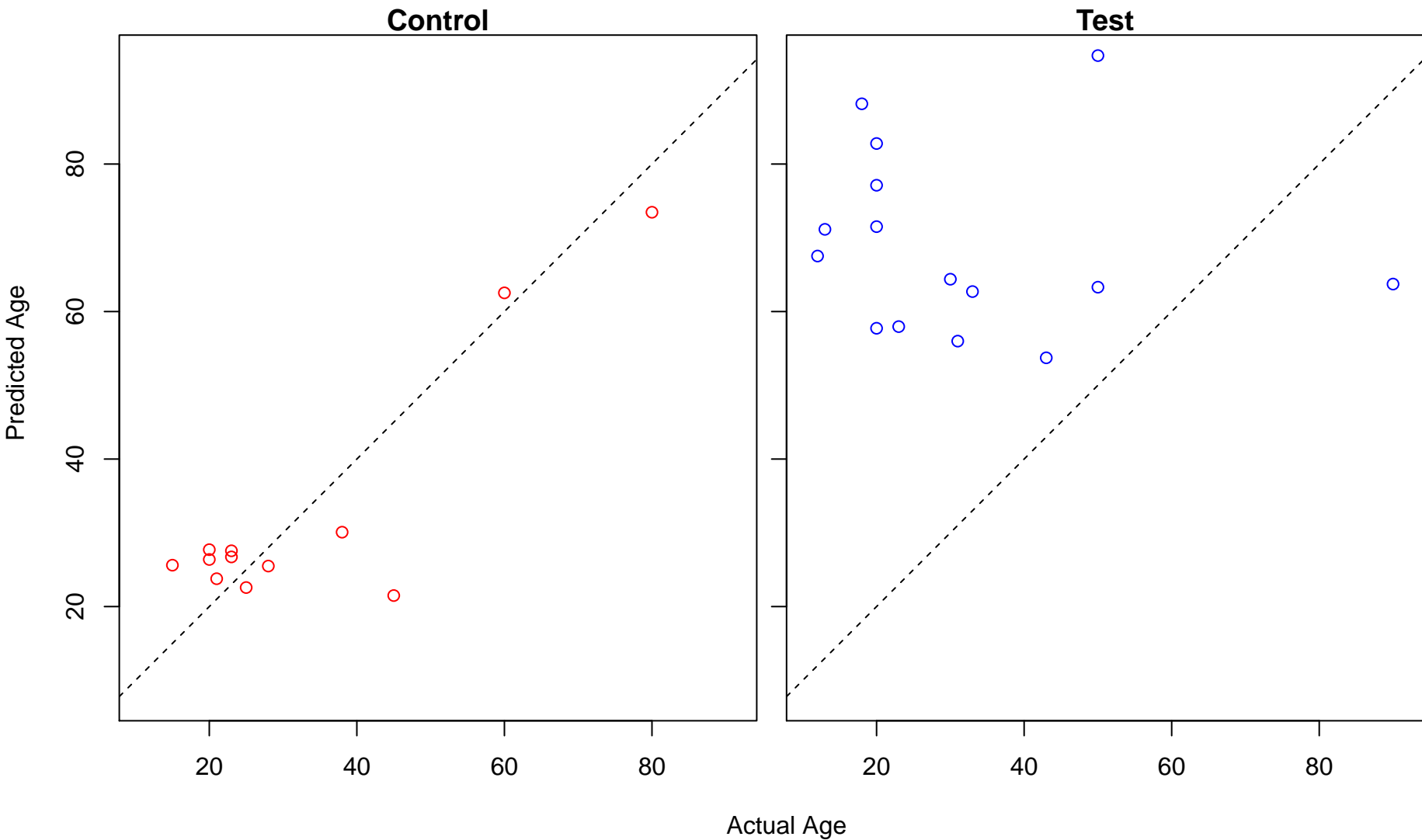
positive regulation of triglyceride metabolic process (Score: 8.432170)



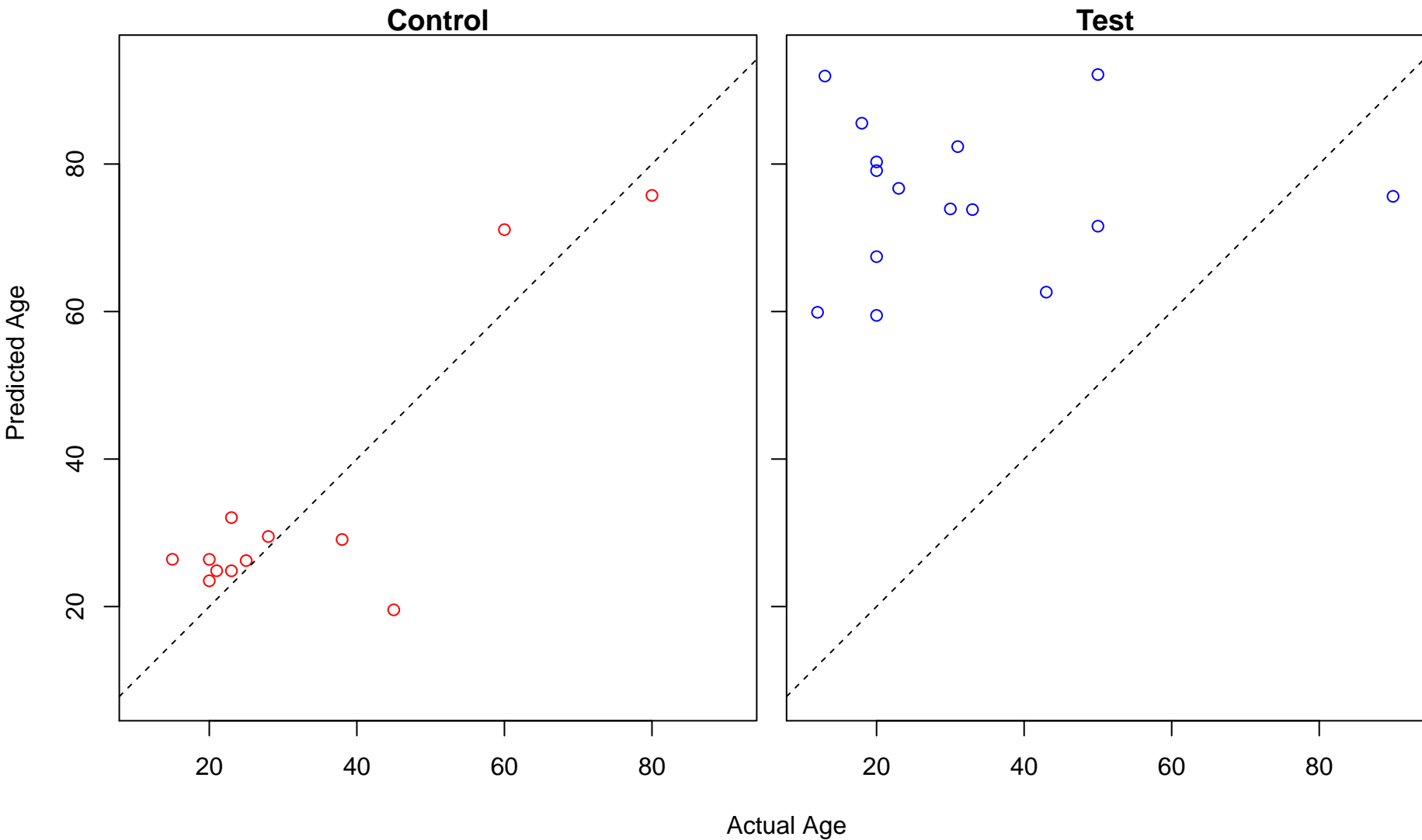
antigen processing and presentation of peptide antigen (Score: 8.430305)



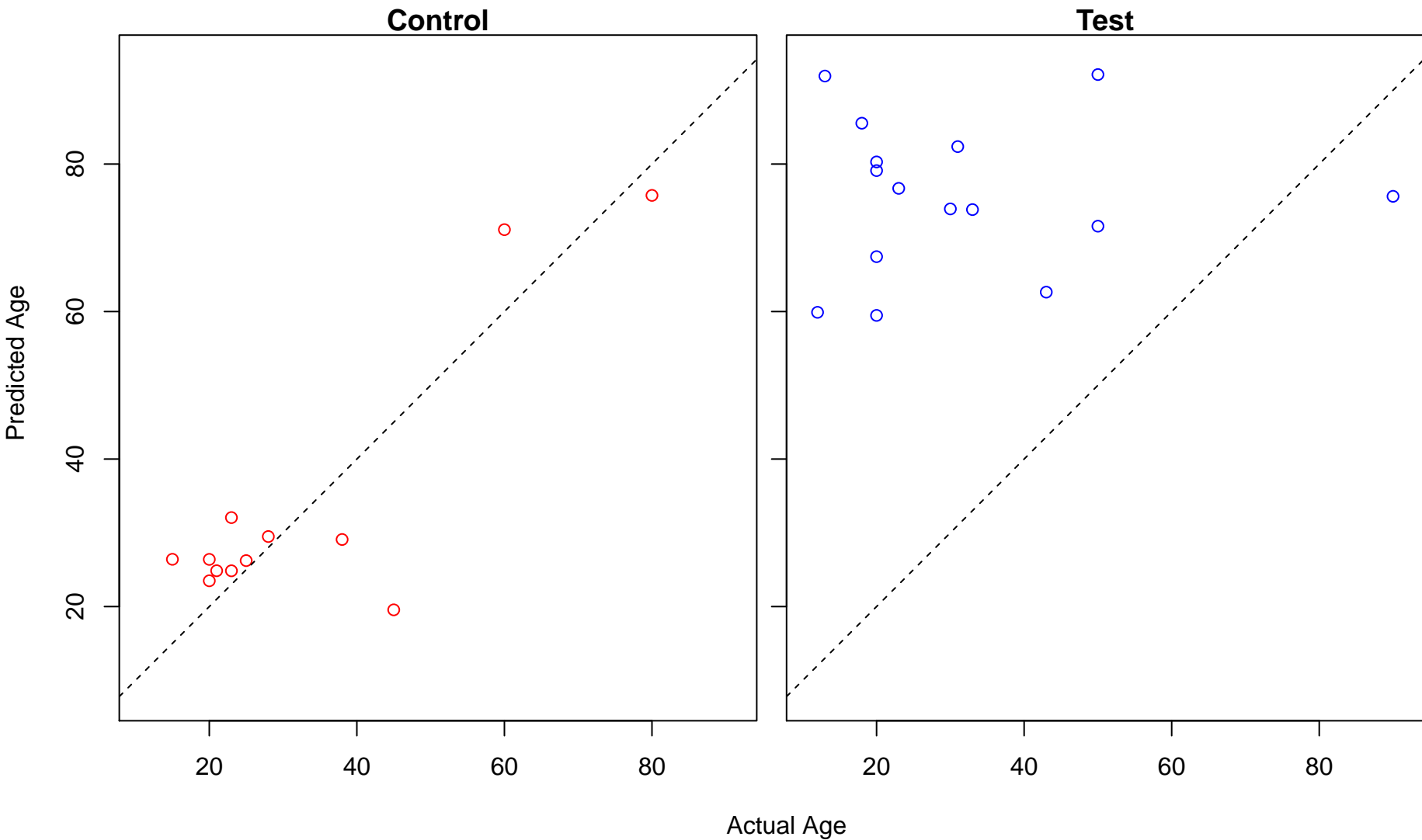
embryonic camera-type eye development (Score: 8.427520)



antigen processing and presentation of exogenous peptide antigen (Score: 8.427493)

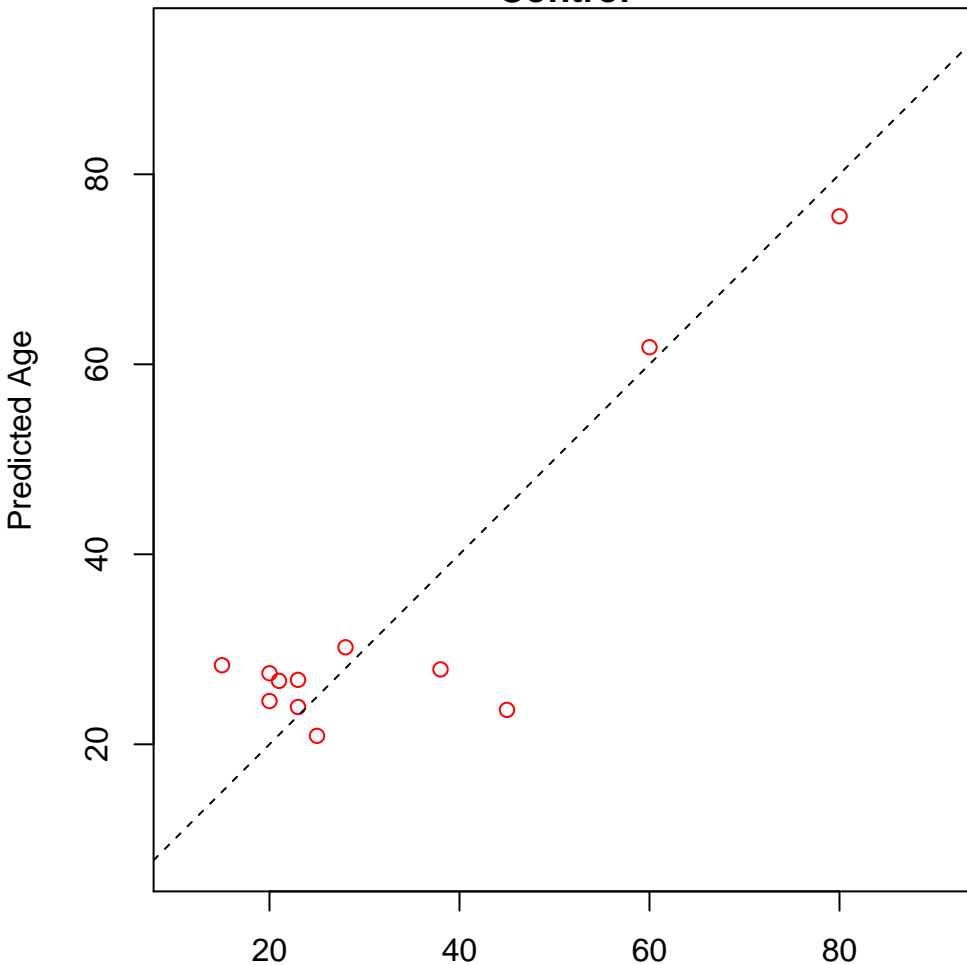


antigen processing and presentation of exogenous antigen (Score: 8.427493)

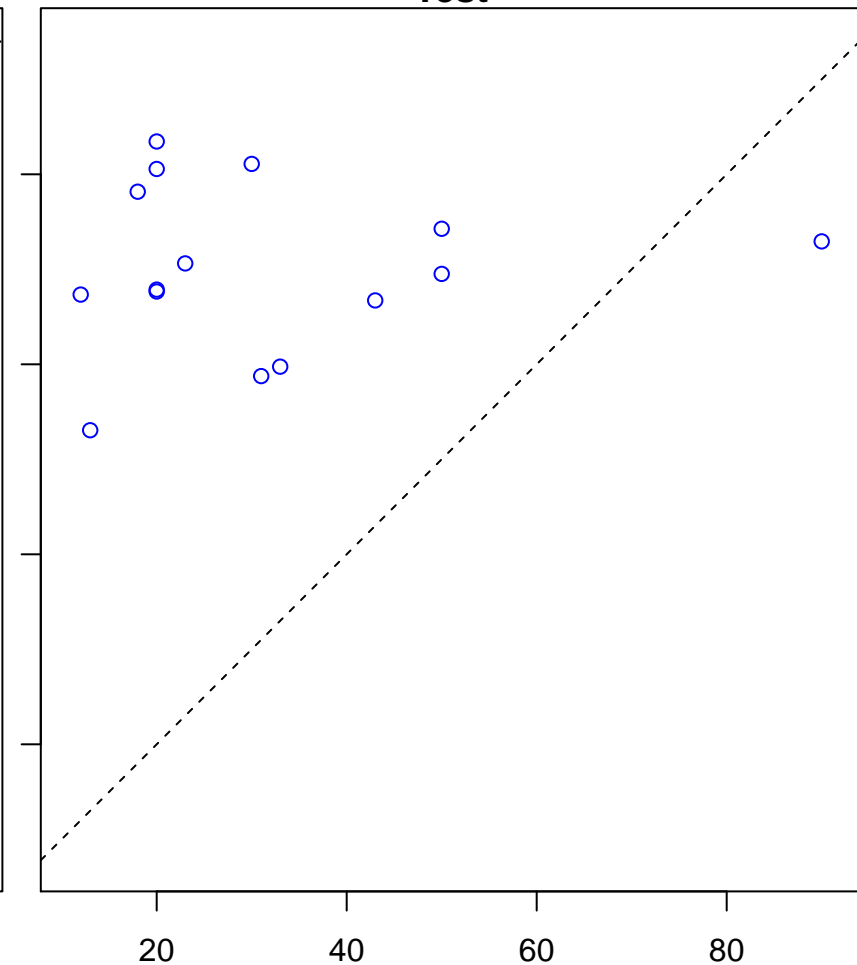


negative regulation of cell proliferation (Score: 8.423959)

Control

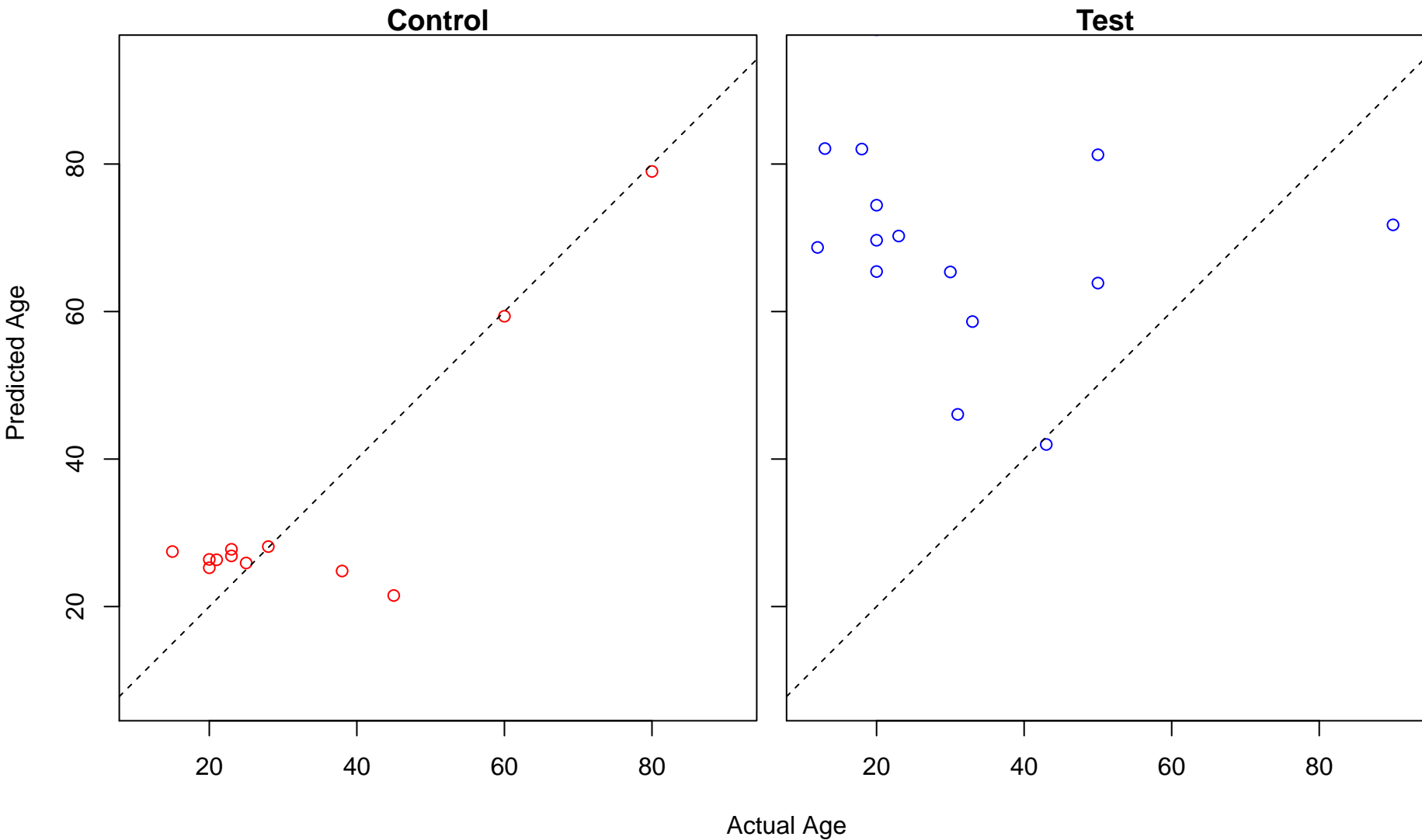


Test

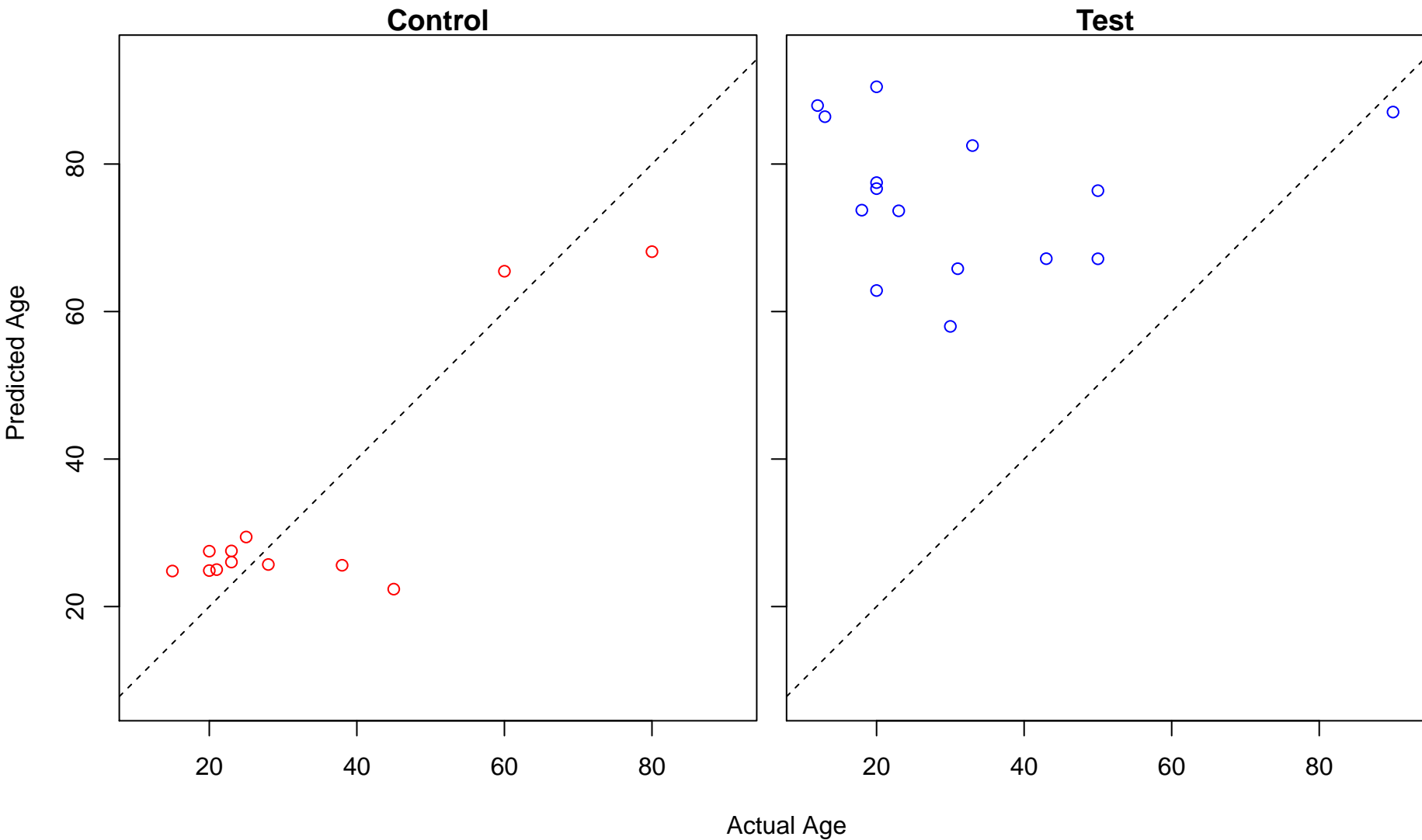


Actual Age

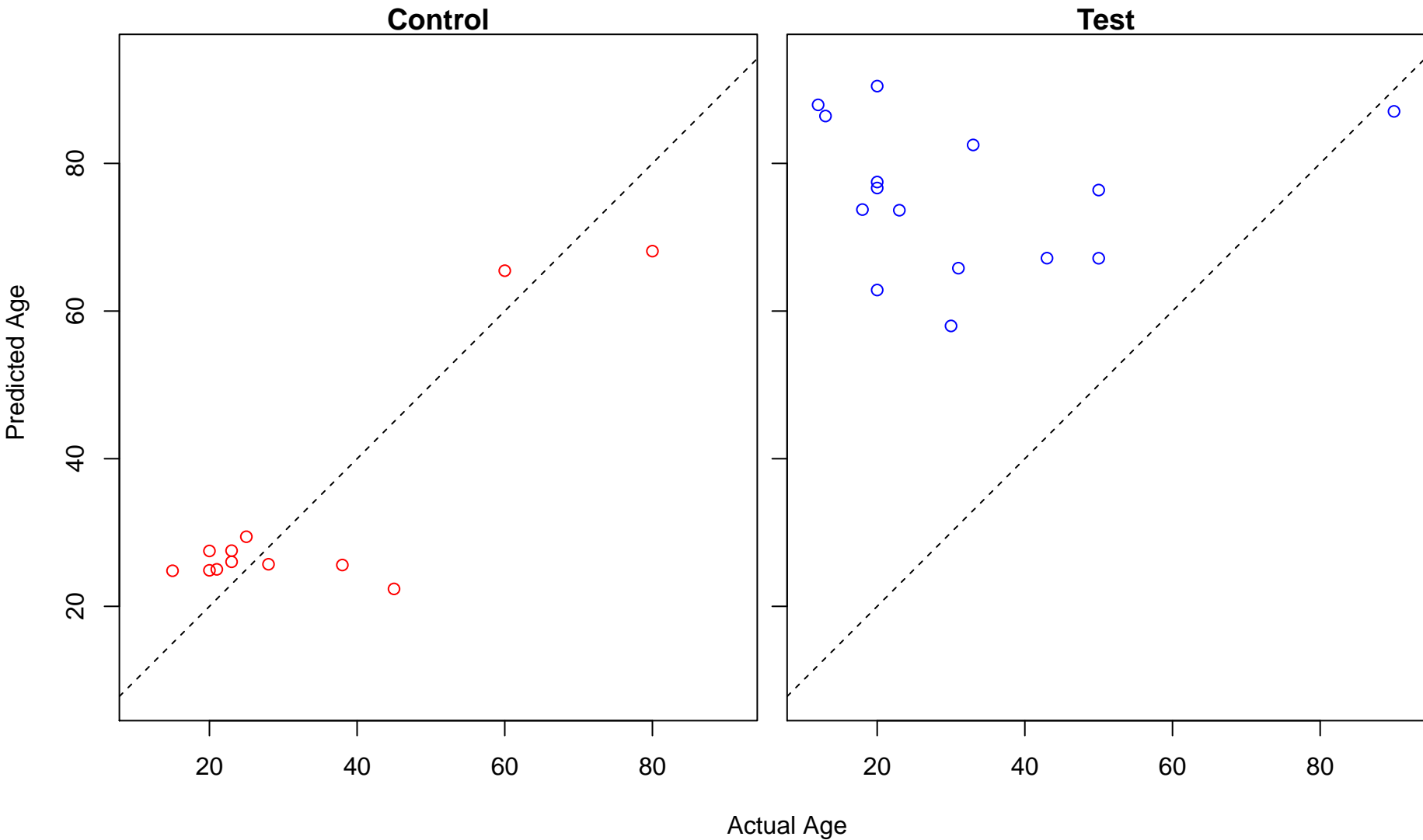
positive regulation of viral process (Score: 8.421055)



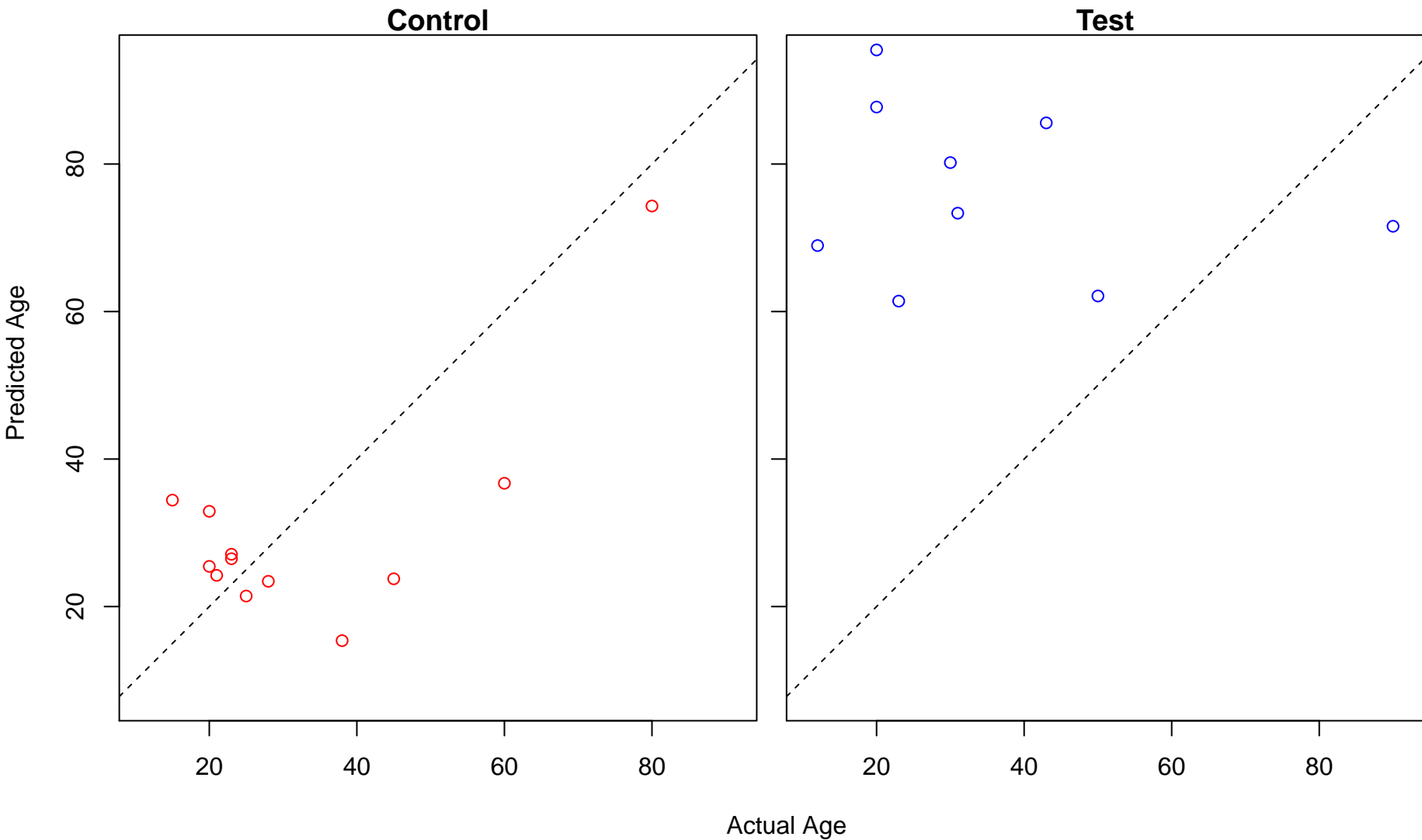
positive regulation of delayed rectifier potassium channel activity (Score: 8.420026)



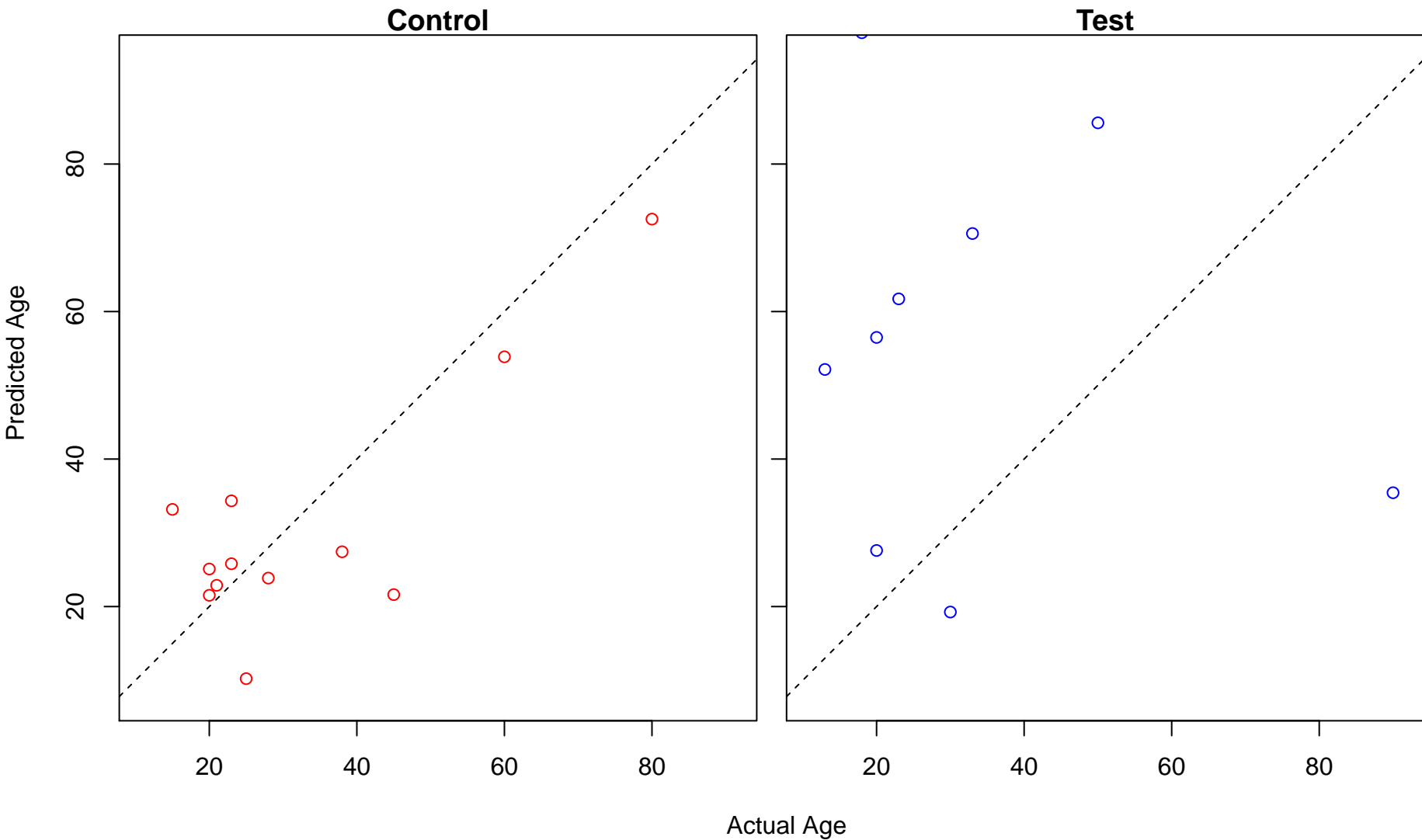
positive regulation of voltage-gated potassium channel activity (Score: 8.420026)



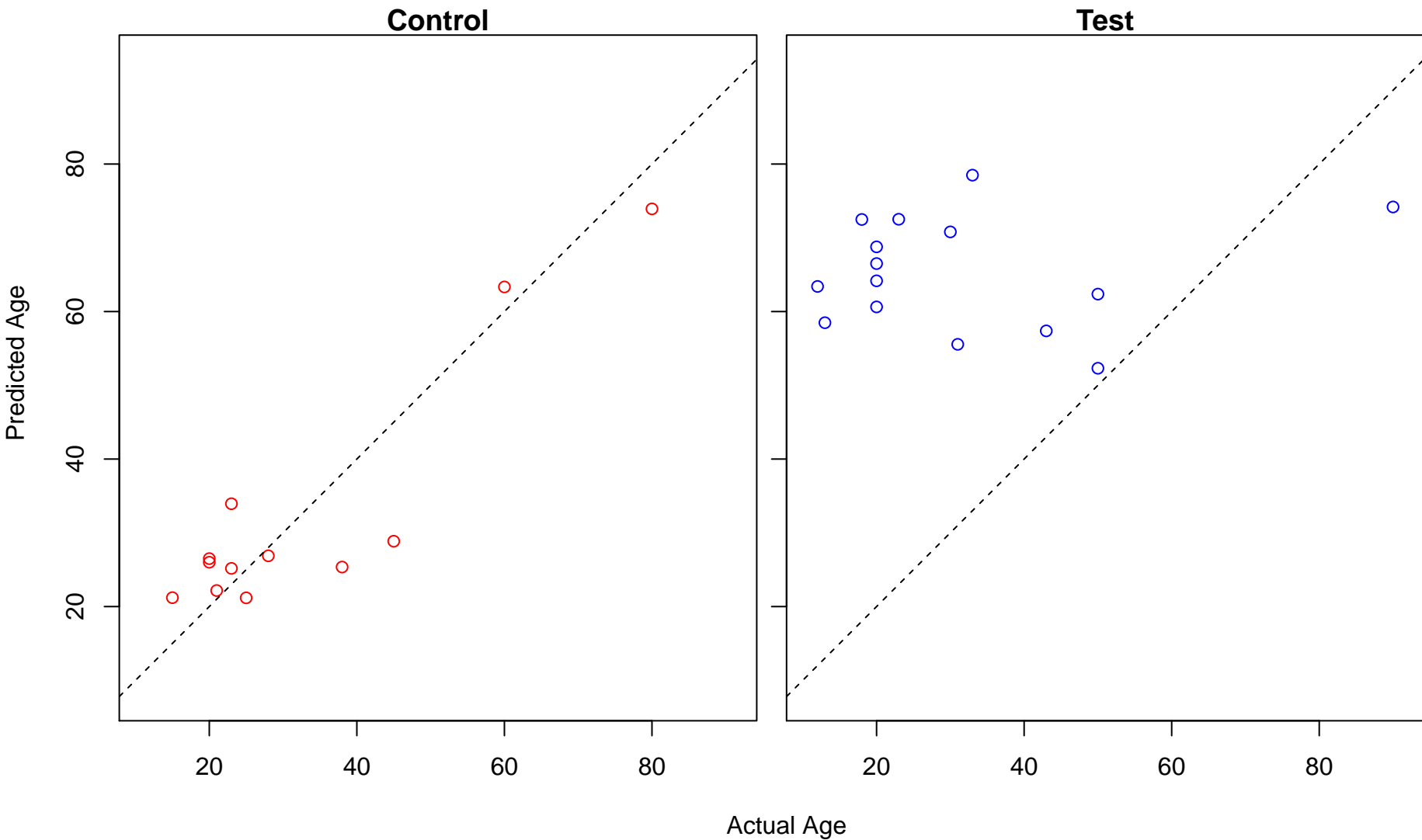
neurotransmitter uptake (Score: 8.413409)



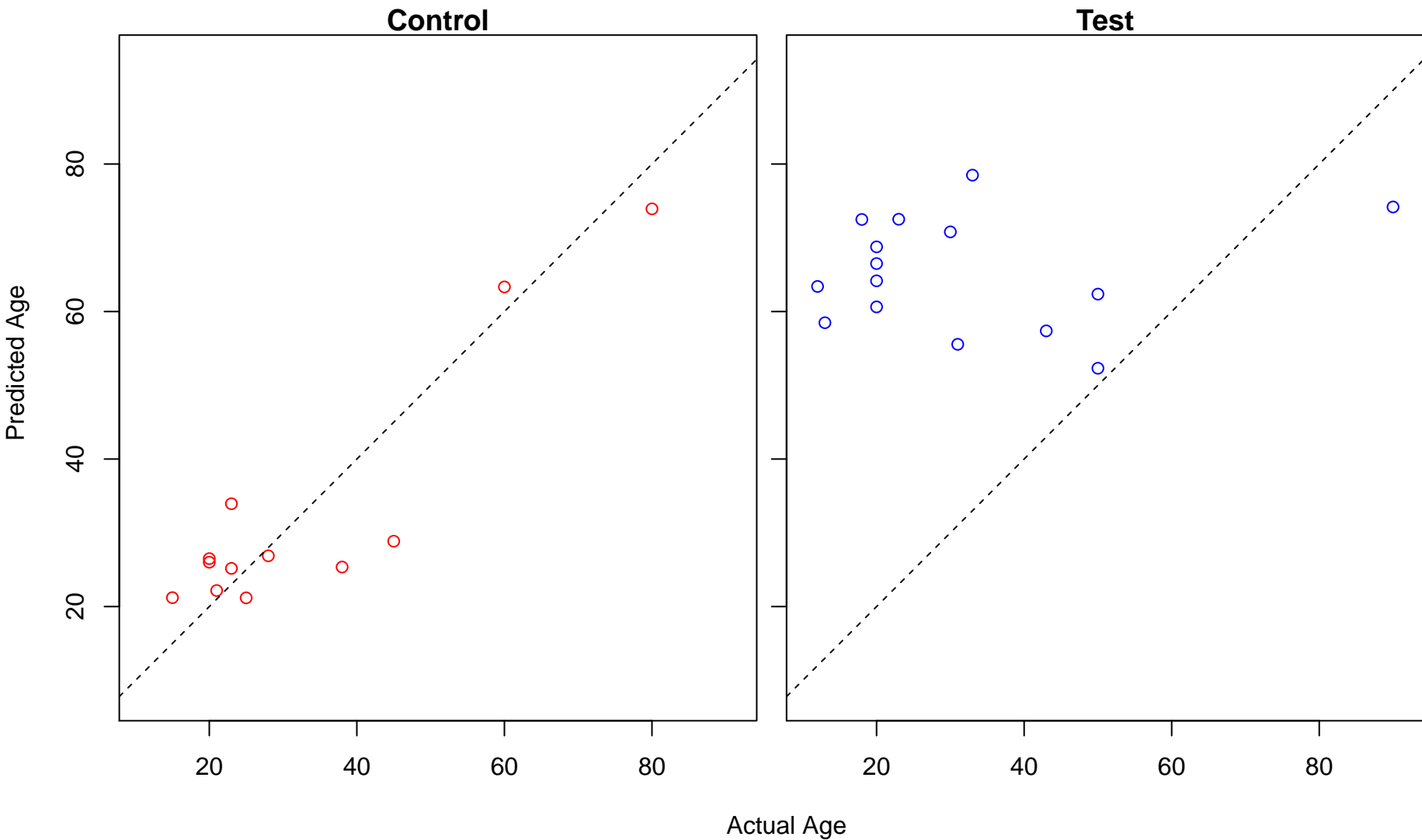
ion homeostasis (Score: 8.409425)



molybdopterin cofactor biosynthetic process (Score: 8.404878)

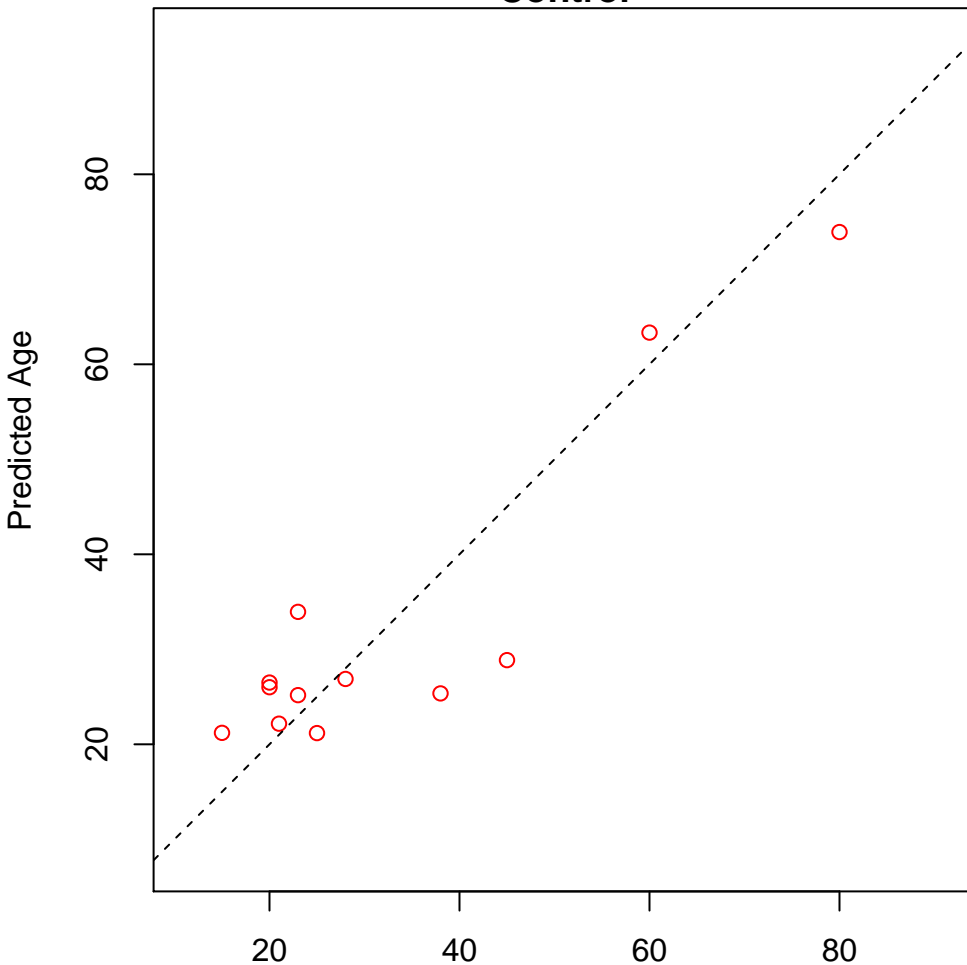


molybdopterin cofactor metabolic process (Score: 8.404878)

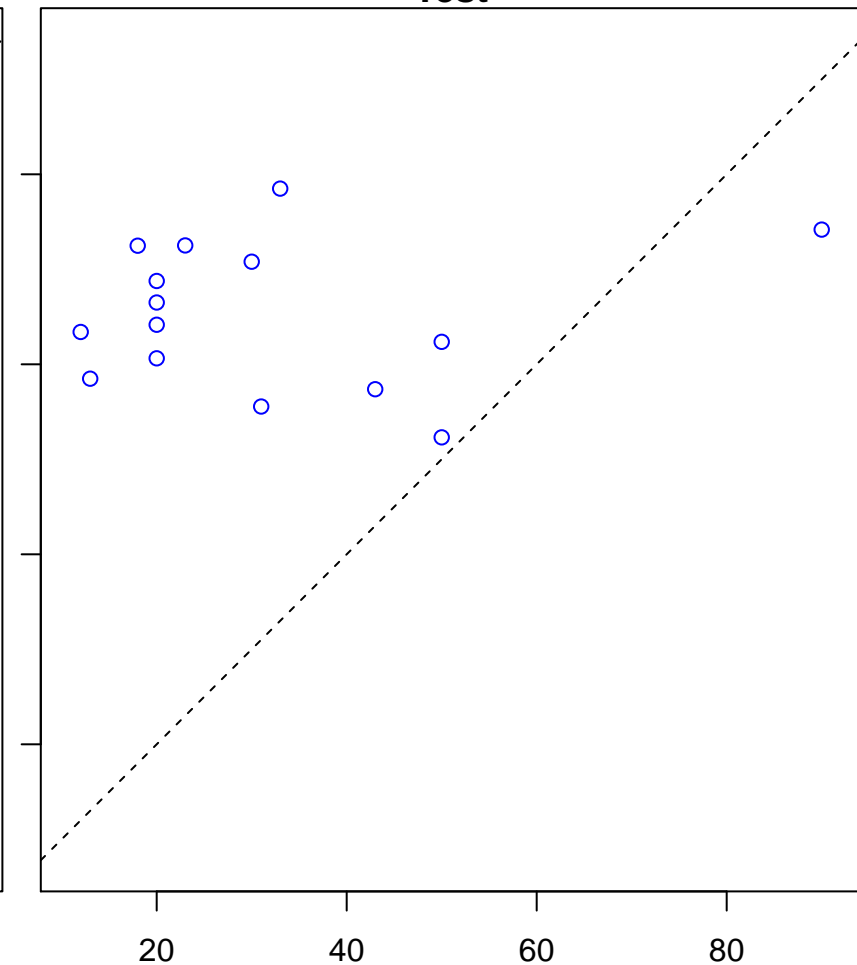


prosthetic group metabolic process (Score: 8.404878)

Control



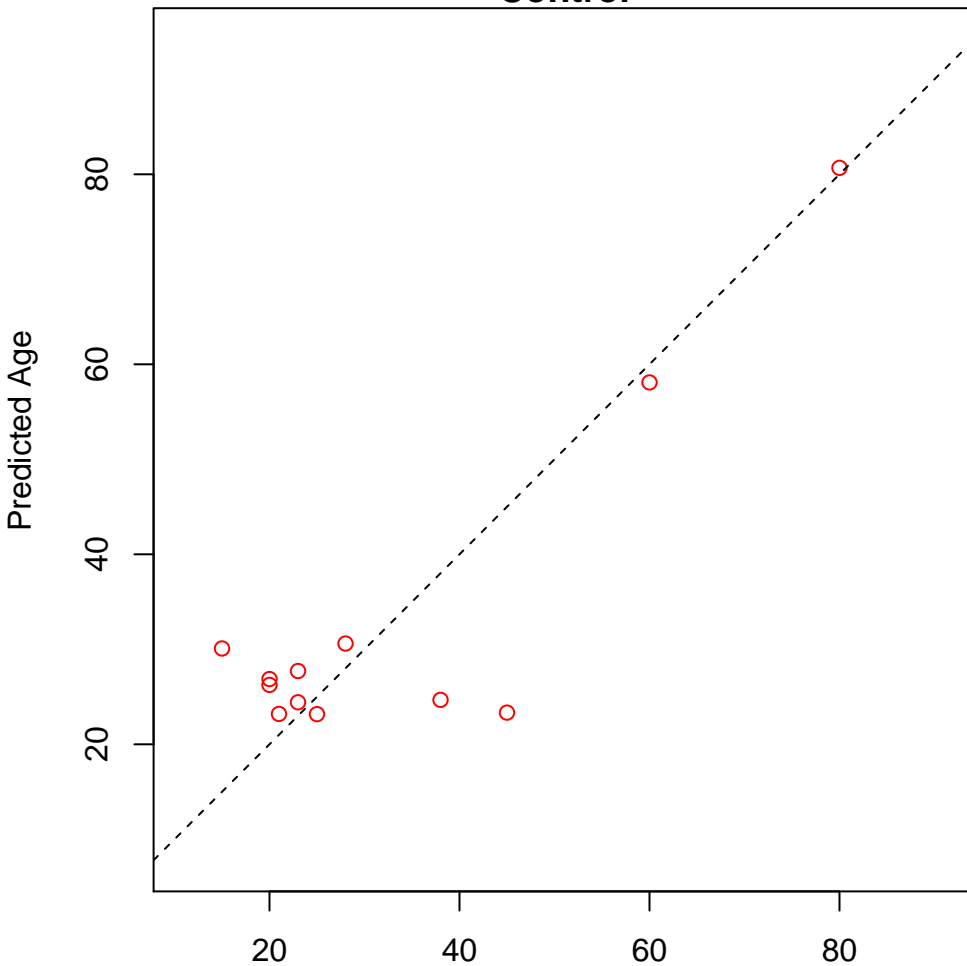
Test



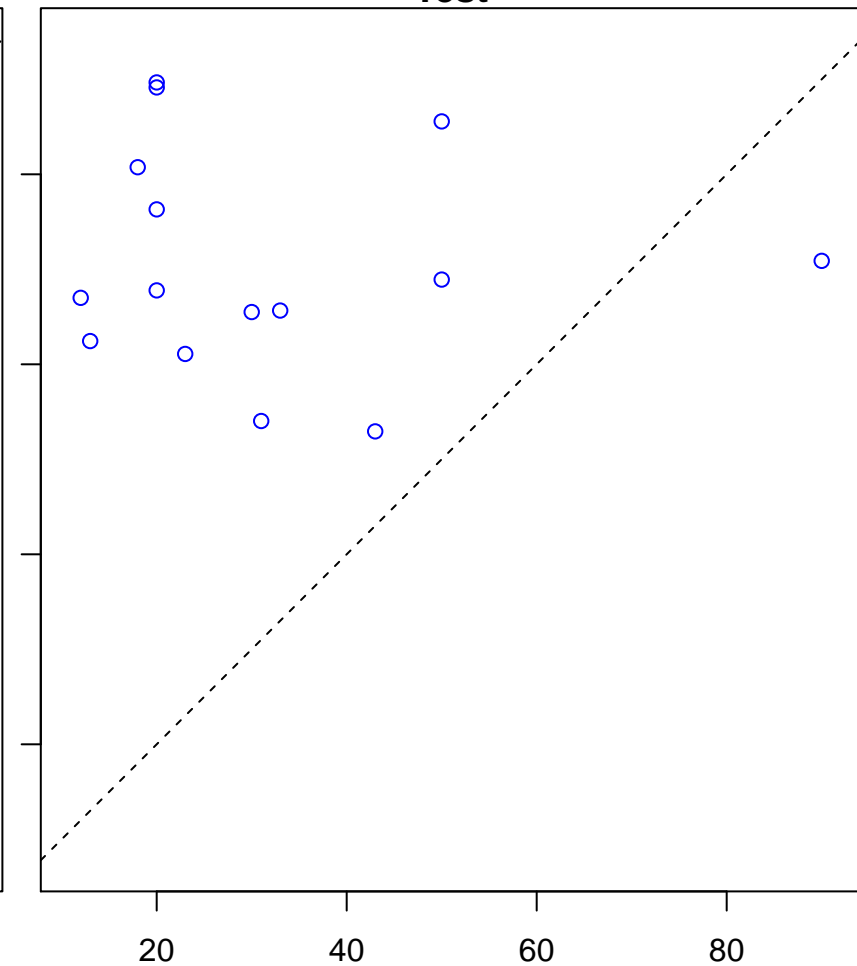
Actual Age

cellular response to amino acid stimulus (Score: 8.404094)

Control

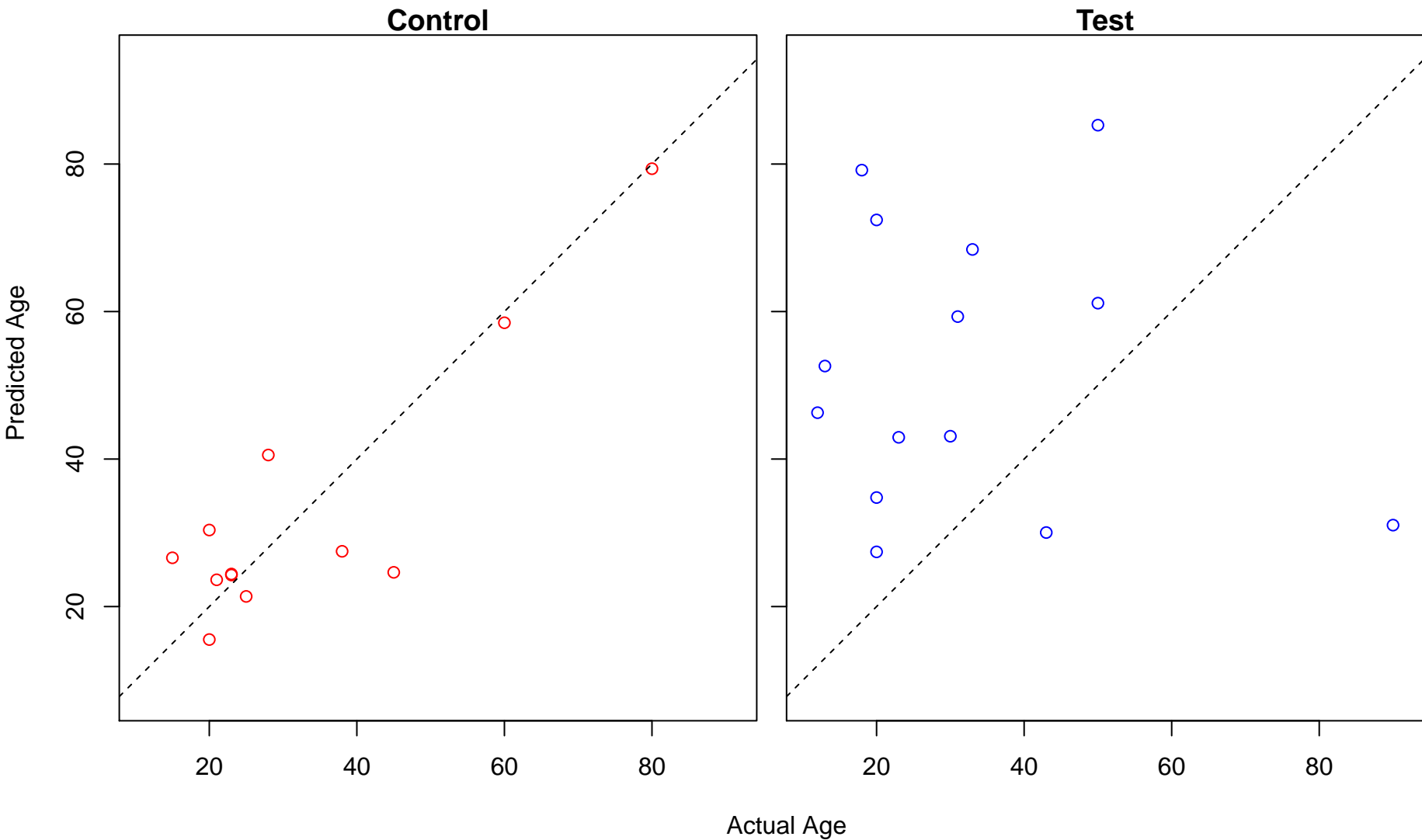


Test

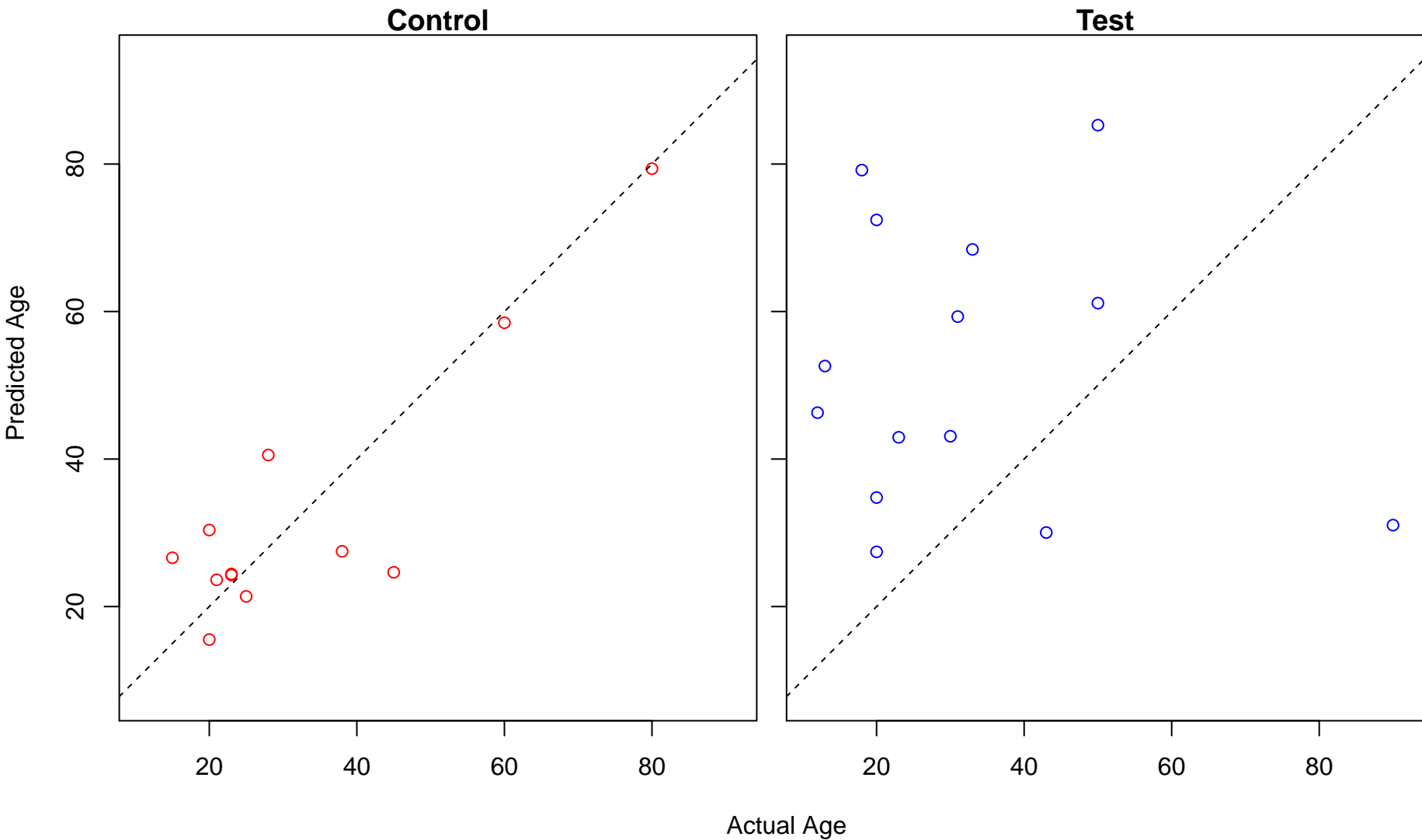


Actual Age

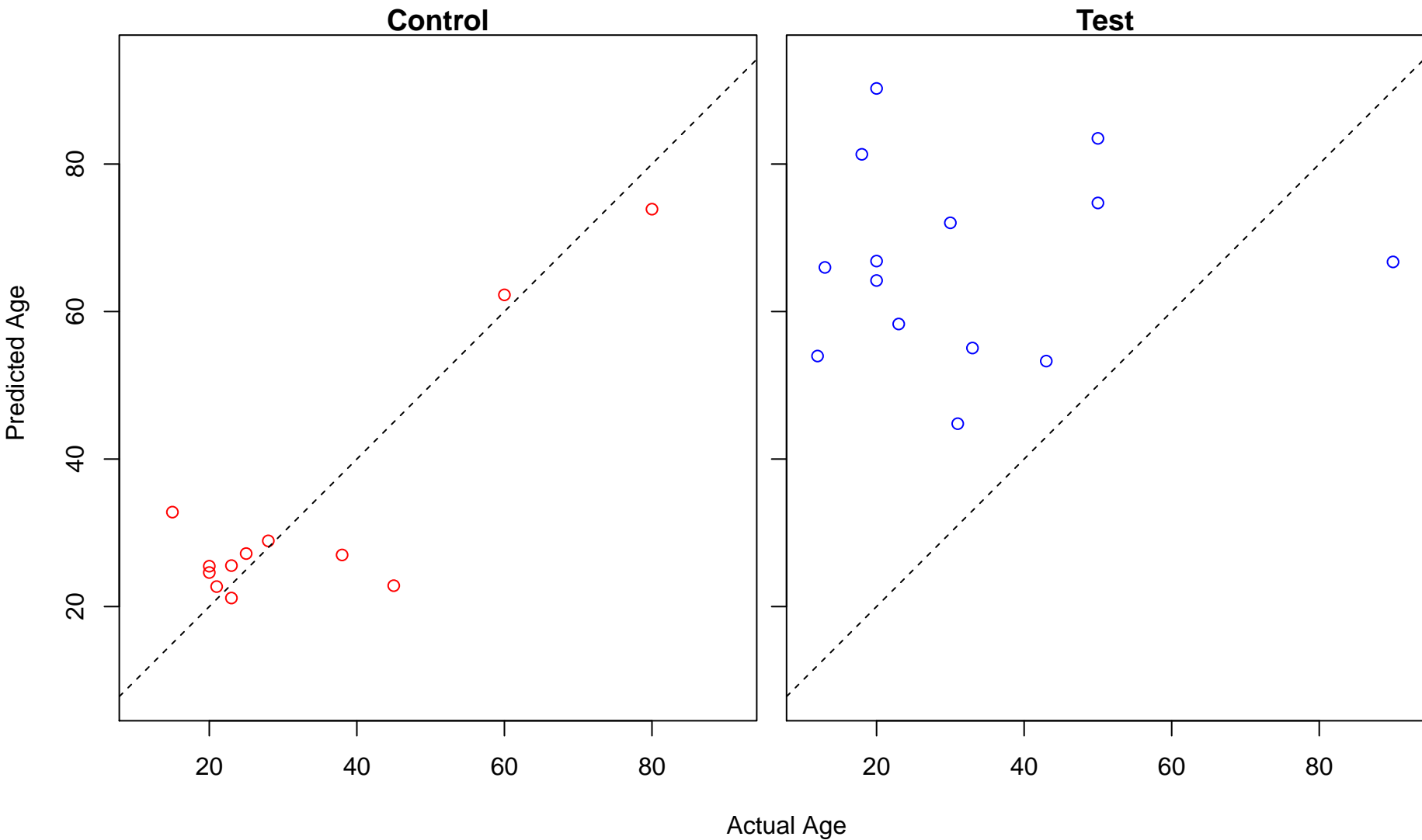
axon guidance (Score: 8.400602)



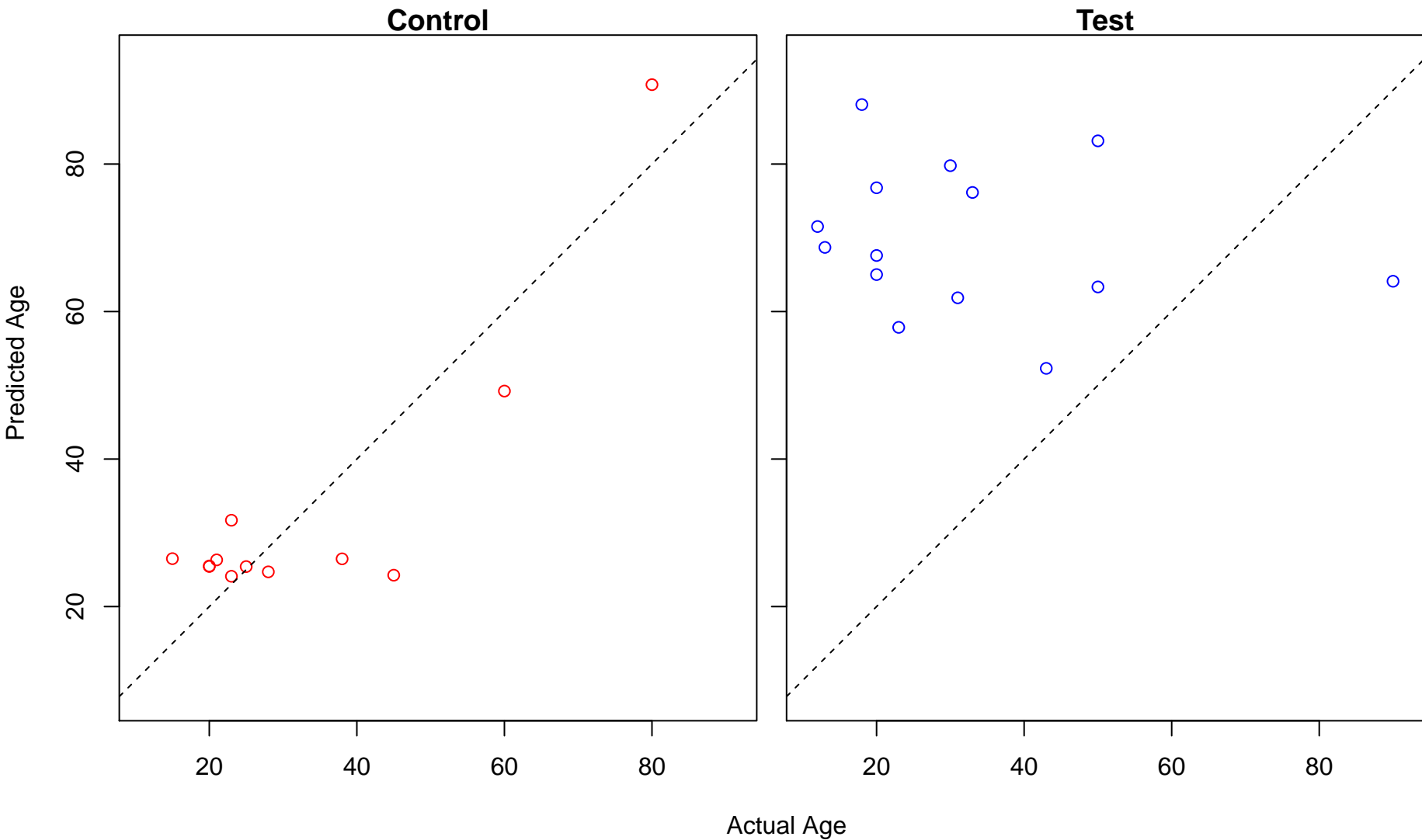
neuron projection guidance (Score: 8.400602)



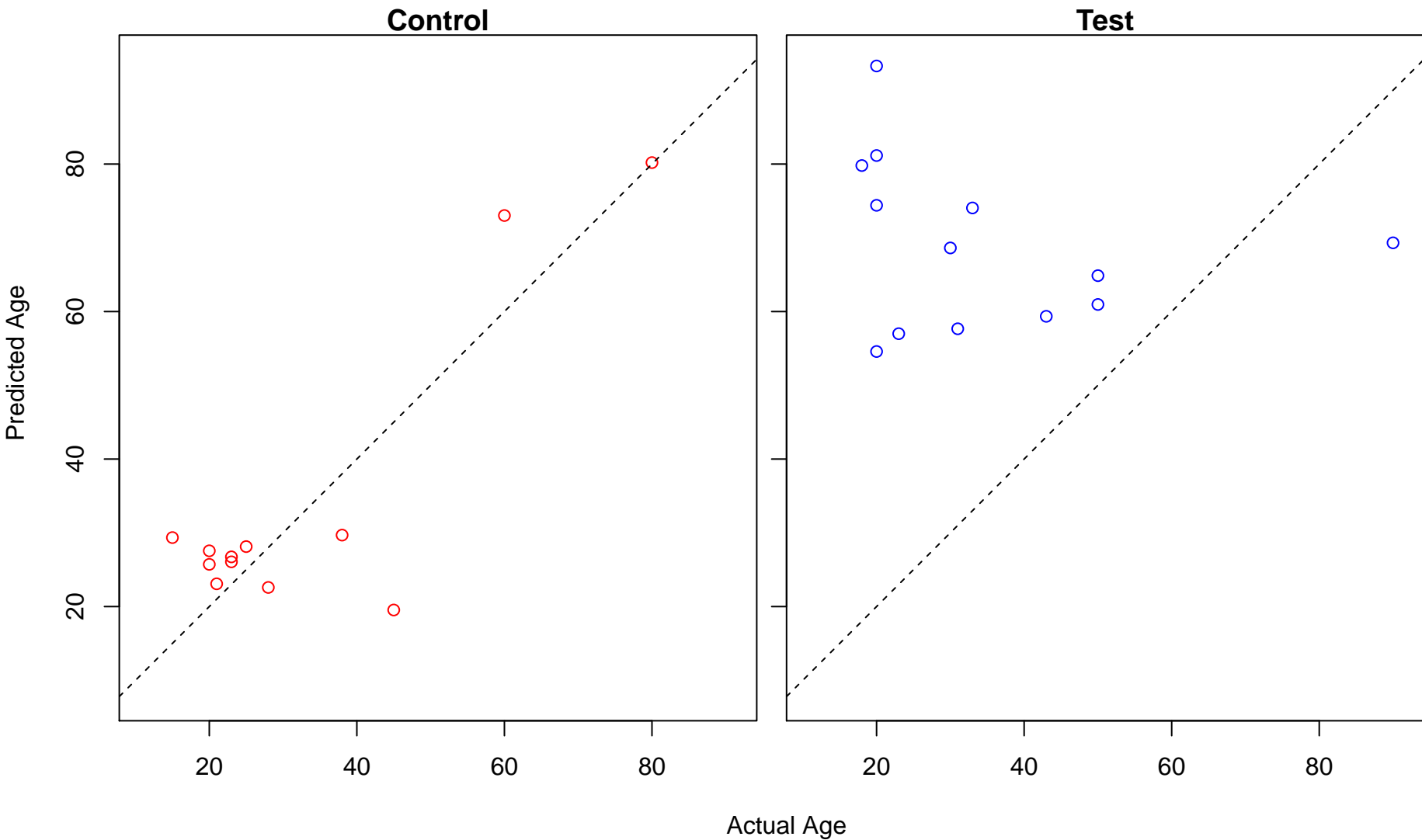
tricarboxylic acid metabolic process (Score: 8.395461)



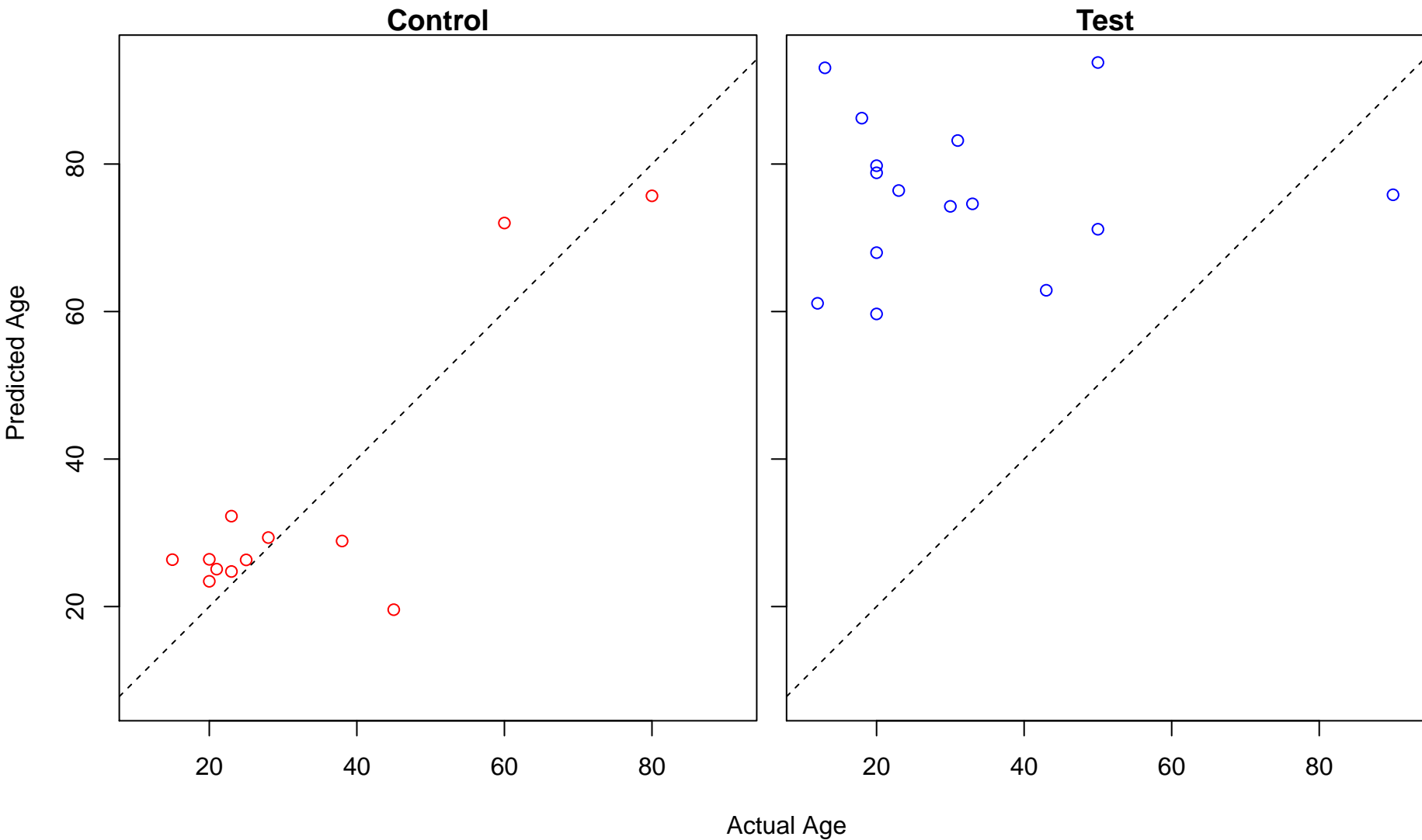
positive regulation of telomerase activity (Score: 8.393939)



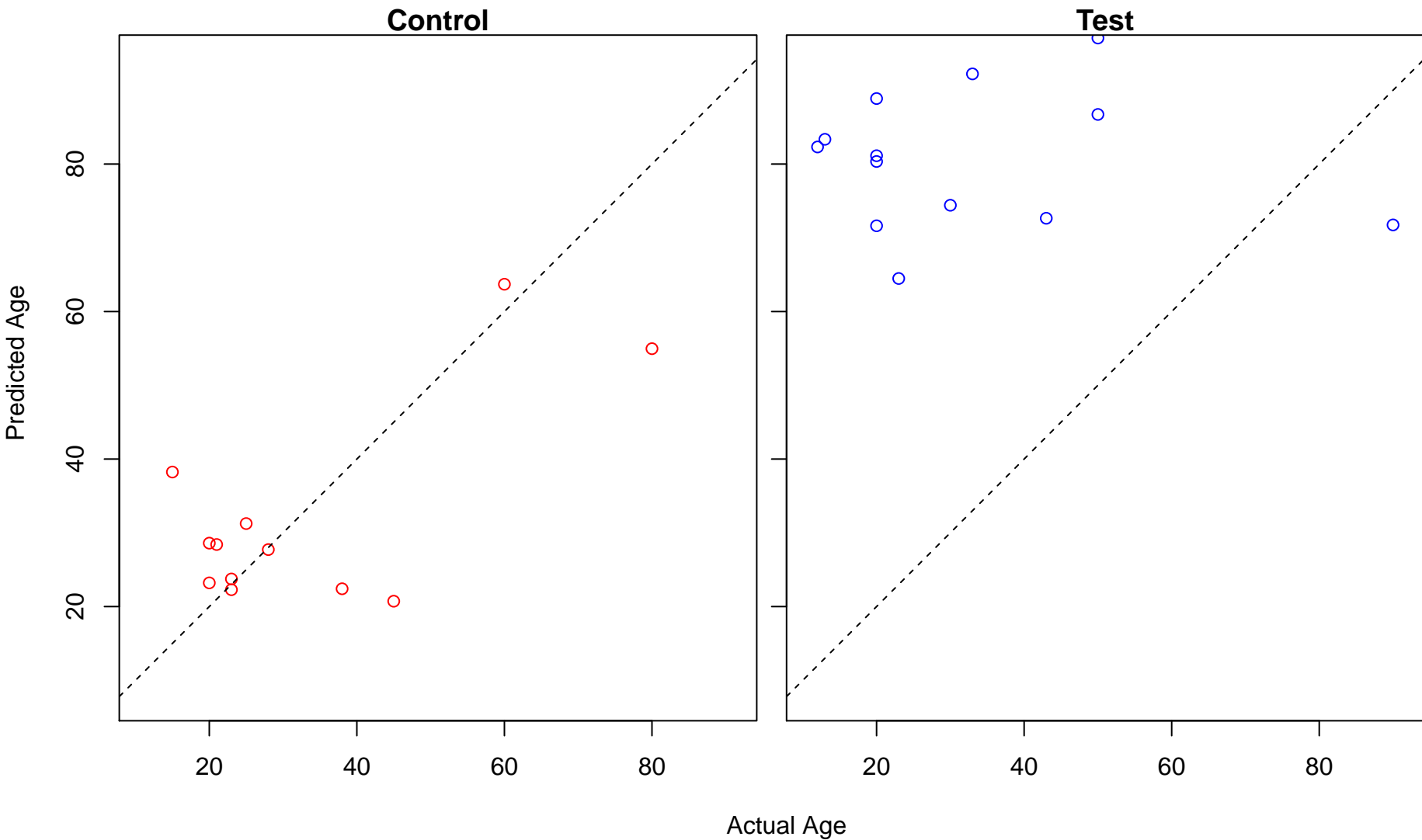
negative regulation by host of viral process (Score: 8.388712)



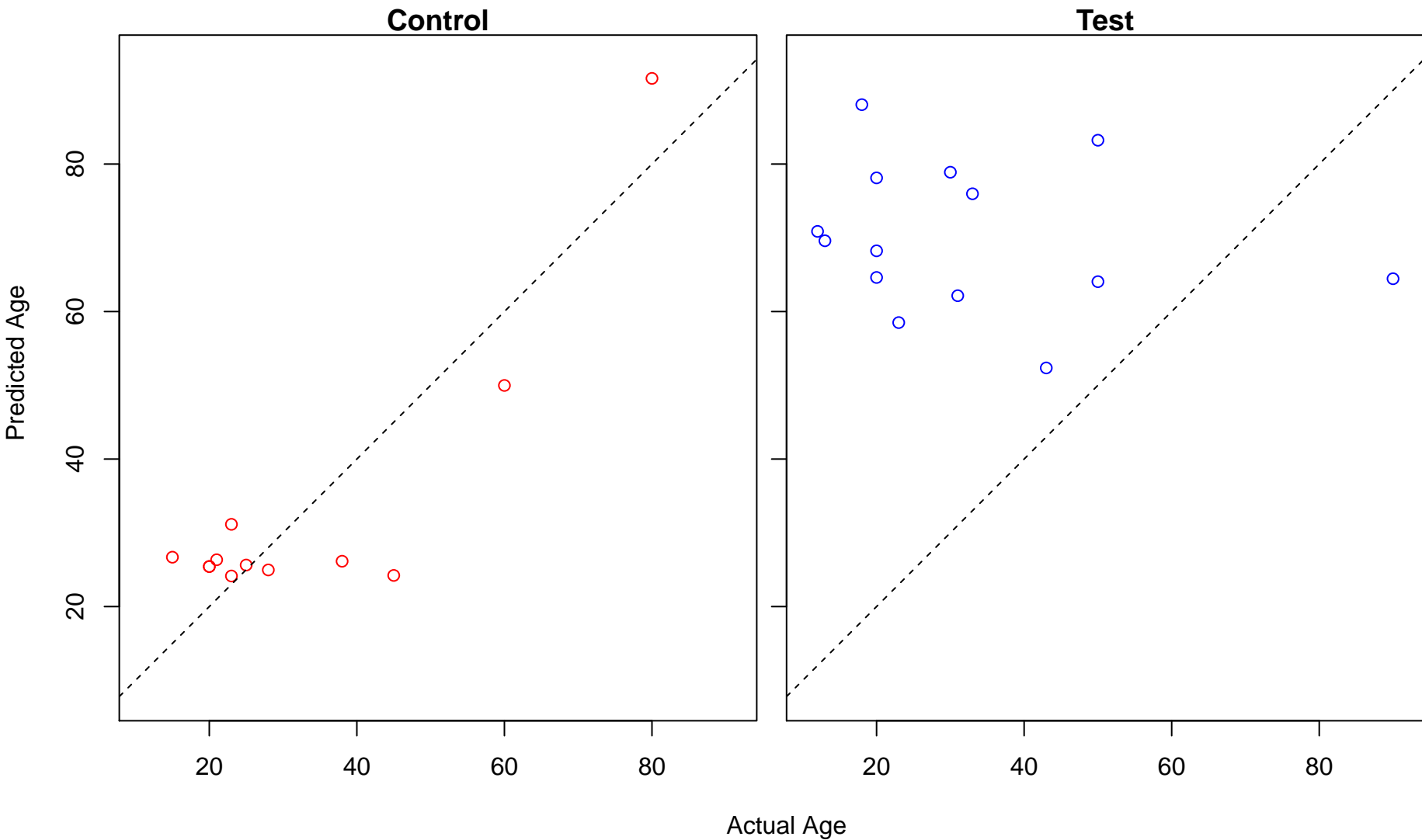
cytokine-mediated signaling pathway (Score: 8.387546)



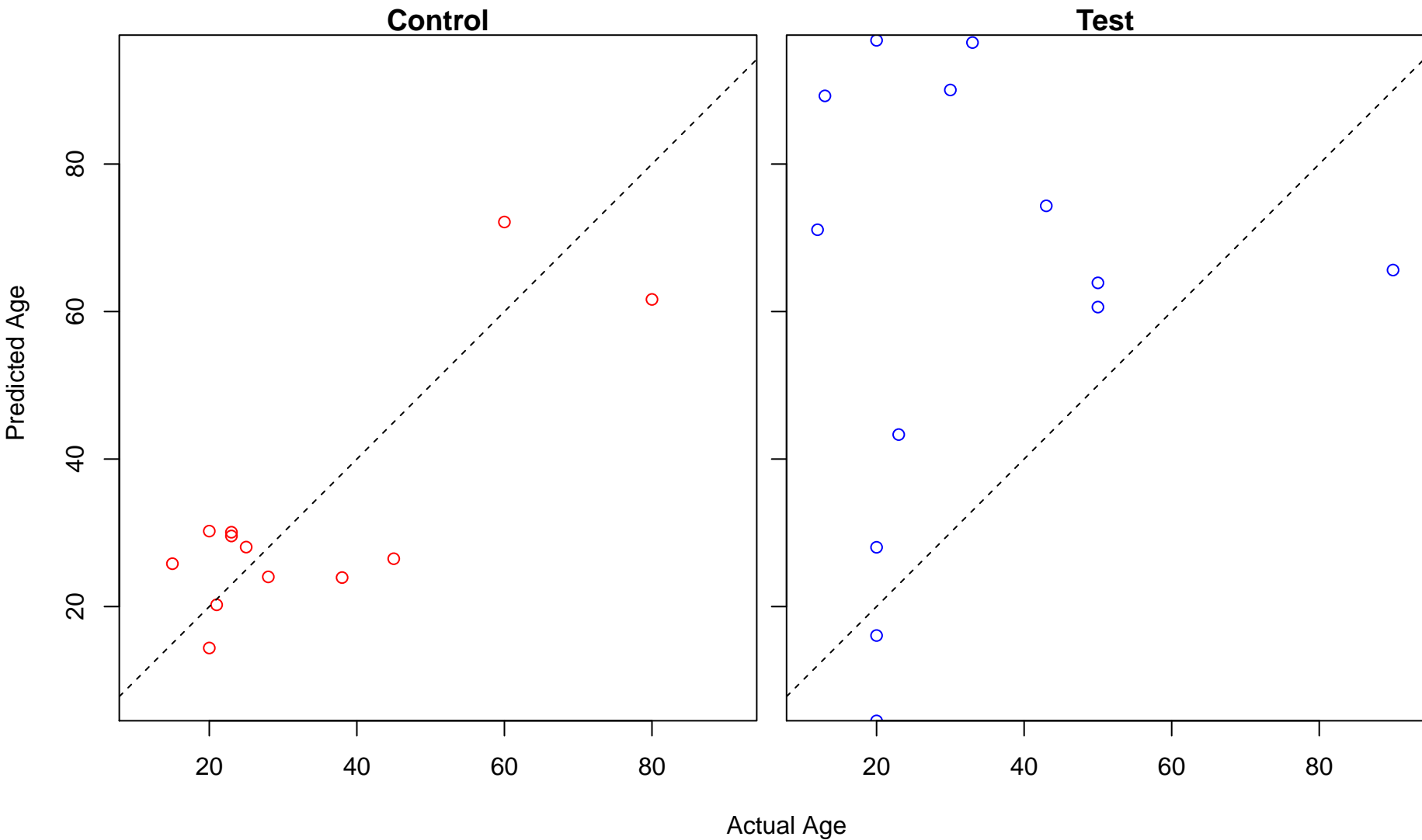
regulation of platelet activation (Score: 8.386890)



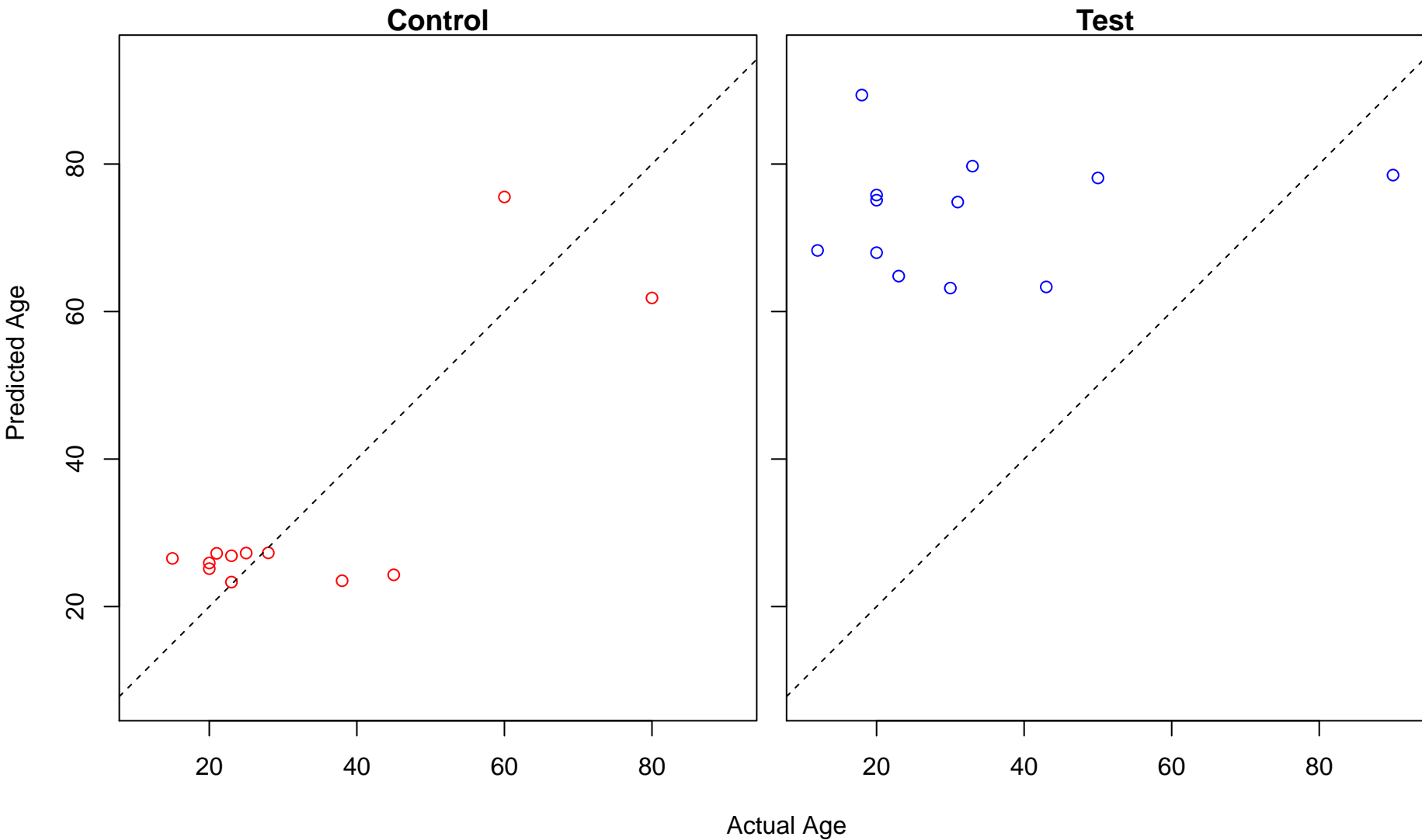
regulation of telomerase activity (Score: 8.378774)



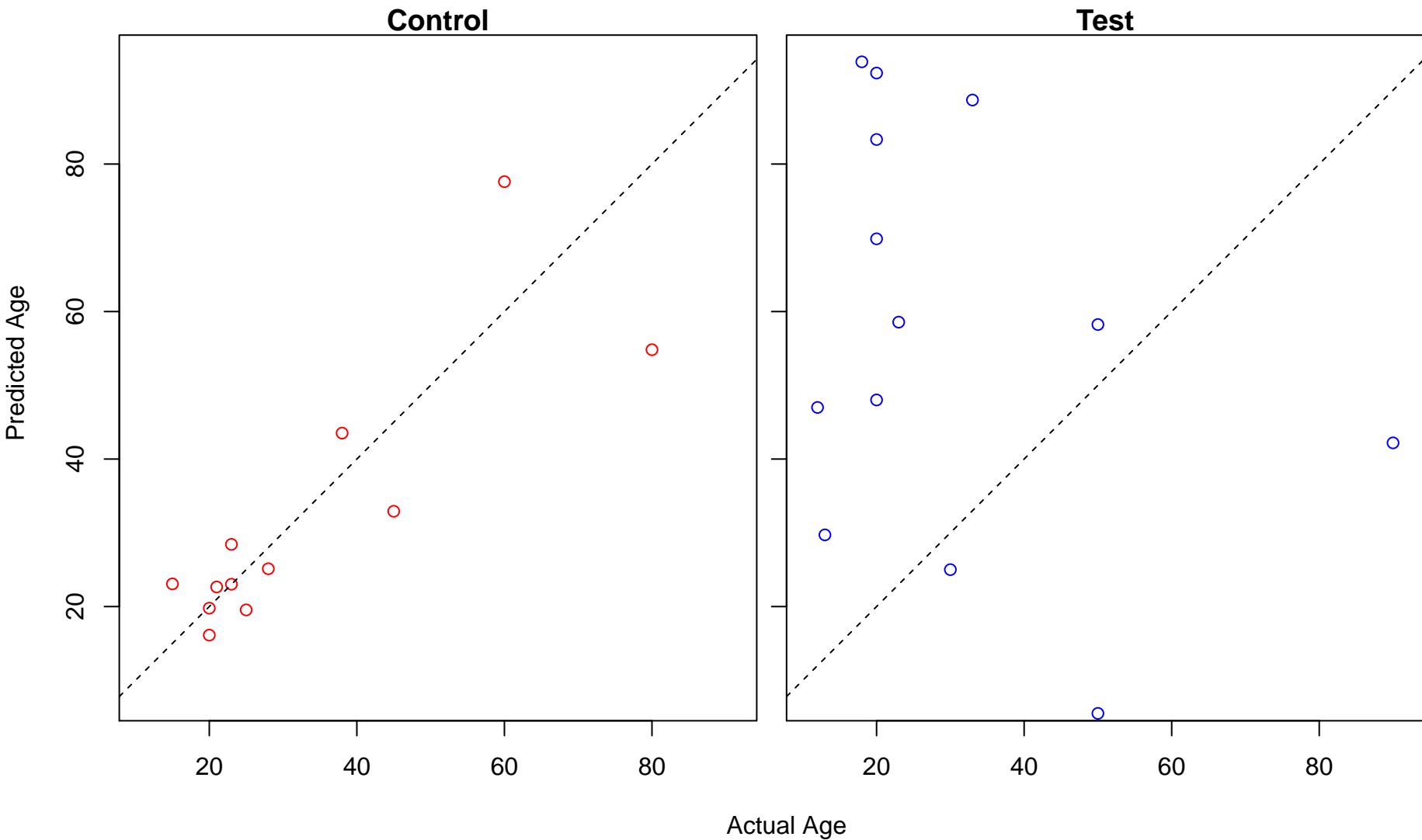
cGMP-mediated signaling (Score: 8.373920)



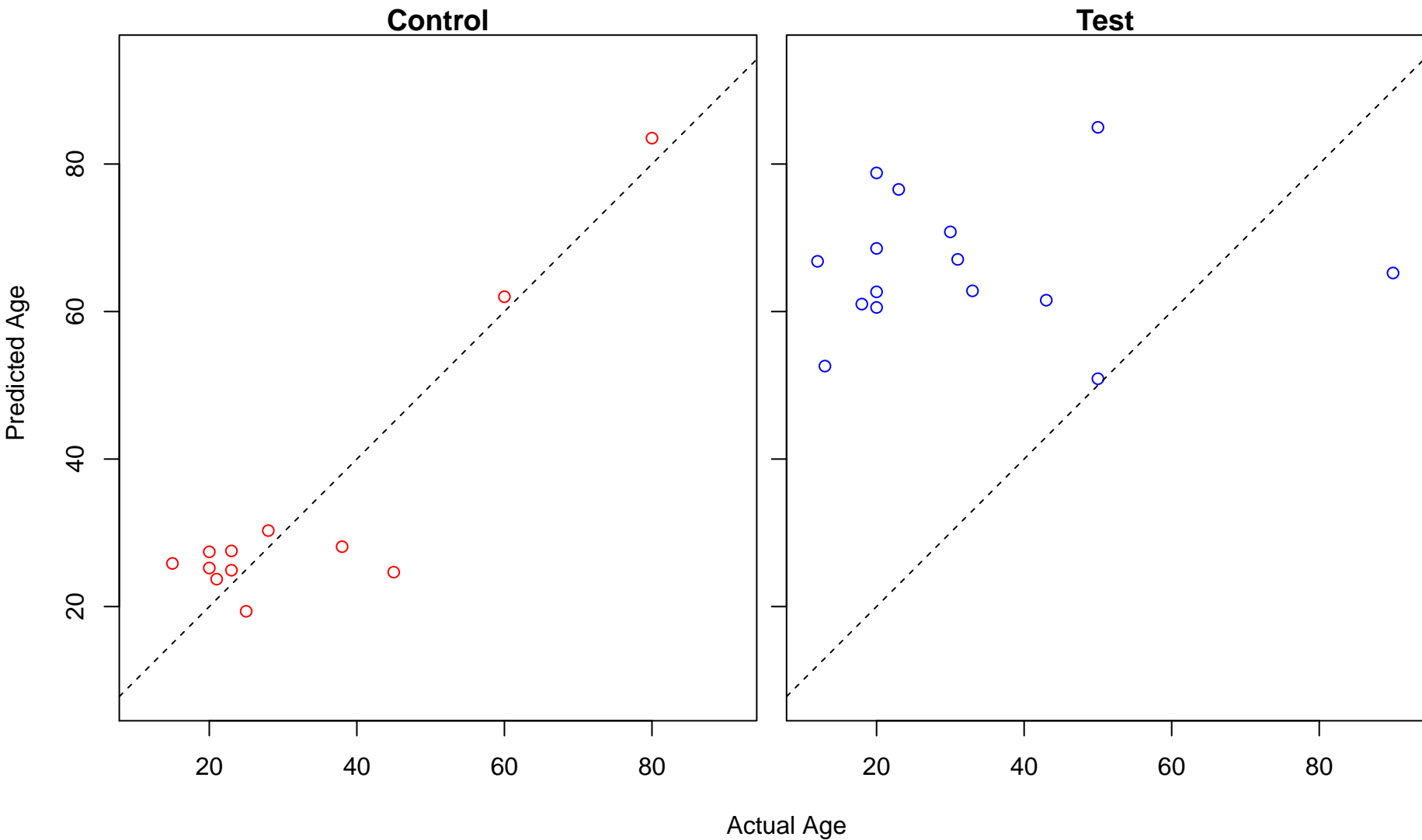
response to virus (Score: 8.373298)



bone morphogenesis (Score: 8.349248)

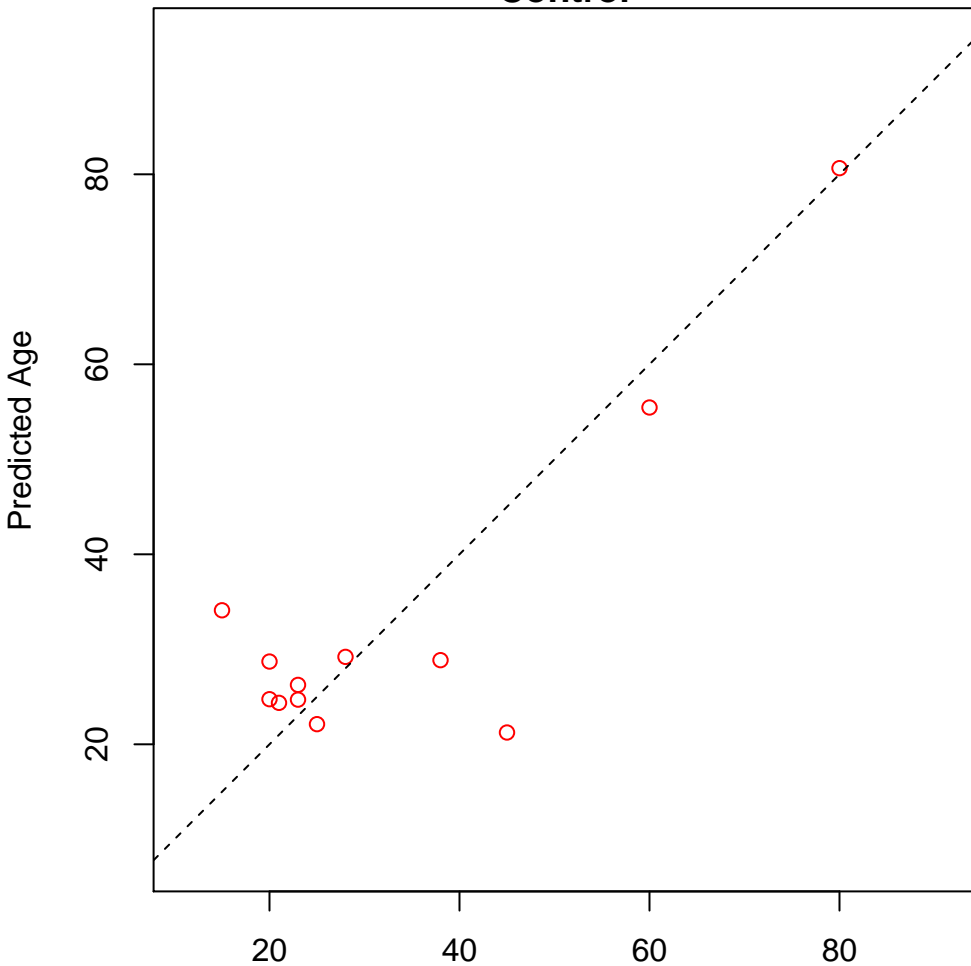


dorsal/ventral axis specification (Score: 8.346712)

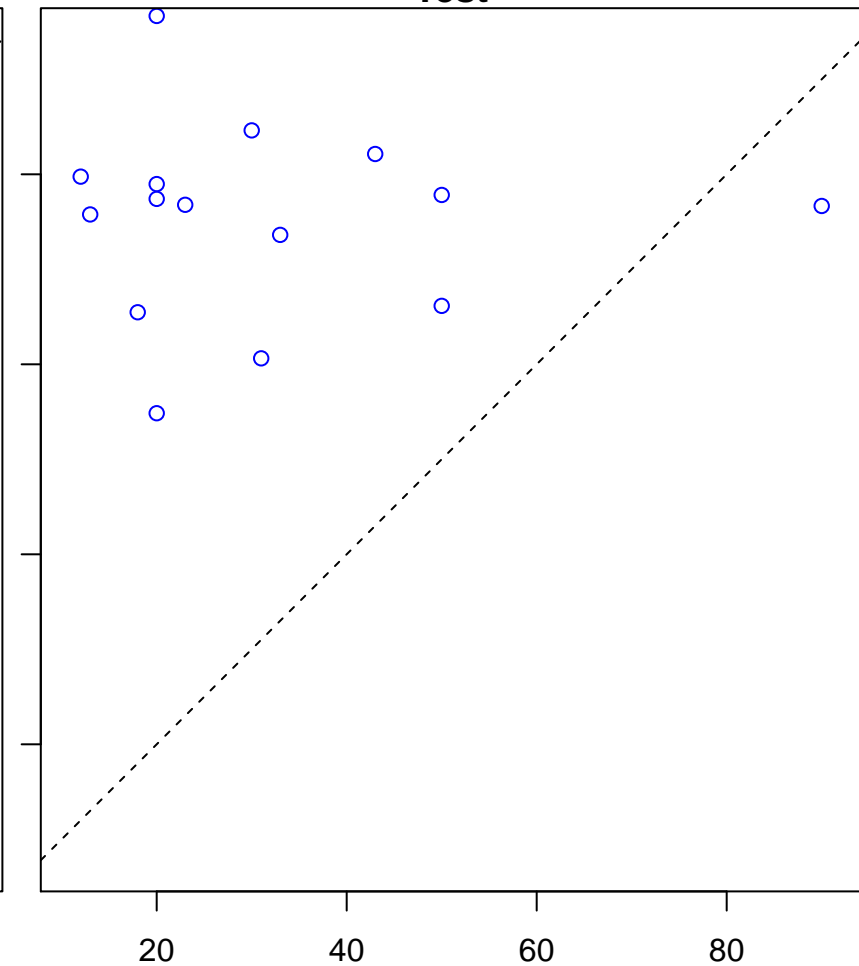


regulation of fatty acid beta-oxidation (Score: 8.341909)

Control

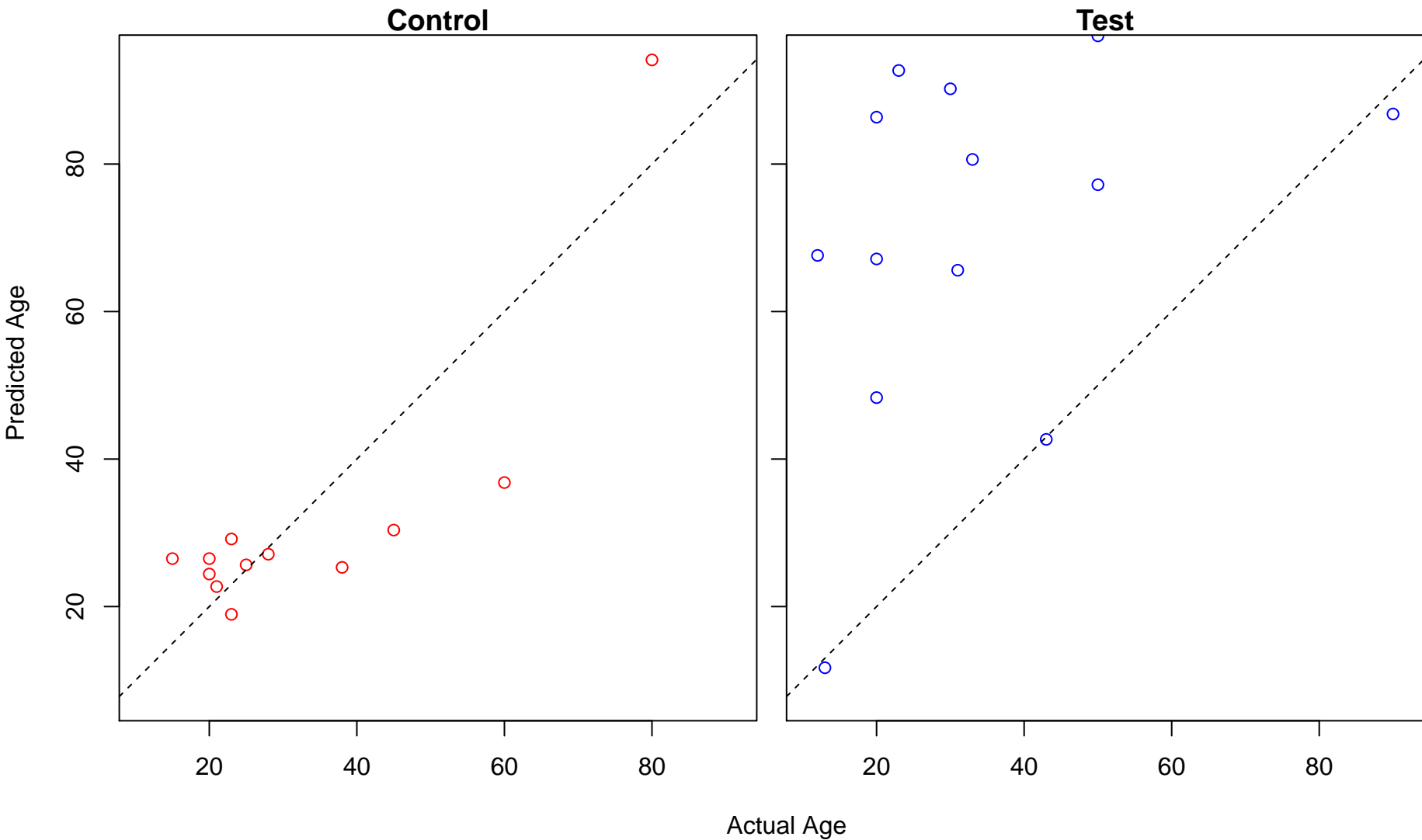


Test

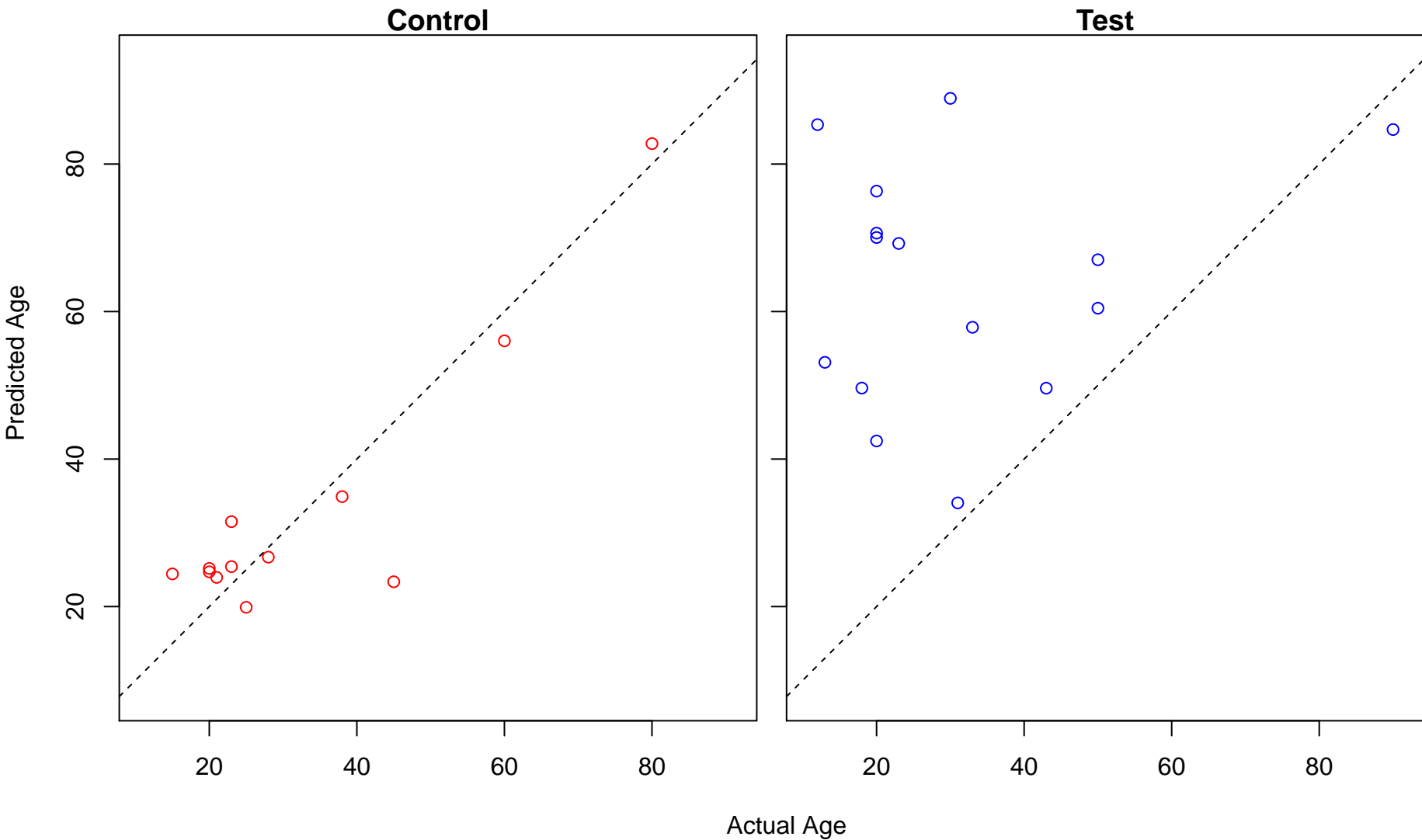


Actual Age

positive regulation of neurotransmitter transport (Score: 8.340658)

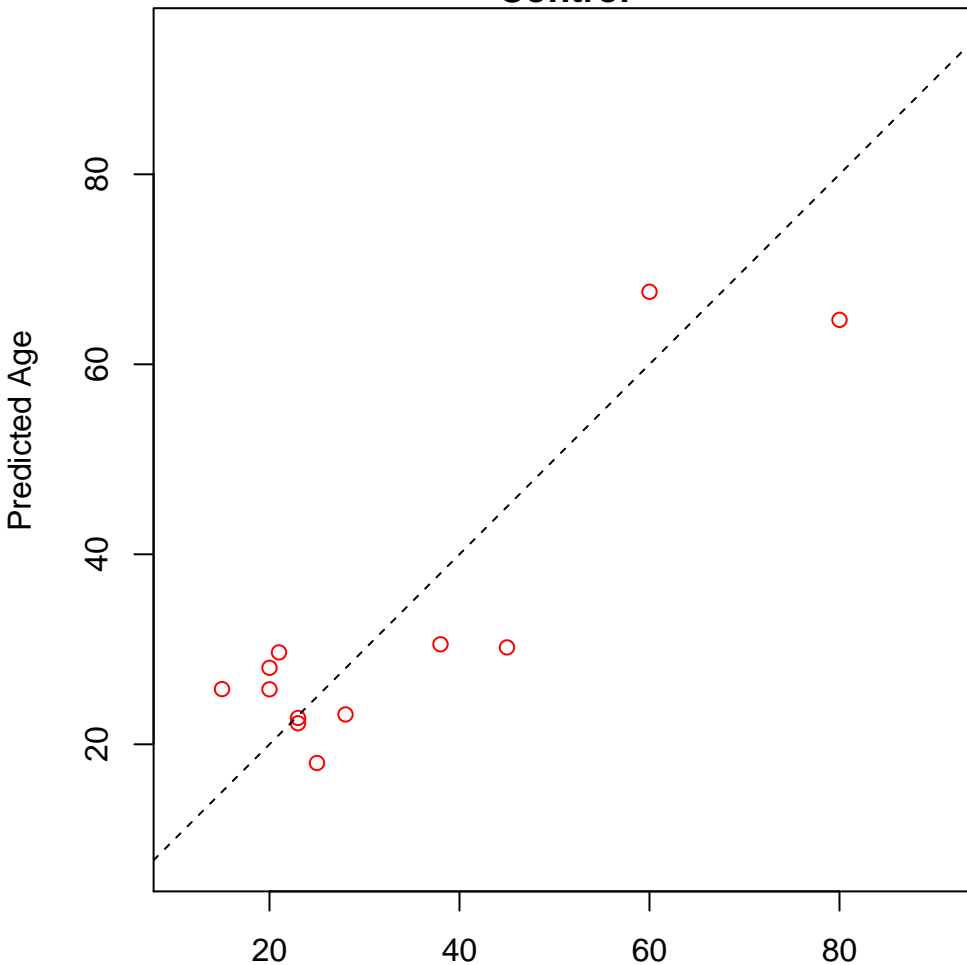


forebrain generation of neurons (Score: 8.334752)

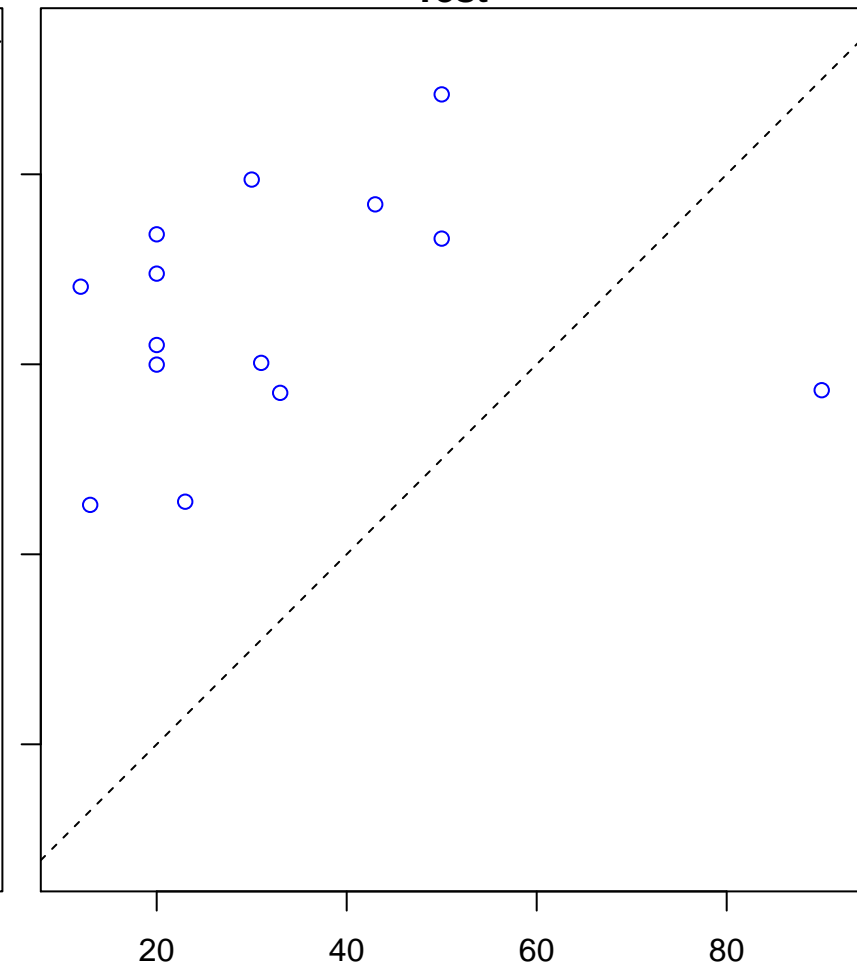


sensory perception of light stimulus (Score: 8.333910)

Control

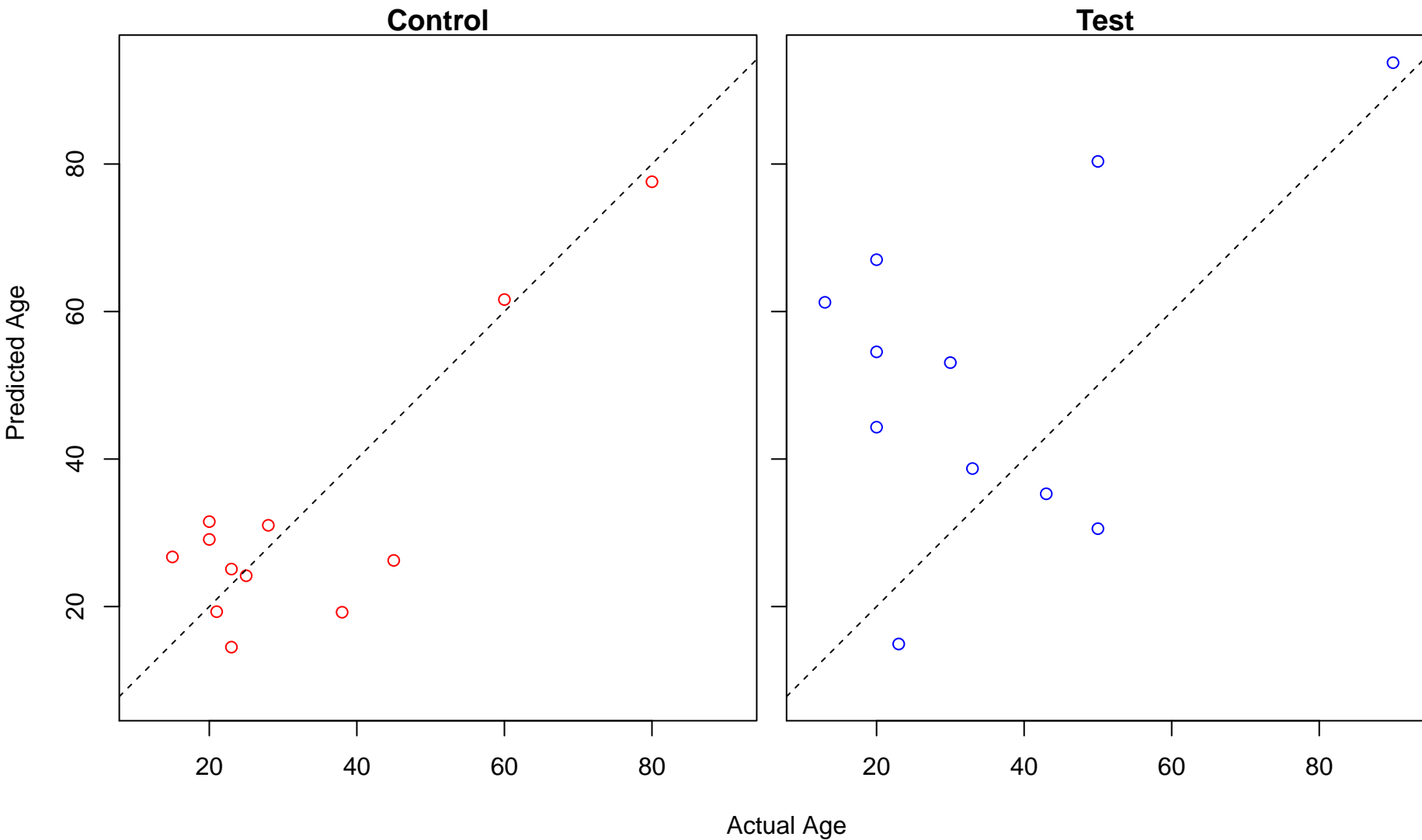


Test

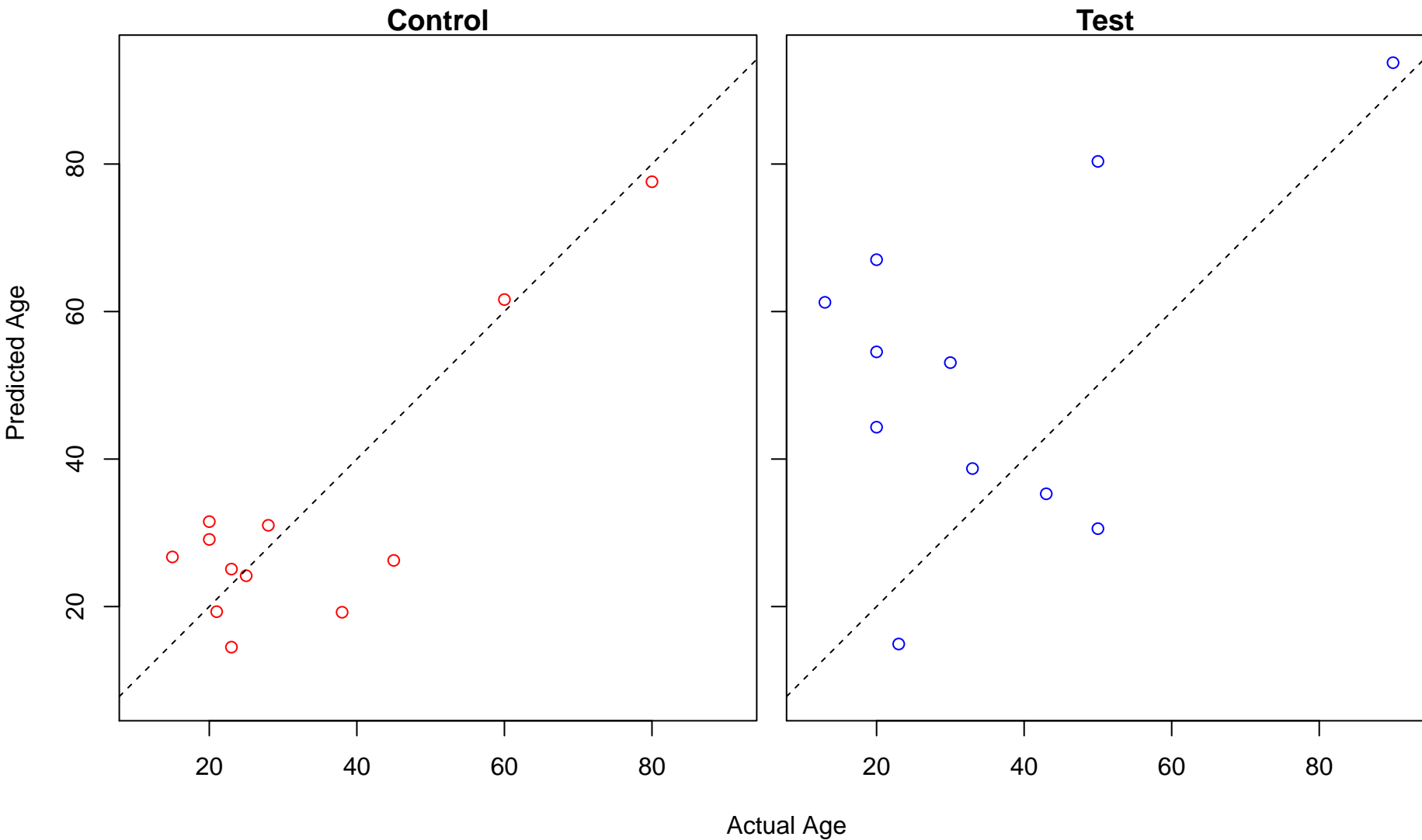


Actual Age

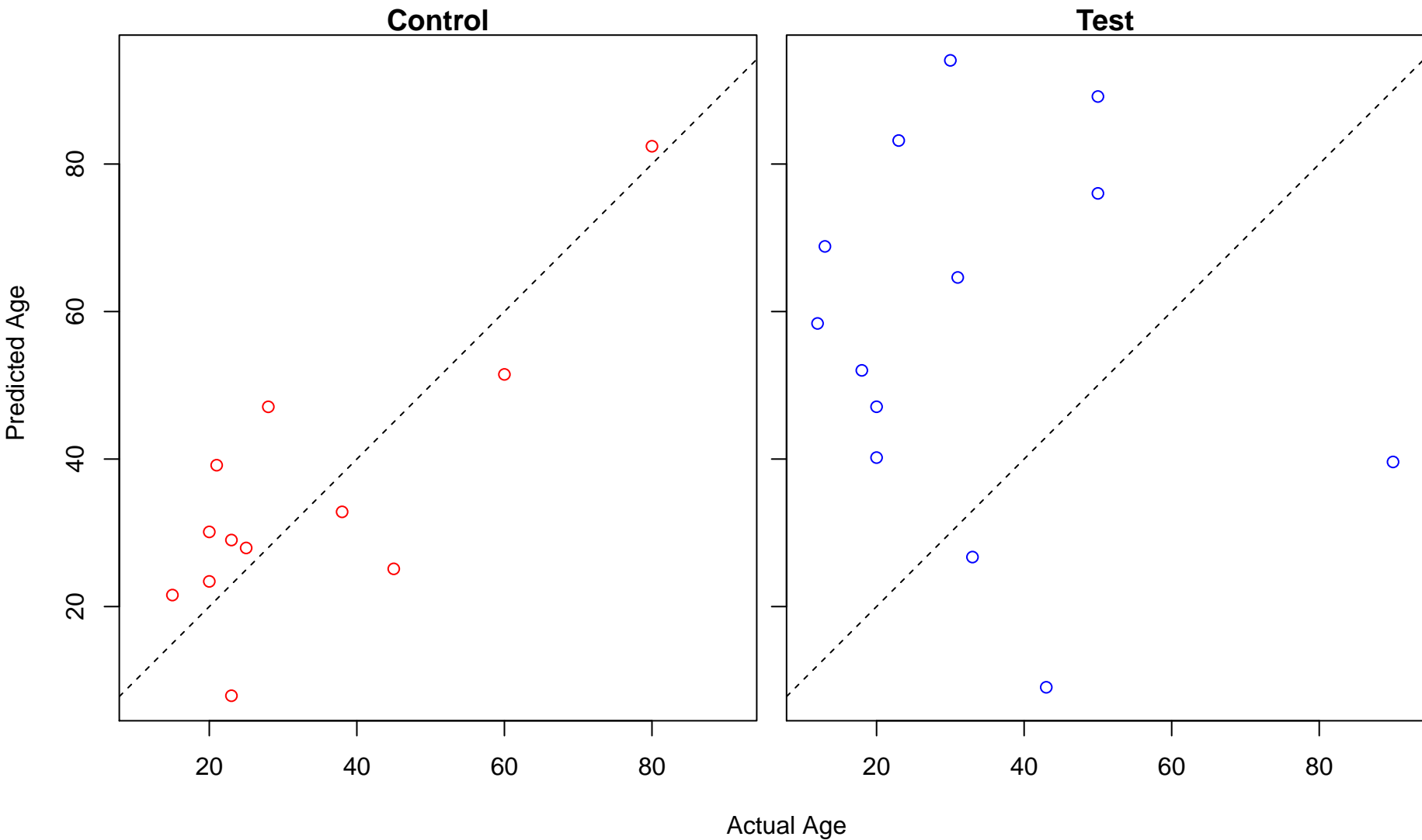
transcription elongation from RNA polymerase III promoter (Score: 8.333721)



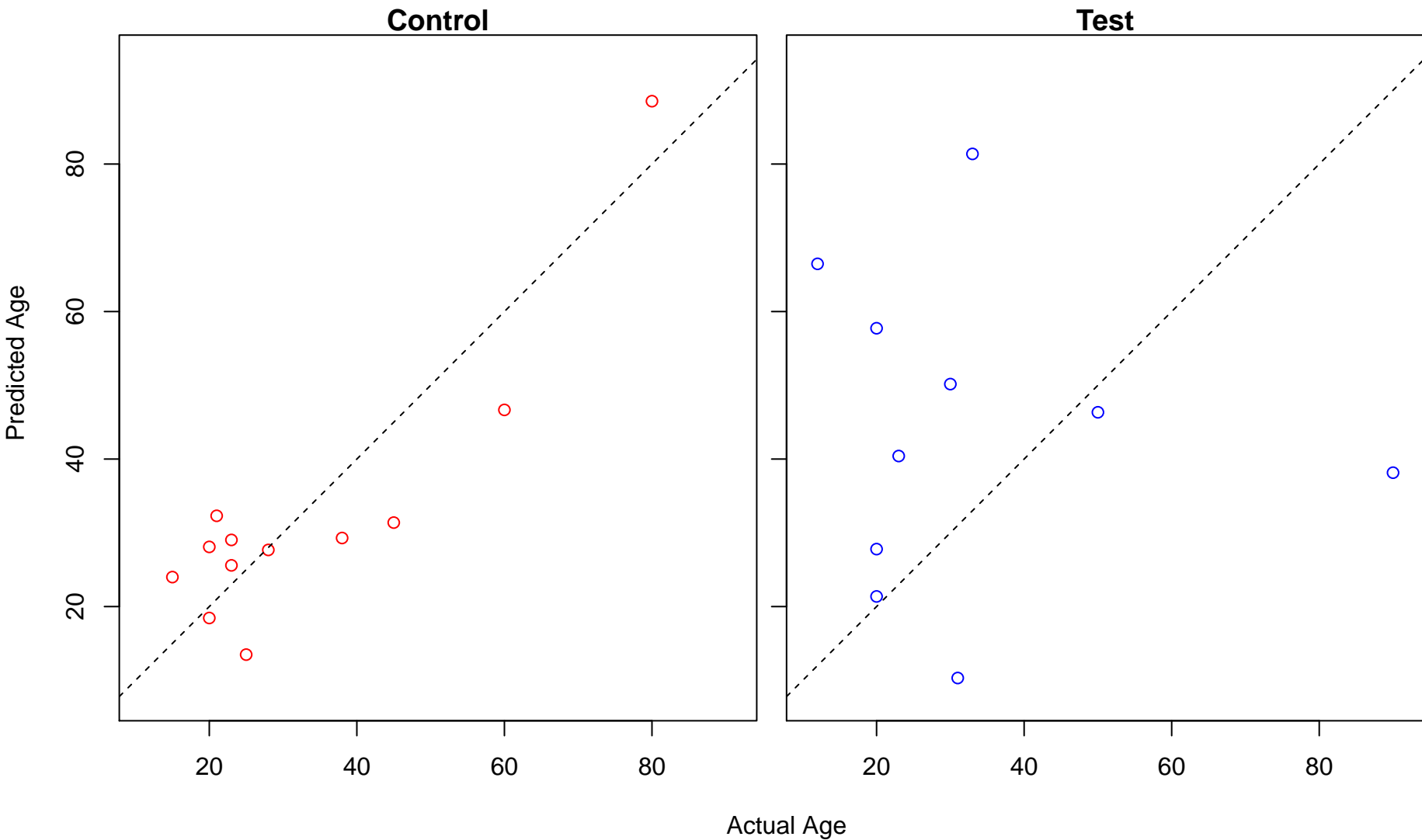
termination of RNA polymerase III transcription (Score: 8.333721)



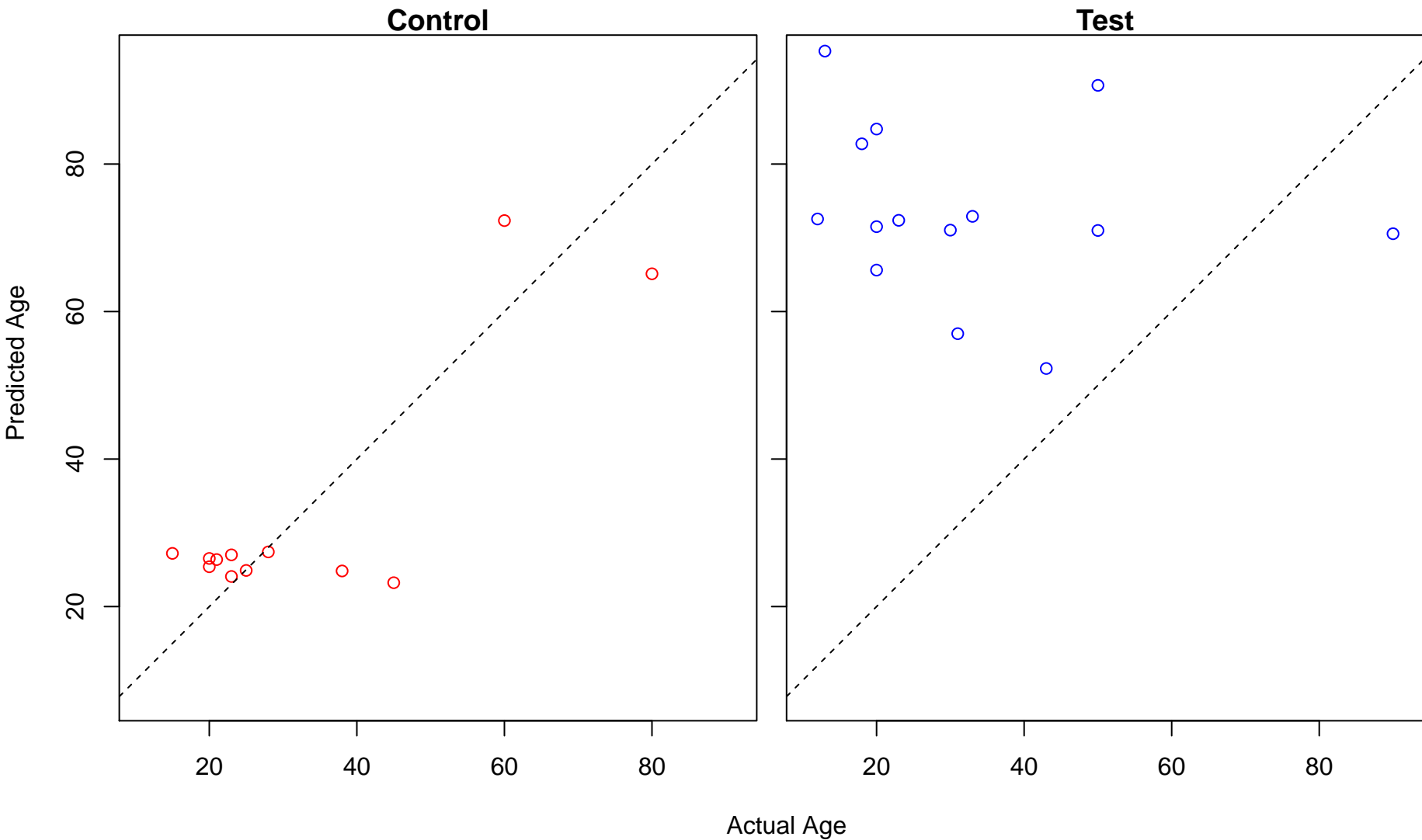
negative regulation of mitochondrion organization (Score: 8.33183)



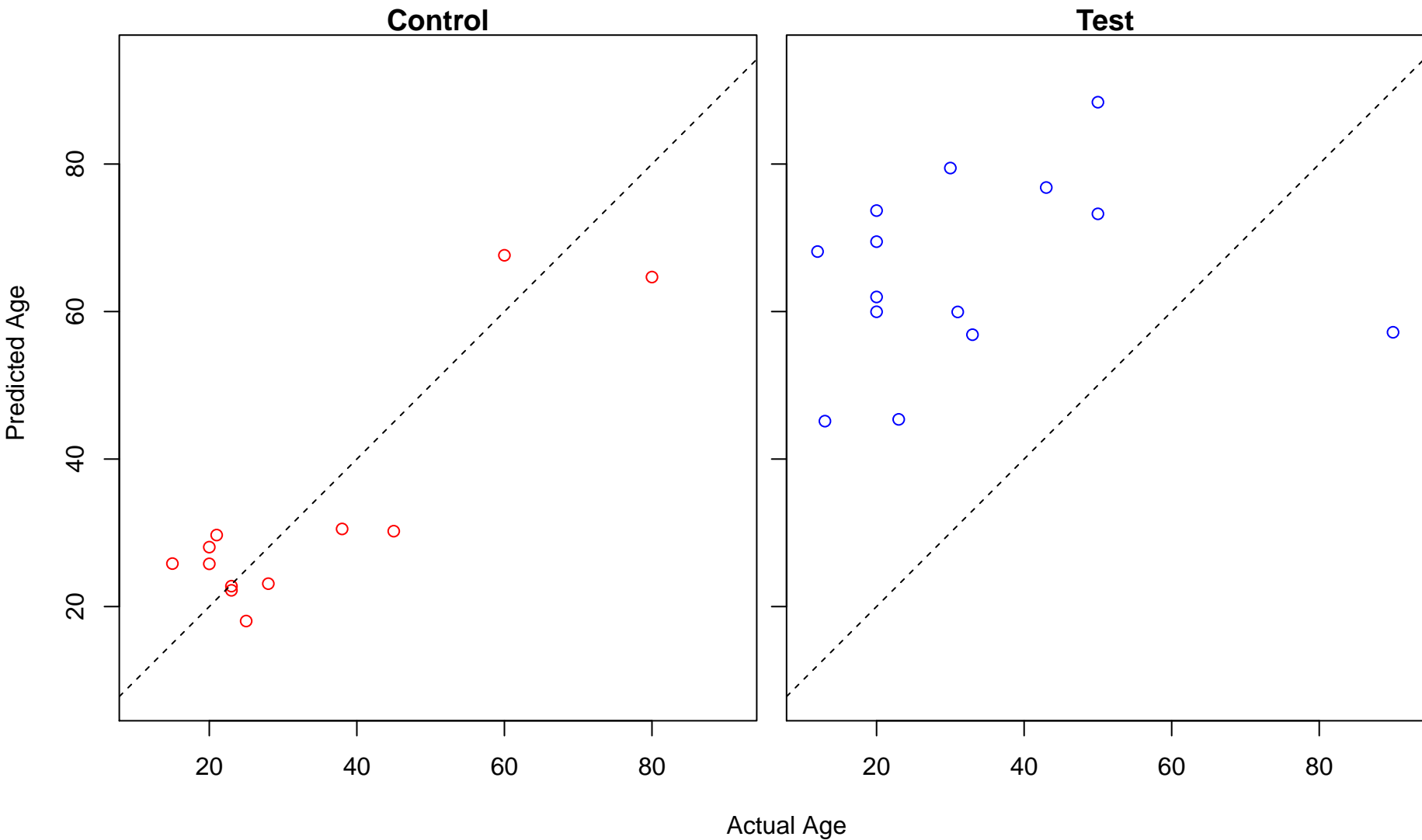
organophosphate ester transport (Score: 8.325892)



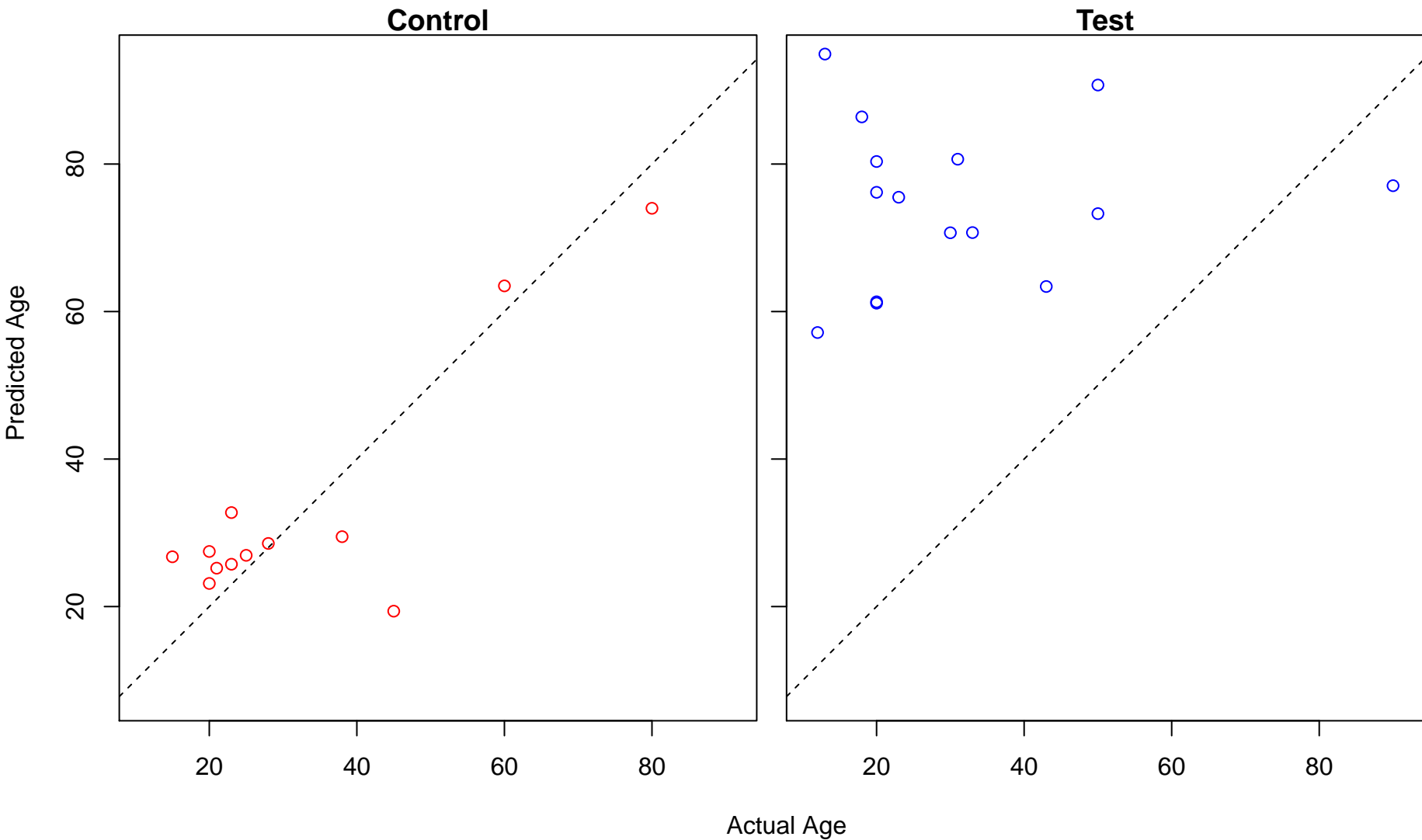
RNA-dependent DNA replication (Score: 8.323081)



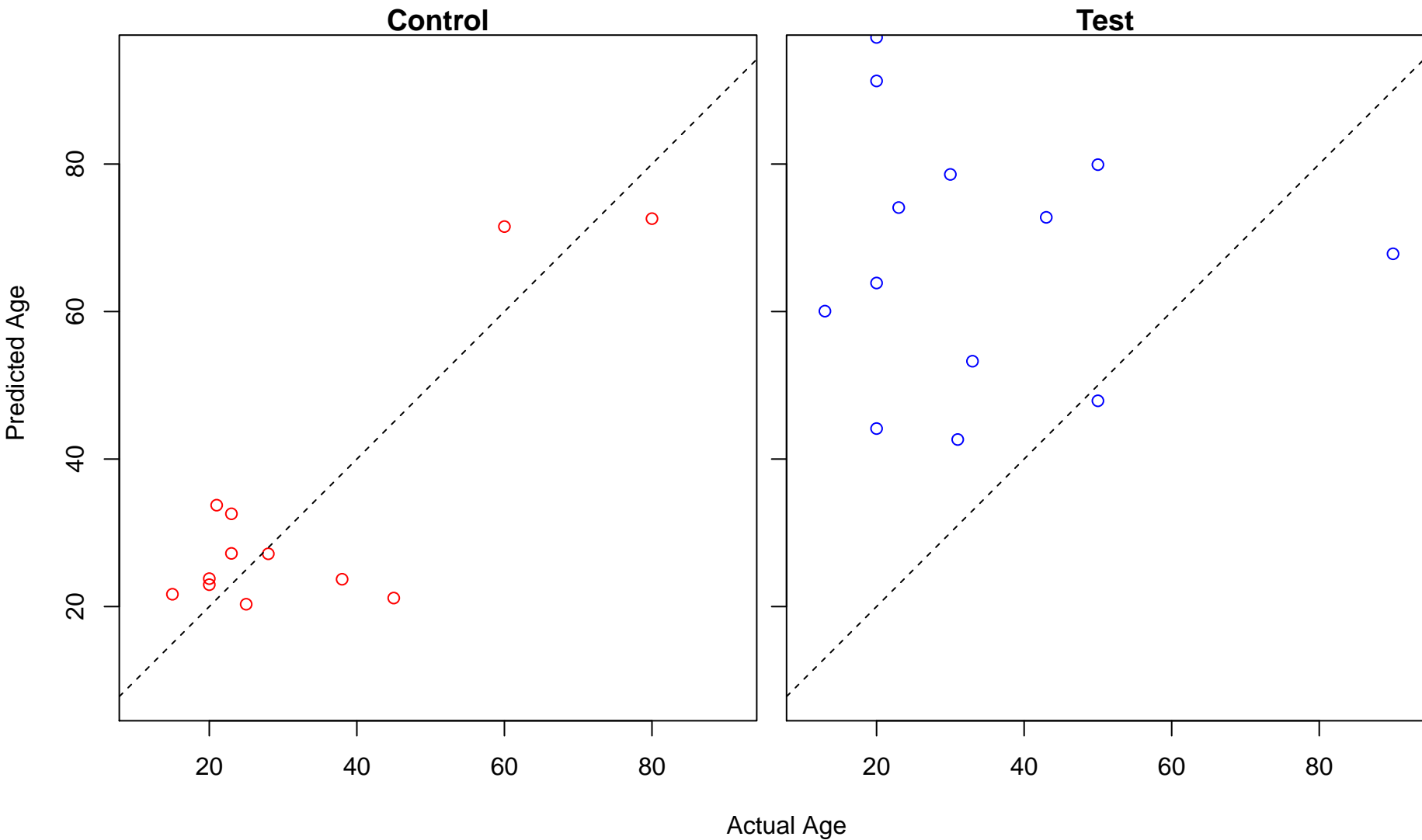
visual perception (Score: 8.322135)



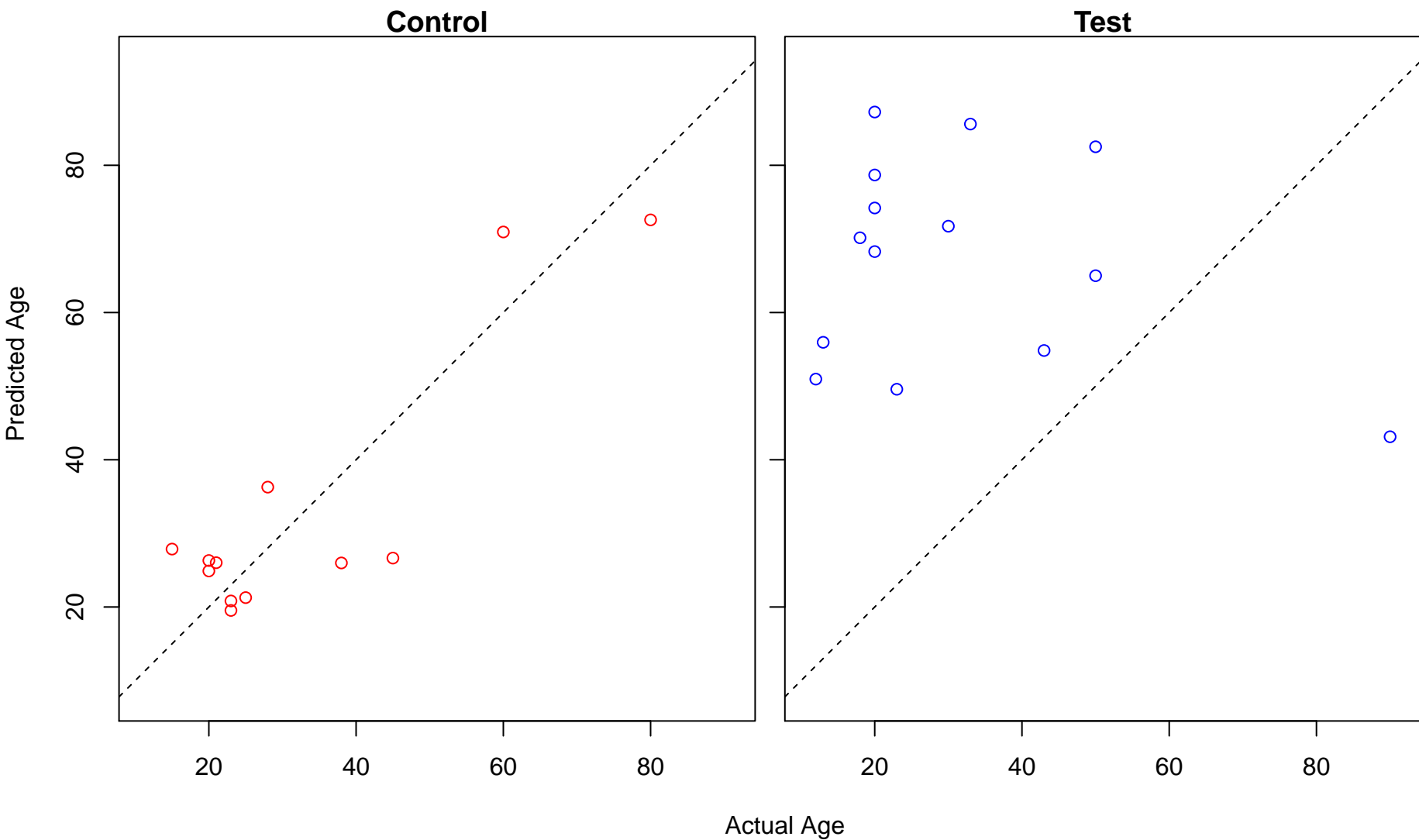
response to interferon-gamma (Score: 8.320078)



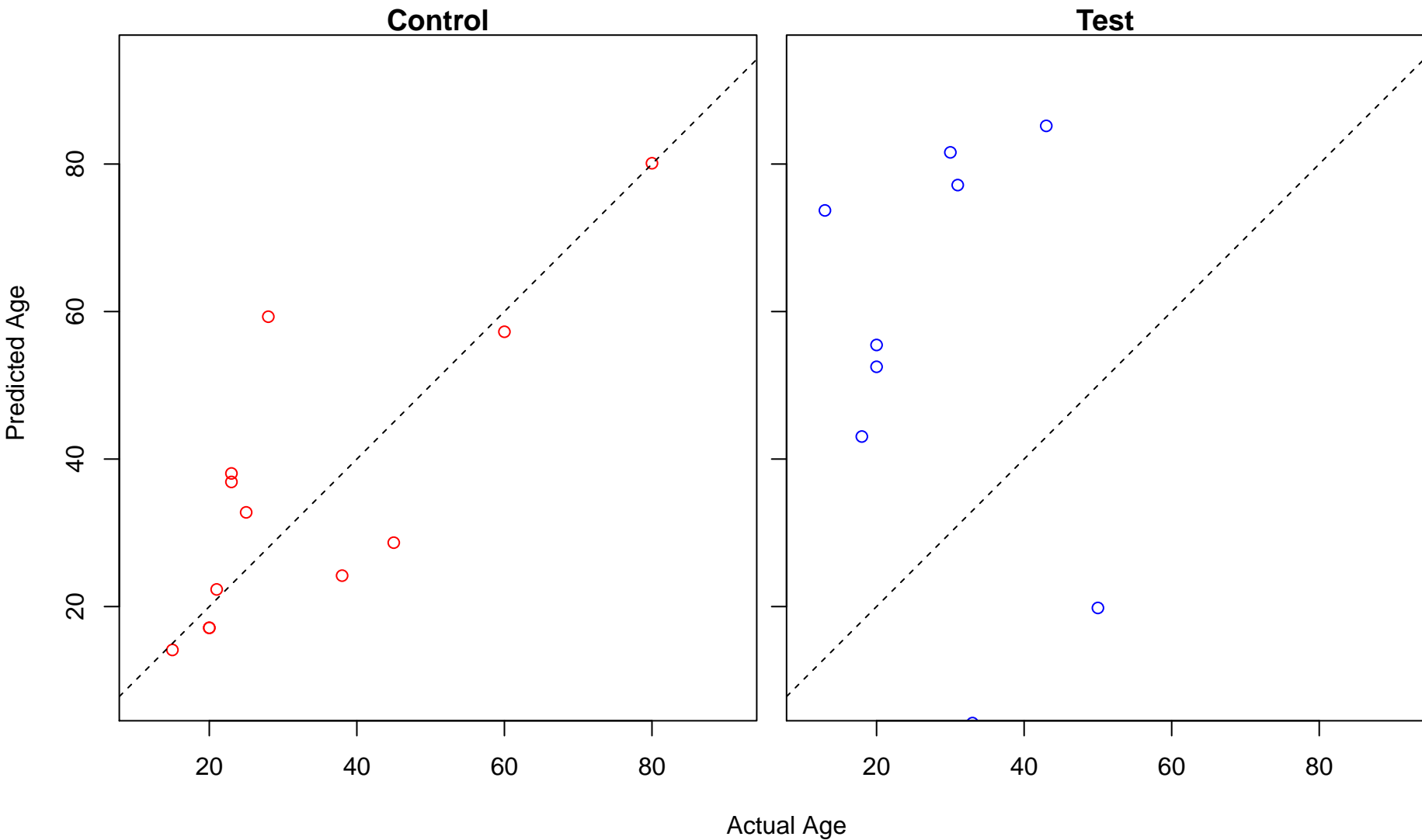
morphogenesis of an epithelial sheet (Score: 8.318587)



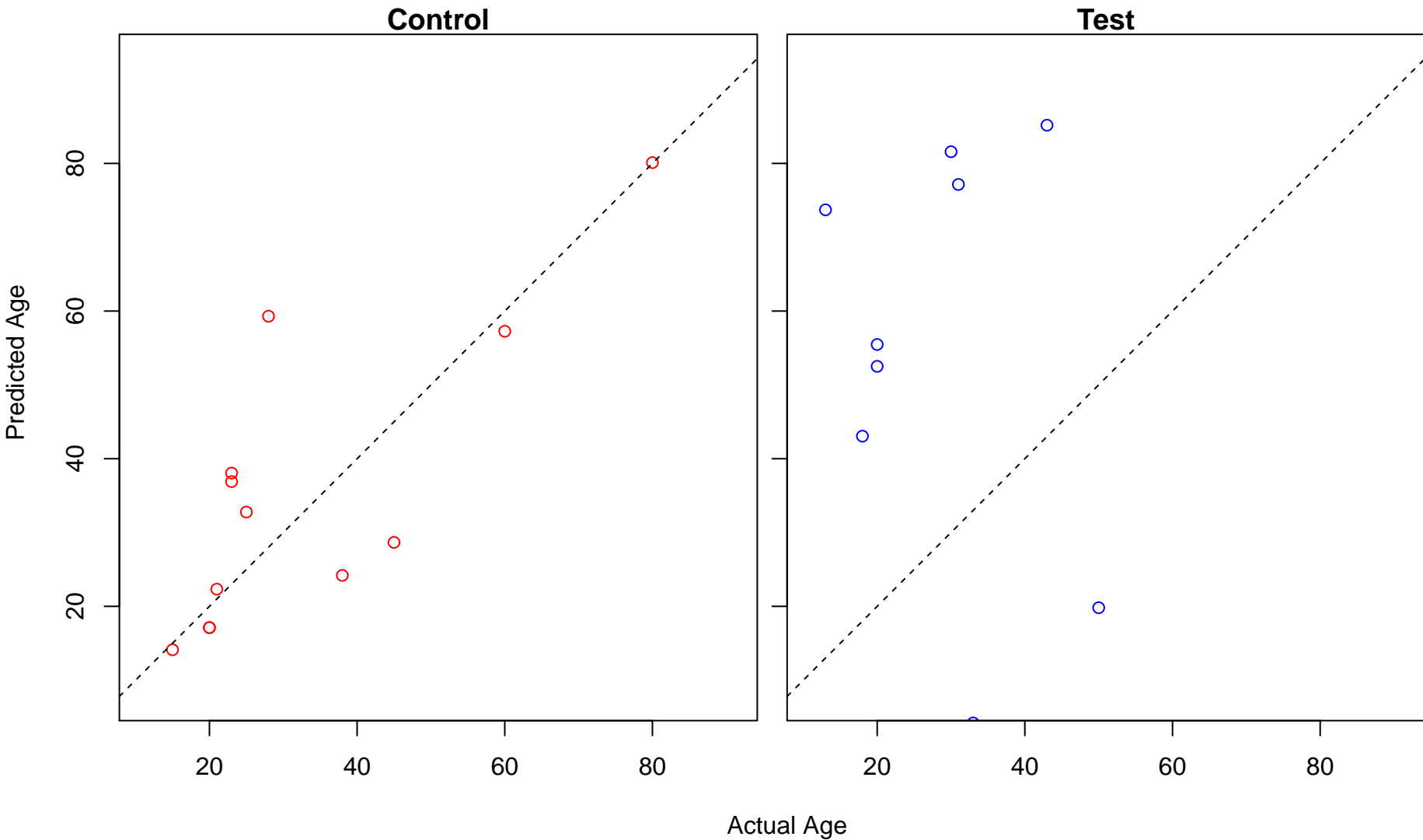
intracellular steroid hormone receptor signaling pathway (Score: 8.314587)



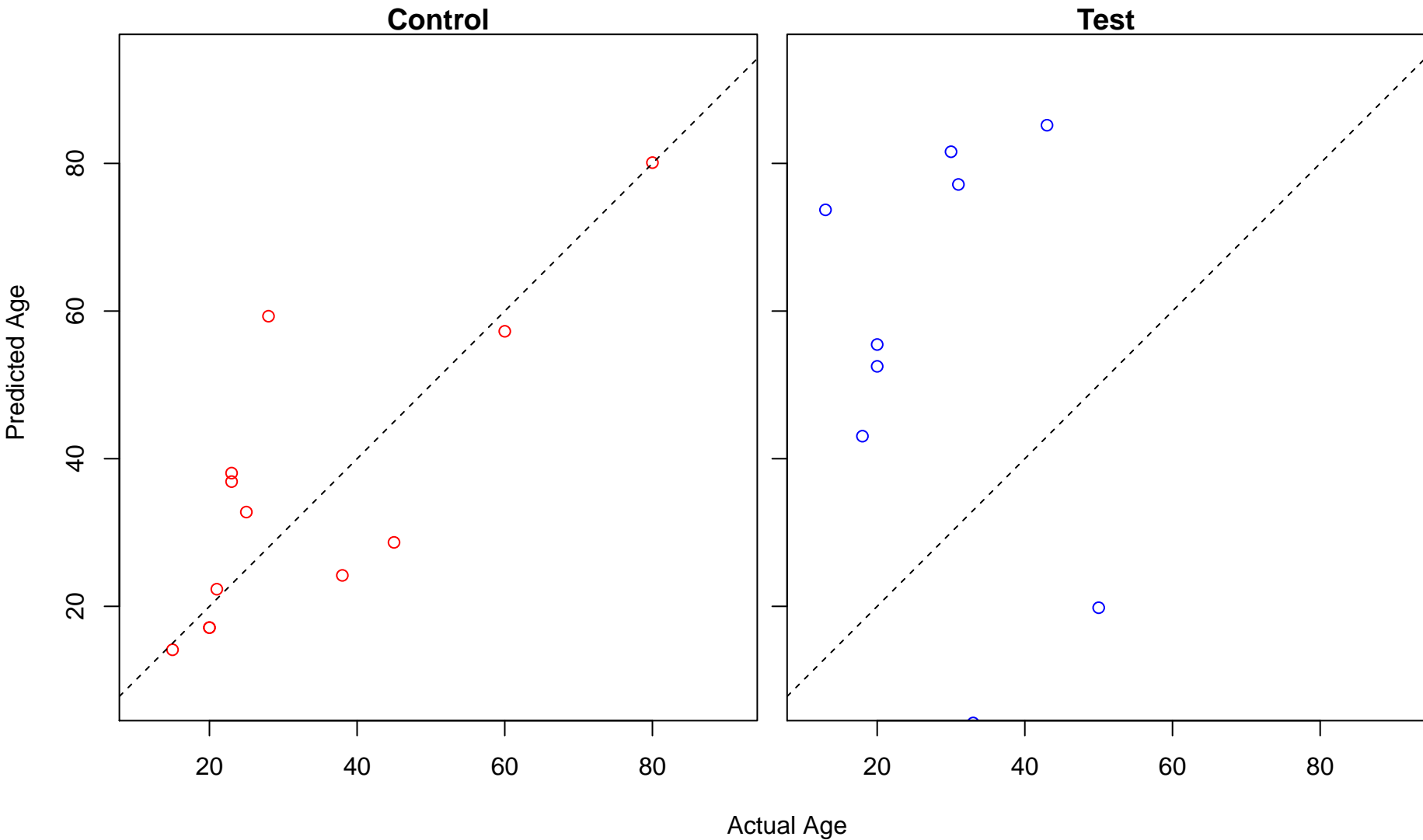
regulation of cilium movement involved in cell motility (Score: 8.312328)



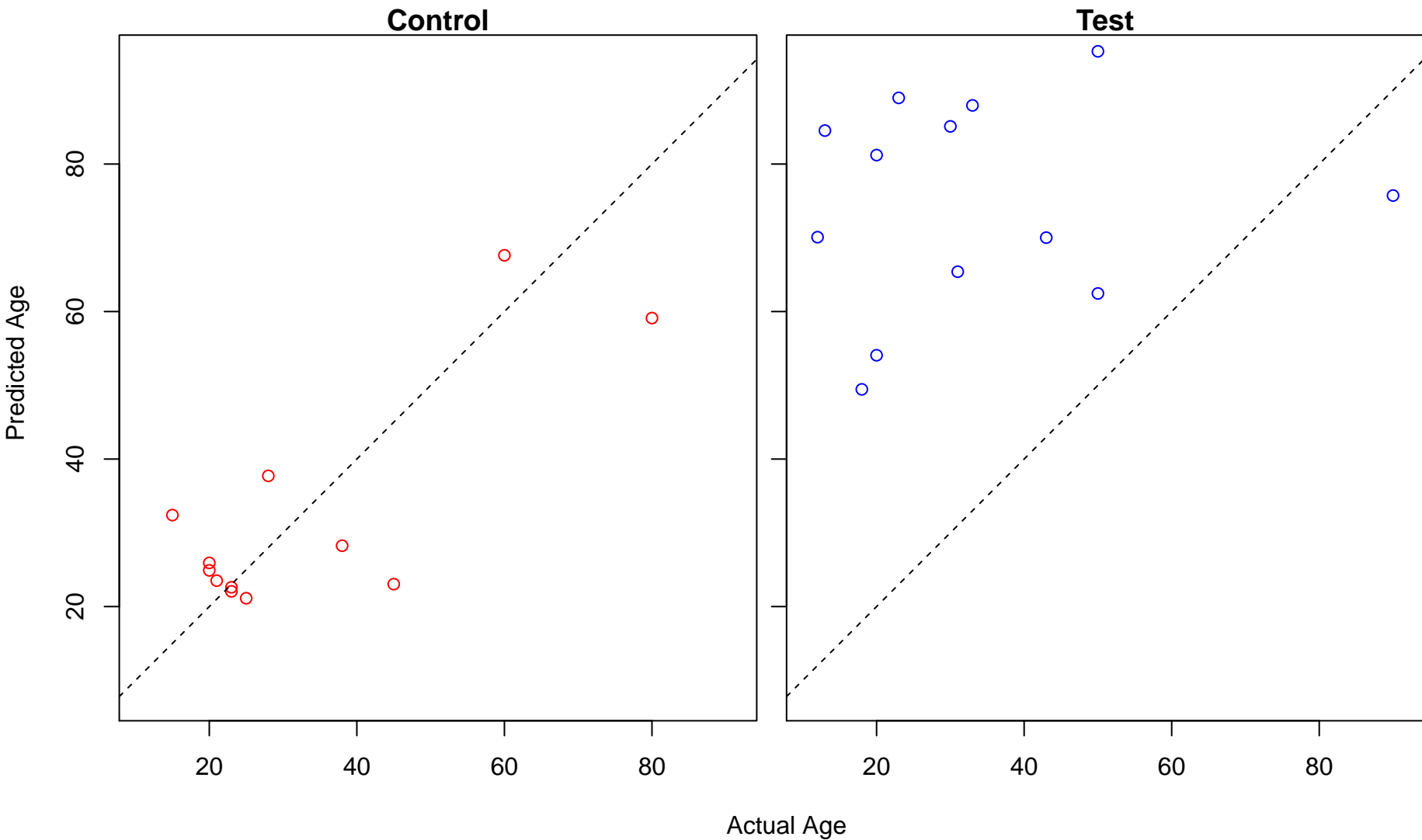
regulation of cilium beat frequency involved in ciliary motility (Score: 8.312328)



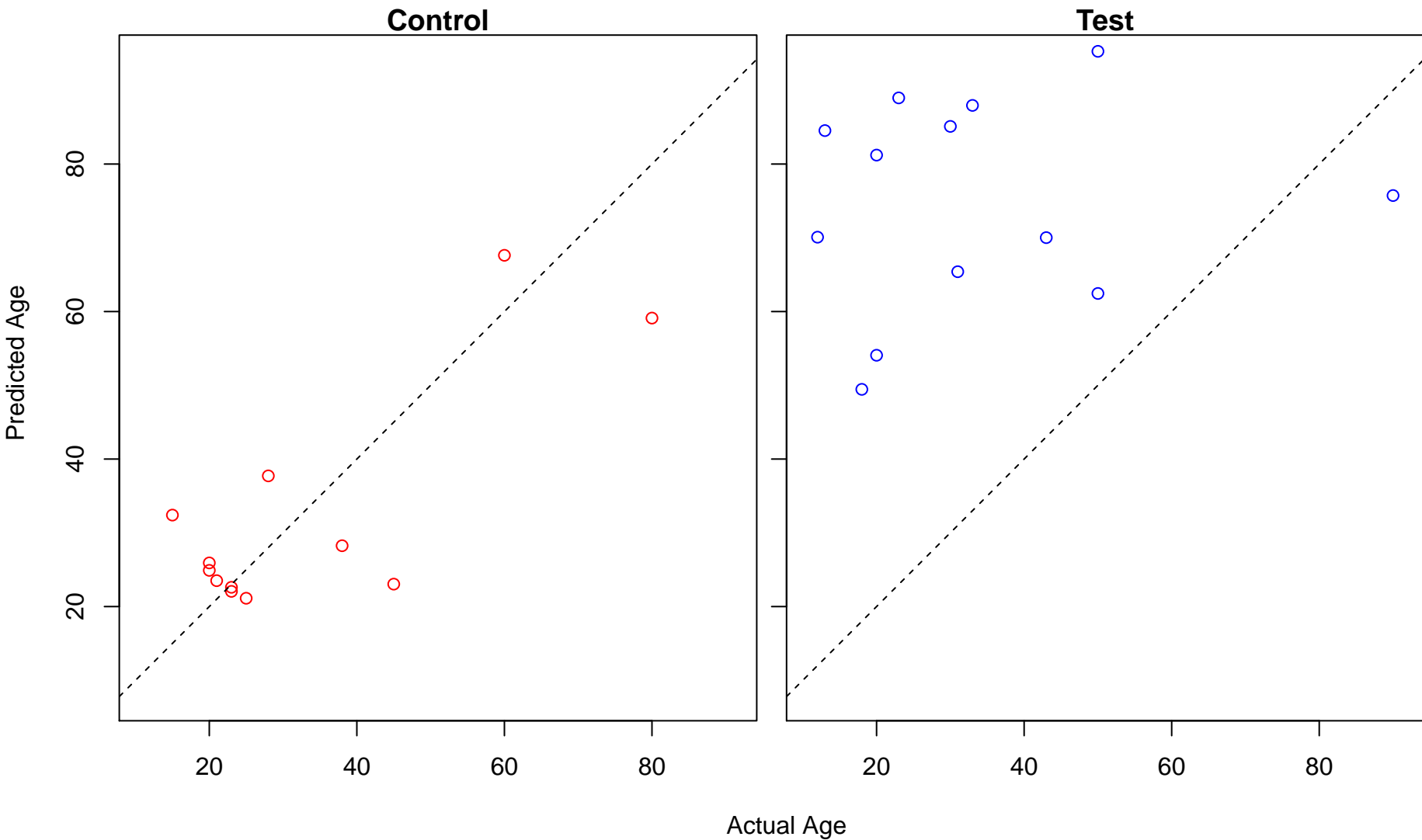
regulation of cilium-dependent cell motility (Score: 8.312328)



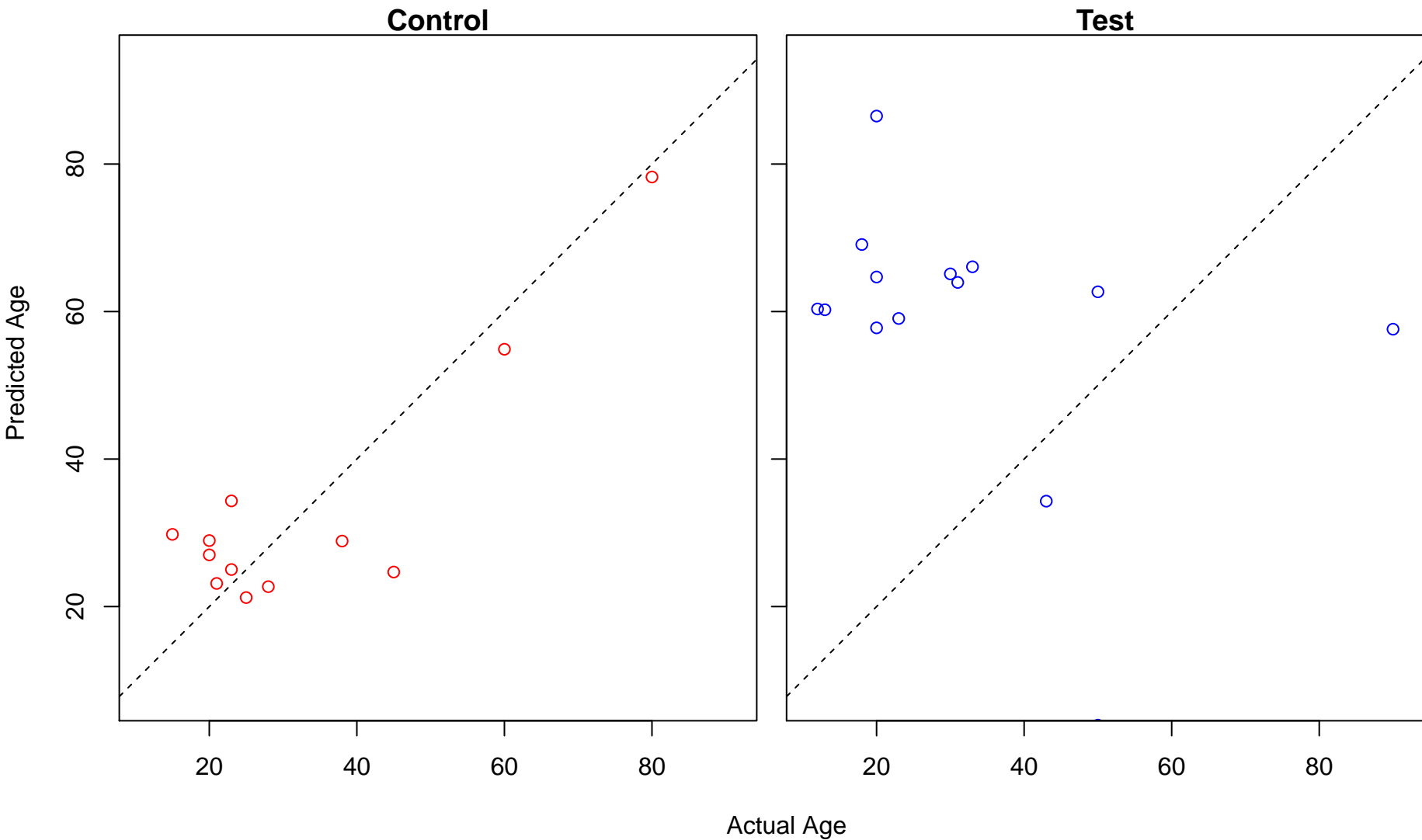
regulation of T cell differentiation in thymus (Score: 8.310059)



regulation of thymocyte aggregation (Score: 8.310059)

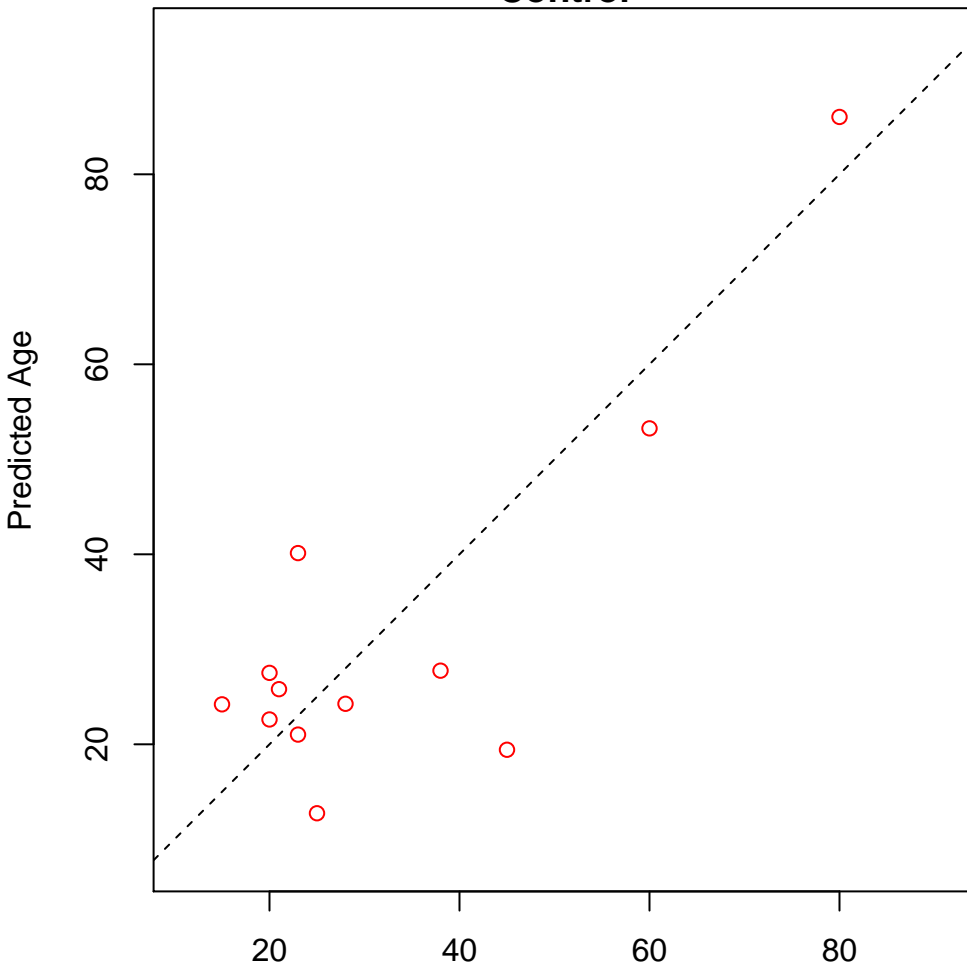


unsaturated fatty acid biosynthetic process (Score: 8.299465)

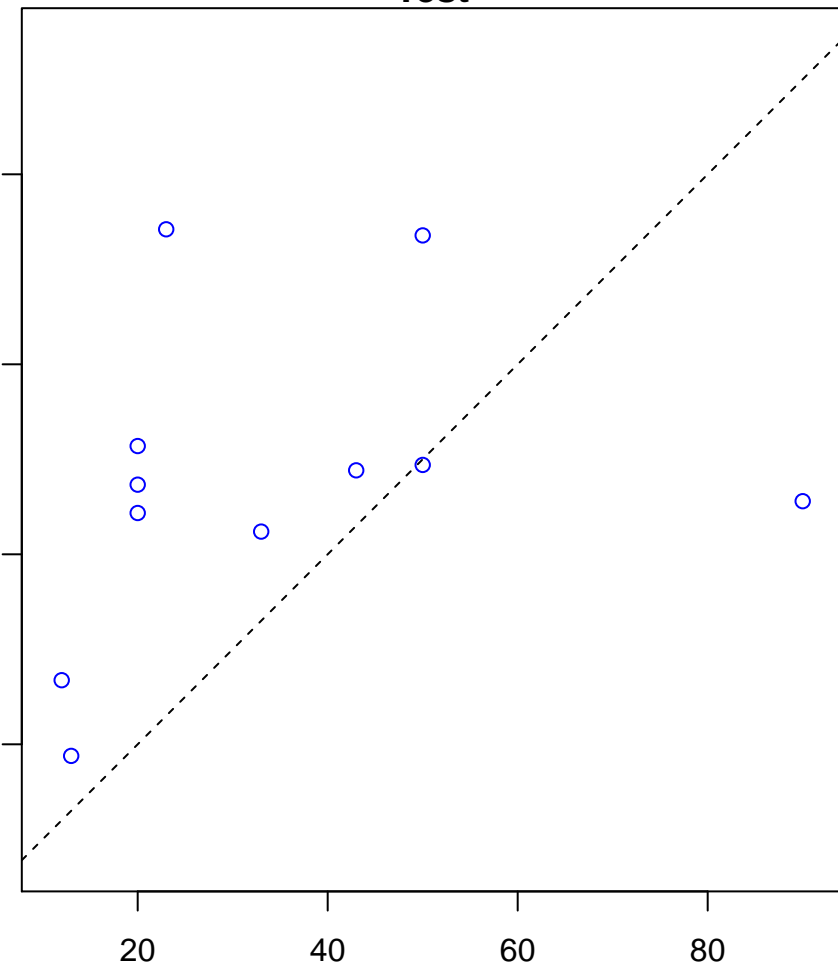


positive regulation of cell-cell adhesion (Score: 8.296905)

Control

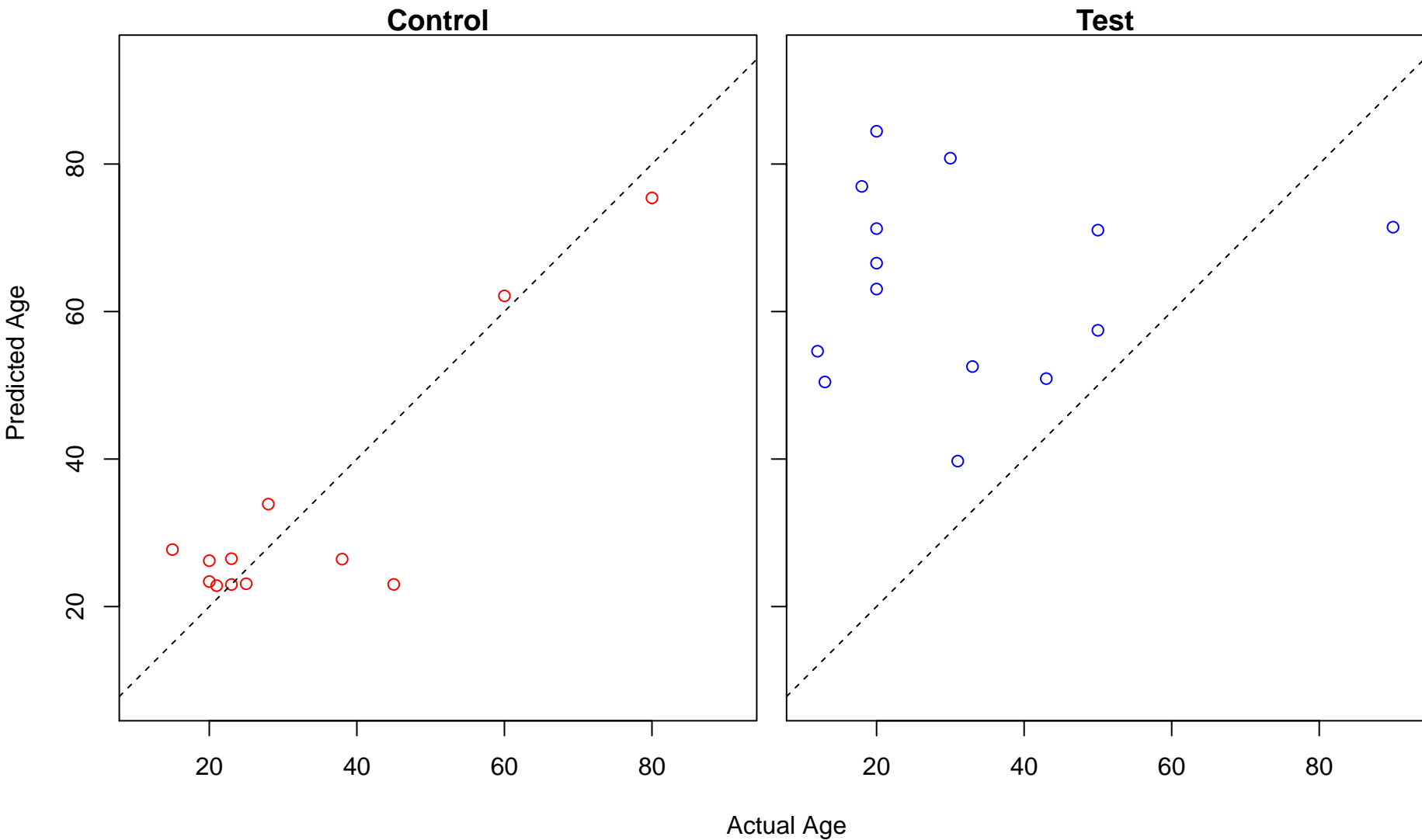


Test

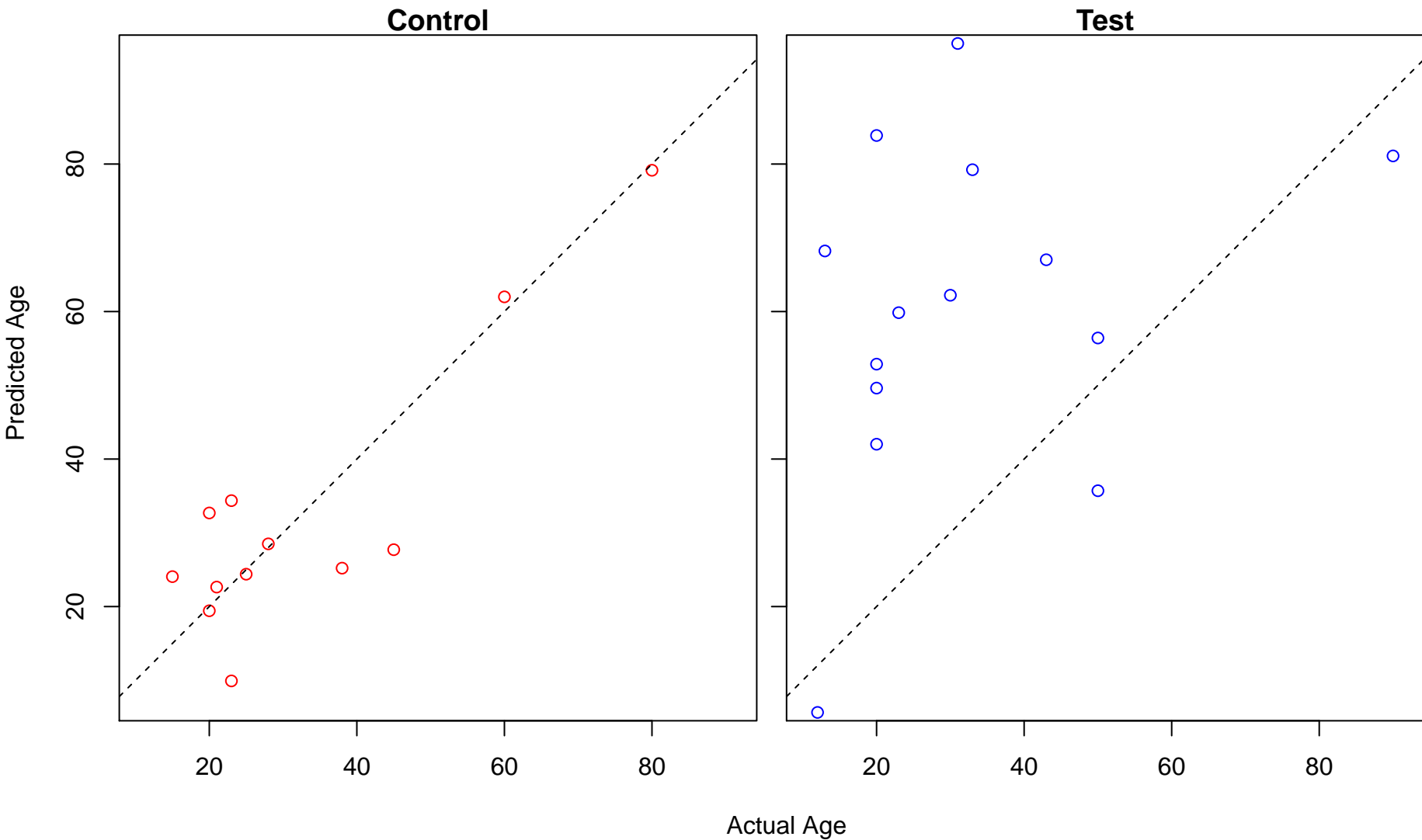


Actual Age

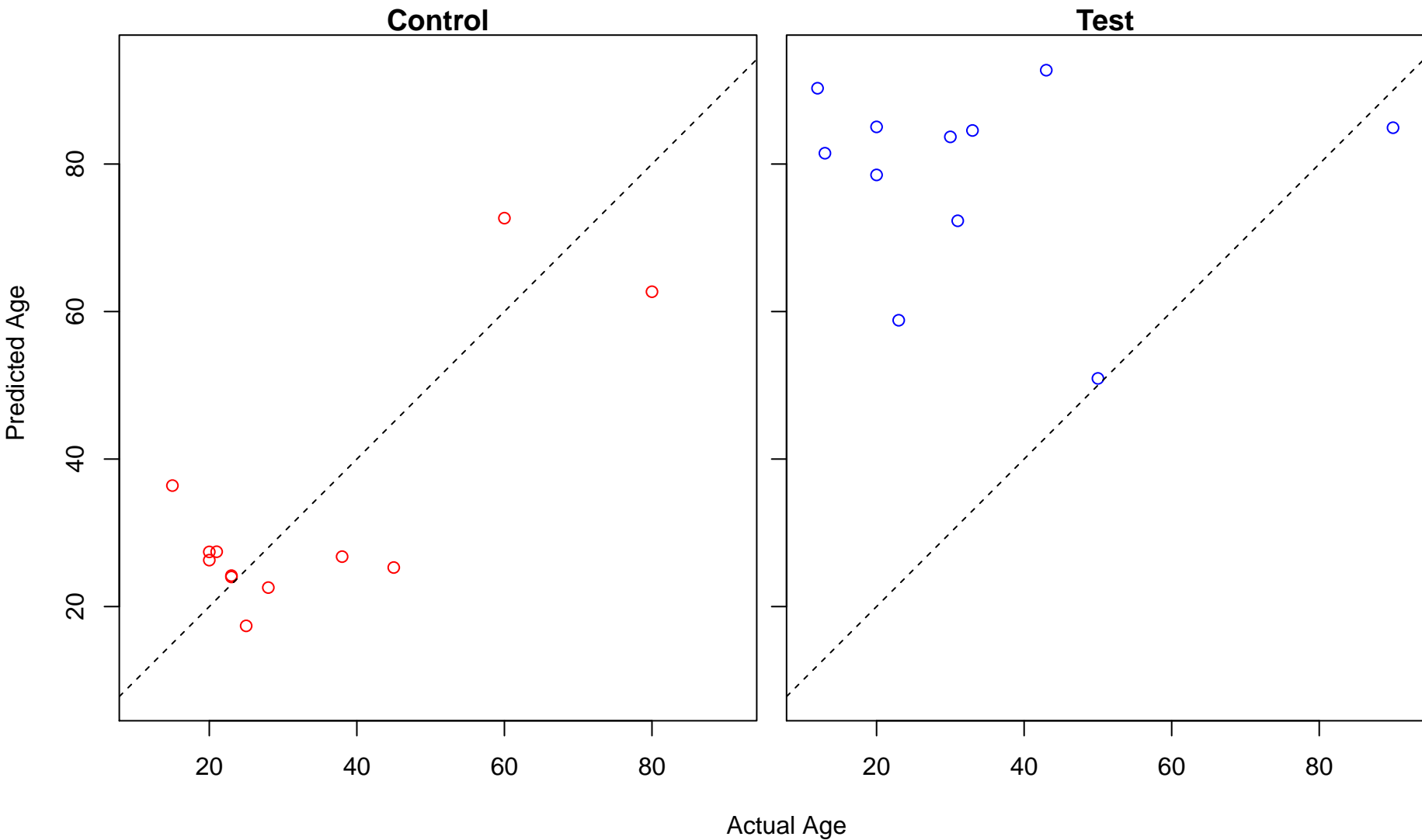
Golgi disassembly (Score: 8.295496)



positive regulation of vasculogenesis (Score: 8.292890)

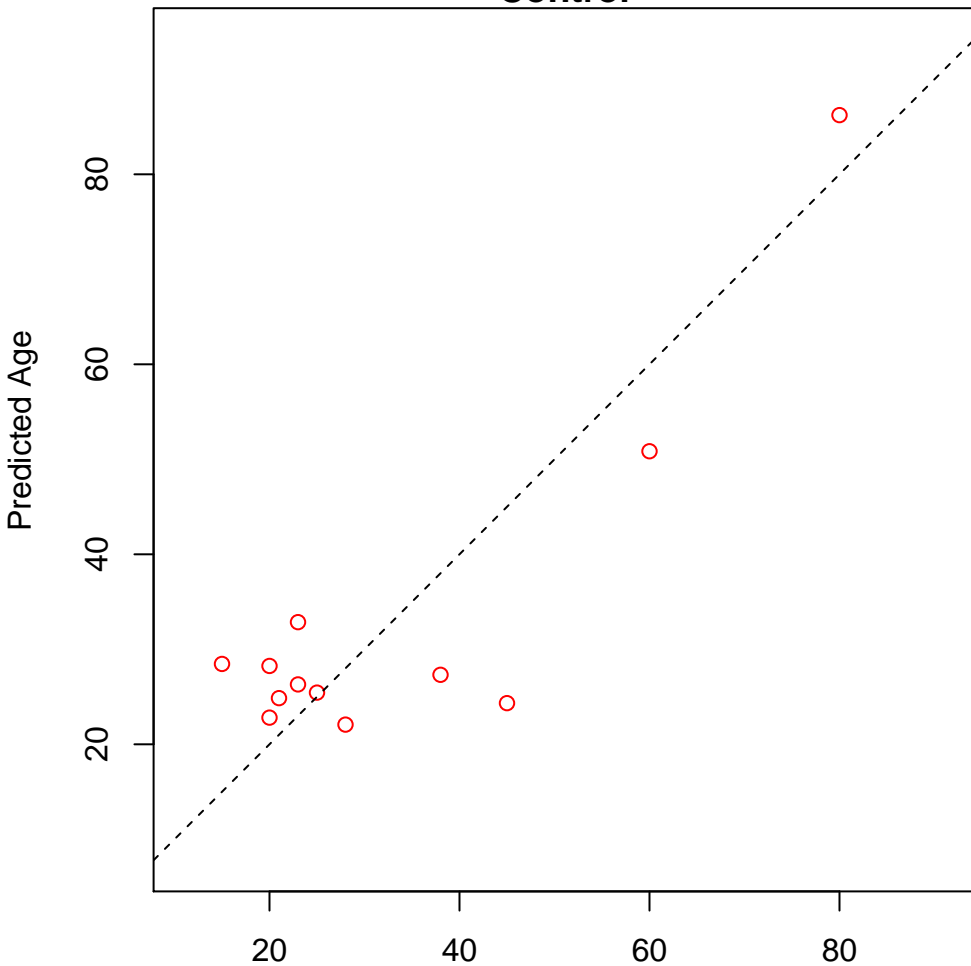


cellular response to carbohydrate stimulus (Score: 8.284225)

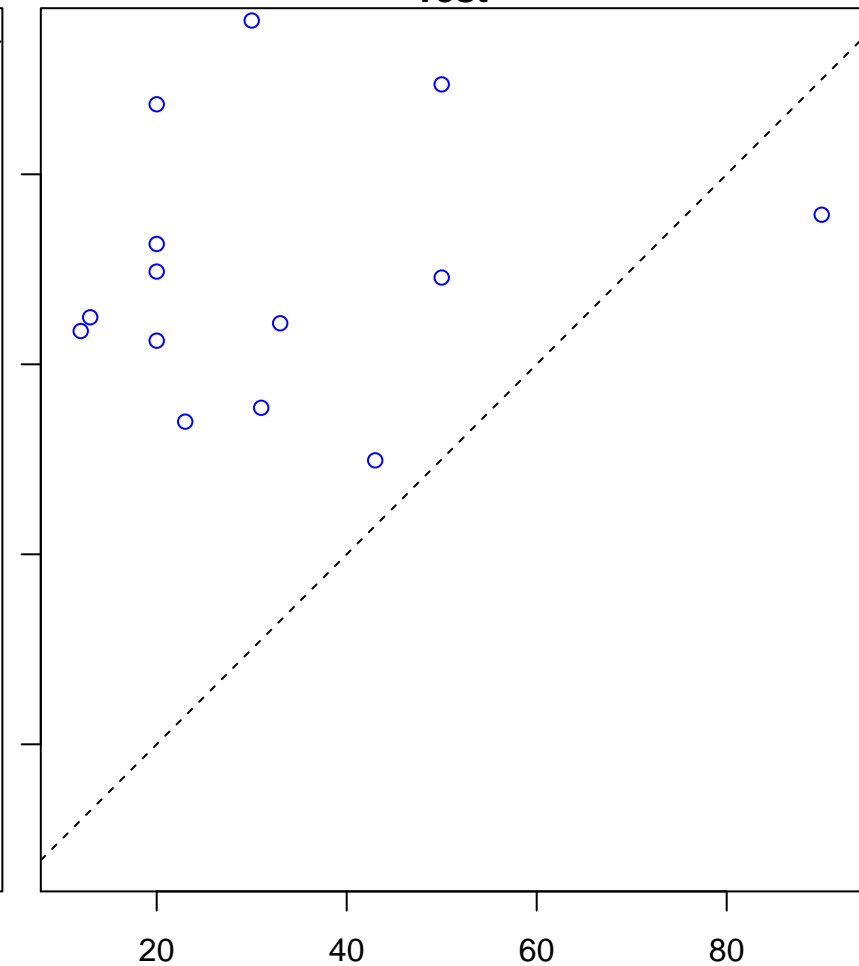


N-acetylneuraminate metabolic process (Score: 8.283779)

Control

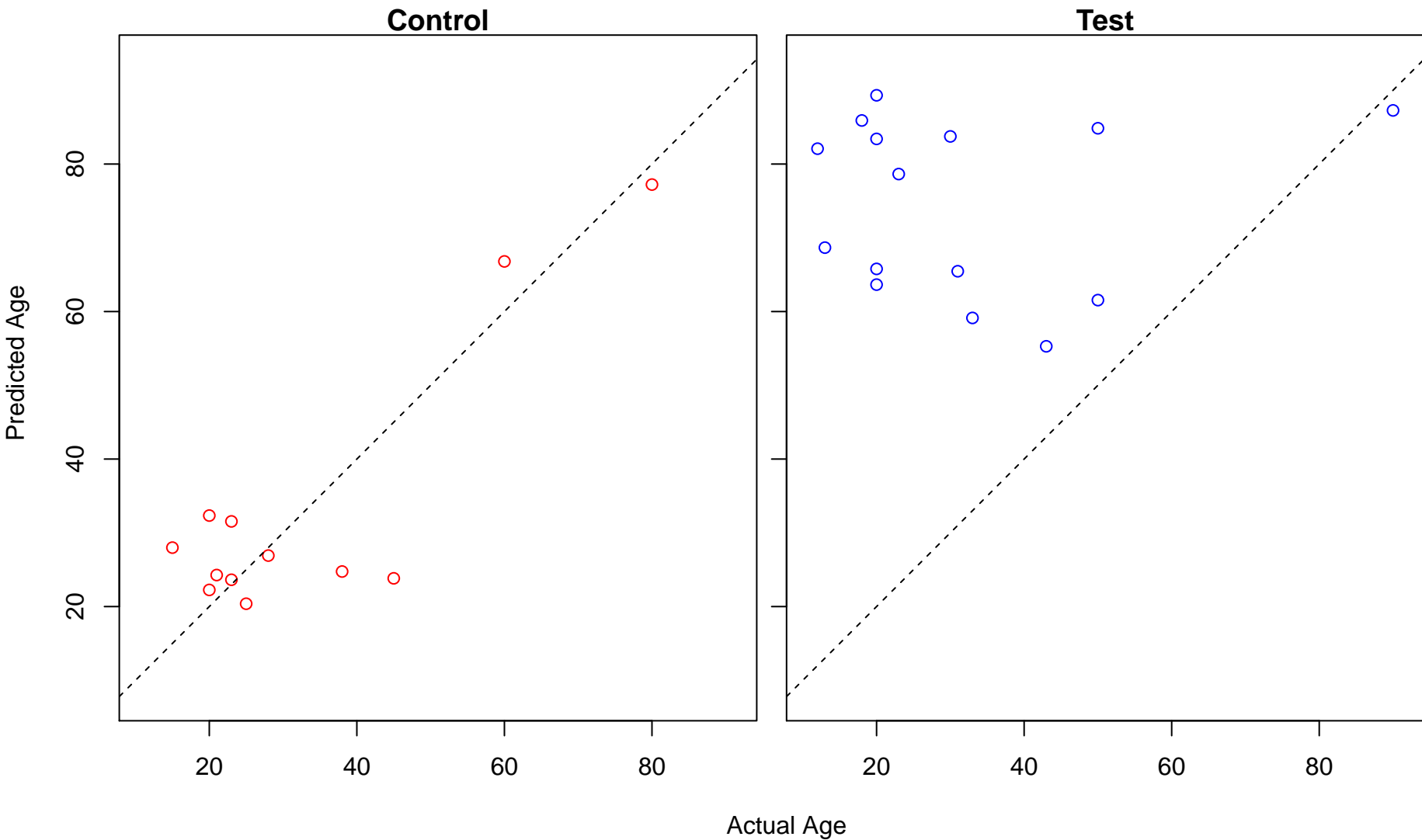


Test

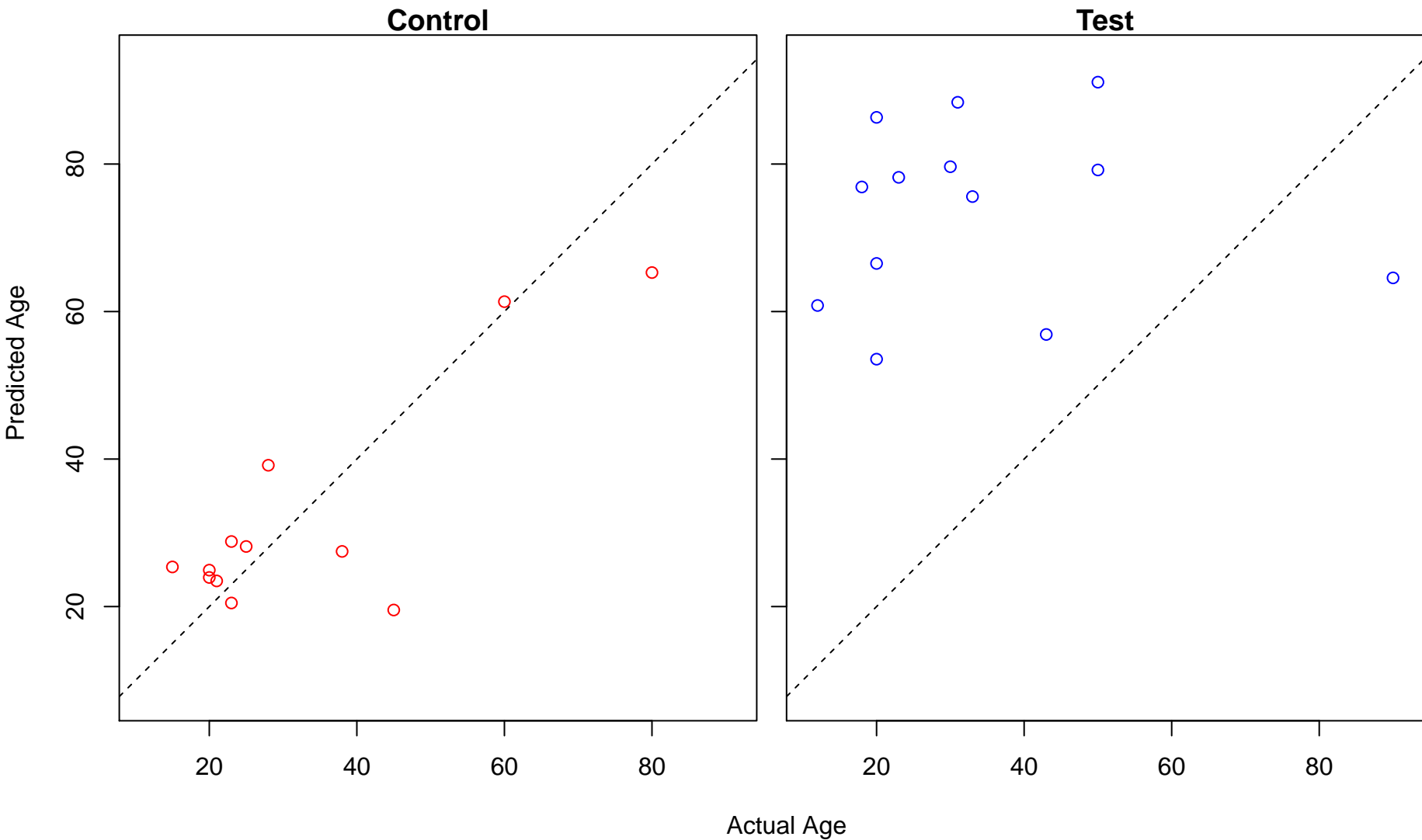


Actual Age

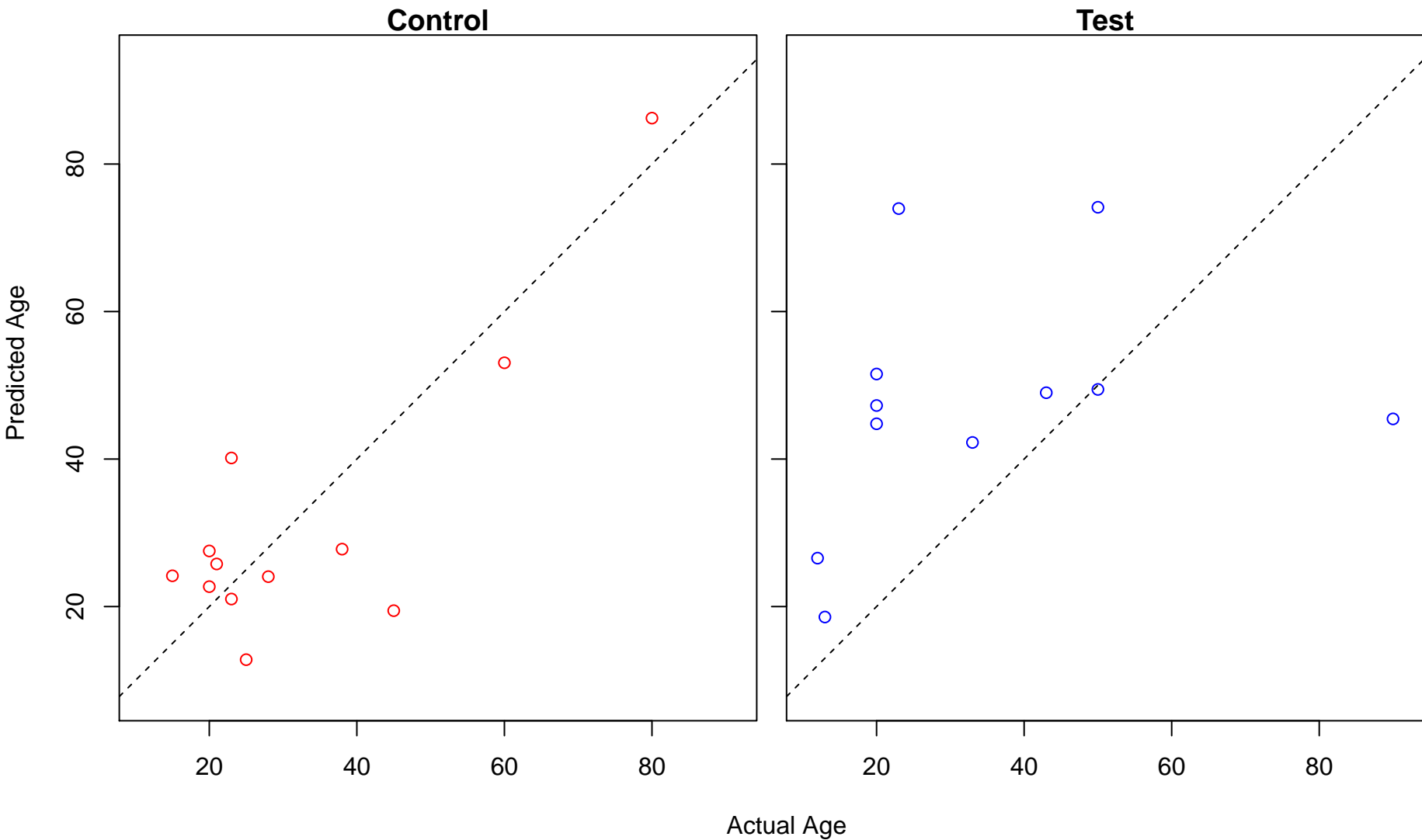
negative regulation of MAP kinase activity (Score: 8.278761)



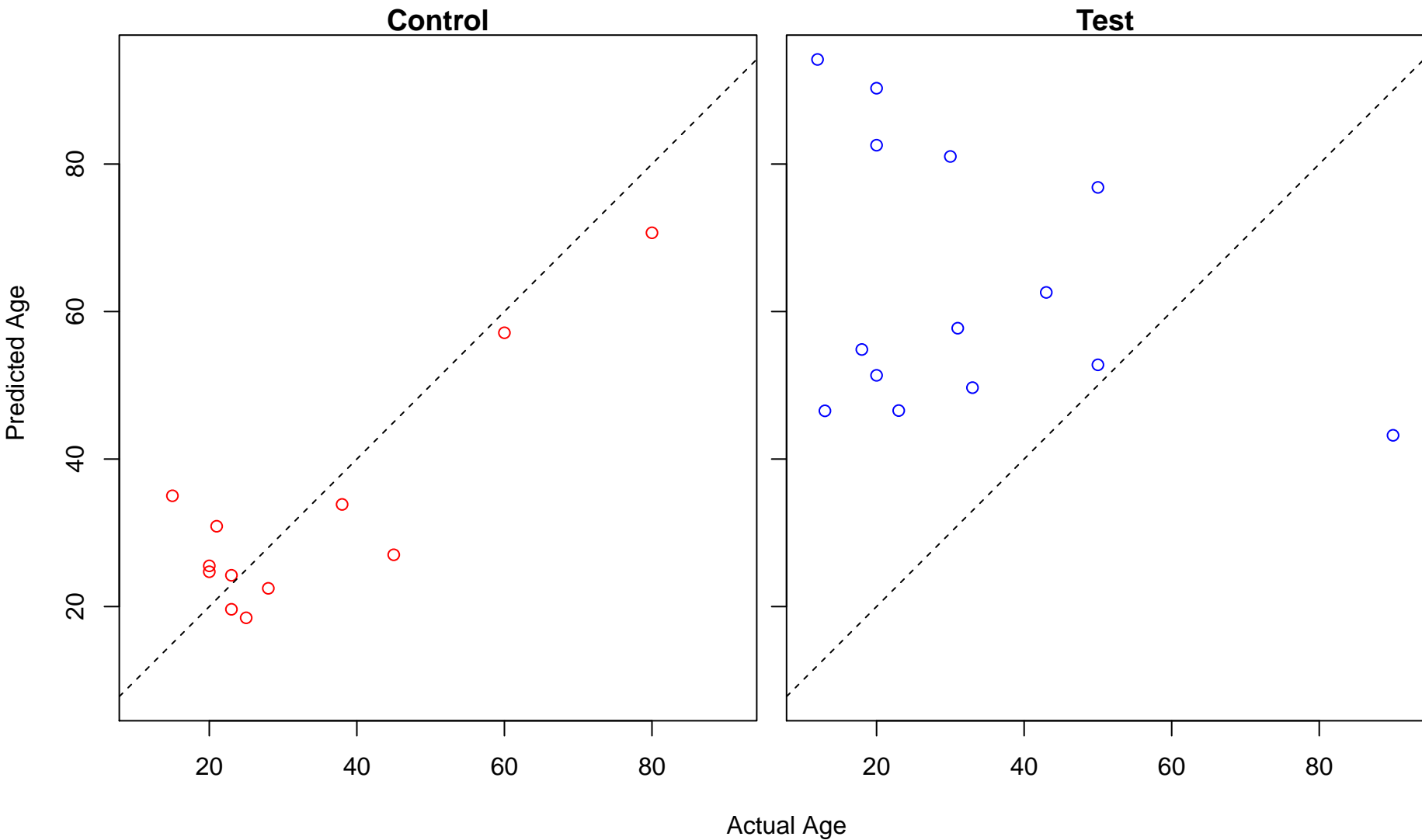
regulation of granulocyte chemotaxis (Score: 8.277561)



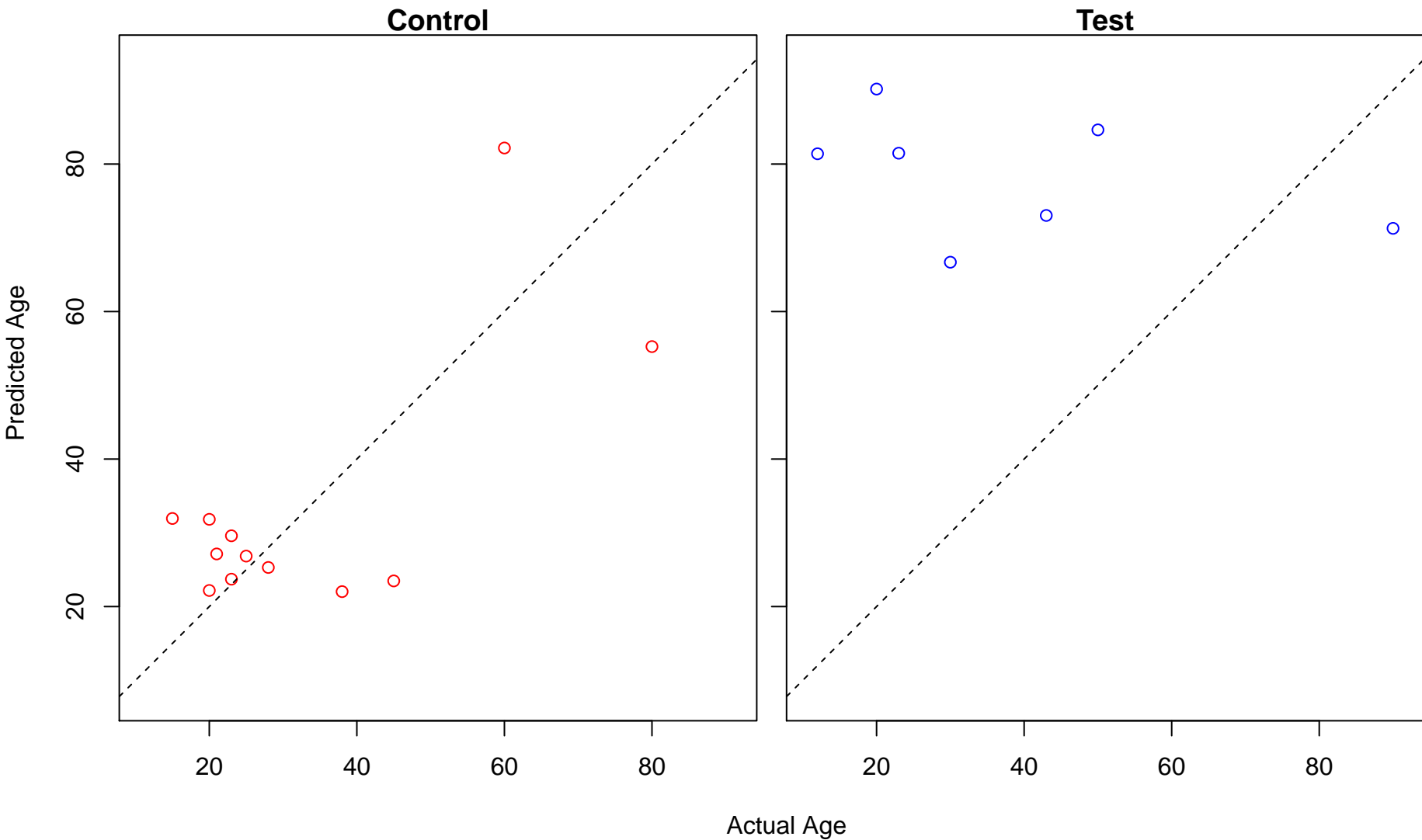
positive regulation of leukocyte cell-cell adhesion (Score: 8.275277)



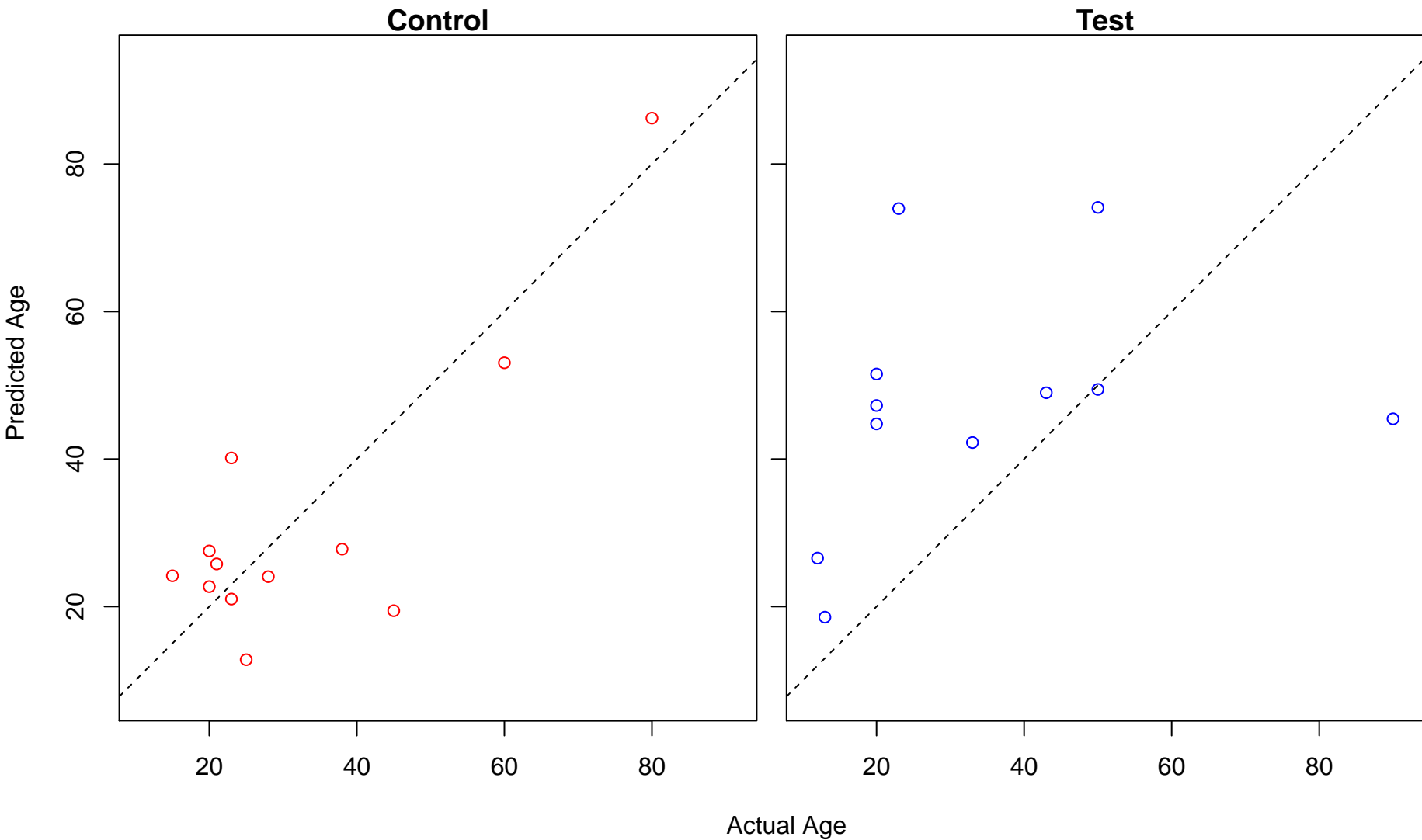
positive regulation of interleukin-1 beta secretion (Score: 8.274109)



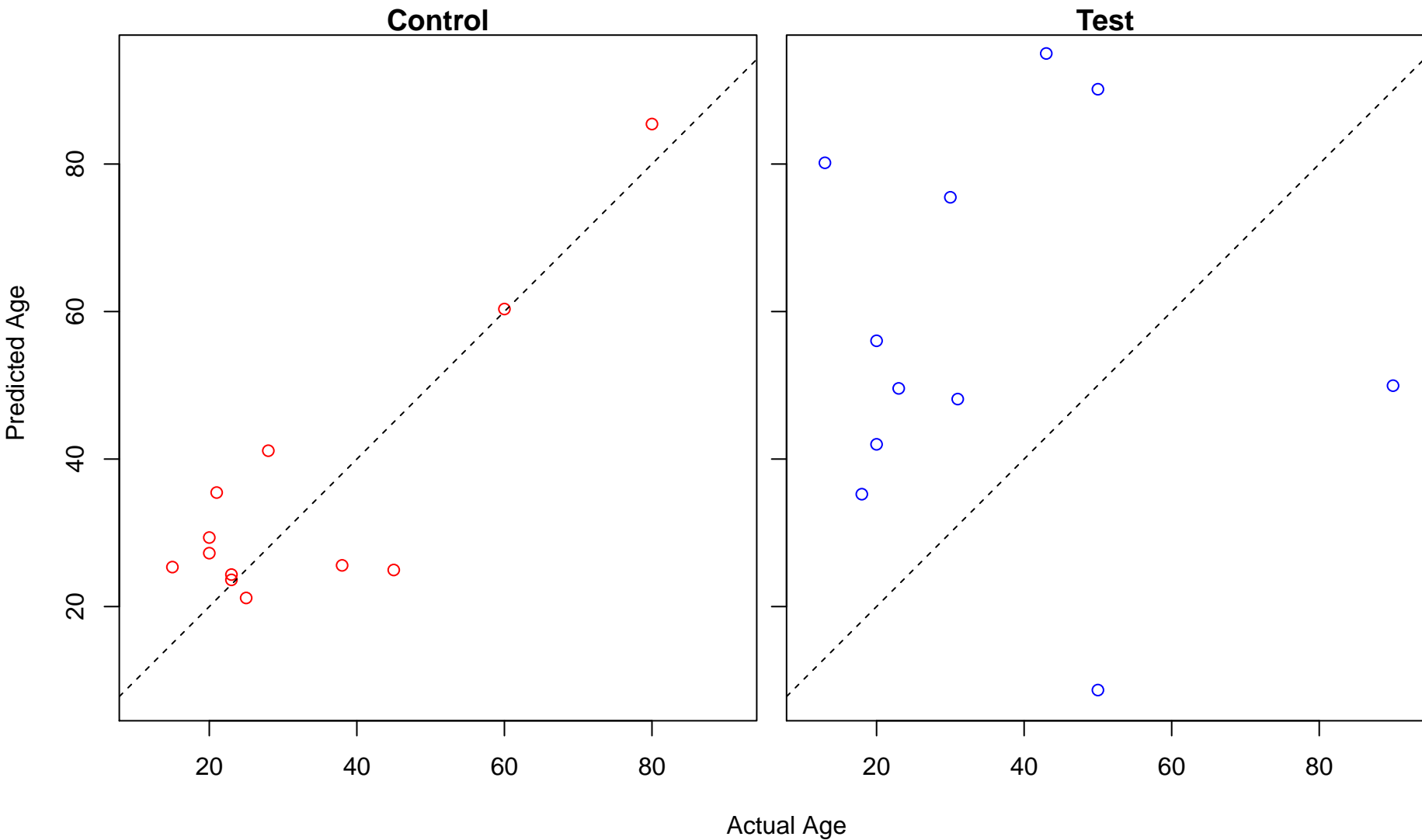
positive regulation of extrinsic apoptotic signaling pathway (Score: 8.273735)



positive regulation of homotypic cell-cell adhesion (Score: 8.272946)

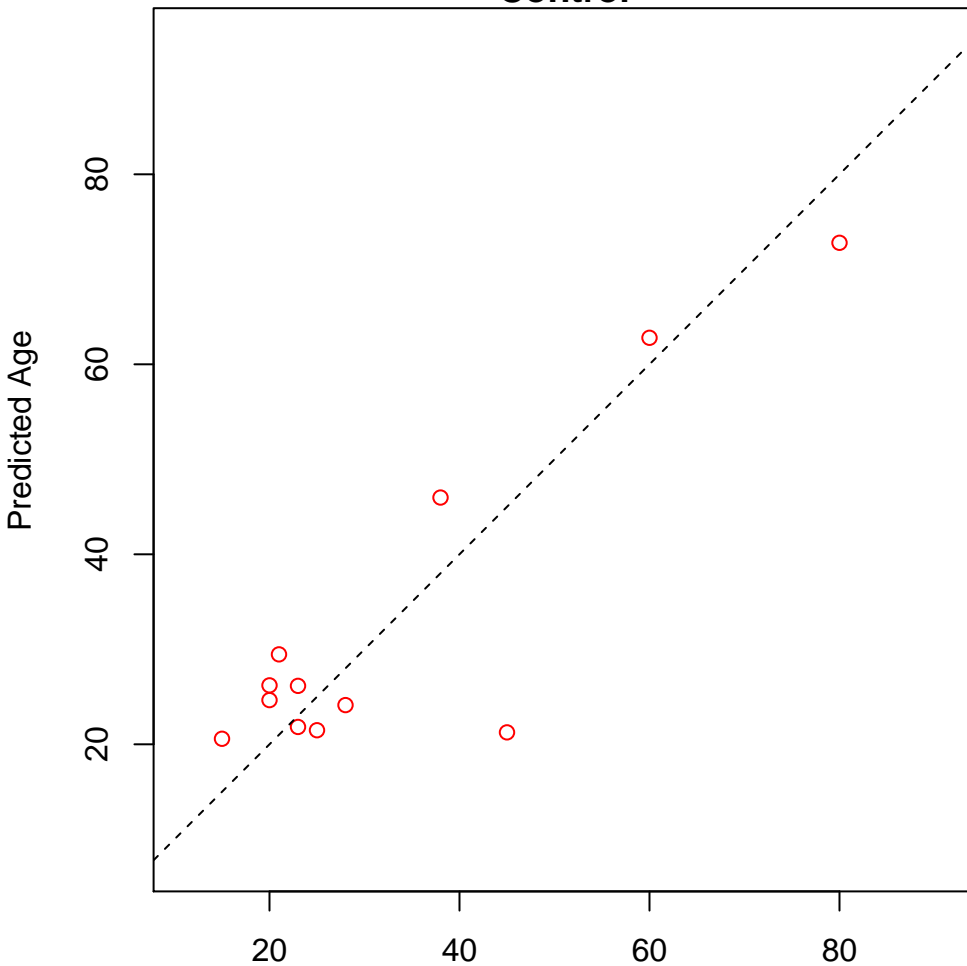


mesenchyme development (Score: 8.272003)

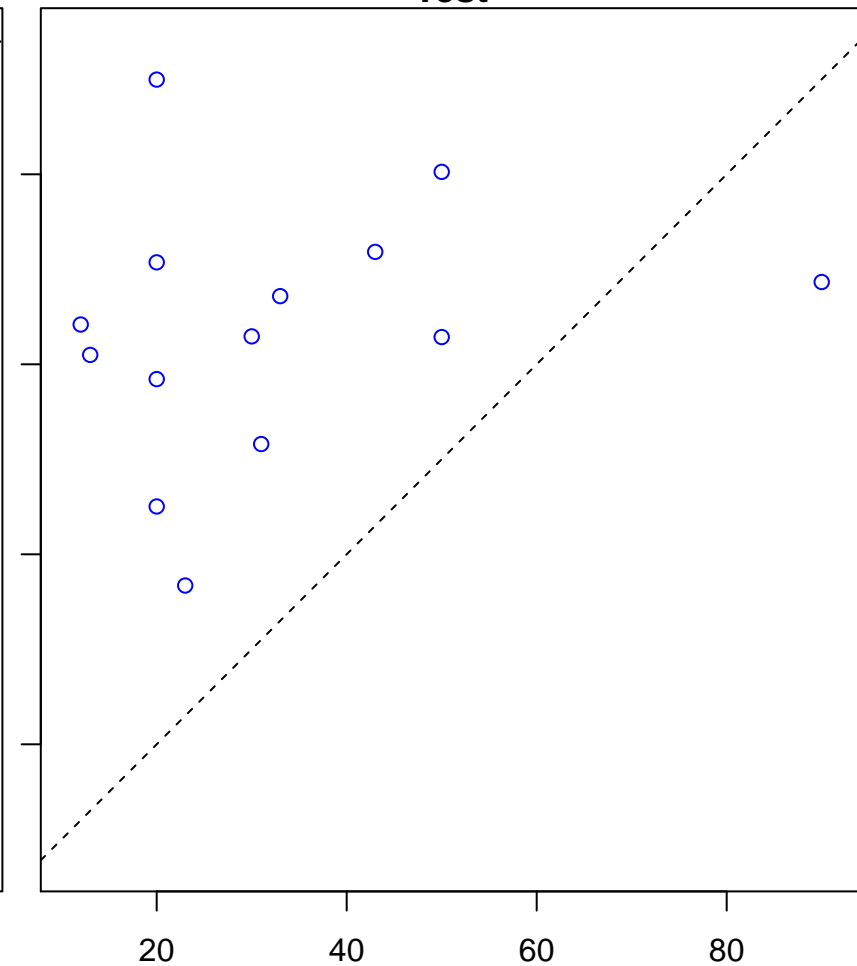


purine nucleobase biosynthetic process (Score: 8.266628)

Control

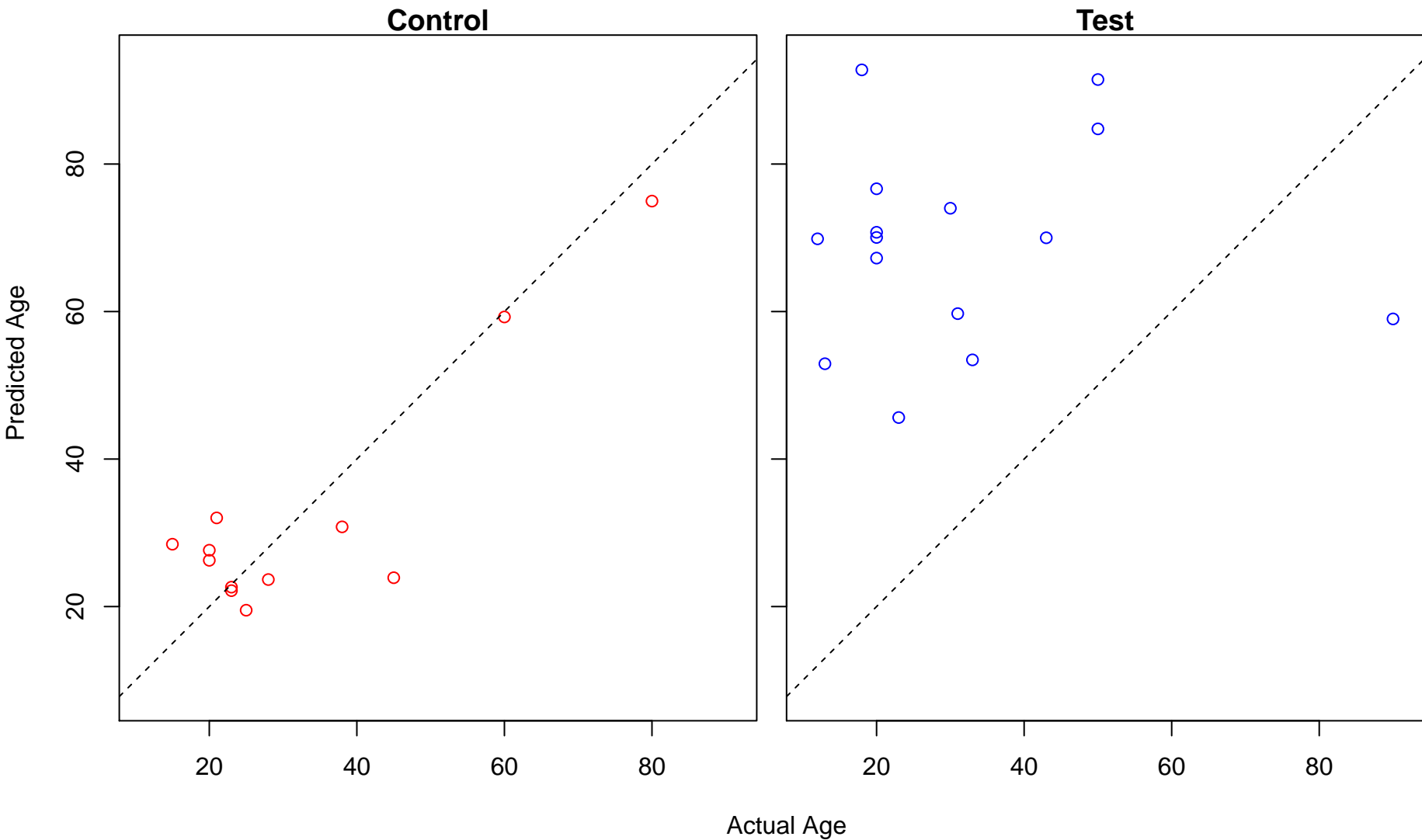


Test

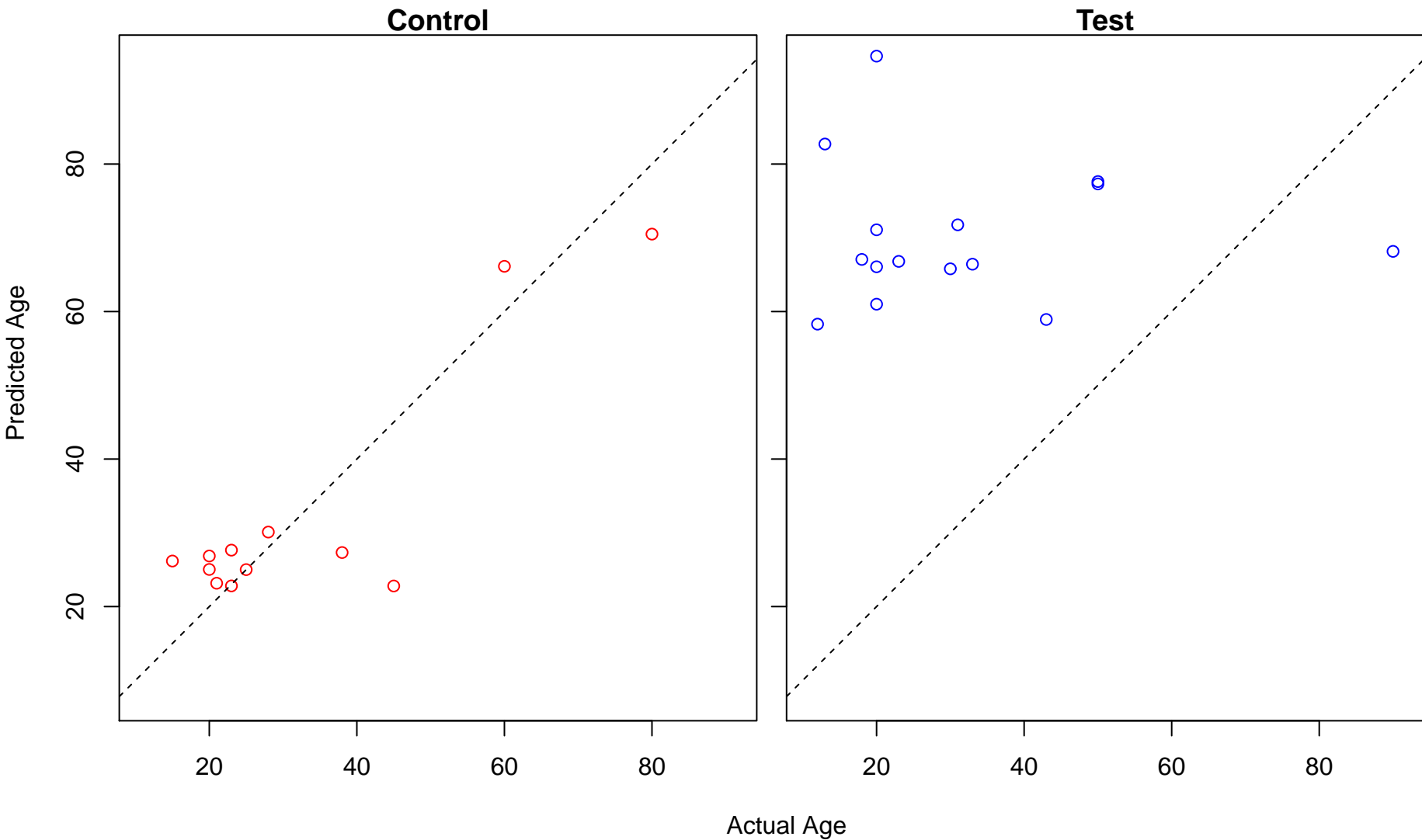


Actual Age

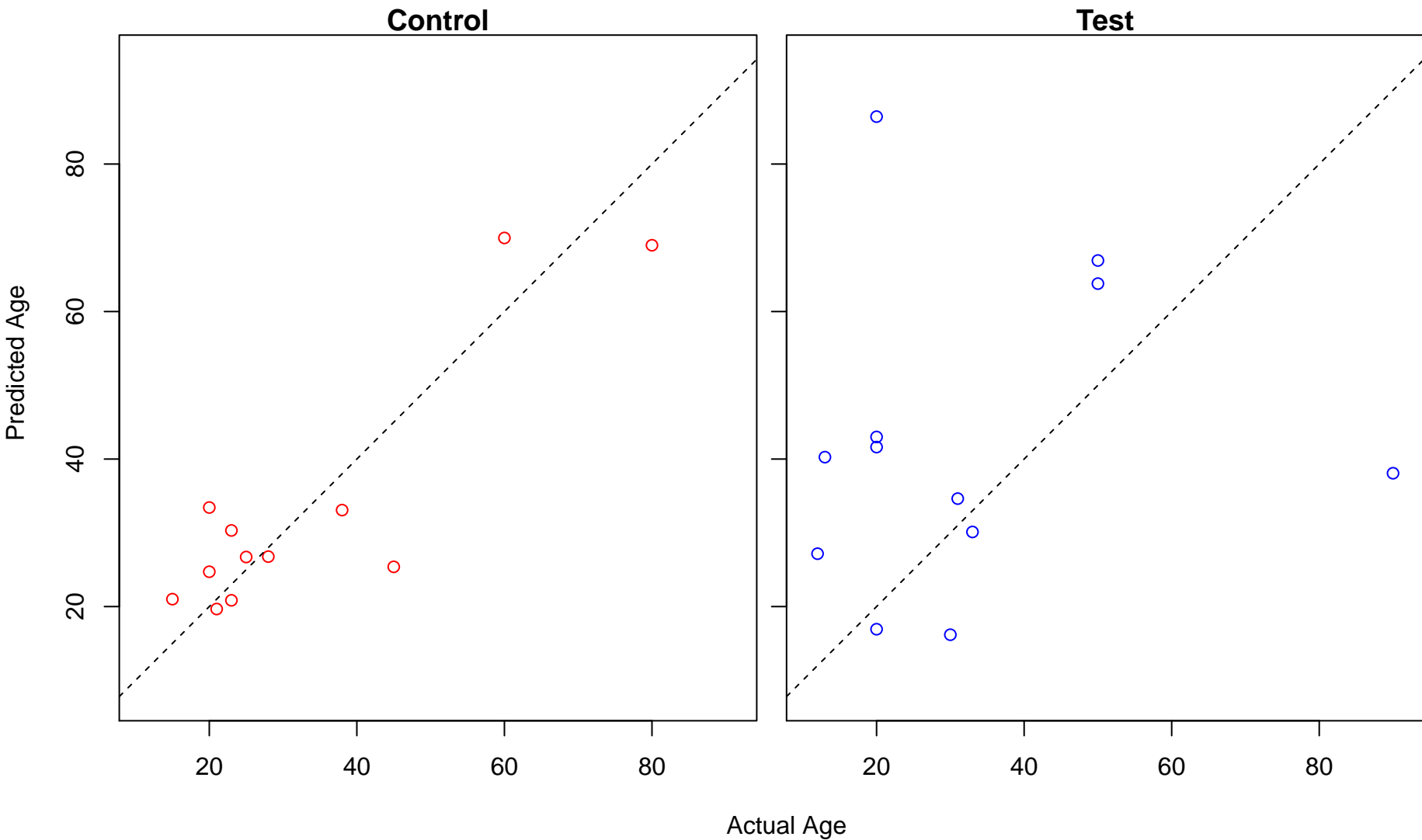
blood vessel morphogenesis (Score: 8.26328)



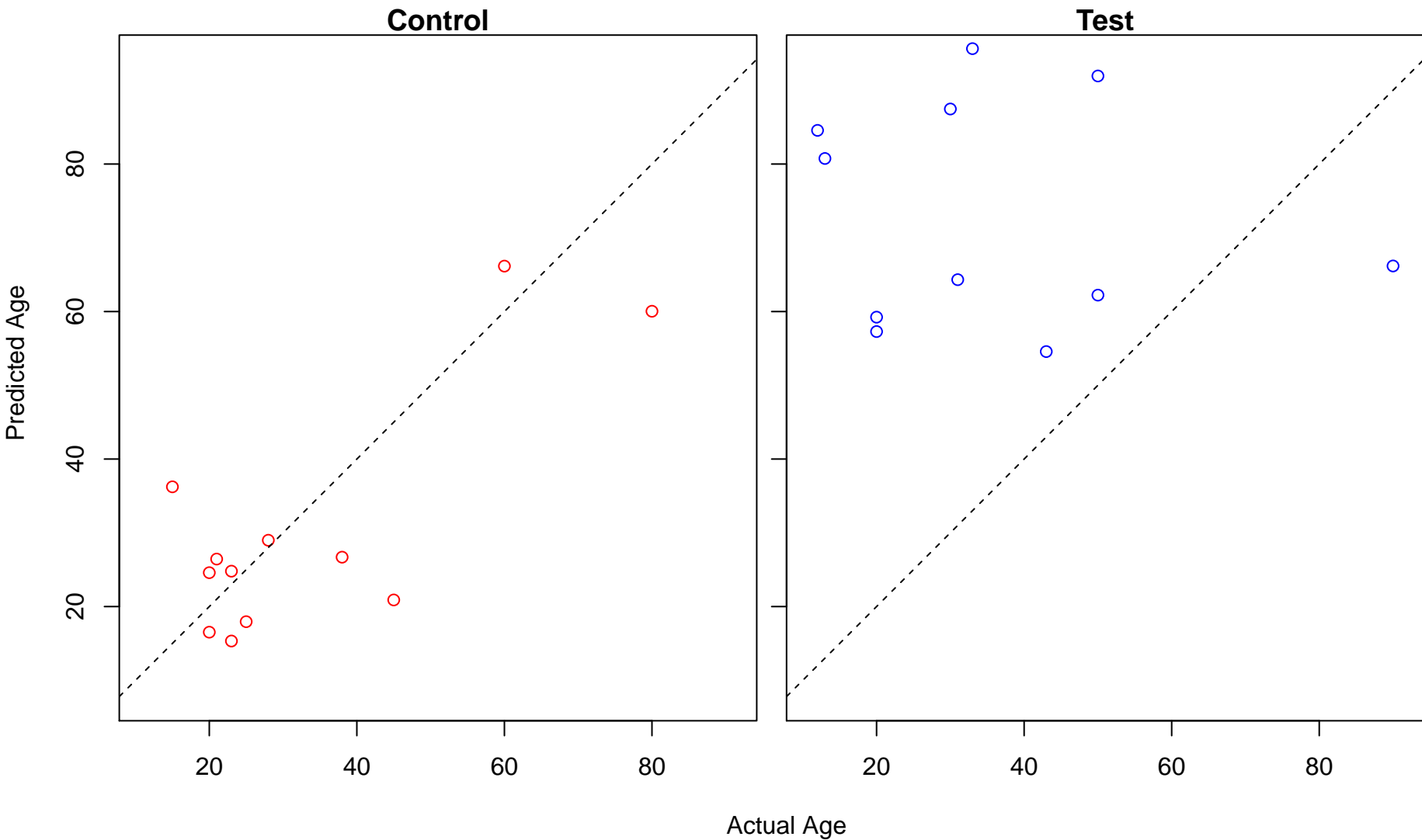
cognition (Score: 8.256727)



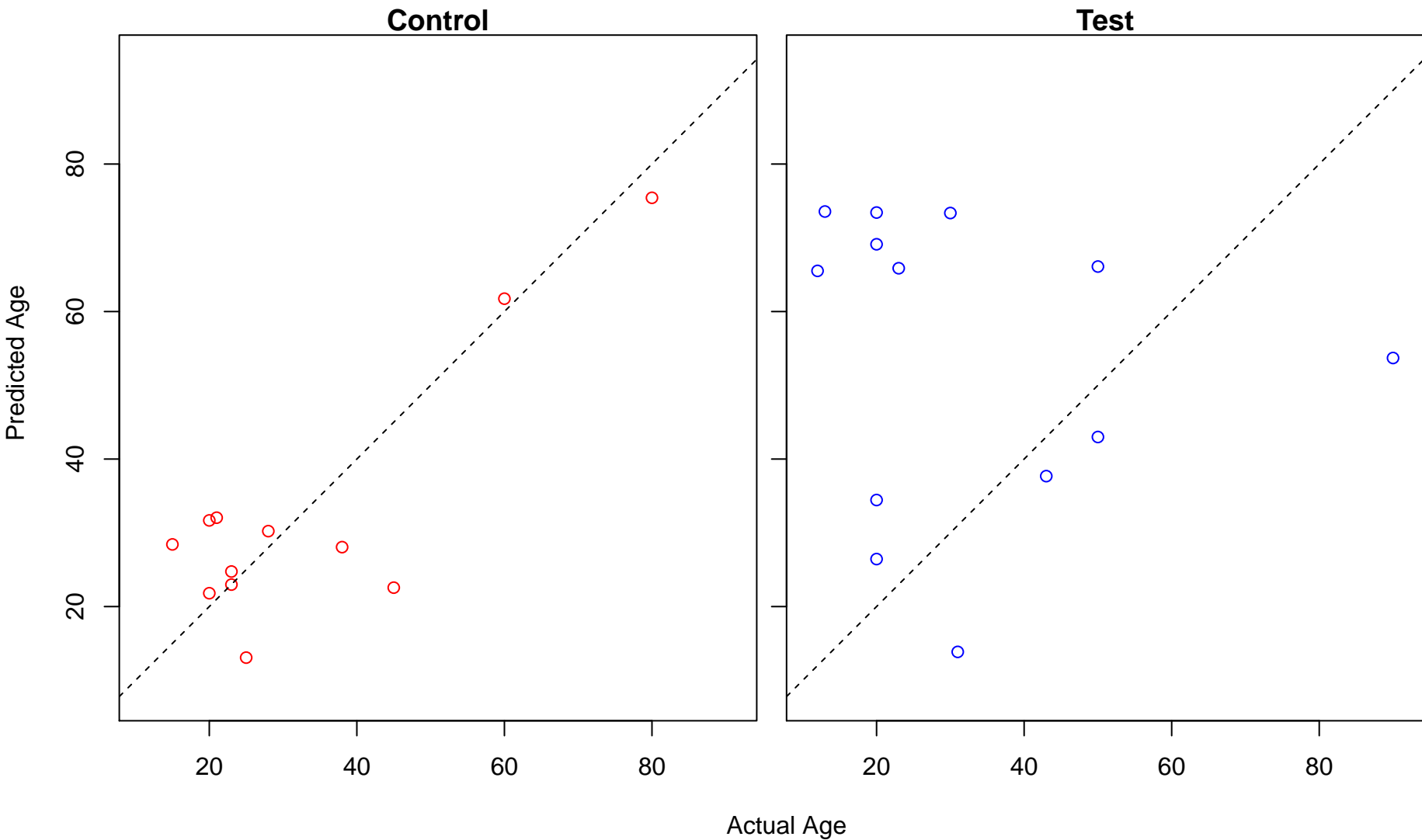
carbohydrate derivative transport (Score: 8.255716)



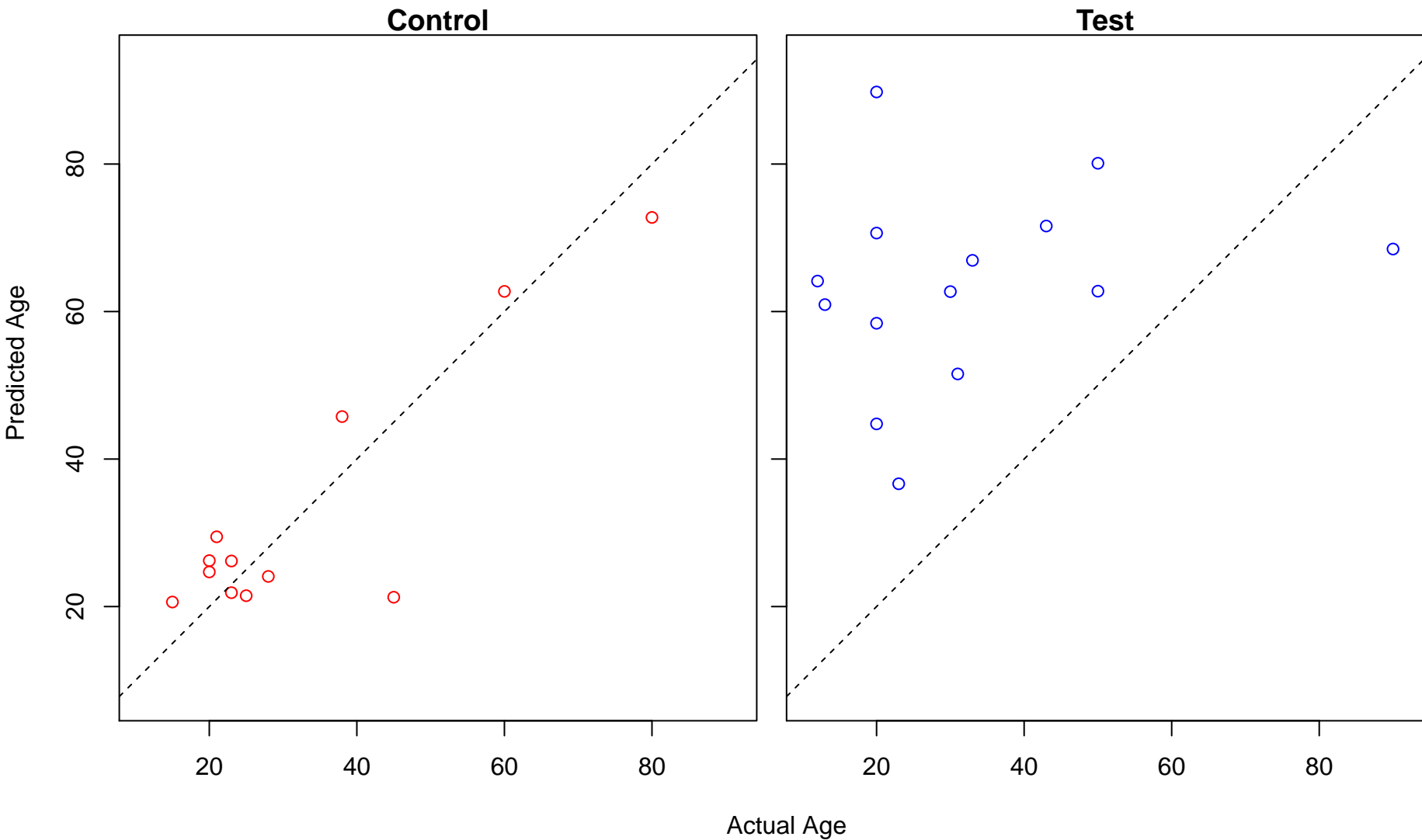
negative regulation of execution phase of apoptosis (Score: 8.254516)



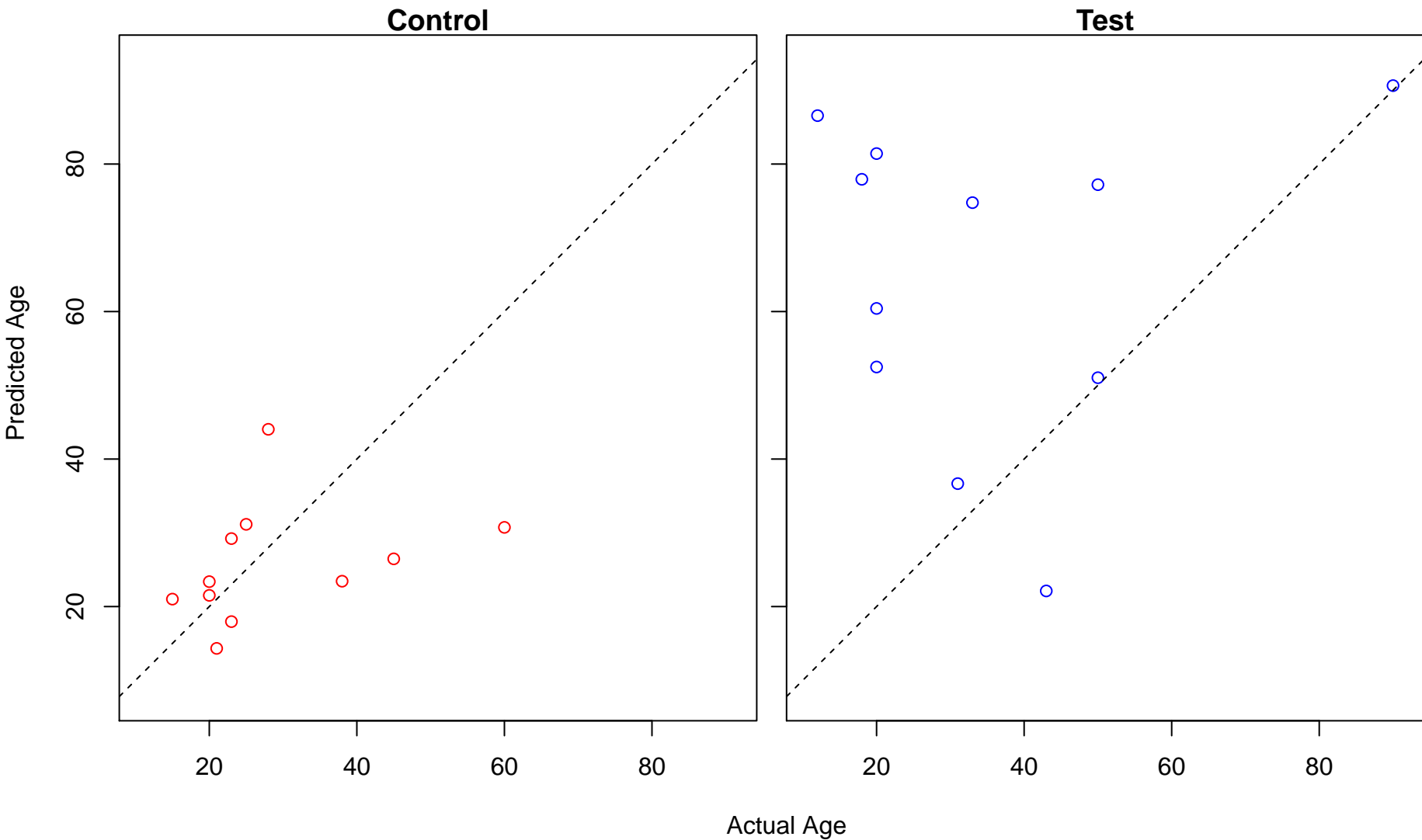
endosome organization (Score: 8.253126)



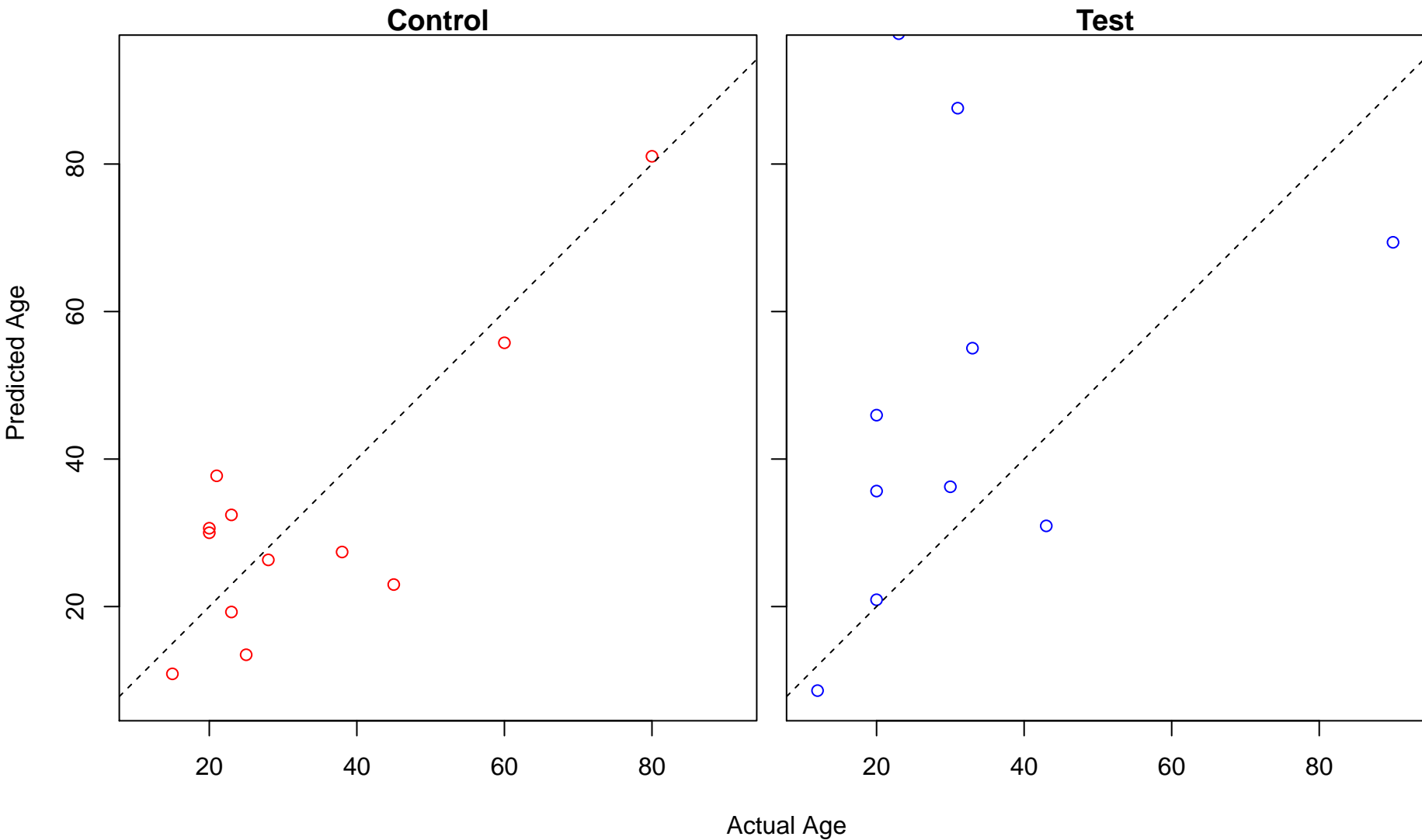
nucleobase biosynthetic process (Score: 8.253048)



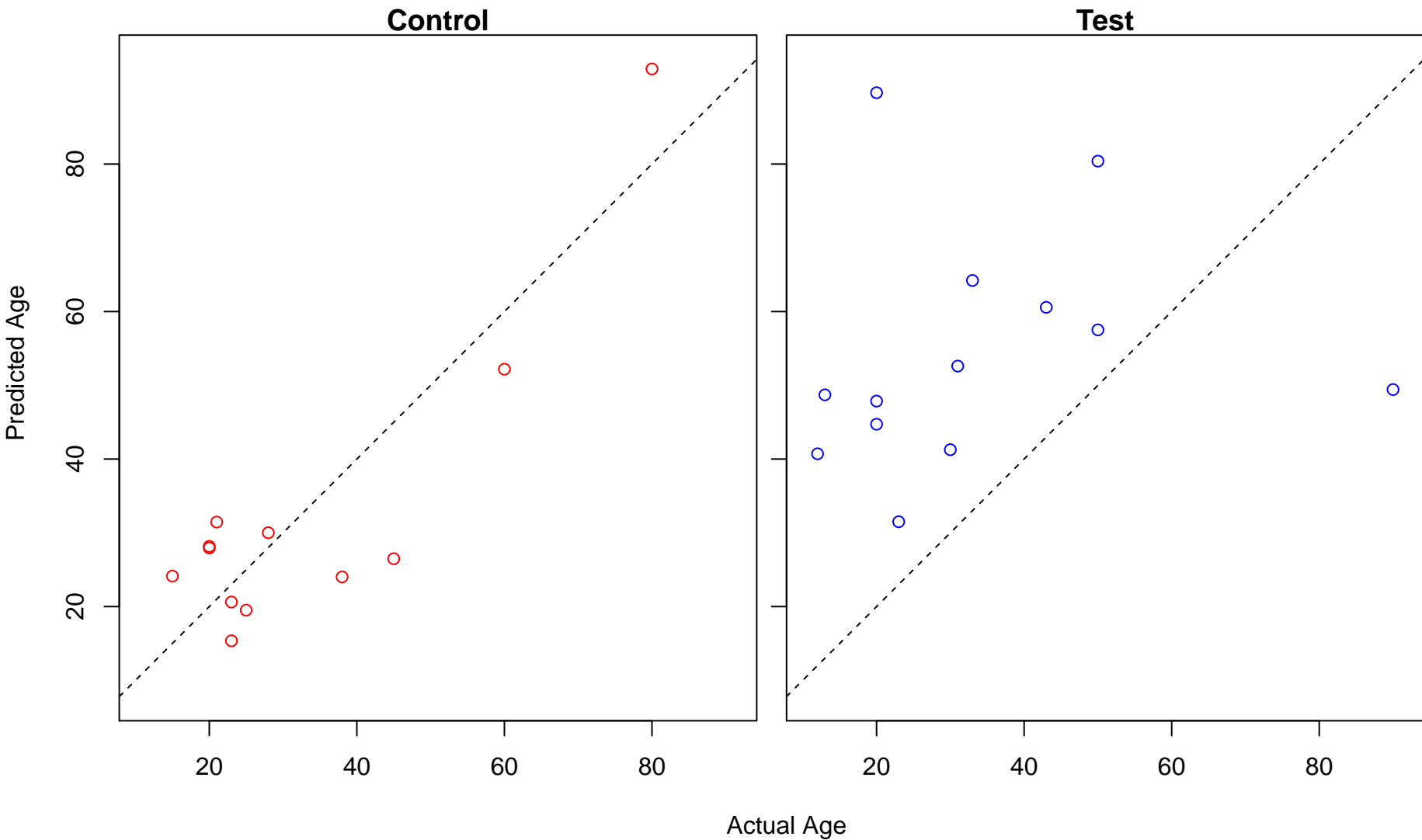
positive regulation of neurotransmitter secretion (Score: 8.251956)



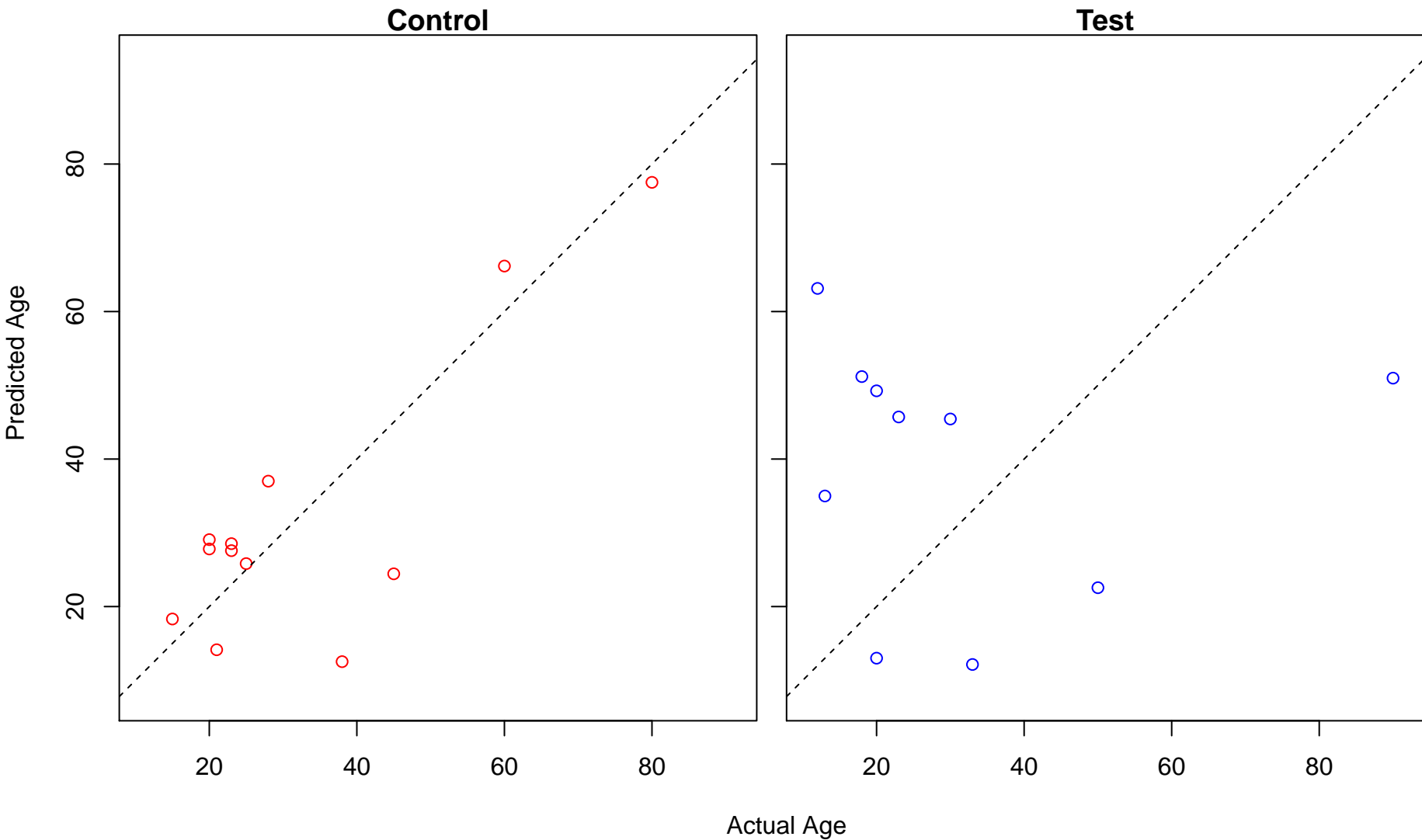
embryonic cranial skeleton morphogenesis (Score: 8.243665)



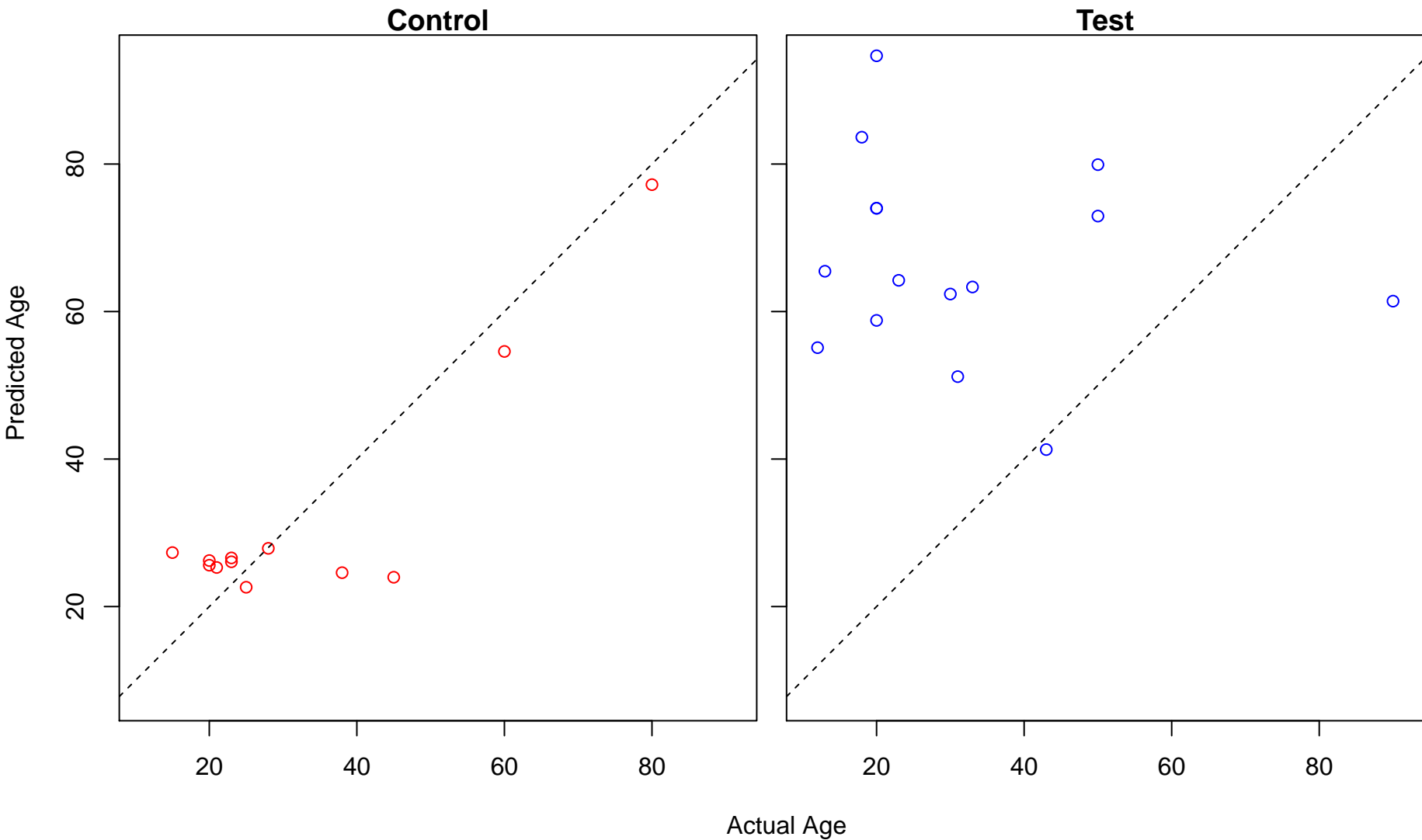
keratinocyte differentiation (Score: 8.243097)



positive regulation of insulin-like growth factor receptor signaling pathway (Score: 8.230980)

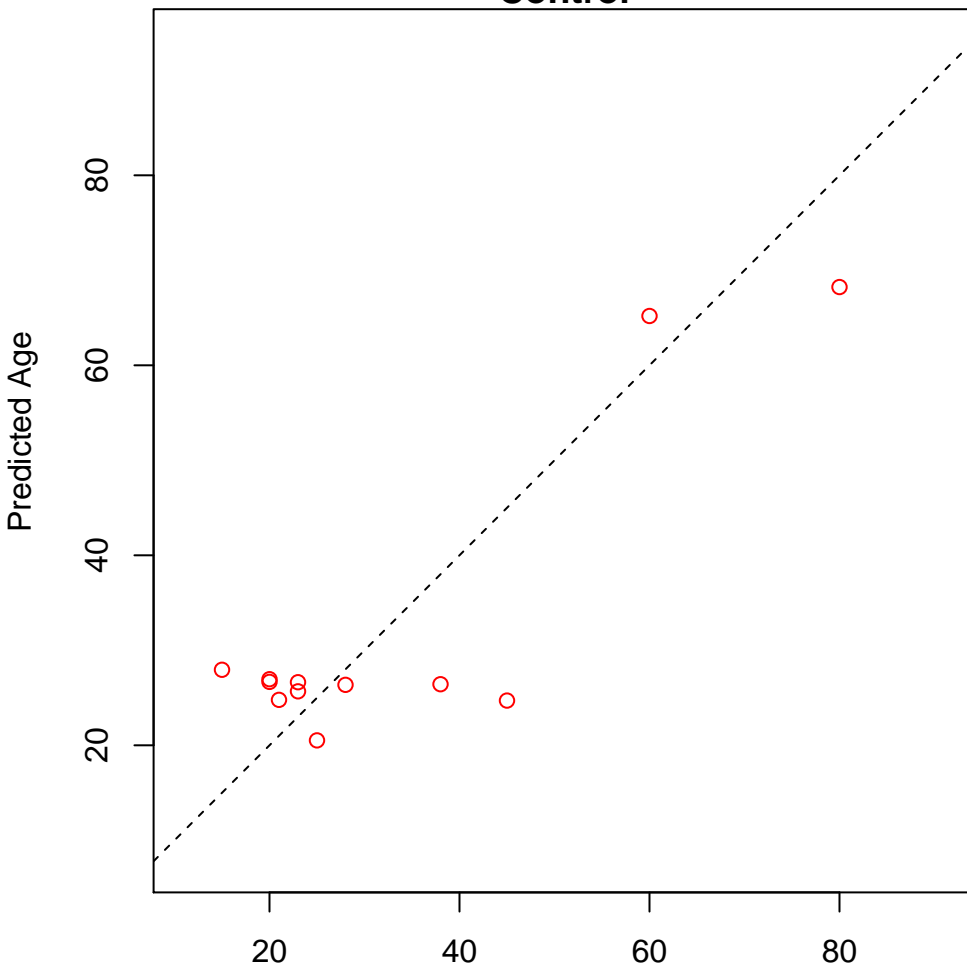


regulation of telomere maintenance via telomerase (Score: 8.230084)

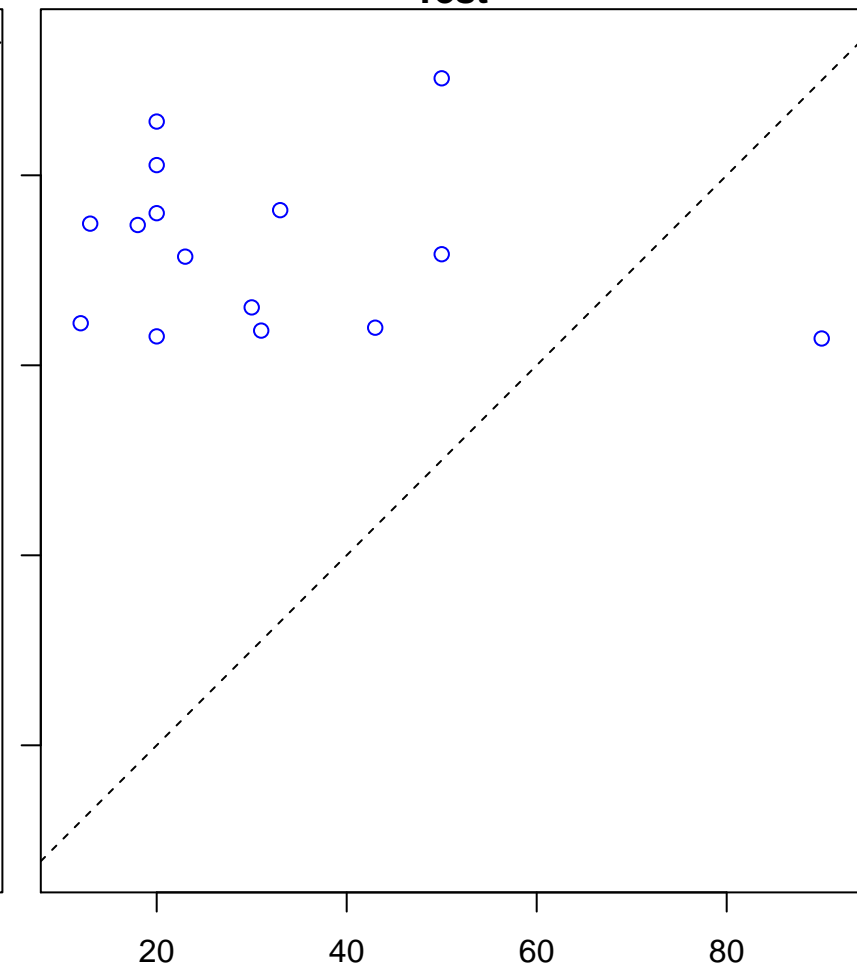


neuromuscular junction development (Score: 8.229460)

Control

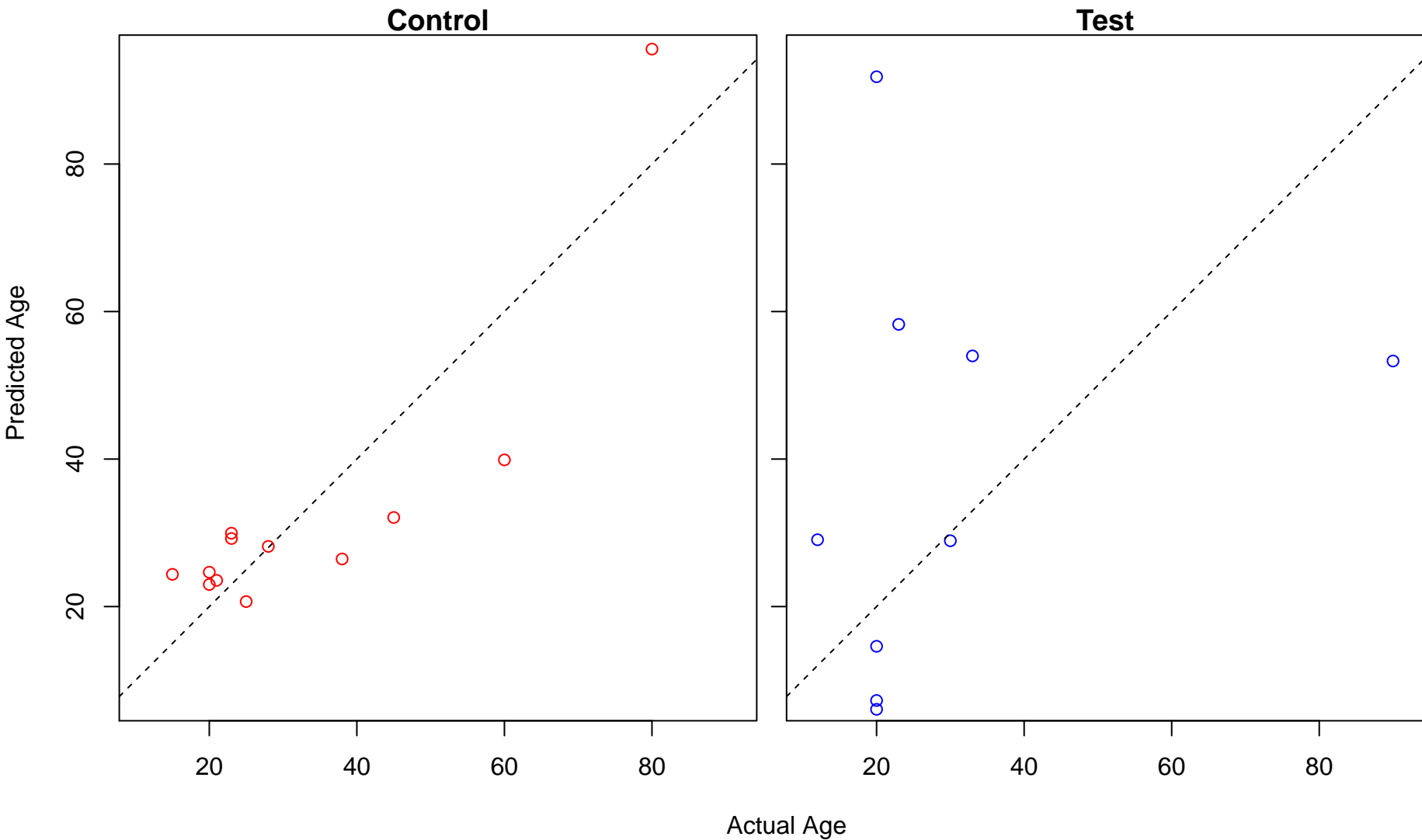


Test

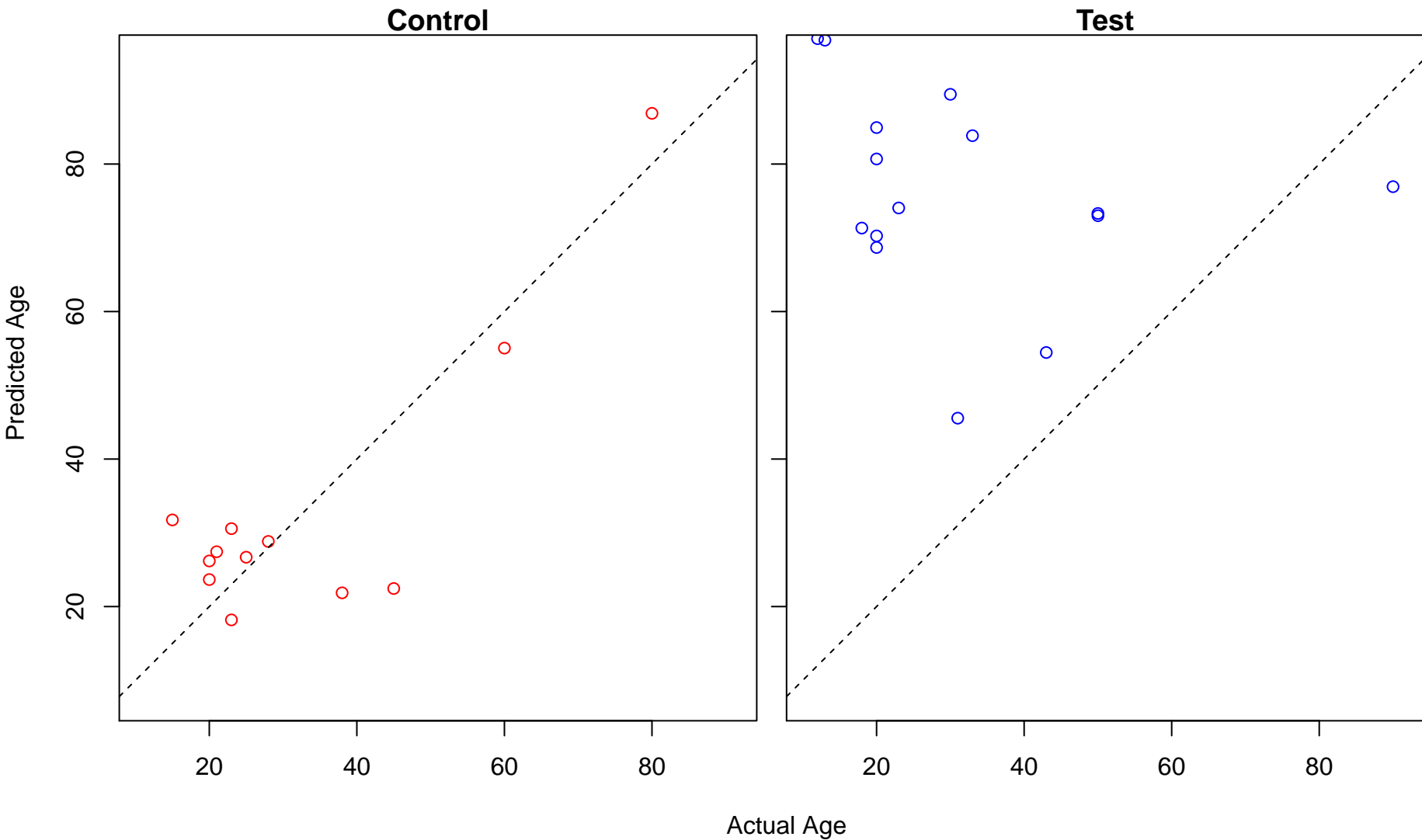


Actual Age

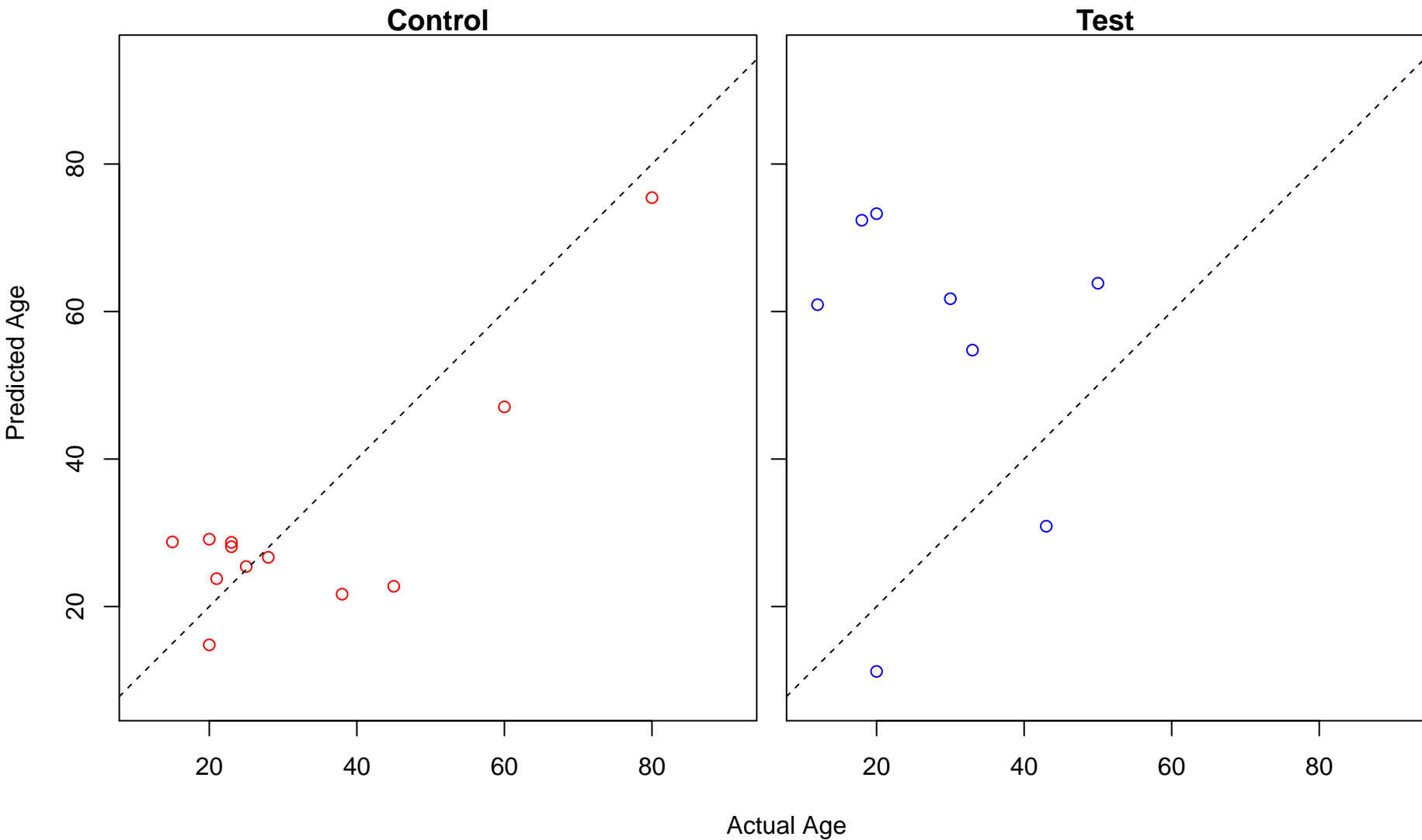
protein deubiquitination (Score: 8.222986)



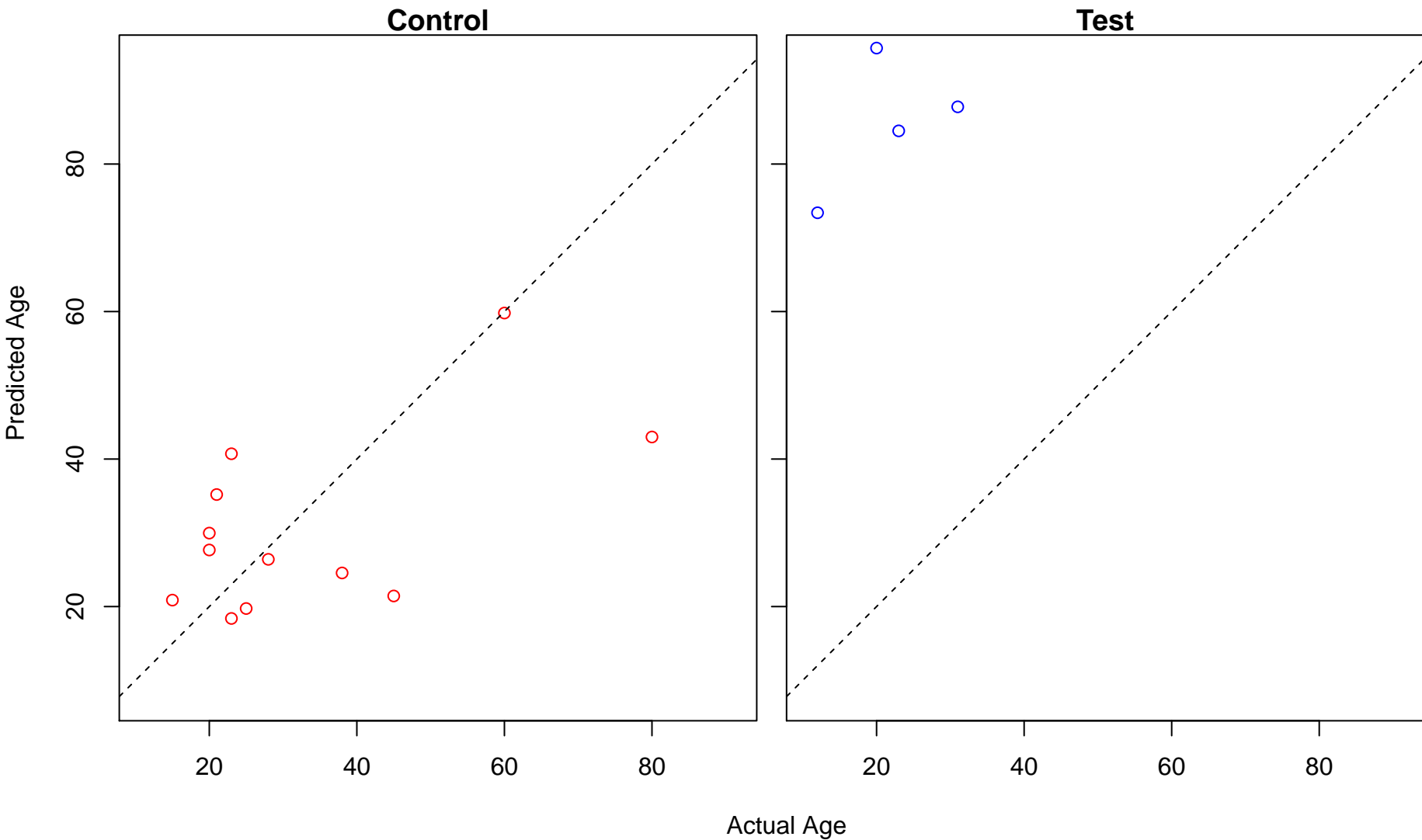
endothelium development (Score: 8.221706)



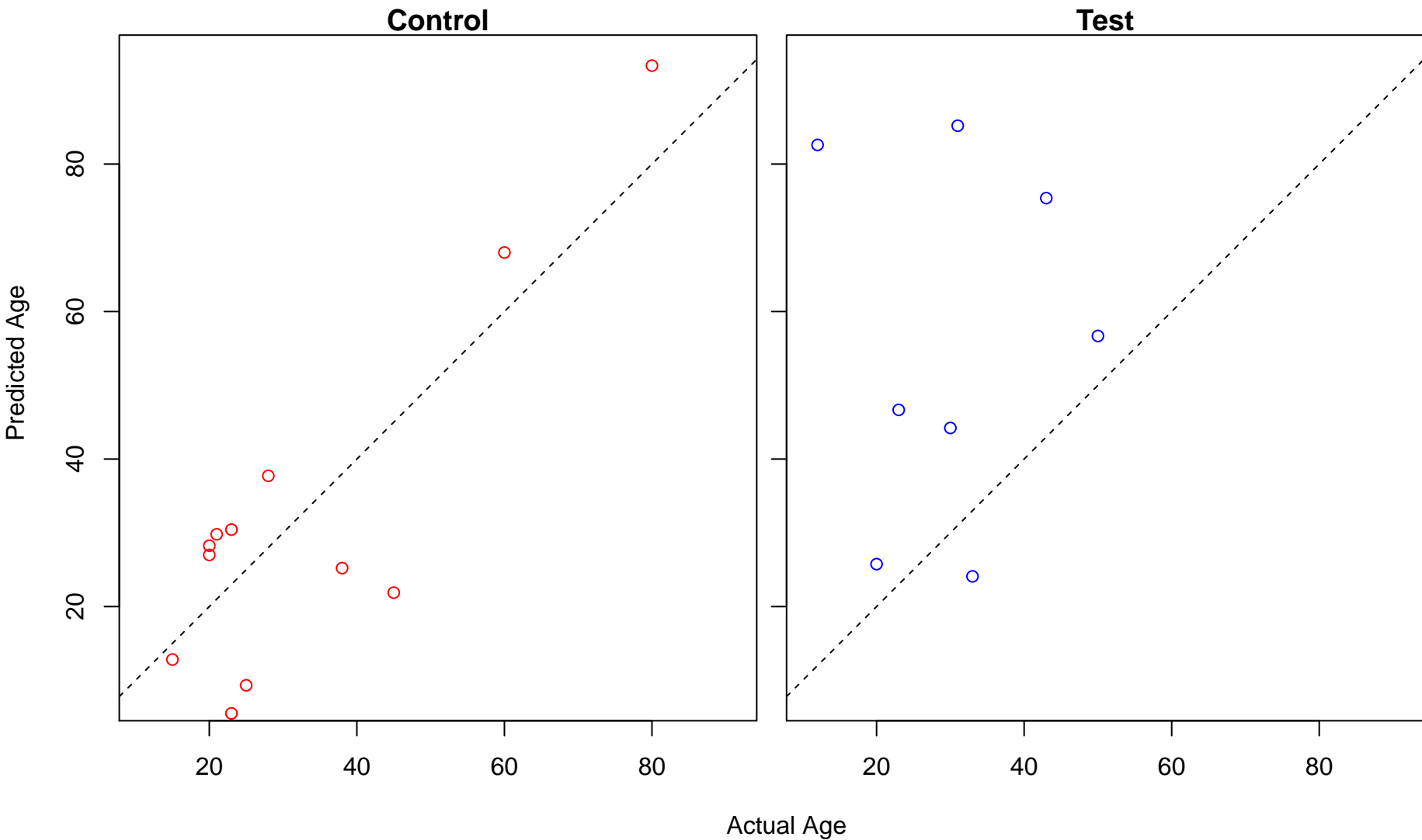
protein heterooligomerization (Score: 8.217584)



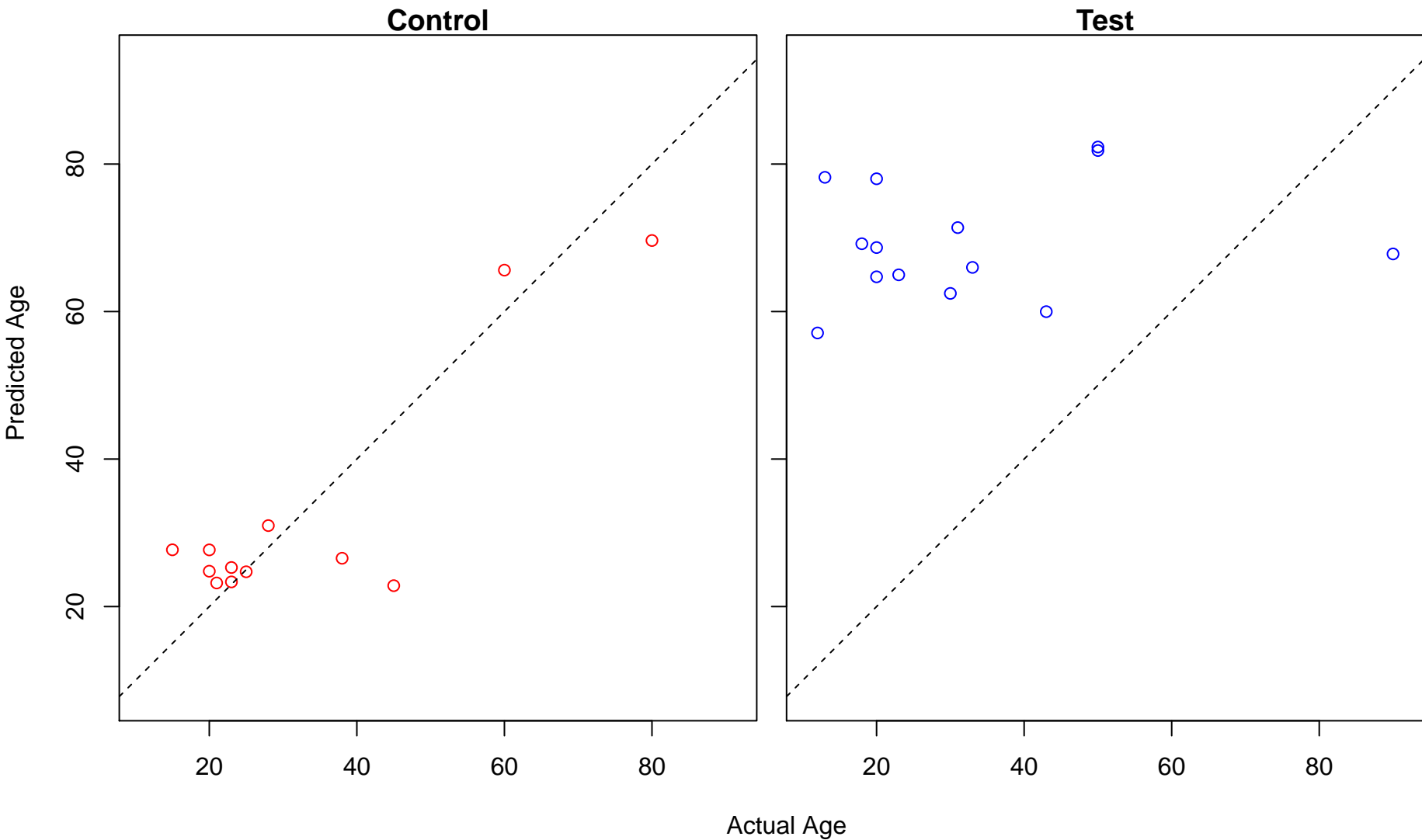
positive regulation of hematopoietic progenitor cell differentiation (Score: 8.212961)



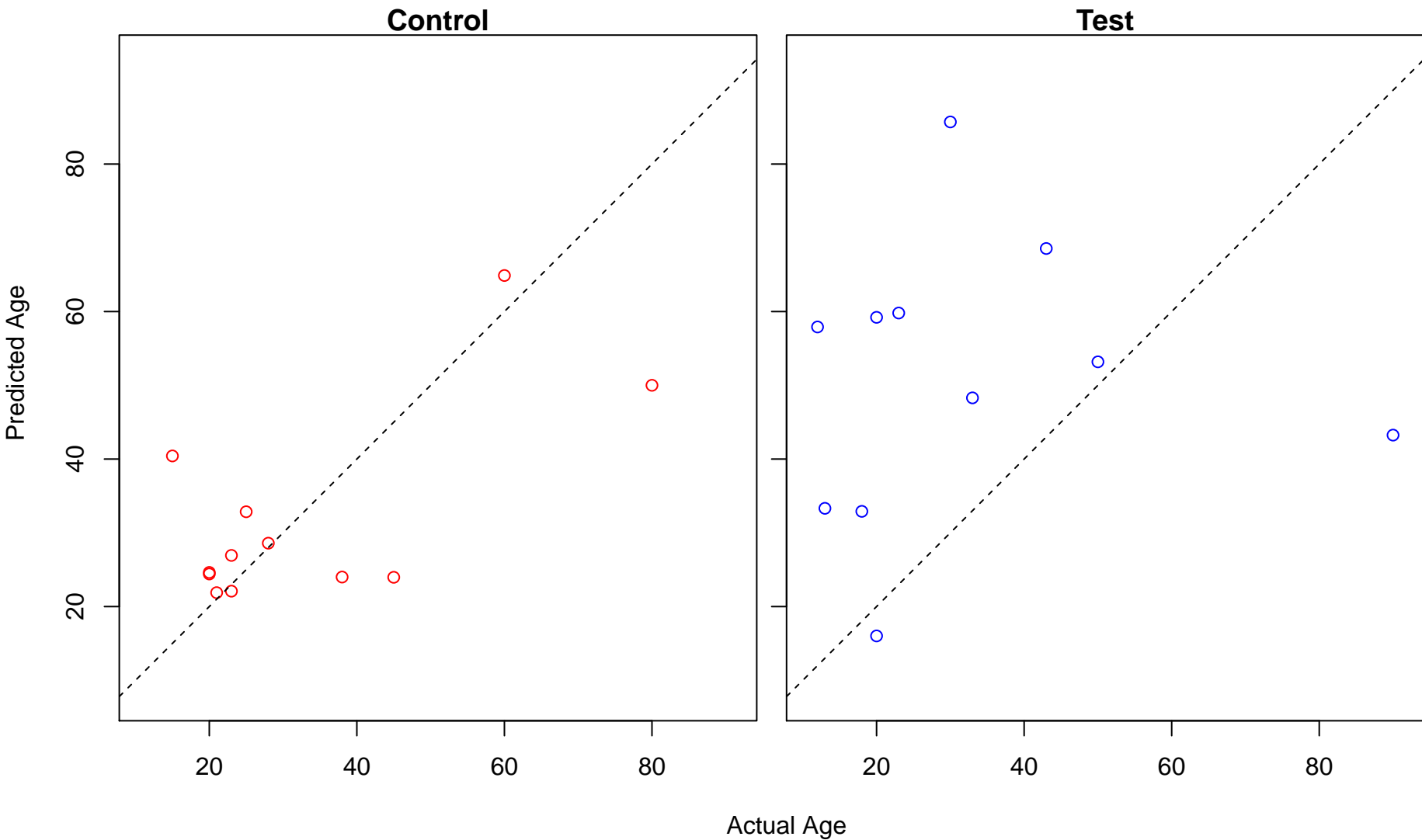
metanephros development (Score: 8.211603)



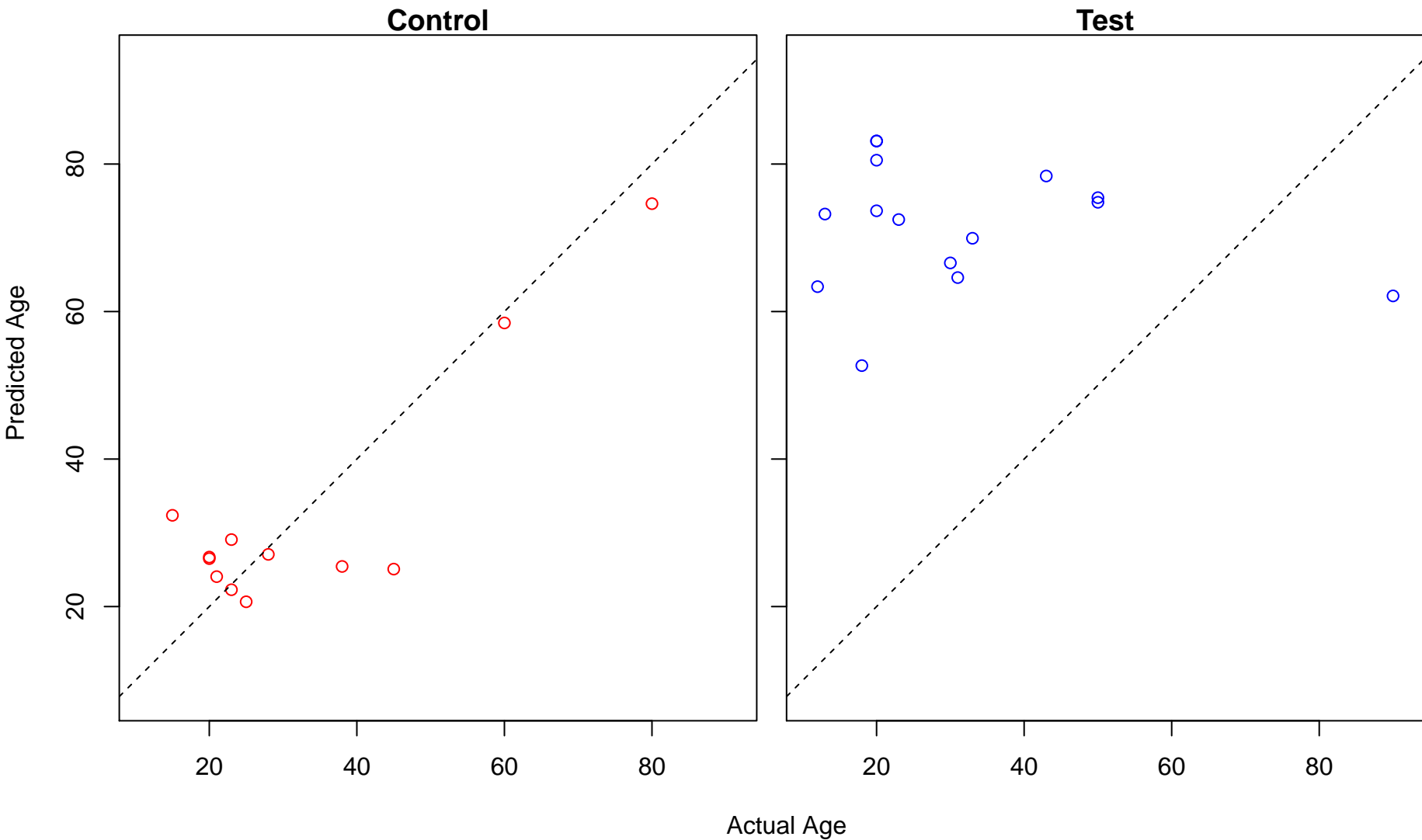
positive regulation of purine nucleotide metabolic process (Score: 8.199013)



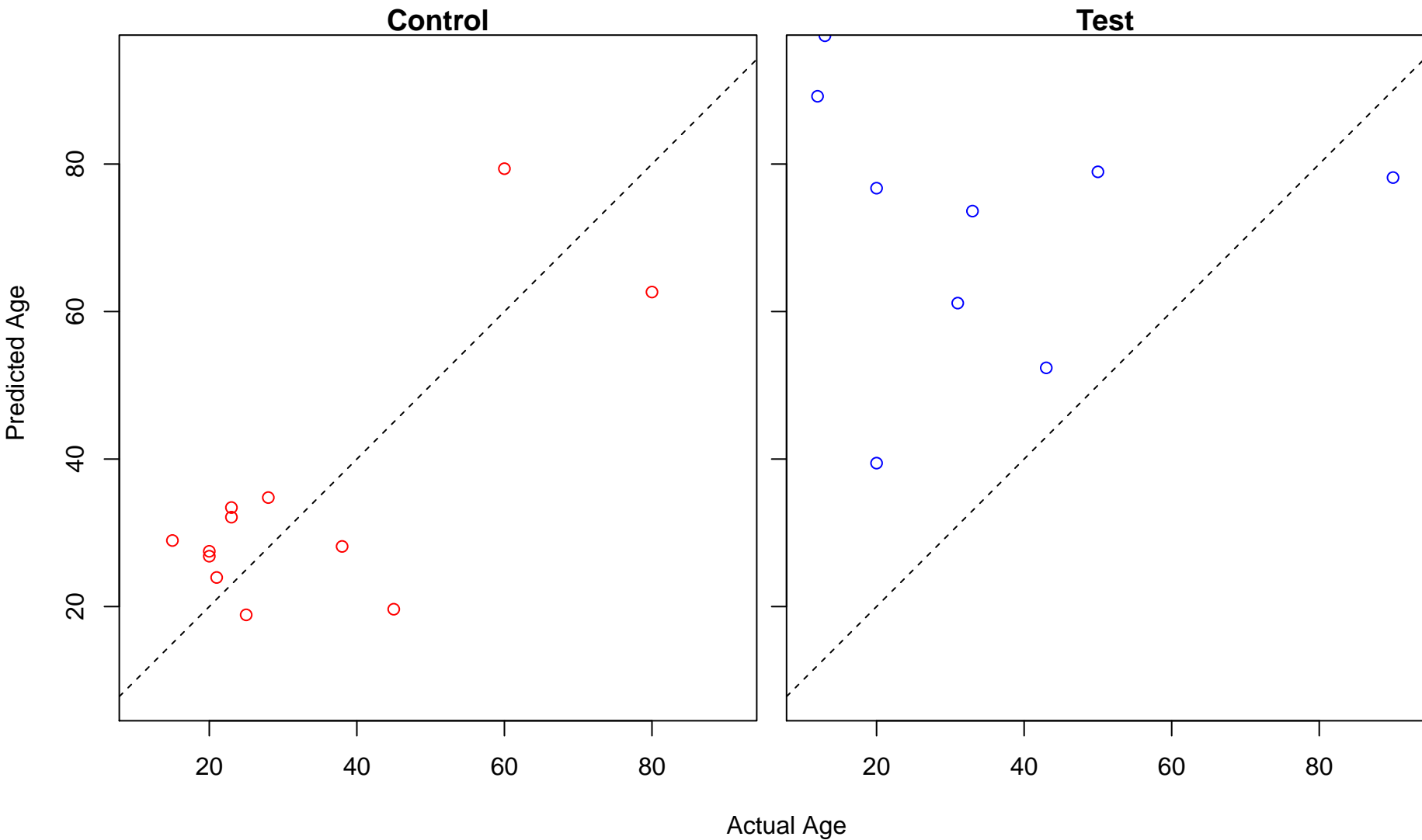
T cell chemotaxis (Score: 8.196789)



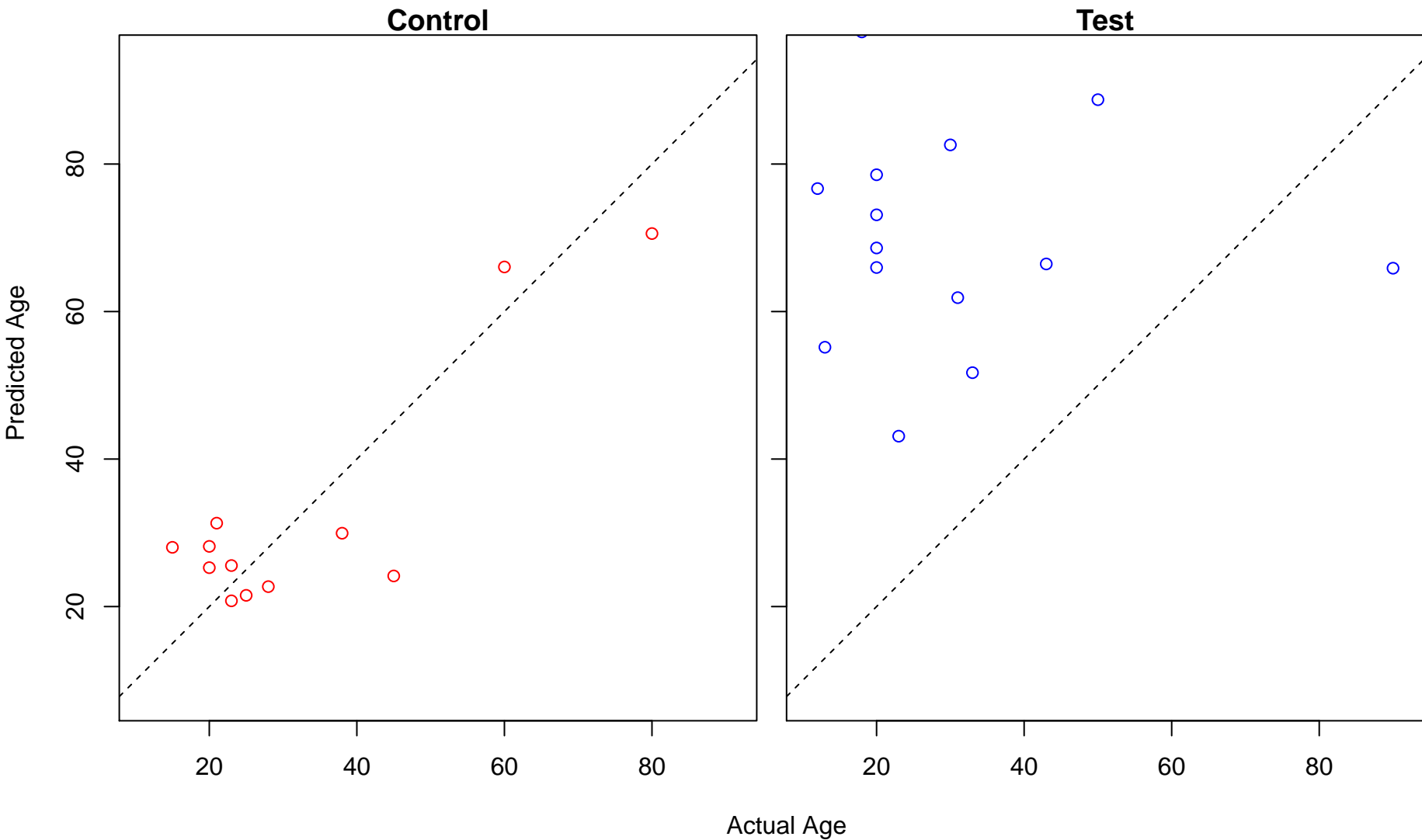
positive regulation by host of viral transcription (Score: 8.190206)



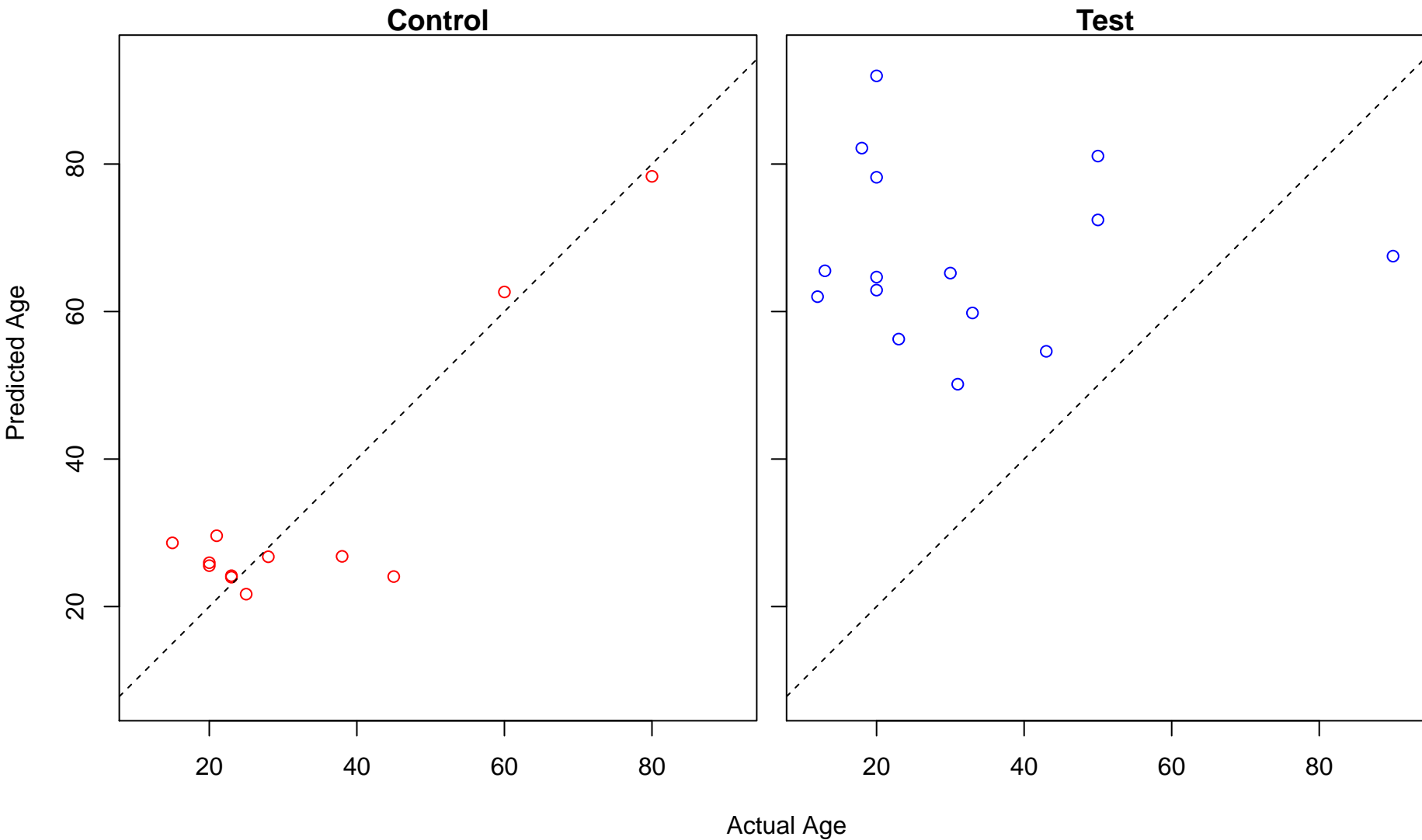
regulation of mitochondrial fission (Score: 8.189997)



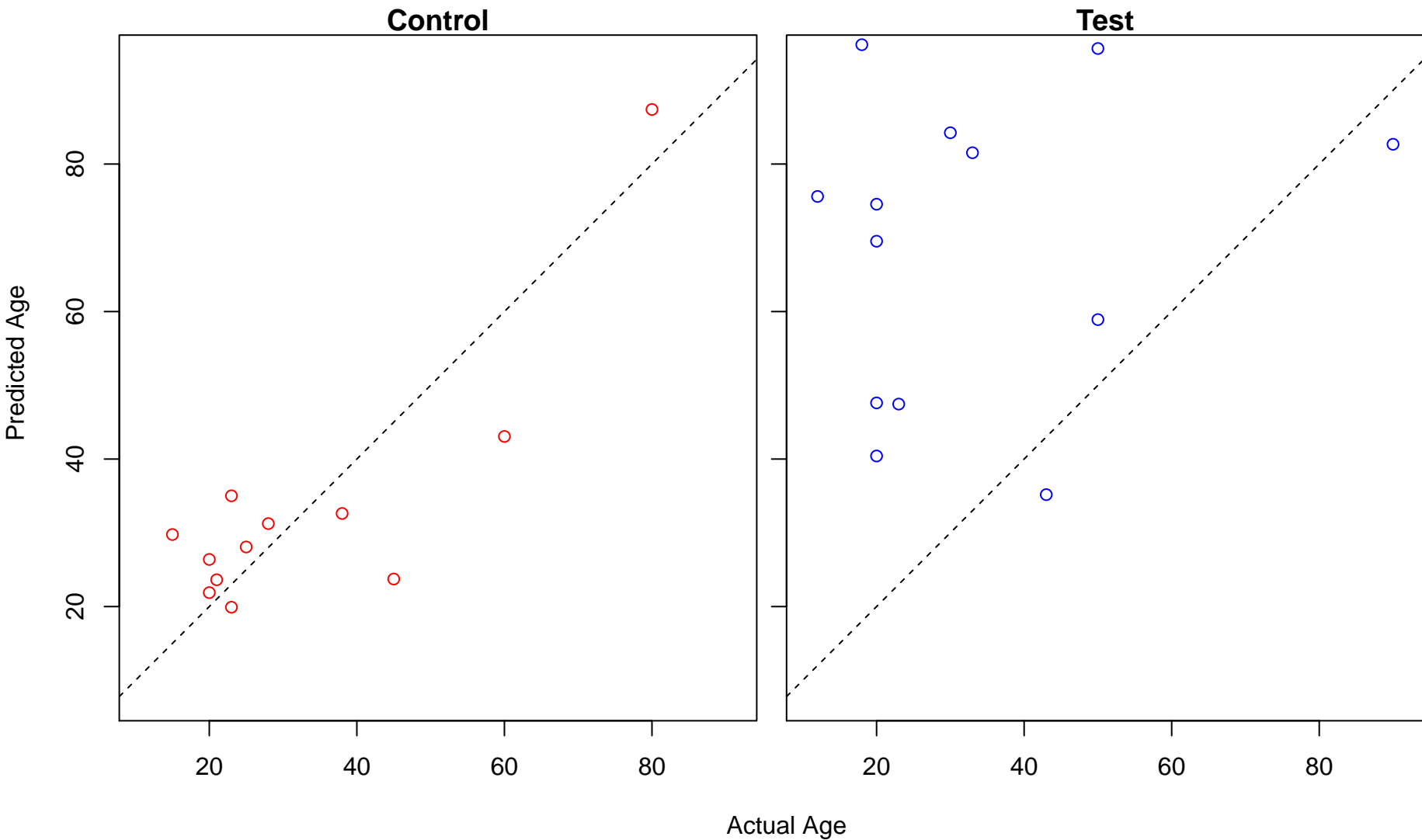
vasculature development (Score: 8.187997)



apoptotic signaling pathway (Score: 8.181401)

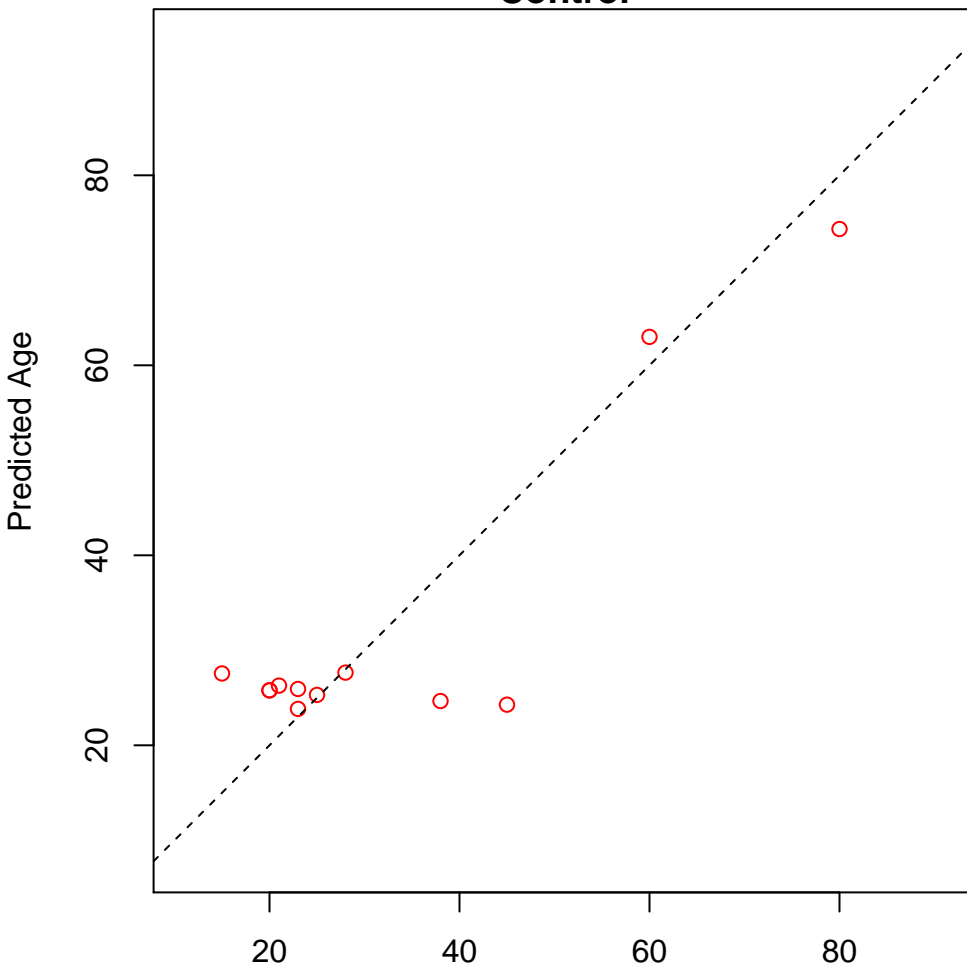


negative regulation of neuron differentiation (Score: 8.174897)

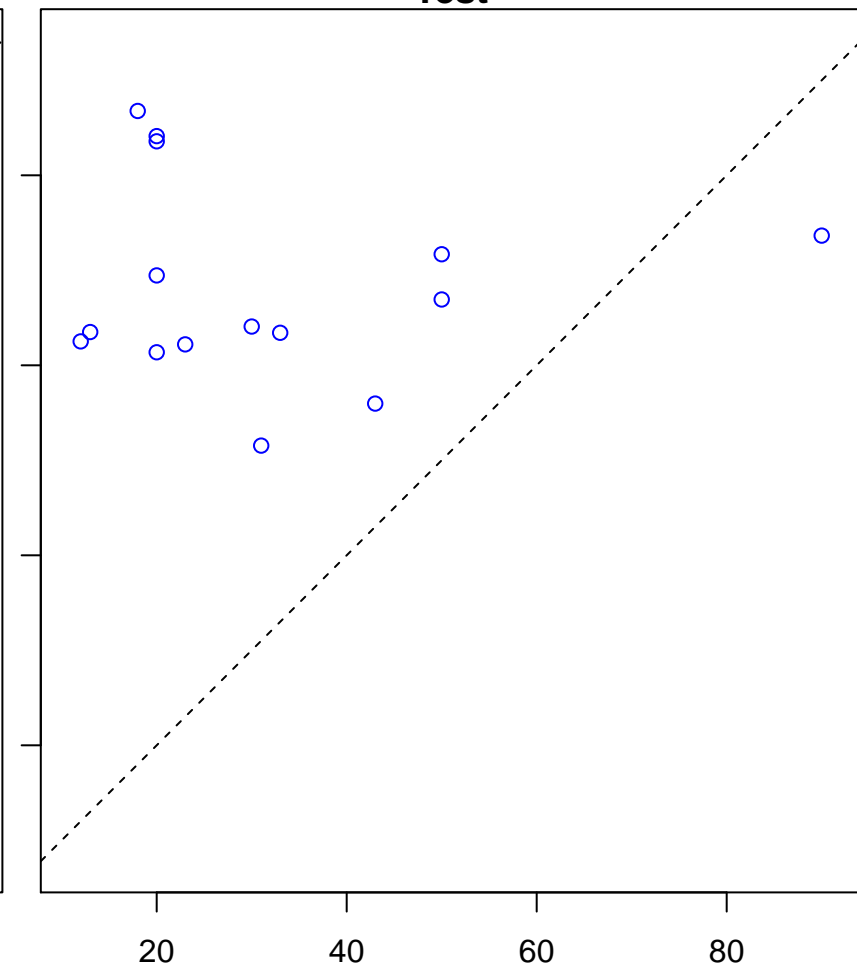


negative regulation of macroautophagy (Score: 8.172579)

Control

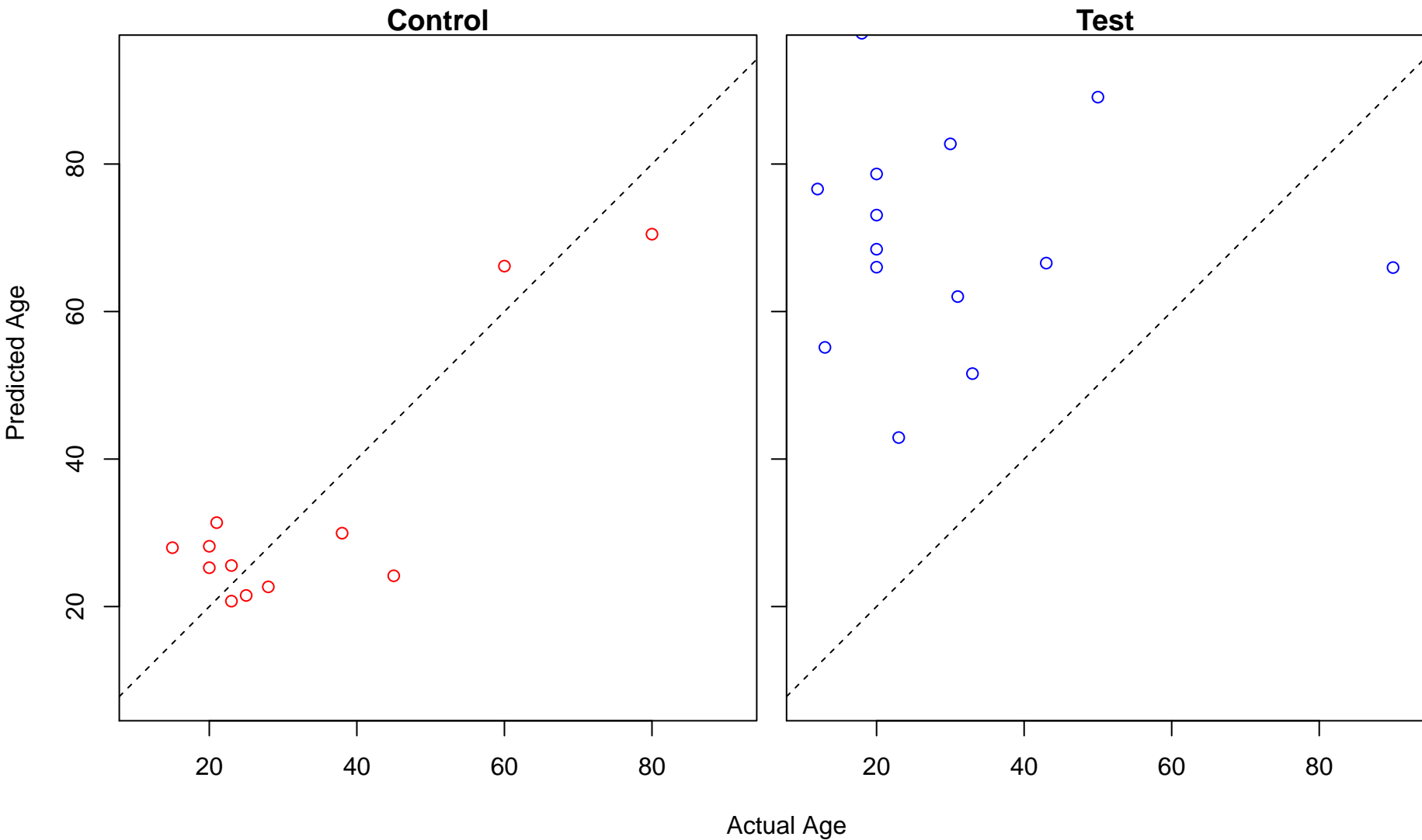


Test



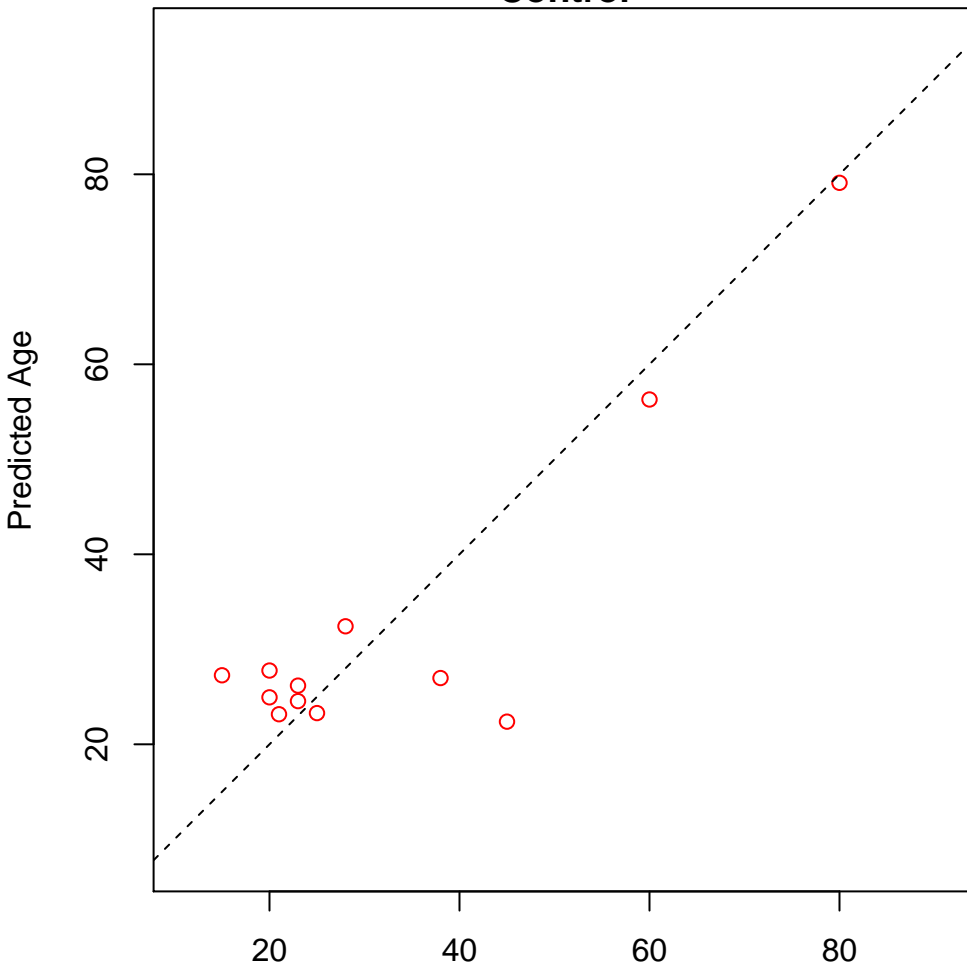
Actual Age

blood vessel development (Score: 8.170099)

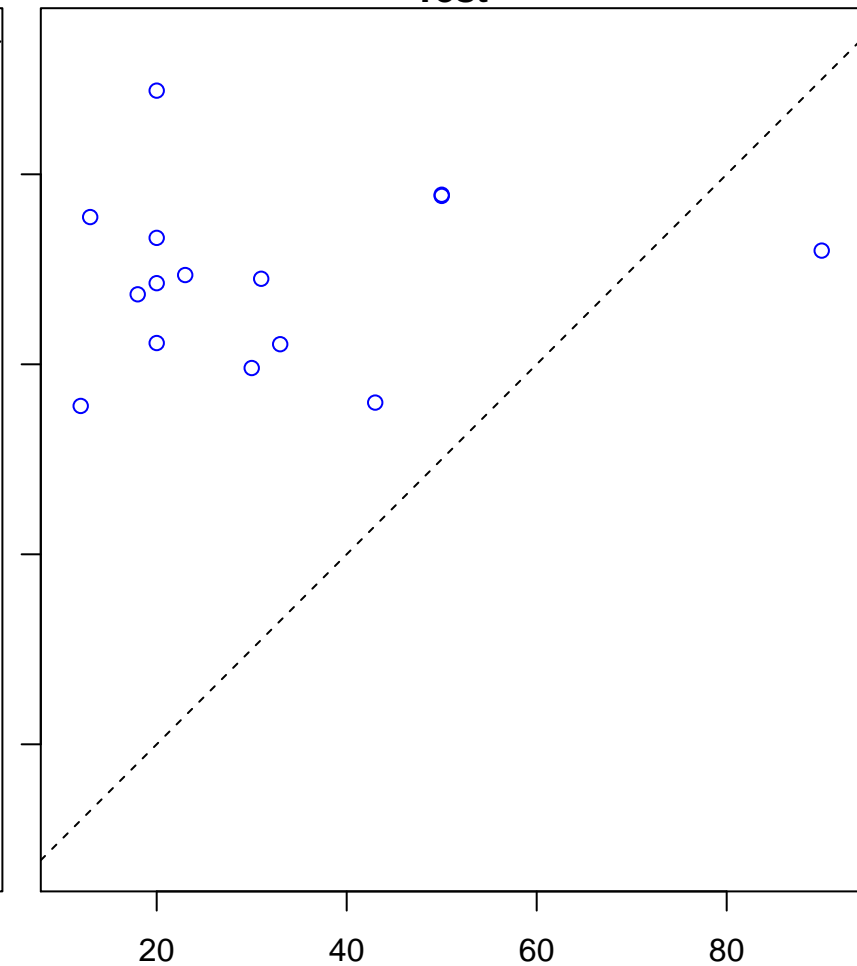


energy reserve metabolic process (Score: 8.169514)

Control

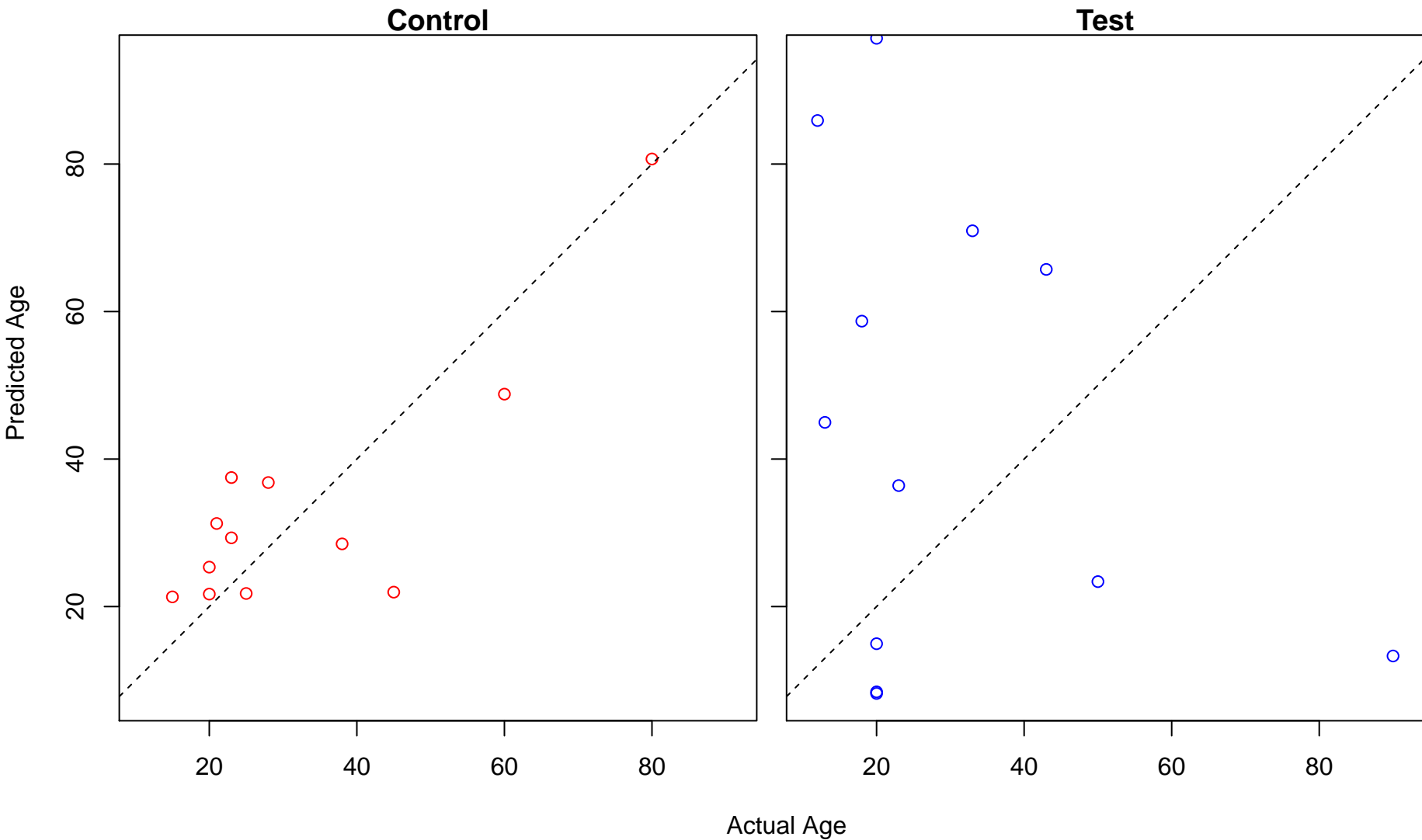


Test

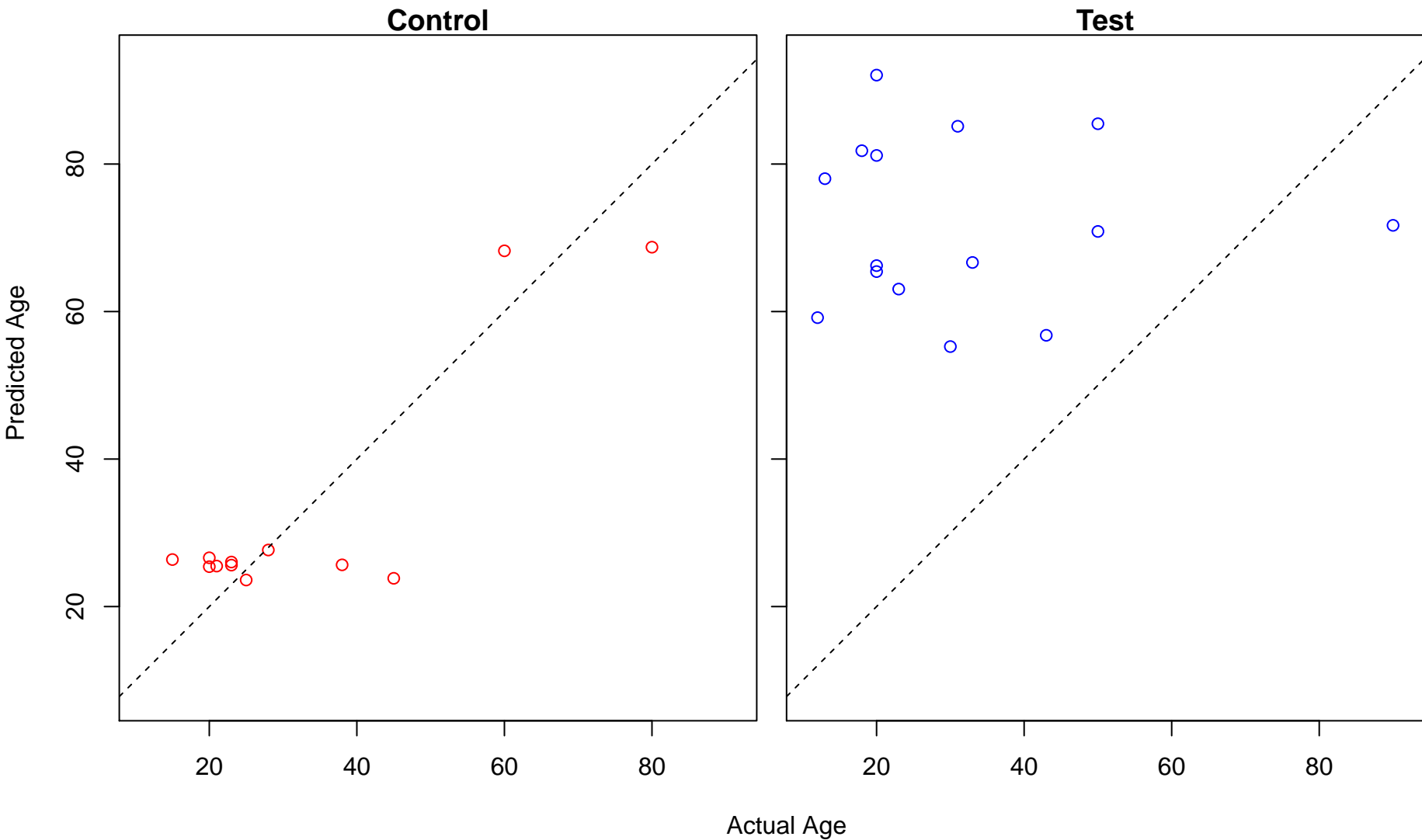


Actual Age

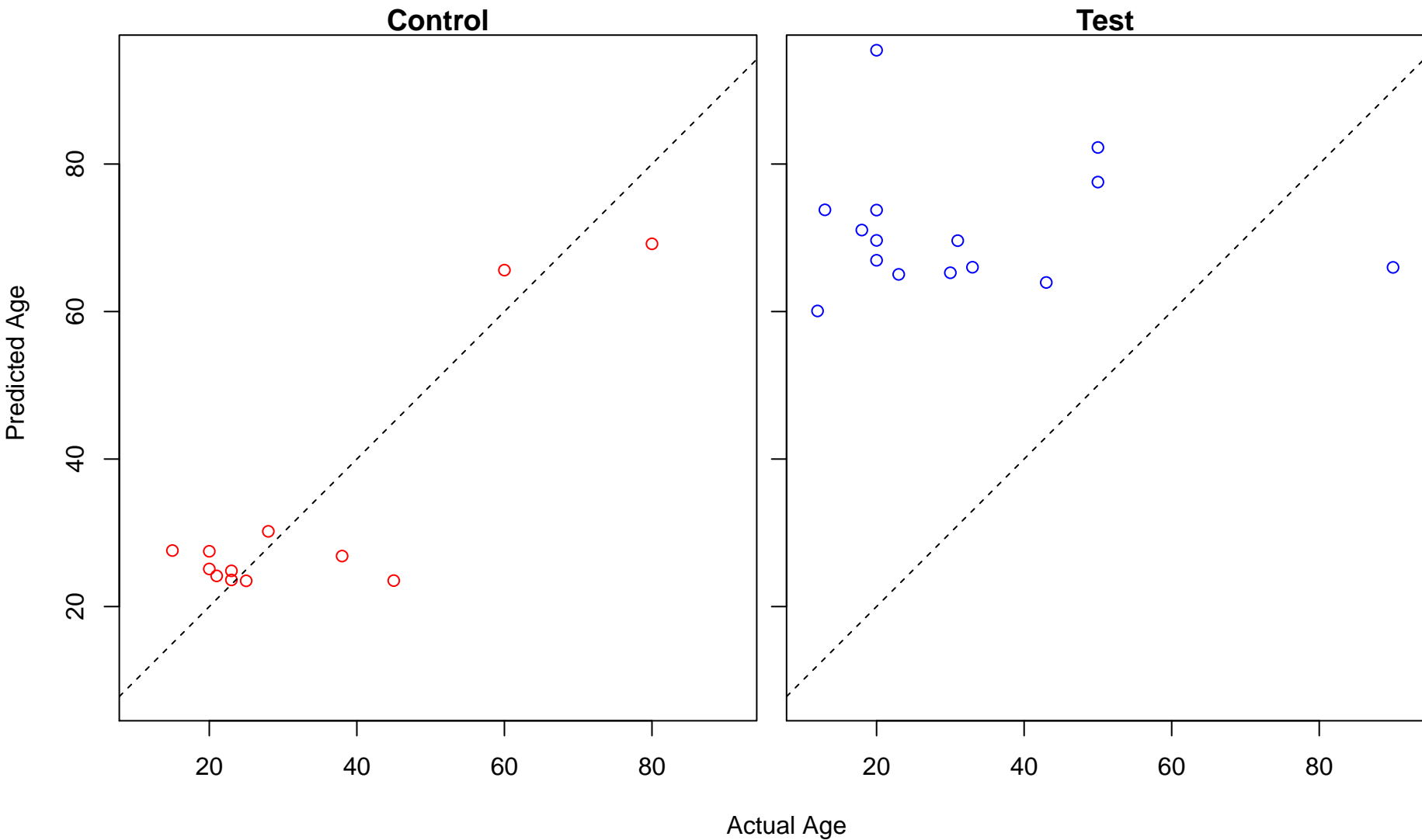
mesoderm development (Score: 8.169190)



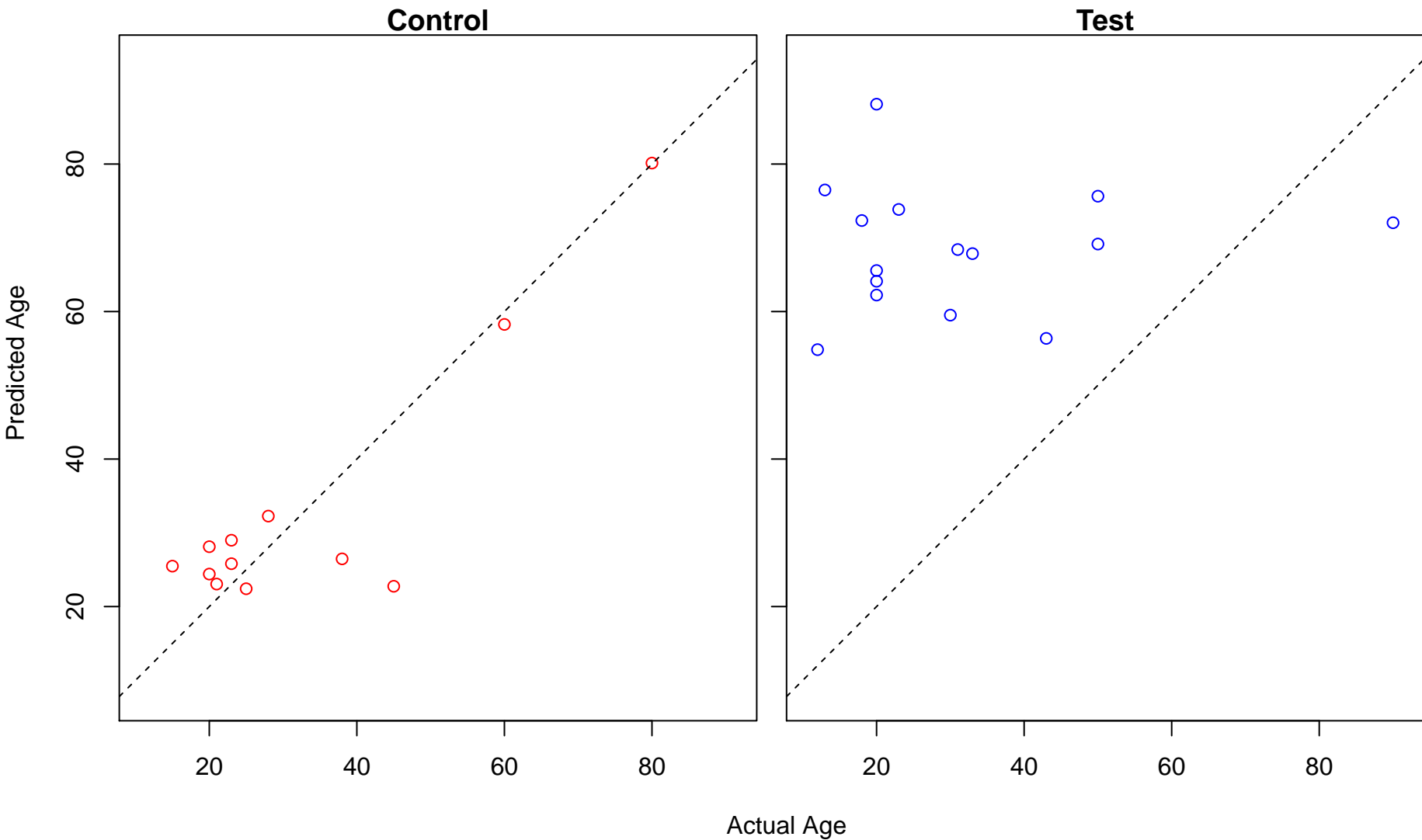
negative regulation of gene expression, epigenetic (Score: 8.168477)



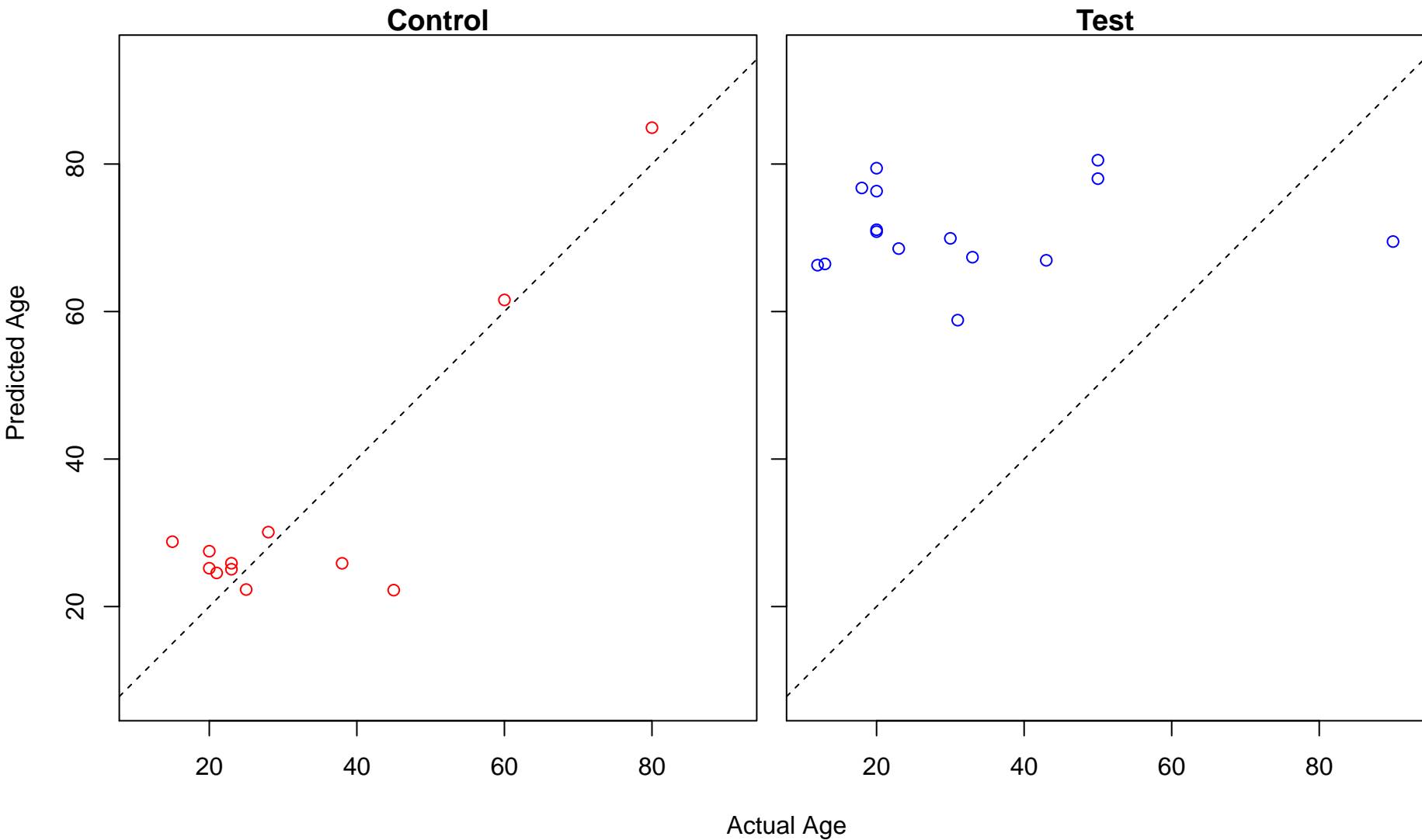
sensory perception (Score: 8.168357)



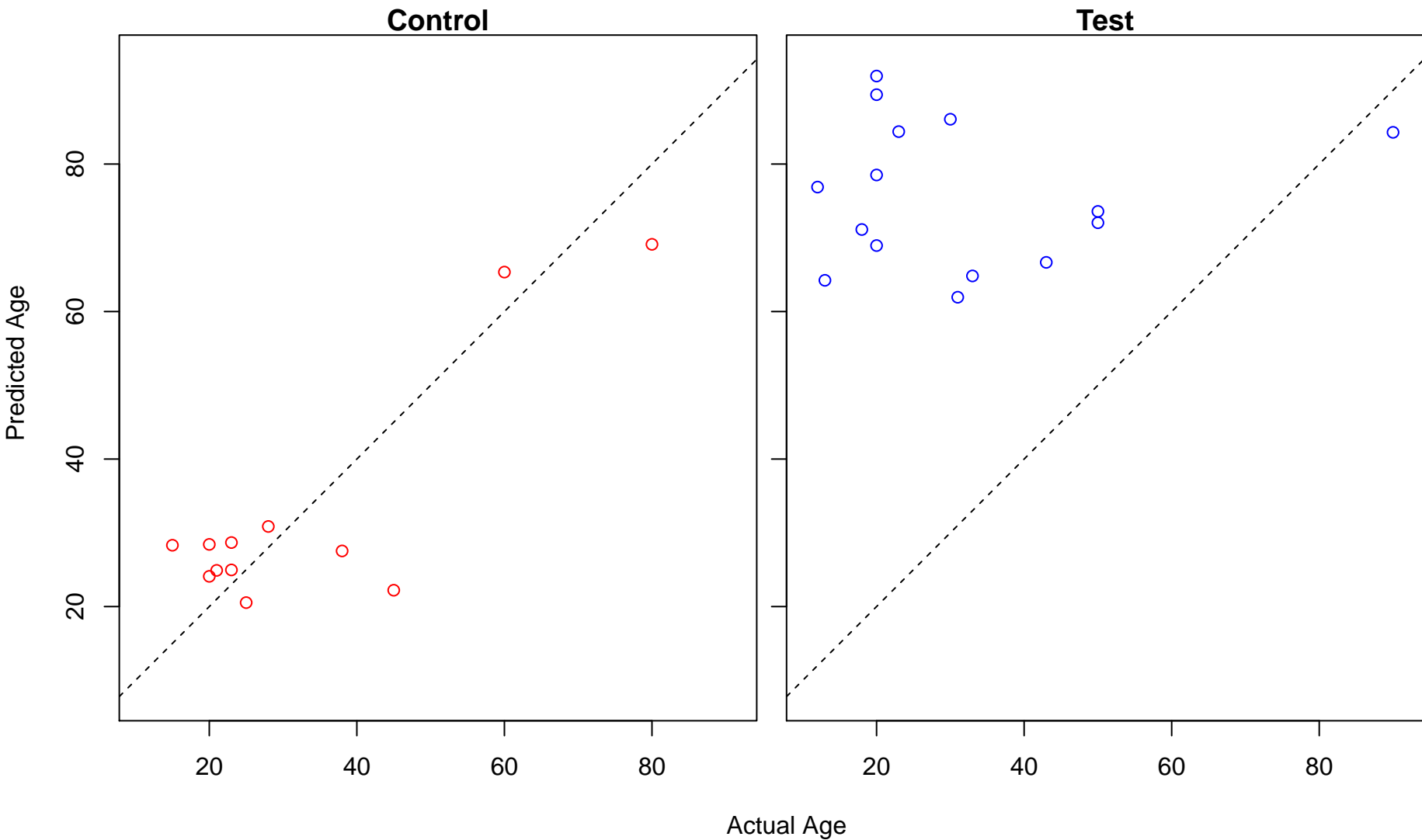
epithelium development (Score: 8.166611)



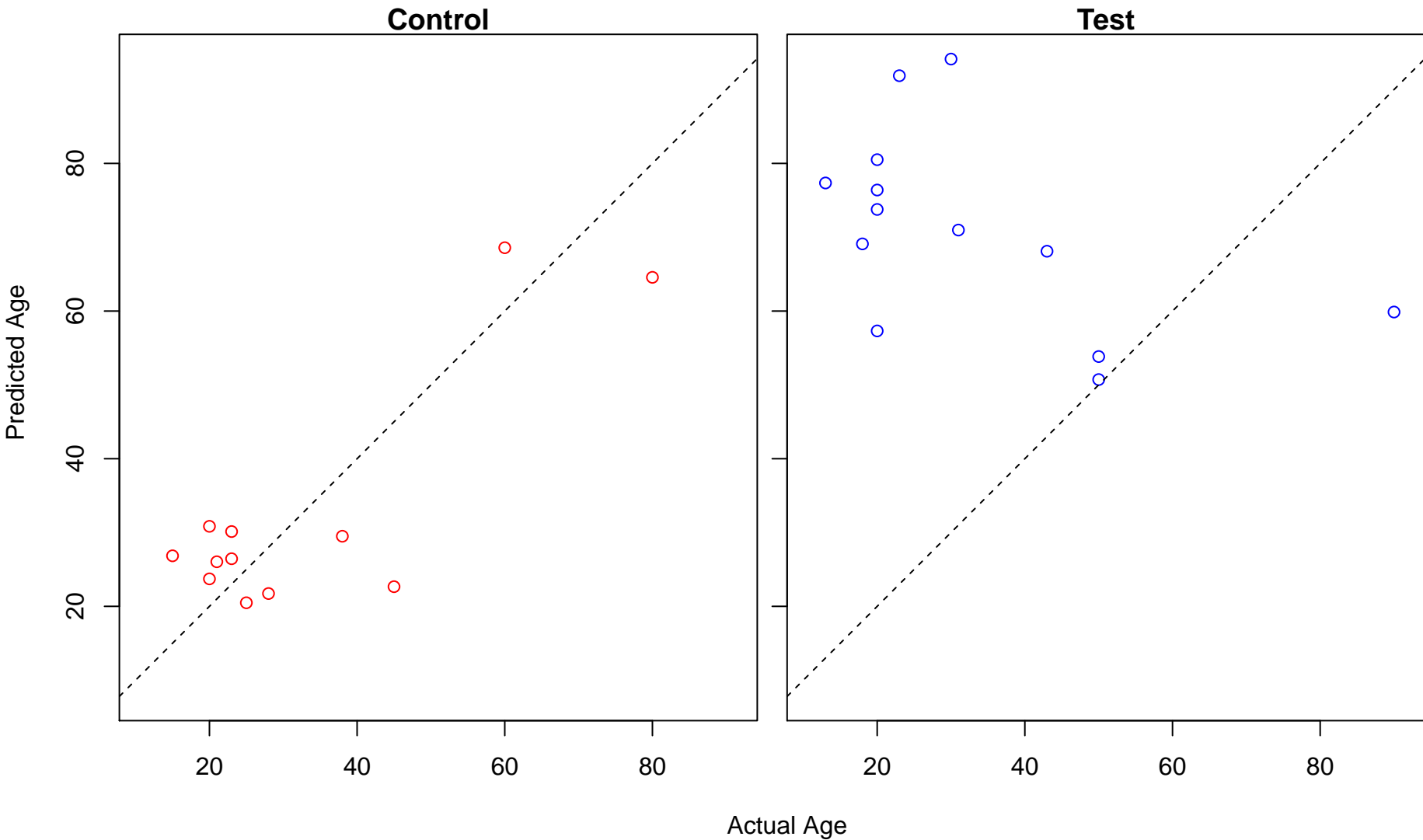
calcium ion transport (Score: 8.163826)



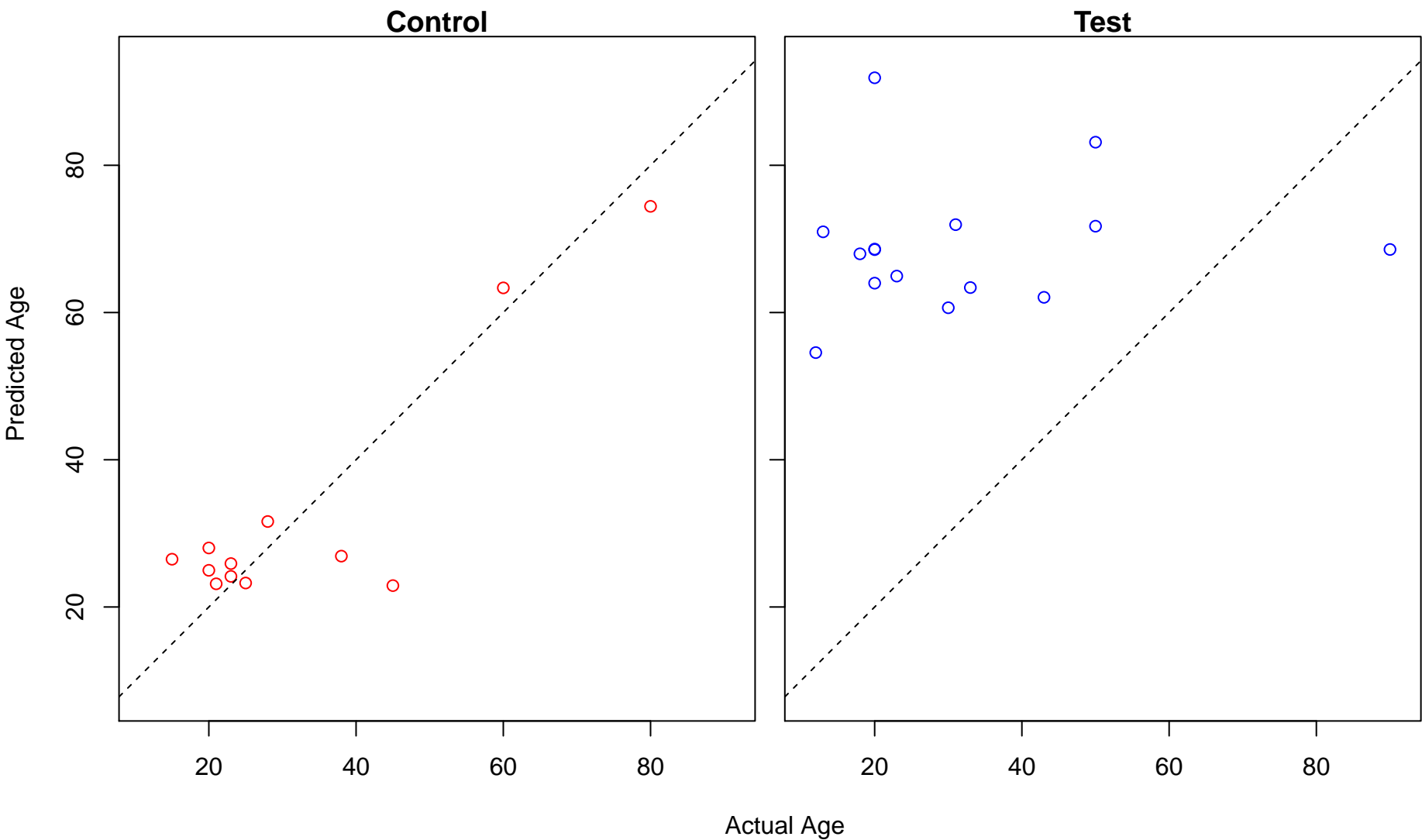
negative regulation of leukocyte proliferation (Score: 8.163352)



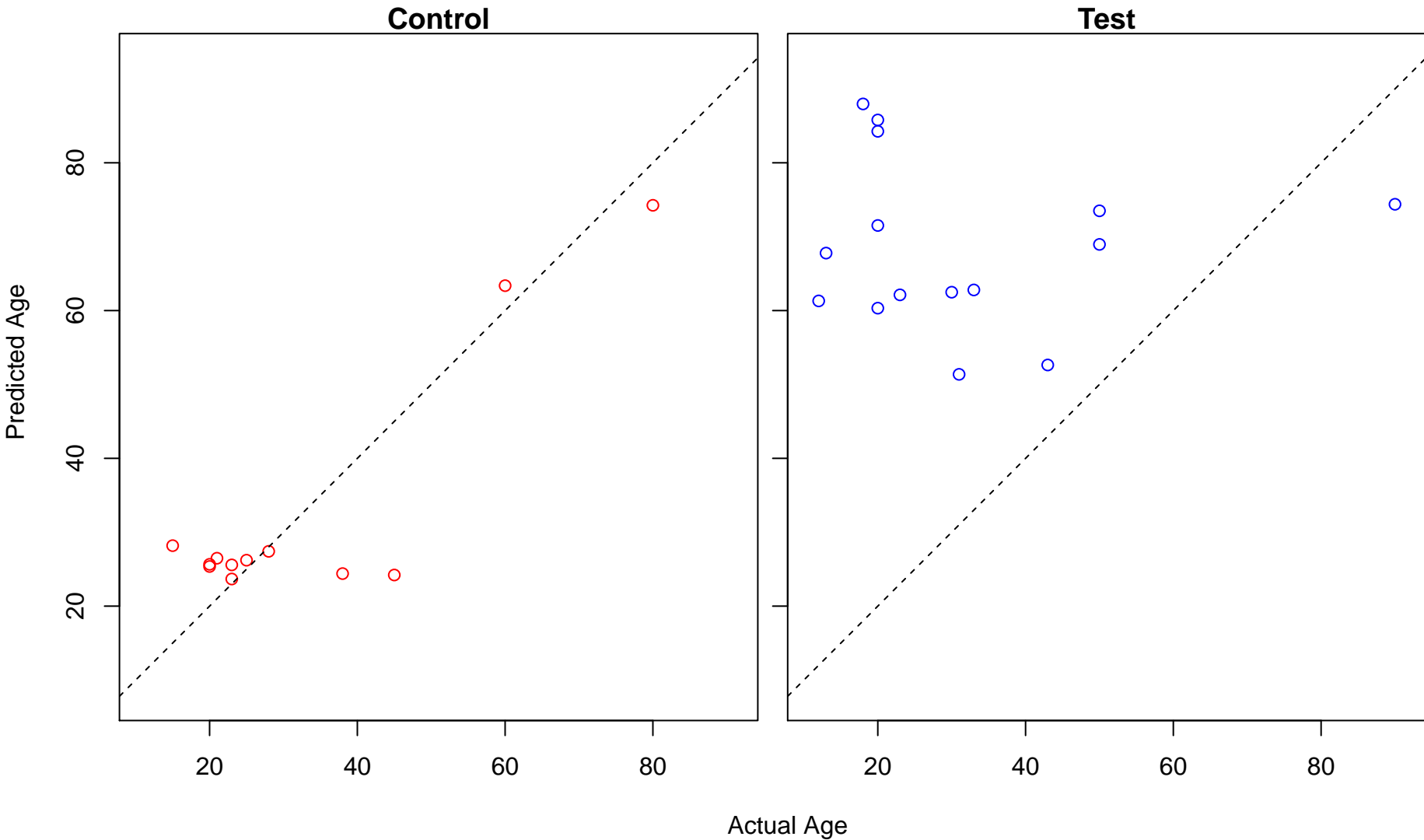
cell differentiation involved in embryonic placenta development (Score: 8.158429)



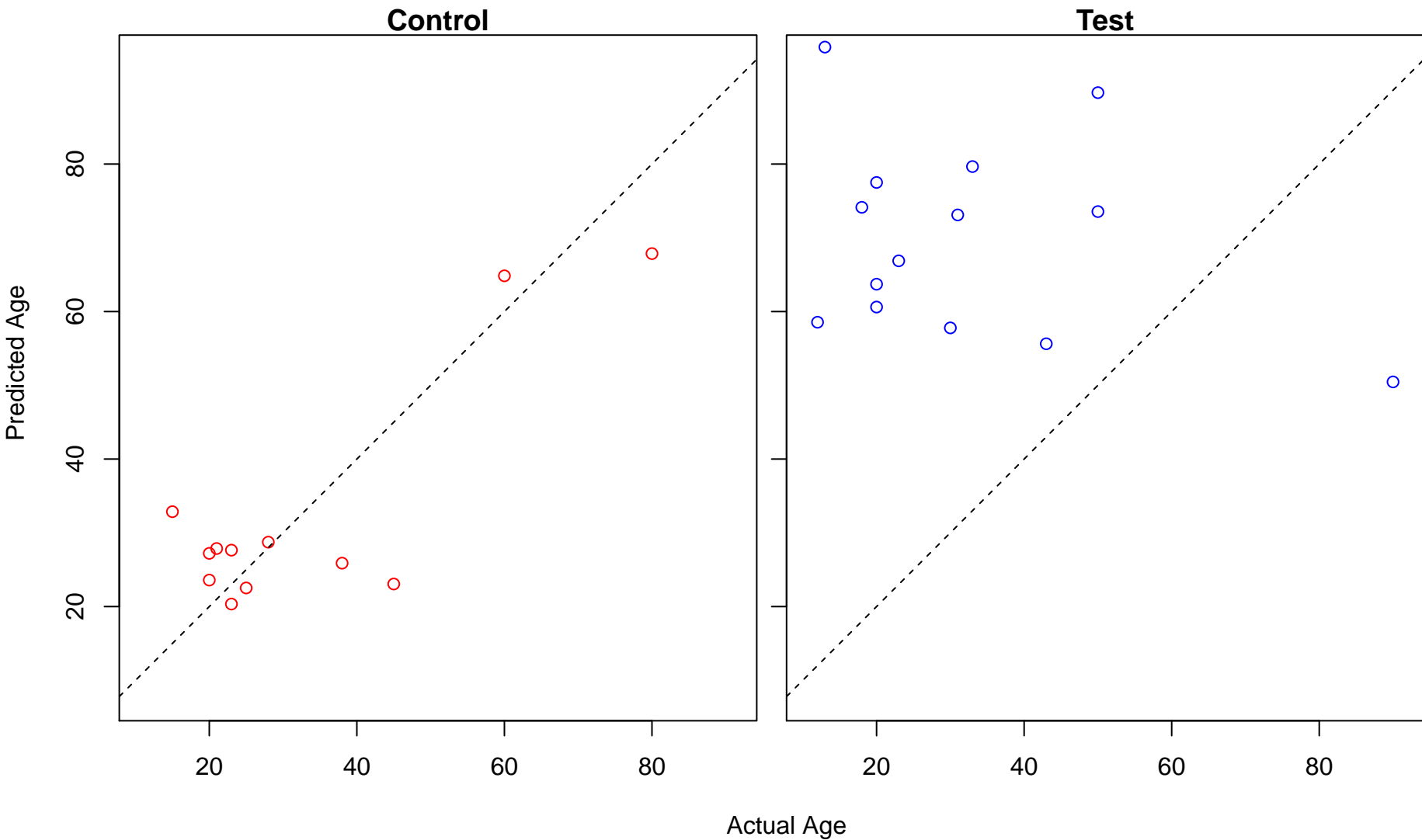
G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (Score: 8.0)



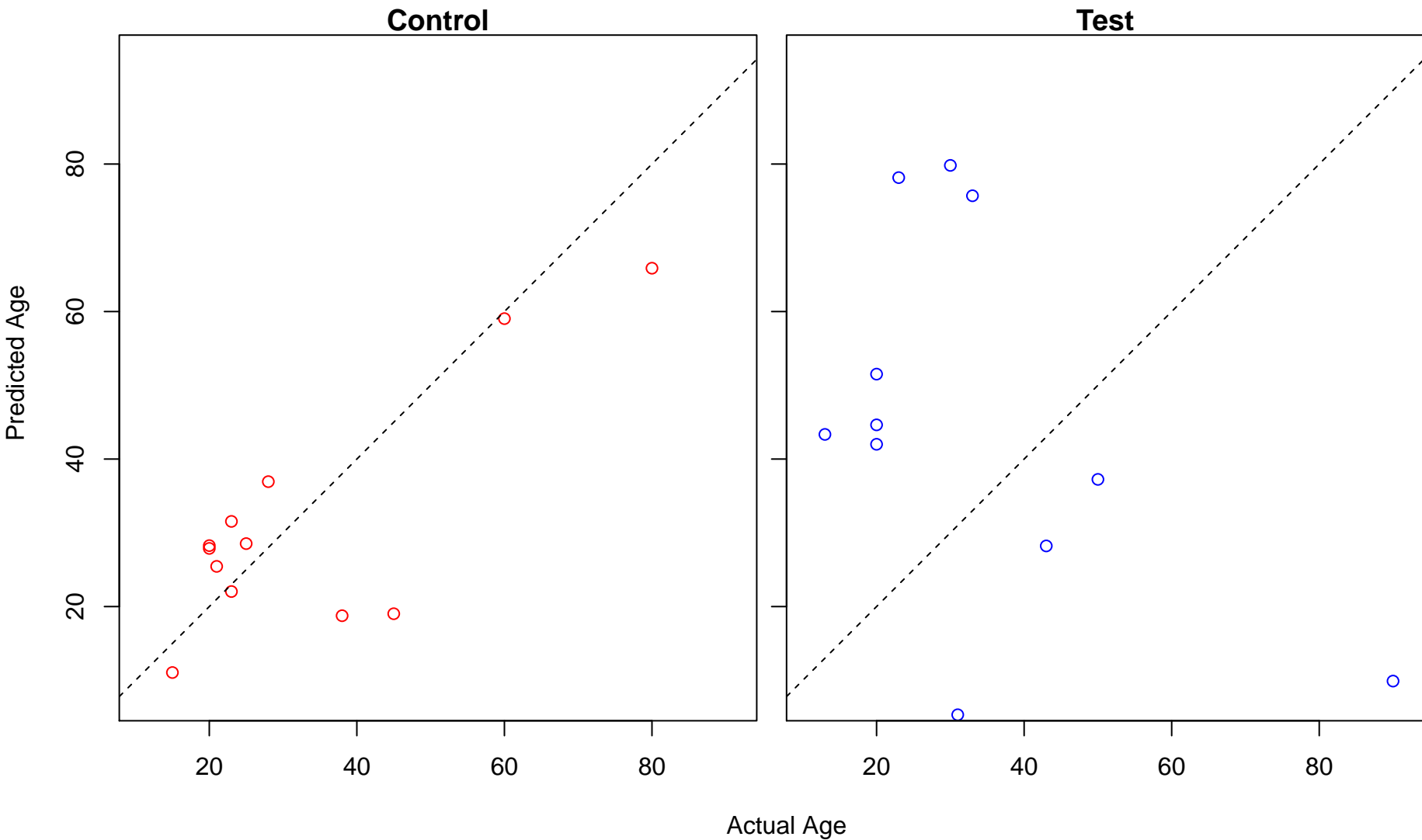
negative regulation of autophagosome assembly (Score: 8.149739)



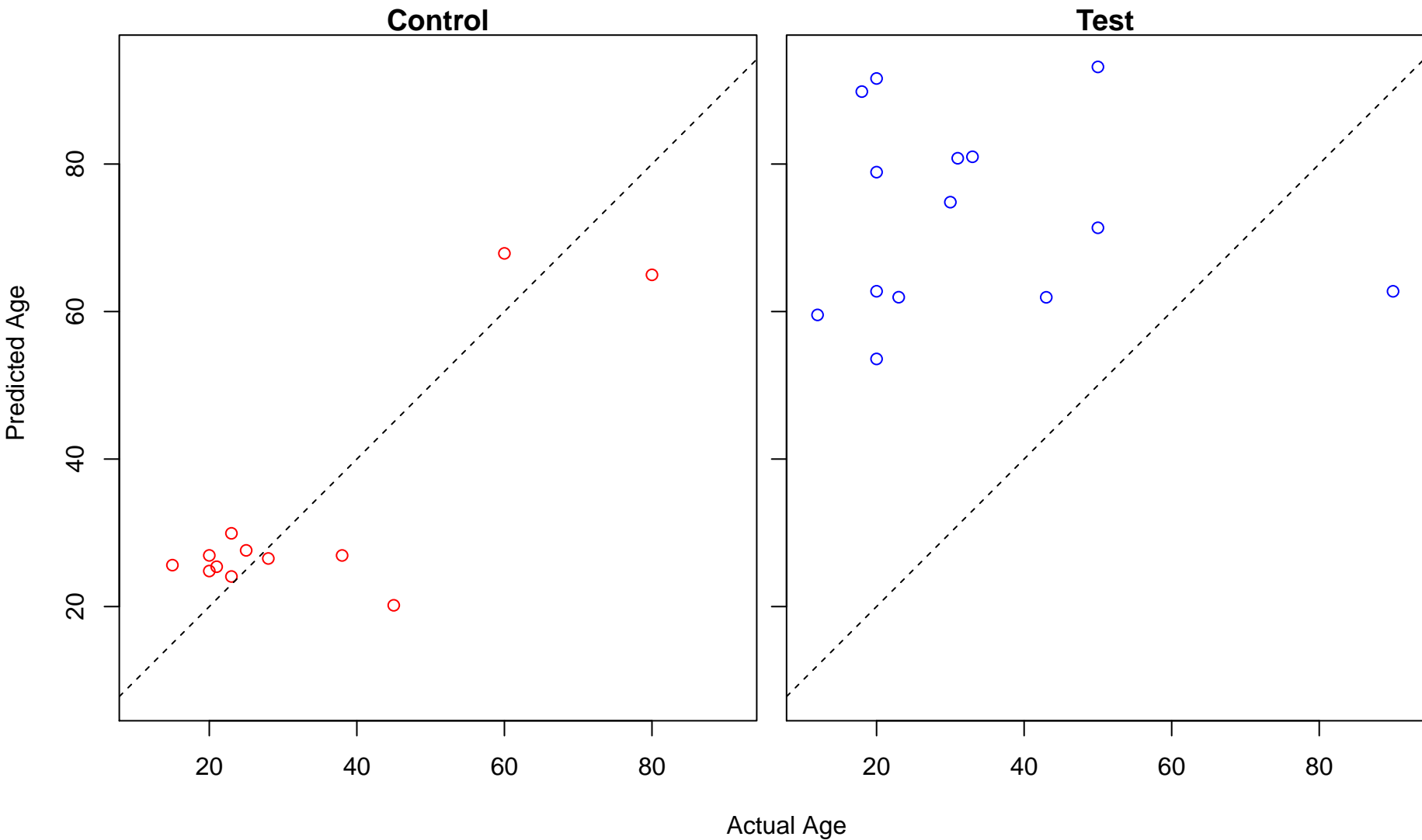
regulation of mitochondrial membrane potential (Score: 8.149633)



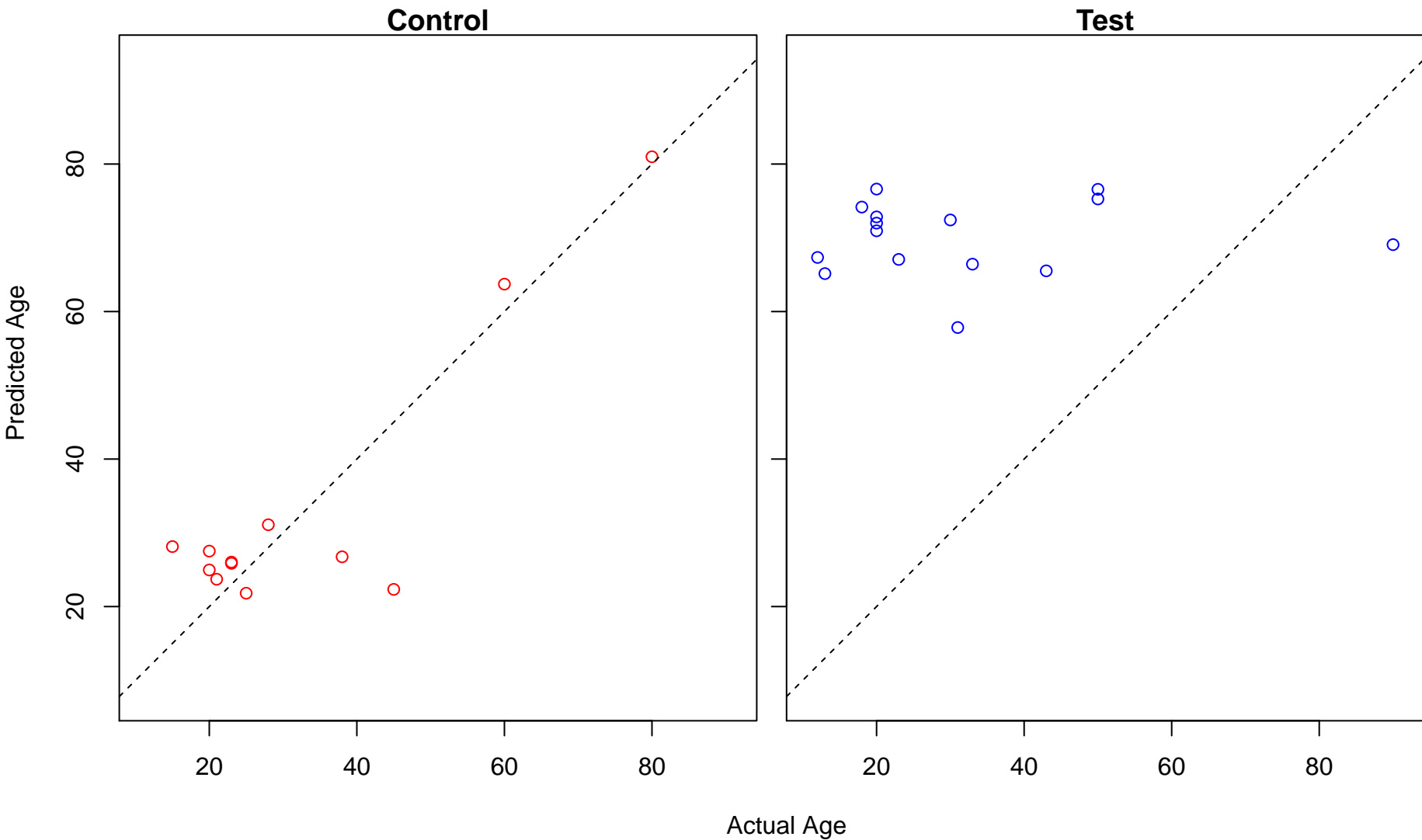
regulation of response to osmotic stress (Score: 8.145159)



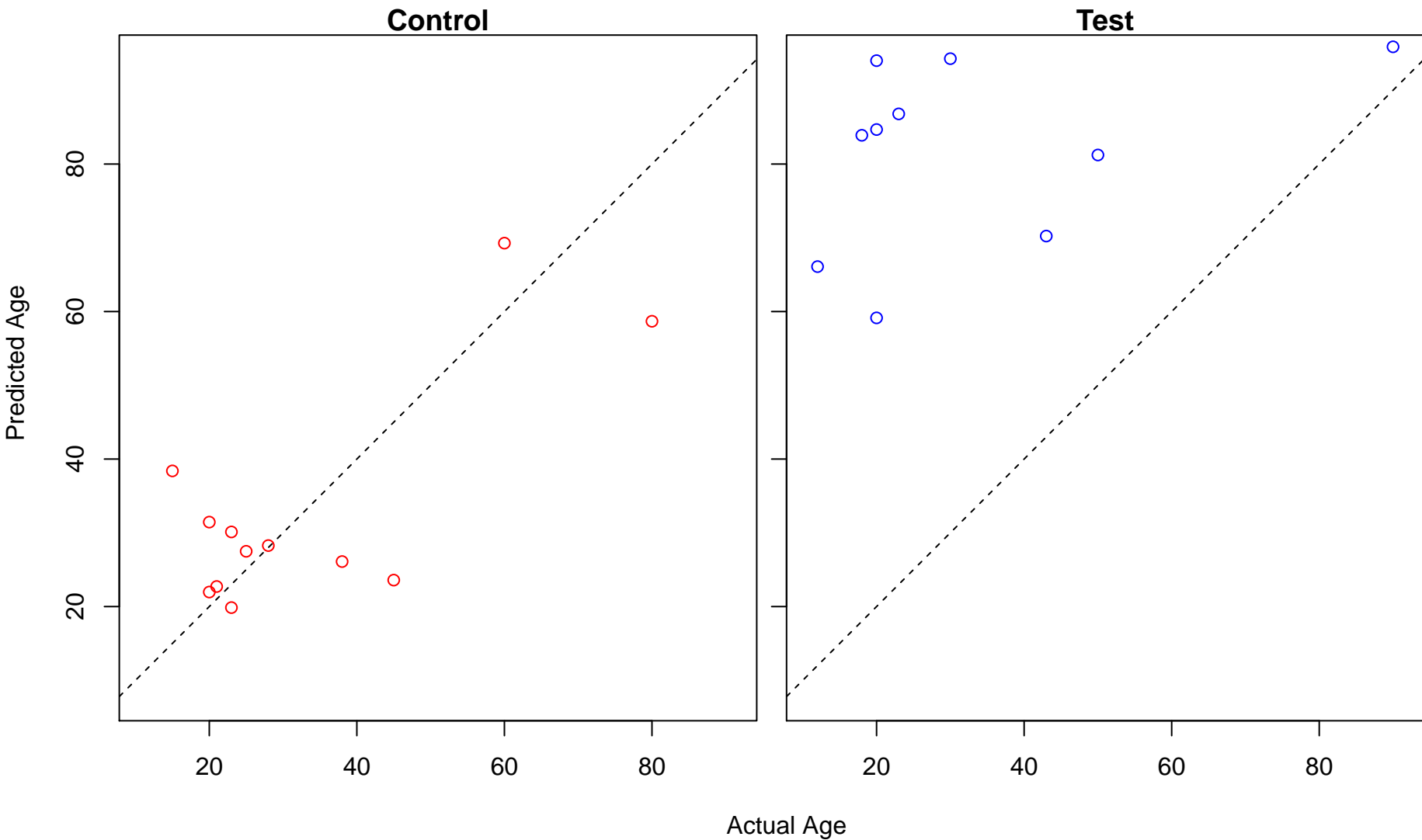
positive regulation of interferon-gamma production (Score: 8.141522)



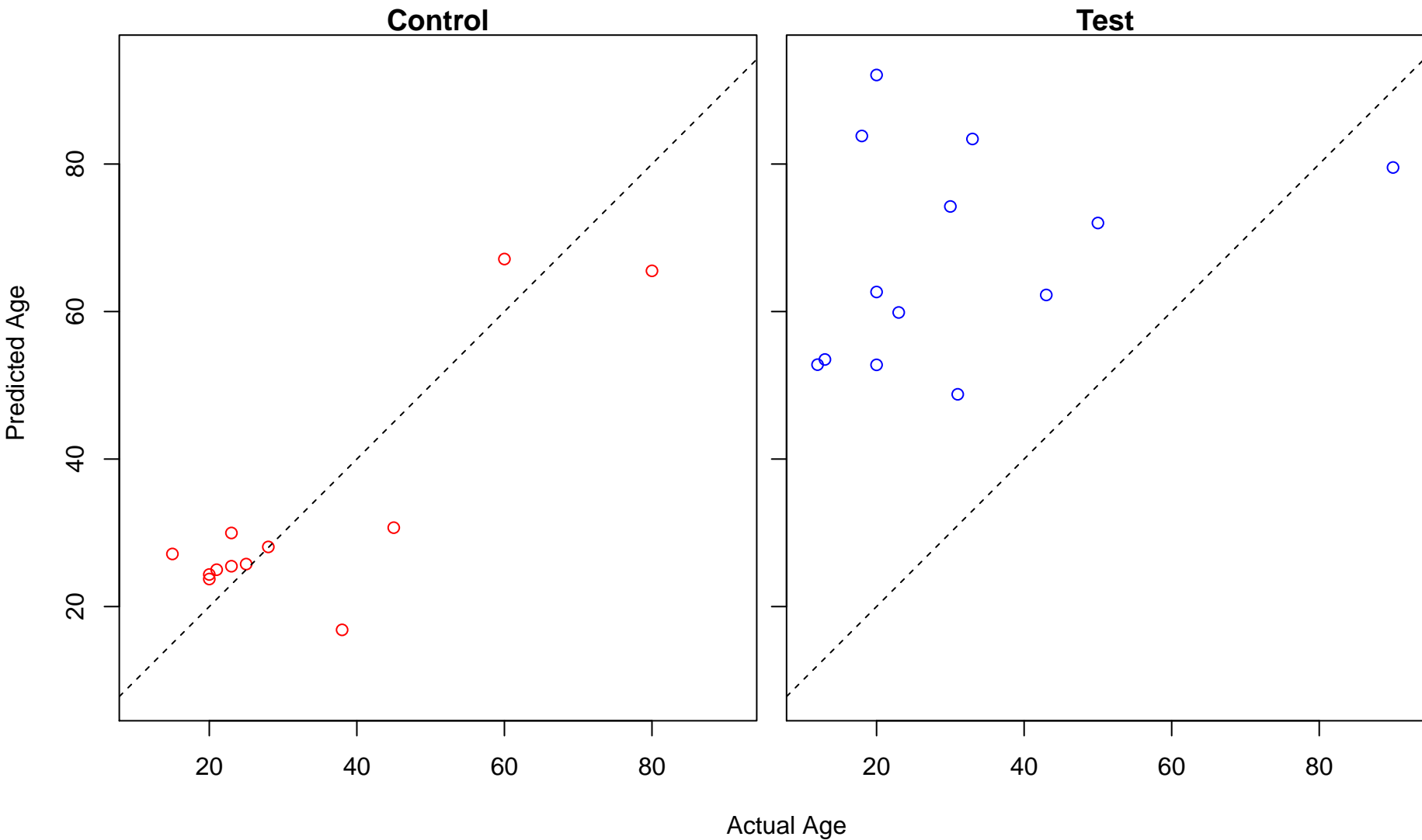
divalent inorganic cation transport (Score: 8.138740)



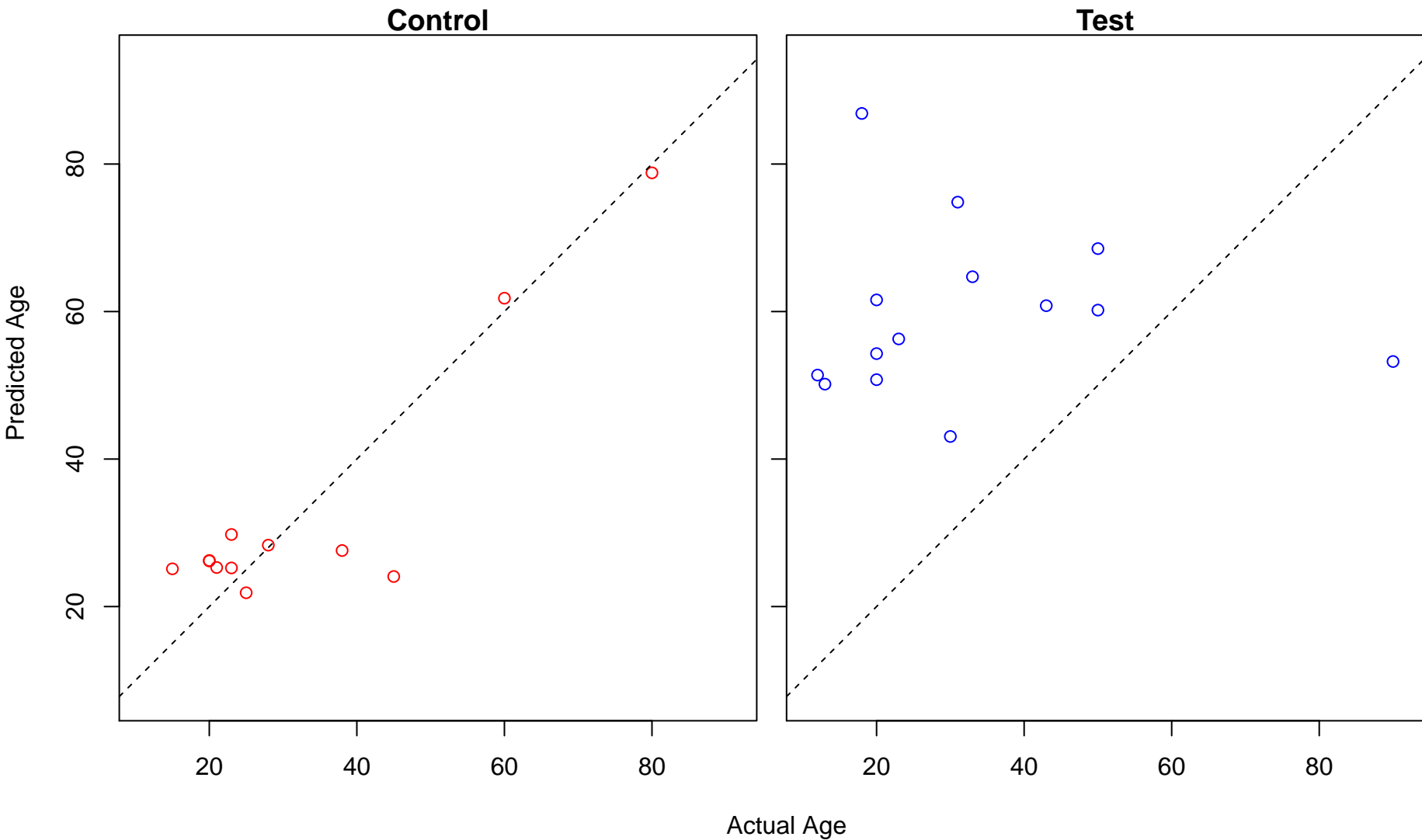
positive regulation of vascular endothelial growth factor receptor signaling pathway (Score: 8.12874)



diacylglycerol metabolic process (Score: 8.125885)

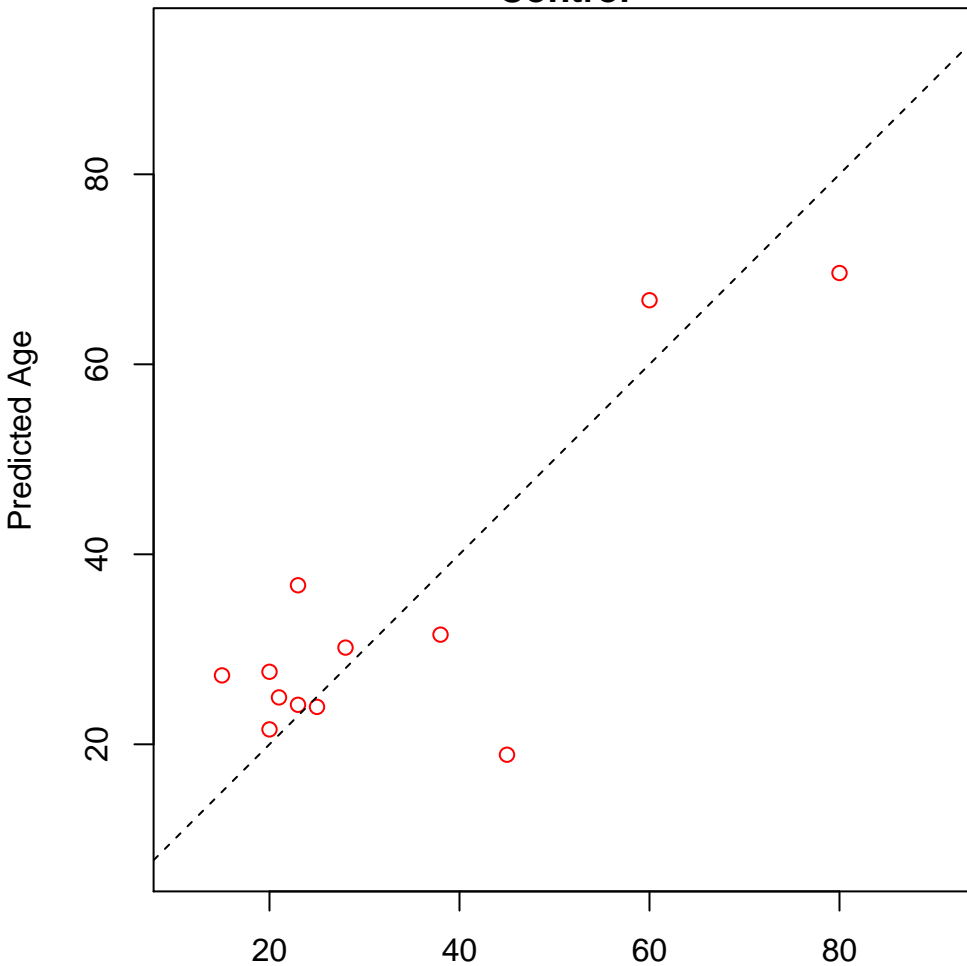


canonical Wnt signaling pathway (Score: 8.123460)

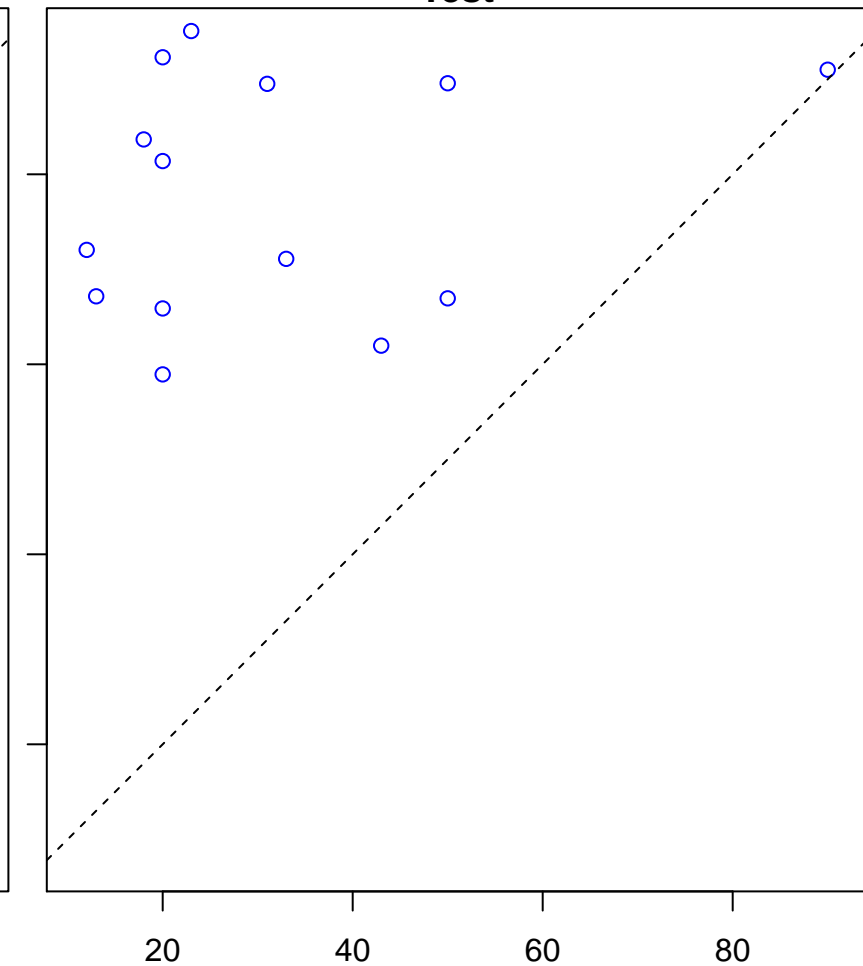


negative regulation of T cell proliferation (Score: 8.123374)

Control



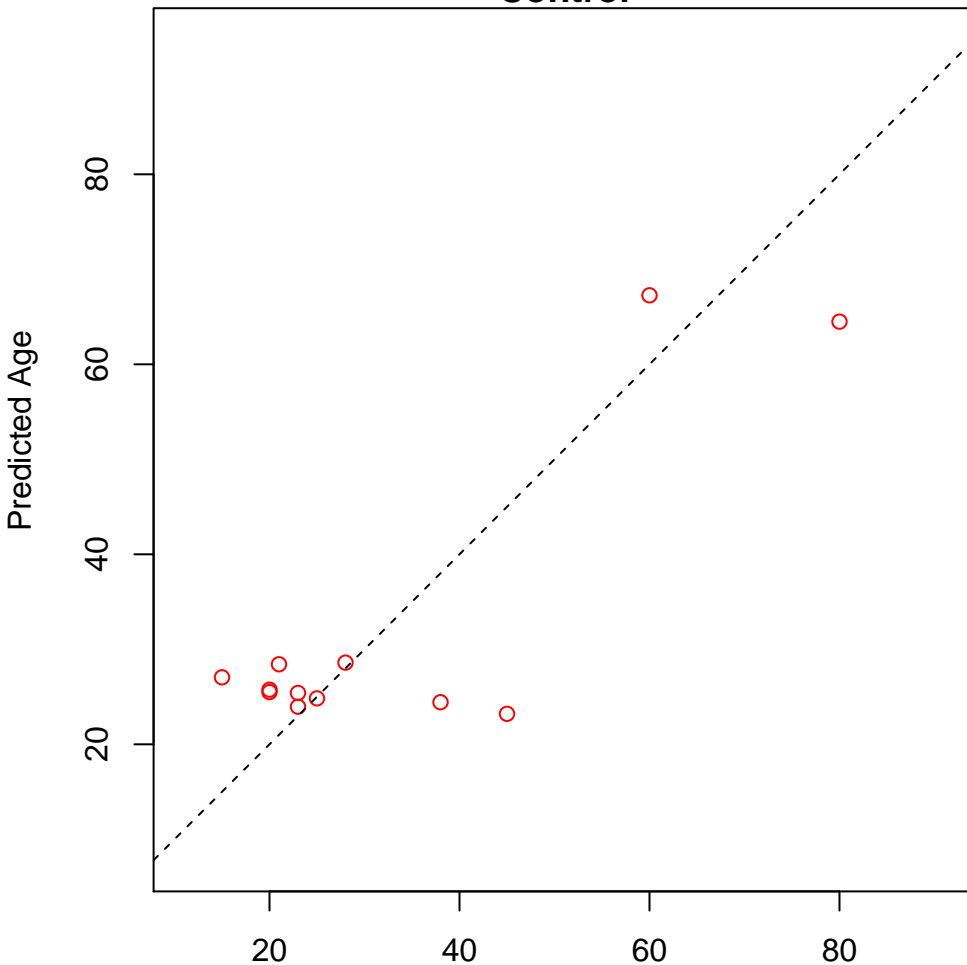
Test



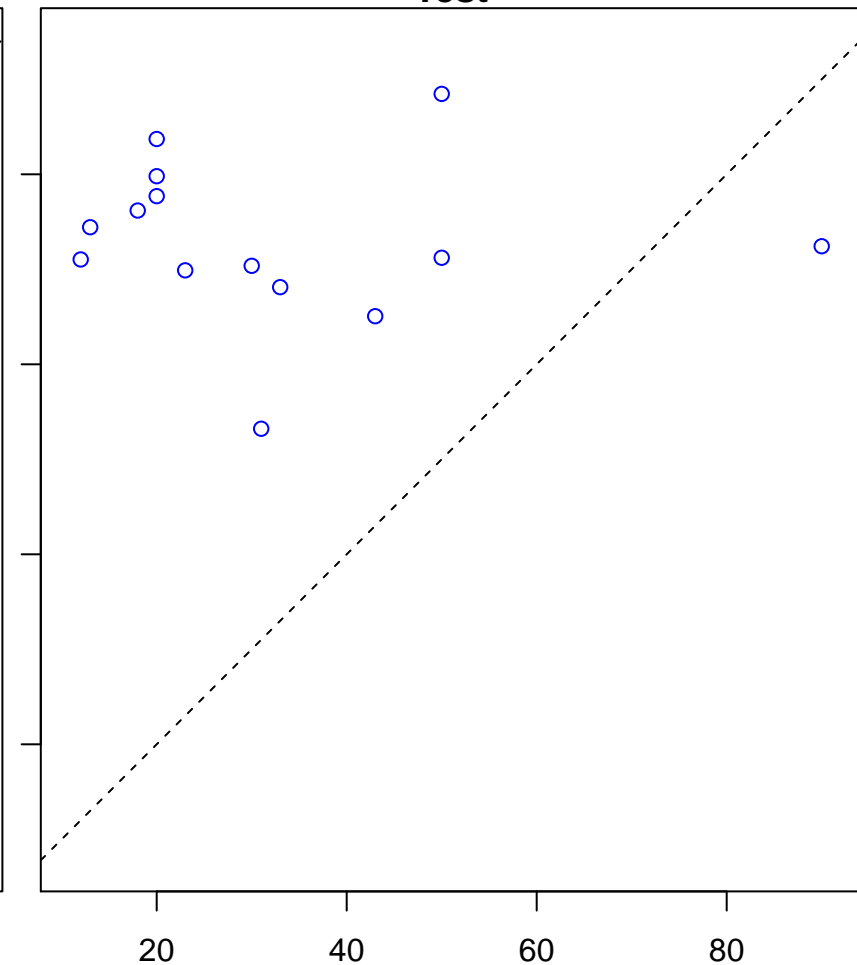
Actual Age

purine nucleotide catabolic process (Score: 8.117058)

Control

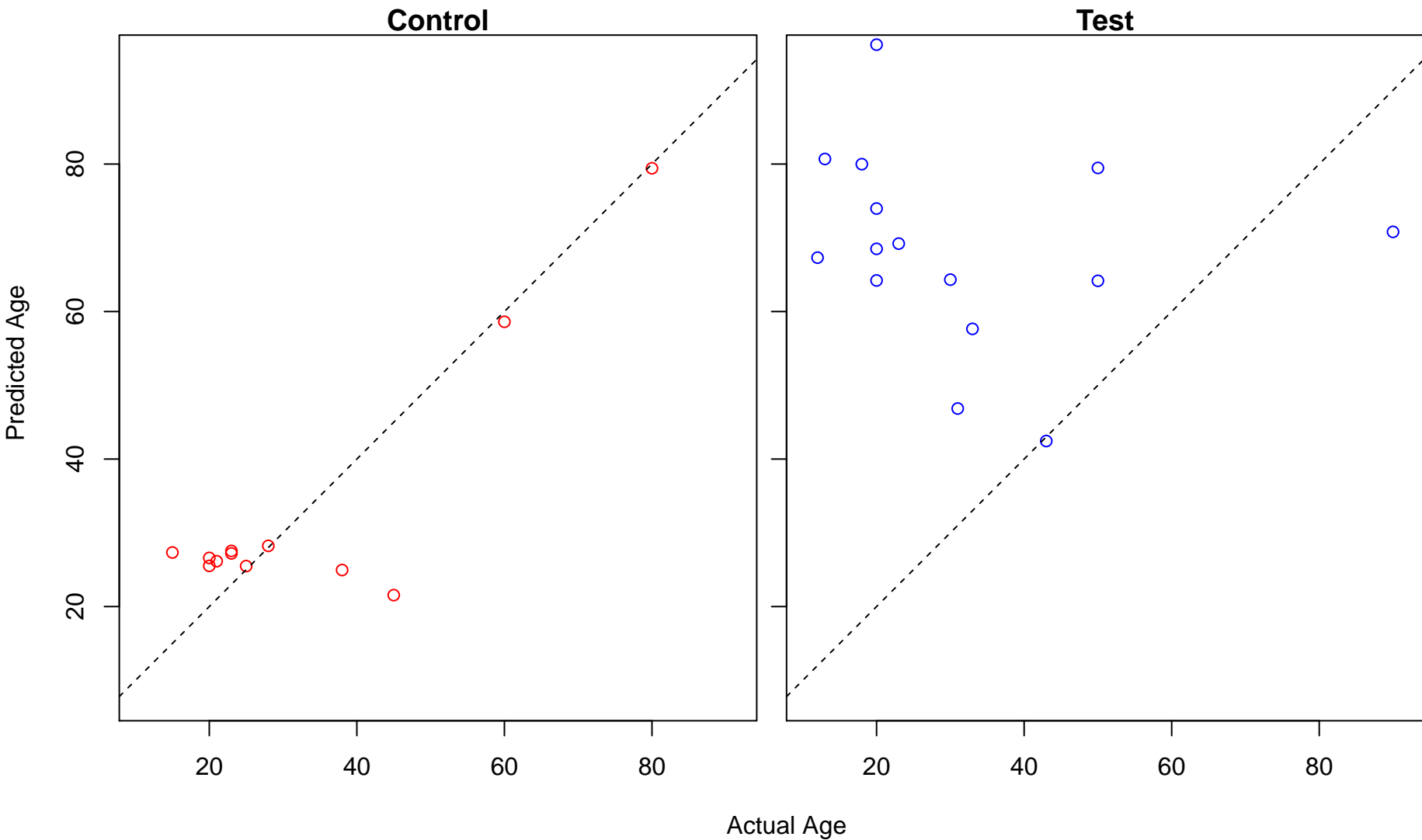


Test

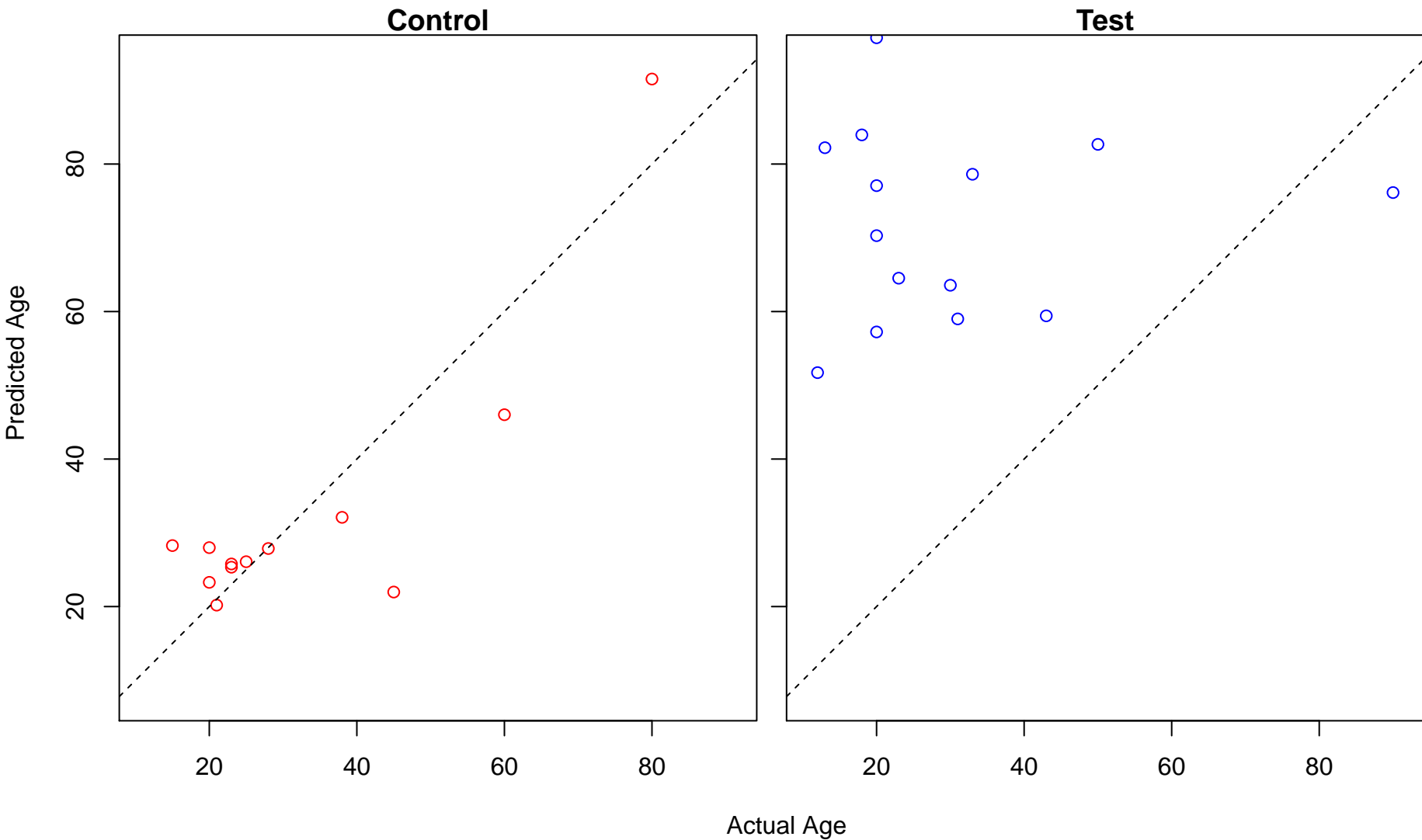


Actual Age

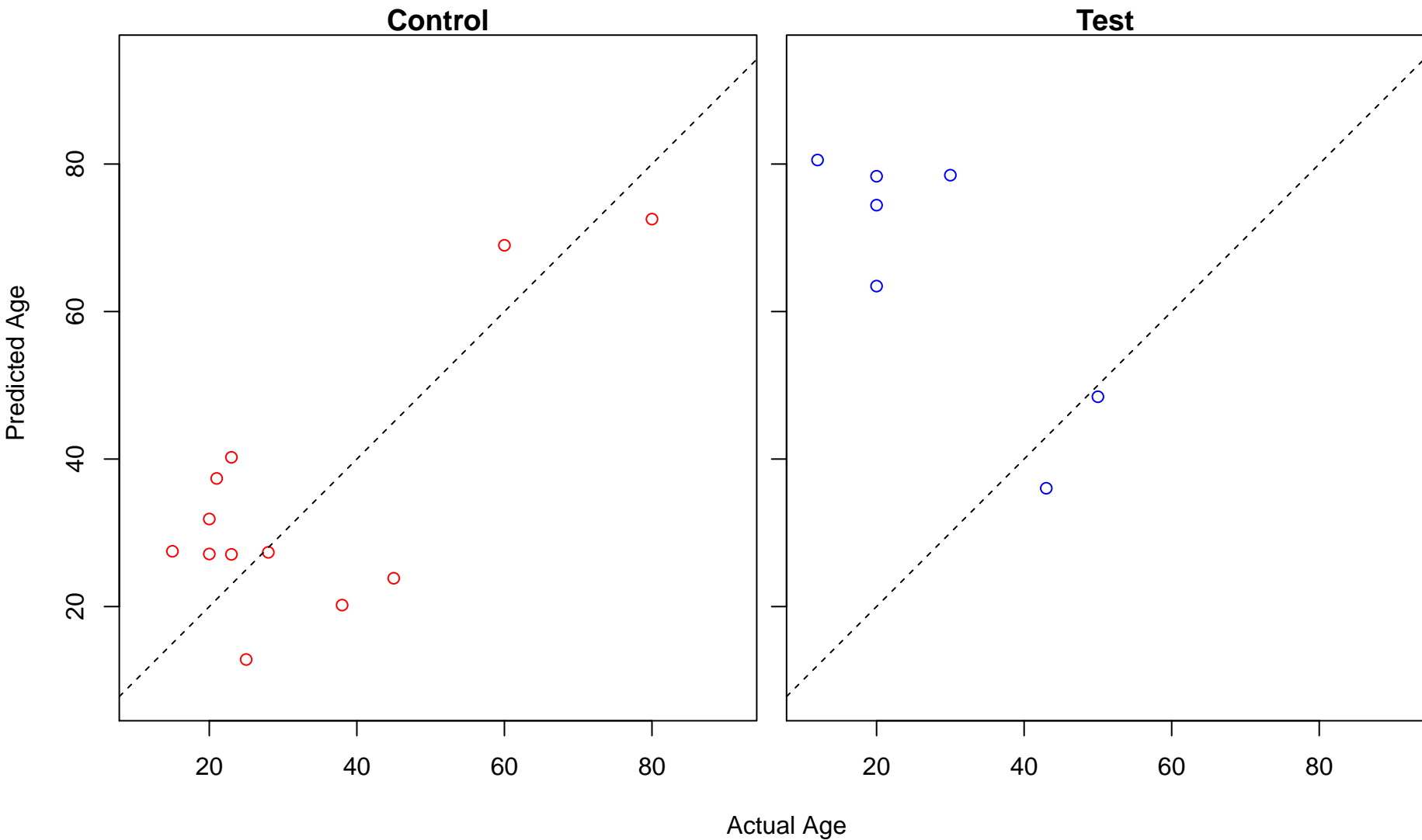
positive regulation of multi-organism process (Score: 8.113432)



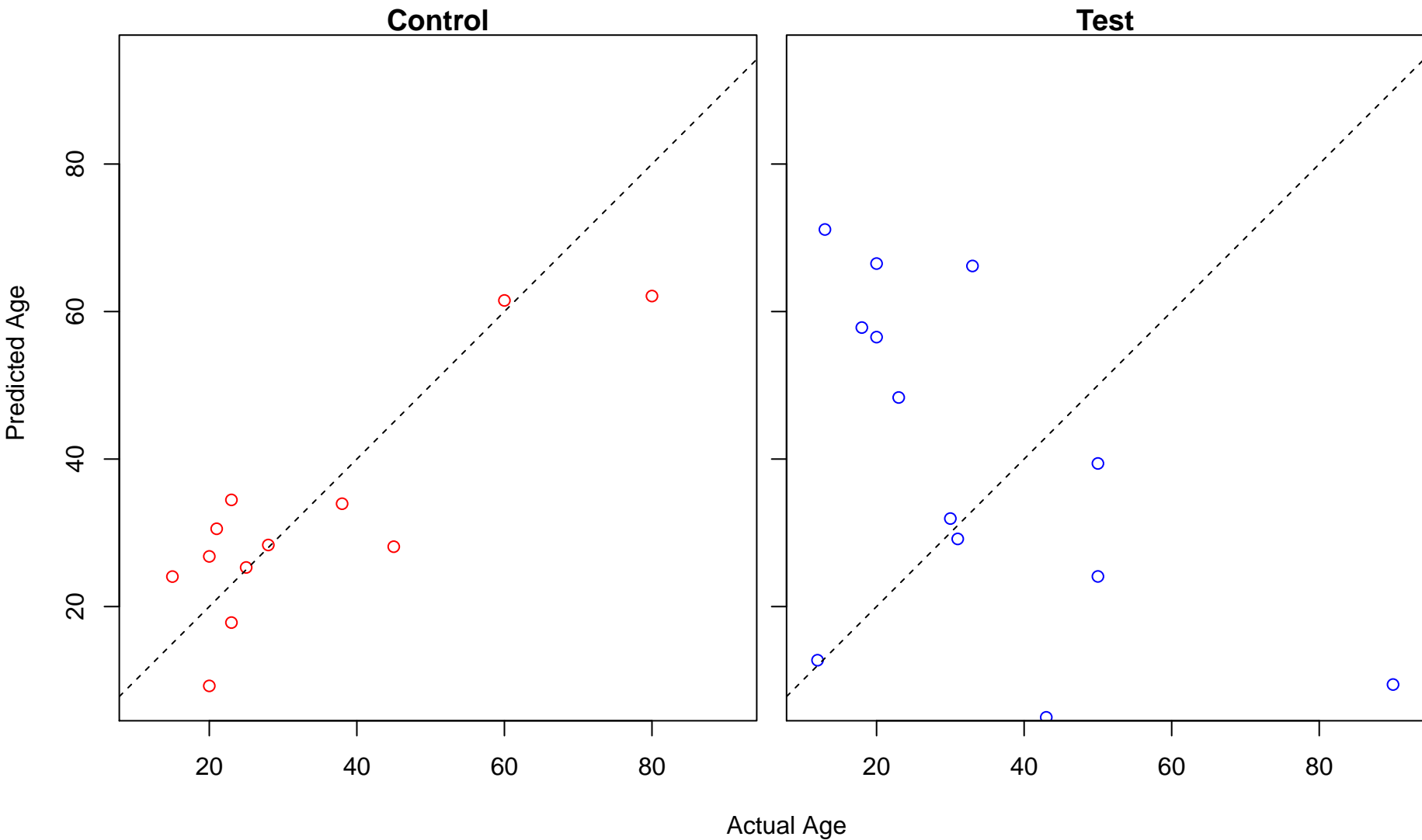
regulation of histone H4 acetylation (Score: 8.110375)



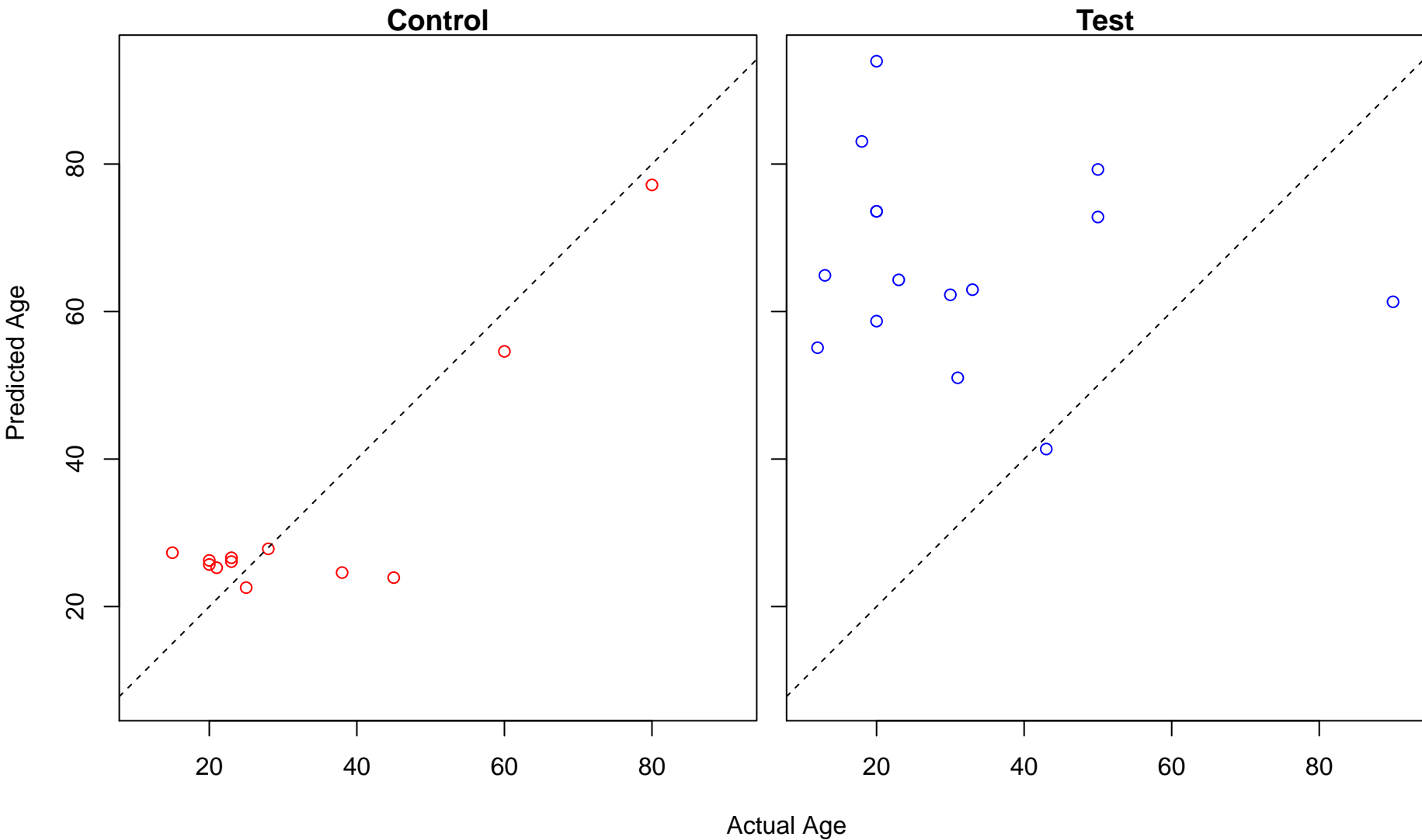
regulation of lipid storage (Score: 8.110016)



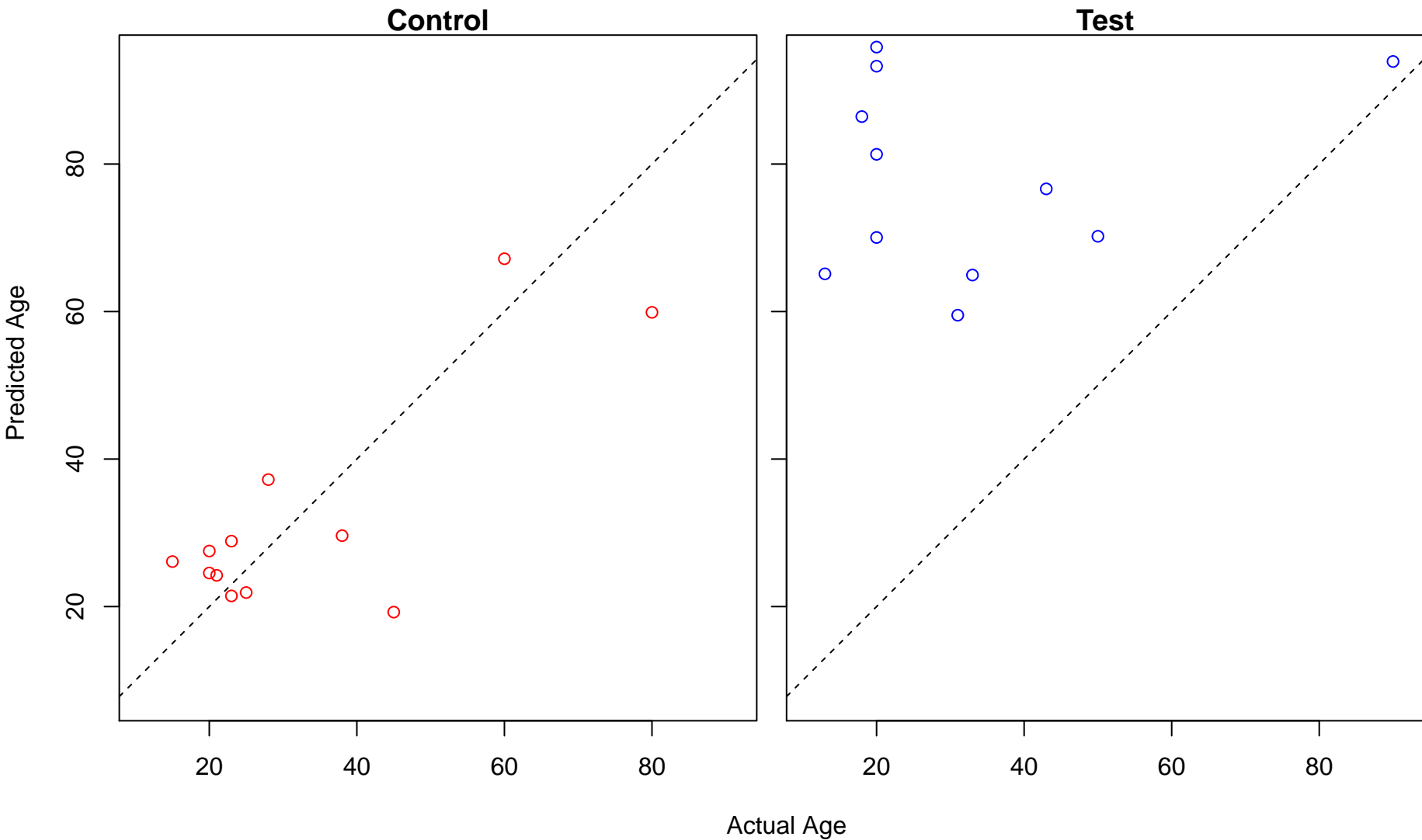
positive regulation of ion transmembrane transporter activity (Score: 8.108747)



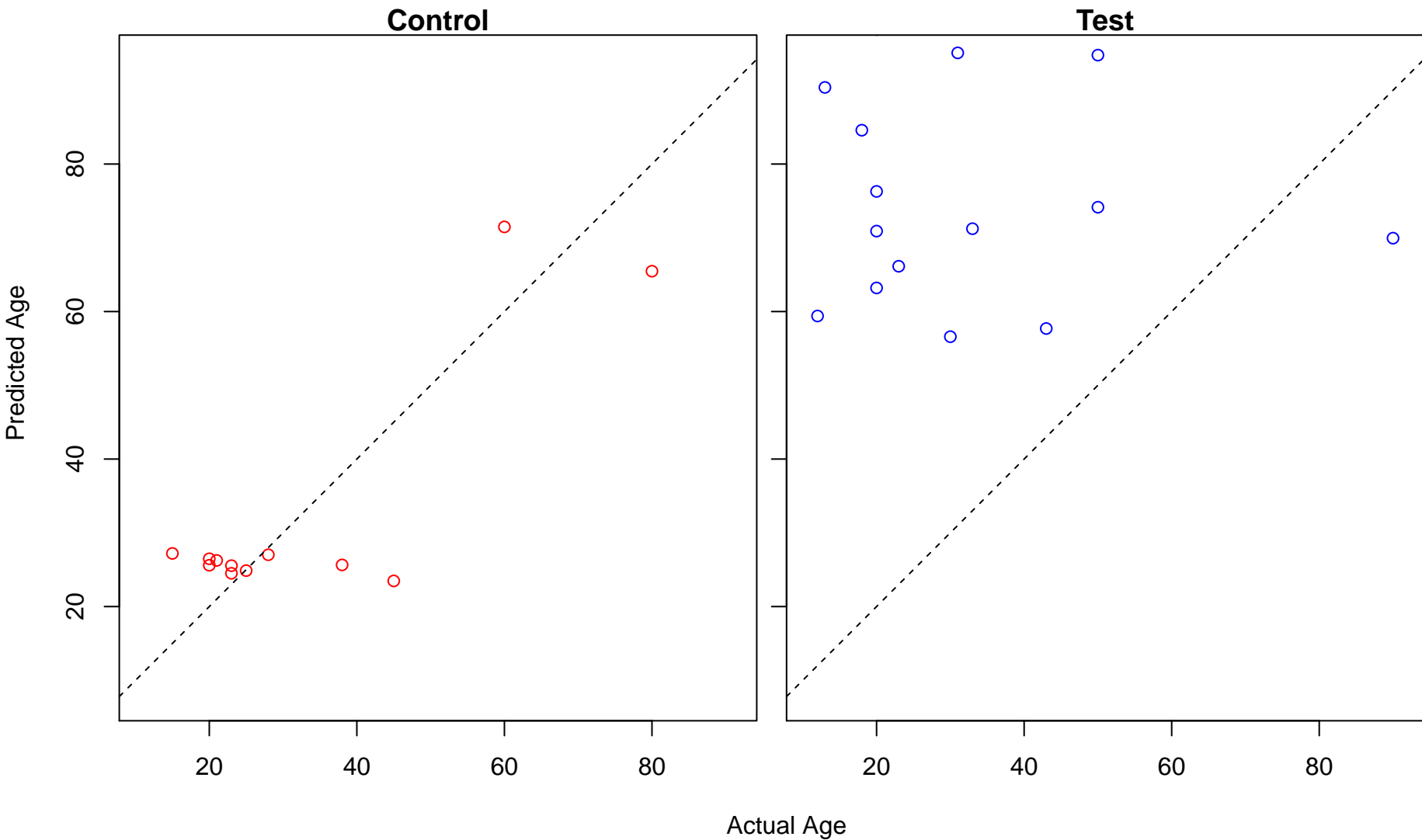
regulation of telomere maintenance via telomere lengthening (Score: 8.104292)



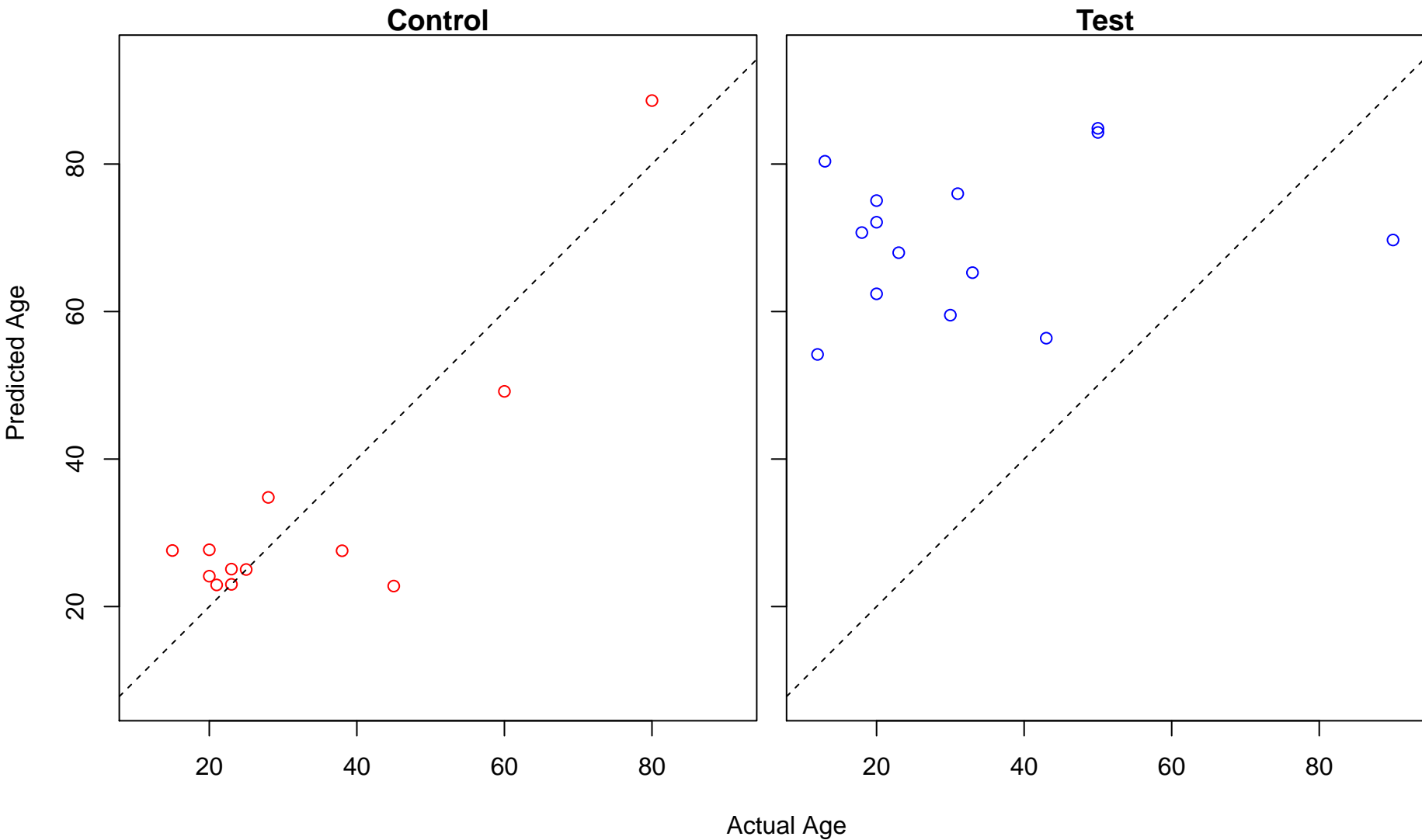
adrenal gland development (Score: 8.101889)



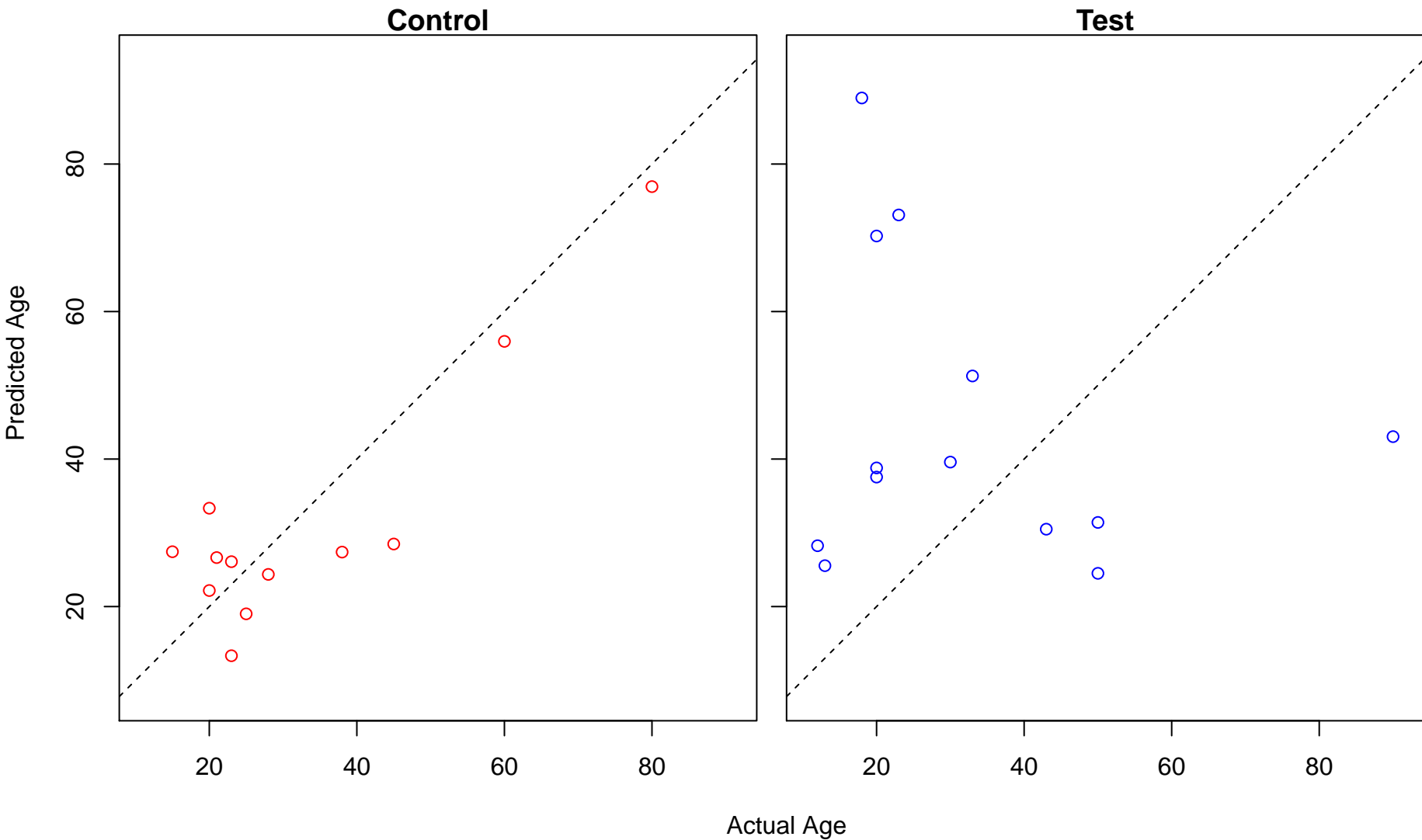
positive regulation of gene expression, epigenetic (Score: 8.100450)



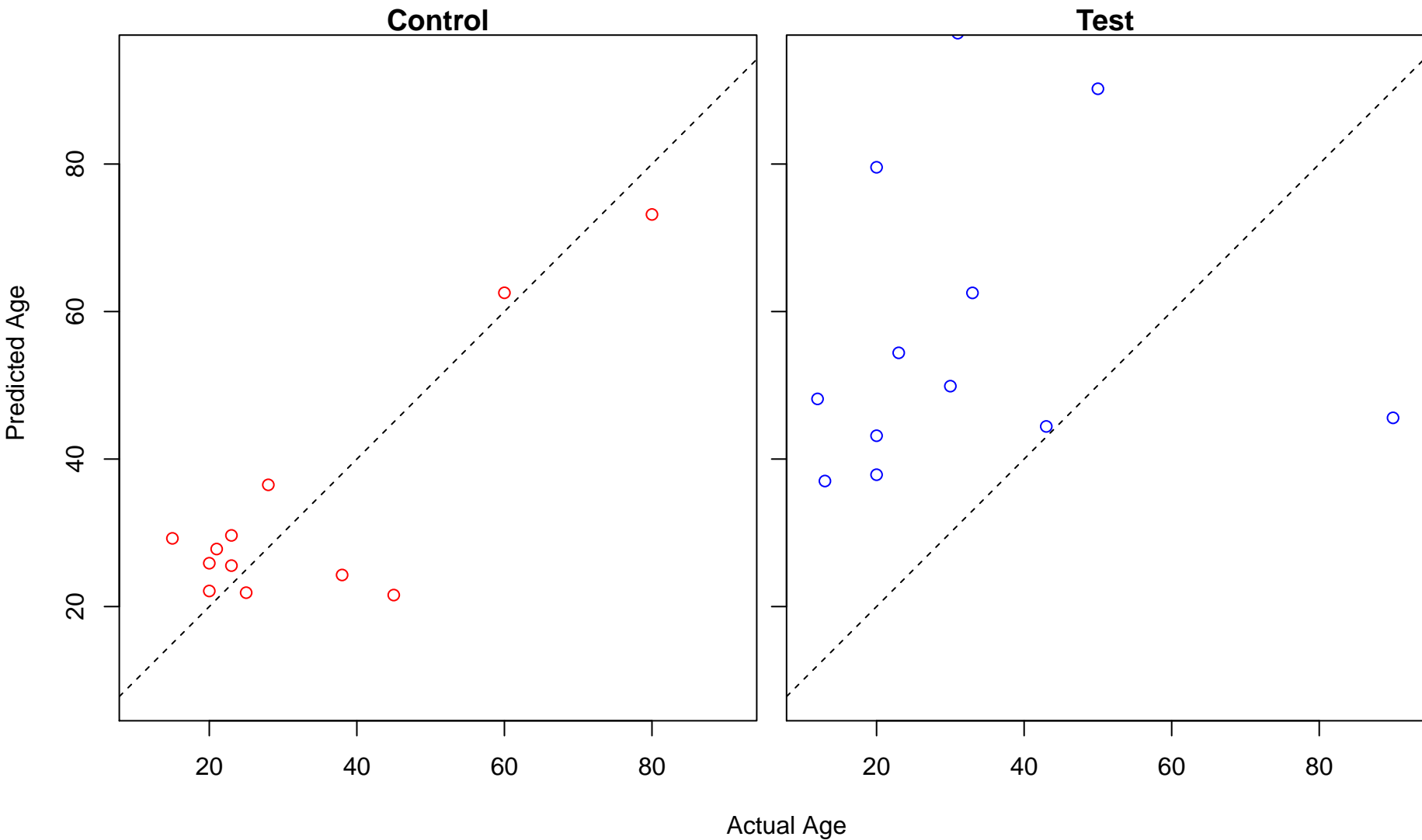
skeletal system development (Score: 8.097056)



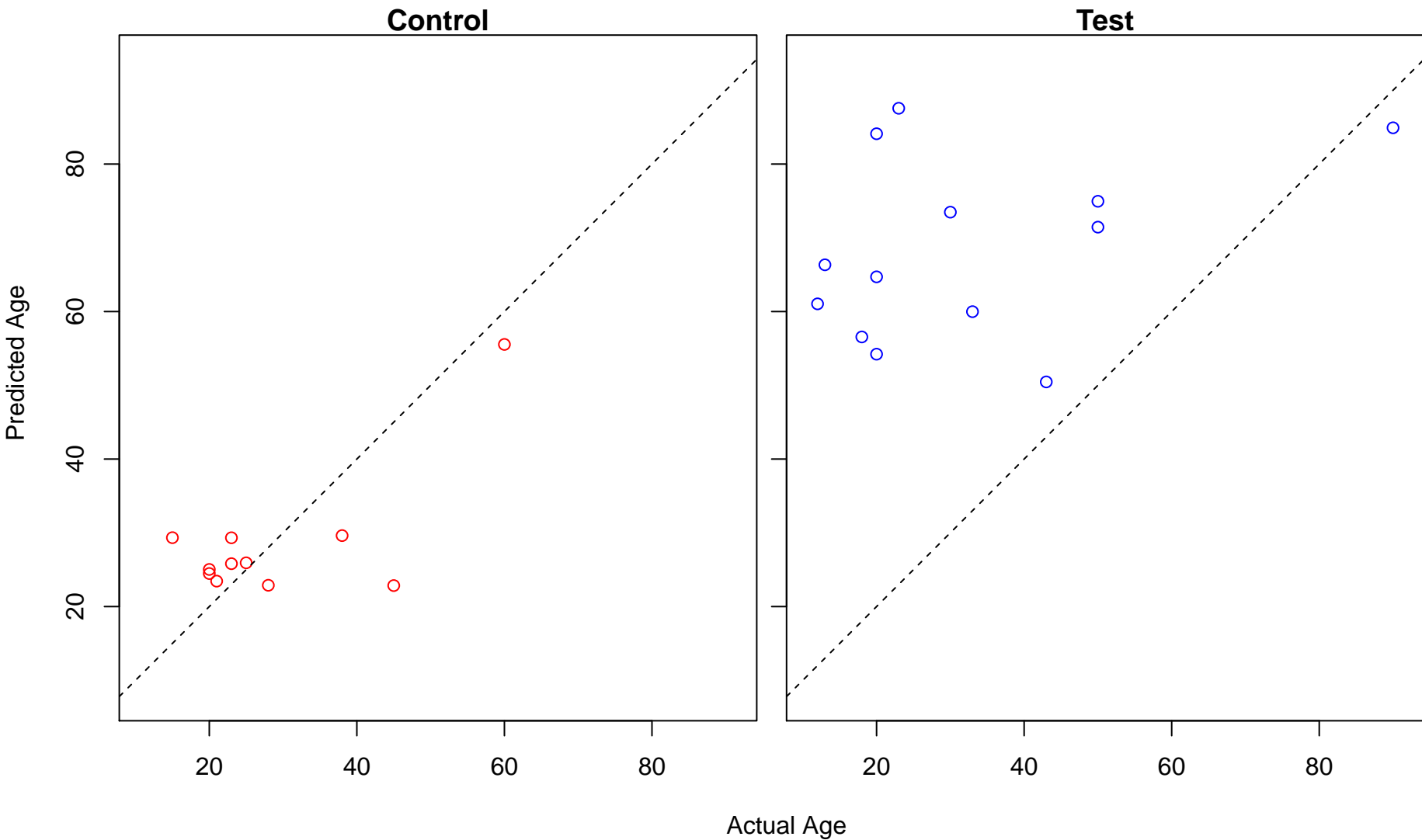
negative regulation of mRNA splicing, via spliceosome (Score: 8.094705)



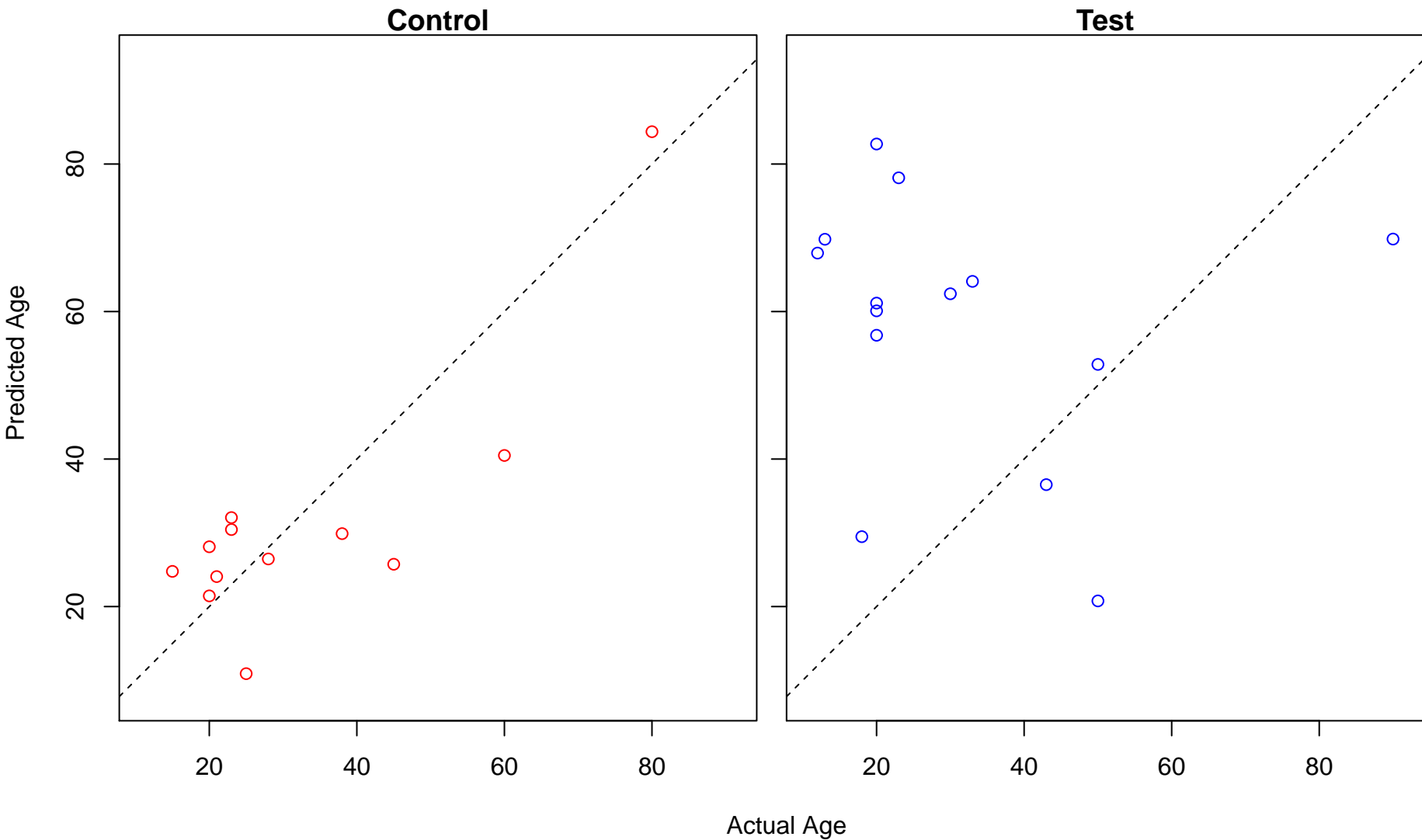
single organismal cell-cell adhesion (Score: 8.094484)



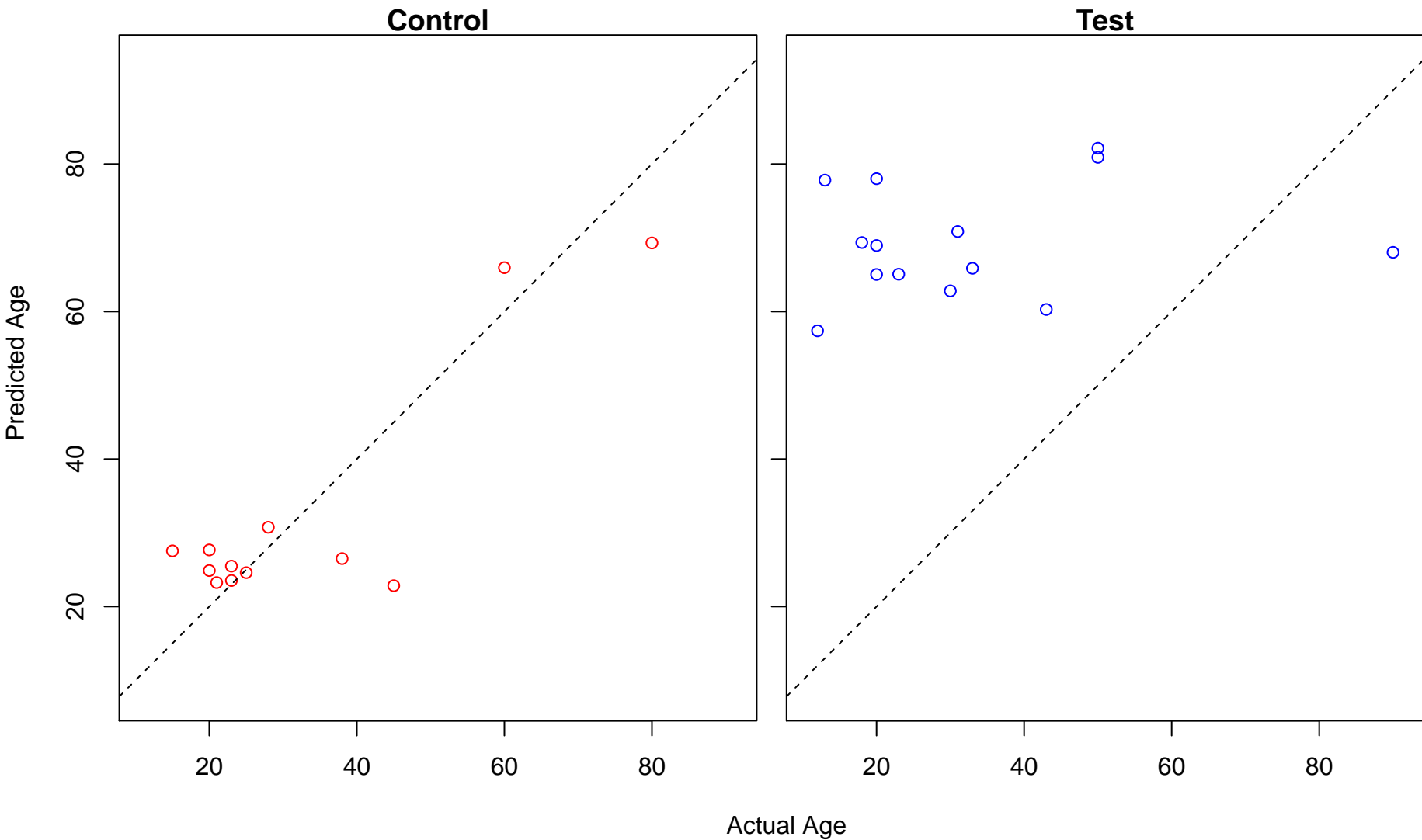
positive regulation of syncytium formation by plasma membrane fusion (Score: 8.093587)



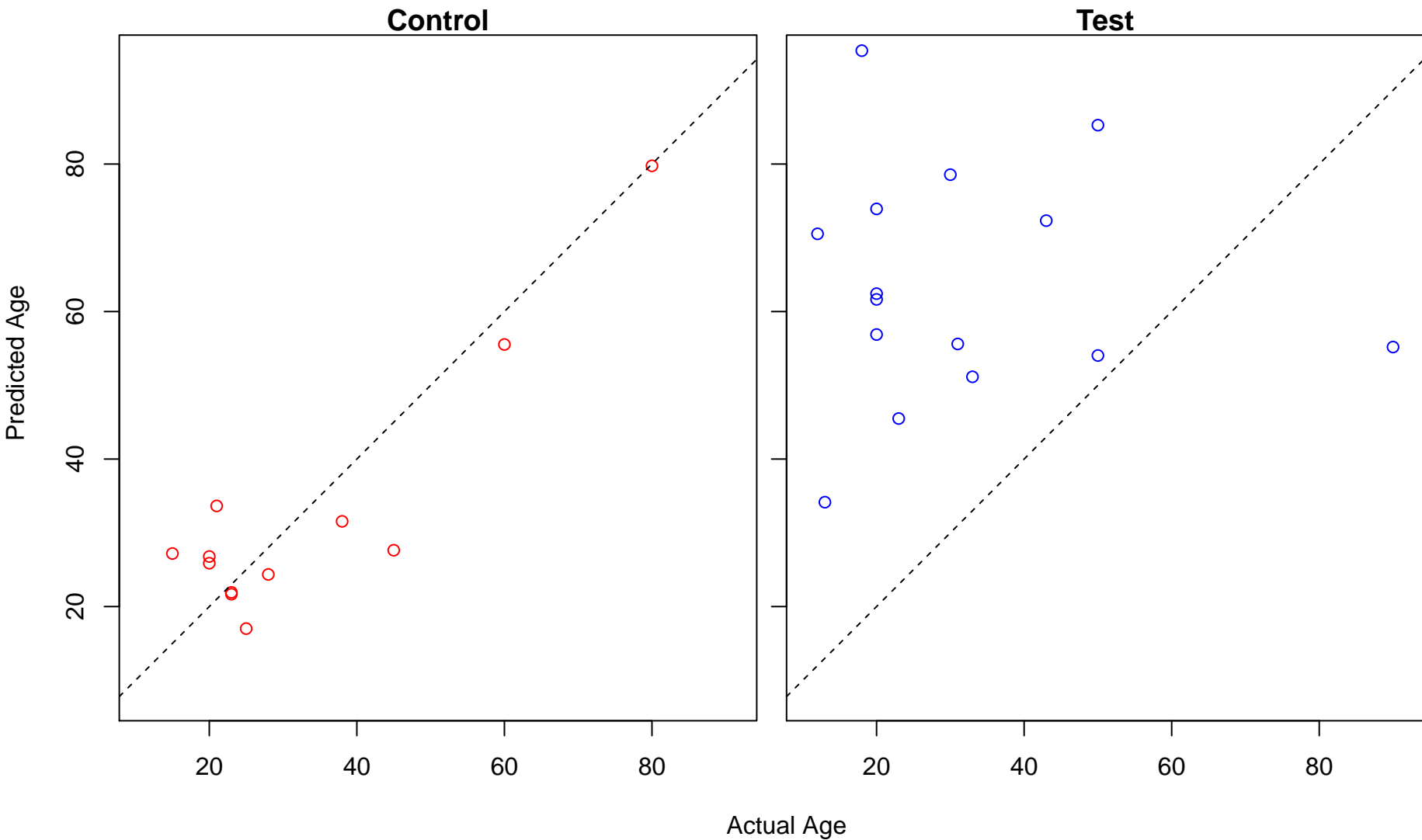
regulation of erythrocyte differentiation (Score: 8.092087)



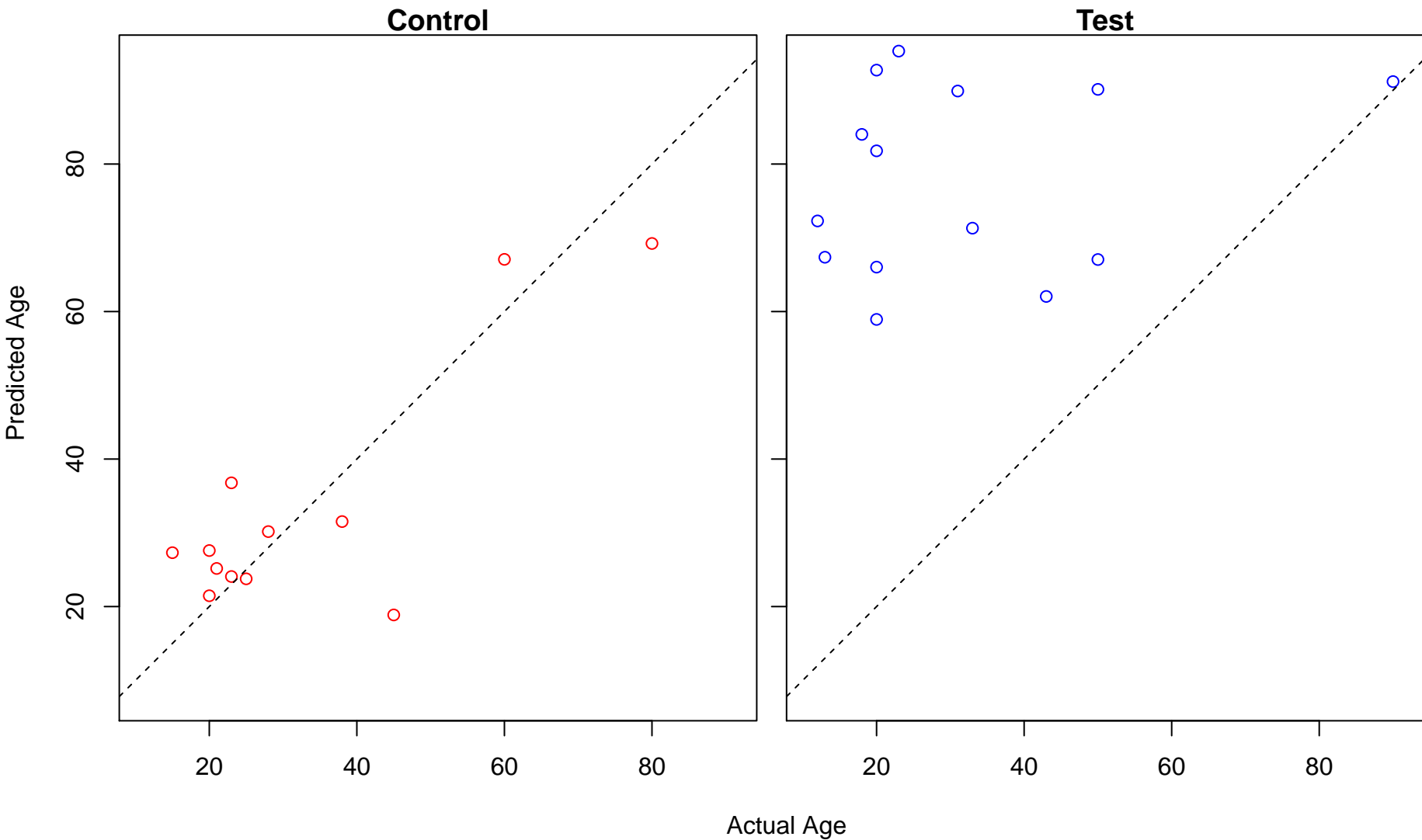
regulation of purine nucleotide metabolic process (Score: 8.091460)



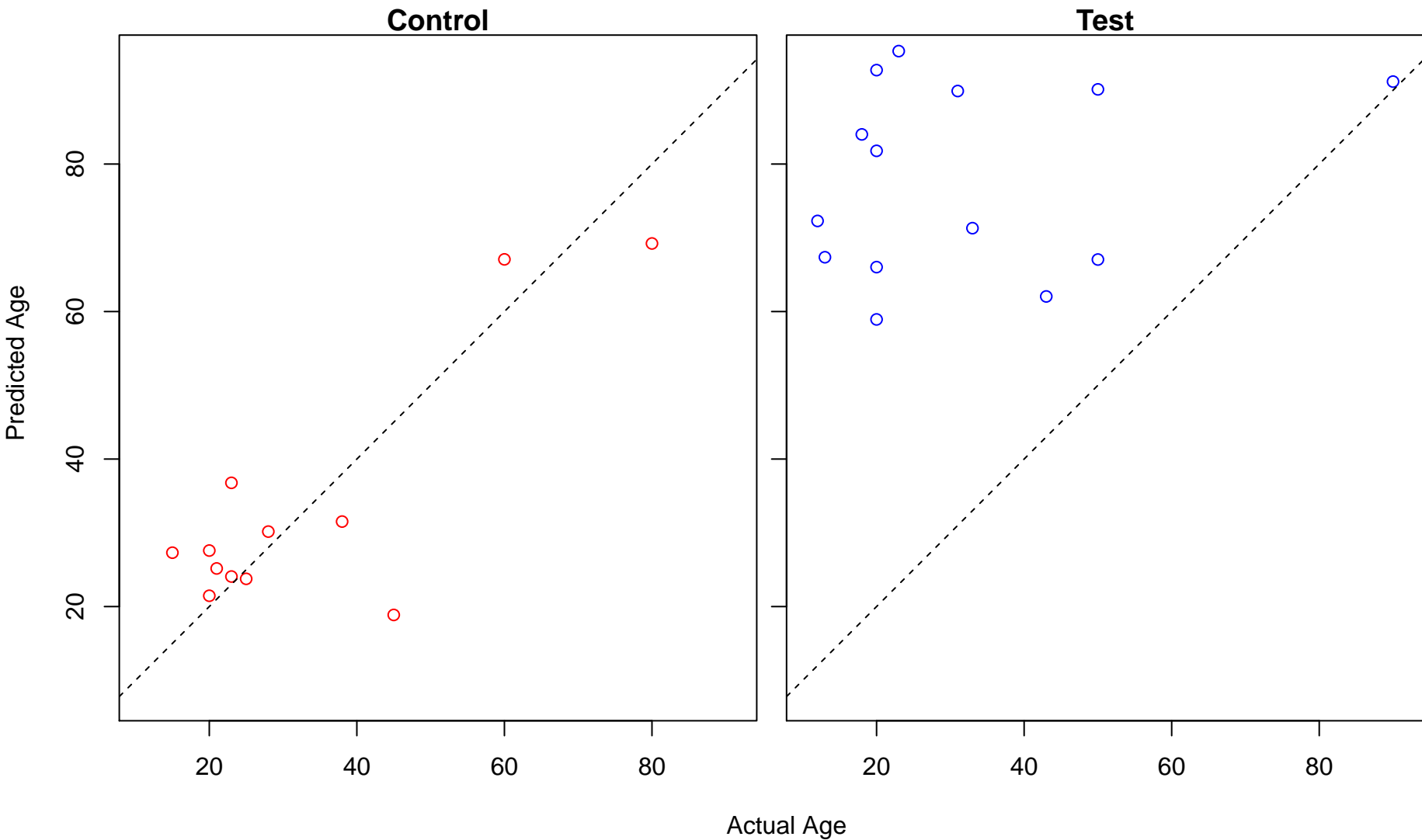
membrane lipid metabolic process (Score: 8.090674)



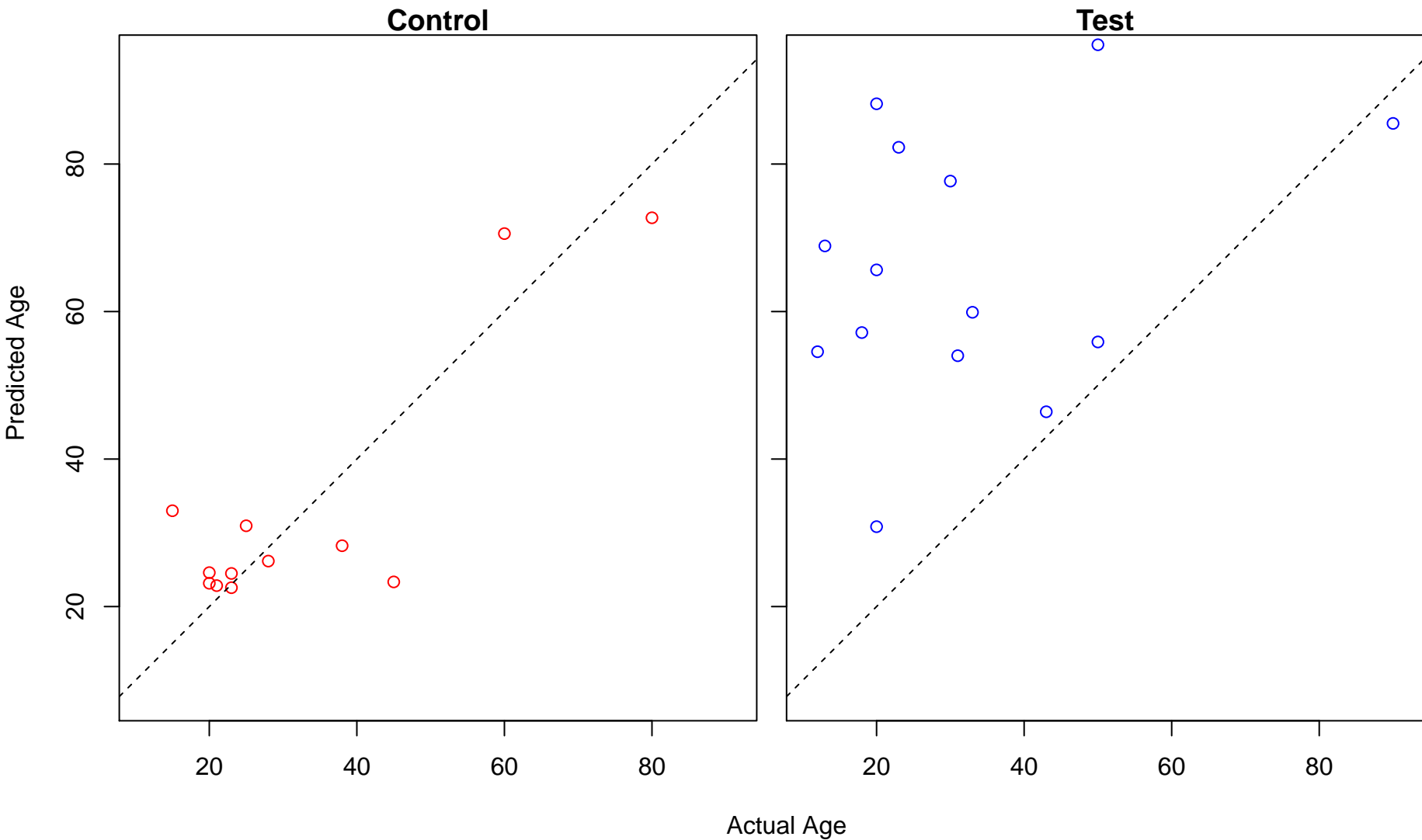
negative regulation of mononuclear cell proliferation (Score: 8.080950)



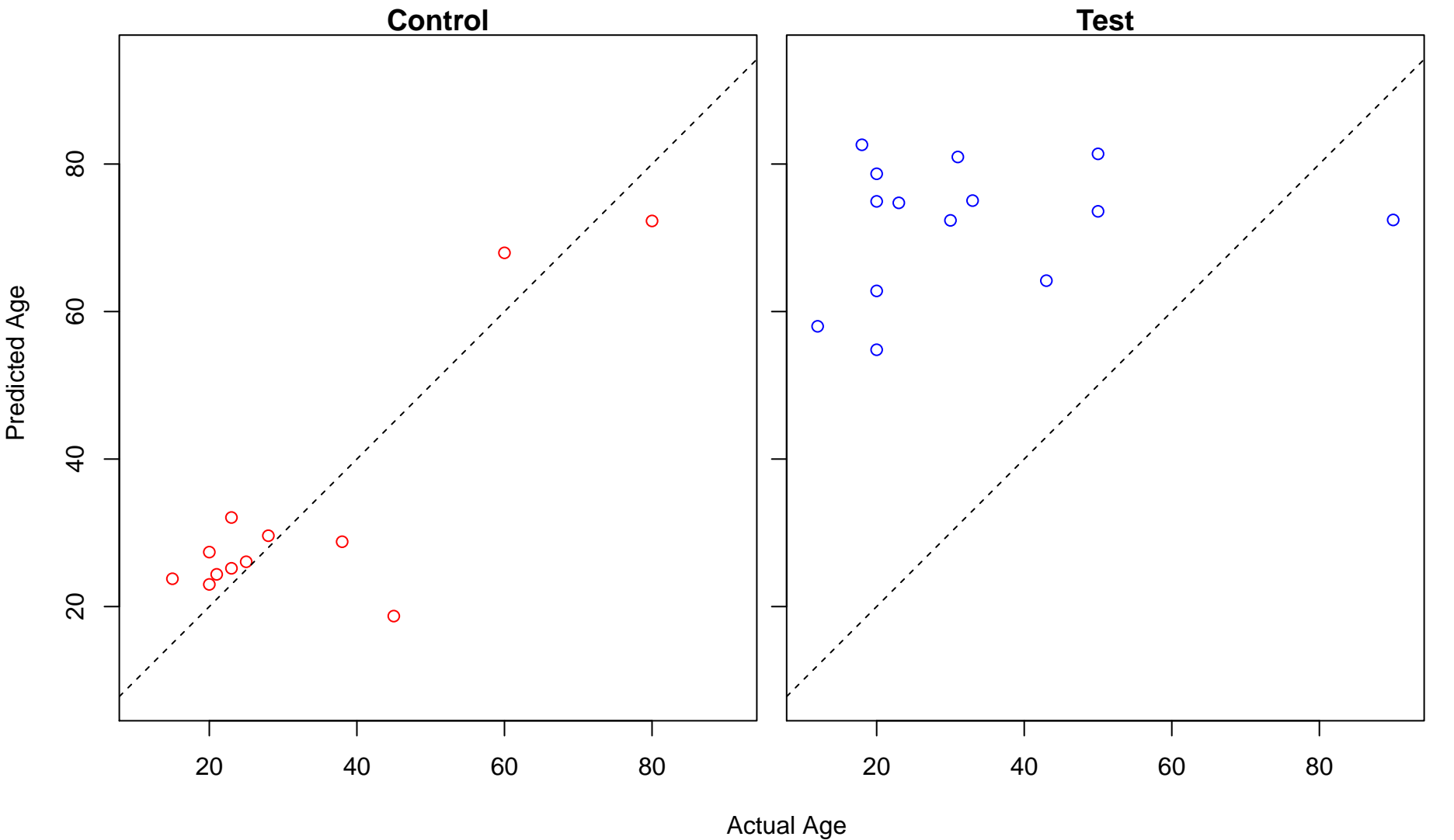
negative regulation of lymphocyte proliferation (Score: 8.080950)



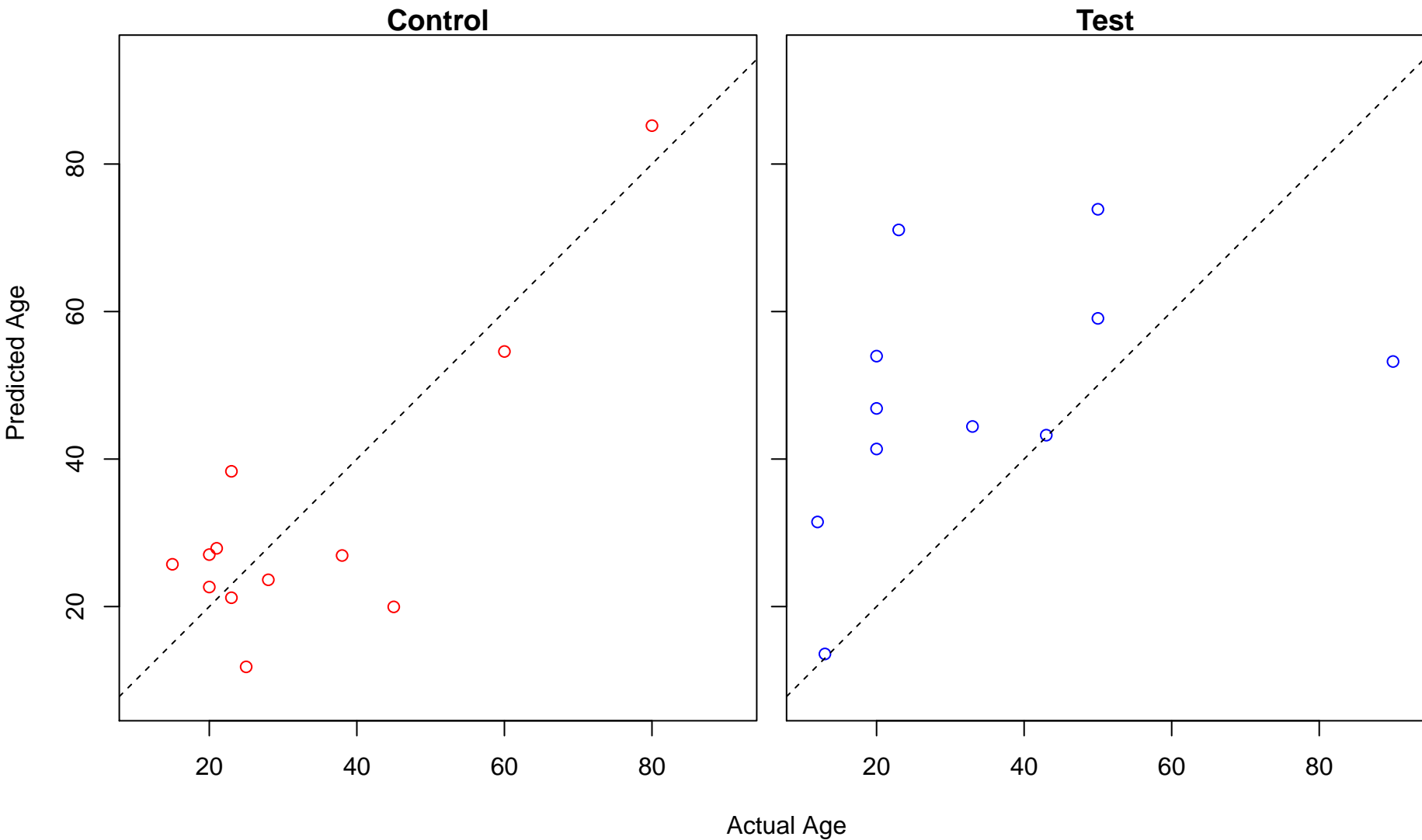
regulation of synaptic plasticity (Score: 8.077973)



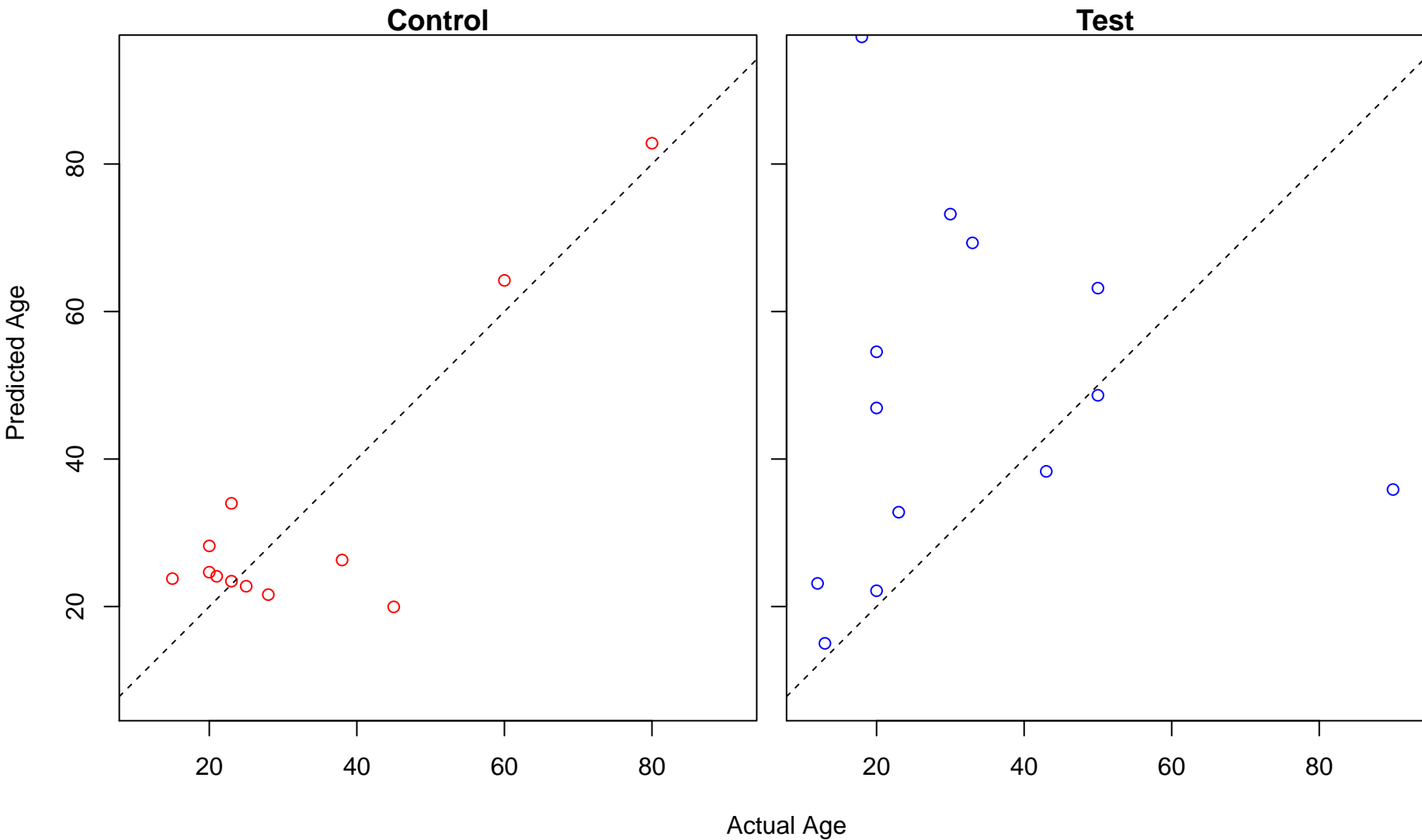
Immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily



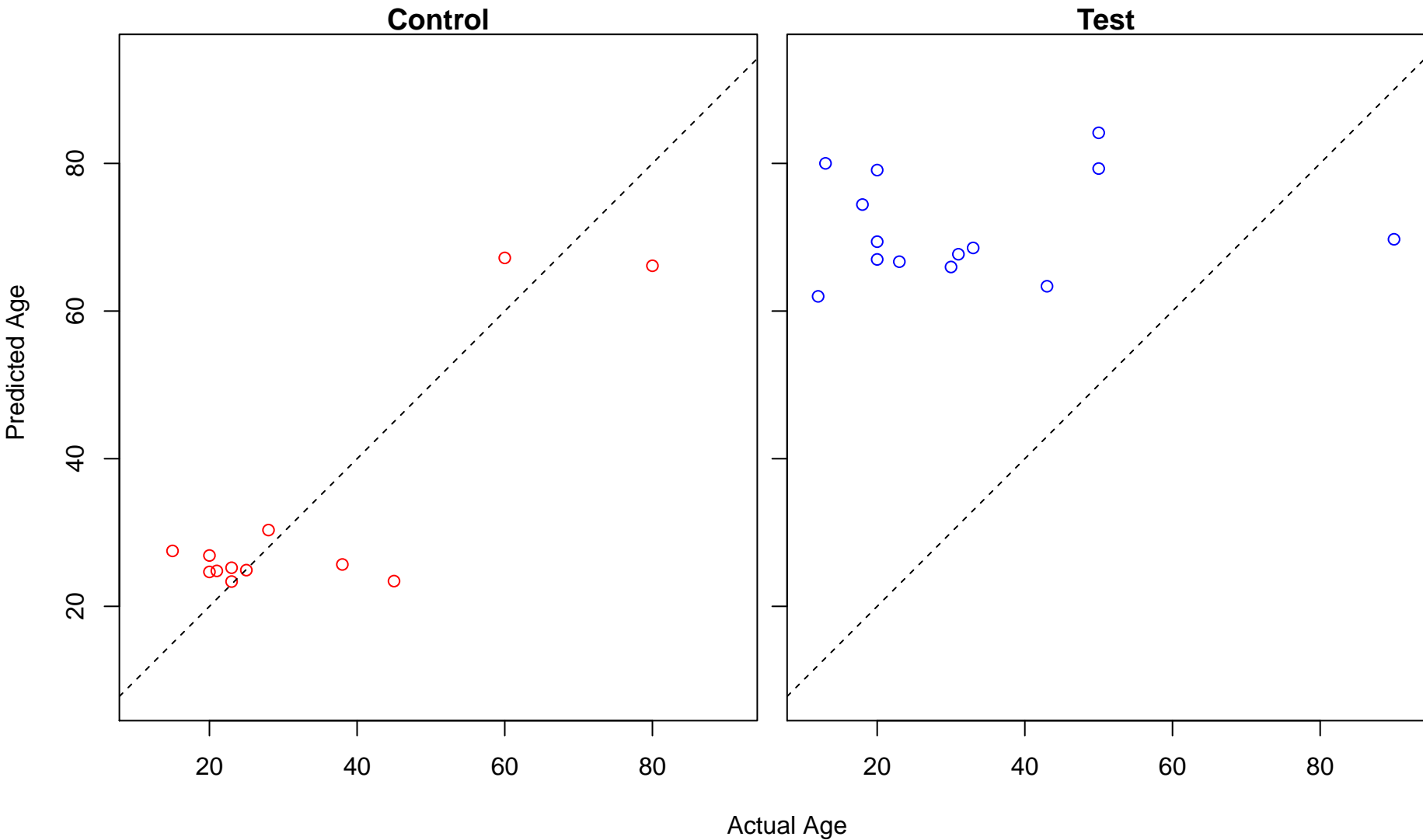
regulation of cell-cell adhesion (Score: 8.069725)



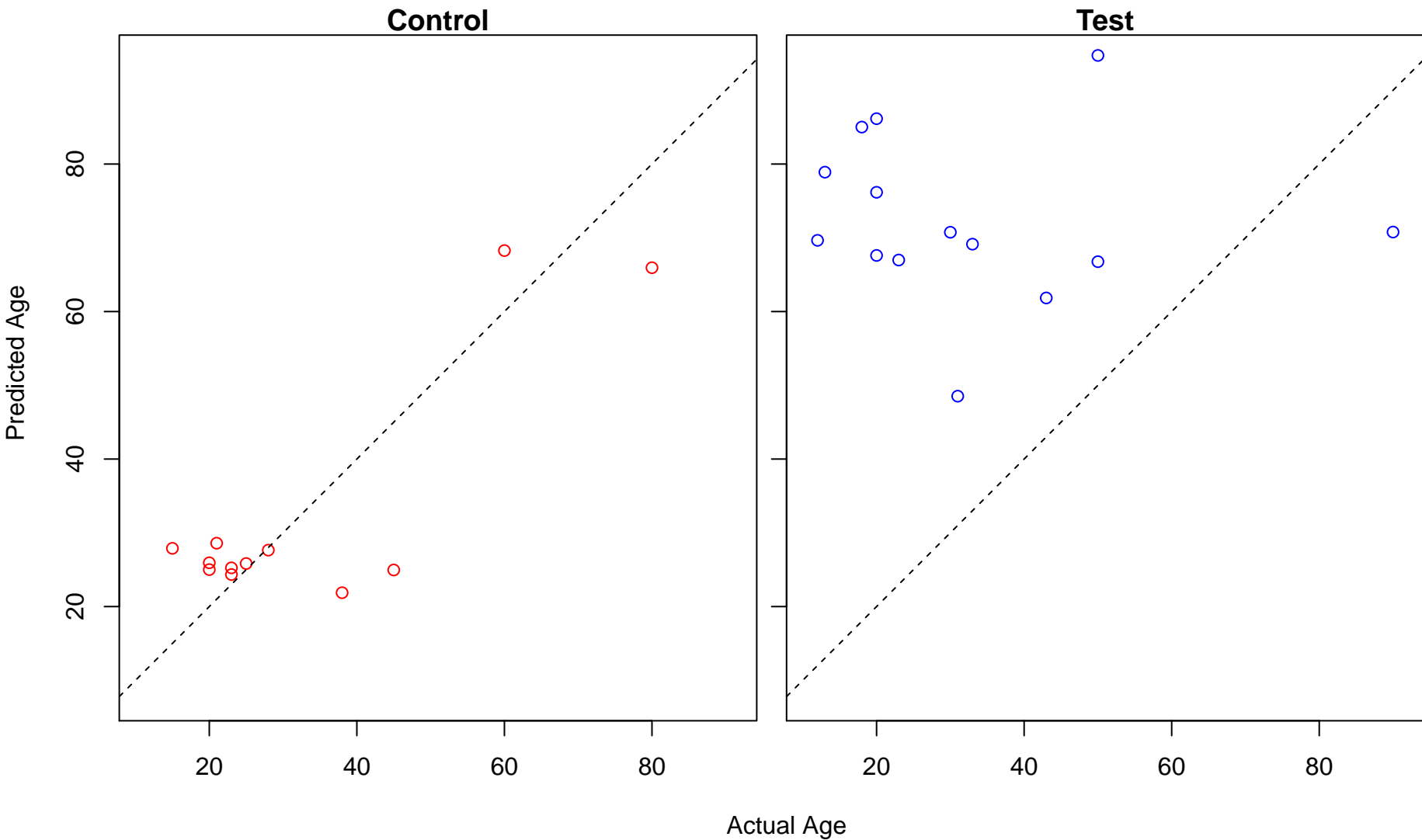
positive regulation of cell adhesion (Score: 8.069088)



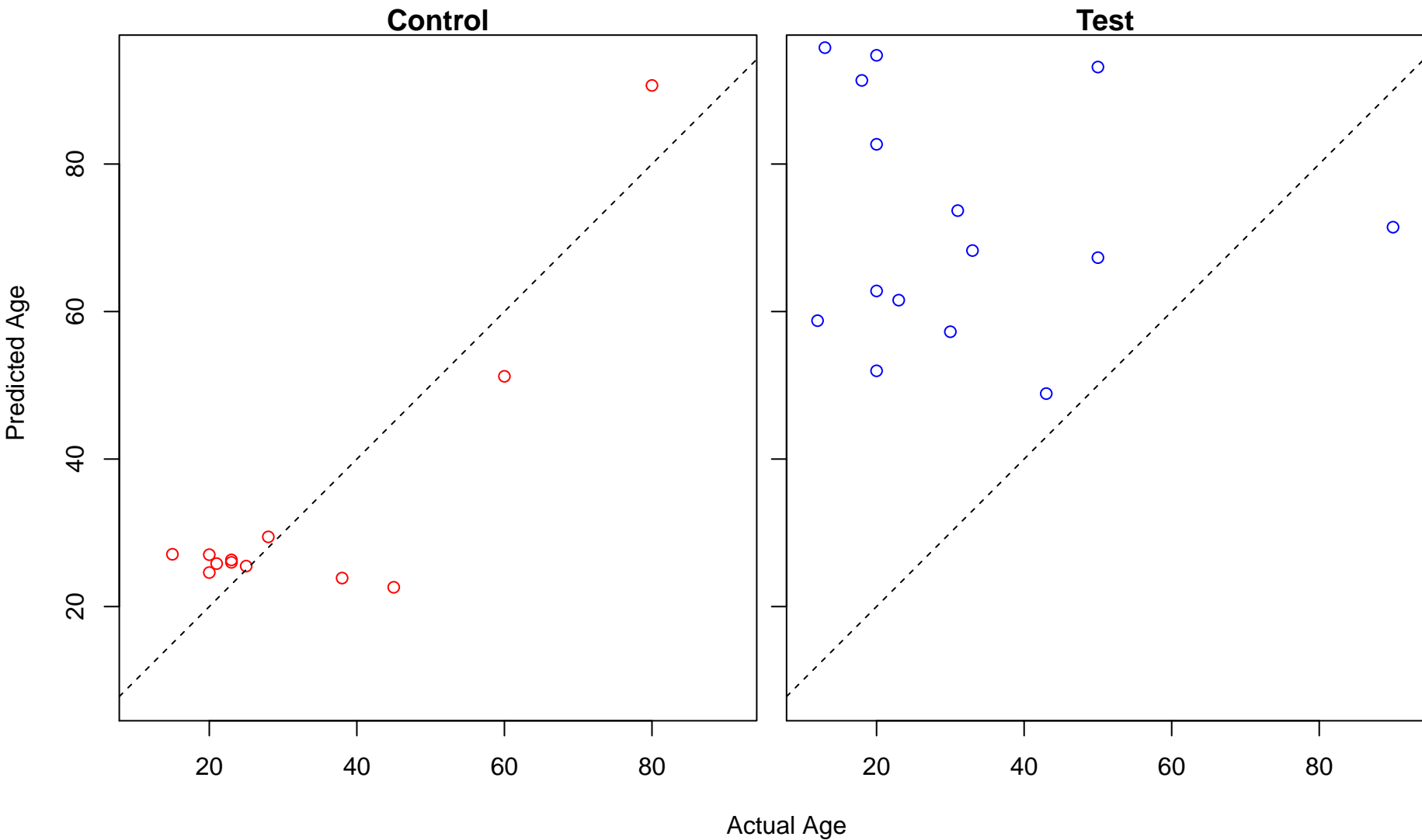
purine ribonucleotide biosynthetic process (Score: 8.067682)



spliceosomal snRNP assembly (Score: 8.066984)

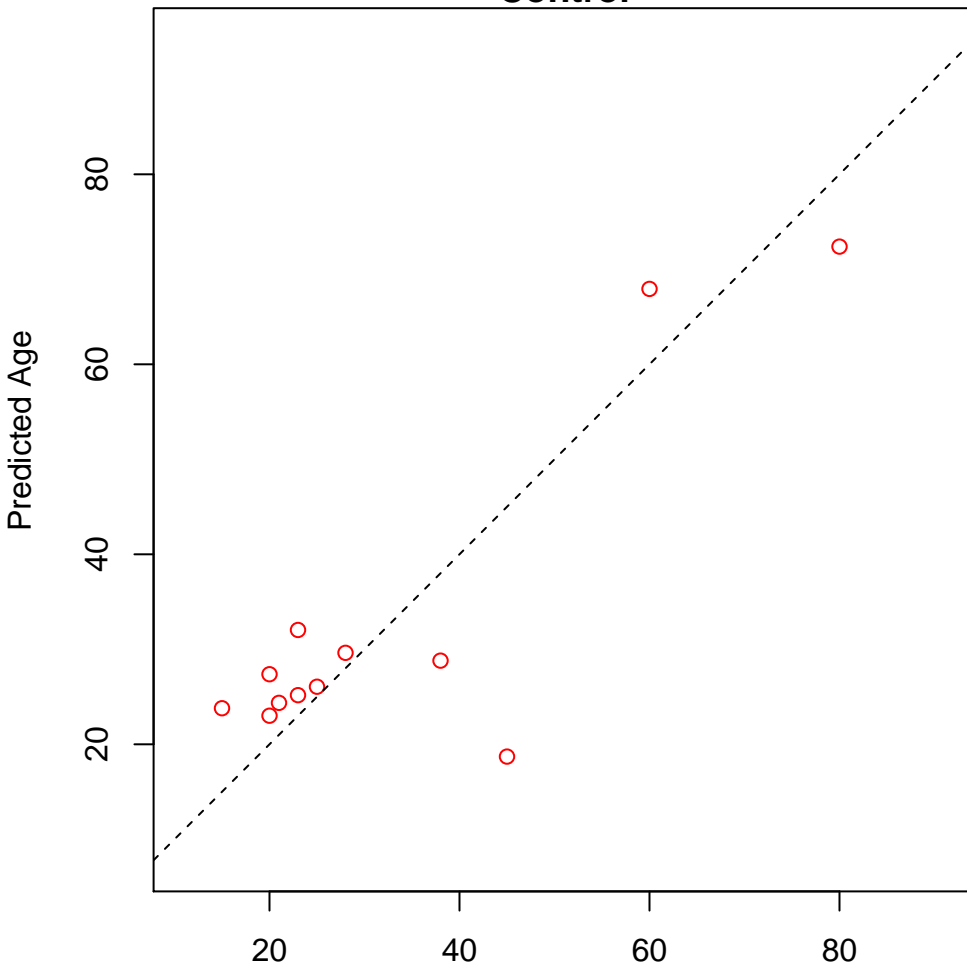


regulation of protein targeting (Score: 8.066869)

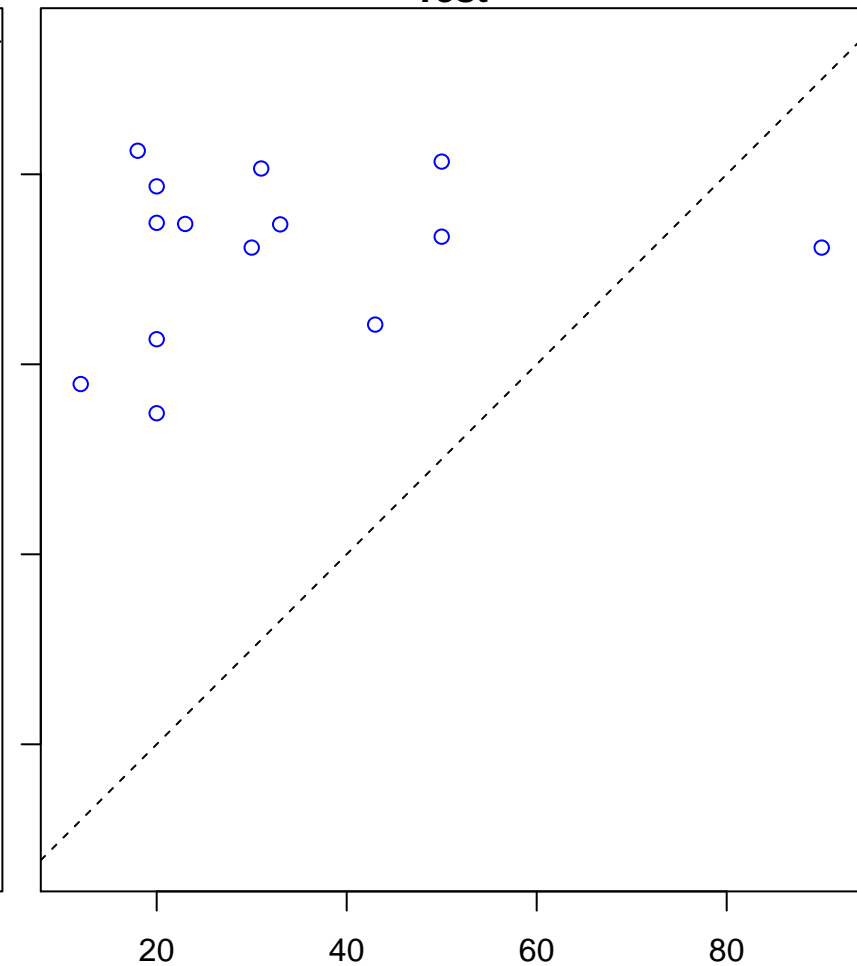


regulation of adaptive immune response (Score: 8.065563)

Control

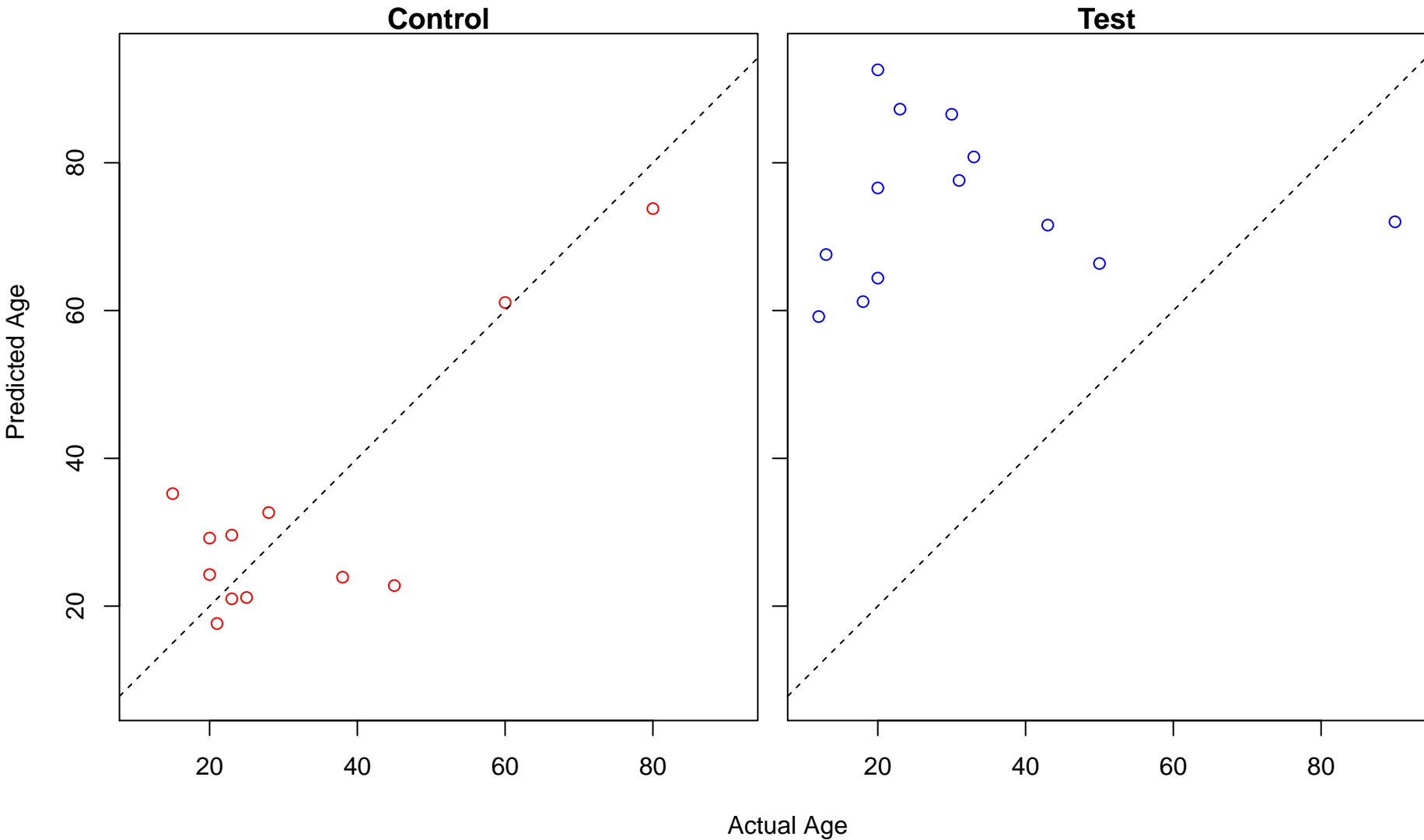


Test

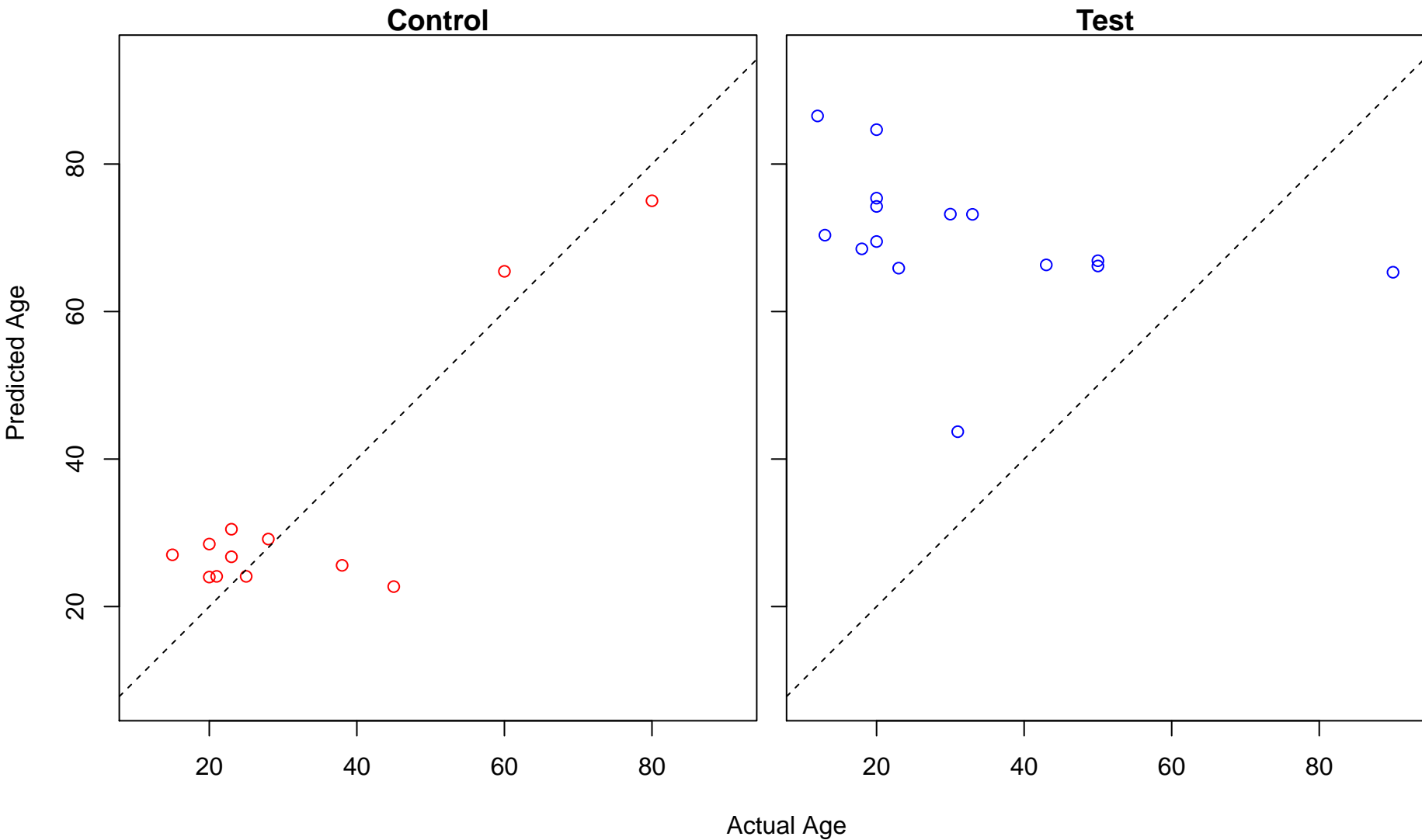


Actual Age

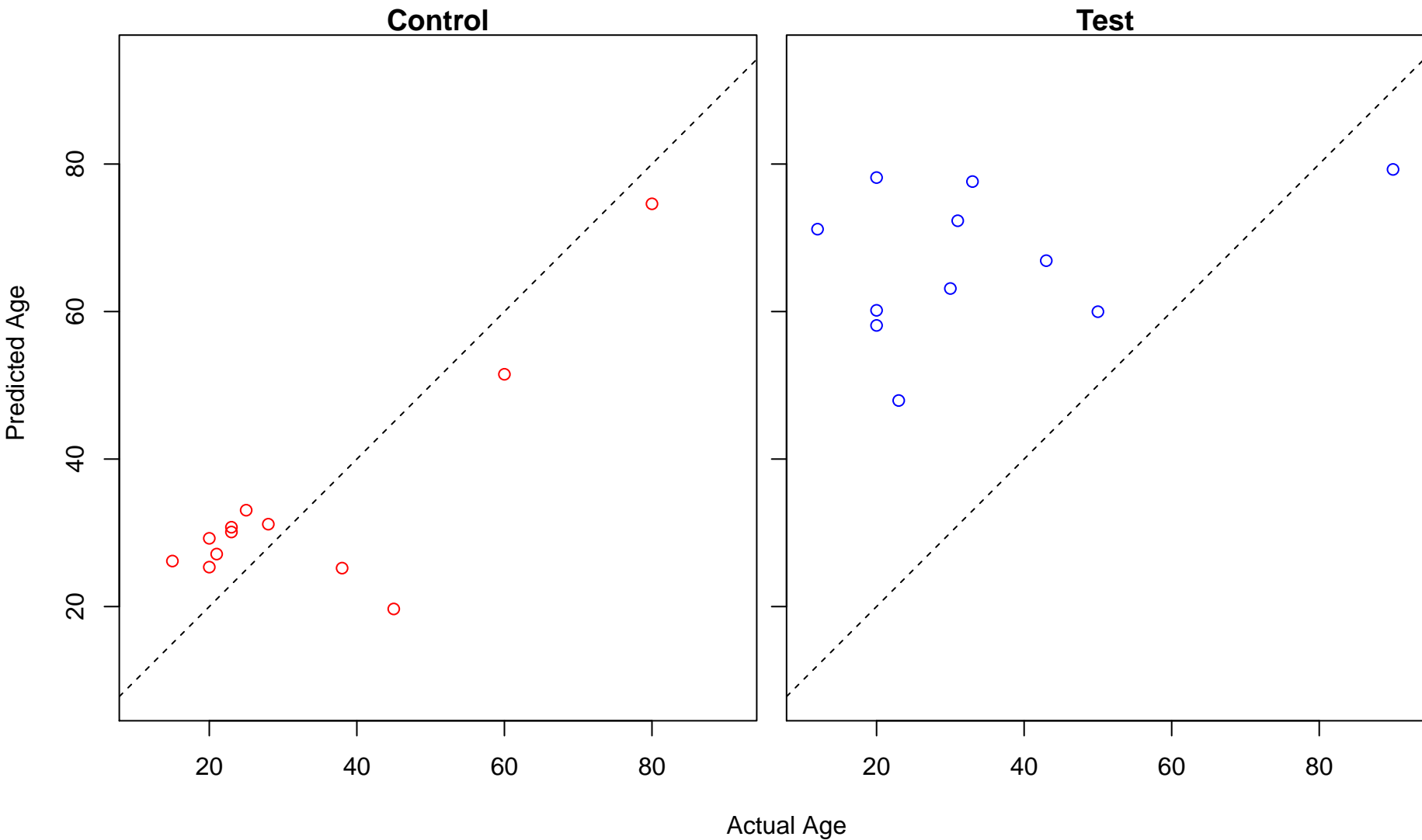
sequestering of extracellular ligand from receptor (Score: 8.063707)



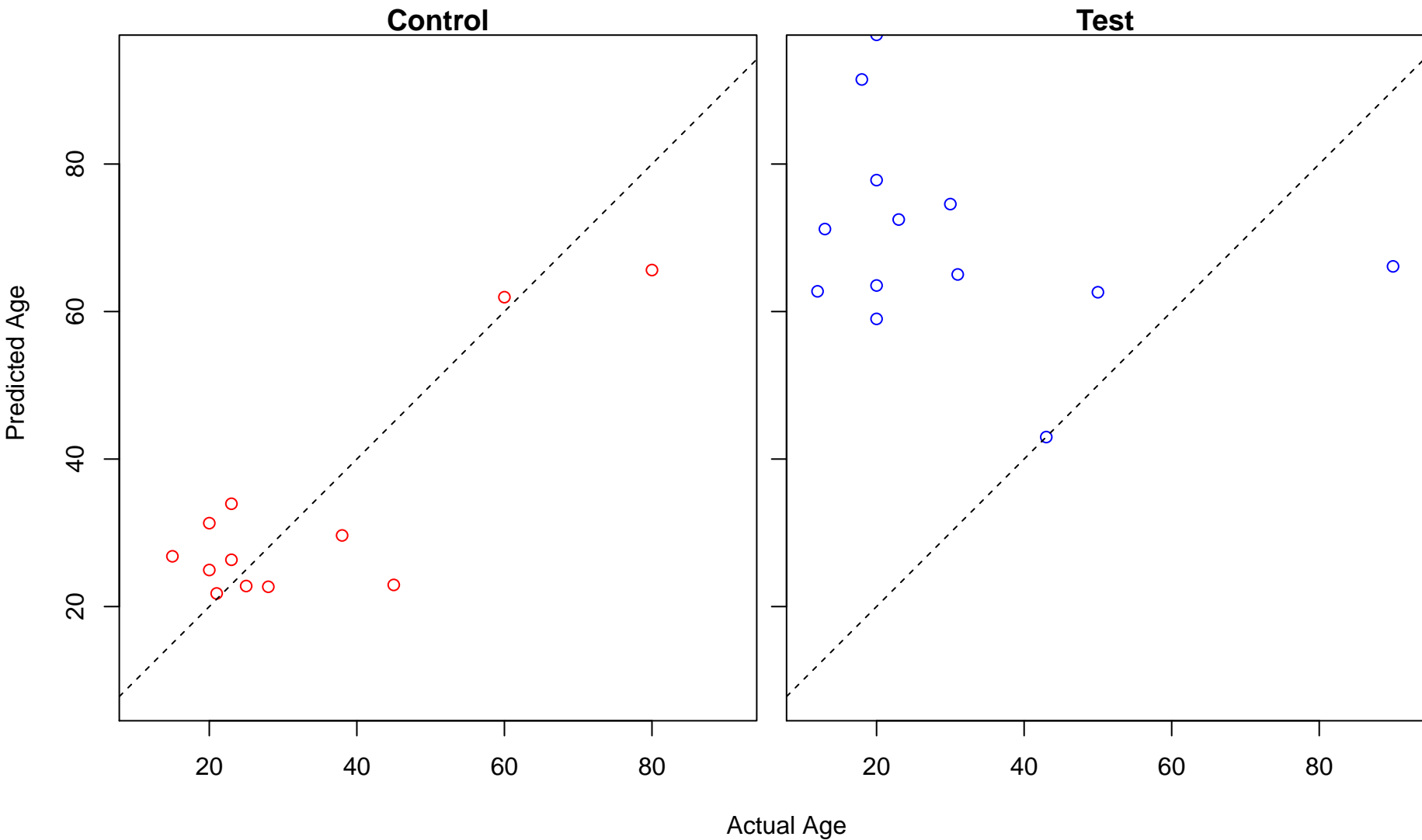
stem cell differentiation (Score: 8.062086)



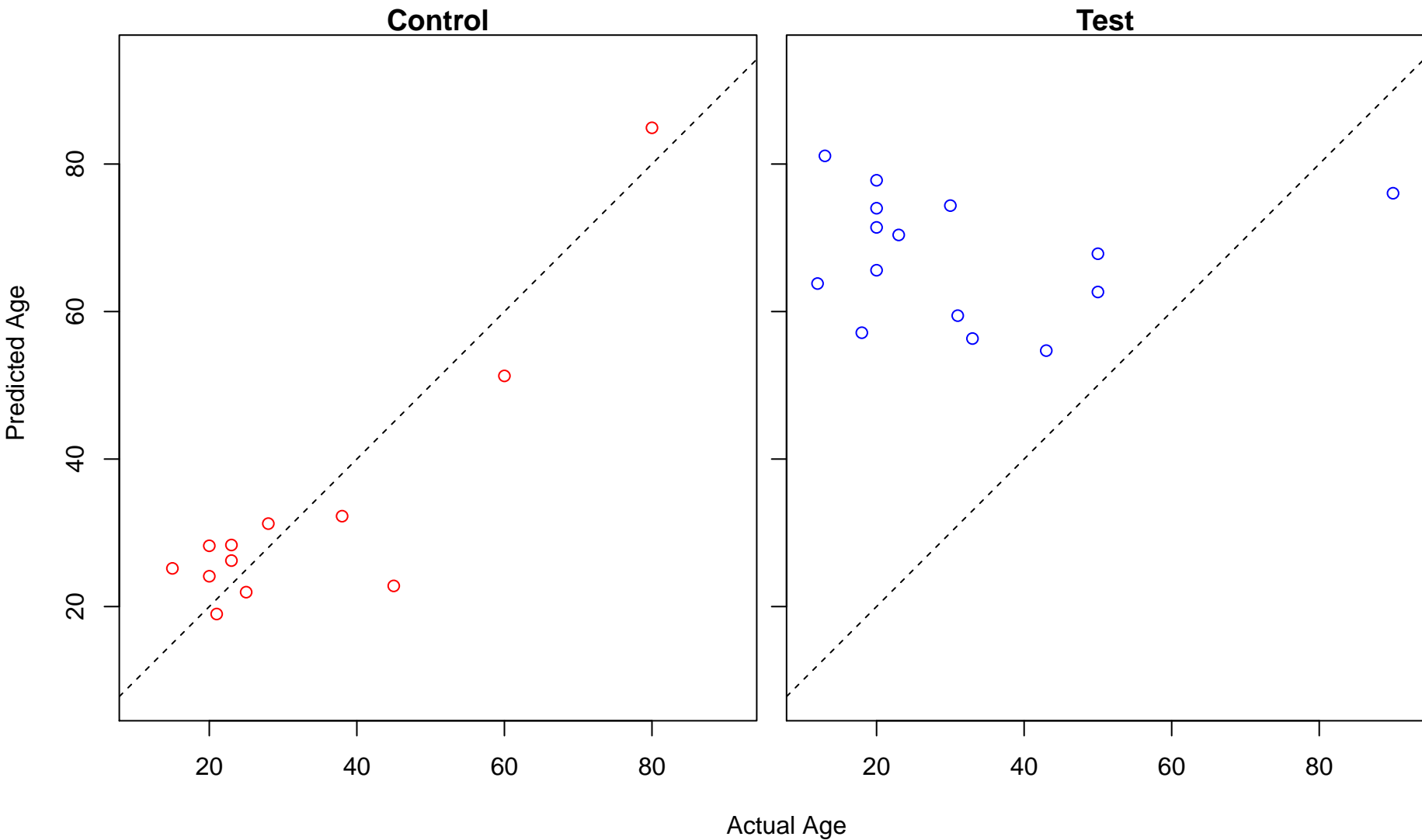
regulation of cell-cell adhesion mediated by integrin (Score: 8.047246)



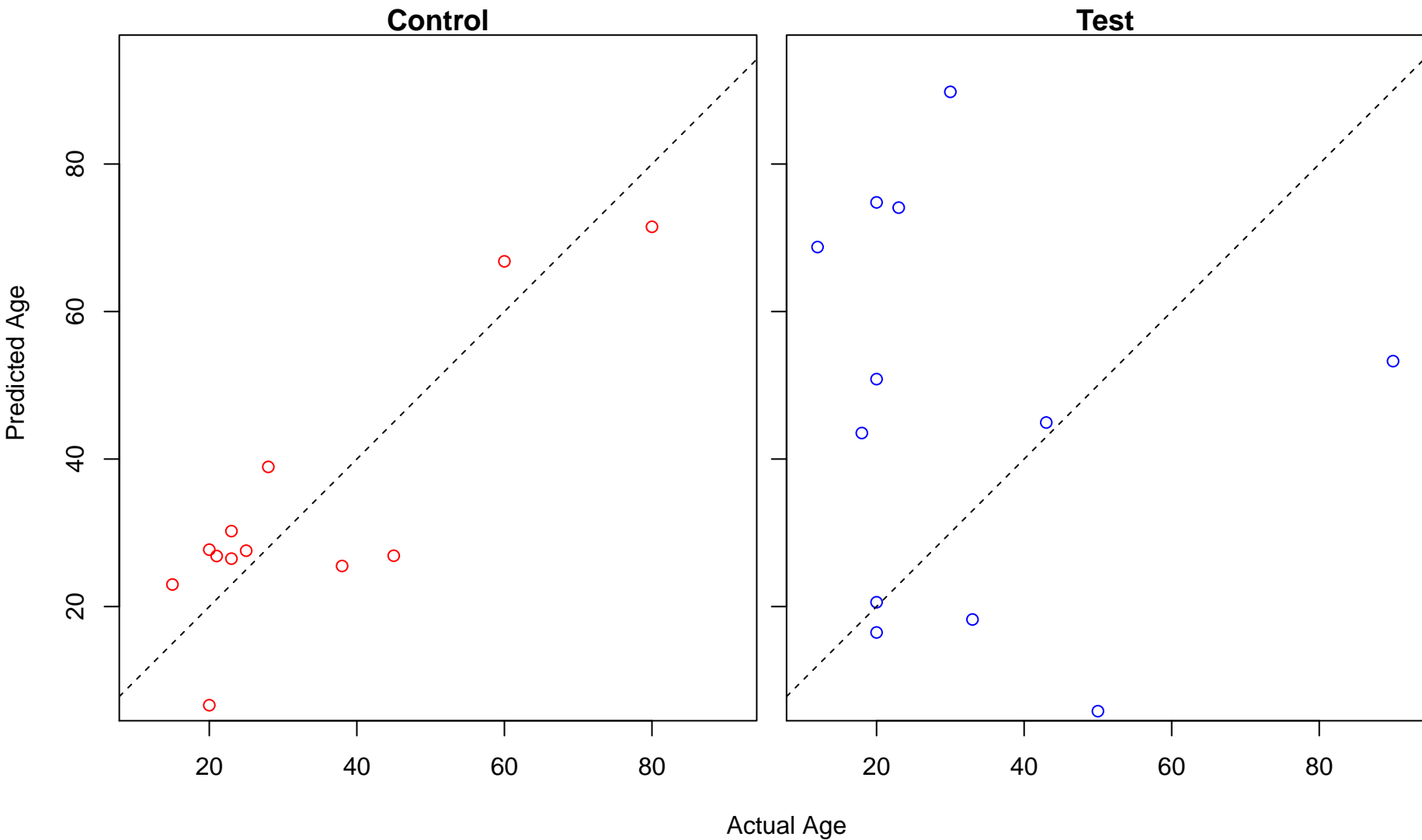
plasma lipoprotein particle clearance (Score: 8.046519)



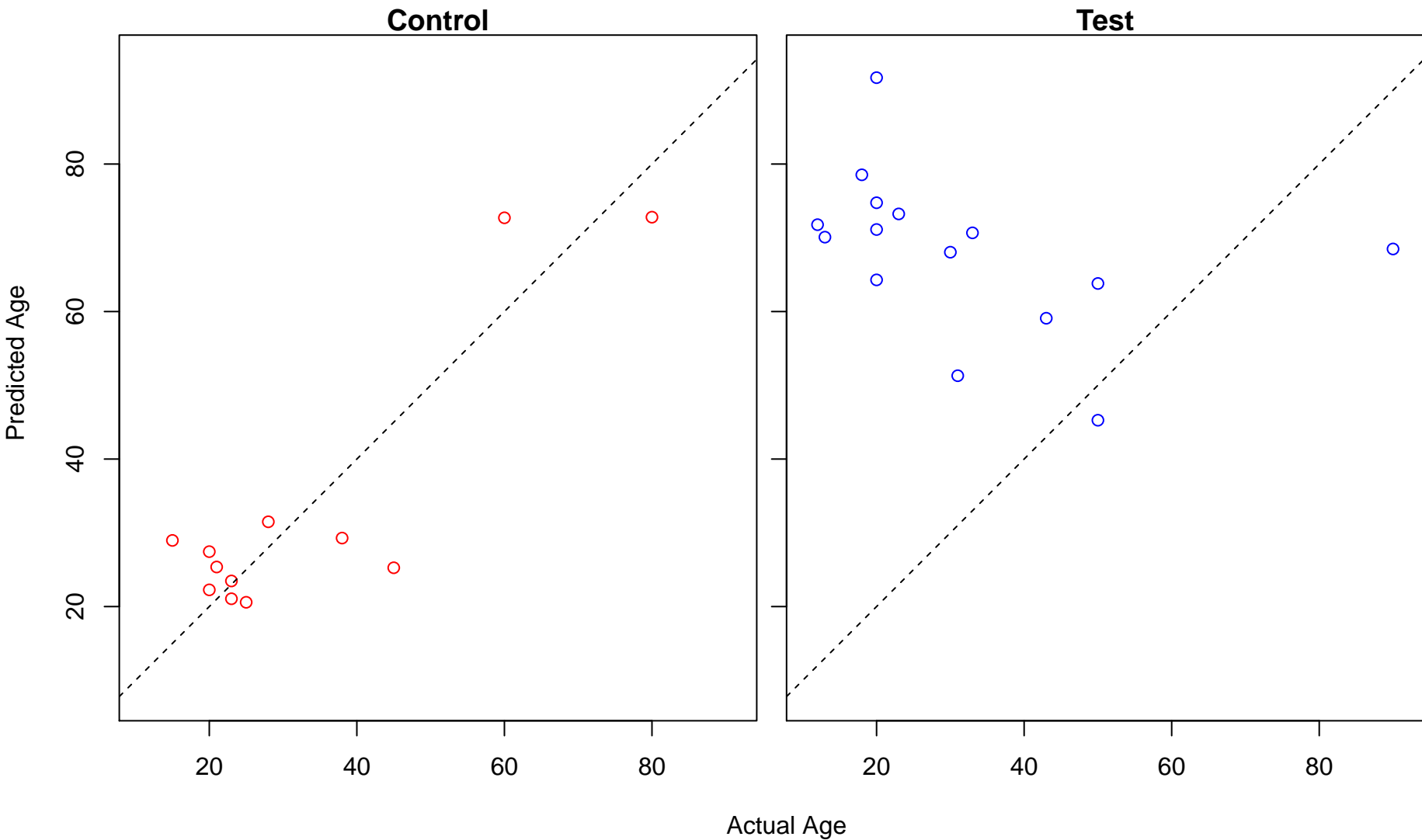
necroptotic signaling pathway (Score: 8.046352)



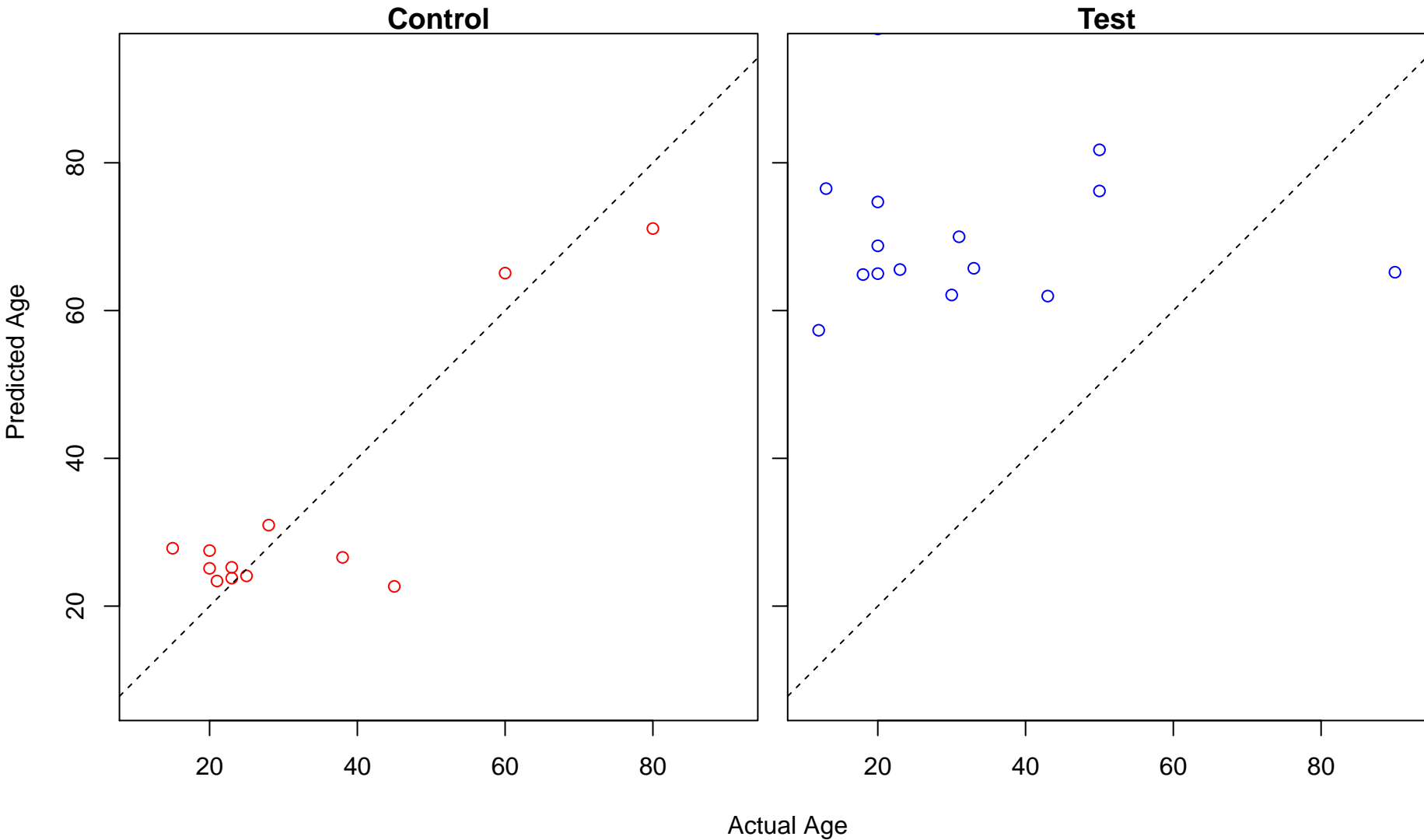
negative regulation of protein catabolic process (Score: 8.044609)



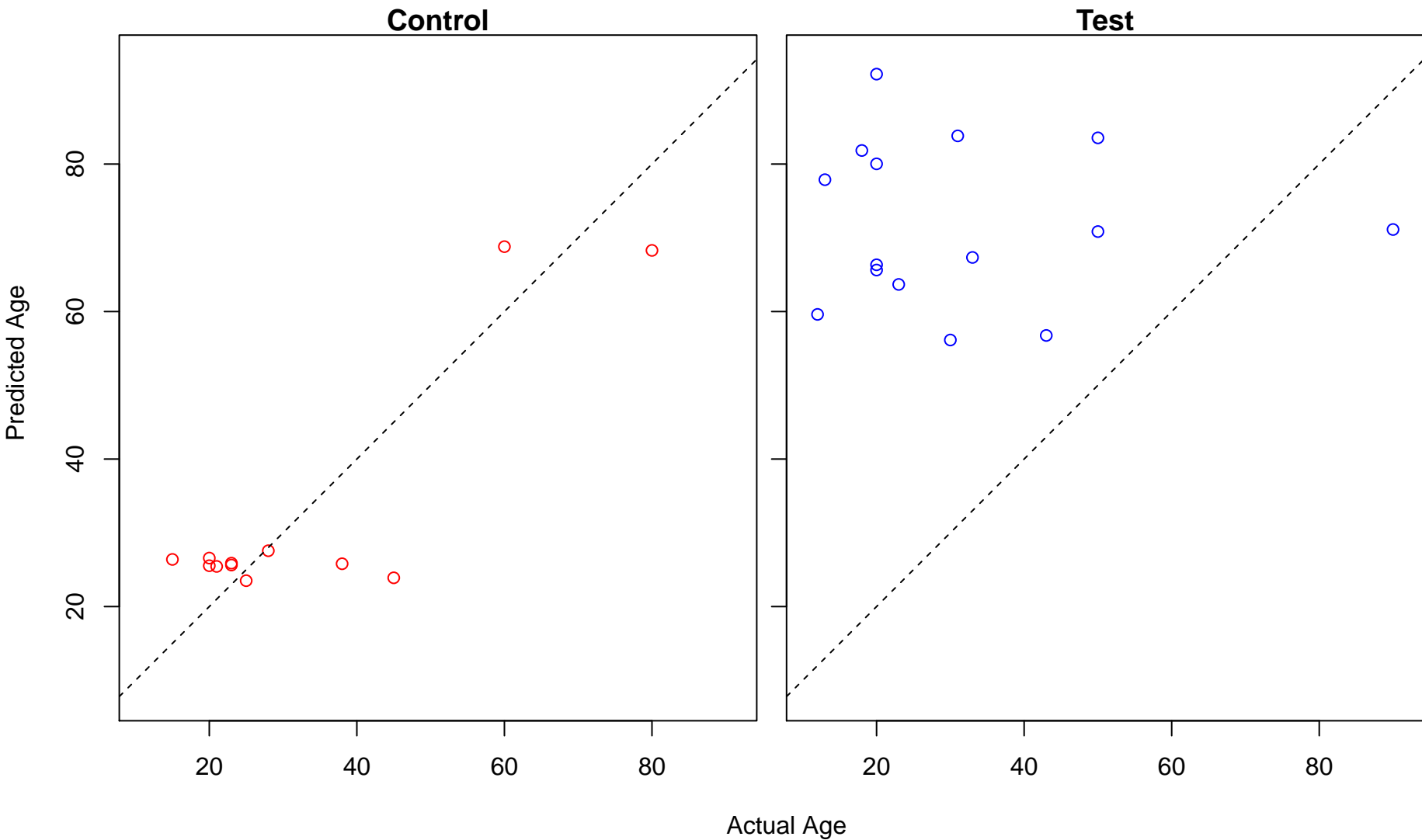
regulation of cellular senescence (Score: 8.039085)



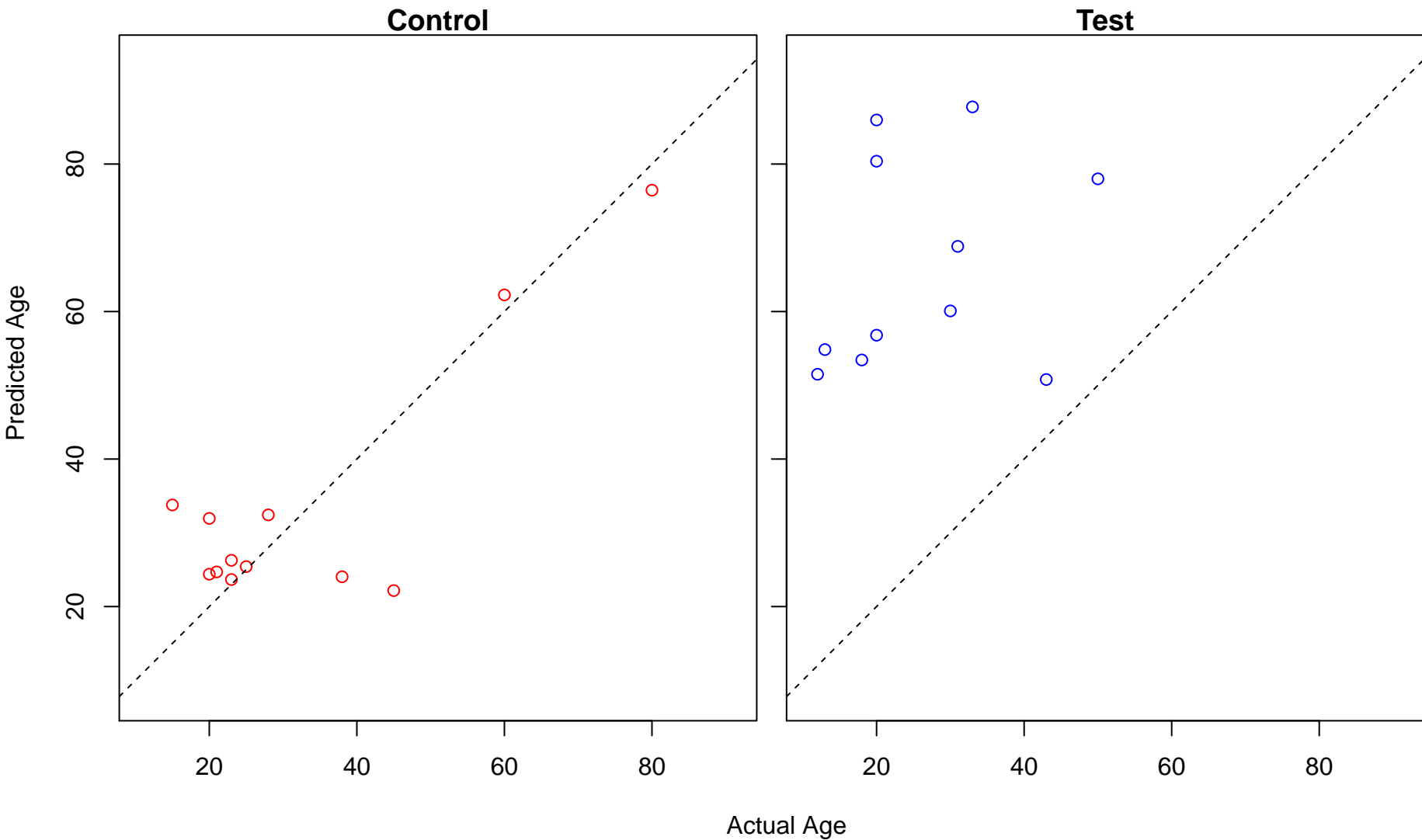
regulation of multicellular organism growth (Score: 8.035106)



telomere organization (Score: 8.034349)

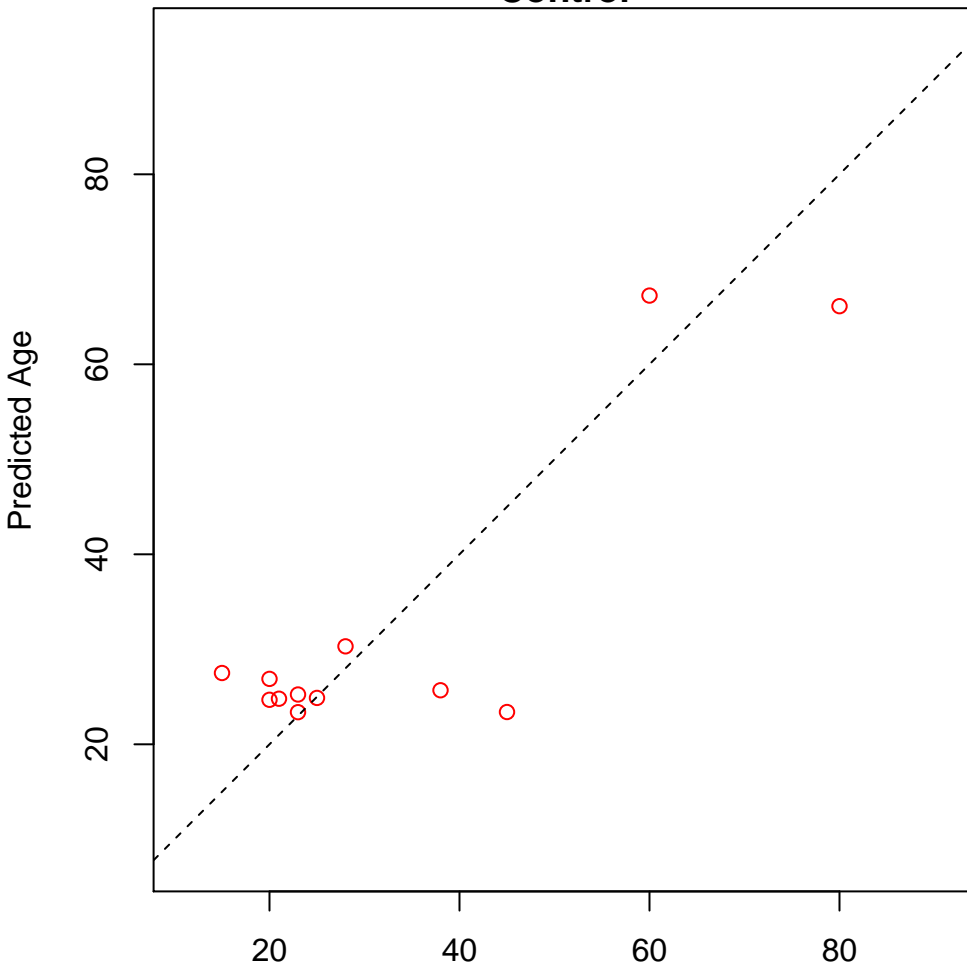


semaphorin-plexin signaling pathway (Score: 8.033836)

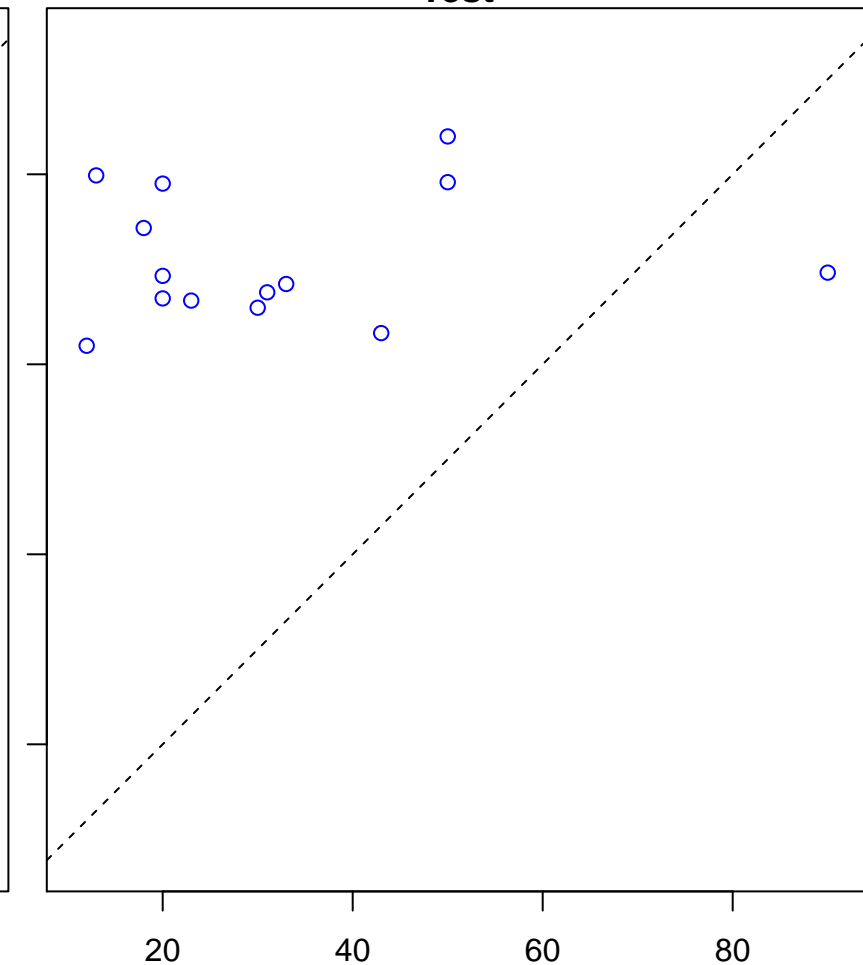


purine nucleotide biosynthetic process (Score: 8.033201)

Control

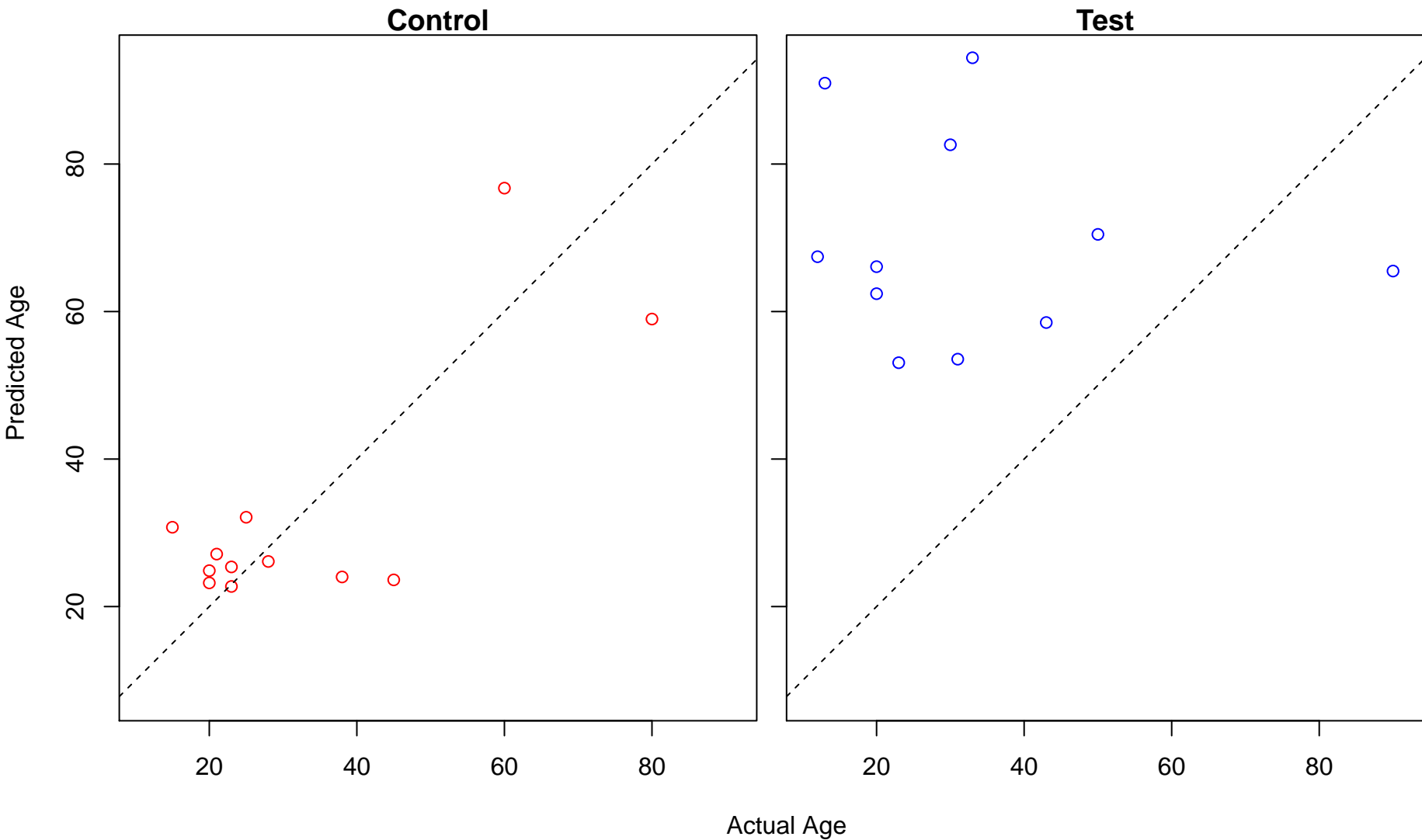


Test

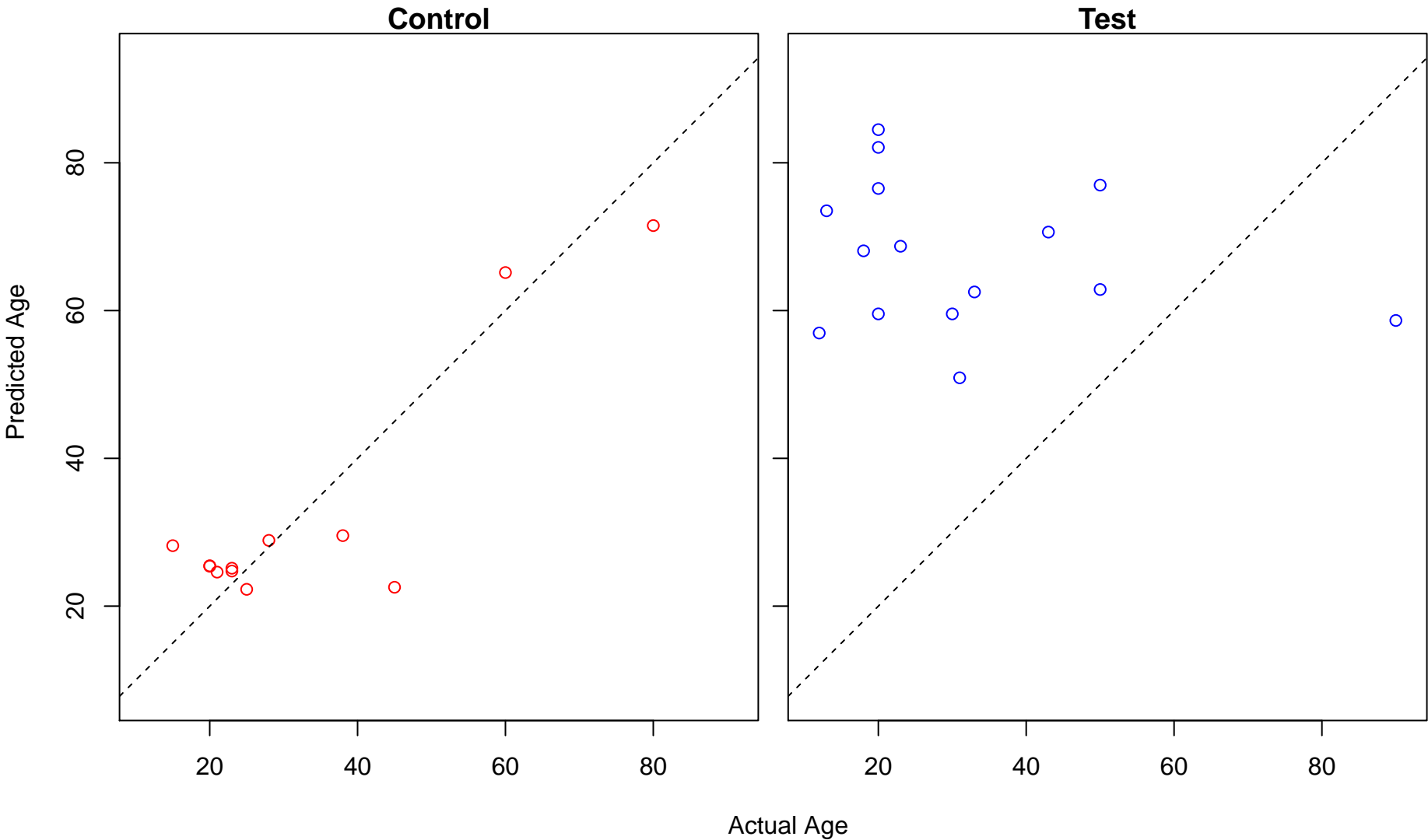


Actual Age

negative regulation of protein autophosphorylation (Score: 8.031960)

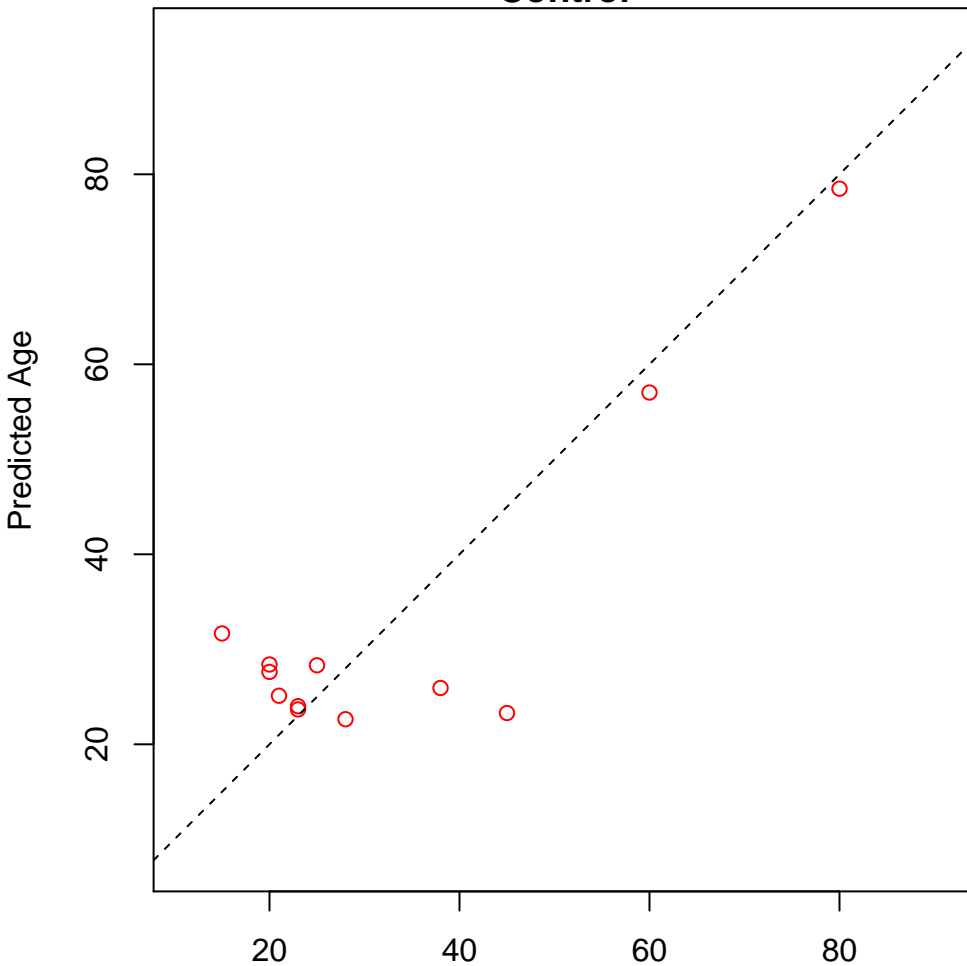


regulation of peroxisome proliferator activated receptor signaling pathway (Score: 8.031313)

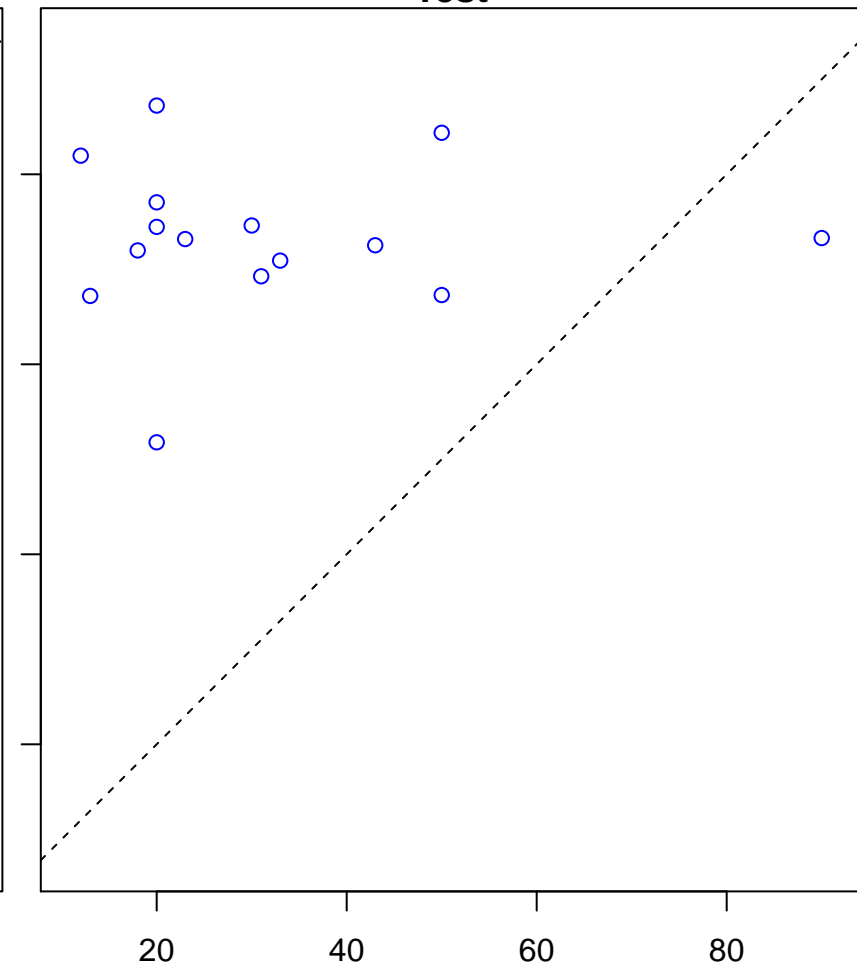


regulation of sequestering of zinc ion (Score: 8.030798)

Control



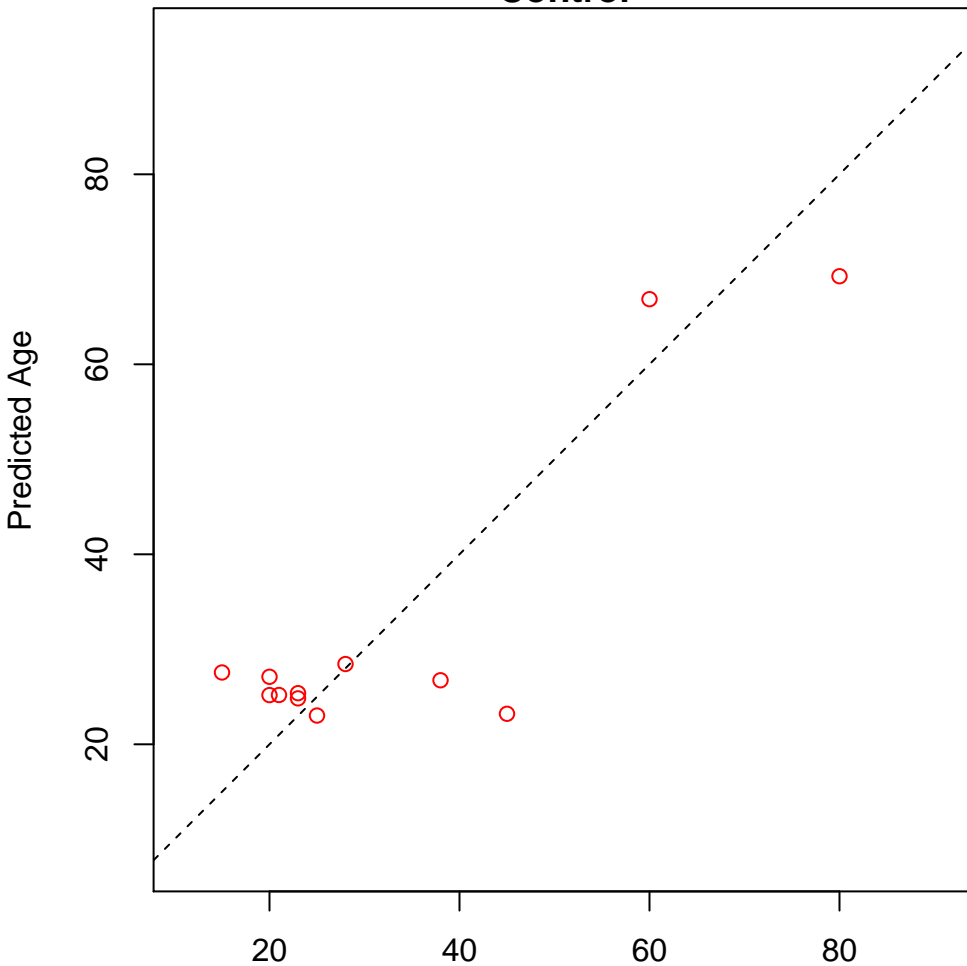
Test



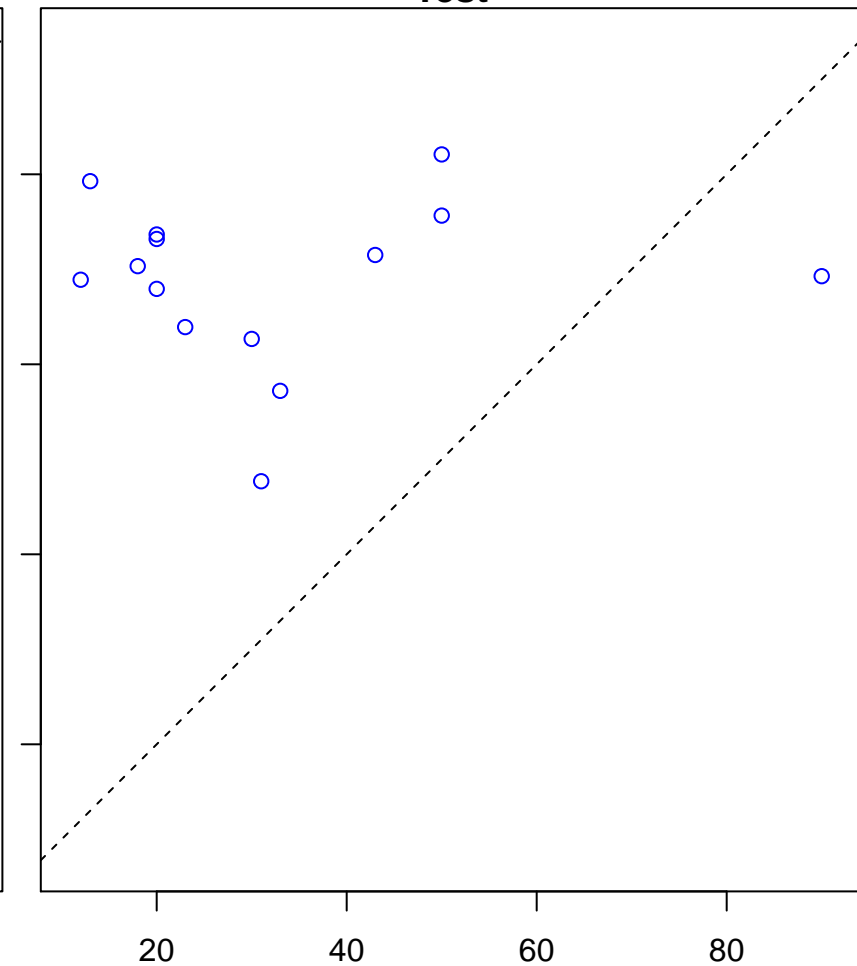
Actual Age

glutathione derivative metabolic process (Score: 8.028965)

Control

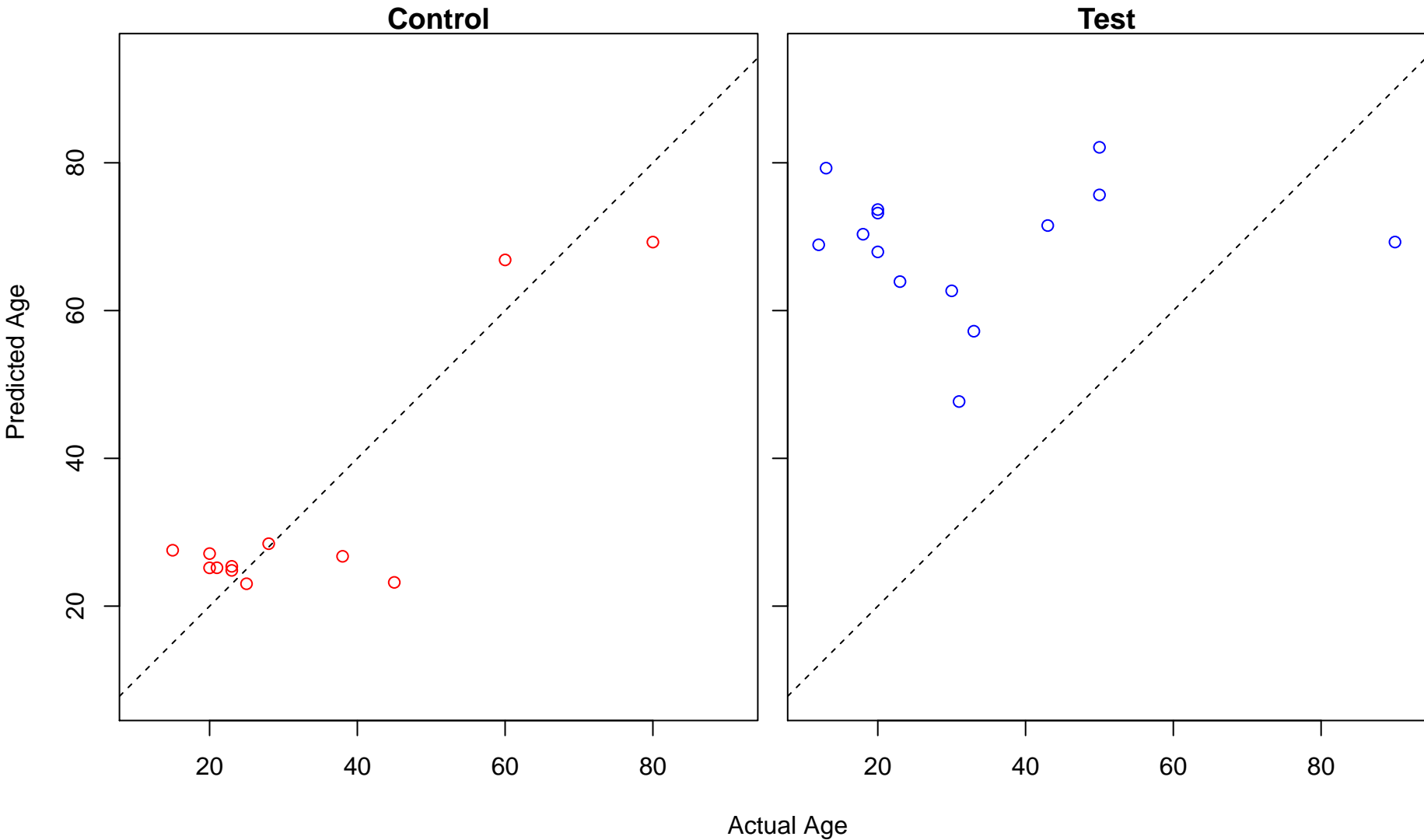


Test

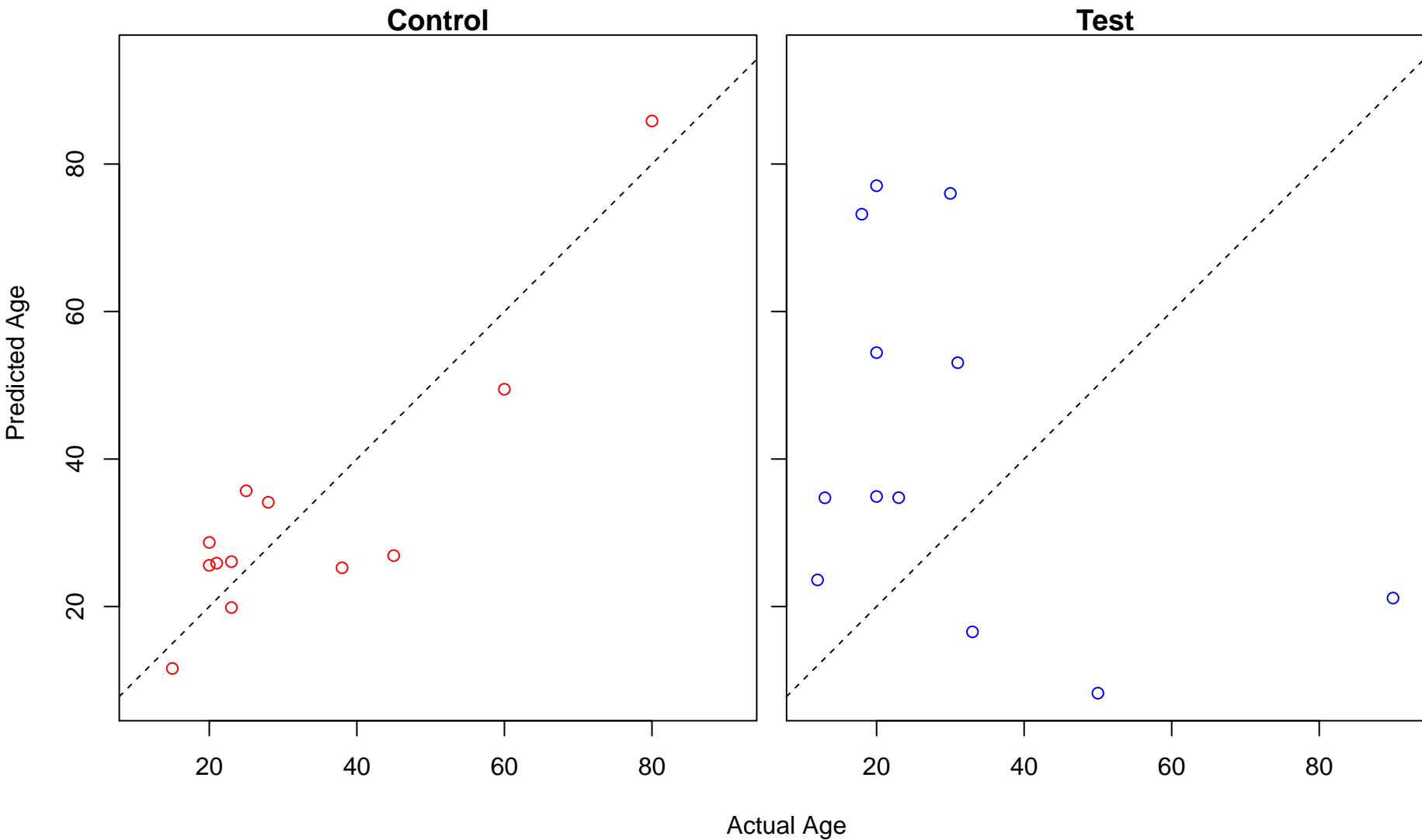


Actual Age

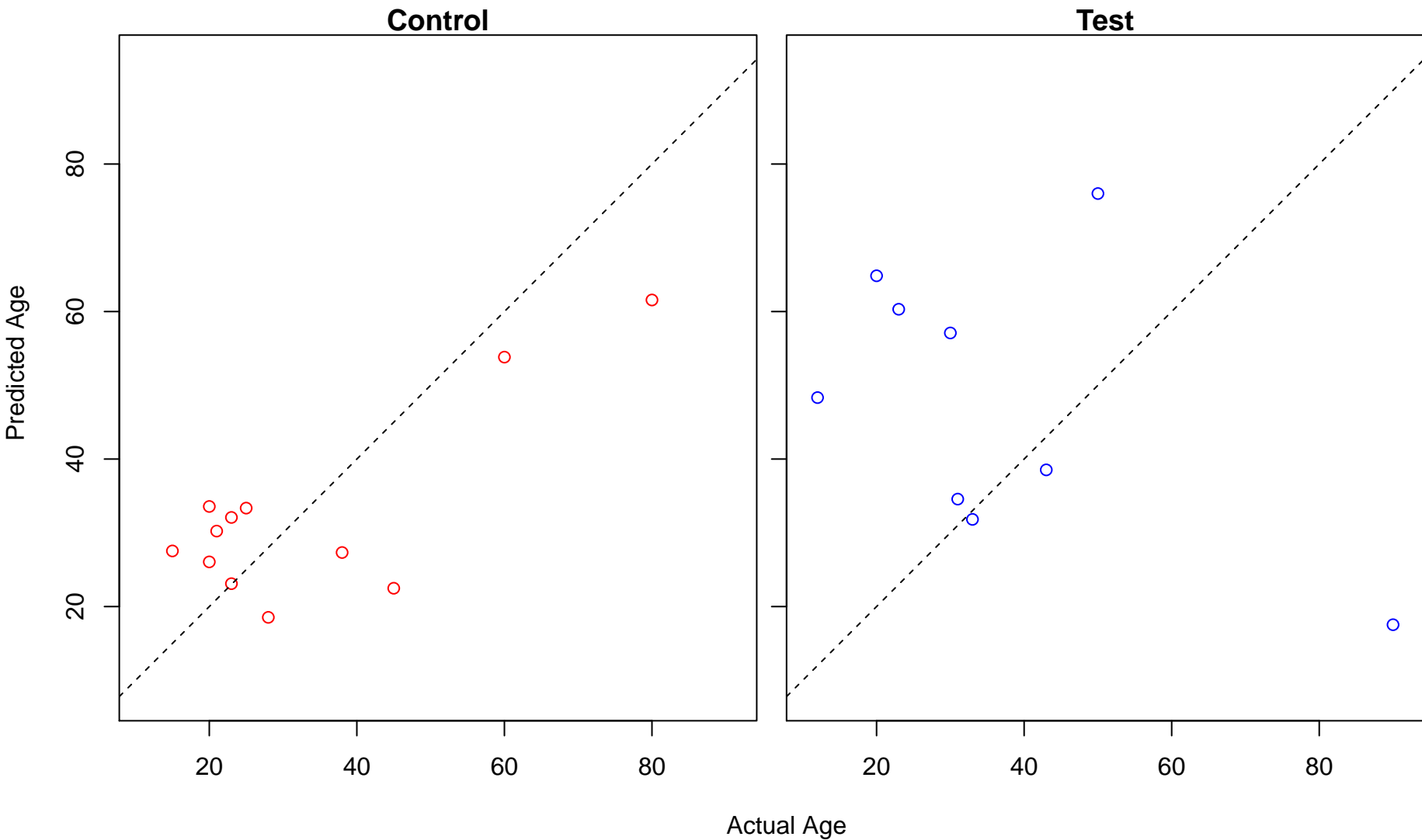
glutathione derivative biosynthetic process (Score: 8.028965)



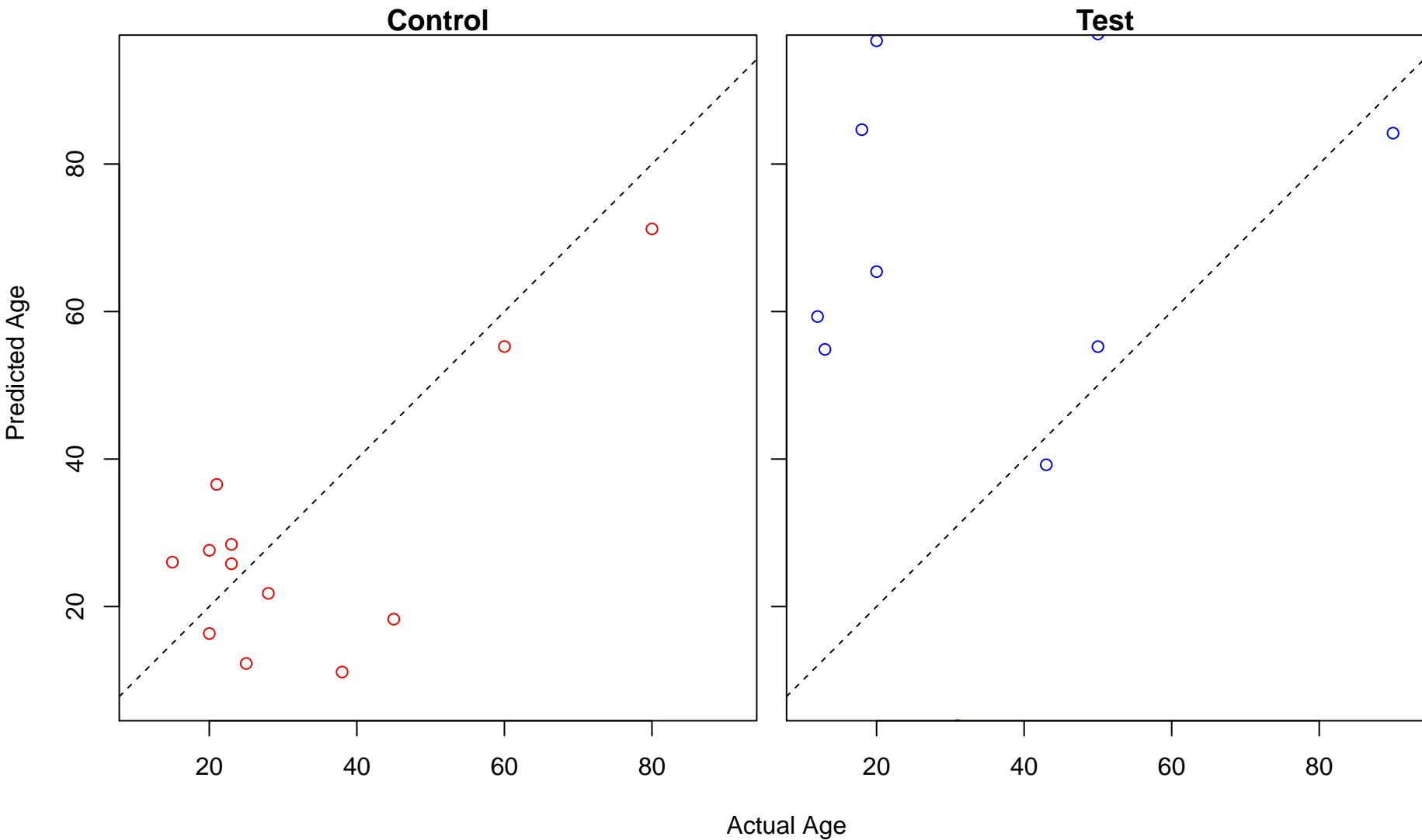
learning (Score: 8.027696)



positive regulation of endothelial cell differentiation (Score: 8.026416)

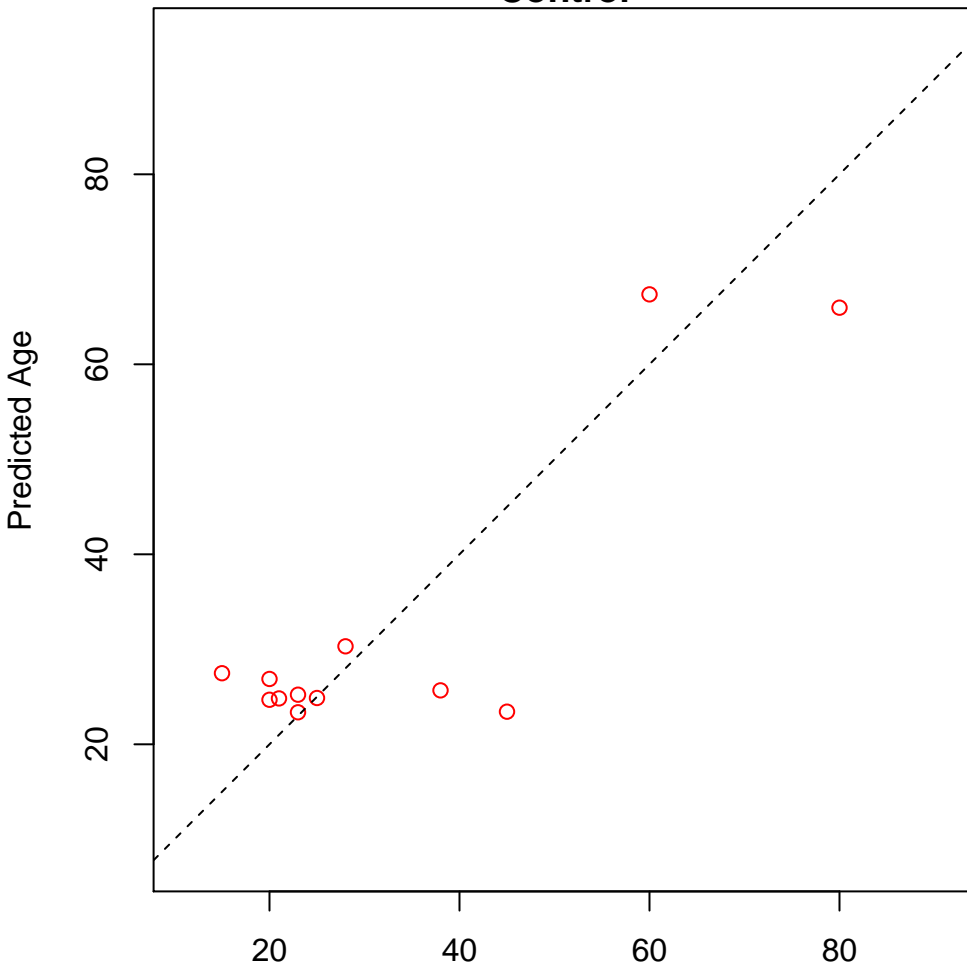


negative regulation of protein export from nucleus (Score: 8.024360)

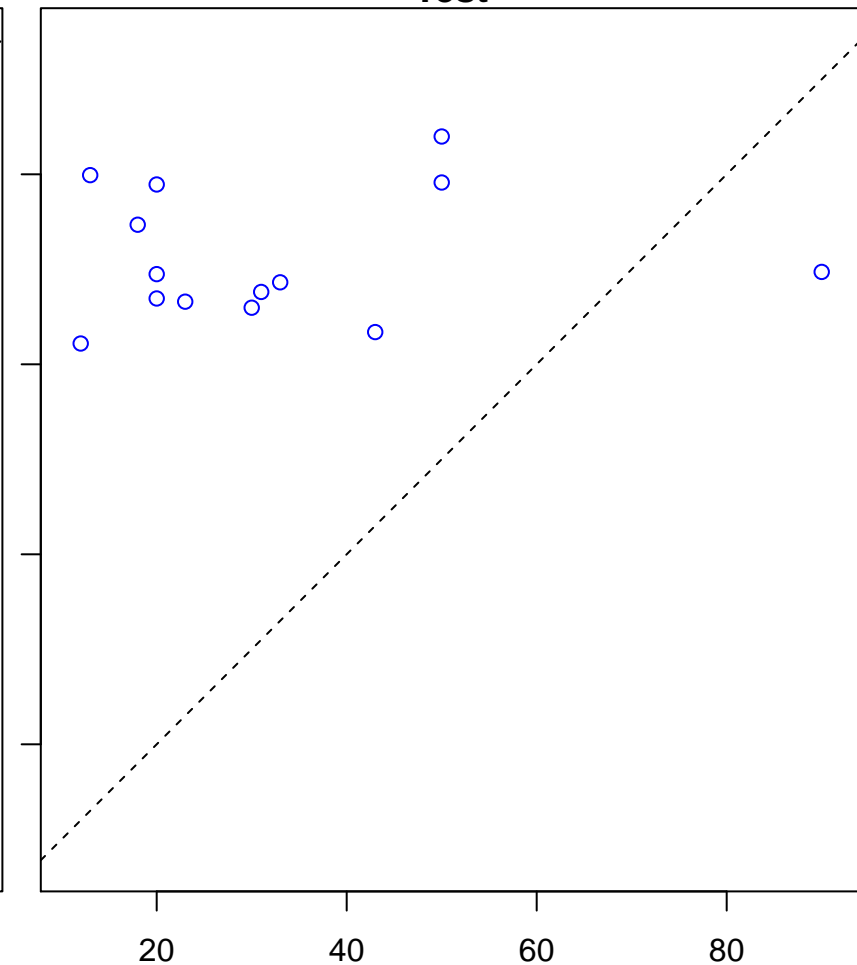


ribonucleotide biosynthetic process (Score: 8.012120)

Control

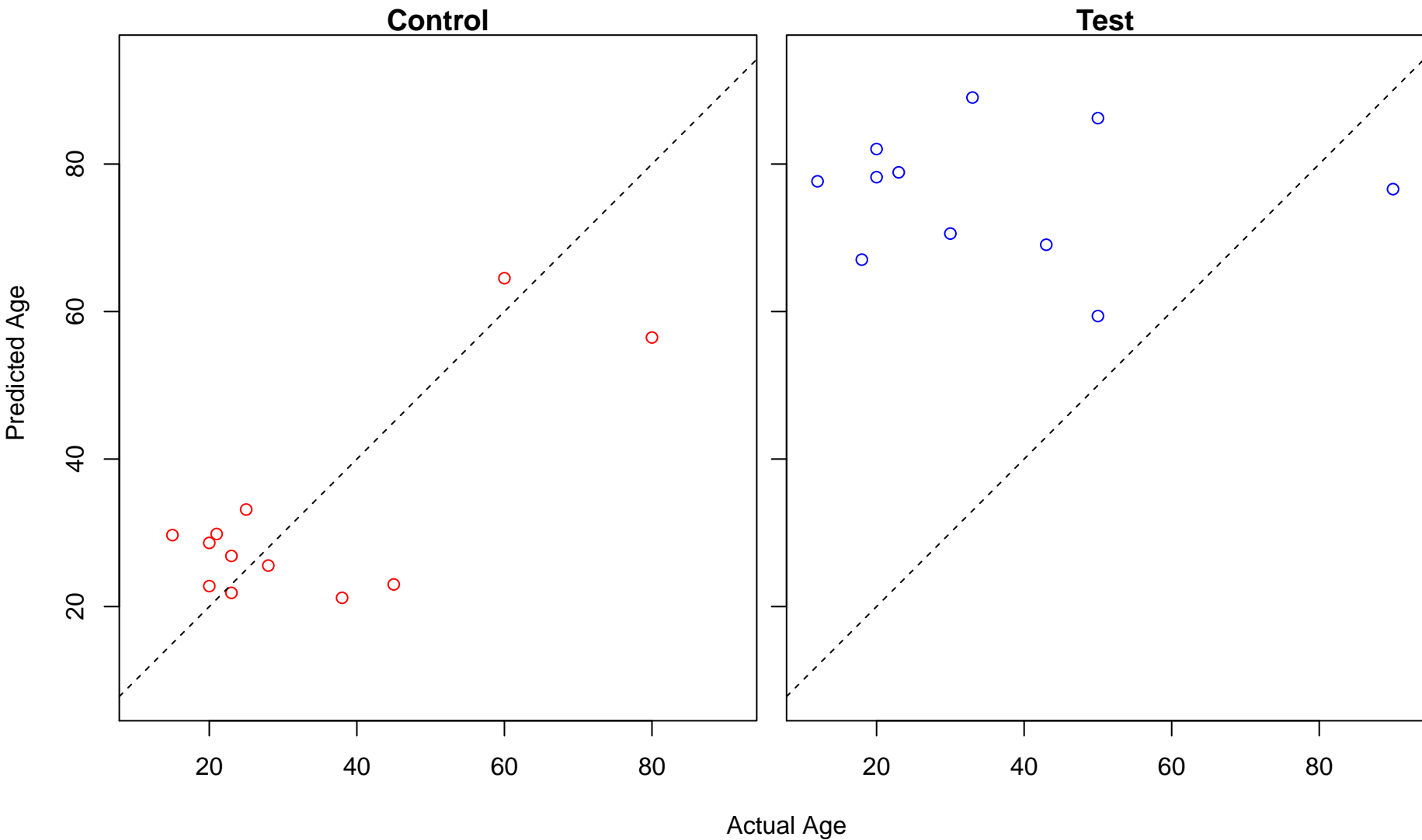


Test

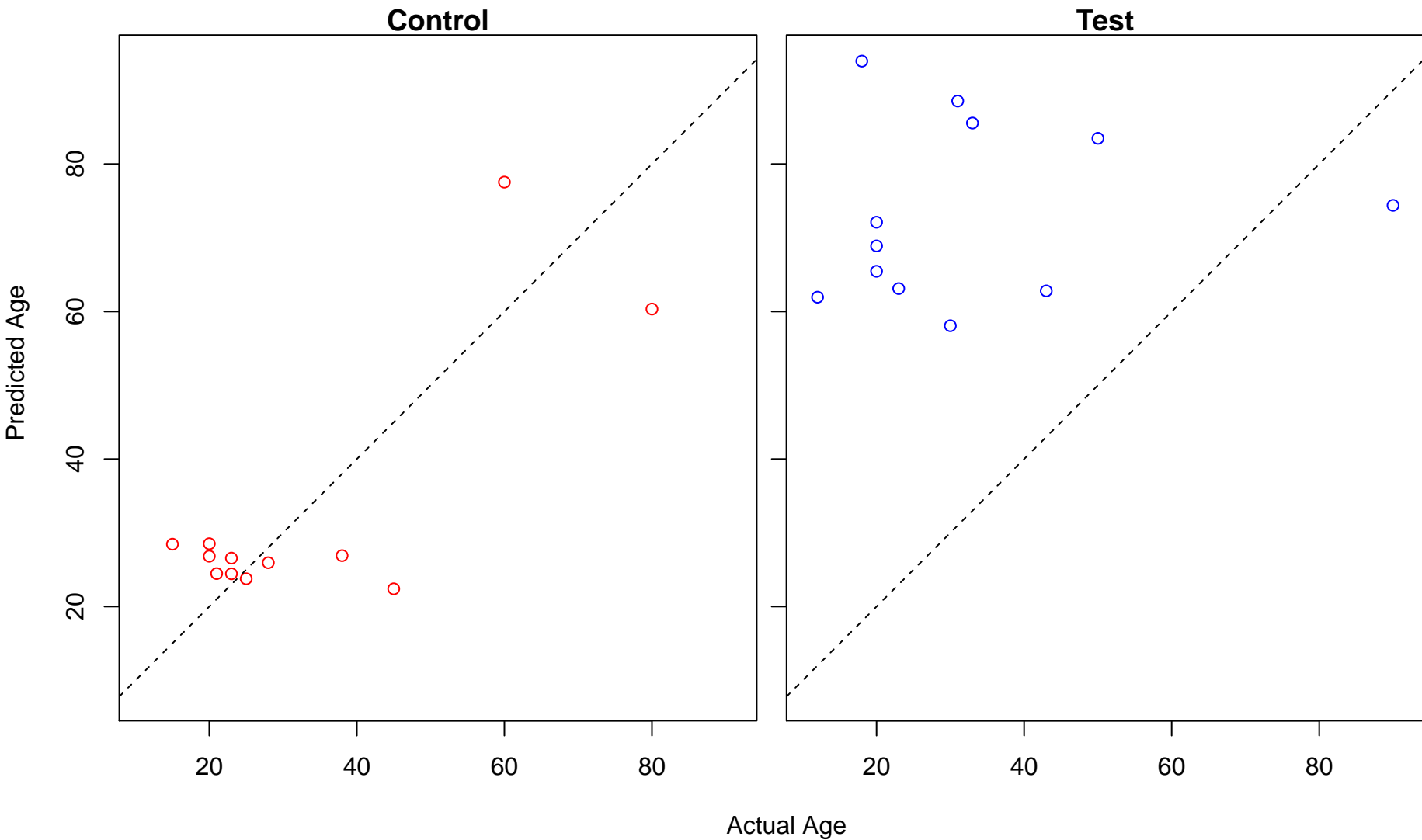


Actual Age

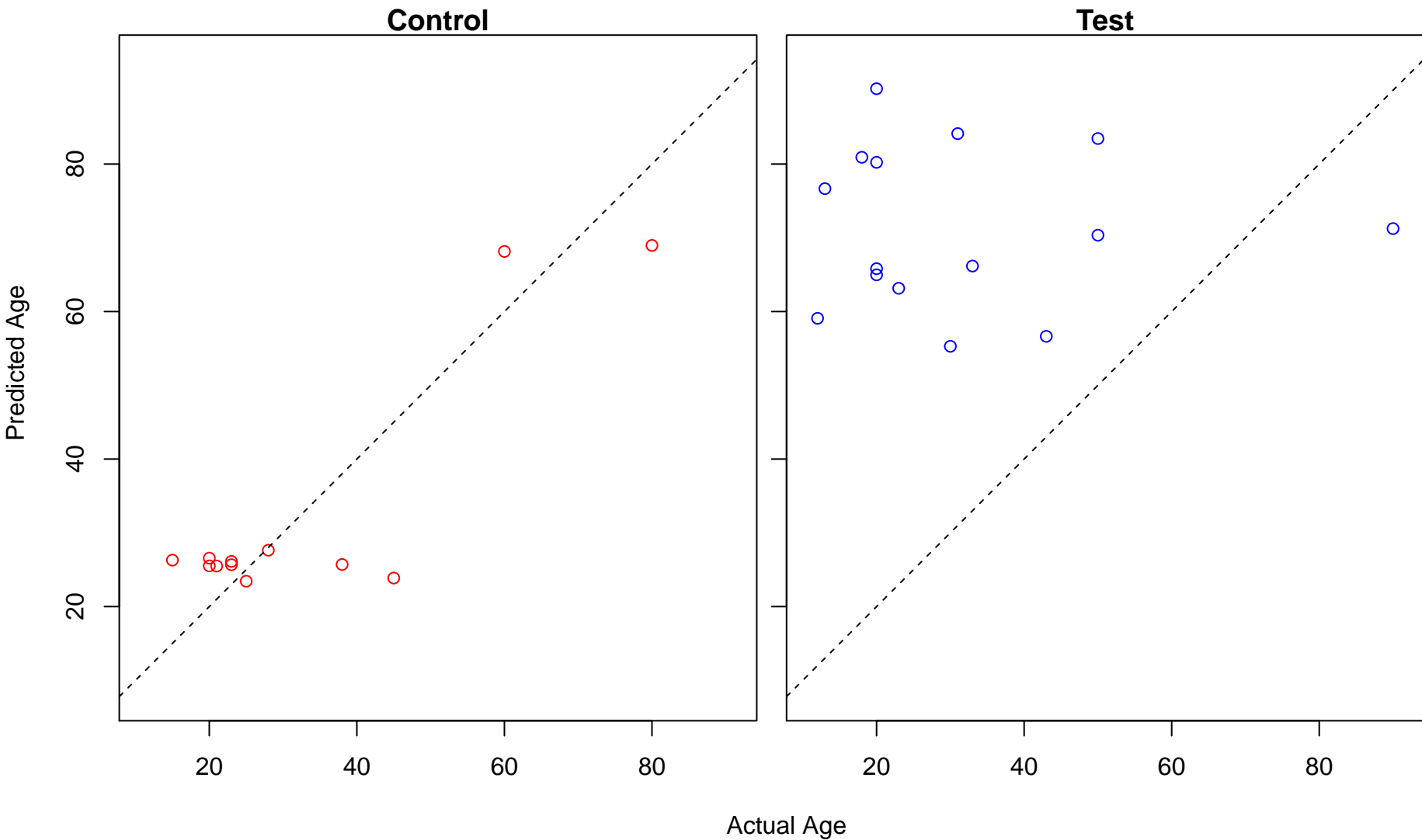
lymphocyte chemotaxis (Score: 8.010596)



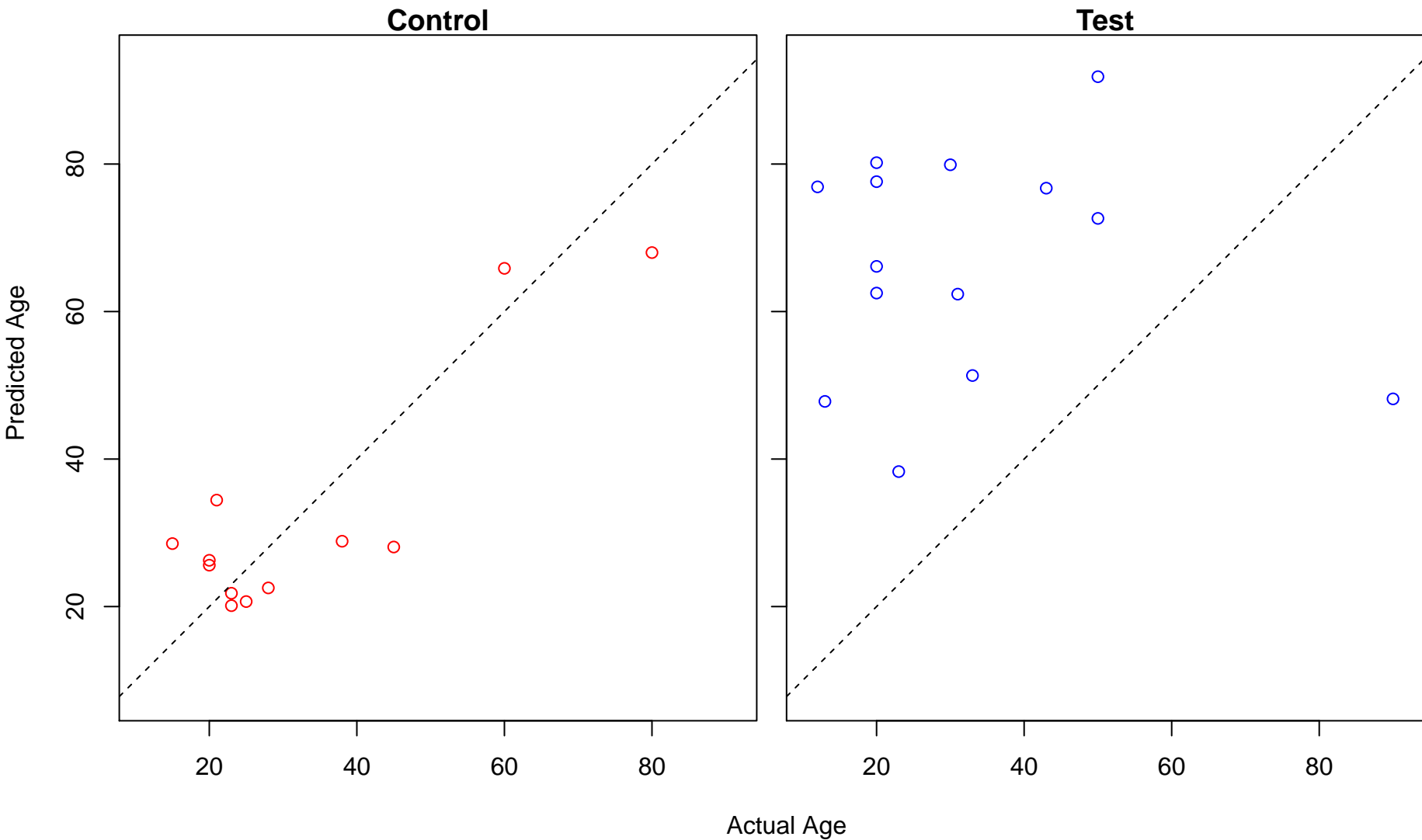
innate immune response in mucosa (Score: 8.008077)



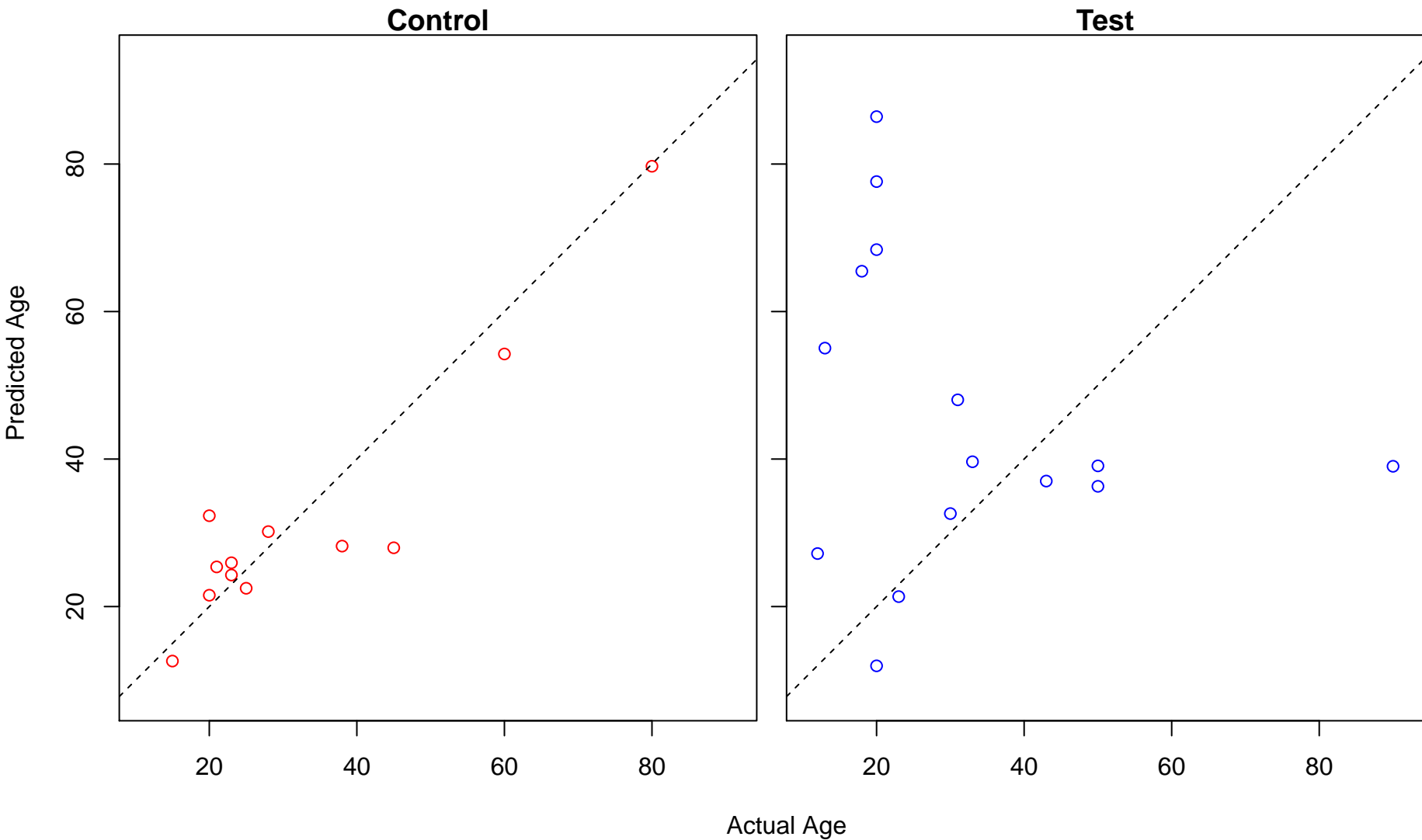
macromolecule methylation (Score: 8.006067)



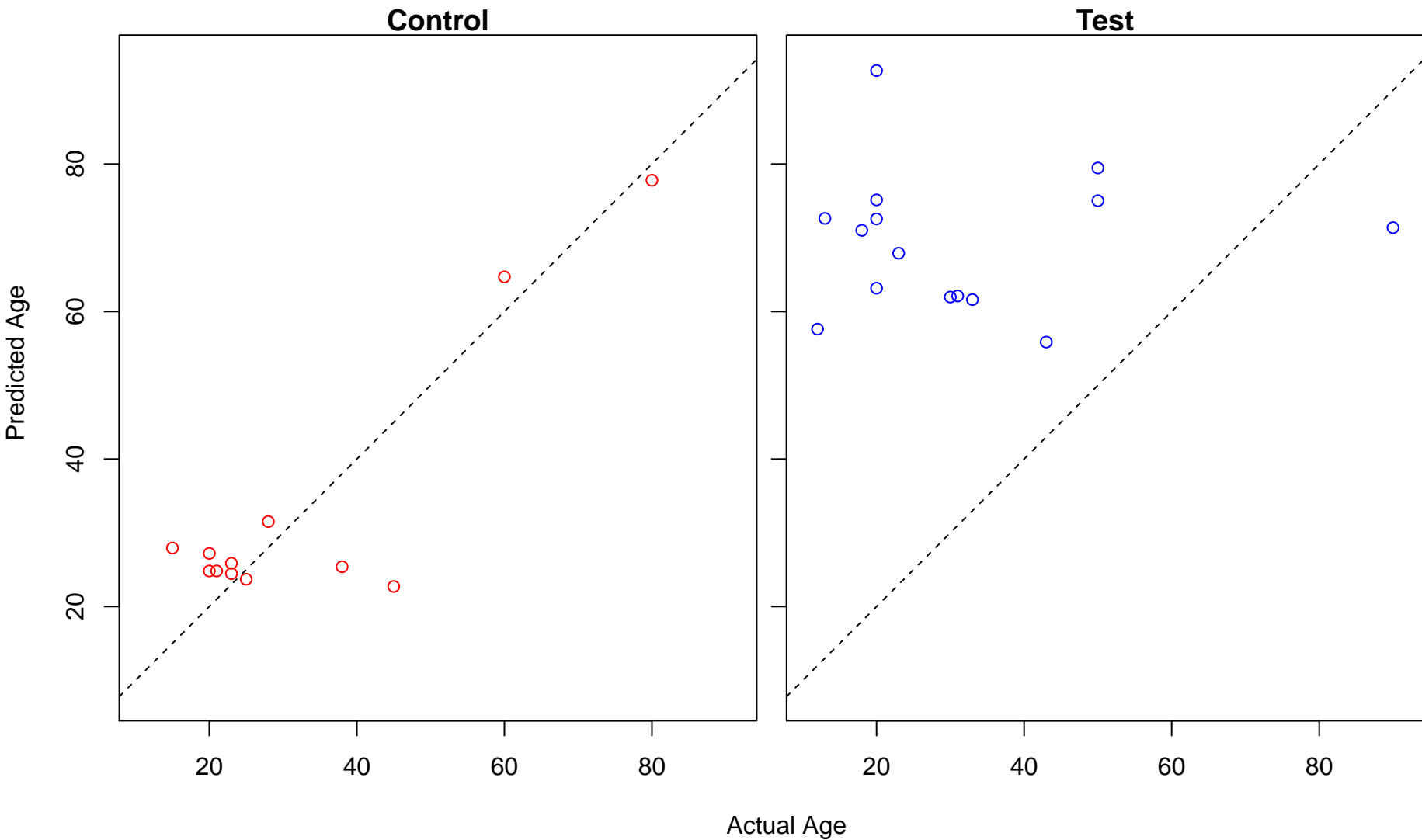
cellular response to reactive oxygen species (Score: 8.005020)



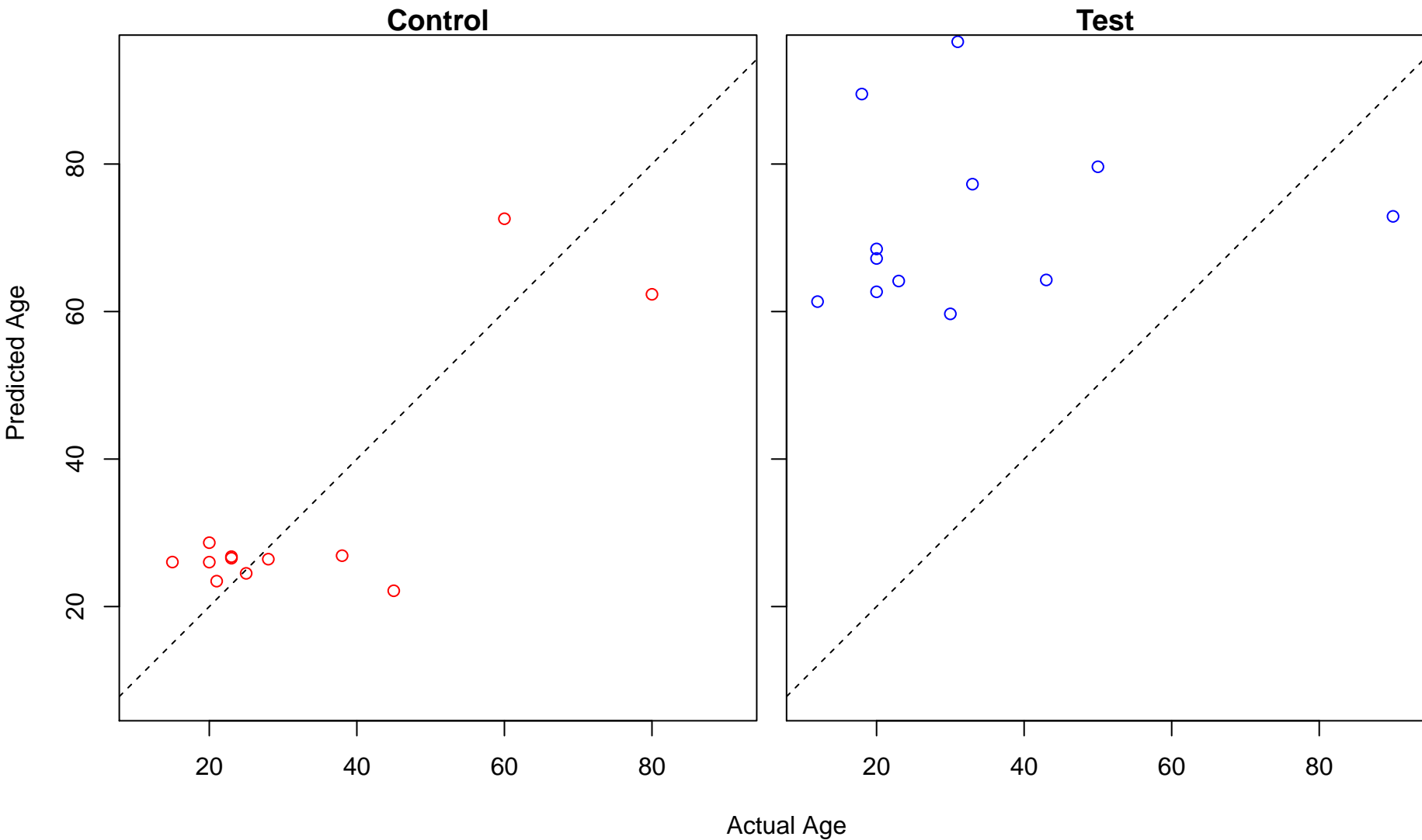
learning or memory (Score: 8.004233)



energy derivation by oxidation of organic compounds (Score: 7.998159)

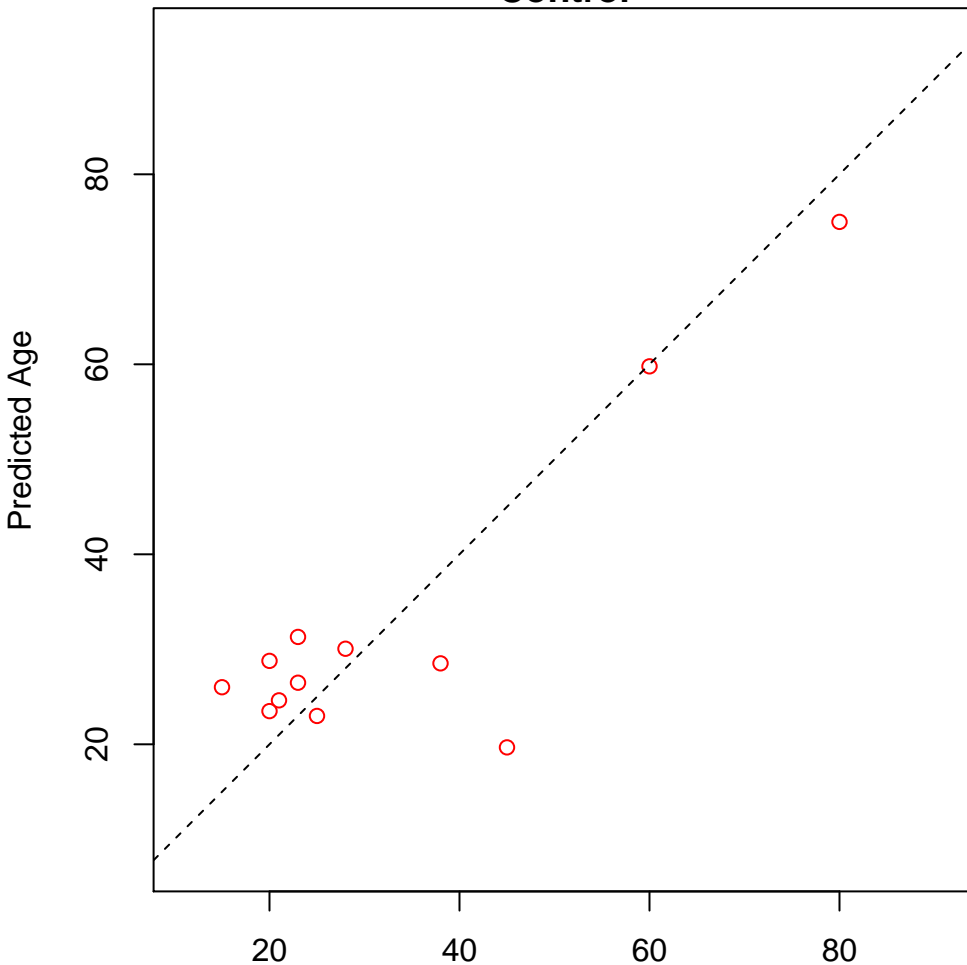


defense response to bacterium (Score: 7.995490)

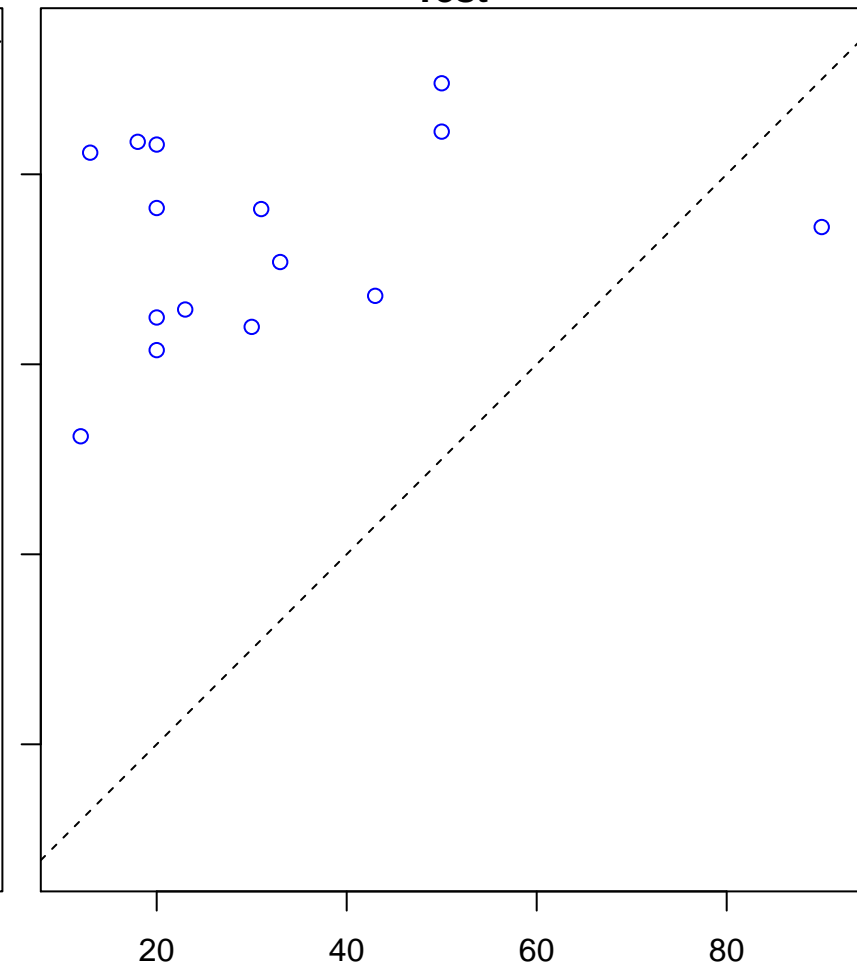


negative regulation of immune response (Score: 7.991960)

Control

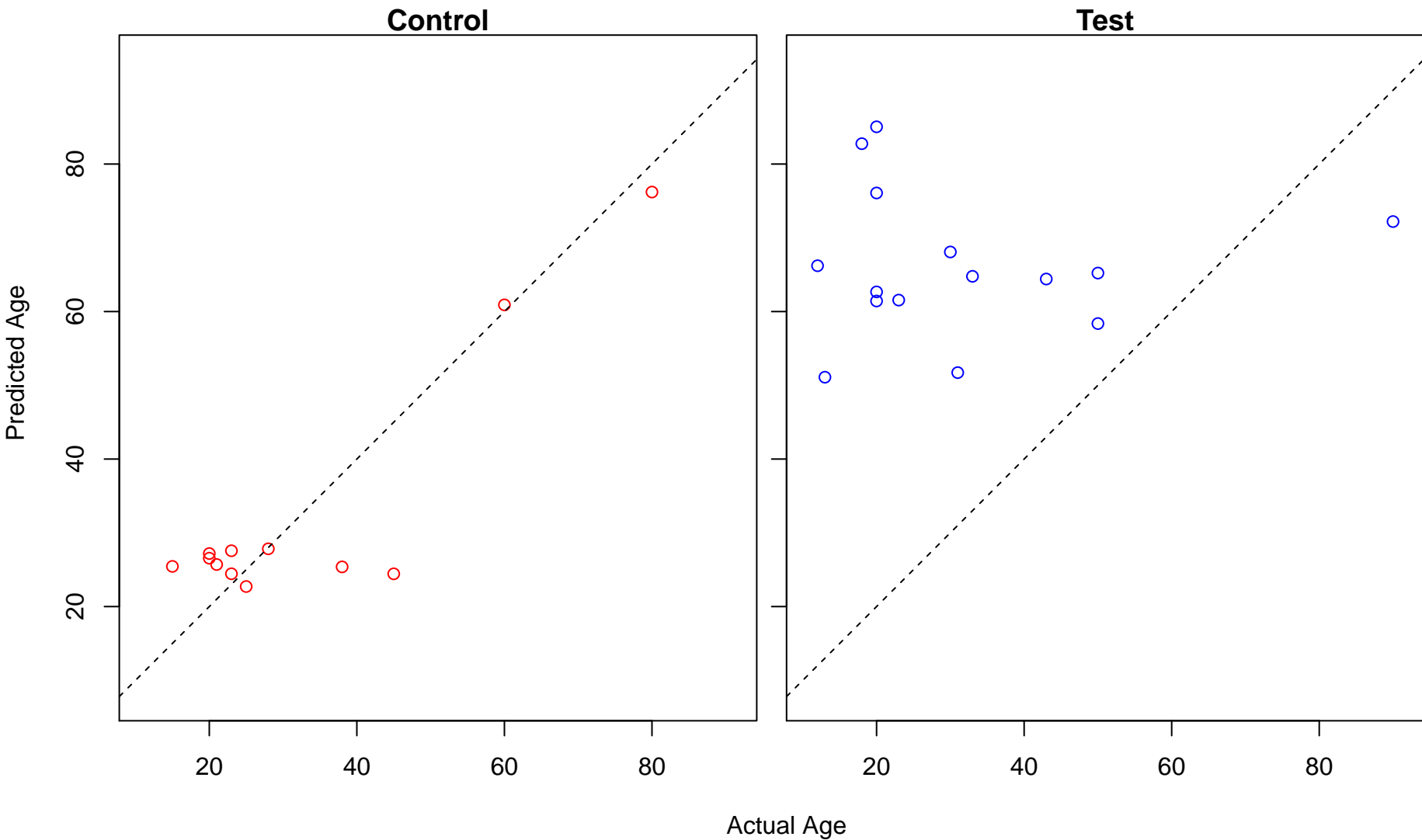


Test

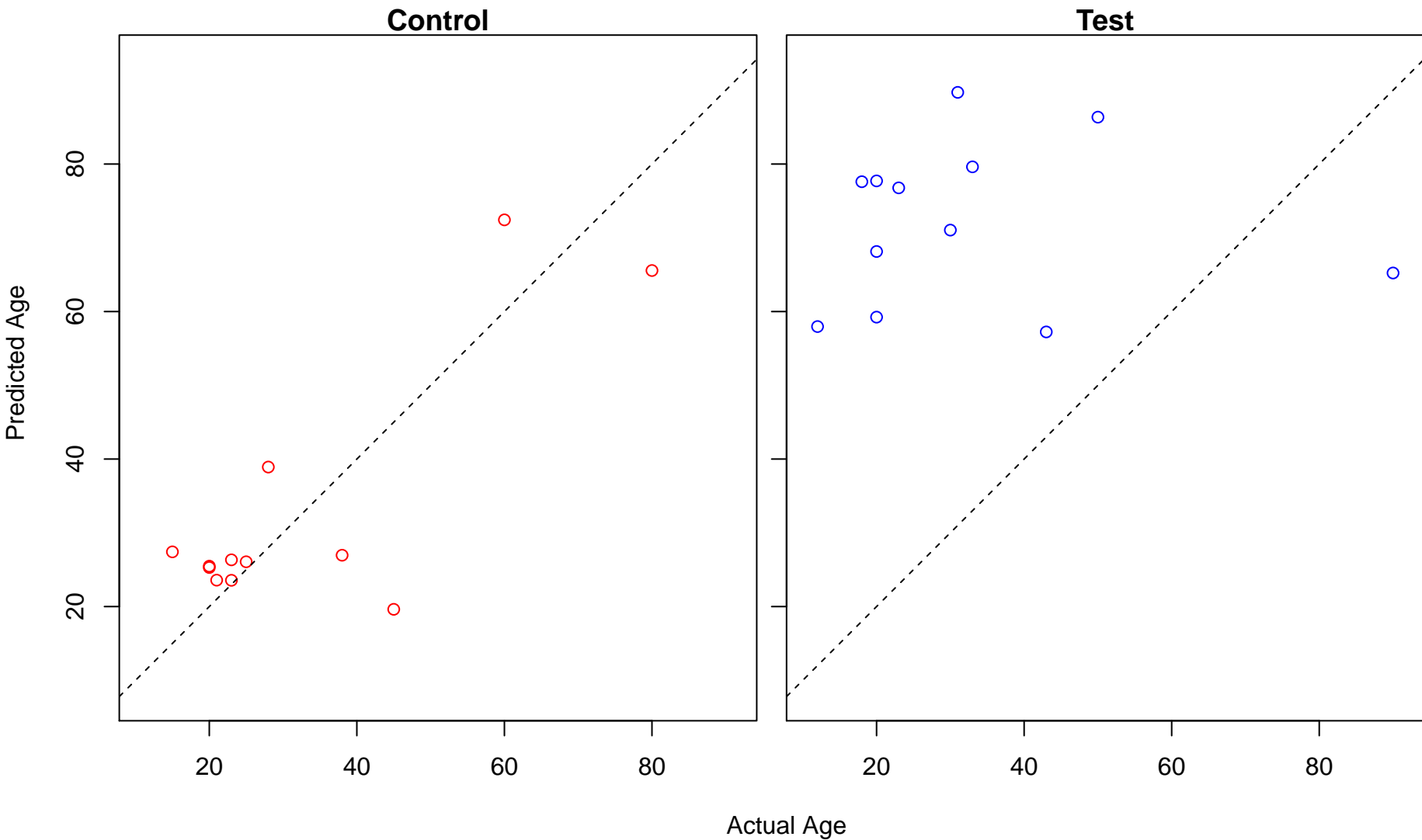


Actual Age

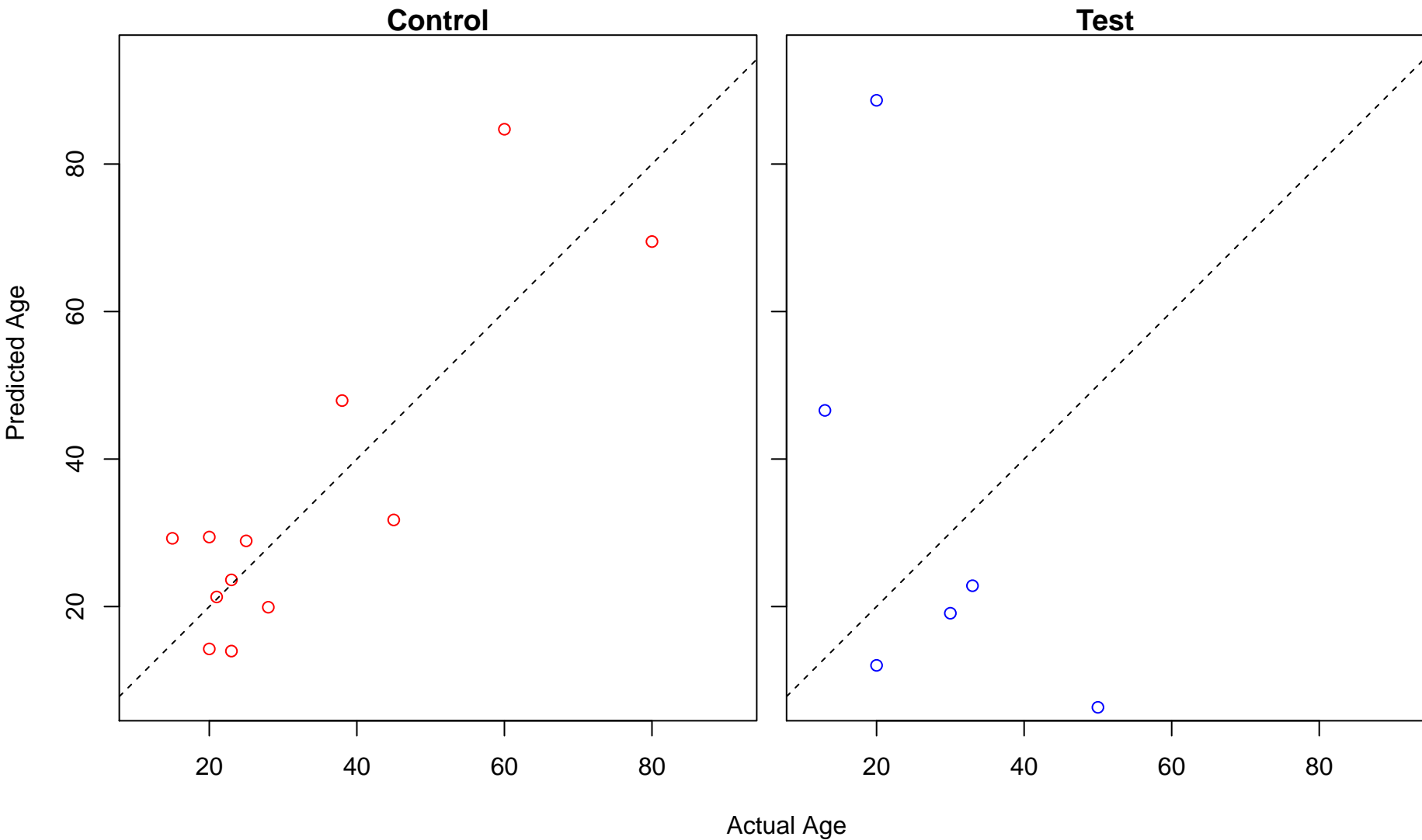
regulation of autophagosome maturation (Score: 7.991377)



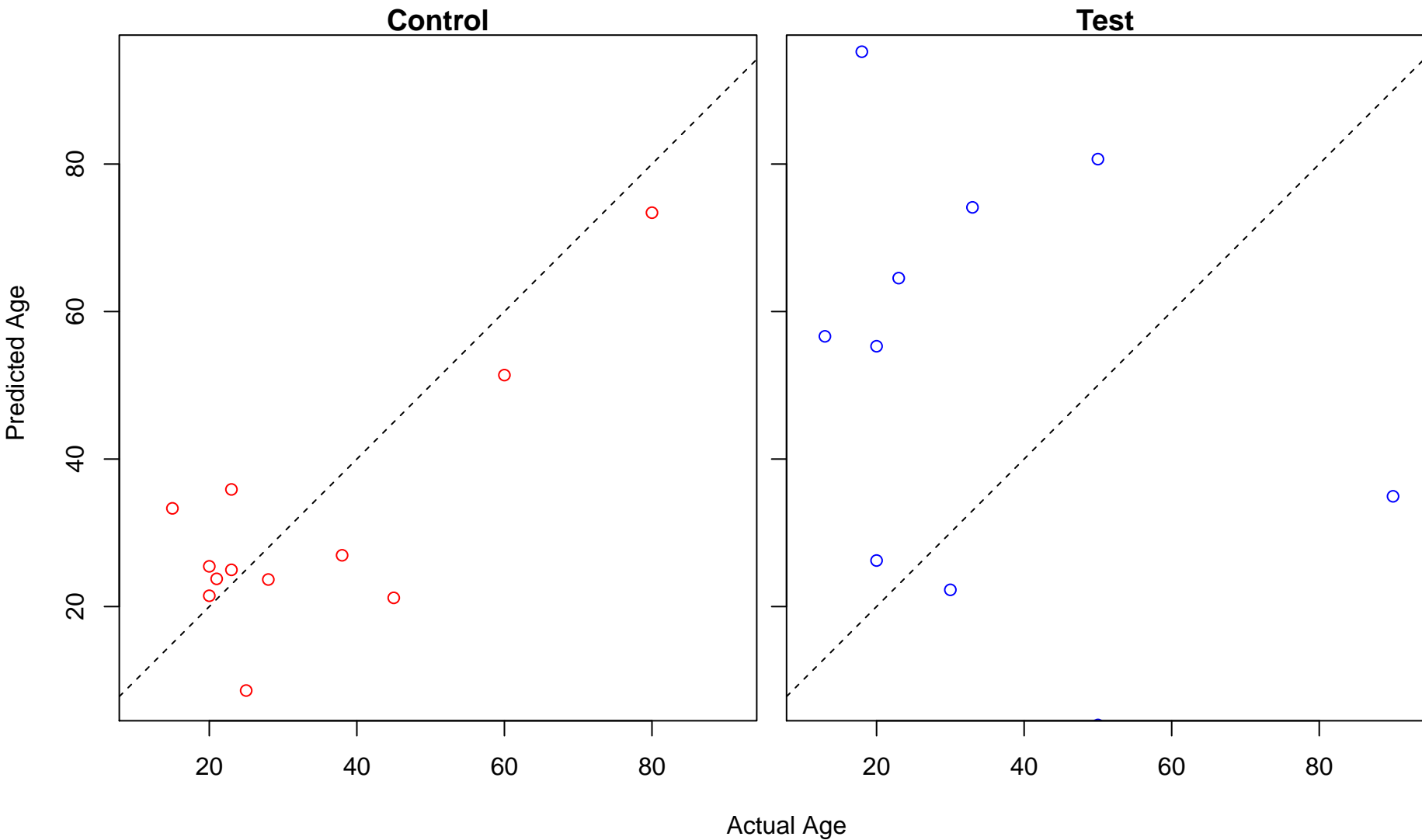
regulation of intrinsic apoptotic signaling pathway by p53 class mediator (Score: 7.980244)



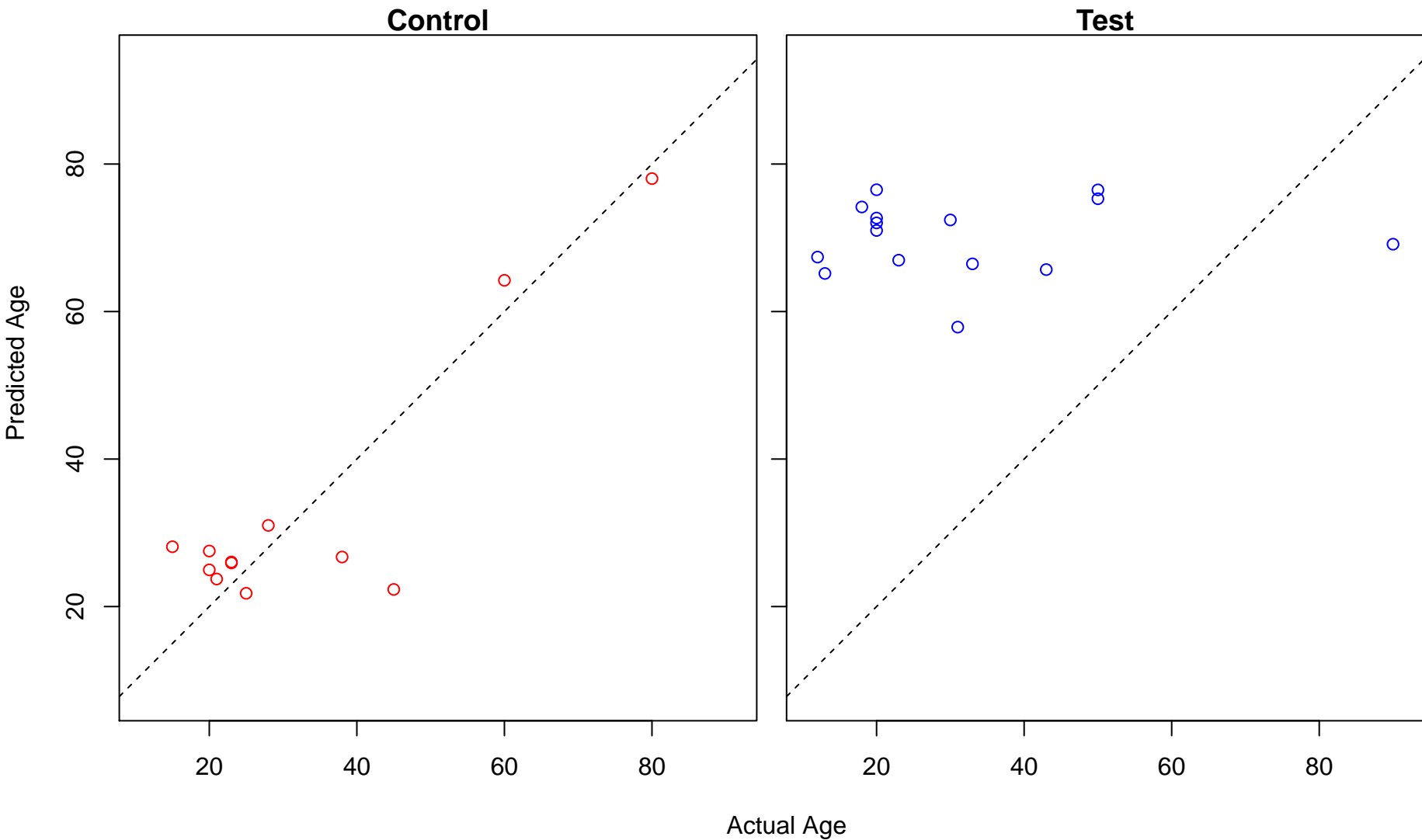
regulation of mesenchymal stem cell differentiation (Score: 7.980116)



cellular chemical homeostasis (Score: 7.978688)

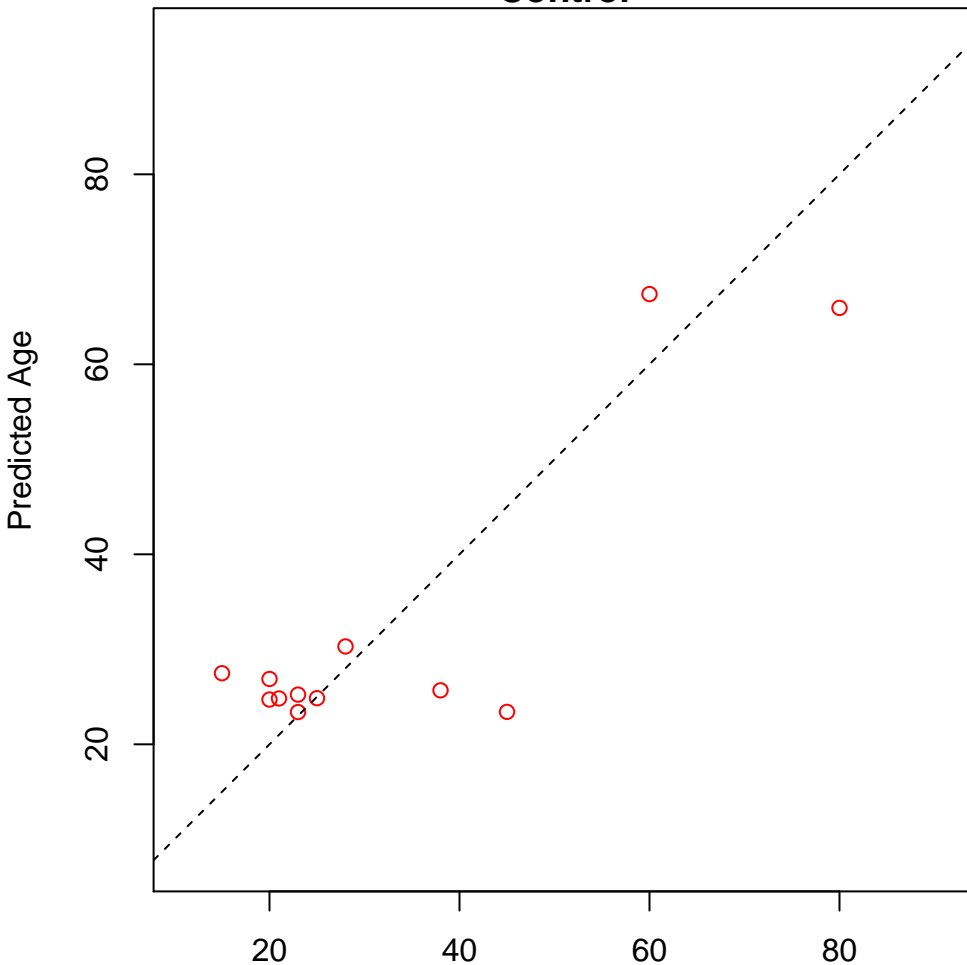


divalent metal ion transport (Score: 7.977641)

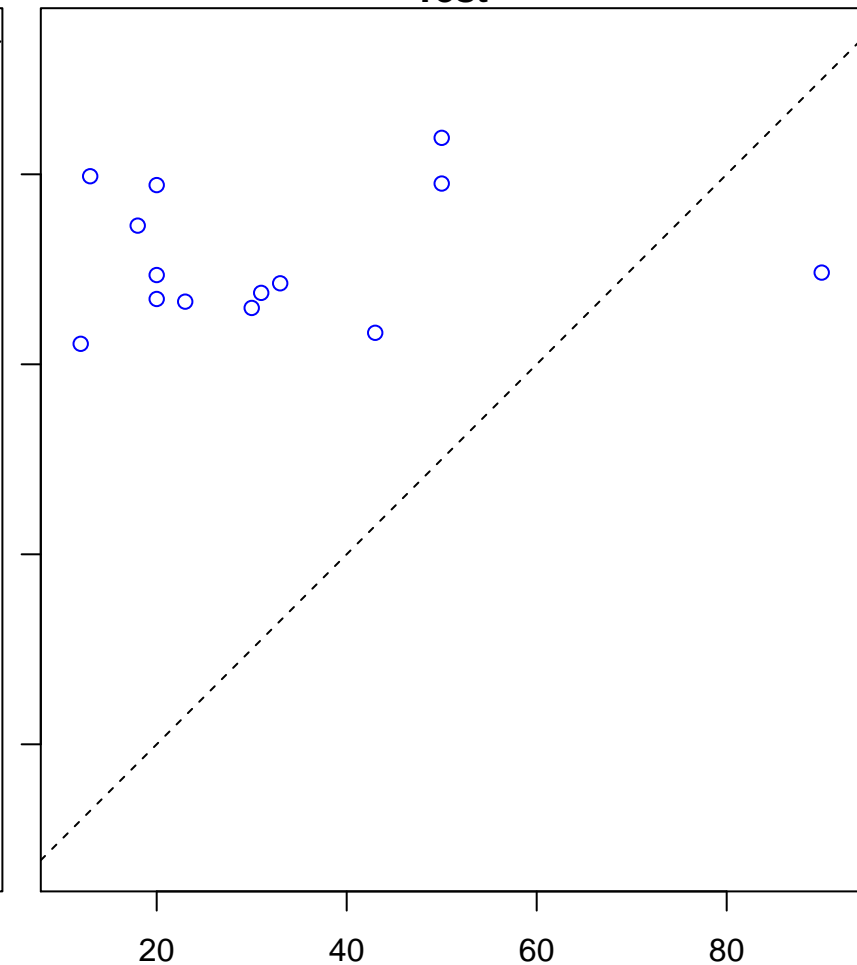


ribose phosphate biosynthetic process (Score: 7.976780)

Control

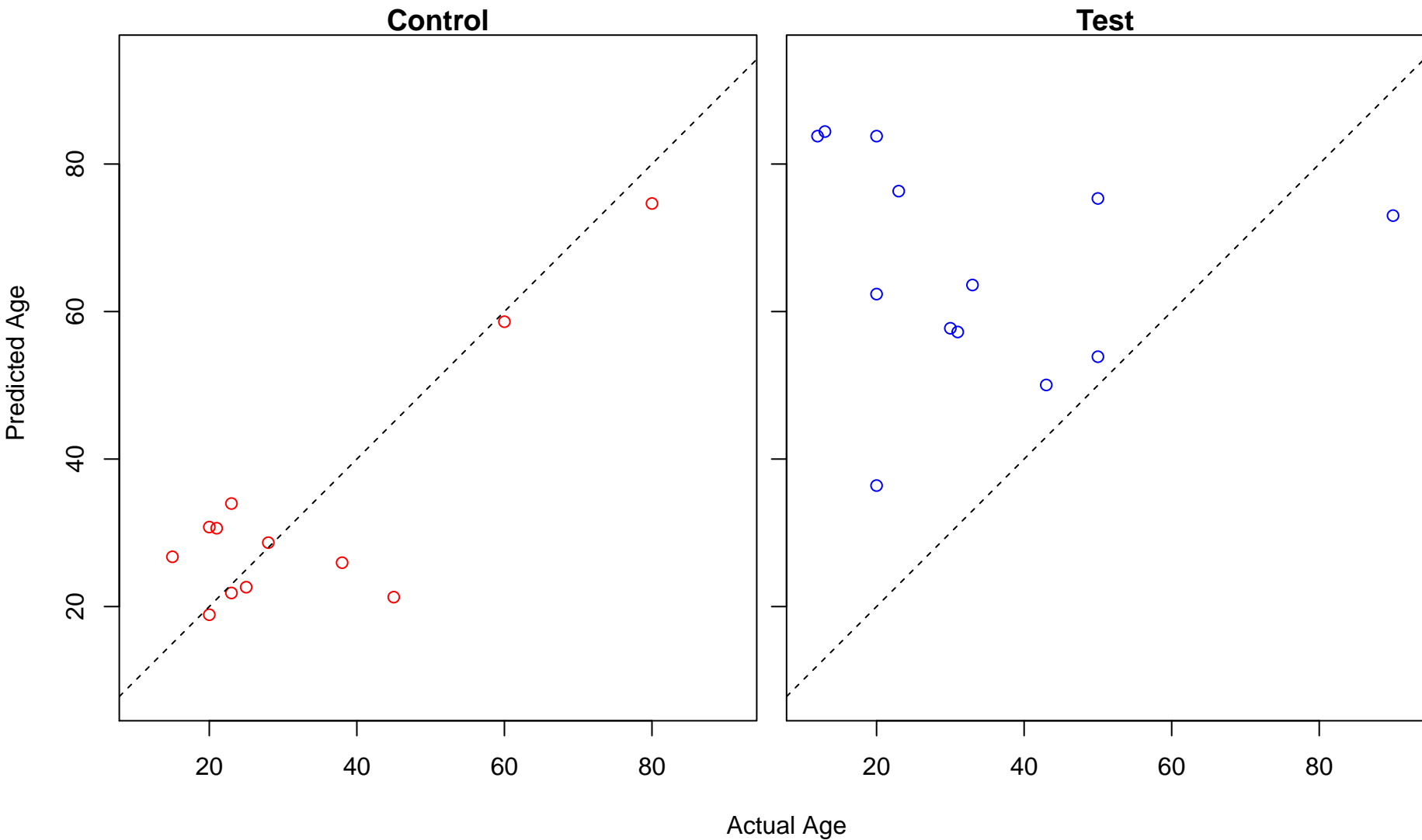


Test

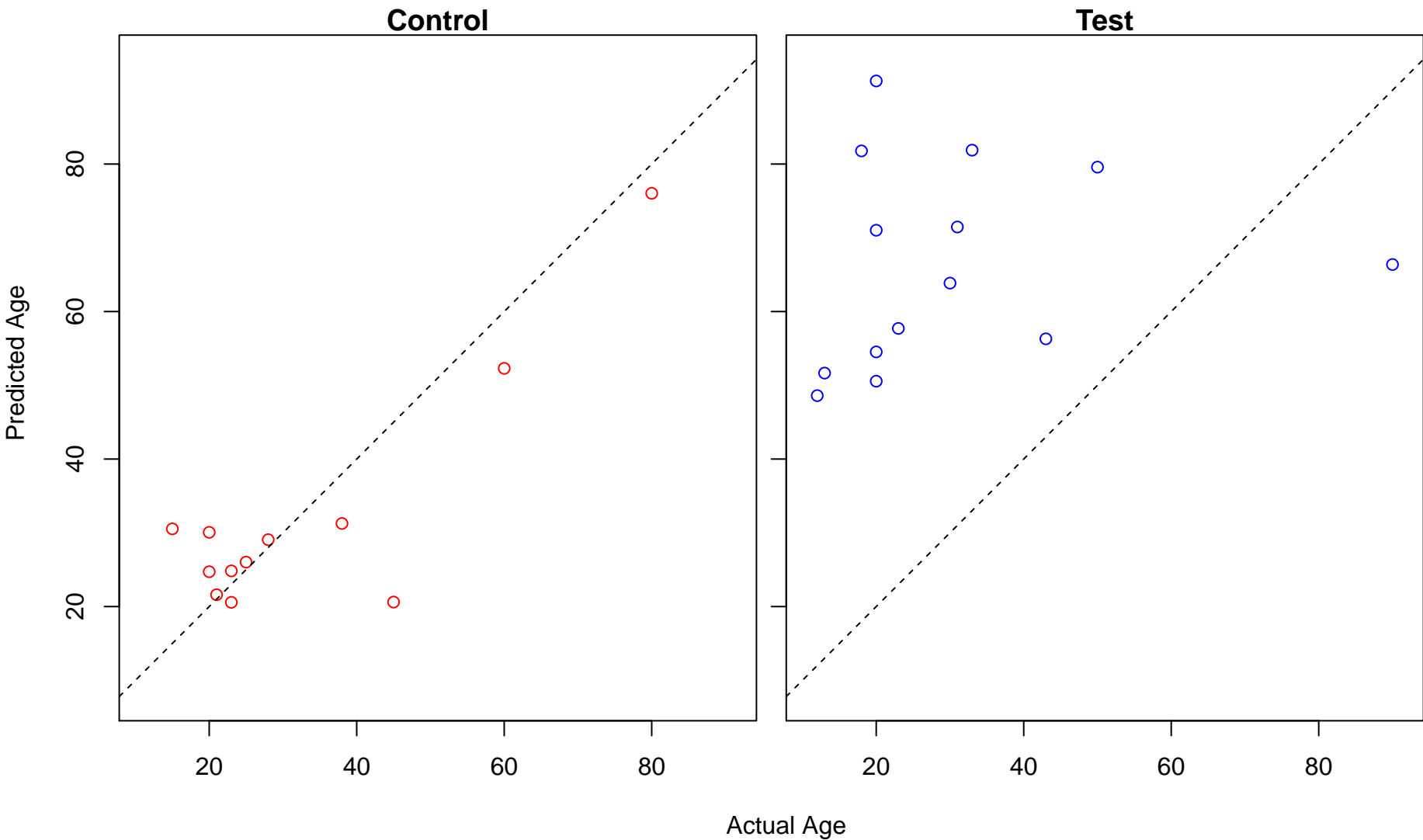


Actual Age

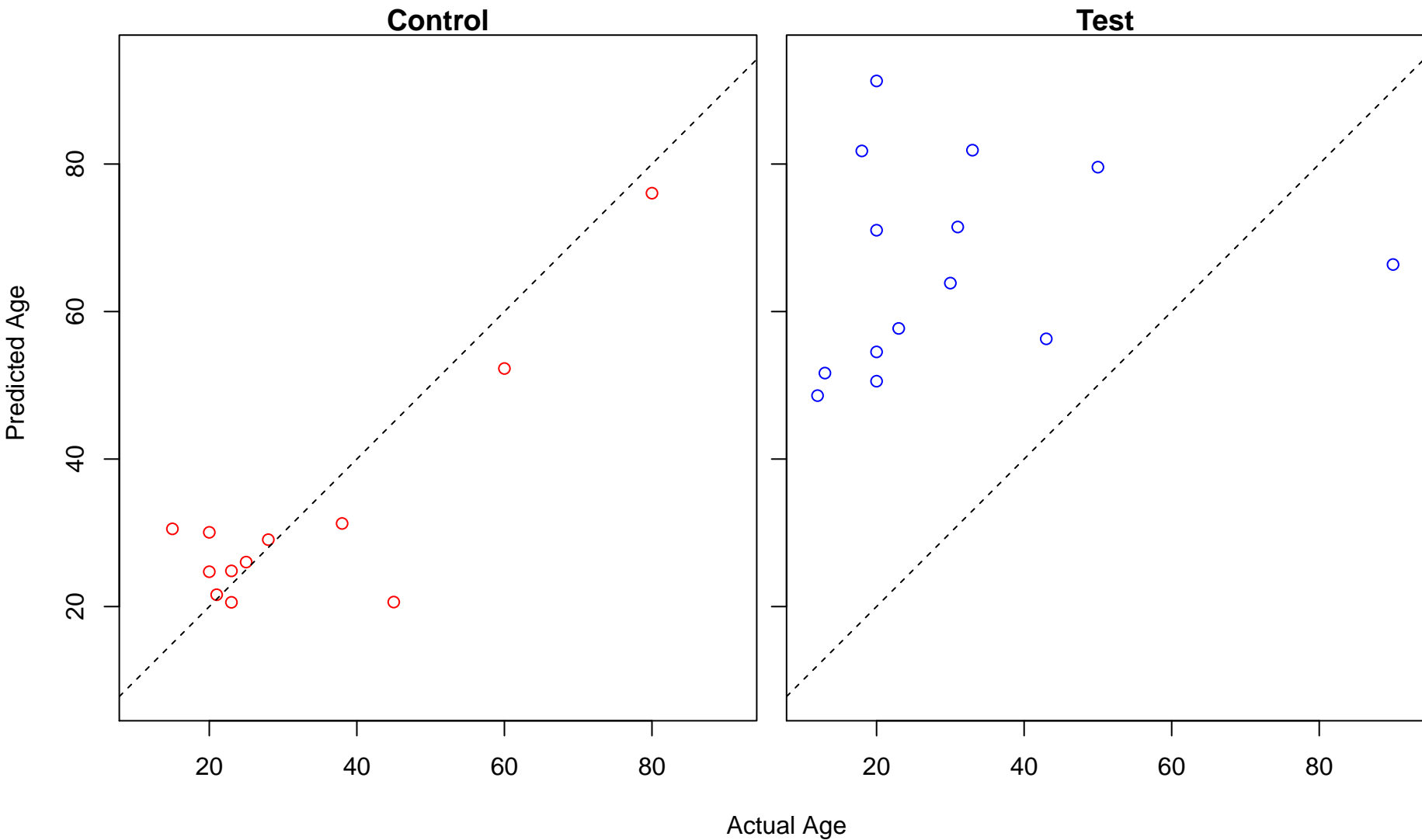
modification by host of symbiont morphology or physiology (Score: 7.973191)



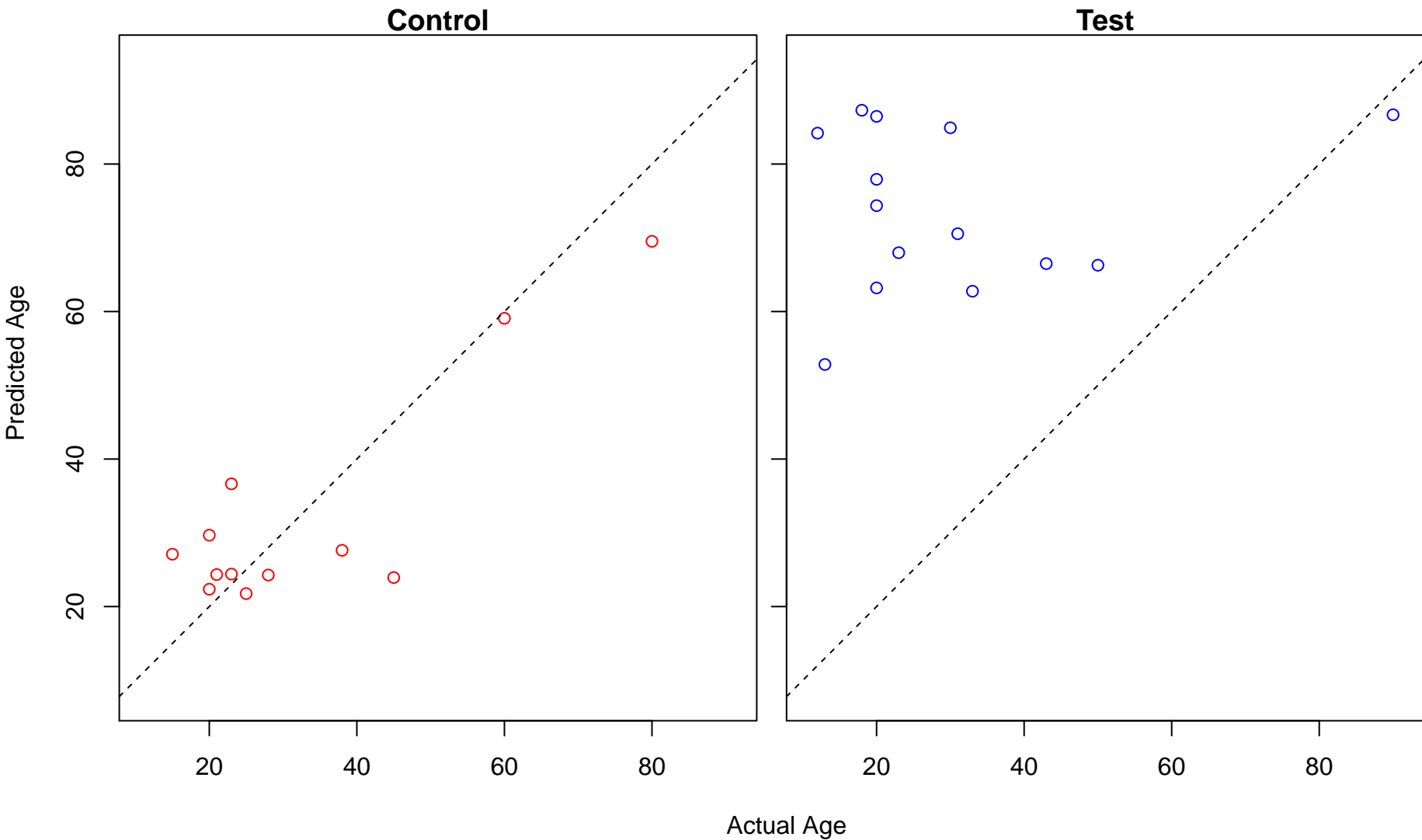
Age response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator



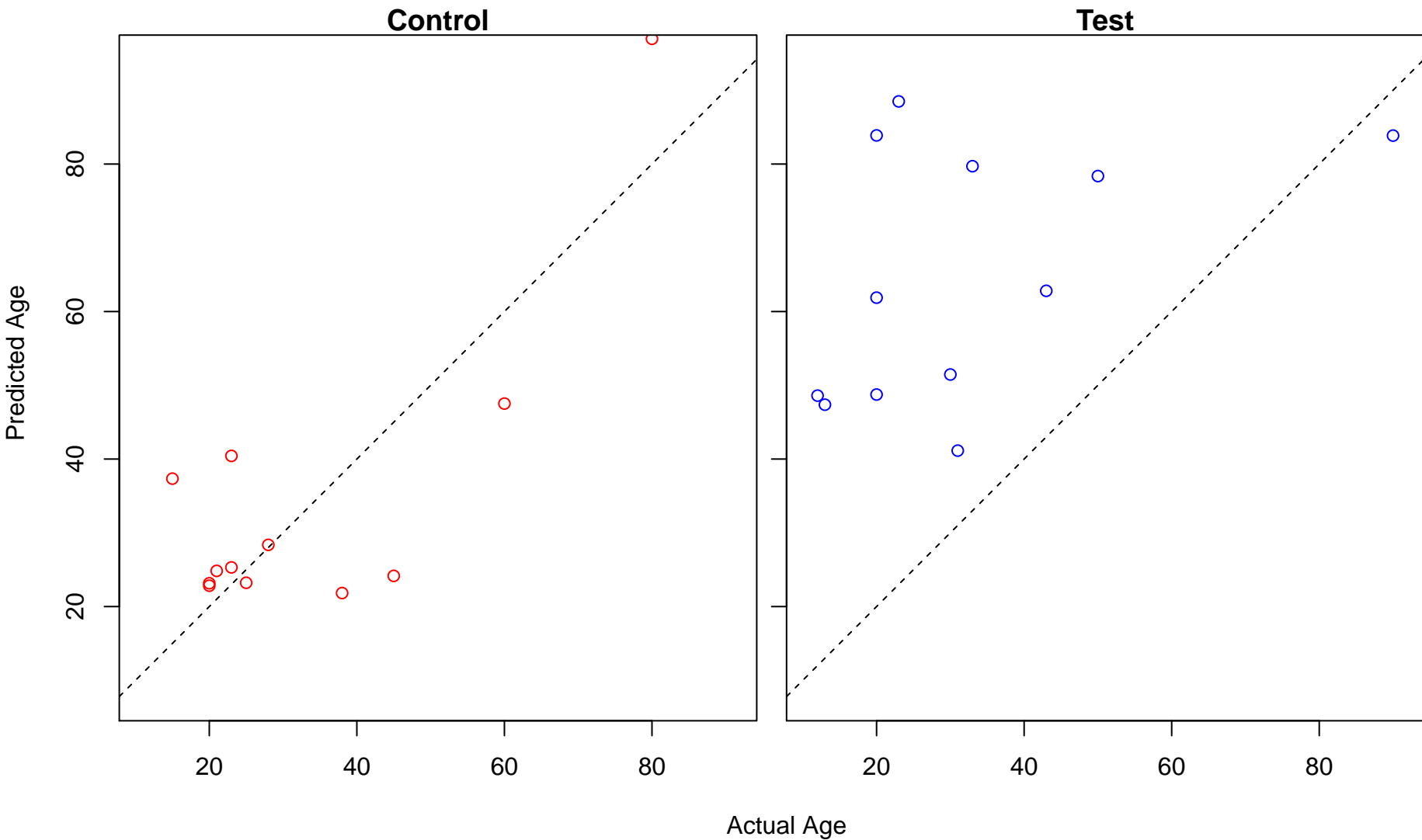
DNA damage response, signal transduction resulting in transcription (Score: 7.971963)



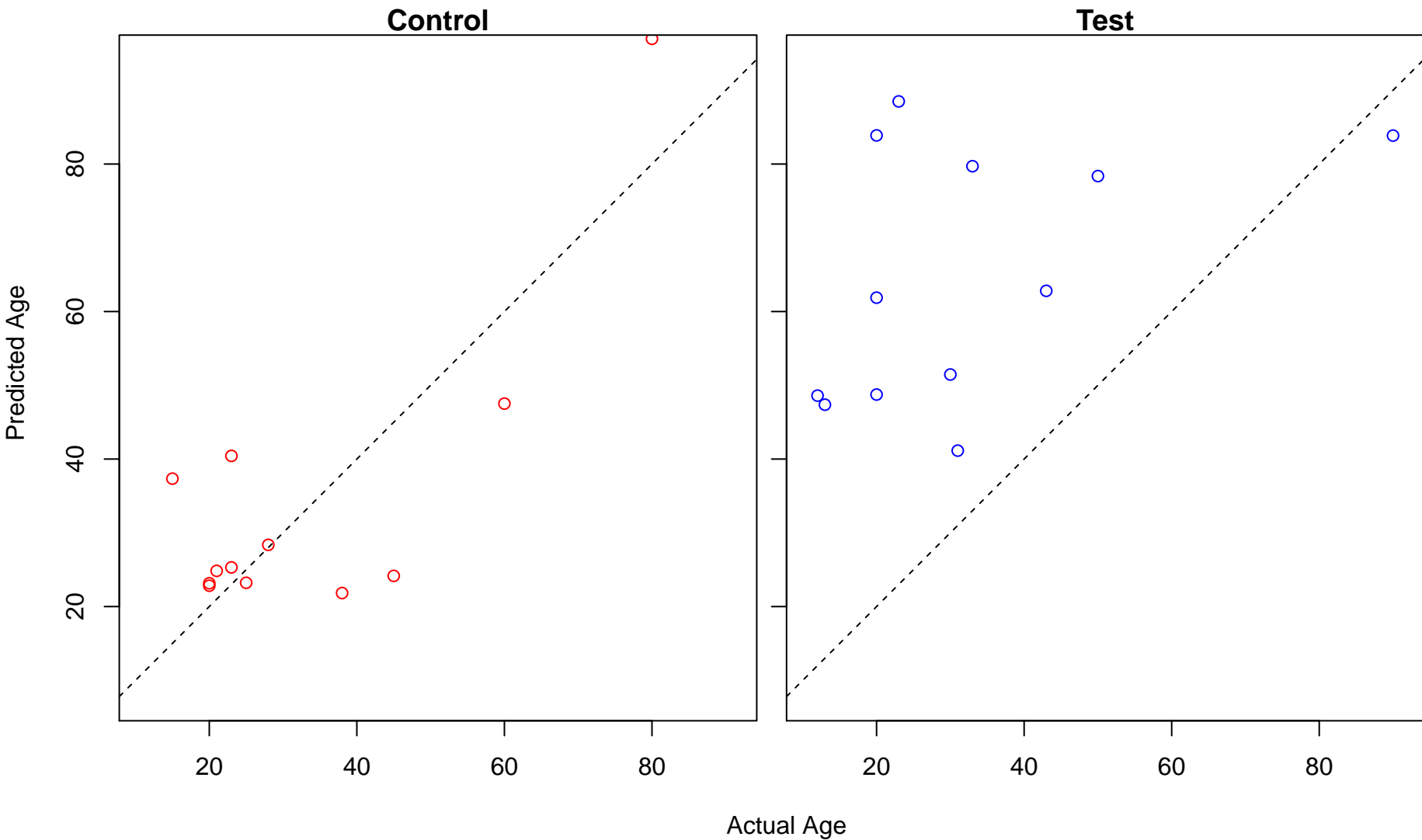
cellular response to interleukin-1 (Score: 7.970568)



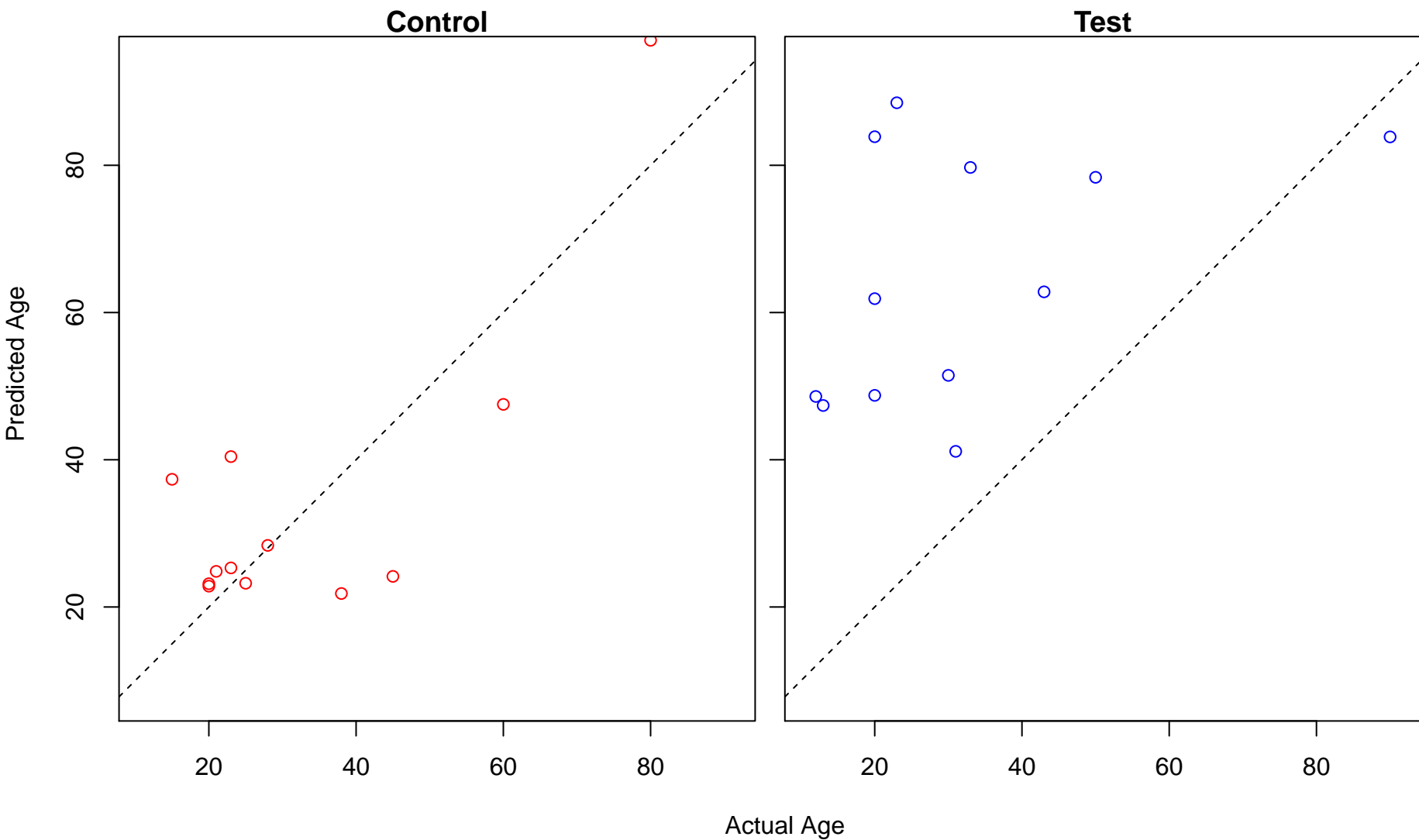
glucuronate catabolic process (Score: 7.958793)



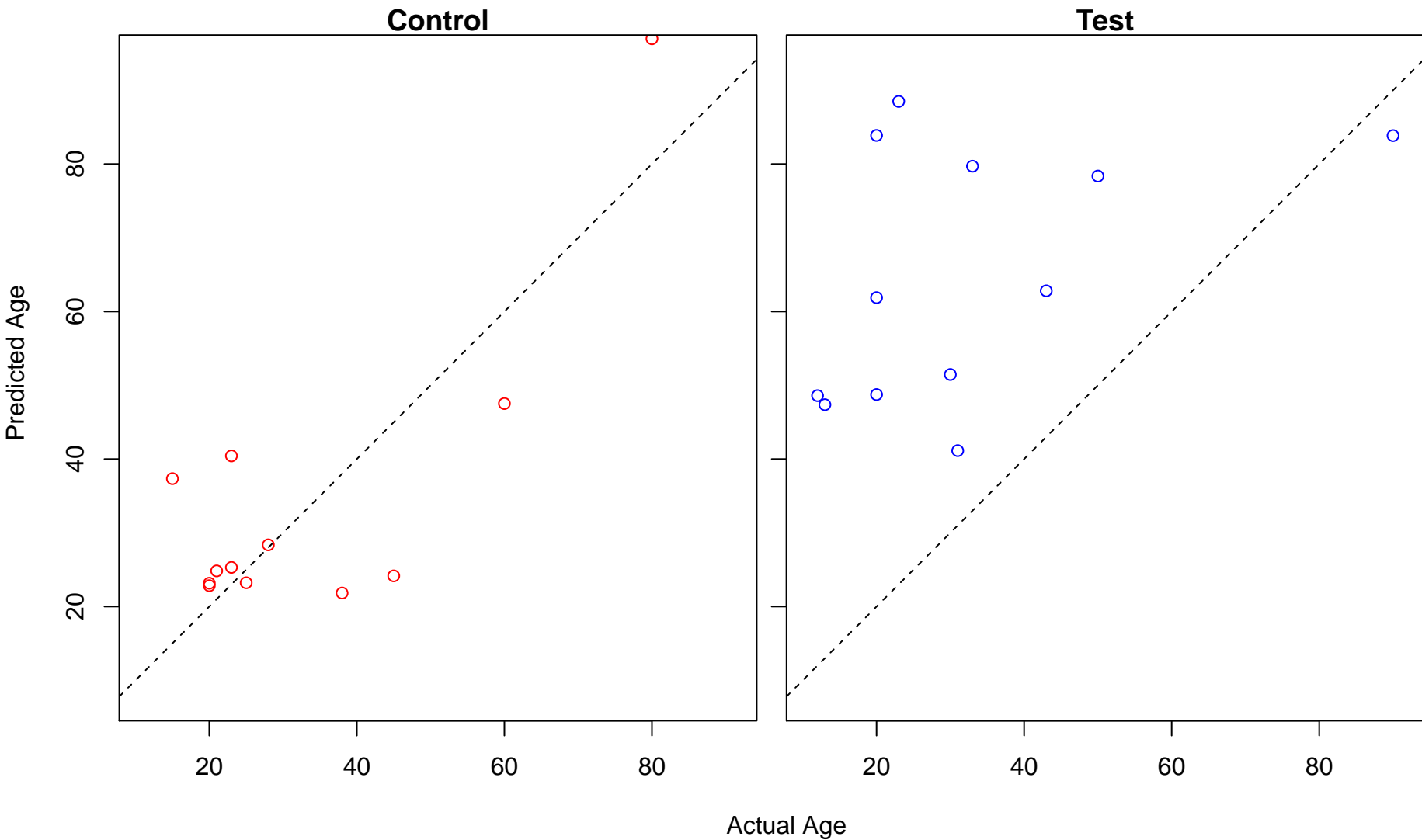
glucuronate catabolic process to xylulose 5-phosphate (Score: 7.958793)



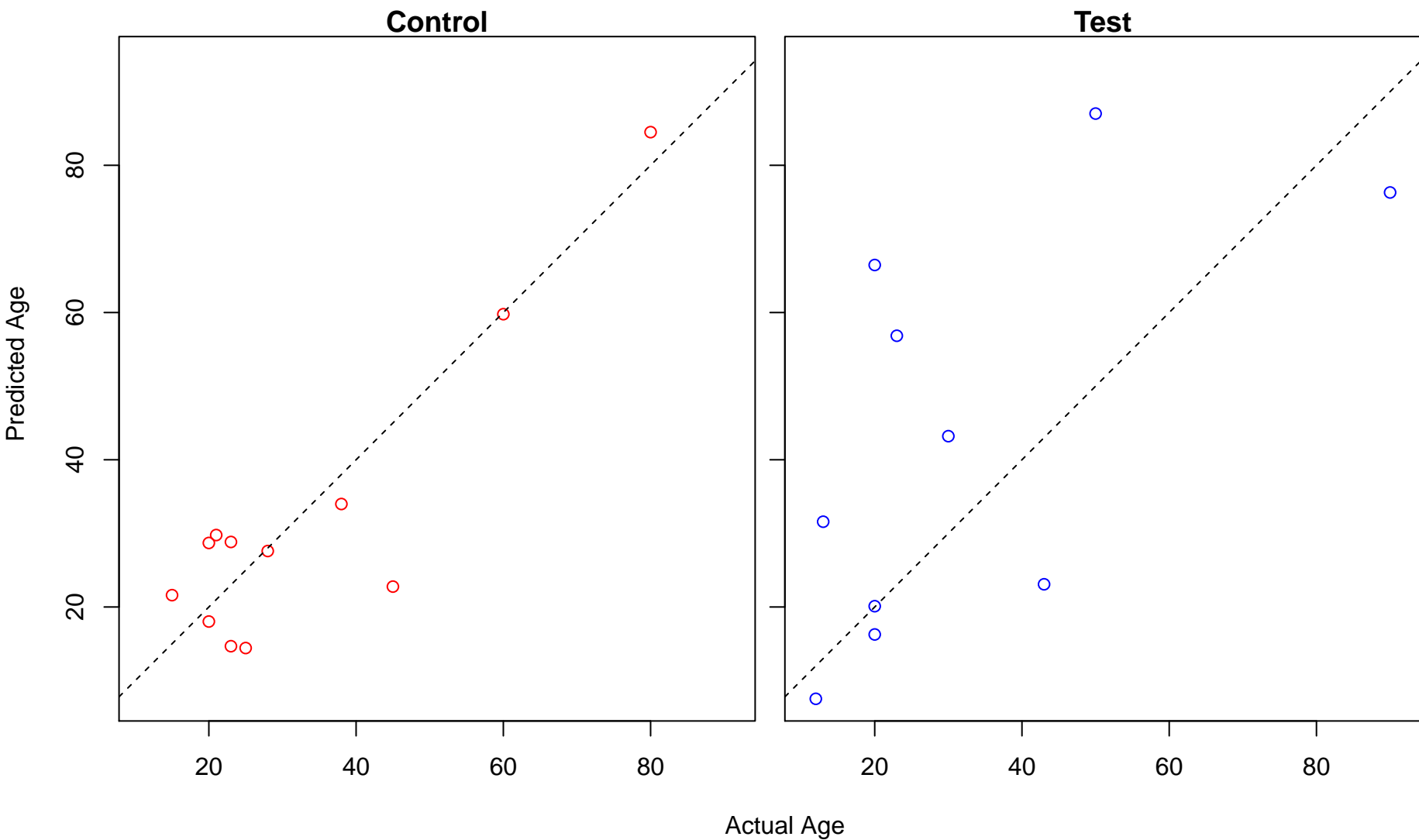
xylulose 5-phosphate metabolic process (Score: 7.958793)



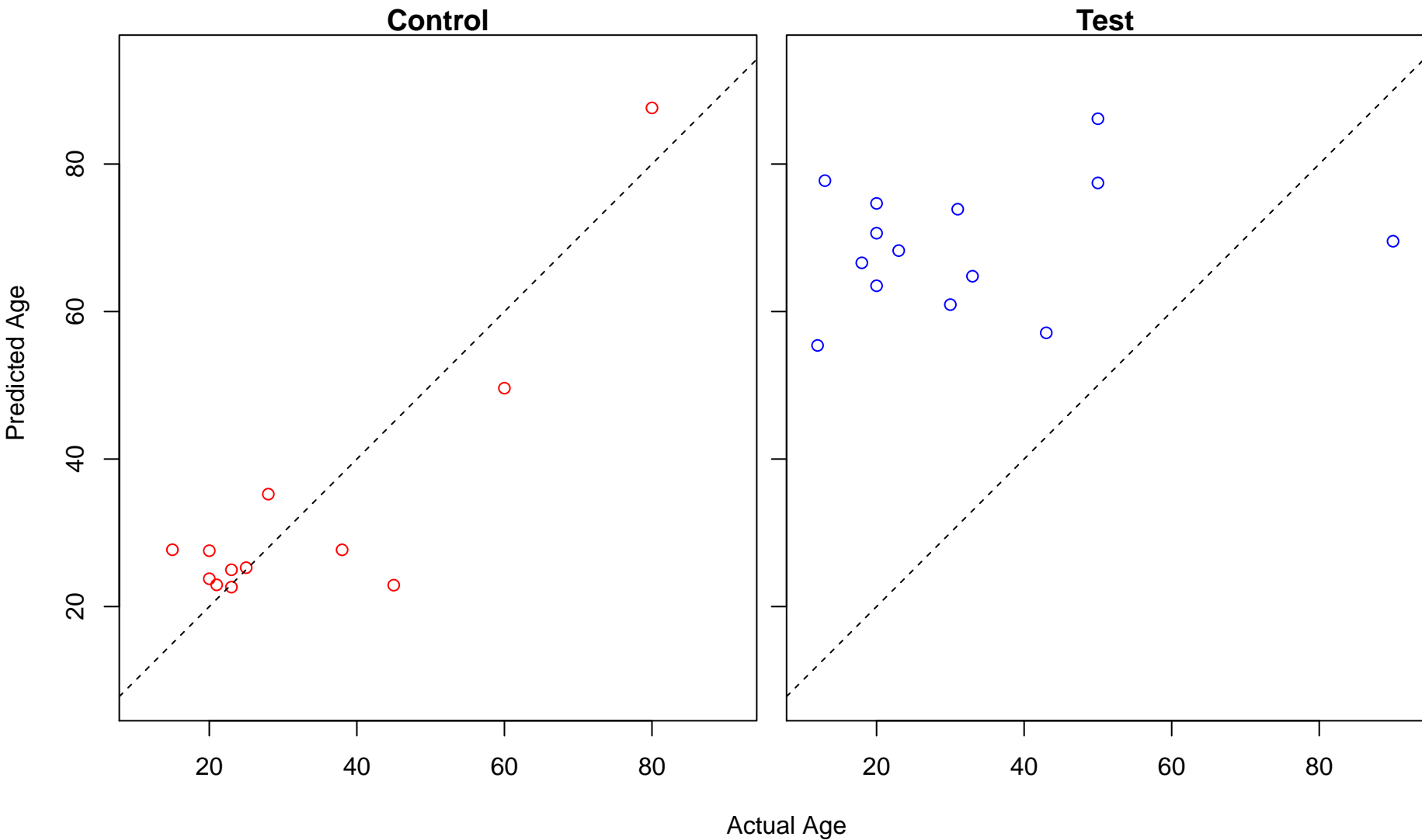
xylulose 5-phosphate biosynthetic process (Score: 7.958793)



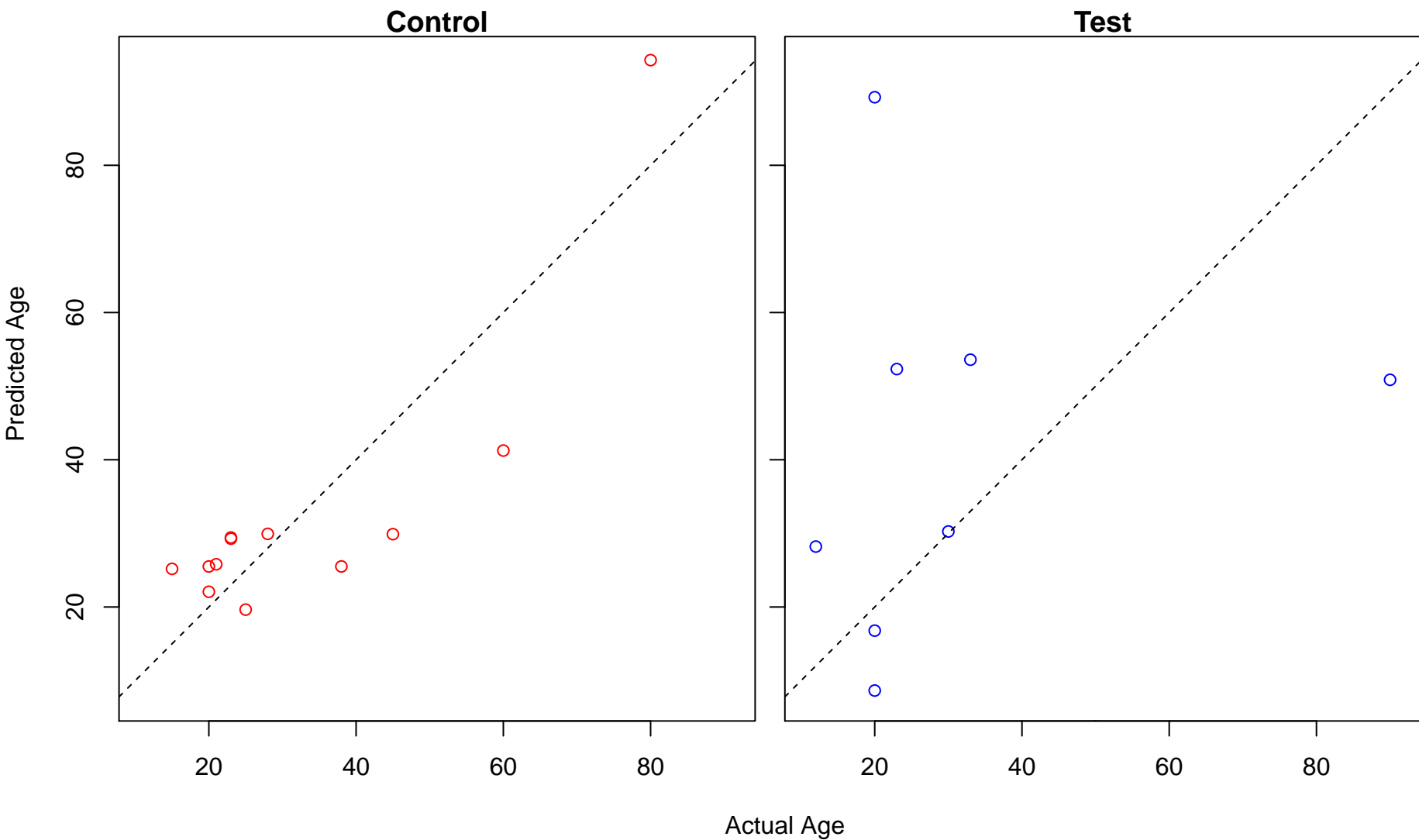
regulation of mesenchymal cell proliferation (Score: 7.957742)



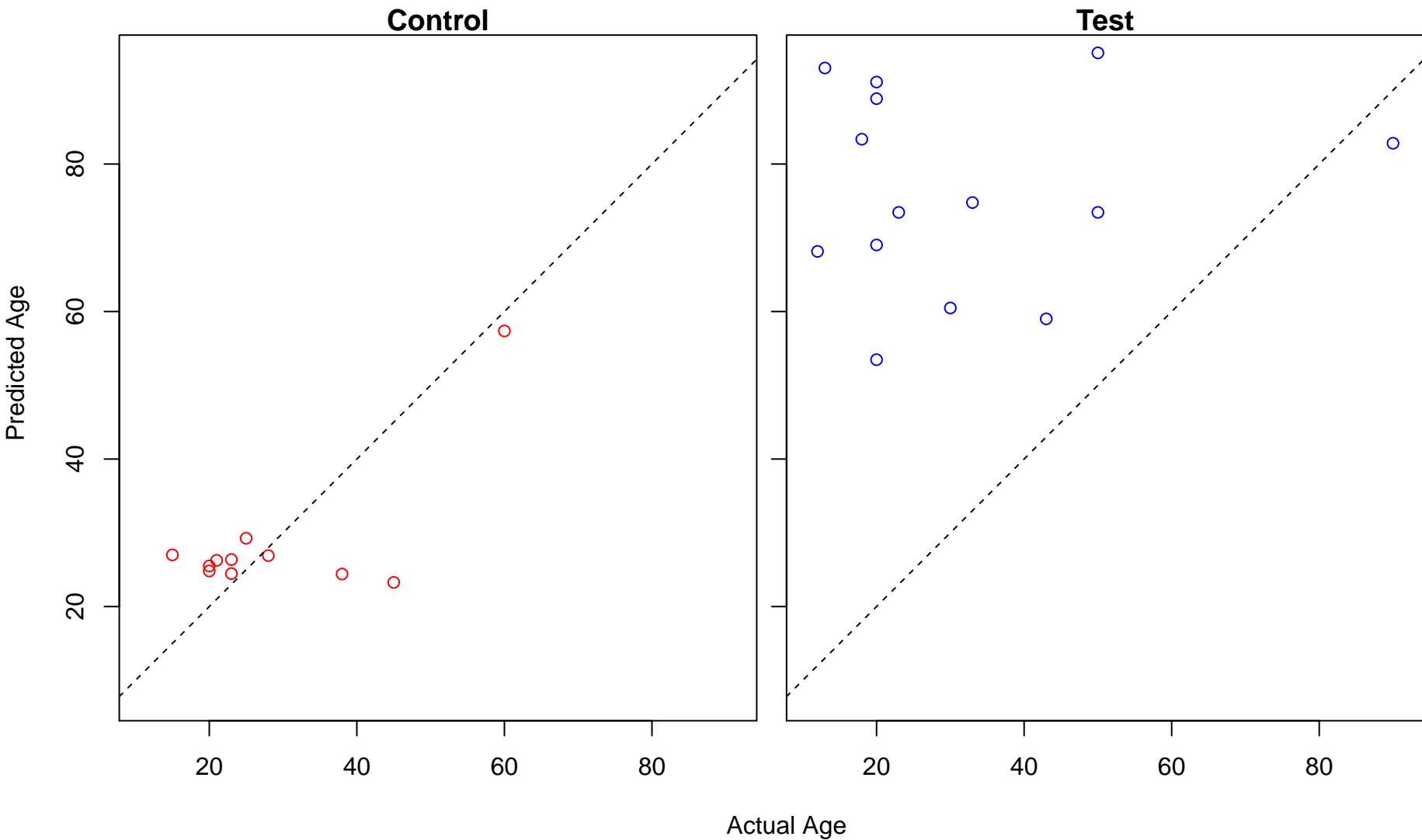
bone development (Score: 7.954042)



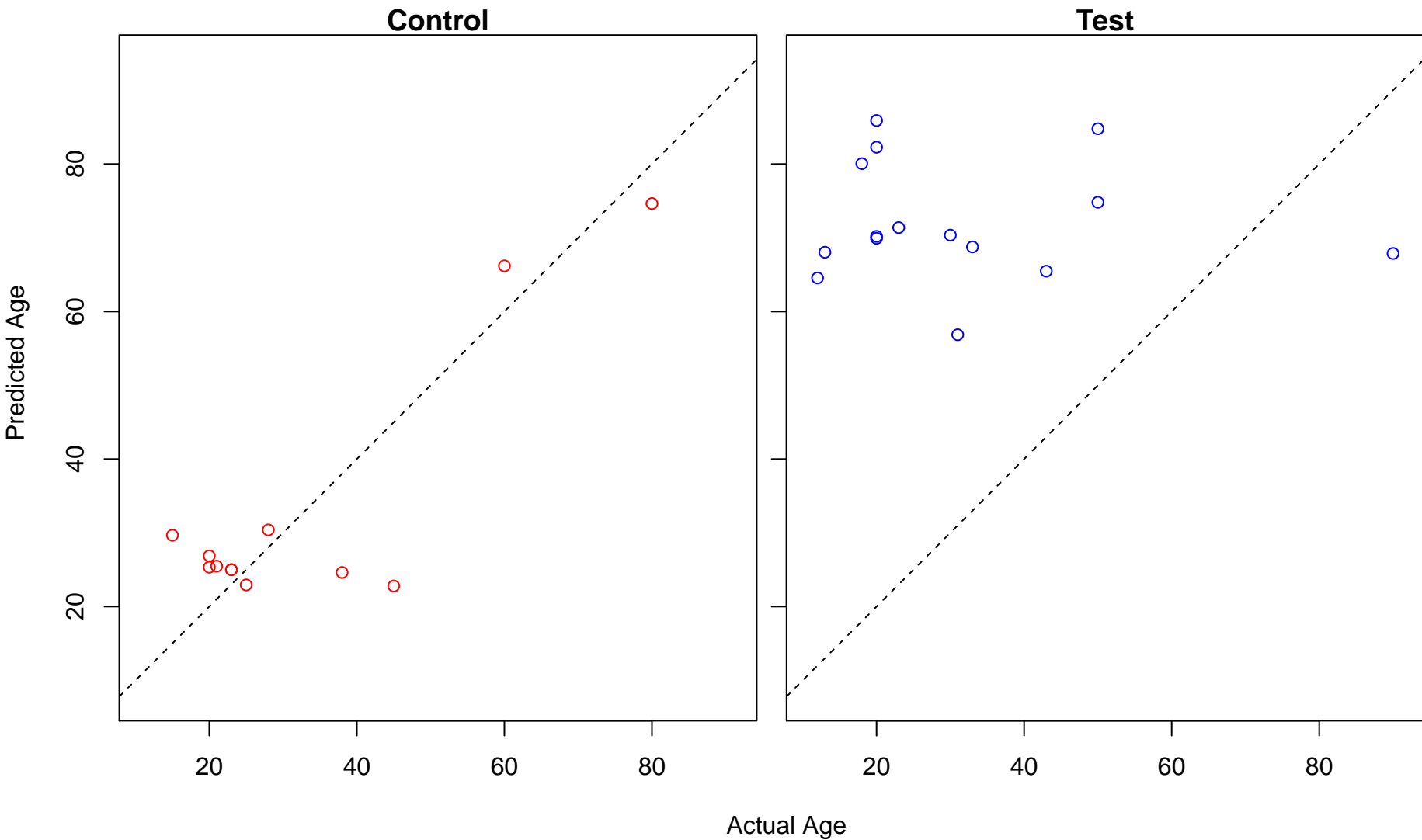
protein modification by small protein removal (Score: 7.952711)



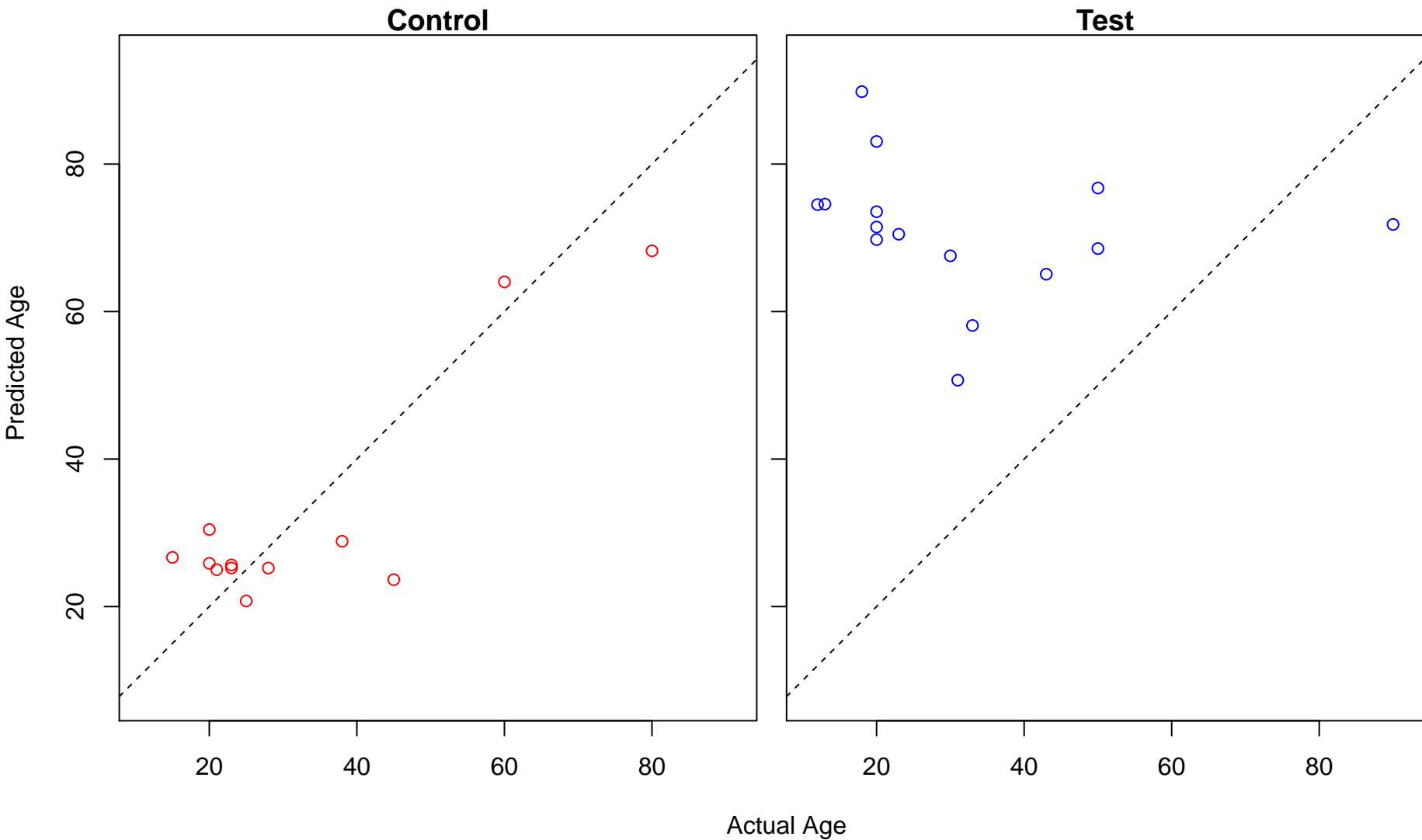
cyclic nucleotide catabolic process (Score: 7.947210)



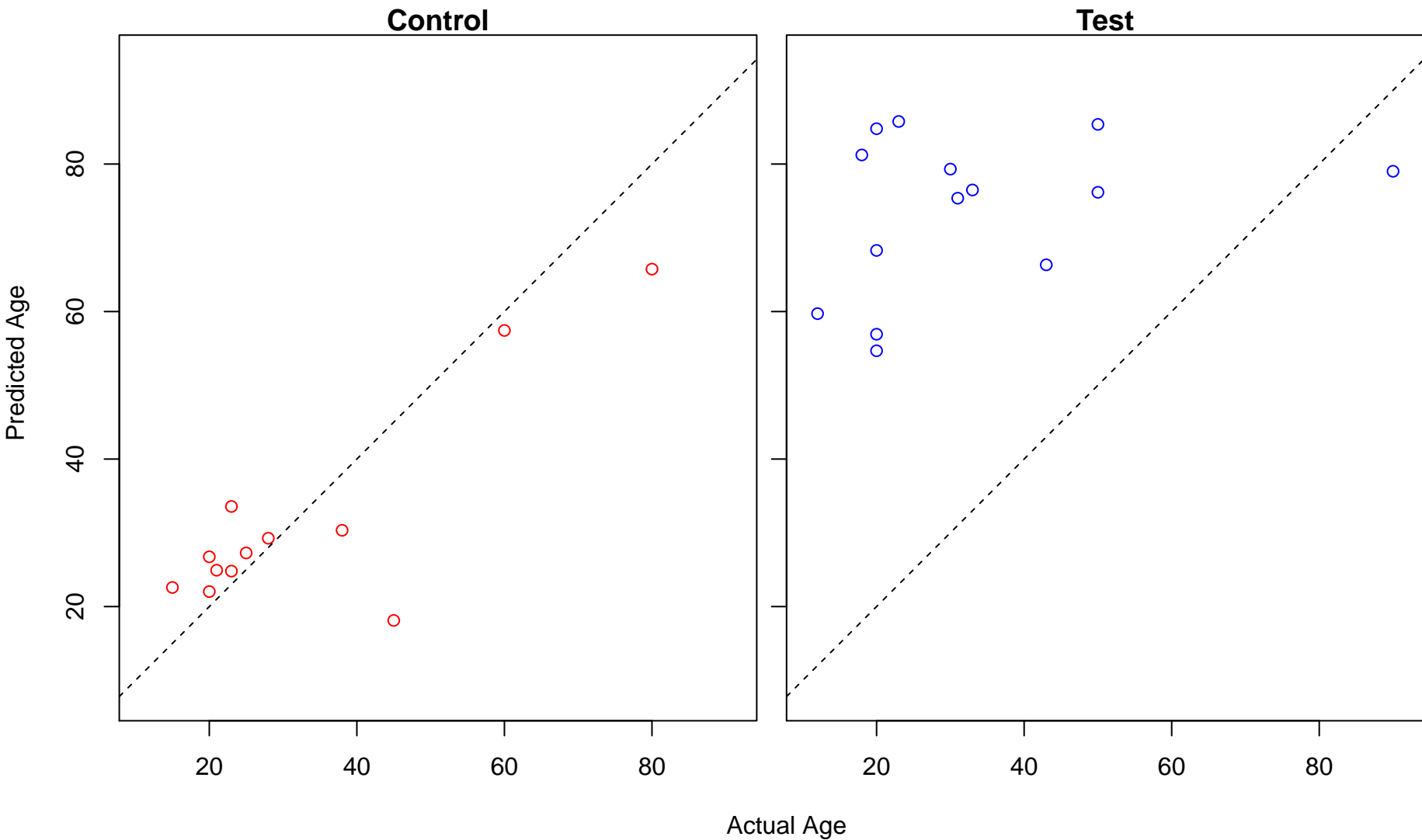
calcium ion import (Score: 7.946352)



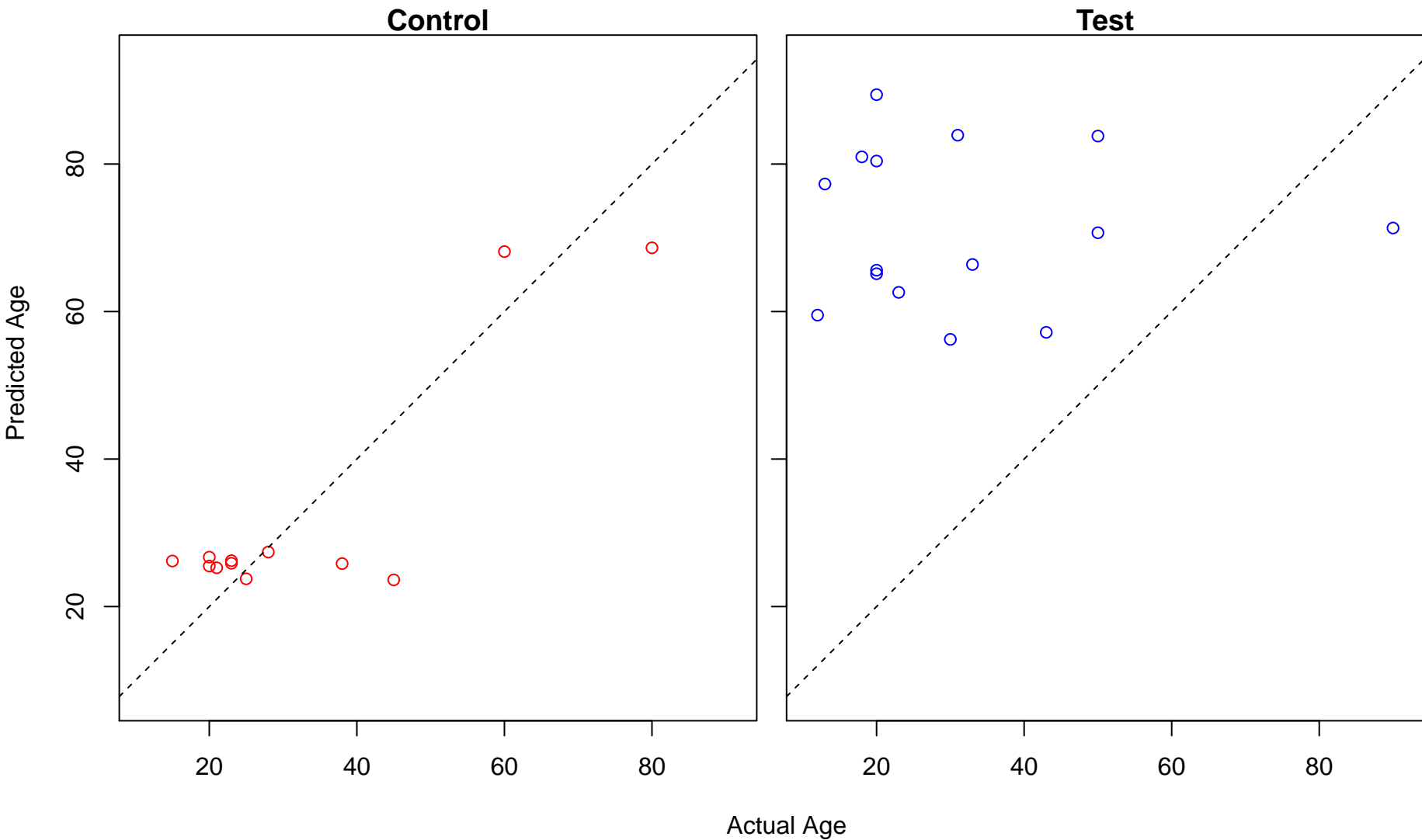
regulation of JUN kinase activity (Score: 7.942731)



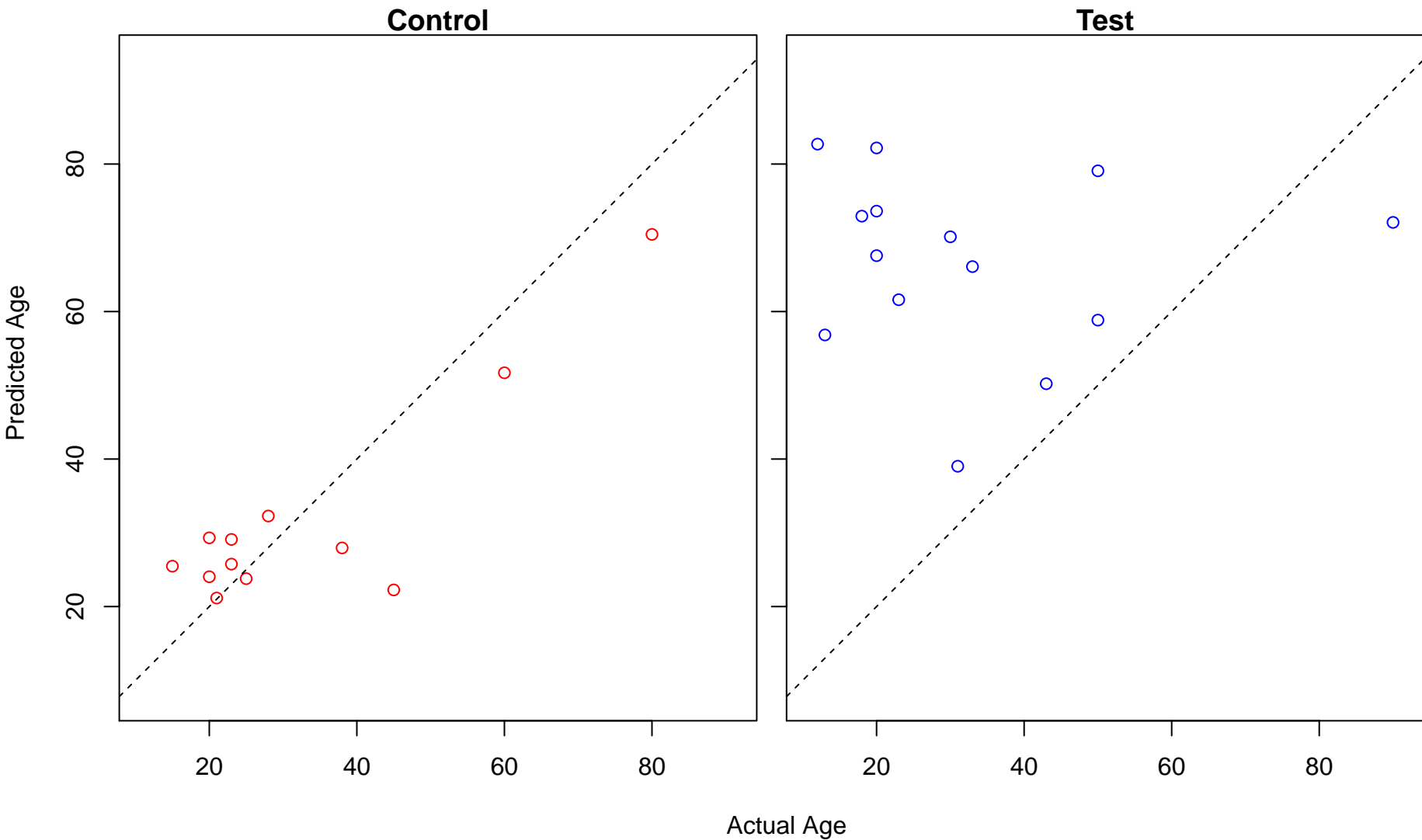
regulation of tolerance induction (Score: 7.938859)



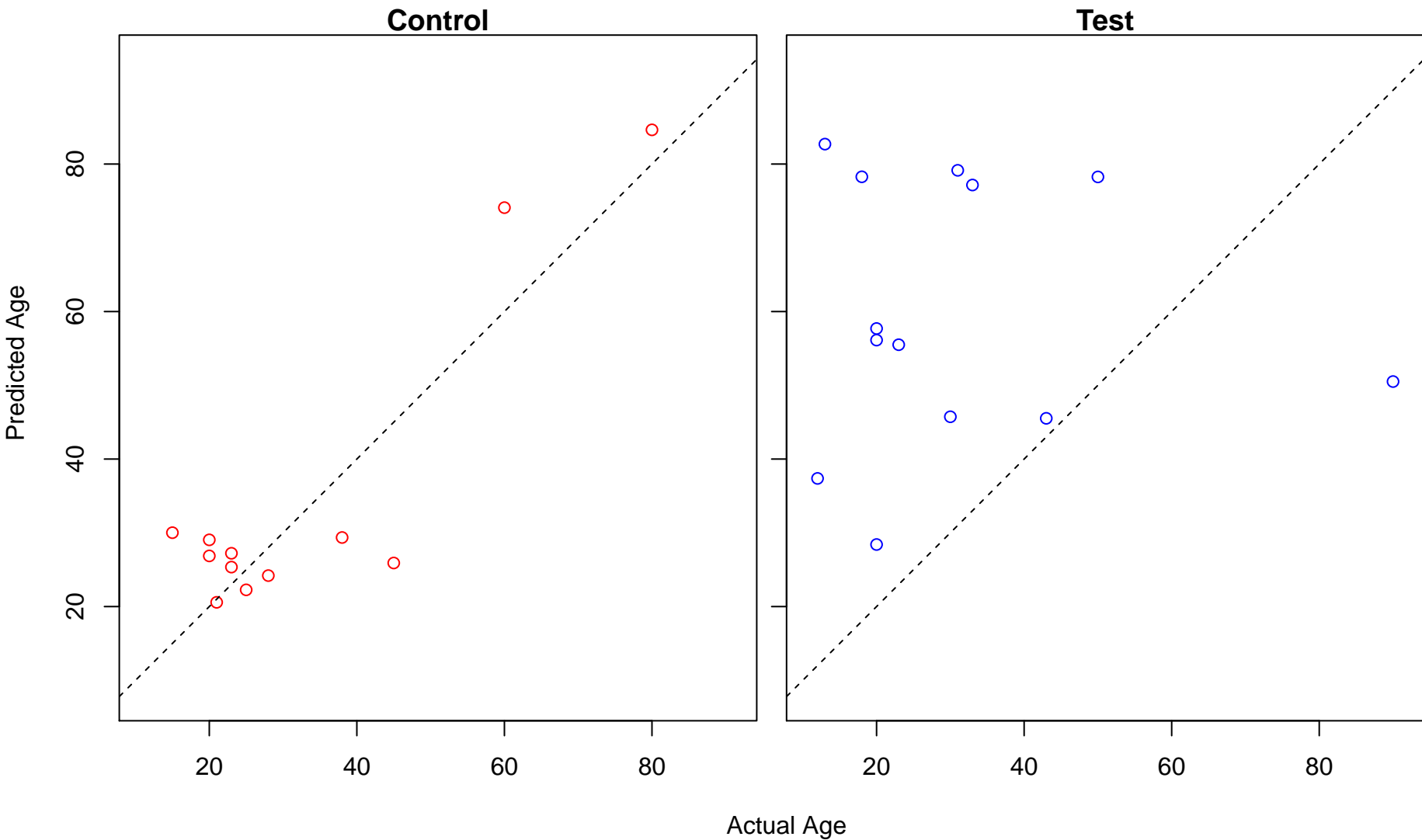
gene silencing by RNA (Score: 7.938378)



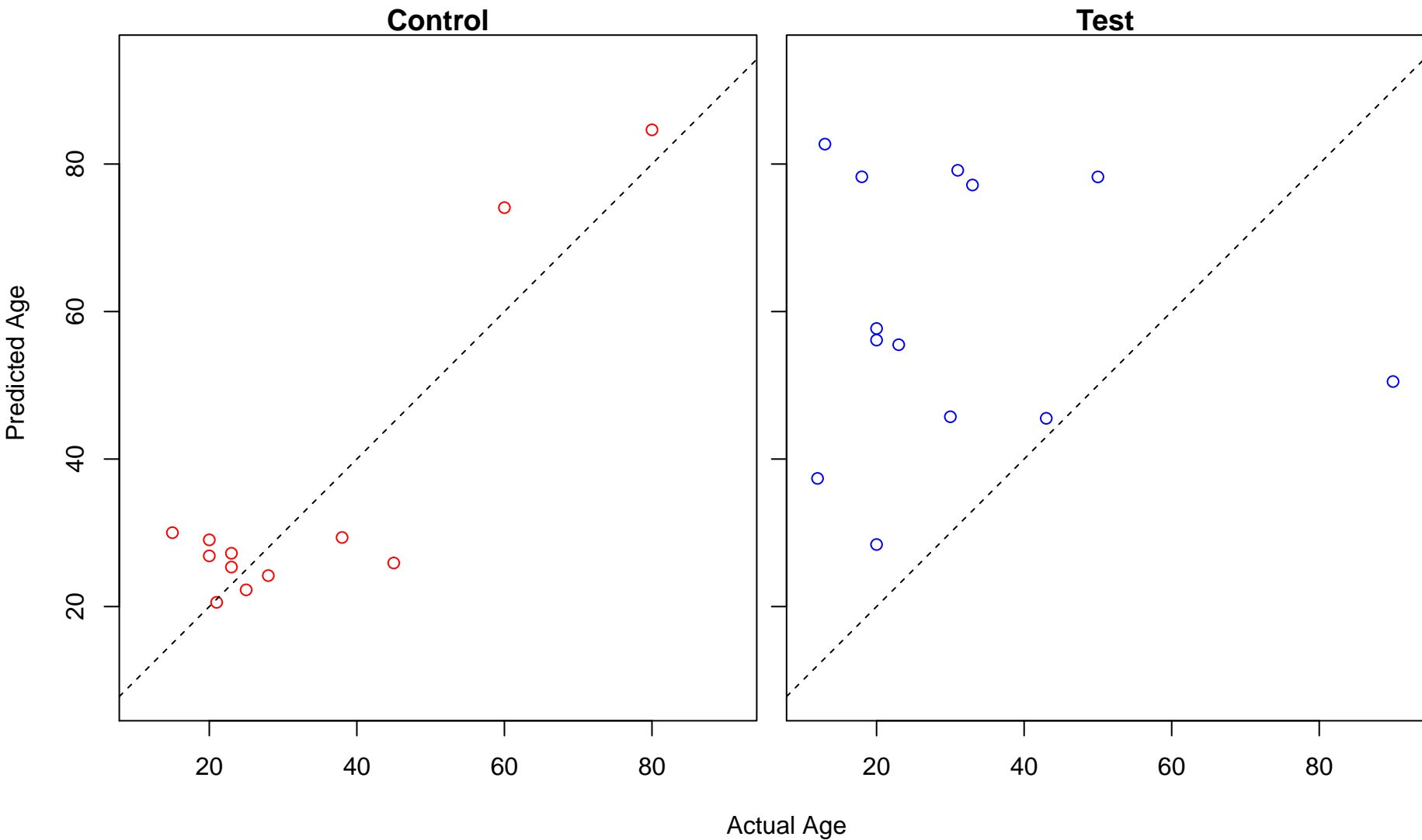
neural crest cell development (Score: 7.936558)



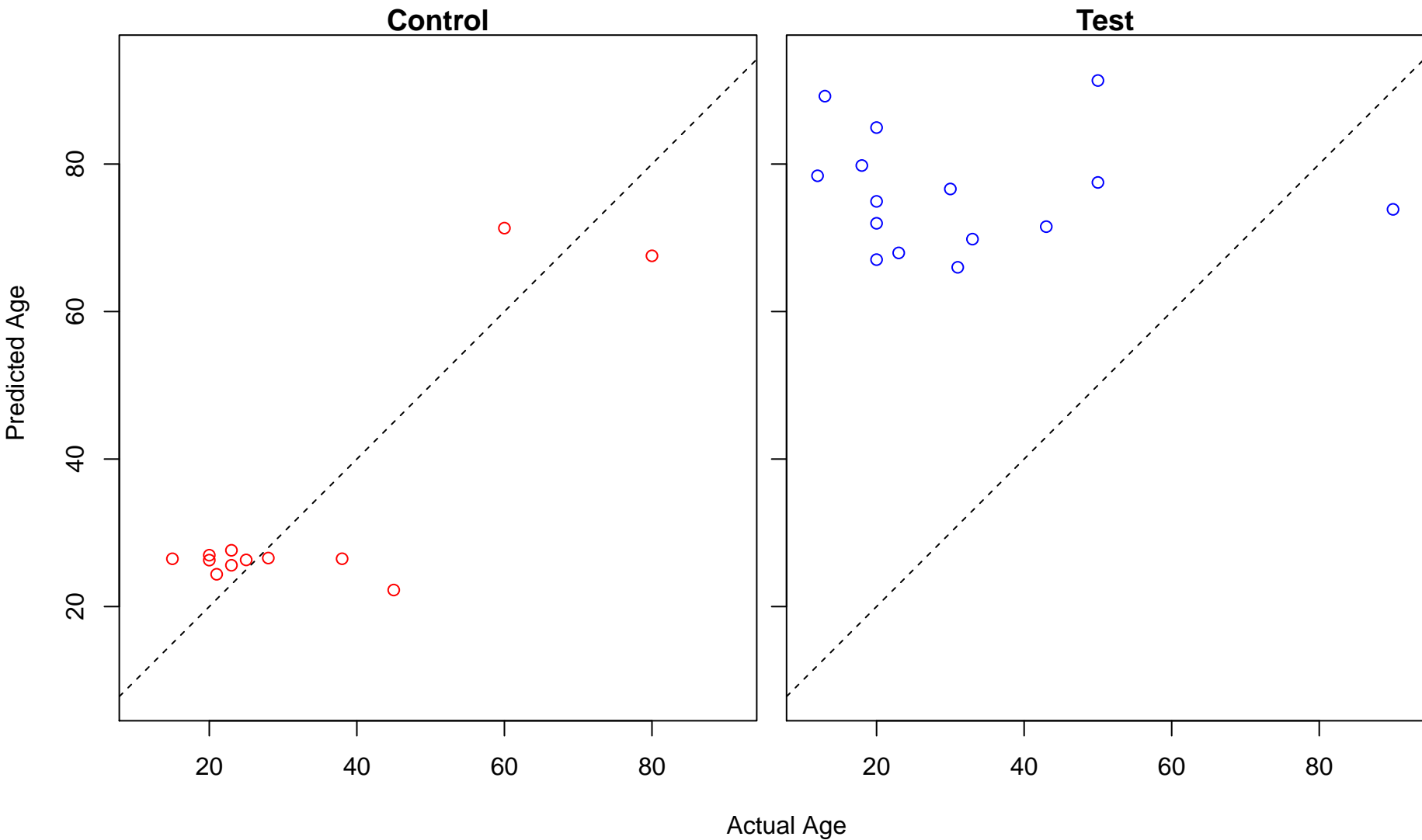
purine ribonucleotide transport (Score: 7.930992)



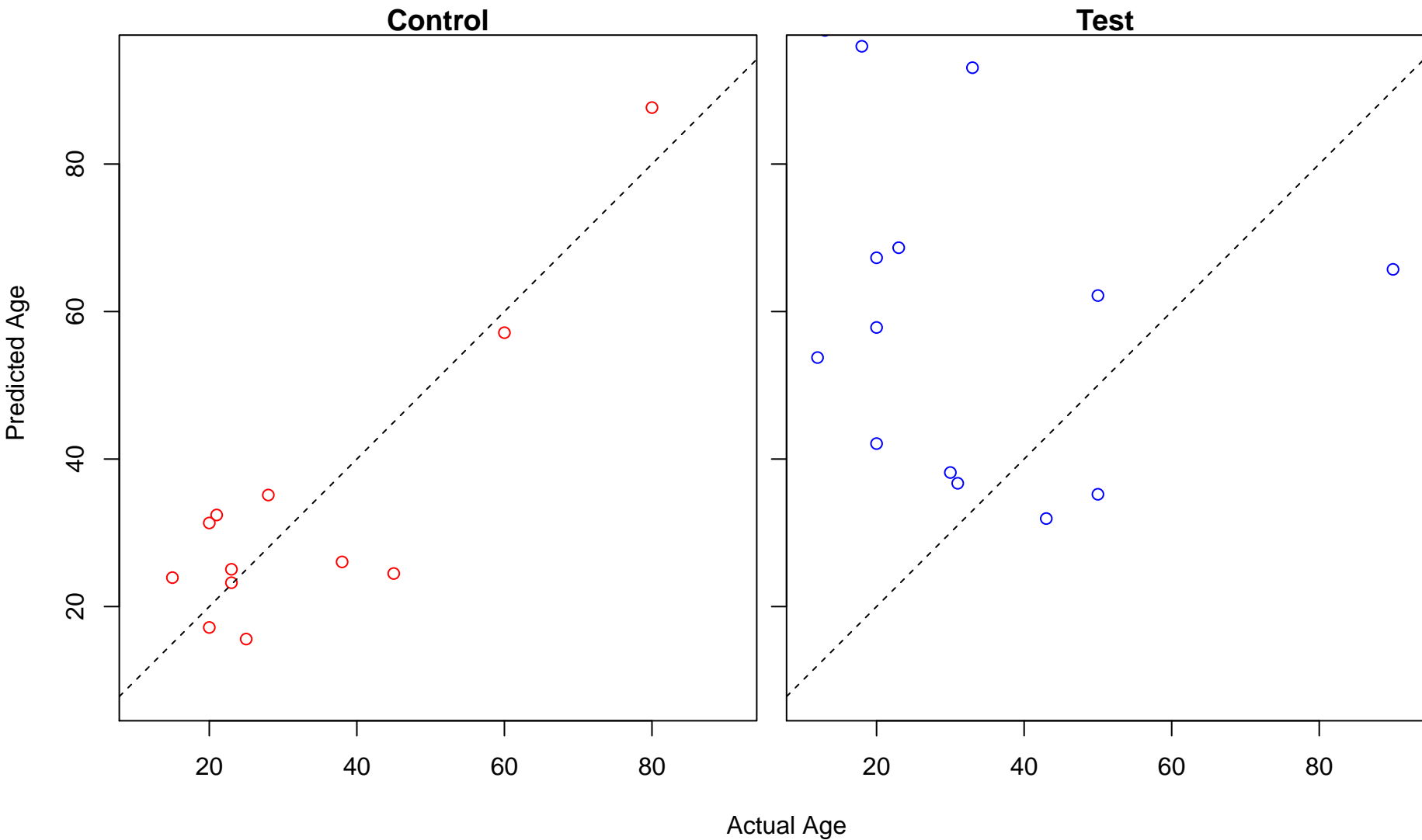
adenine nucleotide transport (Score: 7.930992)



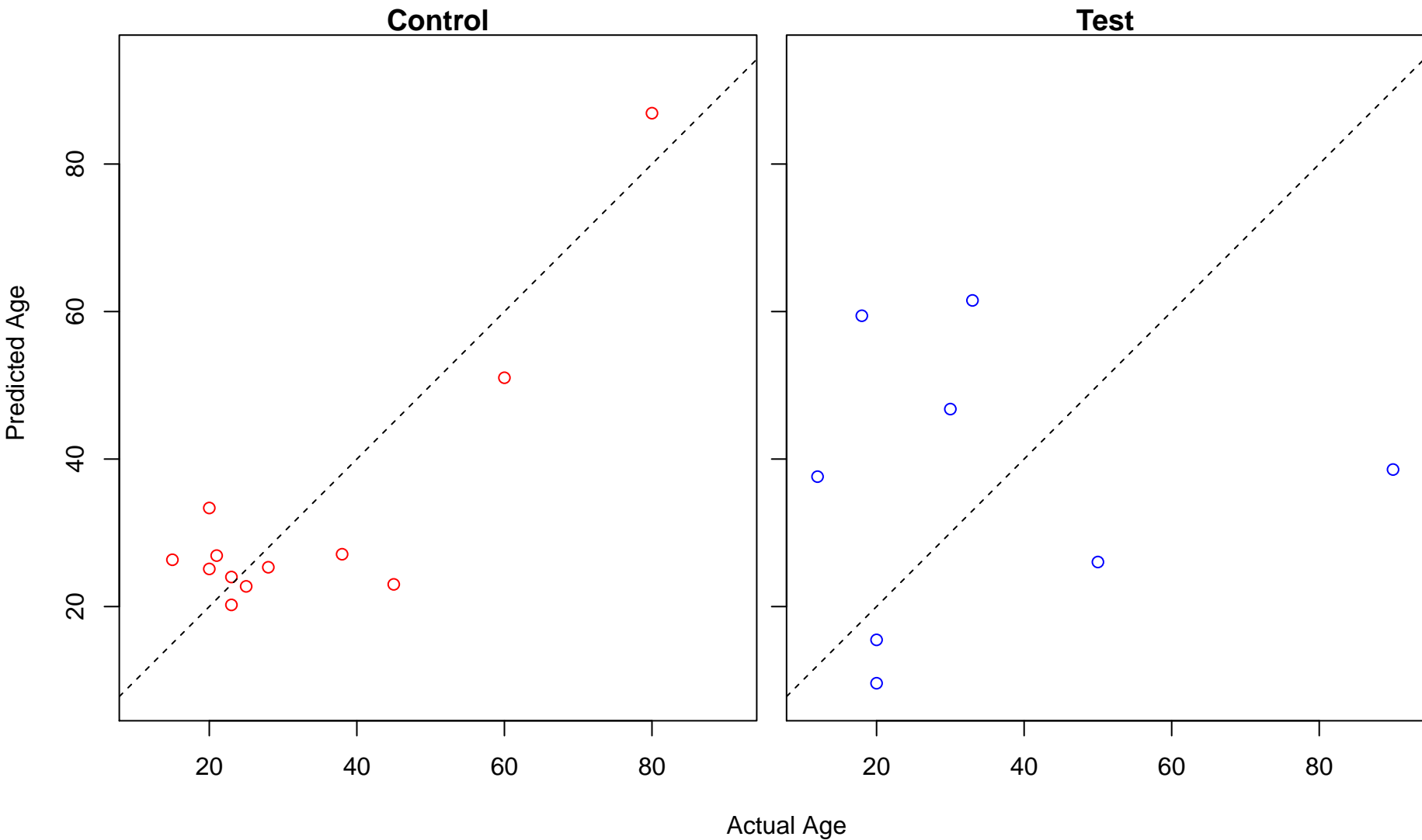
histone H3-K9 methylation (Score: 7.928140)



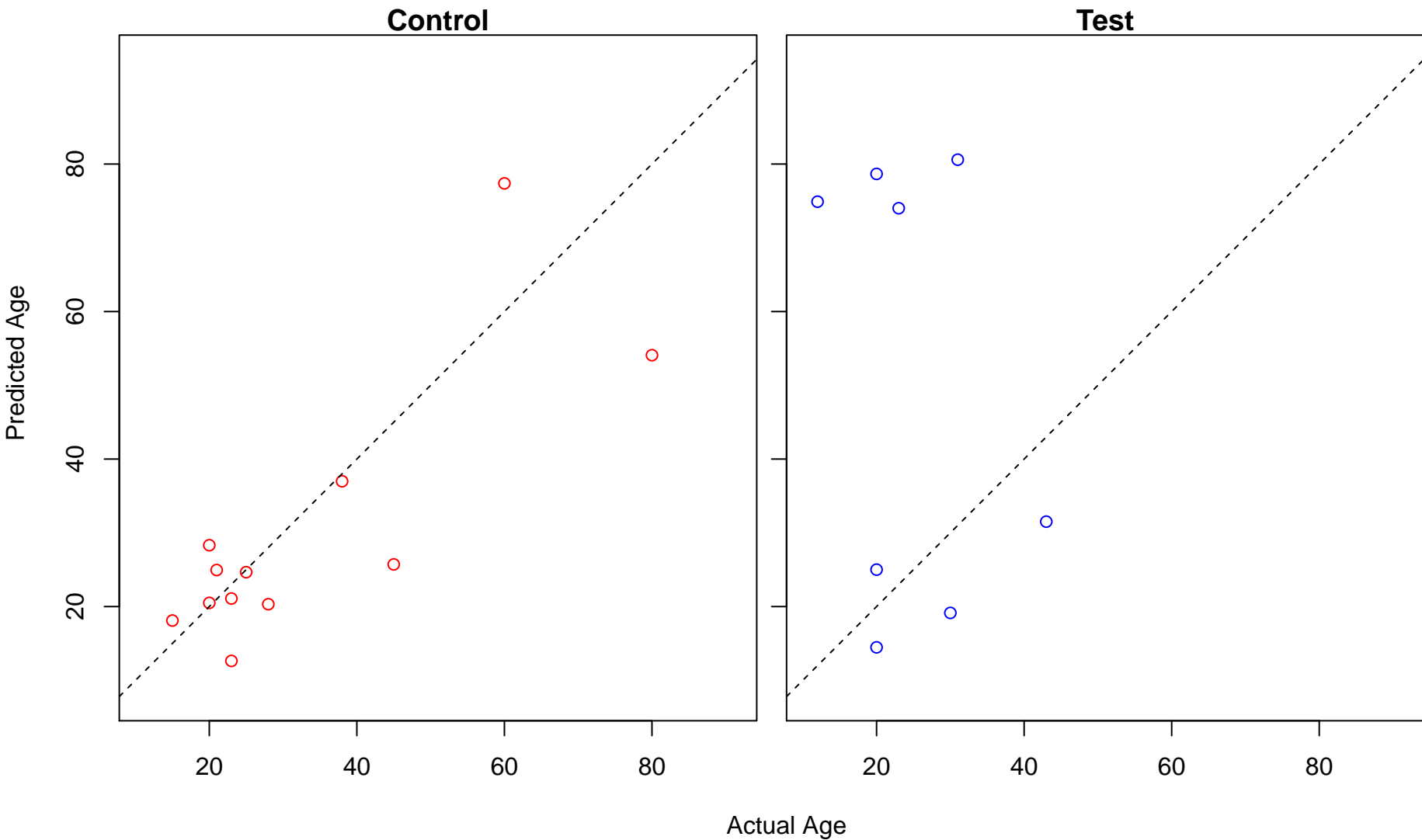
protein localization to membrane (Score: 7.926124)



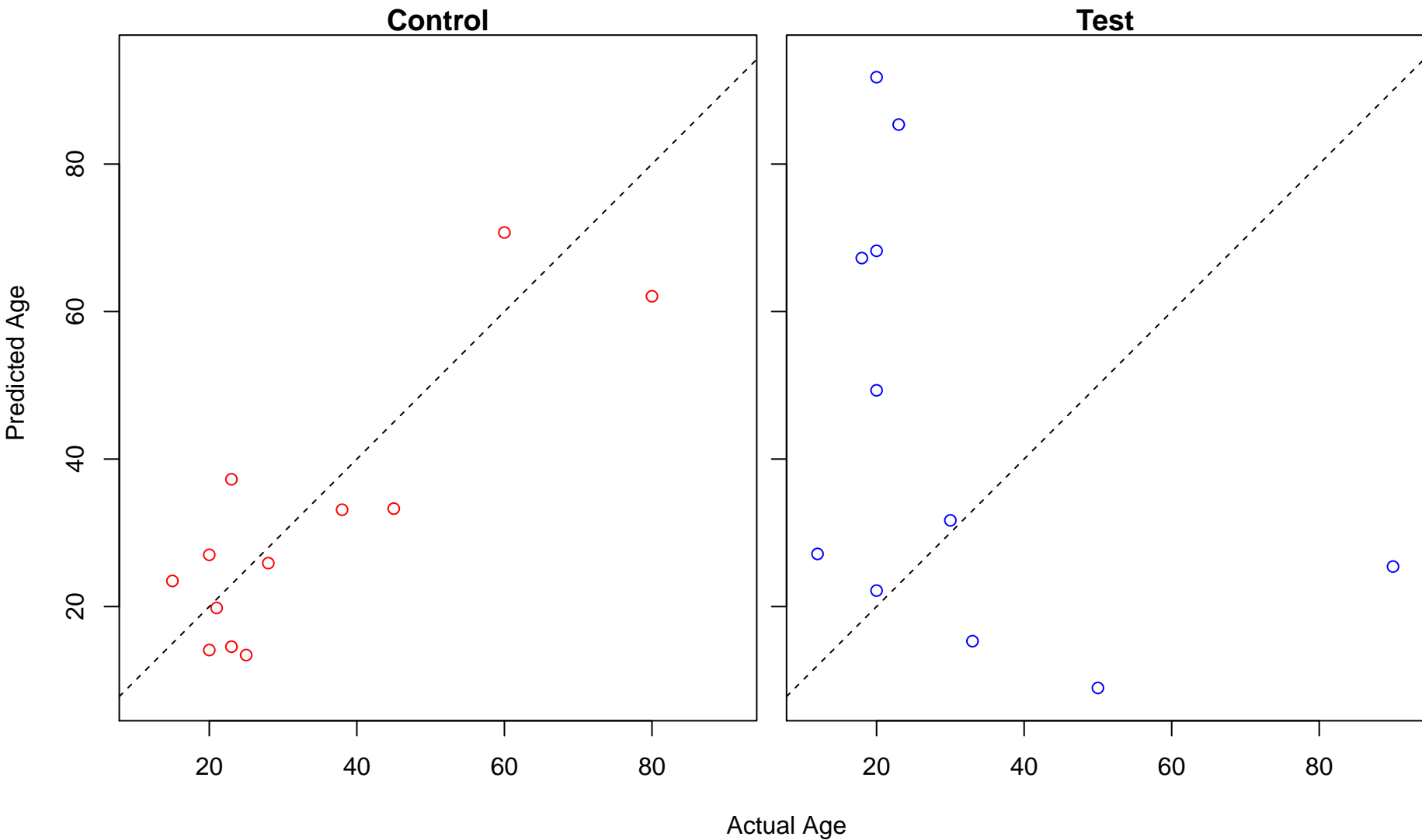
positive regulation of proteolysis (Score: 7.923466)



regulation of hair cycle (Score: 7.919667)

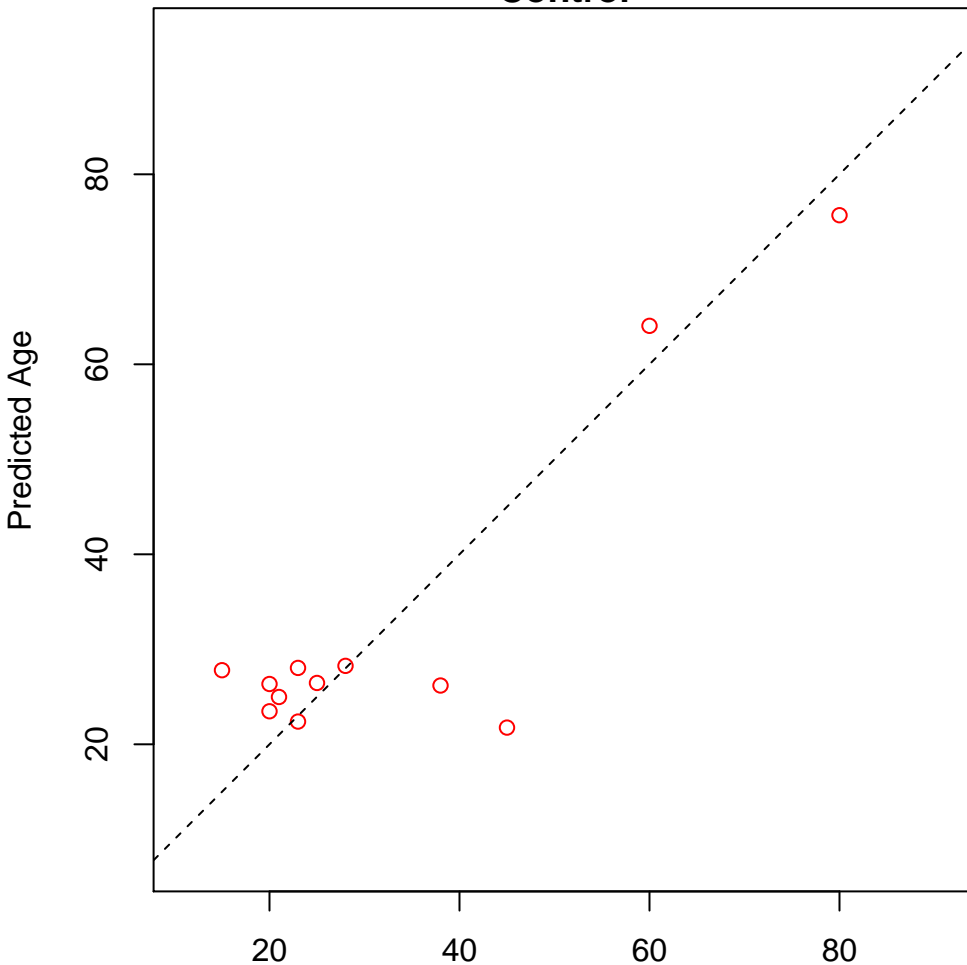


nerve development (Score: 7.919443)

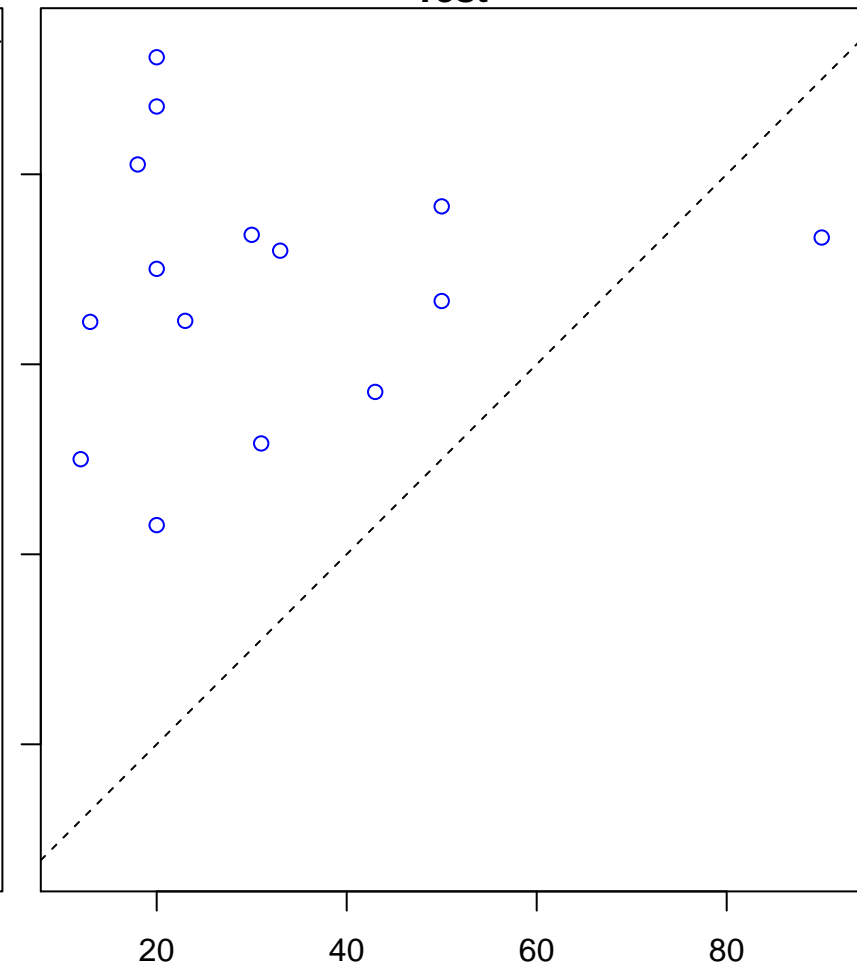


nerve growth factor signaling pathway (Score: 7.911728)

Control

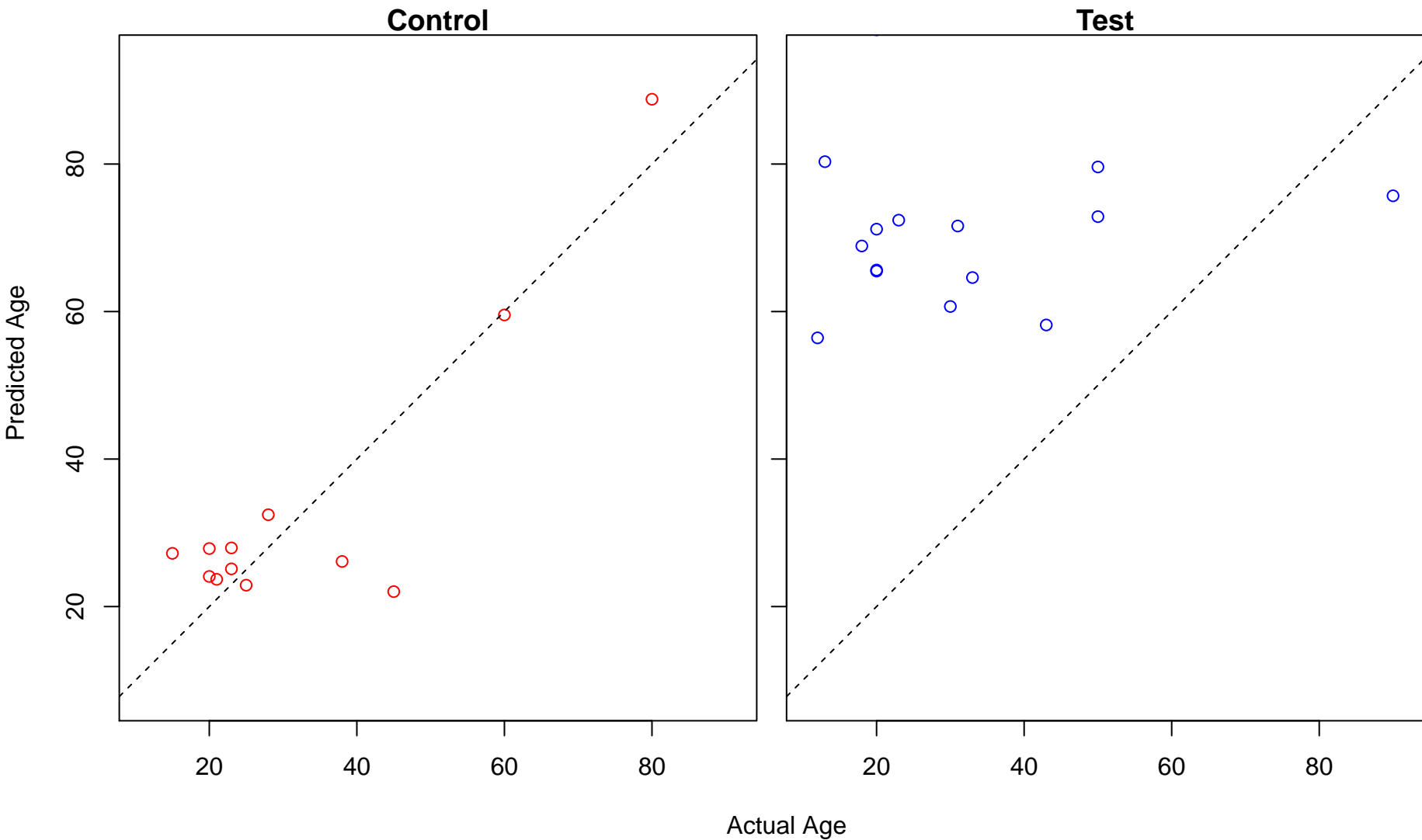


Test

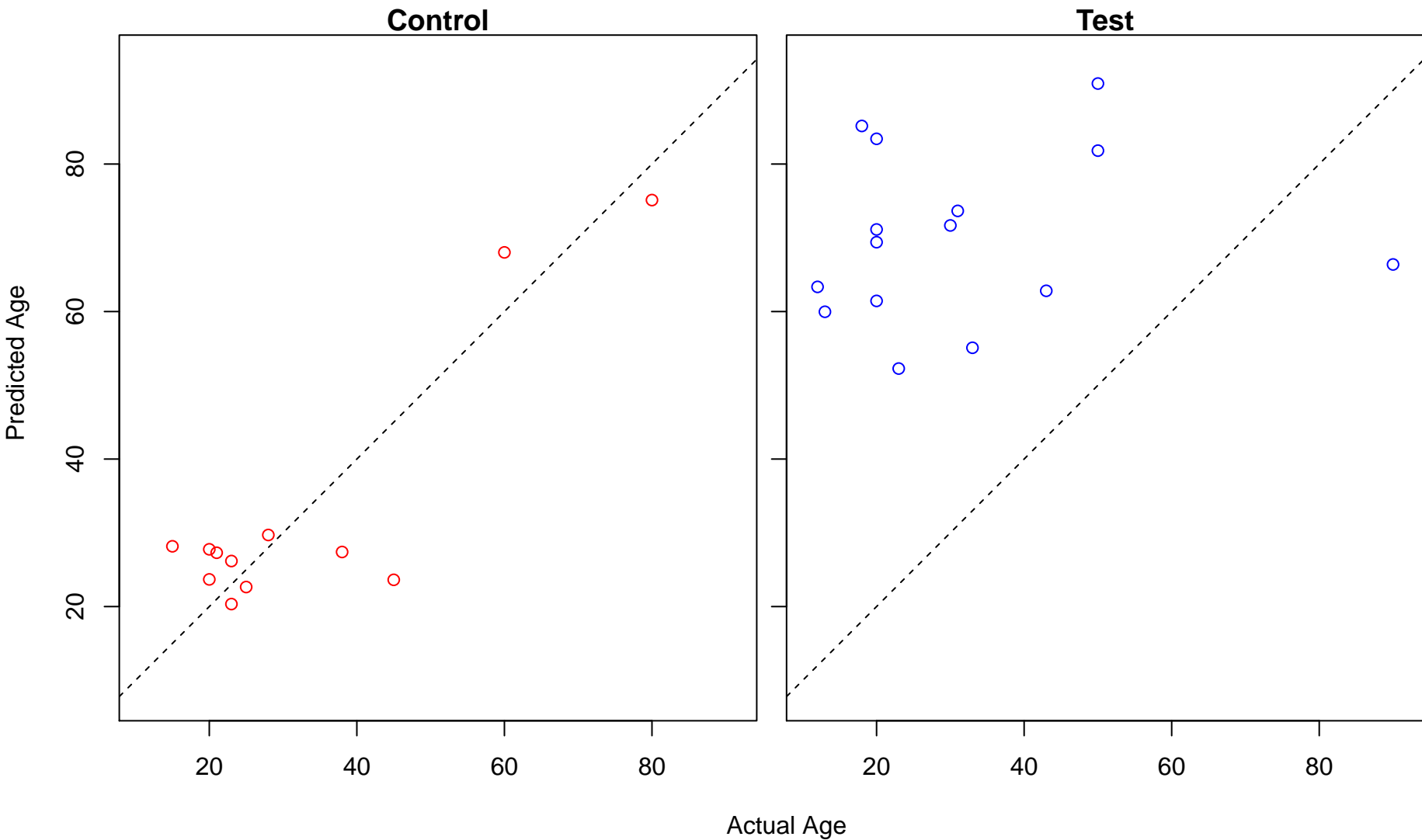


Actual Age

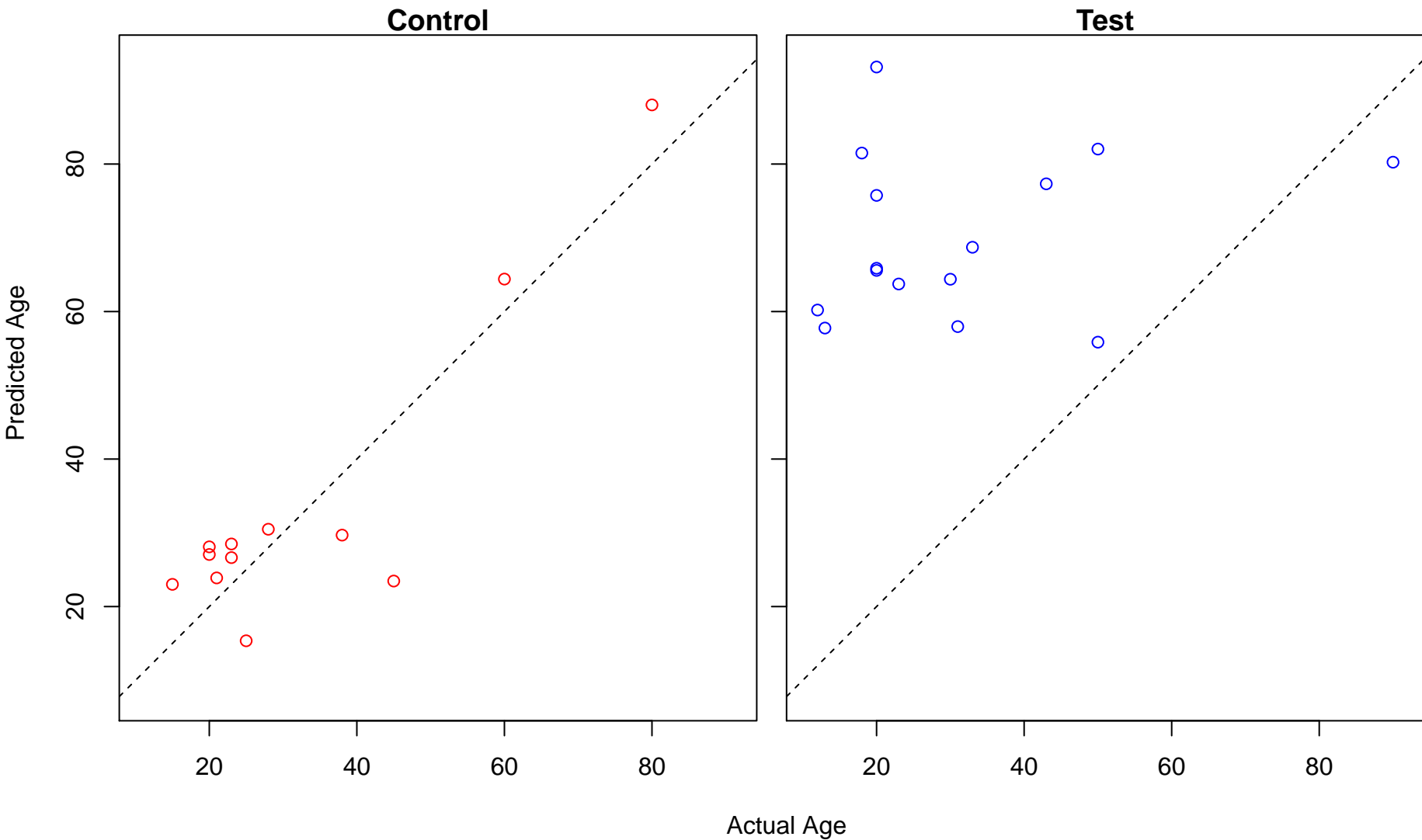
response to lipid (Score: 7.911327)



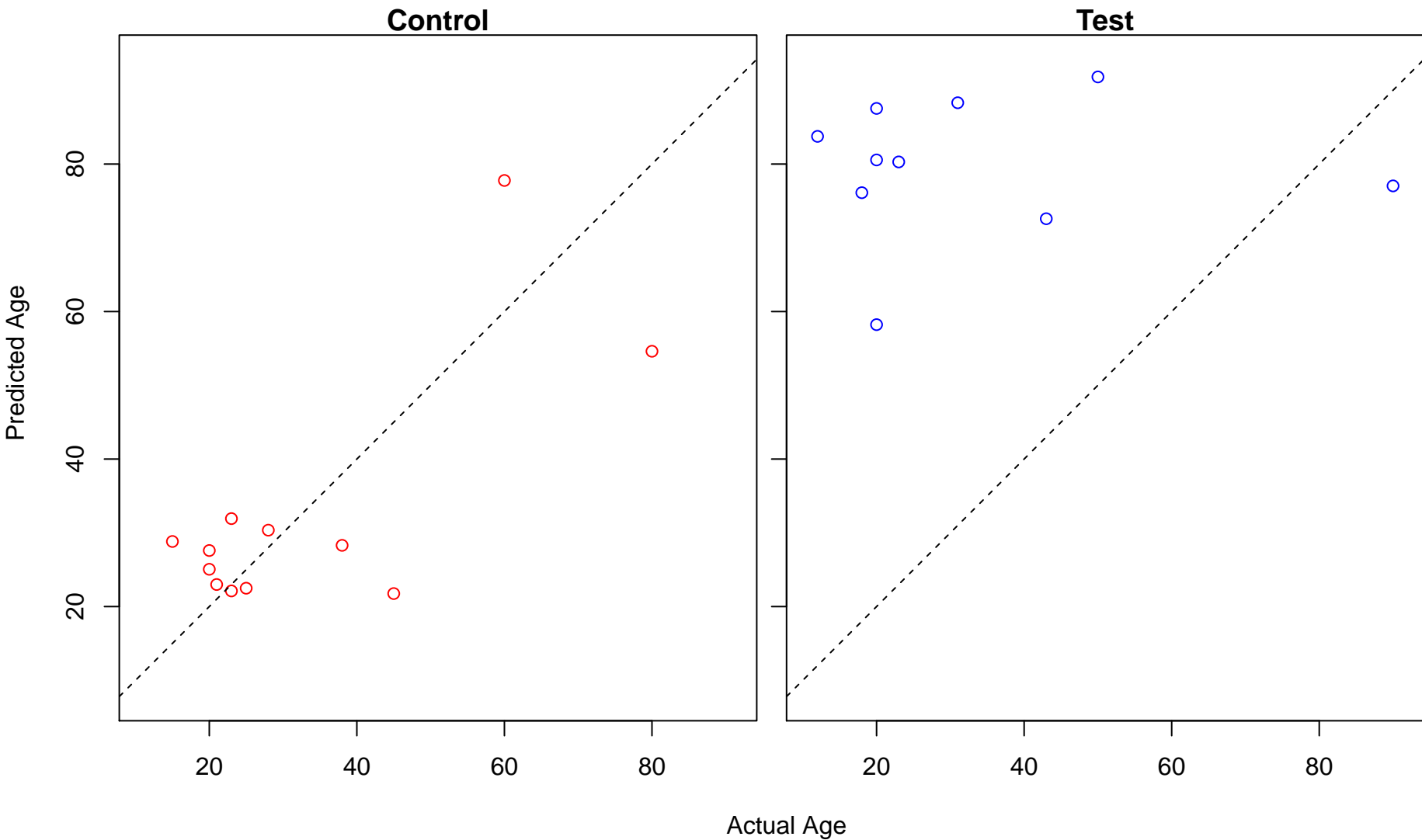
cellular response to organic cyclic compound (Score: 7.910871)



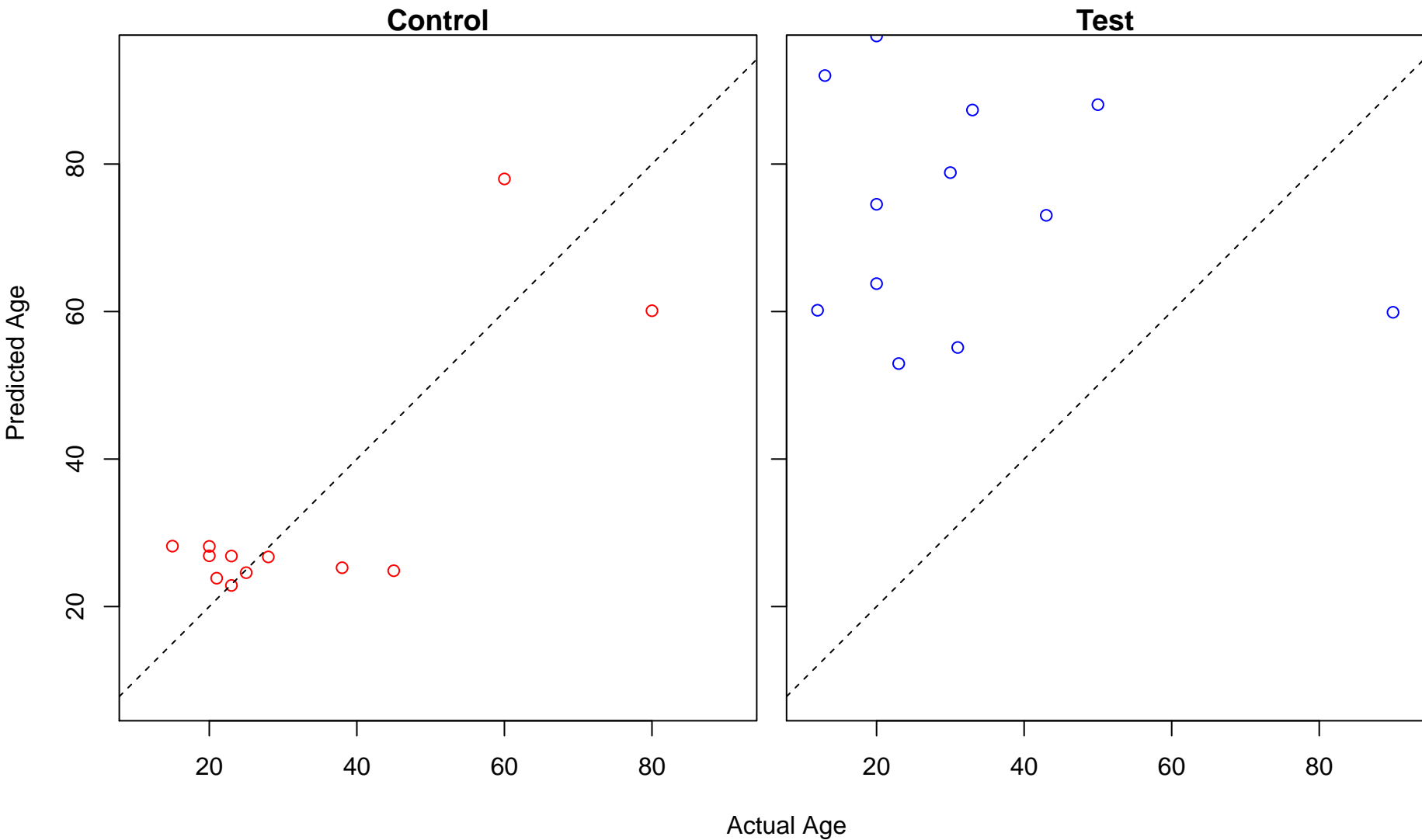
corpus callosum development (Score: 7.906737)



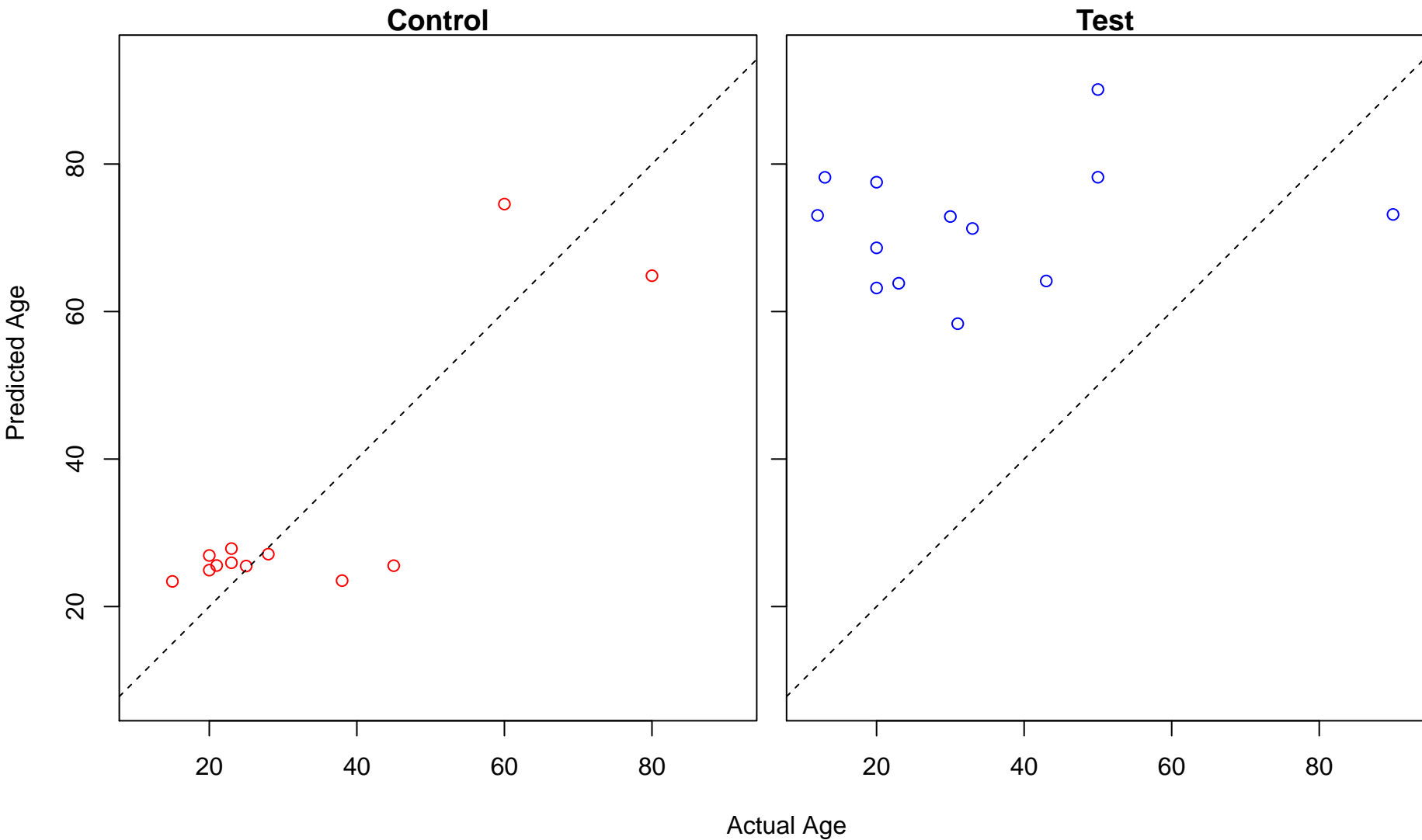
binding of sperm to zona pellucida (Score: 7.905557)



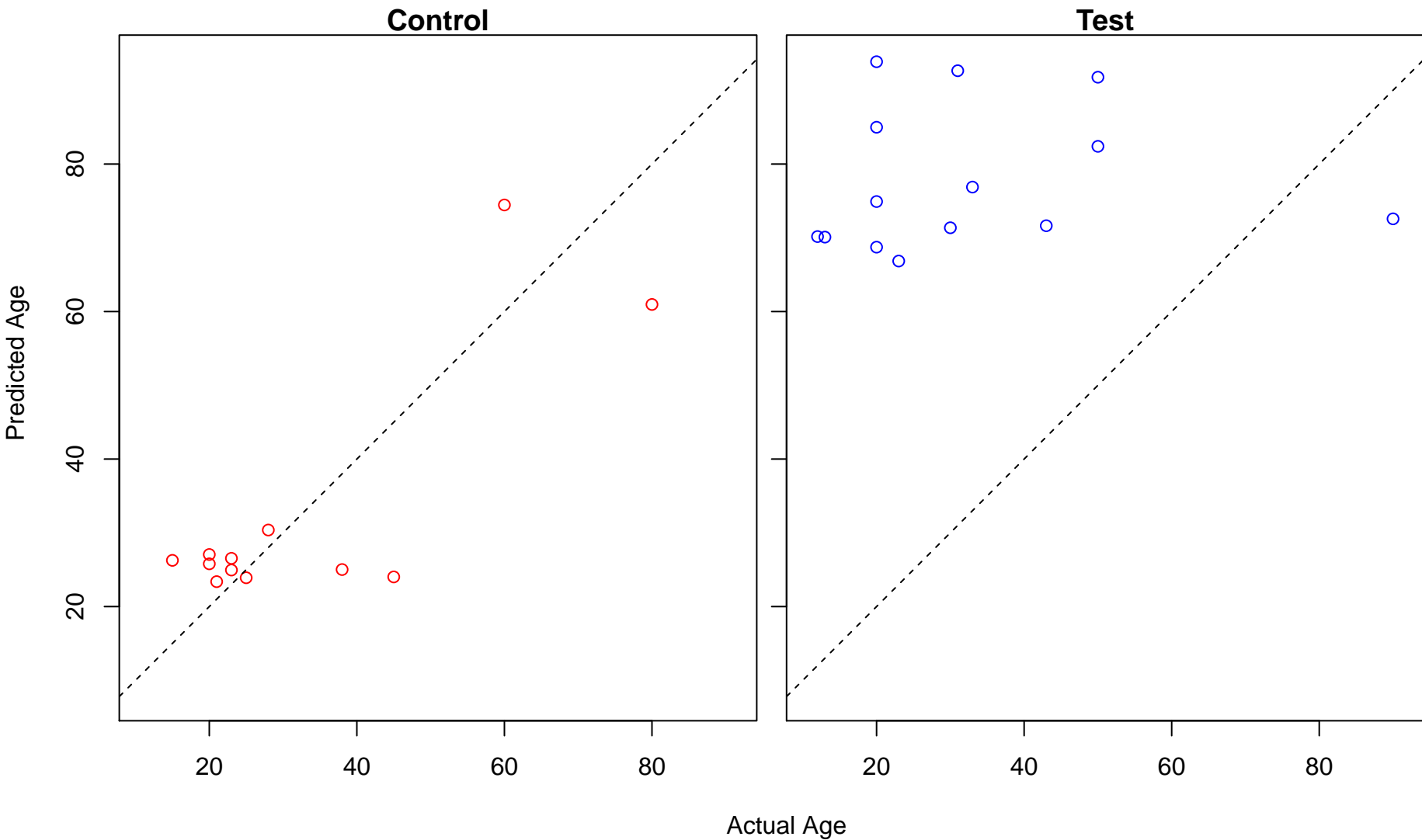
disaccharide metabolic process (Score: 7.903286)



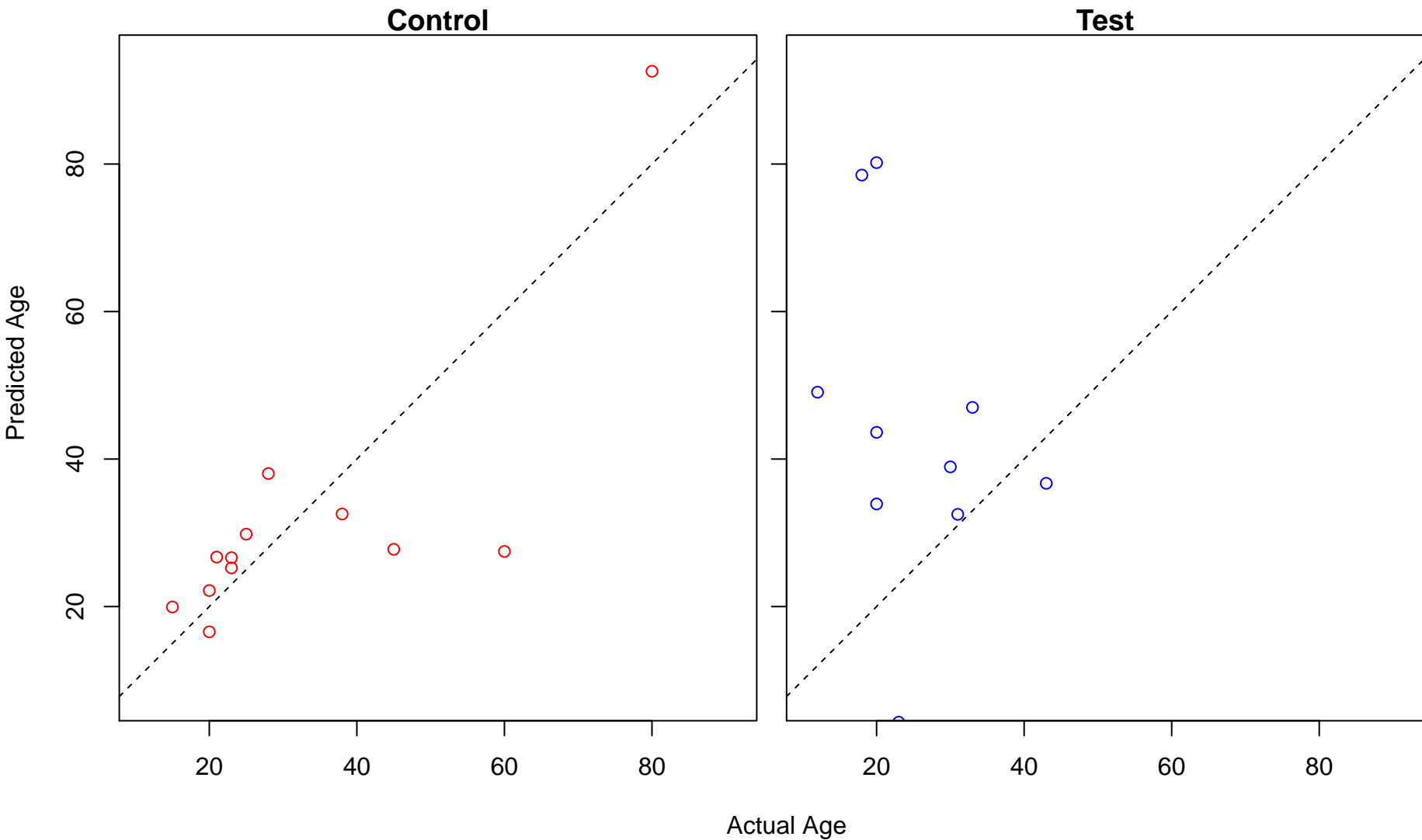
regulation of myotube differentiation (Score: 7.897529)



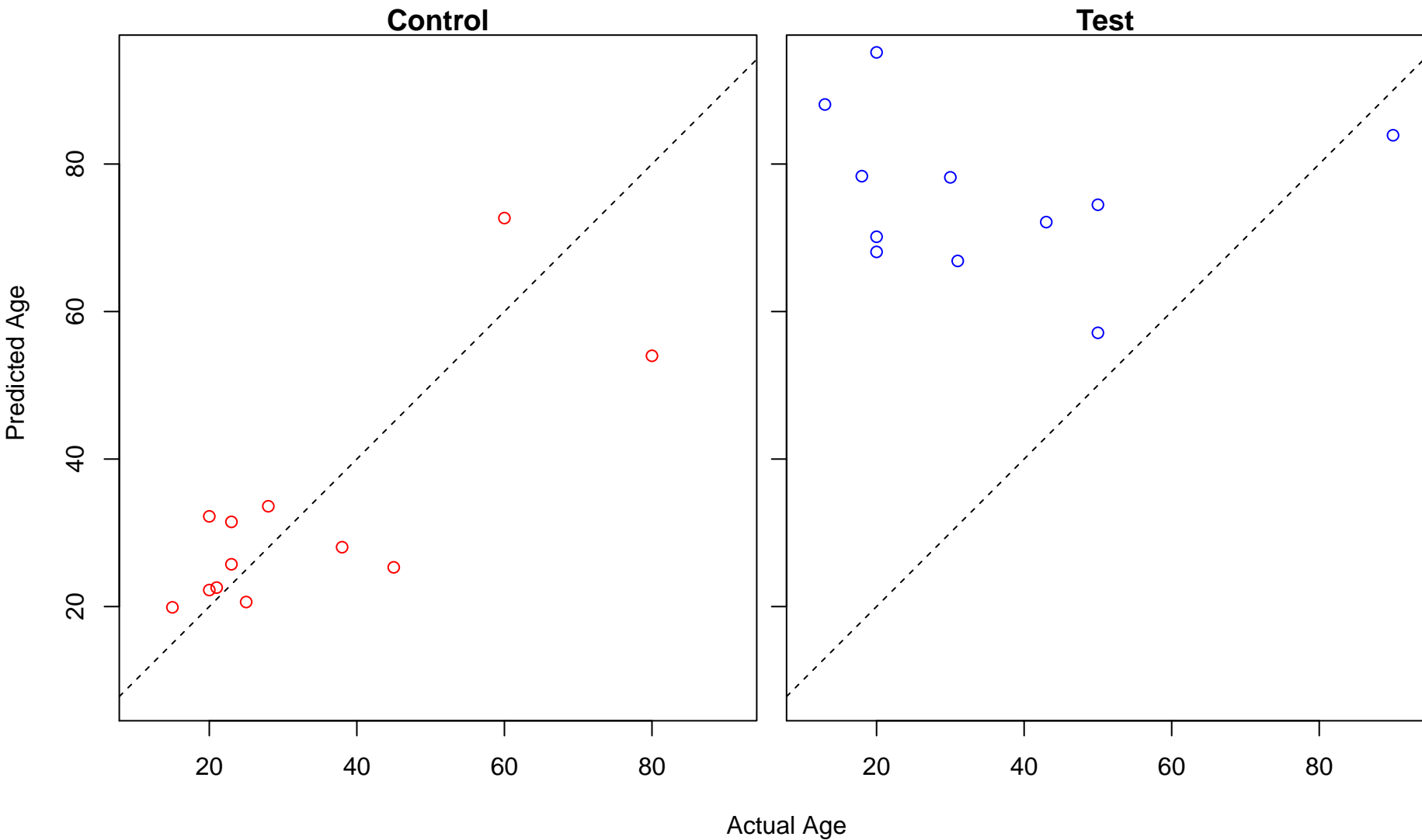
choline transport (Score: 7.896210)



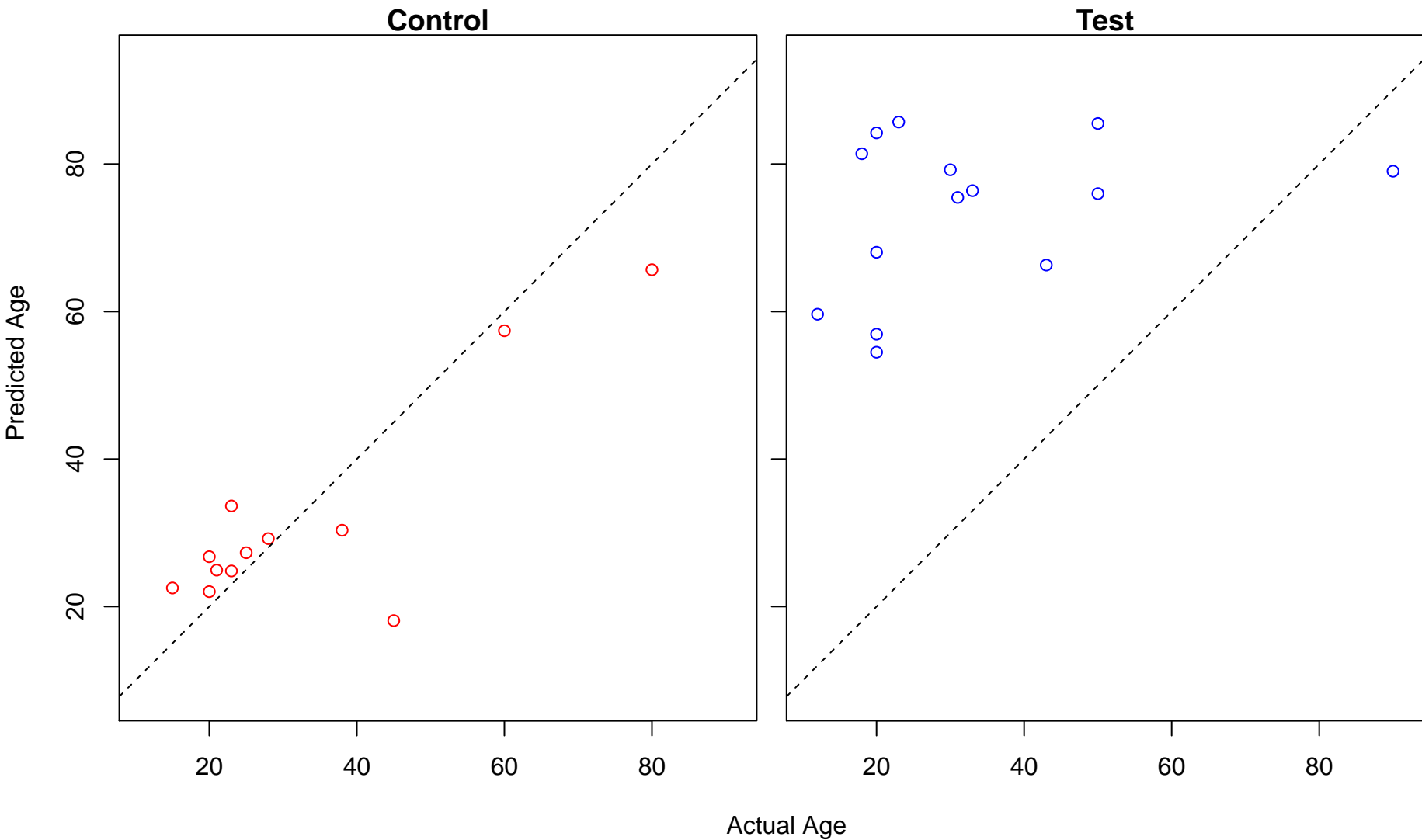
myeloid leukocyte activation (Score: 7.895643)



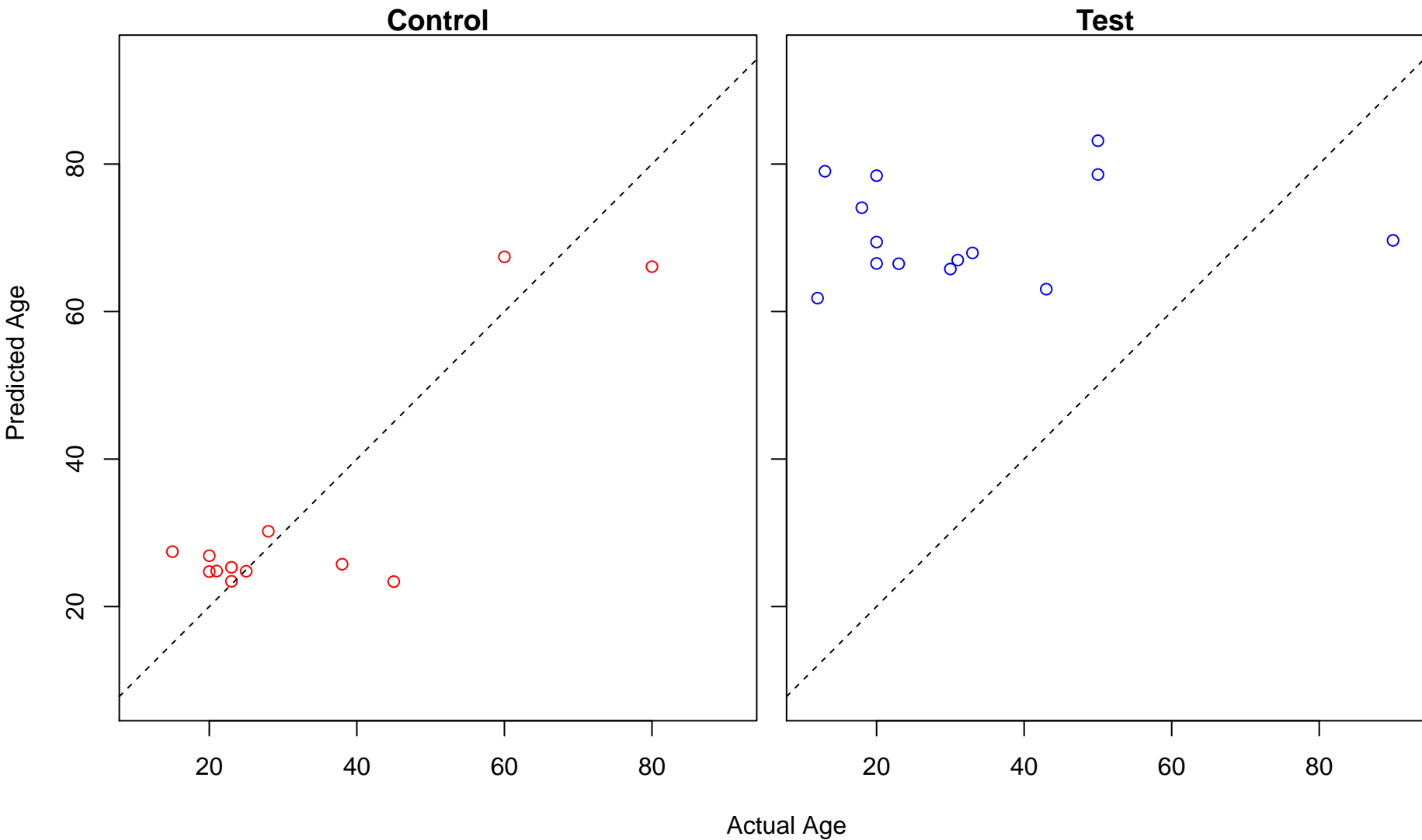
xenobiotic catabolic process (Score: 7.895531)



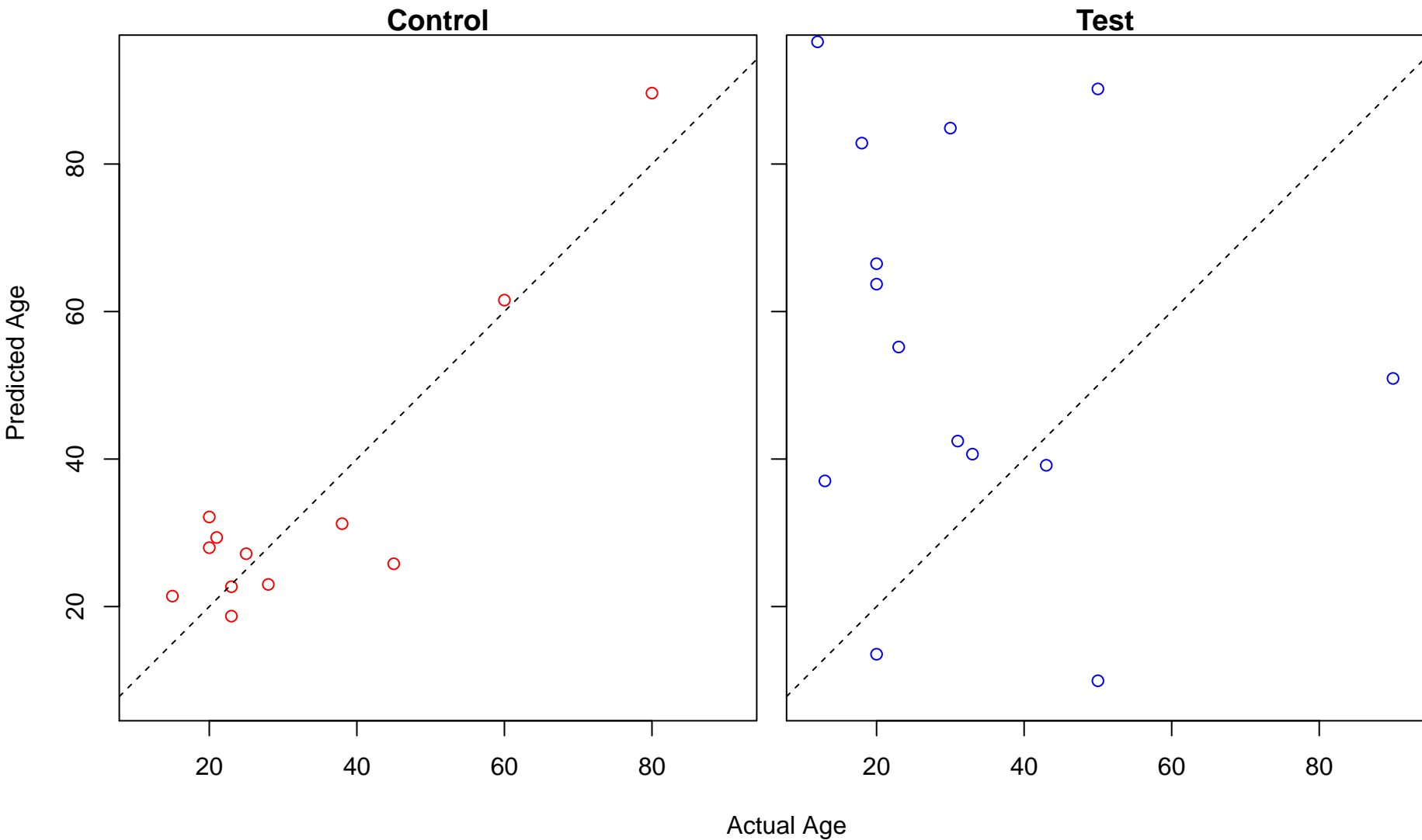
regulation of dendritic cell differentiation (Score: 7.892996)



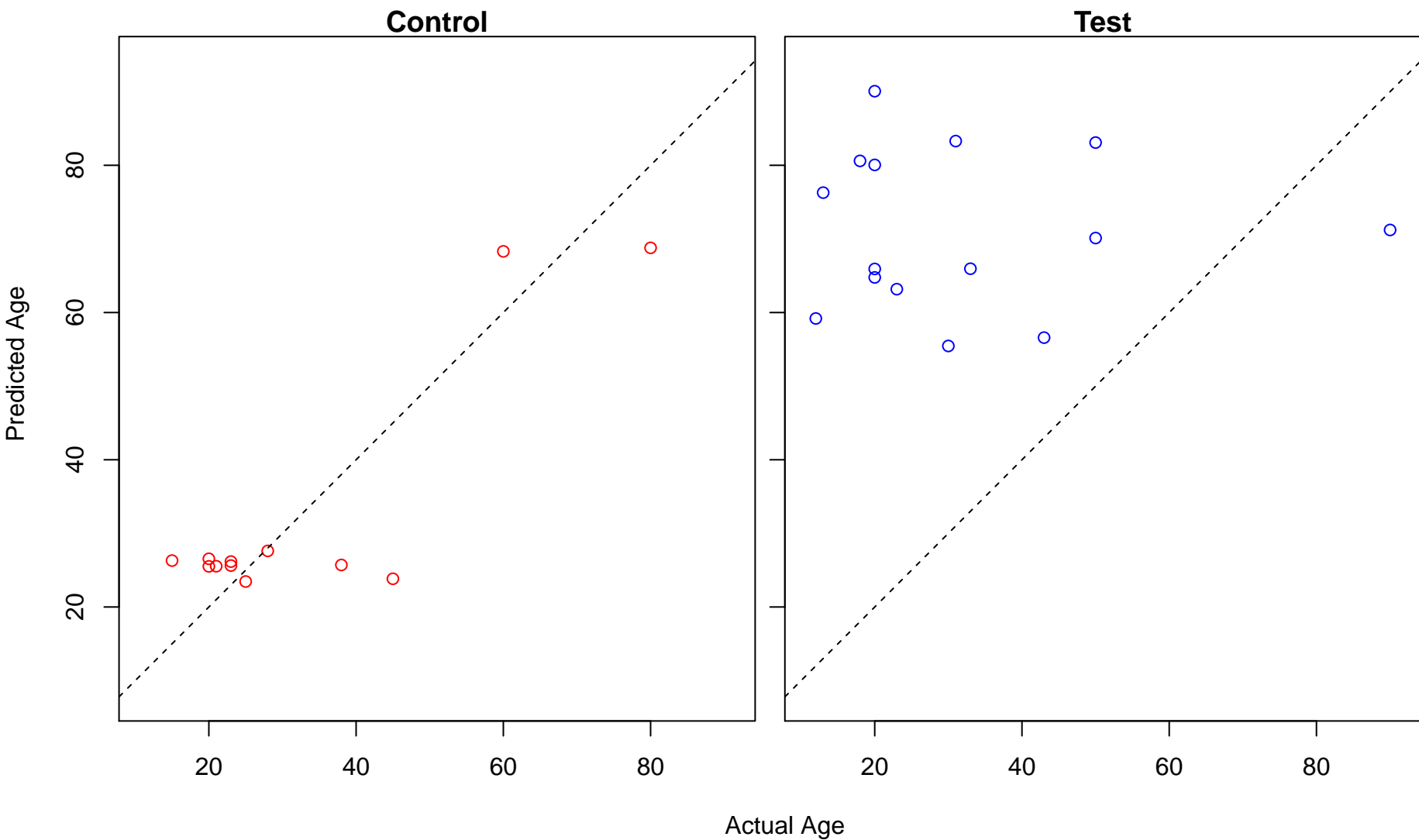
purine-containing compound biosynthetic process (Score: 7.892525)



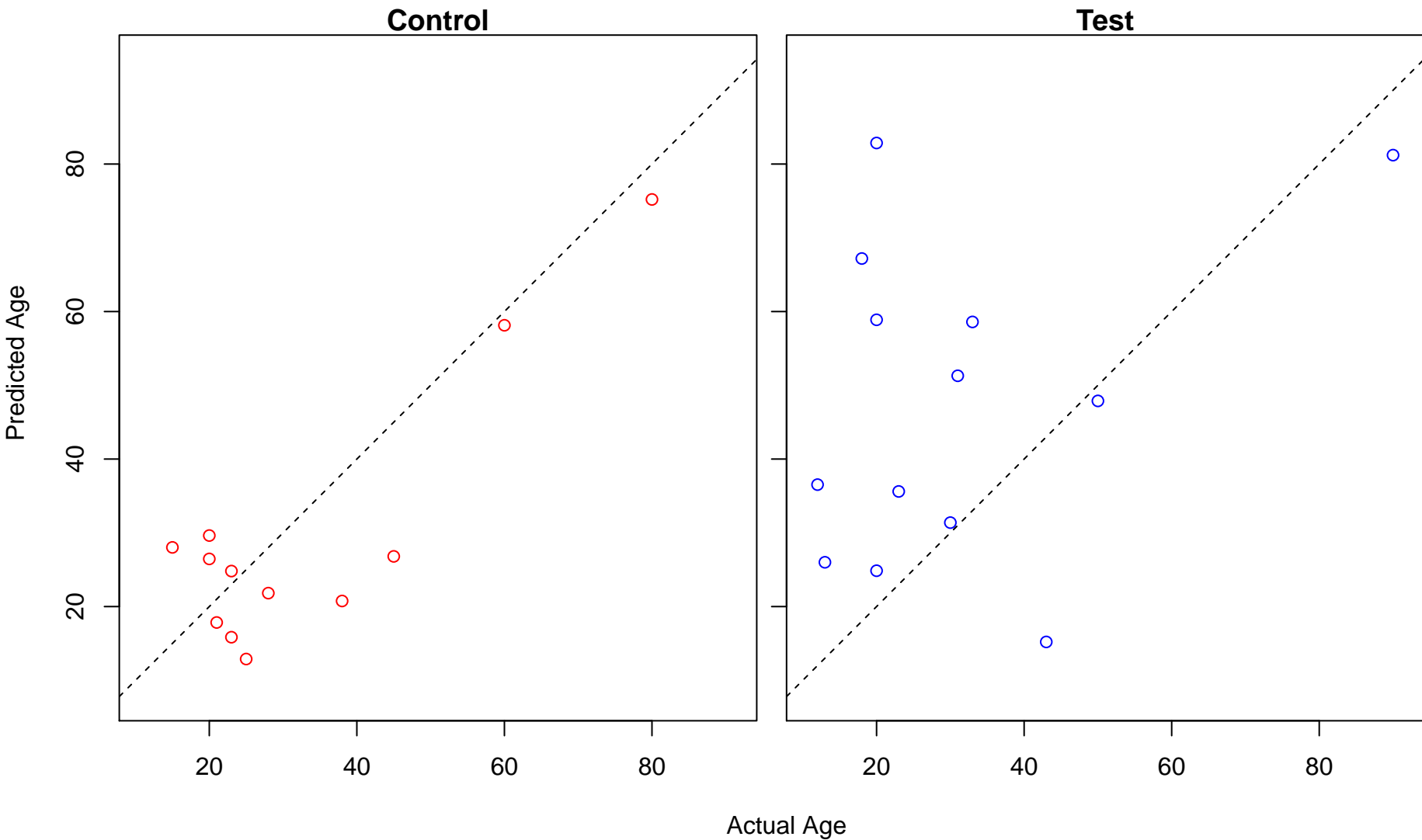
integrin-mediated signaling pathway (Score: 7.892156)



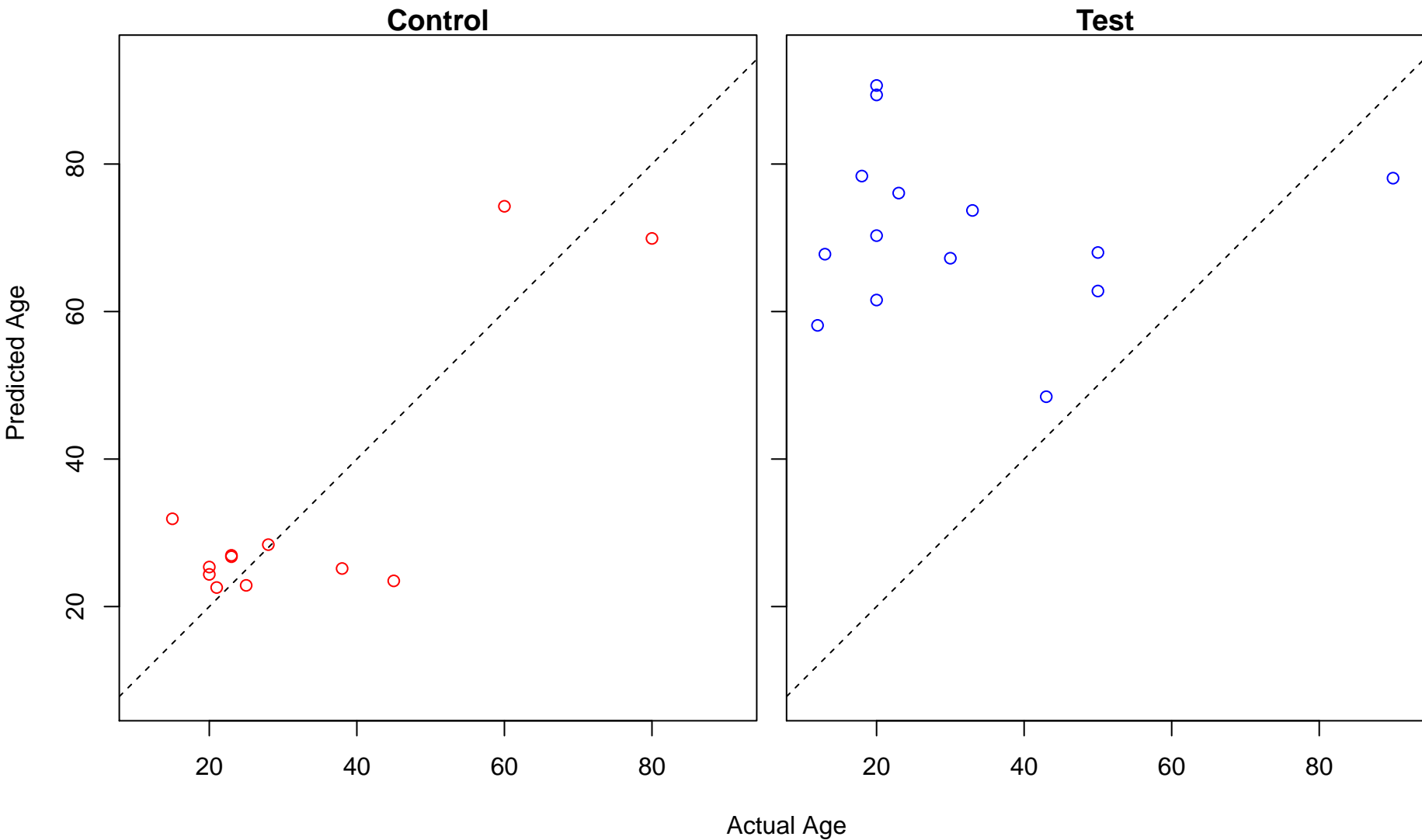
methylation (Score: 7.891878)



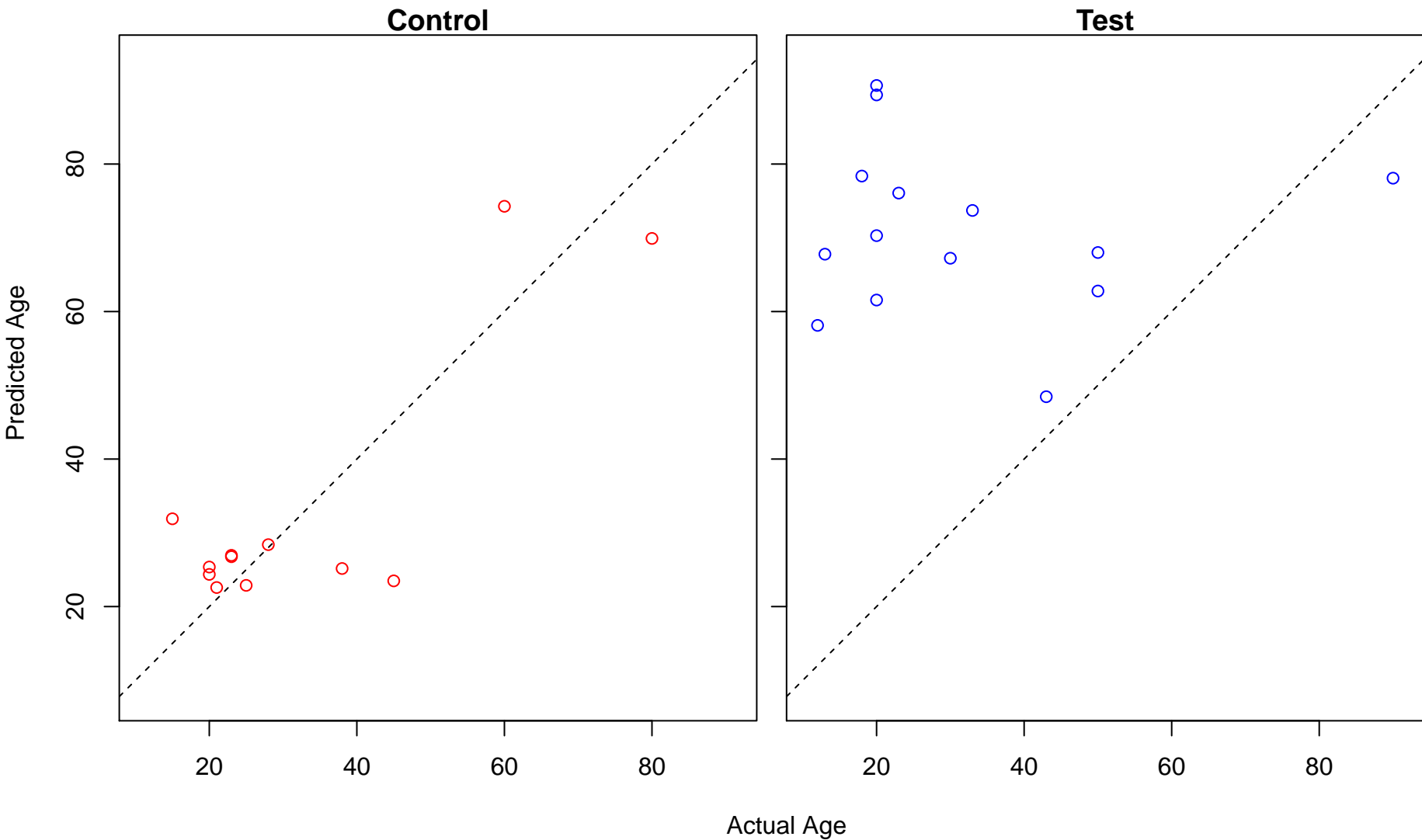
sexual reproduction (Score: 7.889991)



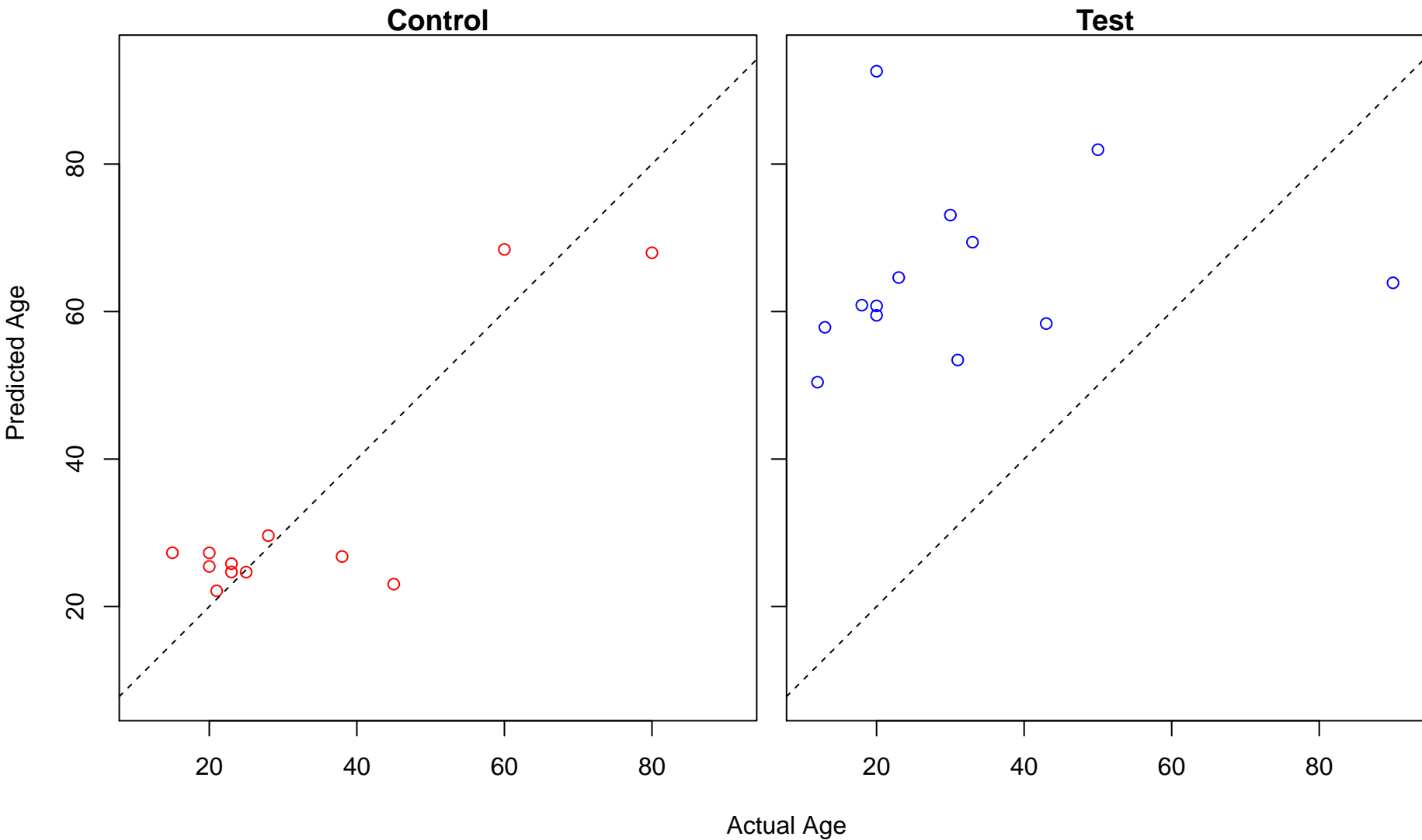
negative regulation of protein import into nucleus (Score: 7.886205)



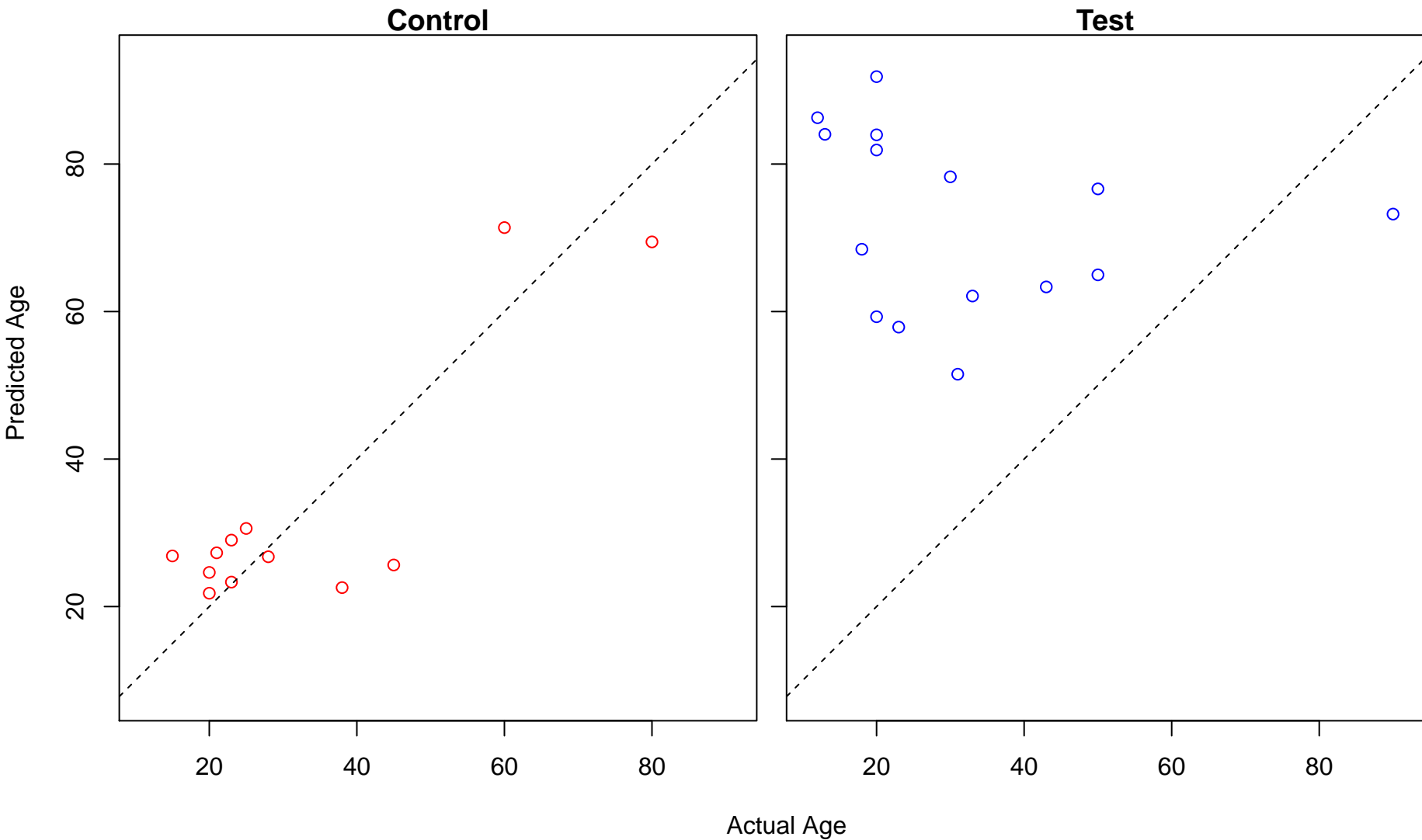
negative regulation of protein import (Score: 7.886205)



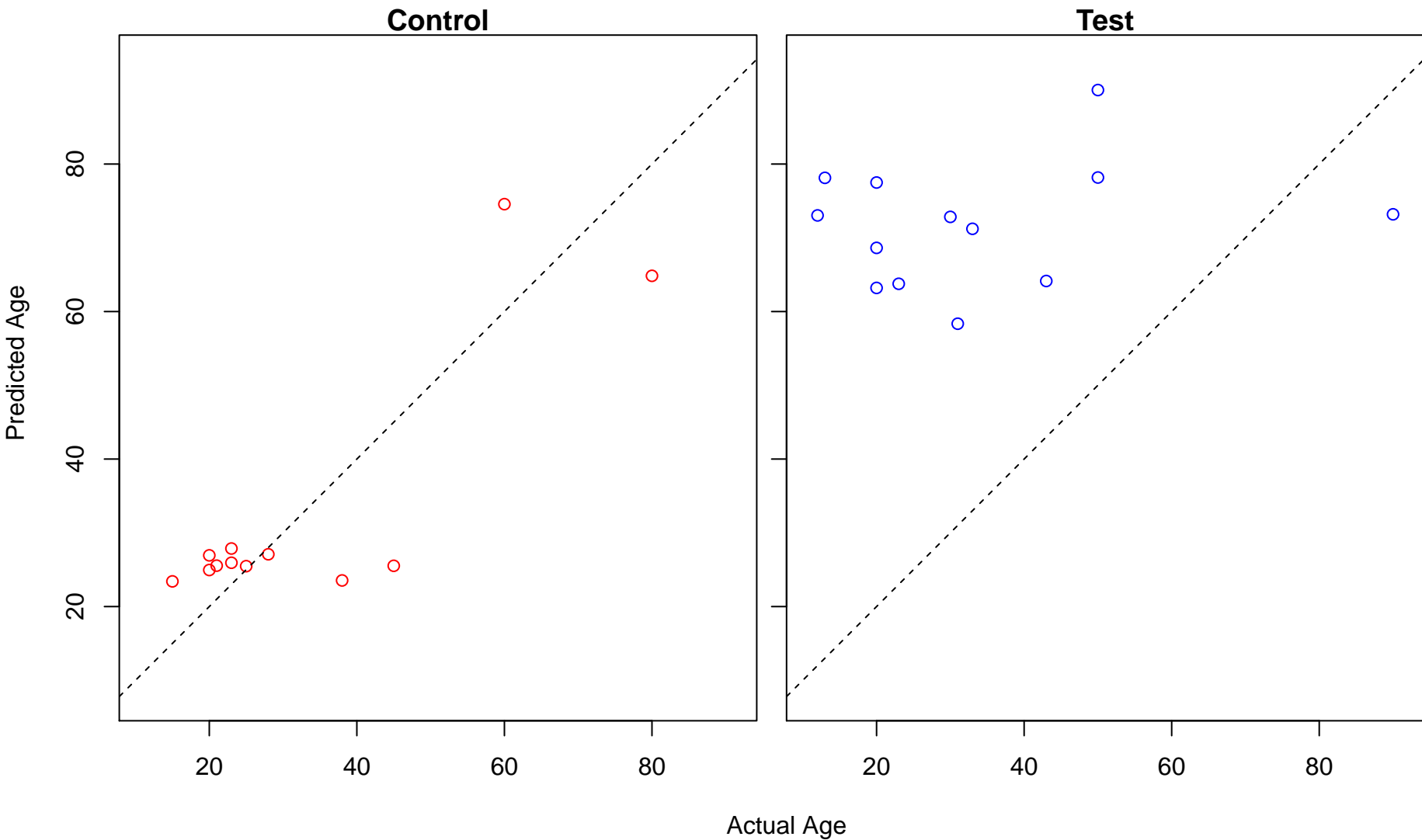
regulation of bone remodeling (Score: 7.885999)



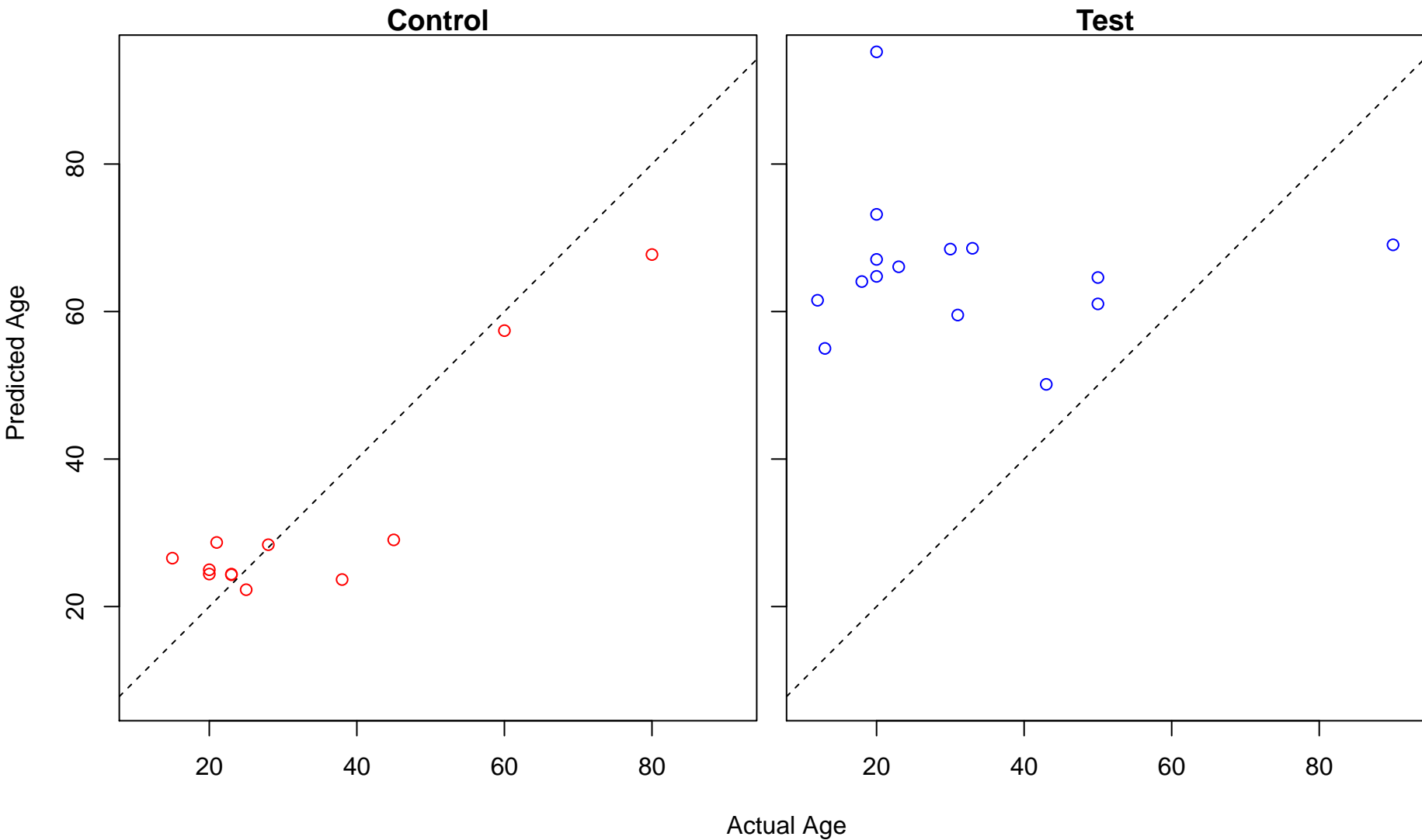
regulation of organ morphogenesis (Score: 7.881157)



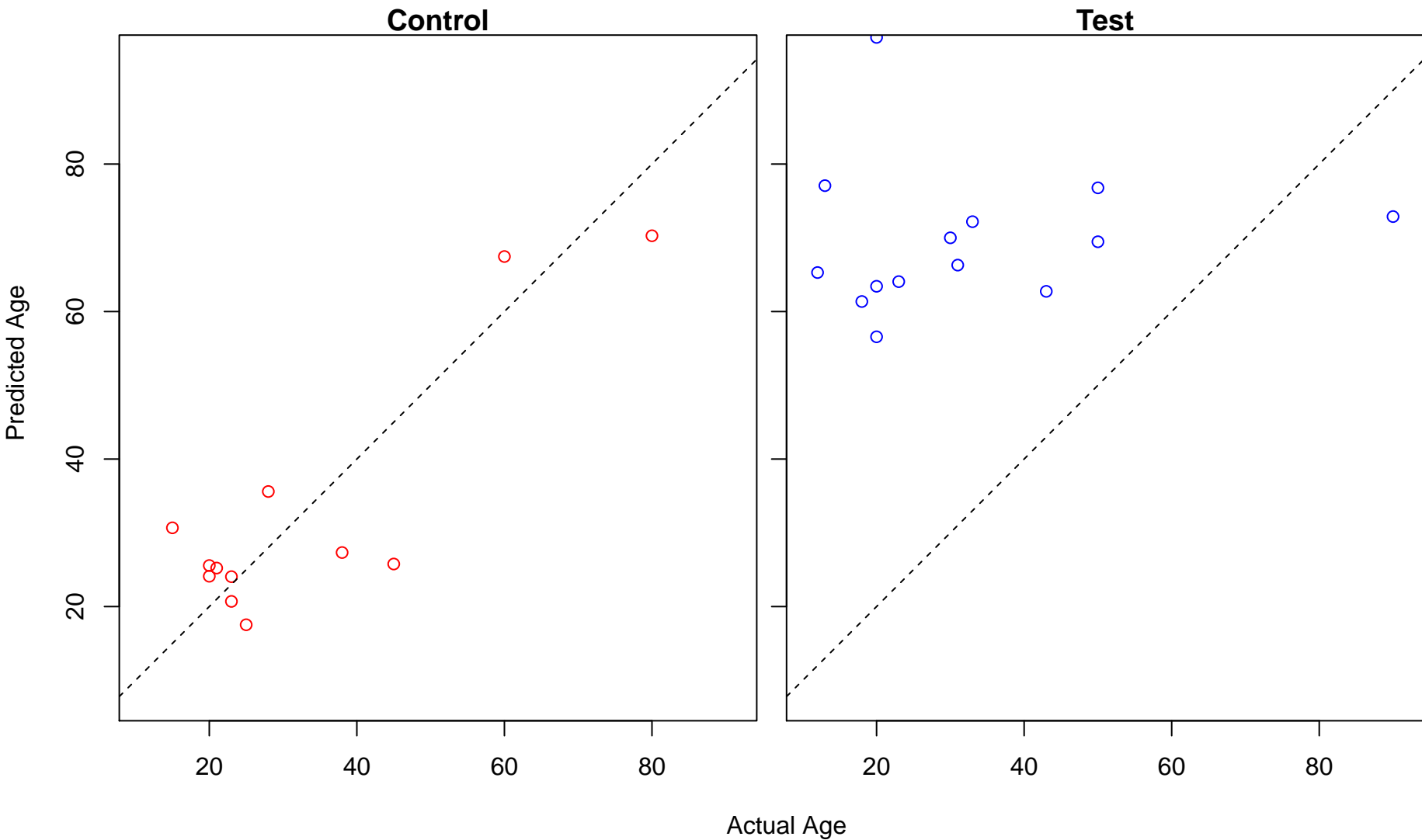
regulation of striated muscle cell differentiation (Score: 7.881130)



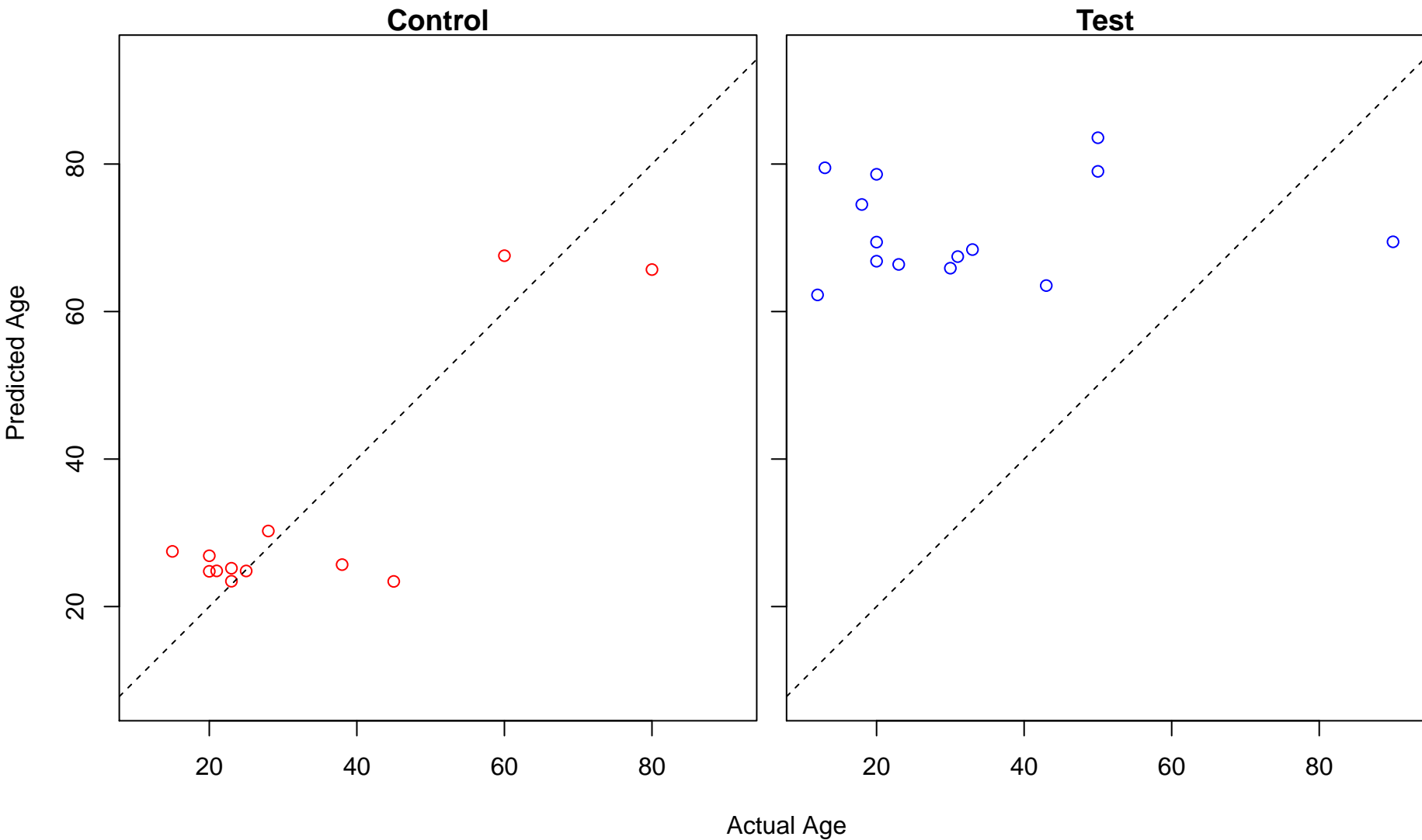
regulation of podosome assembly (Score: 7.879760)



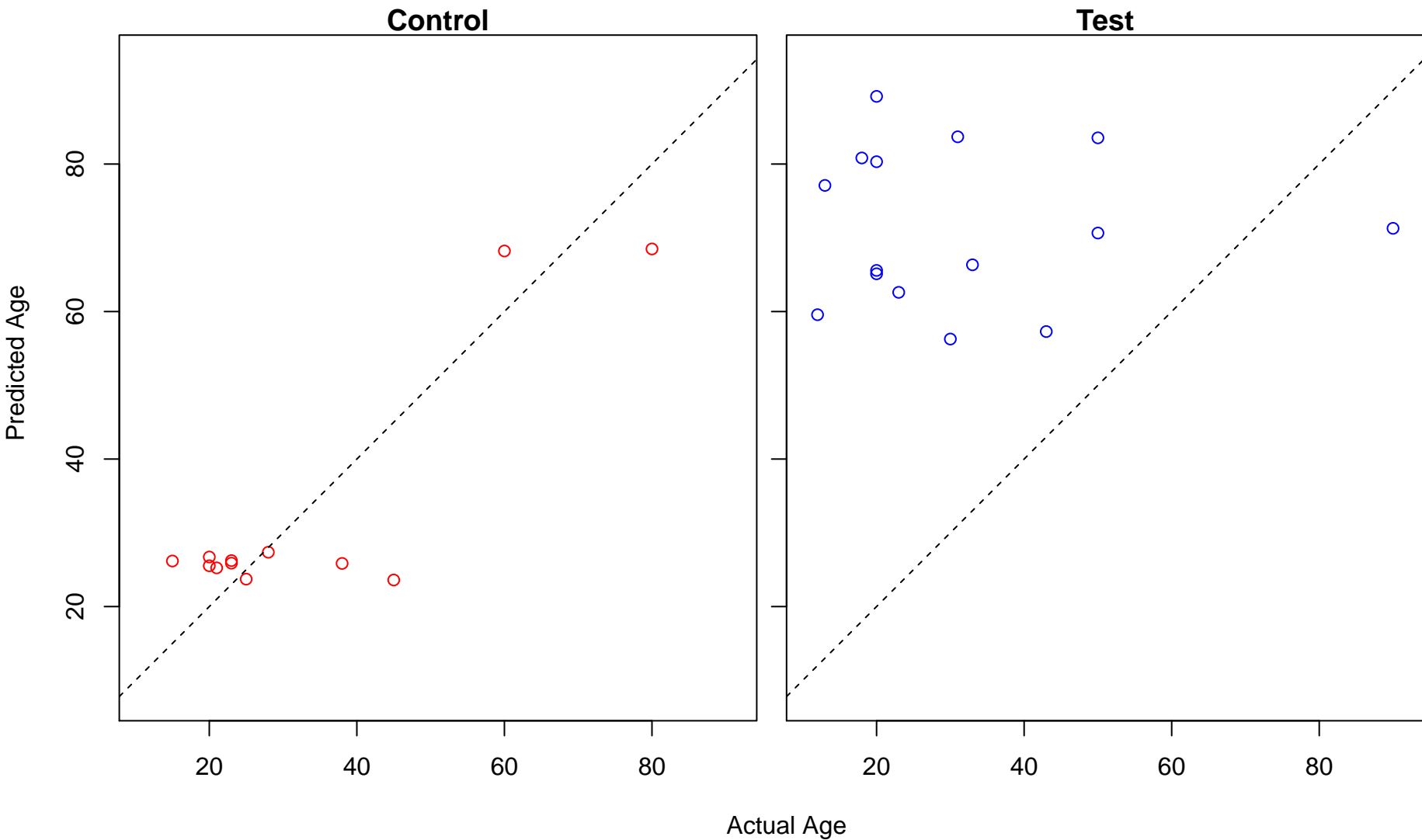
response to UV-B (Score: 7.874167)



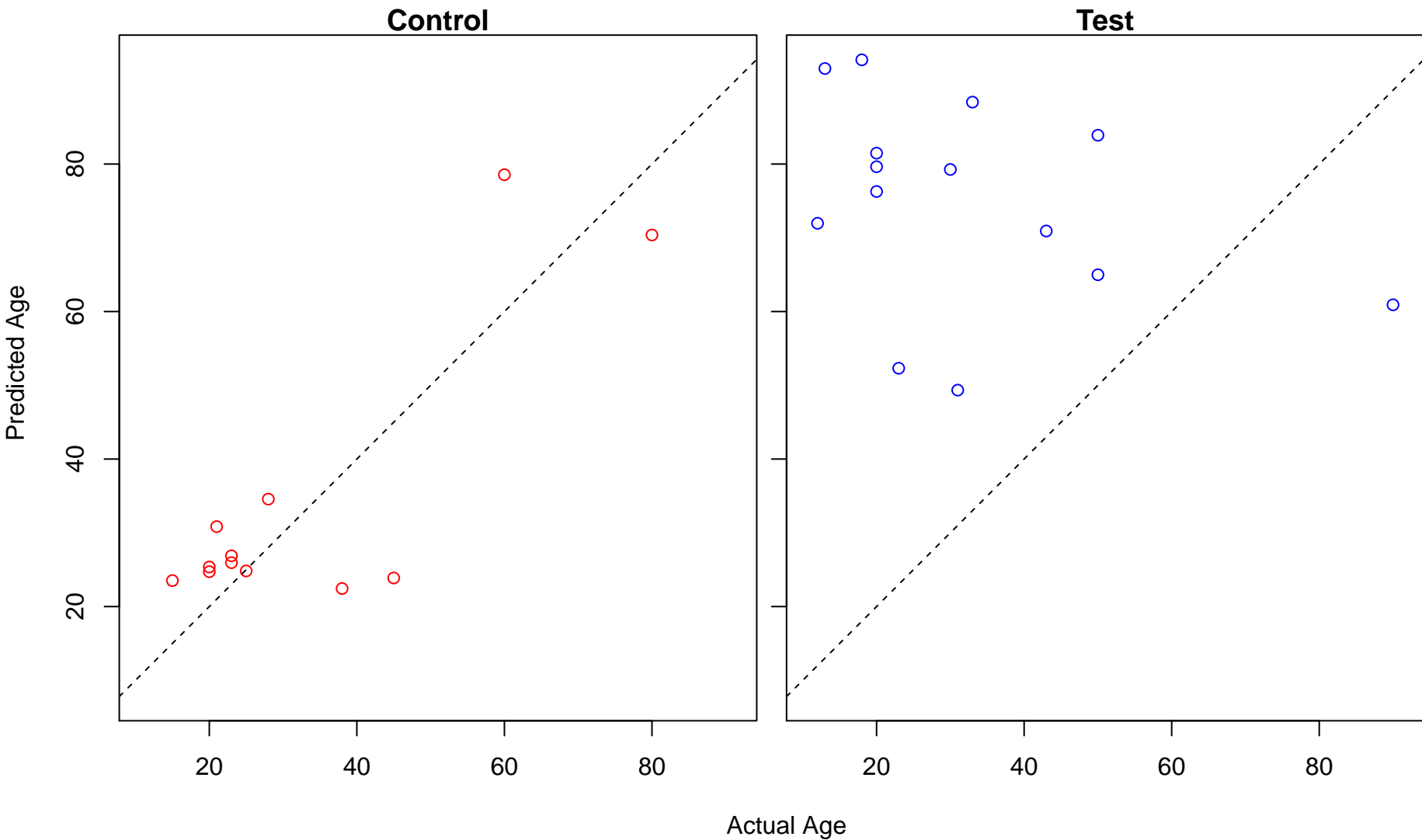
nucleotide biosynthetic process (Score: 7.873551)



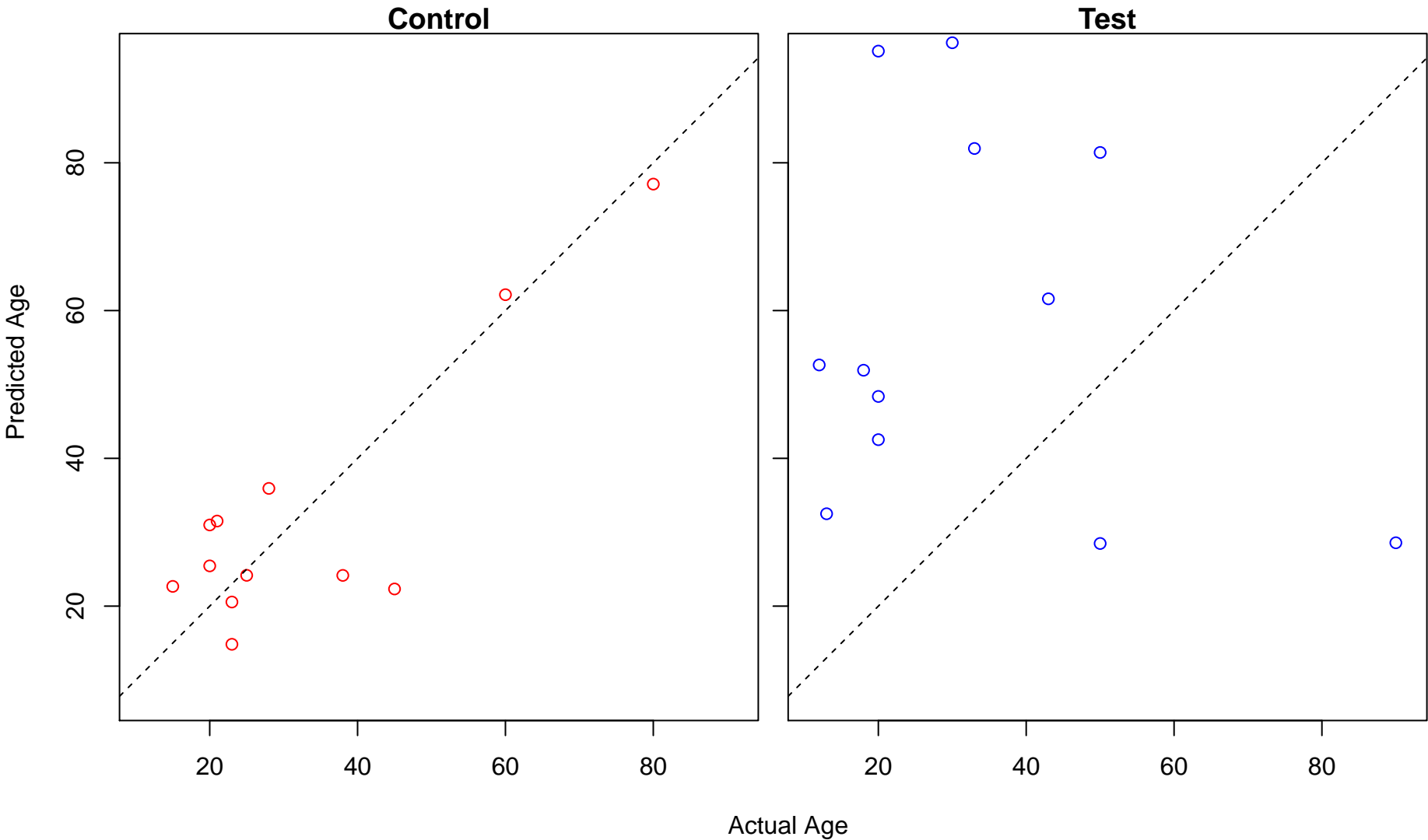
gene silencing (Score: 7.870583)



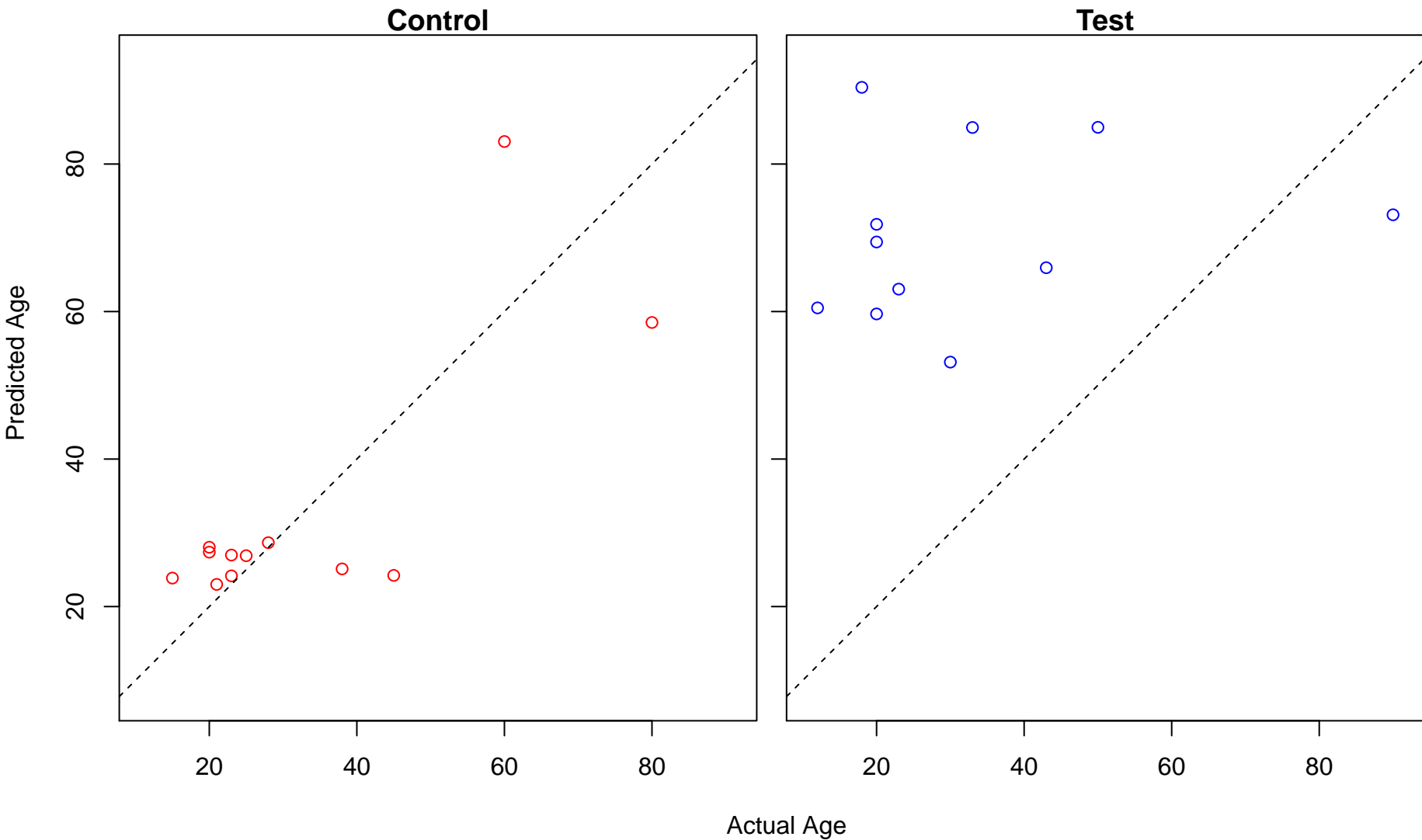
positive regulation of epidermal growth factor-activated receptor activity (Score: 7.870216)



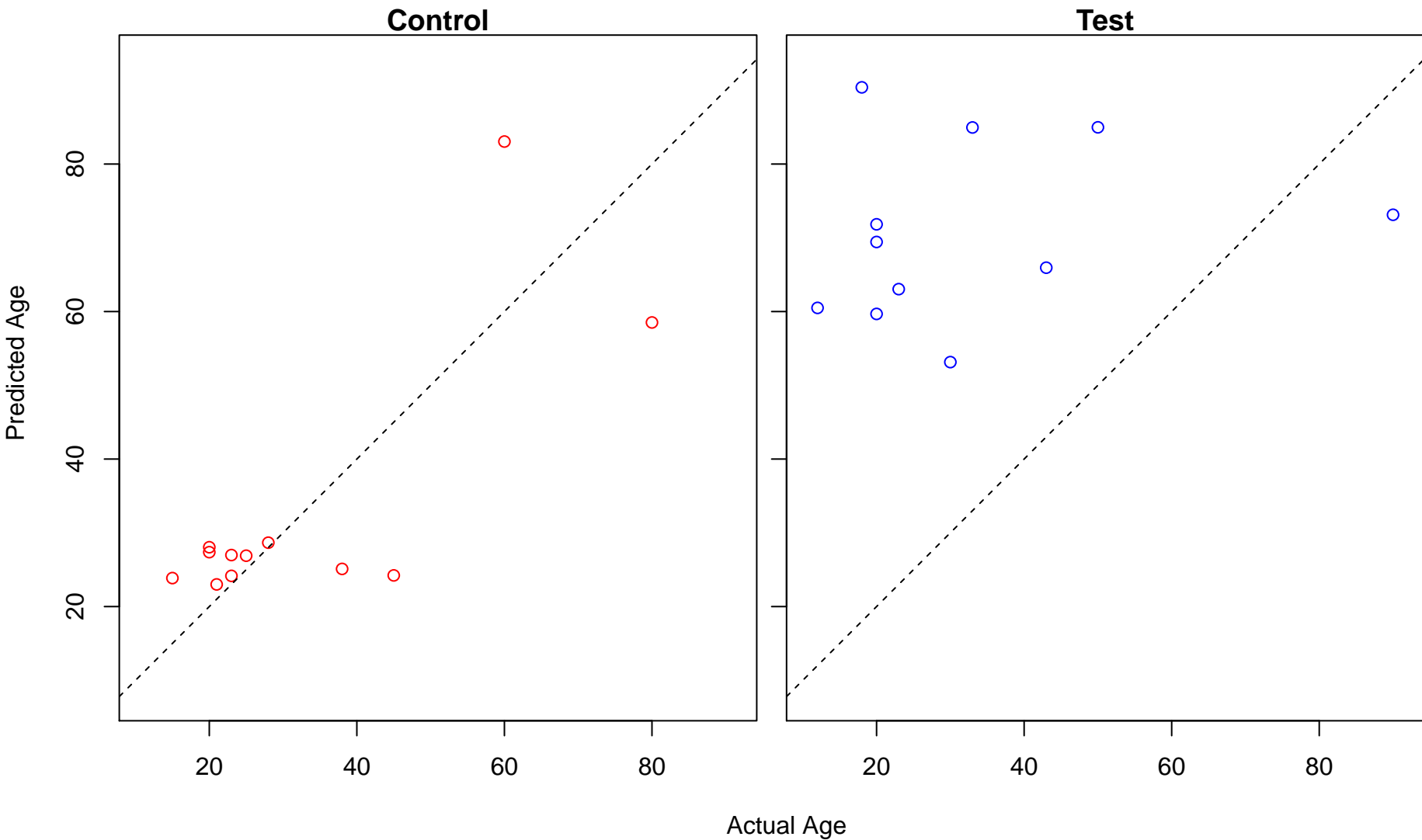
regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 7.869926)



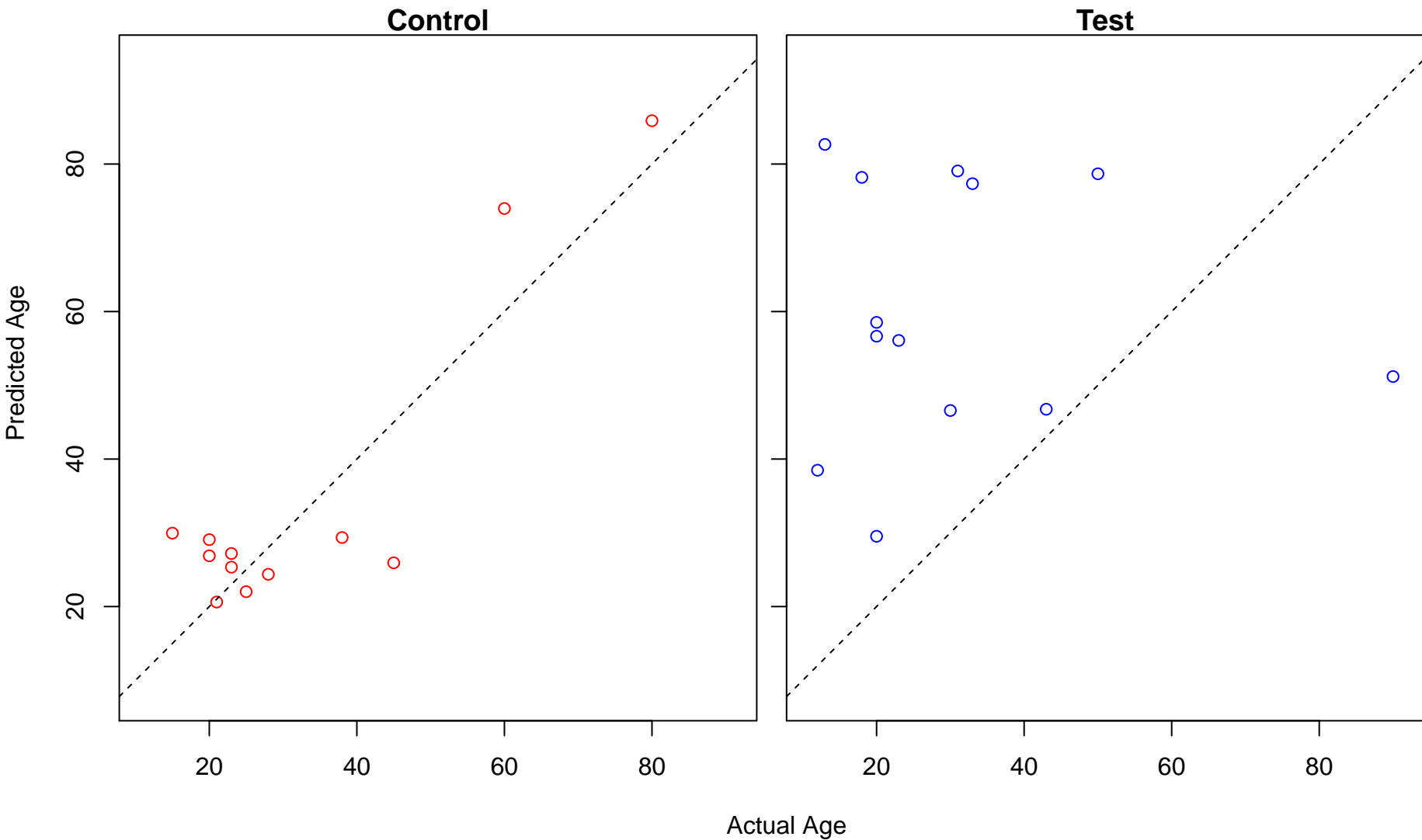
defense response to fungus (Score: 7.865250)



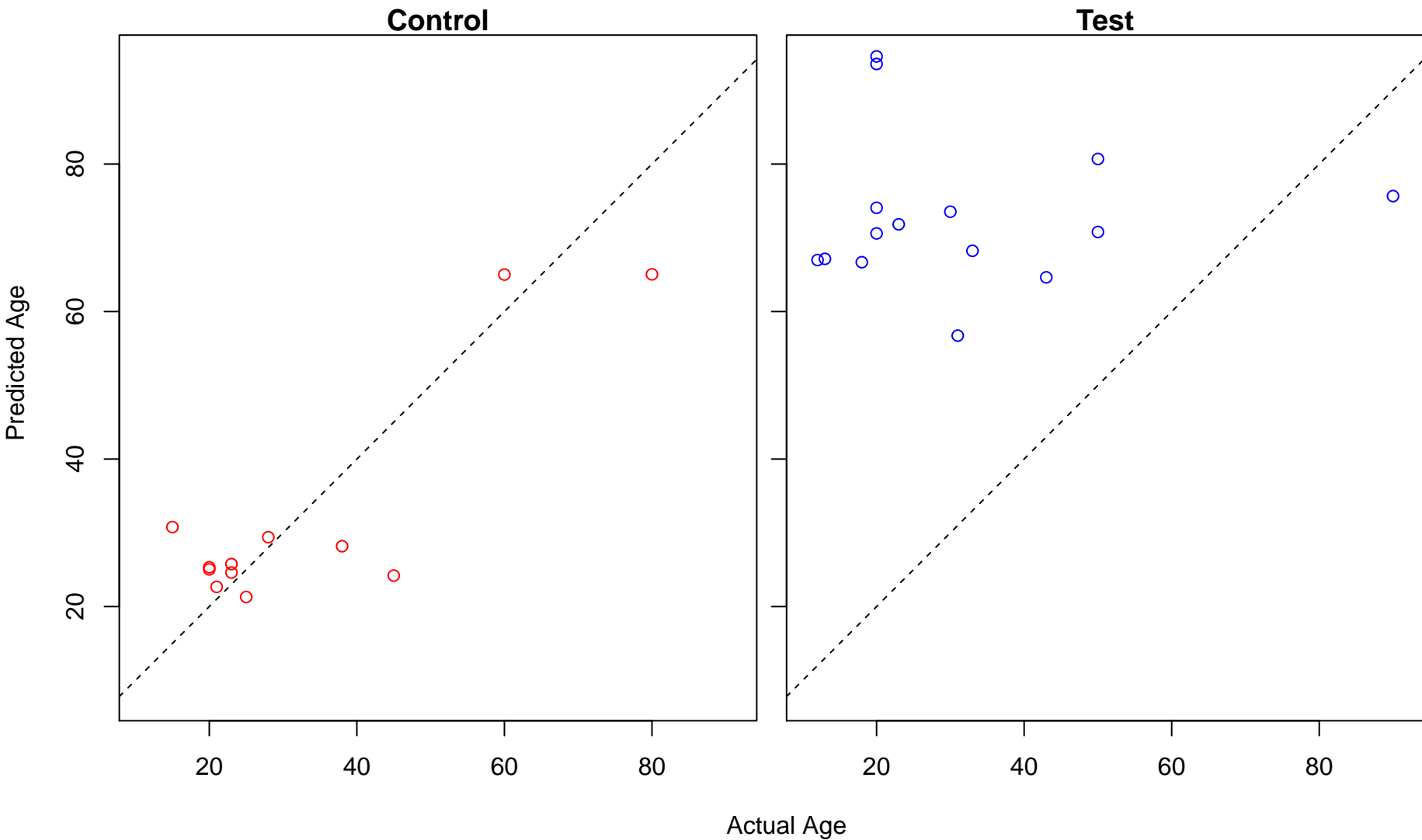
response to fungus (Score: 7.864897)



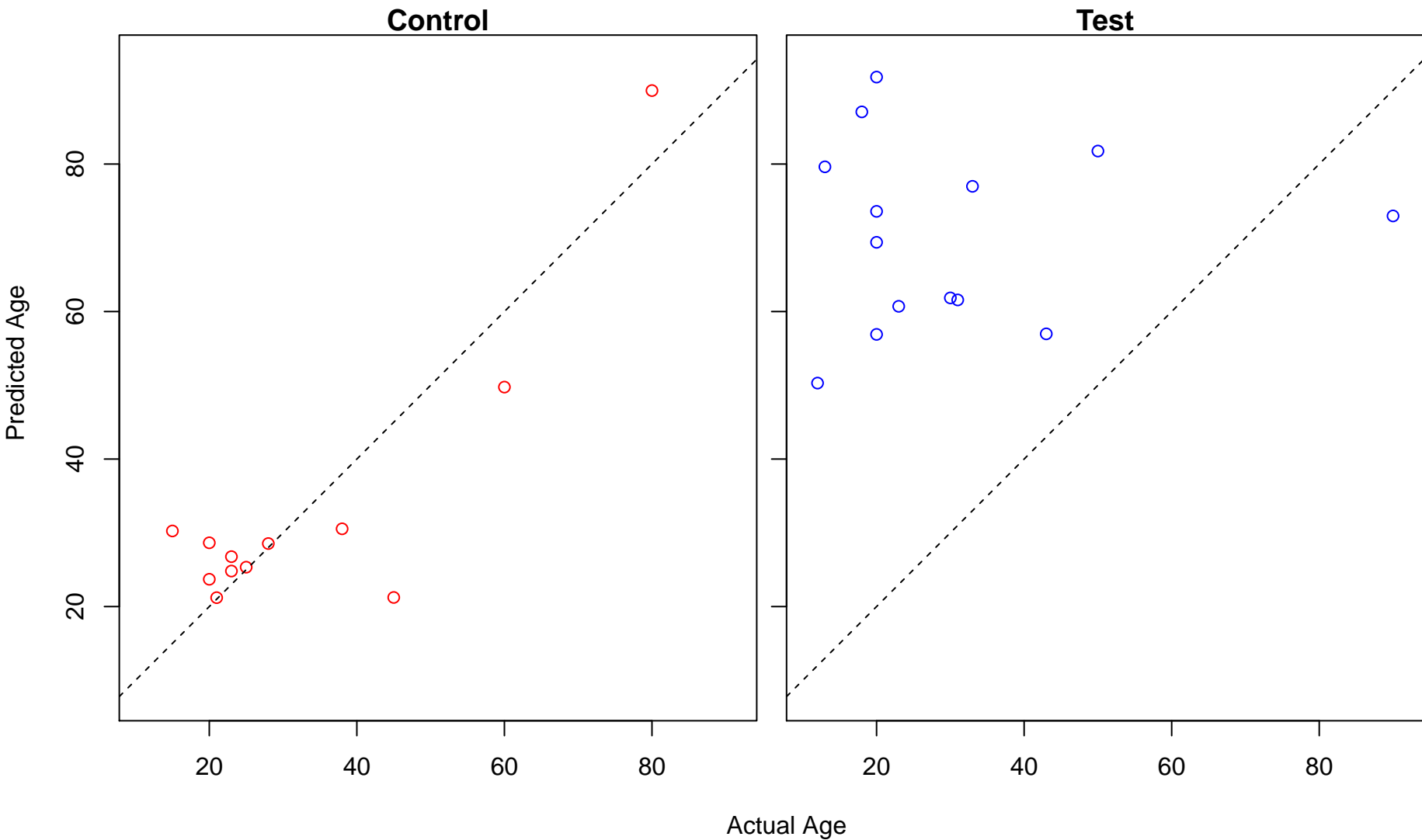
purine nucleotide transport (Score: 7.862513)



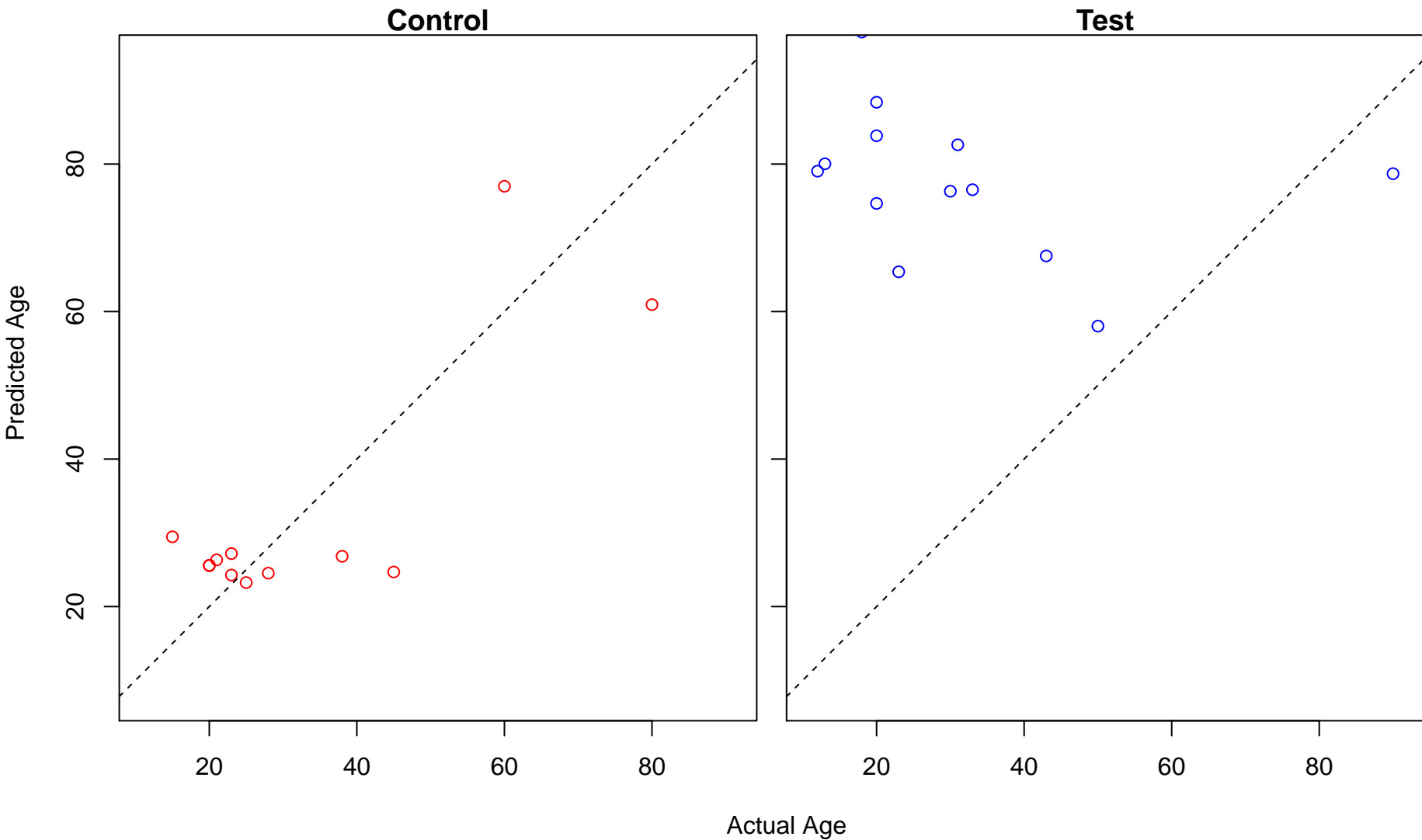
negative regulation of TOR signaling (Score: 7.855082)



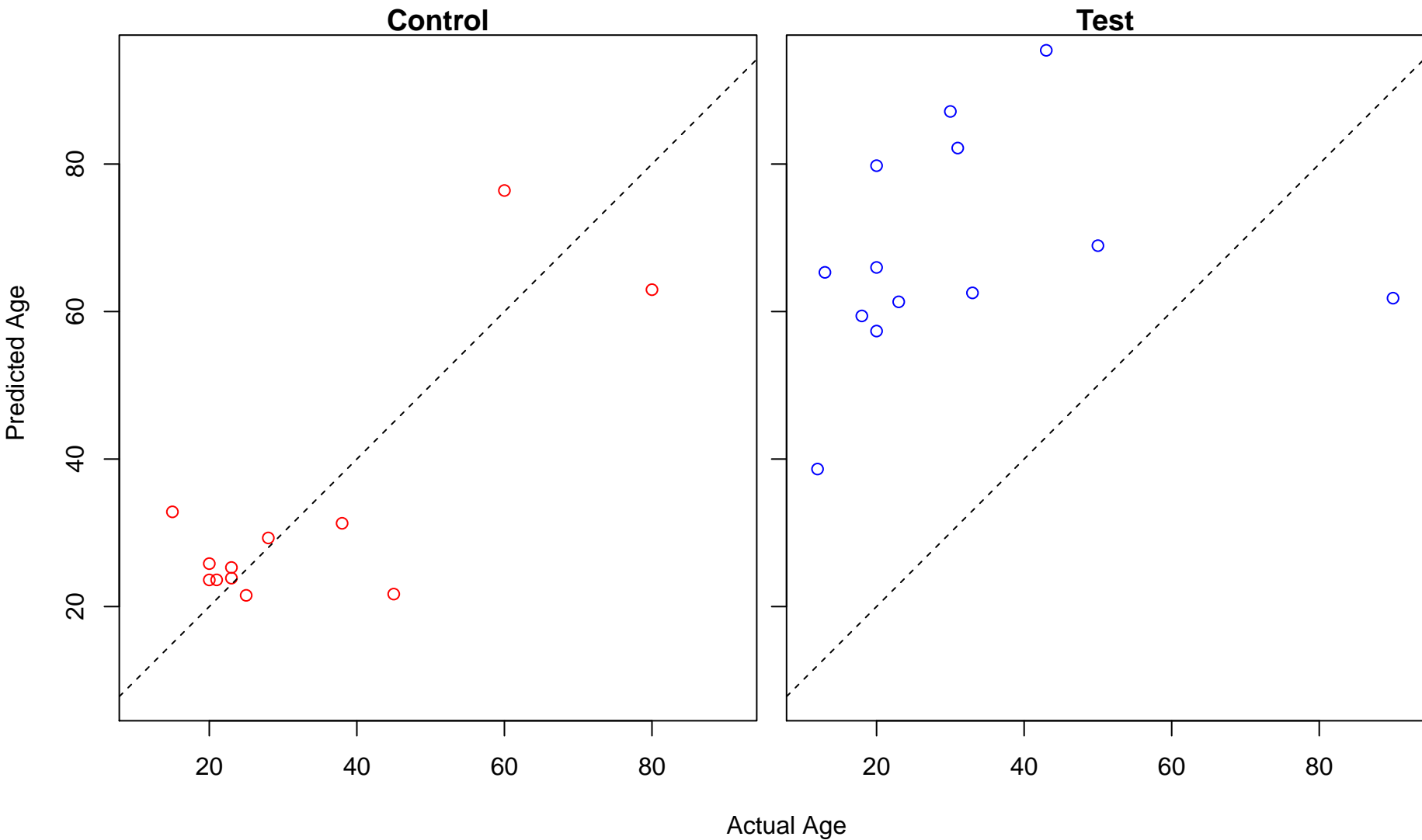
positive regulation of histone acetylation (Score: 7.852989)



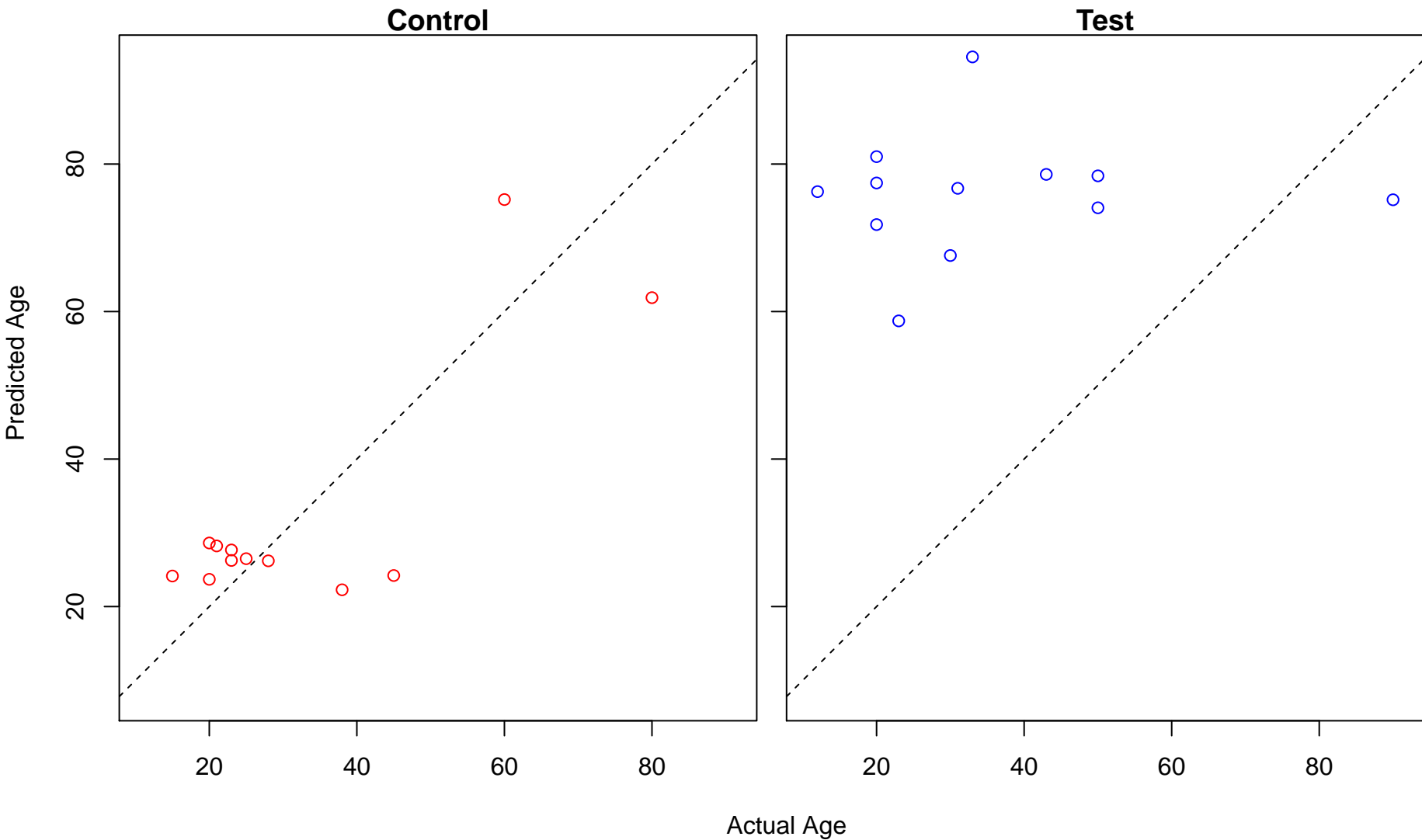
epithelial cell proliferation (Score: 7.850484)



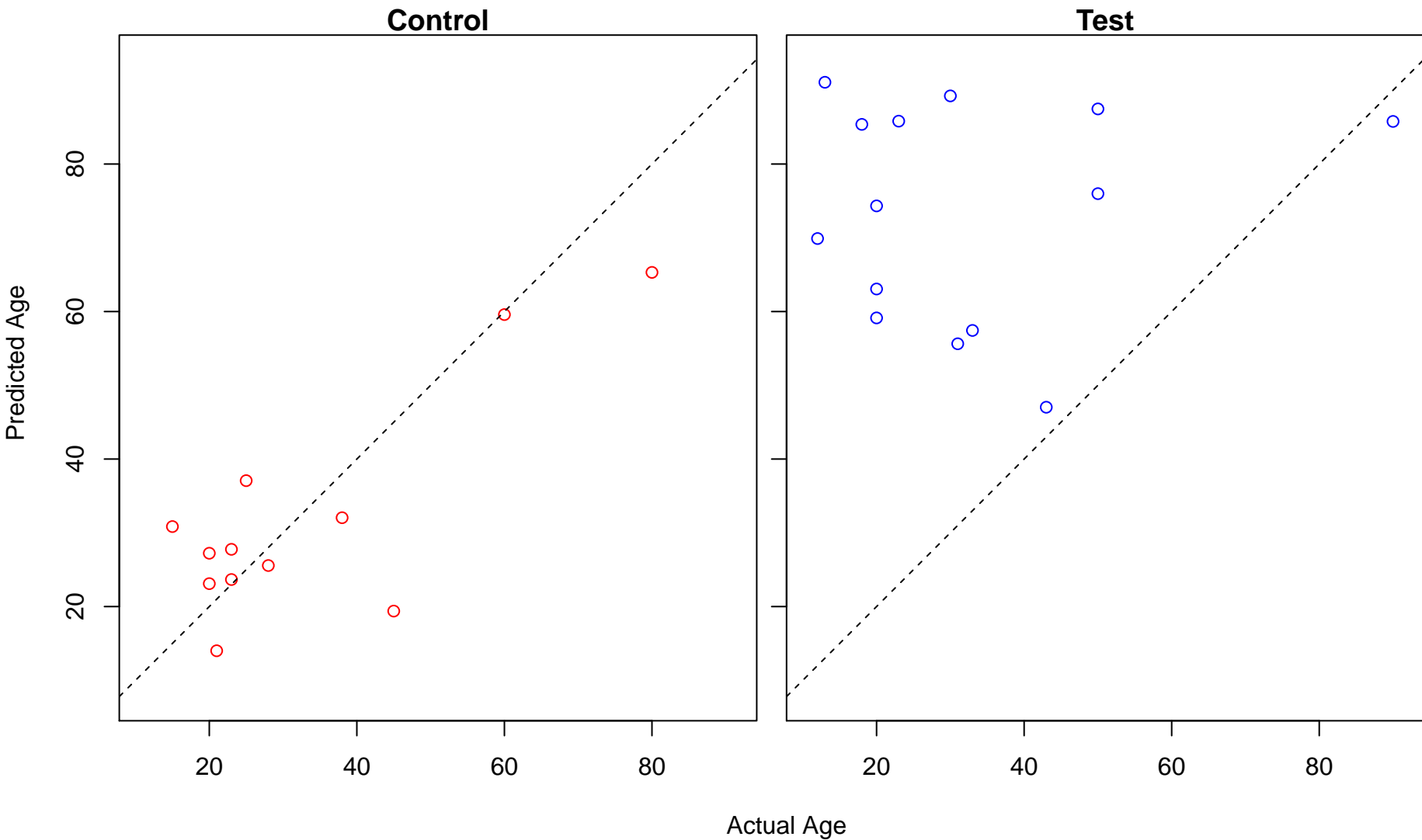
glucosamine-containing compound metabolic process (Score: 7.849696)



L-kynurenine metabolic process (Score: 7.849549)

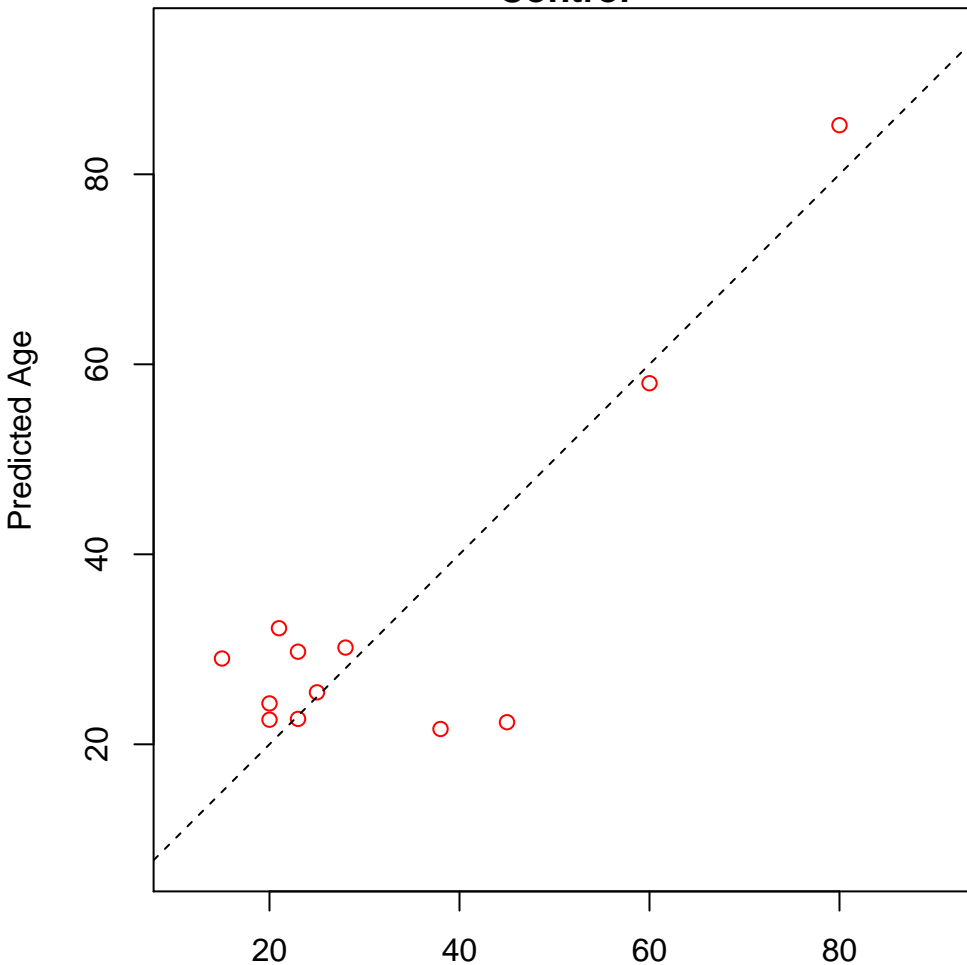


negative regulation of catenin import into nucleus (Score: 7.848558)

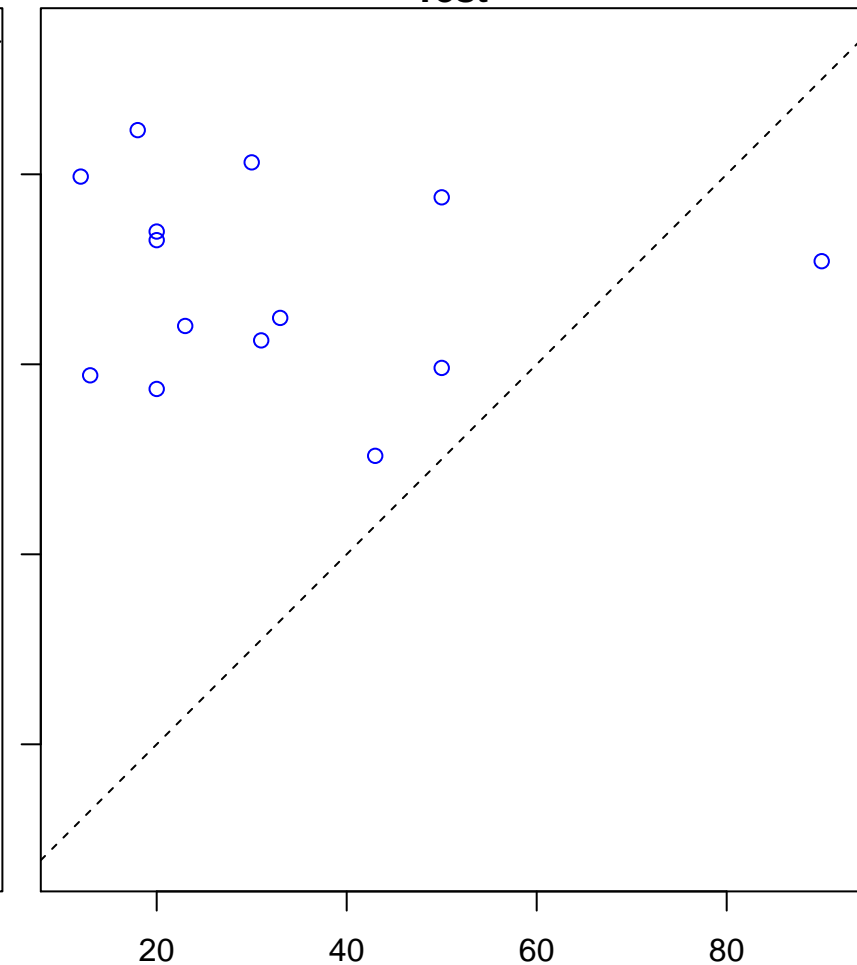


single-organism membrane budding (Score: 7.838243)

Control

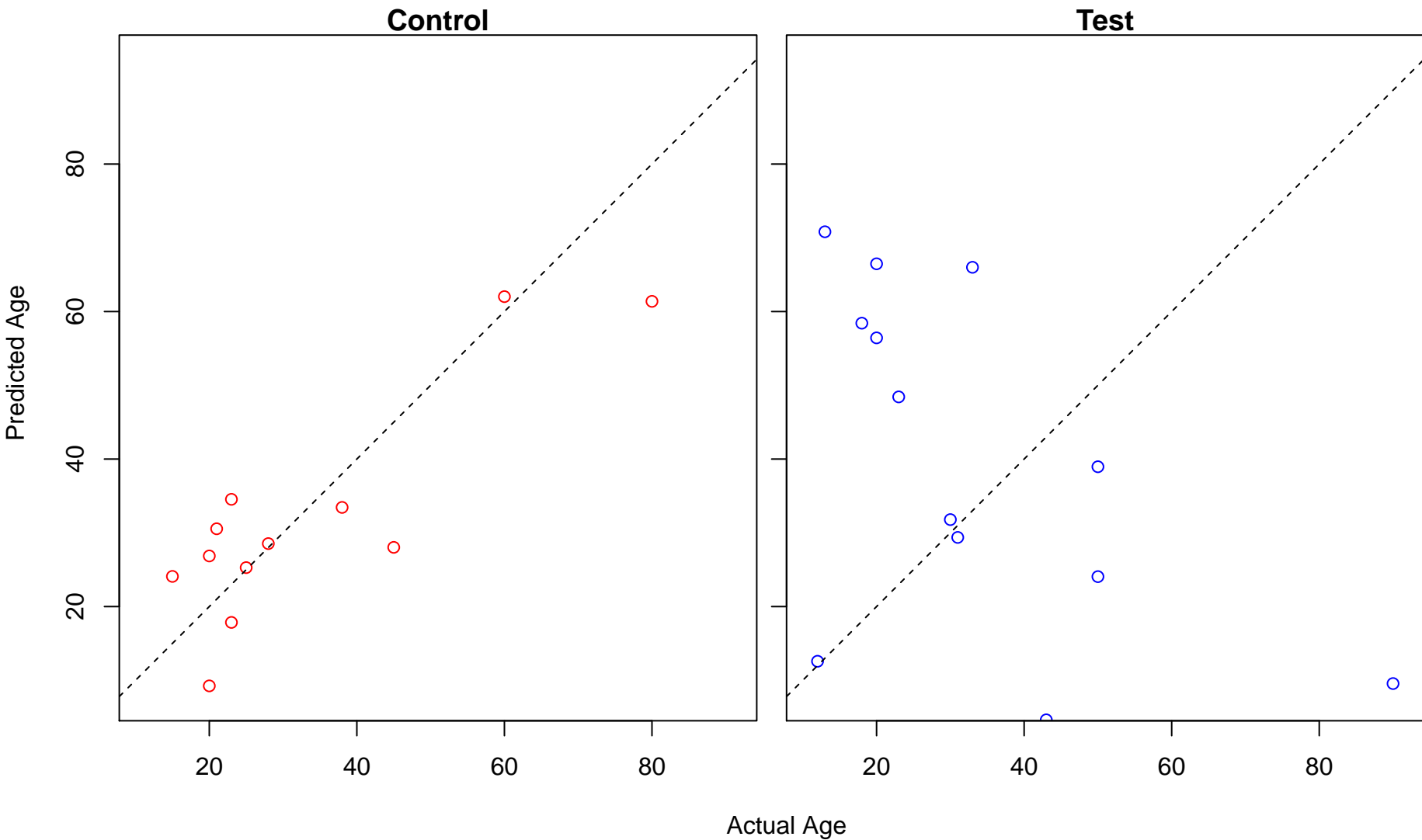


Test

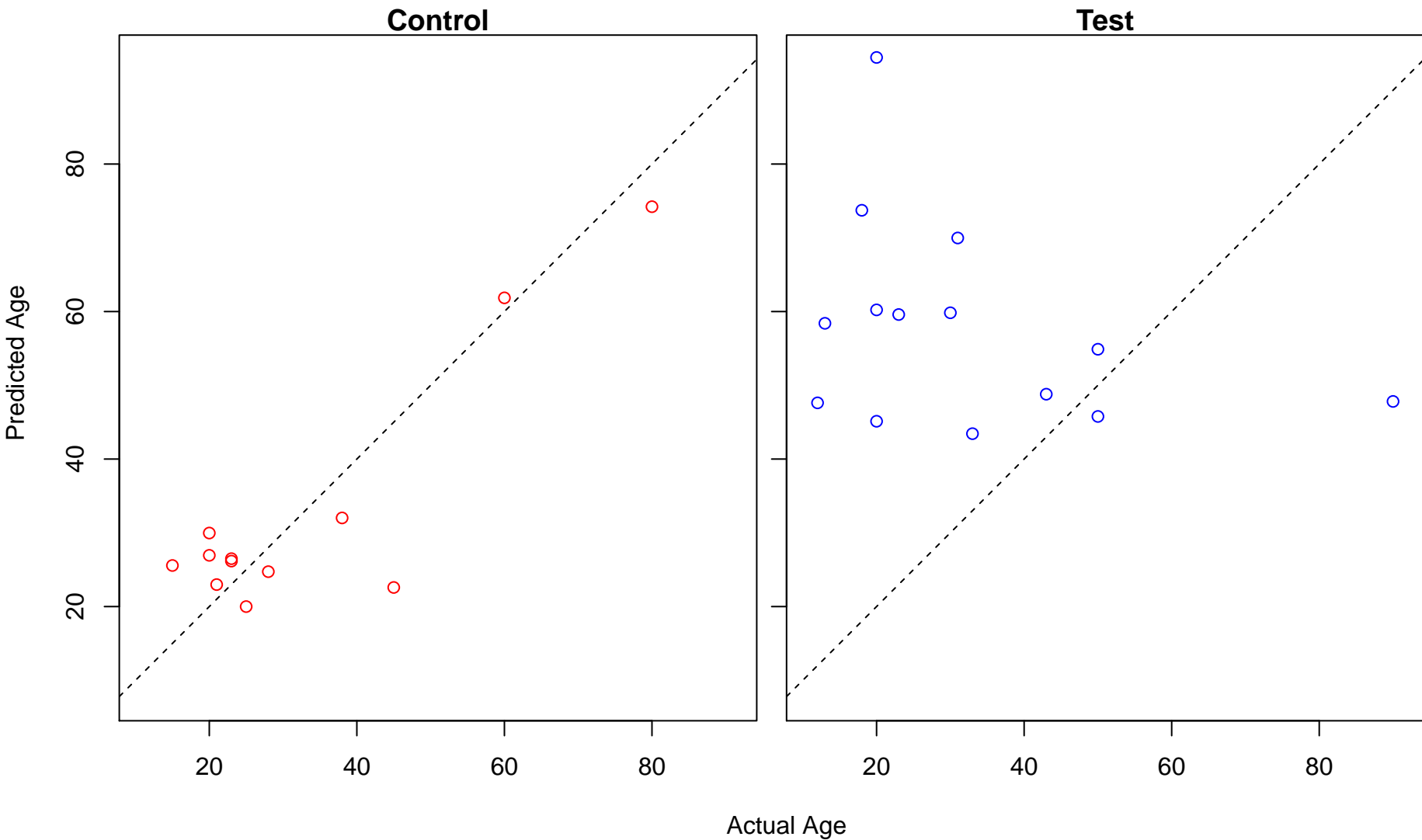


Actual Age

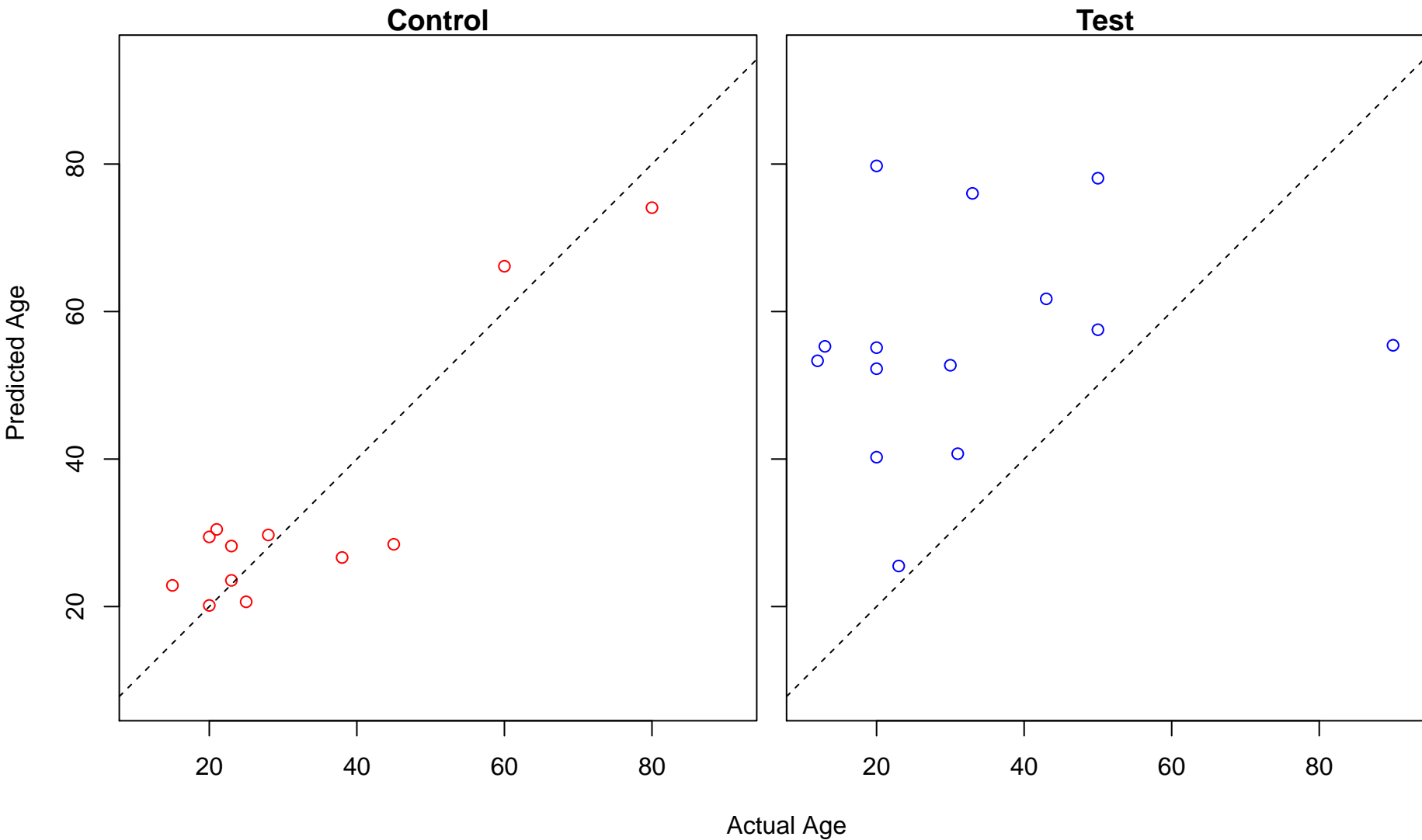
positive regulation of transporter activity (Score: 7.83172)



regulation of transcription involved in G1/S transition of mitotic cell cycle (Score: 7.831444)

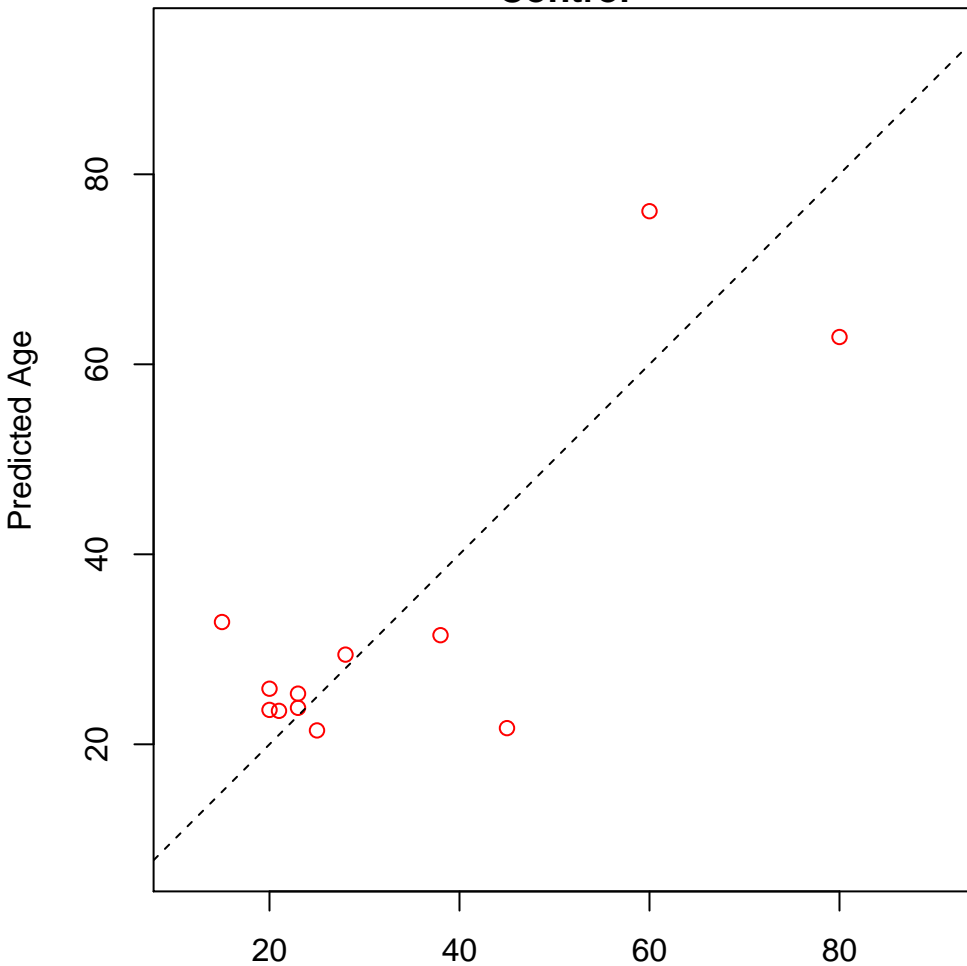


apoptotic mitochondrial changes (Score: 7.829956)

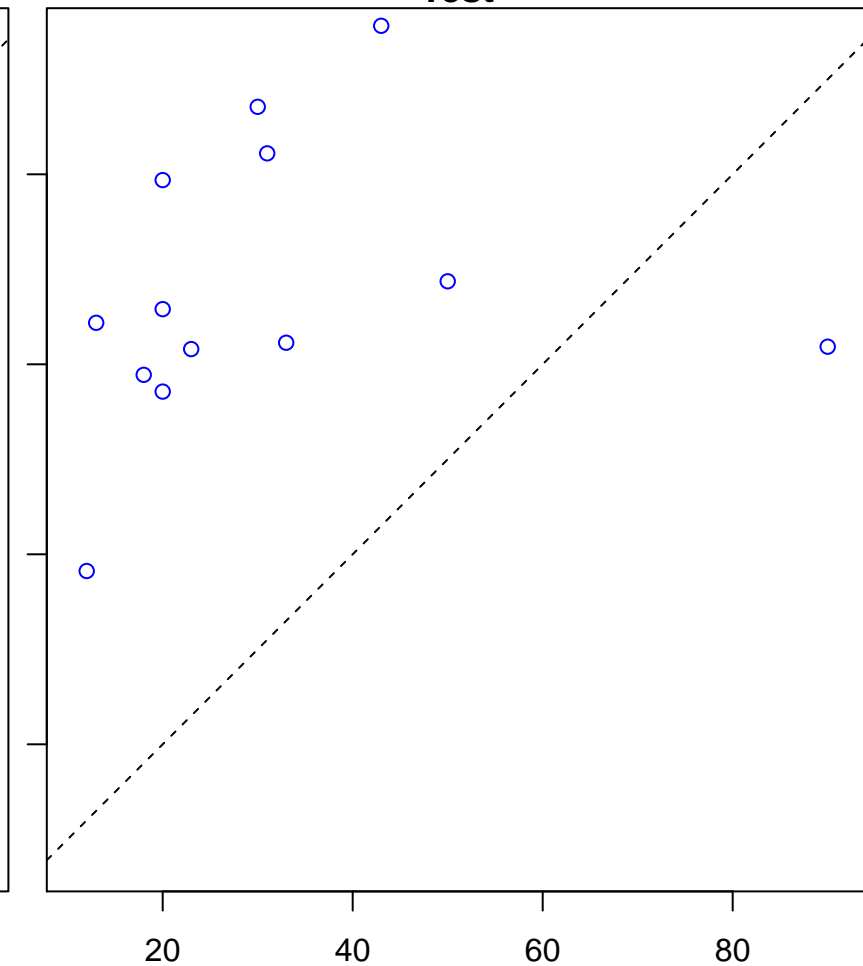


N-acetylglucosamine metabolic process (Score: 7.829315)

Control

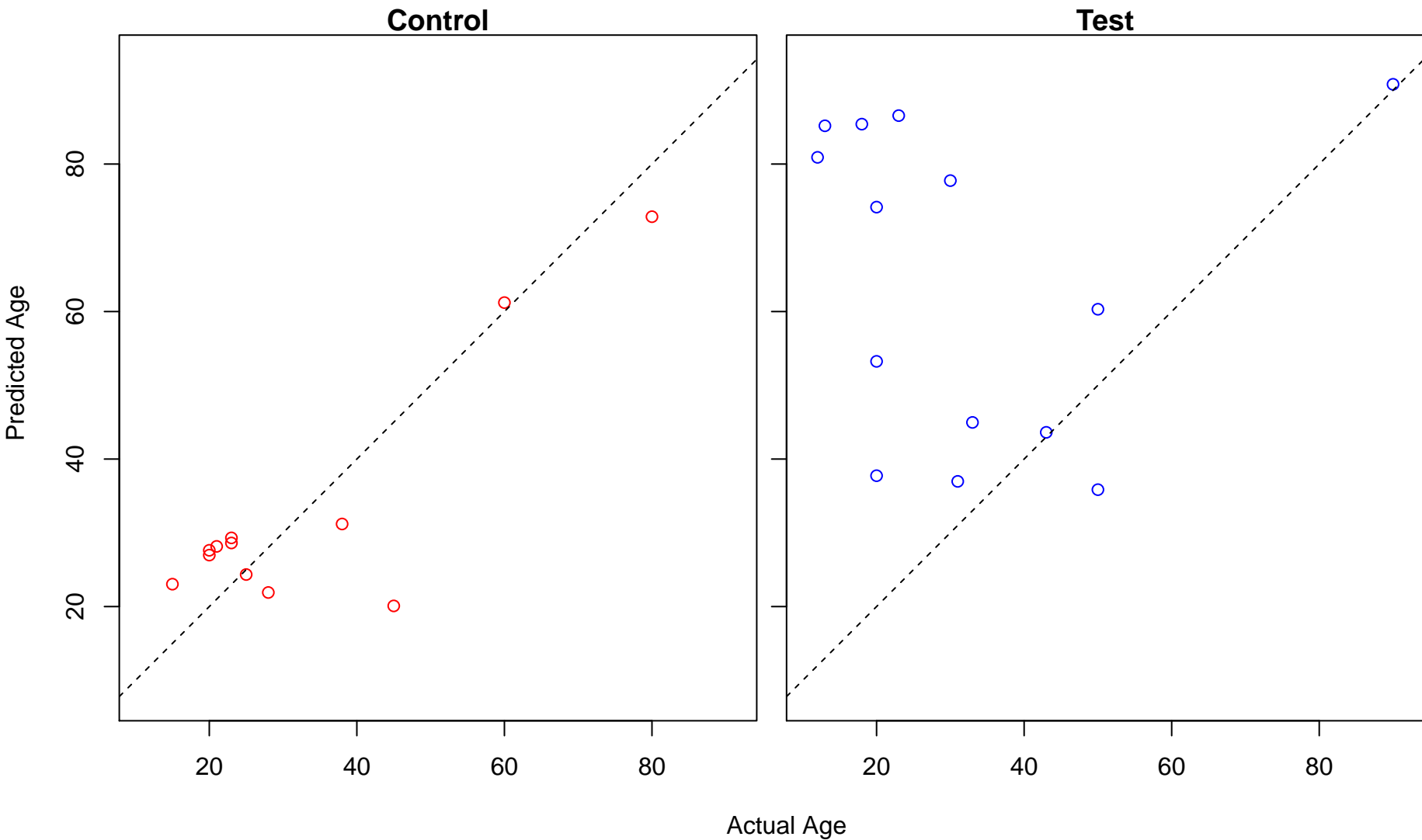


Test

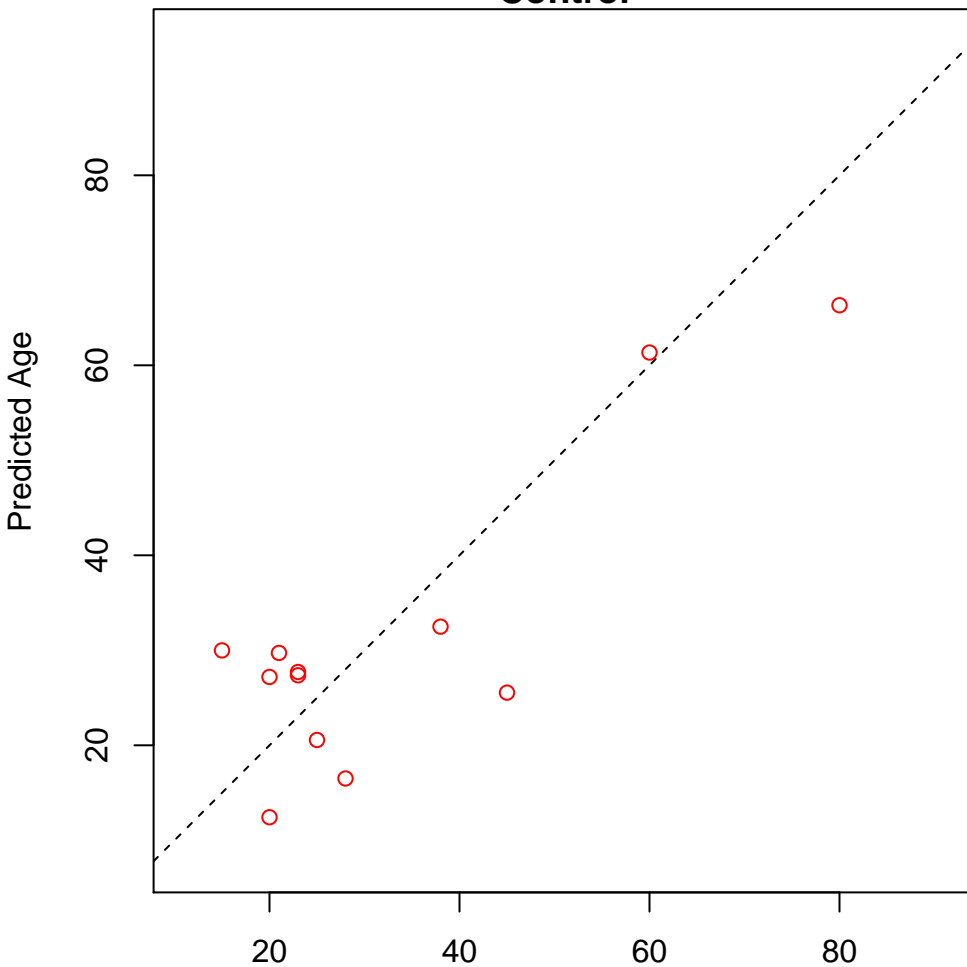


Actual Age

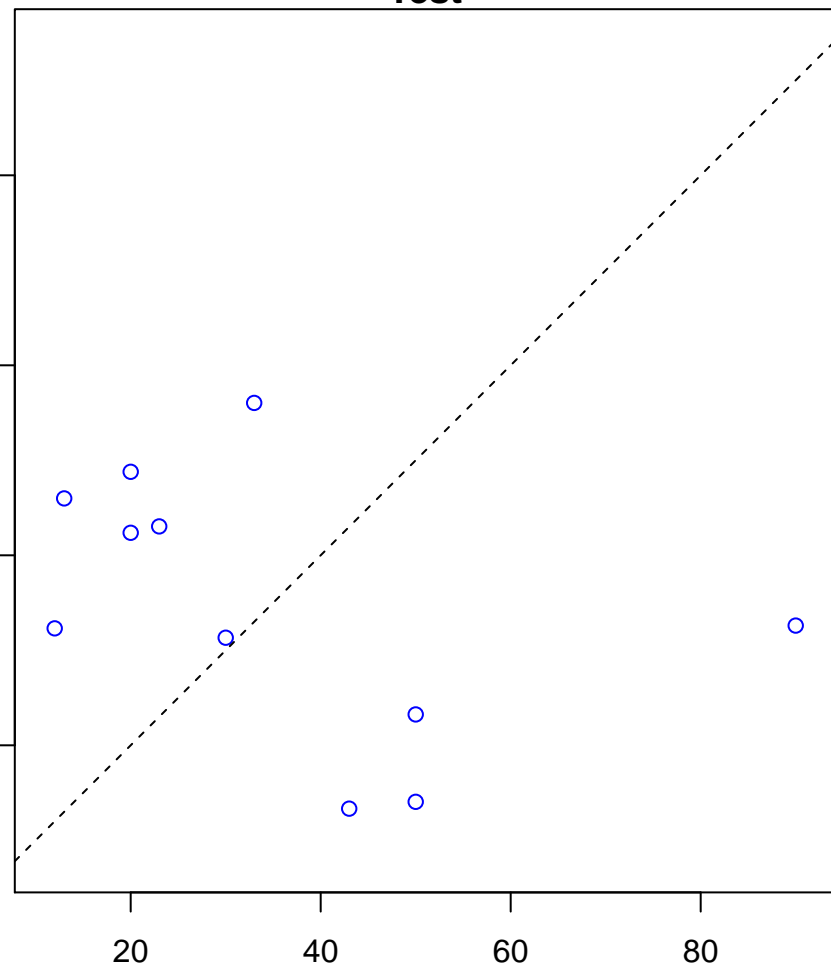
positive regulation of chemokine secretion (Score: 7.828783)



Control

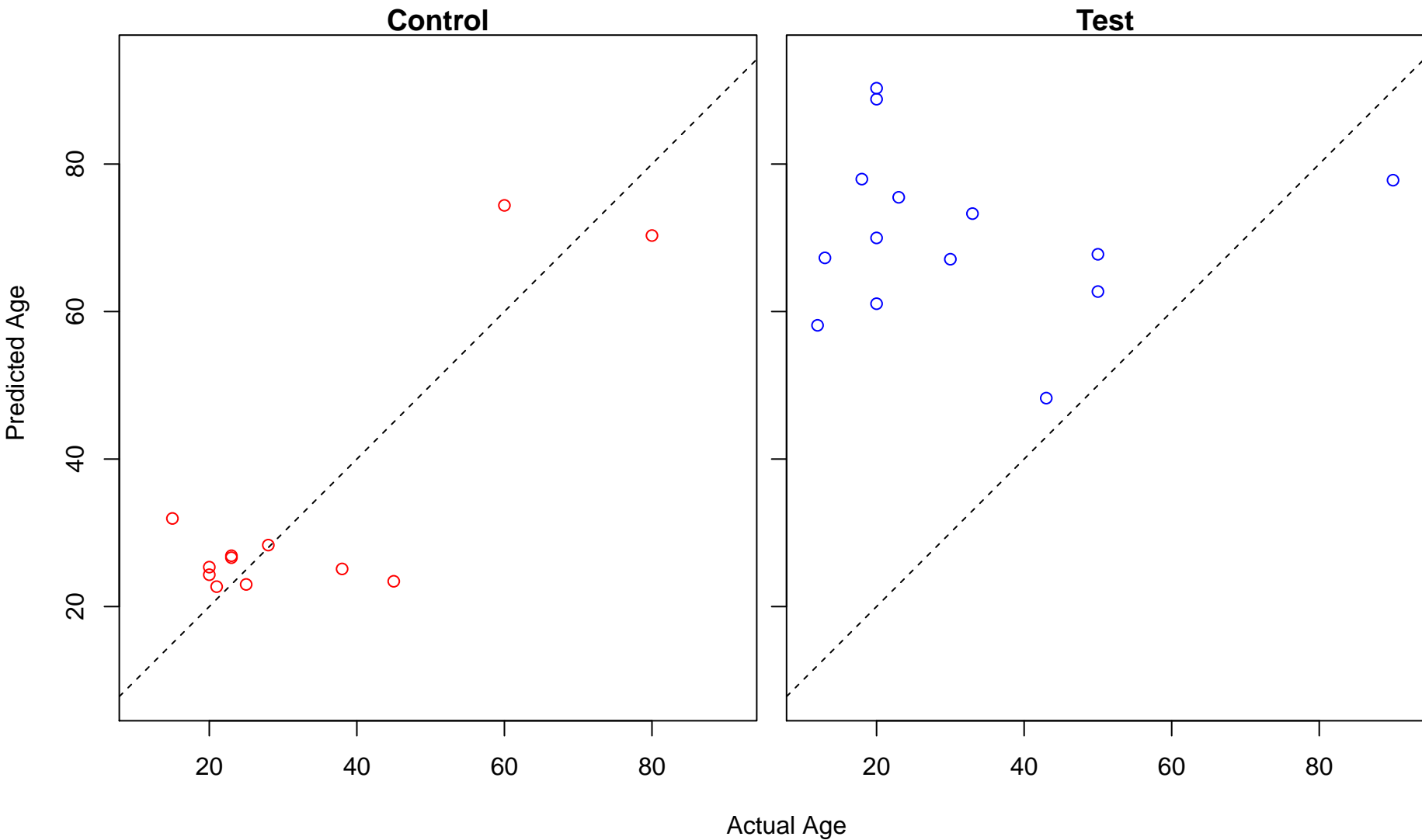


Test

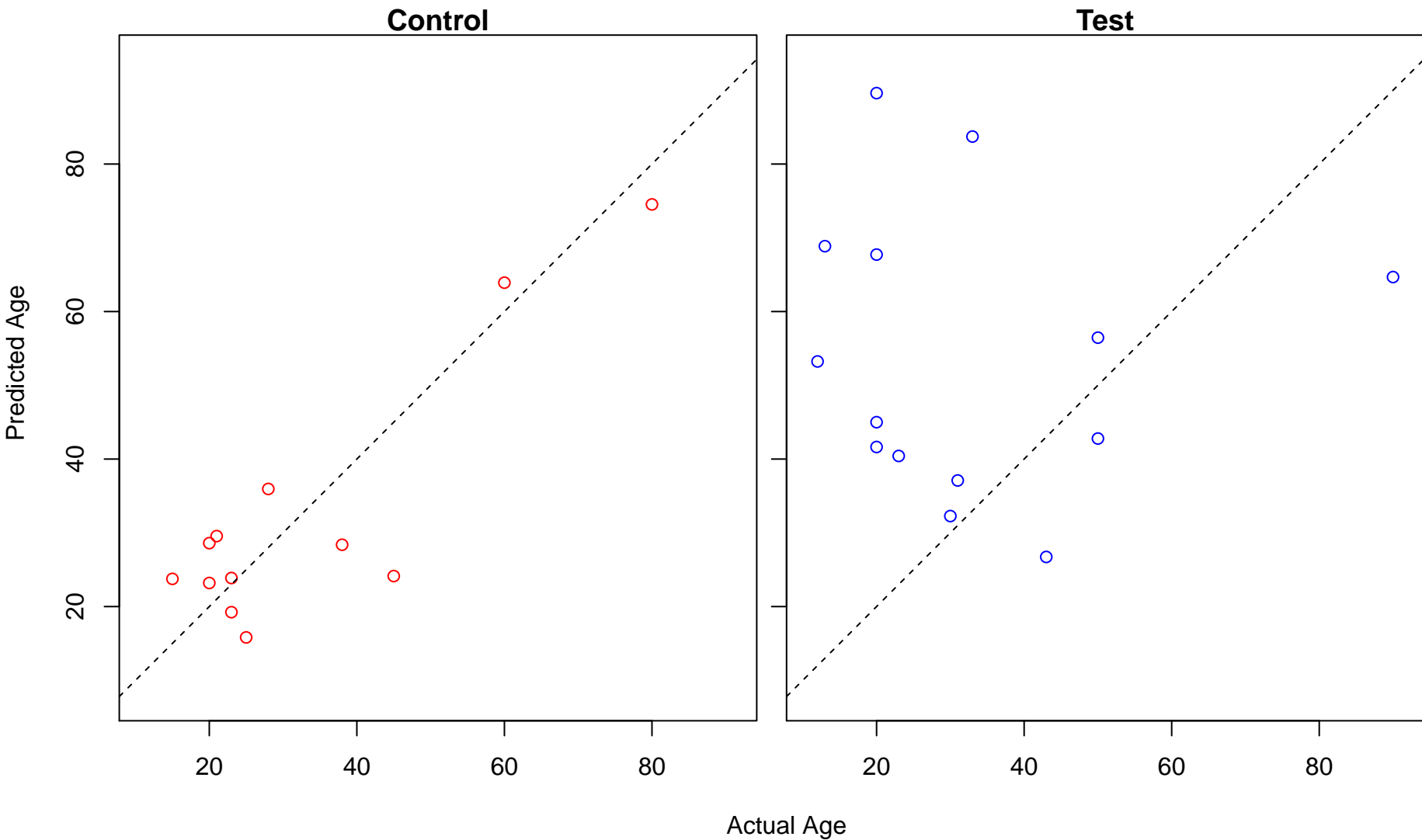


Actual Age

negative regulation of protein localization to nucleus (Score: 7.822620)

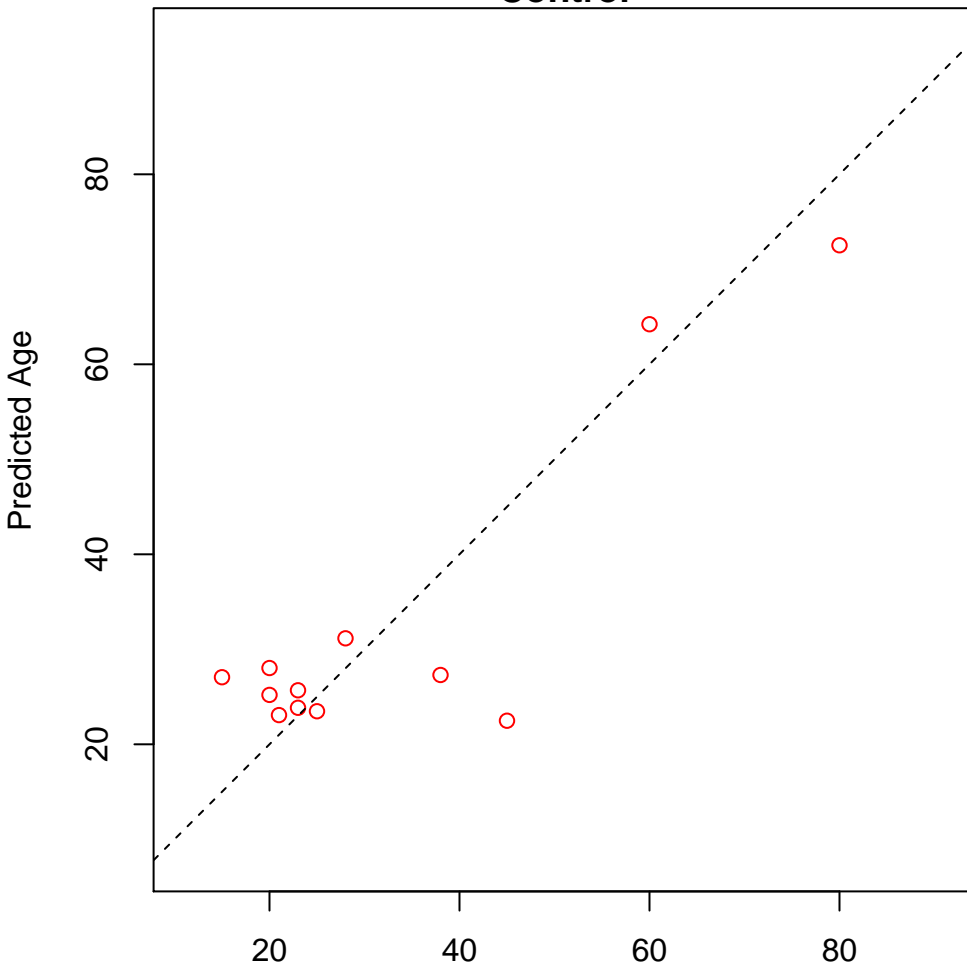


negative regulation of cellular protein localization (Score: 7.818680)

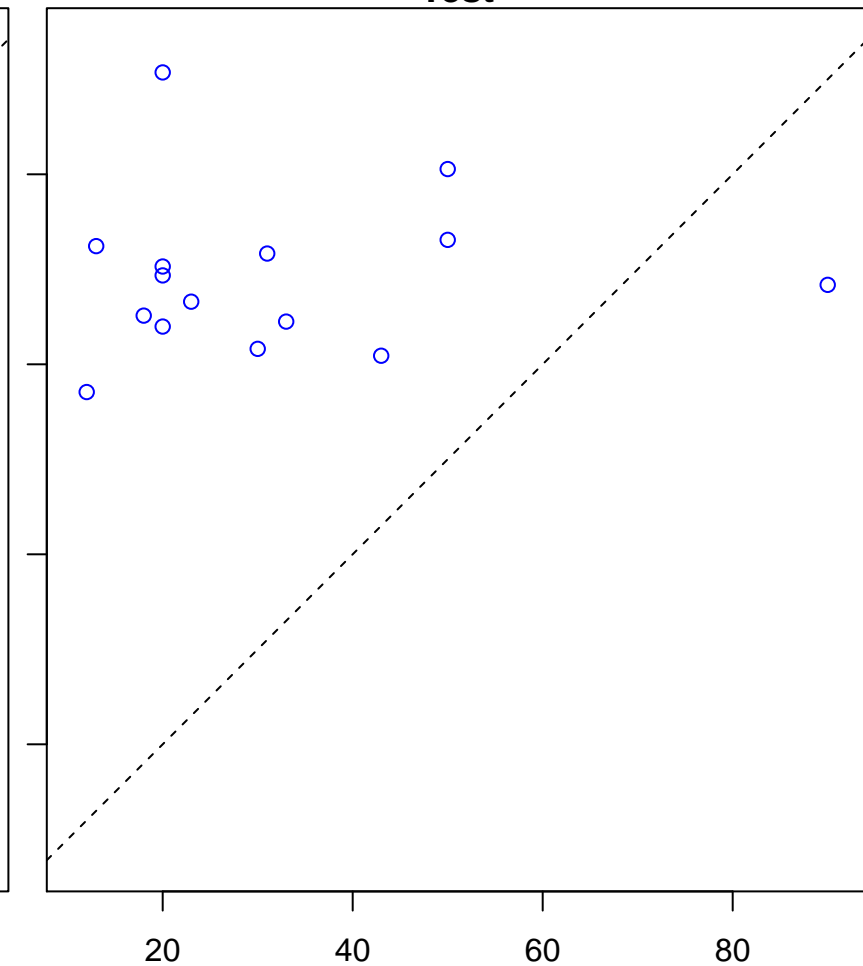


cellular response to glucagon stimulus (Score: 7.816884)

Control

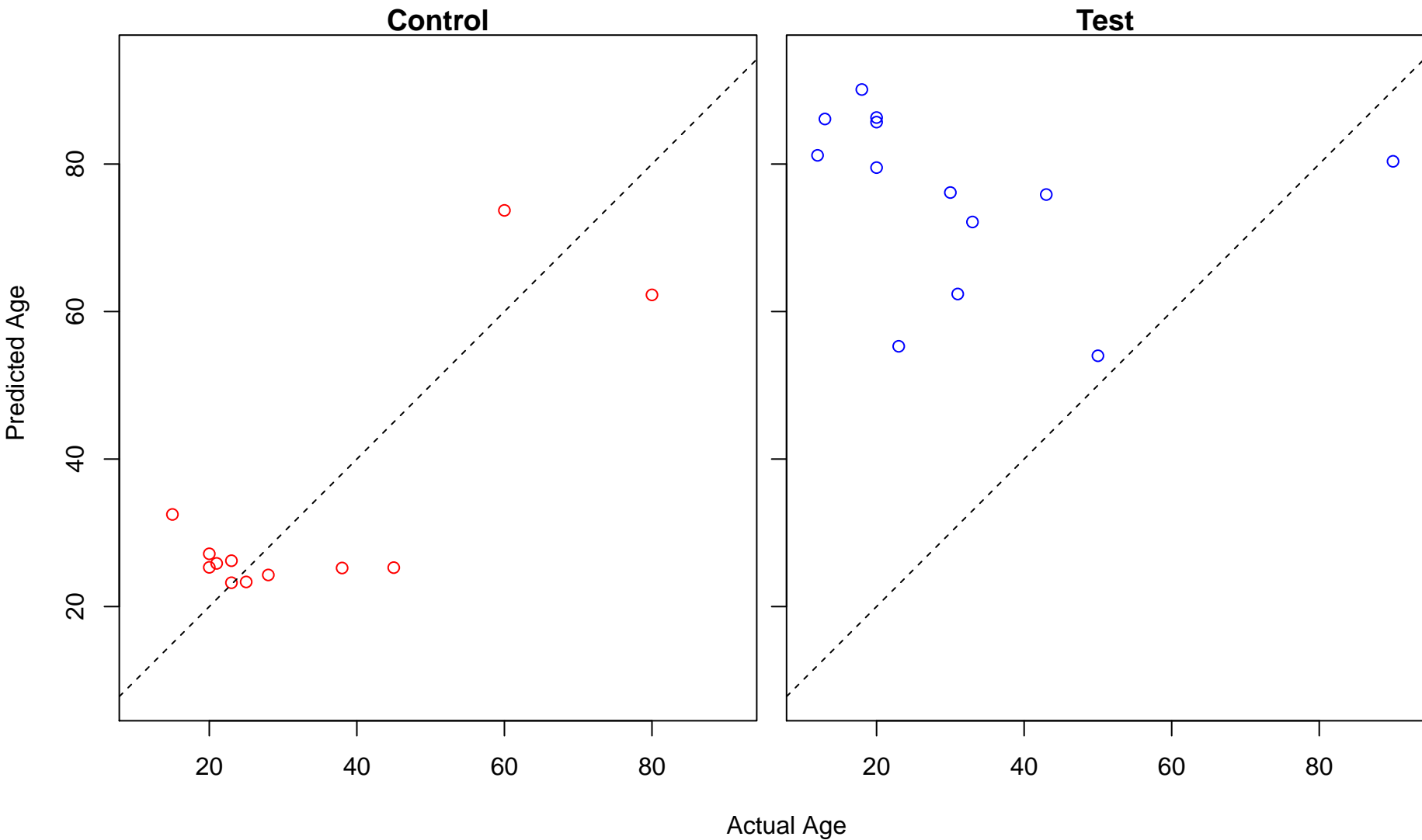


Test

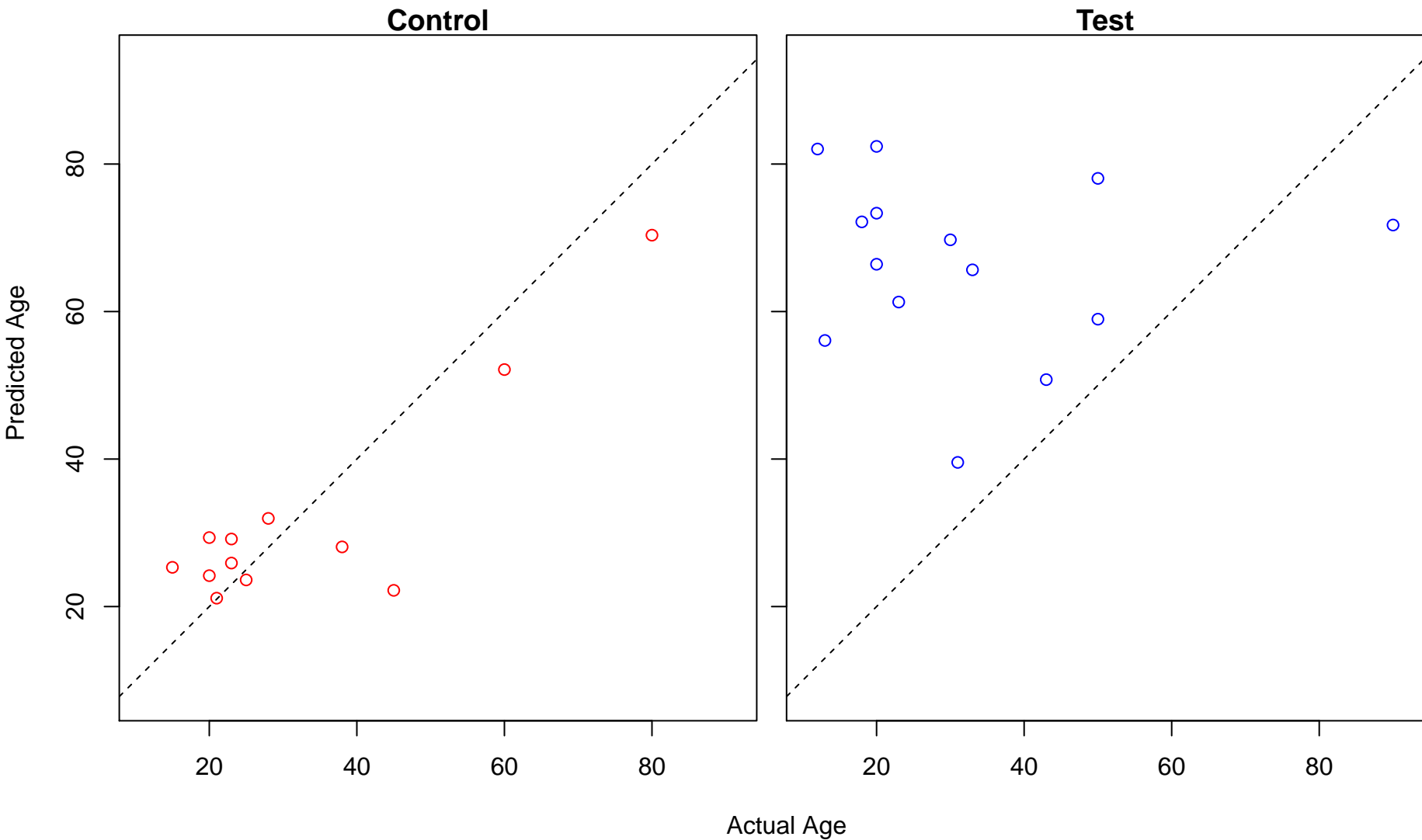


Actual Age

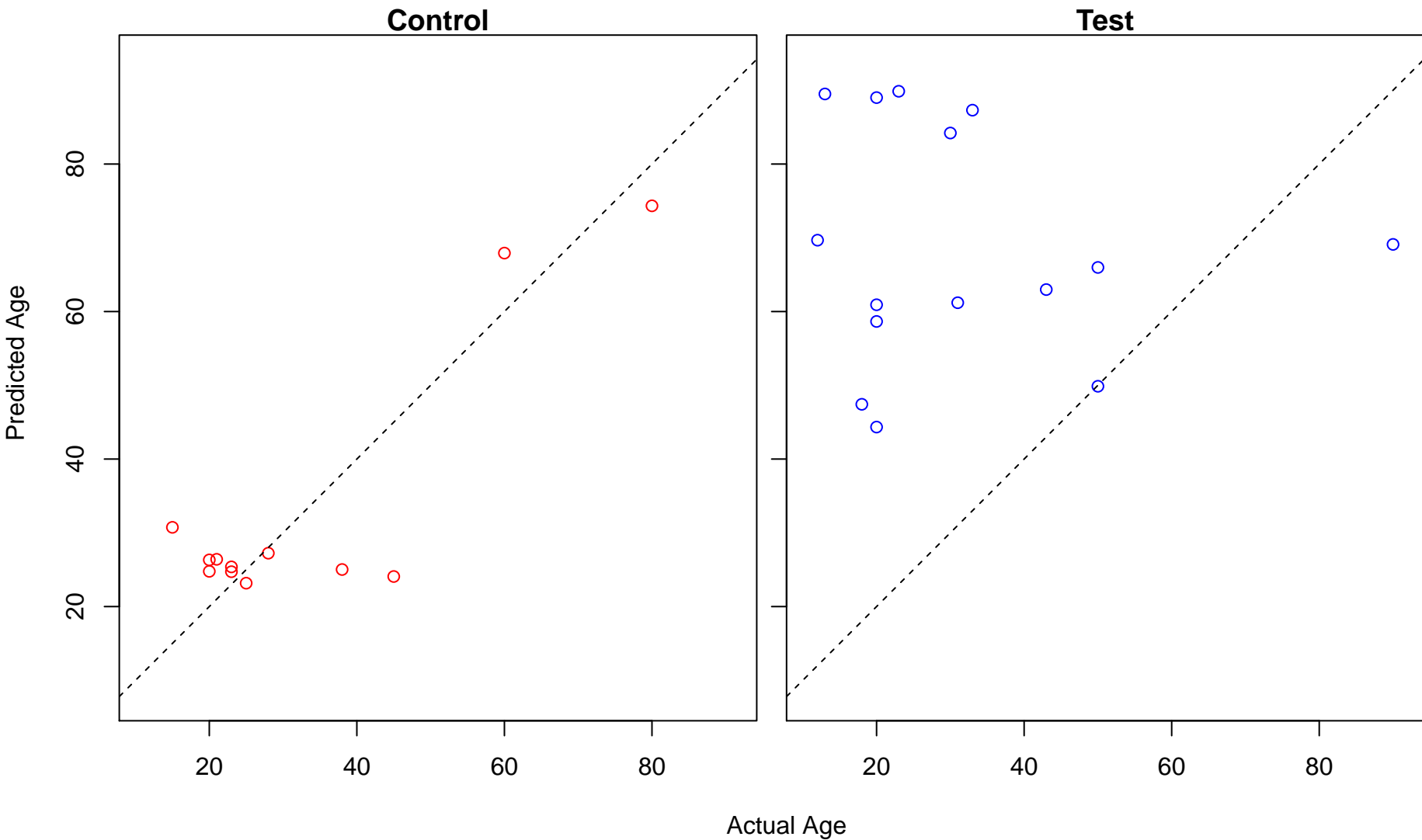
regulation of MHC class II biosynthetic process (Score: 7.816193)



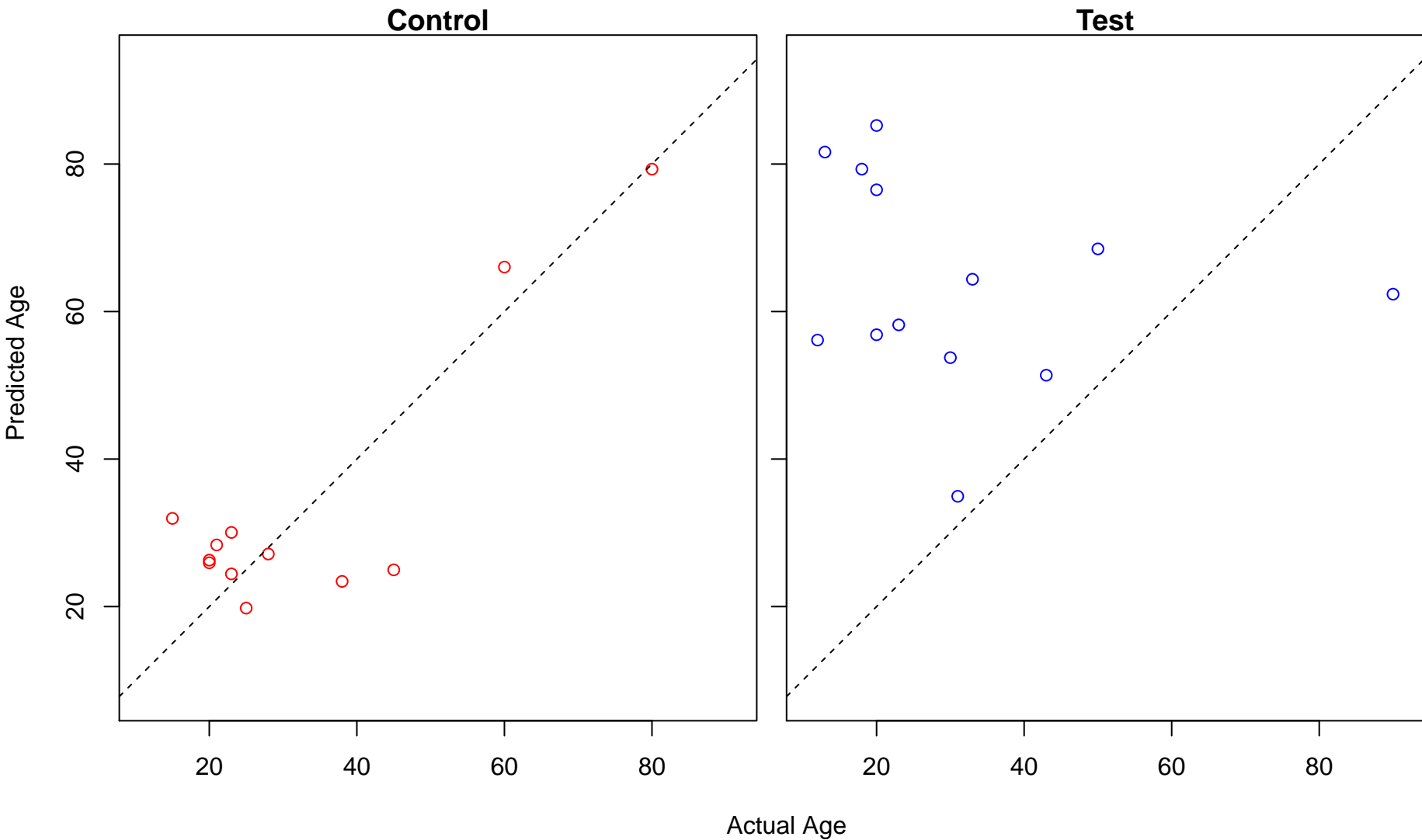
neural crest cell differentiation (Score: 7.813699)



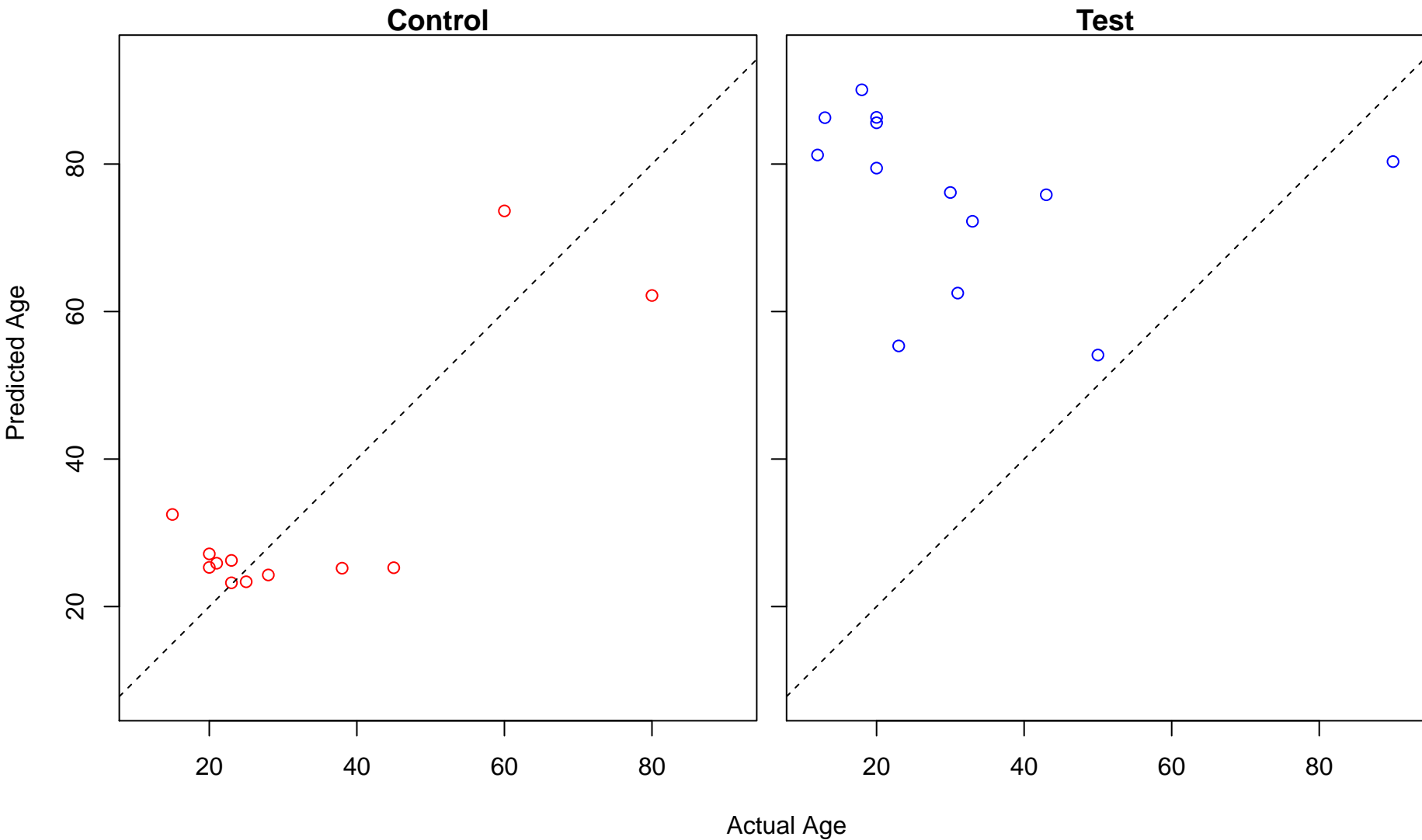
negative regulation of stem cell proliferation (Score: 7.810082)



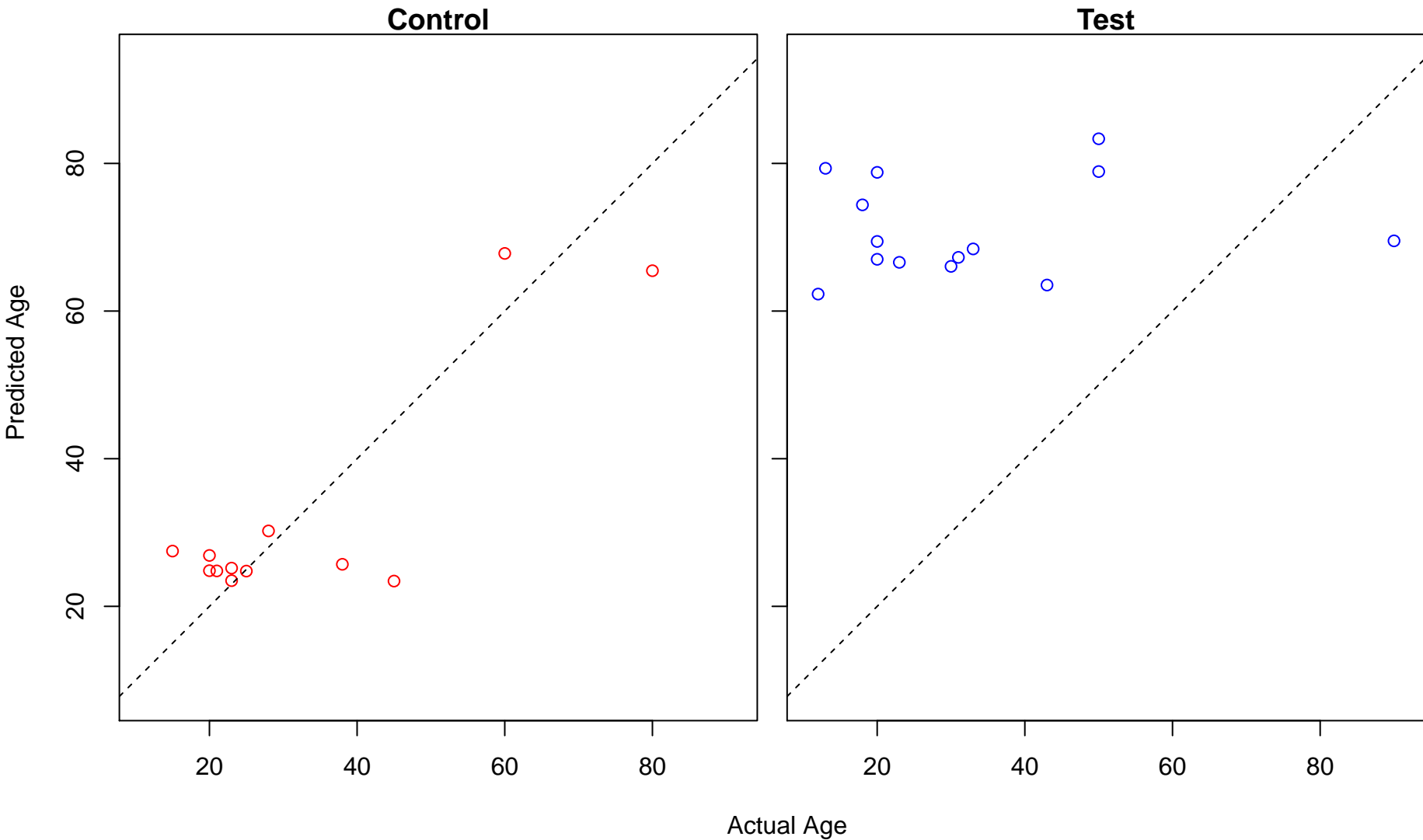
developmental maturation (Score: 7.805467)



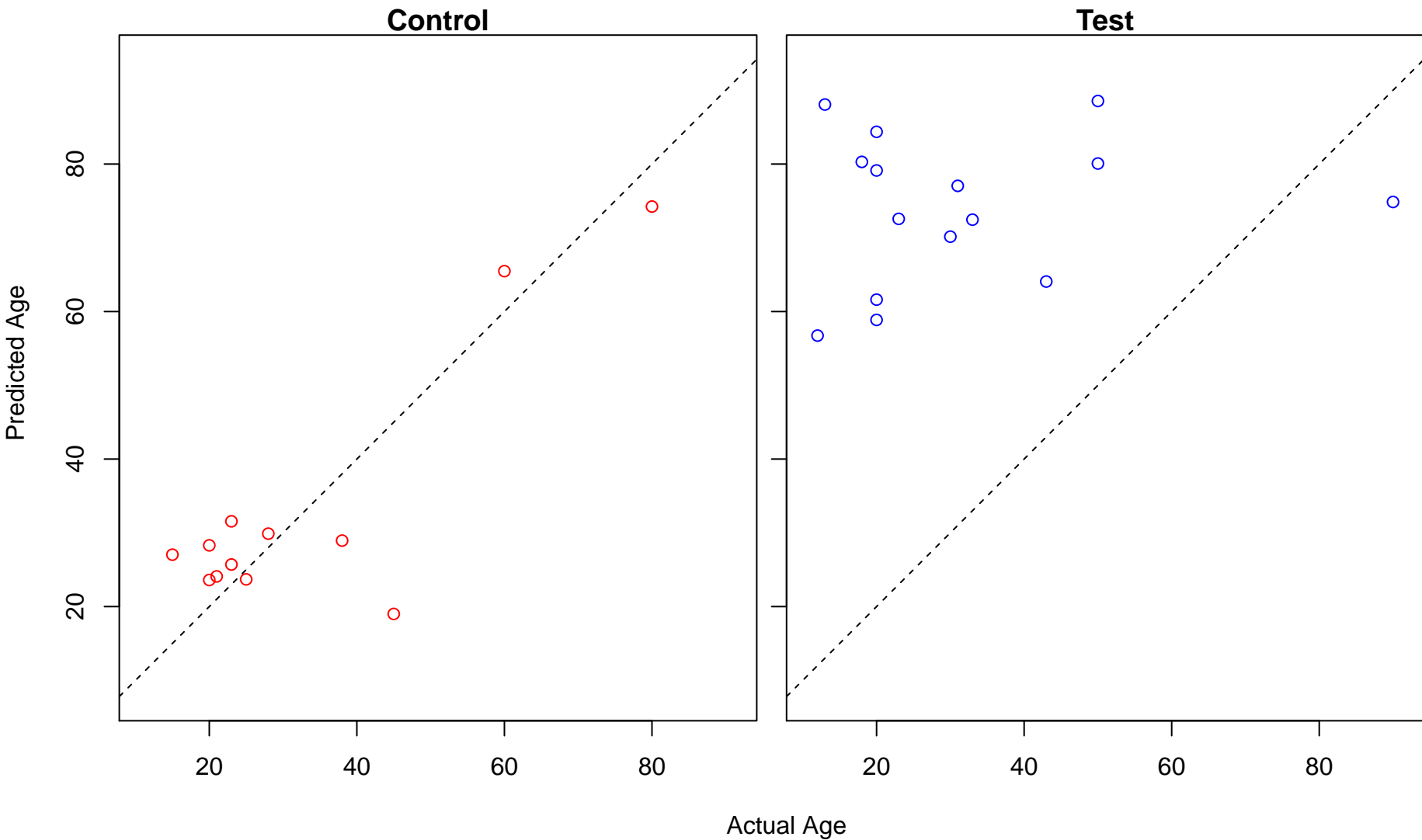
regulation of B cell differentiation (Score: 7.803313)



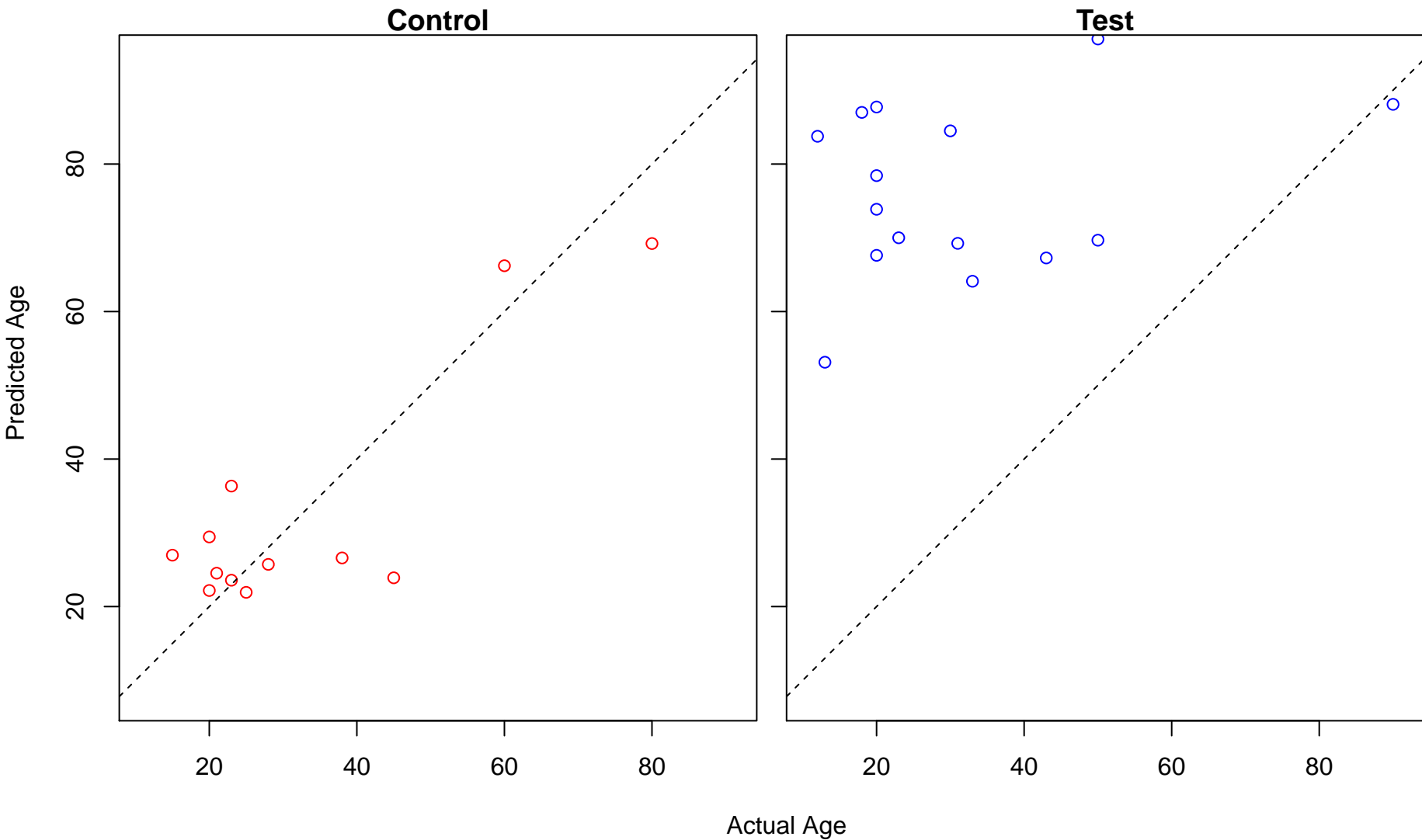
nucleoside phosphate biosynthetic process (Score: 7.803118)



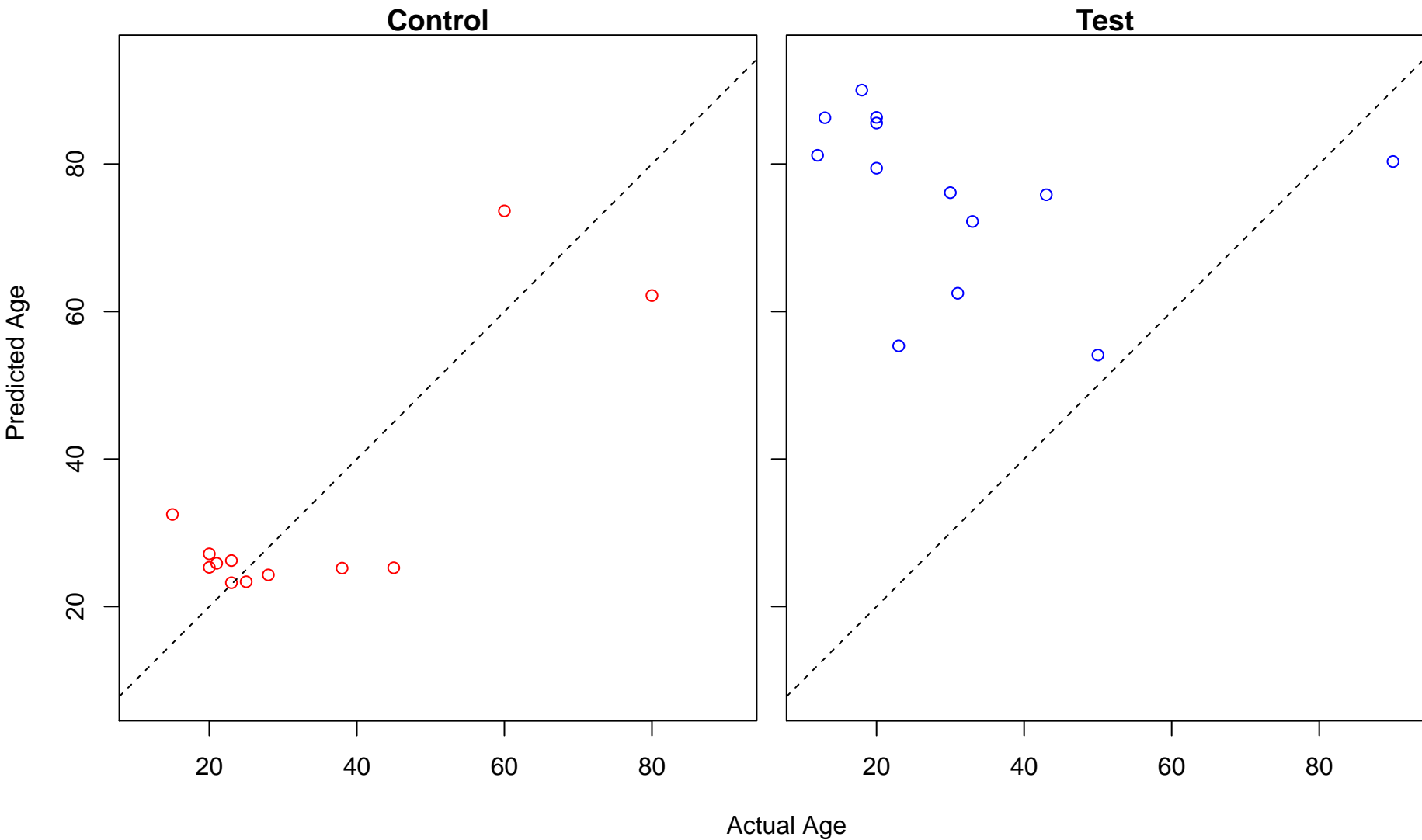
negative regulation of immune system process (Score: 7.799708)



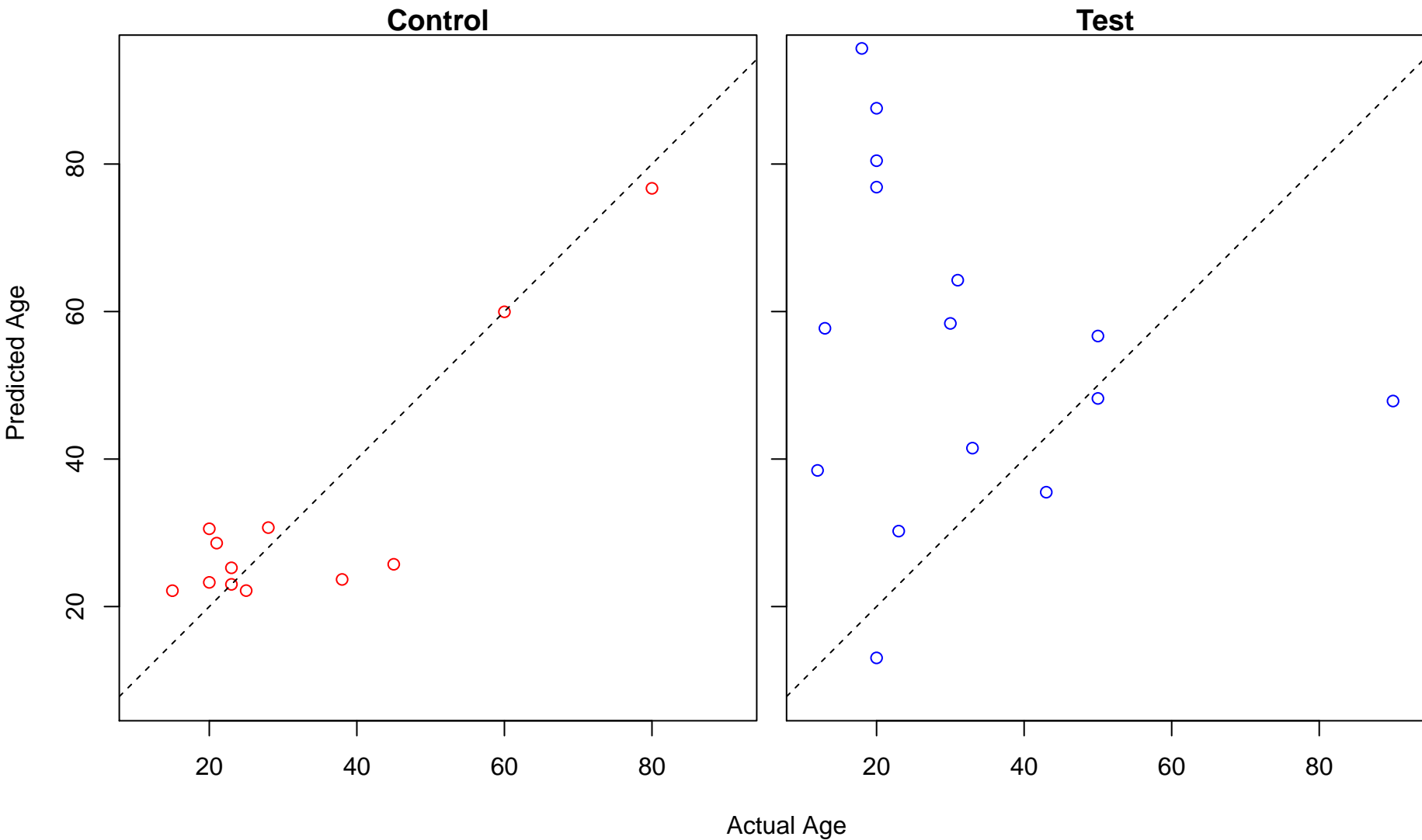
response to interleukin-1 (Score: 7.799313)



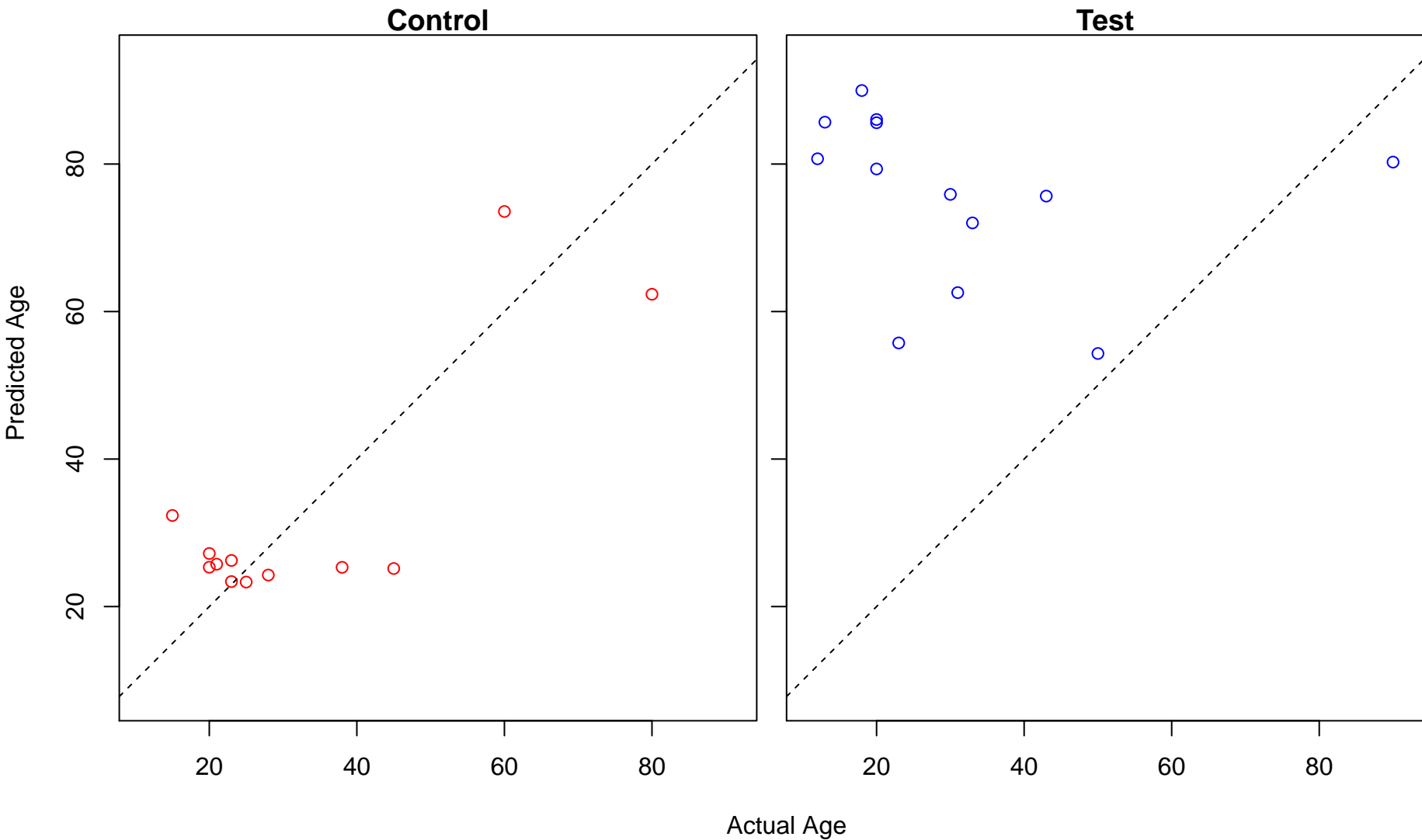
positive regulation of B cell differentiation (Score: 7.794438)



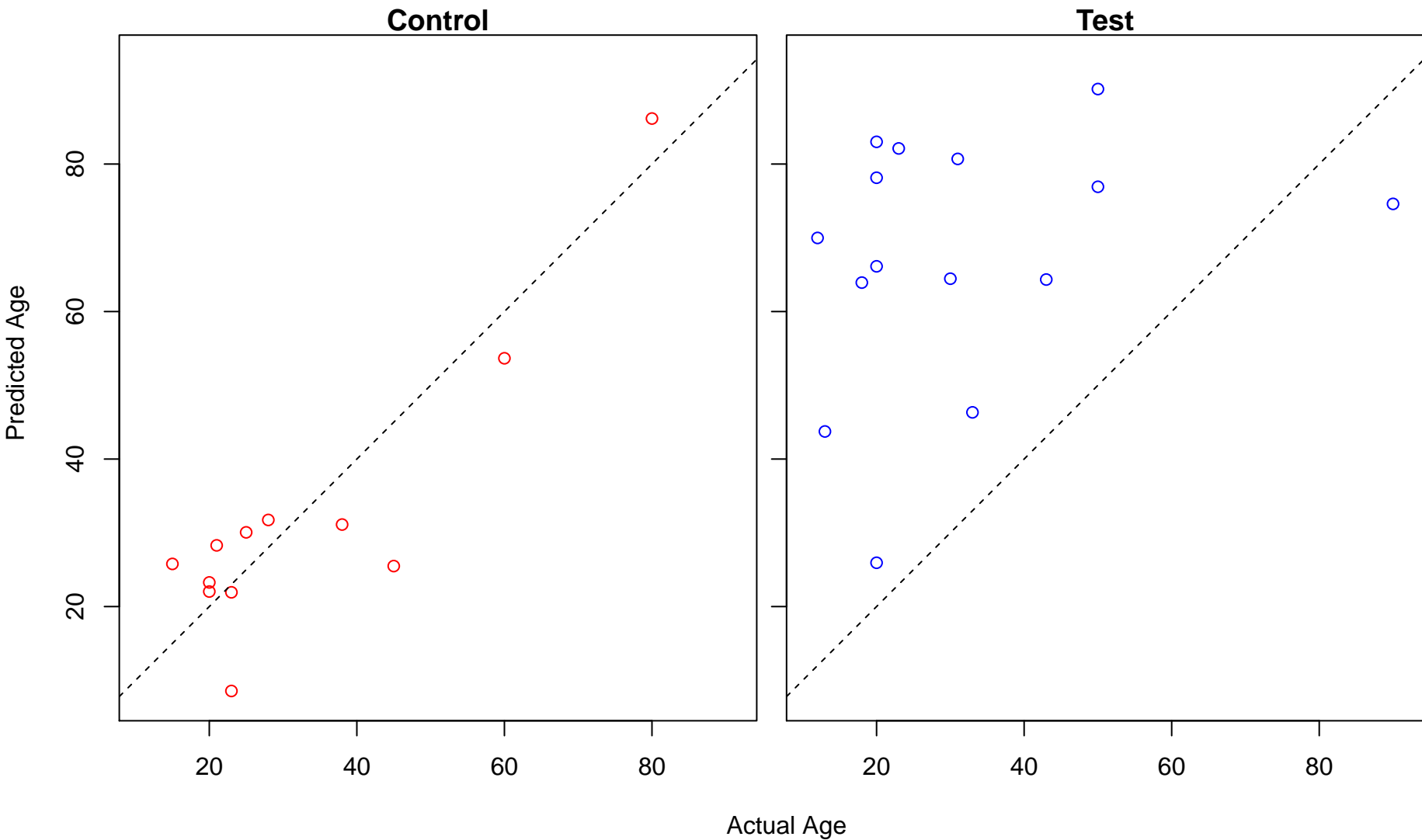
single-organism behavior (Score: 7.789112)



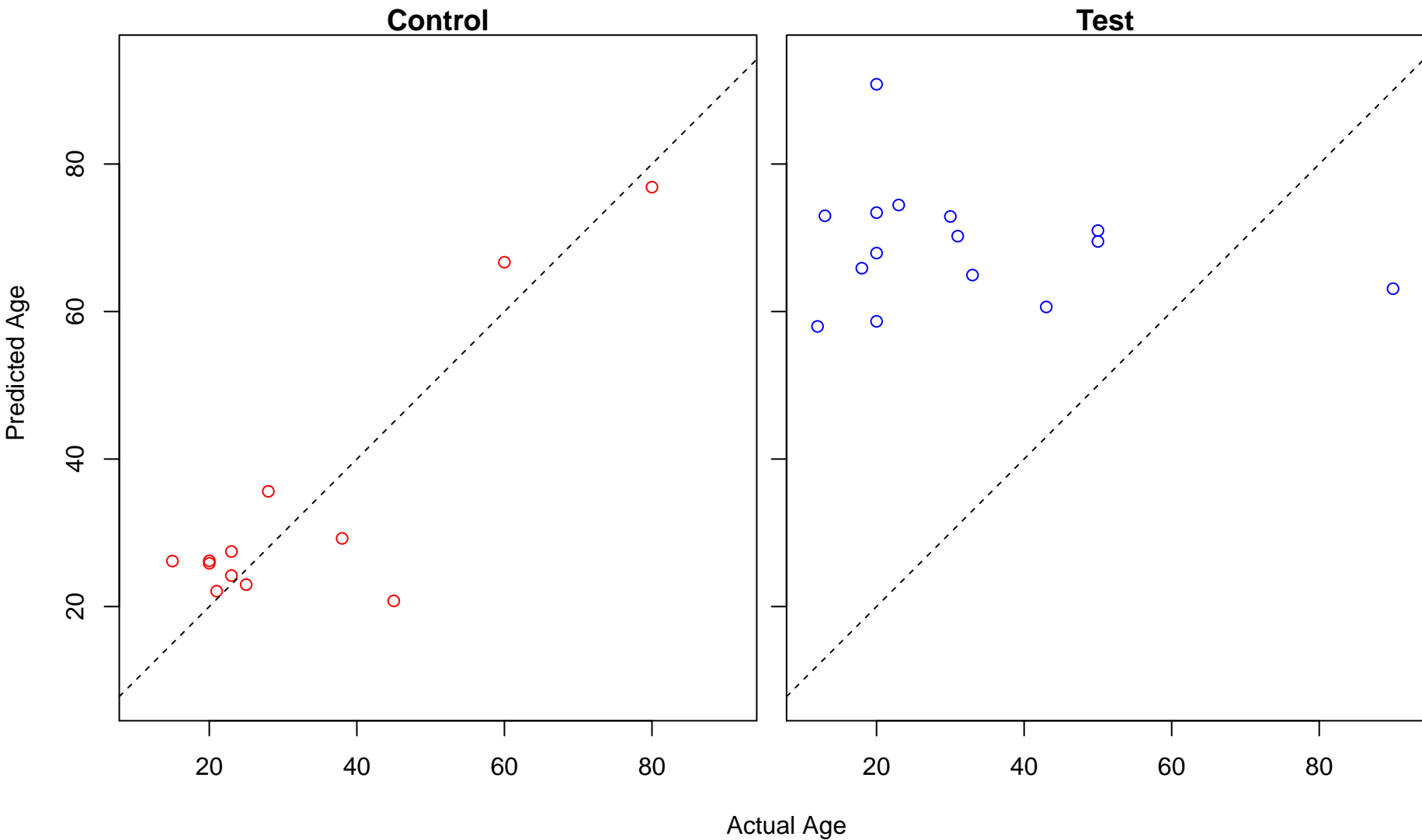
adipose tissue development (Score: 7.788463)



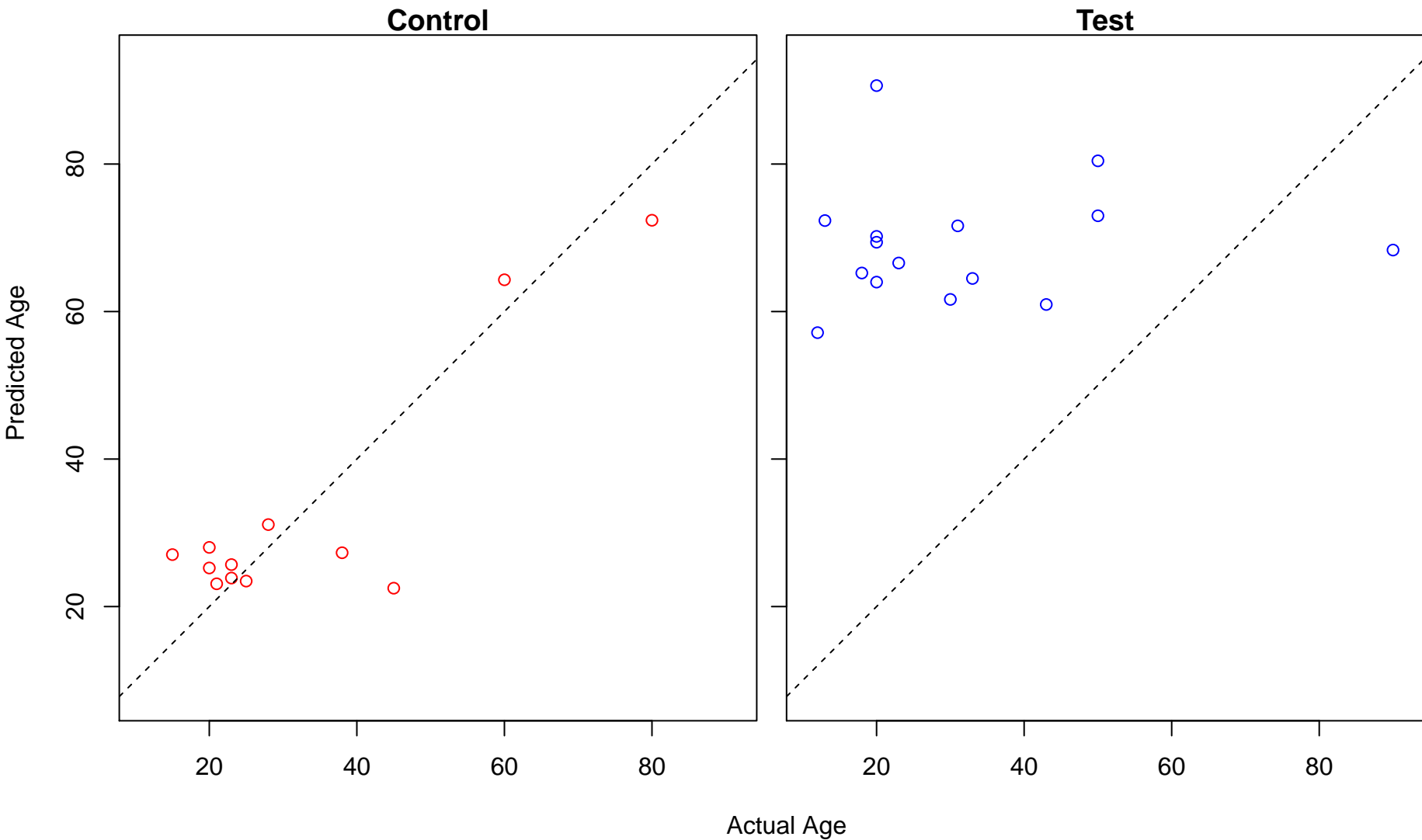
interferon-gamma production (Score: 7.787703)



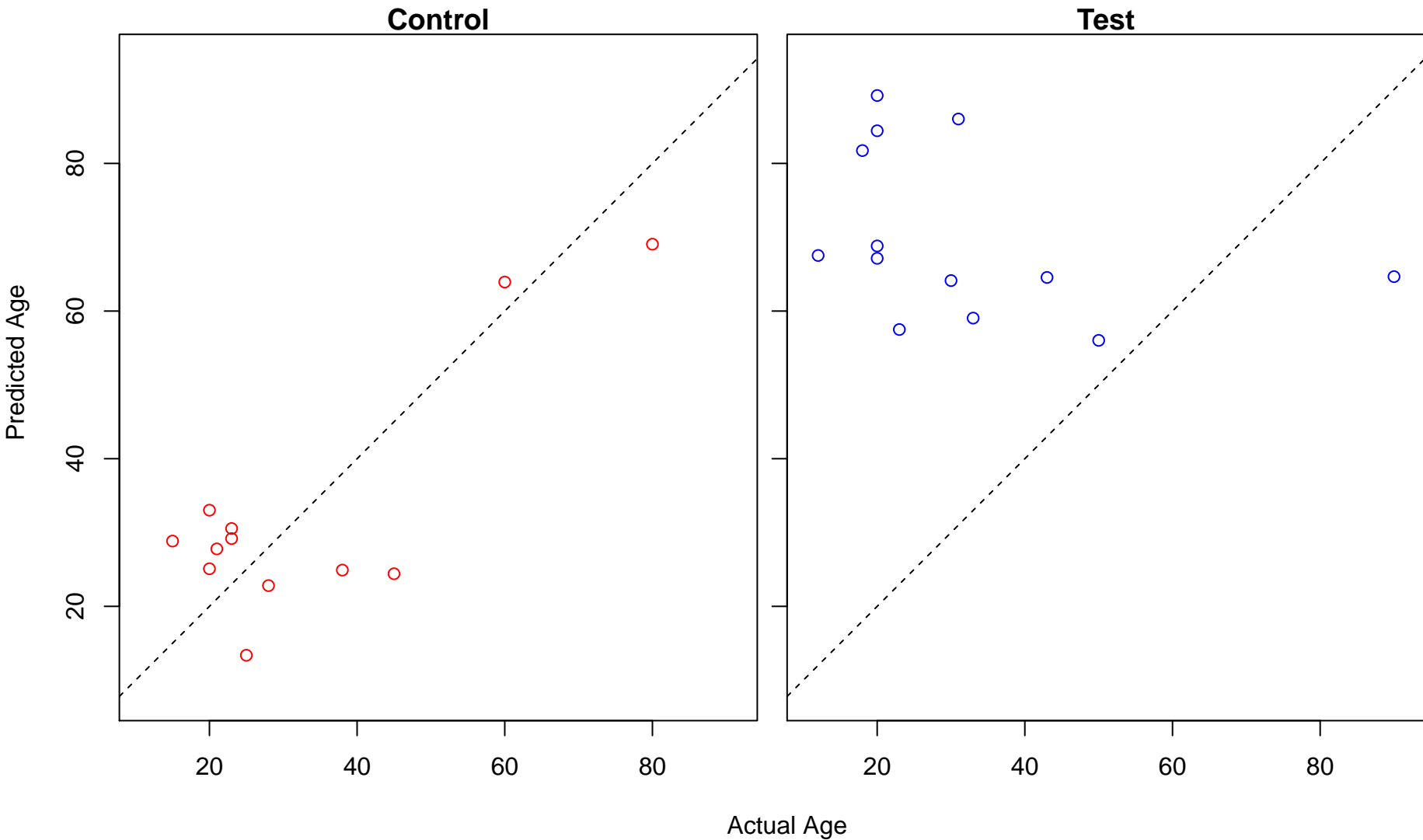
monocarboxylic acid biosynthetic process (Score: 7.786960)



response to glucagon (Score: 7.786080)

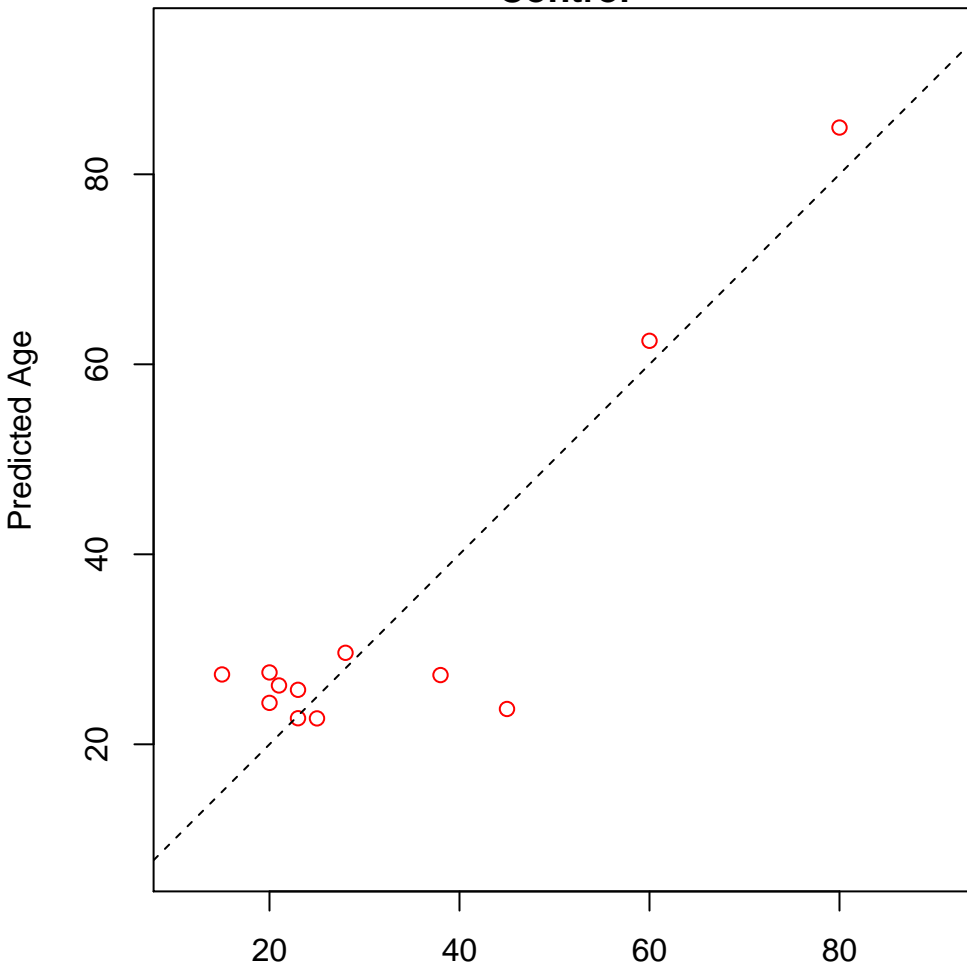


positive regulation of execution phase of apoptosis (Score: 7.780593)

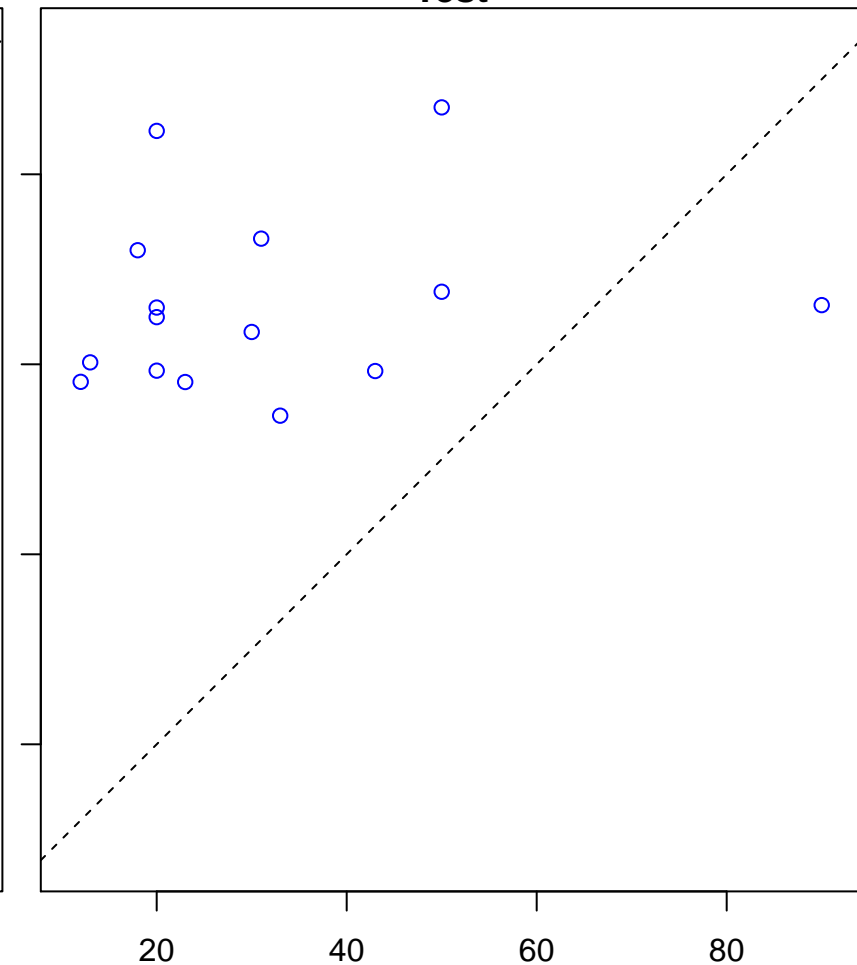


response to organic cyclic compound (Score: 7.772756)

Control

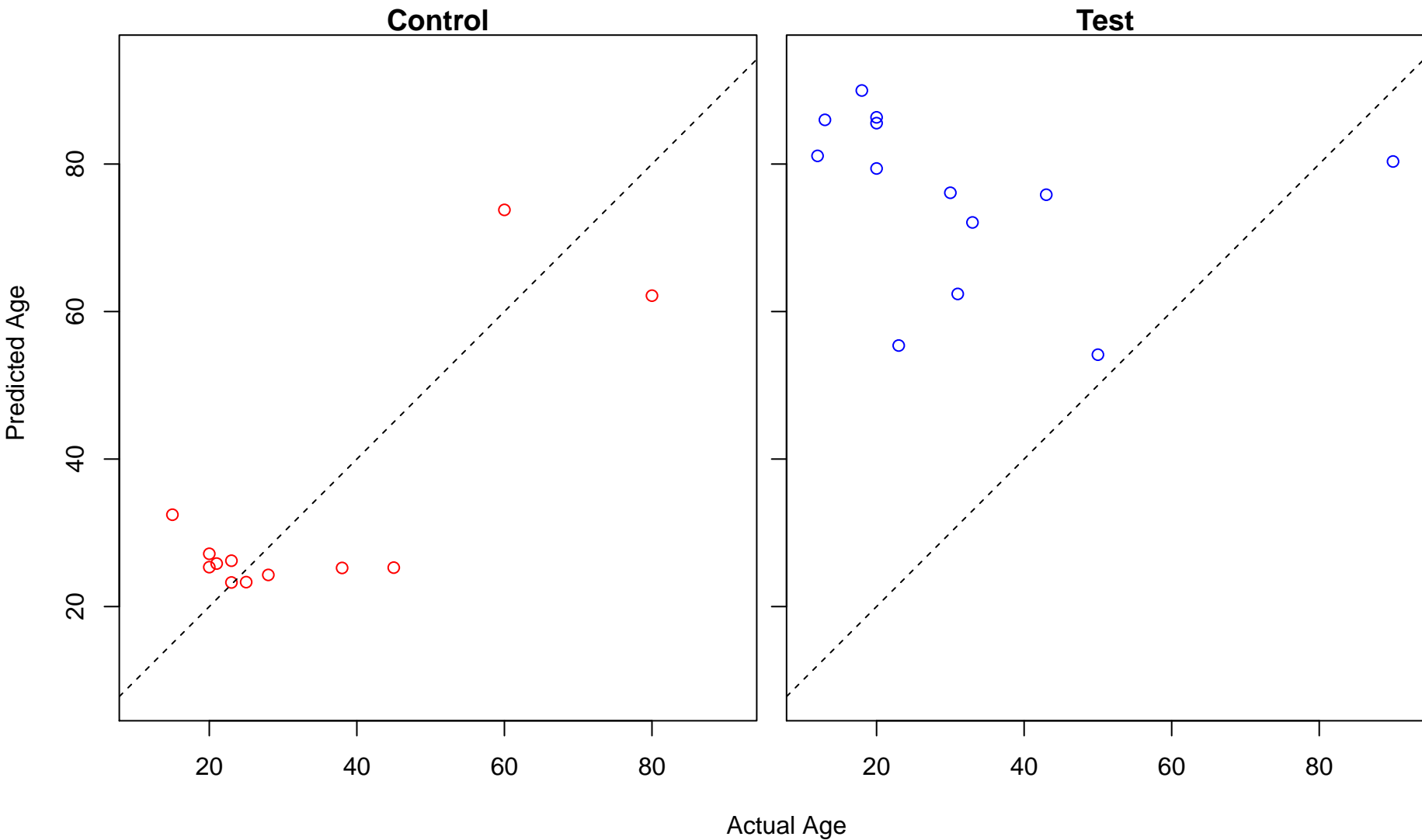


Test

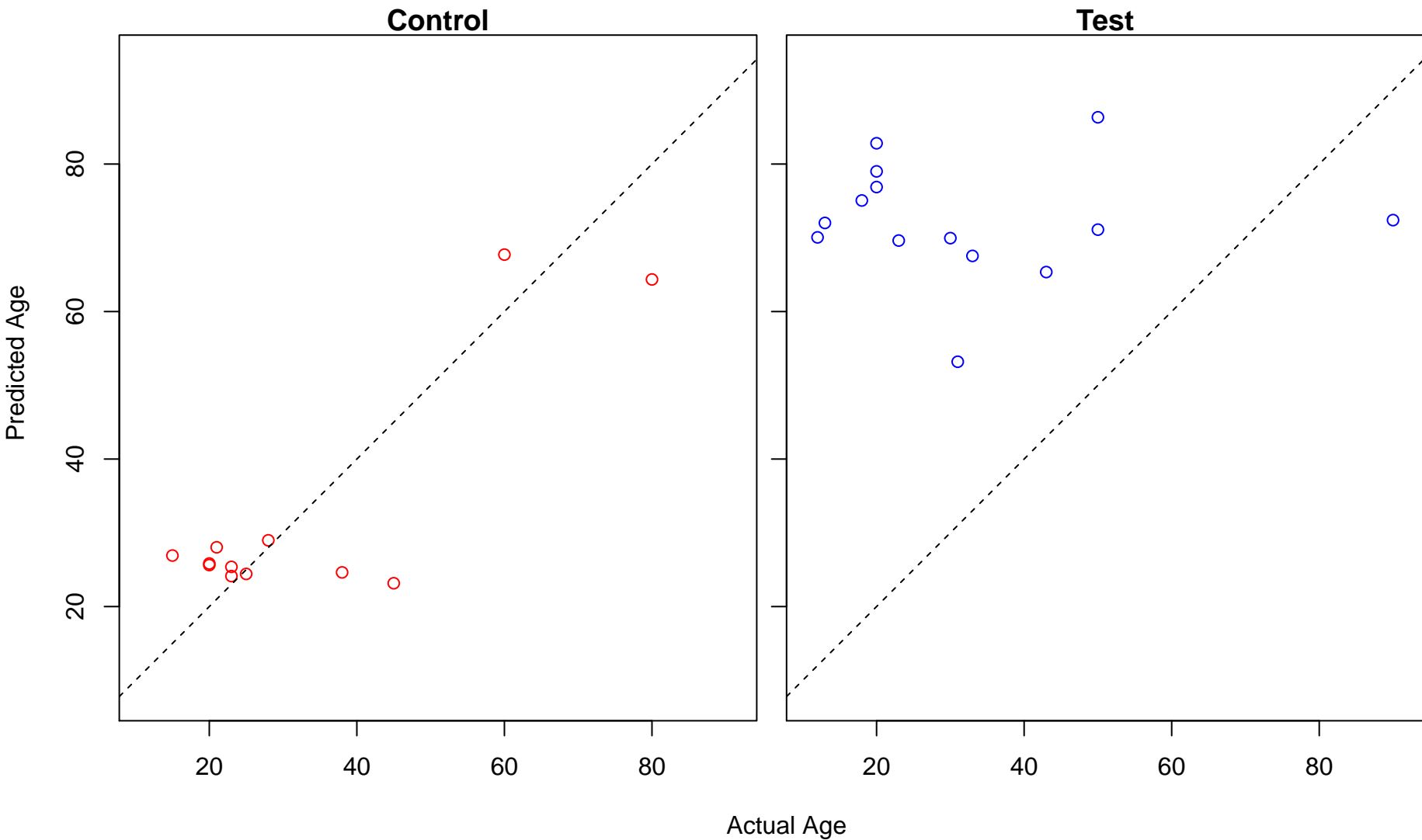


Actual Age

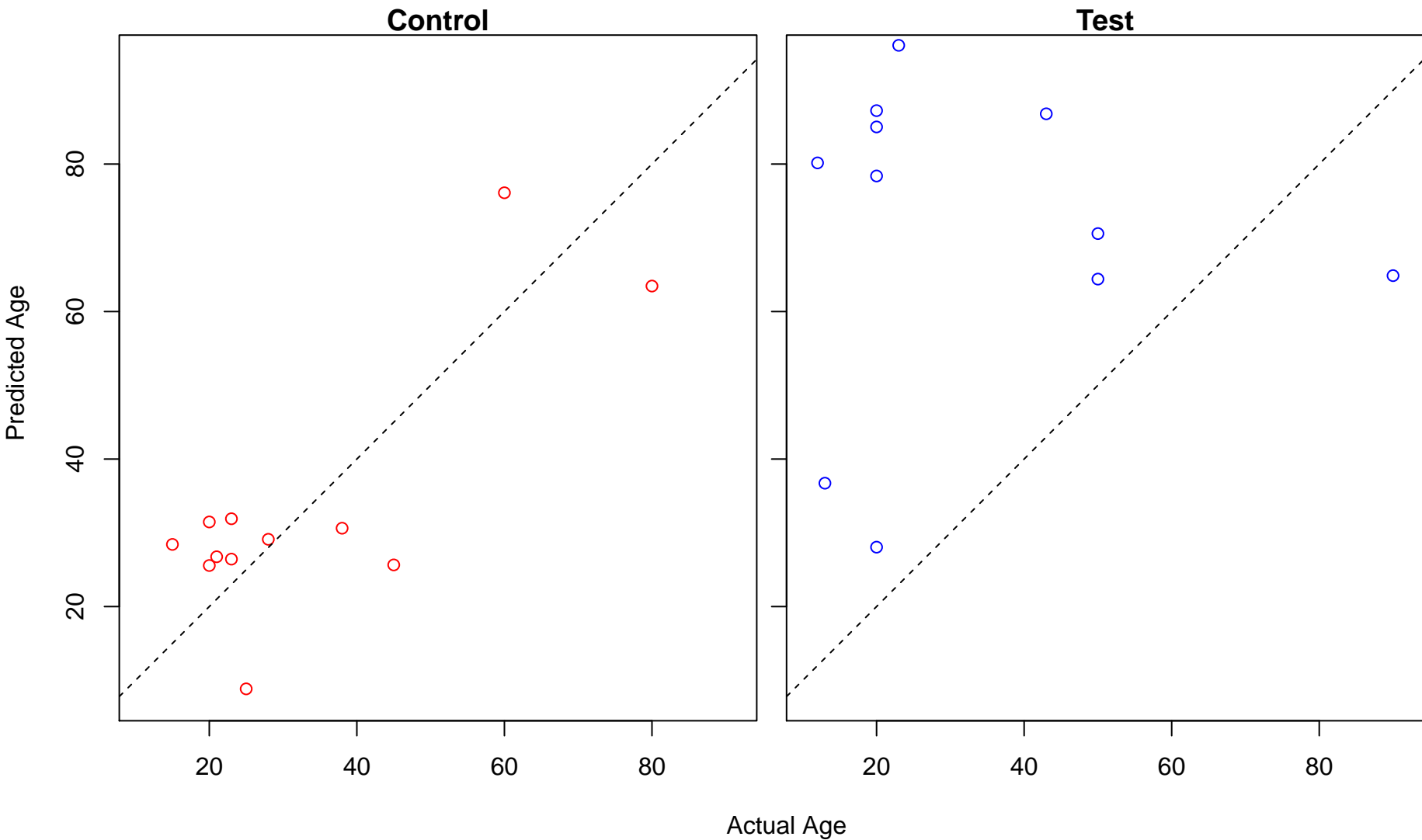
cellular triglyceride homeostasis (Score: 7.771147)



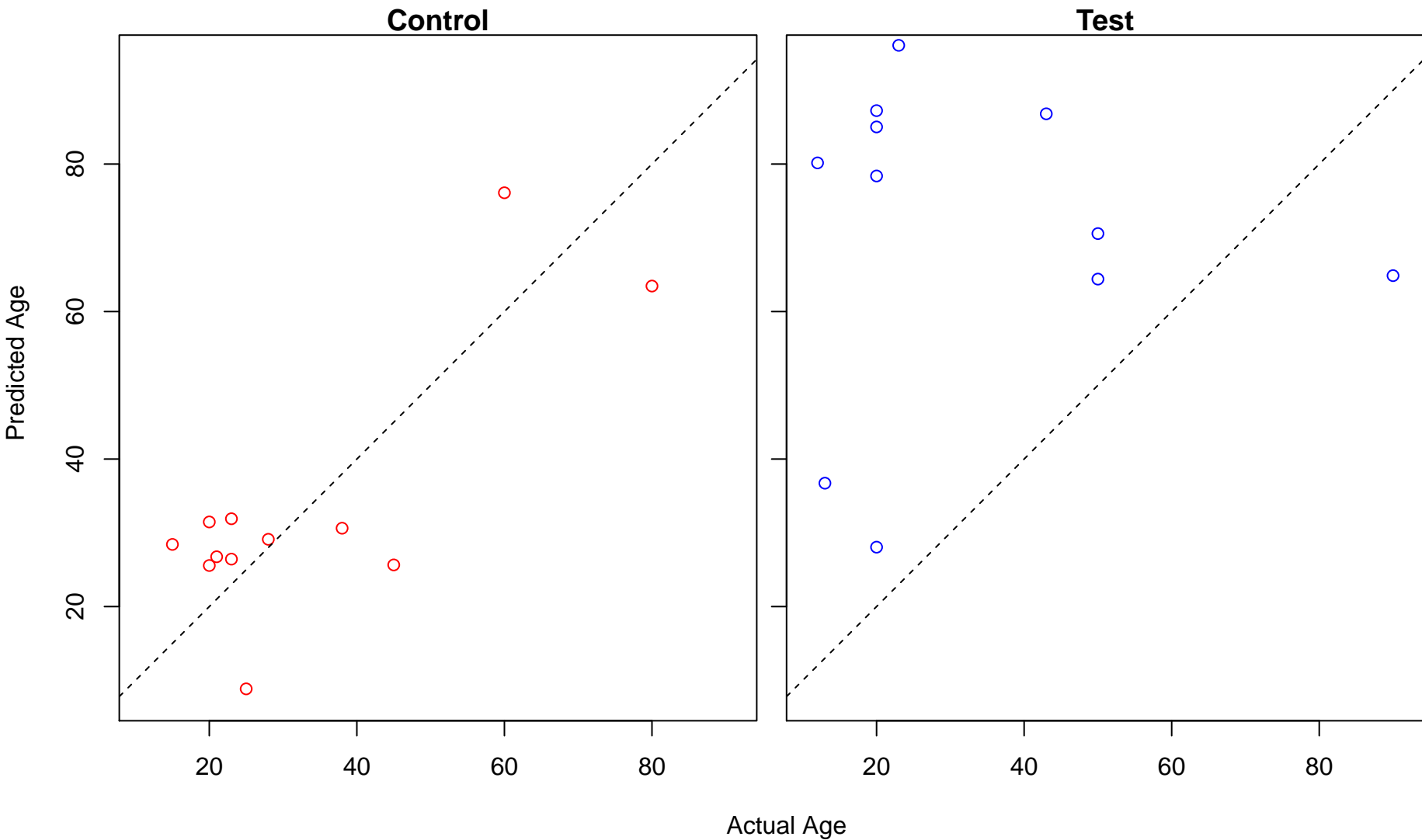
purine-containing compound catabolic process (Score: 7.770522)



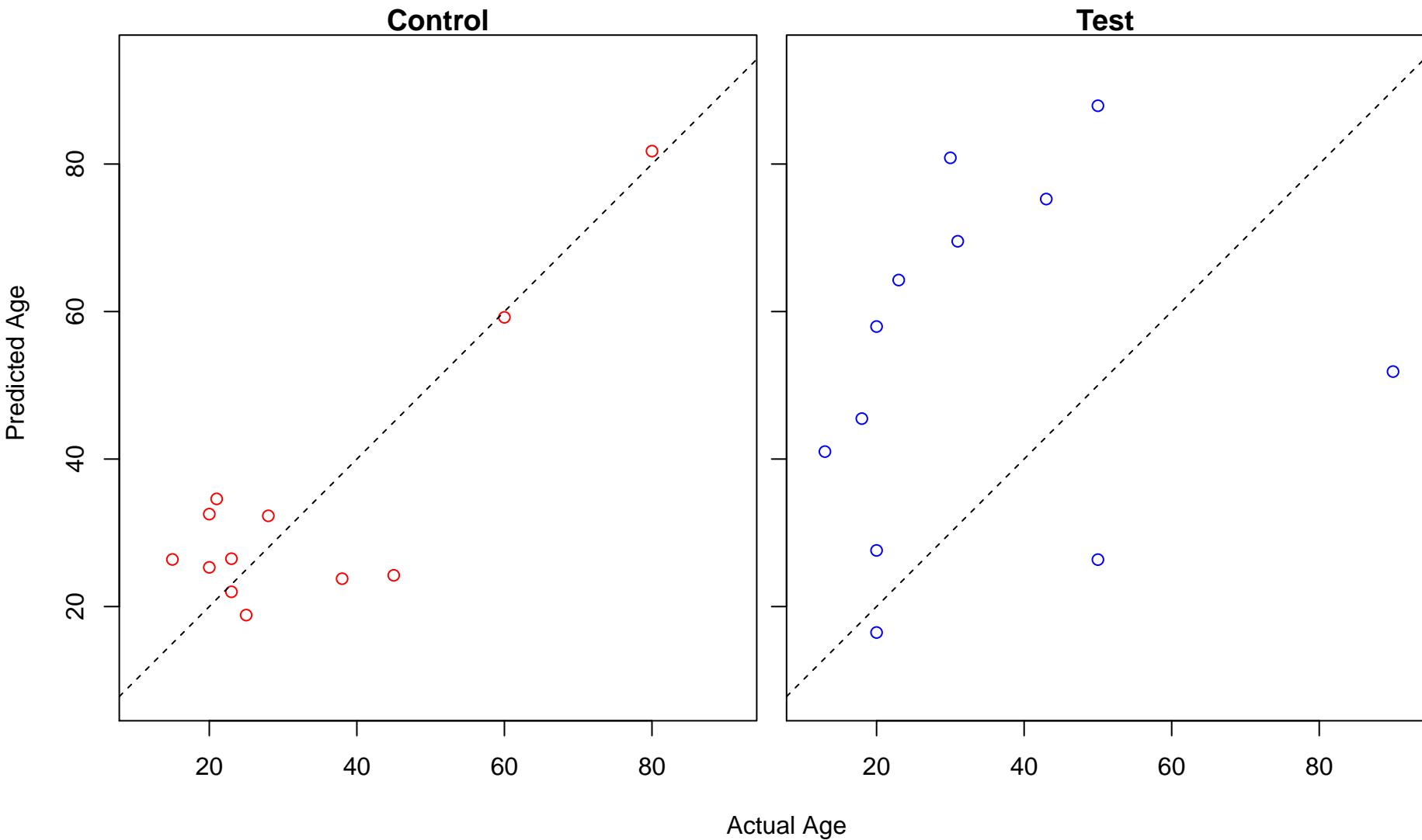
regulation of sphingolipid biosynthetic process (Score: 7.760419)



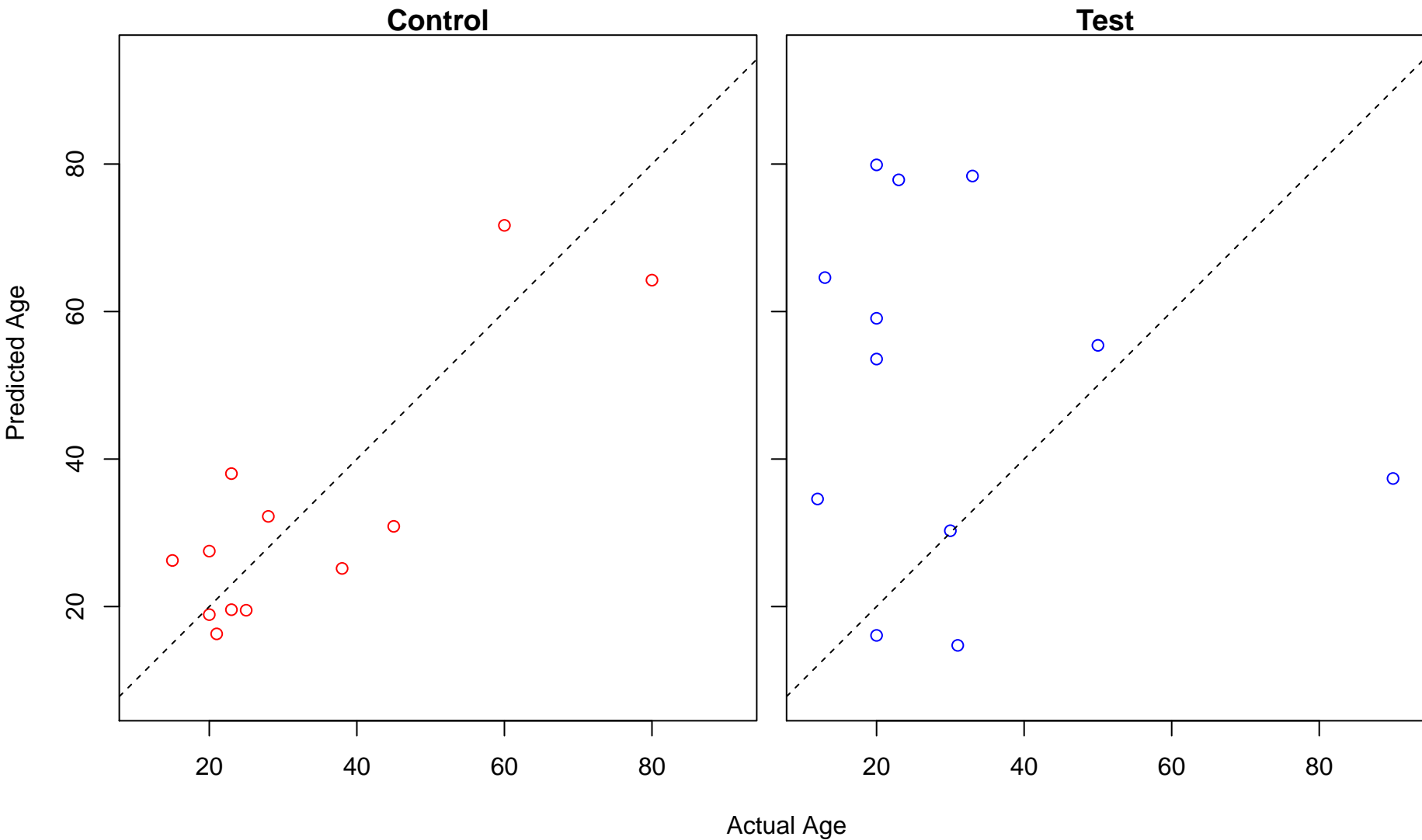
regulation of ceramide biosynthetic process (Score: 7.760419)



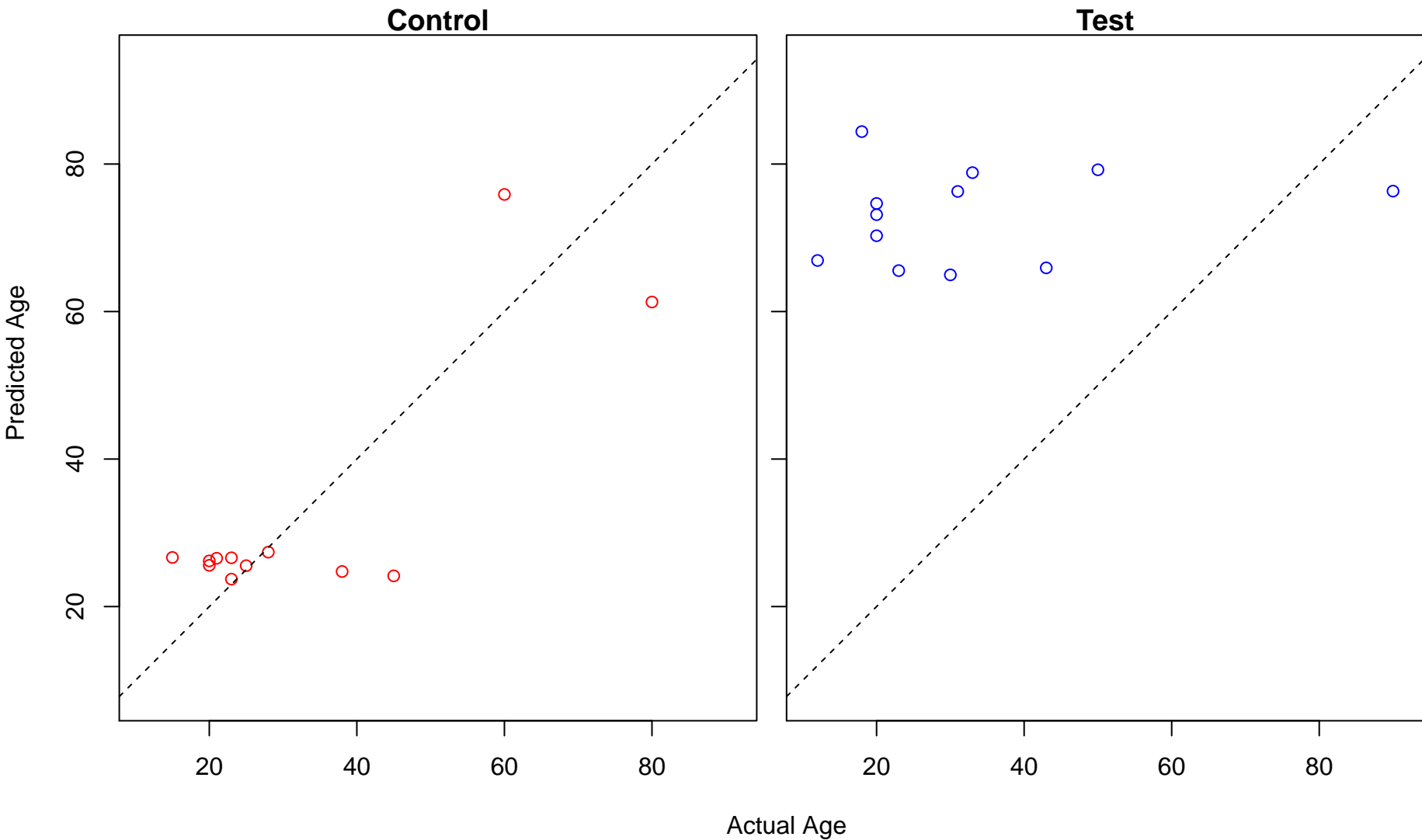
negative regulation of epithelial cell proliferation (Score: 7.760081)



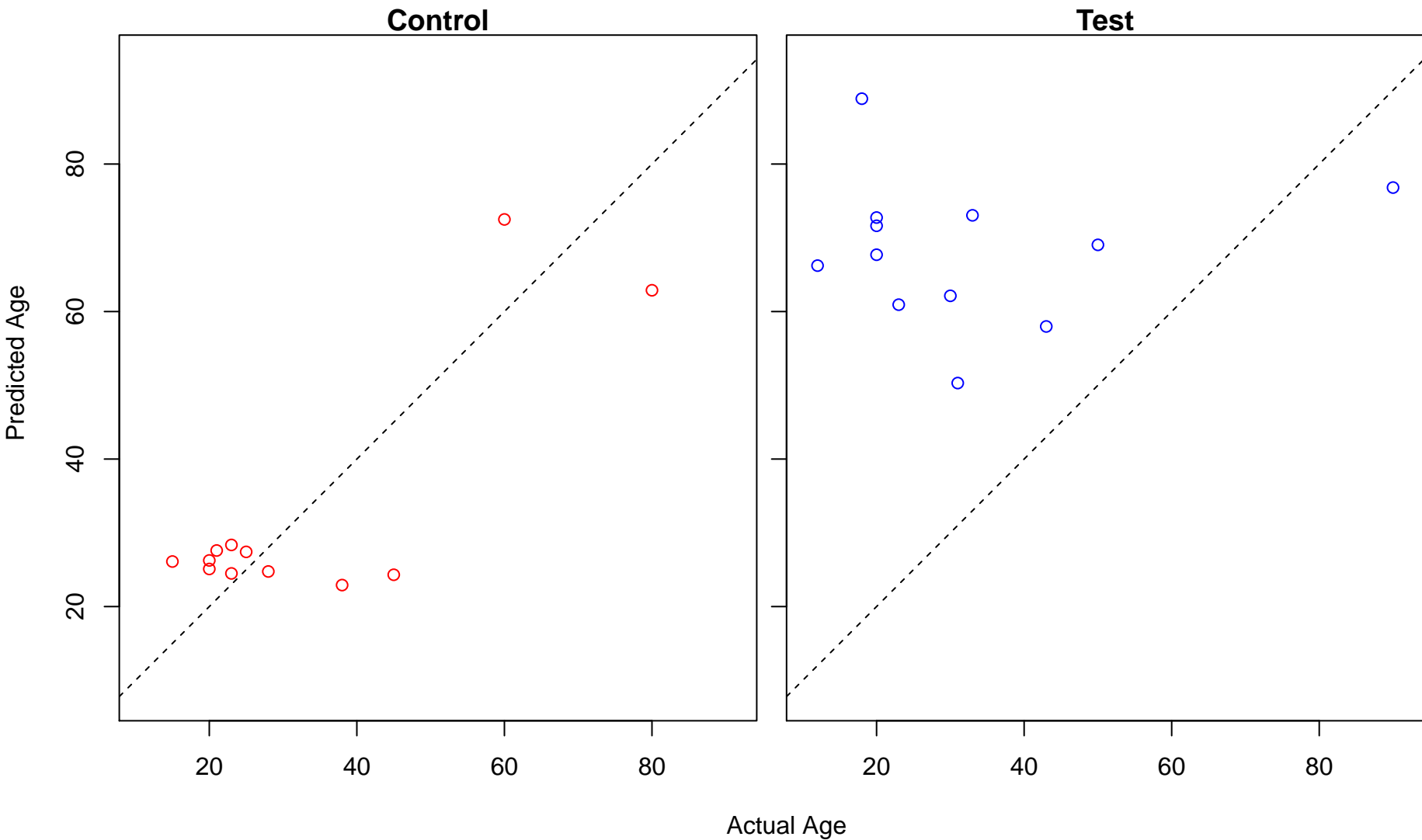
regulation of ubiquitin protein ligase activity (Score: 7.757731)



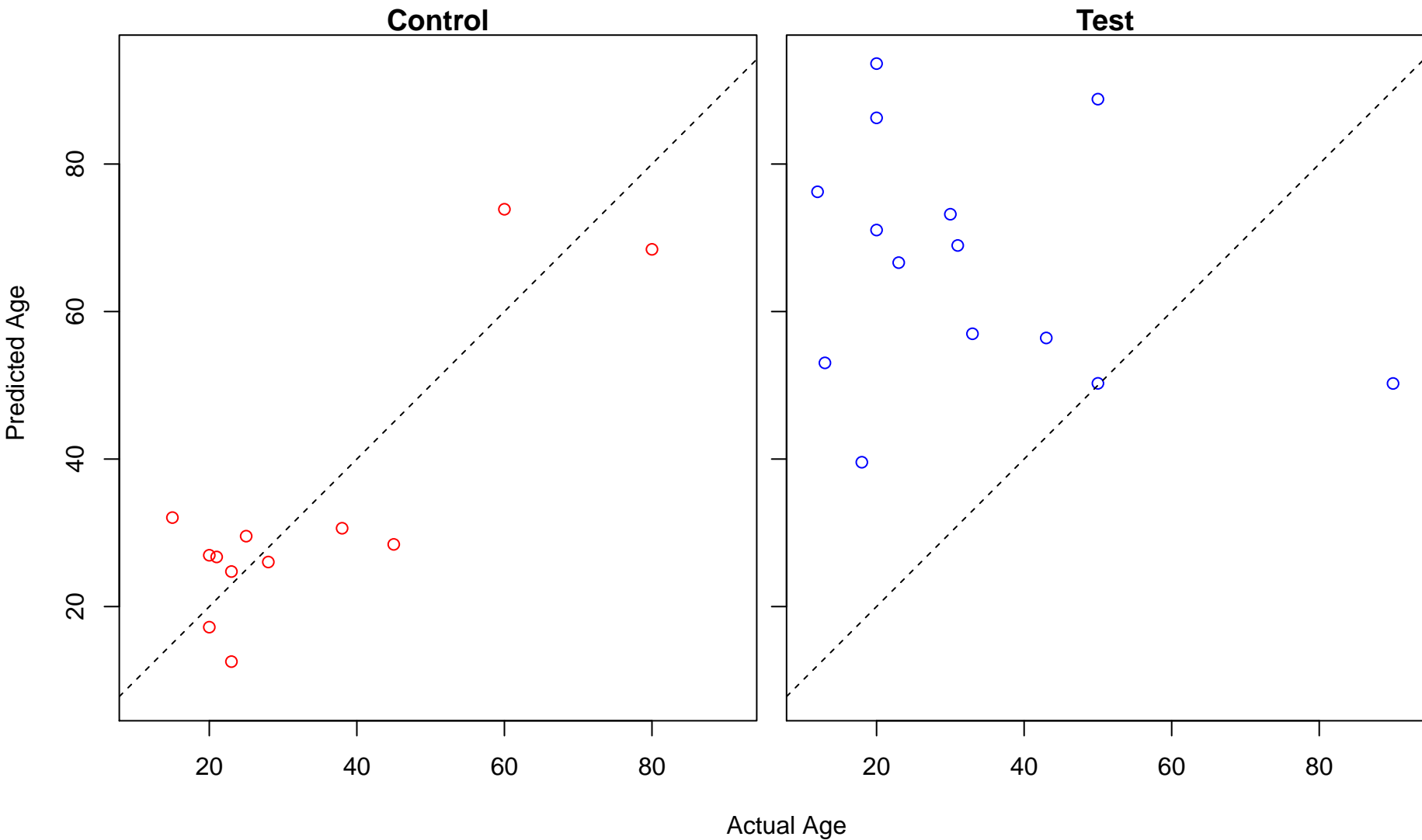
negative regulation of apoptotic signaling pathway (Score: 7.754284)



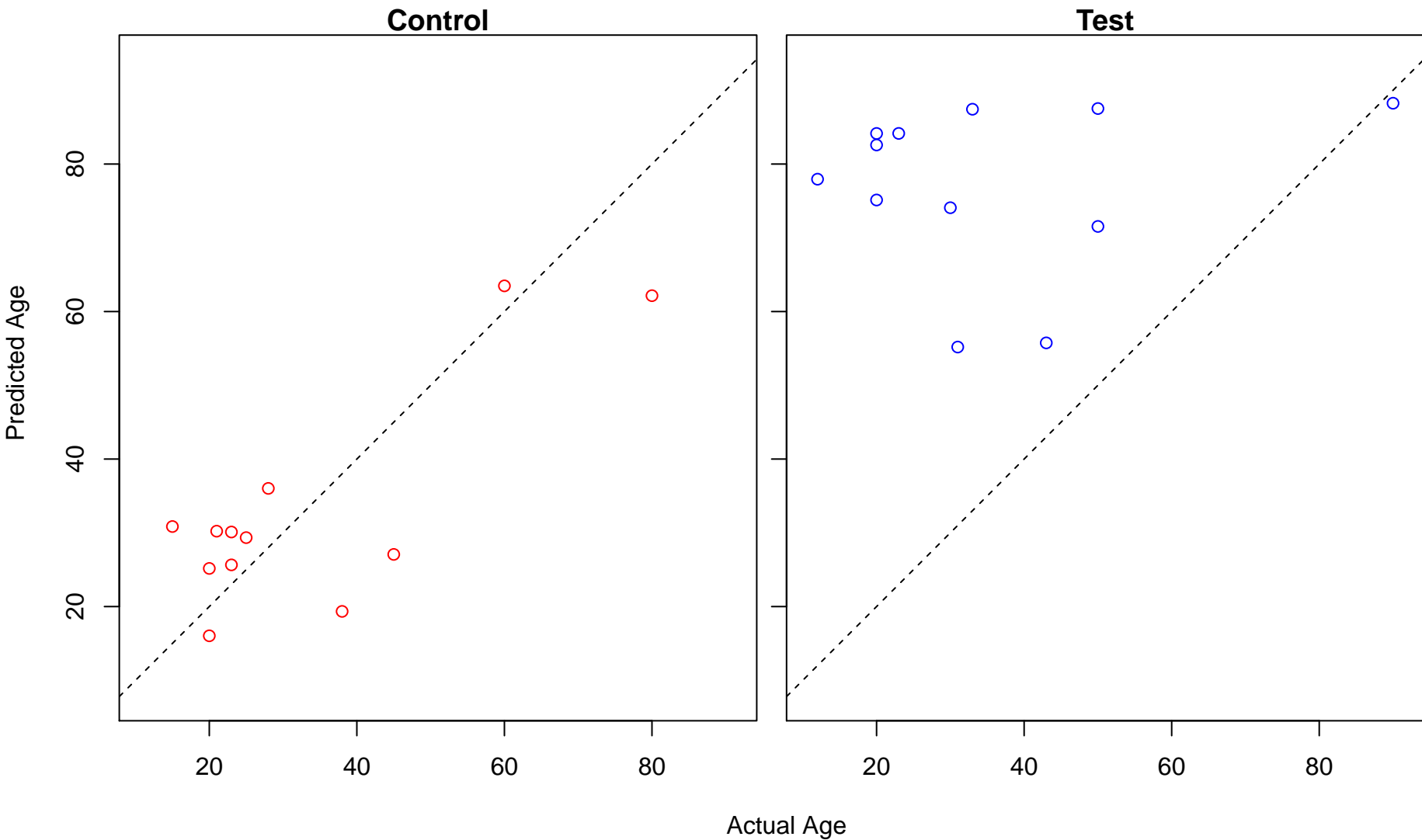
erythrocyte homeostasis (Score: 7.751013)



regulation of ruffle assembly (Score: 7.749523)

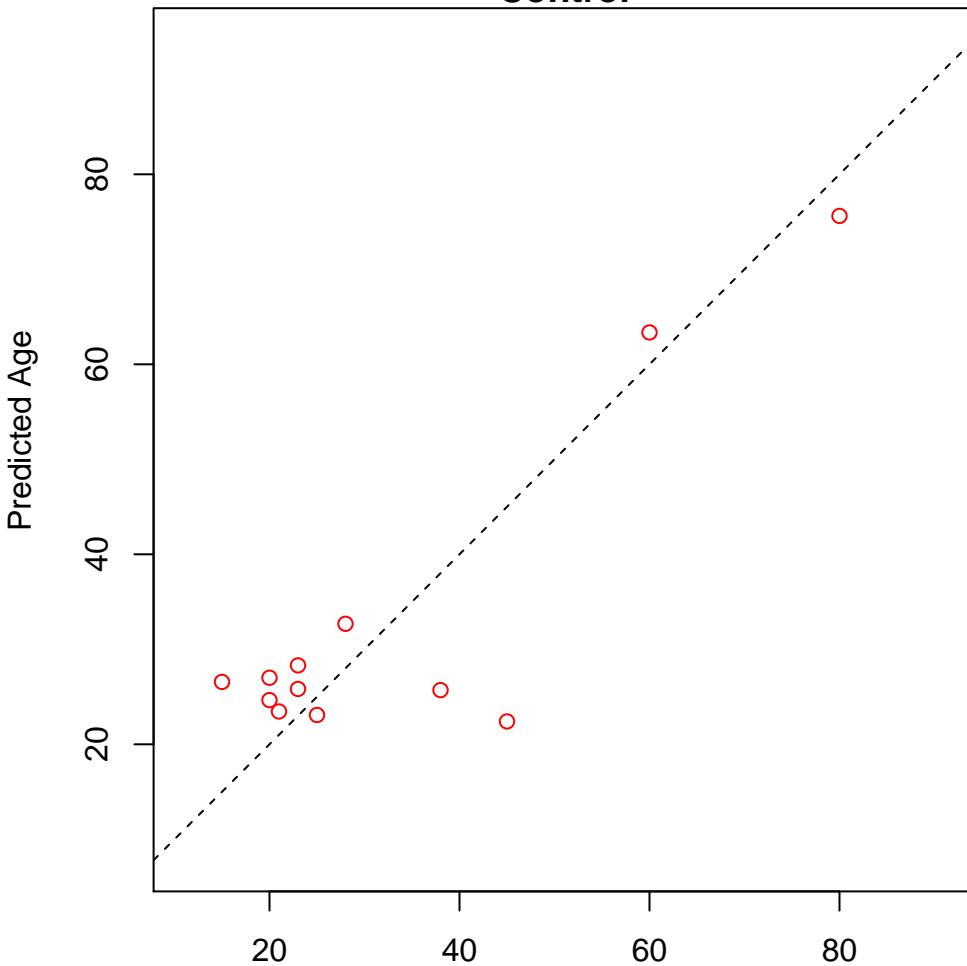


aromatic amino acid family metabolic process (Score: 7.749078)

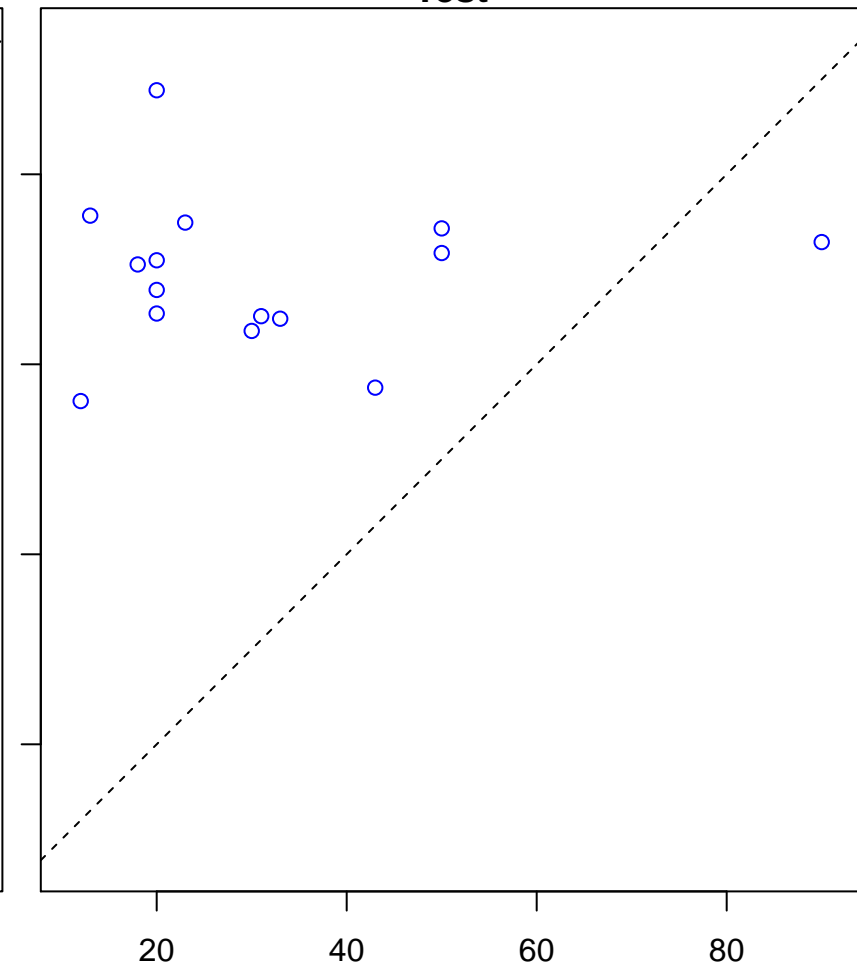


cellular response to hormone stimulus (Score: 7.748986)

Control

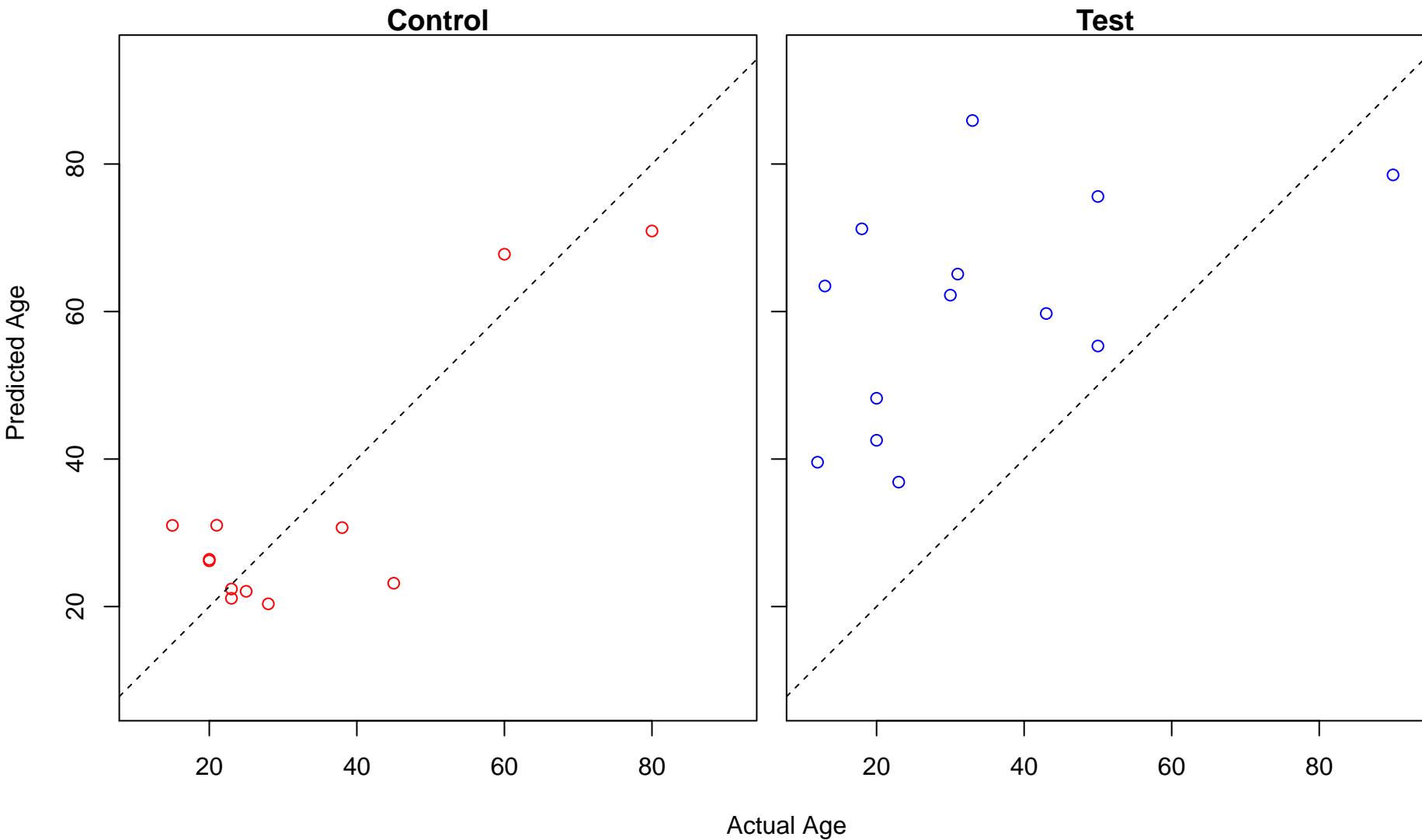


Test

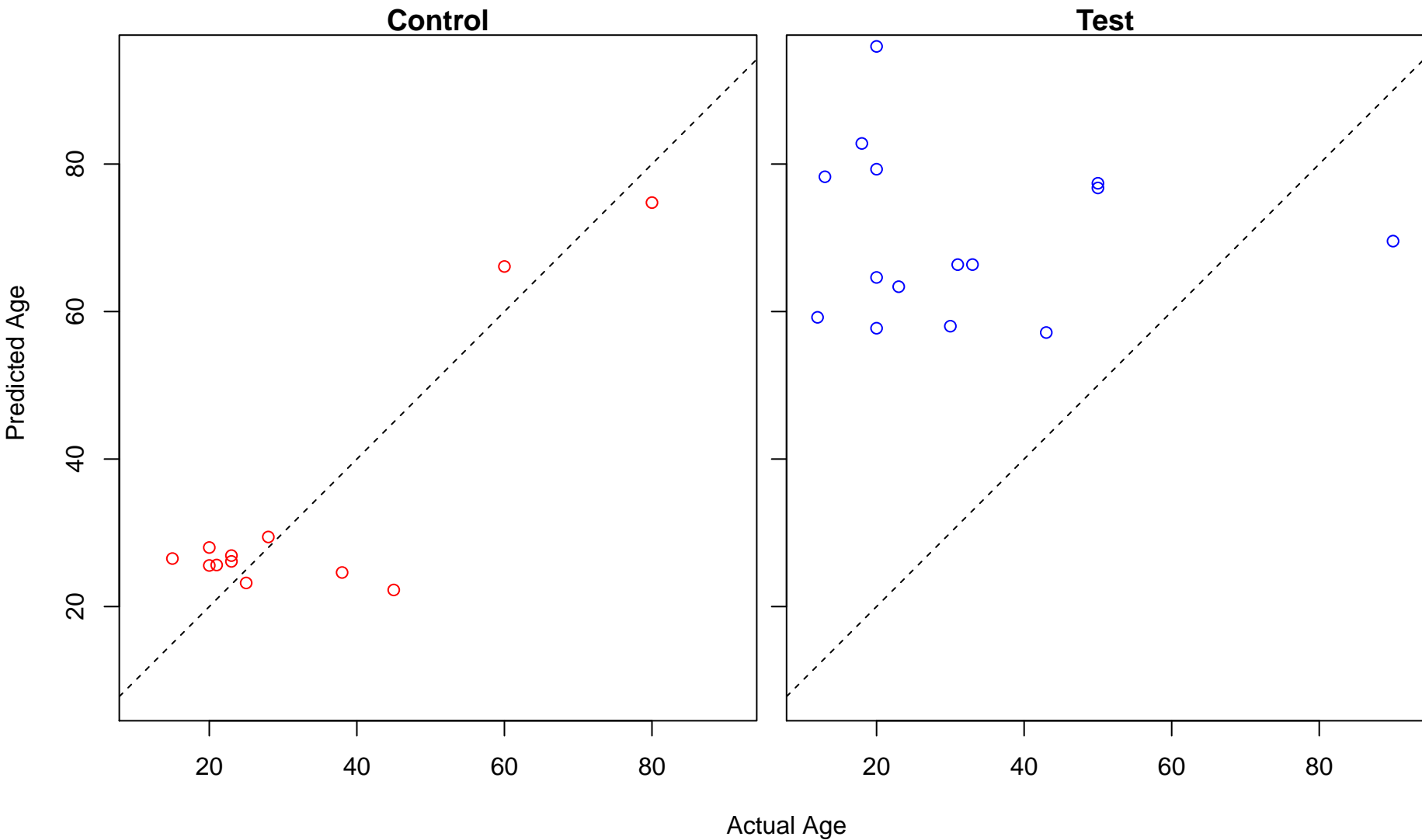


Actual Age

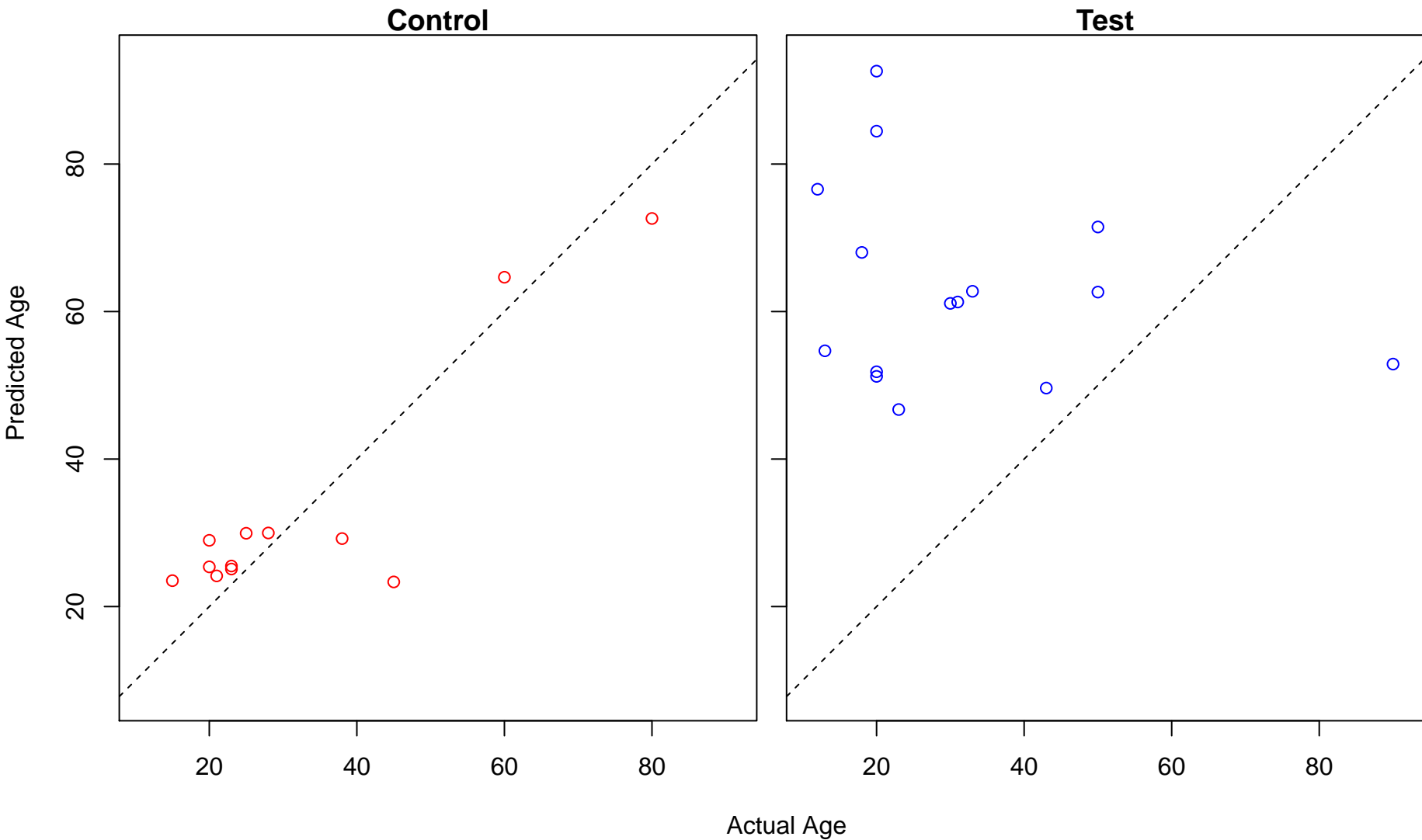
oxidative demethylation (Score: 7.748309)



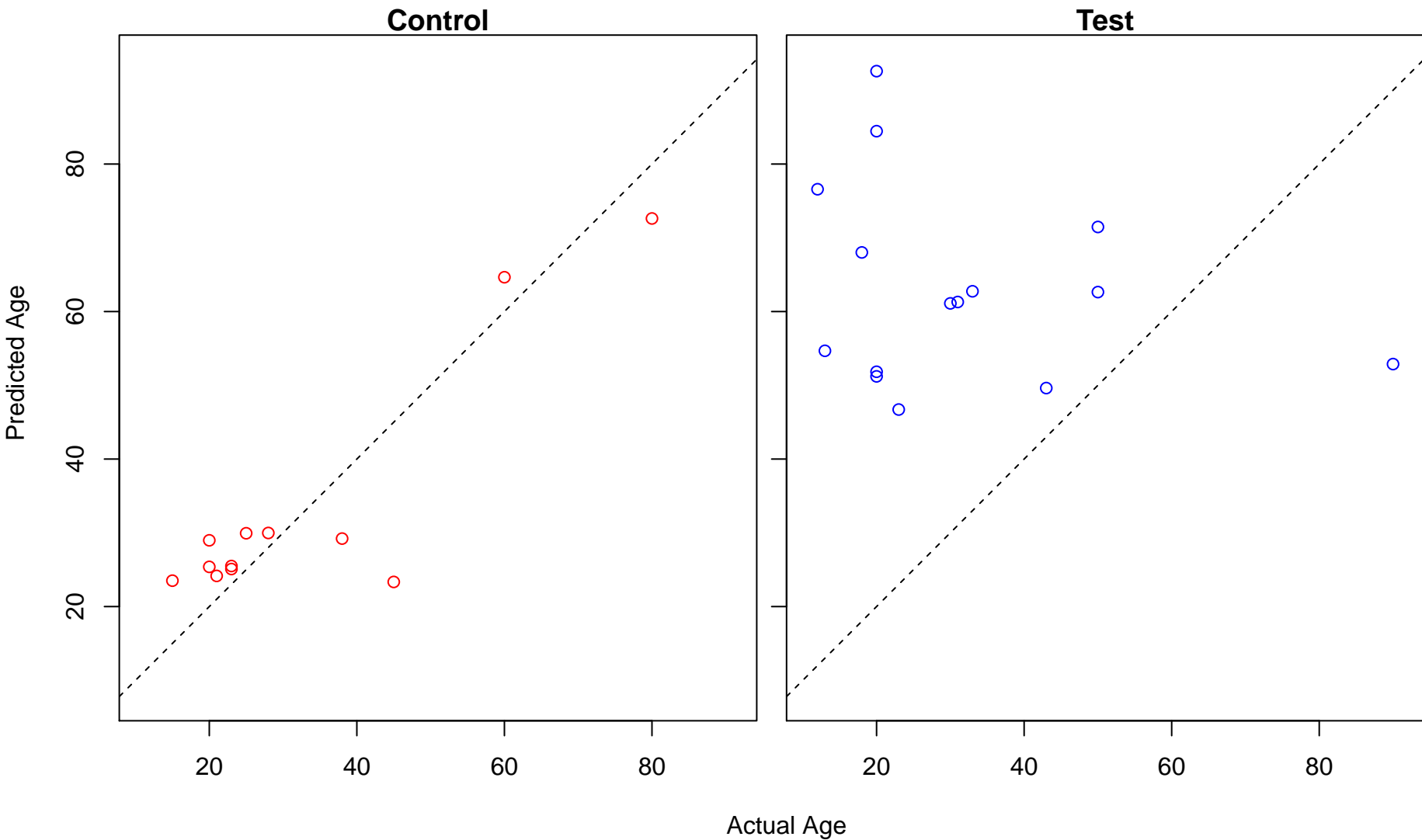
positive regulation of organelle organization (Score: 7.747114)



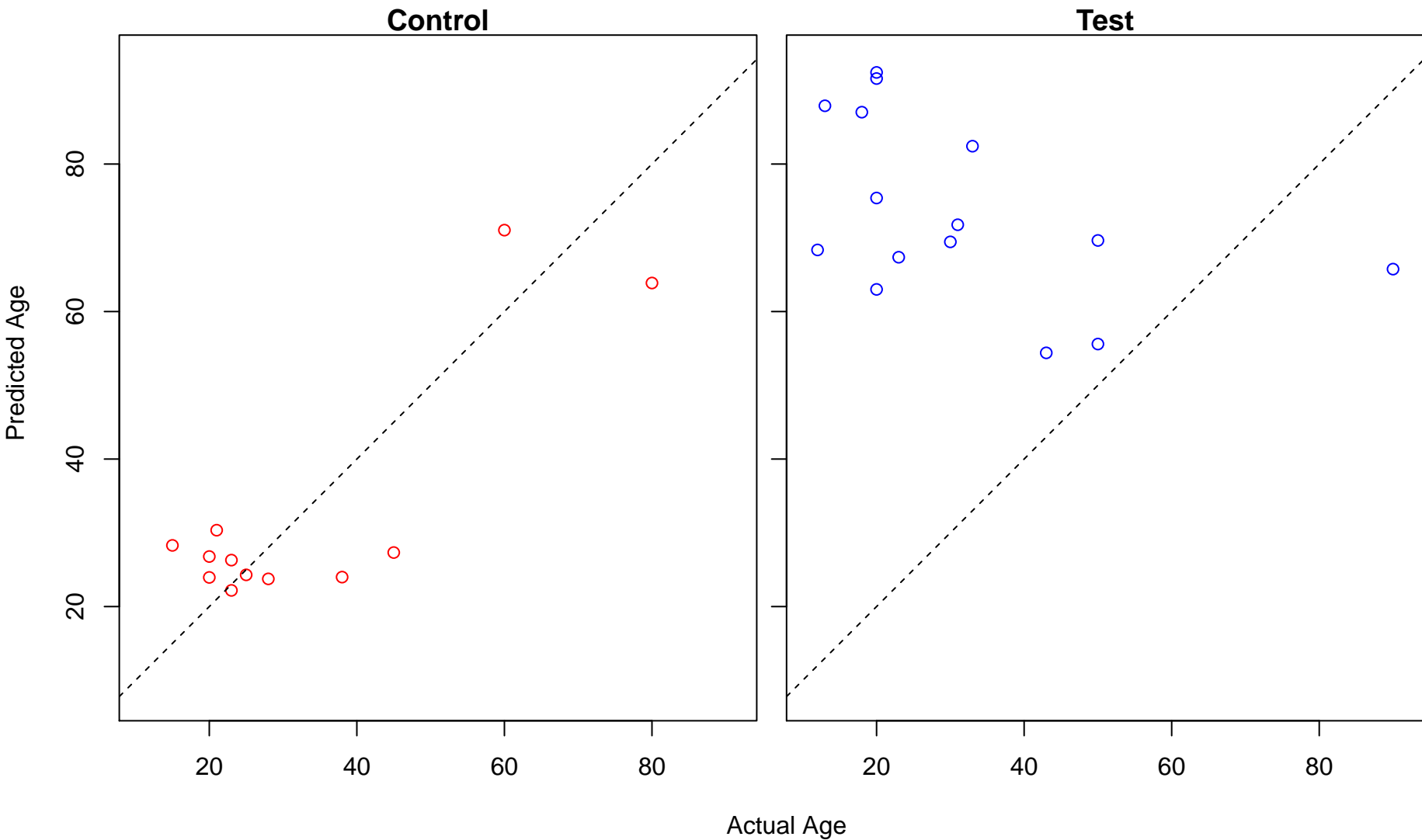
muscle filament sliding (Score: 7.739195)



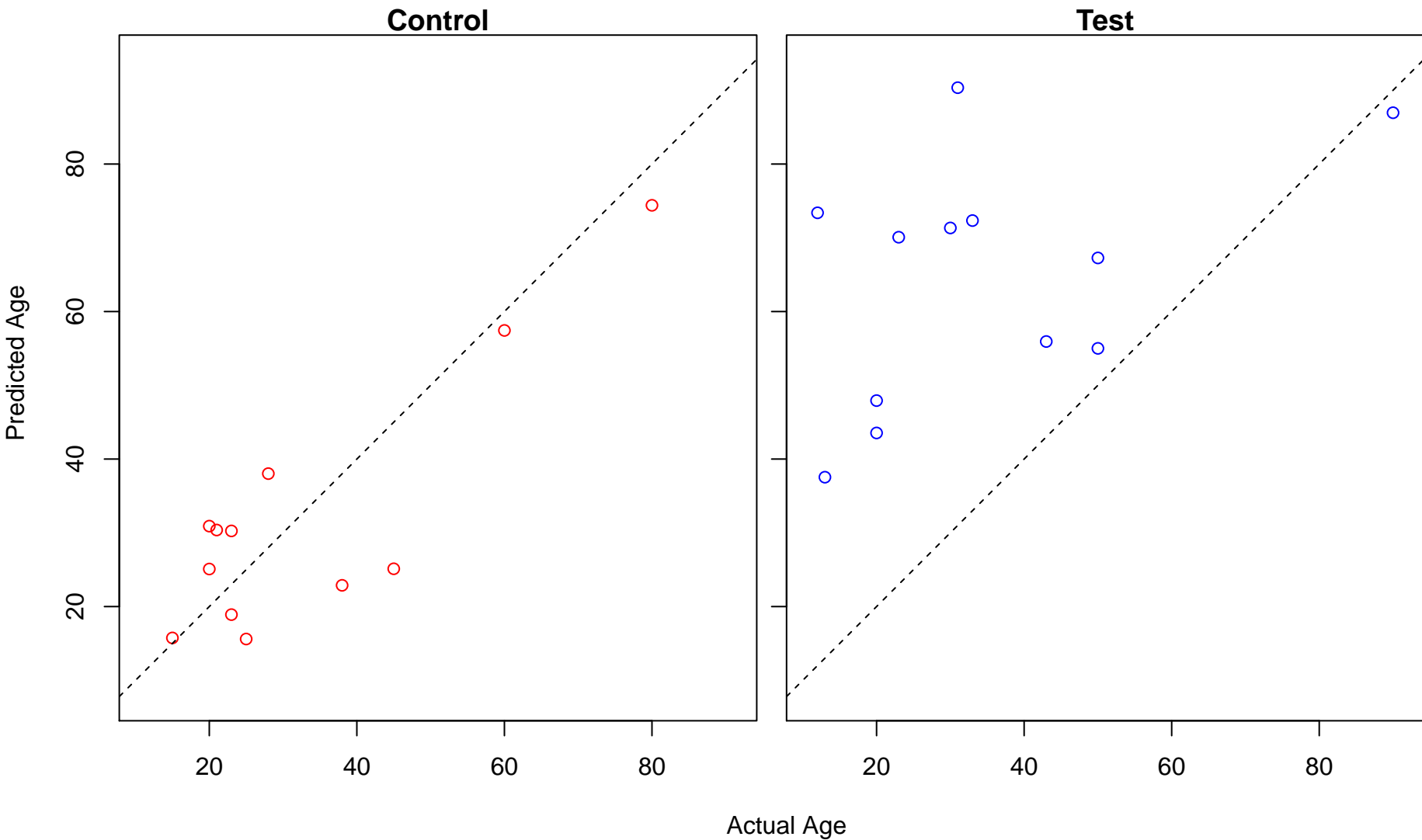
actin-myosin filament sliding (Score: 7.739195)



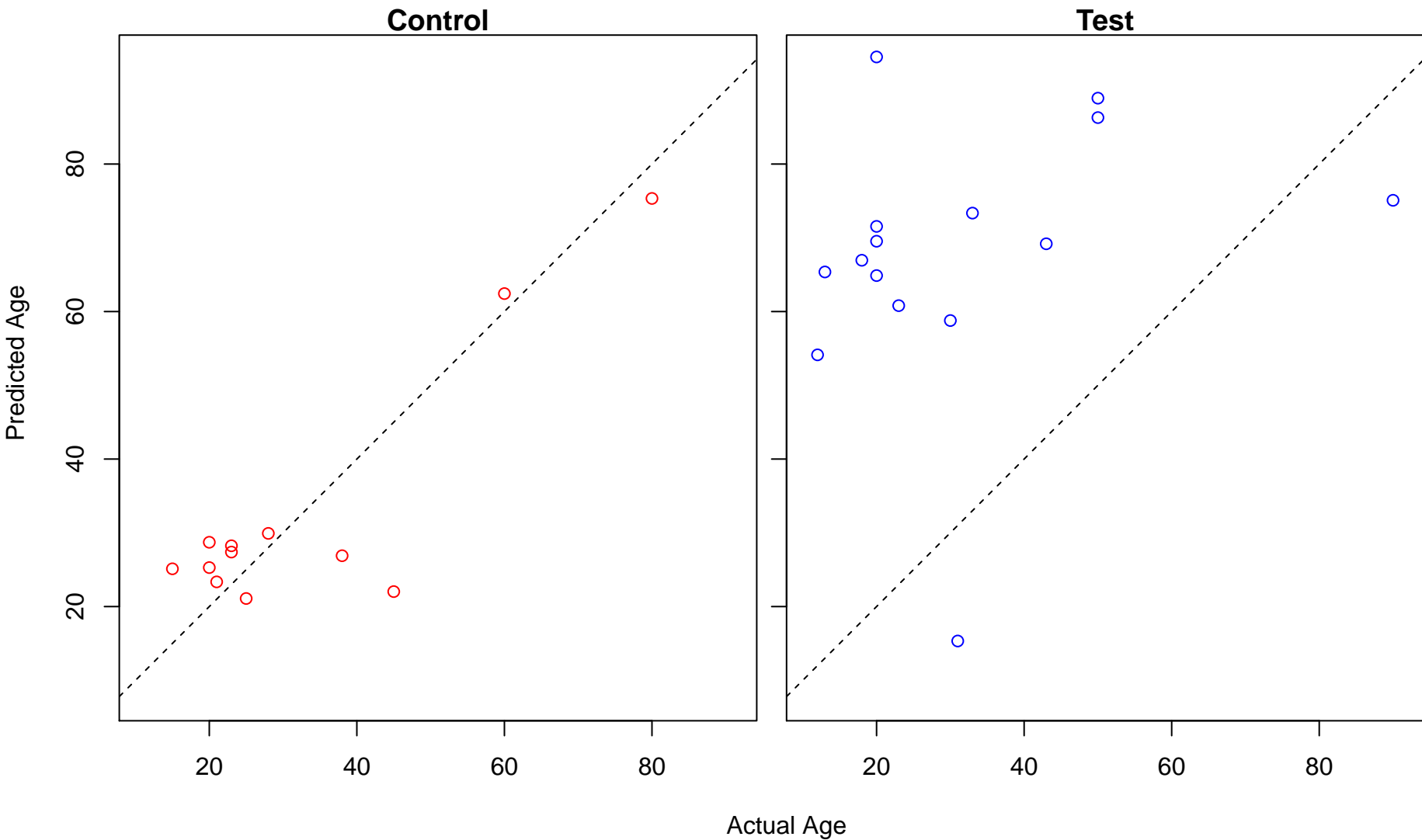
phagosome maturation (Score: 7.737808)



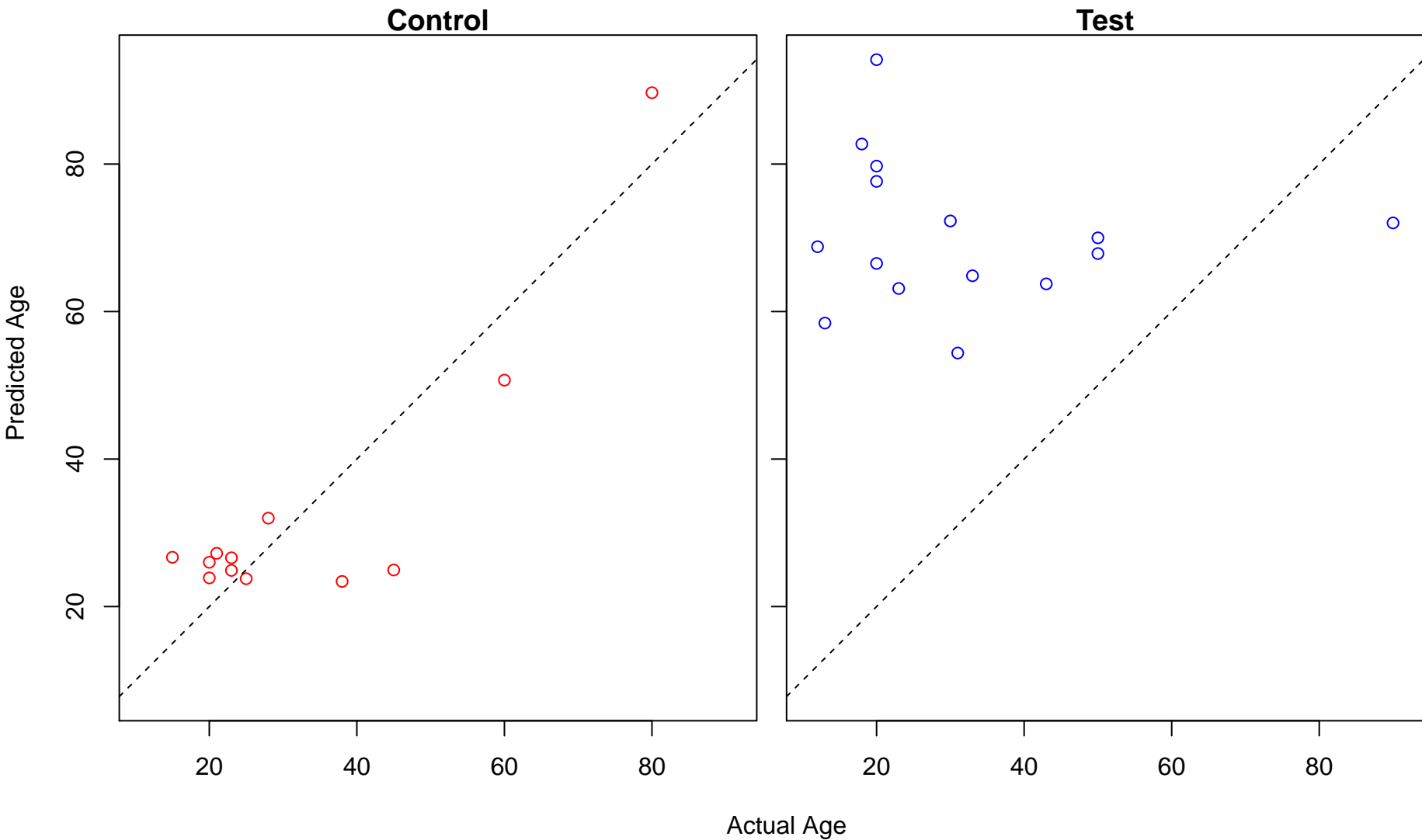
axo-dendritic transport (Score: 7.736818)



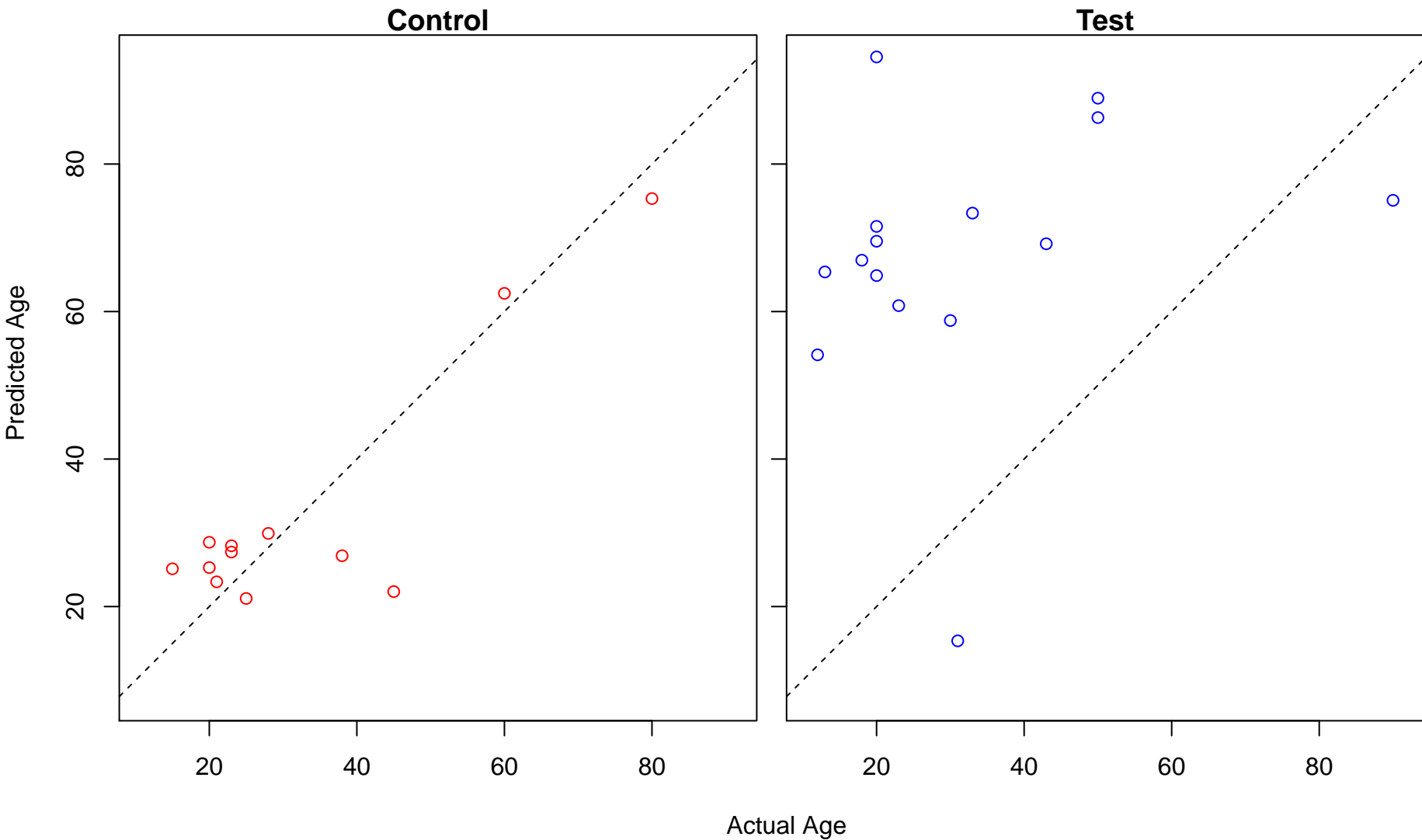
granulocyte migration (Score: 7.725330)



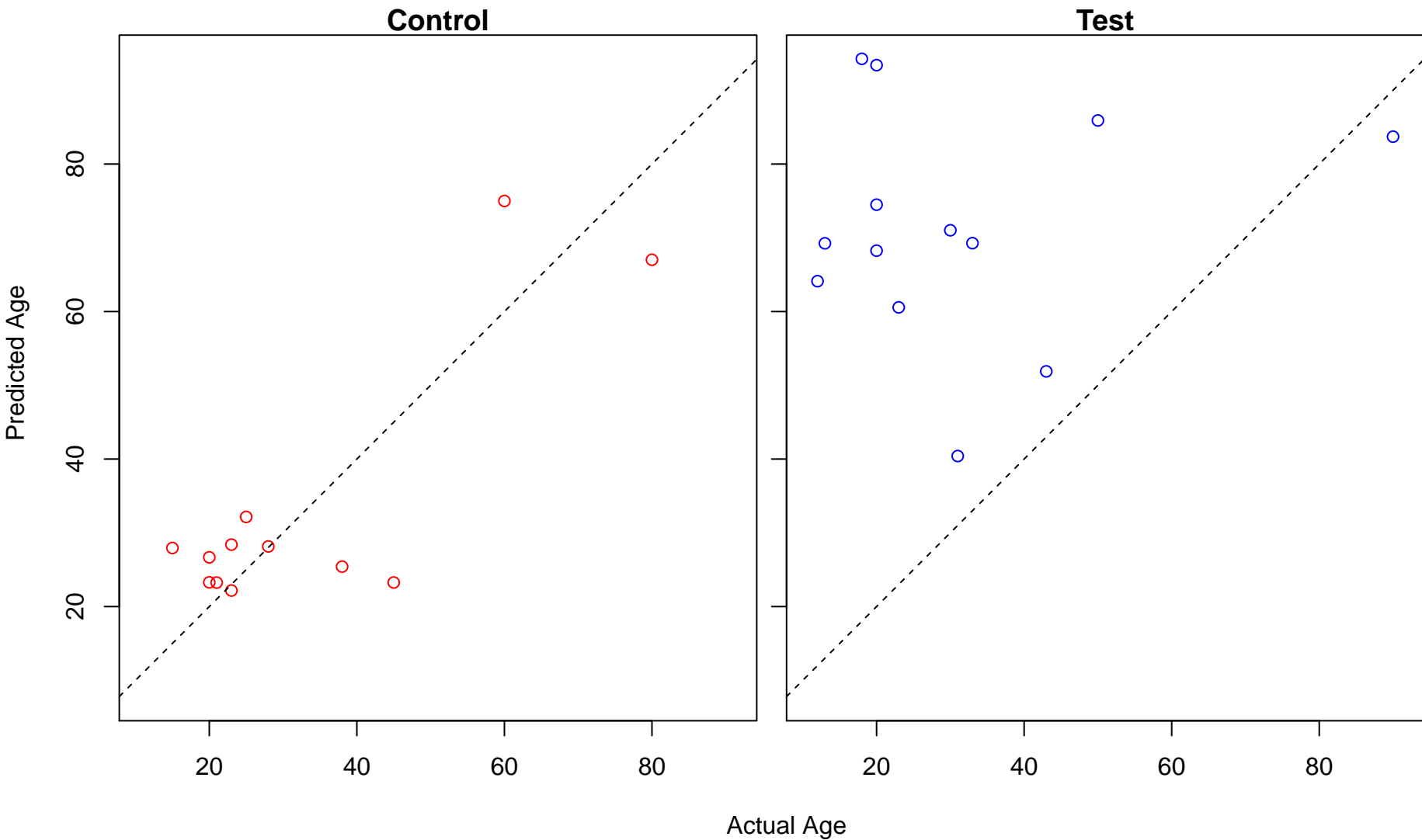
aerobic respiration (Score: 7.721985)



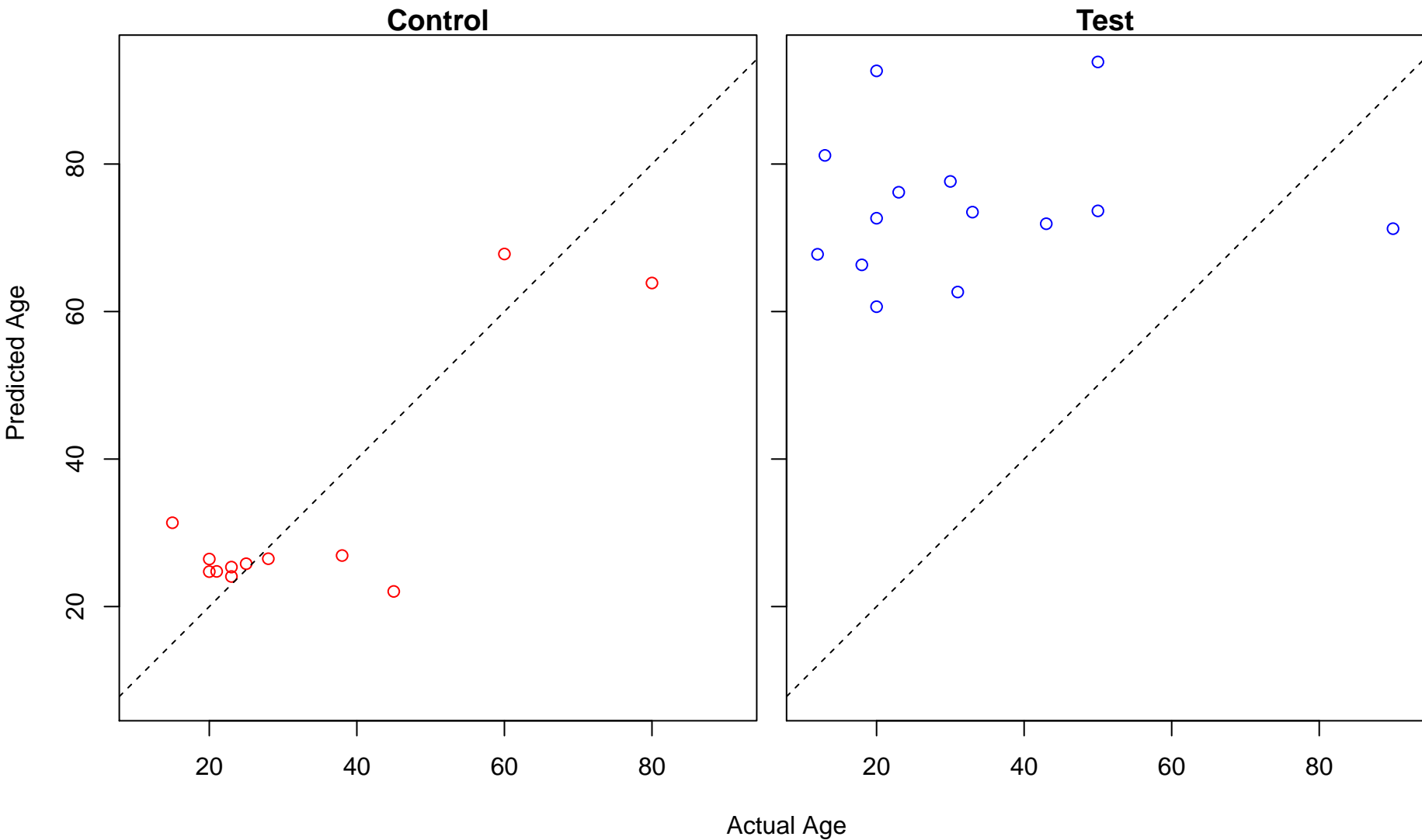
granulocyte chemotaxis (Score: 7.721680)



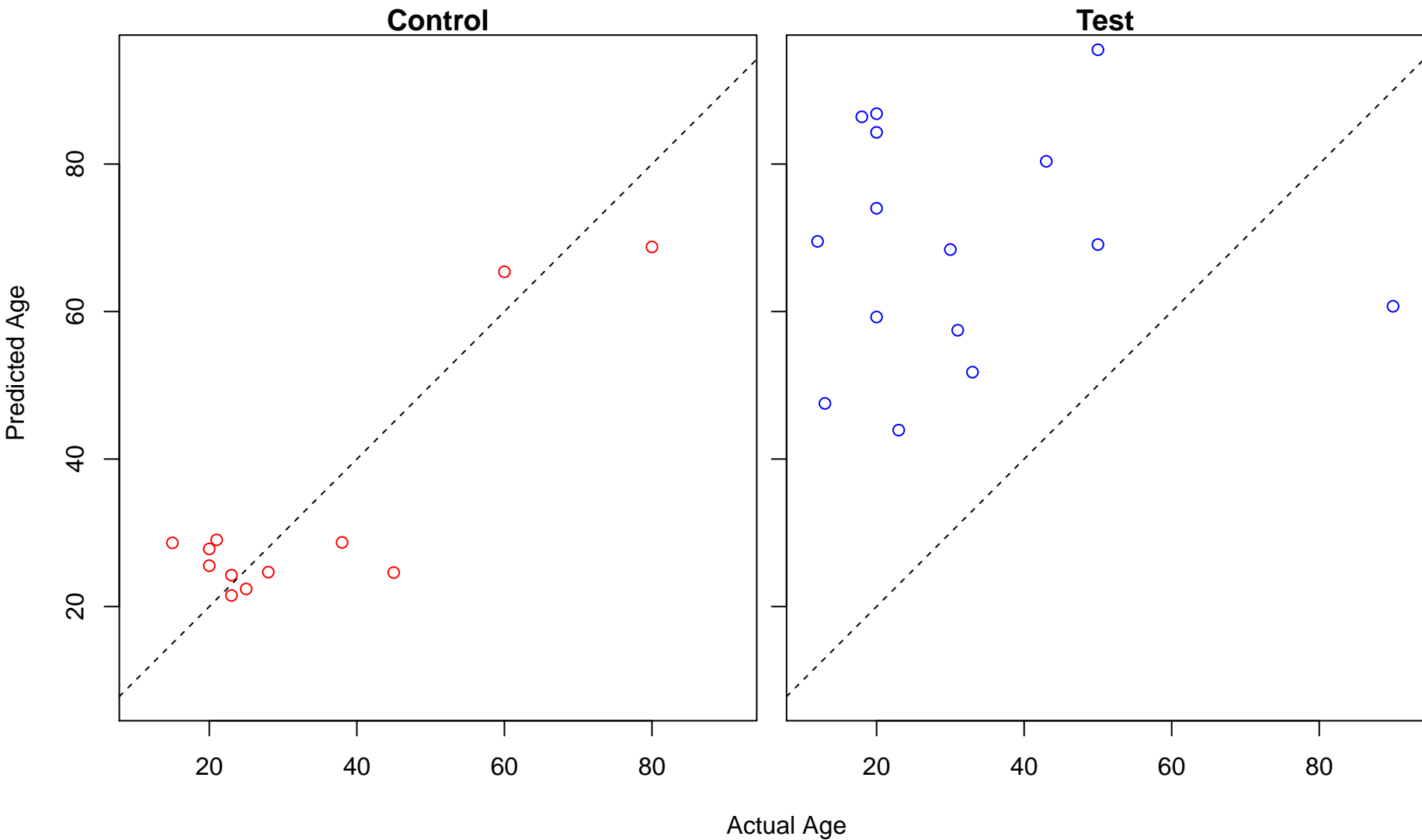
nitrogen cycle metabolic process (Score: 7.721404)



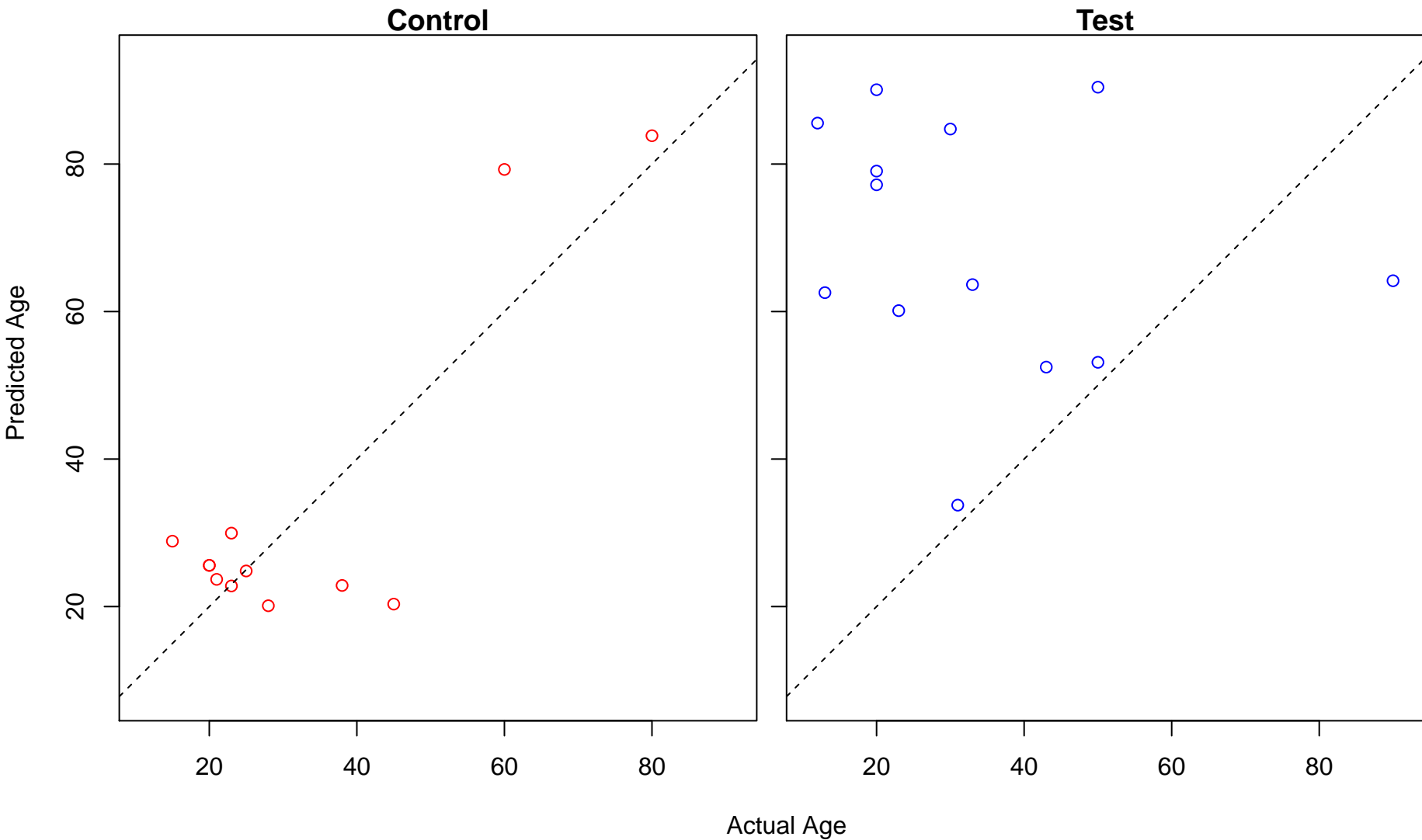
spliceosomal tri-snRNP complex assembly (Score: 7.721099)



cellular response to oxidative stress (Score: 7.720612)

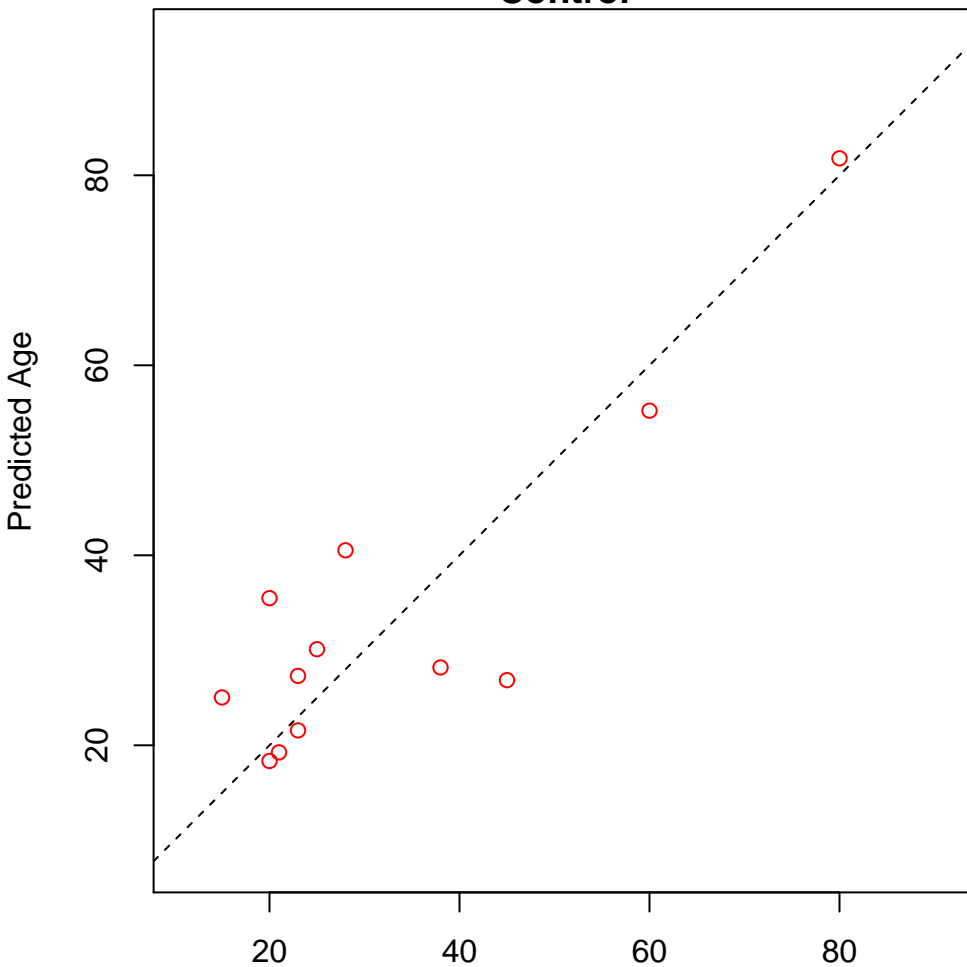


hormone secretion (Score: 7.719713)

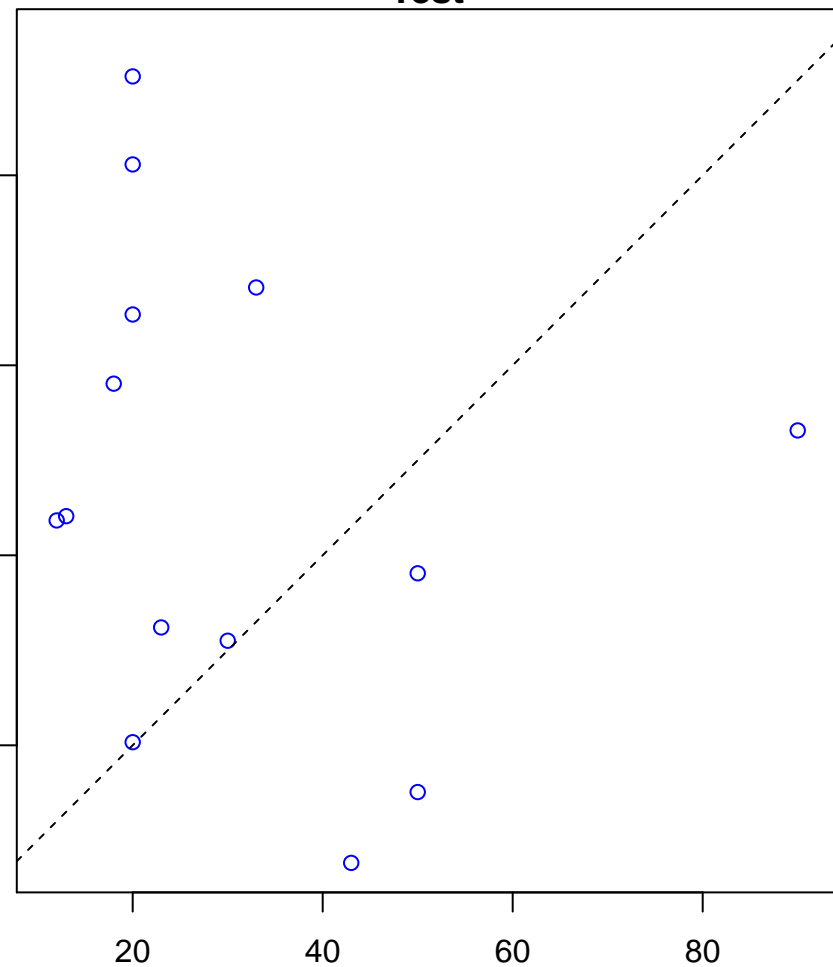


peptidyl-tyrosine phosphorylation (Score: 7.718093)

Control

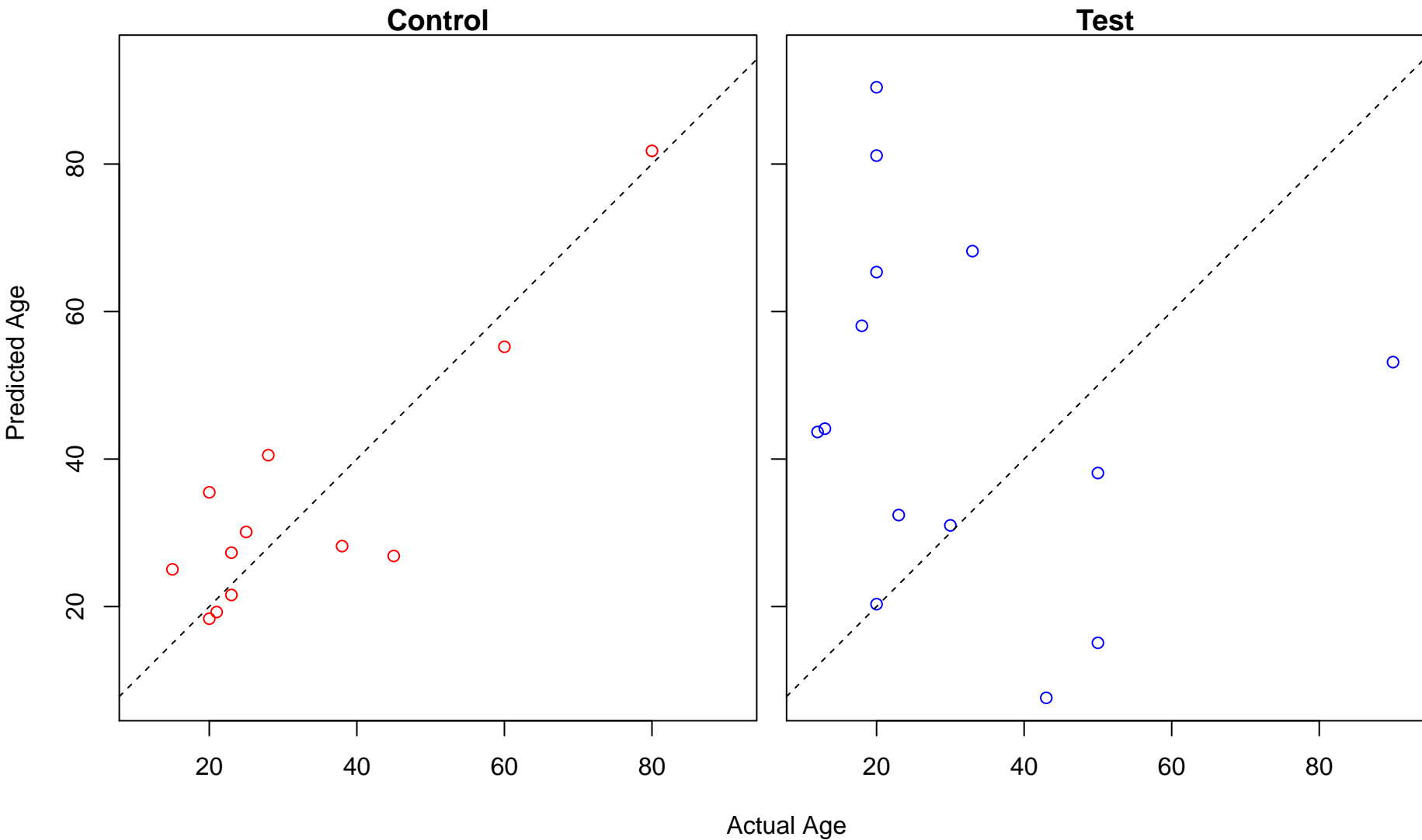


Test

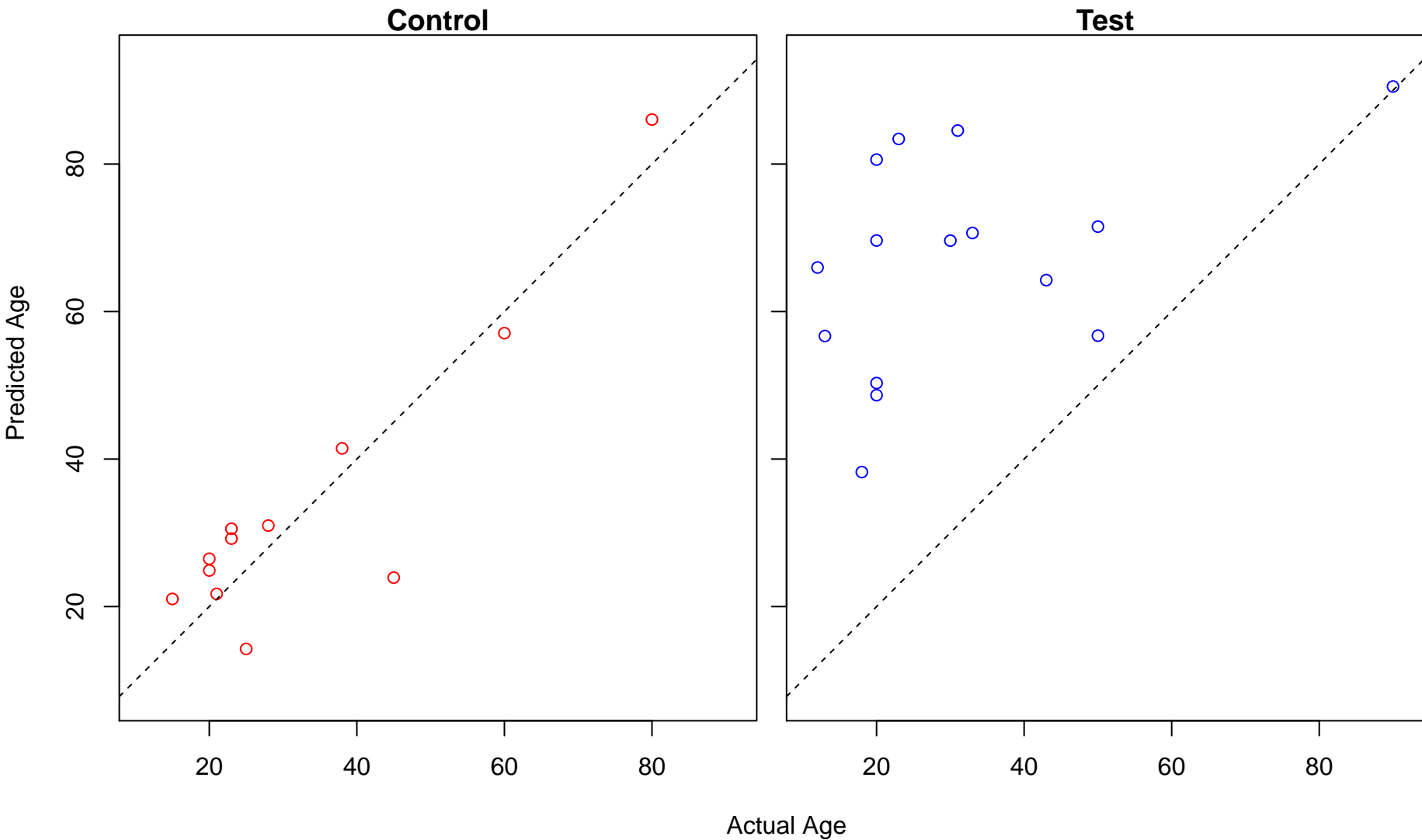


Actual Age

peptidyl-tyrosine modification (Score: 7.718093)

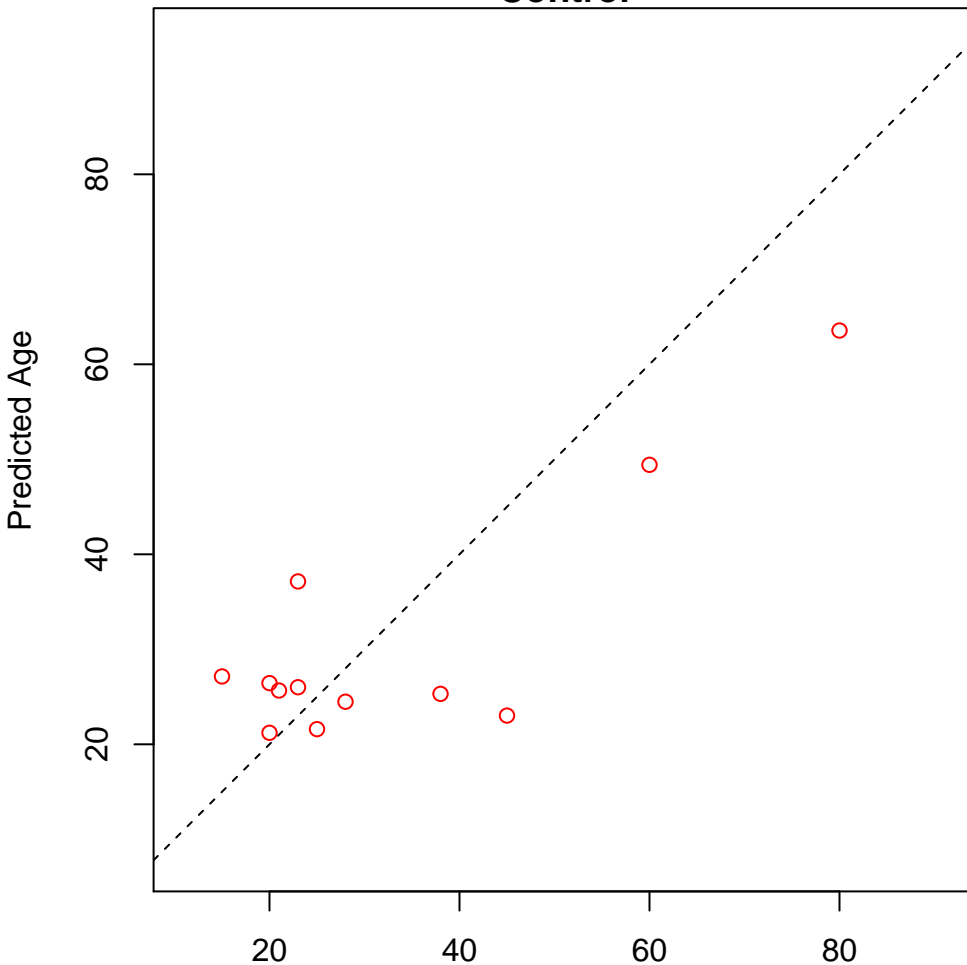


pancreas development (Score: 7.715775)

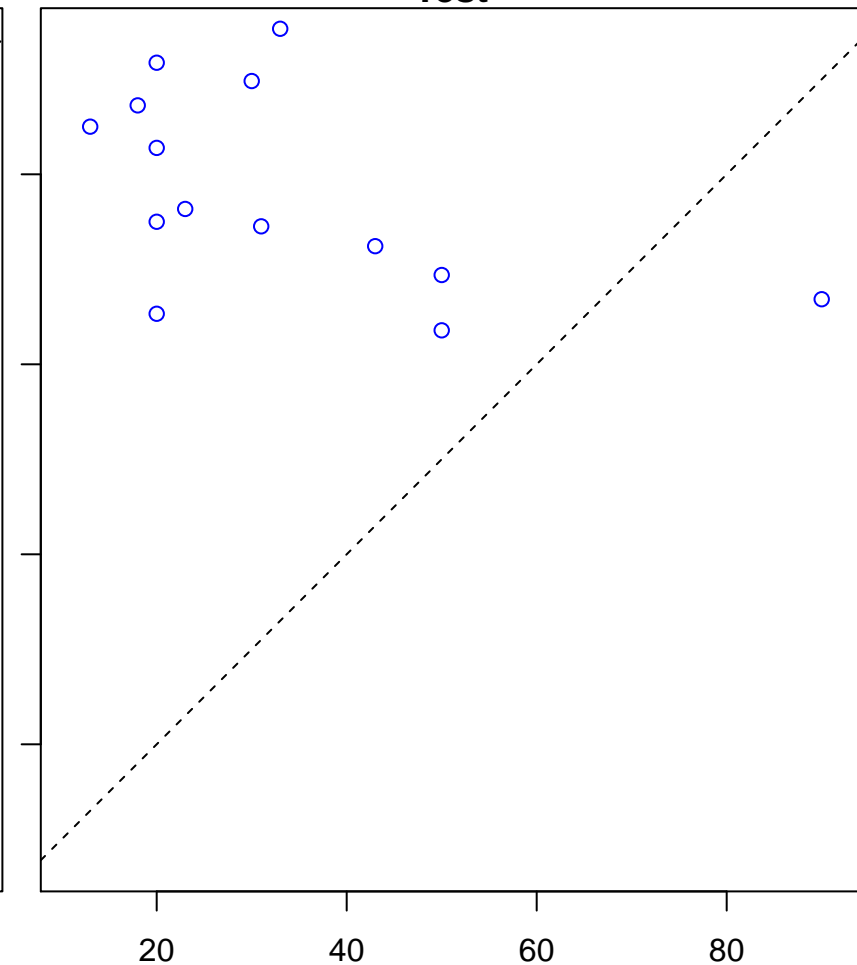


regulation of macrophage differentiation (Score: 7.714151)

Control

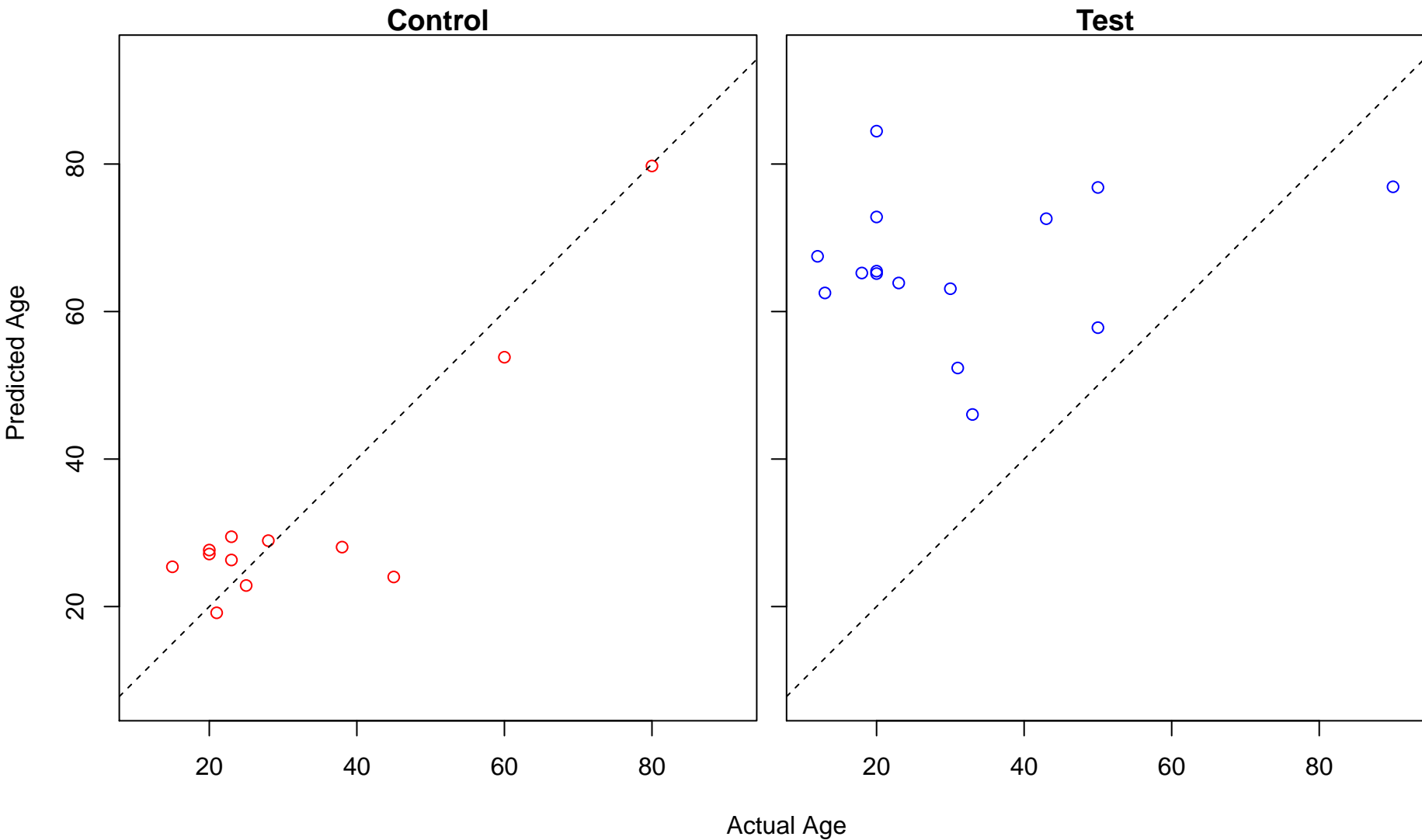


Test

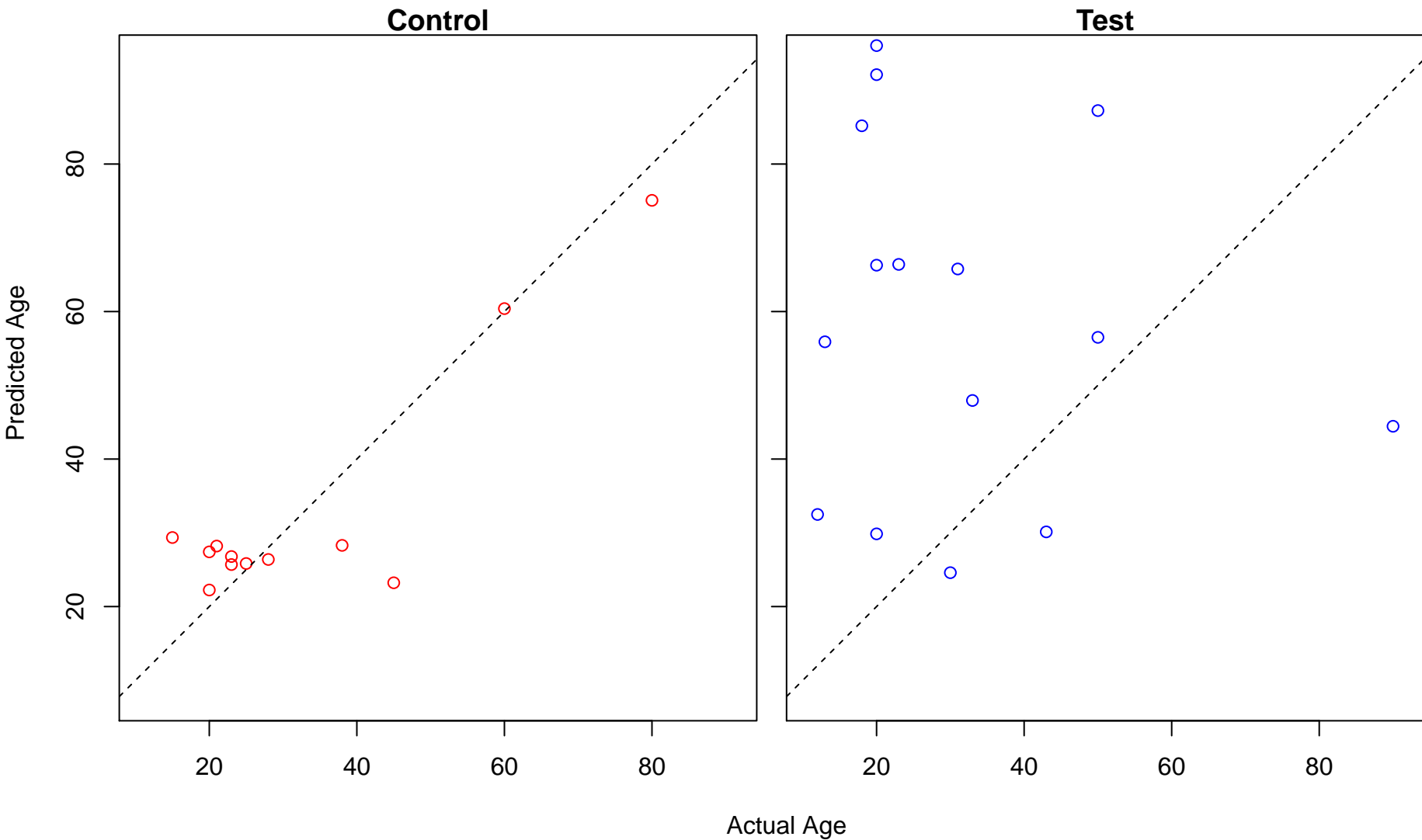


Actual Age

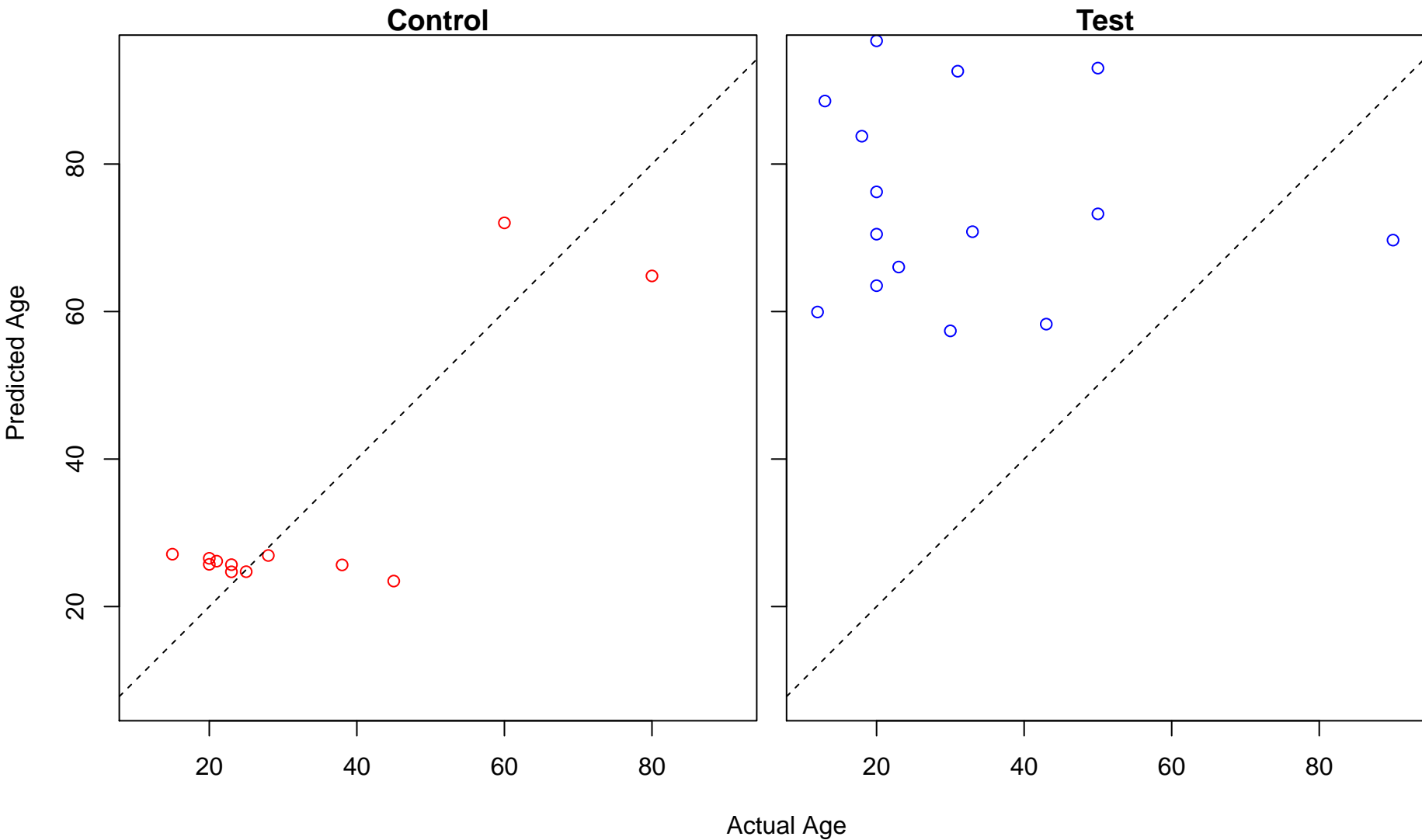
positive regulation of macrophage derived foam cell differentiation (Score: 7.711739)



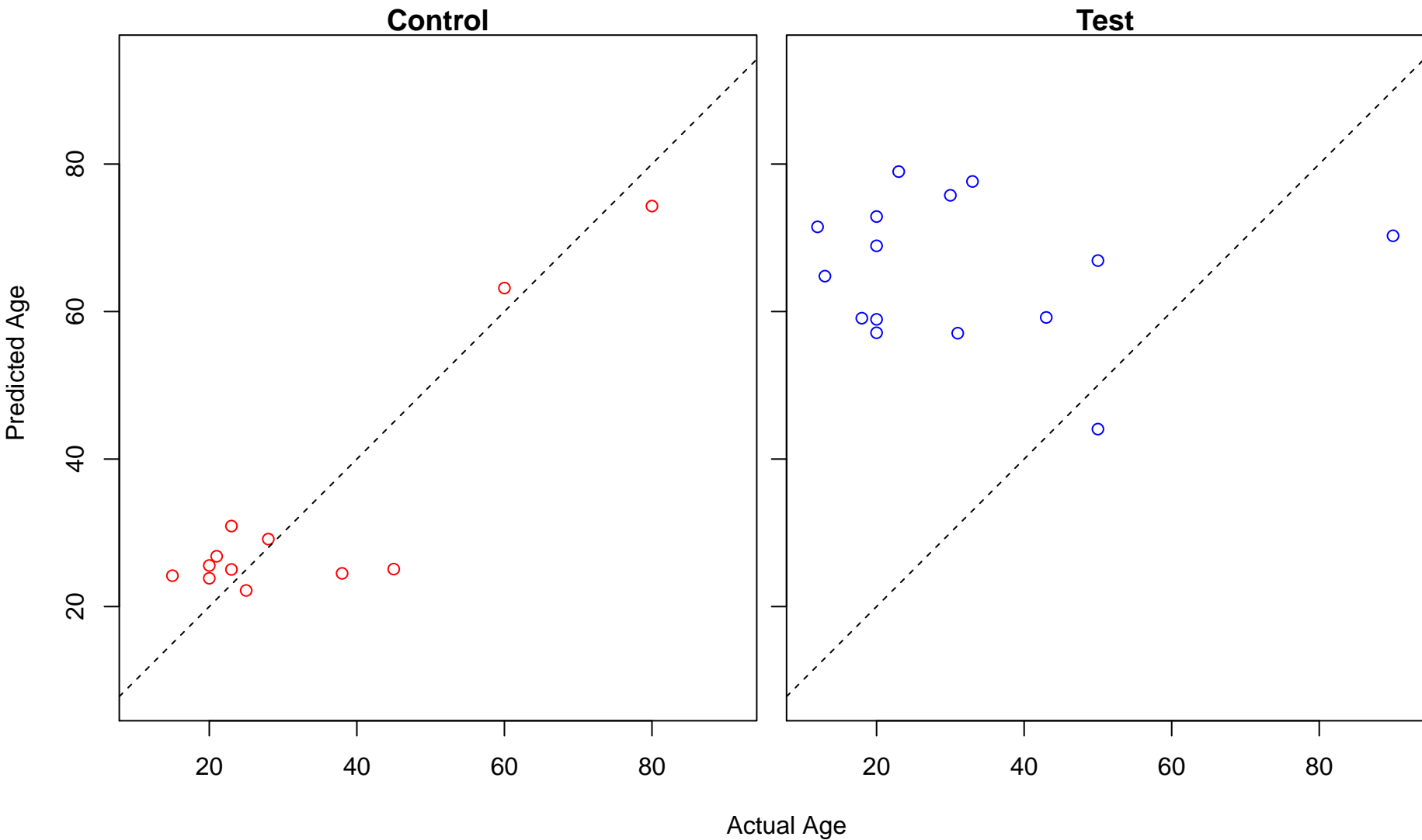
tissue homeostasis (Score: 7.709398)



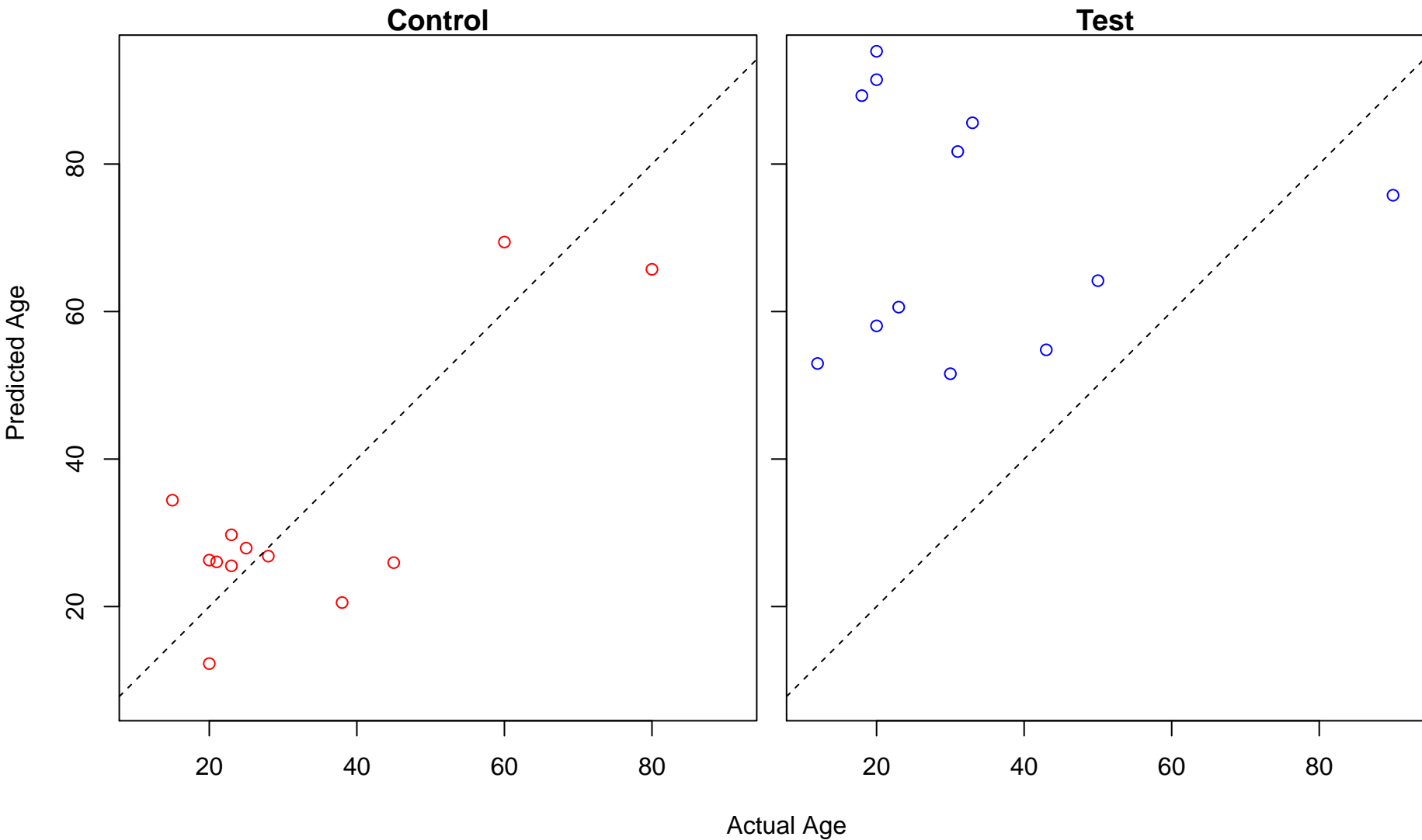
regulation of gene expression, epigenetic (Score: 7.707721)



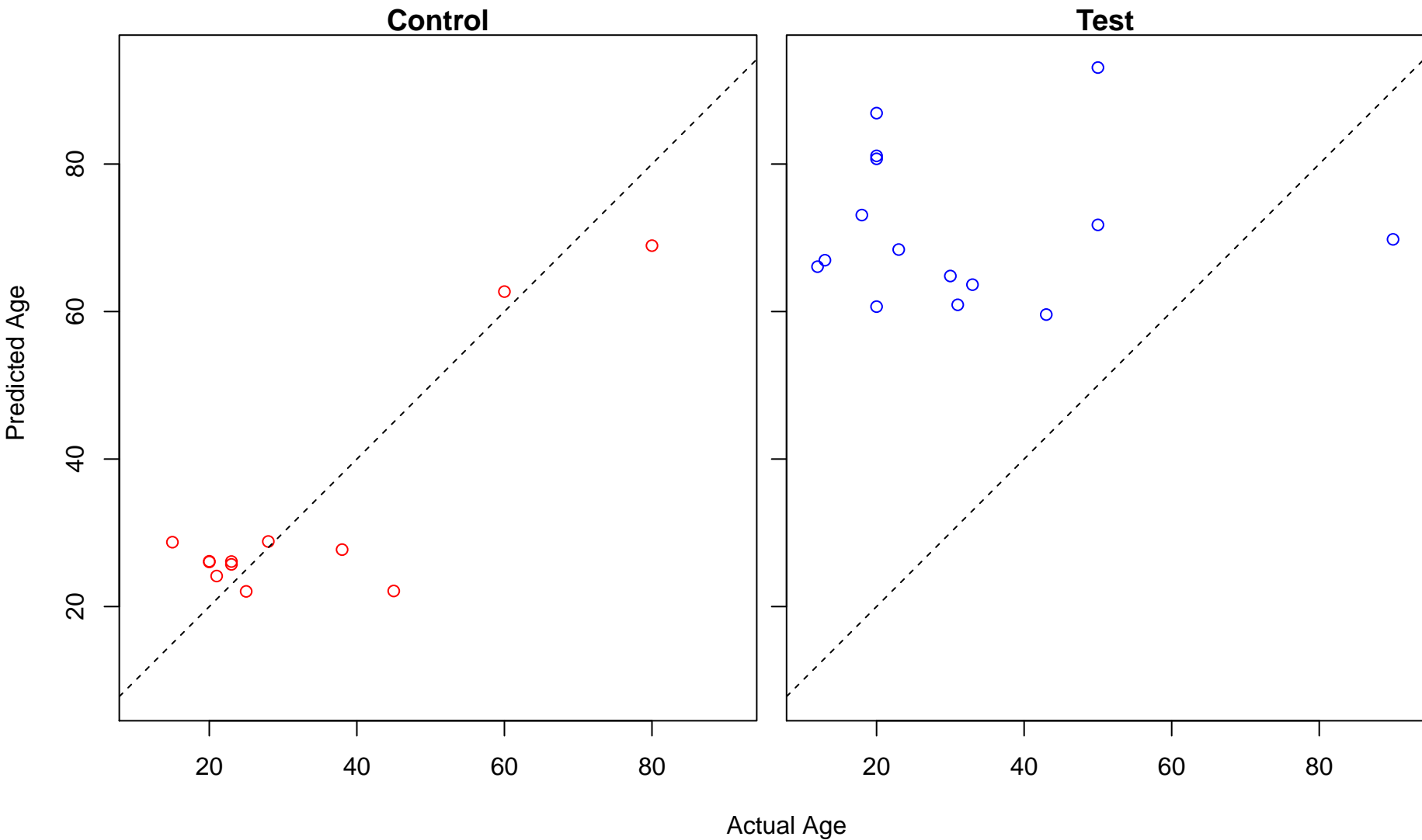
phosphatidylcholine acyl-chain remodeling (Score: 7.706991)



mesenchymal to epithelial transition (Score: 7.705841)

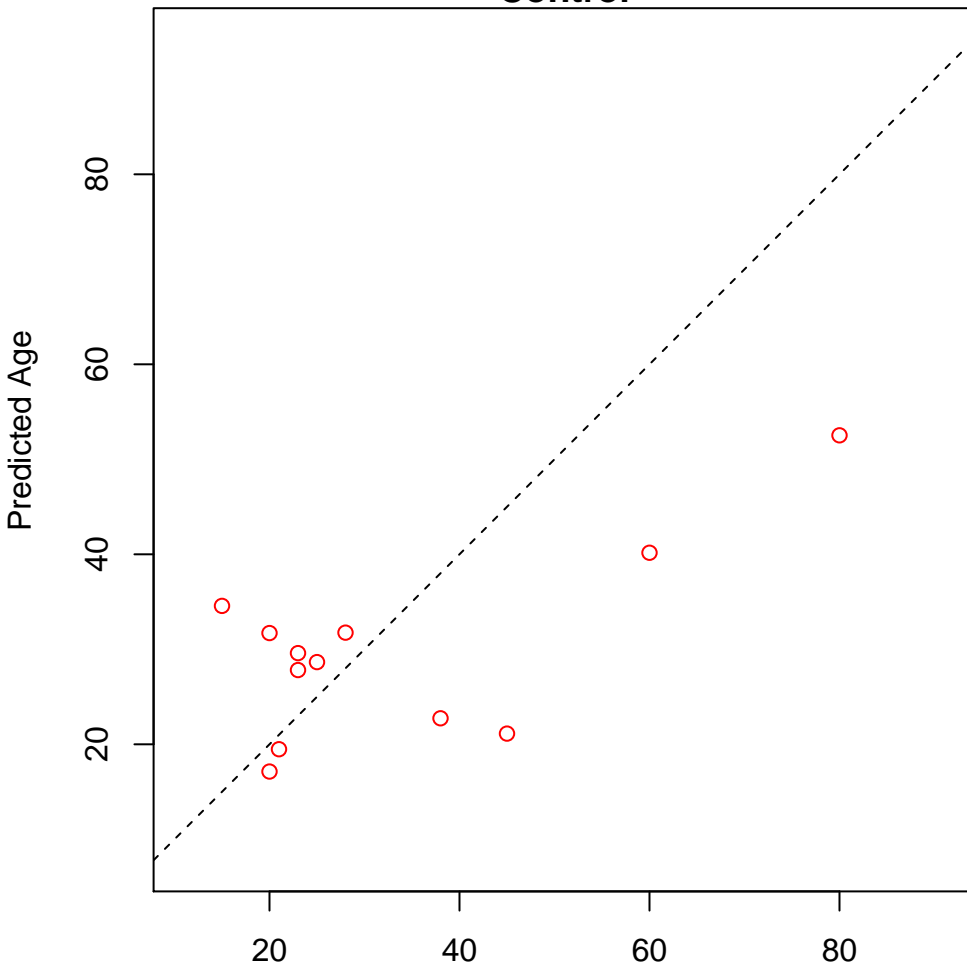


mRNA 3'-splice site recognition (Score: 7.700664)

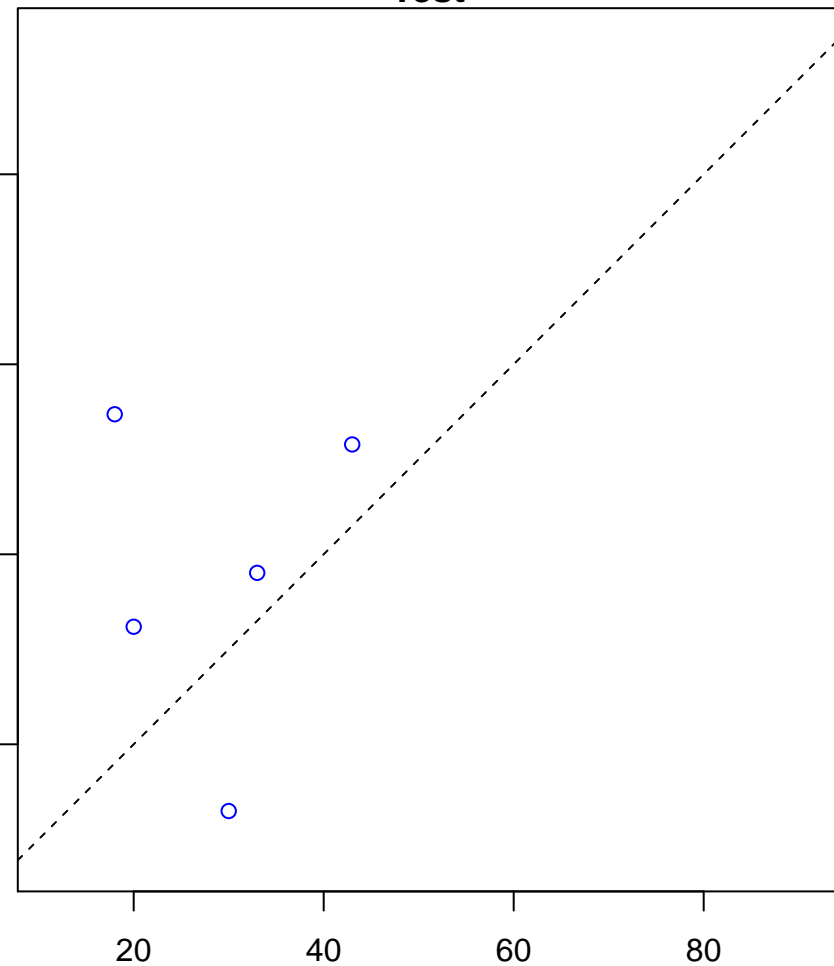


high-density lipoprotein particle clearance (Score: 7.698938)

Control

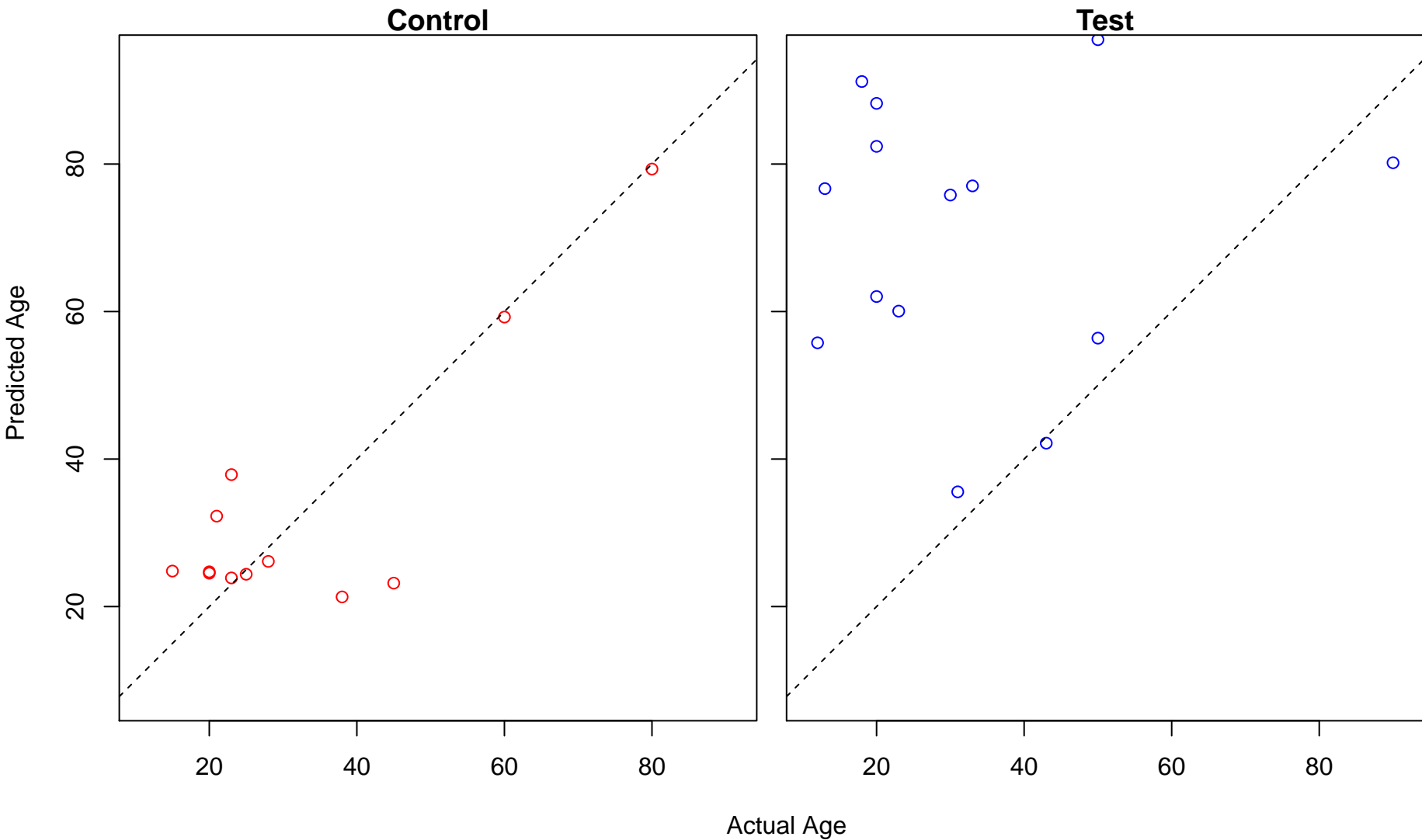


Test

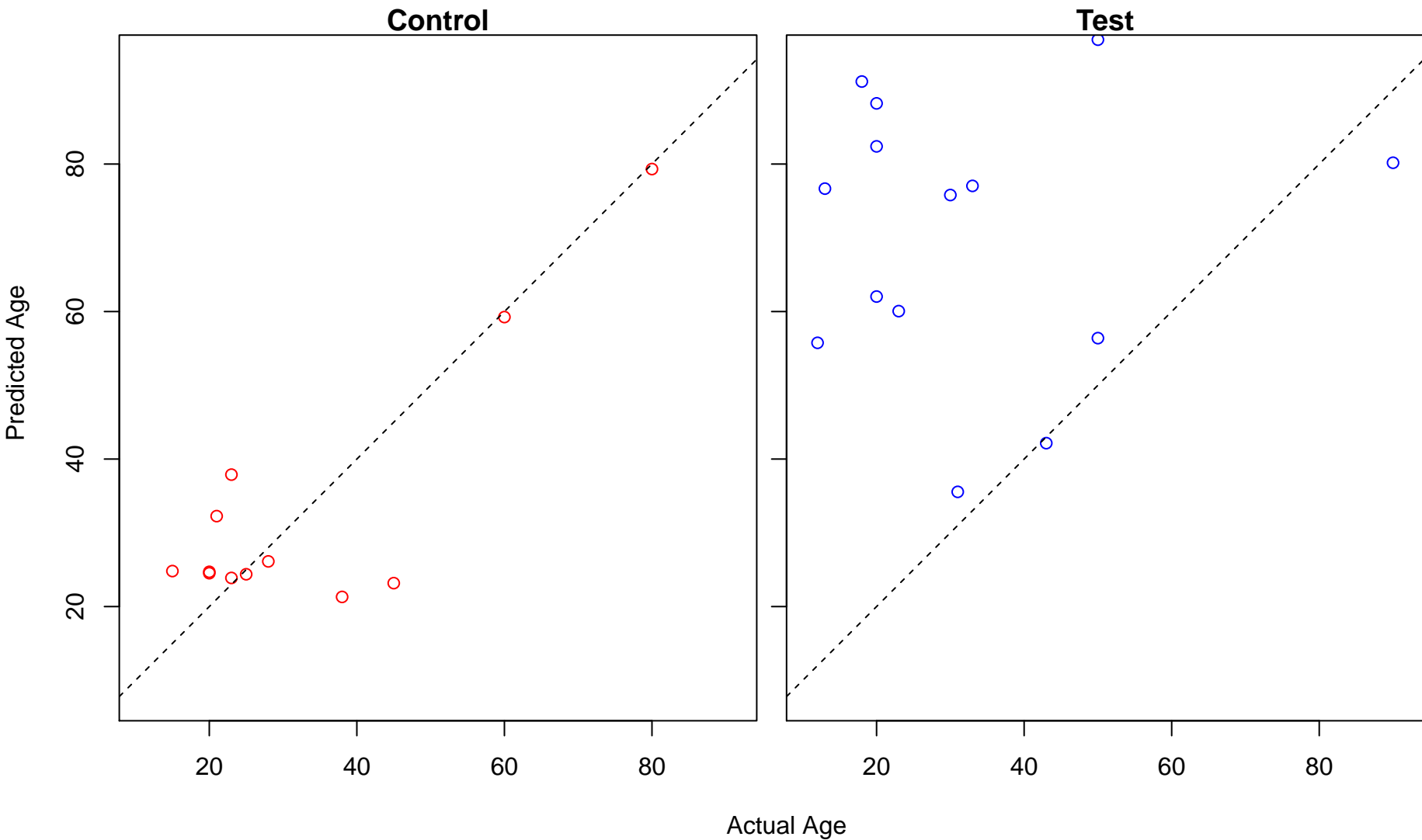


Actual Age

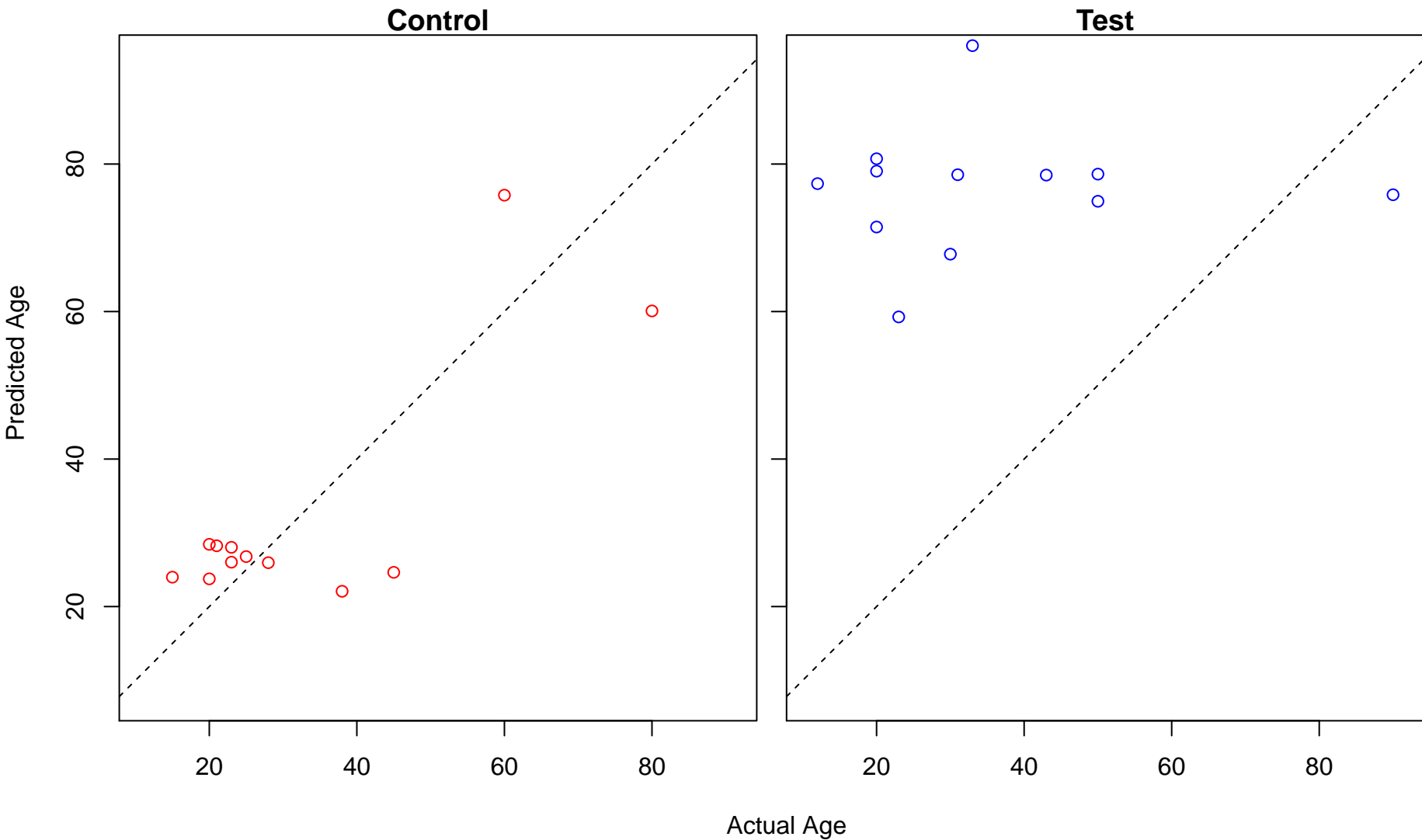
regulation of cofactor metabolic process (Score: 7.683754)



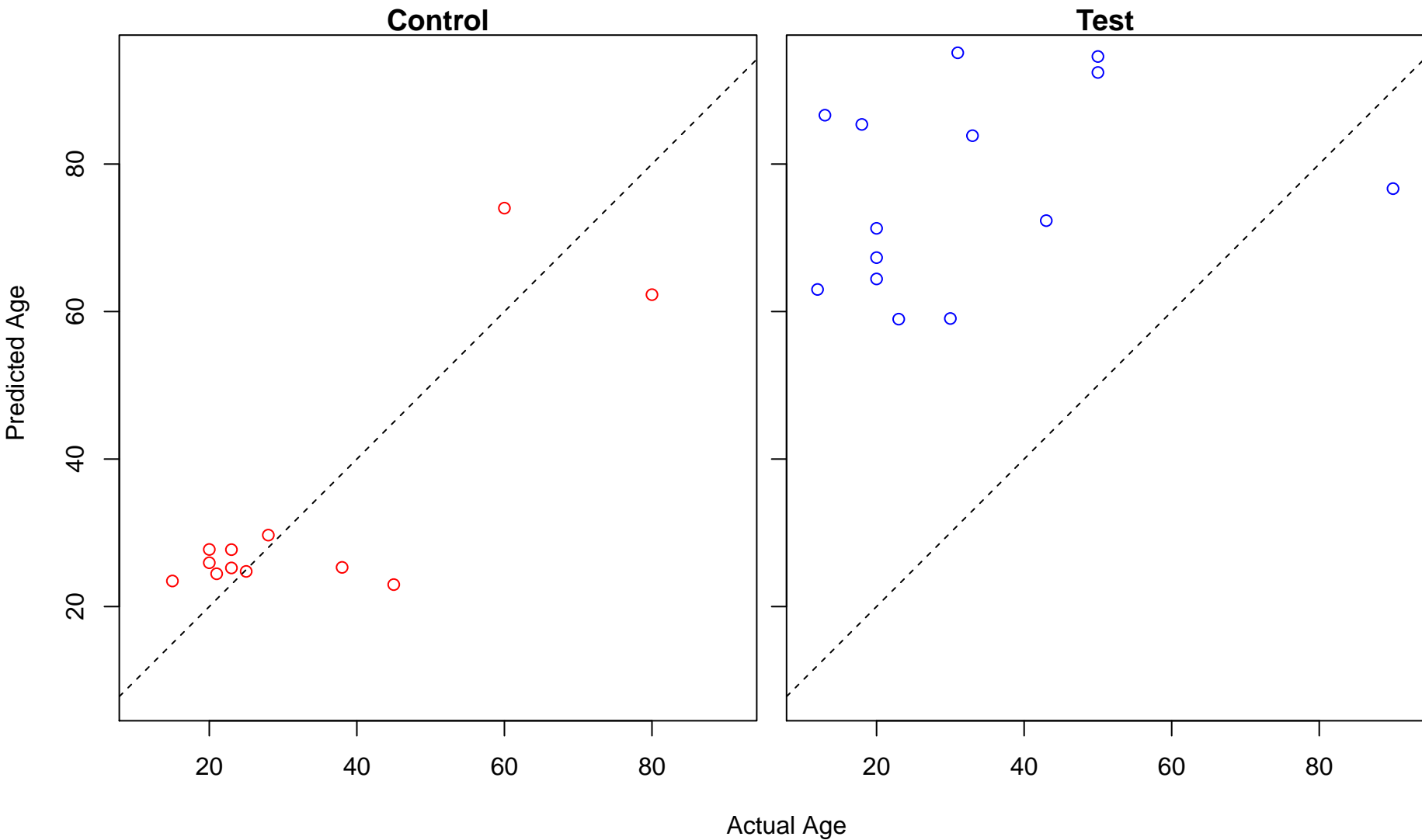
regulation of coenzyme metabolic process (Score: 7.683754)



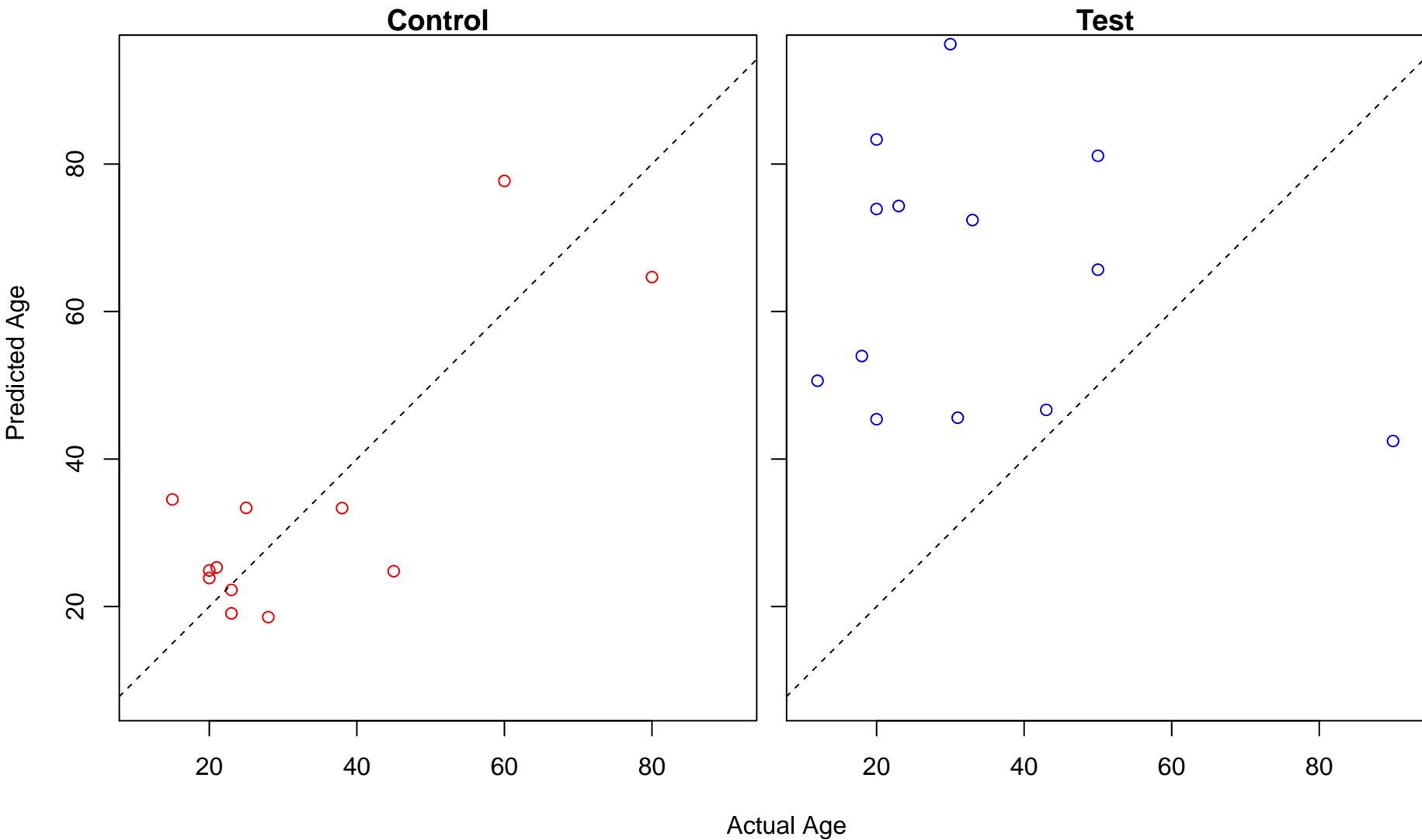
kynurenine metabolic process (Score: 7.682769)



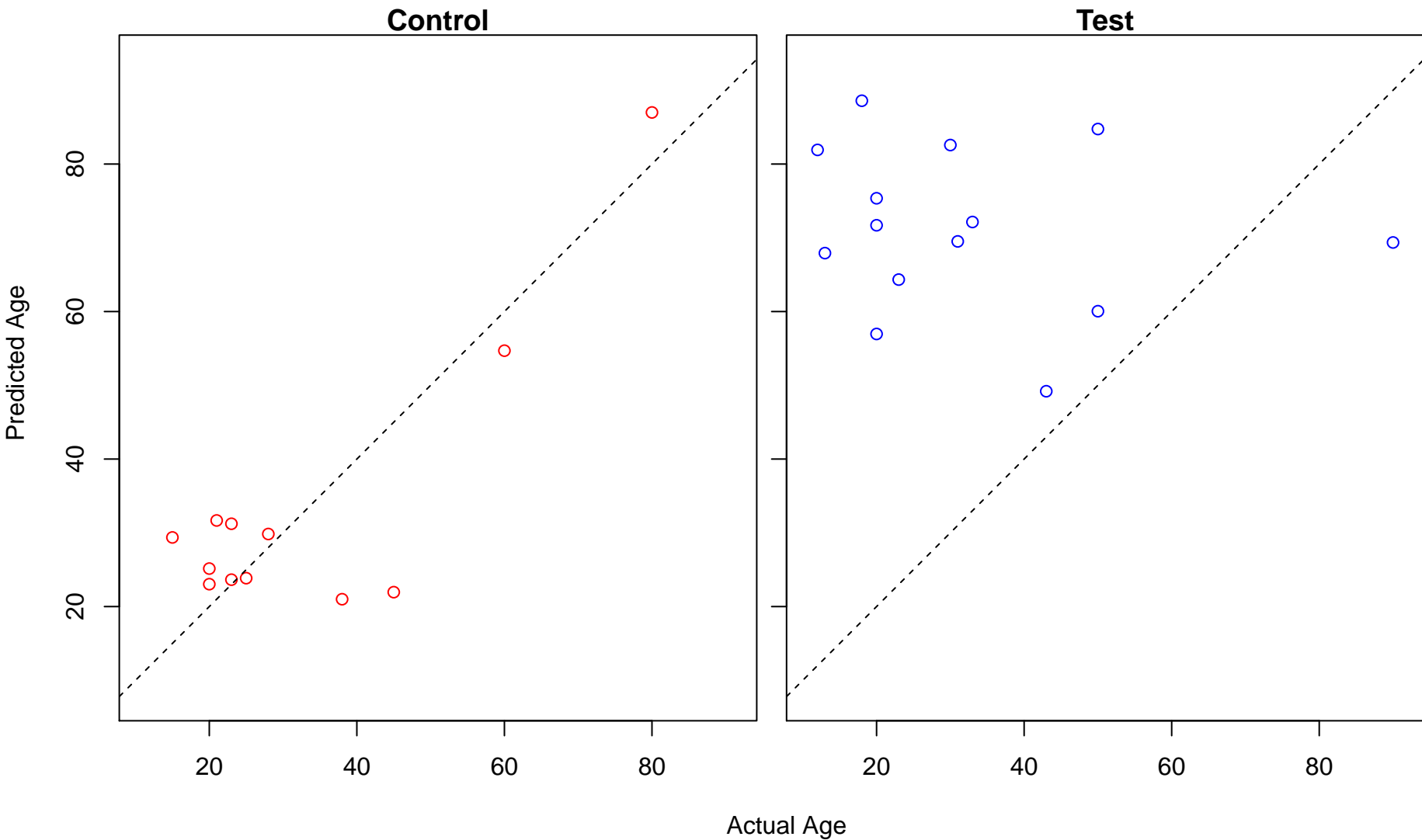
myeloid leukocyte migration (Score: 7.676810)



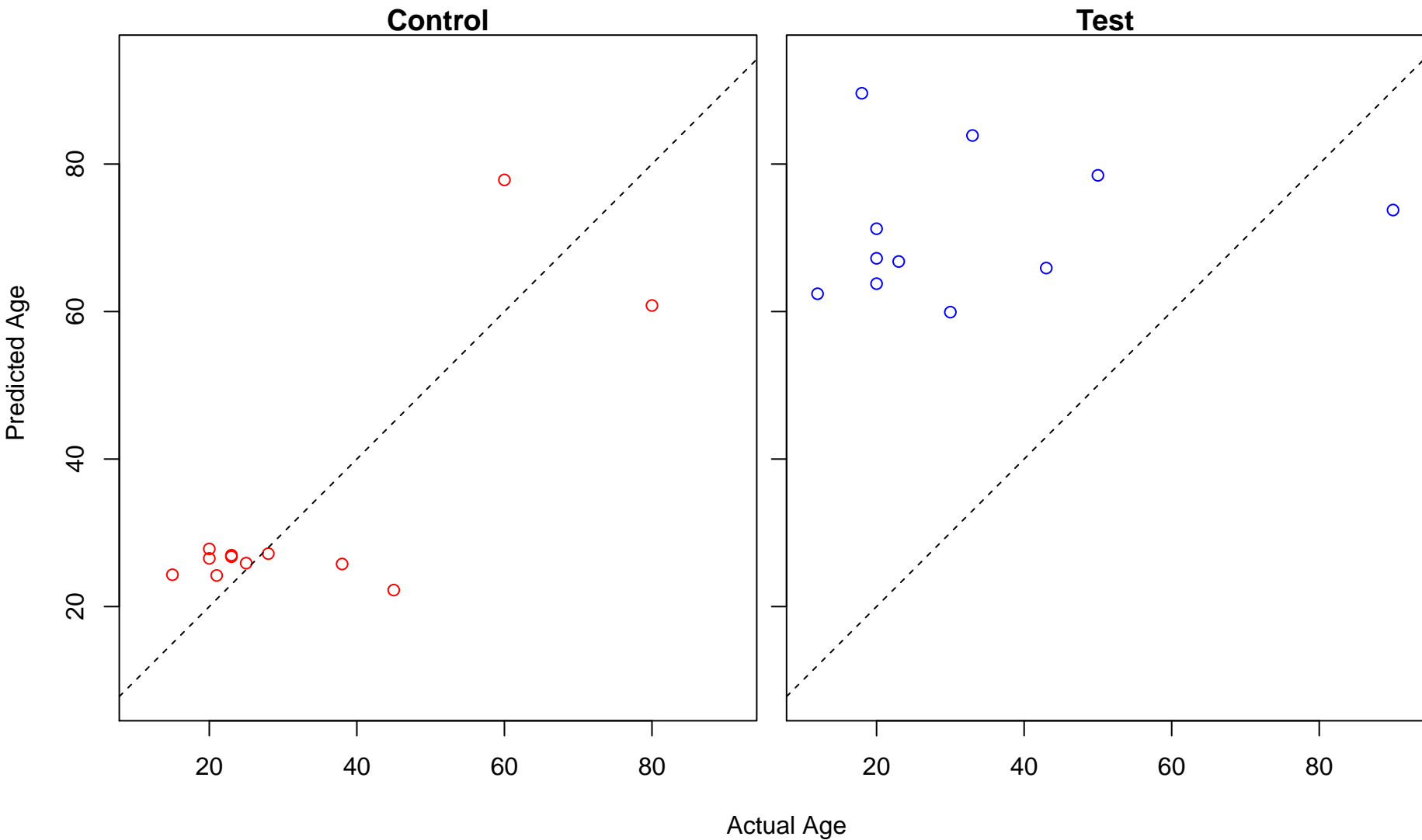
sulfur amino acid transport (Score: 7.676582)



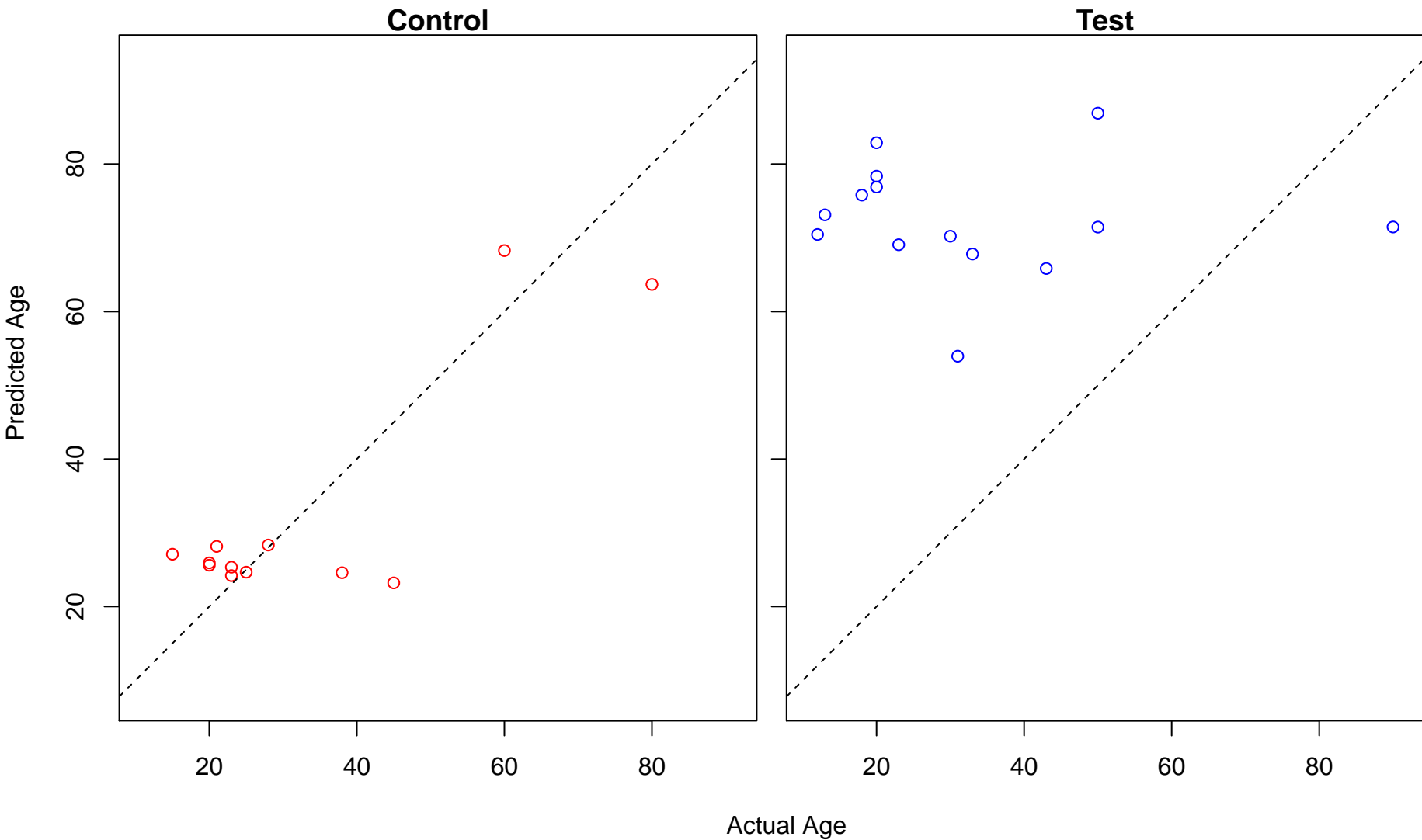
vesicle coating (Score: 7.673202)



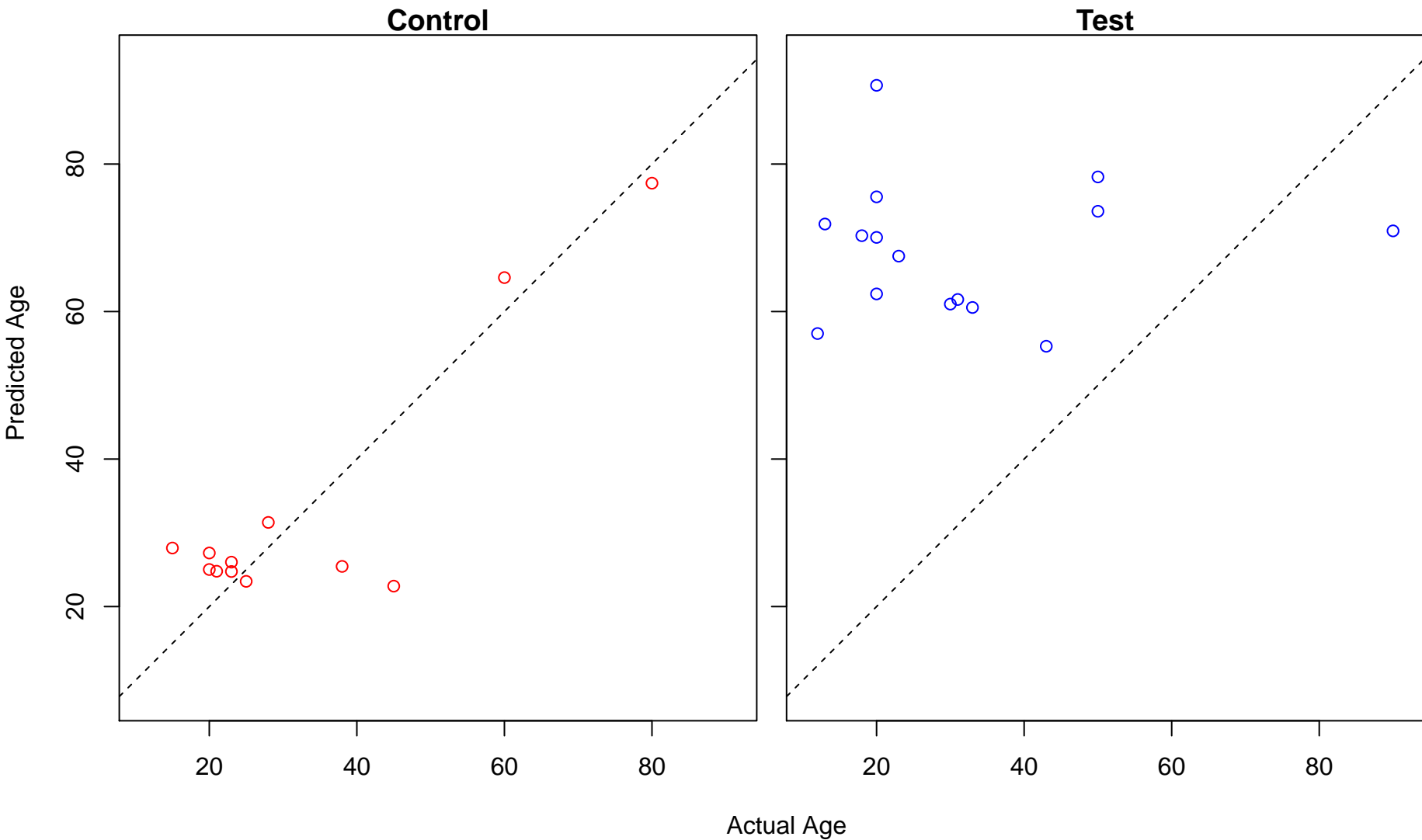
defense response to Gram-positive bacterium (Score: 7.672781)



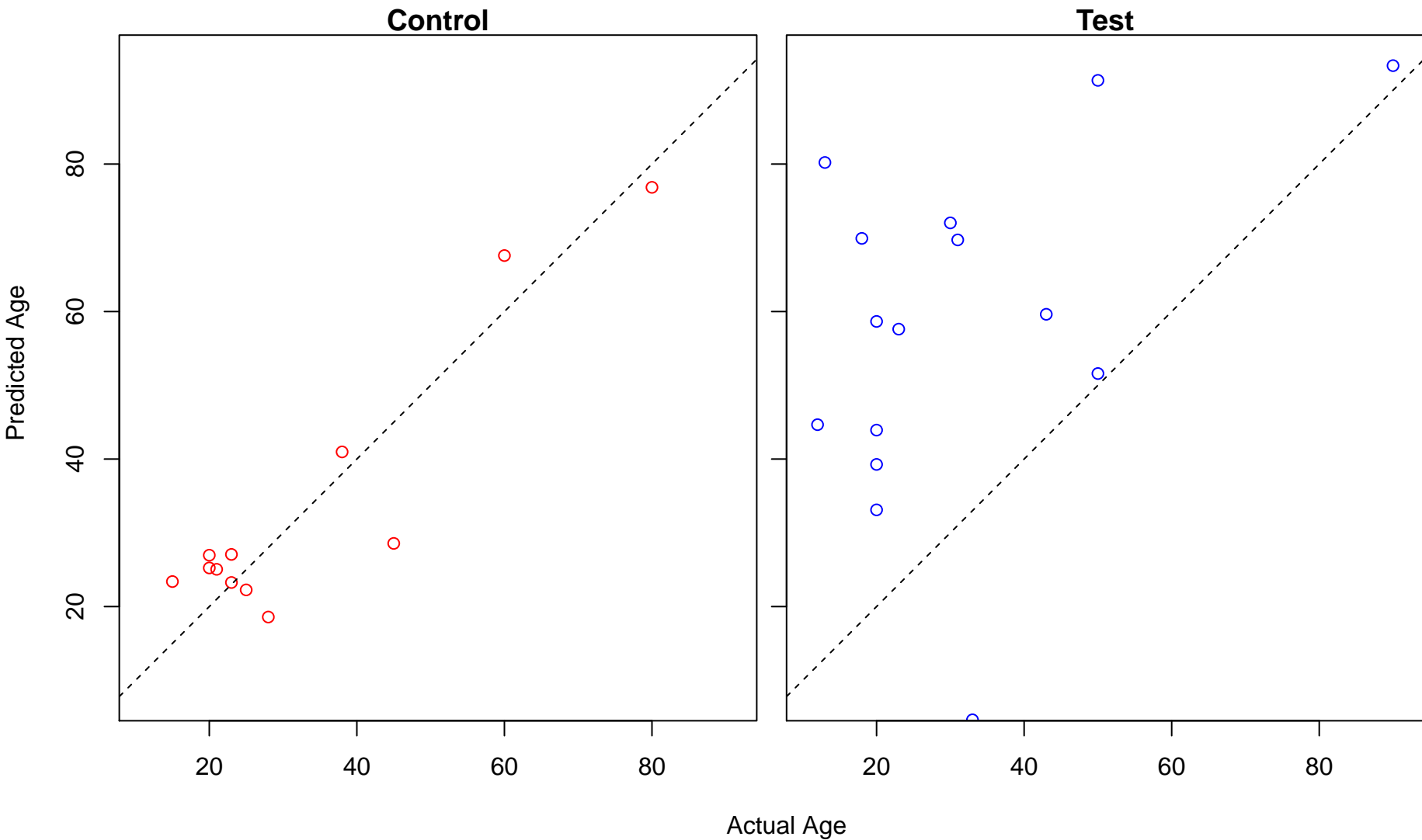
nucleotide catabolic process (Score: 7.671975)



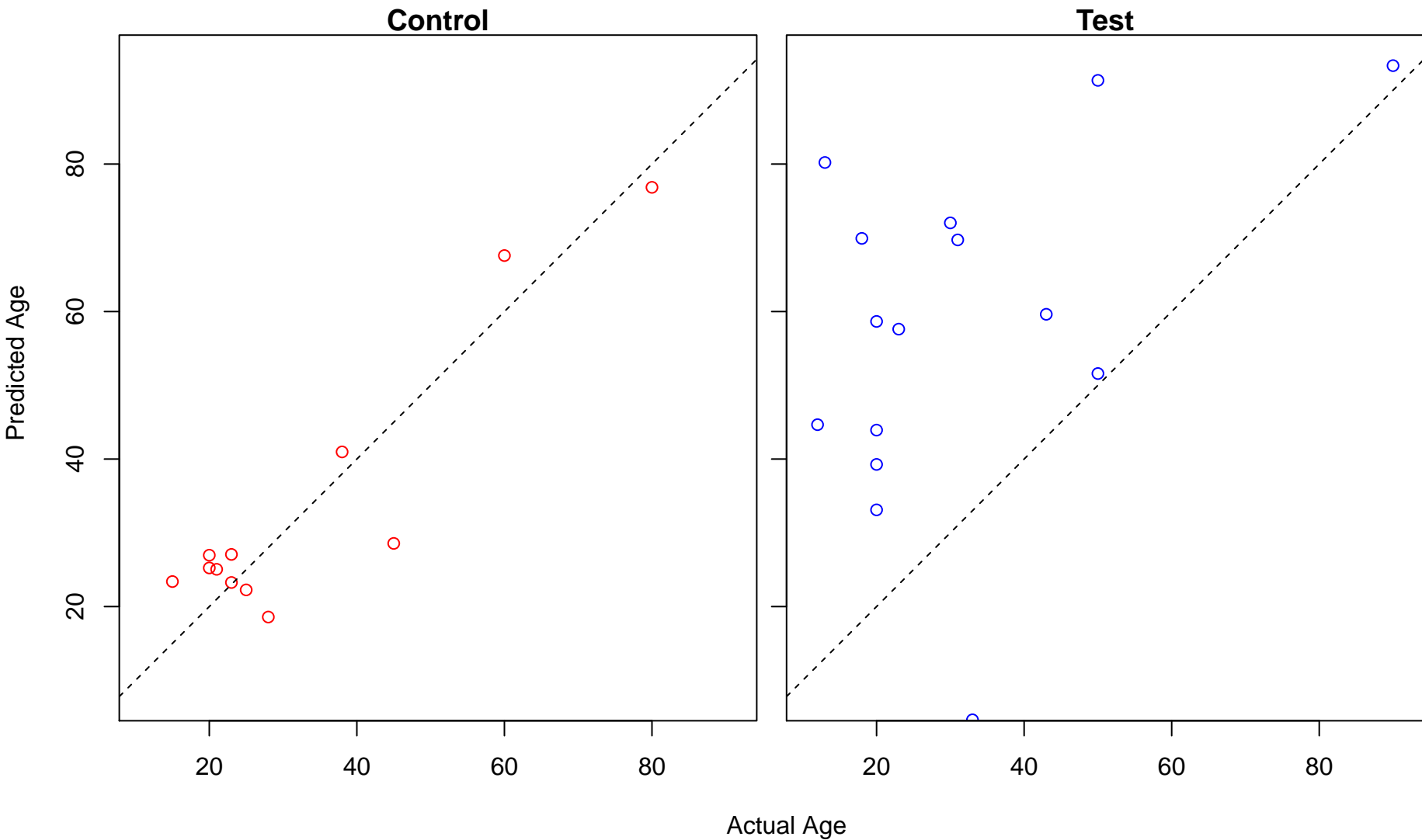
generation of precursor metabolites and energy (Score: 7.671724)



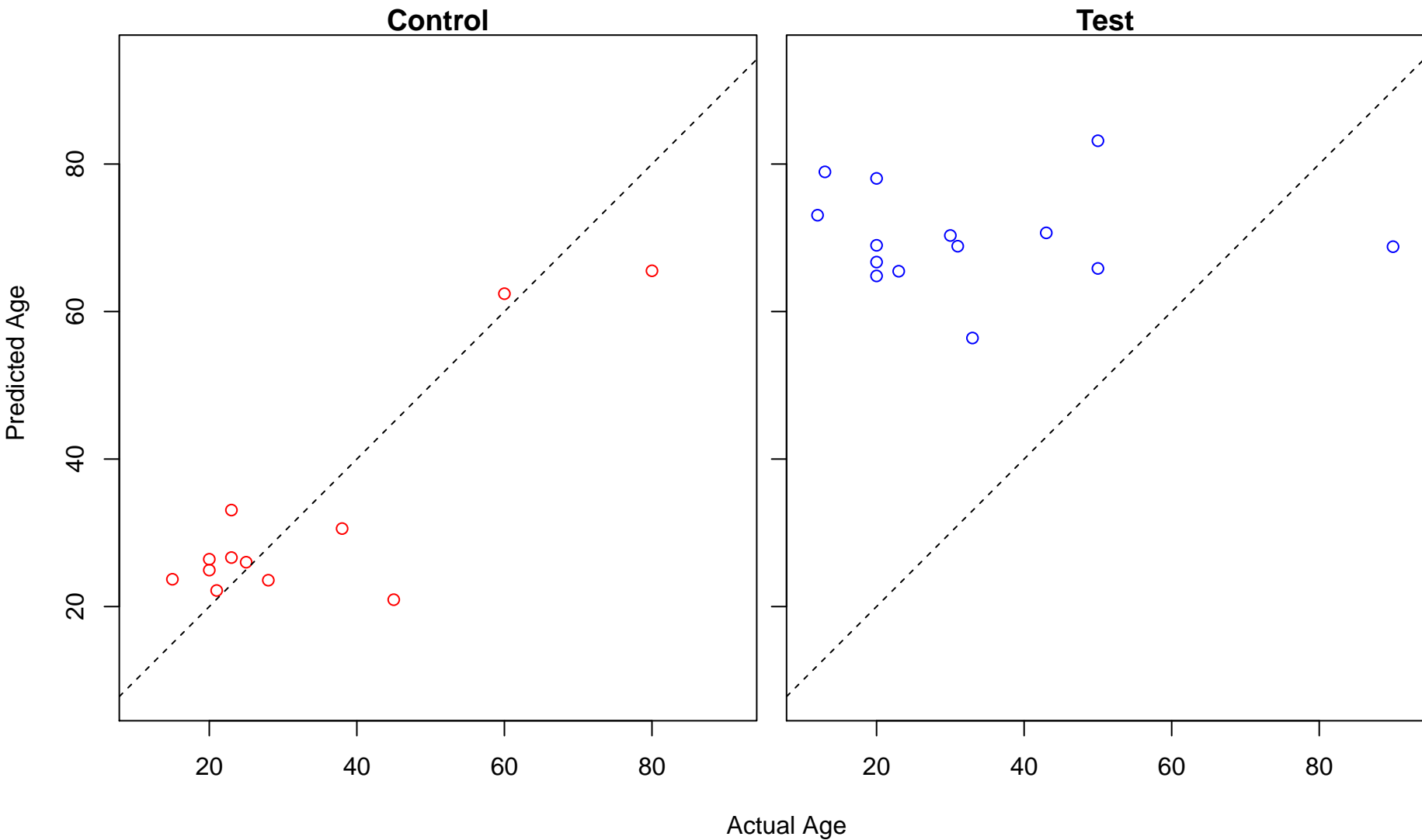
MHC protein complex assembly (Score: 7.671083)



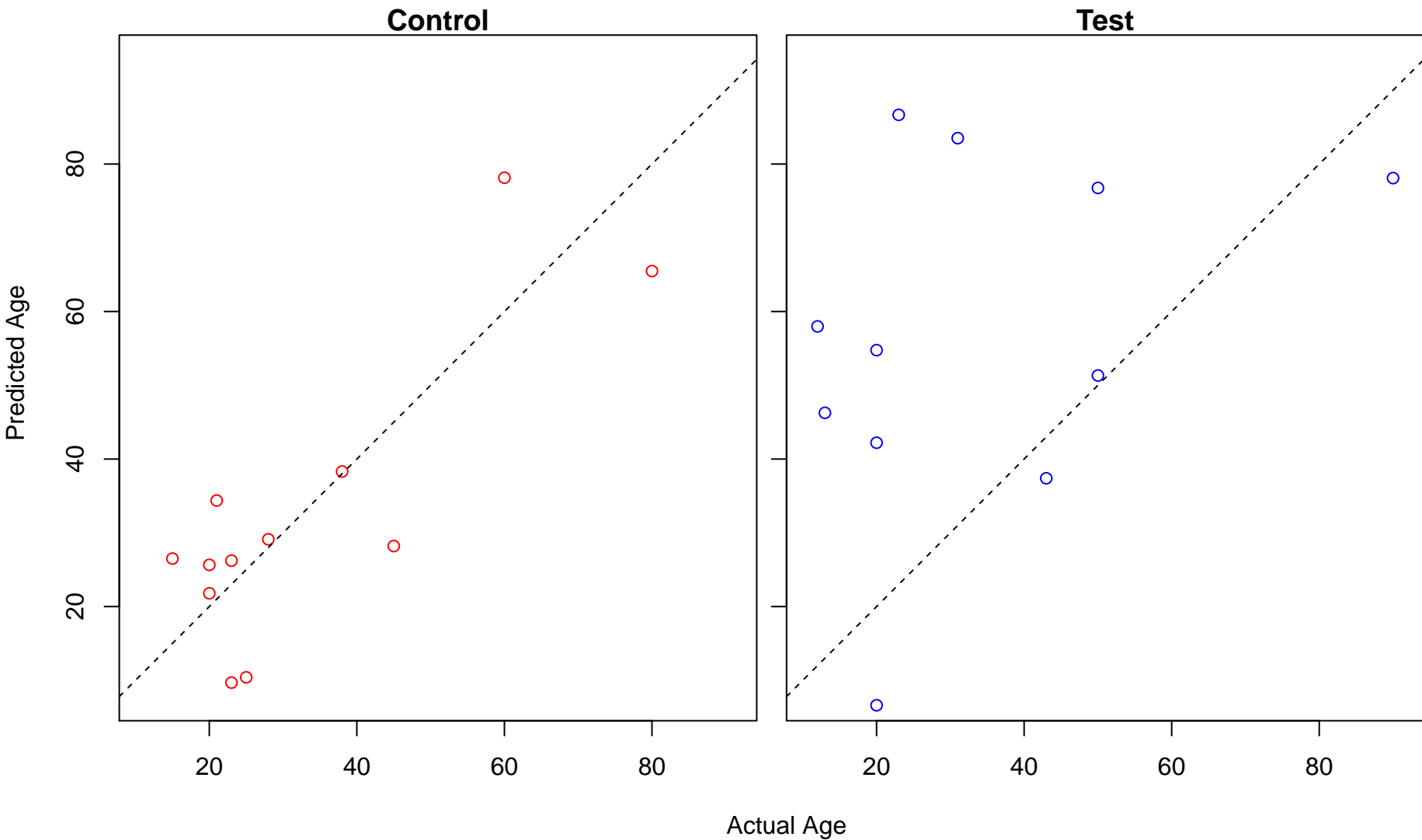
peptide antigen assembly with MHC protein complex (Score: 7.671083)



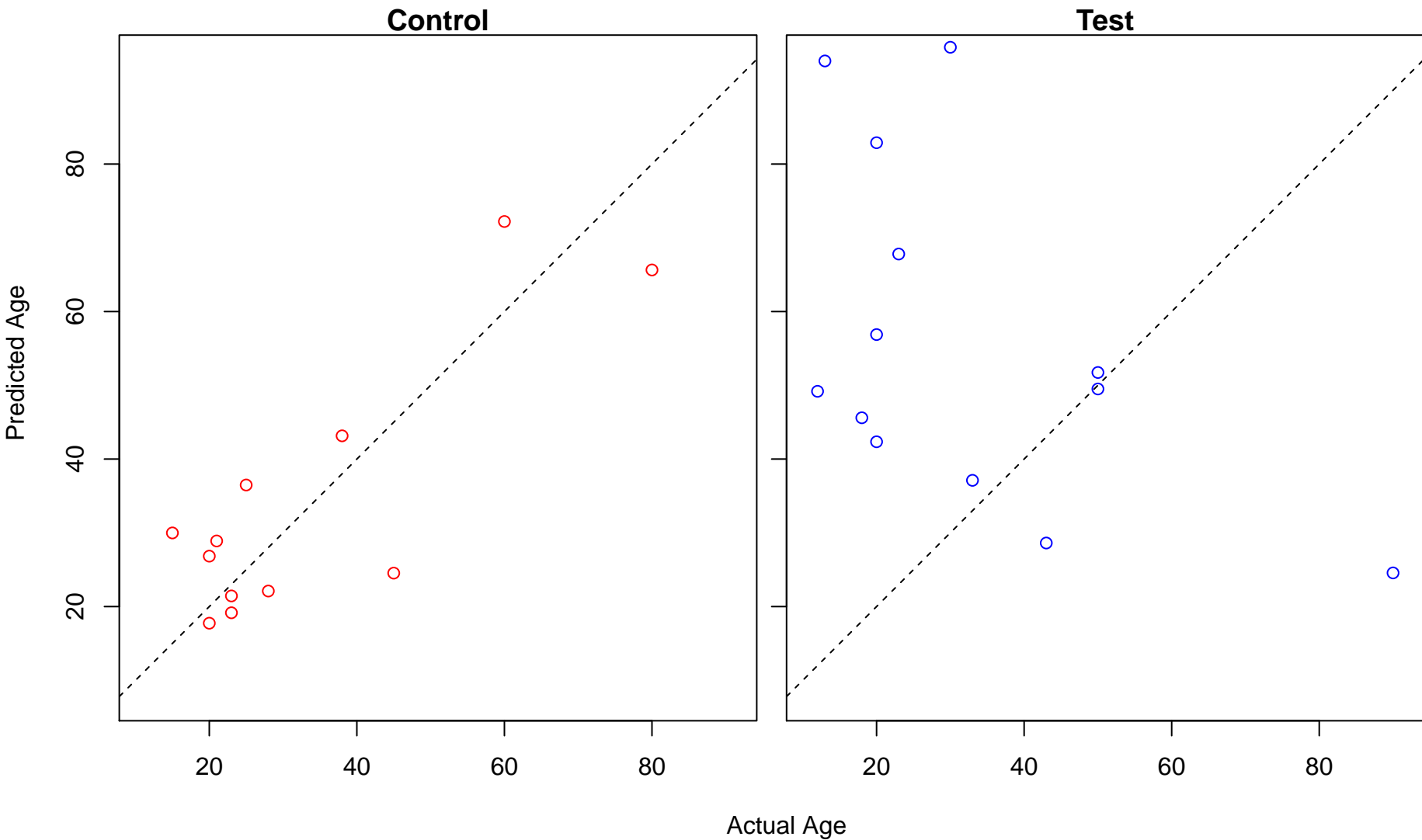
regulation of myoblast differentiation (Score: 7.669245)



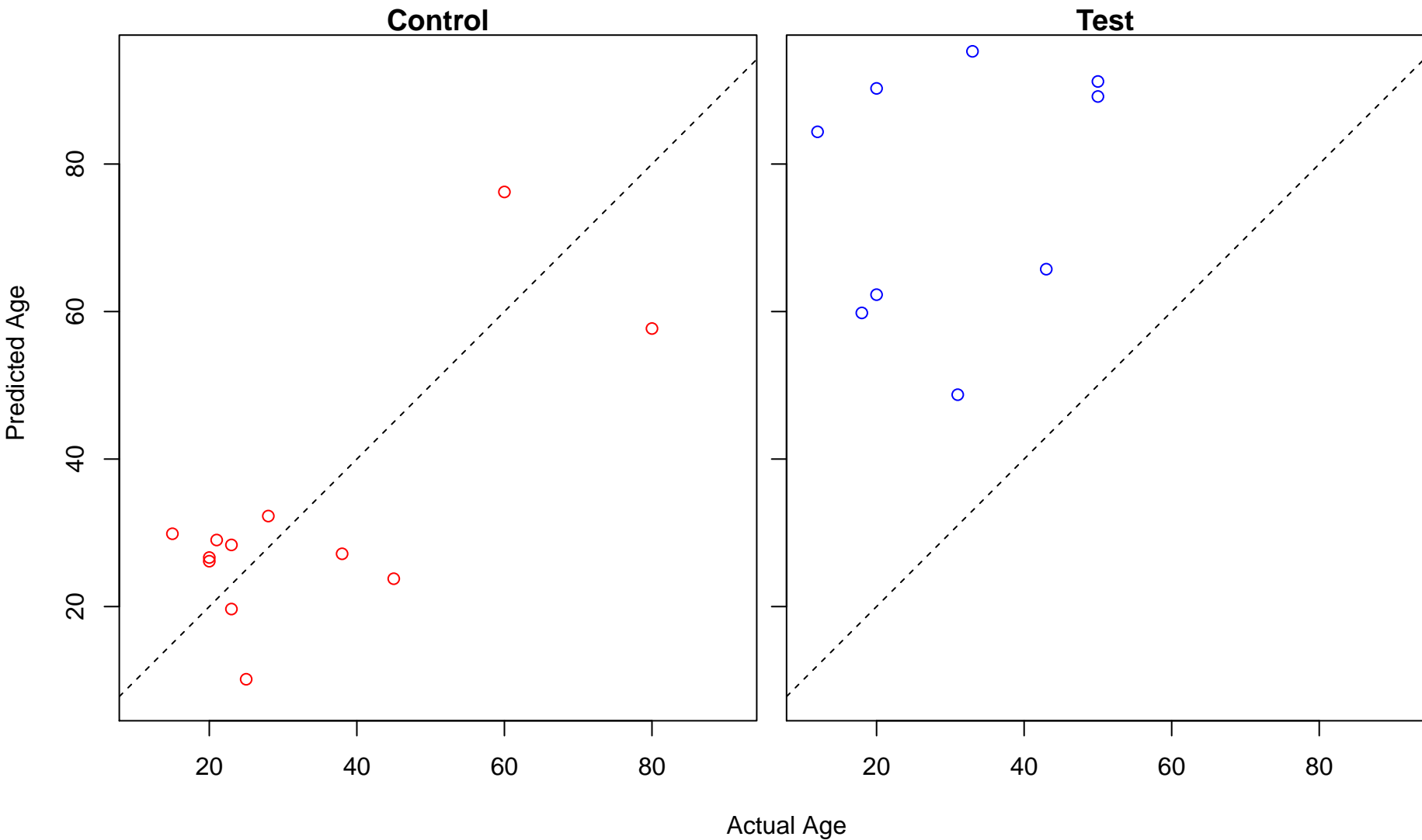
regulation of actin filament depolymerization (Score: 7.668653)



L-cystine transport (Score: 7.668475)

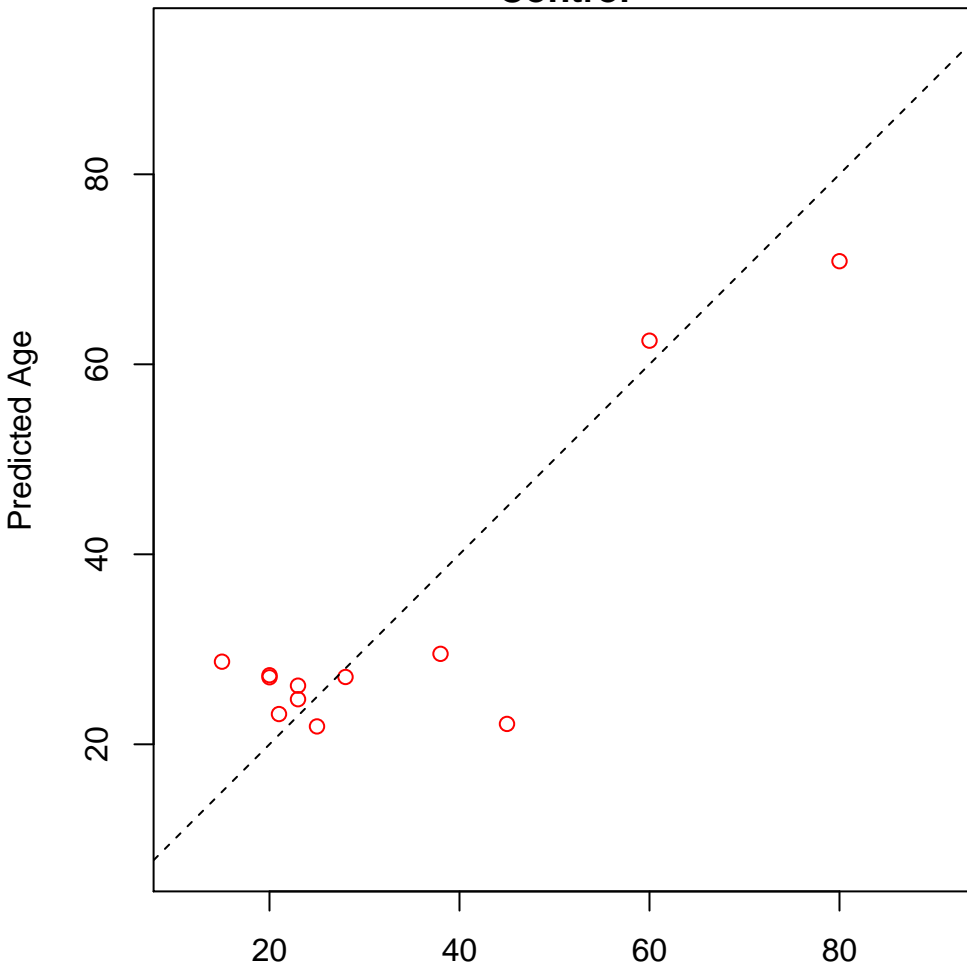


positive regulation of lipoprotein lipase activity (Score: 7.666843)

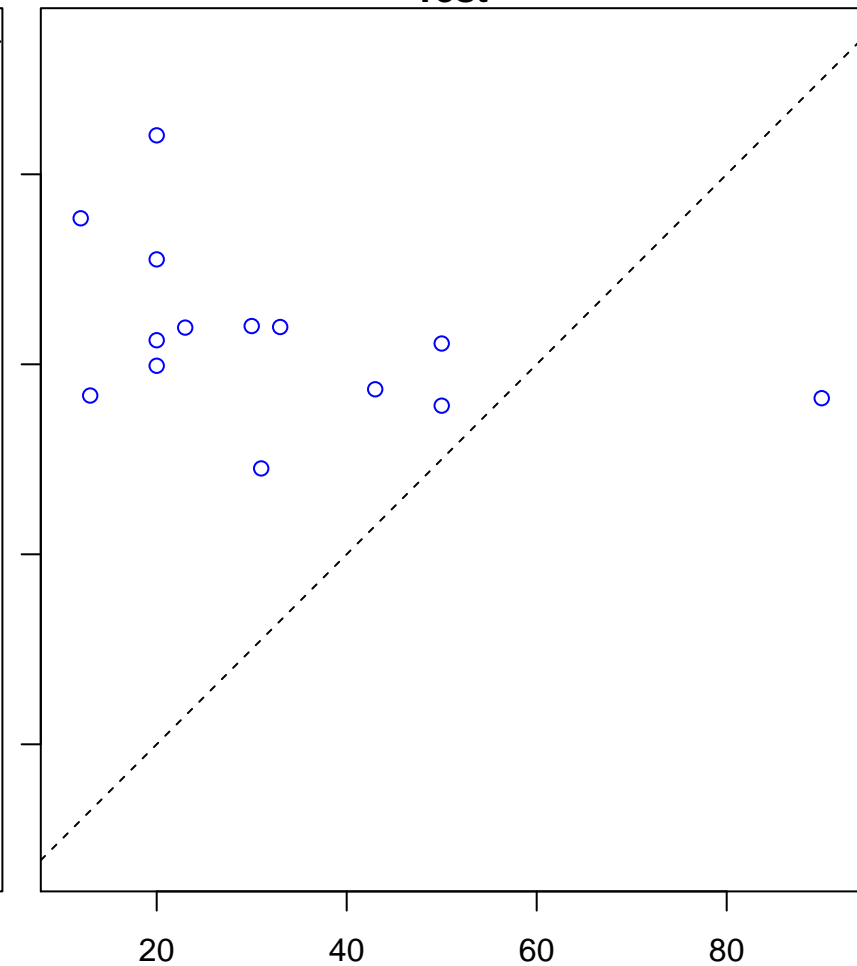


lymphatic endothelial cell differentiation (Score: 7.666107)

Control

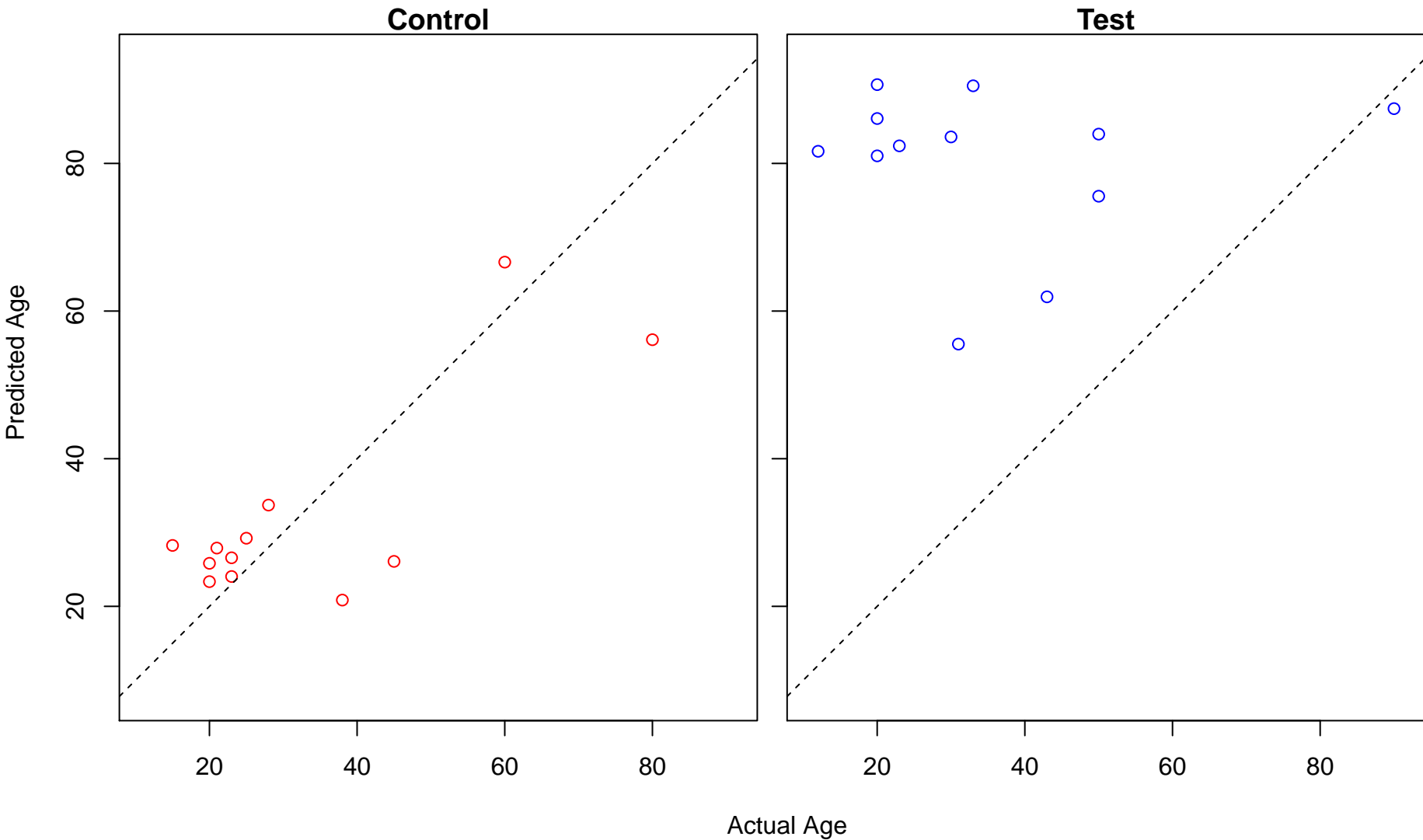


Test

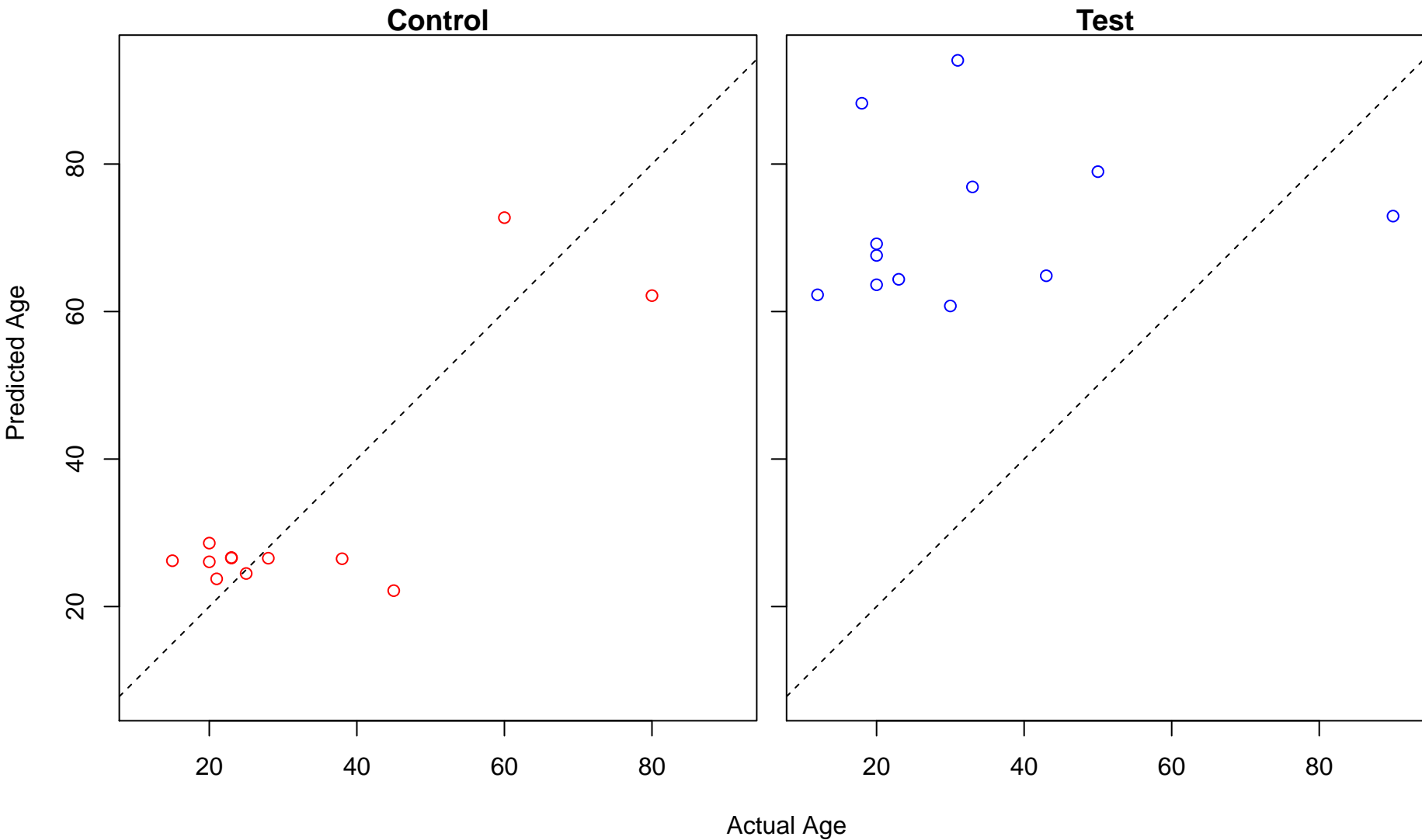


Actual Age

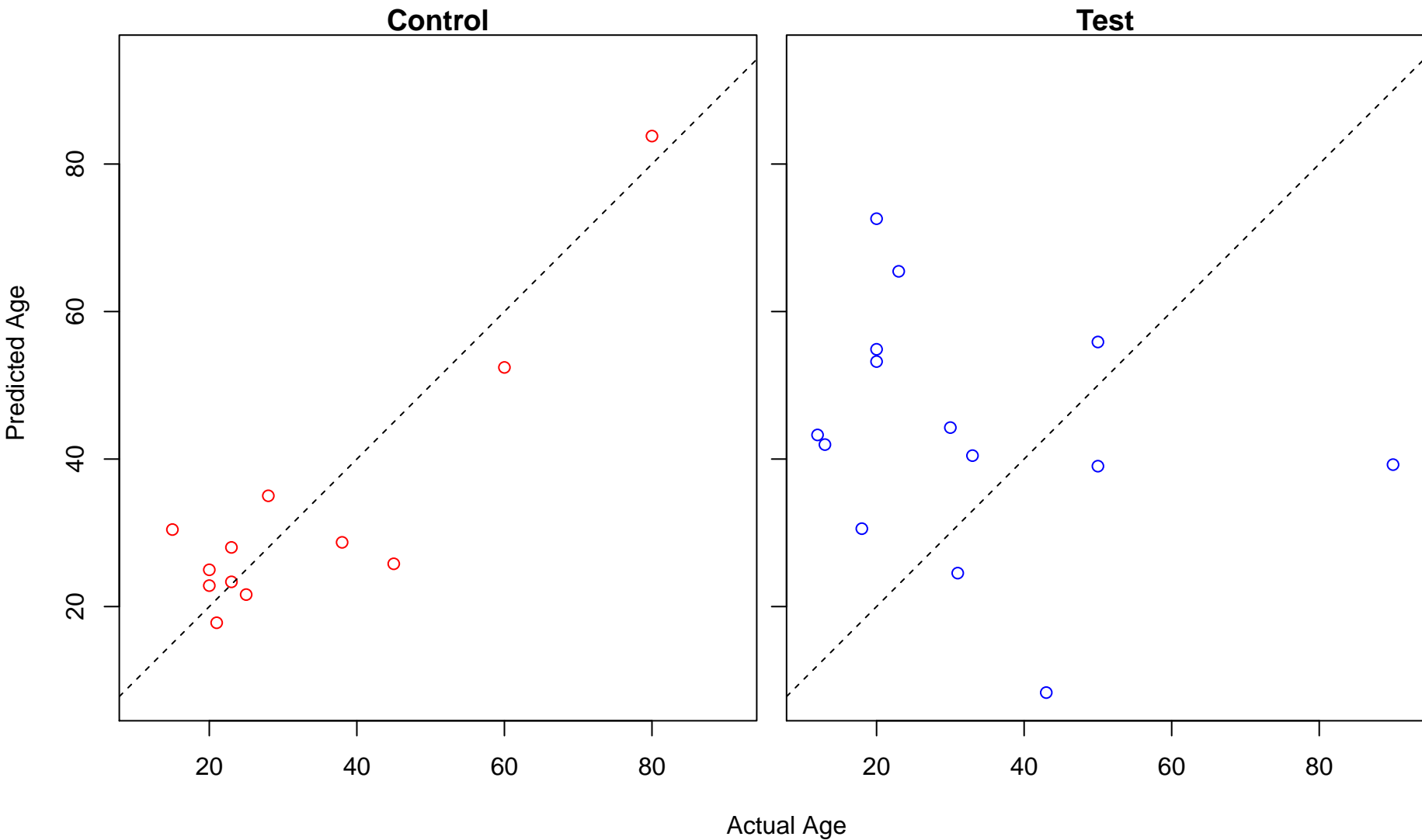
aromatic amino acid family catabolic process (Score: 7.663835)



defense response to other organism (Score: 7.663656)

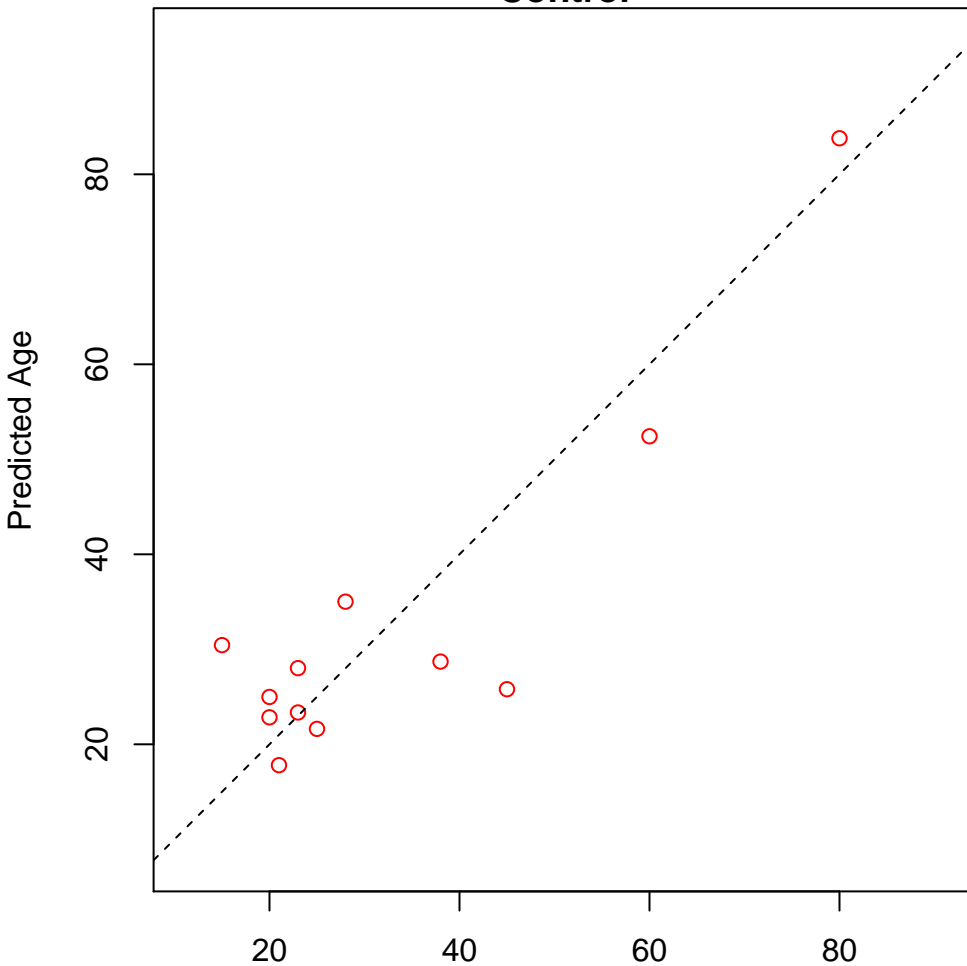


Schwann cell development (Score: 7.661312)

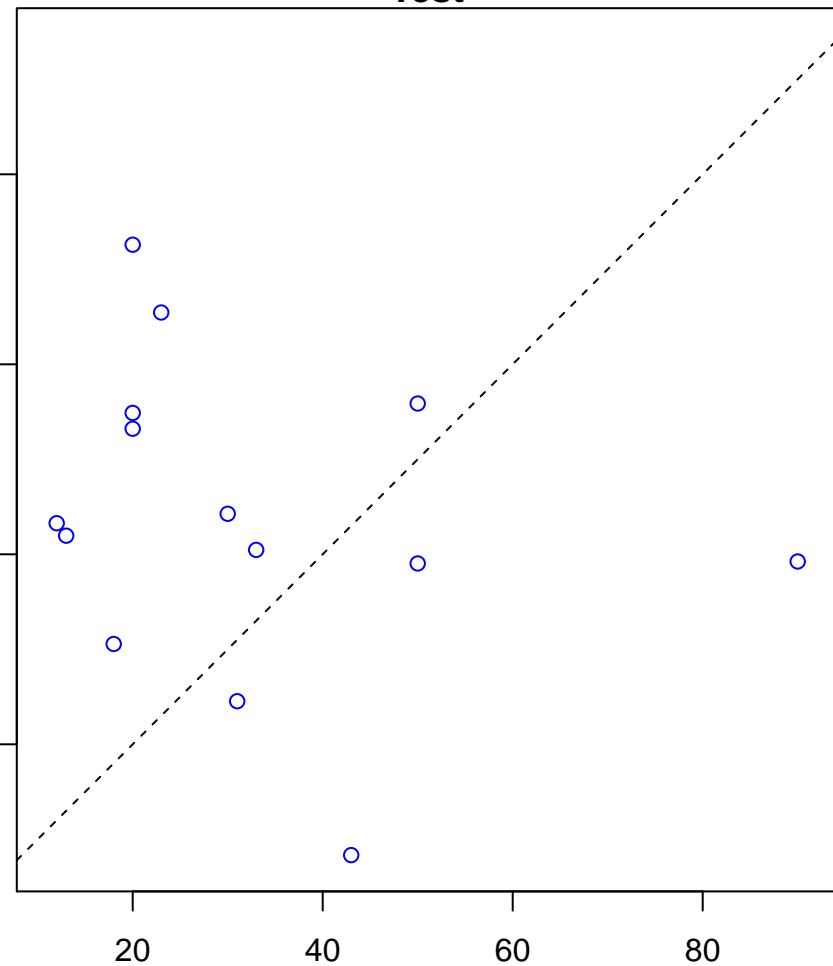


myelination in peripheral nervous system (Score: 7.661312)

Control

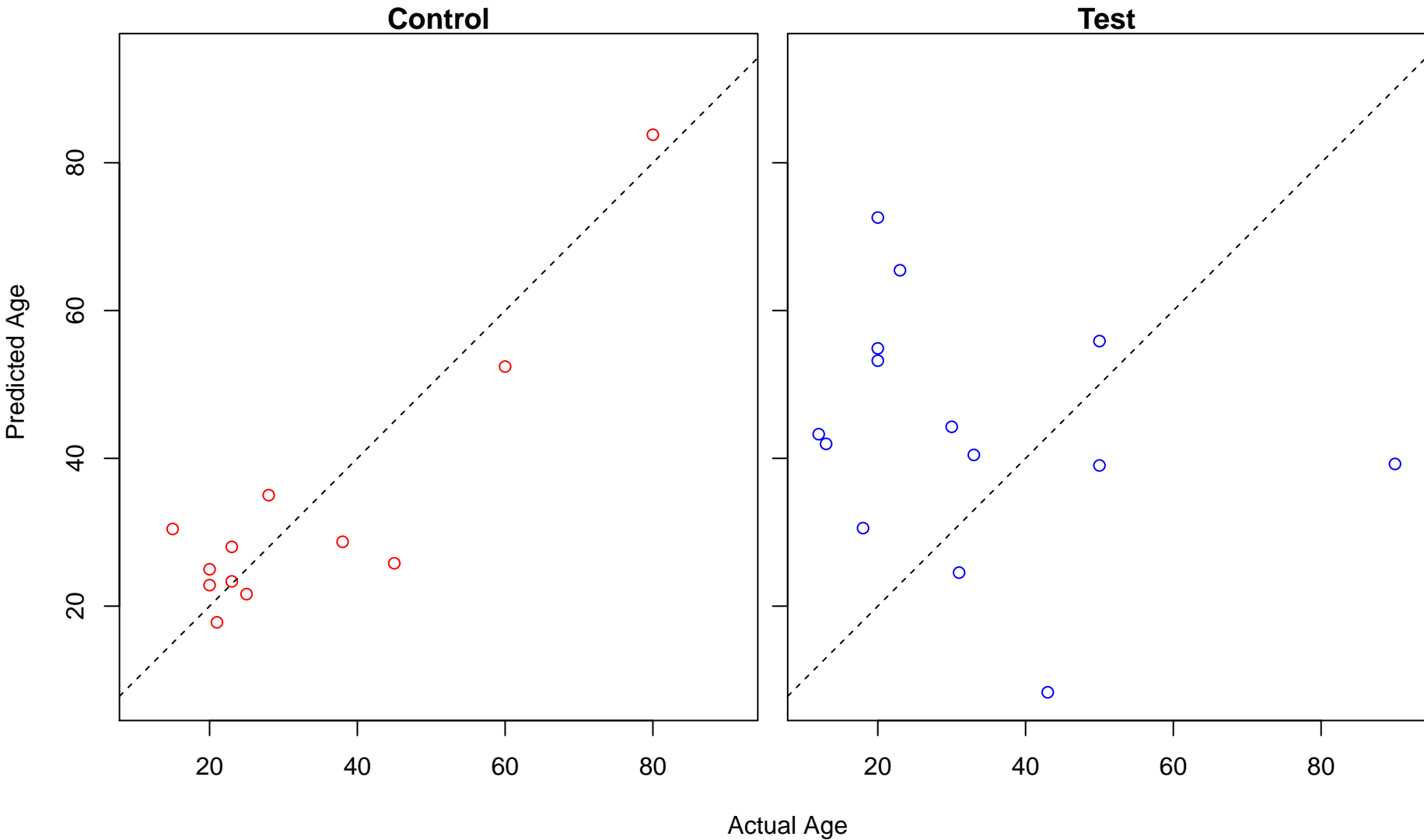


Test

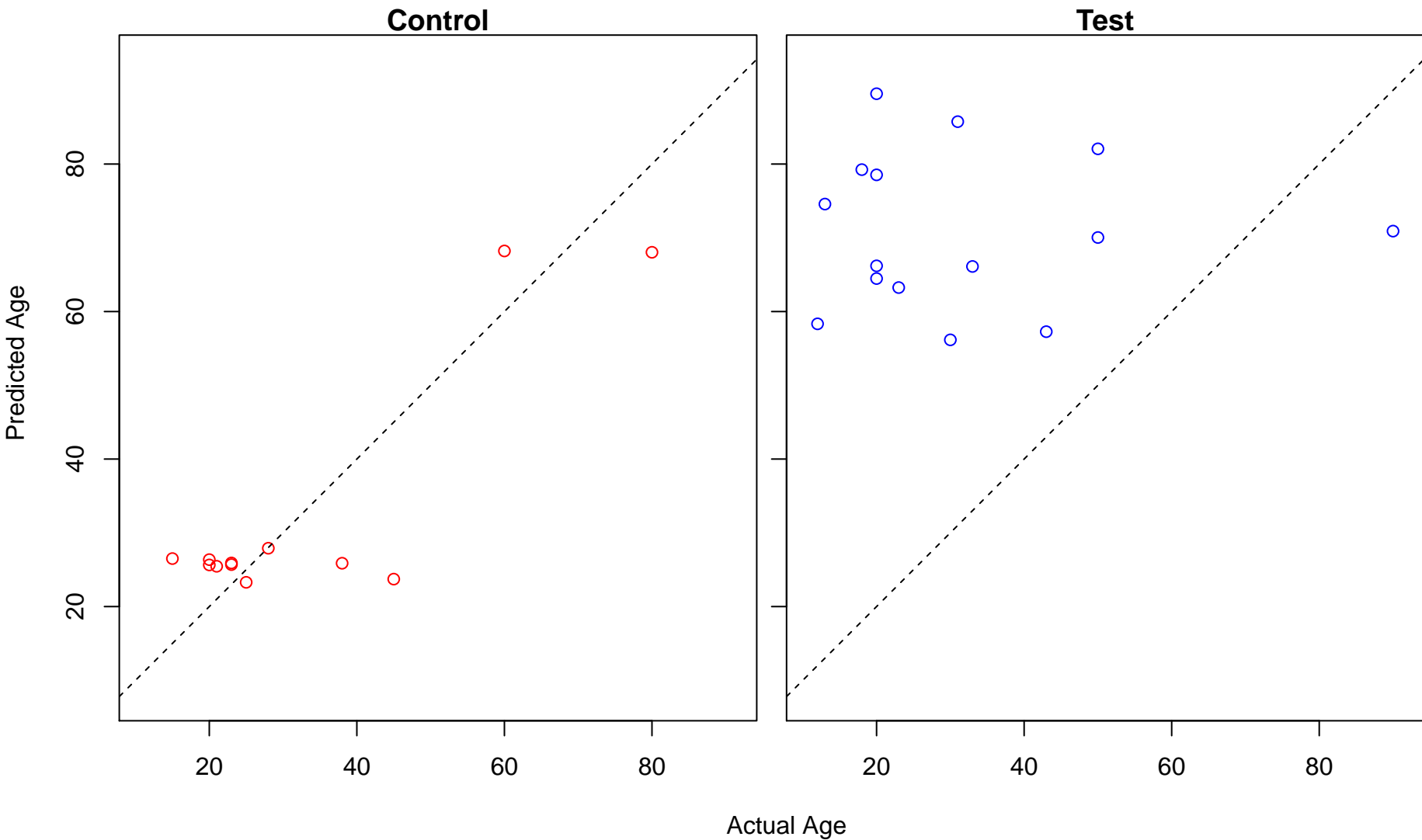


Actual Age

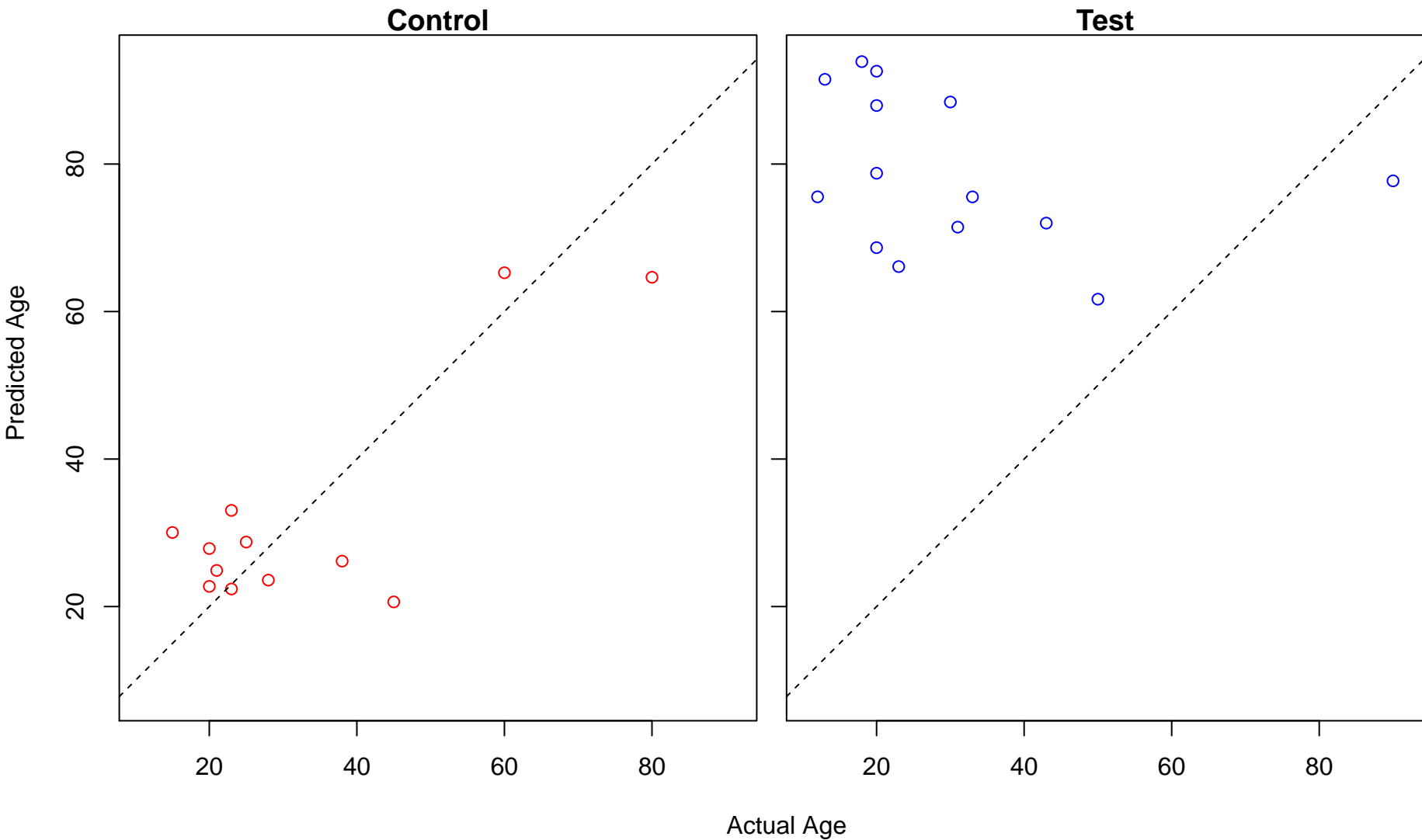
peripheral nervous system axon ensheathment (Score: 7.661312)



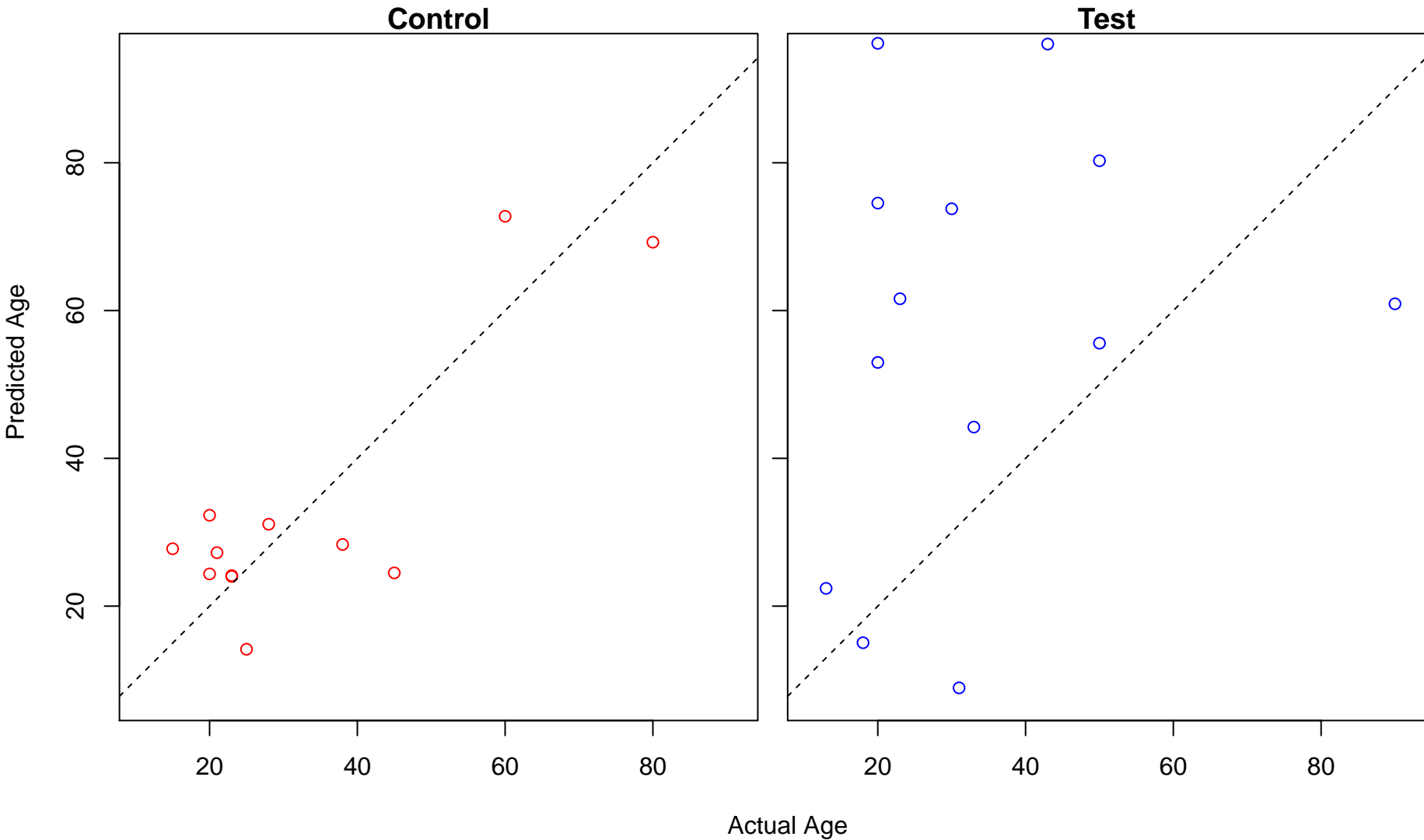
positive regulation of cell growth (Score: 7.660612)



positive regulation of immunoglobulin production (Score: 7.658563)

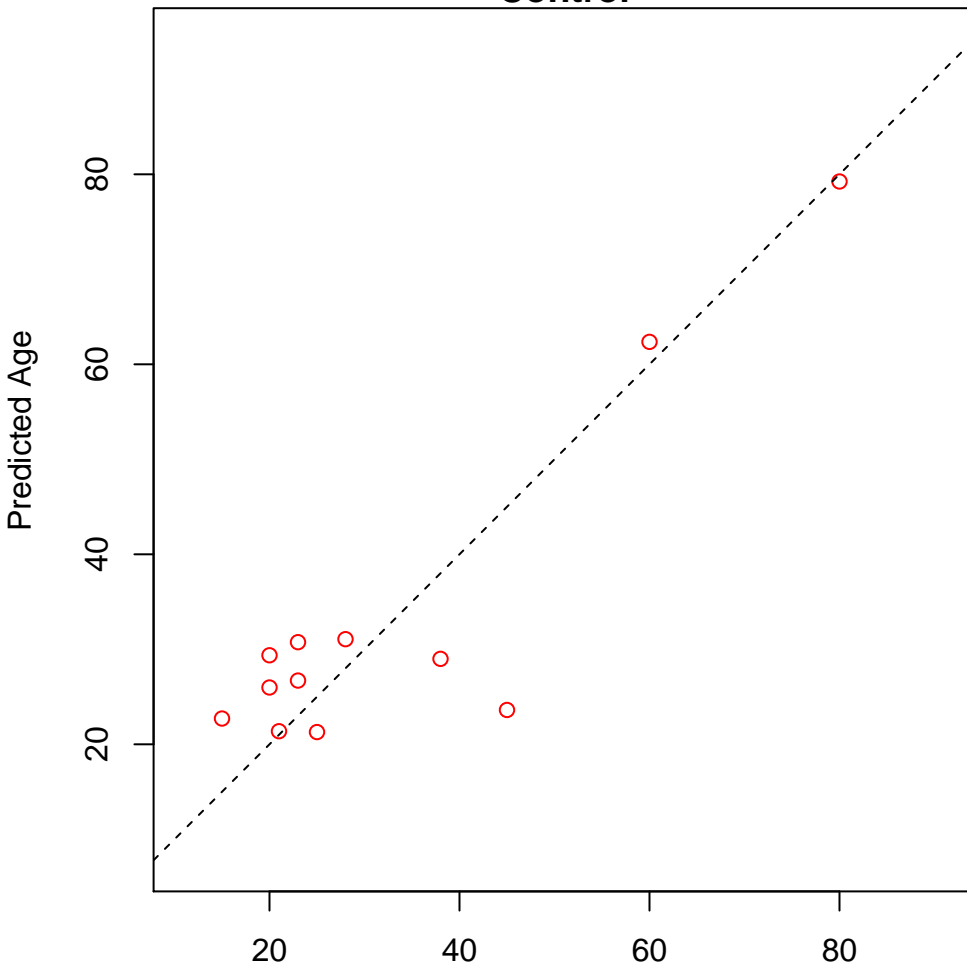


regulation of hormone biosynthetic process (Score: 7.656573)

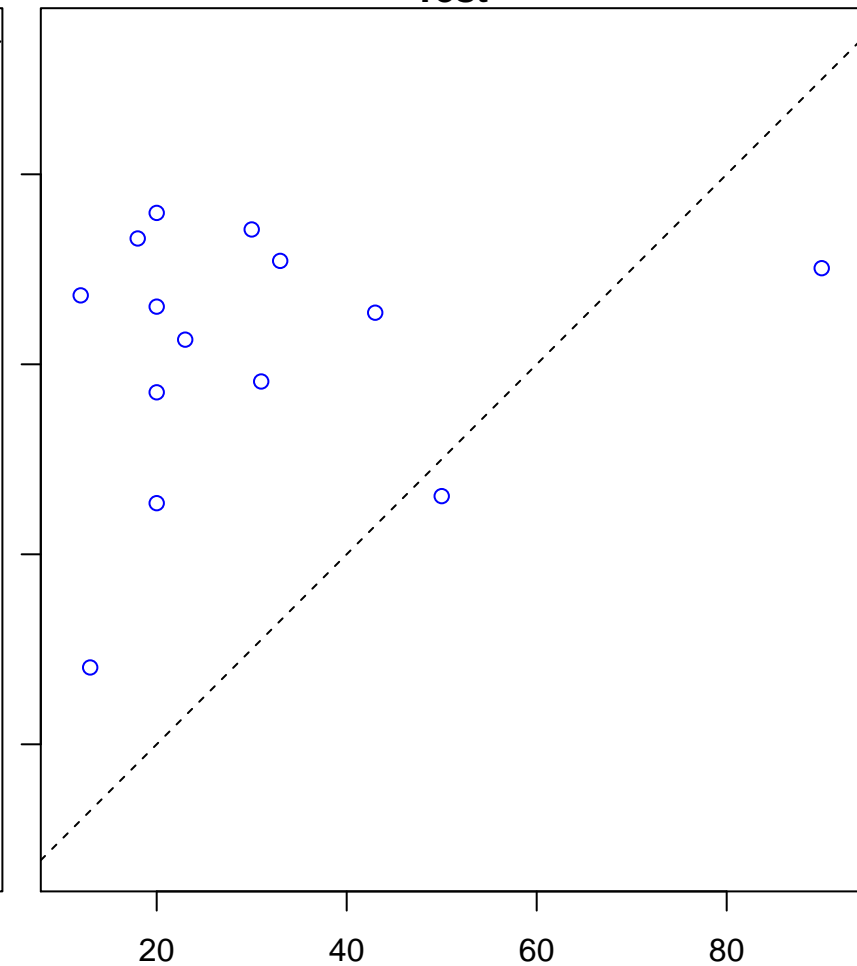


regulation of collagen metabolic process (Score: 7.652091)

Control

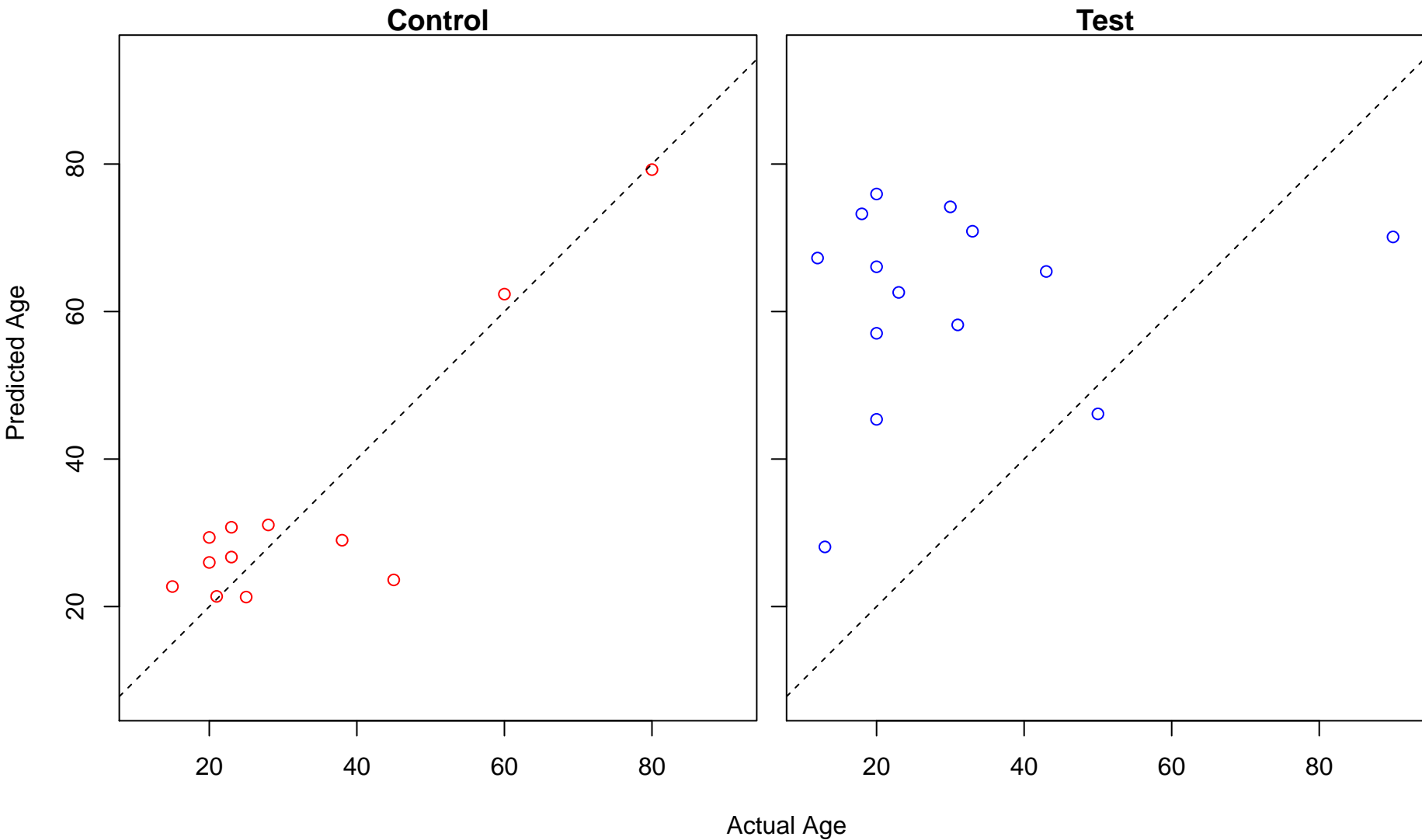


Test

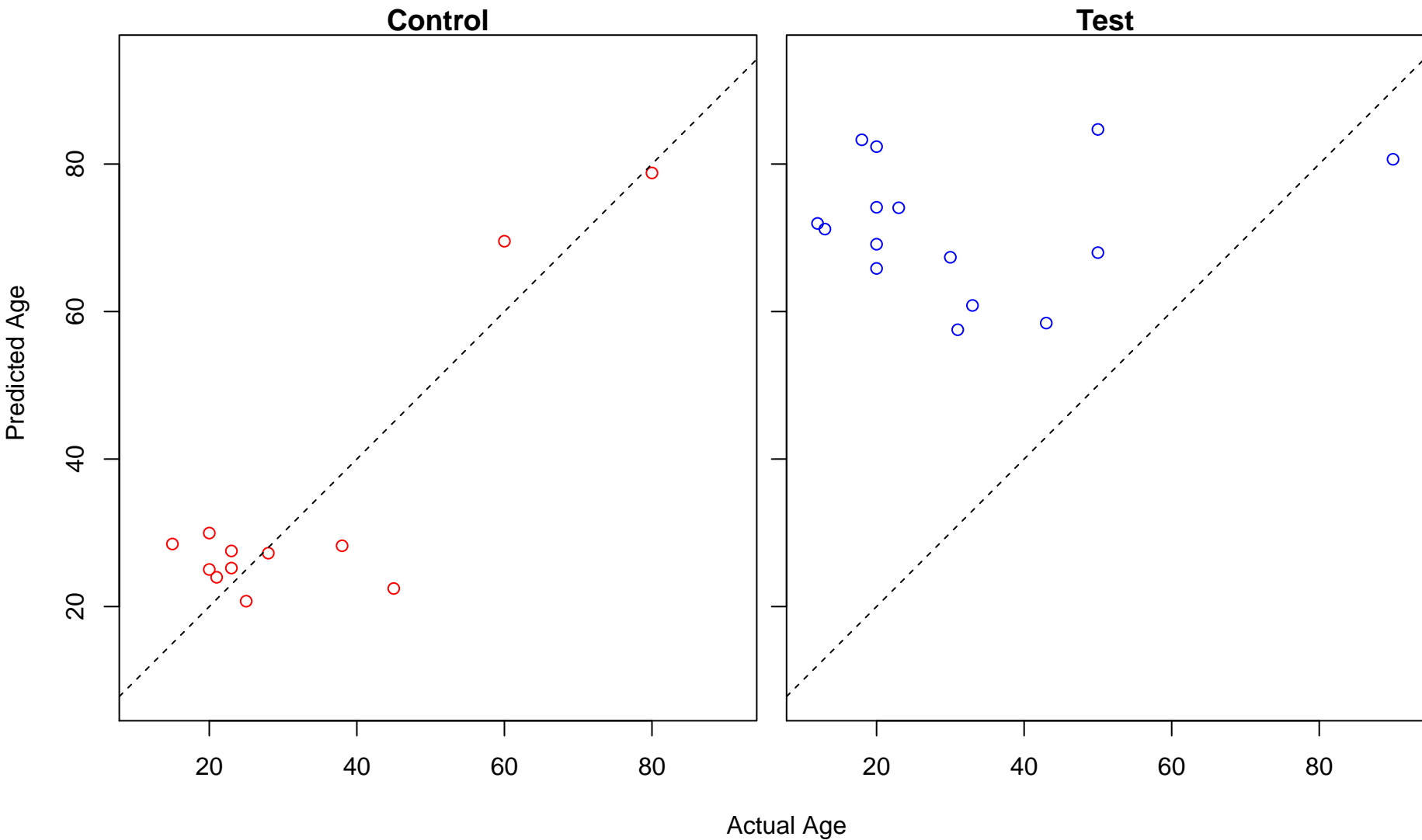


Actual Age

regulation of multicellular organismal metabolic process (Score: 7.652091)

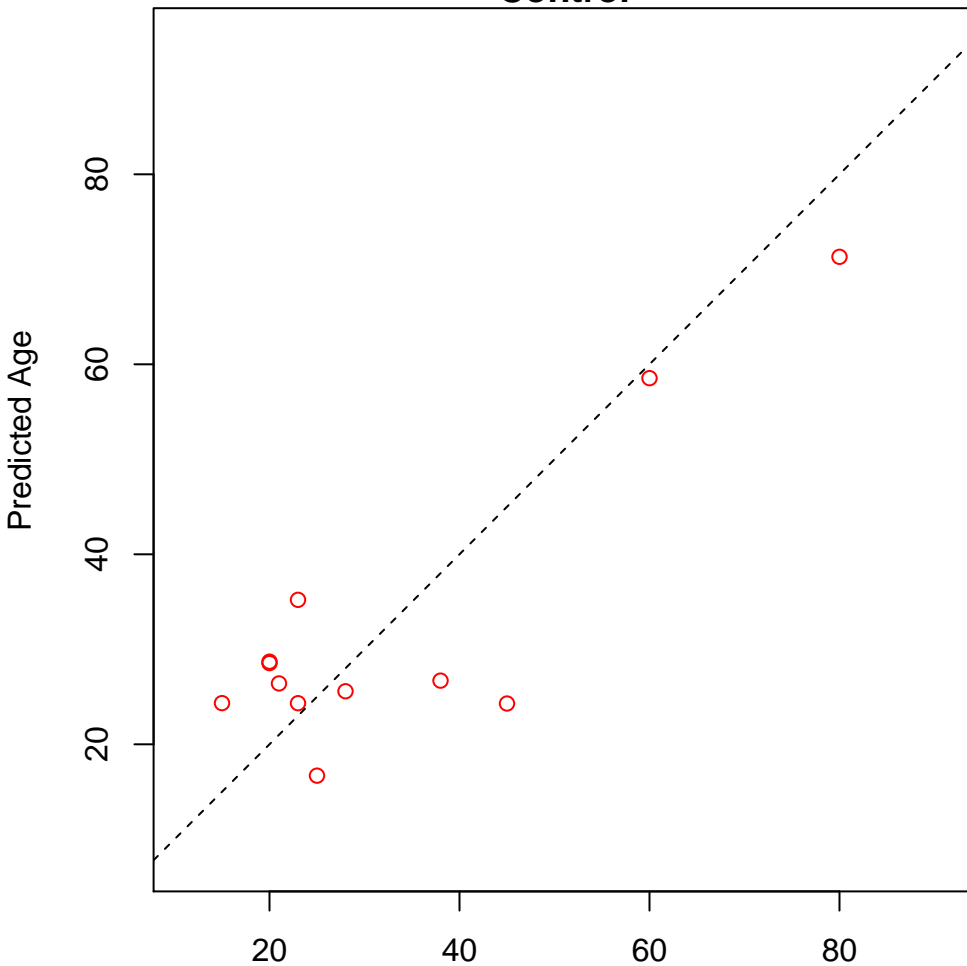


negative regulation of transferase activity (Score: 7.651071)

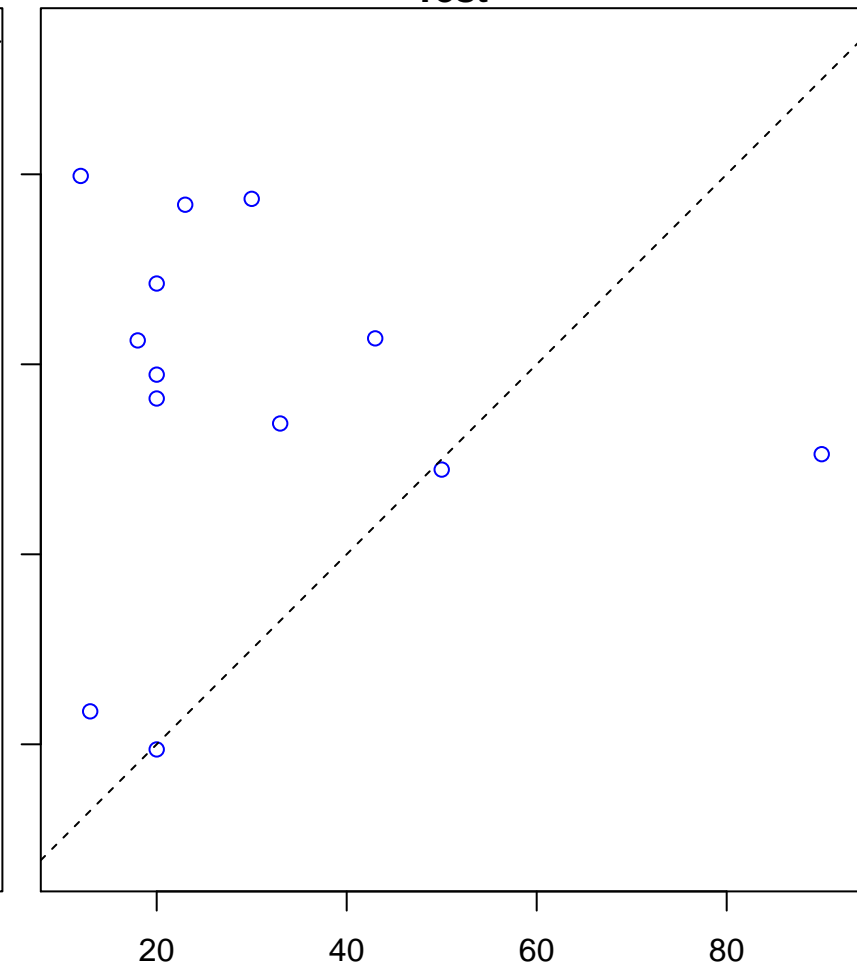


phosphatidylserine metabolic process (Score: 7.648401)

Control

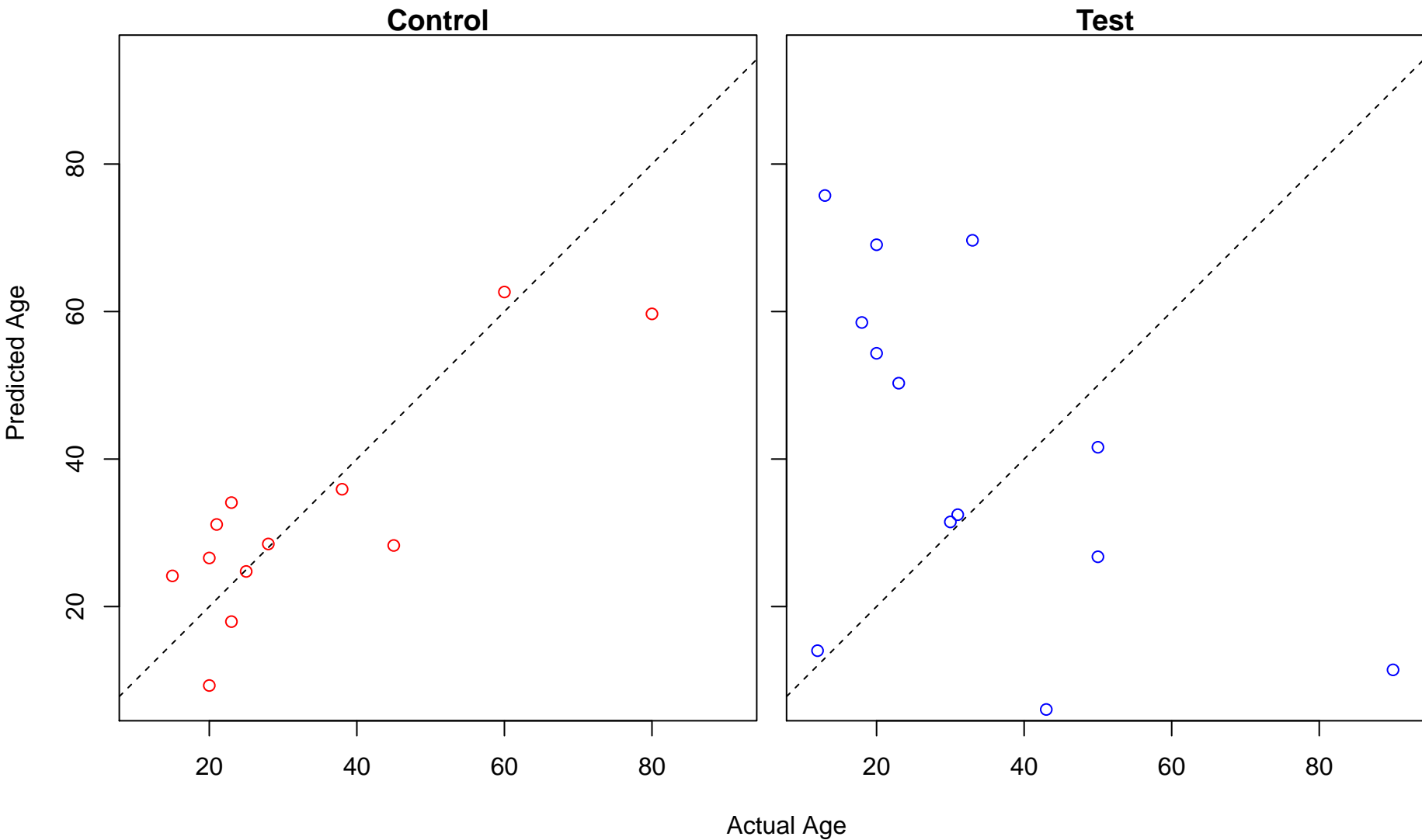


Test

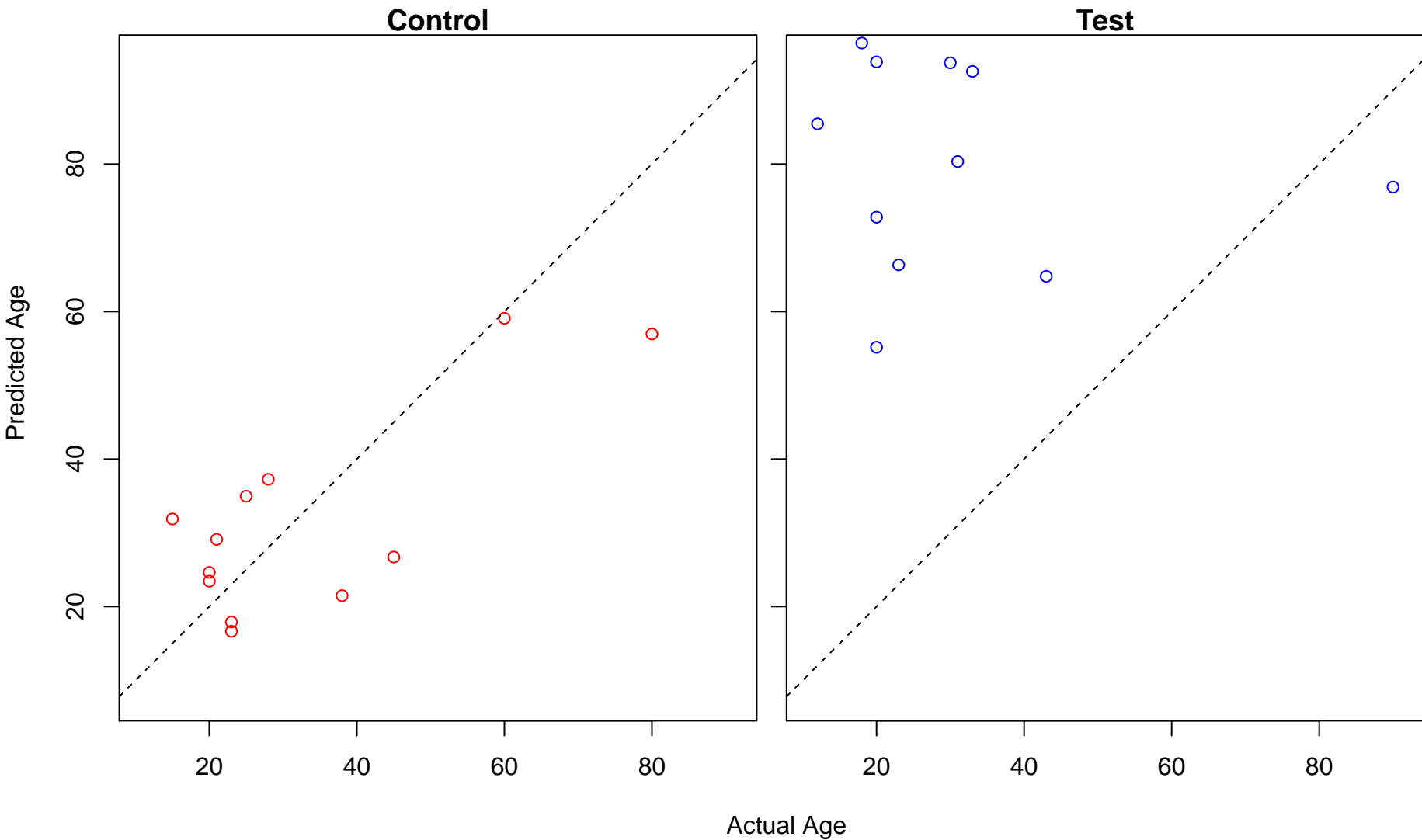


Actual Age

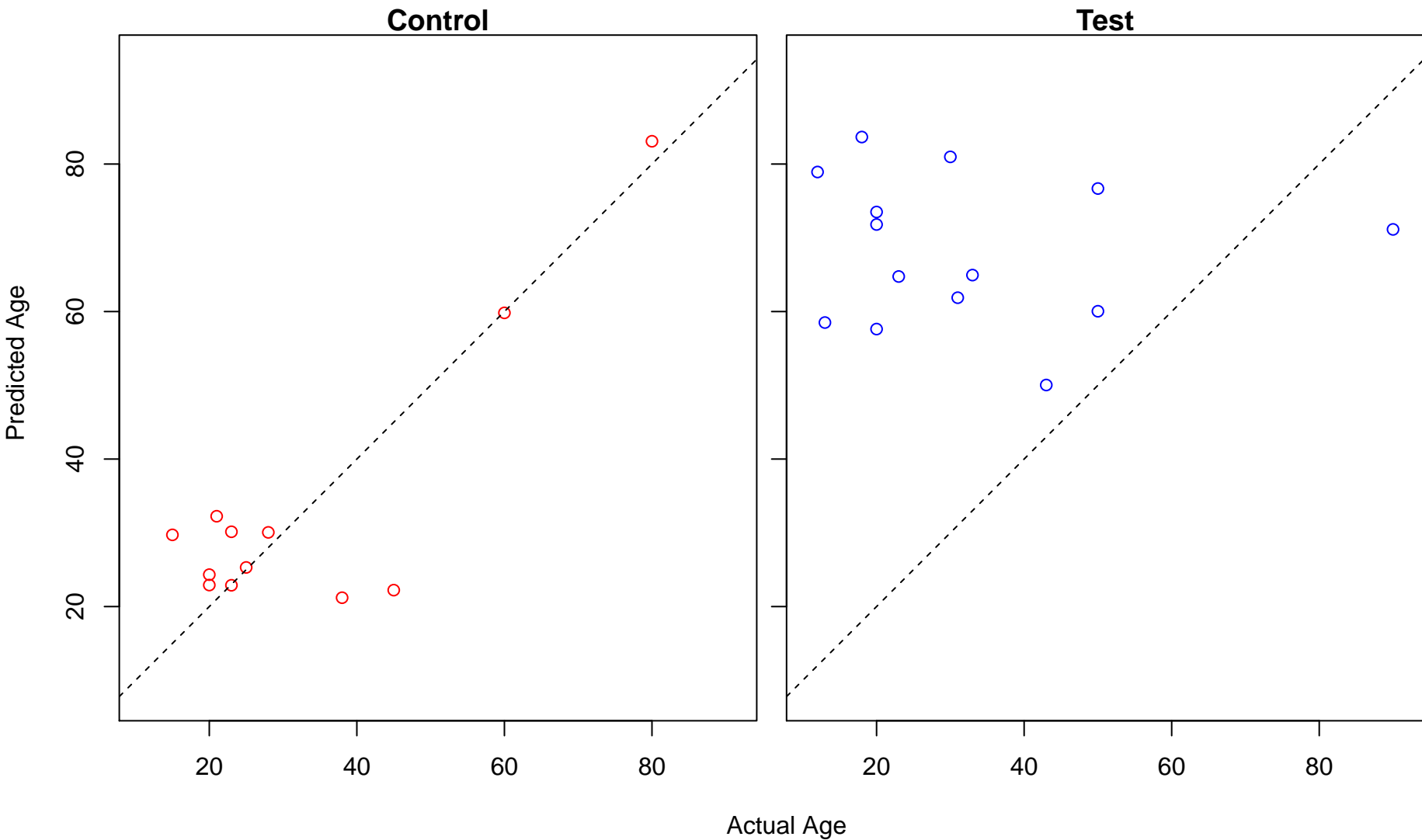
positive regulation of cation transmembrane transport (Score: 7.644424)



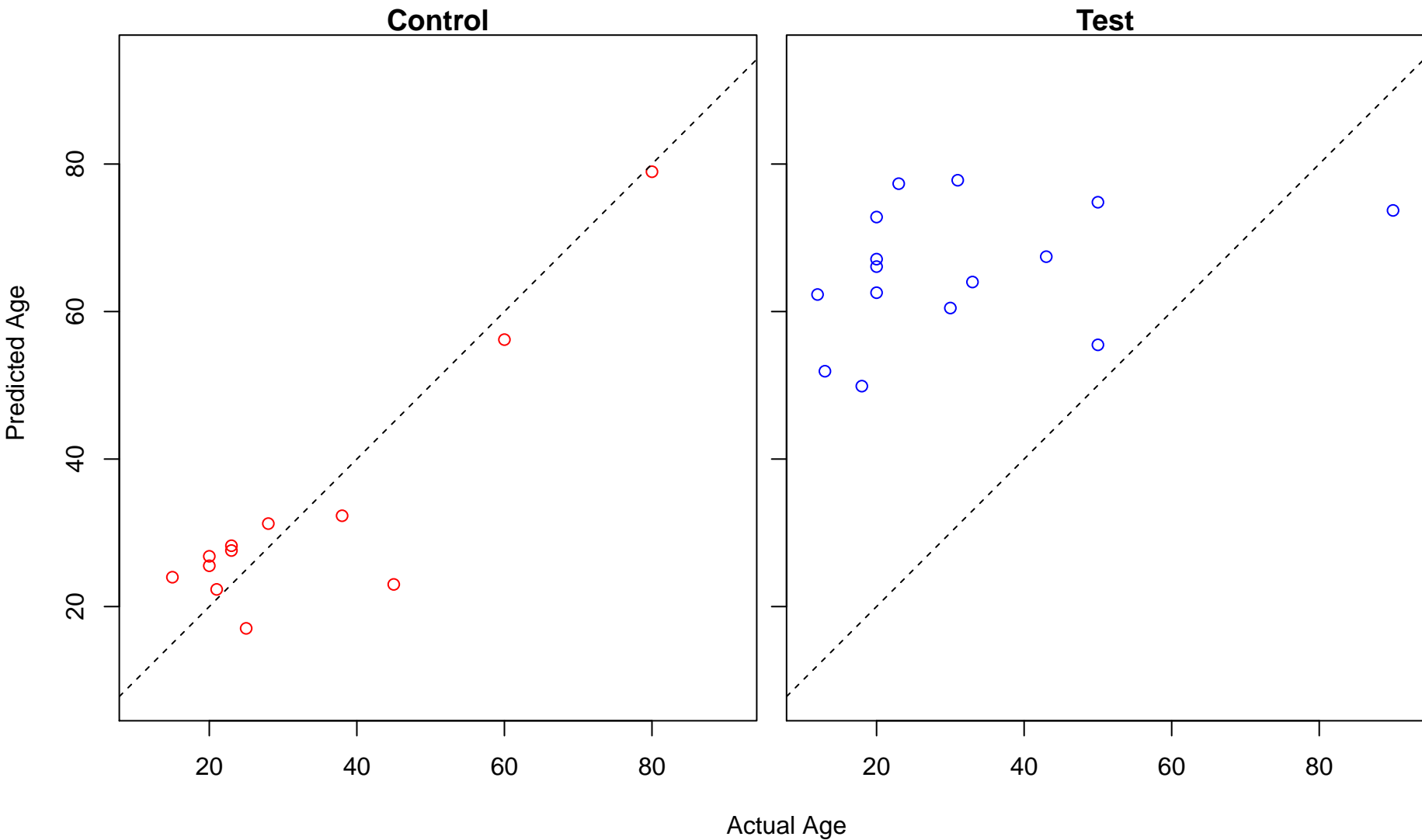
riboflavin transport (Score: 7.641789)



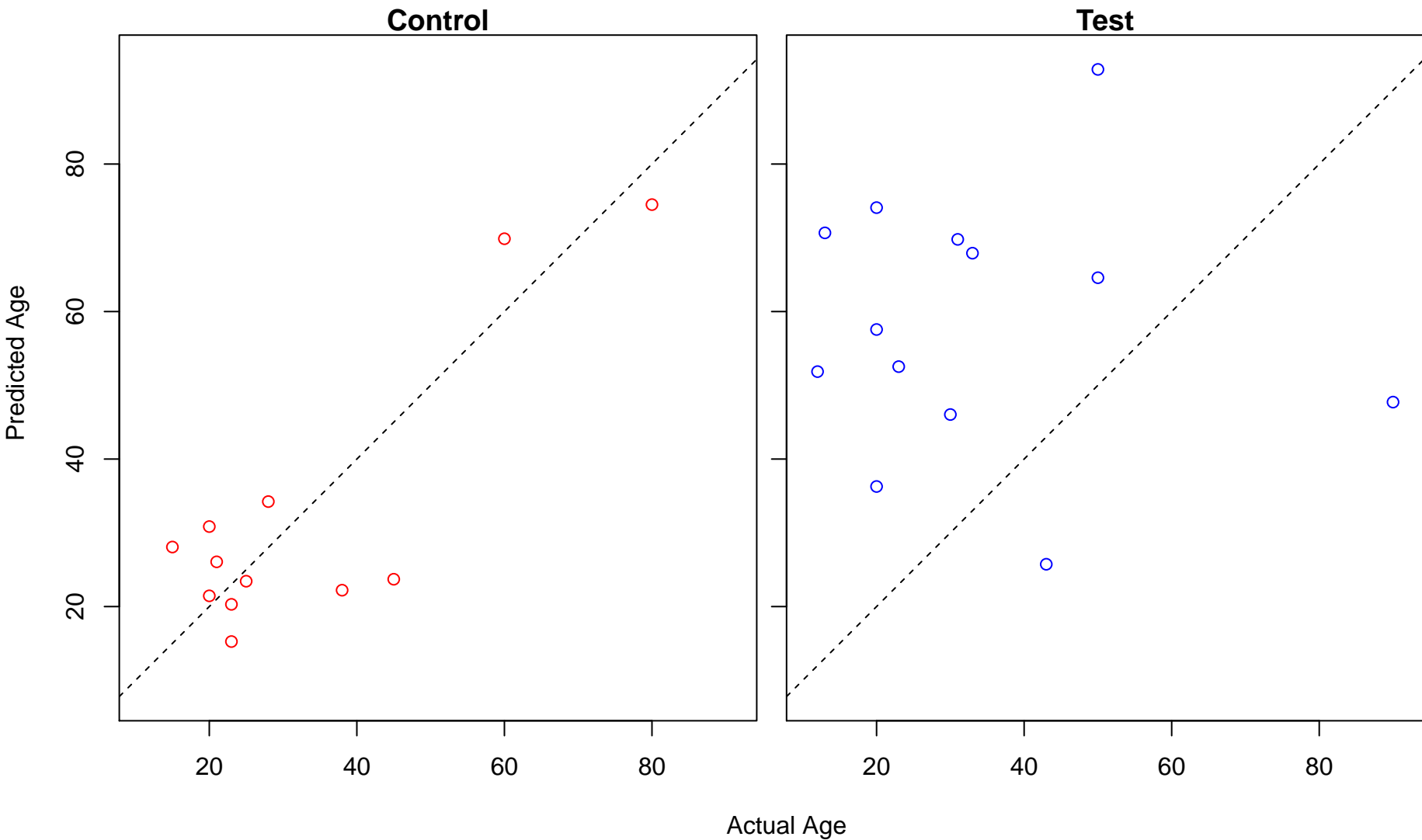
localization within membrane (Score: 7.637413)



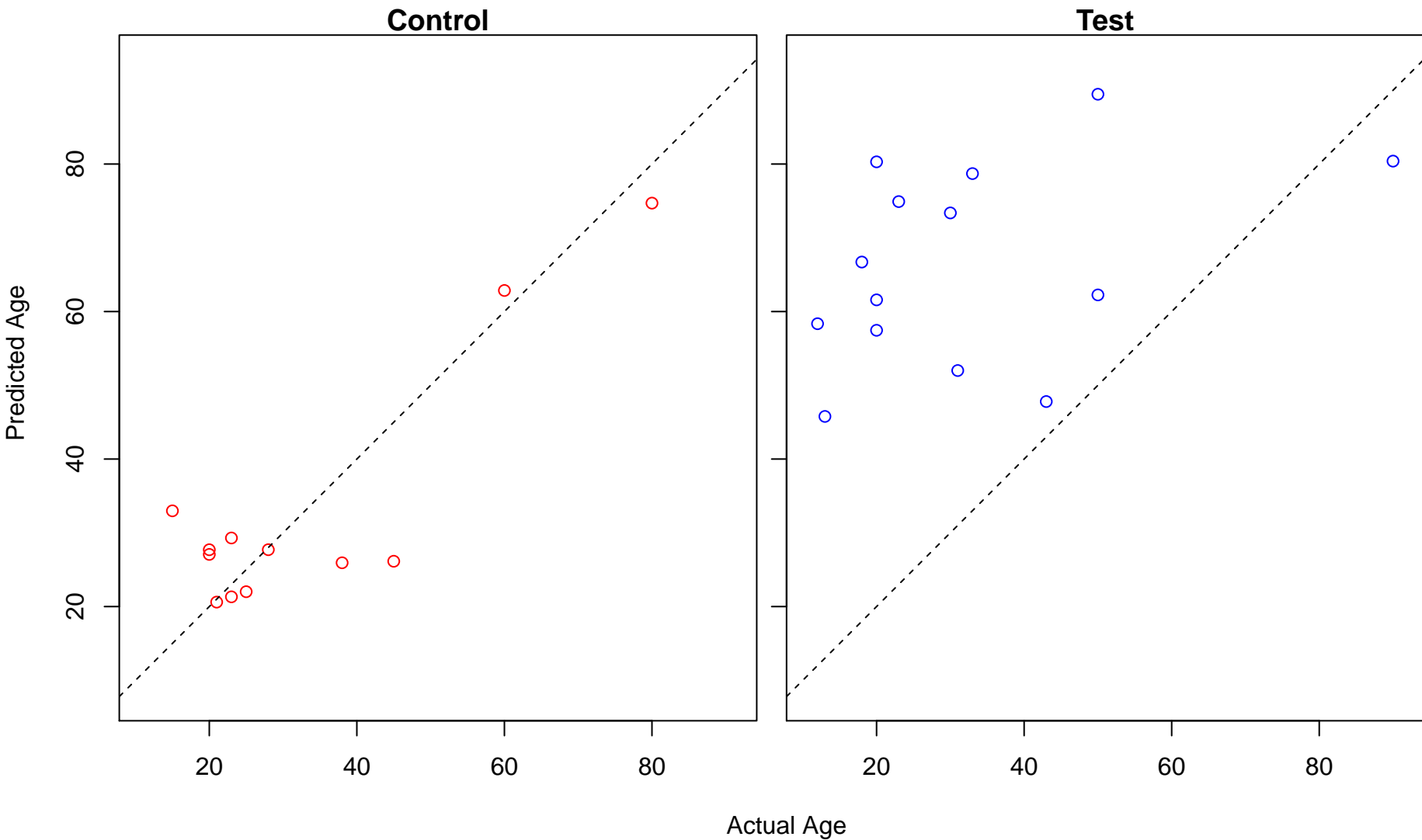
embryonic organ morphogenesis (Score: 7.633991)



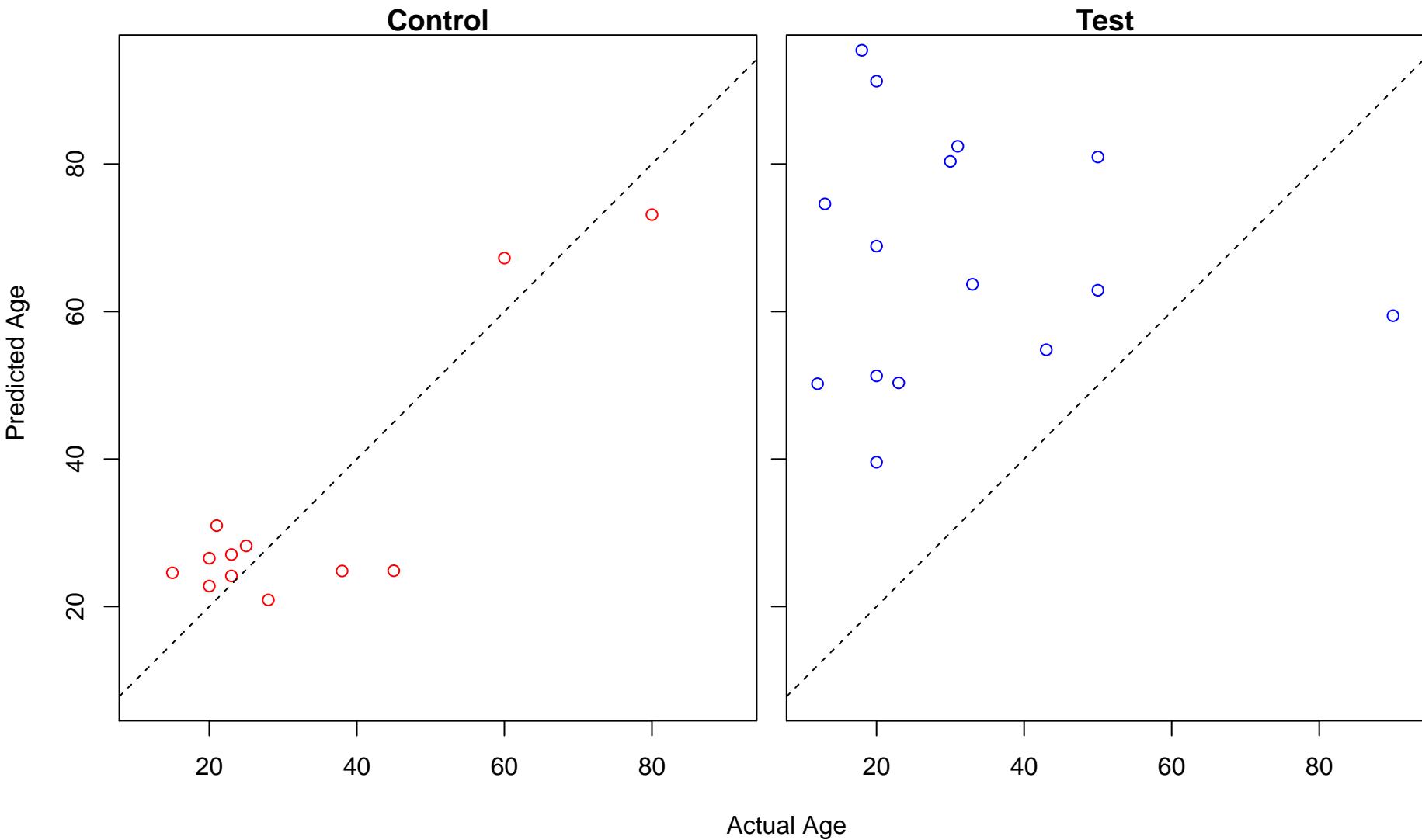
RNA processing (Score: 7.626004)



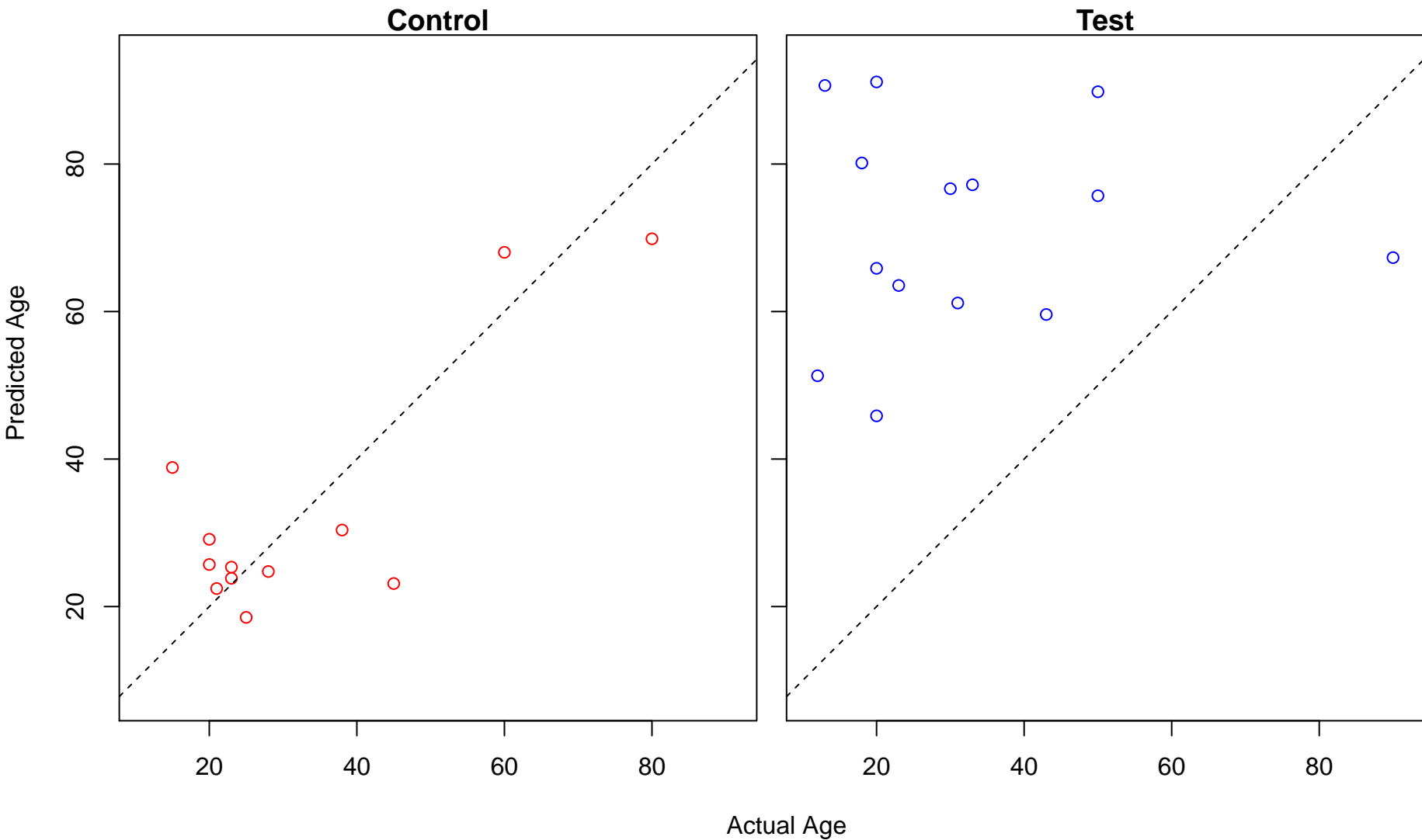
presynaptic process involved in synaptic transmission (Score: 7.623958)



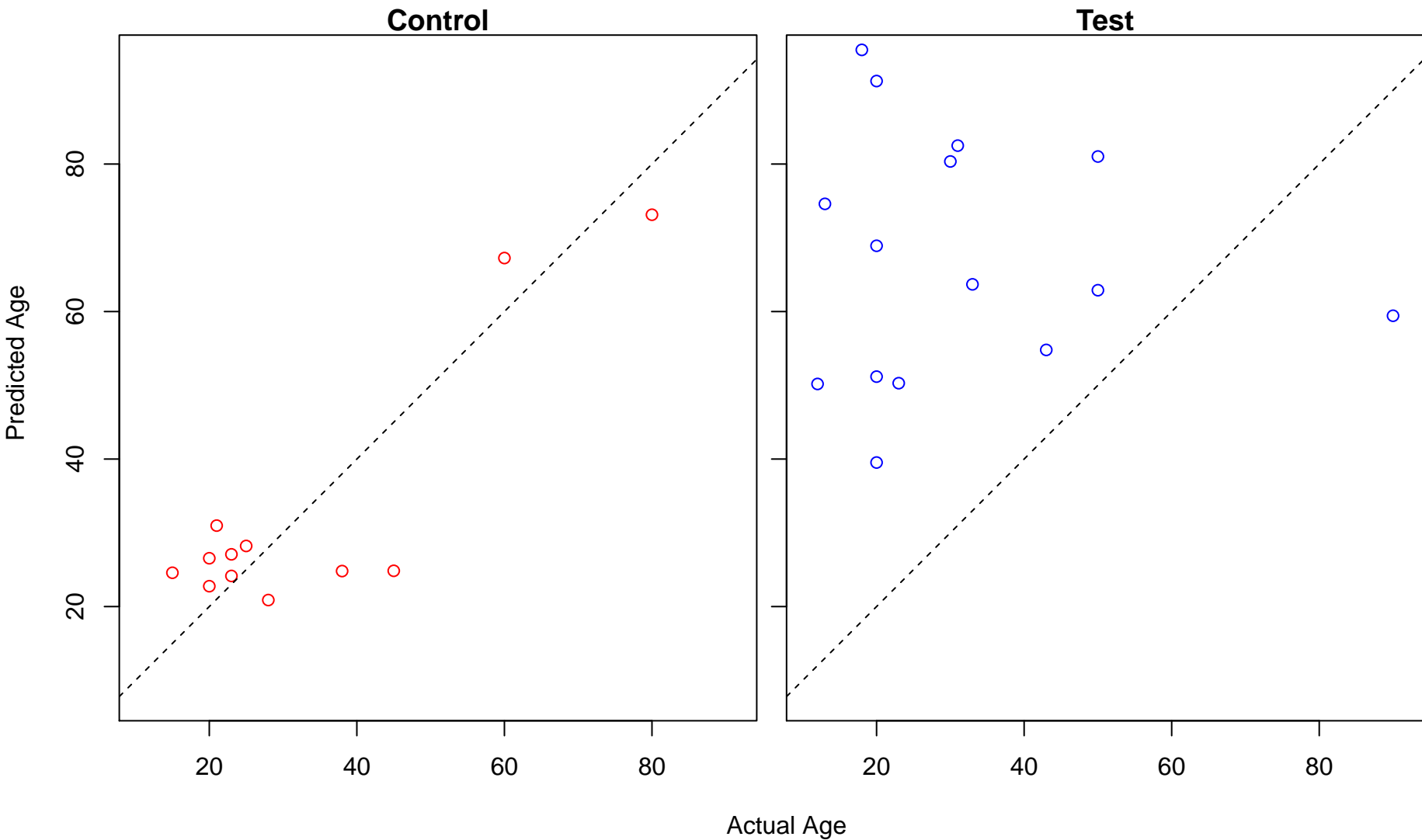
response to acidic pH (Score: 7.622090)



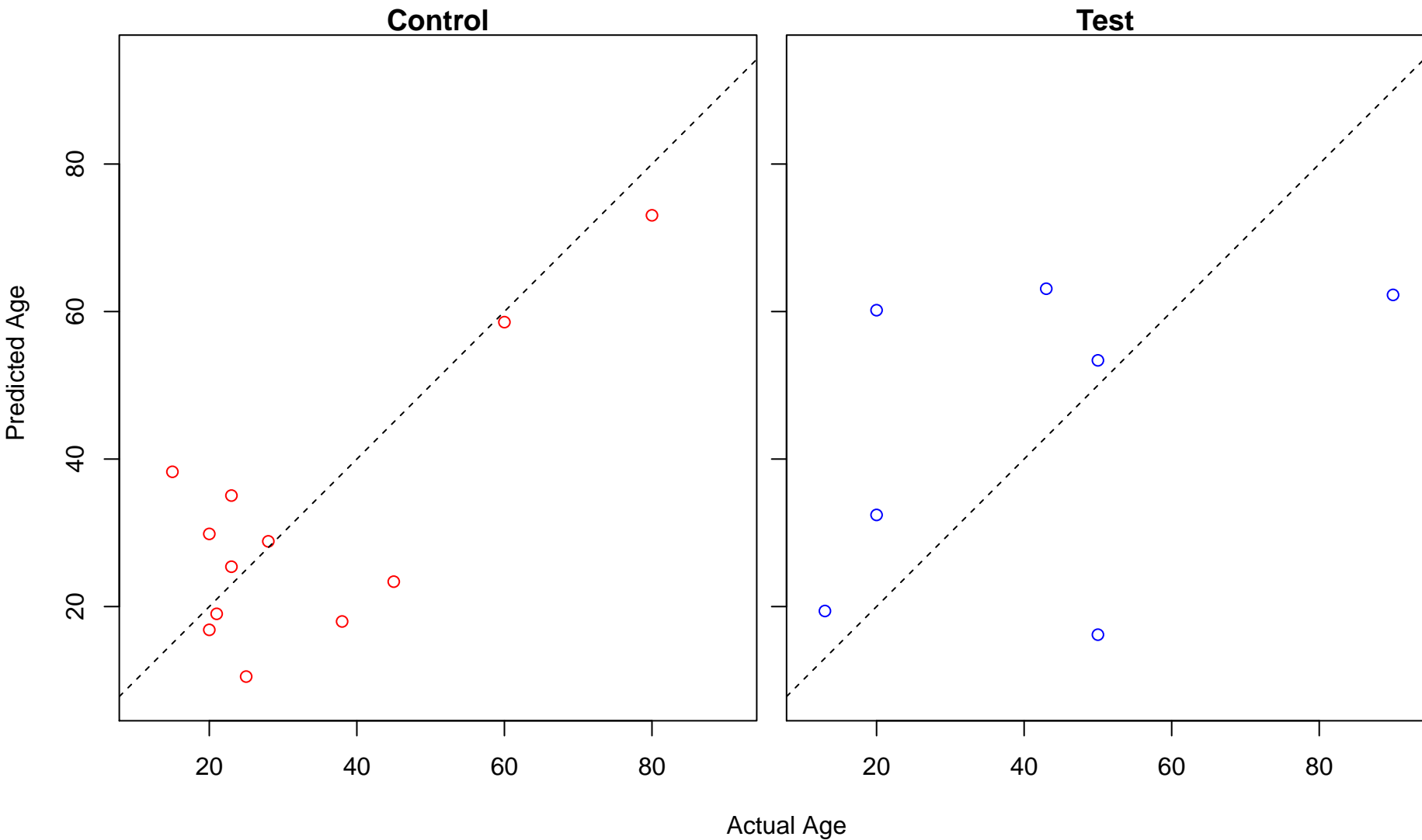
sphingolipid catabolic process (Score: 7.618839)



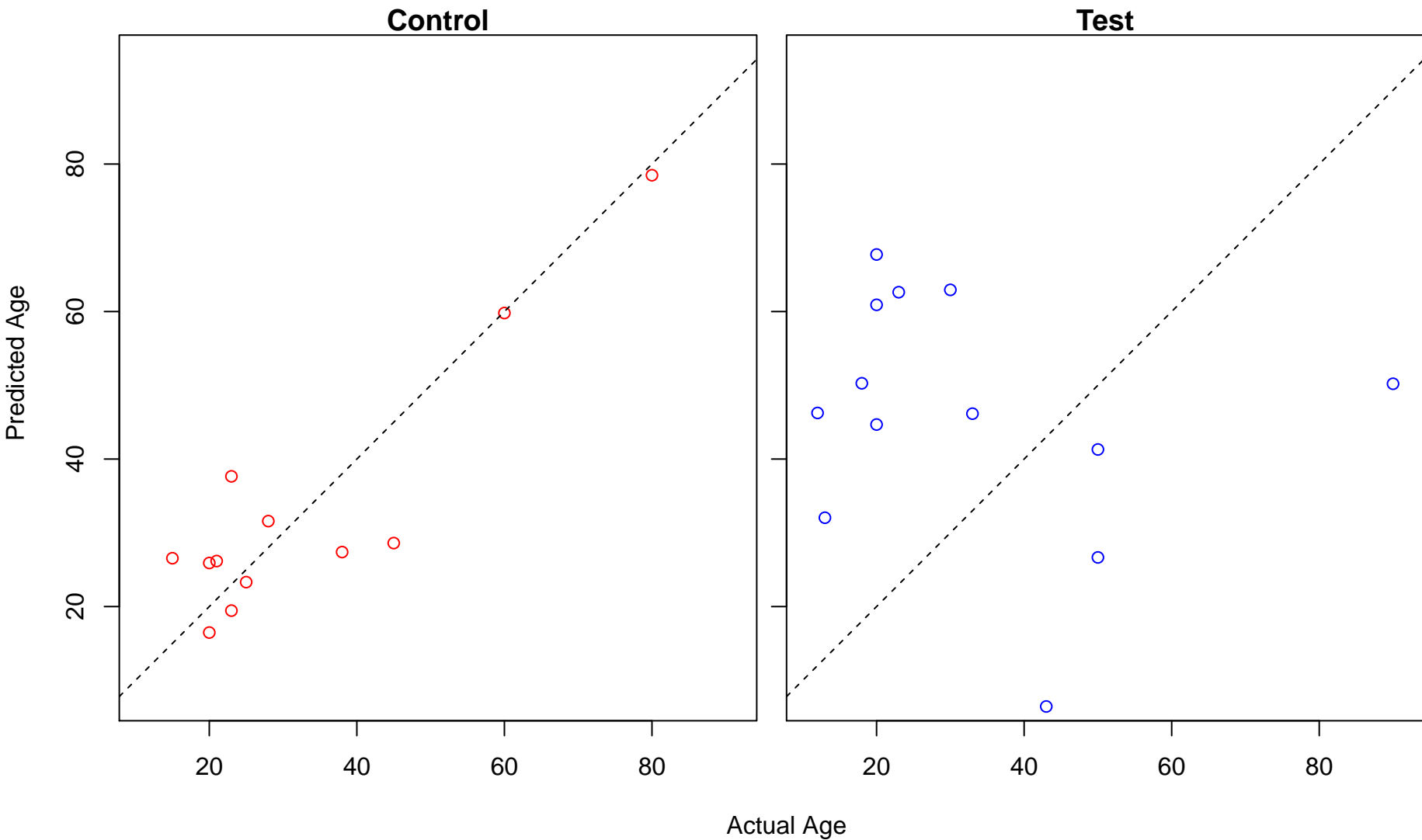
response to pH (Score: 7.616130)



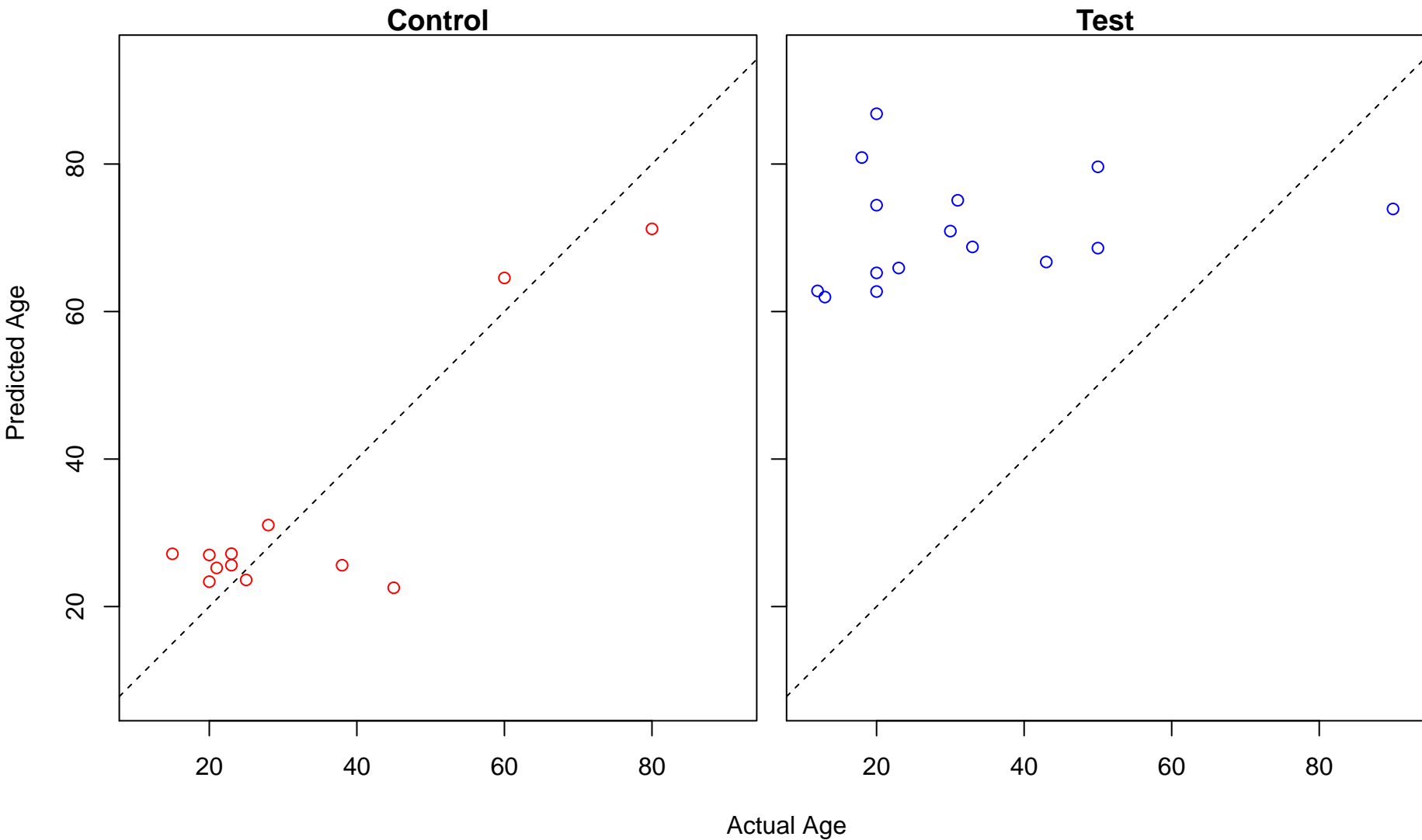
negative regulation of lipoprotein metabolic process (Score: 7.614791)



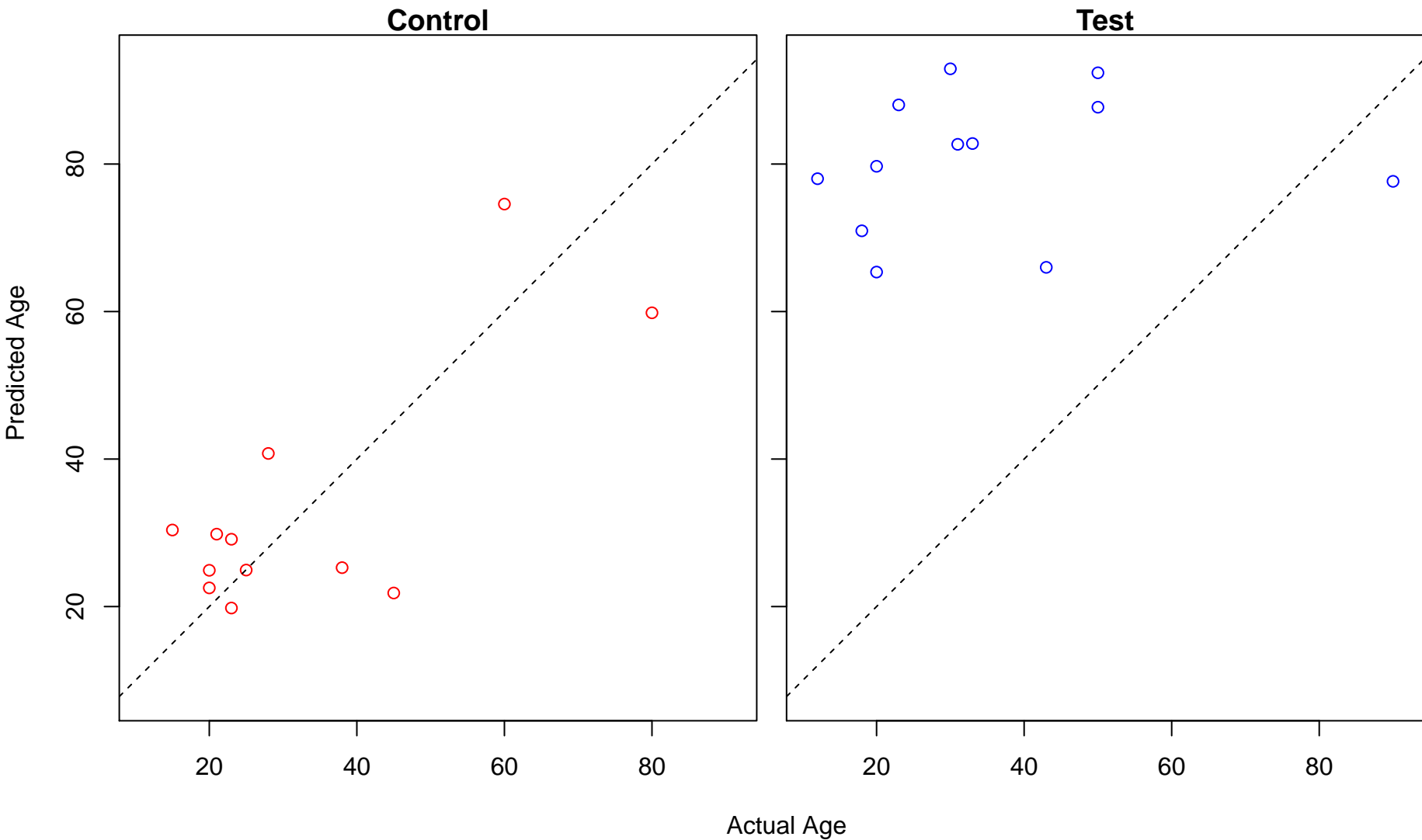
positive regulation of nervous system development (Score: 7.613256)



negative regulation of cell differentiation (Score: 7.608919)

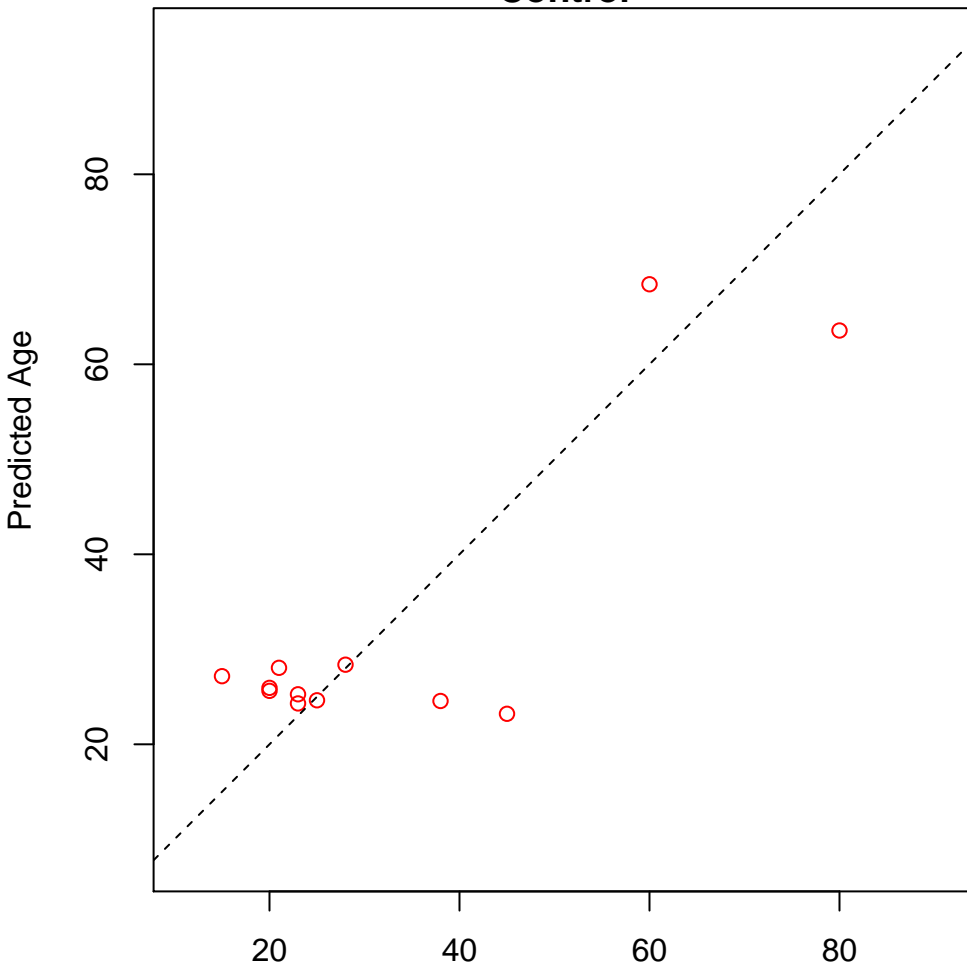


regulation of fibroblast proliferation (Score: 7.605721)

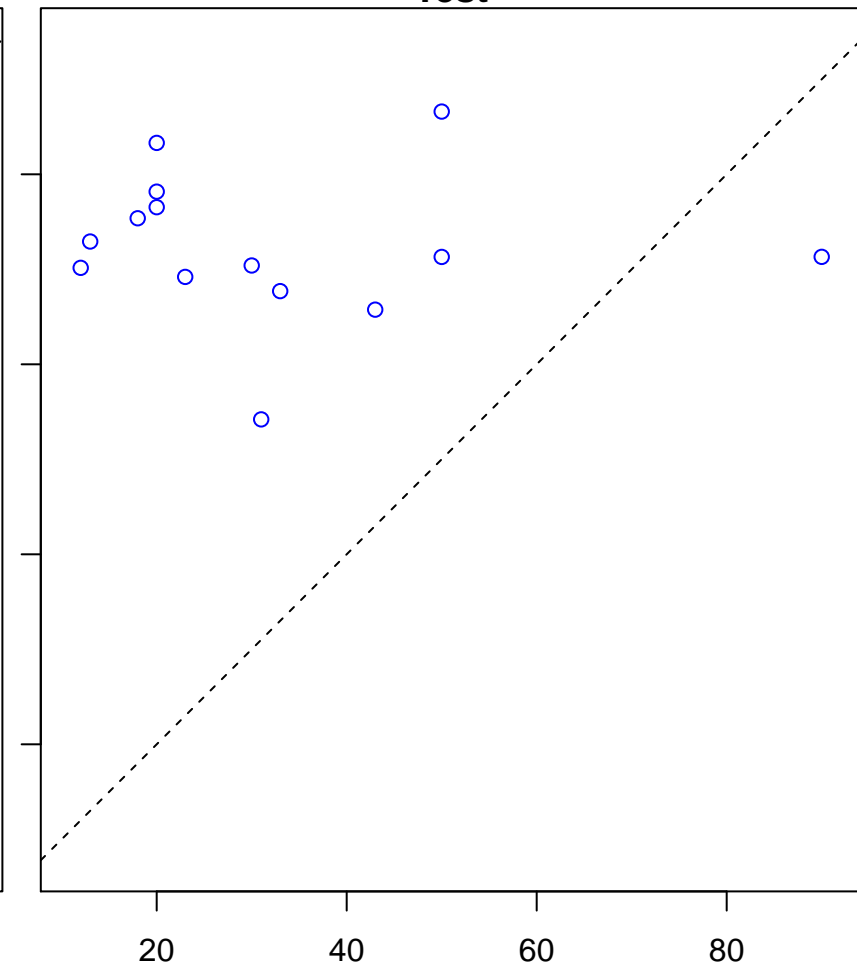


nucleoside phosphate catabolic process (Score: 7.595525)

Control



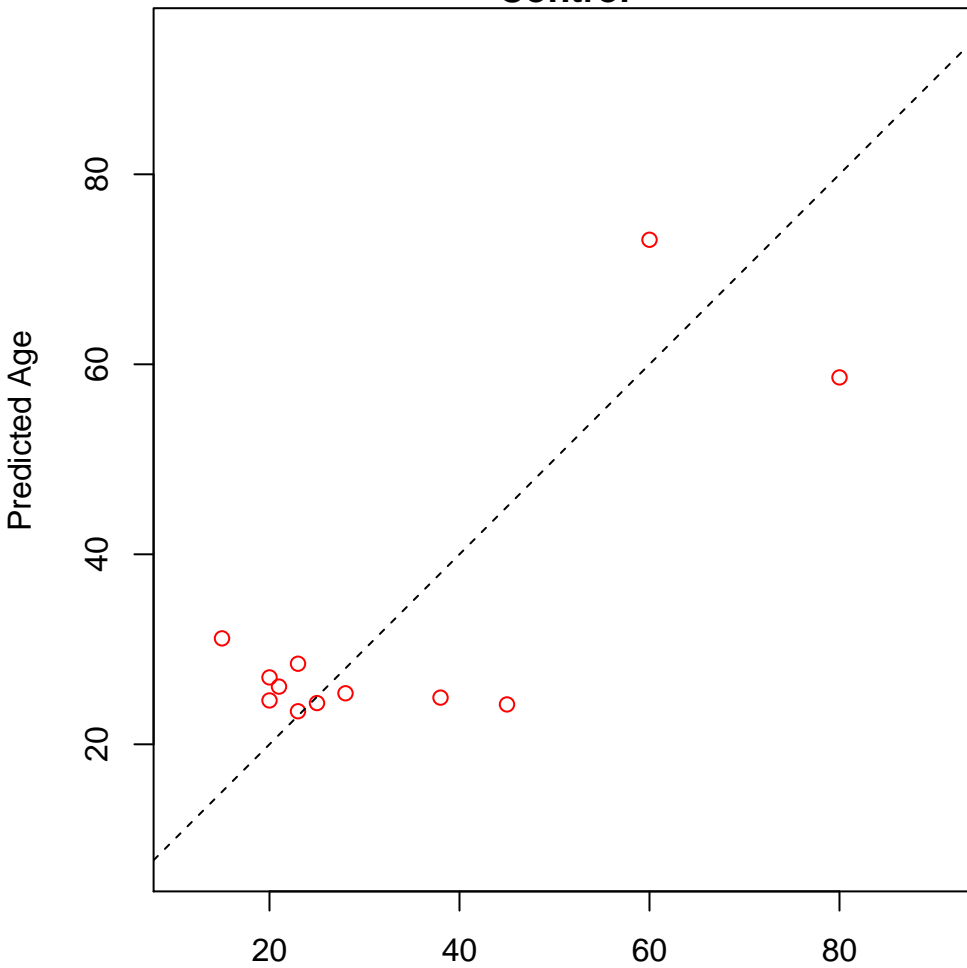
Test



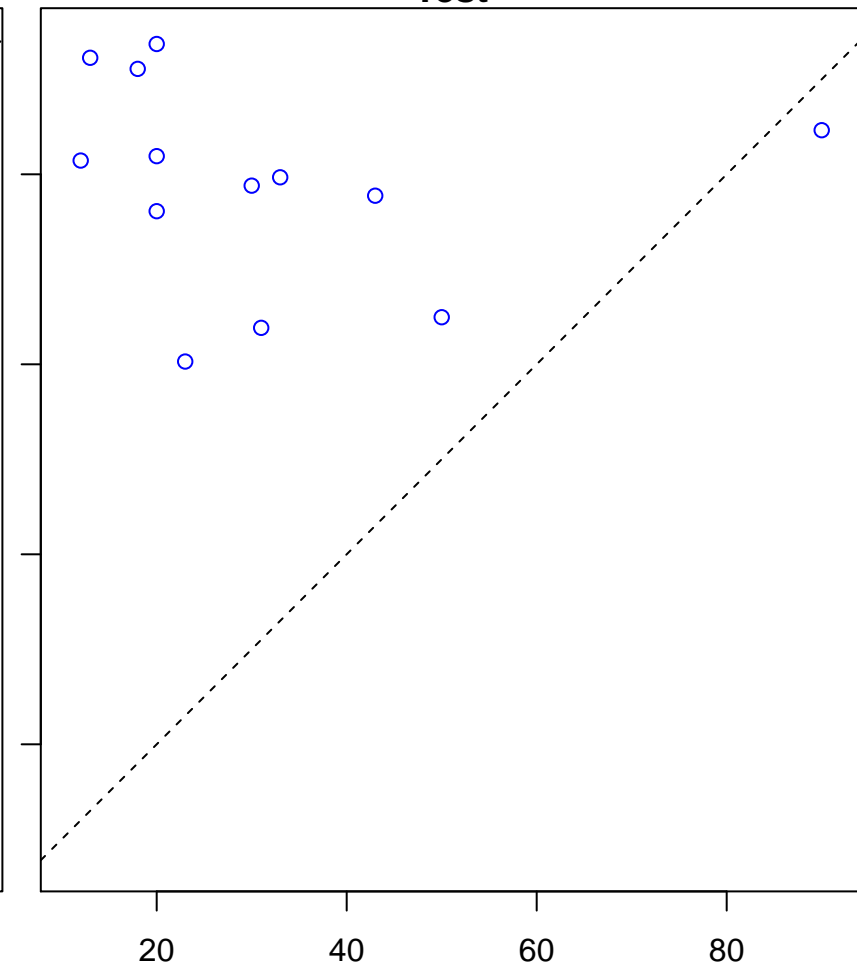
Actual Age

phosphatidylinositol 3-kinase signaling (Score: 7.595448)

Control

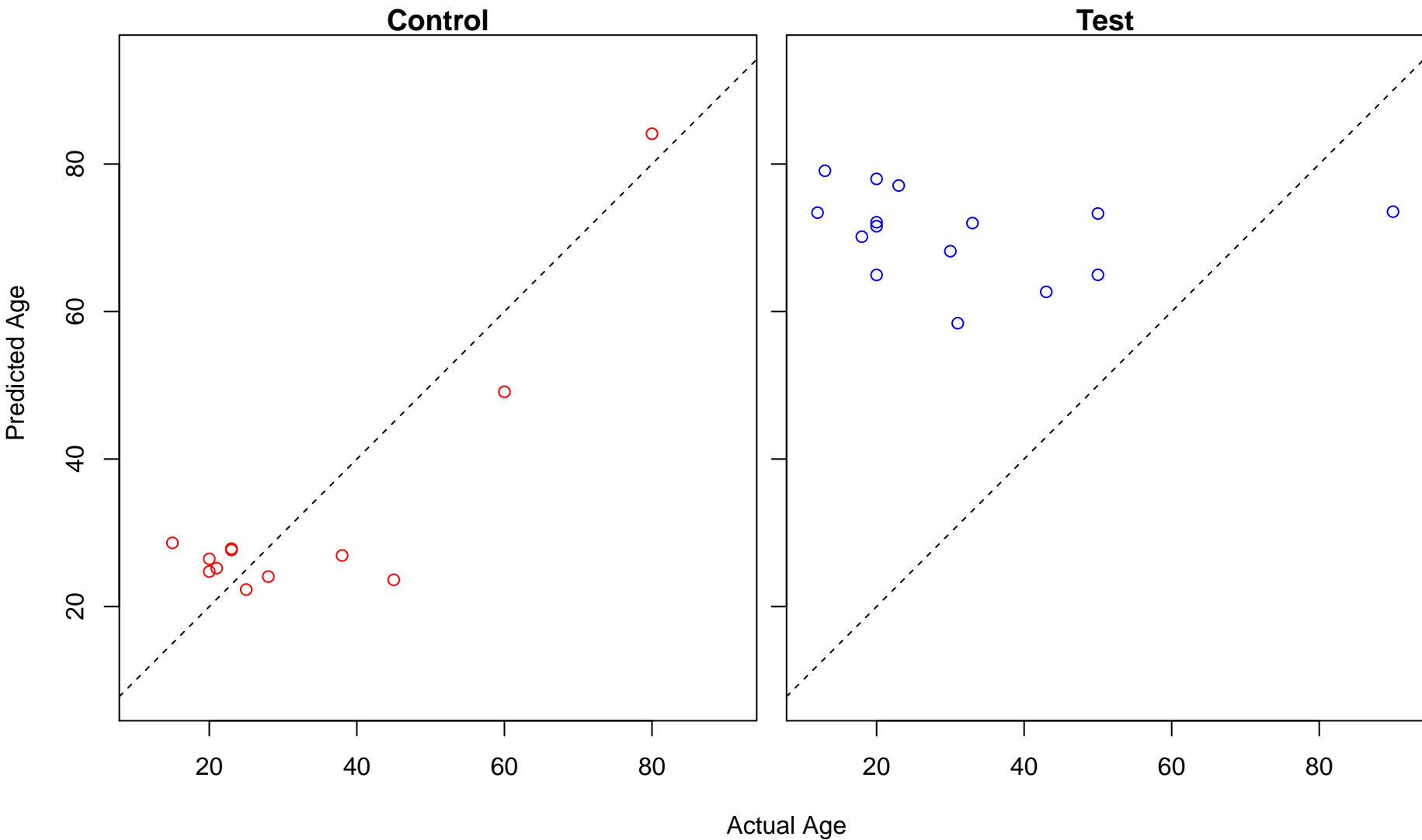


Test

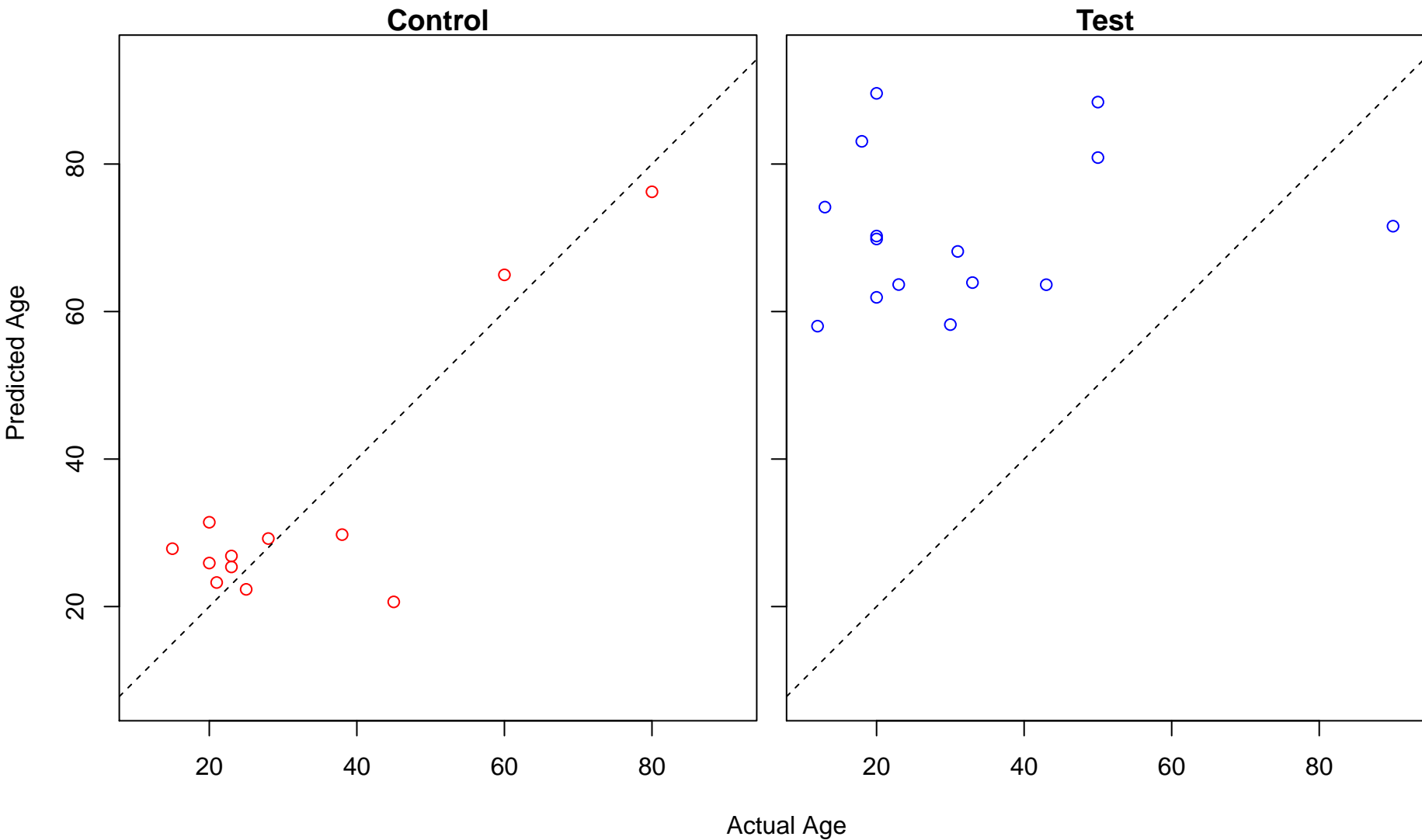


Actual Age

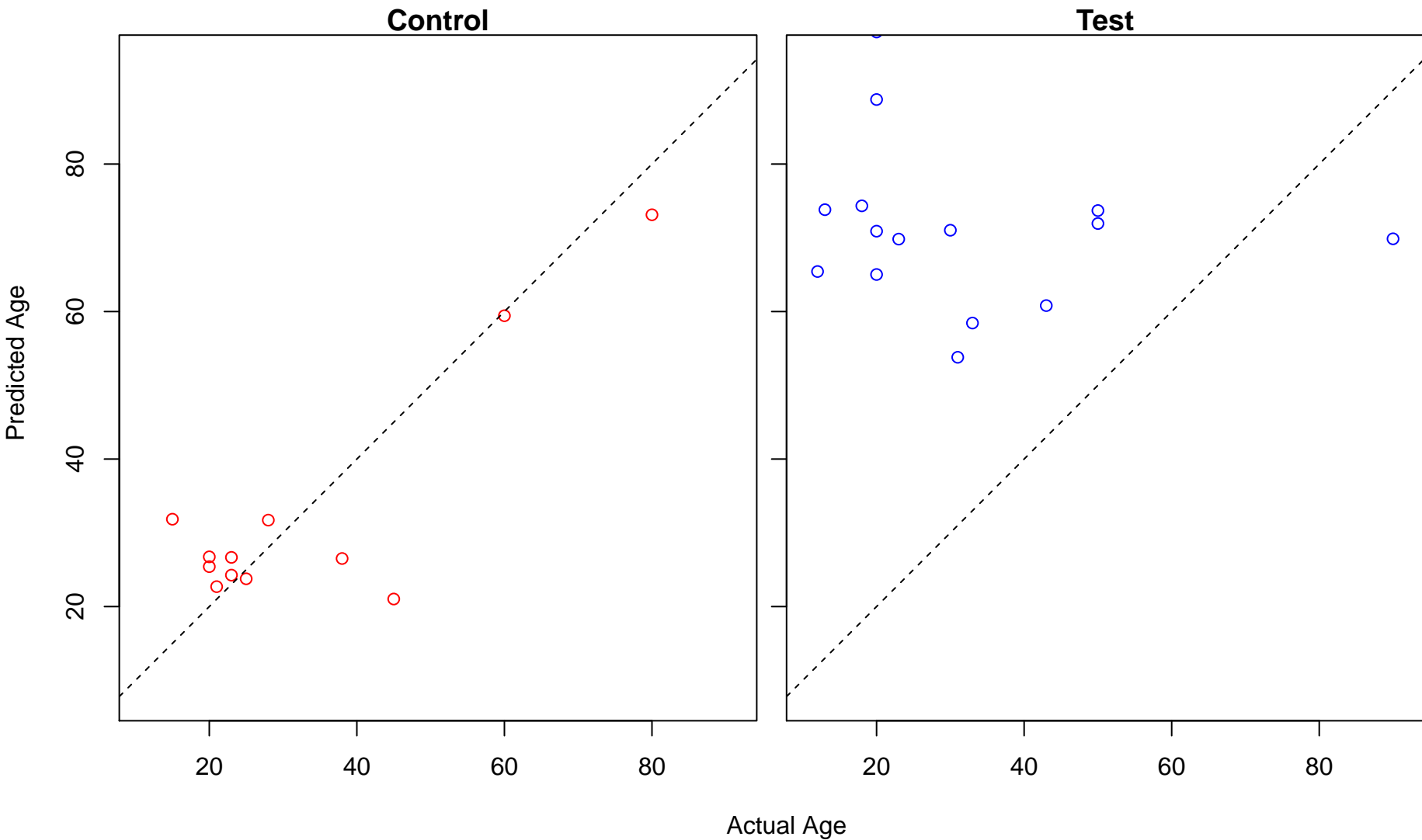
positive regulation of erythrocyte differentiation (Score: 7.593638)



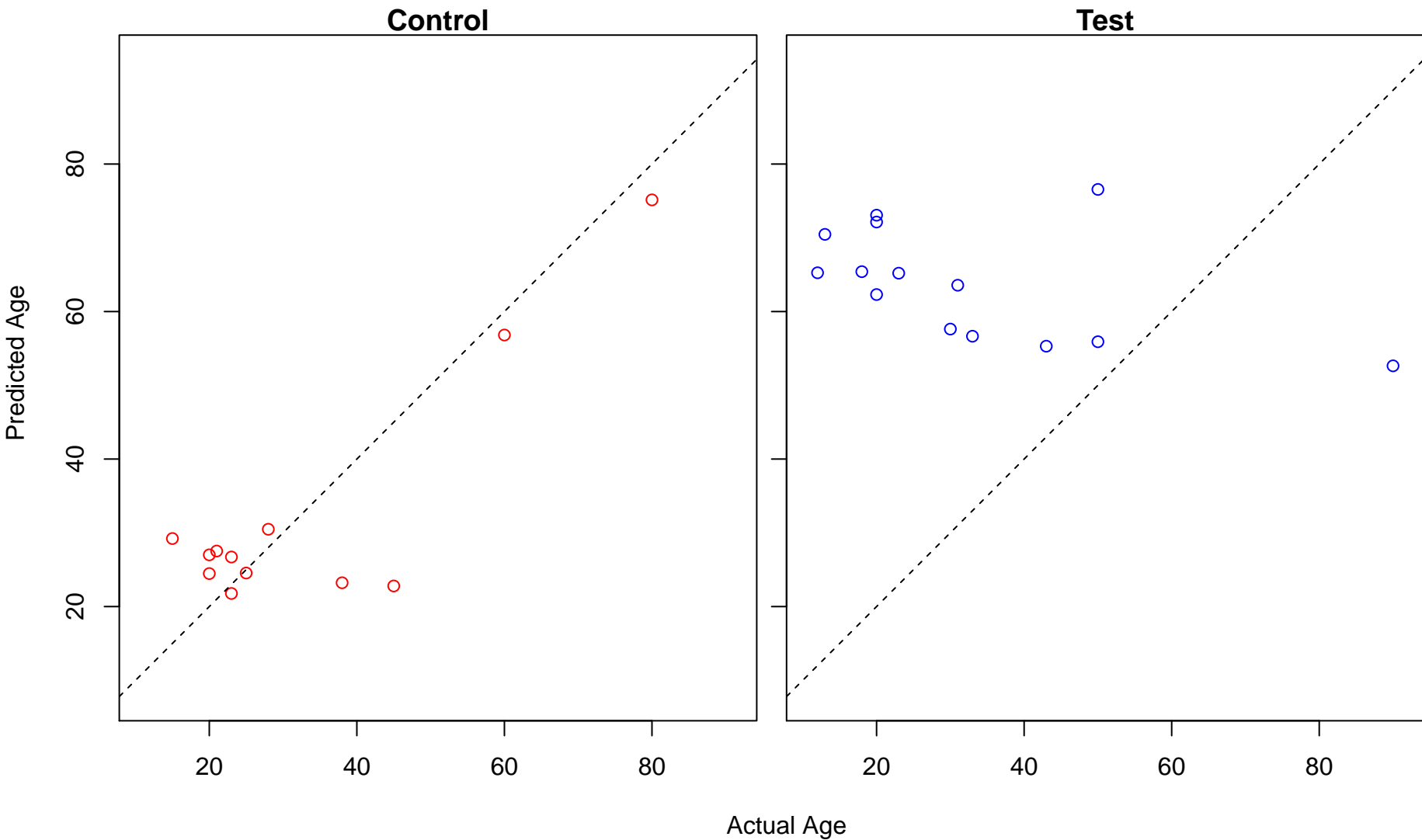
positive regulation of cellular component movement (Score: 7.593265)



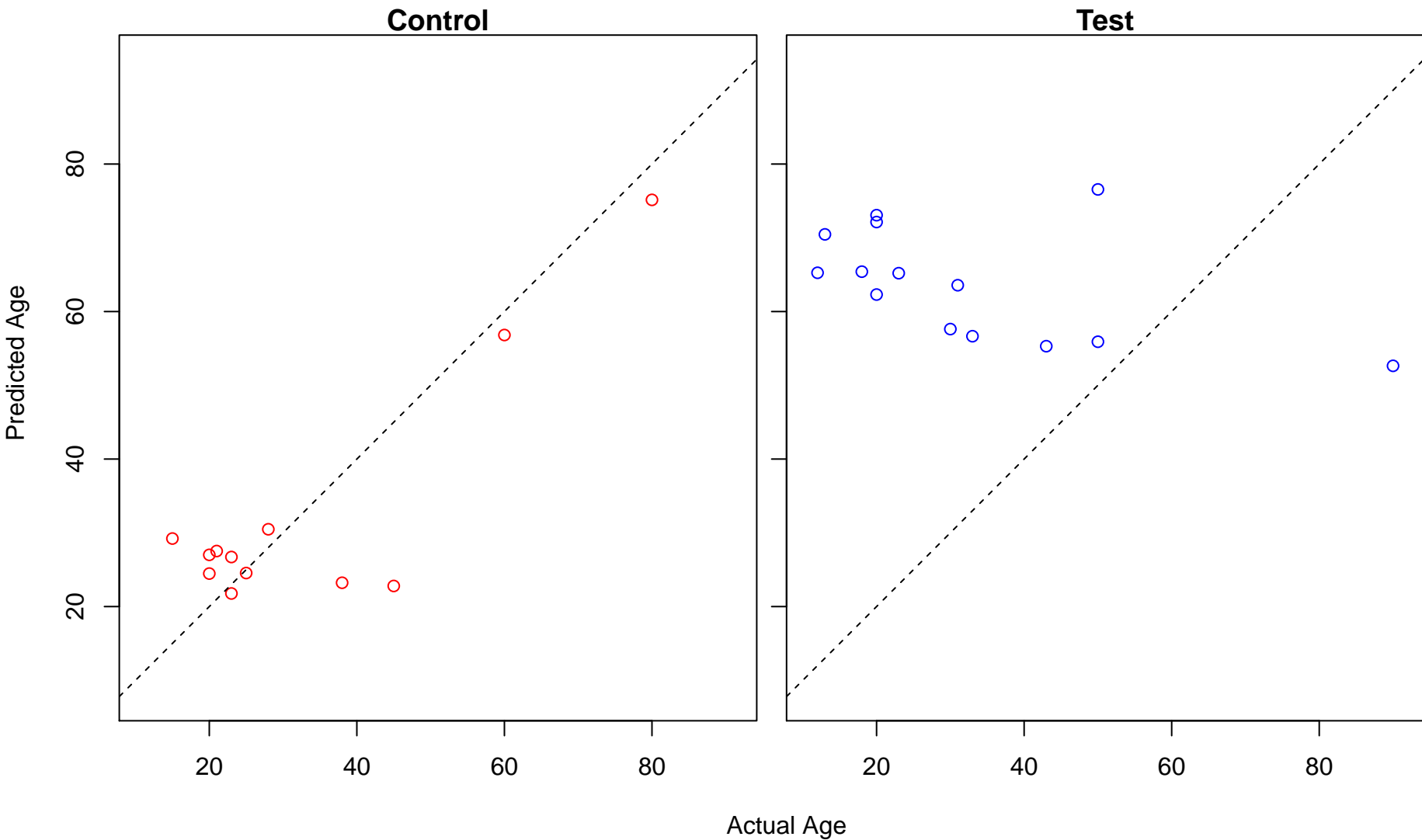
regulation of pathway-restricted SMAD protein phosphorylation (Score: 7.591975)



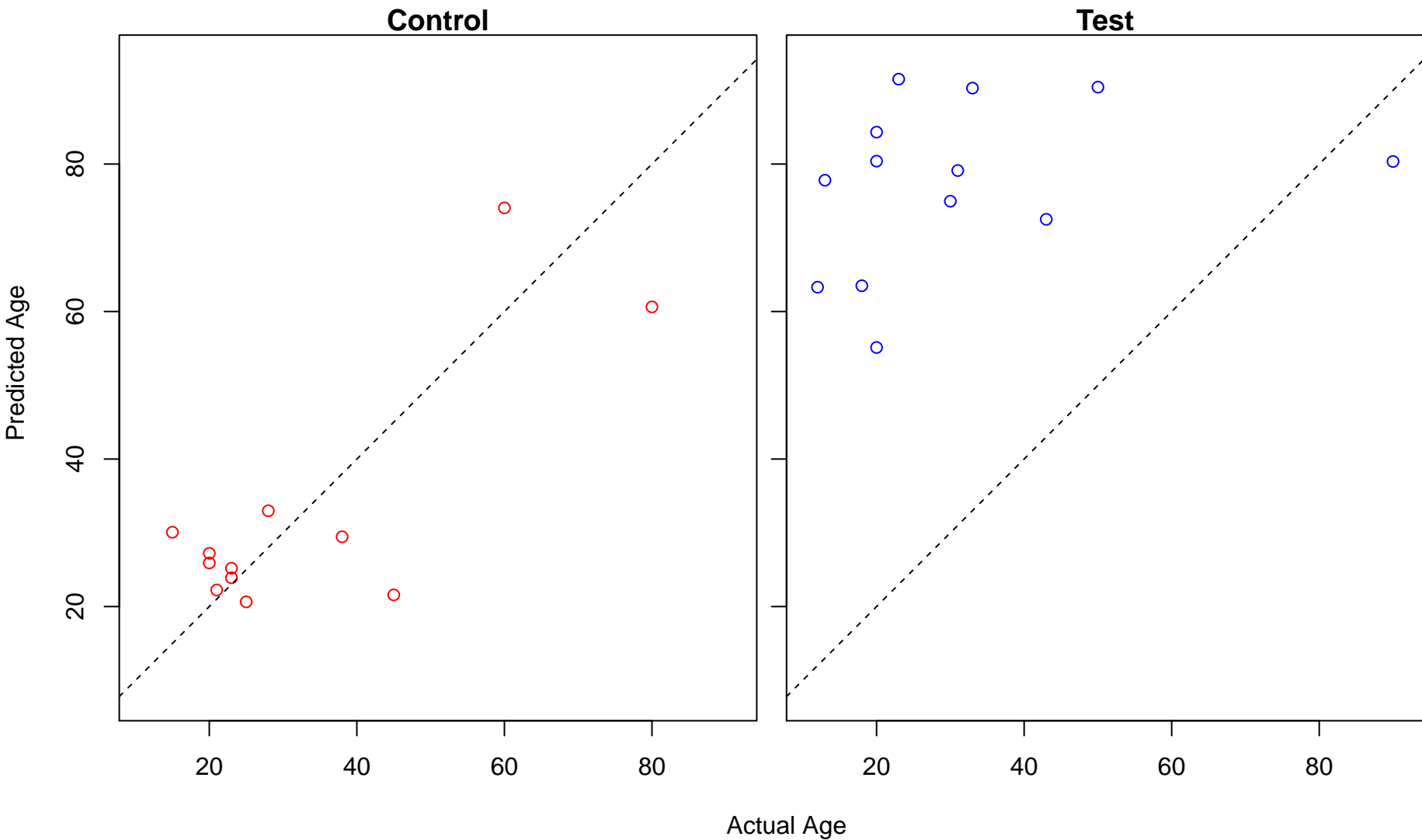
negative regulation of steroid biosynthetic process (Score: 7.585633)



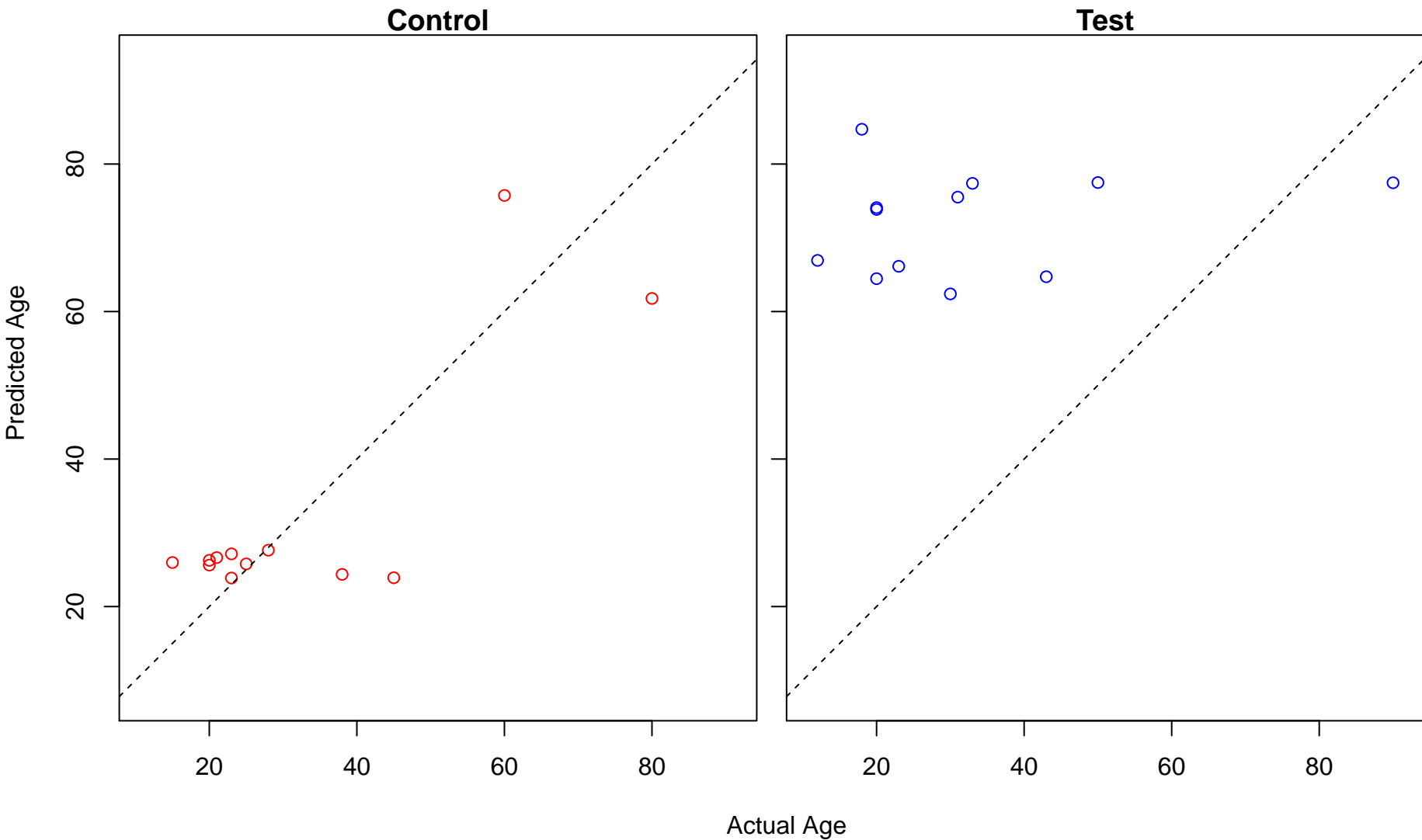
negative regulation of steroid metabolic process (Score: 7.585633)



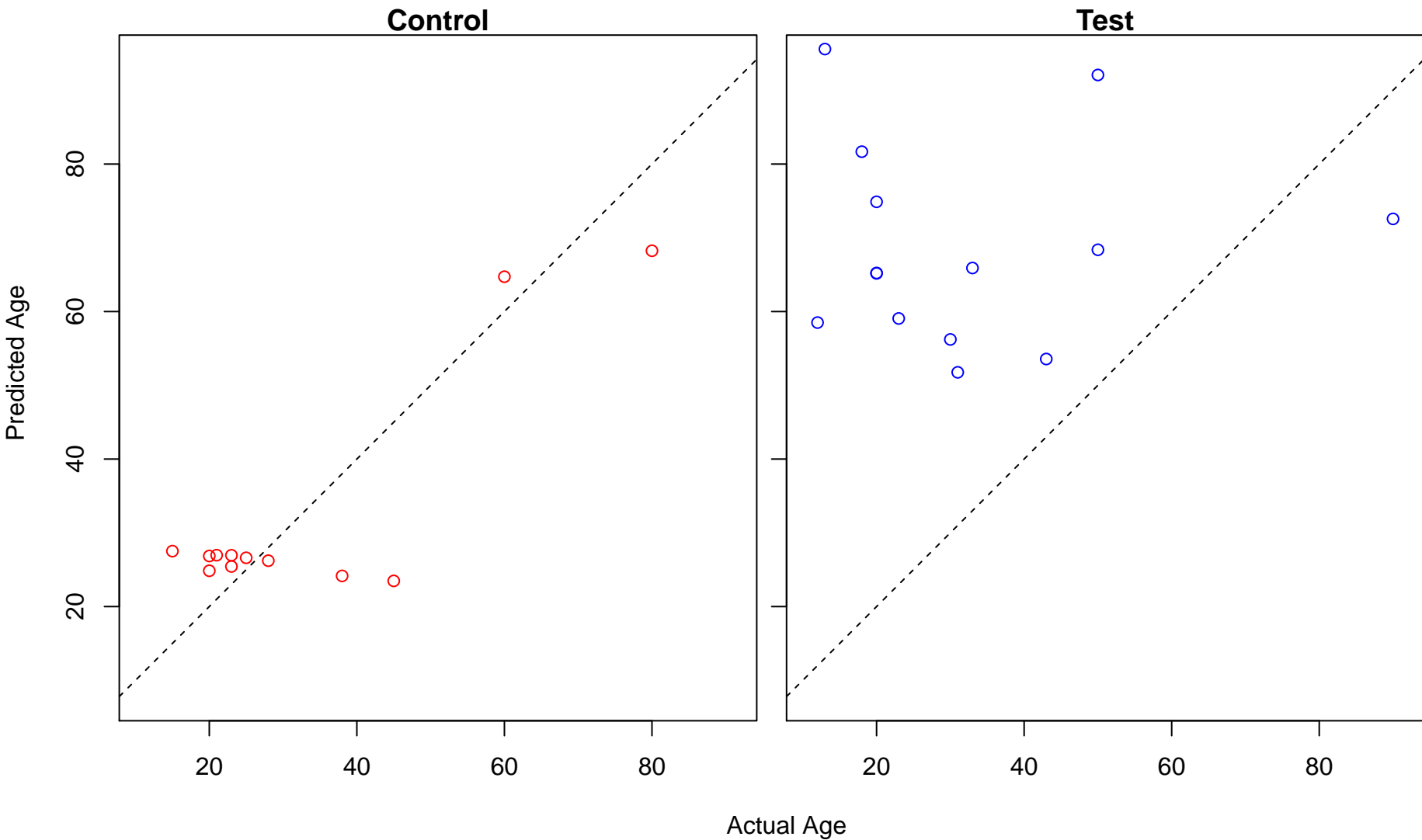
regulation of neuron migration (Score: 7.583885)



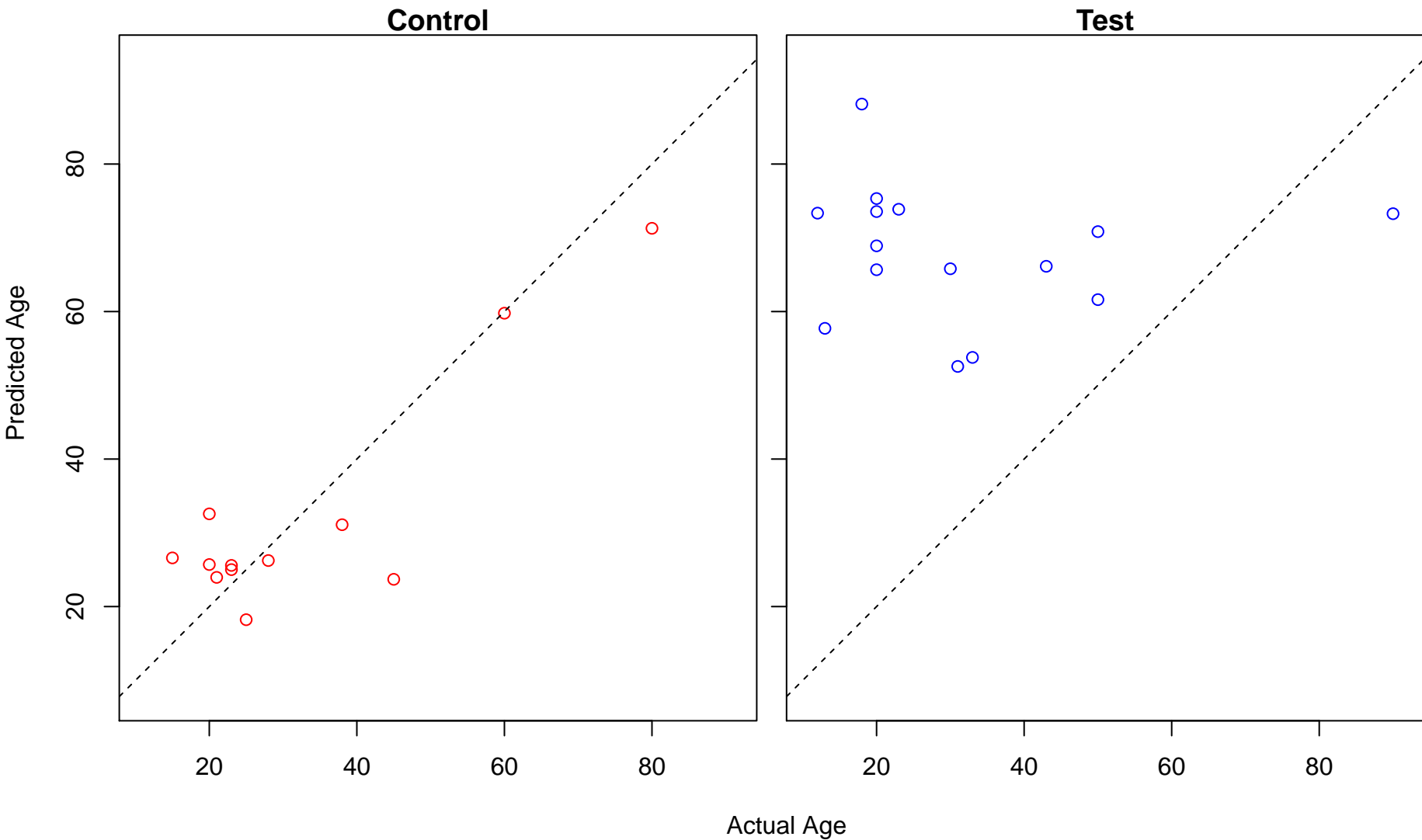
regulation of response to DNA damage stimulus (Score: 7.580760)



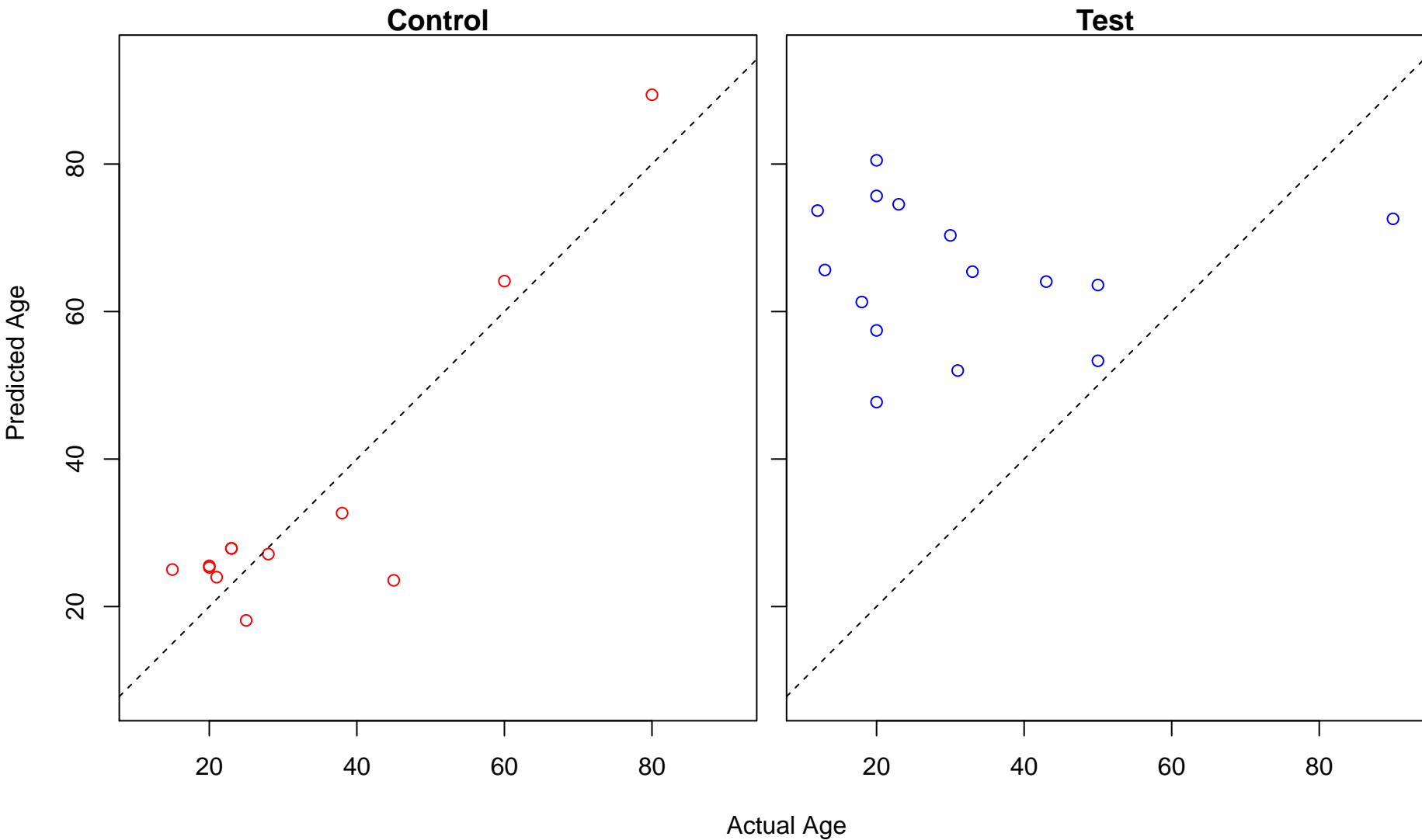
translational initiation (Score: 7.579941)



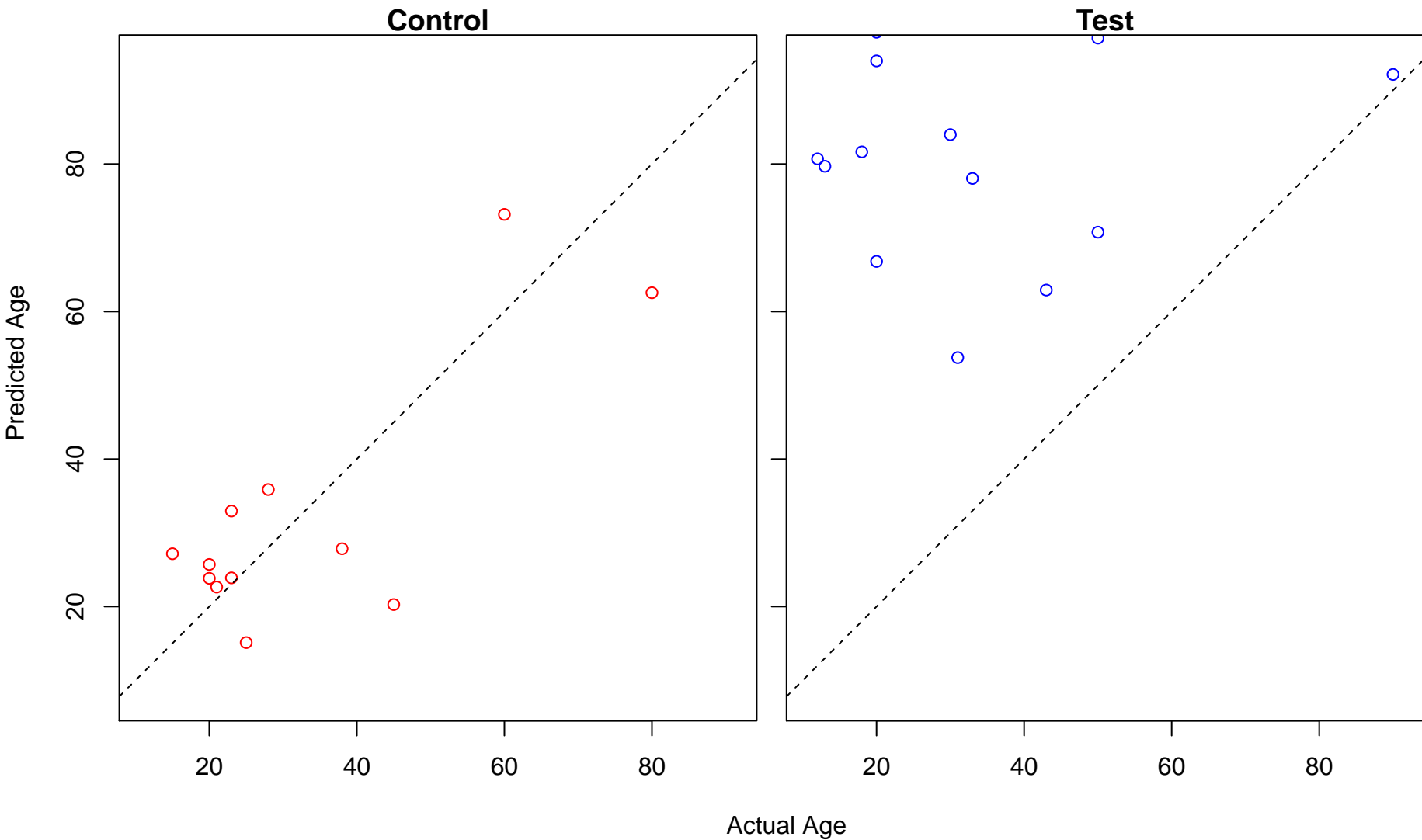
negative regulation of JUN kinase activity (Score: 7.575810)



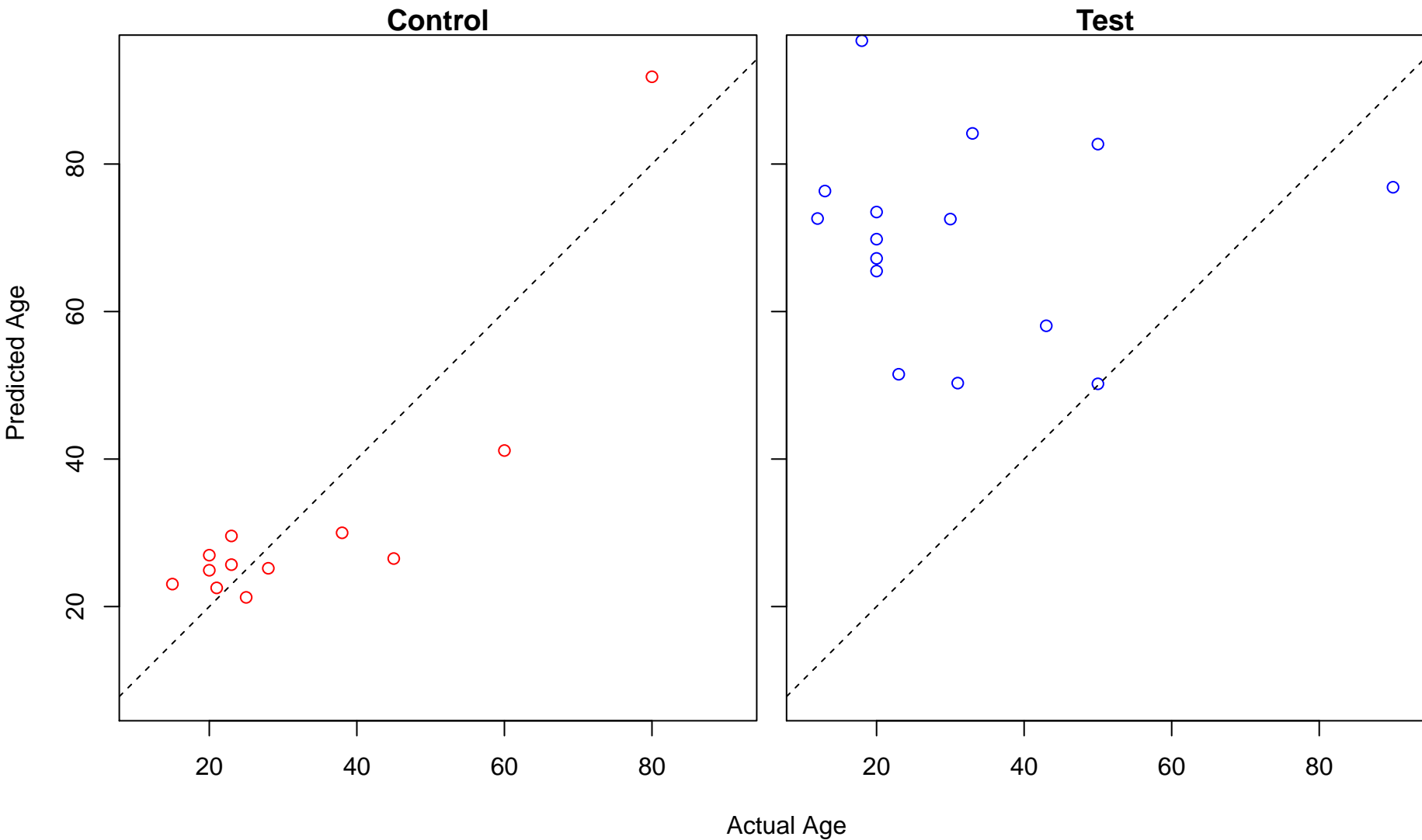
central nervous system neuron axonogenesis (Score: 7.573311)



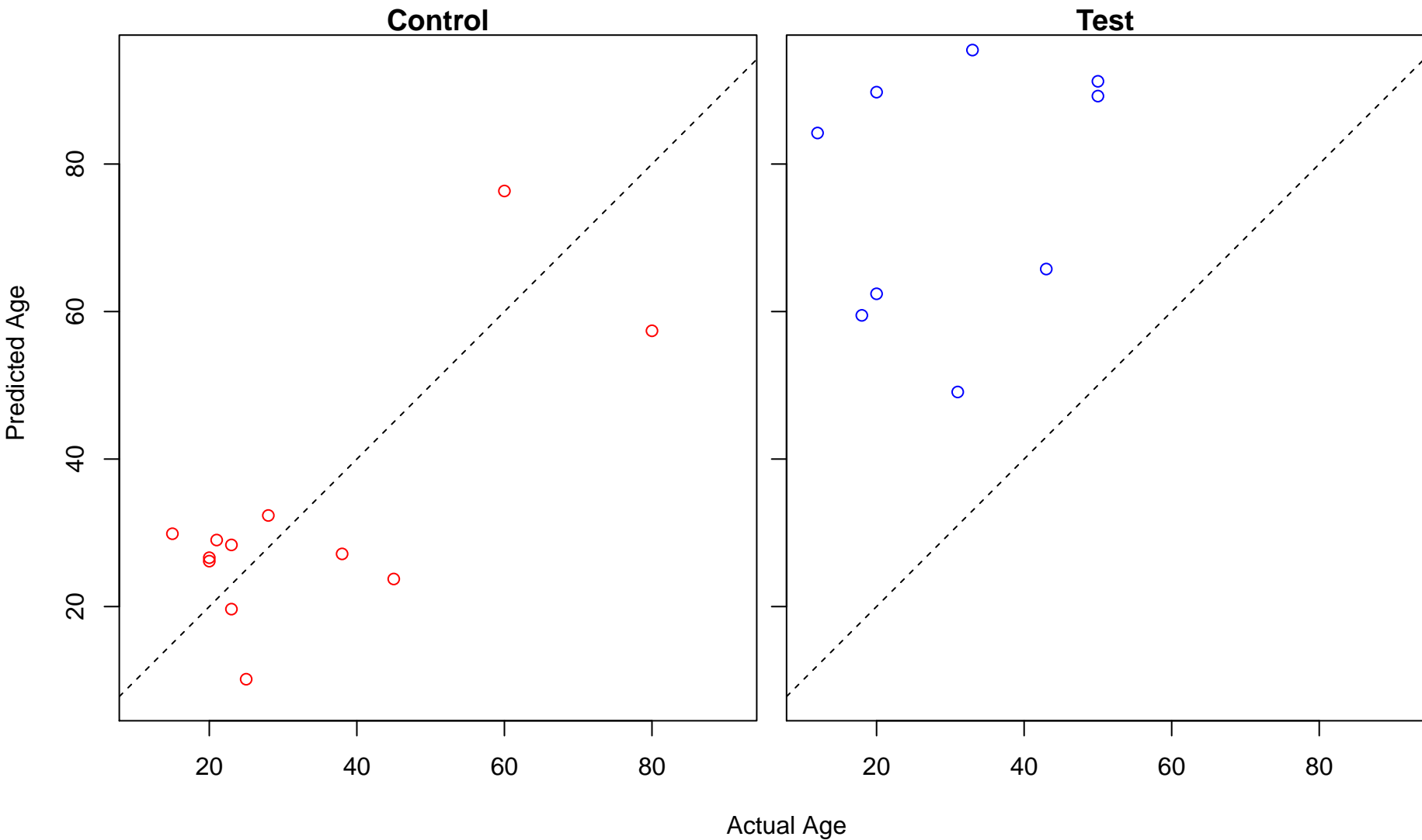
spliceosomal complex assembly (Score: 7.570481)



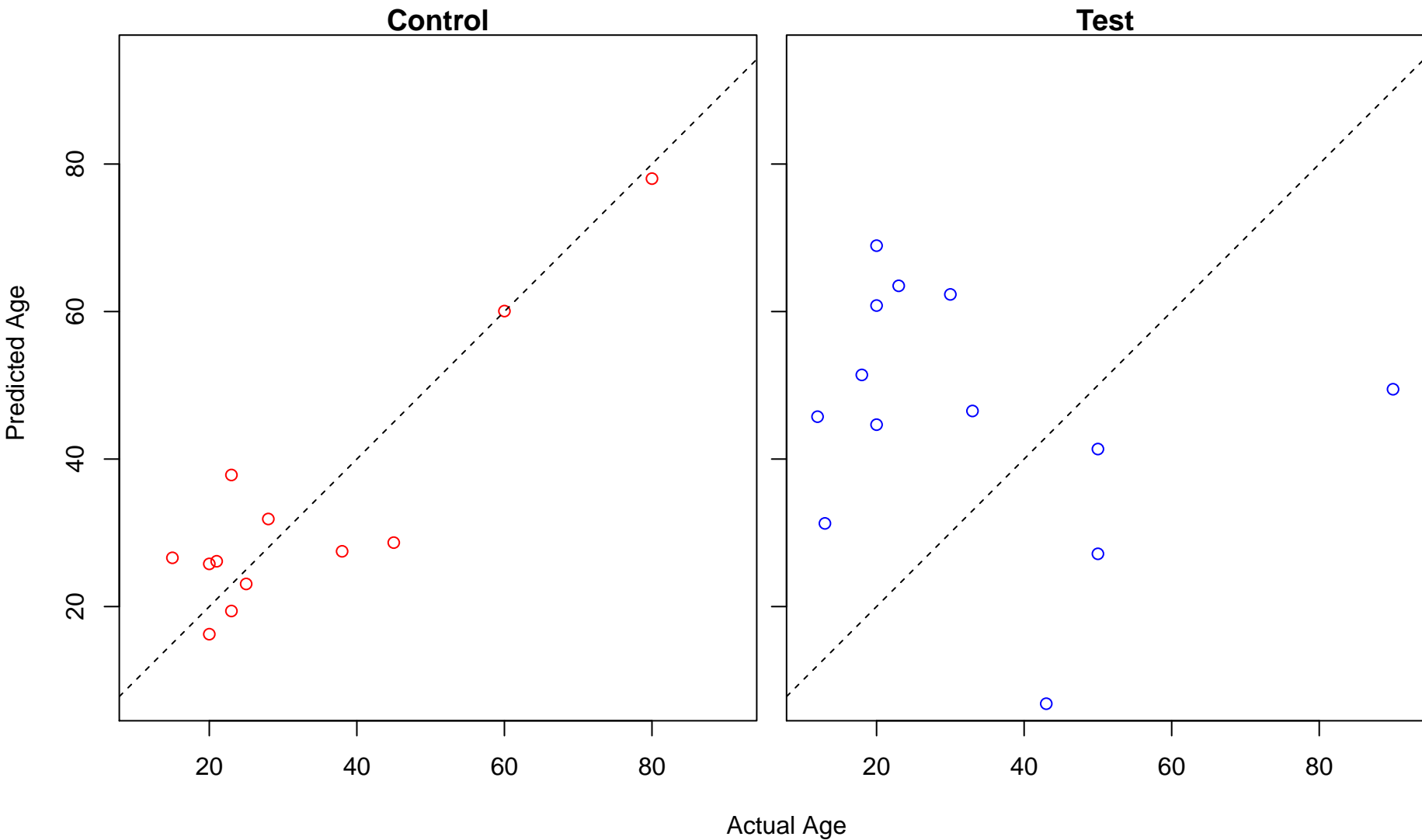
pyrimidine-containing compound catabolic process (Score: 7.563379)



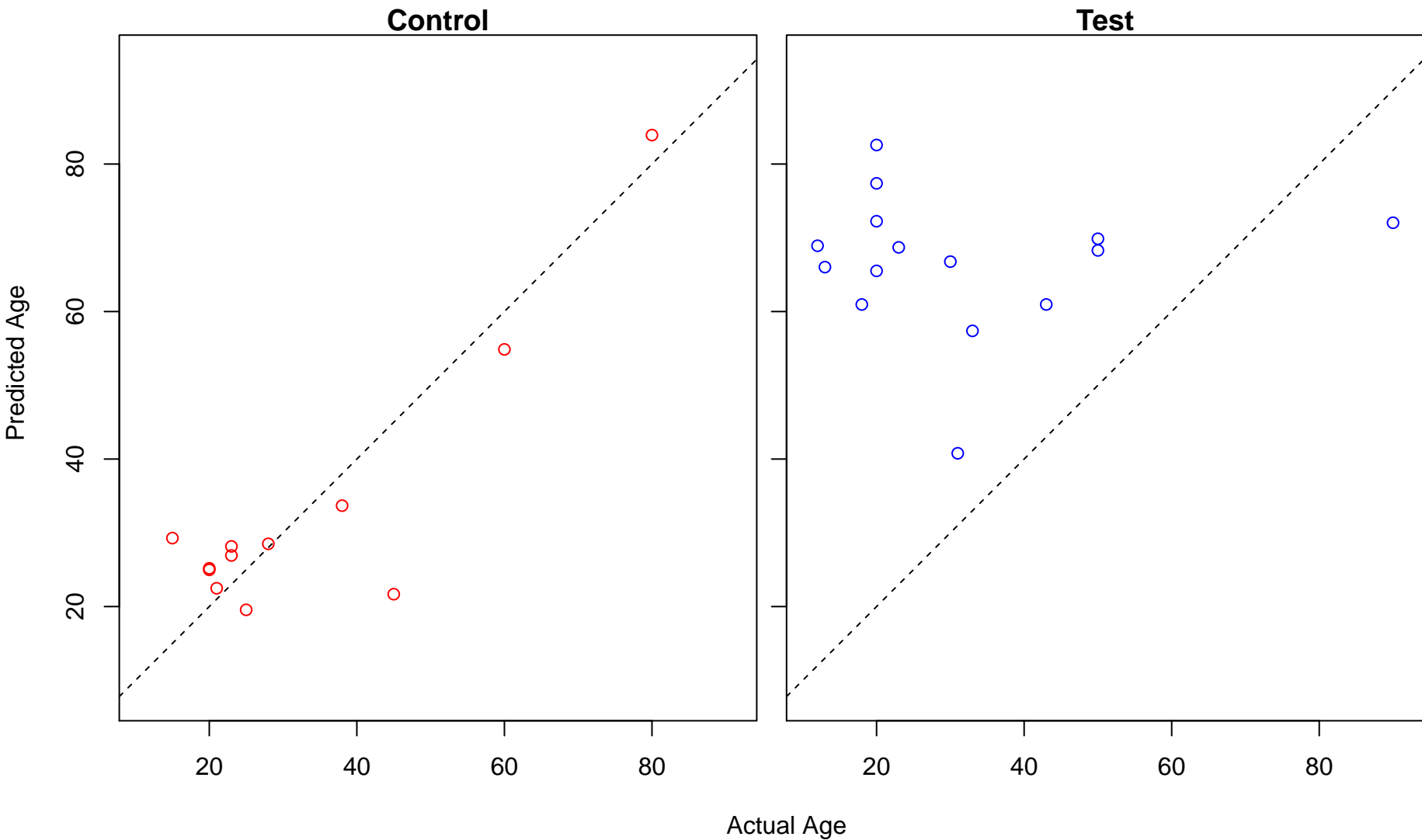
positive regulation of triglyceride lipase activity (Score: 7.560224)



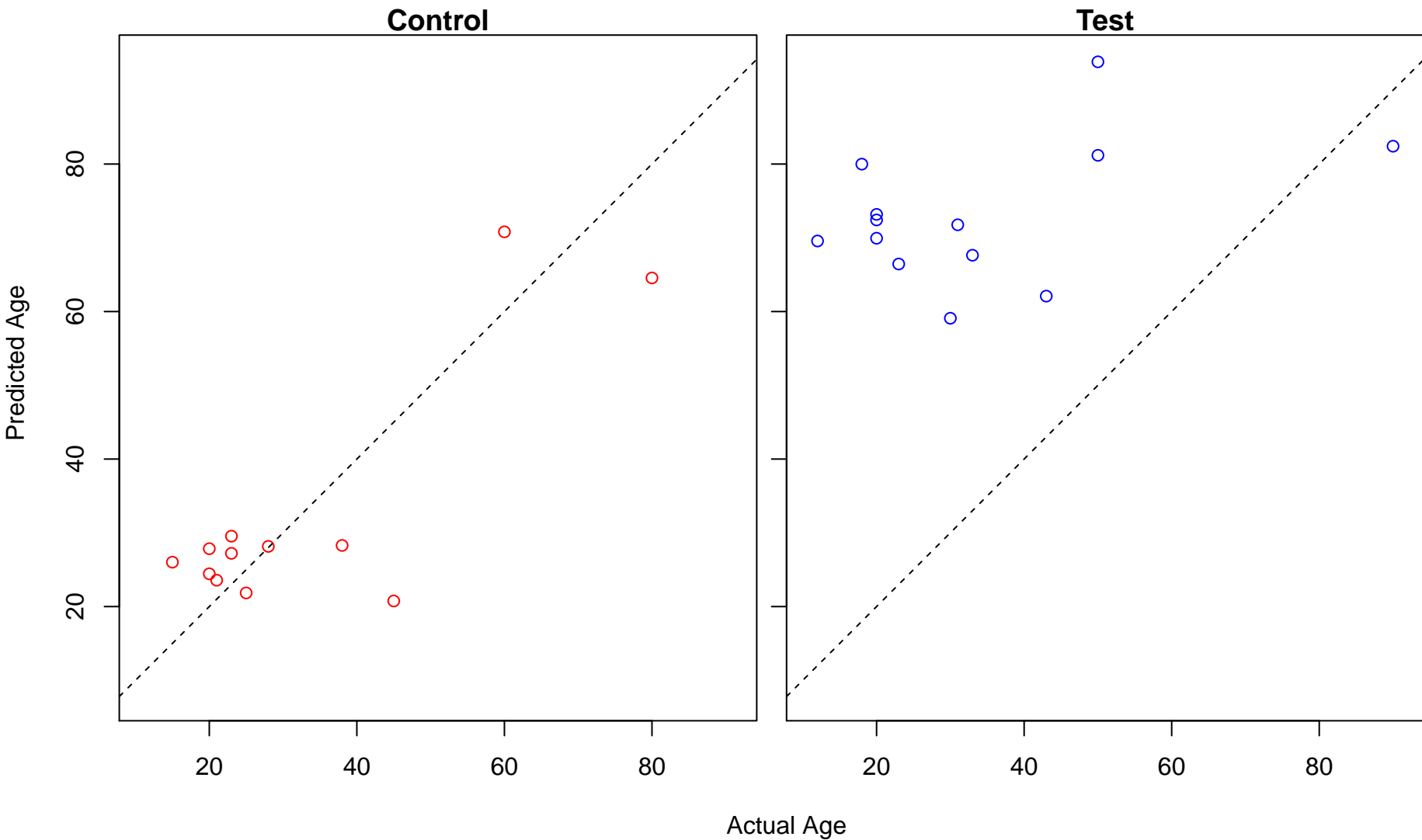
positive regulation of neurogenesis (Score: 7.555860)



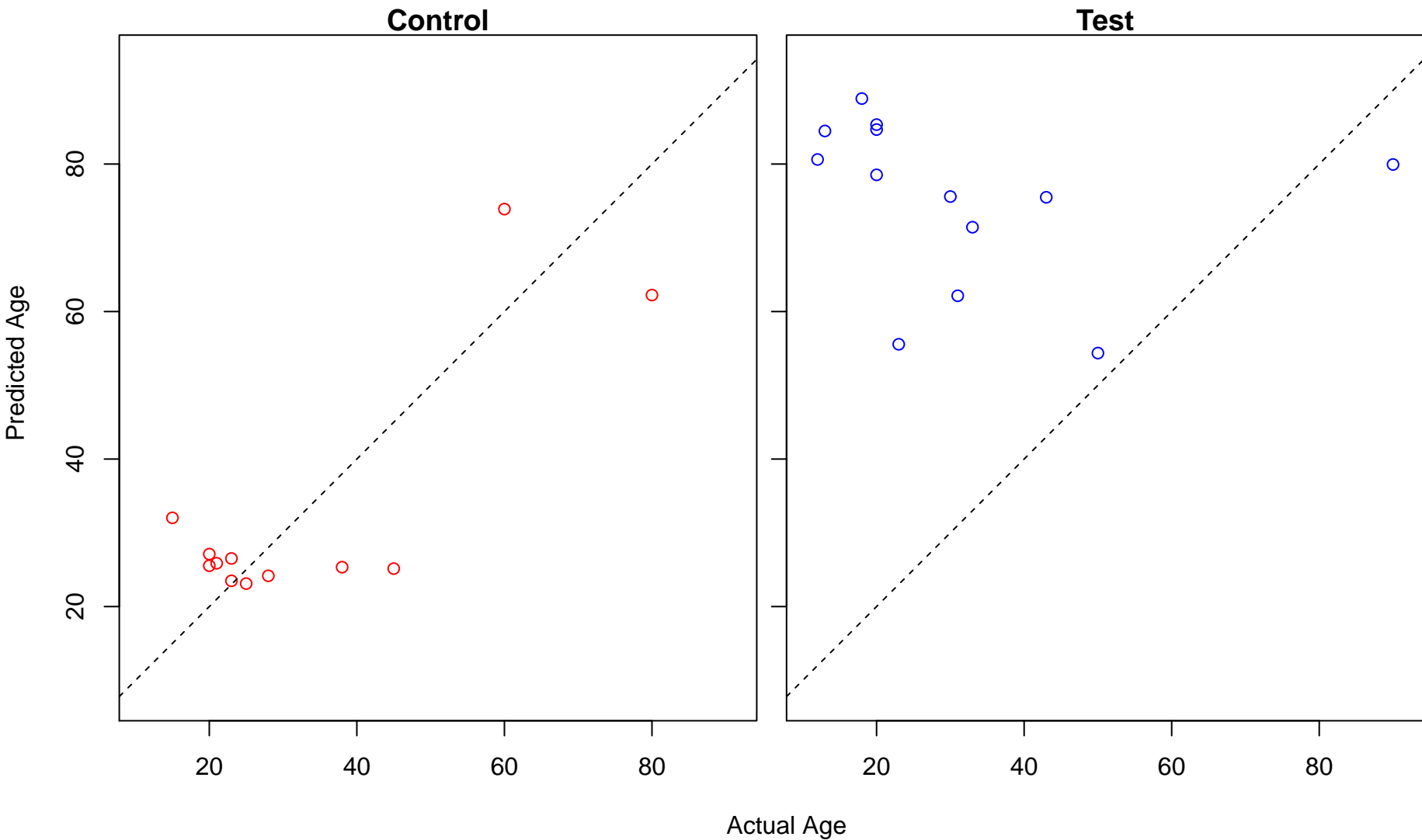
mesonephros development (Score: 7.552047)



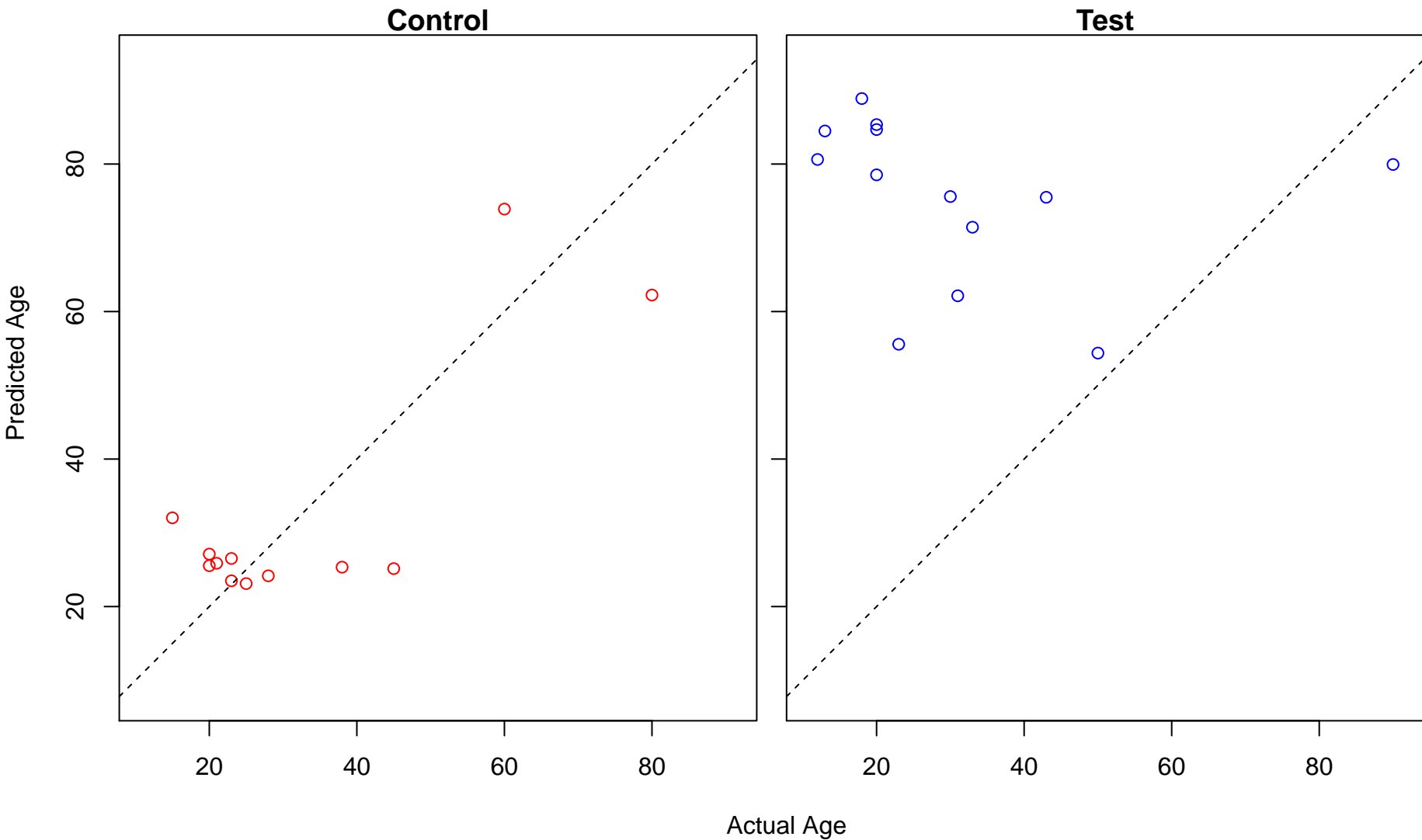
negative regulation of viral genome replication (Score: 7.550437)



acylglycerol homeostasis (Score: 7.550106)

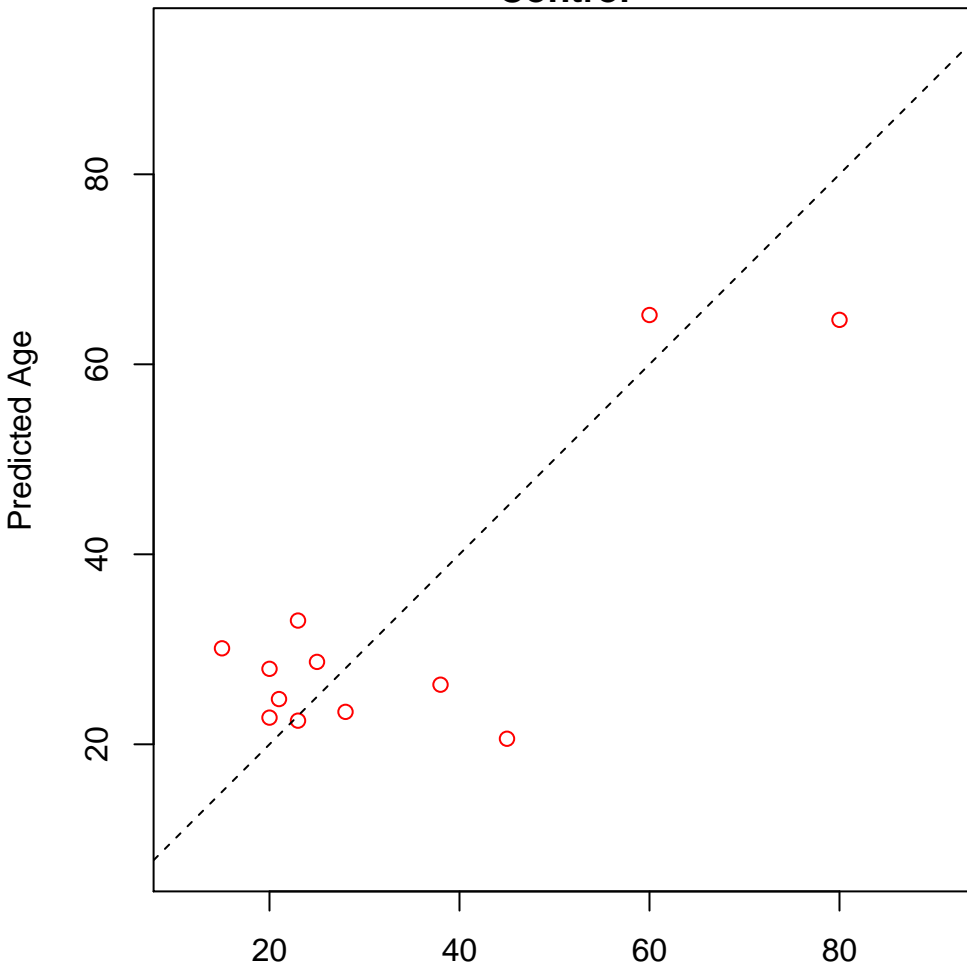


triglyceride homeostasis (Score: 7.550106)

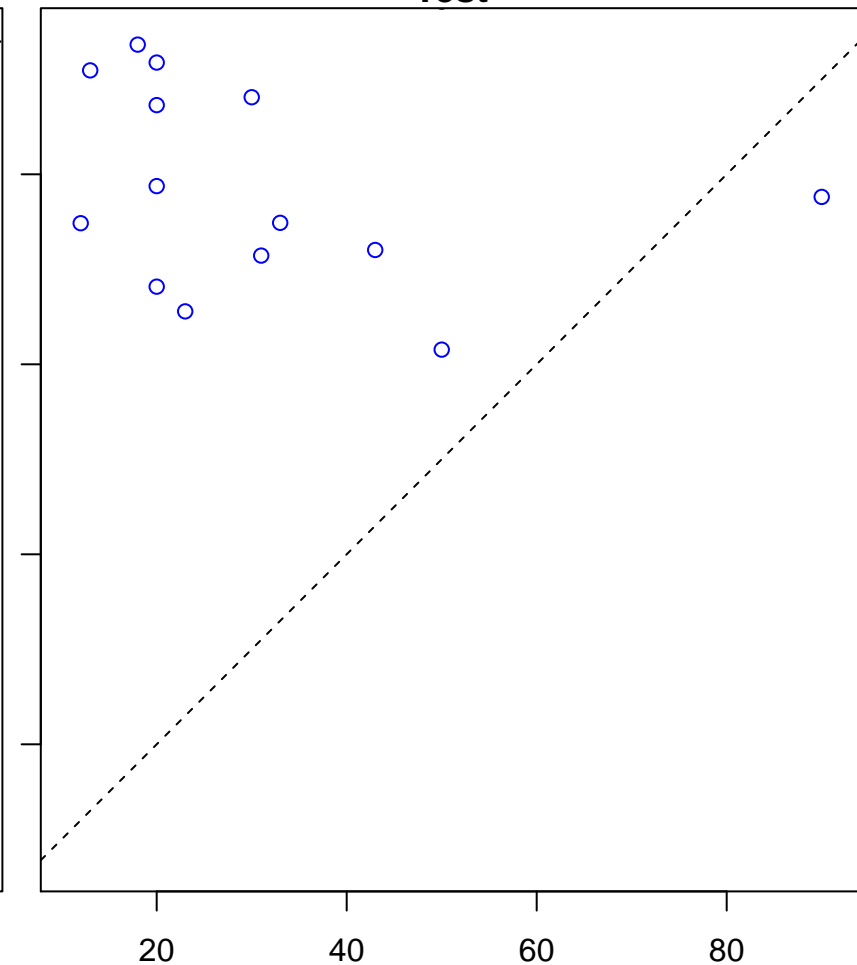


regulation of immunoglobulin secretion (Score: 7.545921)

Control

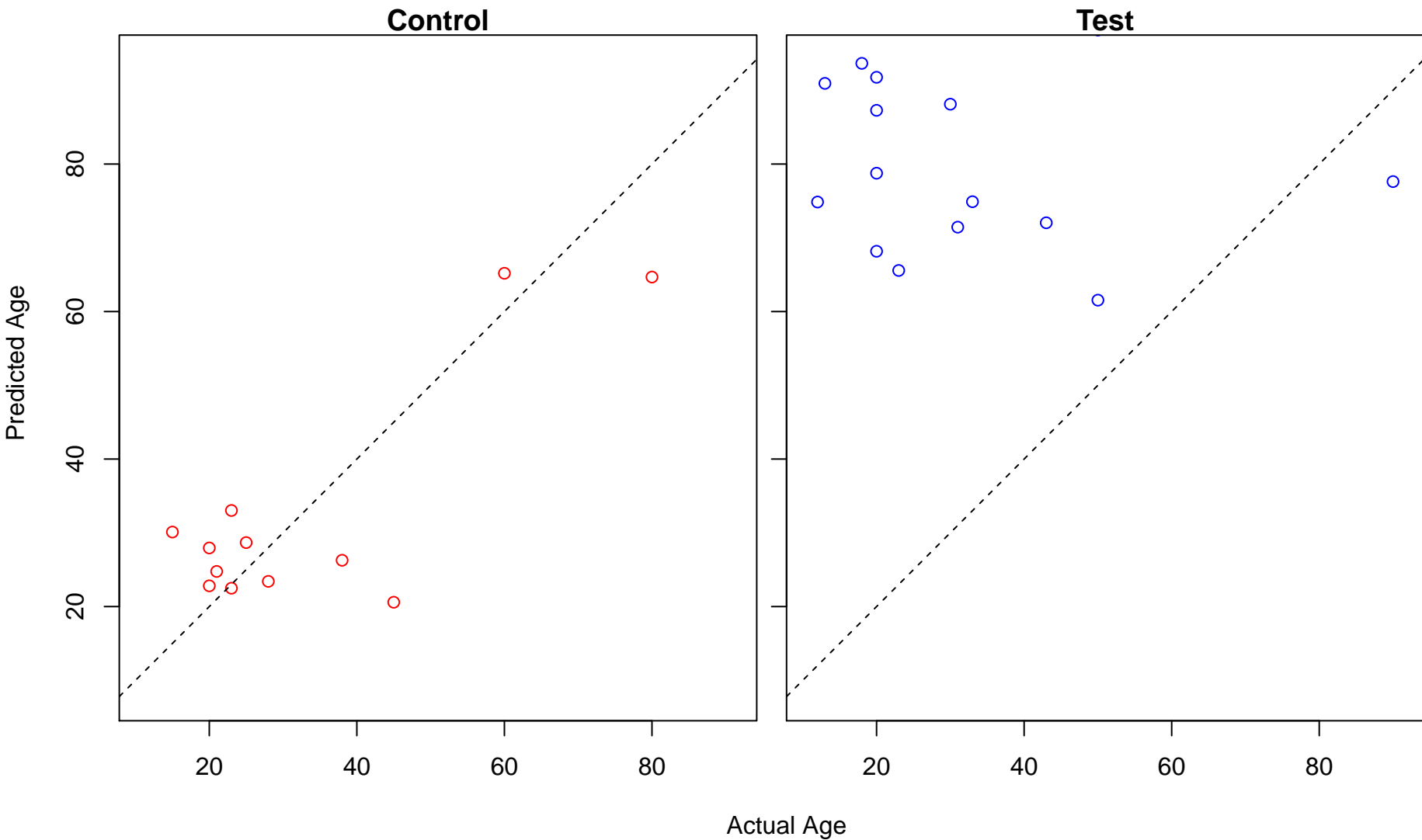


Test



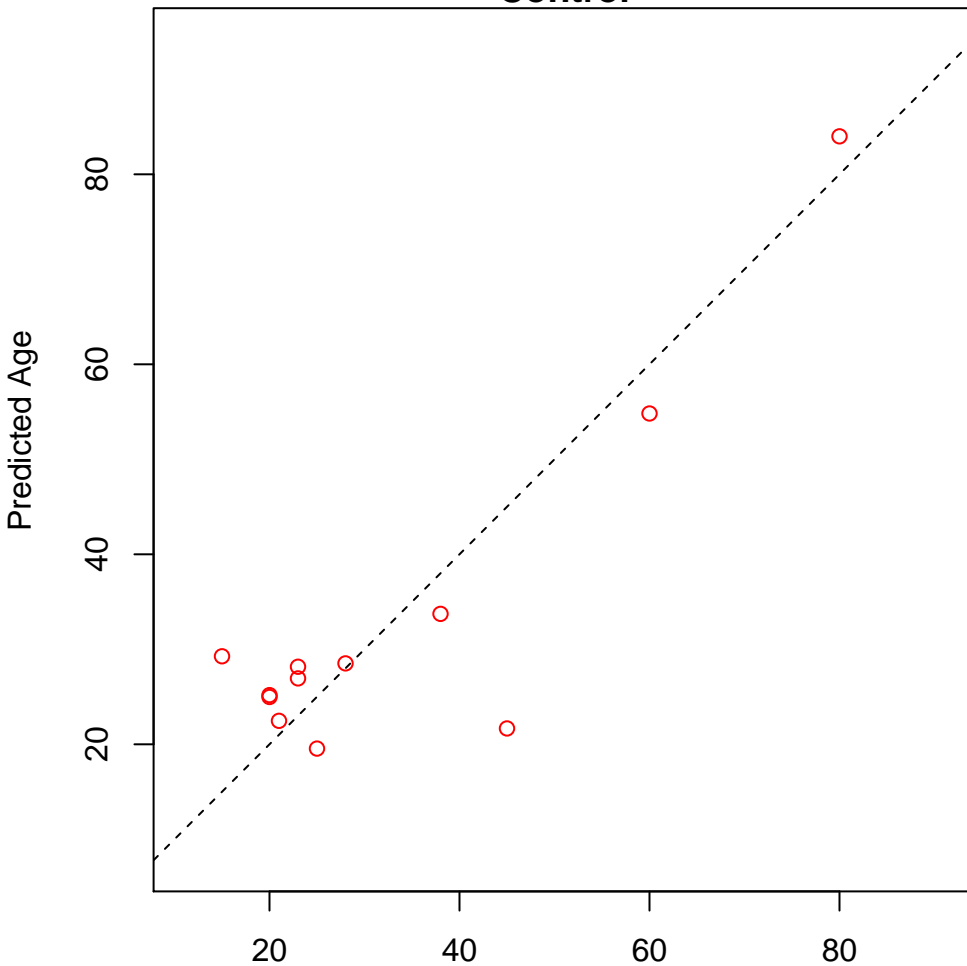
Actual Age

positive regulation of immunoglobulin secretion (Score: 7.545921)

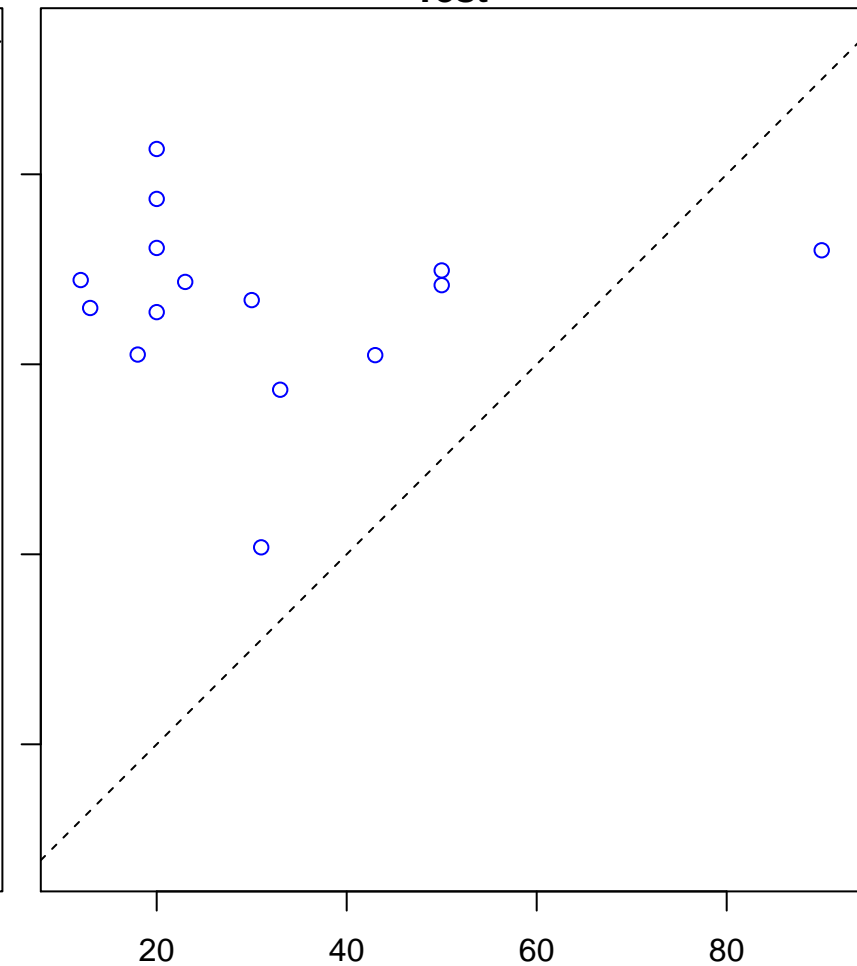


mesonephric epithelium development (Score: 7.545821)

Control



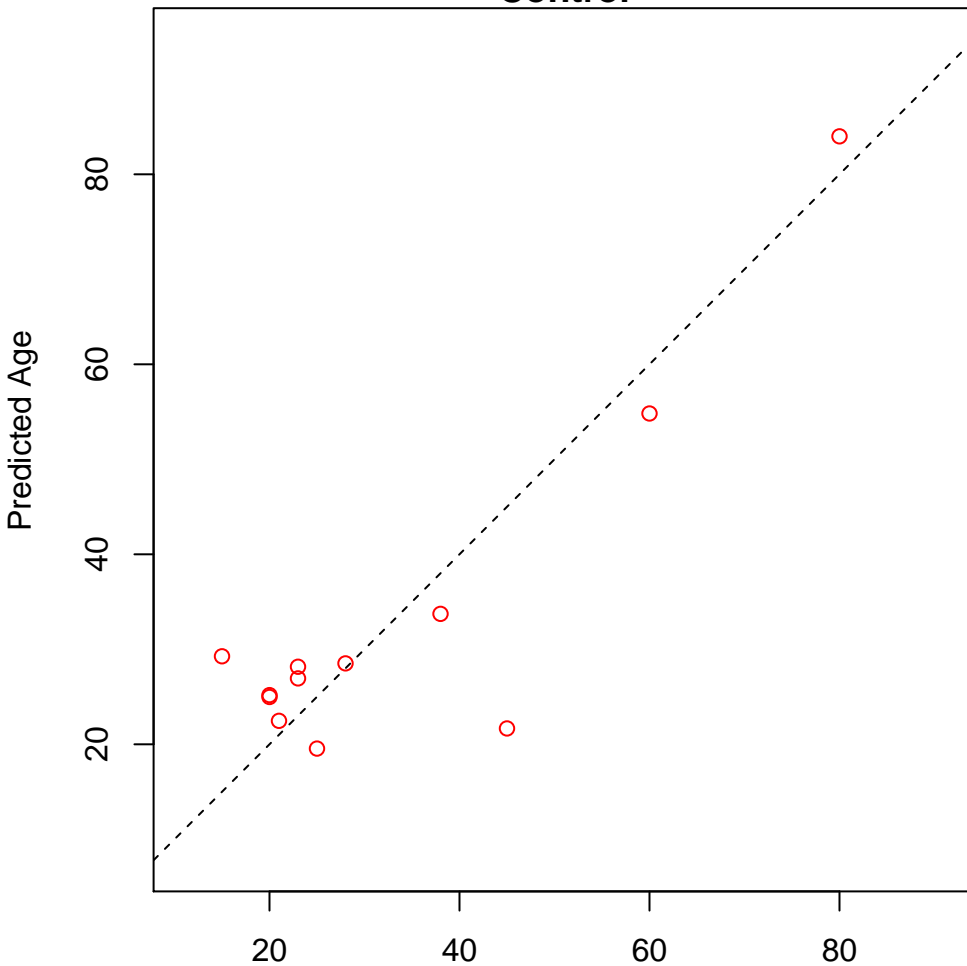
Test



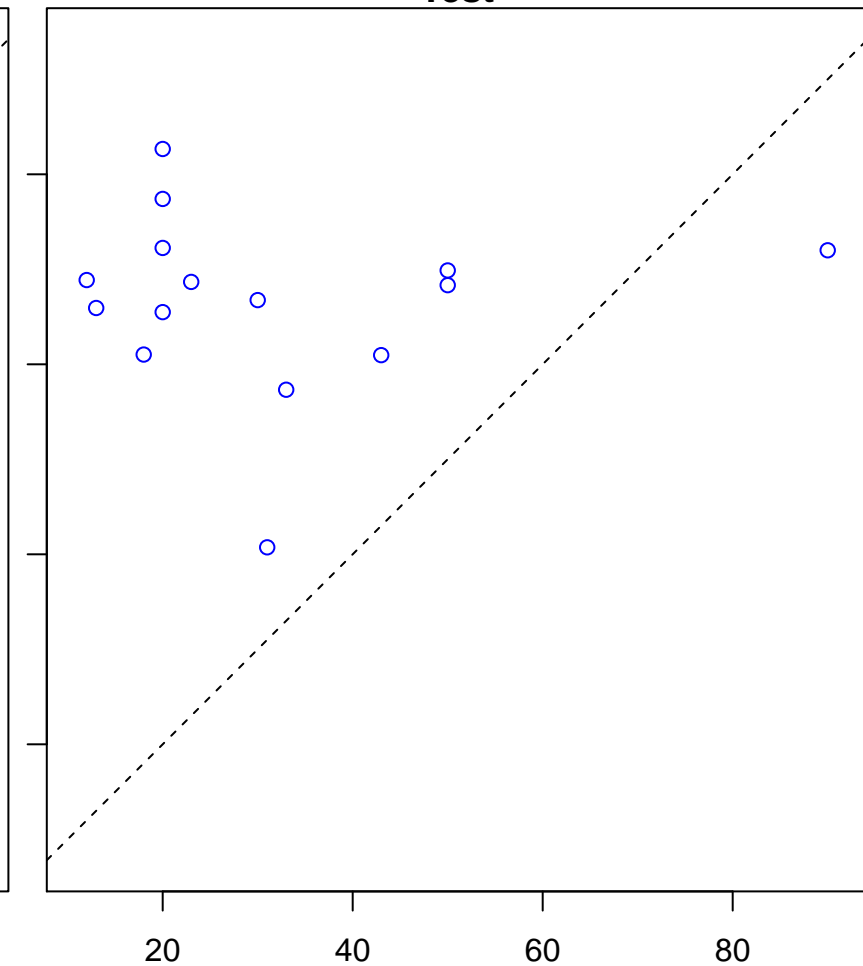
Actual Age

mesonephric tubule development (Score: 7.545821)

Control

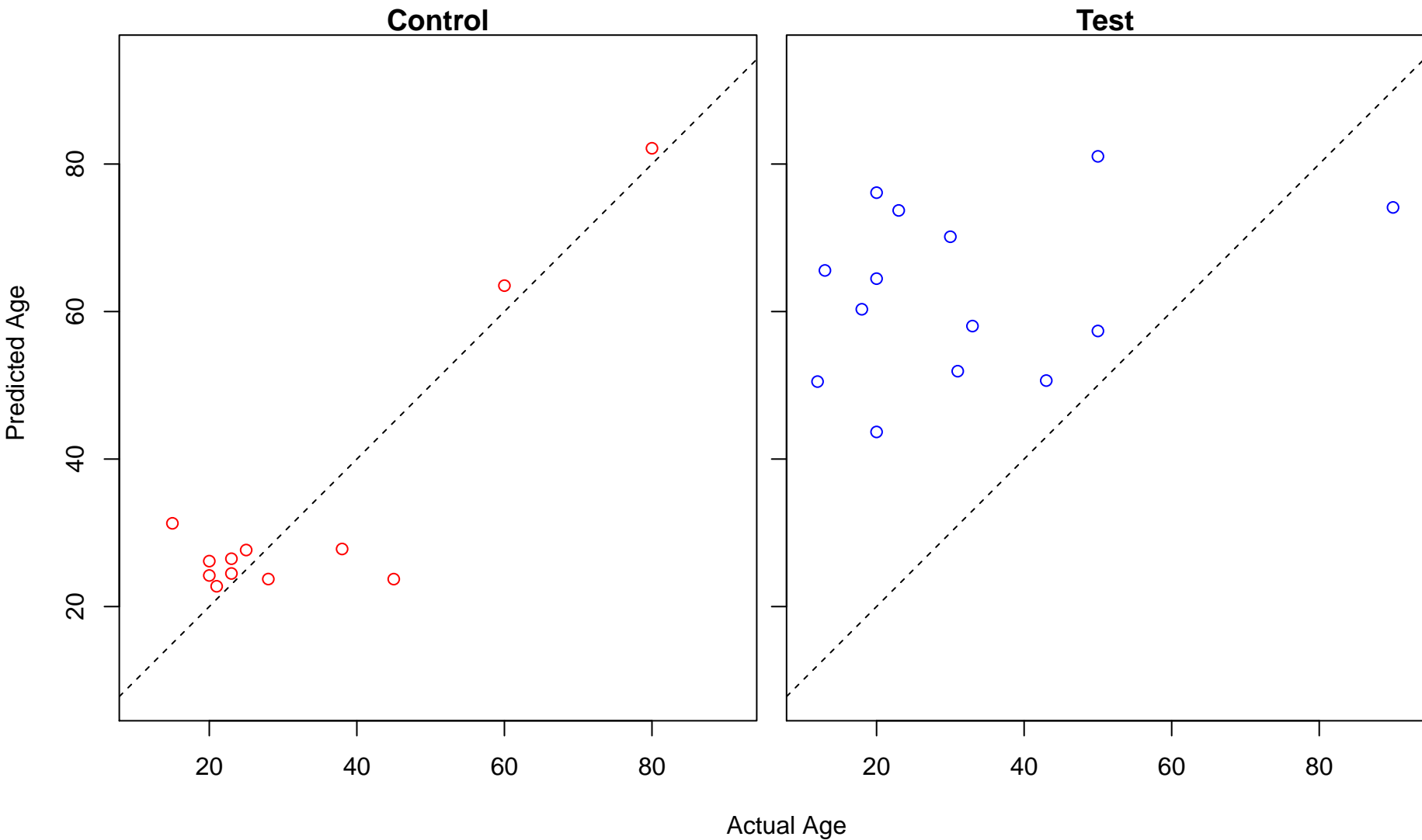


Test

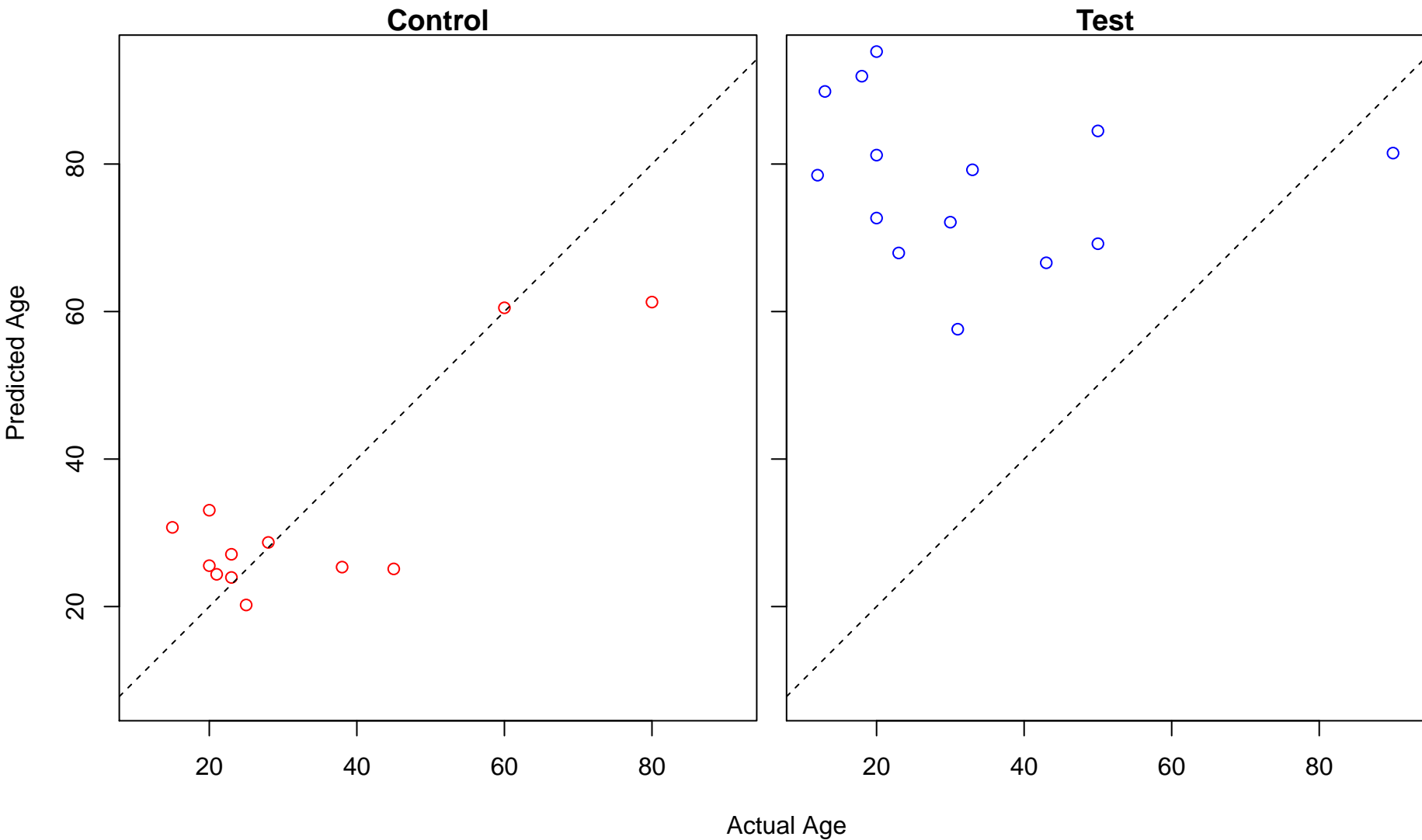


Actual Age

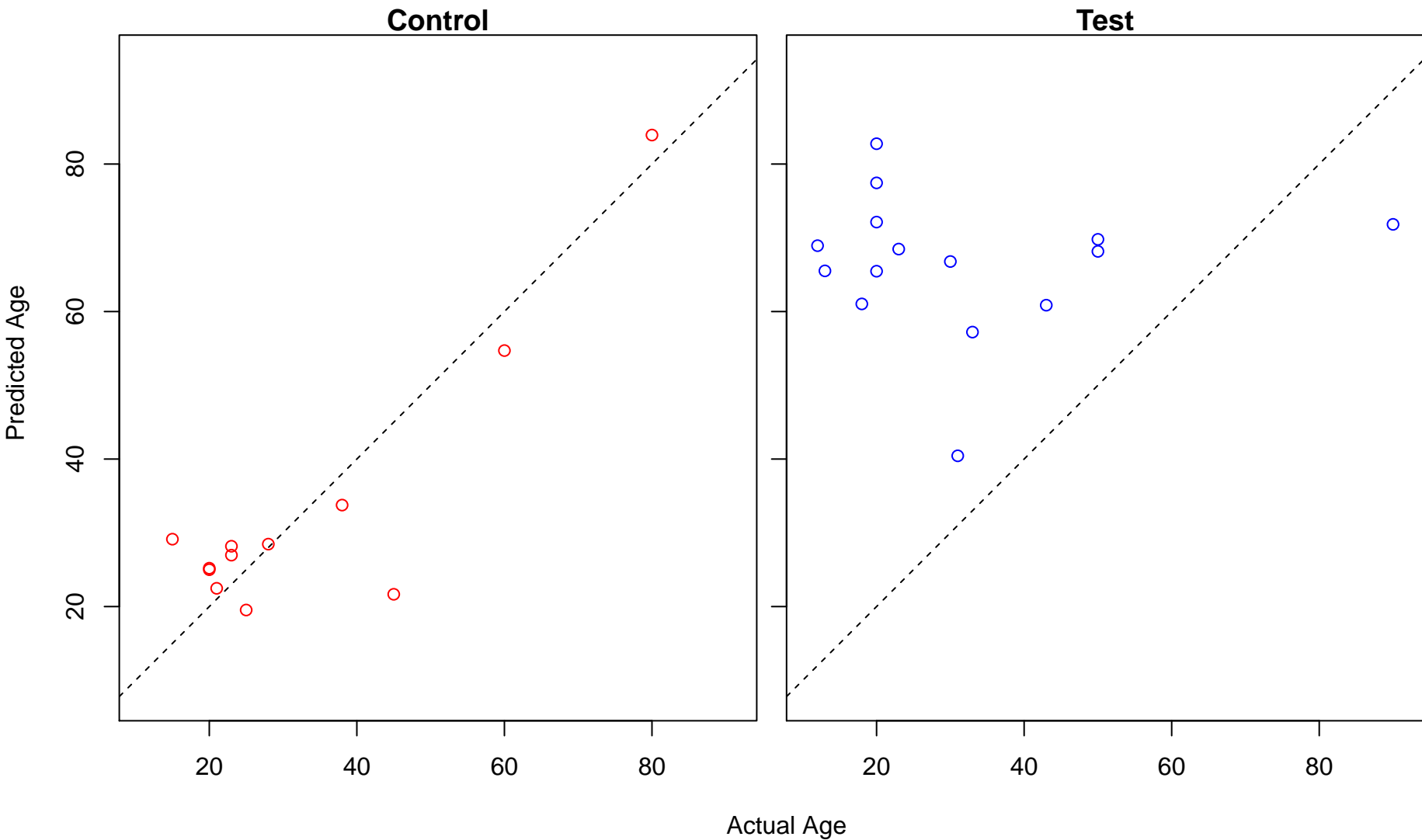
regulation of synapse structure or activity (Score: 7.543091)



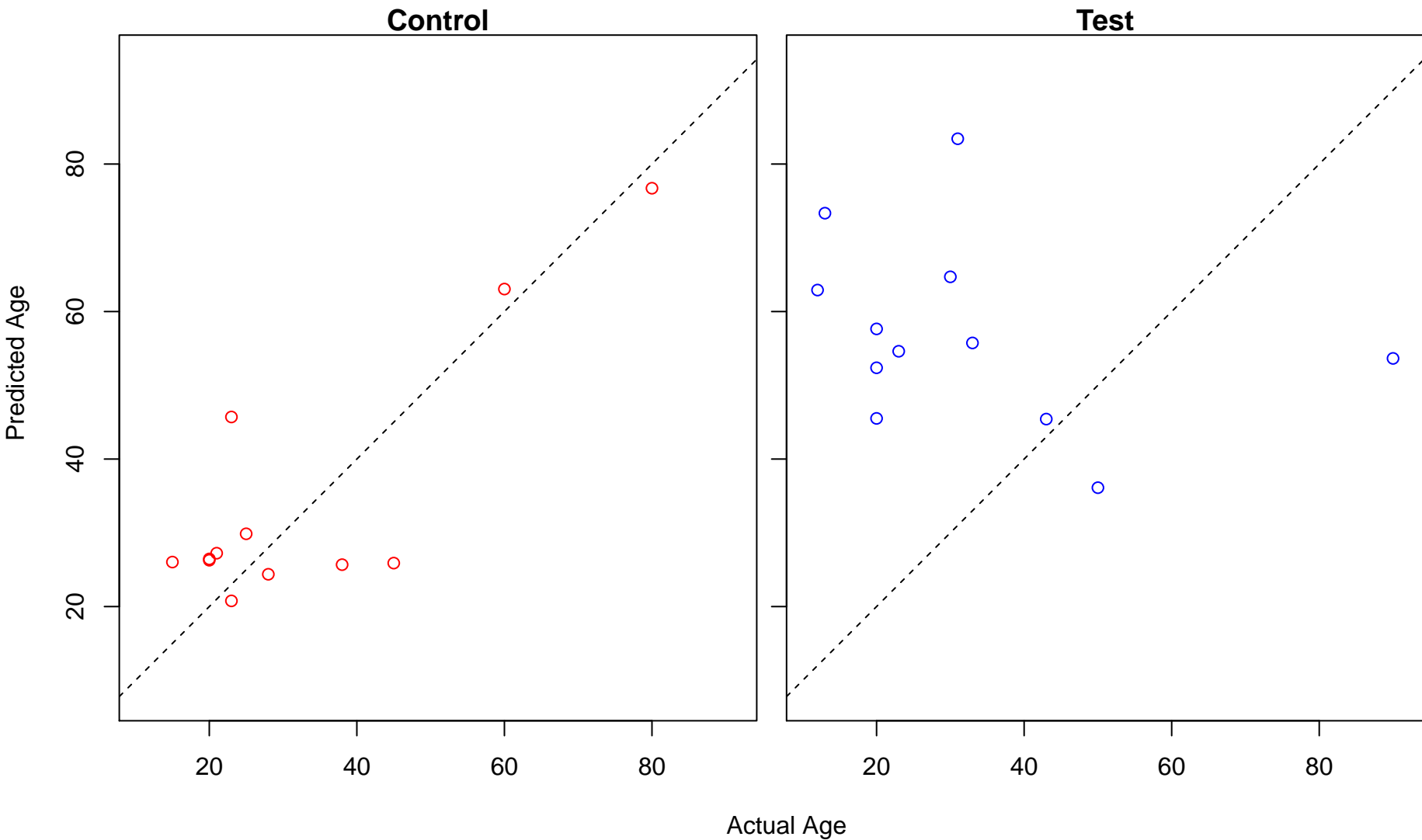
negative regulation of cytokine production involved in immune response (Score: 7.542651)



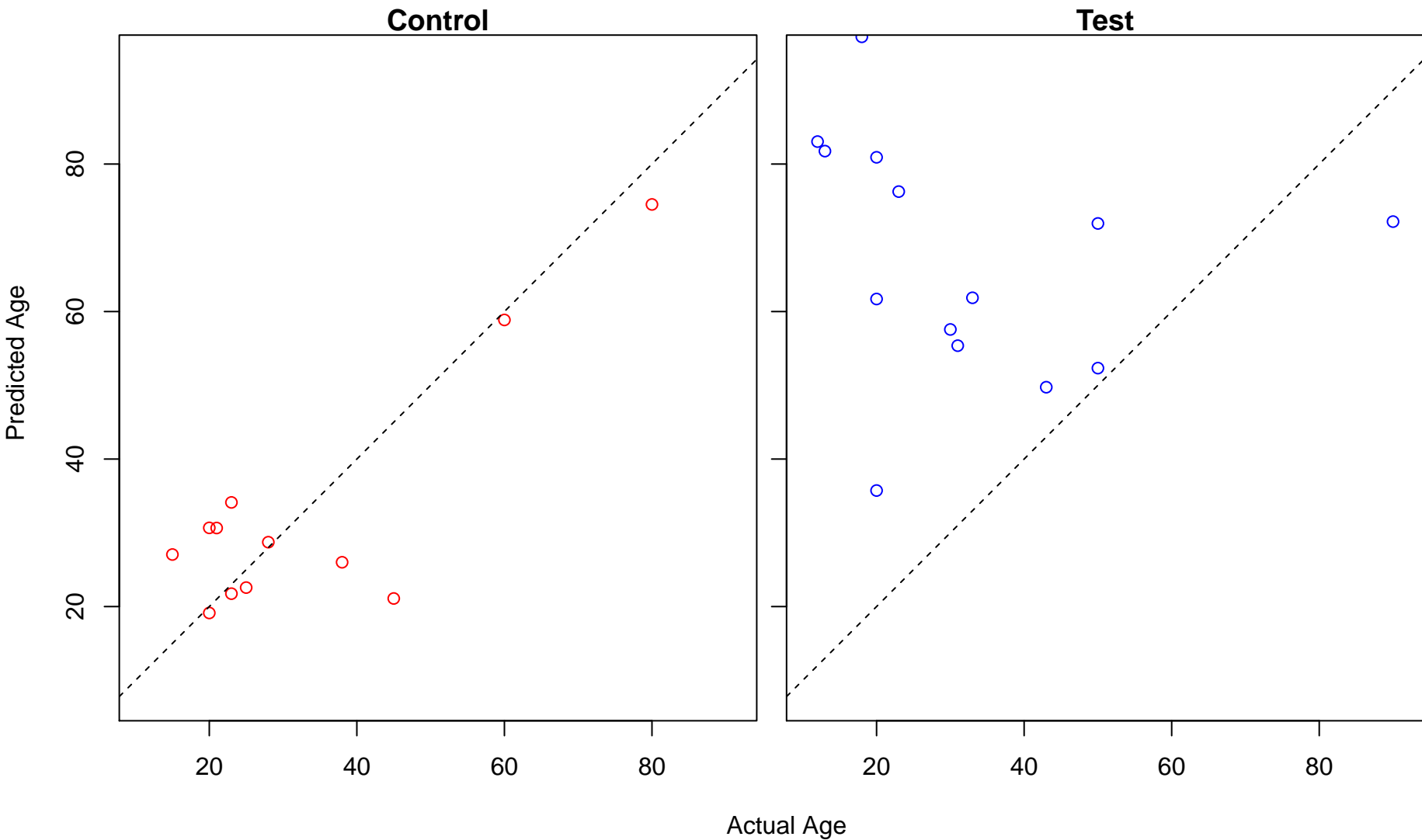
ureteric bud development (Score: 7.541661)



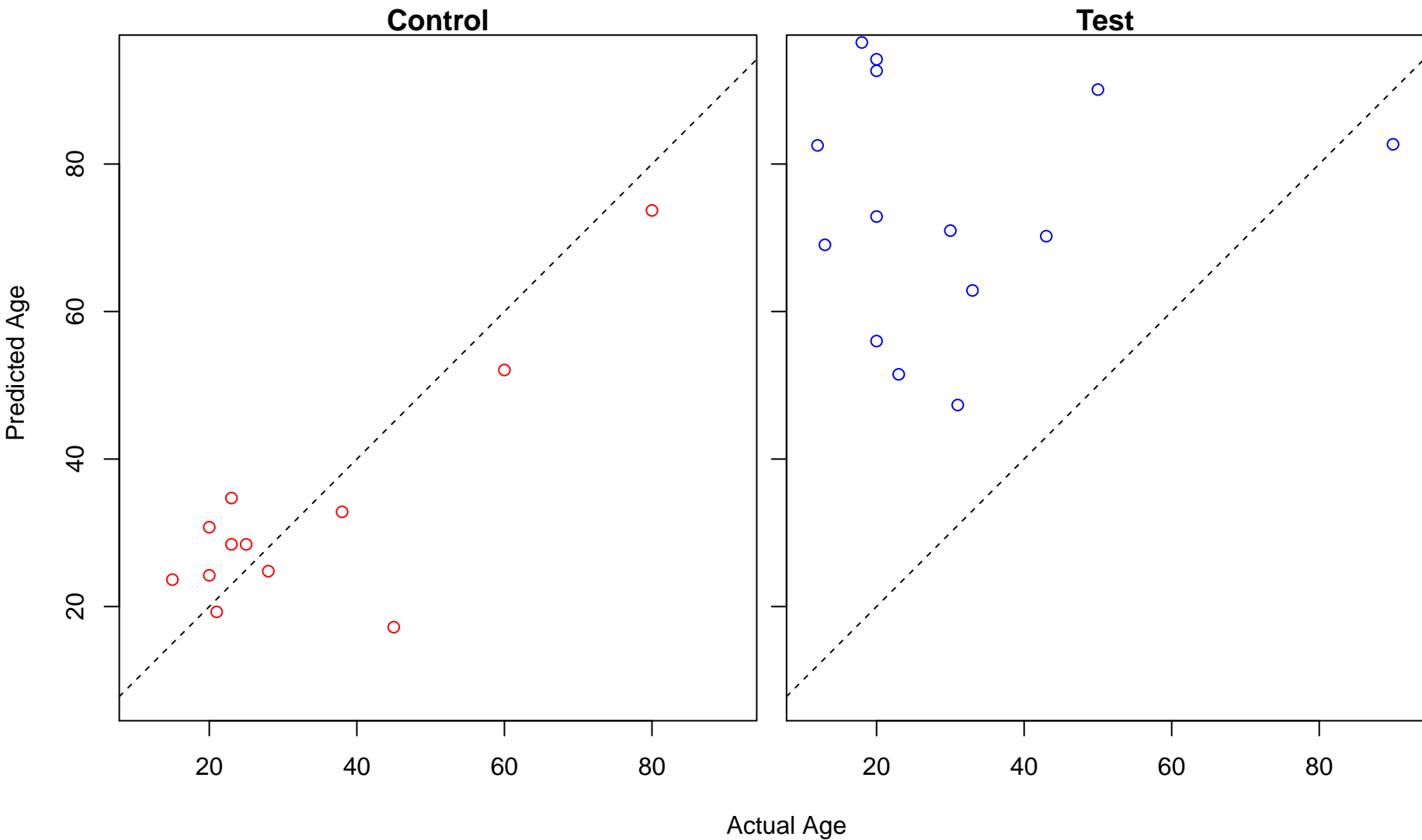
regulation of meiotic cell cycle (Score: 7.537503)



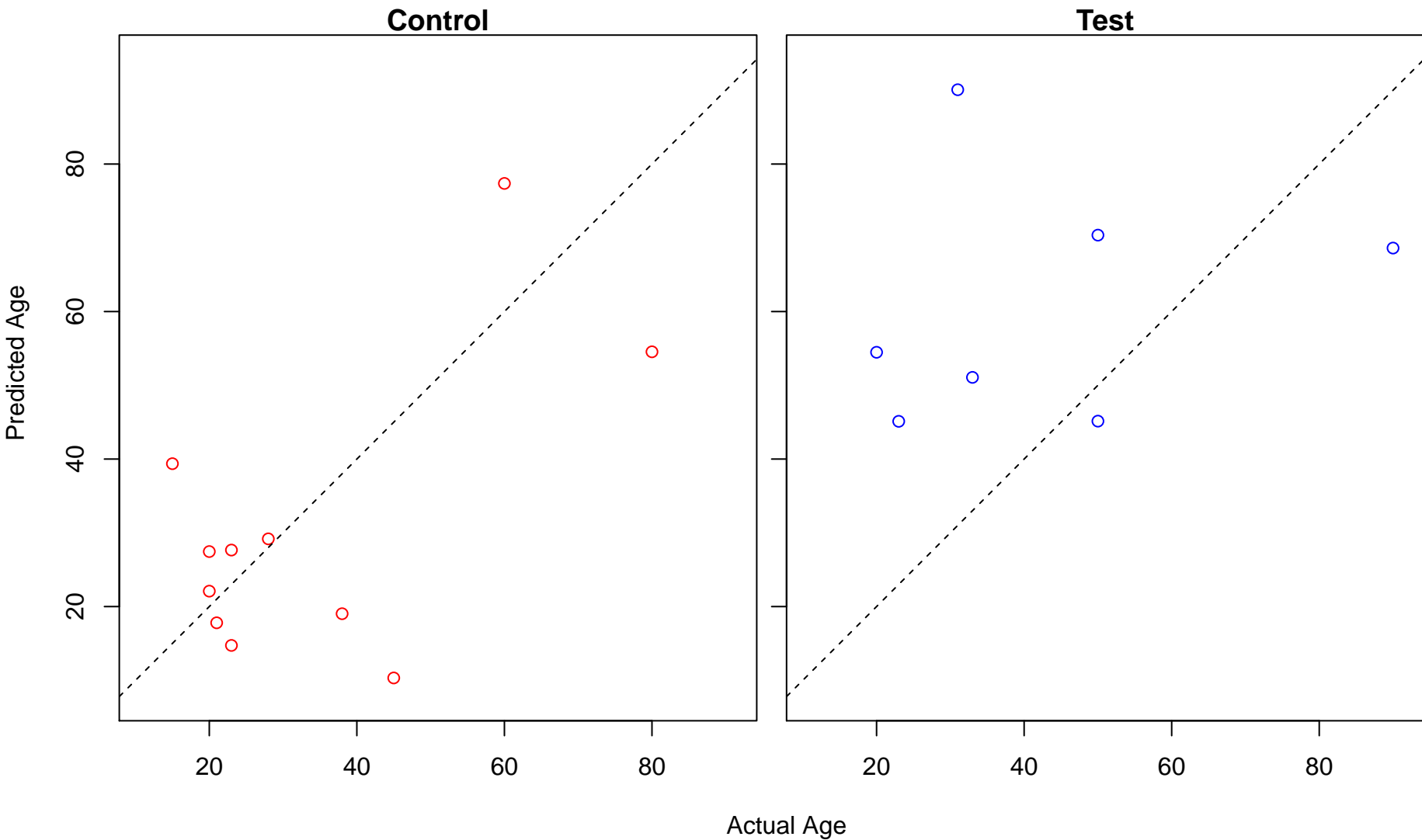
interaction with symbiont (Score: 7.537462)



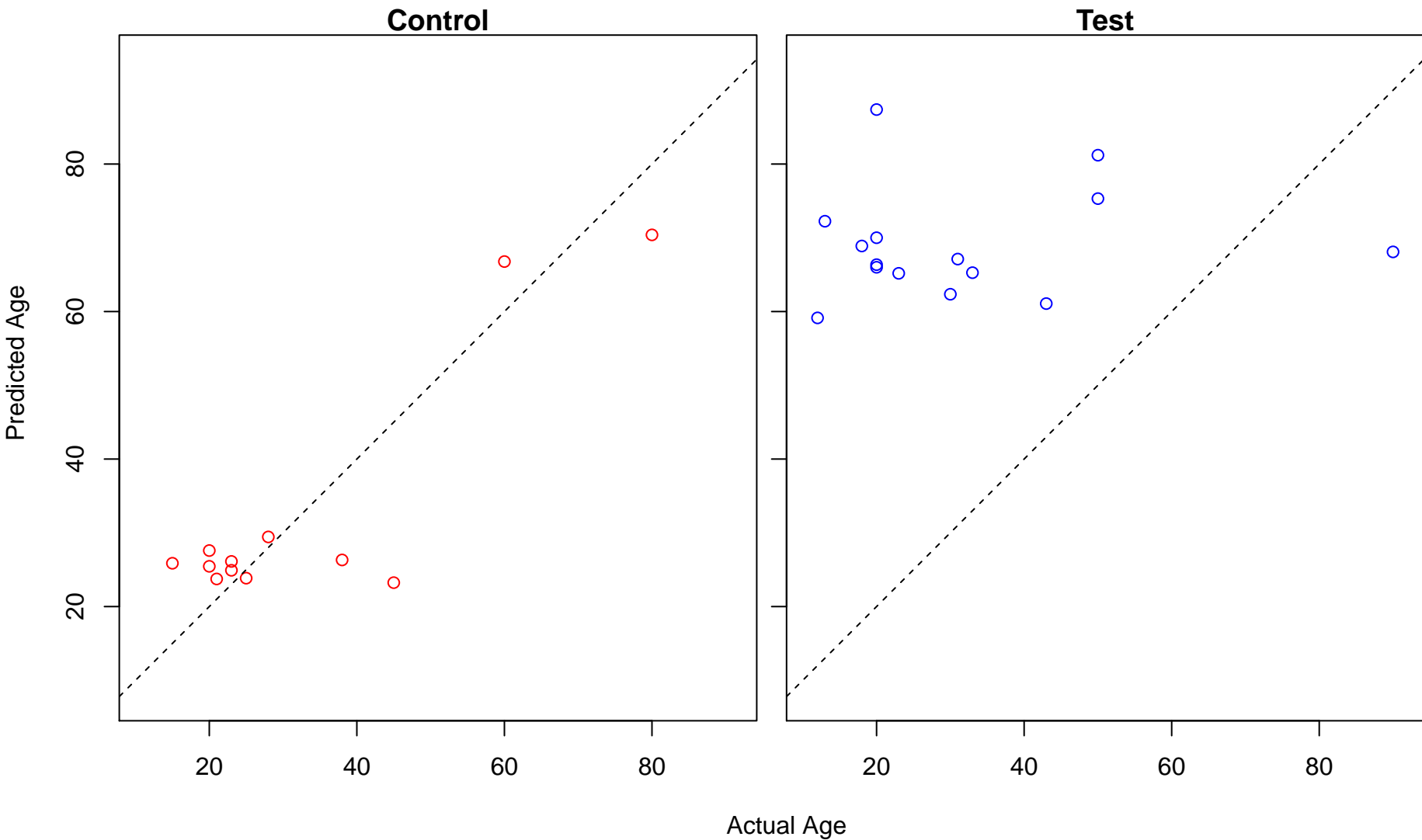
exocrine system development (Score: 7.535108)



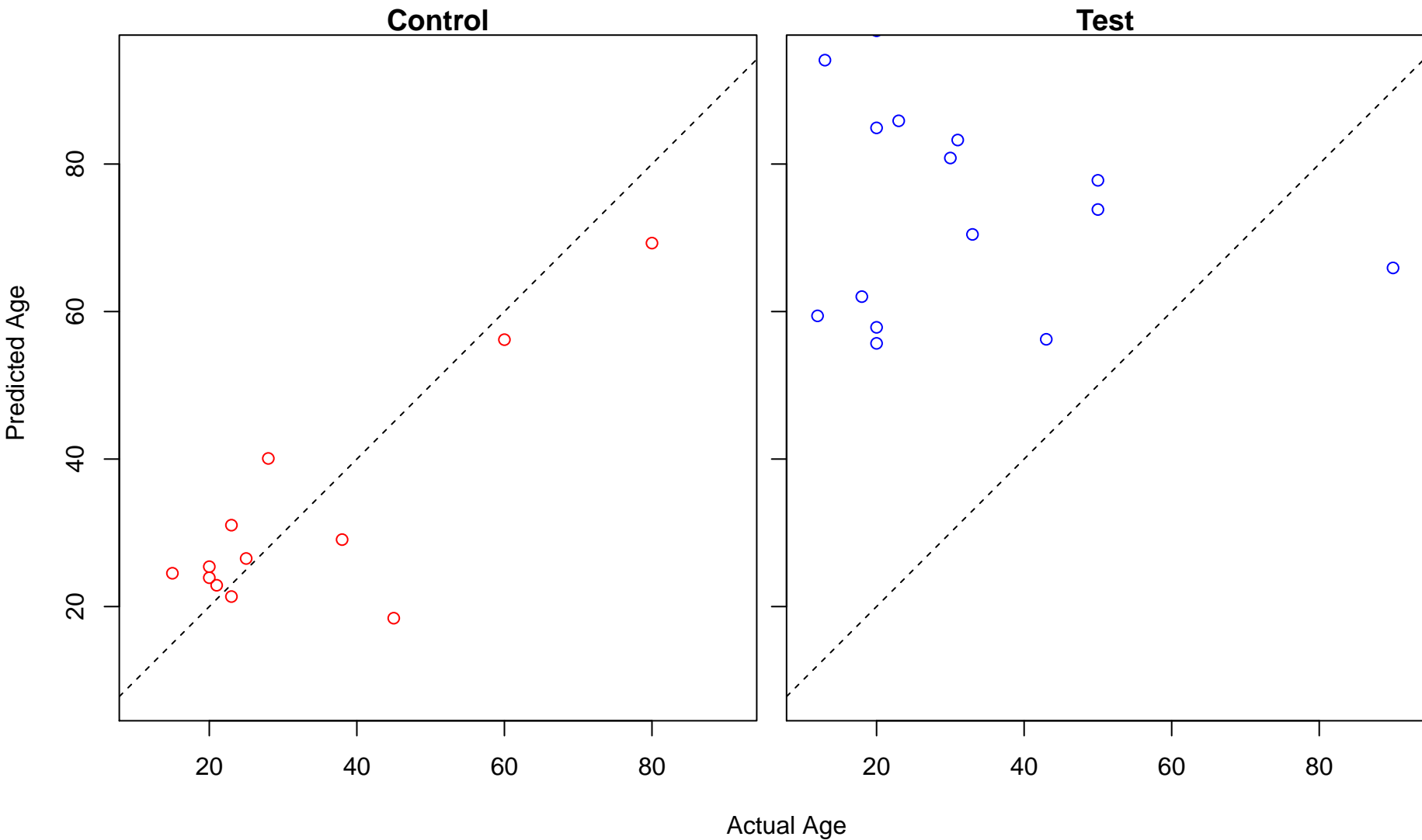
positive regulation of tumor necrosis factor biosynthetic process (Score: 7.526785)



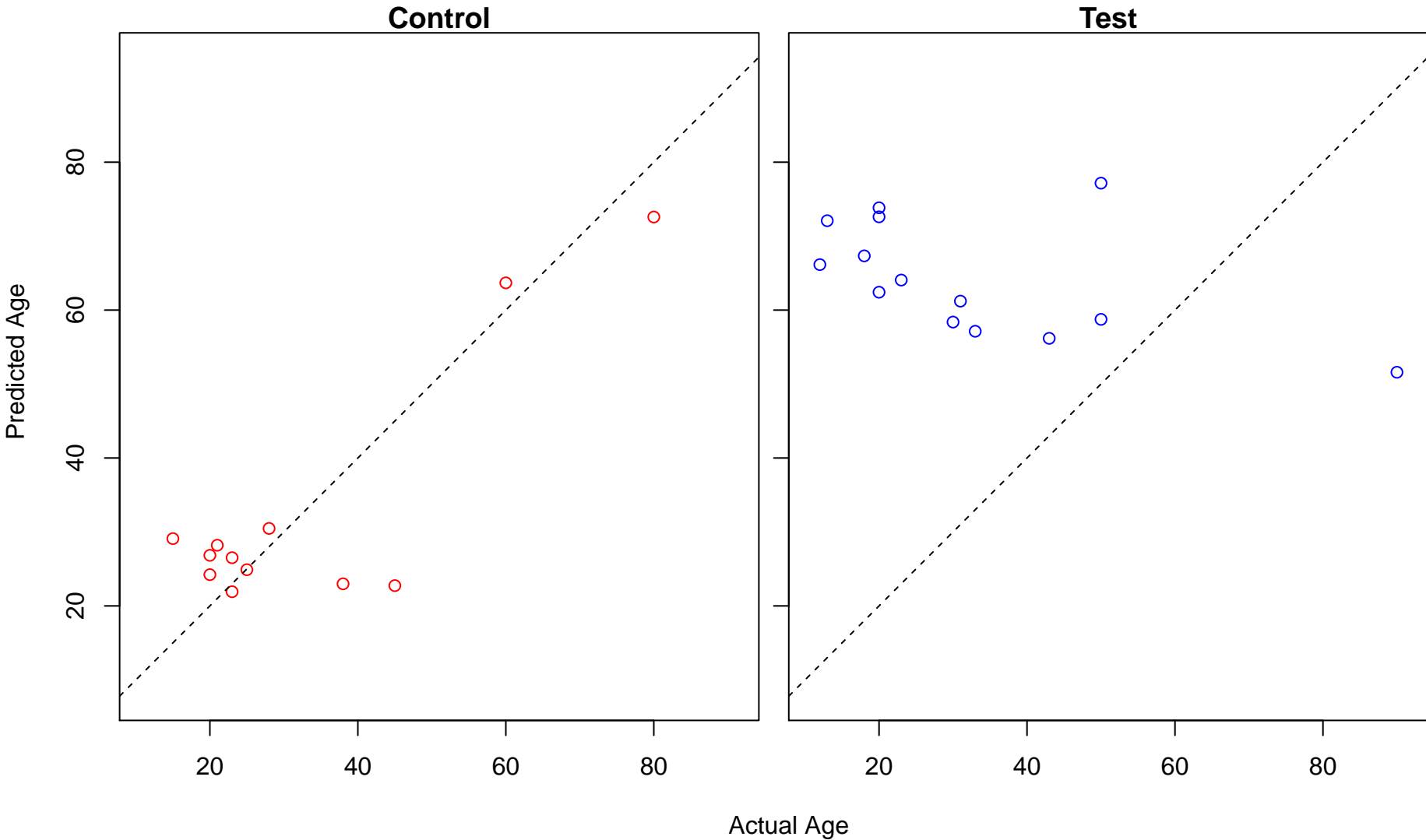
developmental growth (Score: 7.525679)



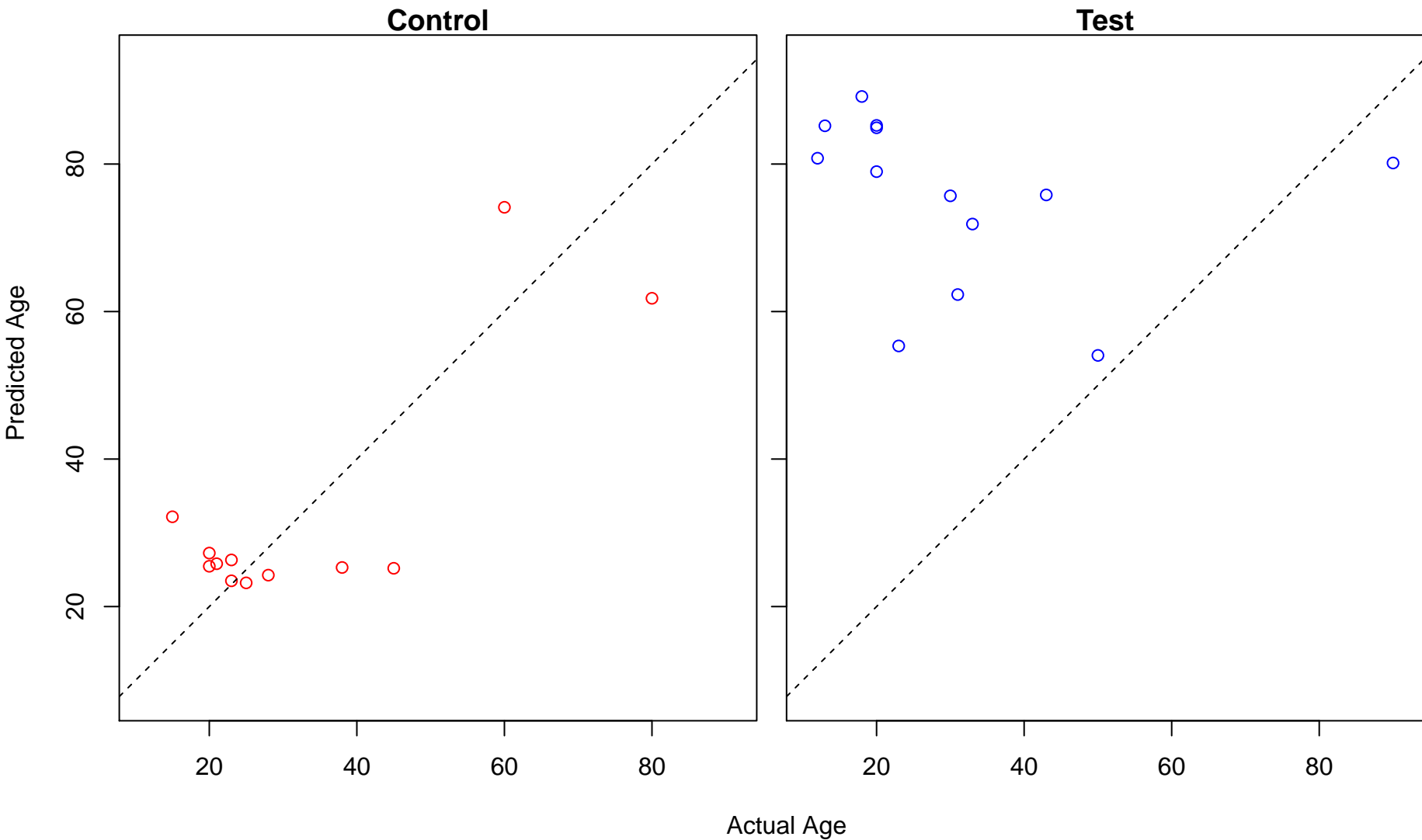
regulation of B cell proliferation (Score: 7.522379)



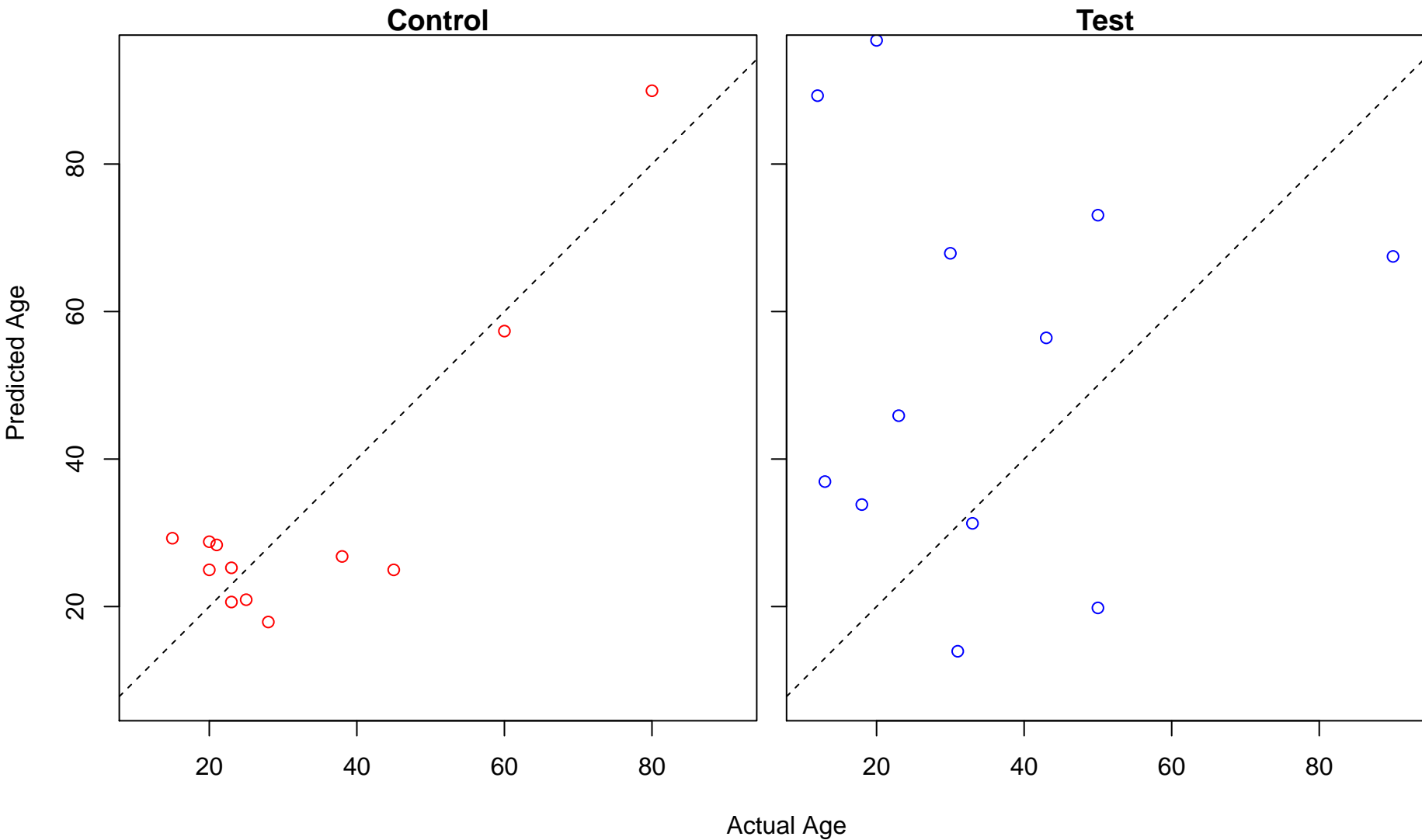
regulation of cholesterol biosynthetic process (Score: 7.520643)



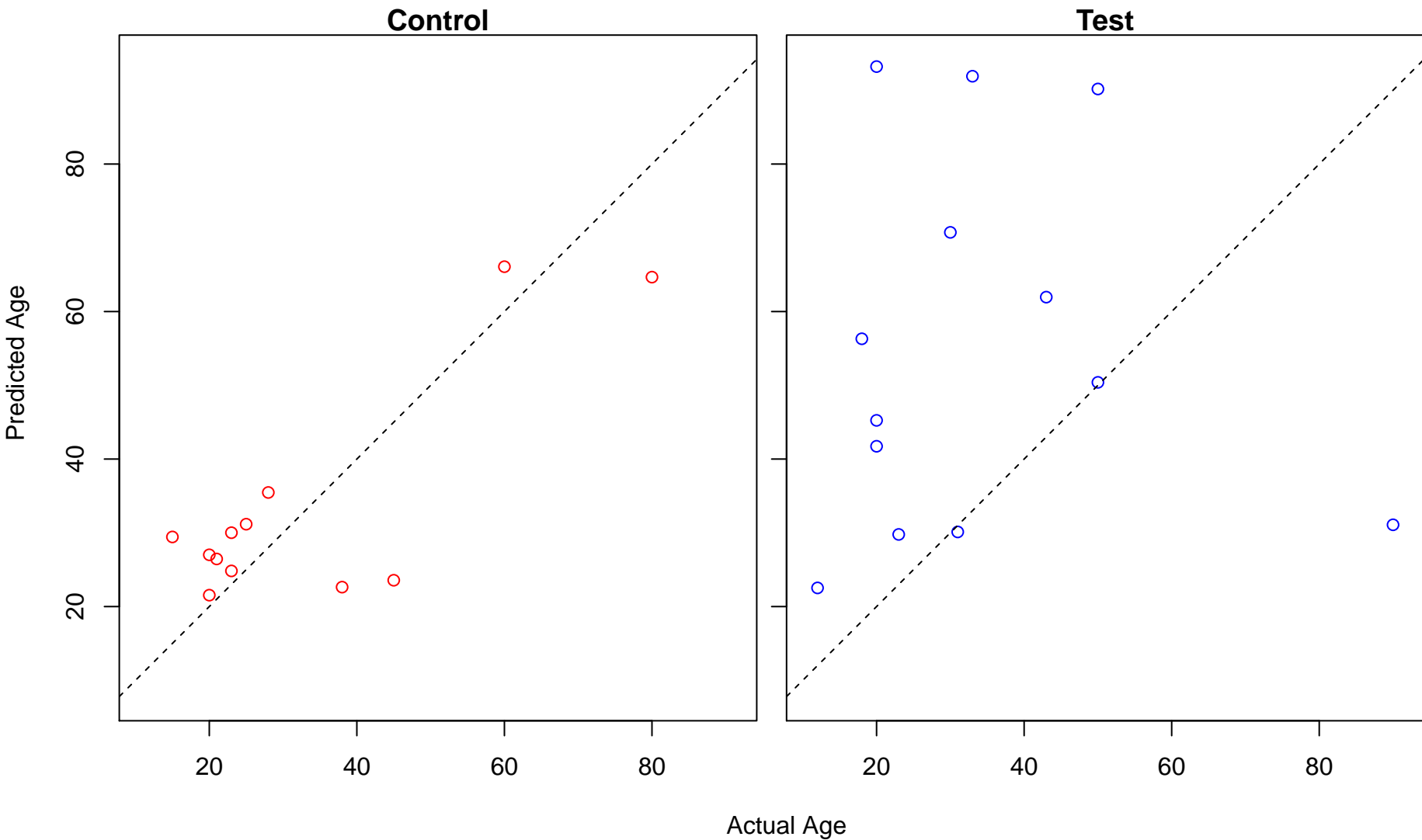
fatty acid homeostasis (Score: 7.513777)



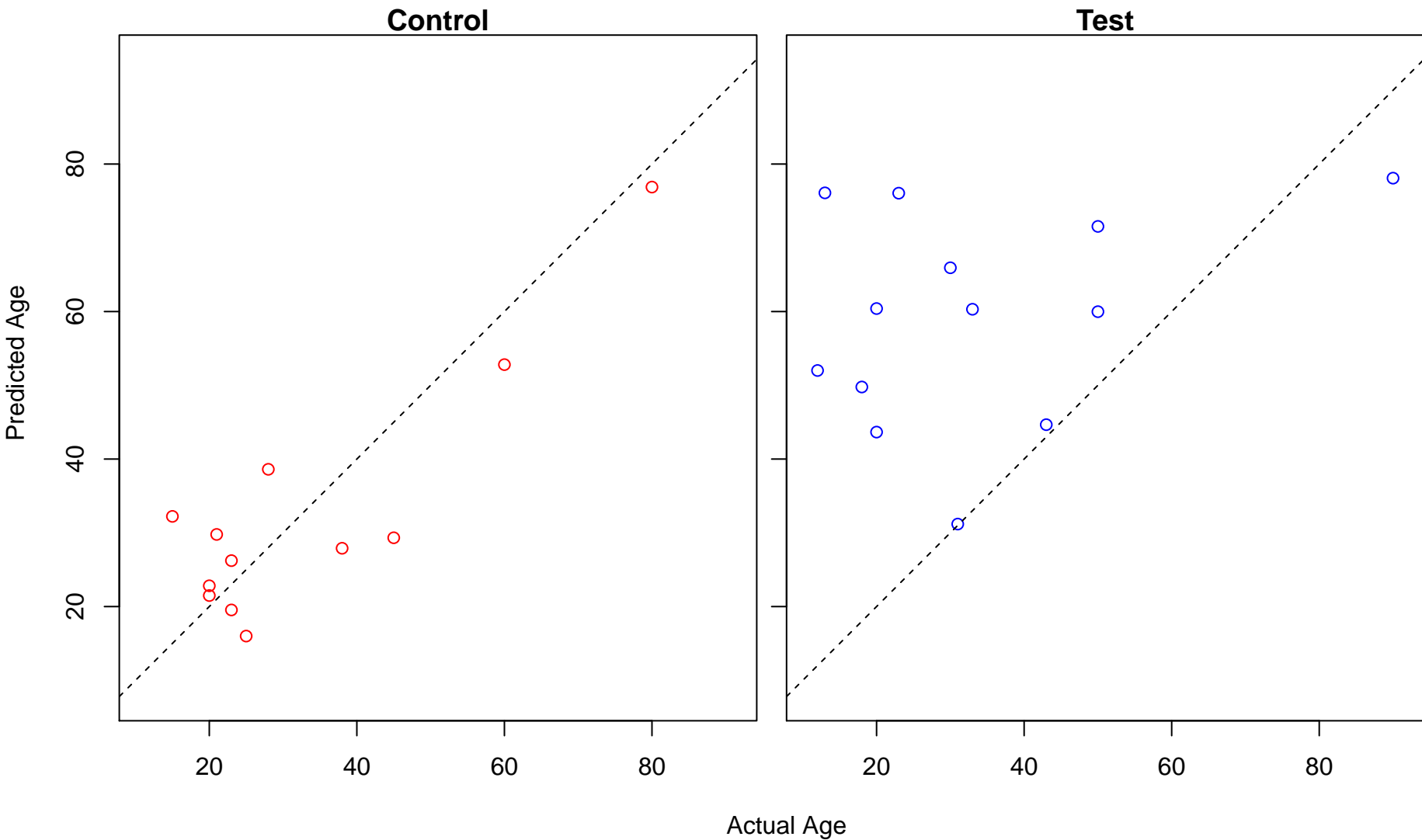
negative regulation of cytoskeleton organization (Score: 7.513526)



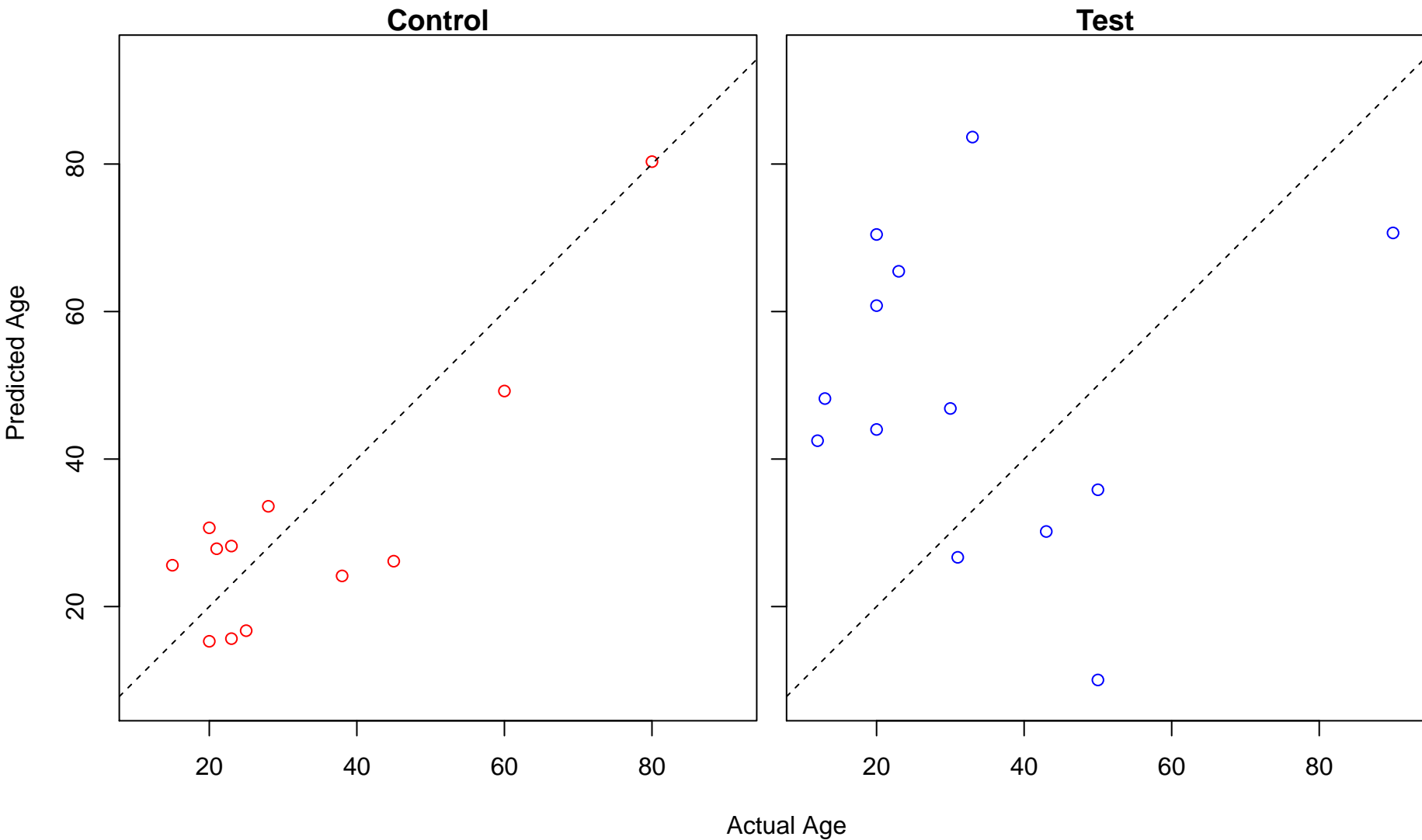
meiotic chromosome segregation (Score: 7.505474)



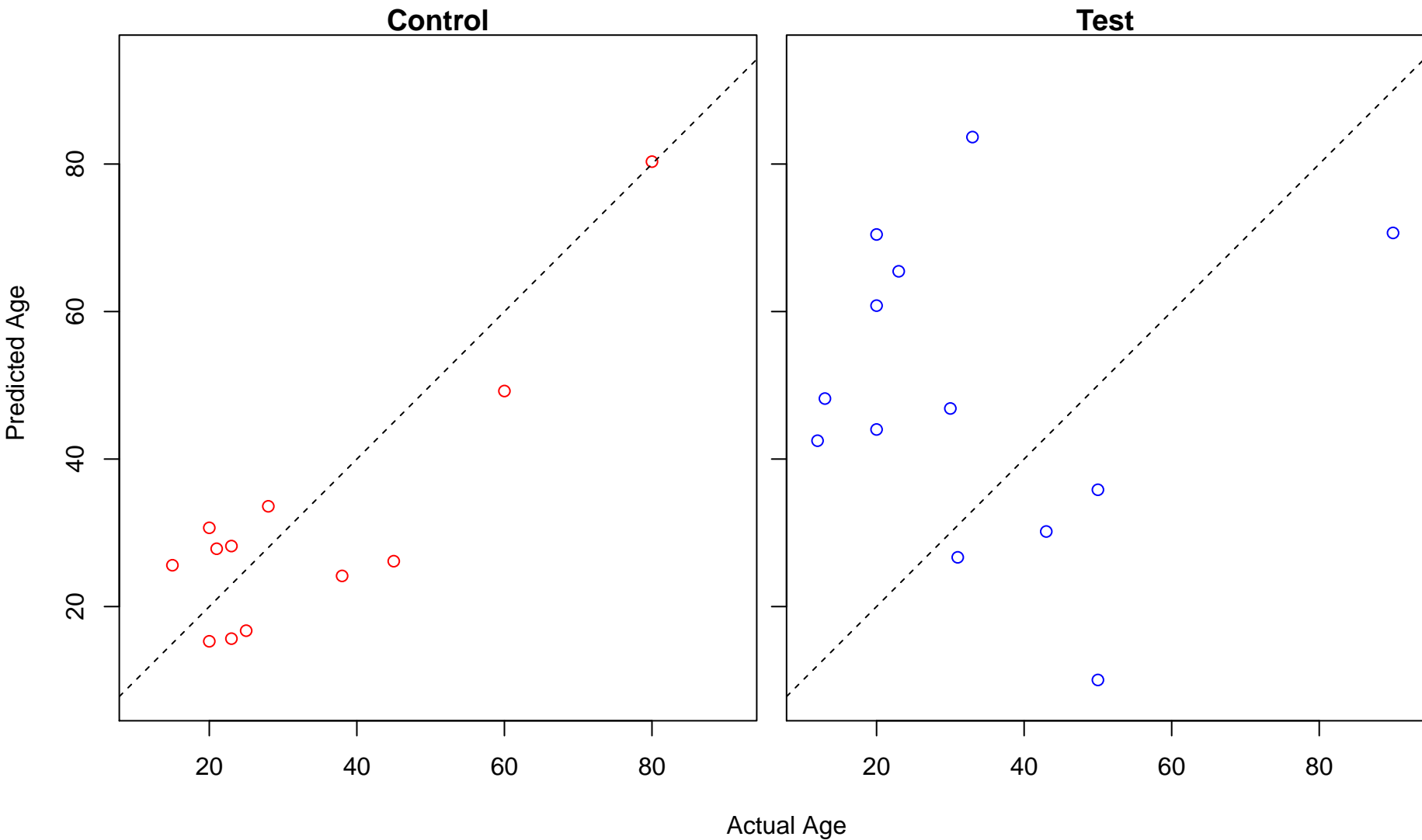
response to zinc ion (Score: 7.504803)



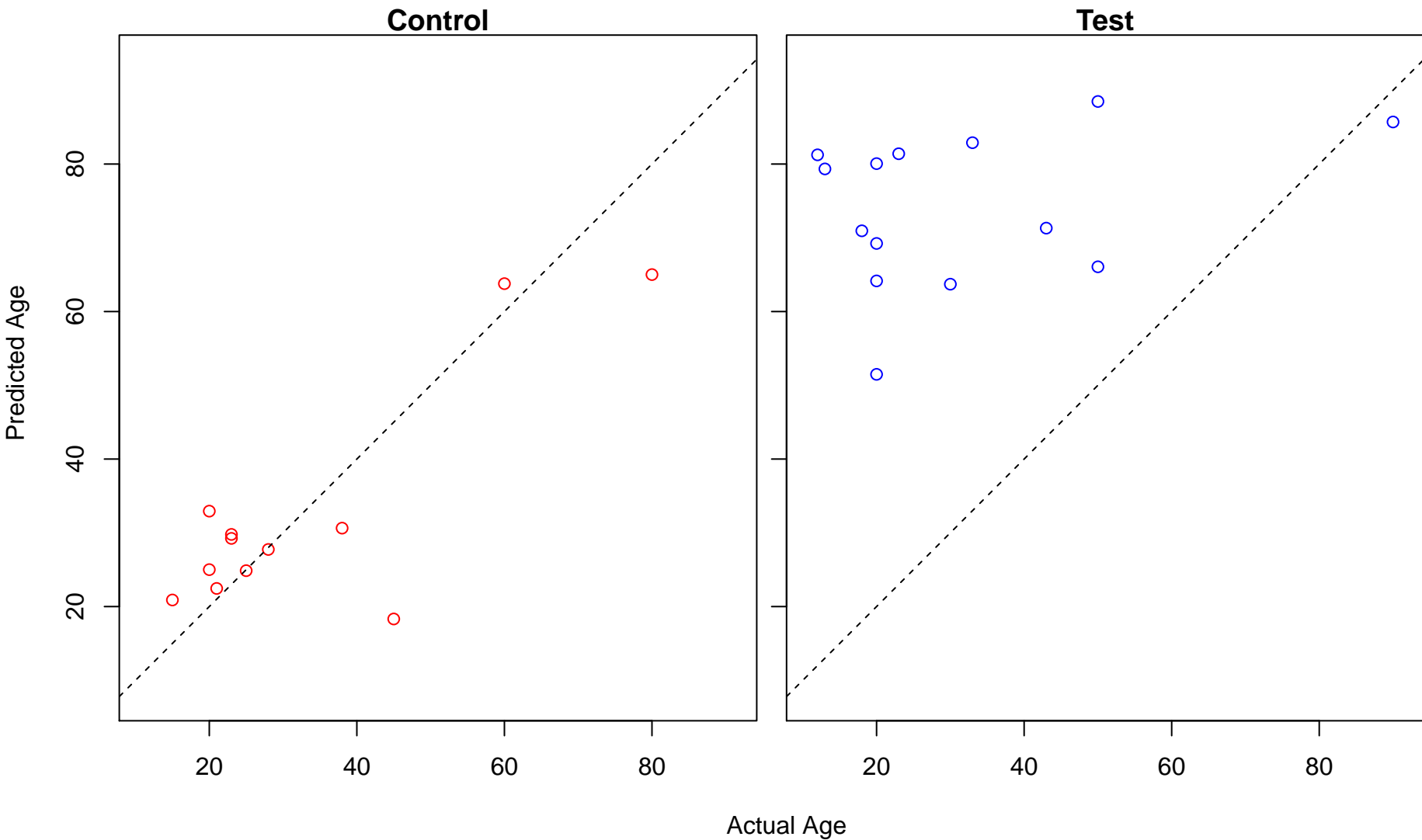
nucleic acid transport (Score: 7.503787)



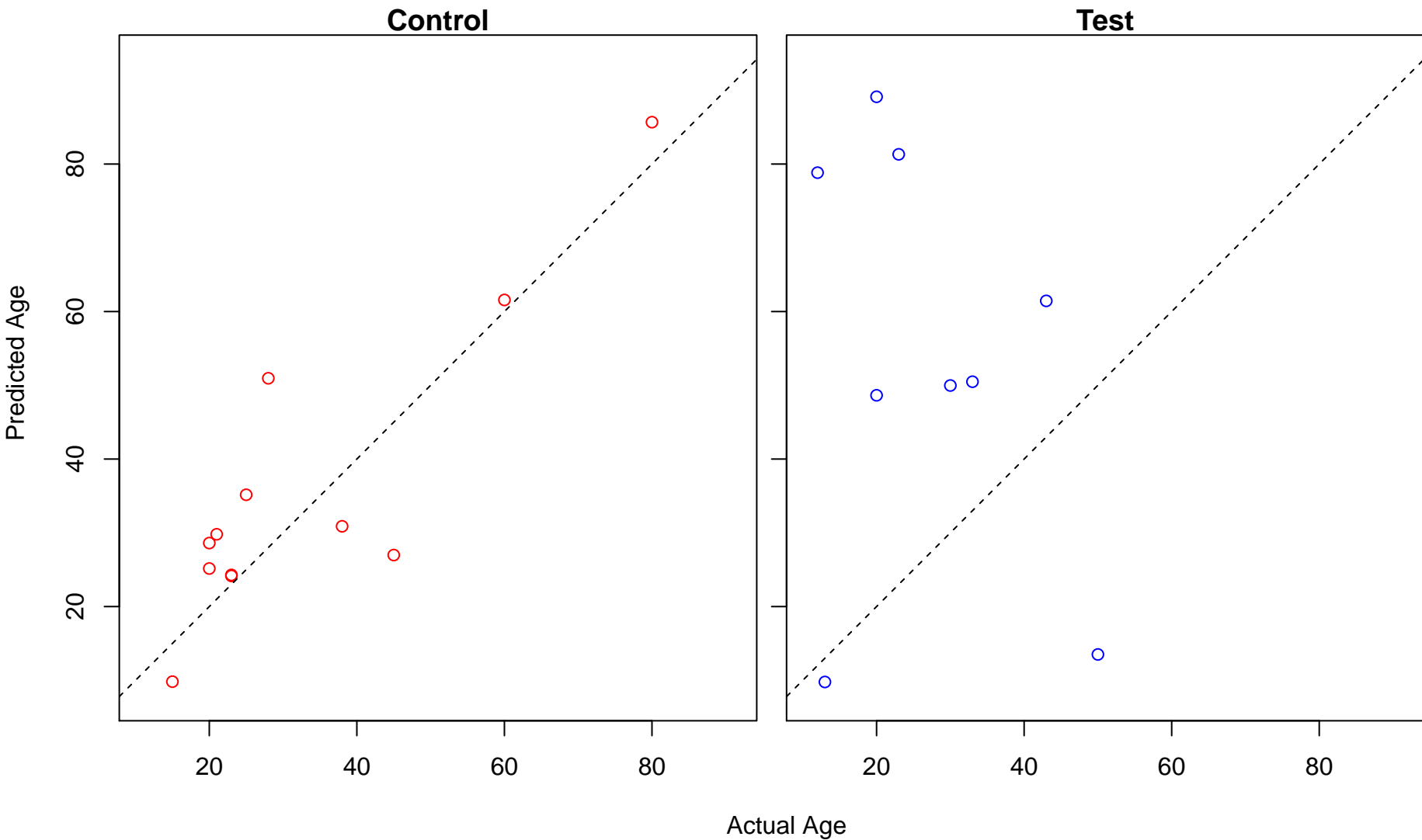
RNA transport (Score: 7.503787)



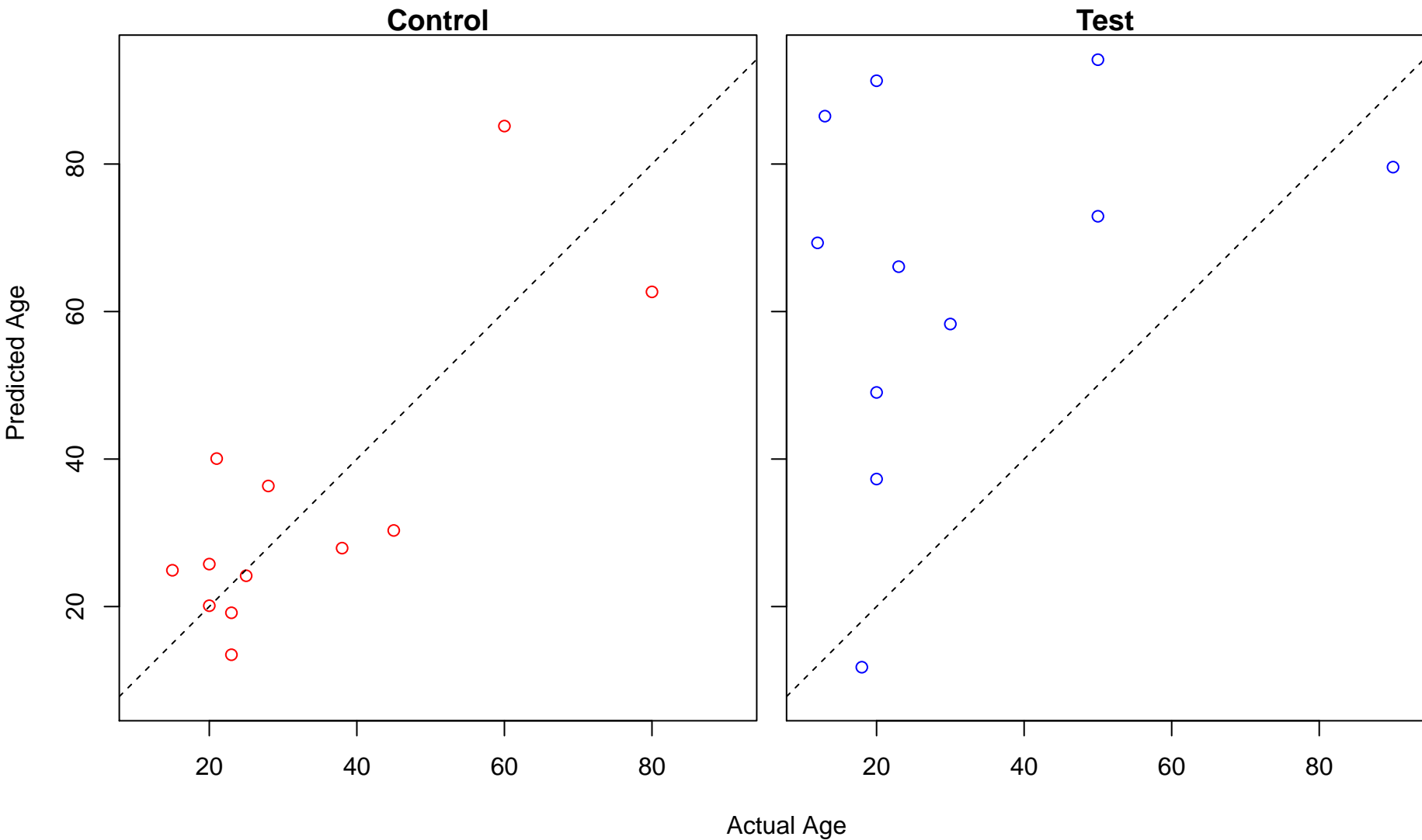
negative regulation of striated muscle contraction (Score: 7.503278)



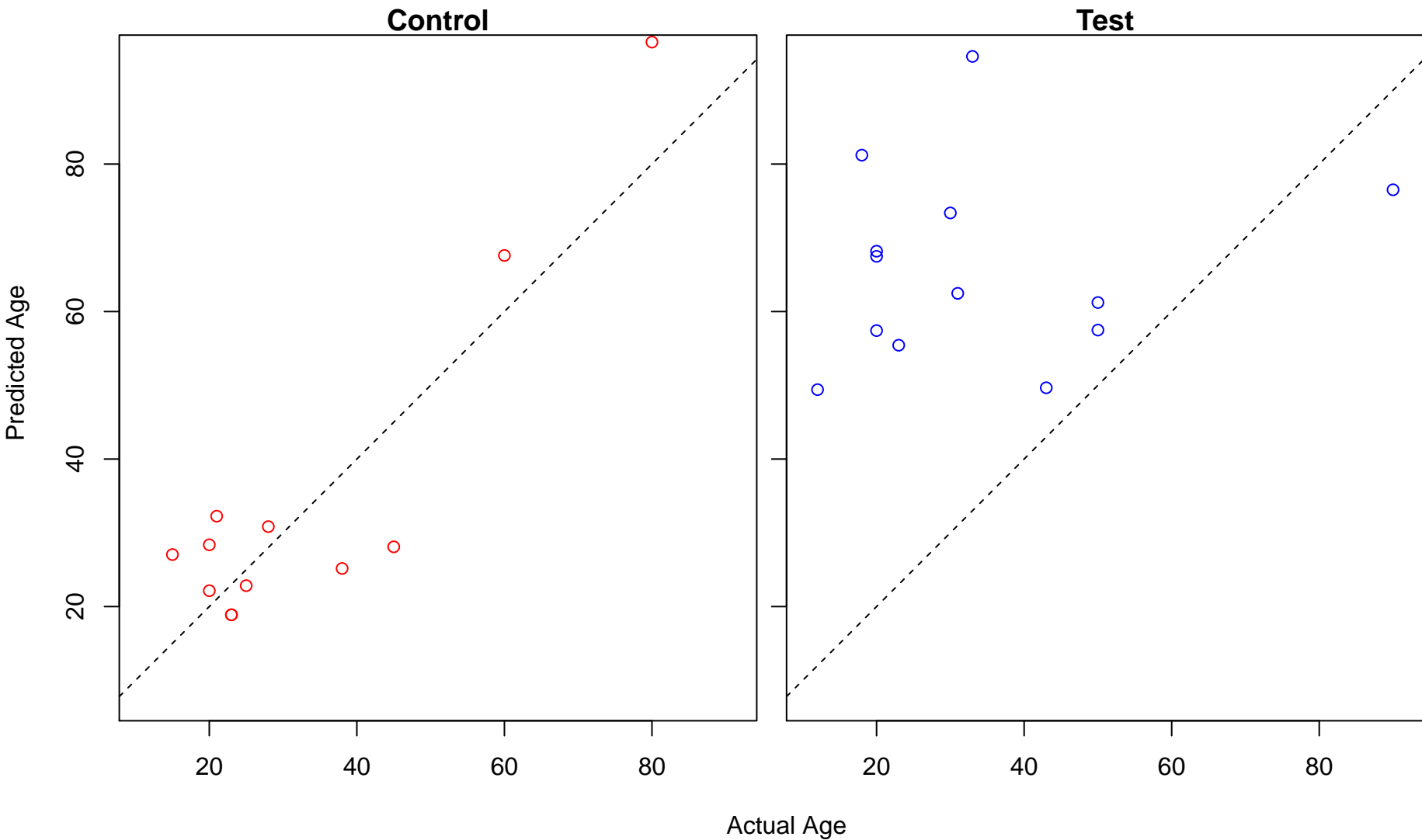
positive regulation of phosphatidylinositol 3-kinase signaling (Score: 7.497402)



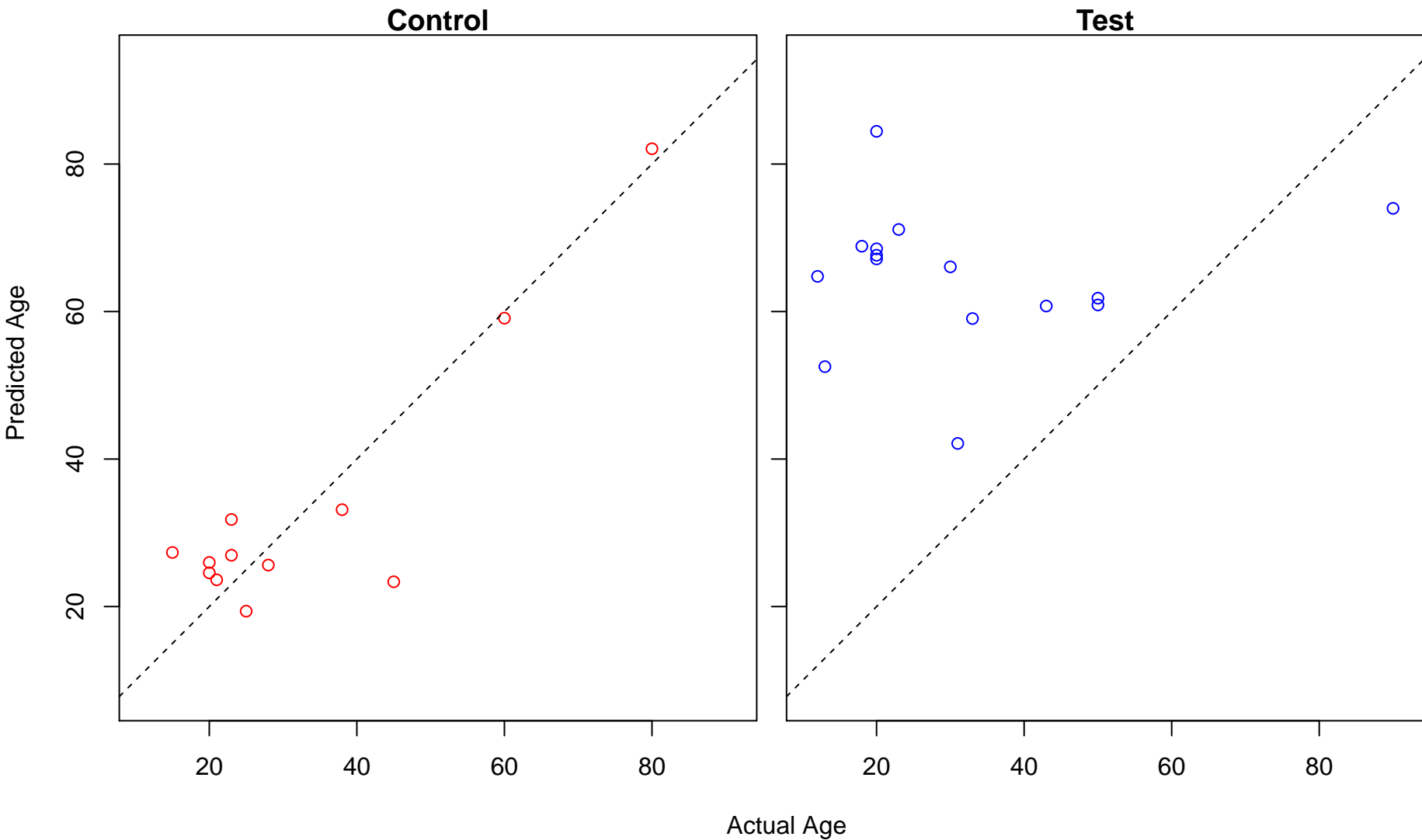
negative regulation of phagocytosis (Score: 7.493589)



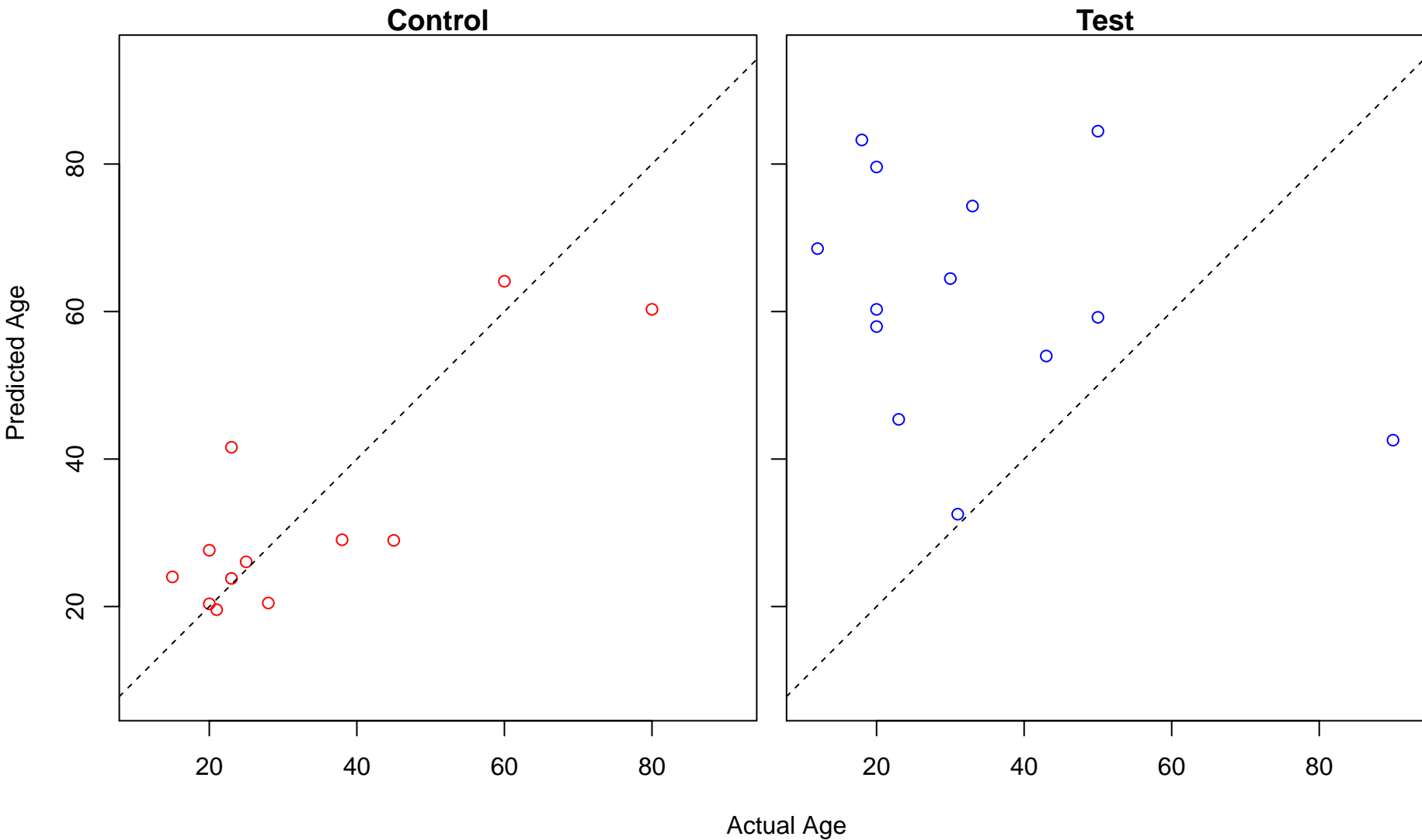
negative regulation of keratinocyte proliferation (Score: 7.492413)



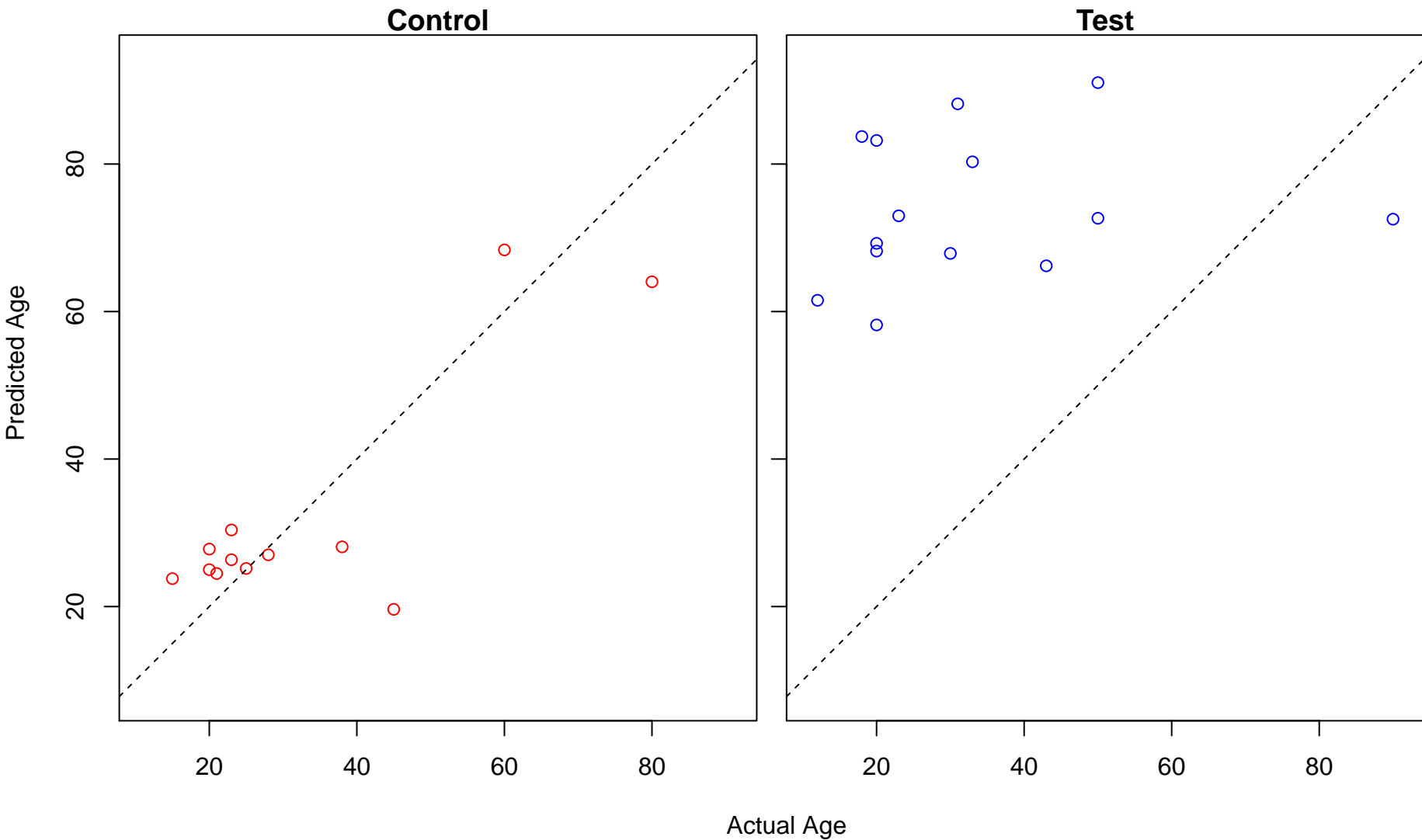
negative regulation of leukocyte migration (Score: 7.489811)



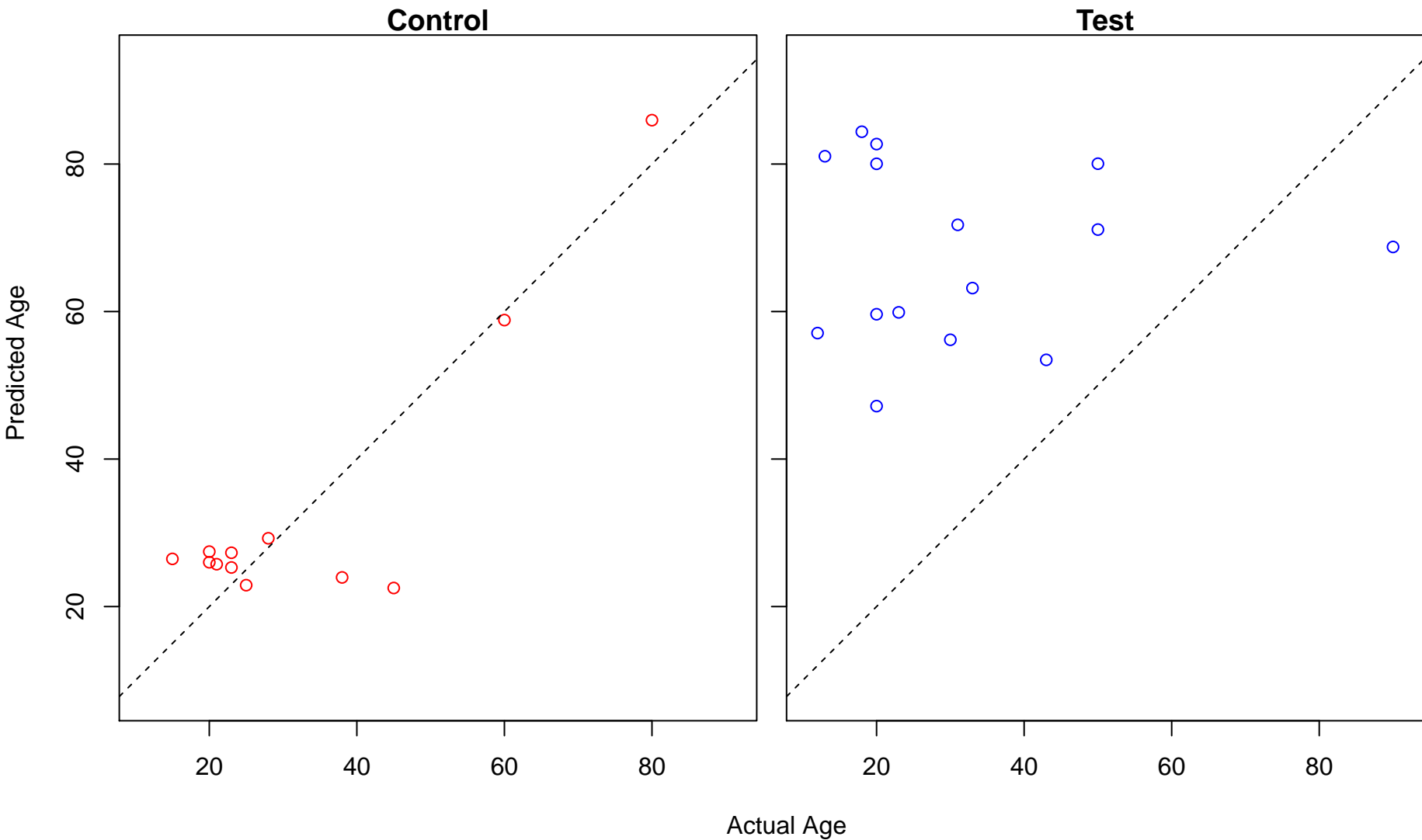
regulation of phosphatidylinositol biosynthetic process (Score: 7.487975)



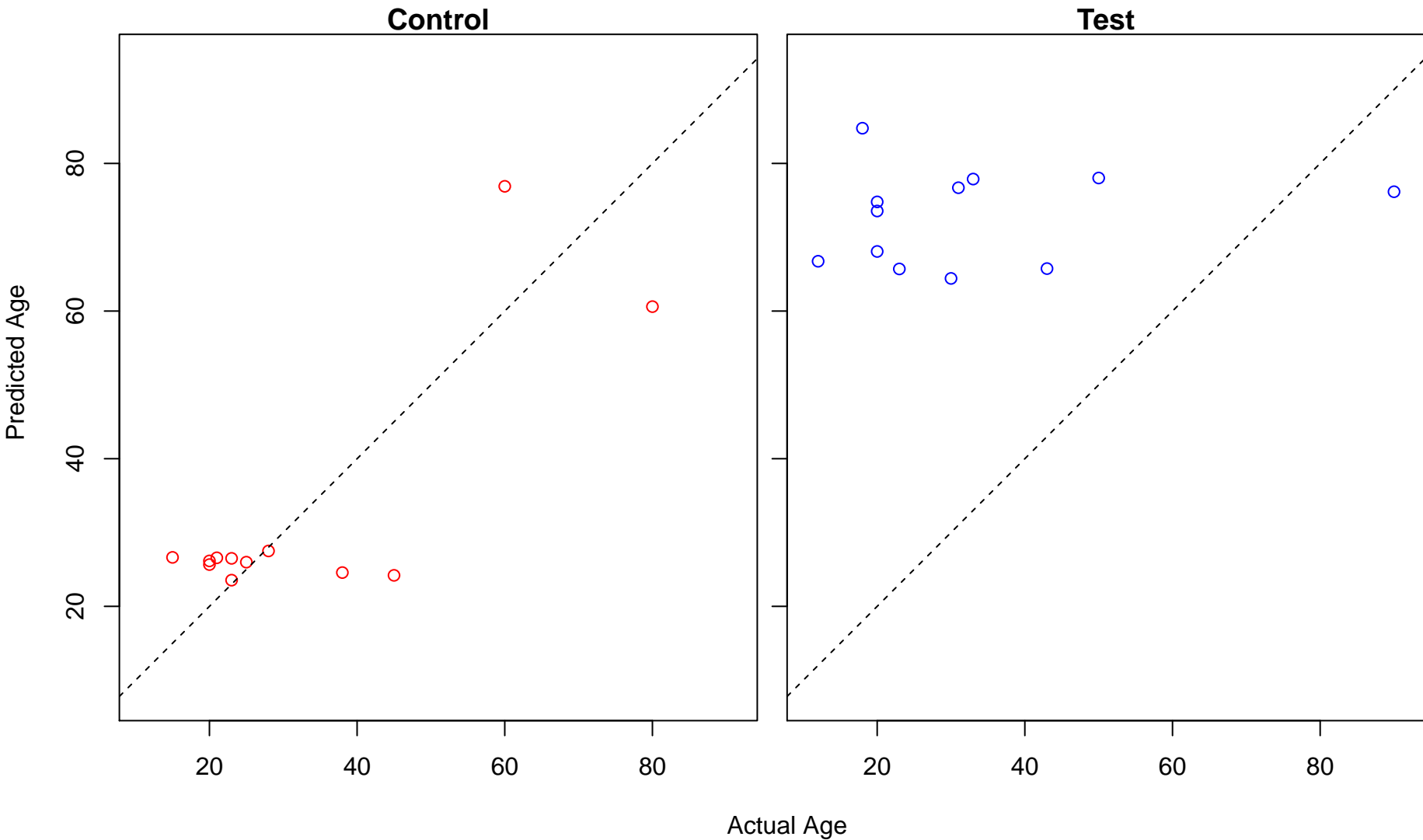
positive regulation of T cell mediated immunity (Score: 7.487519)



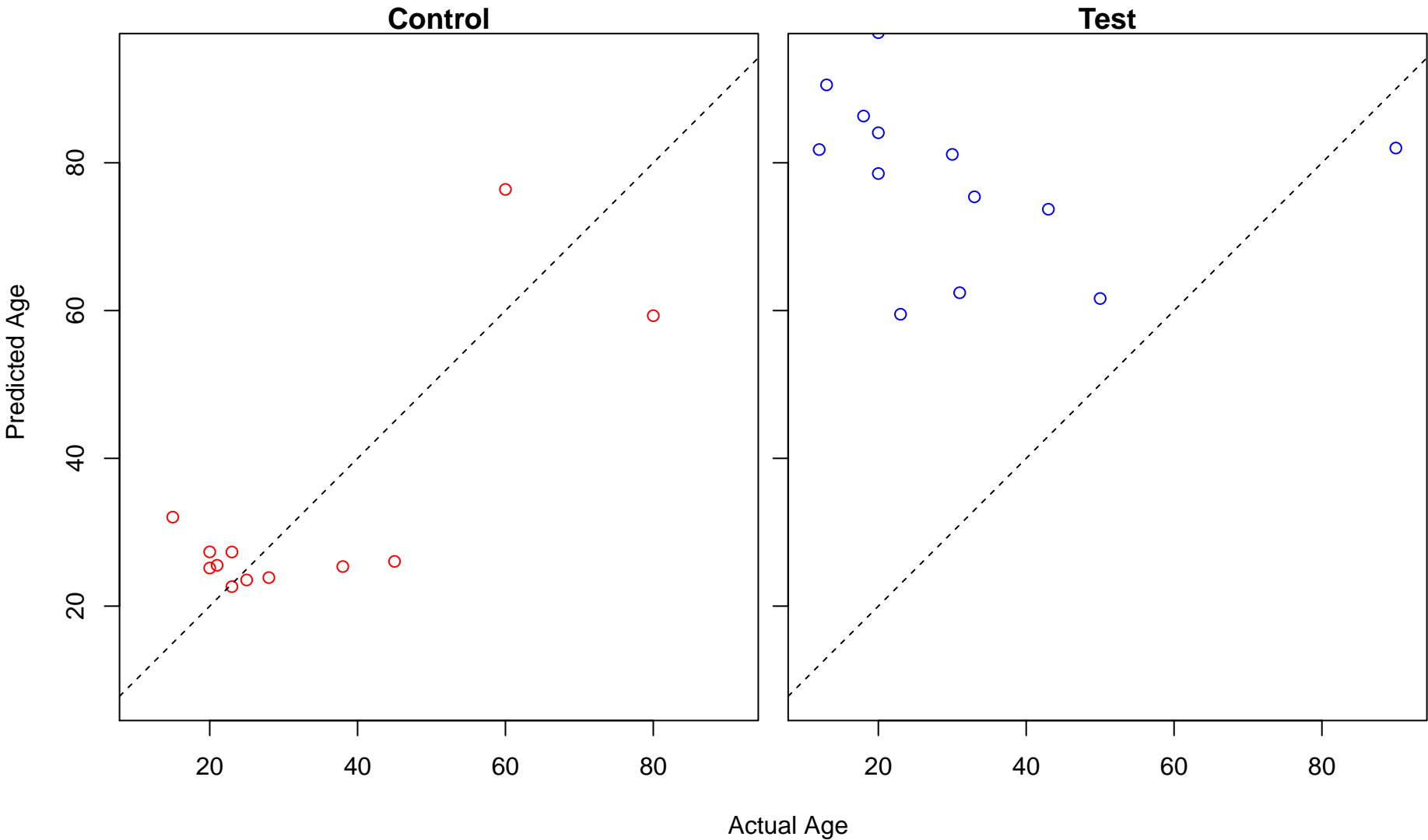
positive regulation of cytoplasmic transport (Score: 7.487155)



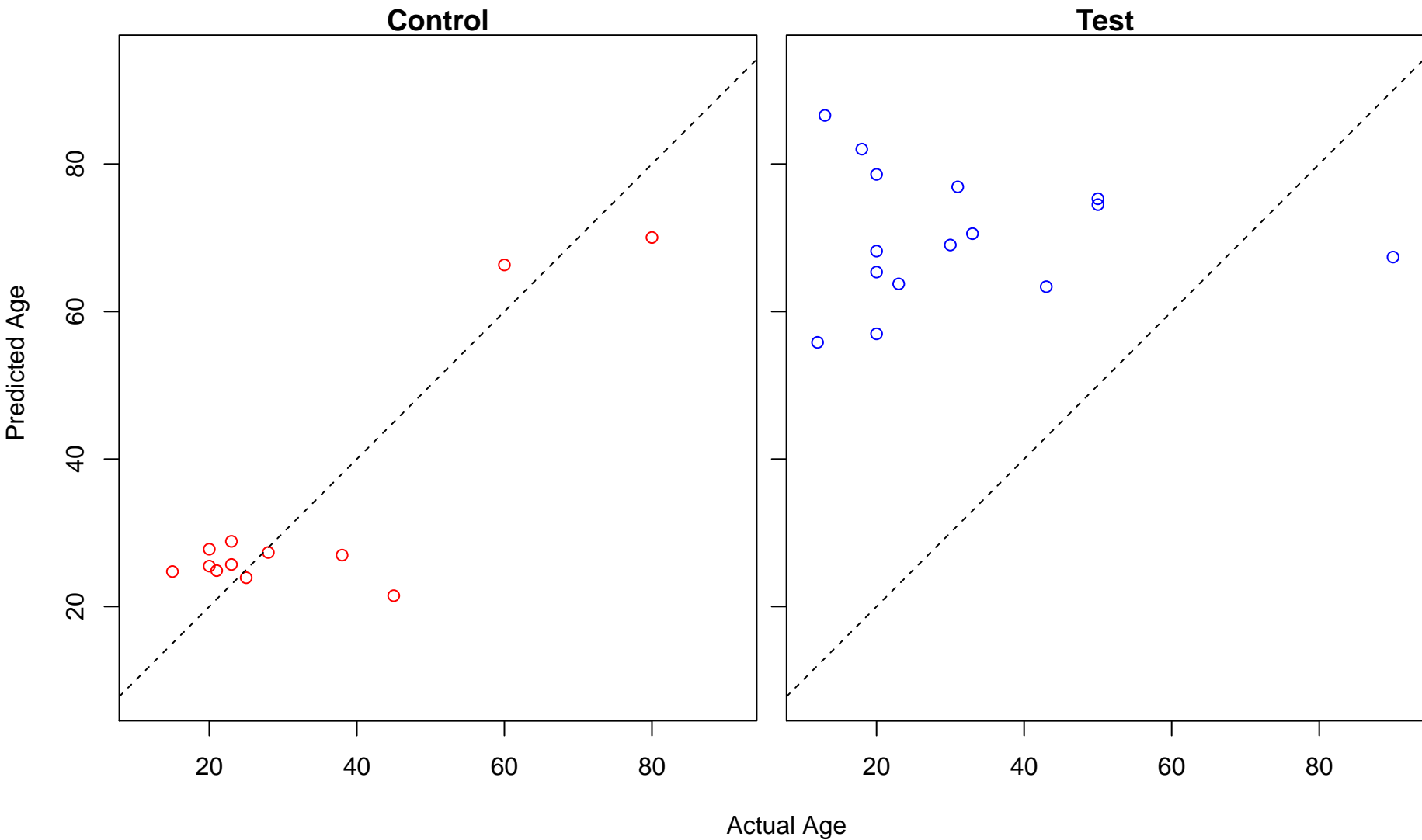
negative regulation of intrinsic apoptotic signaling pathway (Score: 7.484698)



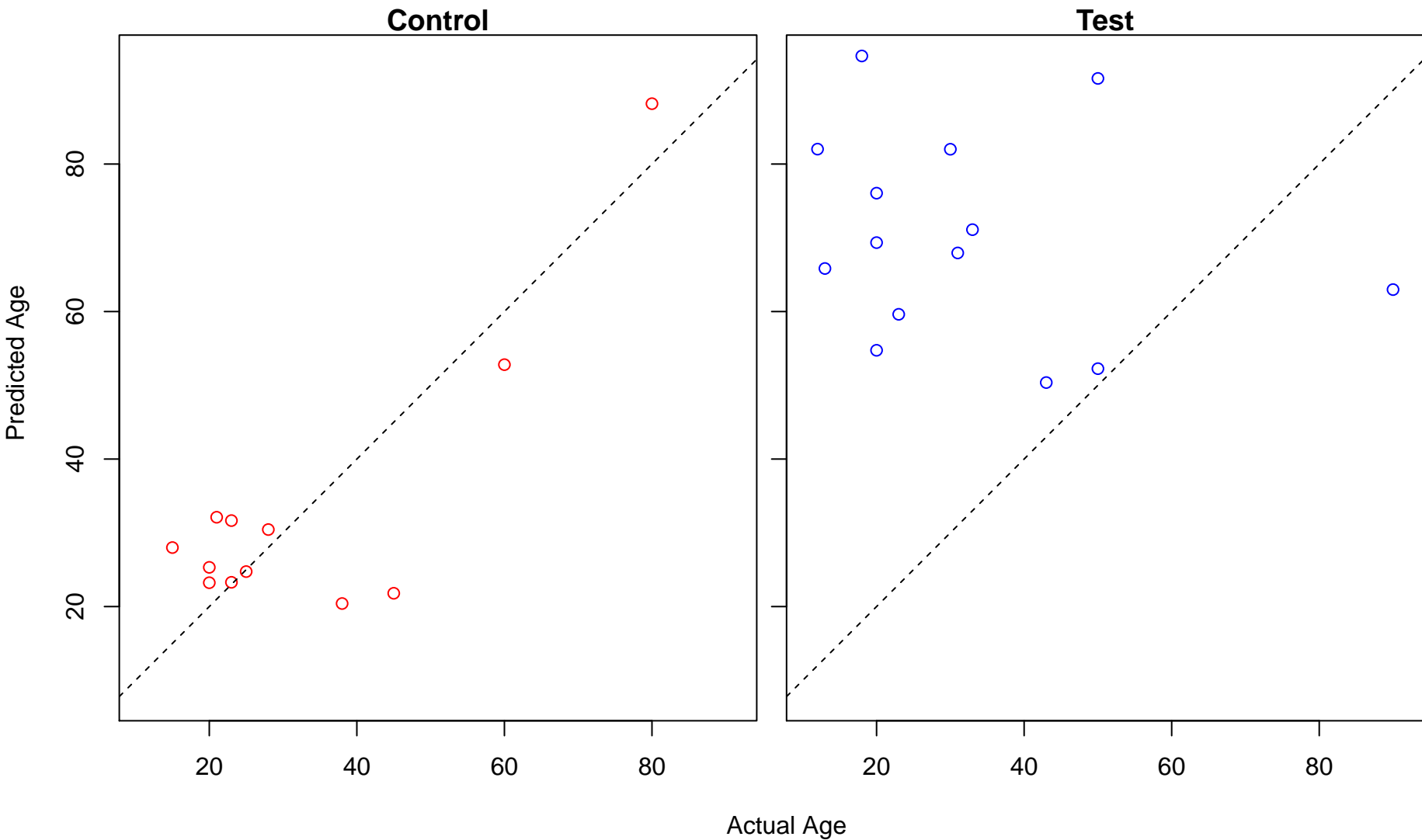
cellular response to vascular endothelial growth factor stimulus (Score: 7.483304)



positive regulation of alpha-beta T cell activation (Score: 7.482591)

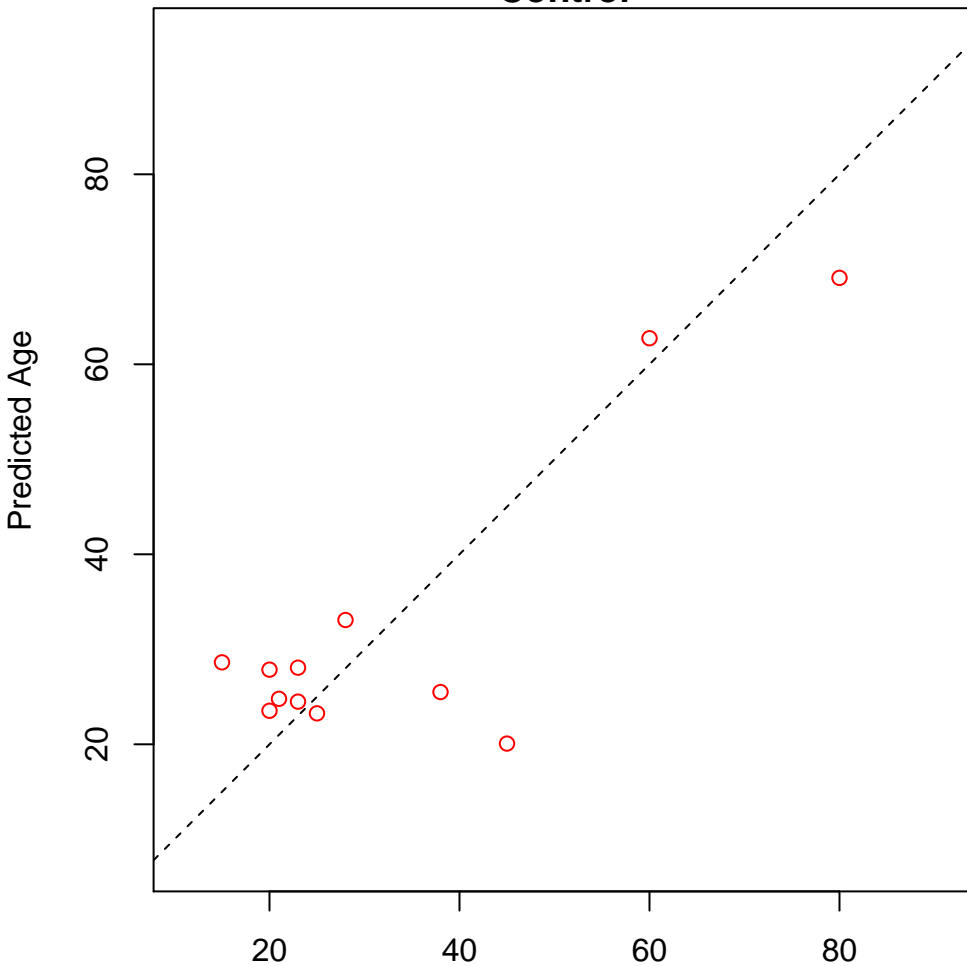


COPII-coated vesicle budding (Score: 7.480595)

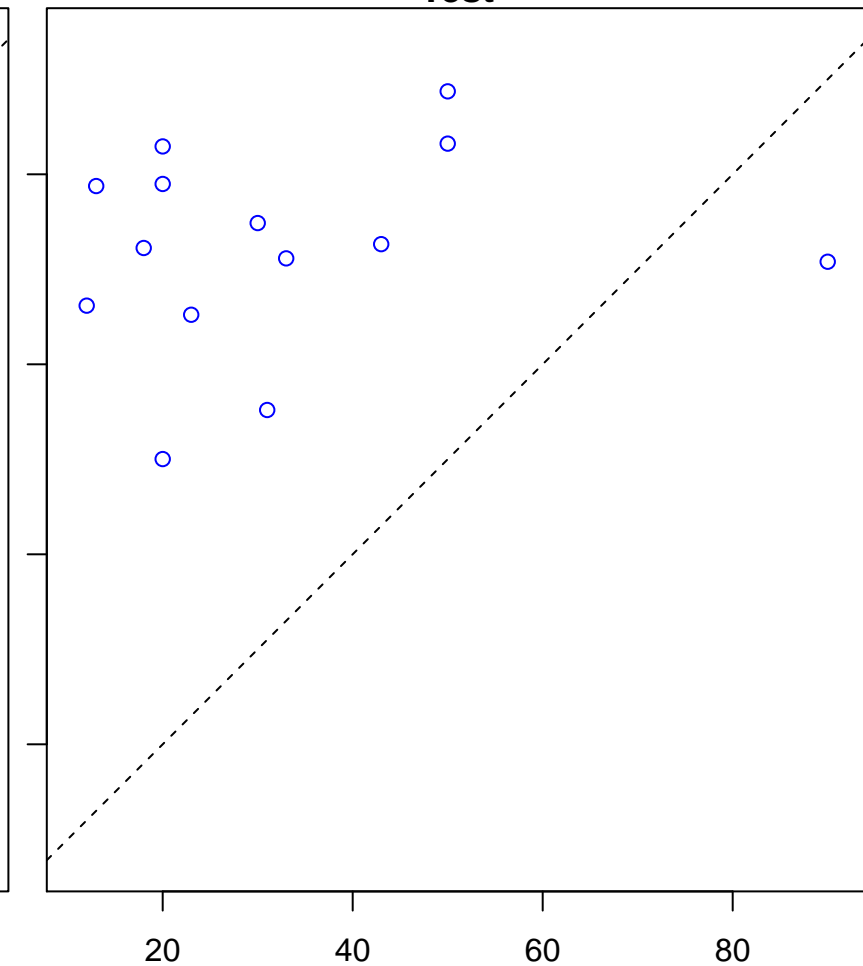


fatty acid elongation, saturated fatty acid (Score: 7.476779)

Control

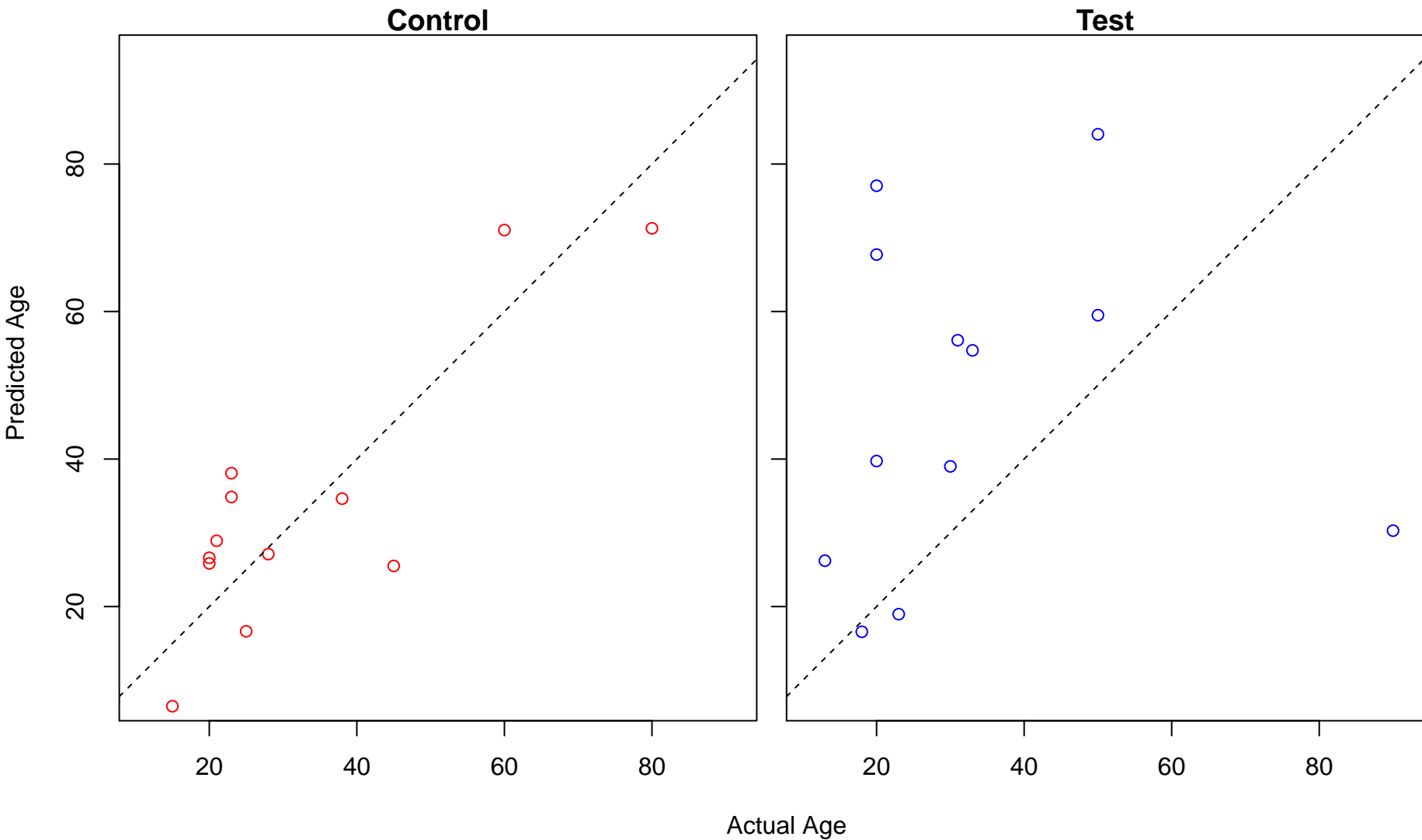


Test

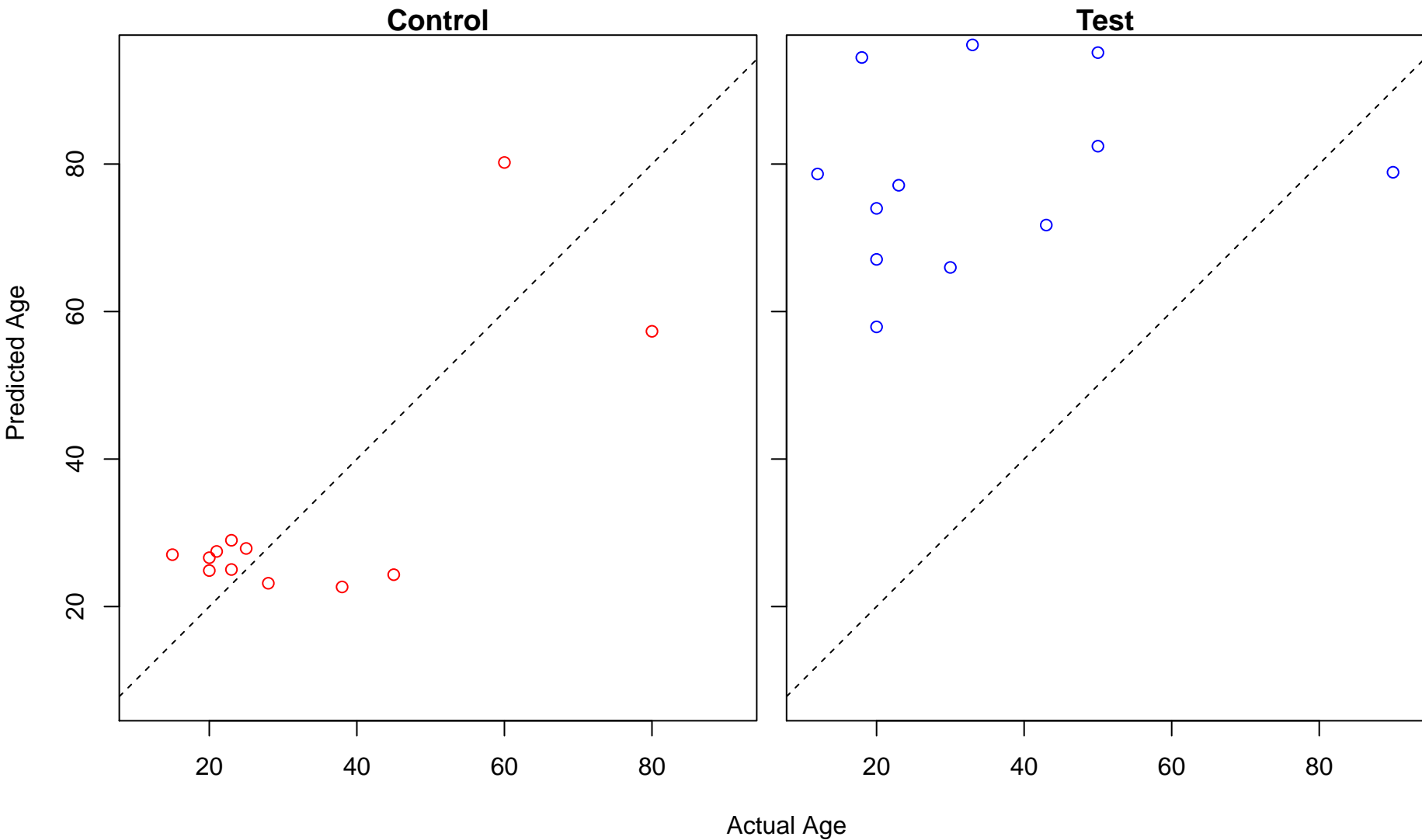


Actual Age

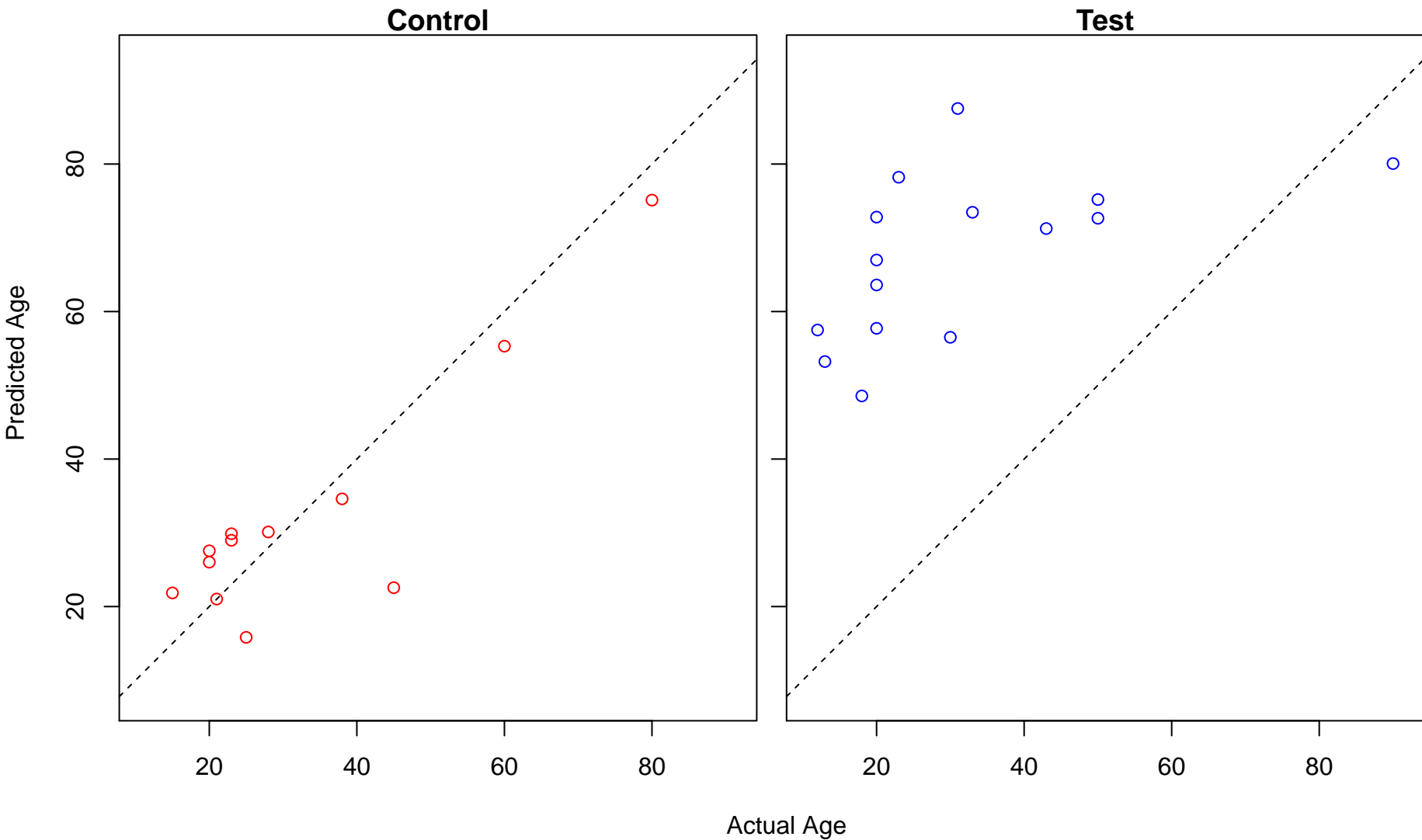
lipid digestion (Score: 7.472265)



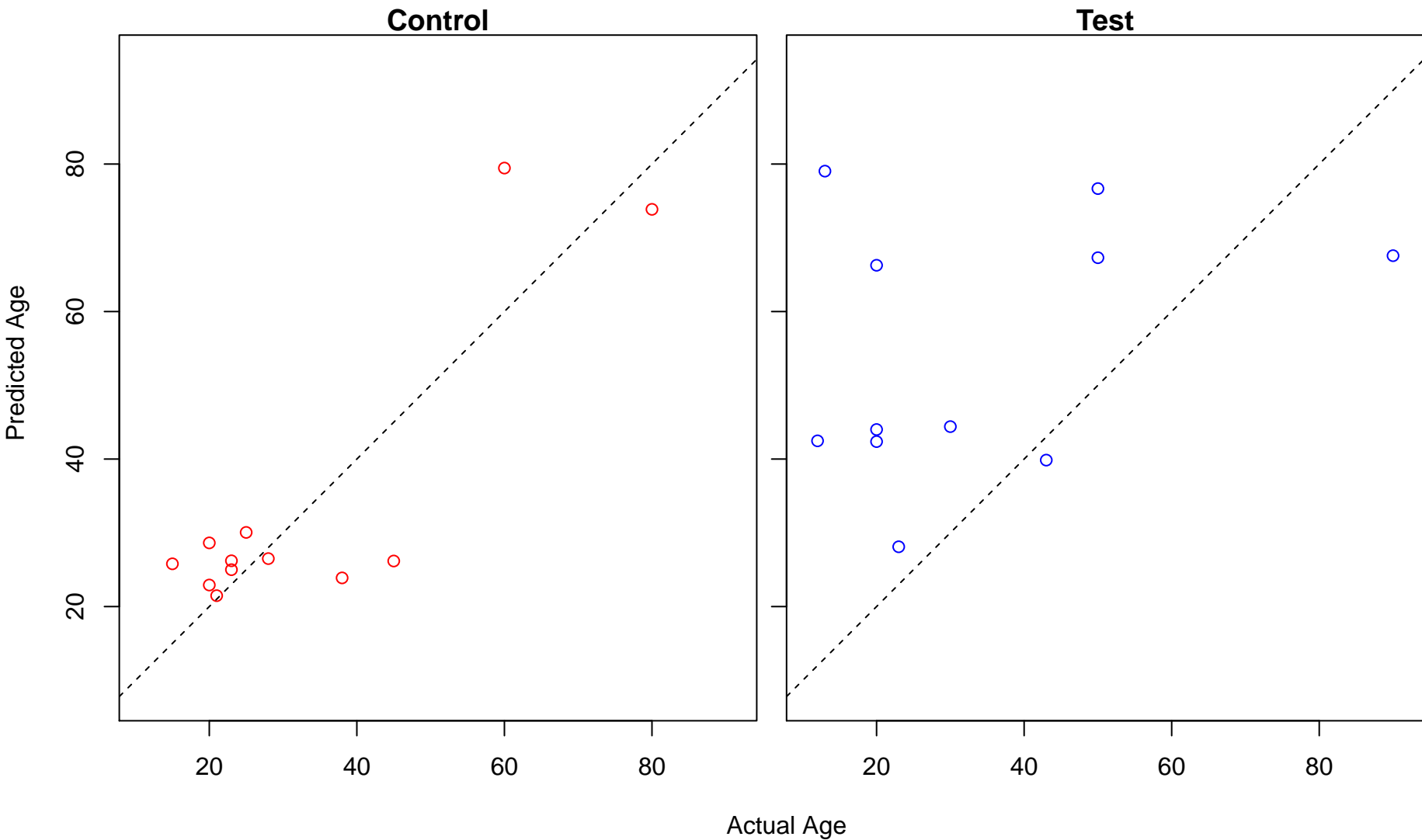
brown fat cell differentiation (Score: 7.471228)



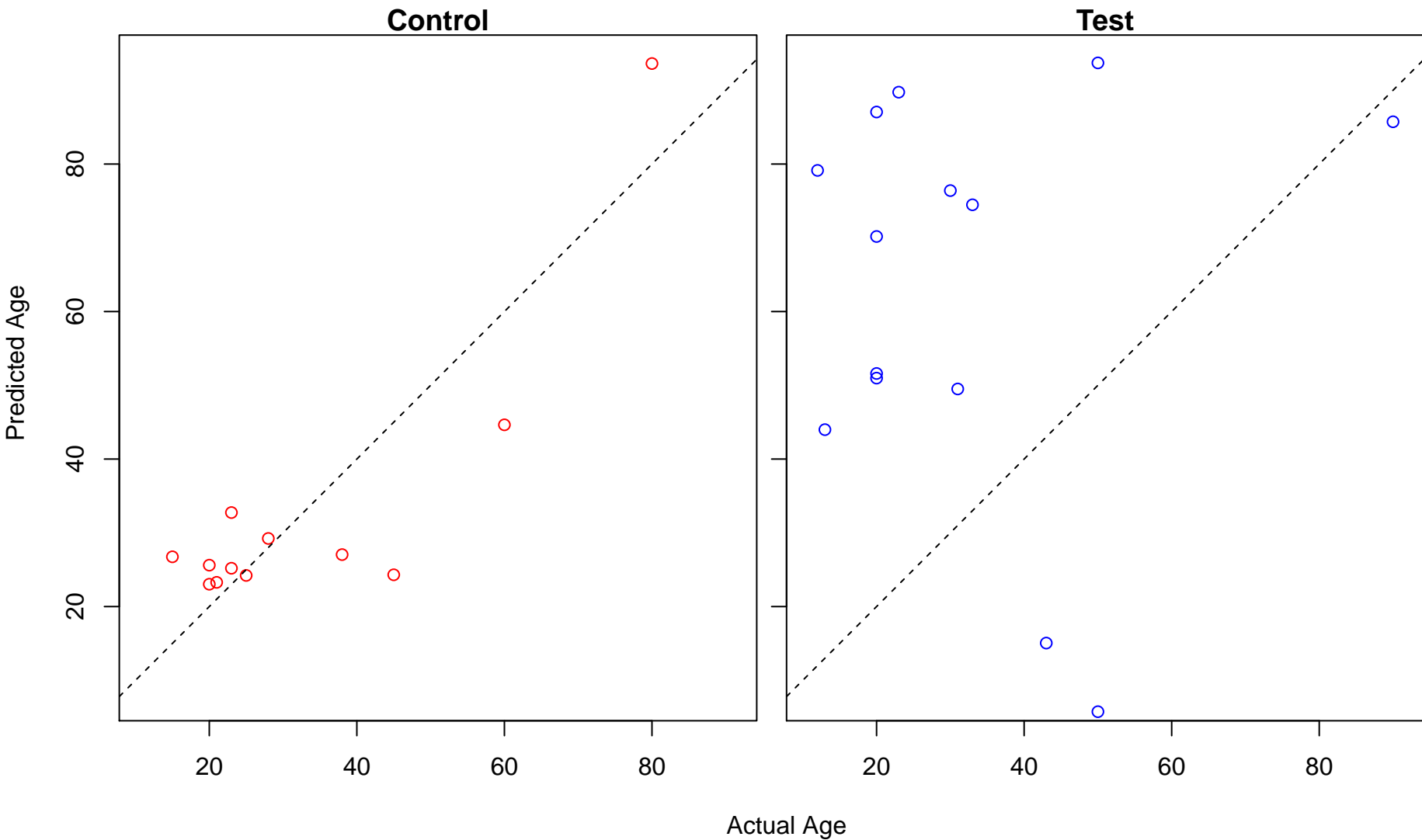
regulation of microtubule-based movement (Score: 7.470062)



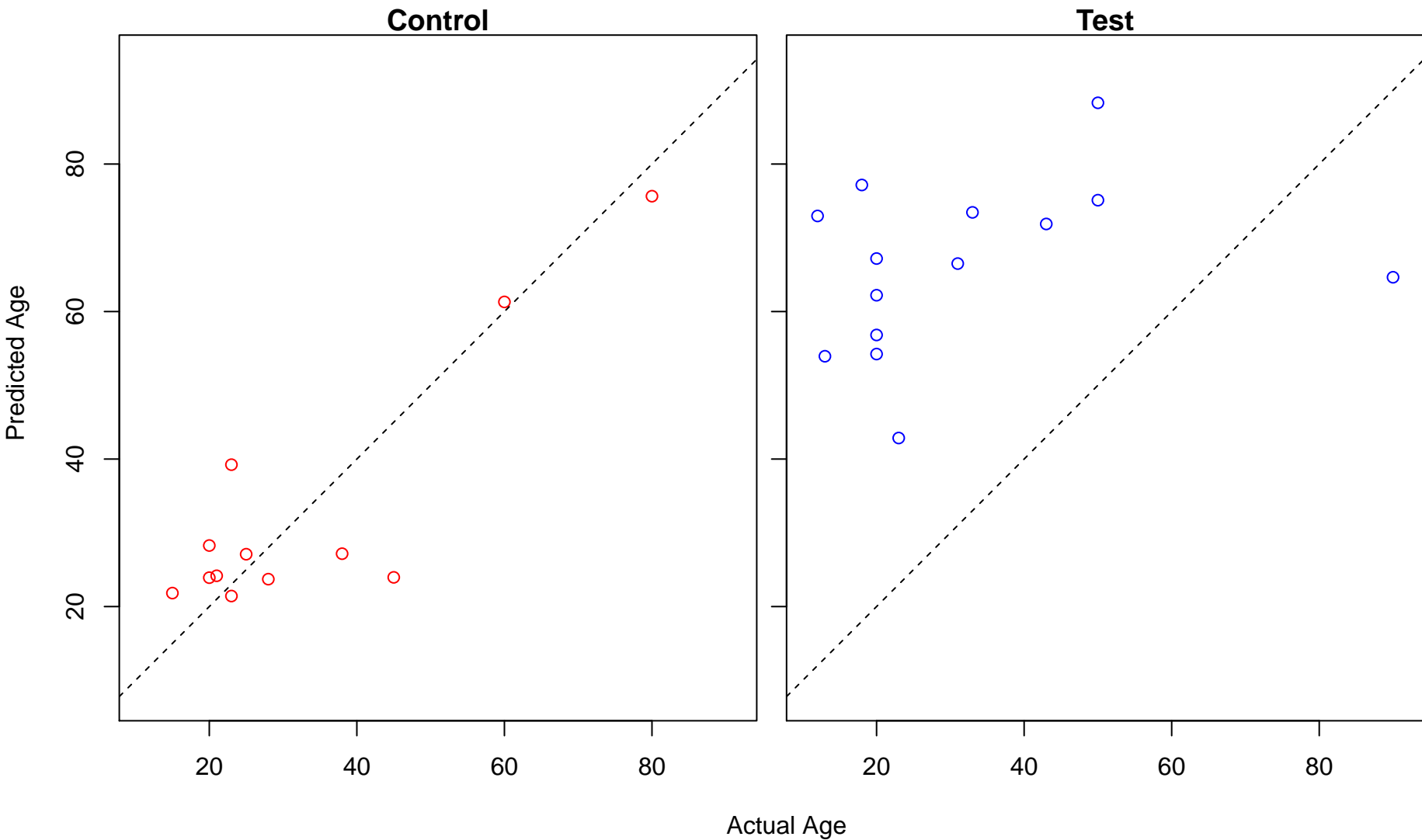
positive regulation of endoplasmic reticulum unfolded protein response (Score: 7.459478)



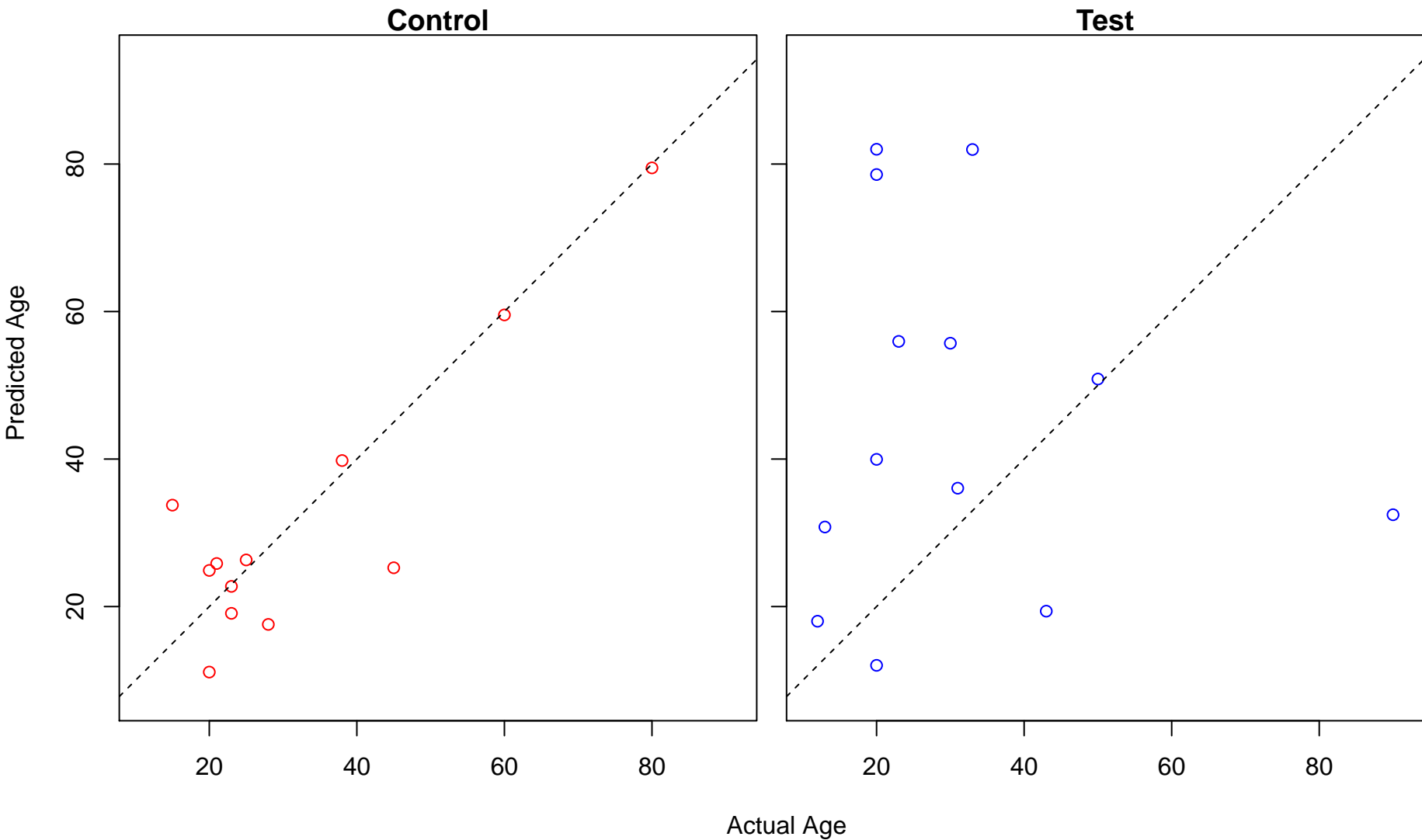
glycerolipid biosynthetic process (Score: 7.454548)



cell fate commitment involved in formation of primary germ layer (Score: 7.449953)

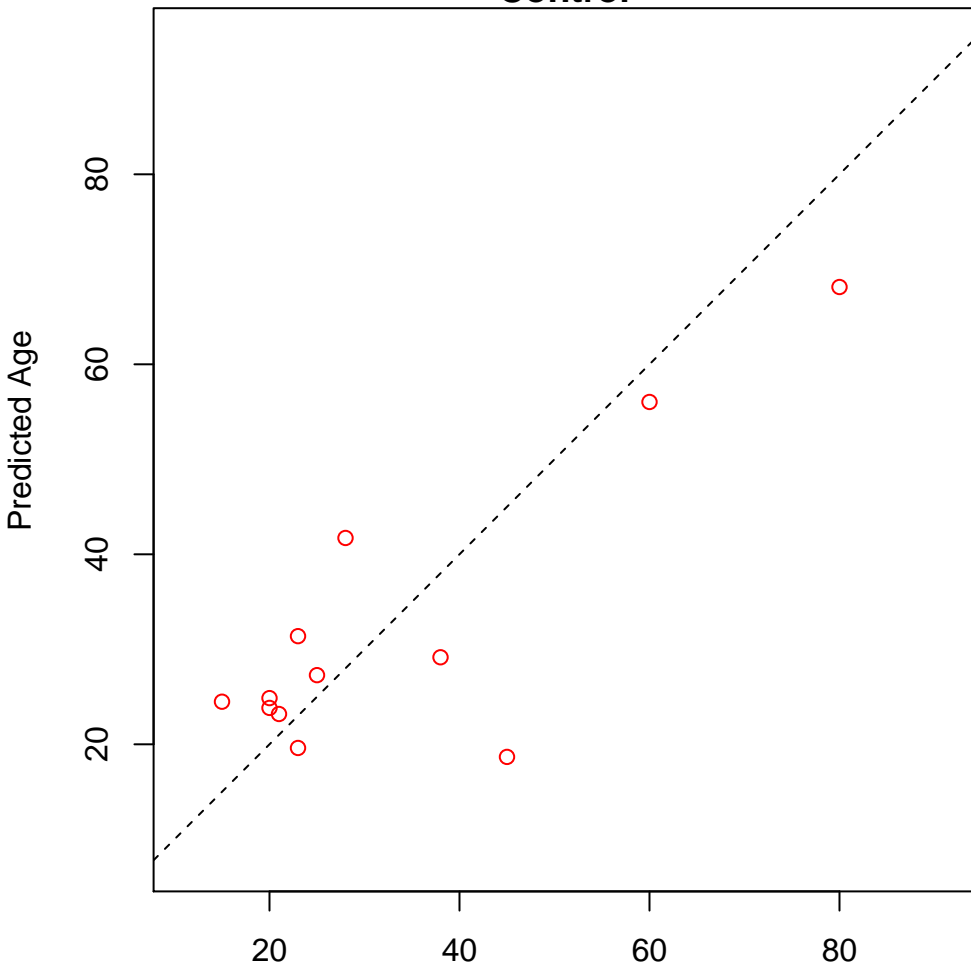


lysosome localization (Score: 7.449454)

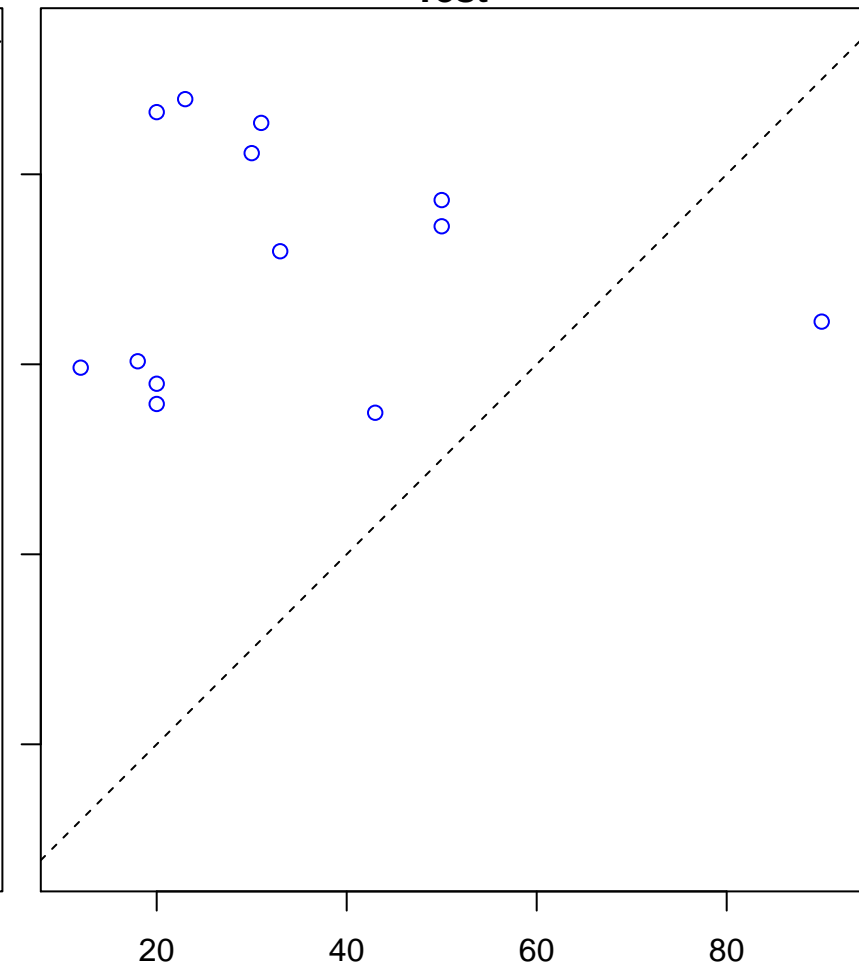


positive regulation of B cell proliferation (Score: 7.446661)

Control

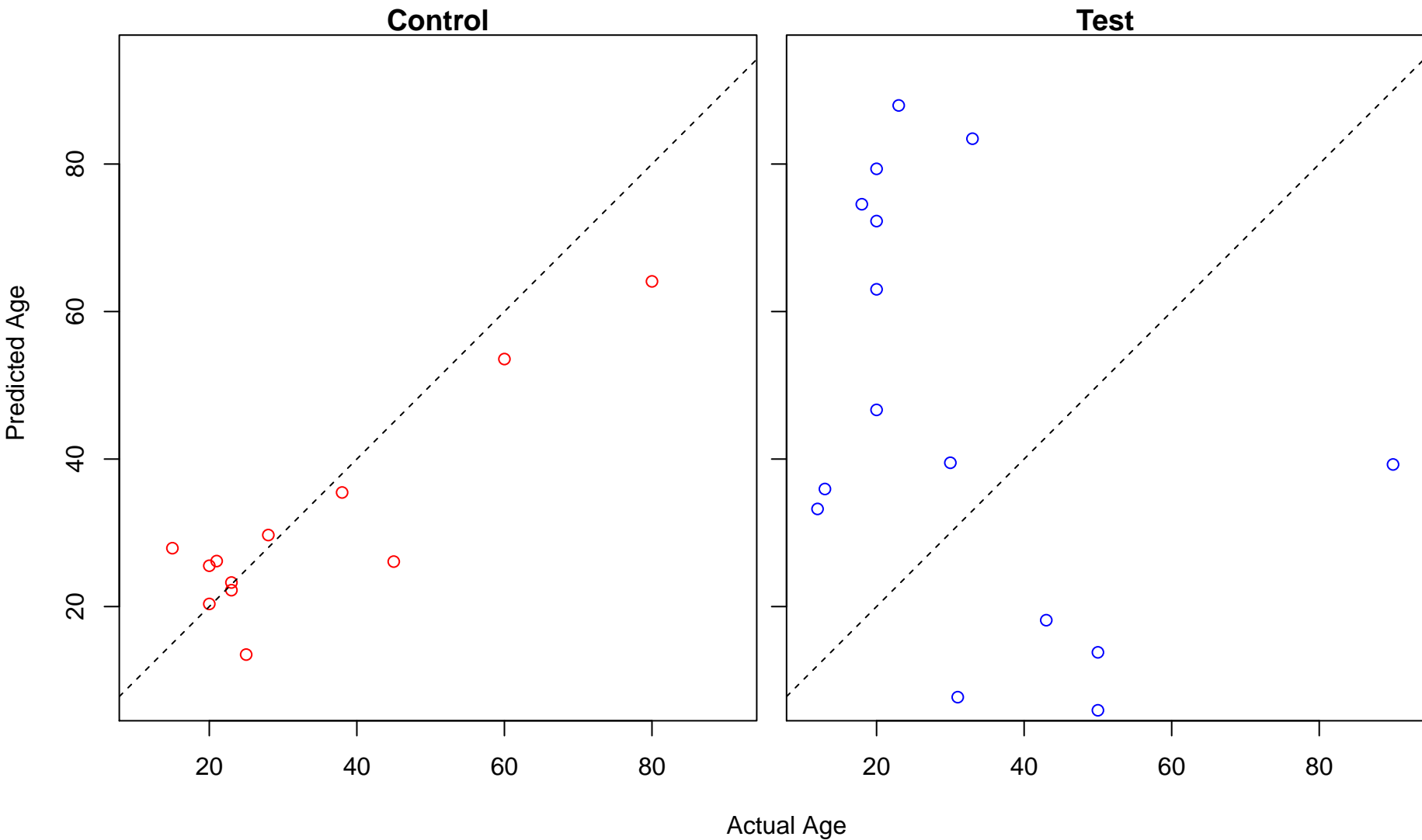


Test

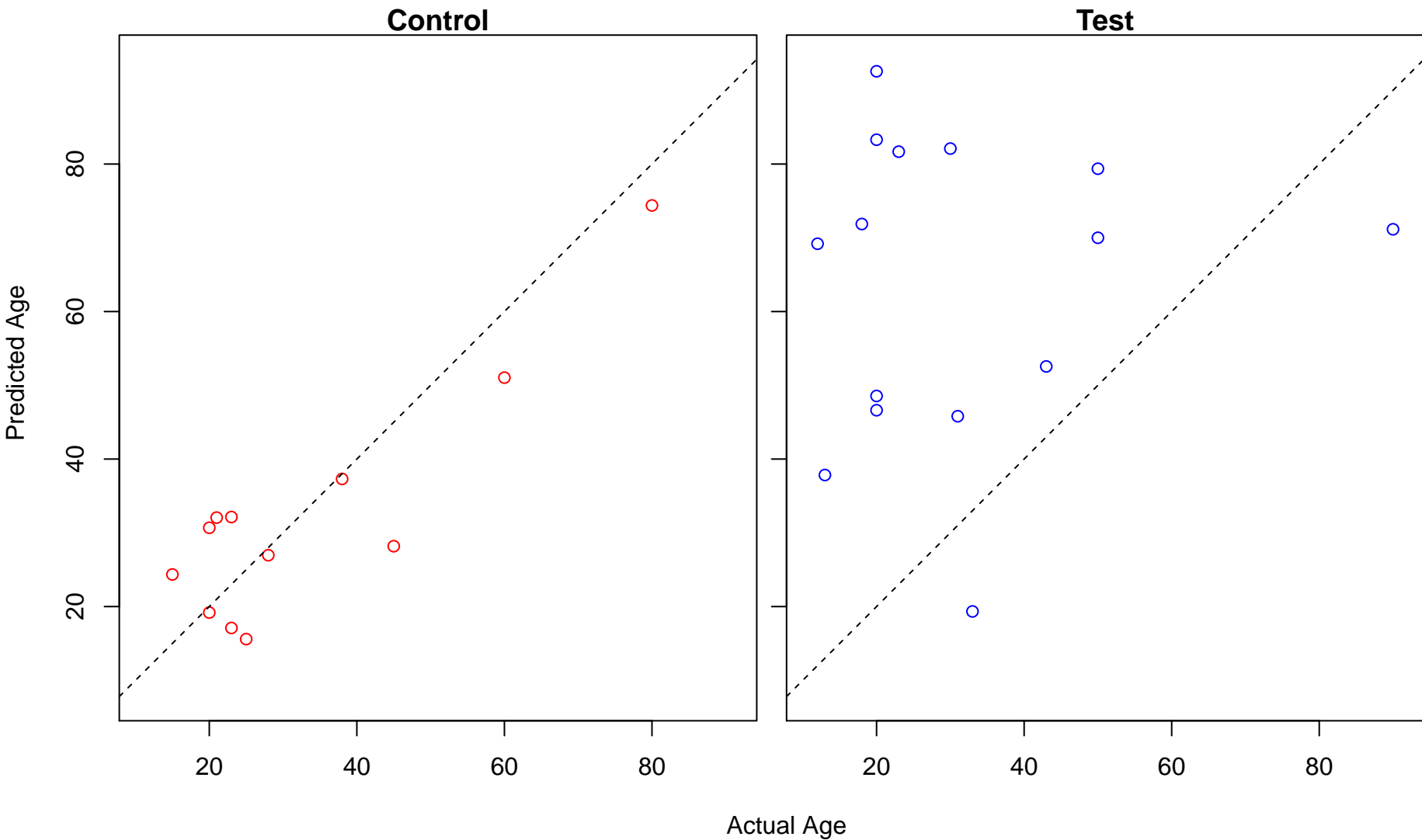


Actual Age

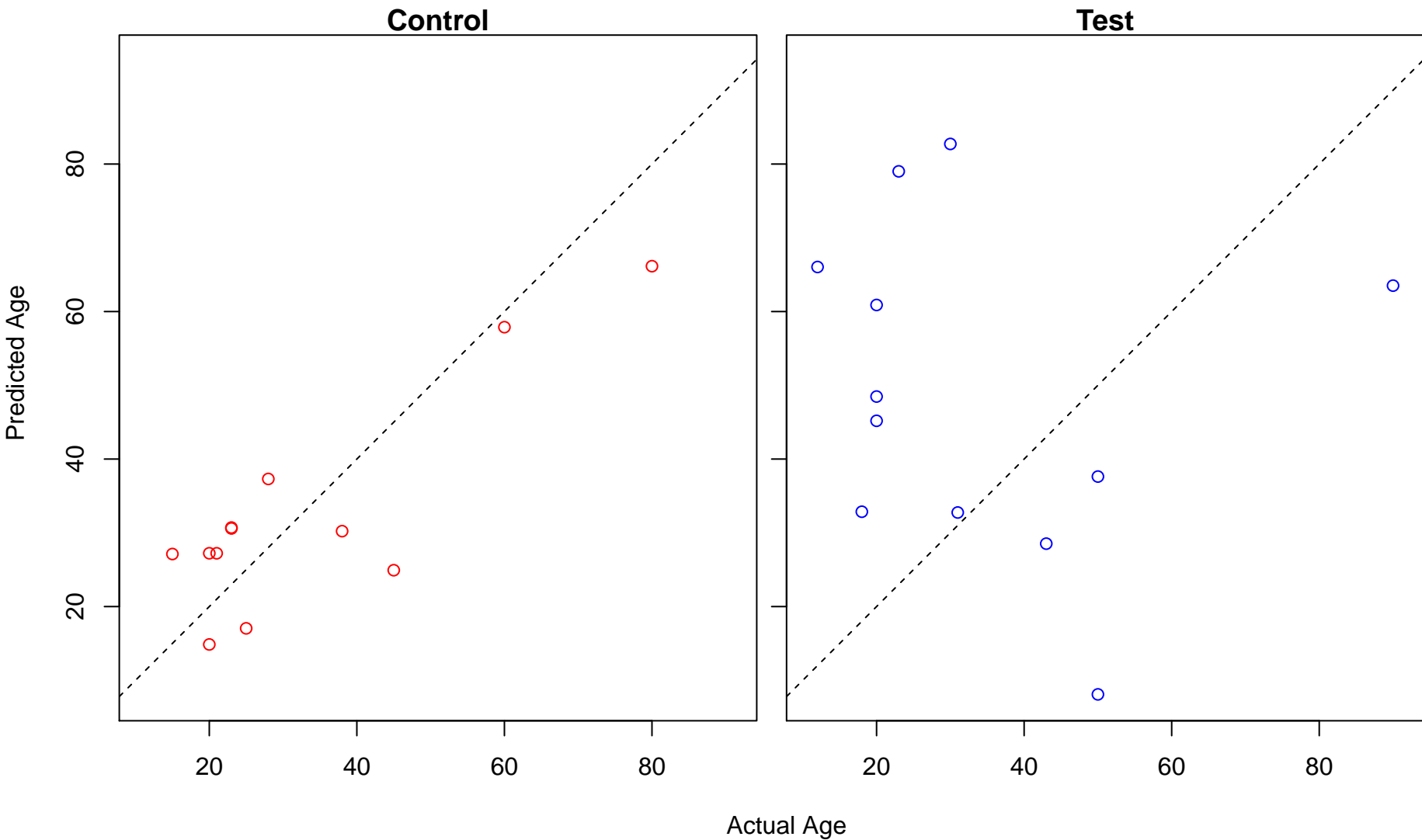
modulation by virus of host morphology or physiology (Score: 7.440550)



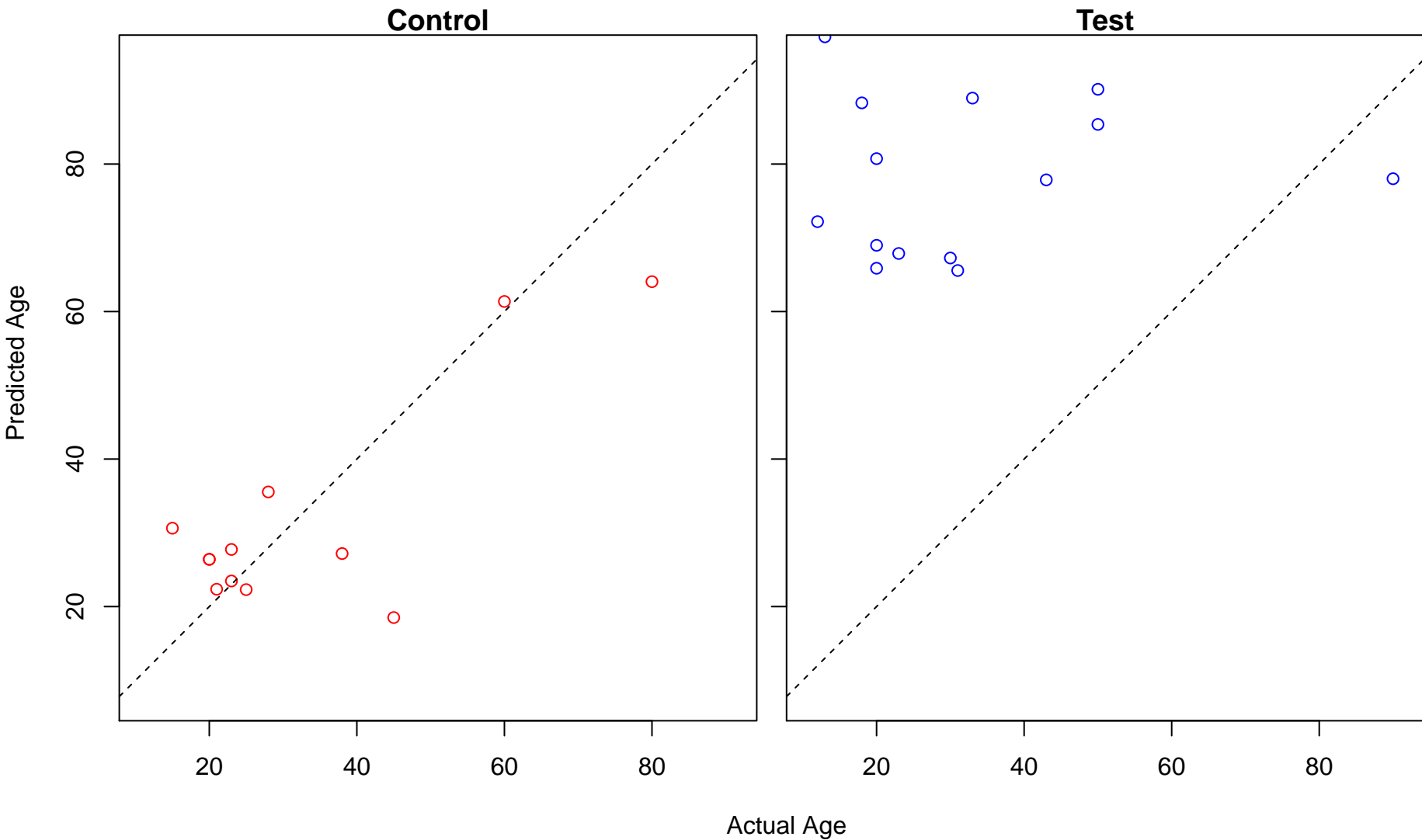
camera-type eye morphogenesis (Score: 7.440316)



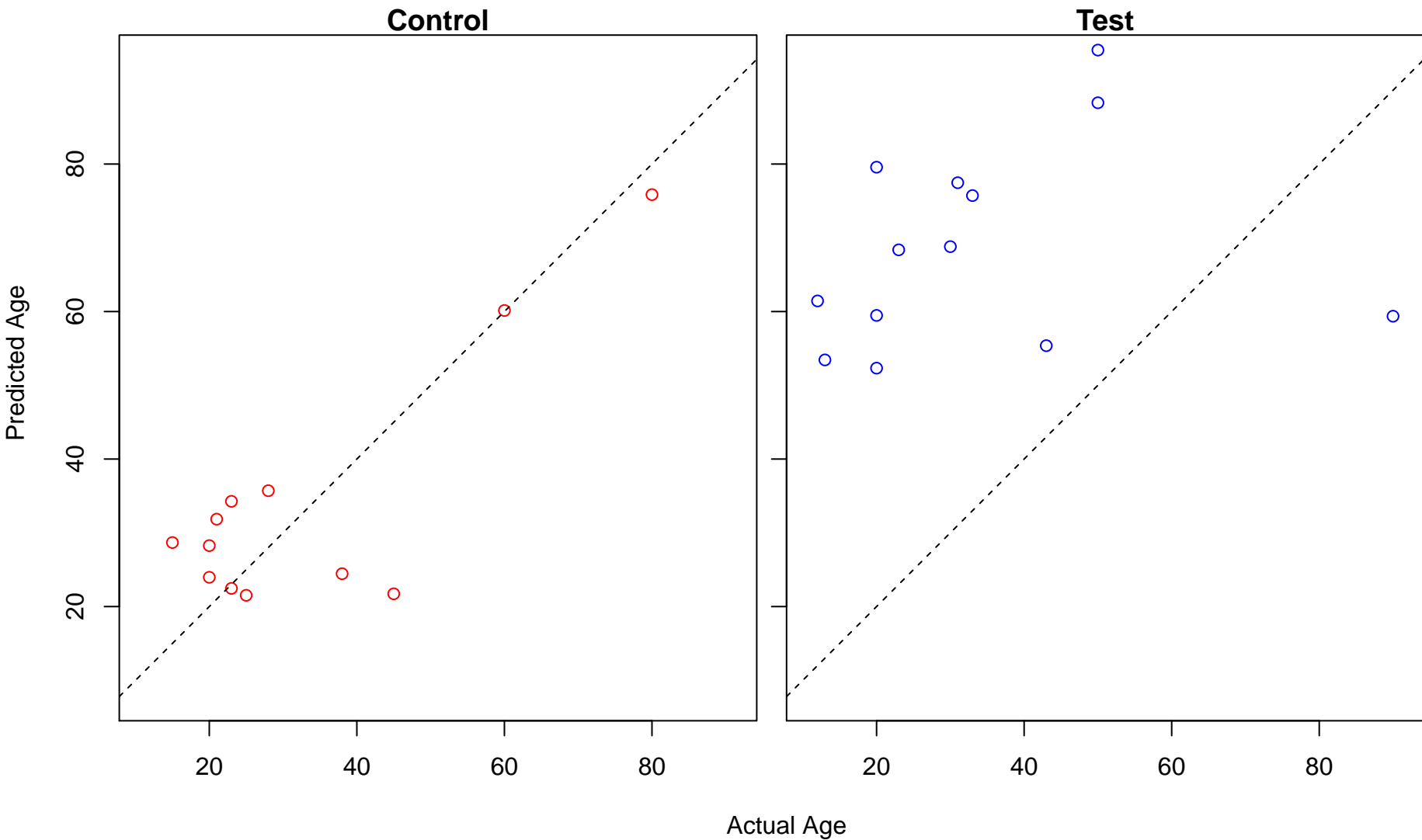
endothelial cell activation (Score: 7.437455)



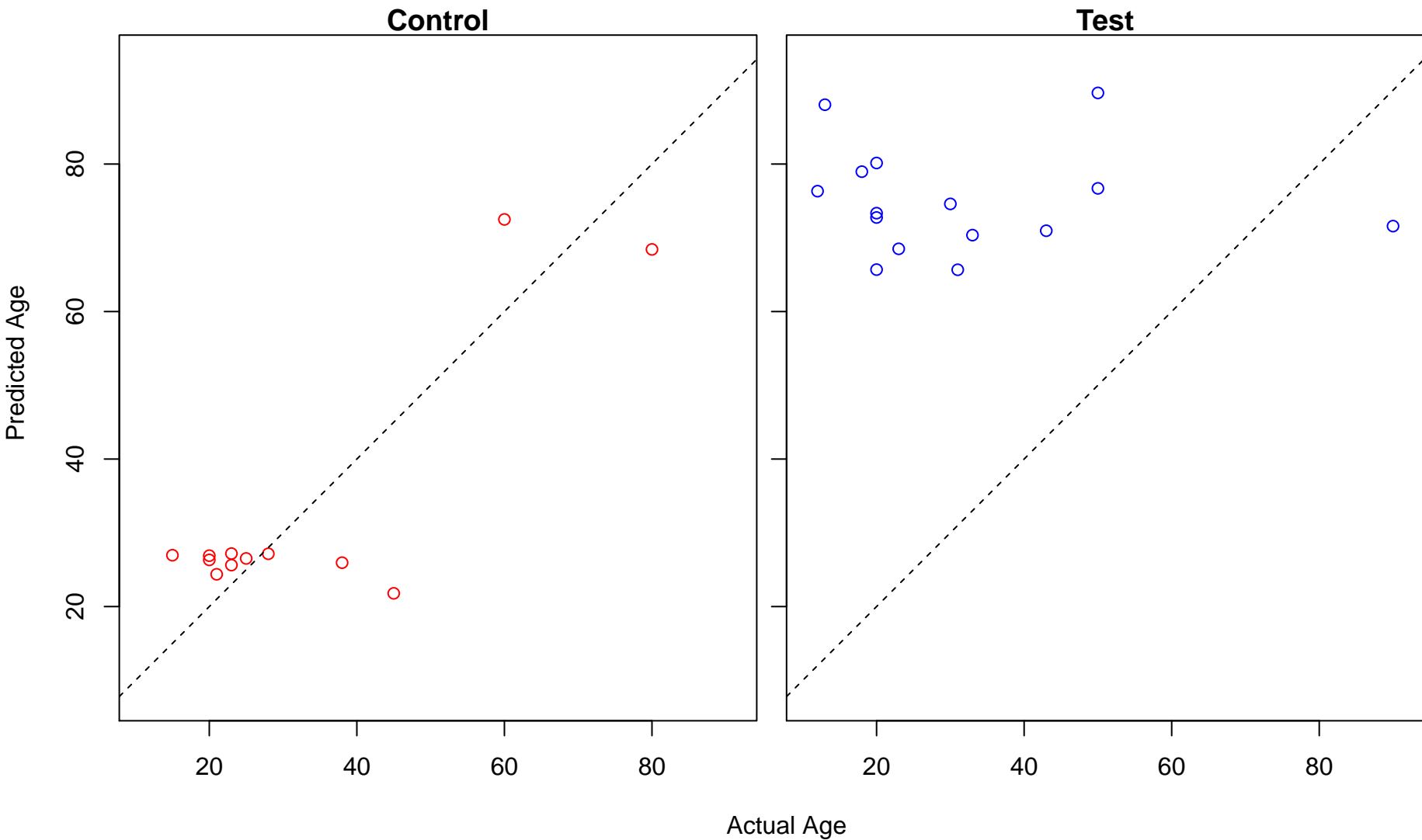
osteoblast development (Score: 7.436427)



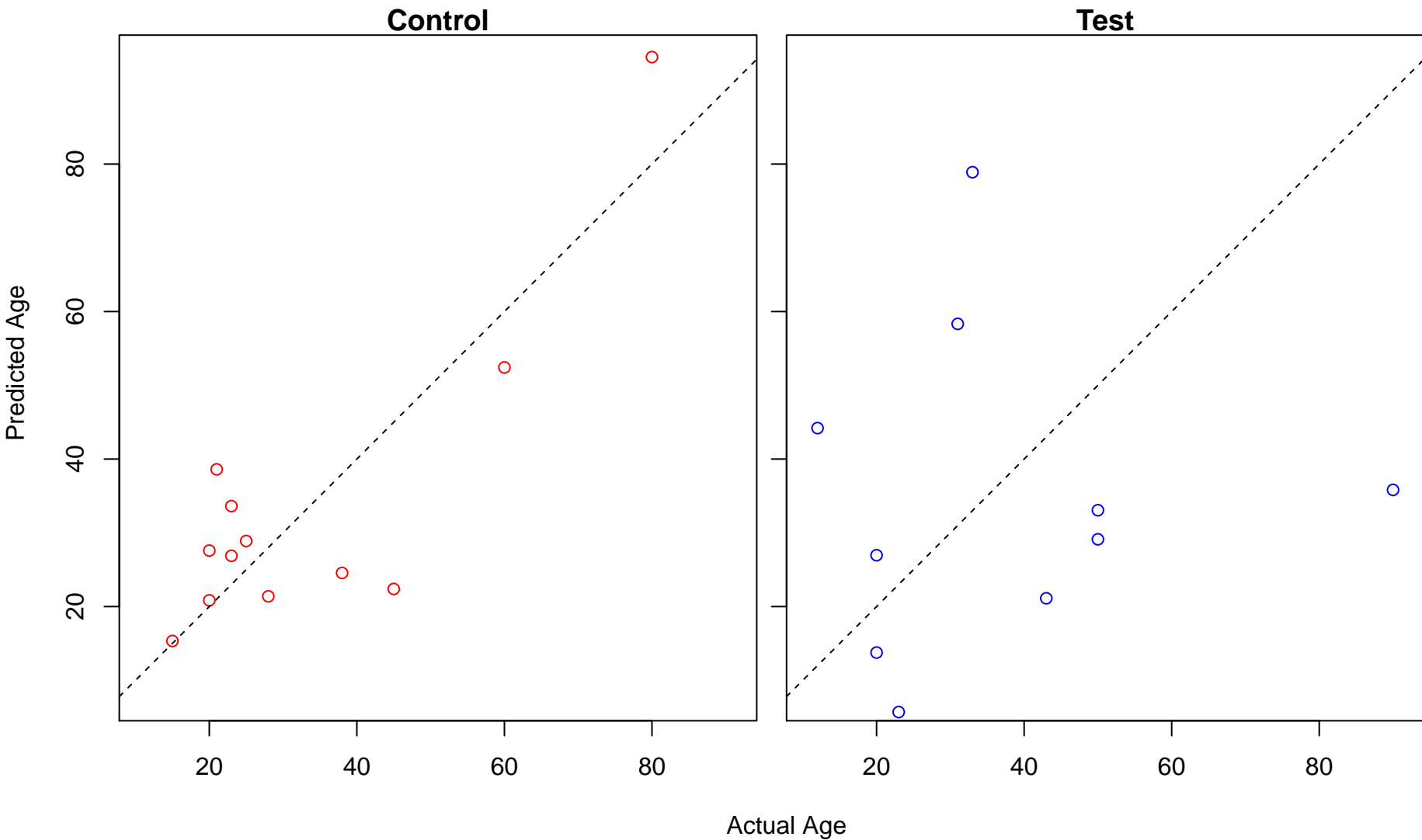
single organism cell adhesion (Score: 7.434727)



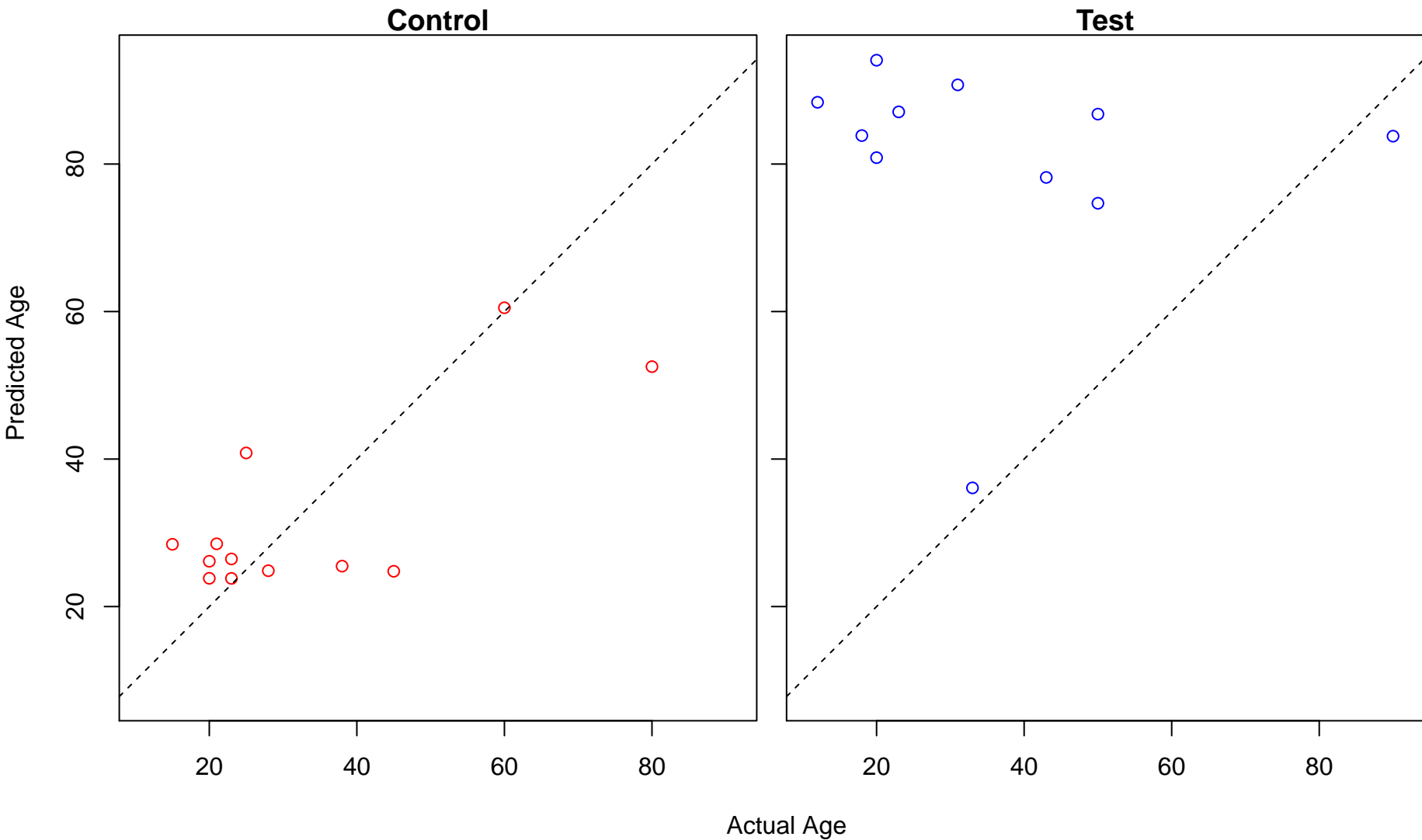
histone H3-K9 modification (Score: 7.431580)



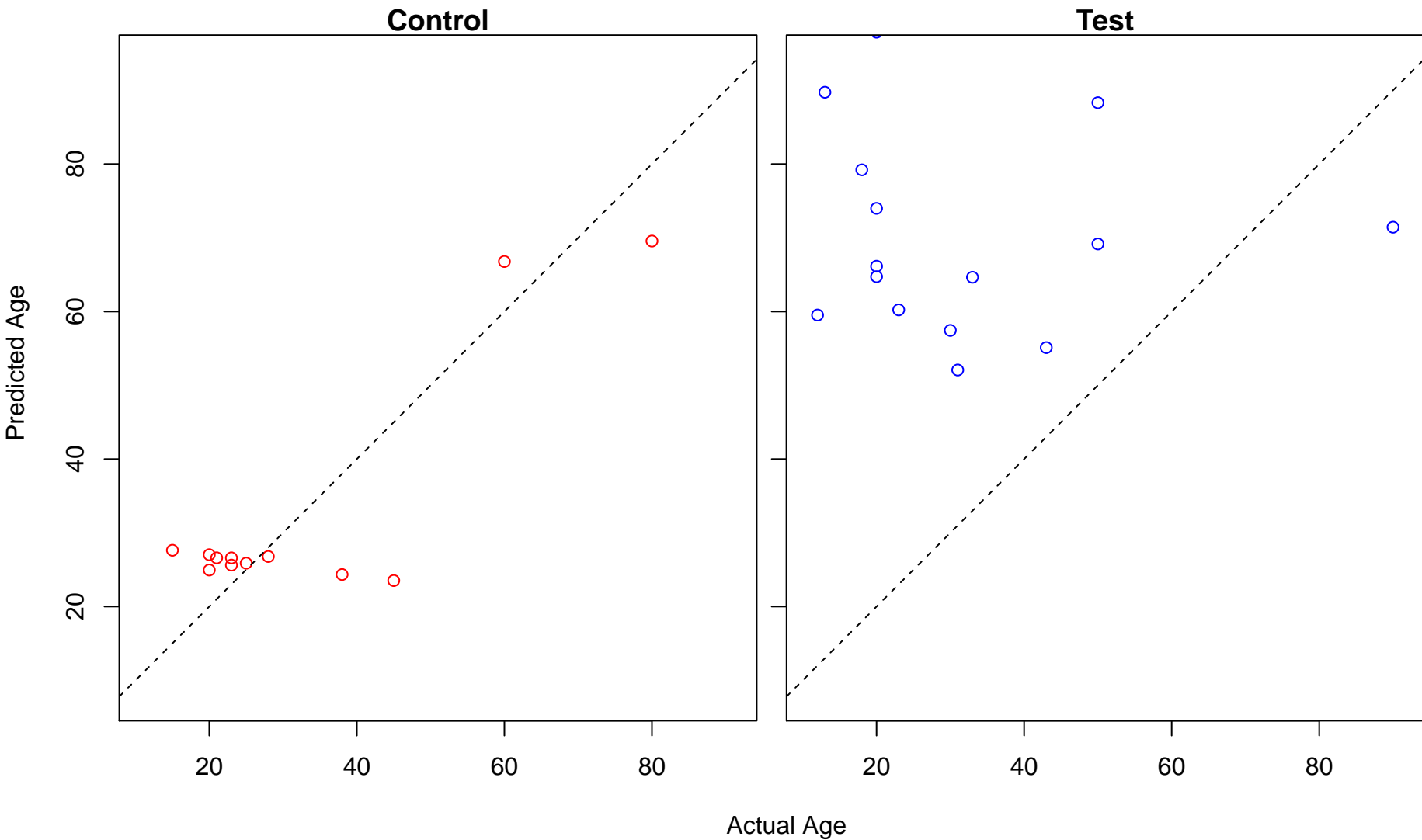
deoxyribonucleoside monophosphate metabolic process (Score: 7.429534)



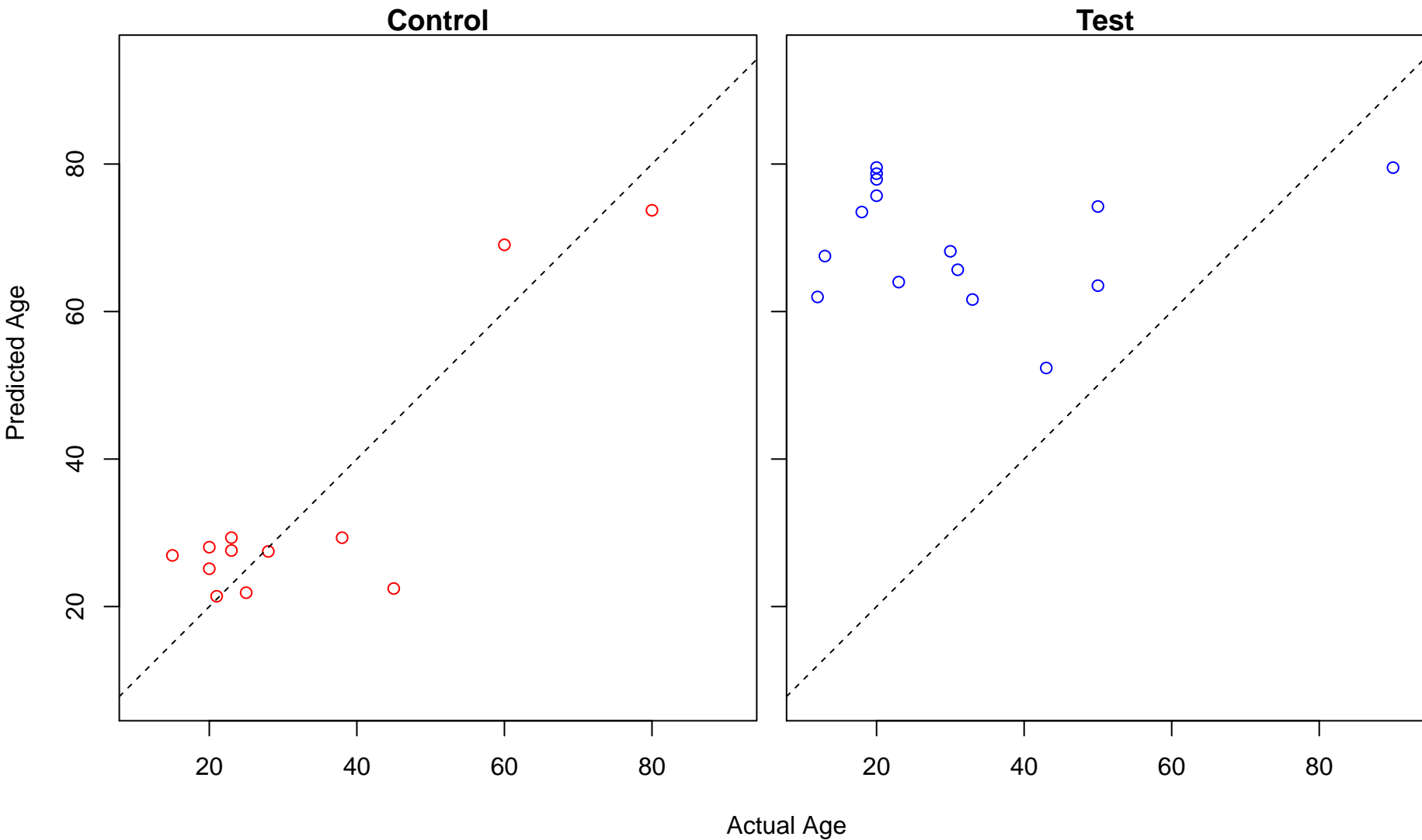
response to progesterone (Score: 7.428383)



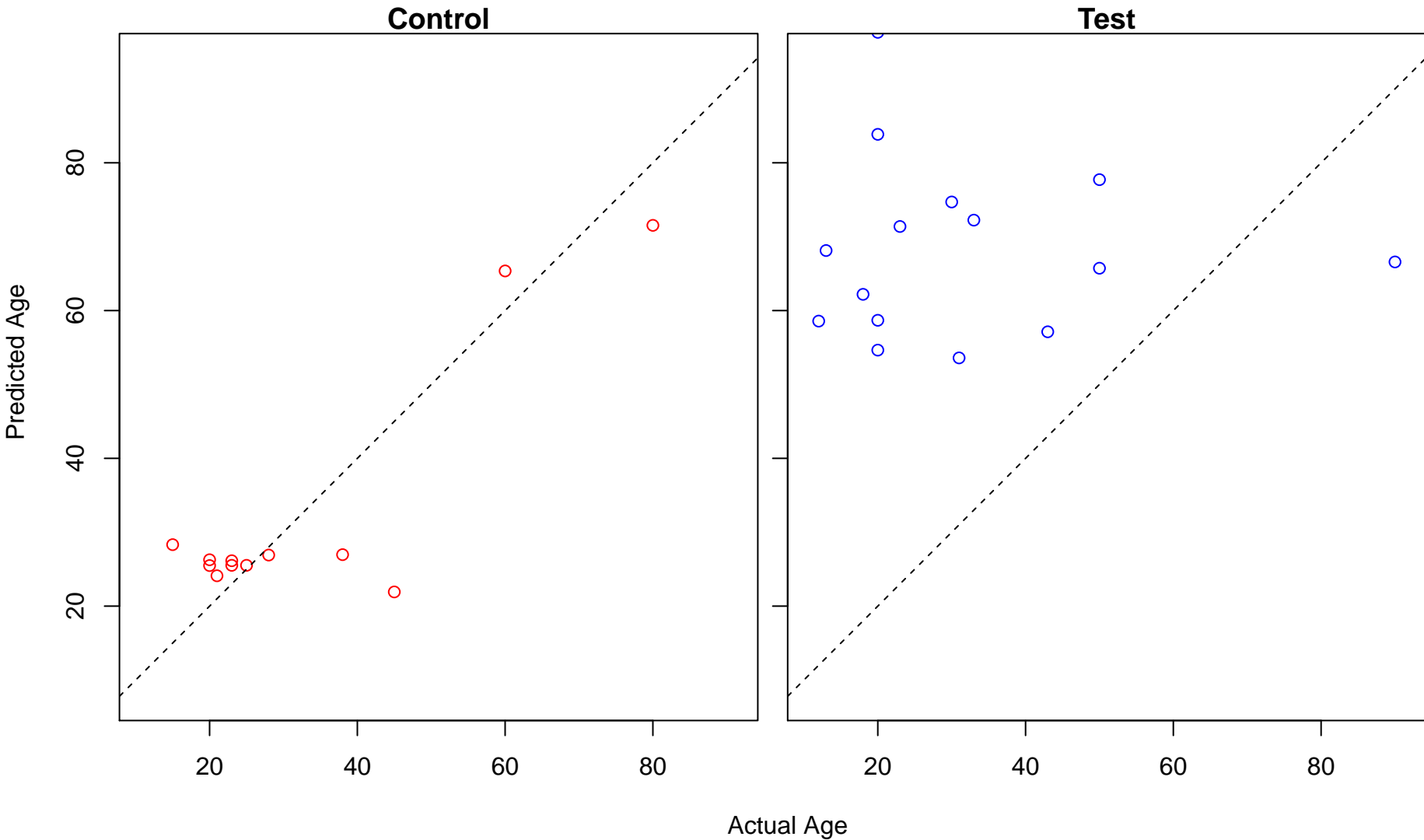
peptide metabolic process (Score: 7.425986)



synapse organization (Score: 7.424334)

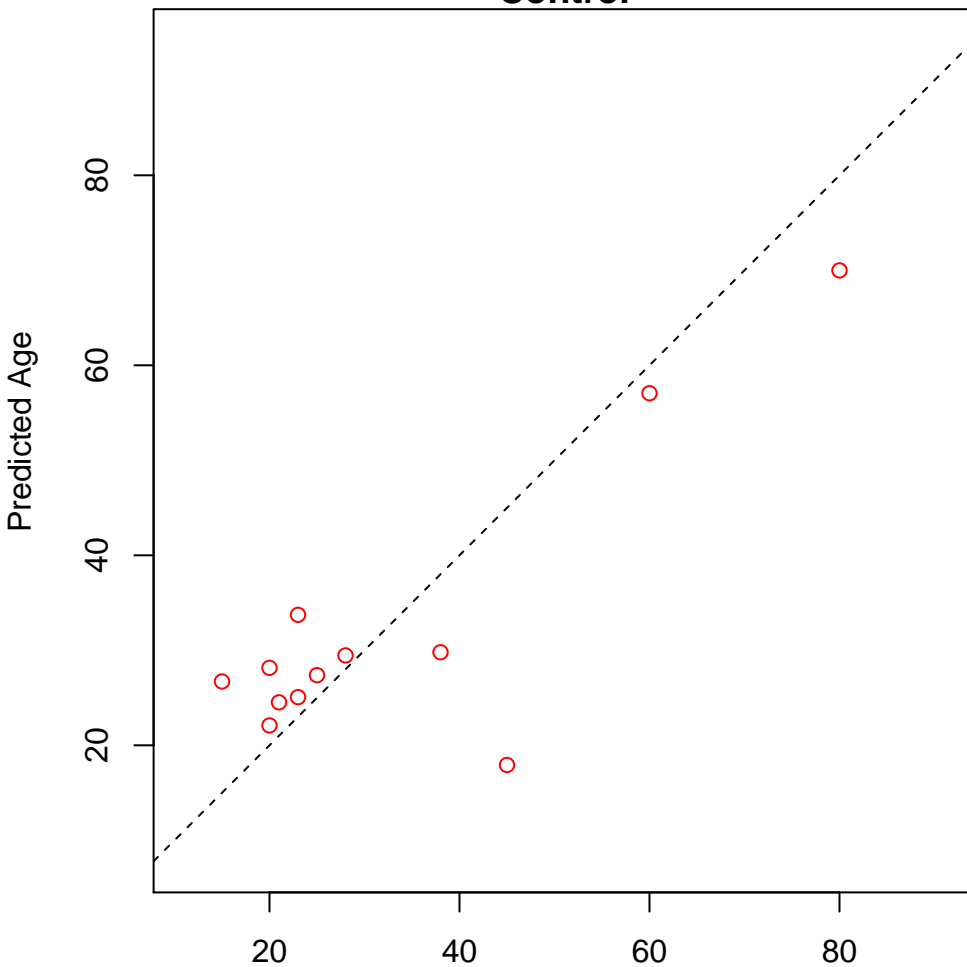


plasma membrane to endosome transport (Score: 7.423450)

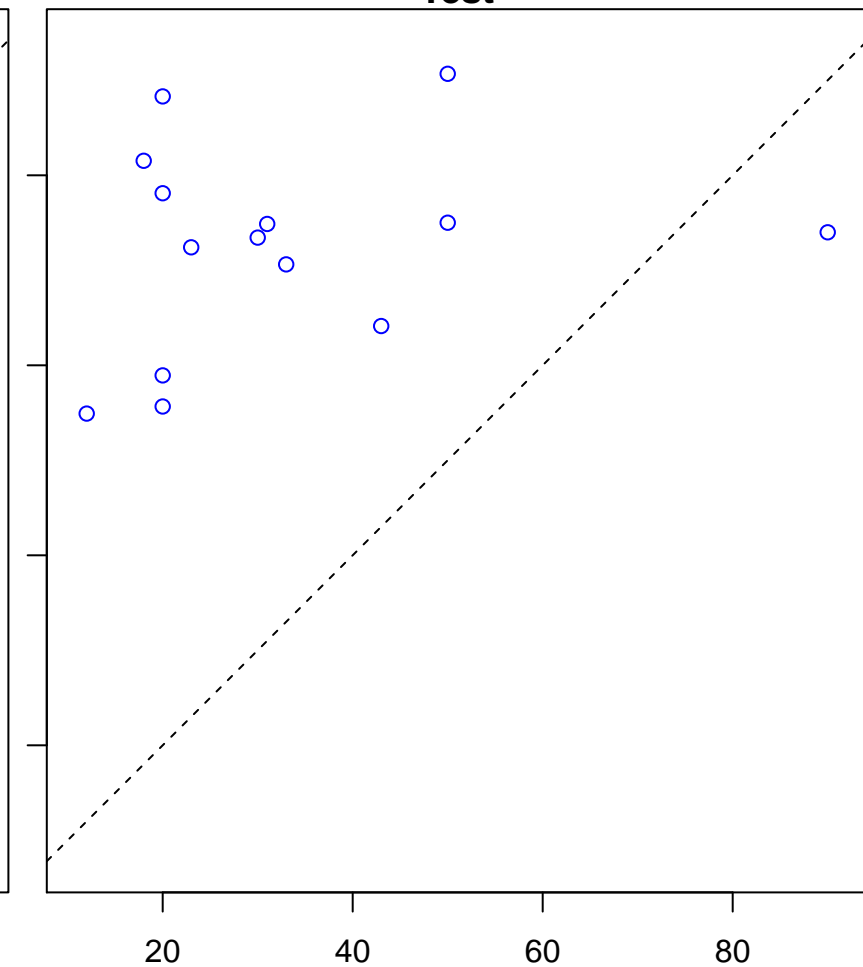


negative regulation of defense response (Score: 7.414404)

Control

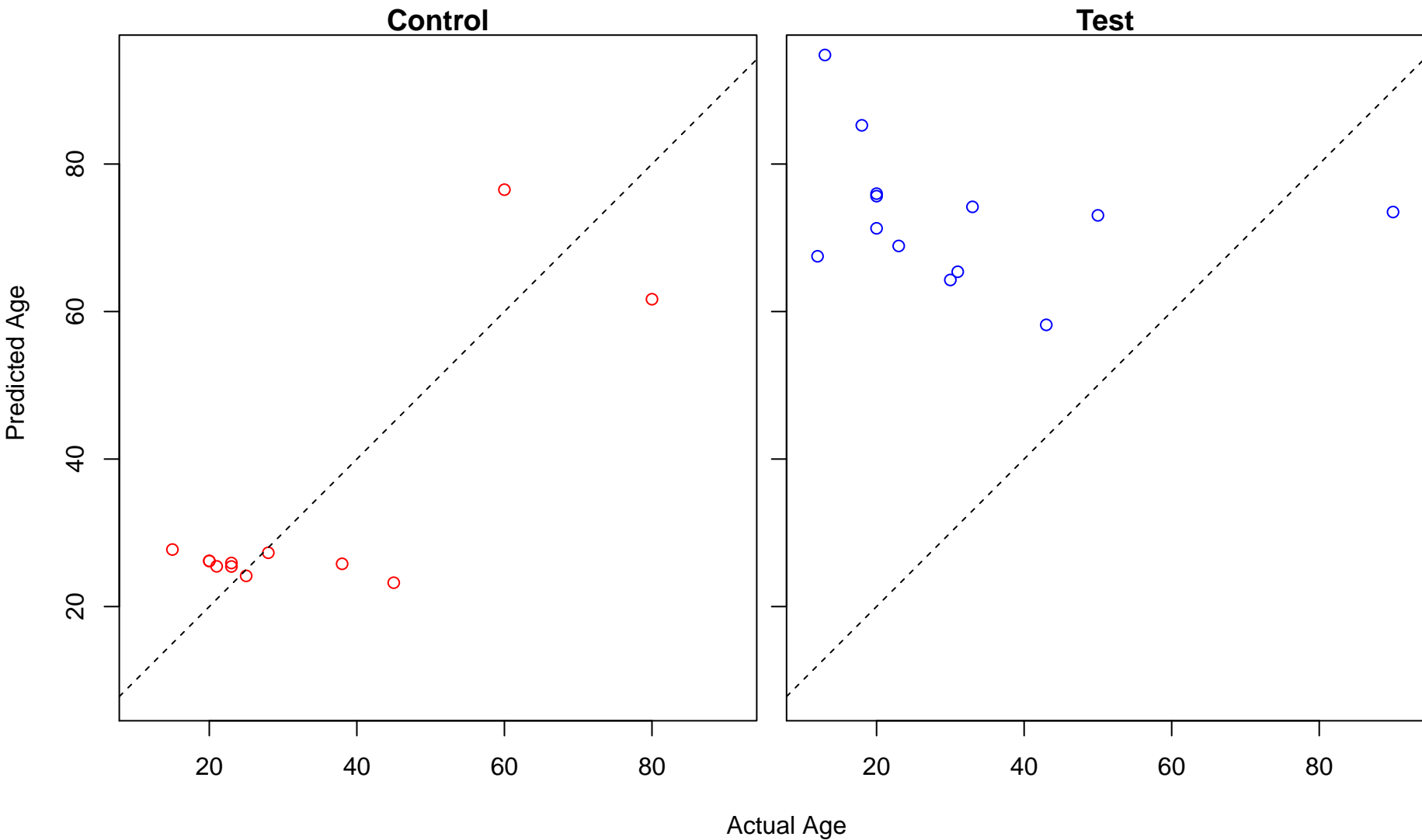


Test

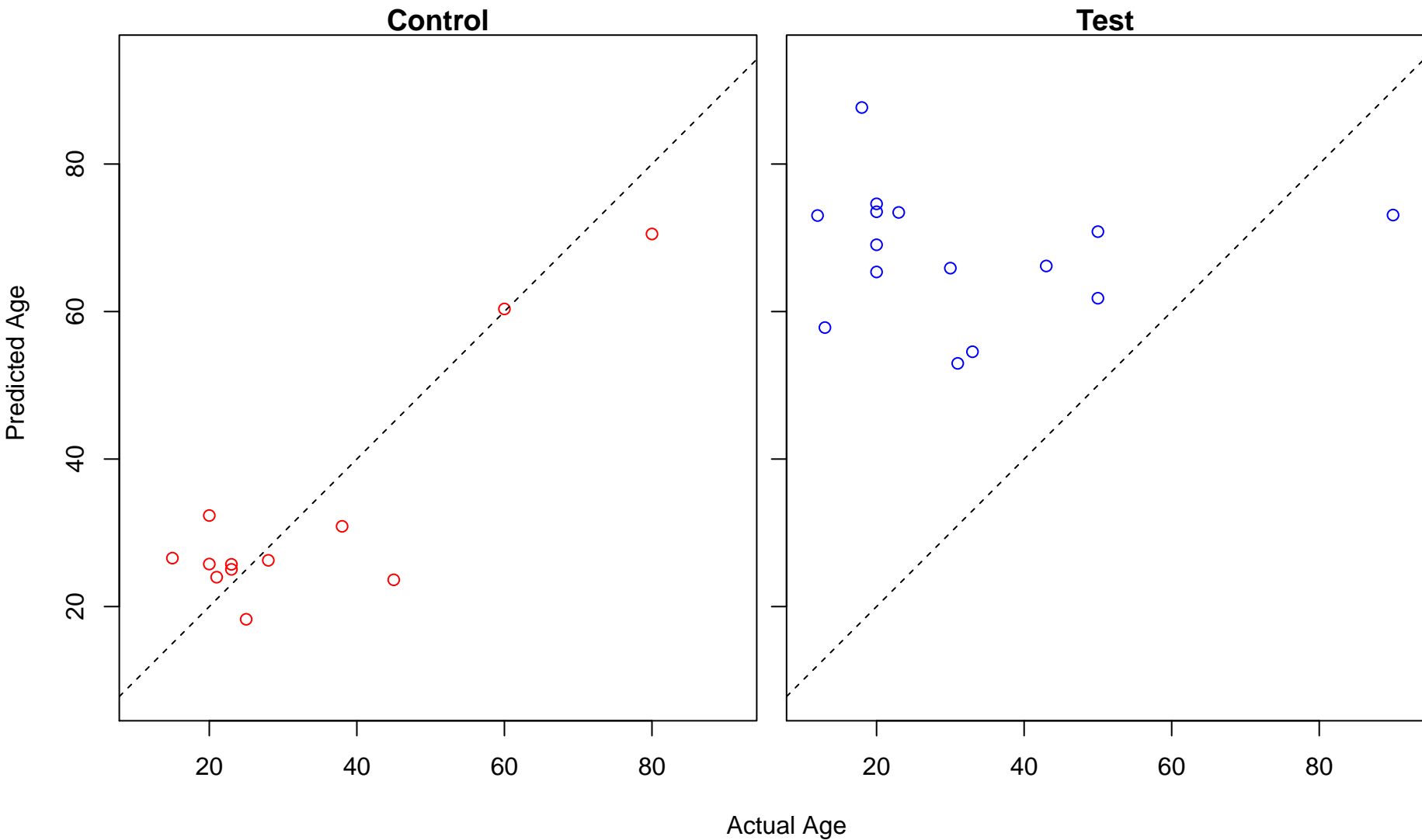


Actual Age

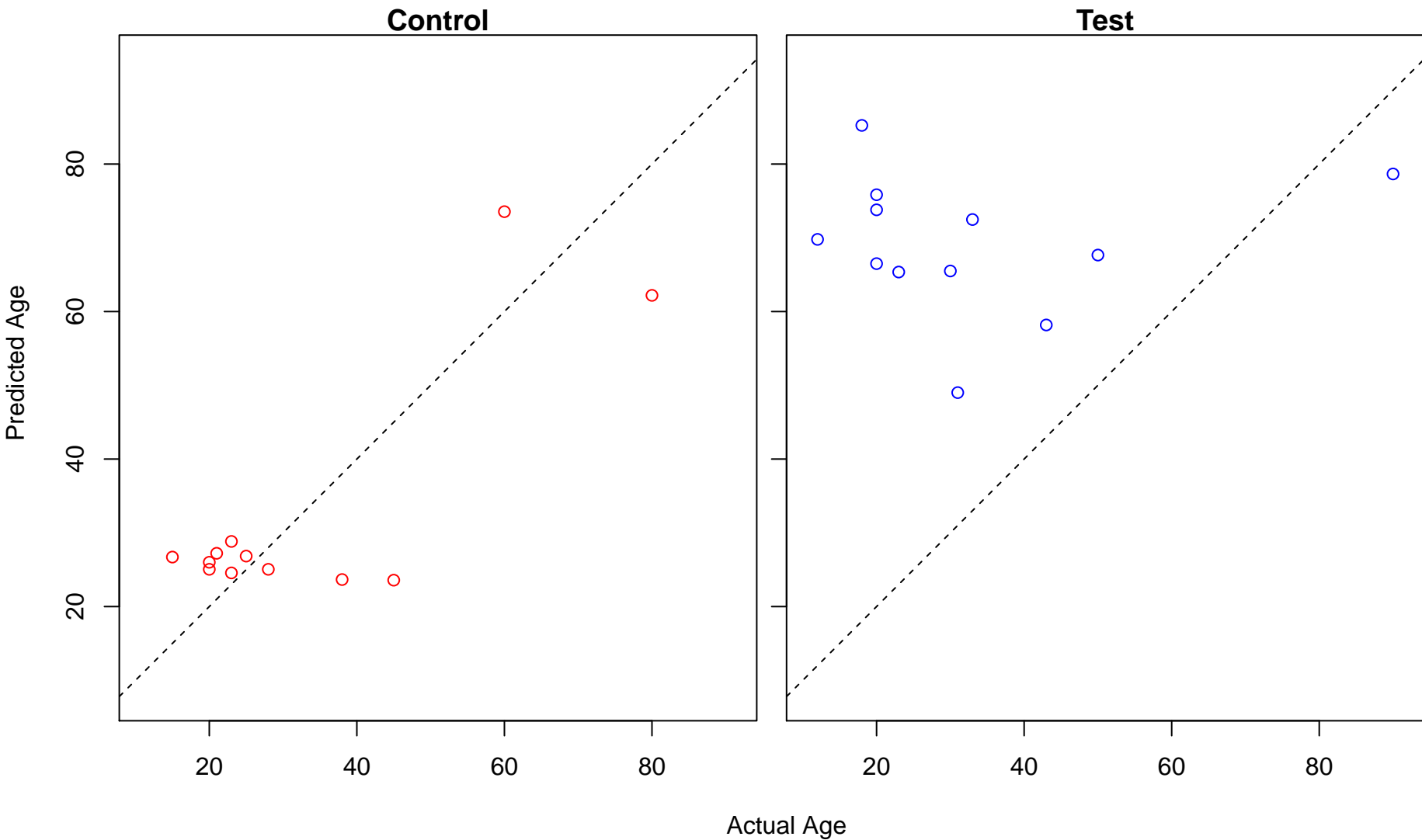
virion assembly (Score: 7.414196)



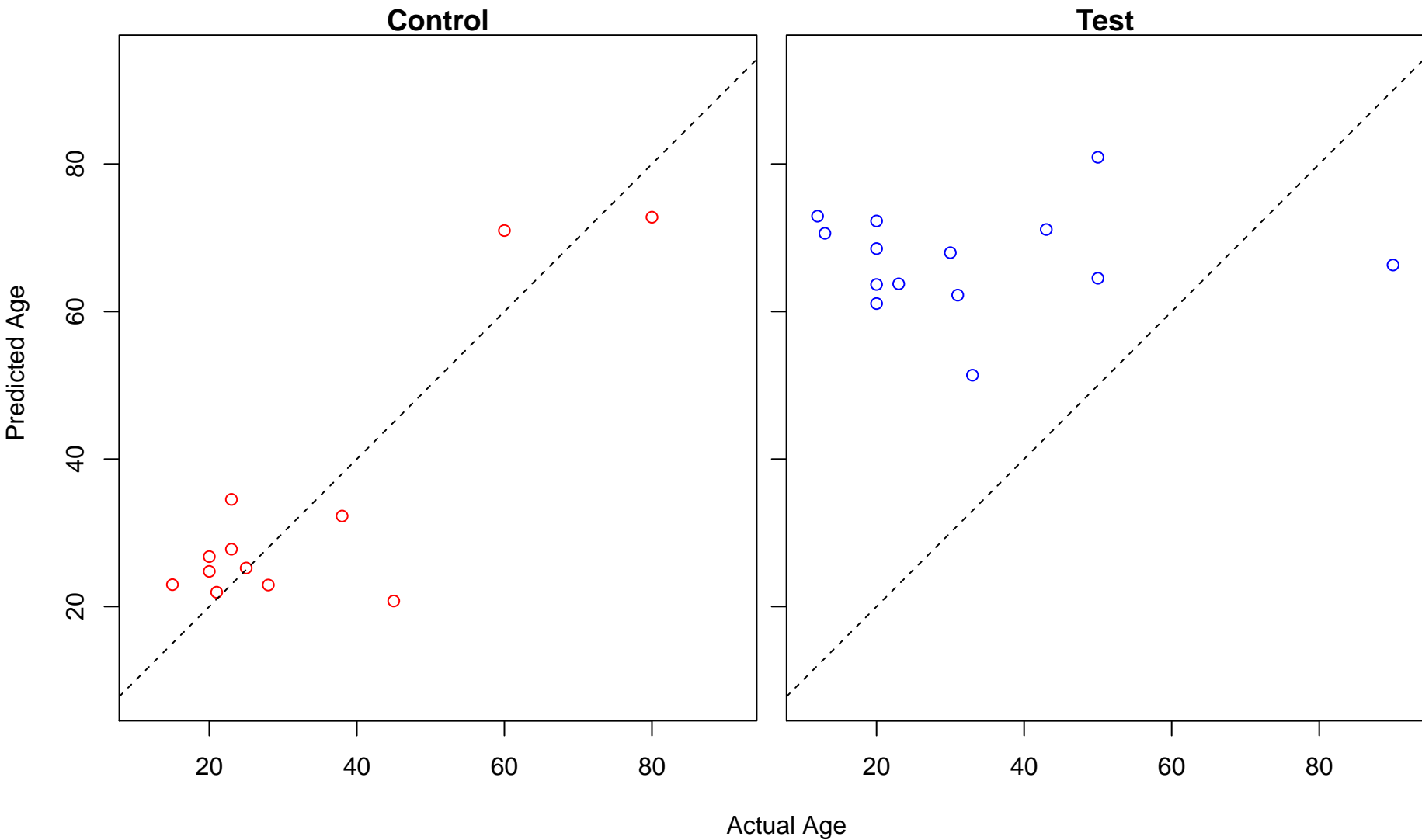
negative regulation of JNK cascade (Score: 7.406291)



ribosomal small subunit biogenesis (Score: 7.403426)

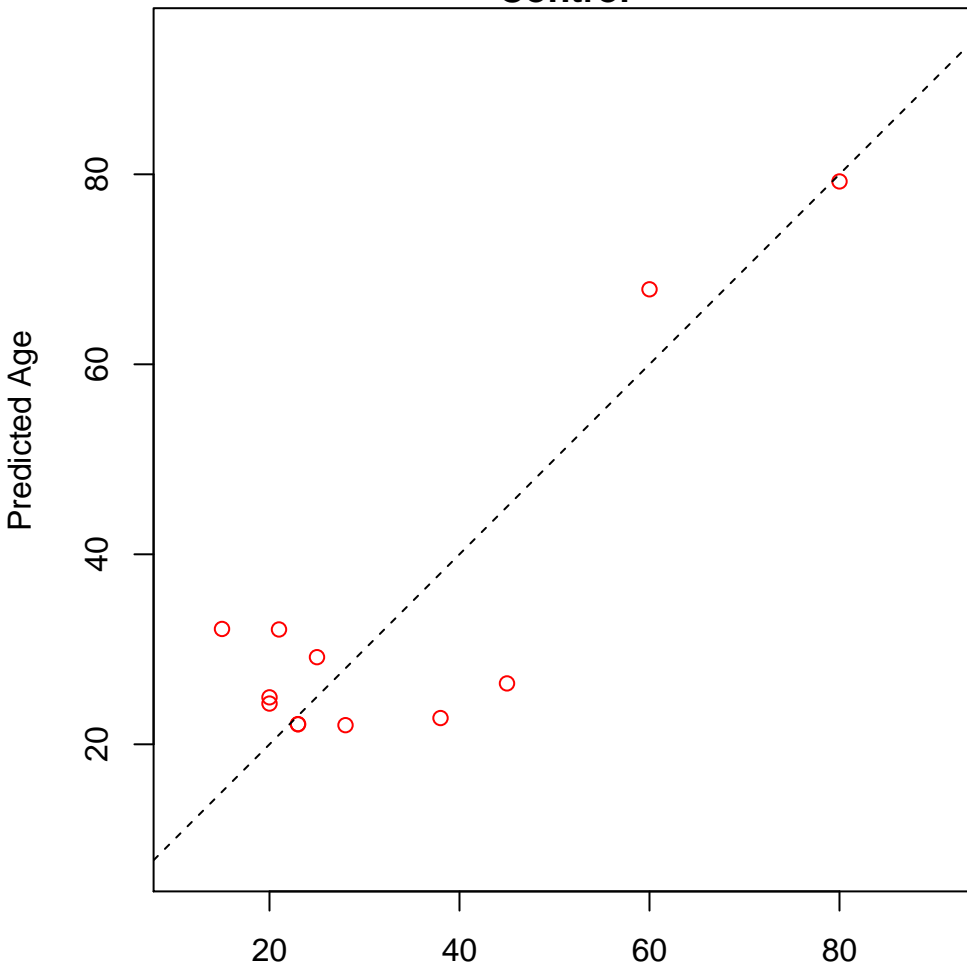


positive regulation of myoblast differentiation (Score: 7.401909)

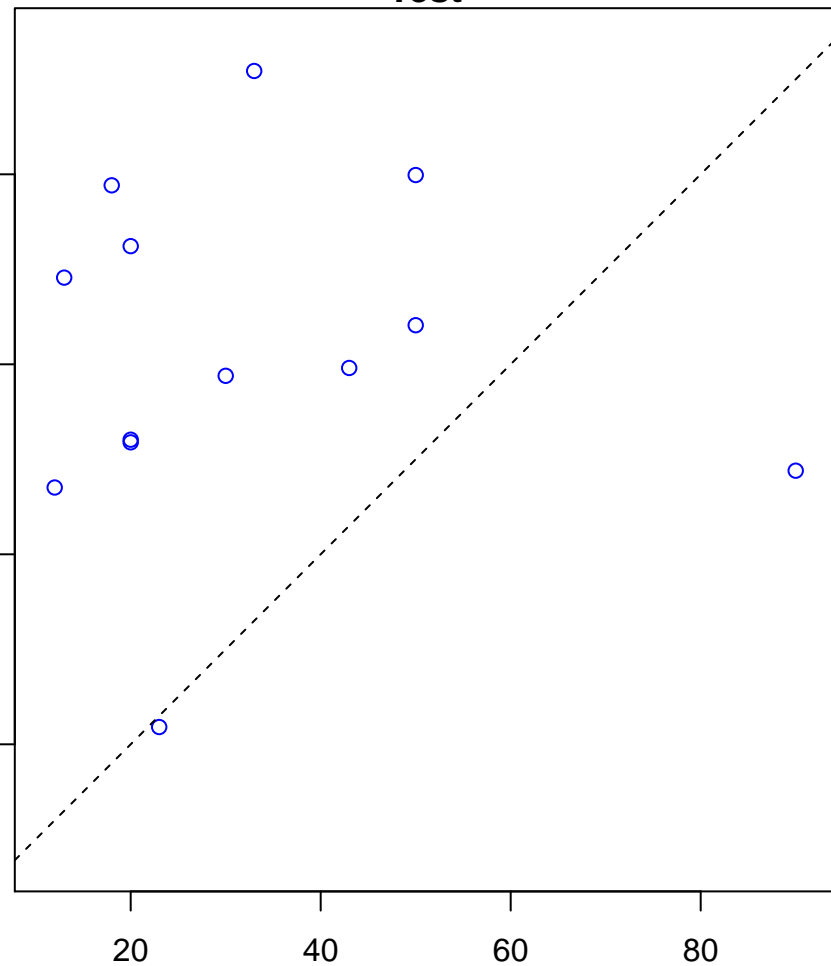


regulation of cell-substrate adhesion (Score: 7.398425)

Control

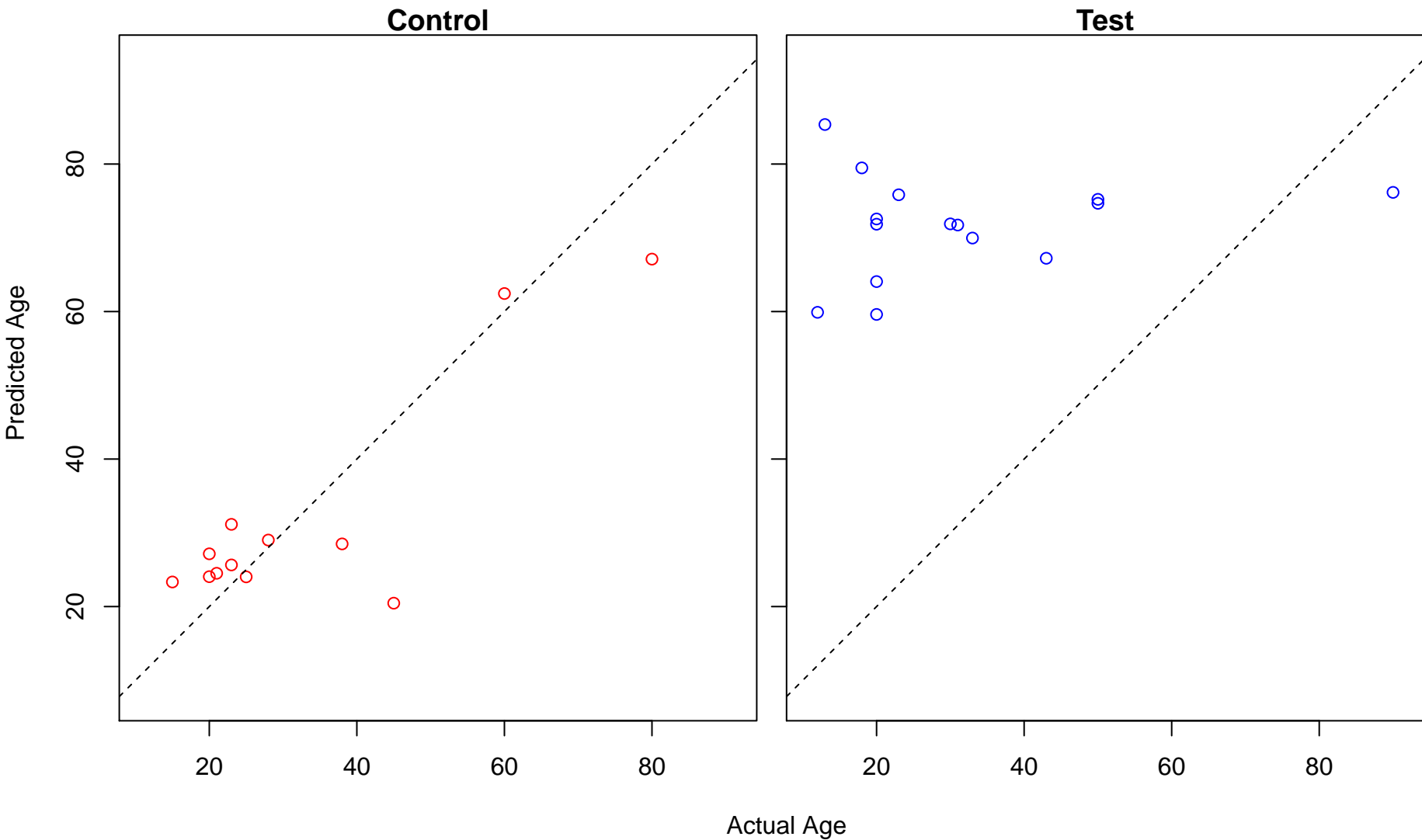


Test

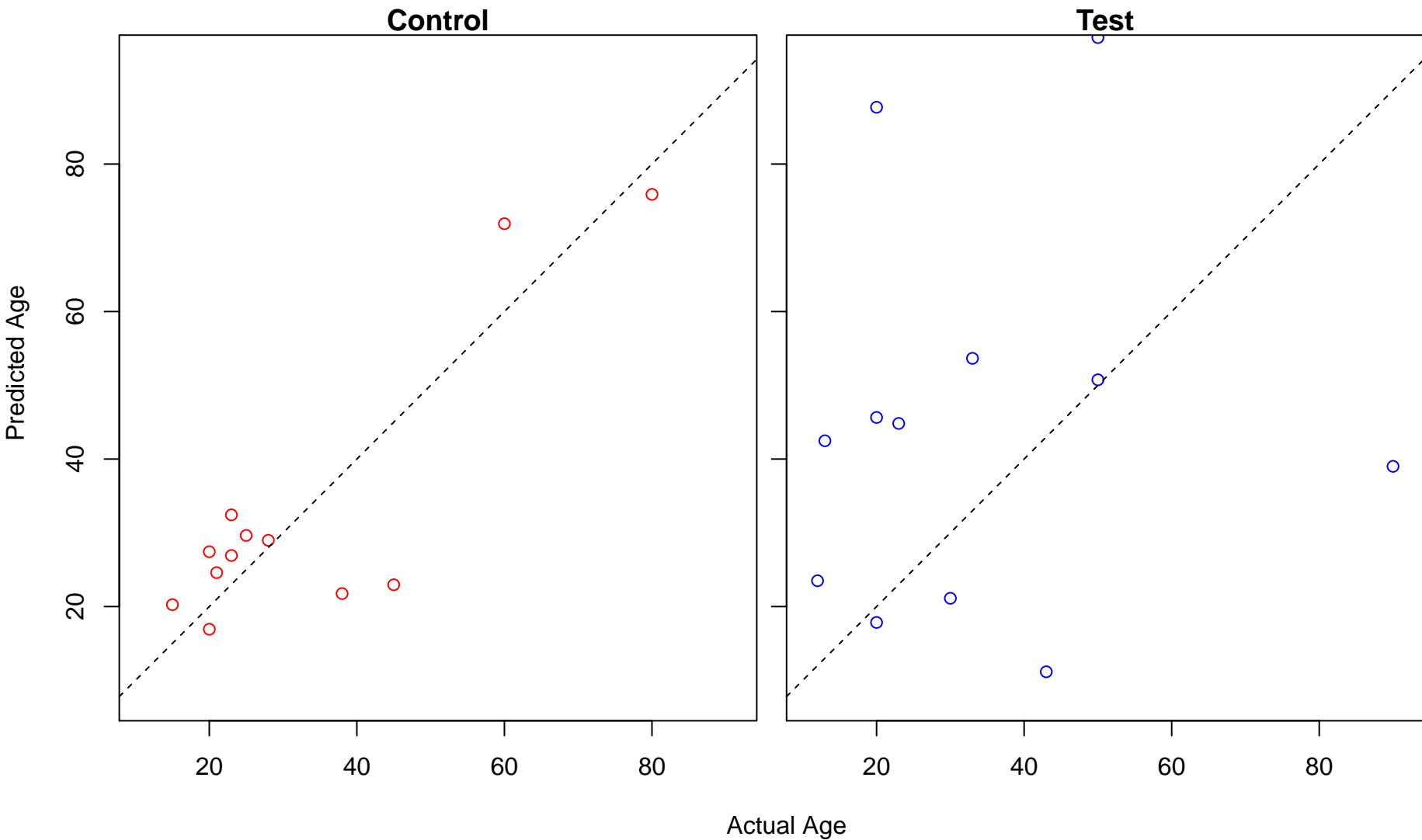


Actual Age

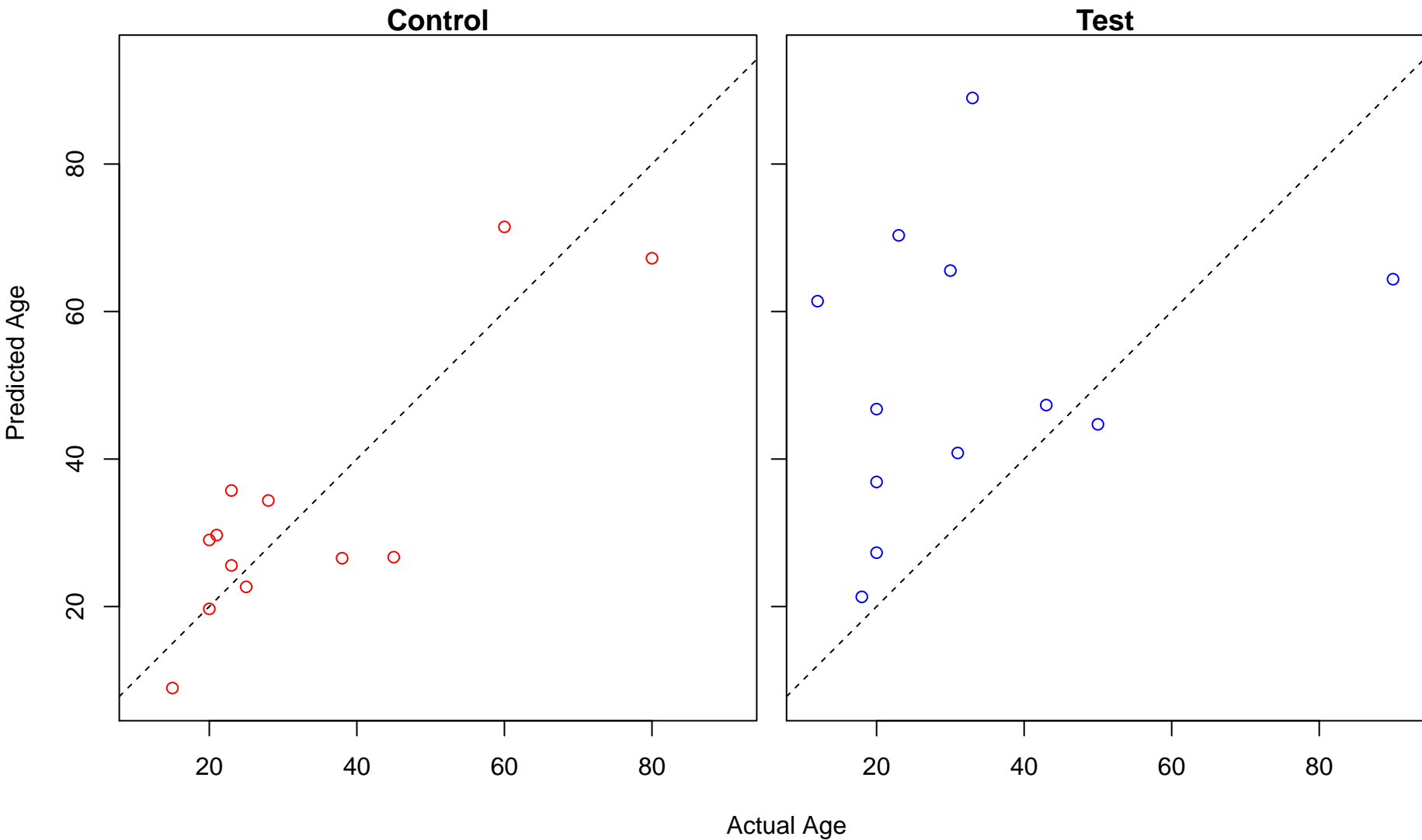
regulation of leukocyte differentiation (Score: 7.398114)



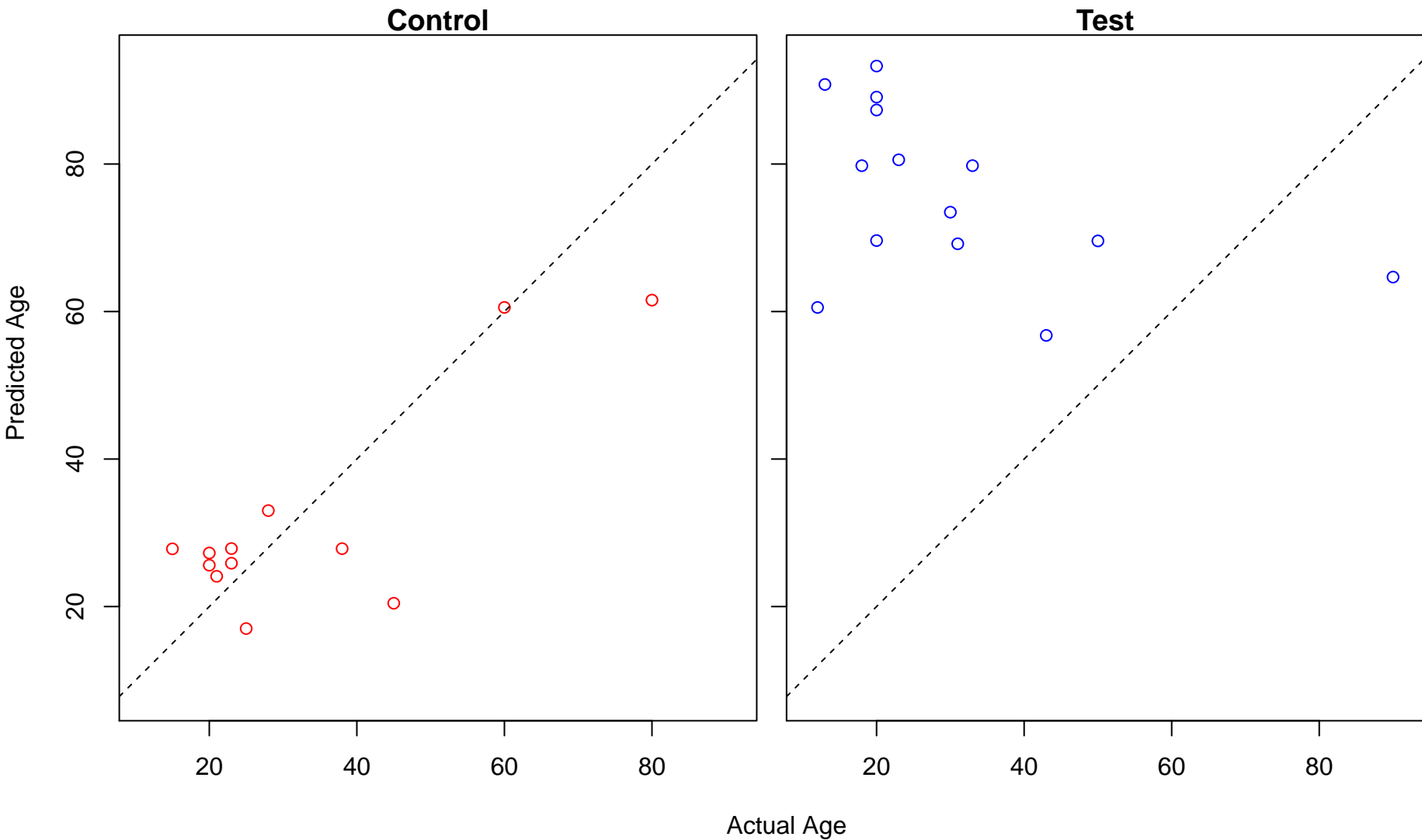
negative regulation of DNA biosynthetic process (Score: 7.396199)



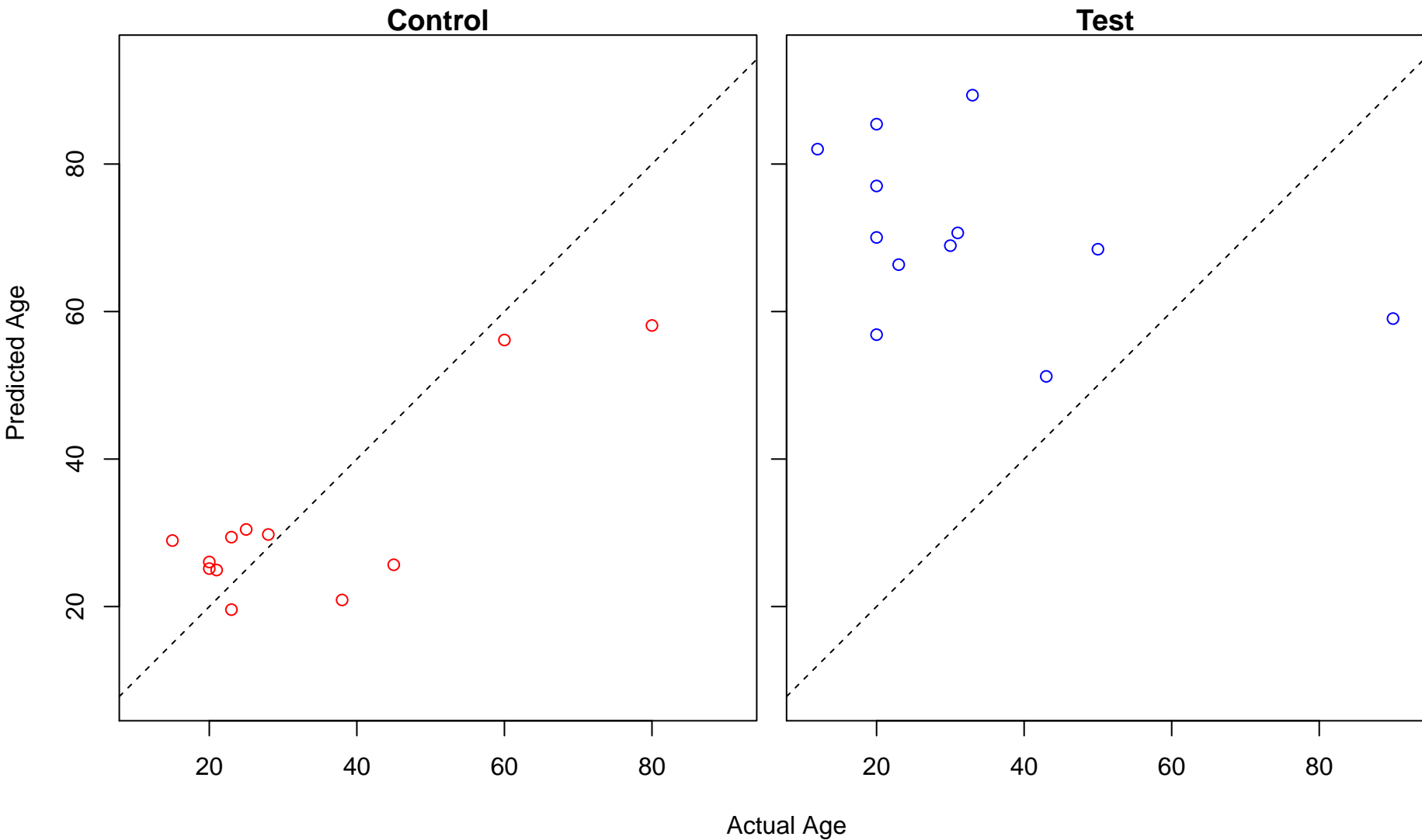
regulation of defense response to bacterium (Score: 7.390530)



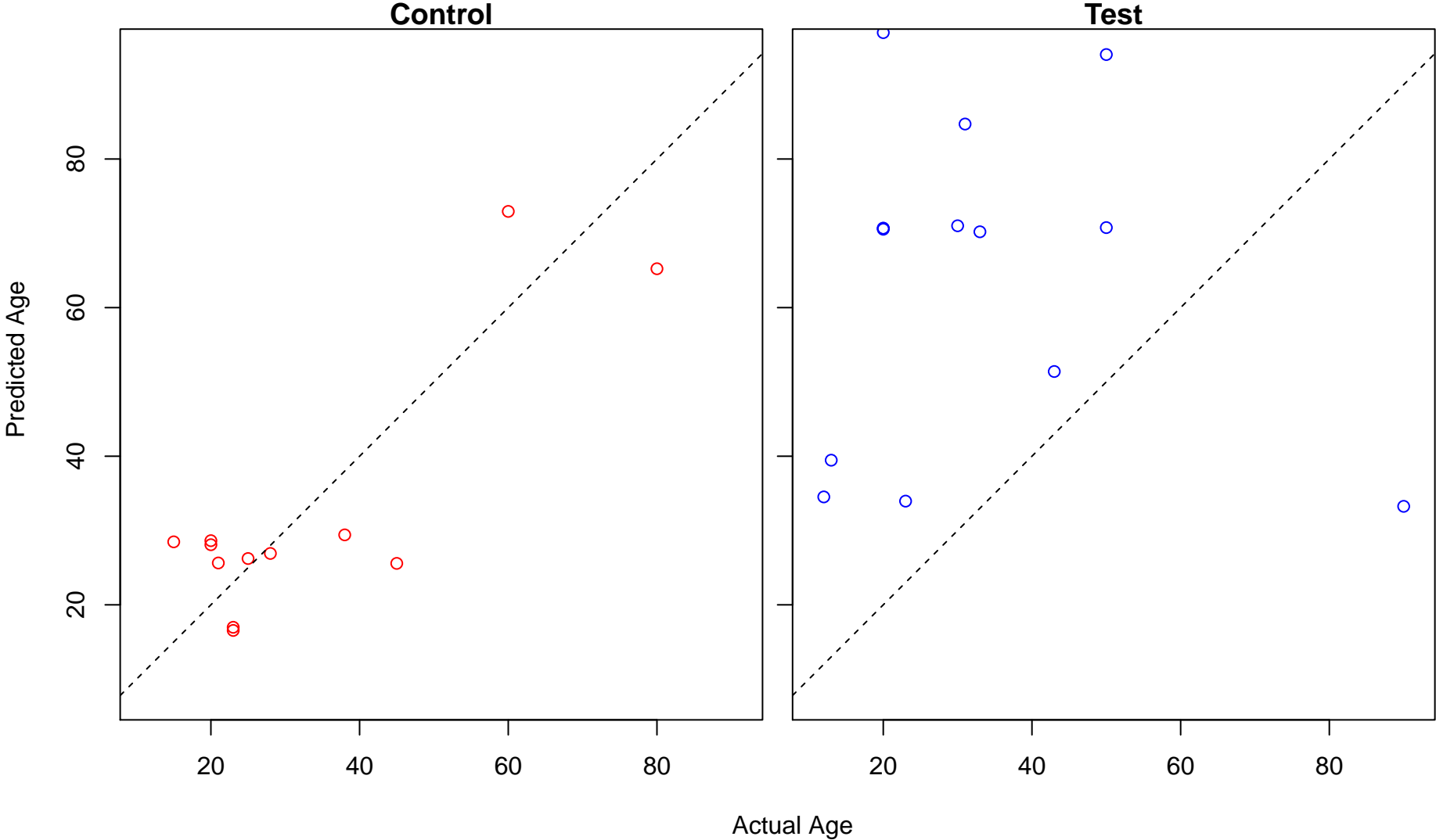
negative regulation of cardiac muscle cell differentiation (Score: 7.389202)



positive regulation of the force of heart contraction (Score: 7.386985)

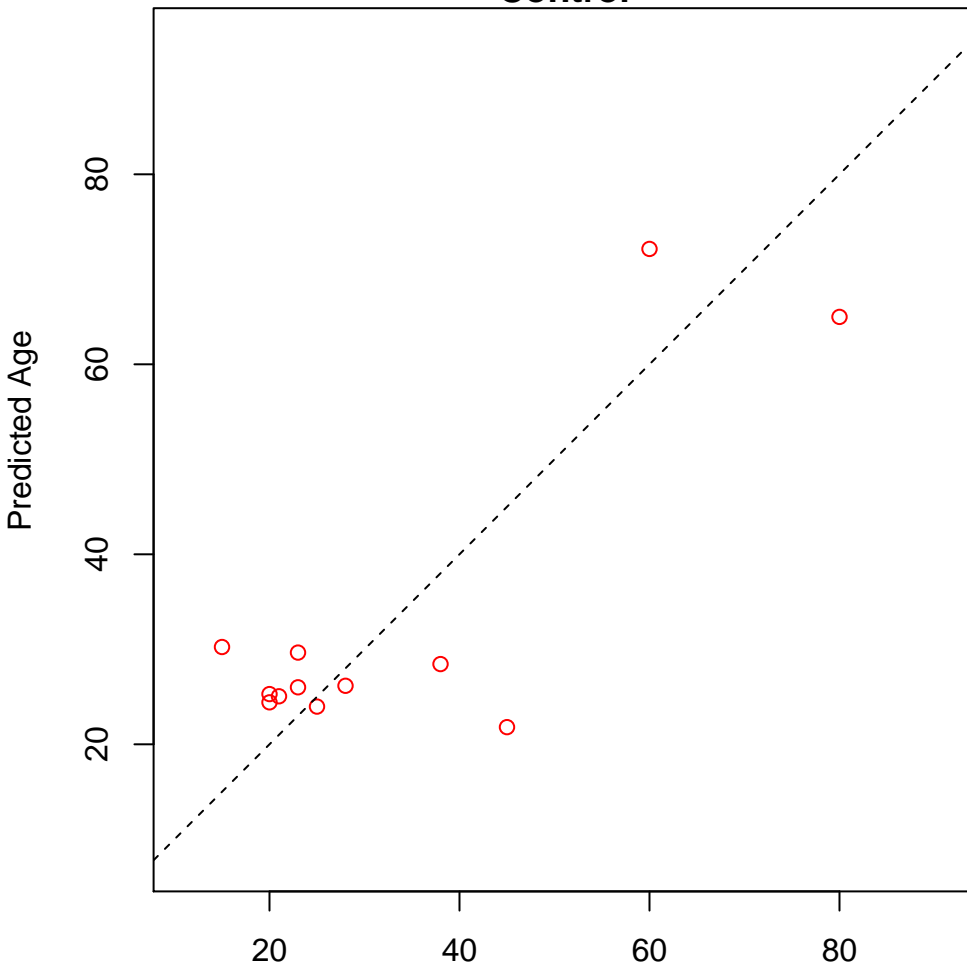


calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules (Score: 7.385)

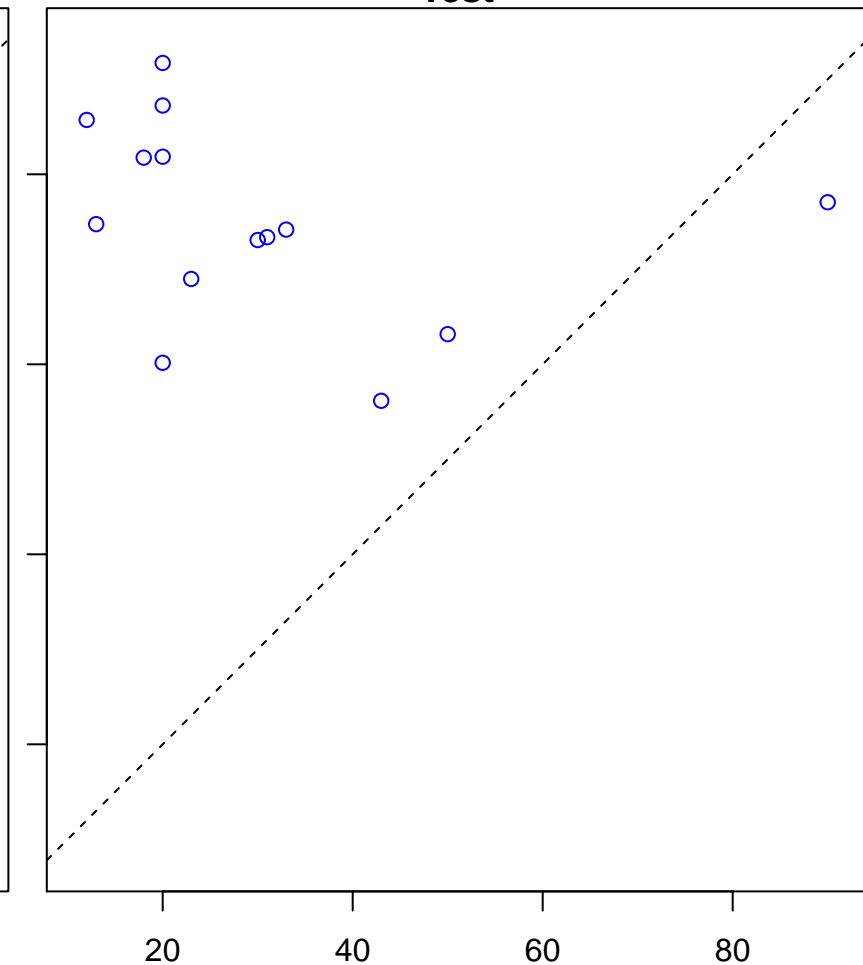


regulation of myeloid cell differentiation (Score: 7.385298)

Control

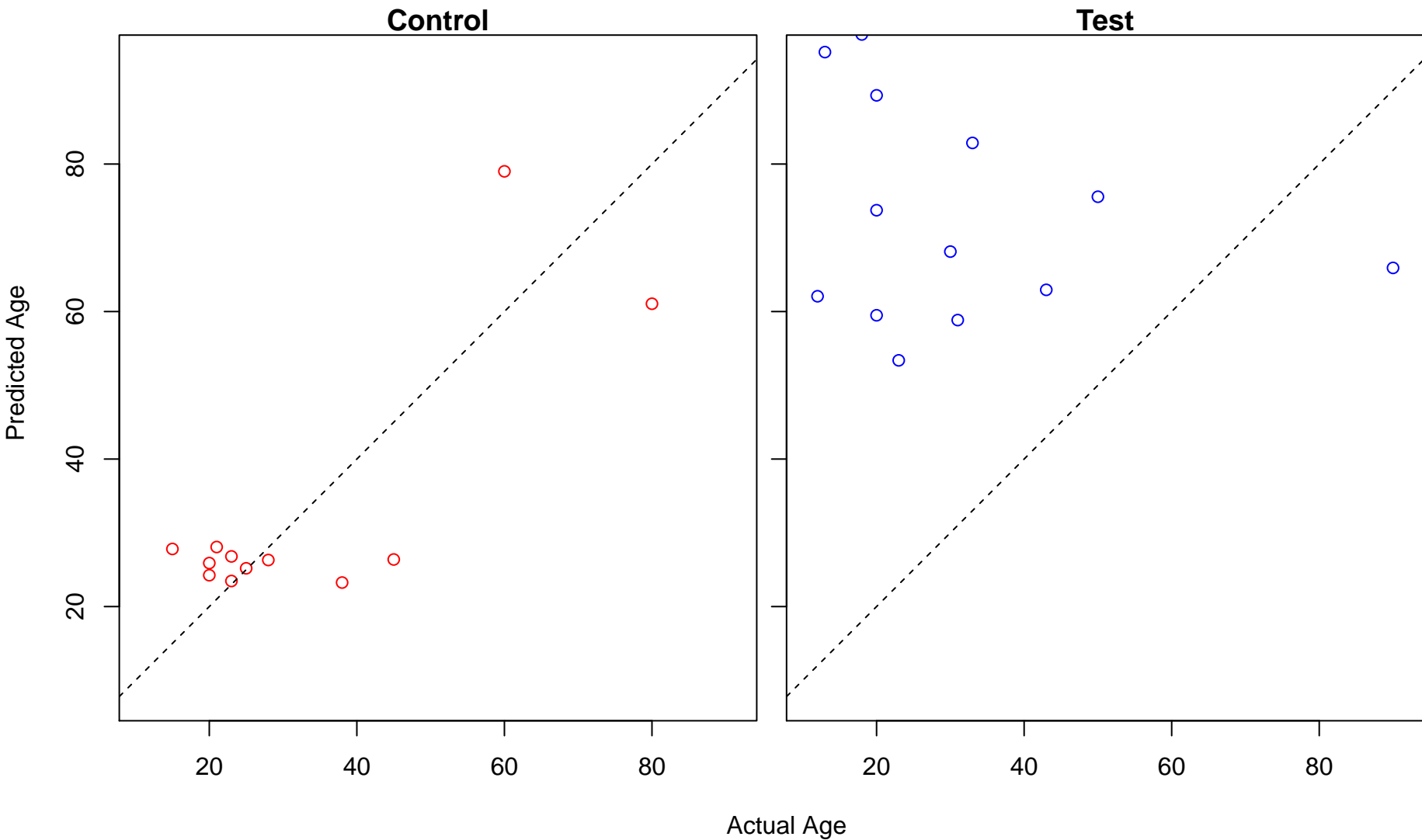


Test



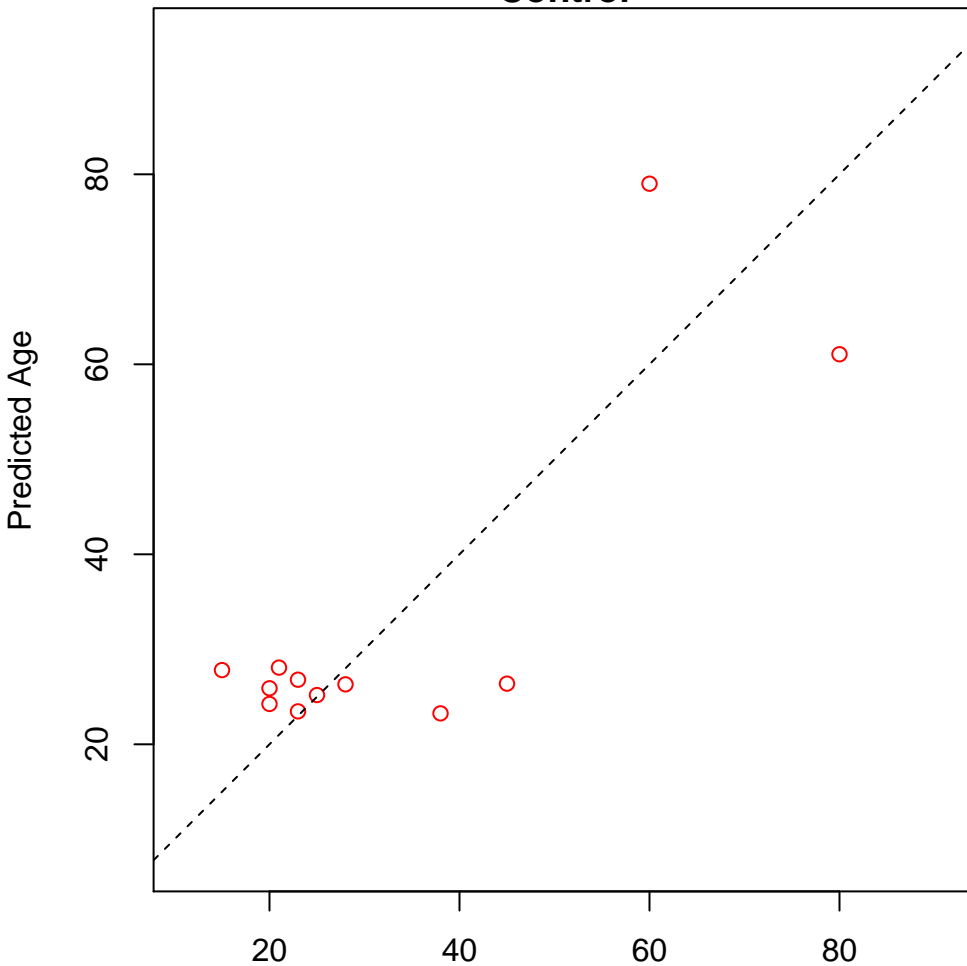
Actual Age

endosome to melanosome transport (Score: 7.381685)

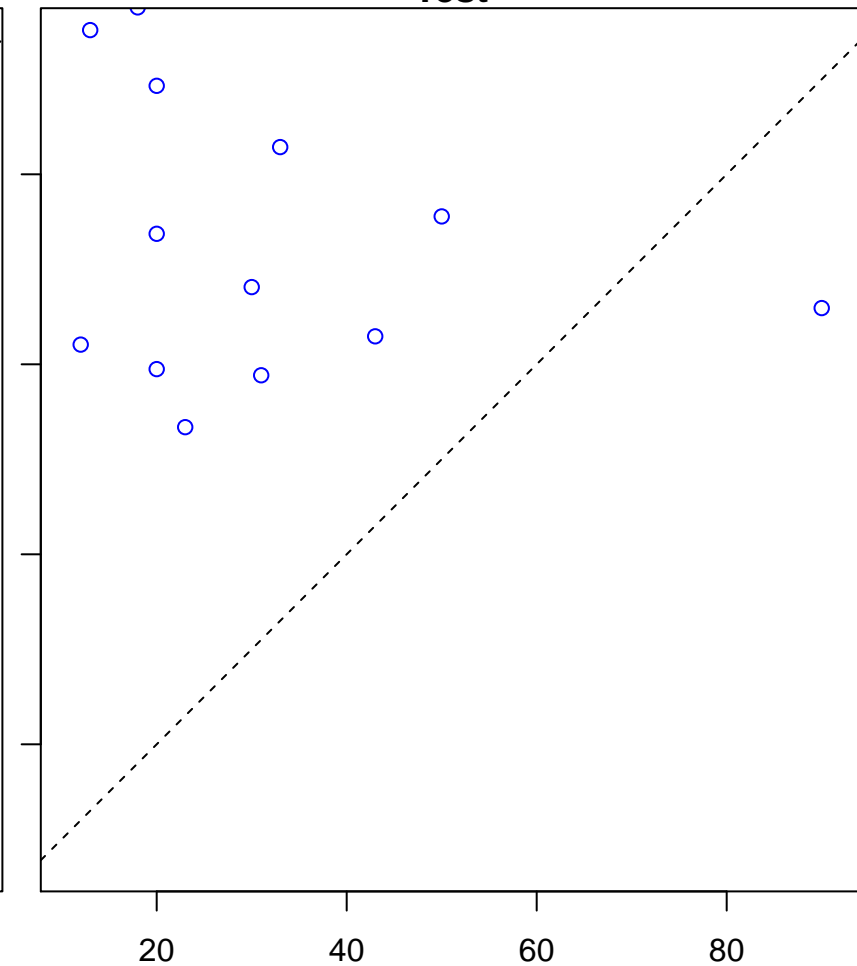


endosome to pigment granule transport (Score: 7.381685)

Control

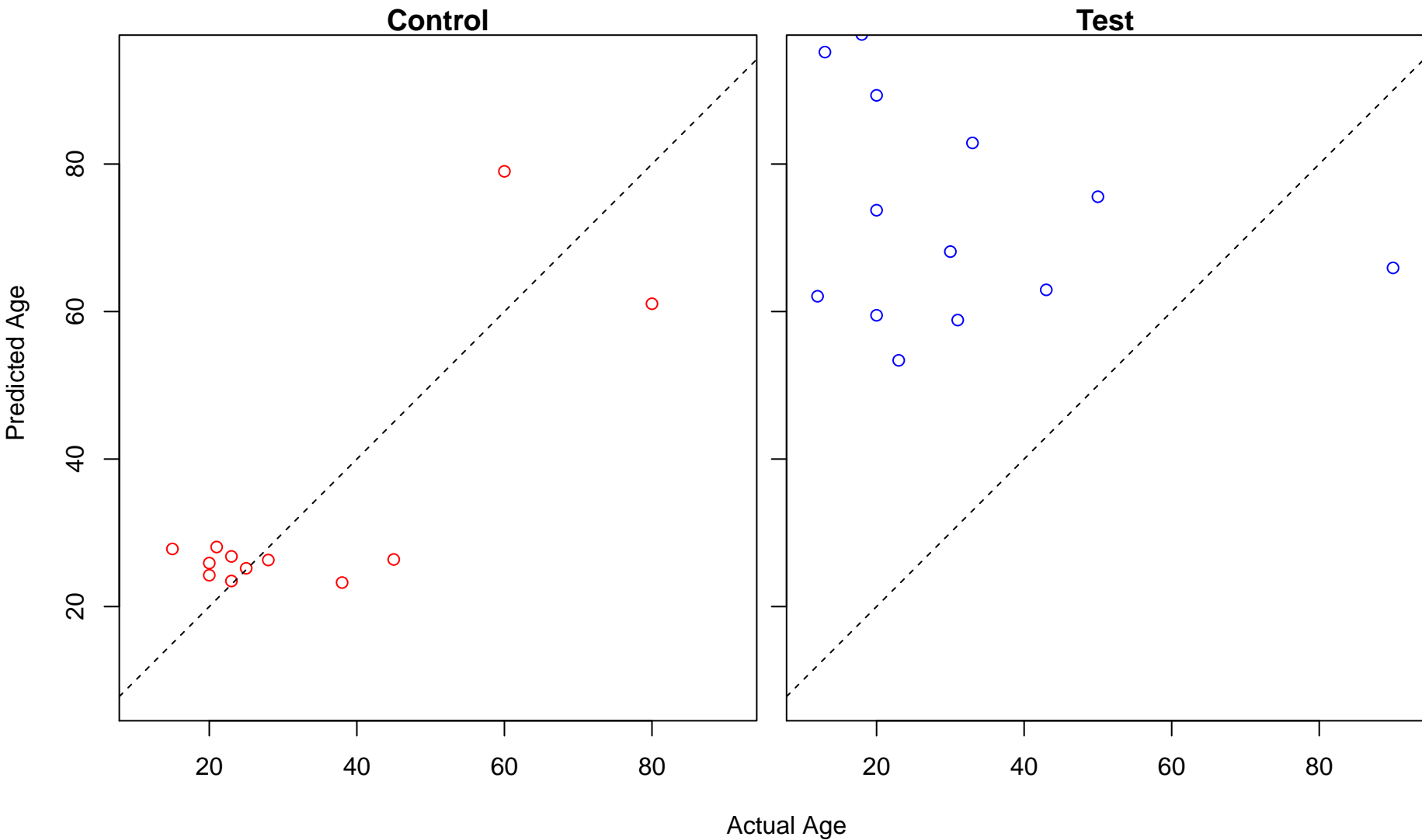


Test

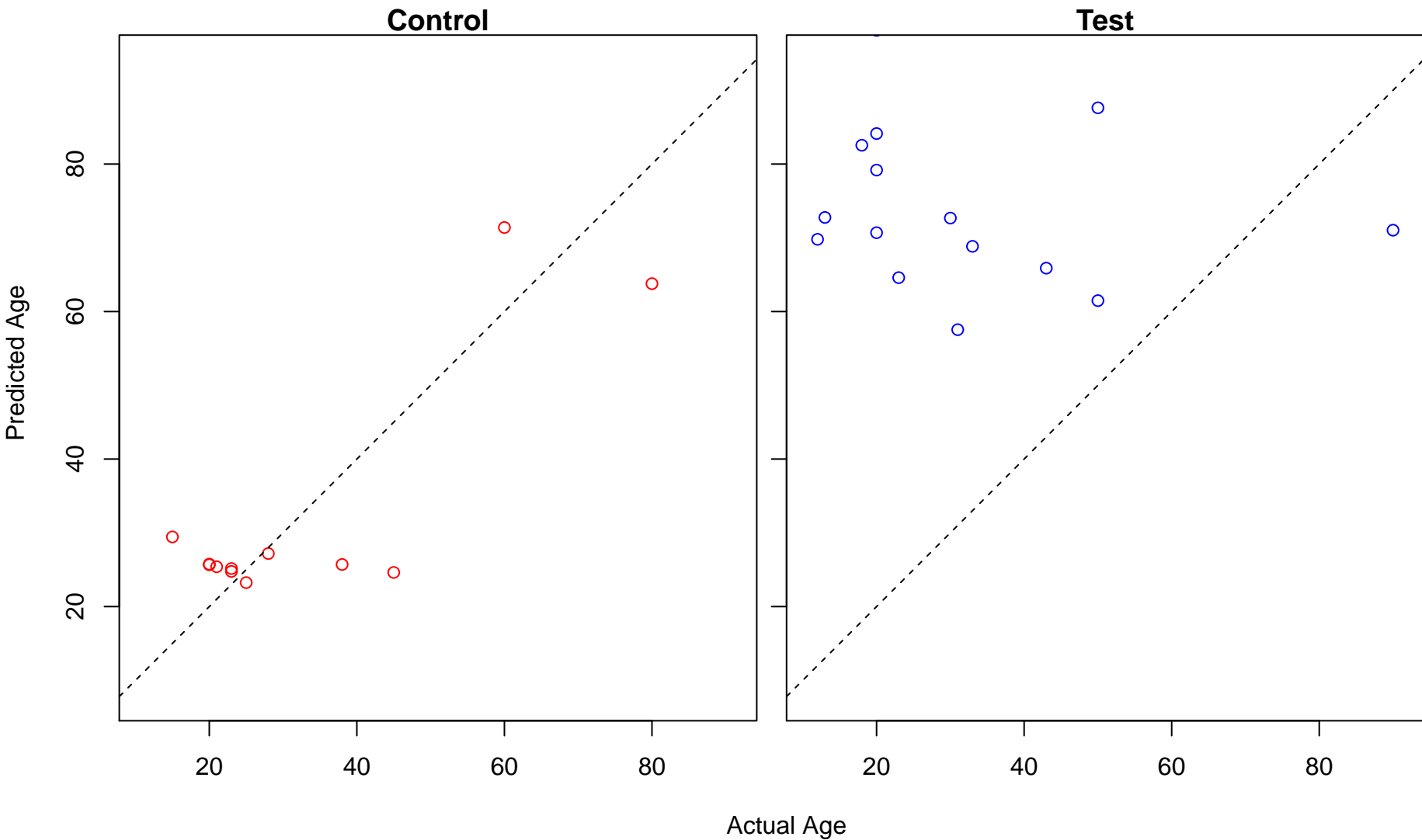


Actual Age

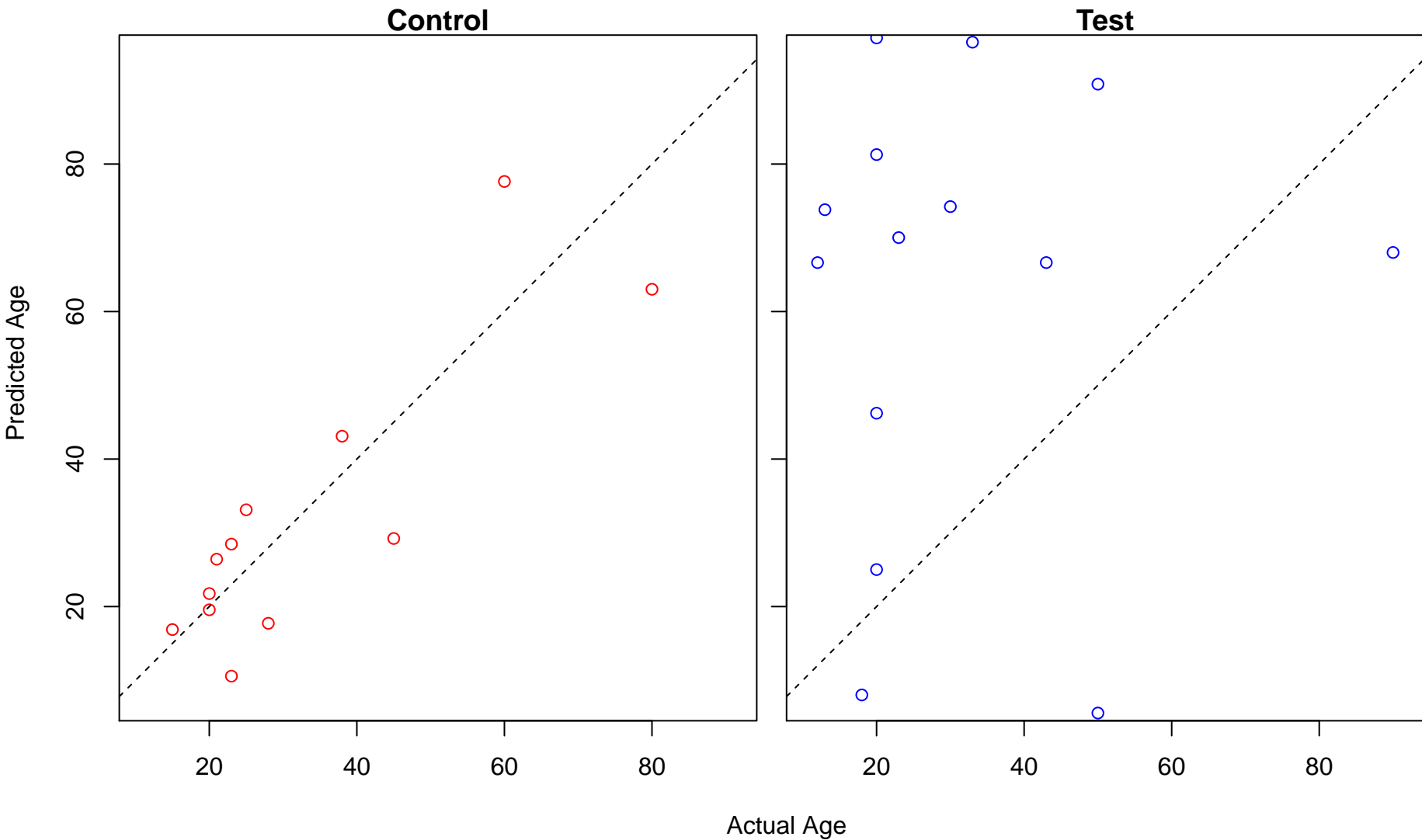
pigment granule maturation (Score: 7.381685)



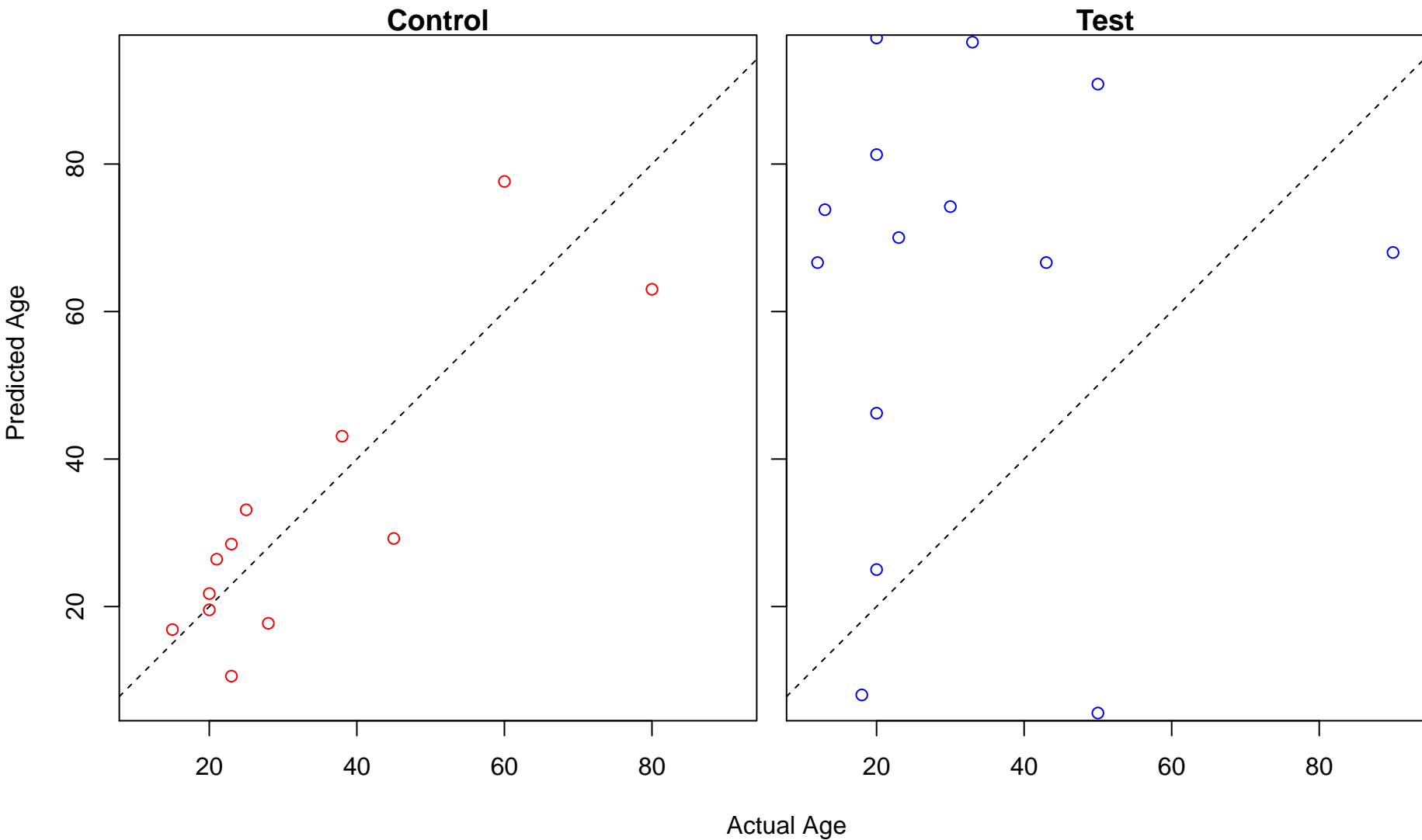
regulation of TOR signaling (Score: 7.375716)



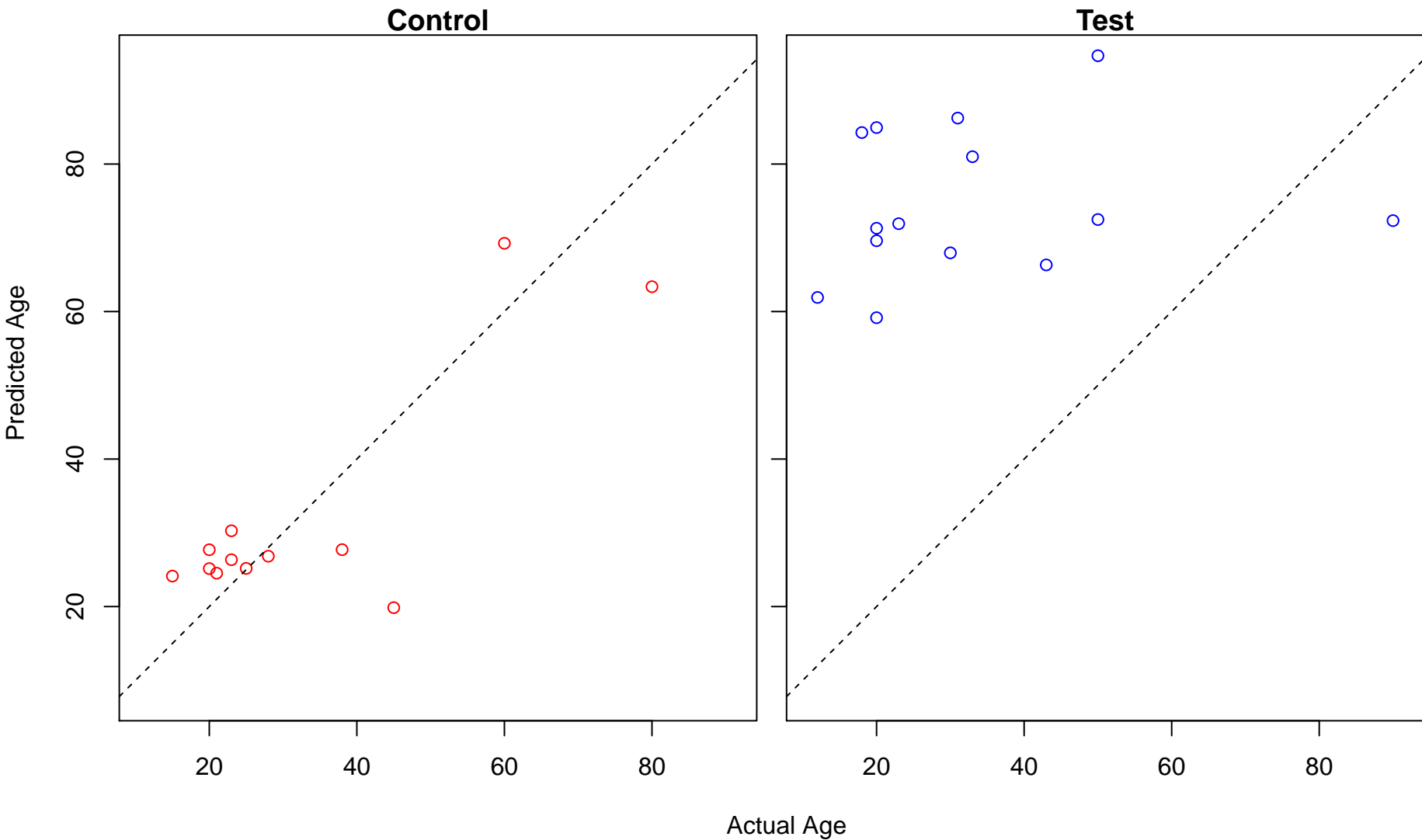
negative regulation of chondrocyte differentiation (Score: 7.375448)



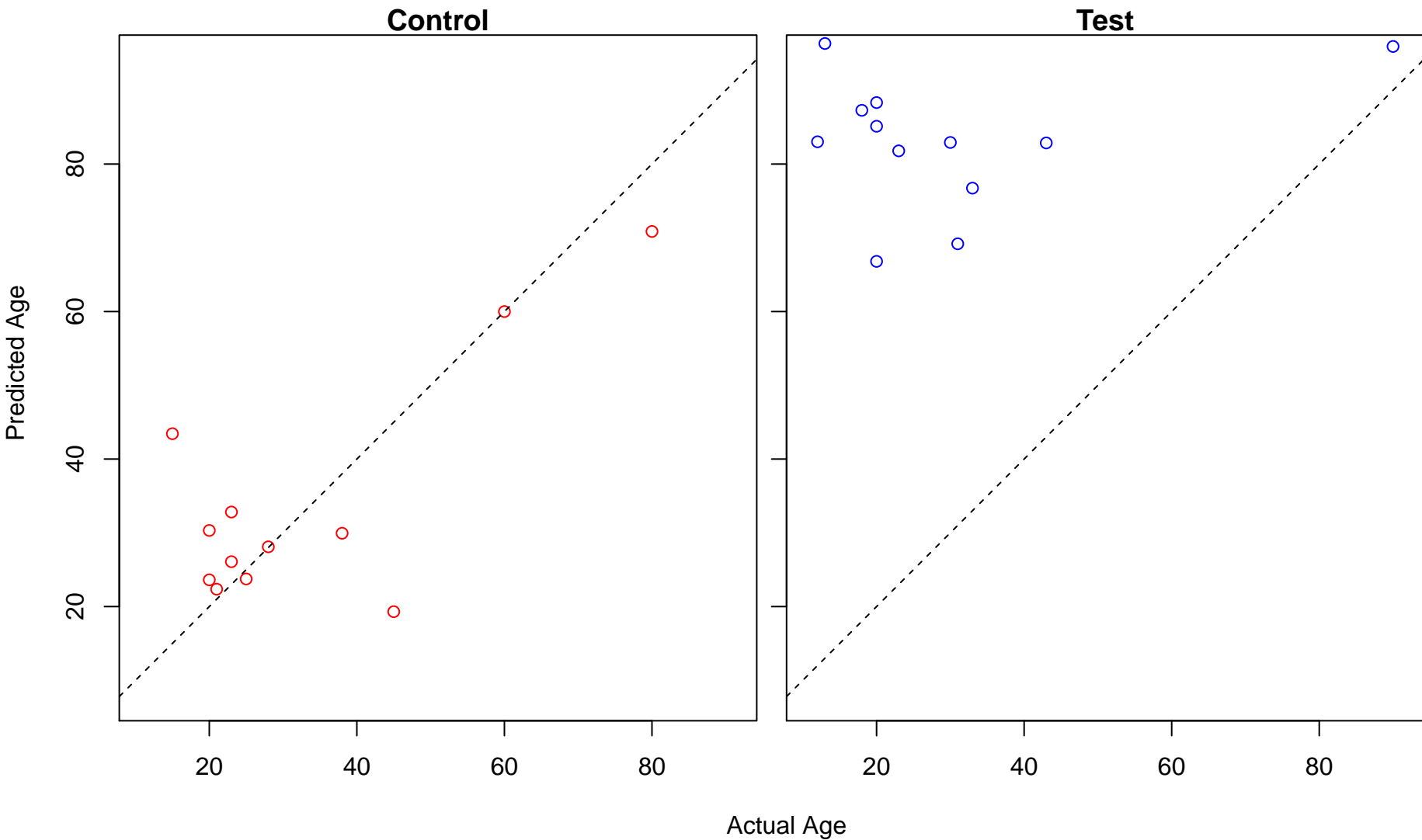
negative regulation of cartilage development (Score: 7.375448)



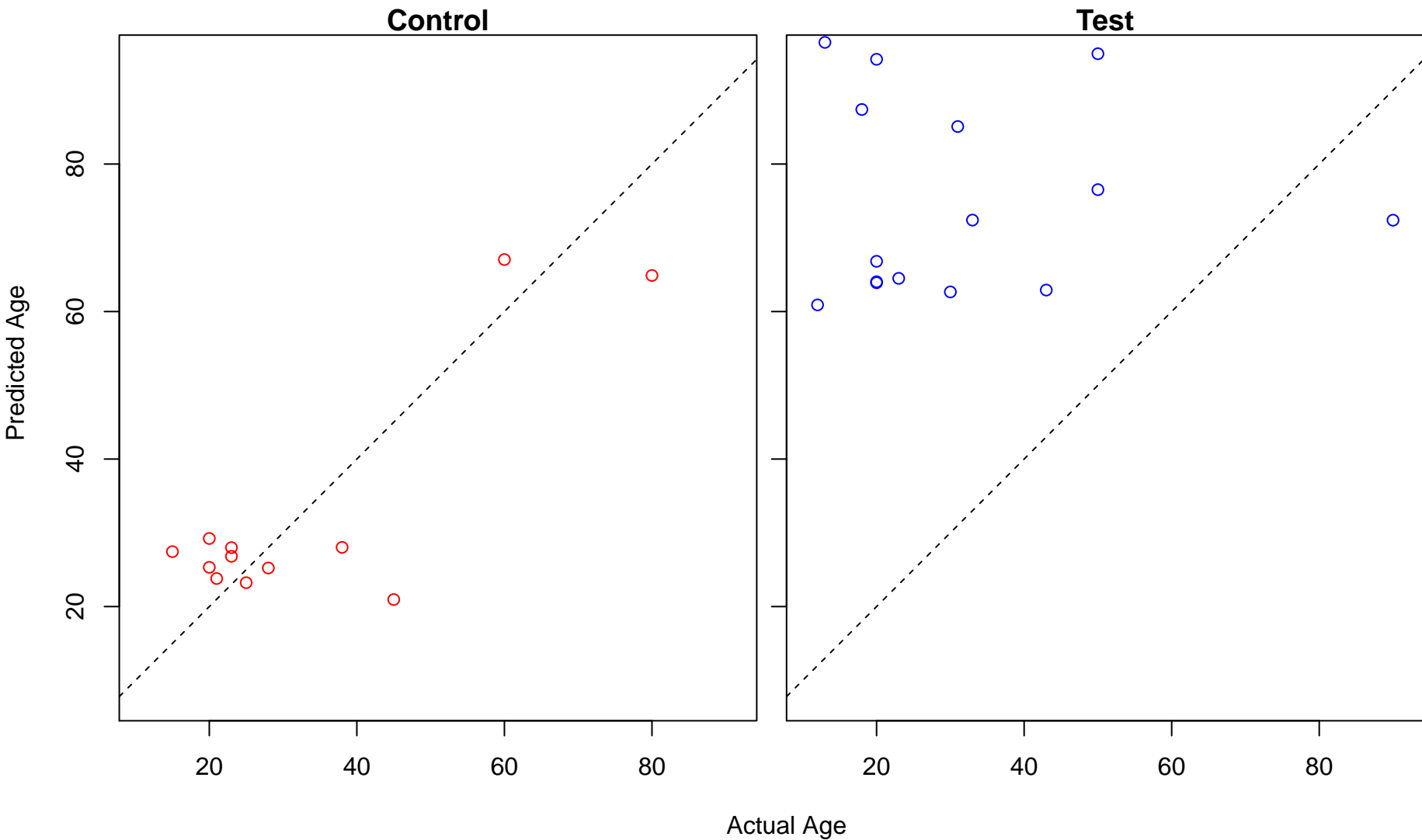
positive regulation of leukocyte mediated immunity (Score: 7.373133)



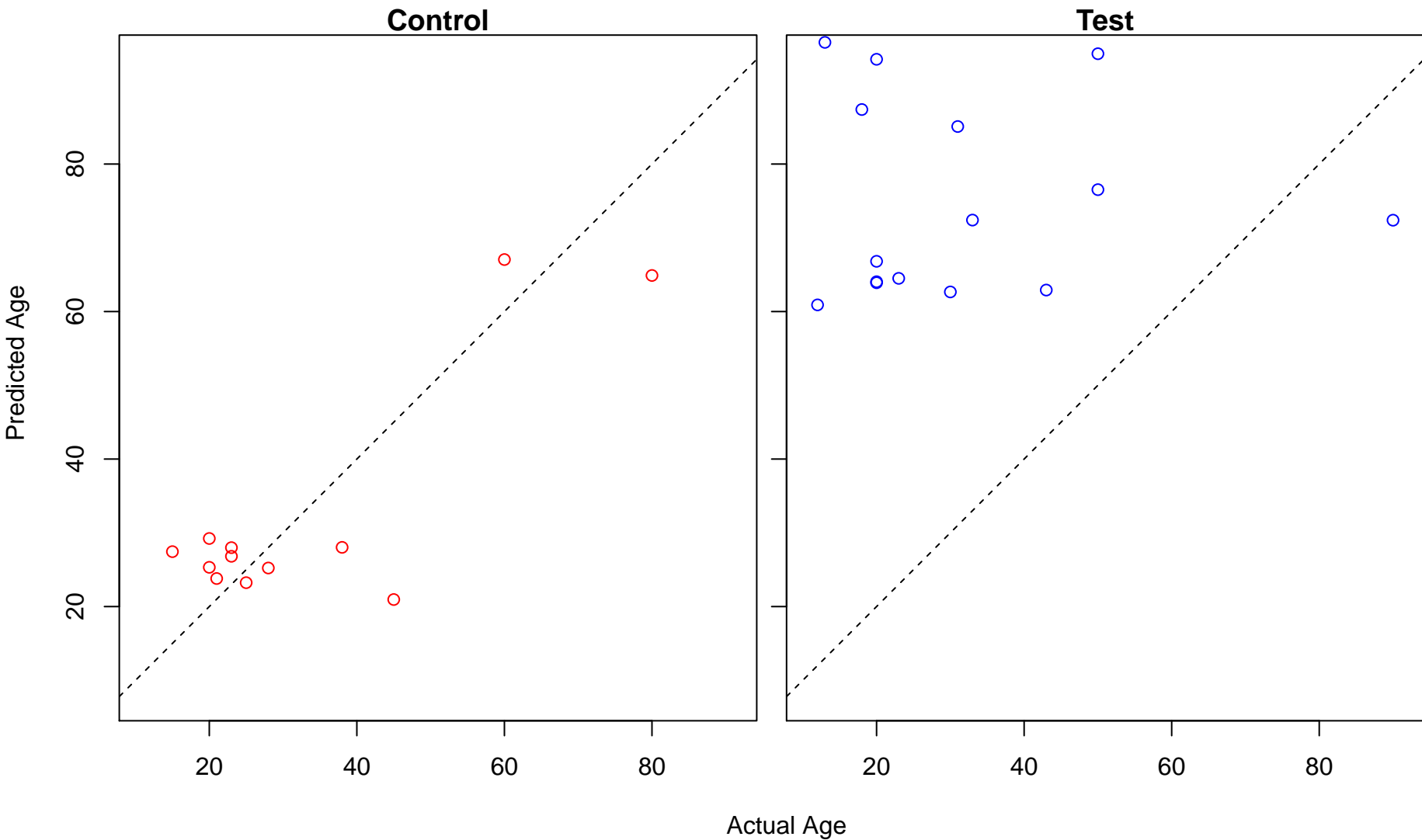
regulation of fibroblast growth factor receptor signaling pathway (Score: 7.371580)



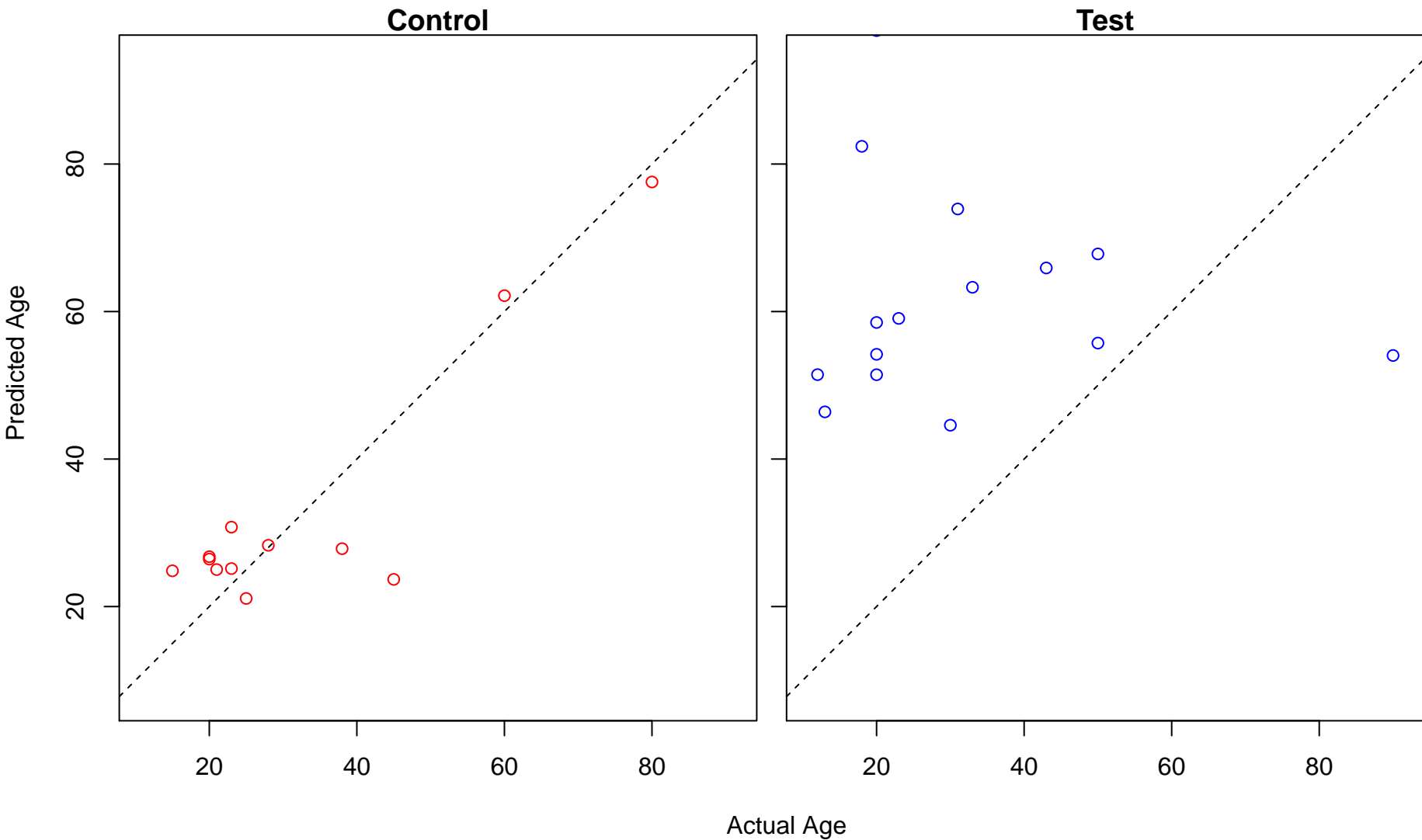
antibacterial humoral response (Score: 7.369603)



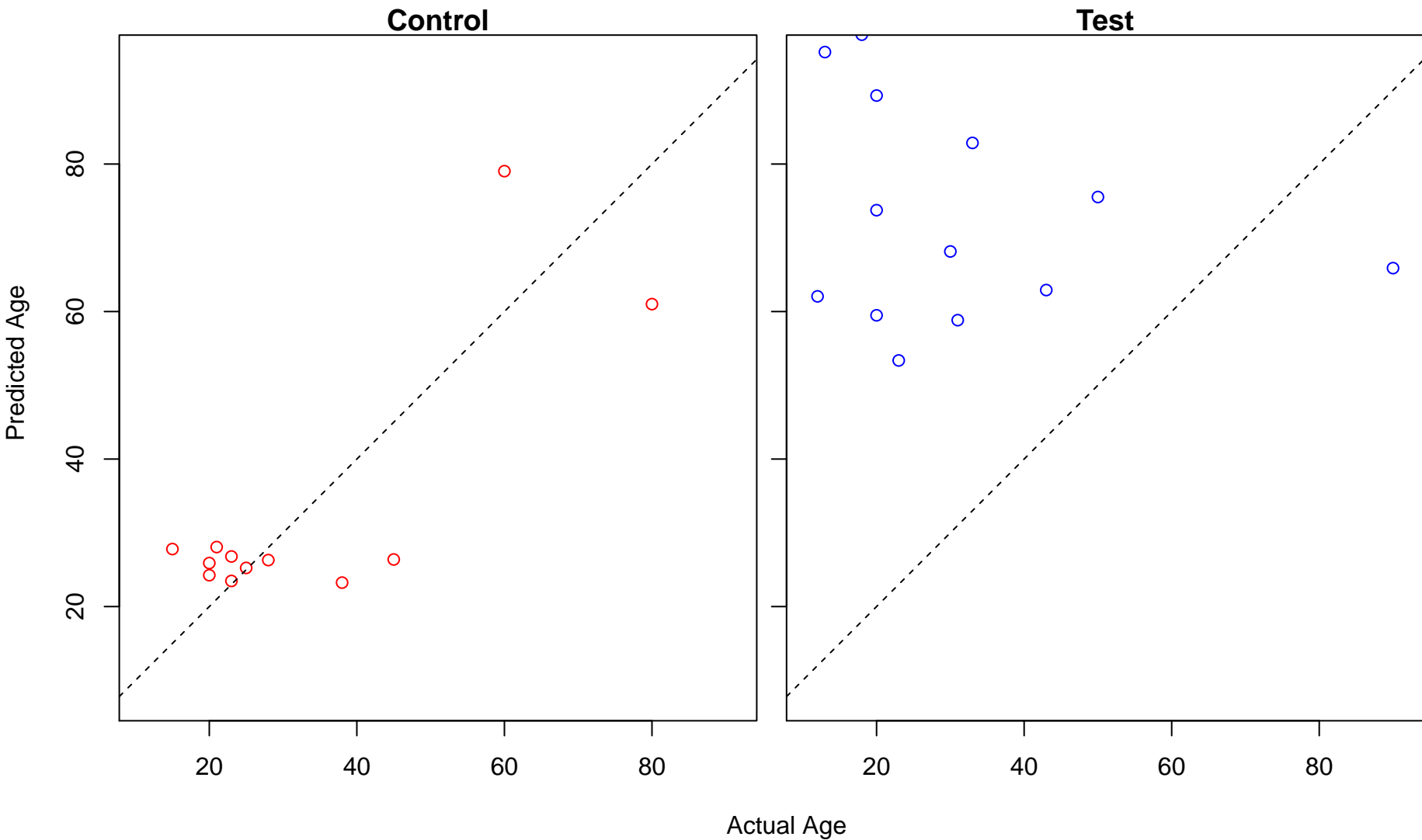
antimicrobial humoral response (Score: 7.369595)



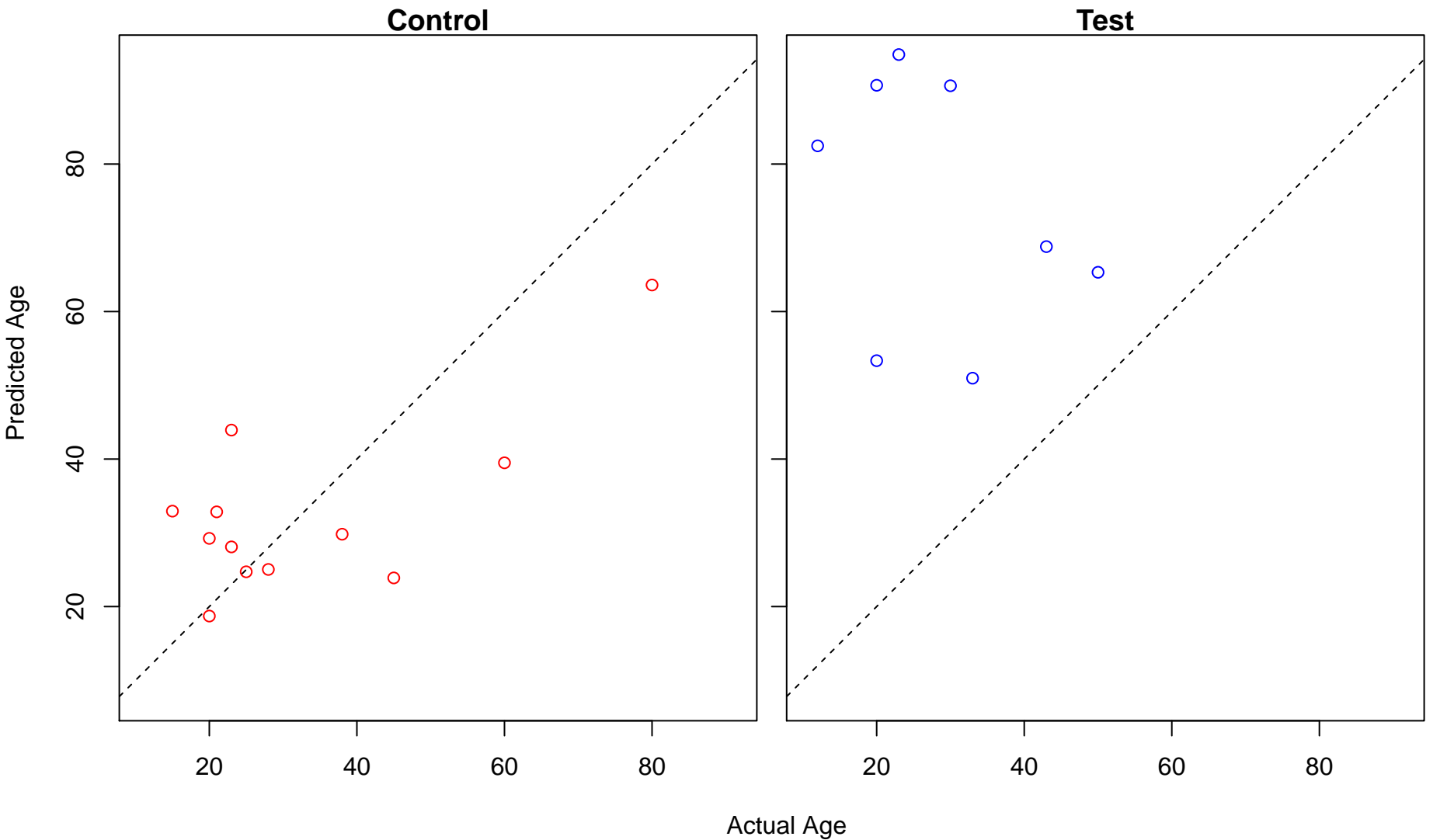
Wnt signaling pathway (Score: 7.368984)



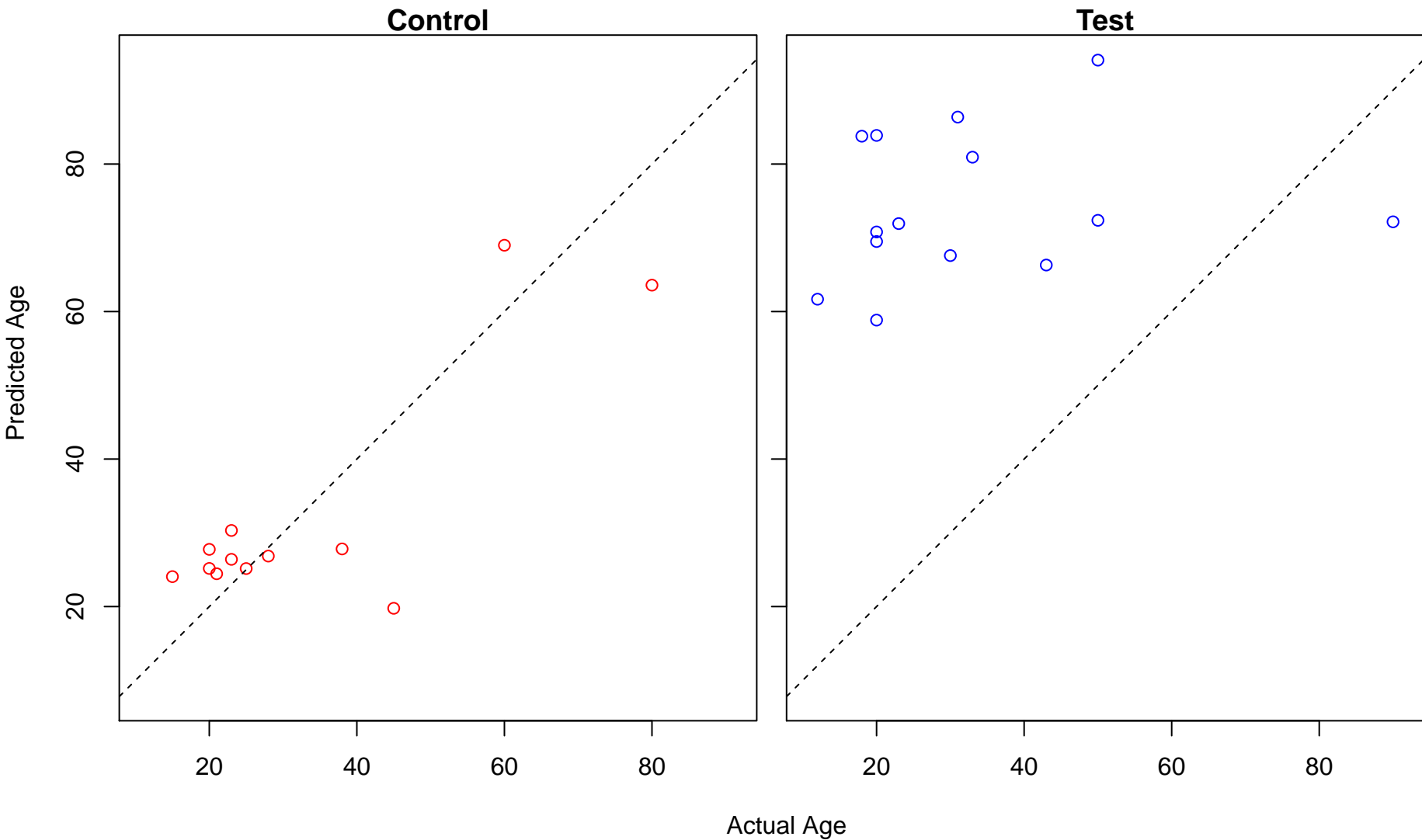
pigment cell differentiation (Score: 7.366480)



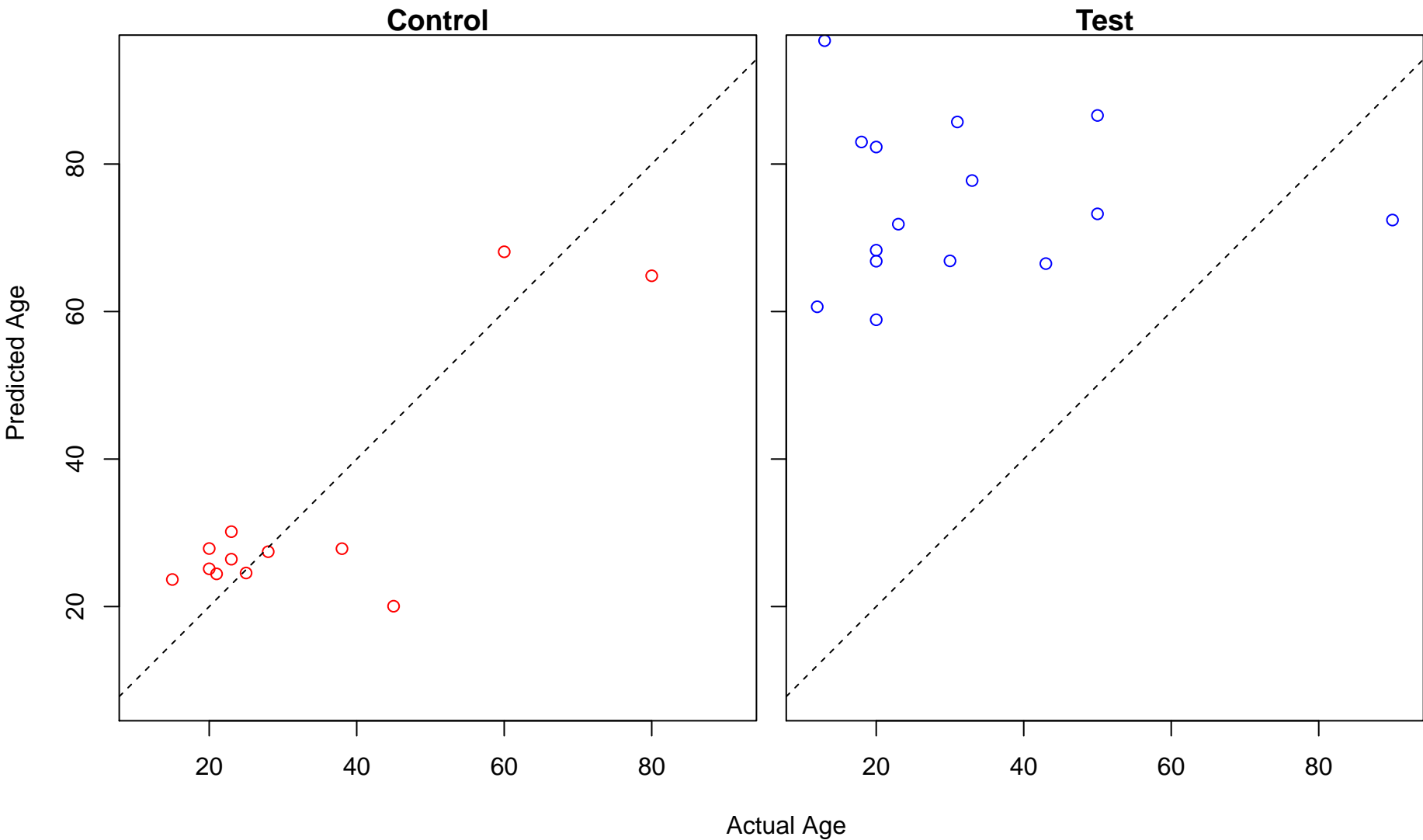
Correlation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II (Score)



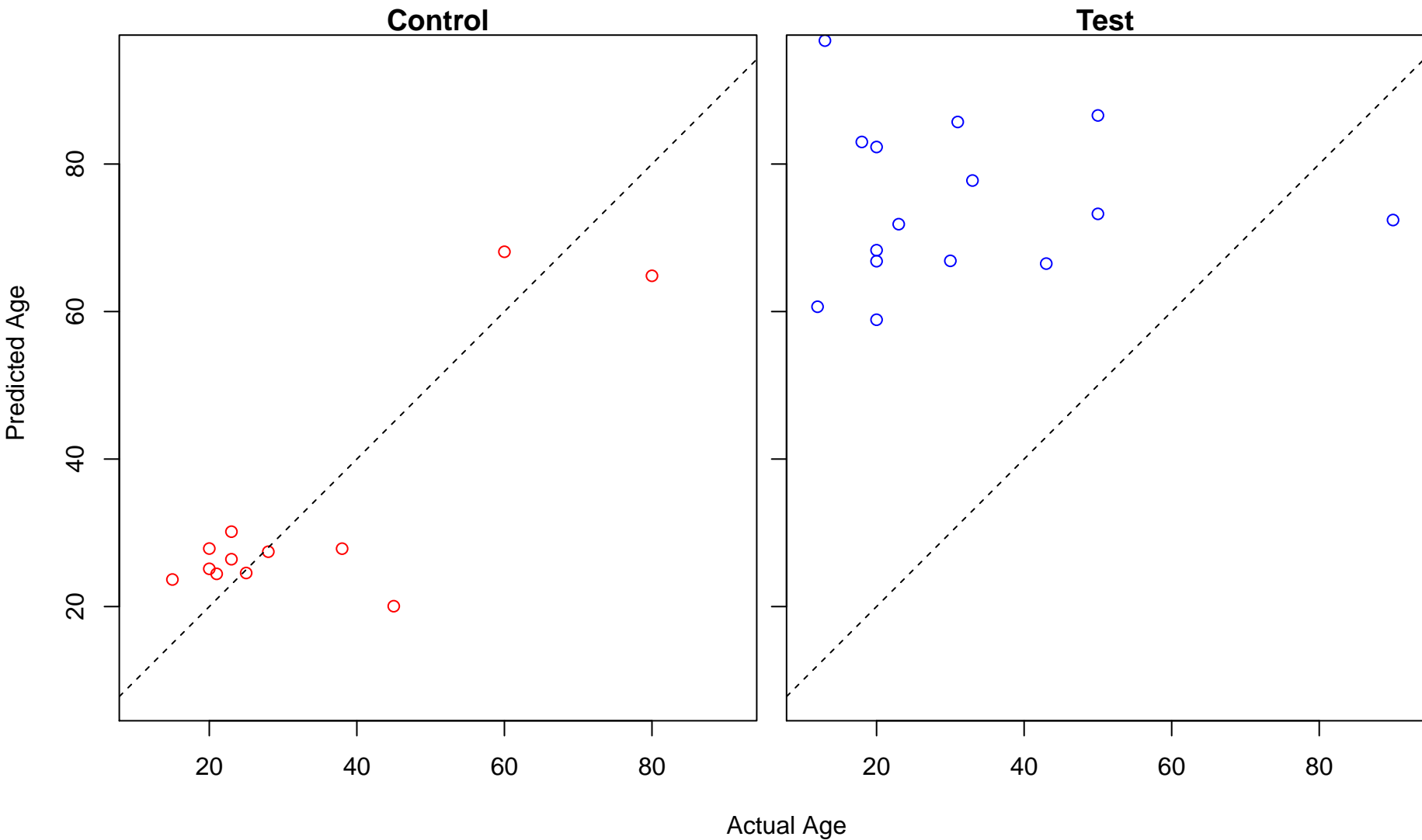
positive regulation of lymphocyte mediated immunity (Score: 7.363141)



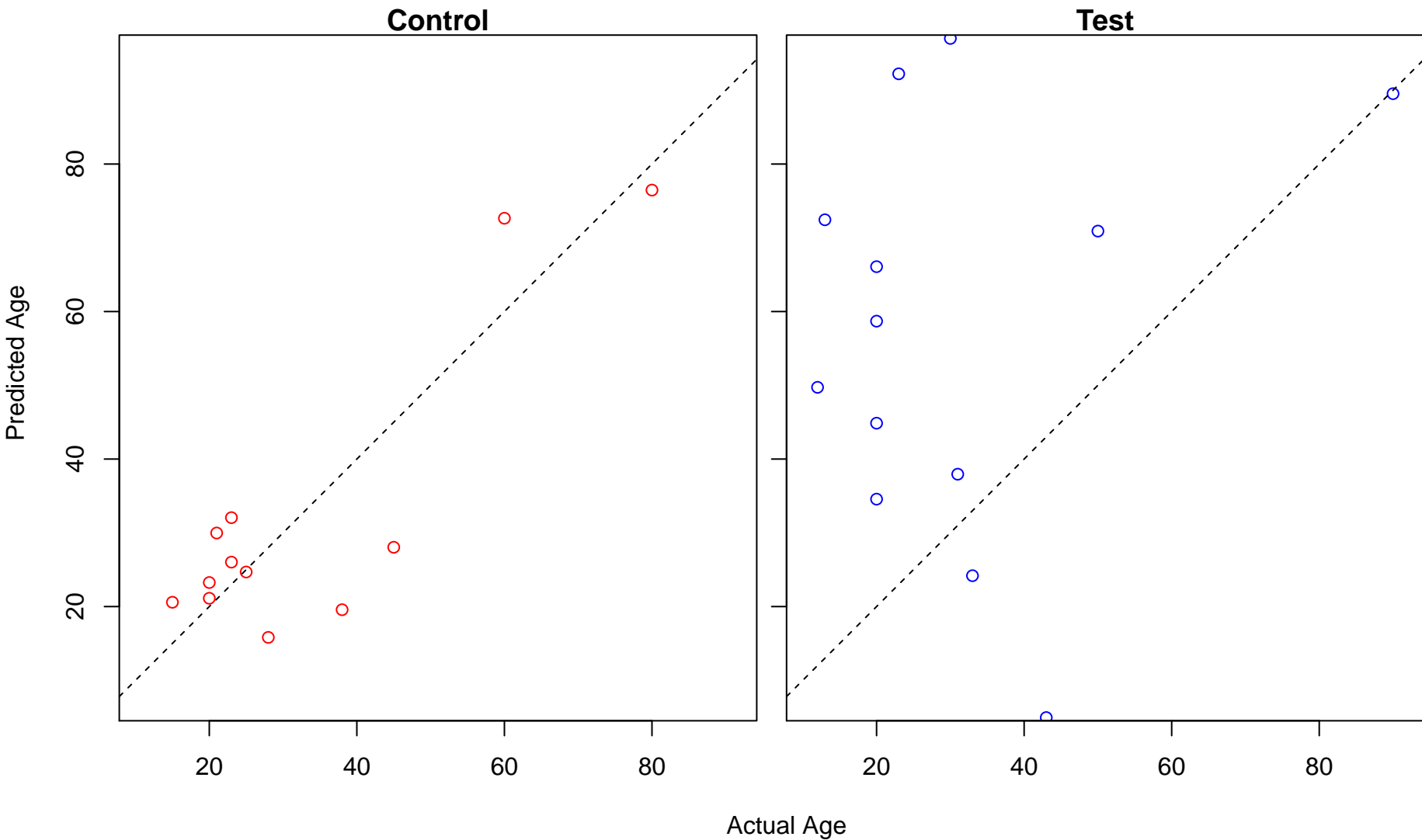
ve immune response based on somatic recombination of immune receptors built from immunoglobulin su



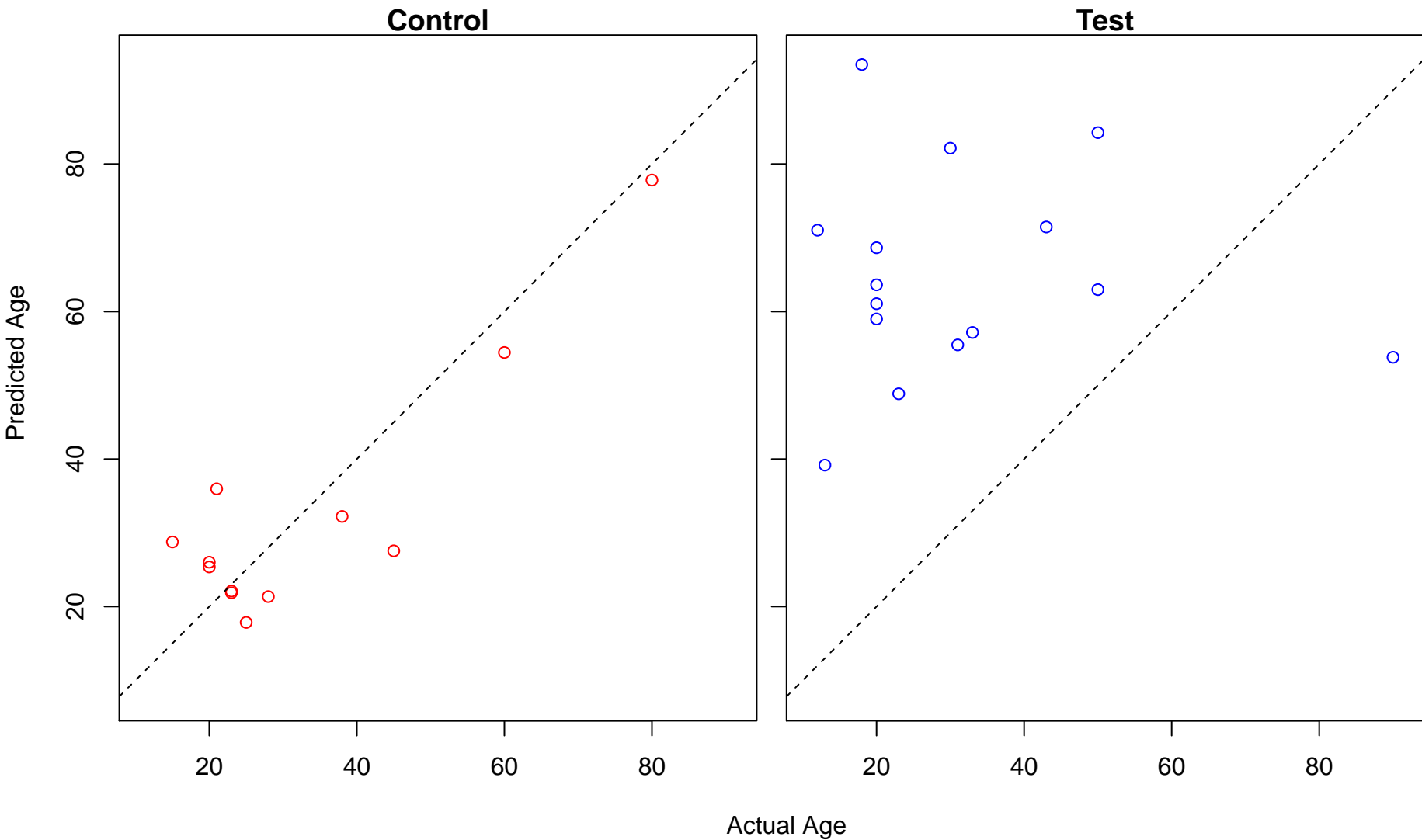
positive regulation of adaptive immune response (Score: 7.362646)



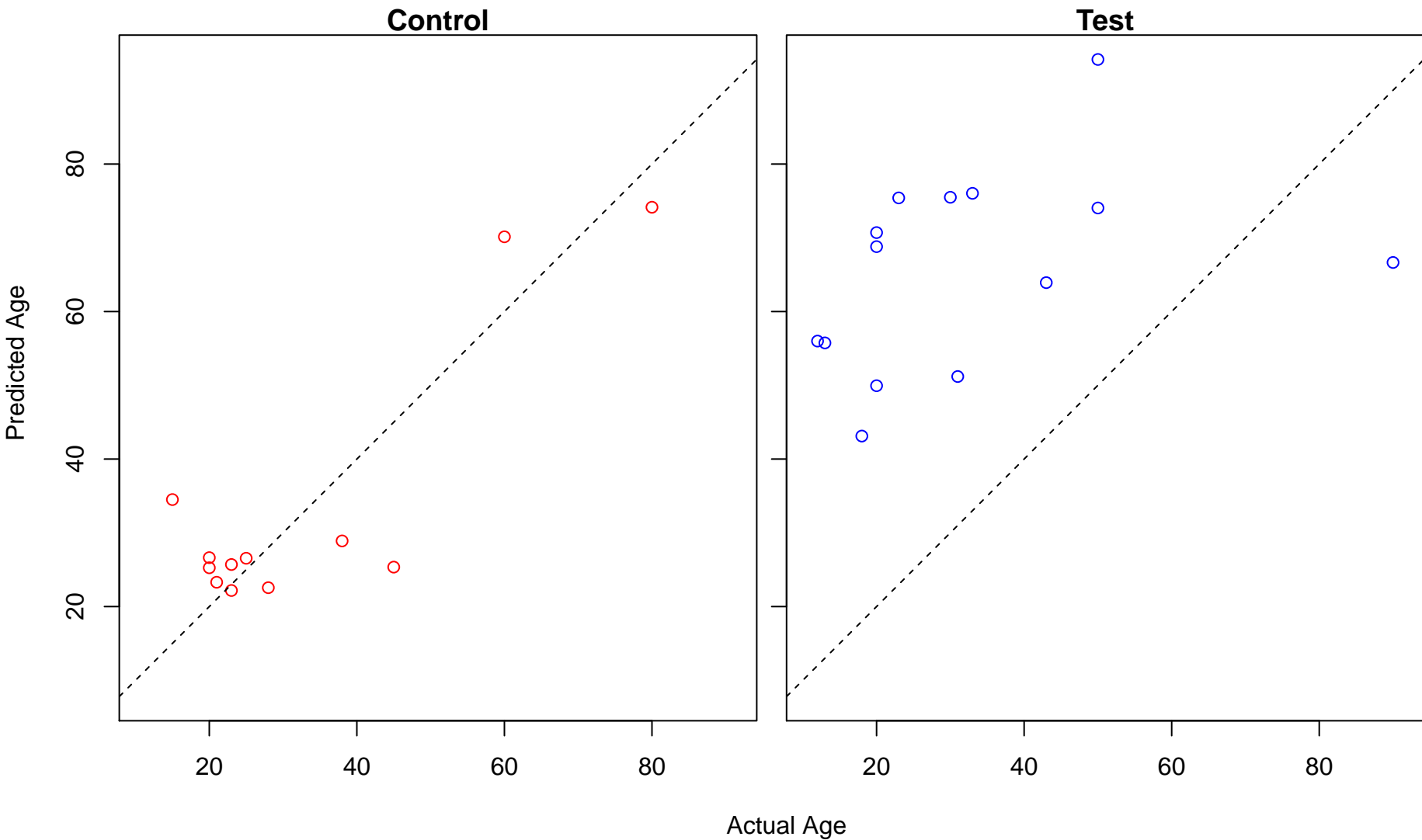
coenzyme A metabolic process (Score: 7.362422)



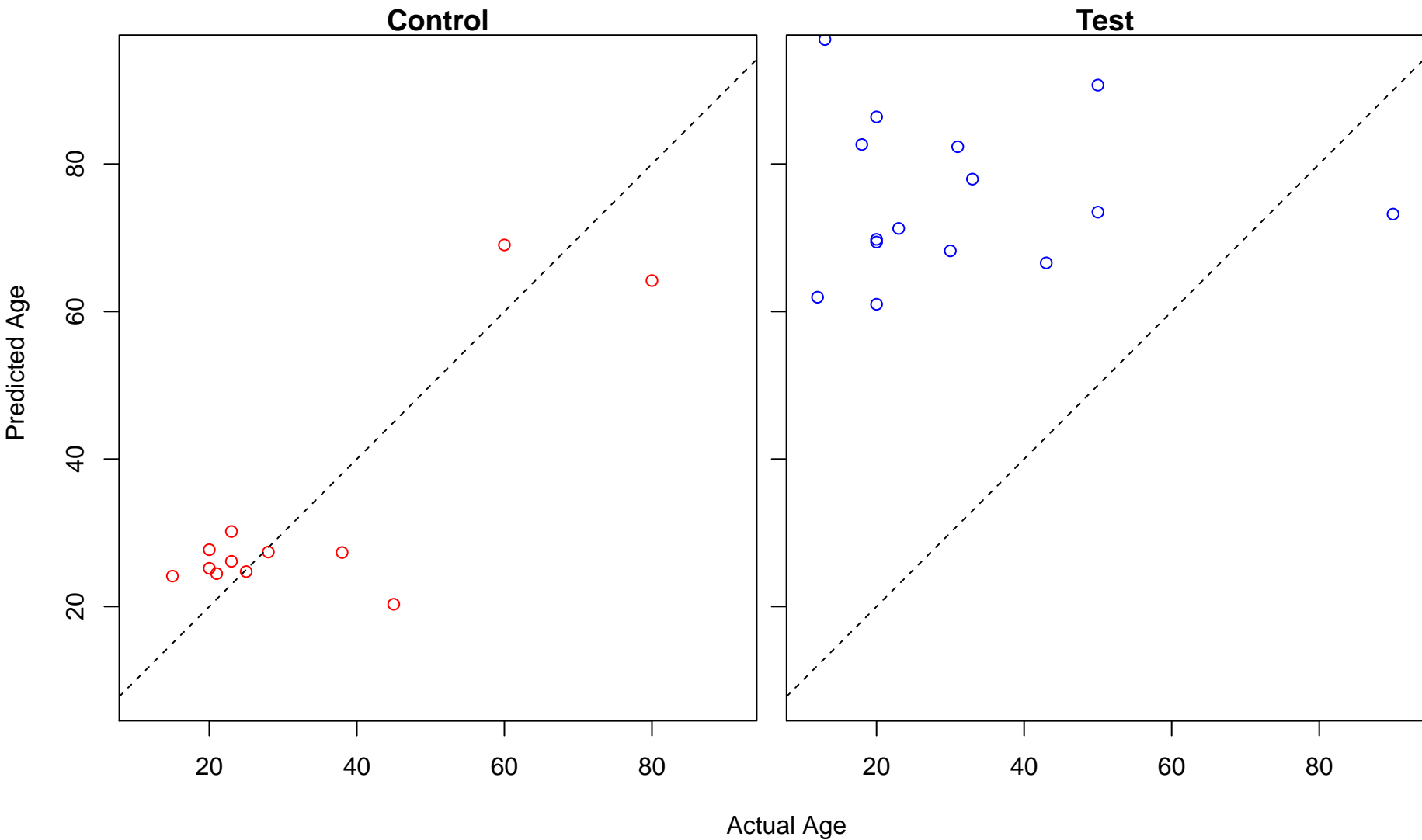
sterol metabolic process (Score: 7.353276)



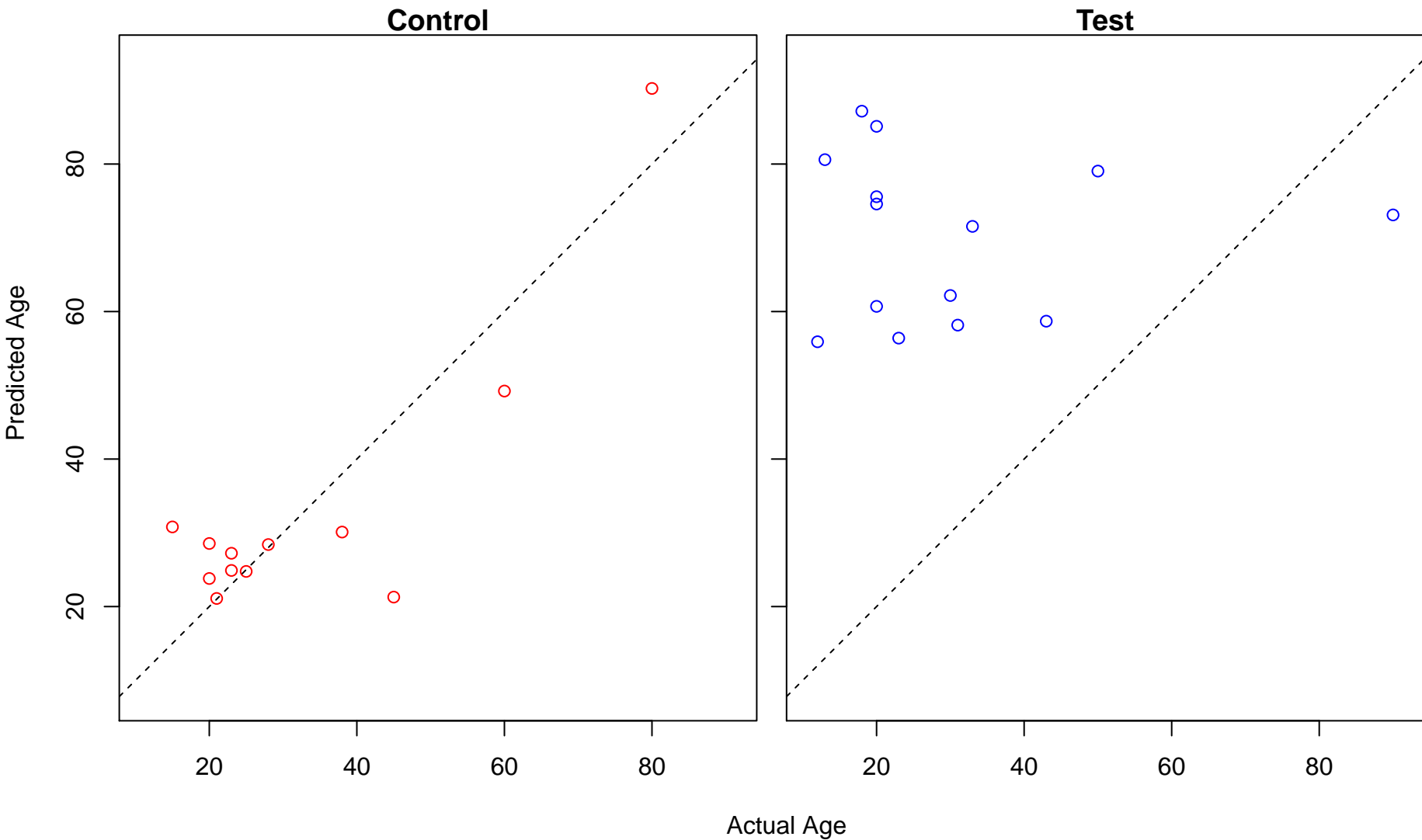
glycolipid catabolic process (Score: 7.352676)



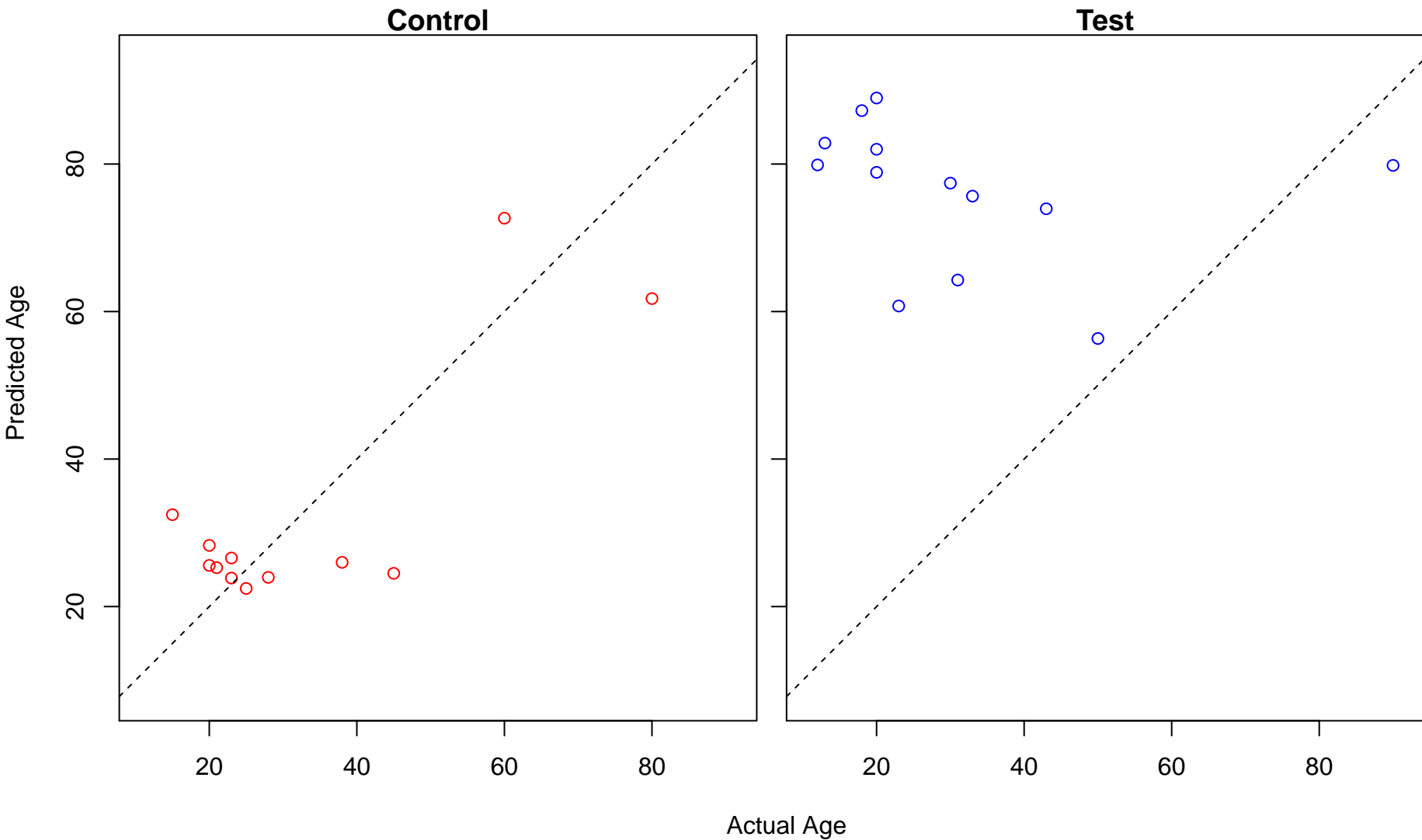
positive regulation of immune effector process (Score: 7.351516)



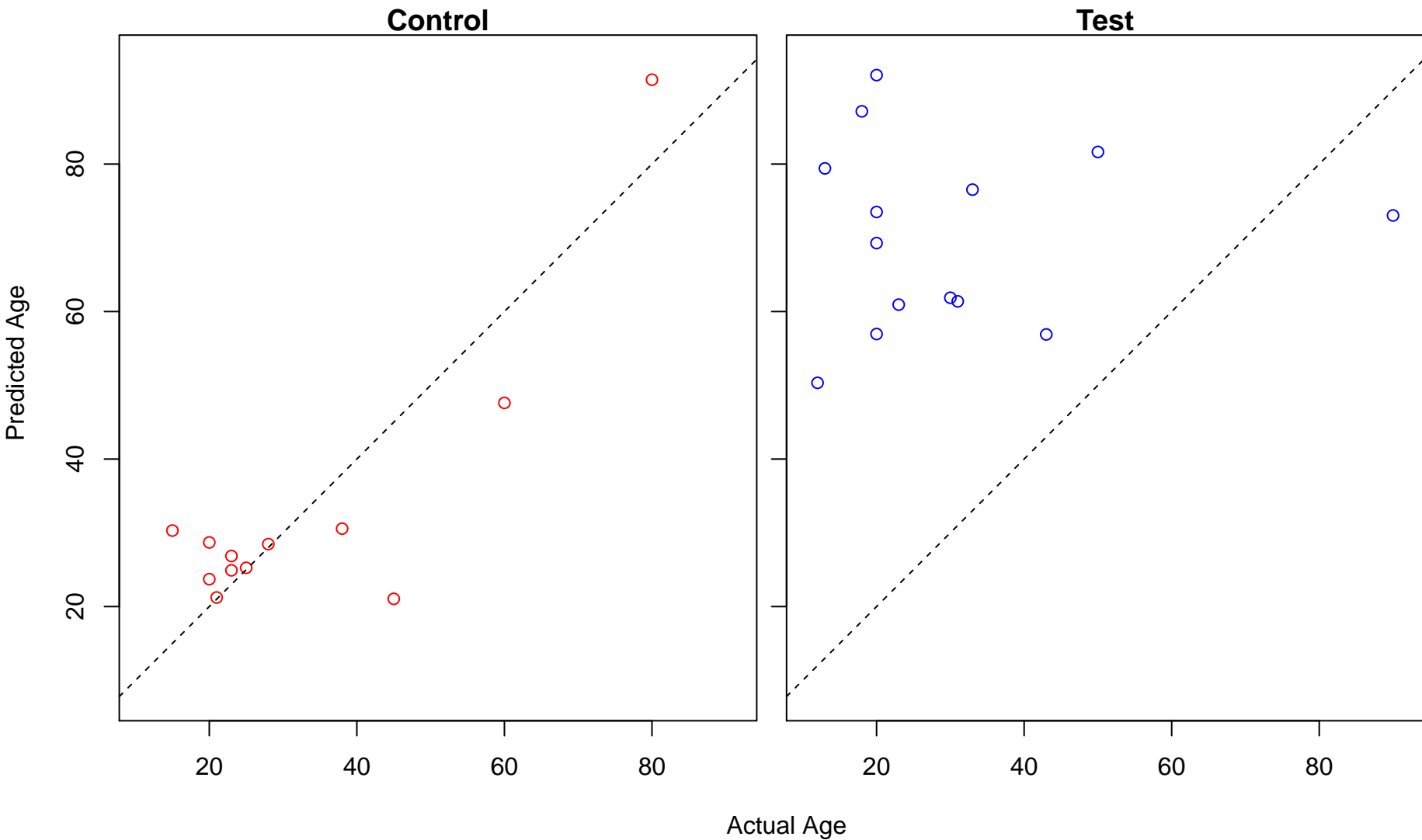
positive regulation of protein acetylation (Score: 7.344954)



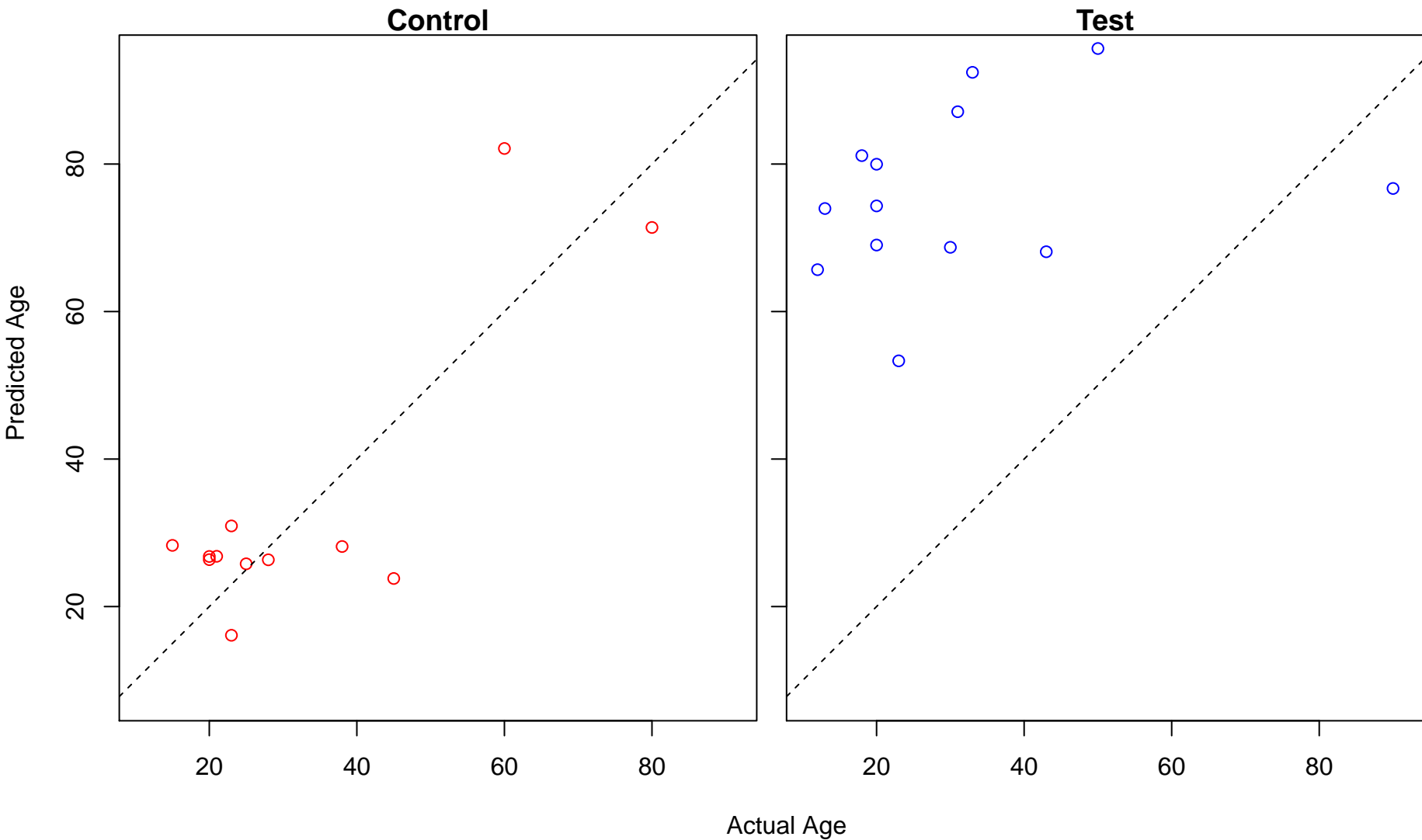
anion homeostasis (Score: 7.341662)



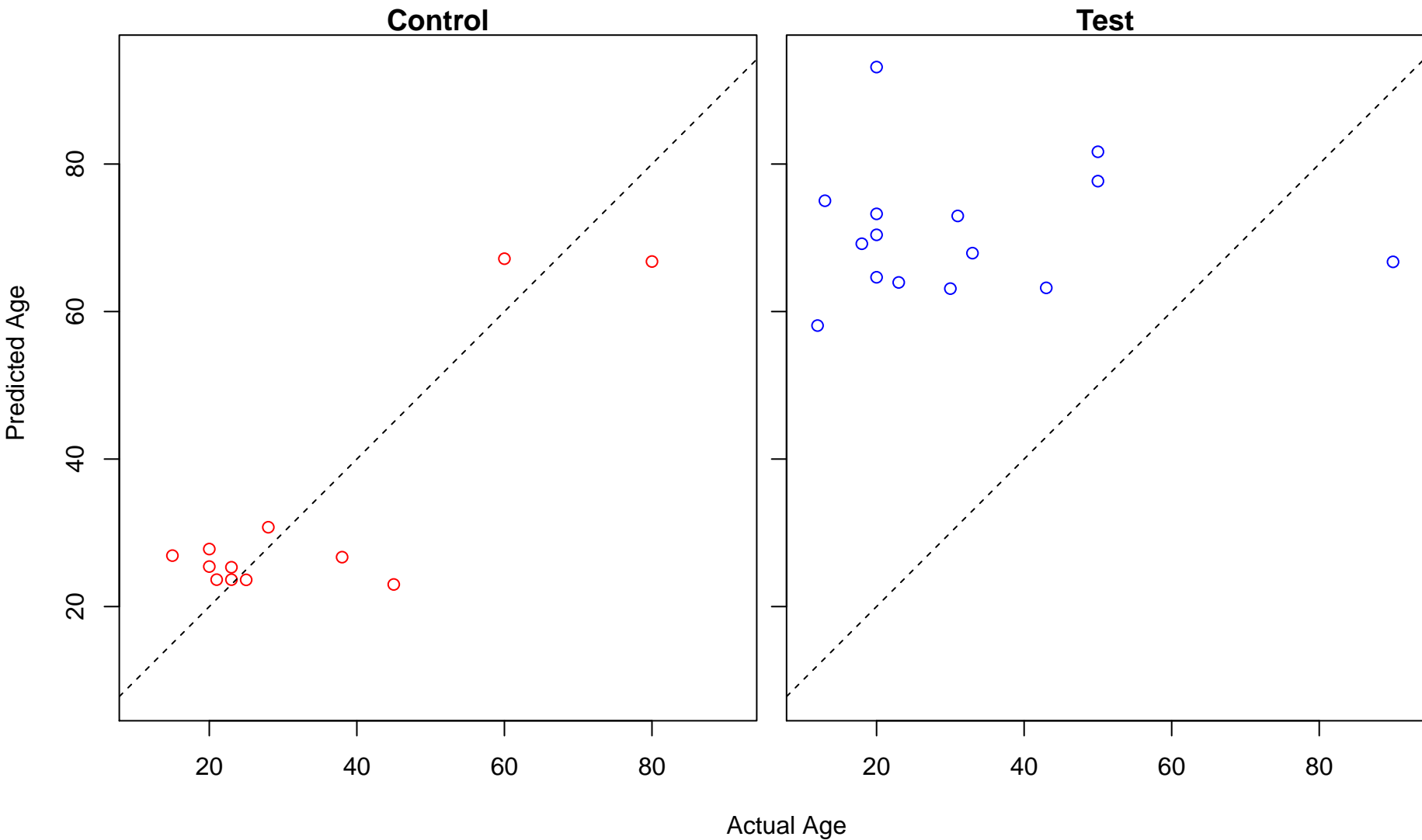
positive regulation of peptidyl-lysine acetylation (Score: 7.341392)



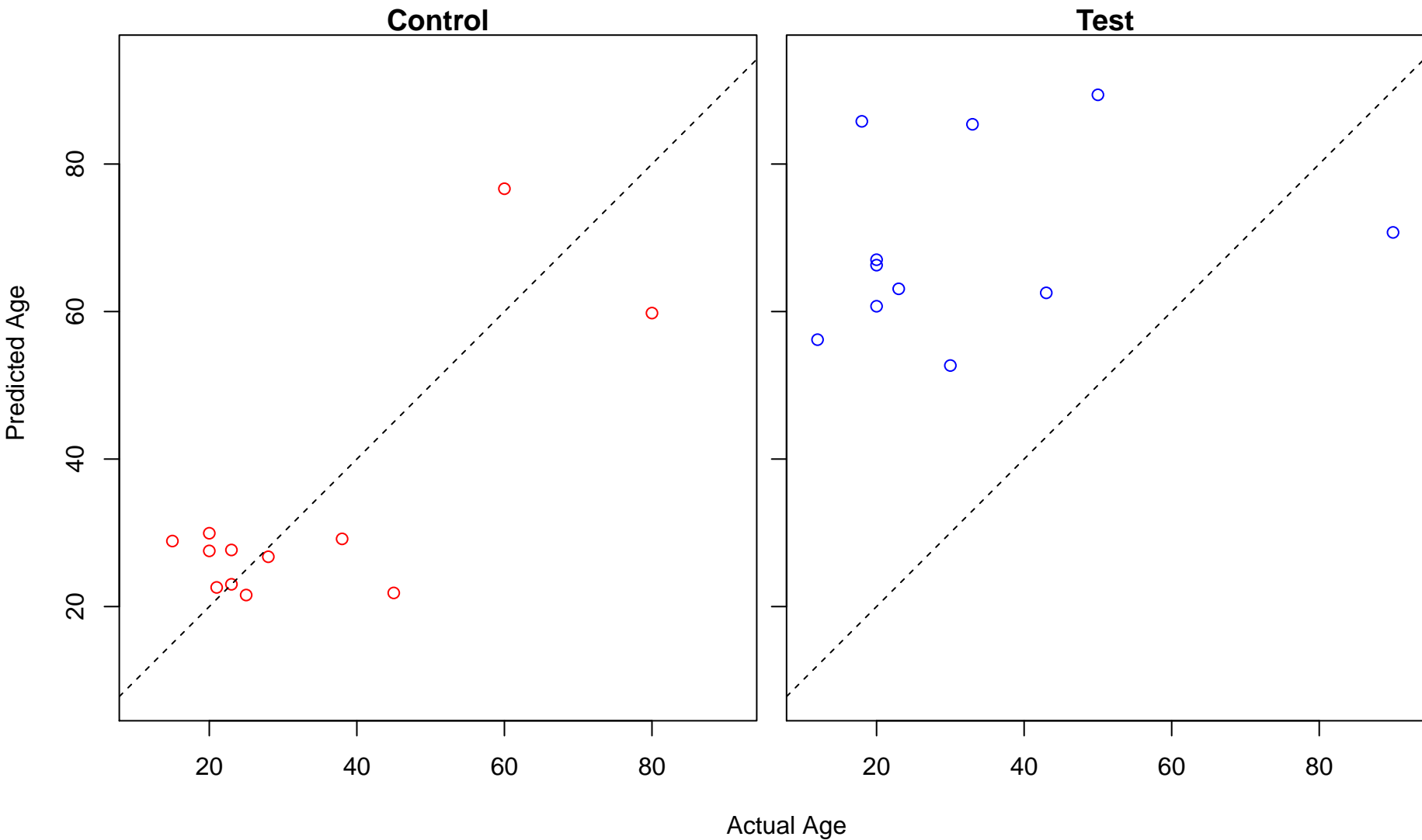
regulation of fibroblast migration (Score: 7.338656)



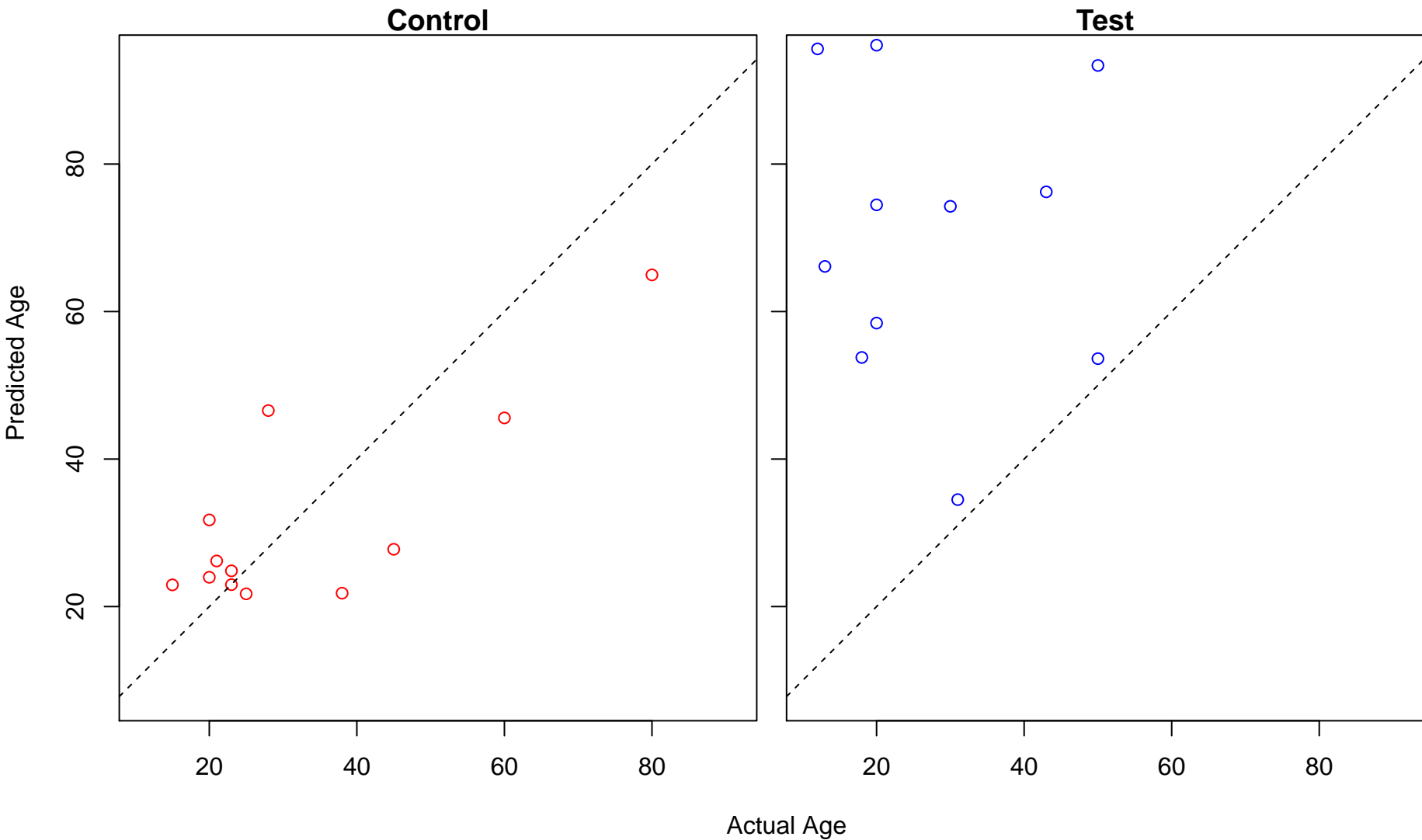
negative regulation of developmental growth (Score: 7.335766)



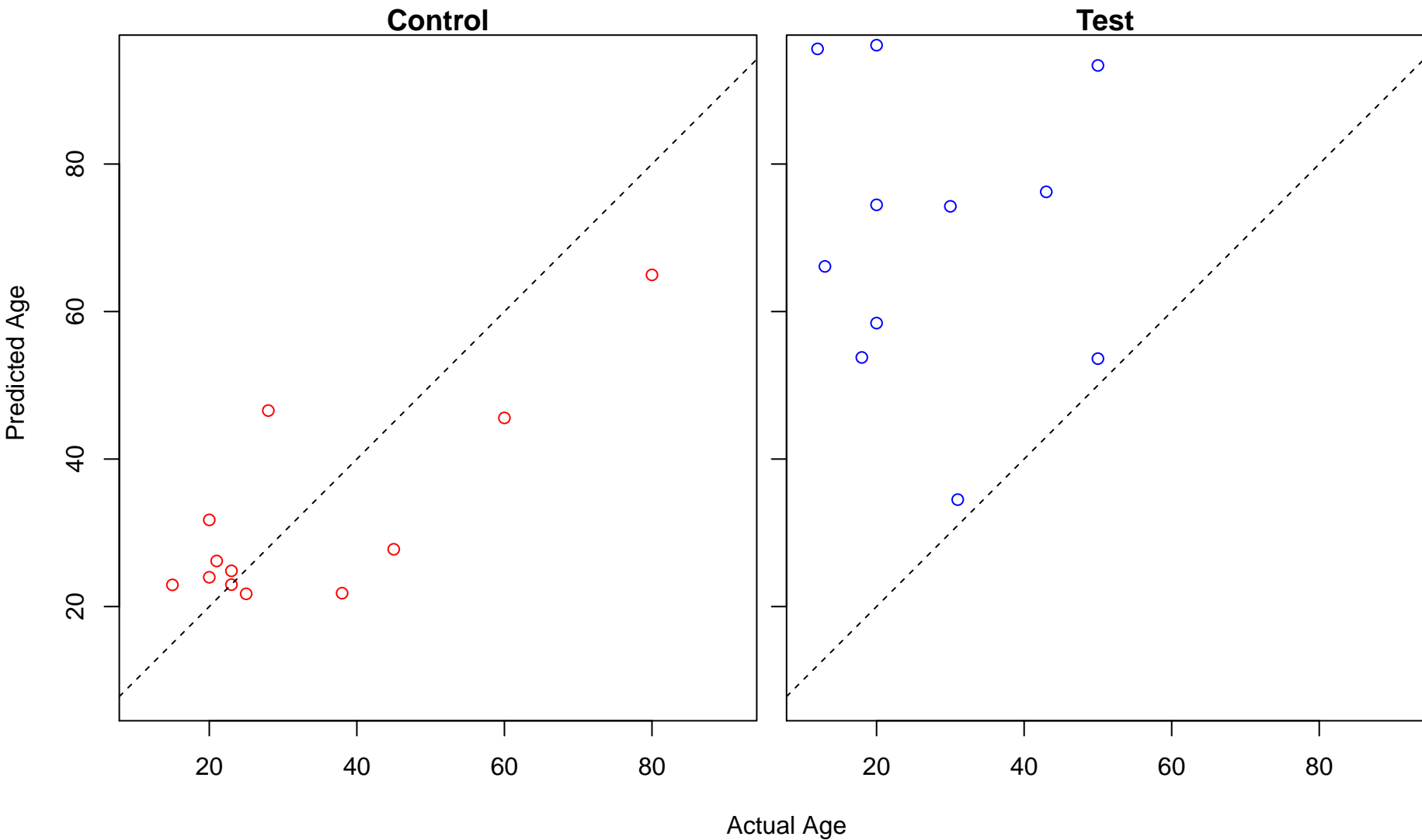
negative regulation of toll-like receptor 4 signaling pathway (Score: 7.335418)



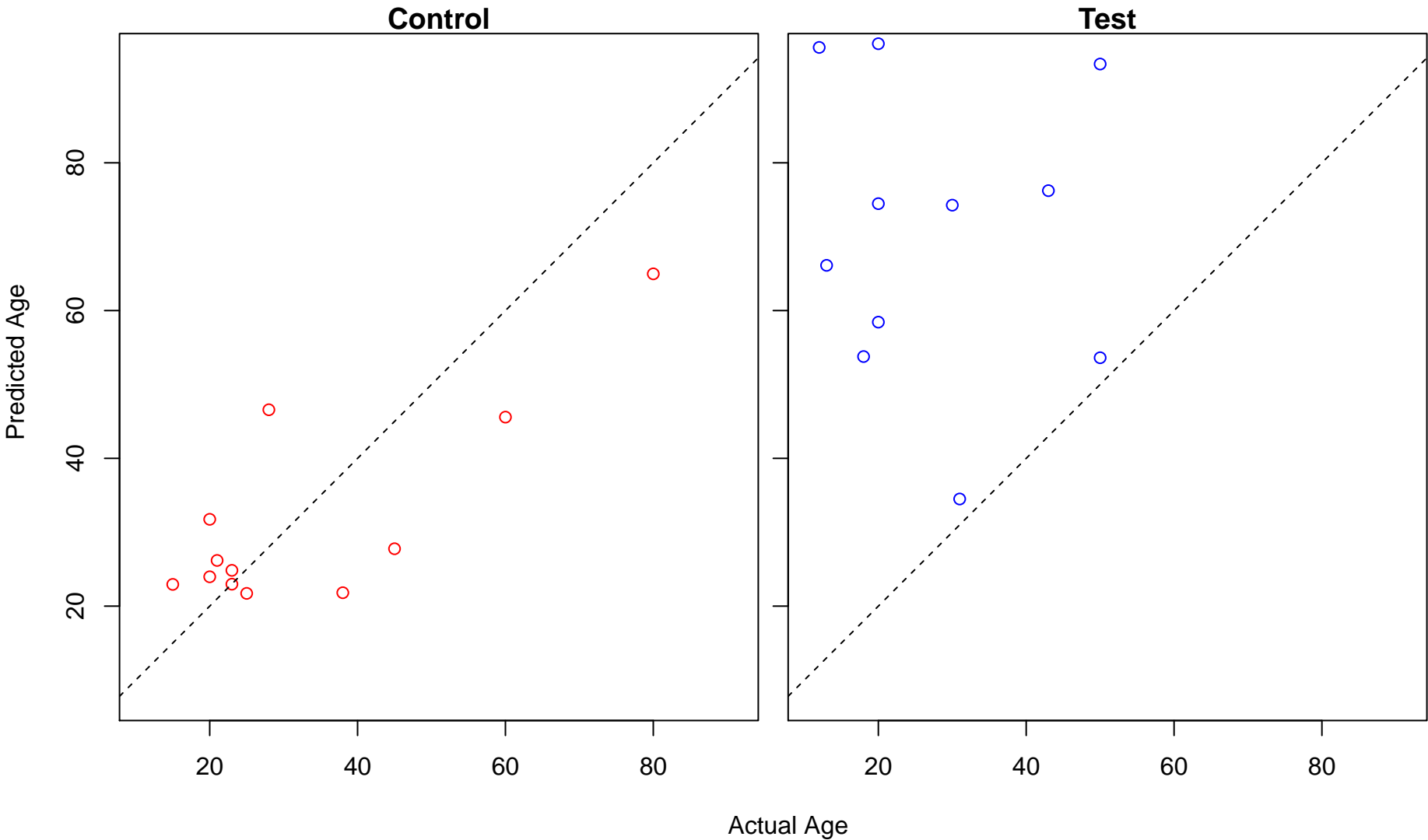
L-phenylalanine metabolic process (Score: 7.334078)



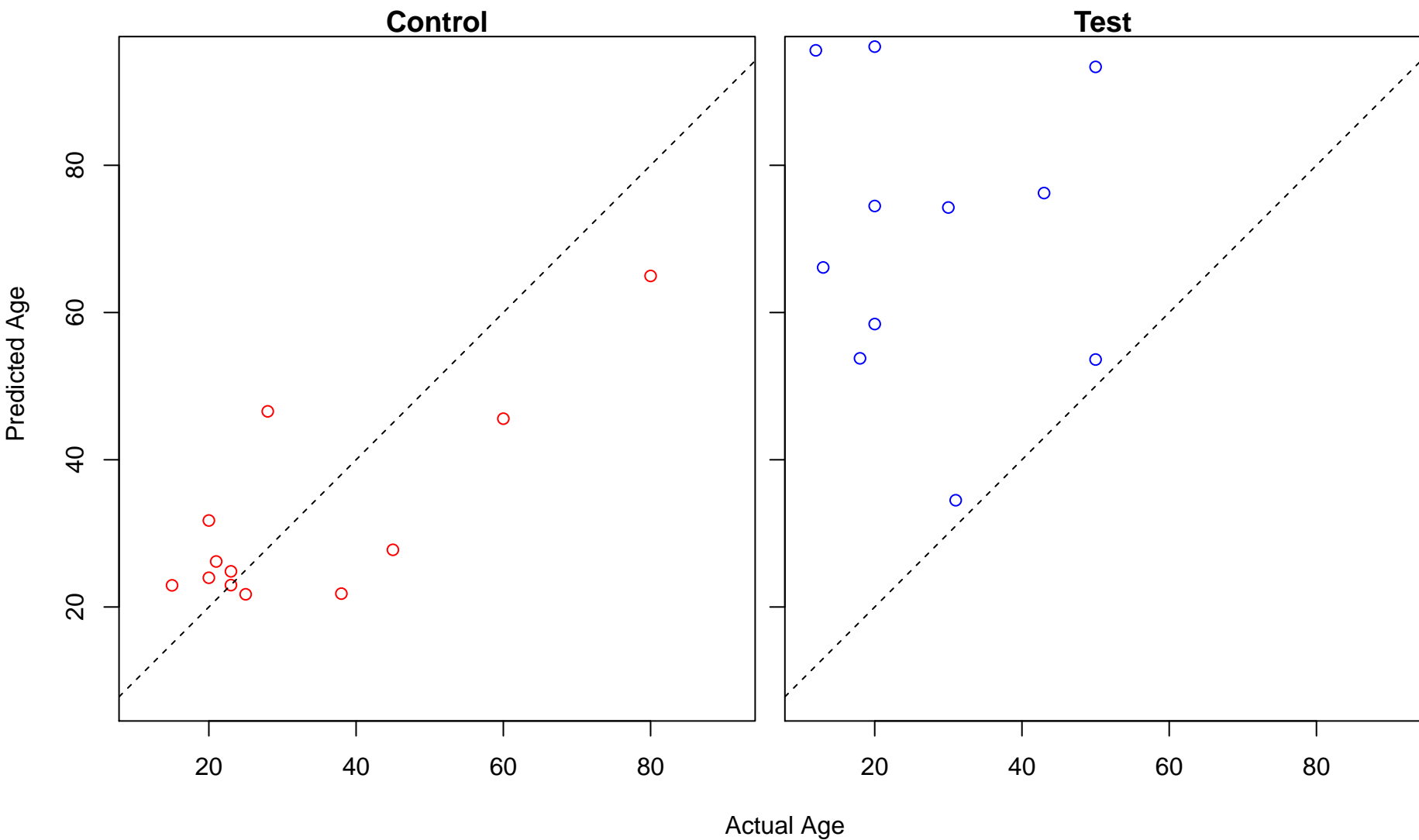
L-phenylalanine catabolic process (Score: 7.334078)



erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process (Score: 7.33407)

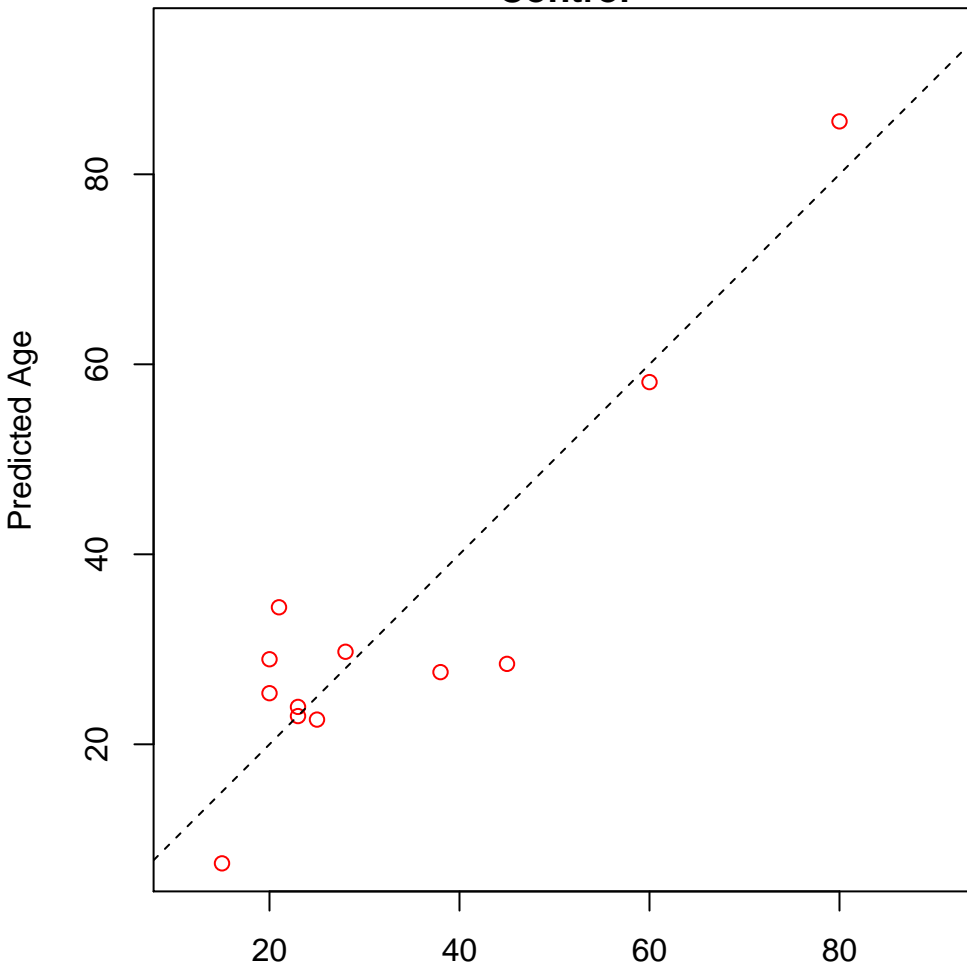


erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process (Score: 7.33407)

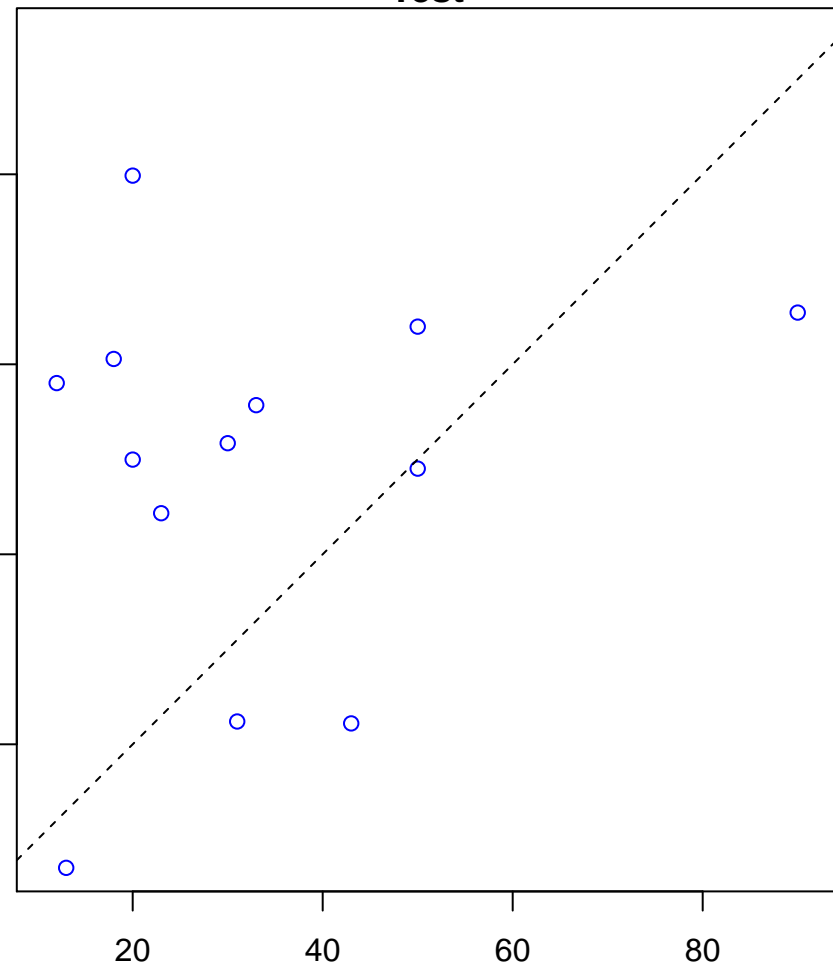


anterograde synaptic vesicle transport (Score: 7.332859)

Control



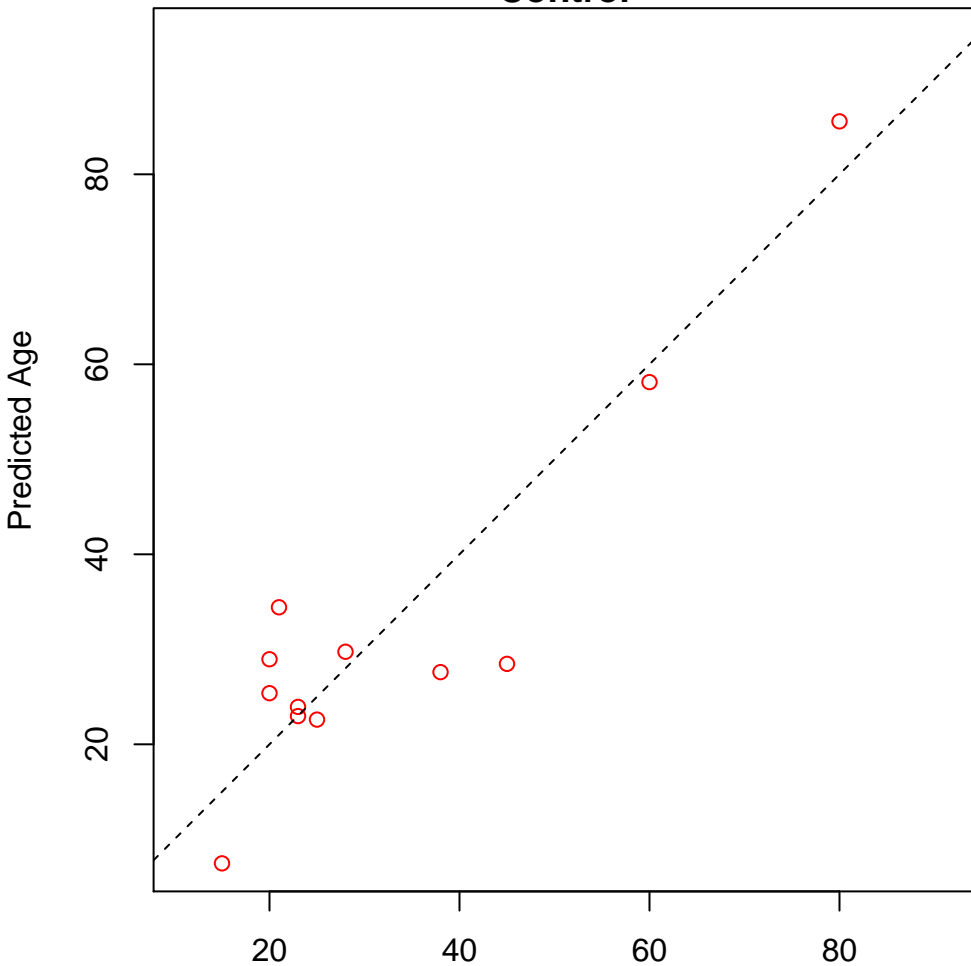
Test



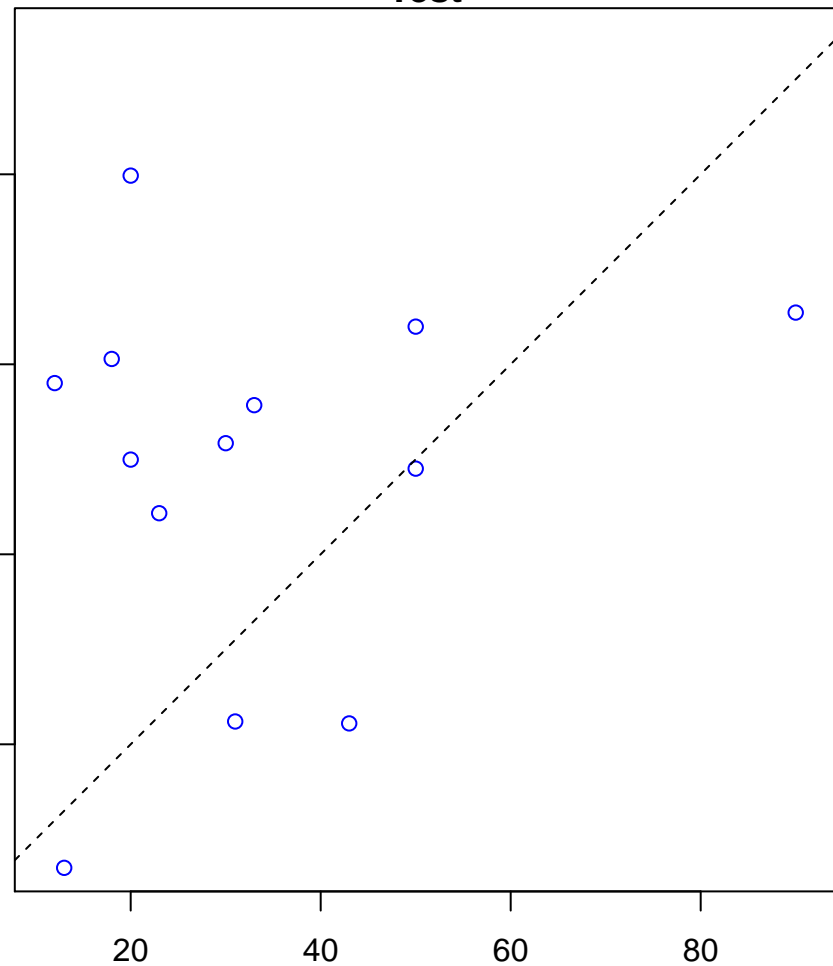
Actual Age

synaptic vesicle cytoskeletal transport (Score: 7.332859)

Control

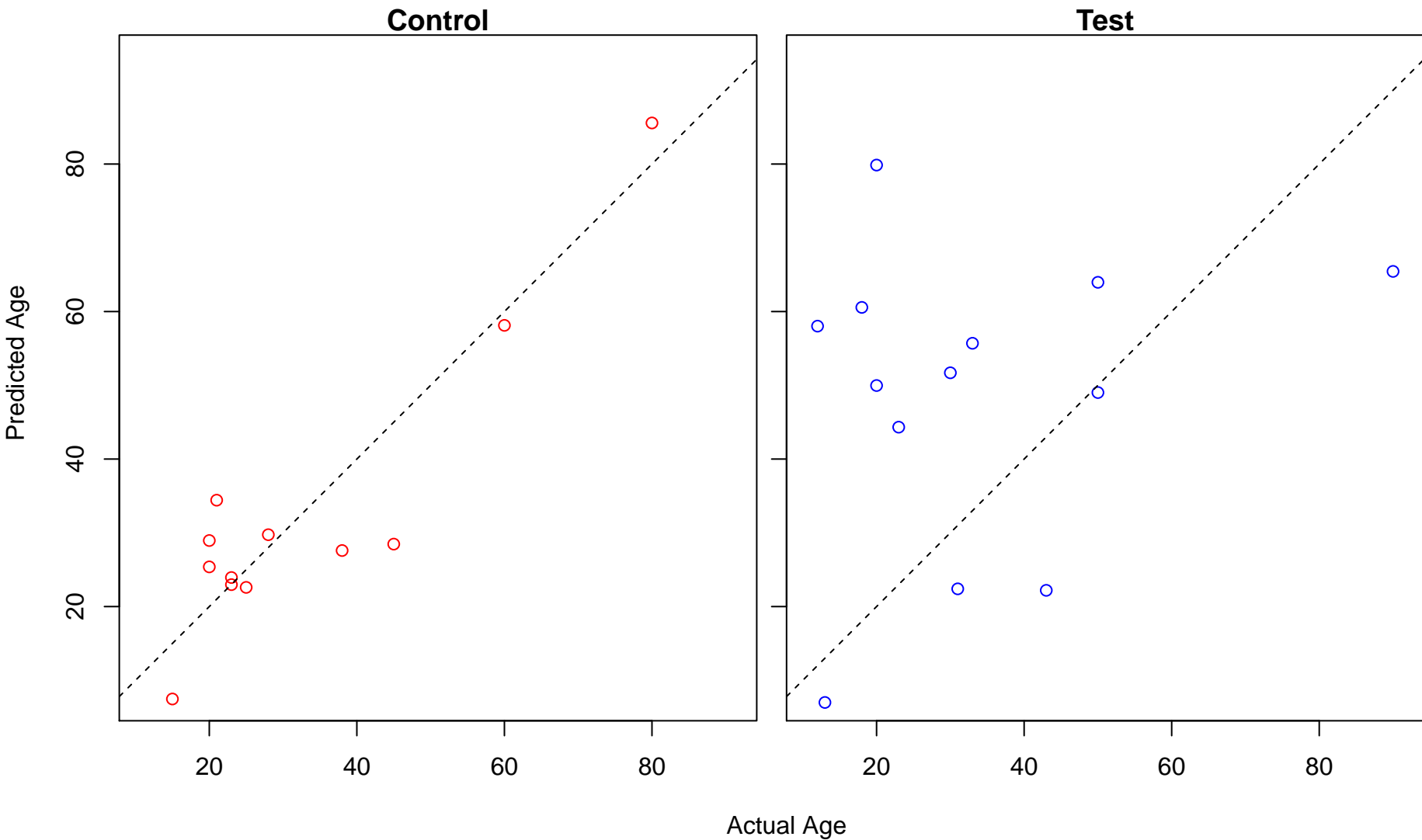


Test

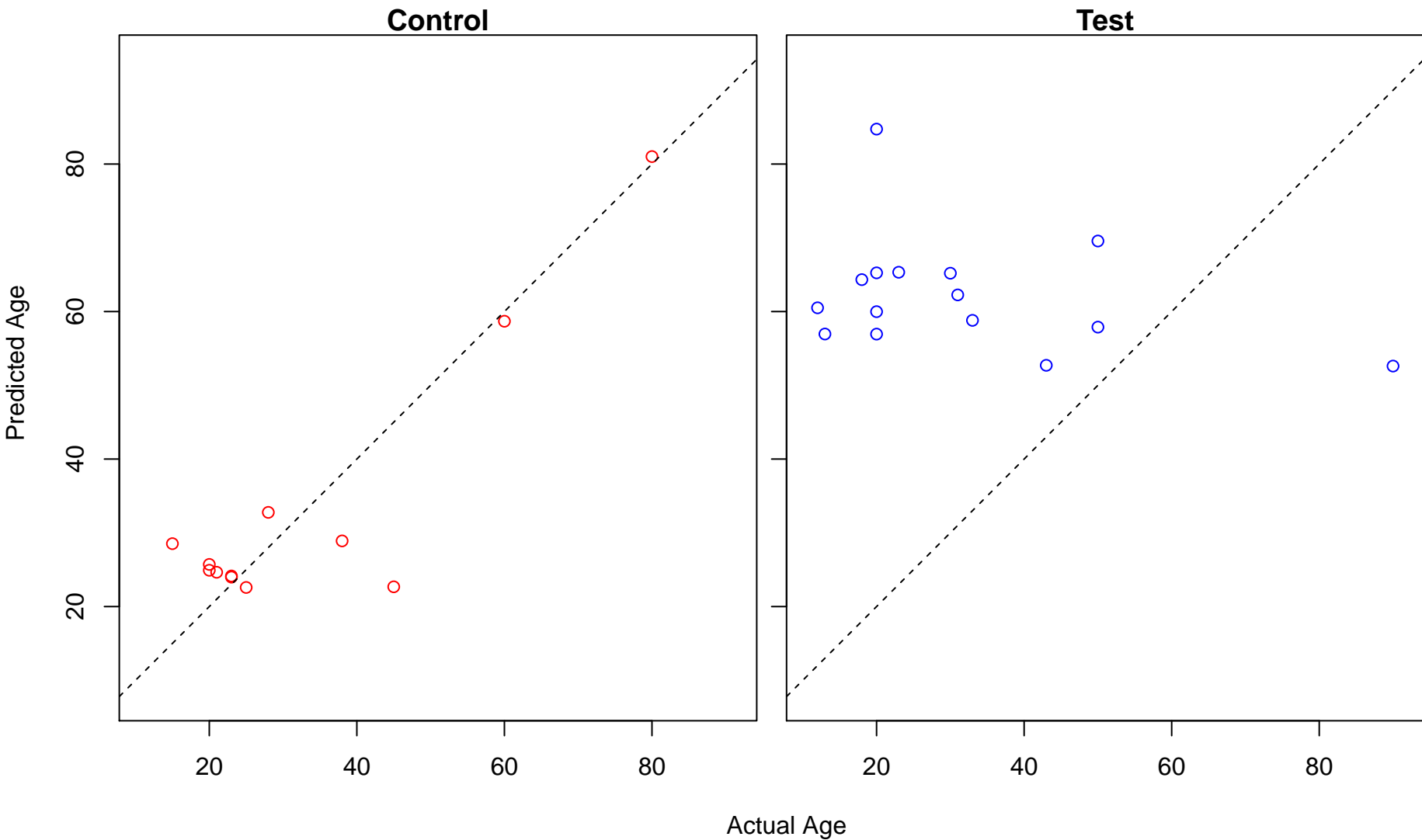


Actual Age

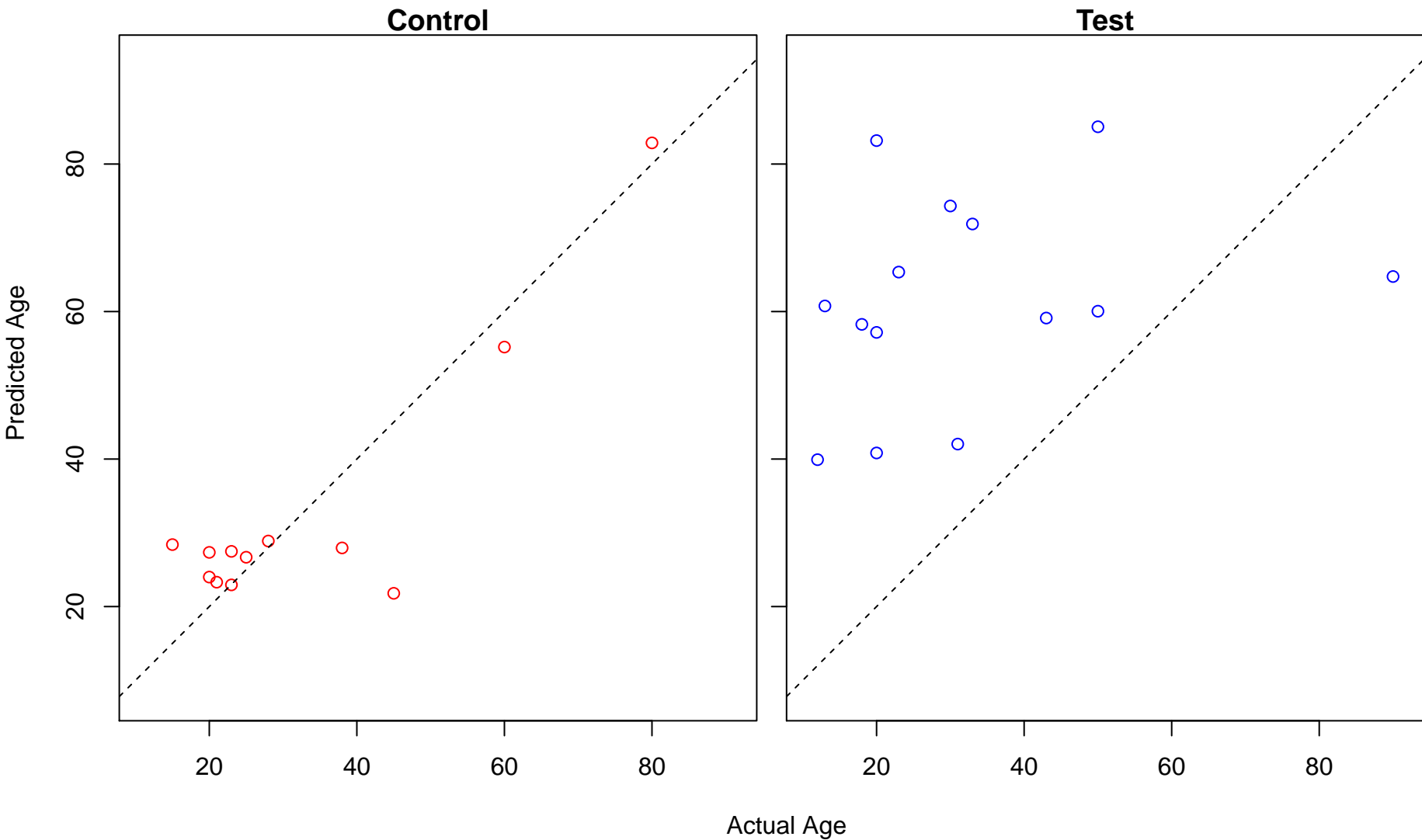
synaptic vesicle transport along microtubule (Score: 7.332859)



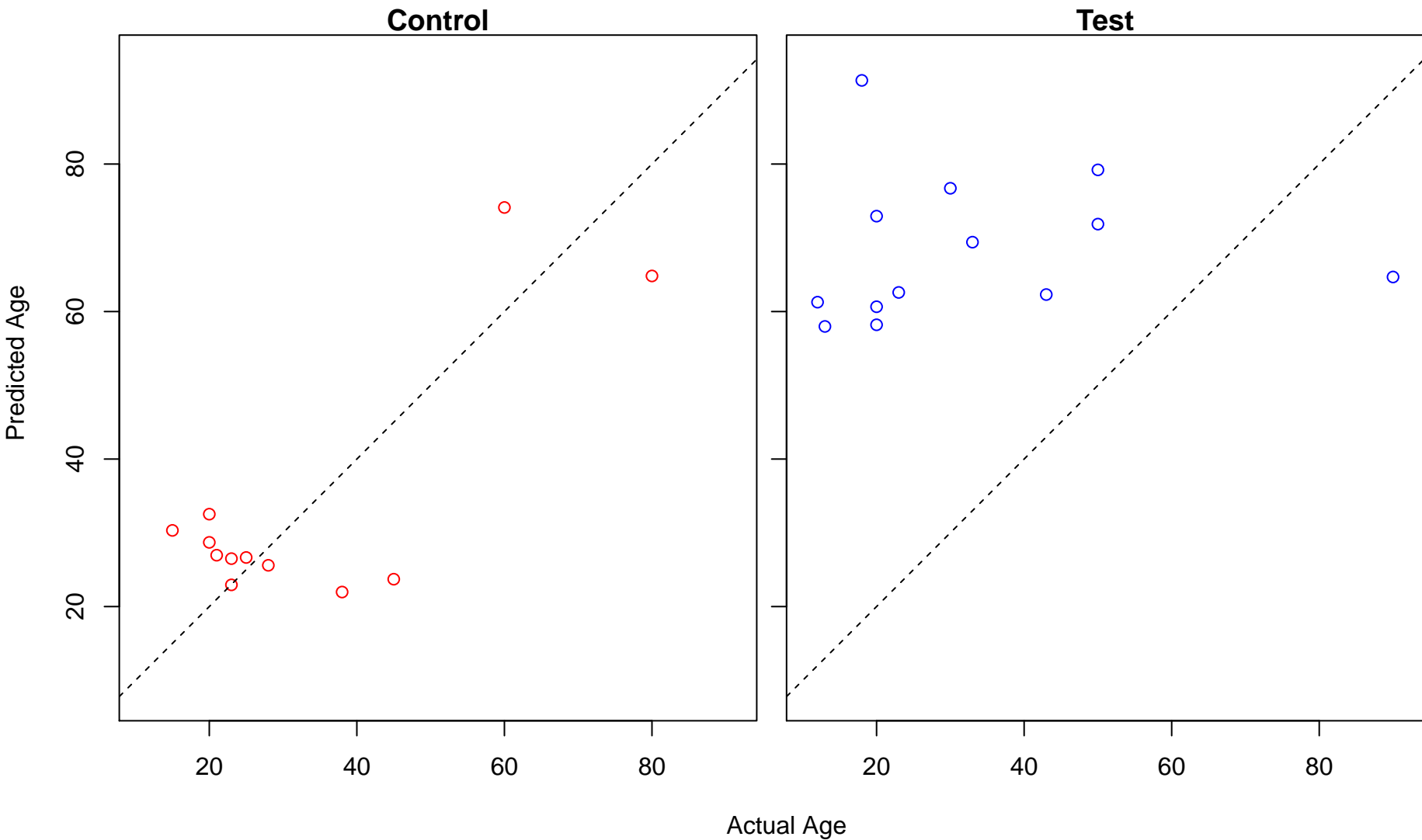
SMAD protein complex assembly (Score: 7.324762)



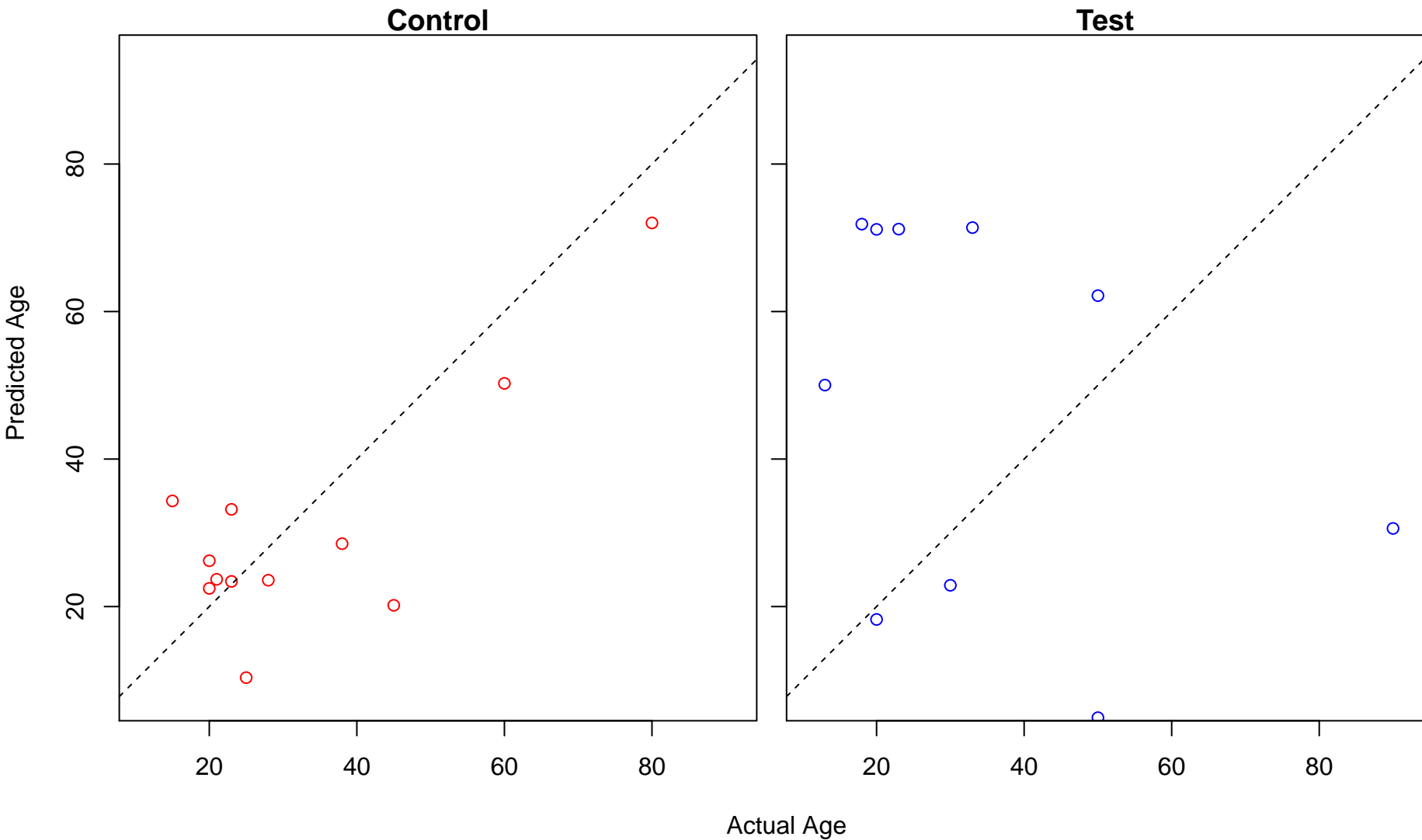
neuropeptide signaling pathway (Score: 7.321173)



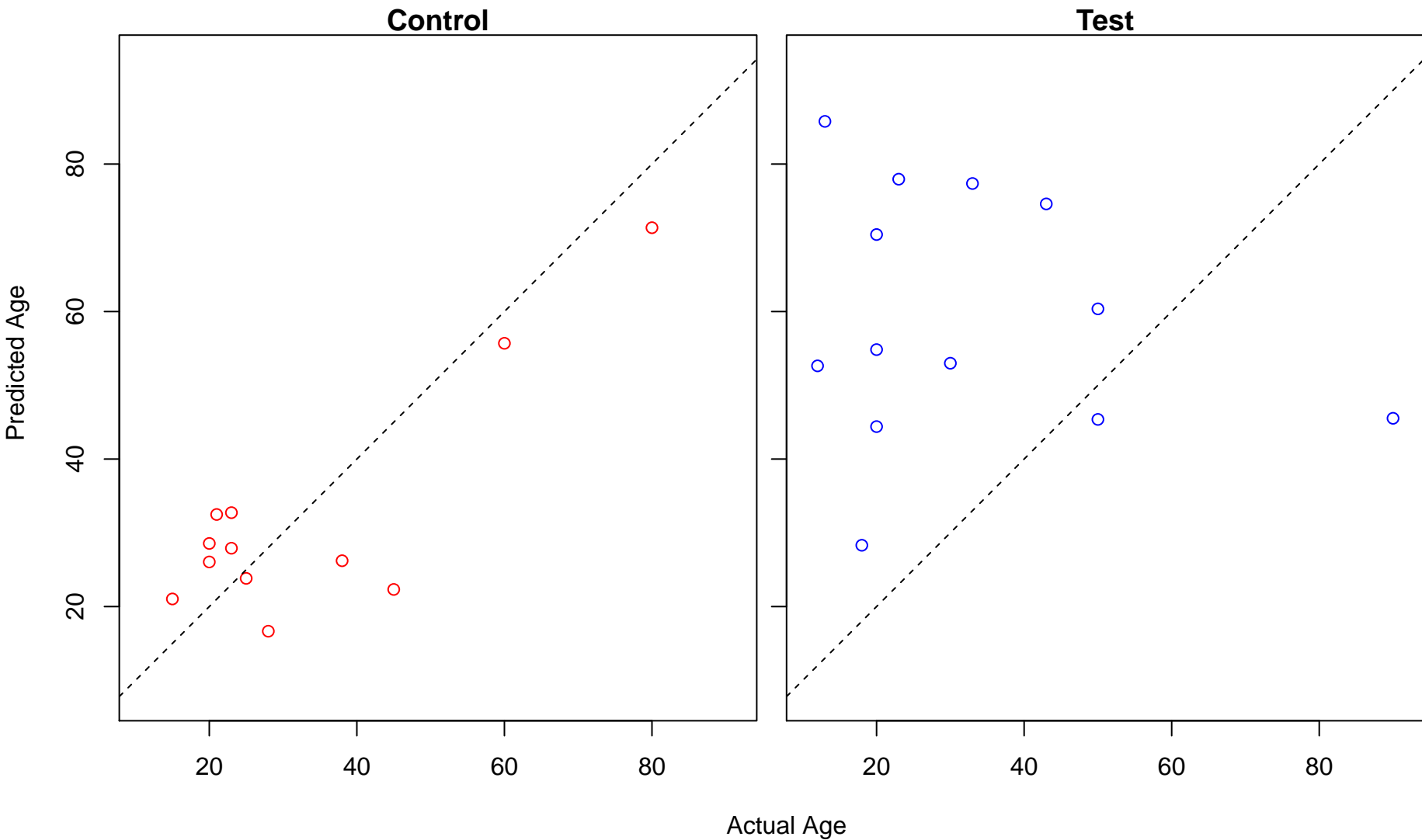
regulation of anion transport (Score: 7.318517)



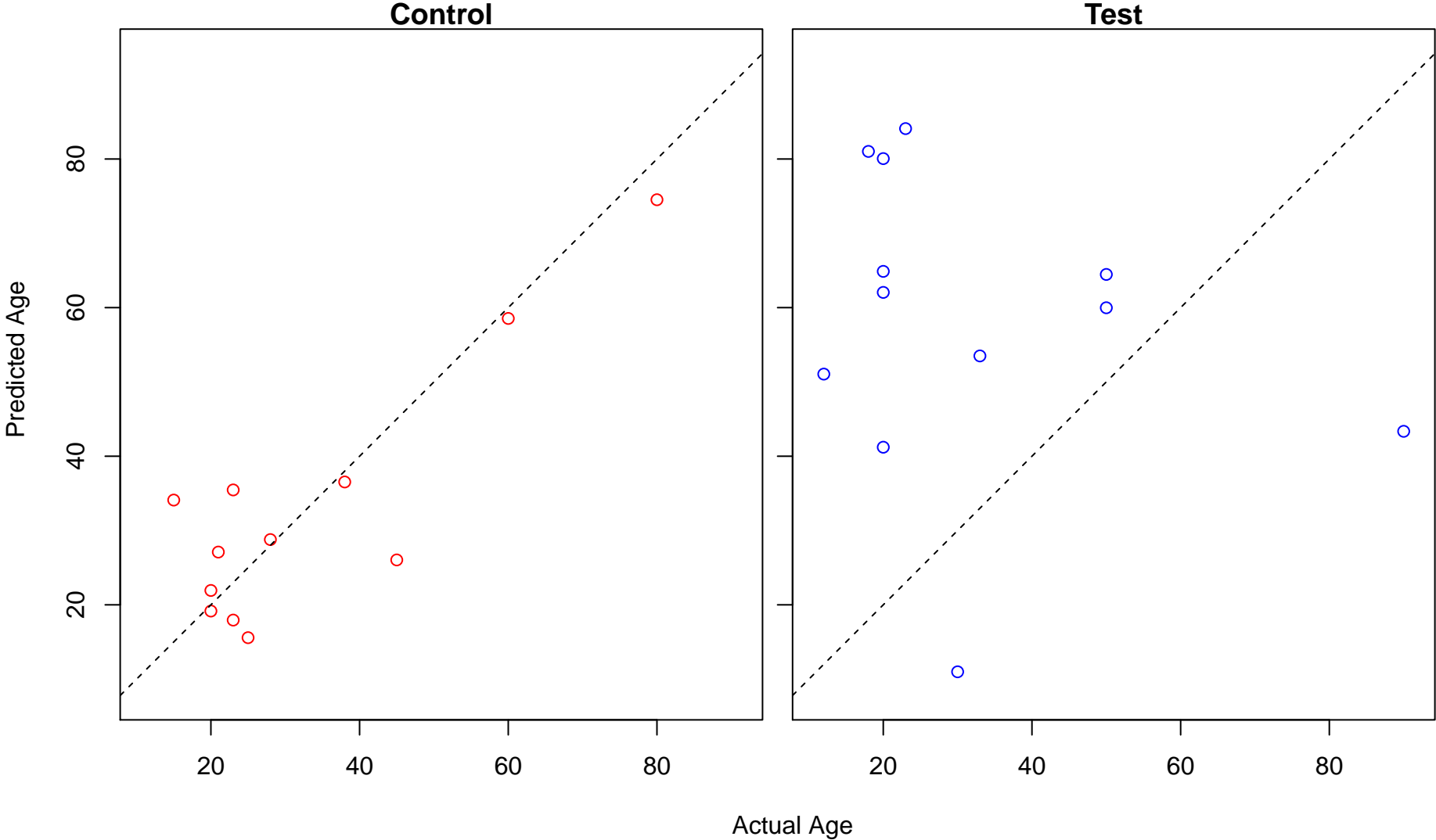
cellular metal ion homeostasis (Score: 7.316481)



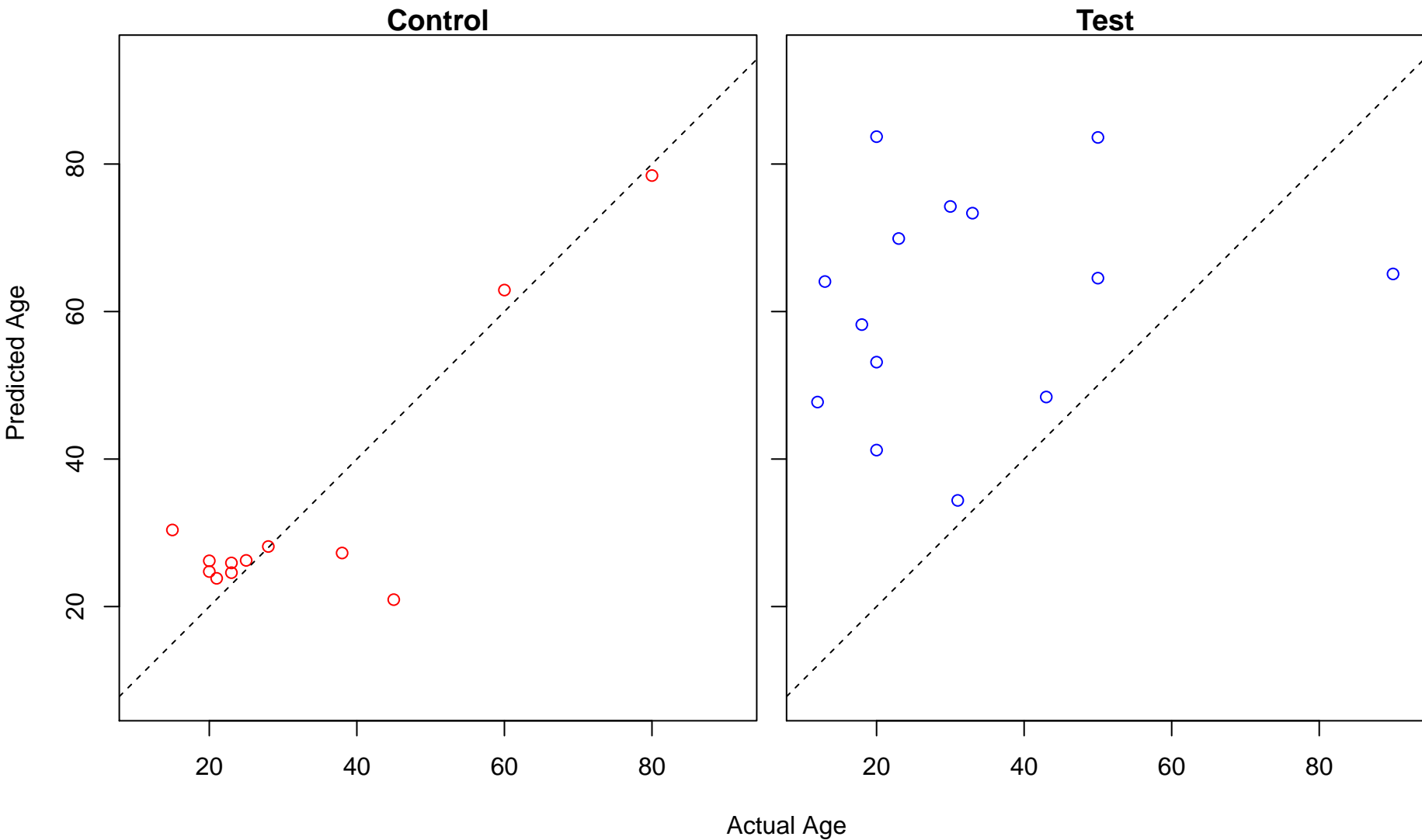
polyol transport (Score: 7.314907)



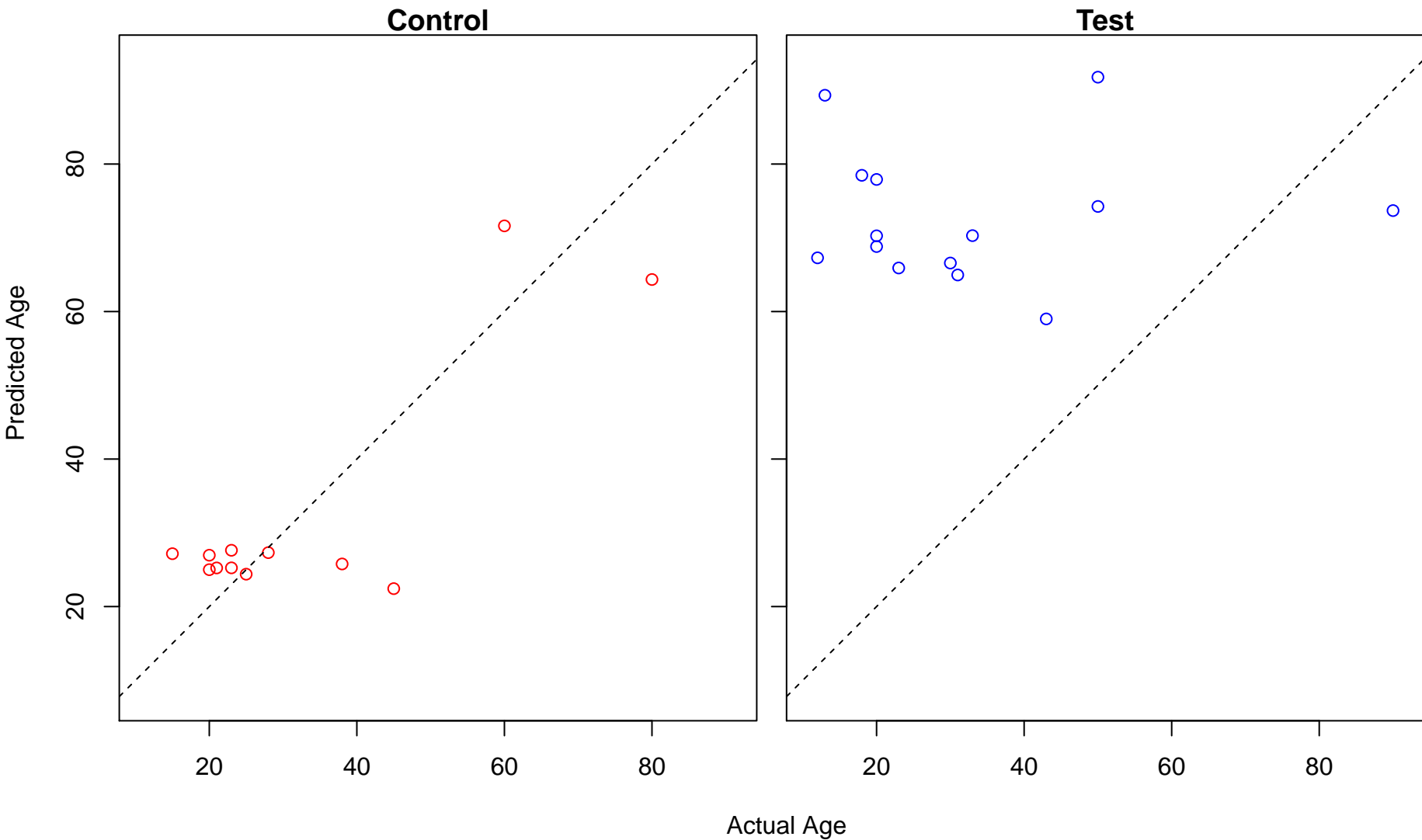
production of miRNAs involved in gene silencing by miRNA (Score: 7.311411)



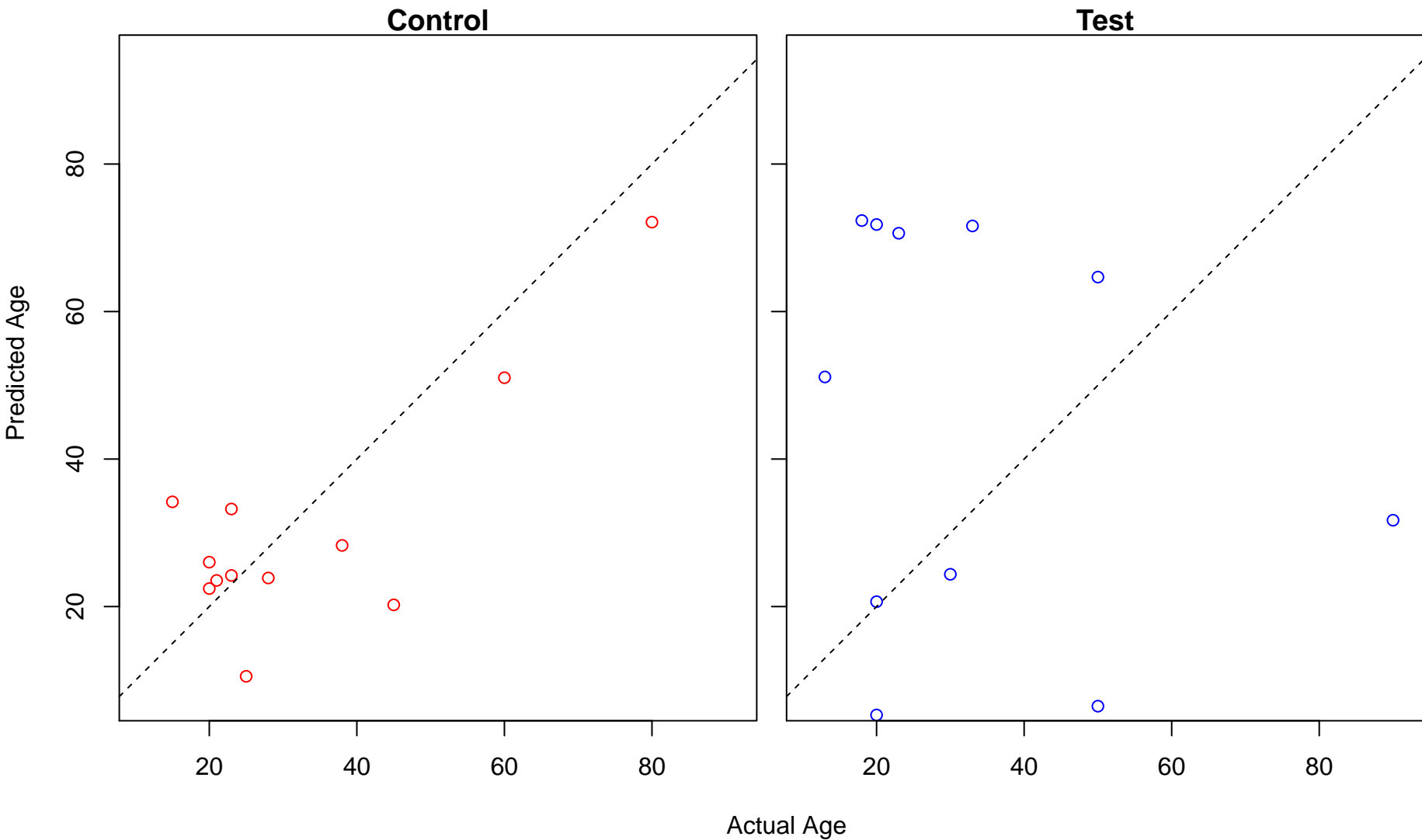
endosome transport via multivesicular body sorting pathway (Score: 7.309059)



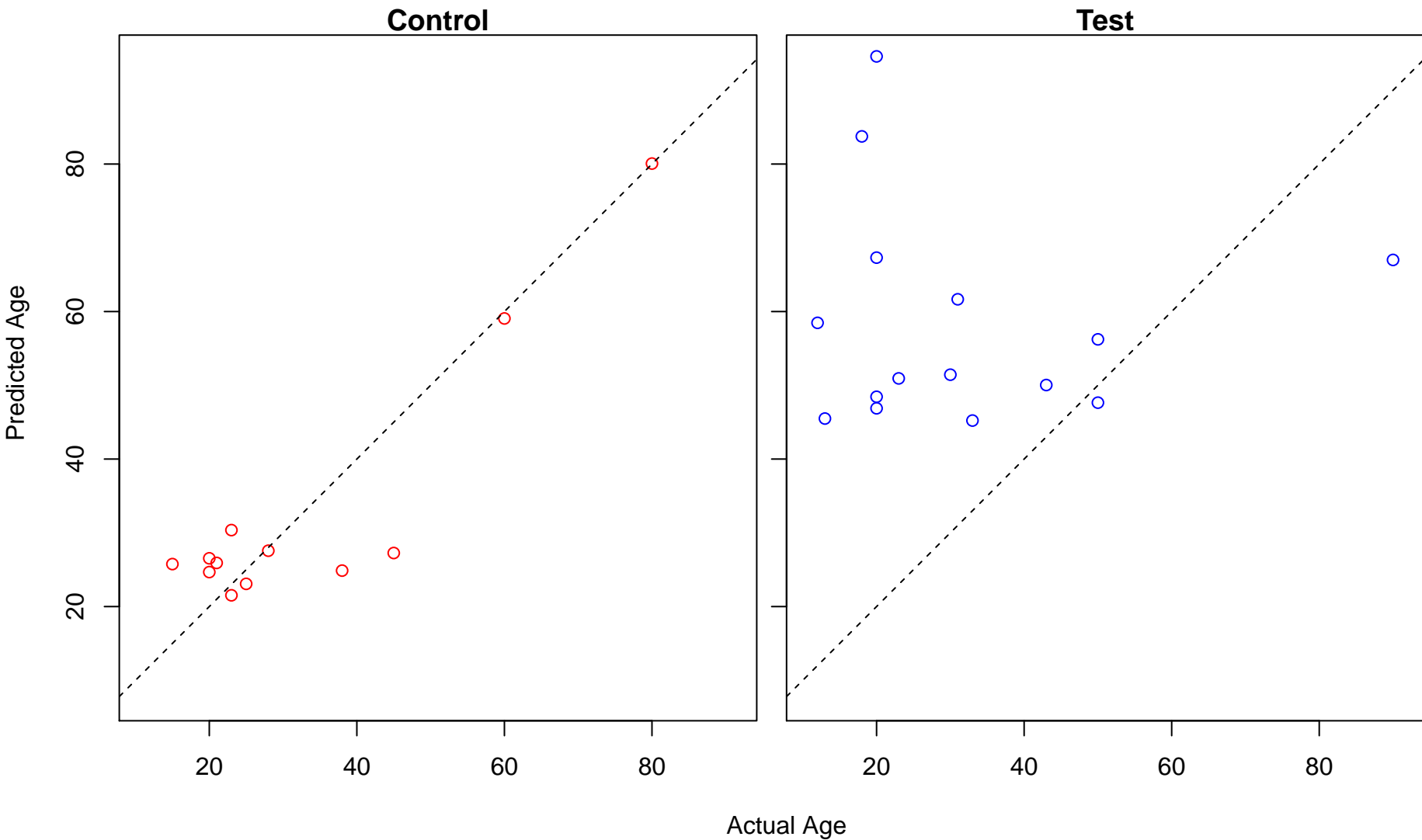
regulation of viral process (Score: 7.304941)



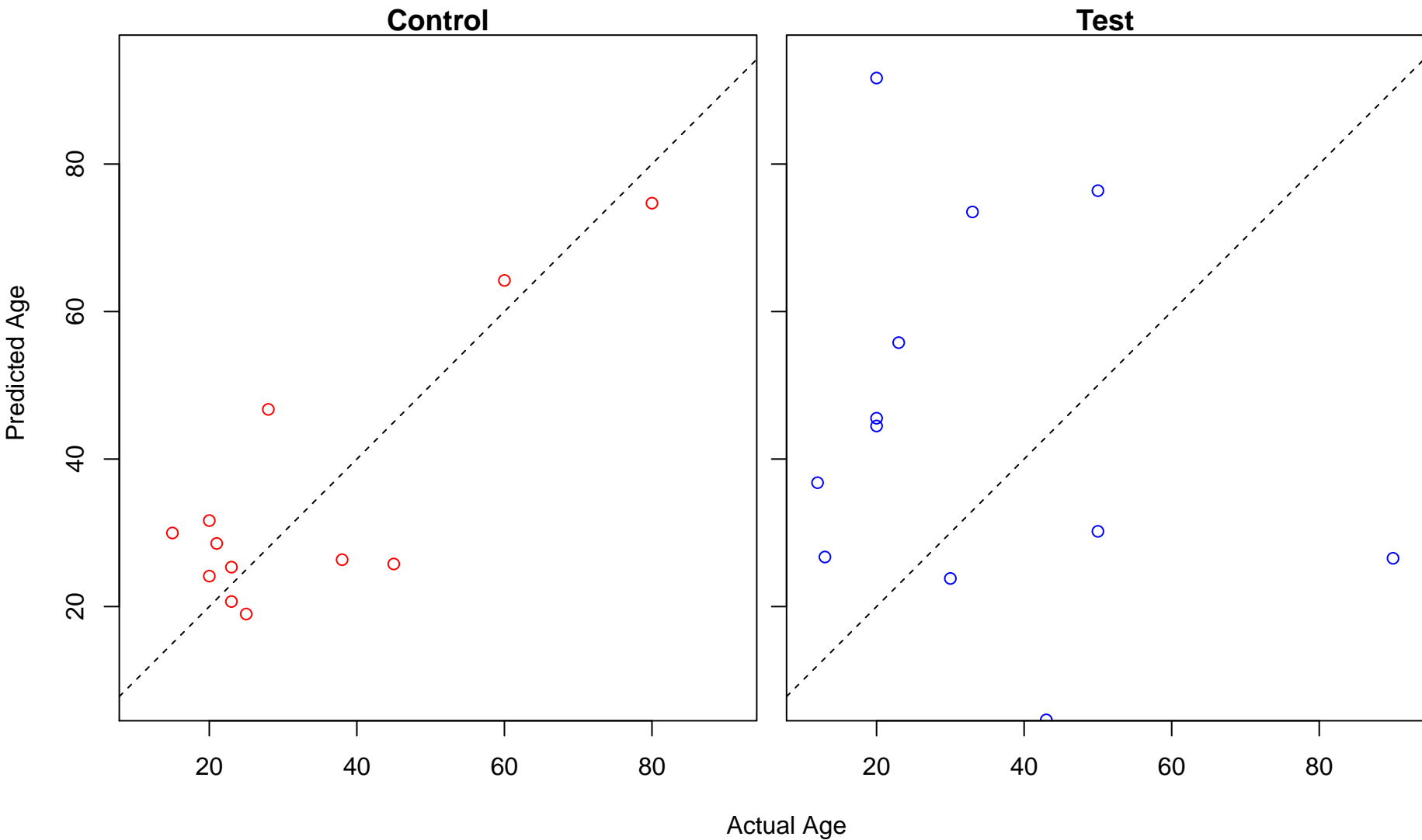
metal ion homeostasis (Score: 7.301931)



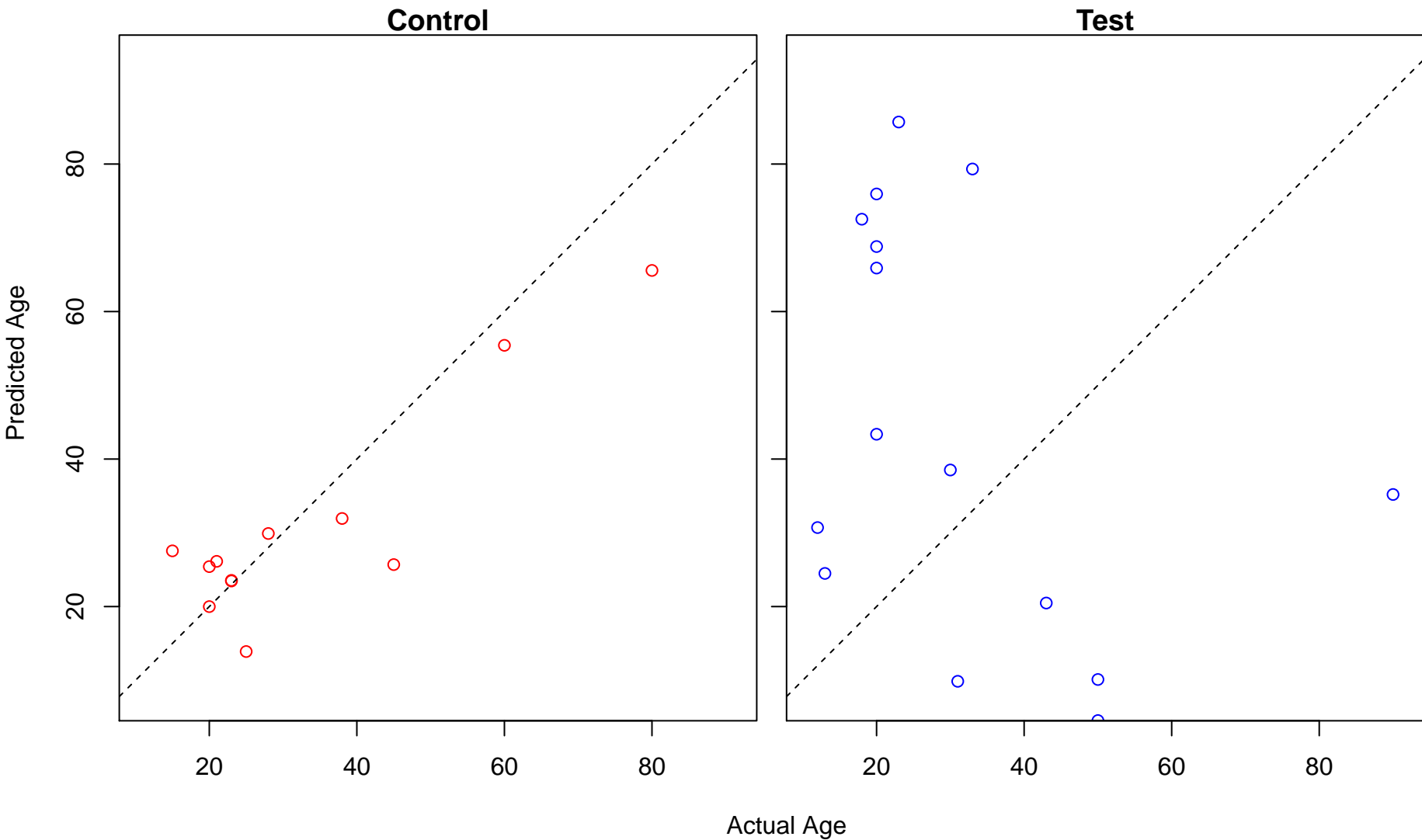
entrainment of circadian clock (Score: 7.298981)



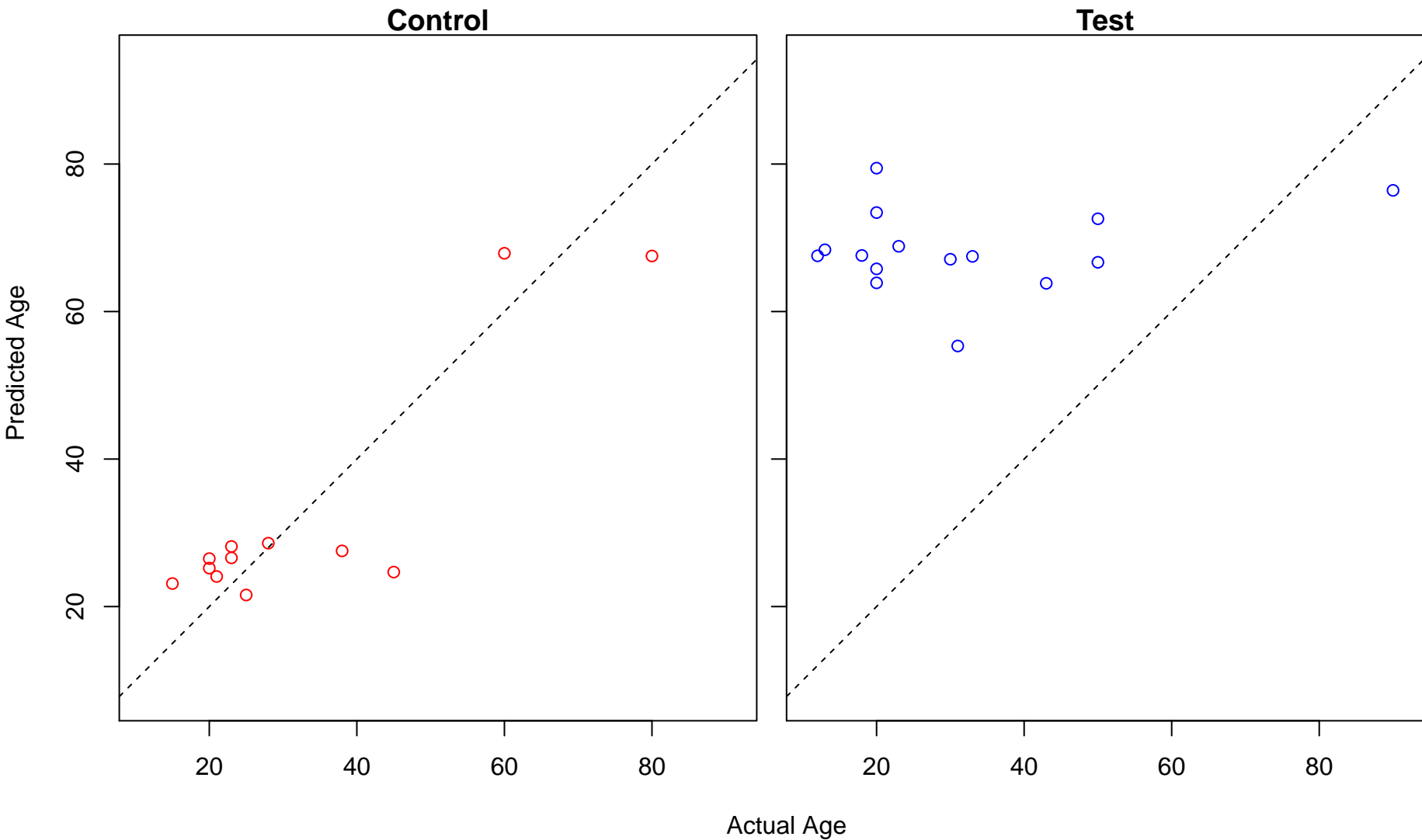
positive regulation of RNA splicing (Score: 7.298217)



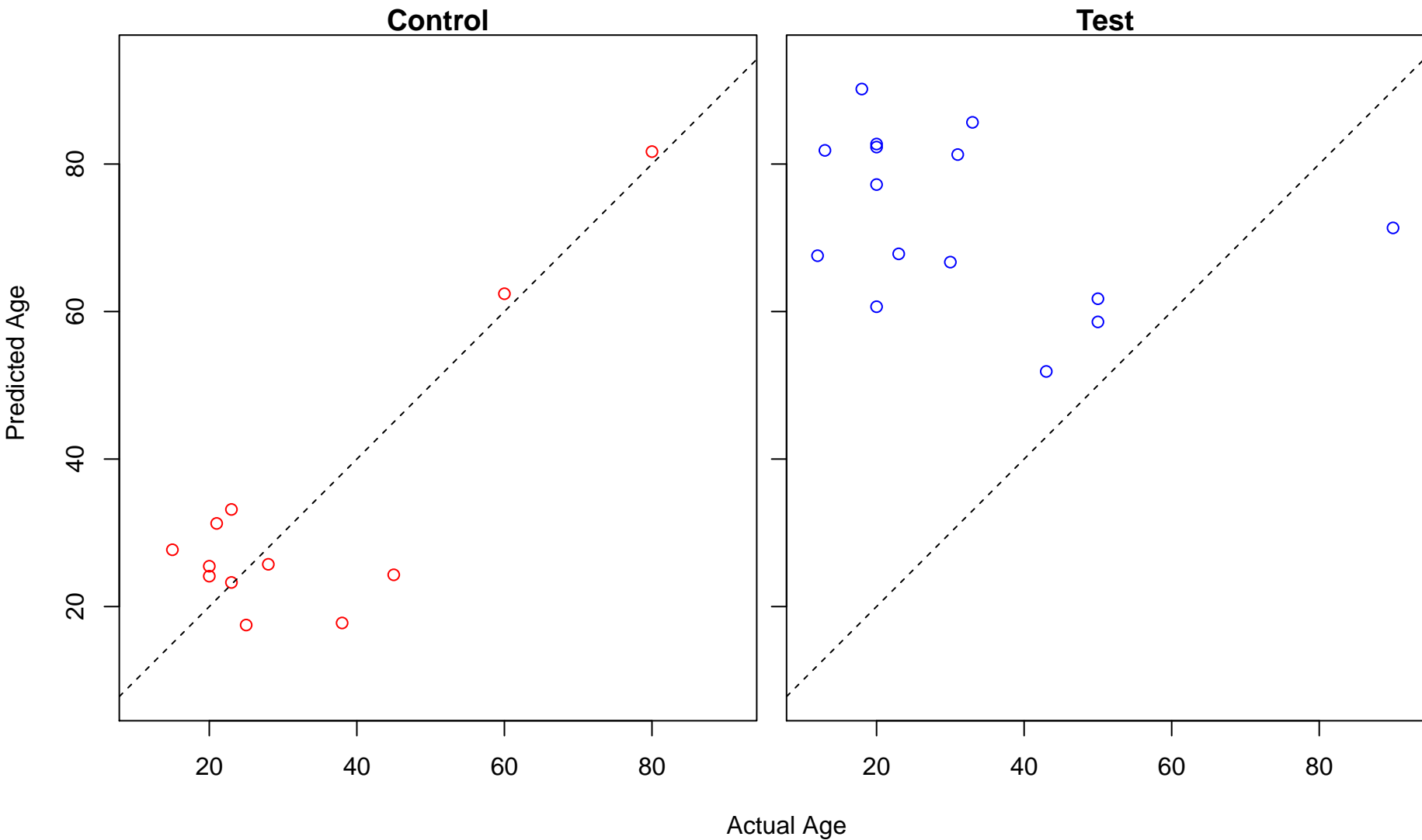
modification by symbiont of host morphology or physiology (Score: 7.296023)



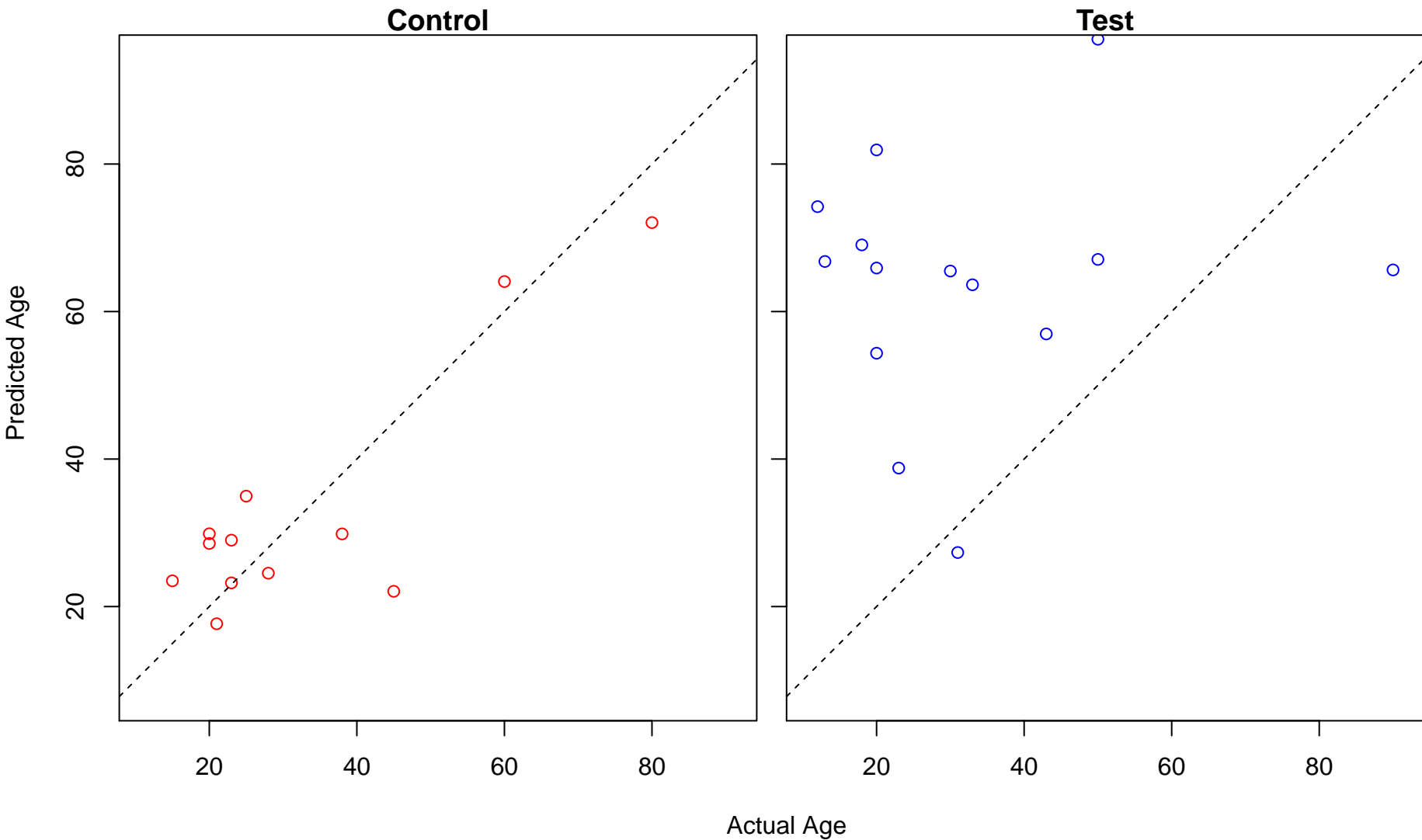
heart development (Score: 7.294658)



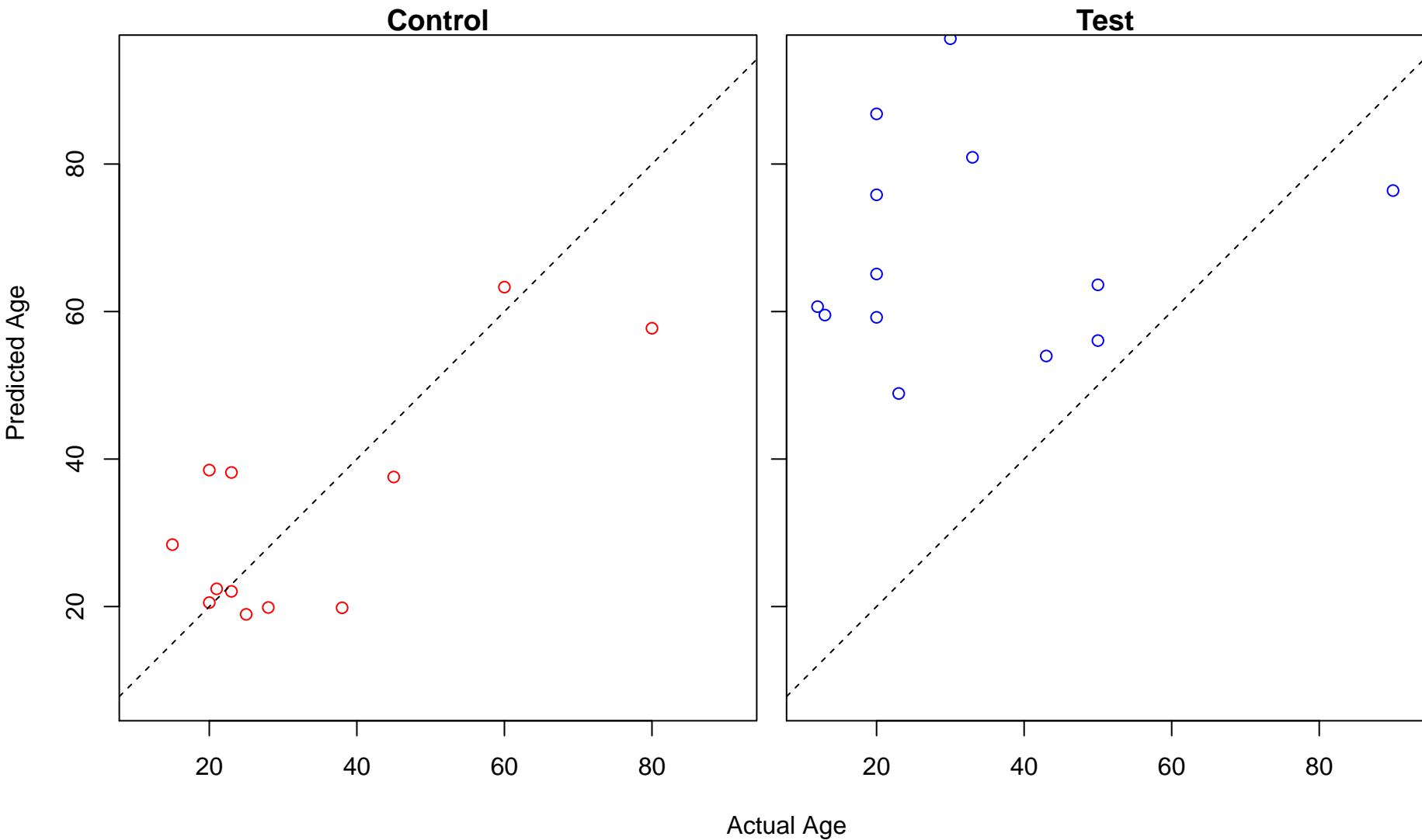
receptor metabolic process (Score: 7.293179)



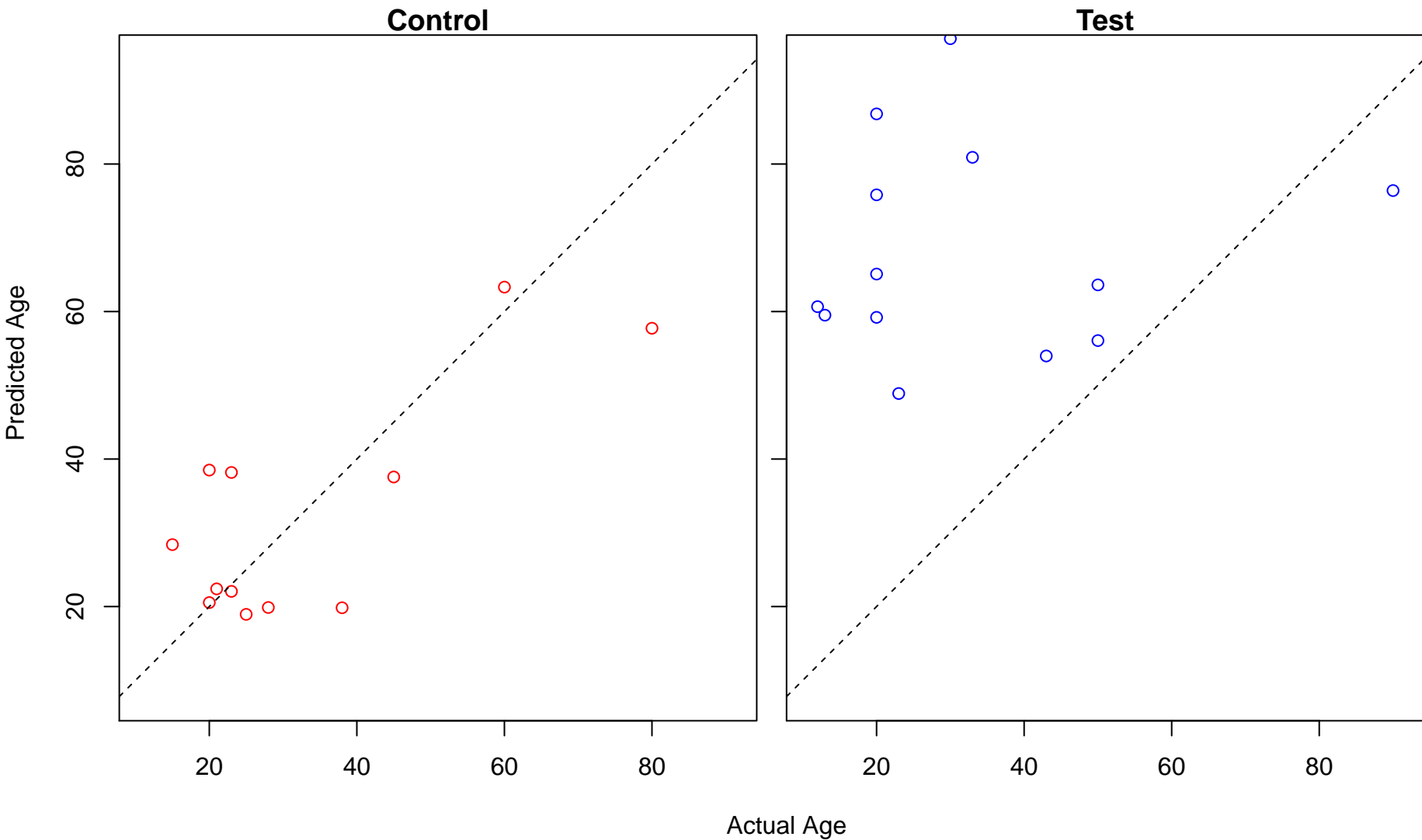
positive regulation of heart rate (Score: 7.290425)



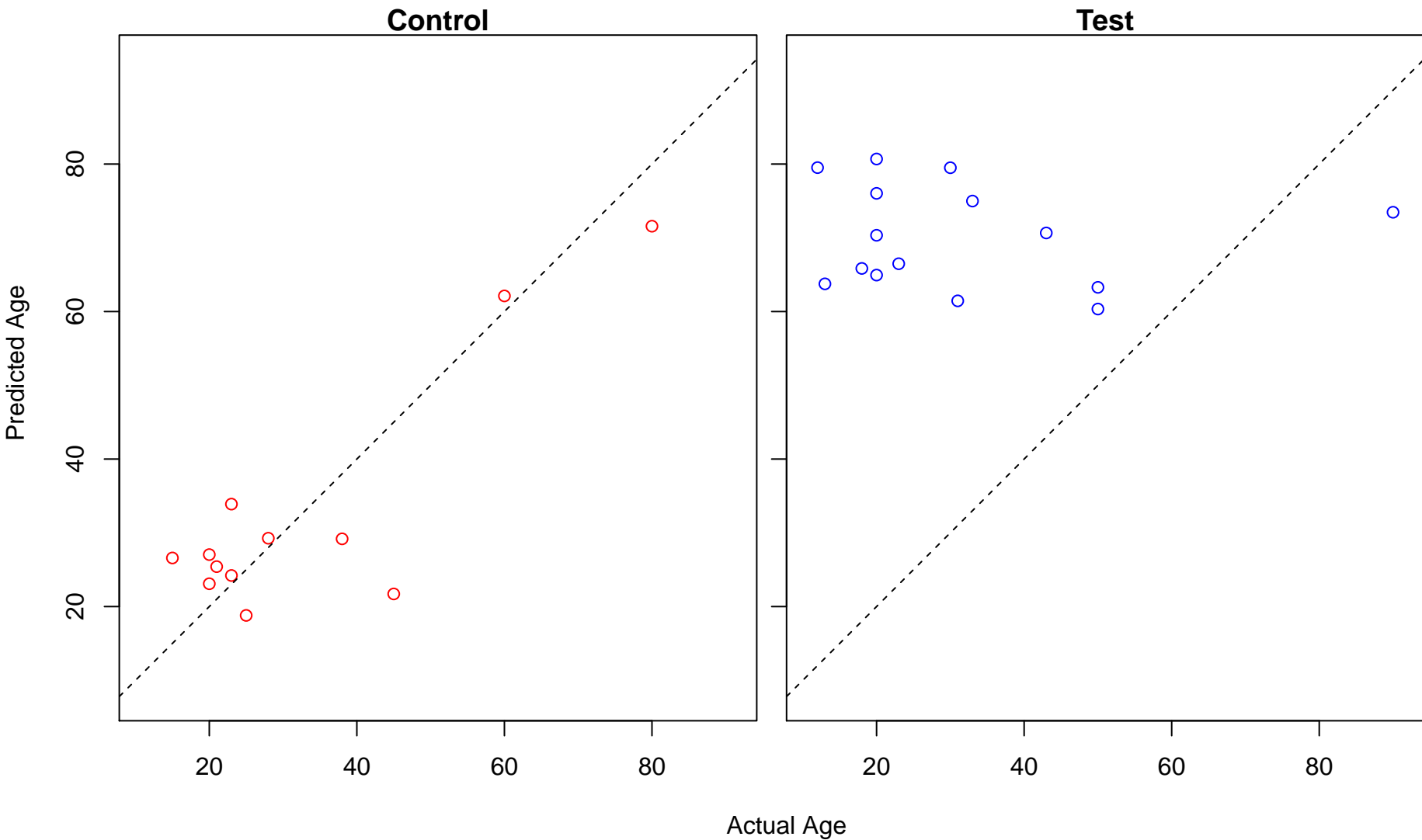
negative regulation of protein activation cascade (Score: 7.289912)



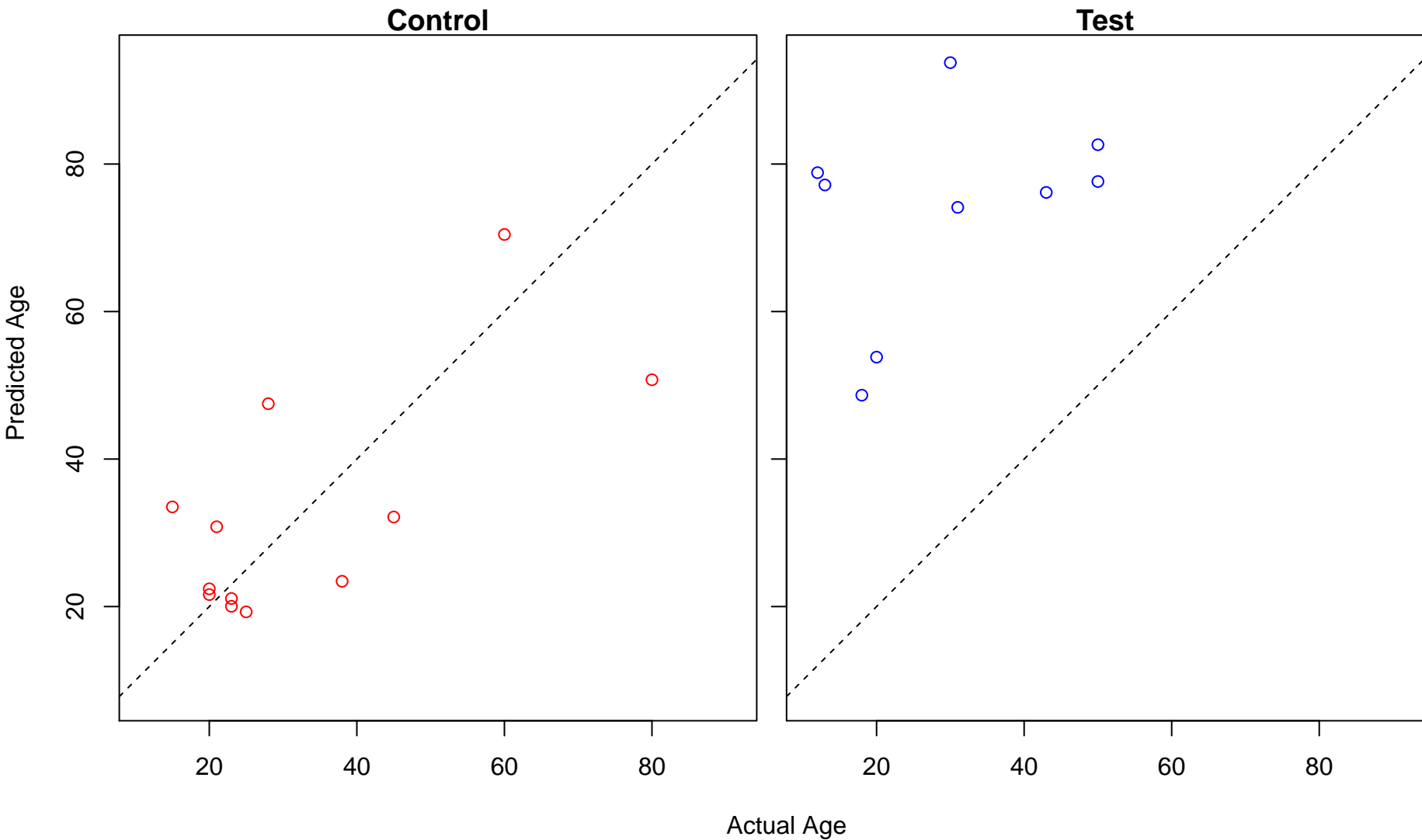
negative regulation of complement activation (Score: 7.289560)



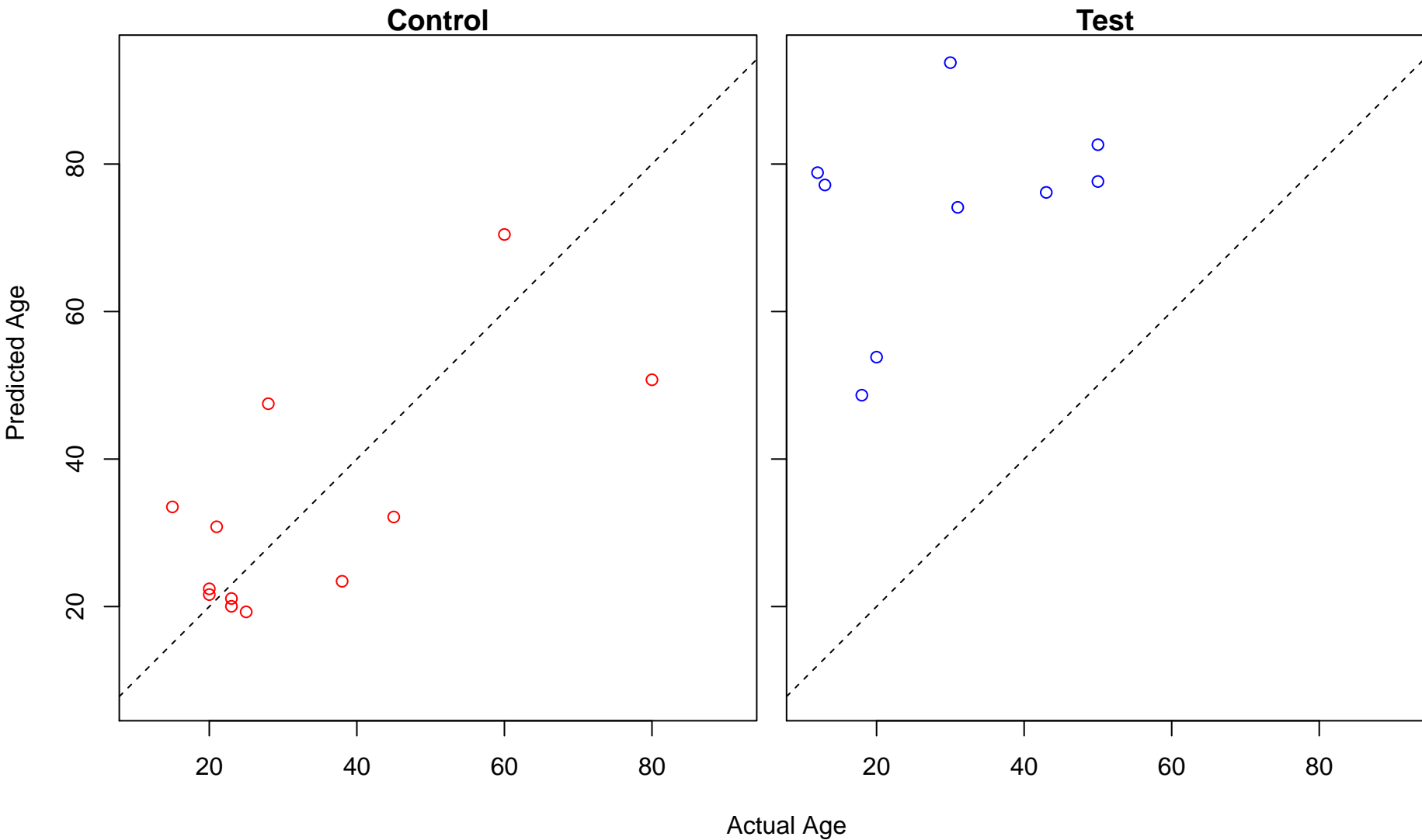
estrogen biosynthetic process (Score: 7.288516)



multicellular organismal movement (Score: 7.288138)

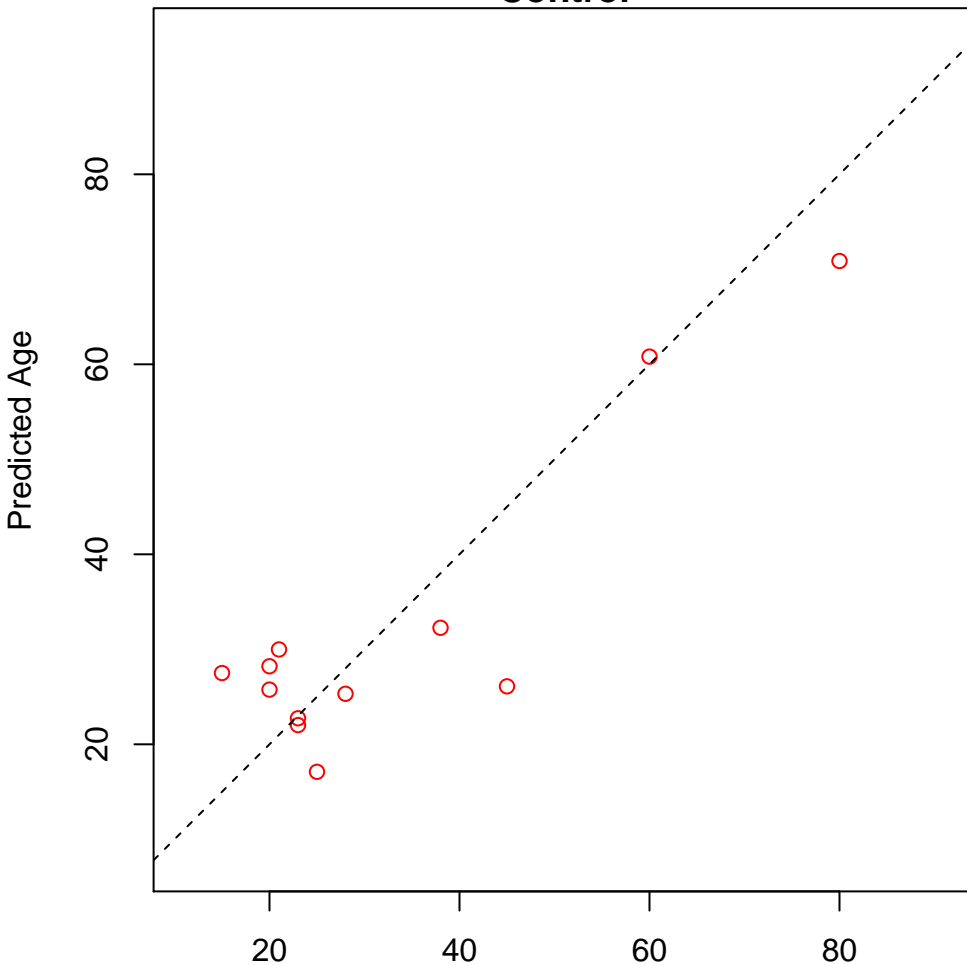


musculoskeletal movement (Score: 7.288138)

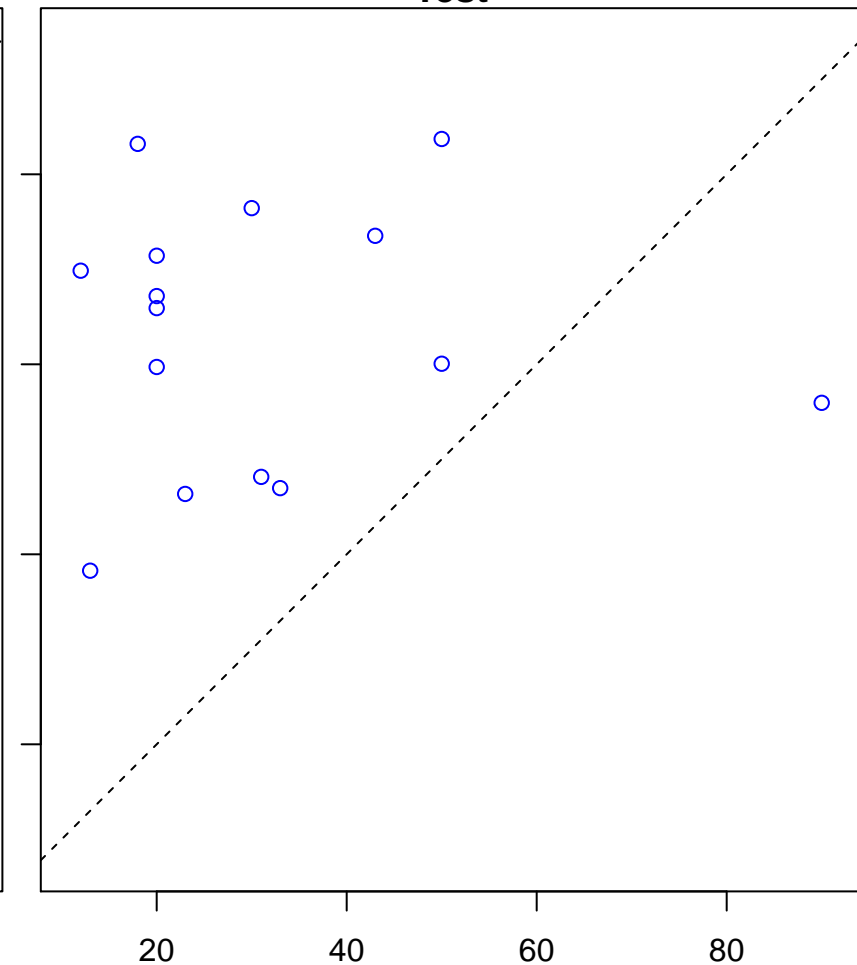


primary alcohol metabolic process (Score: 7.276198)

Control



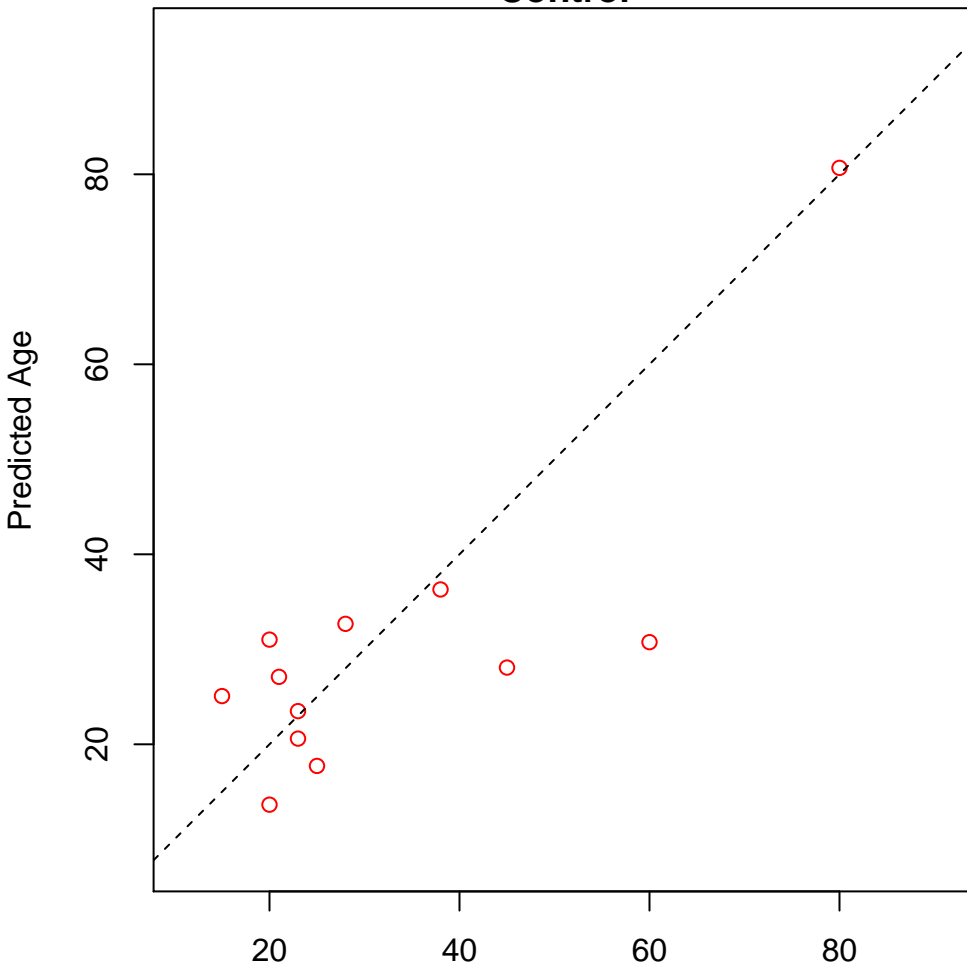
Test



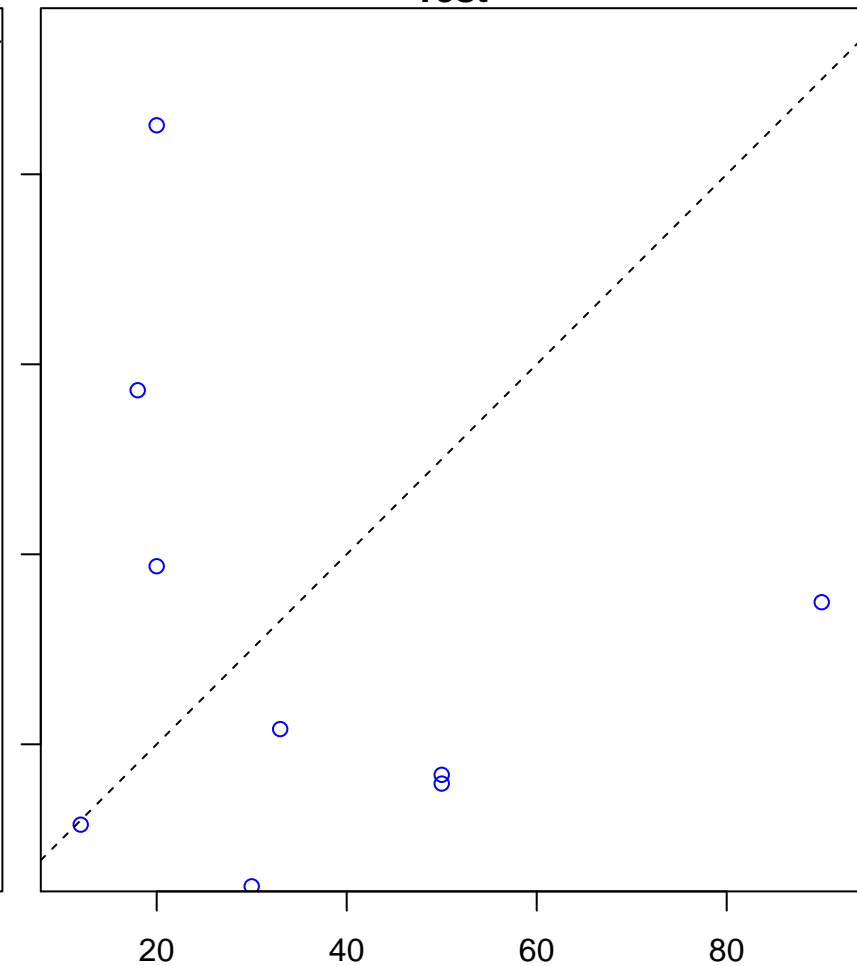
Actual Age

skeletal muscle organ development (Score: 7.276184)

Control

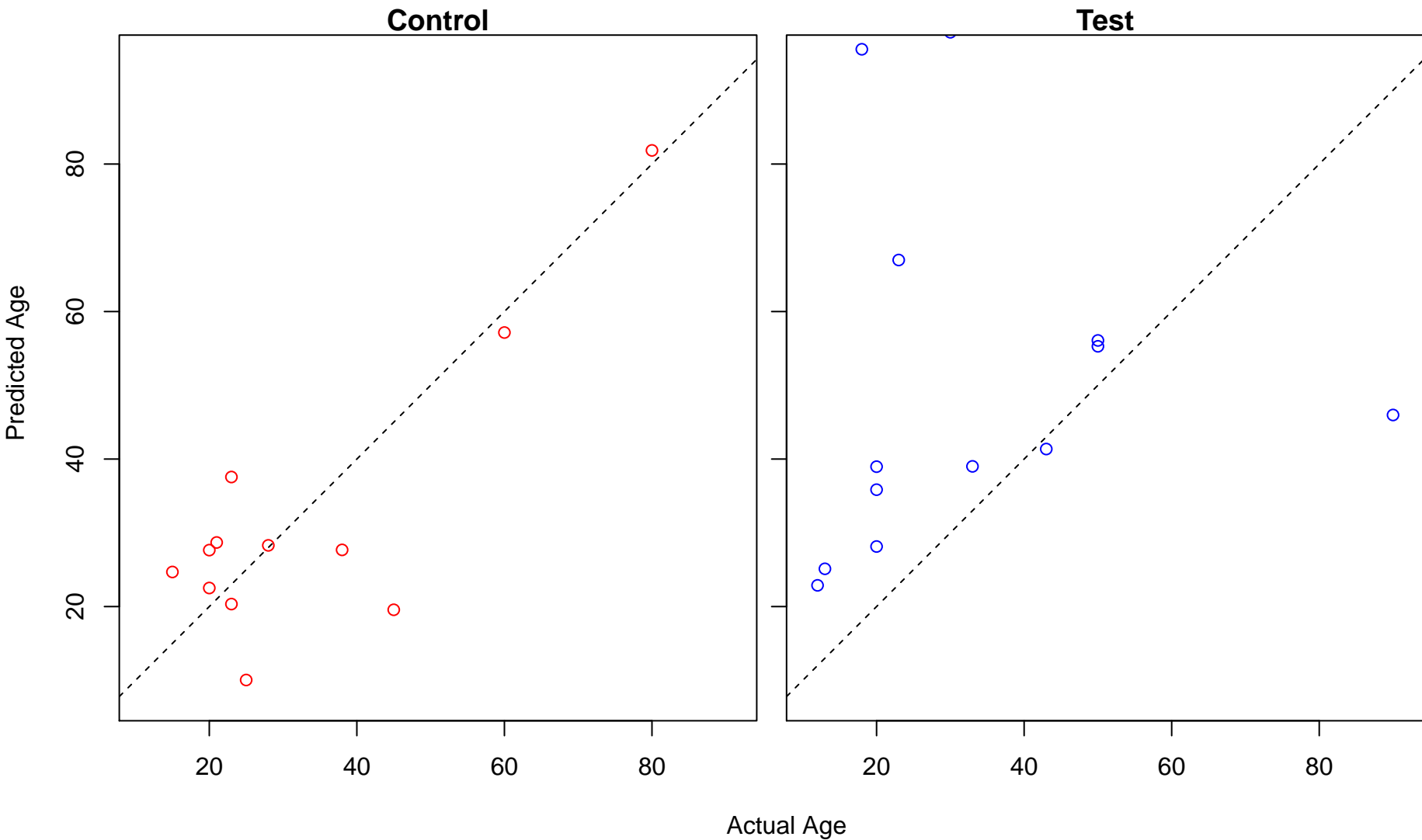


Test

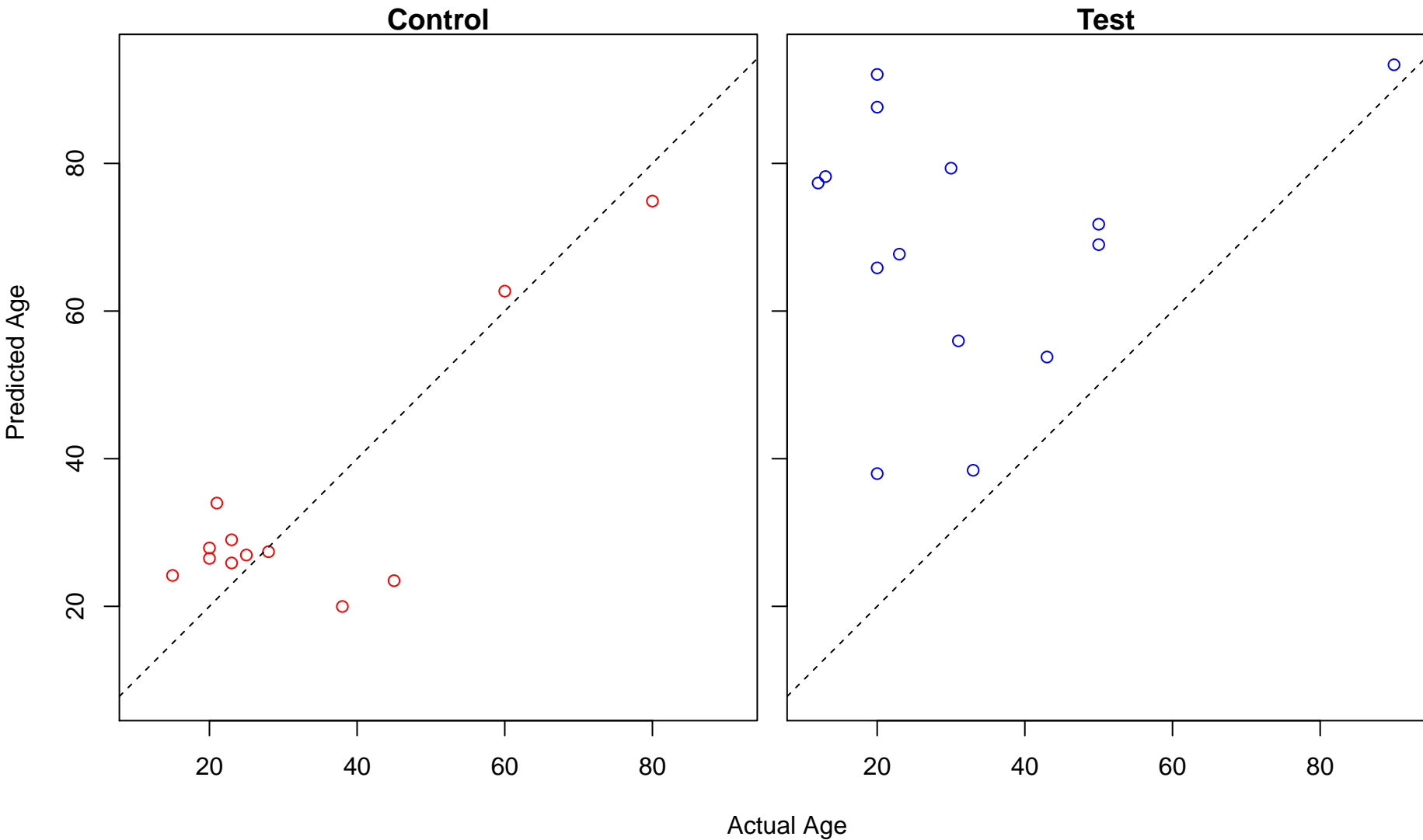


Actual Age

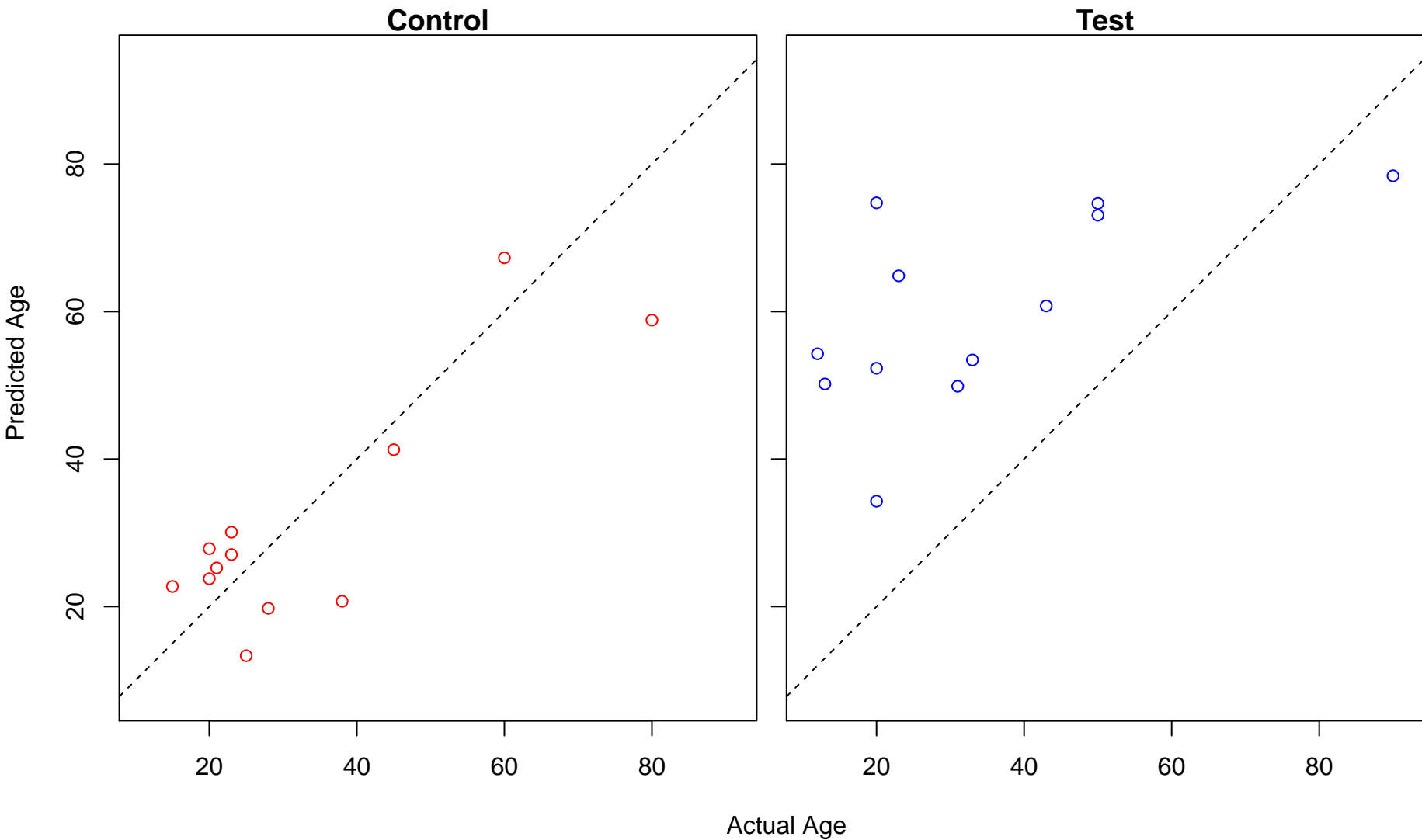
regulation of lymphocyte activation (Score: 7.274216)



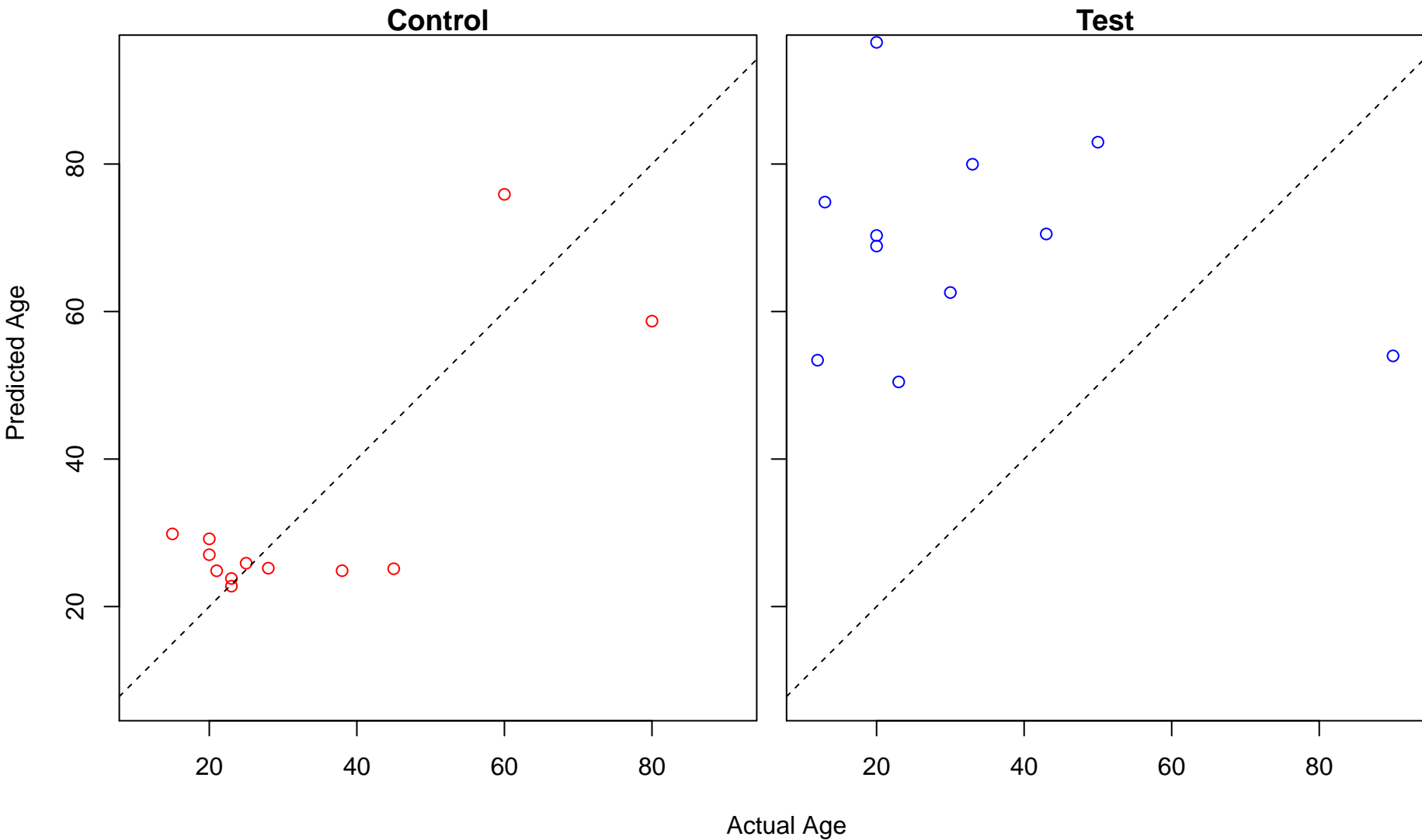
negative regulation of endoplasmic reticulum calcium ion concentration (Score: 7.270862)



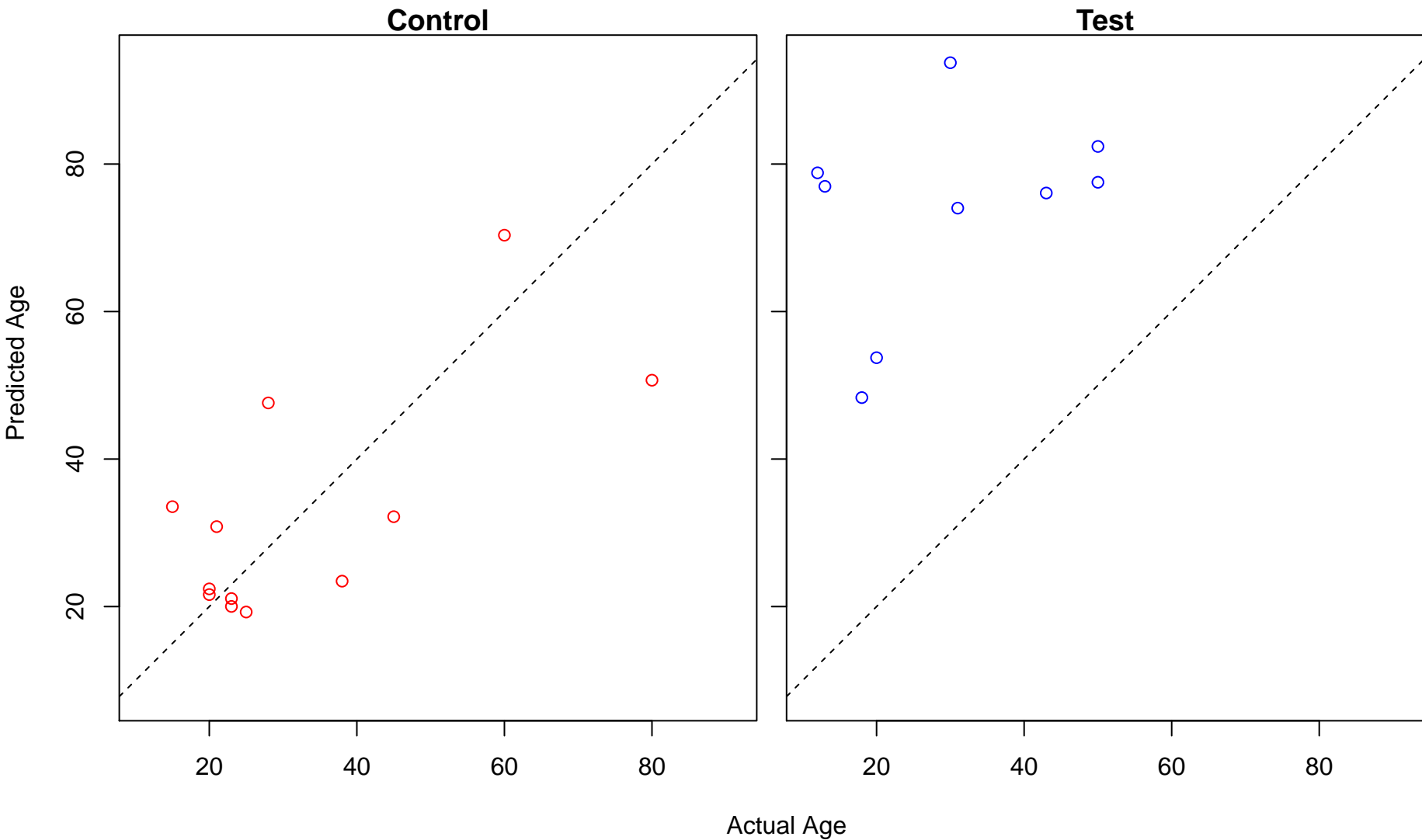
response to cocaine (Score: 7.268822)



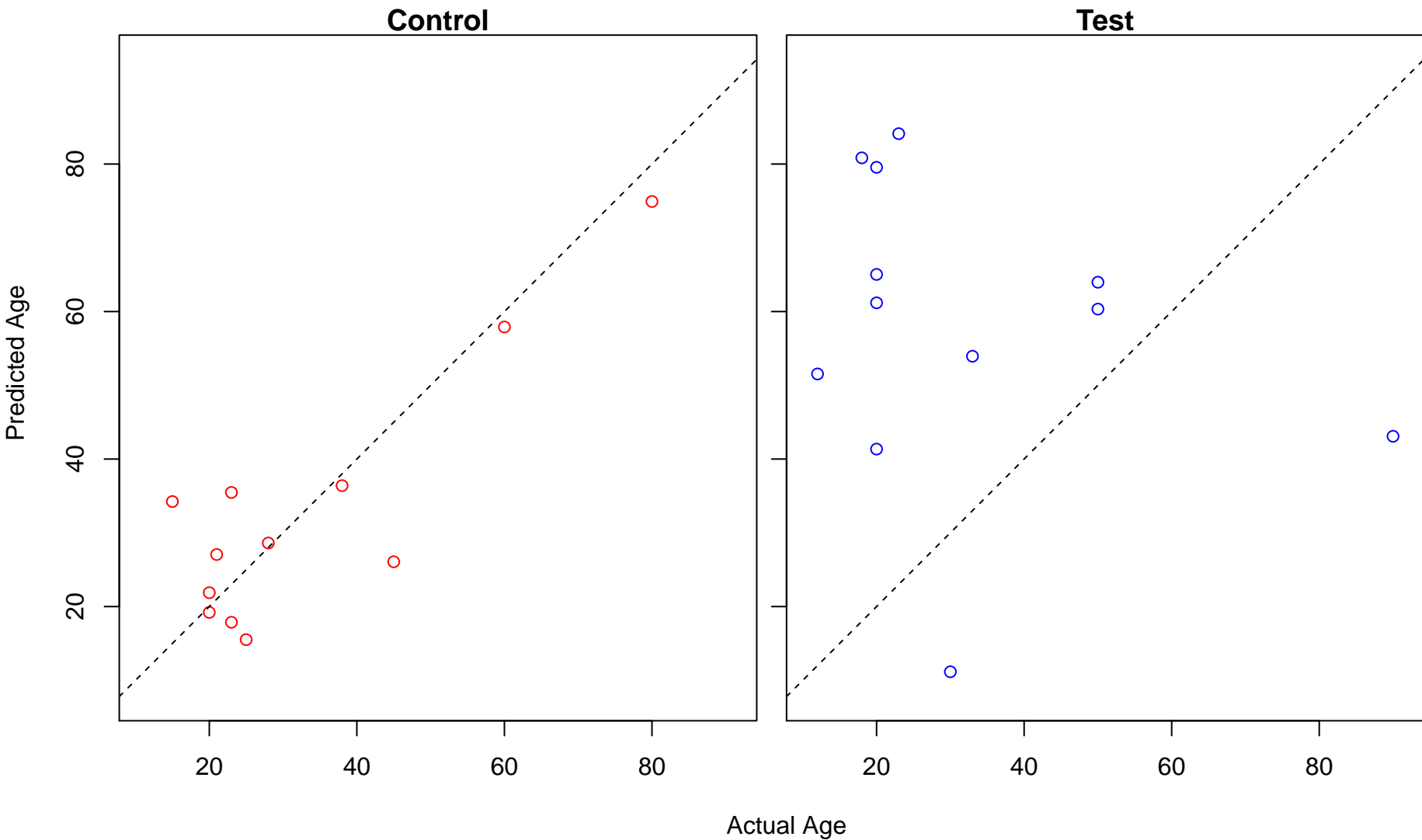
hexose transmembrane transport (Score: 7.268149)



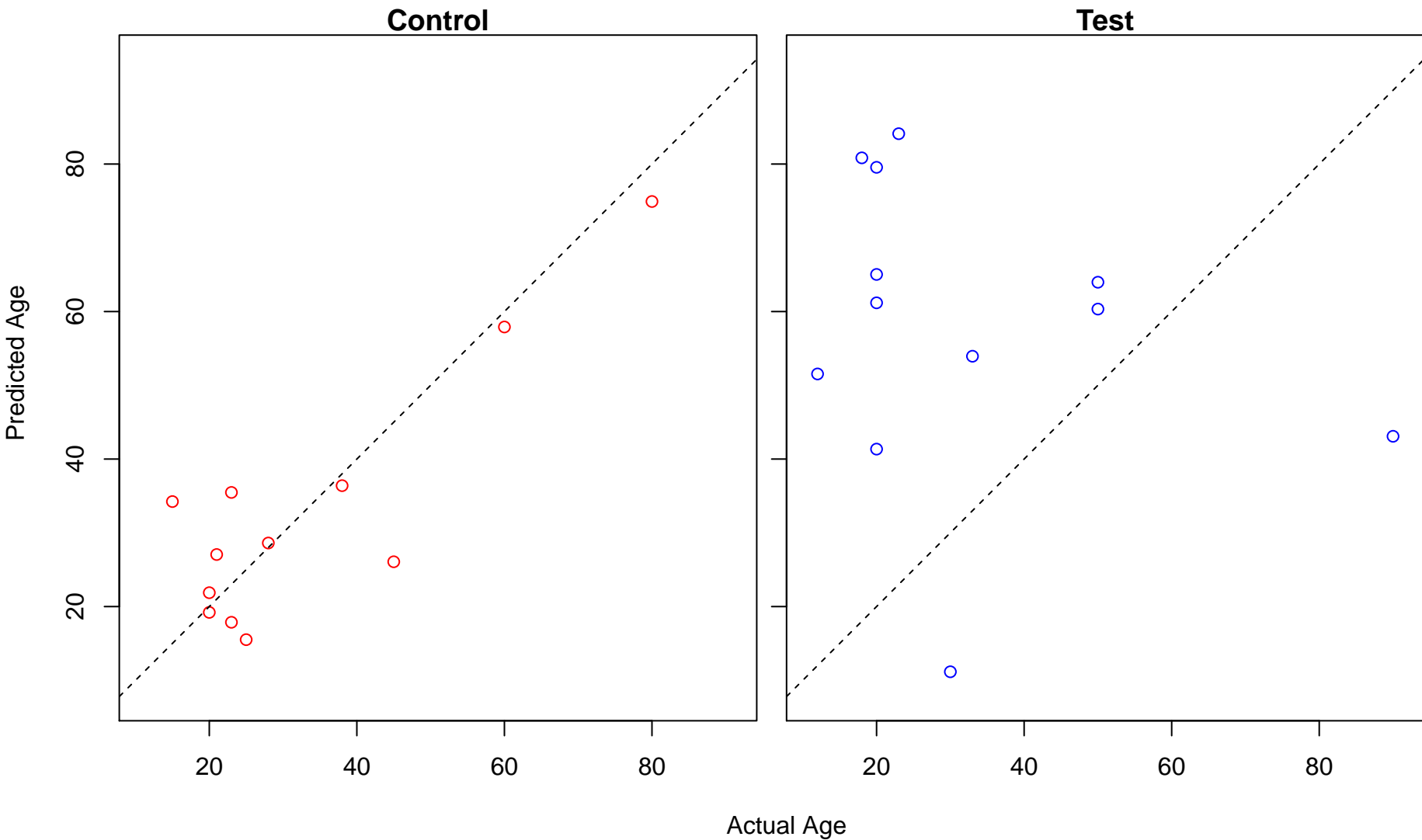
skeletal muscle contraction (Score: 7.266287)



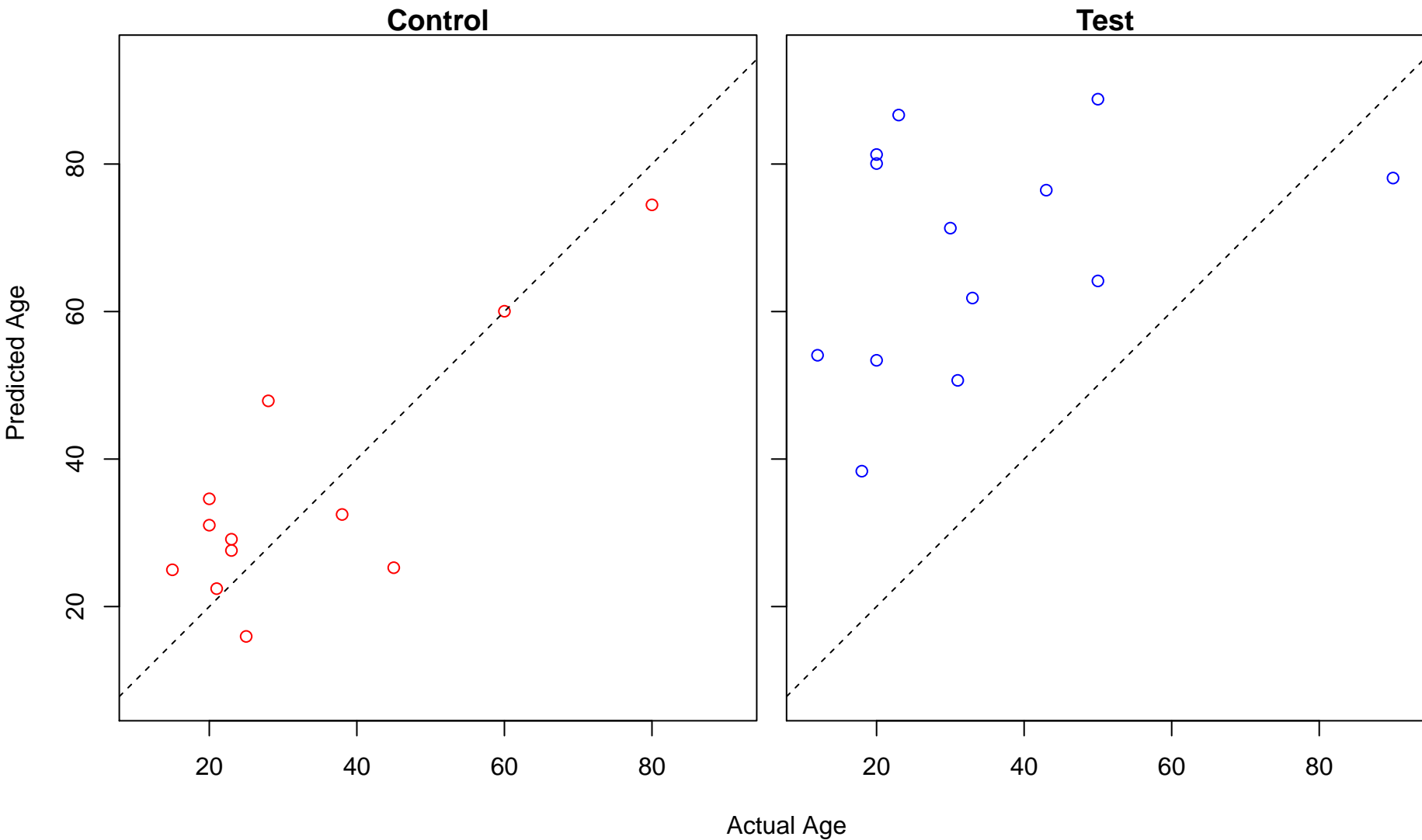
dsRNA fragmentation (Score: 7.263385)



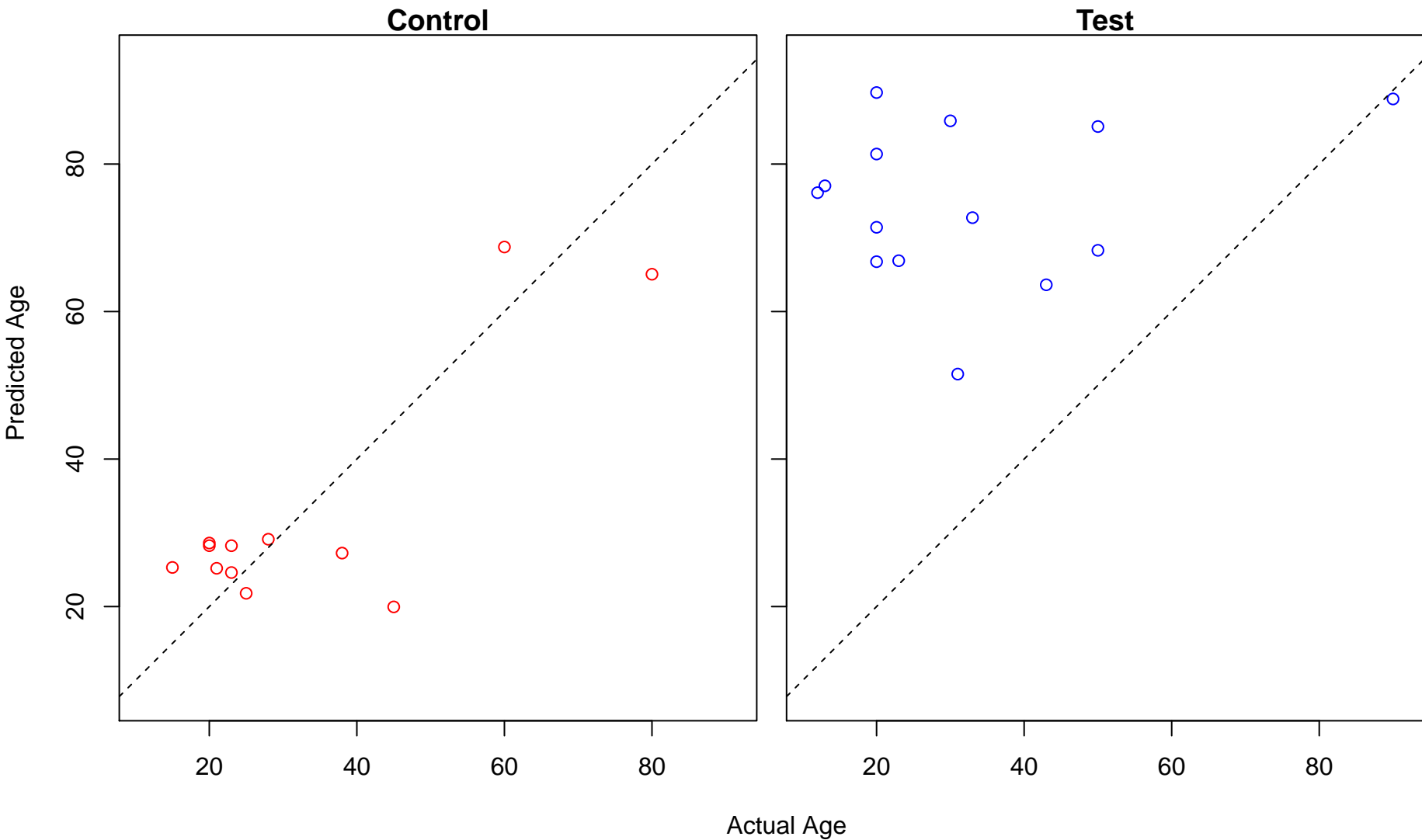
production of small RNA involved in gene silencing by RNA (Score: 7.263385)



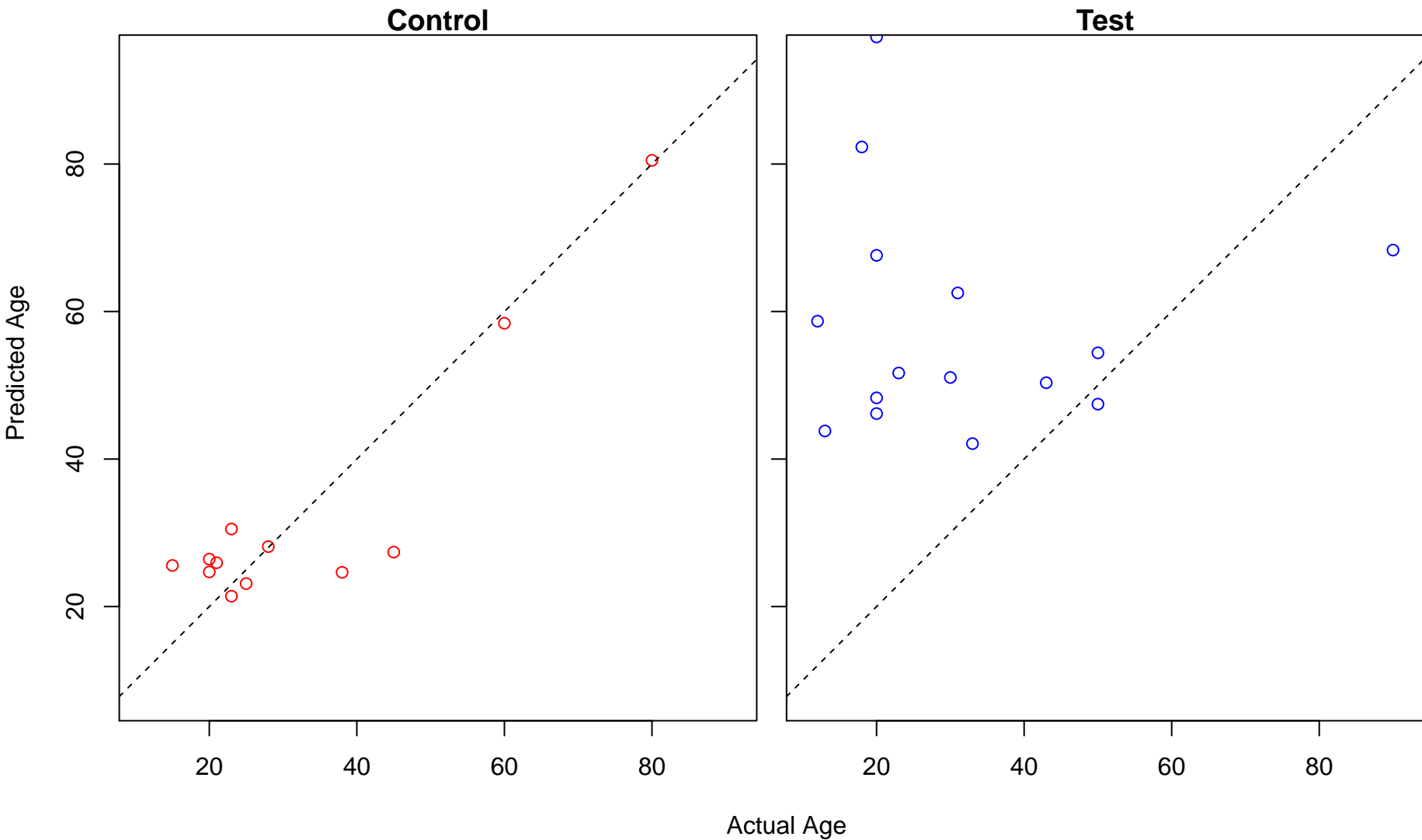
extracellular matrix assembly (Score: 7.257748)



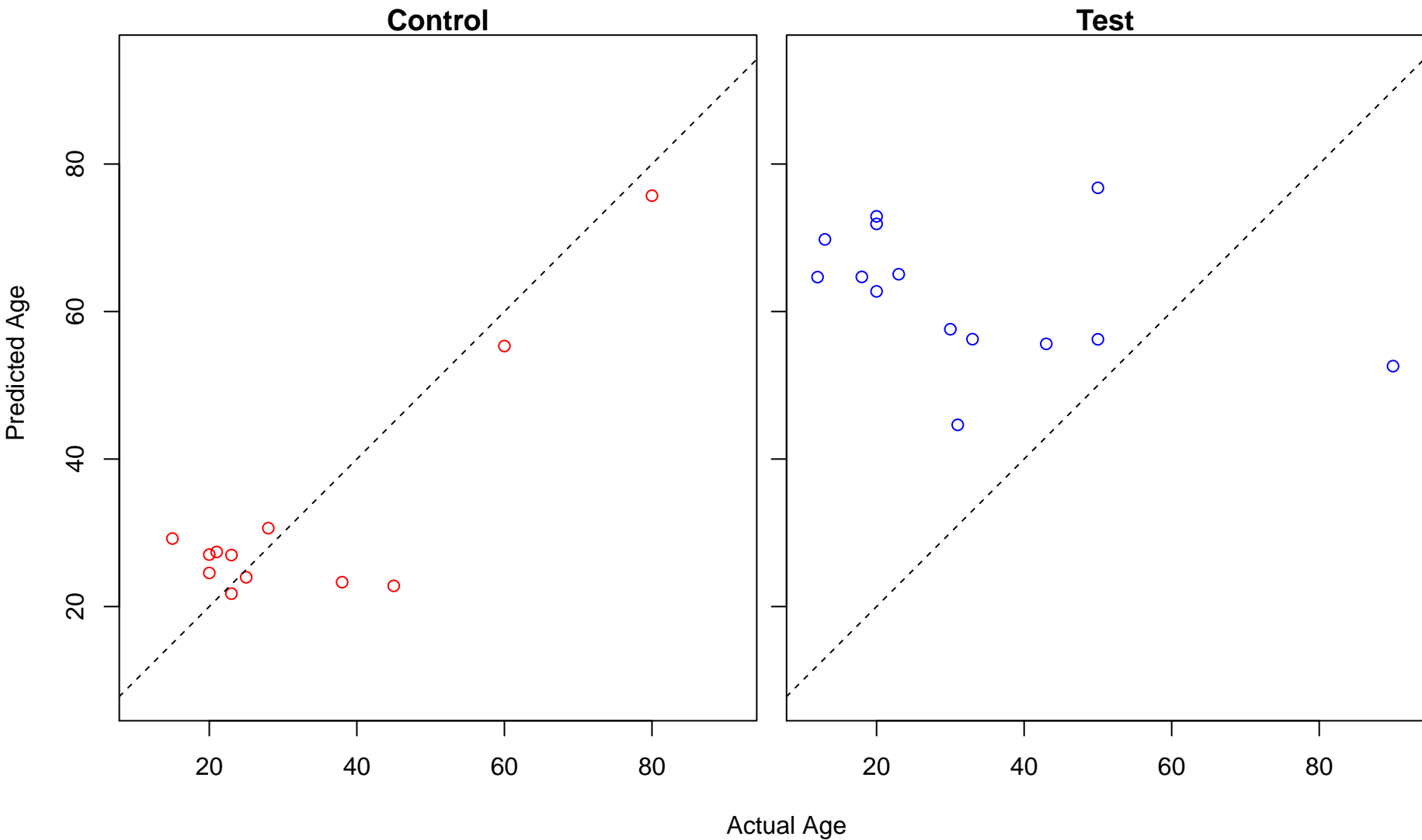
negative regulation of cytokinesis (Score: 7.256707)



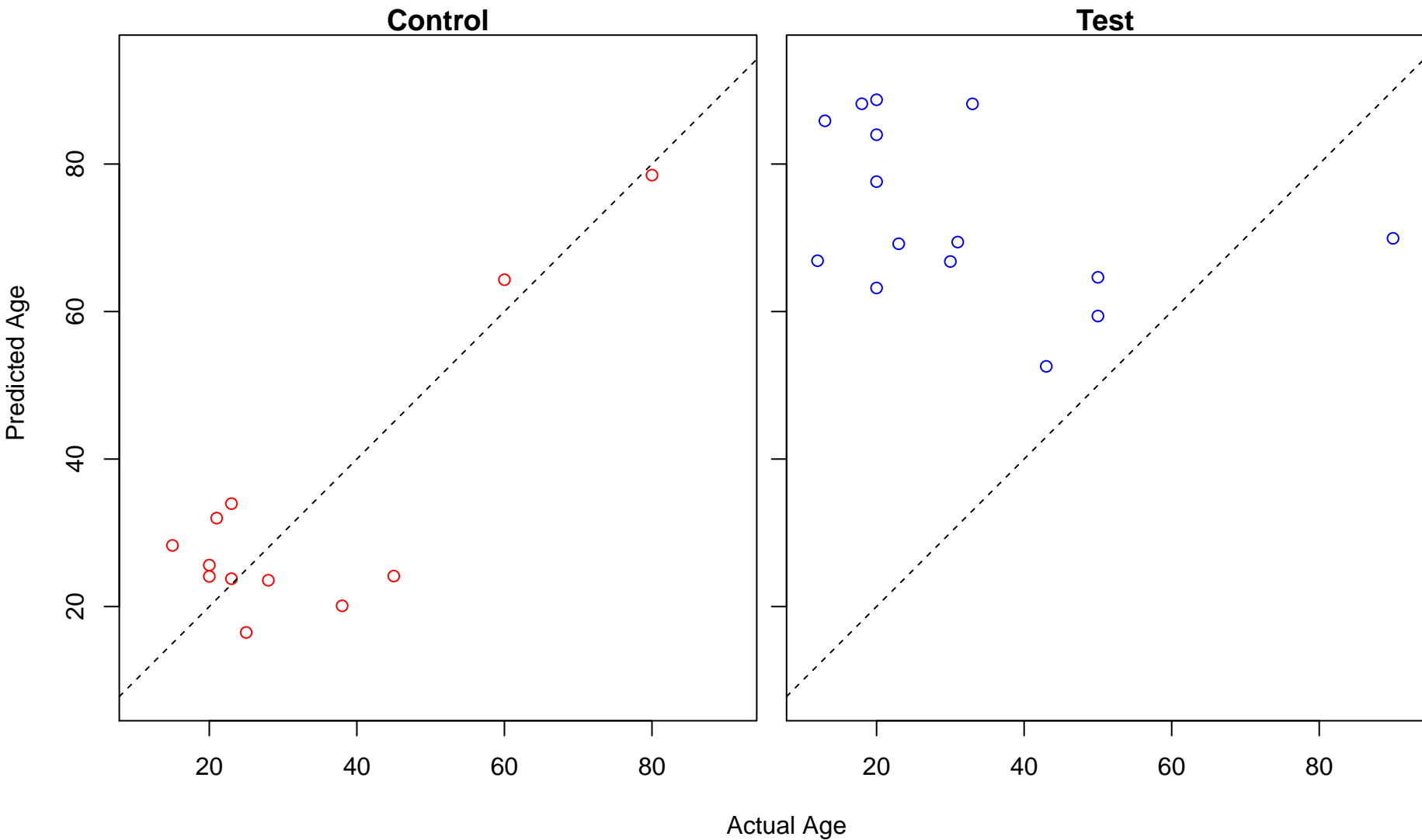
glycerolipid catabolic process (Score: 7.255770)



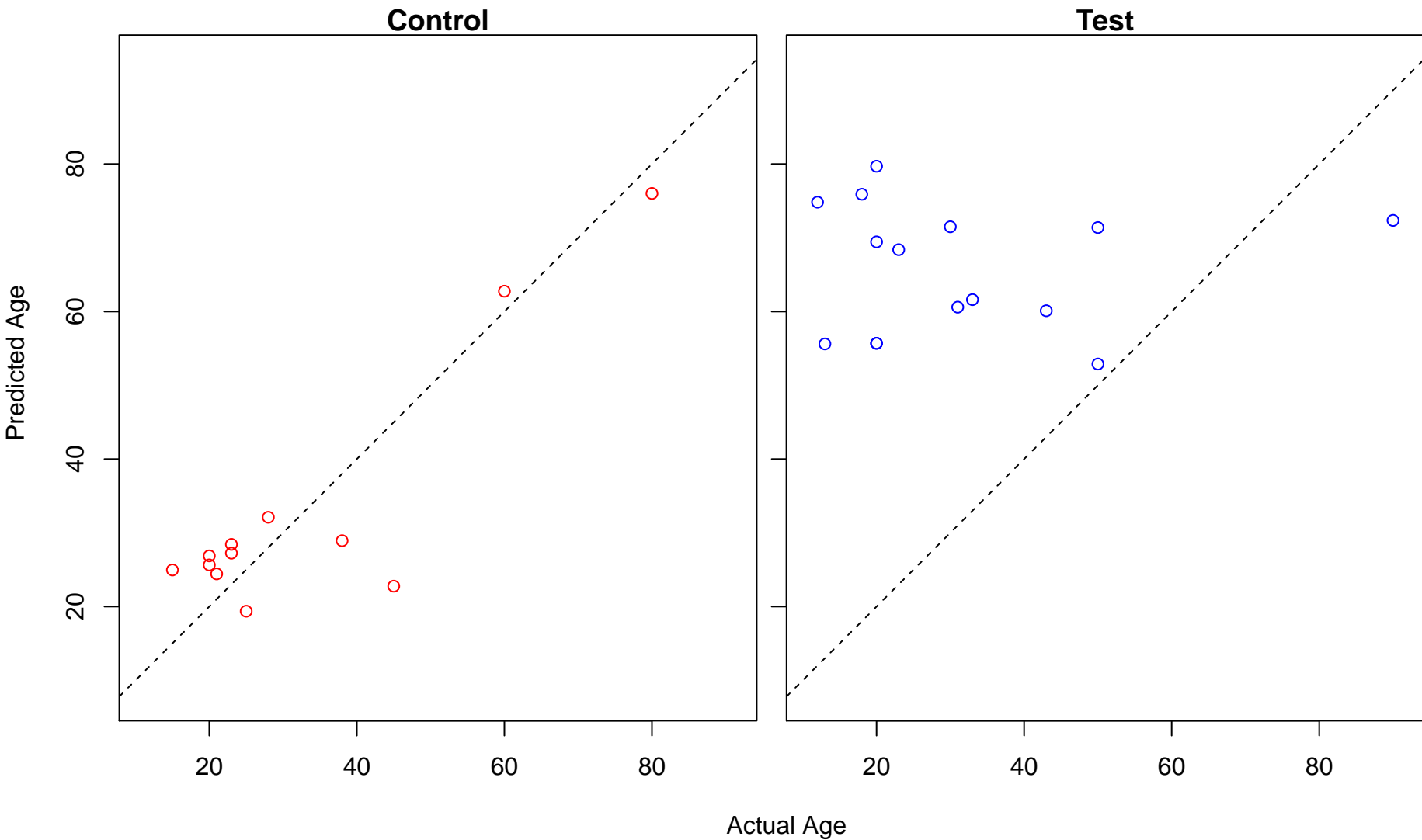
negative regulation of alcohol biosynthetic process (Score: 7.254937)



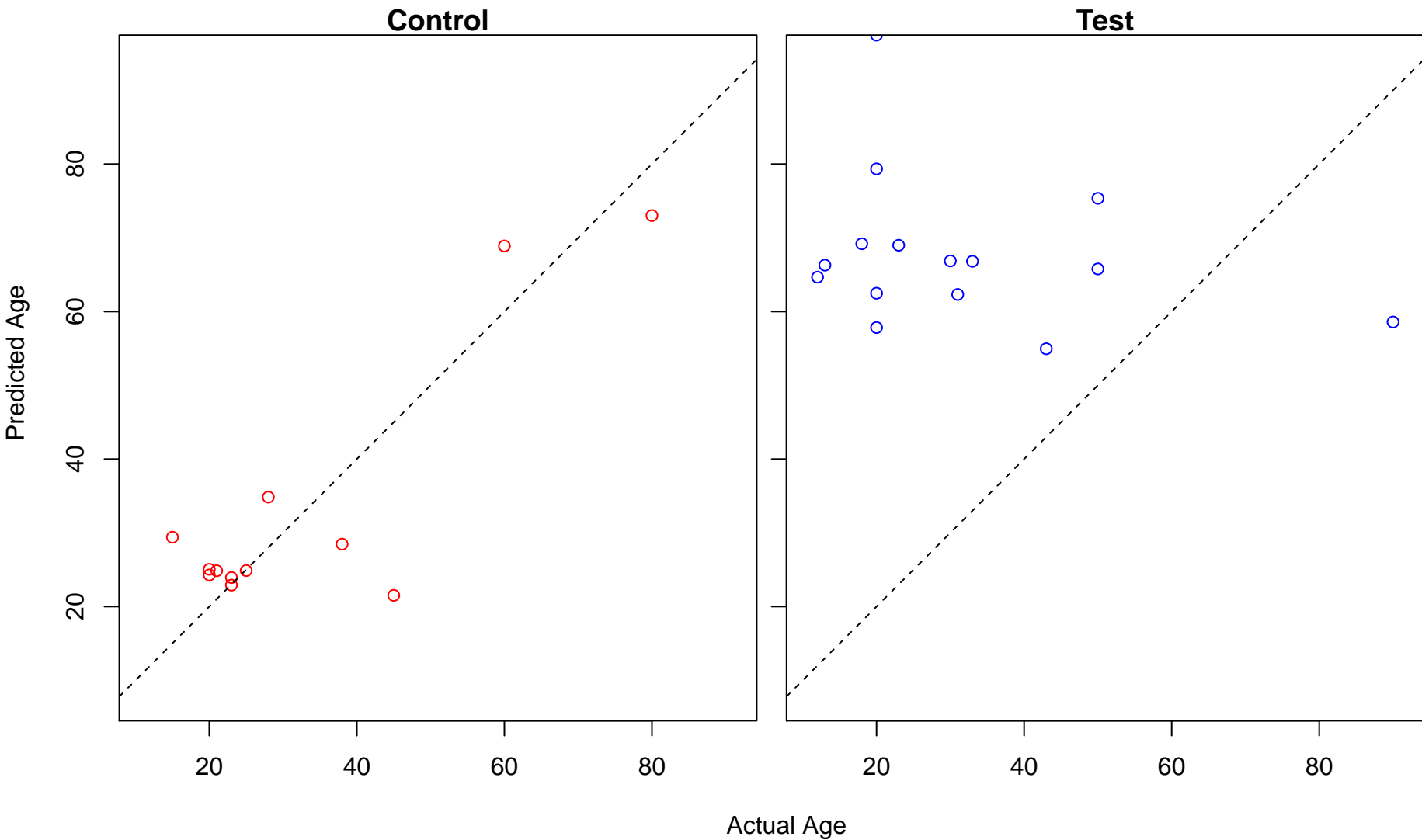
receptor internalization (Score: 7.254088)



histone H2B ubiquitination (Score: 7.252337)

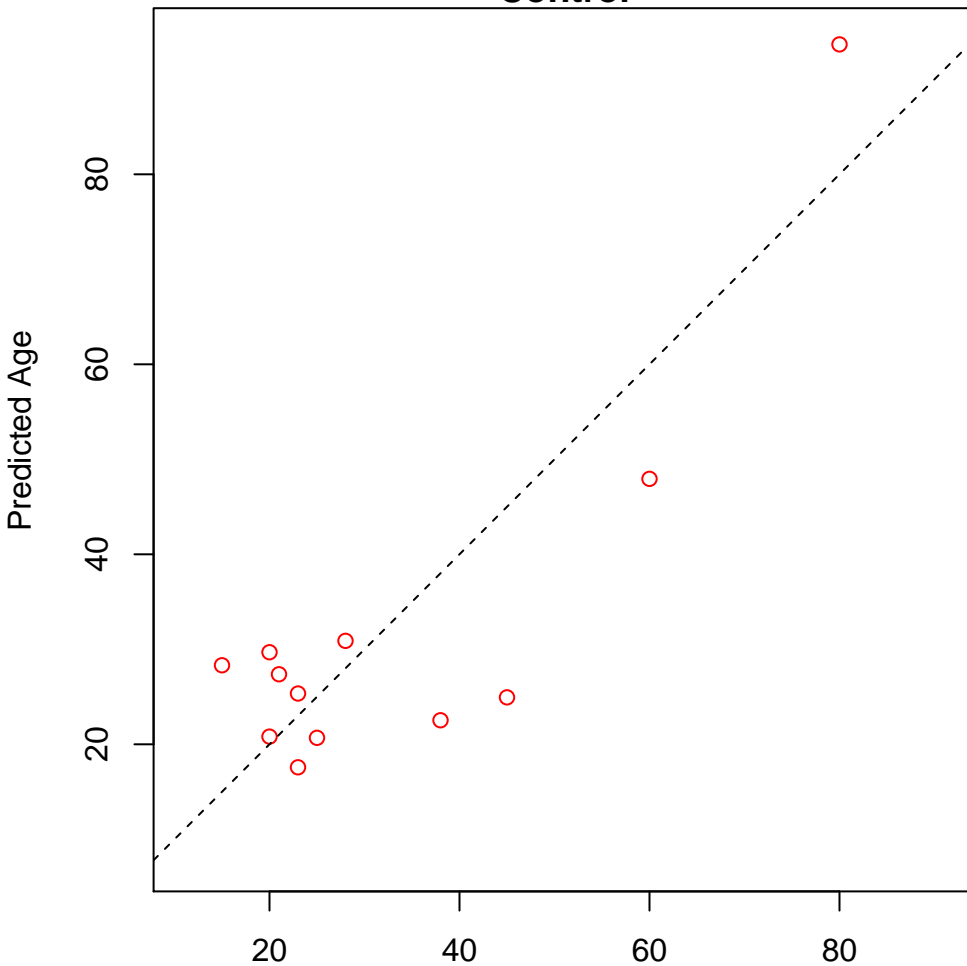


regulation of activin receptor signaling pathway (Score: 7.251892)

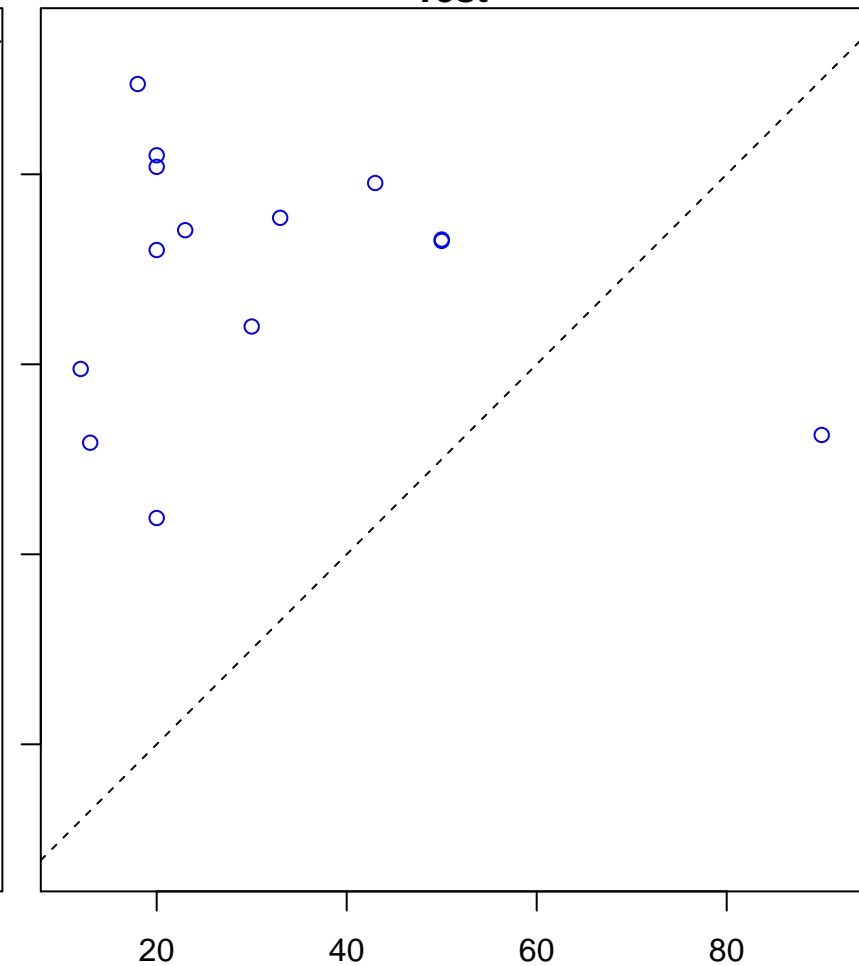


protein folding in endoplasmic reticulum (Score: 7.251731)

Control

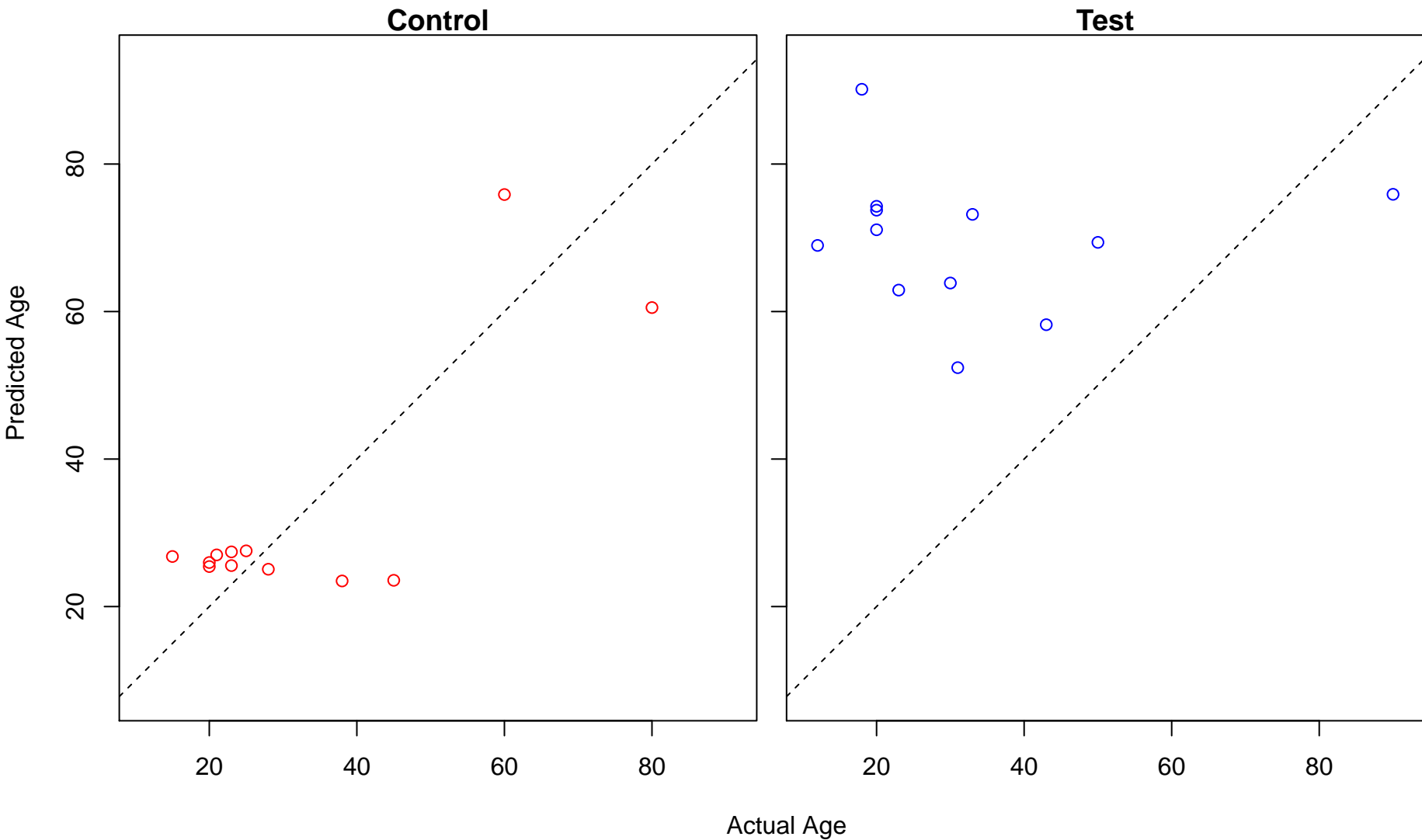


Test

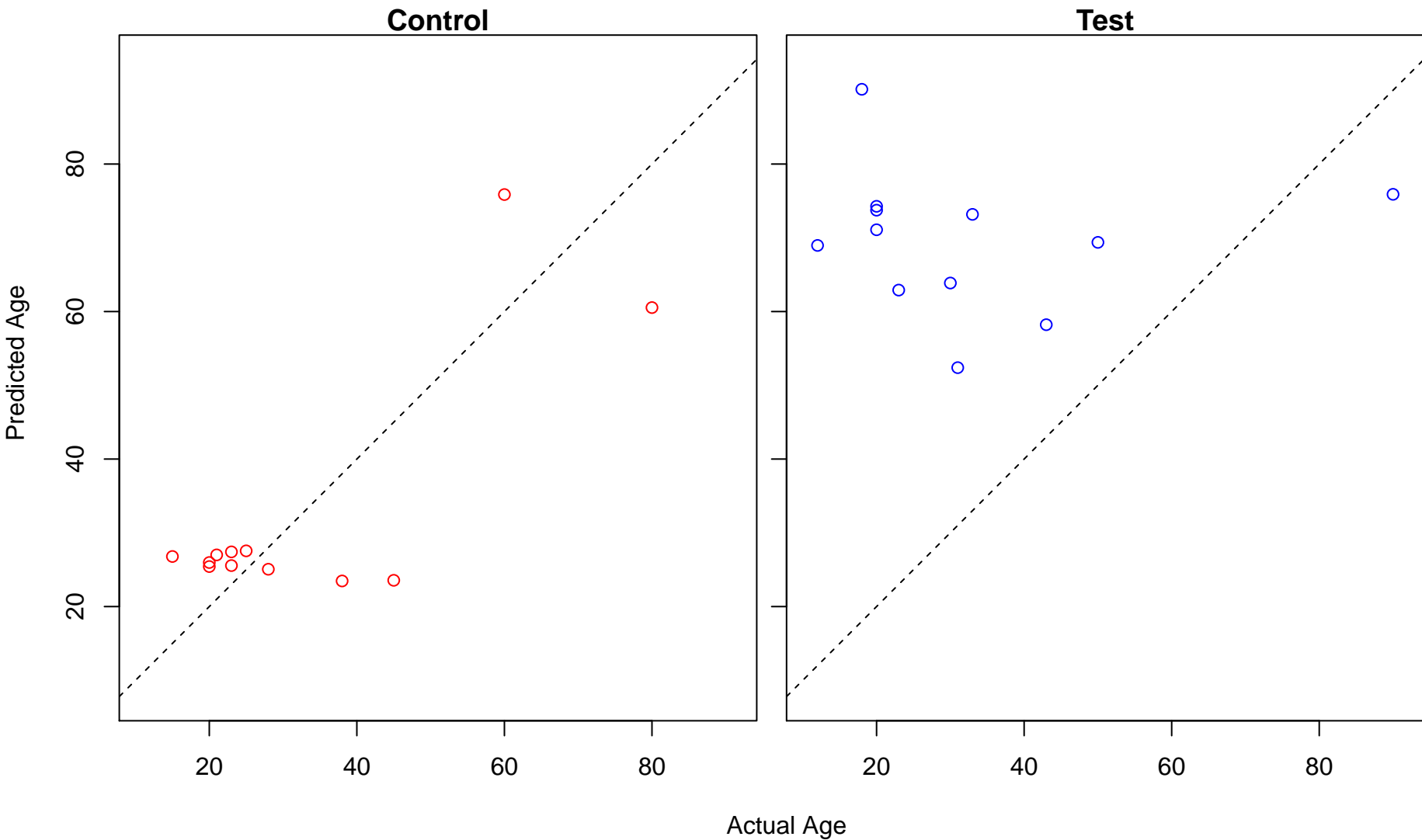


Actual Age

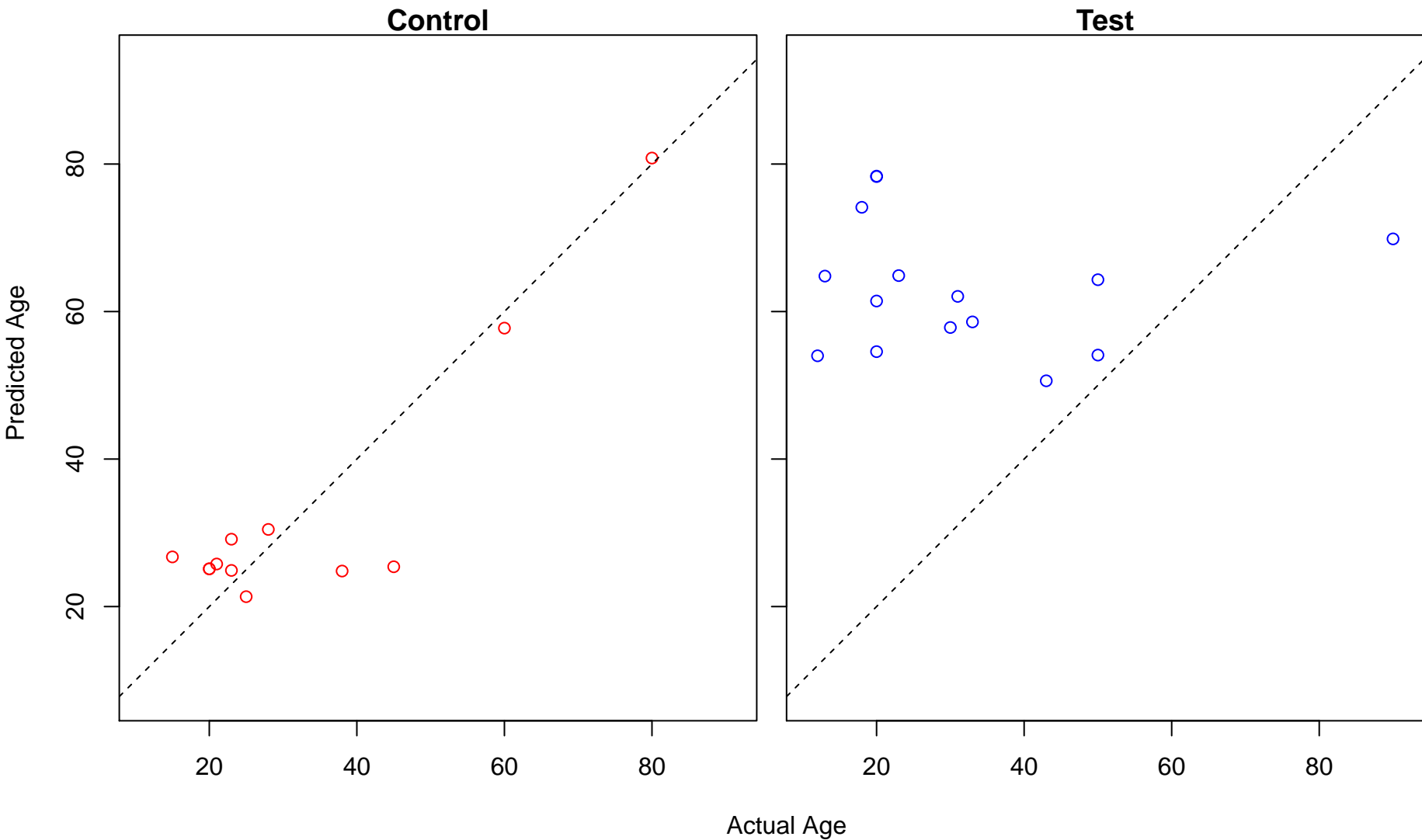
multi-organism metabolic process (Score: 7.251081)



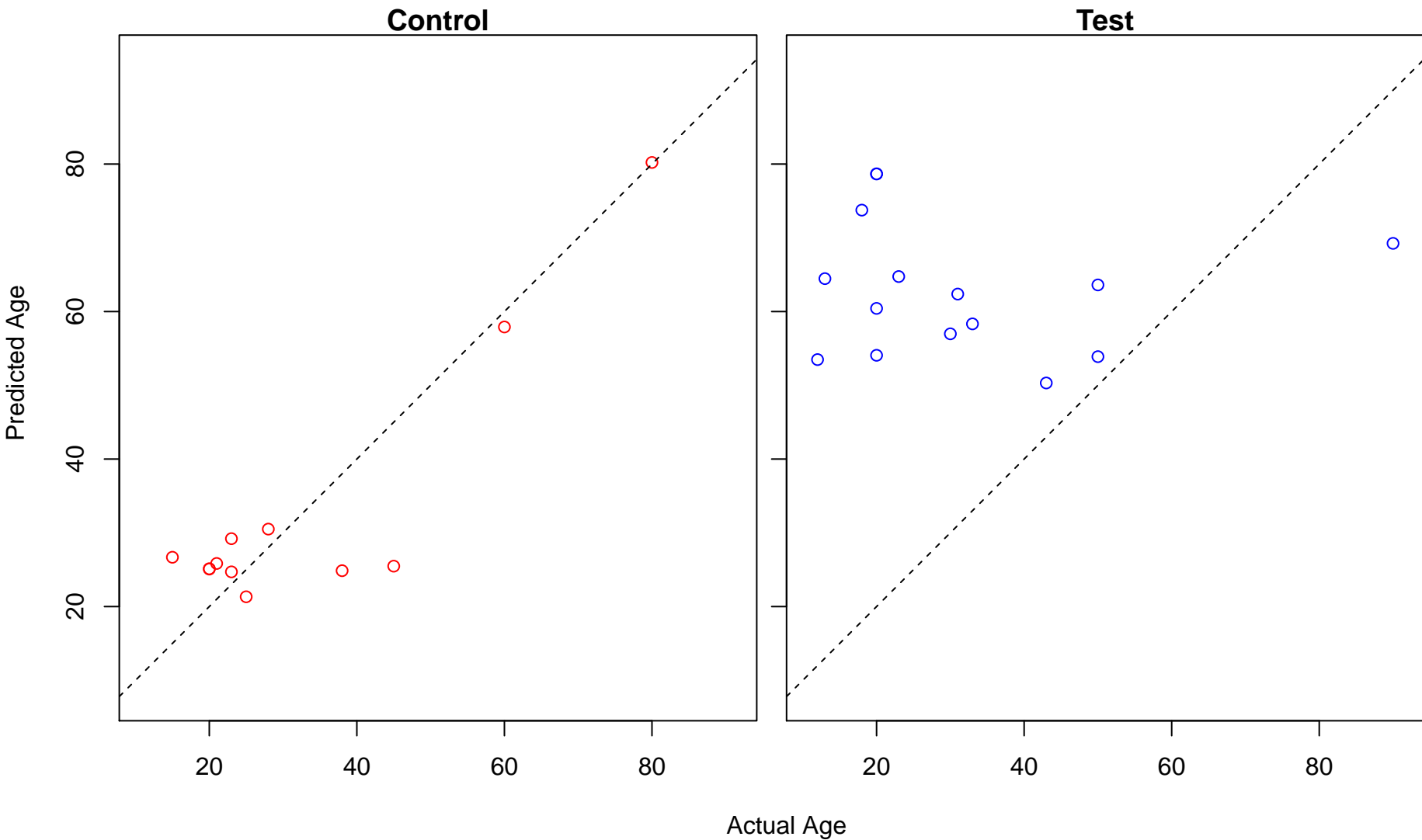
viral gene expression (Score: 7.251039)



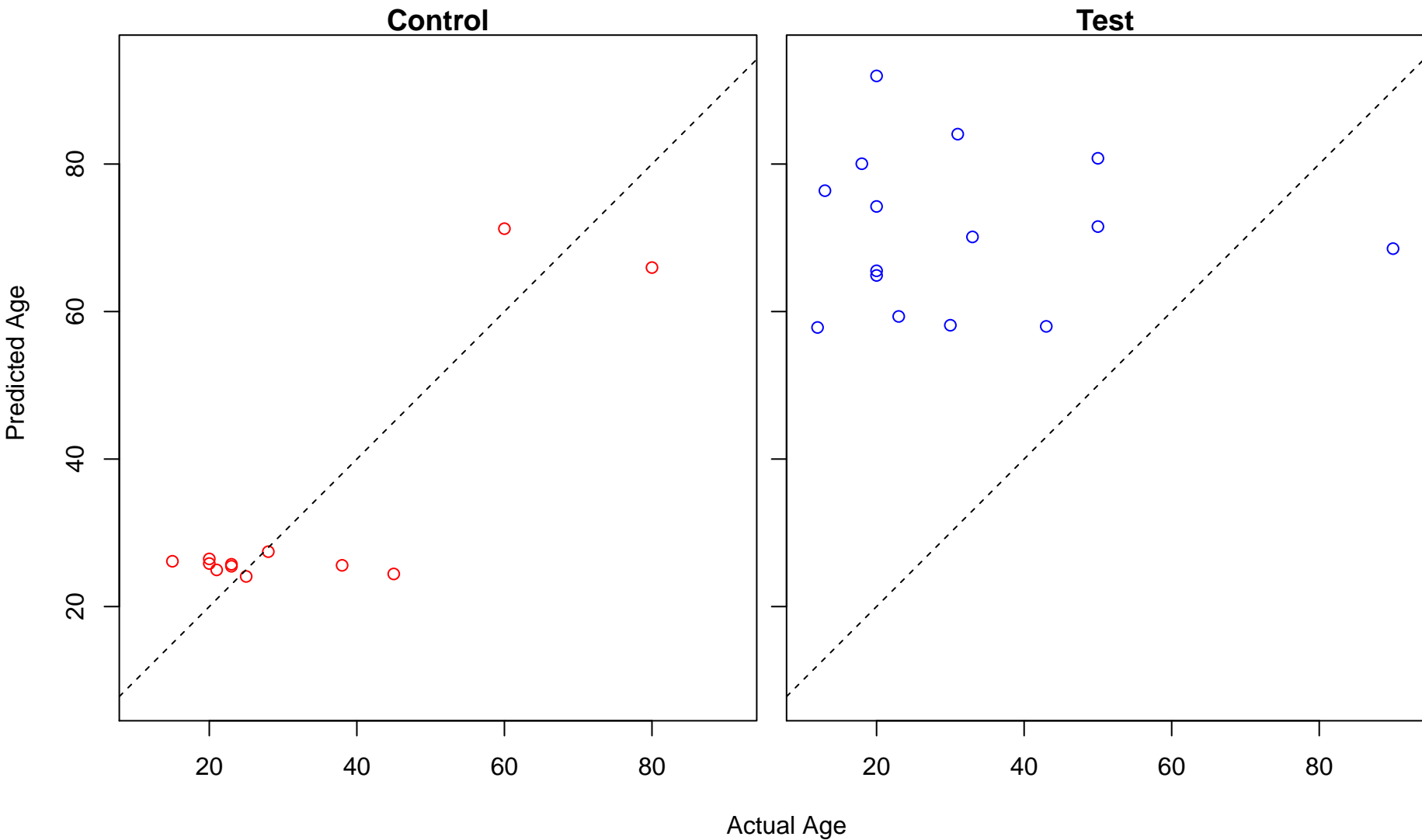
response to radiation (Score: 7.250639)



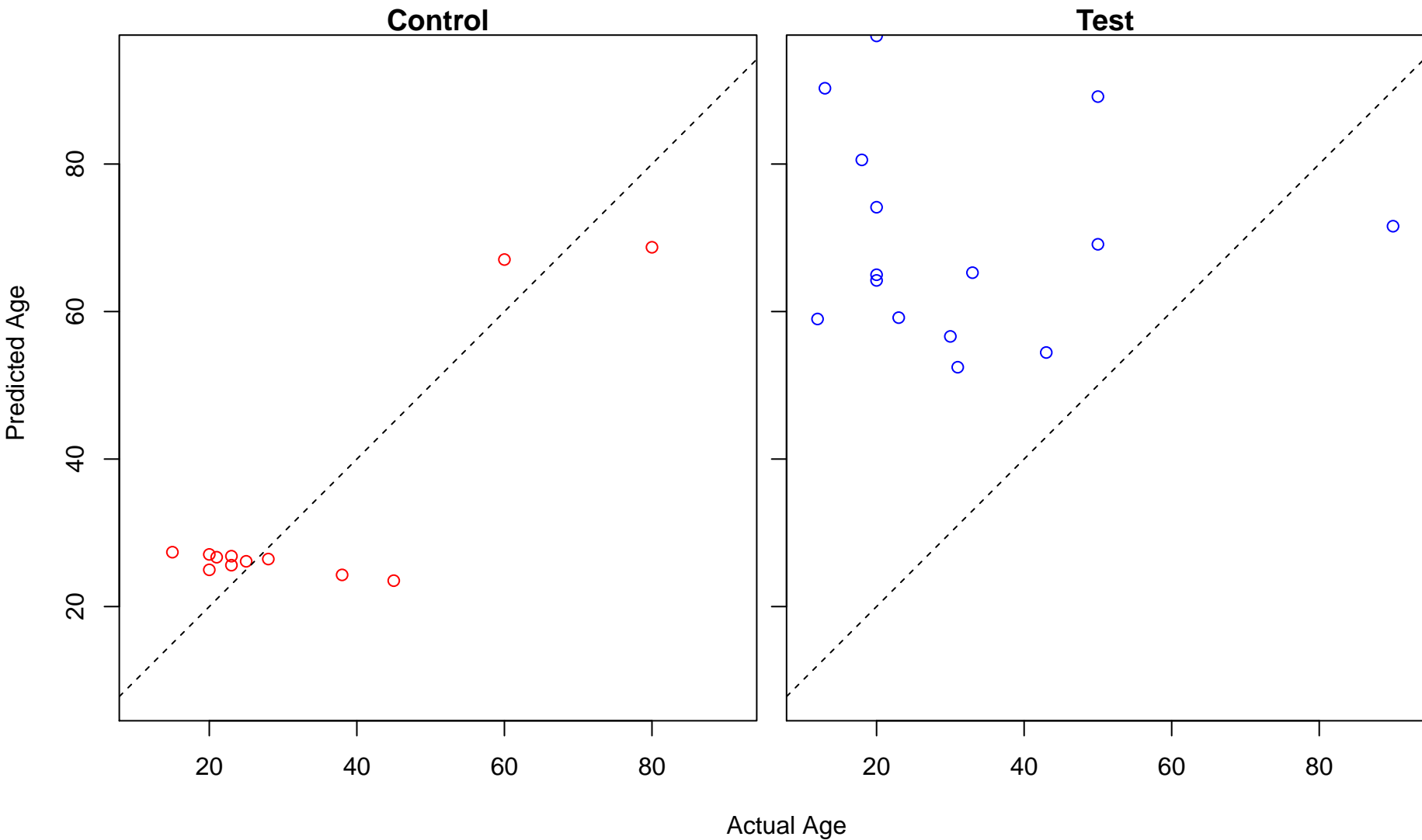
response to light stimulus (Score: 7.249552)



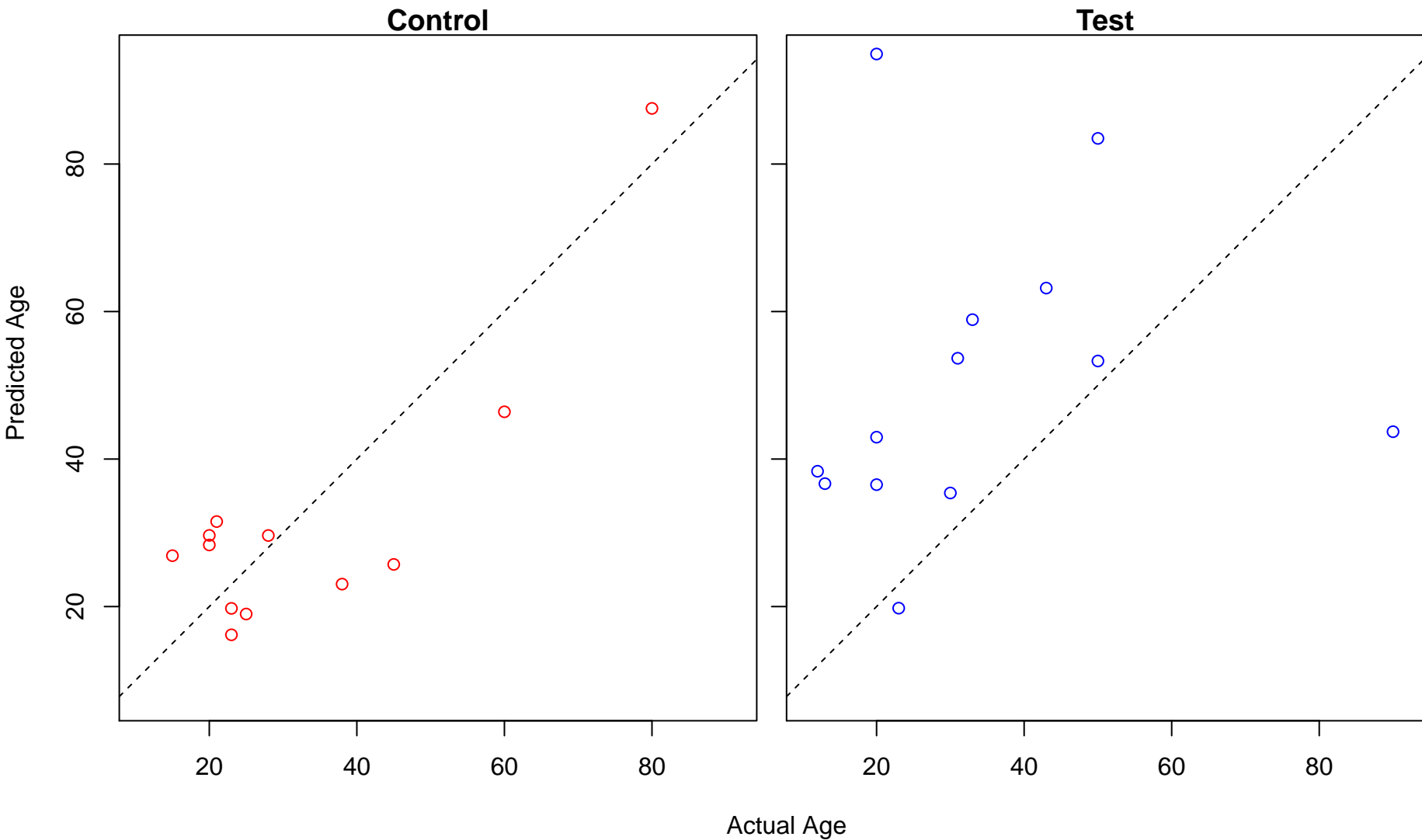
positive regulation of growth (Score: 7.249090)



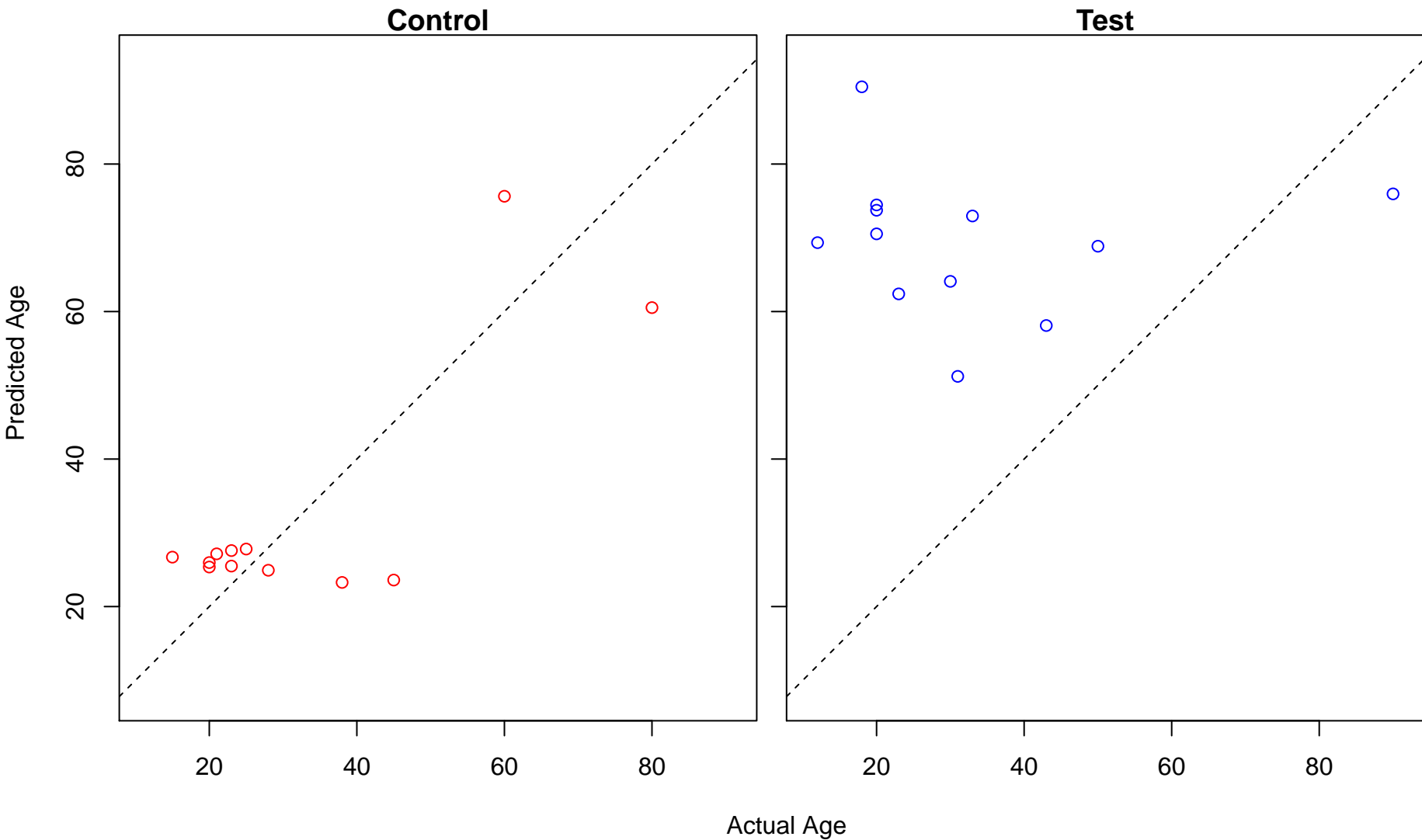
amide biosynthetic process (Score: 7.248063)



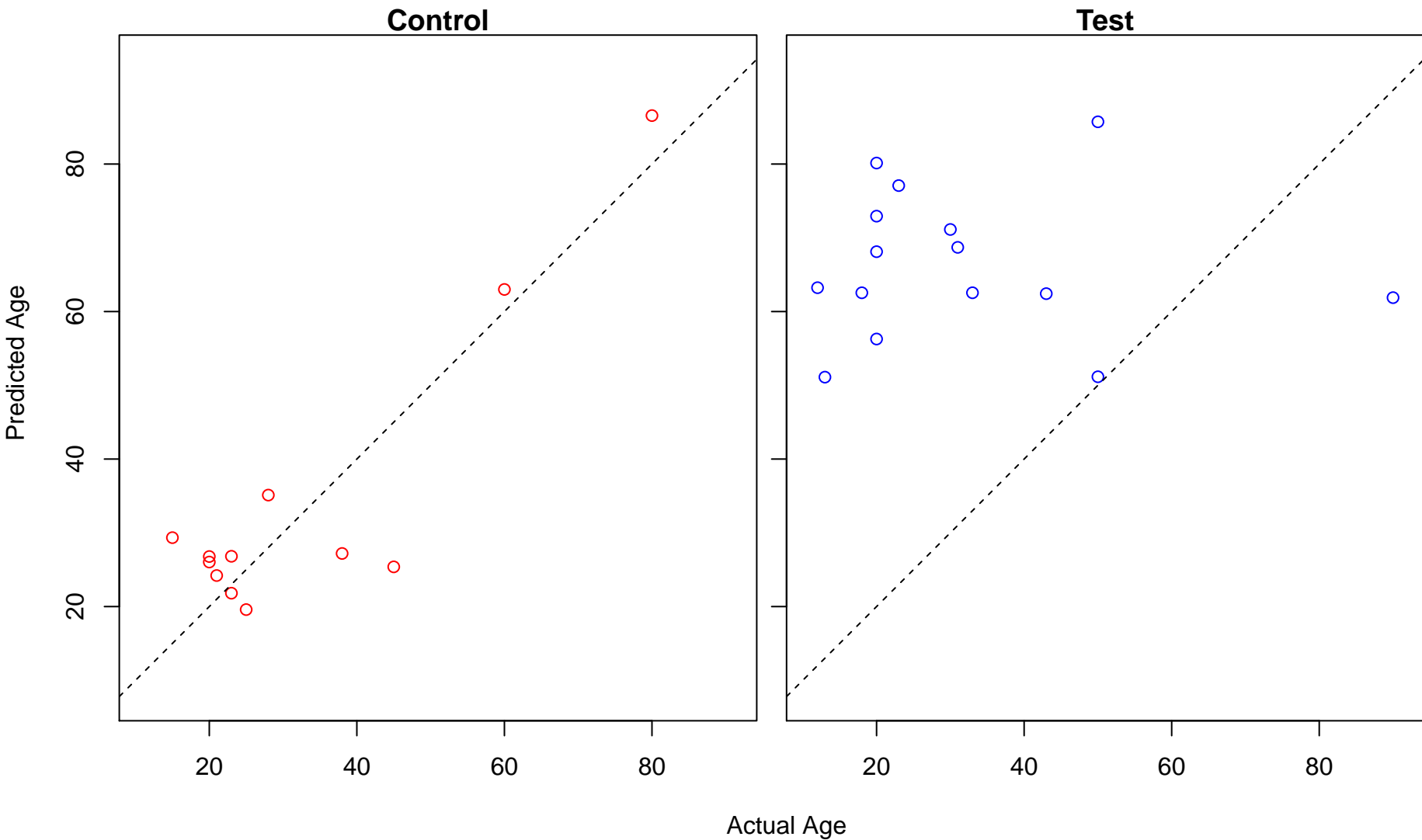
epidermal cell differentiation (Score: 7.246166)



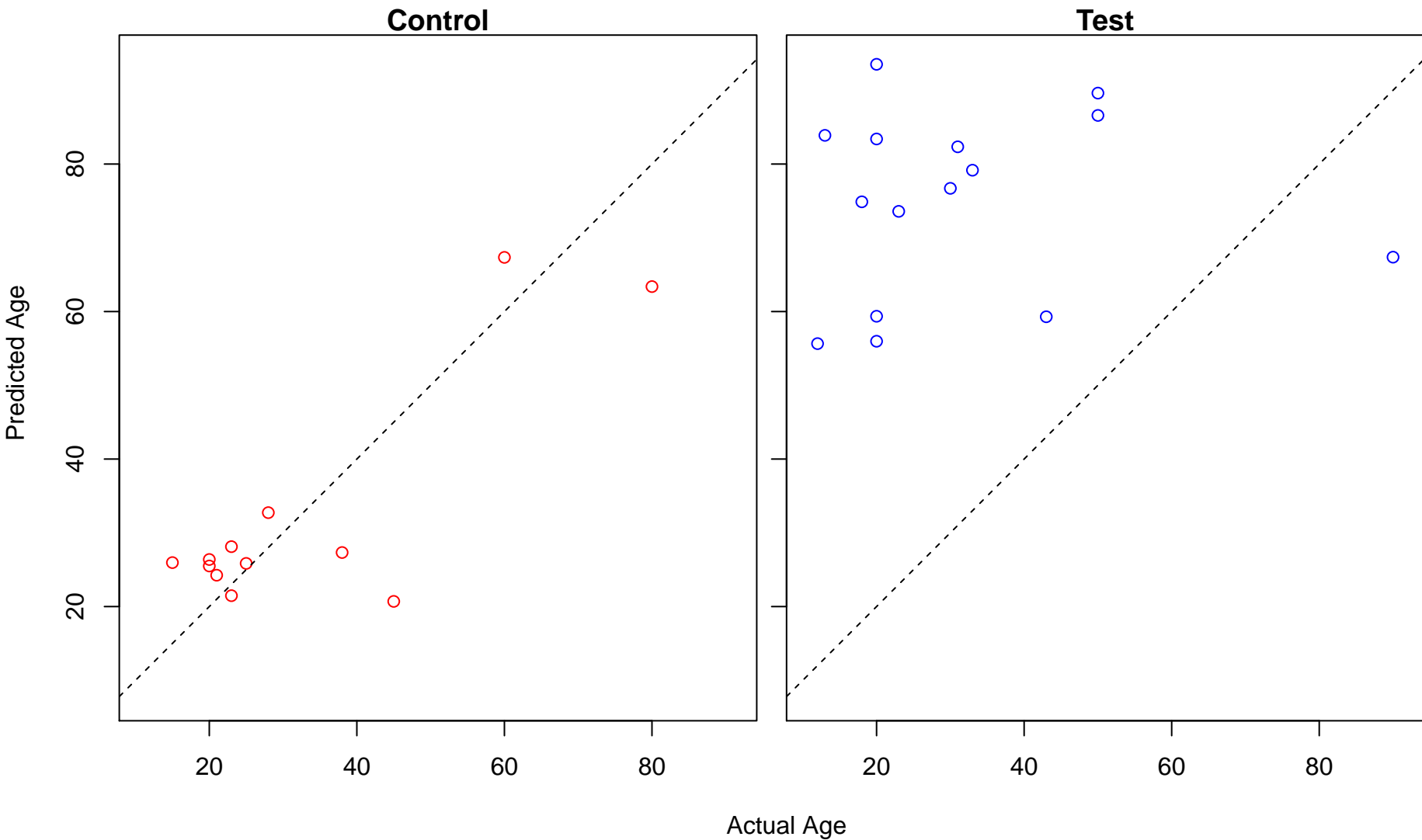
selenocysteine metabolic process (Score: 7.244808)



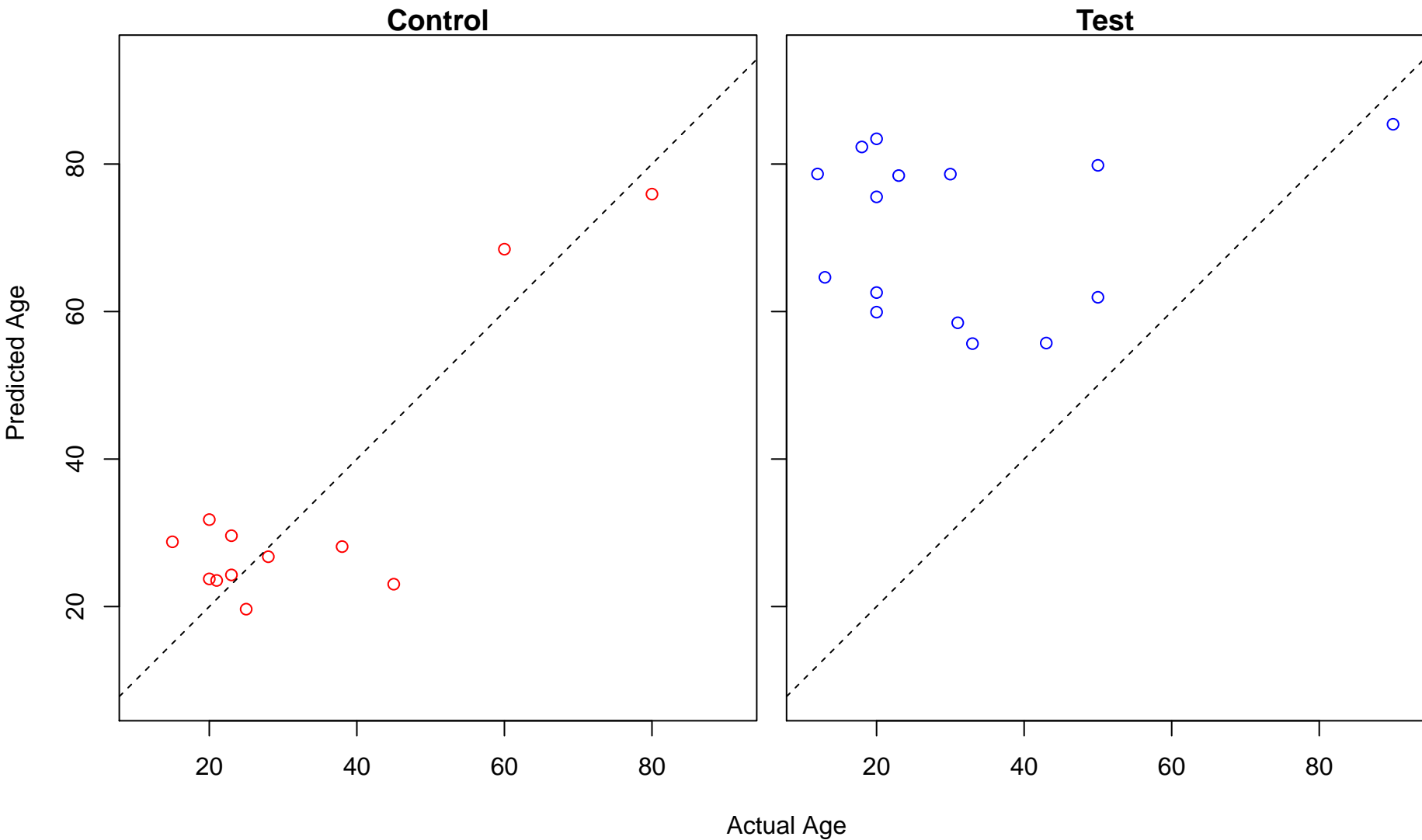
embryonic axis specification (Score: 7.242747)



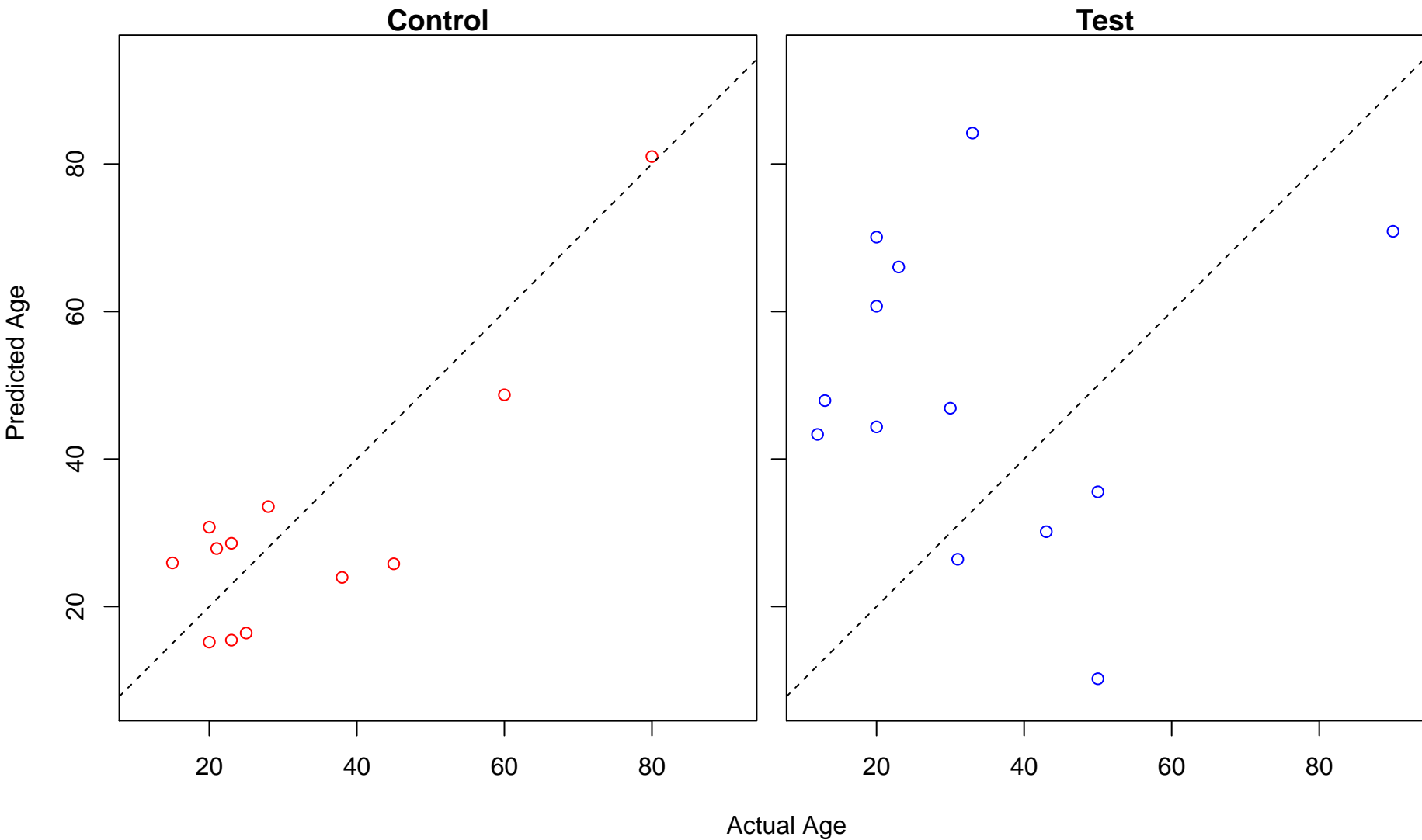
negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator (Score: 7.24092)



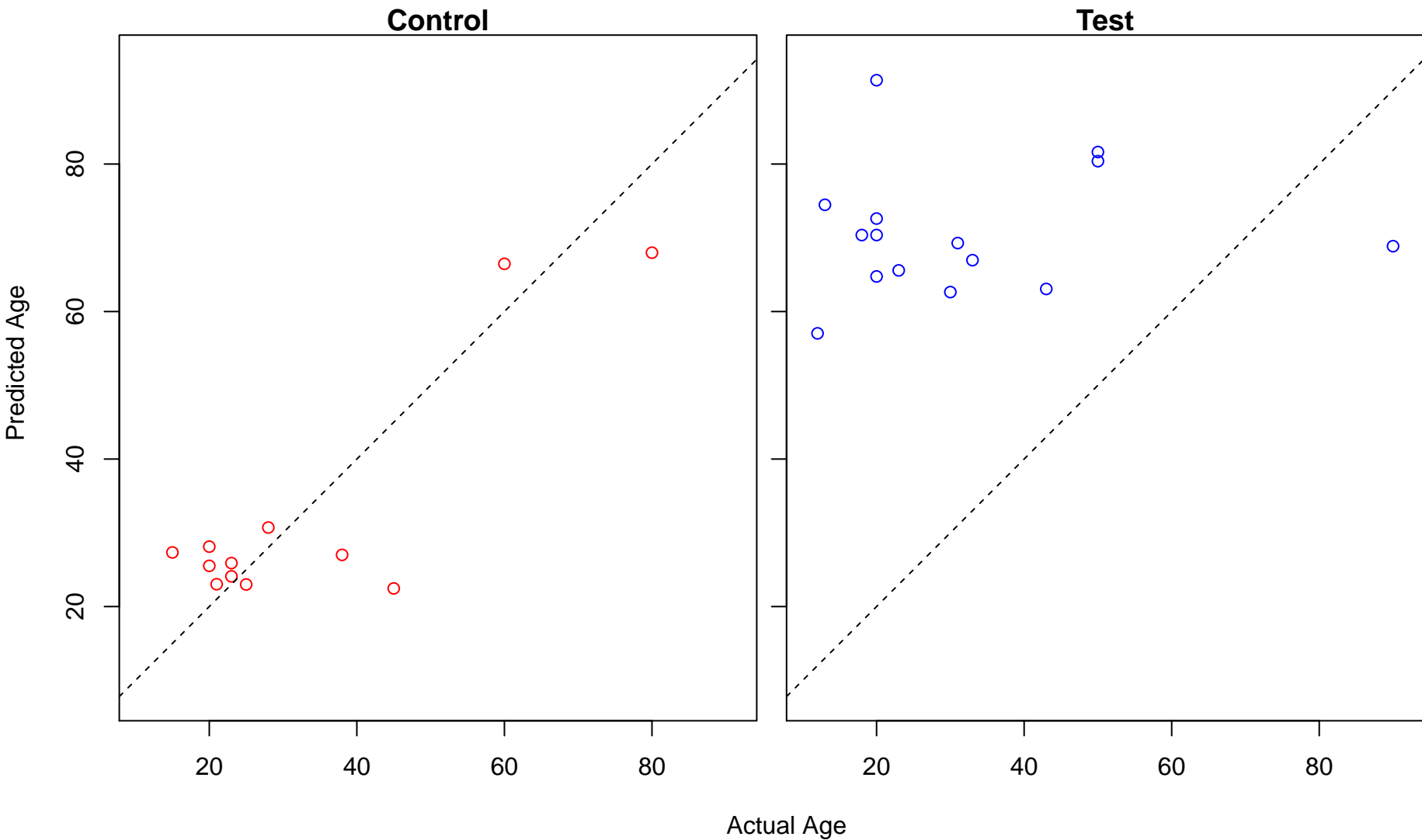
negative regulation of MAPK cascade (Score: 7.240855)



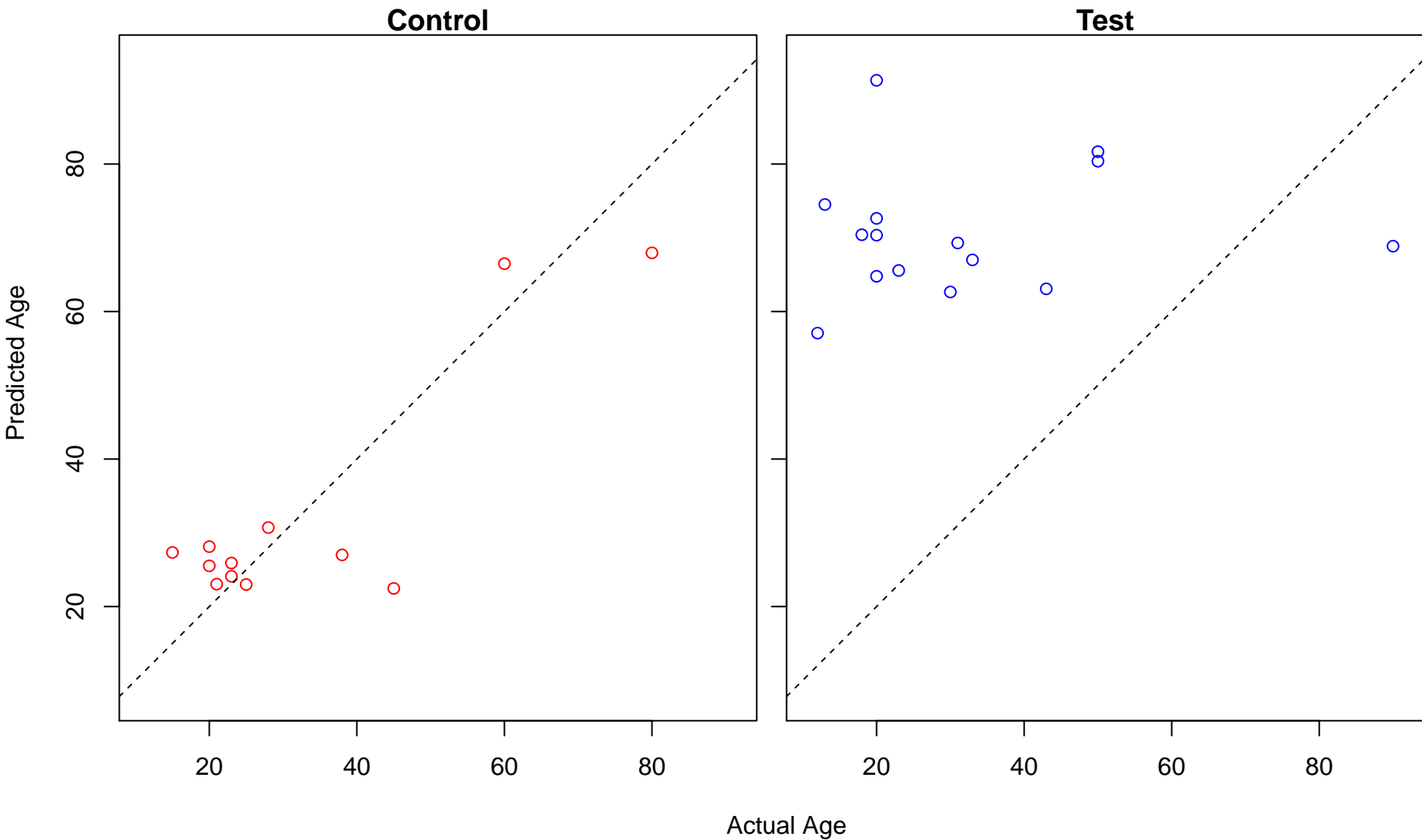
establishment of RNA localization (Score: 7.232700)



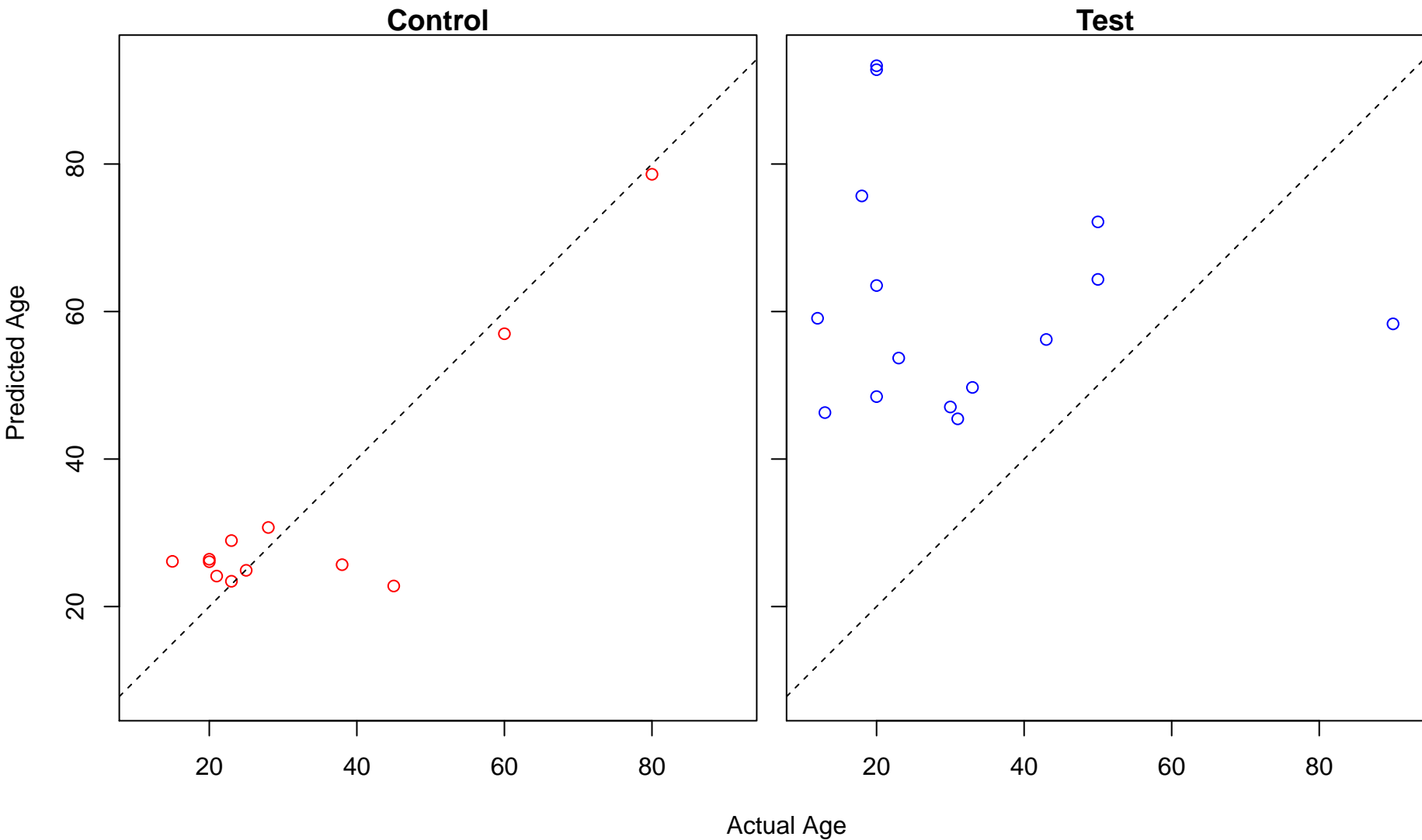
water transport (Score: 7.229047)



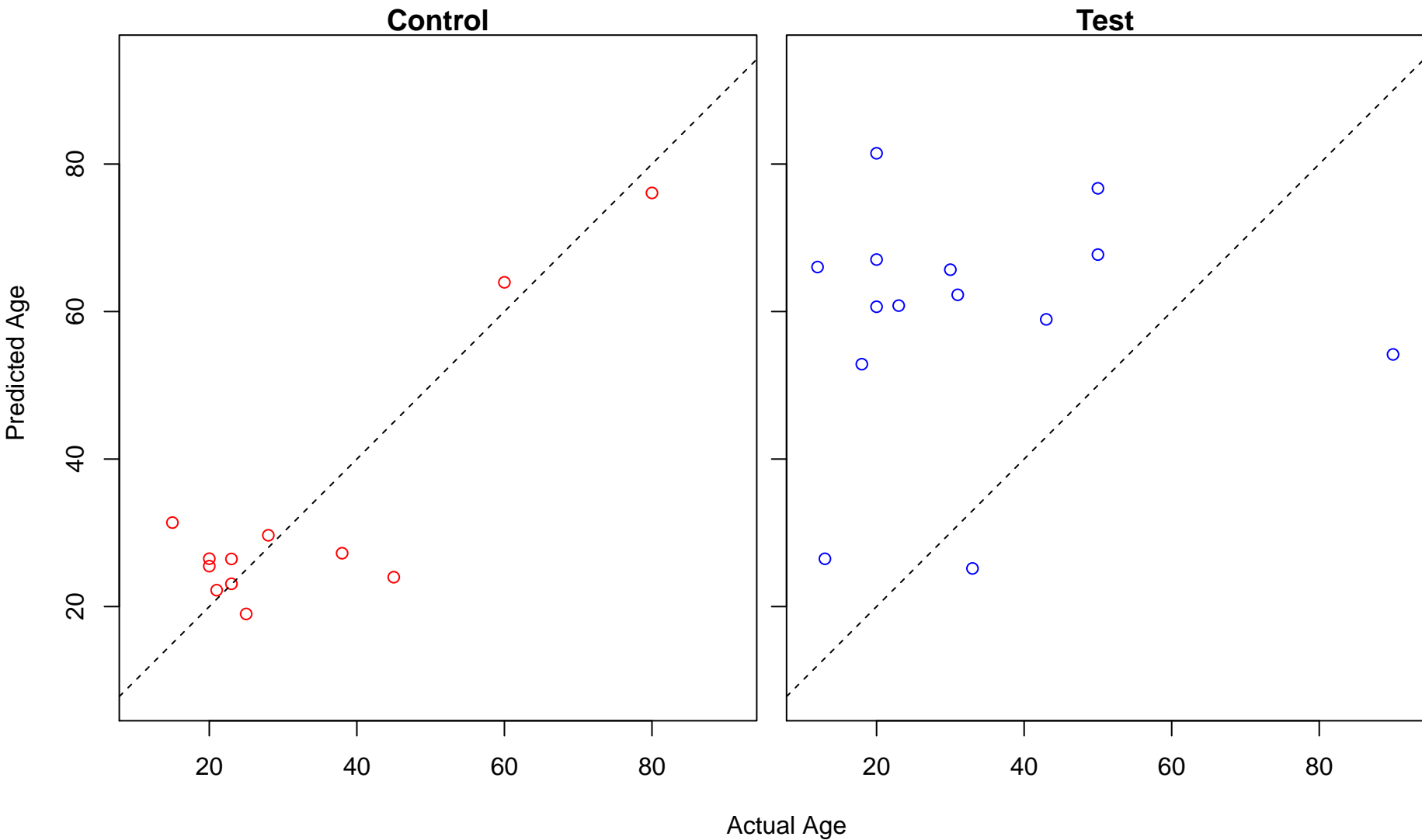
fluid transport (Score: 7.227395)



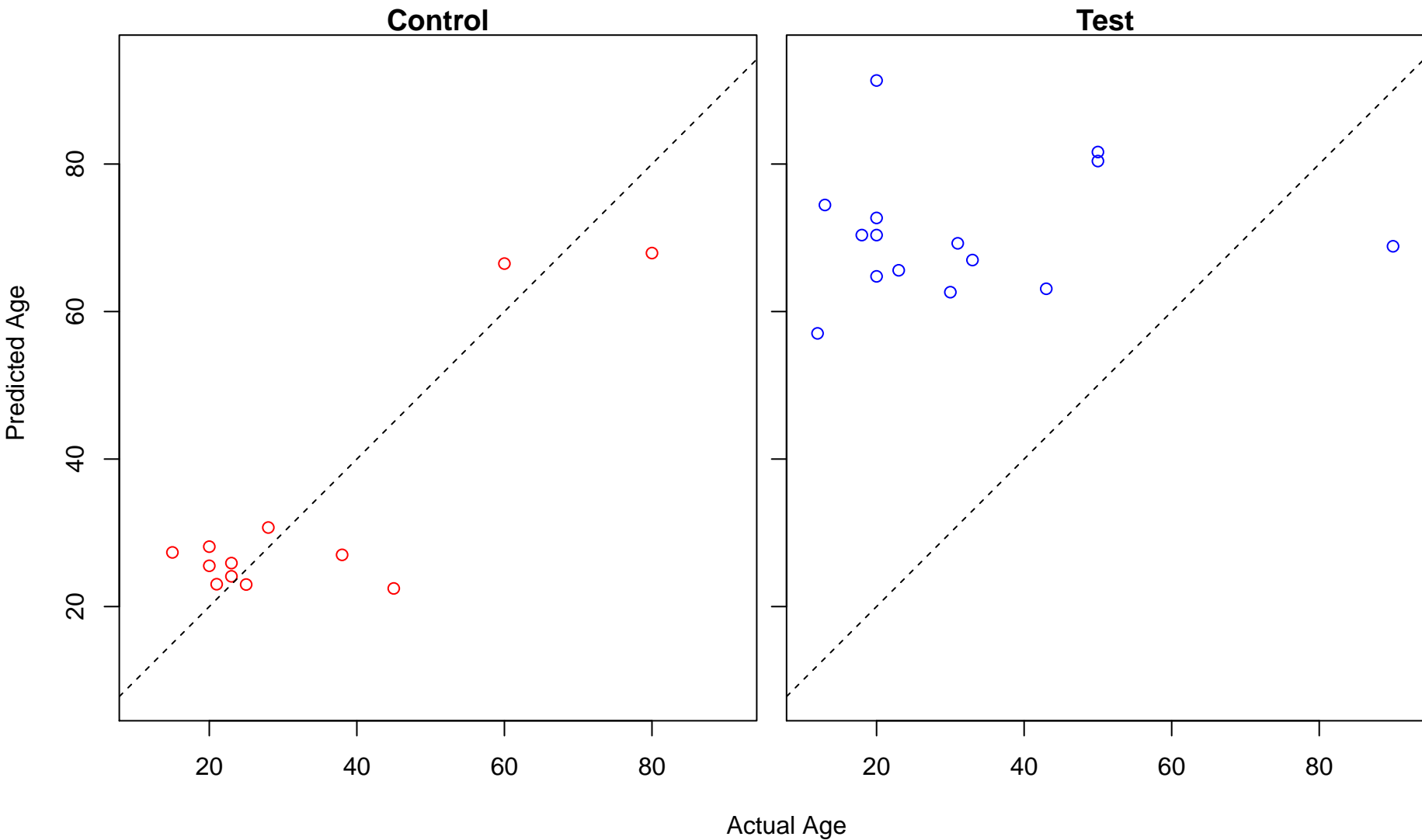
SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (Score: 7.227304)



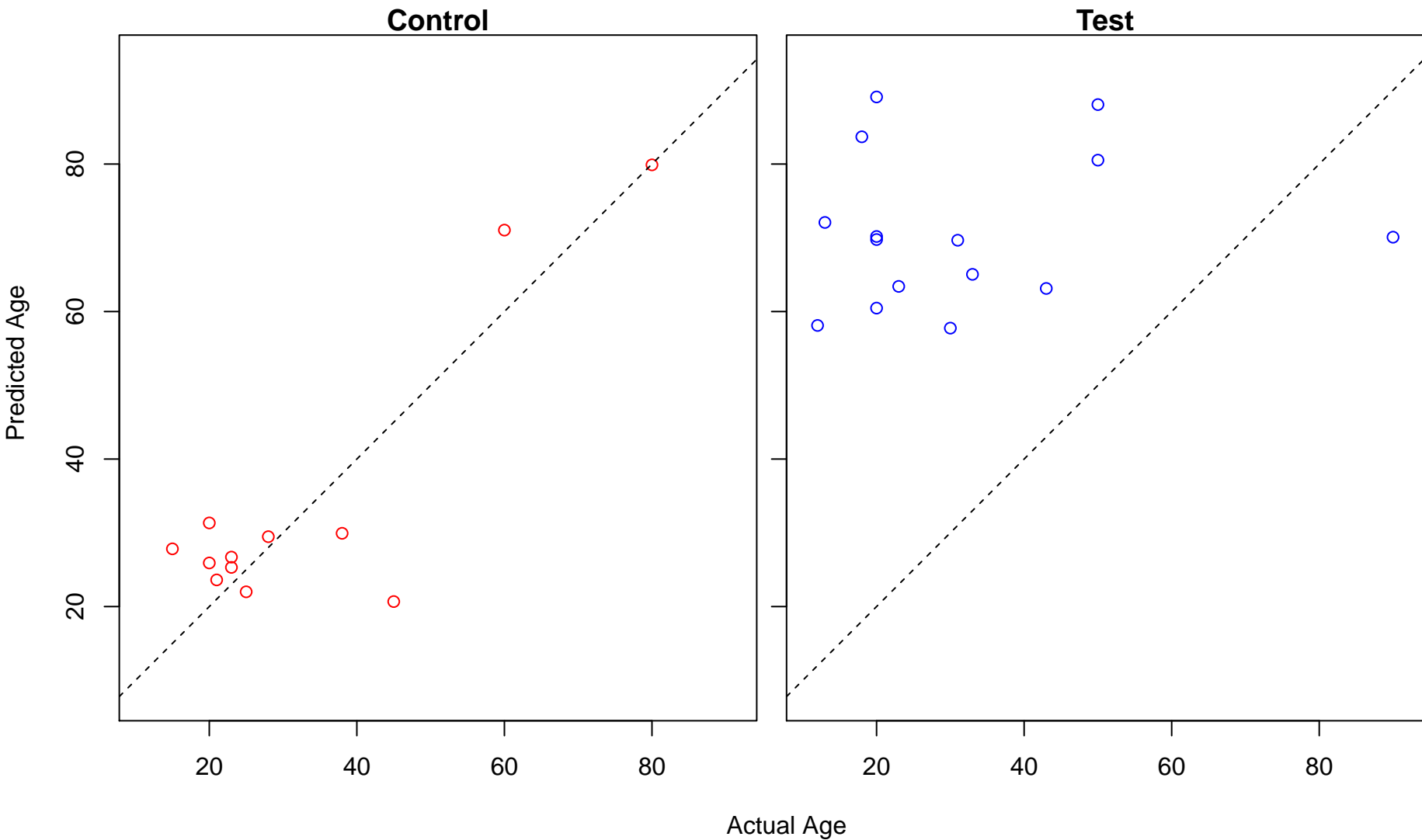
regulation of retinoic acid receptor signaling pathway (Score: 7.221341)



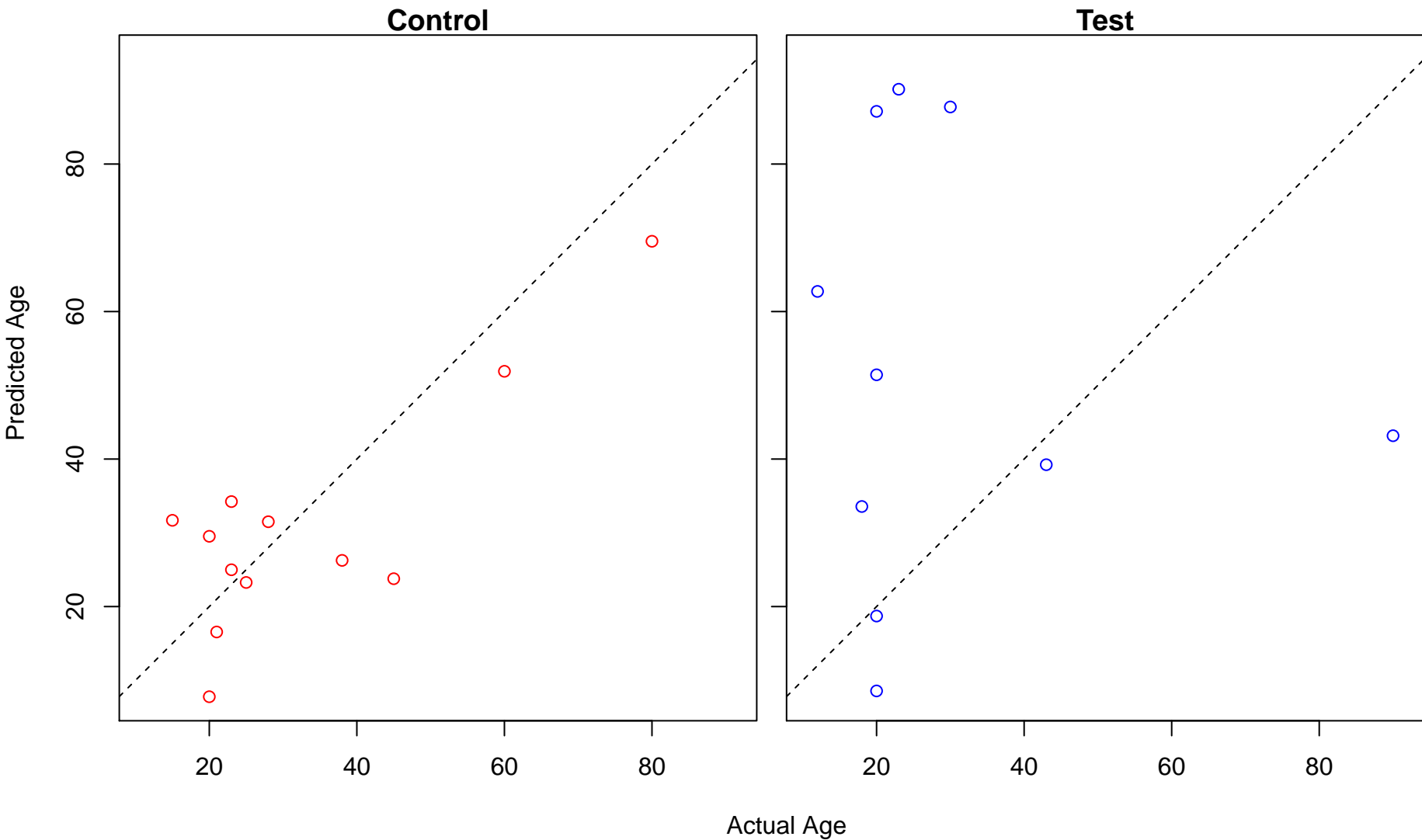
renal water homeostasis (Score: 7.218560)



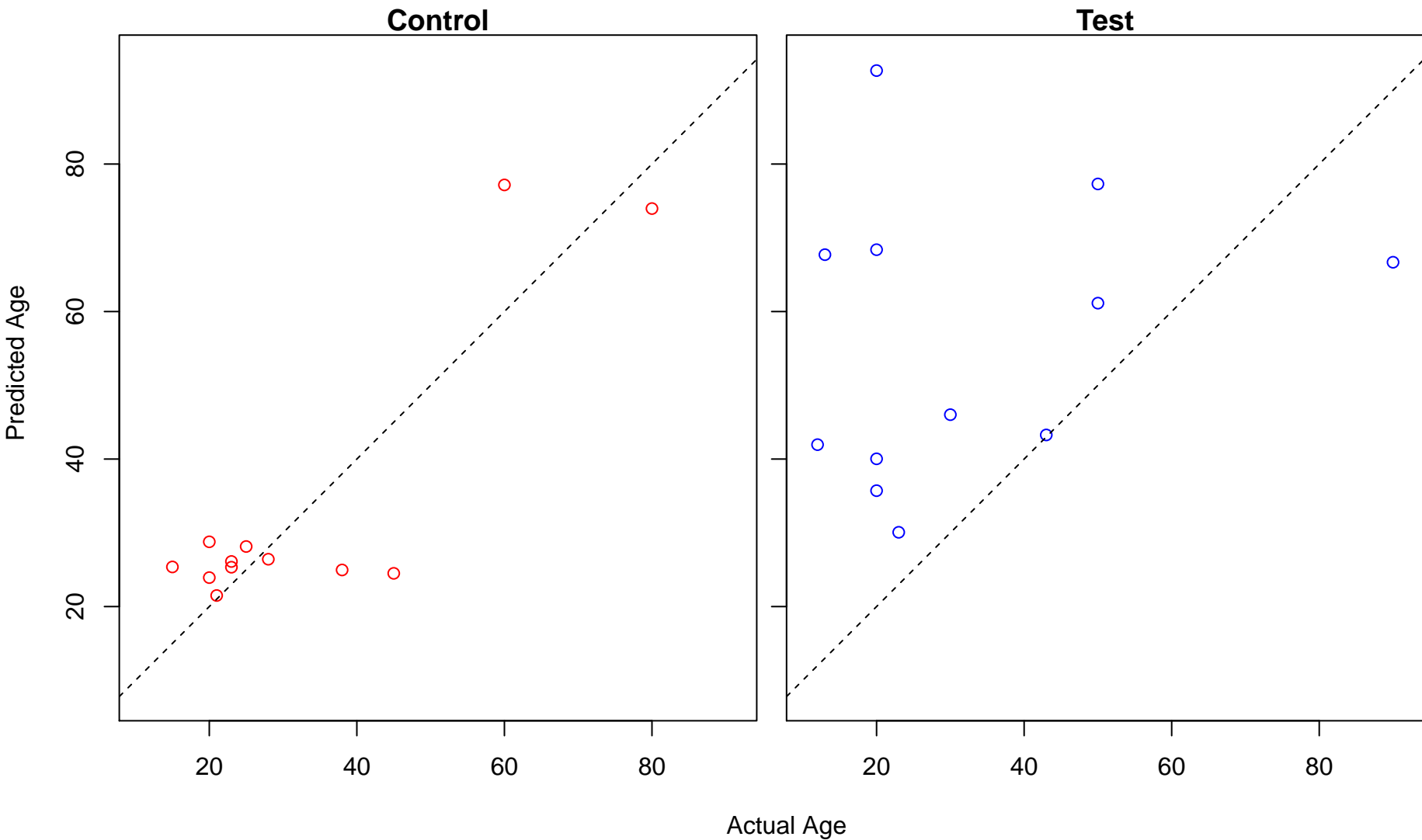
positive regulation of cell motility (Score: 7.218143)



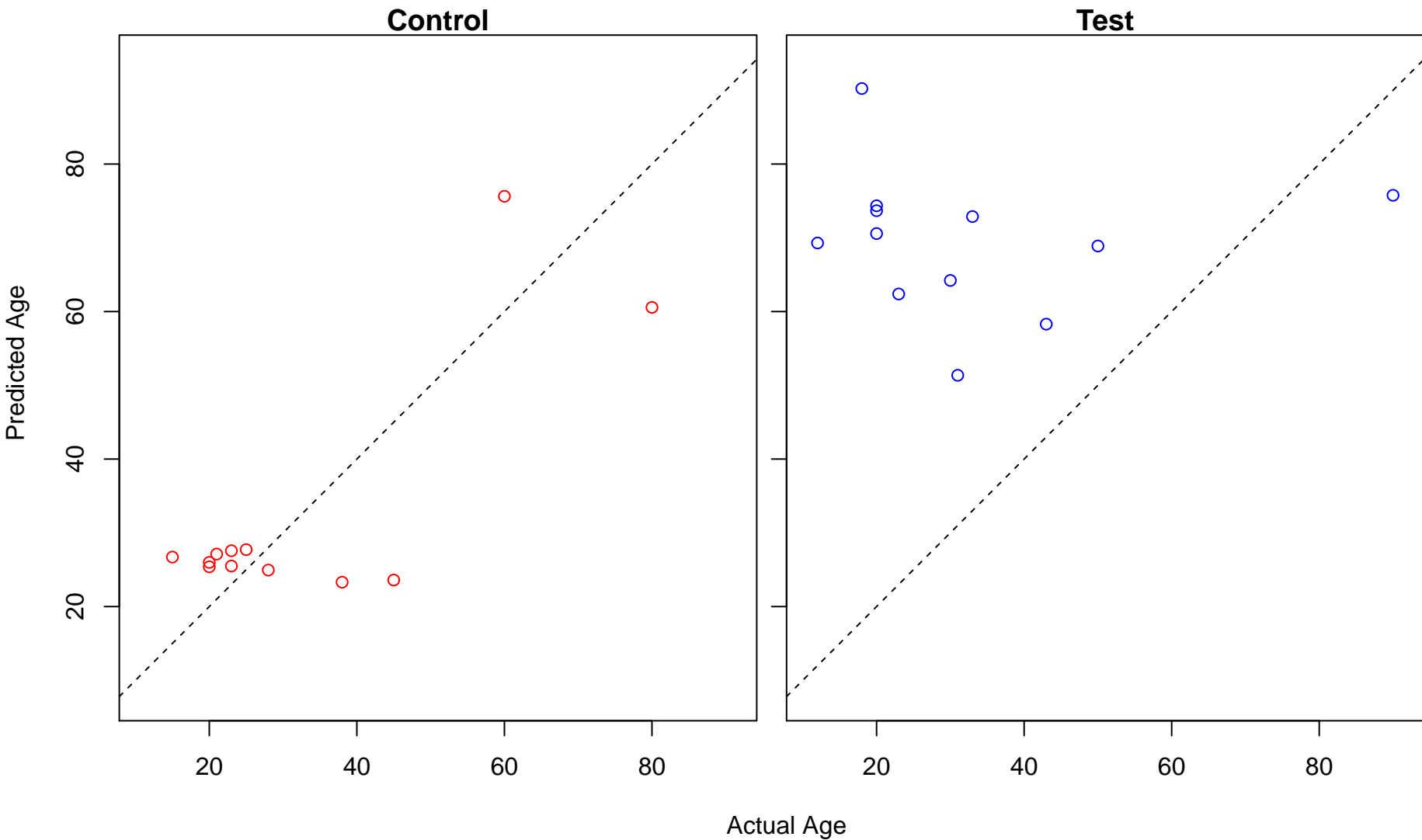
negative regulation of cellular protein catabolic process (Score: 7.216831)



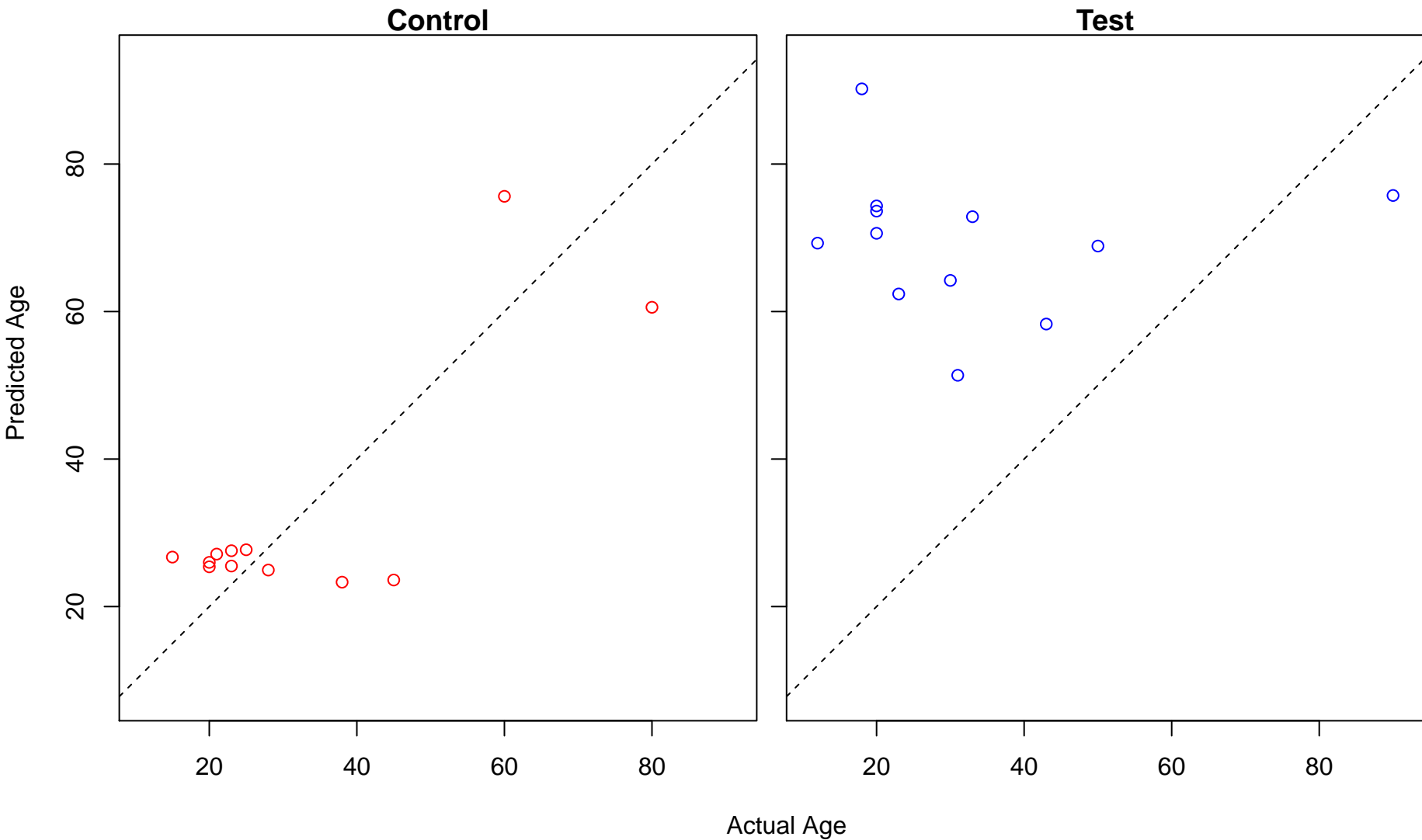
regulation of endoplasmic reticulum unfolded protein response (Score: 7.207049)



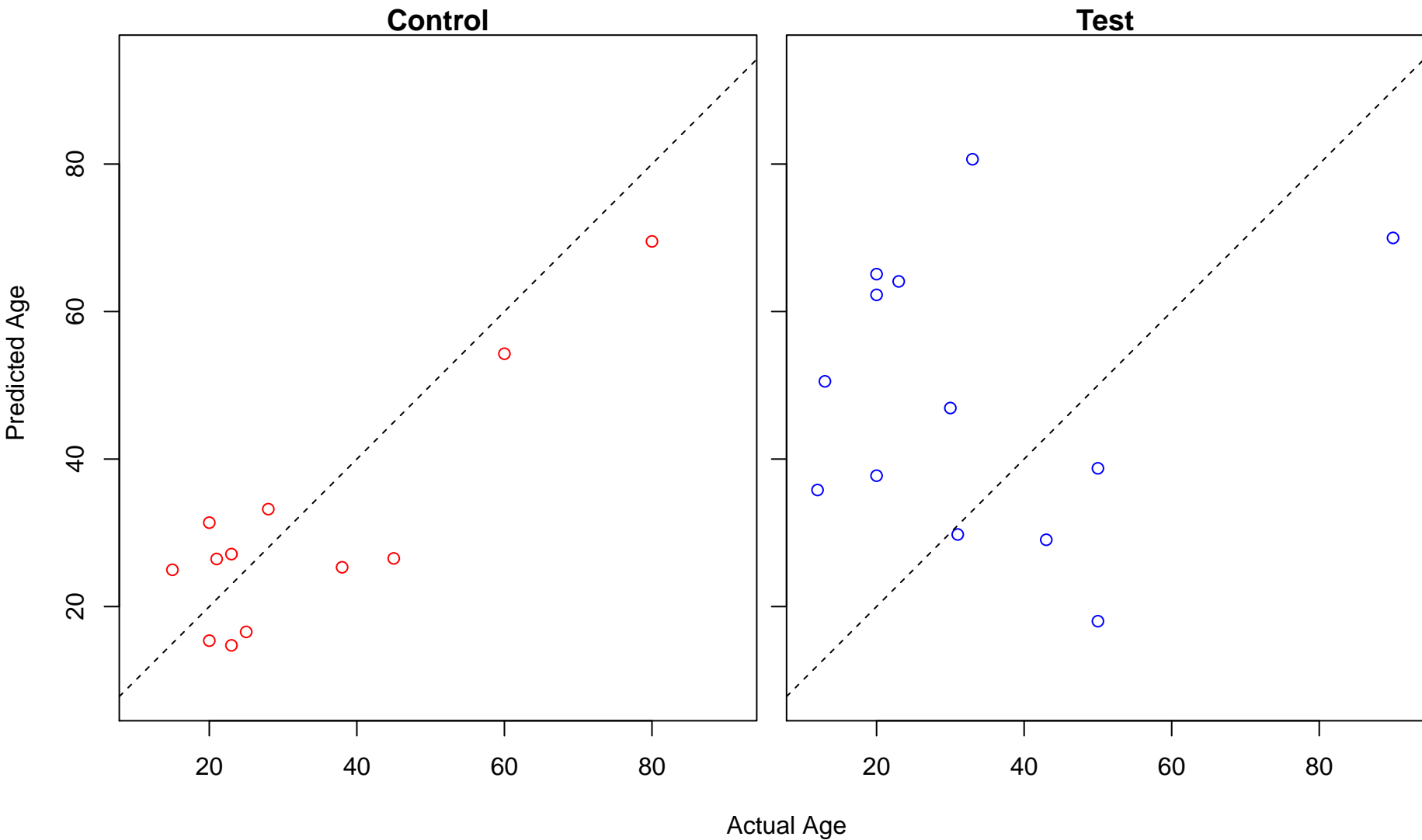
SRP-dependent cotranslational protein targeting to membrane (Score: 7.206121)



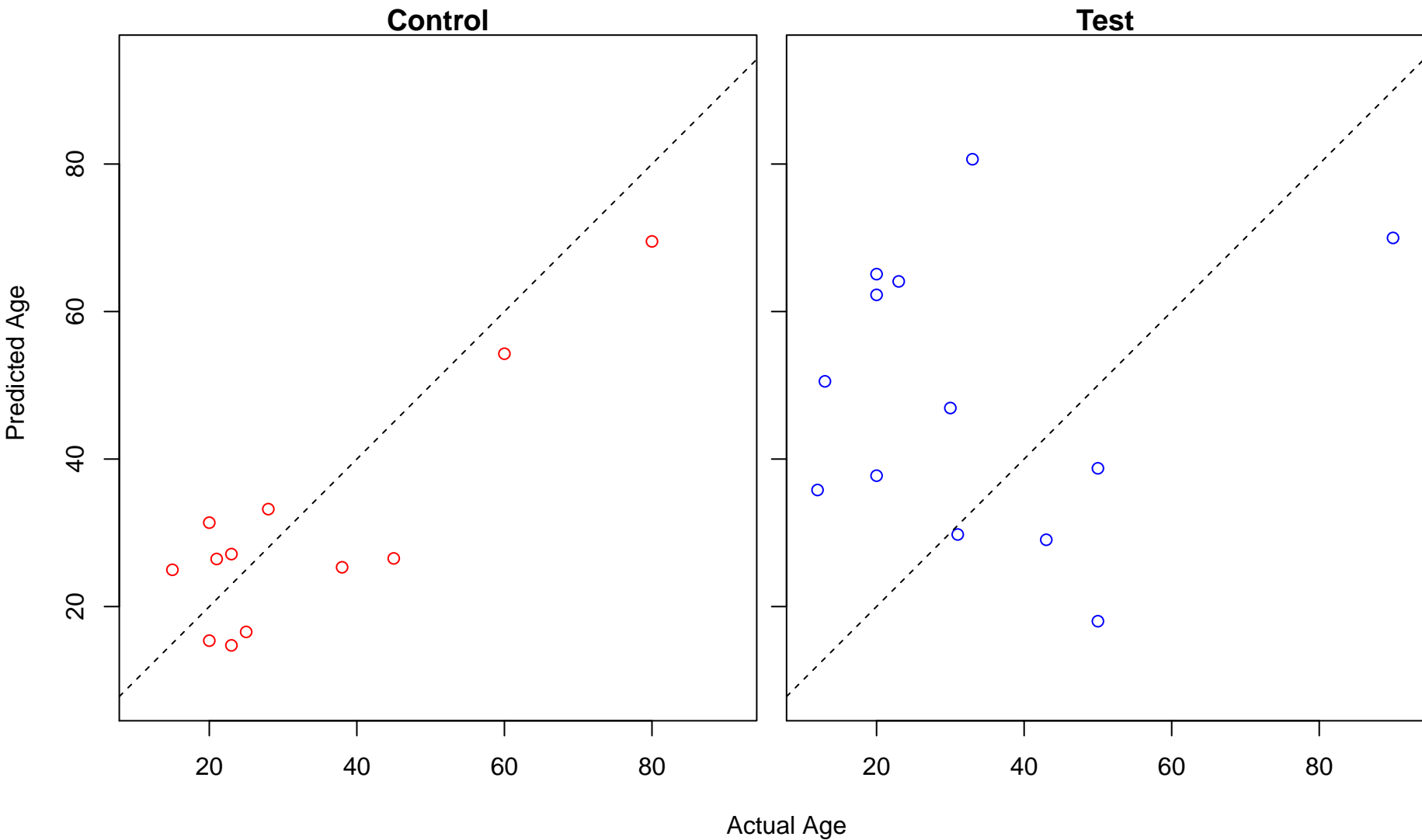
protein targeting to ER (Score: 7.201262)



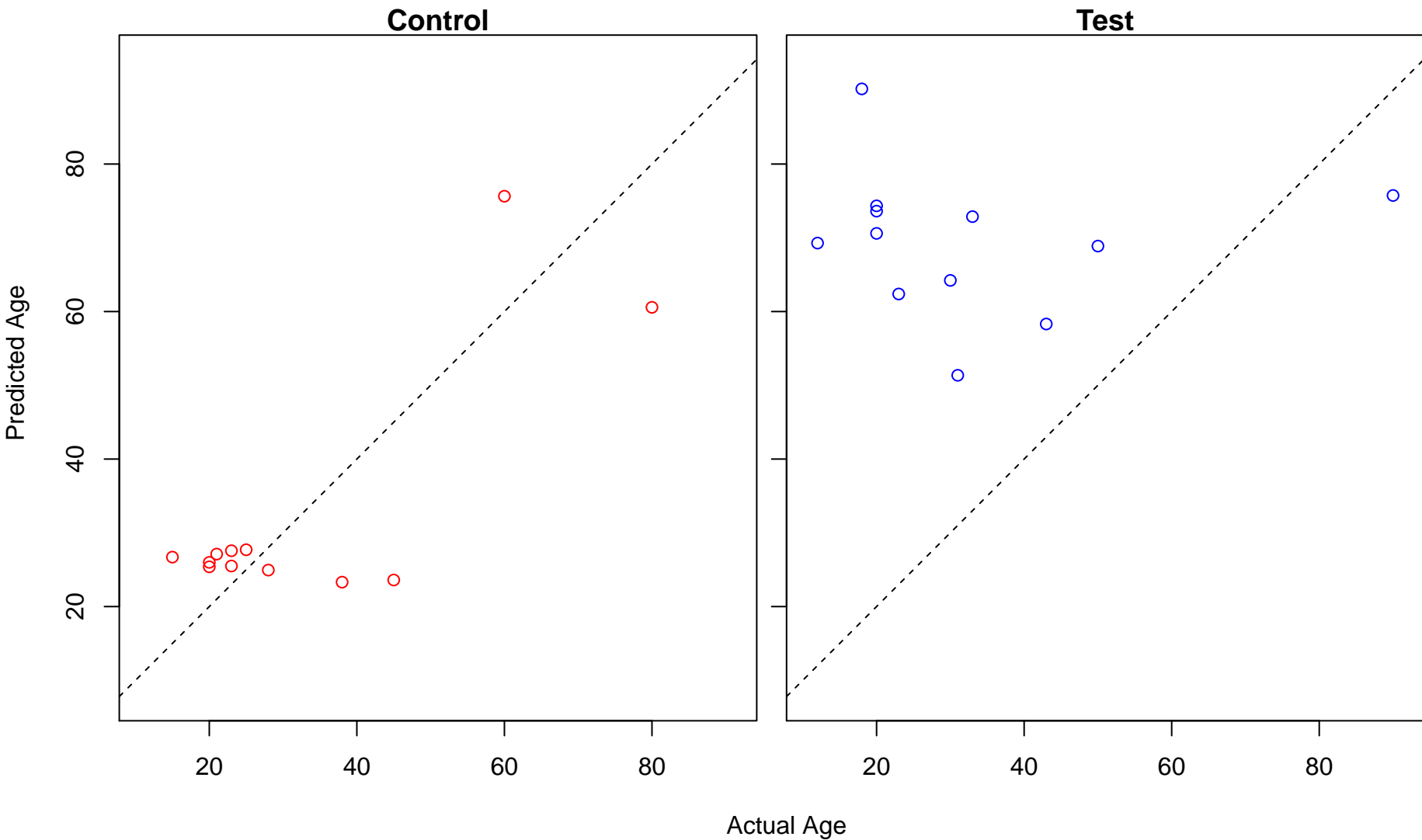
mRNA export from nucleus (Score: 7.201008)



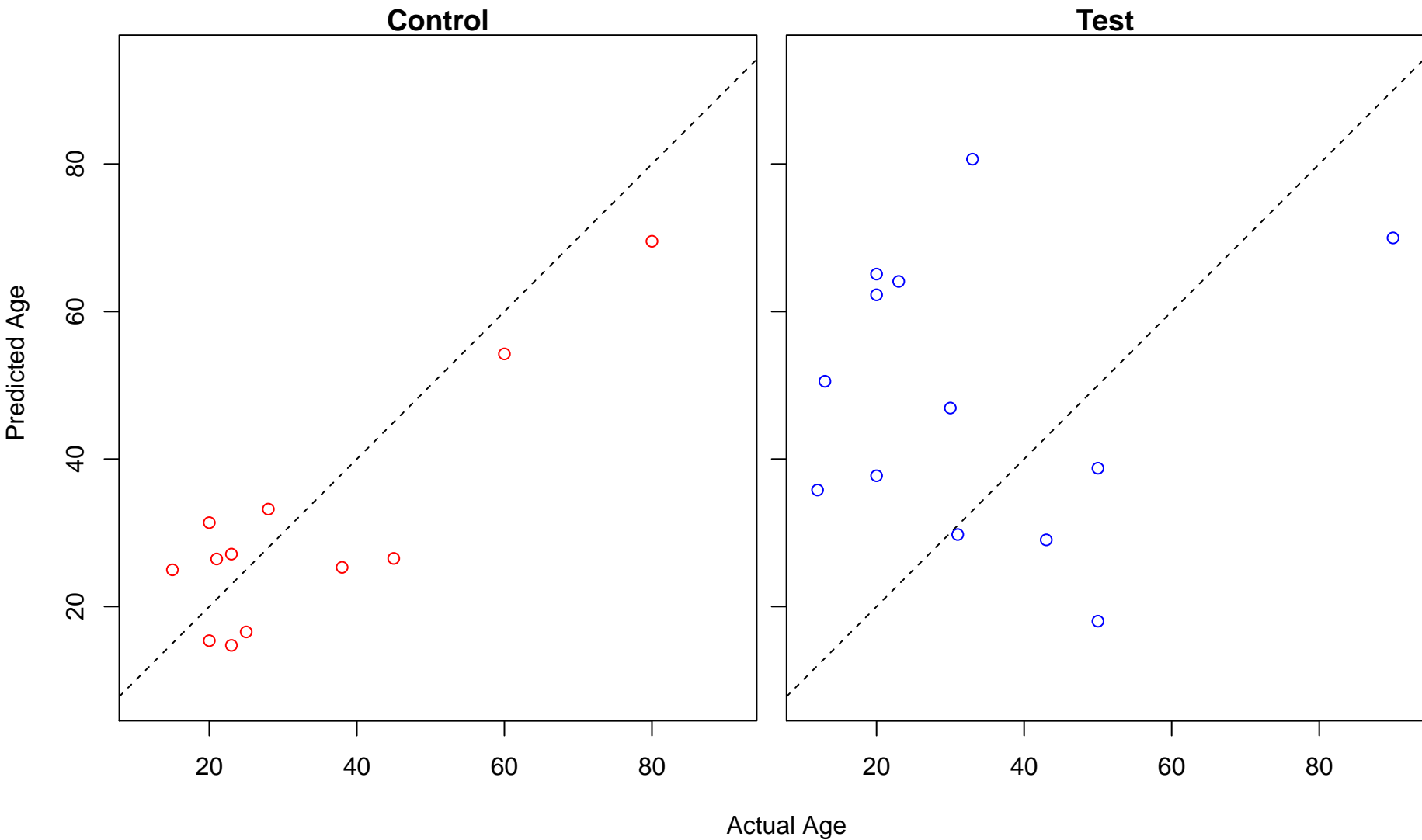
mRNA-containing ribonucleoprotein complex export from nucleus (Score: 7.201008)



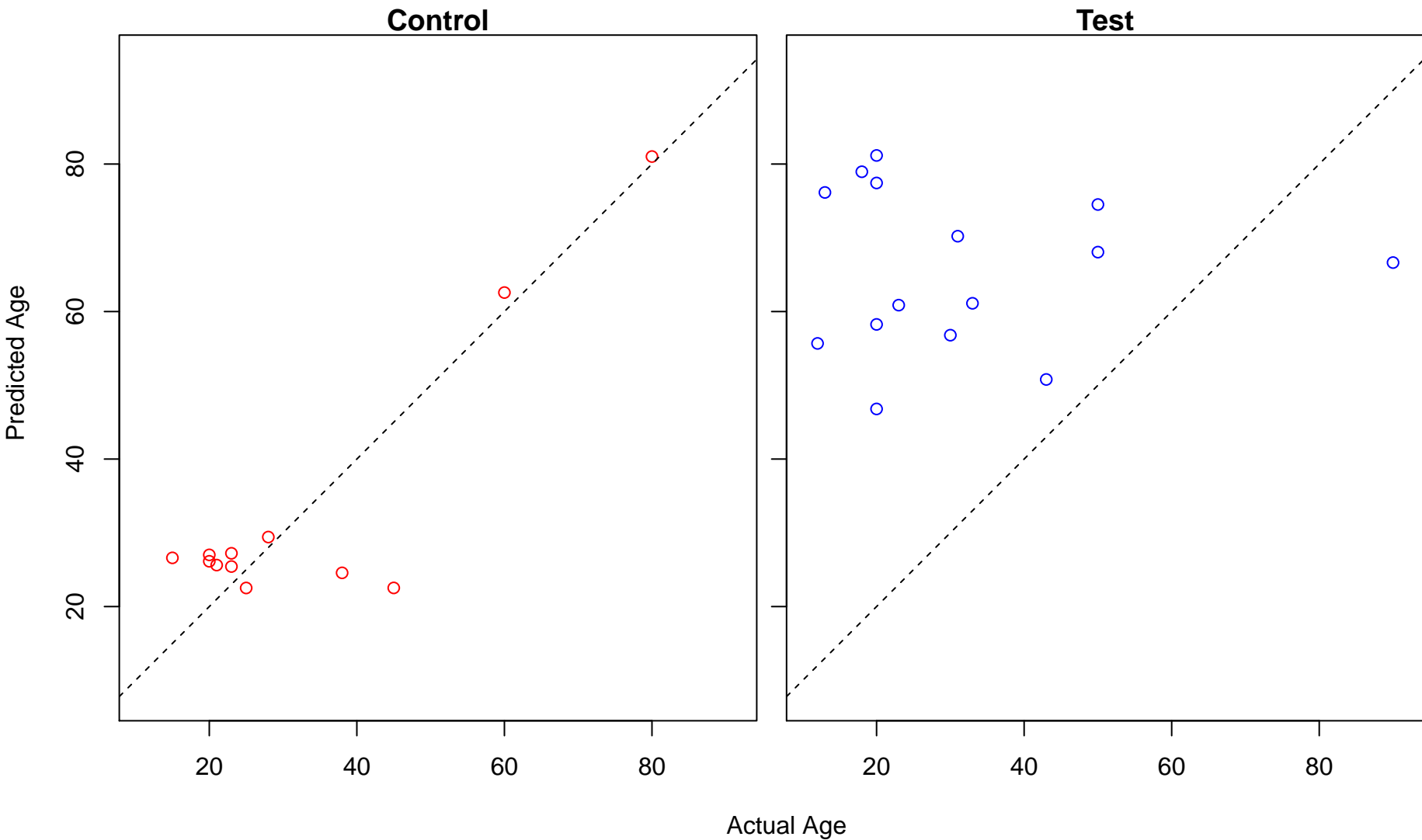
cotranslational protein targeting to membrane (Score: 7.200260)



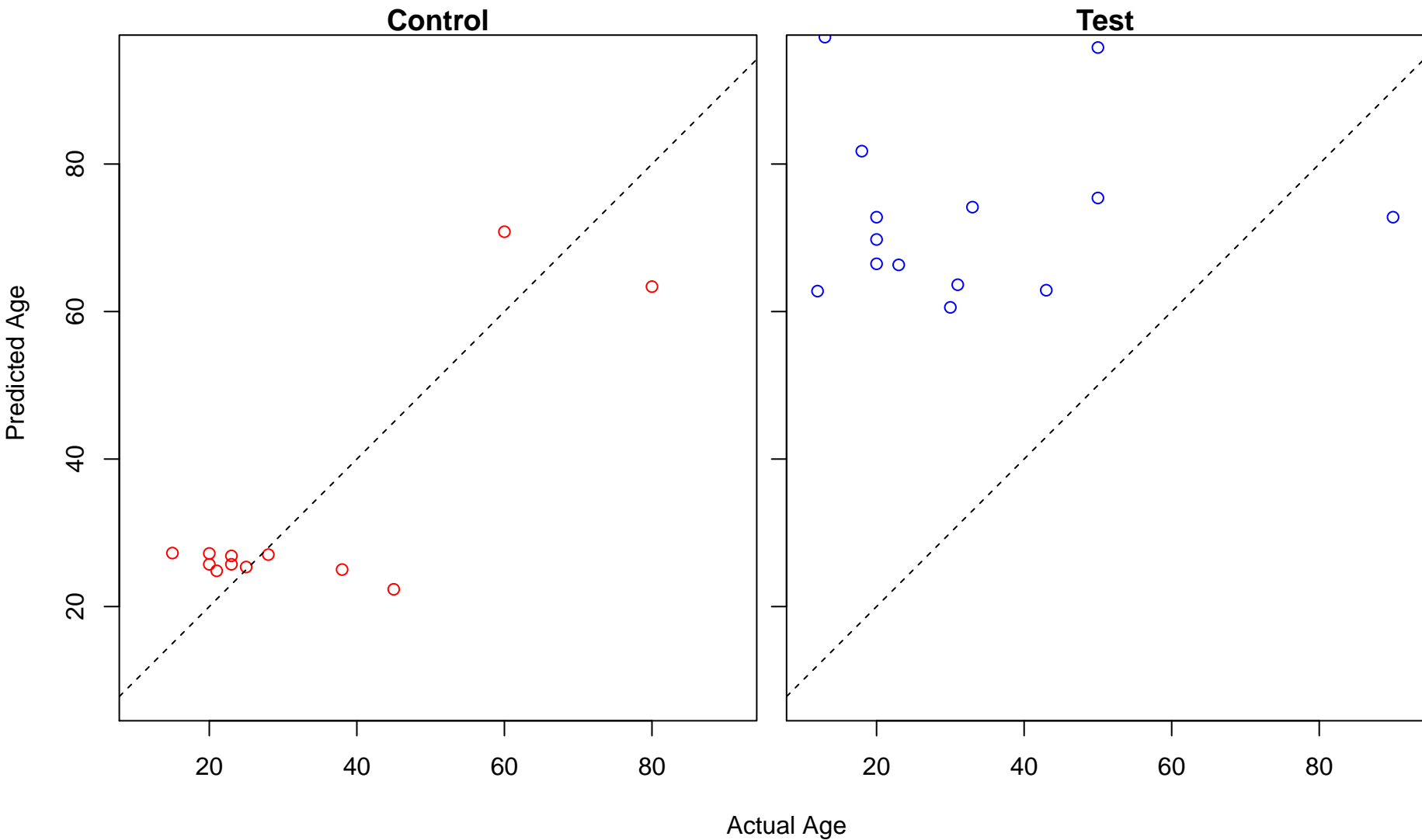
mRNA transport (Score: 7.199479)



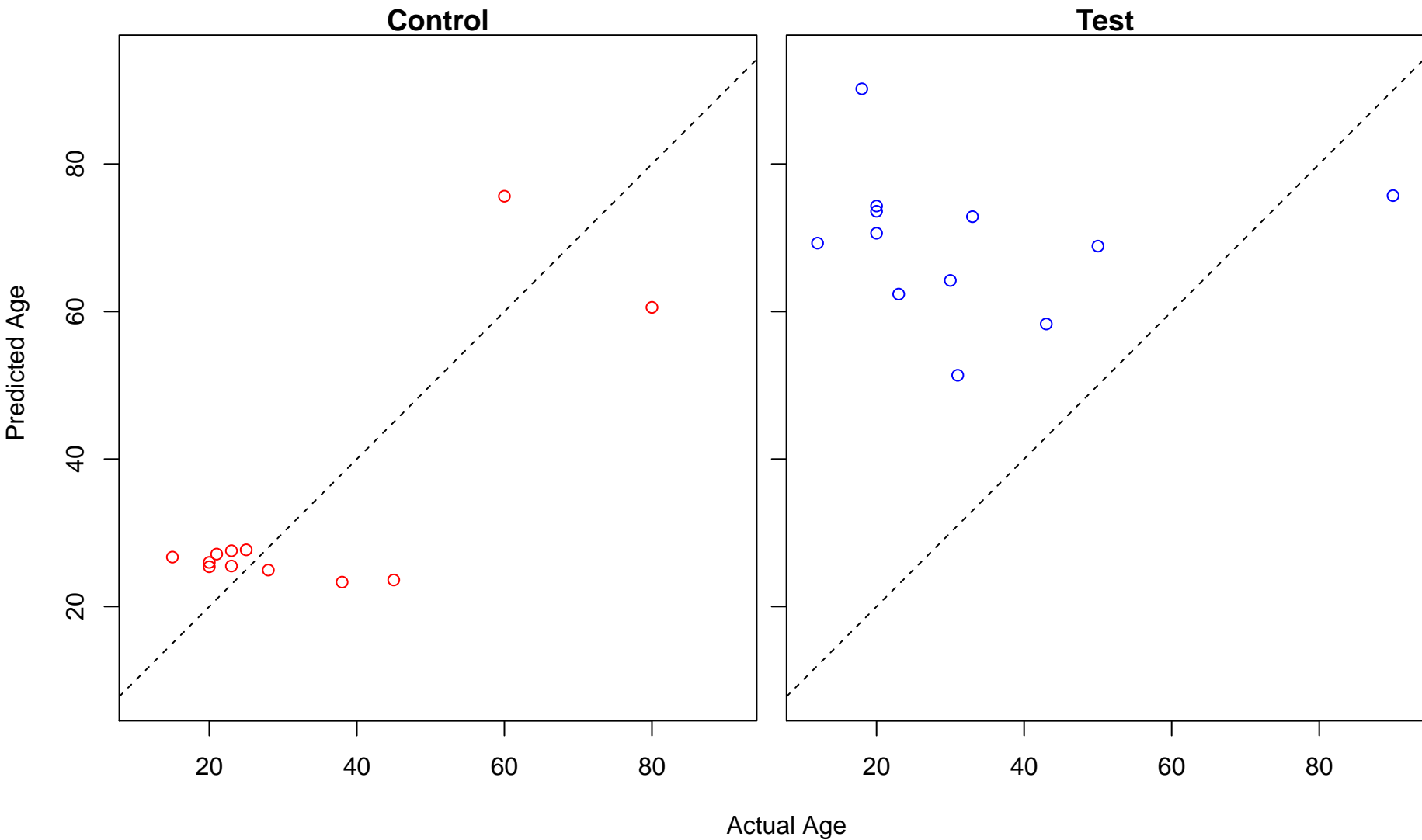
regulation of cytoplasmic transport (Score: 7.197594)



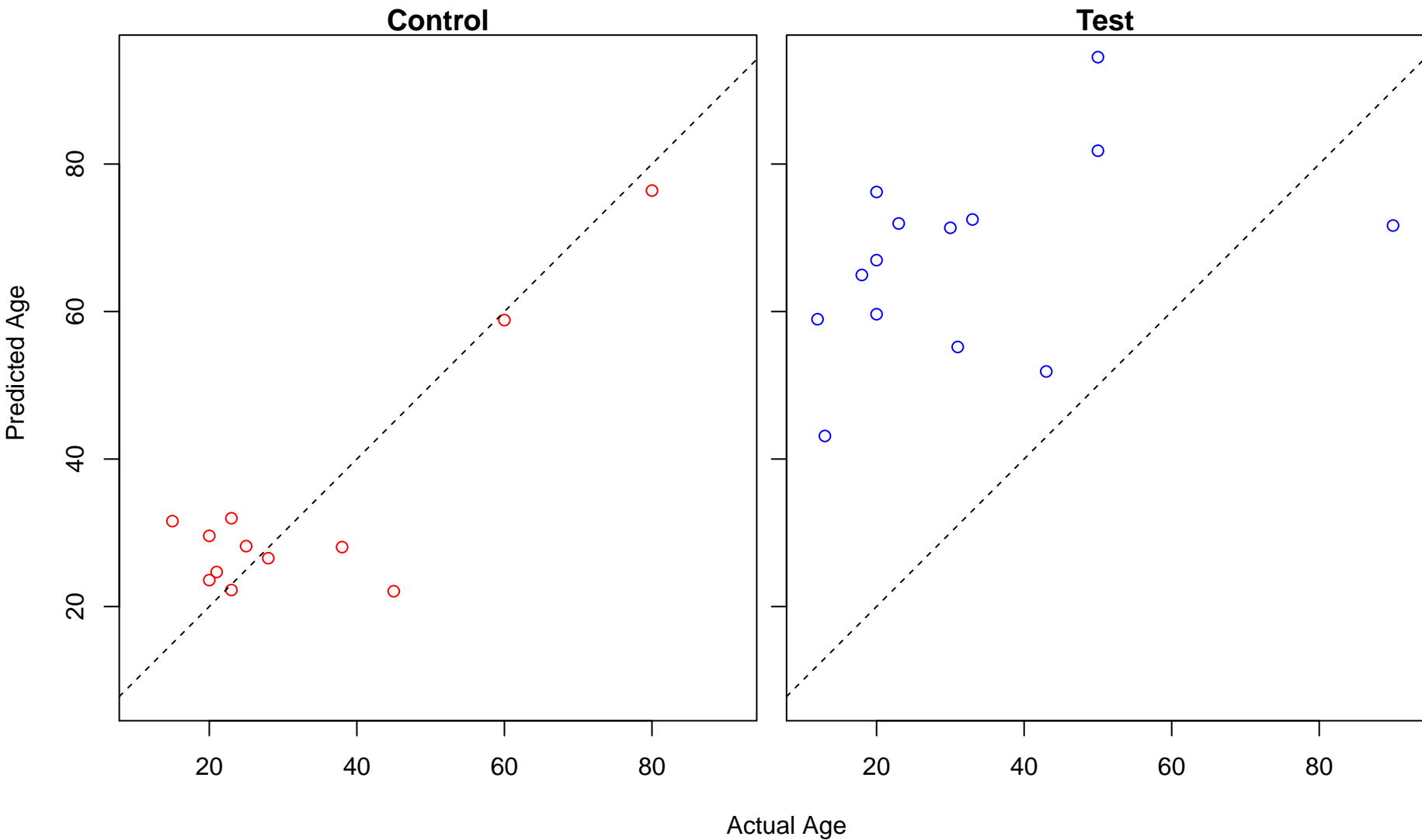
cell proliferation (Score: 7.194841)



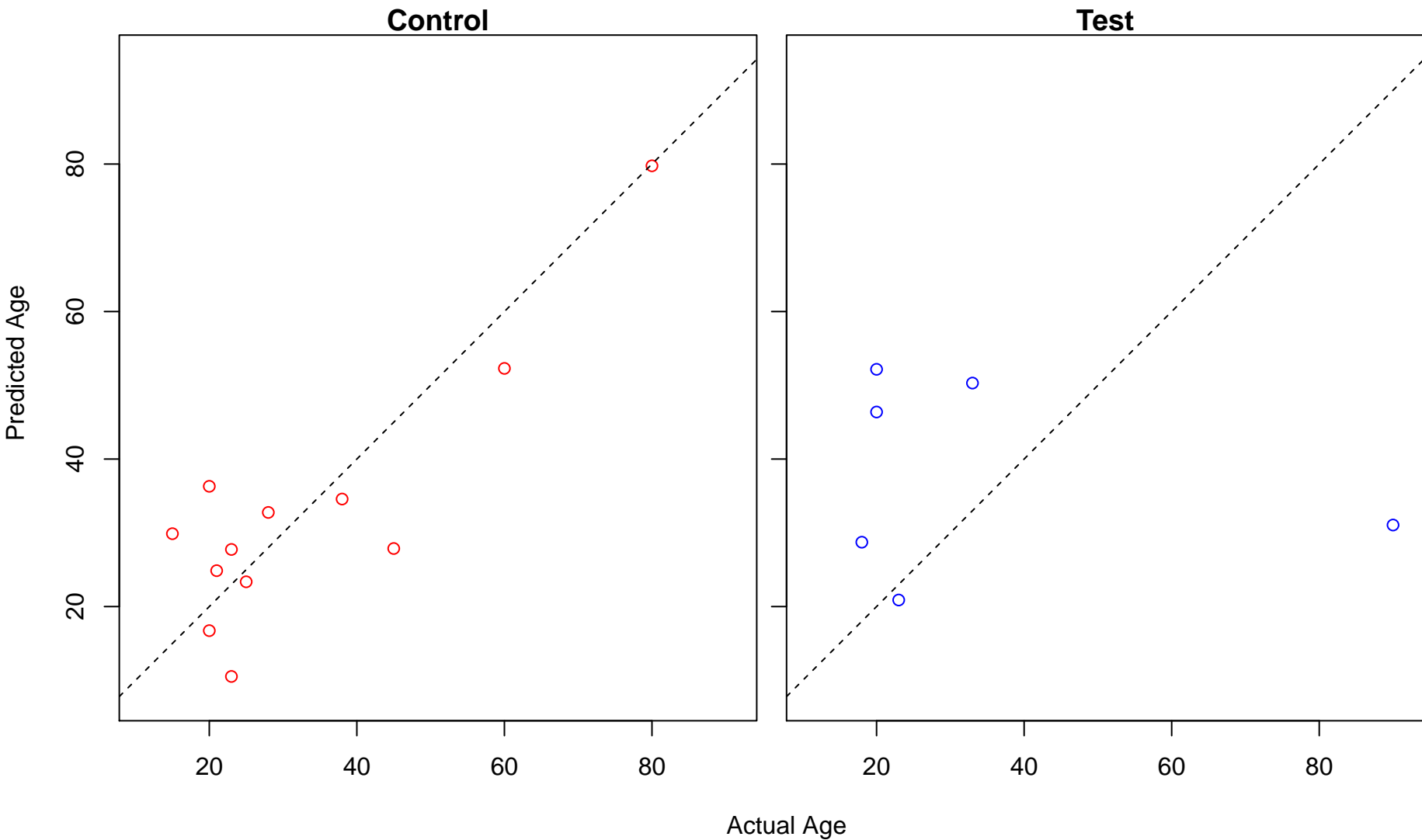
establishment of protein localization to endoplasmic reticulum (Score: 7.193683)



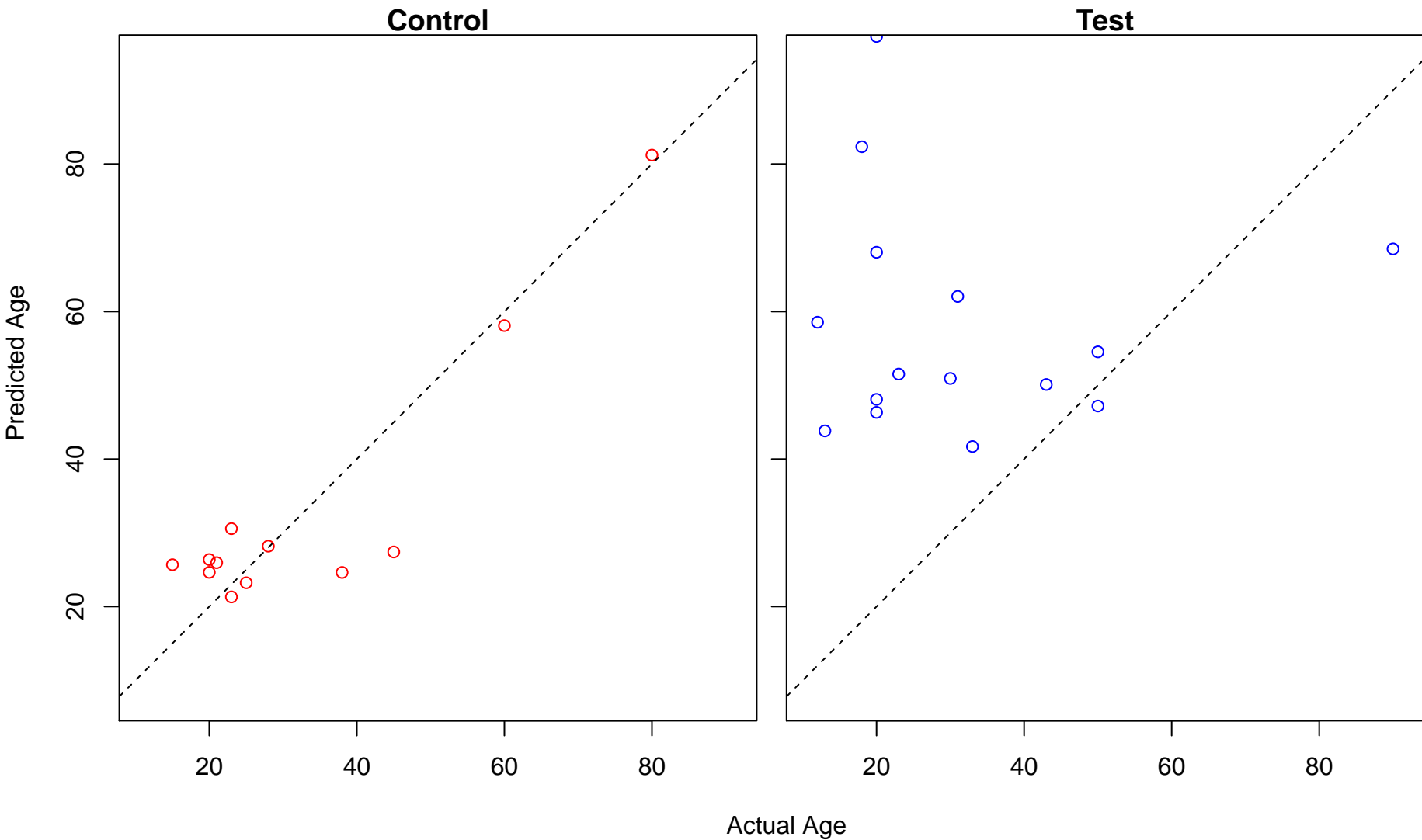
sphingoid biosynthetic process (Score: 7.193494)



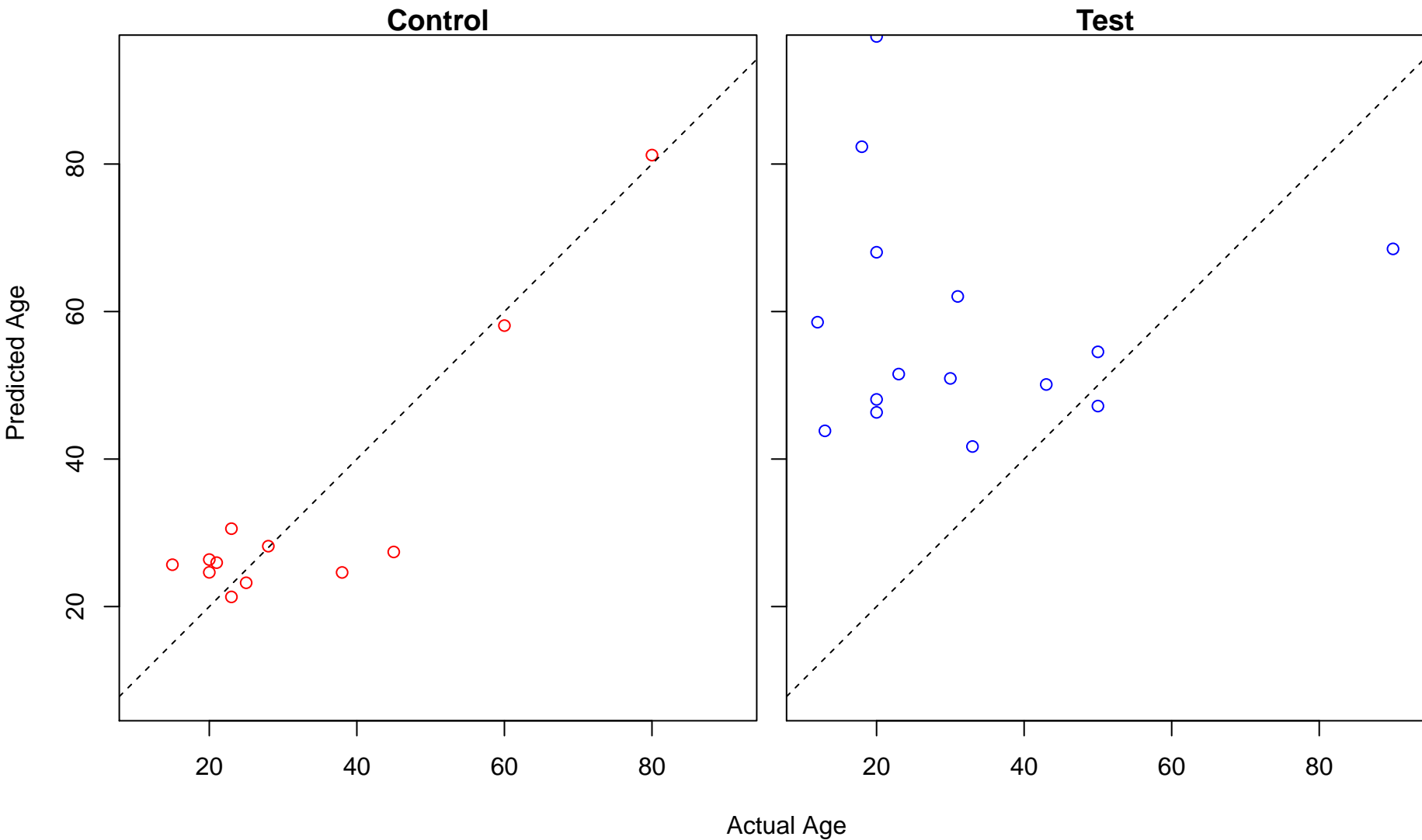
regulation of cAMP-dependent protein kinase activity (Score: 7.187748)



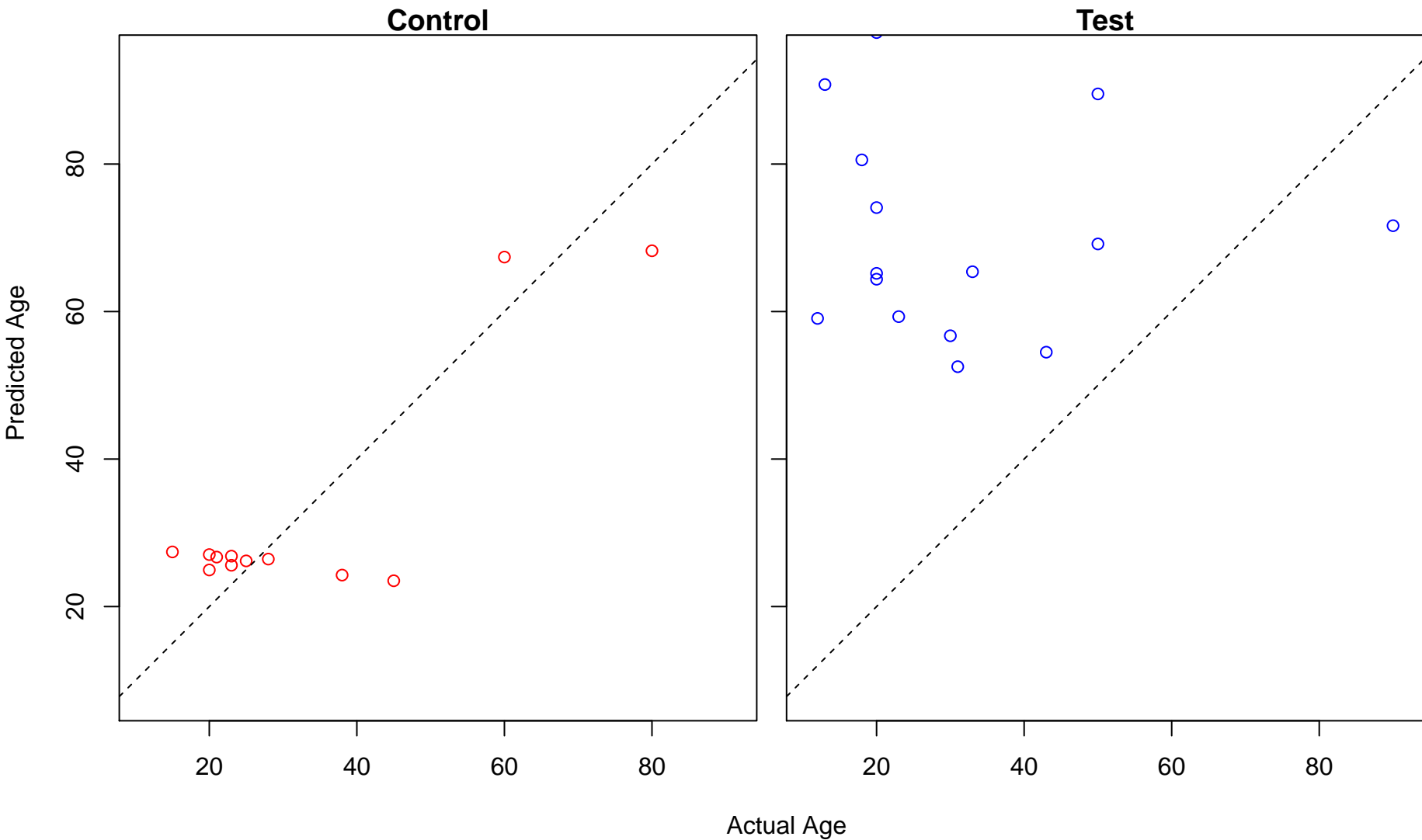
neutral lipid catabolic process (Score: 7.184544)



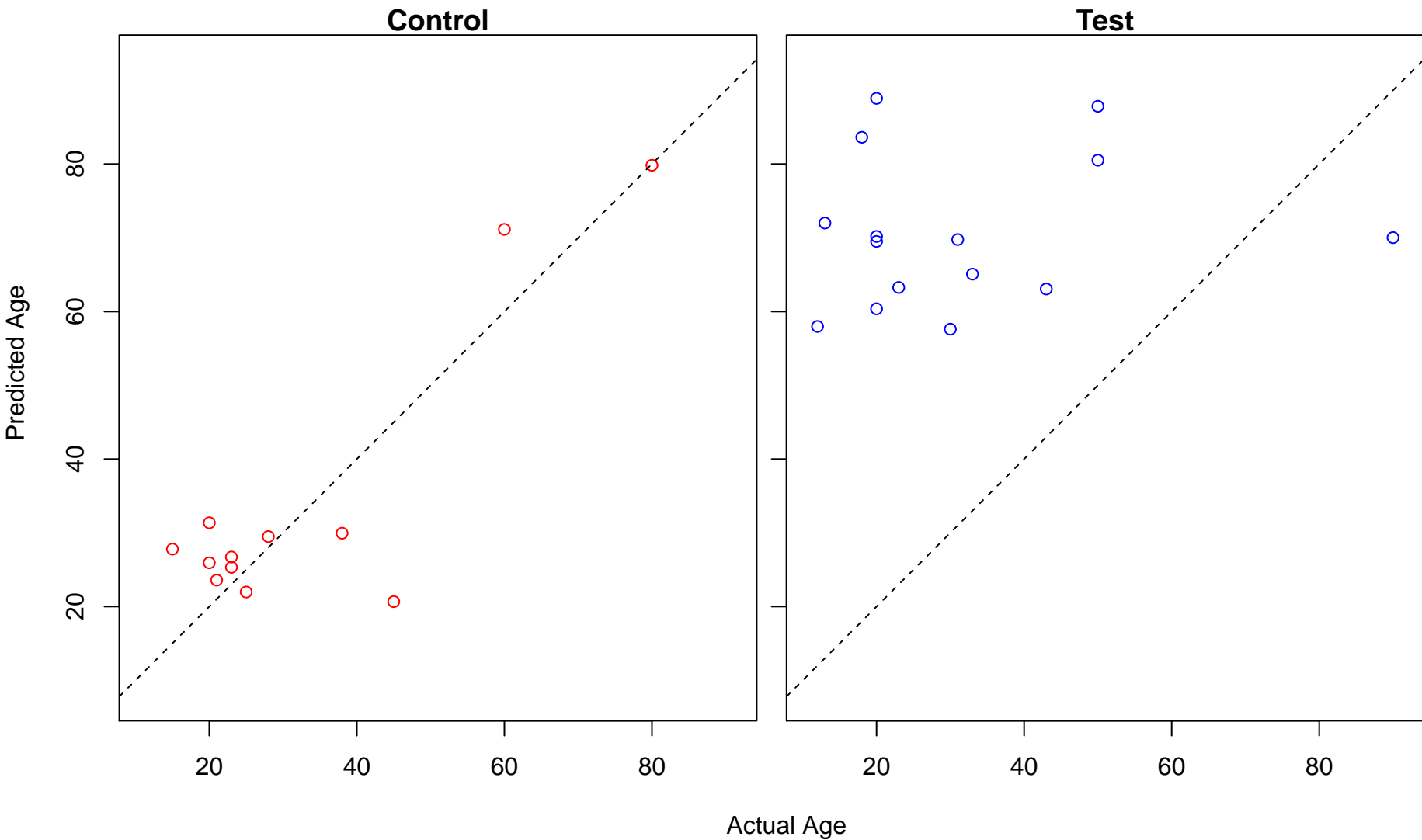
acylglycerol catabolic process (Score: 7.184544)



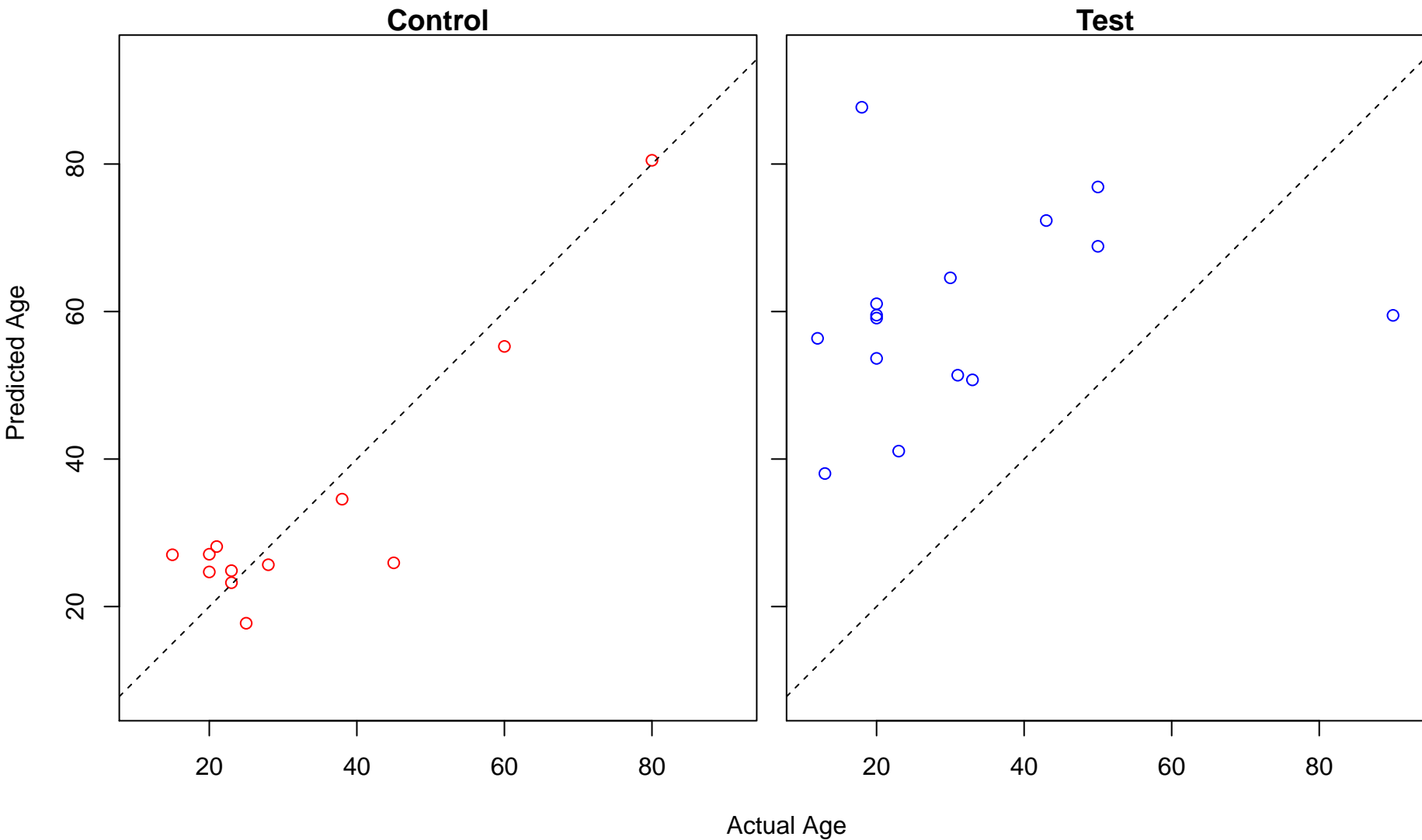
peptide biosynthetic process (Score: 7.183218)



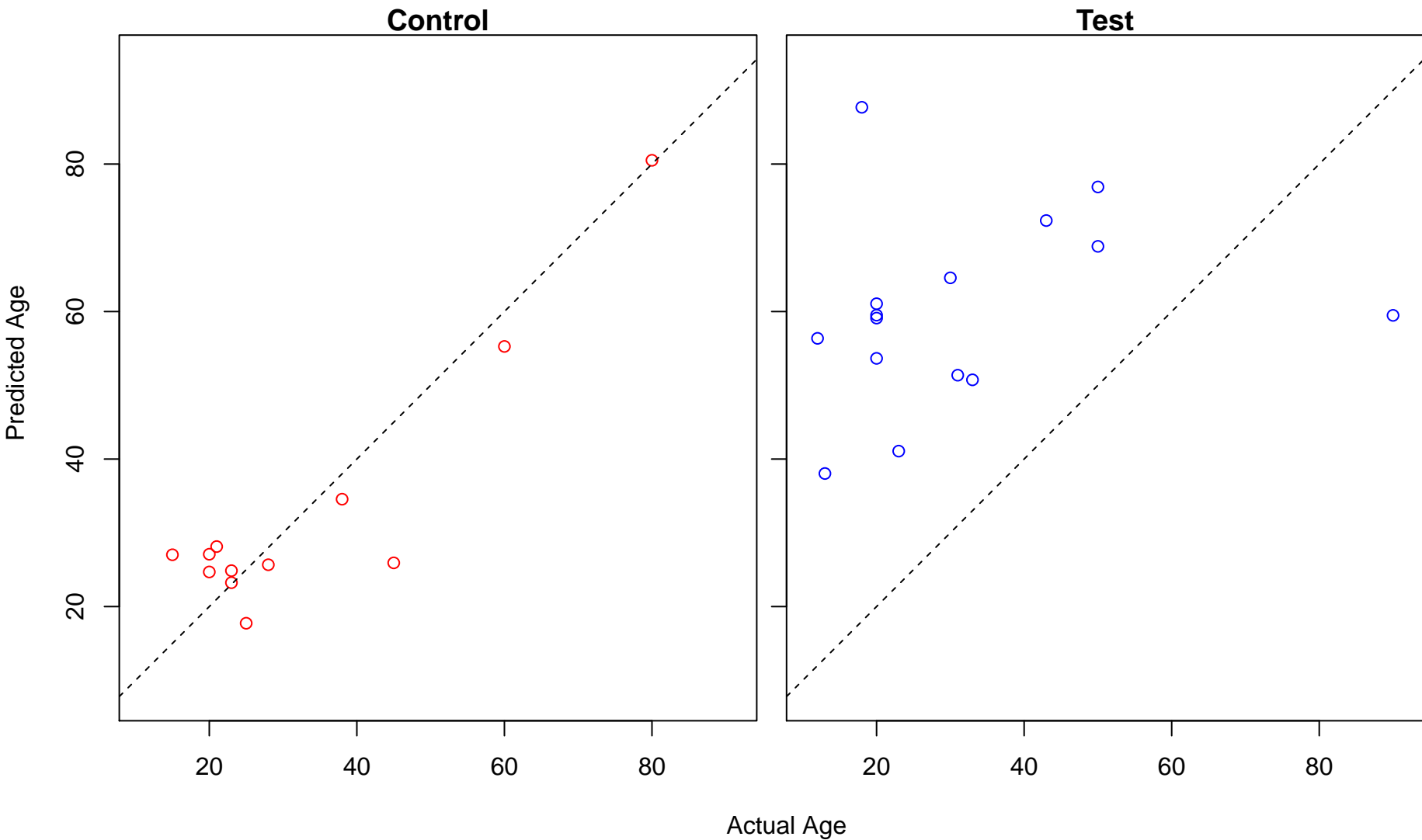
positive regulation of cell migration (Score: 7.177325)



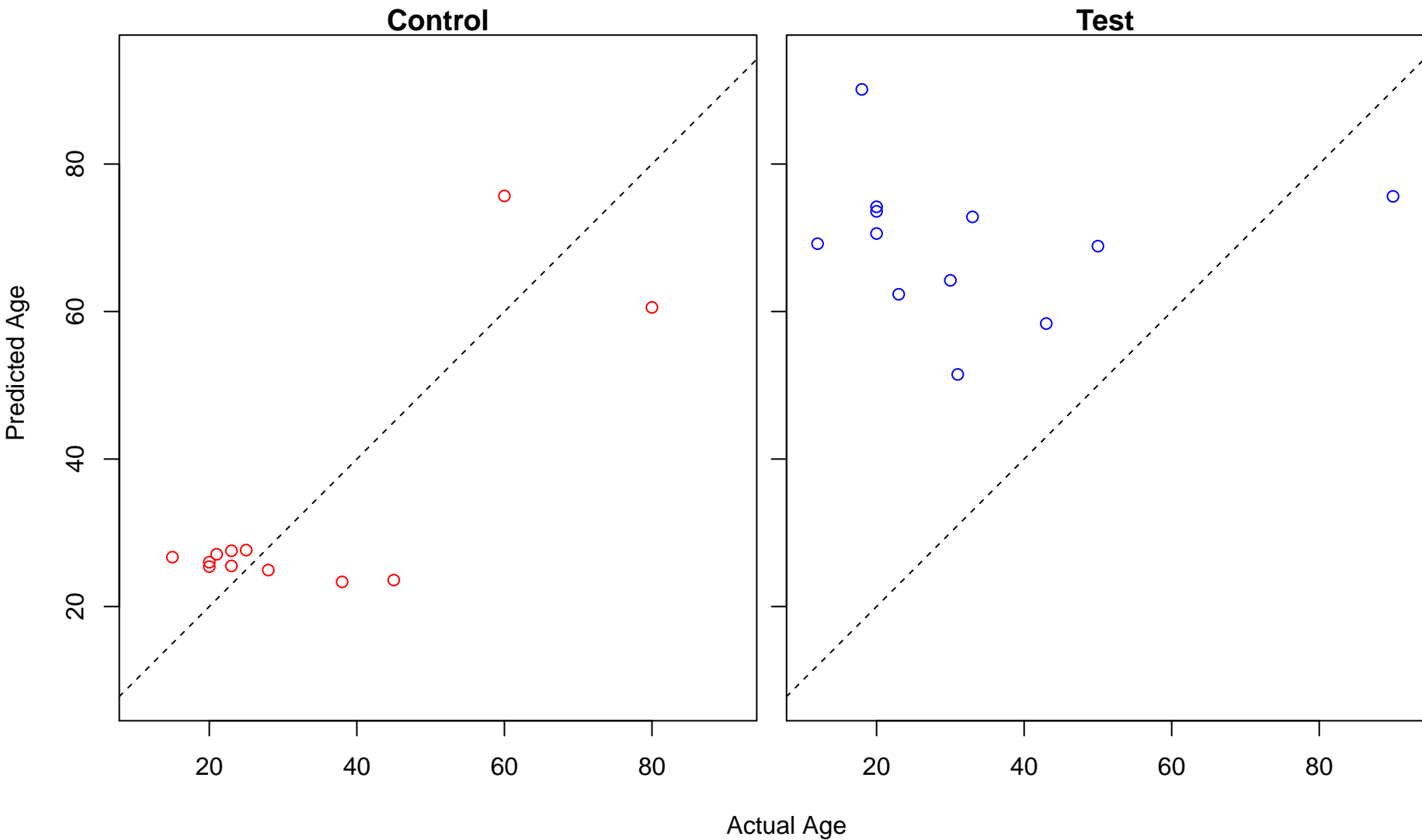
diterpenoid metabolic process (Score: 7.170954)



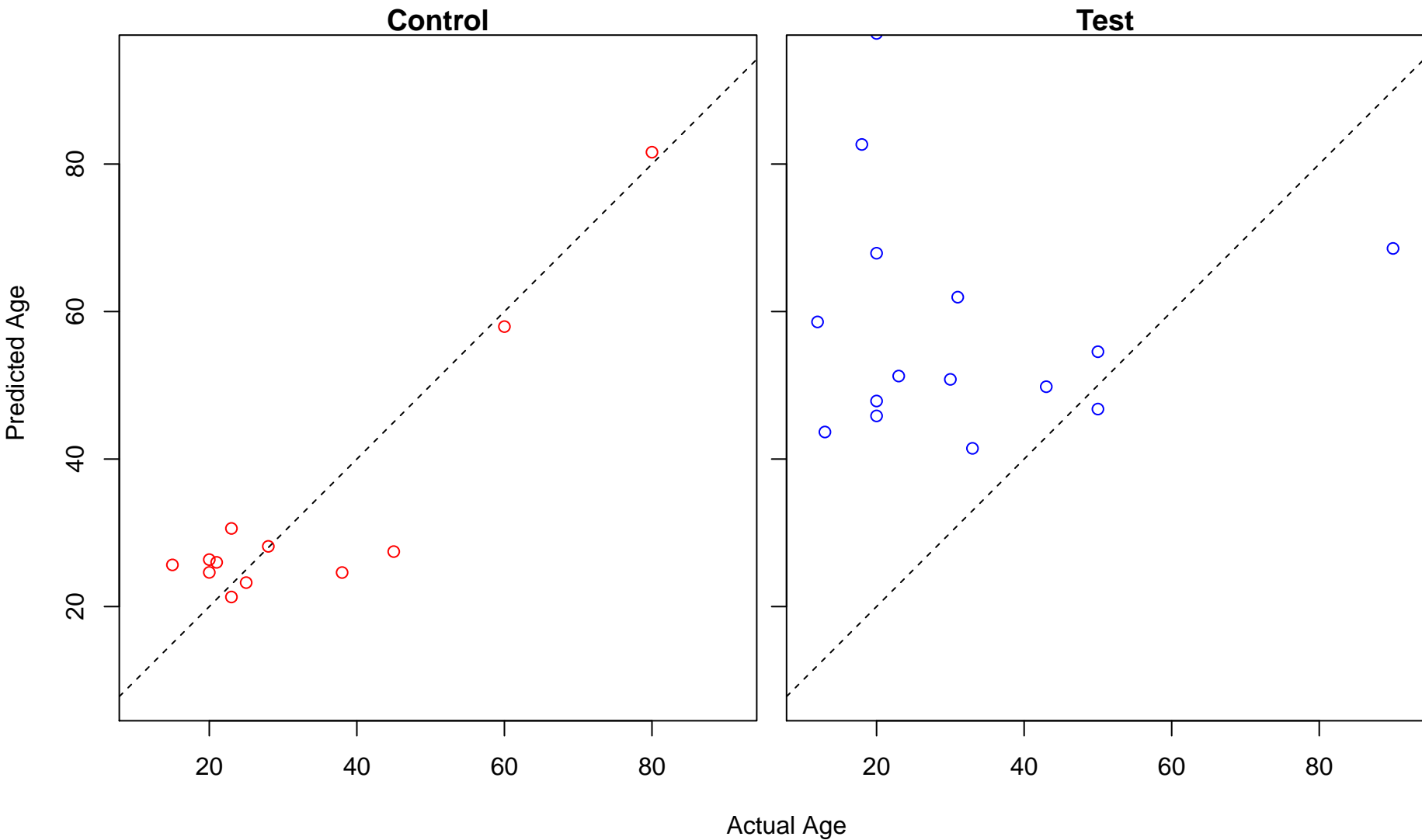
terpenoid metabolic process (Score: 7.170530)



protein localization to endoplasmic reticulum (Score: 7.169462)

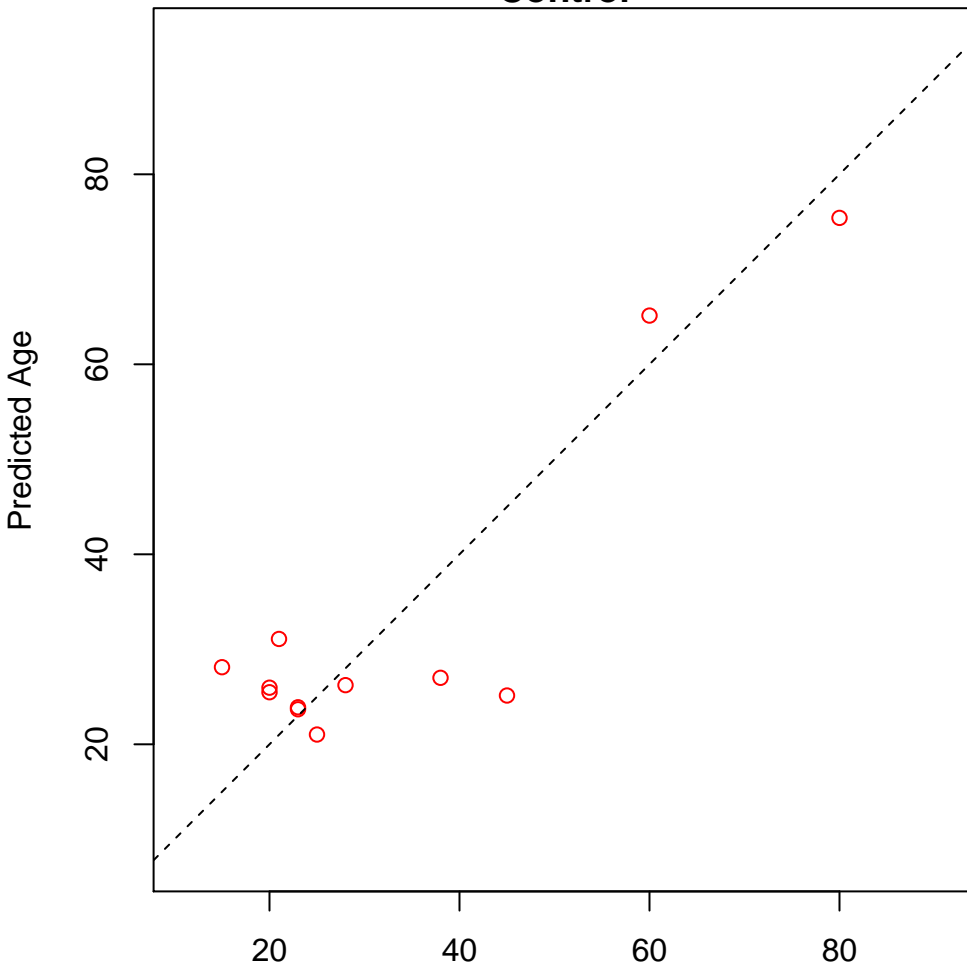


triglyceride catabolic process (Score: 7.169079)

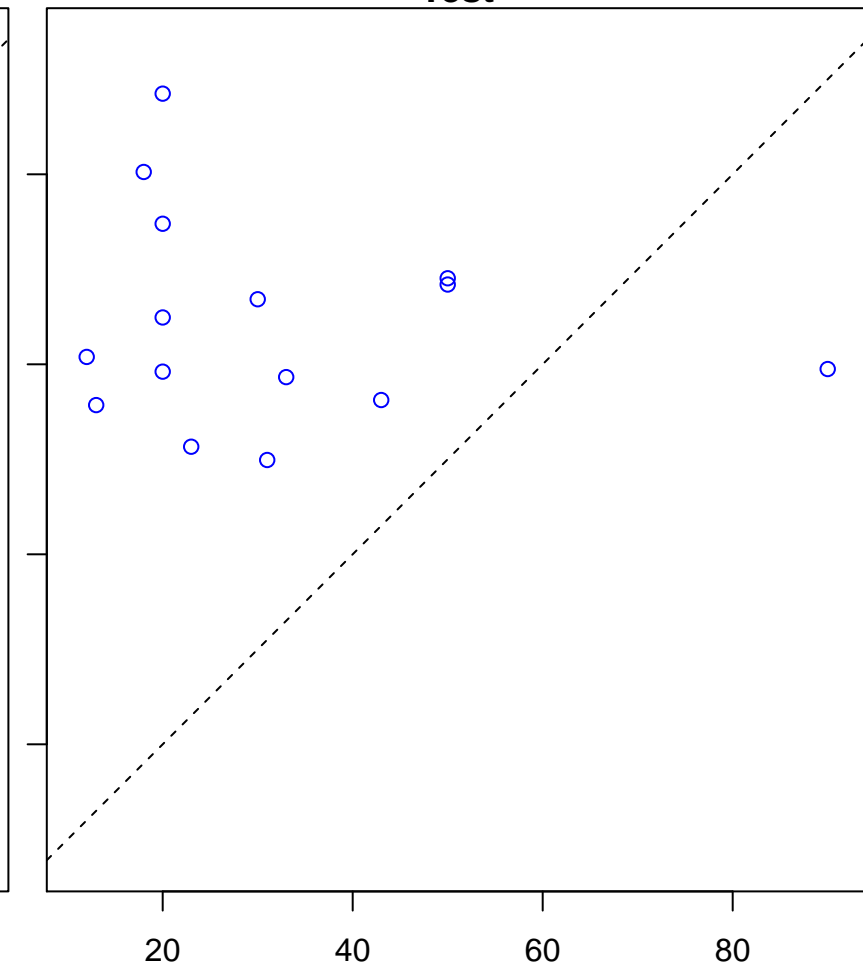


intrinsic apoptotic signaling pathway (Score: 7.166216)

Control

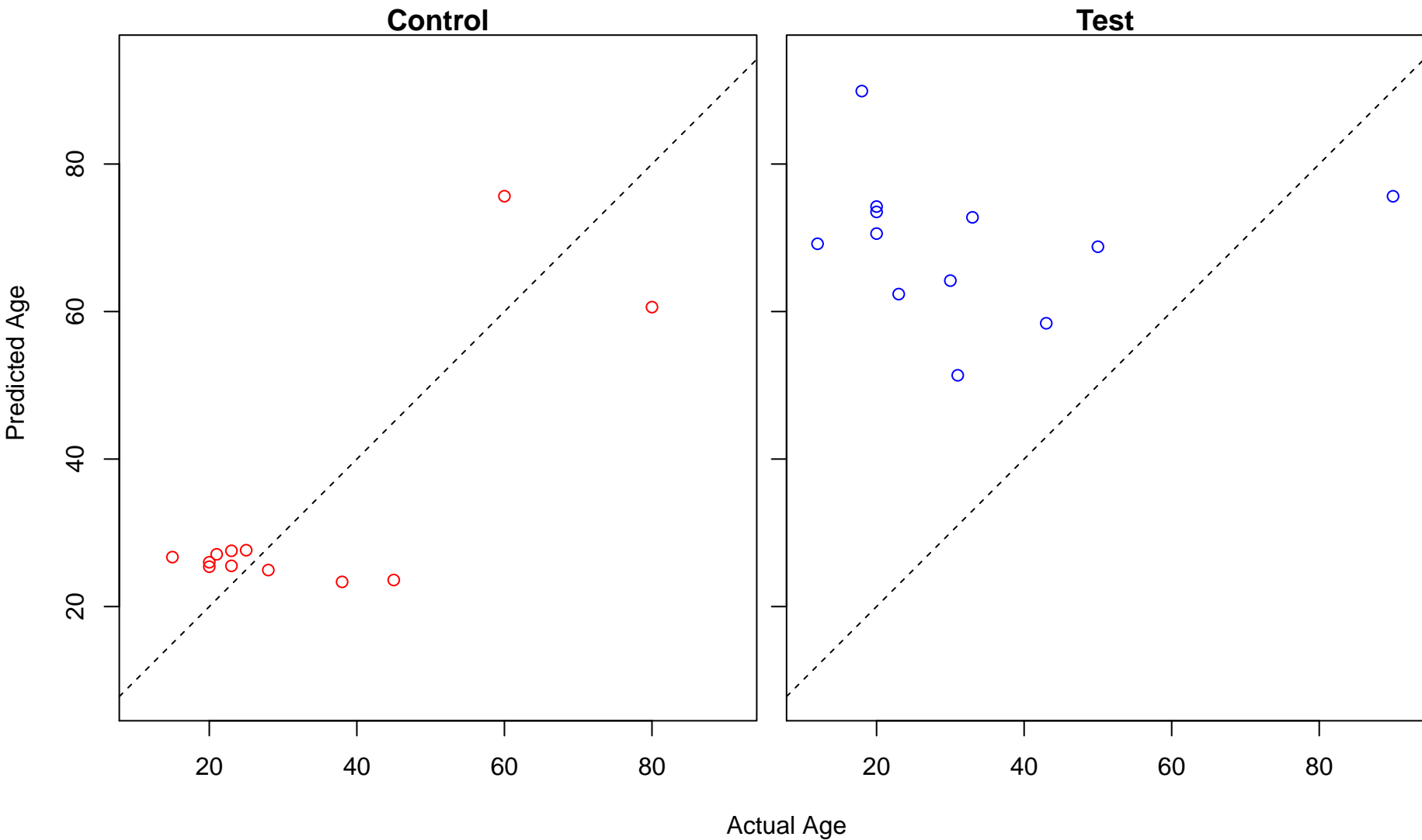


Test

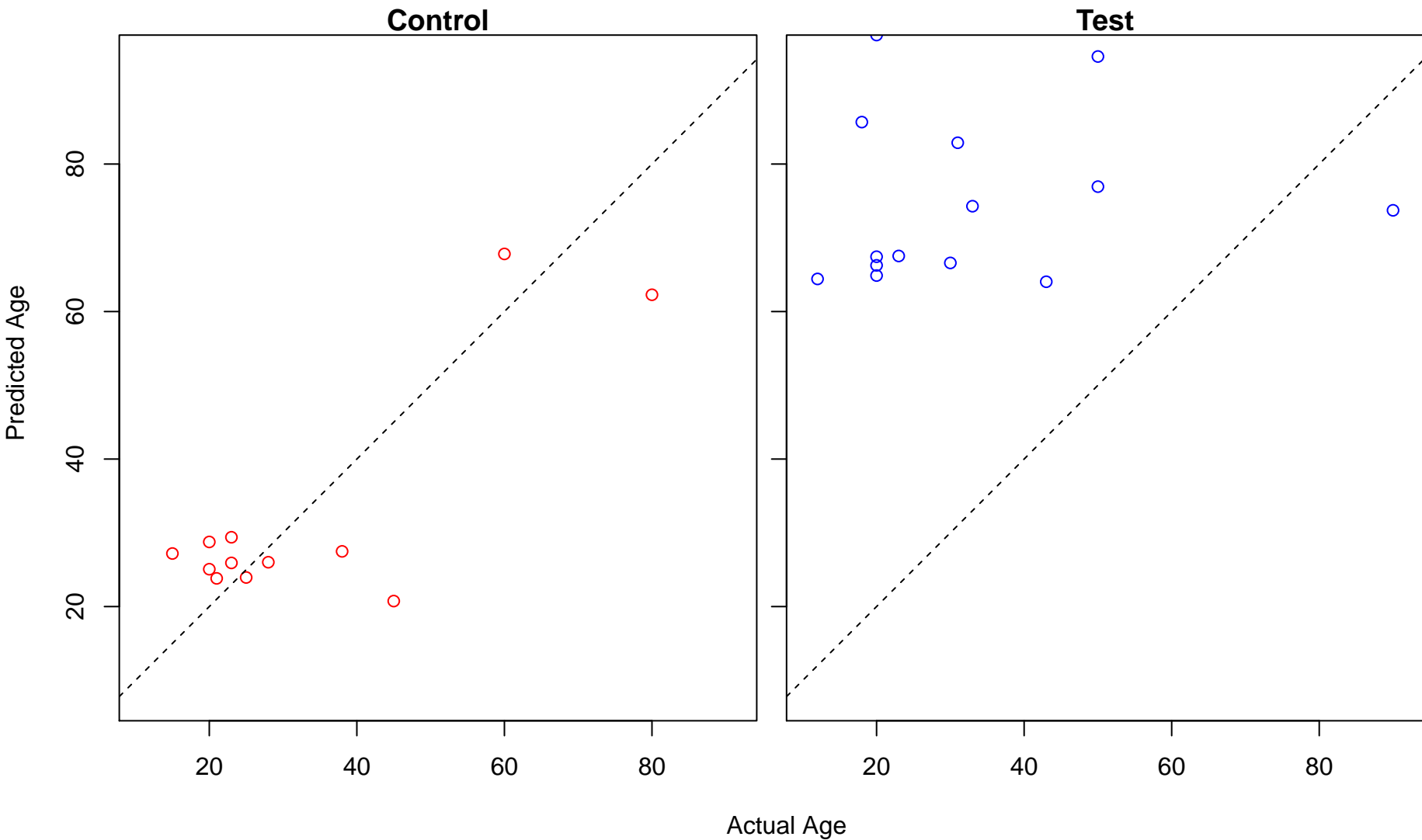


Actual Age

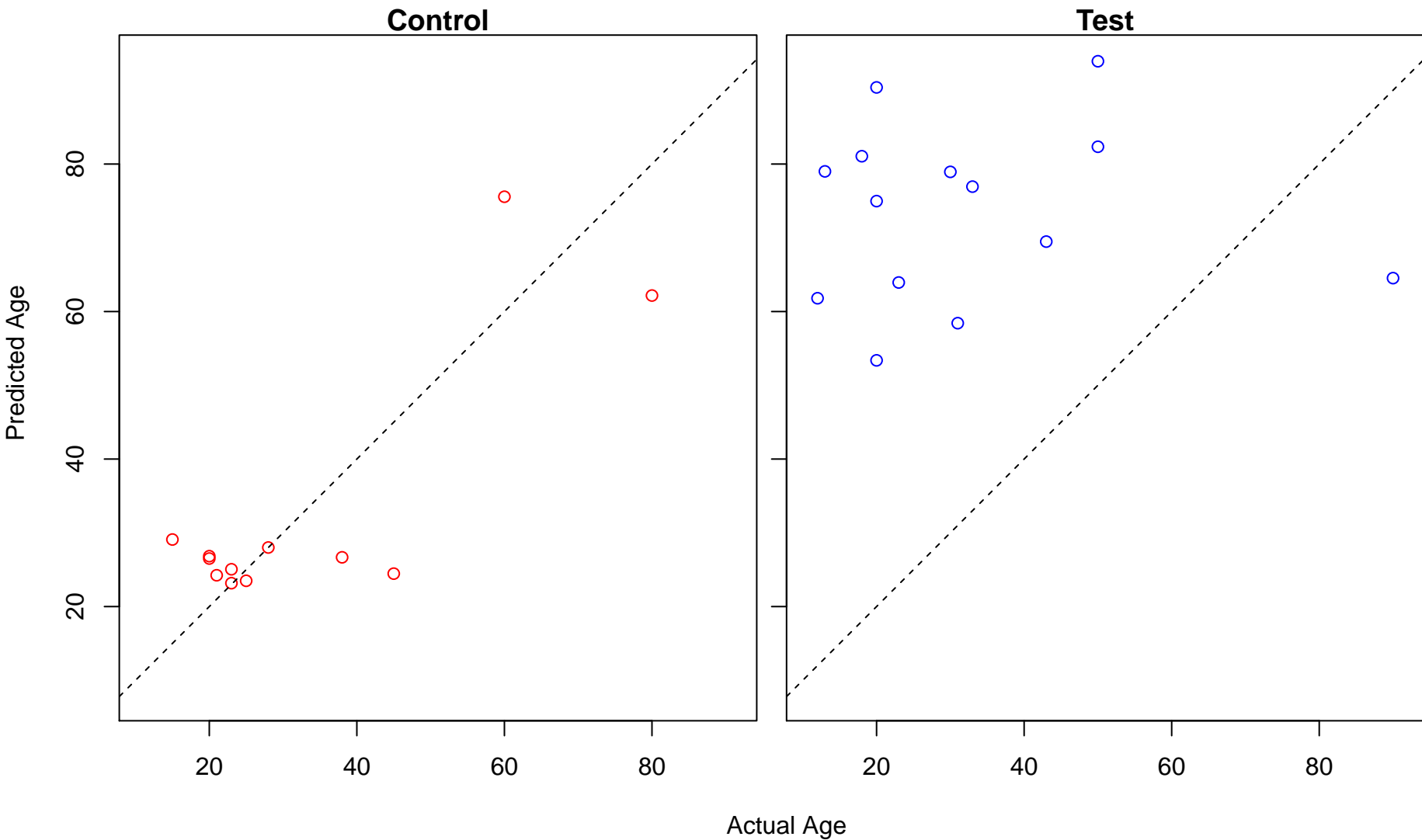
protein targeting to membrane (Score: 7.163536)



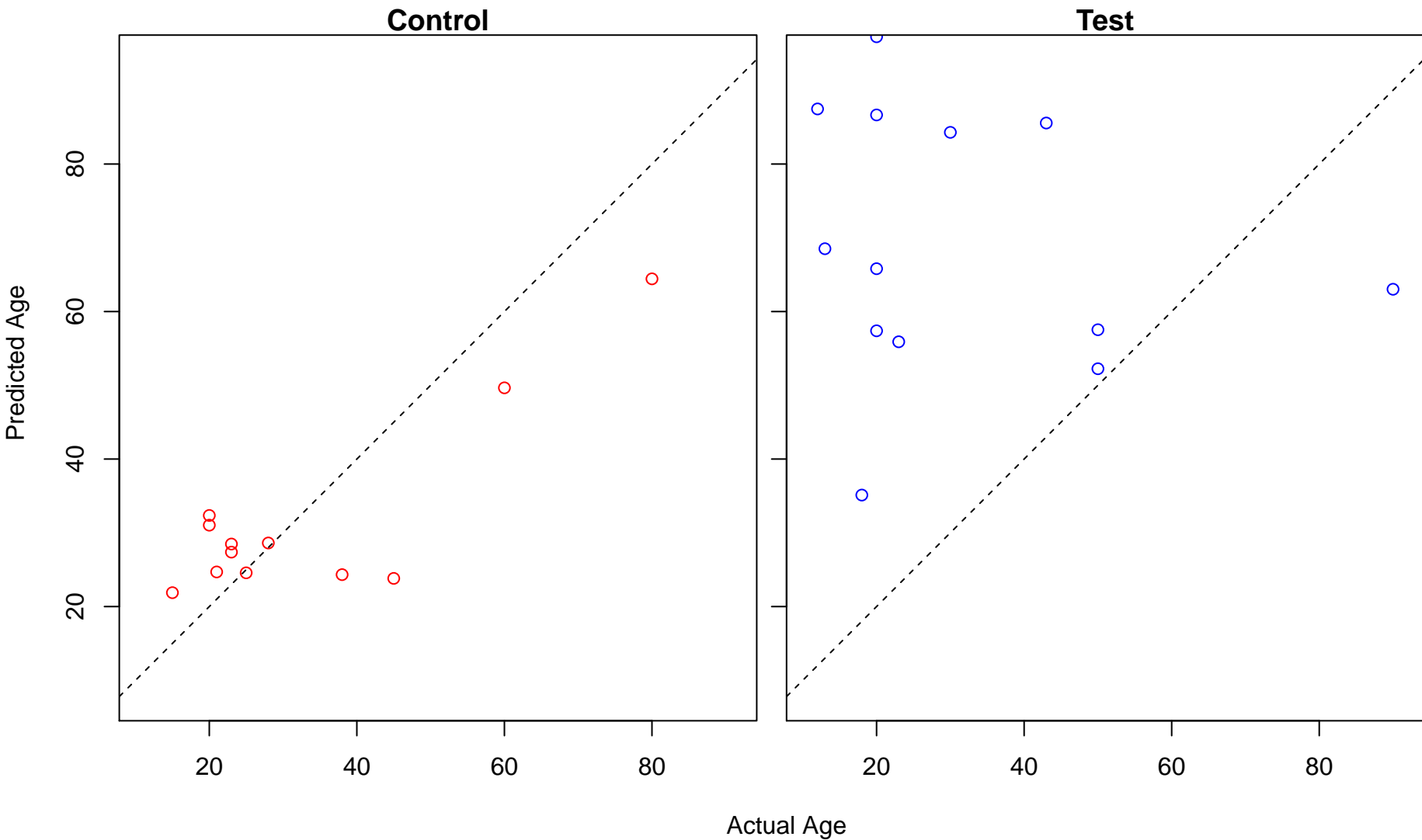
humoral immune response (Score: 7.160453)



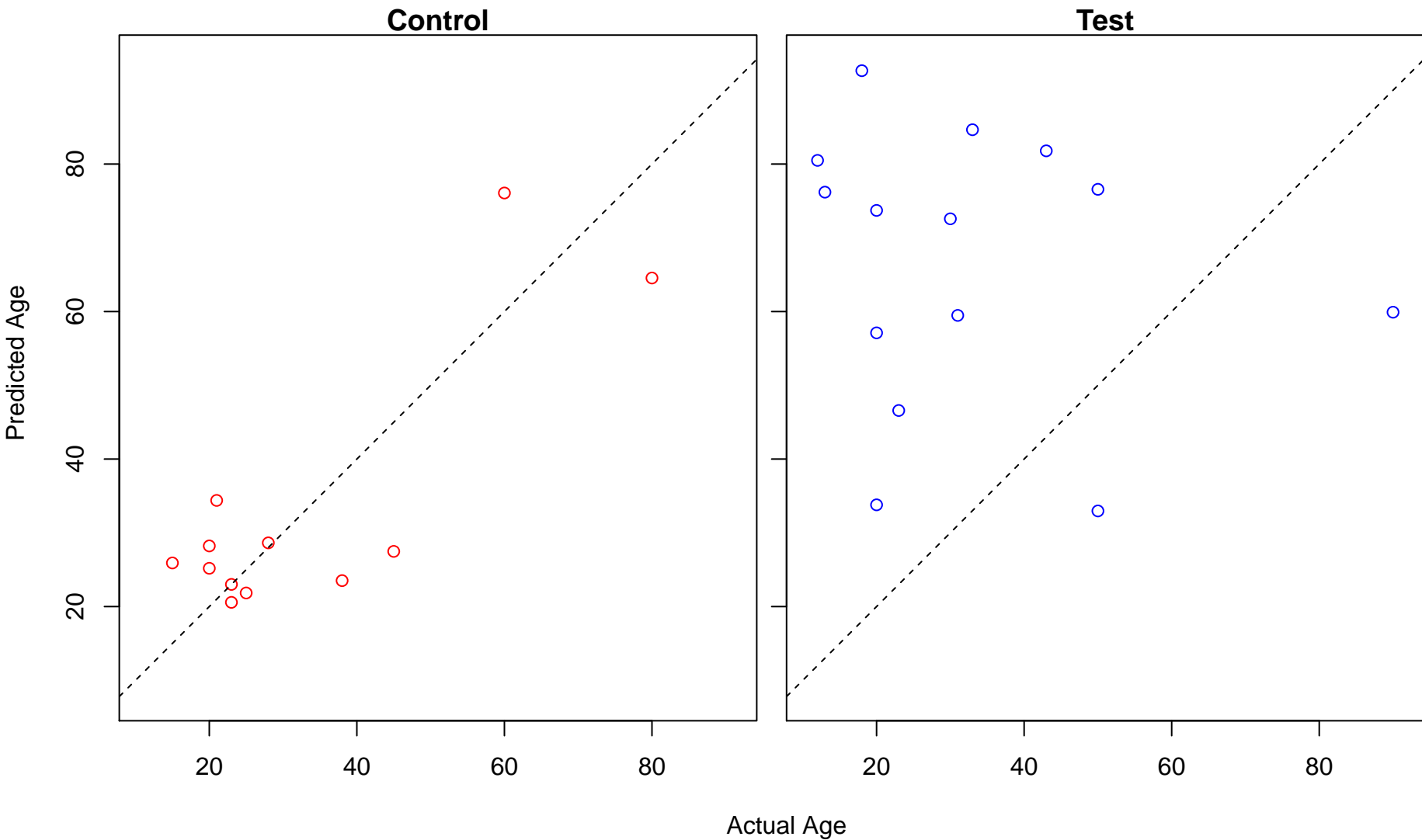
oligosaccharide biosynthetic process (Score: 7.158658)



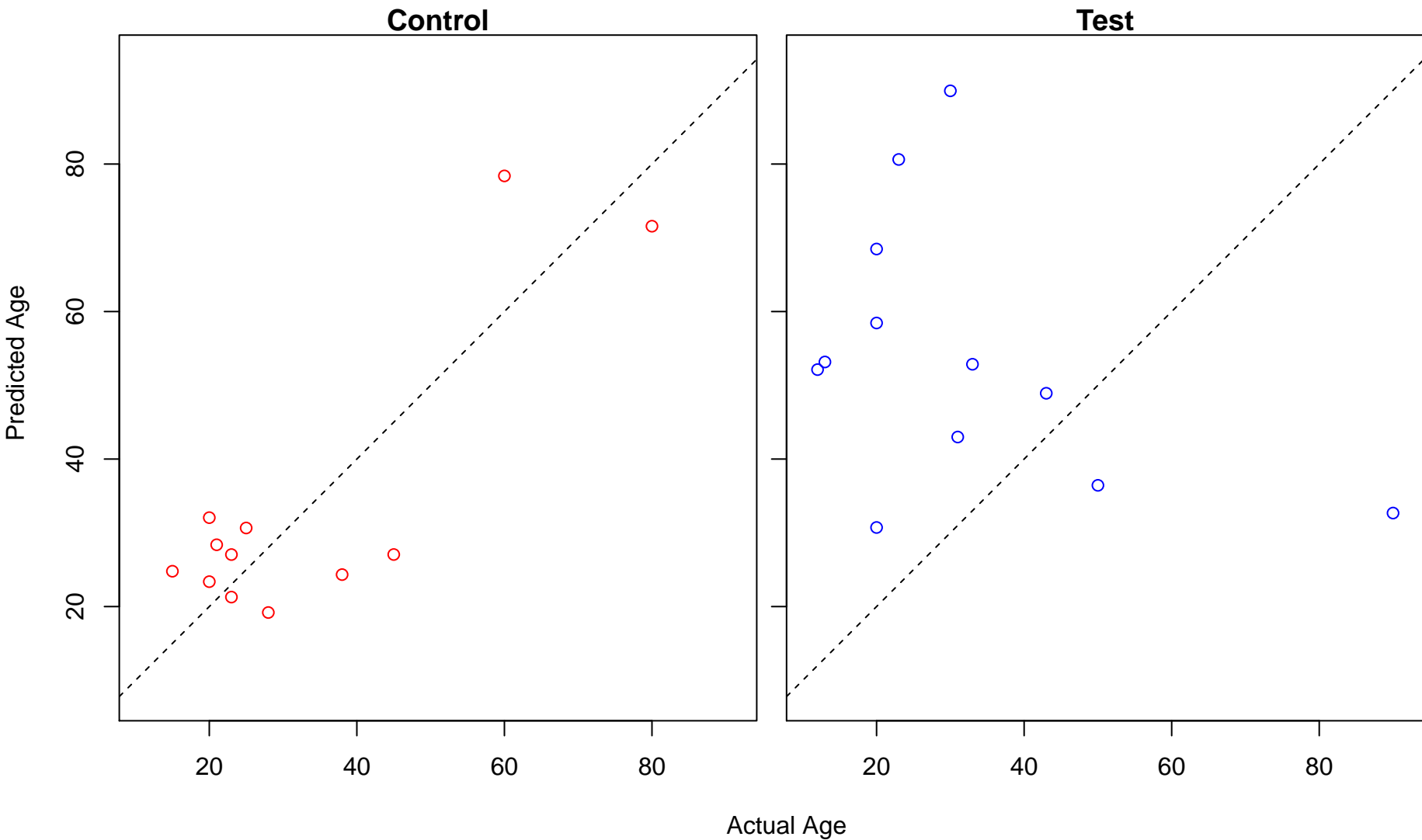
oxalate transport (Score: 7.15625)



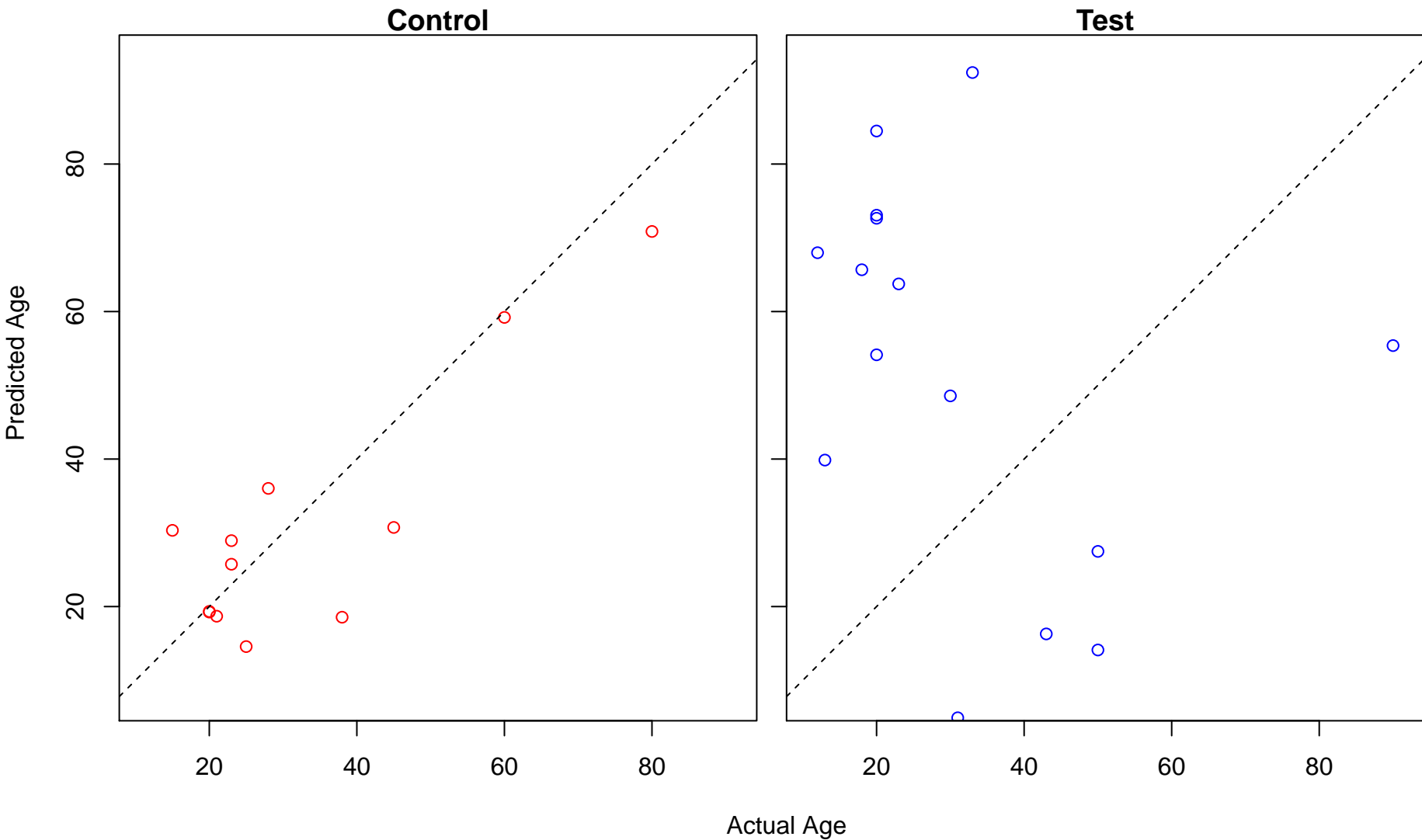
kinetochore assembly (Score: 7.155911)



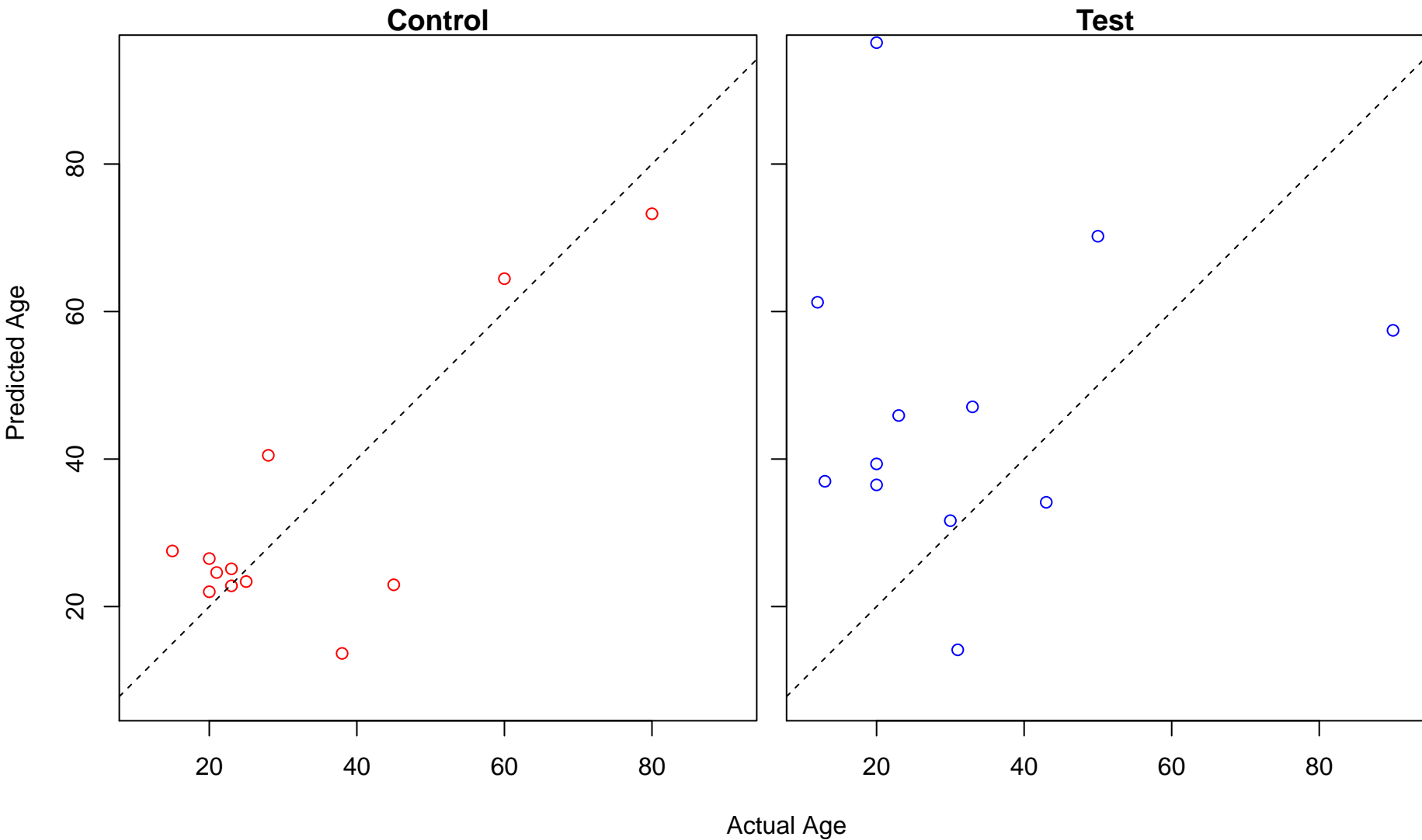
proteasome assembly (Score: 7.152791)



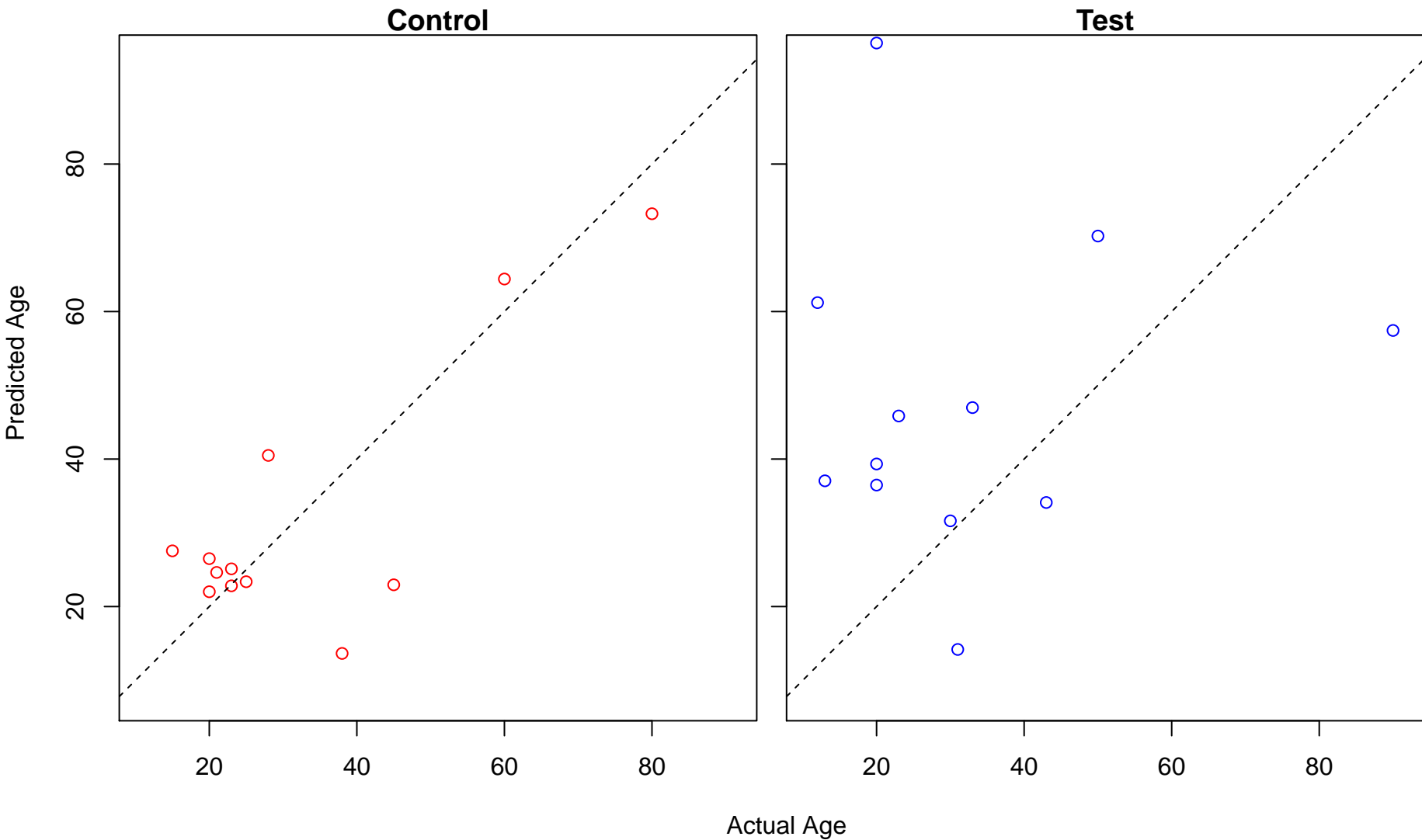
cellular process involved in reproduction in multicellular organism (Score: 7.148766)



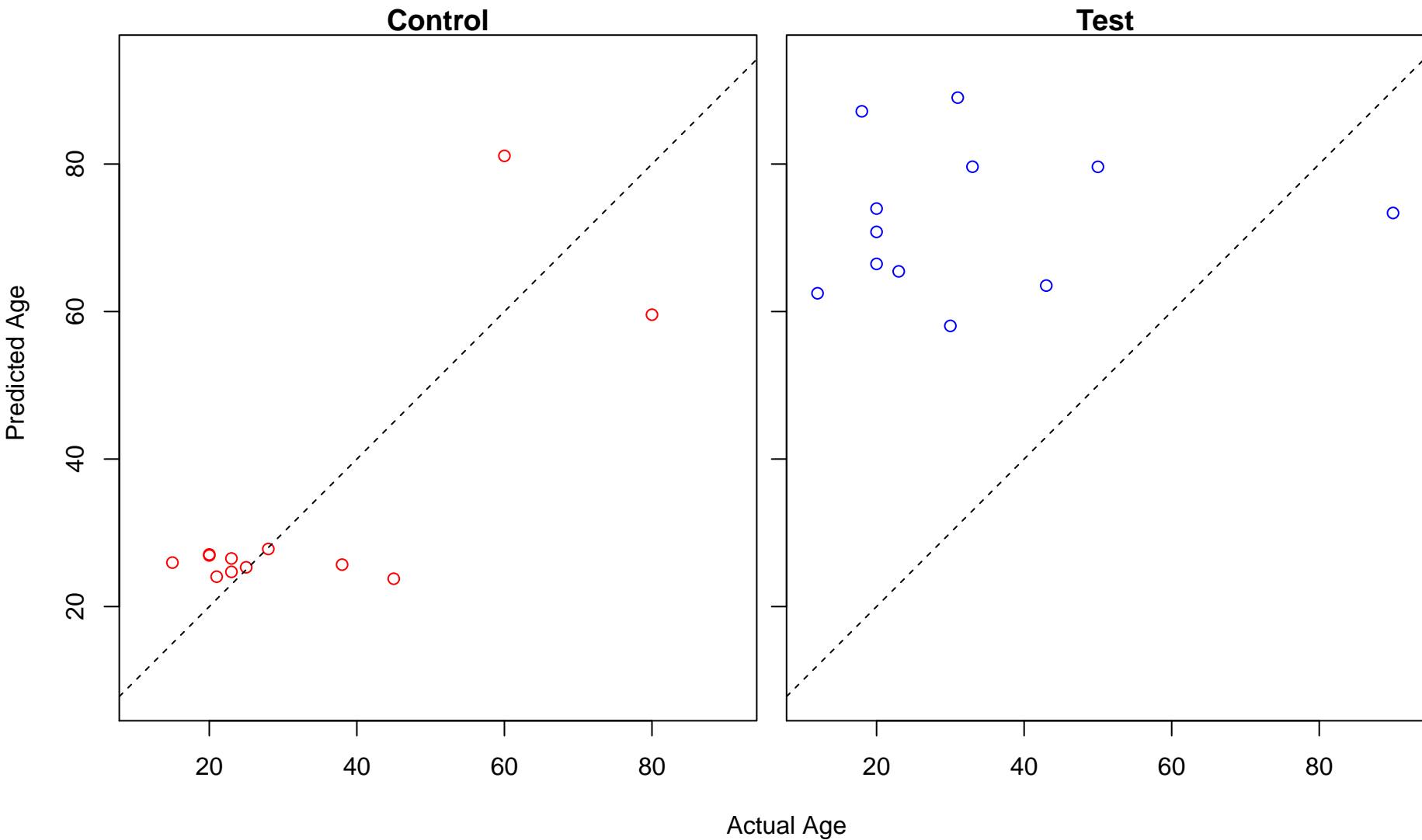
glycosyl compound biosynthetic process (Score: 7.148181)



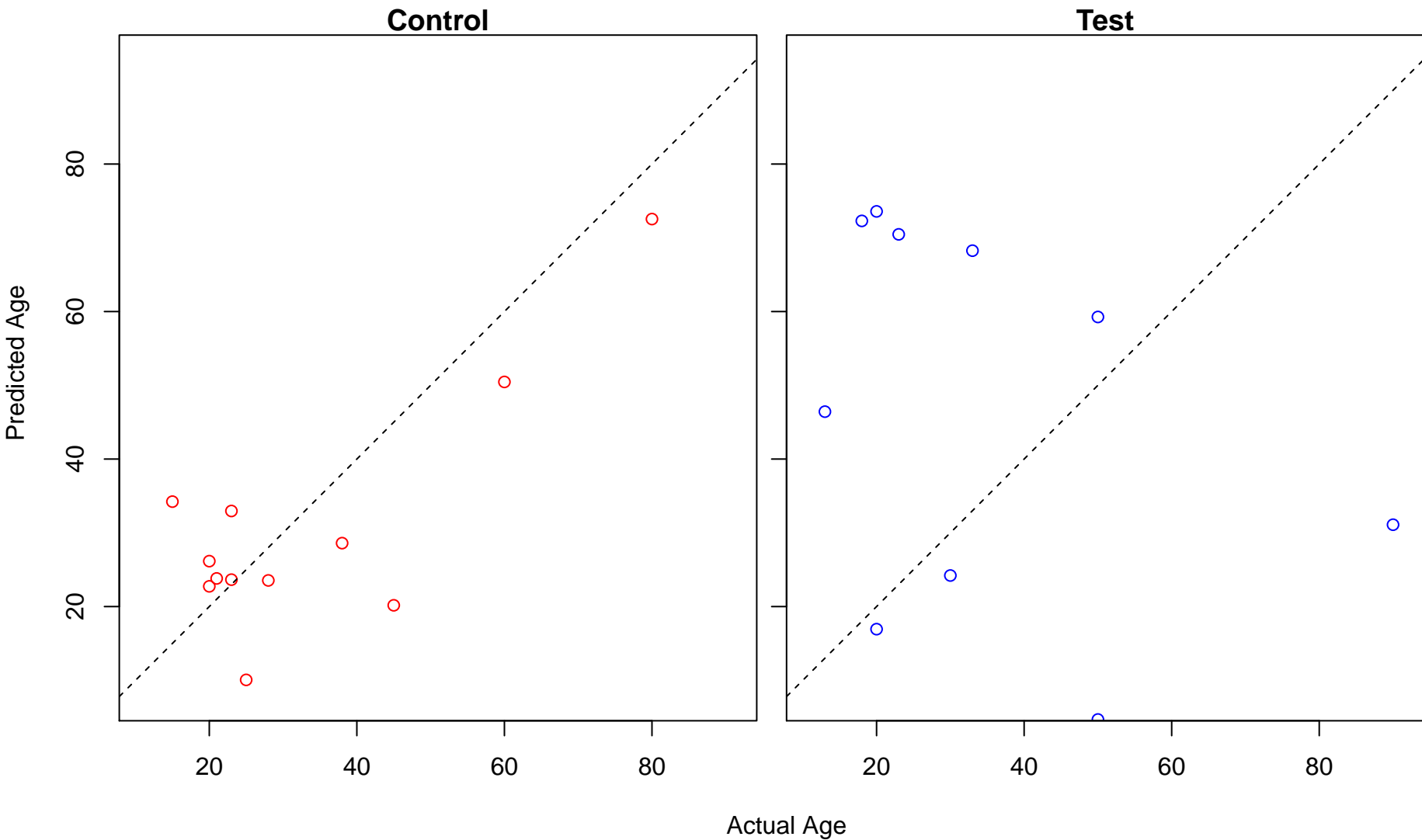
nucleoside biosynthetic process (Score: 7.146172)



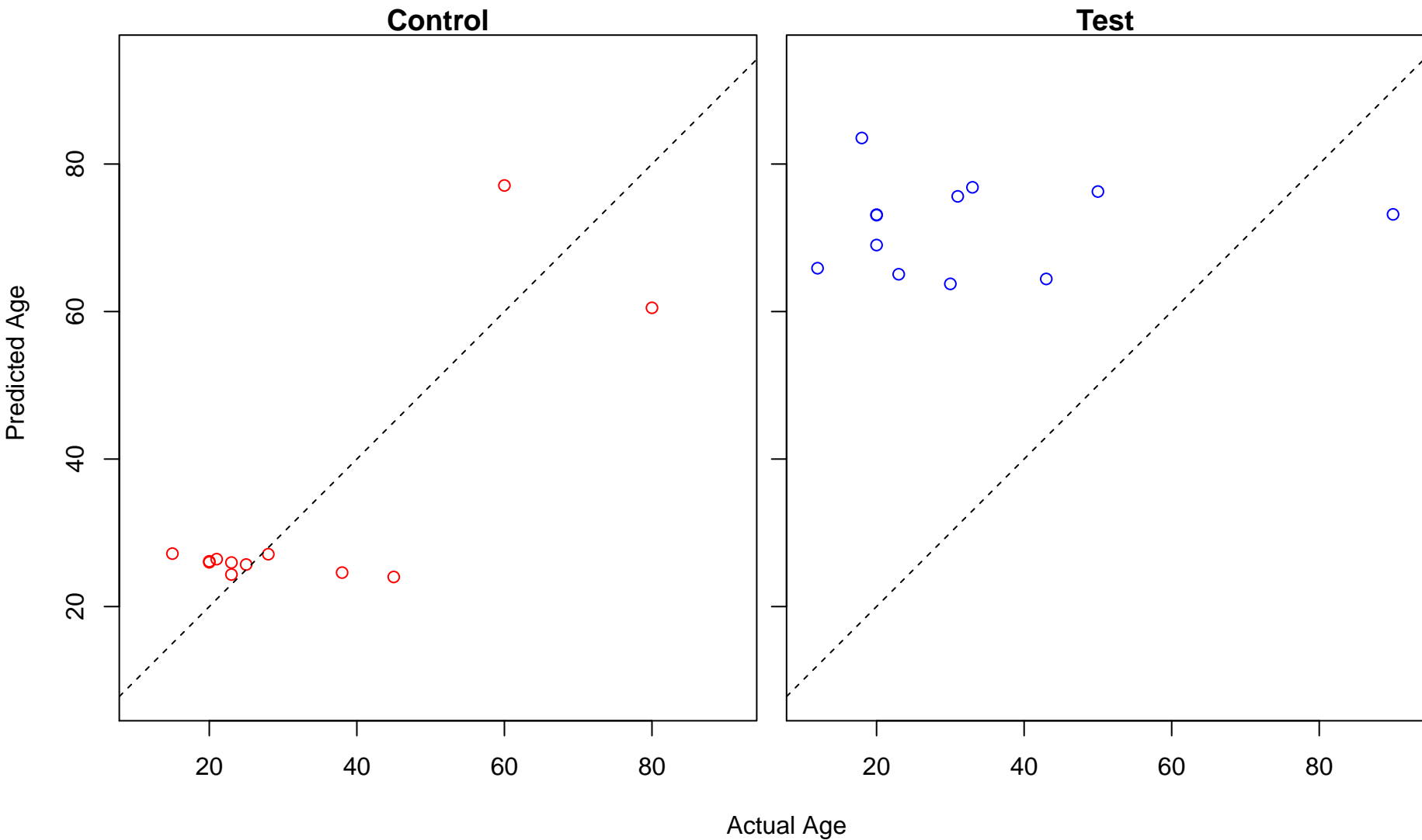
negative regulation of cell cycle G1/S phase transition (Score: 7.144587)



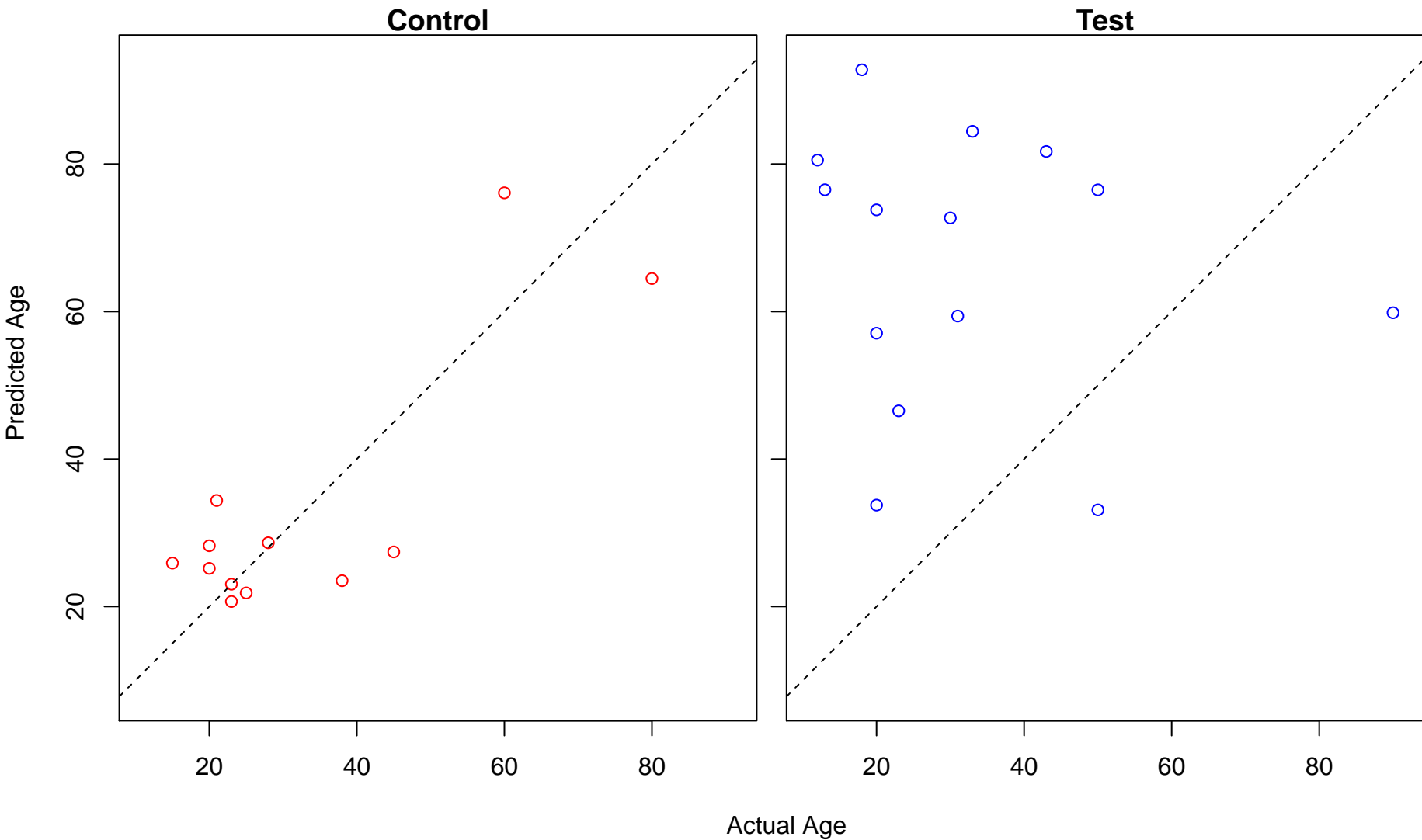
cellular cation homeostasis (Score: 7.143272)



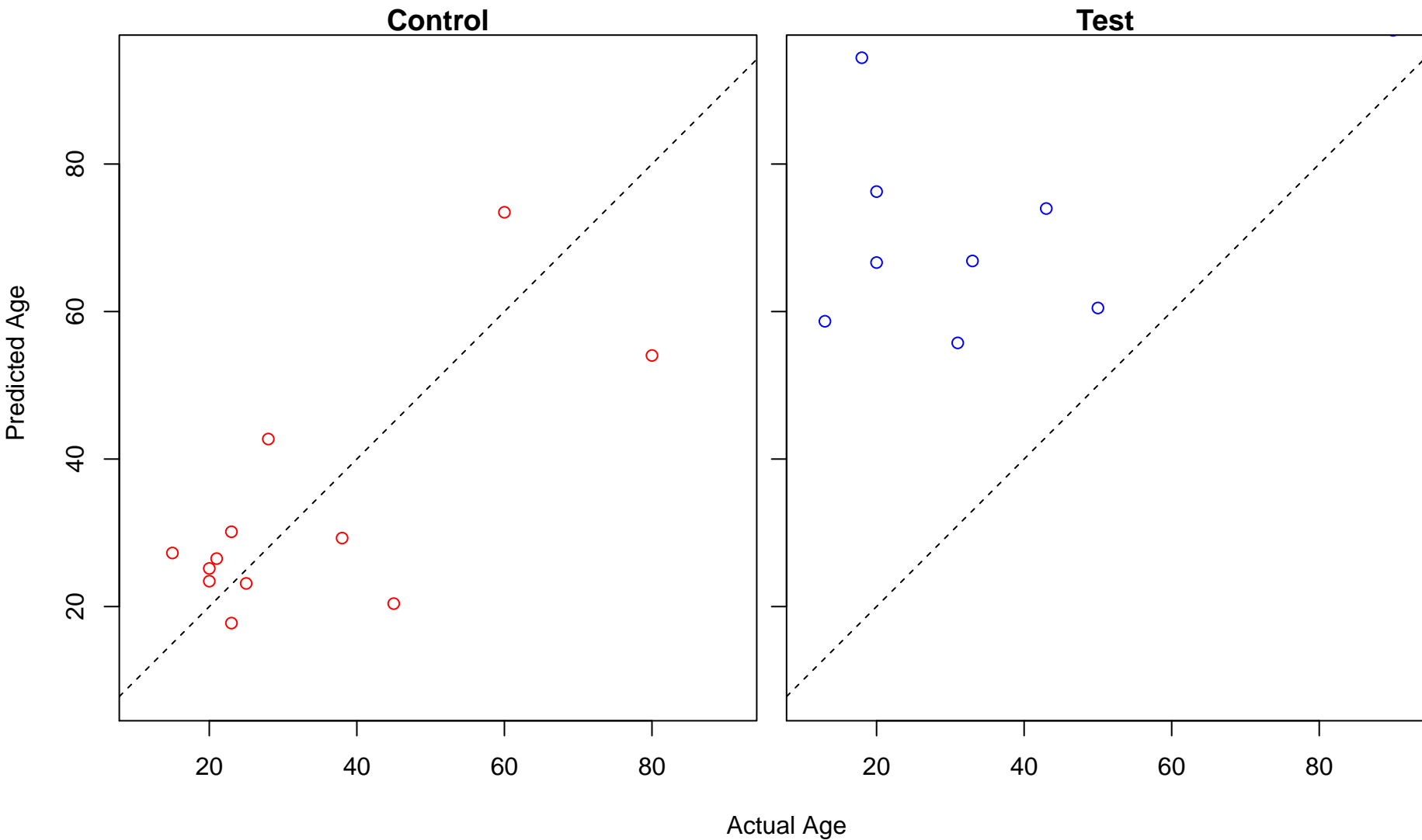
regulation of intrinsic apoptotic signaling pathway (Score: 7.140413)



kinetochore organization (Score: 7.138638)

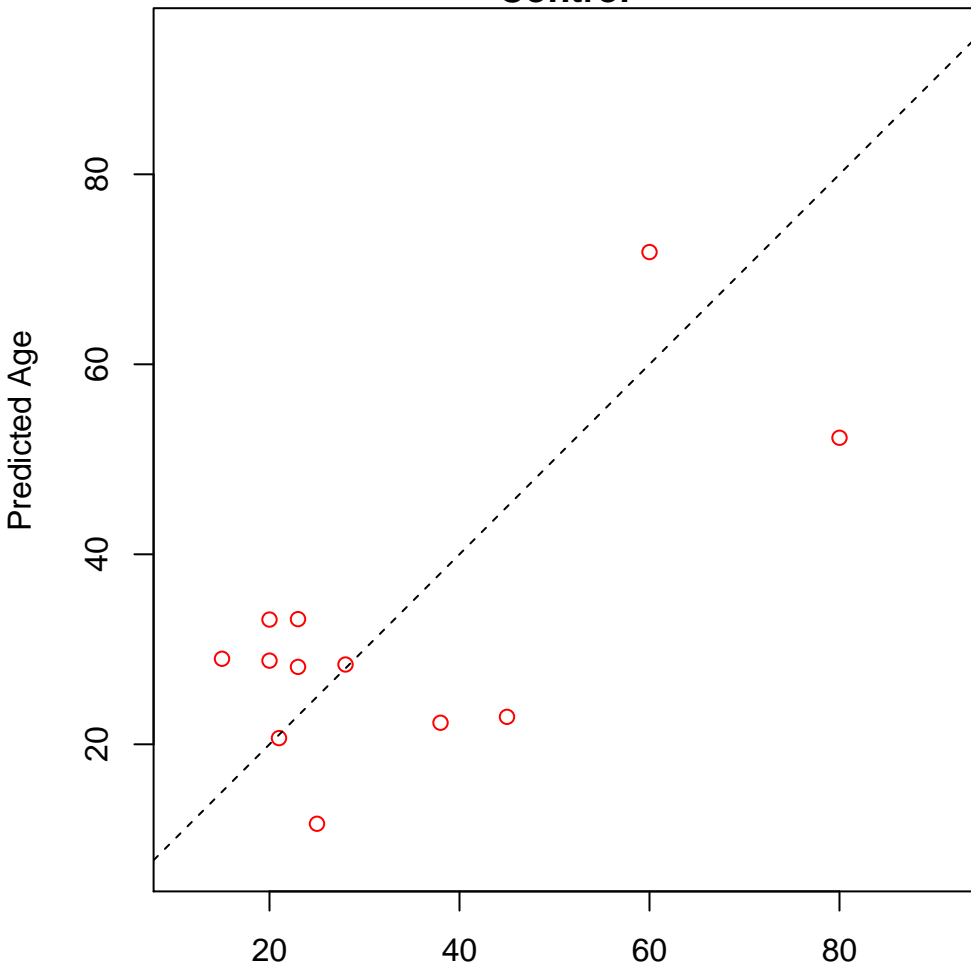


lateral mesoderm development (Score: 7.137723)

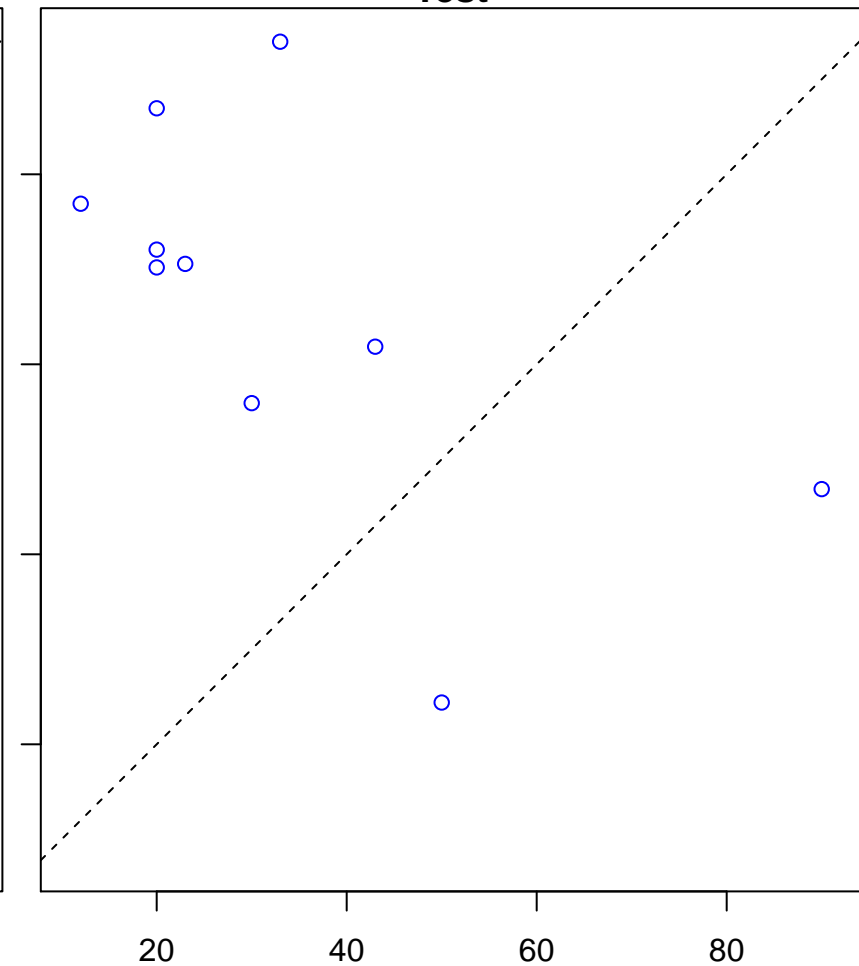


hematopoietic stem cell differentiation (Score: 7.132114)

Control

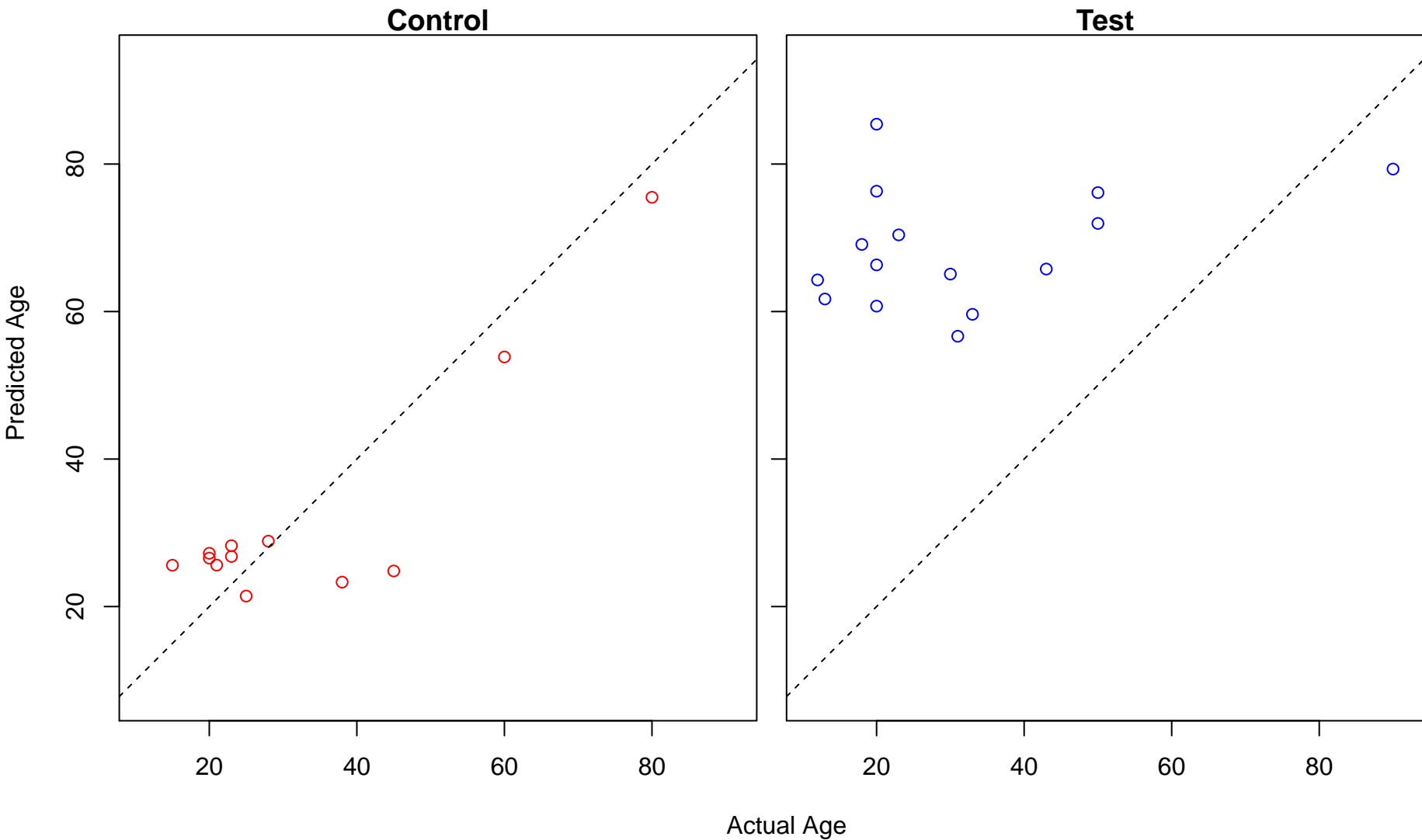


Test

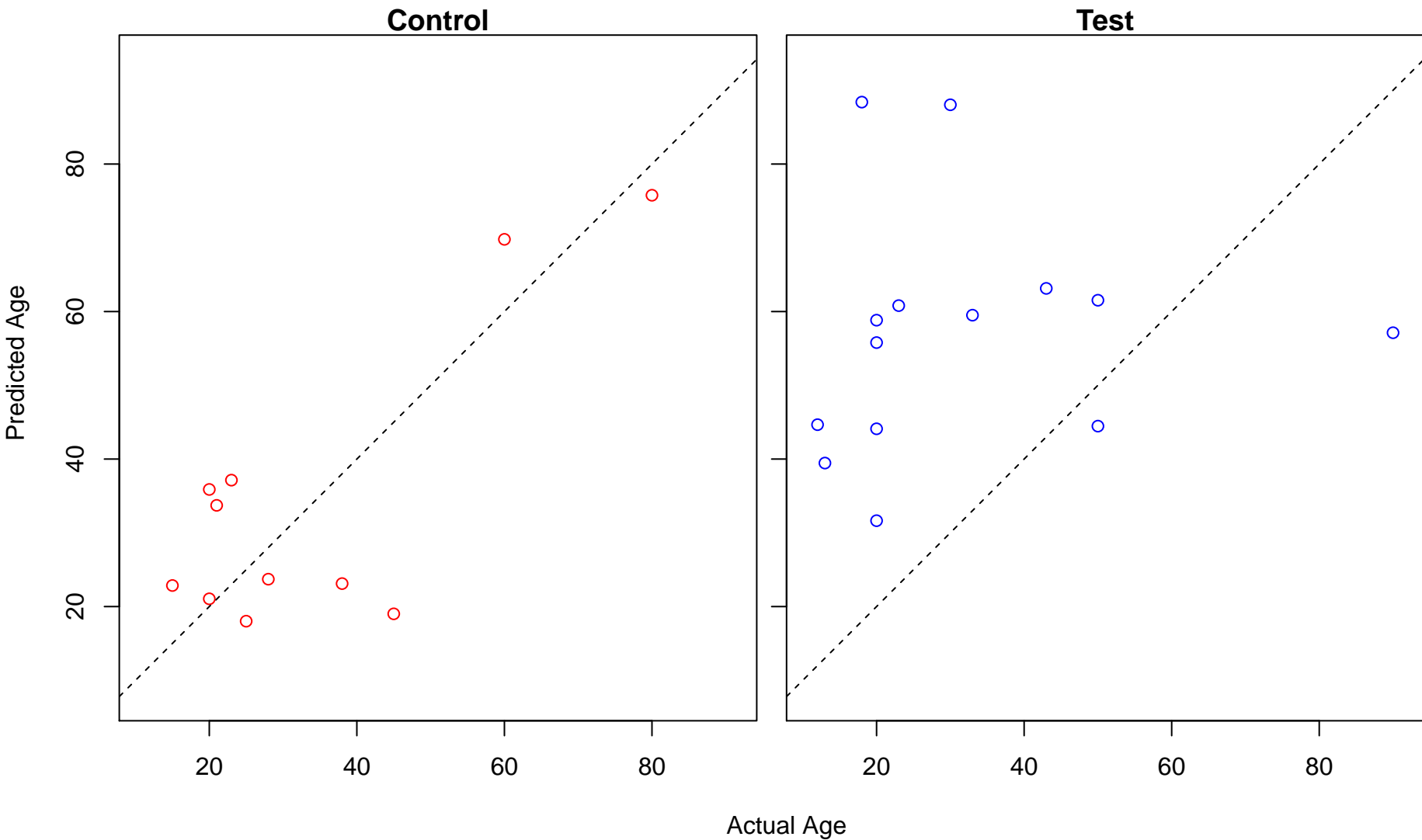


Actual Age

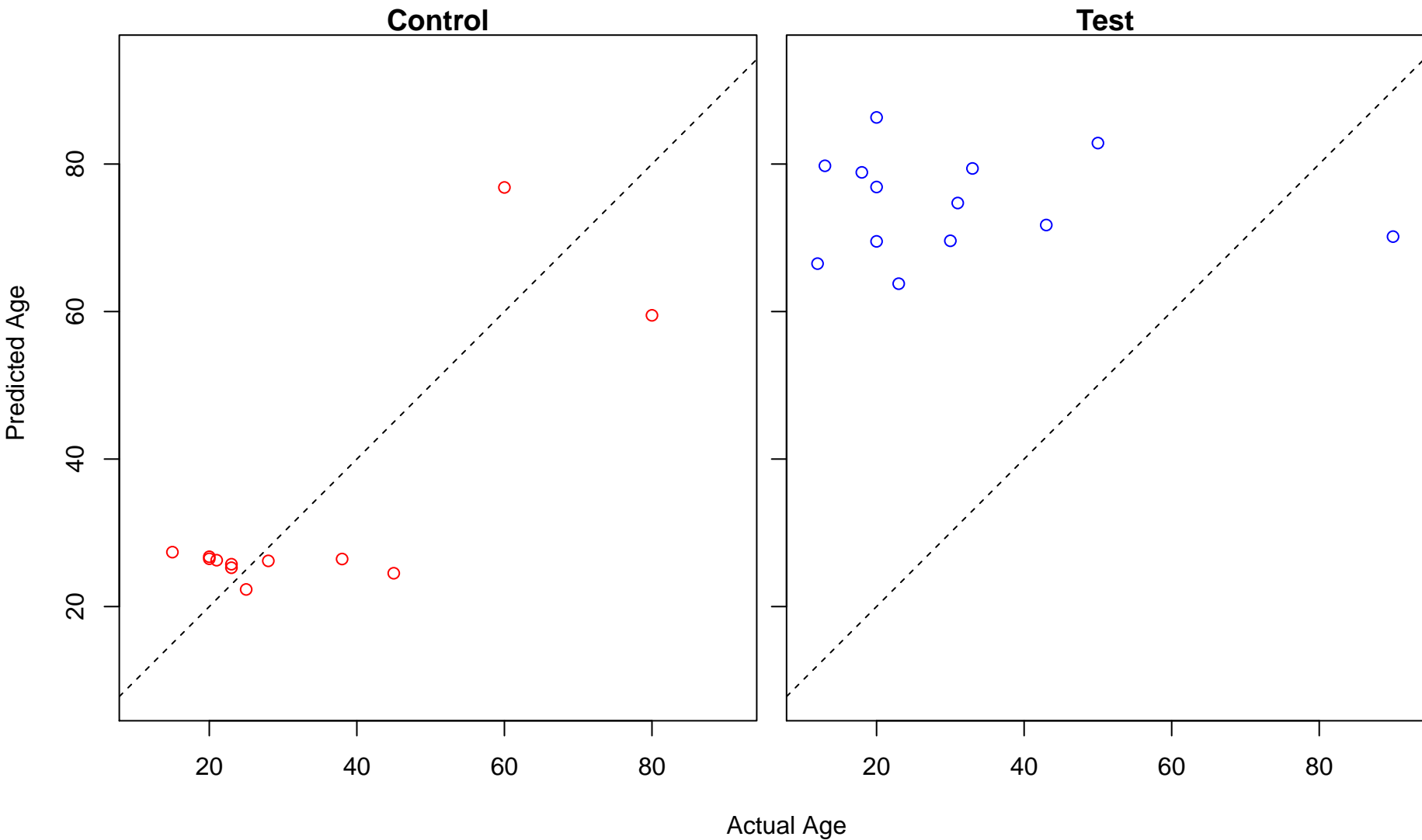
protein geranylgeranylation (Score: 7.132010)



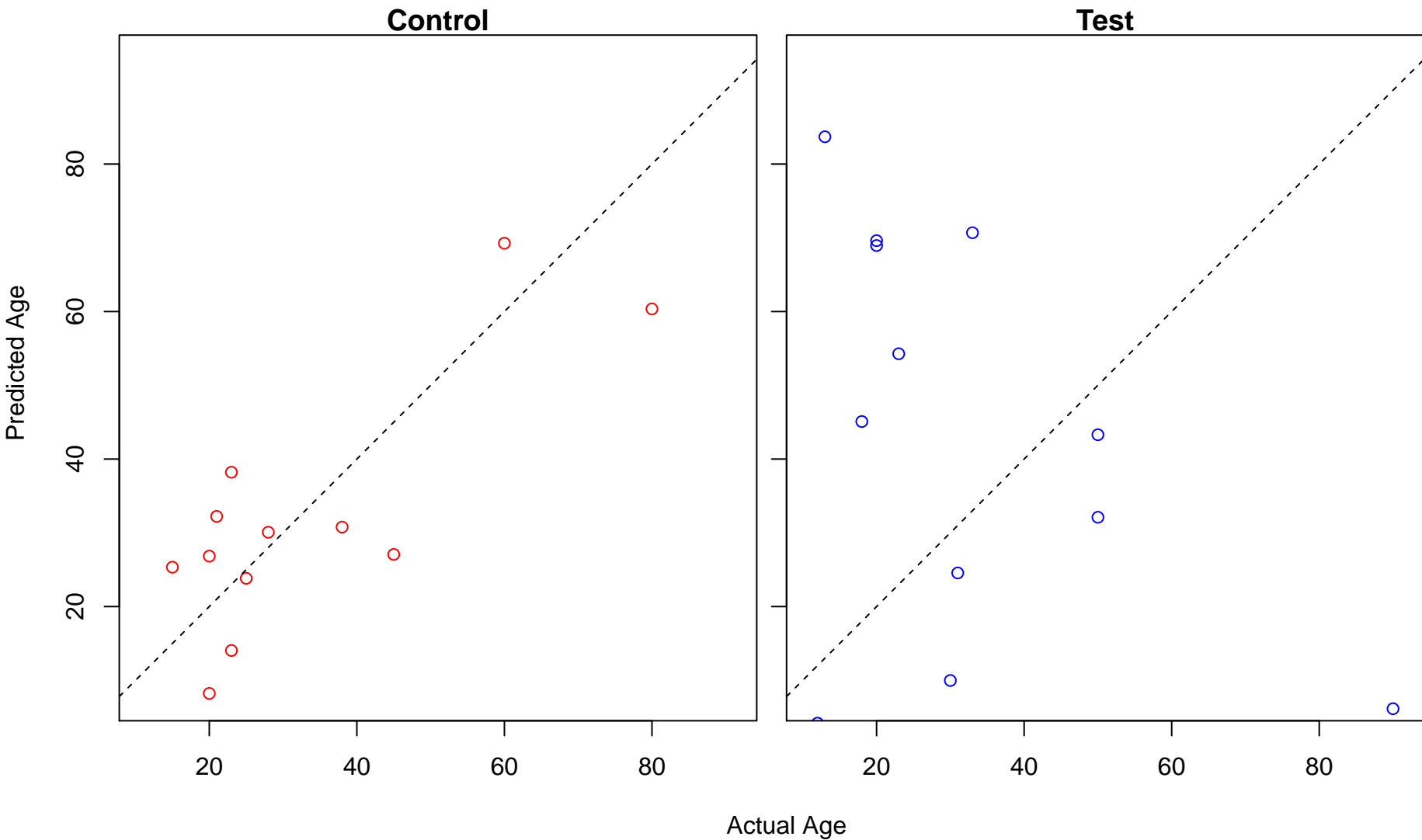
B cell activation (Score: 7.130550)



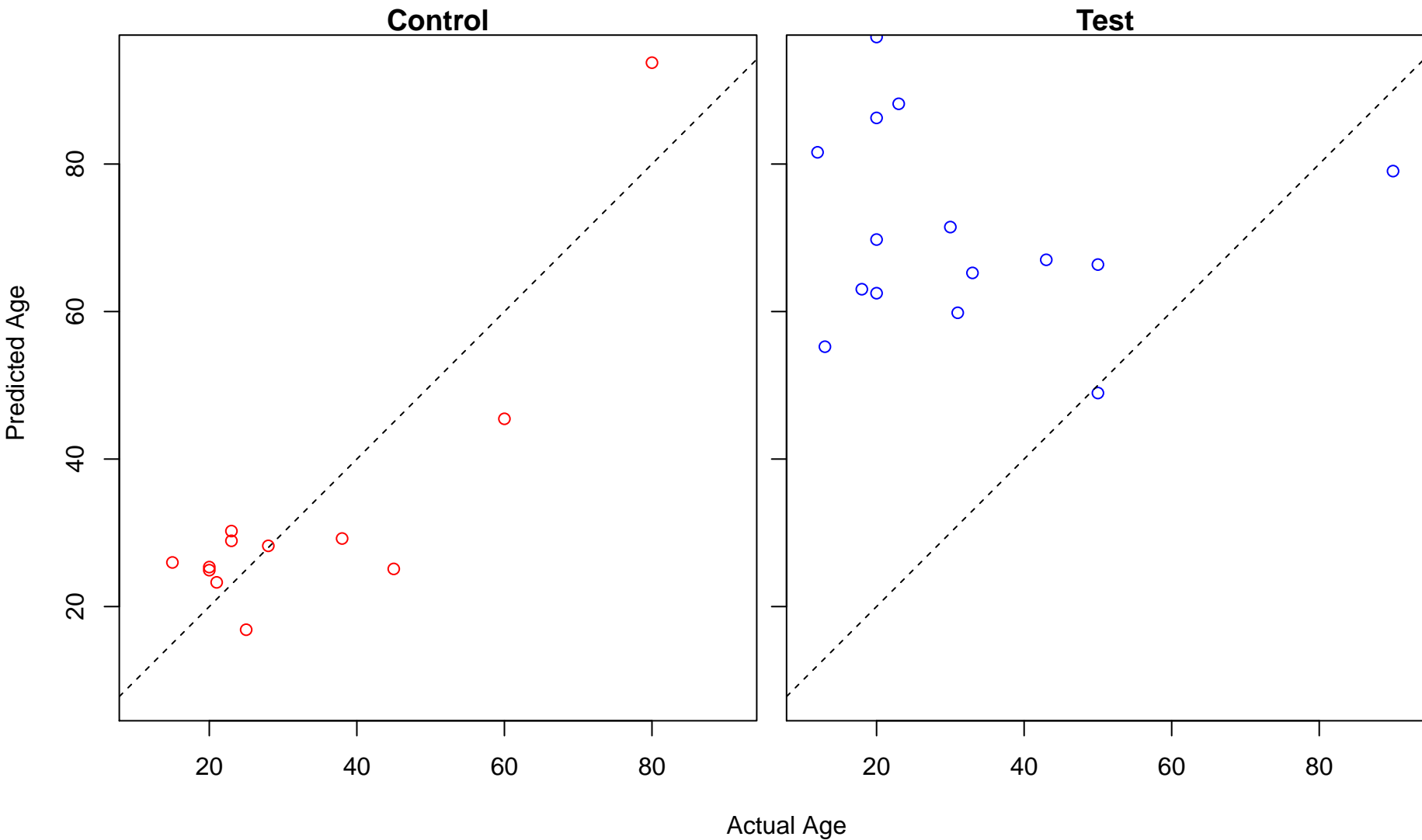
negative regulation of extrinsic apoptotic signaling pathway (Score: 7.129986)



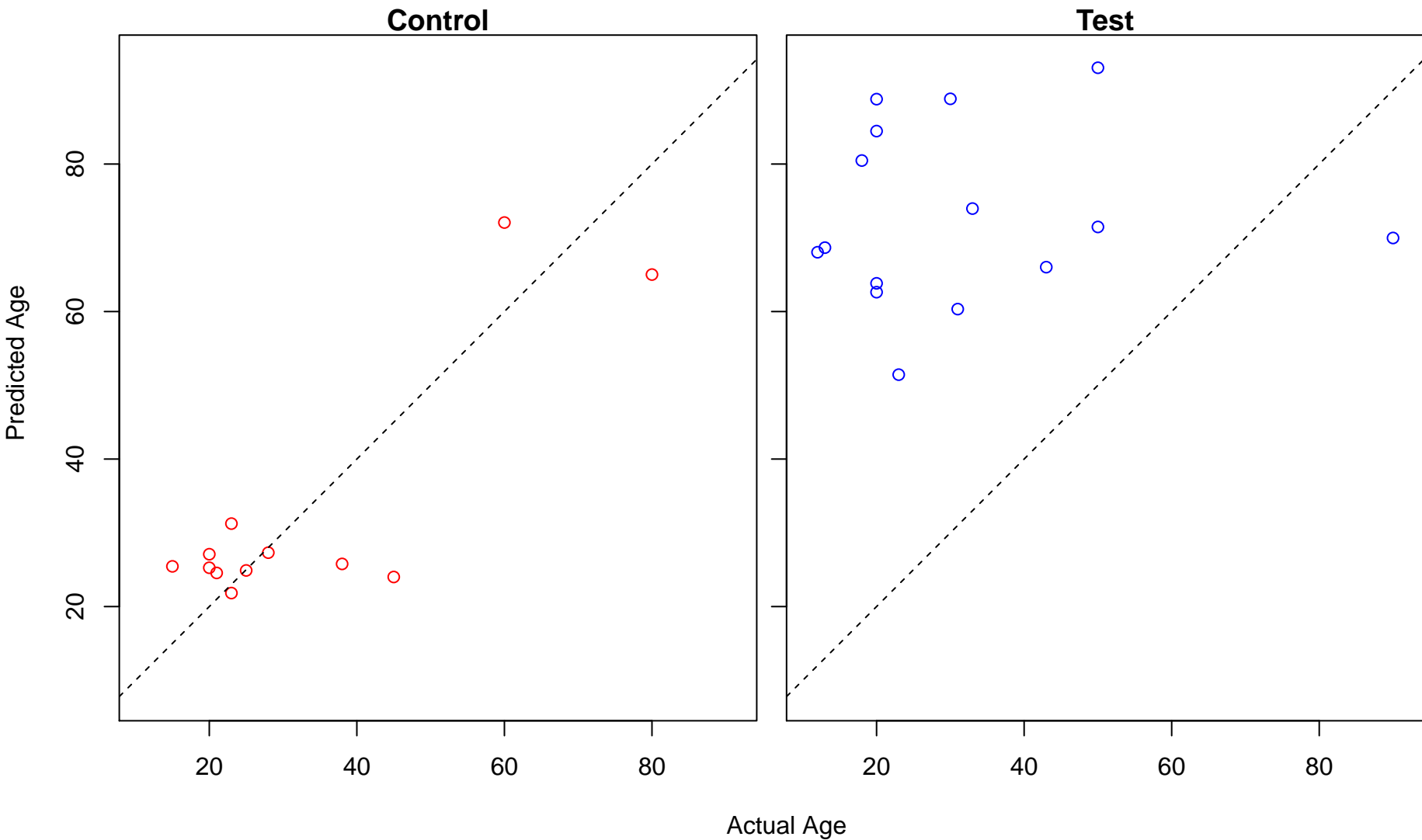
positive regulation of calcium ion transmembrane transporter activity (Score: 7.128373)



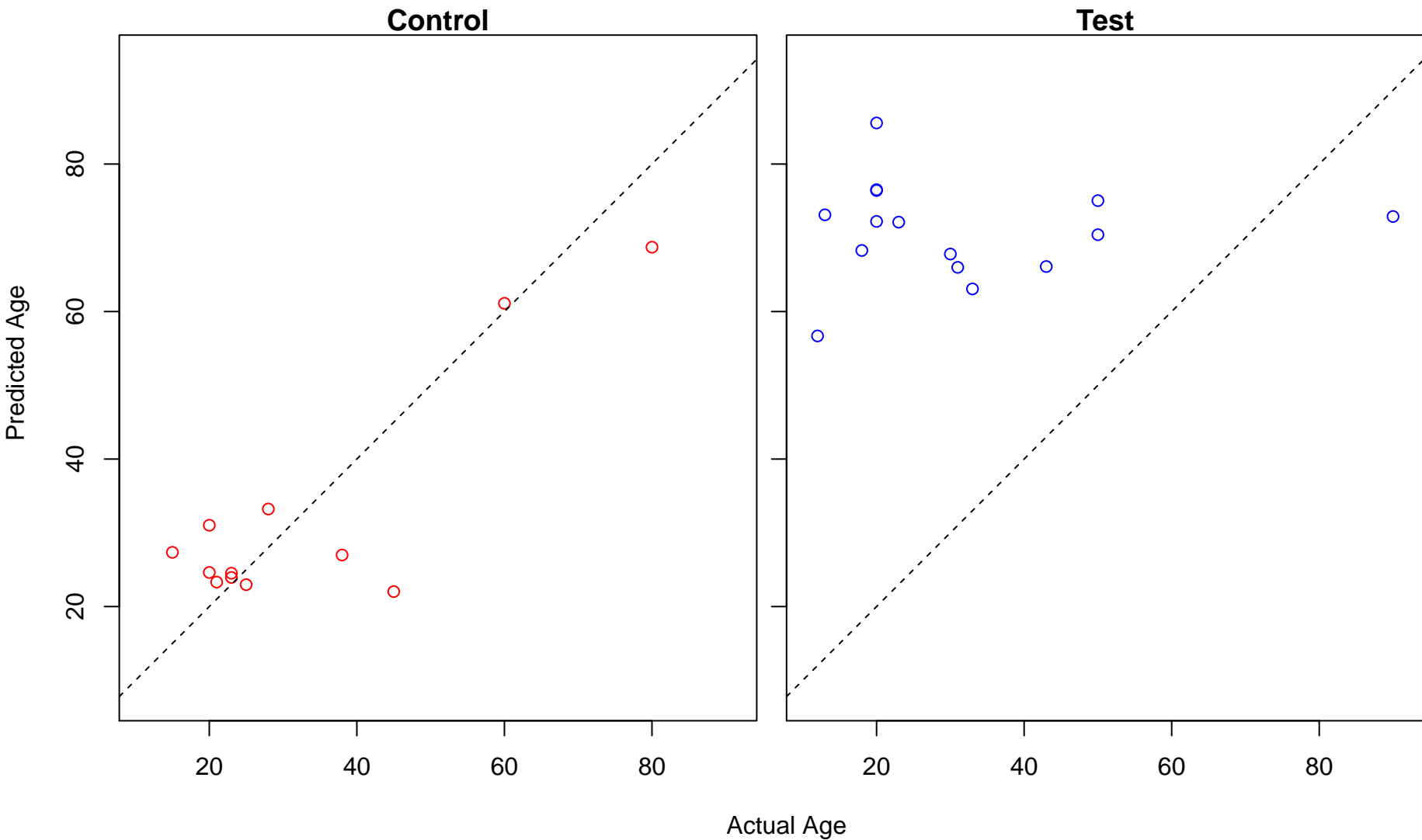
G2 DNA damage checkpoint (Score: 7.128150)



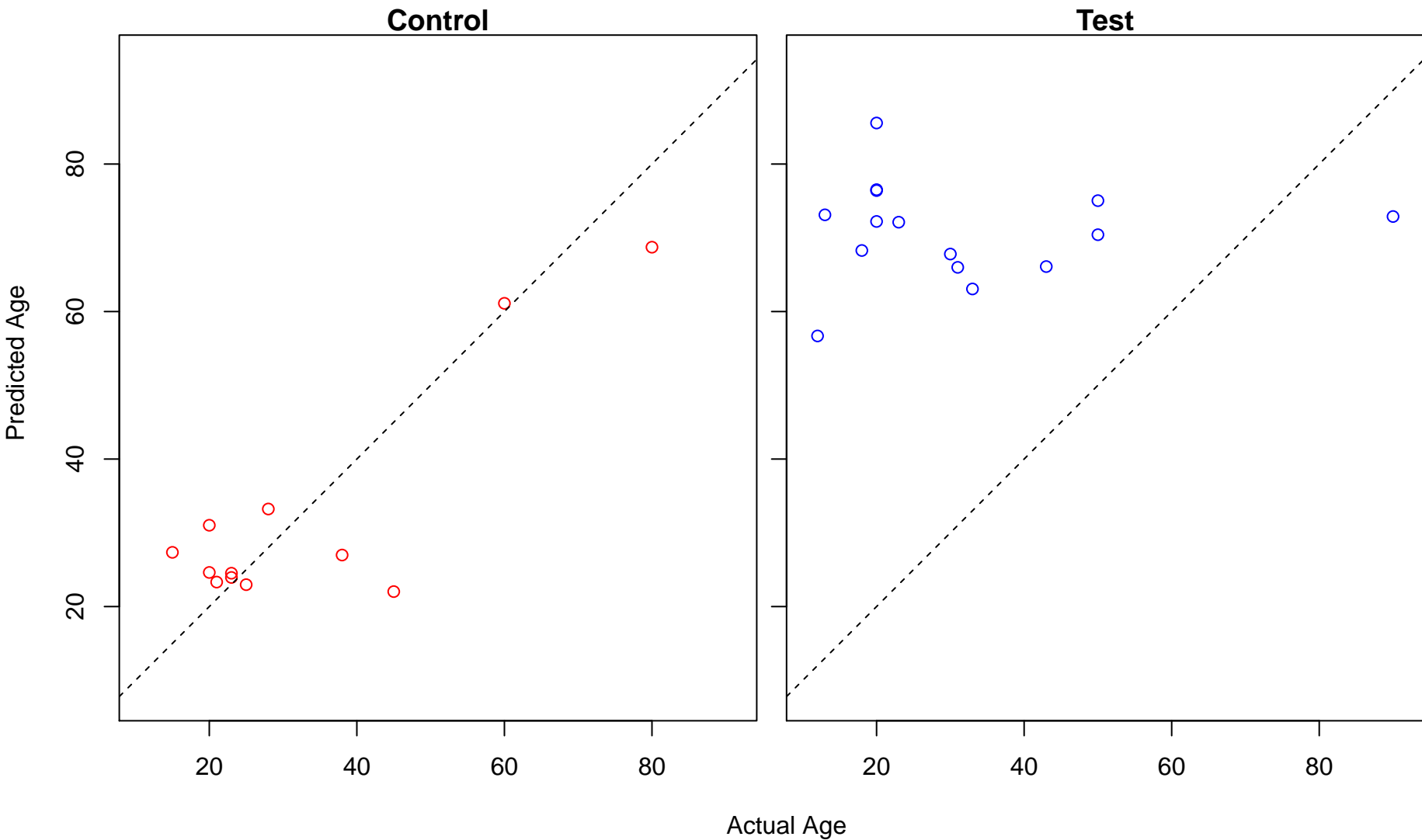
negative regulation of cytokine biosynthetic process (Score: 7.123499)



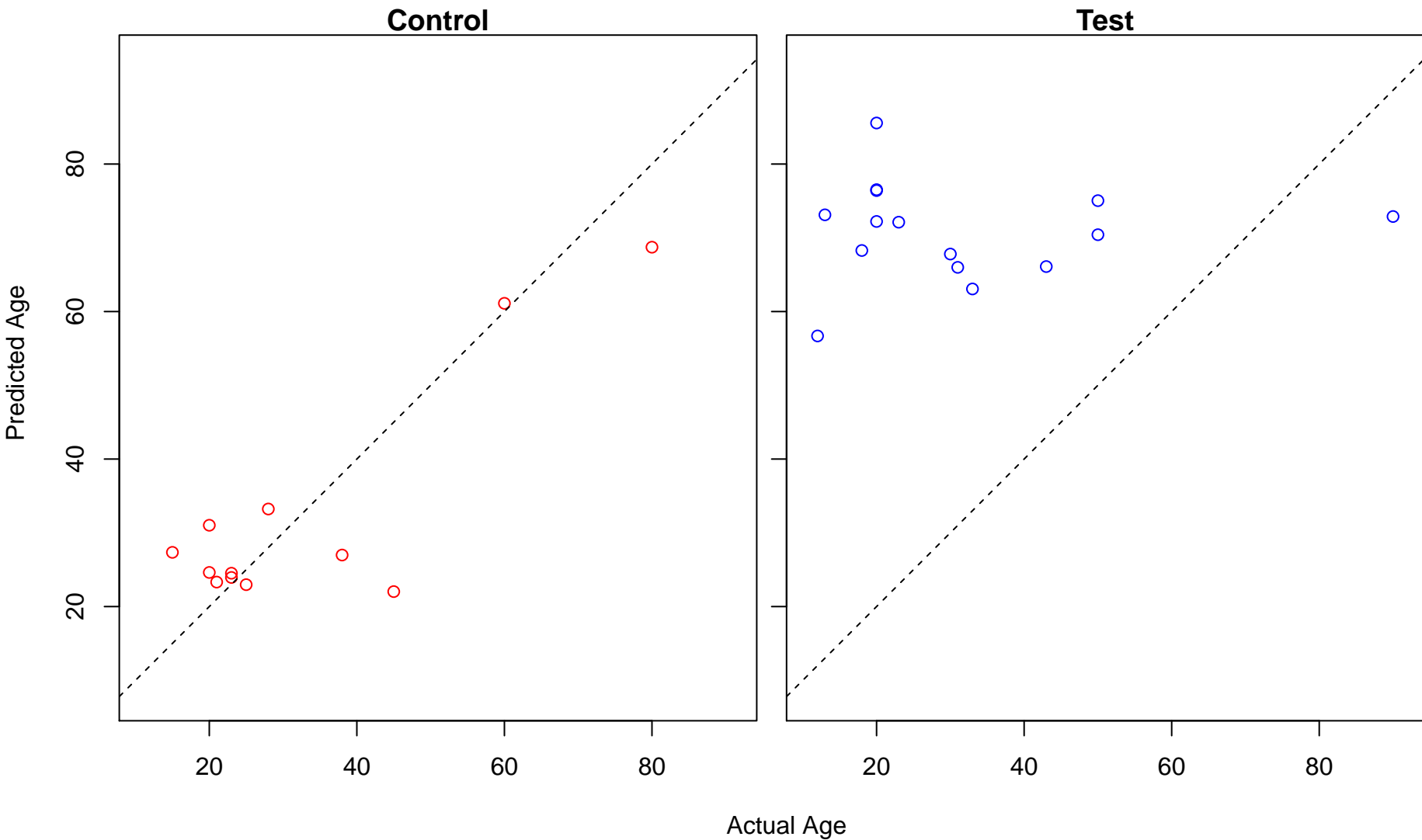
hemostasis (Score: 7.122649)



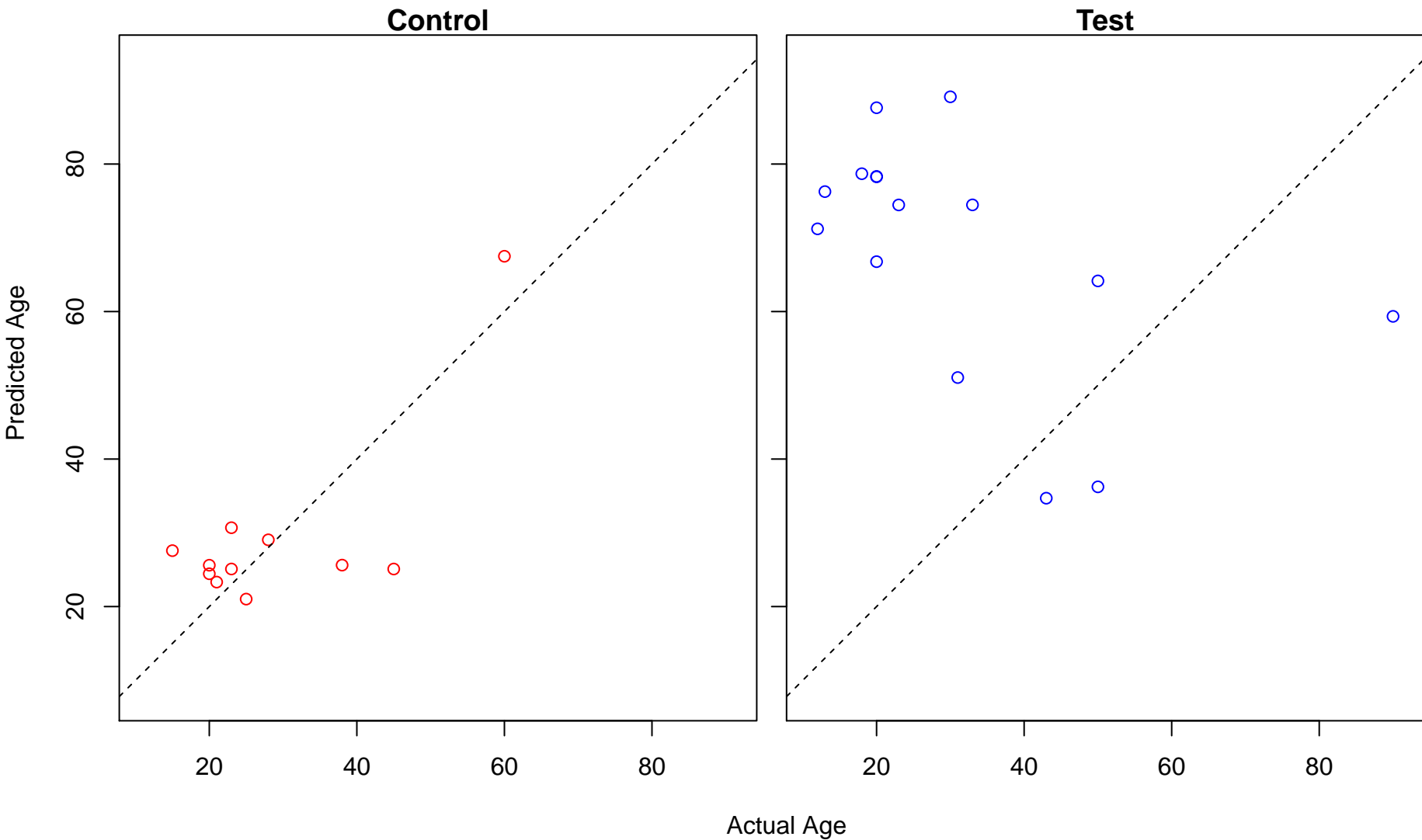
blood coagulation (Score: 7.122293)



coagulation (Score: 7.122293)

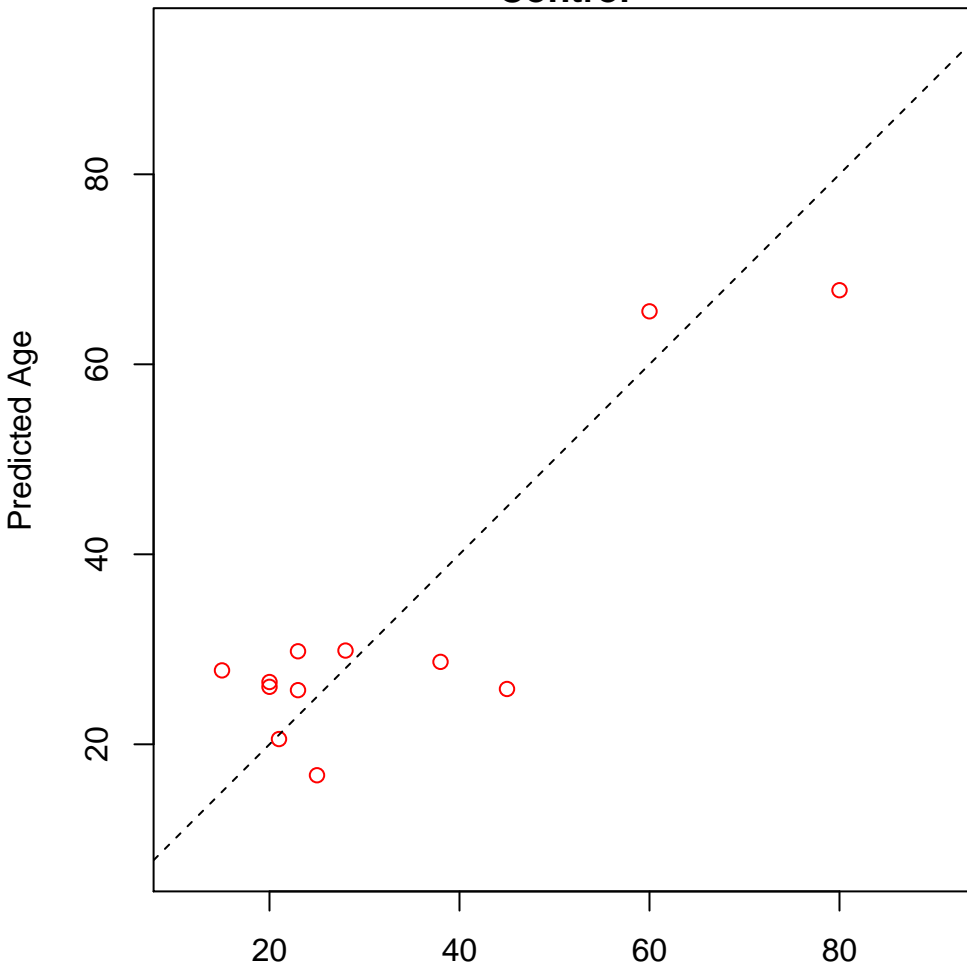


neutral amino acid transport (Score: 7.122264)

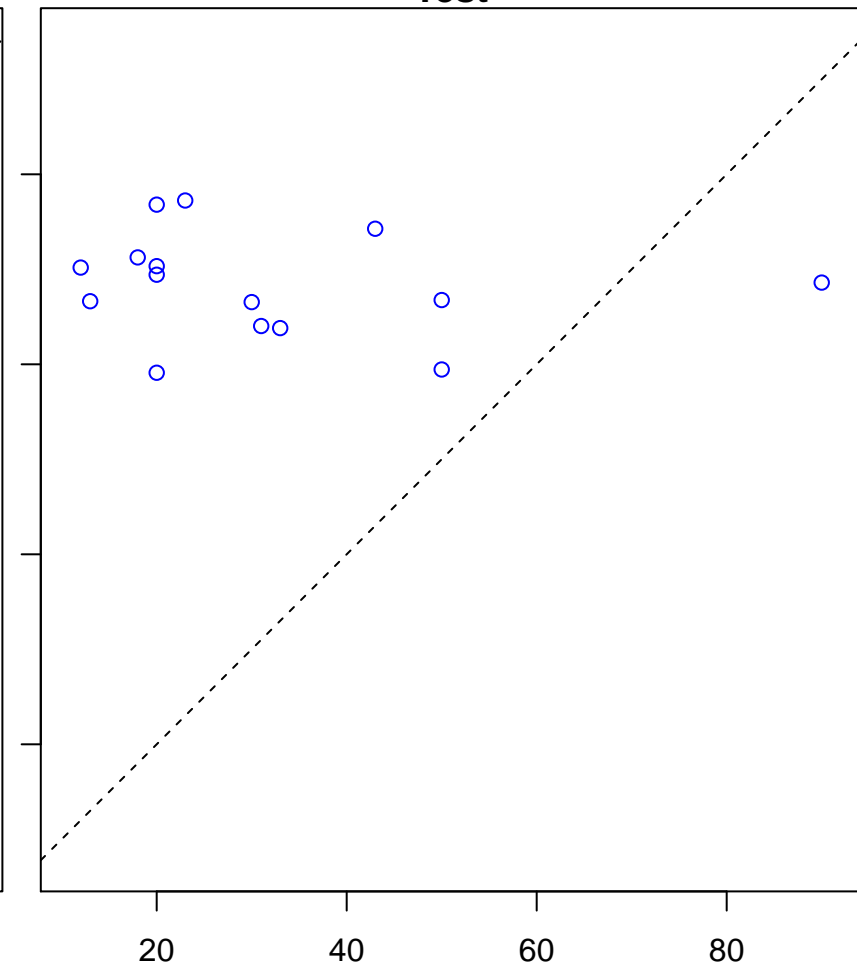


metanephric tubule development (Score: 7.115036)

Control



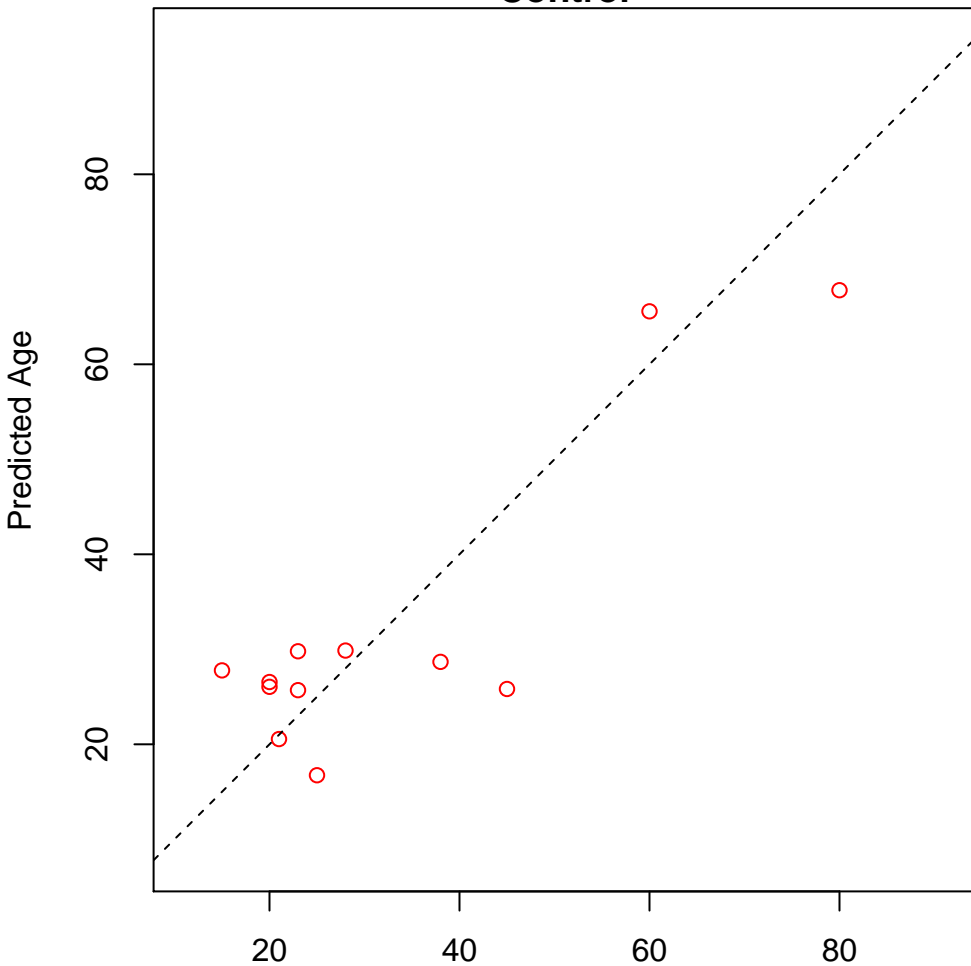
Test



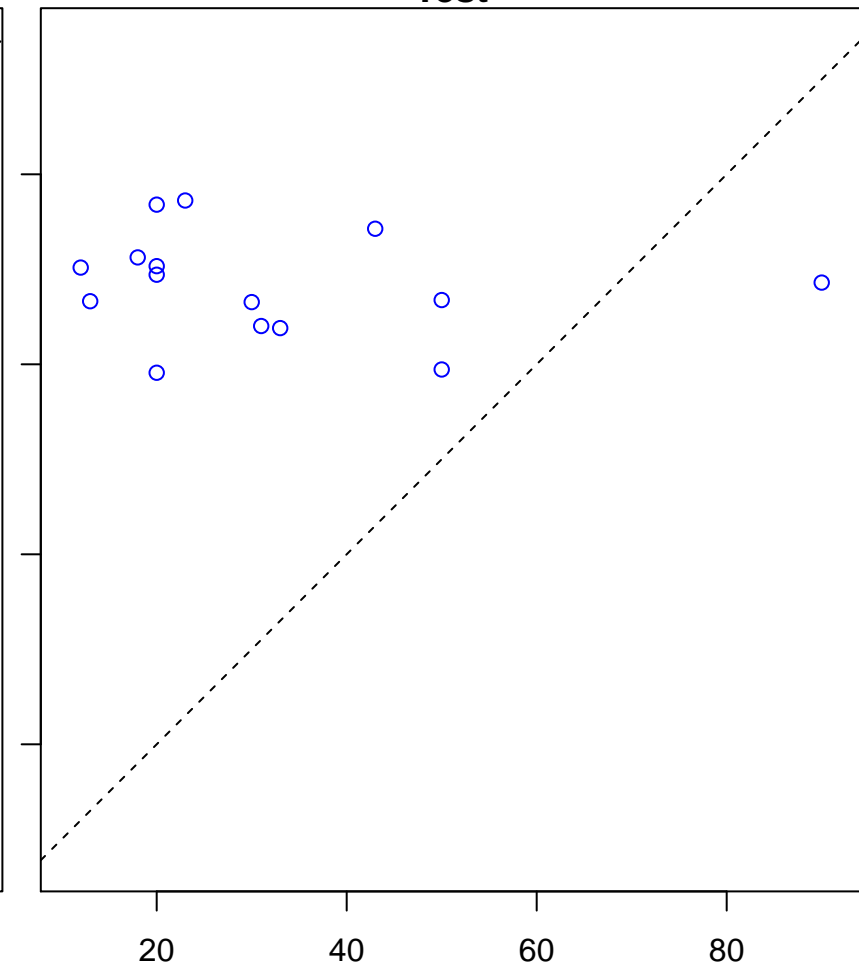
Actual Age

metanephric nephron tubule development (Score: 7.115036)

Control

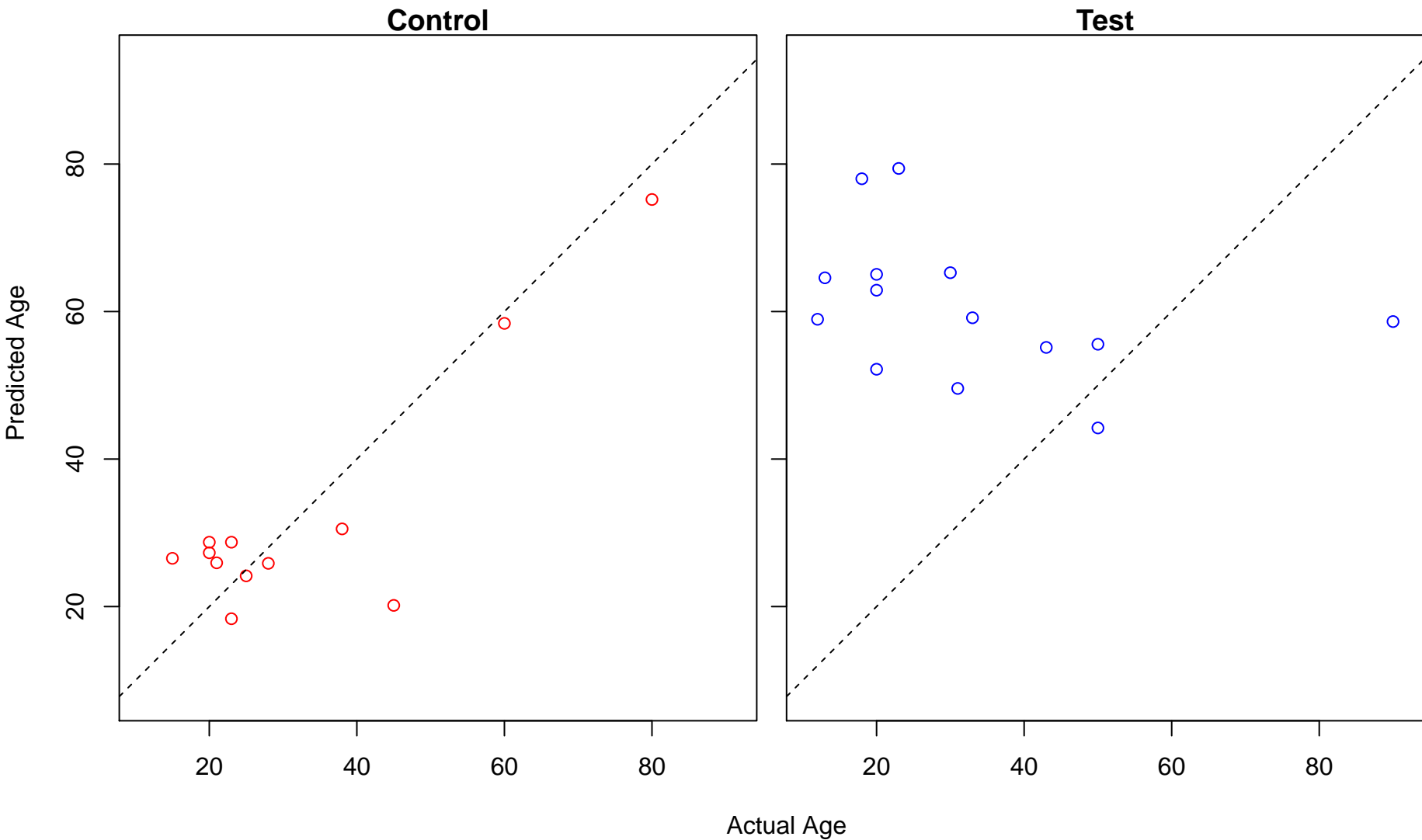


Test

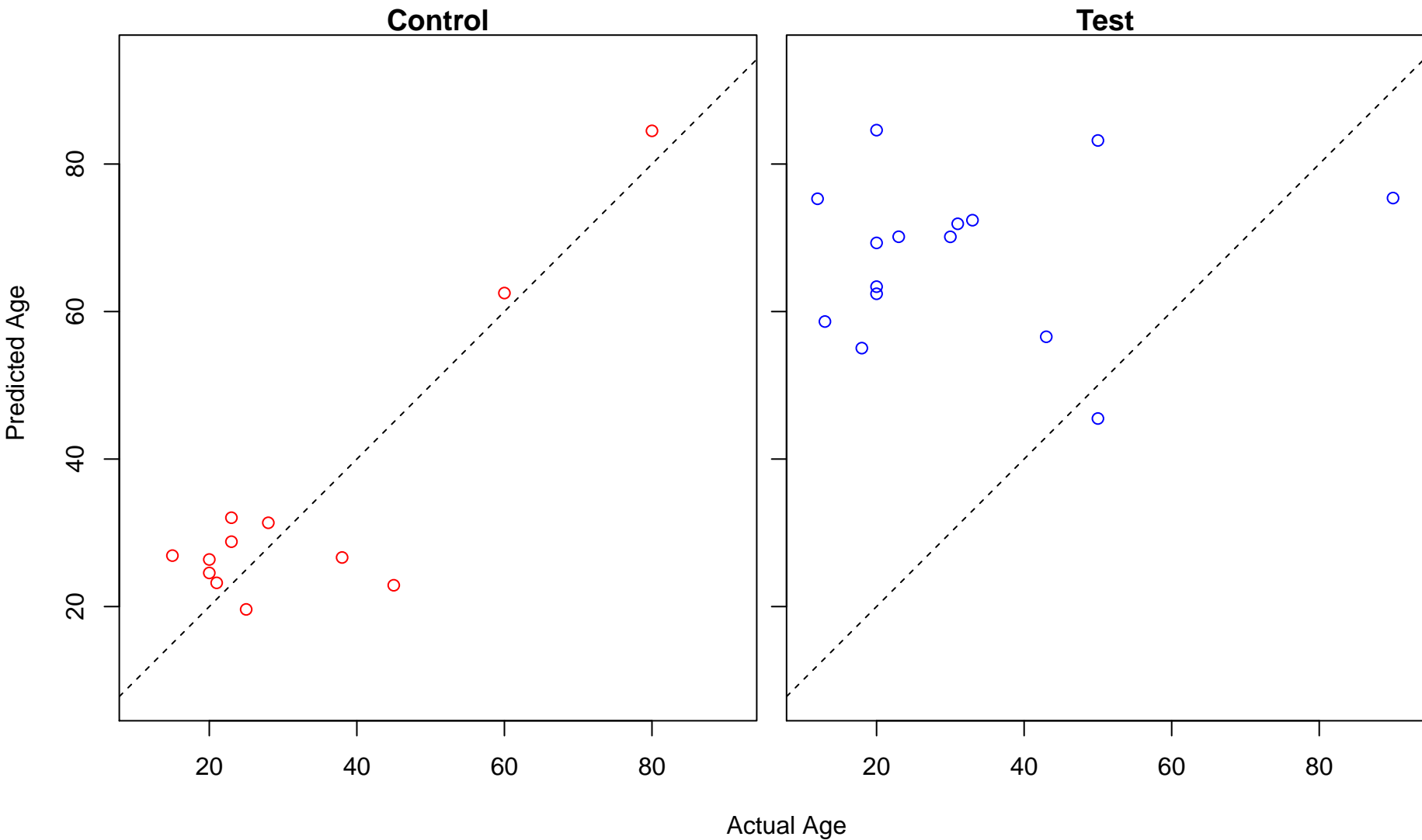


Actual Age

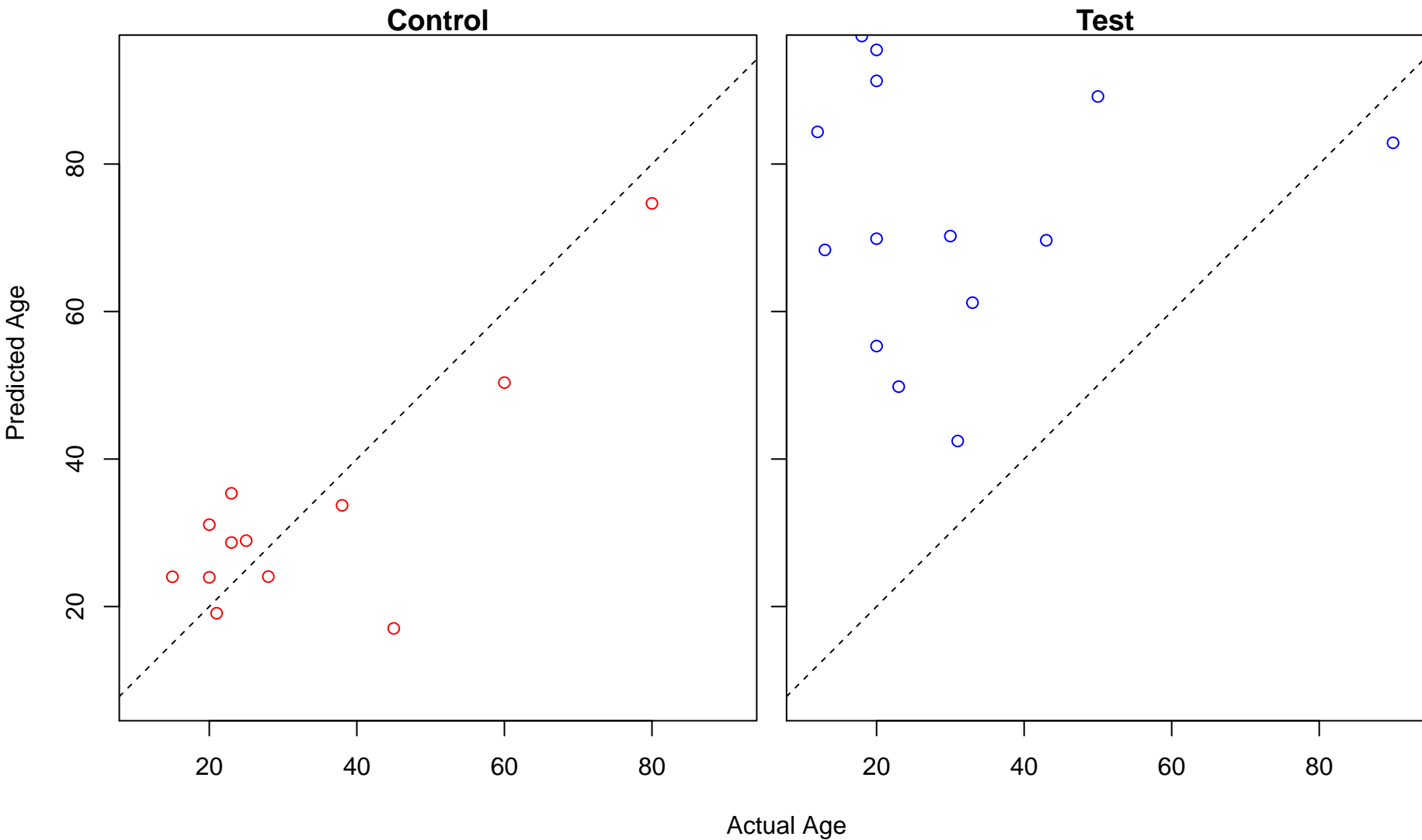
negative regulation of metanephros development (Score: 7.114511)



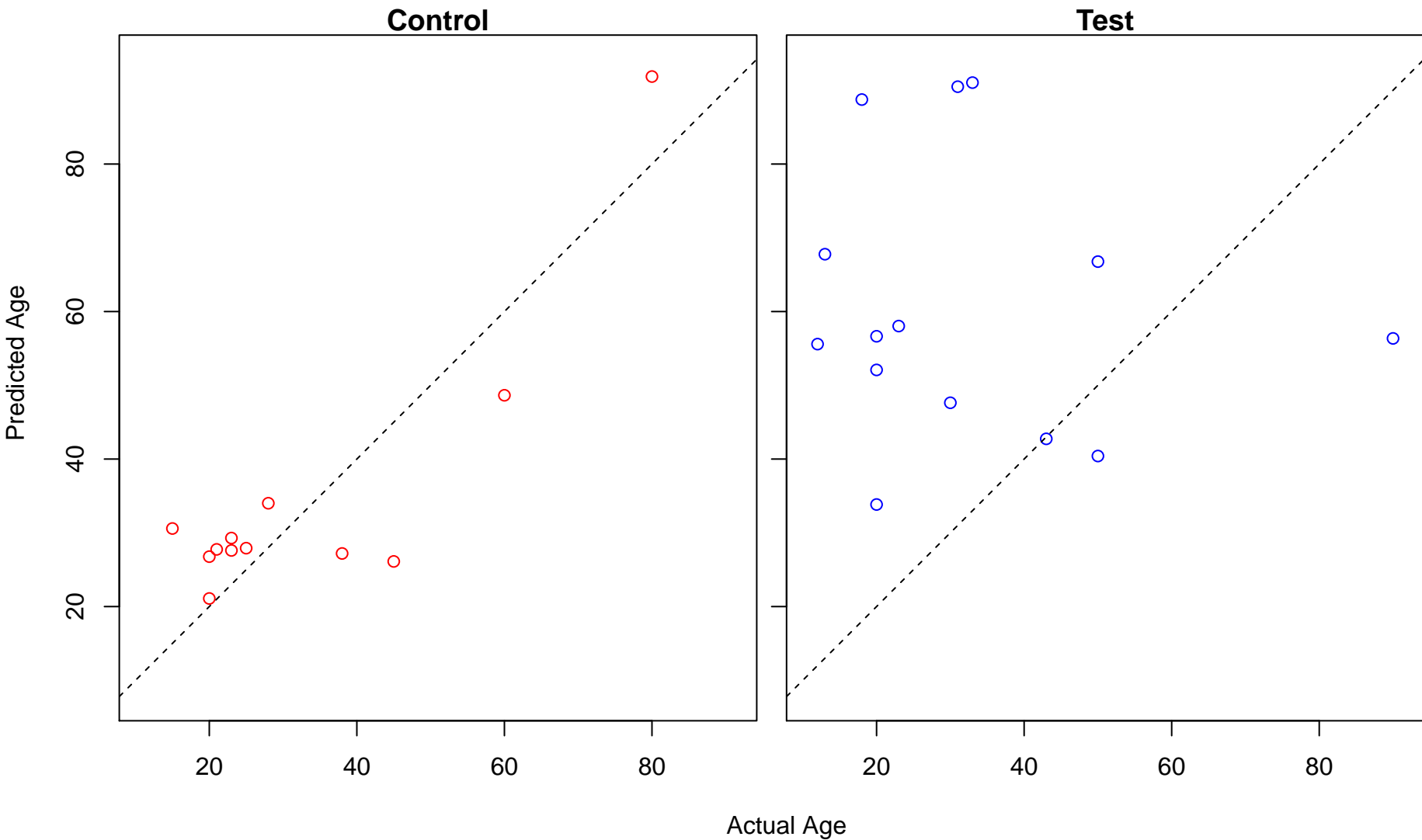
regulation of isotype switching (Score: 7.112973)



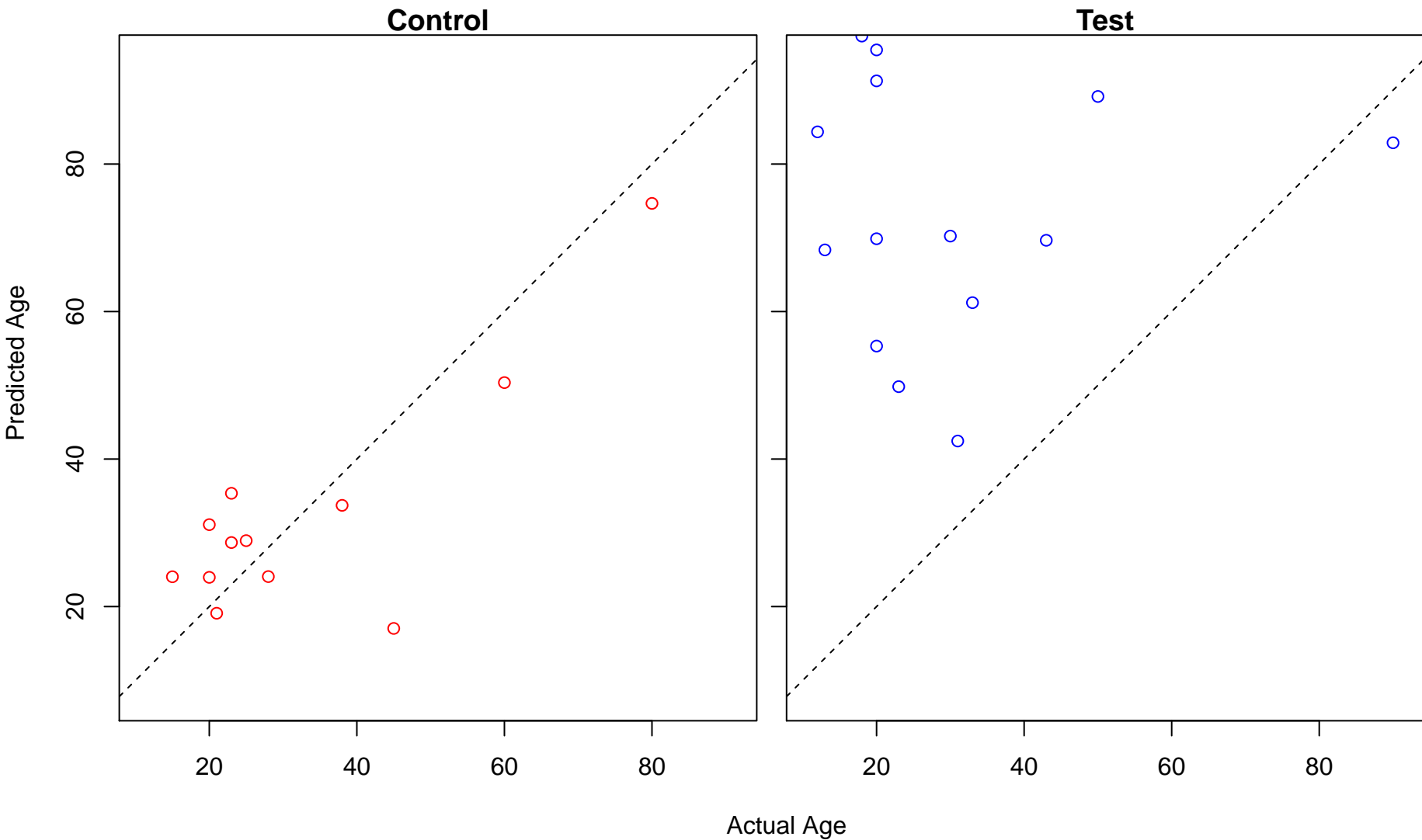
salivary gland morphogenesis (Score: 7.112228)



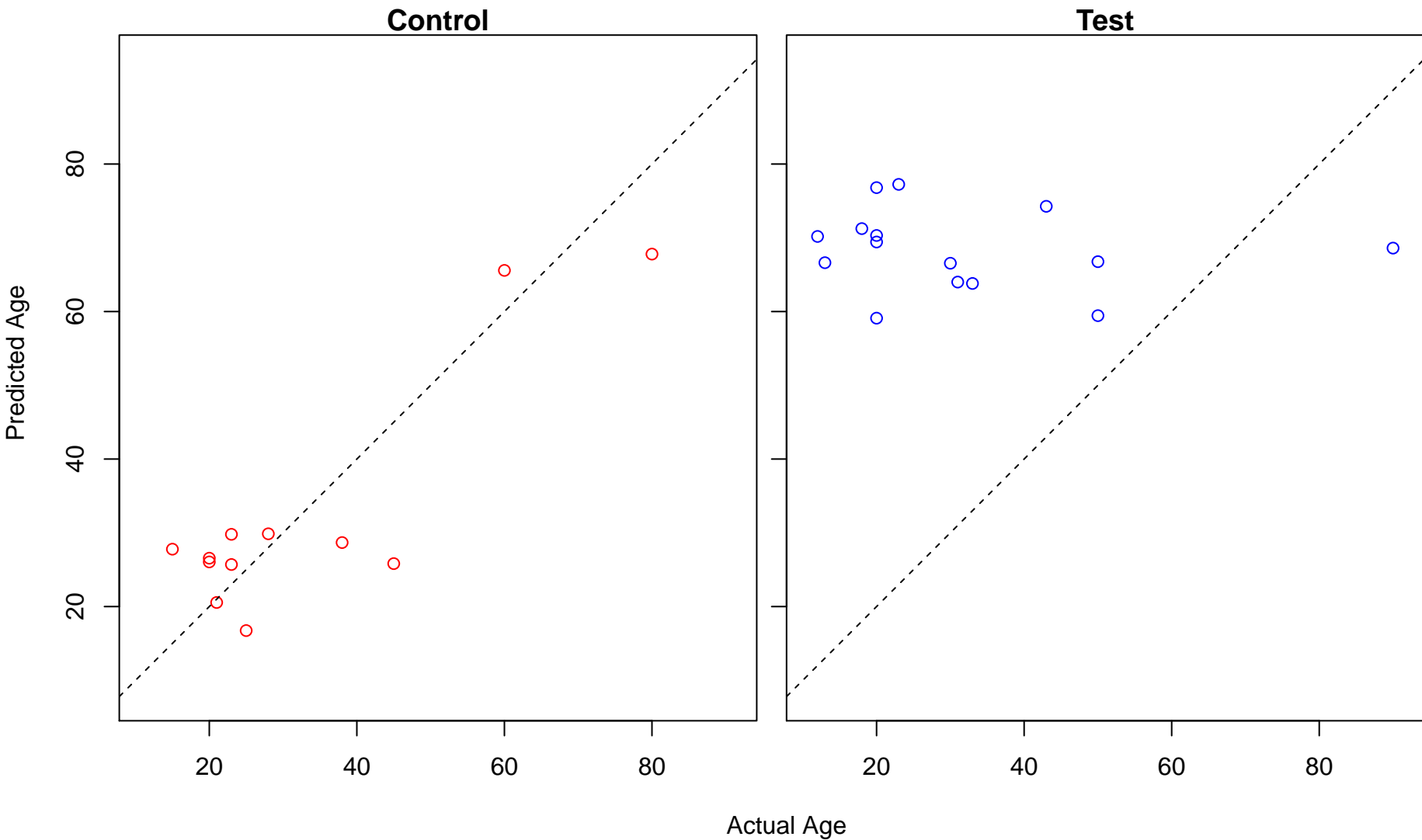
regulation of neurogenesis (Score: 7.112209)



salivary gland development (Score: 7.112090)

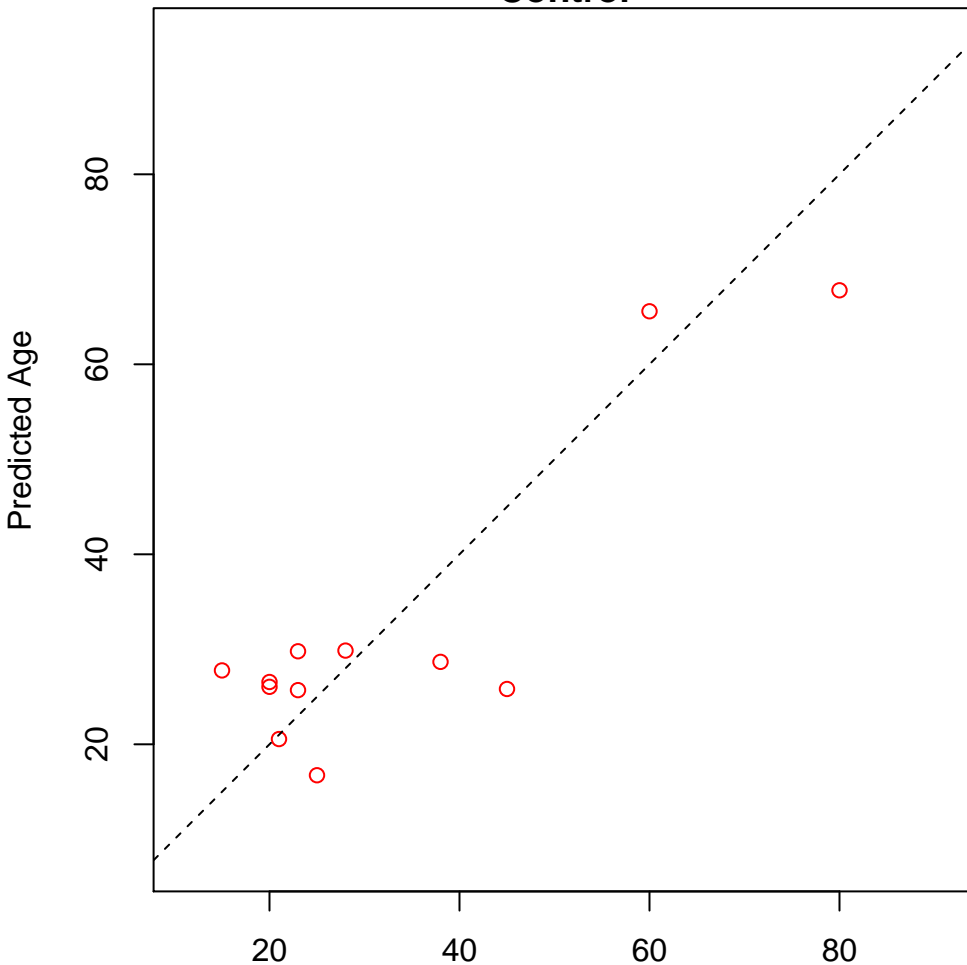


metanephric nephron epithelium development (Score: 7.111479)

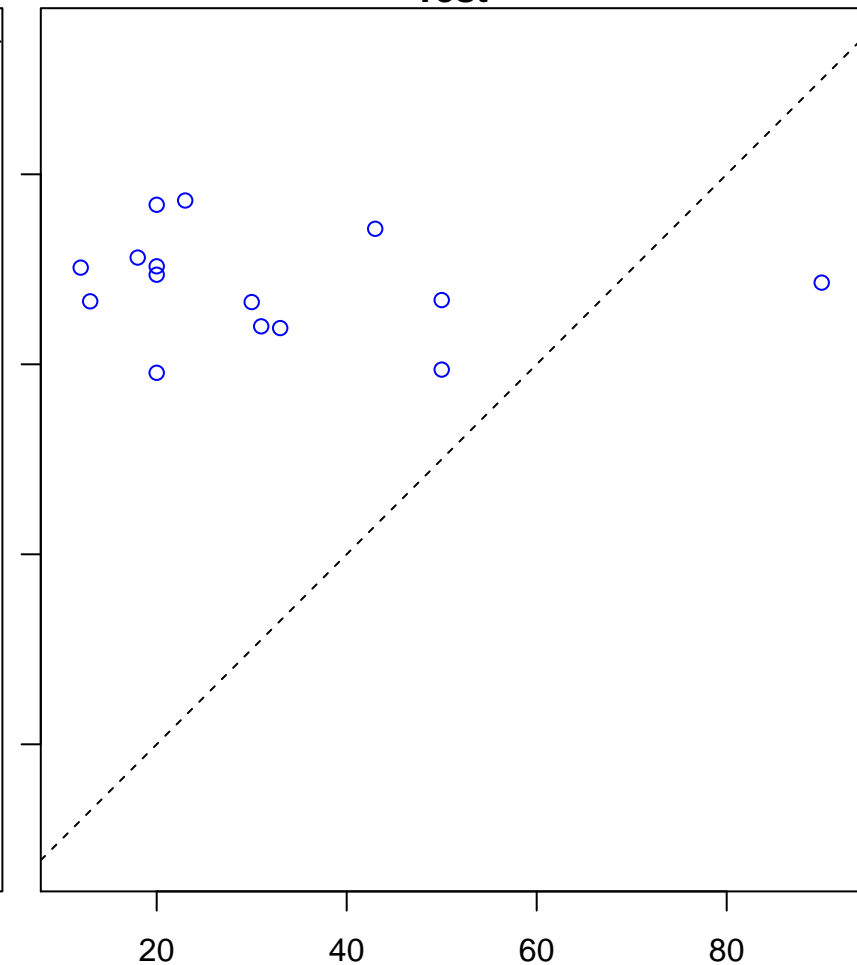


metanephric epithelium development (Score: 7.110936)

Control

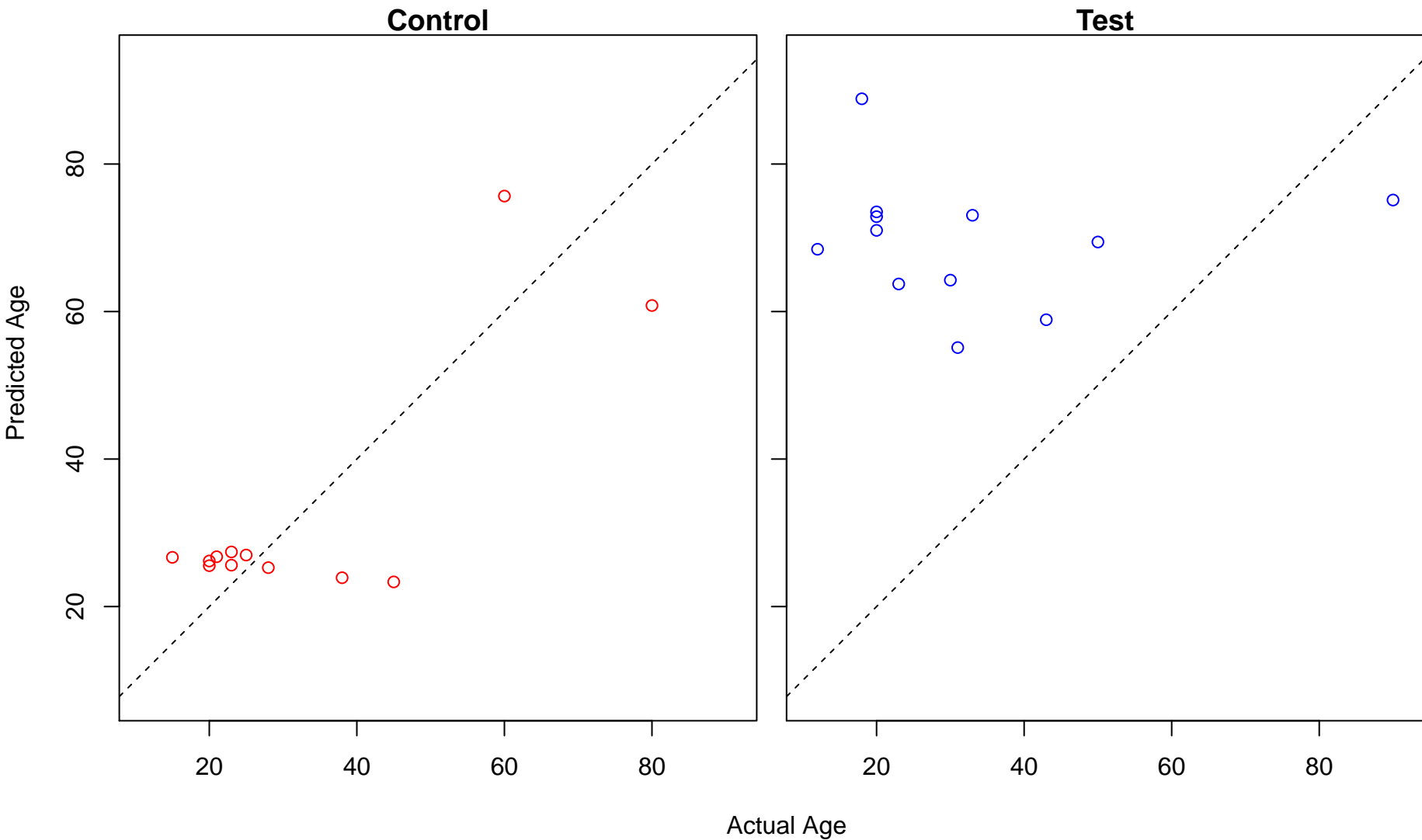


Test

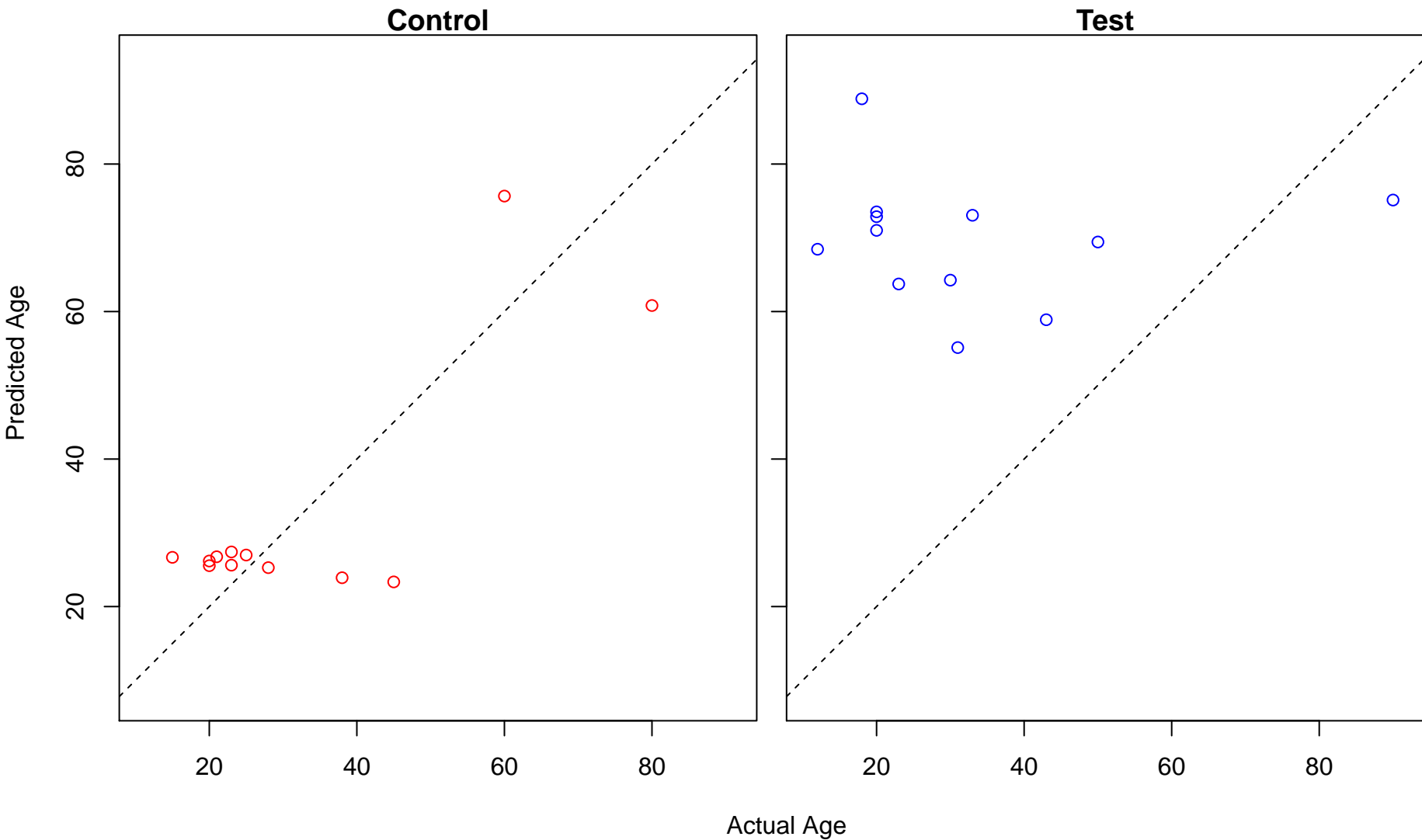


Actual Age

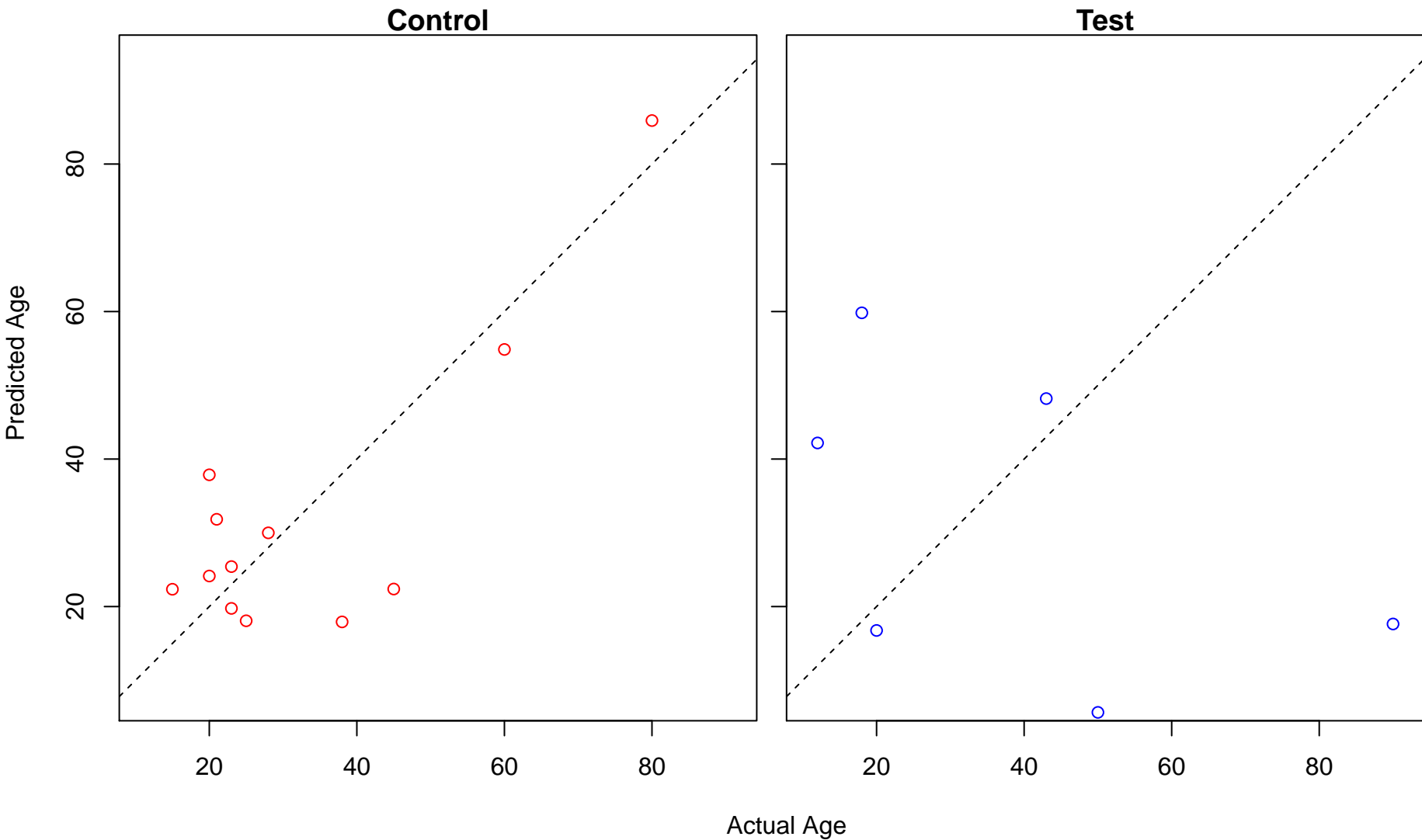
viral process (Score: 7.109519)



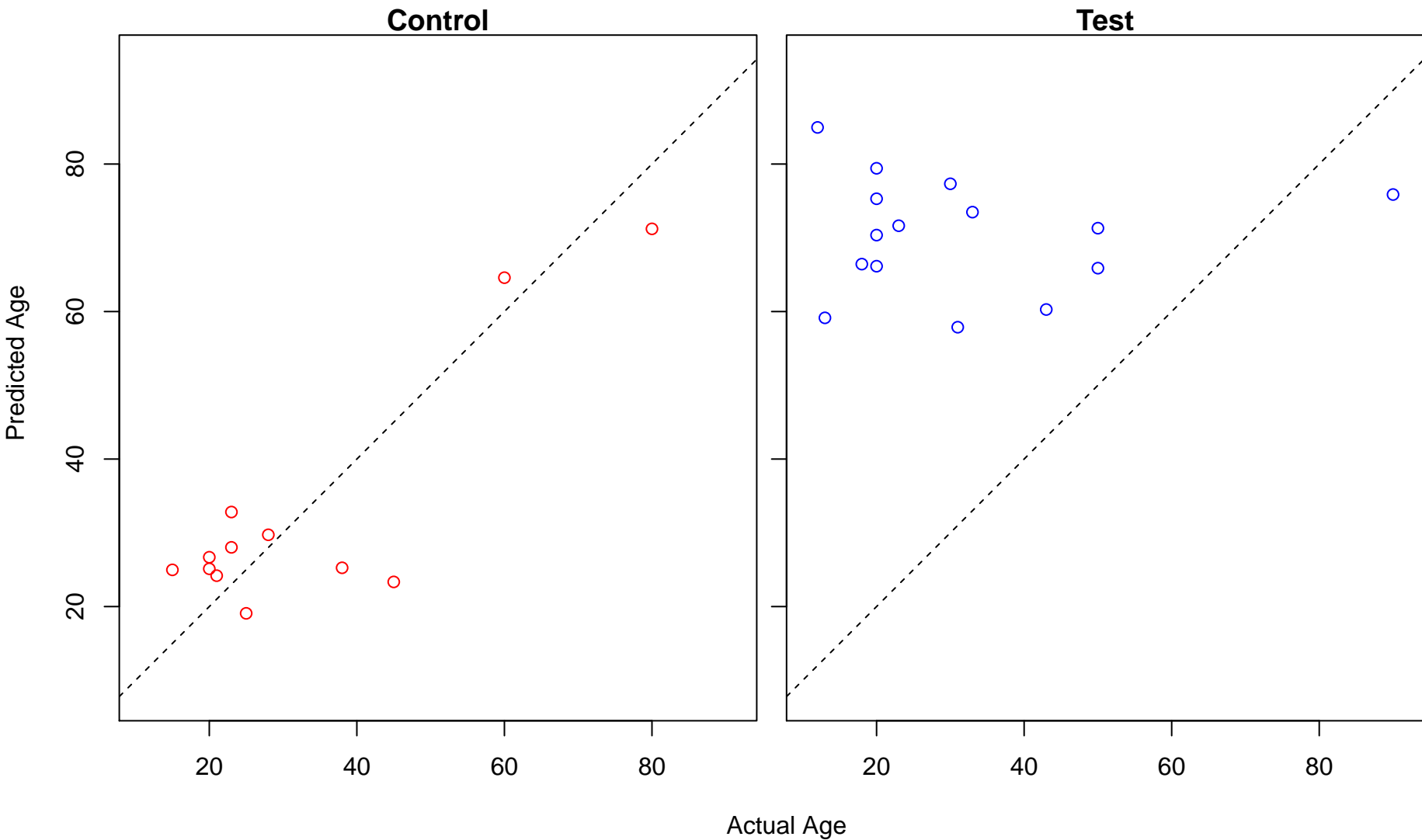
multi-organism cellular process (Score: 7.109491)



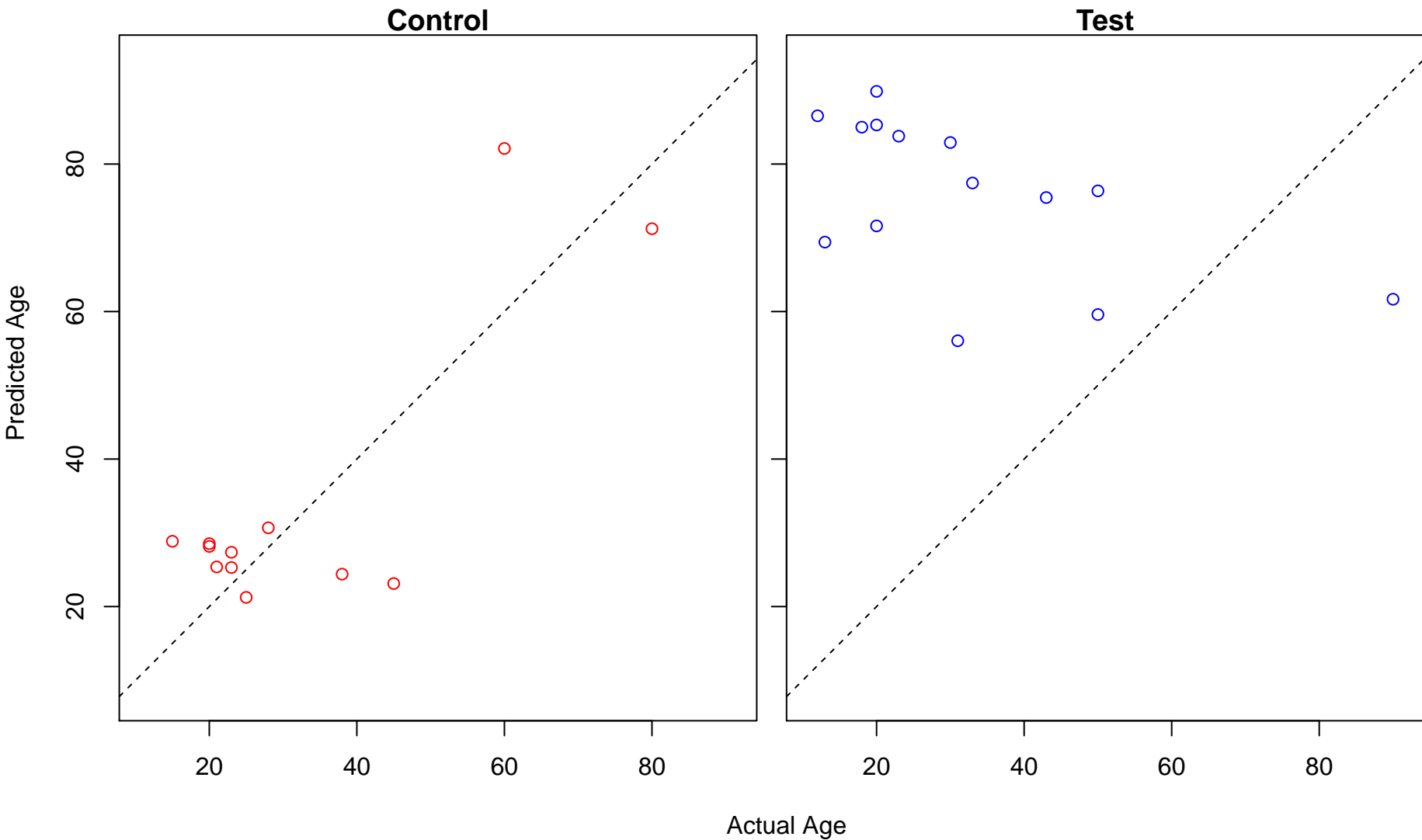
response to steroid hormone (Score: 7.108769)



positive regulation of isotype switching (Score: 7.108279)

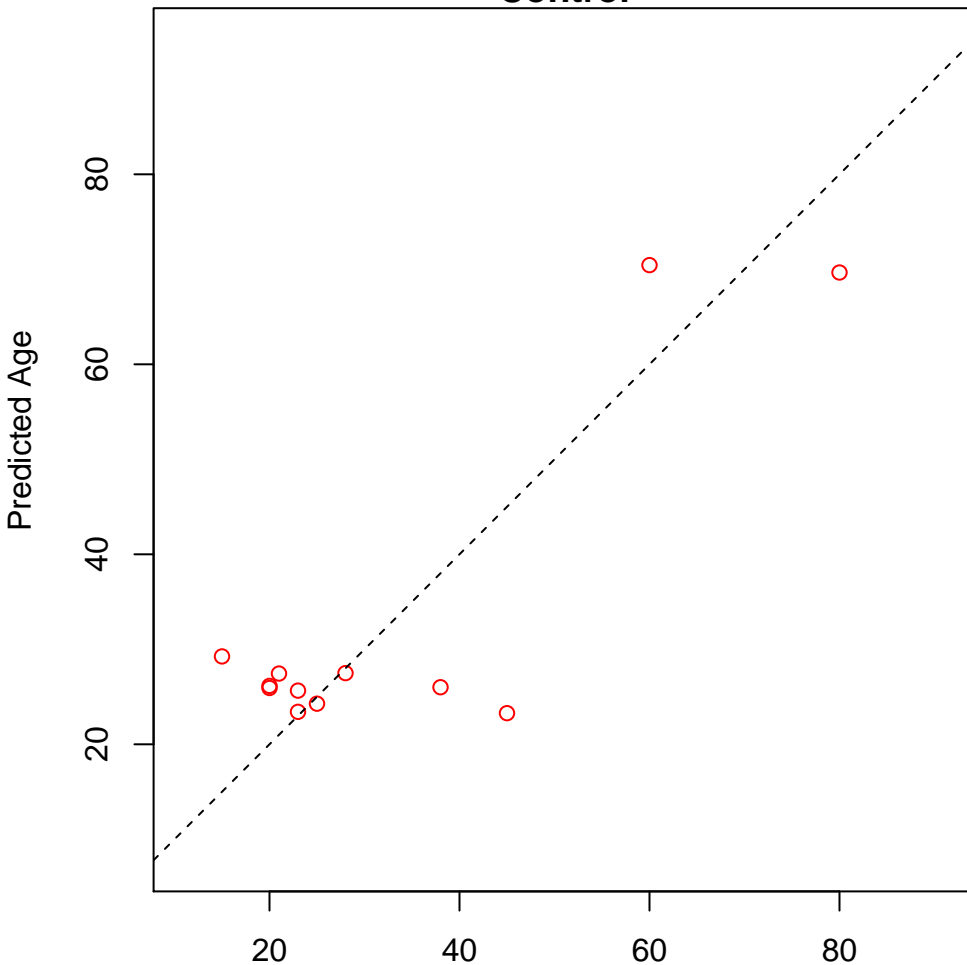


regulation of glucocorticoid metabolic process (Score: 7.107956)

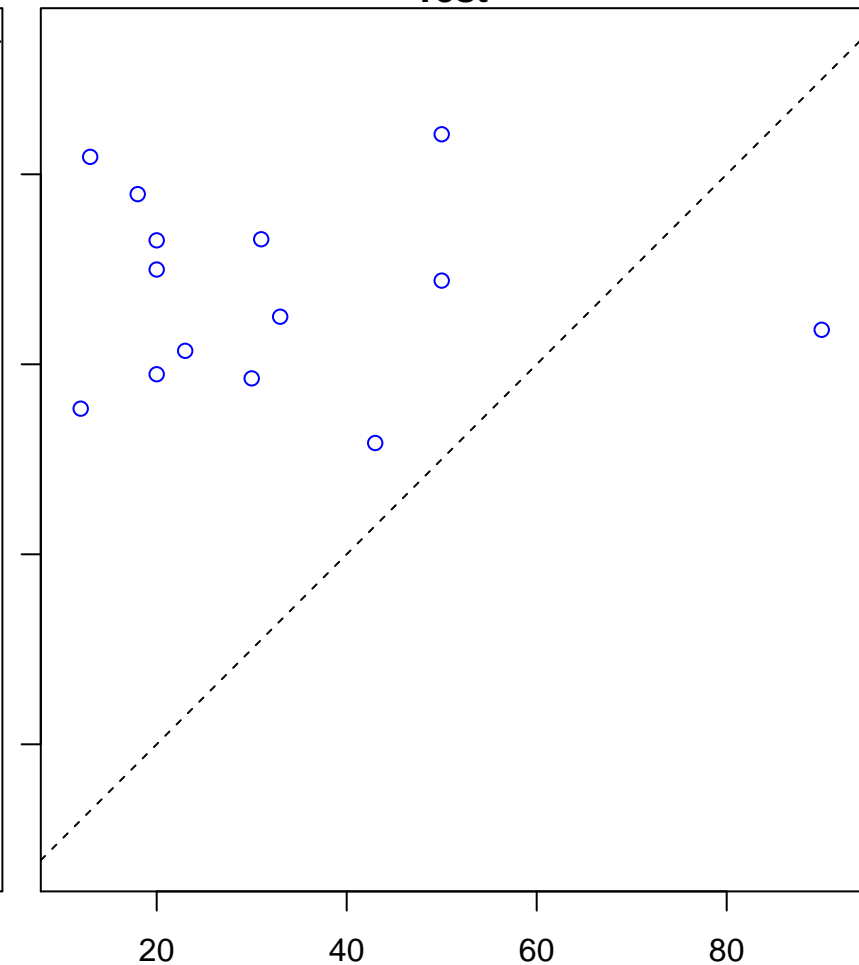


central nervous system development (Score: 7.106781)

Control

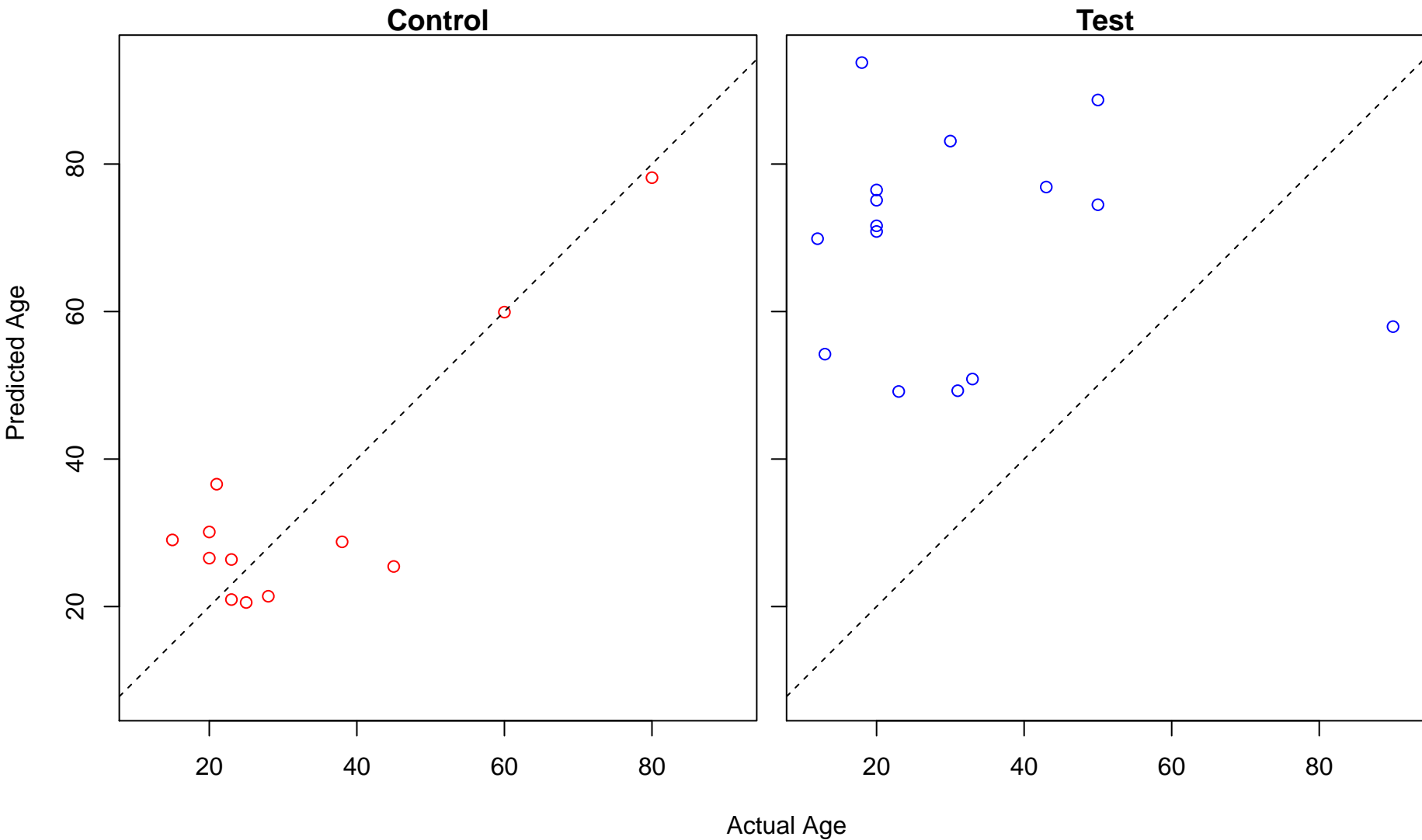


Test

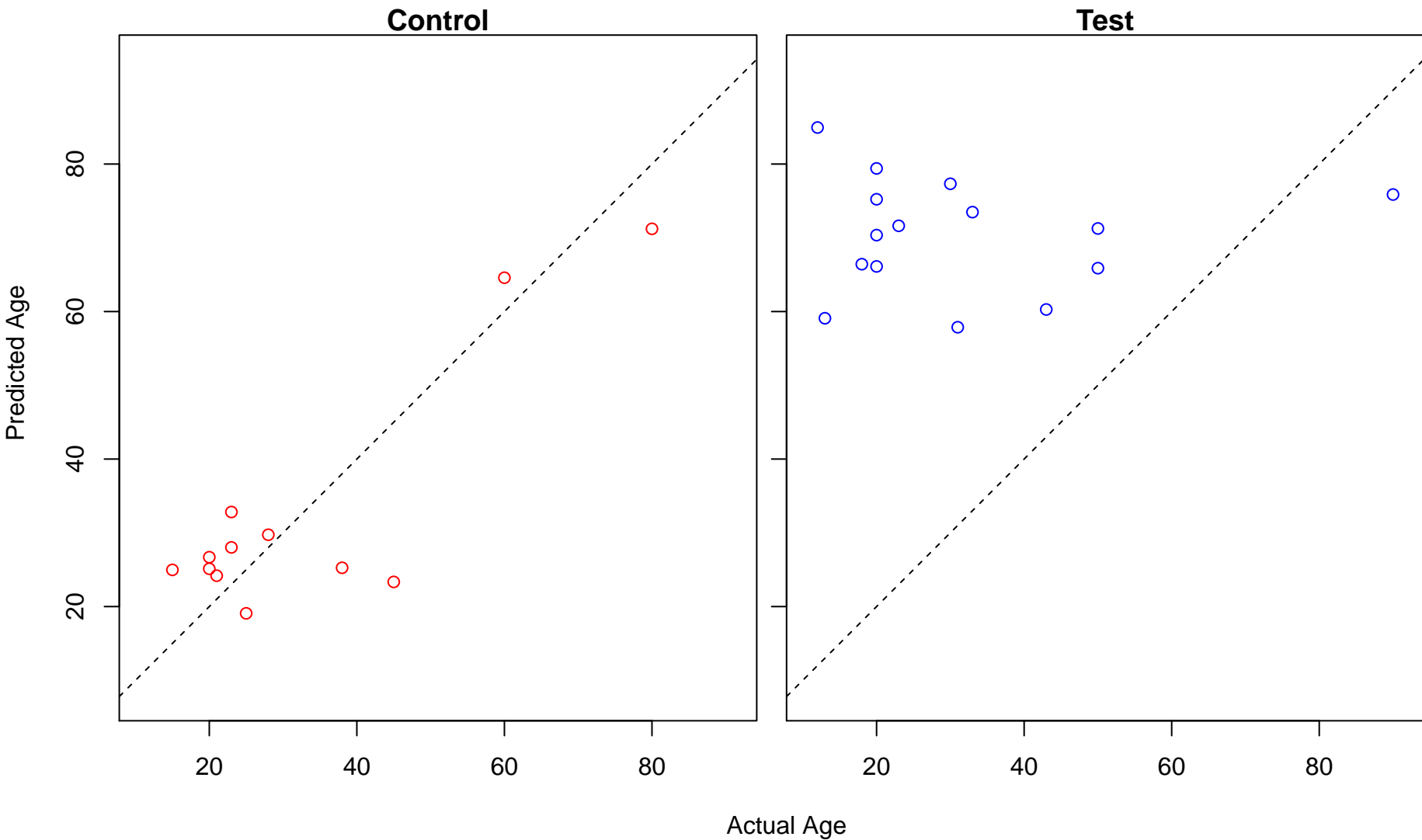


Actual Age

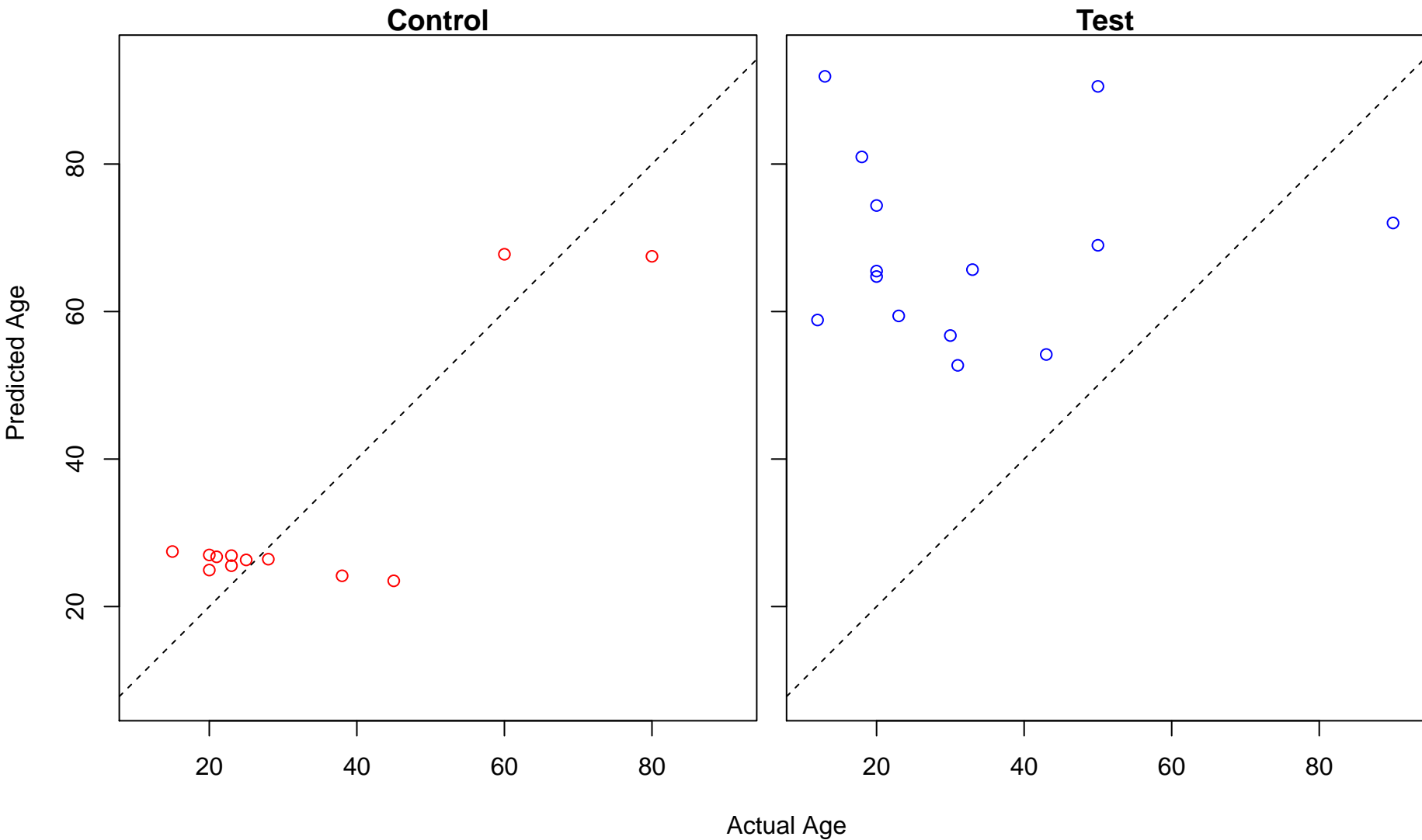
response to hydrogen peroxide (Score: 7.104935)



positive regulation of DNA recombination (Score: 7.104009)

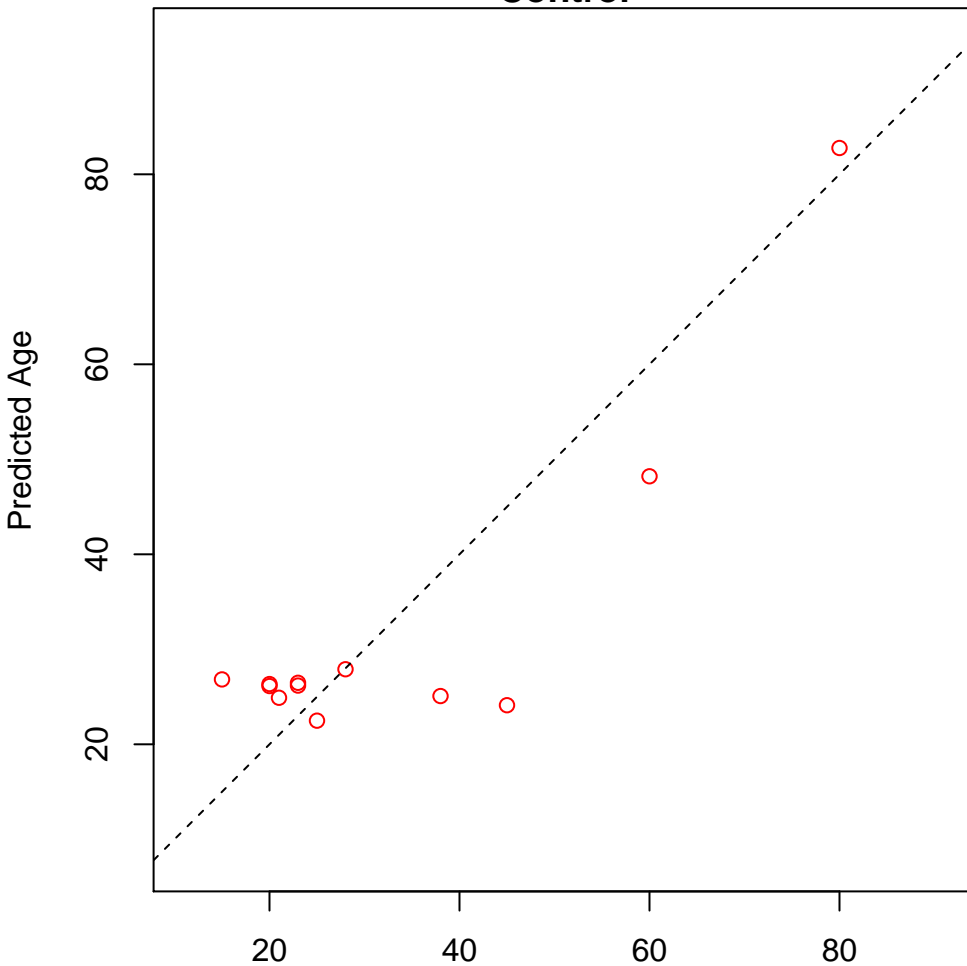


translation (Score: 7.103681)

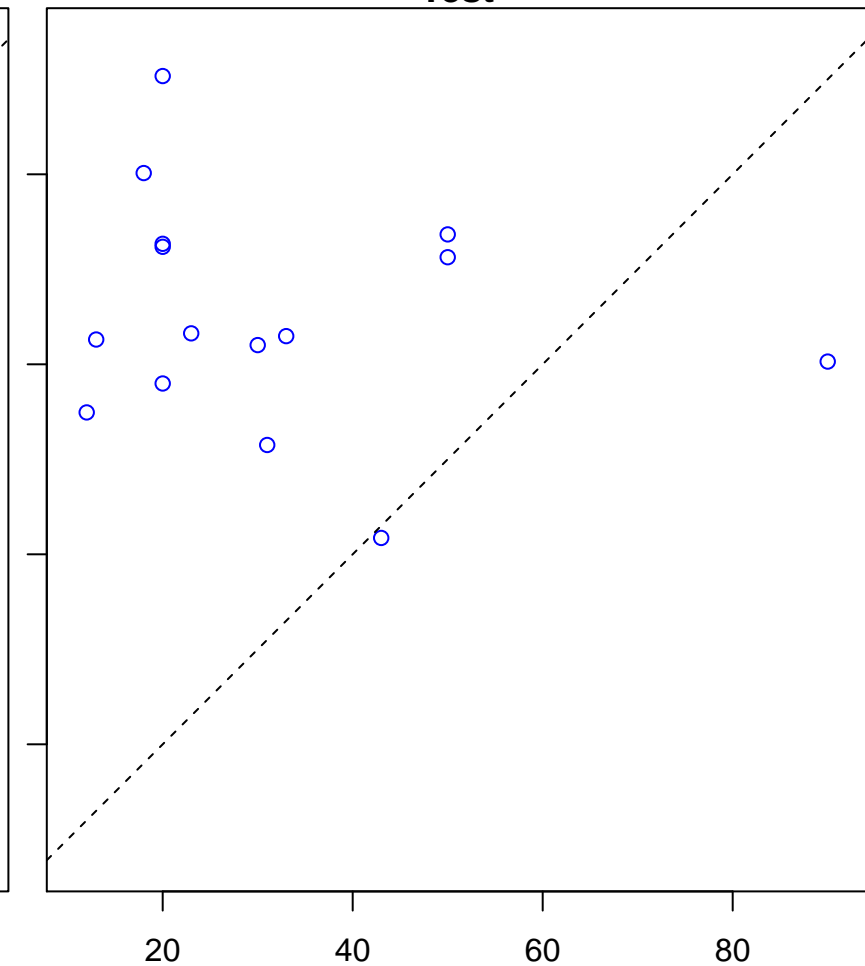


regulation of telomere maintenance (Score: 7.100060)

Control

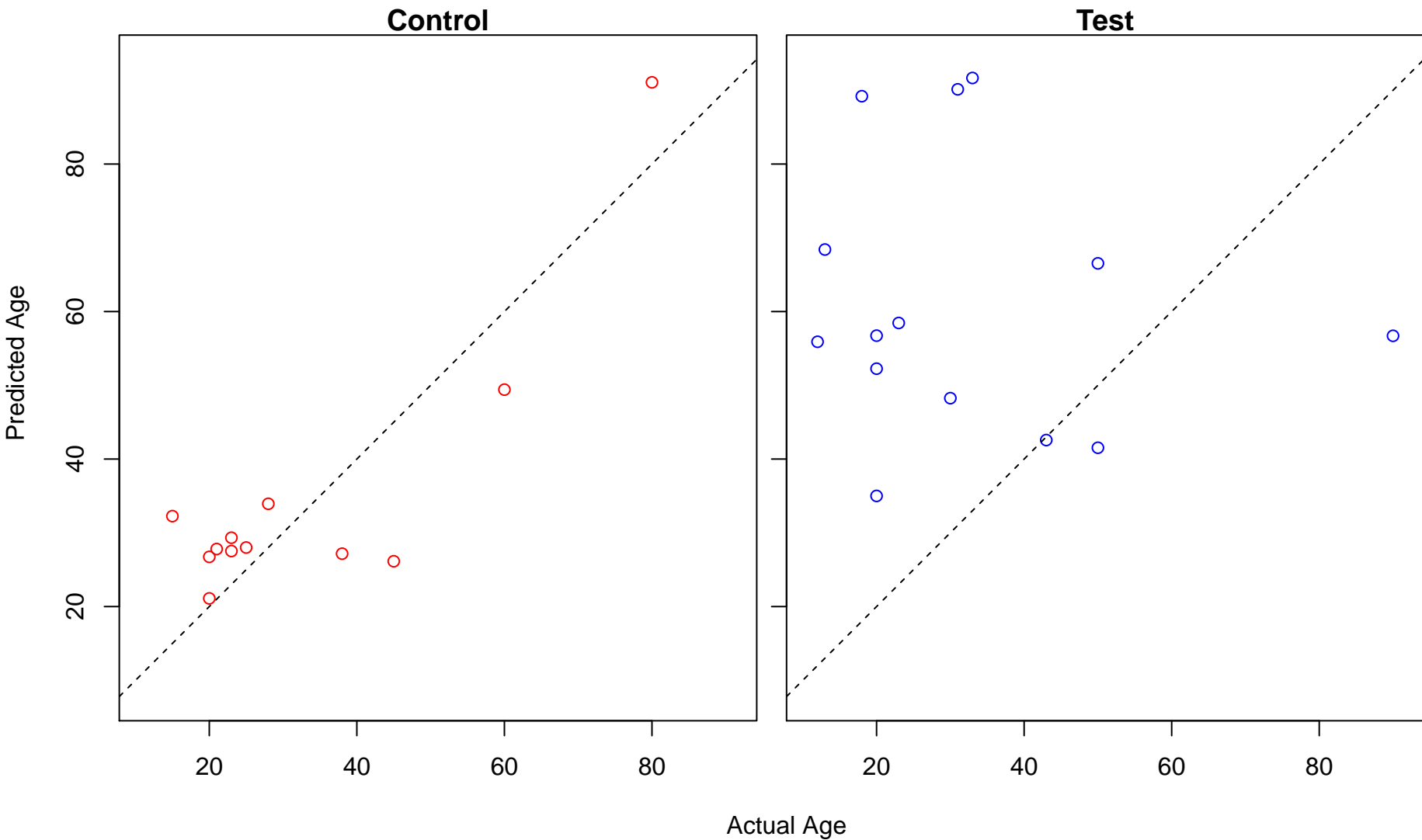


Test

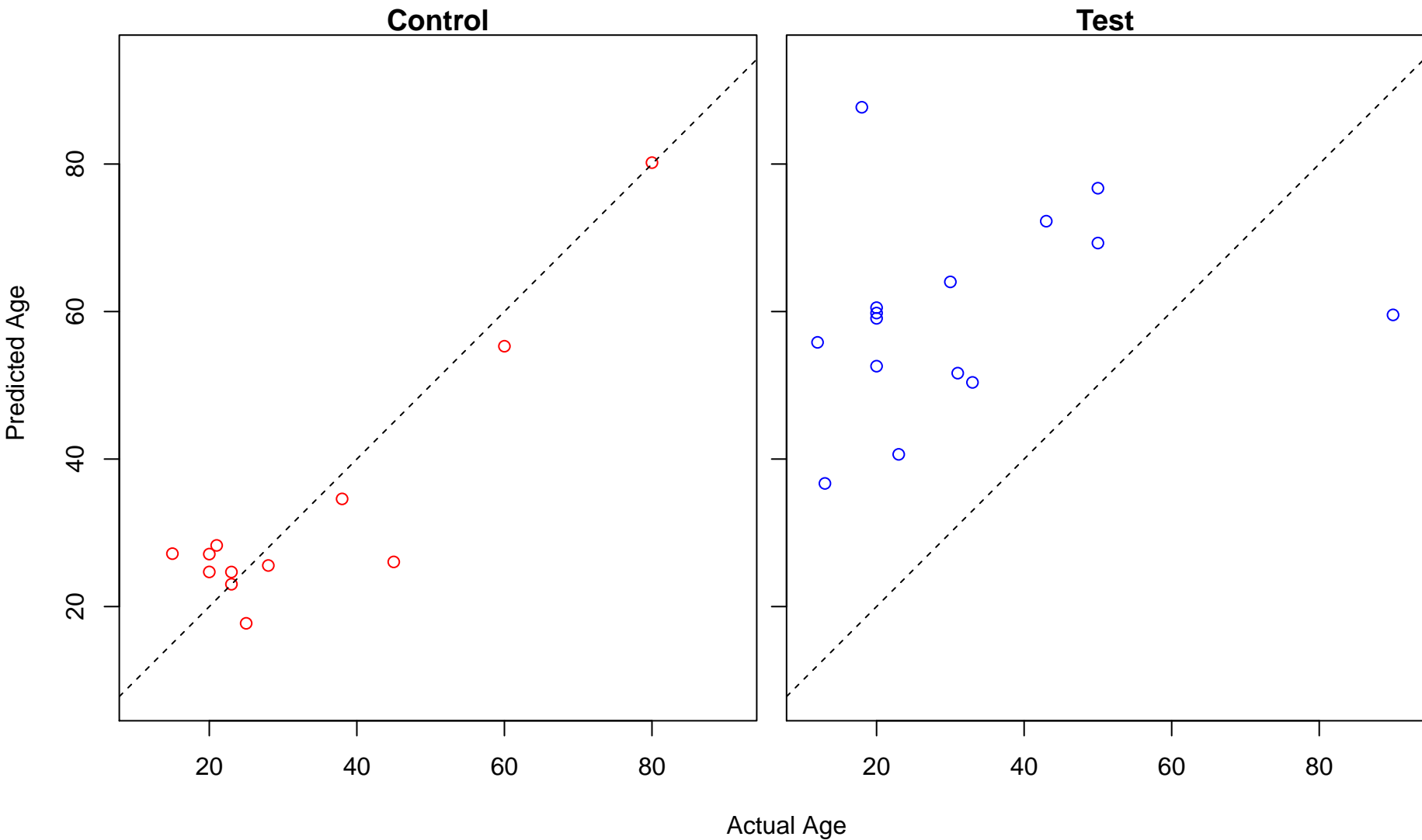


Actual Age

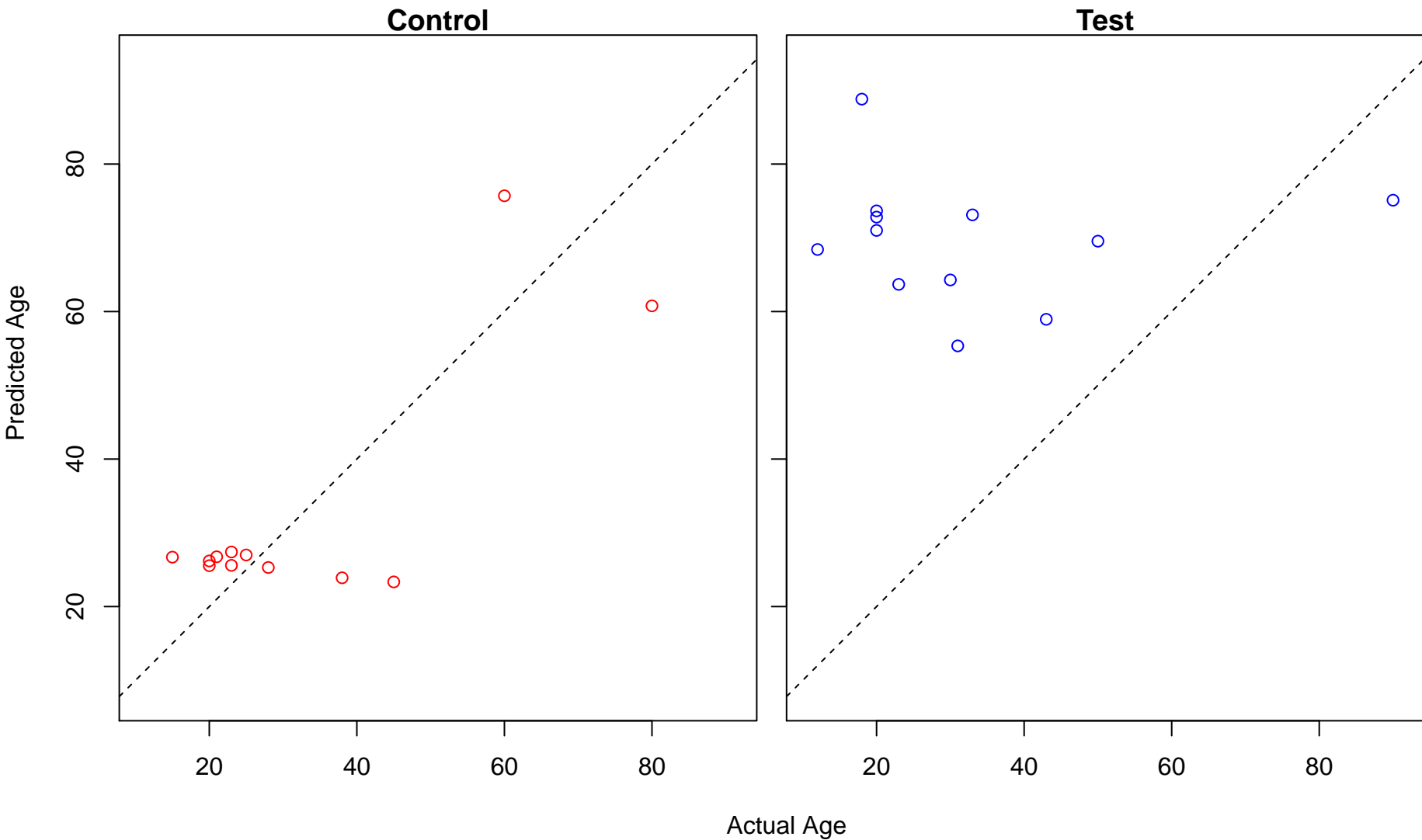
regulation of nervous system development (Score: 7.099930)



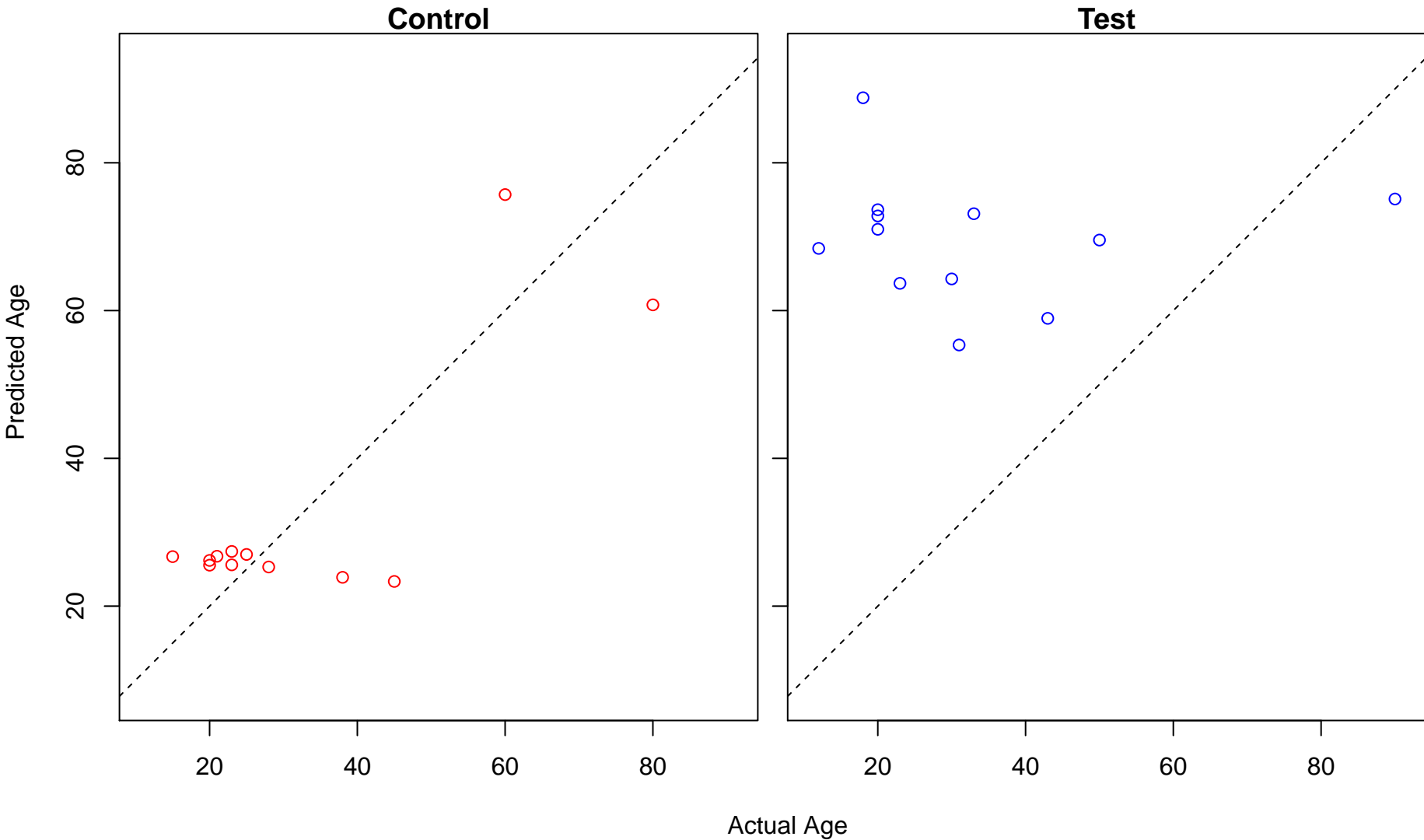
retinoid metabolic process (Score: 7.099284)



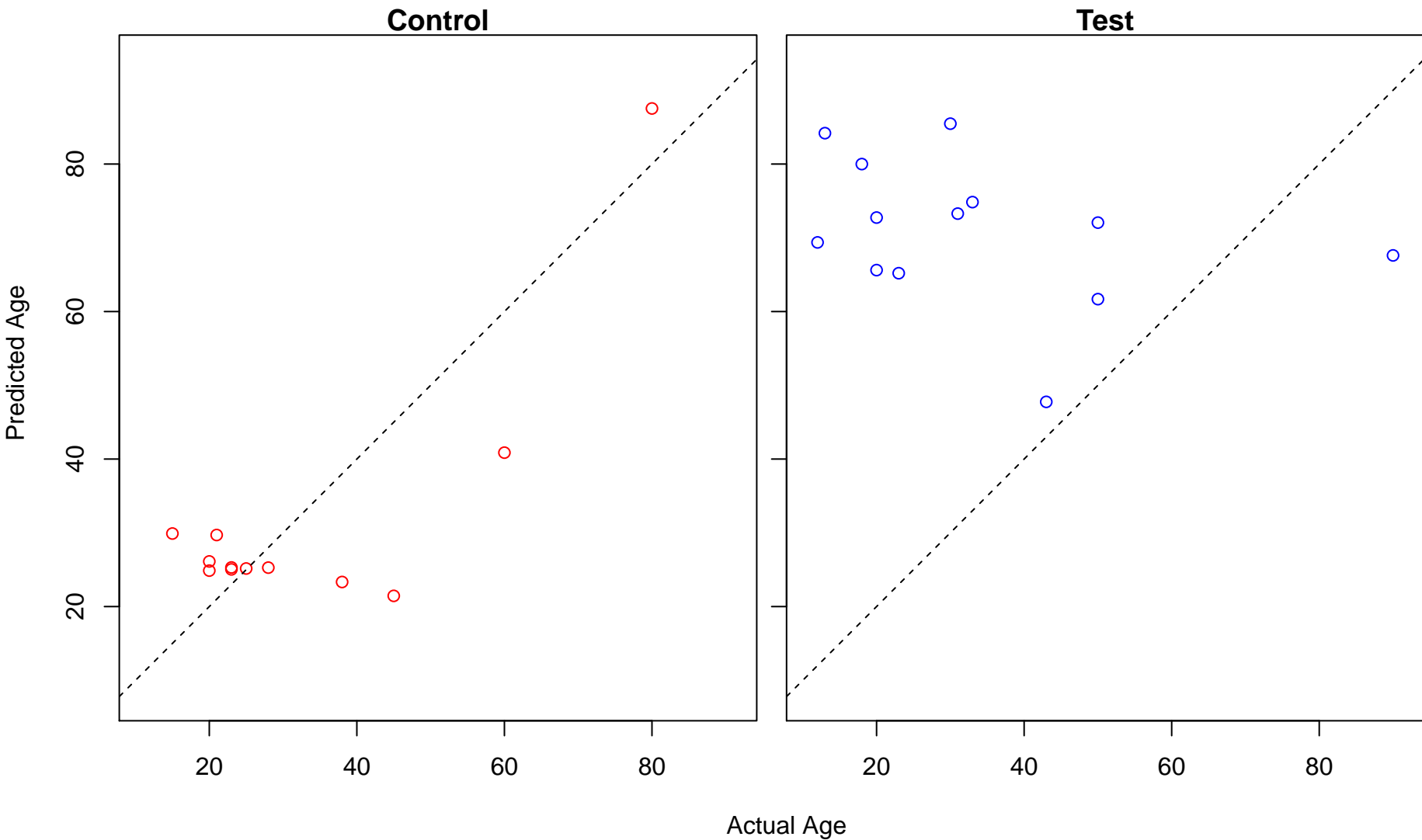
symbiosis, encompassing mutualism through parasitism (Score: 7.097864)



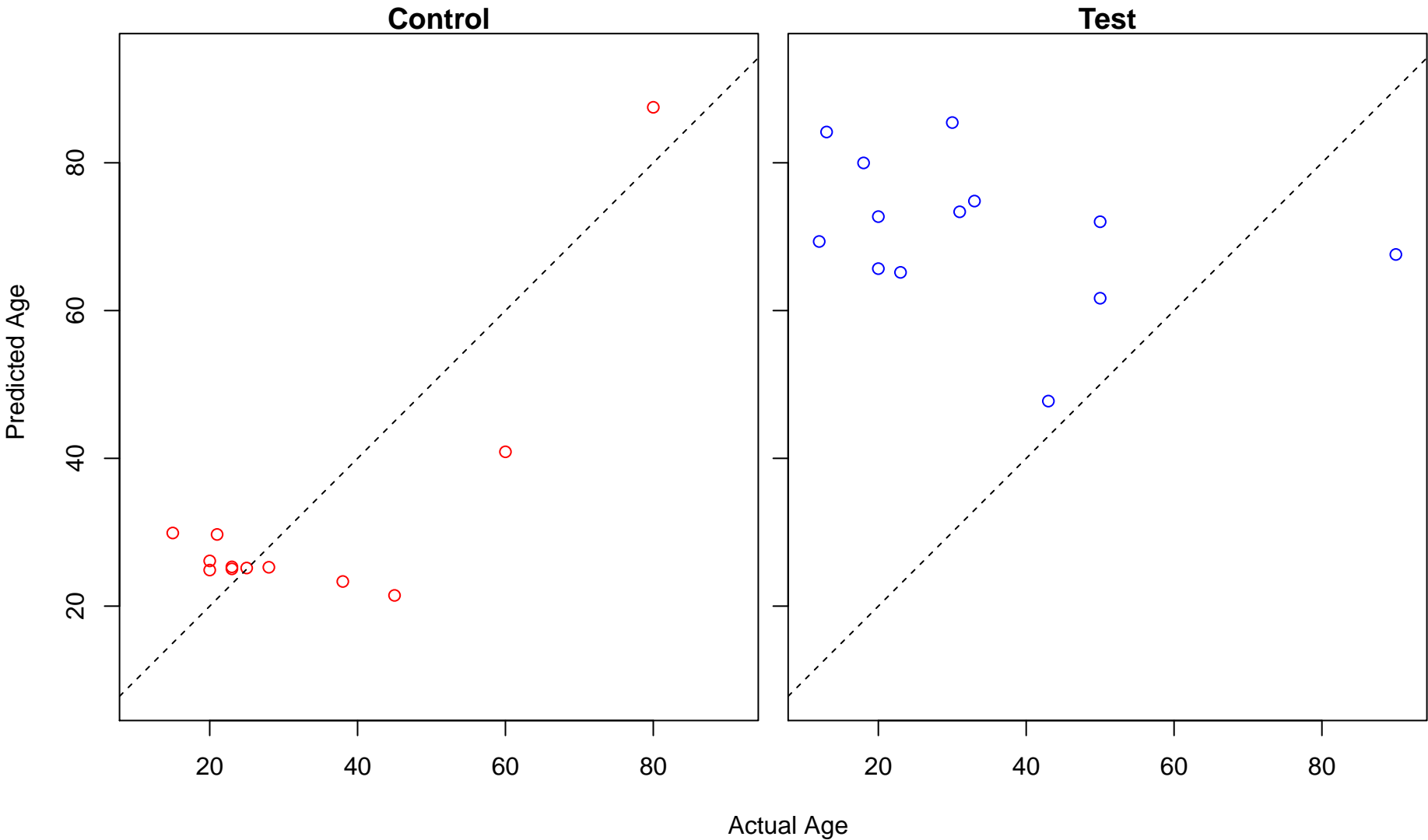
interspecies interaction between organisms (Score: 7.097864)



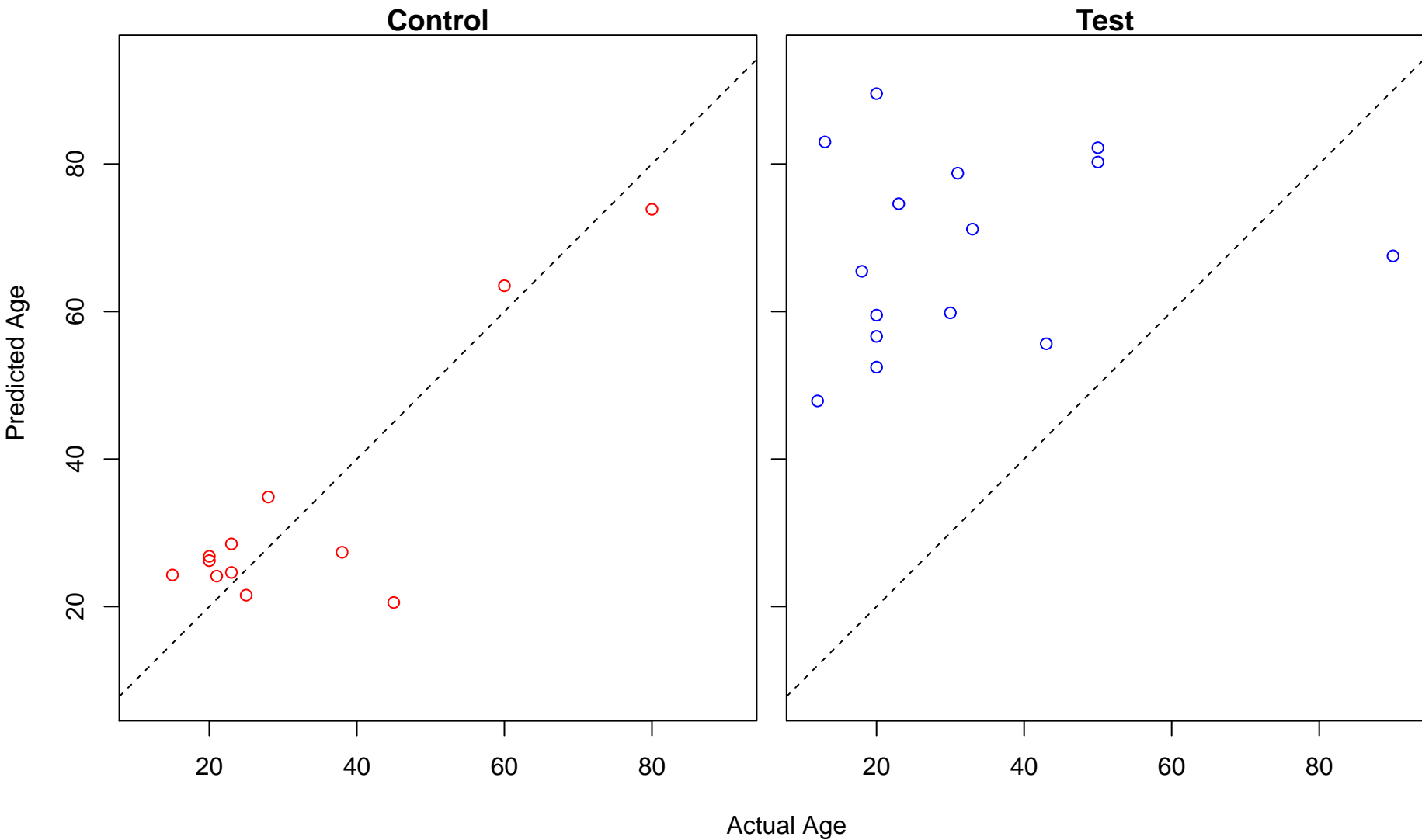
regulation of tumor necrosis factor production (Score: 7.095640)



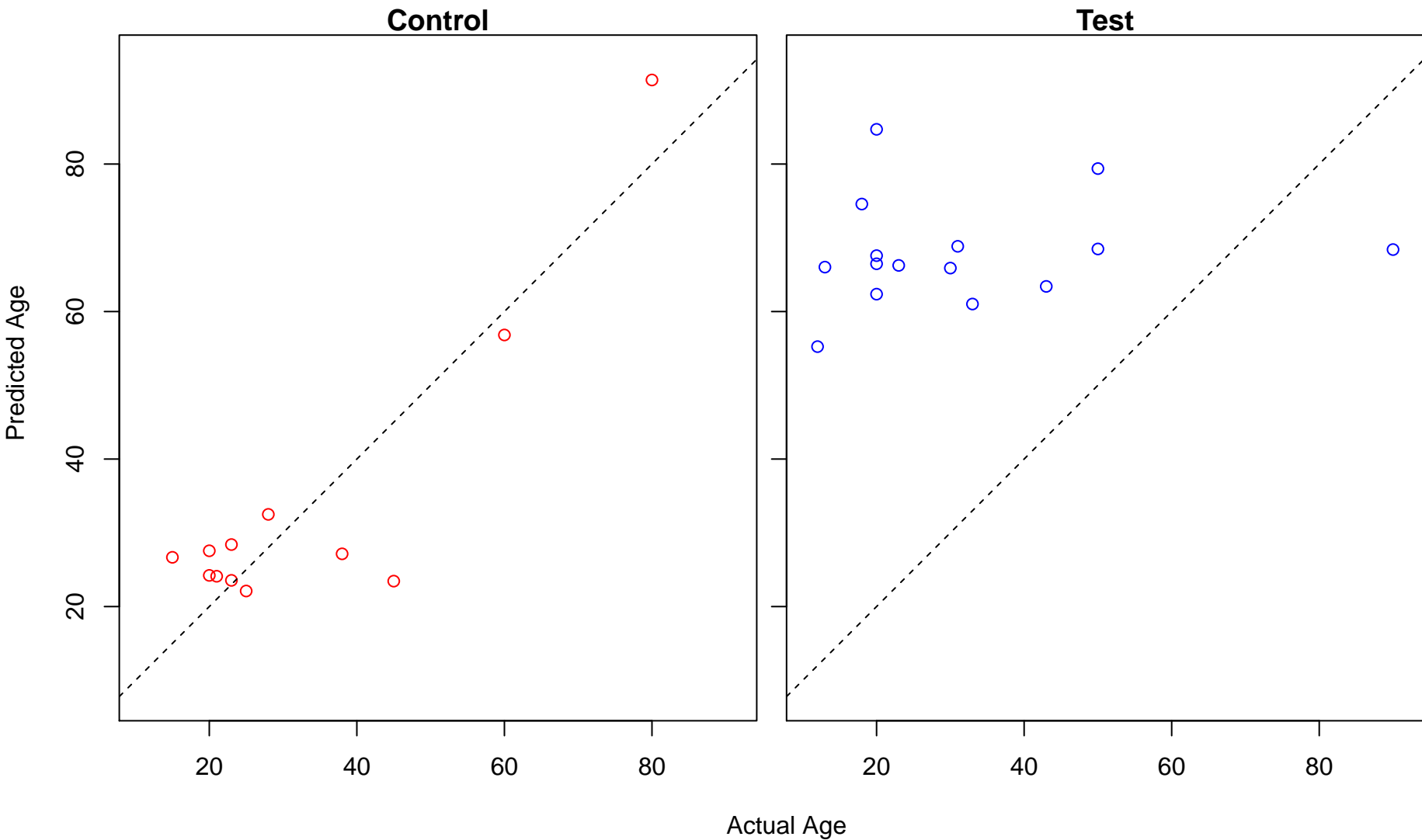
regulation of tumor necrosis factor superfamily cytokine production (Score: 7.095570)



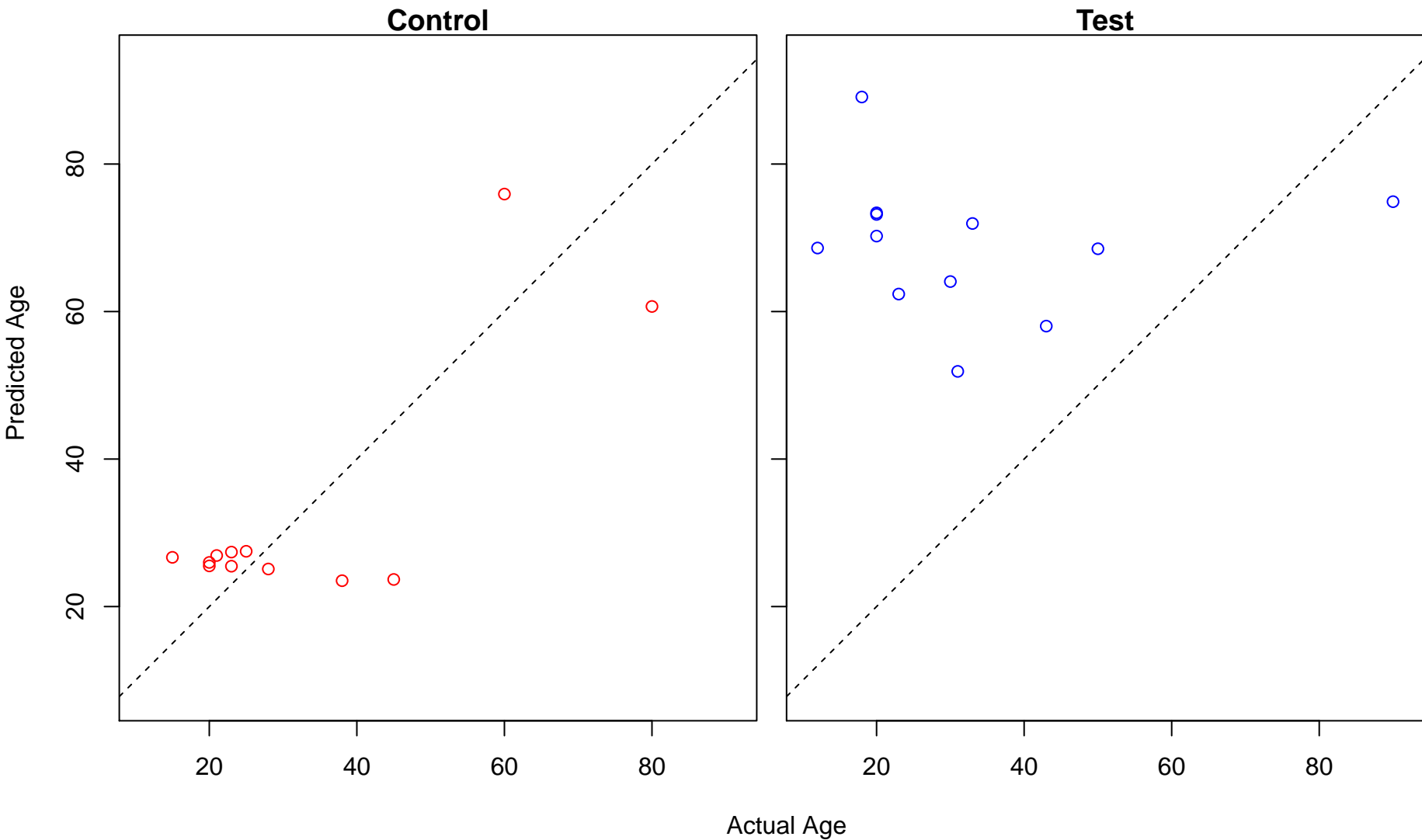
regulation of peptidyl-tyrosine phosphorylation (Score: 7.094105)



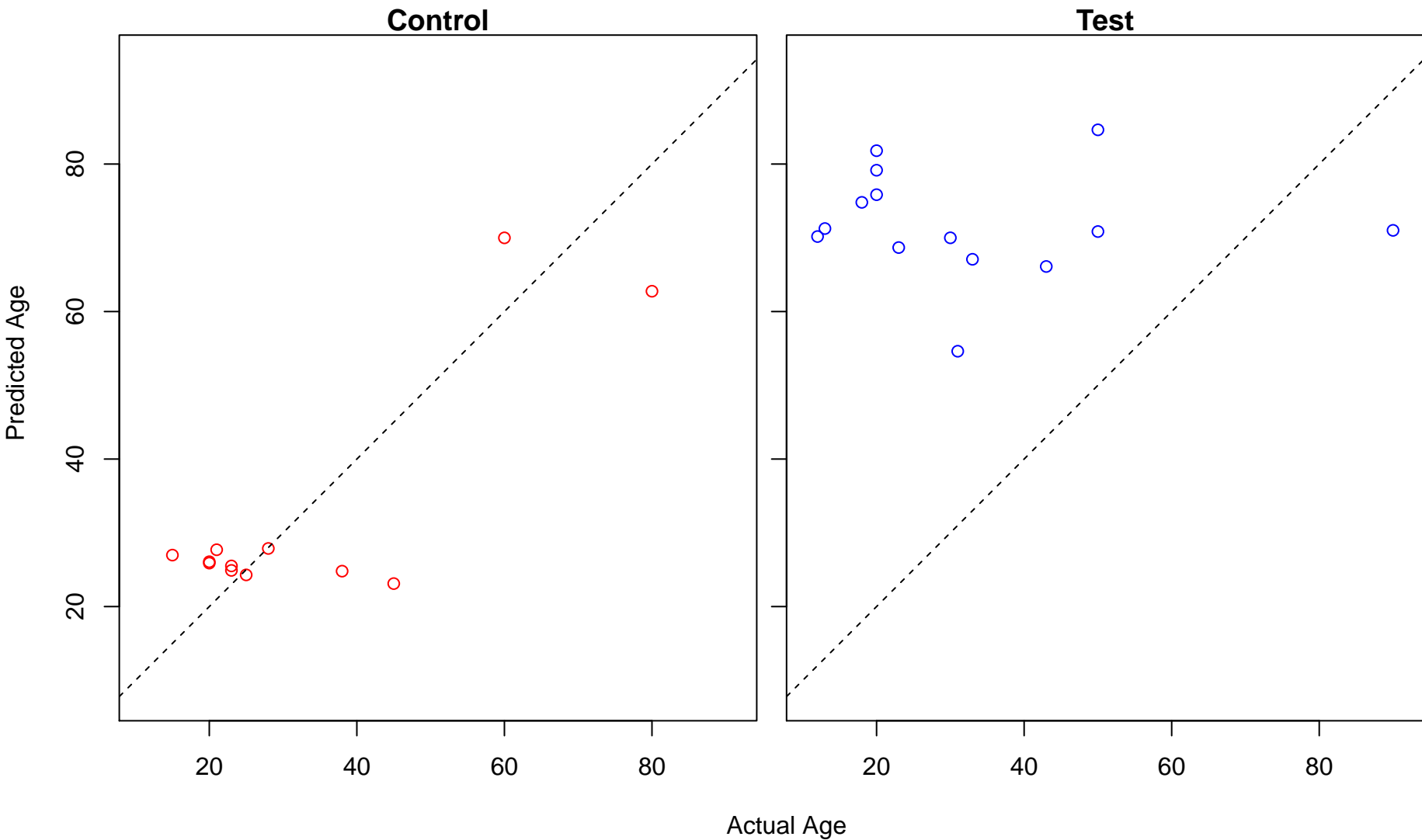
regulation of hormone levels (Score: 7.093049)



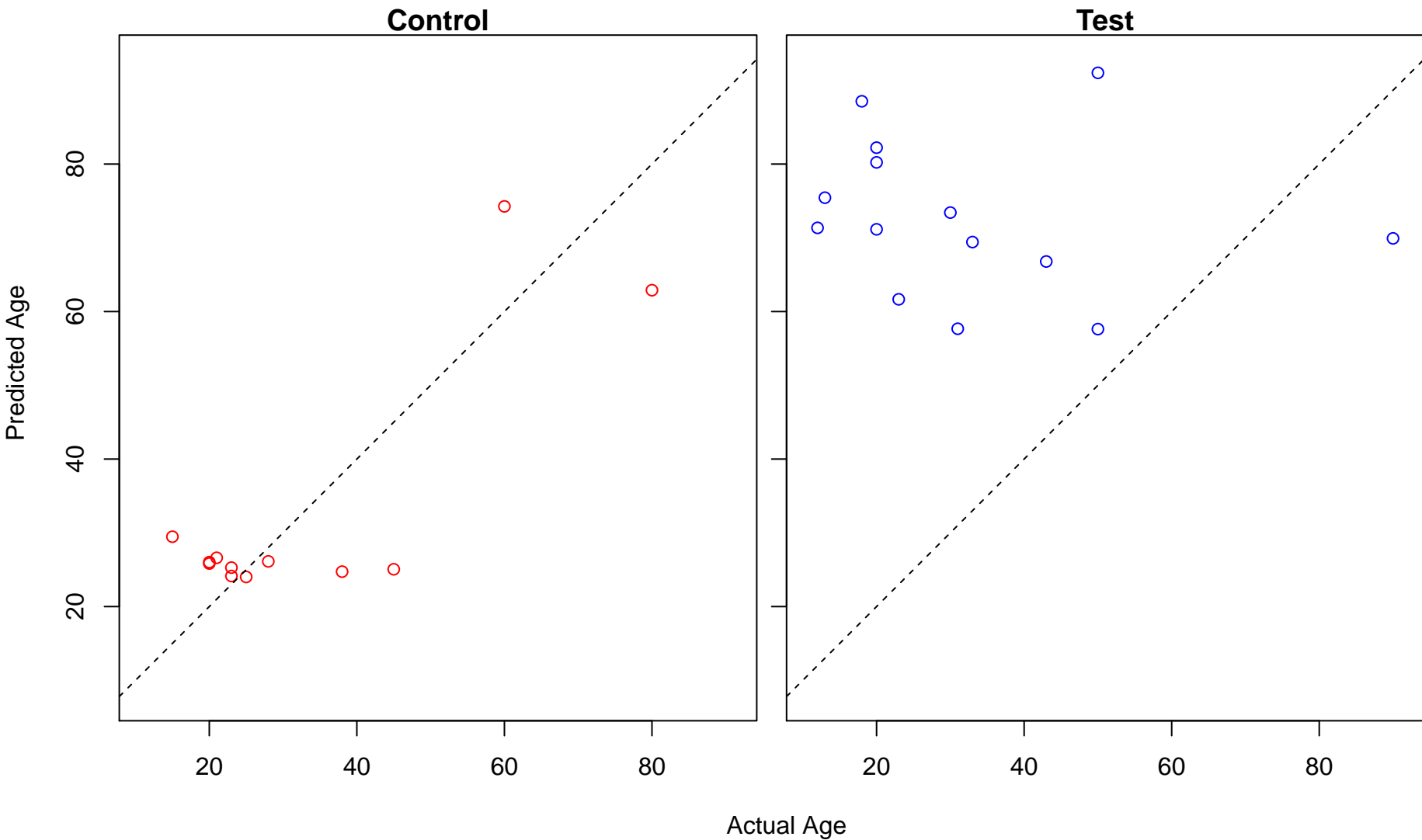
protein complex disassembly (Score: 7.092550)



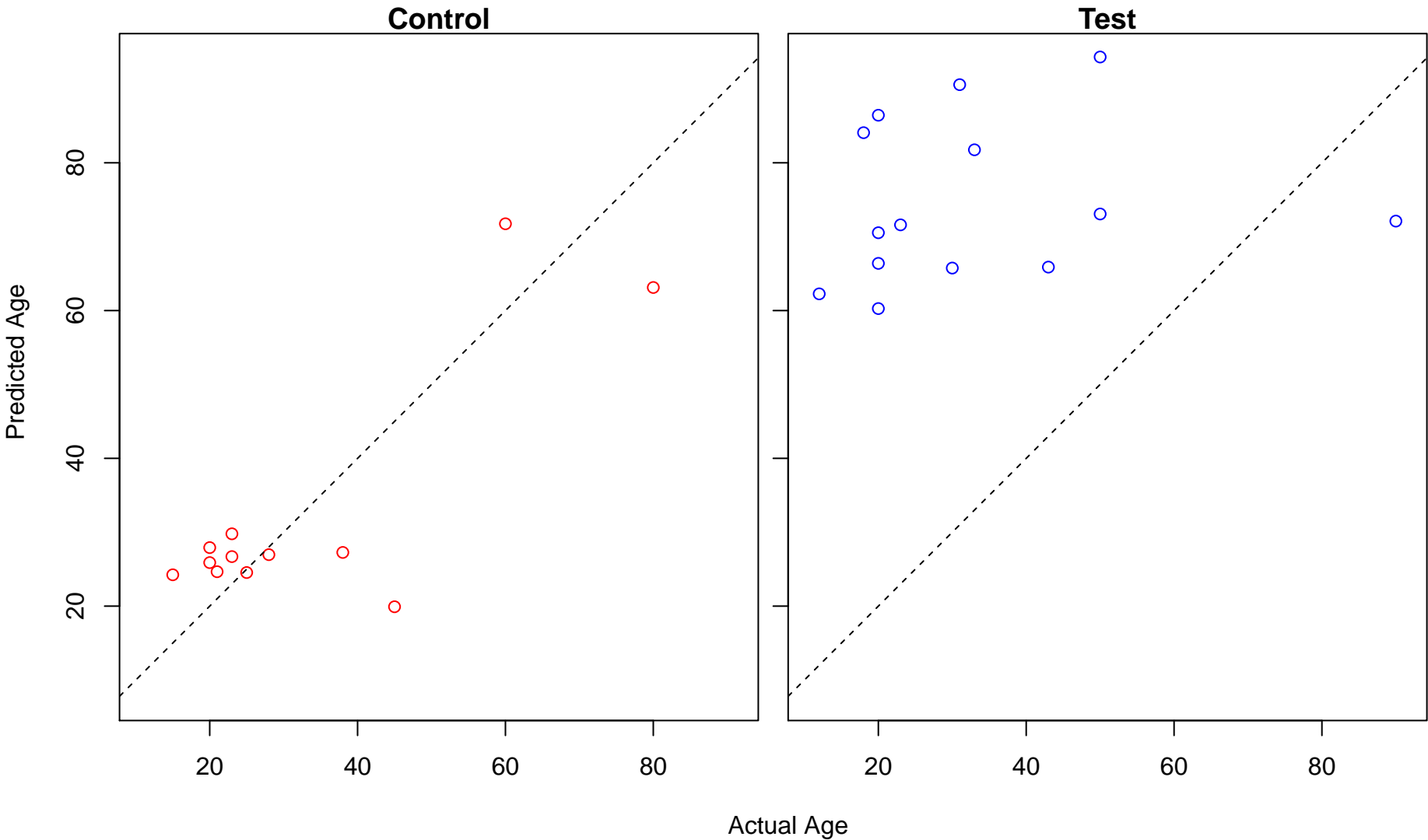
organophosphate catabolic process (Score: 7.088443)



positive regulation of TOR signaling (Score: 7.087393)

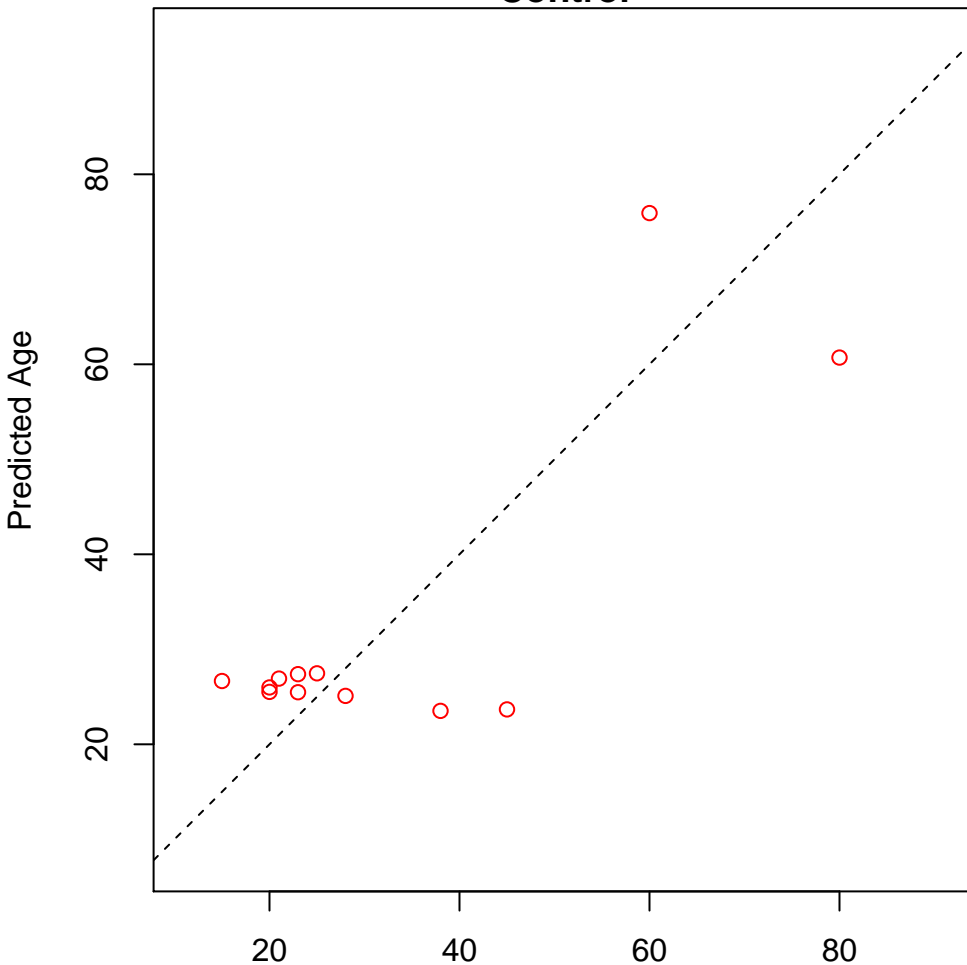


positive regulation of production of molecular mediator of immune response (Score: 7.086694)

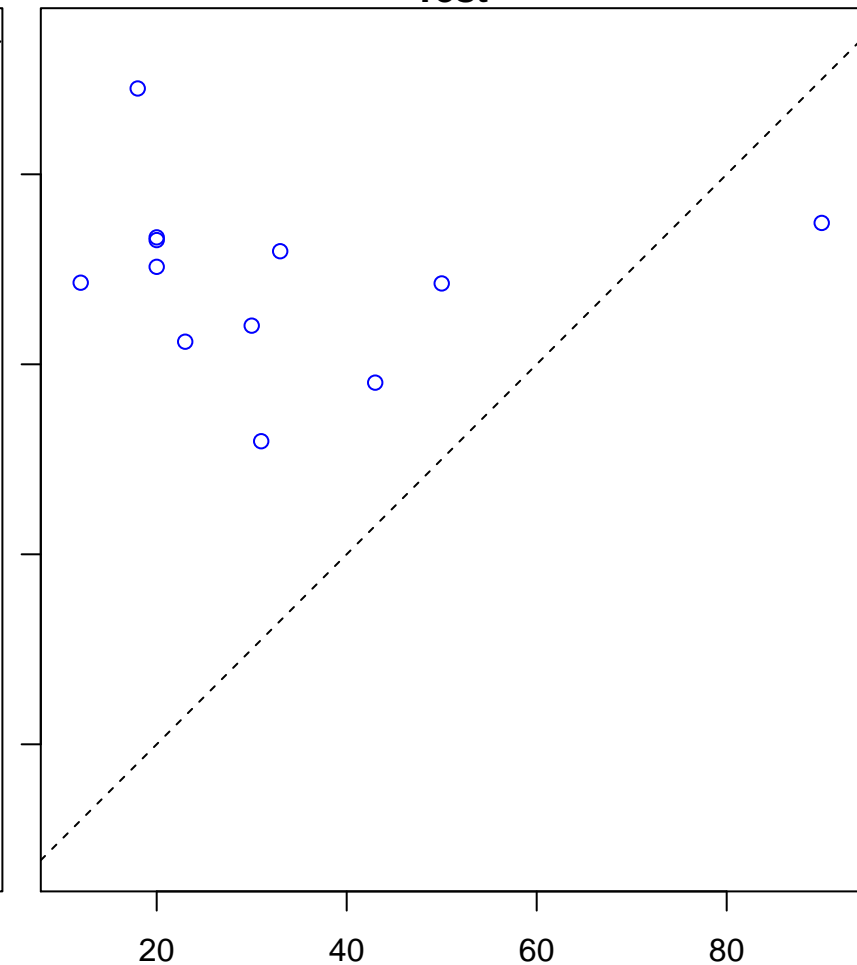


macromolecular complex disassembly (Score: 7.083665)

Control

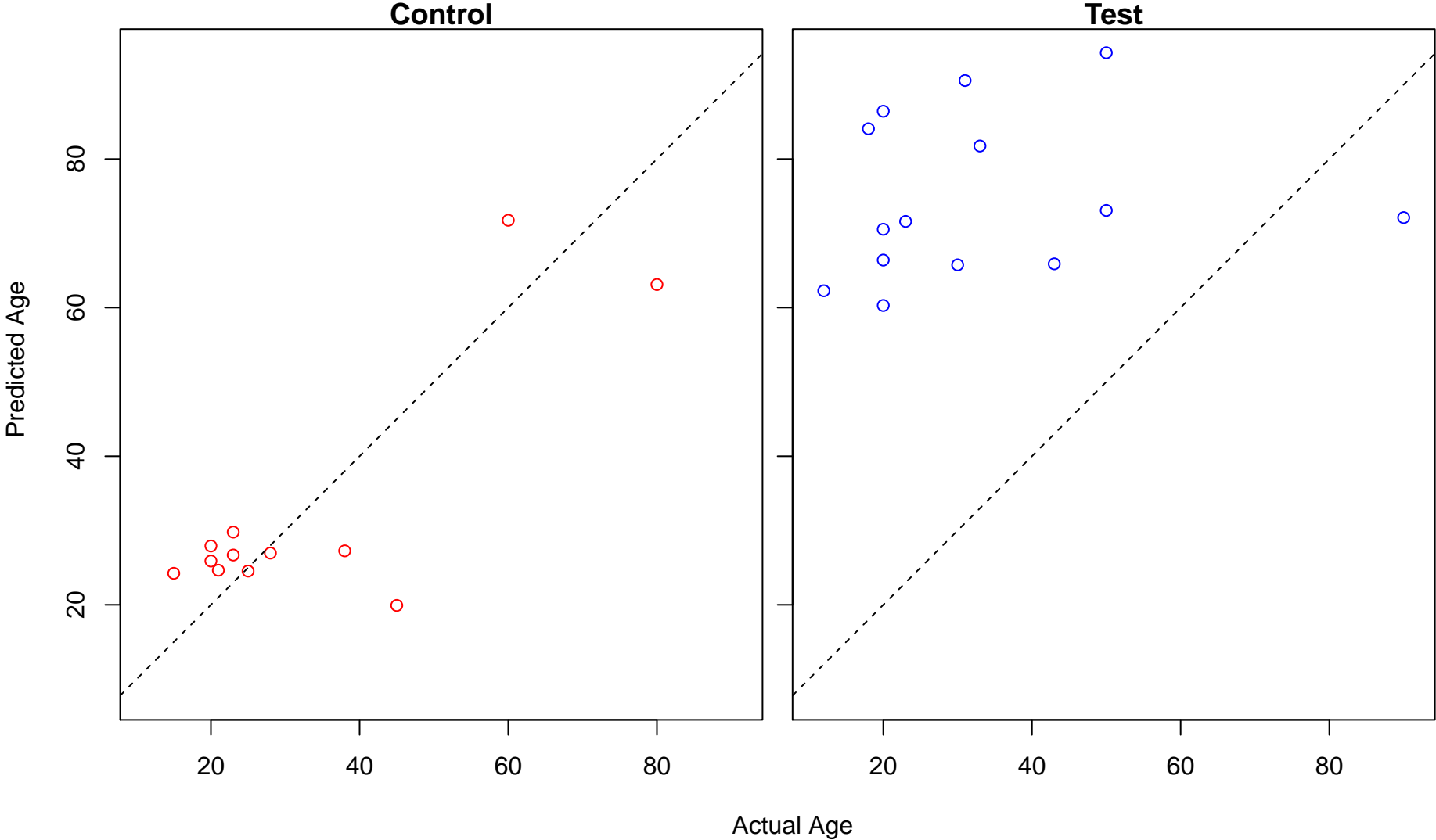


Test

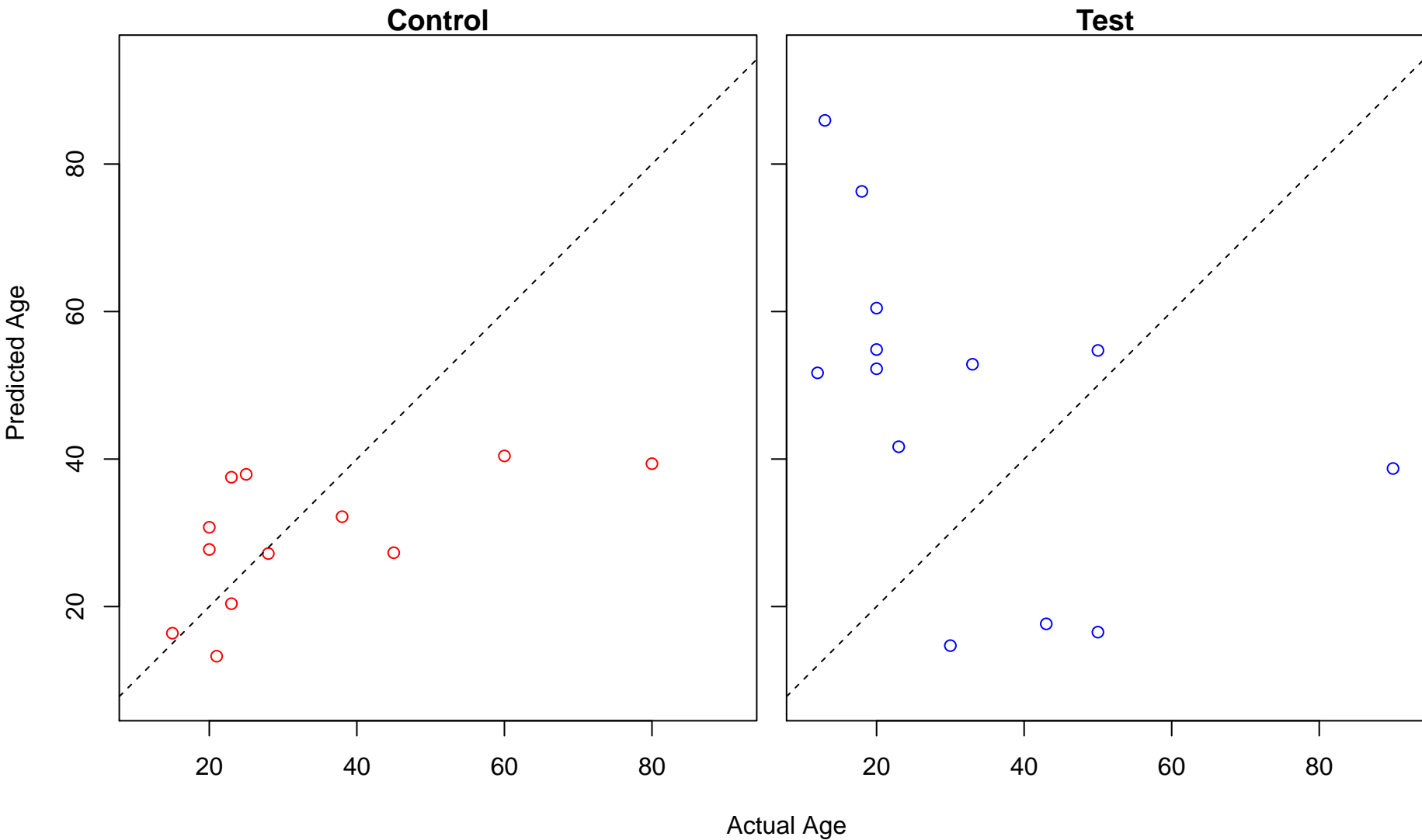


Actual Age

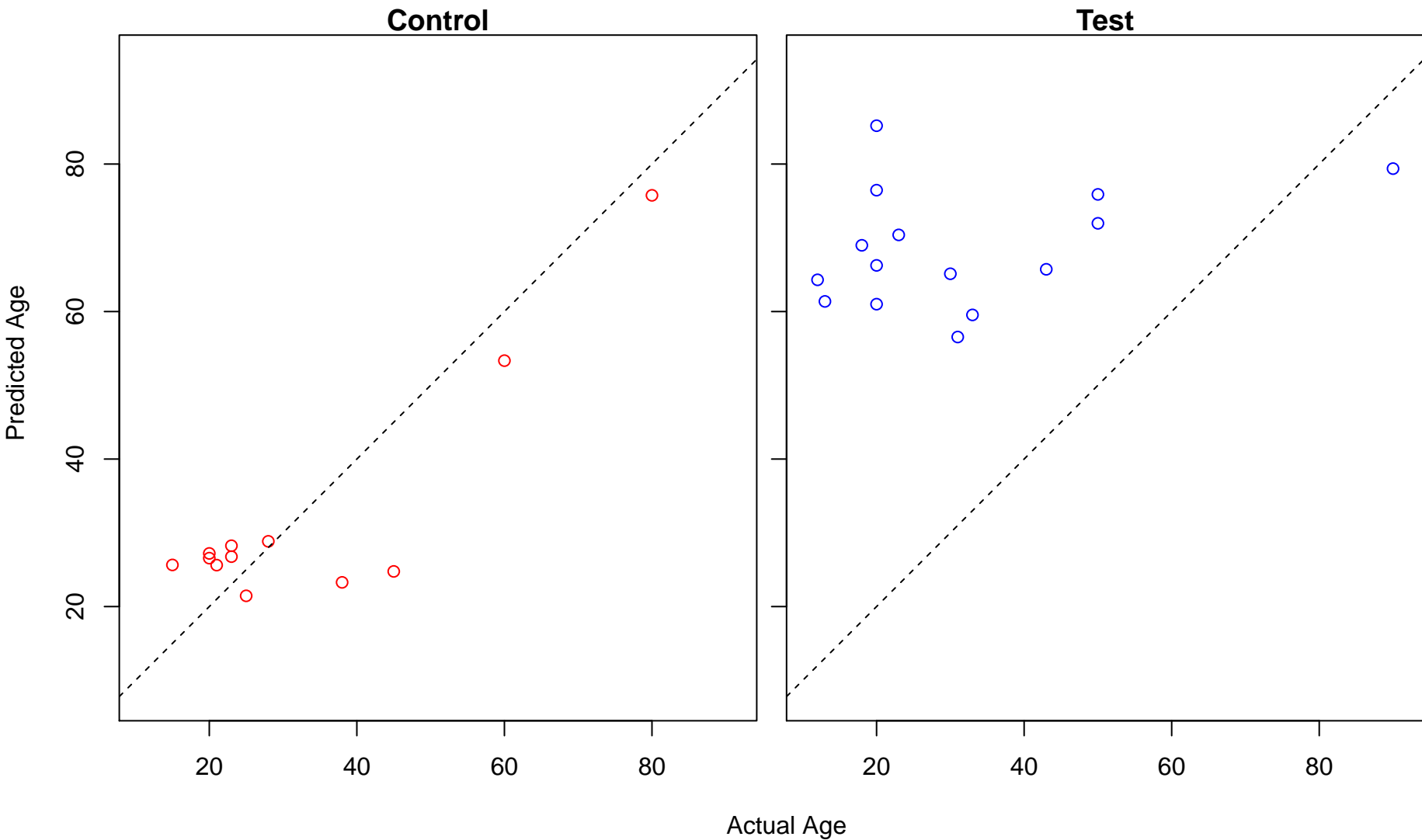
regulation of production of molecular mediator of immune response (Score: 7.083193)



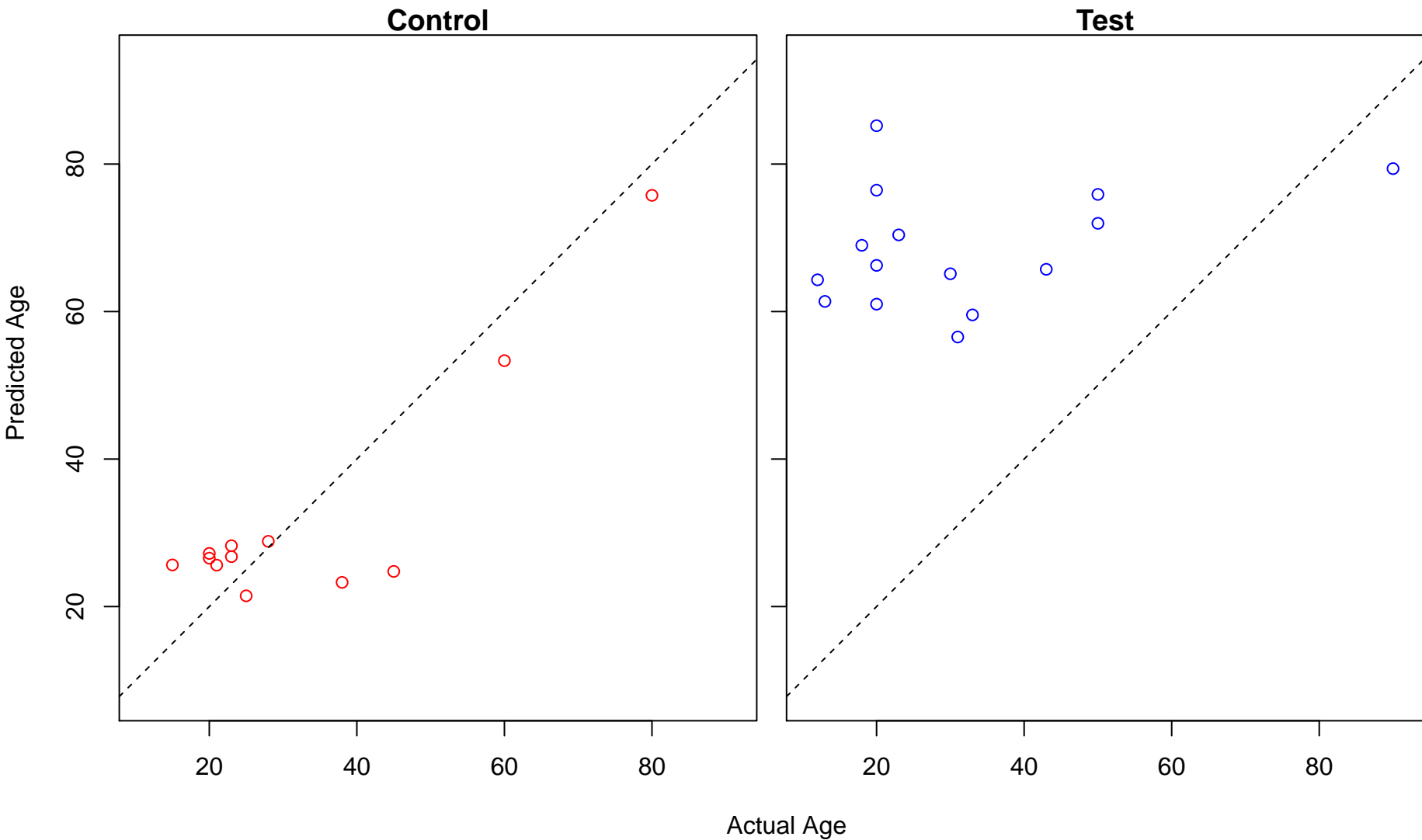
negative regulation of cytokine secretion involved in immune response (Score: 7.082687)



protein prenylation (Score: 7.079648)

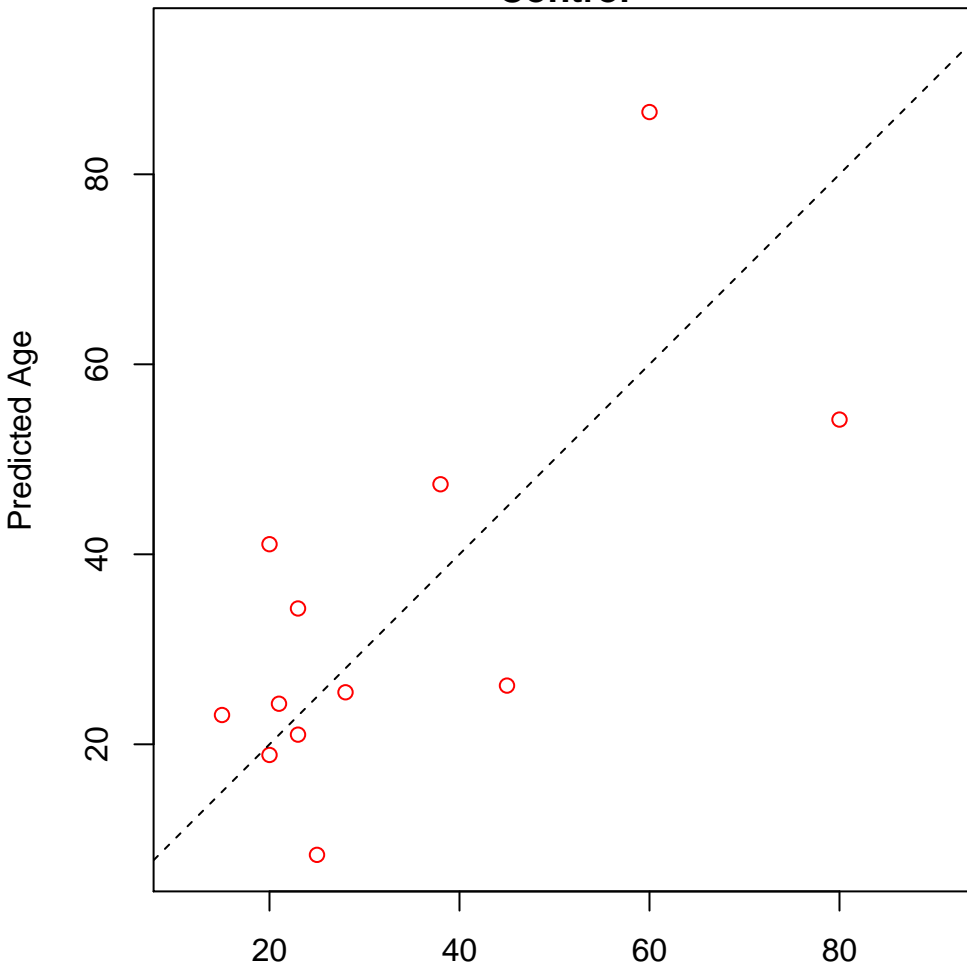


prenylation (Score: 7.079648)

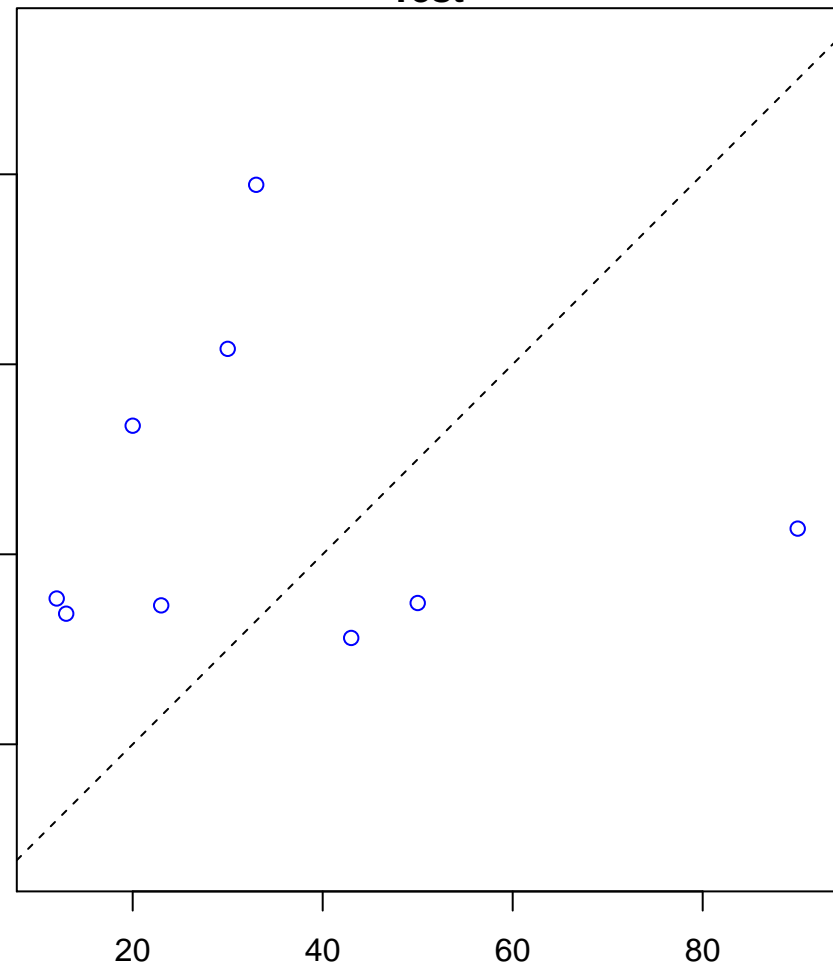


fat-soluble vitamin catabolic process (Score: 7.079265)

Control



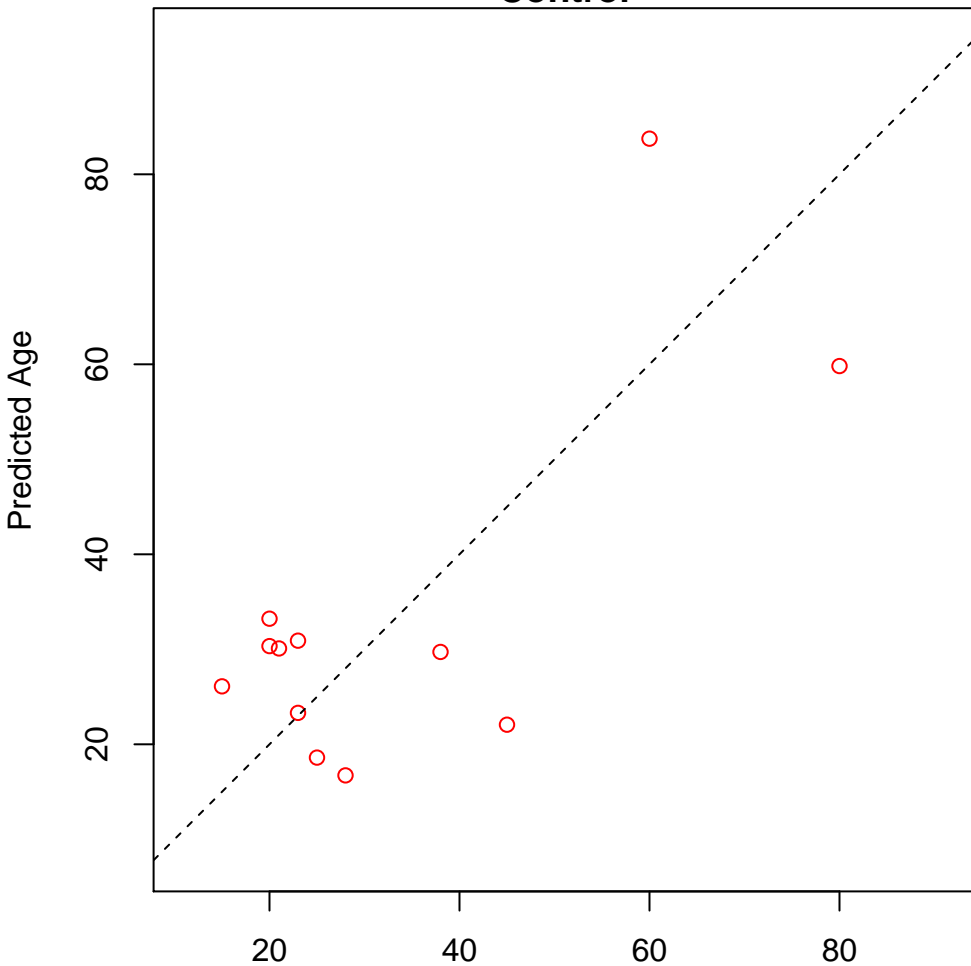
Test



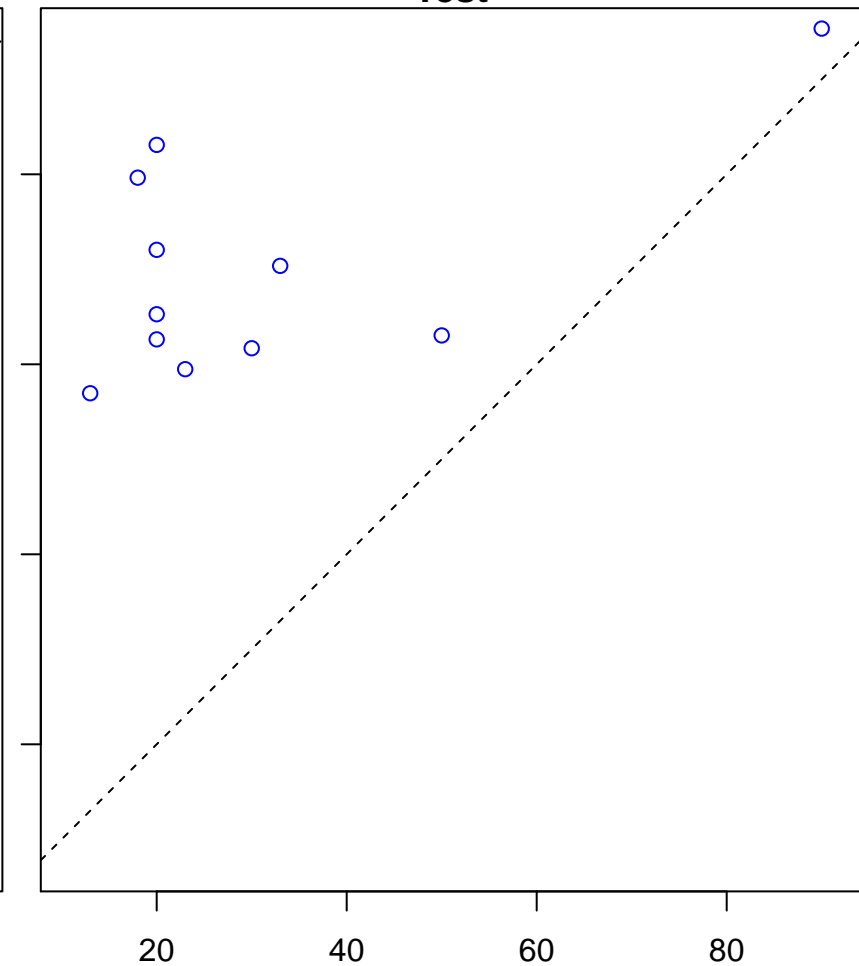
Actual Age

L-glutamate transmembrane transport (Score: 7.078588)

Control

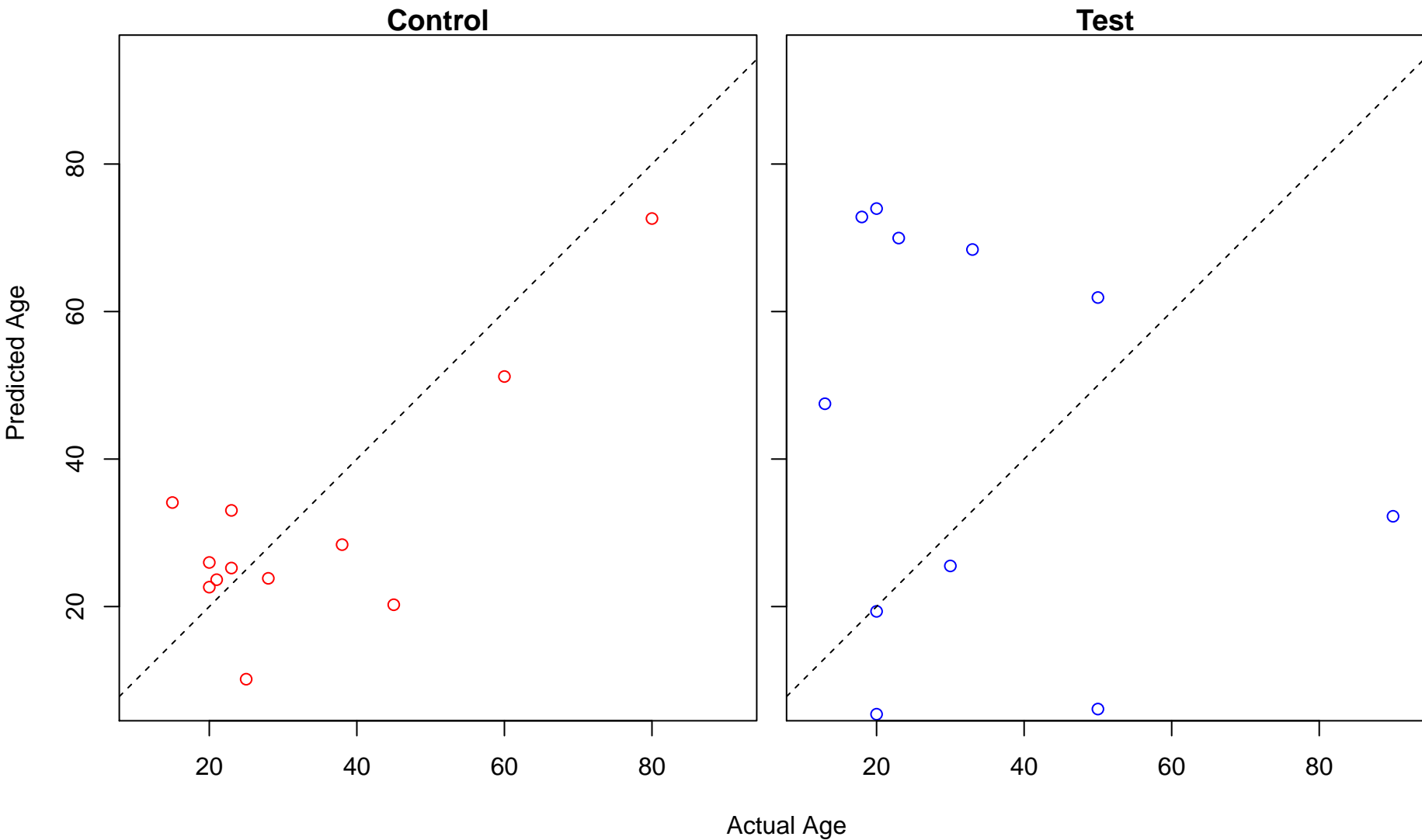


Test

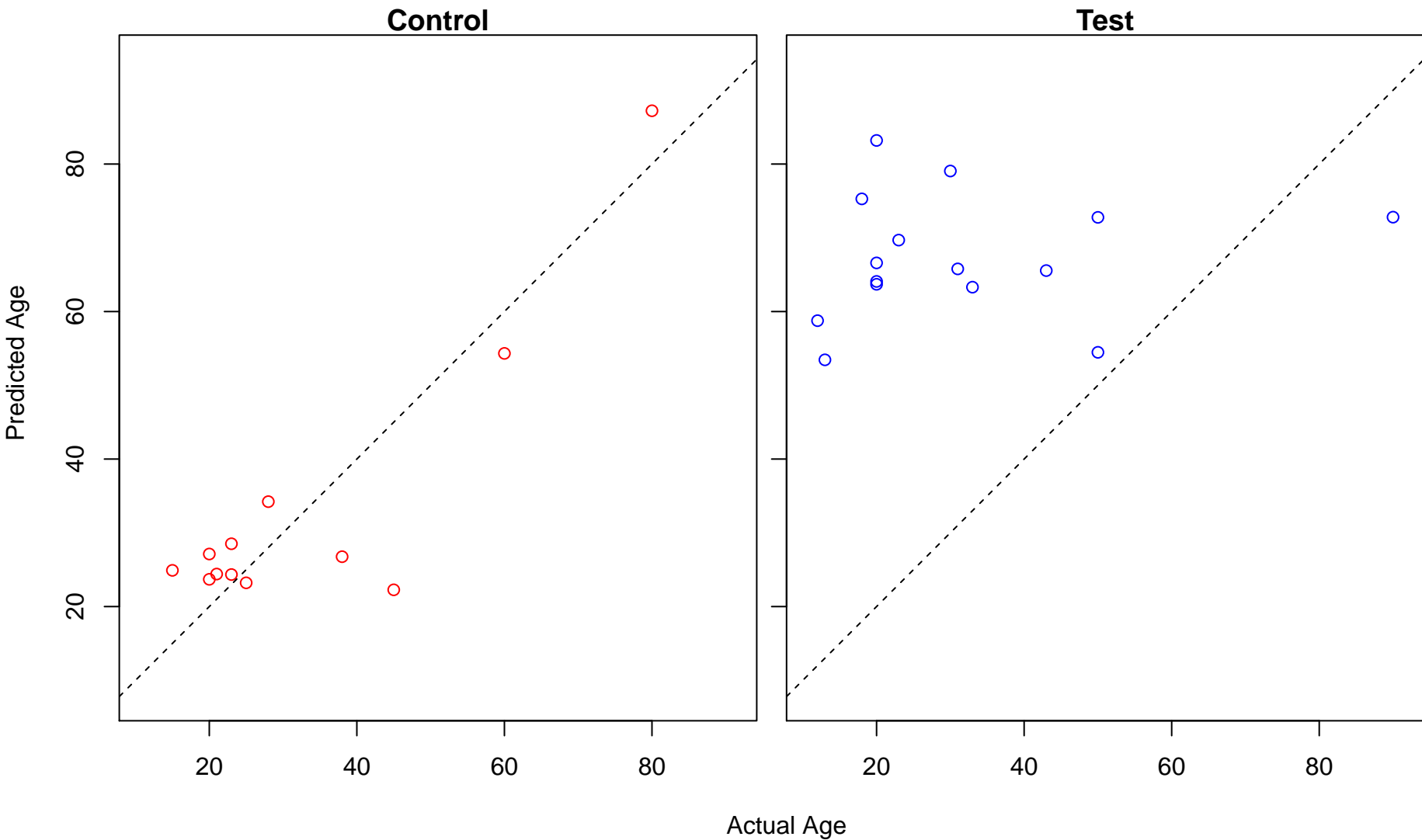


Actual Age

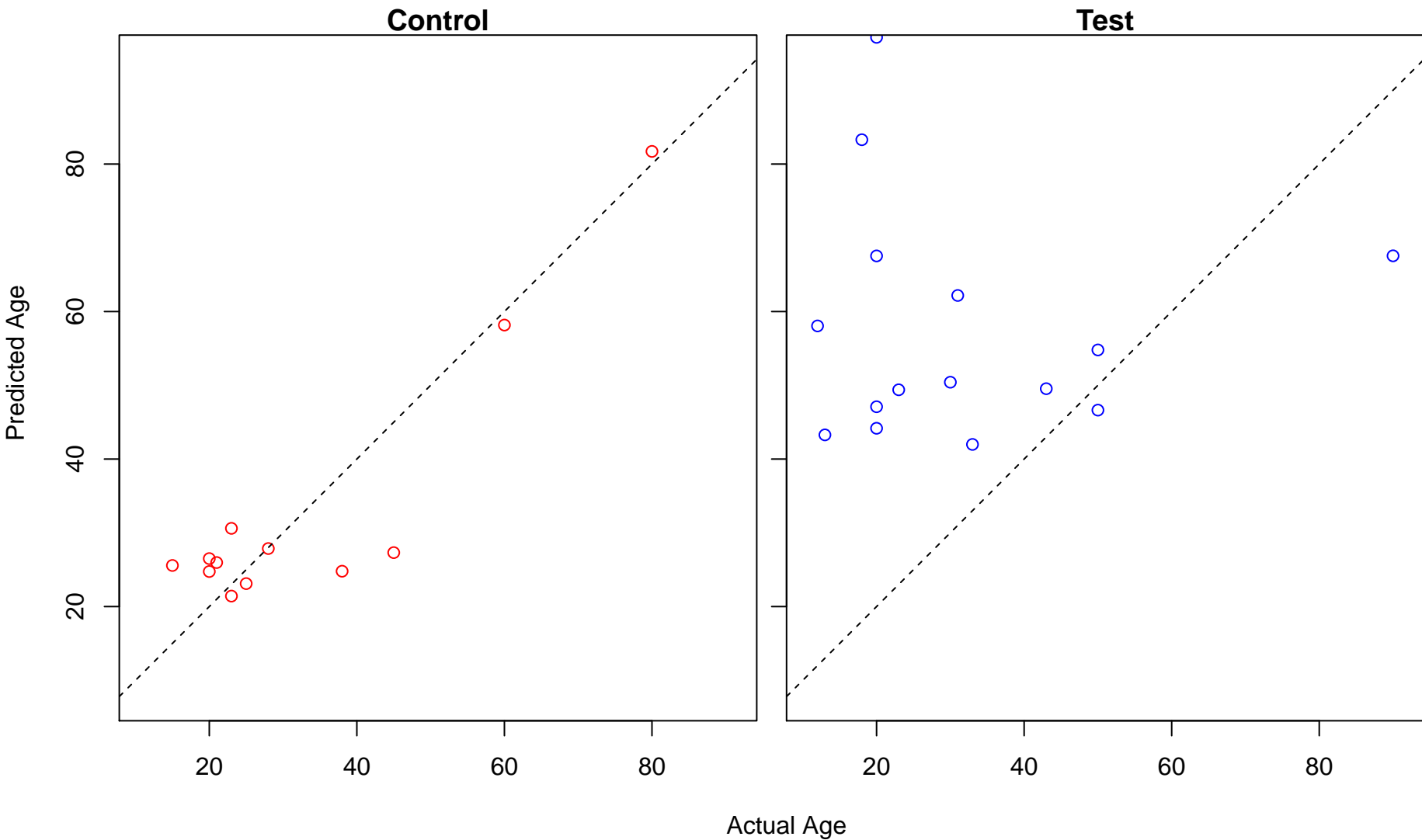
cation homeostasis (Score: 7.077538)



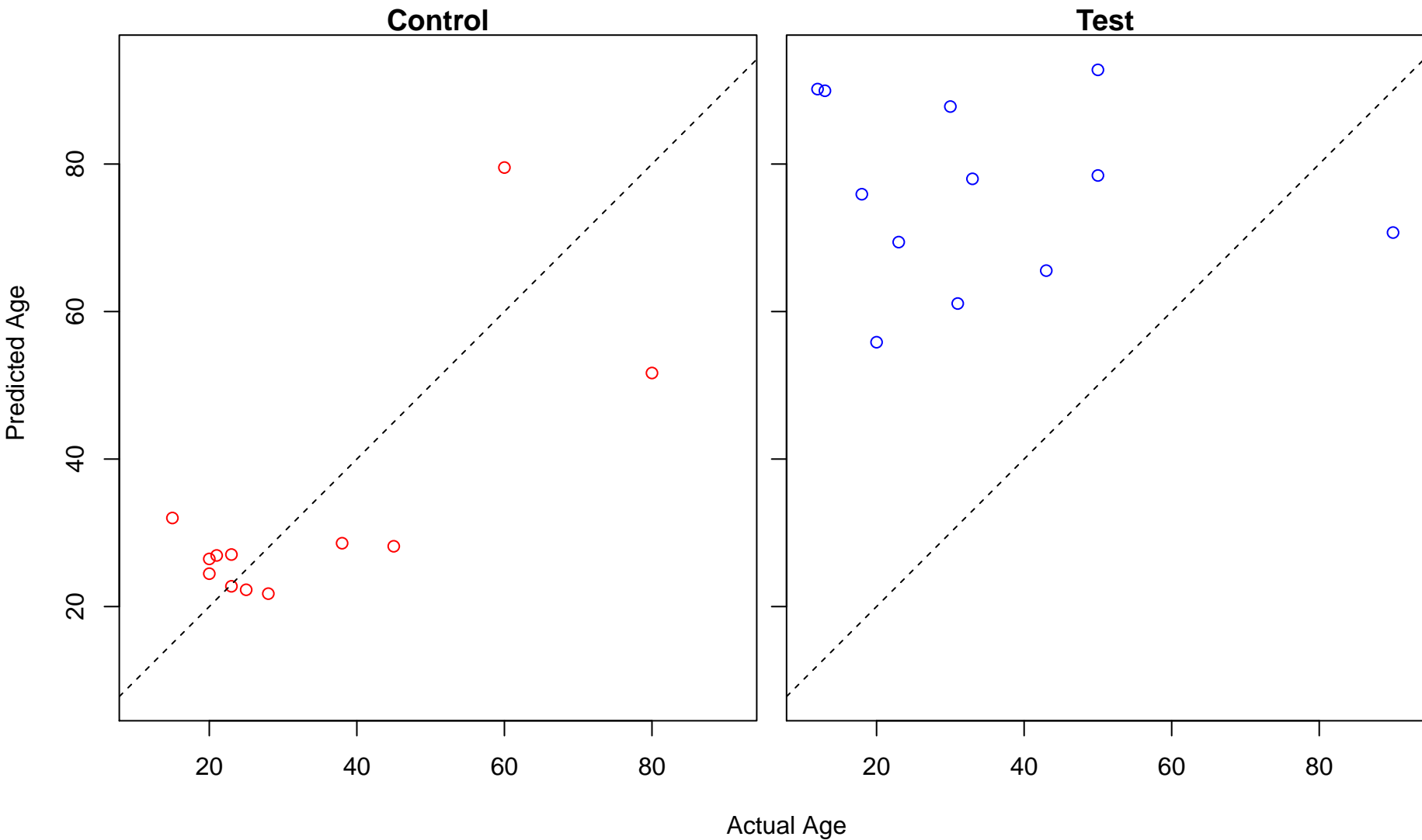
negative regulation of hemopoiesis (Score: 7.077506)



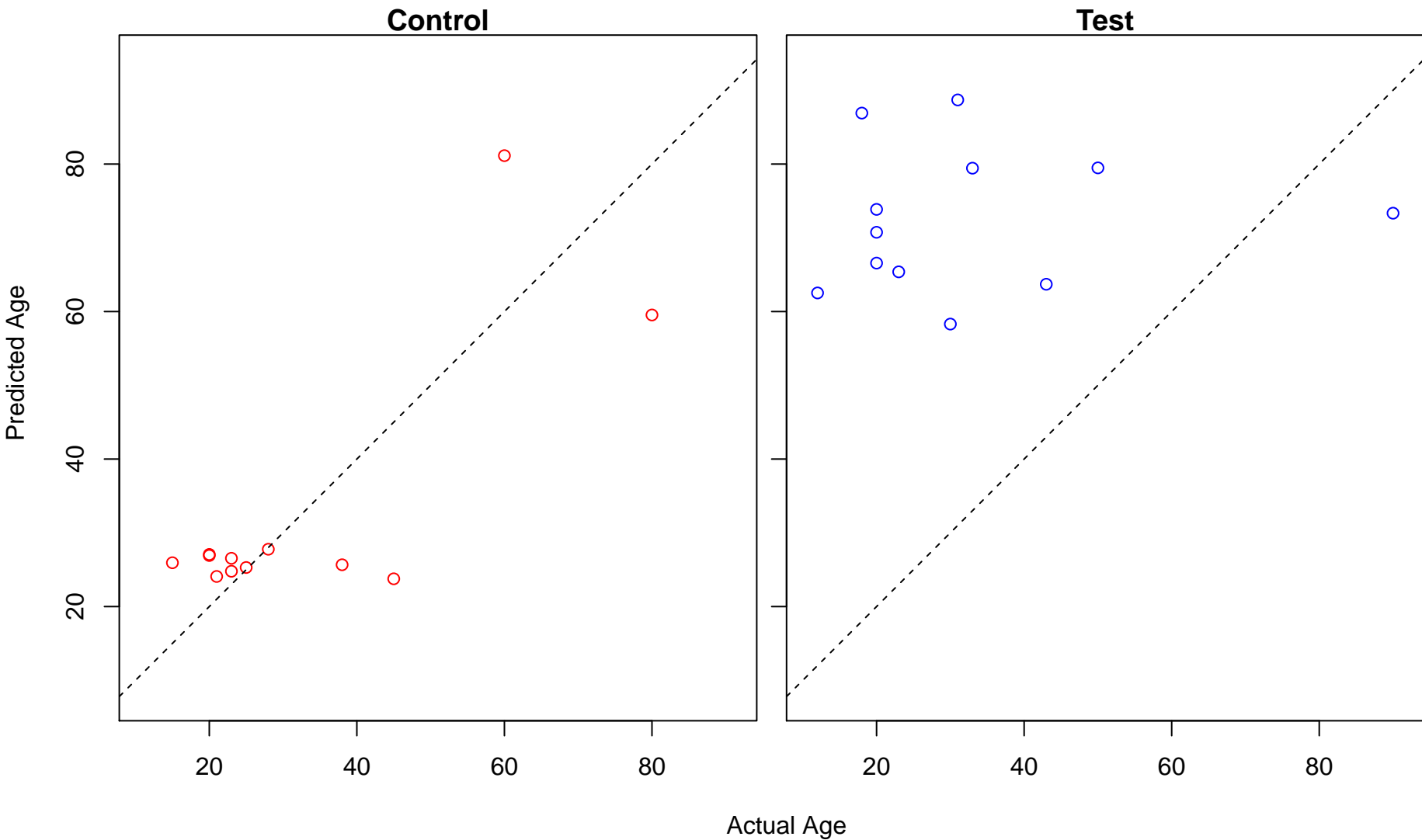
photoperiodism (Score: 7.076671)



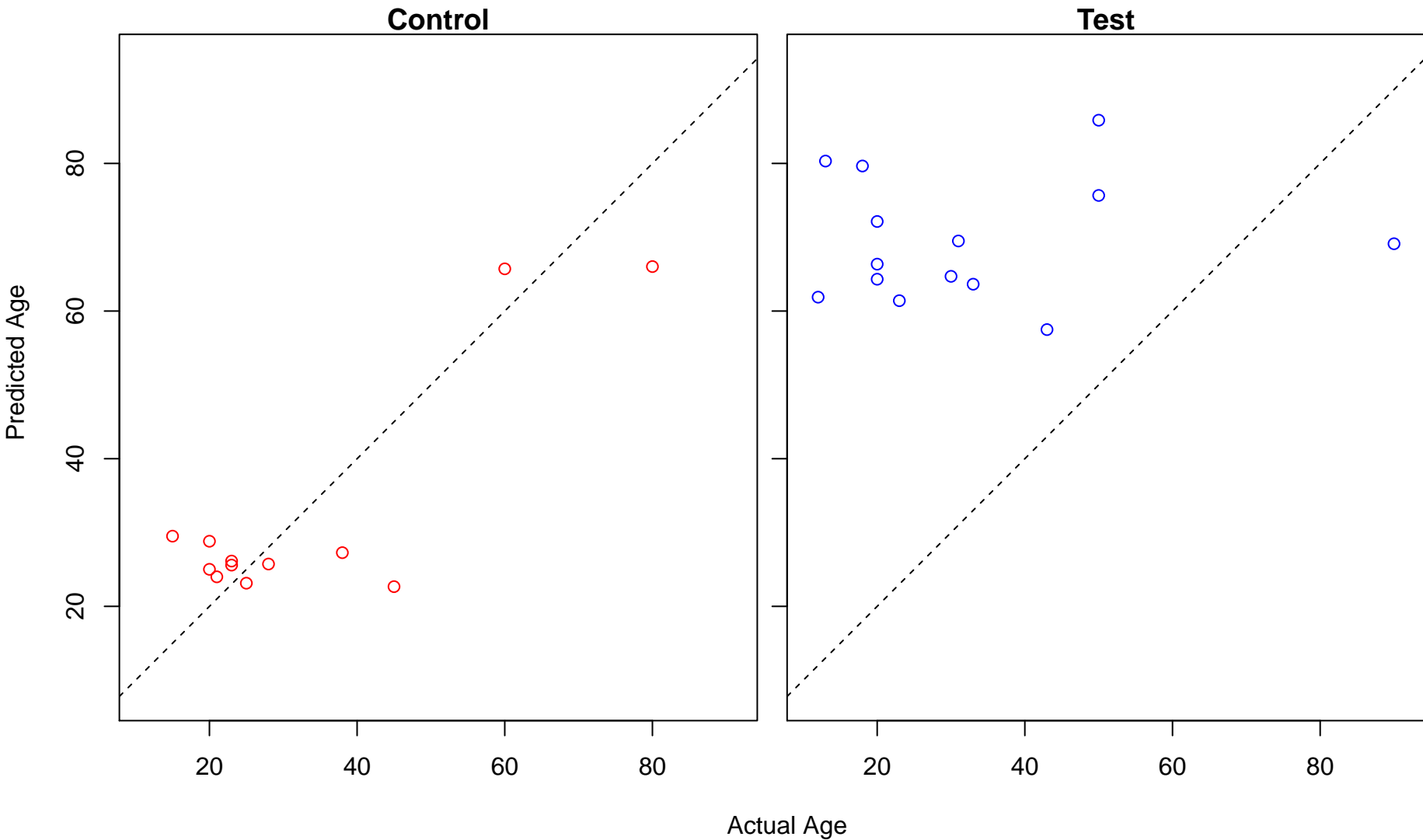
positive regulation of interleukin-1 beta production (Score: 7.074985)



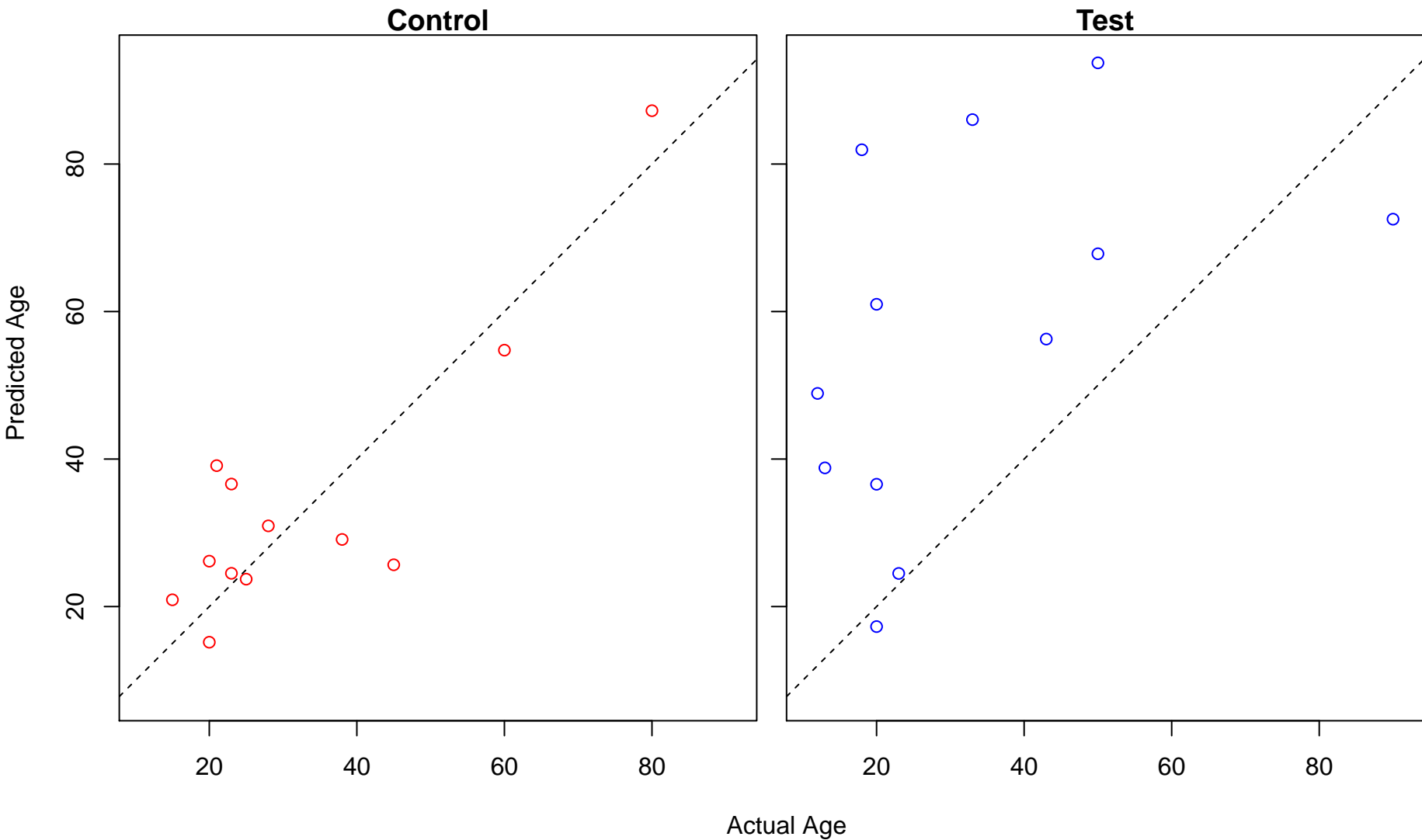
regulation of cell cycle G1/S phase transition (Score: 7.074774)



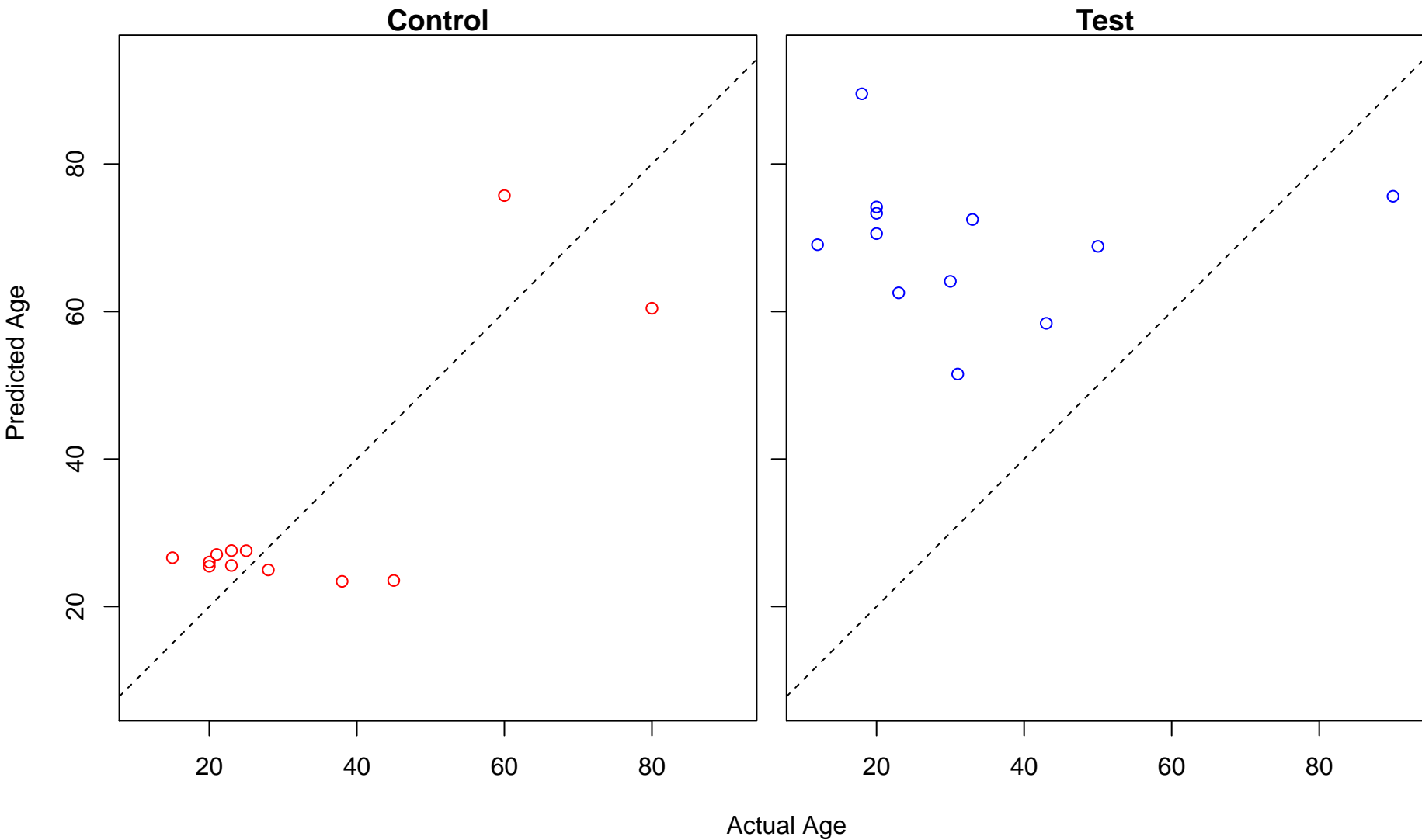
regulation of symbiosis, encompassing mutualism through parasitism (Score: 7.074404)



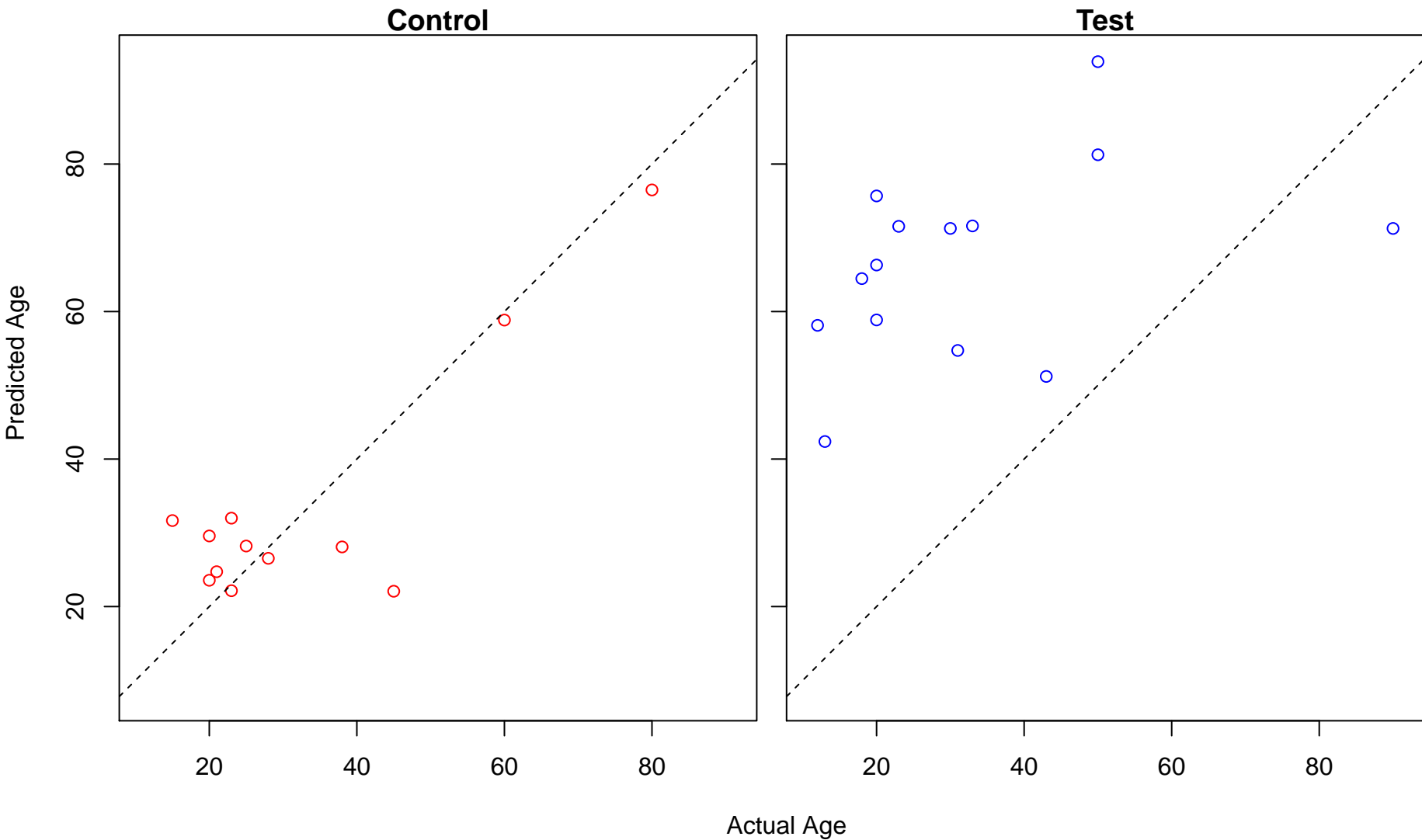
post-embryonic development (Score: 7.074066)



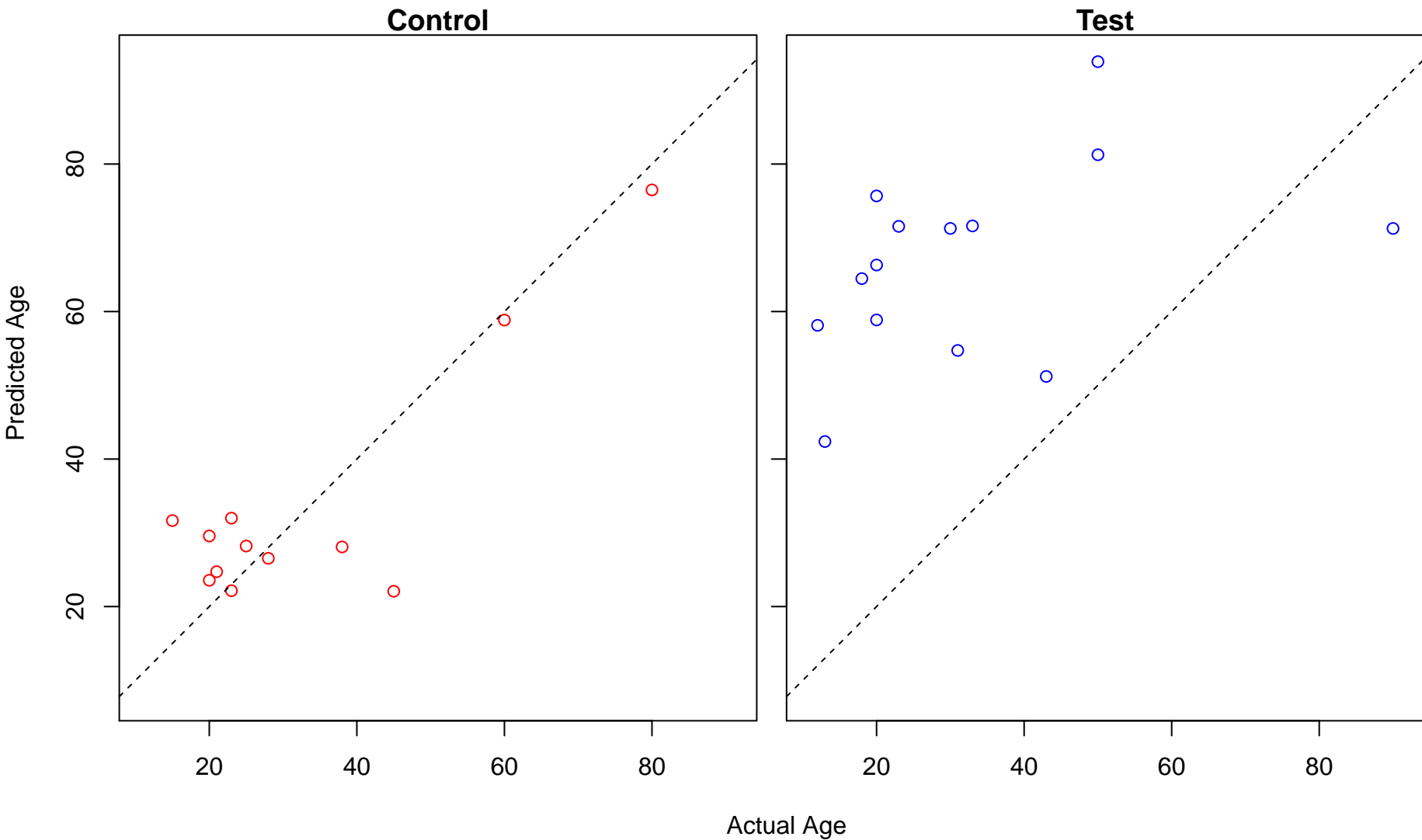
nucleobase-containing compound catabolic process (Score: 7.071034)



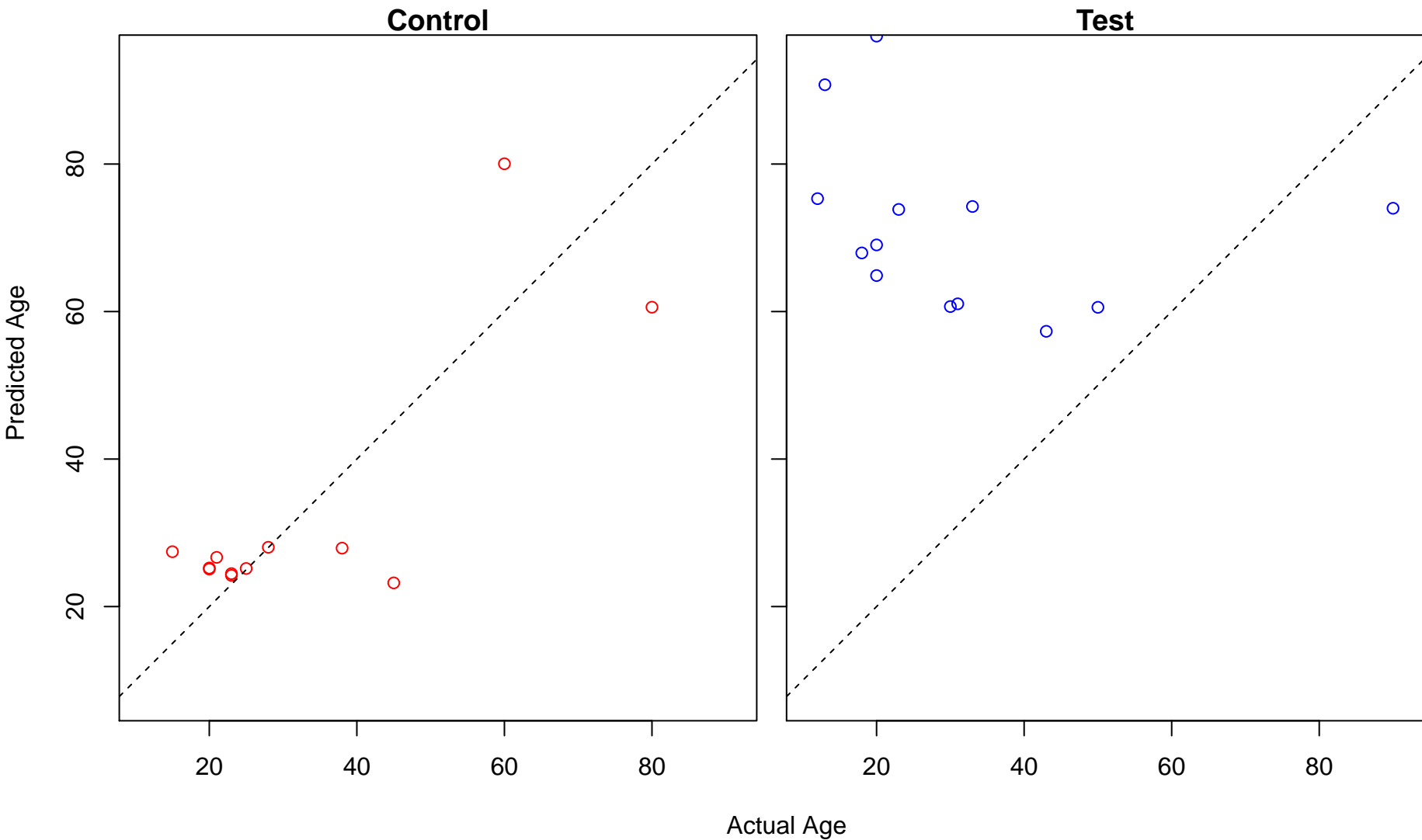
diol biosynthetic process (Score: 7.068936)



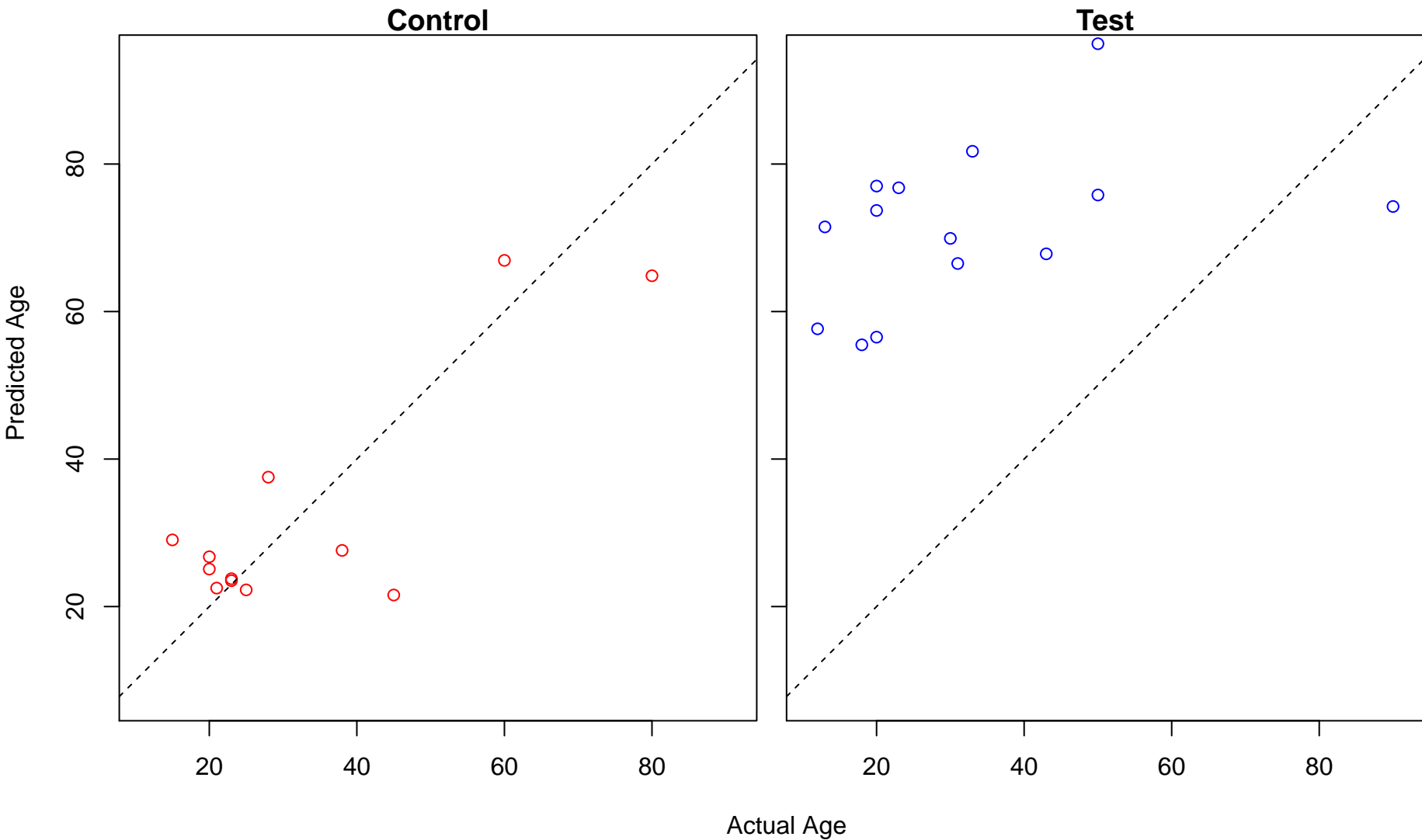
sphingosine biosynthetic process (Score: 7.068936)



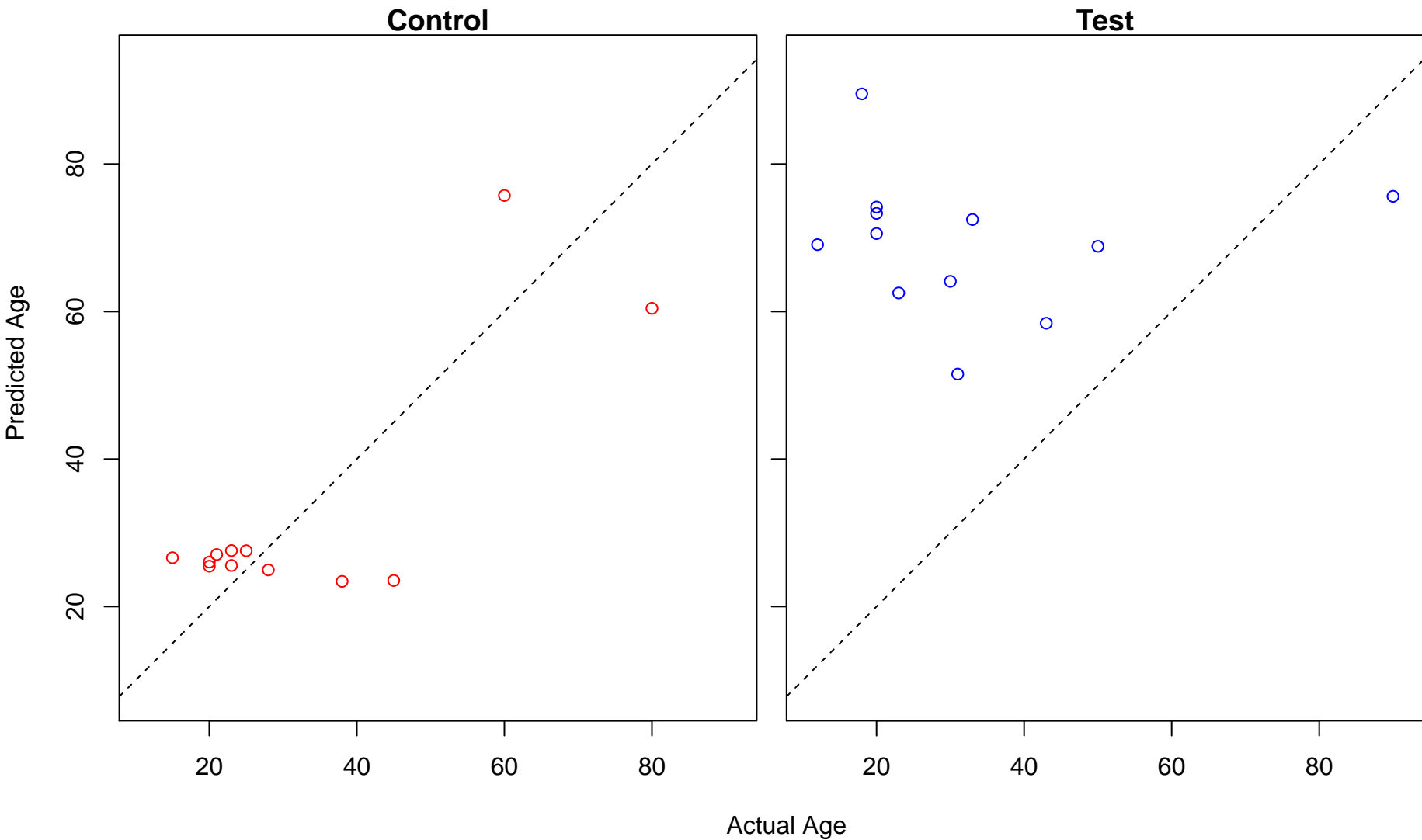
leukocyte mediated cytotoxicity (Score: 7.066753)



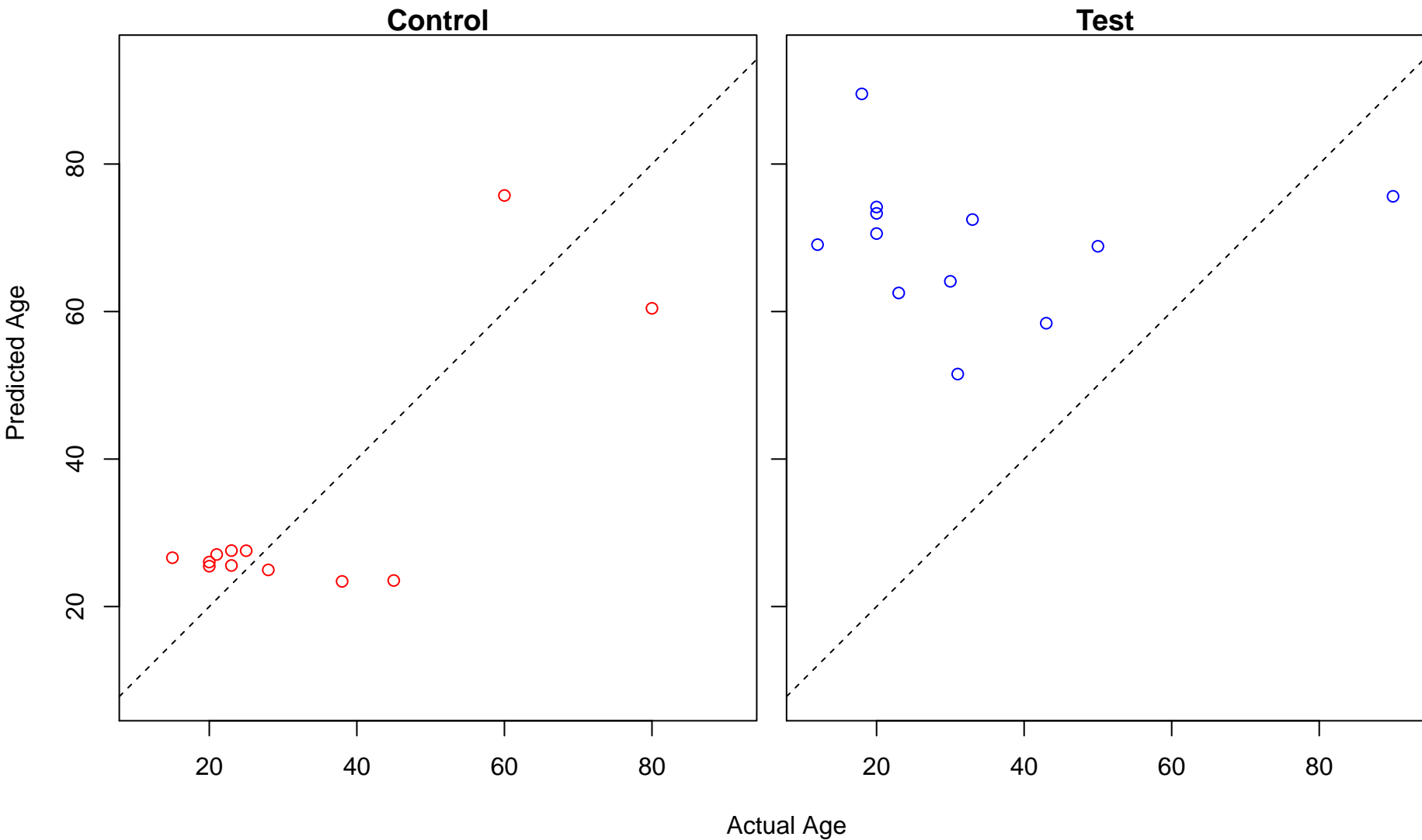
regulation of extracellular matrix disassembly (Score: 7.066434)



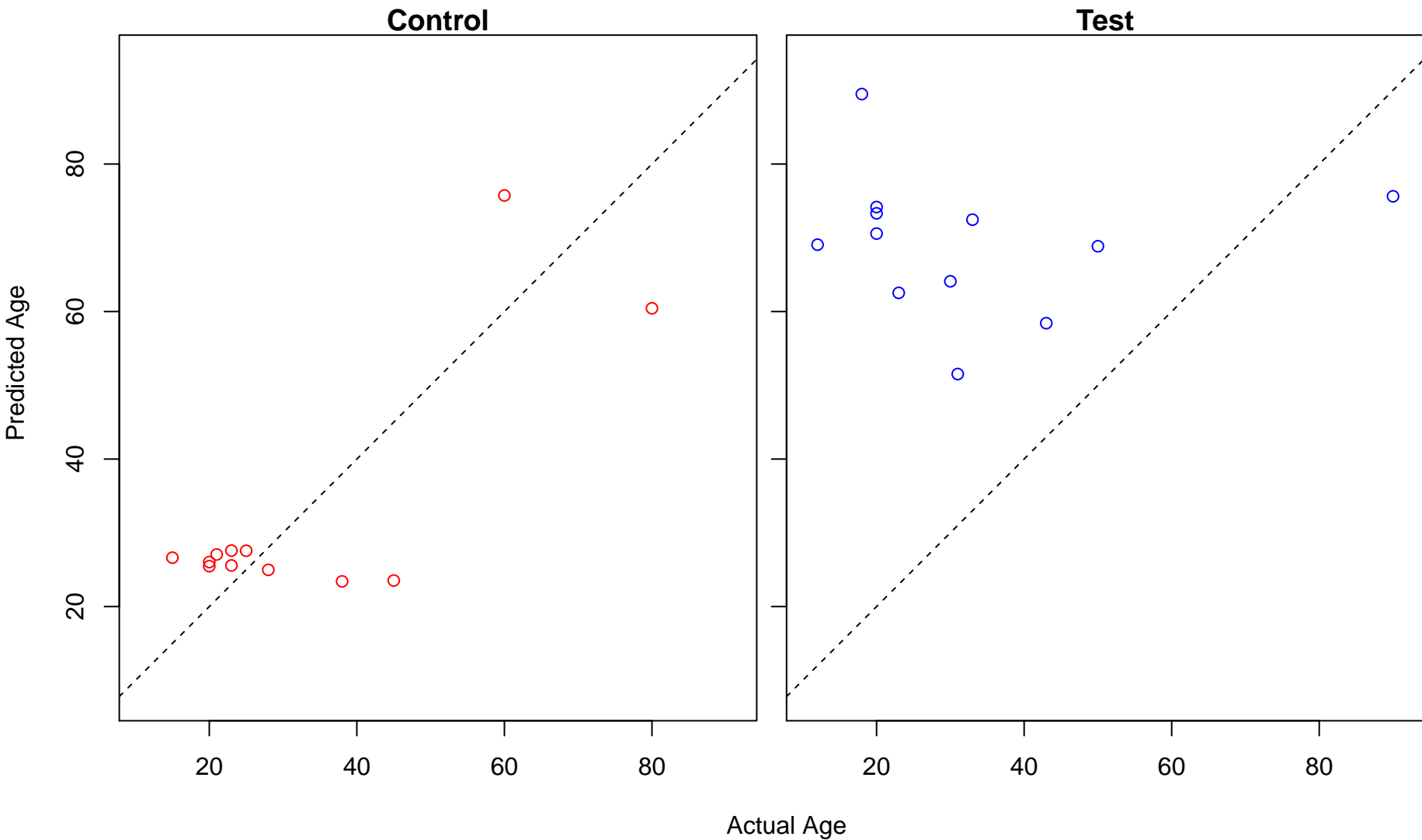
cellular nitrogen compound catabolic process (Score: 7.065315)



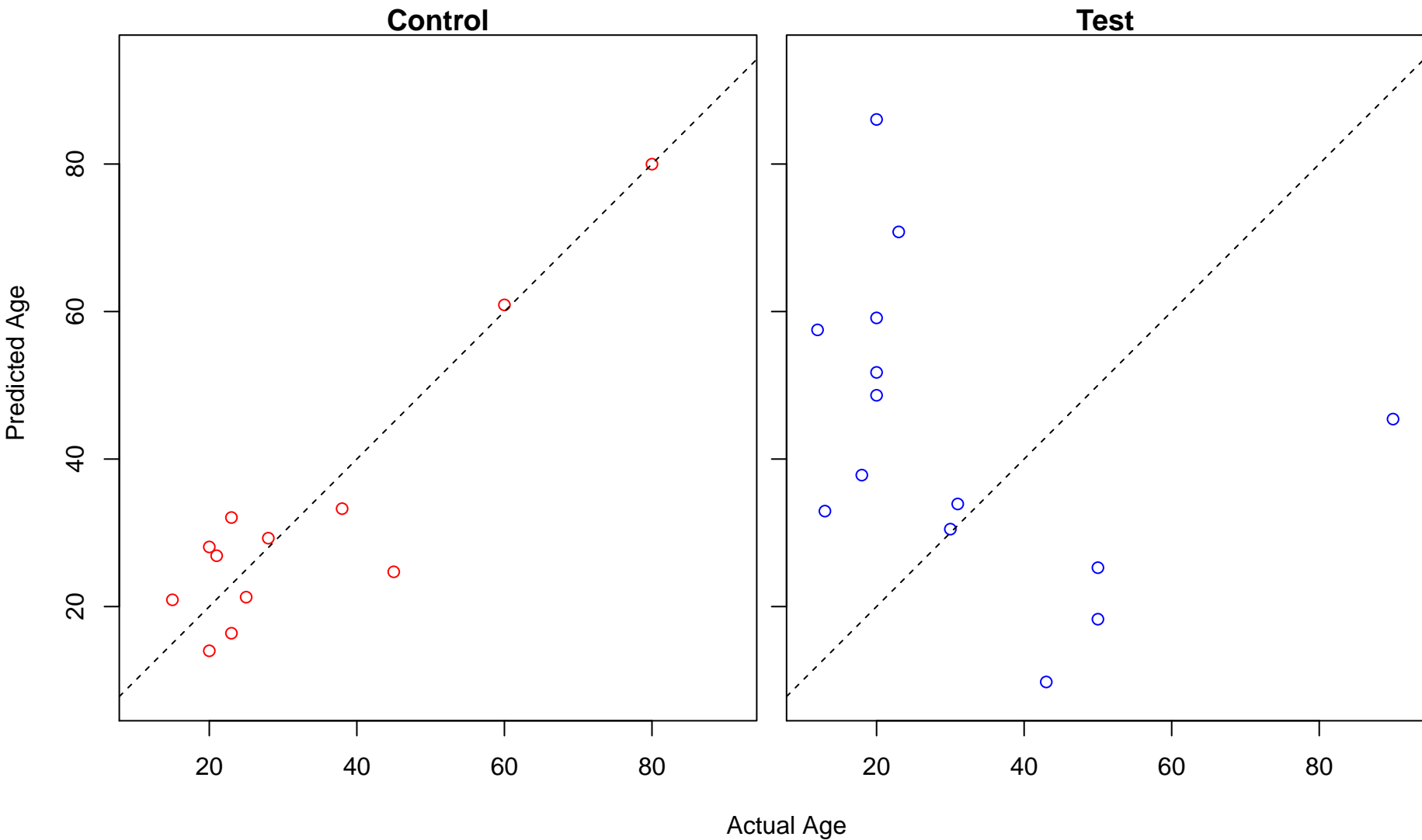
heterocycle catabolic process (Score: 7.064831)



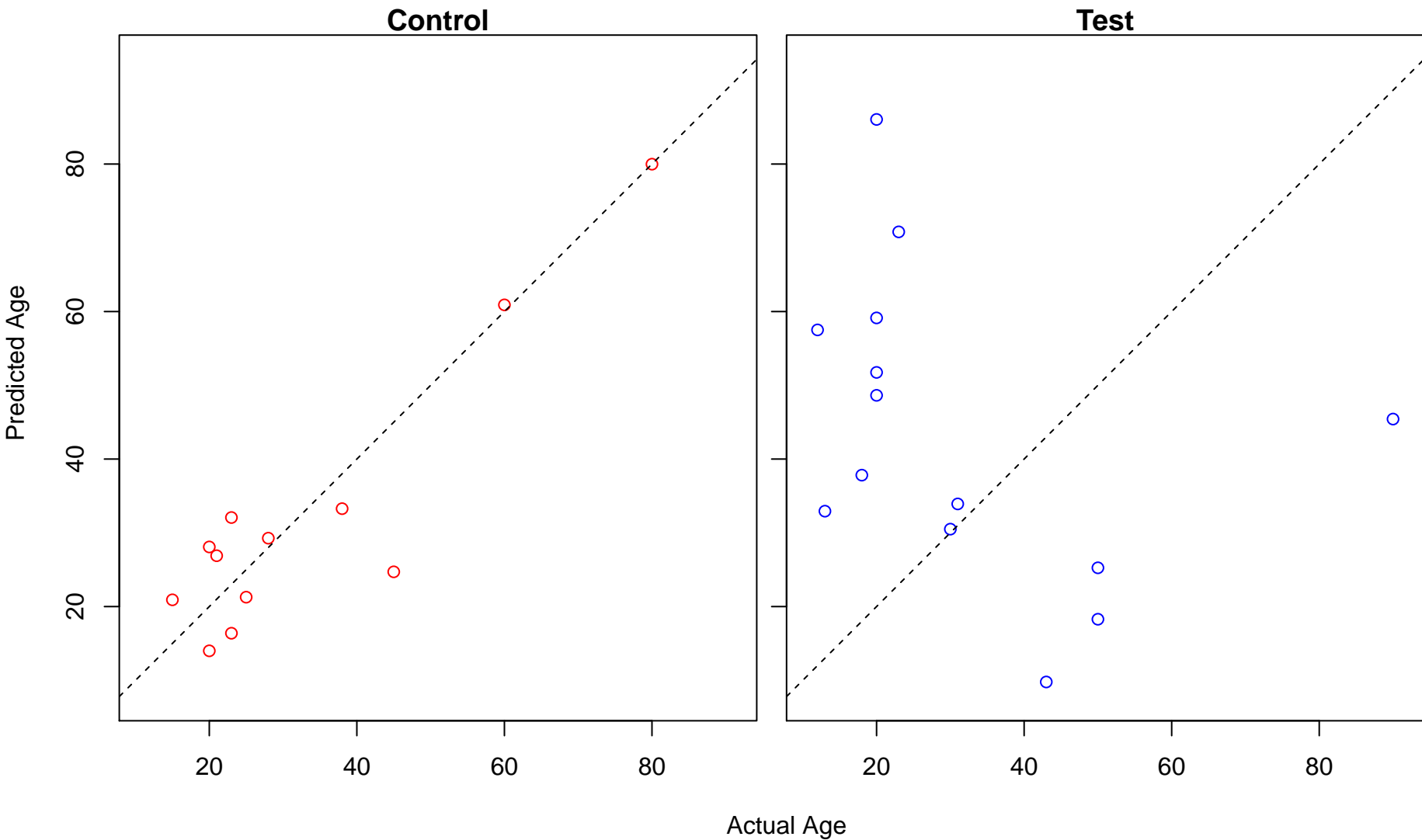
aromatic compound catabolic process (Score: 7.063262)



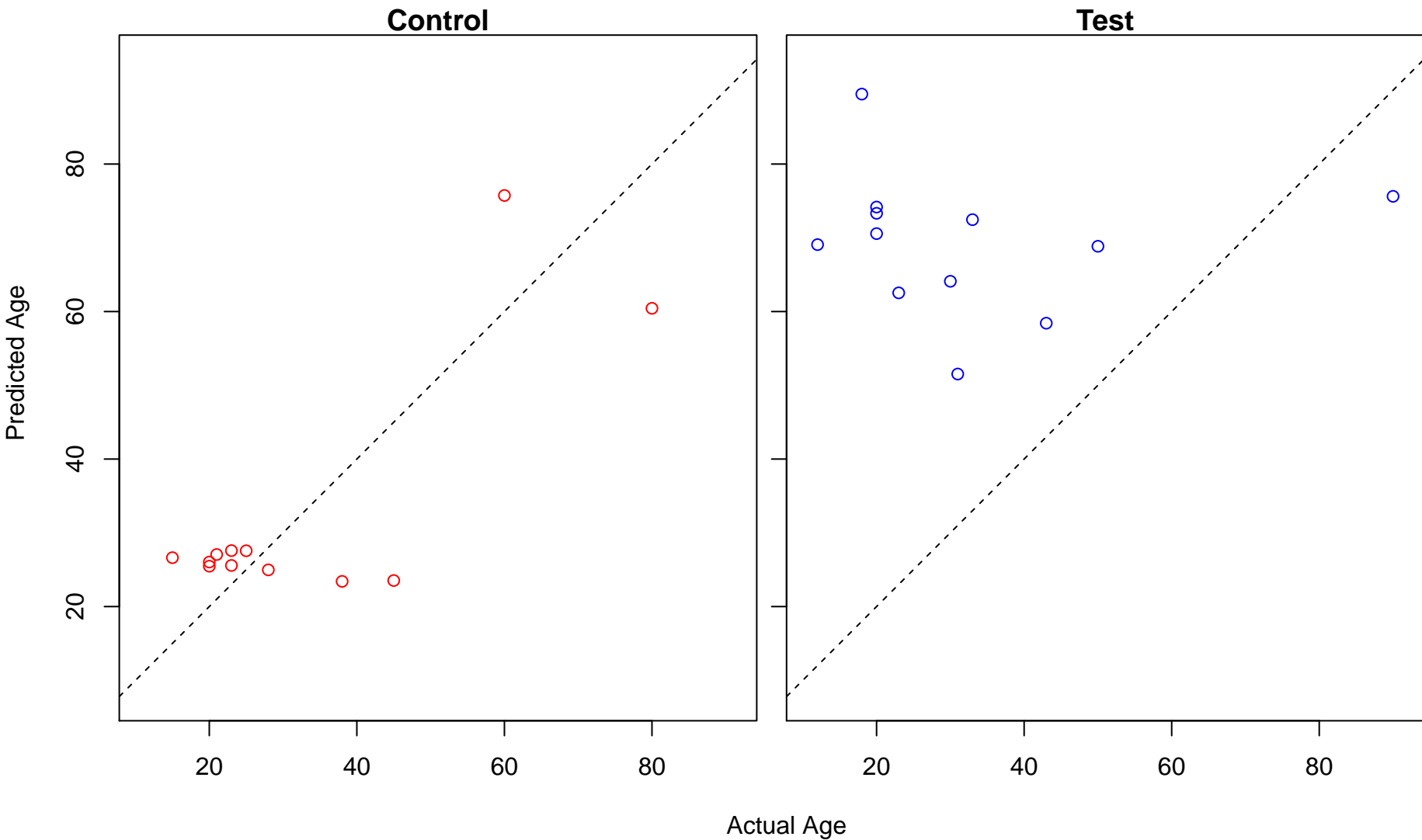
response to thyroid hormone (Score: 7.063023)



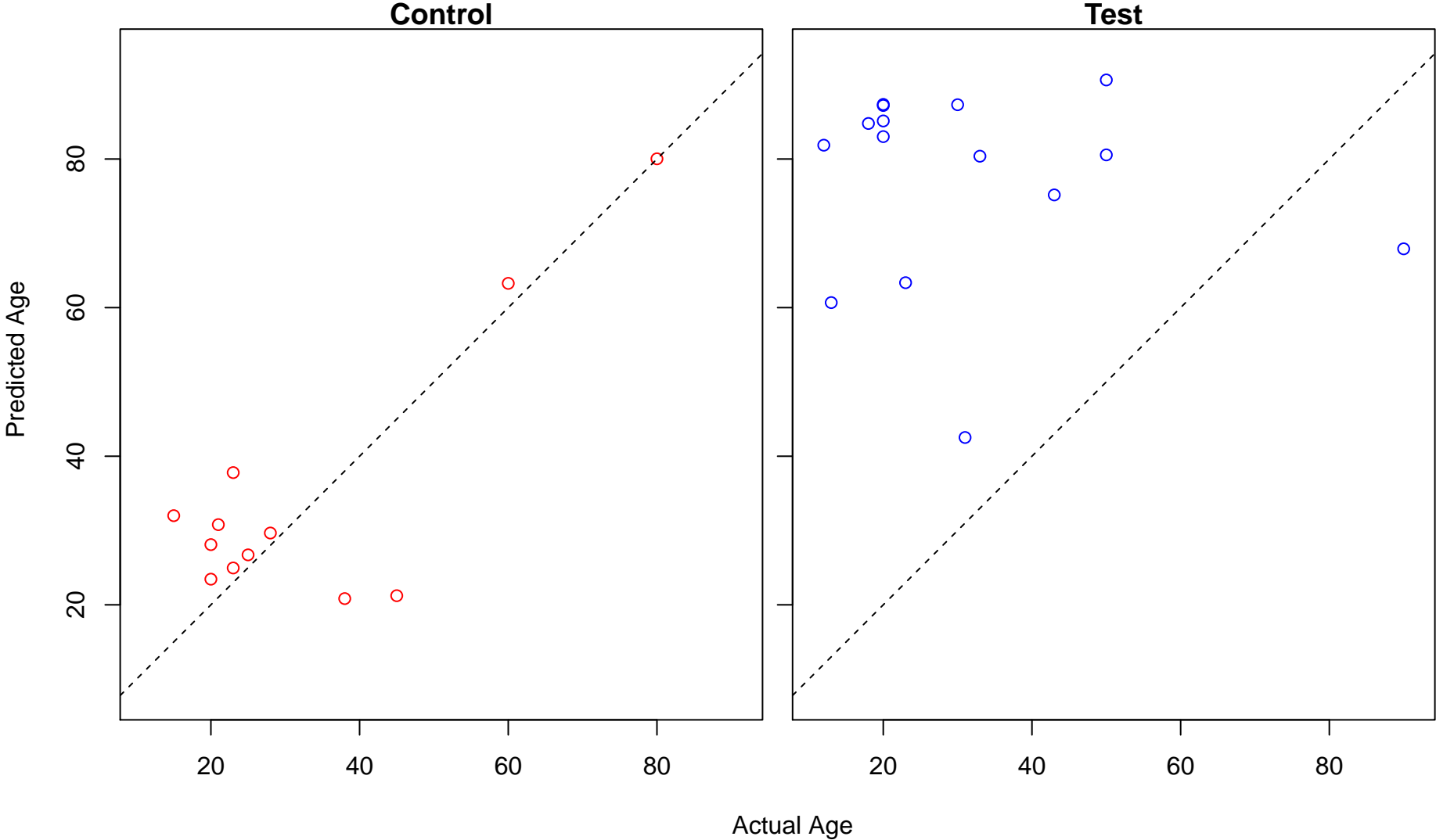
cellular response to thyroid hormone stimulus (Score: 7.062956)



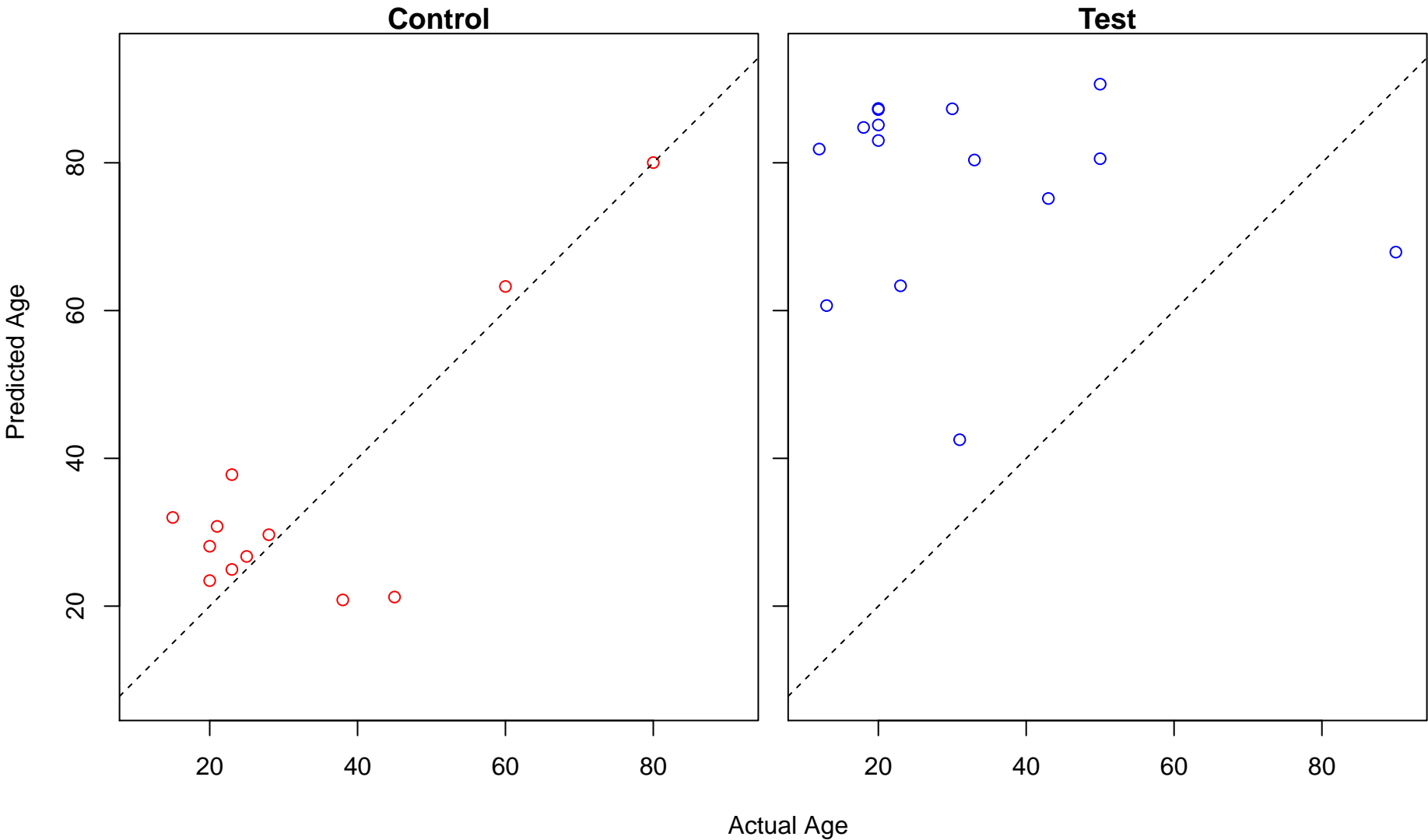
organic cyclic compound catabolic process (Score: 7.062934)



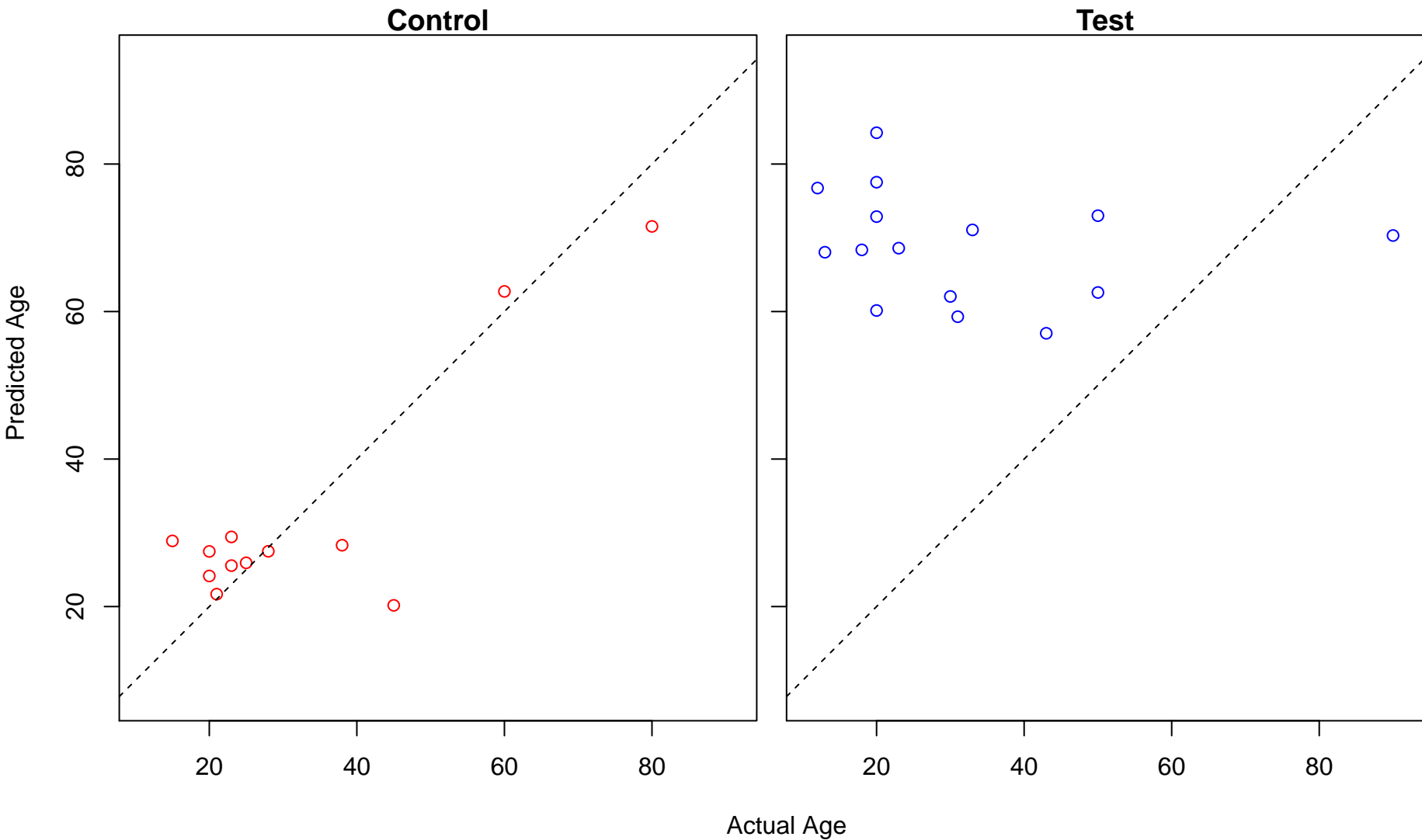
positive regulation of mitochondrial membrane permeability involved in apoptotic process (Score: 7.06)



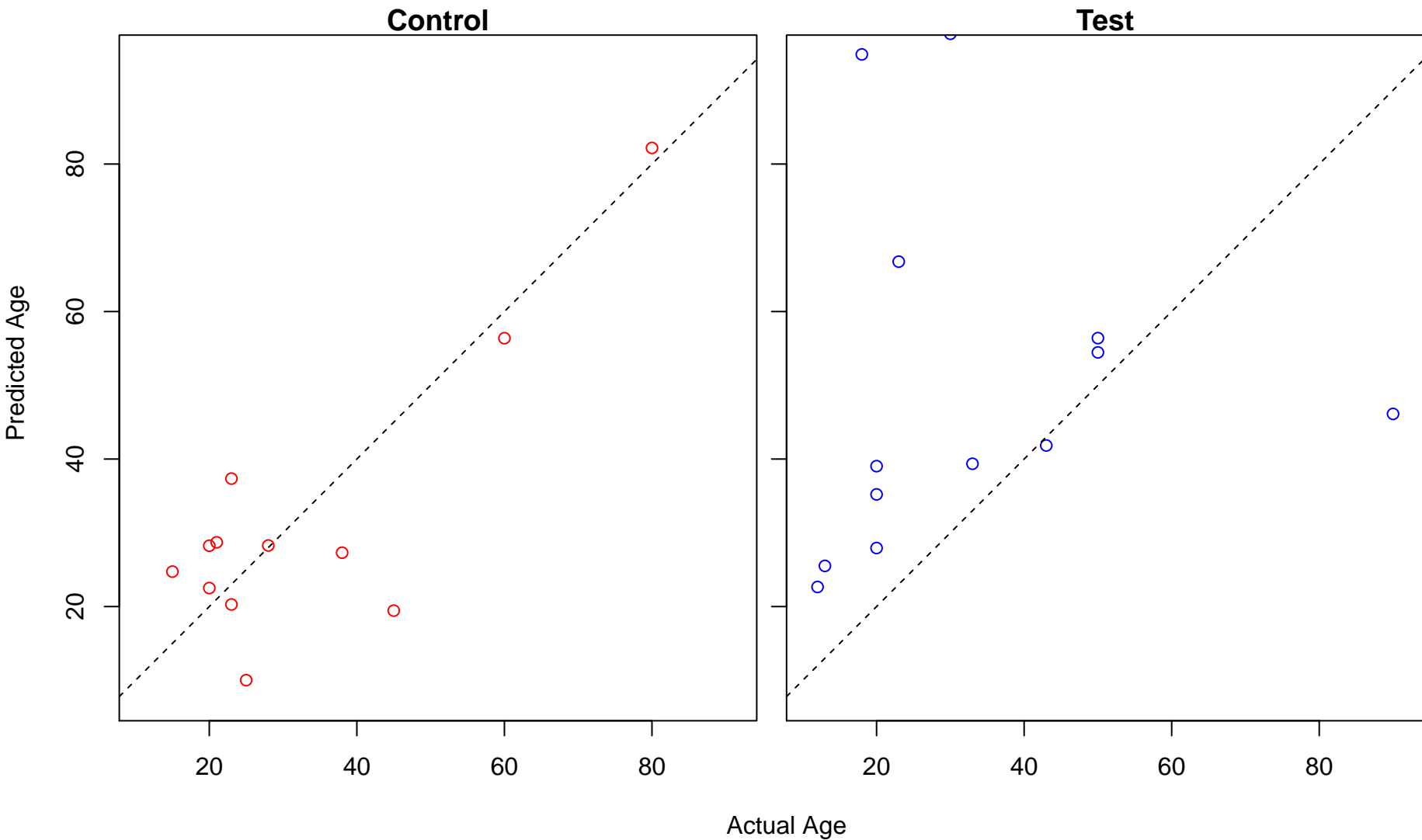
mitochondrial outer membrane permeabilization involved in programmed cell death (Score: 7.06219)



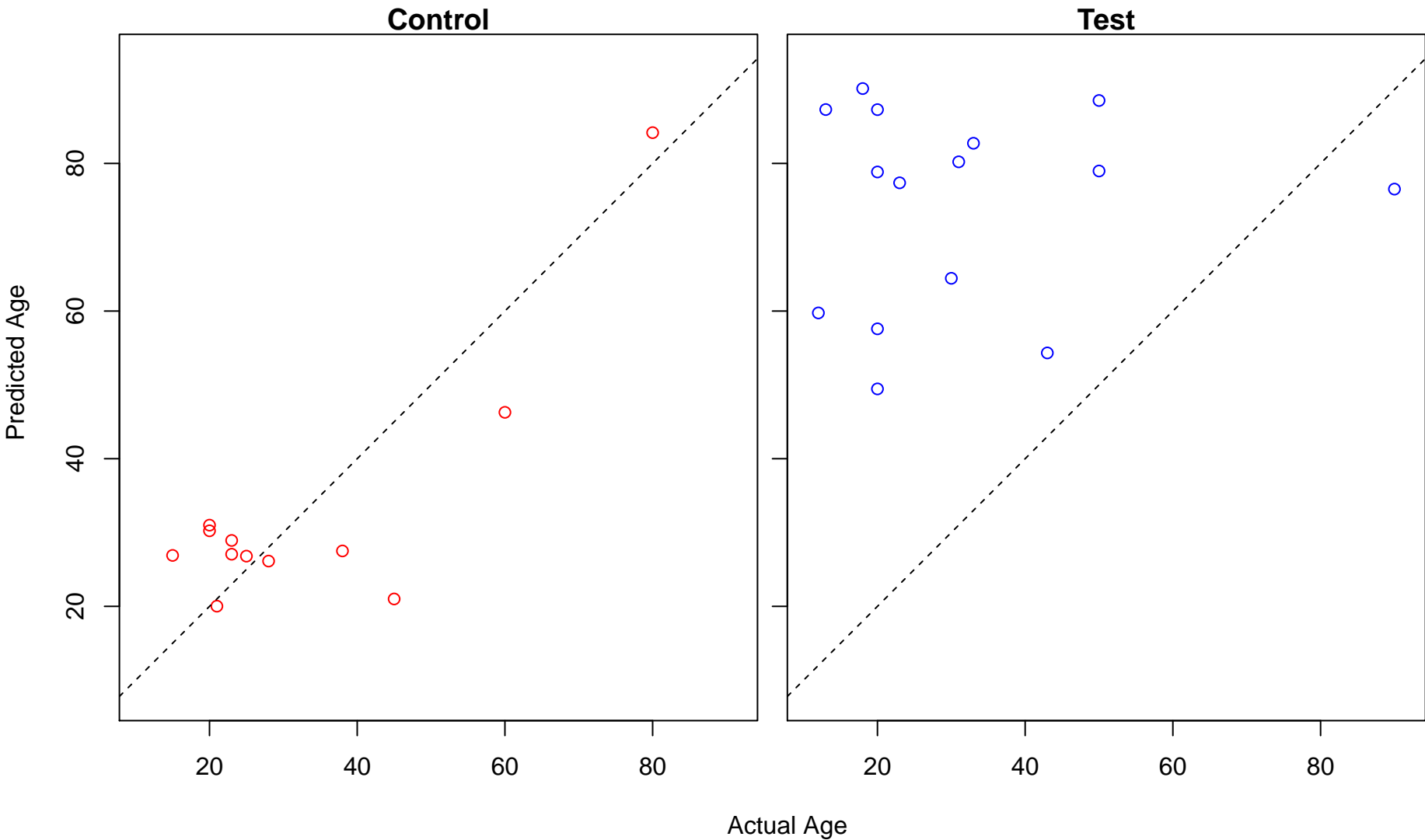
regulation of osteoblast differentiation (Score: 7.057634)



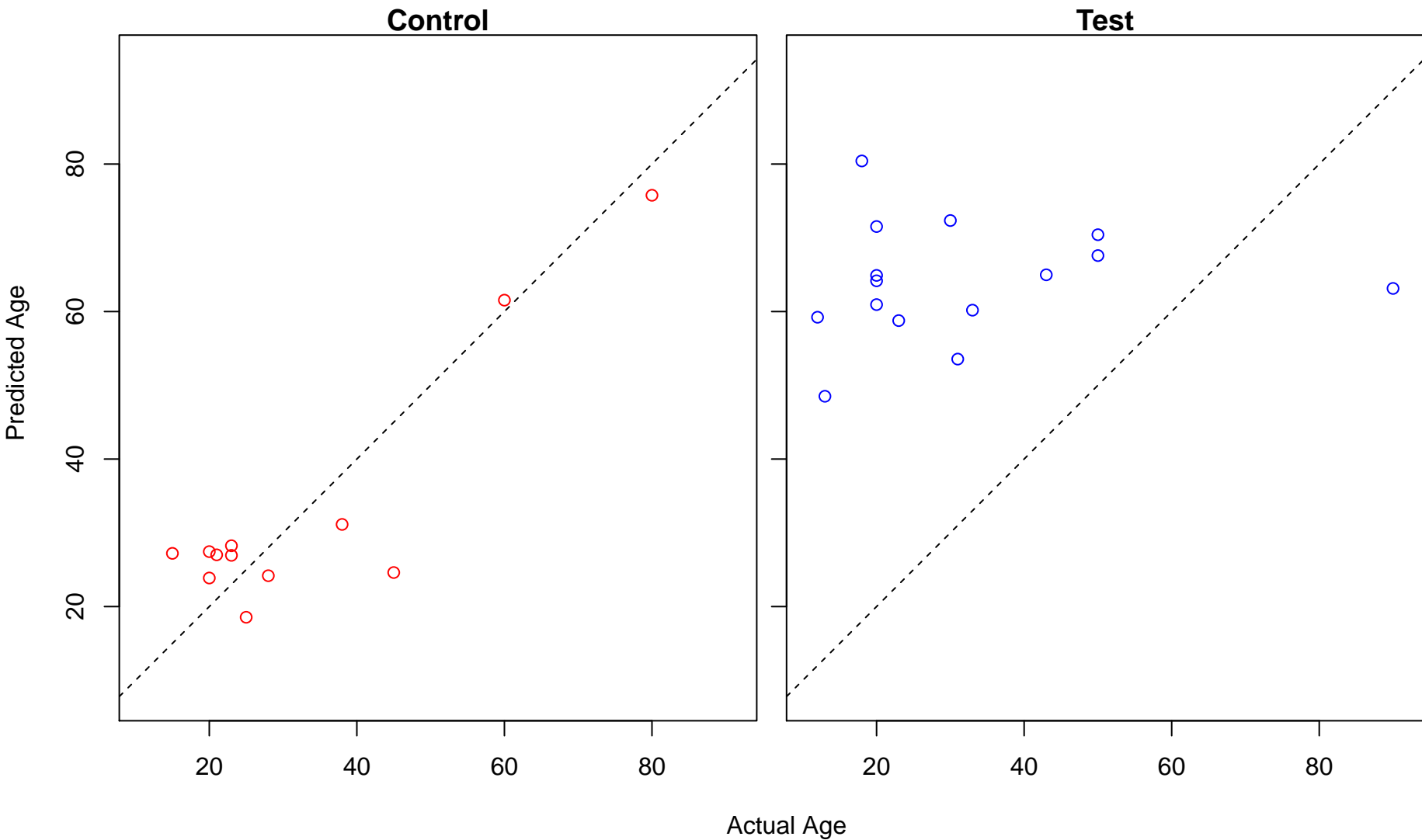
regulation of leukocyte activation (Score: 7.057213)



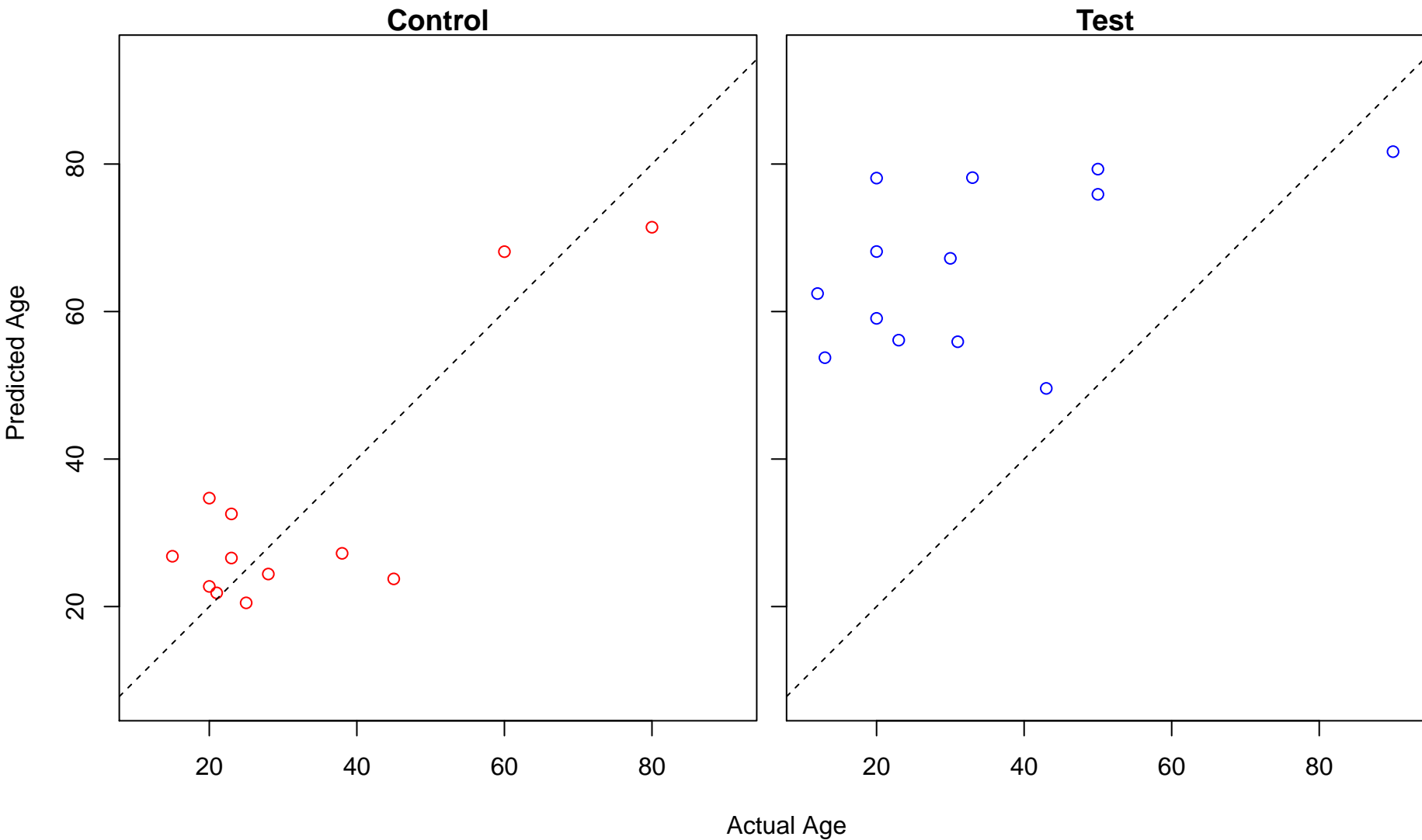
negative regulation of vascular endothelial growth factor signaling pathway (Score: 7.057196)



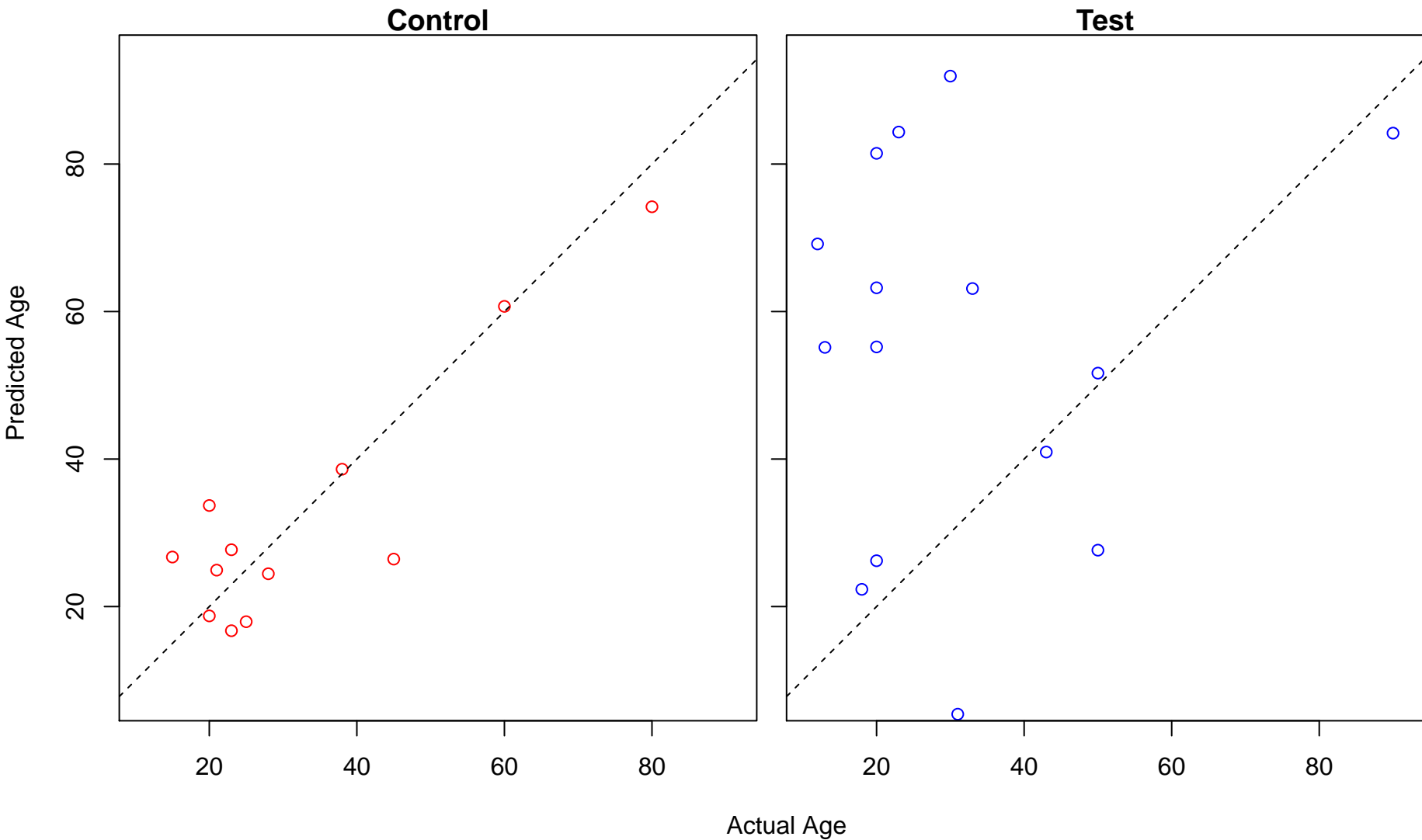
steroid metabolic process (Score: 7.052902)



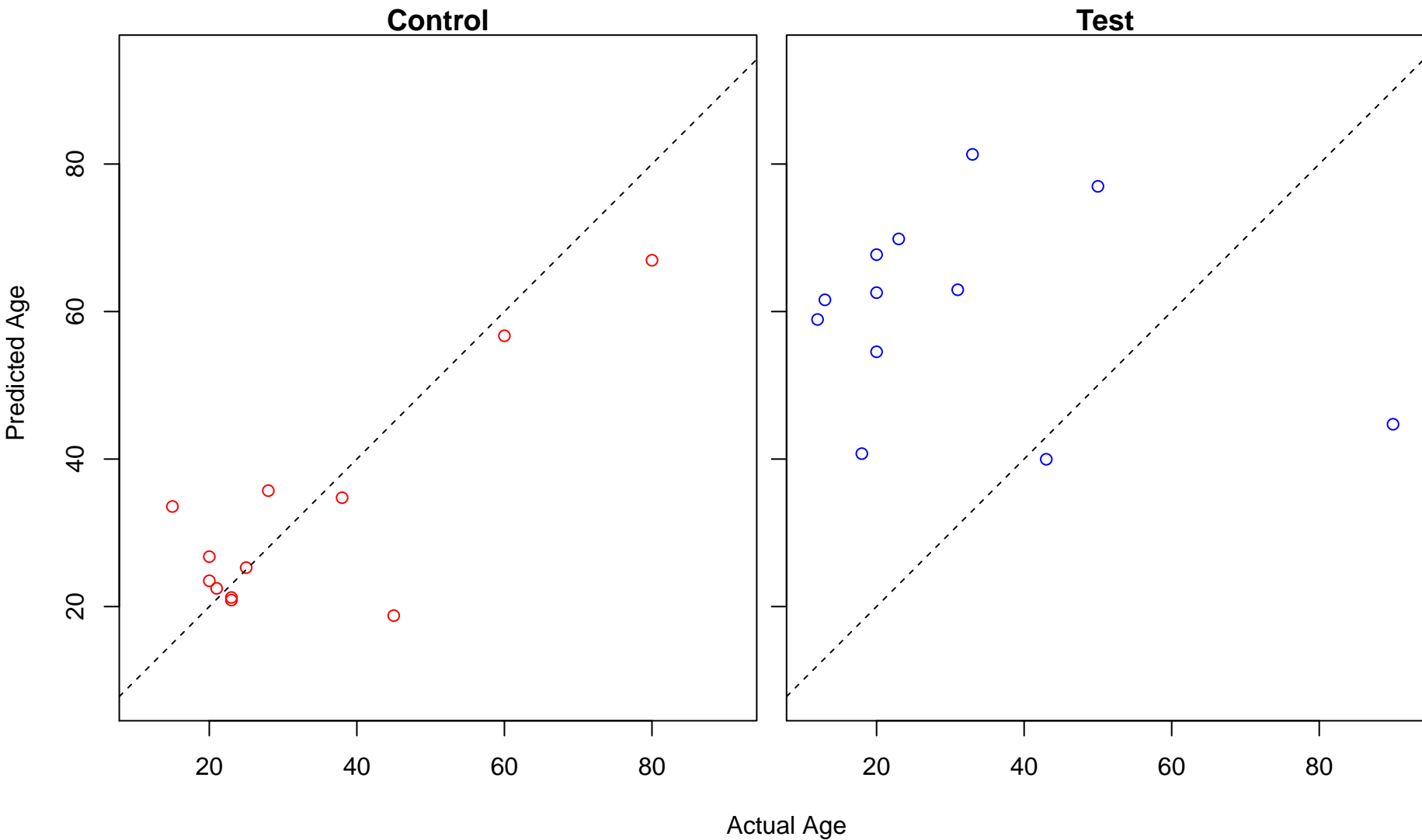
glutamate secretion (Score: 7.050998)



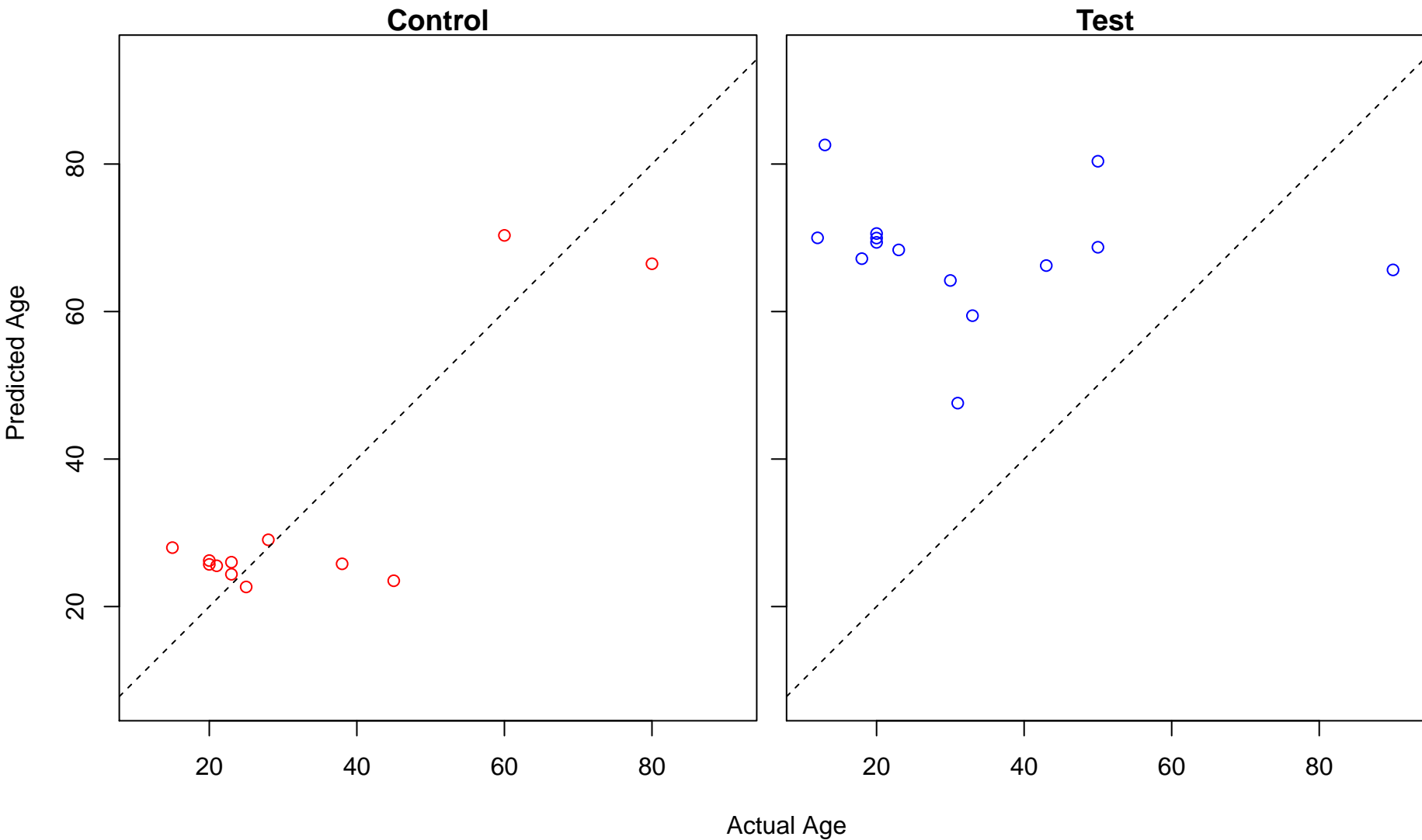
endocrine system development (Score: 7.049930)



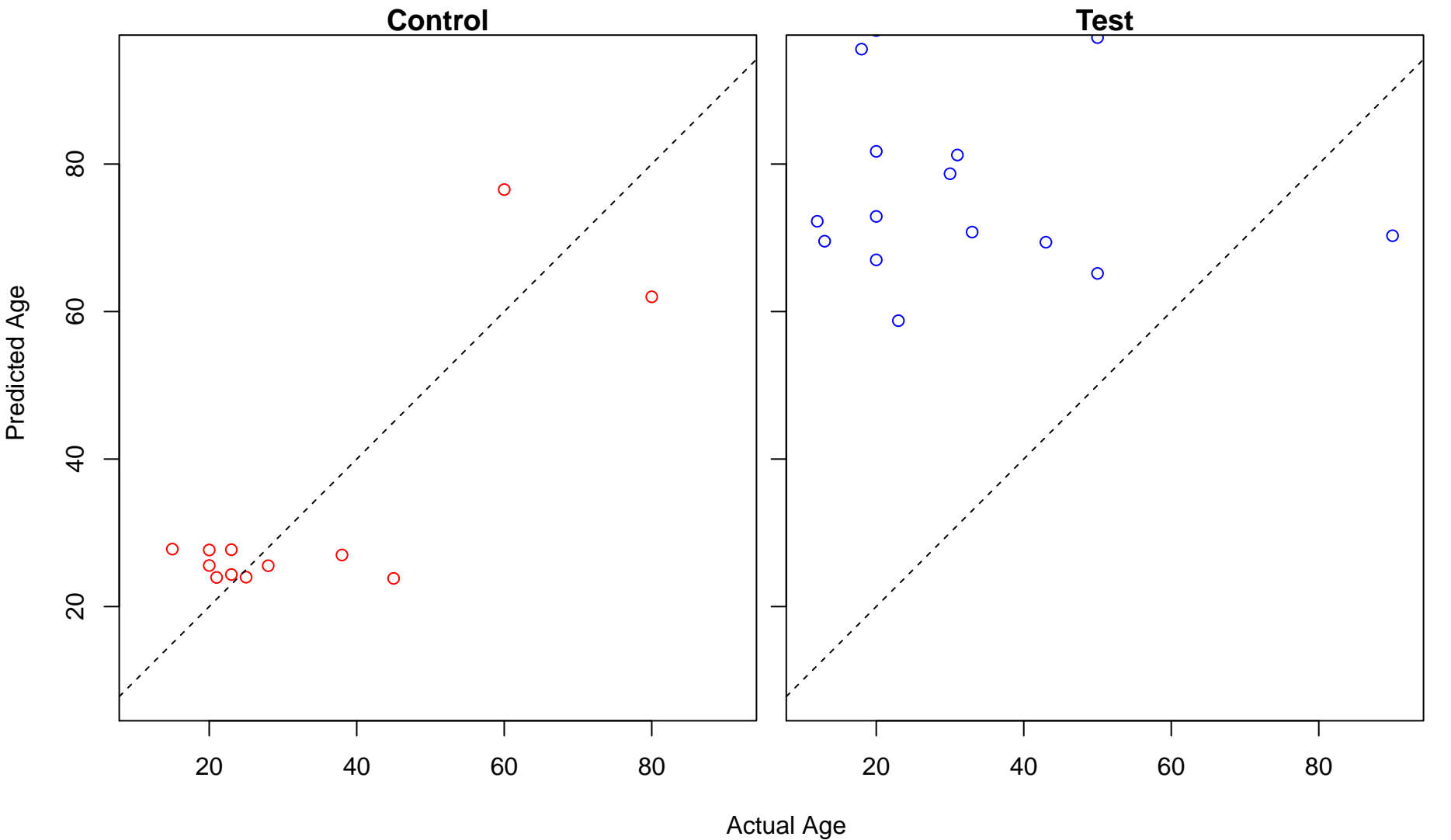
one-carbon compound transport (Score: 7.049711)



glutathione metabolic process (Score: 7.049160)

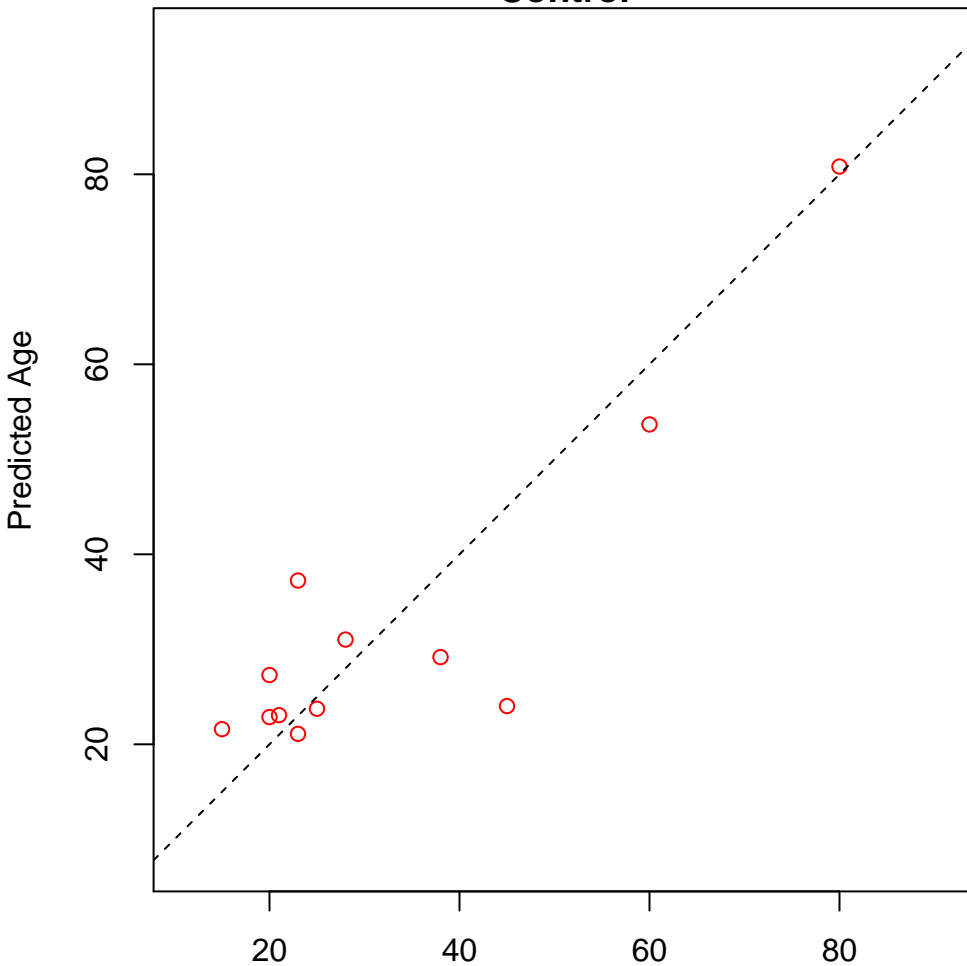


regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress

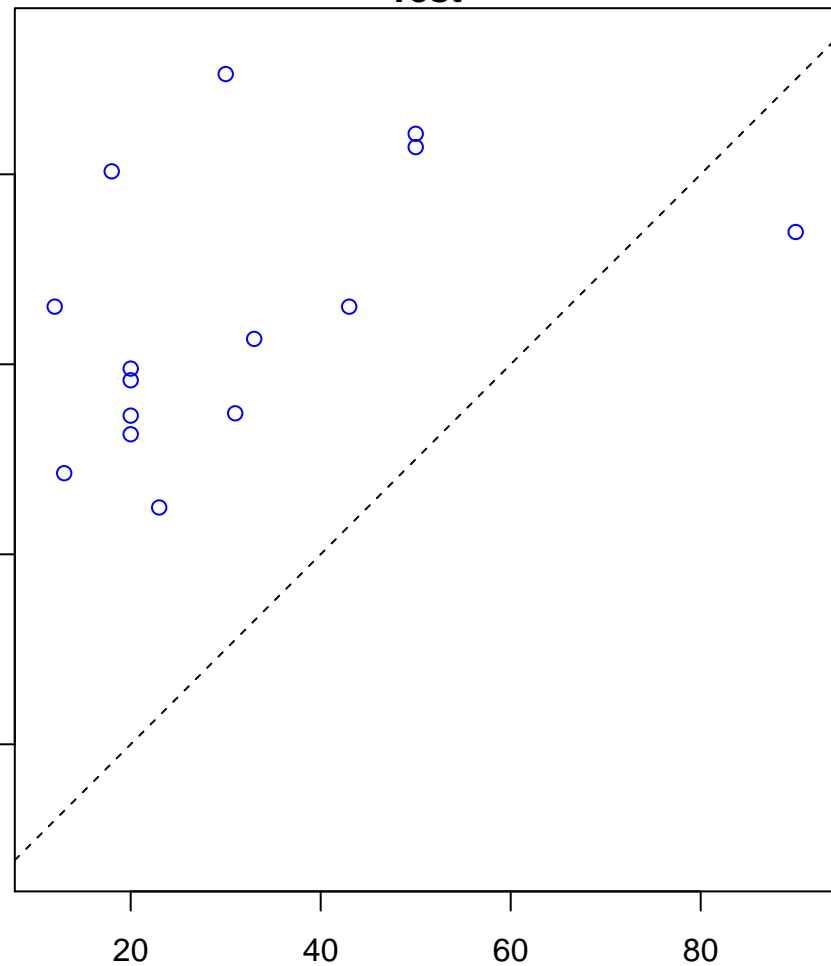


mesodermal cell fate commitment (Score: 7.045408)

Control

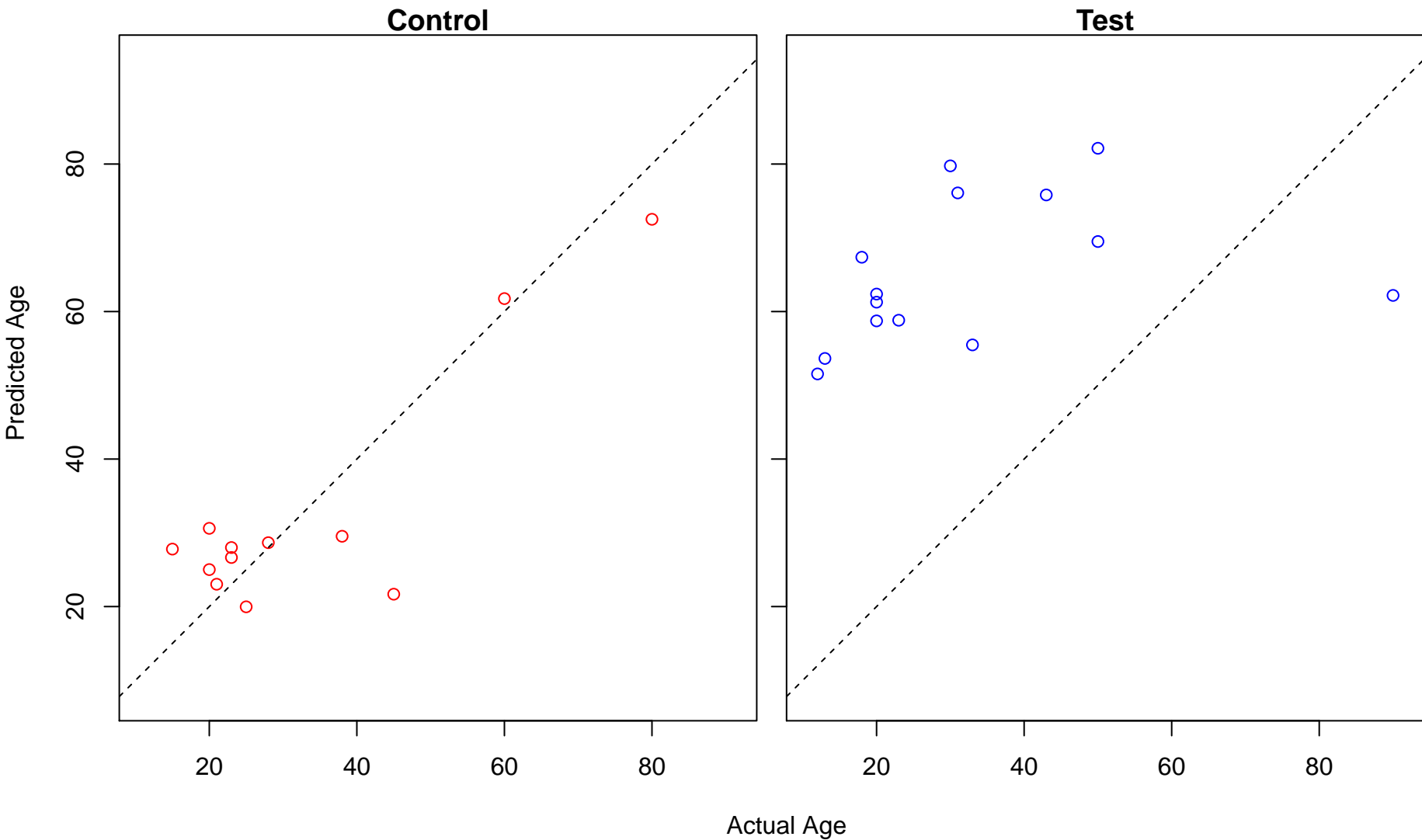


Test

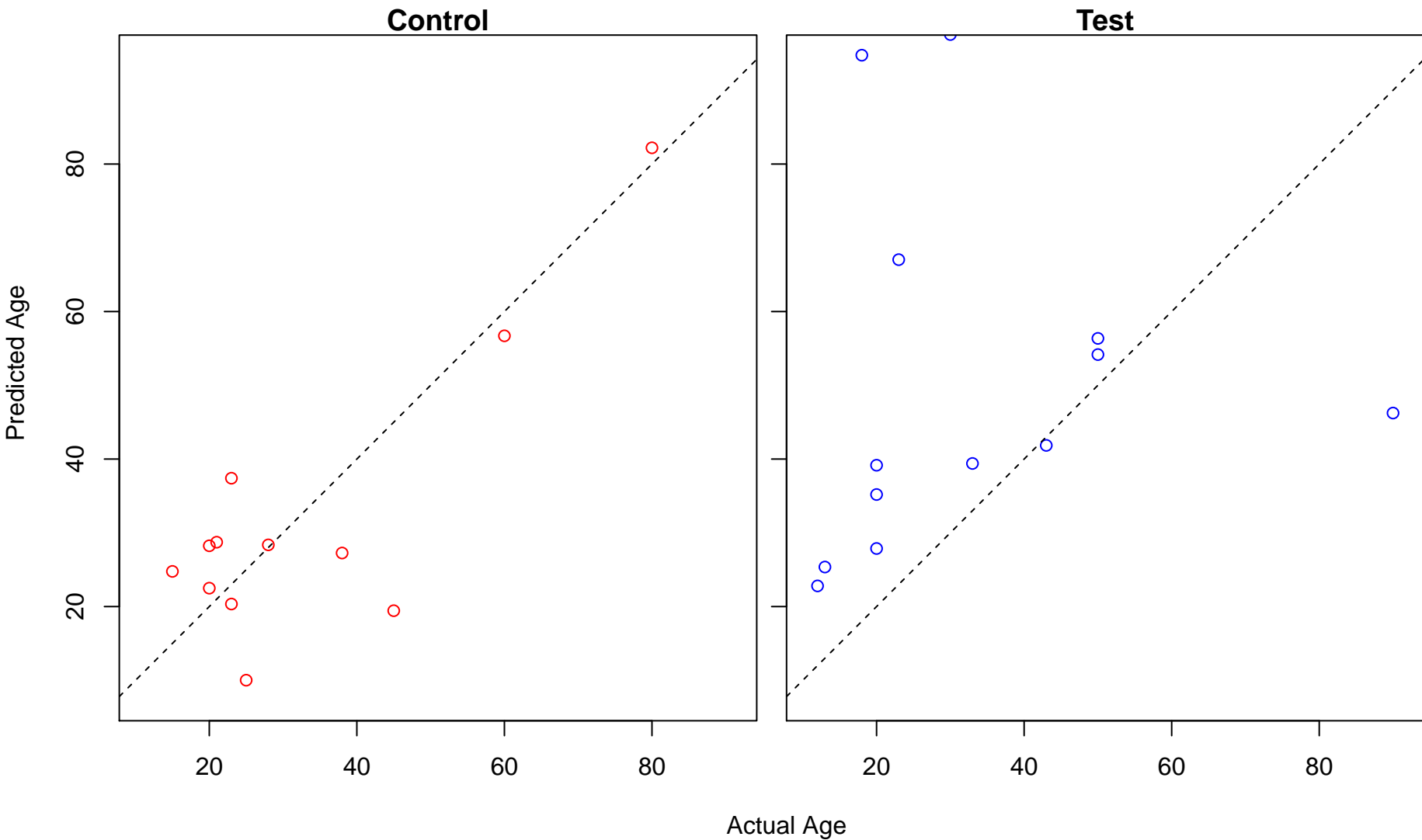


Actual Age

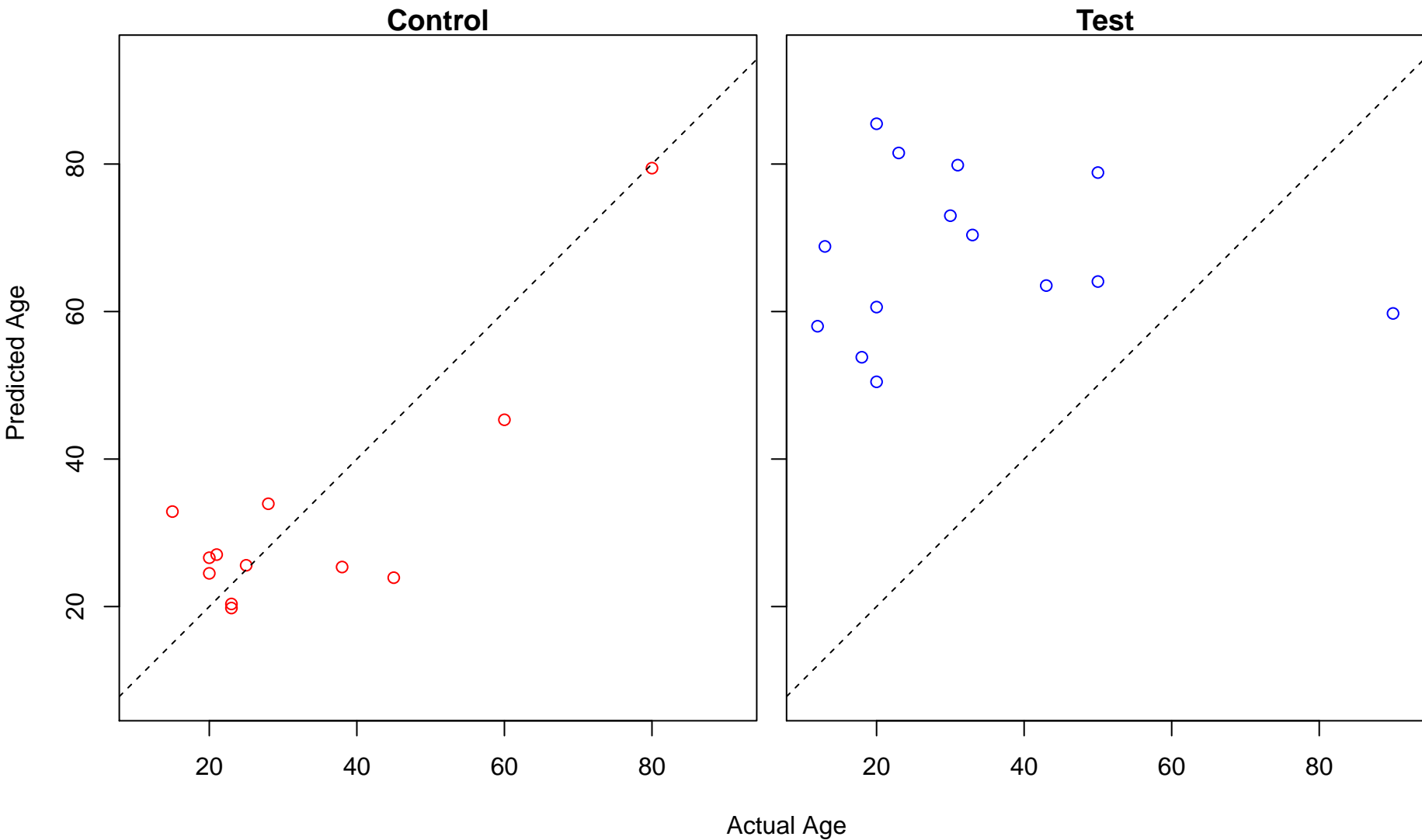
keratan sulfate metabolic process (Score: 7.045083)



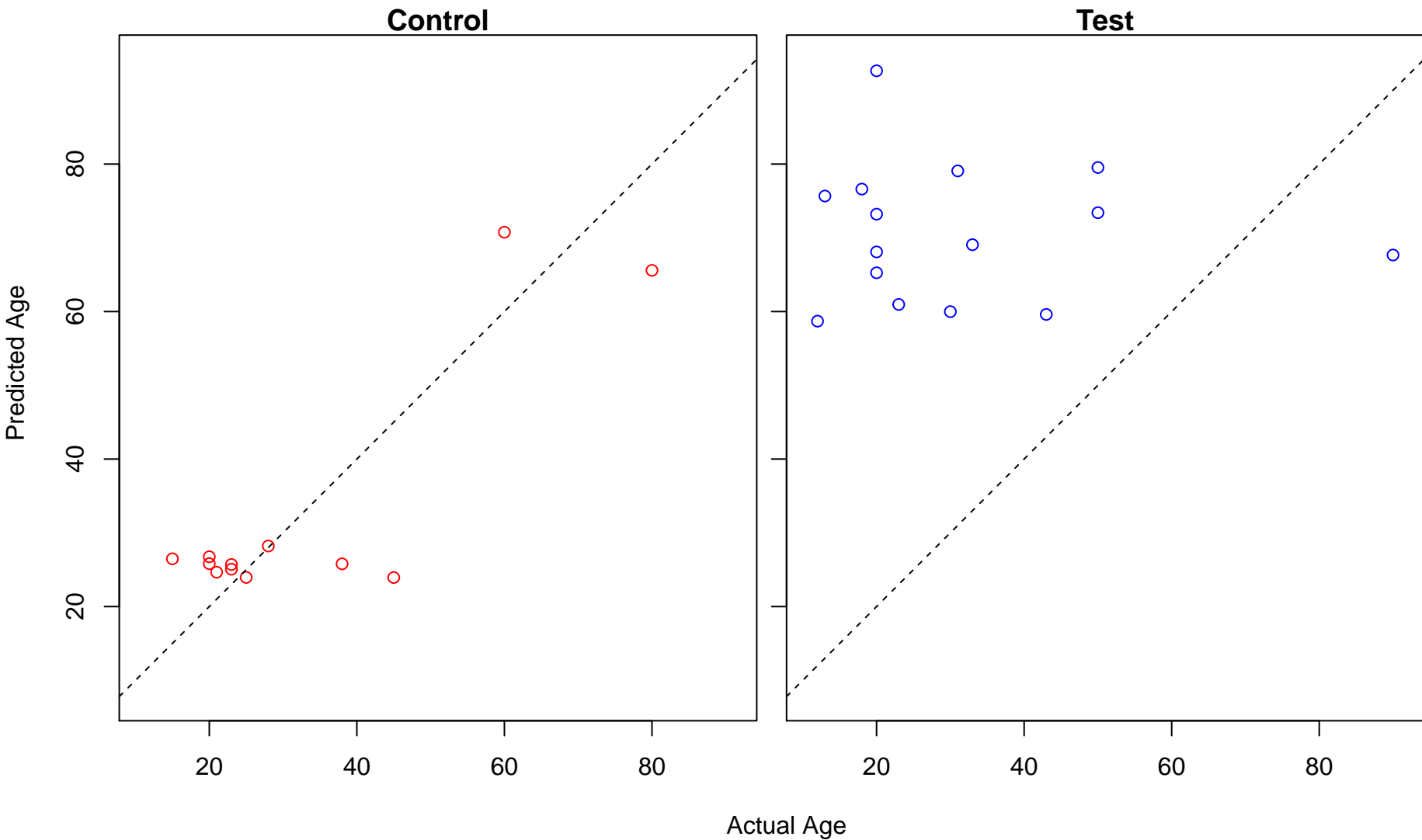
regulation of cell activation (Score: 7.042887)



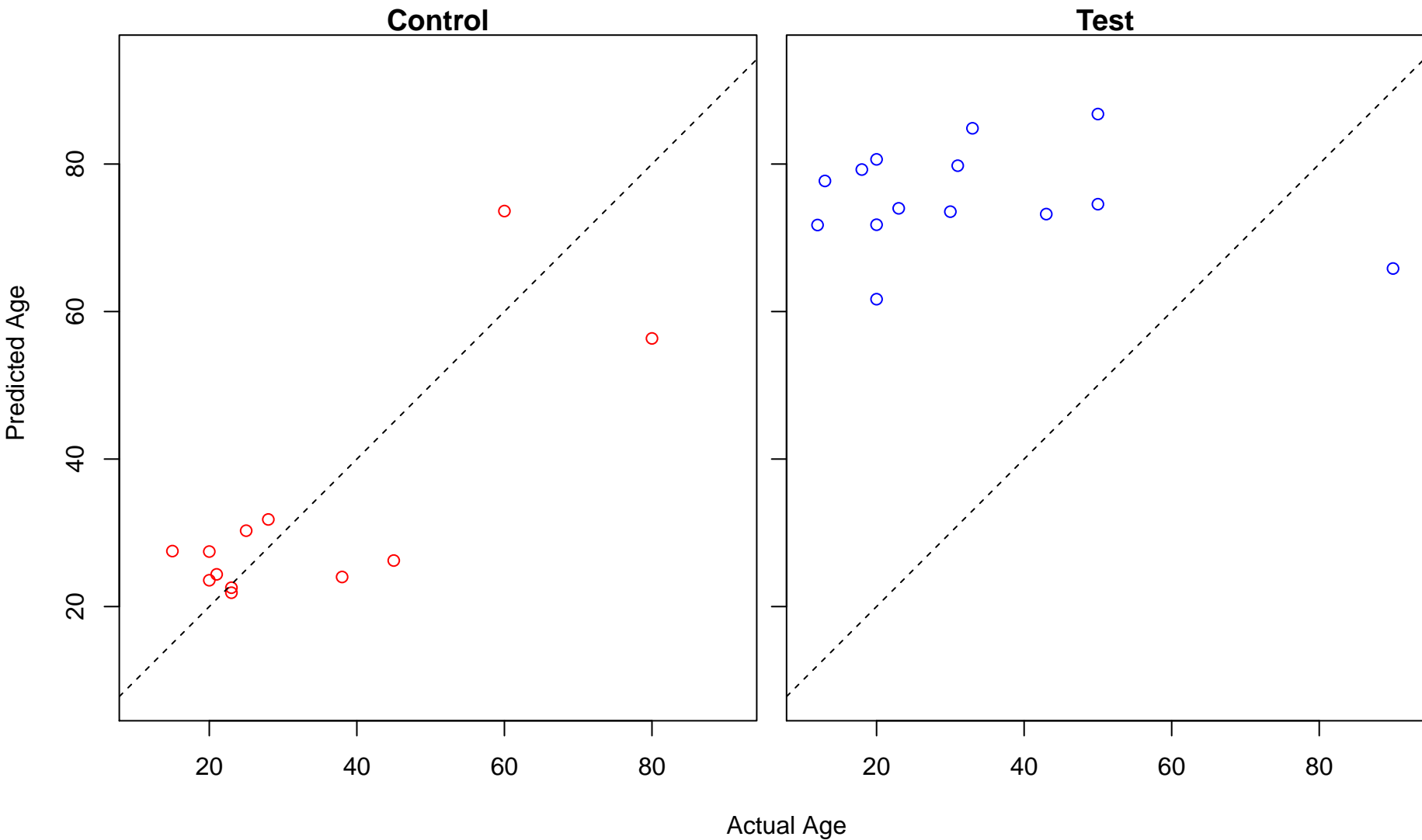
response to ischemia (Score: 7.041638)



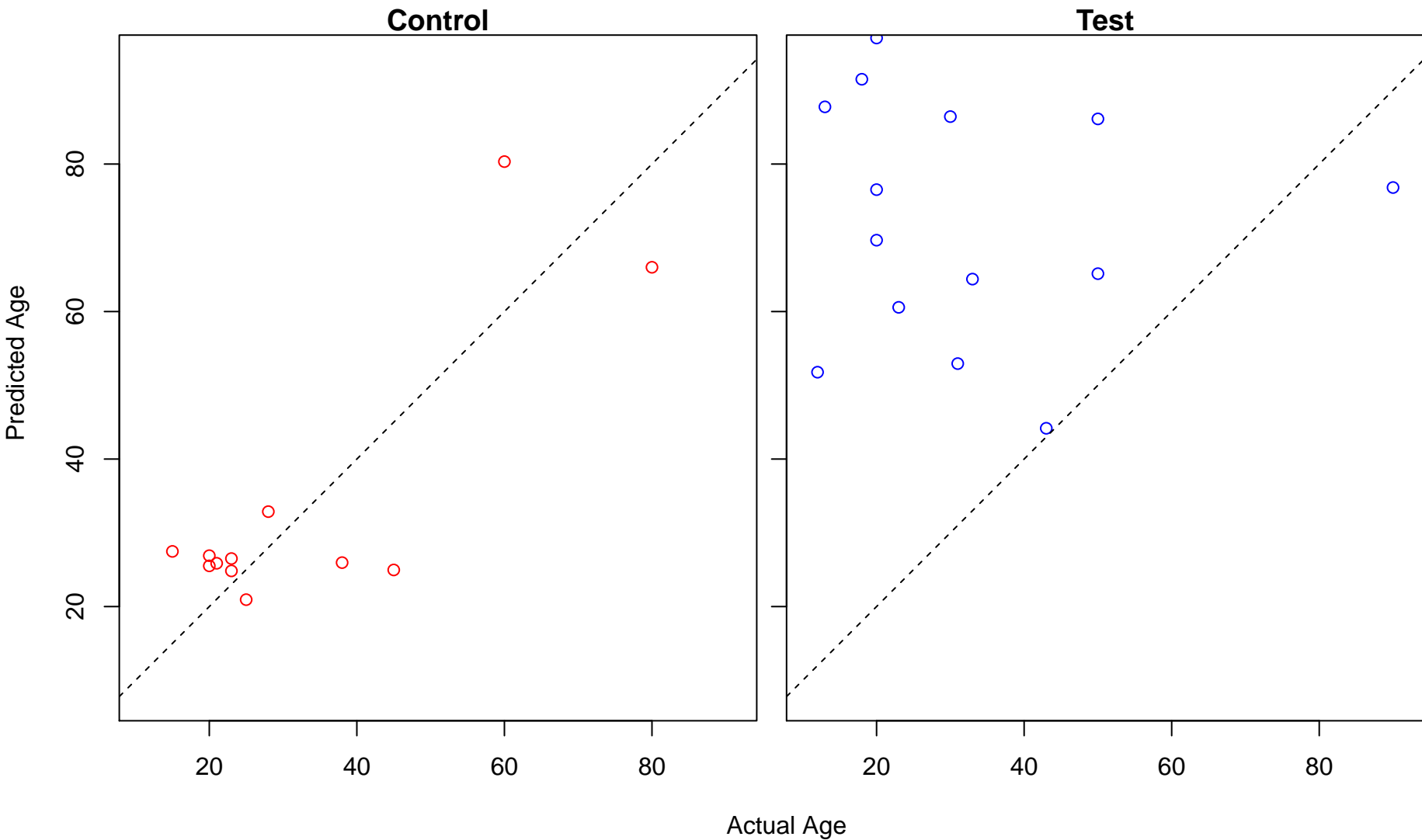
regulation of growth (Score: 7.041619)



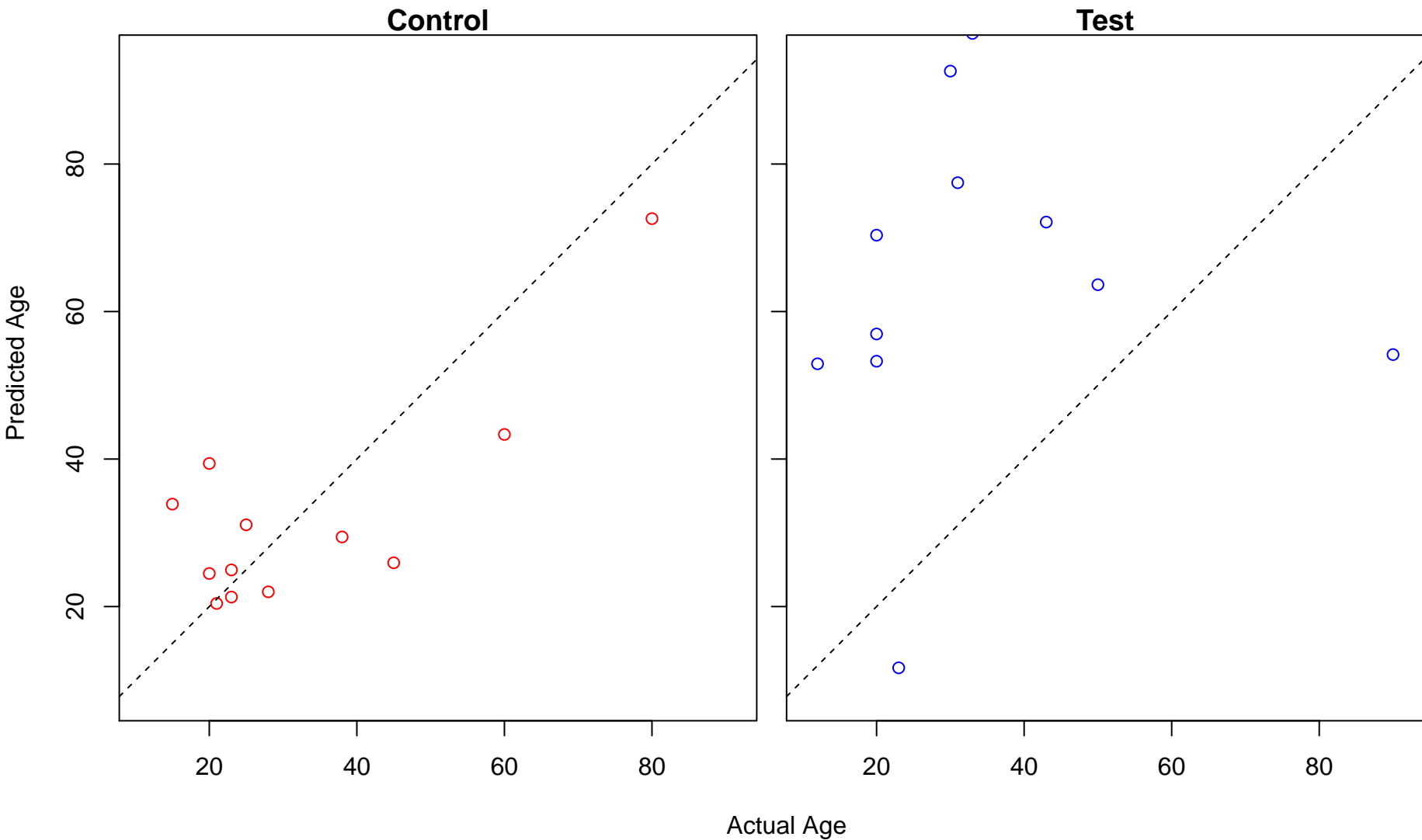
heterochromatin assembly (Score: 7.040587)



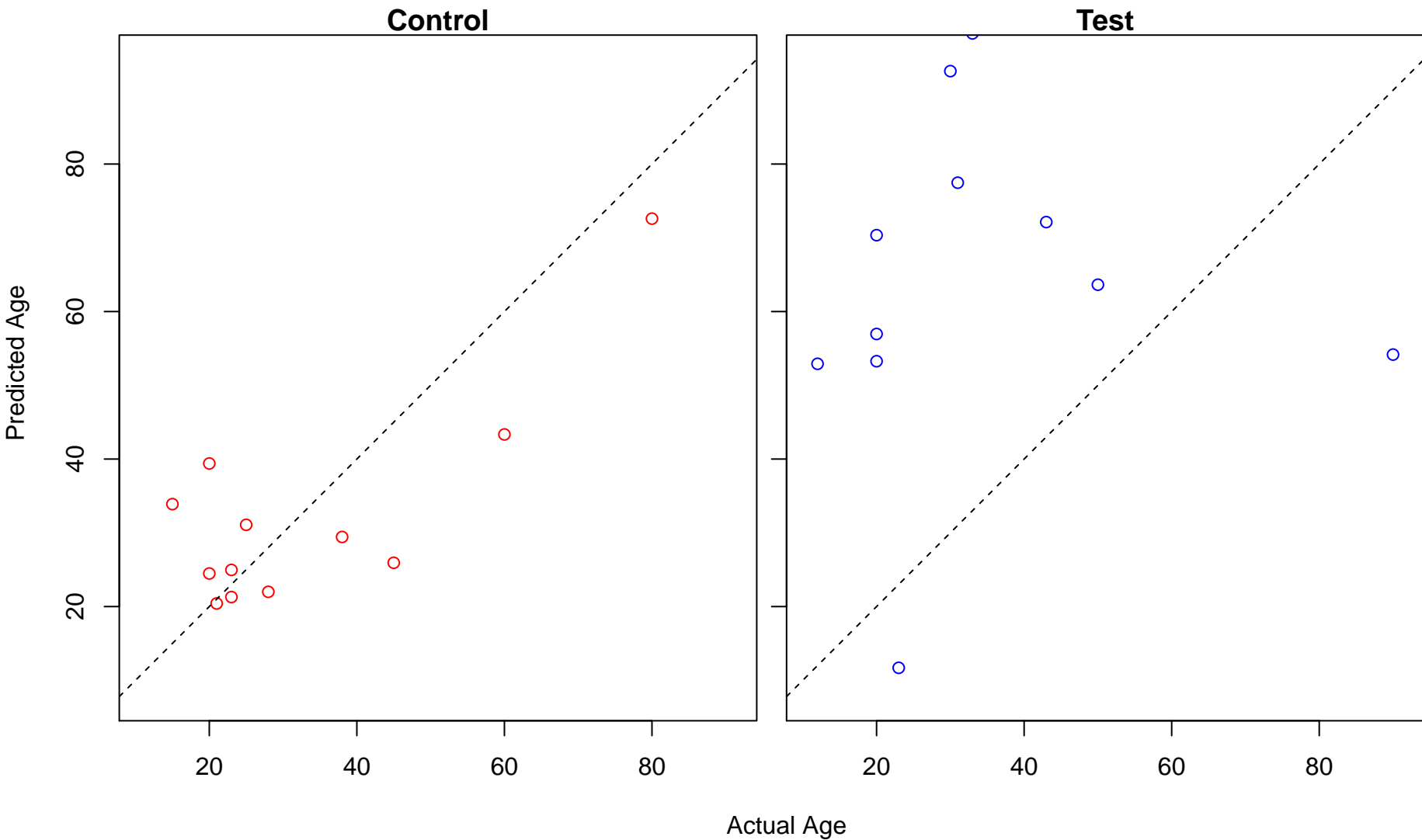
calcium ion regulated exocytosis (Score: 7.038545)



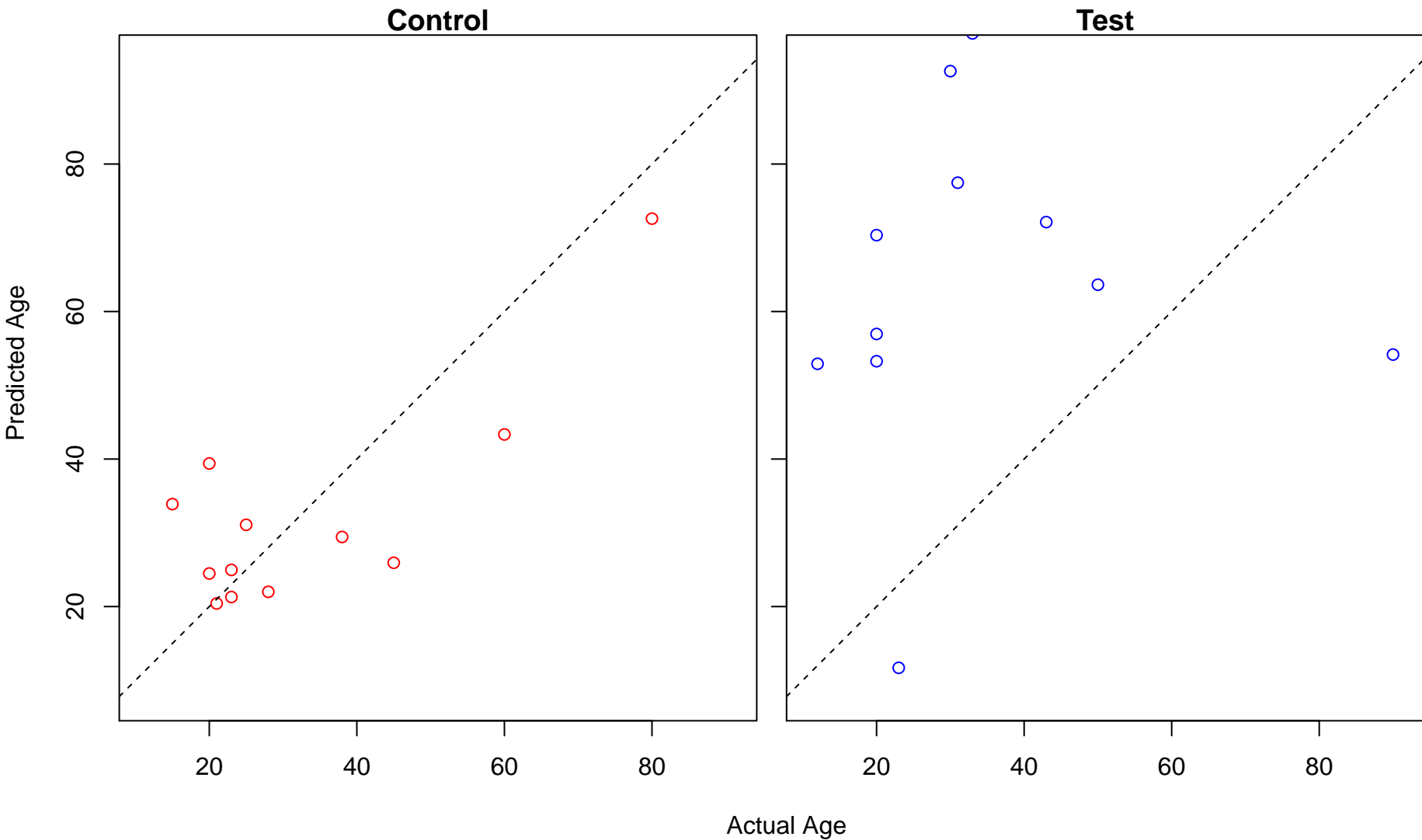
leukotriene catabolic process (Score: 7.037525)



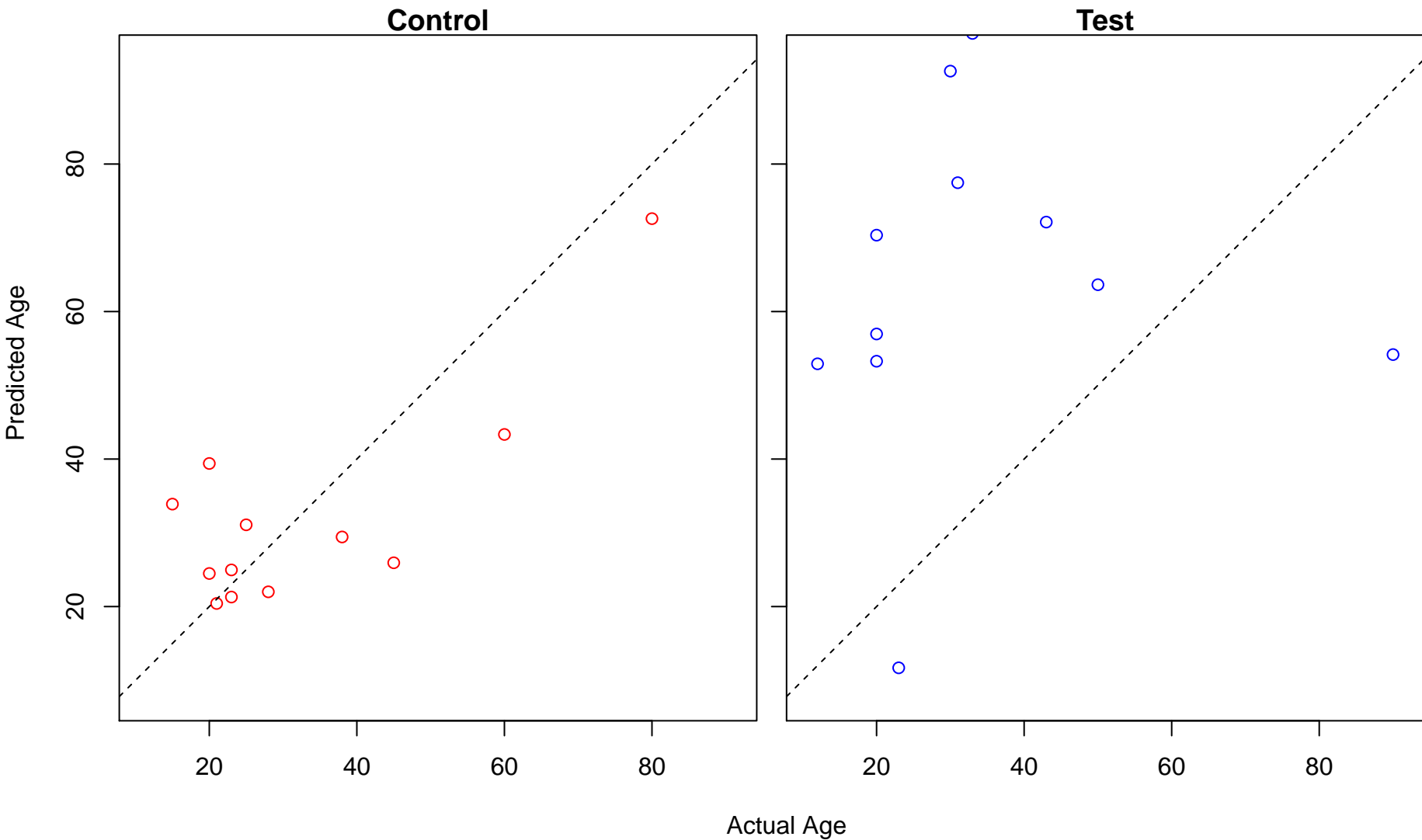
leukotriene B4 catabolic process (Score: 7.037525)



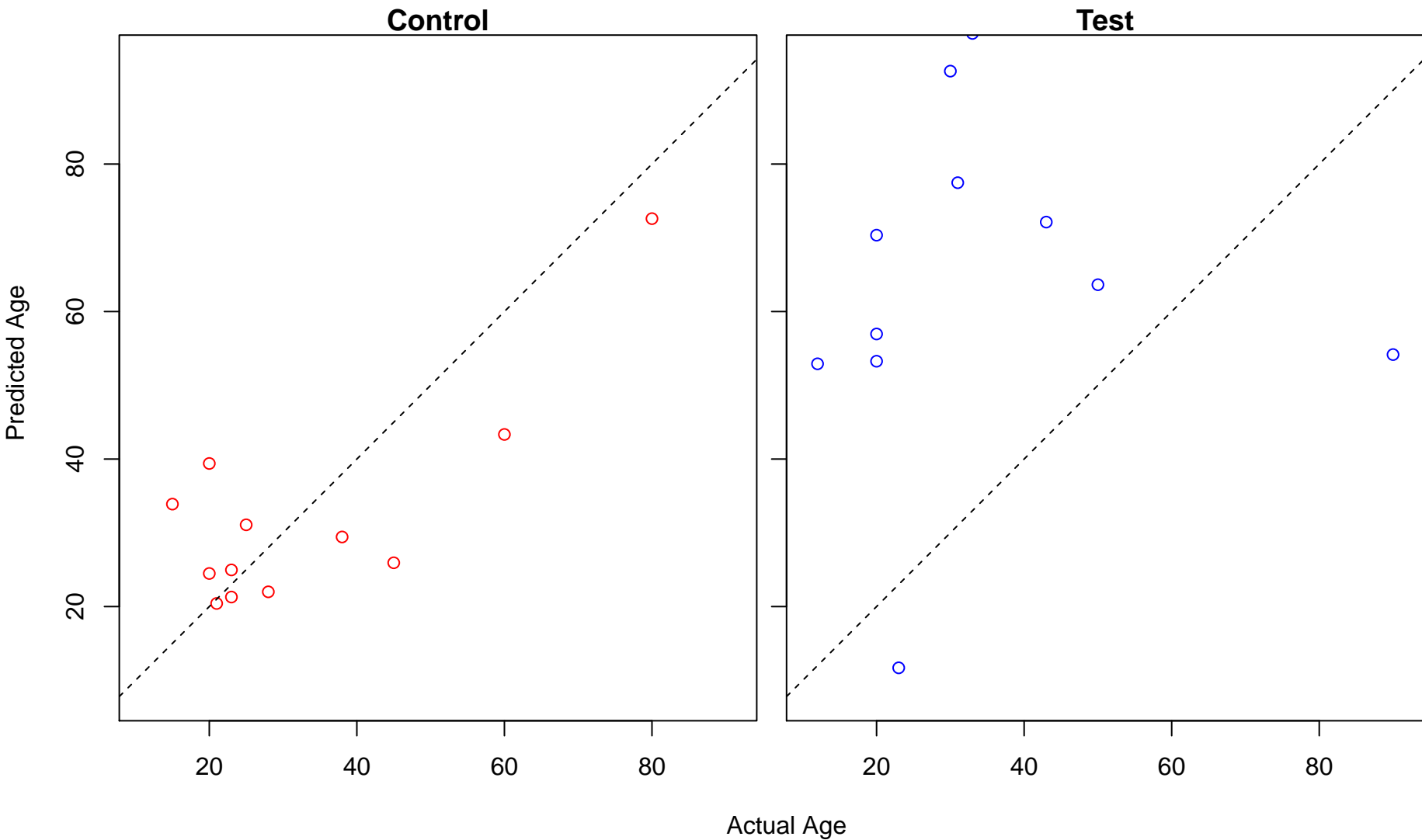
leukotriene B4 metabolic process (Score: 7.037525)



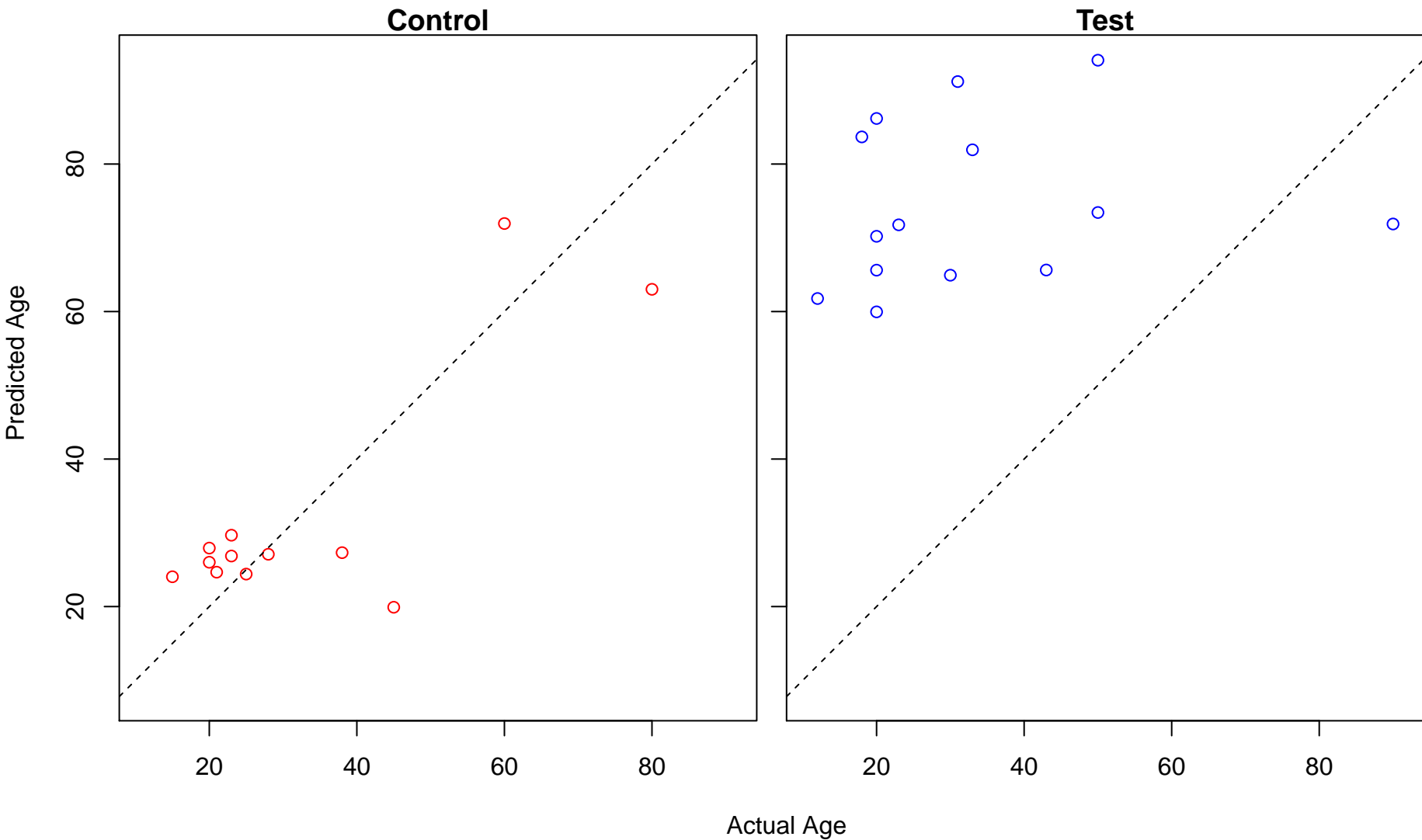
icosanoid catabolic process (Score: 7.037525)



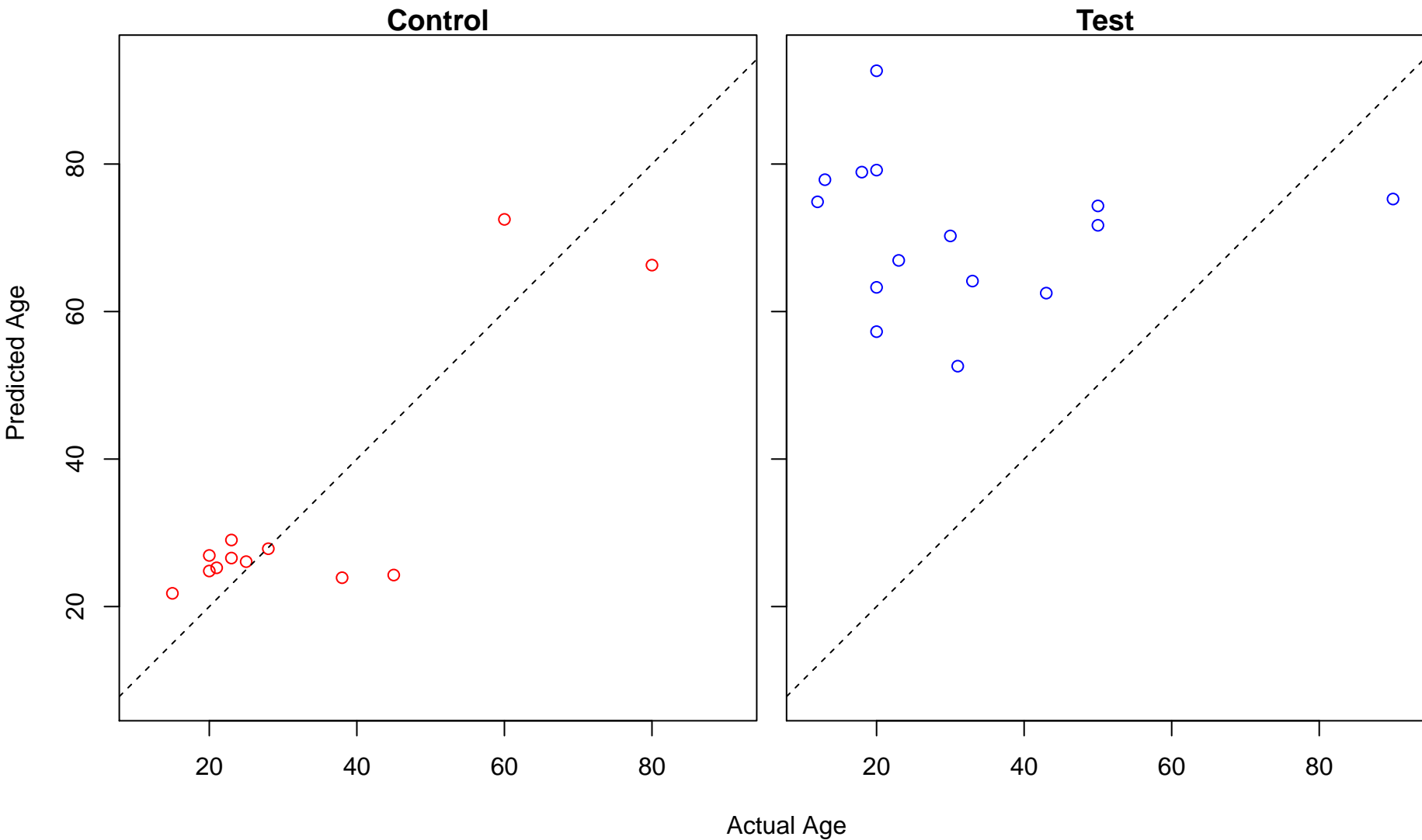
fatty acid derivative catabolic process (Score: 7.037525)



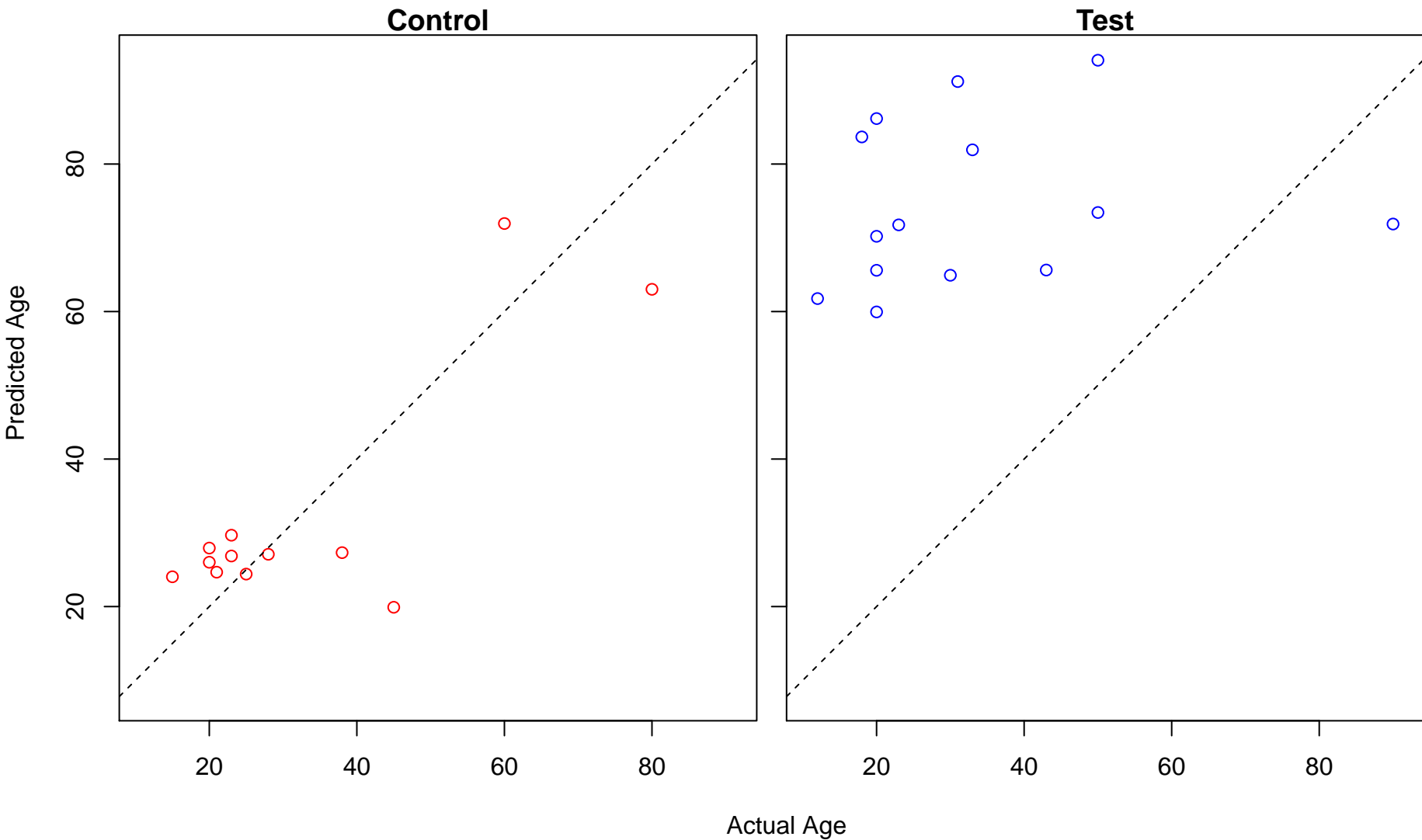
regulation of cytokine production involved in immune response (Score: 7.036802)



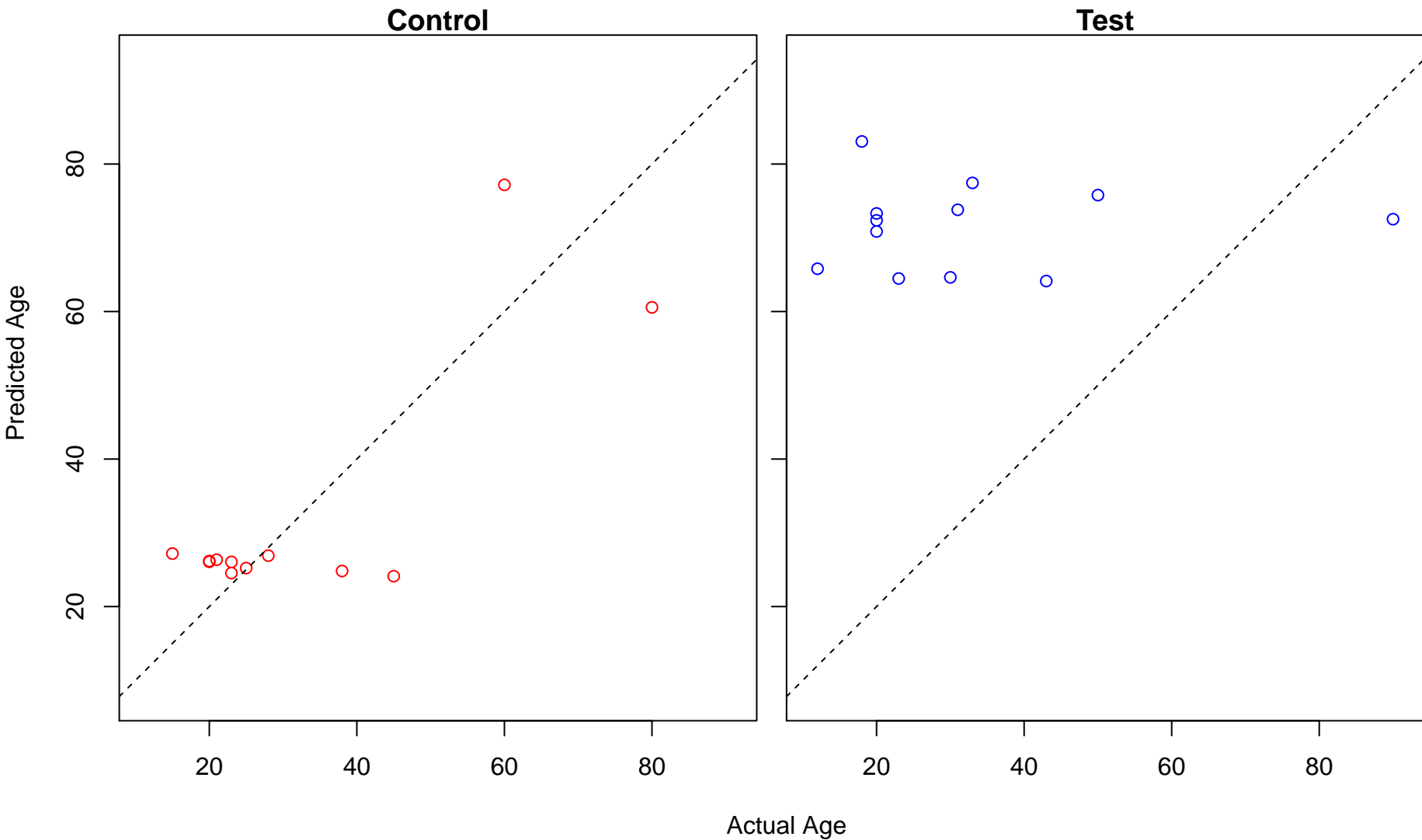
skeletal muscle tissue regeneration (Score: 7.036276)



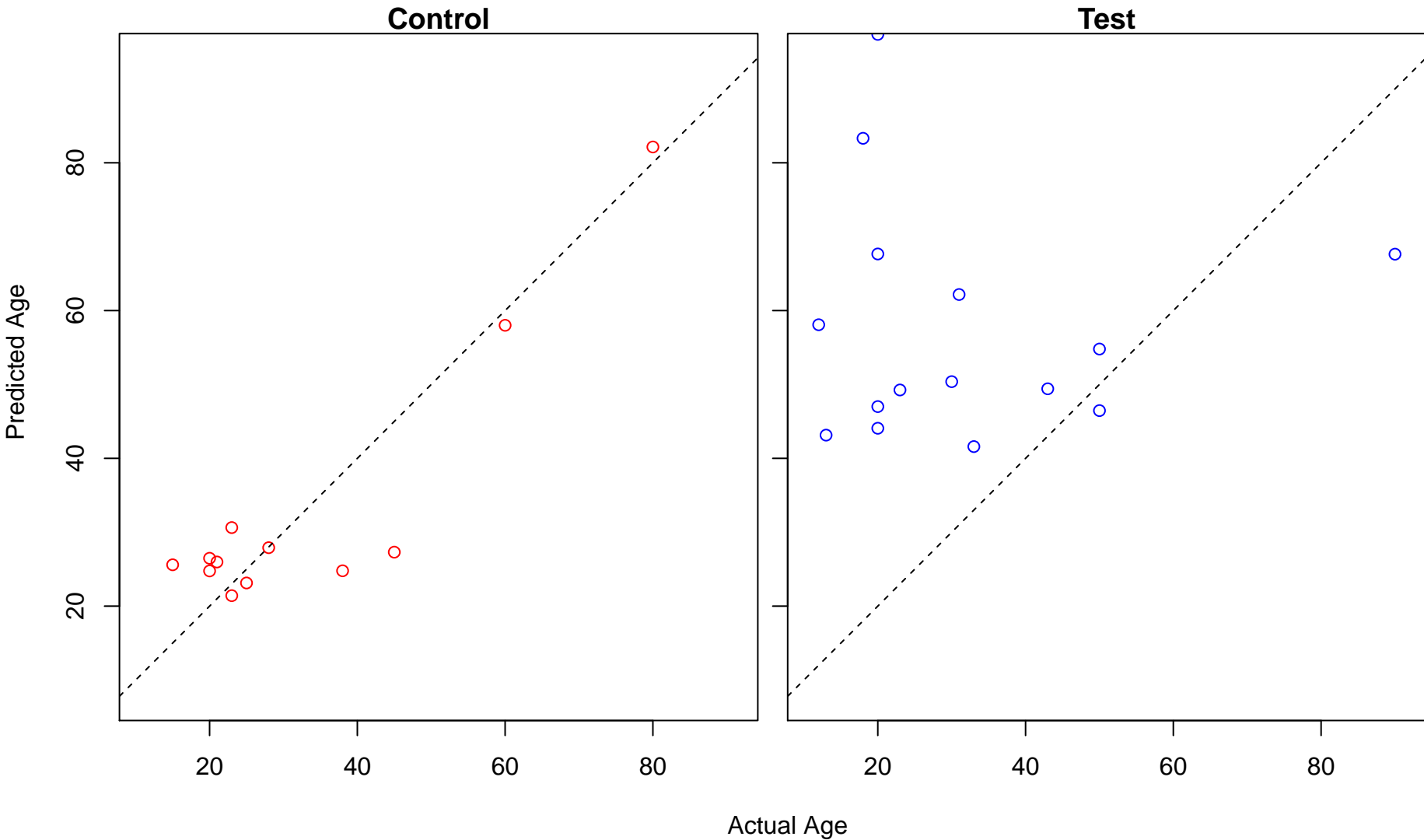
positive regulation of cytokine production involved in immune response (Score: 7.035773)



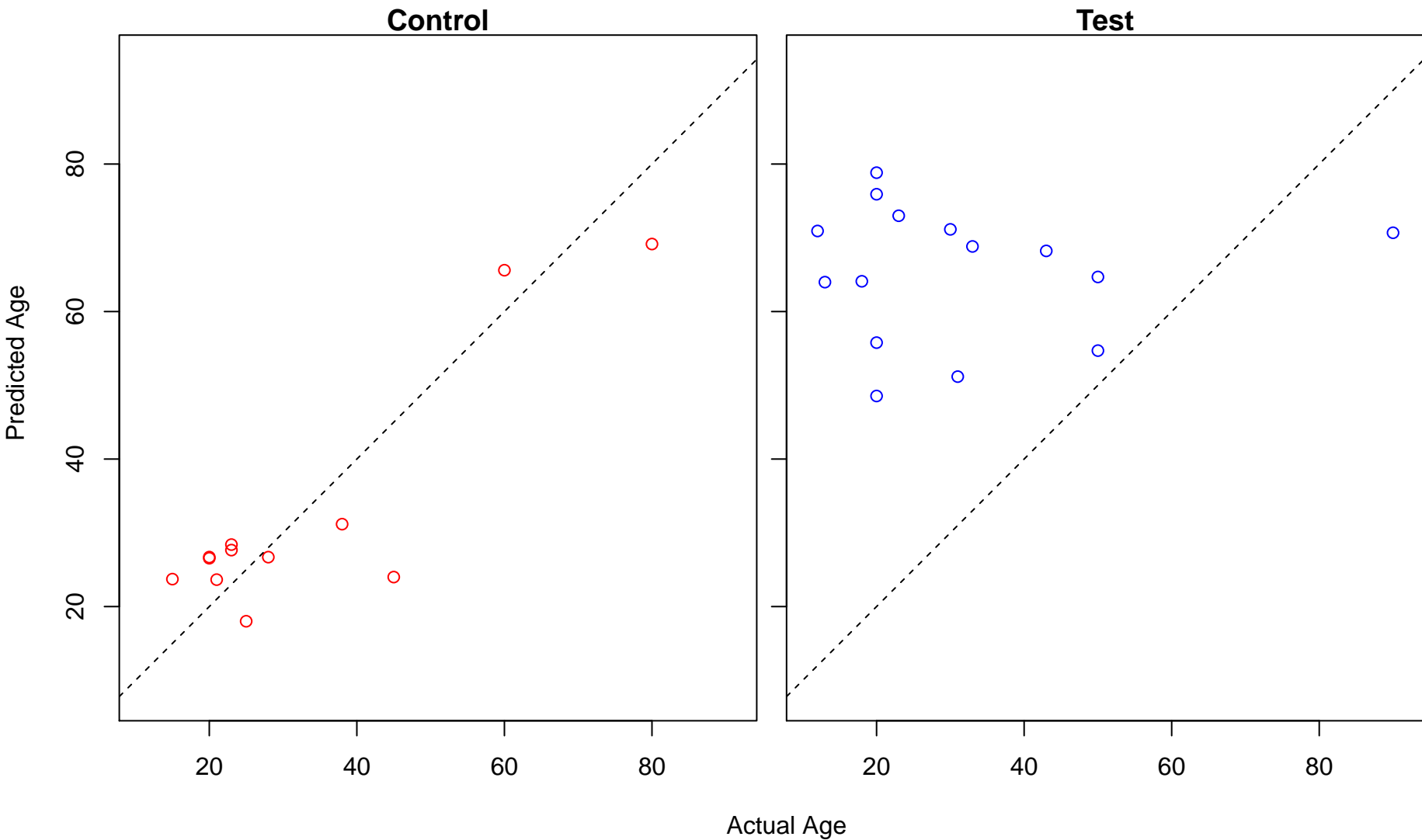
regulation of apoptotic signaling pathway (Score: 7.035257)



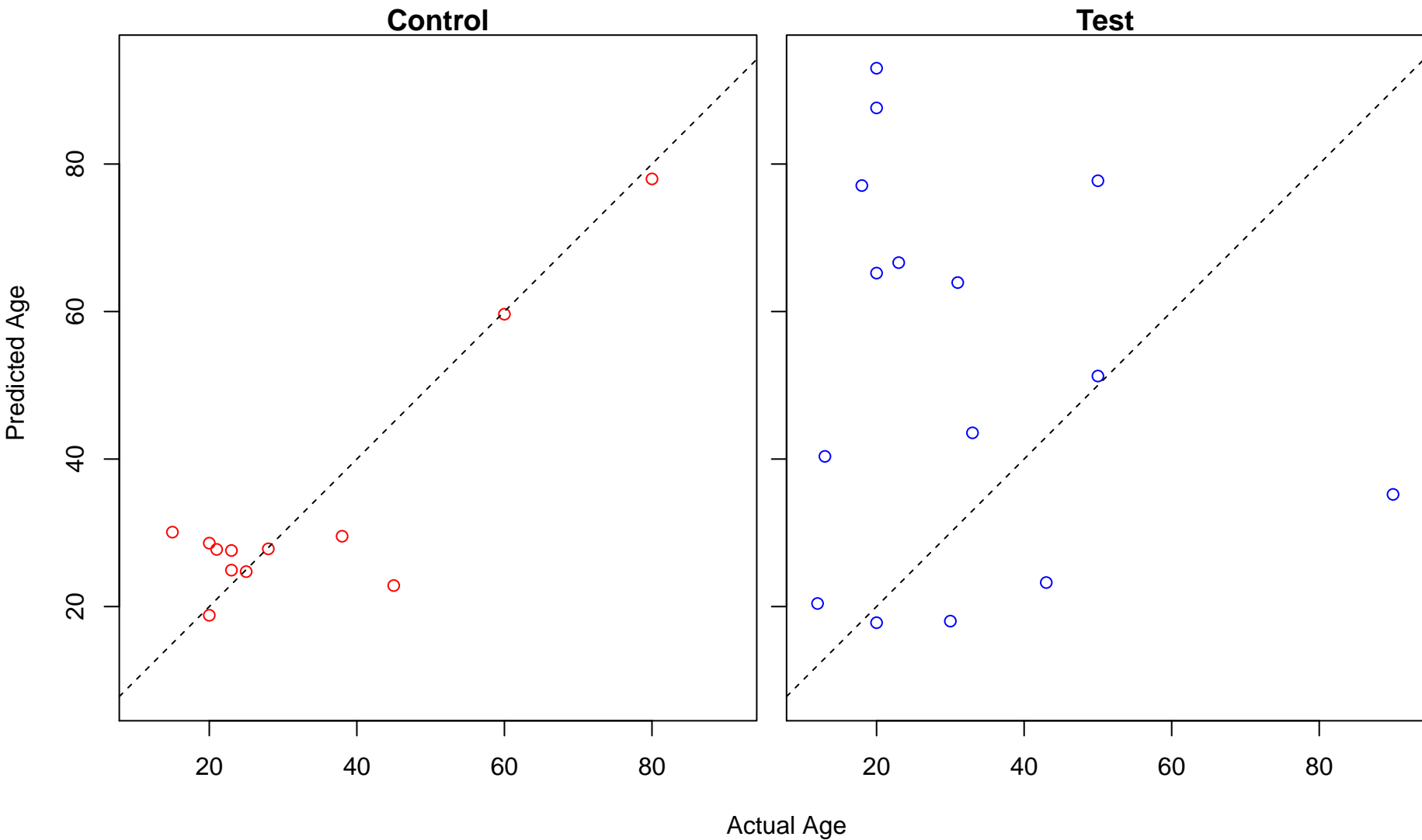
entrainment of circadian clock by photoperiod (Score: 7.033997)



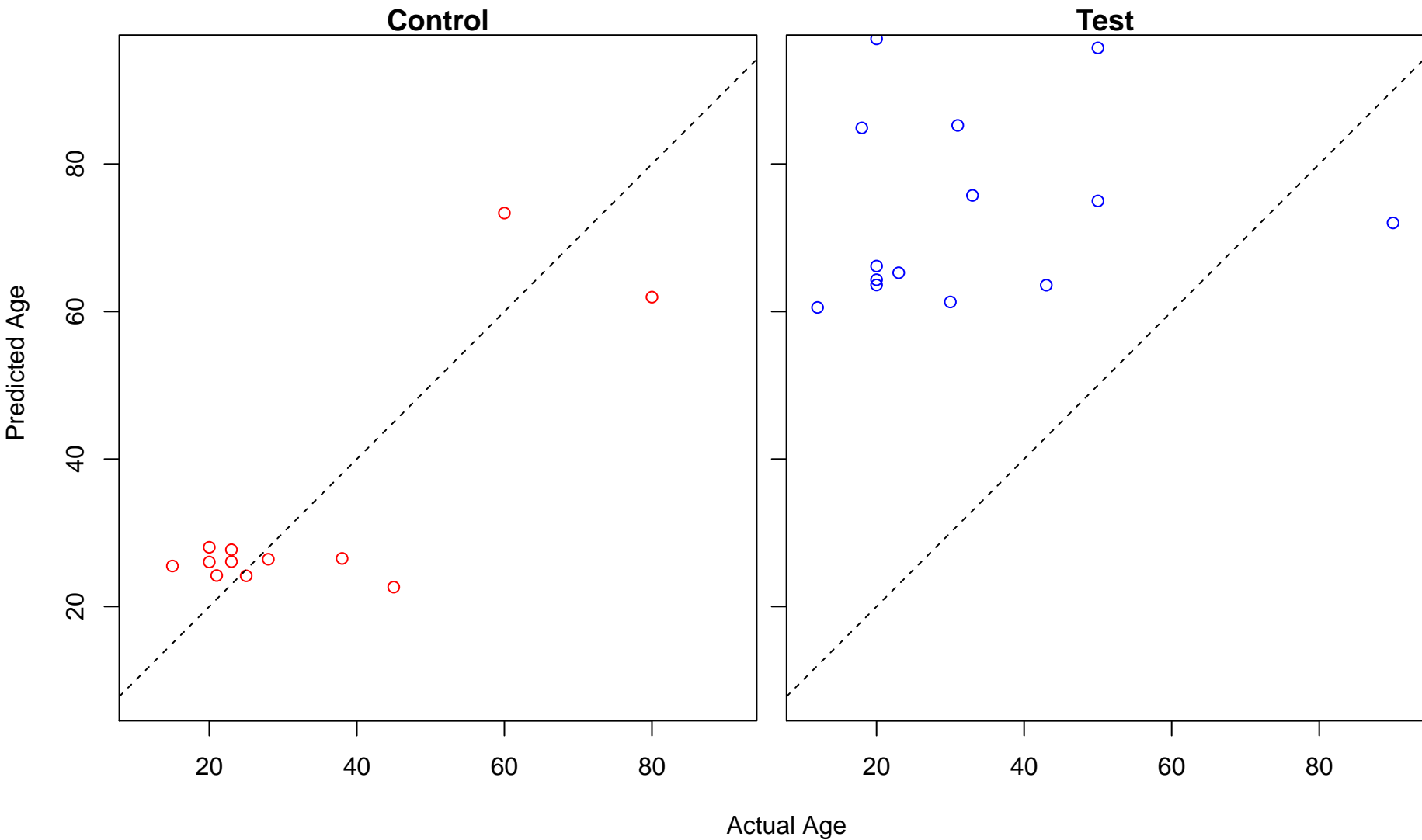
central nervous system projection neuron axonogenesis (Score: 7.031747)



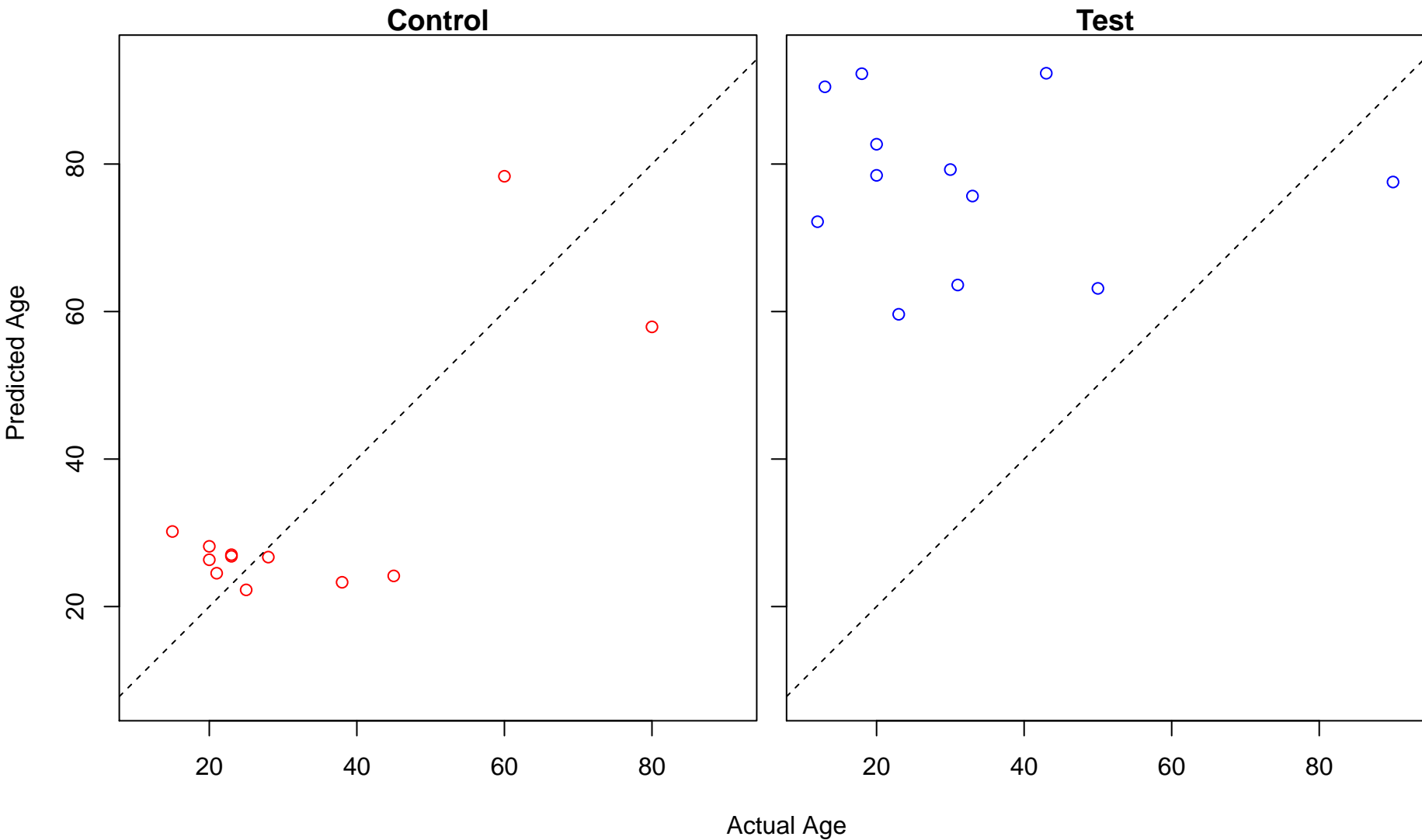
retina homeostasis (Score: 7.028746)



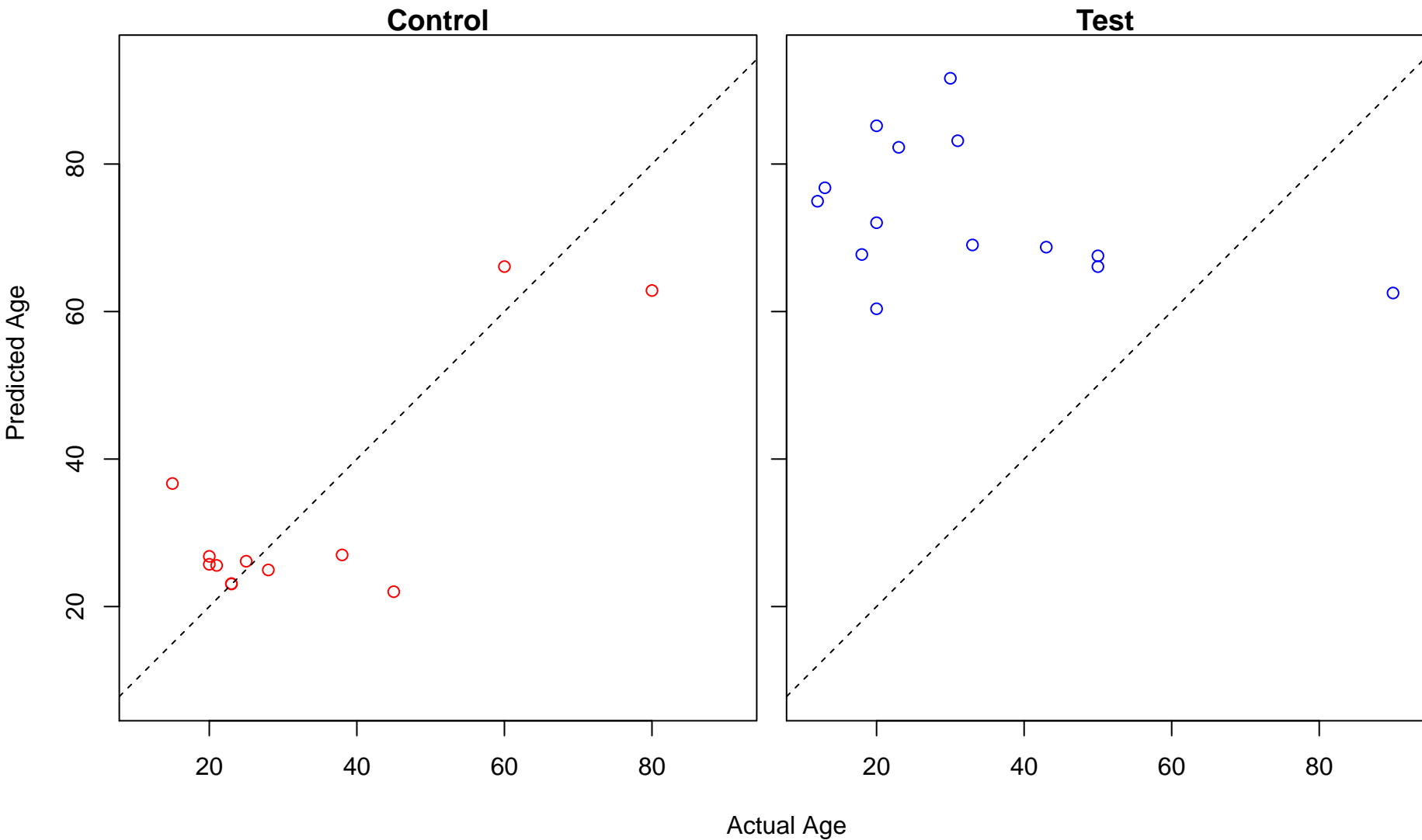
response to bacterium (Score: 7.028679)



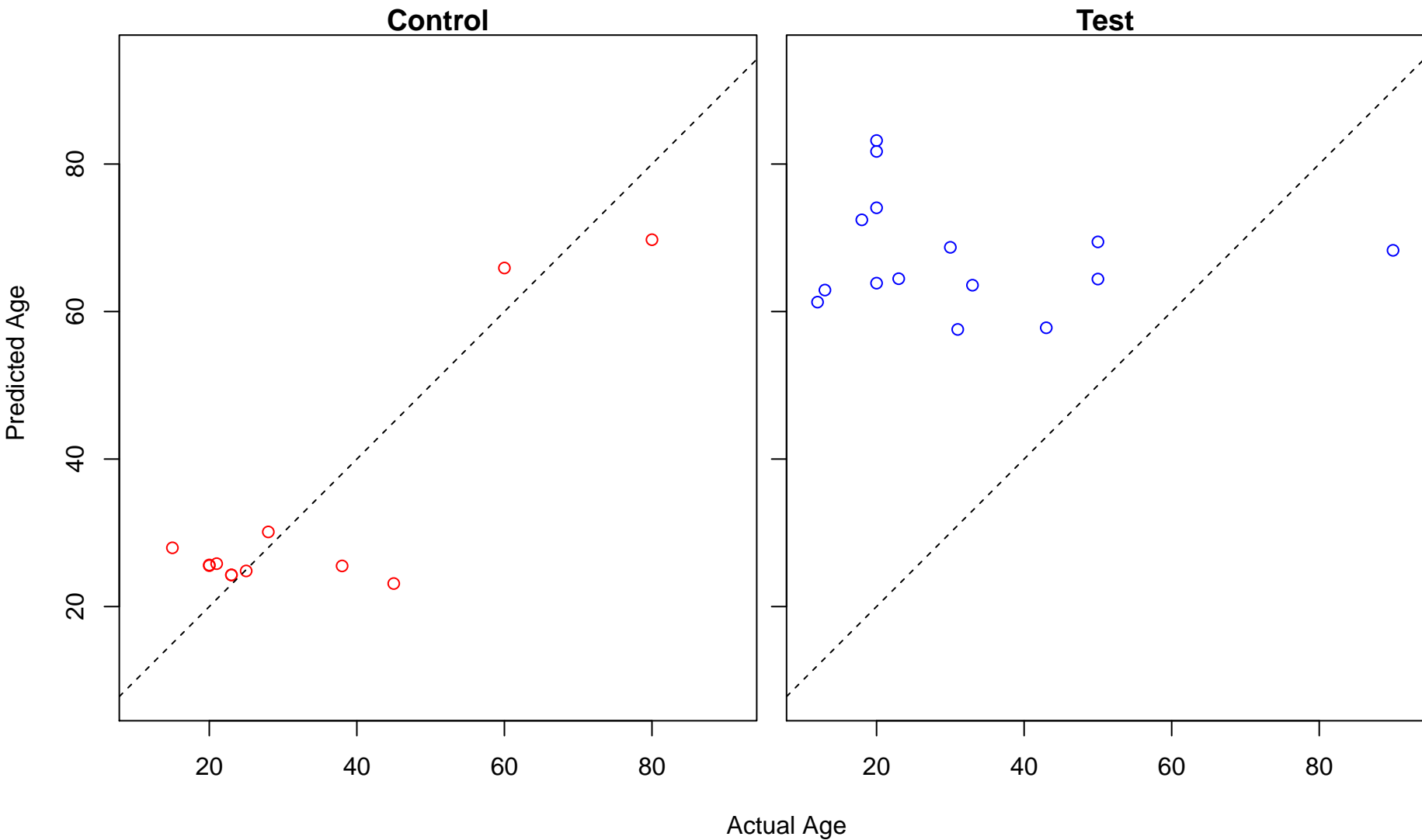
regulation of actin cytoskeleton reorganization (Score: 7.024565)



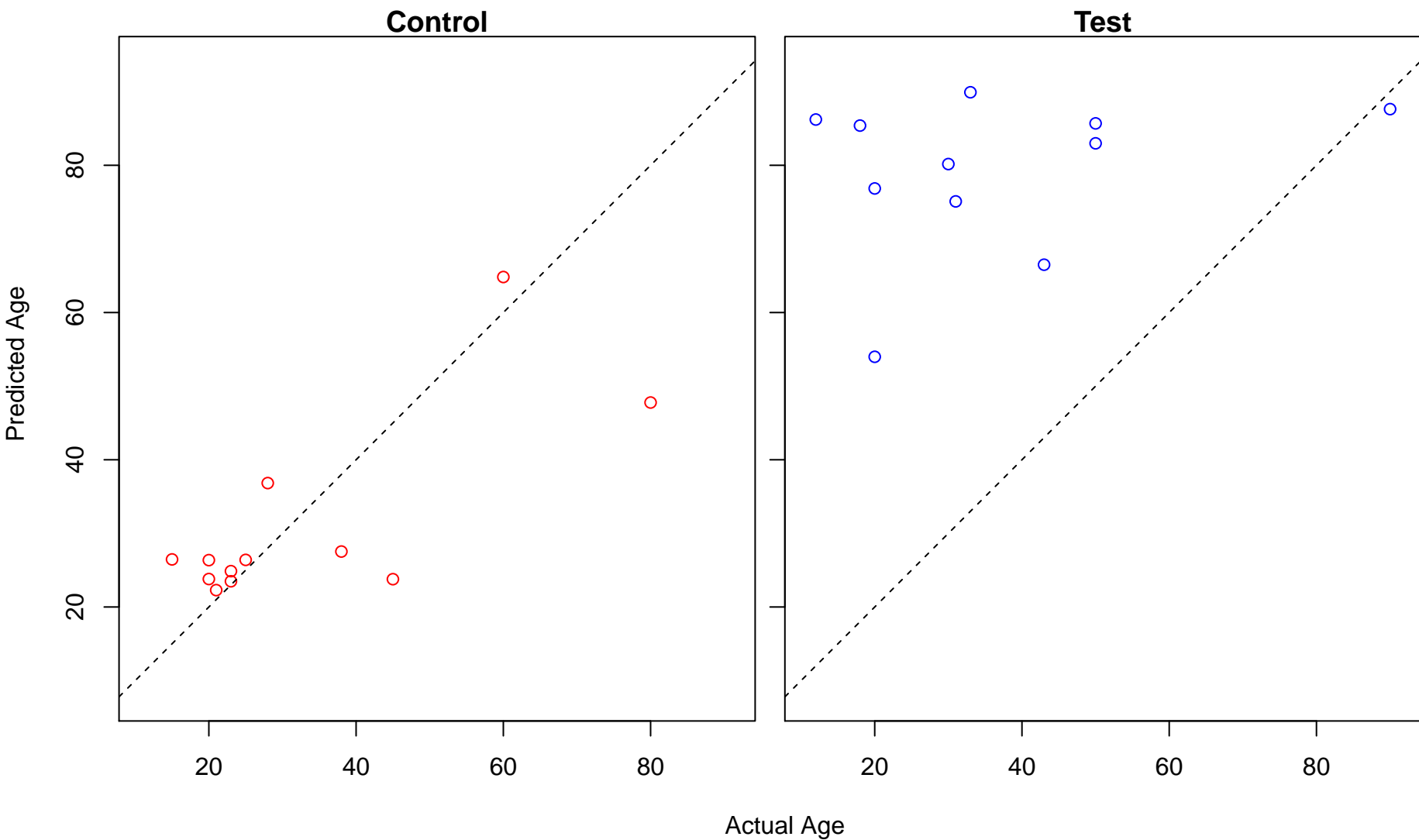
astrocyte differentiation (Score: 7.022814)



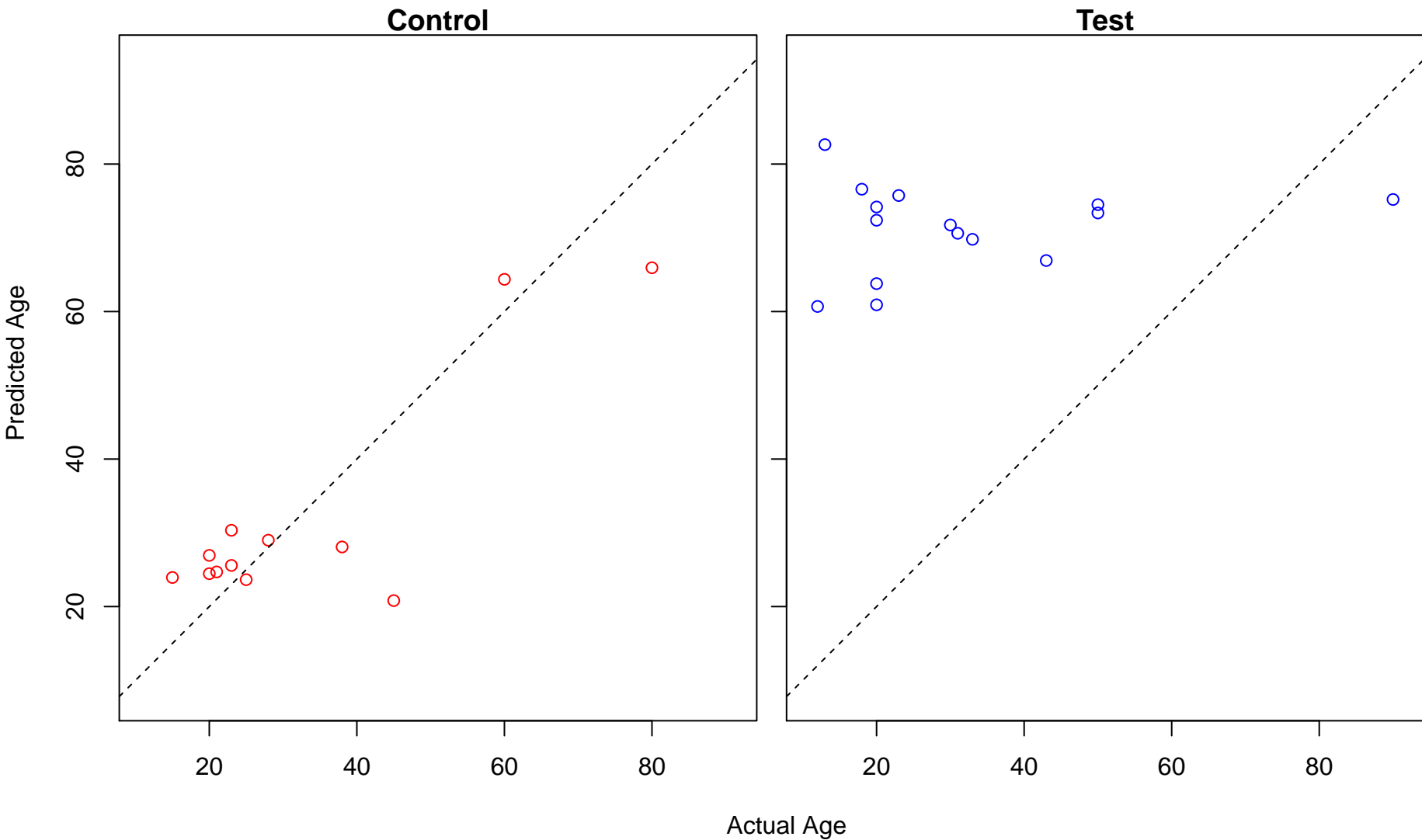
negative regulation of autophagy (Score: 7.017406)



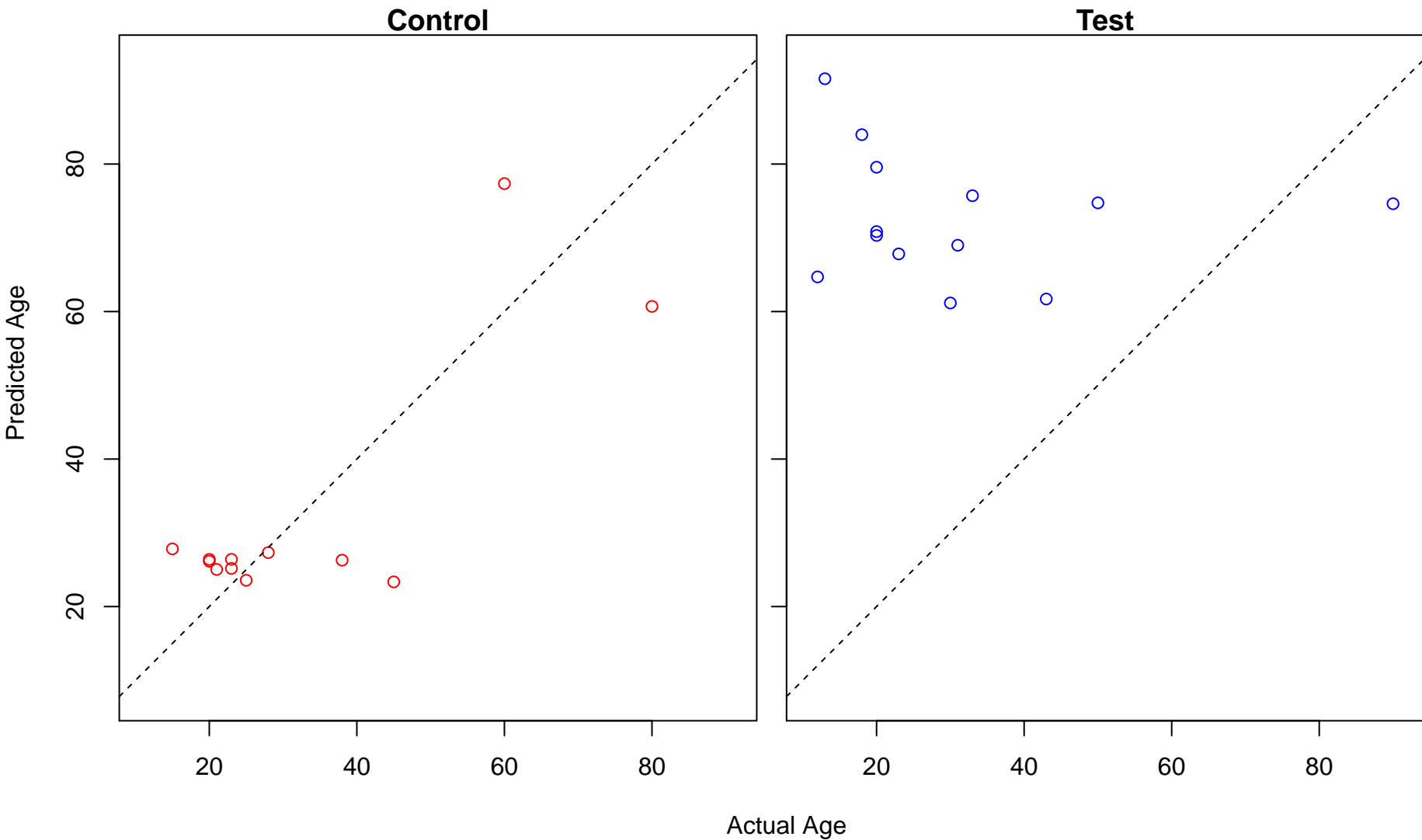
positive regulation of synapse maturation (Score: 7.017089)



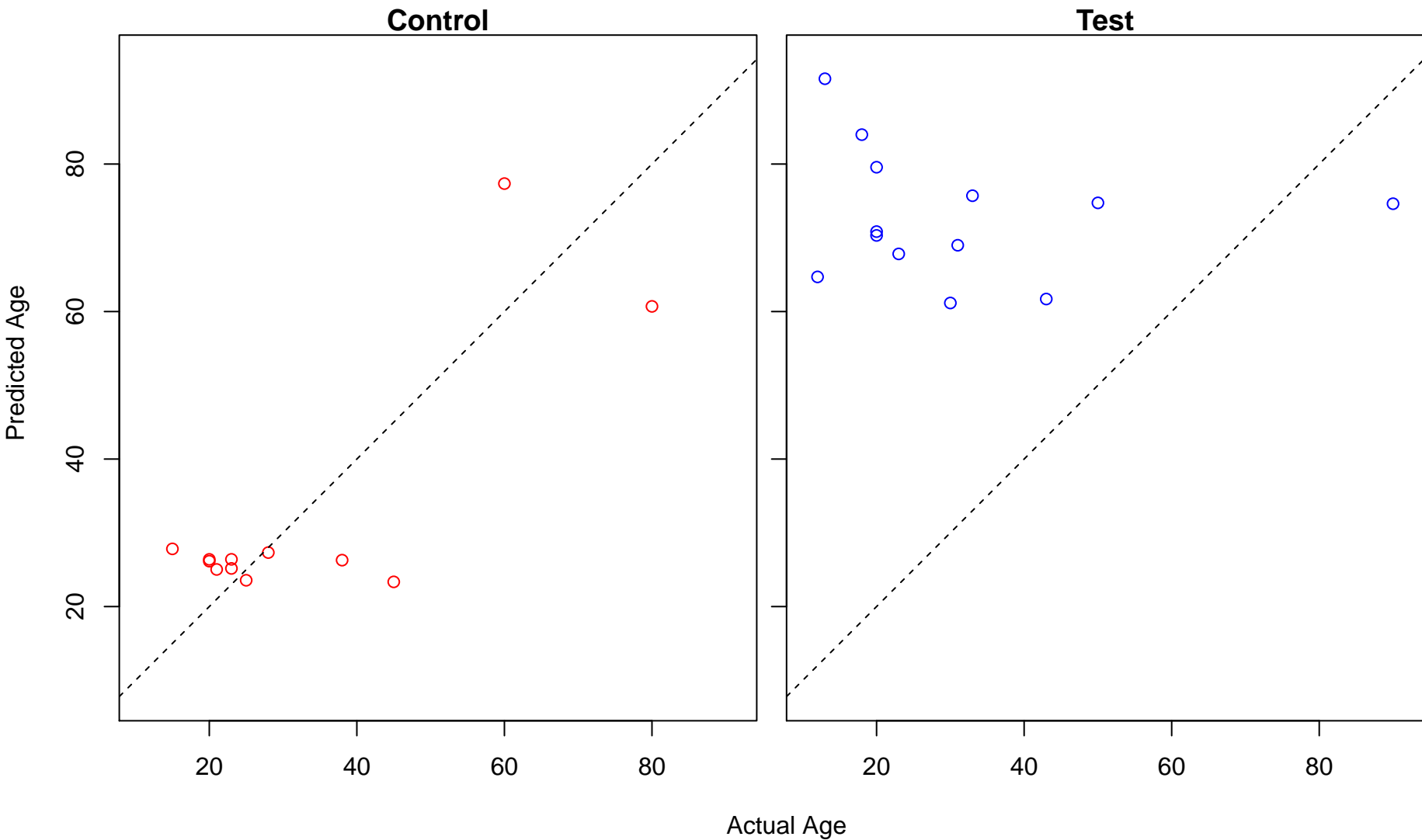
regulation of hemopoiesis (Score: 7.014158)



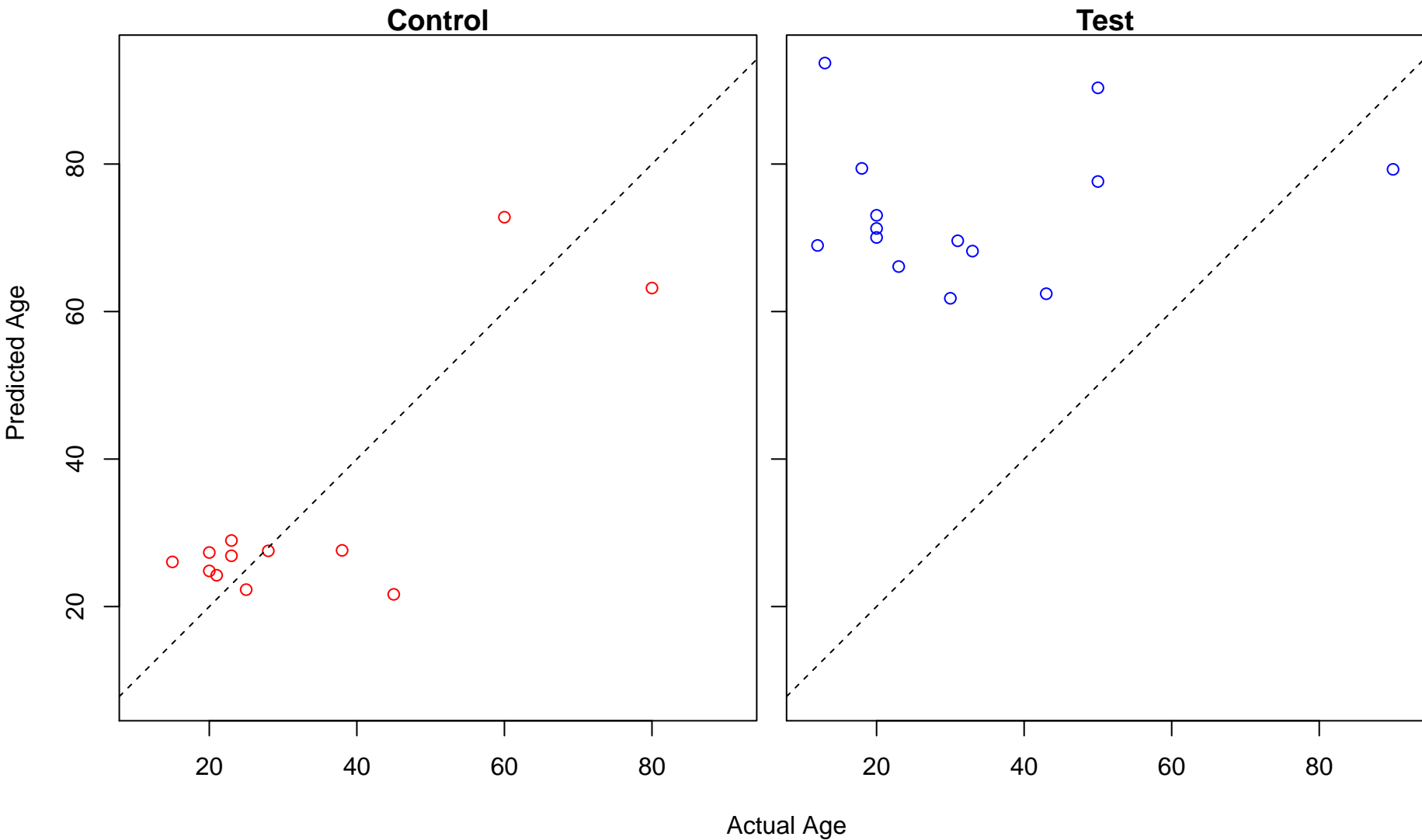
intracellular transport of virus (Score: 7.011528)



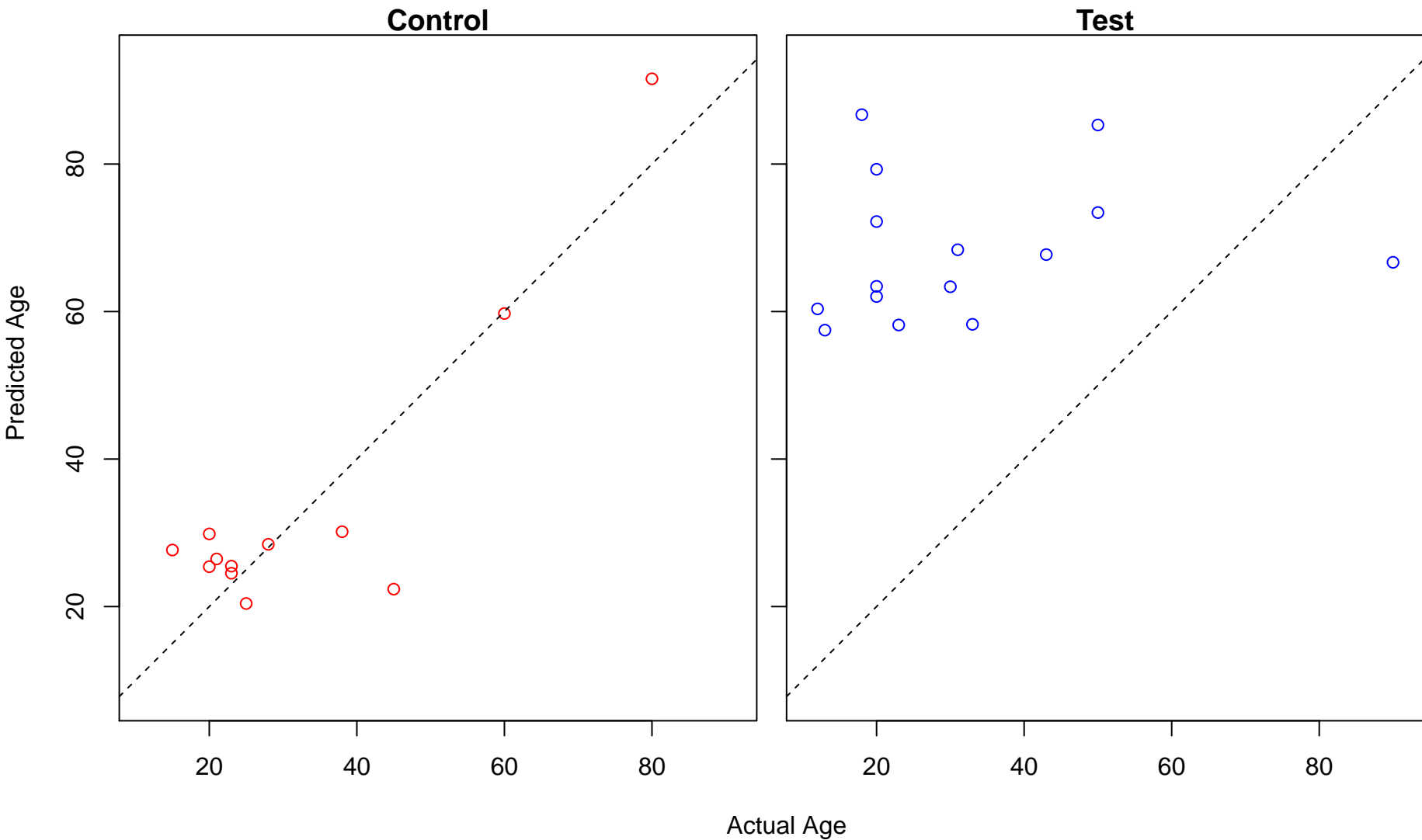
multi-organism intracellular transport (Score: 7.011528)



negative regulation of viral process (Score: 7.009524)

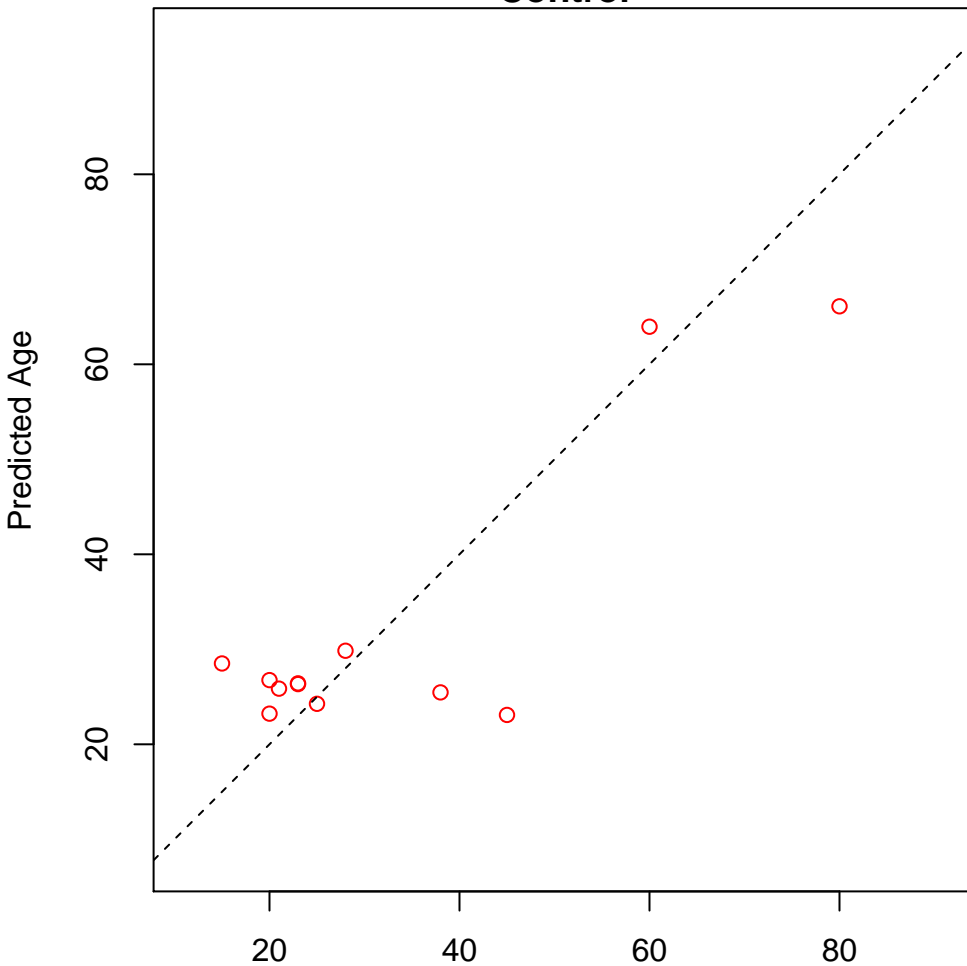


regulation of cell motility (Score: 7.008900)

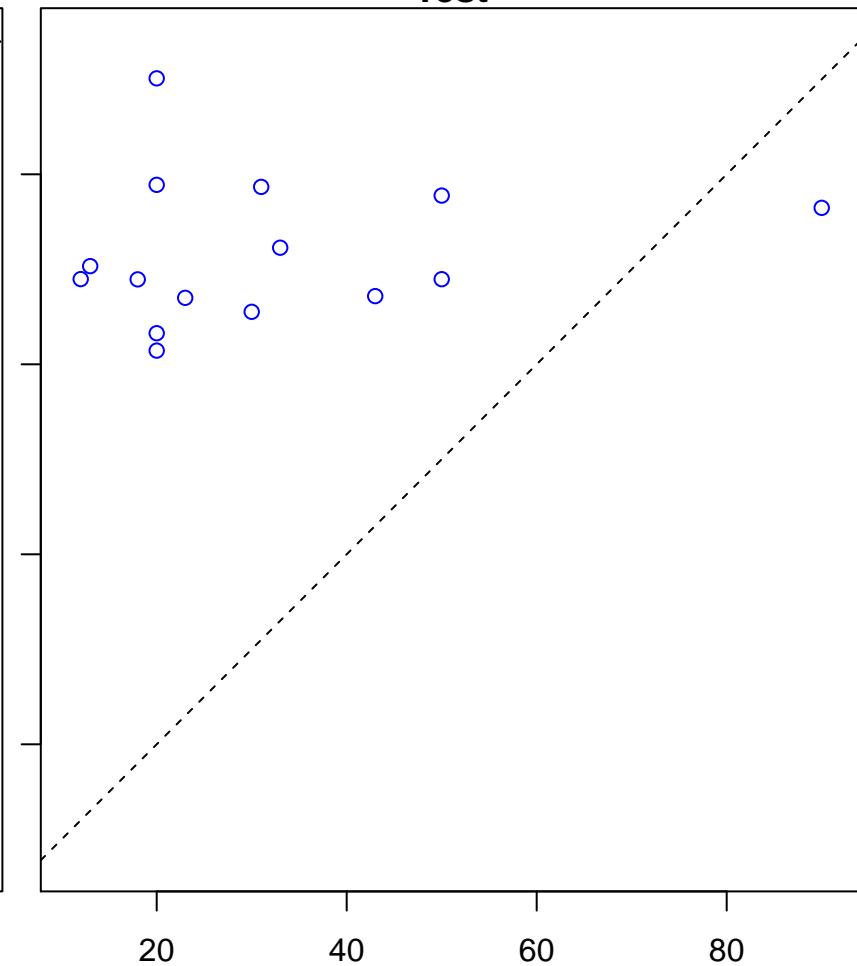


negative regulation of cell development (Score: 7.008830)

Control

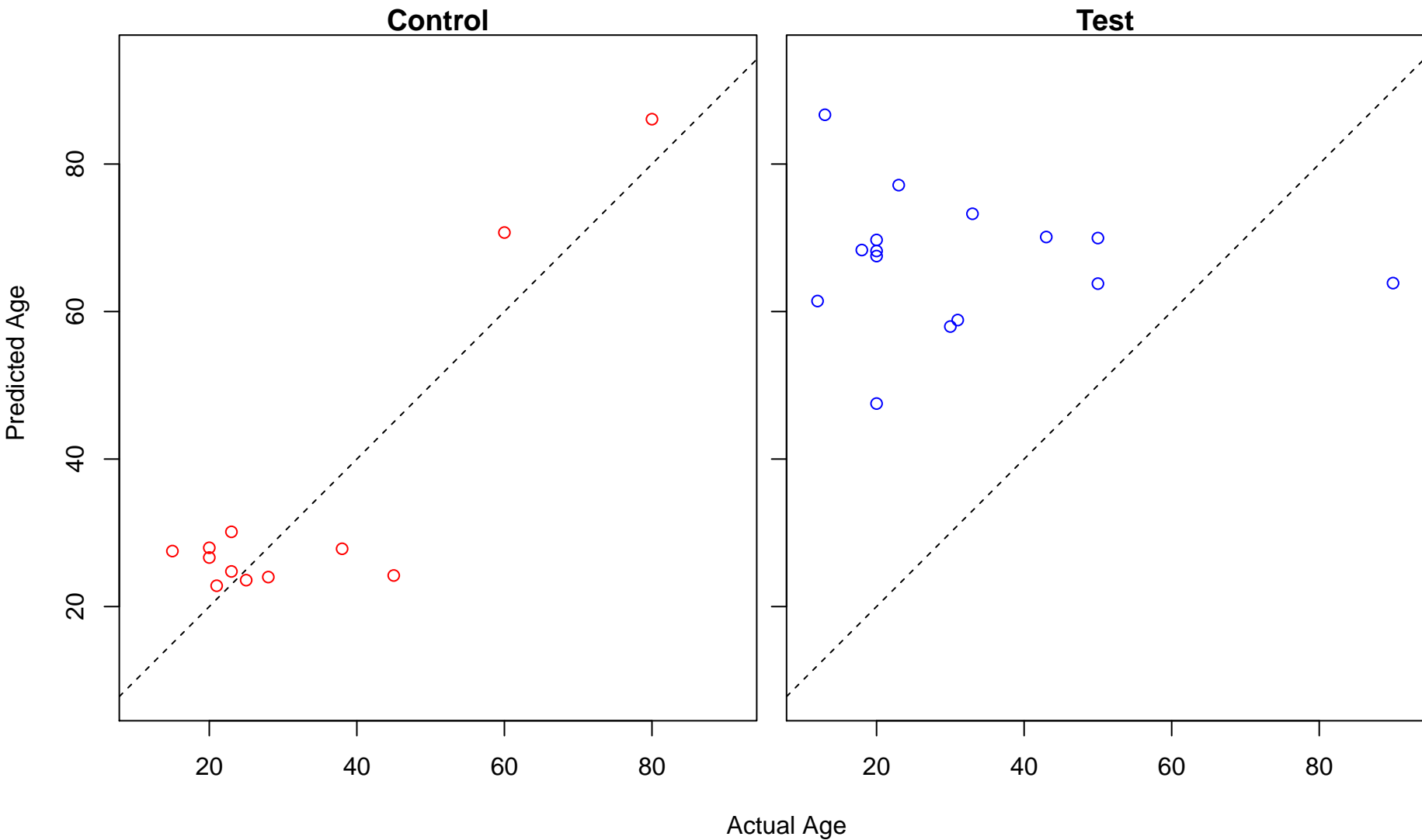


Test

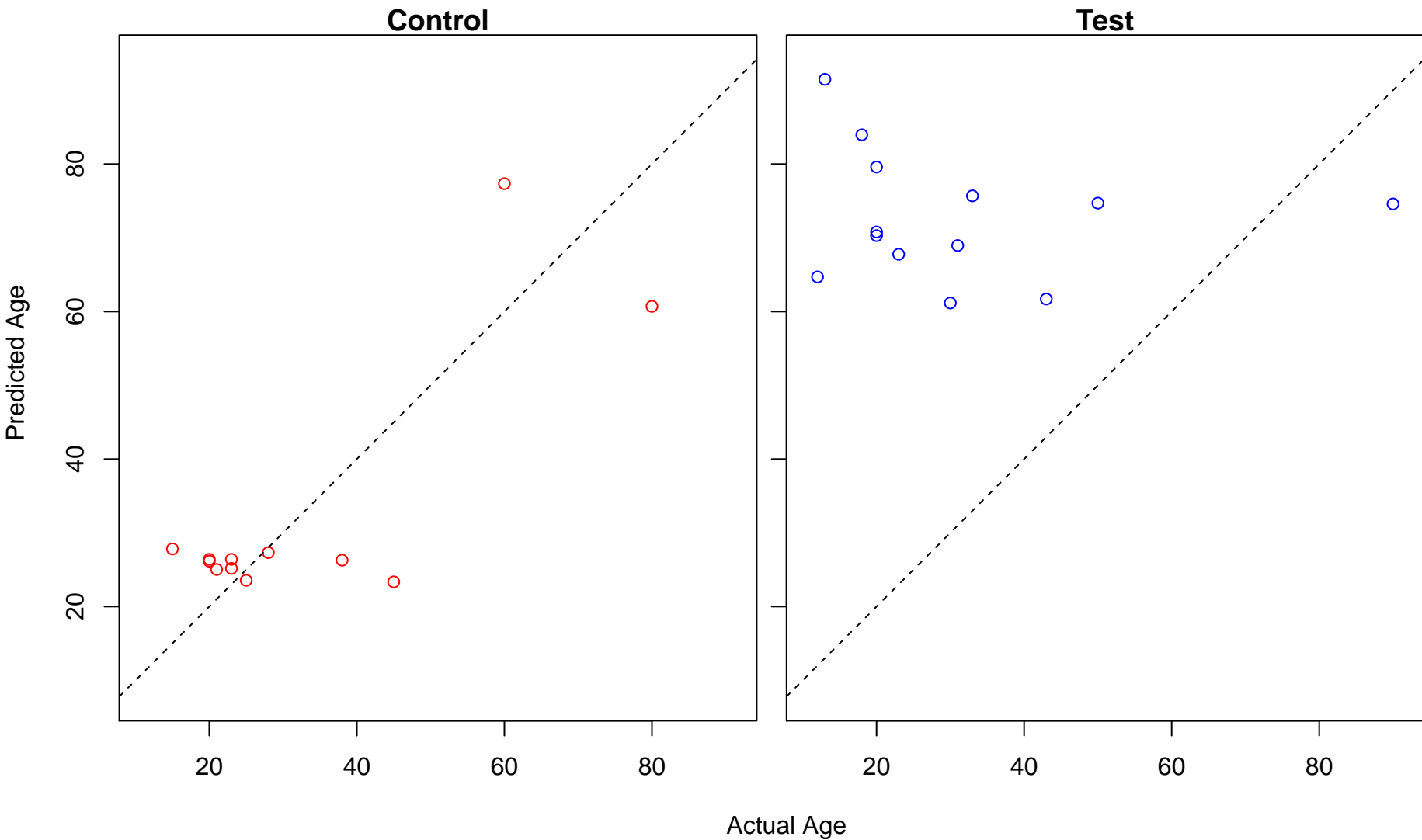


Actual Age

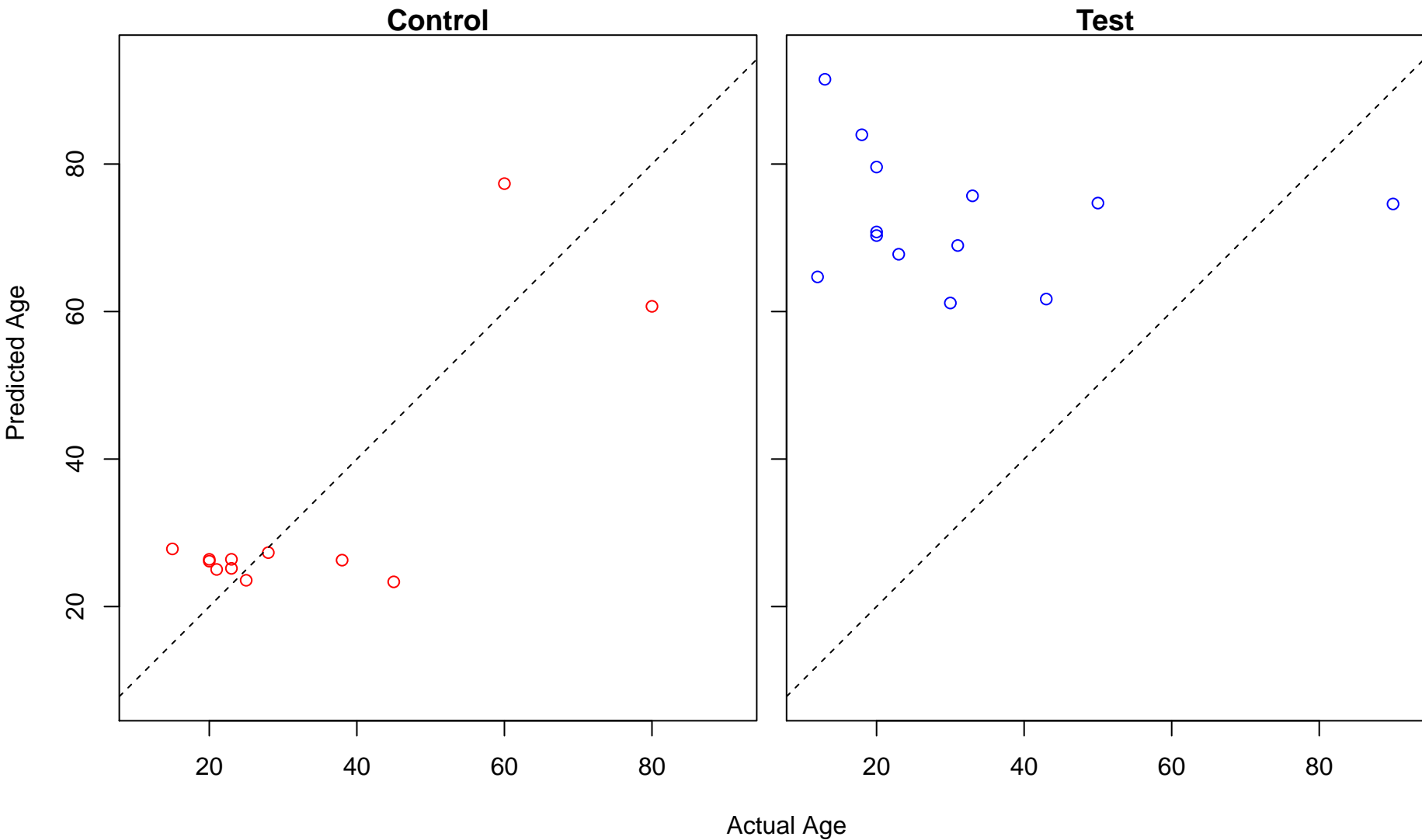
negative regulation of receptor biosynthetic process (Score: 7.005811)



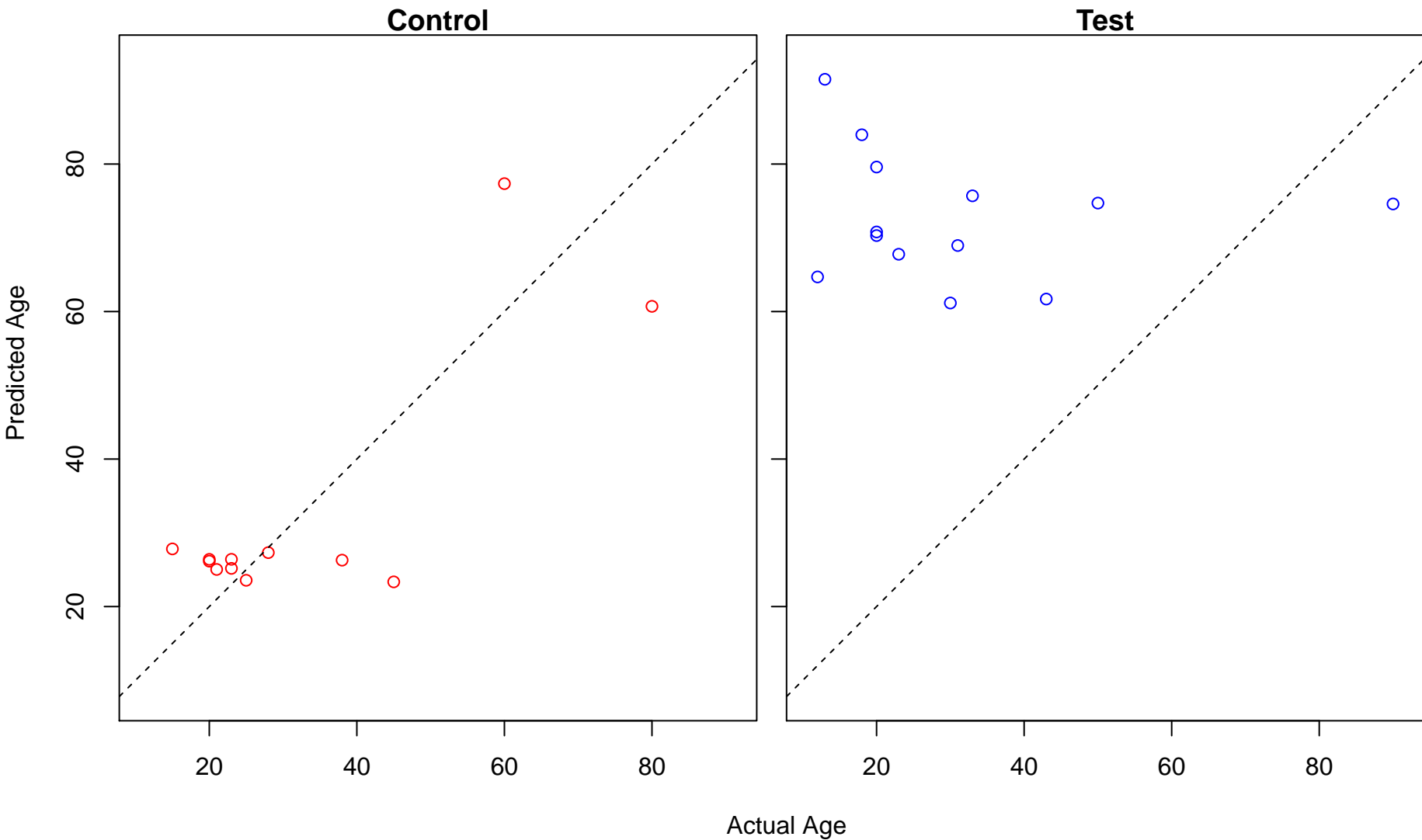
multi-organism transport (Score: 7.004841)



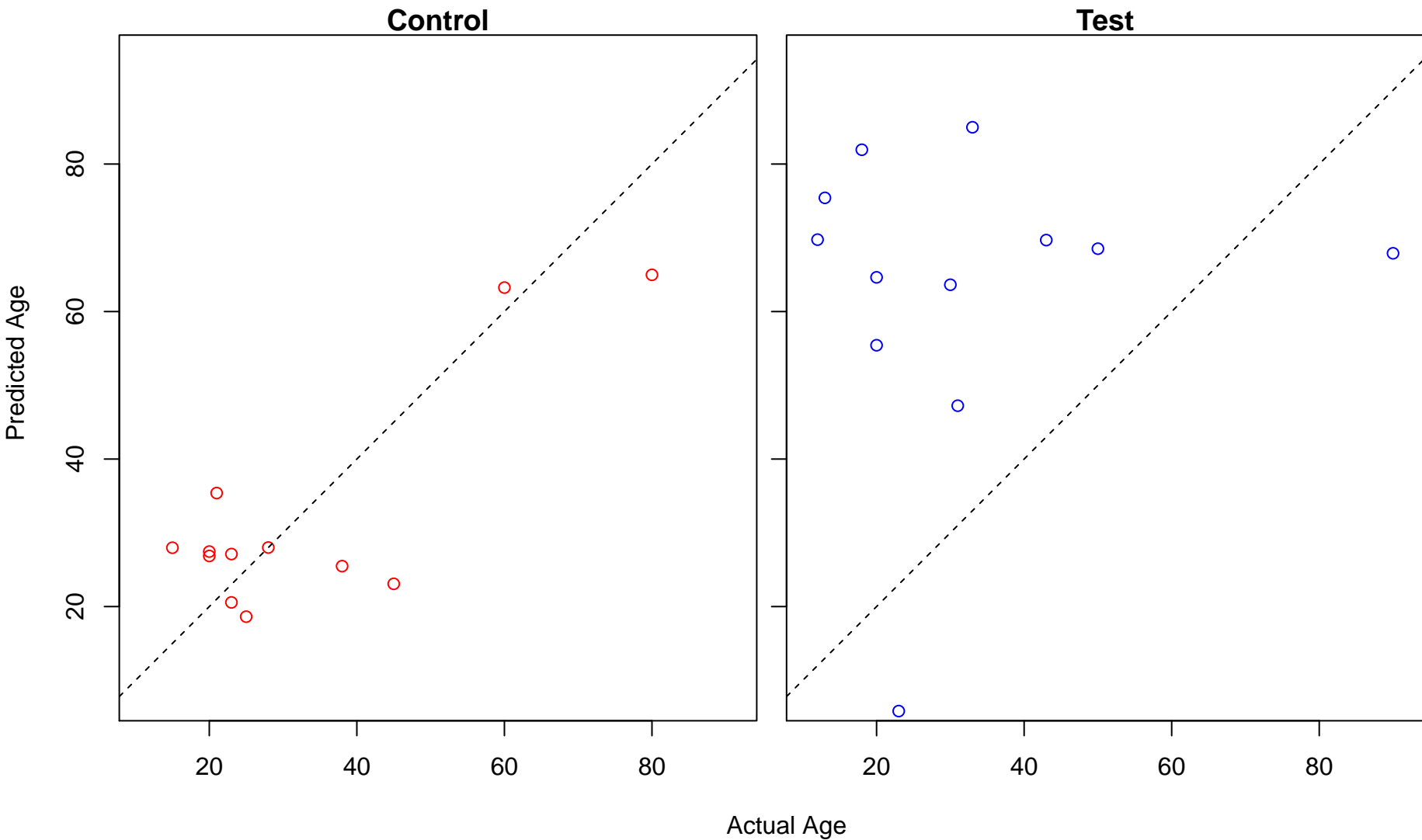
transport of virus (Score: 7.004841)



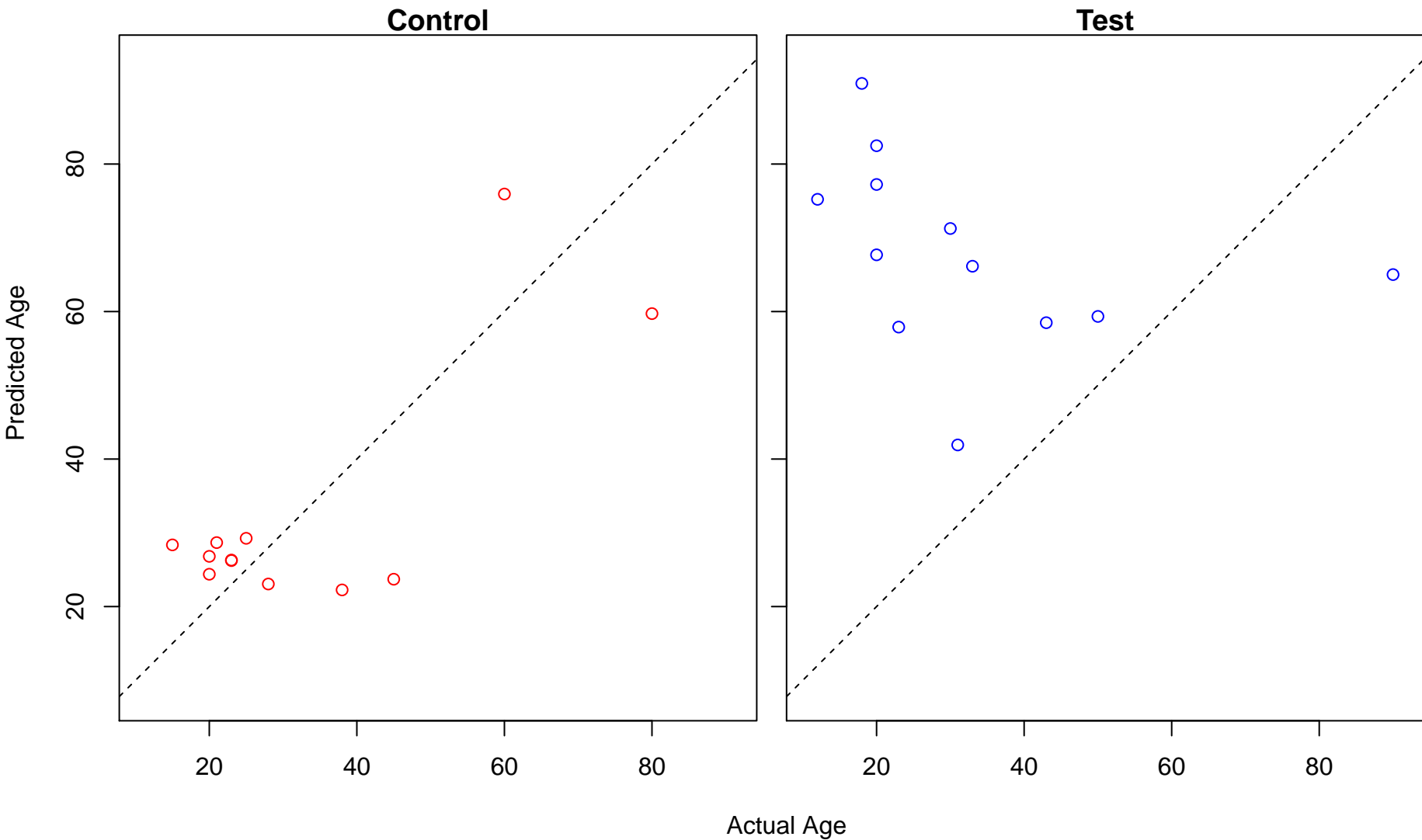
multi-organism localization (Score: 7.004841)



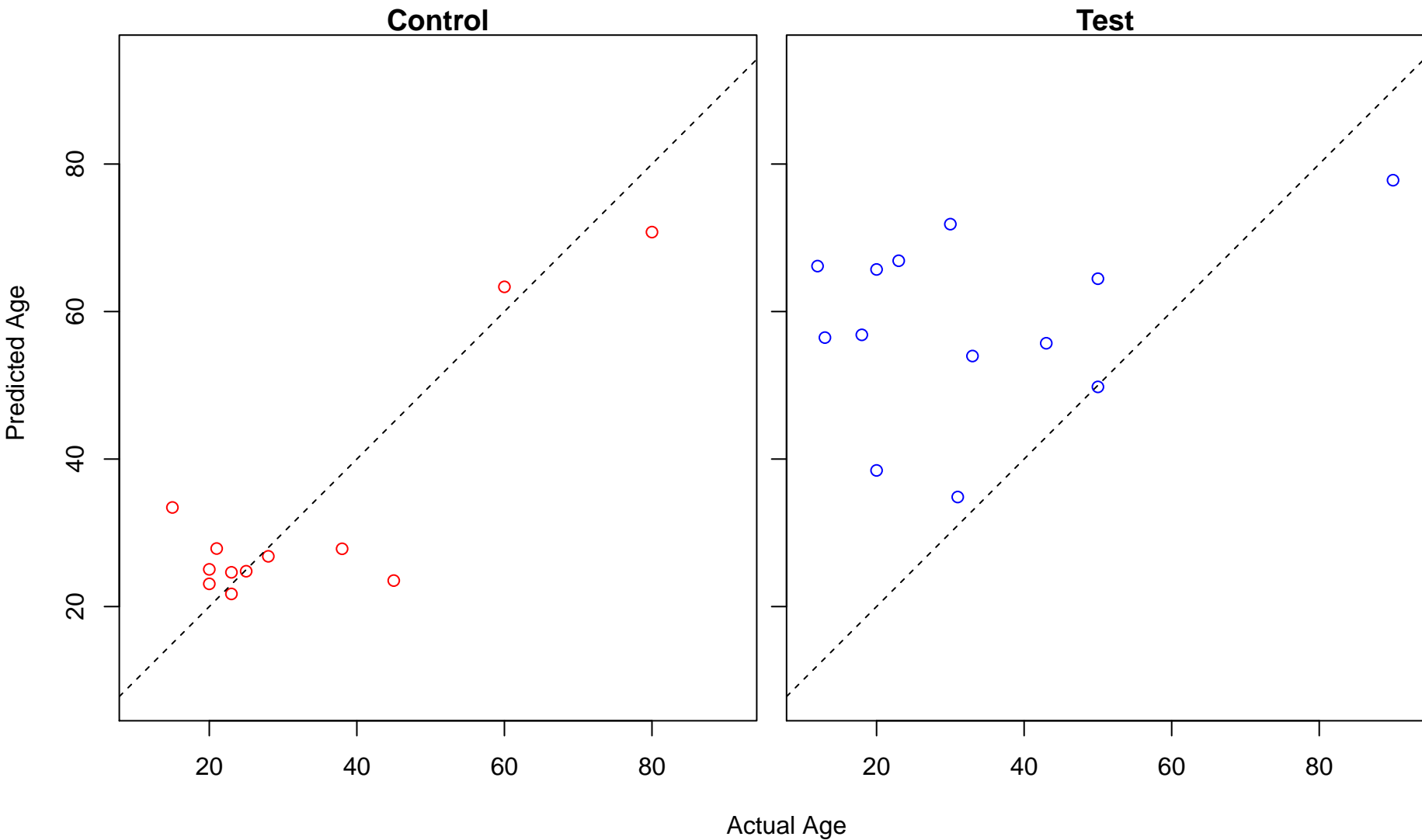
activation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 7.002777)



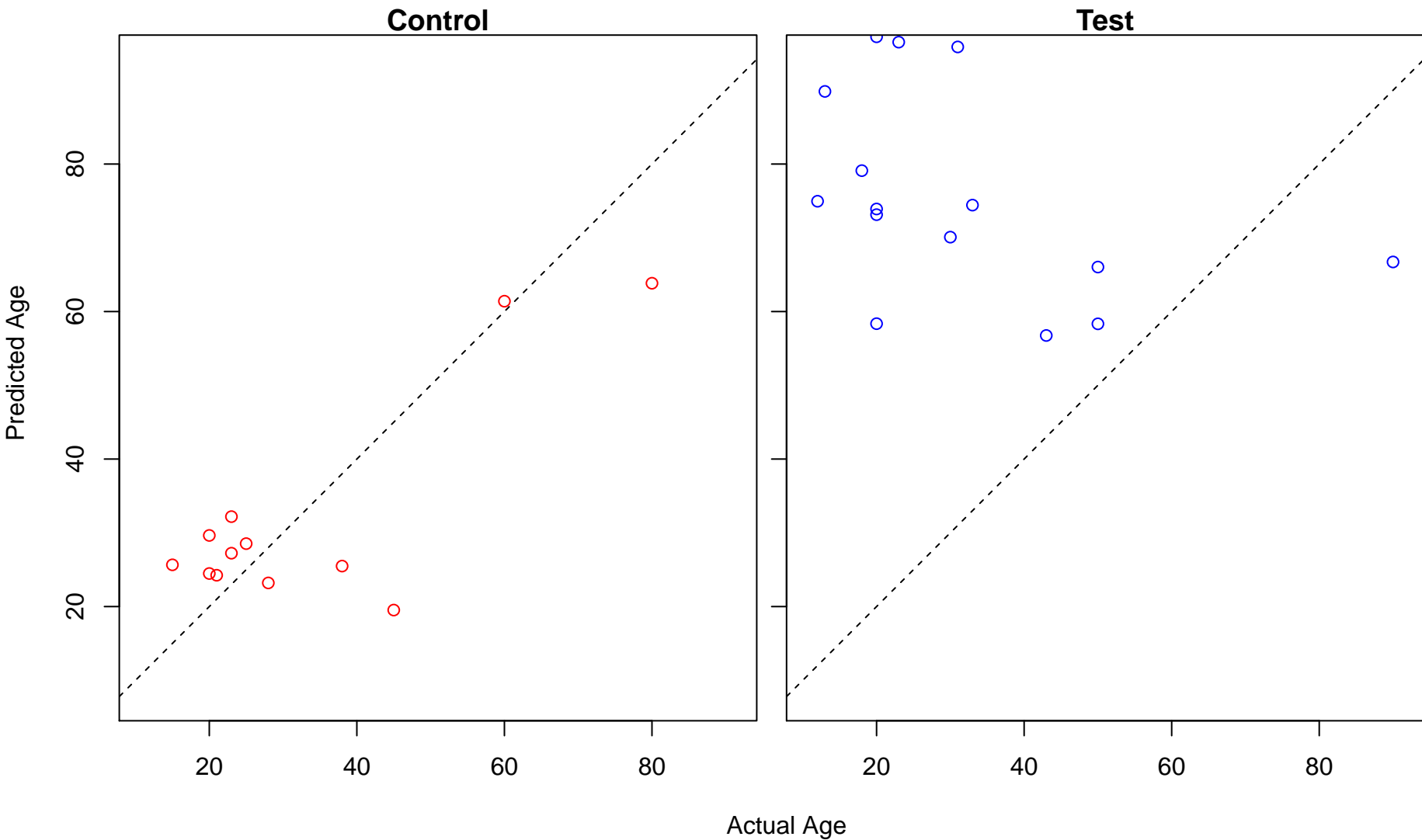
regulation of execution phase of apoptosis (Score: 6.998861)



negative regulation of cell aging (Score: 6.998819)

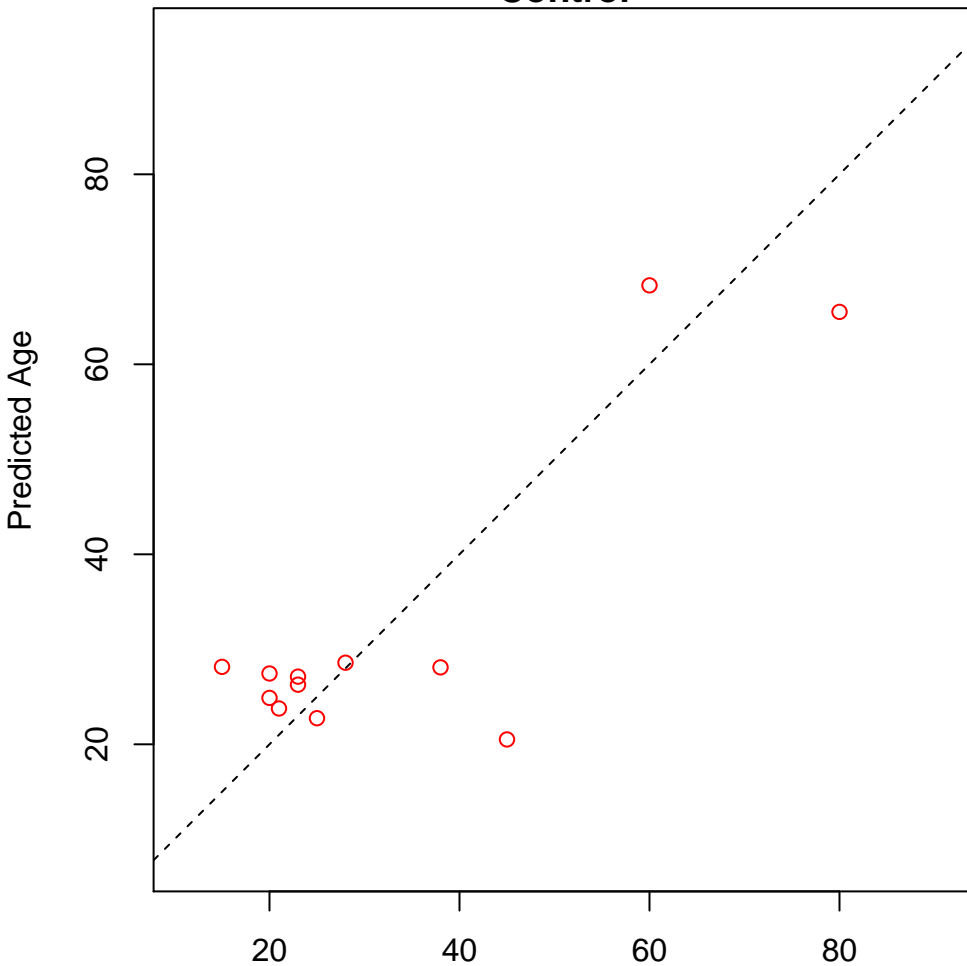


response to interferon-beta (Score: 6.997954)

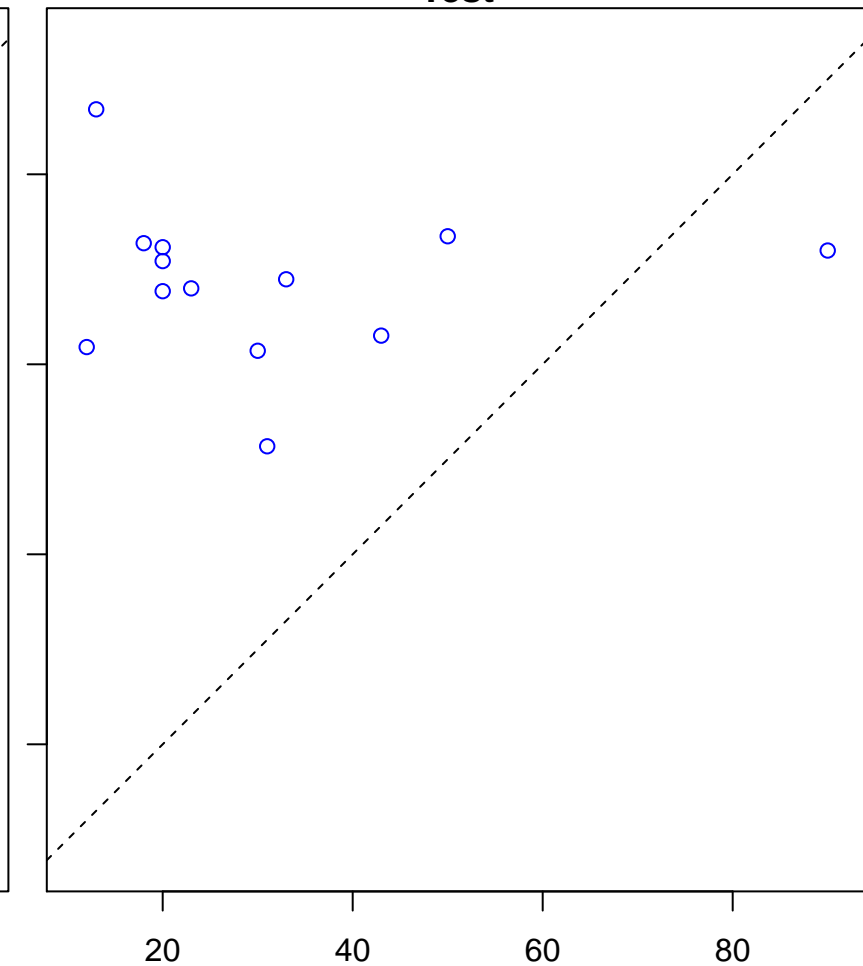


multi-organism reproductive process (Score: 6.994938)

Control



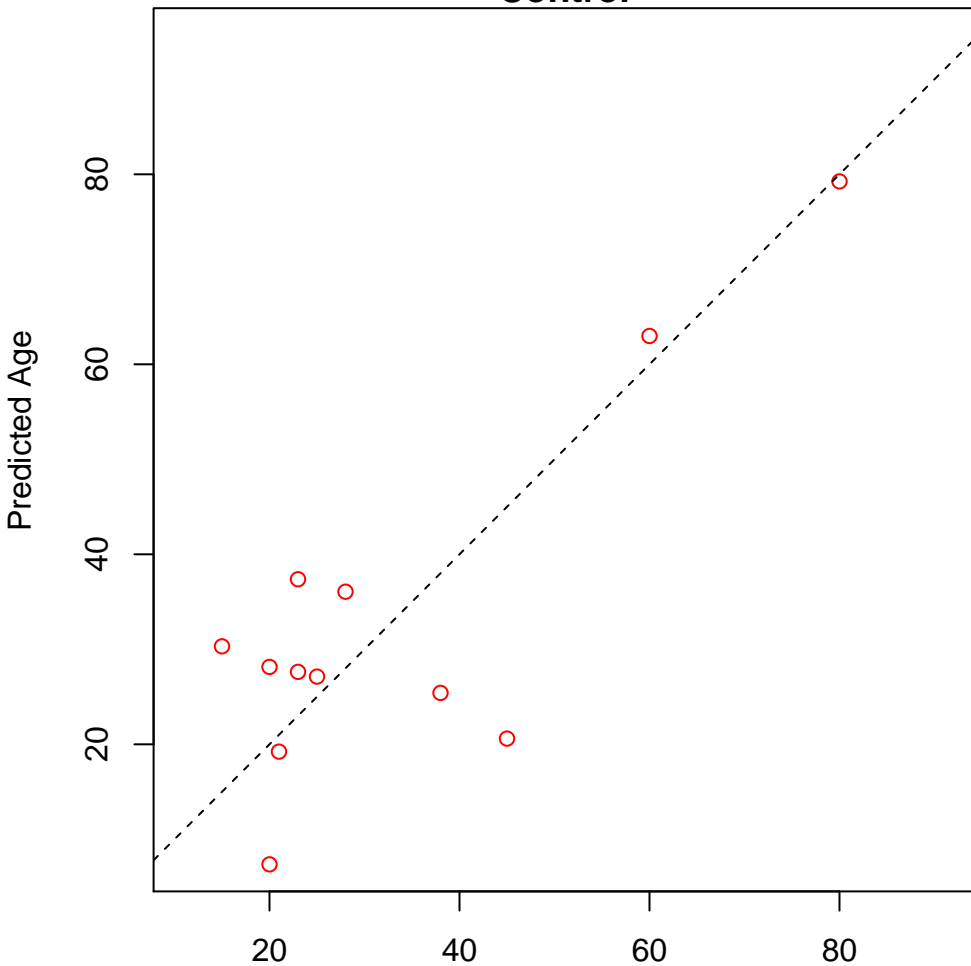
Test



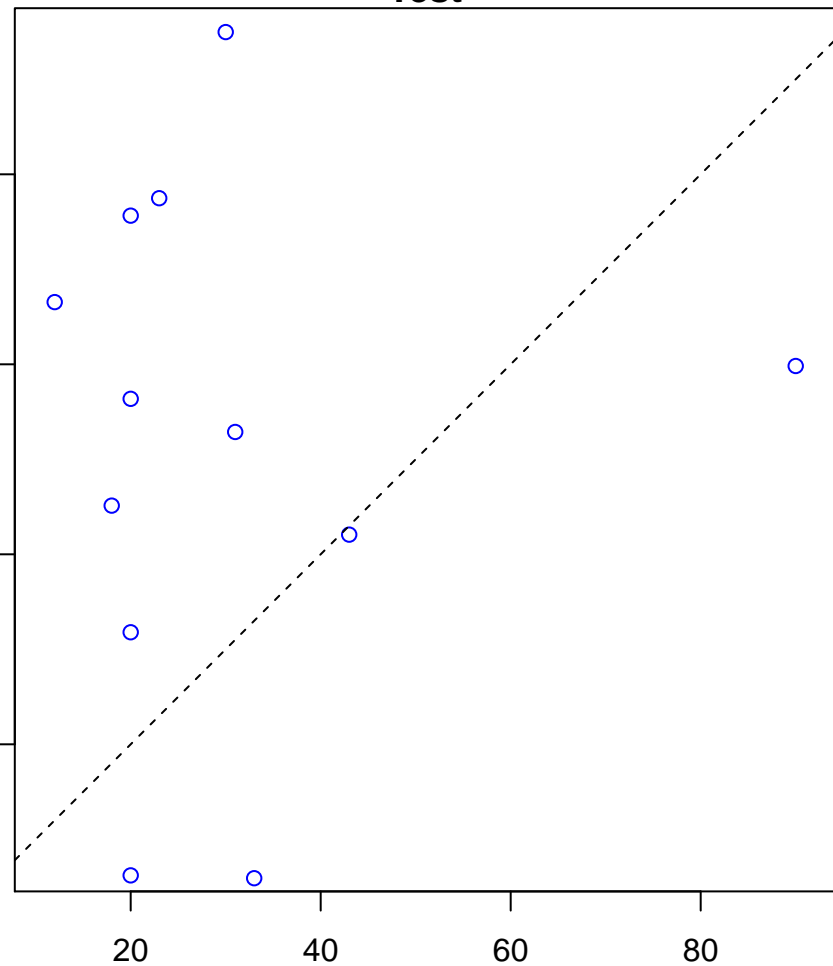
Actual Age

negative regulation of catabolic process (Score: 6.994732)

Control

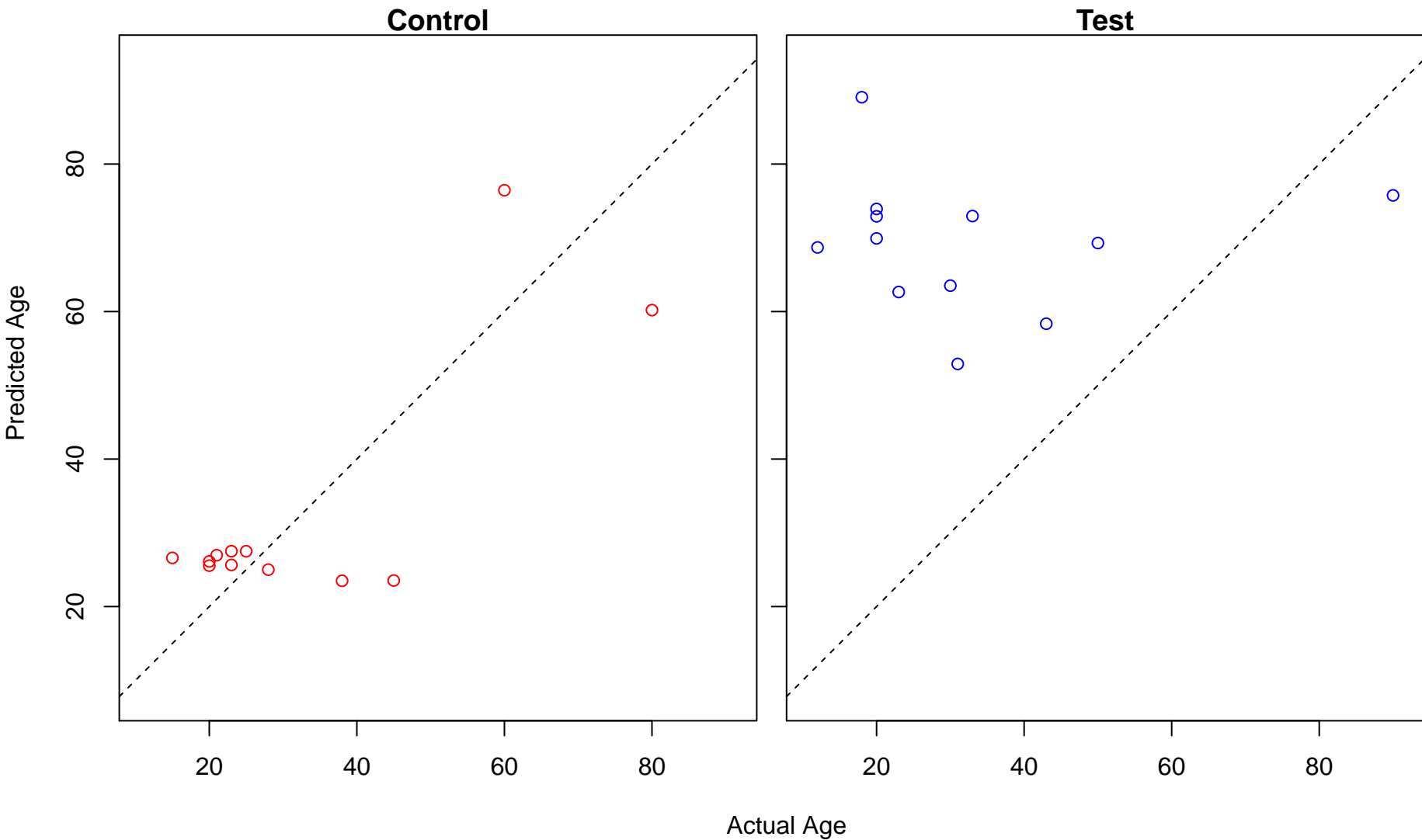


Test

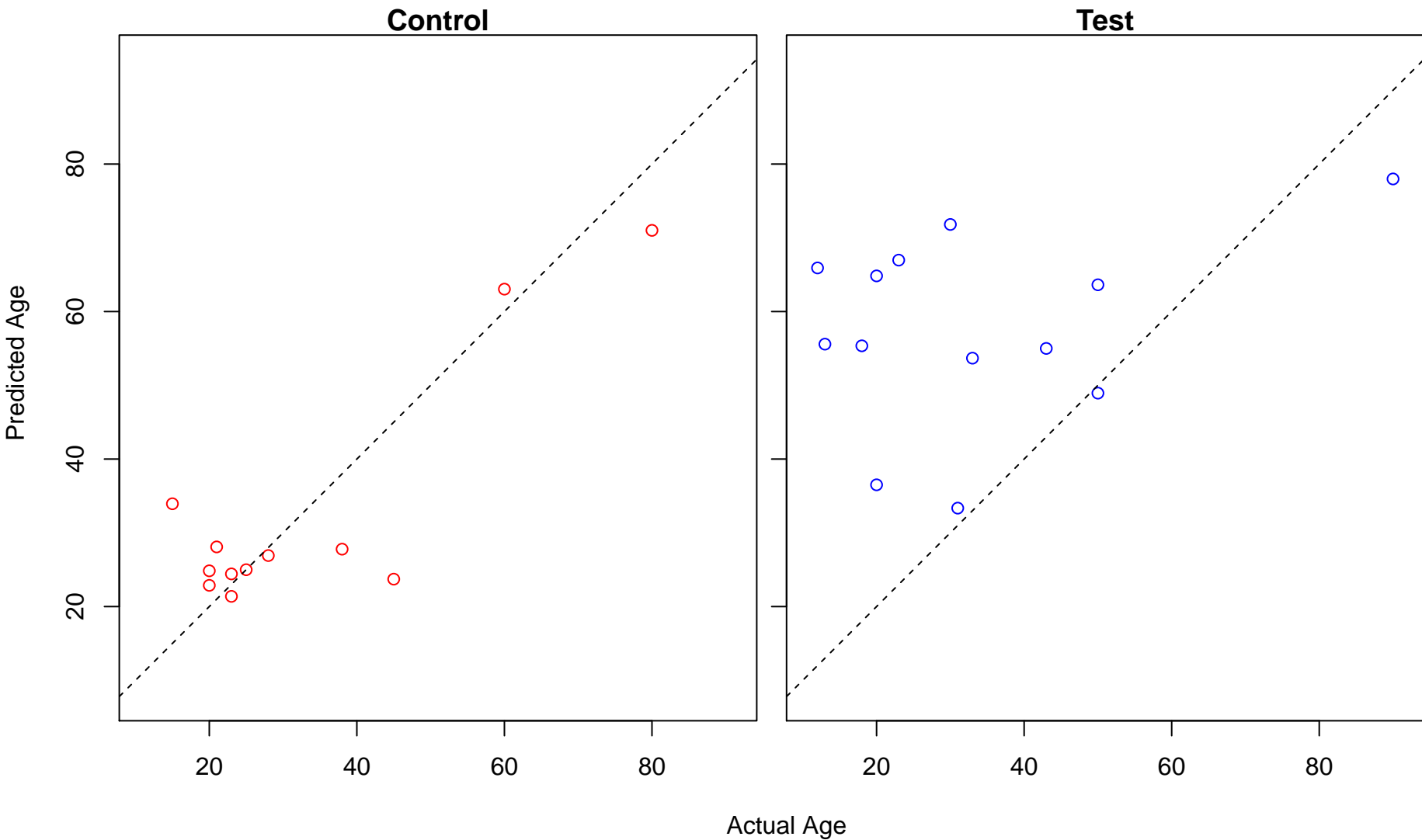


Actual Age

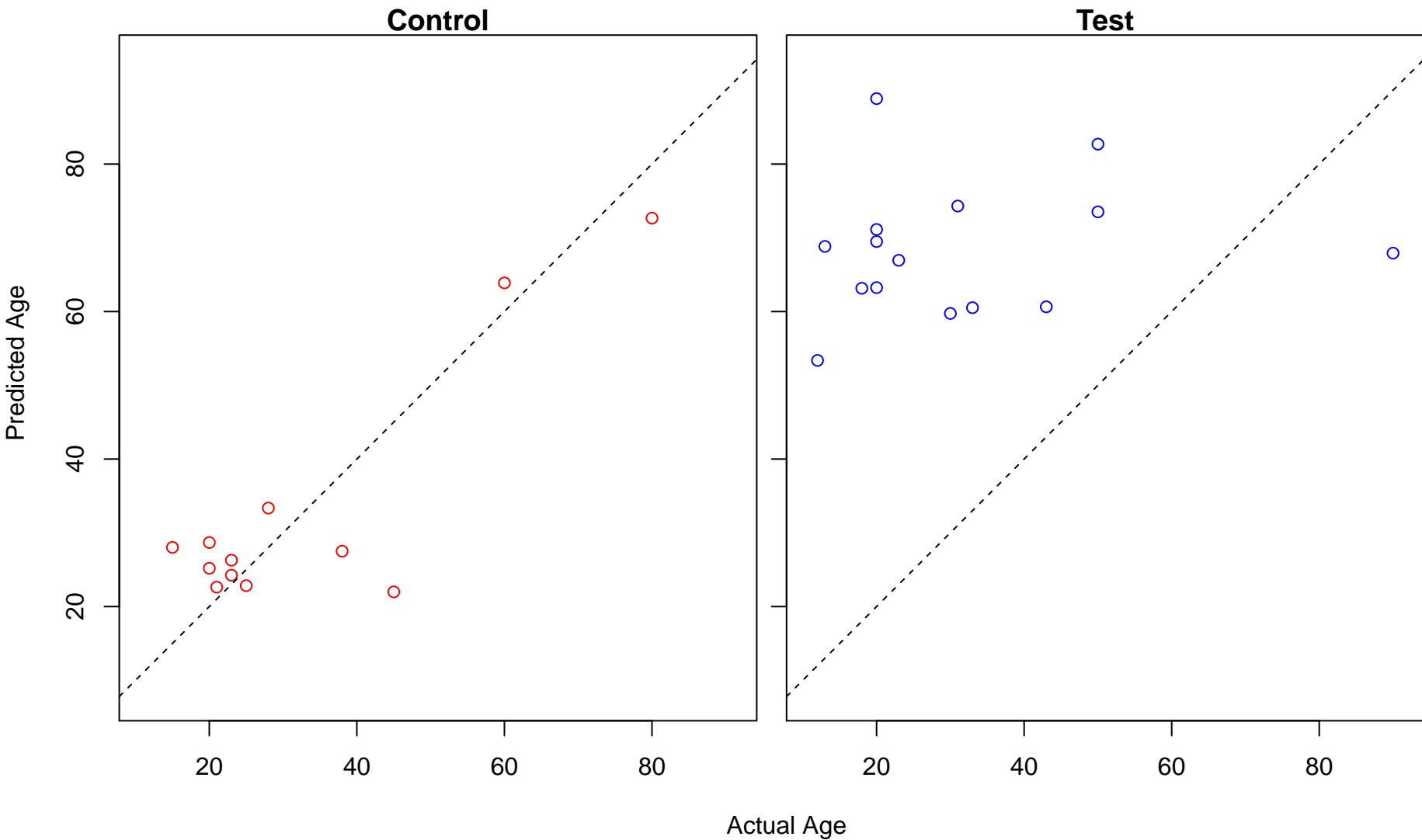
translational elongation (Score: 6.994312)



positive regulation of protein kinase A signaling (Score: 6.989513)

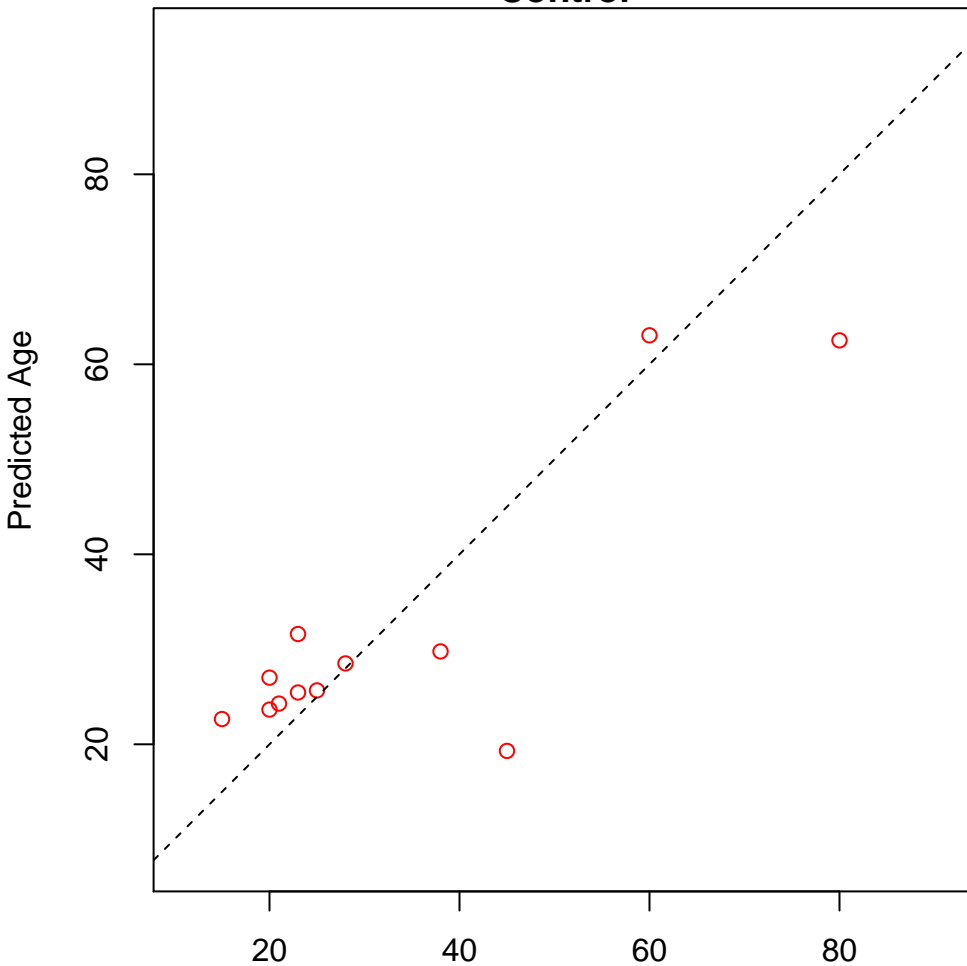


regulation of peptide secretion (Score: 6.989286)

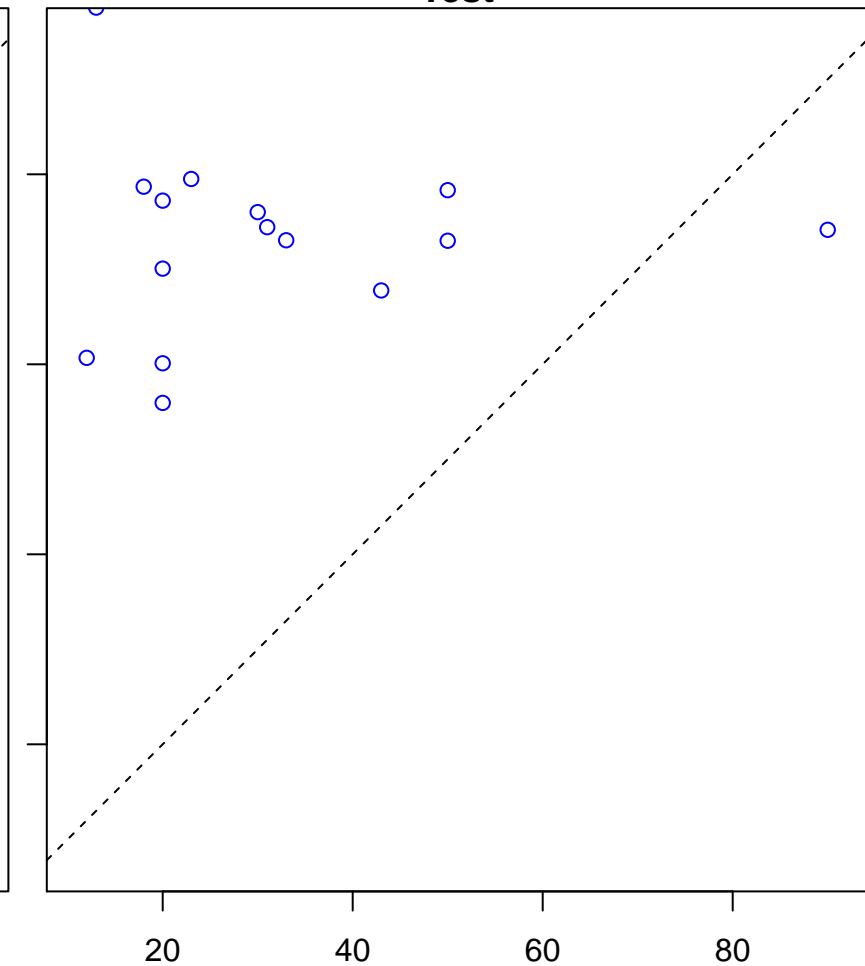


regulation of interleukin-12 production (Score: 6.988060)

Control

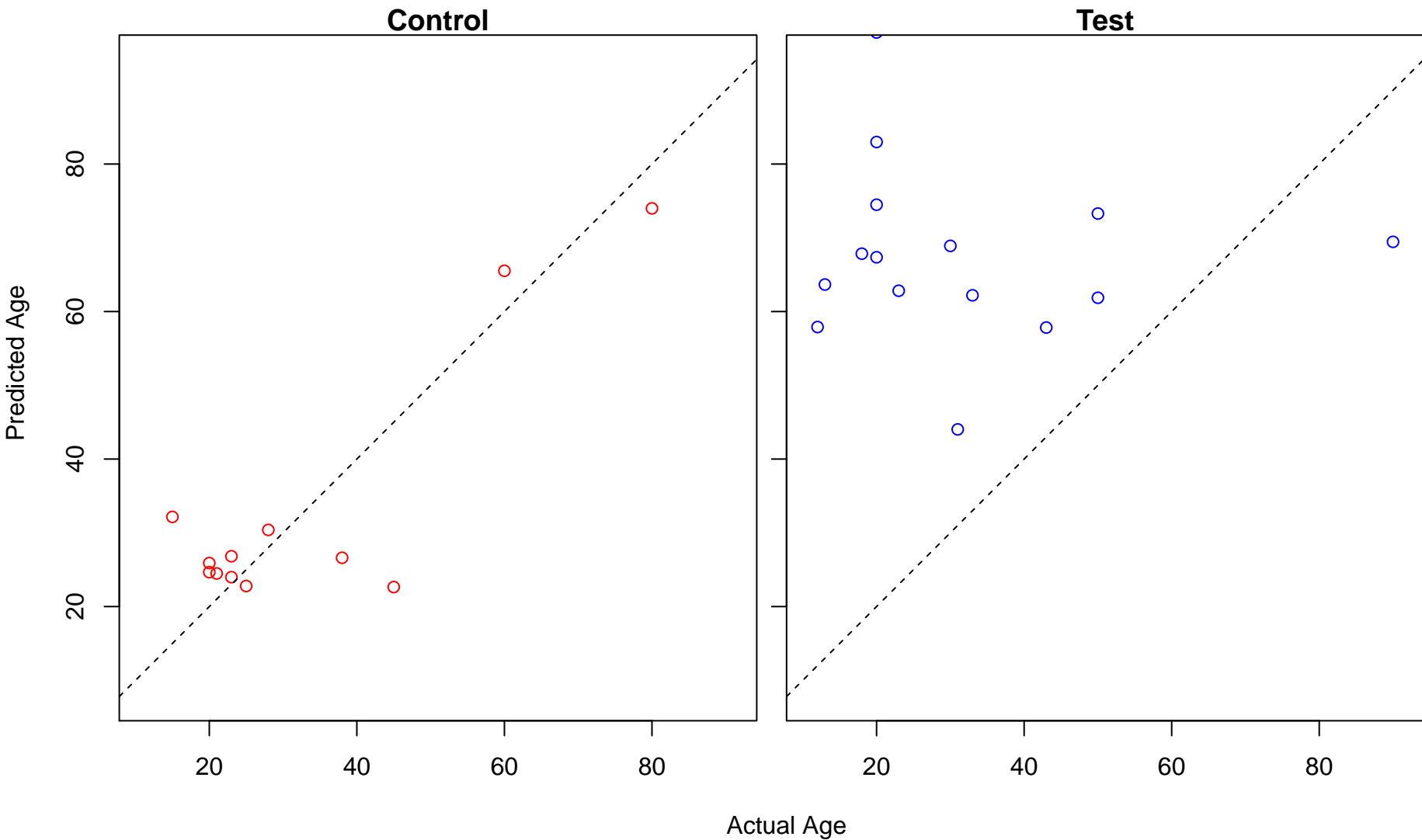


Test

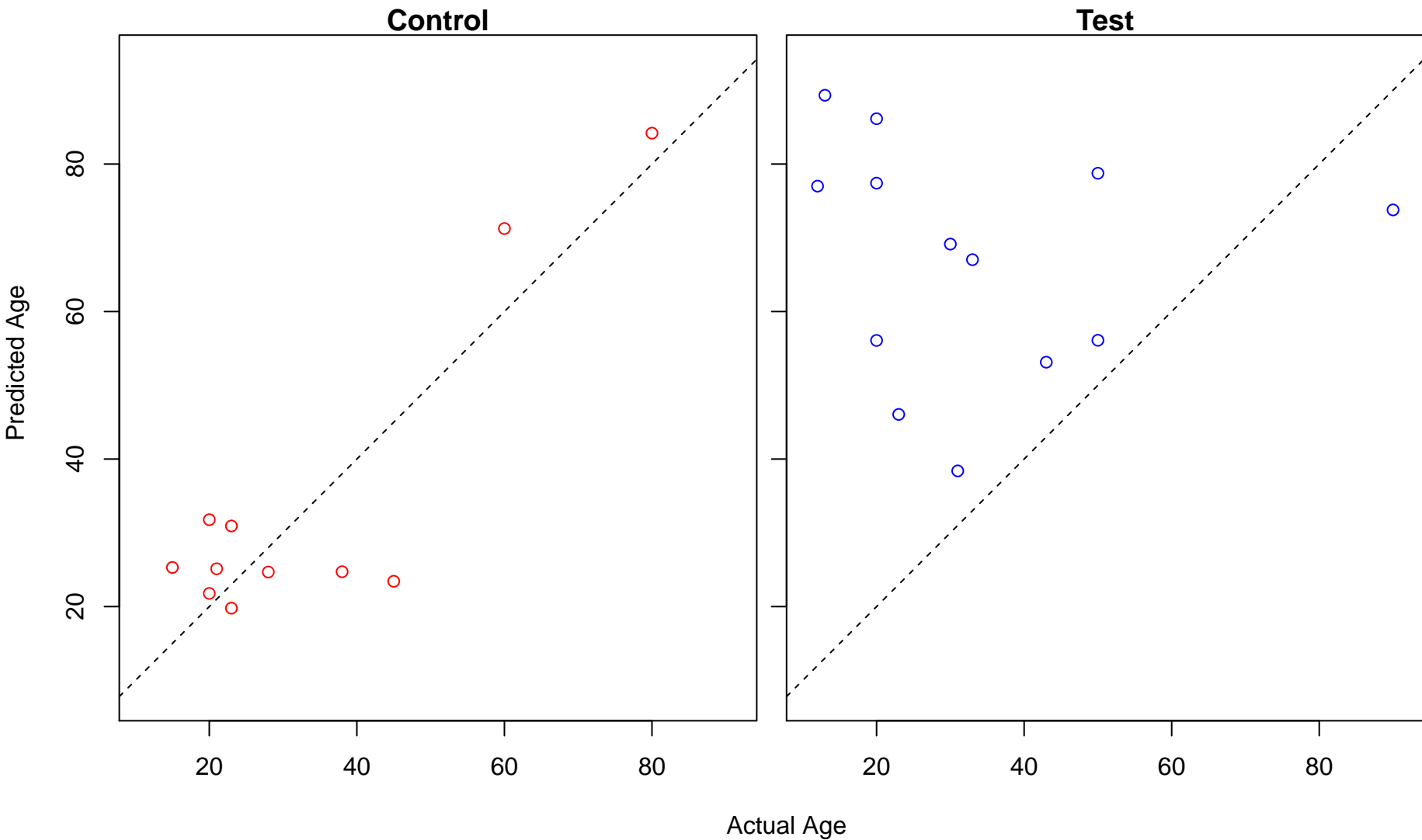


Actual Age

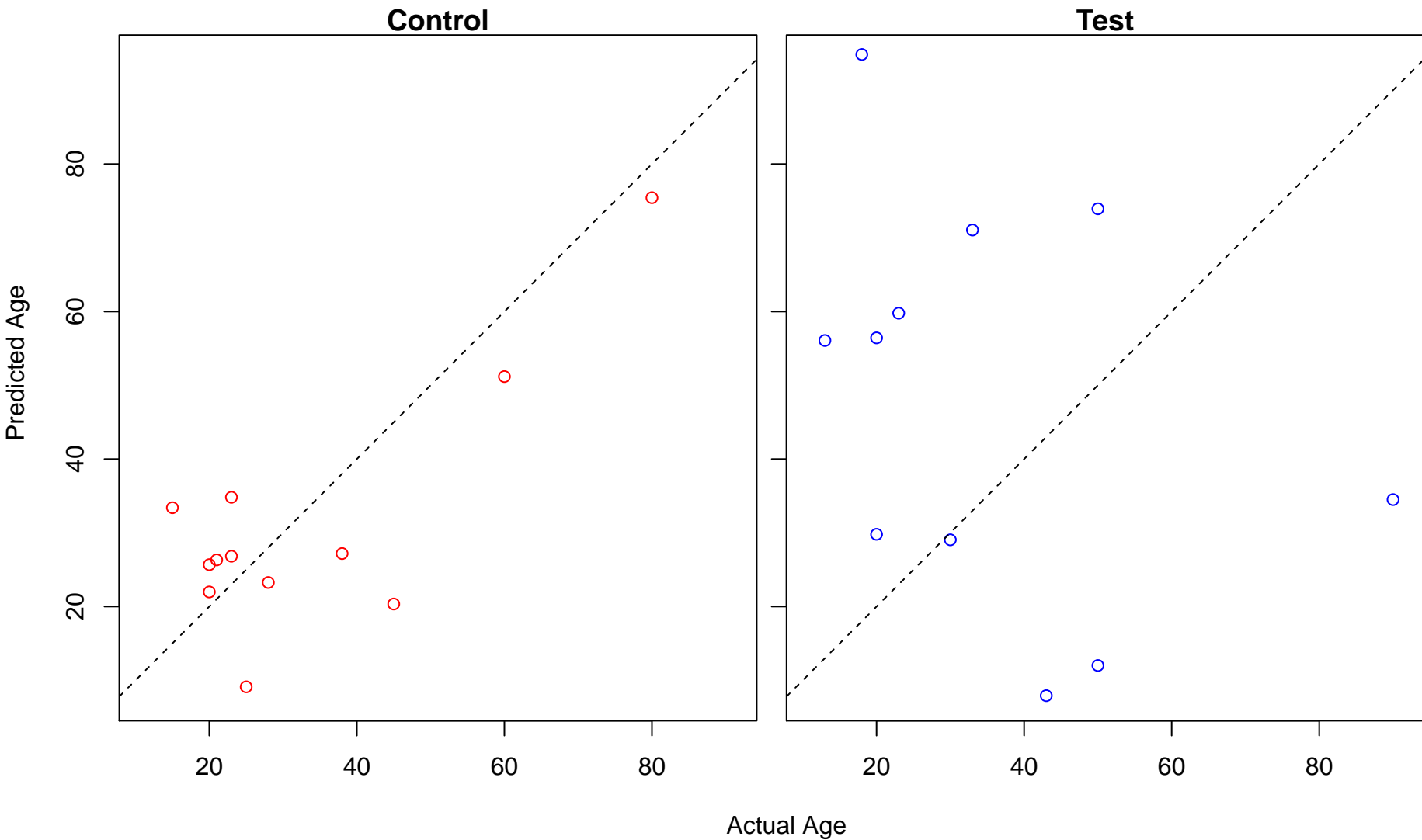
regulation of autophagy (Score: 6.986851)



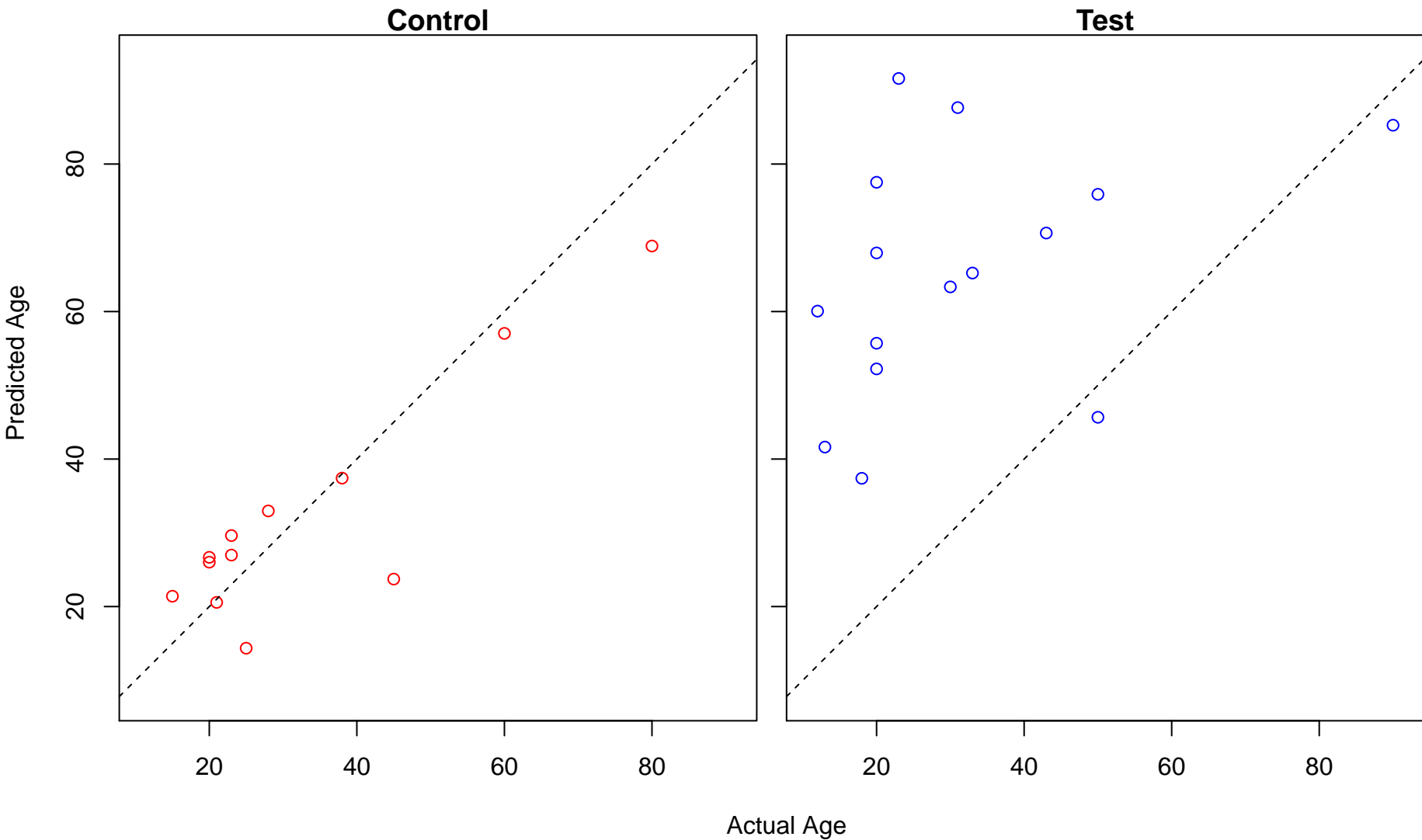
ISG15-protein conjugation (Score: 6.986332)



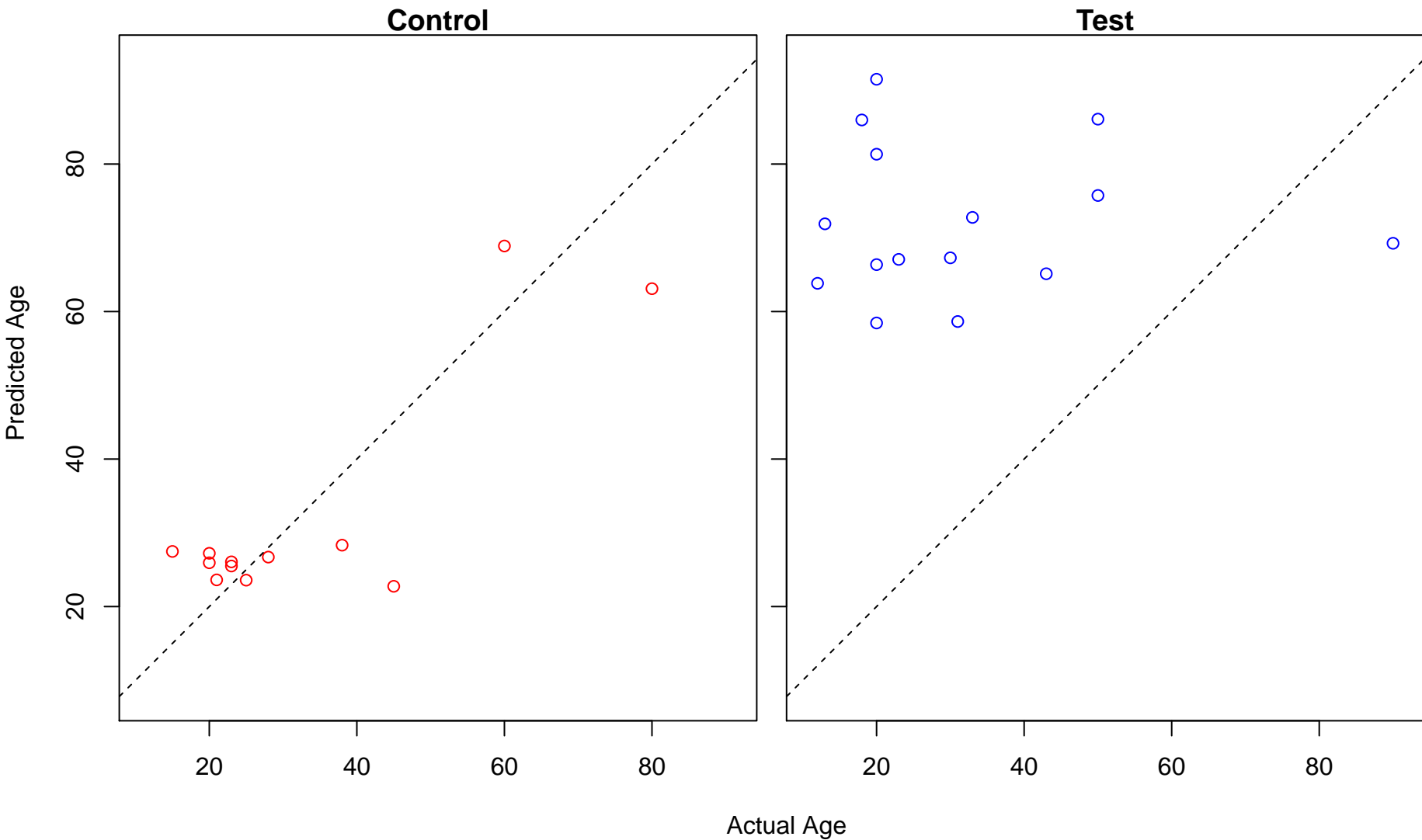
cellular homeostasis (Score: 6.984454)



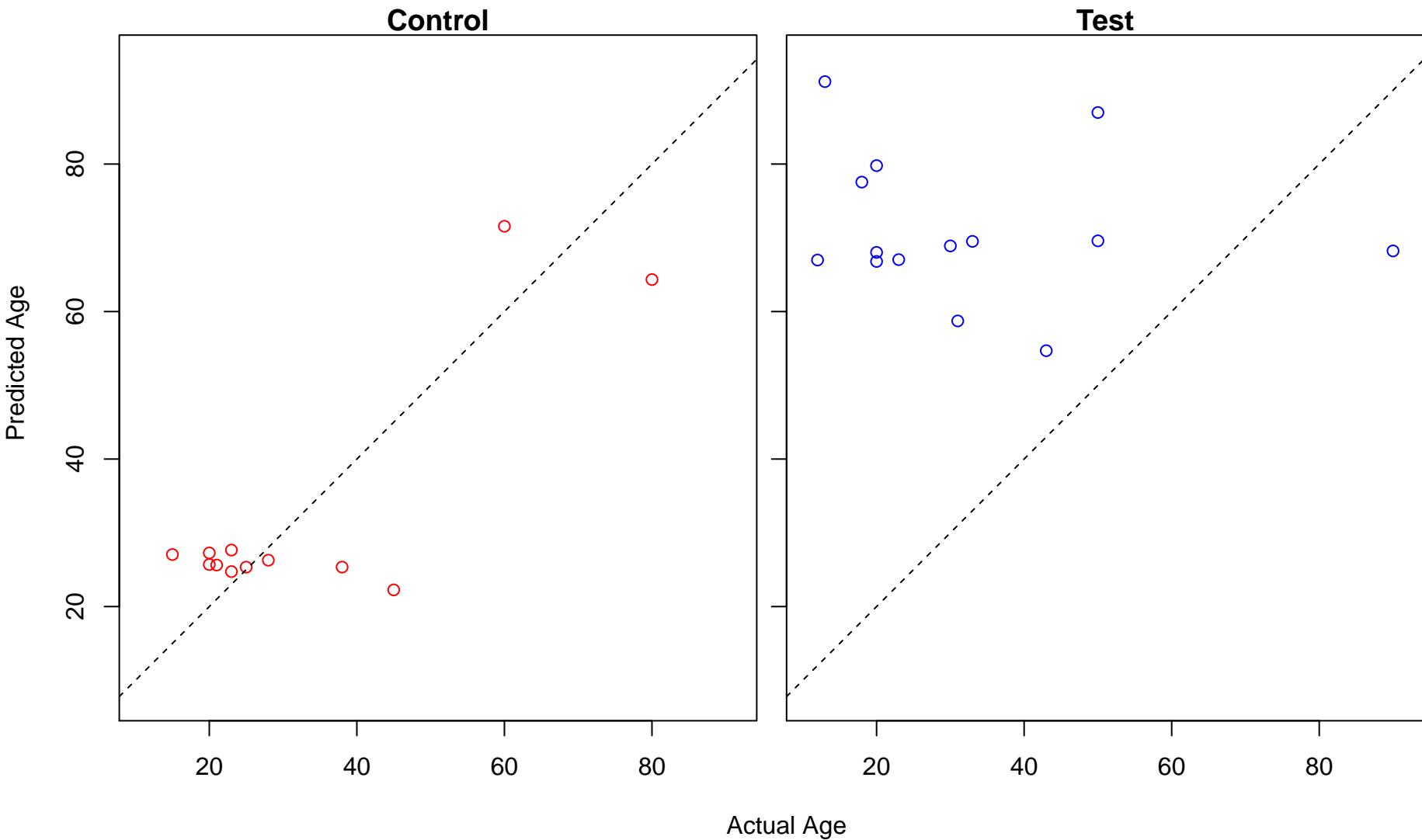
motile cilium assembly (Score: 6.982330)



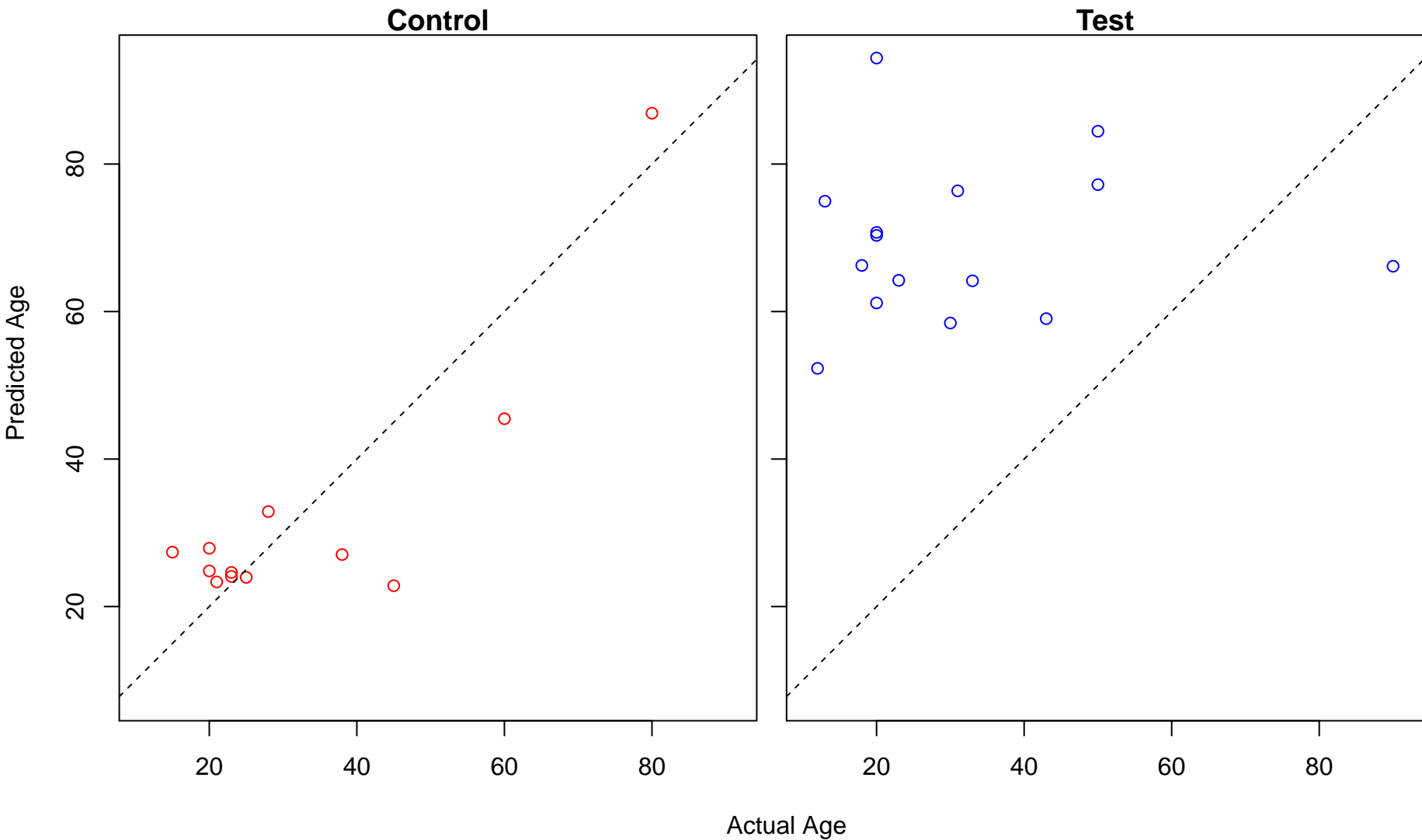
activation of GTPase activity (Score: 6.981863)



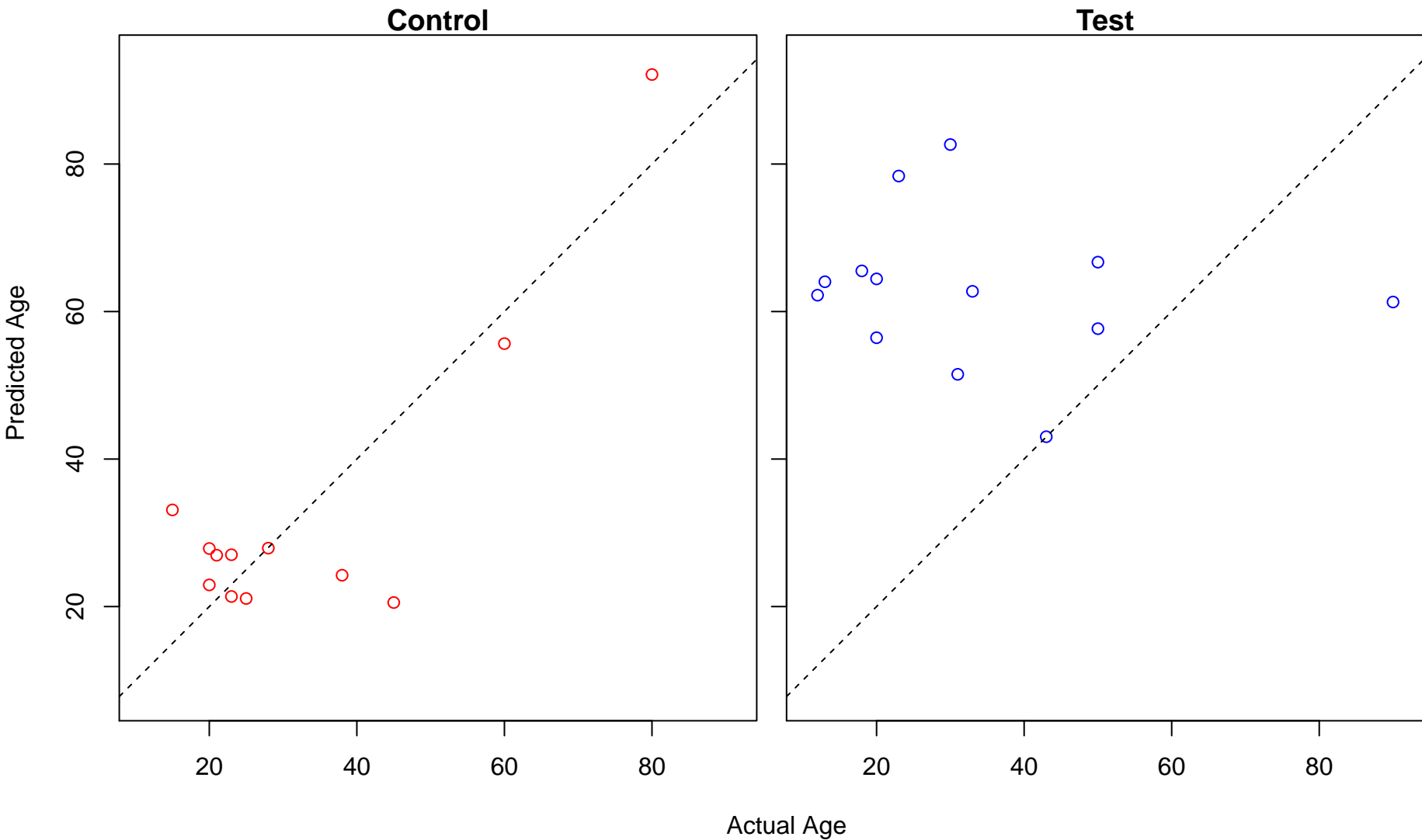
positive regulation of viral genome replication (Score: 6.980753)



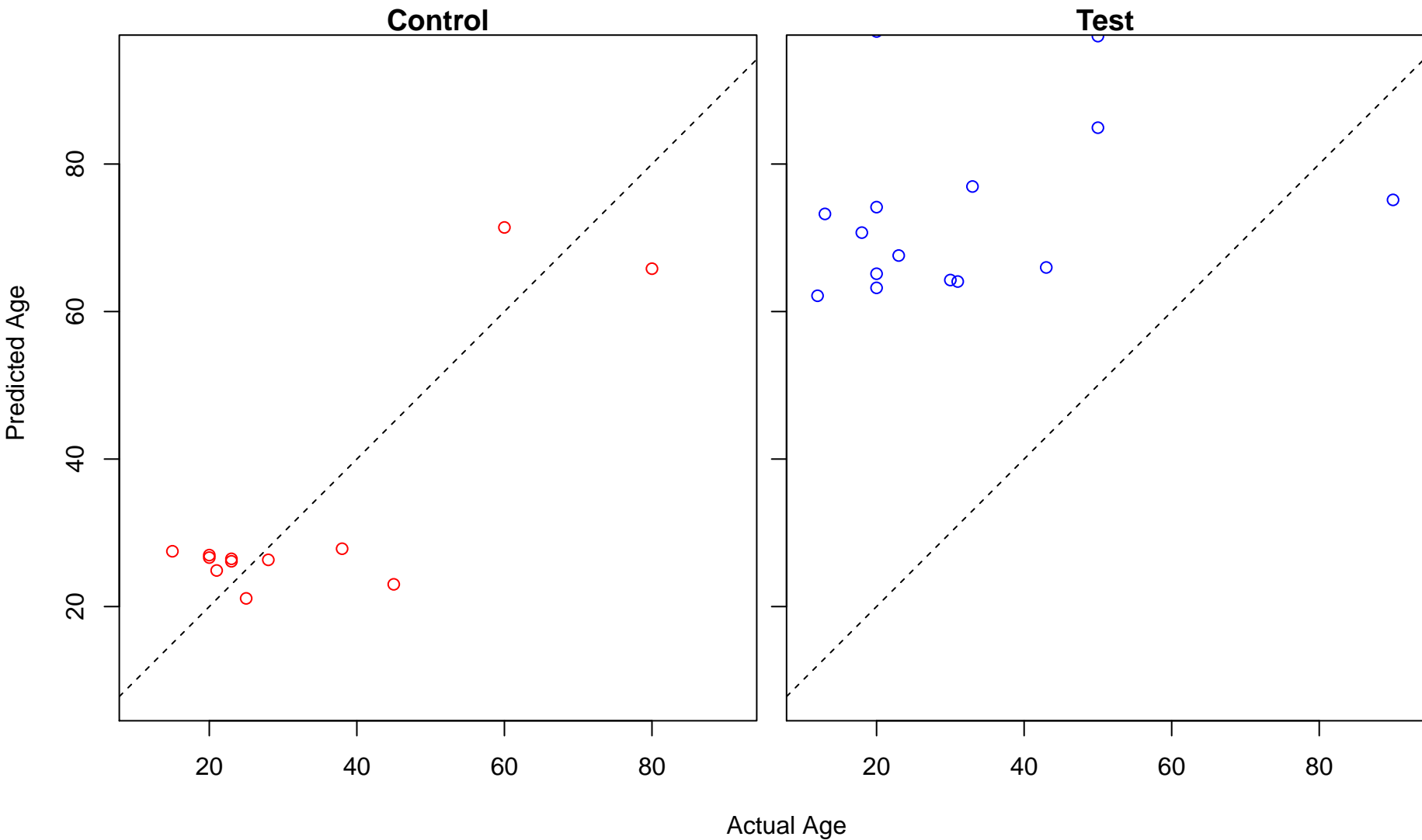
positive regulation of cyclic nucleotide metabolic process (Score: 6.979550)



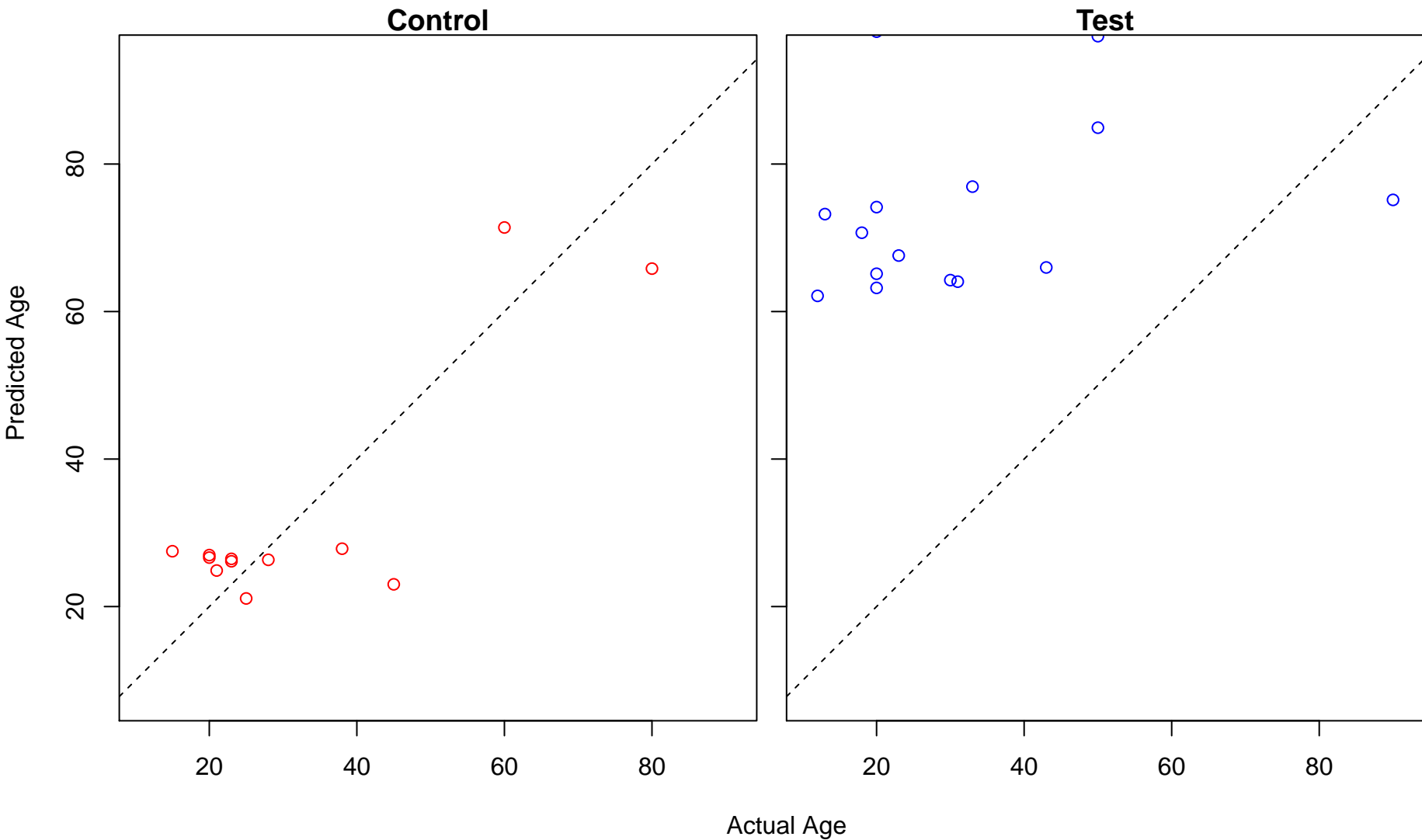
histone H4-R3 methylation (Score: 6.978786)



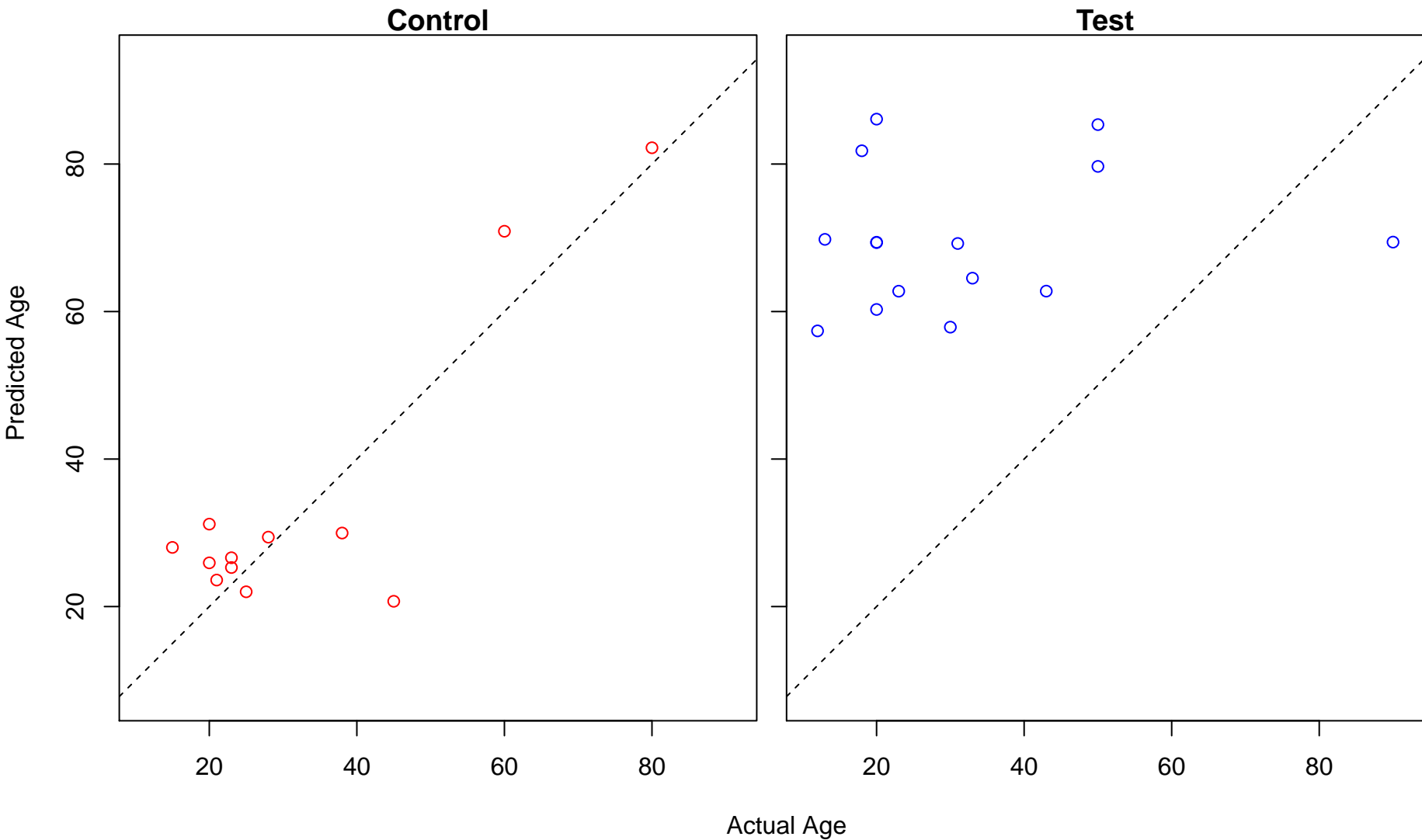
negative regulation of antigen receptor-mediated signaling pathway (Score: 6.975026)



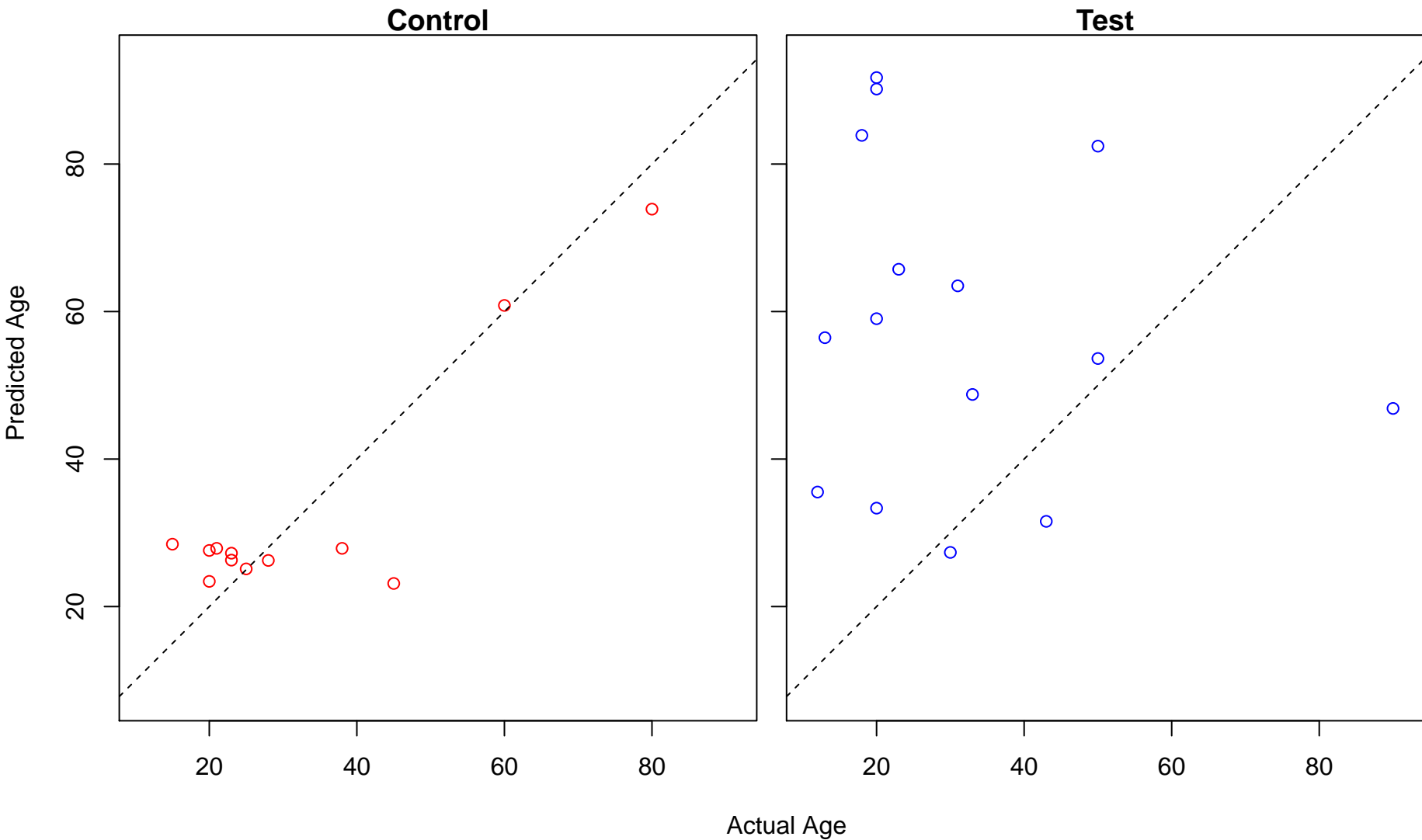
negative regulation of T cell receptor signaling pathway (Score: 6.973816)



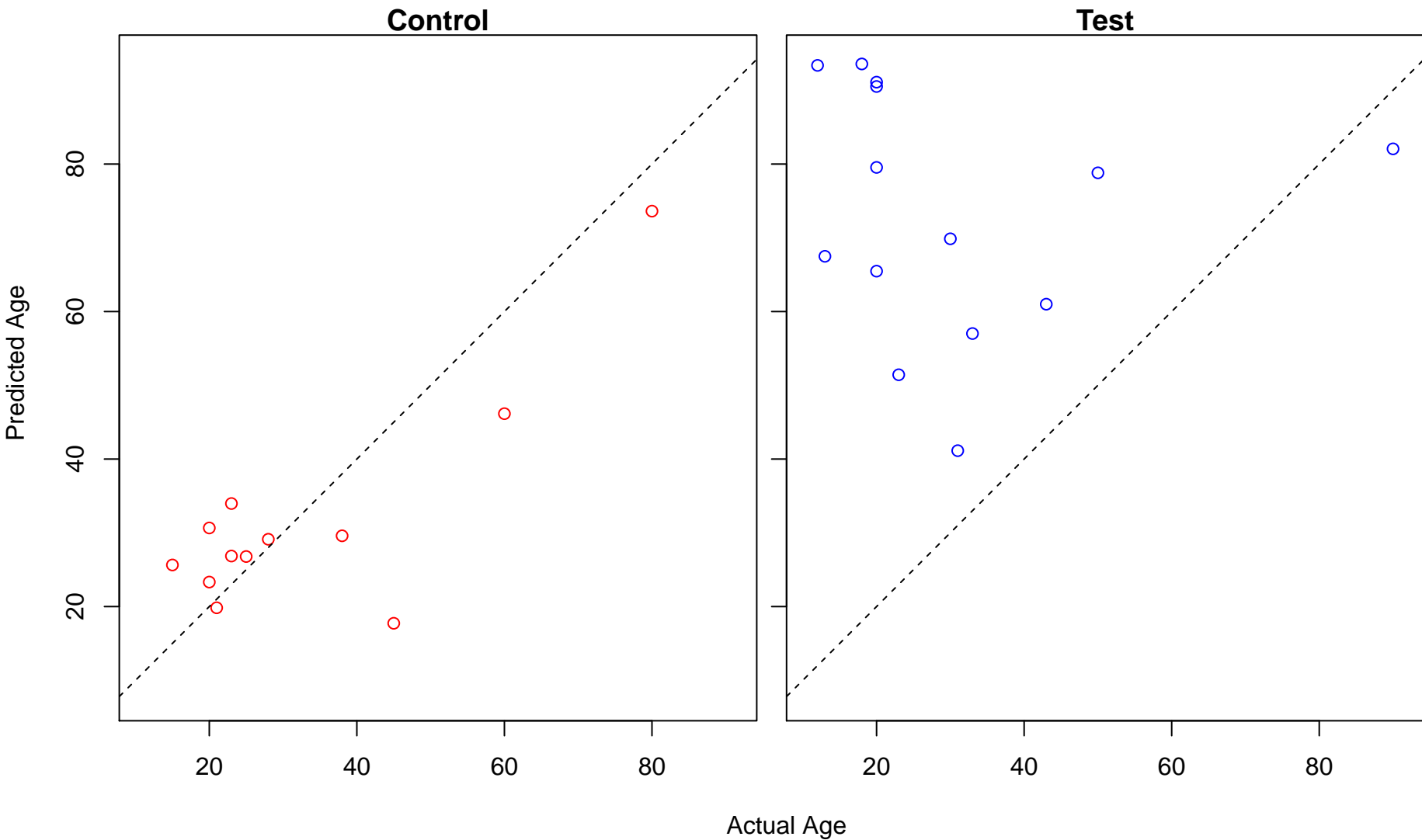
positive regulation of locomotion (Score: 6.972241)



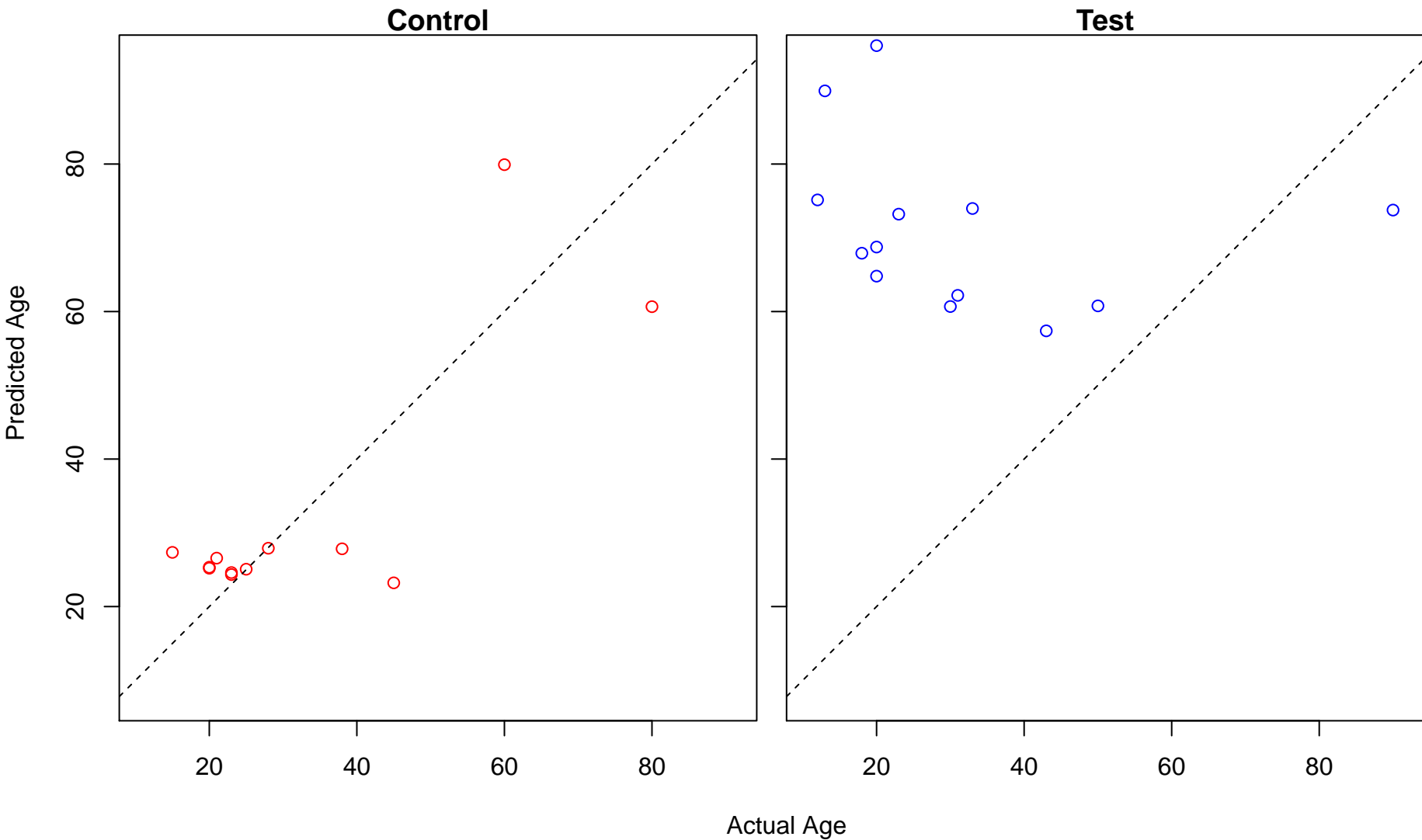
anatomical structure homeostasis (Score: 6.971618)



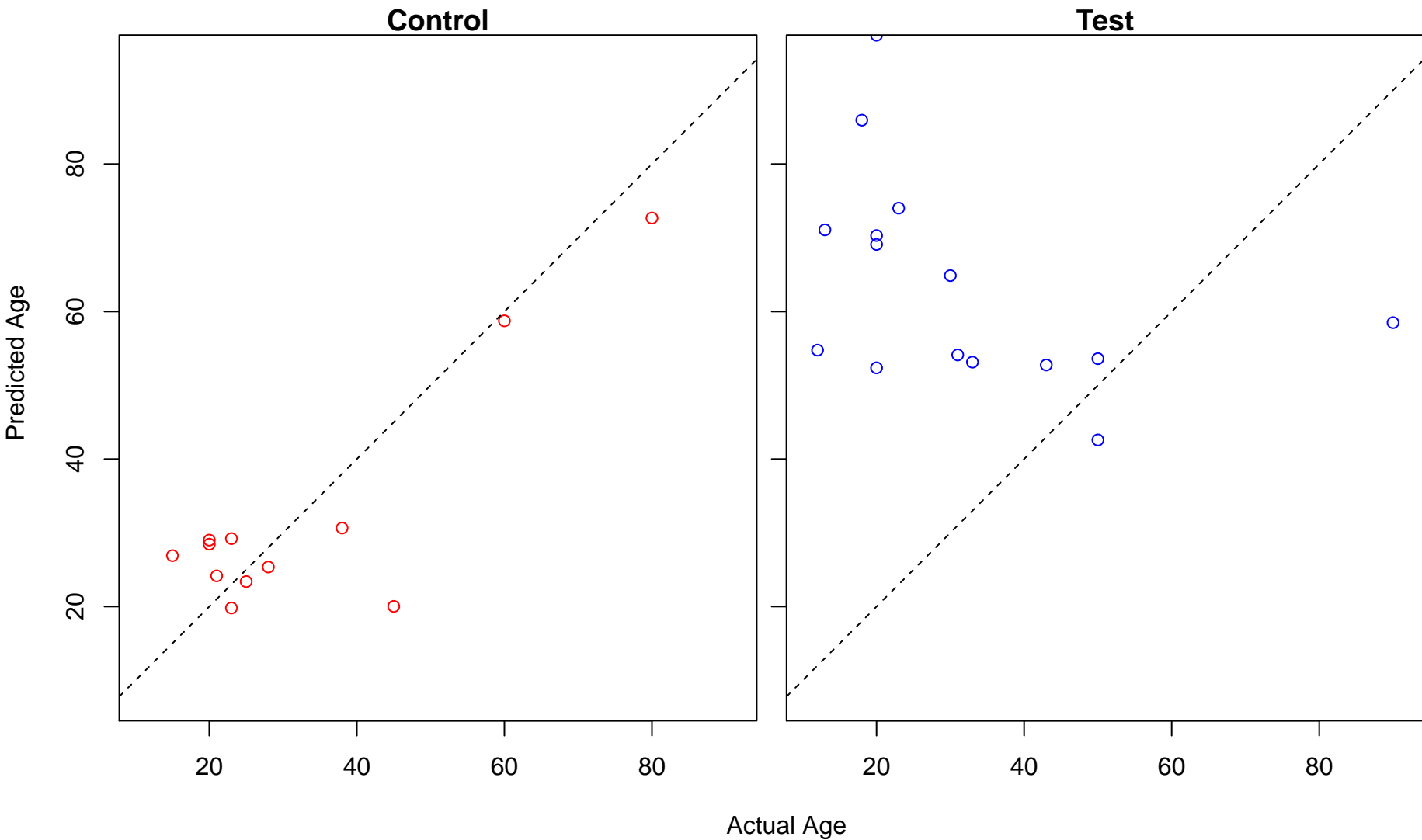
organ formation (Score: 6.969672)



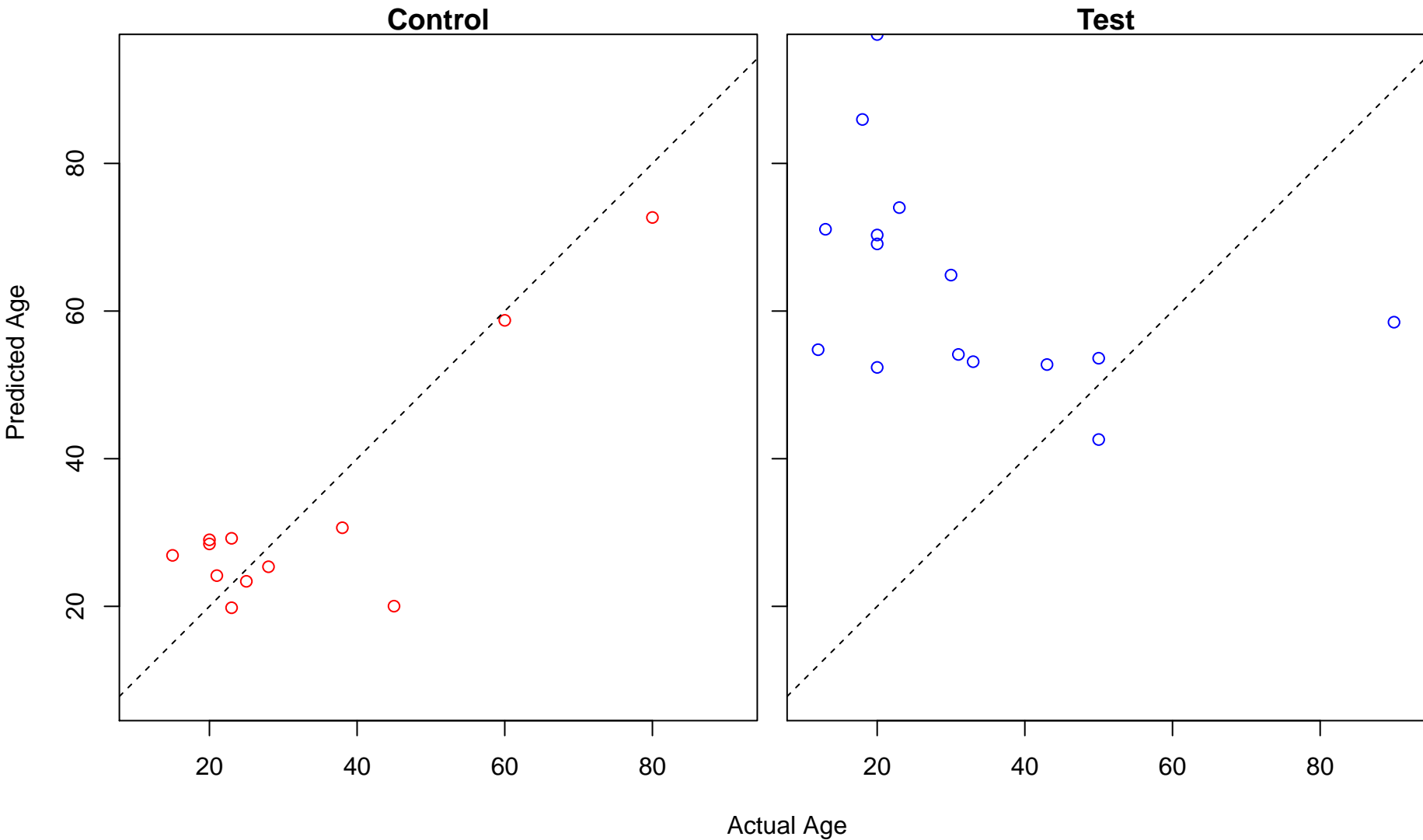
cell killing (Score: 6.965009)



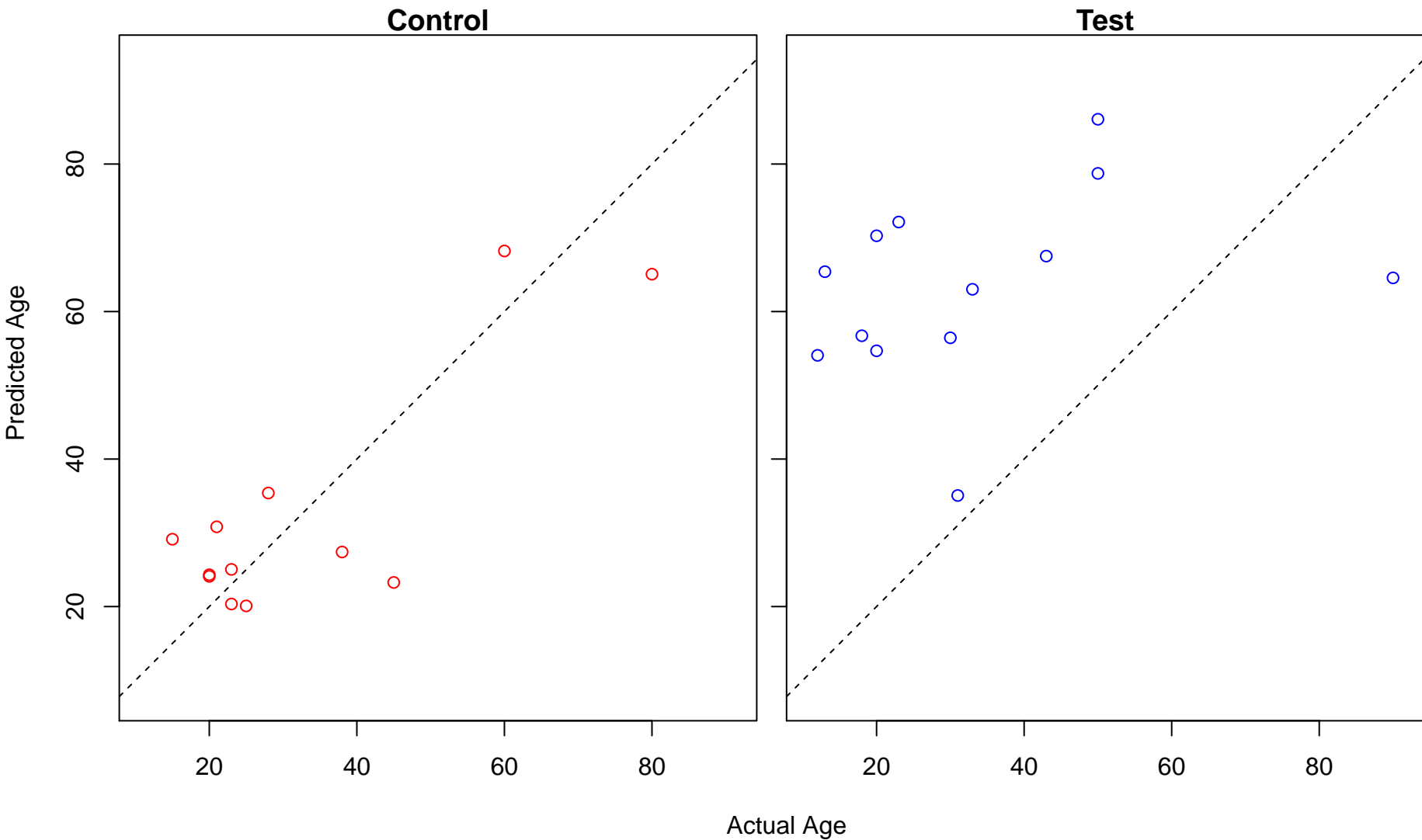
mesenchymal cell differentiation involved in kidney development (Score: 6.964765)



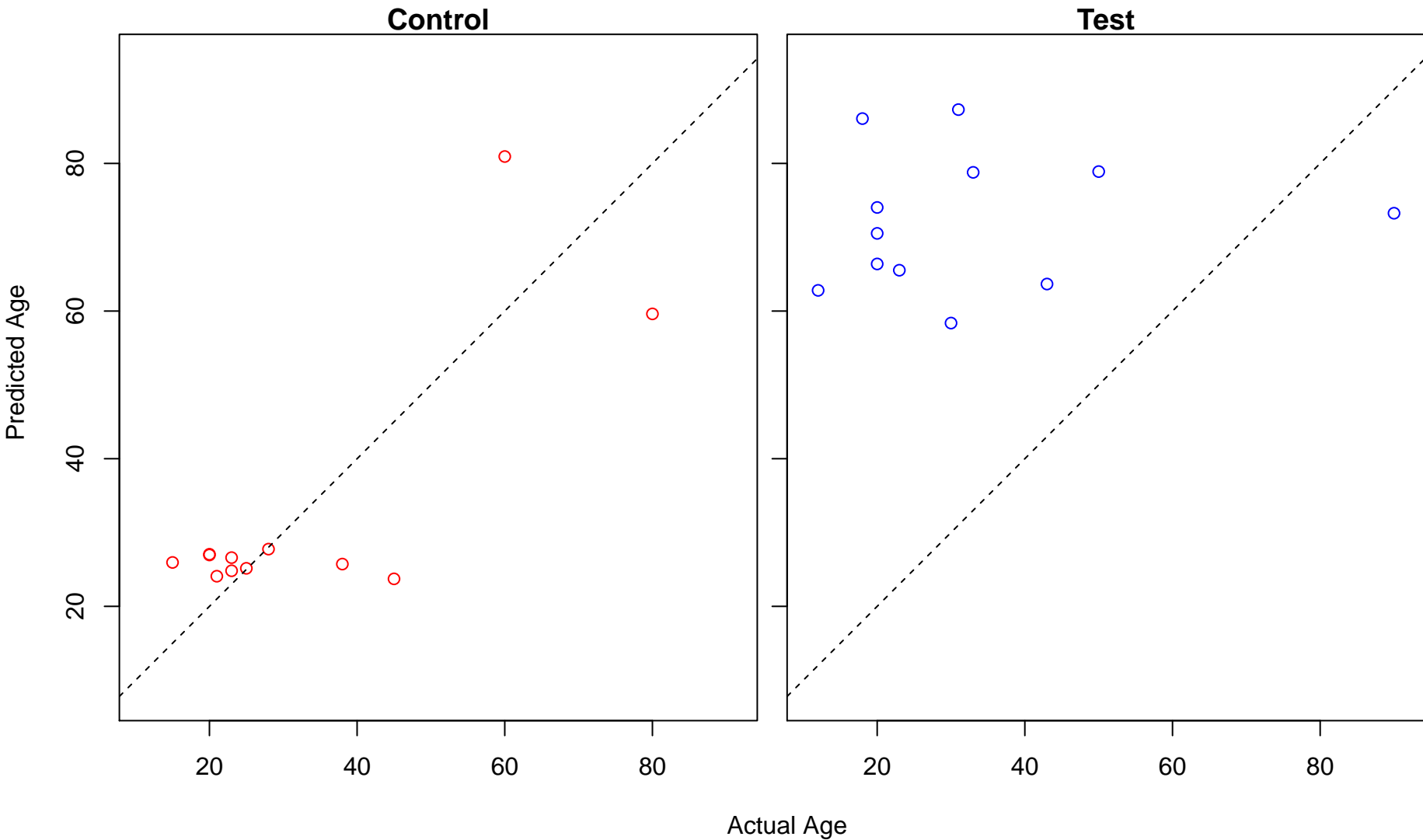
mesenchymal cell differentiation involved in renal system development (Score: 6.964765)



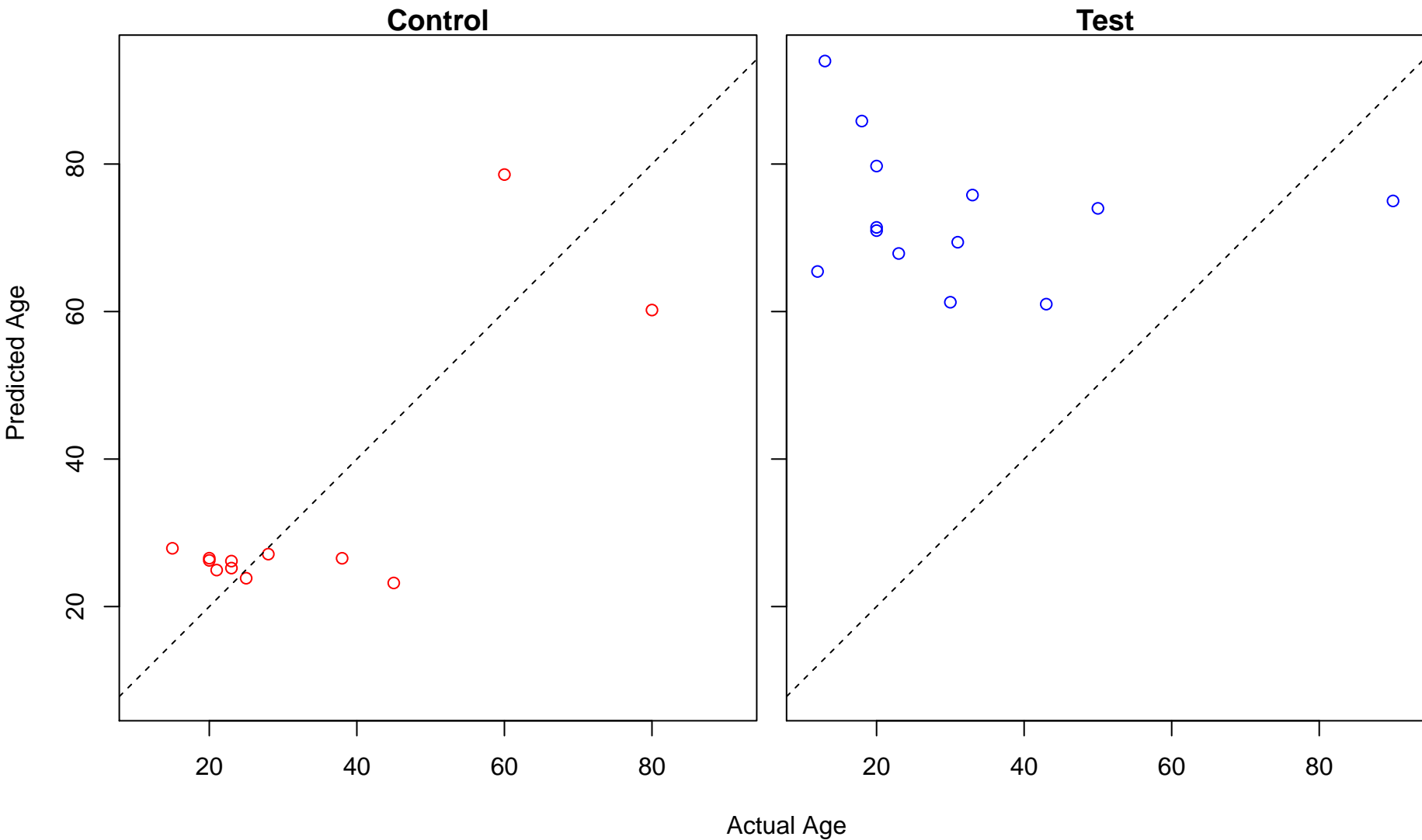
lipxygenase pathway (Score: 6.962847)



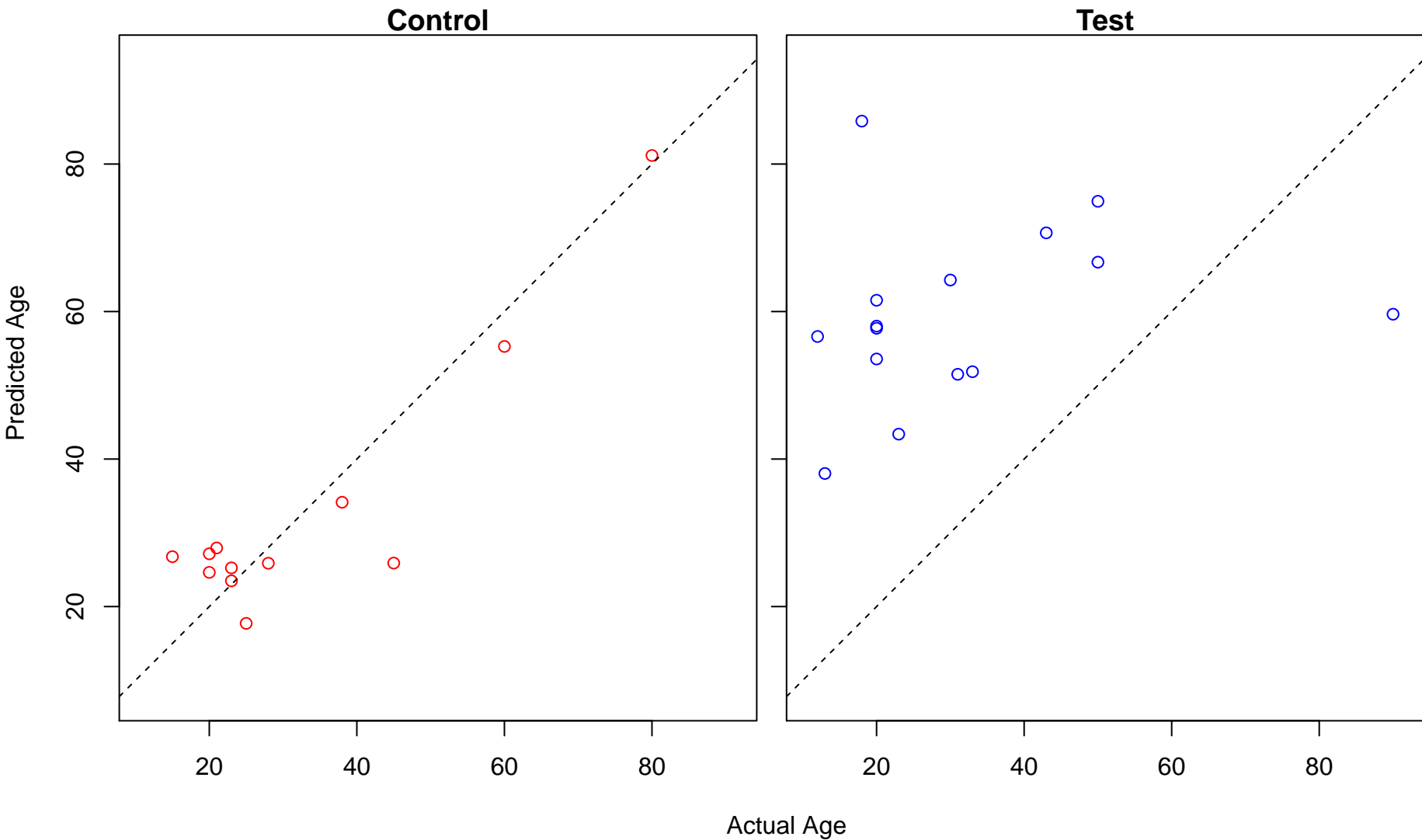
negative regulation of cell cycle phase transition (Score: 6.962016)



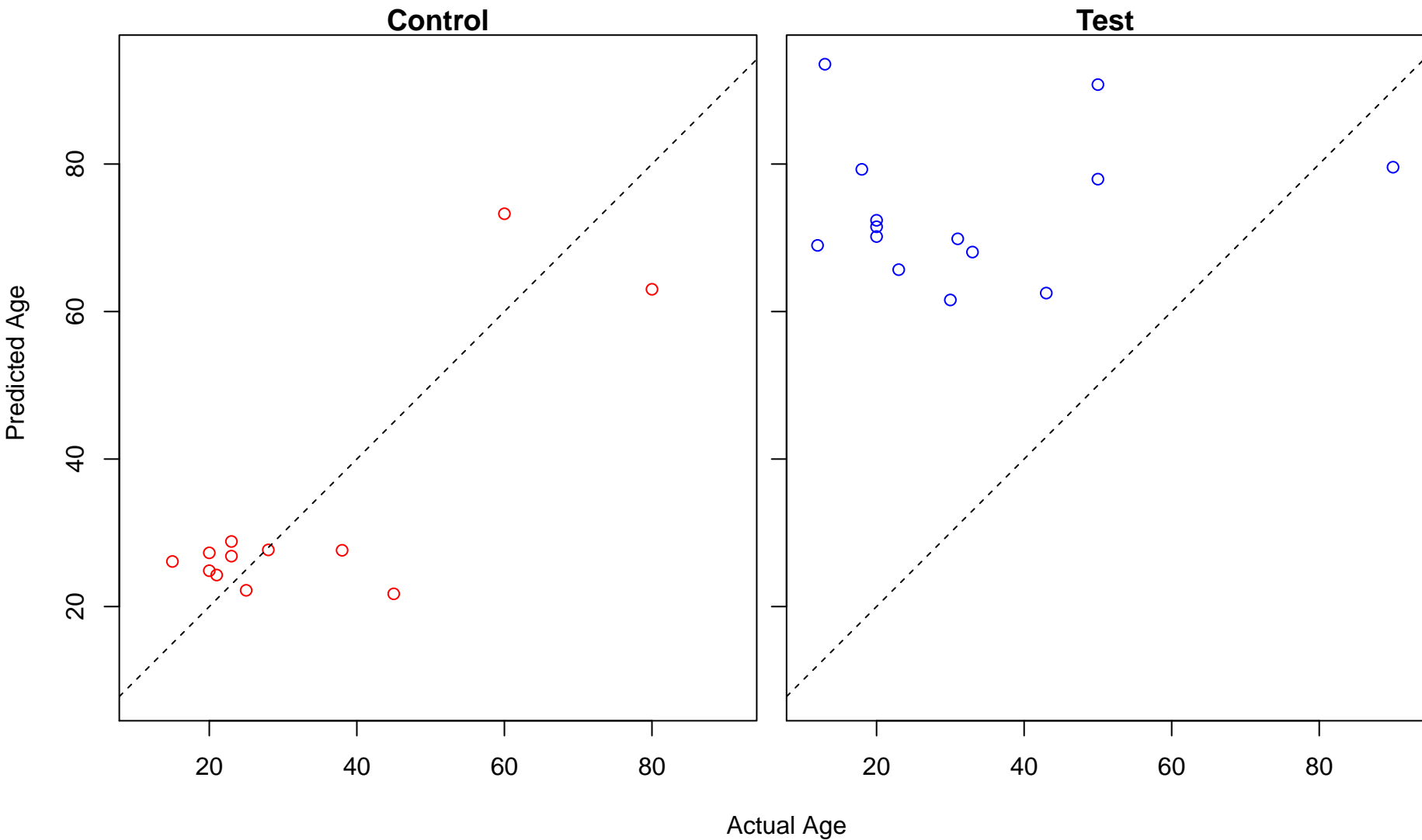
regulation of transcription from RNA polymerase II promoter in response to hypoxia (Score: 6.95829)



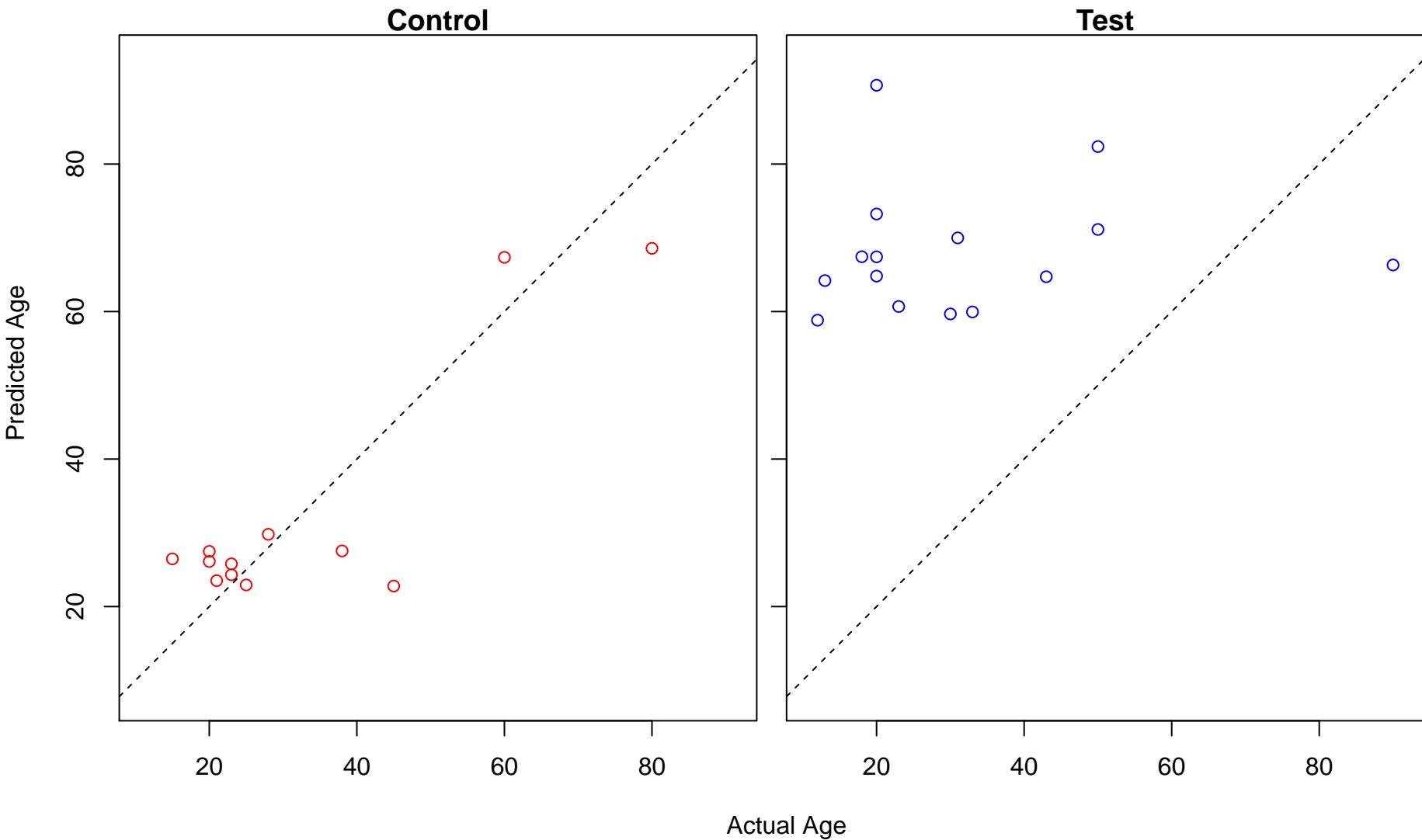
isoprenoid metabolic process (Score: 6.954537)



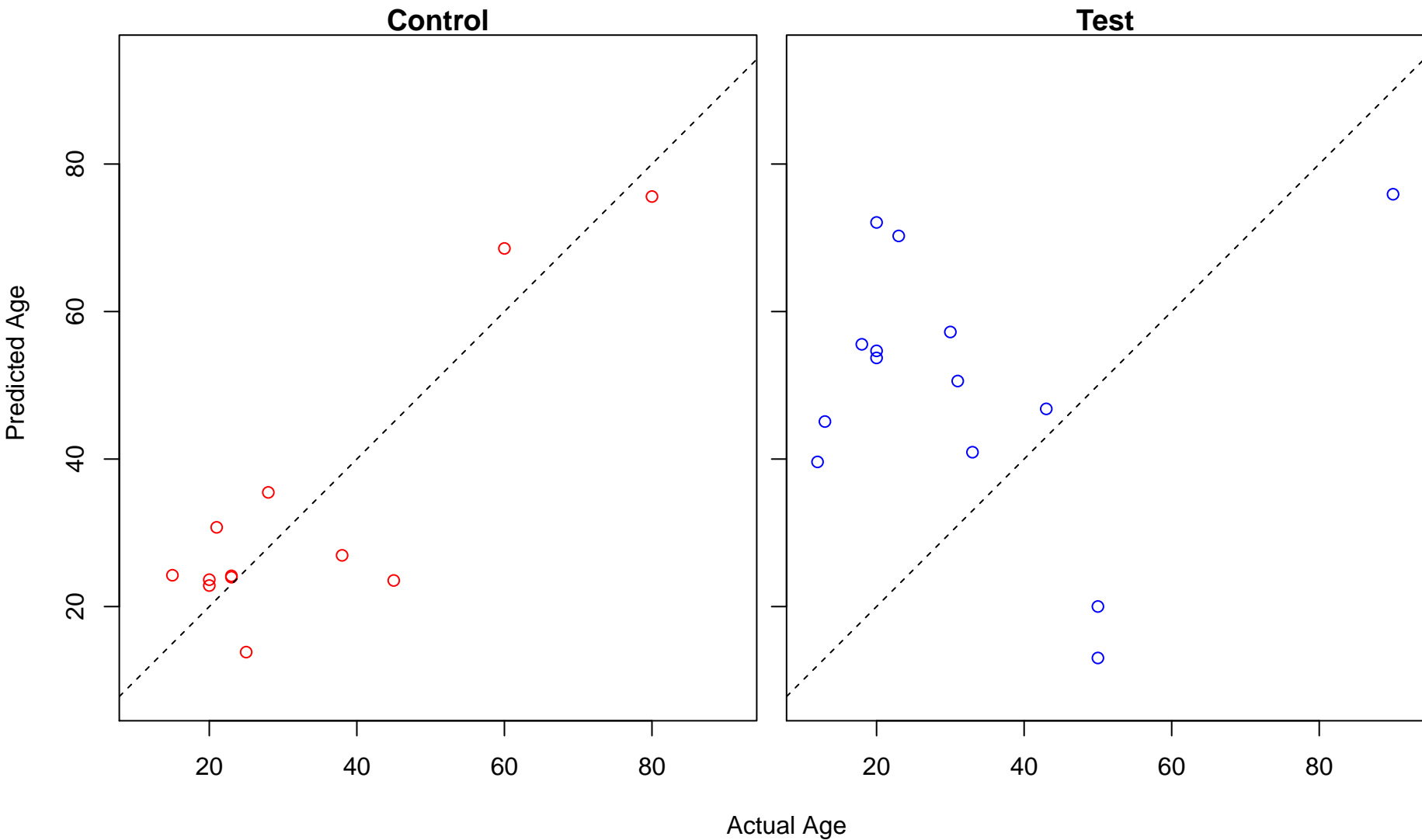
negative regulation of viral life cycle (Score: 6.954487)



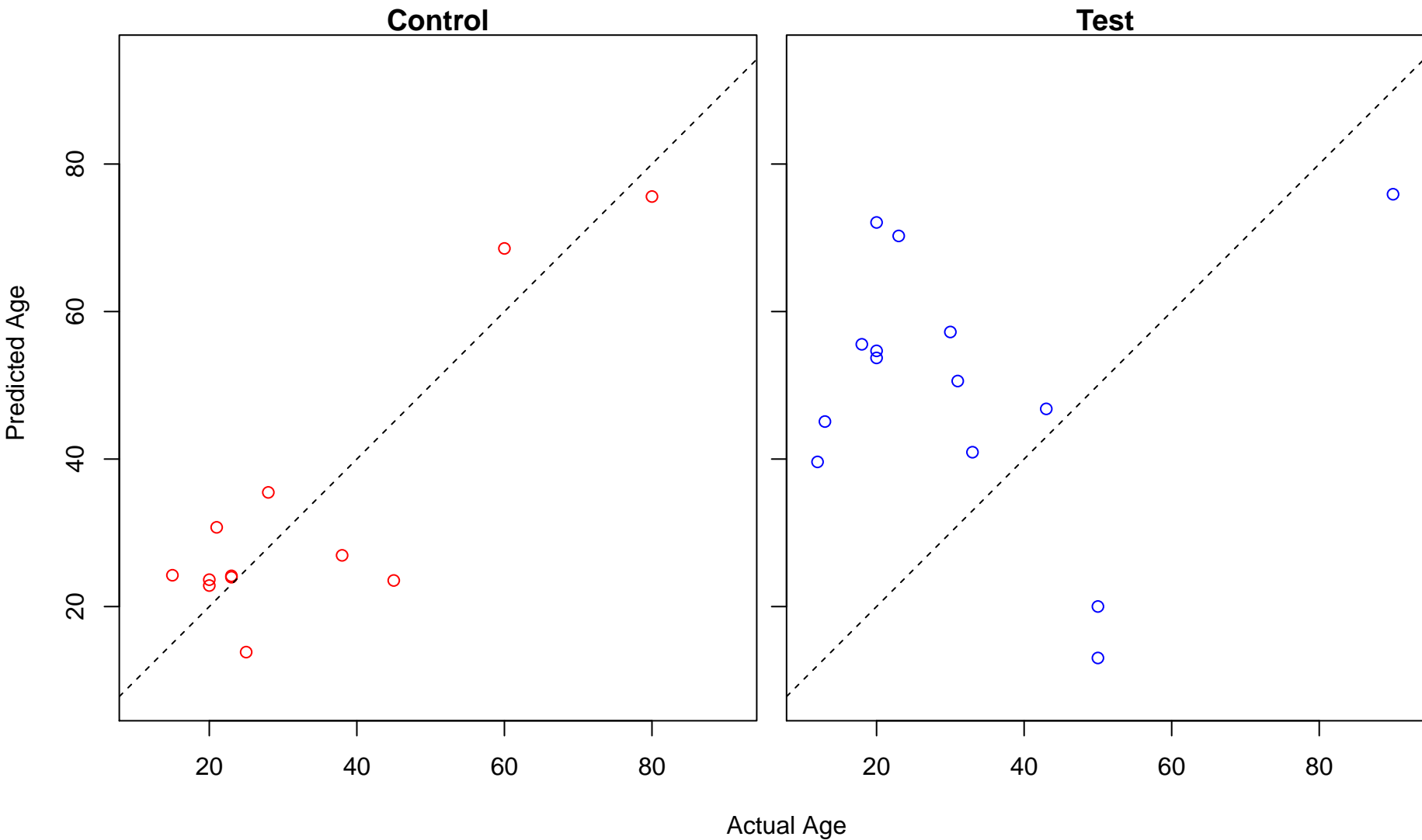
skin development (Score: 6.950678)



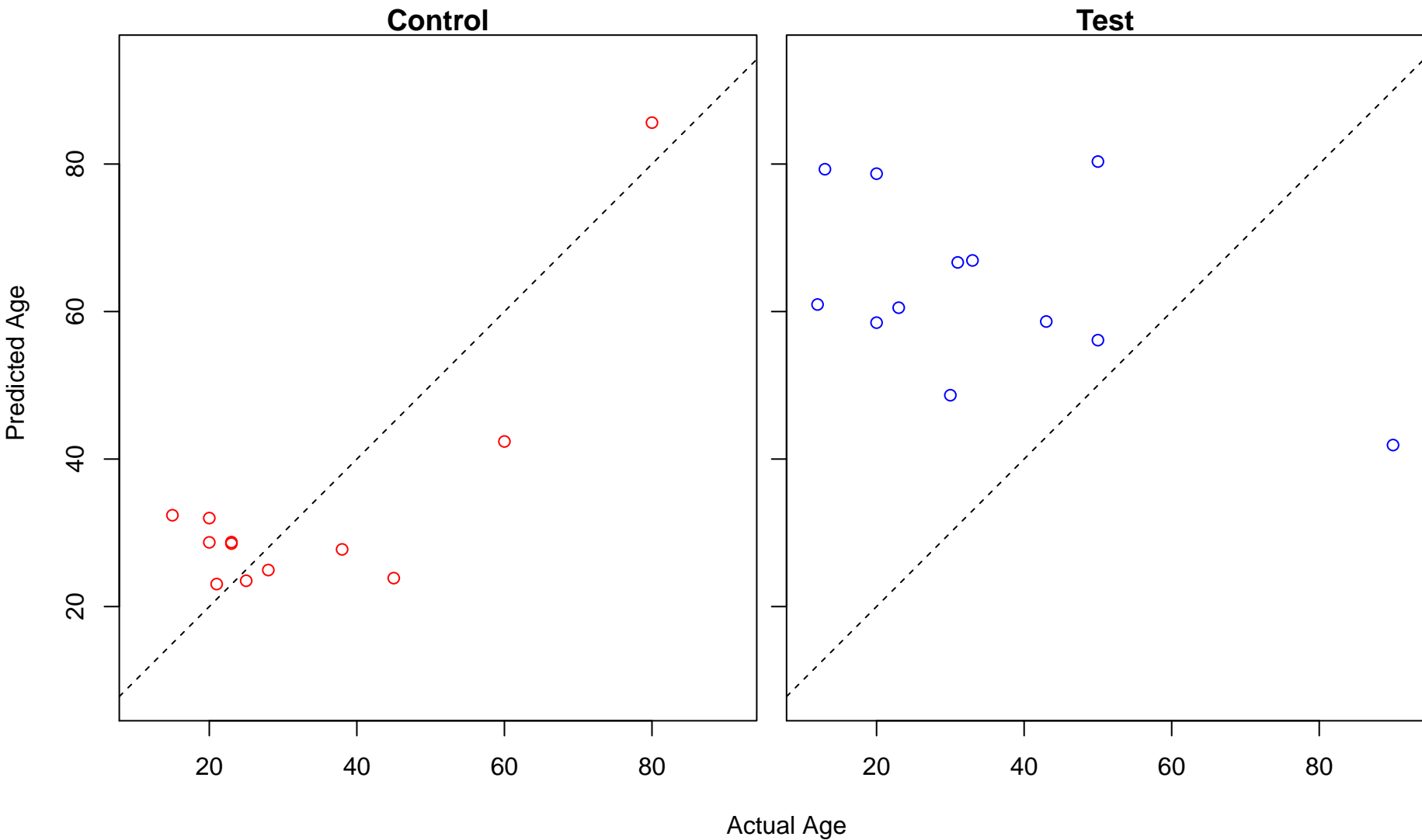
male gonad development (Score: 6.947388)



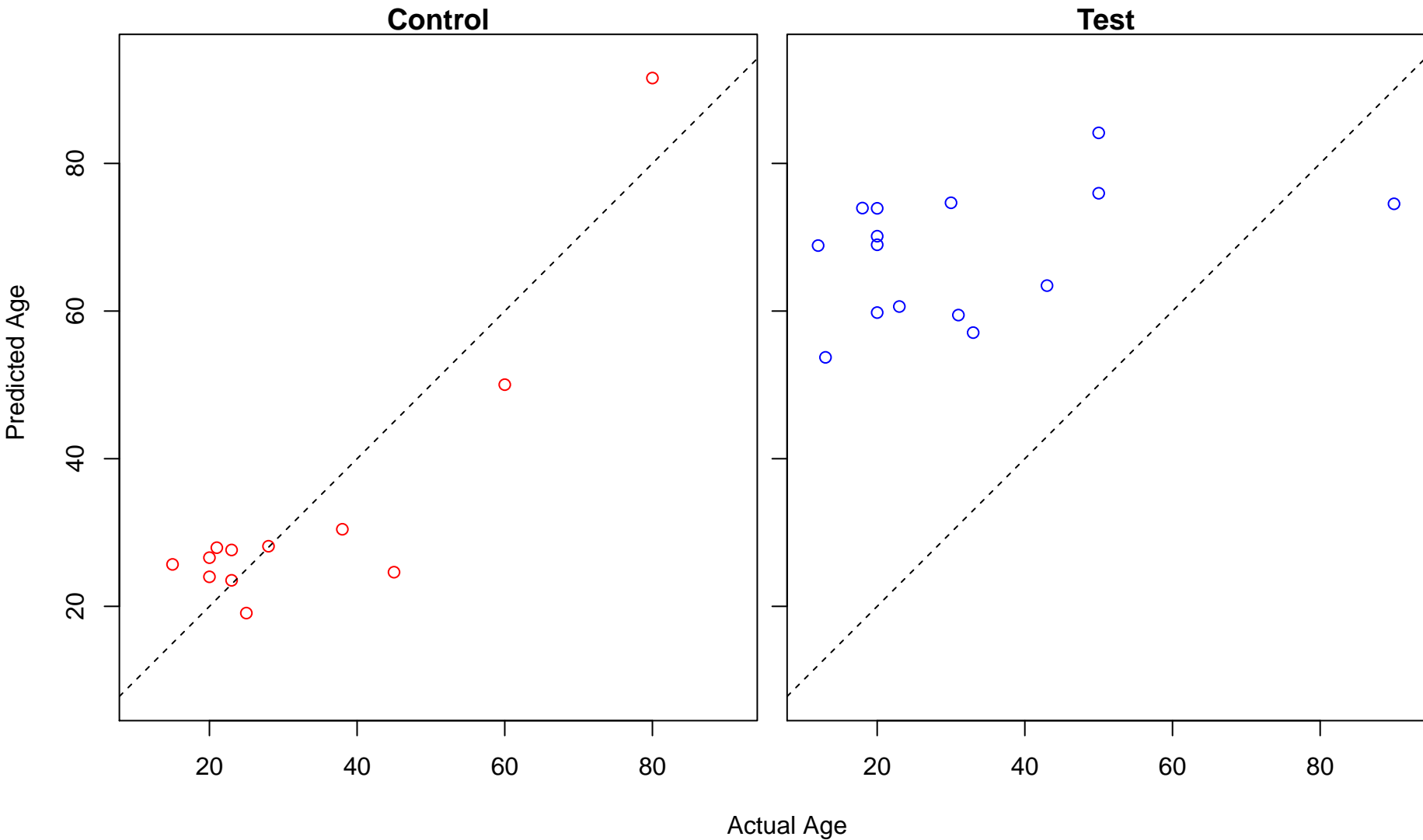
development of primary male sexual characteristics (Score: 6.947388)



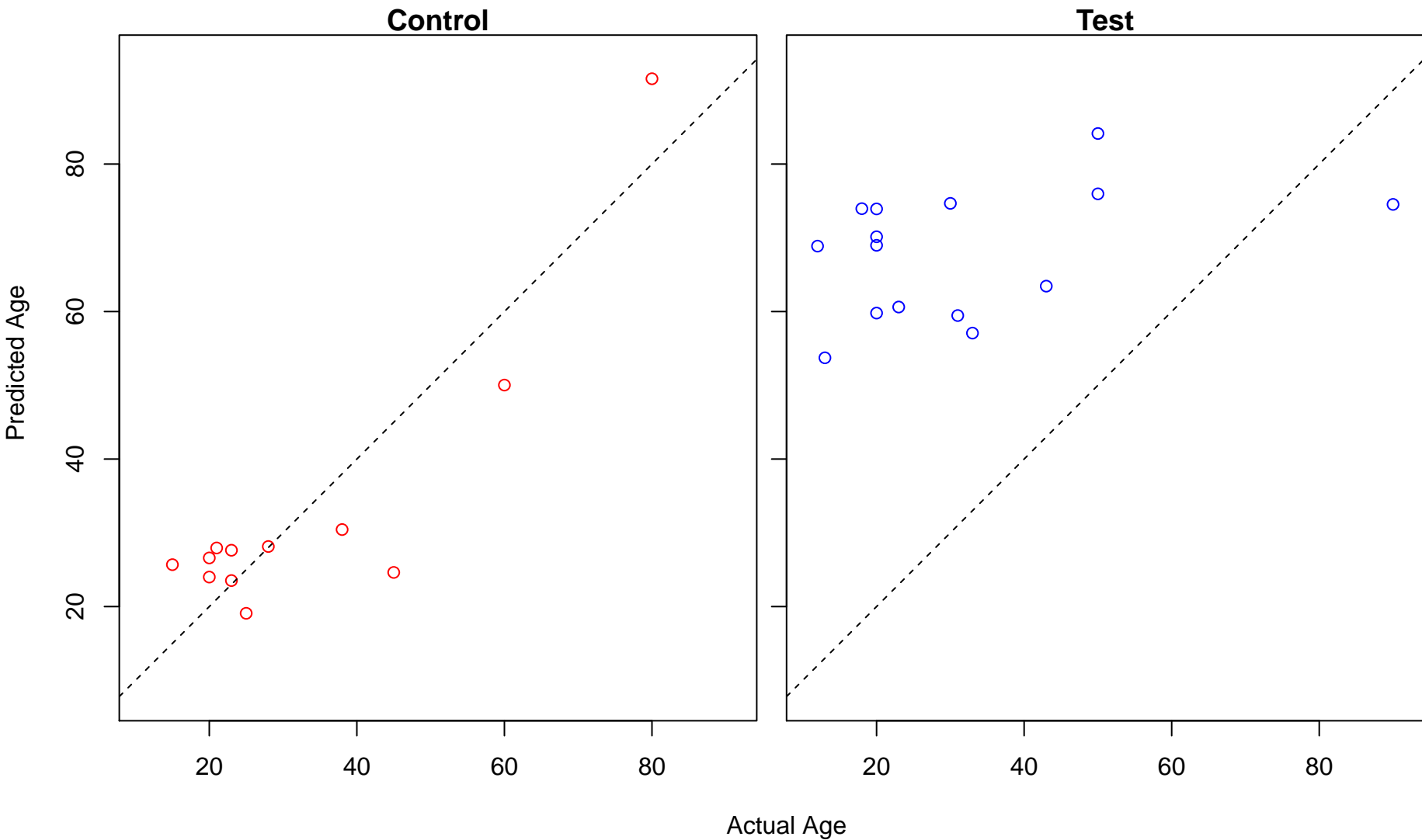
heparan sulfate proteoglycan metabolic process (Score: 6.946654)



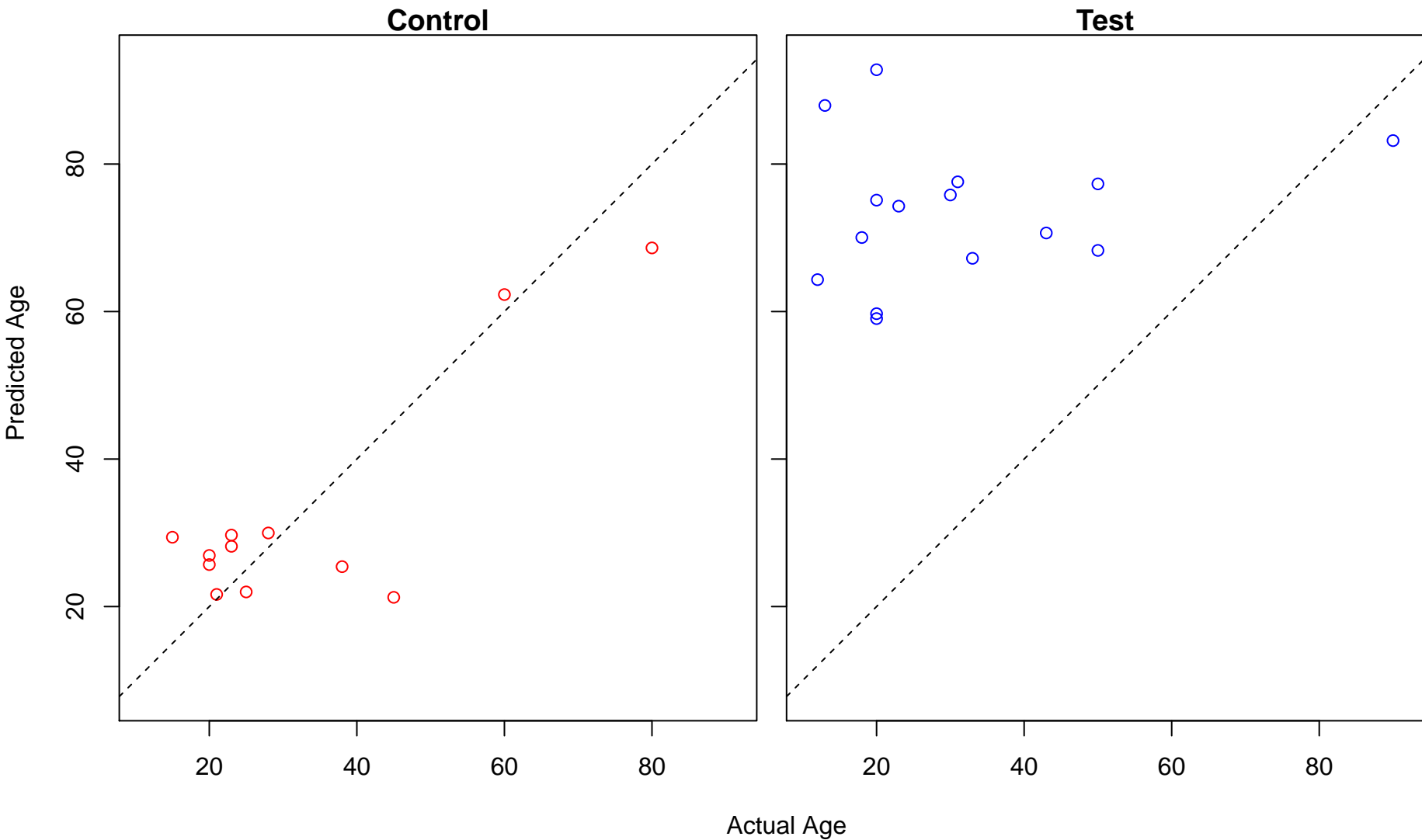
cardiovascular system development (Score: 6.946038)



circulatory system development (Score: 6.946038)

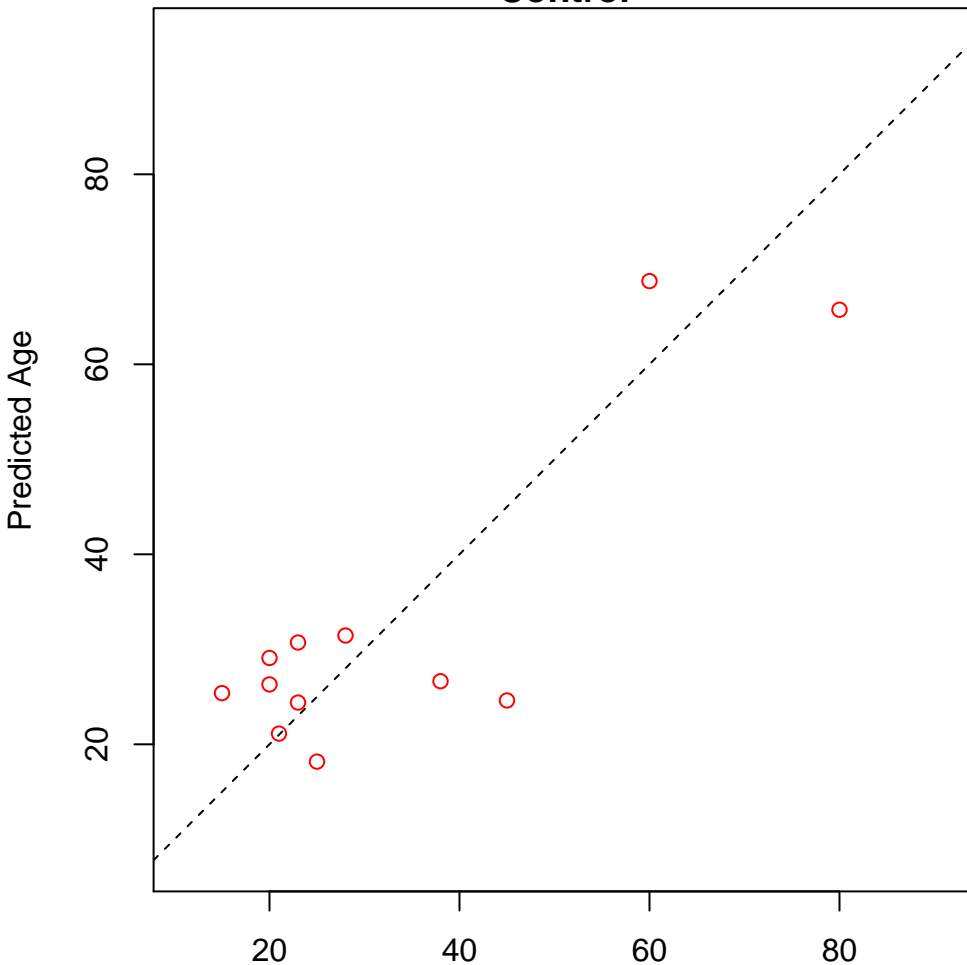


T cell apoptotic process (Score: 6.944886)

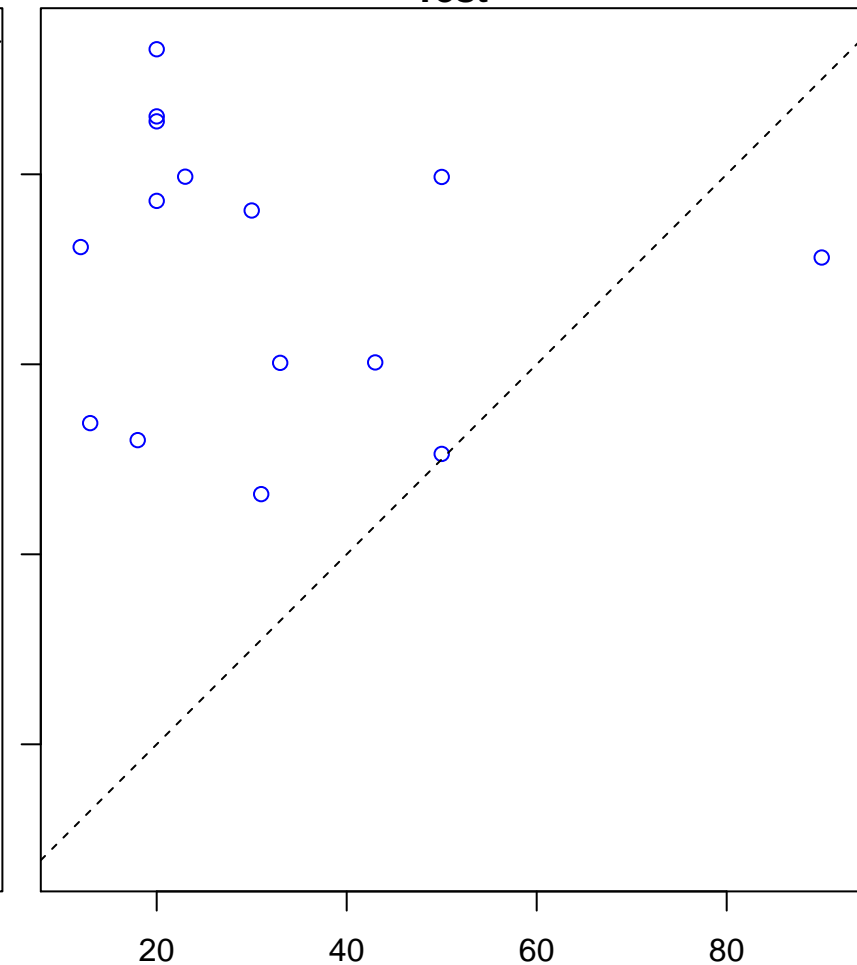


angiogenesis involved in wound healing (Score: 6.944213)

Control

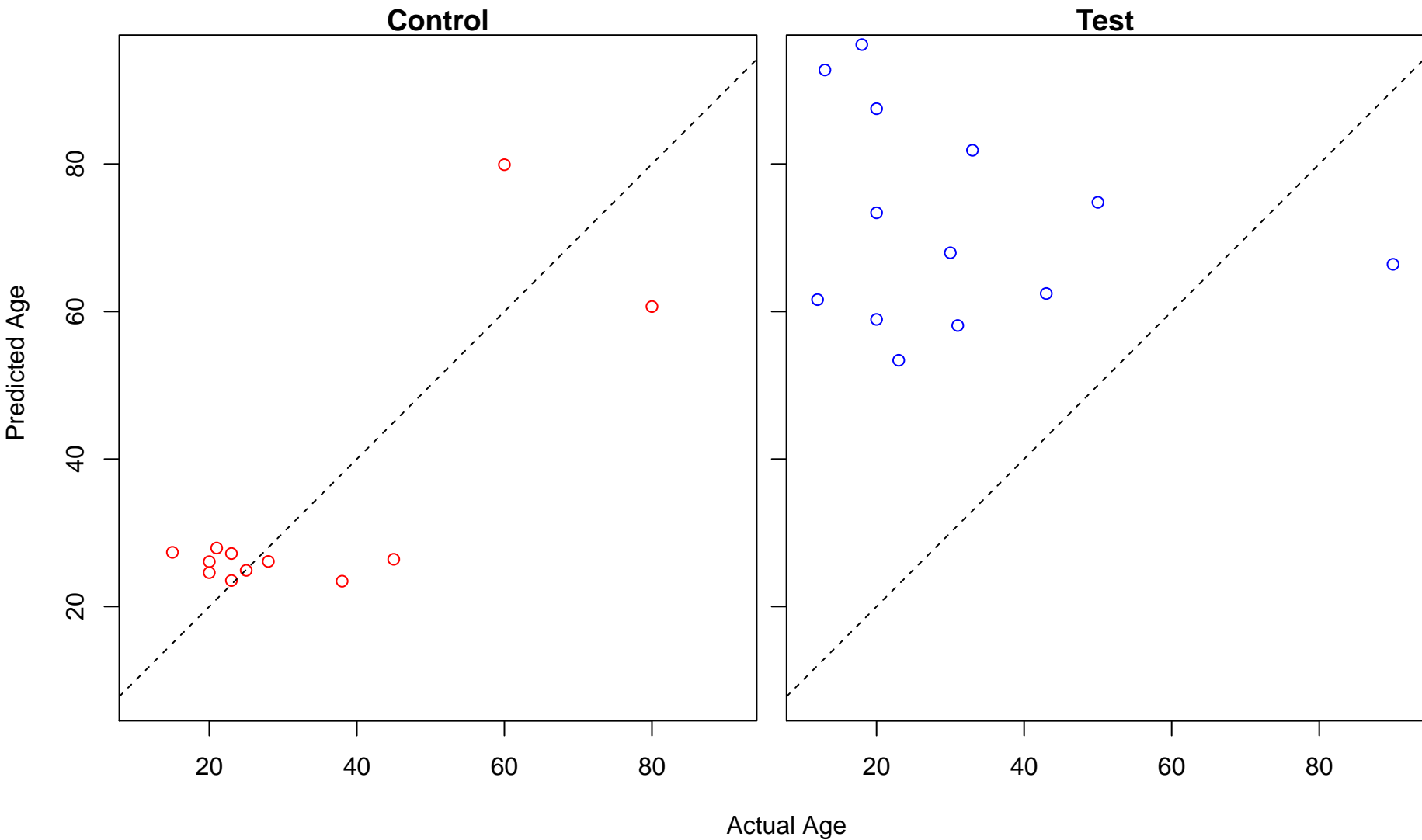


Test

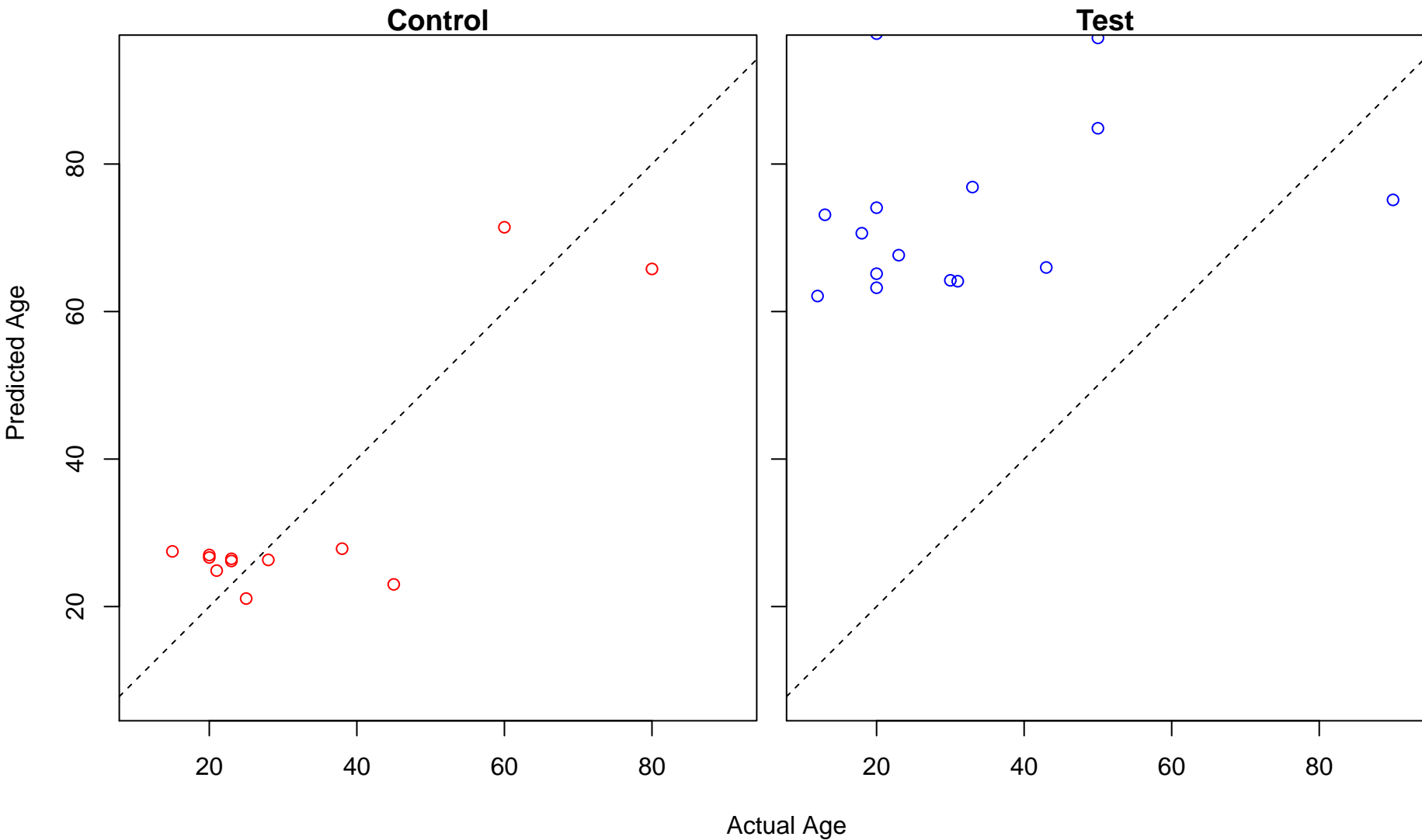


Actual Age

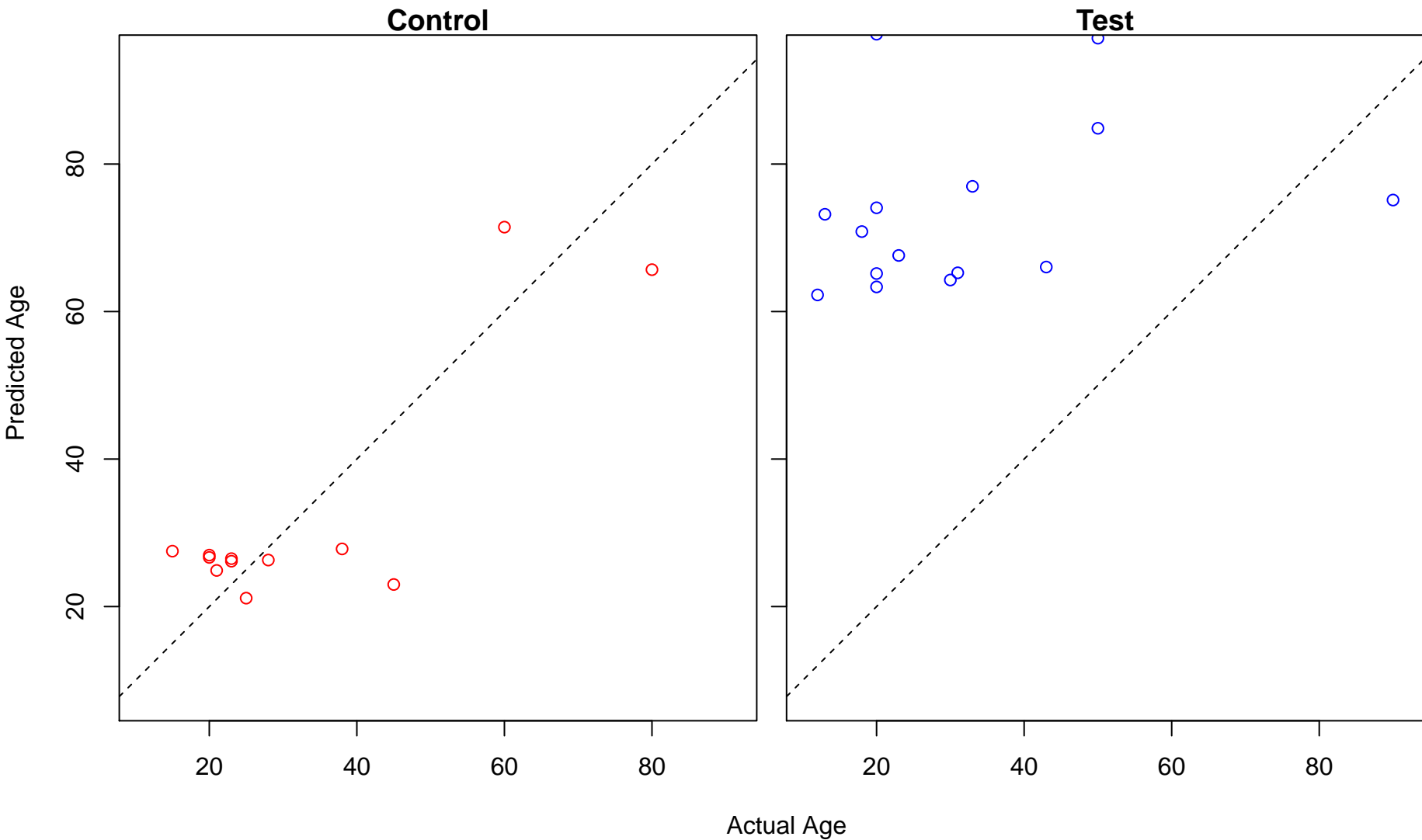
positive regulation of receptor internalization (Score: 6.943713)



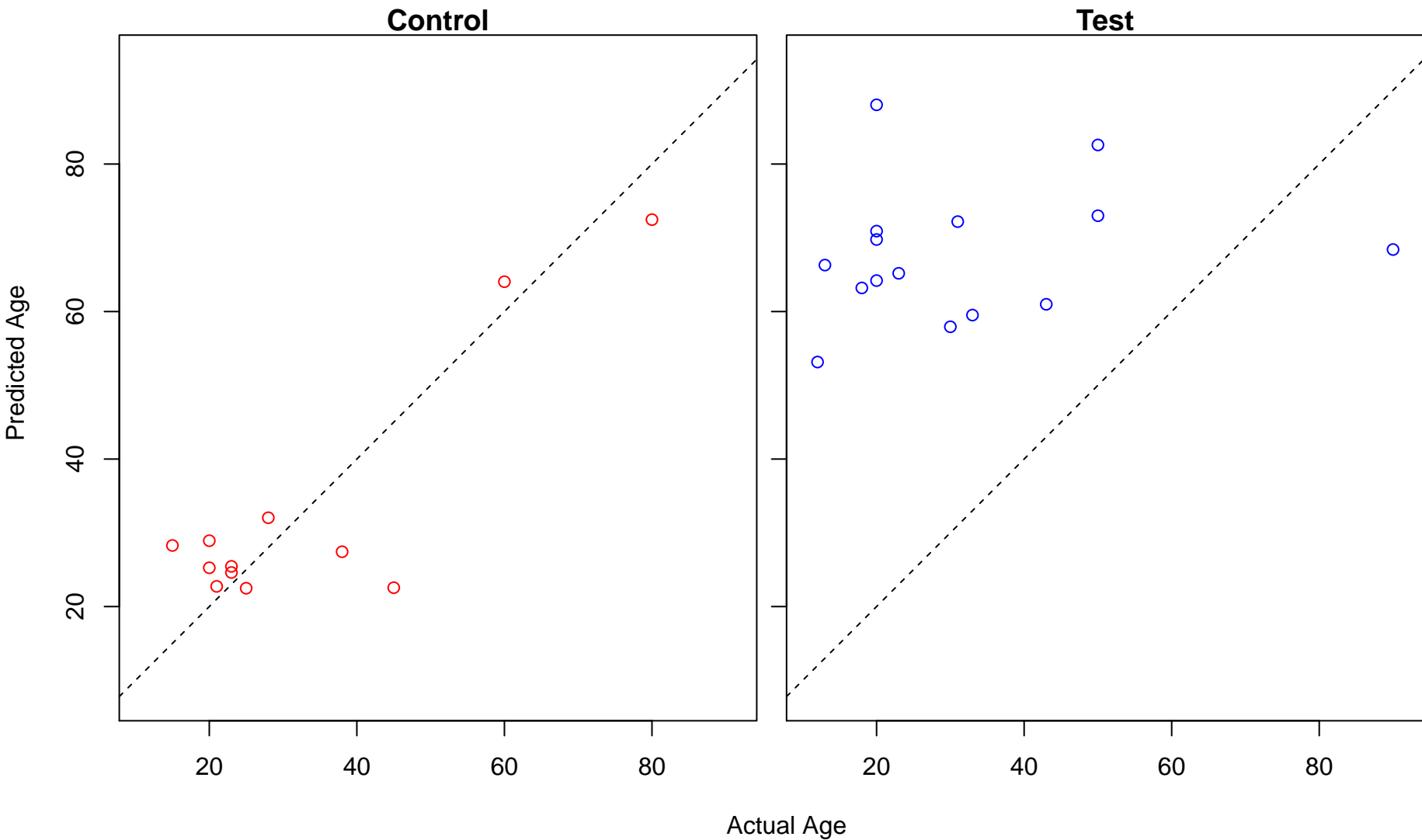
regulation of T cell receptor signaling pathway (Score: 6.943091)



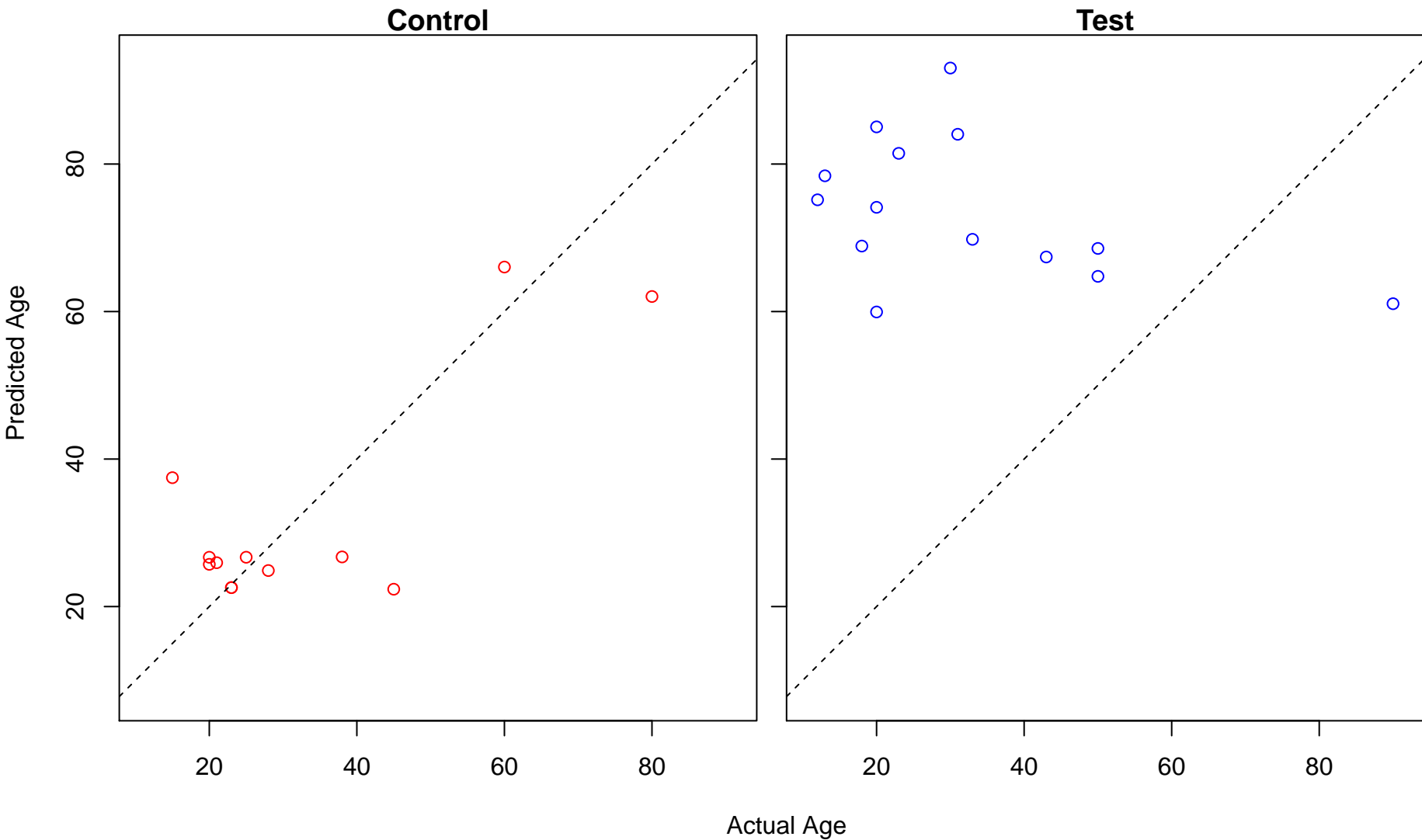
regulation of antigen receptor-mediated signaling pathway (Score: 6.941403)



regulation of insulin secretion (Score: 6.940882)

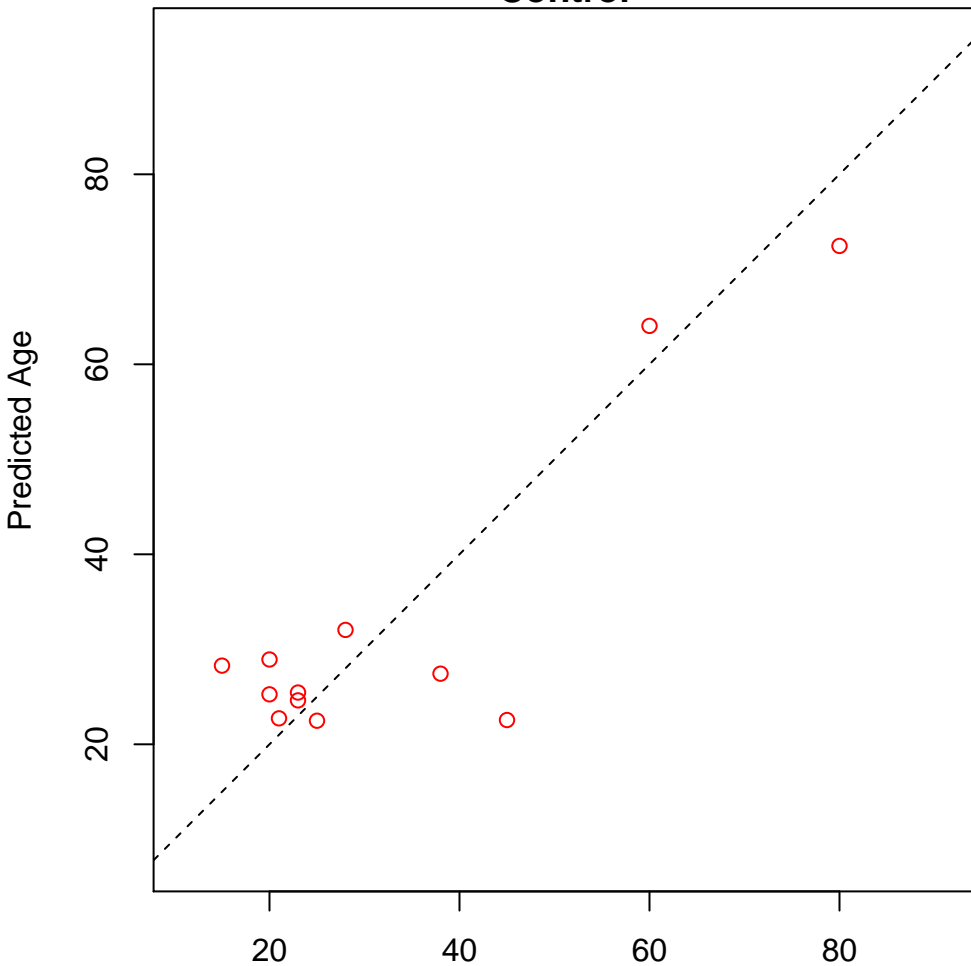


regulation of feeding behavior (Score: 6.939650)

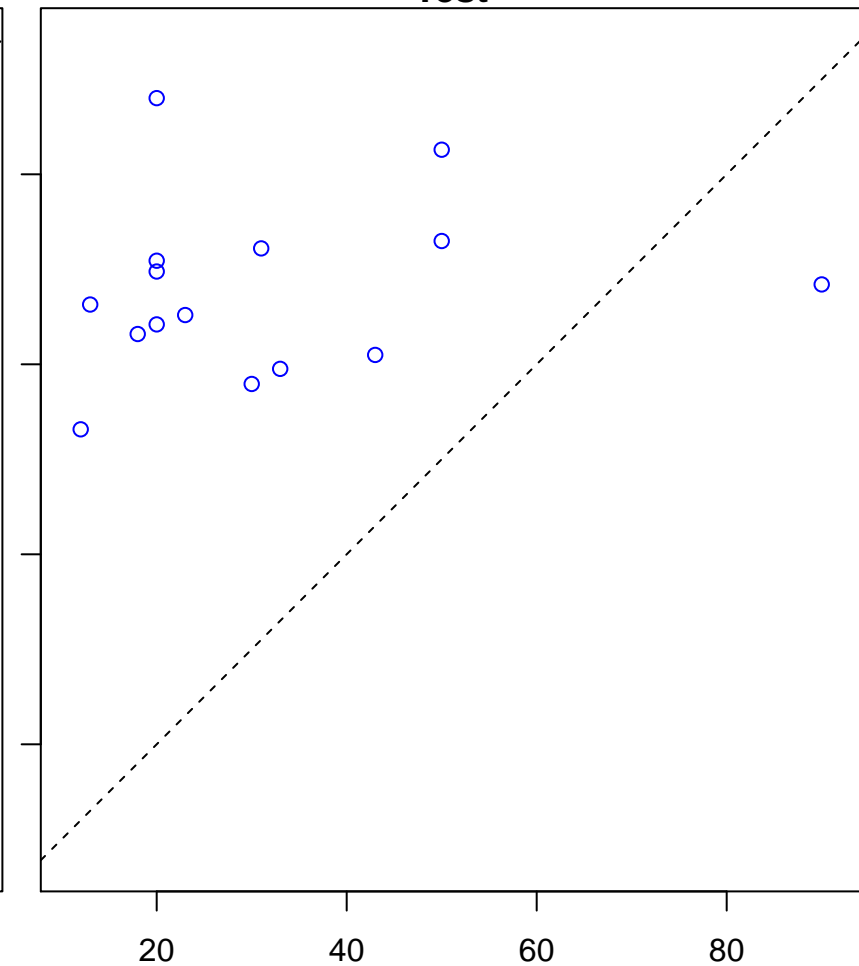


regulation of peptide hormone secretion (Score: 6.939497)

Control

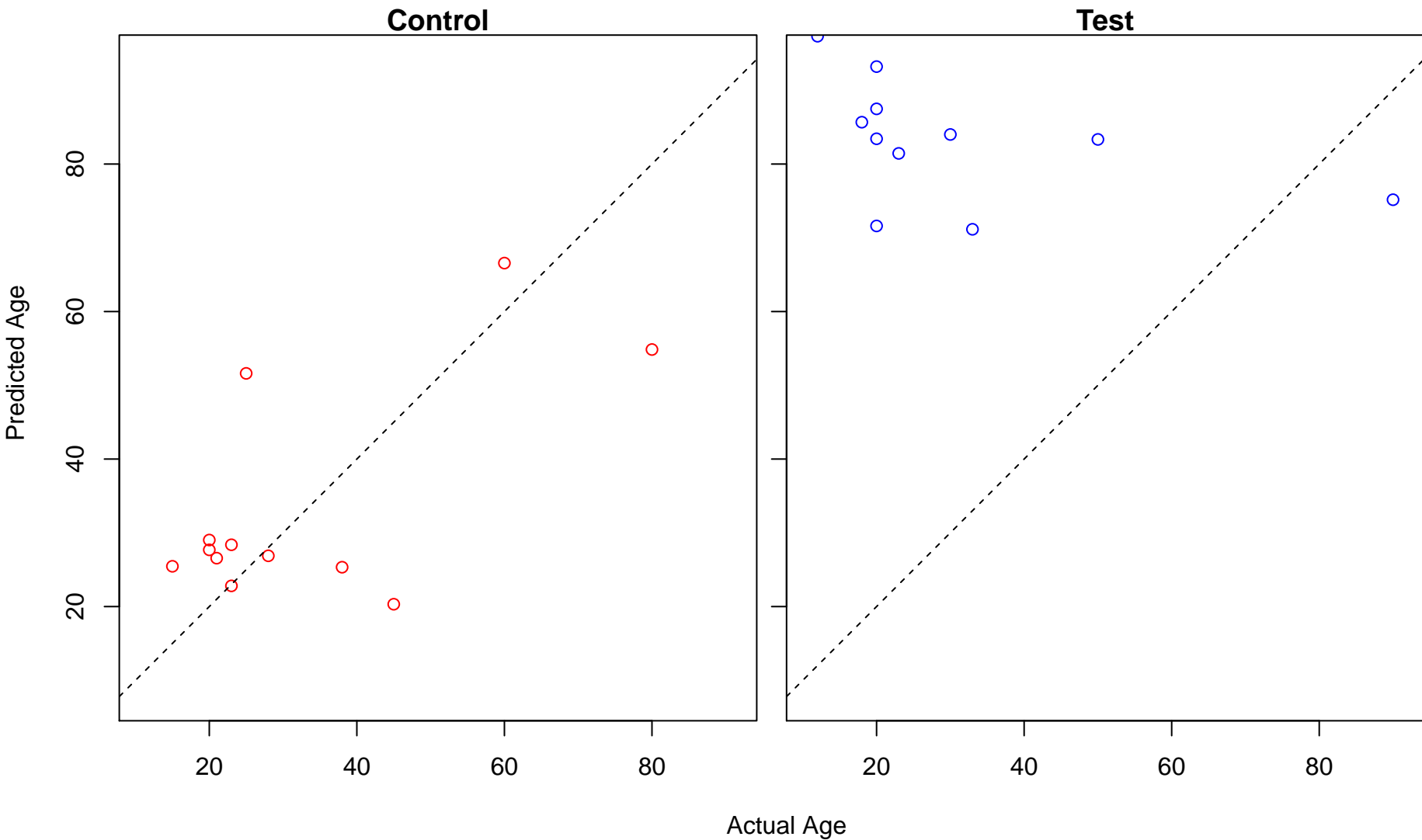


Test

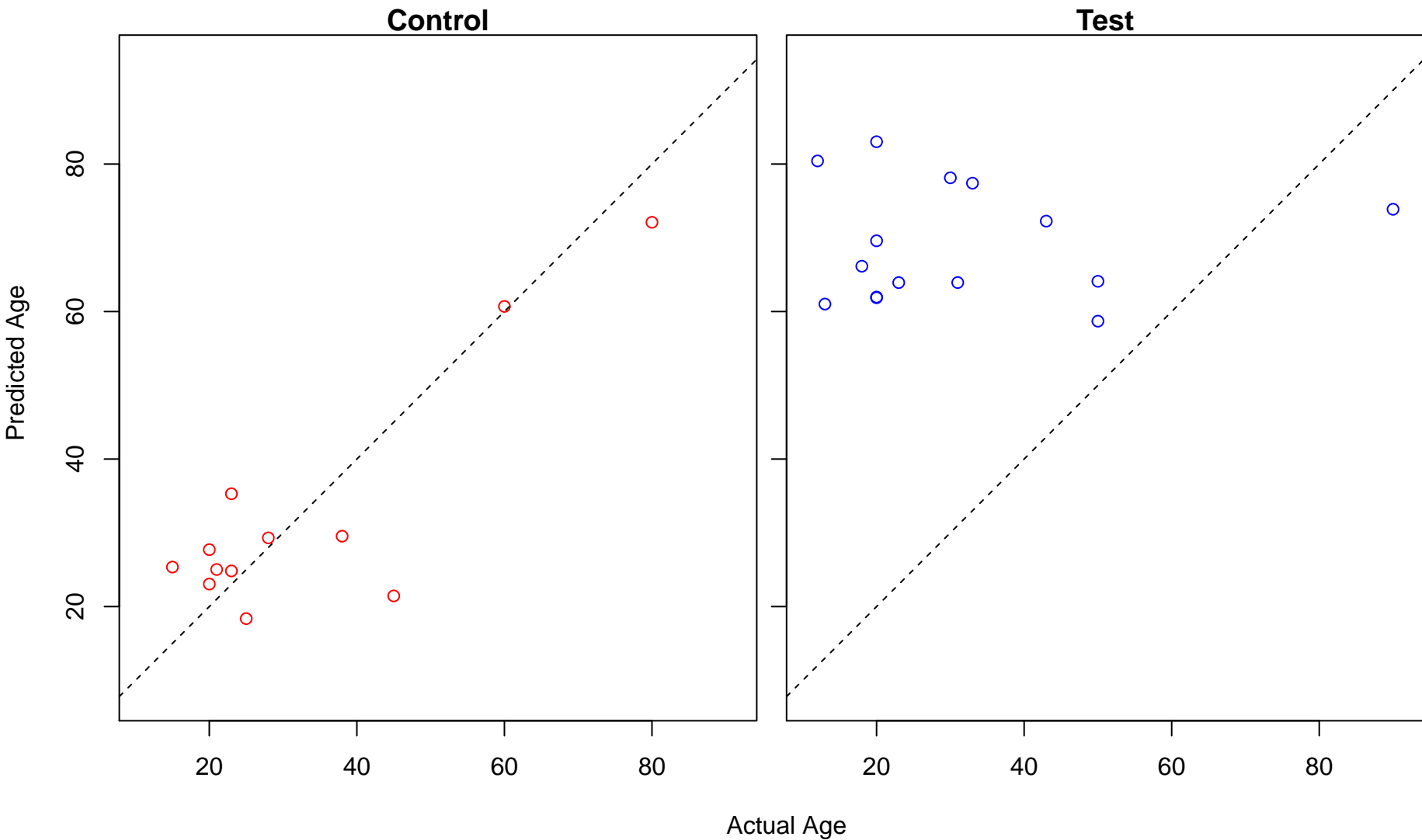


Actual Age

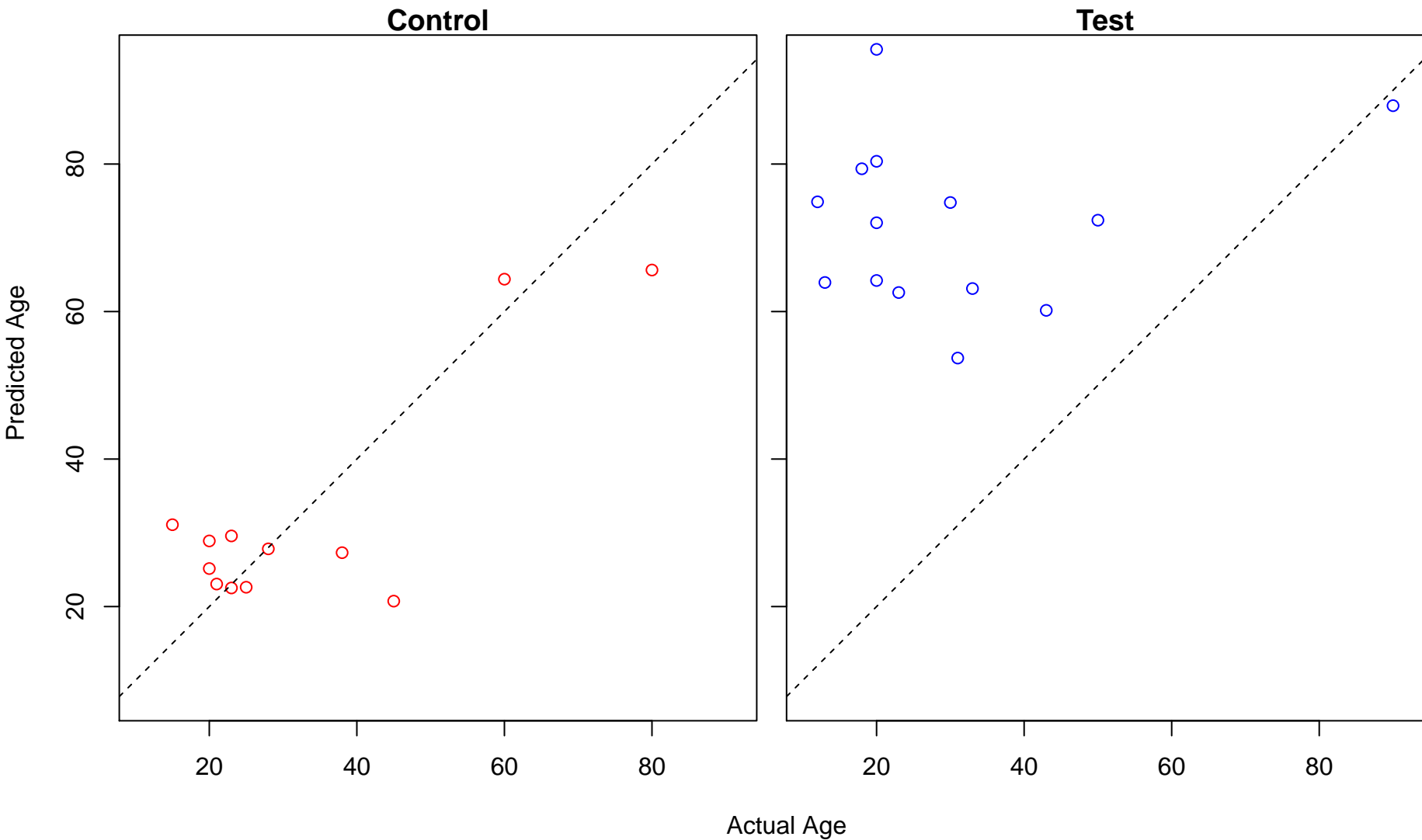
positive regulation of activation of Janus kinase activity (Score: 6.934471)



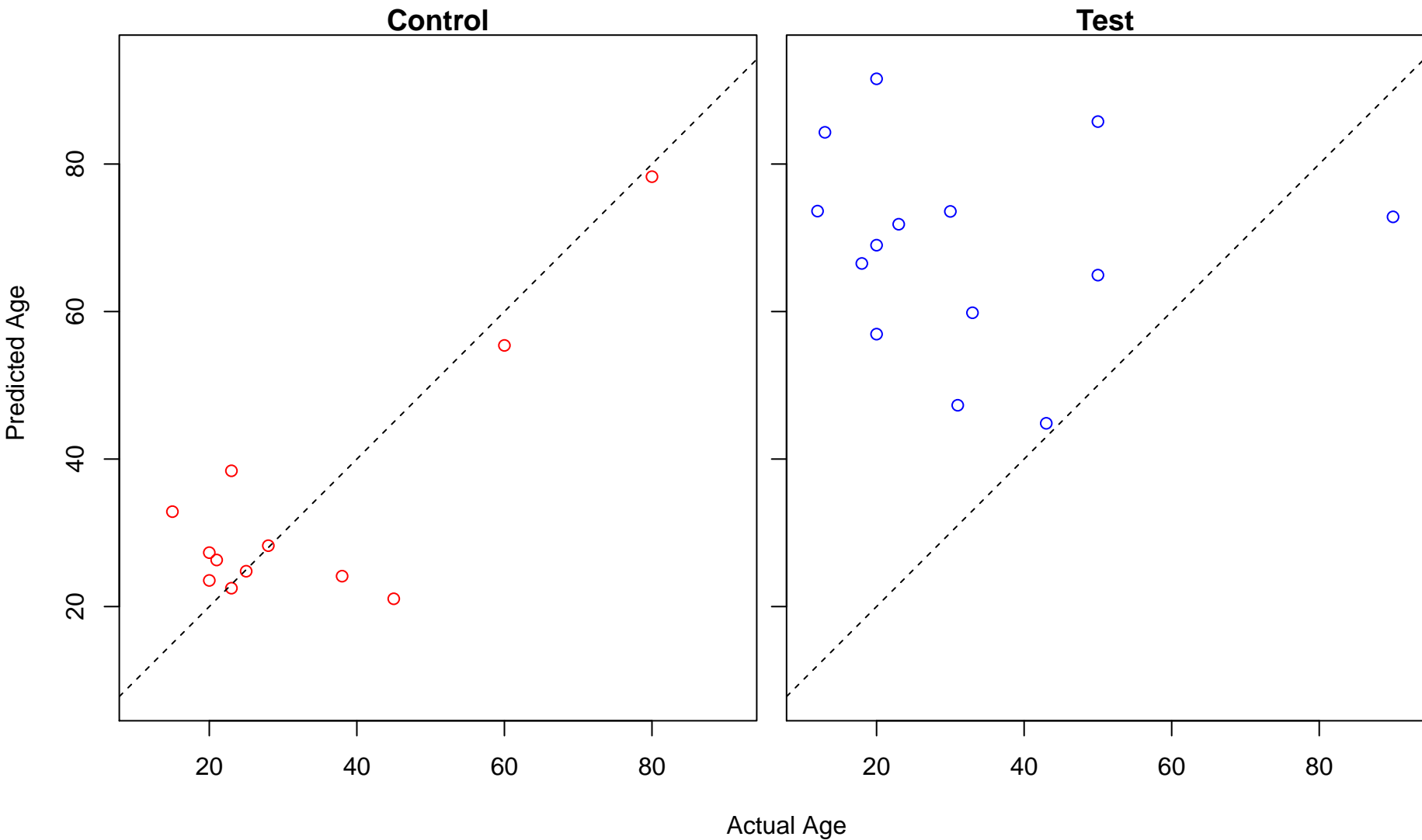
hormone catabolic process (Score: 6.932990)



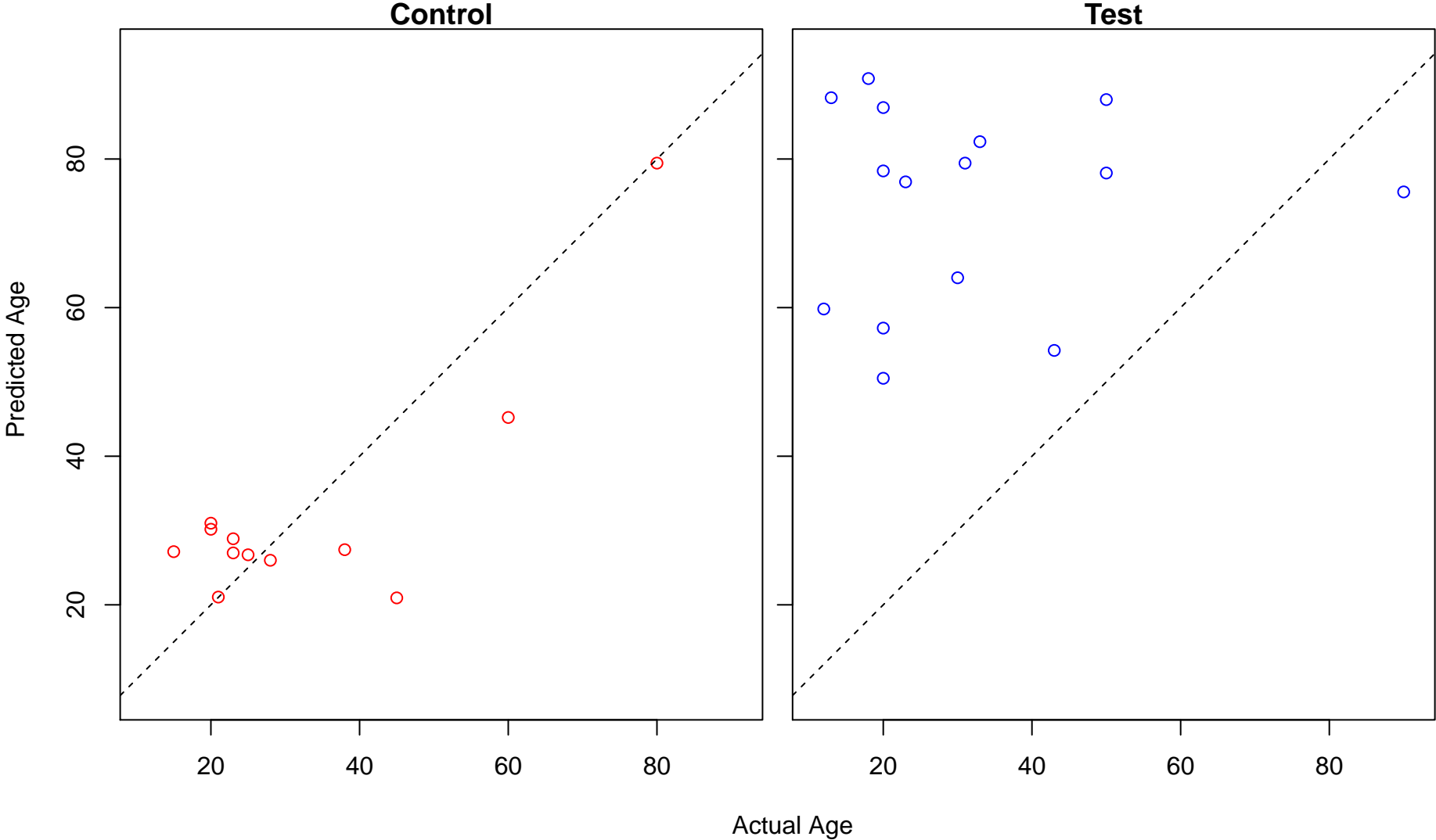
mammary gland morphogenesis (Score: 6.929046)



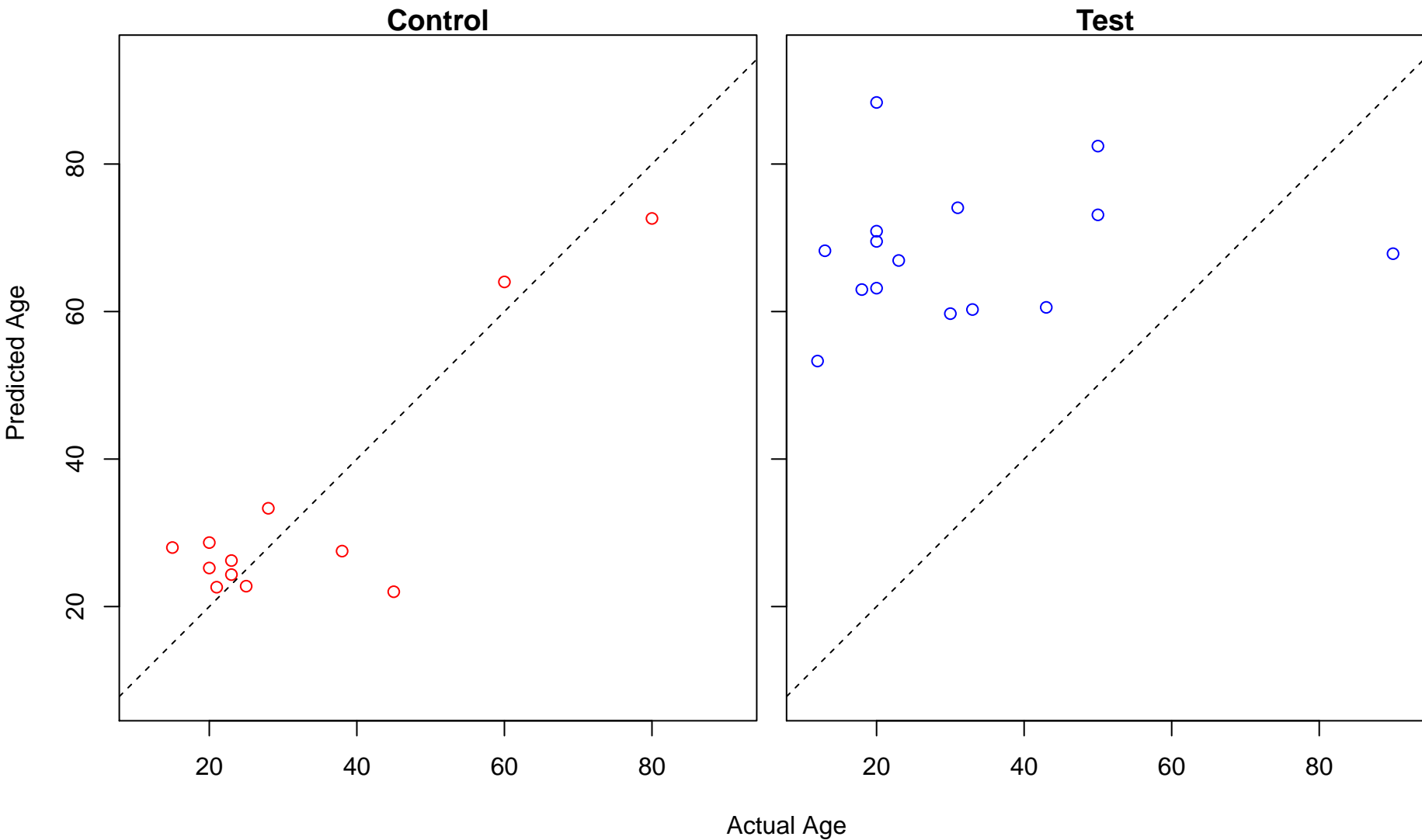
positive regulation of protein secretion (Score: 6.928535)



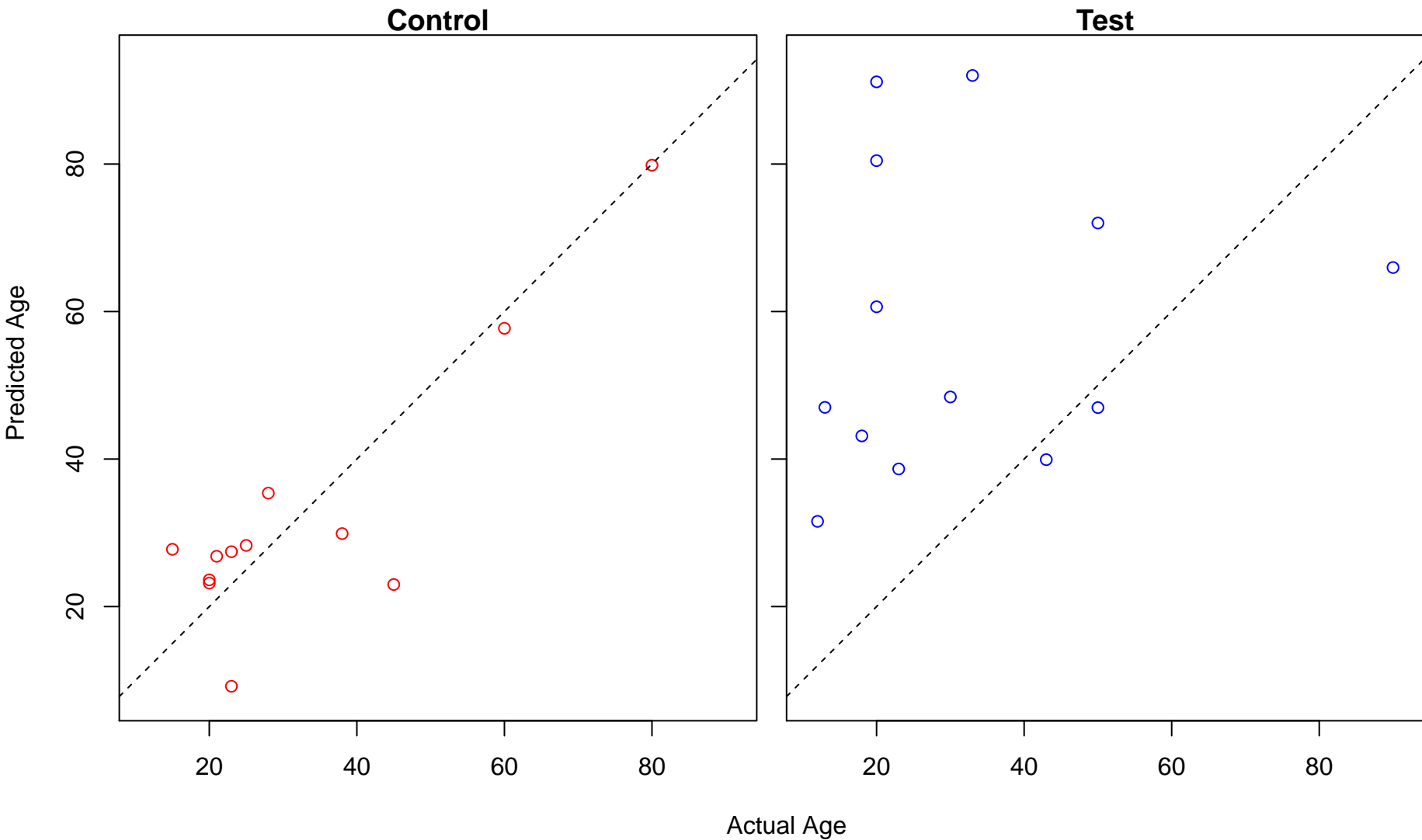
negative regulation of cellular response to vascular endothelial growth factor stimulus (Score: 6.9262)



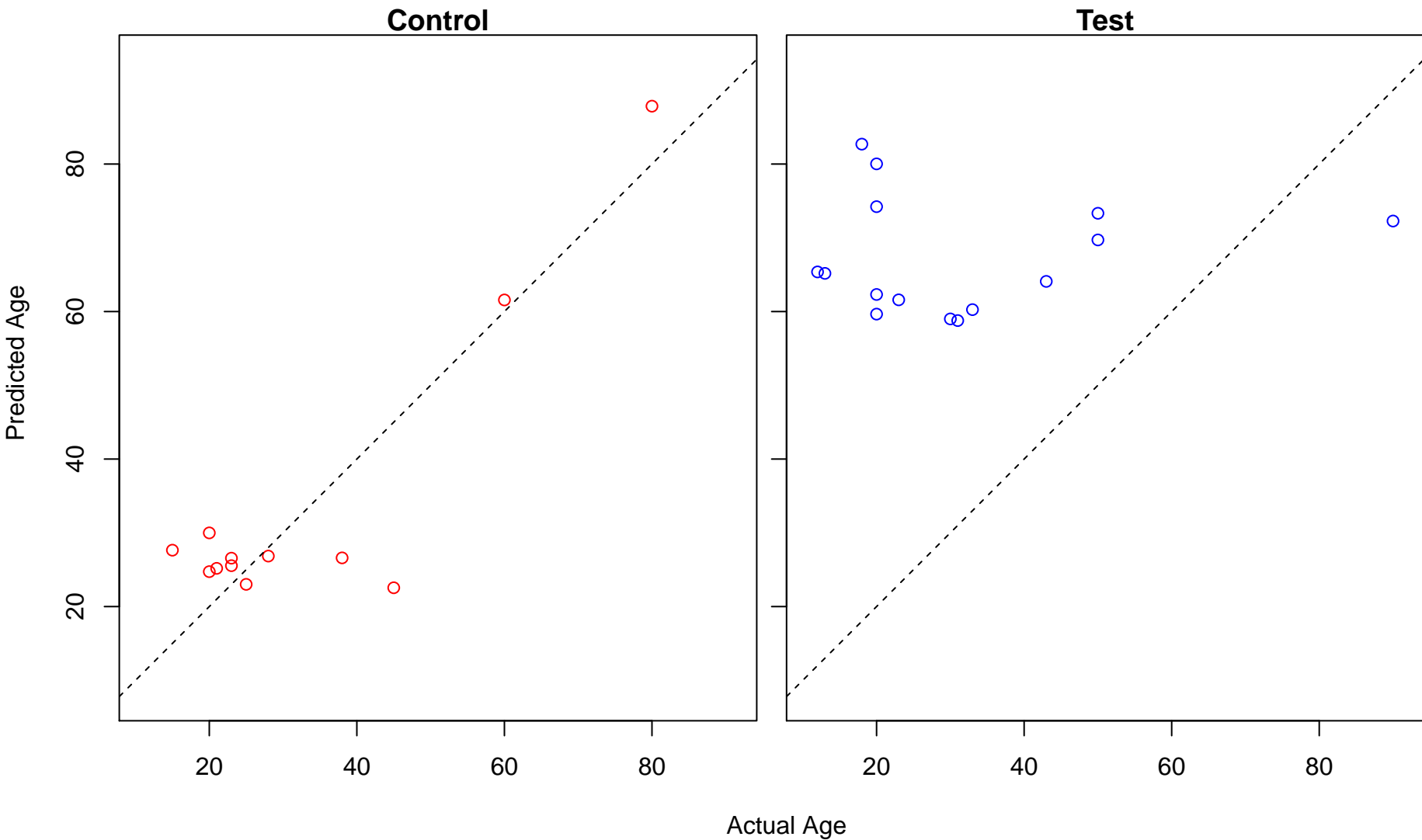
regulation of peptide transport (Score: 6.925377)



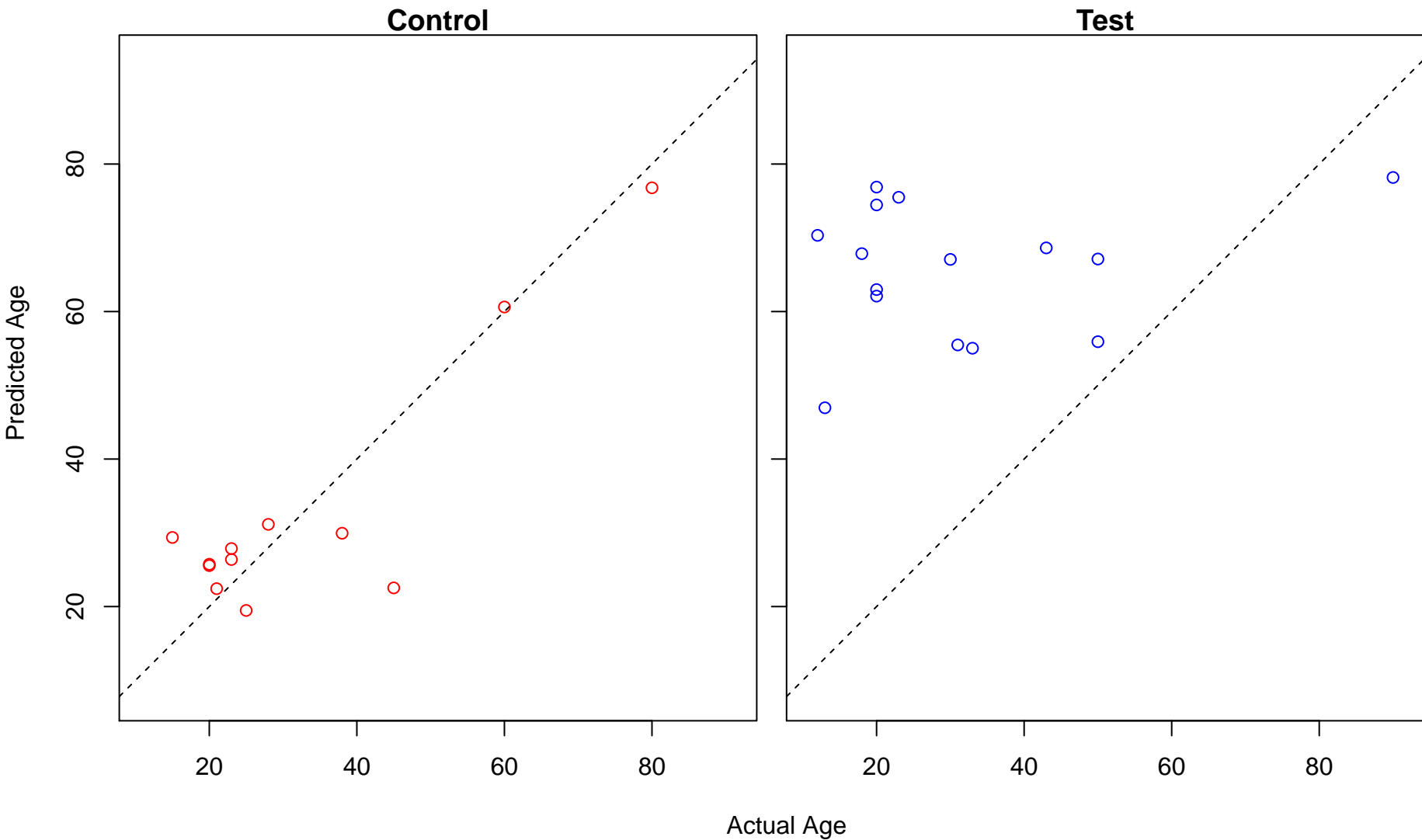
prostate gland development (Score: 6.924916)



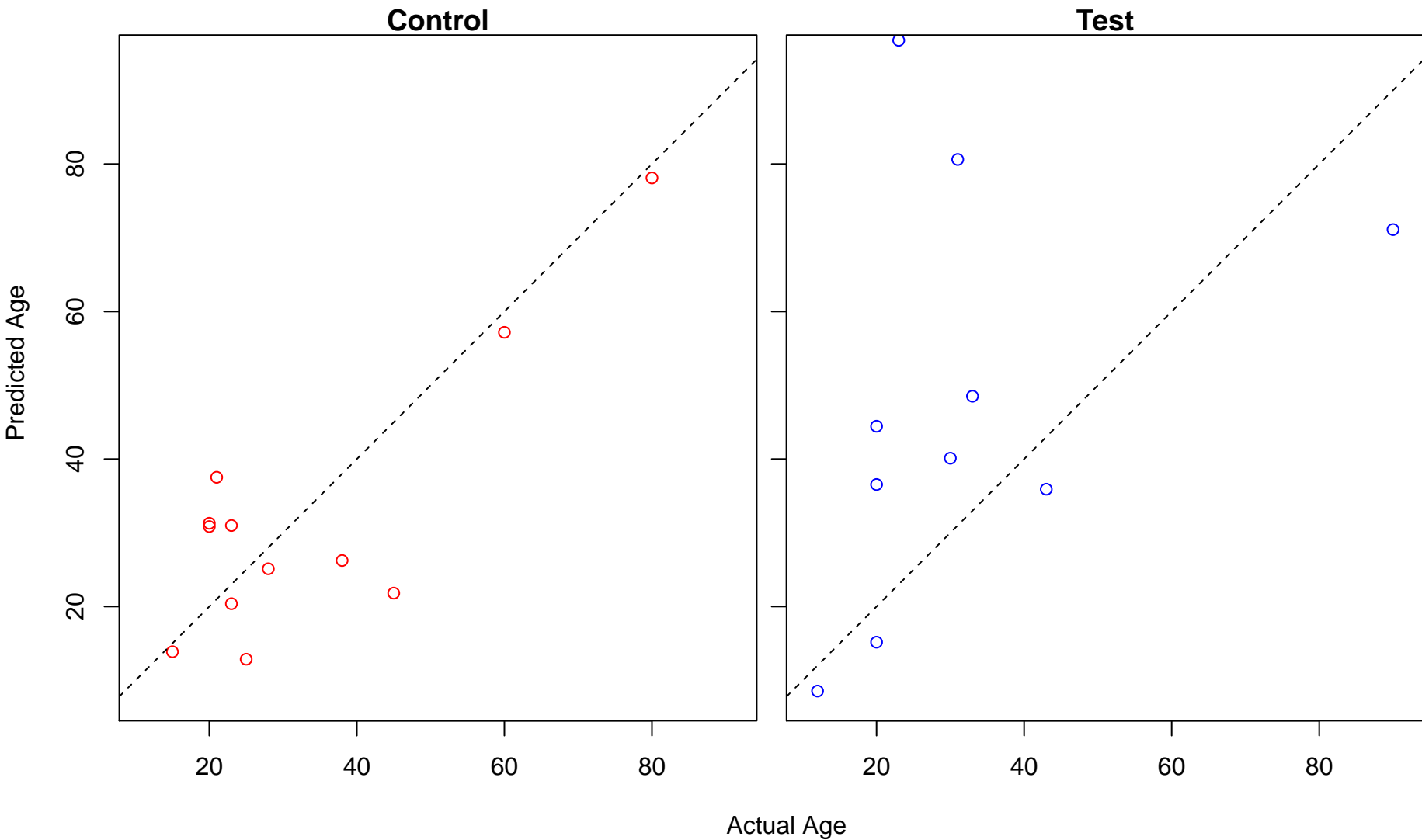
regulation of cell development (Score: 6.924809)



neuron migration (Score: 6.923918)

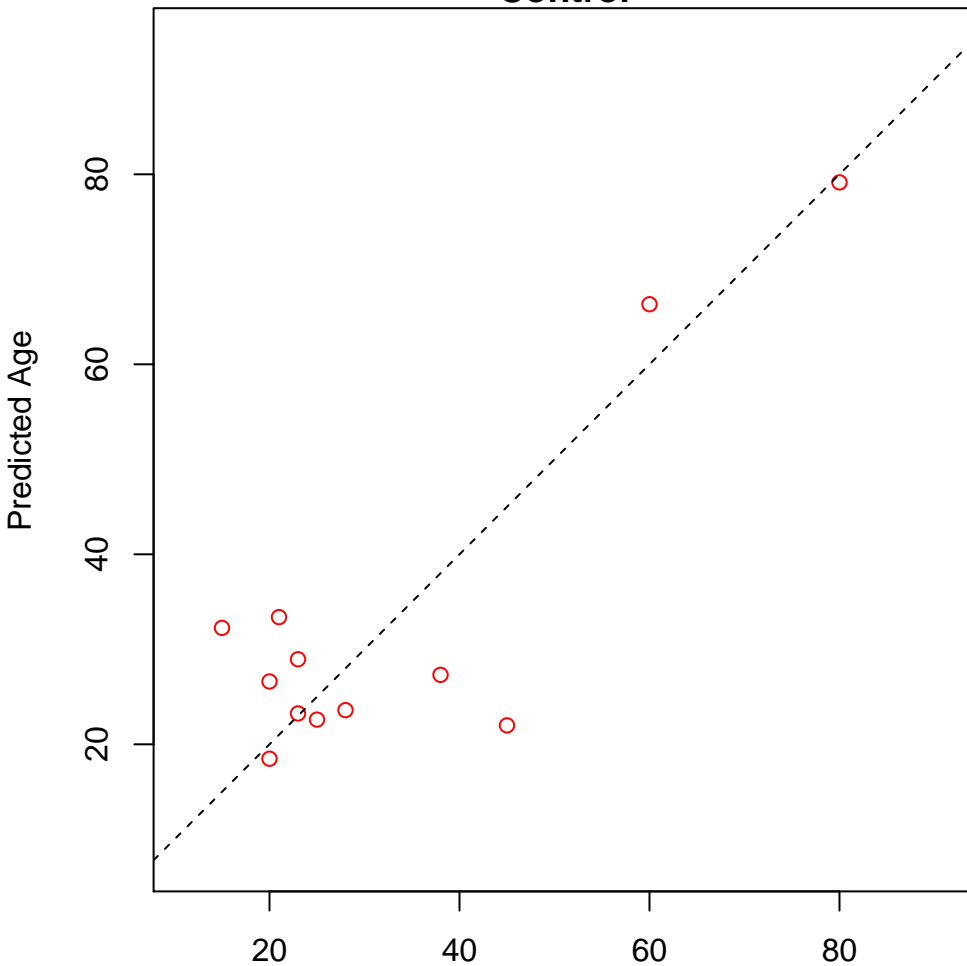


cranial skeletal system development (Score: 6.920630)

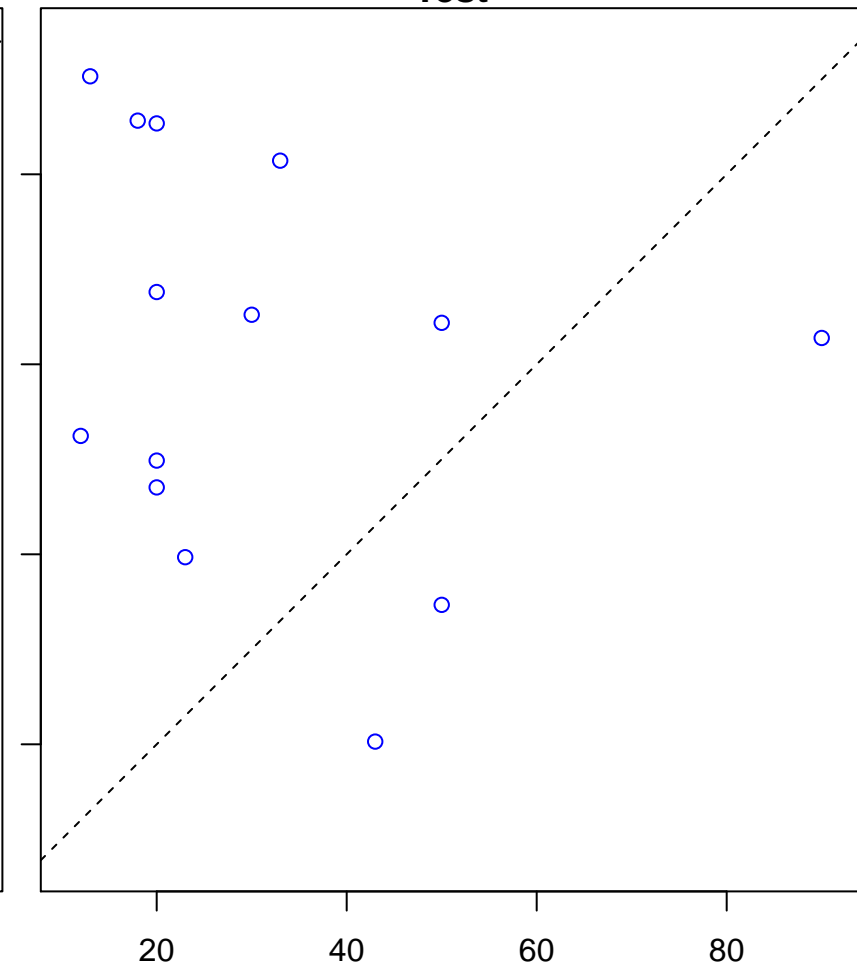


regulation of nucleocytoplasmic transport (Score: 6.918183)

Control

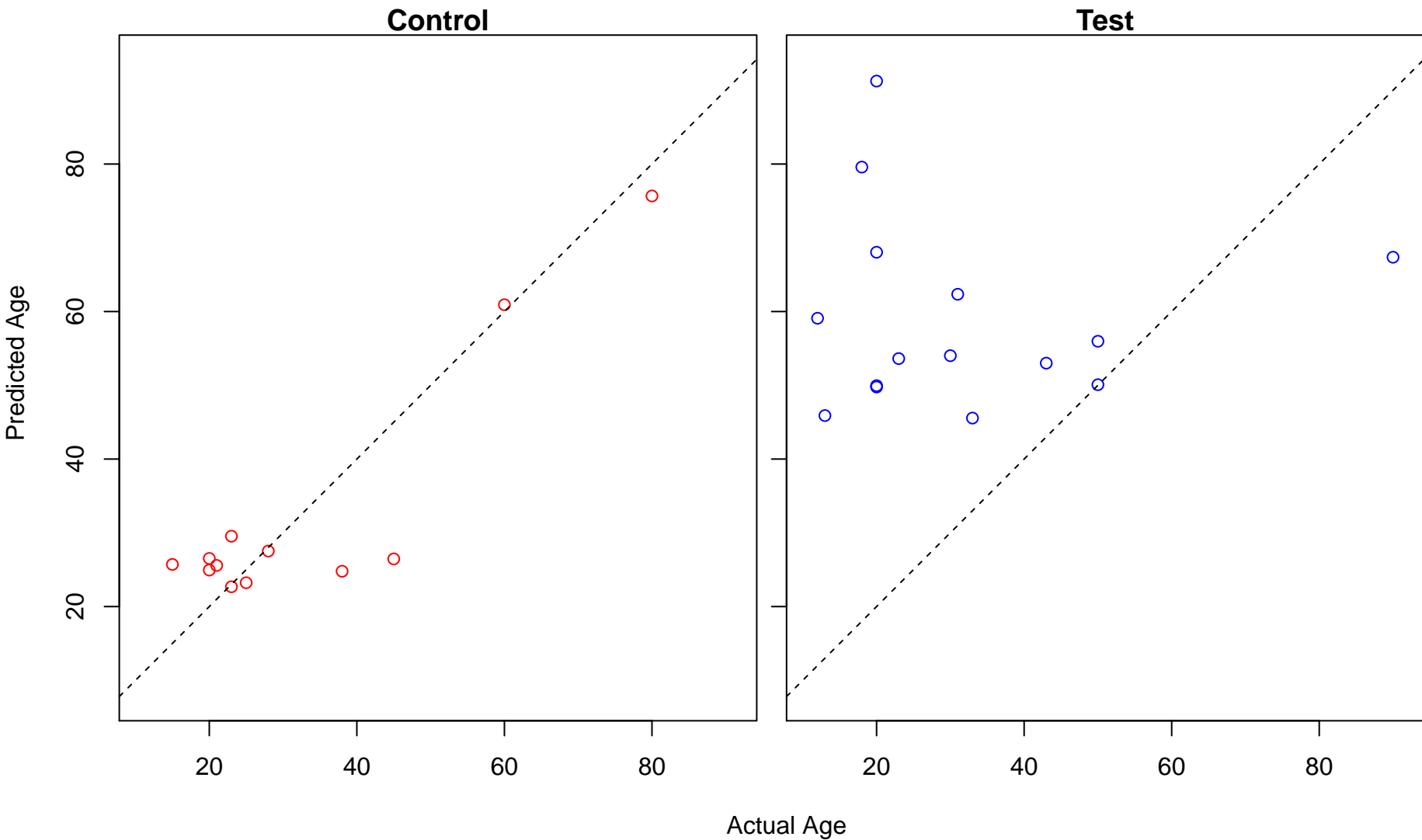


Test

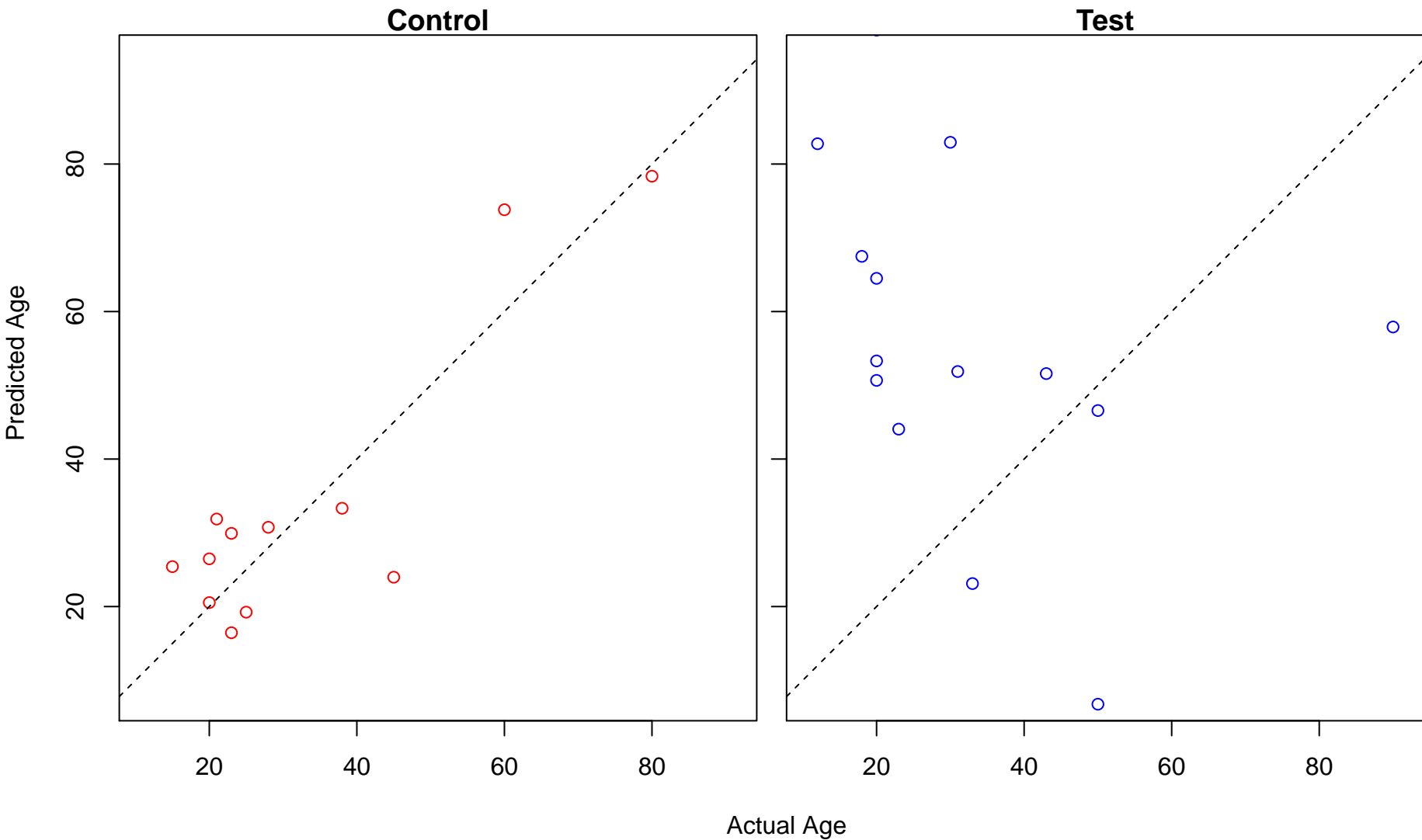


Actual Age

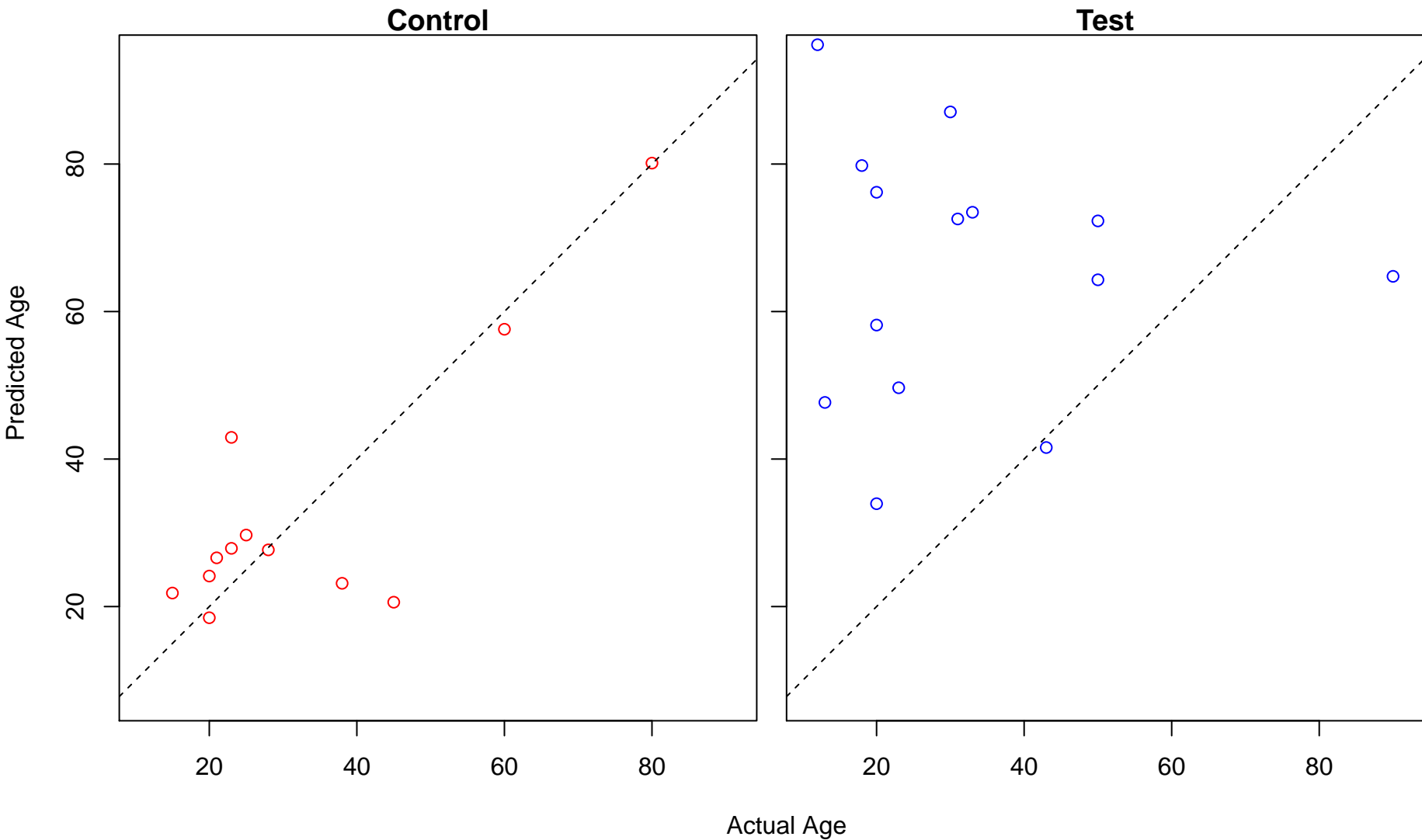
triglyceride metabolic process (Score: 6.917162)



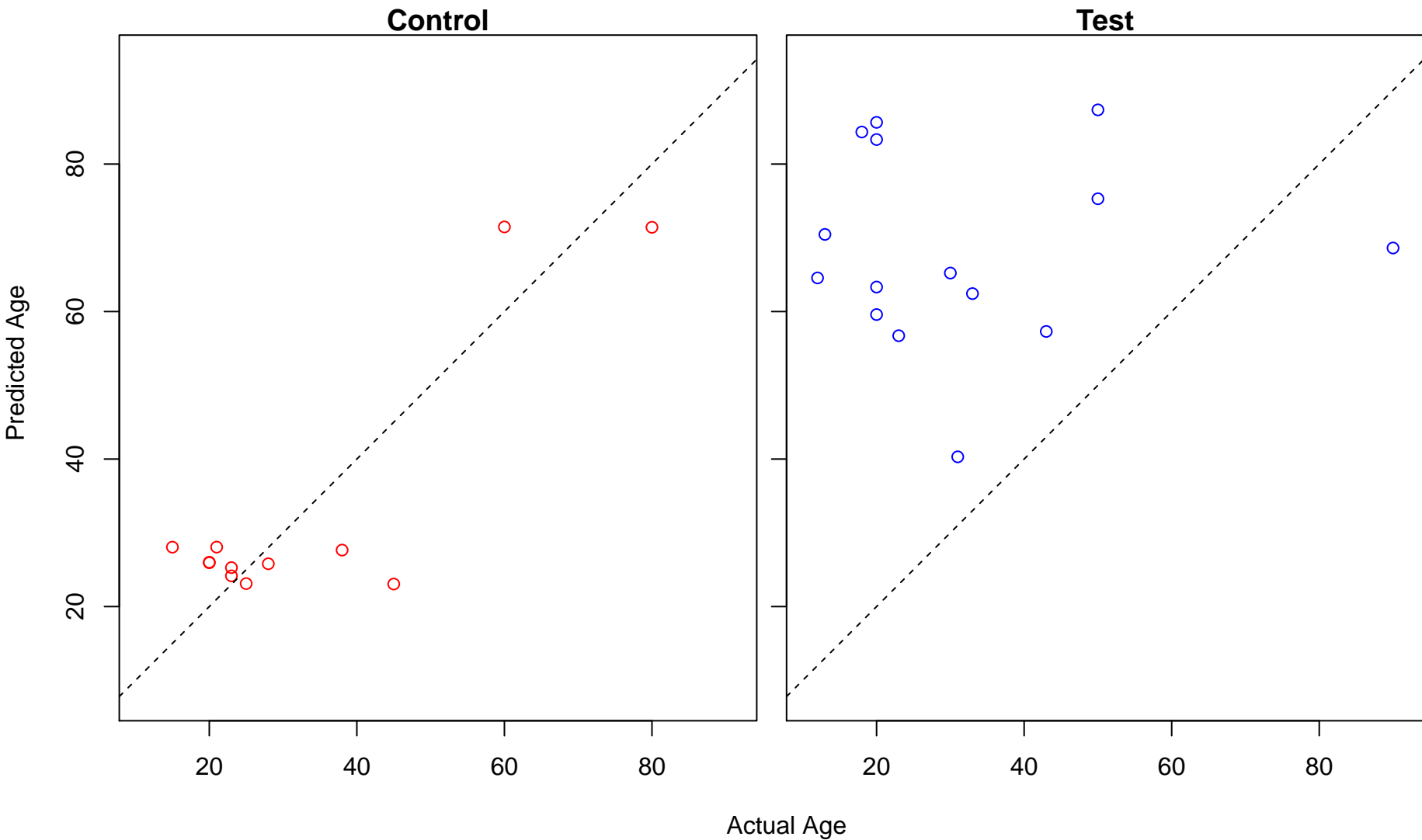
regulation of type I interferon-mediated signaling pathway (Score: 6.914819)



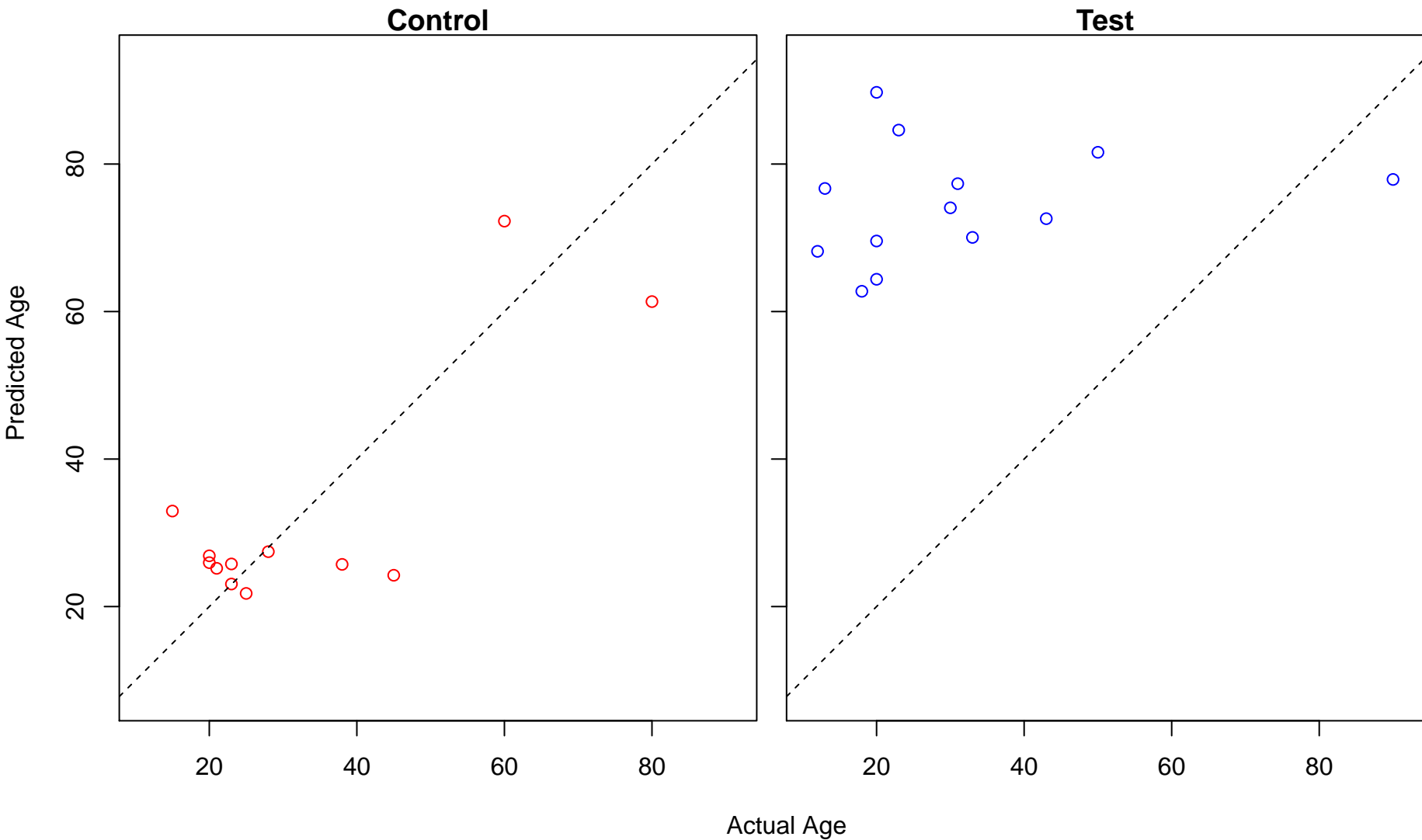
endocrine process (Score: 6.912551)



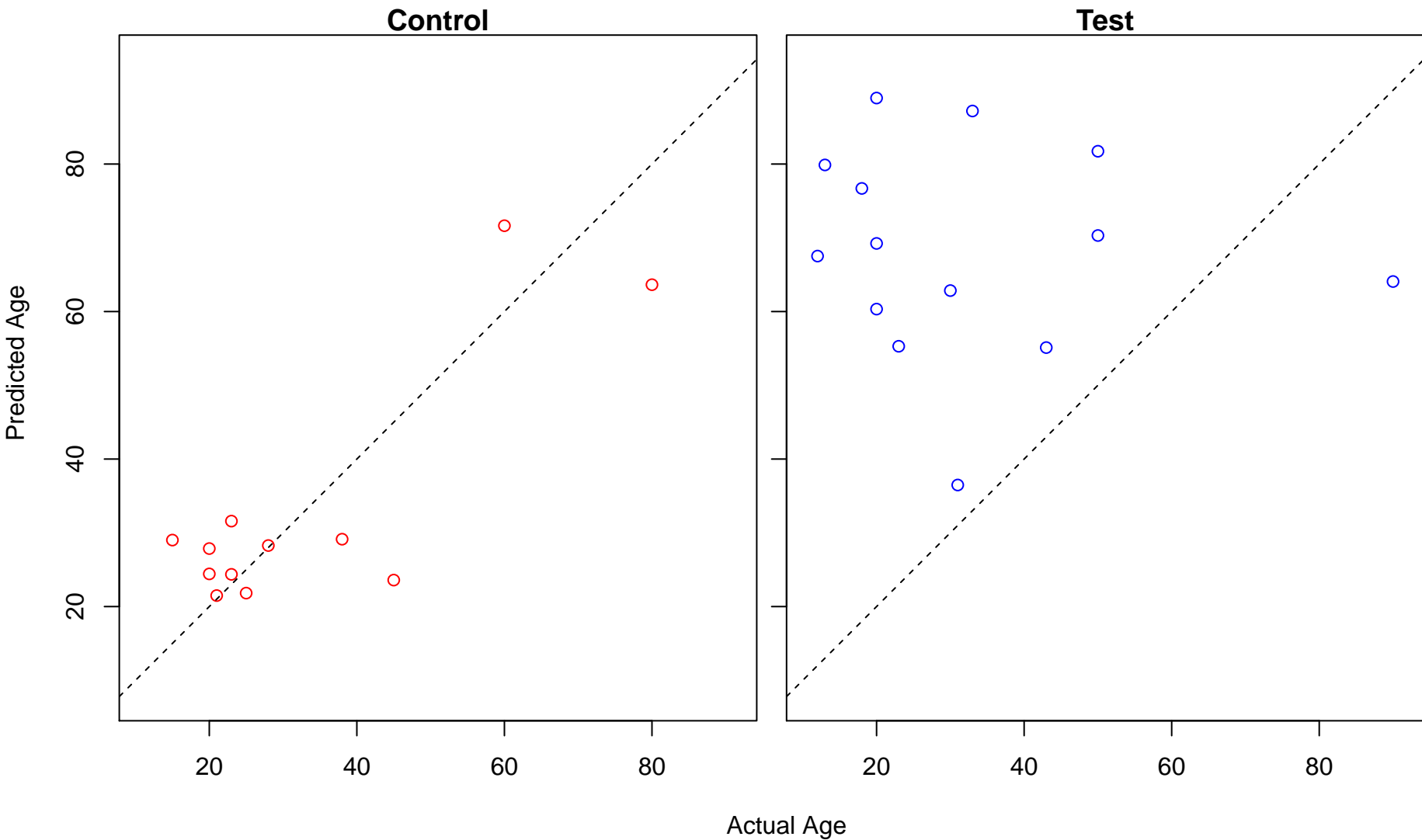
regulation of sequence-specific DNA binding transcription factor activity (Score: 6.911120)



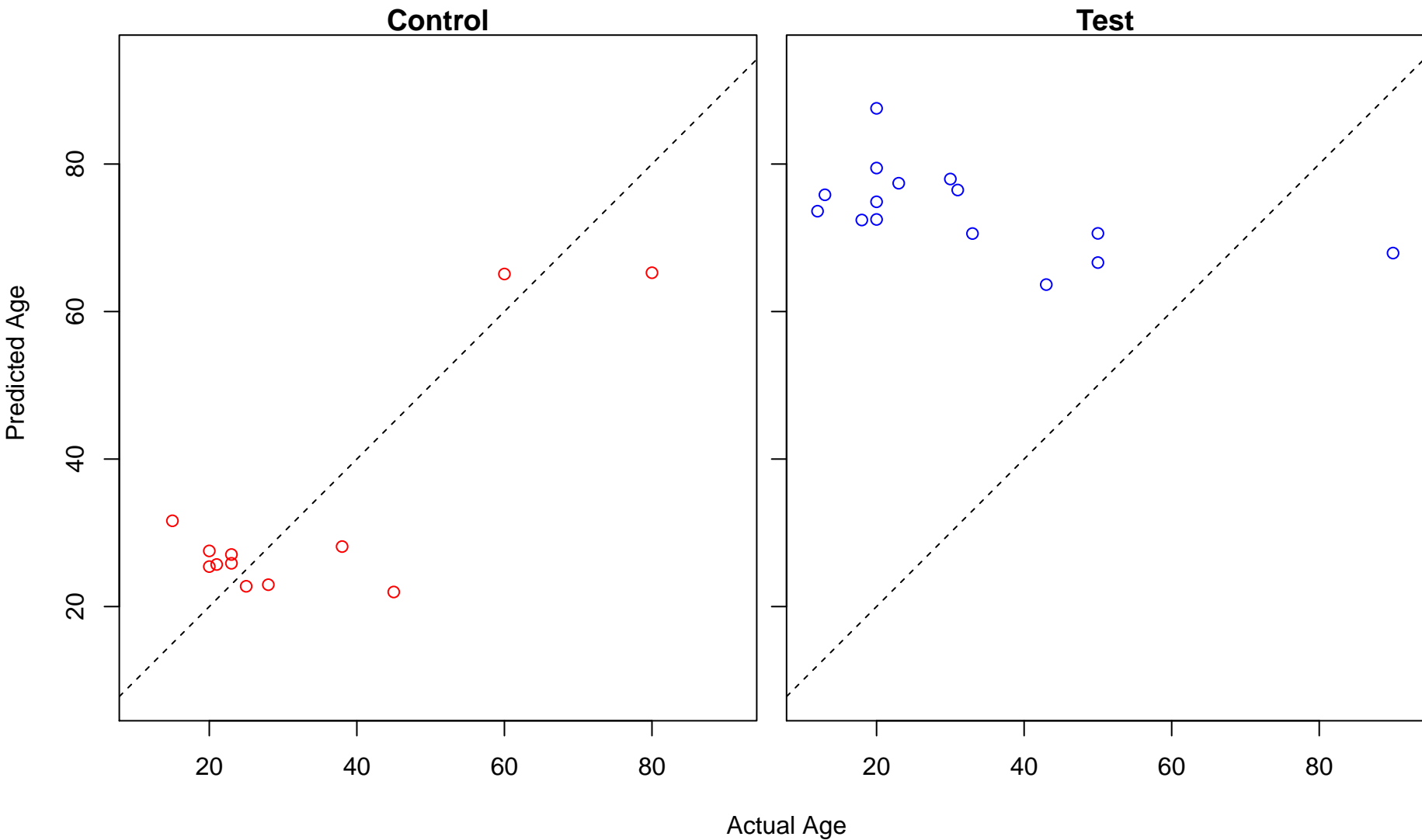
negative regulation of smoothened signaling pathway (Score: 6.910560)



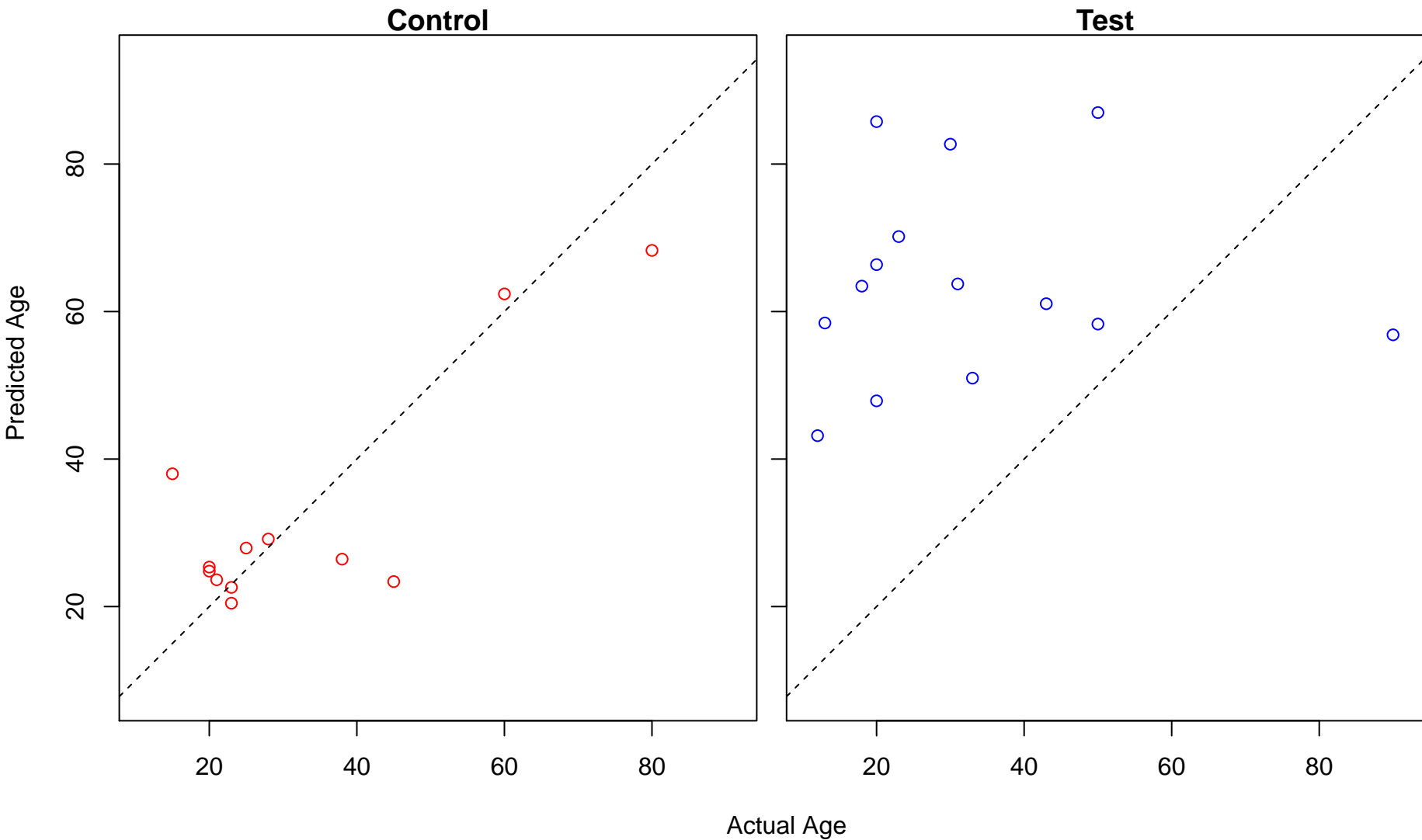
platelet-derived growth factor receptor-beta signaling pathway (Score: 6.909360)



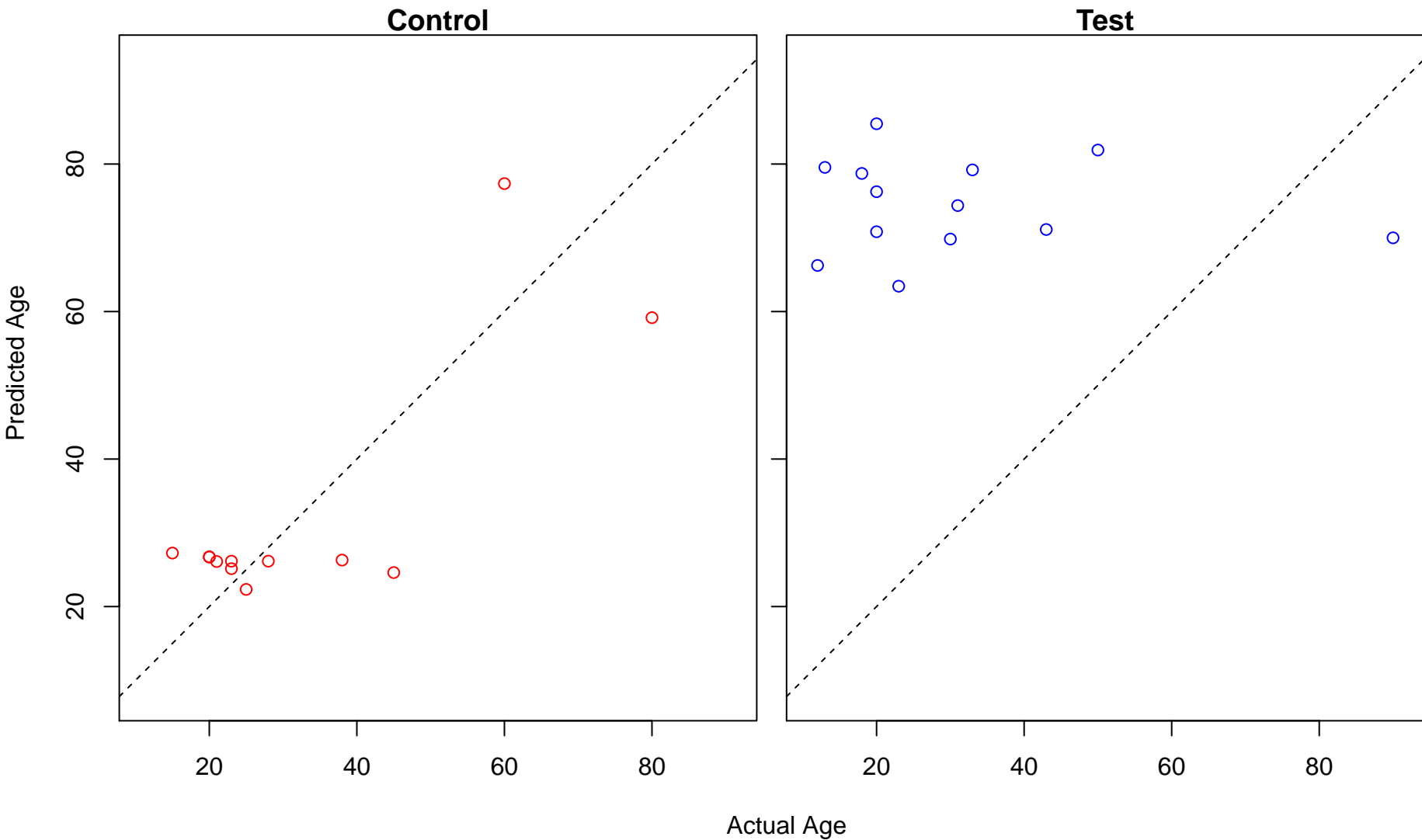
response to growth hormone (Score: 6.909126)



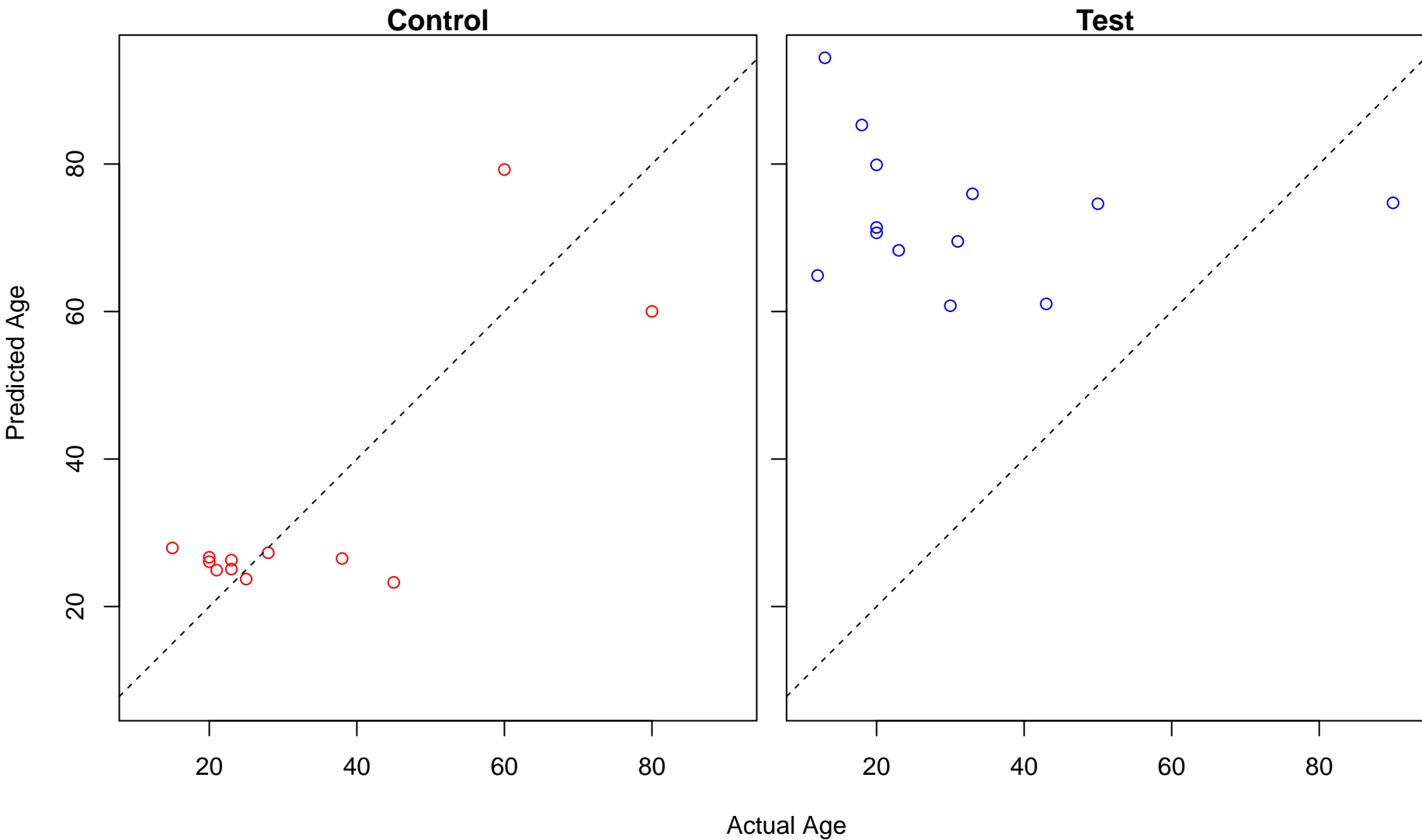
2-oxoglutarate metabolic process (Score: 6.906068)



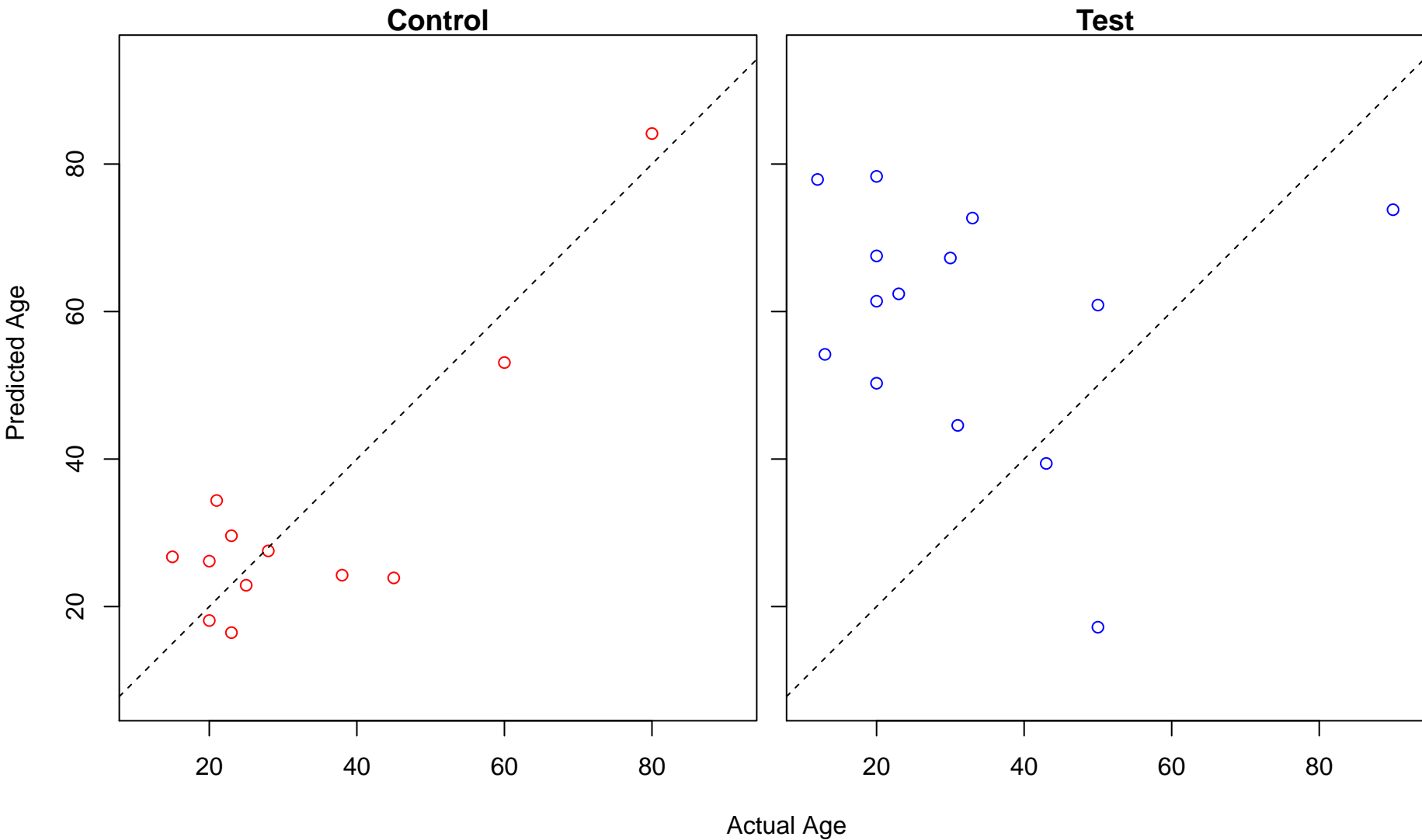
regulation of extrinsic apoptotic signaling pathway (Score: 6.904706)



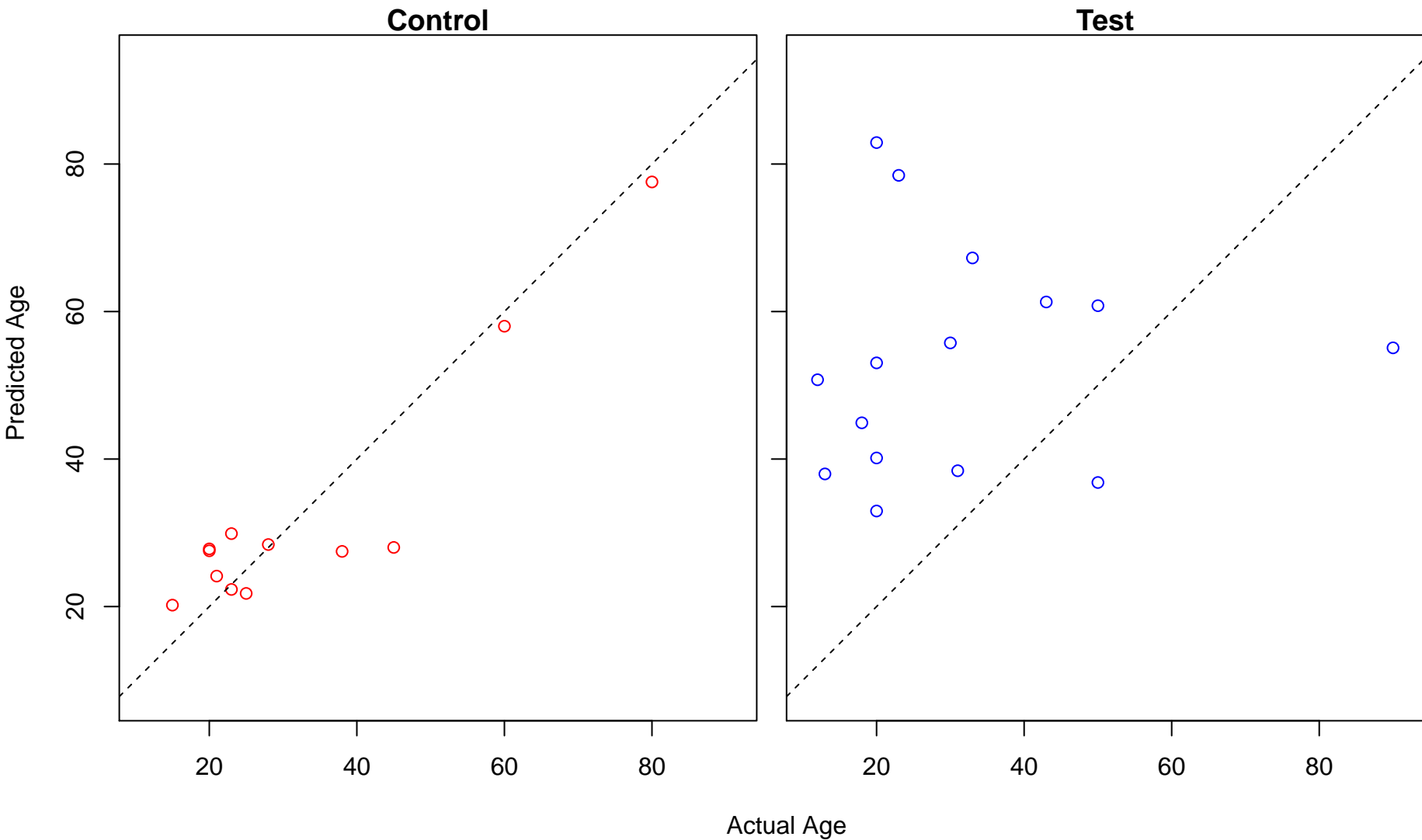
nucleotide-excision repair, DNA gap filling (Score: 6.901189)



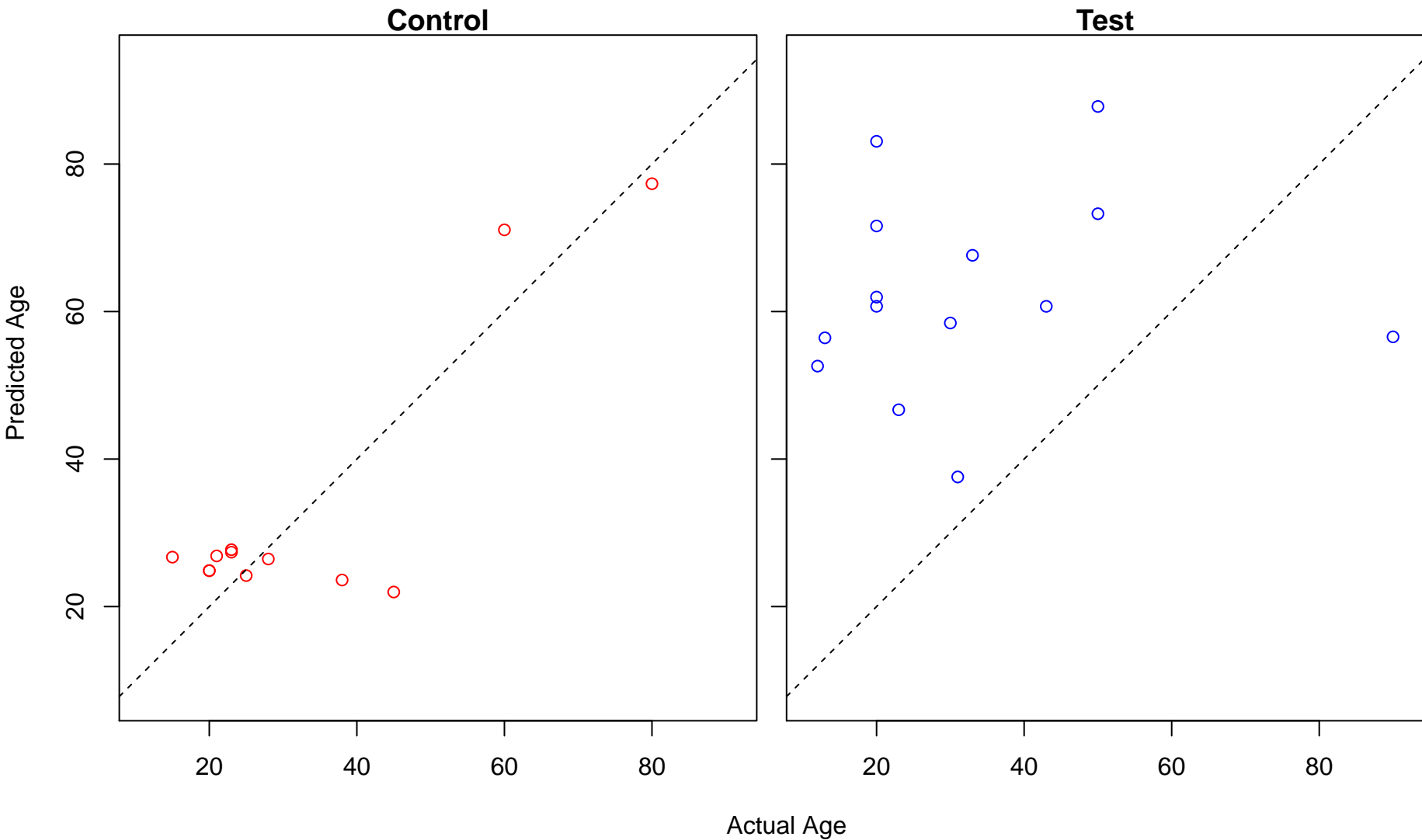
guanosine-containing compound metabolic process (Score: 6.894457)



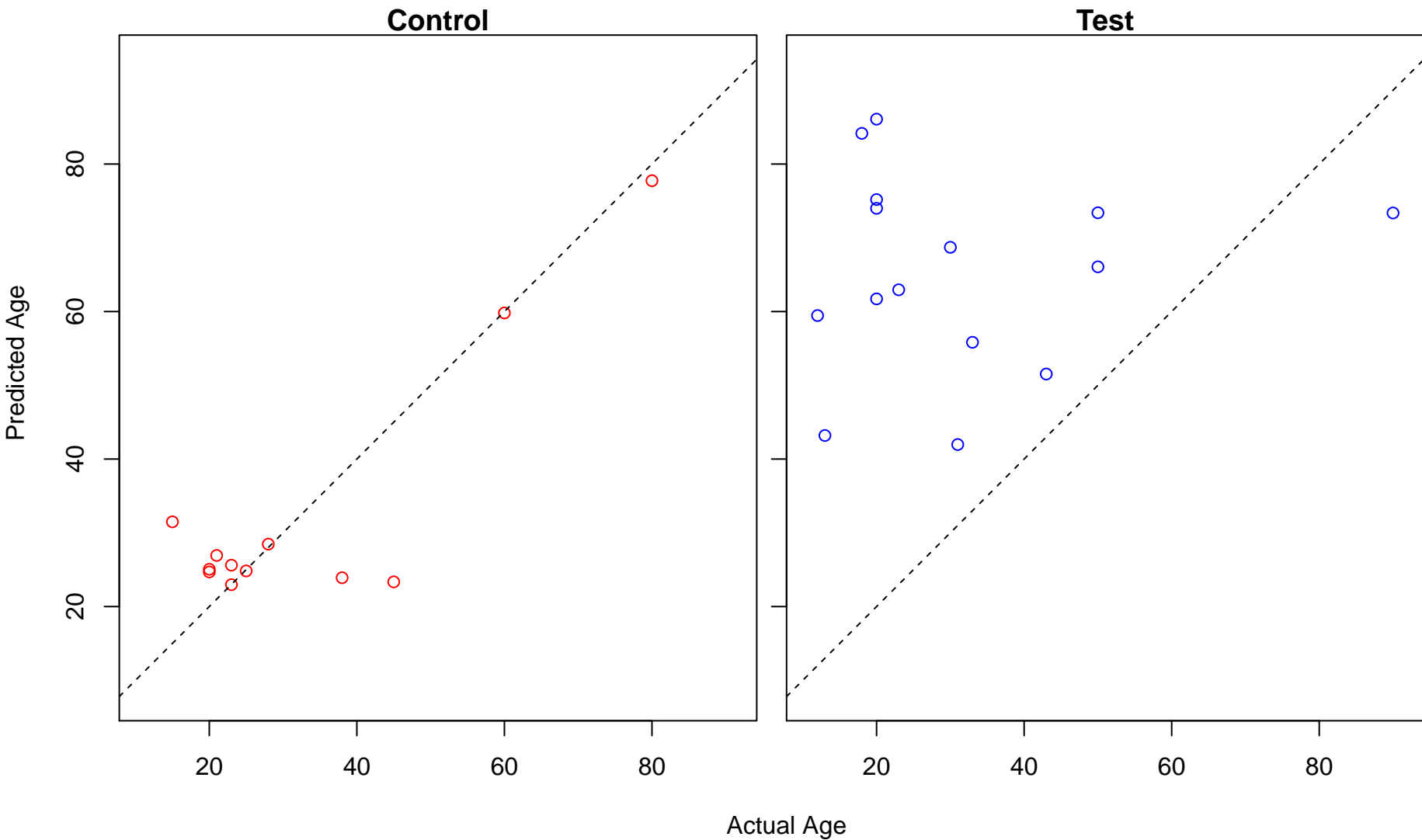
positive regulation of tyrosine phosphorylation of Stat5 protein (Score: 6.890299)



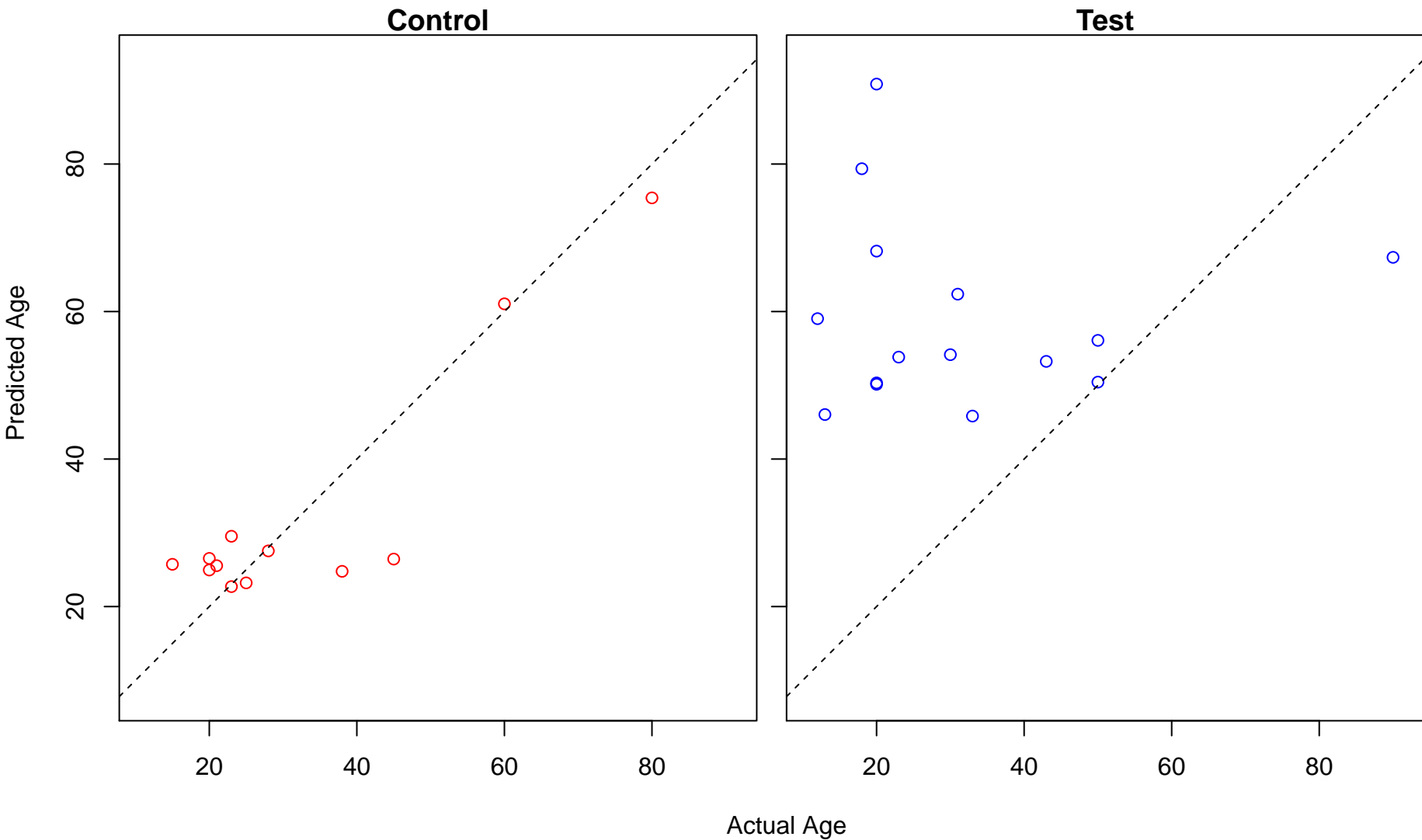
regulation of muscle cell differentiation (Score: 6.888704)



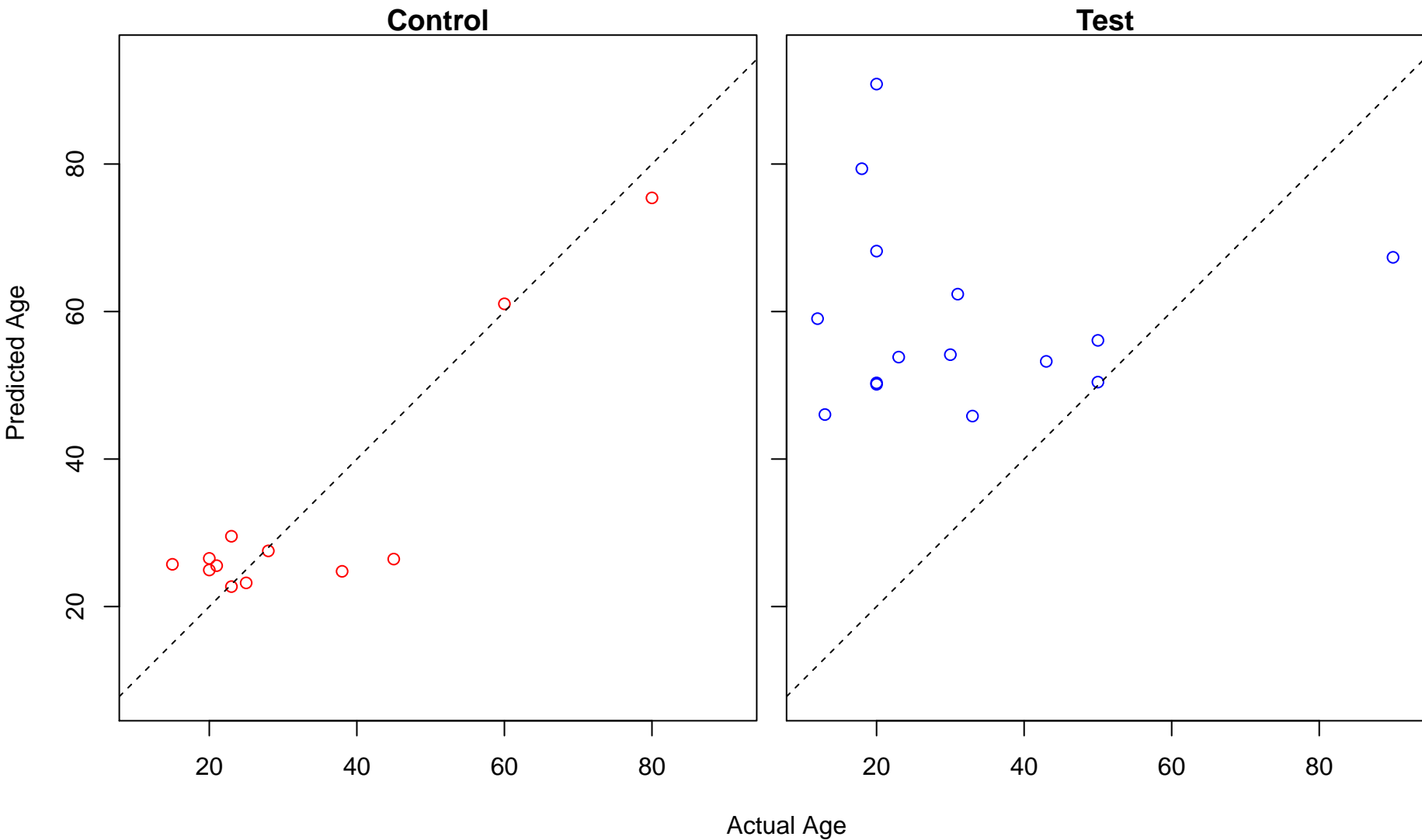
positive regulation of viral release from host cell (Score: 6.888490)



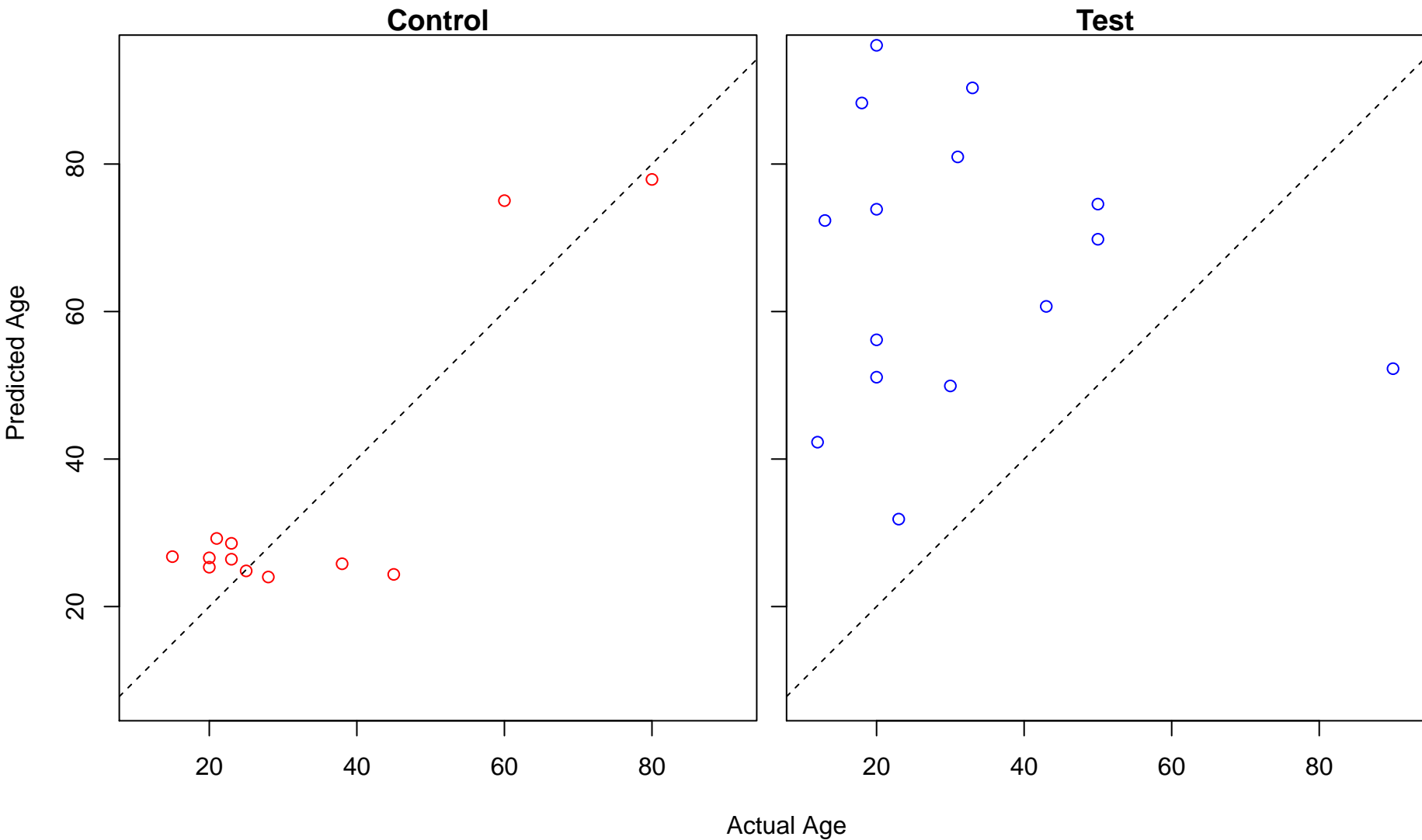
neutral lipid metabolic process (Score: 6.888051)



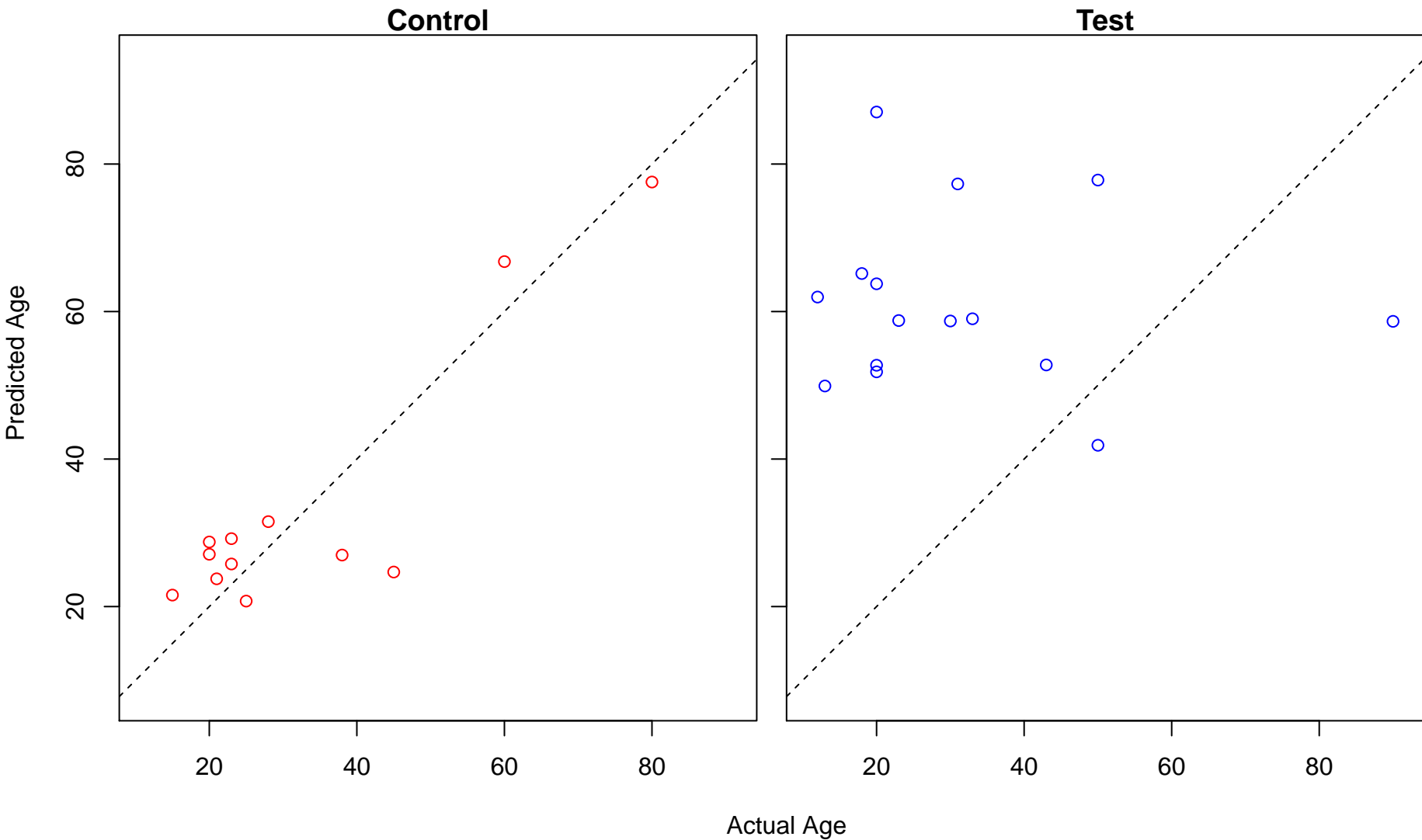
acylglycerol metabolic process (Score: 6.888051)



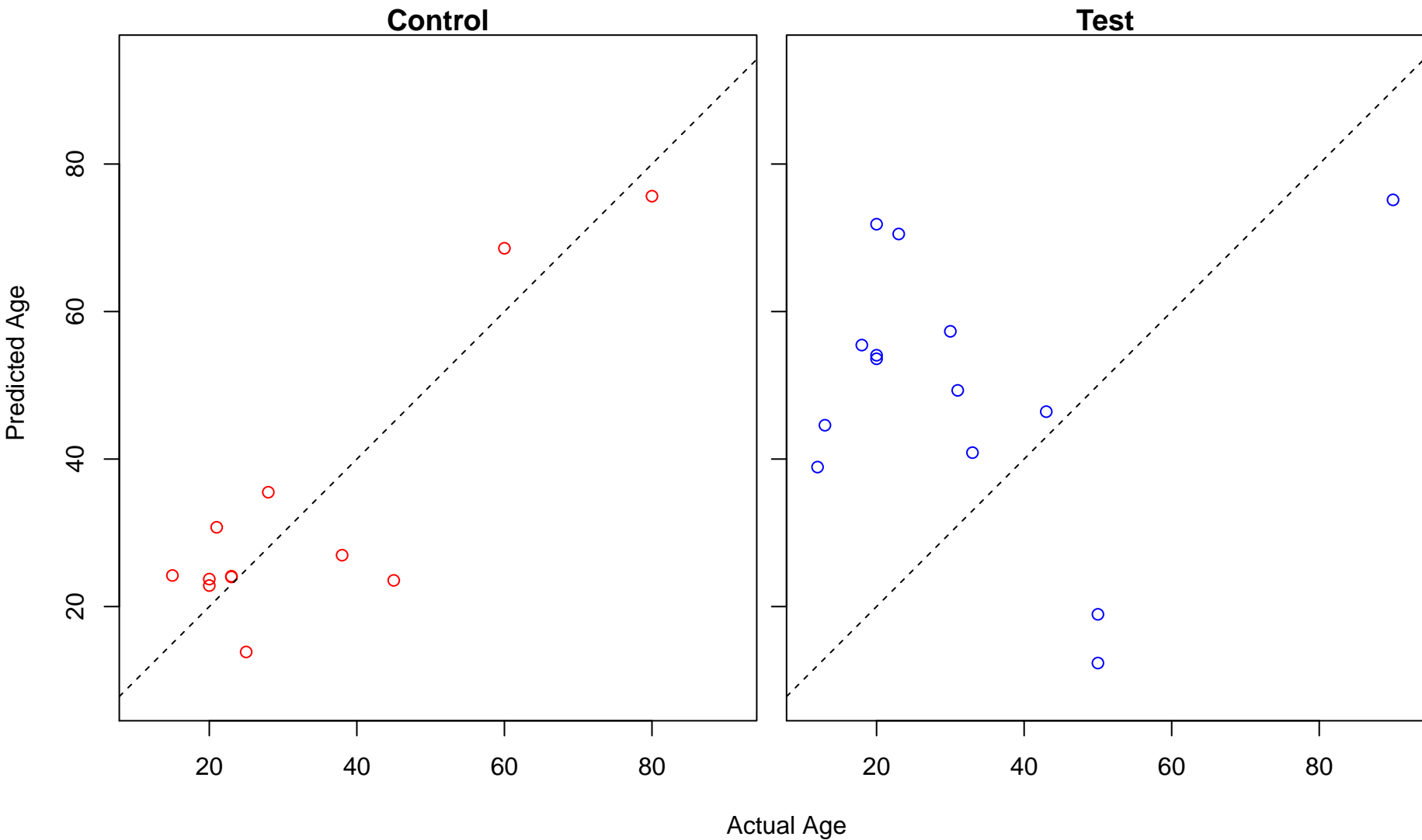
positive regulation of cell-substrate adhesion (Score: 6.885818)



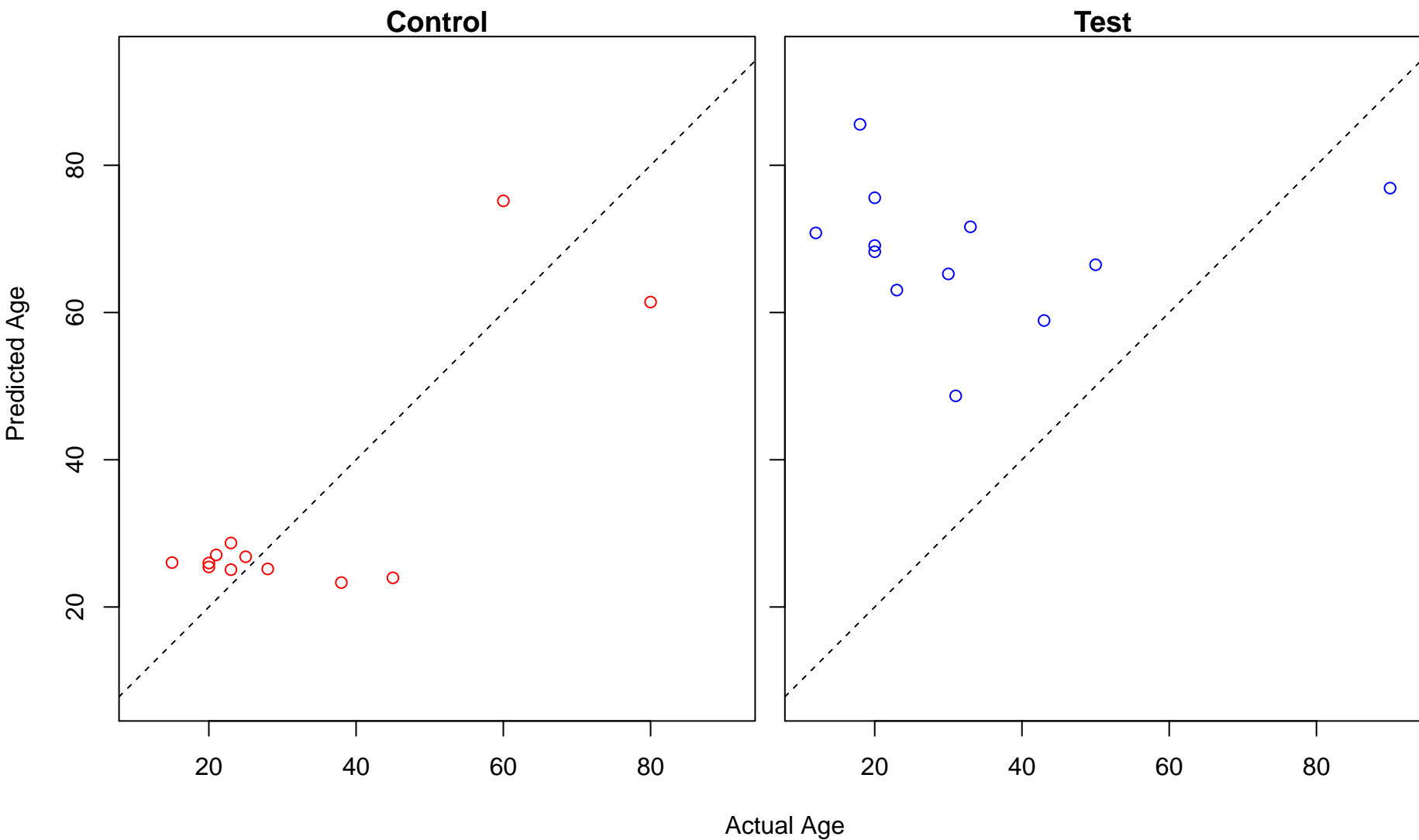
telomere capping (Score: 6.883747)



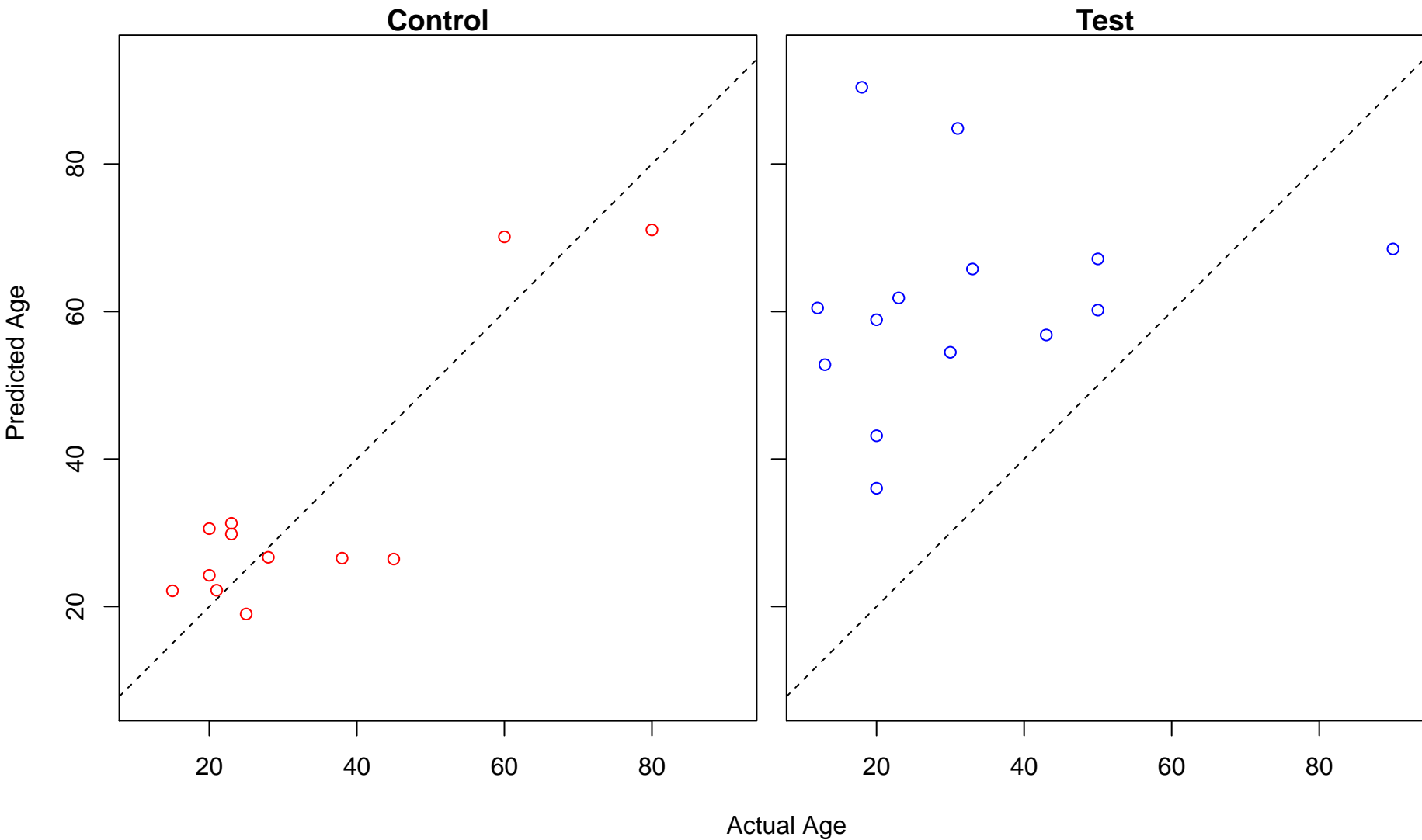
male sex differentiation (Score: 6.883289)



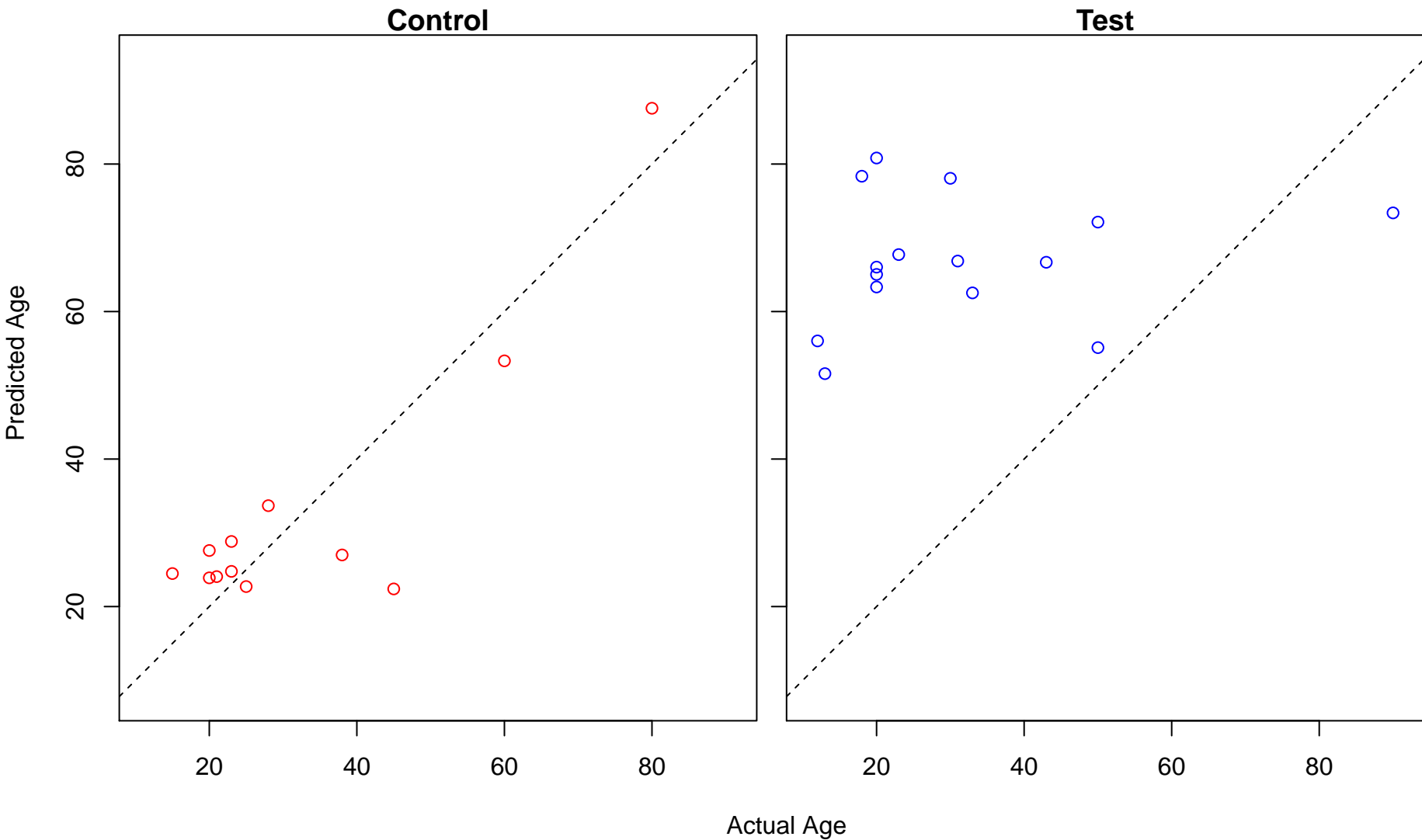
rRNA processing (Score: 6.882997)



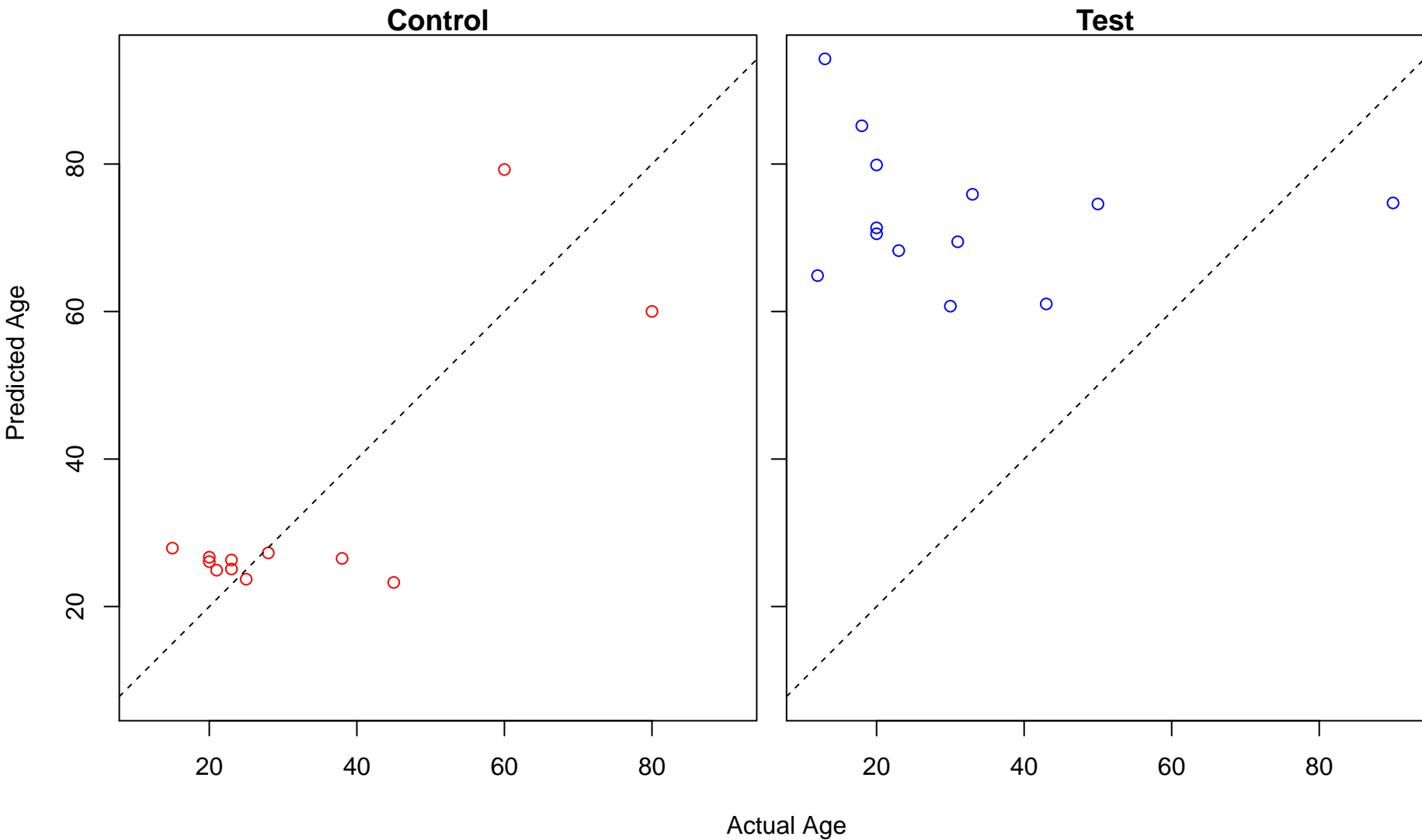
regulation of endosome size (Score: 6.882146)



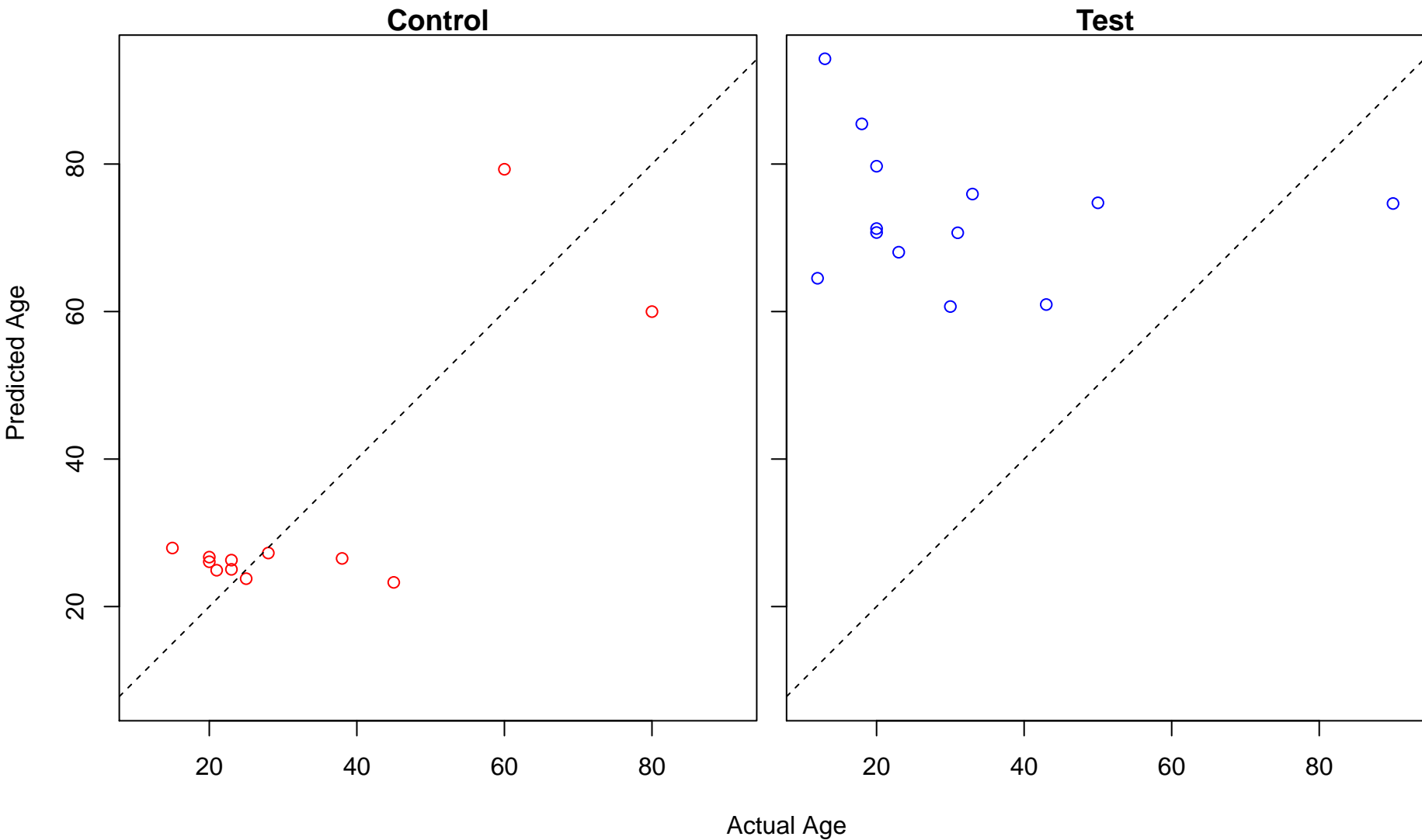
regulation of T cell differentiation (Score: 6.881851)



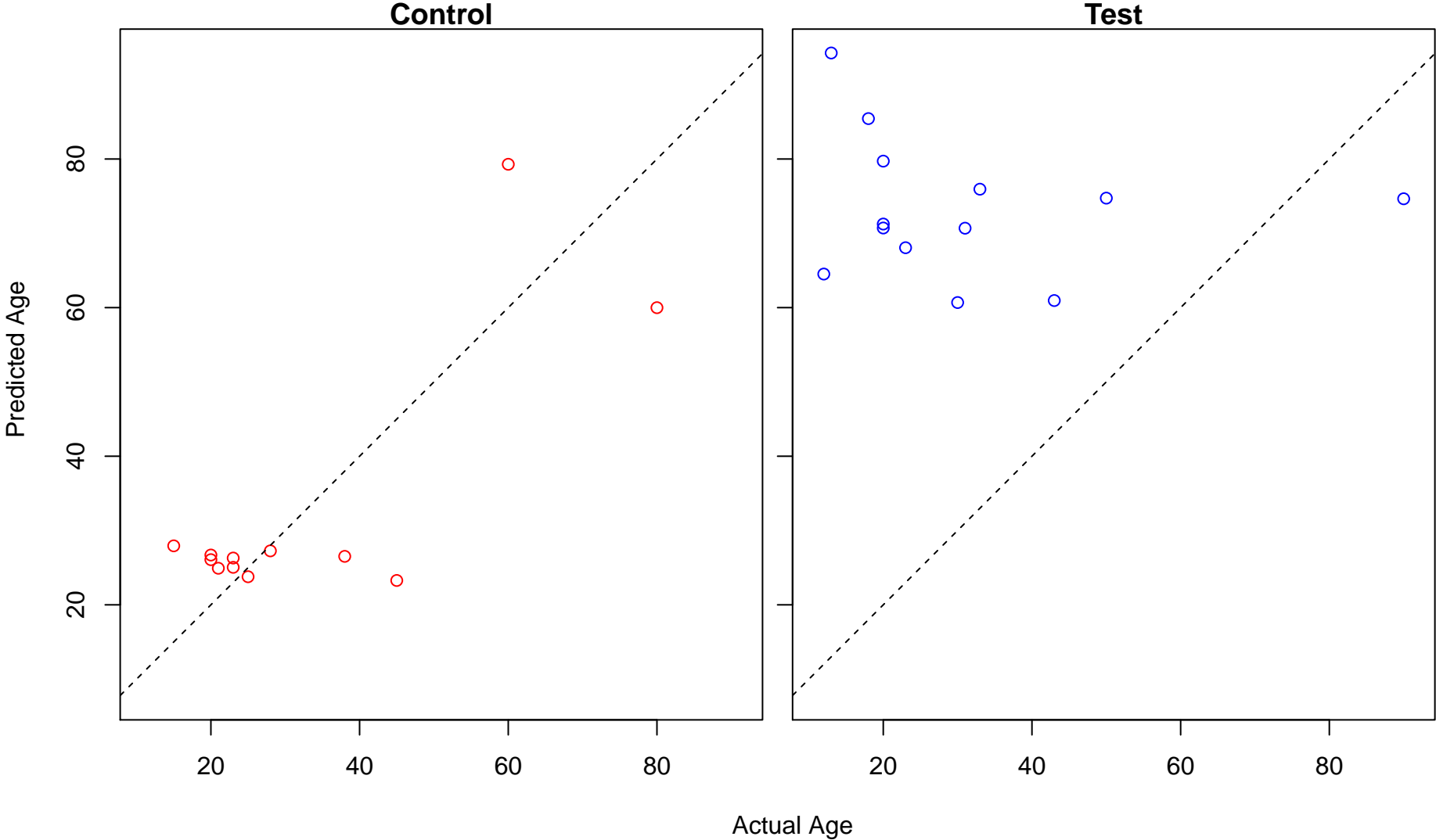
error-prone translesion synthesis (Score: 6.881321)



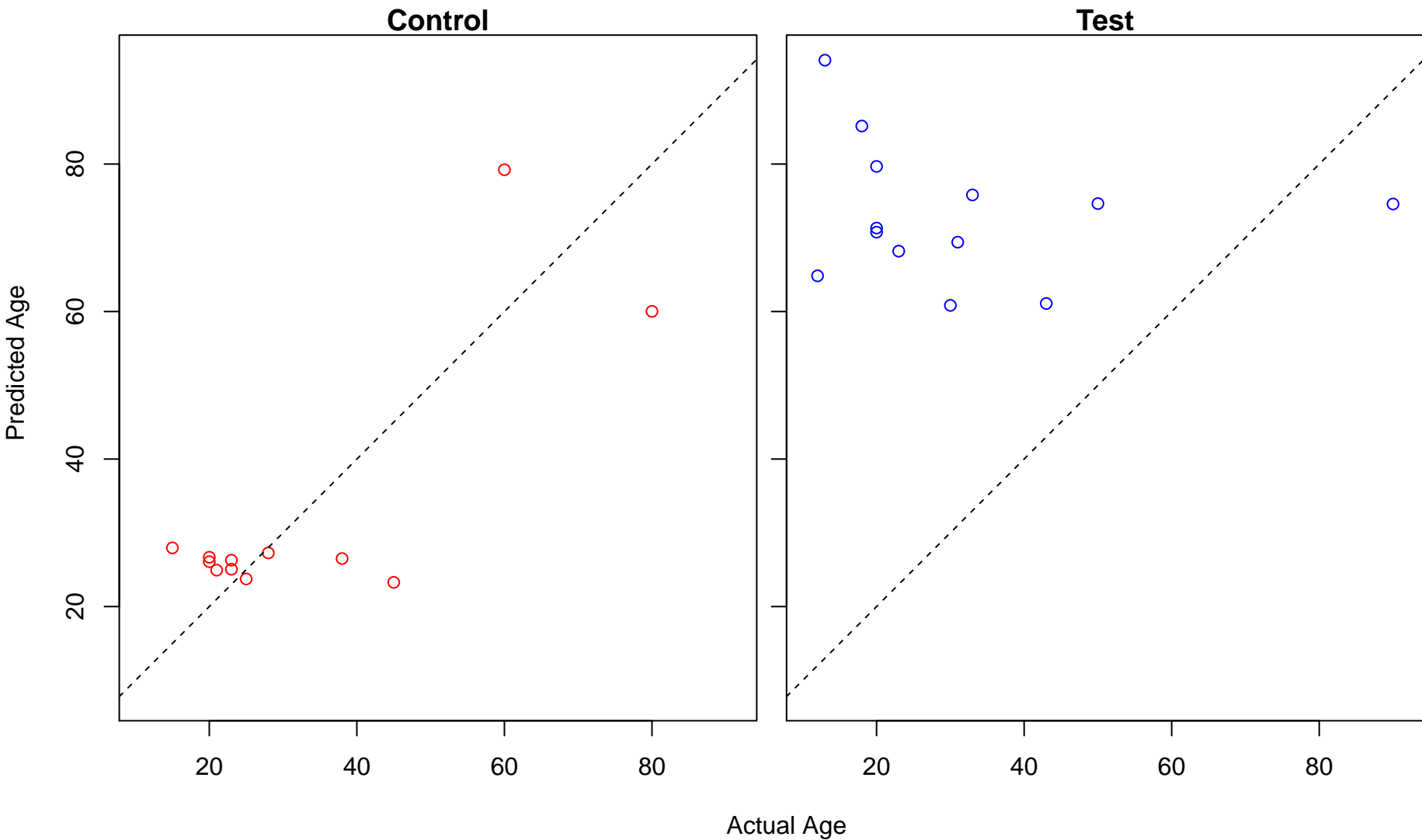
nucleotide-binding oligomerization domain containing signaling pathway (Score: 6.879687)



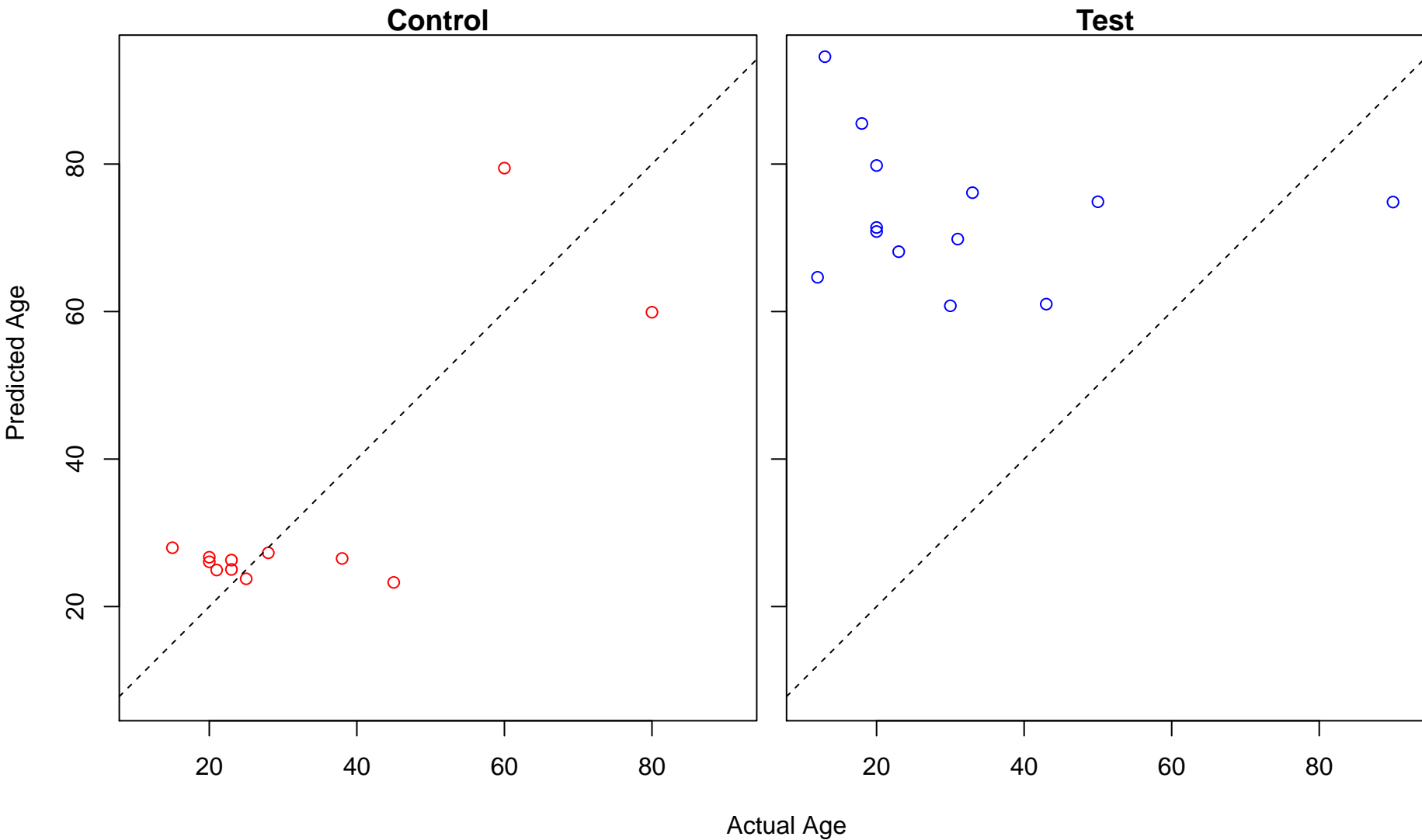
cytoplasmic pattern recognition receptor signaling pathway (Score: 6.879383)



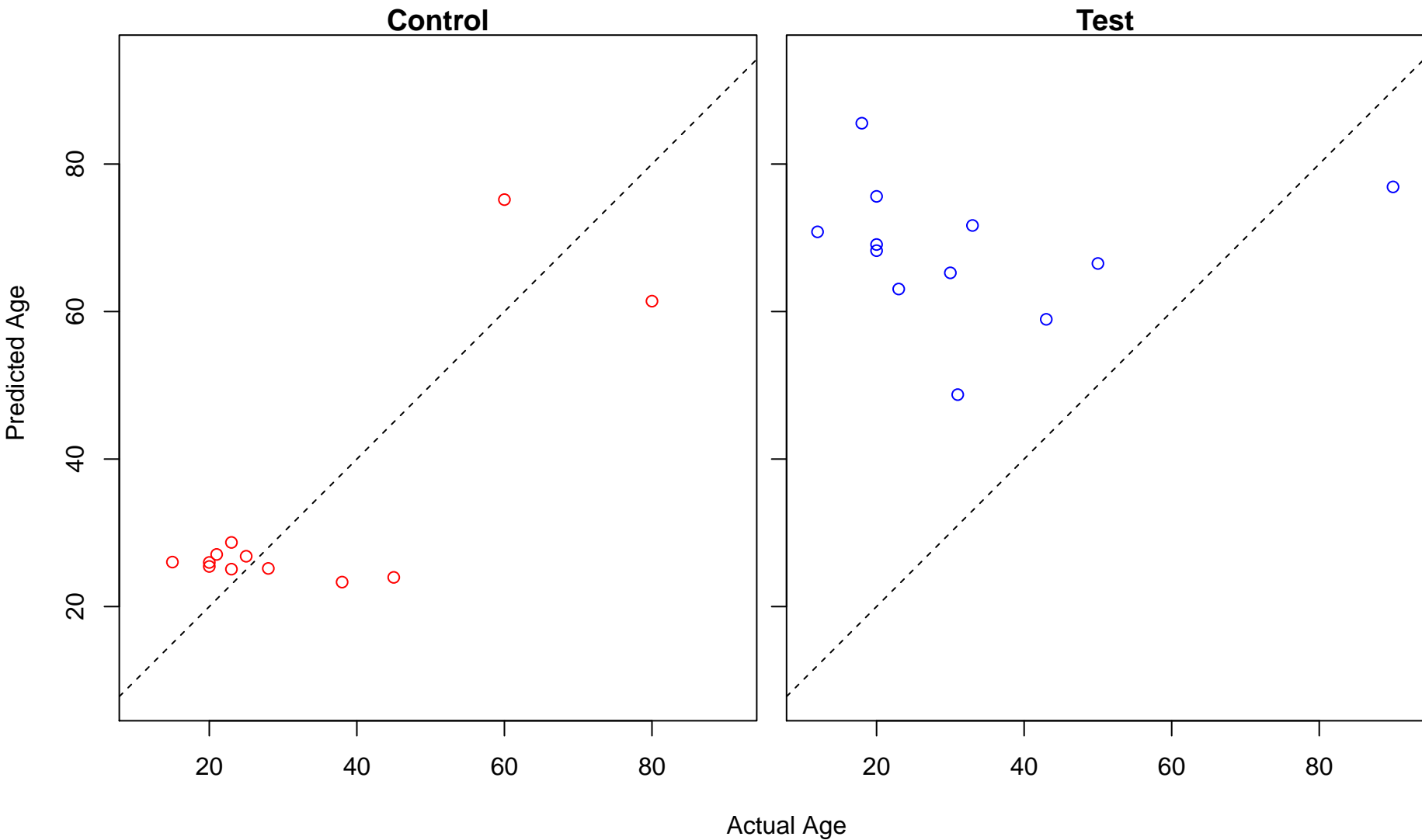
error-free translesion synthesis (Score: 6.878624)



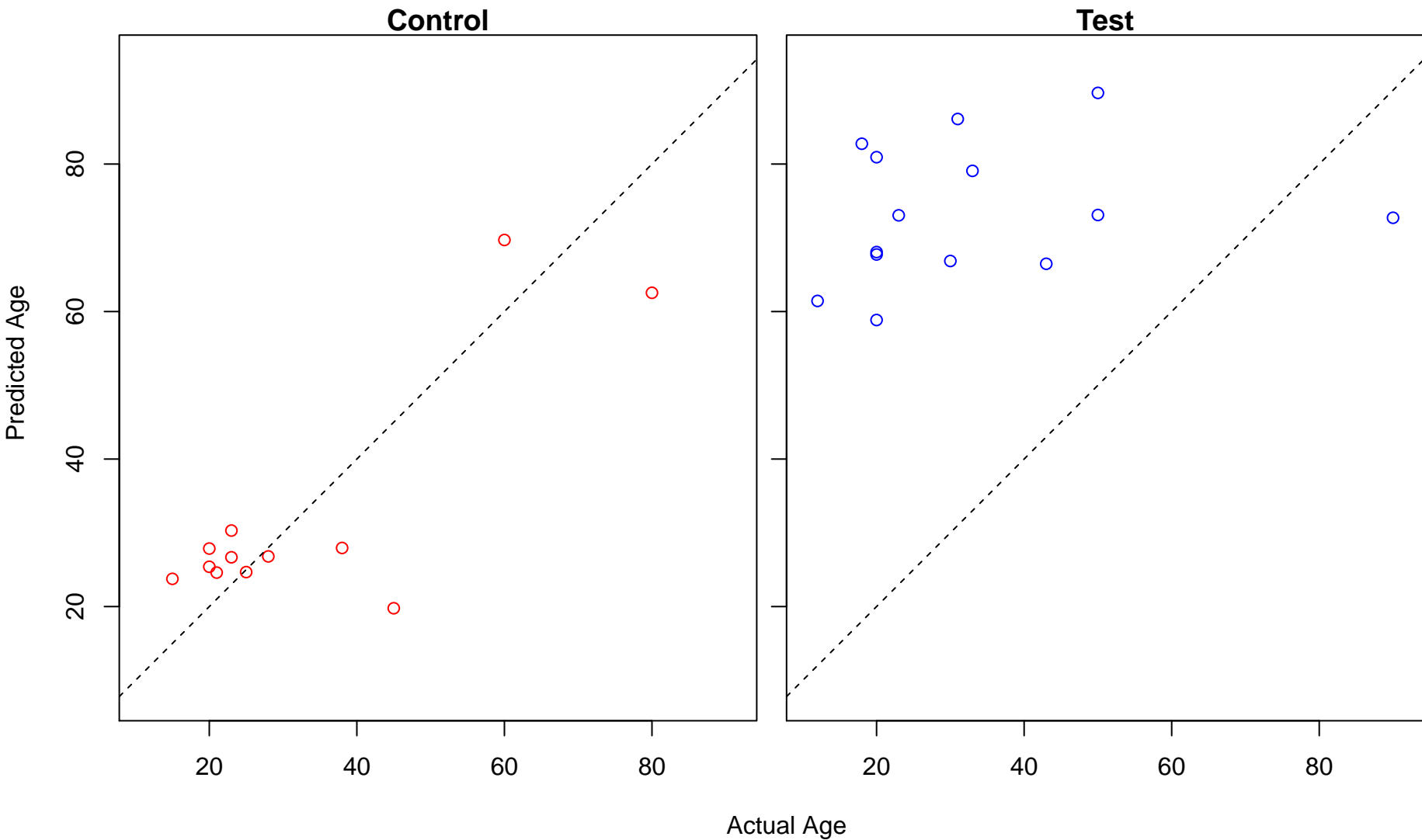
viral protein processing (Score: 6.878093)



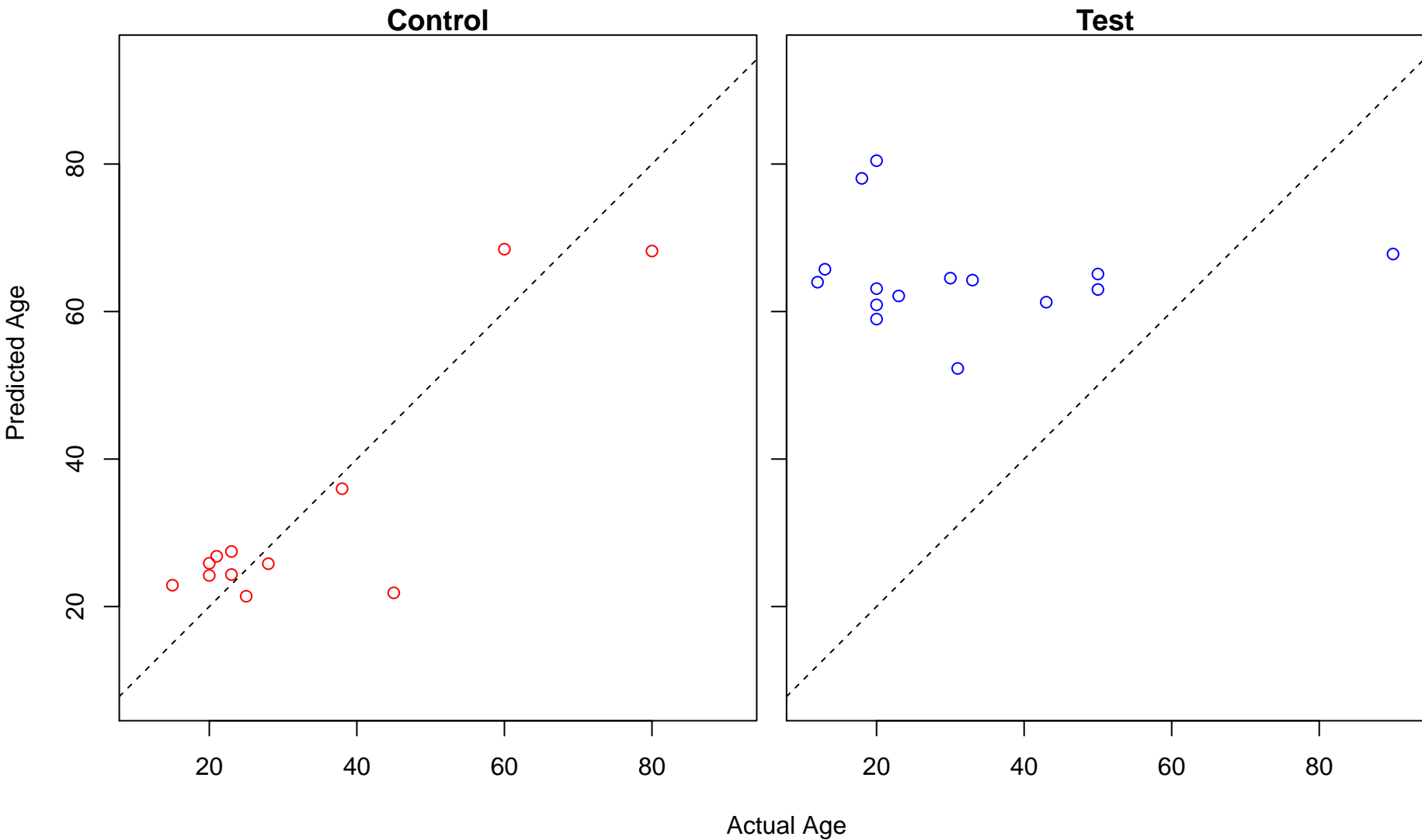
rRNA metabolic process (Score: 6.876988)



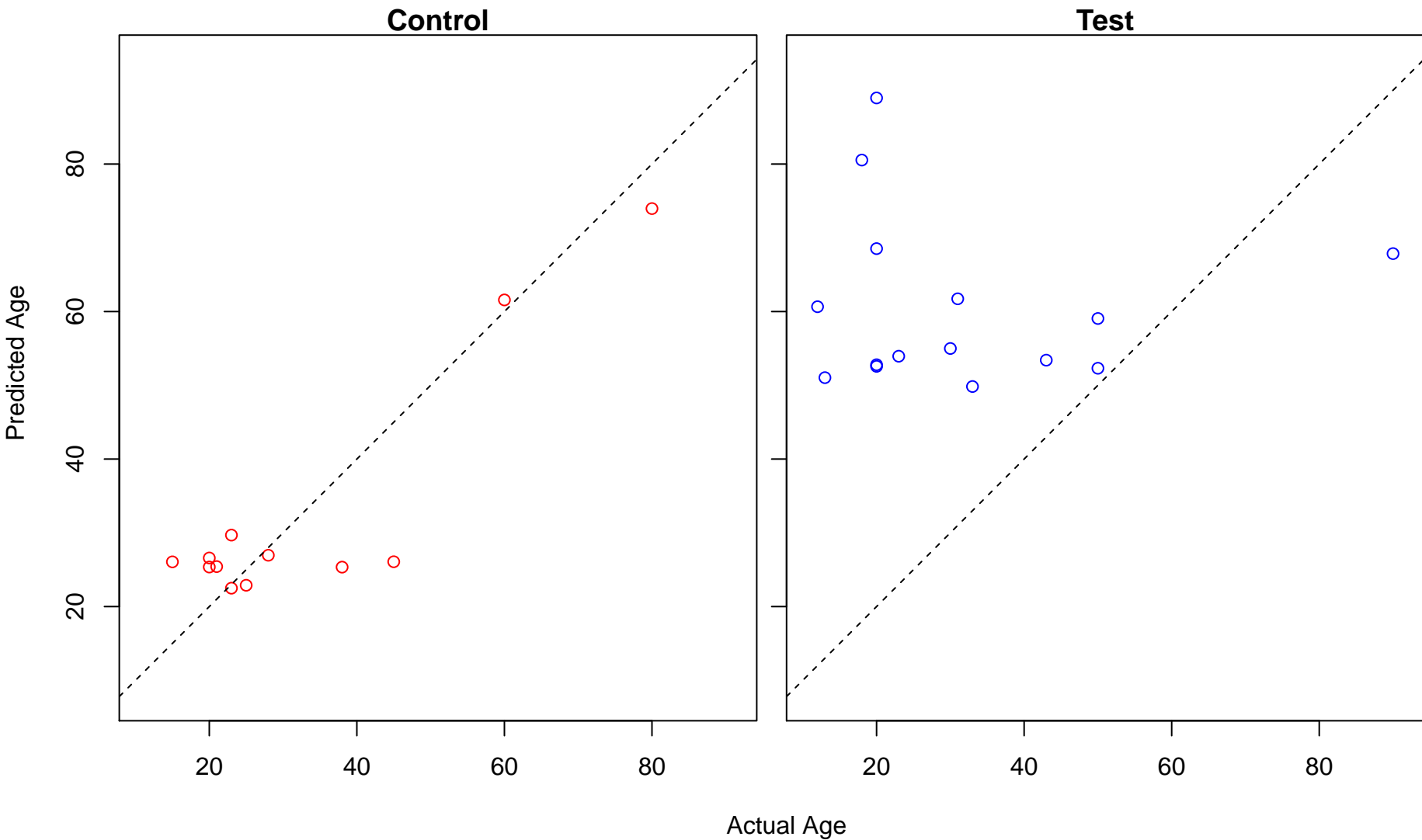
regulation of T cell mediated immunity (Score: 6.876296)



nucleoside salvage (Score: 6.874396)

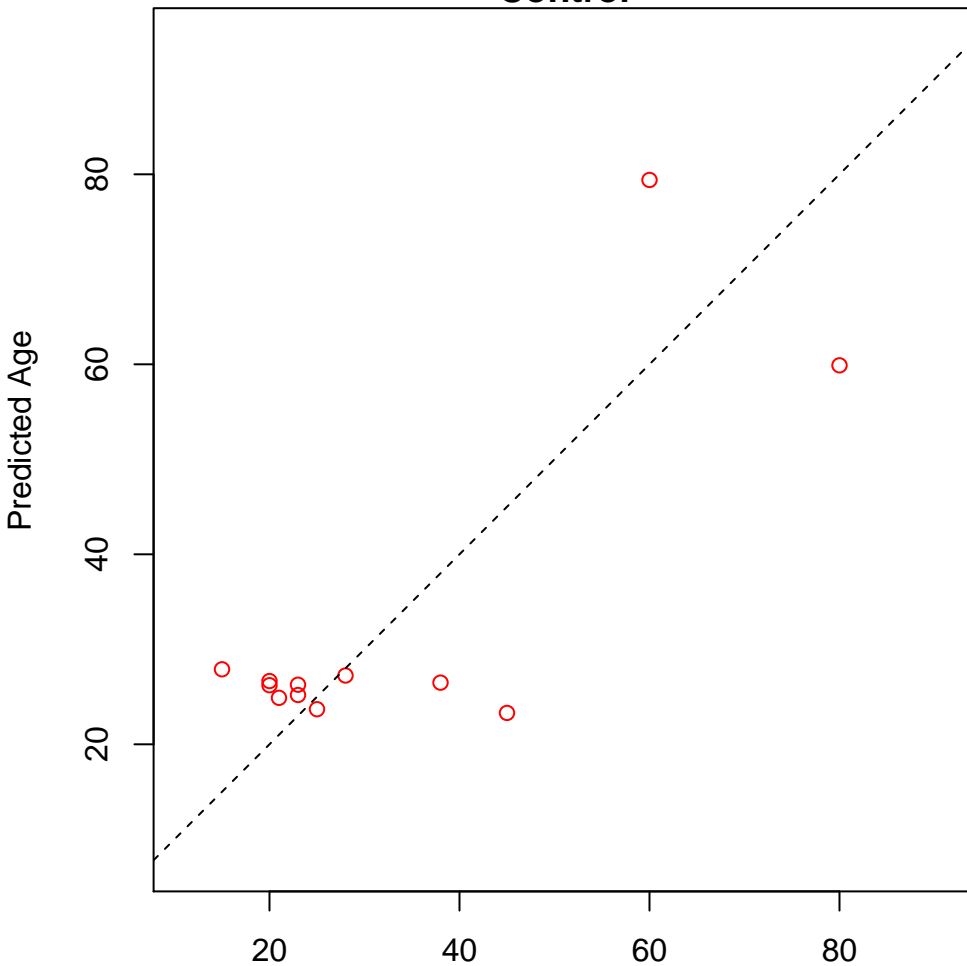


regulation of circadian rhythm (Score: 6.874099)

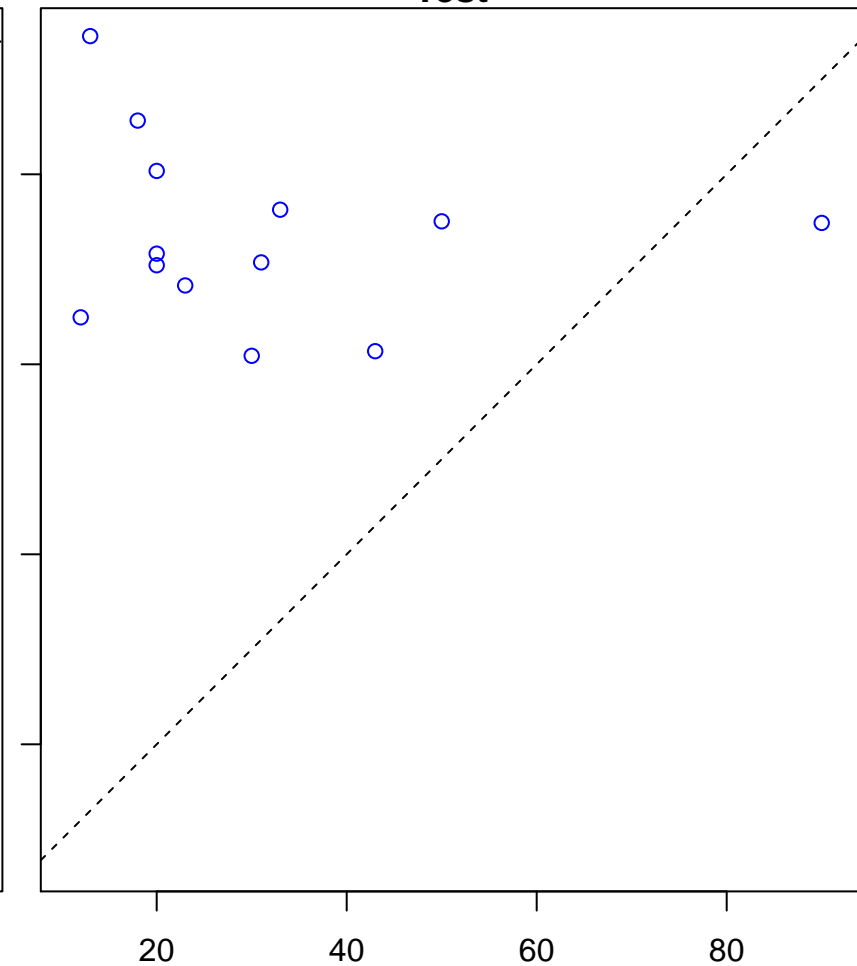


programmed necrotic cell death (Score: 6.873487)

Control

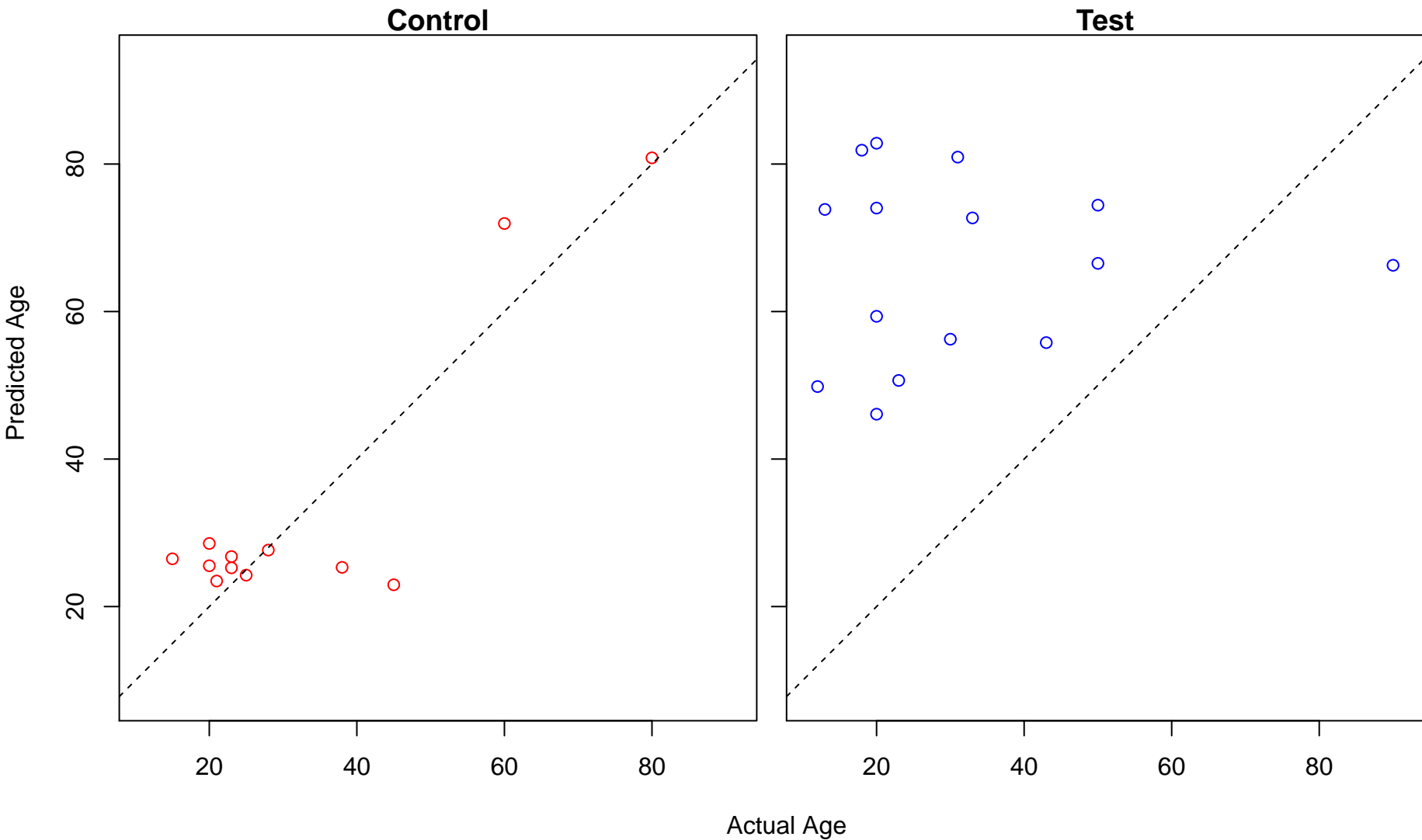


Test



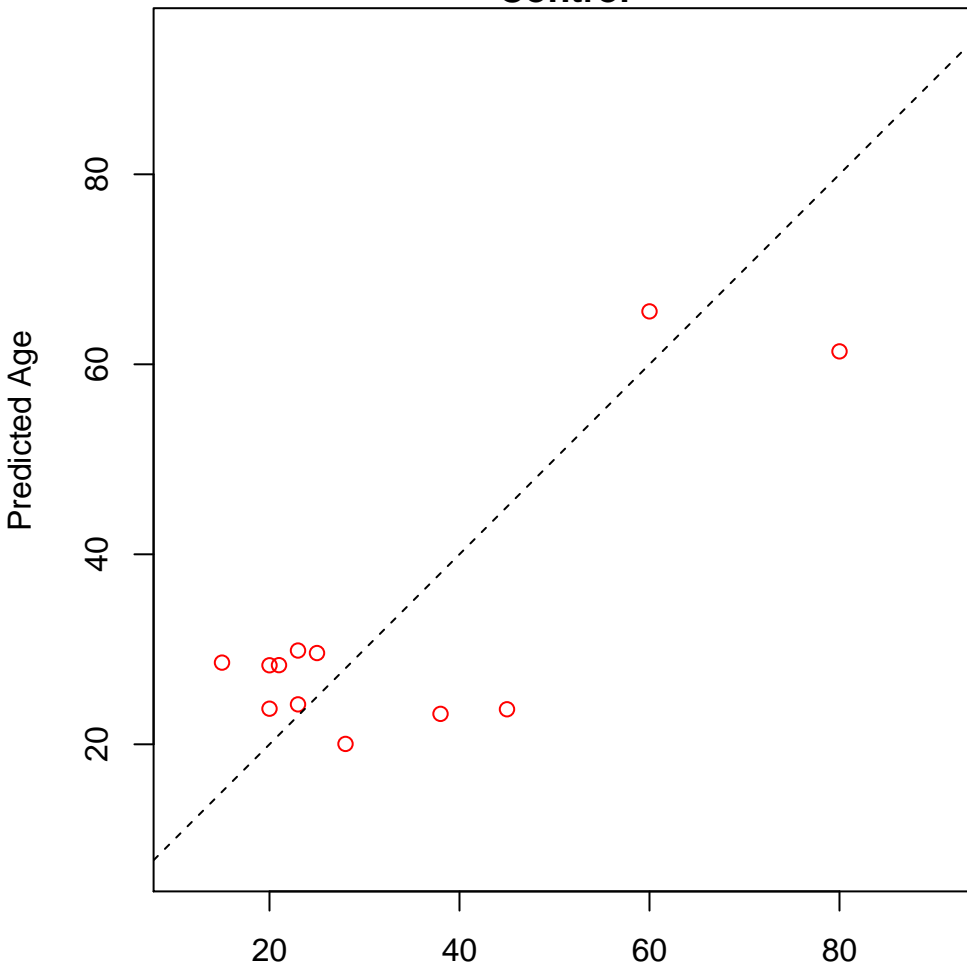
Actual Age

positive regulation of cellular protein localization (Score: 6.872479)

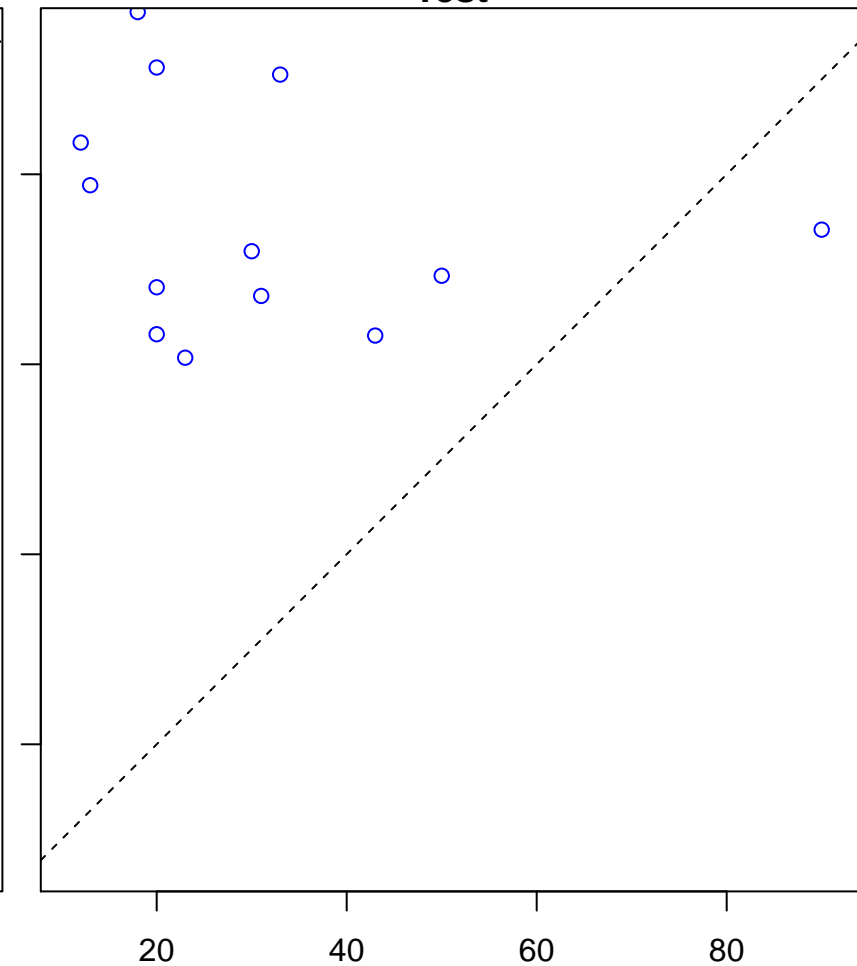


sulfur amino acid catabolic process (Score: 6.871863)

Control

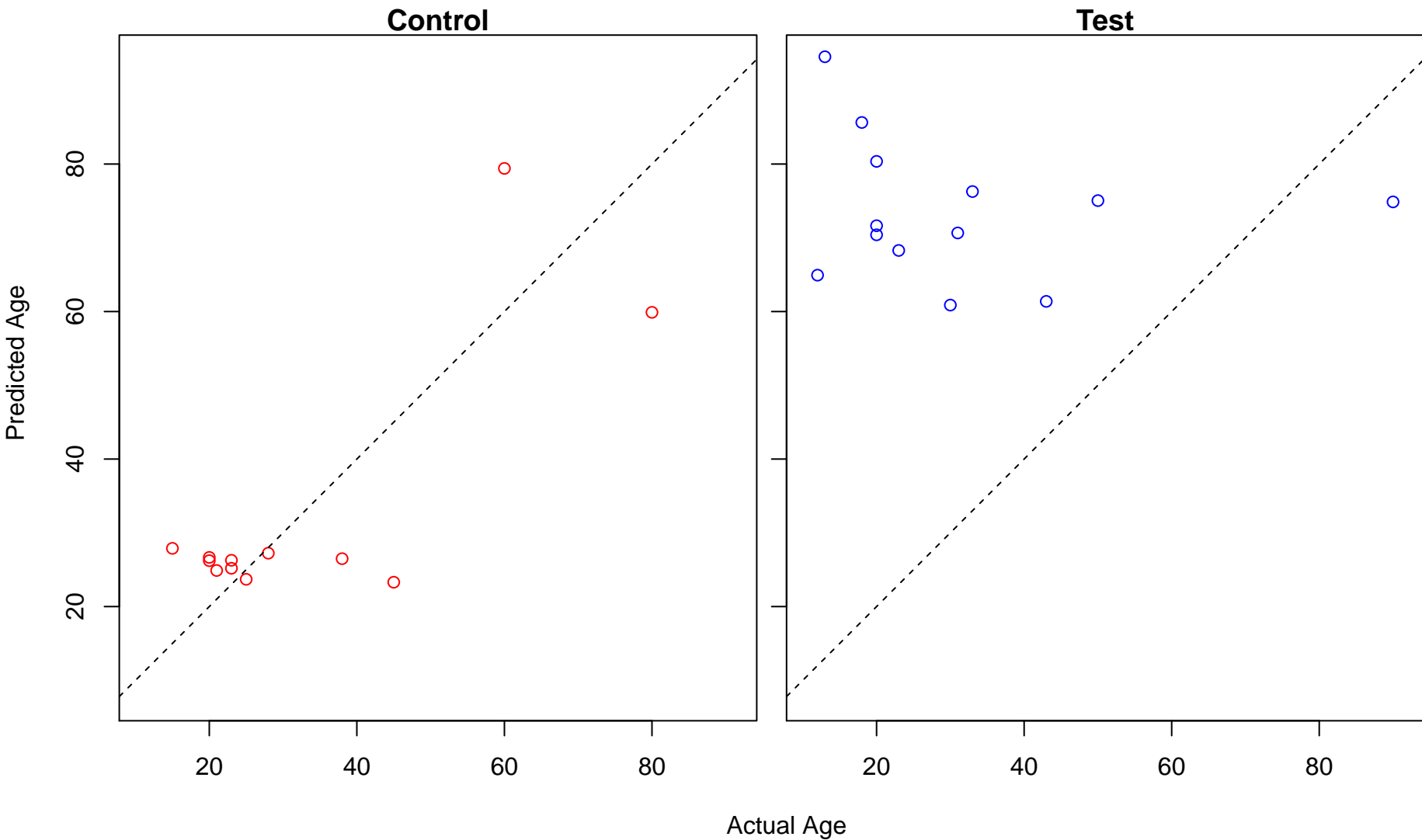


Test



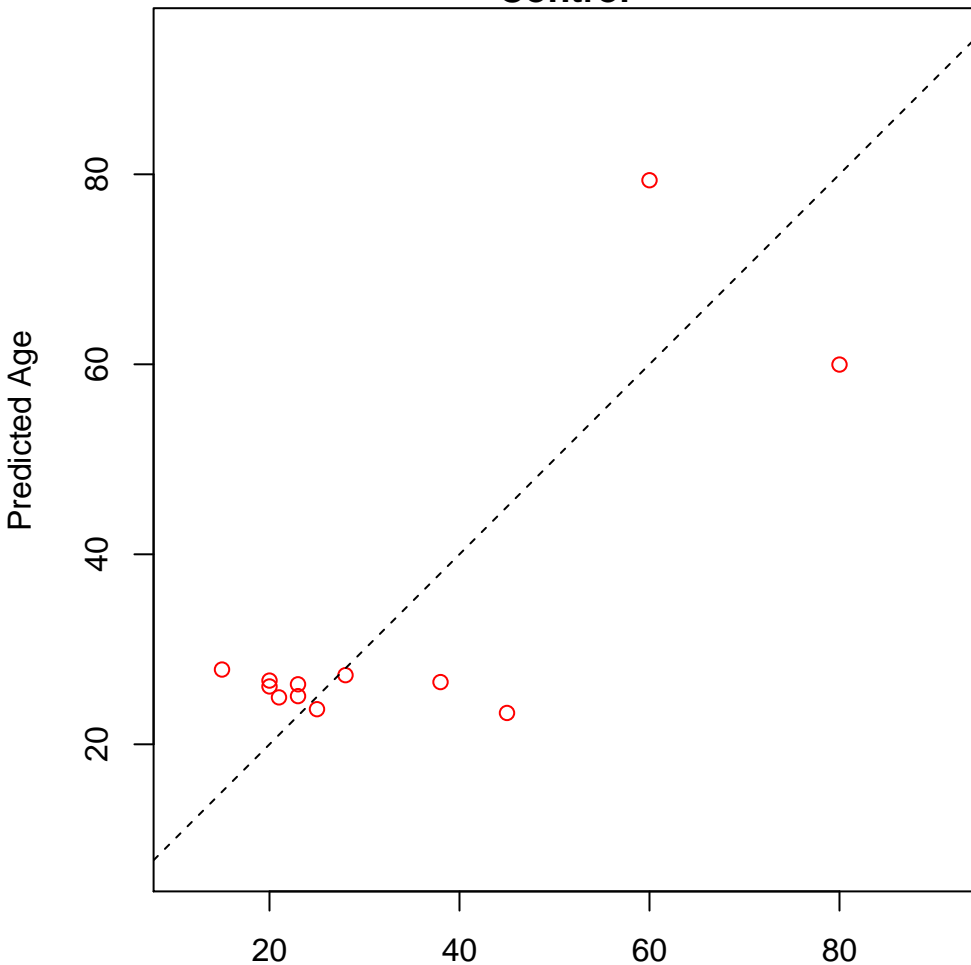
Actual Age

necroptotic process (Score: 6.870796)

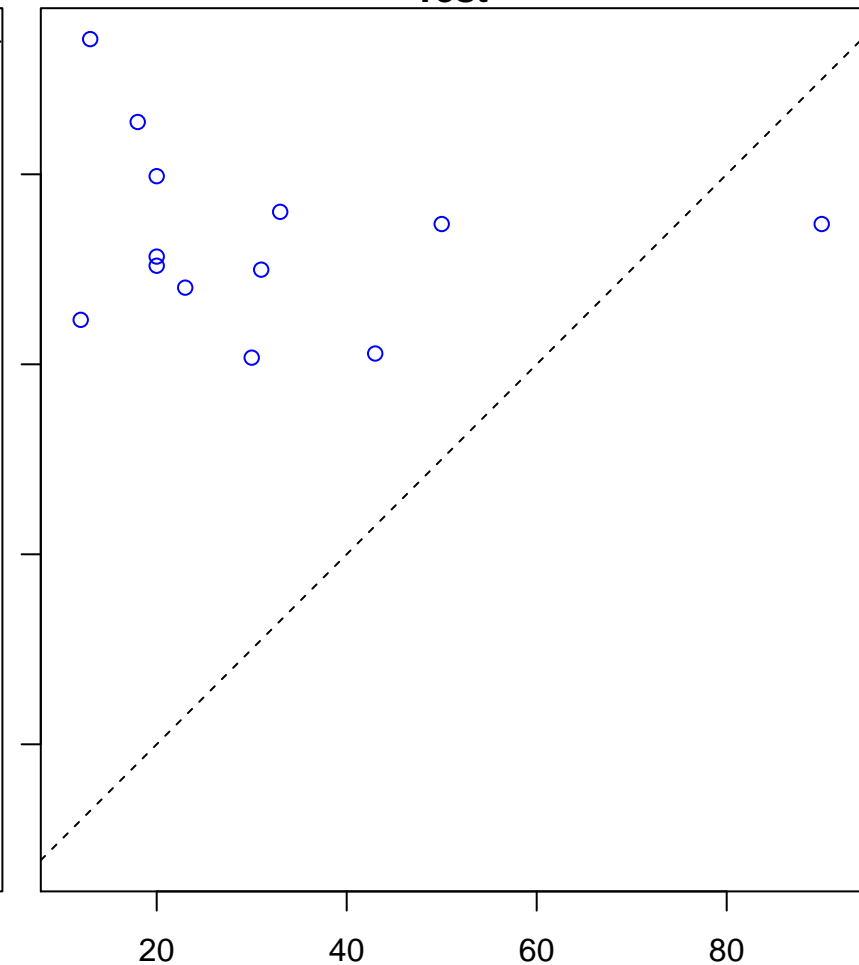


I-kappaB kinase/NF-kappaB signaling (Score: 6.864507)

Control

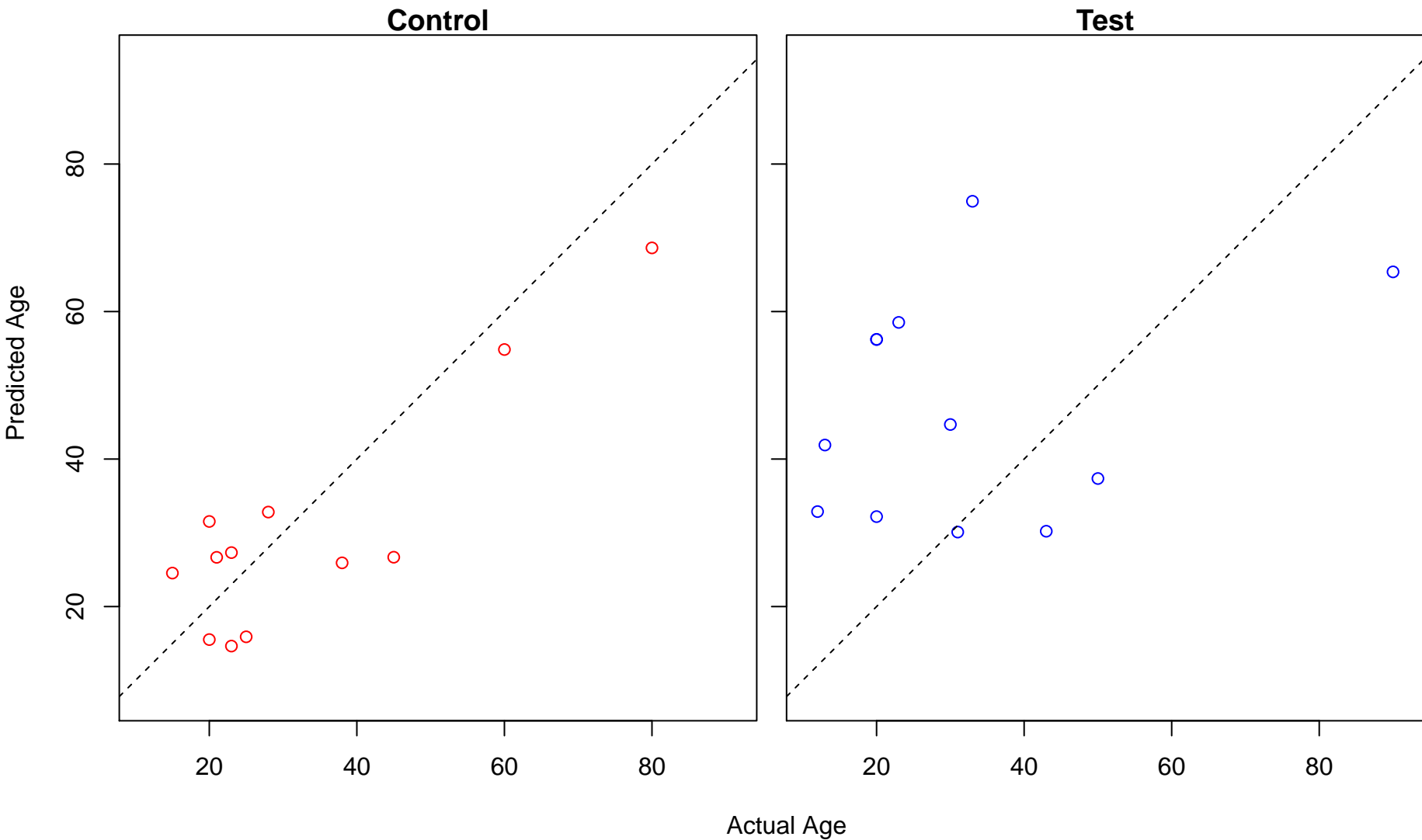


Test



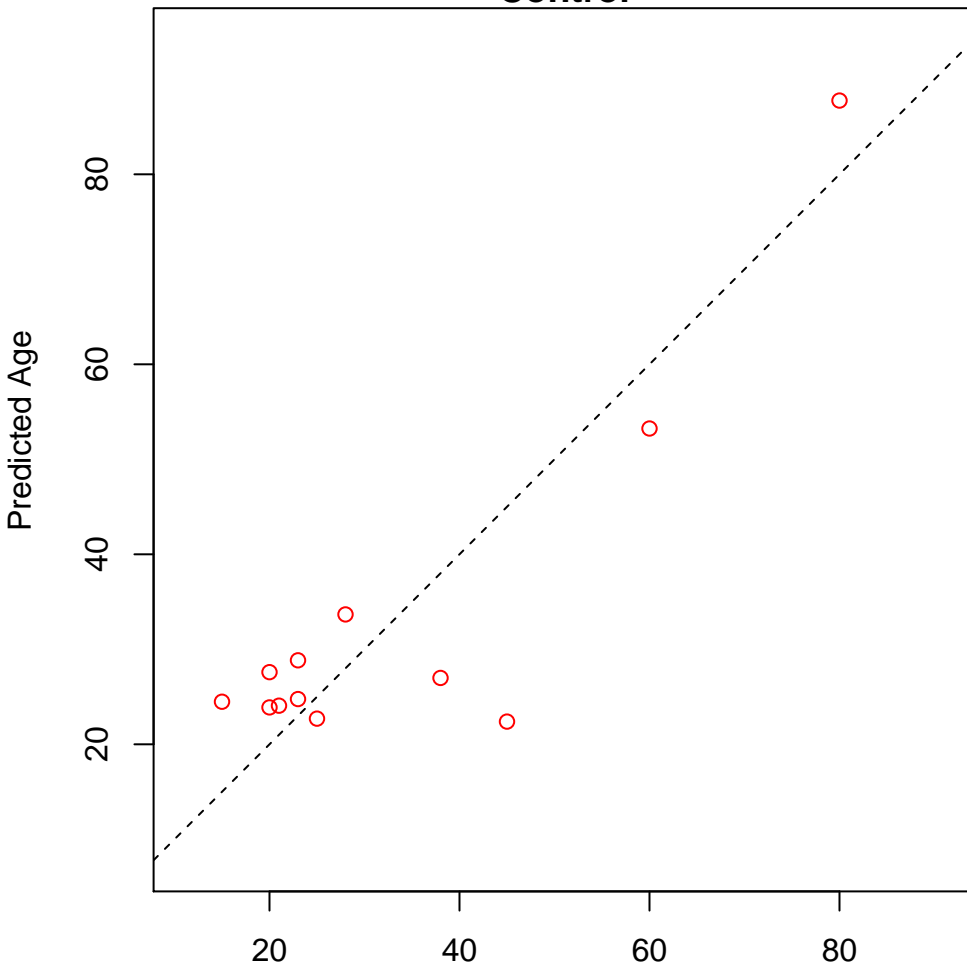
Actual Age

RNA export from nucleus (Score: 6.861495)

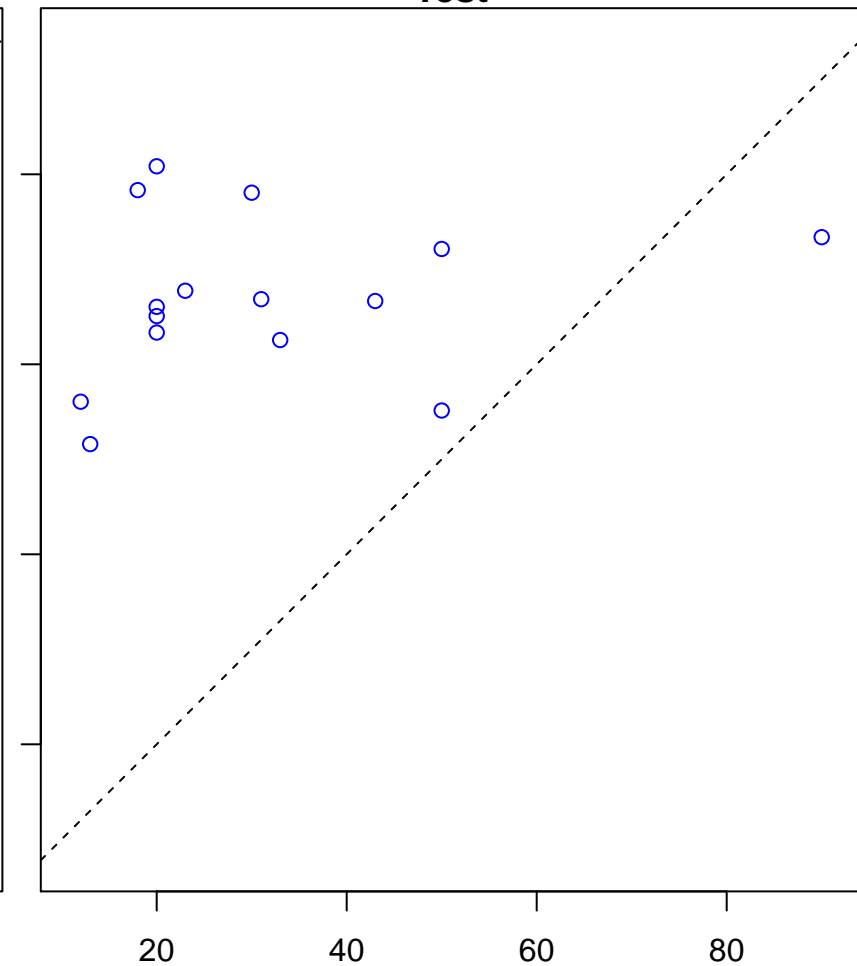


regulation of lymphocyte differentiation (Score: 6.858893)

Control

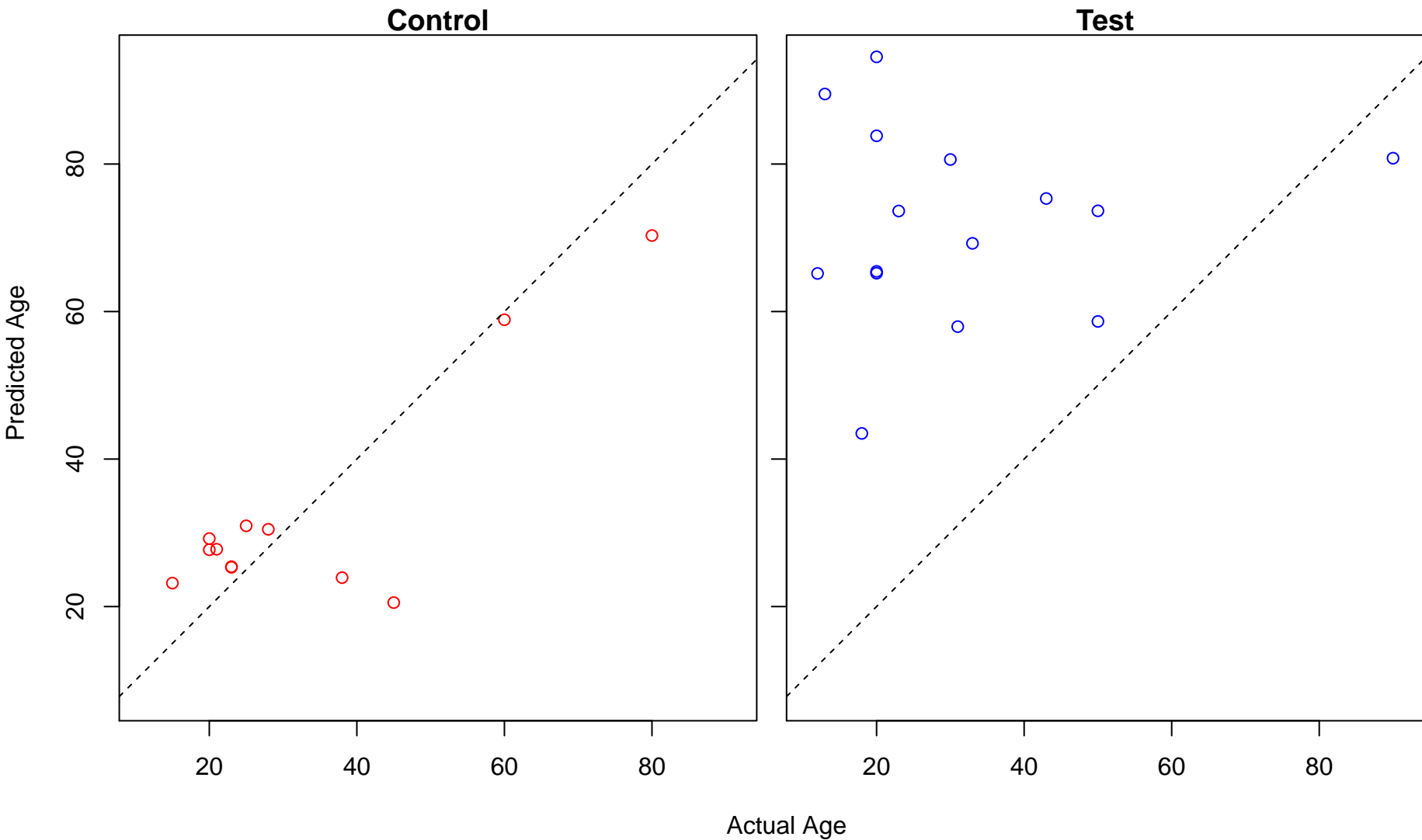


Test

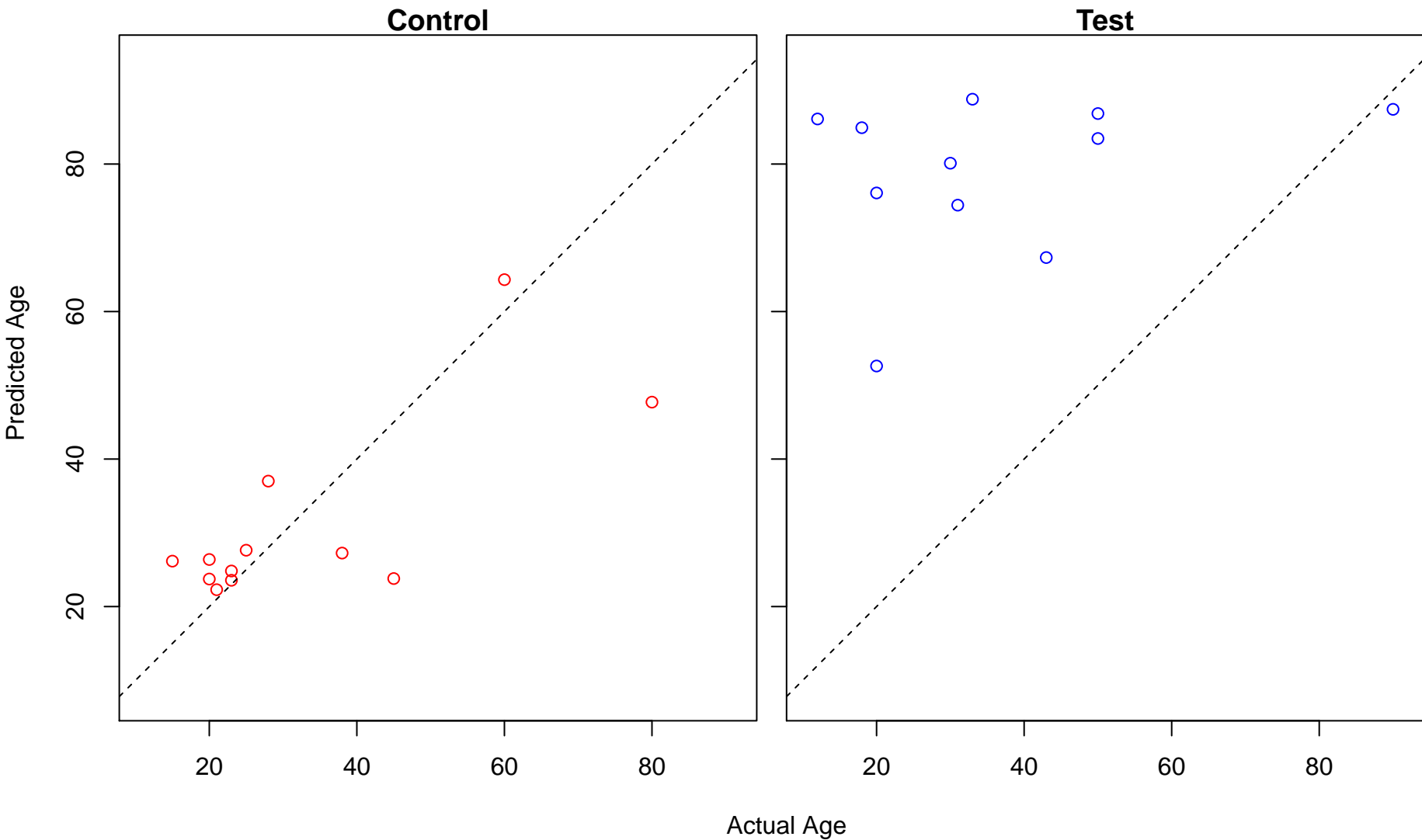


Actual Age

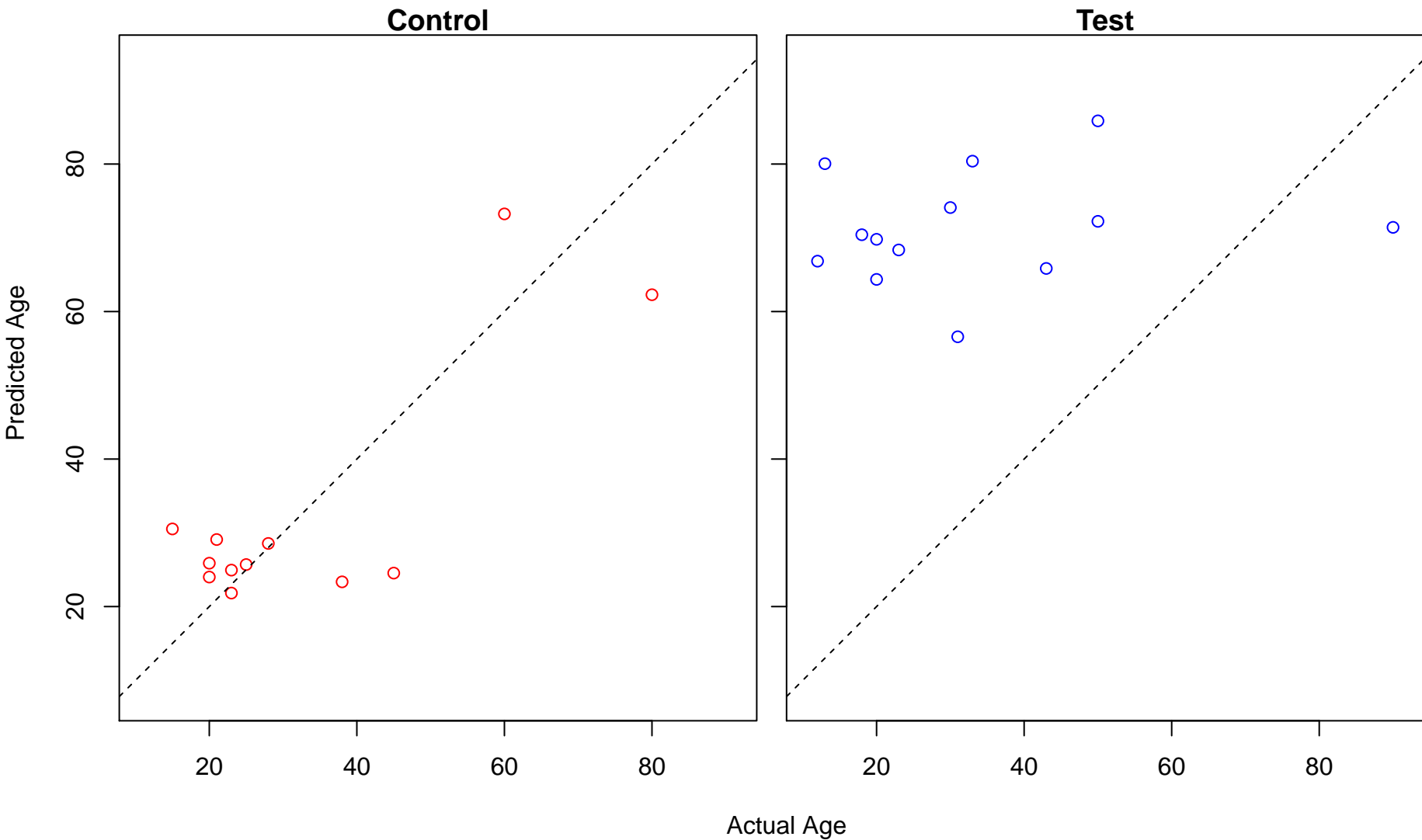
regulation of norepinephrine secretion (Score: 6.858174)



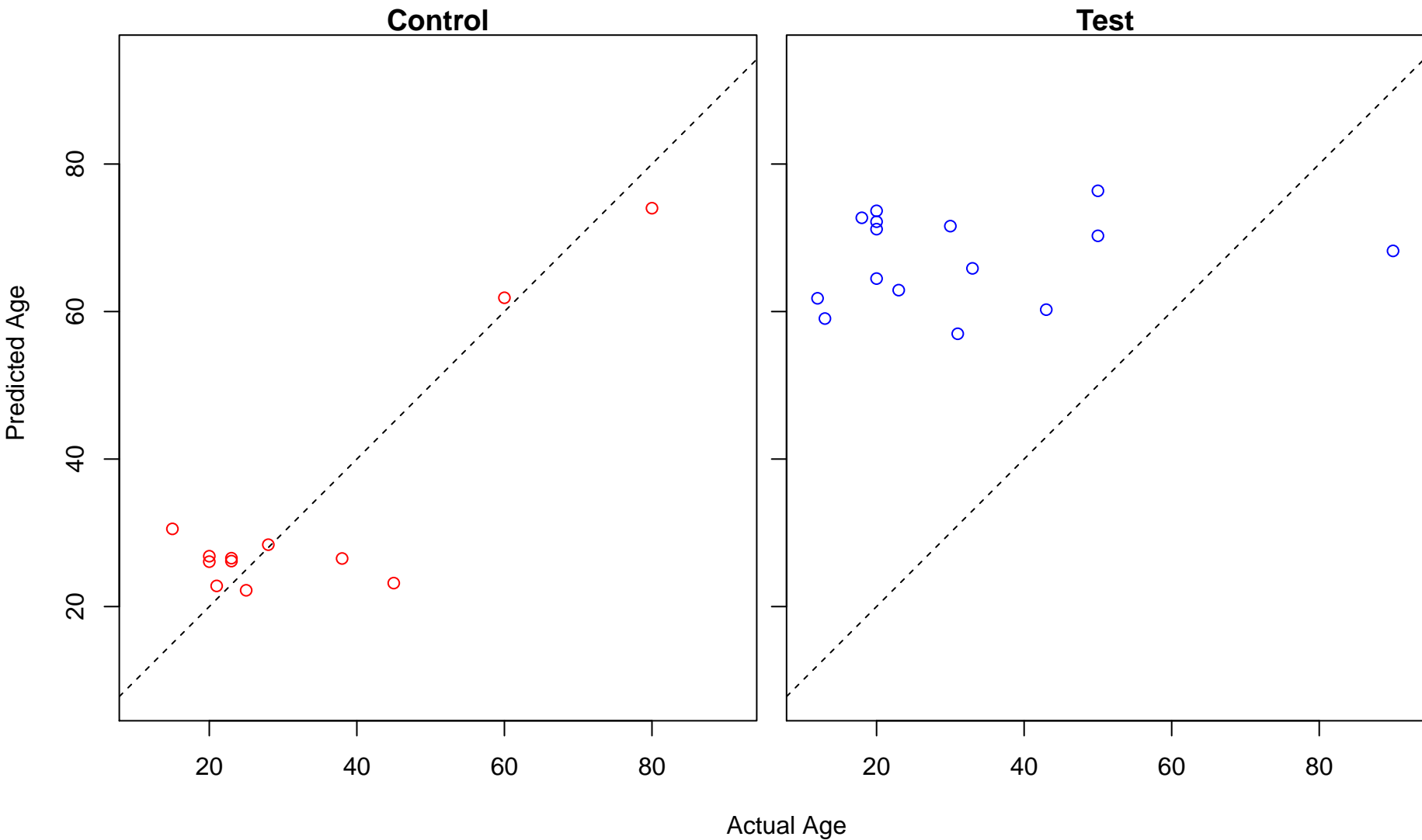
regulation of synapse maturation (Score: 6.854919)



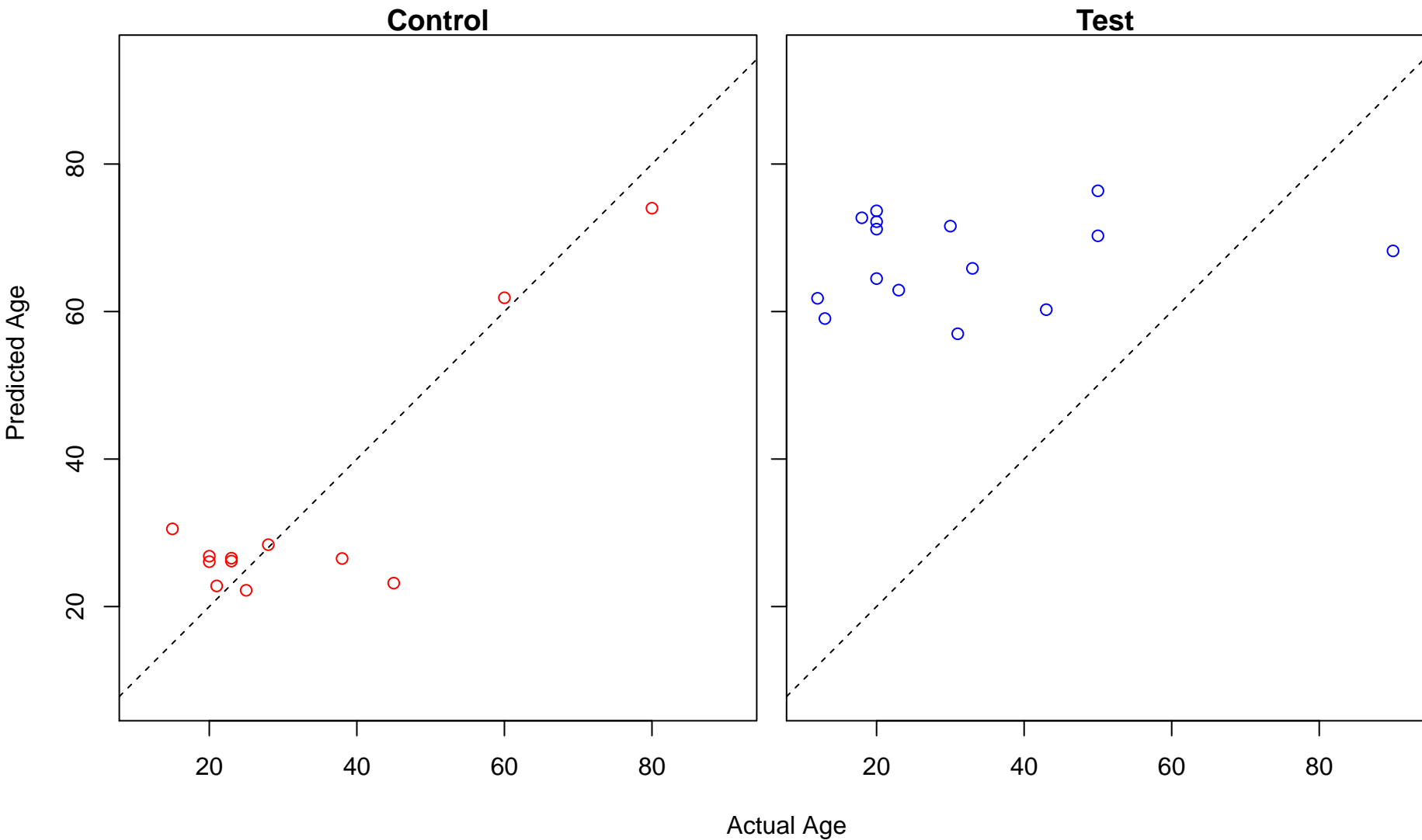
rRNA transcription (Score: 6.853411)



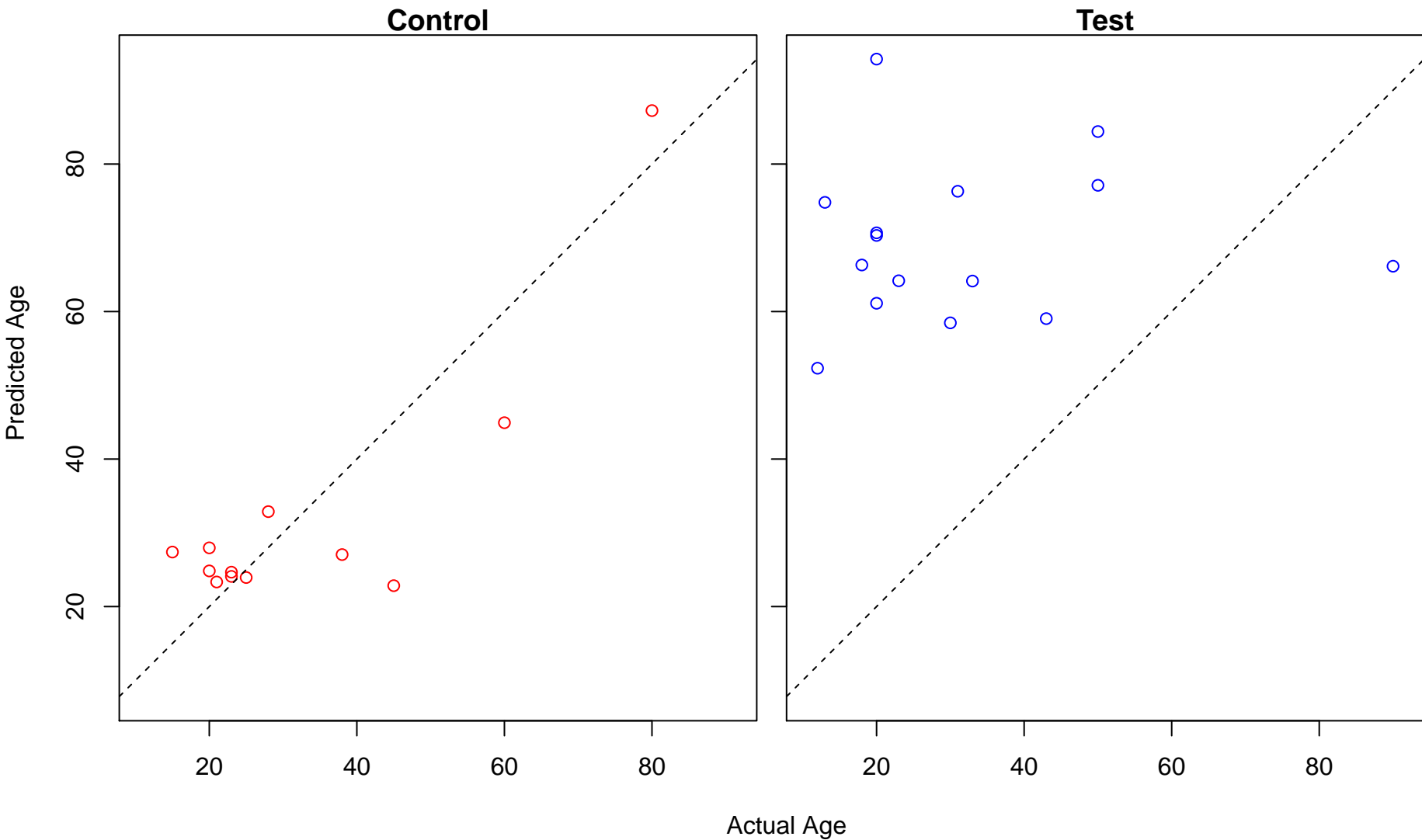
positive regulation of response to extracellular stimulus (Score: 6.853034)



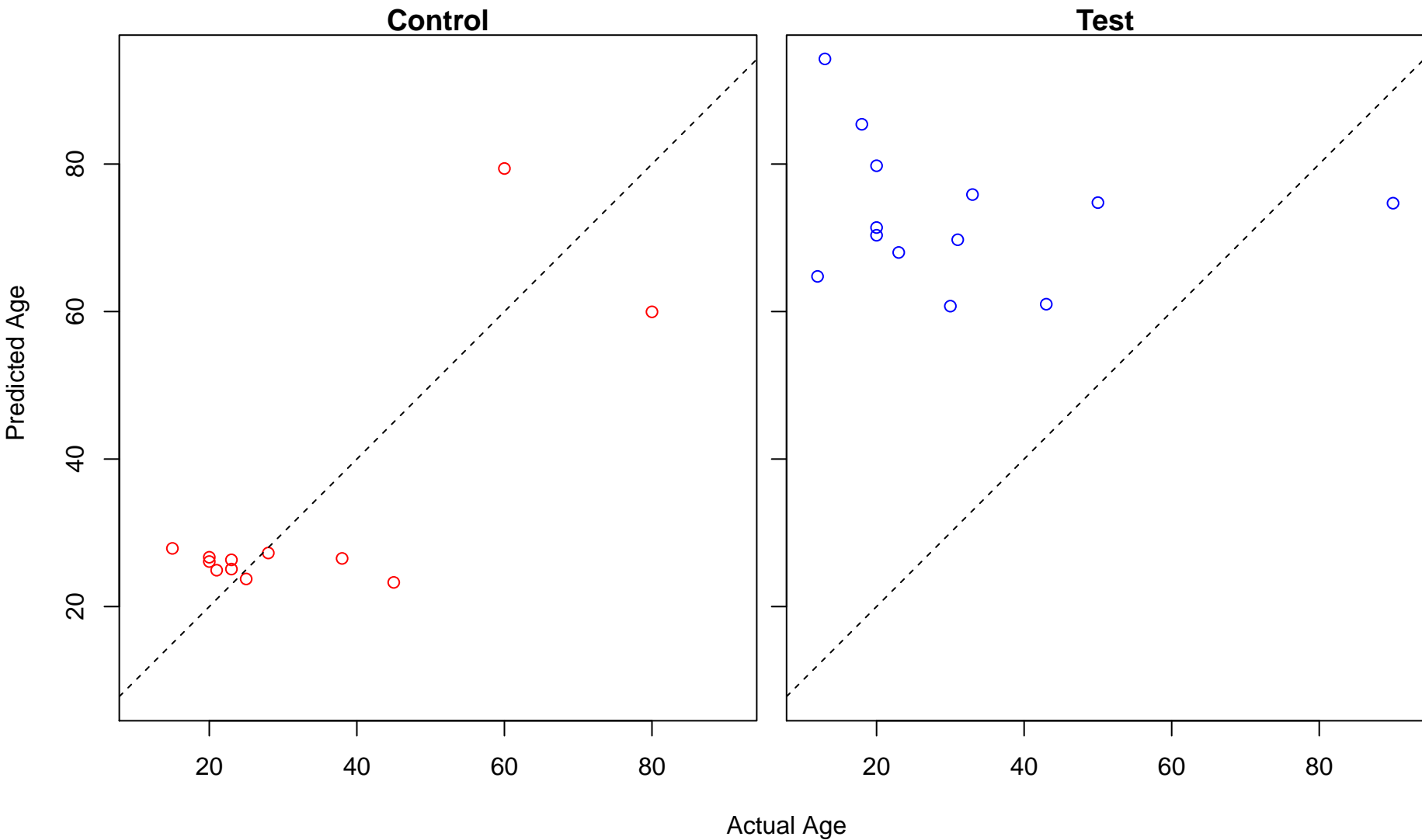
positive regulation of response to nutrient levels (Score: 6.853034)



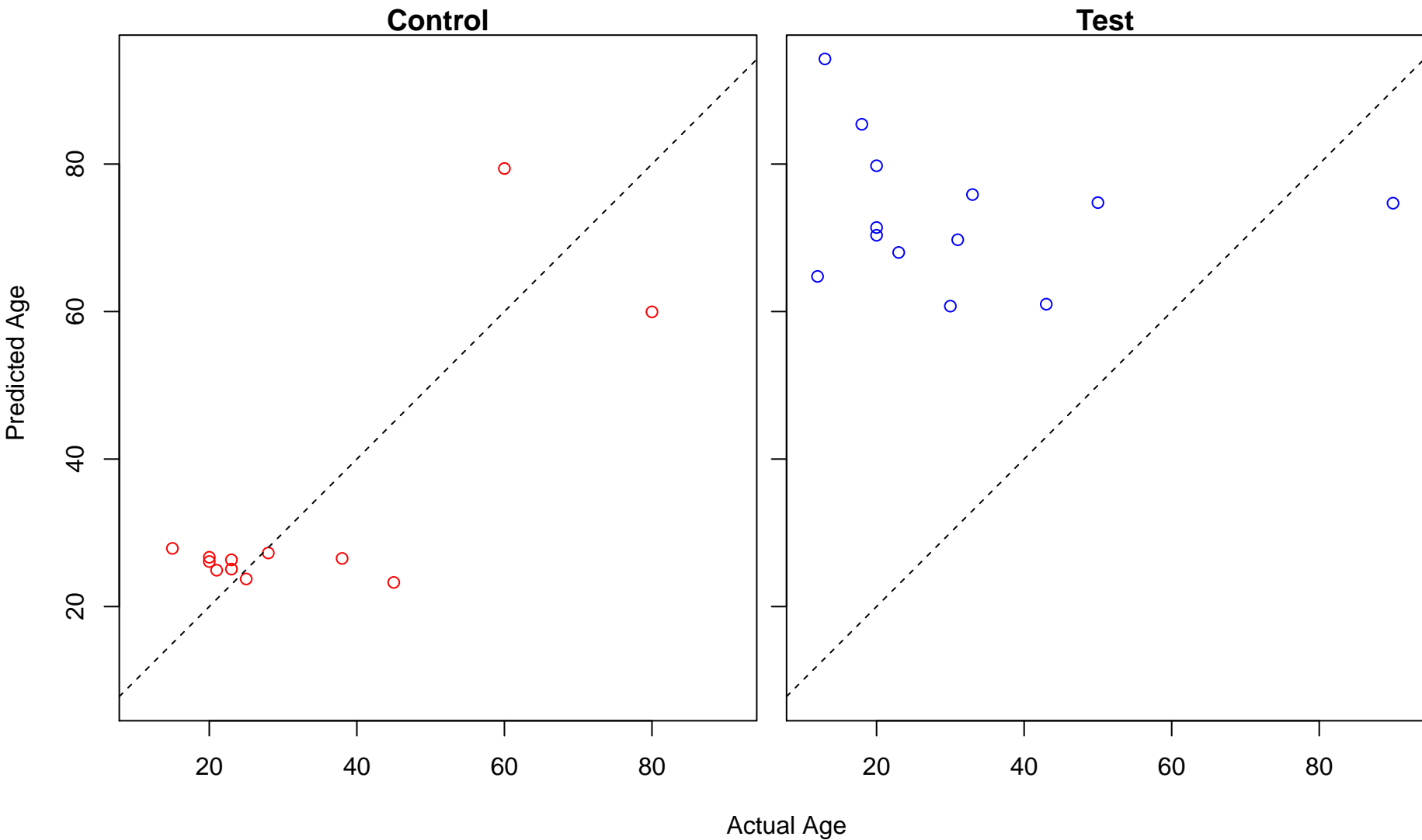
regulation of cyclic nucleotide metabolic process (Score: 6.853000)



glycogen biosynthetic process (Score: 6.851637)

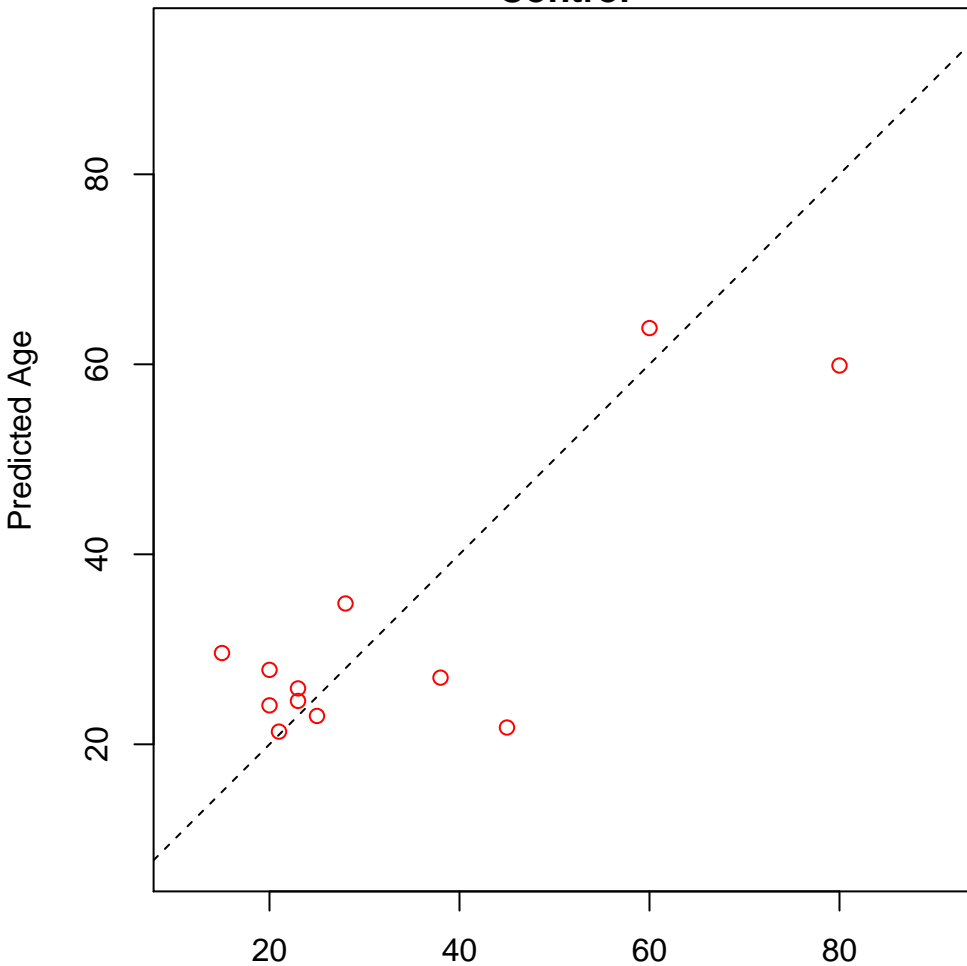


glucan biosynthetic process (Score: 6.851637)

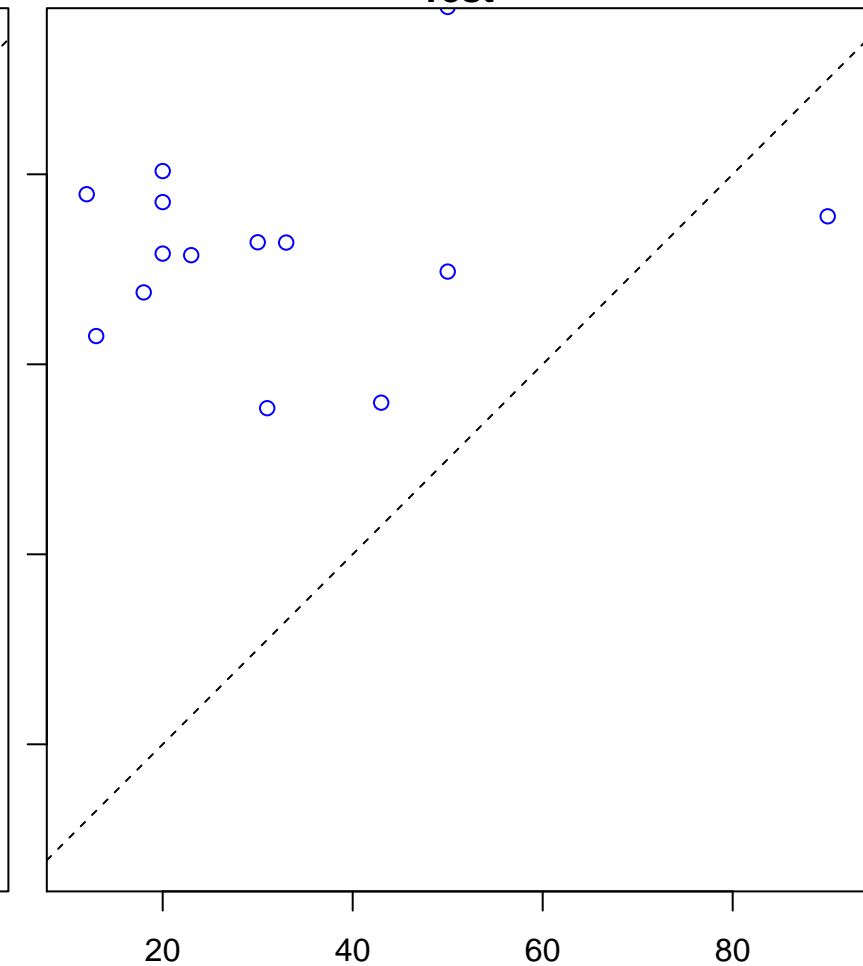


embryonic epithelial tube formation (Score: 6.850974)

Control

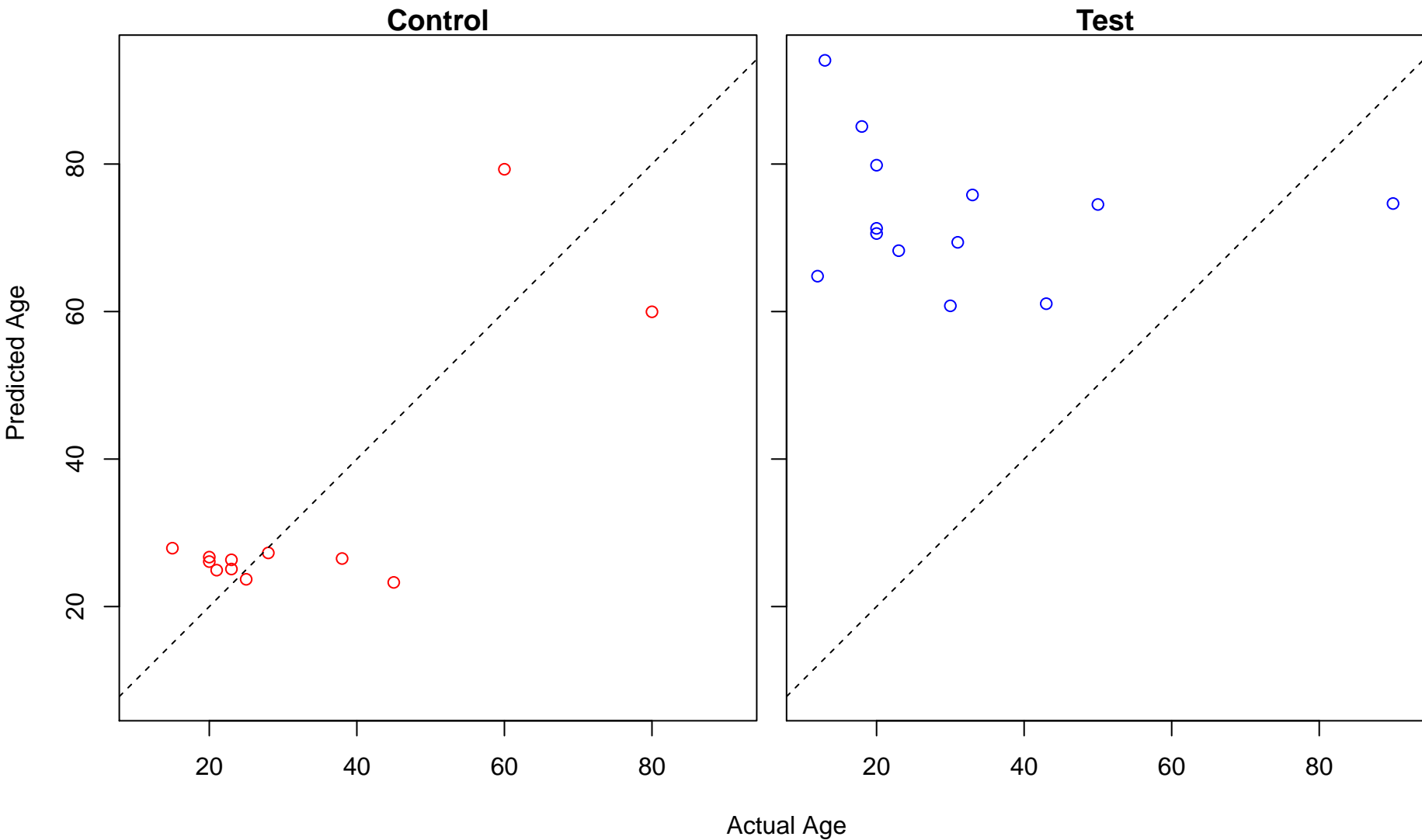


Test

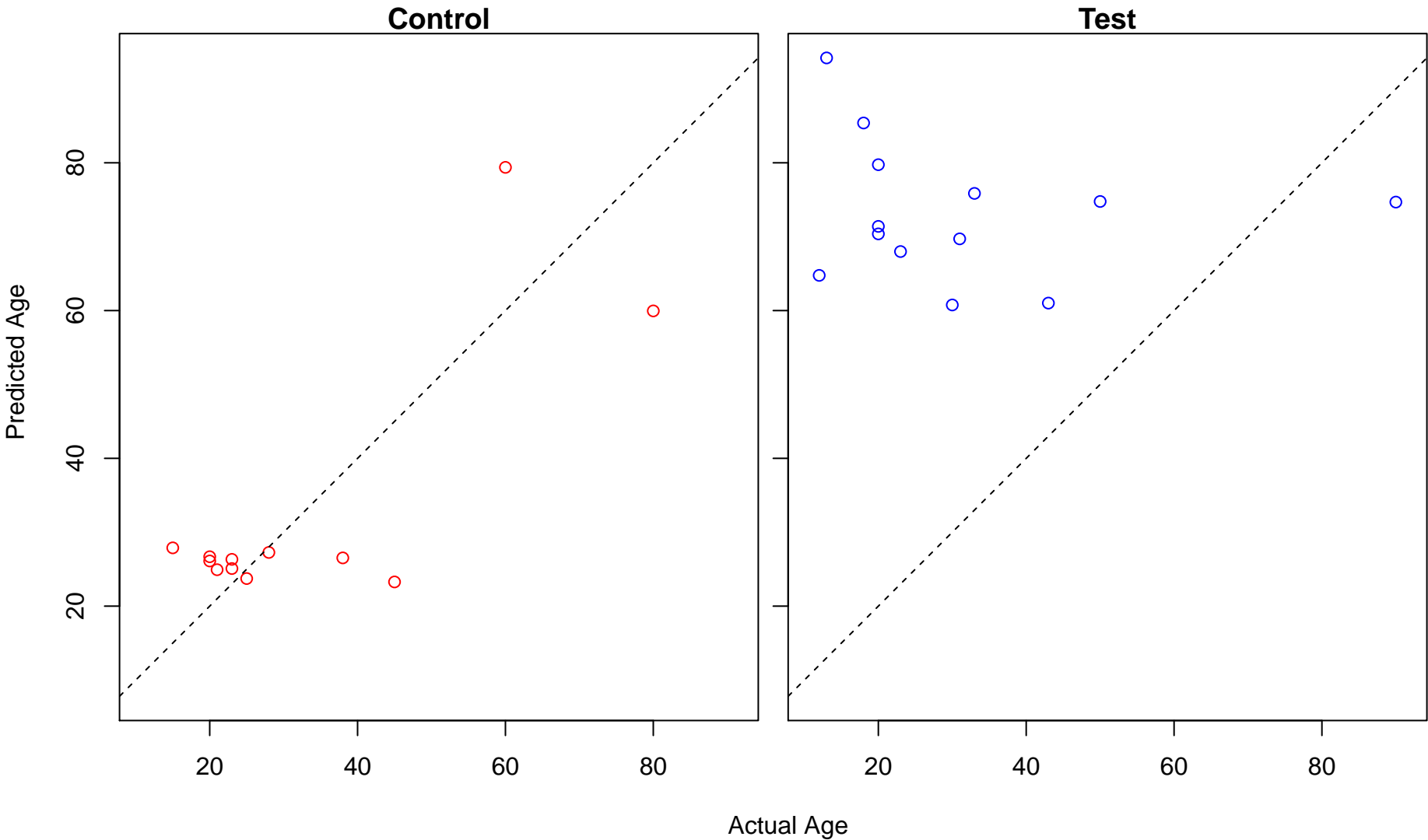


Actual Age

interstrand cross-link repair (Score: 6.847151)

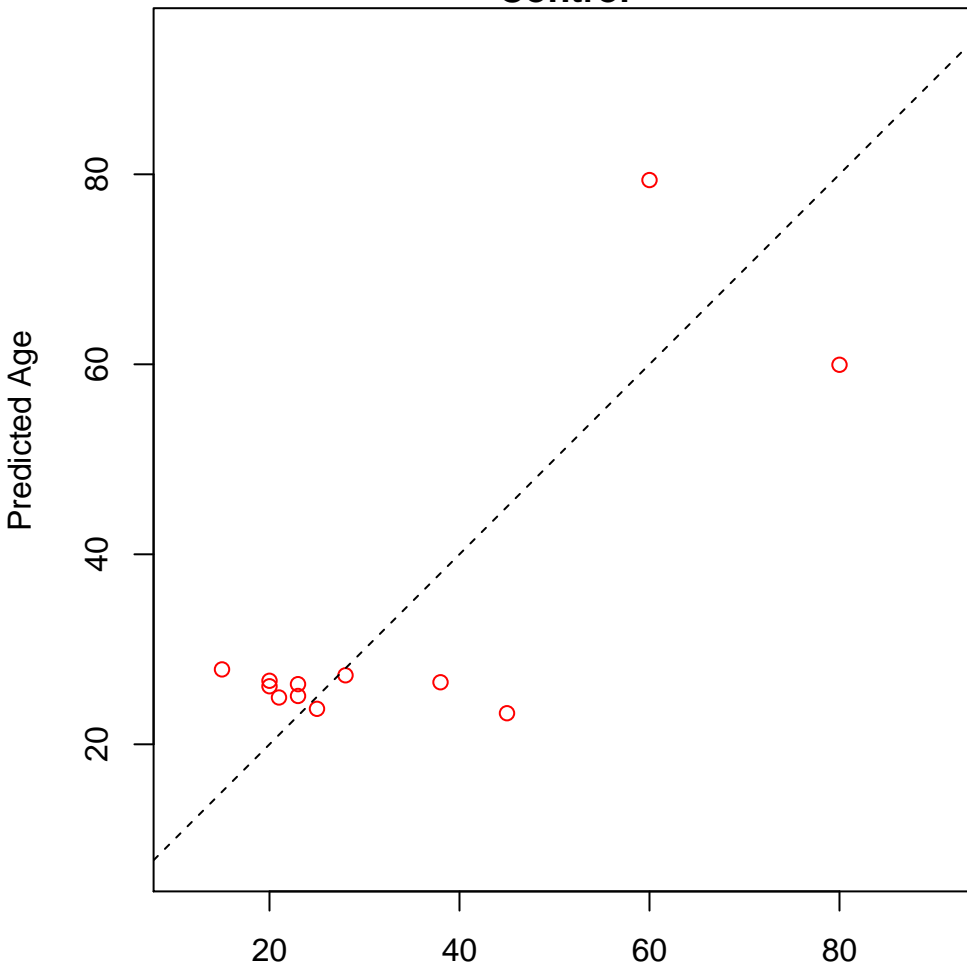


cellular carbohydrate biosynthetic process (Score: 6.846835)

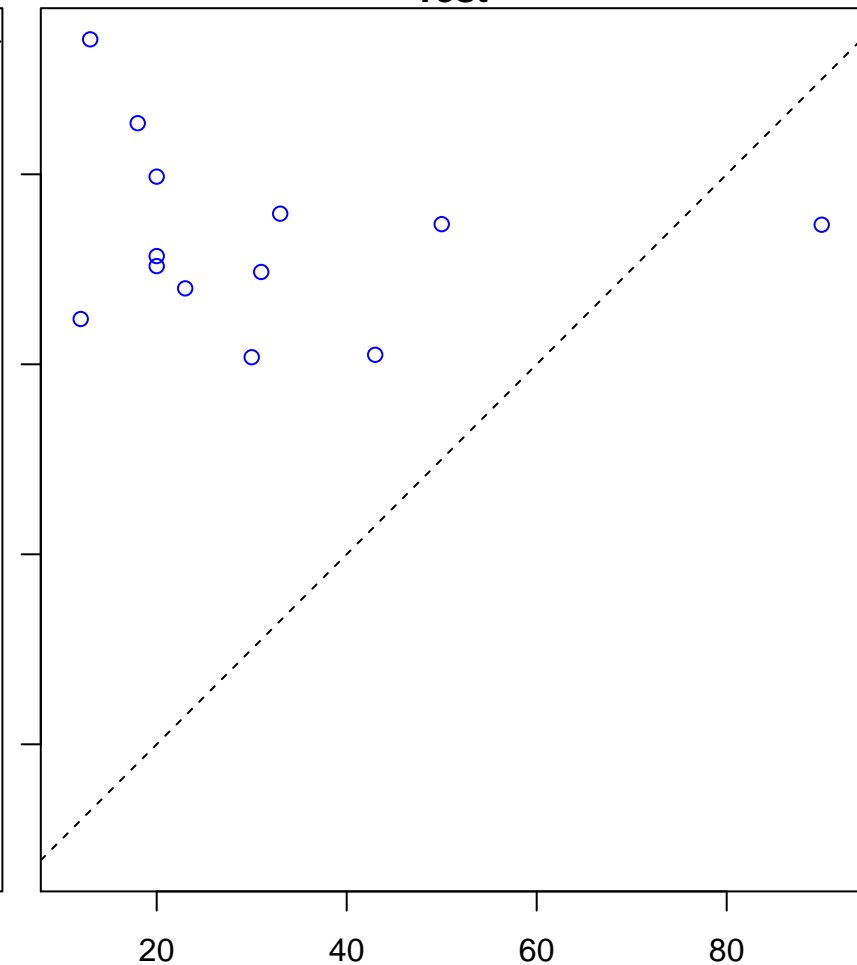


polysaccharide biosynthetic process (Score: 6.844687)

Control

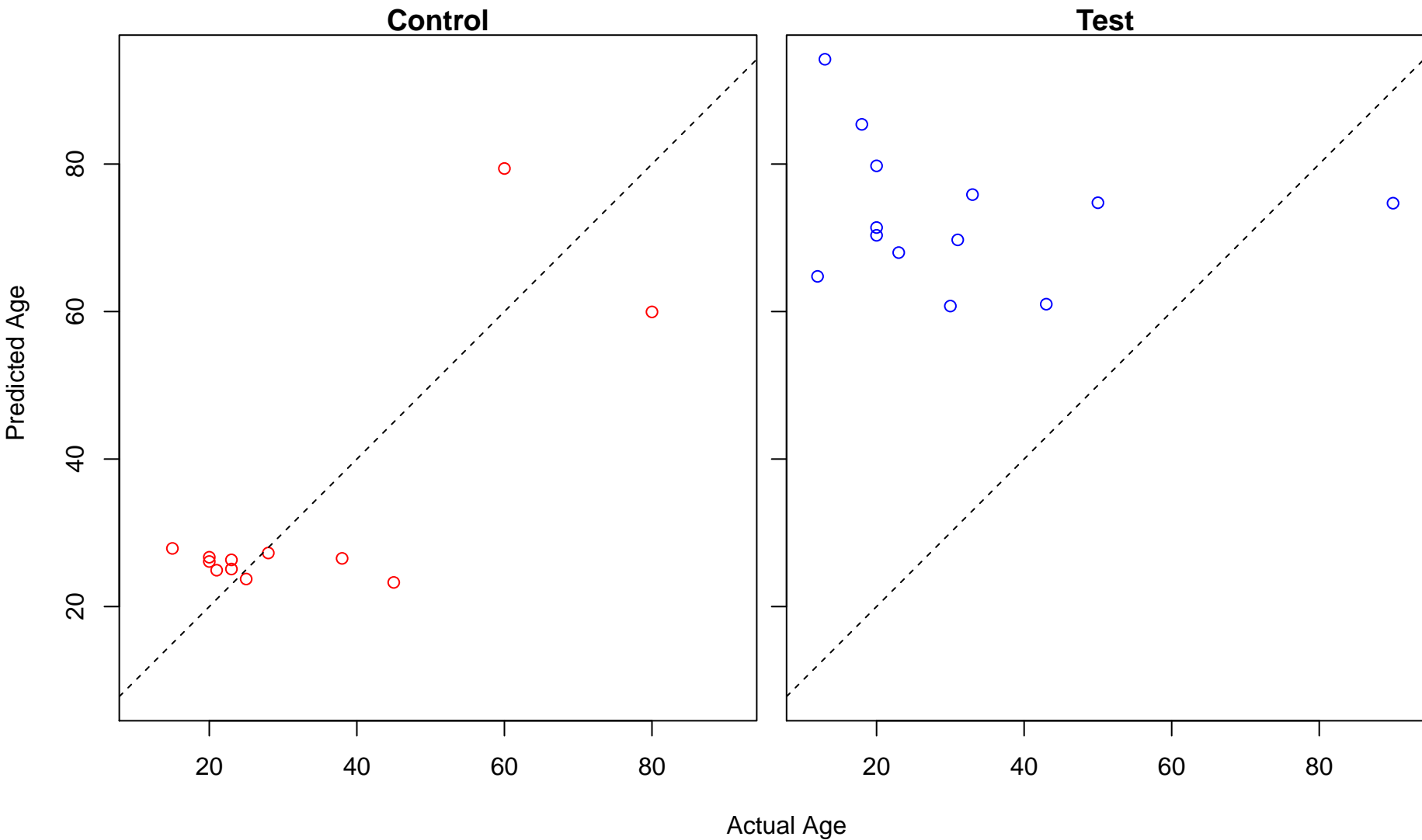


Test



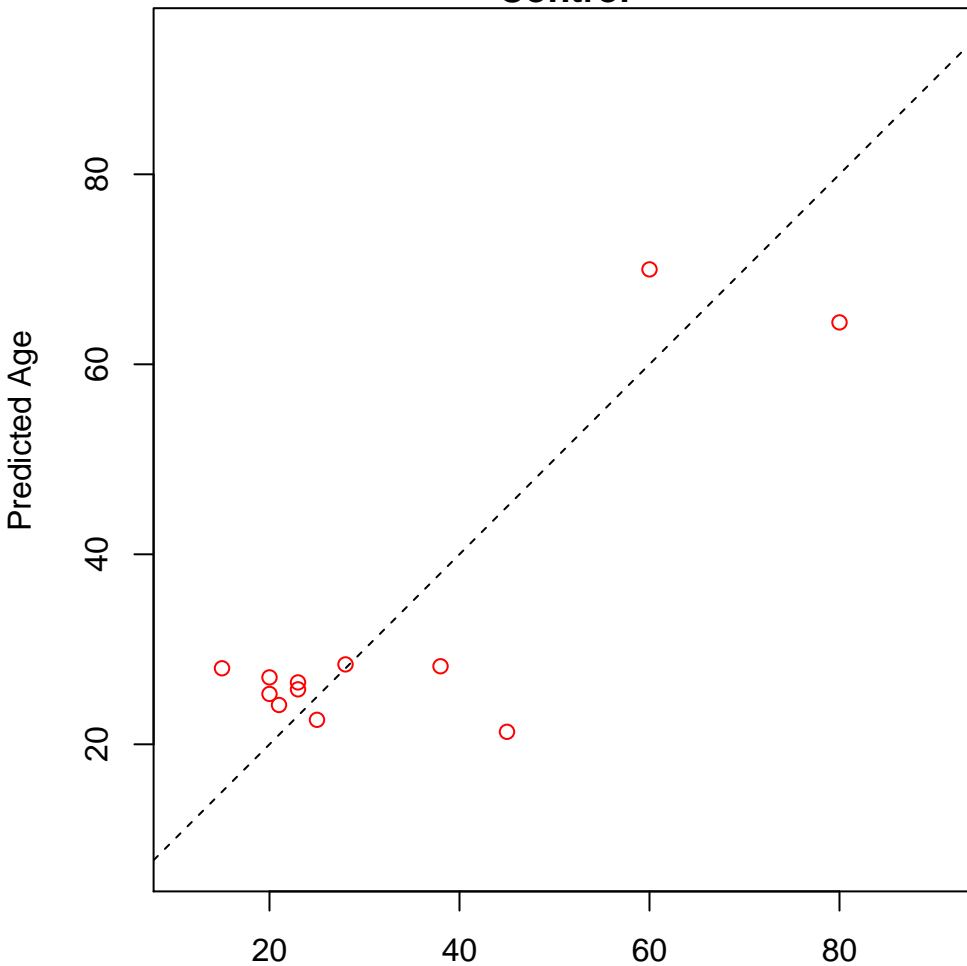
Actual Age

cellular polysaccharide biosynthetic process (Score: 6.844687)

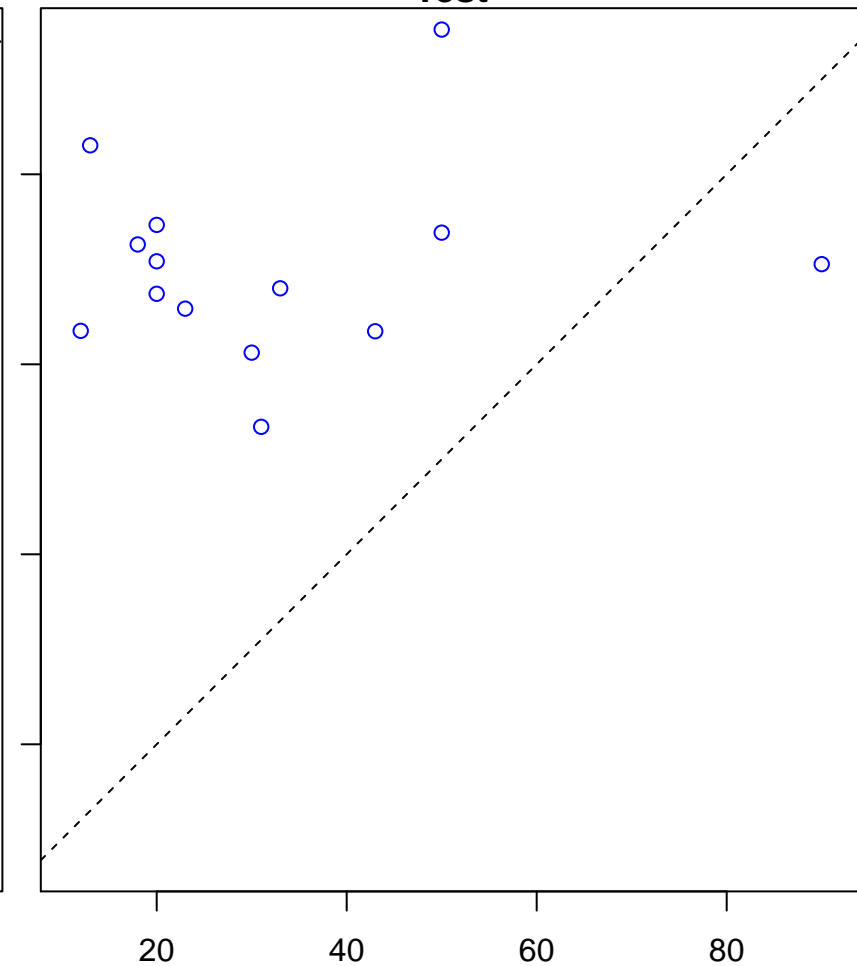


single organism reproductive process (Score: 6.844134)

Control



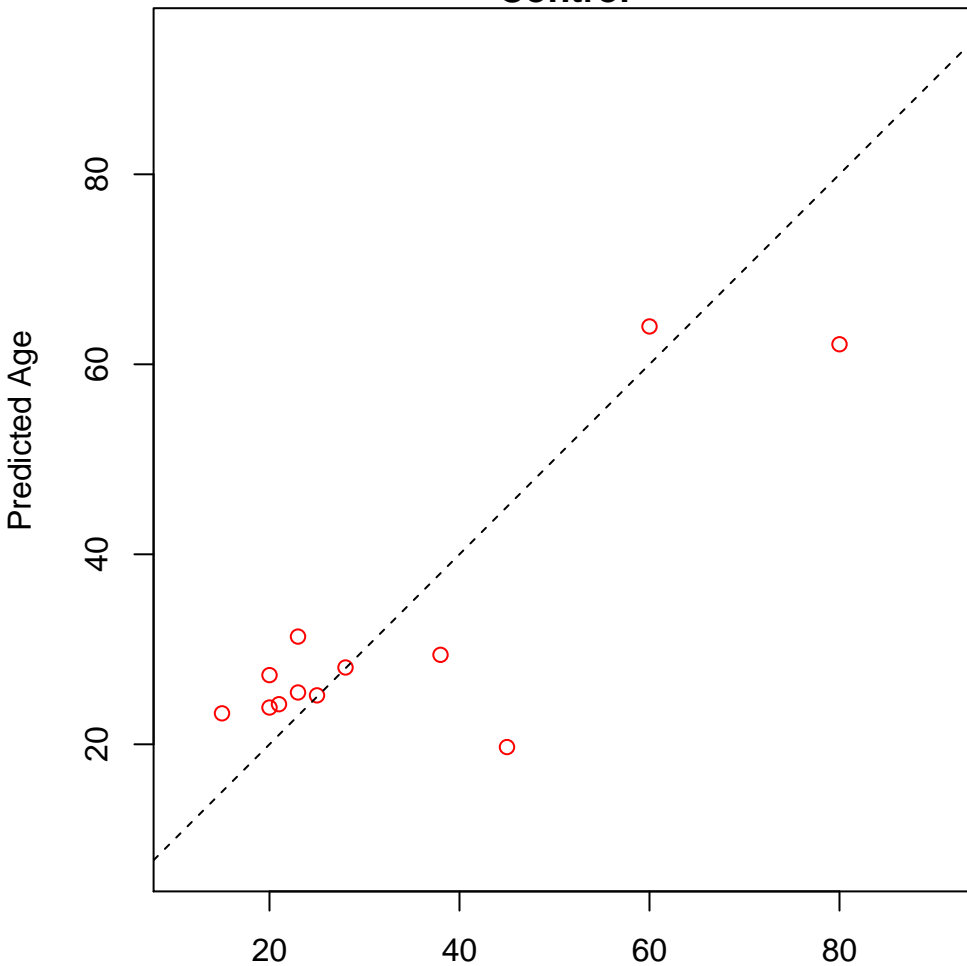
Test



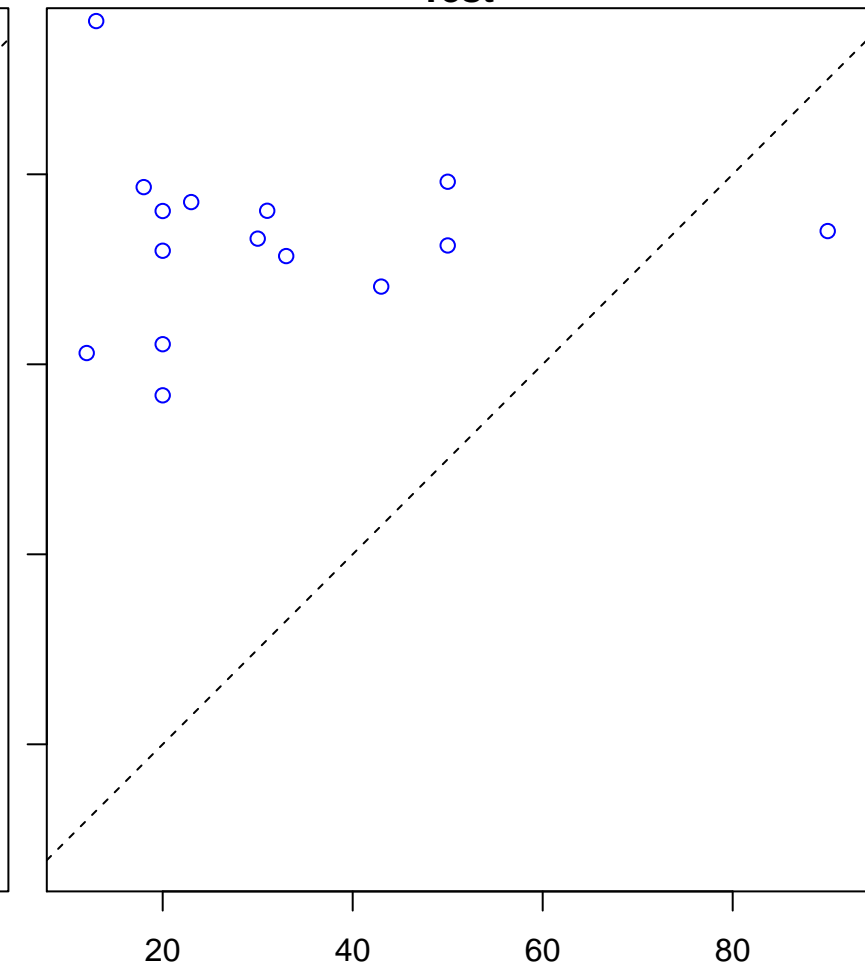
Actual Age

regulation of interleukin-6 production (Score: 6.842977)

Control

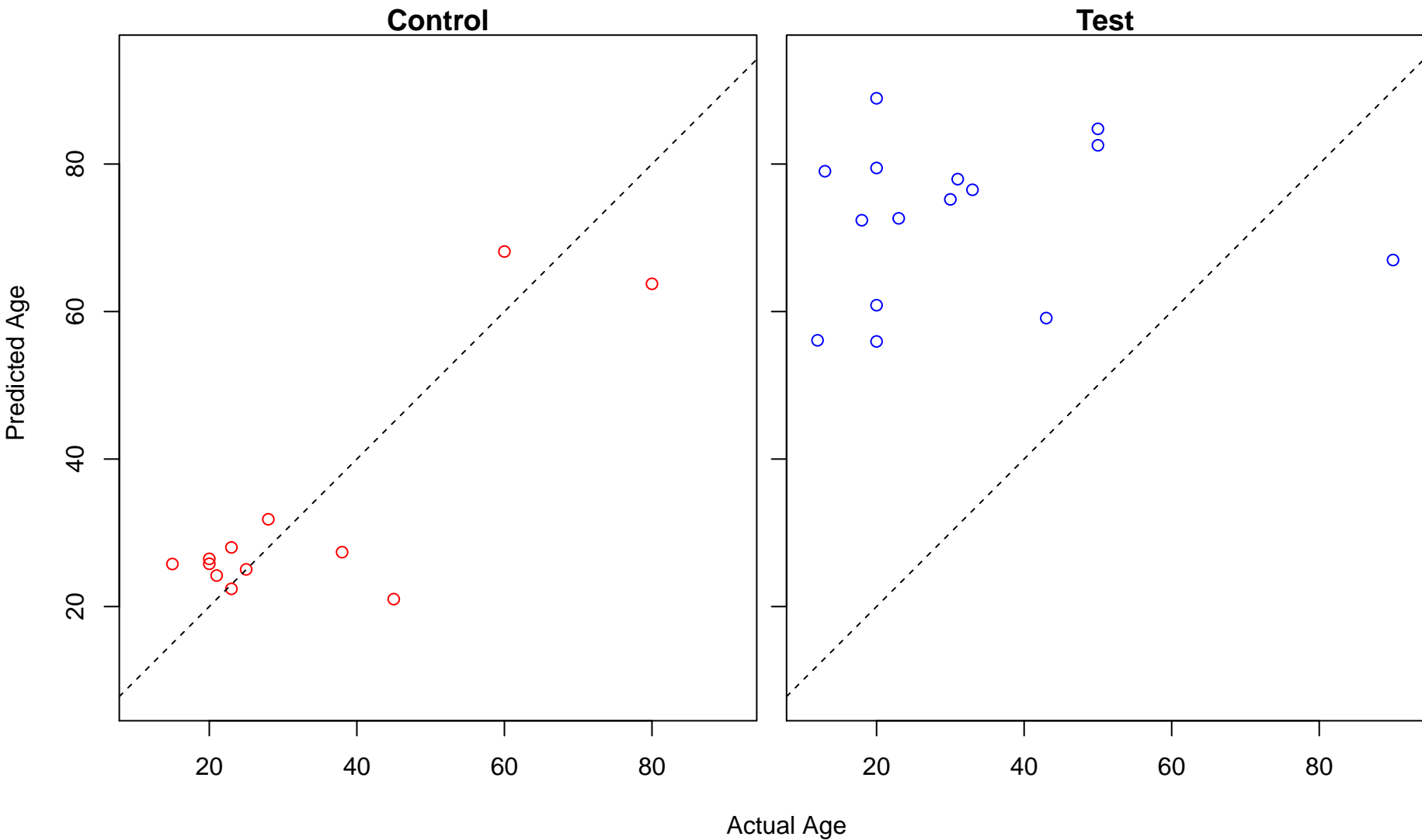


Test

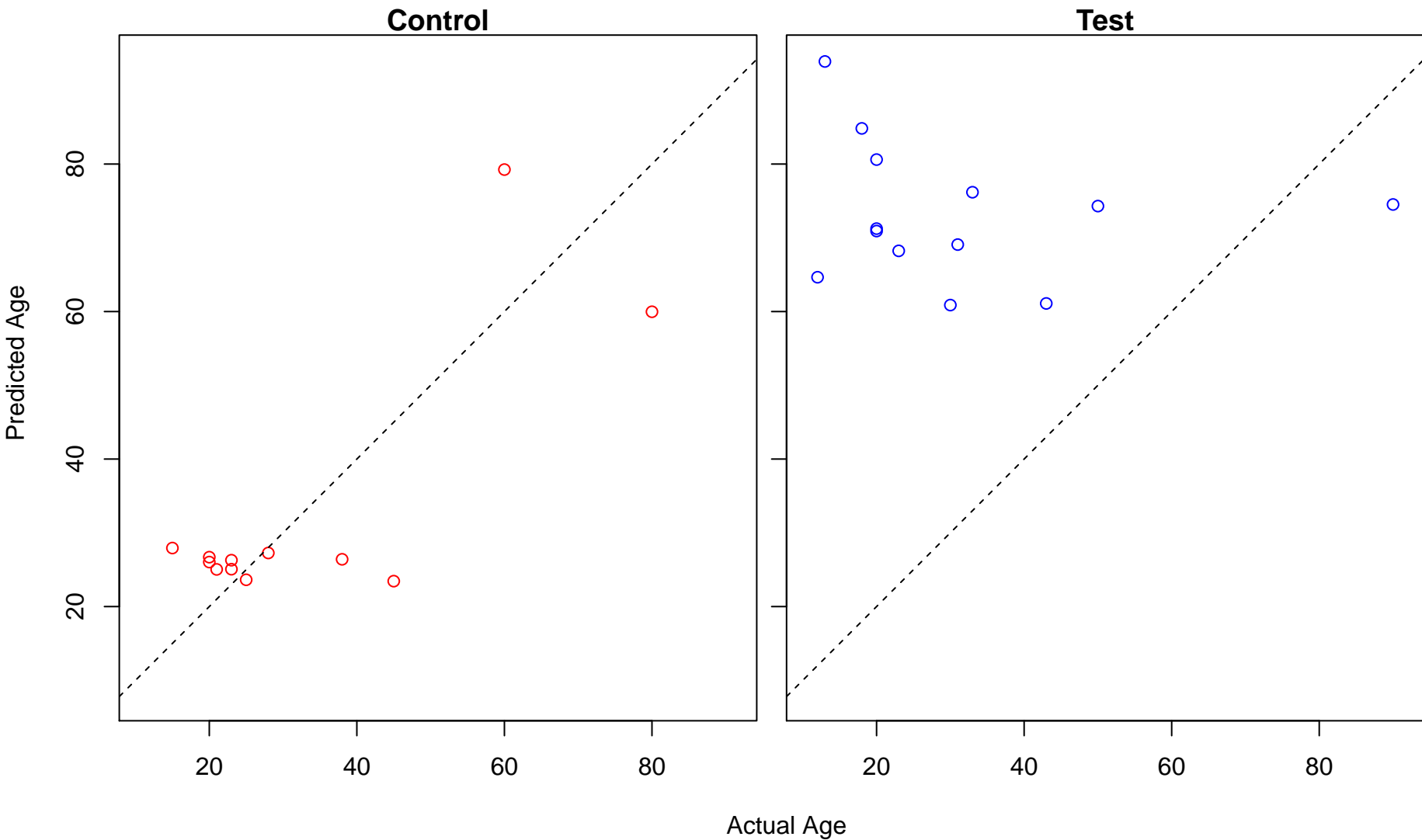


Actual Age

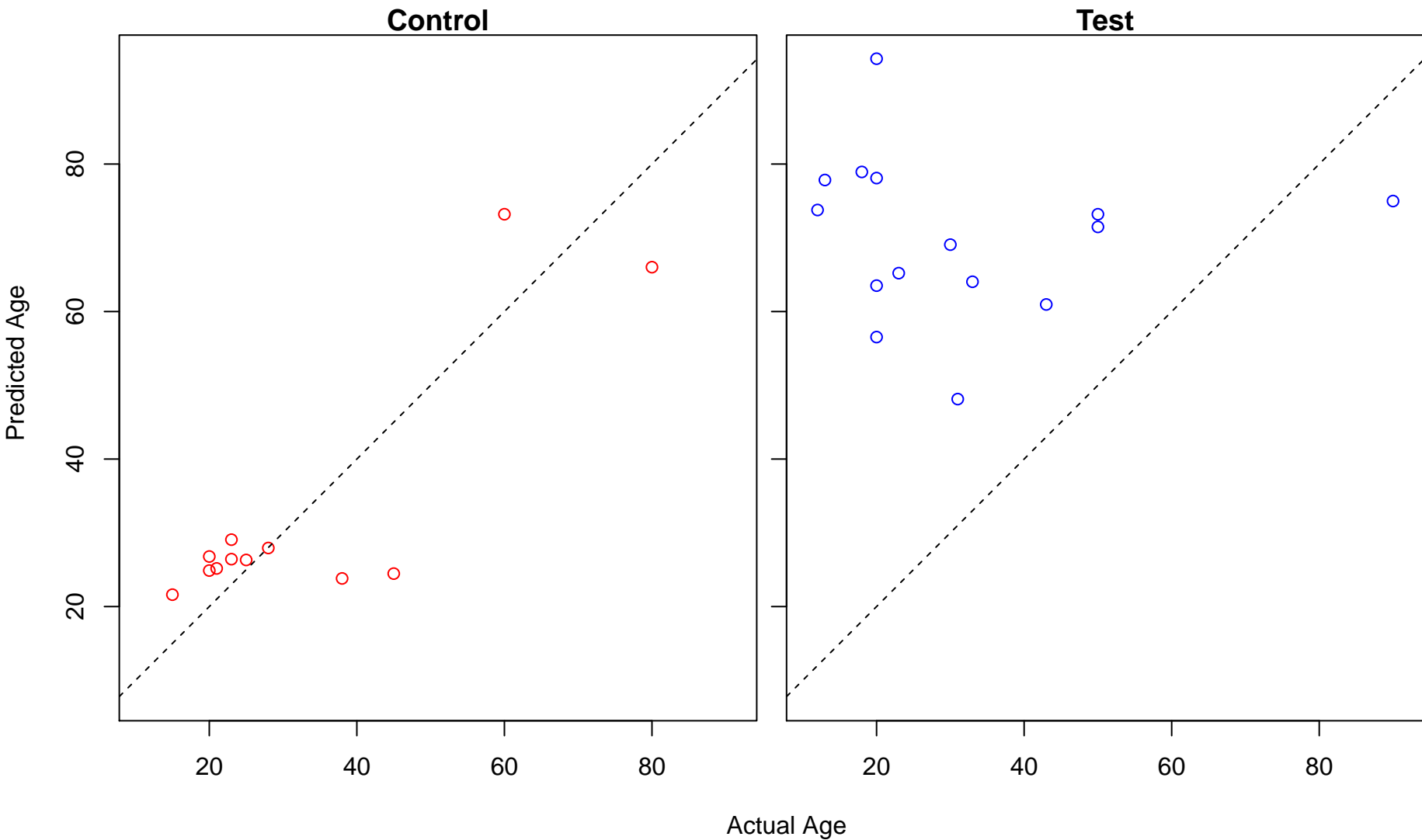
negative regulation of signal transduction by p53 class mediator (Score: 6.837698)



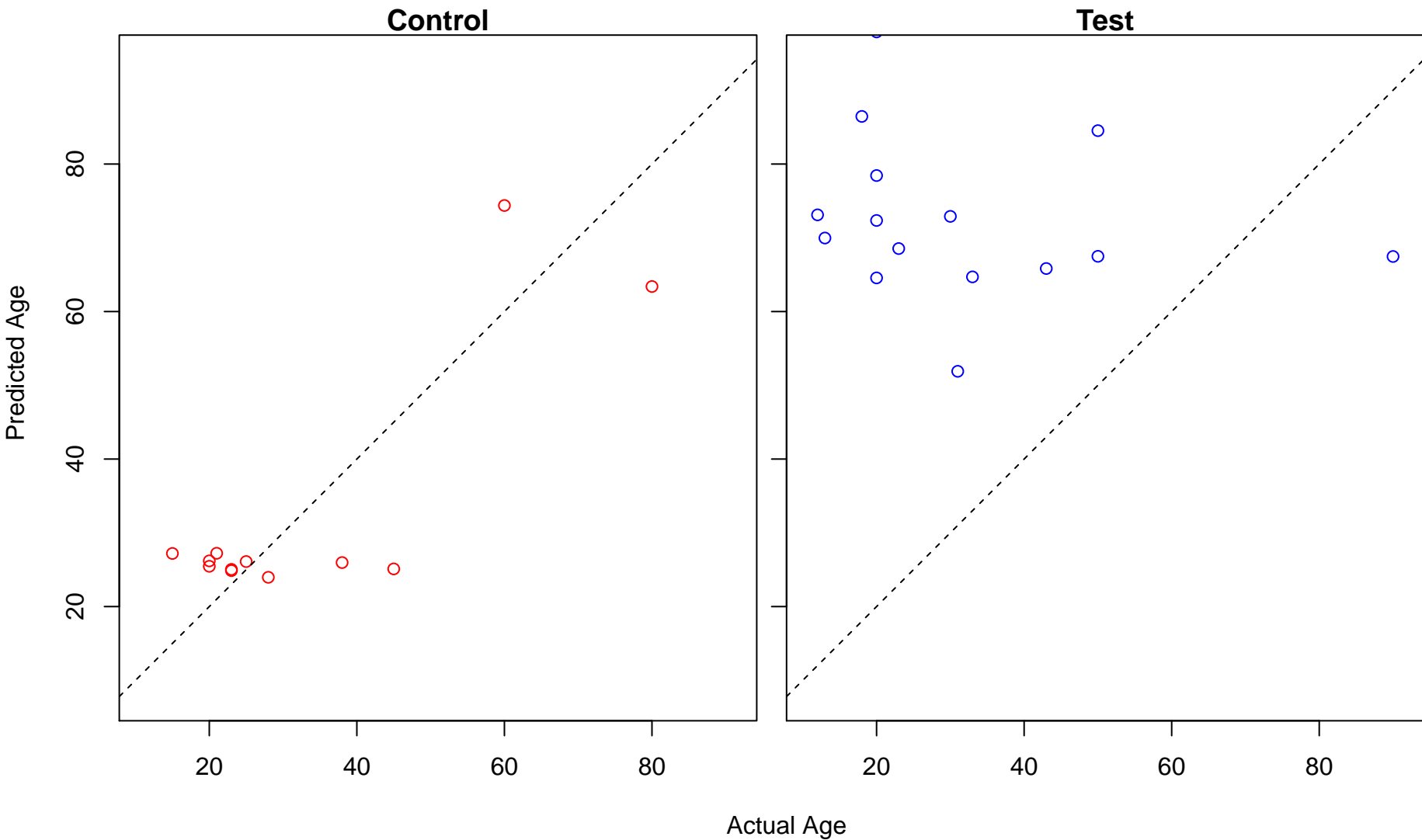
JNK cascade (Score: 6.833574)



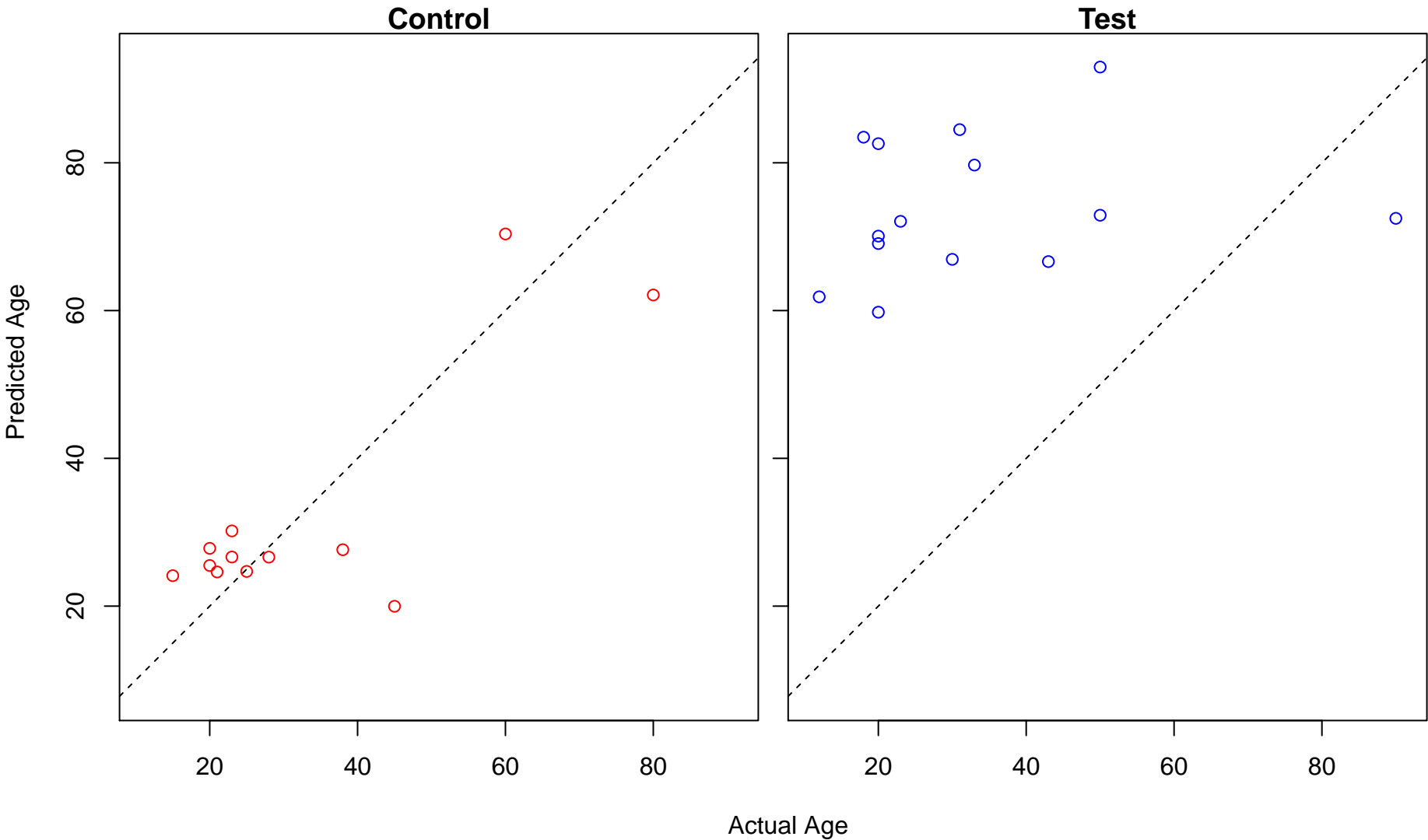
positive regulation of skeletal muscle tissue development (Score: 6.833358)



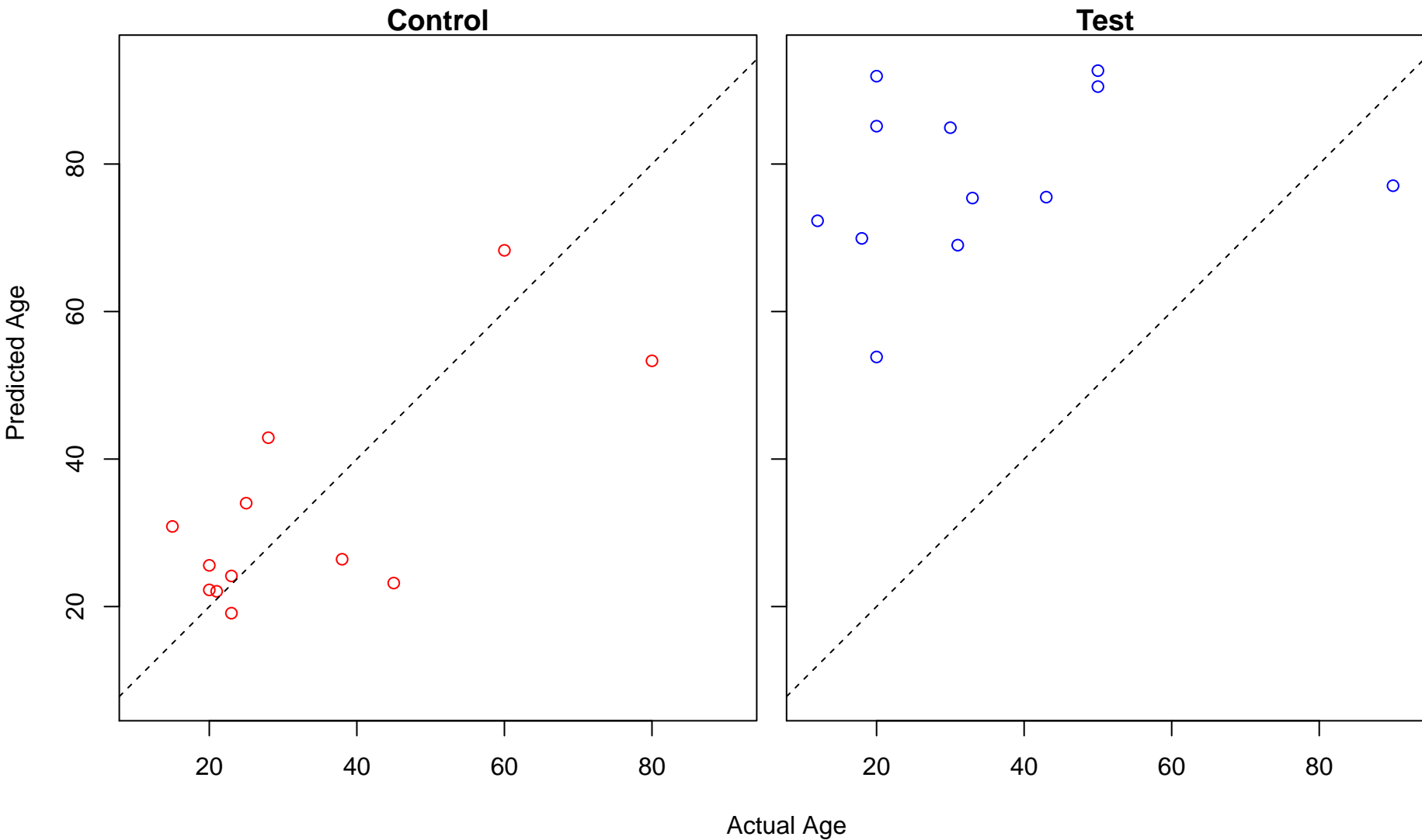
negative regulation of lyase activity (Score: 6.831993)



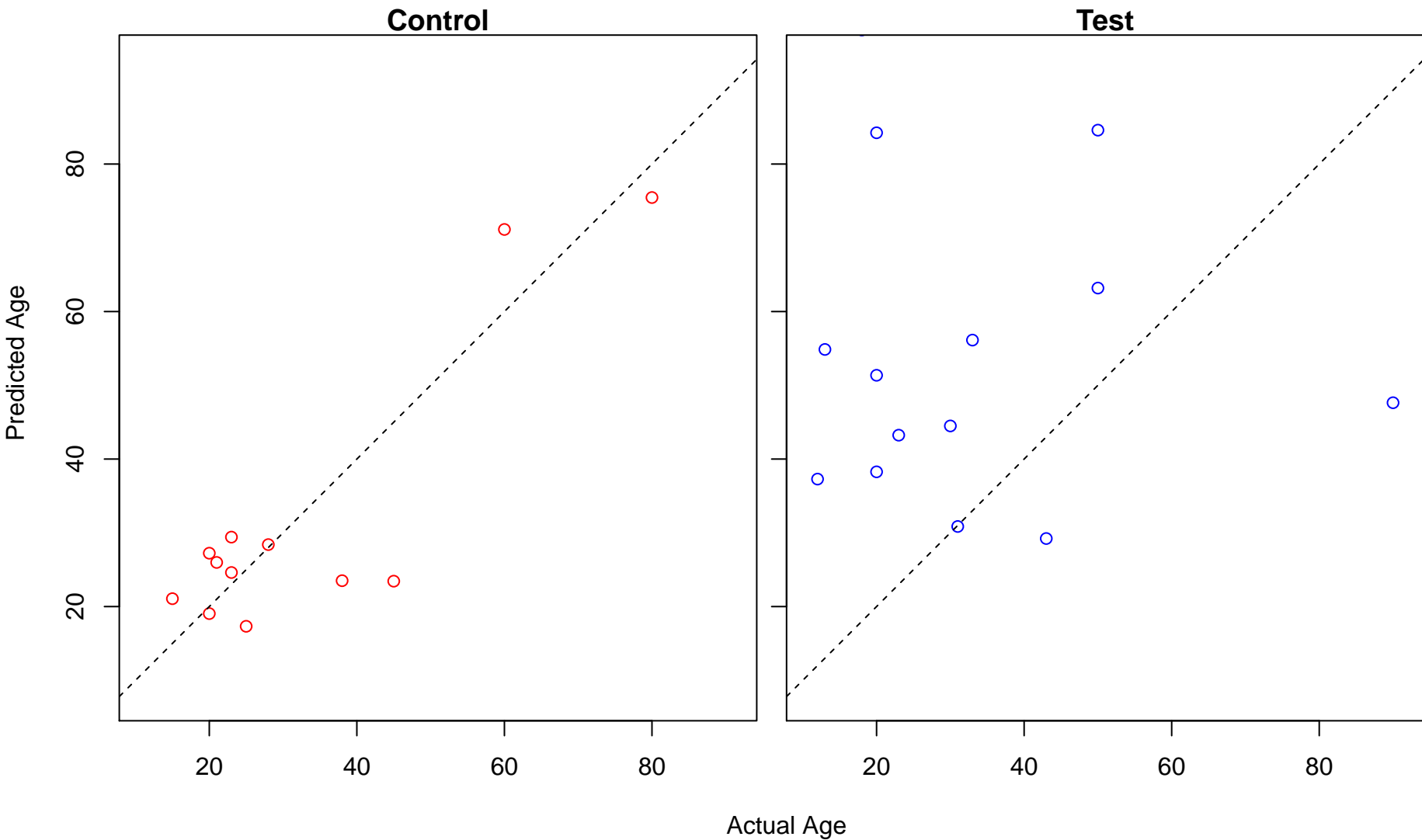
regulation of leukocyte mediated immunity (Score: 6.829311)



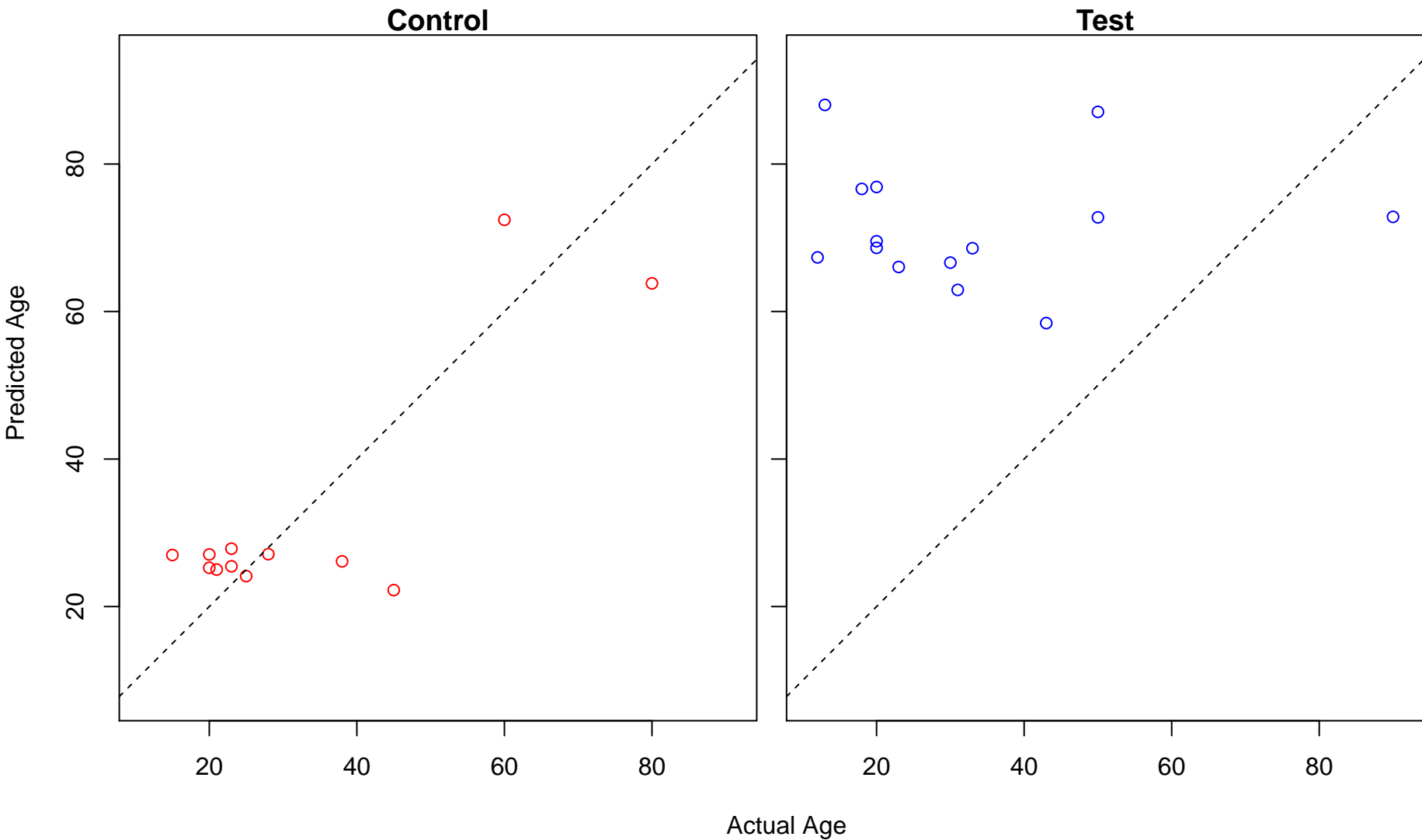
T cell selection (Score: 6.827581)



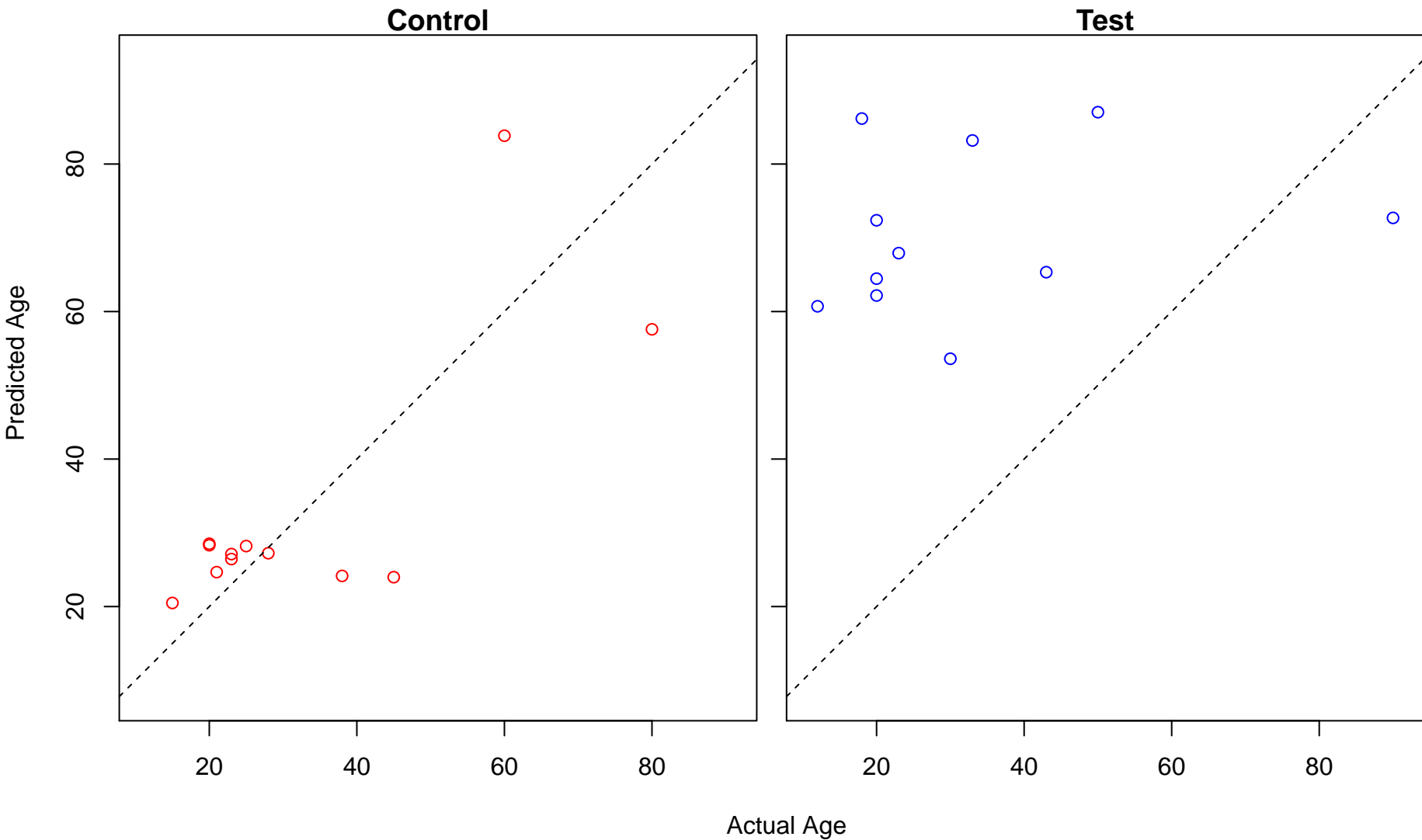
negative regulation of telomerase activity (Score: 6.824060)



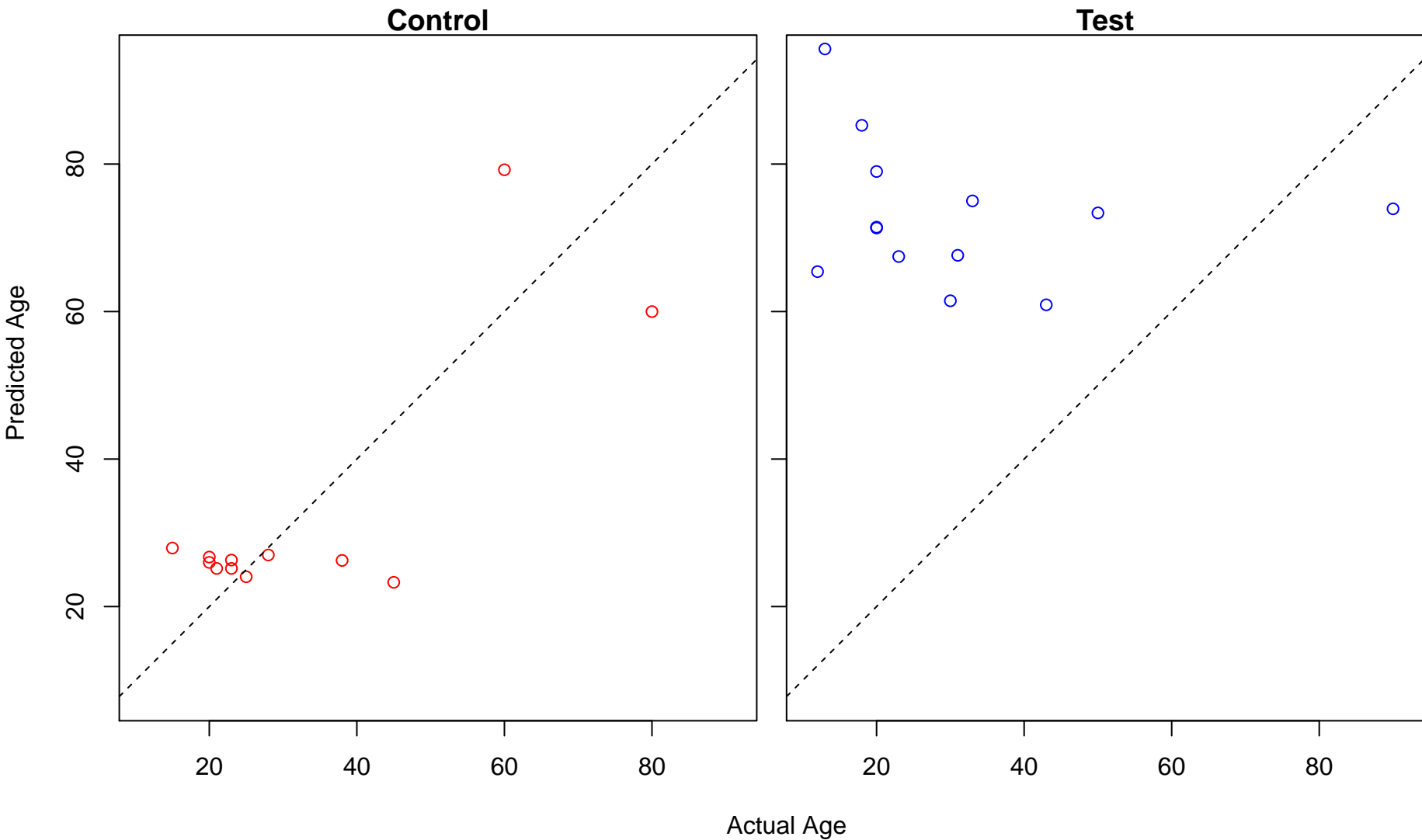
regulation of viral life cycle (Score: 6.823690)



negative regulation of anoikis (Score: 6.823689)

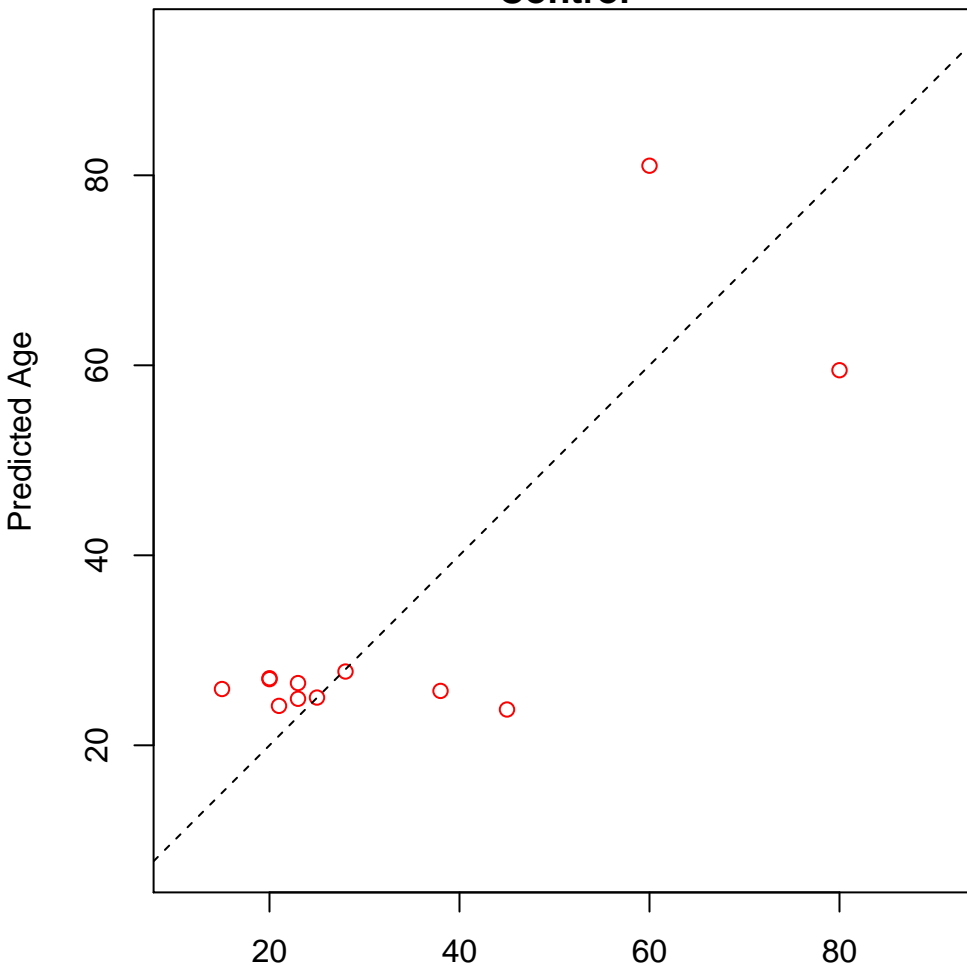


DNA damage response, detection of DNA damage (Score: 6.821545)

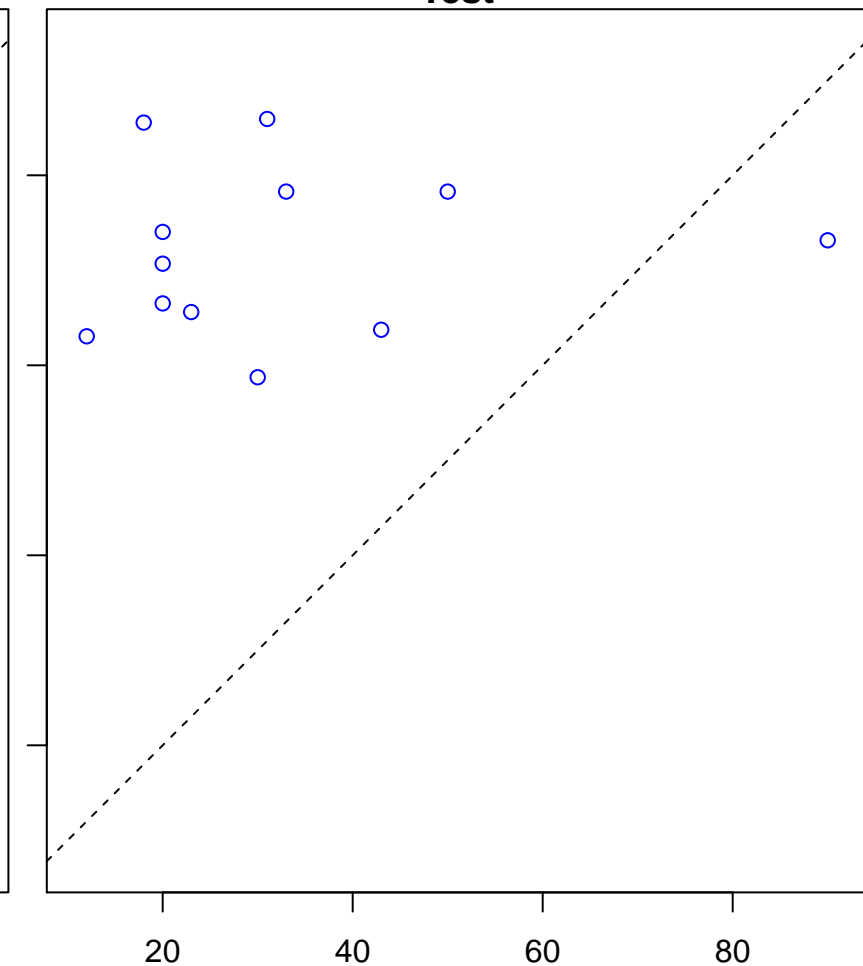


negative regulation of cell cycle process (Score: 6.821051)

Control

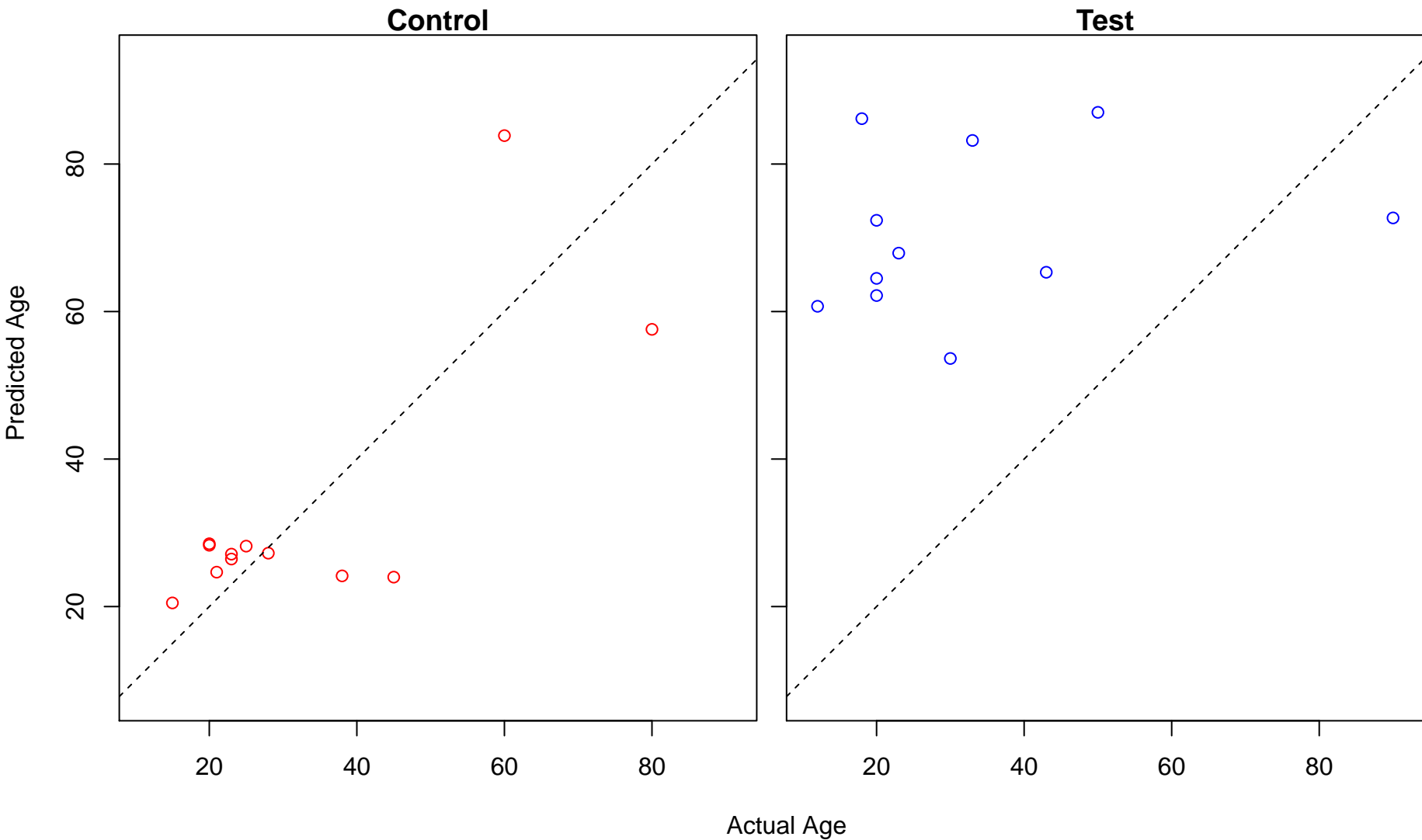


Test

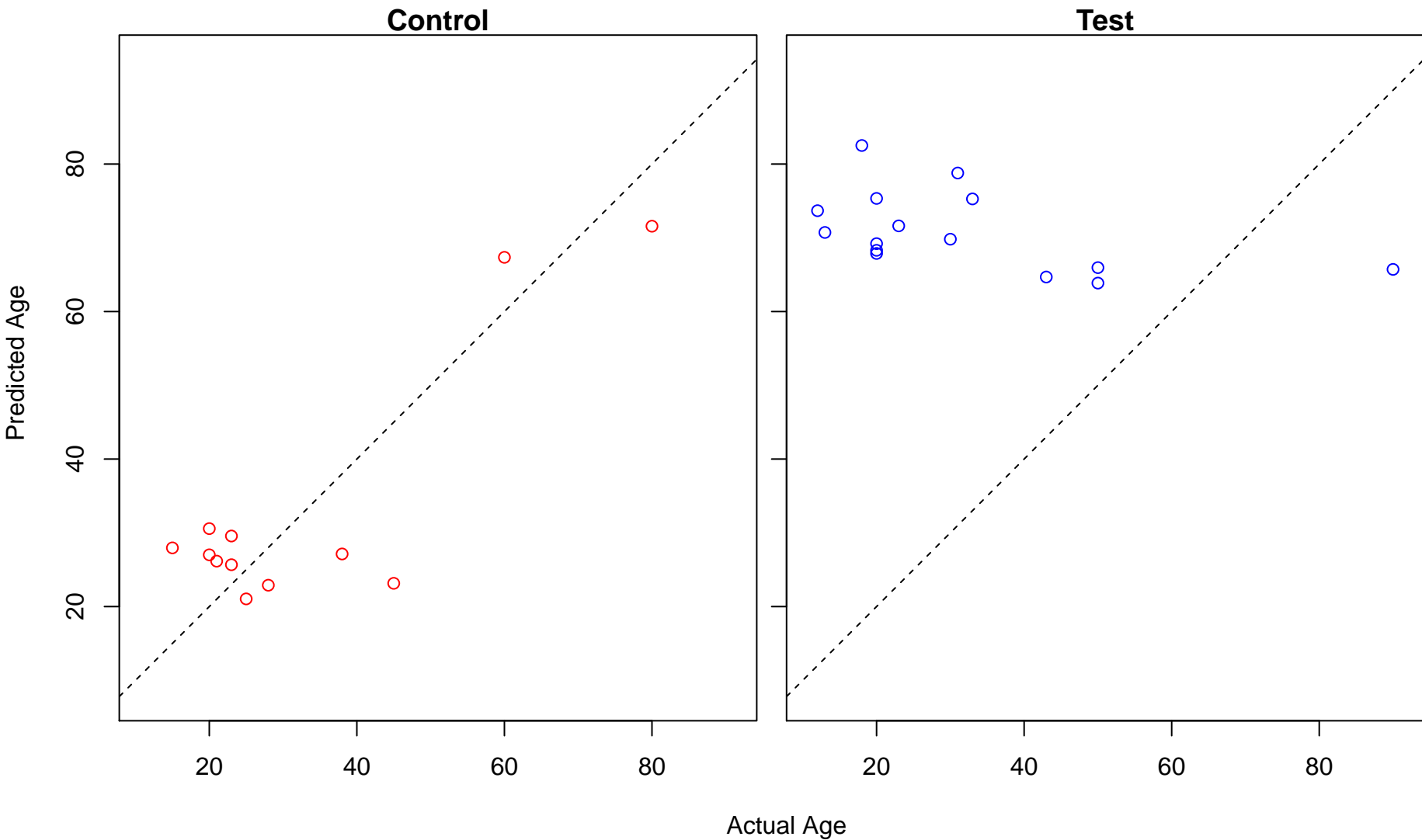


Actual Age

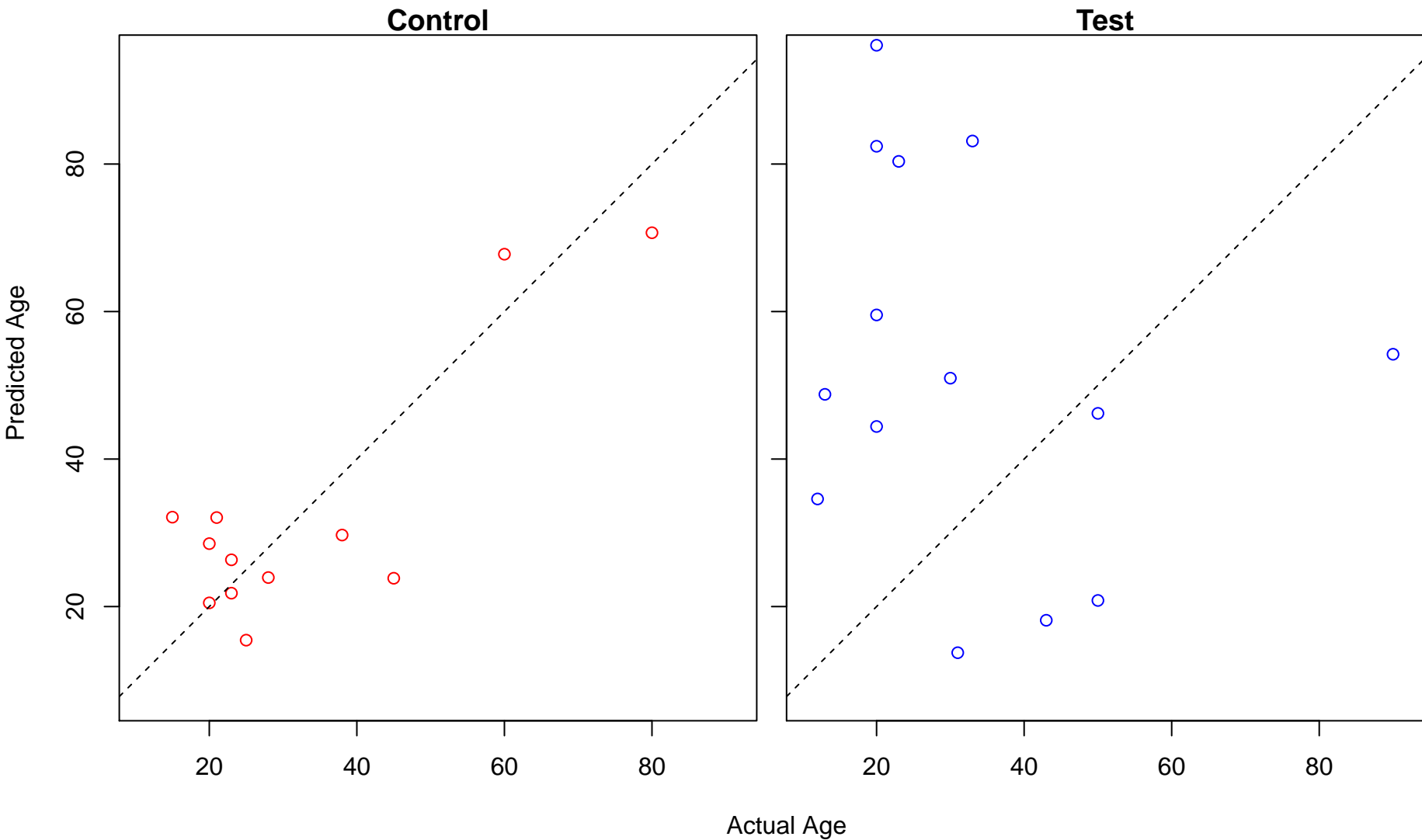
regulation of anoikis (Score: 6.820904)



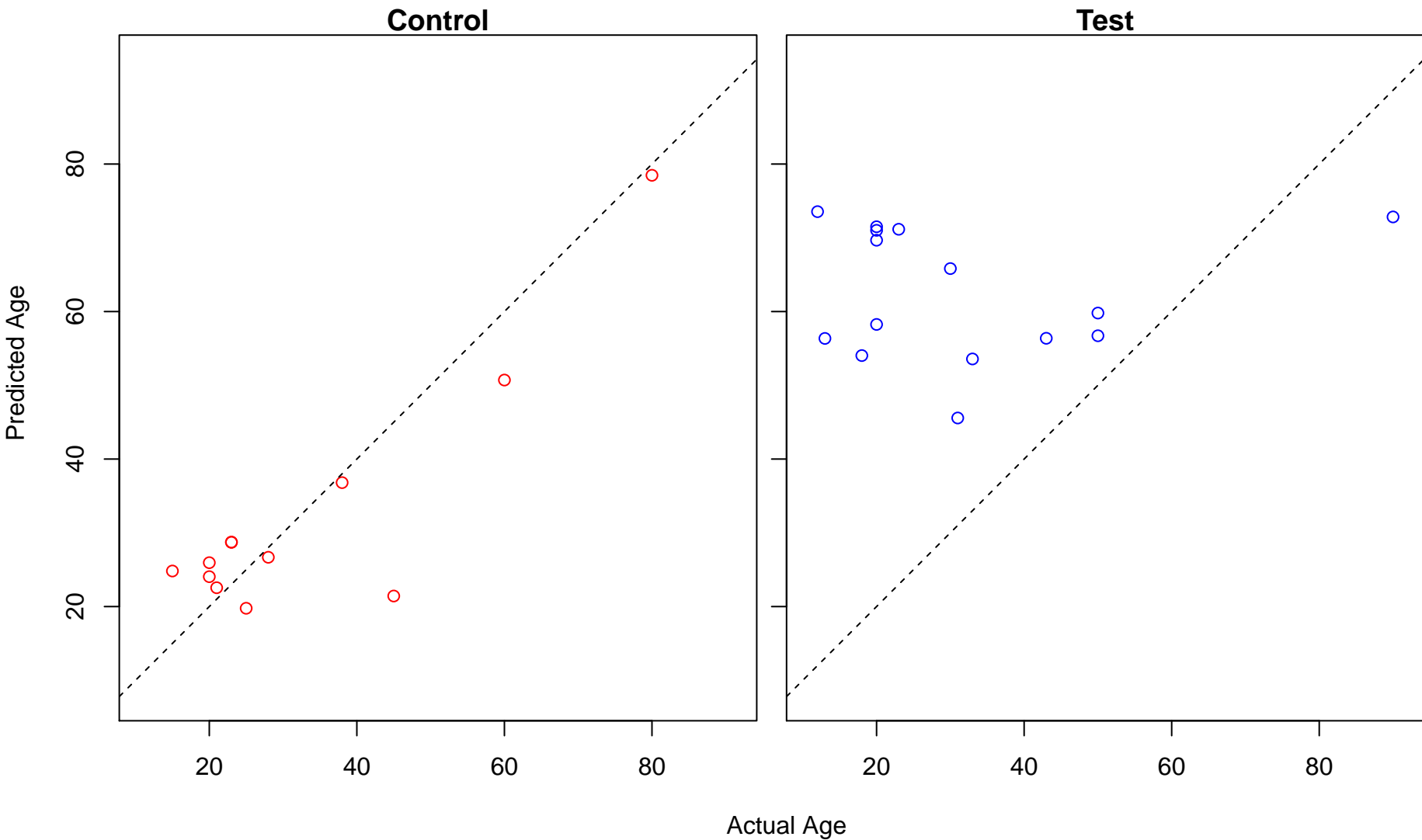
pteridine-containing compound metabolic process (Score: 6.817135)



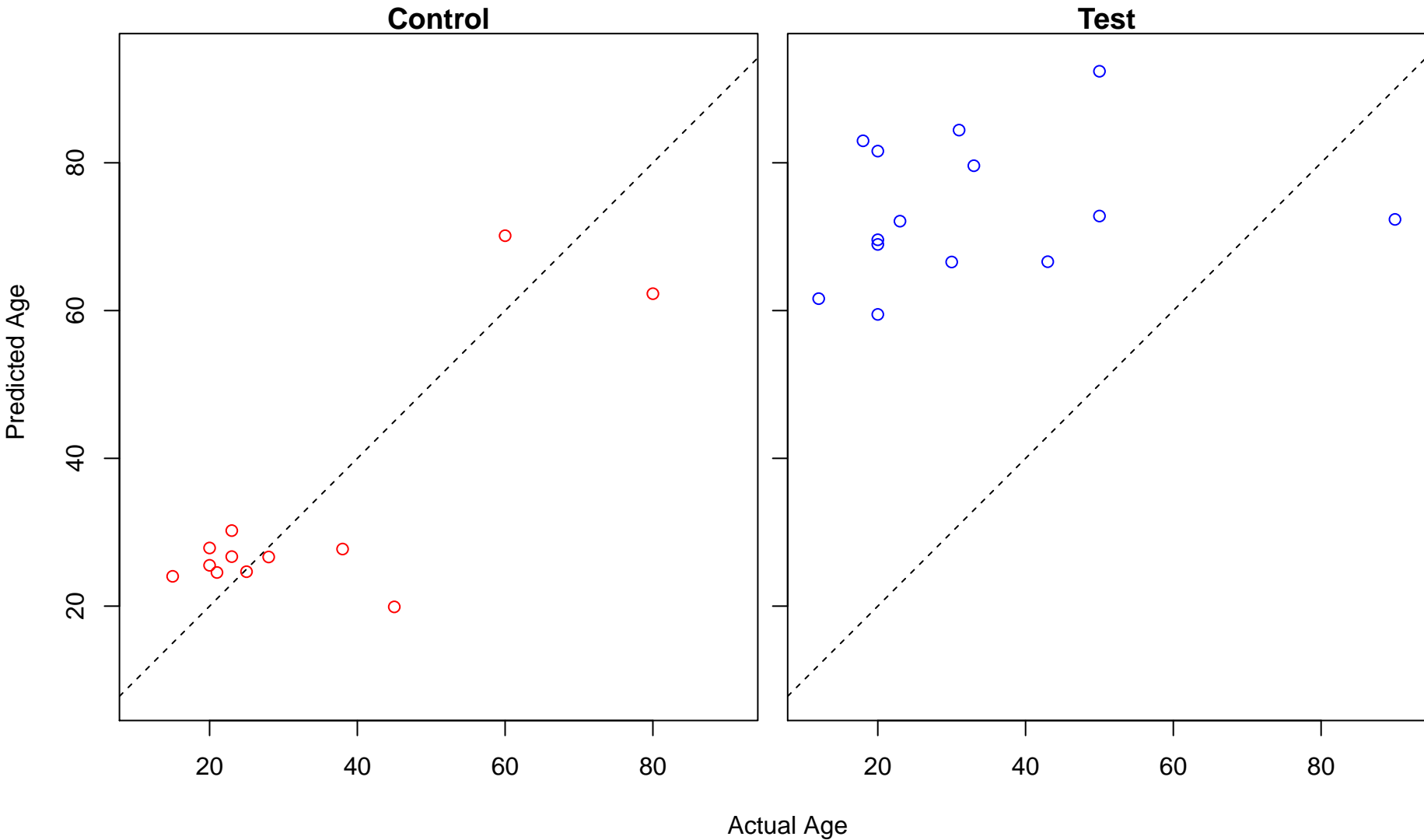
regulation of mitotic spindle organization (Score: 6.813936)



apoptotic process involved in development (Score: 6.813291)

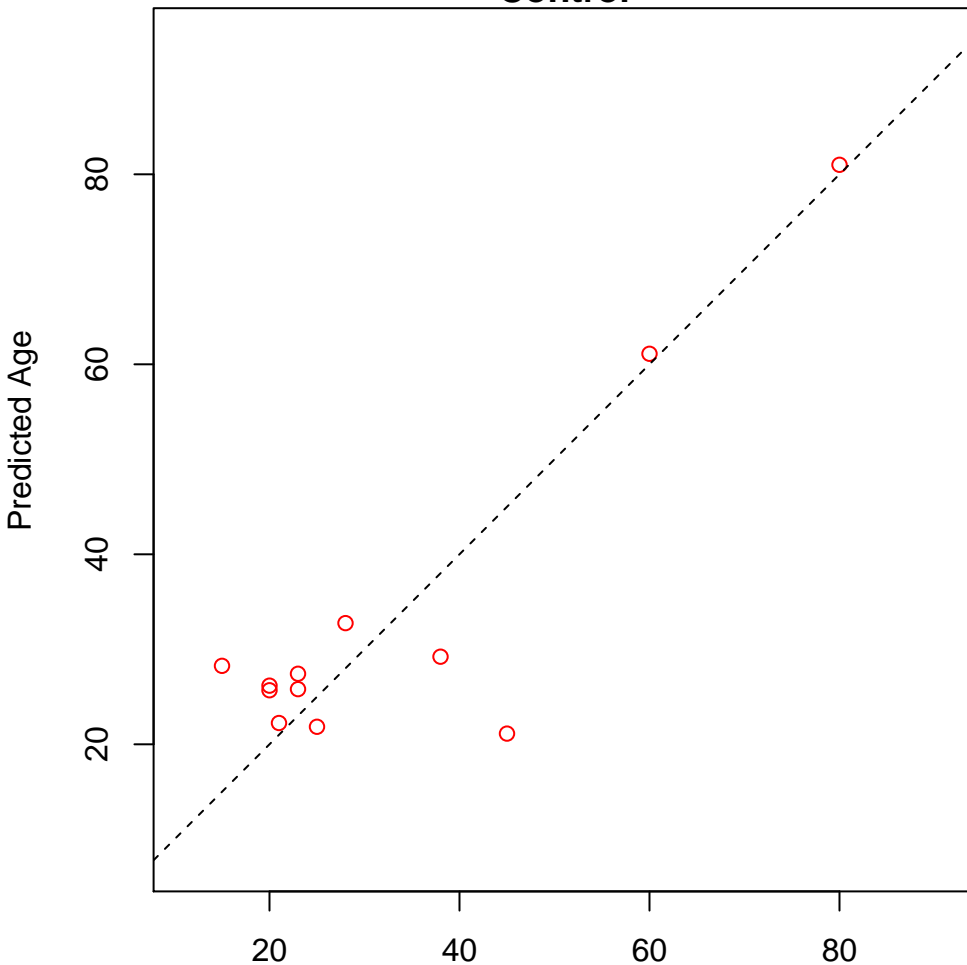


regulation of lymphocyte mediated immunity (Score: 6.812885)

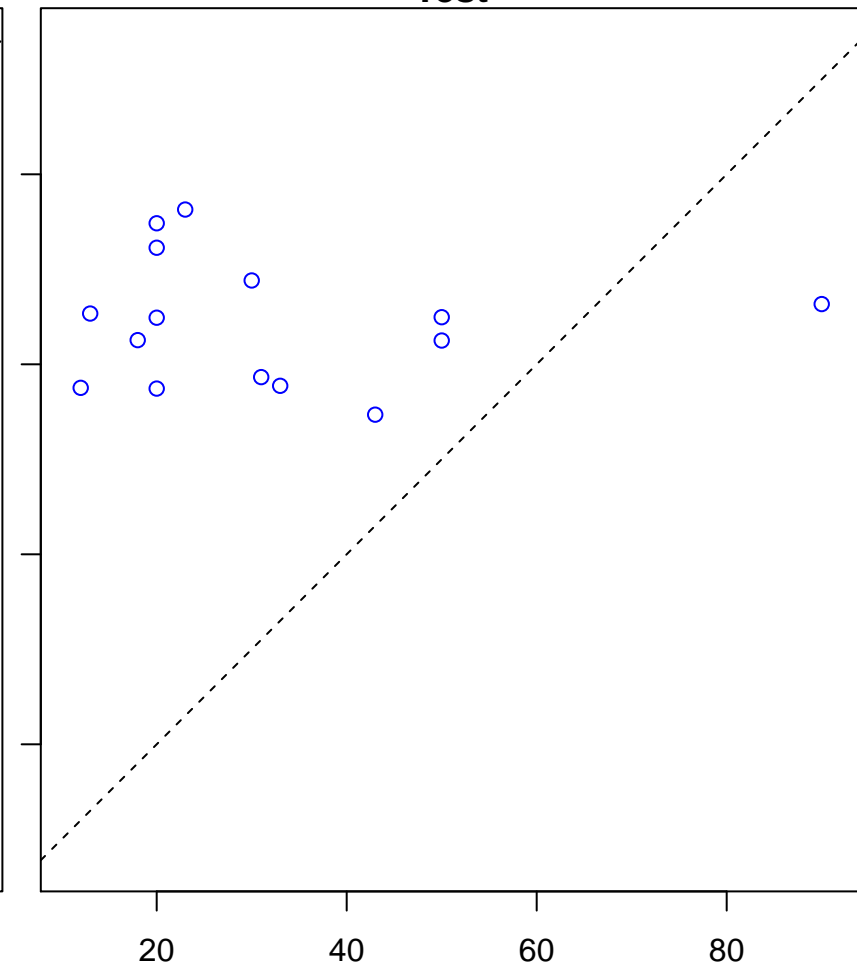


small molecule biosynthetic process (Score: 6.812128)

Control

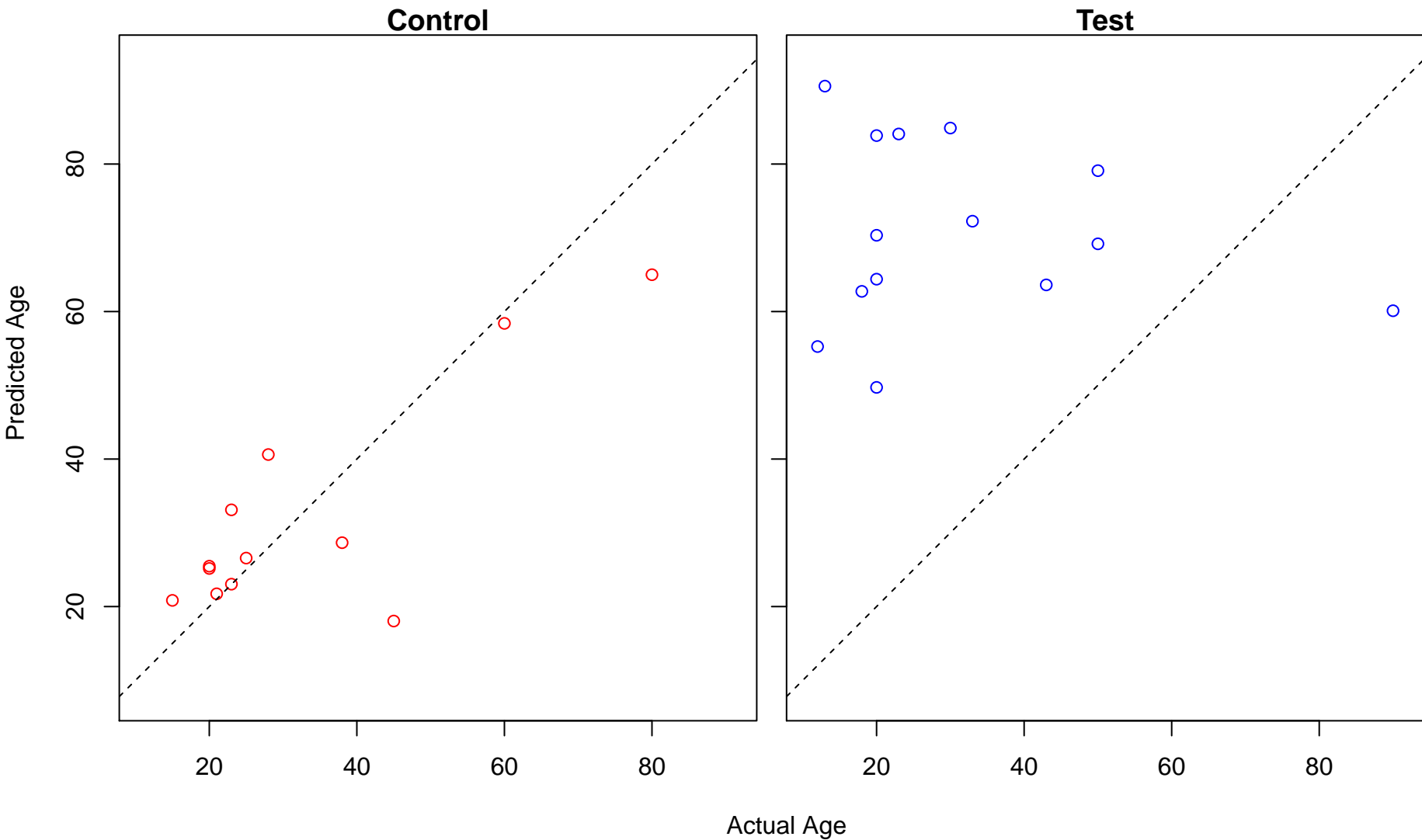


Test

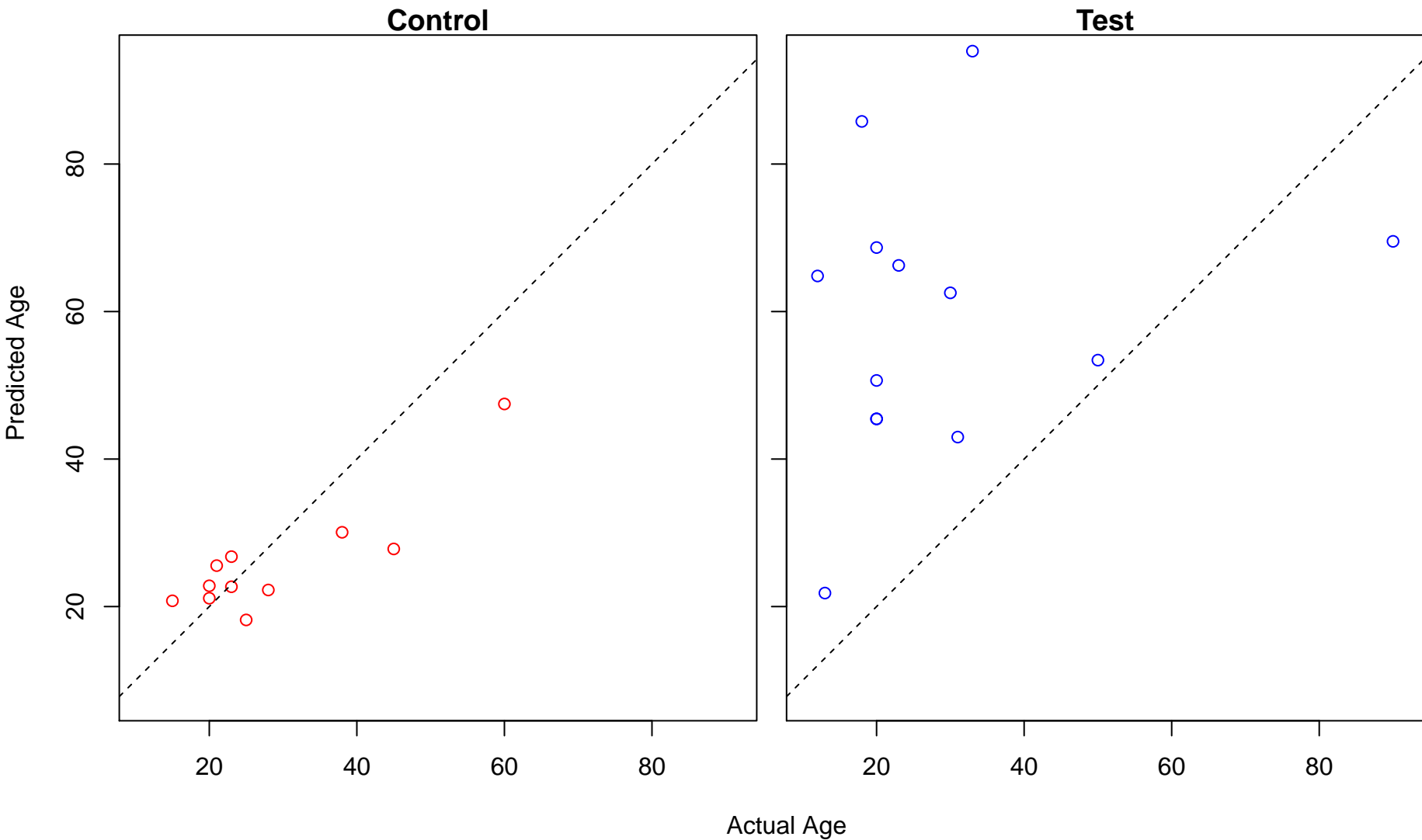


Actual Age

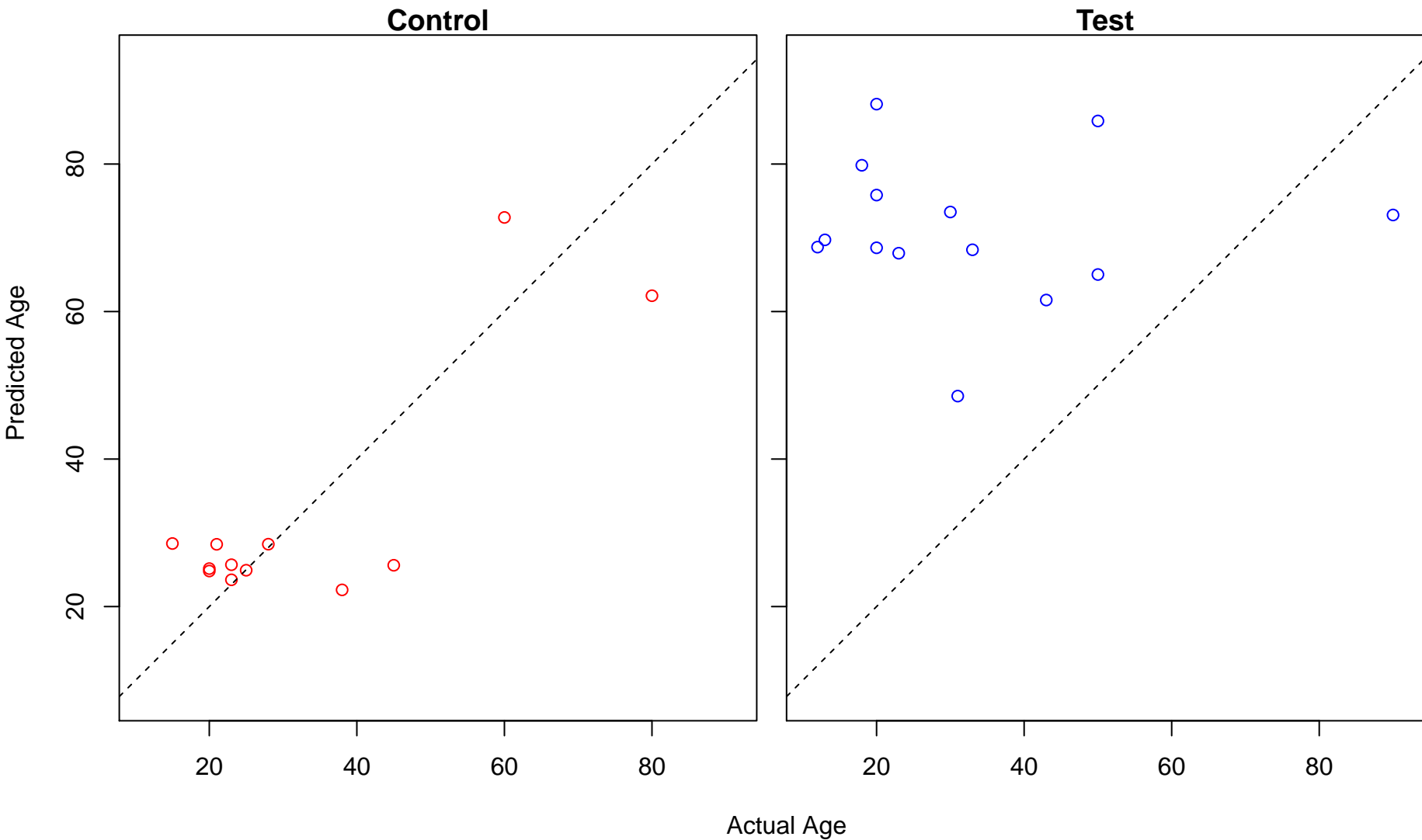
positive regulation of chemokine production (Score: 6.810357)



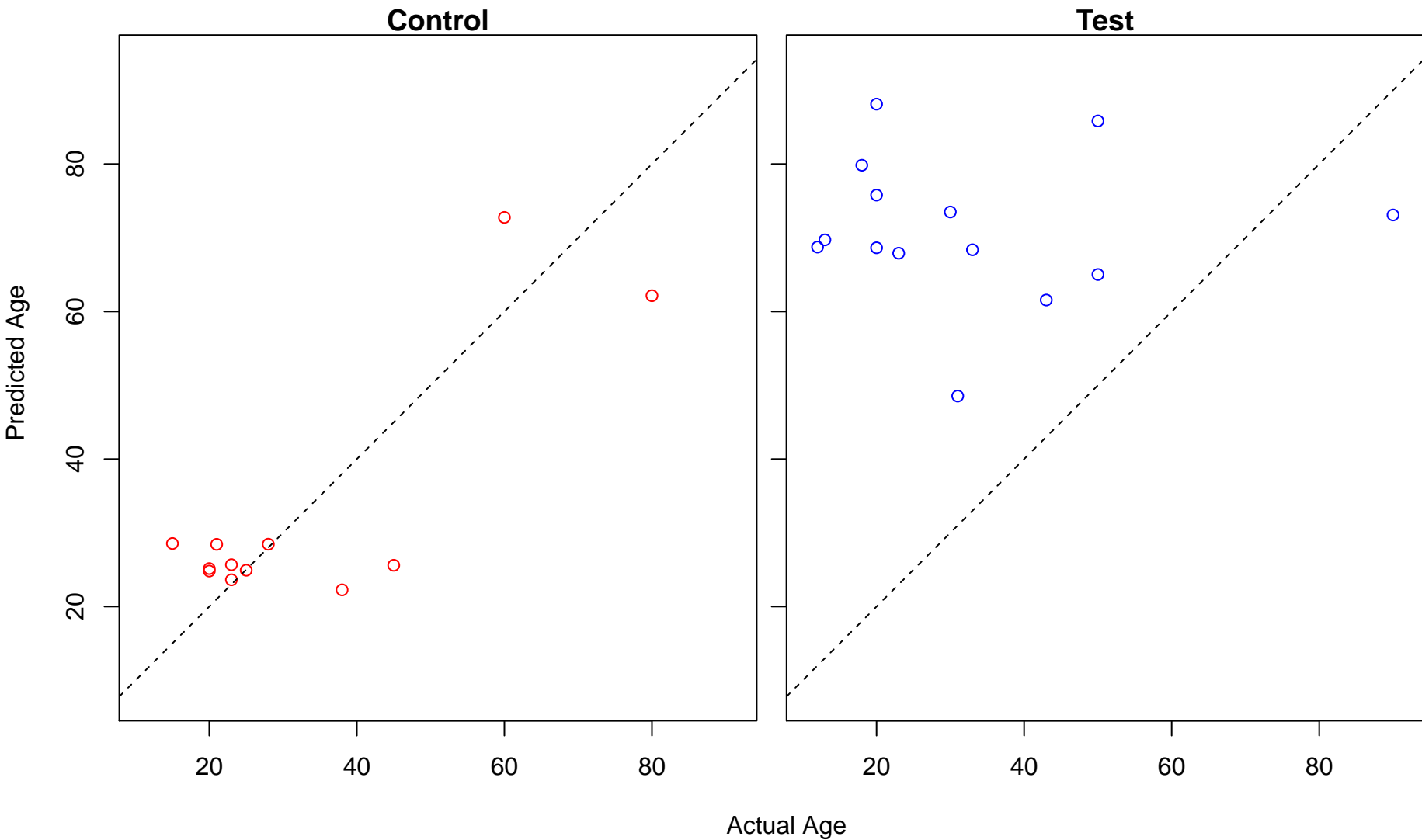
RNA polyadenylation (Score: 6.807848)



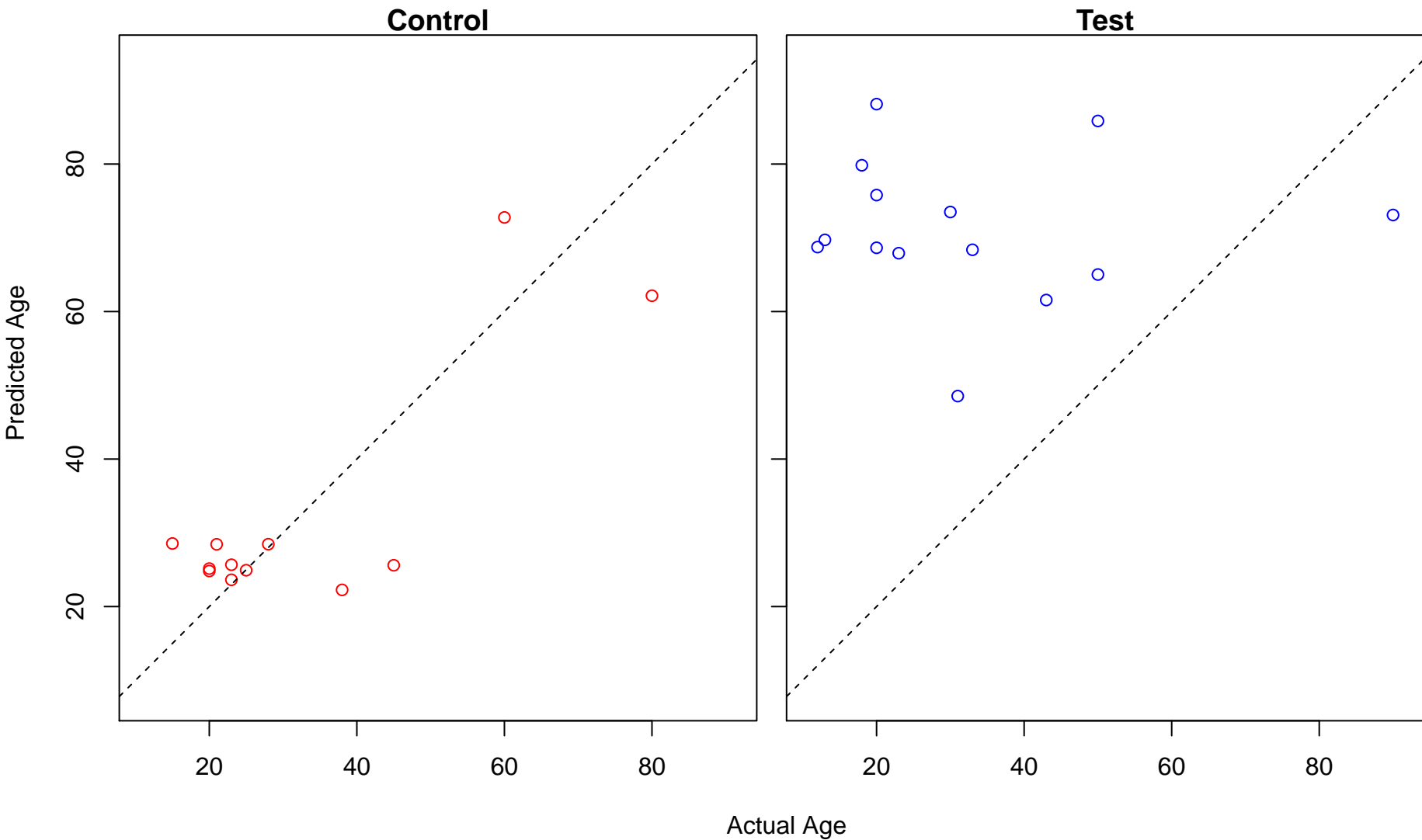
NADH dehydrogenase complex assembly (Score: 6.807834)



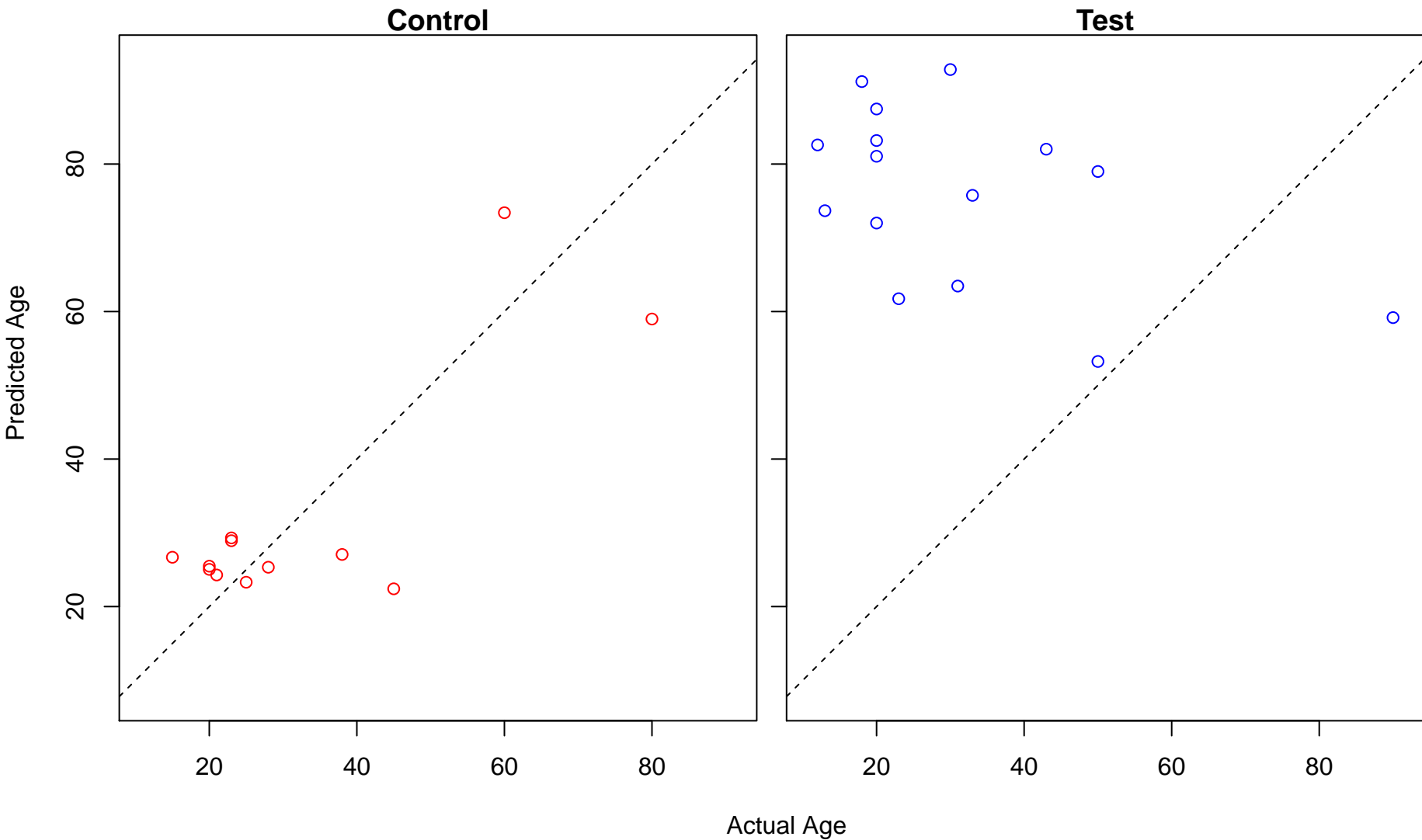
mitochondrial respiratory chain complex I assembly (Score: 6.807834)



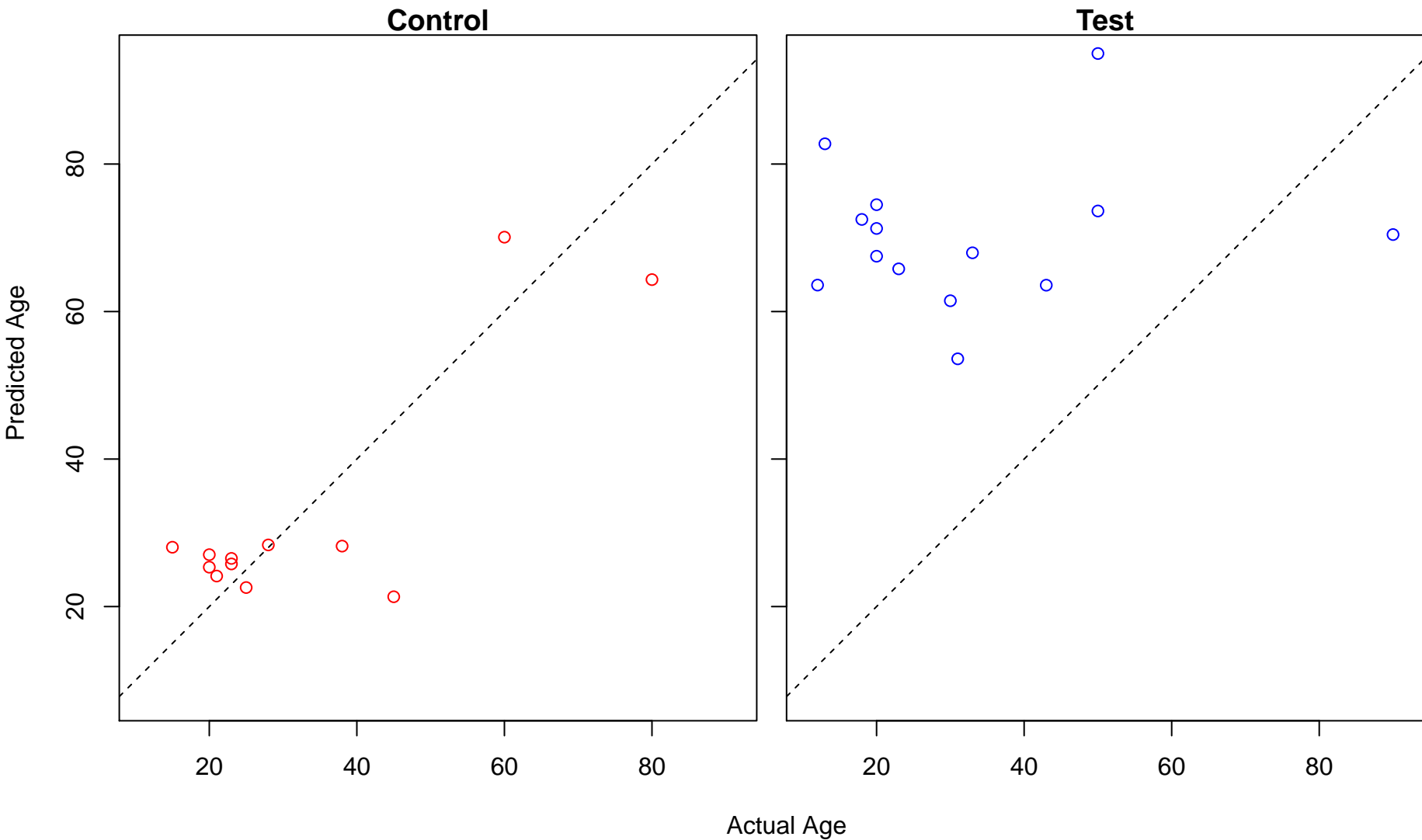
mitochondrial respiratory chain complex I biogenesis (Score: 6.807834)



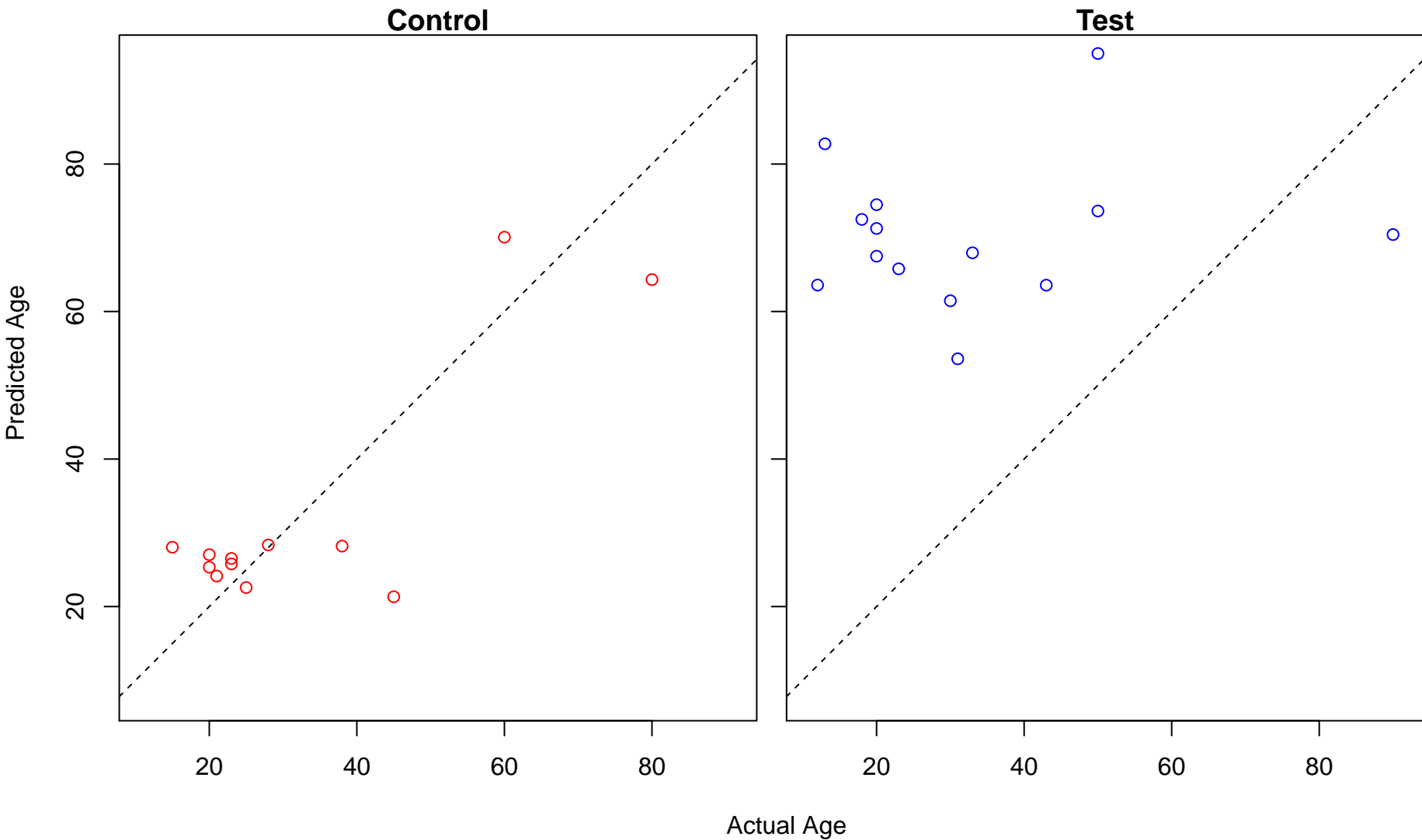
mitotic sister chromatid cohesion (Score: 6.803936)



reproductive process (Score: 6.798700)

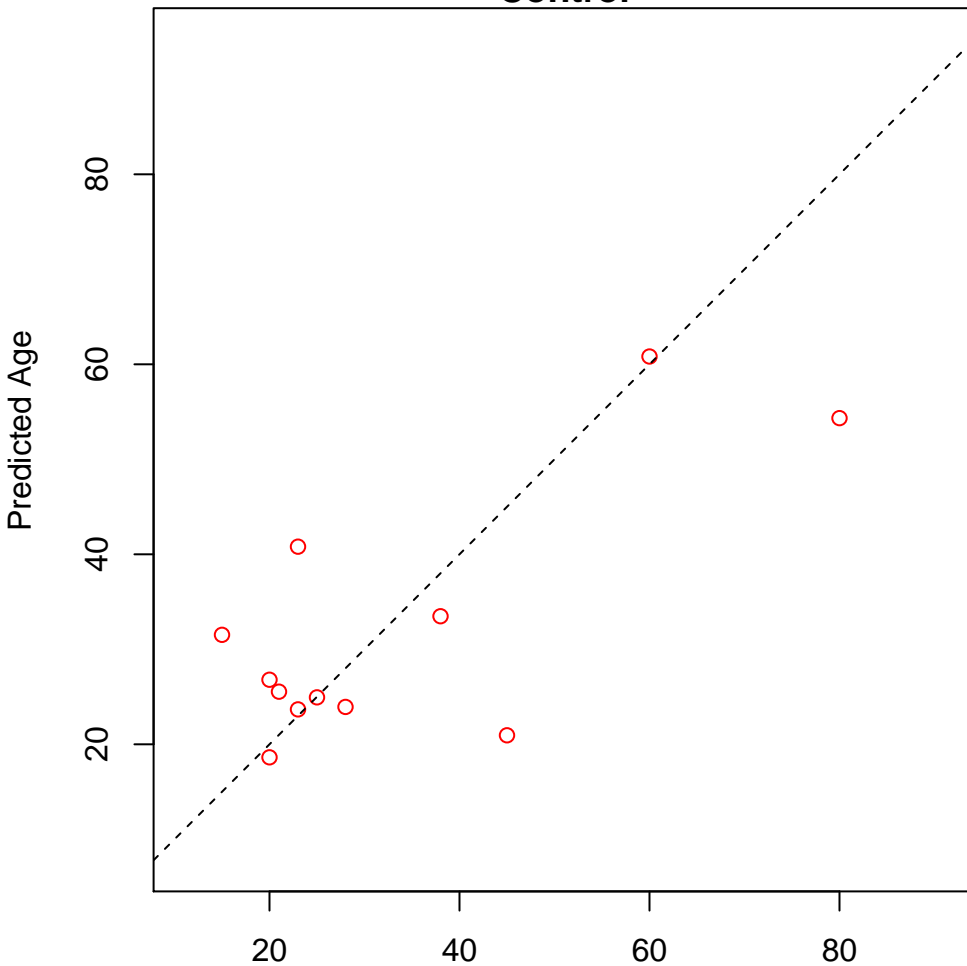


reproduction (Score: 6.798700)

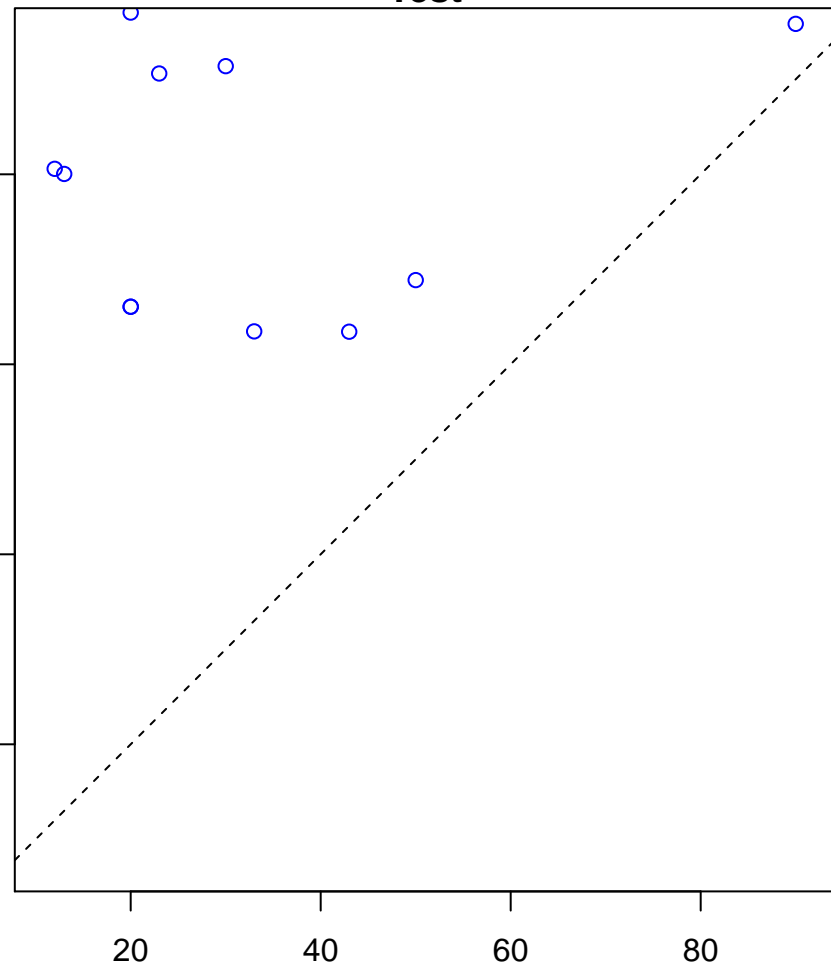


regulation of interleukin-4 production (Score: 6.798668)

Control

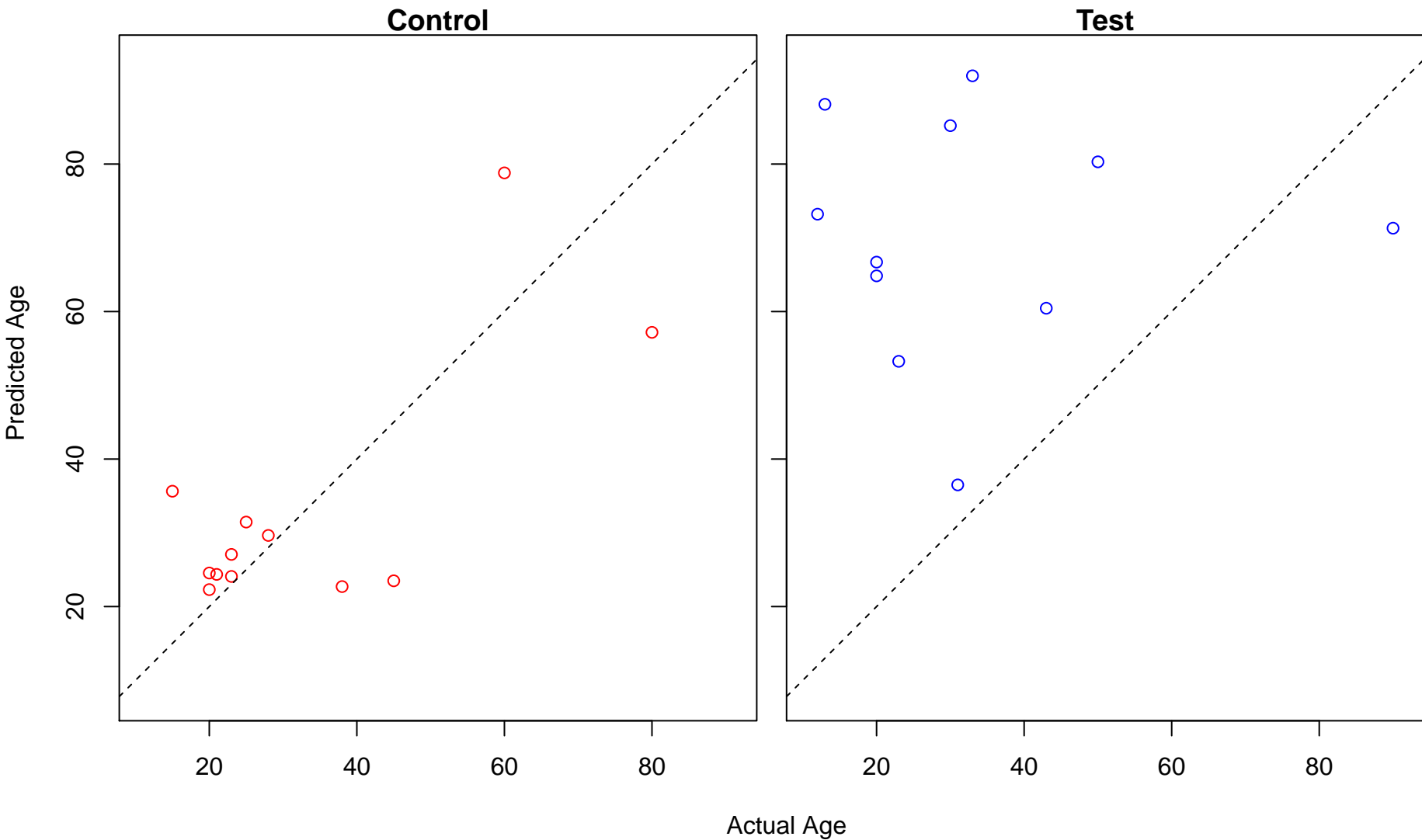


Test

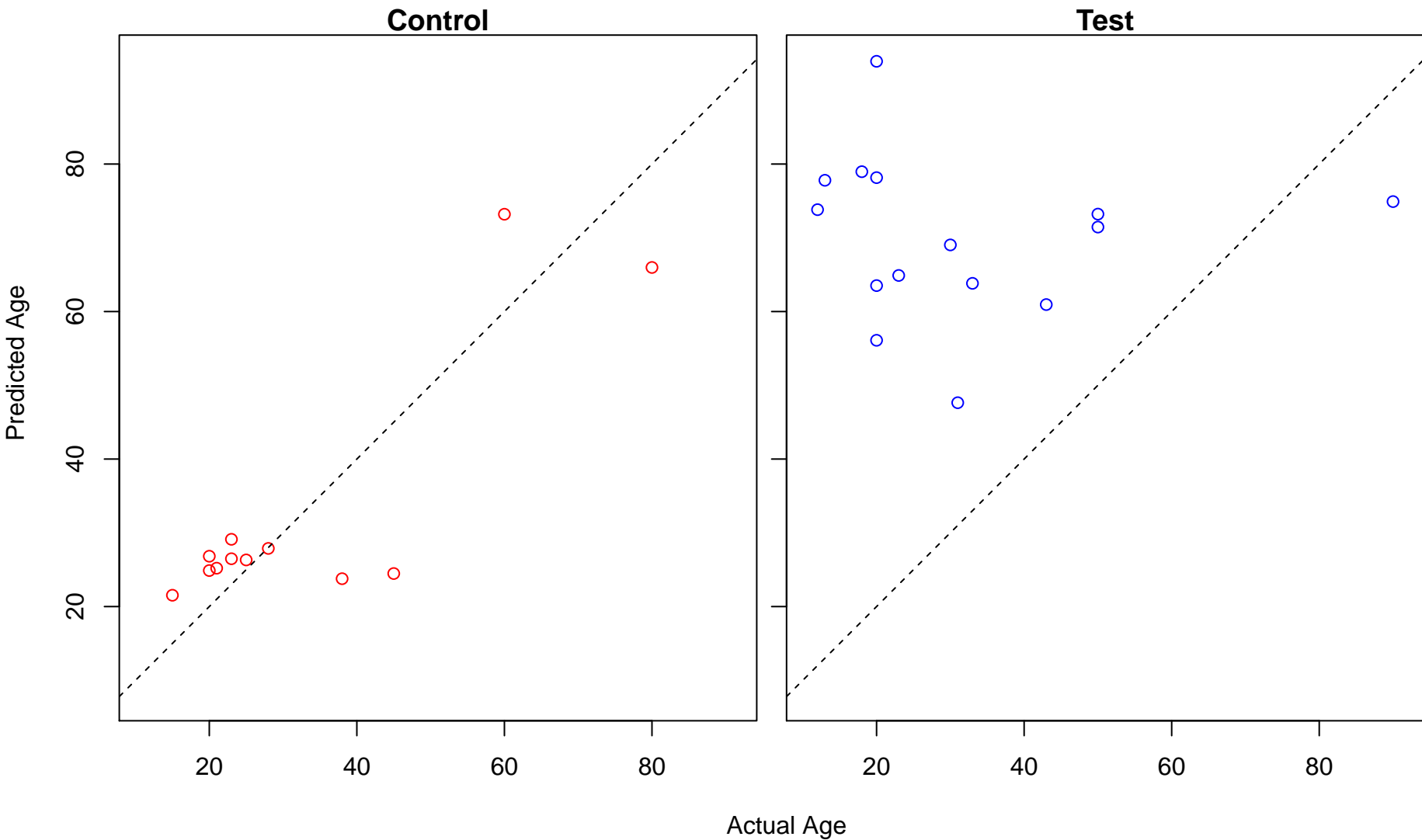


Actual Age

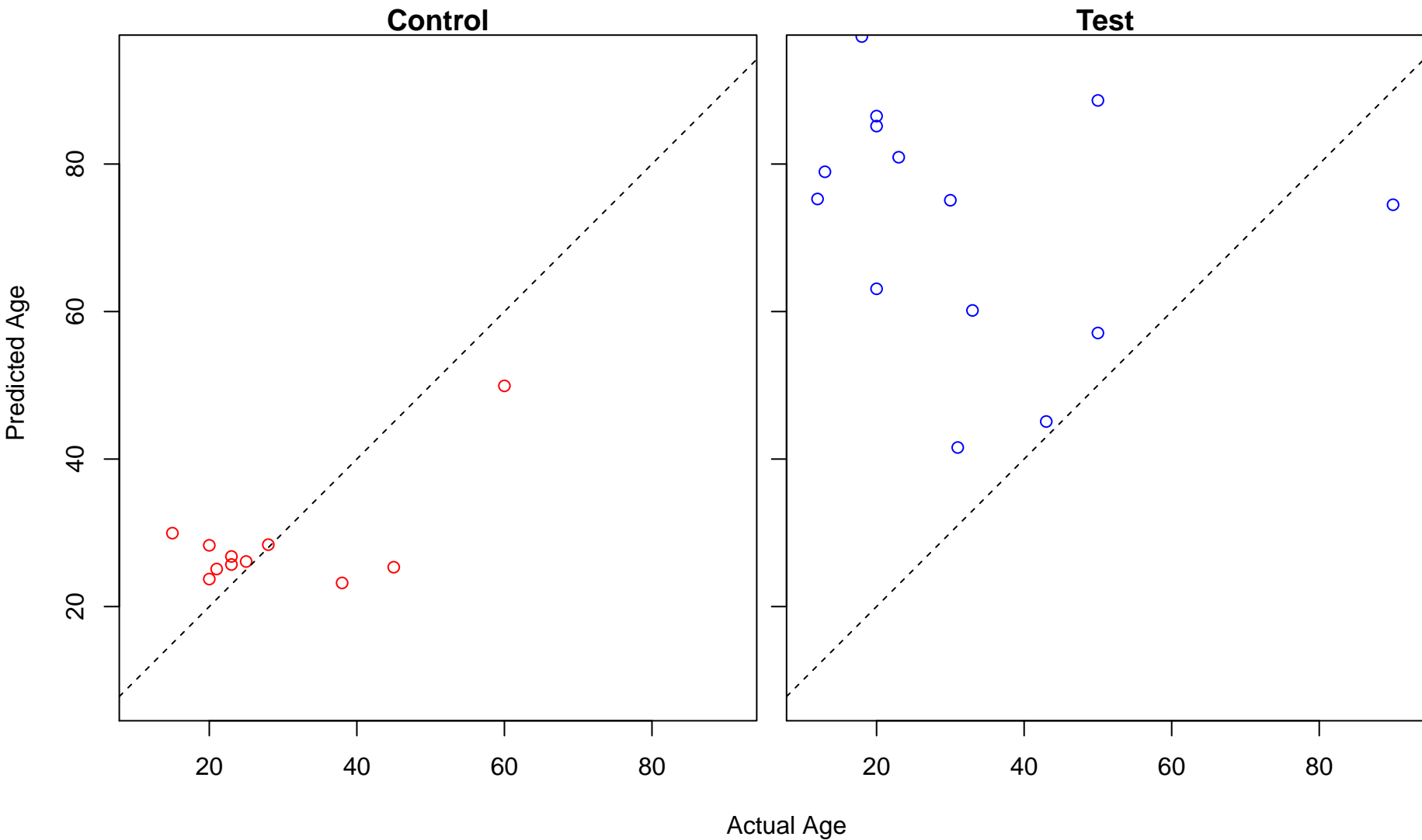
hyaluronan catabolic process (Score: 6.796255)



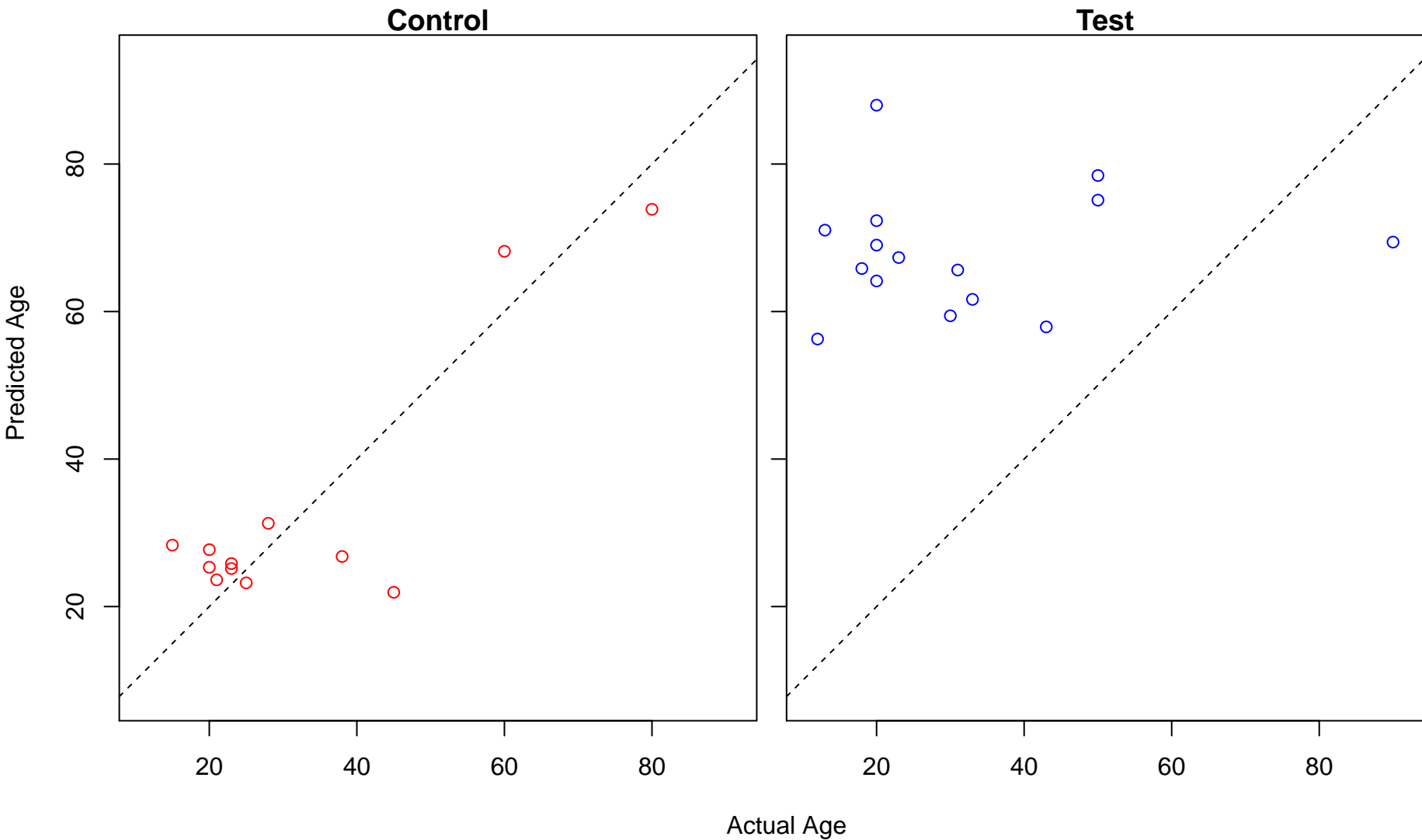
negative regulation of striated muscle cell apoptotic process (Score: 6.794978)



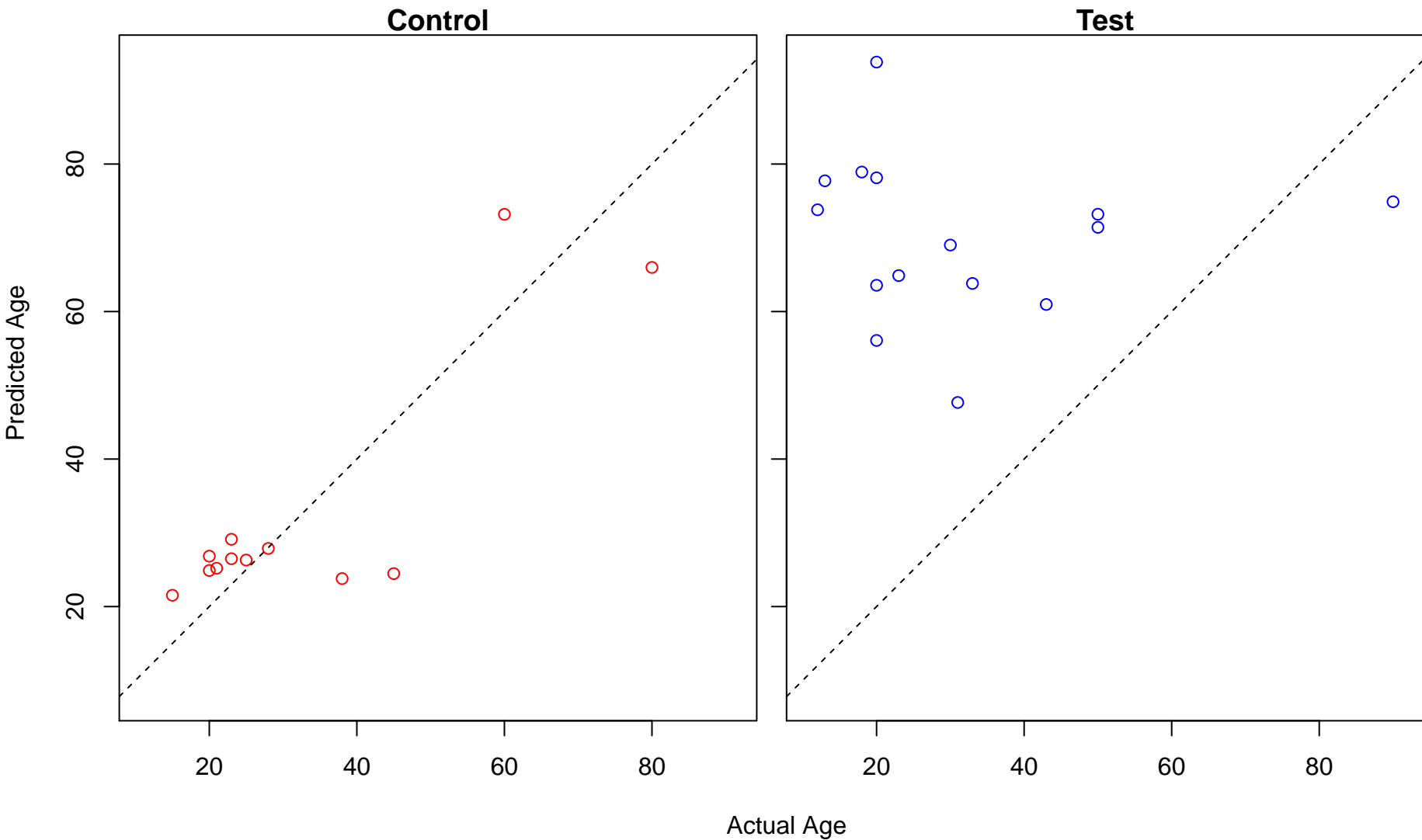
misfolded or incompletely synthesized protein catabolic process (Score: 6.794803)



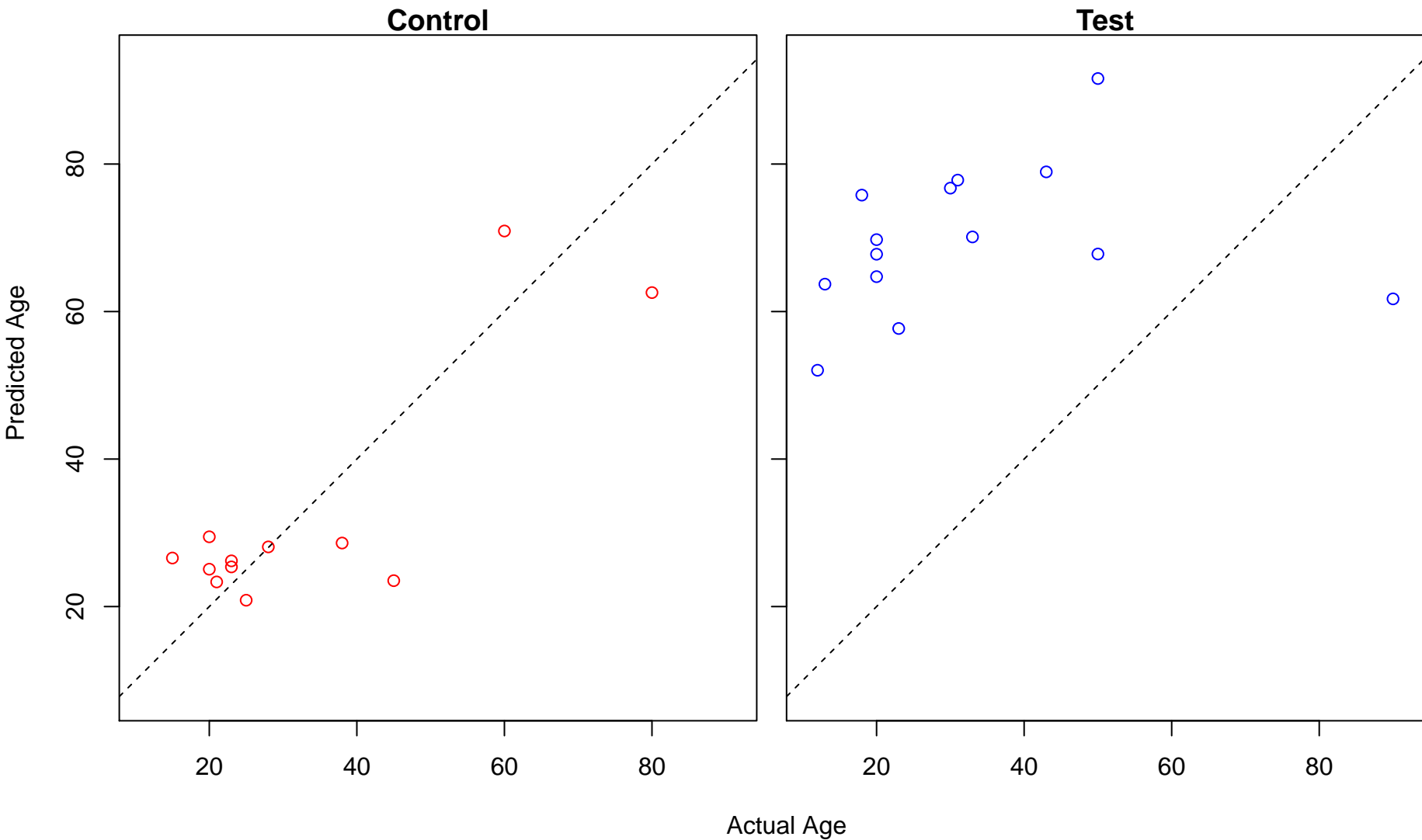
response to peptide (Score: 6.791392)



negative regulation of muscle cell apoptotic process (Score: 6.790755)

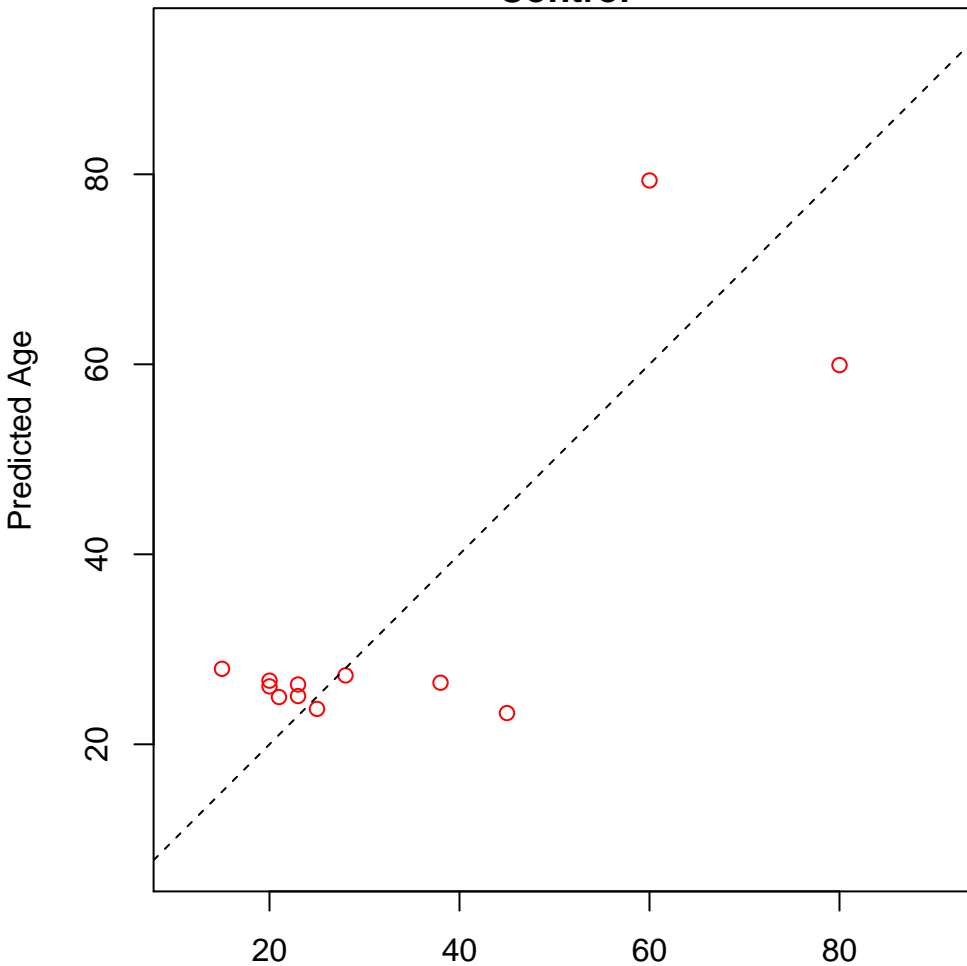


keratan sulfate biosynthetic process (Score: 6.789782)

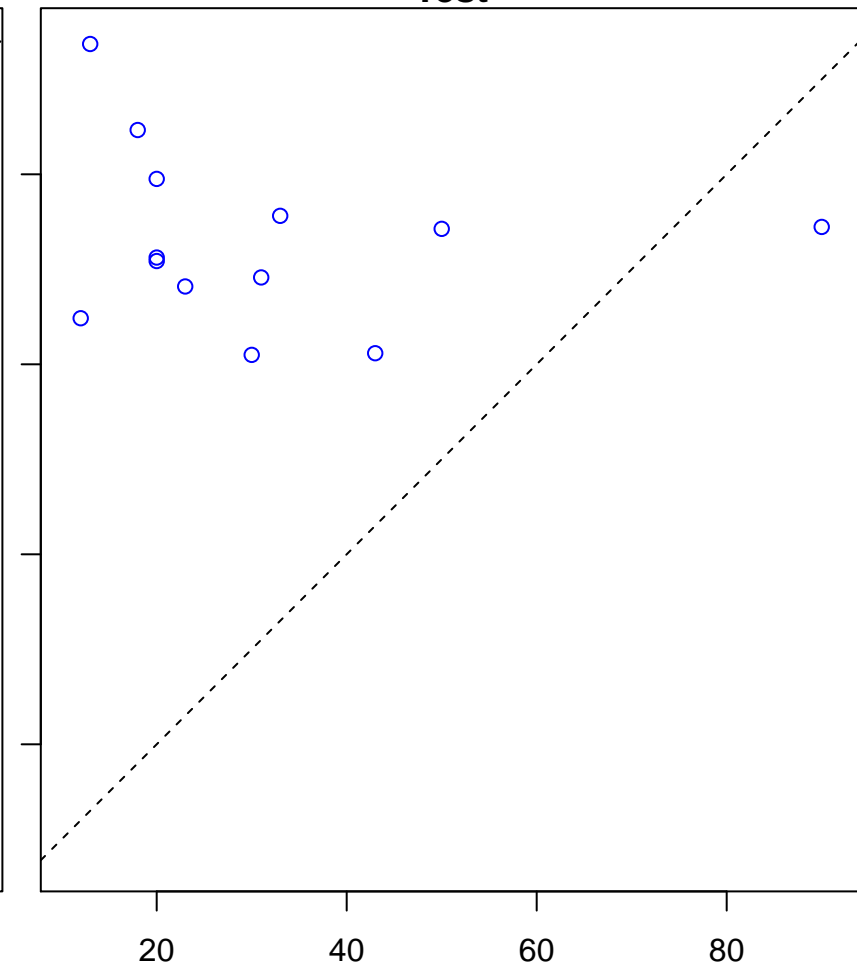


nucleotide-excision repair, DNA incision (Score: 6.789121)

Control

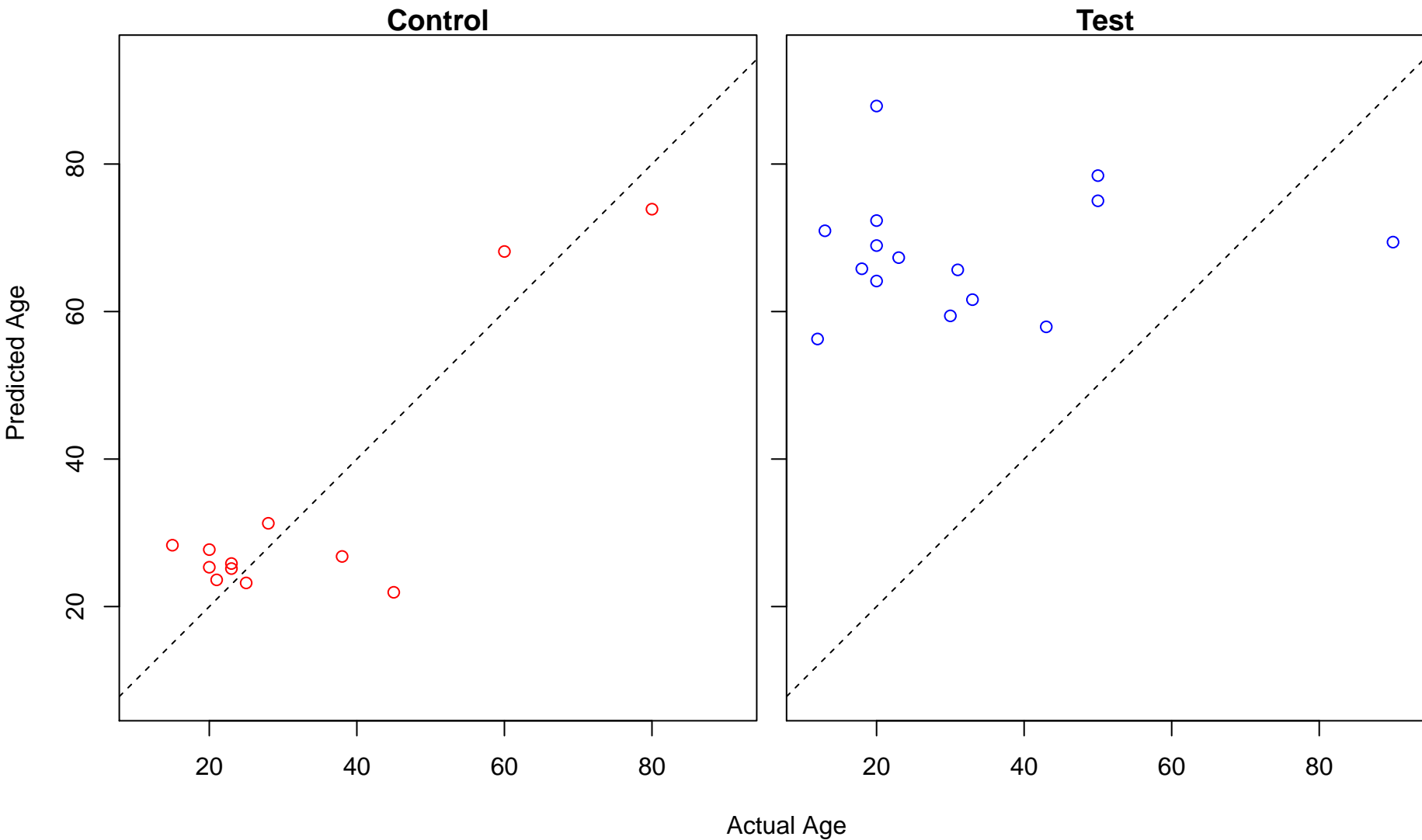


Test

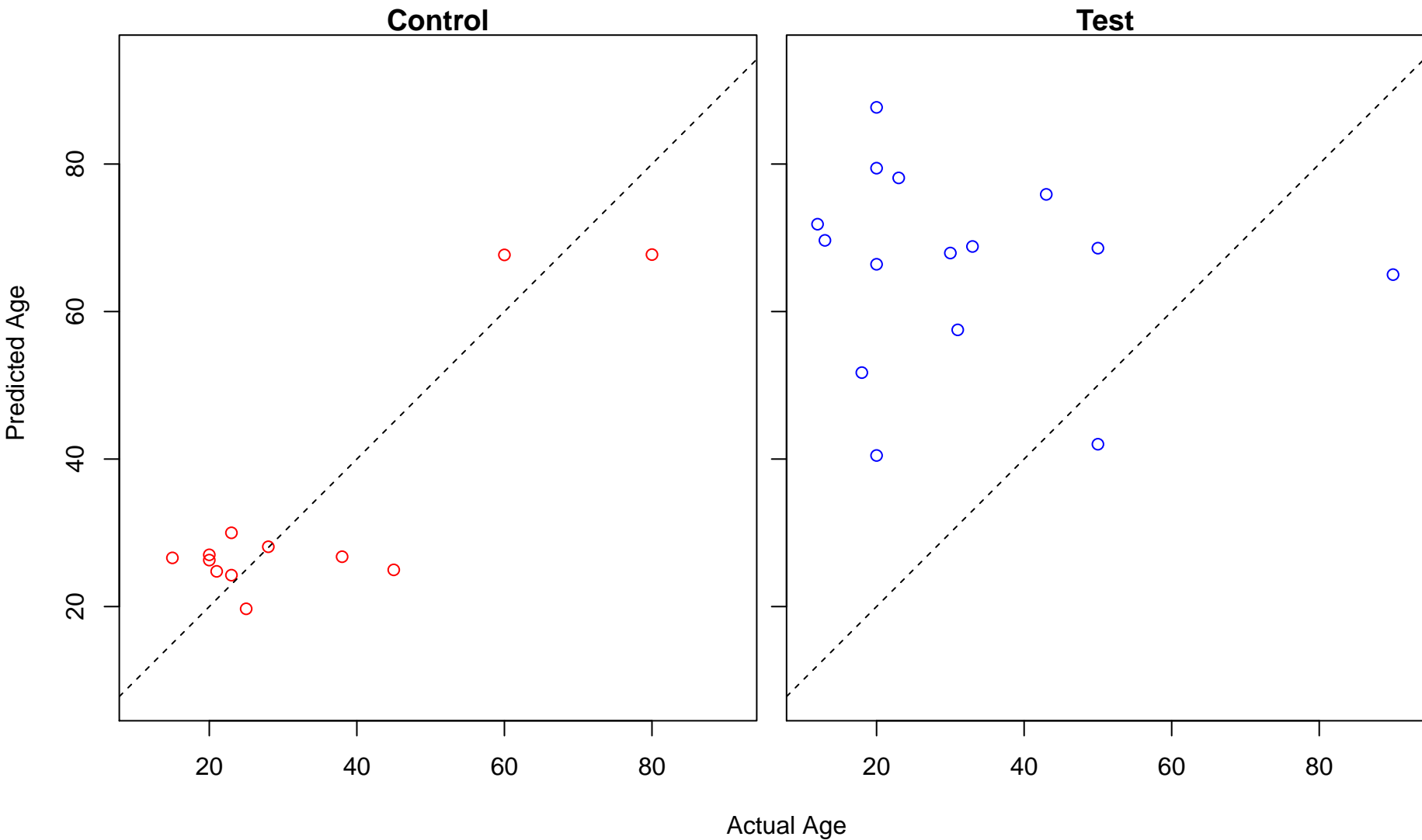


Actual Age

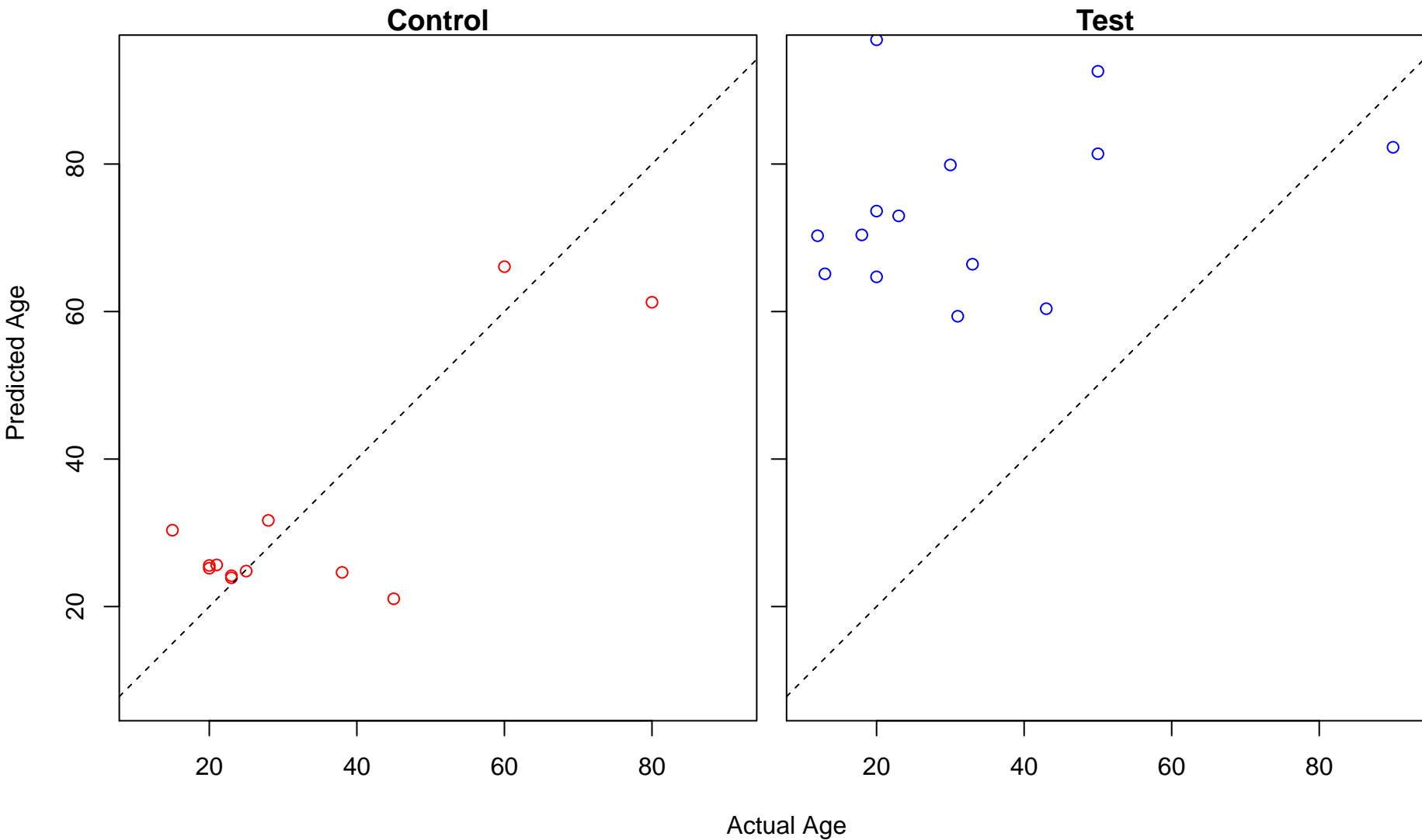
response to peptide hormone (Score: 6.786896)



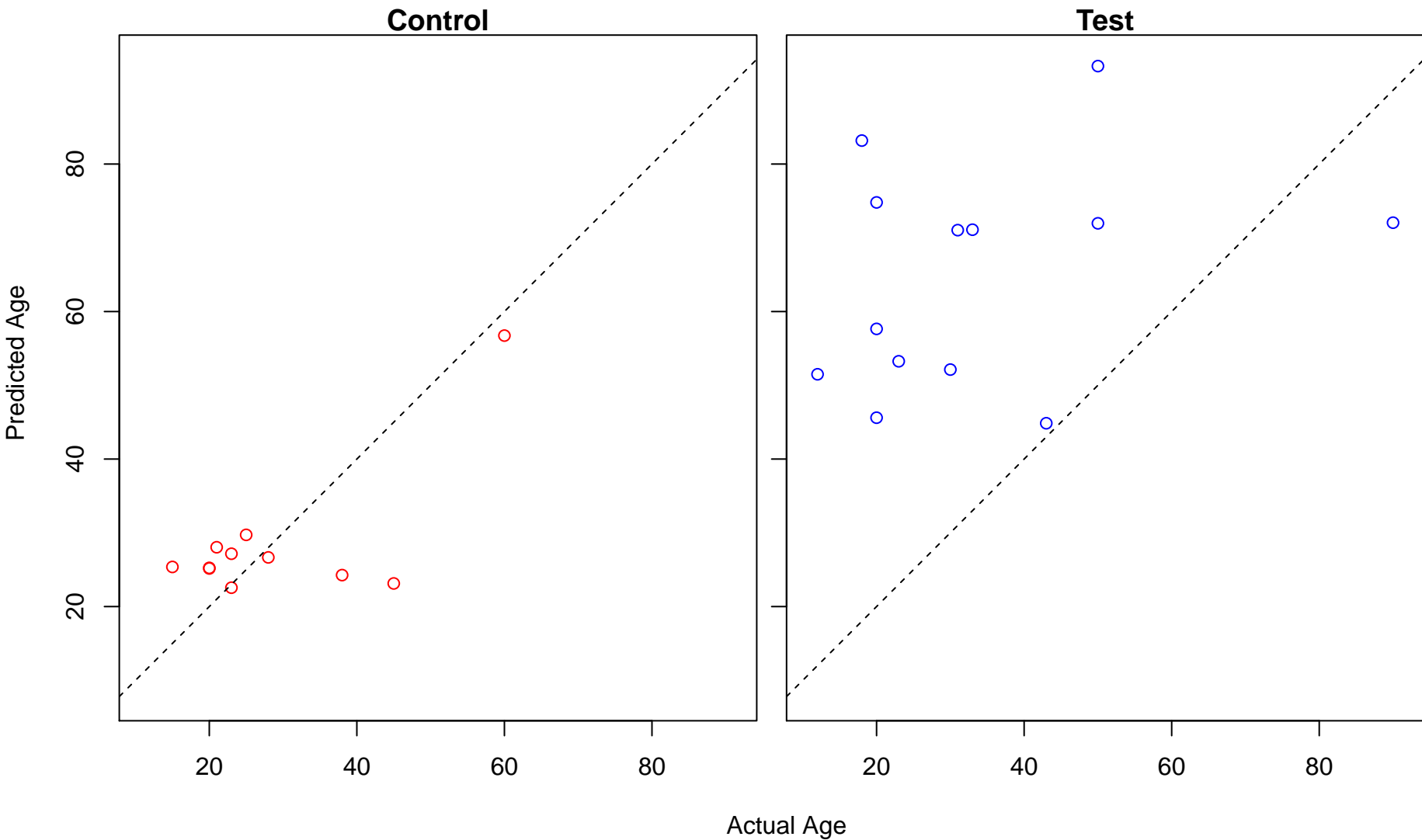
negative regulation of DNA binding (Score: 6.785997)



regulation of transcription from RNA polymerase I promoter (Score: 6.785532)

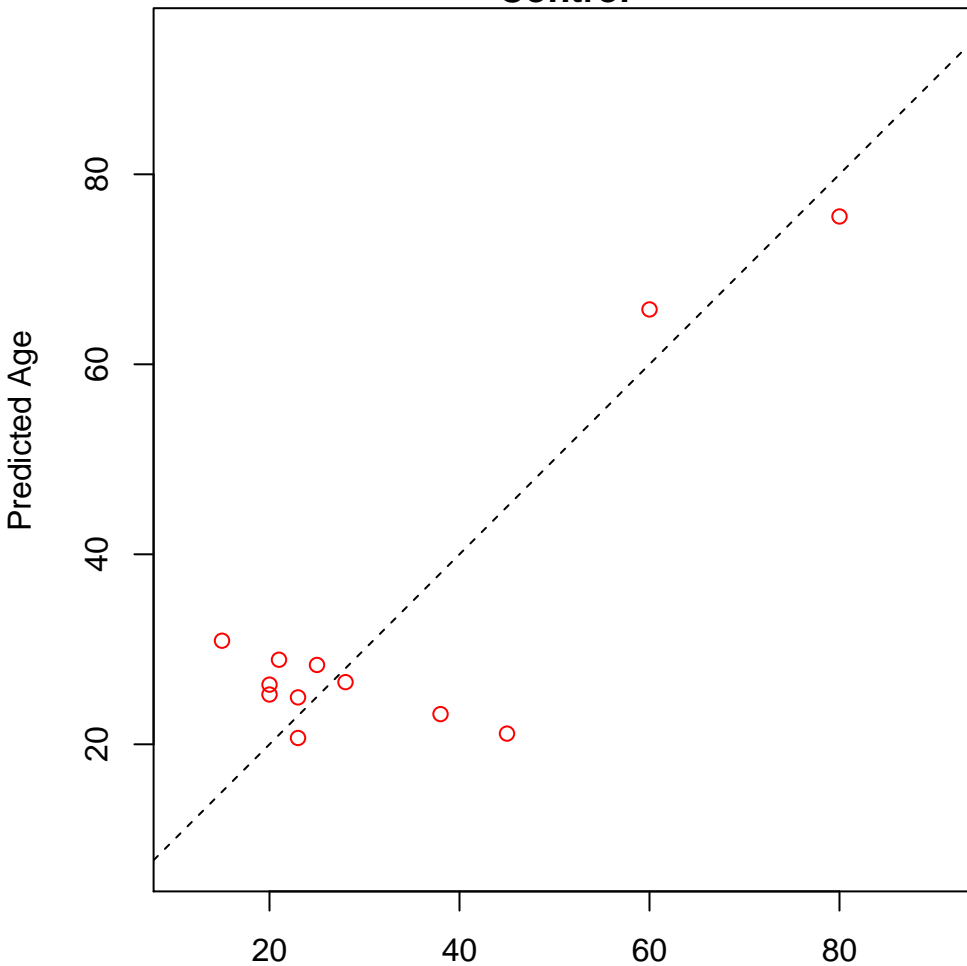


regulation of intrinsic apoptotic signaling pathway in response to DNA damage (Score: 6.781672)

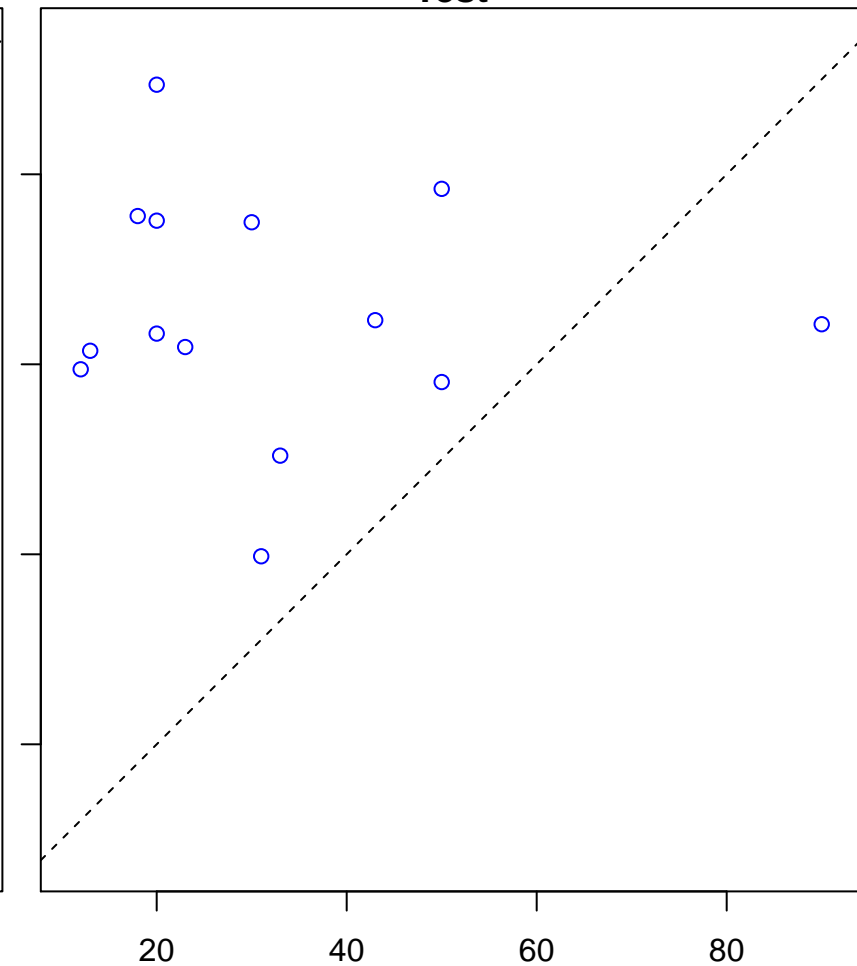


regulation of receptor catabolic process (Score: 6.781412)

Control

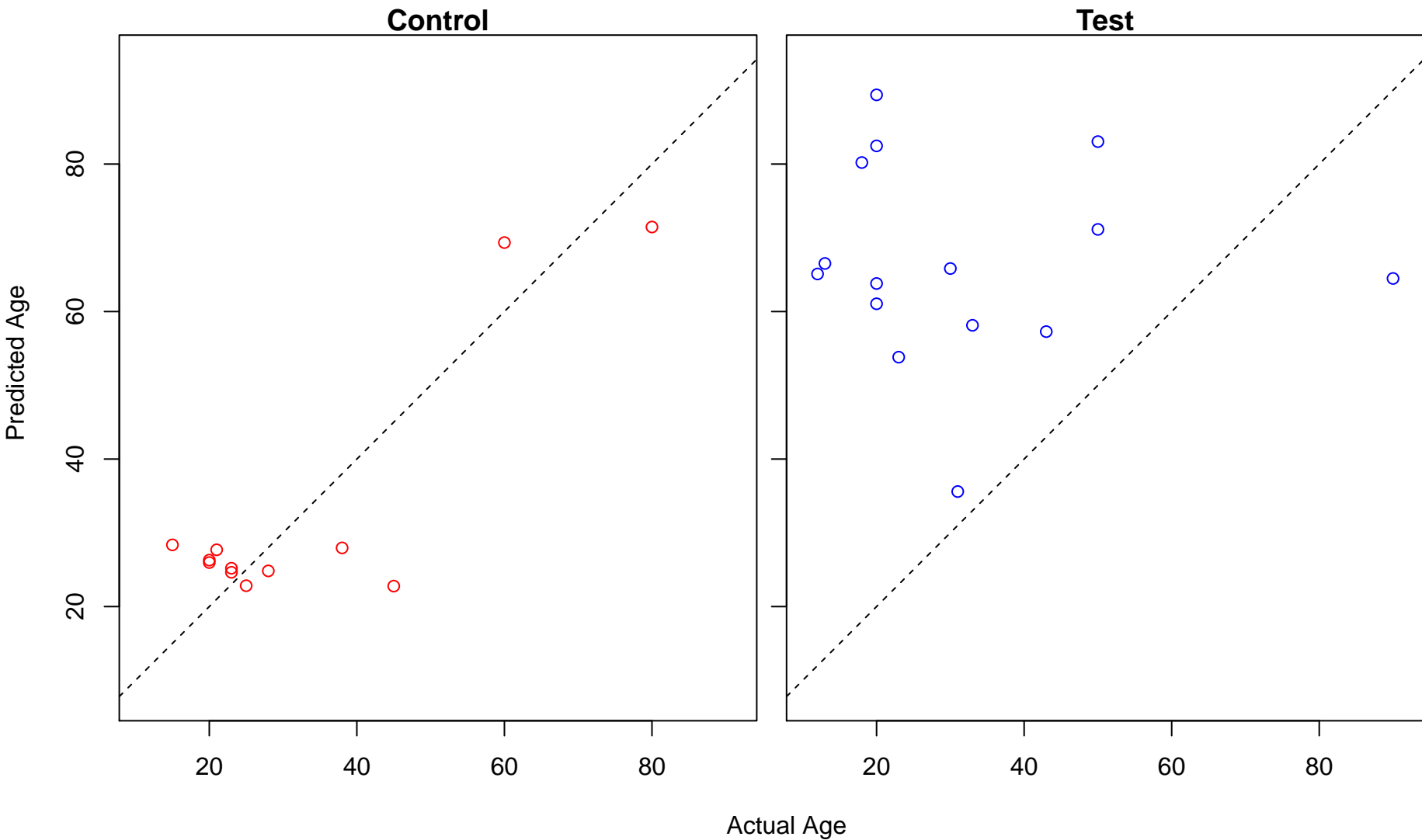


Test

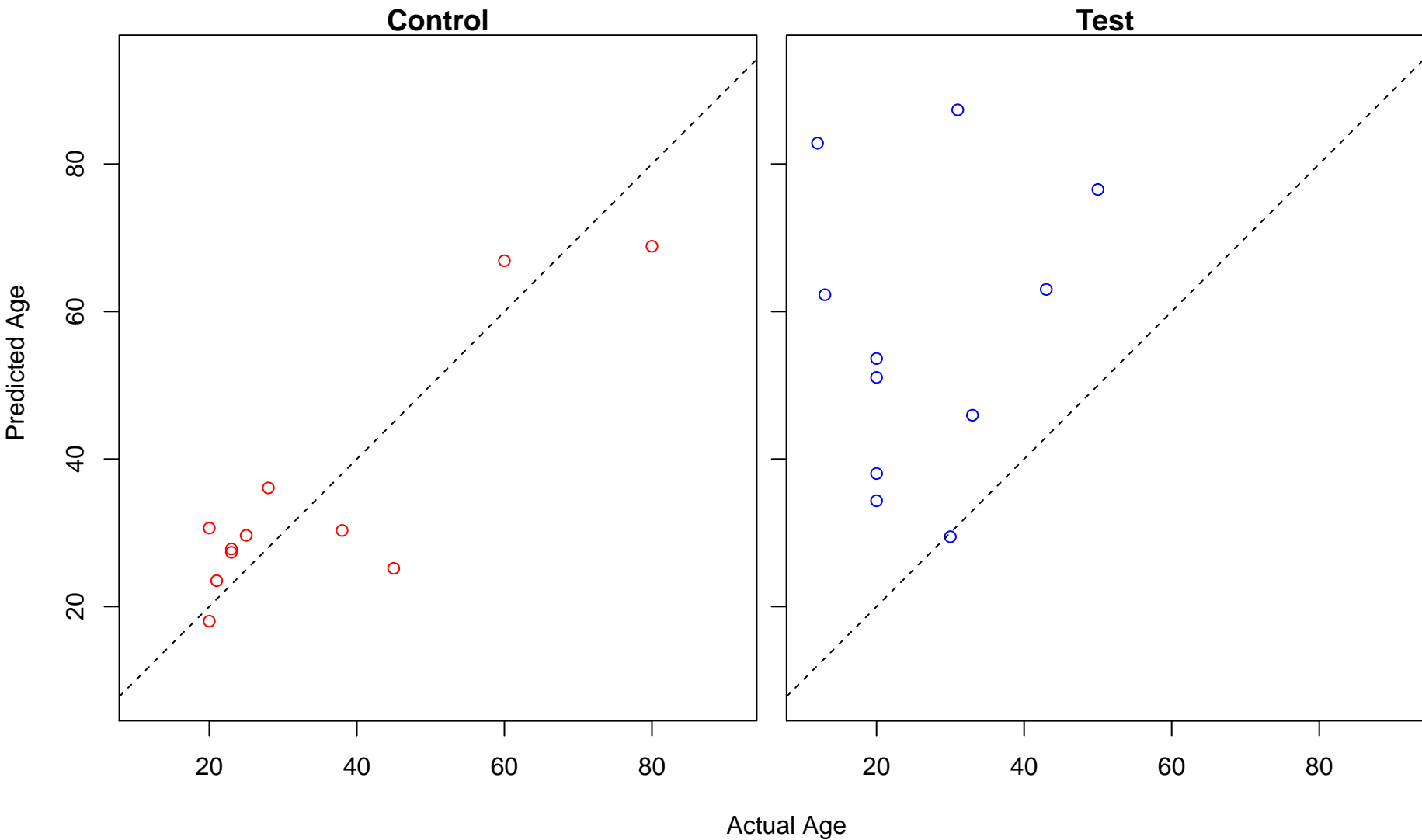


Actual Age

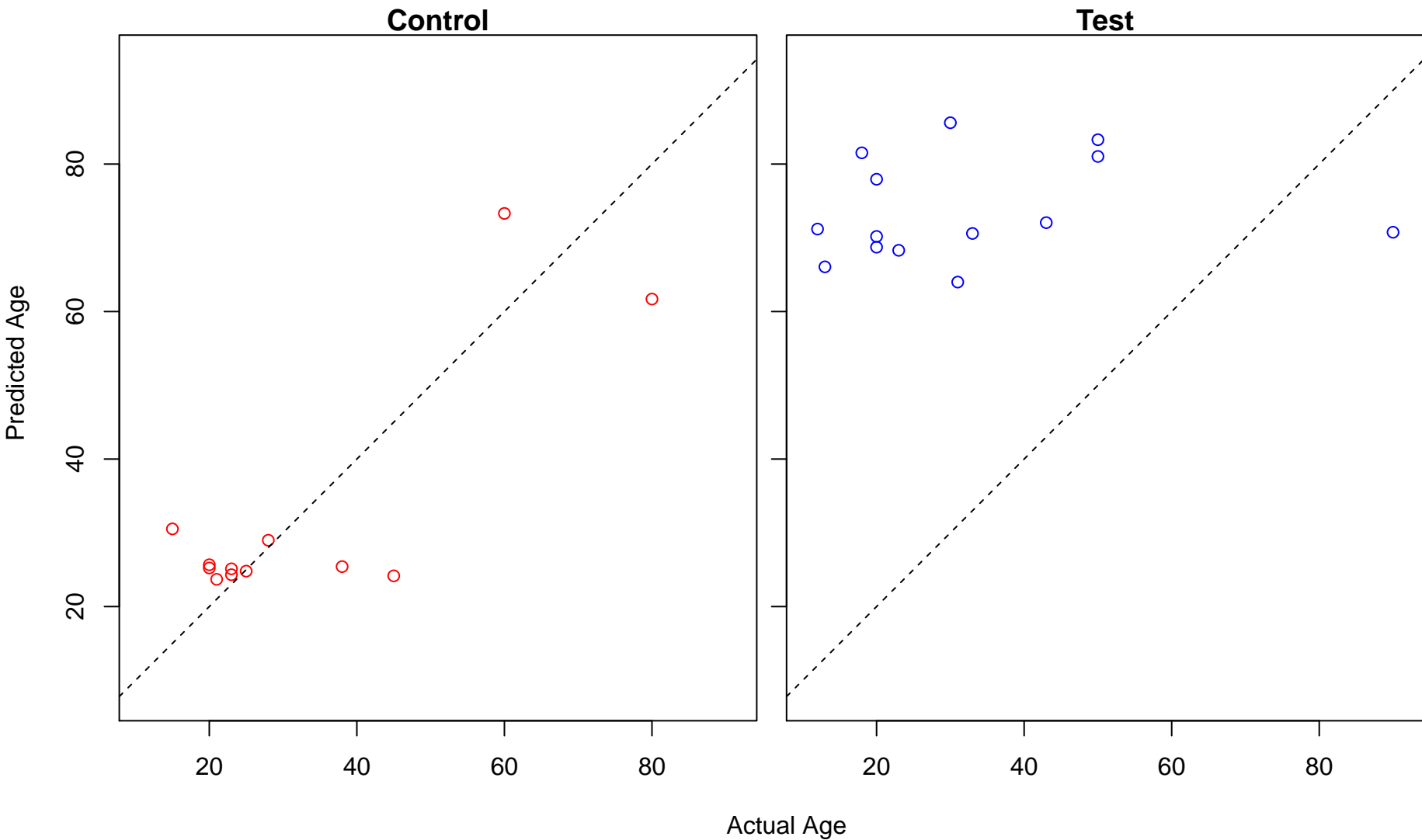
positive regulation of programmed cell death (Score: 6.779653)



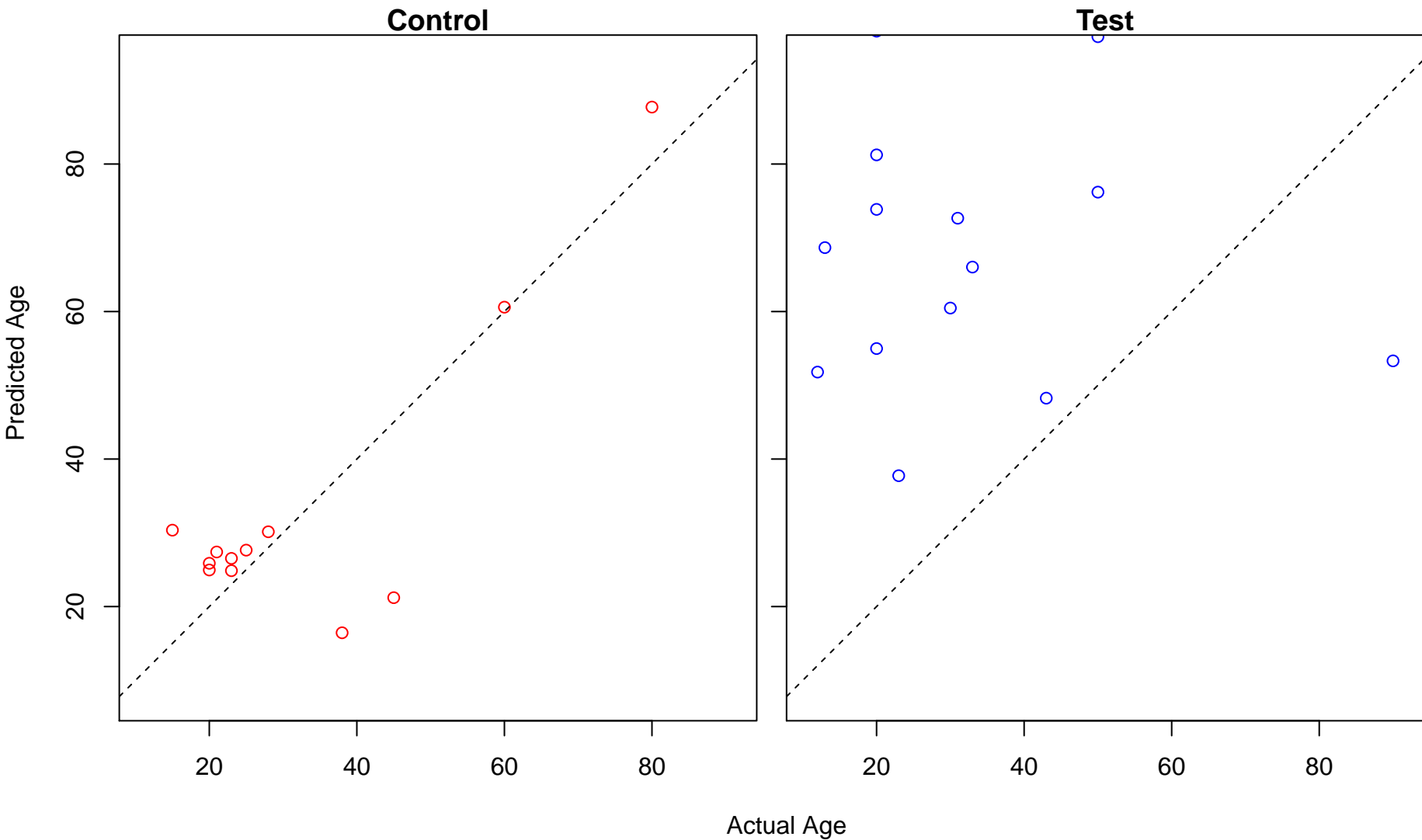
negative regulation of tumor necrosis factor–mediated signaling pathway (Score: 6.778852)



carbohydrate phosphorylation (Score: 6.777451)

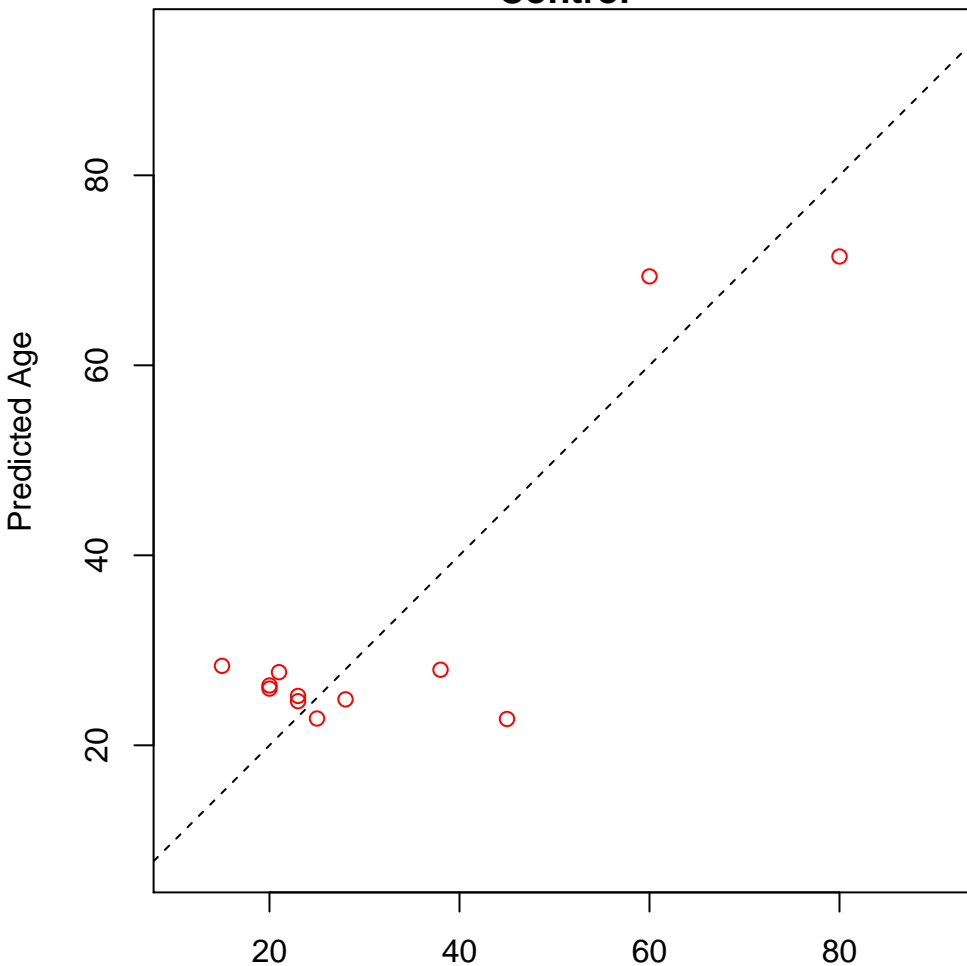


regulation of integrin-mediated signaling pathway (Score: 6.777352)

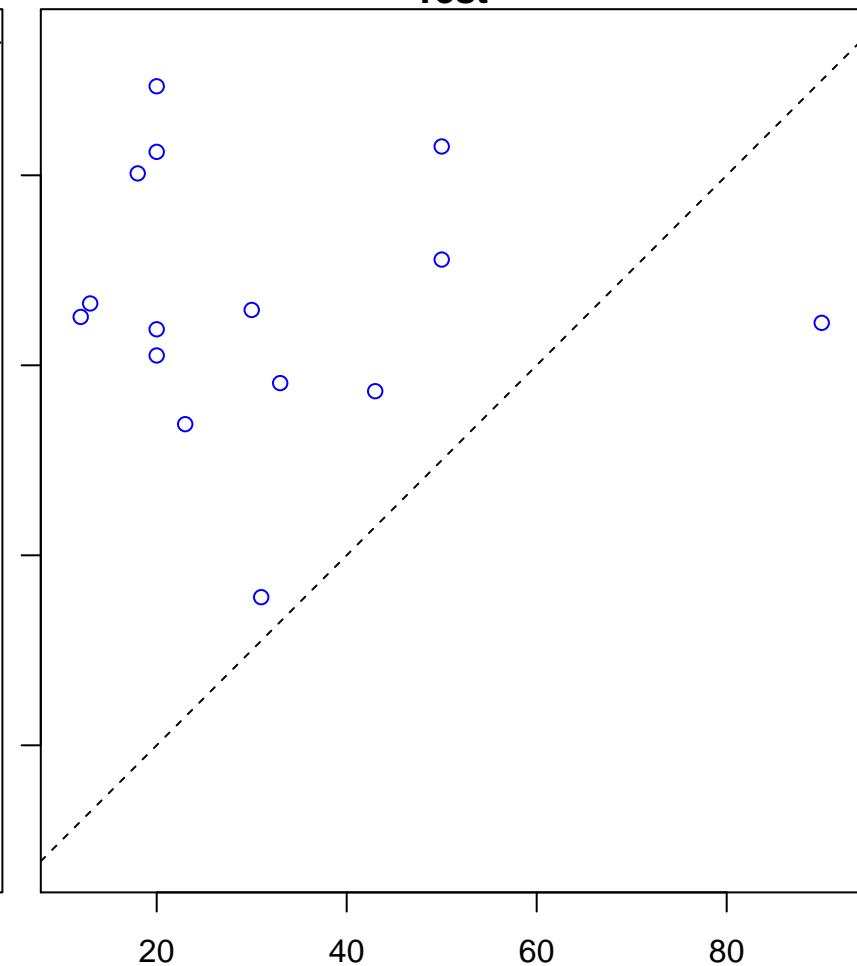


positive regulation of apoptotic process (Score: 6.776359)

Control

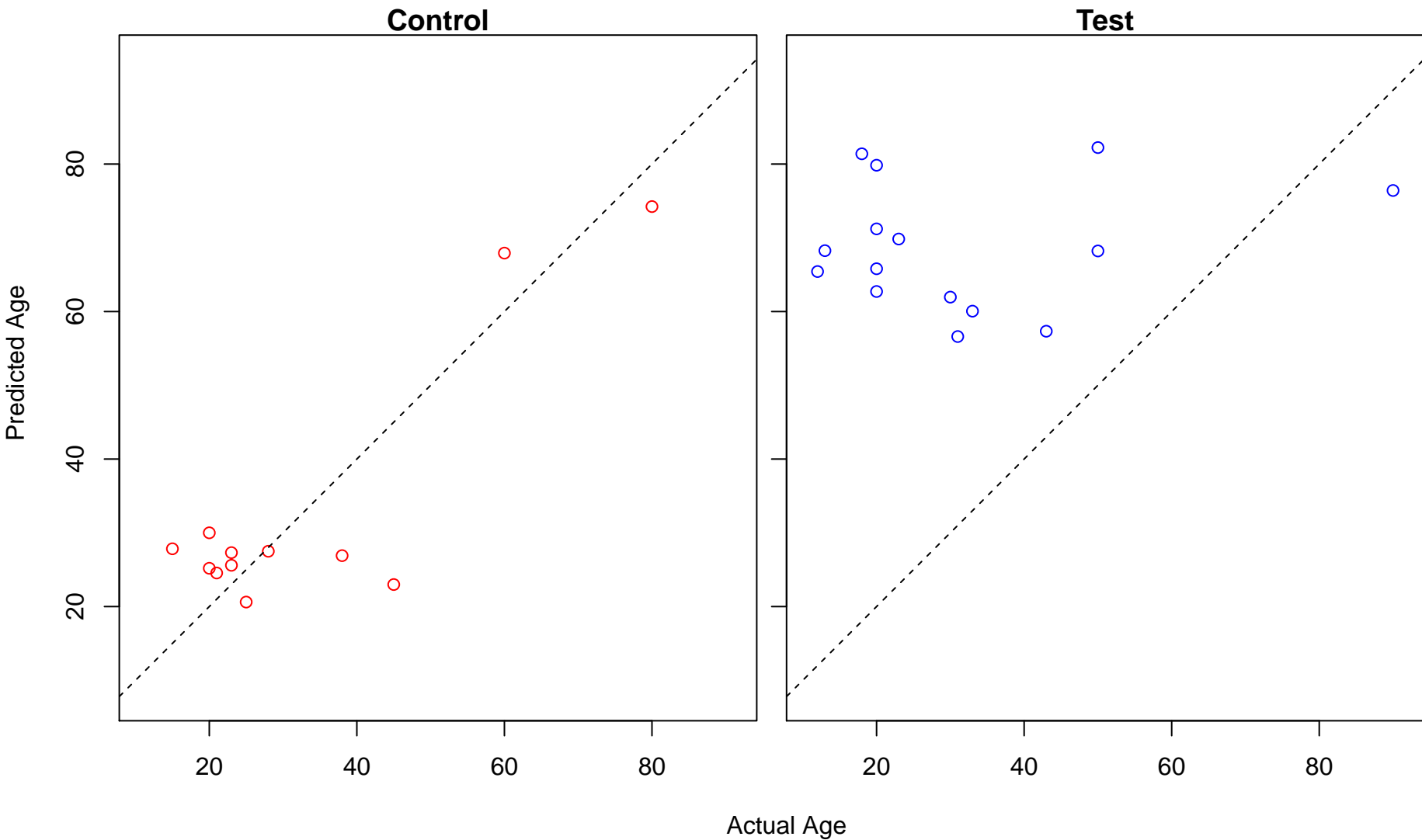


Test

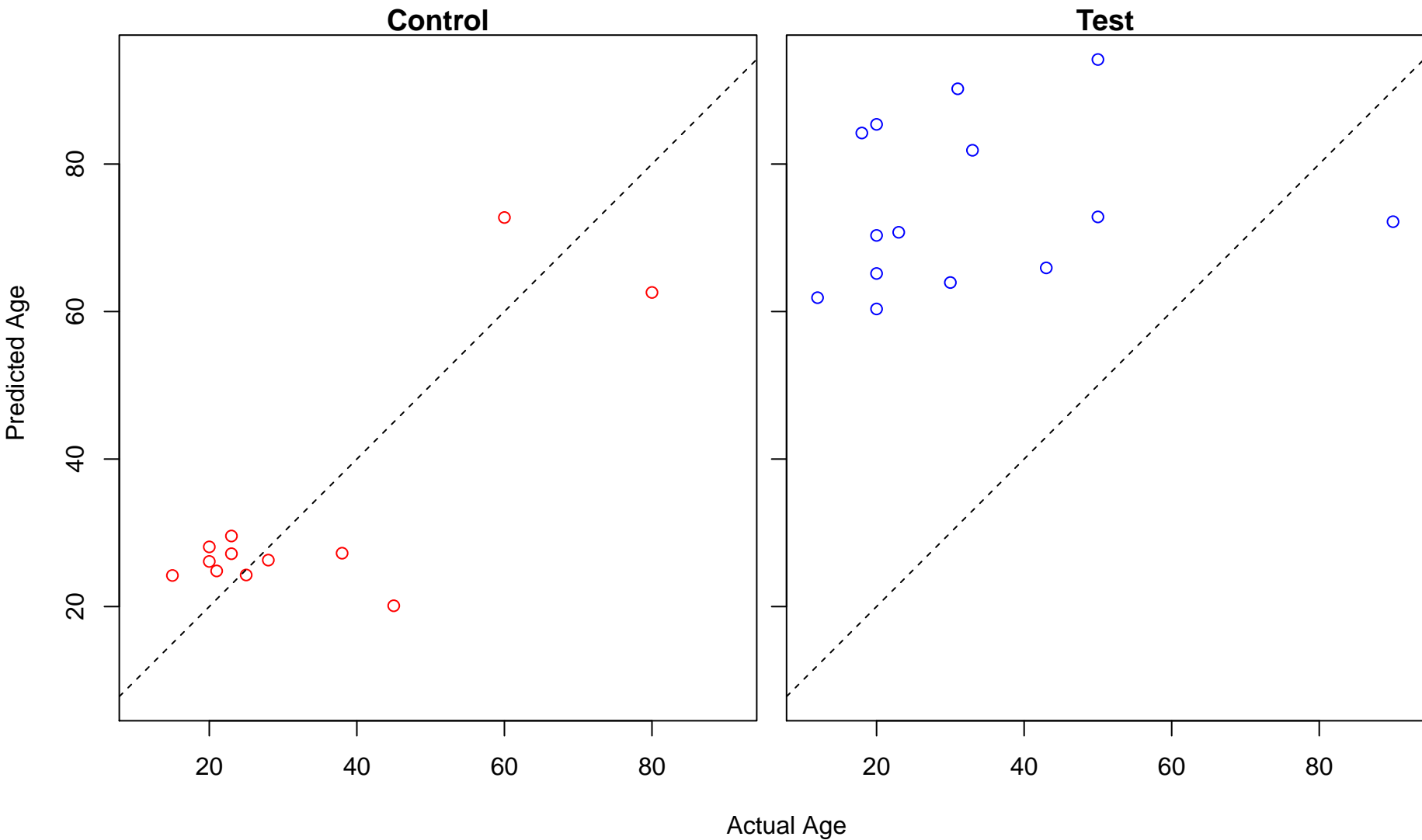


Actual Age

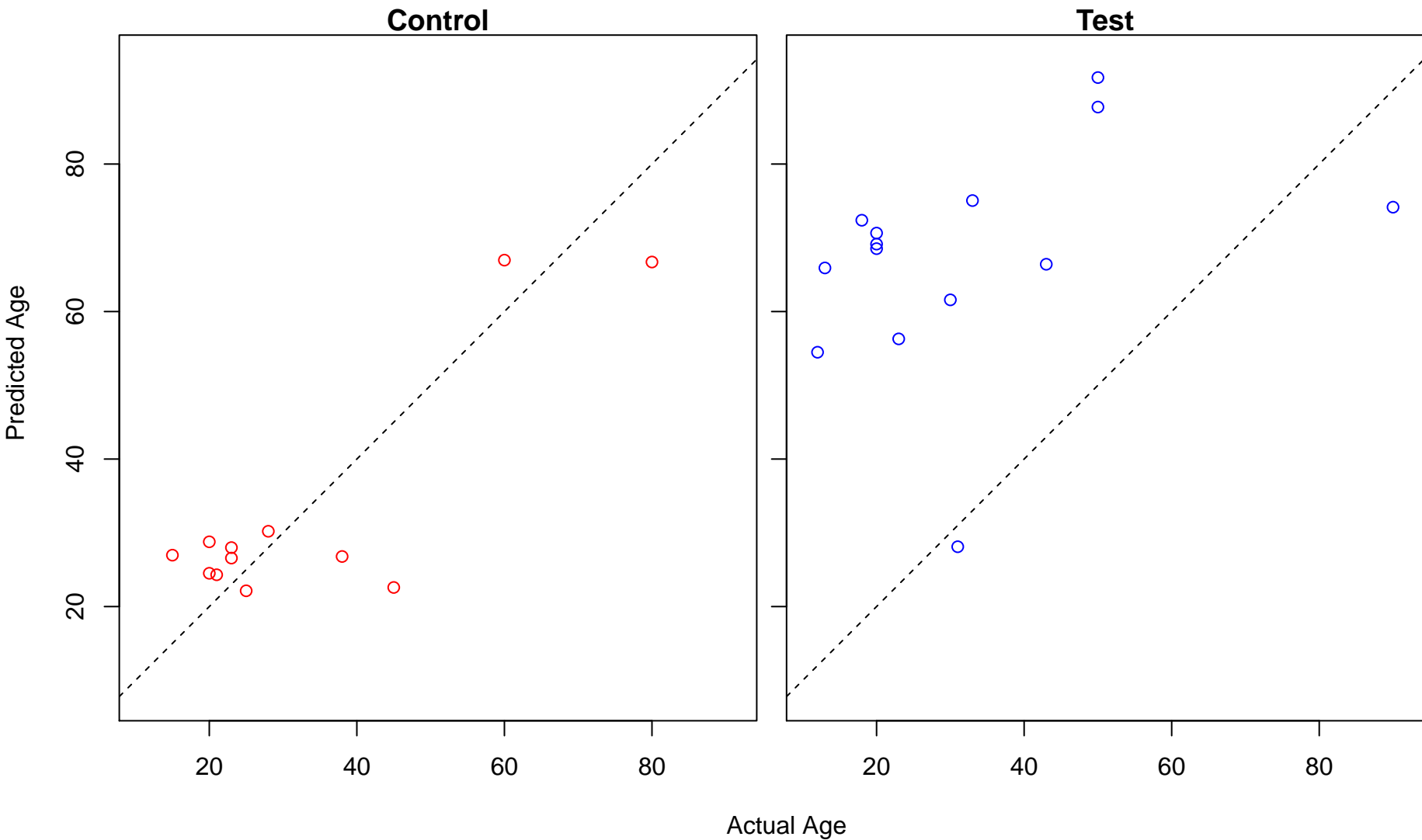
regulation of MAP kinase activity (Score: 6.774685)



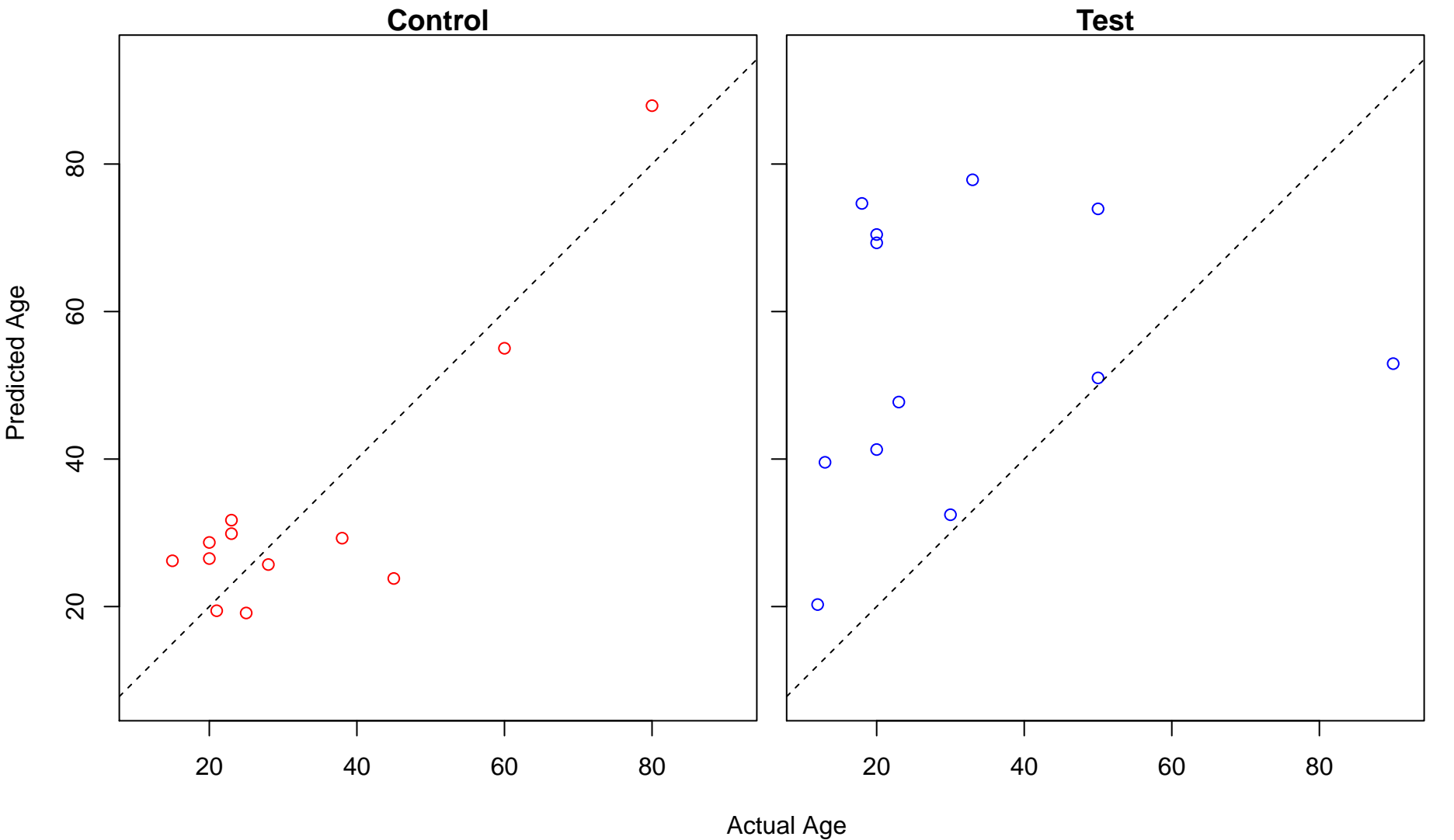
positive regulation of T cell cytokine production (Score: 6.772187)



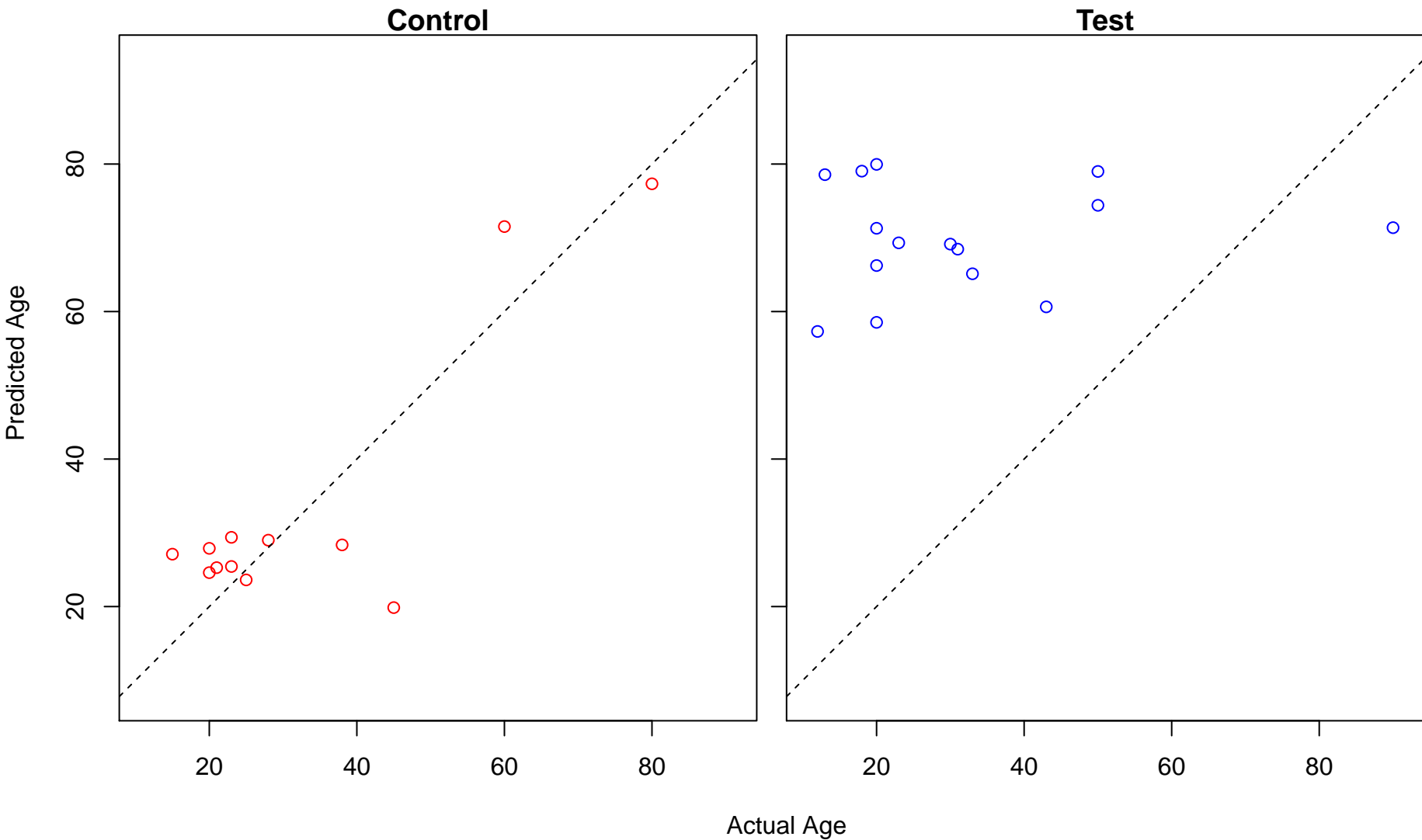
cell chemotaxis (Score: 6.771745)



of T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting c

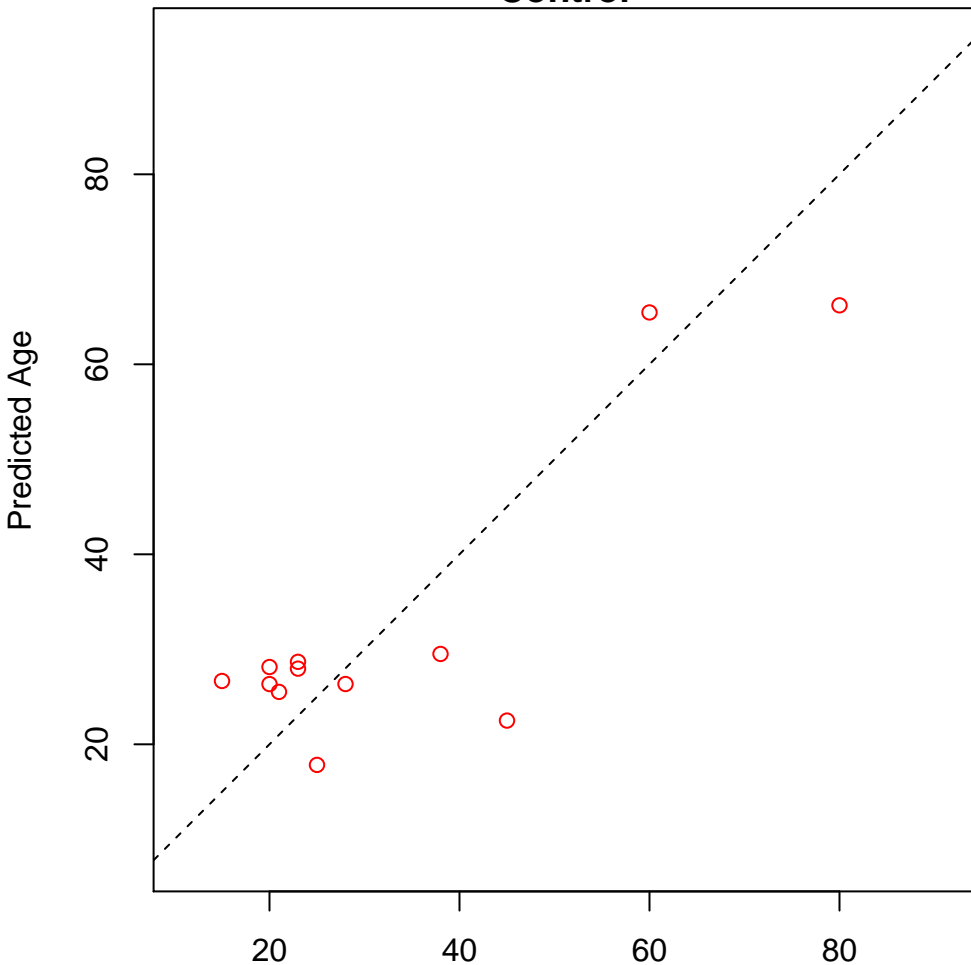


regulation of cytokine production (Score: 6.767558)

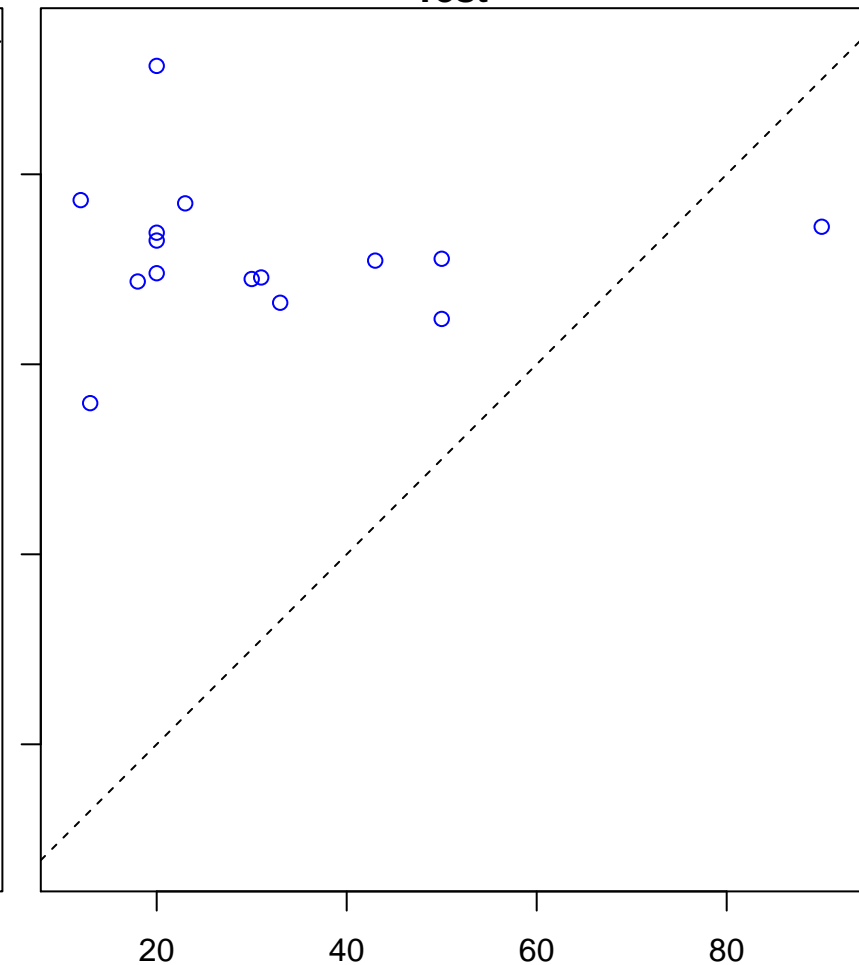


glycosaminoglycan metabolic process (Score: 6.766465)

Control

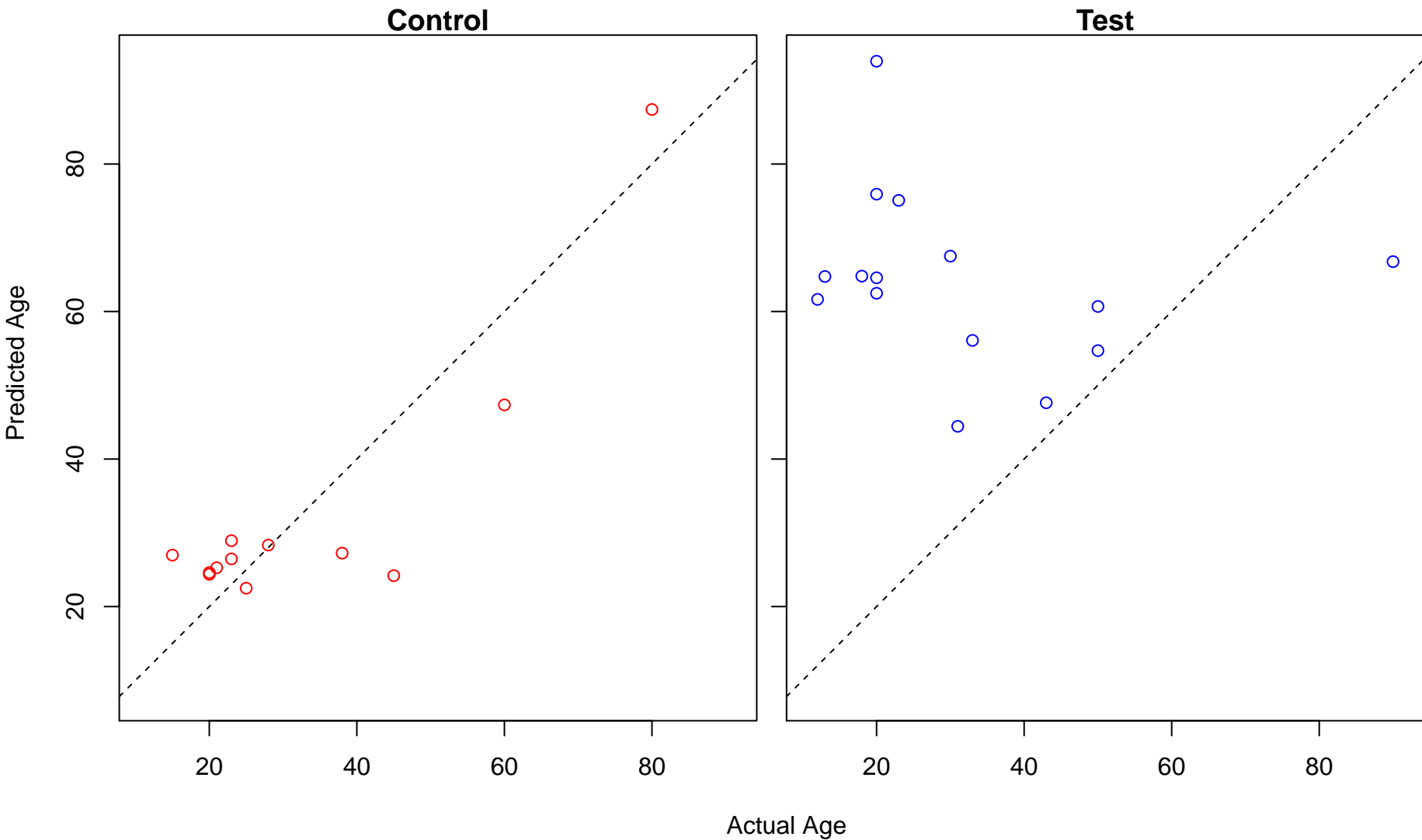


Test

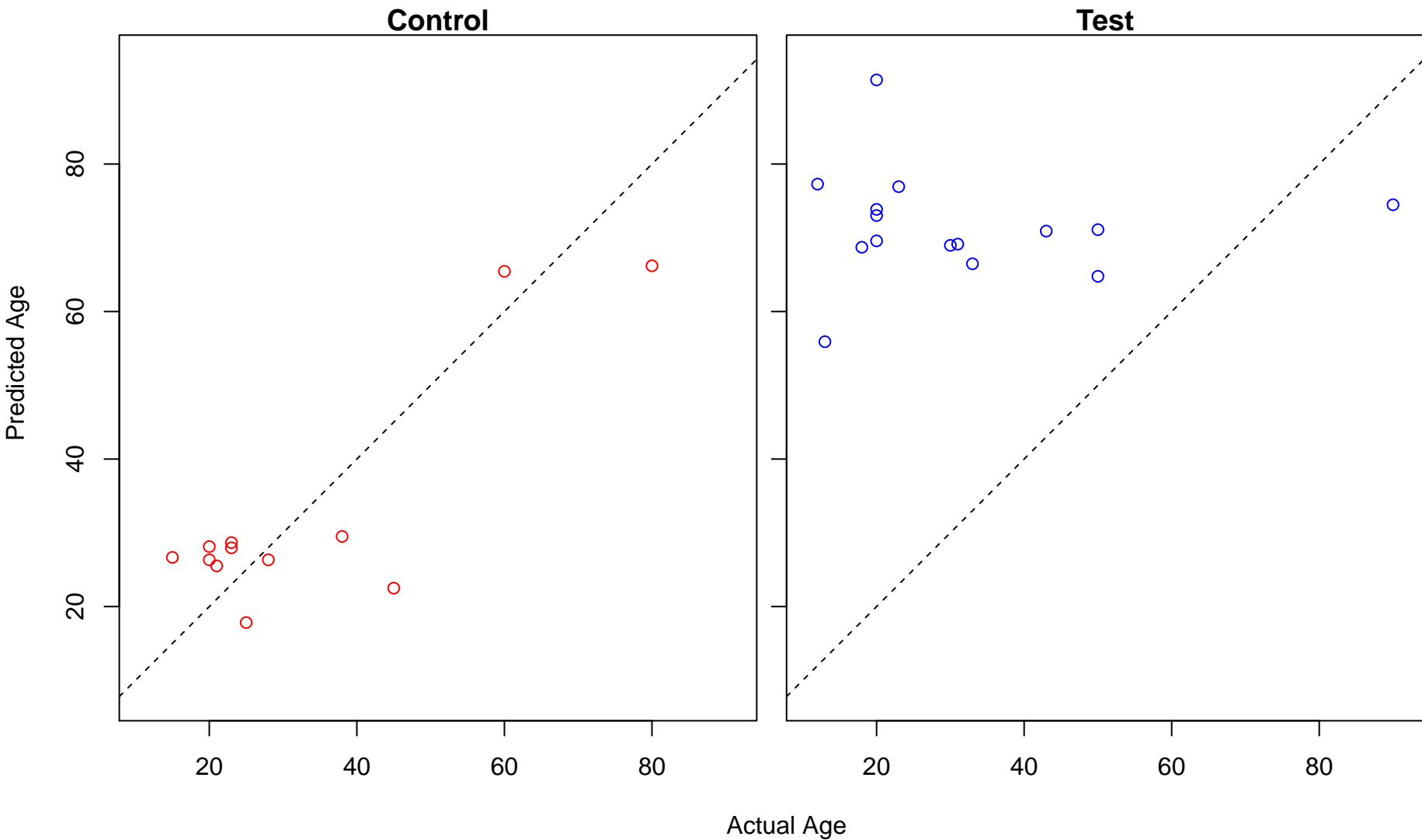


Actual Age

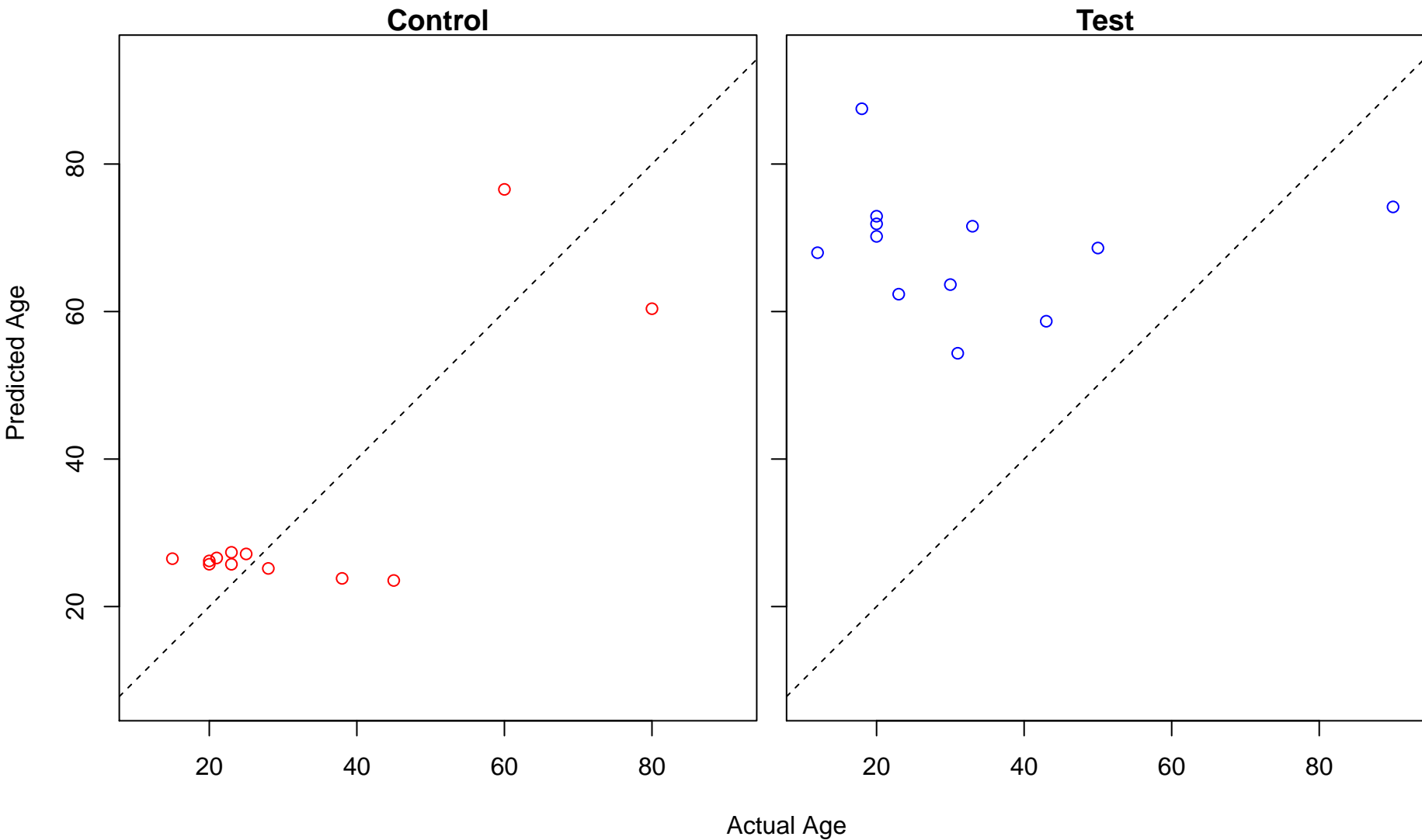
regulation of cellular amine metabolic process (Score: 6.766018)



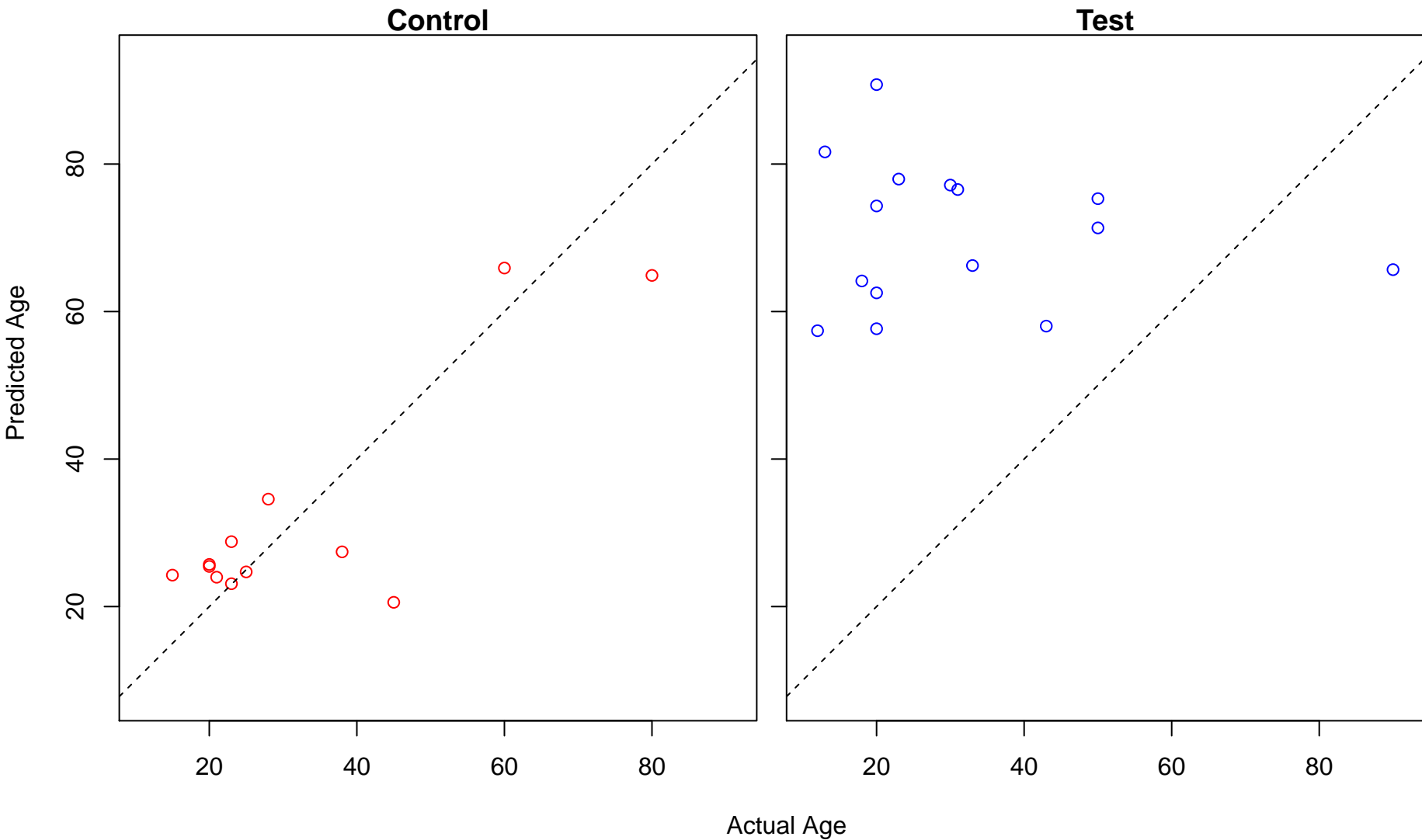
aminoglycan metabolic process (Score: 6.765249)



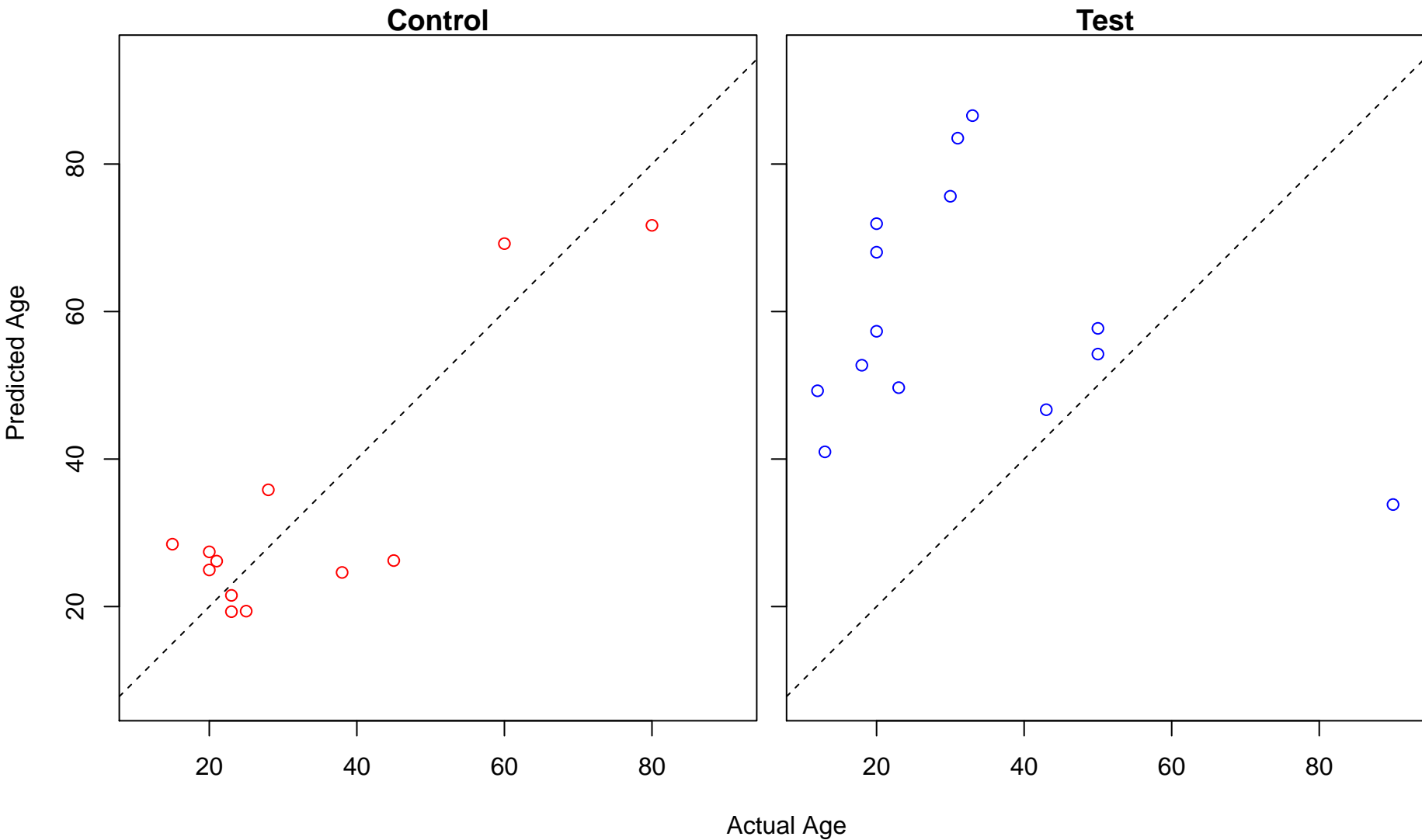
mRNA metabolic process (Score: 6.764772)



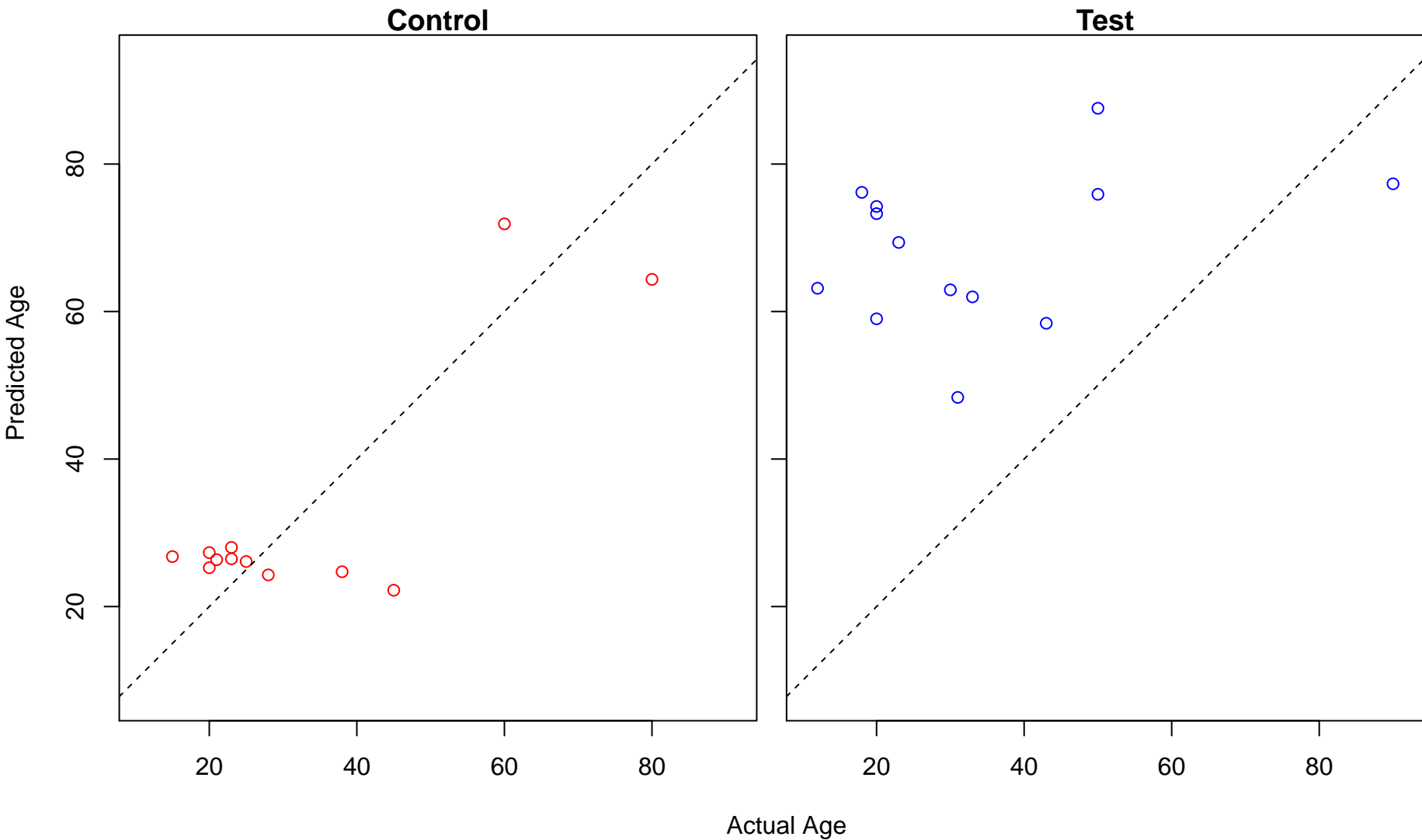
negative regulation of DNA damage response, signal transduction by p53 class mediator (Score: 6.764)



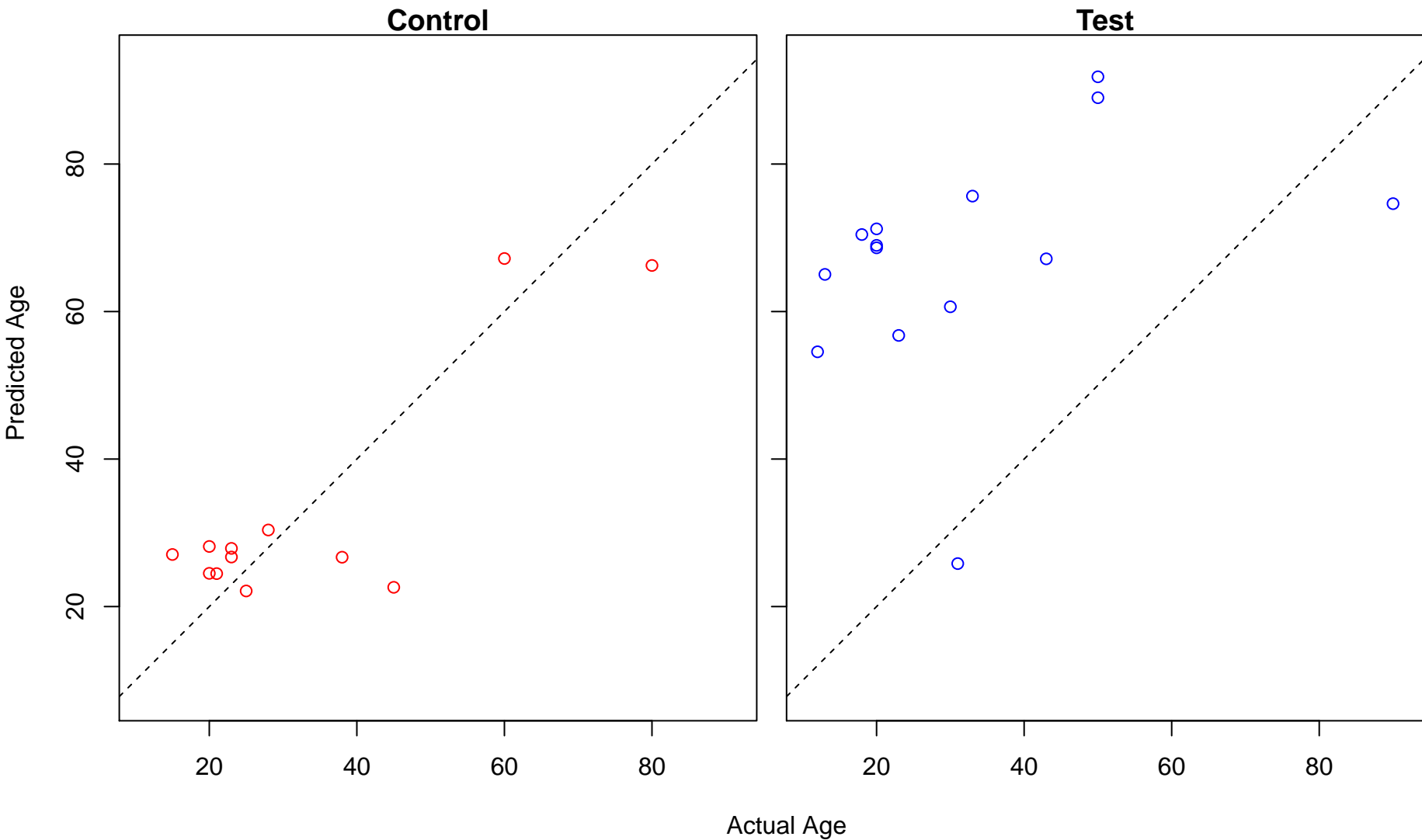
androgen receptor signaling pathway (Score: 6.759593)



negative regulation of translational initiation (Score: 6.756402)

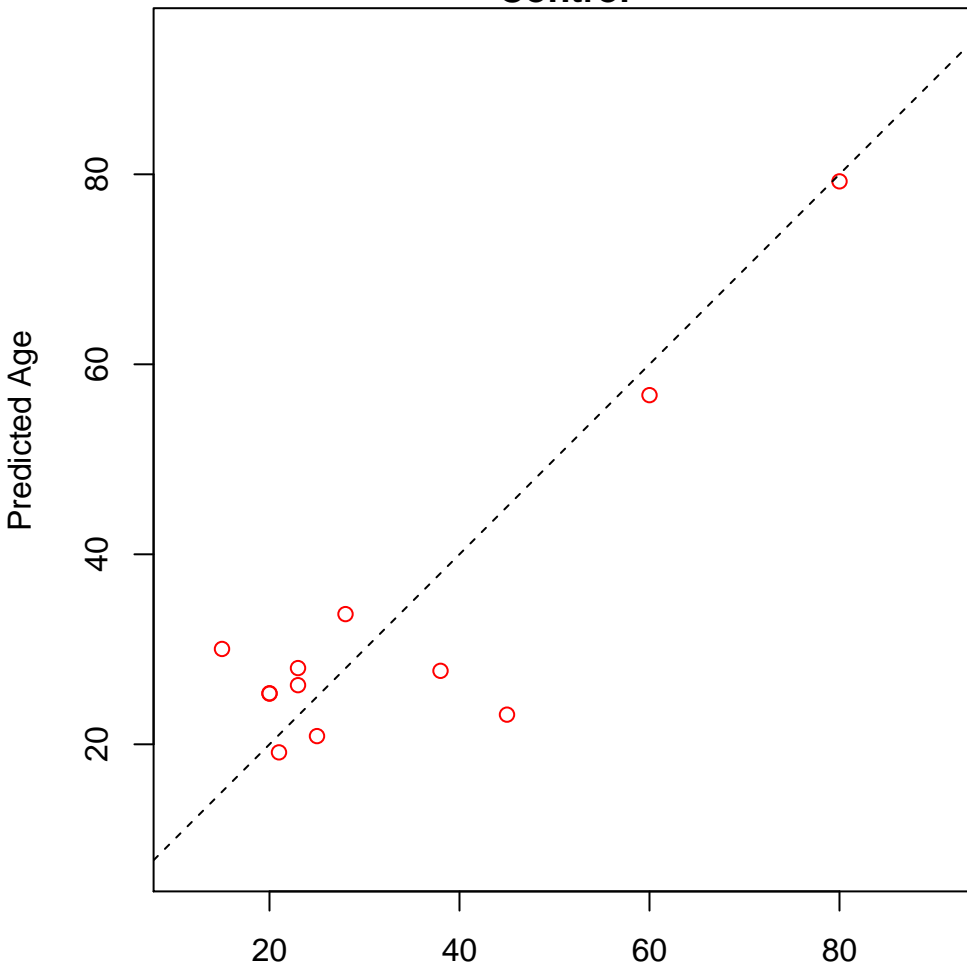


leukocyte chemotaxis (Score: 6.754907)

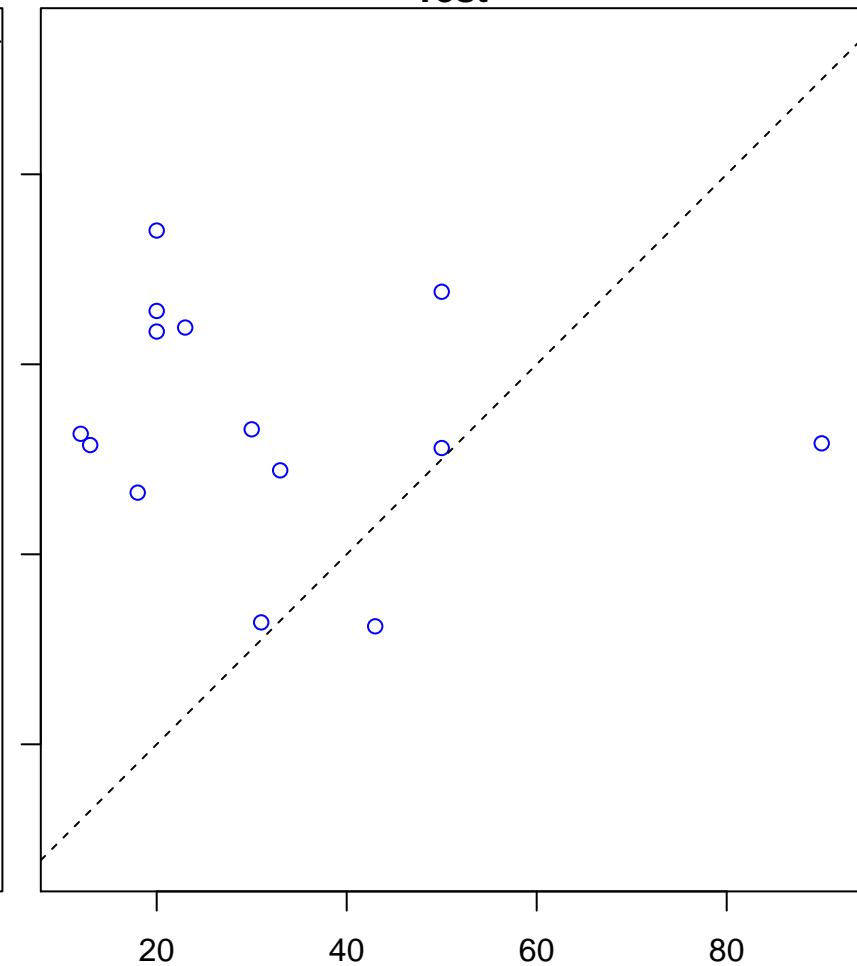


peripheral nervous system development (Score: 6.754587)

Control

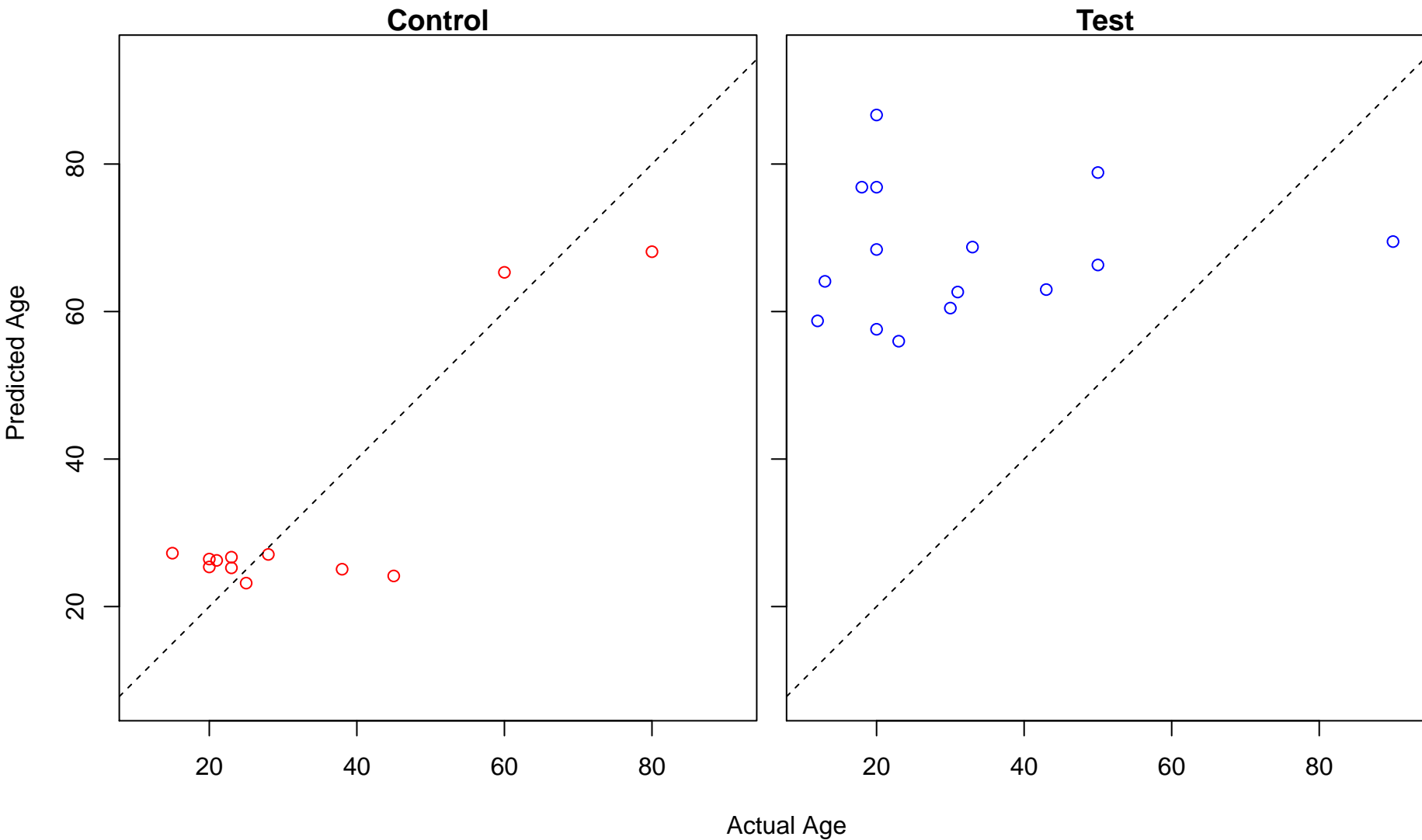


Test

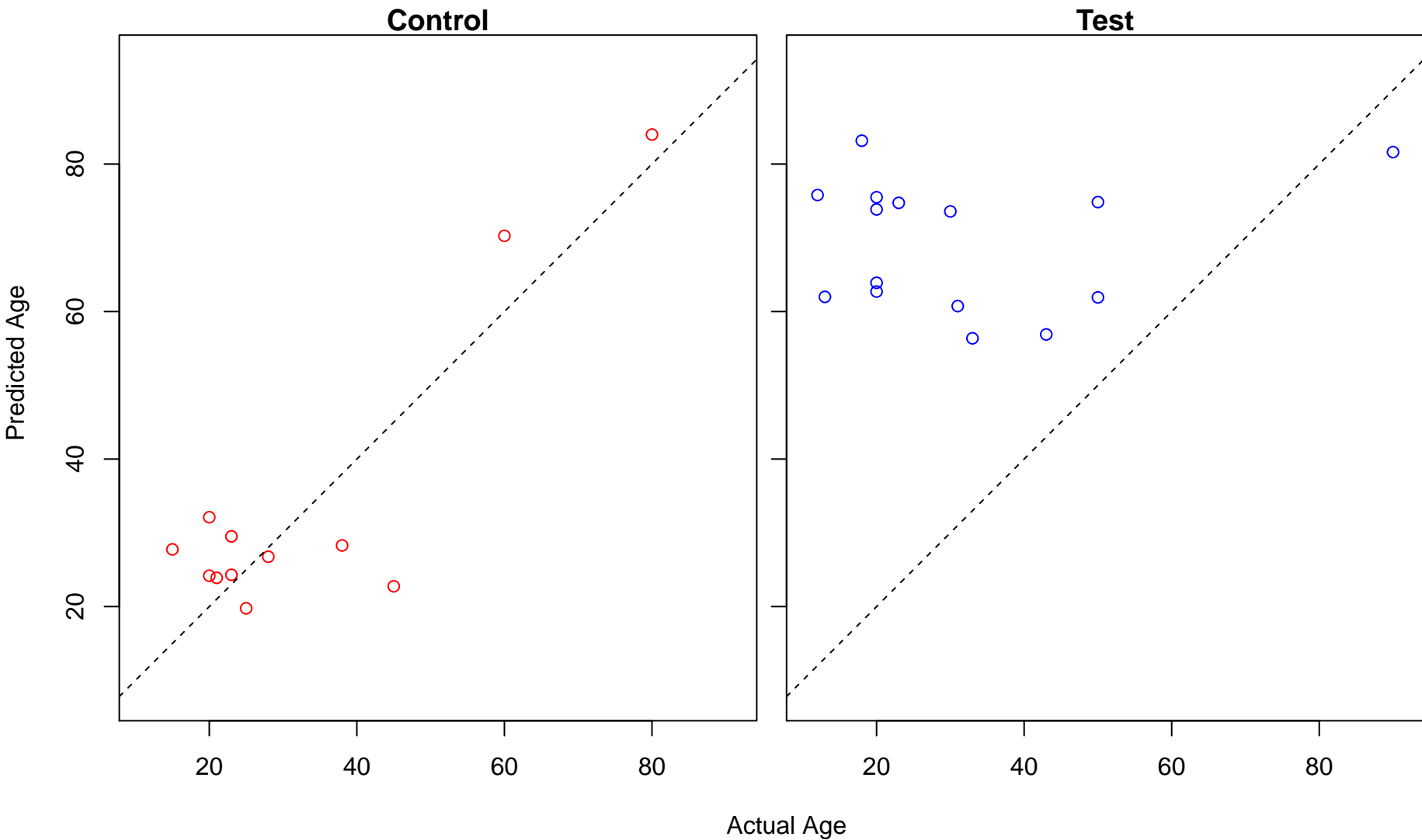


Actual Age

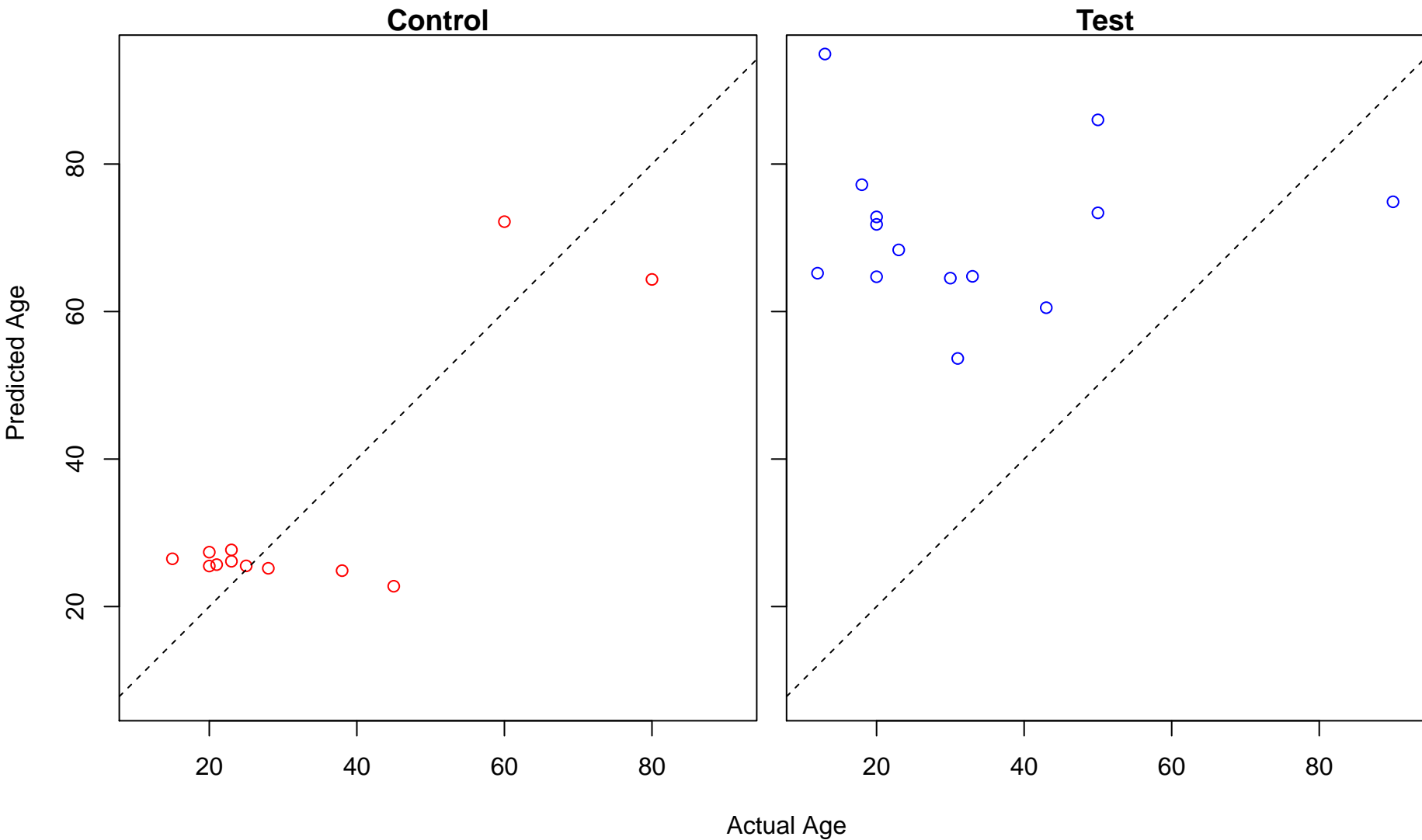
establishment or maintenance of cell polarity (Score: 6.751527)



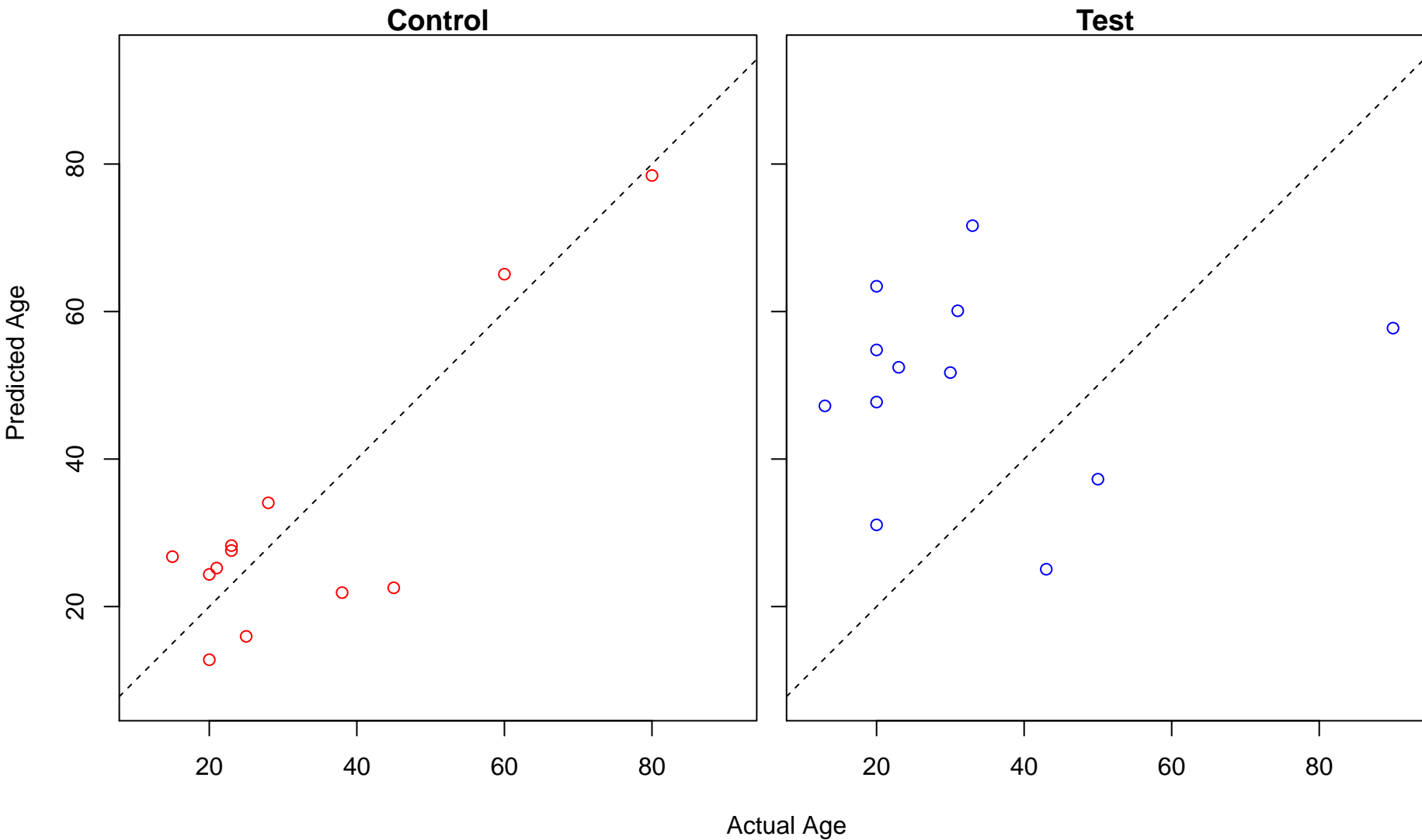
negative regulation of protein serine/threonine kinase activity (Score: 6.746030)



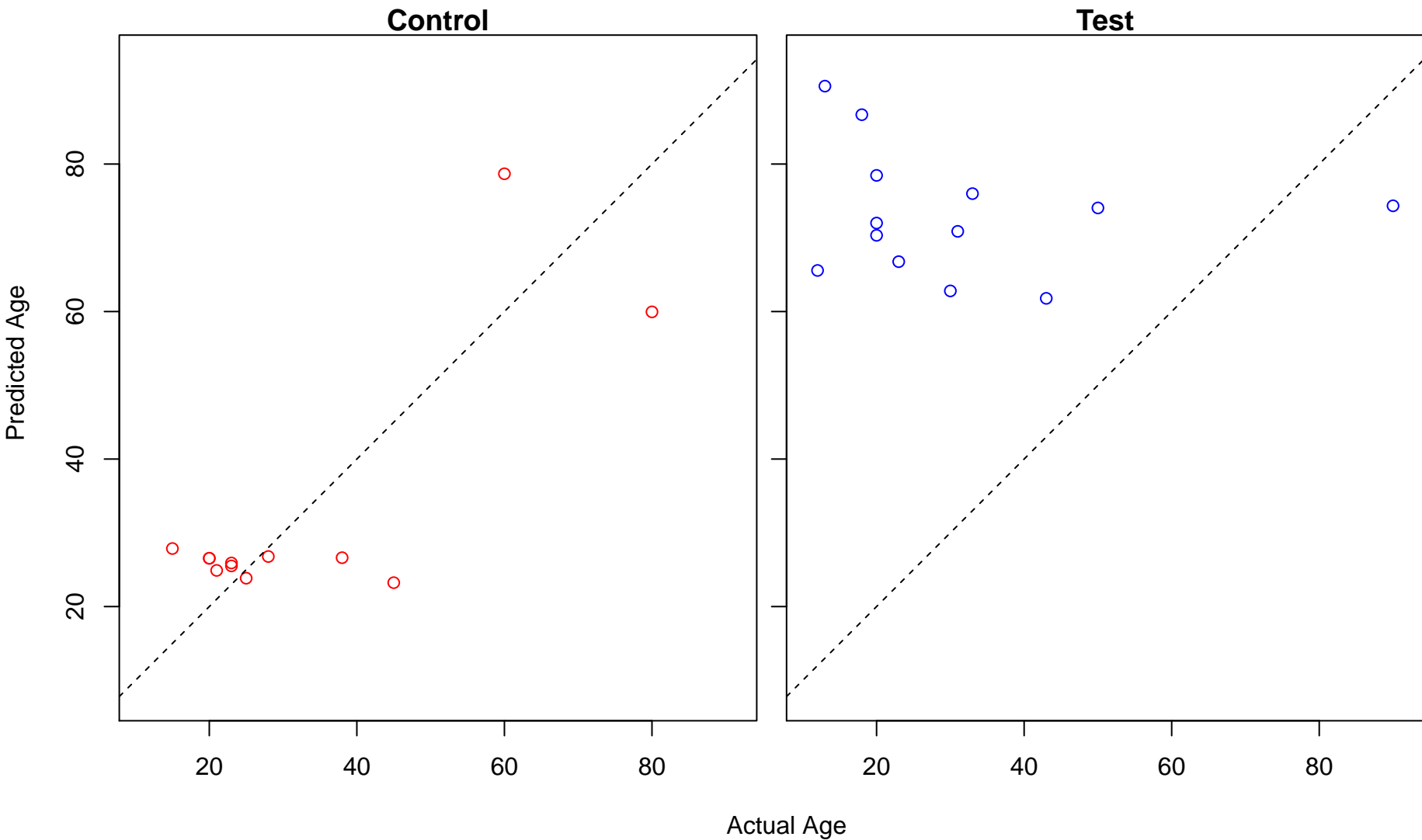
regulation of translational initiation (Score: 6.743195)



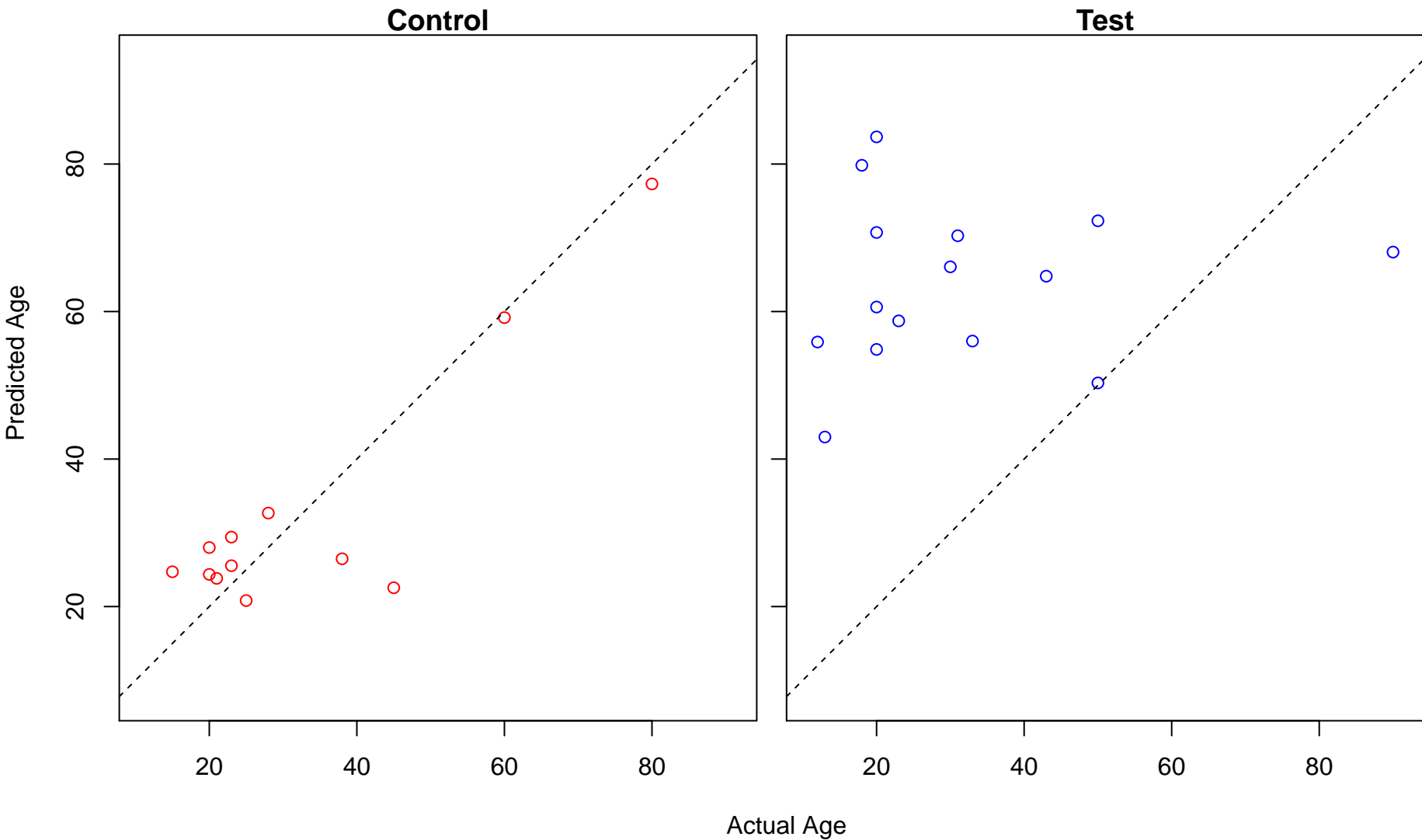
histone mRNA metabolic process (Score: 6.742840)



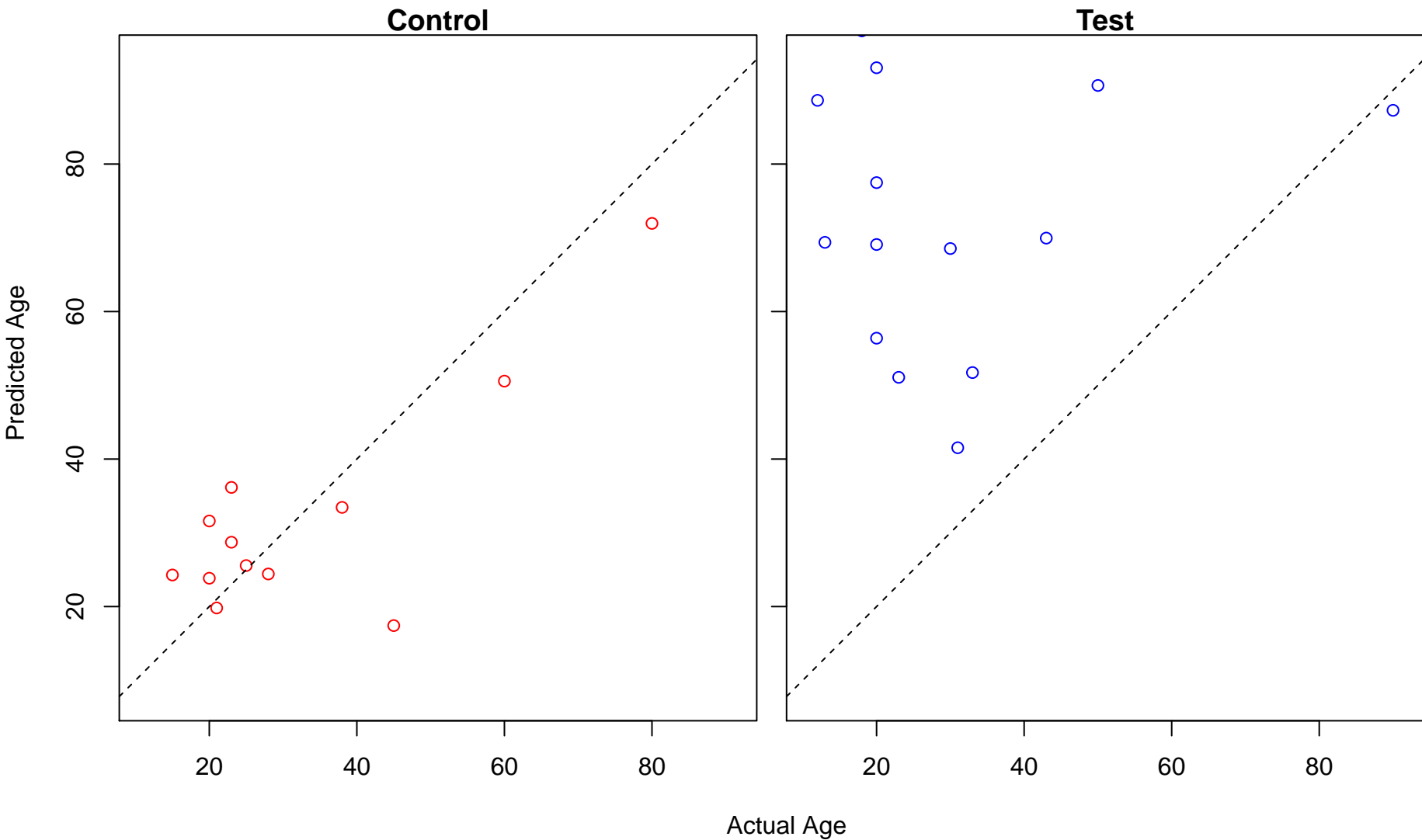
regulation of transcription from RNA polymerase II promoter in response to stress (Score: 6.74226)



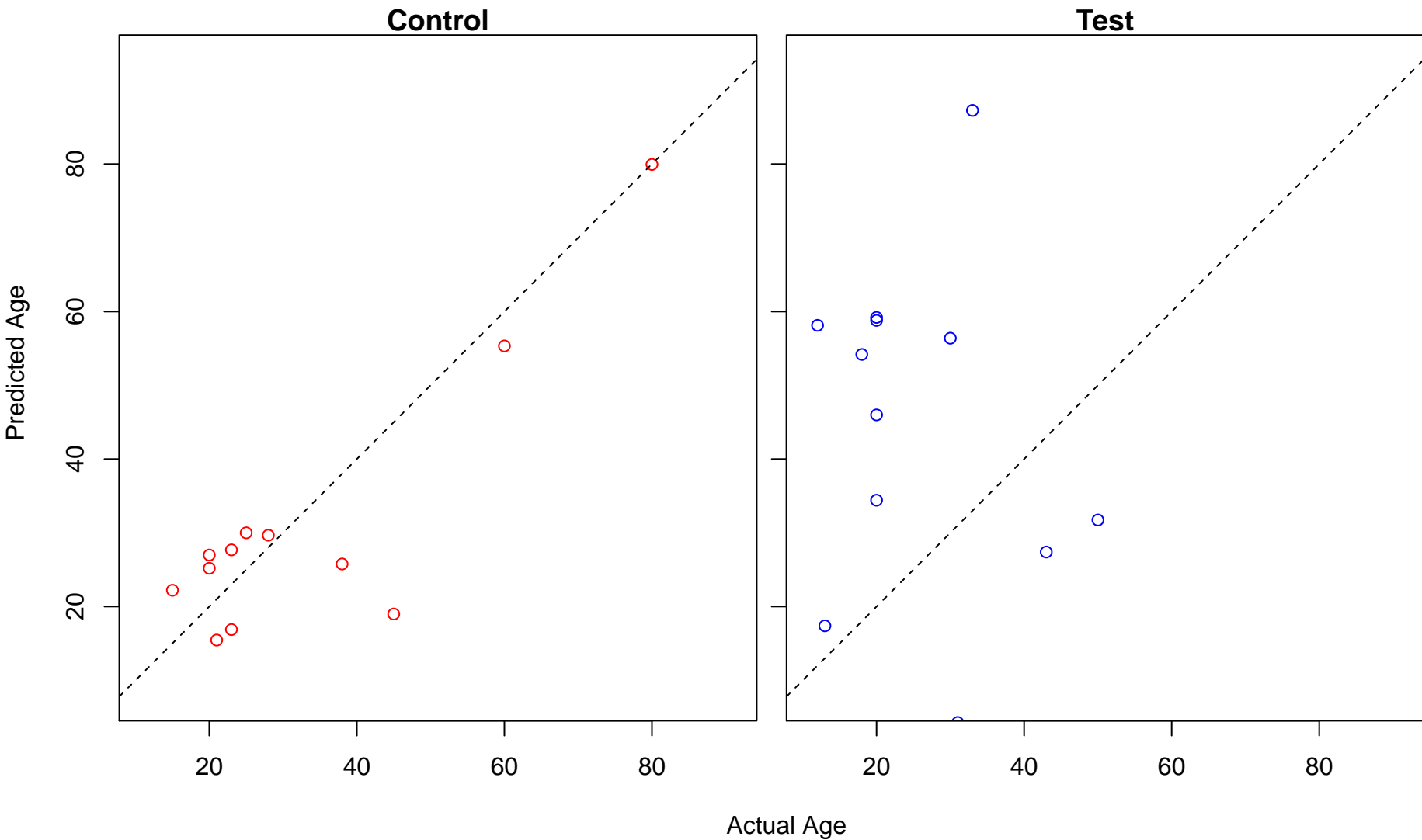
lymphocyte aggregation (Score: 6.740825)



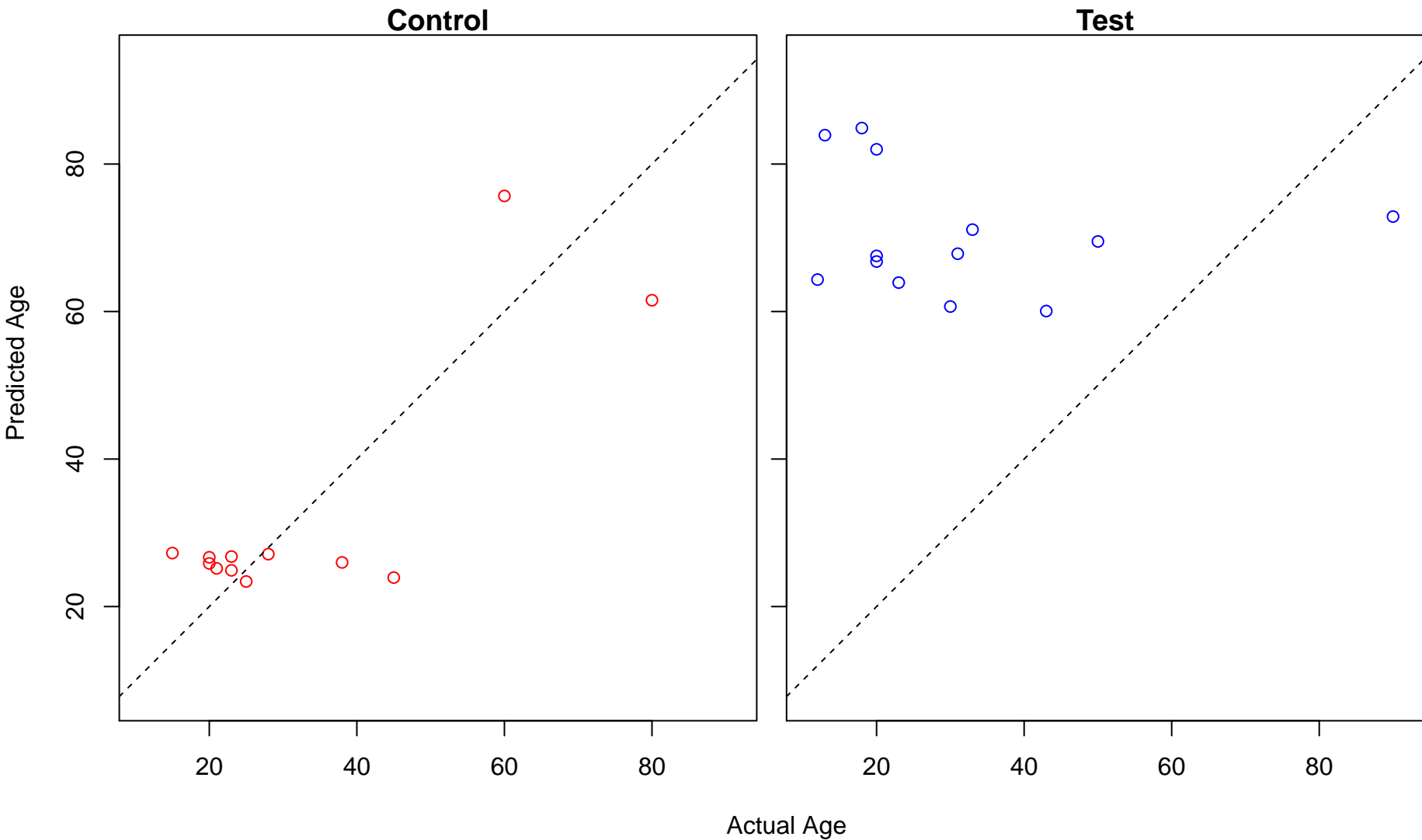
specification of organ identity (Score: 6.738206)



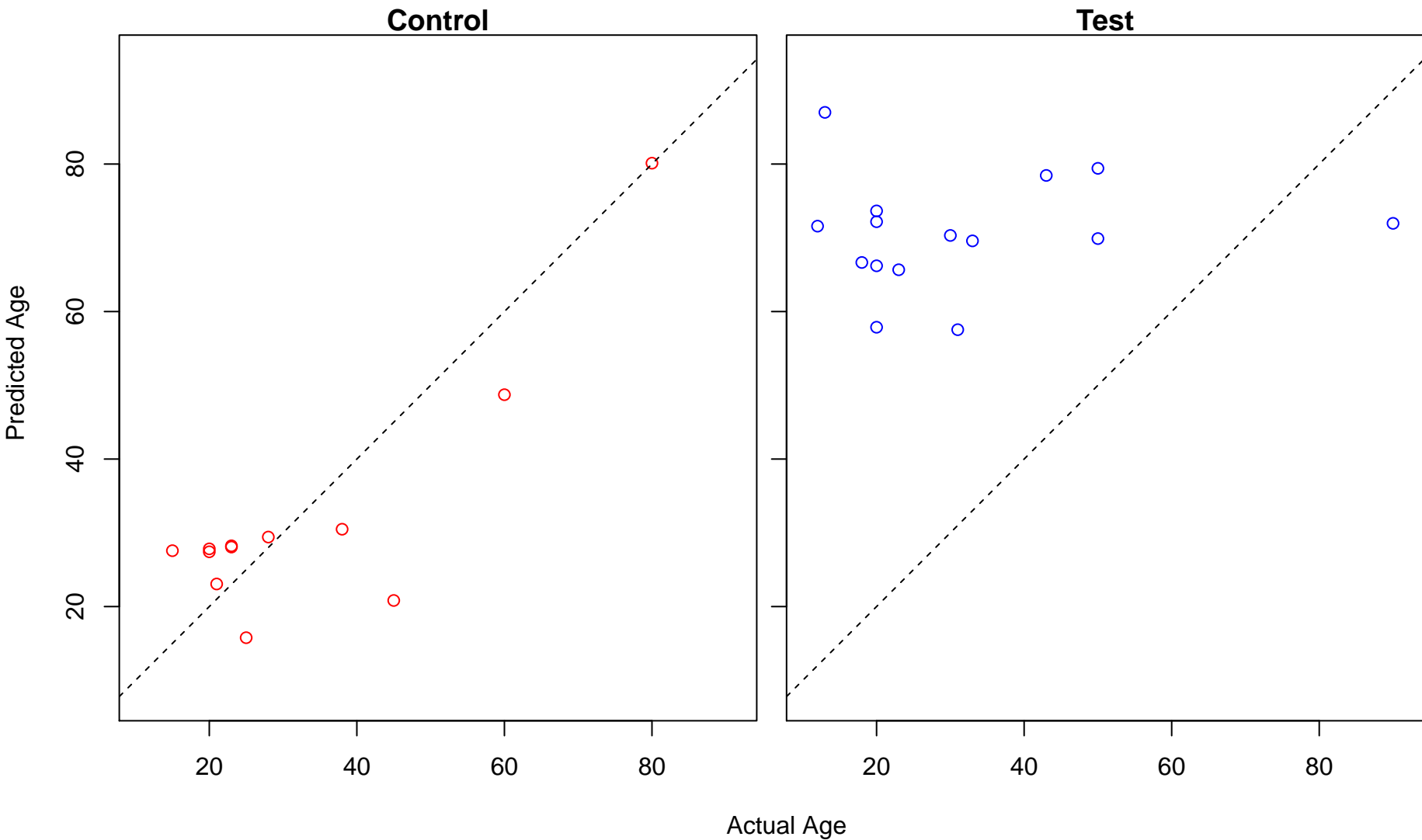
membrane tubulation (Score: 6.735521)



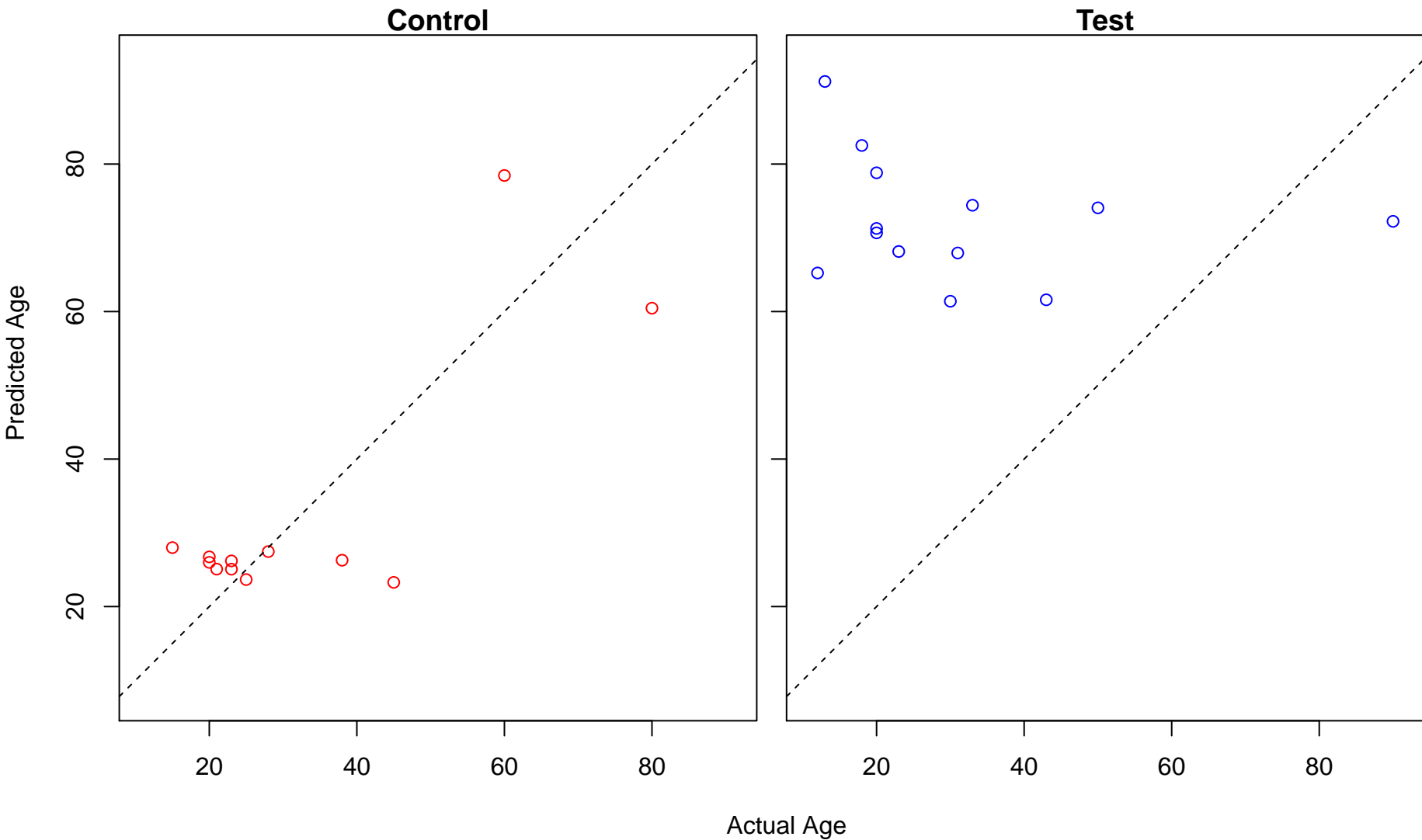
regulation of cellular response to growth factor stimulus (Score: 6.735029)



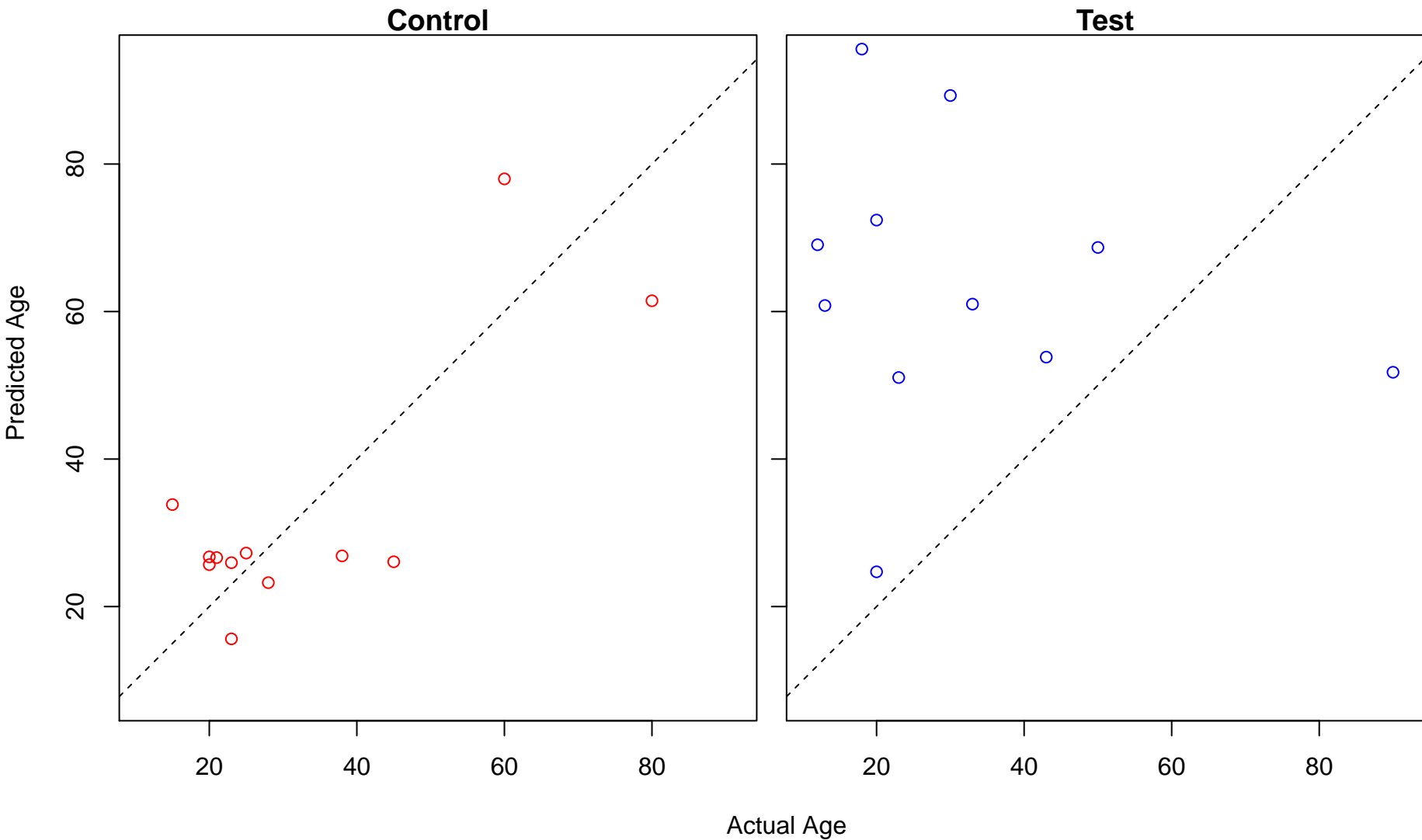
adult locomotory behavior (Score: 6.730845)



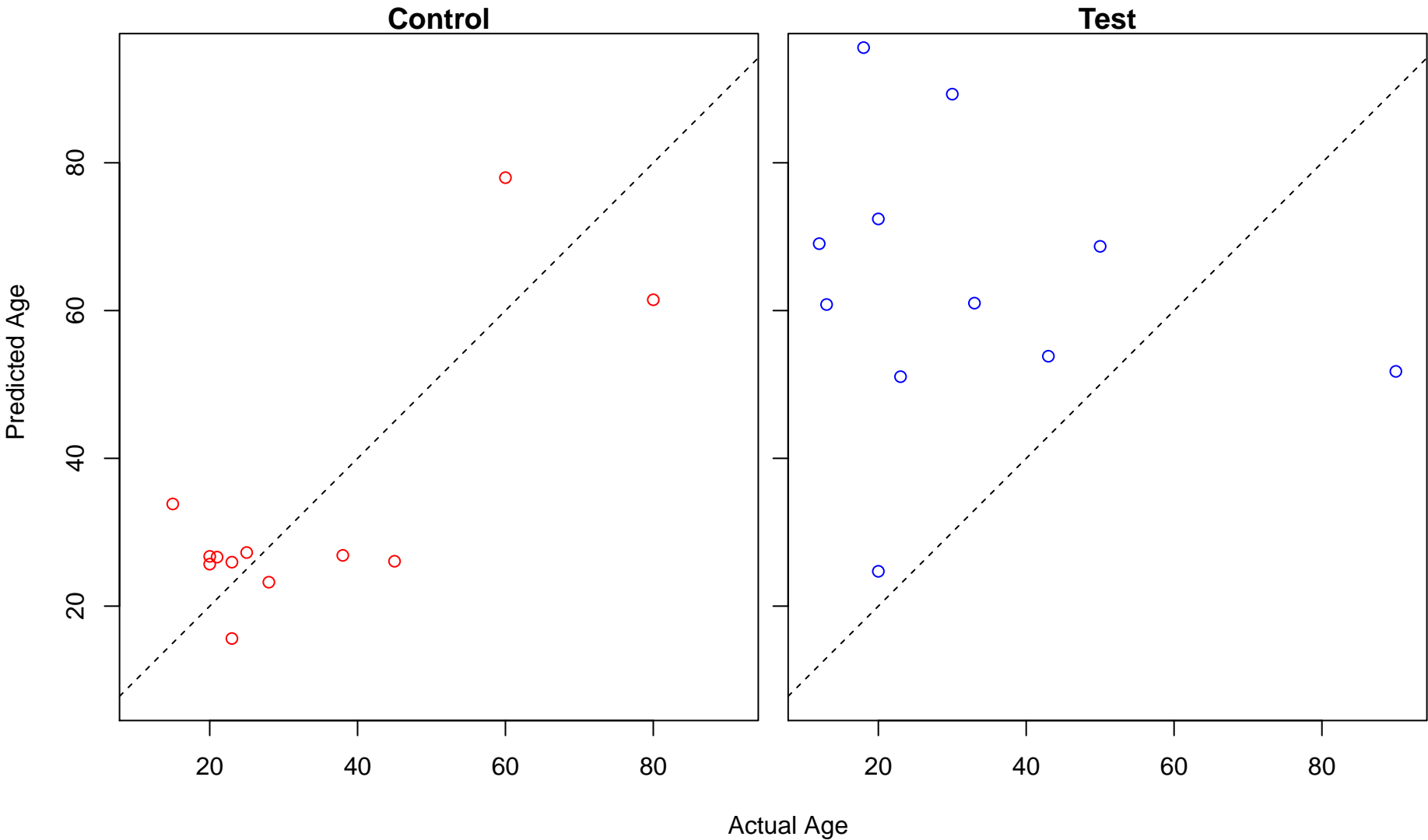
activation of MAPK activity (Score: 6.730696)



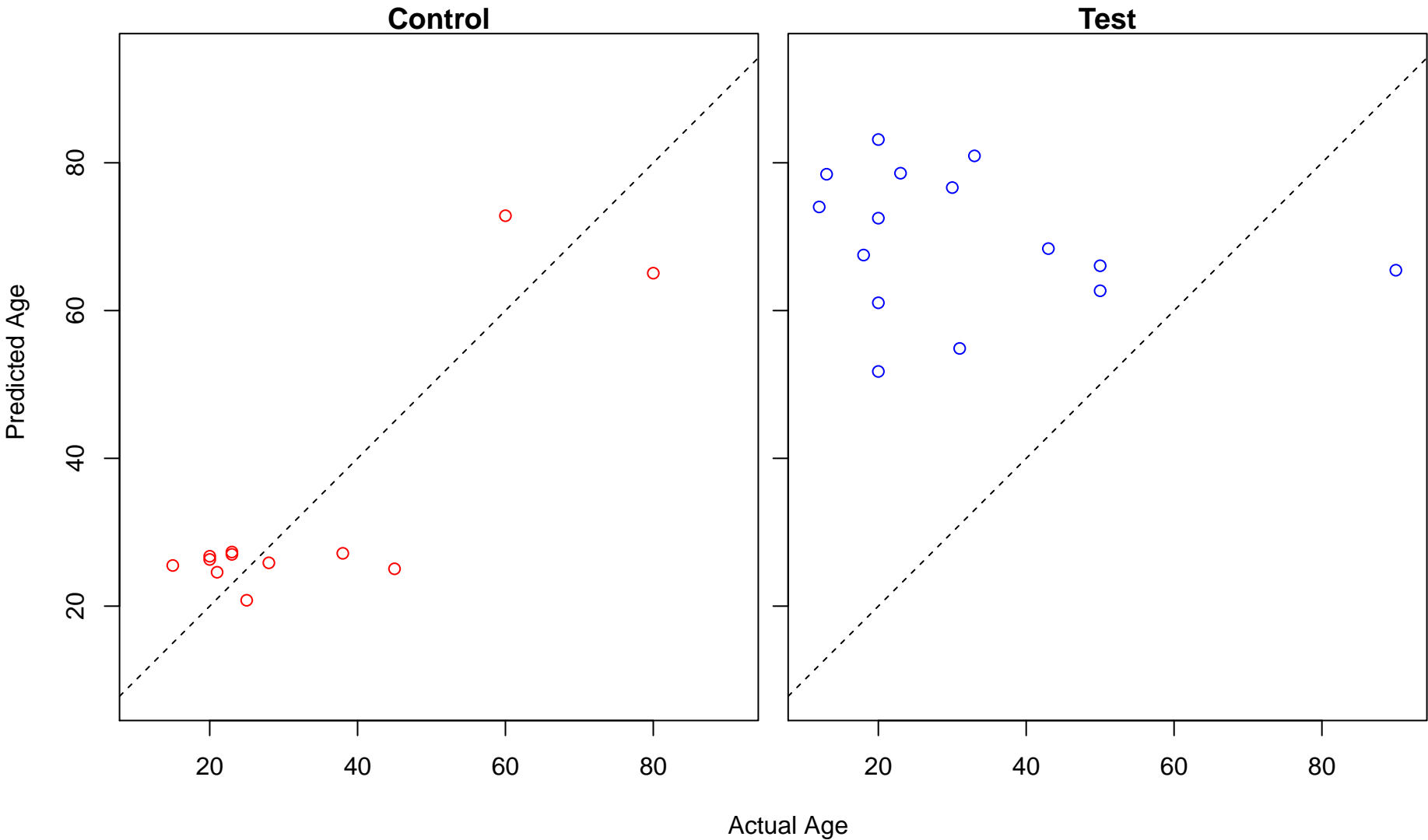
membrane repolarization during action potential (Score: 6.724271)



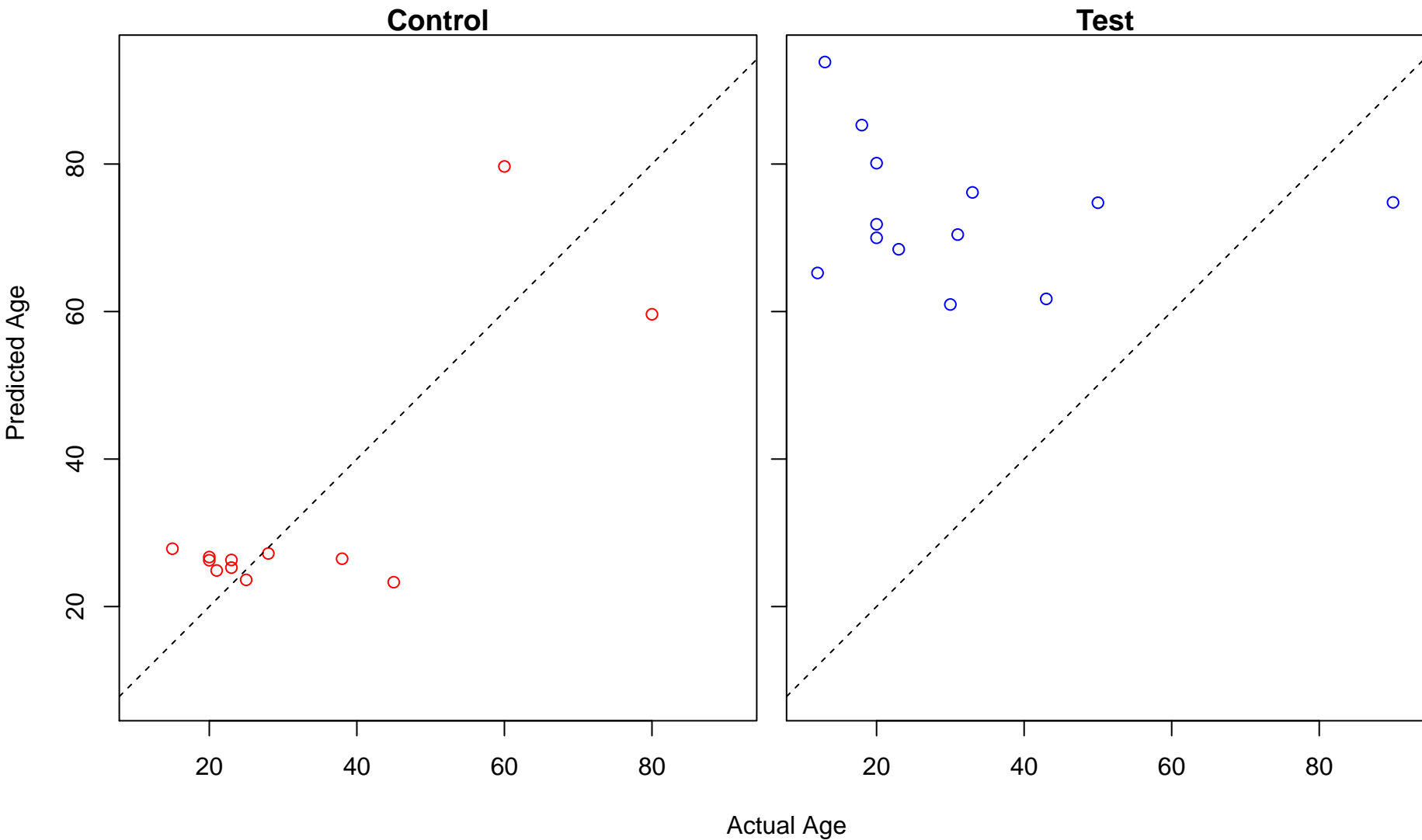
membrane repolarization during cardiac muscle cell action potential (Score: 6.724271)



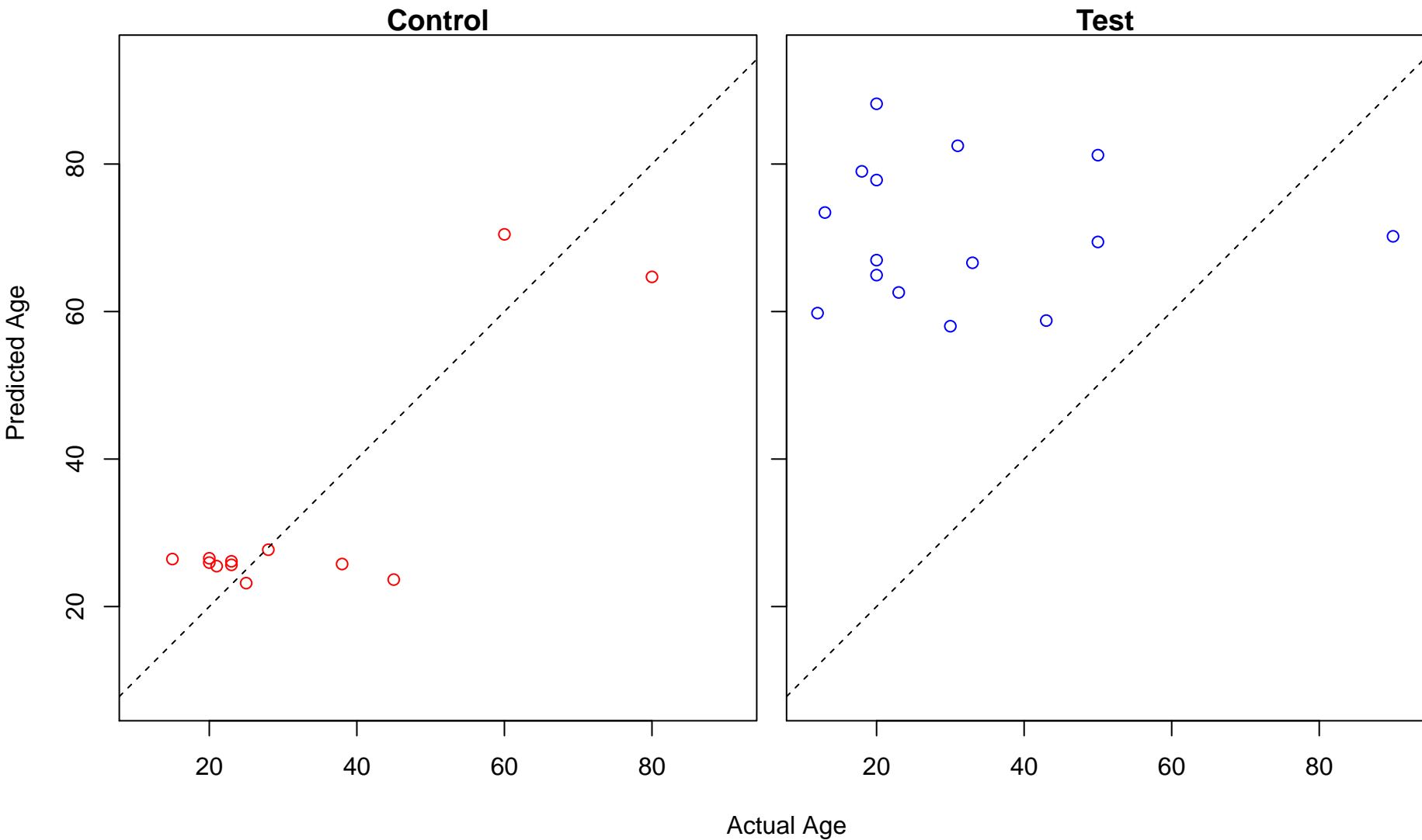
negative regulation of pri-miRNA transcription from RNA polymerase II promoter (Score: 6.723183)



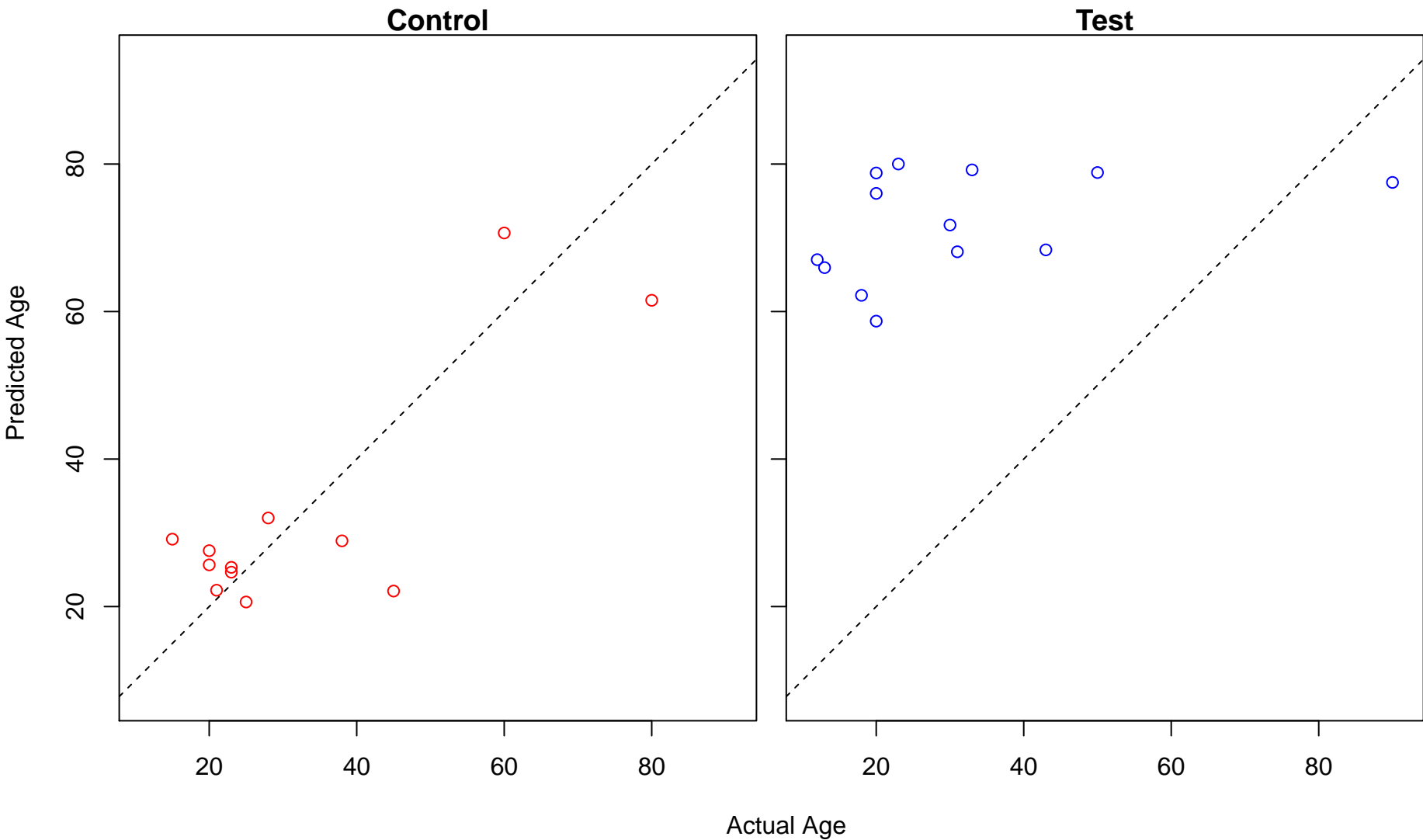
necrotic cell death (Score: 6.722357)



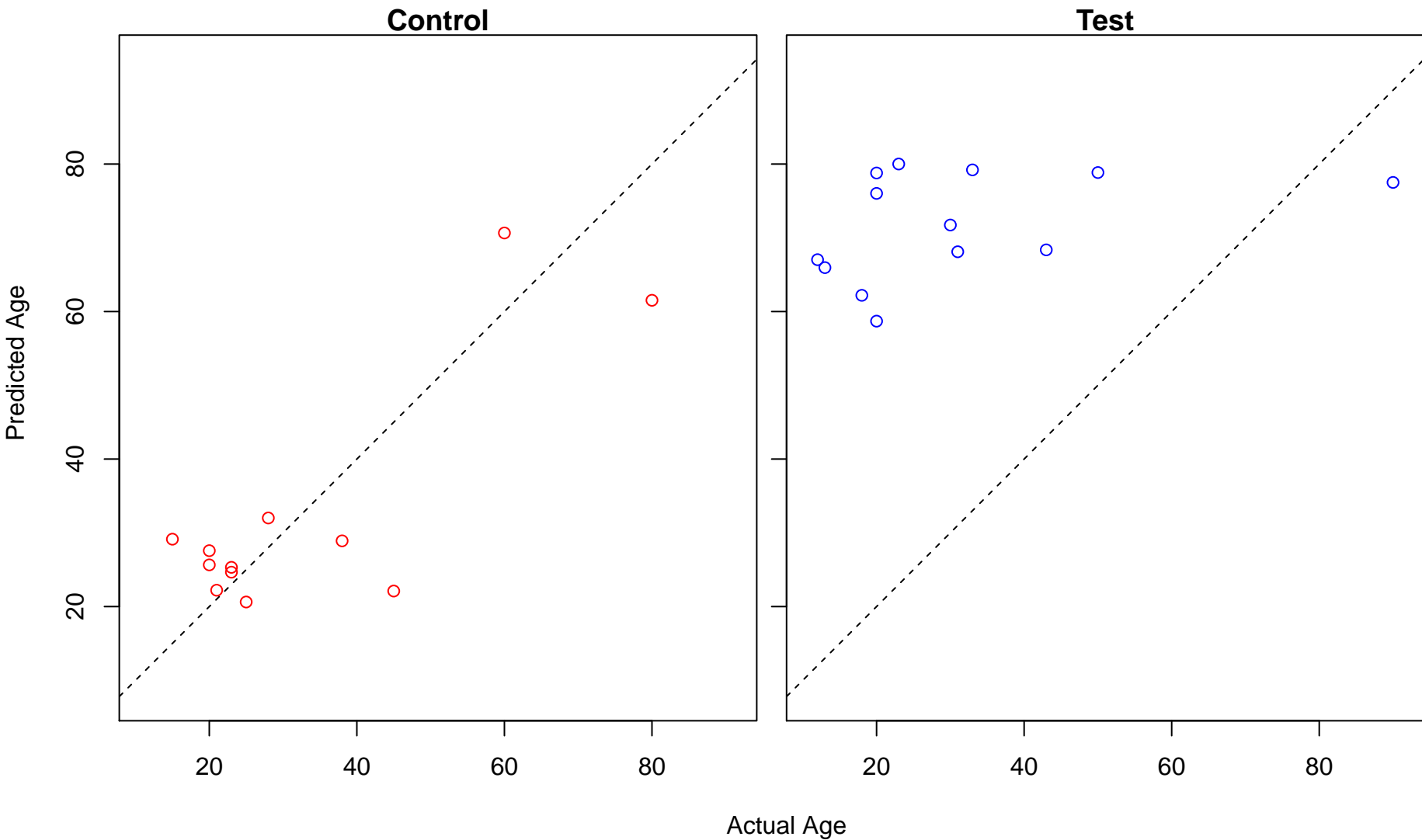
regulation of cell growth (Score: 6.722031)



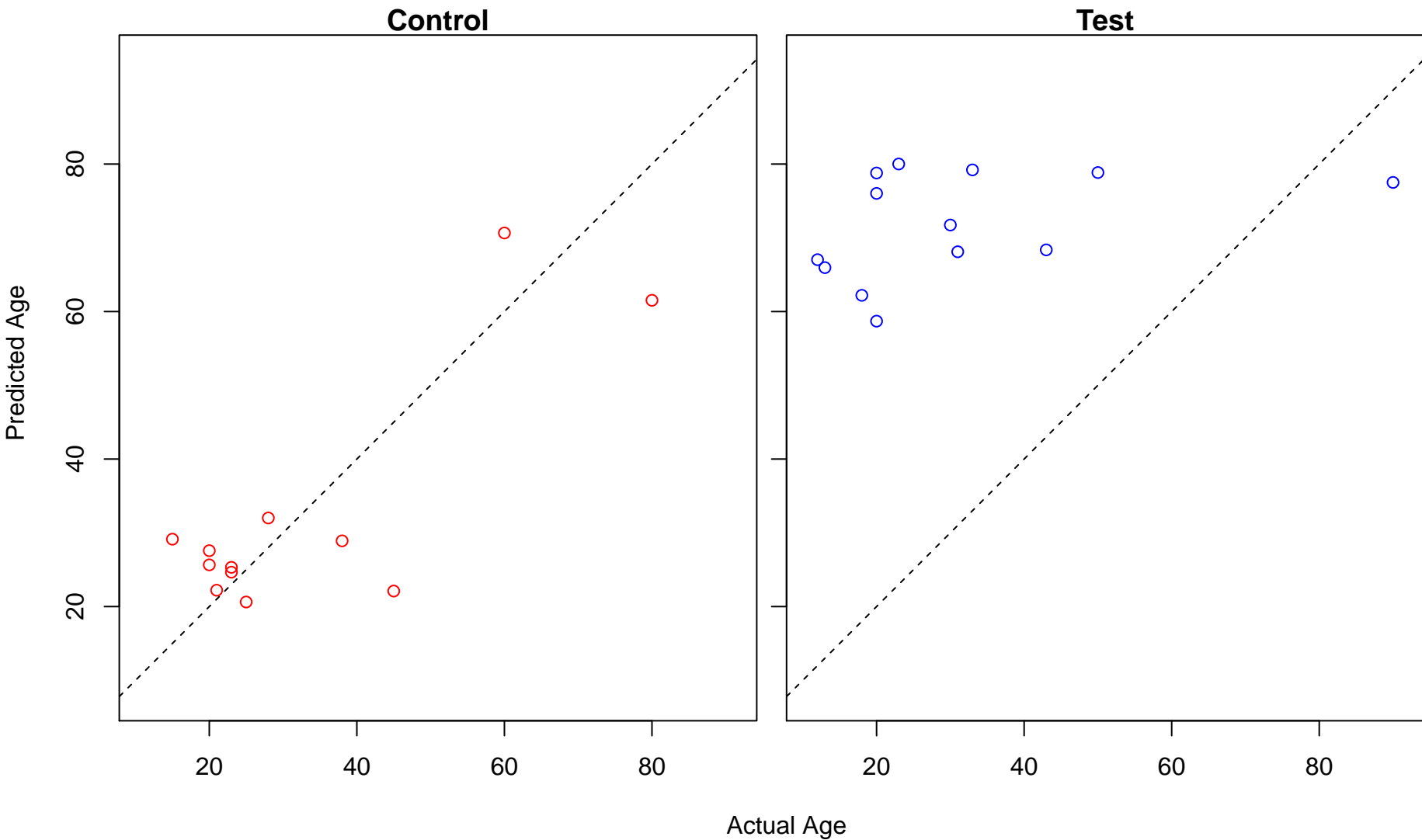
neural tube closure (Score: 6.721456)



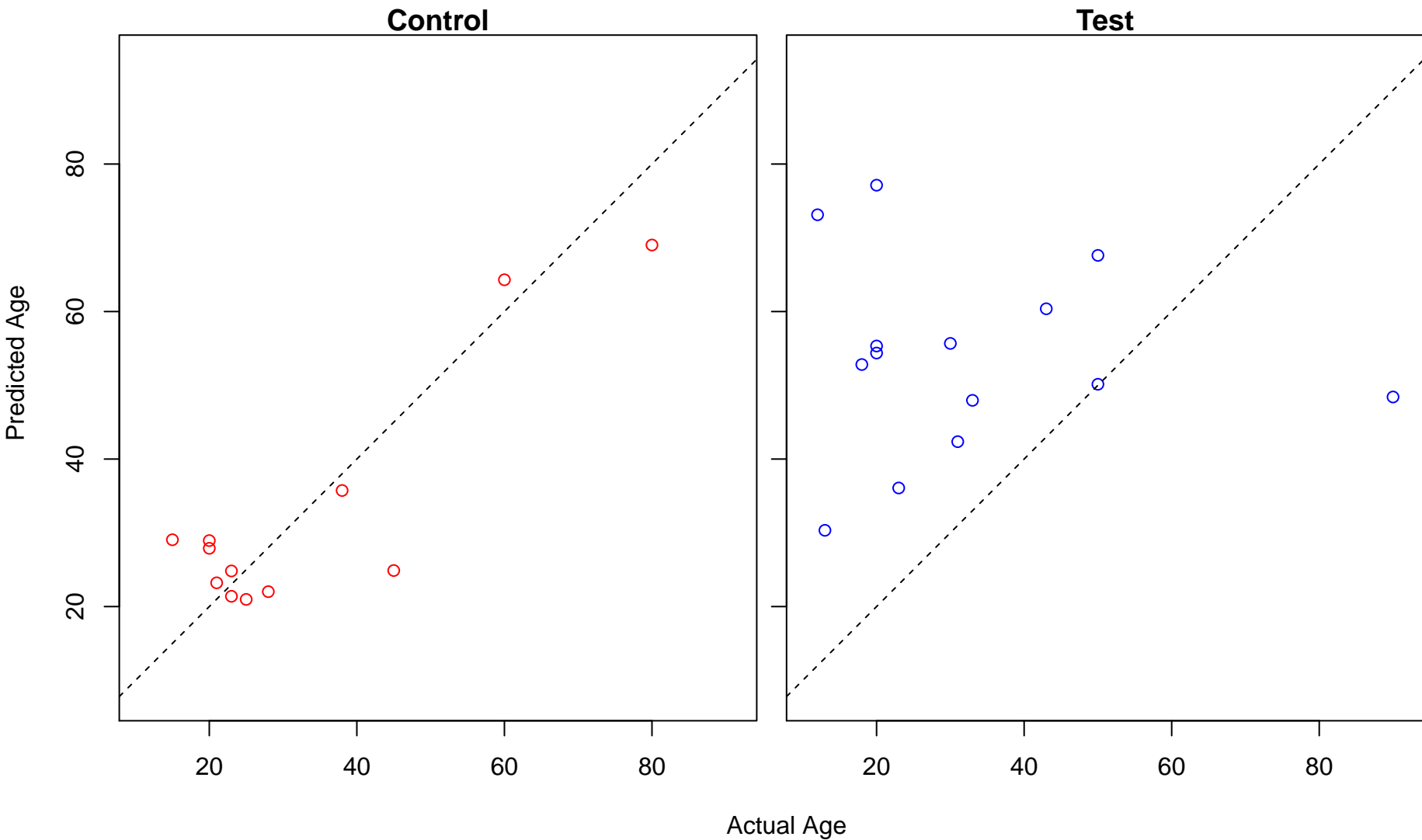
primary neural tube formation (Score: 6.721456)



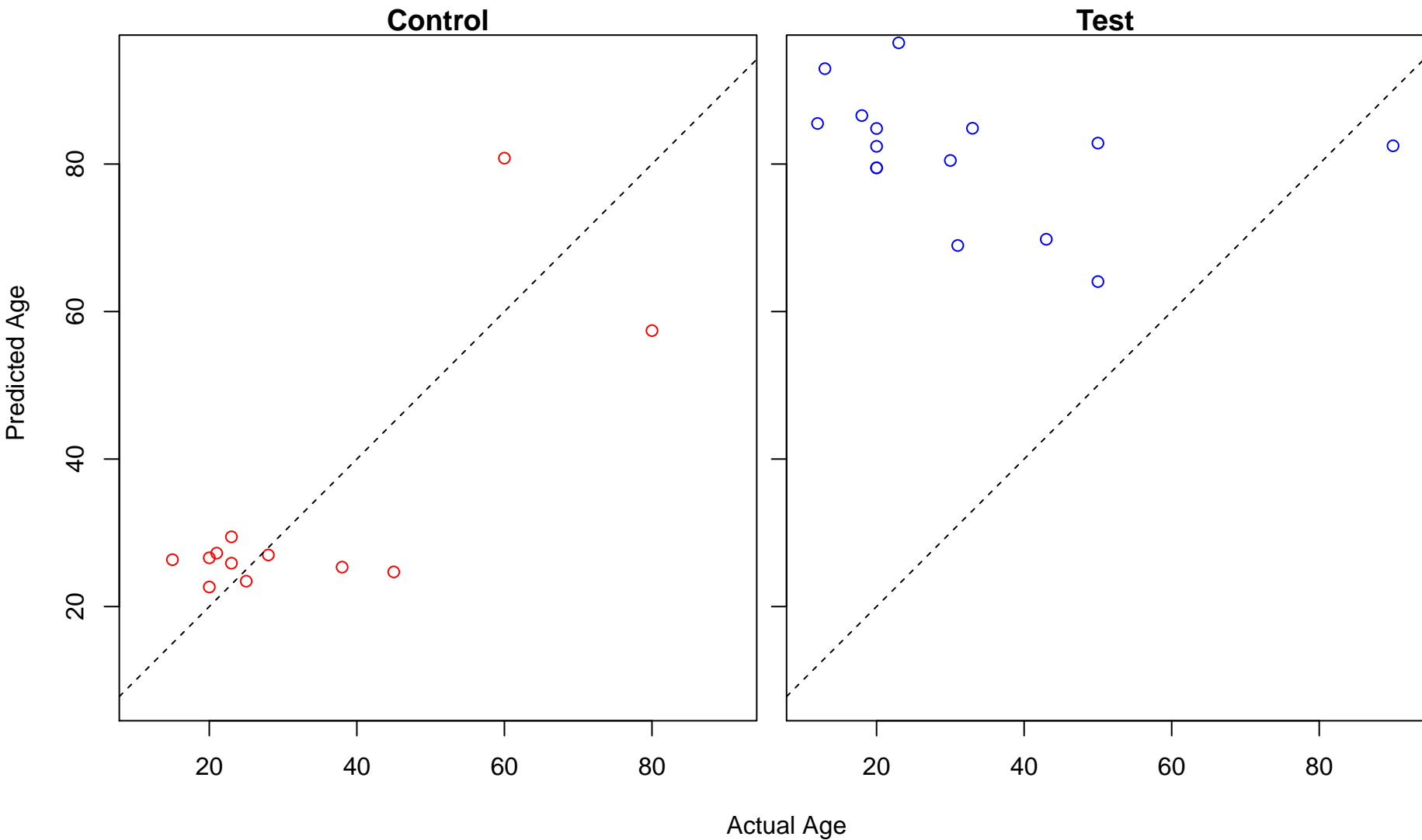
tube closure (Score: 6.721456)



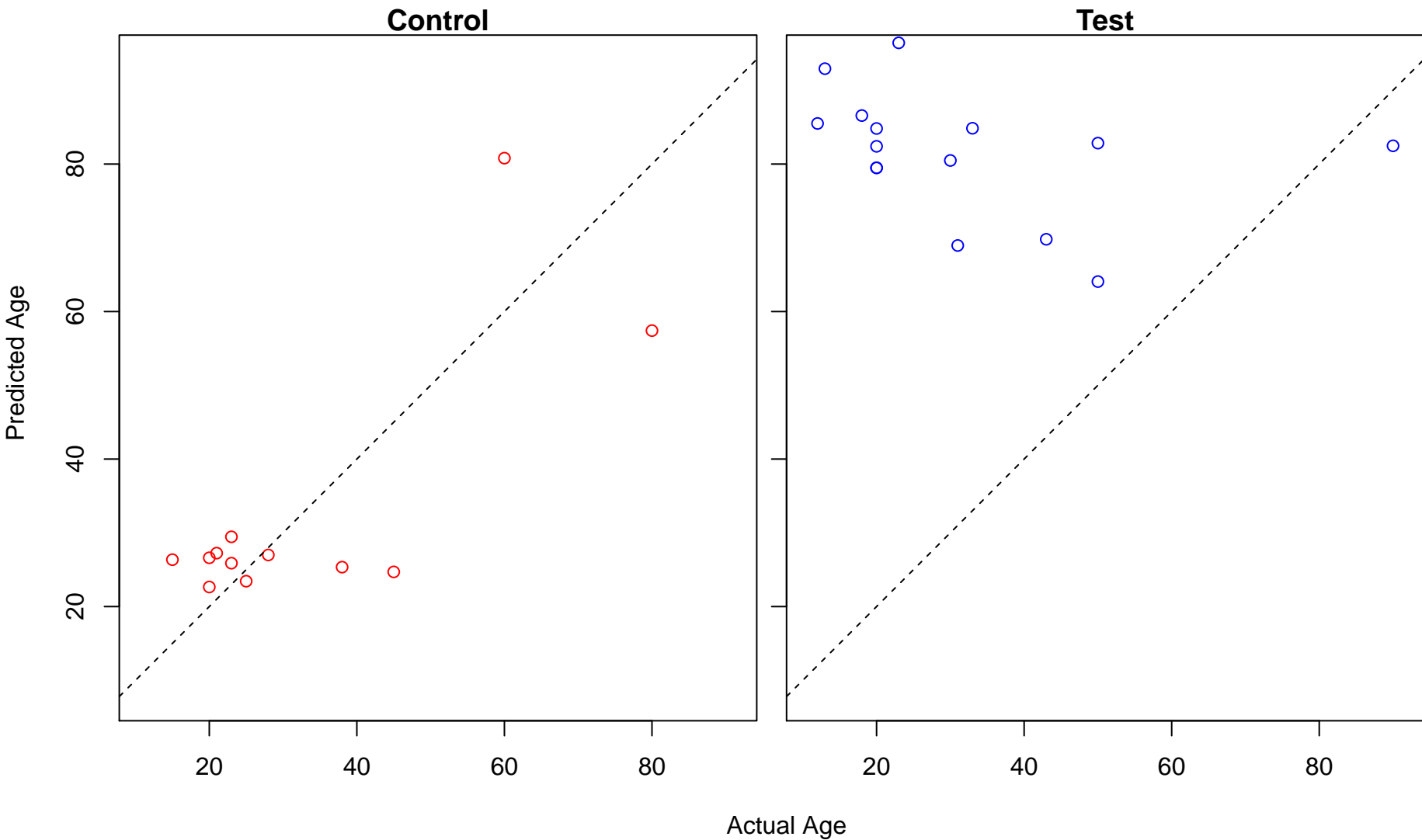
terpenoid catabolic process (Score: 6.720966)



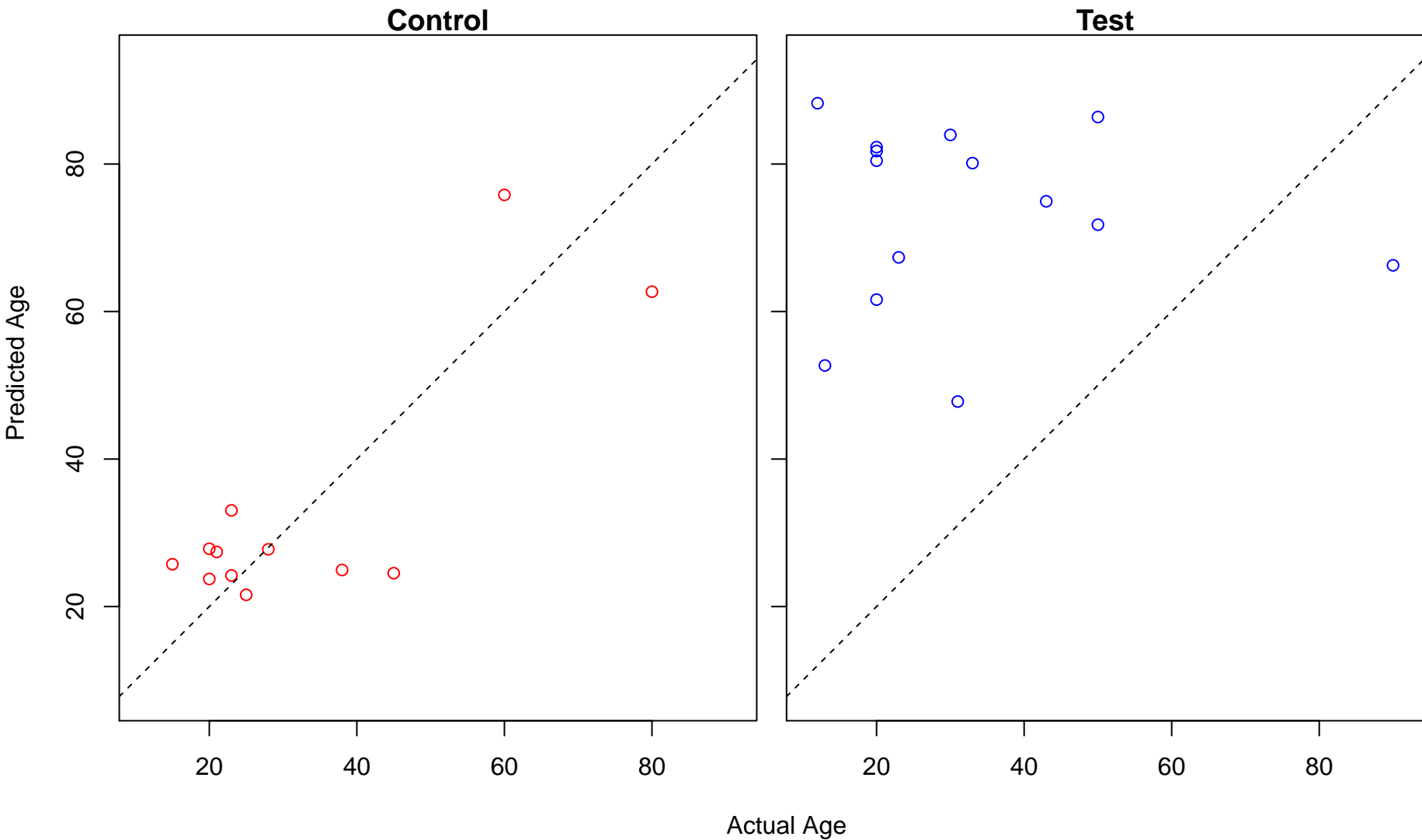
pyrimidine-containing compound salvage (Score: 6.720614)



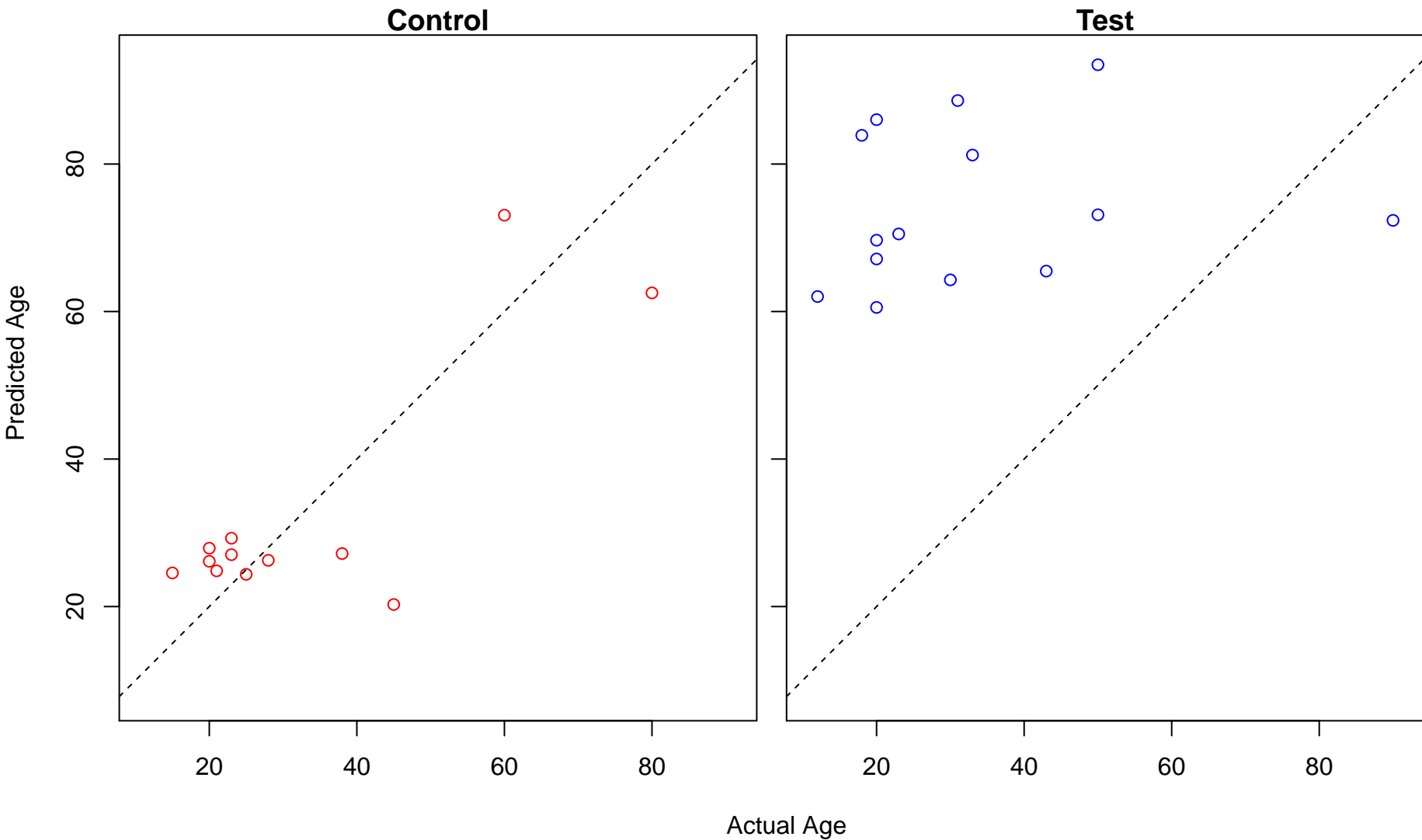
pyrimidine nucleoside salvage (Score: 6.720614)



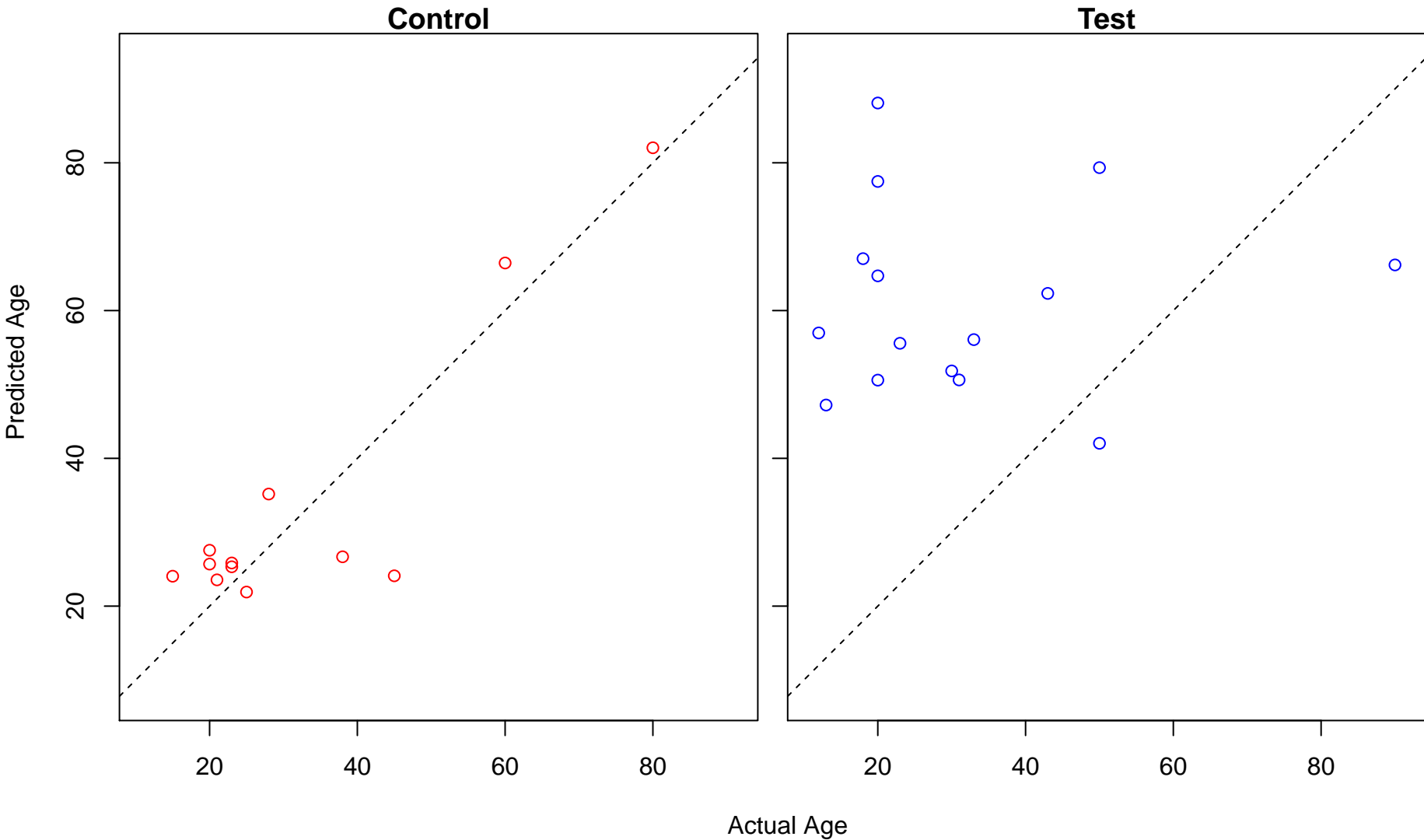
regulation of mitochondrial membrane permeability involved in apoptotic process (Score: 6.717436)



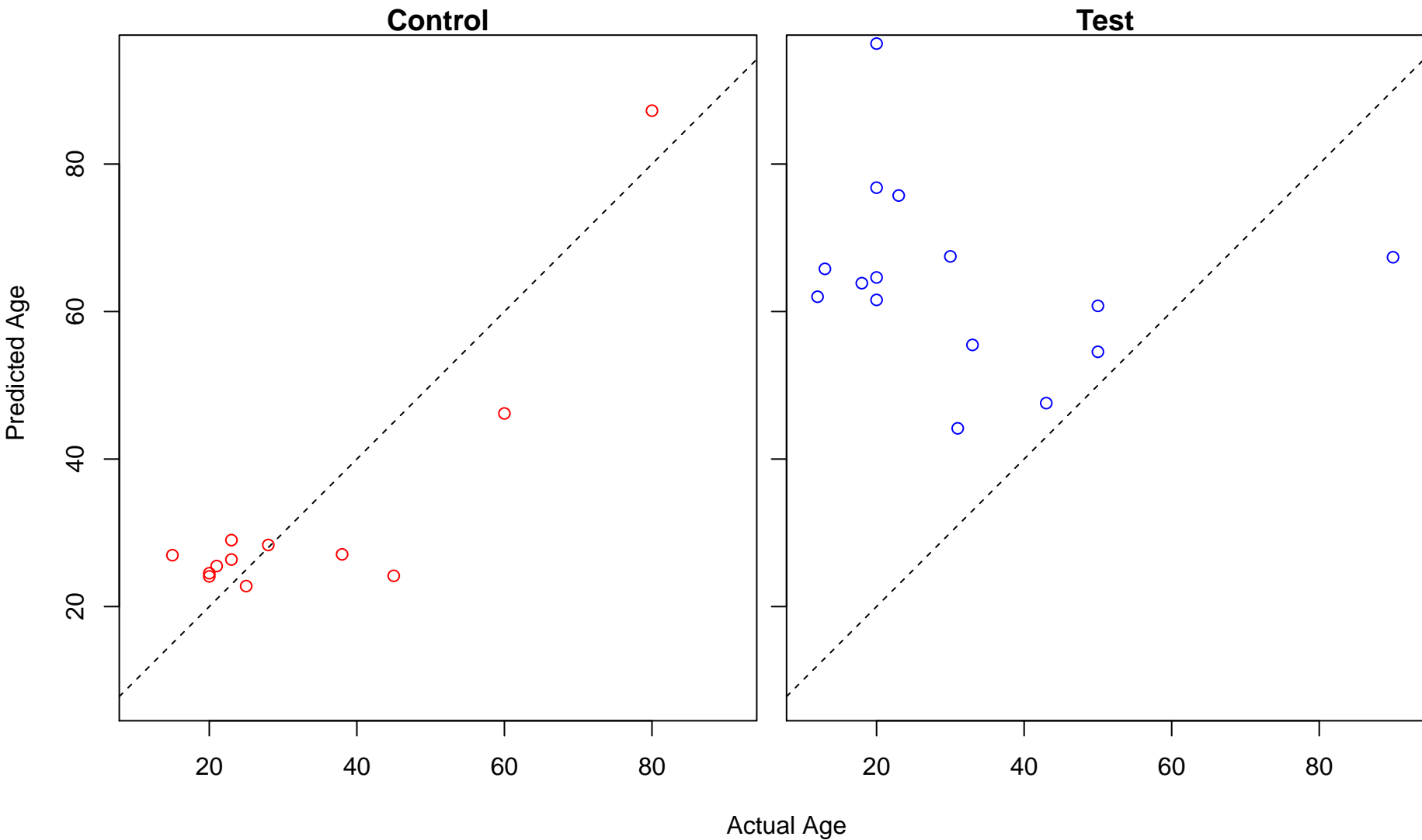
regulation of defense response to virus by virus (Score: 6.713499)



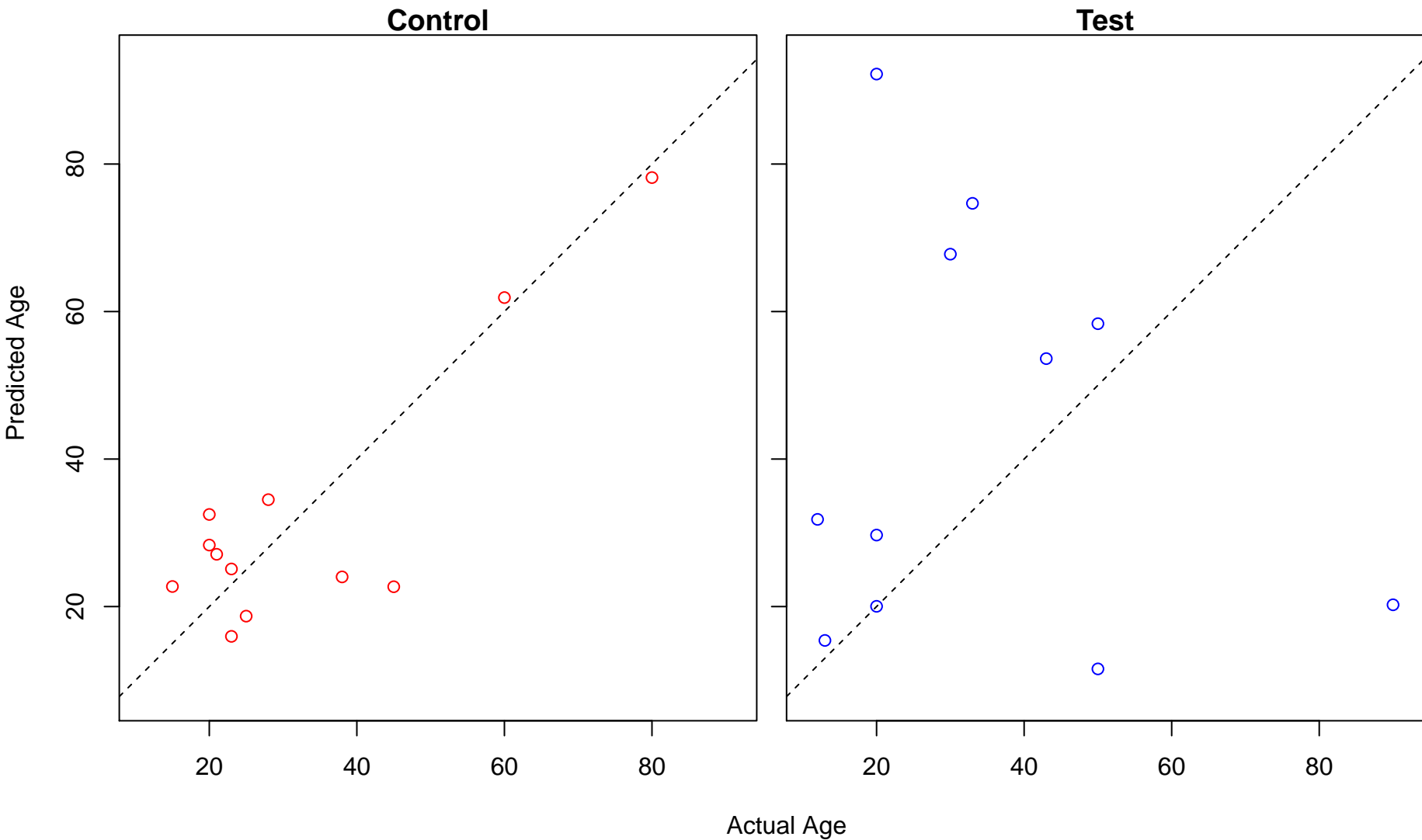
preassembly of GPI anchor in ER membrane (Score: 6.713407)



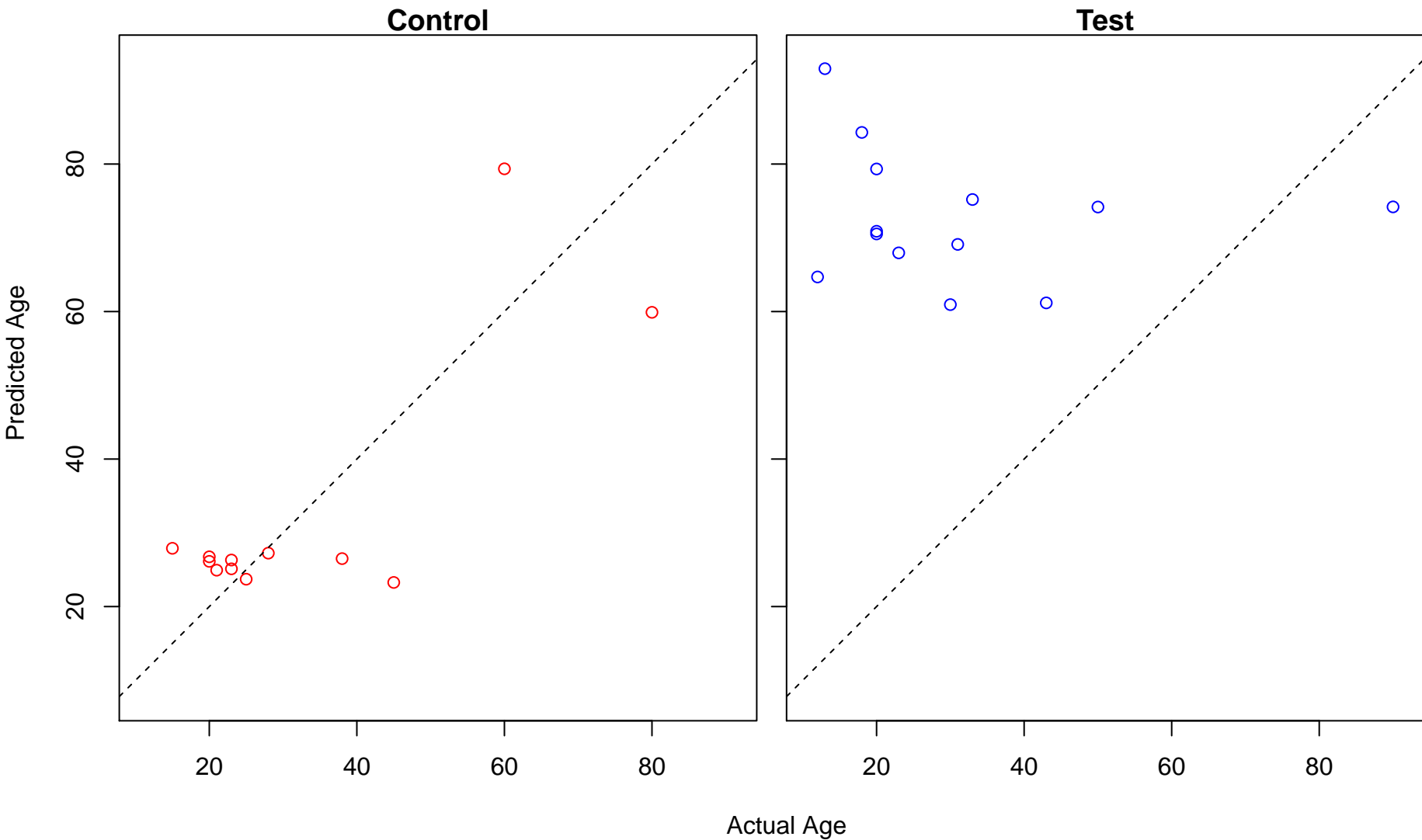
regulation of cellular amino acid metabolic process (Score: 6.711291)



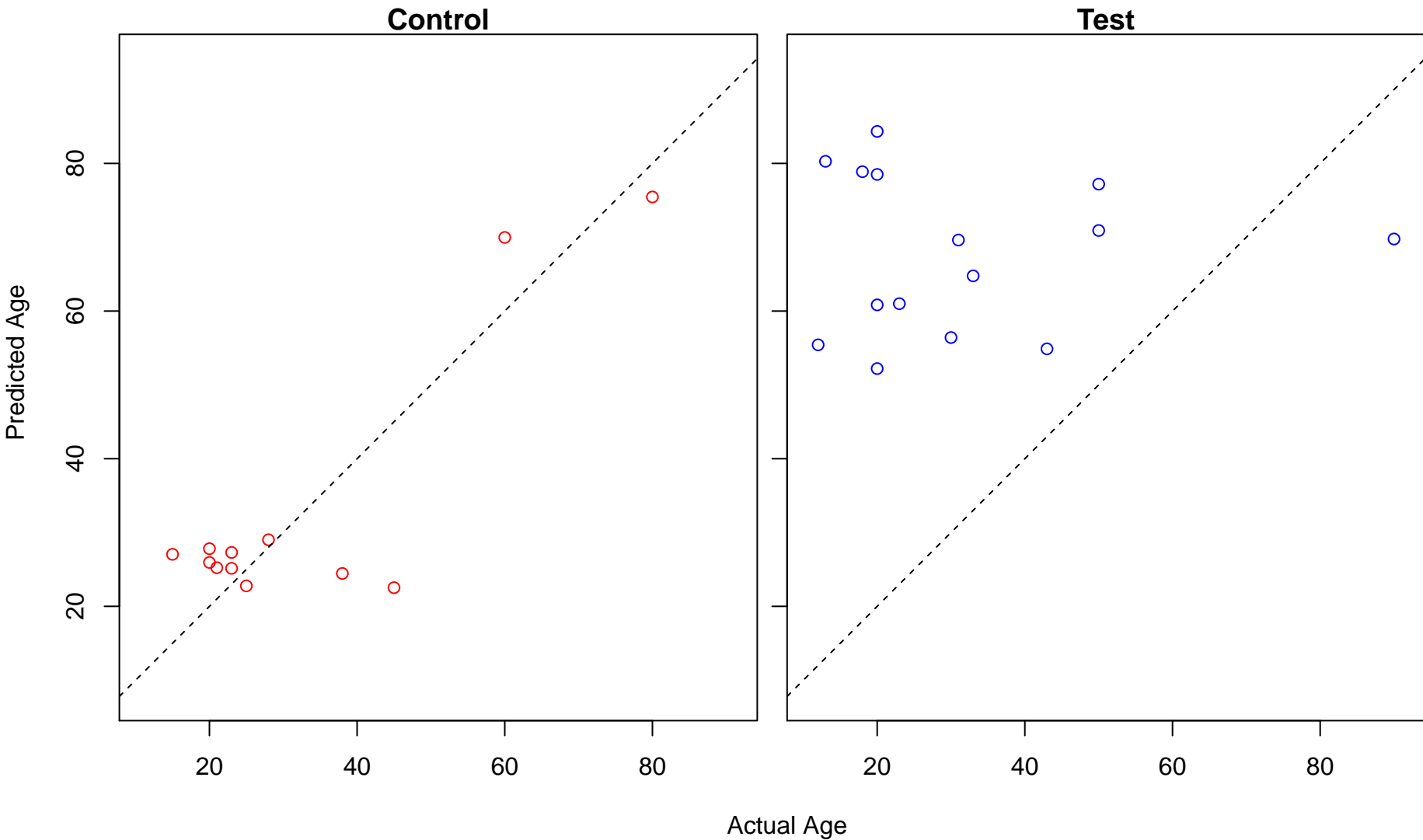
positive regulation of endopeptidase activity (Score: 6.709541)



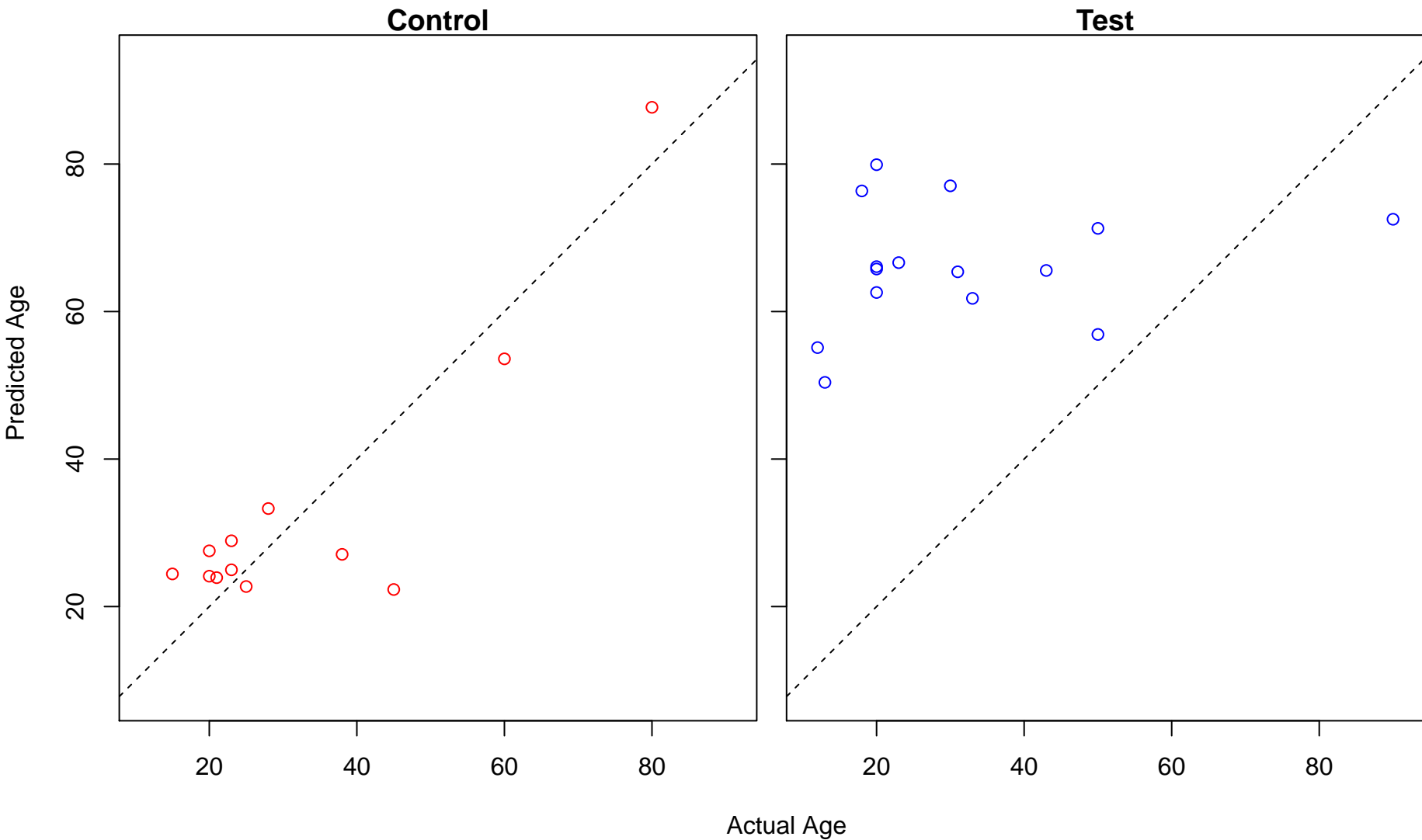
translesion synthesis (Score: 6.700064)



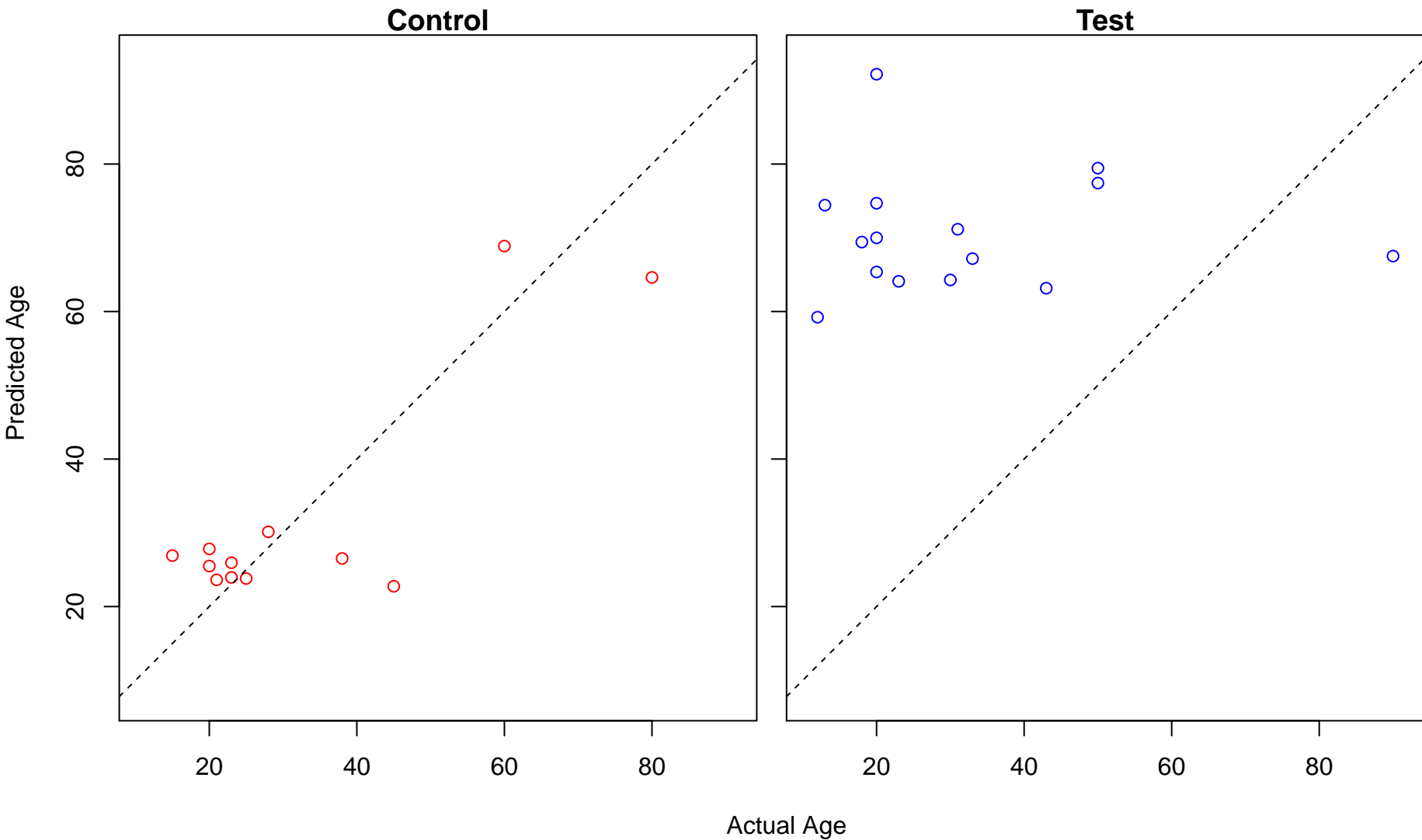
positive regulation of intracellular transport (Score: 6.699343)



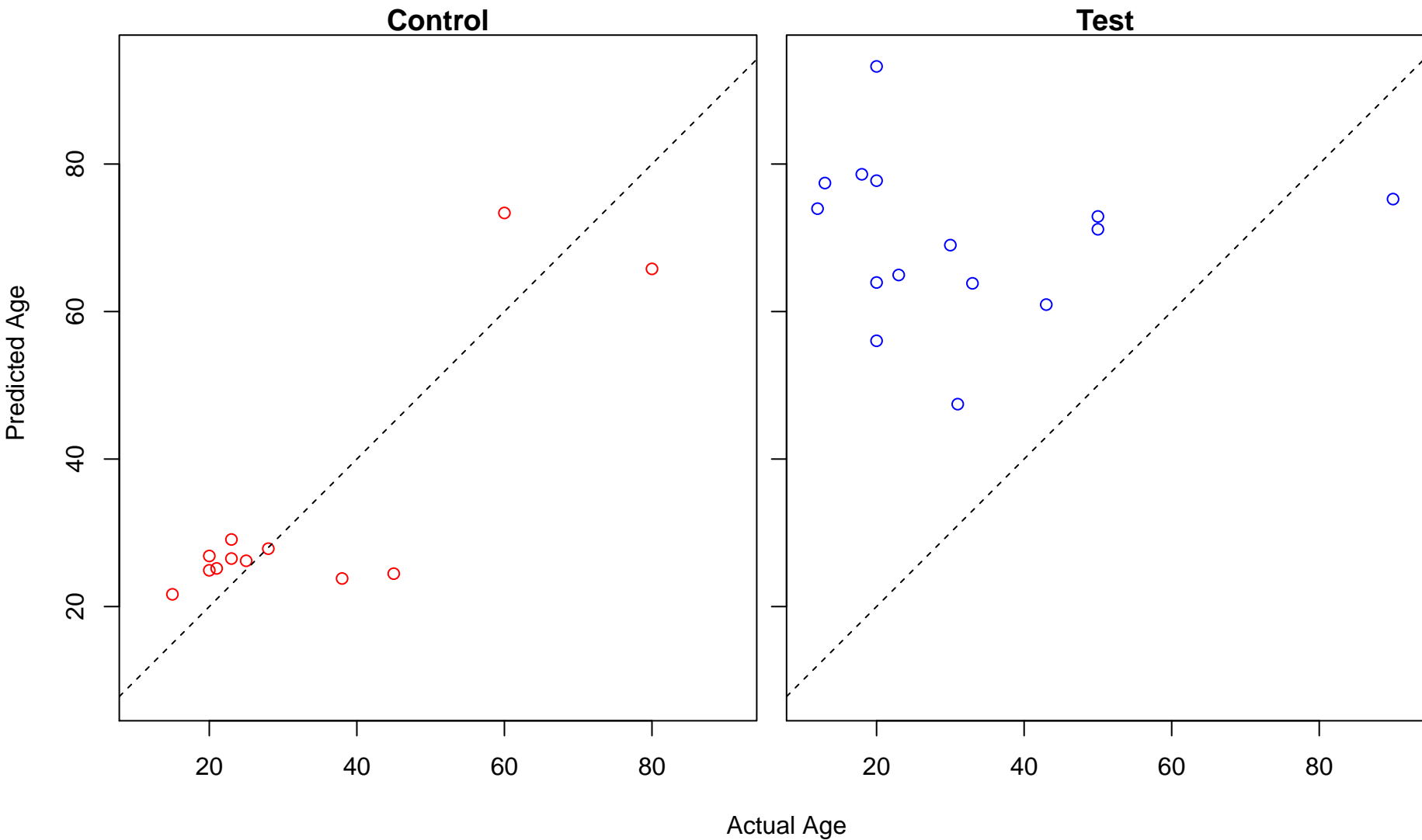
positive regulation of leukocyte differentiation (Score: 6.698514)



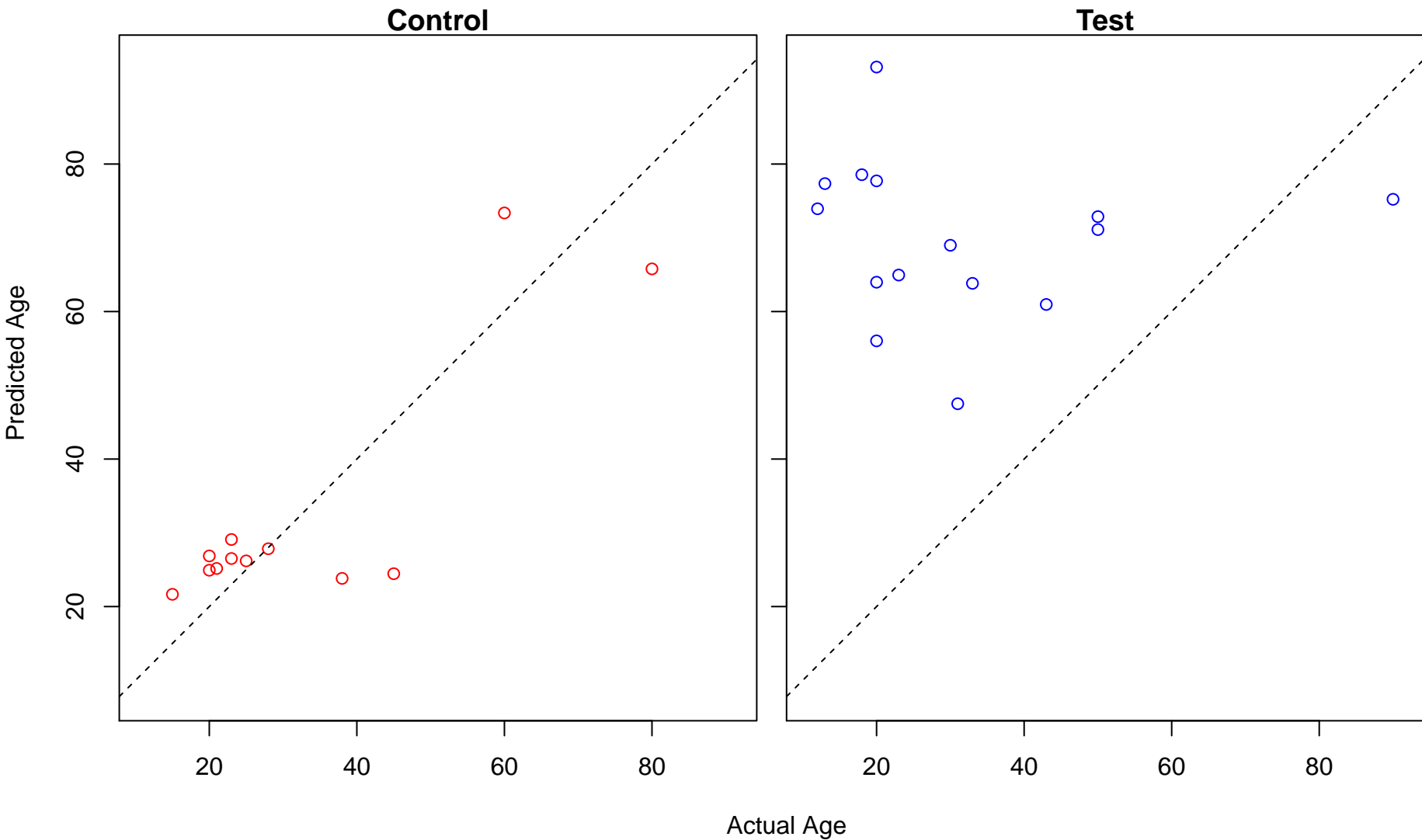
negative regulation of growth (Score: 6.696914)



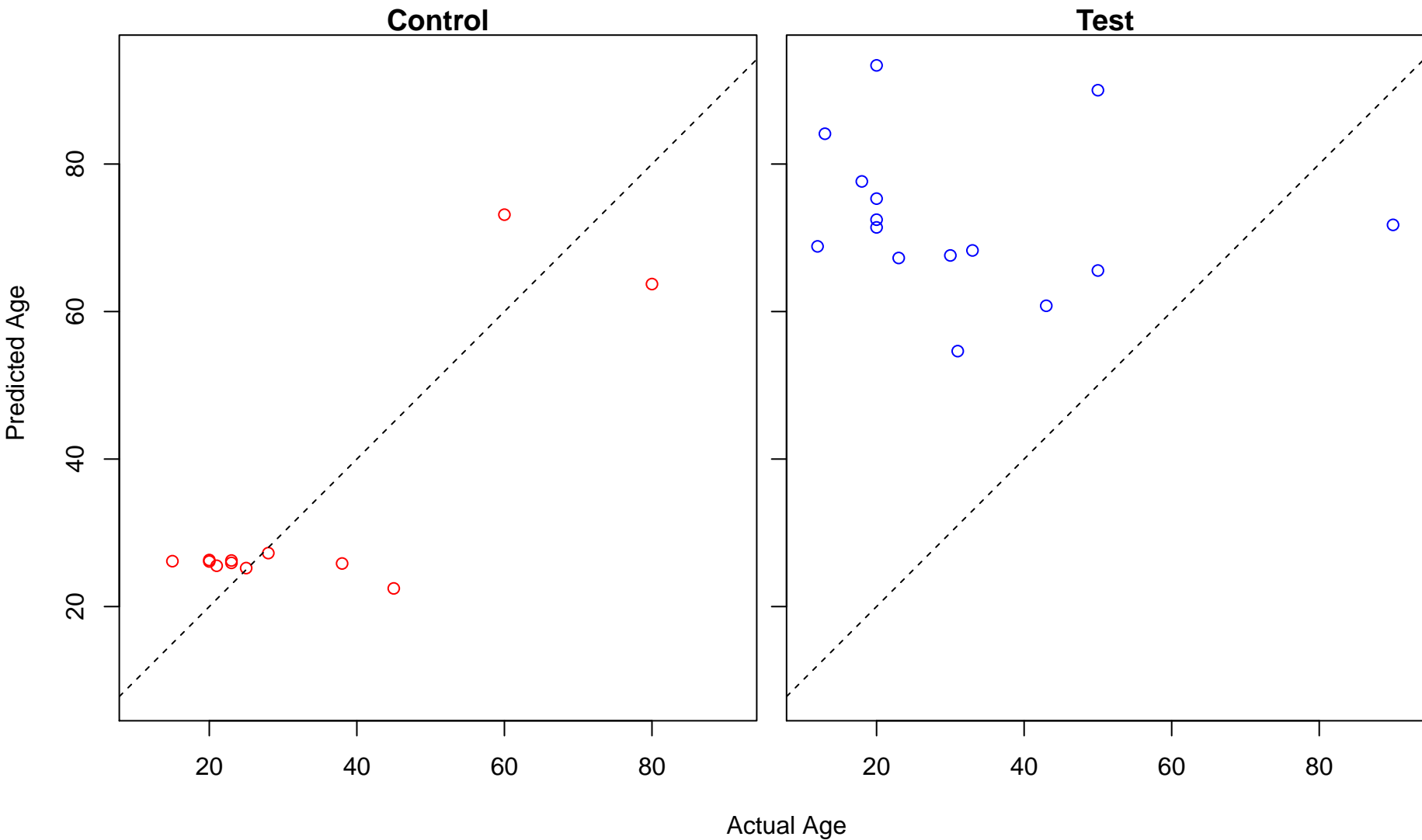
regulation of striated muscle cell apoptotic process (Score: 6.692787)



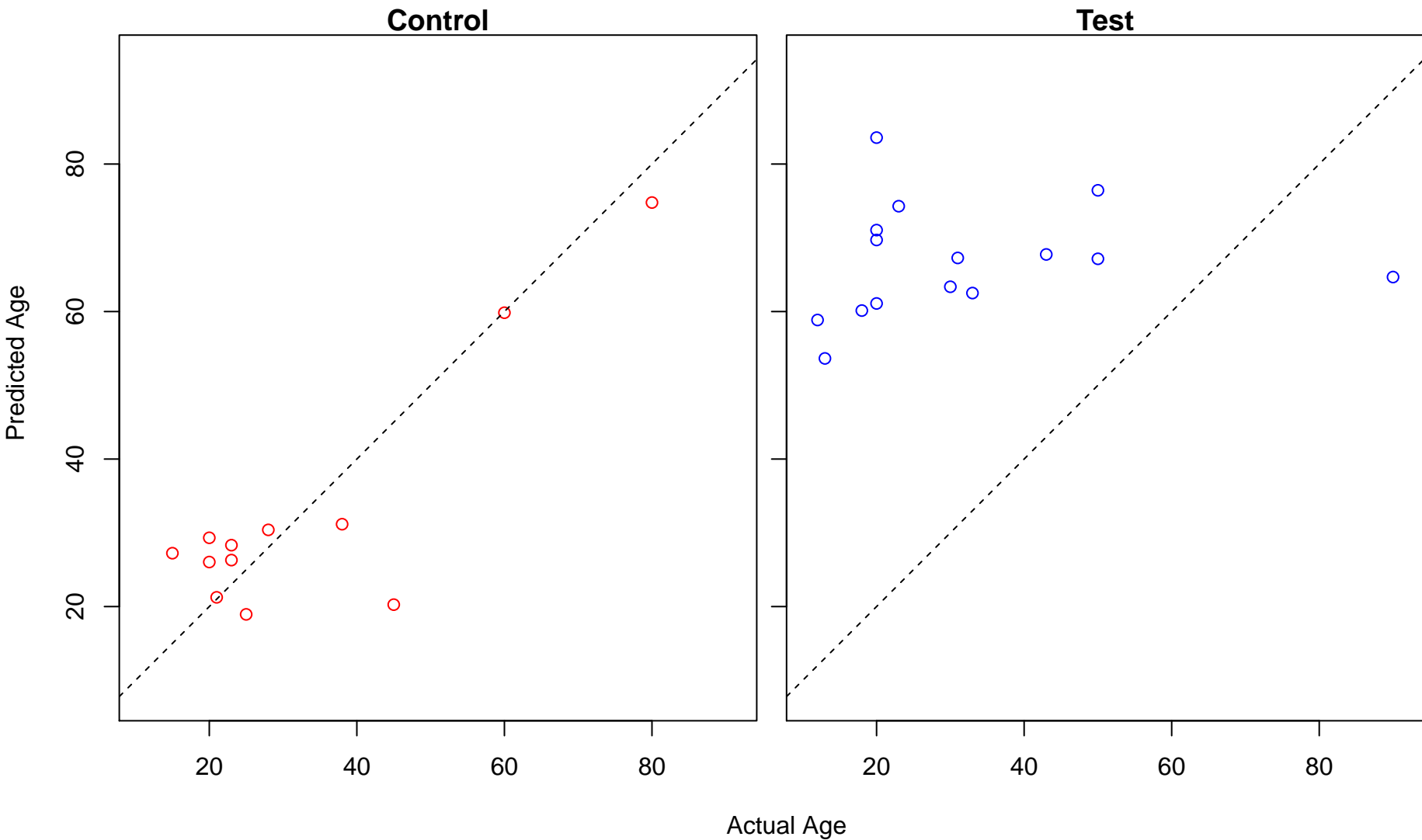
regulation of muscle cell apoptotic process (Score: 6.687775)



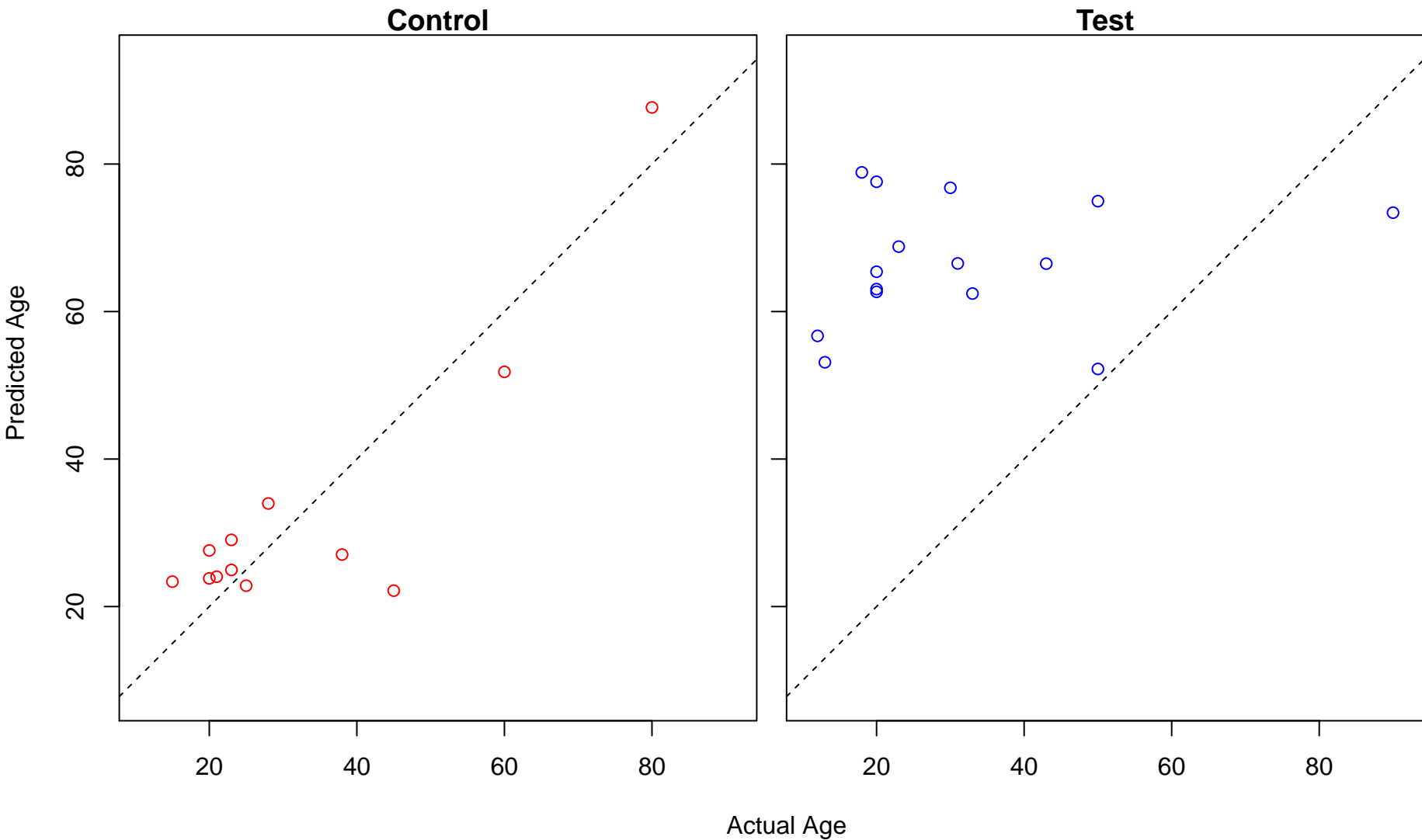
negative regulation of RNA splicing (Score: 6.686895)



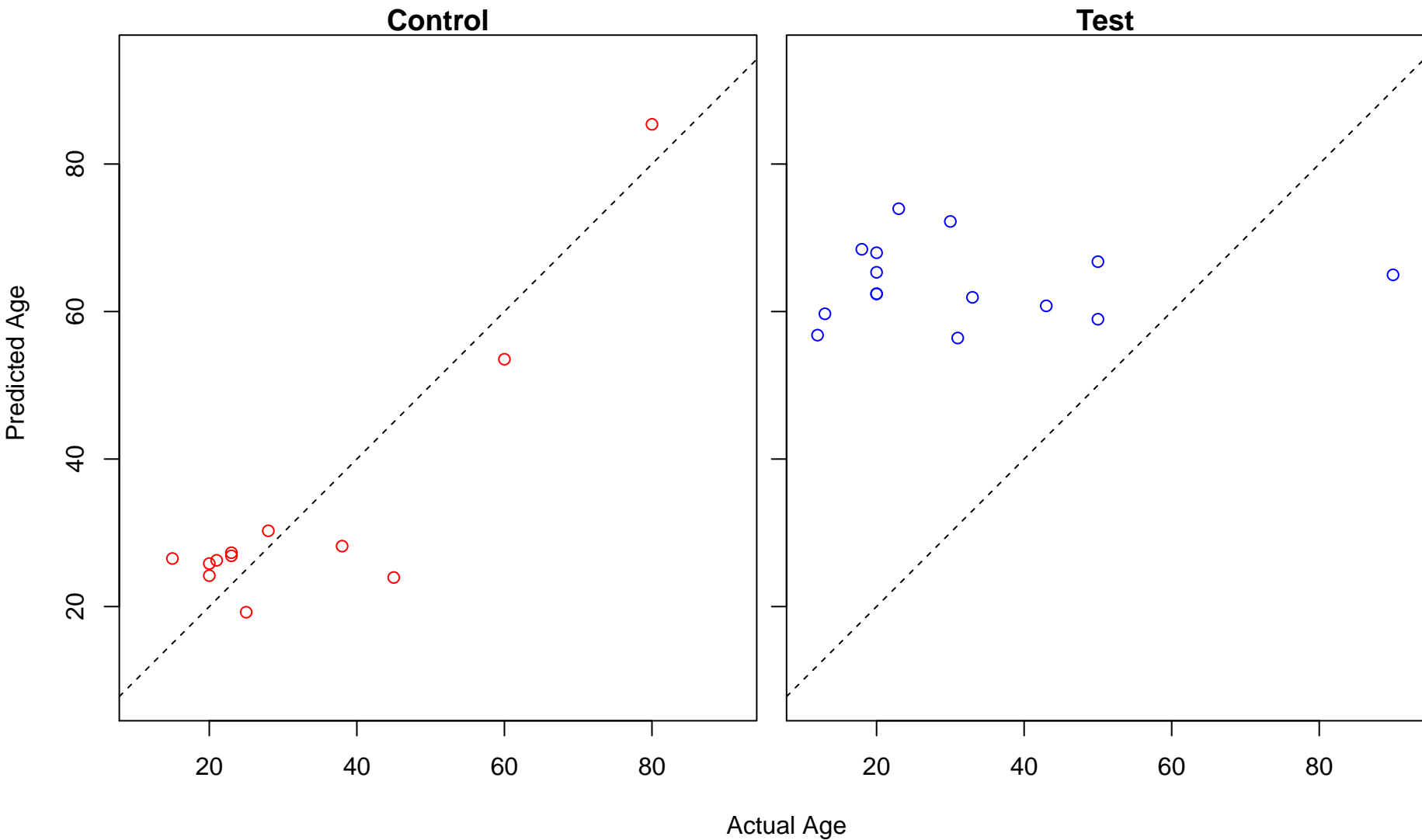
sarcoplasmic reticulum calcium ion transport (Score: 6.685184)



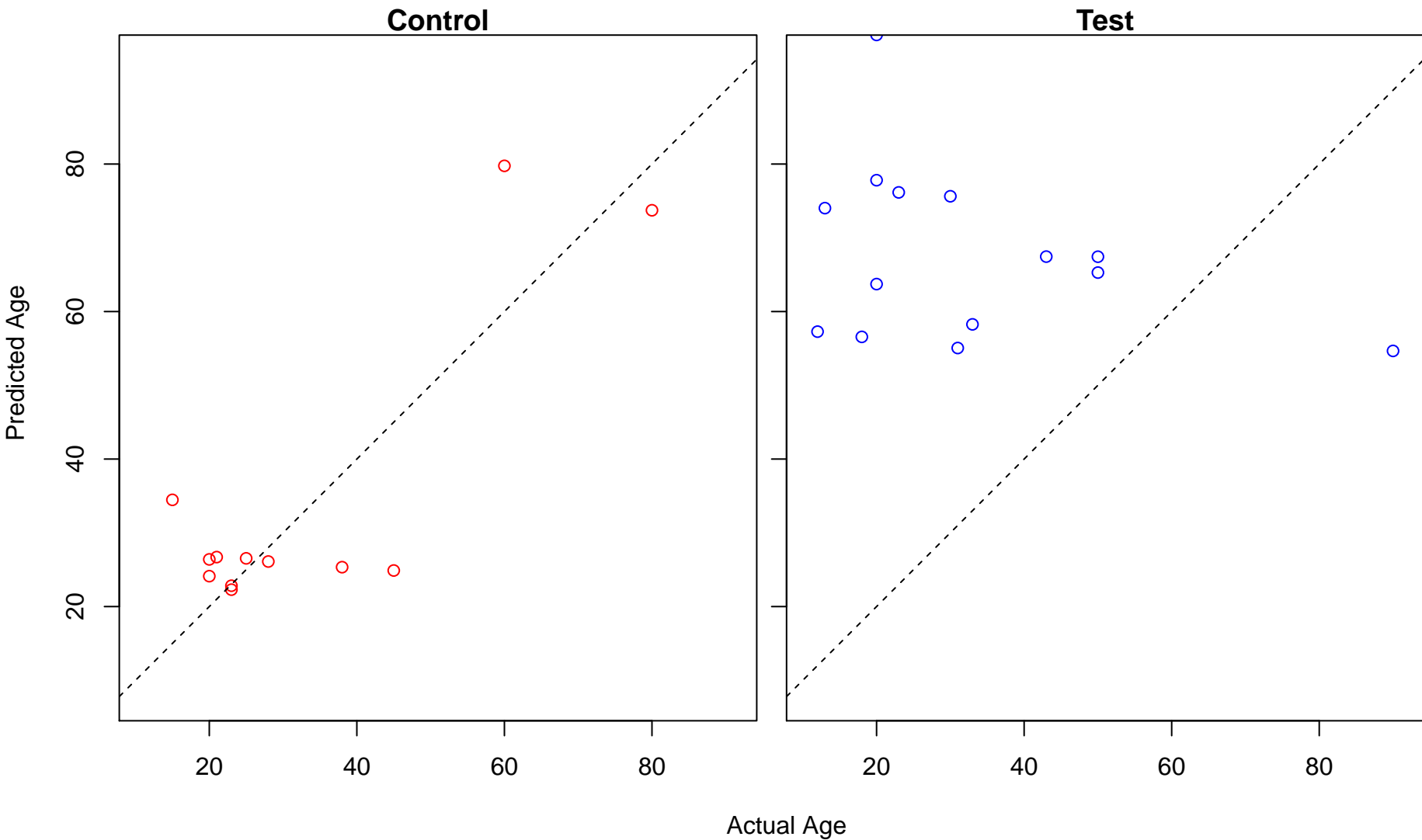
negative regulation of leukocyte differentiation (Score: 6.684788)



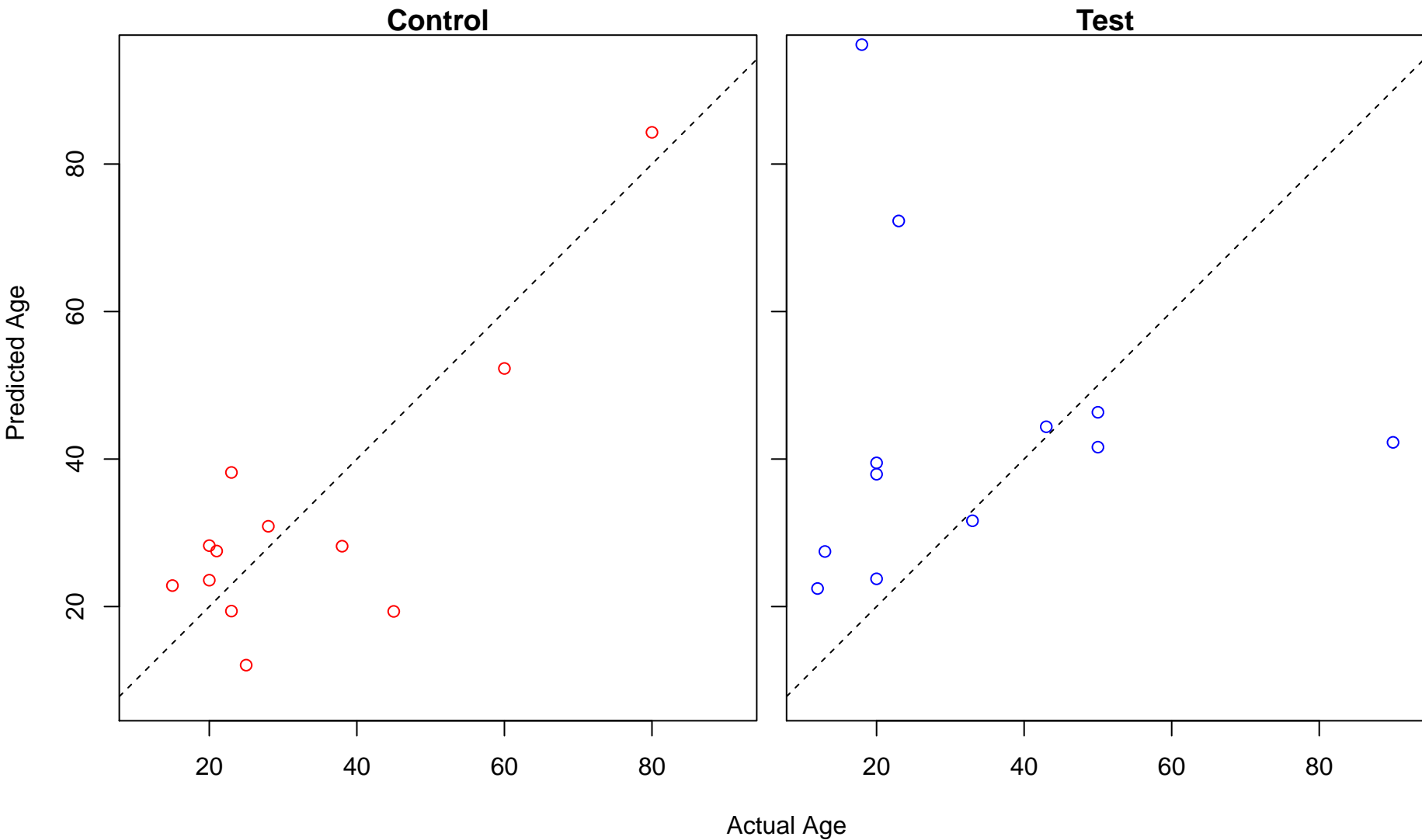
organic hydroxy compound metabolic process (Score: 6.683979)



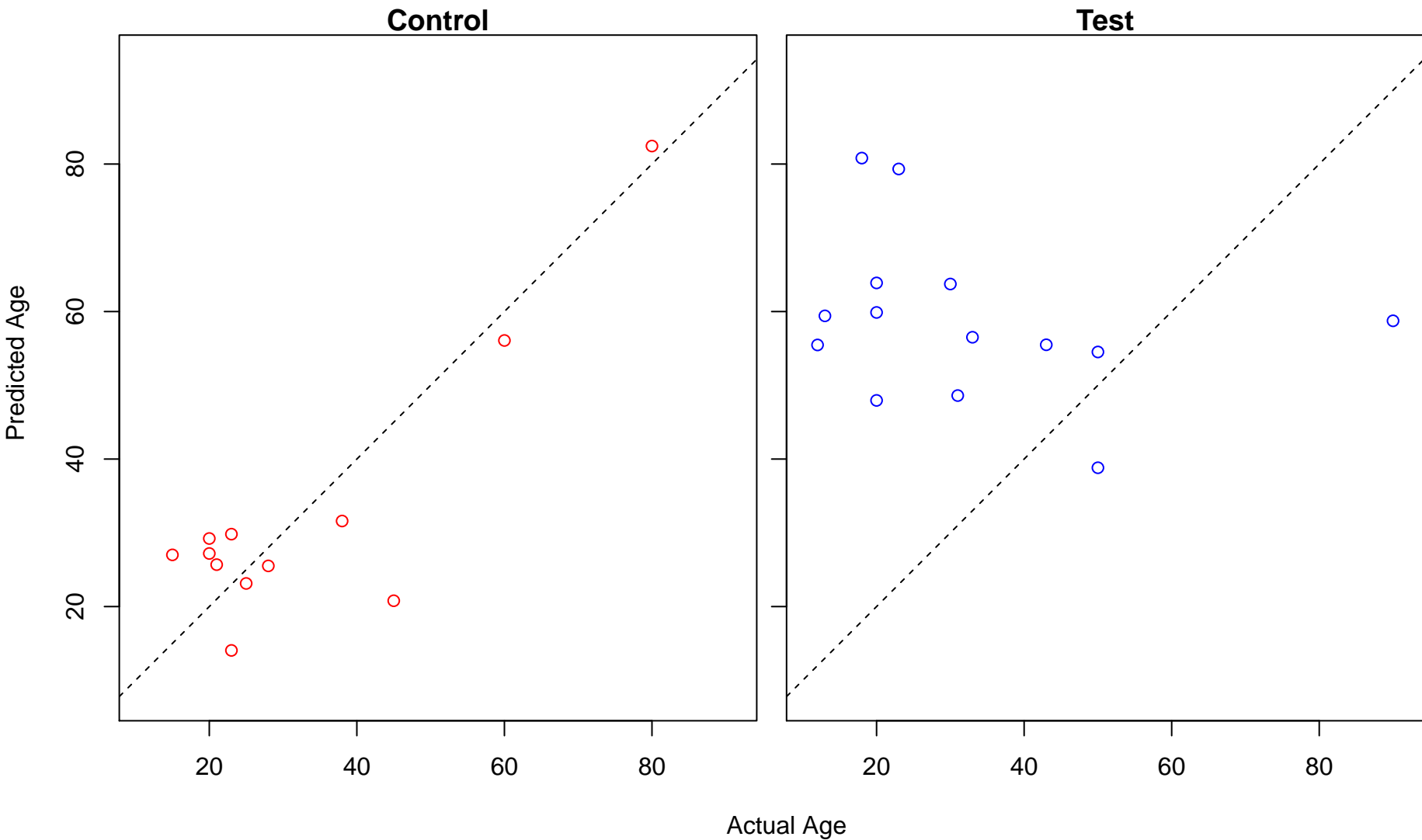
adhesion of symbiont to host (Score: 6.682963)



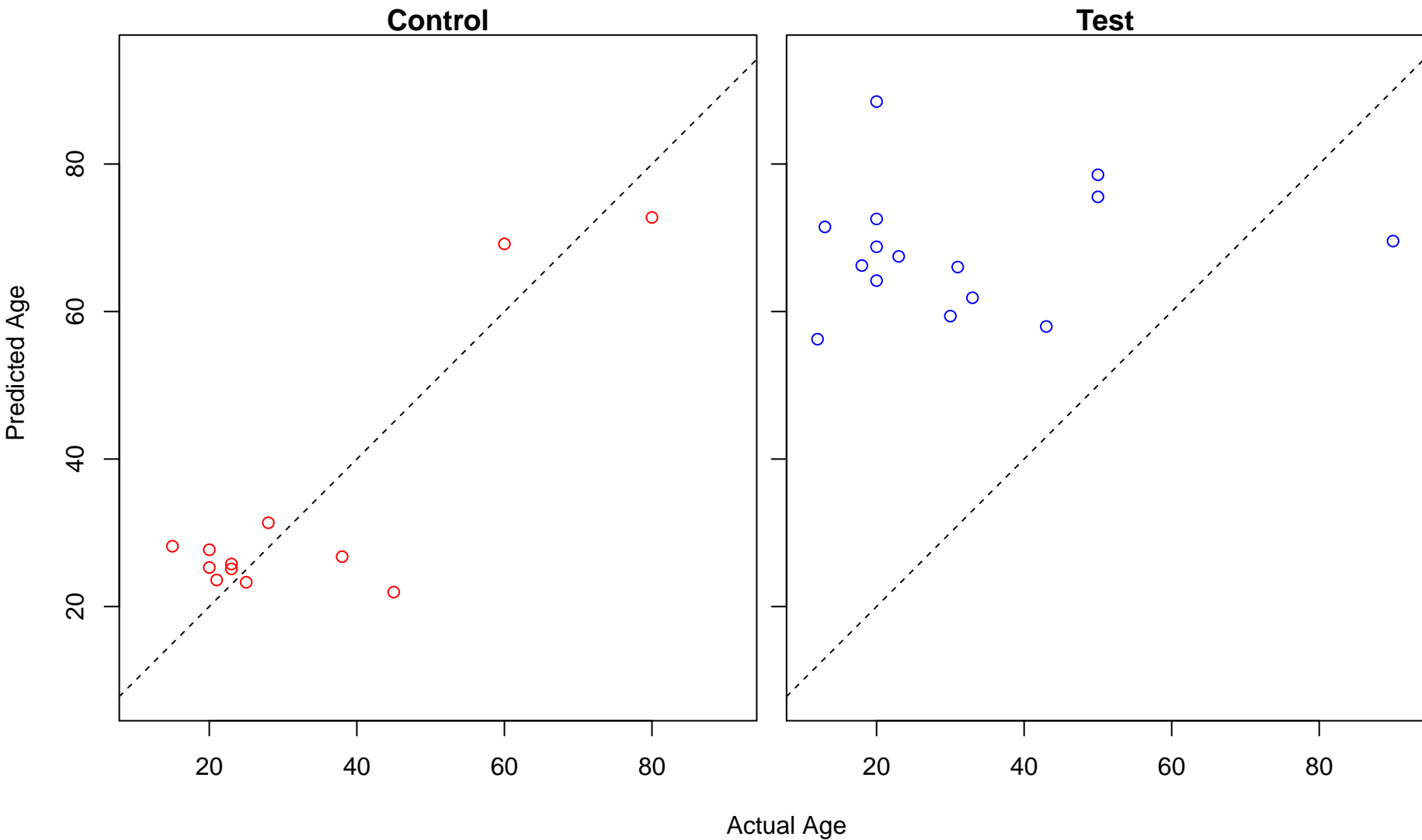
positive regulation of lymphocyte activation (Score: 6.682754)



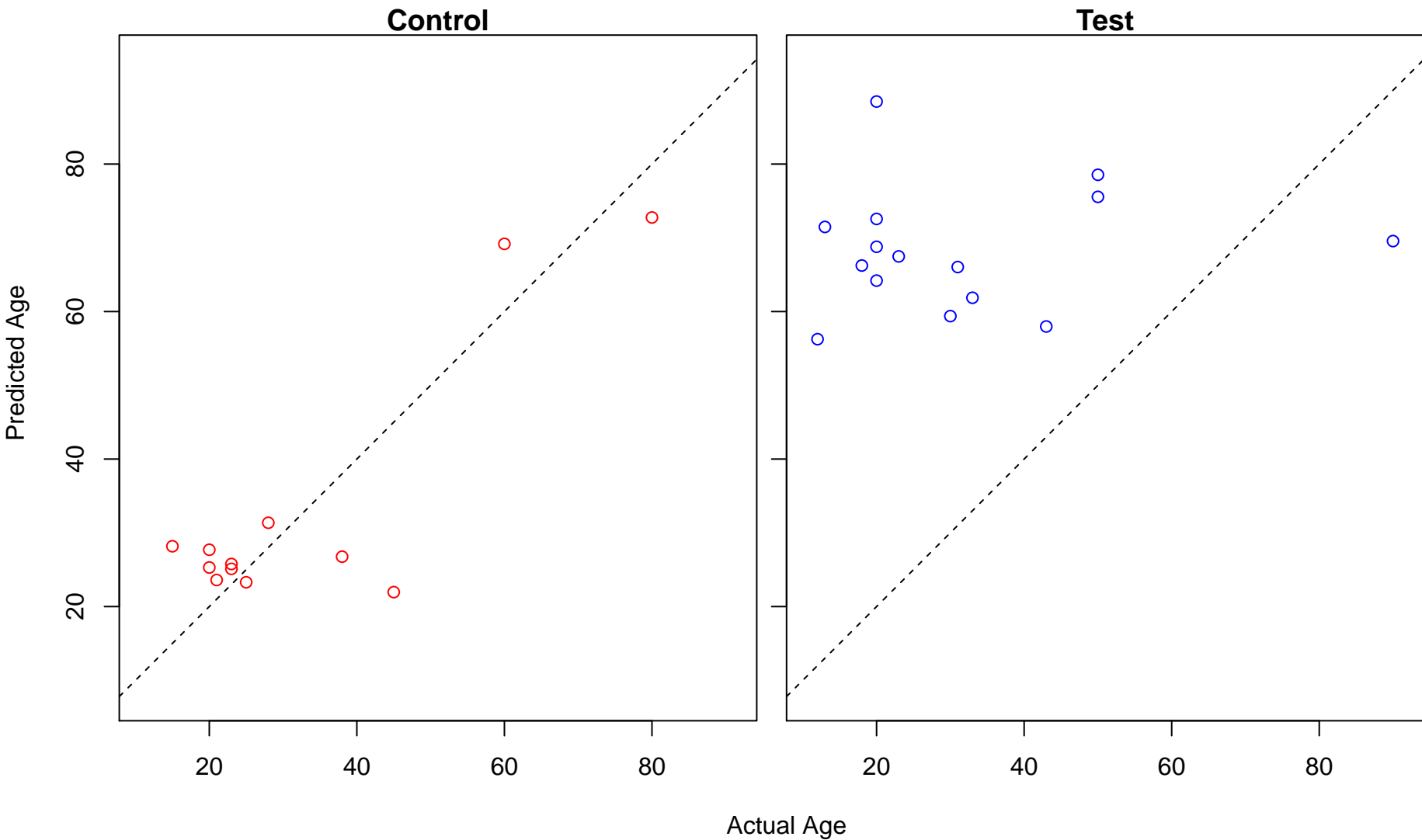
cell differentiation involved in metanephros development (Score: 6.678649)



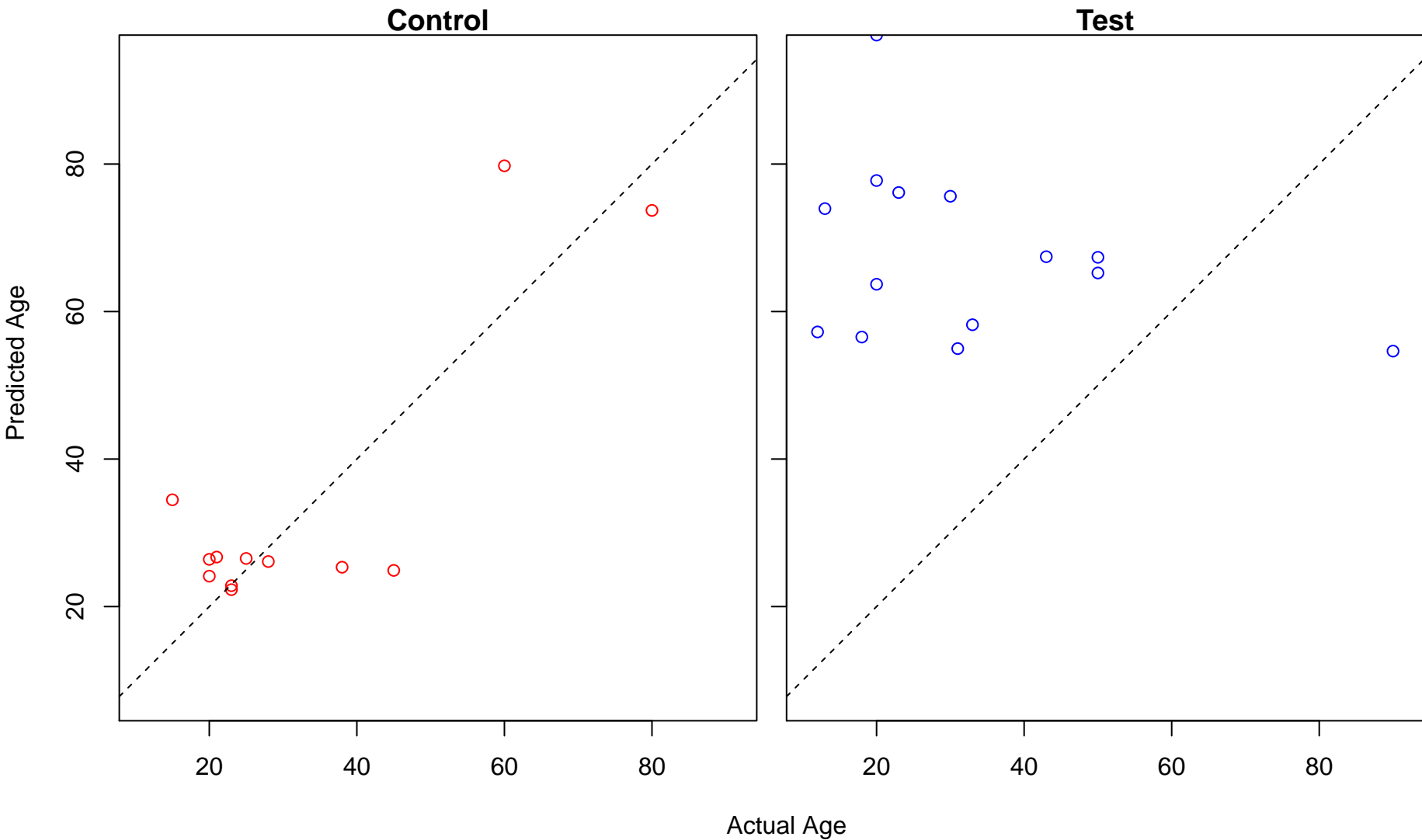
cellular response to peptide hormone stimulus (Score: 6.676696)



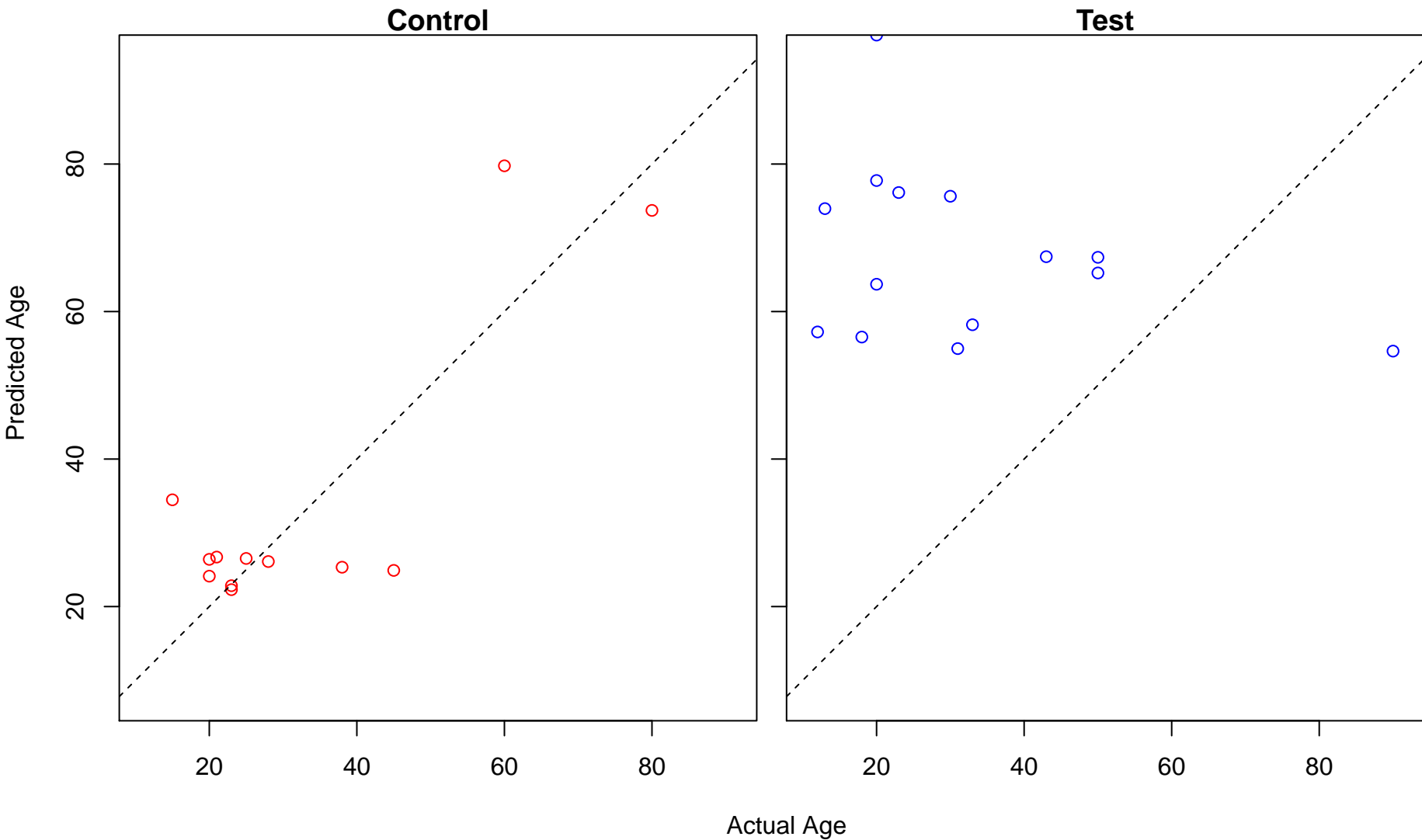
cellular response to peptide (Score: 6.676210)



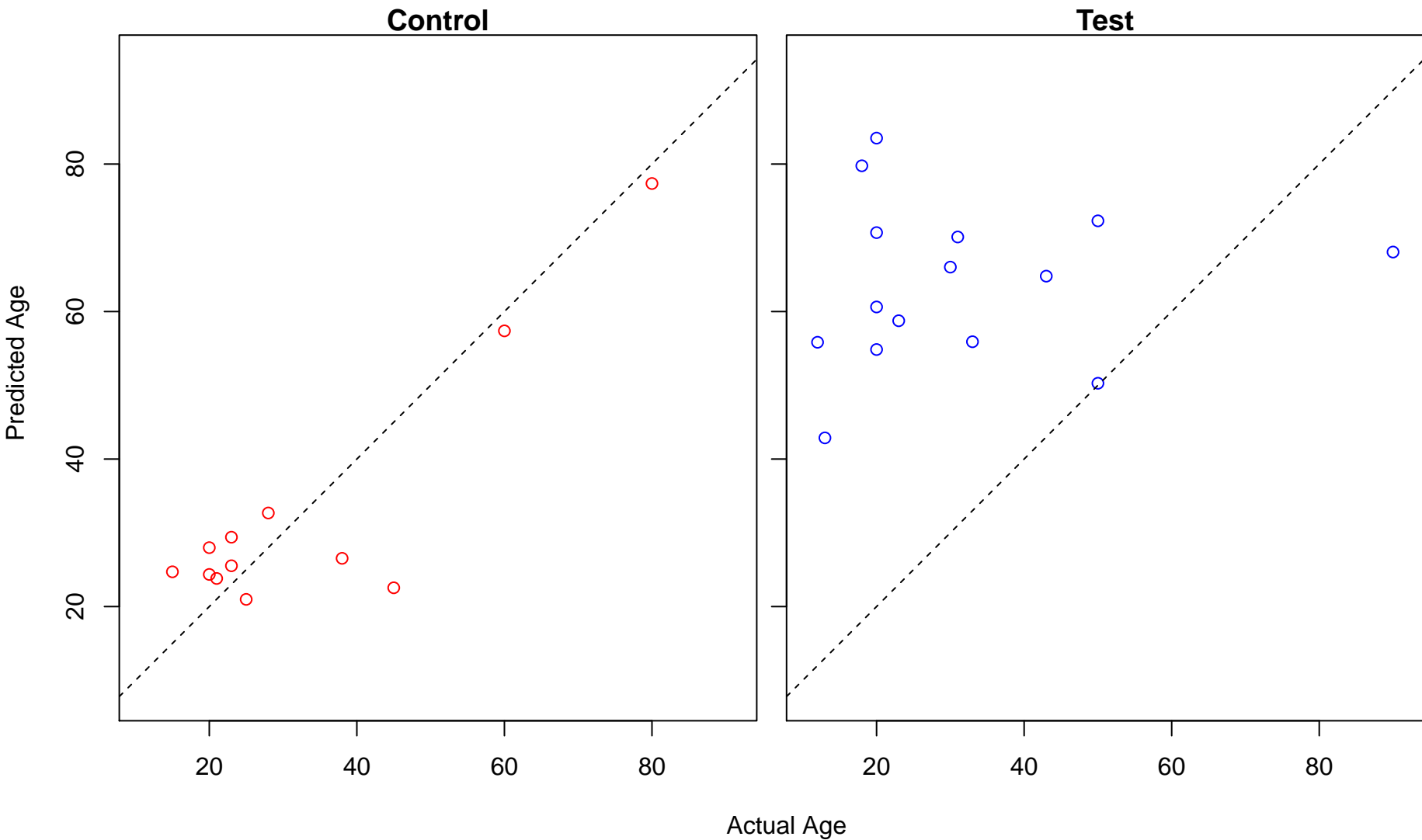
virion attachment to host cell (Score: 6.676091)



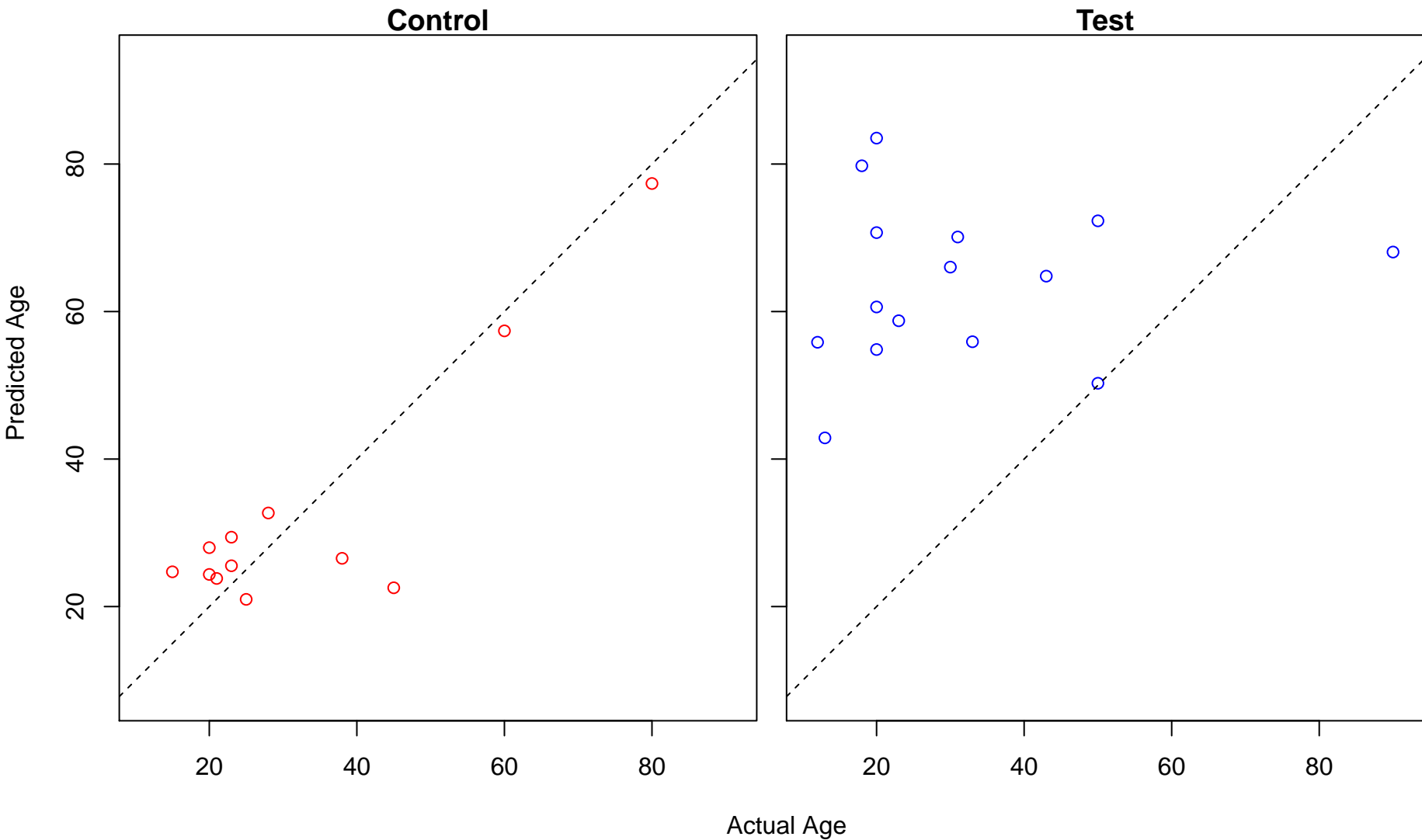
adhesion of symbiont to host cell (Score: 6.676091)



T cell activation (Score: 6.675794)

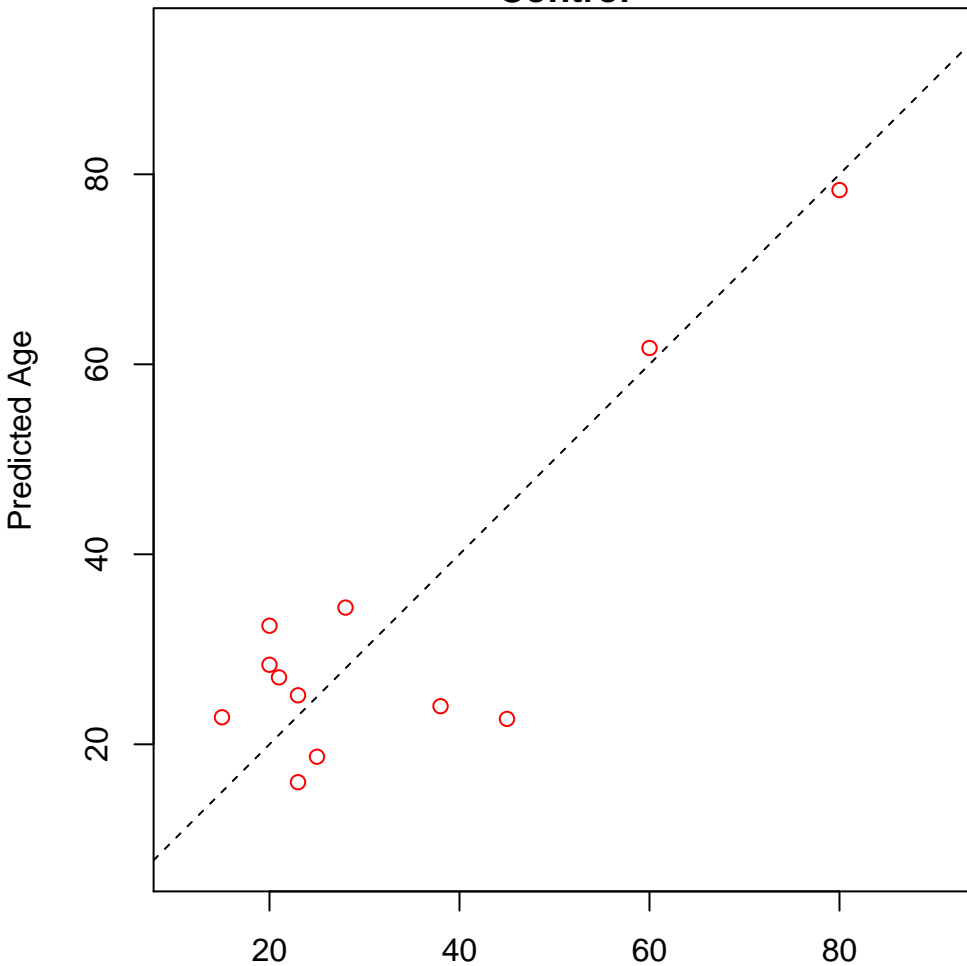


T cell aggregation (Score: 6.675794)

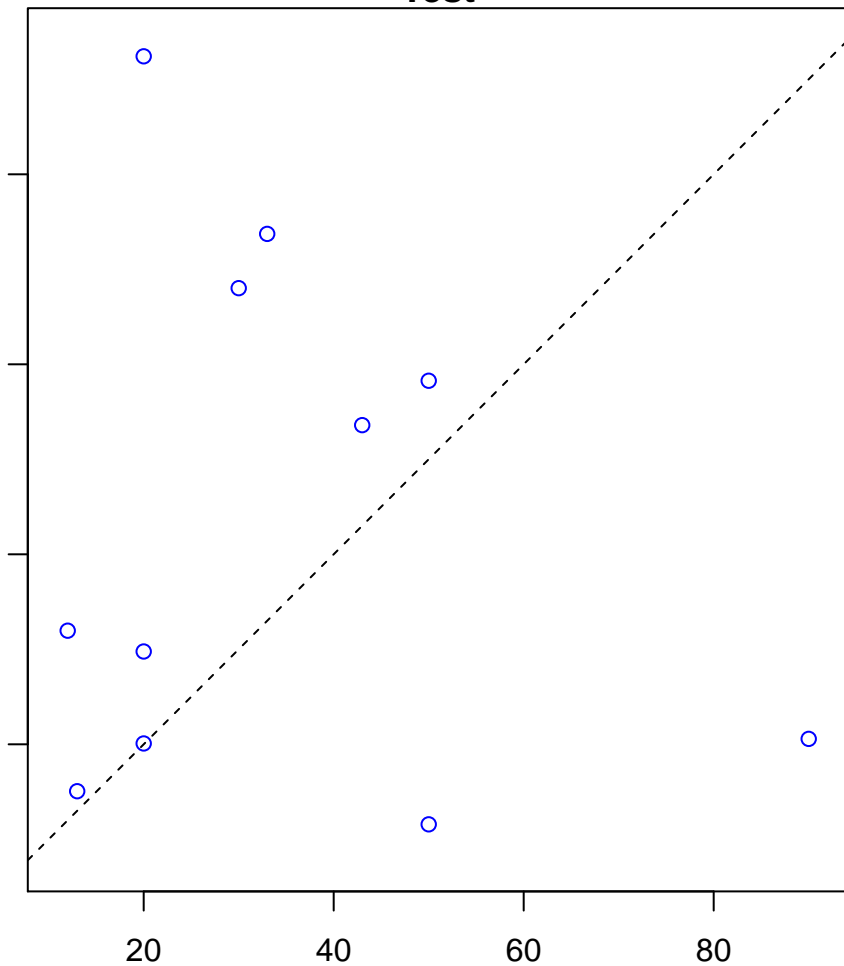


positive regulation of peptidase activity (Score: 6.674388)

Control

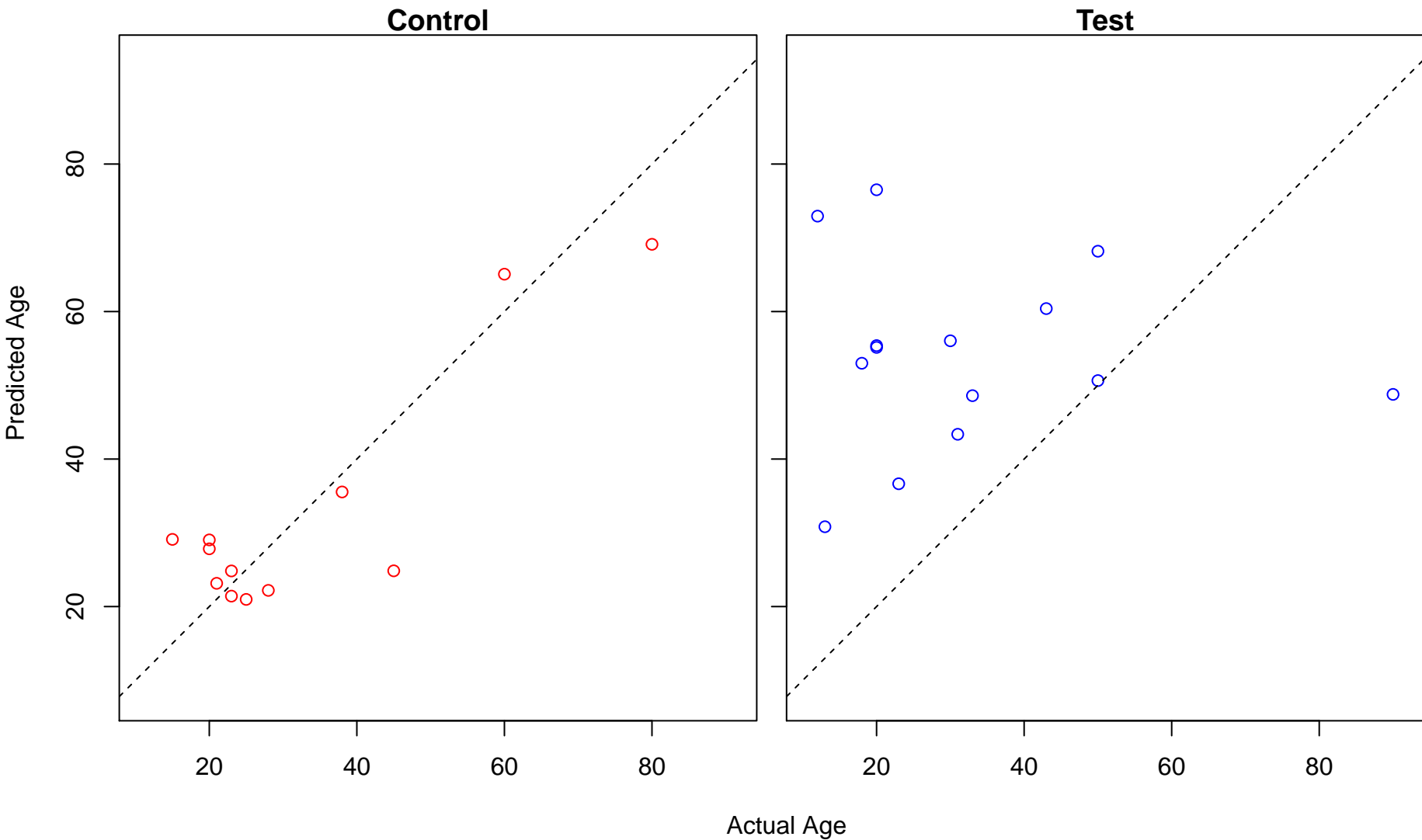


Test



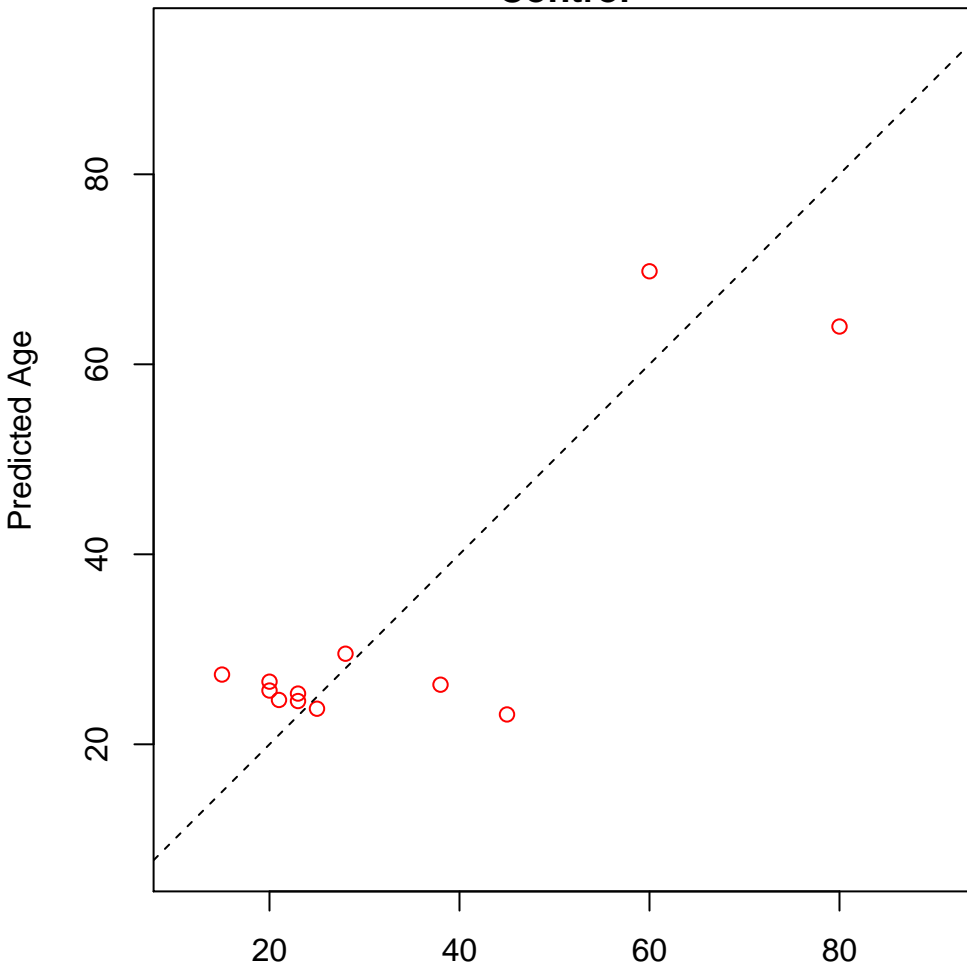
Actual Age

isoprenoid catabolic process (Score: 6.672988)

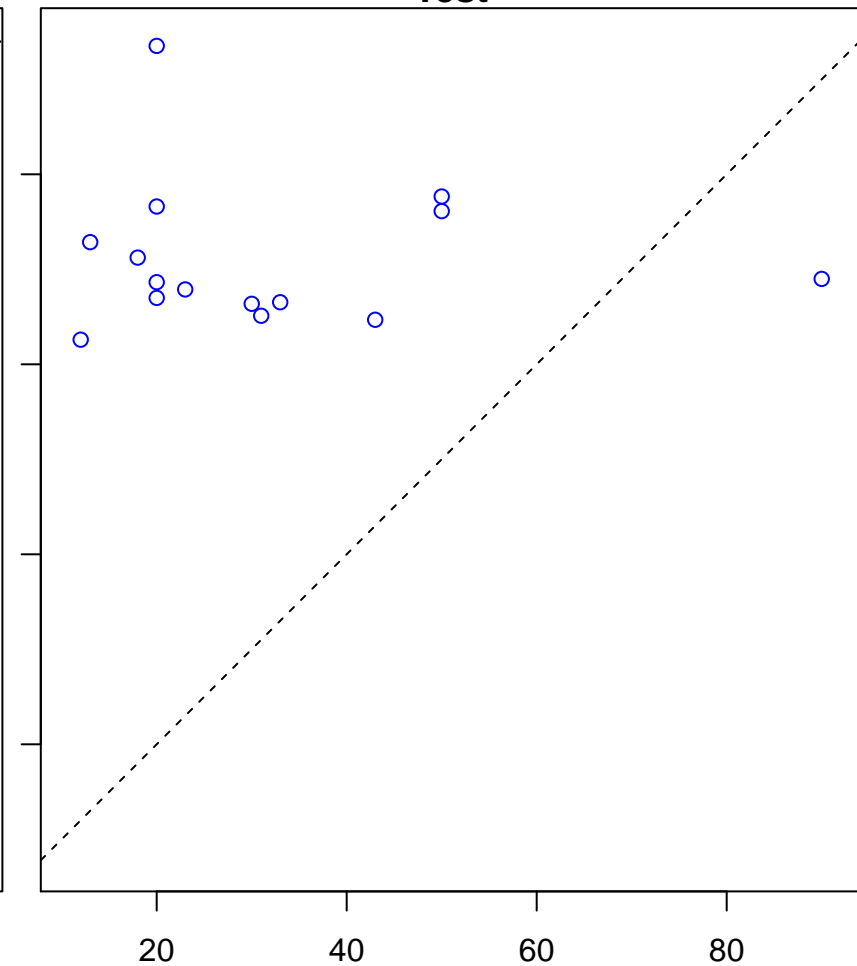


organophosphate biosynthetic process (Score: 6.672373)

Control

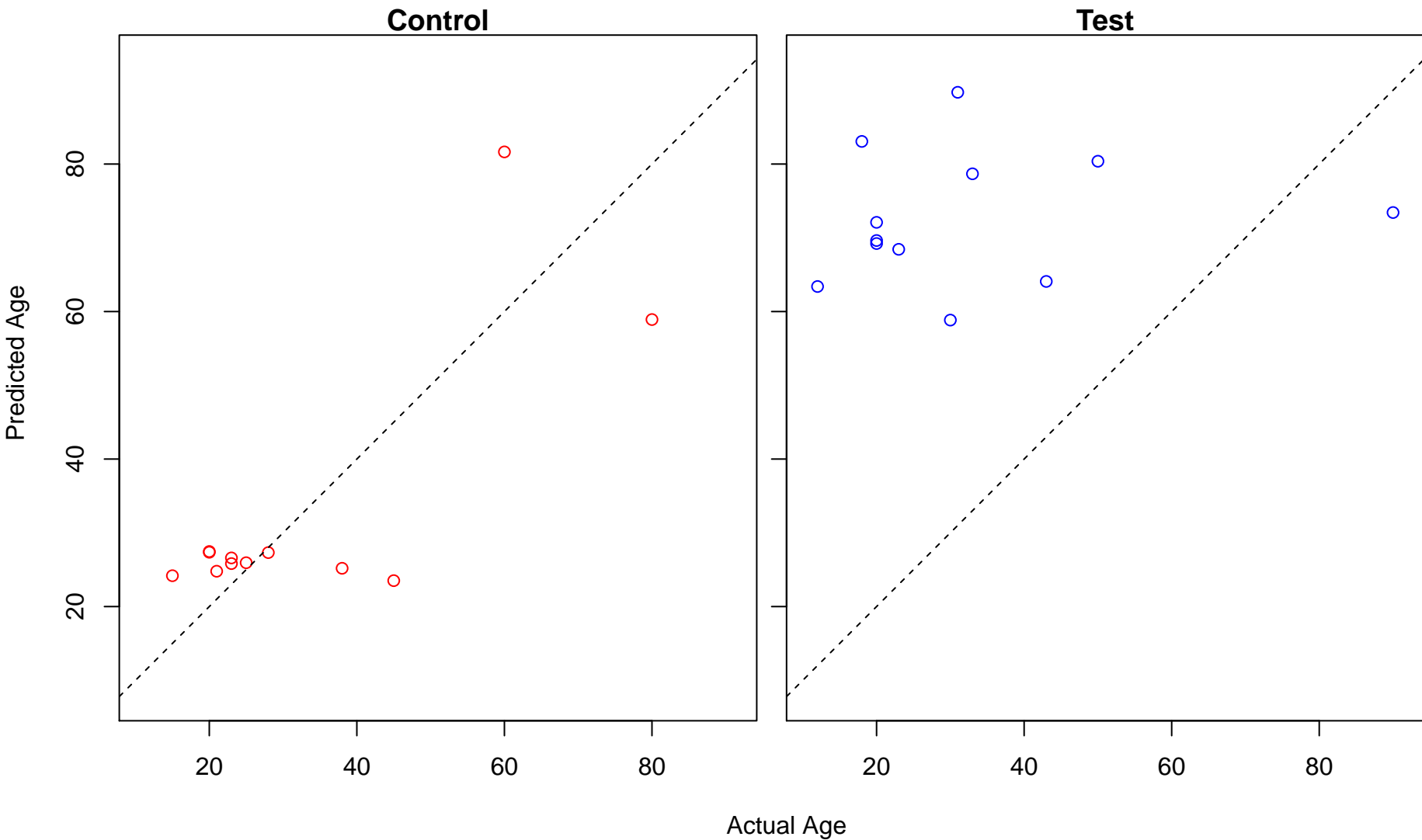


Test

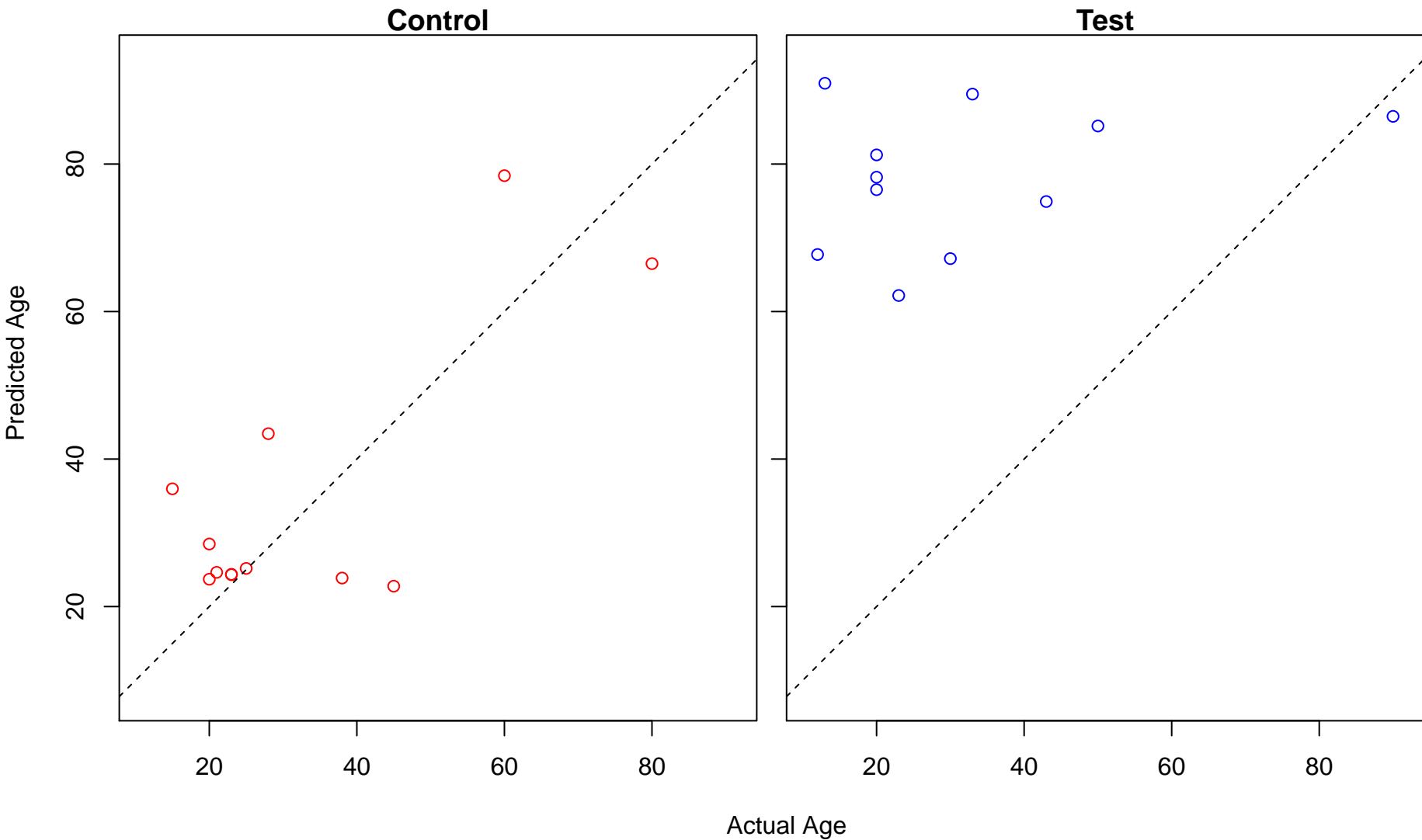


Actual Age

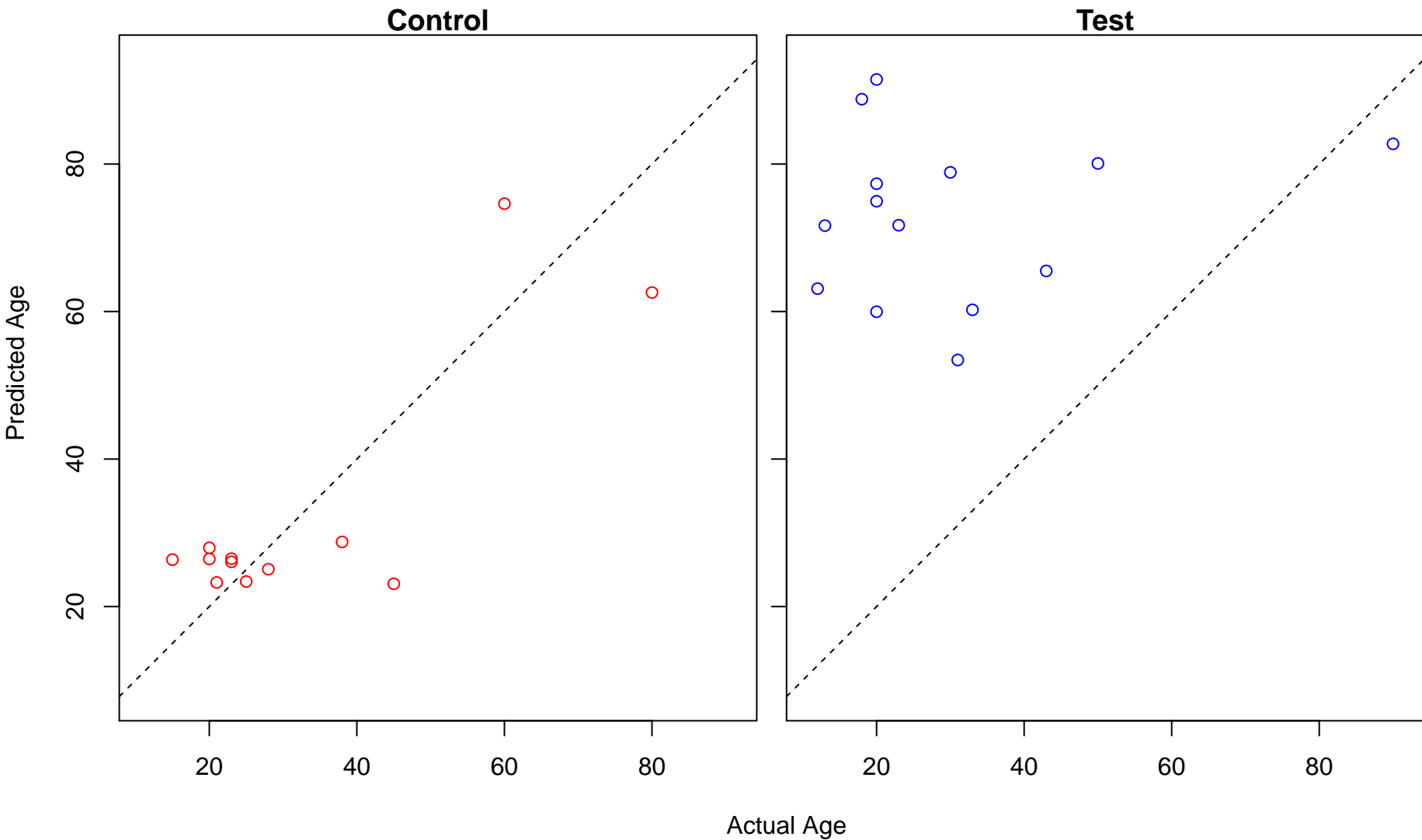
regulation of I-kappaB kinase/NF-kappaB signaling (Score: 6.671635)



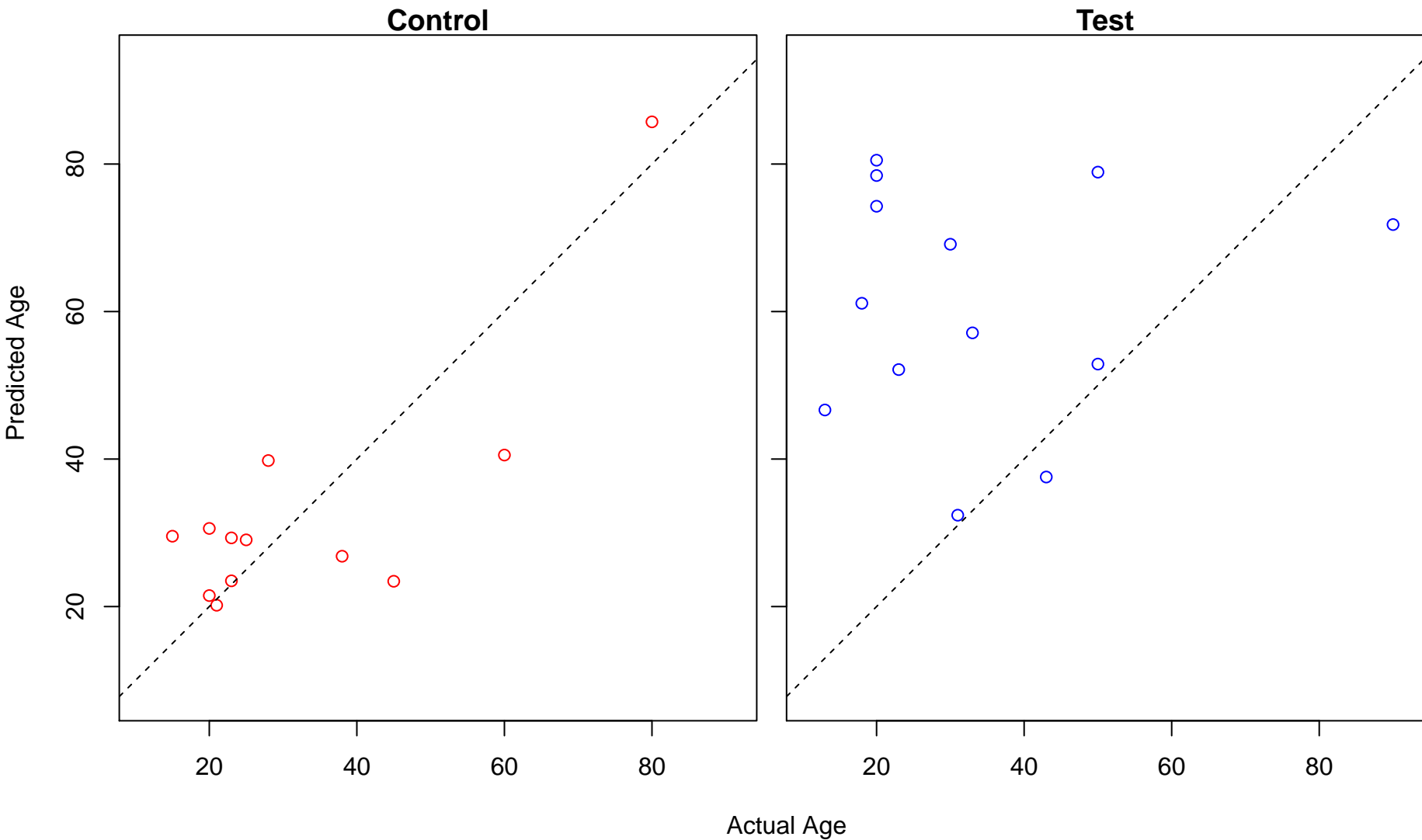
lamellipodium assembly (Score: 6.671613)



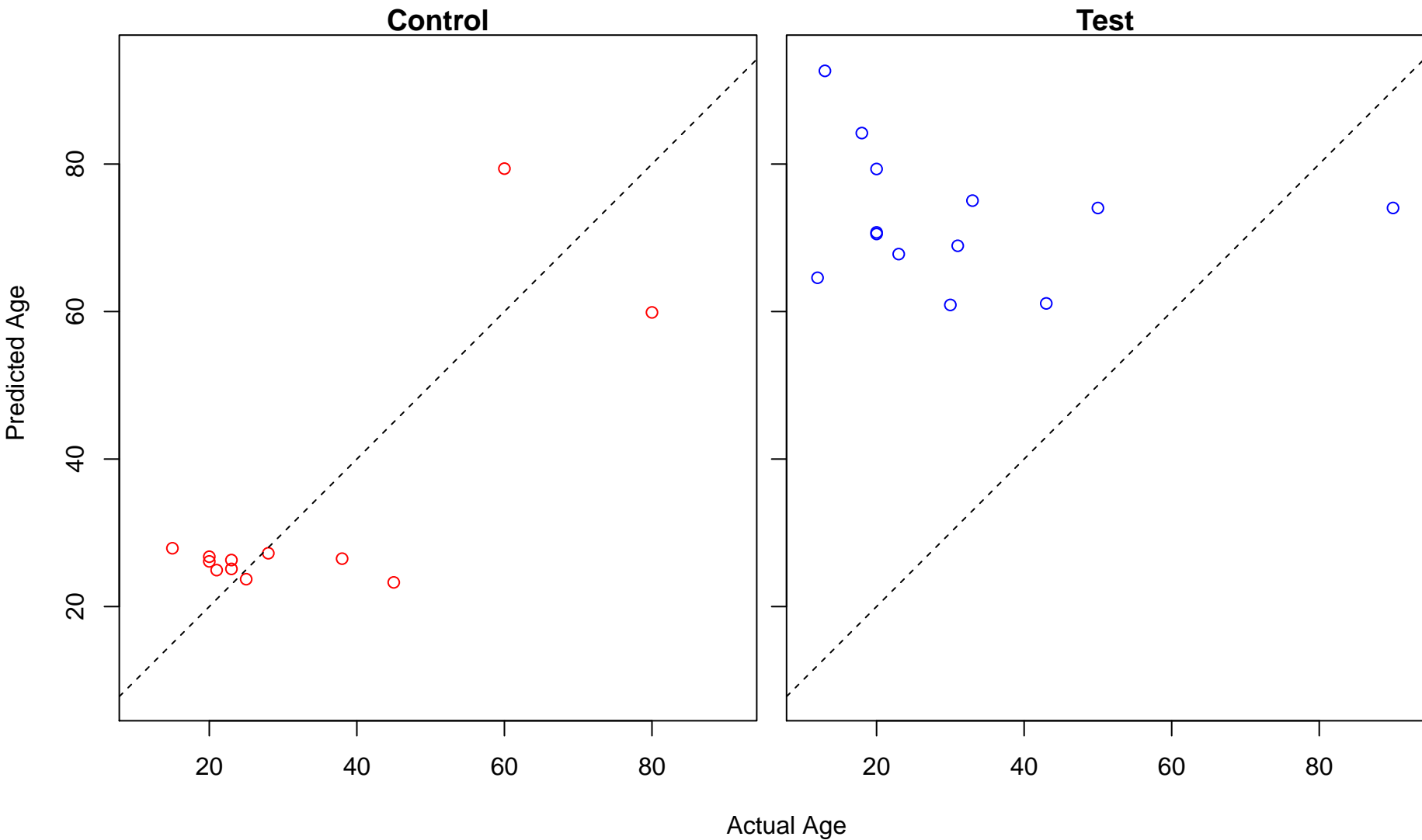
myofibril assembly (Score: 6.669858)



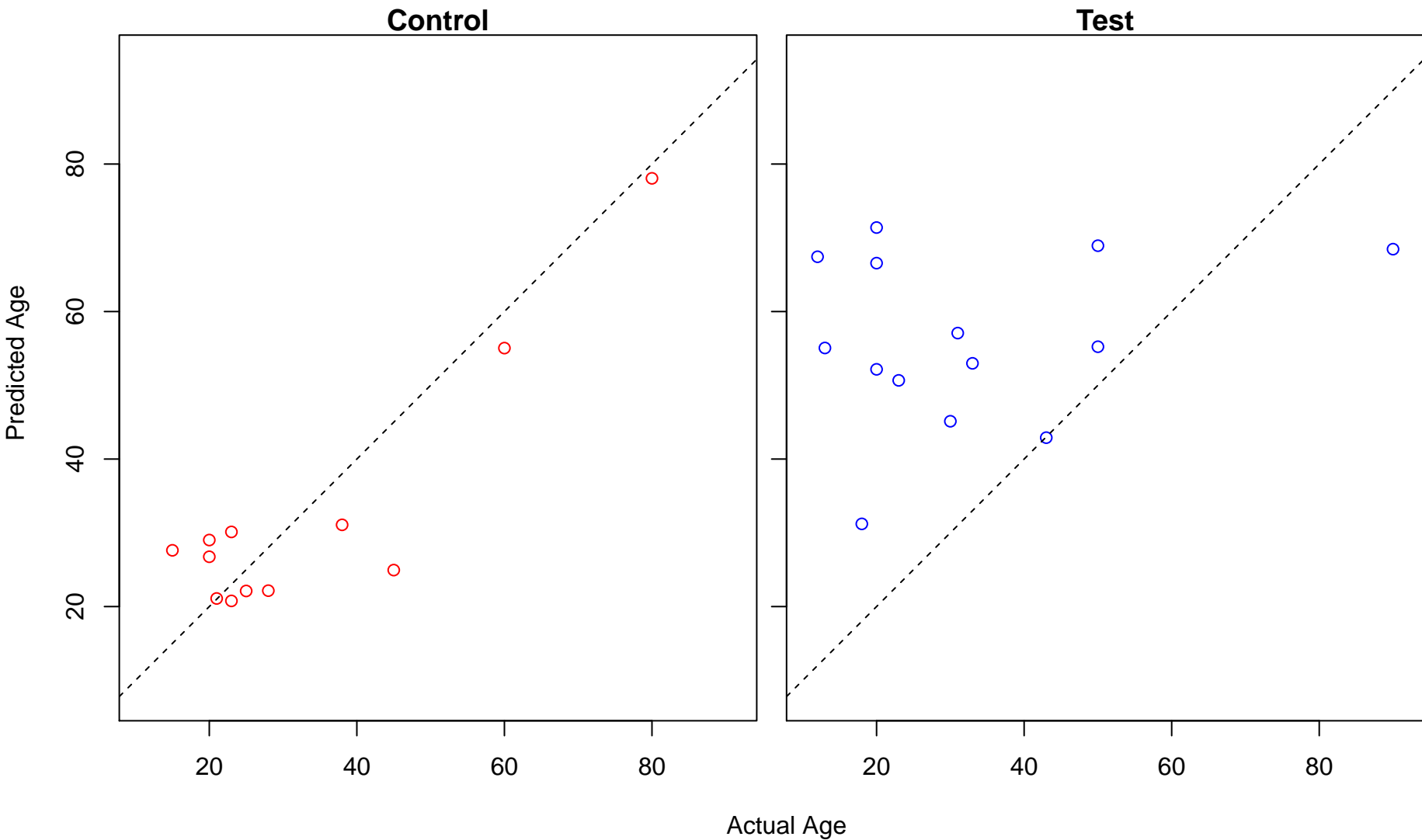
cellular response to vitamin (Score: 6.669820)



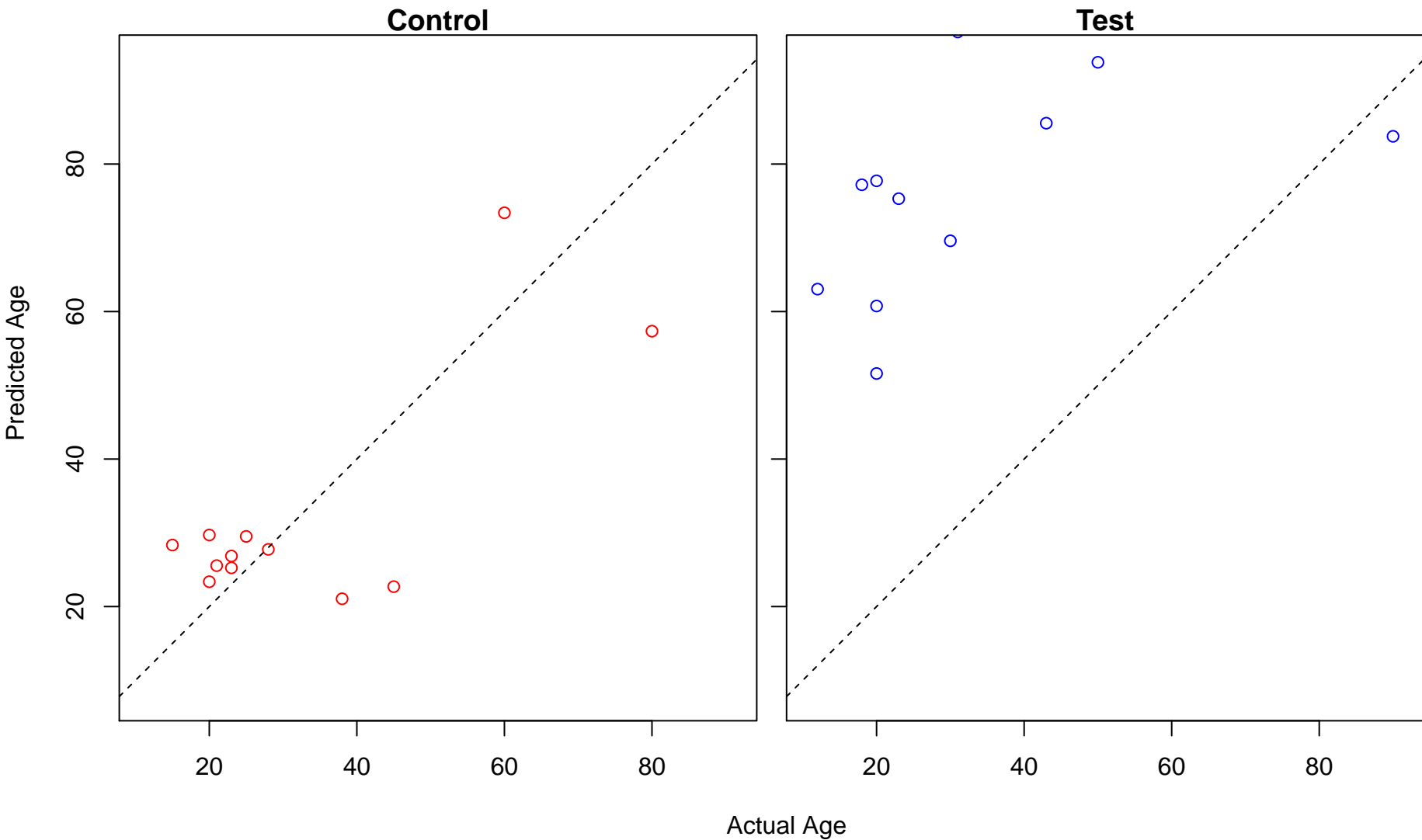
postreplication repair (Score: 6.666800)



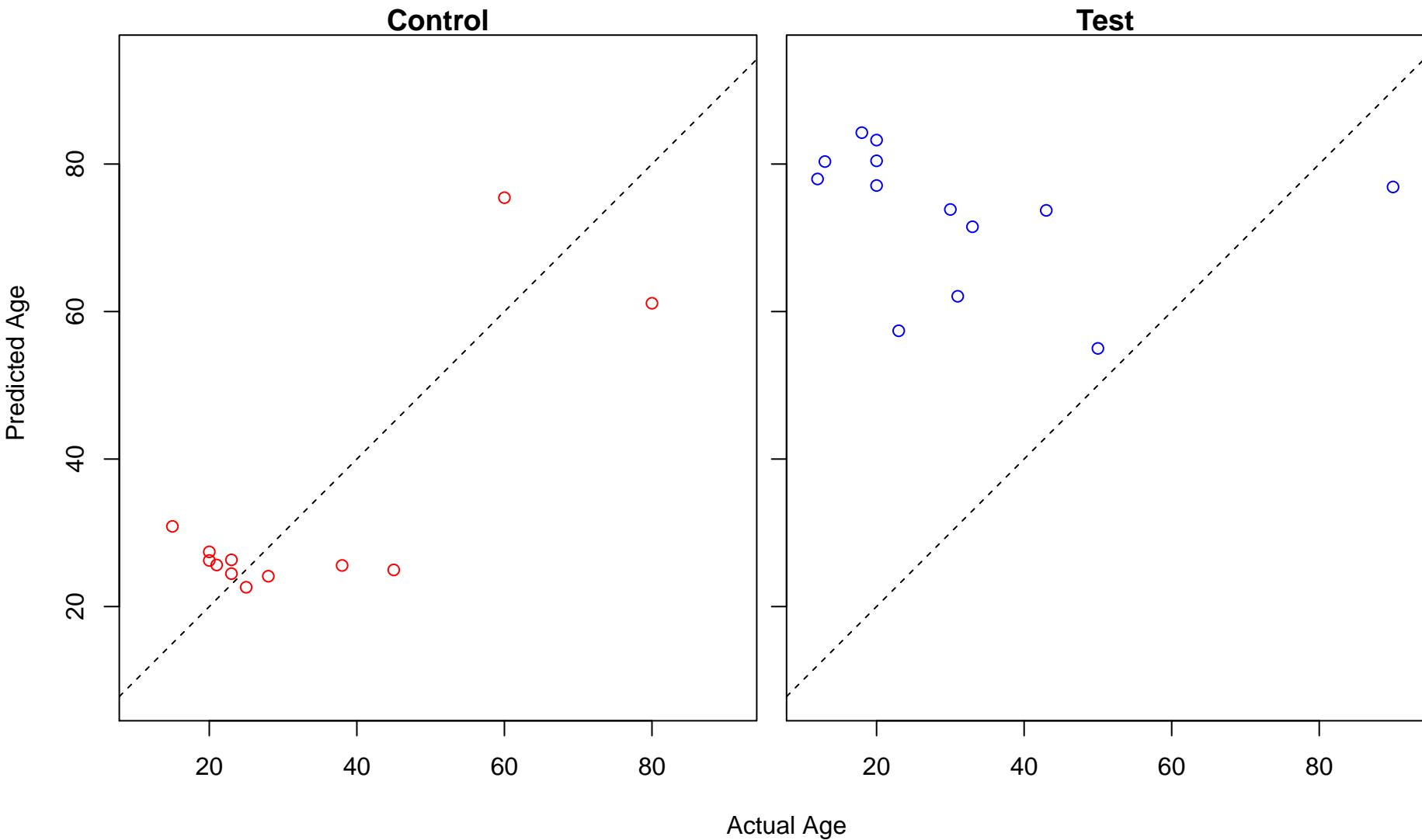
modified amino acid transport (Score: 6.666406)



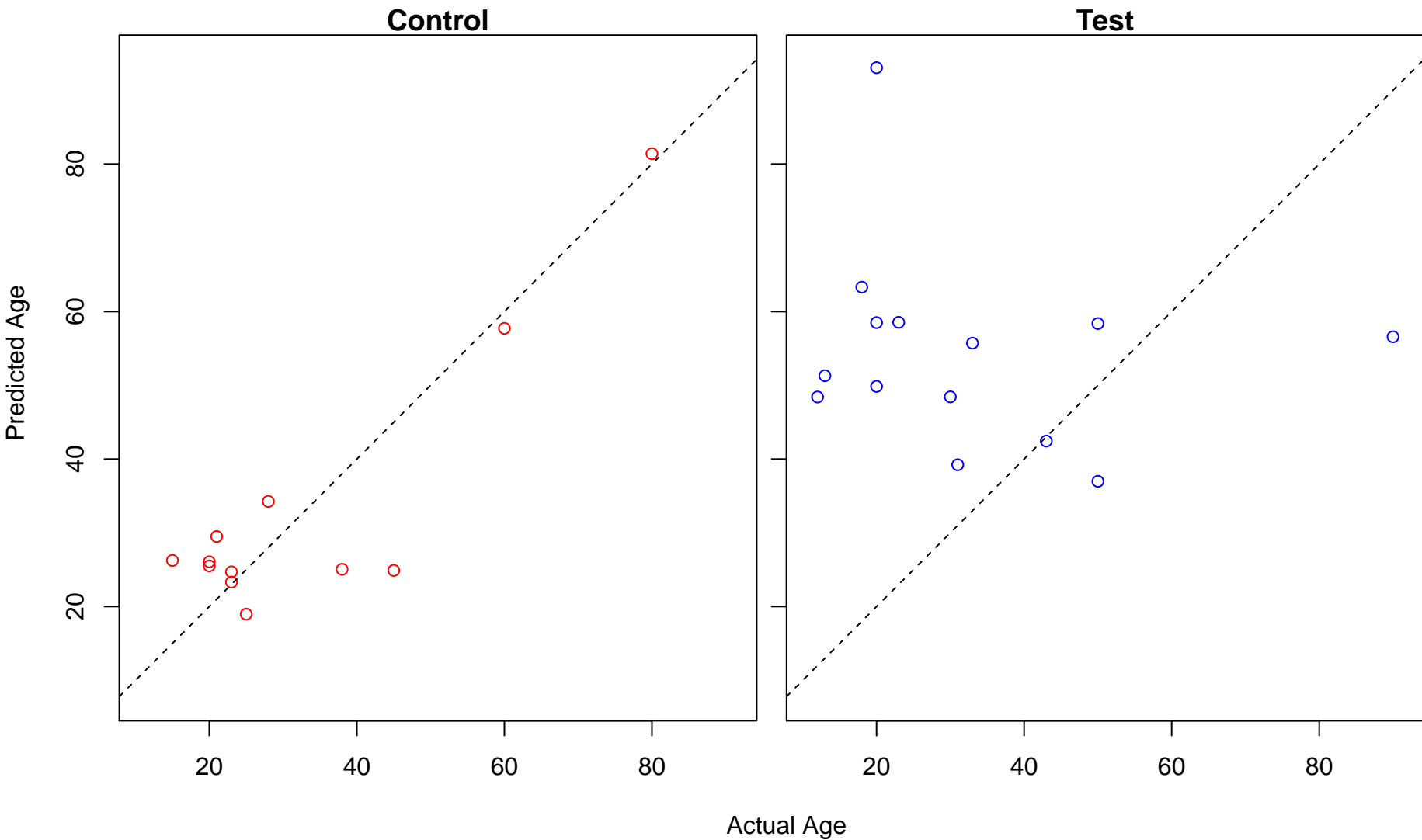
chromosome condensation (Score: 6.664782)



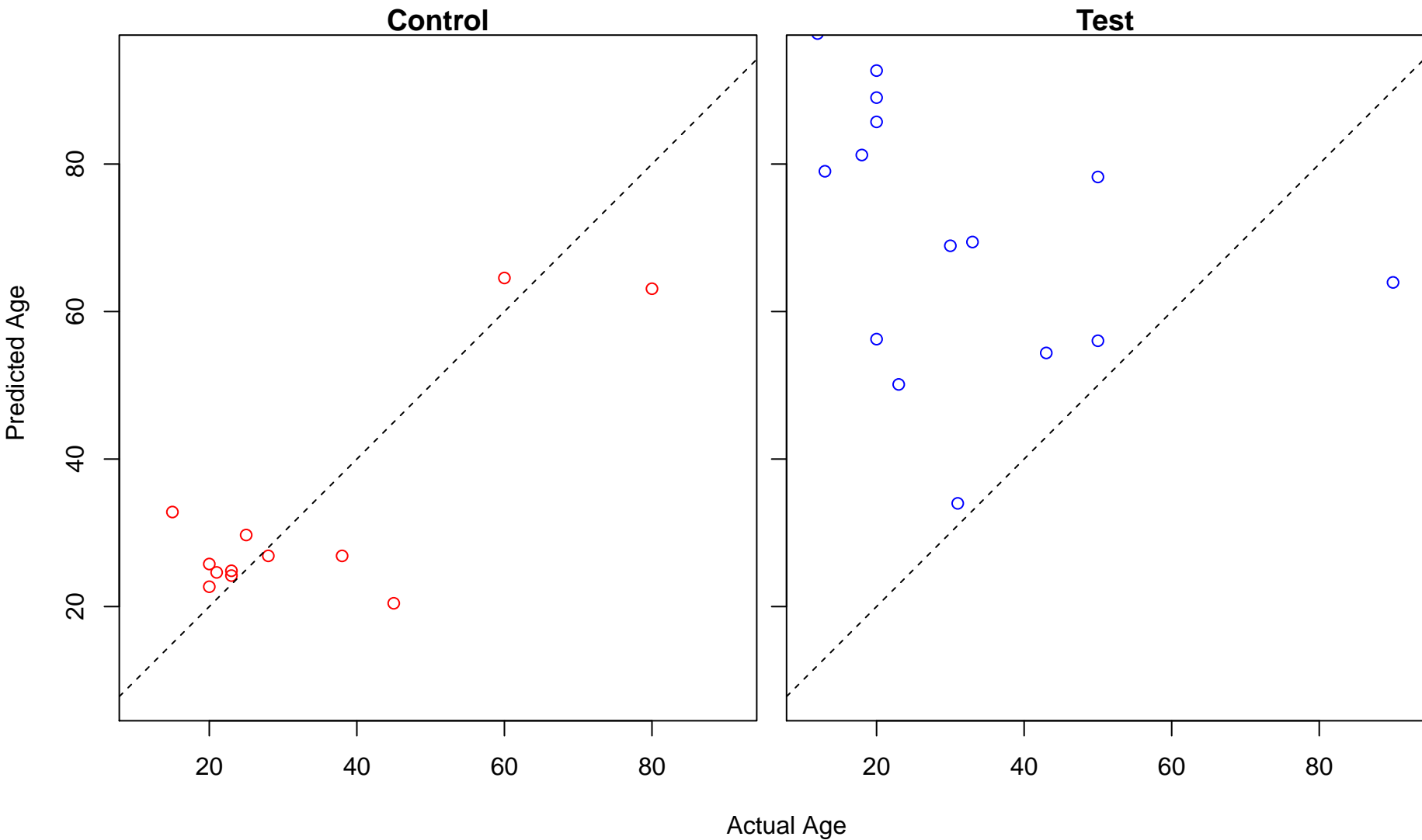
endothelial cell proliferation (Score: 6.660878)



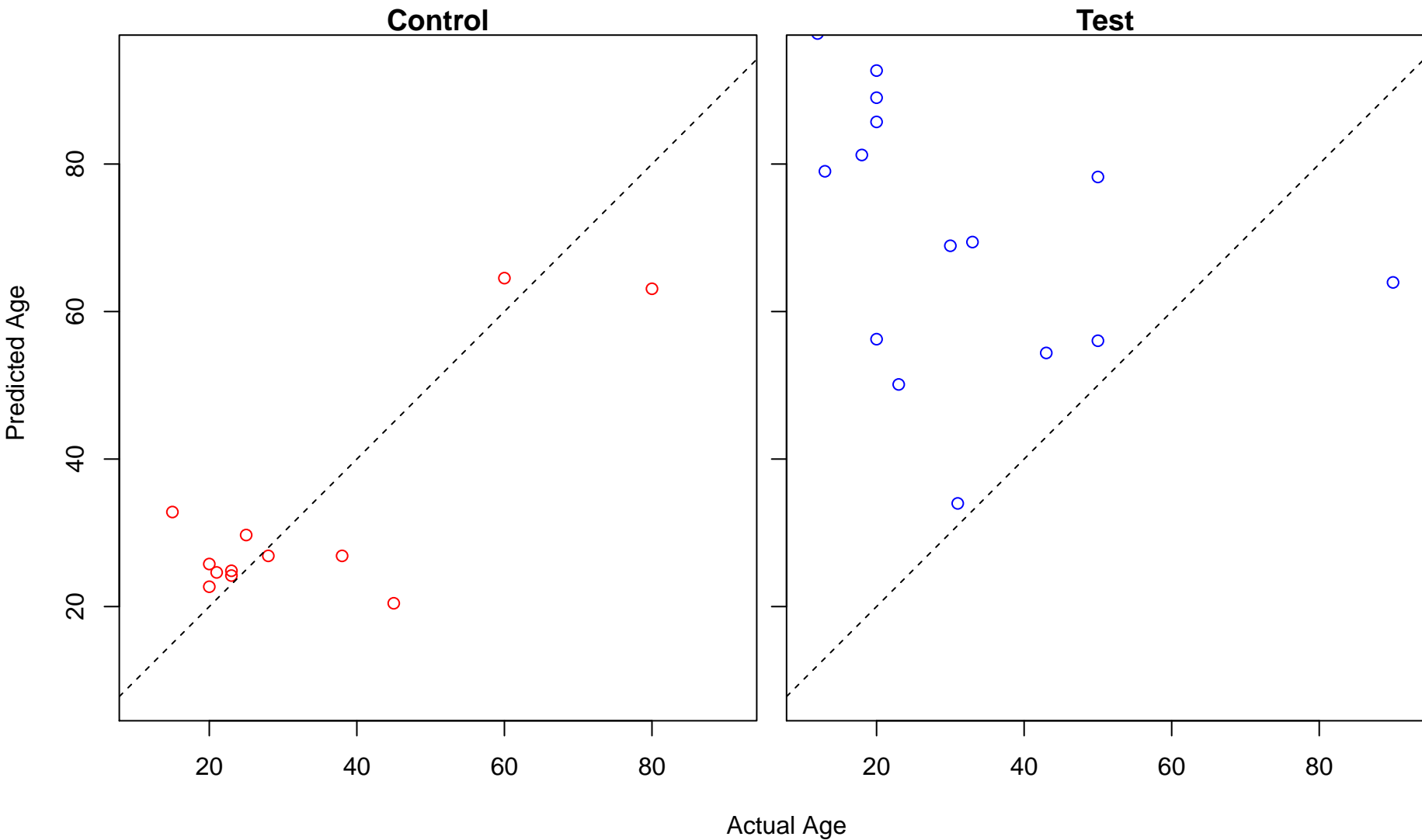
histone lysine methylation (Score: 6.657656)



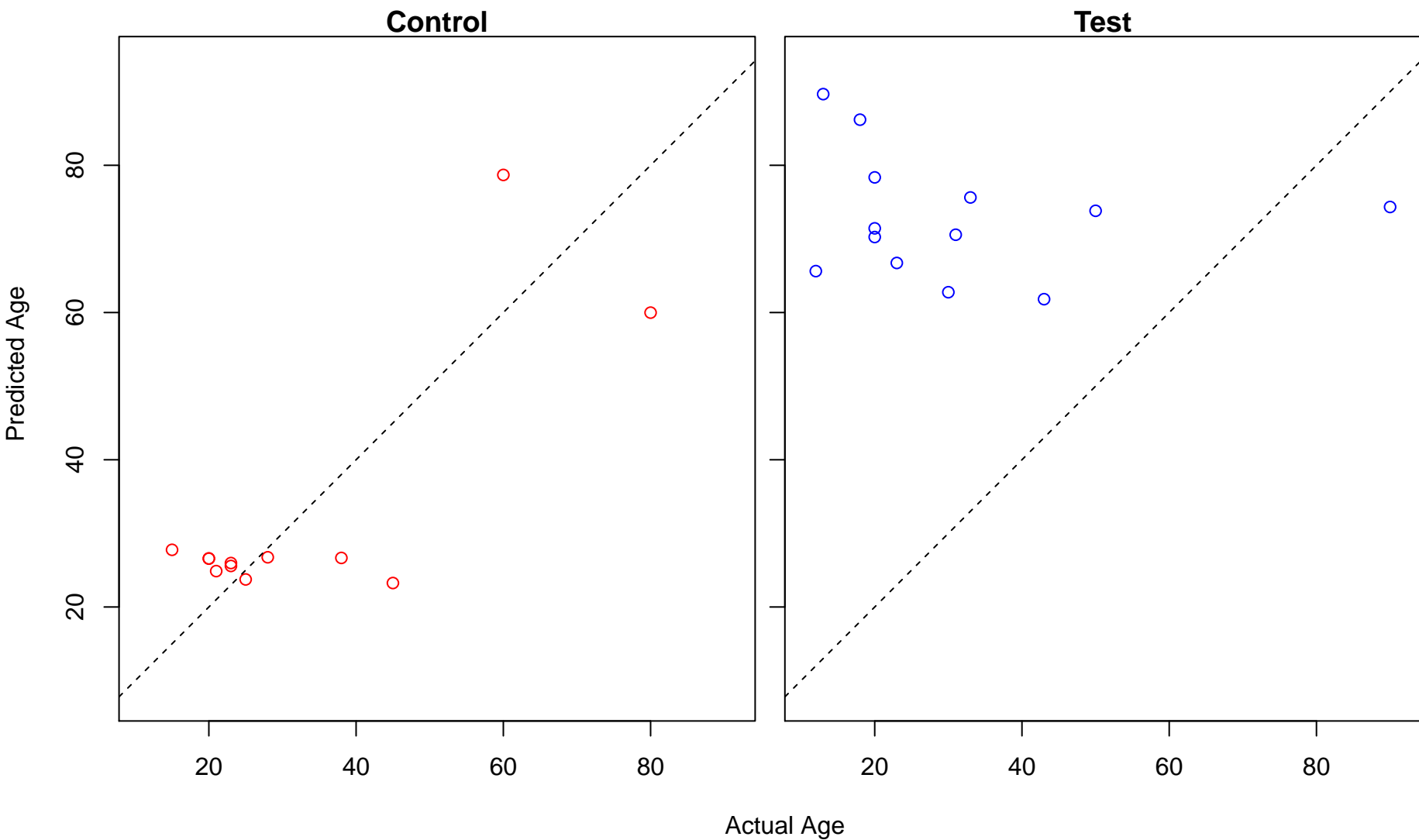
positive regulation of bone mineralization (Score: 6.655936)



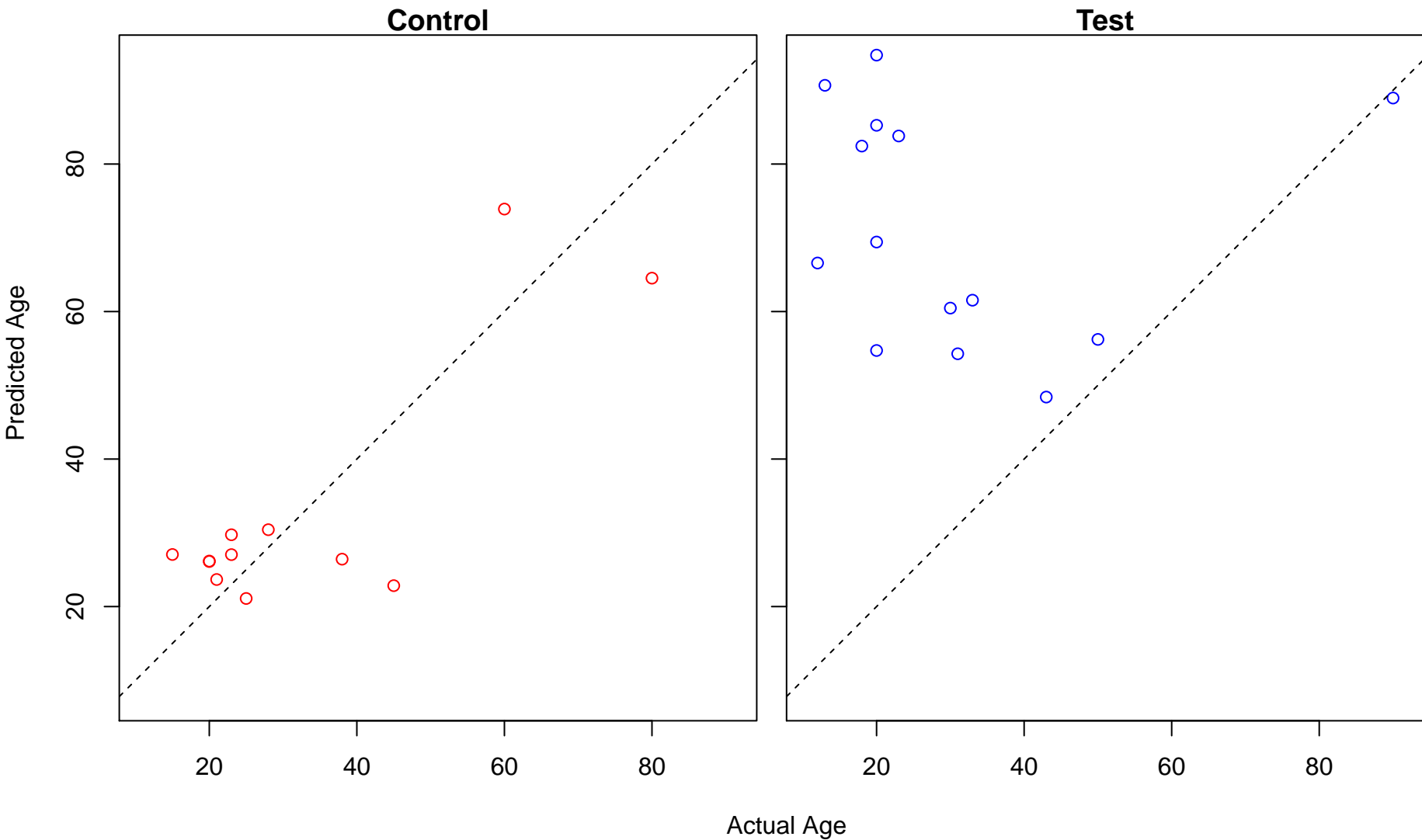
positive regulation of biomineral tissue development (Score: 6.655616)



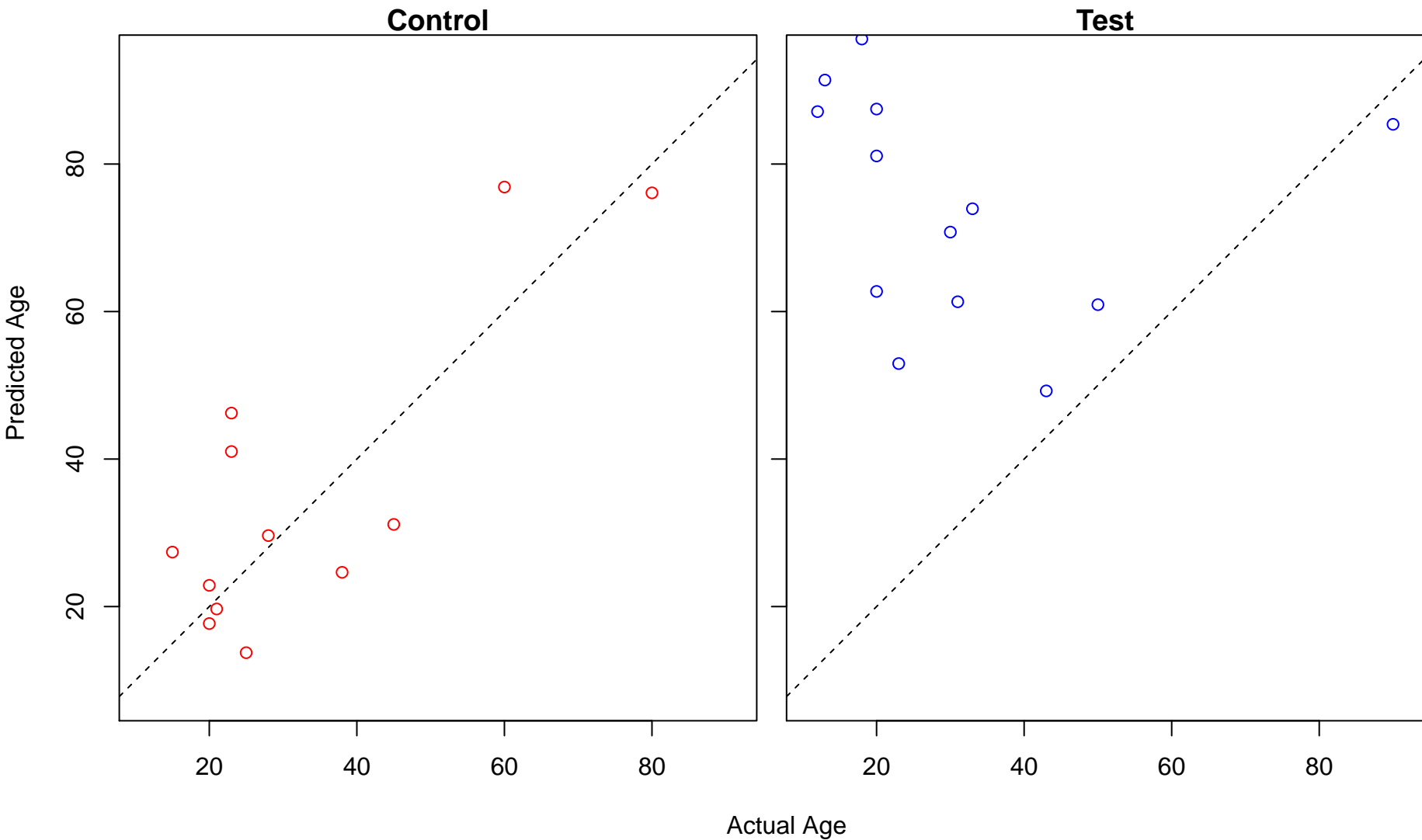
regulation of DNA-templated transcription in response to stress (Score: 6.655328)



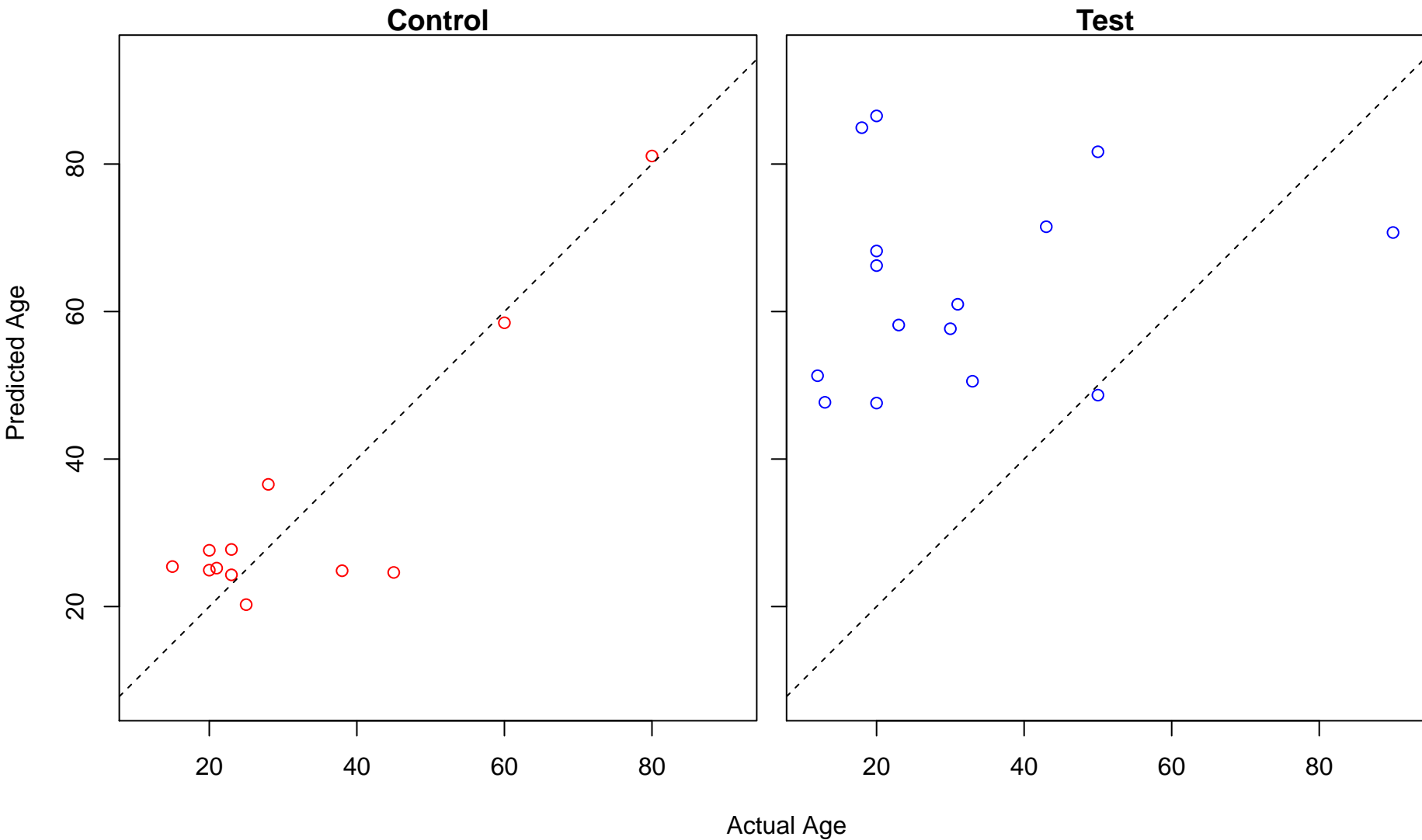
carbohydrate biosynthetic process (Score: 6.650268)



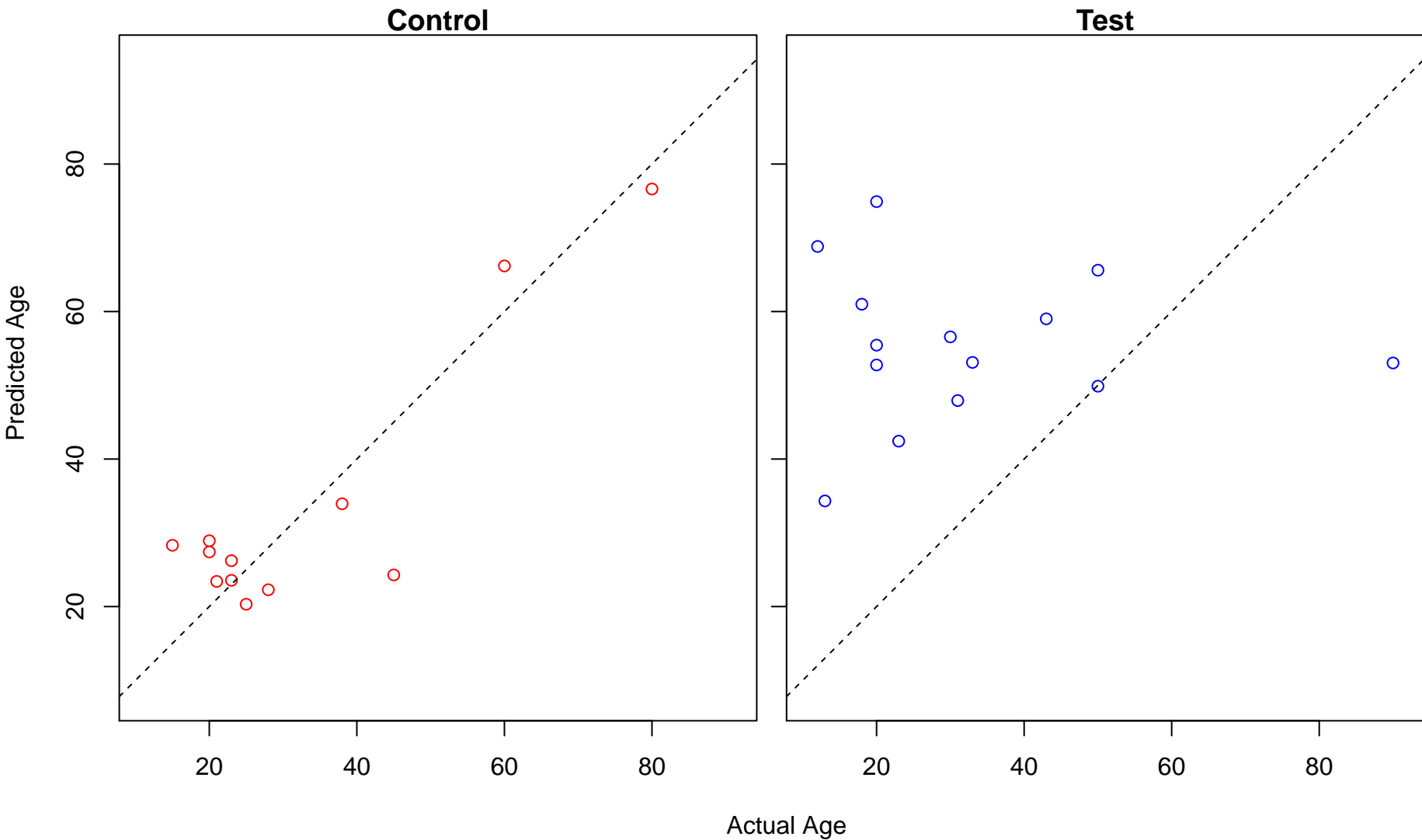
positive regulation of metanephros development (Score: 6.649680)



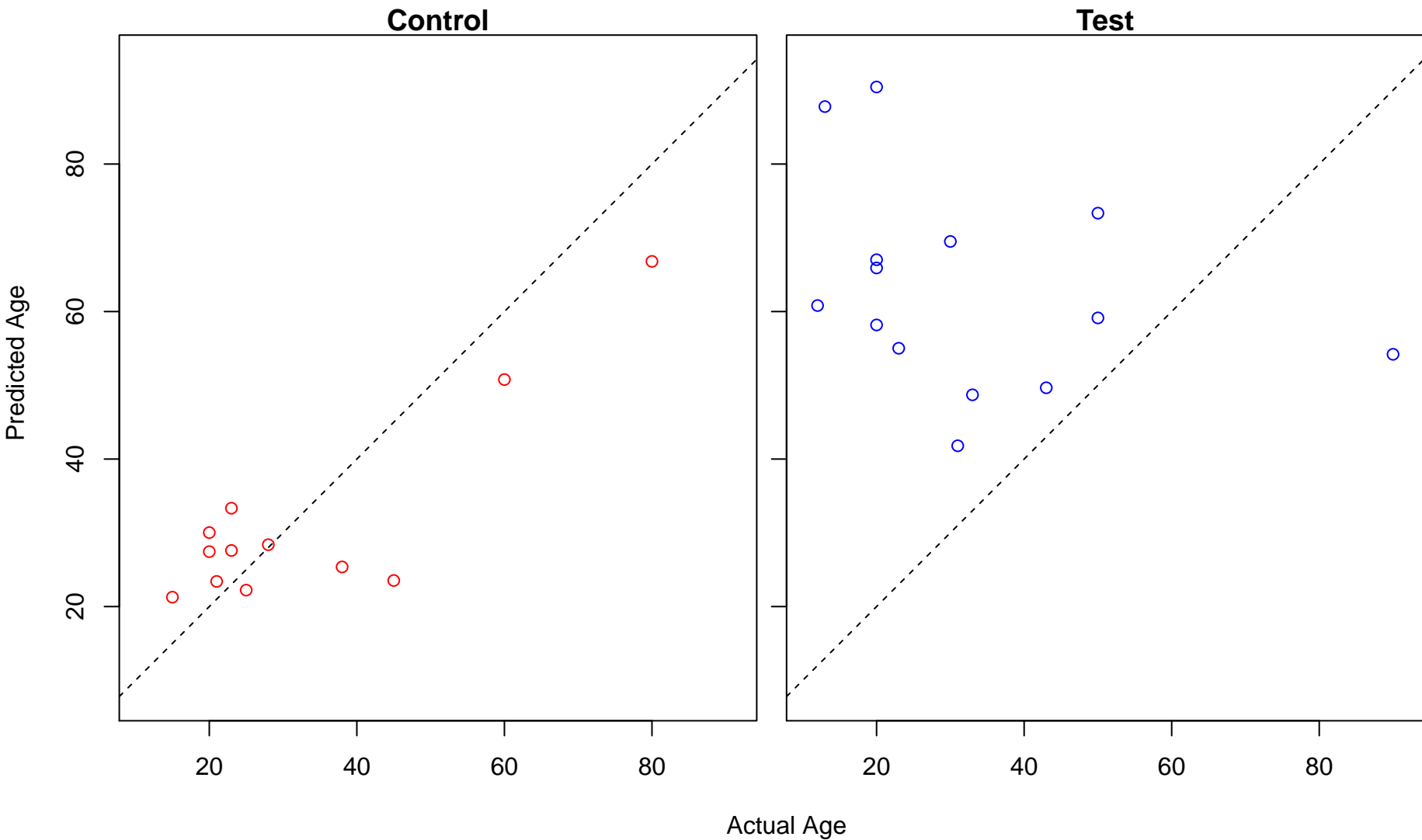
negative regulation of T-helper cell differentiation (Score: 6.649344)



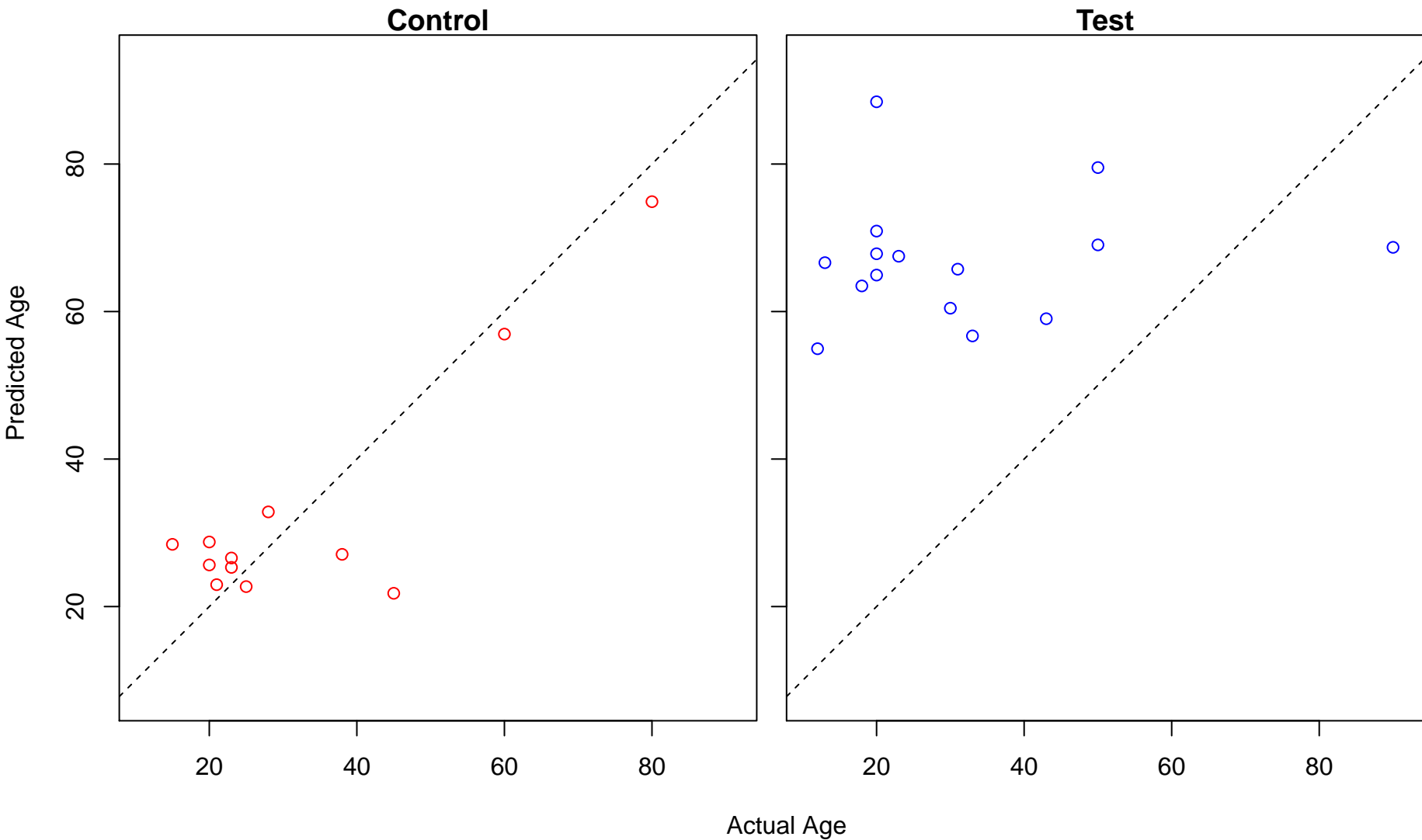
alcohol catabolic process (Score: 6.644698)



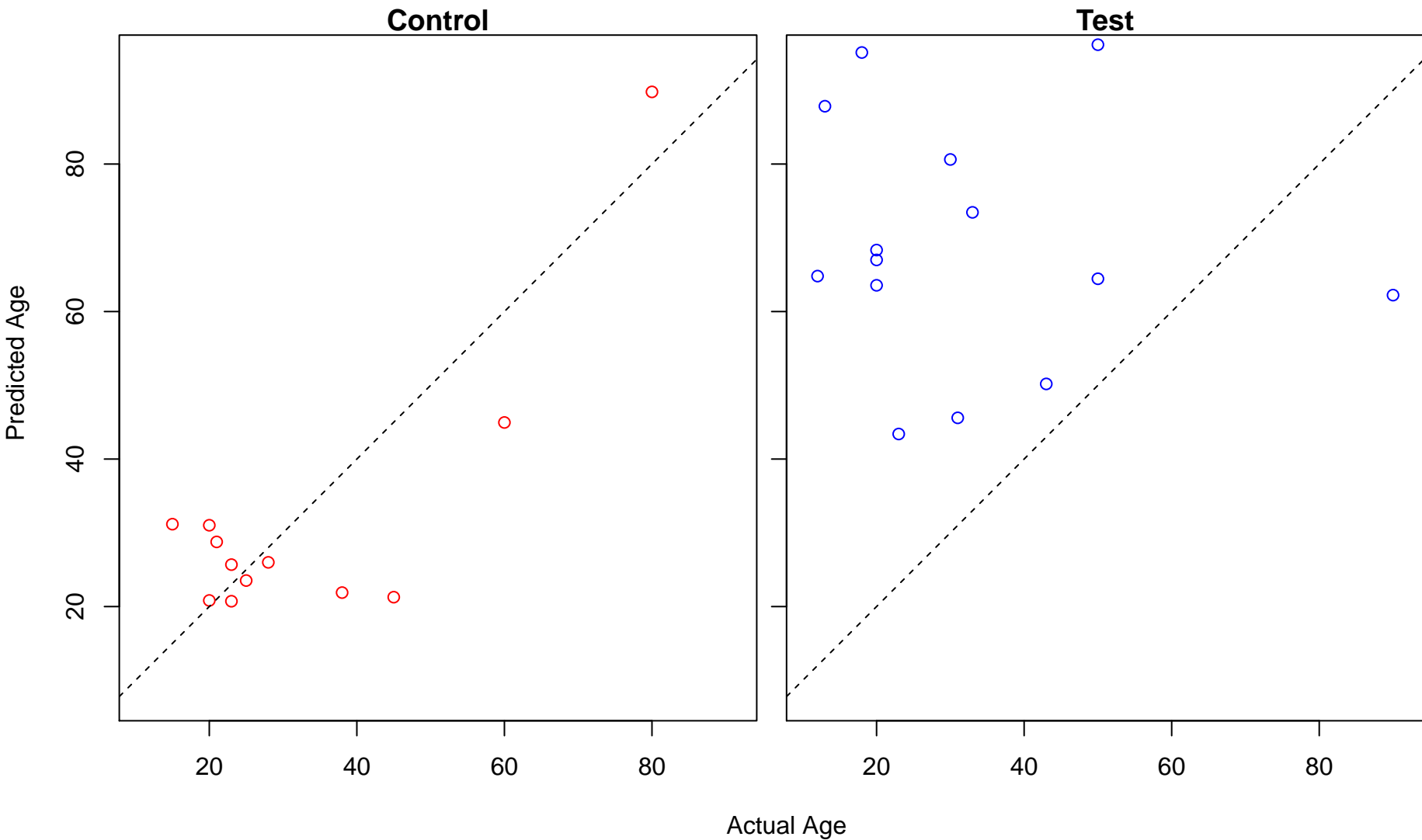
regulation of microtubule polymerization or depolymerization (Score: 6.644348)



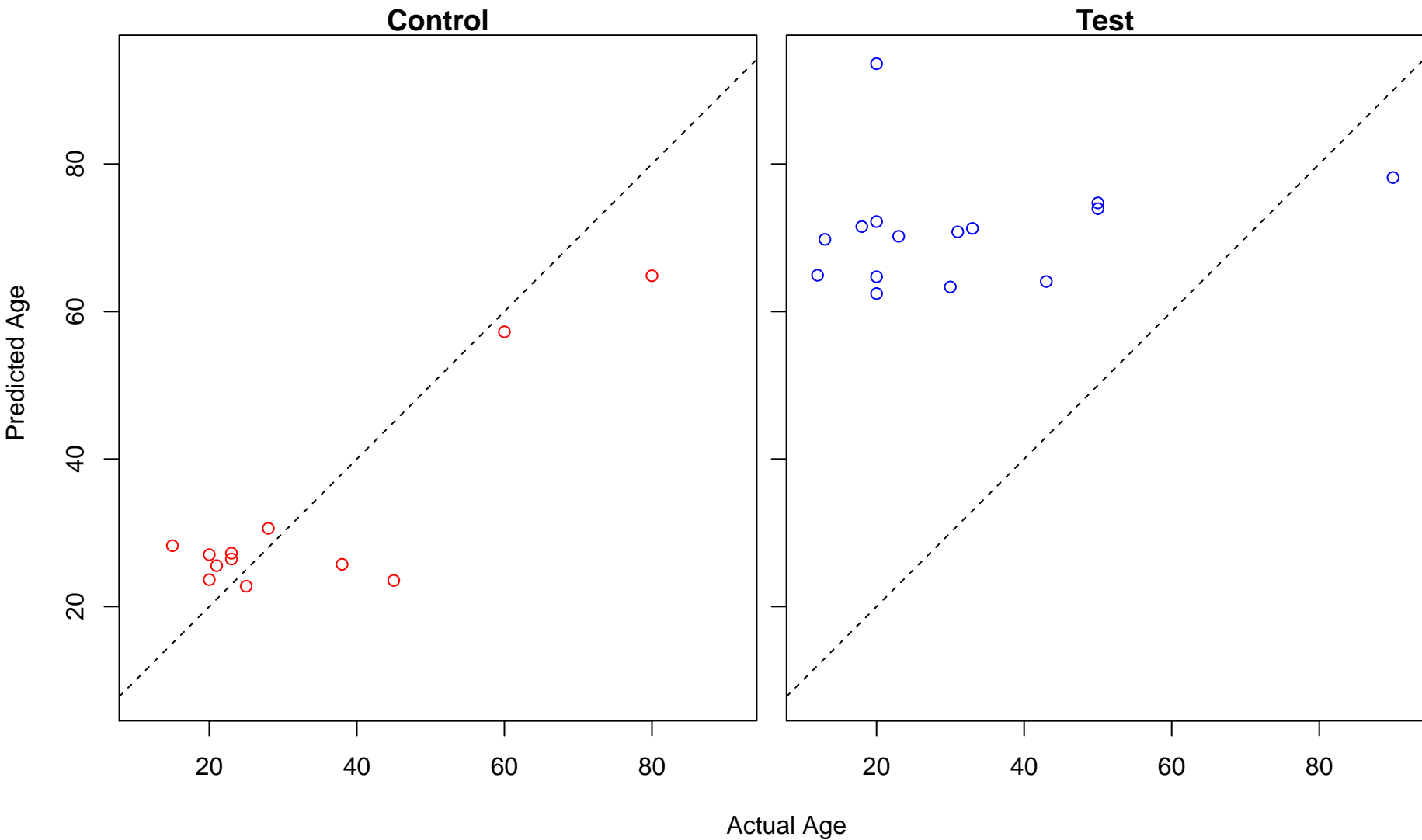
regulation of secretion (Score: 6.636250)



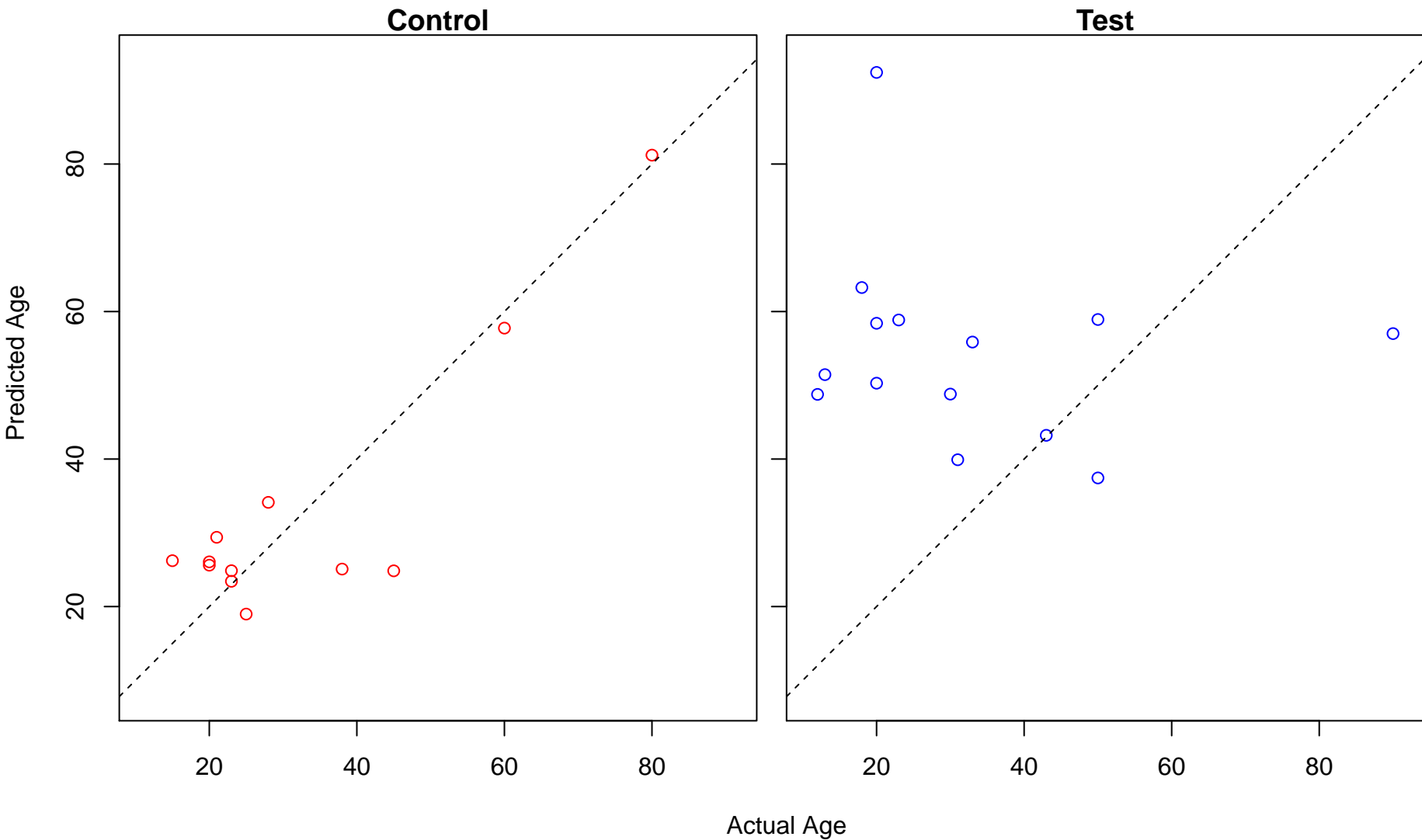
glycoprotein biosynthetic process (Score: 6.636085)



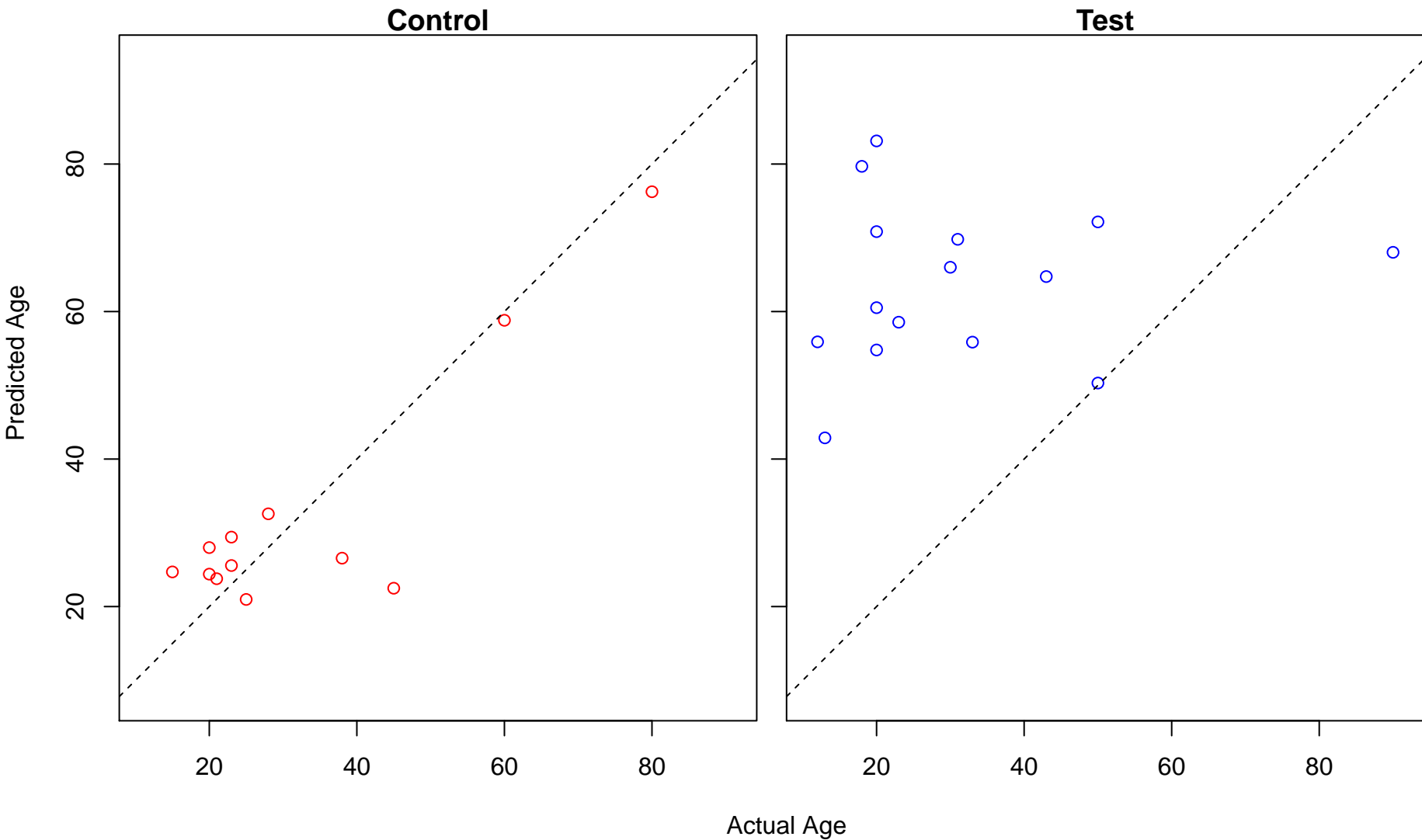
negative regulation of neurogenesis (Score: 6.635342)



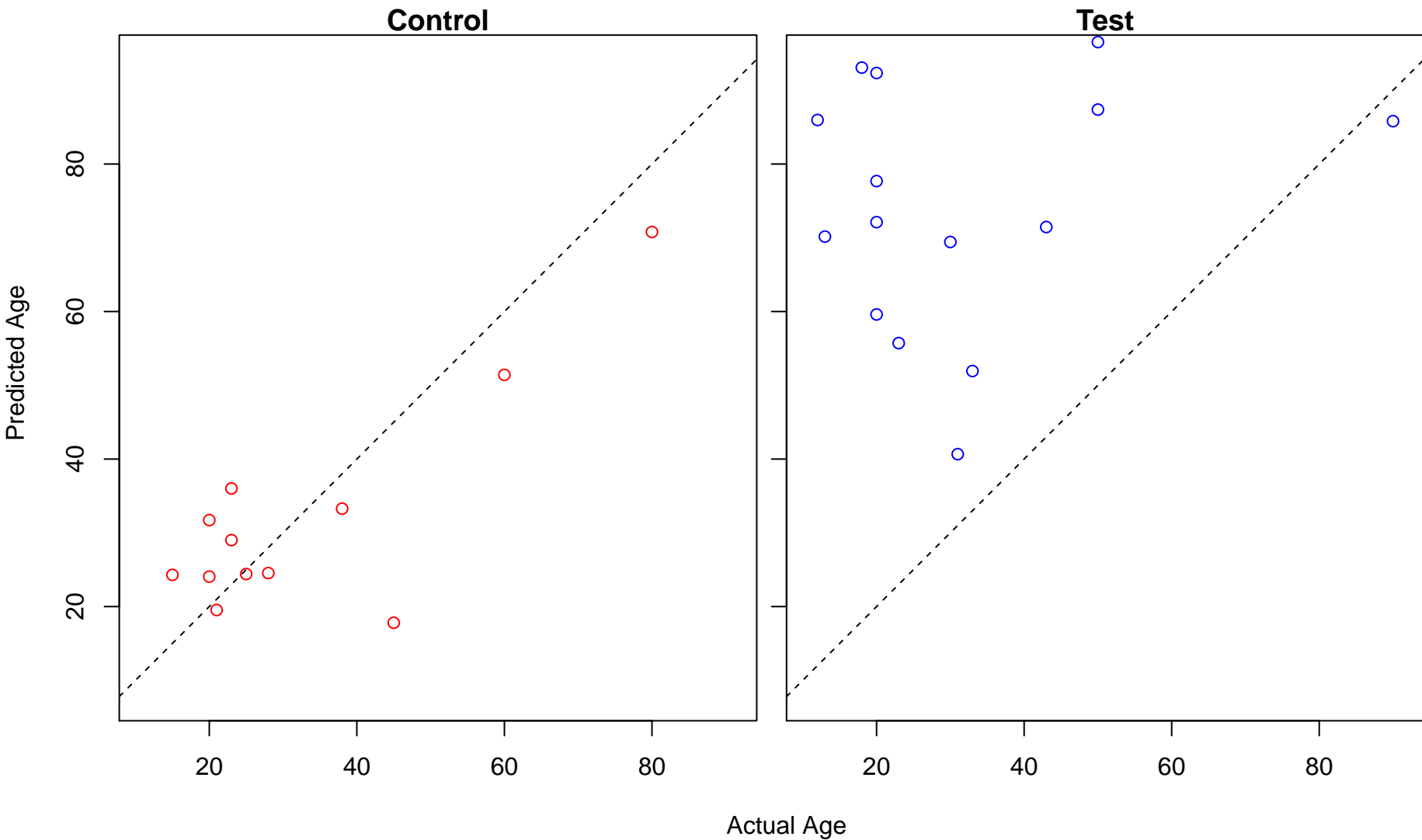
peptidyl-lysine methylation (Score: 6.634295)



lymphocyte activation (Score: 6.633762)

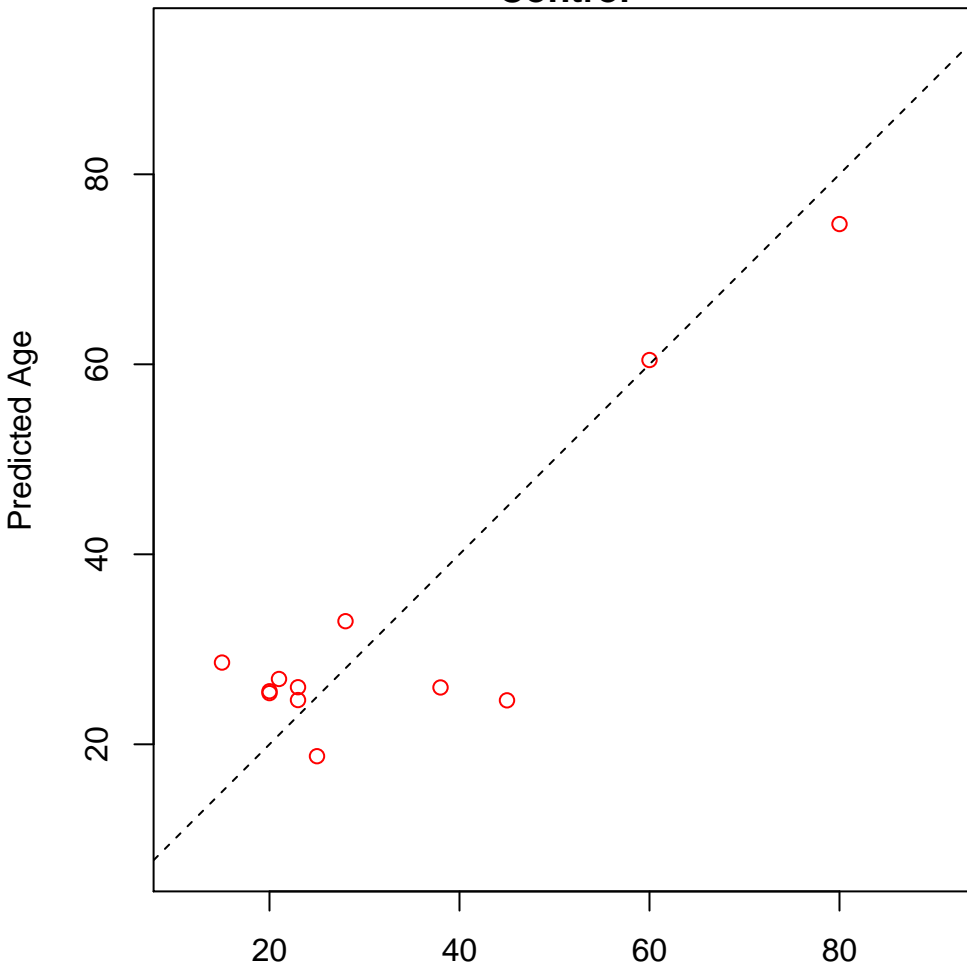


regulation of smooth muscle cell differentiation (Score: 6.633417)

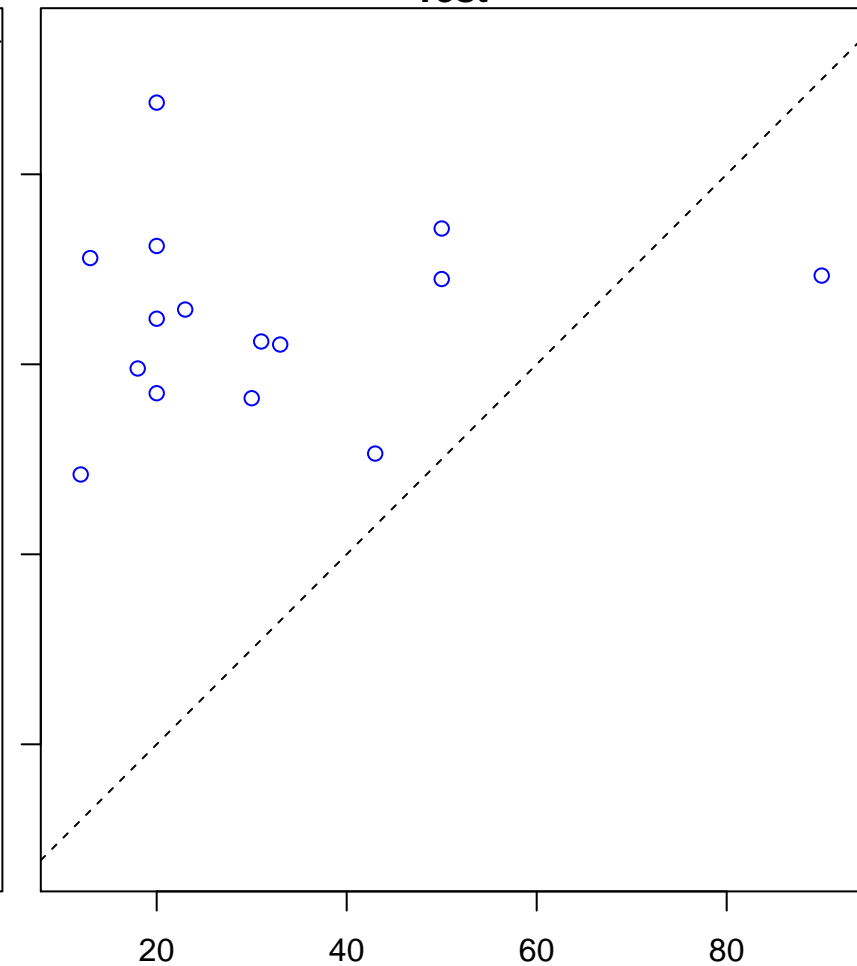


cellular response to abiotic stimulus (Score: 6.633133)

Control



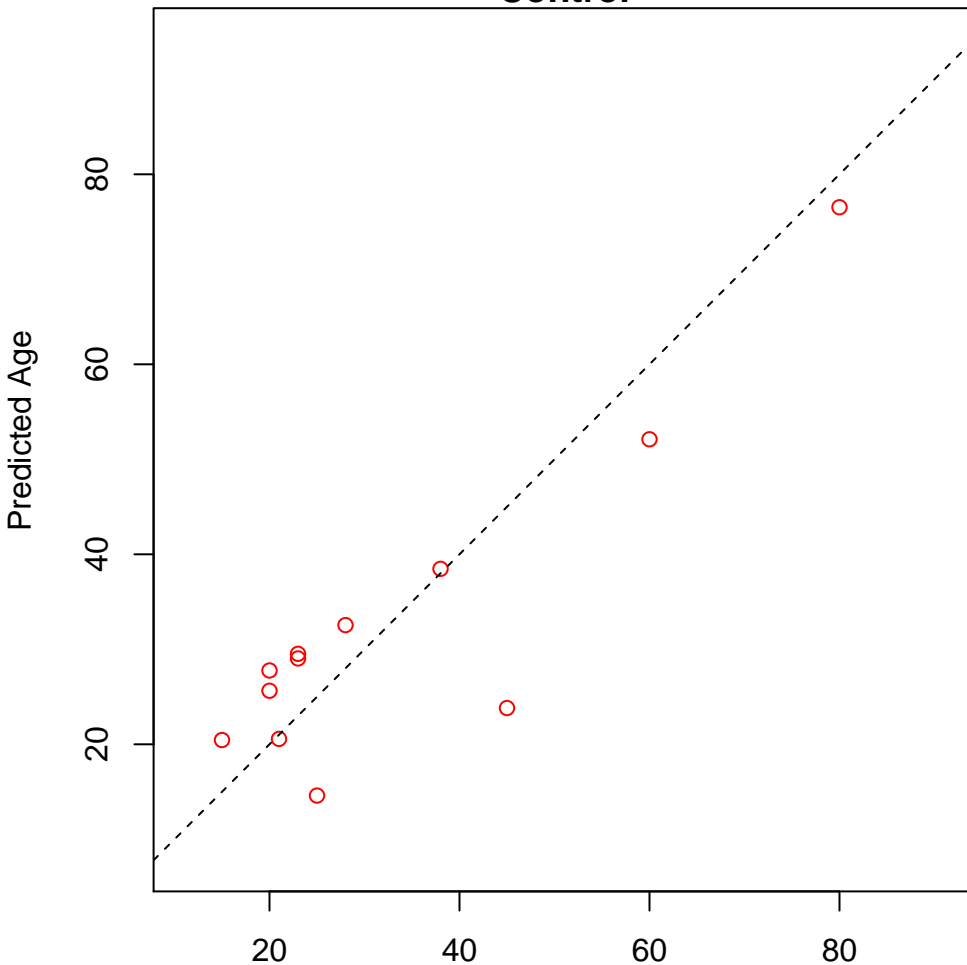
Test



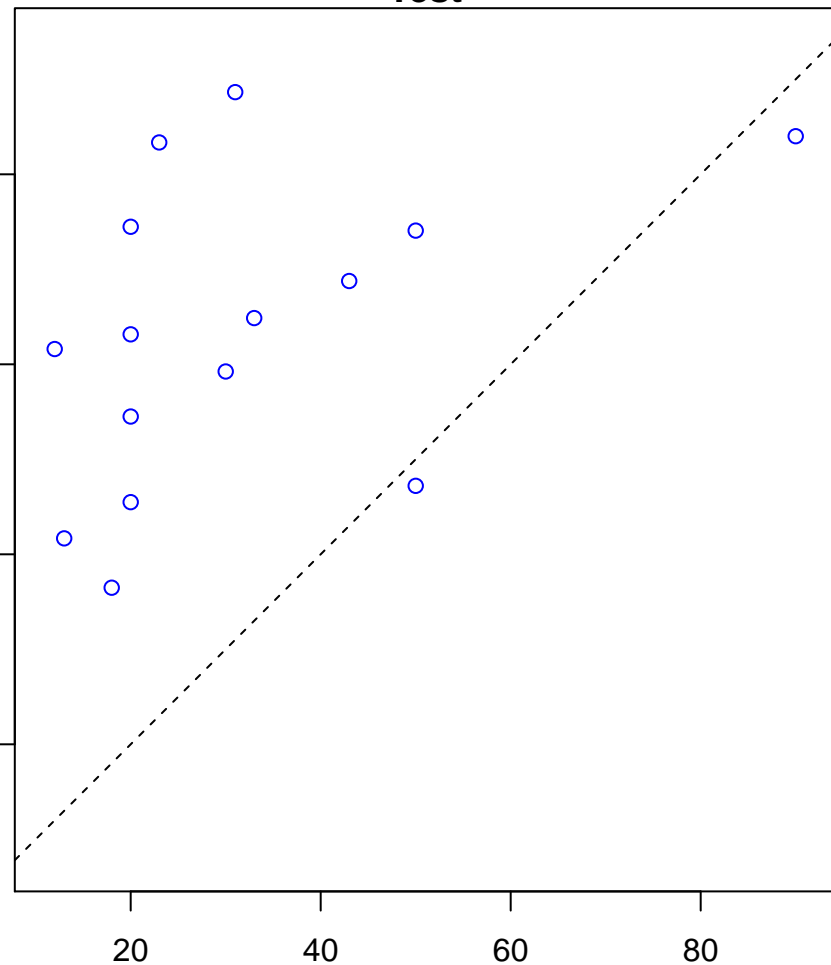
Actual Age

embryonic heart tube development (Score: 6.631655)

Control

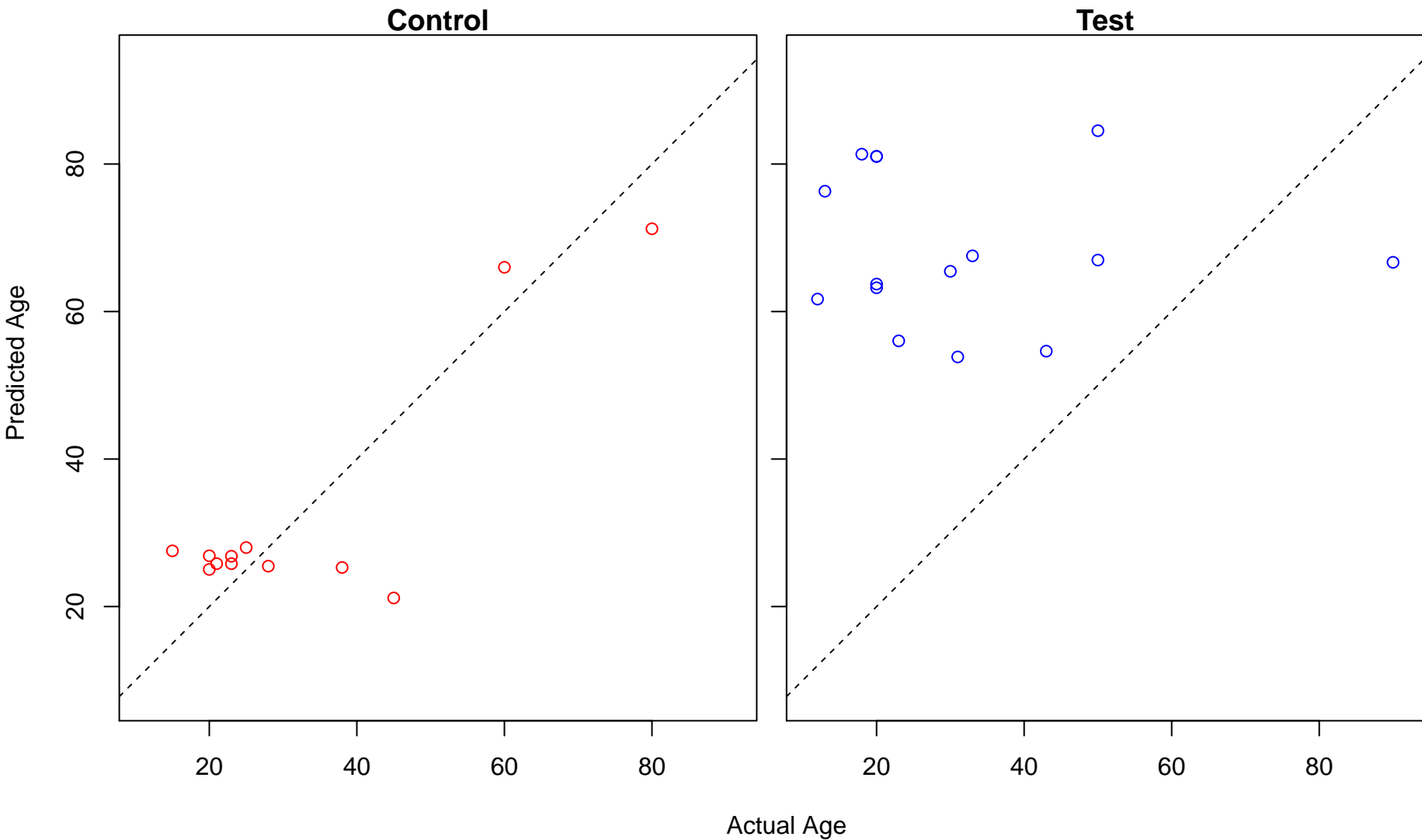


Test

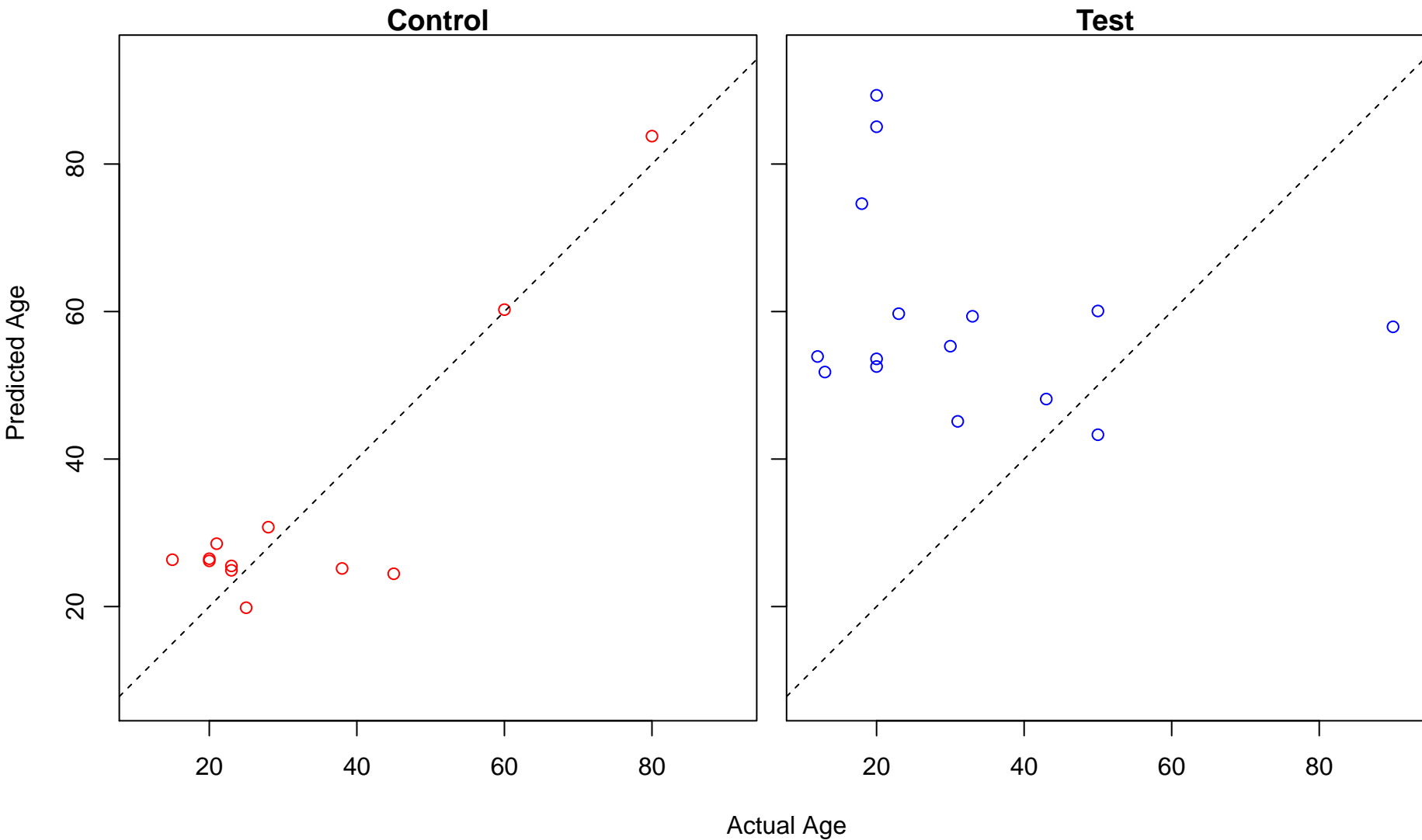


Actual Age

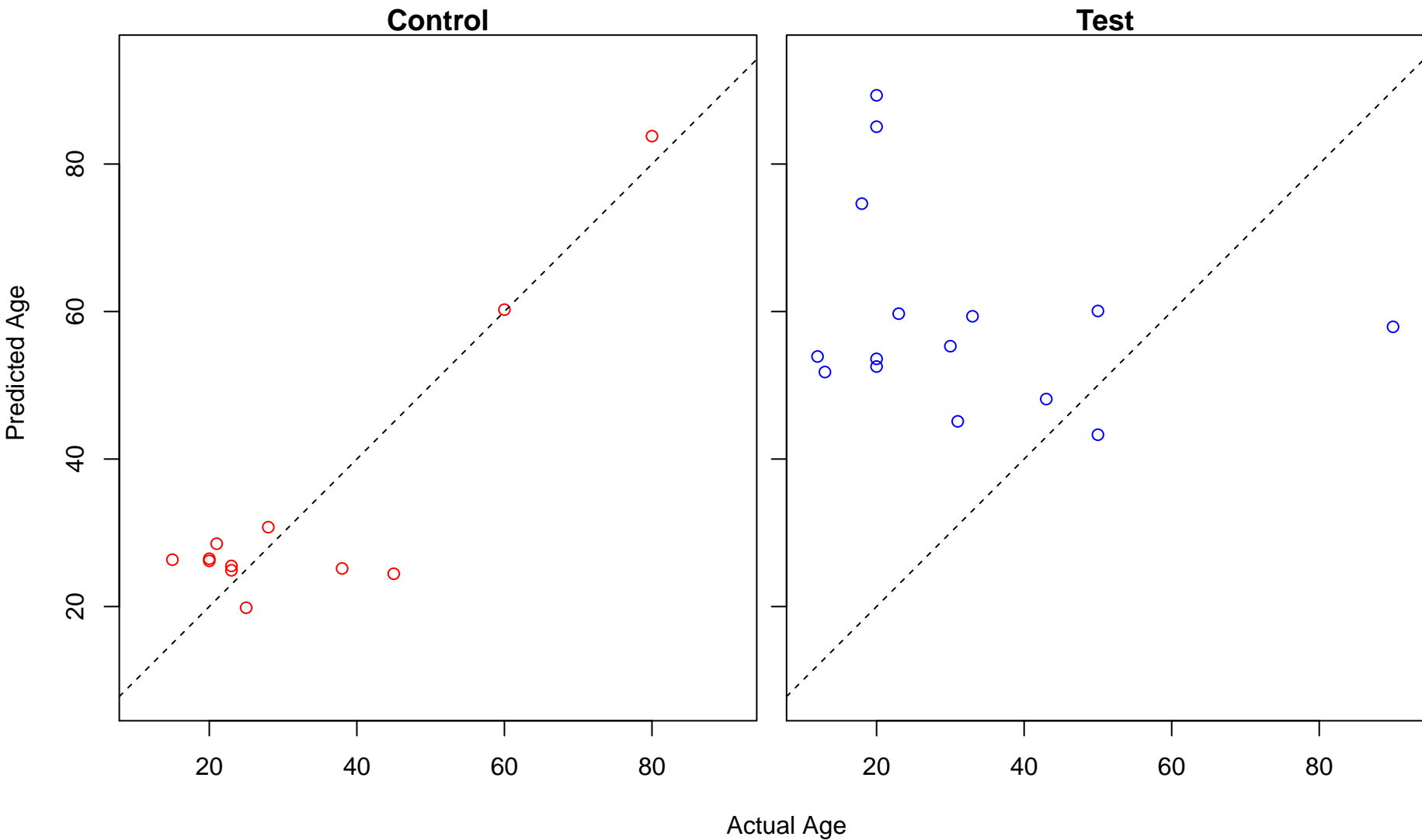
mRNA 3'-end processing (Score: 6.629902)



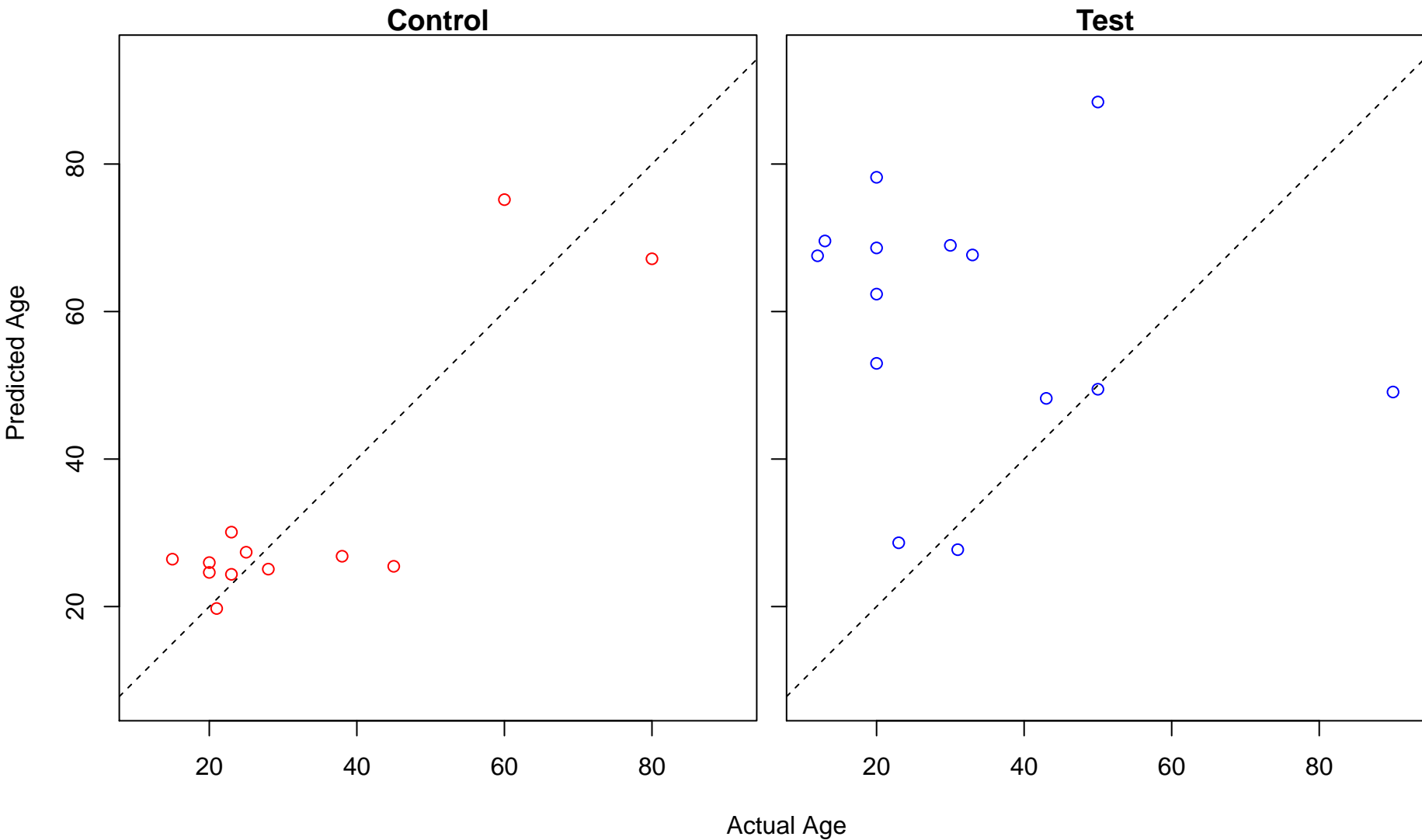
protein methylation (Score: 6.629220)



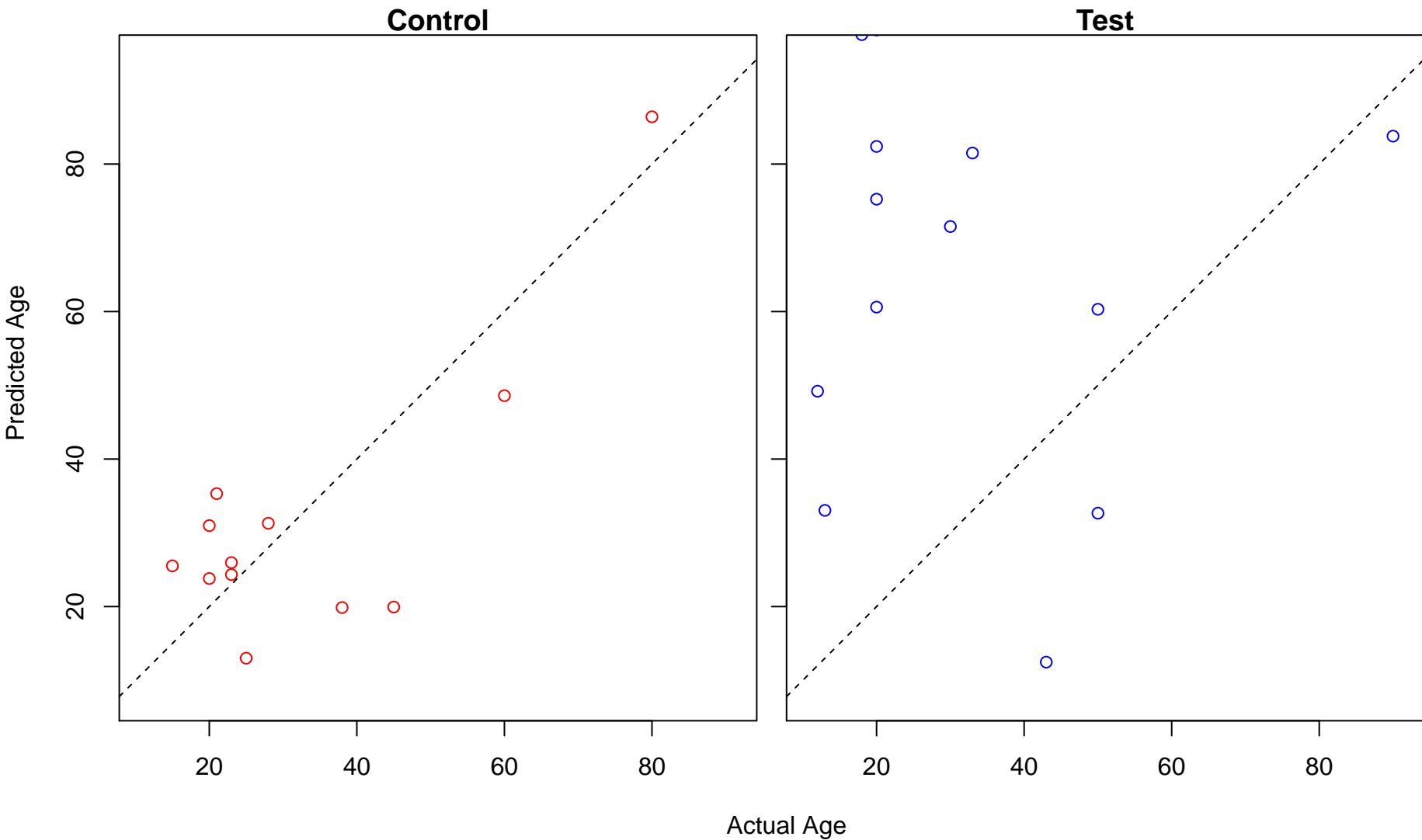
protein alkylation (Score: 6.629220)



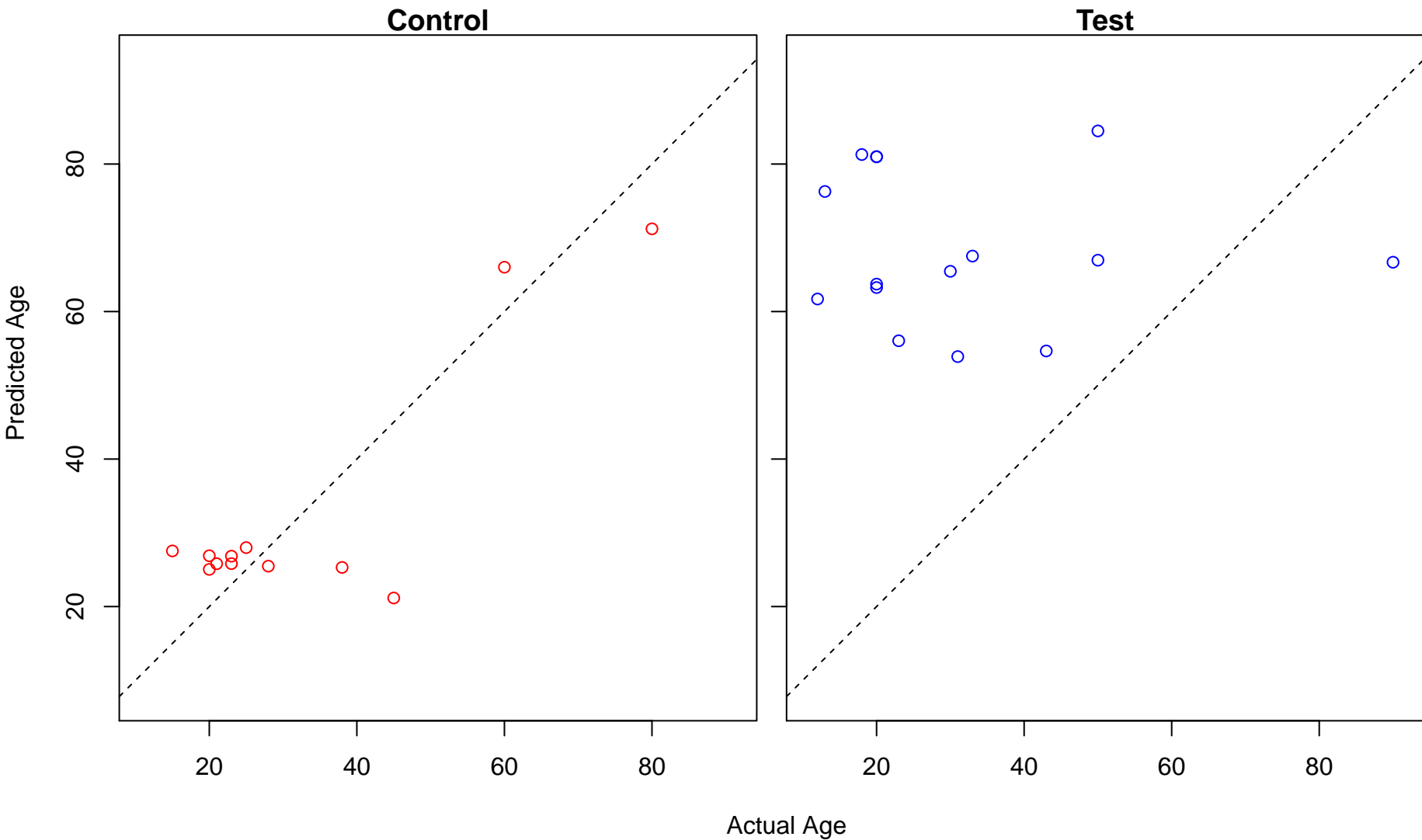
valine metabolic process (Score: 6.628139)



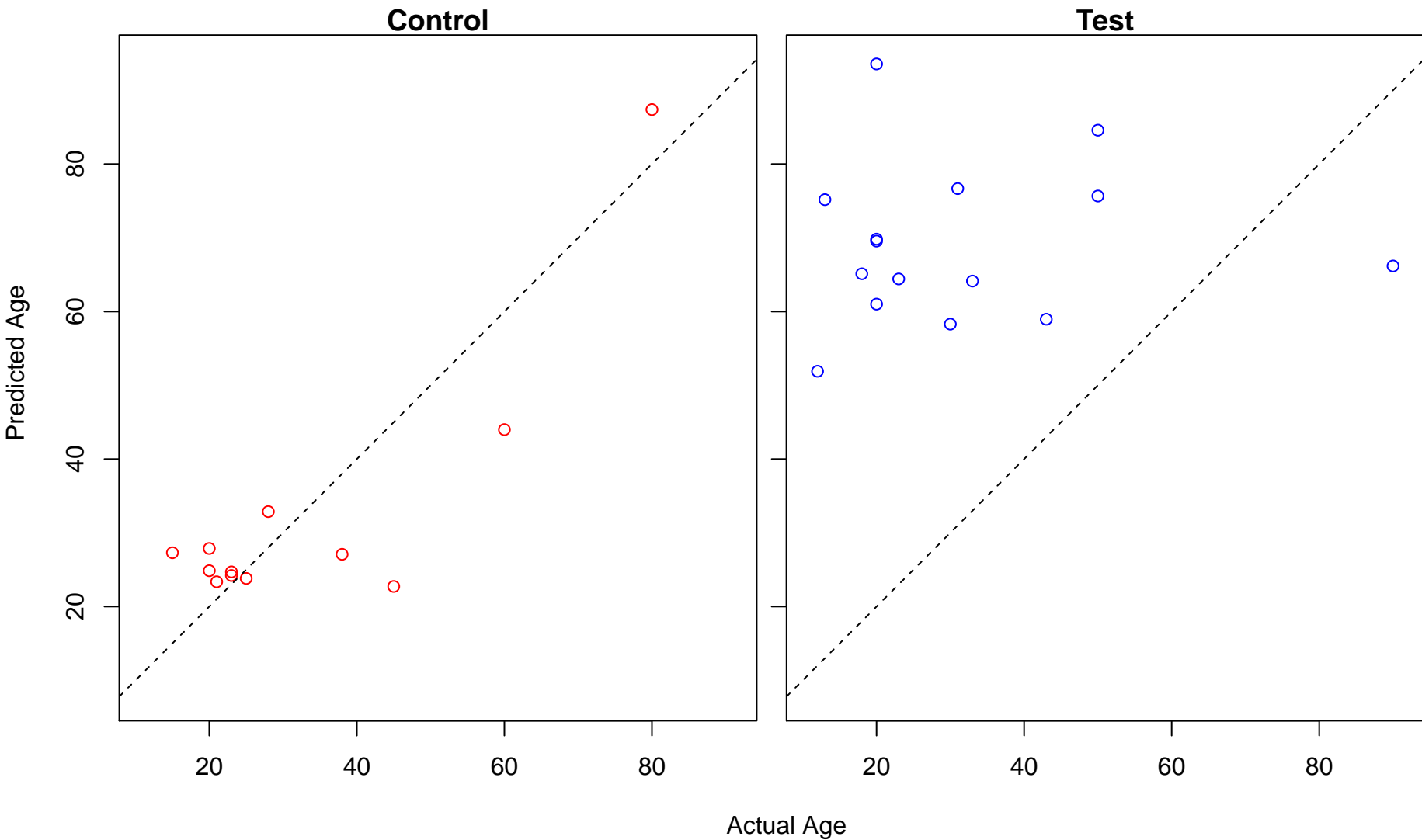
non-recombinational repair (Score: 6.627414)



RNA 3'-end processing (Score: 6.626114)

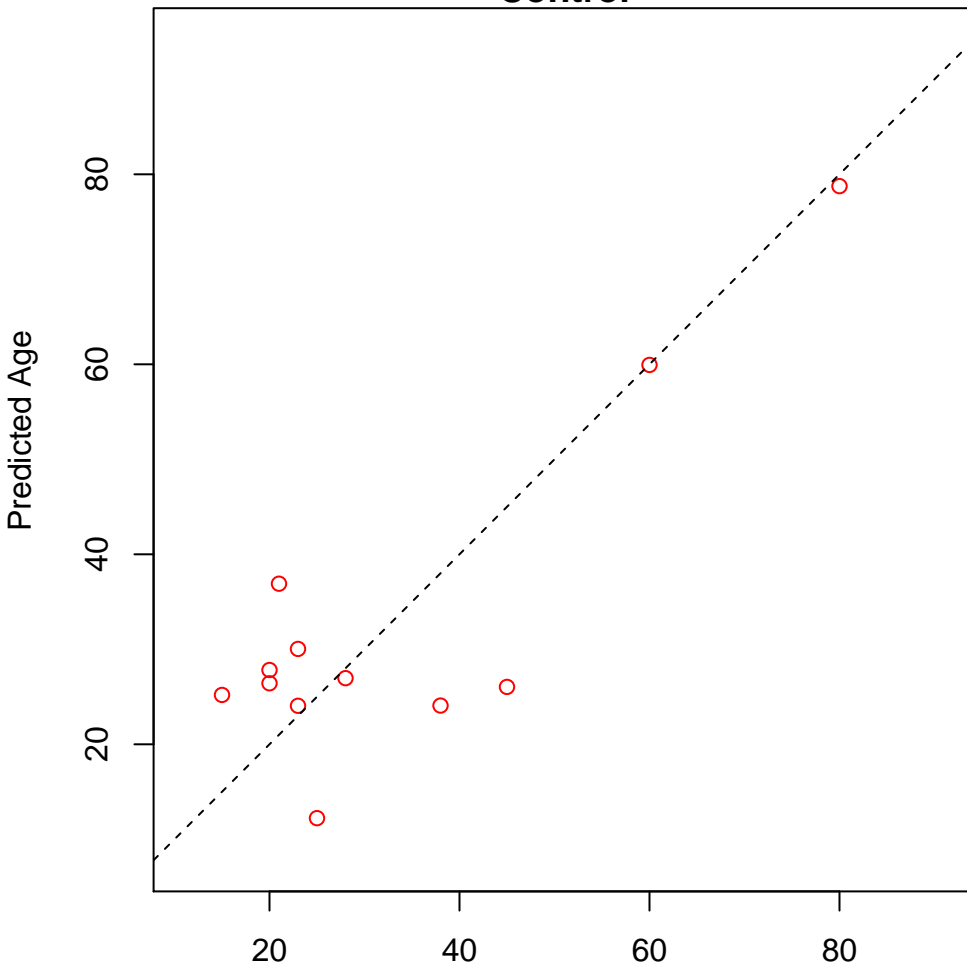


positive regulation of nucleotide metabolic process (Score: 6.624974)

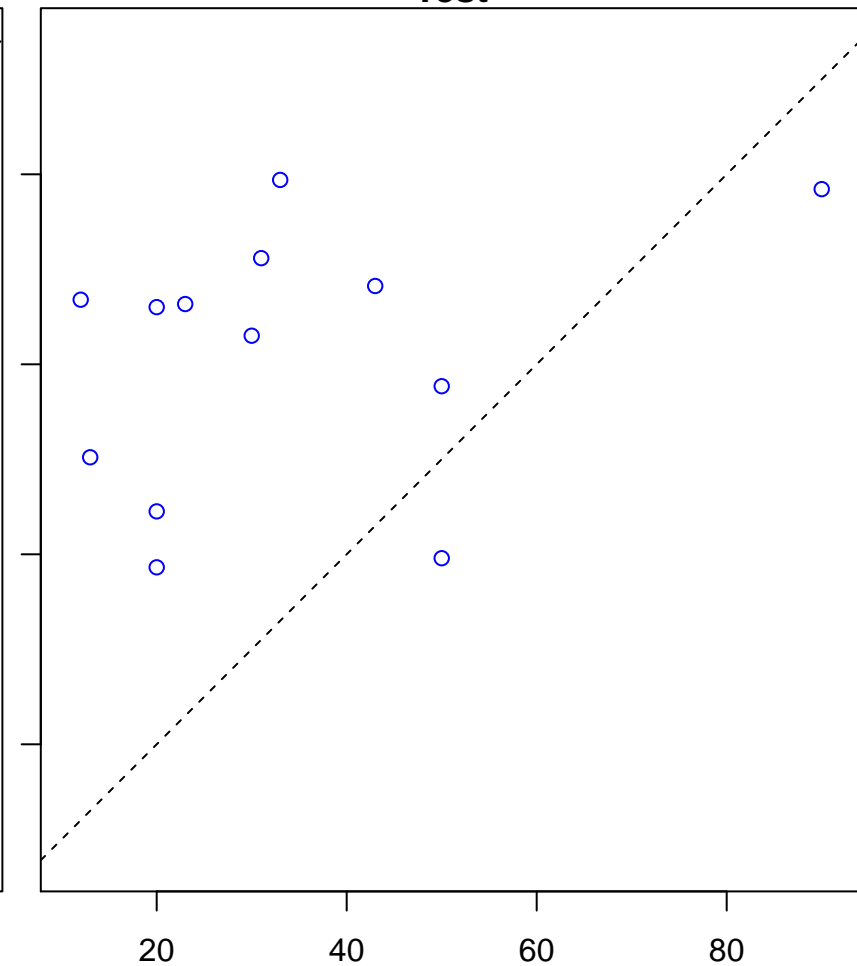


regulation of sequestering of triglyceride (Score: 6.619592)

Control

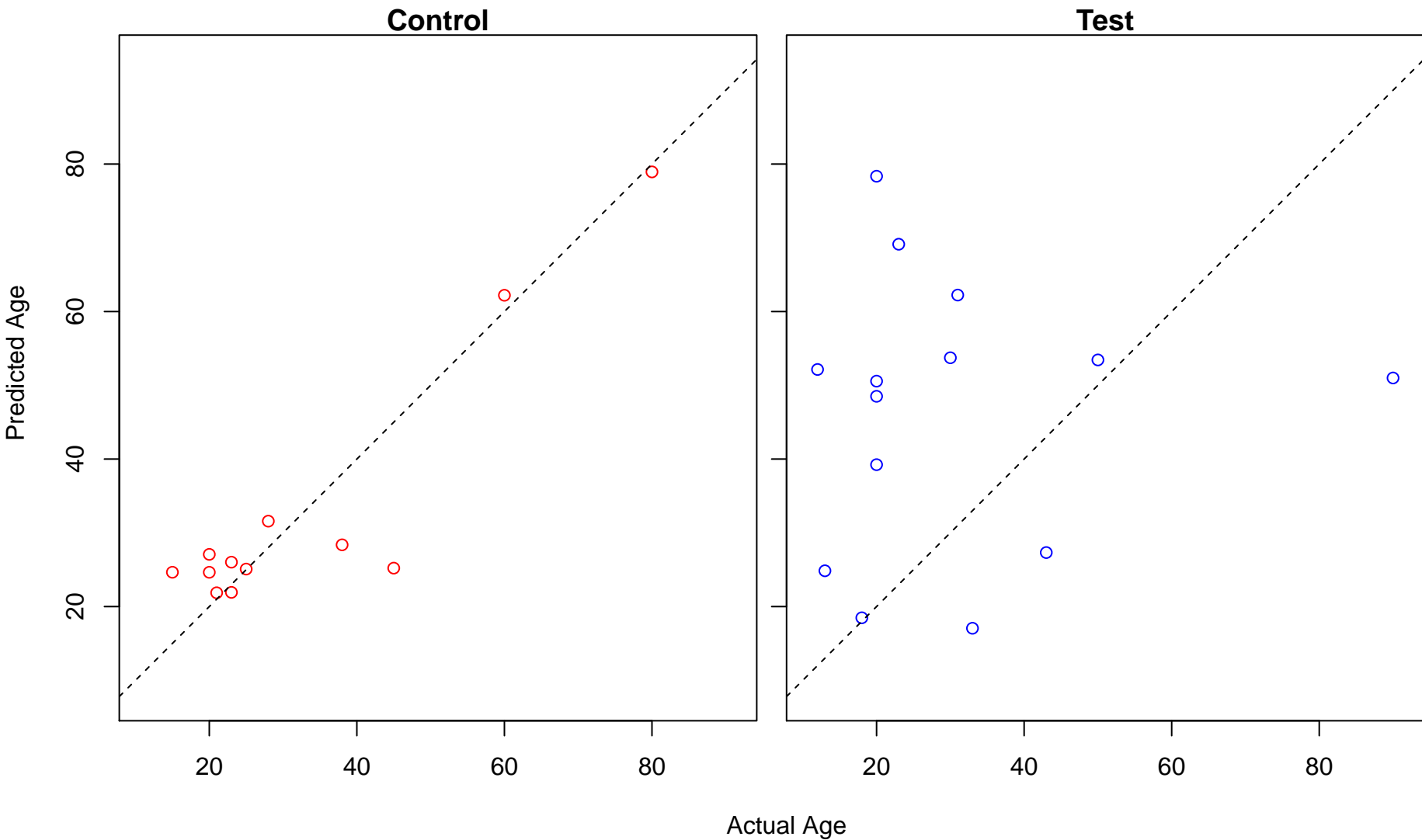


Test

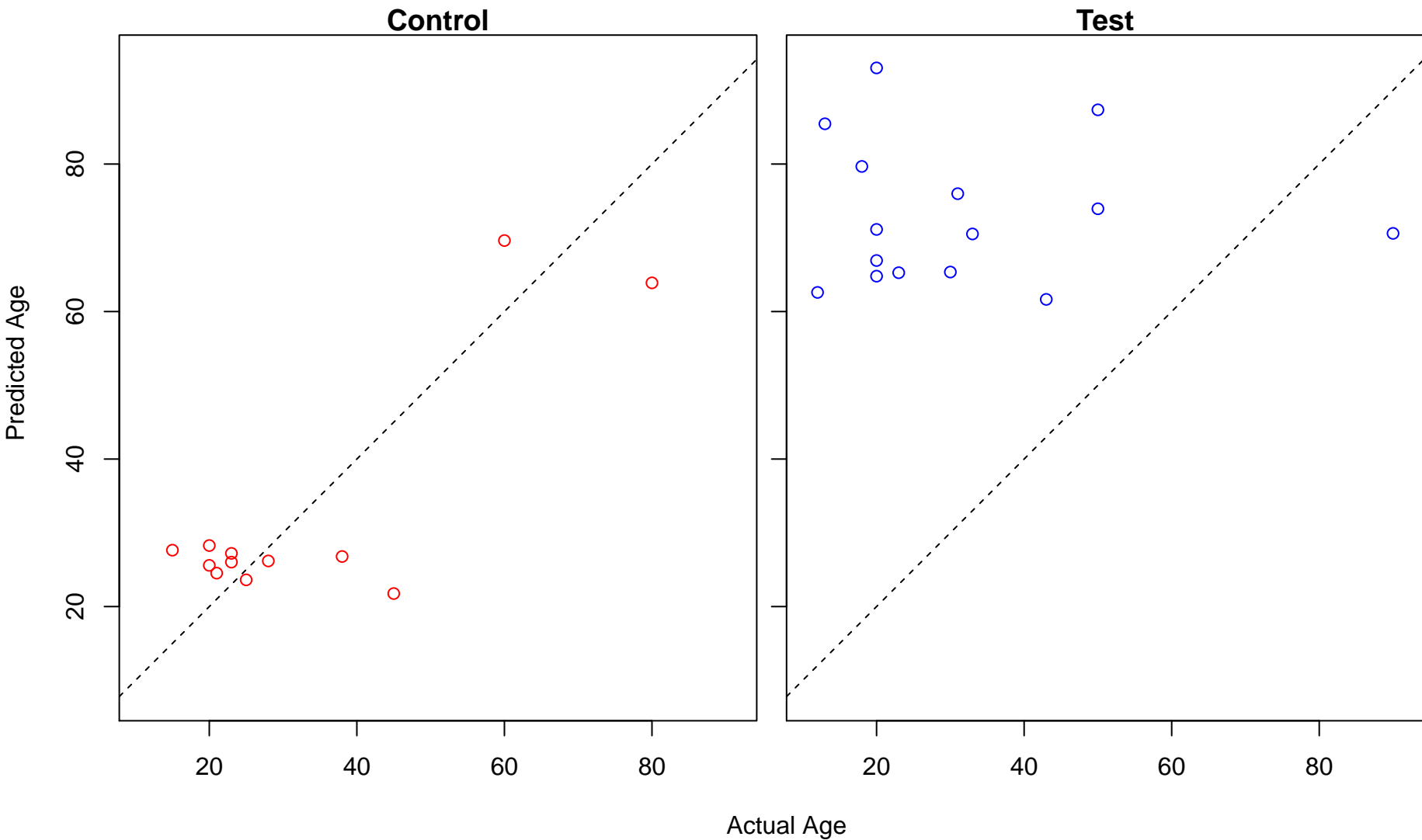


Actual Age

response to nutrient levels (Score: 6.619495)

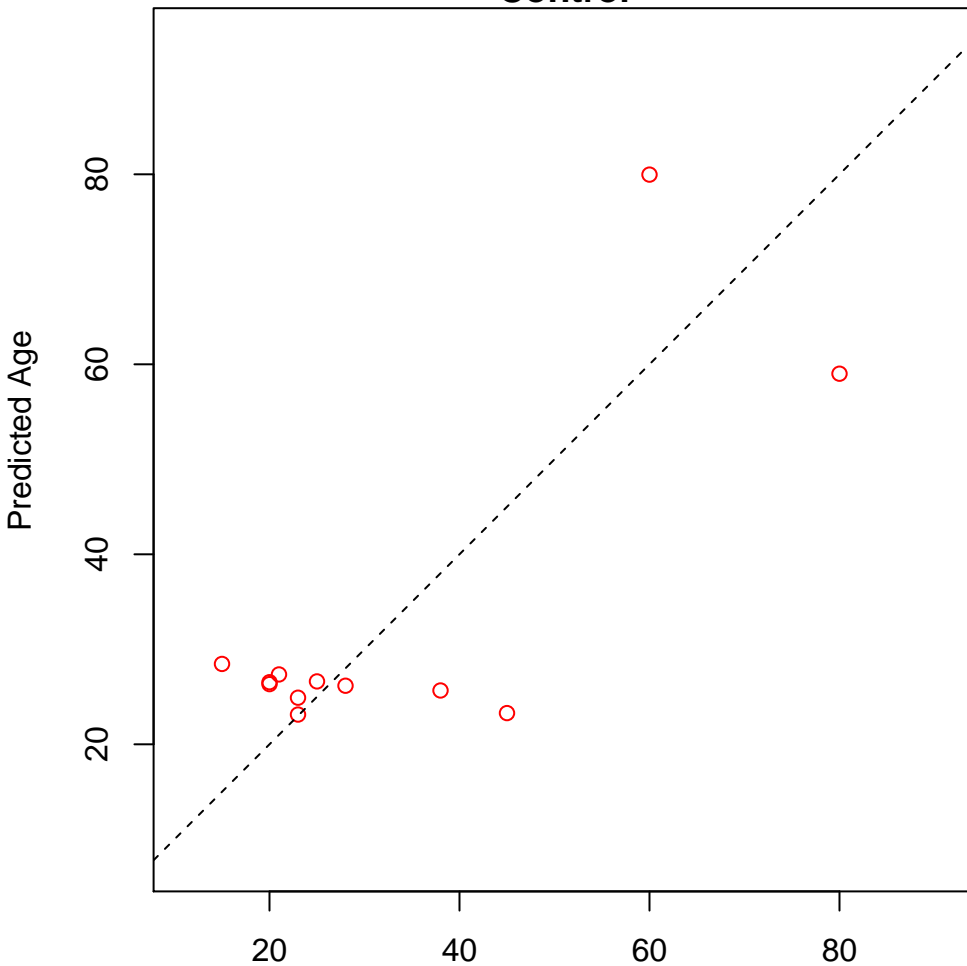


regulation of multi-organism process (Score: 6.619349)

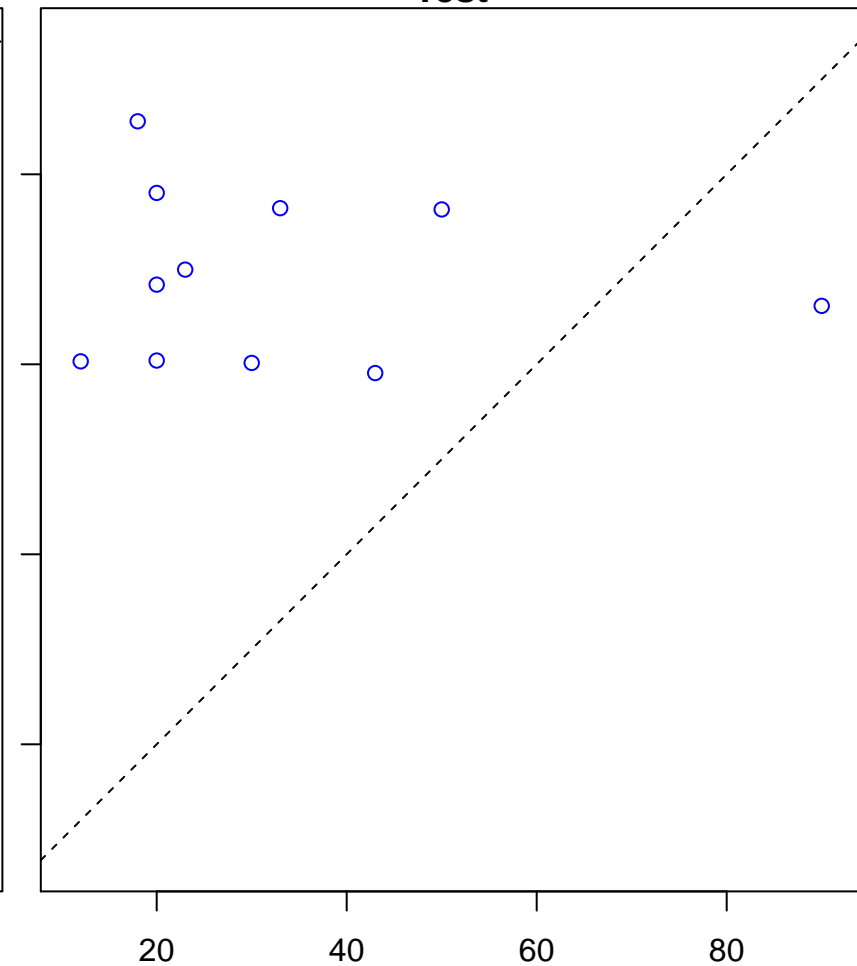


ATP-dependent chromatin remodeling (Score: 6.616090)

Control

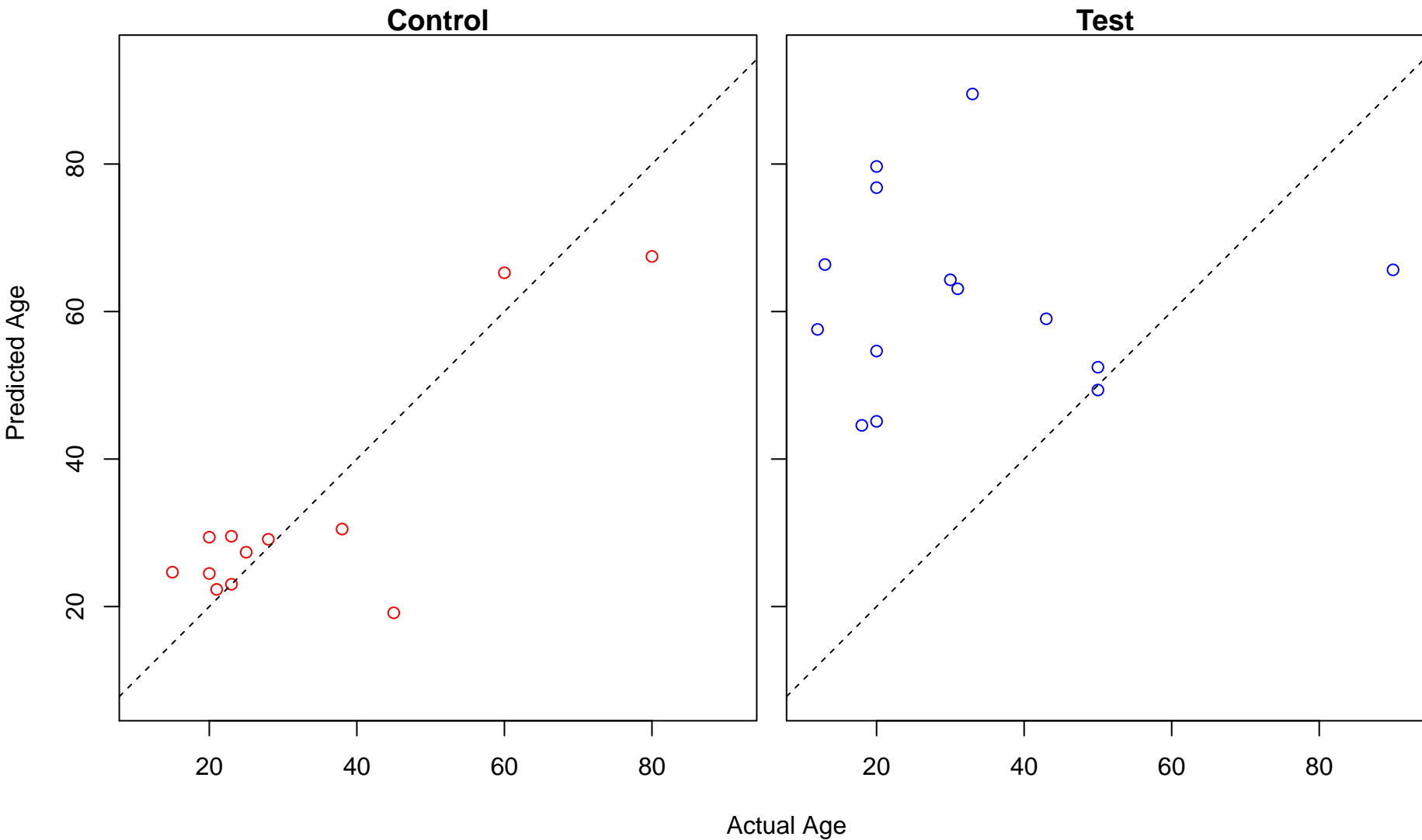


Test

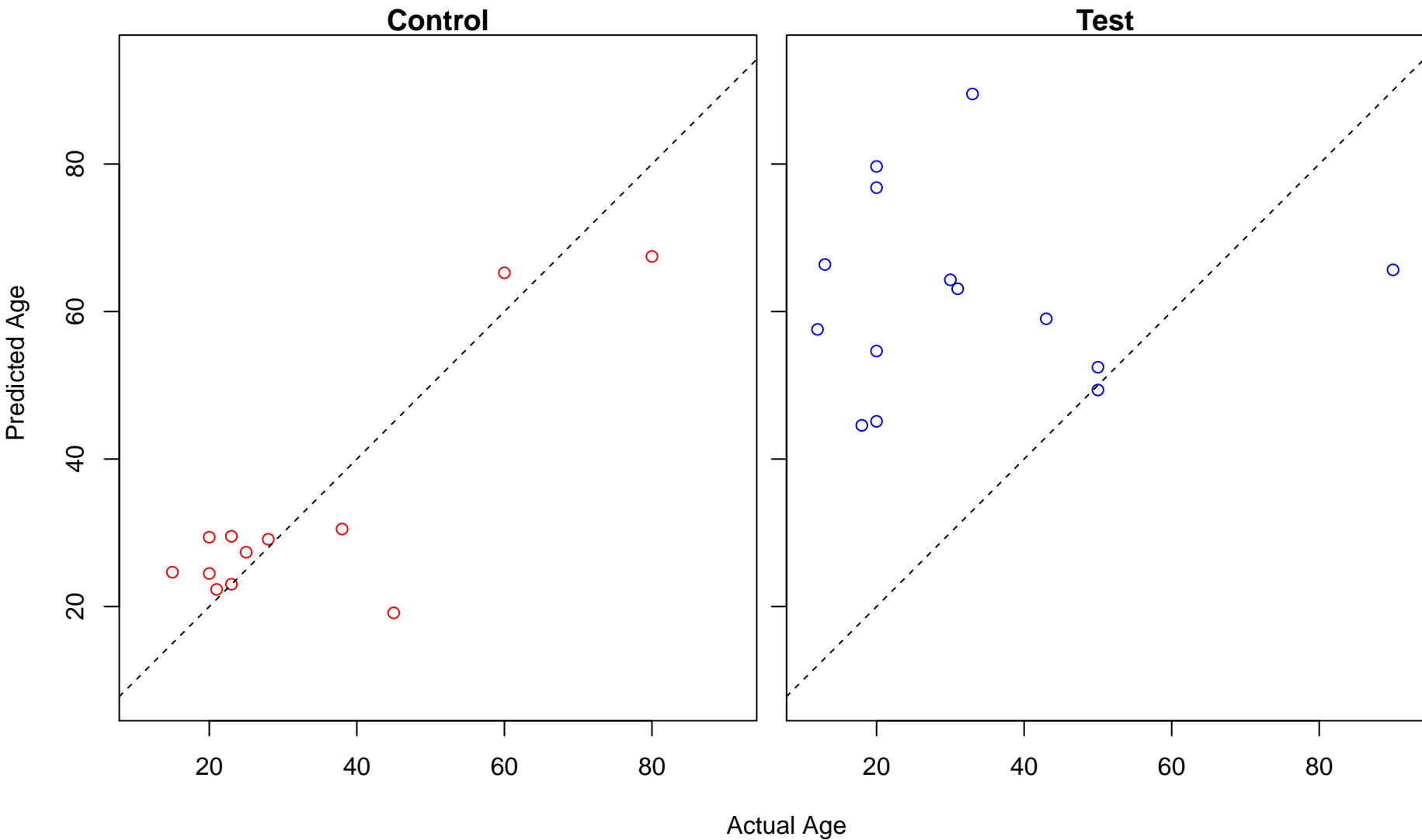


Actual Age

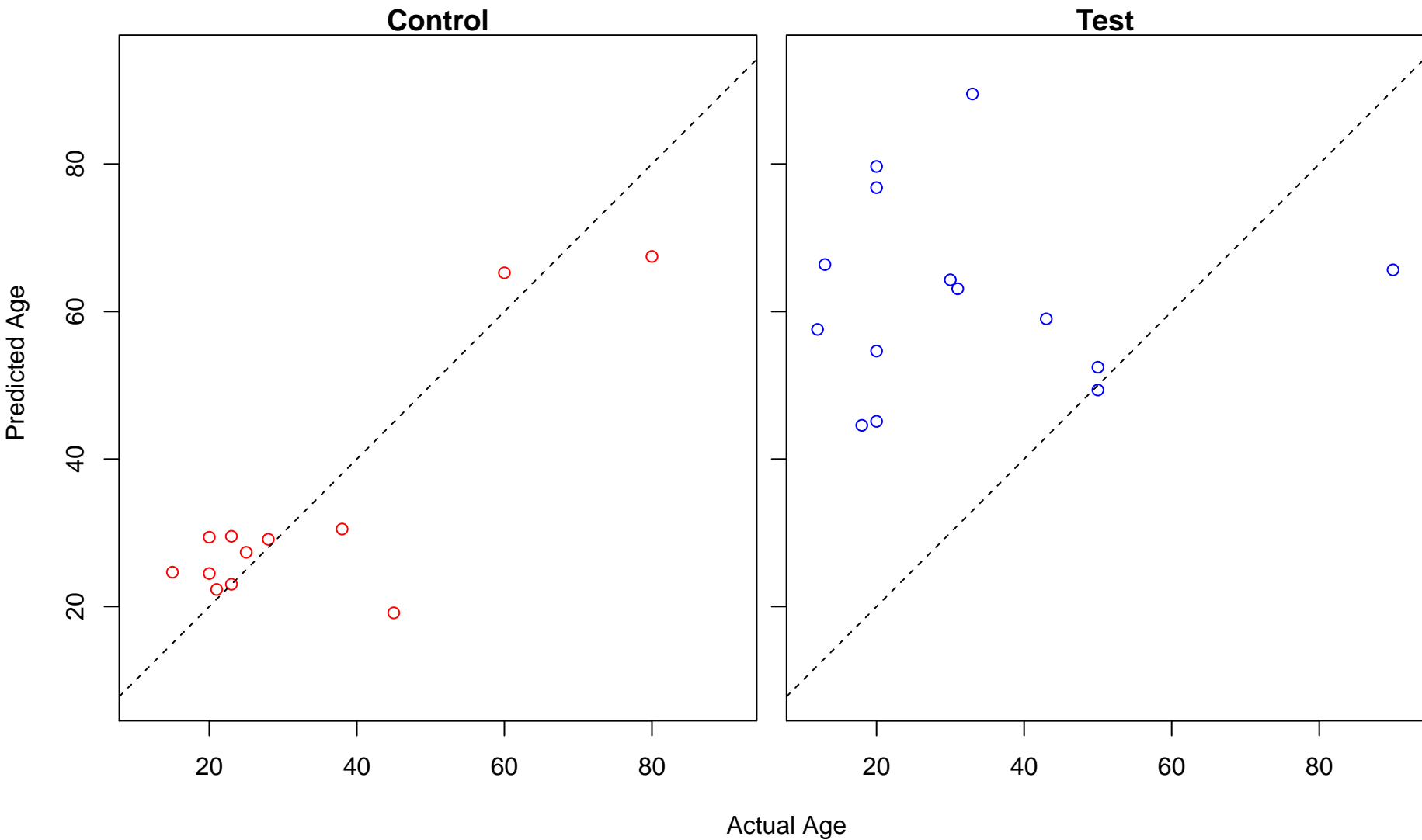
response to caffeine (Score: 6.615723)



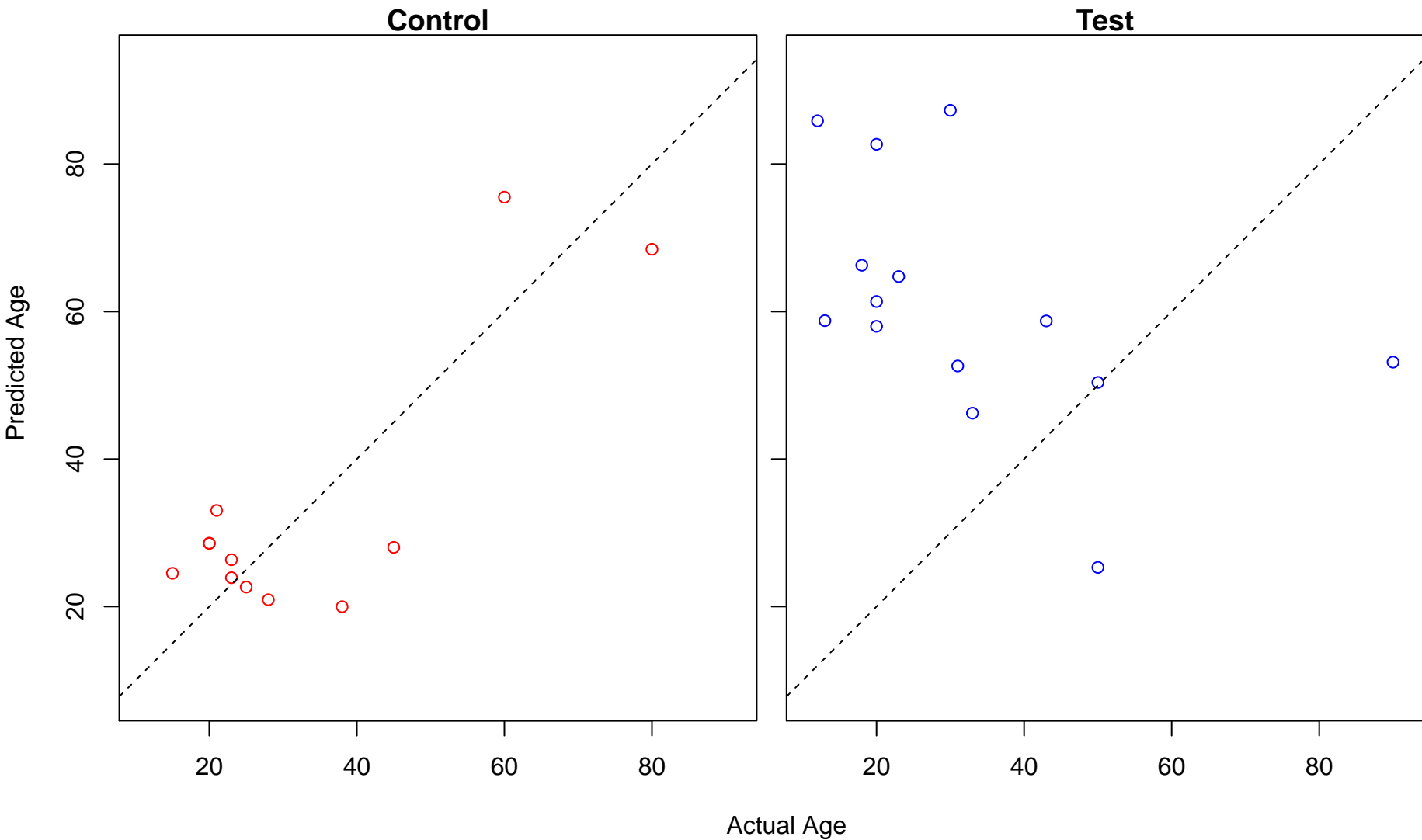
cellular response to caffeine (Score: 6.615723)



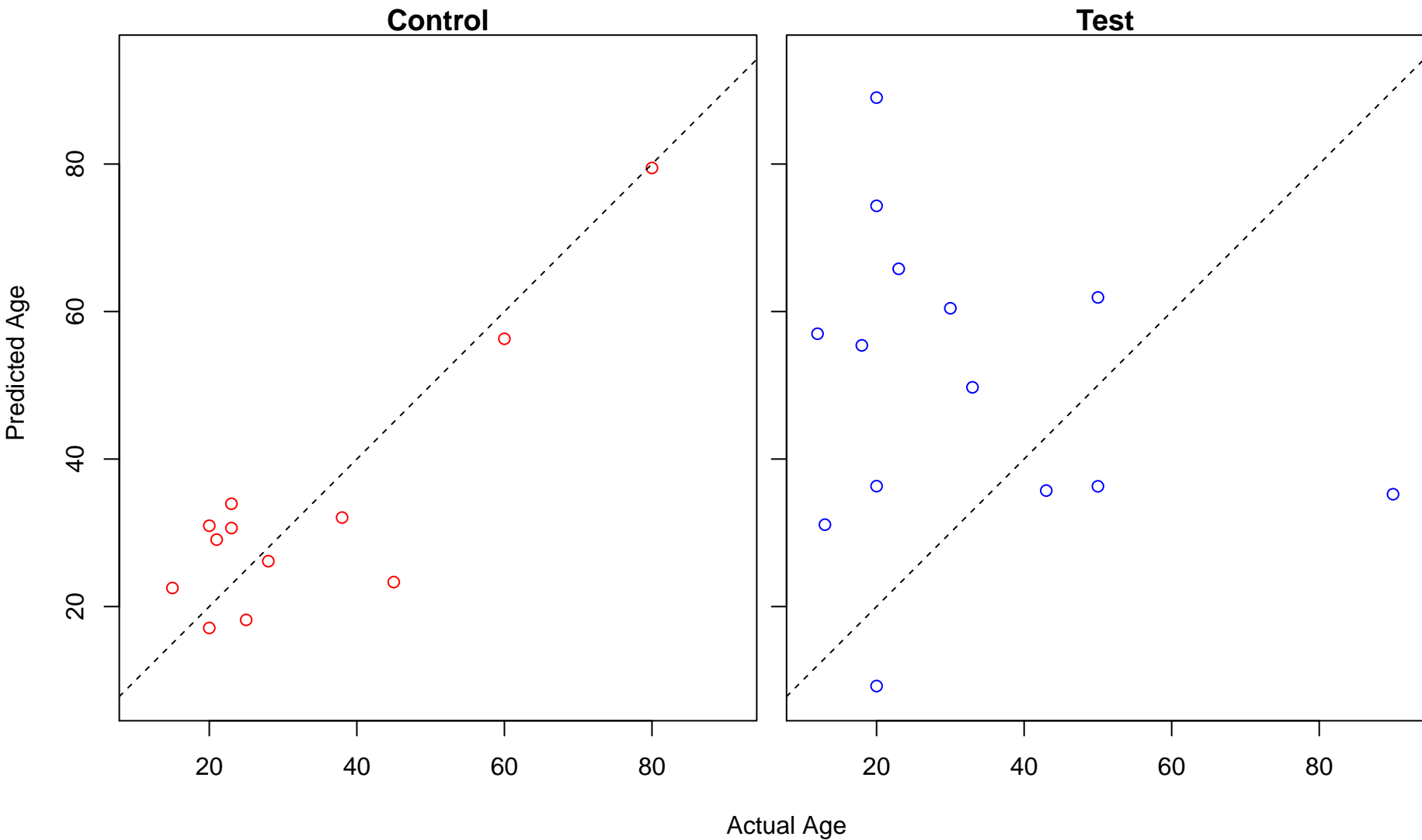
cellular response to purine-containing compound (Score: 6.615723)



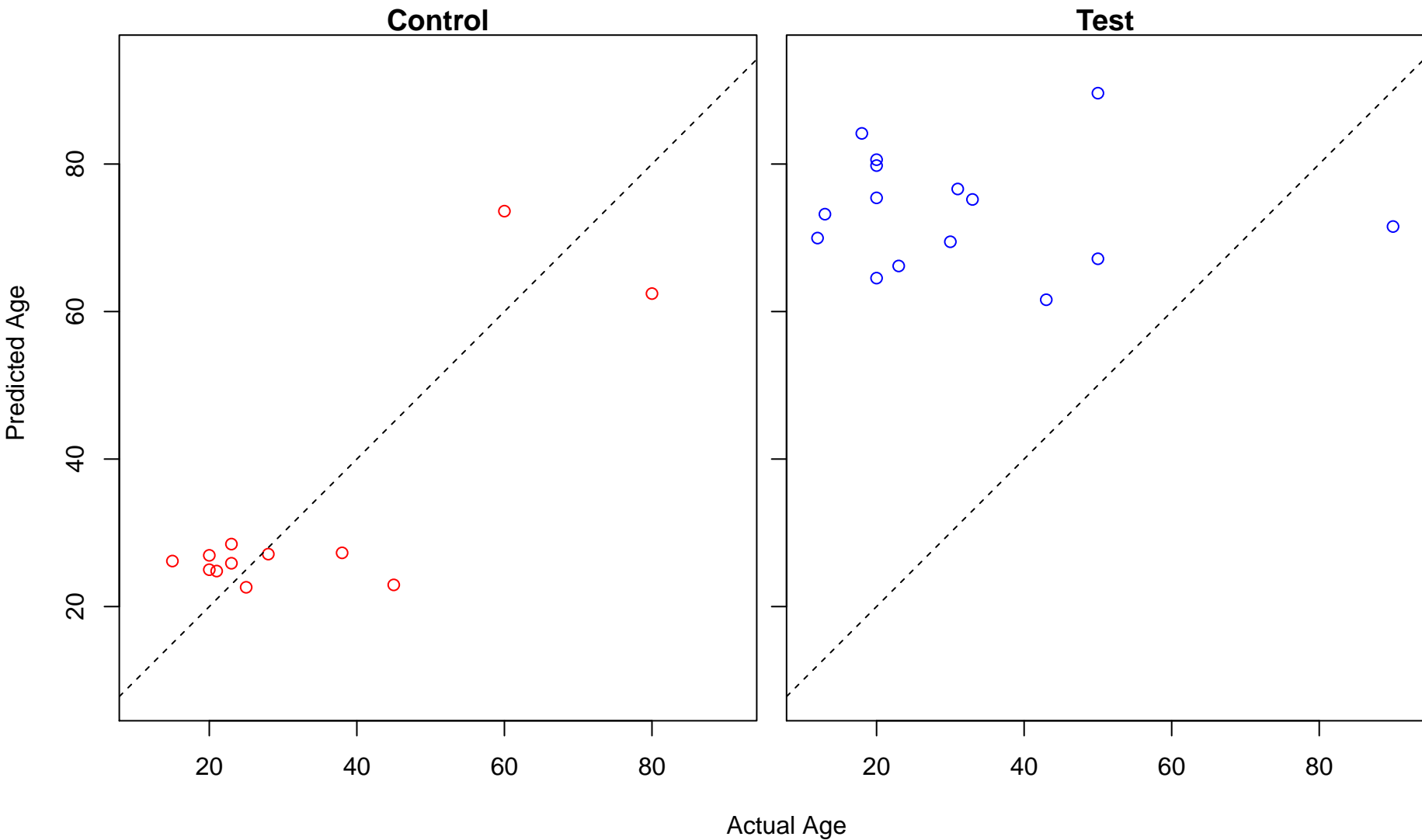
rRNA-containing ribonucleoprotein complex export from nucleus (Score: 6.615028)



immune effector process (Score: 6.614086)

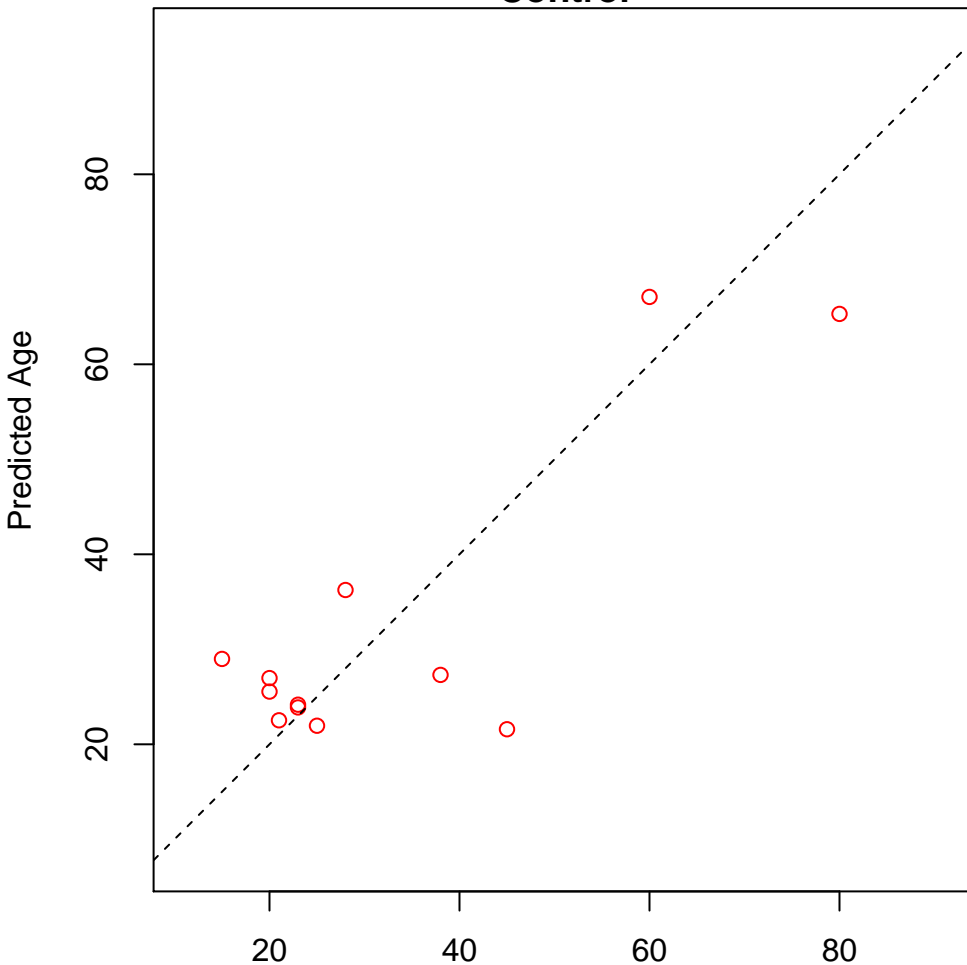


regulation of myeloid leukocyte differentiation (Score: 6.613432)

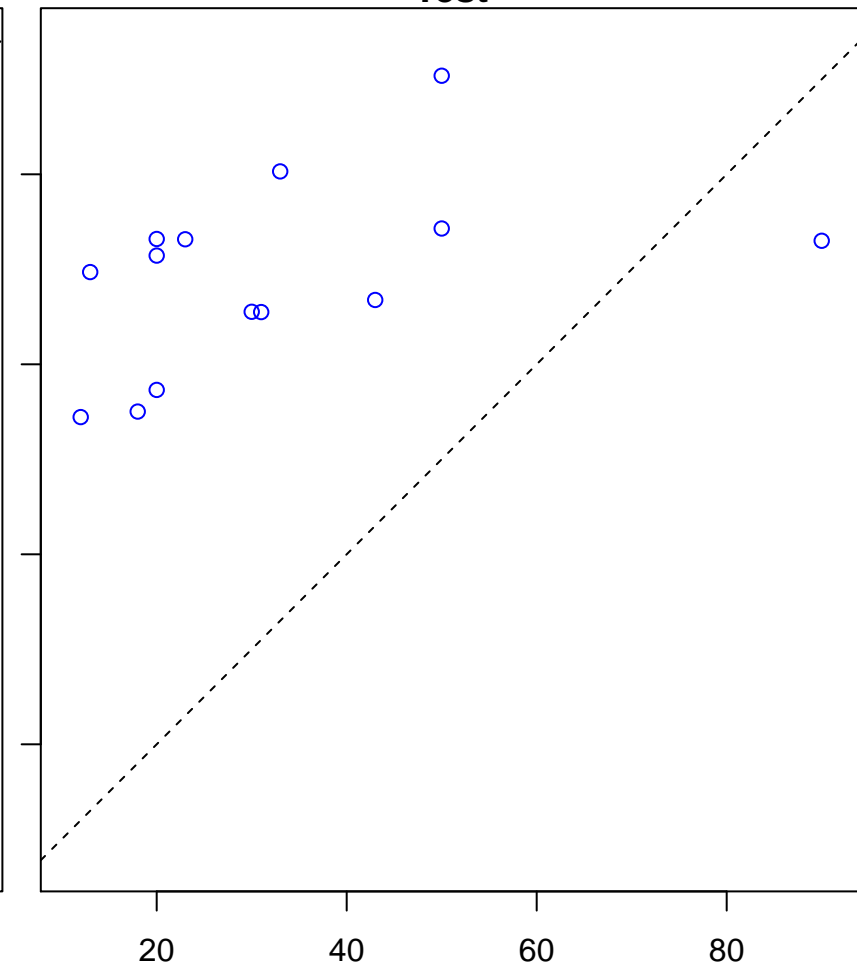


collagen-activated signaling pathway (Score: 6.611071)

Control

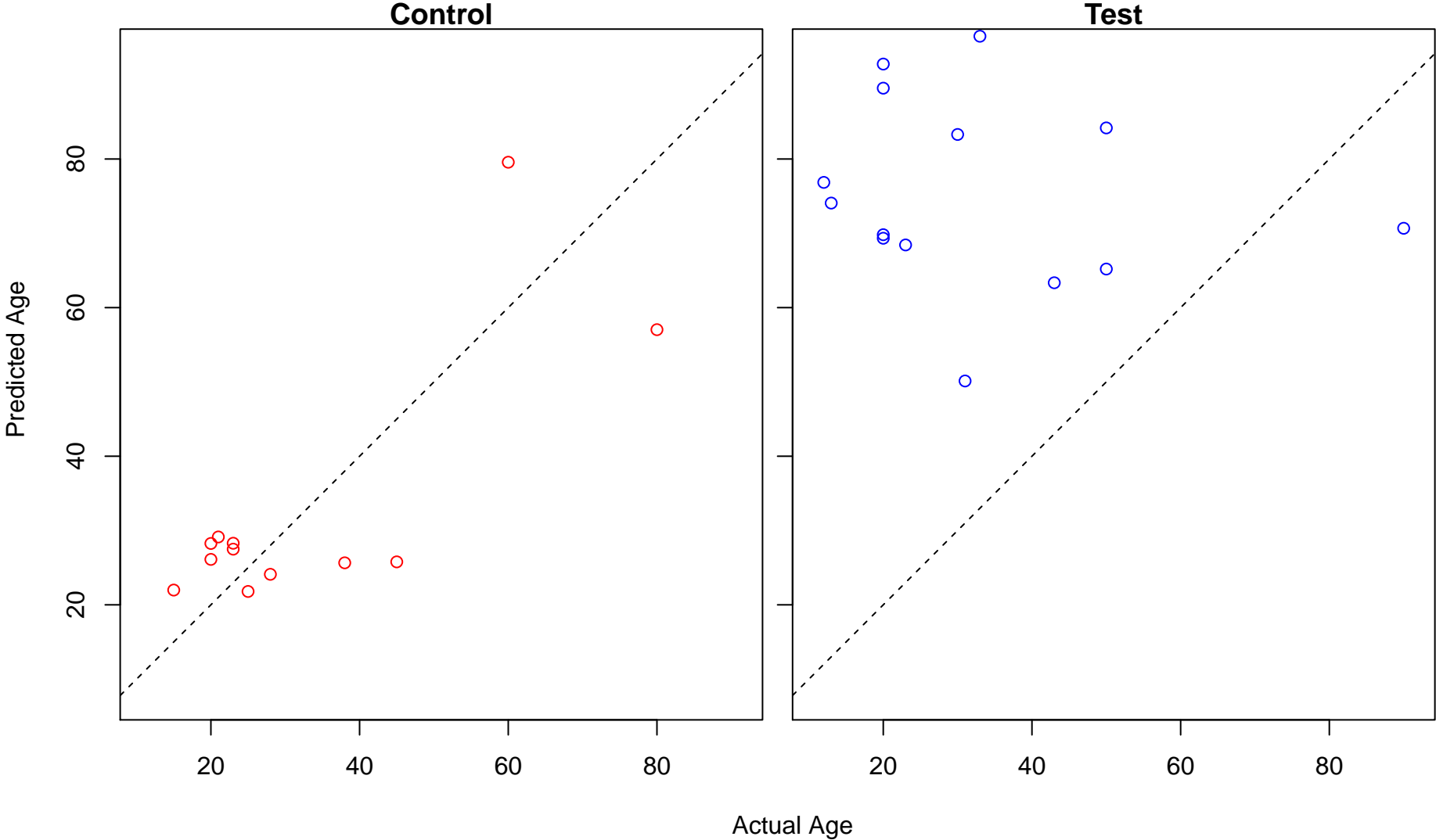


Test

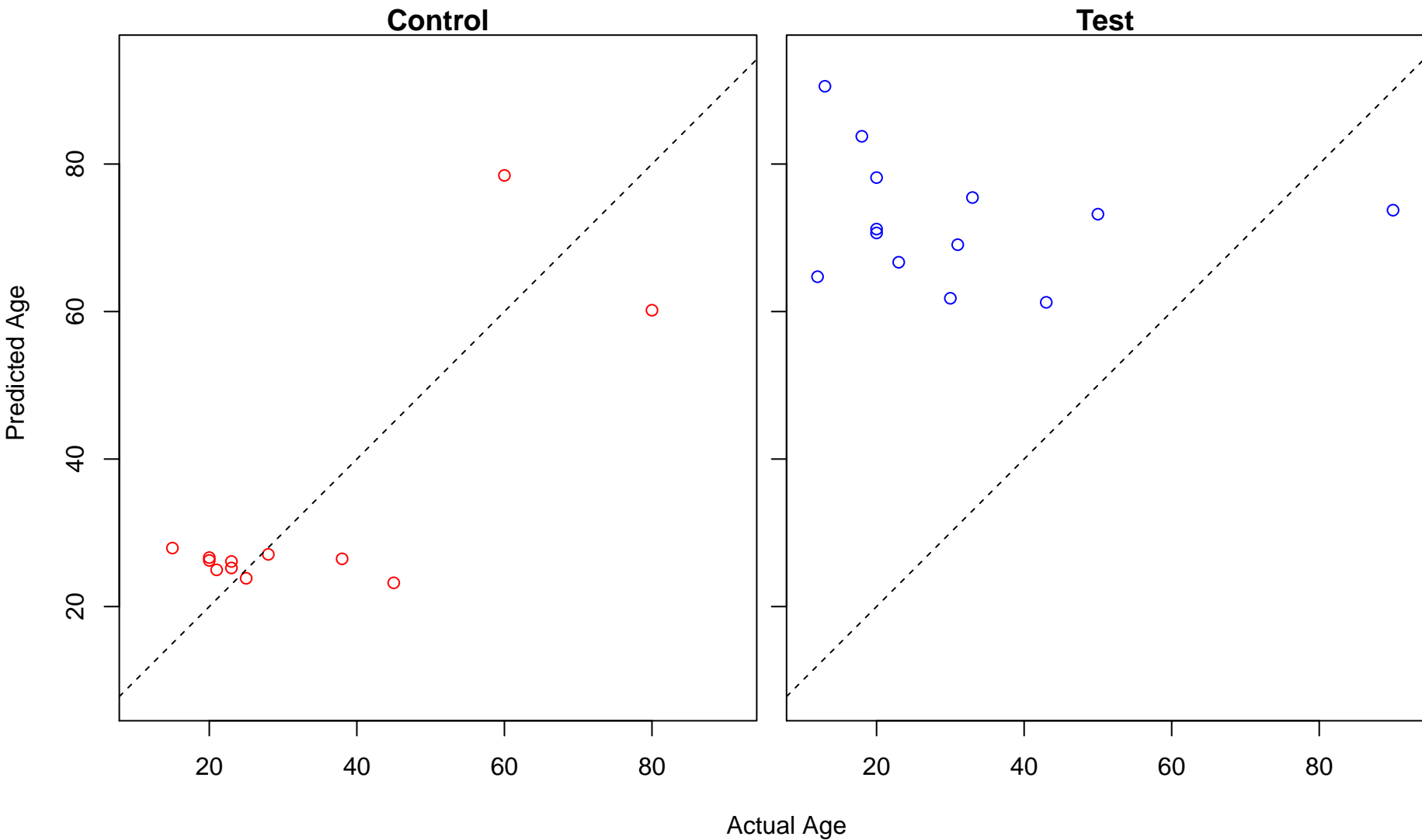


Actual Age

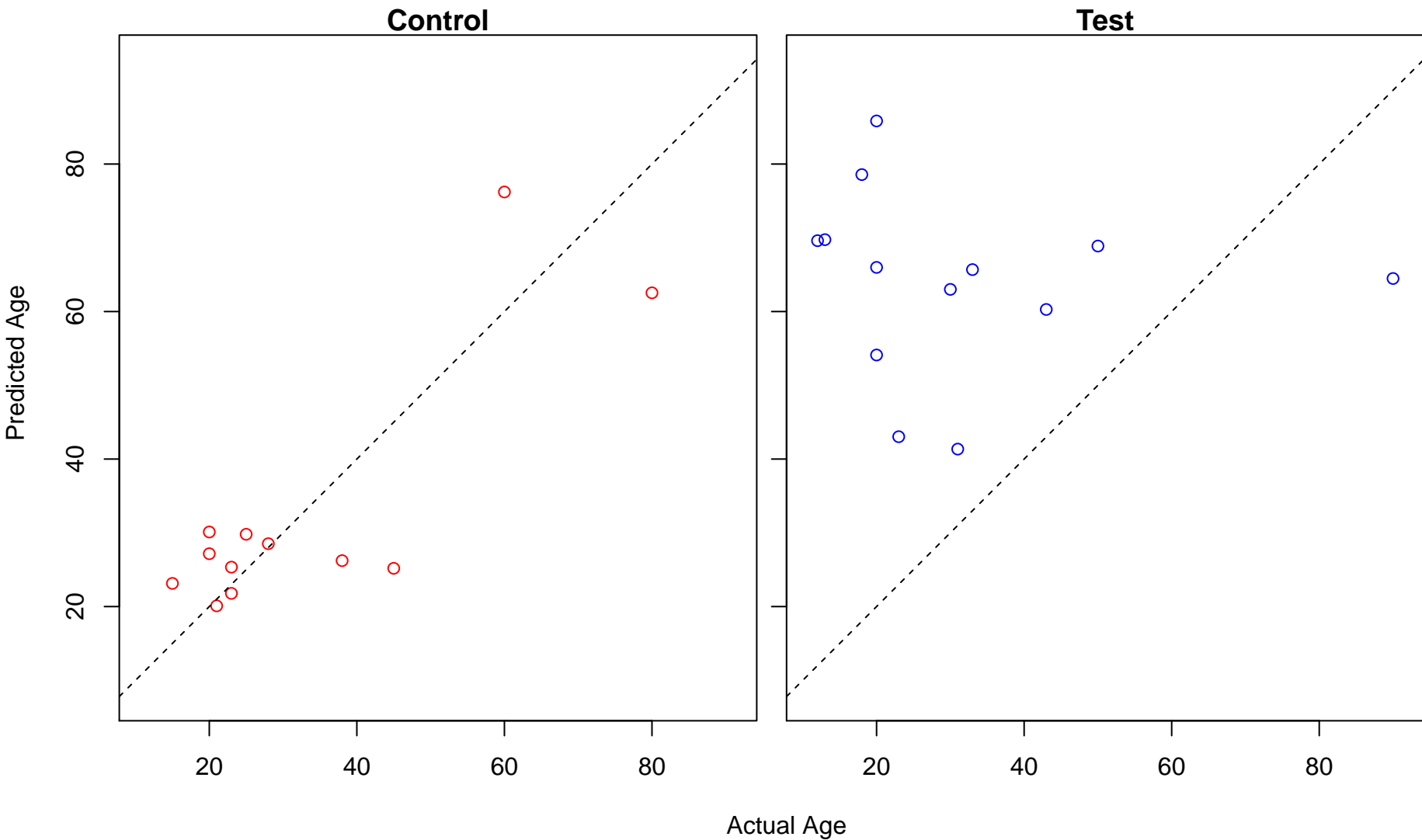
regulation of dopamine receptor signaling pathway (Score: 6.609571)



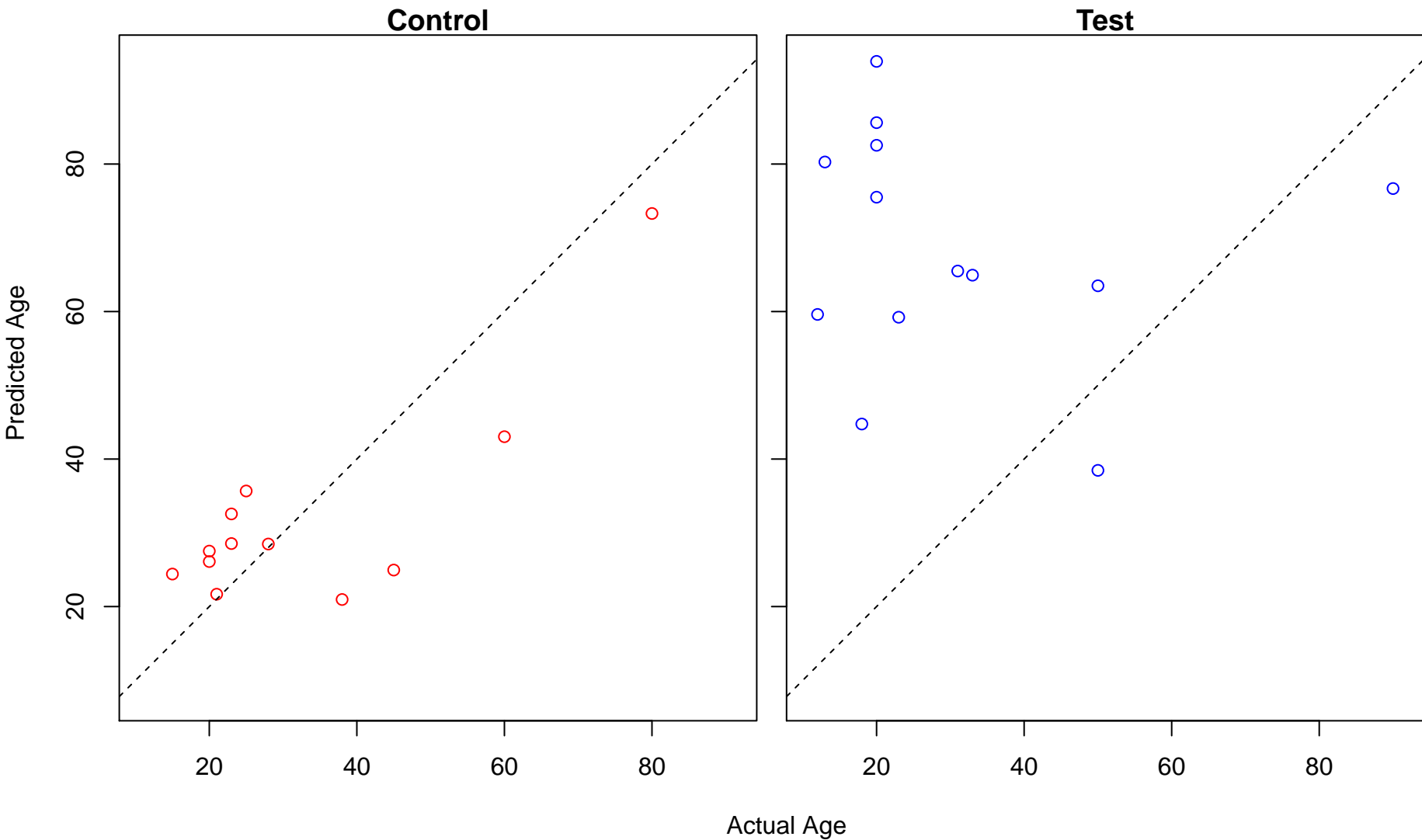
cellular response to hypoxia (Score: 6.608160)



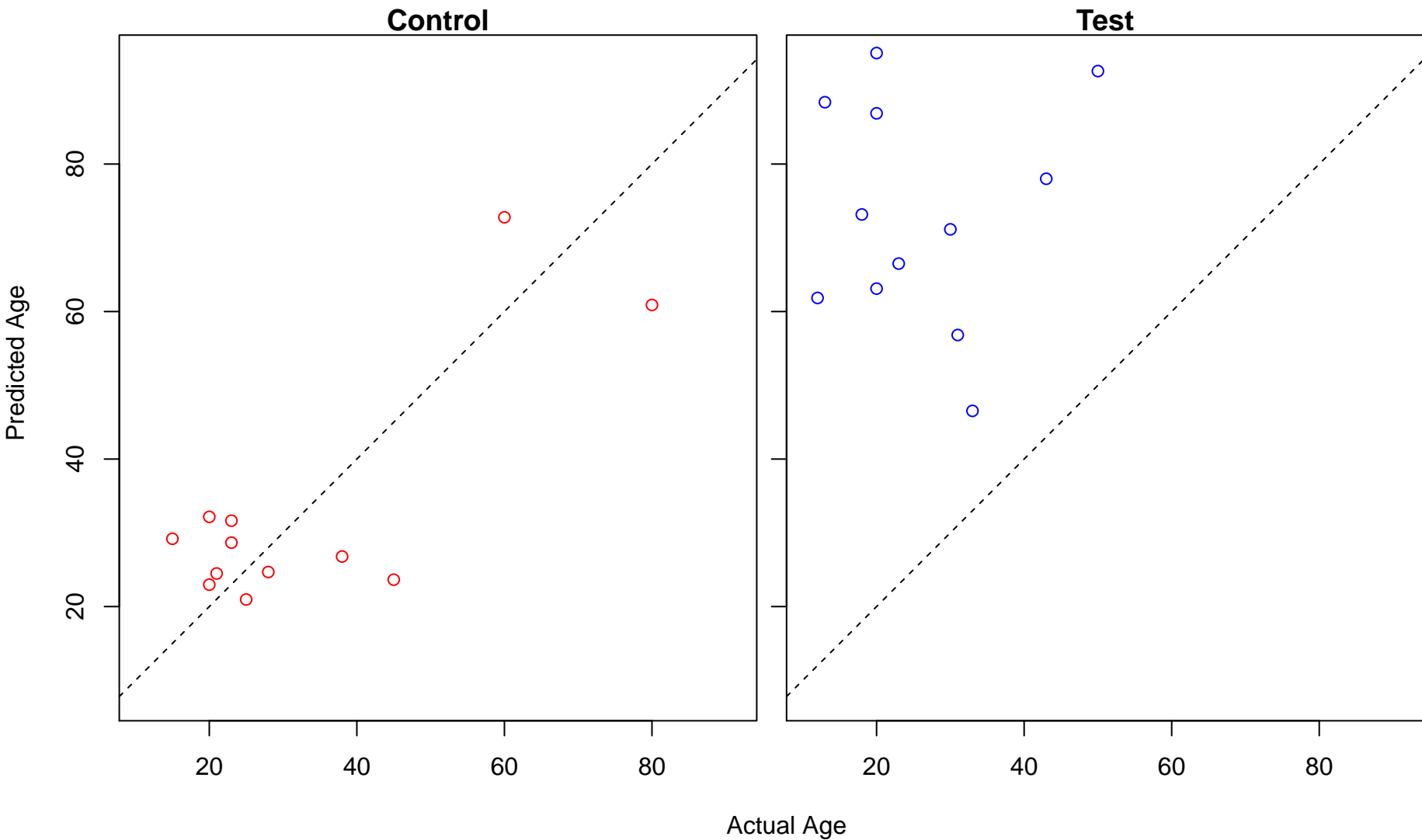
regulation of vascular smooth muscle cell proliferation (Score: 6.606360)



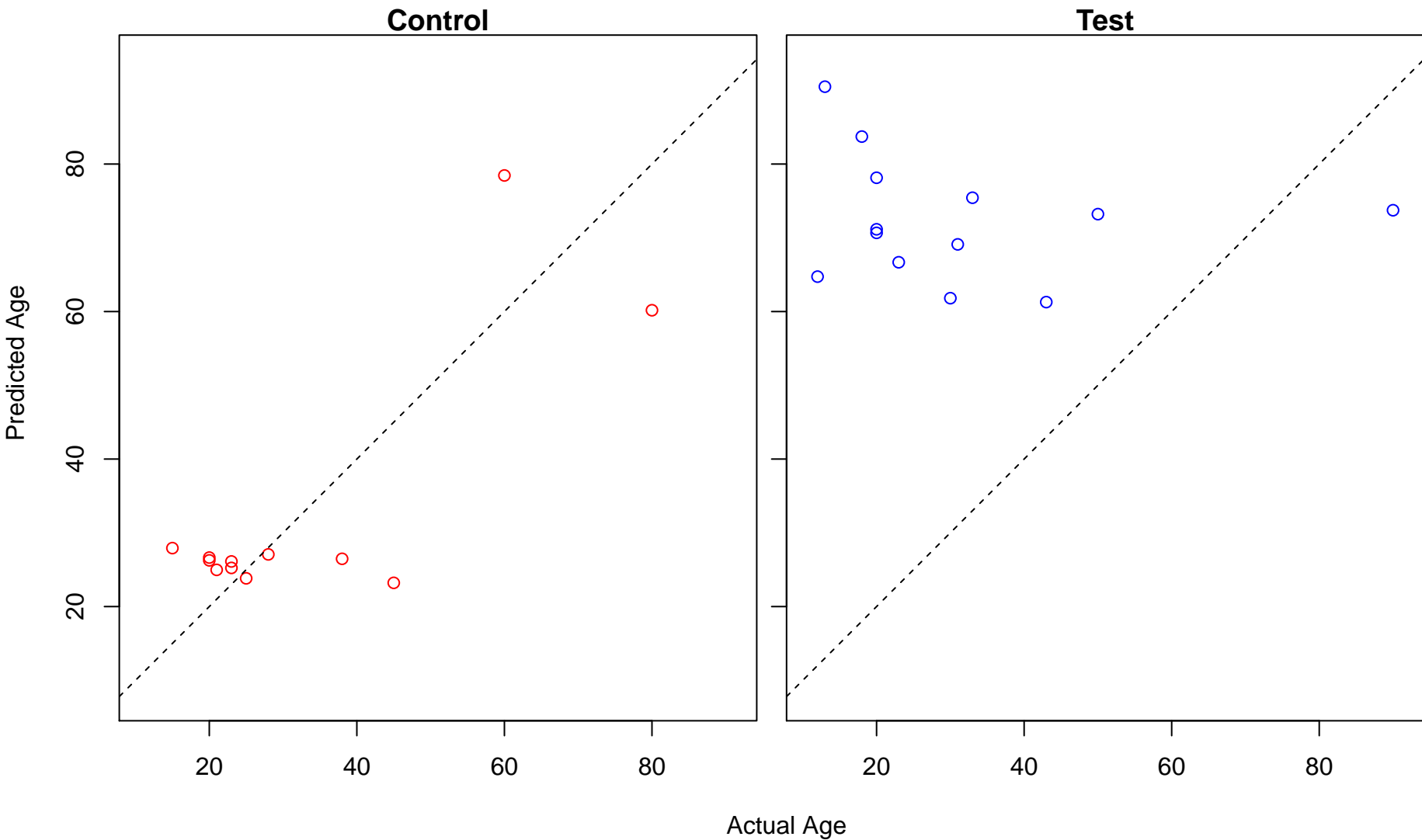
regulation of natural killer cell proliferation (Score: 6.604975)



negative regulation of inflammatory response (Score: 6.603957)

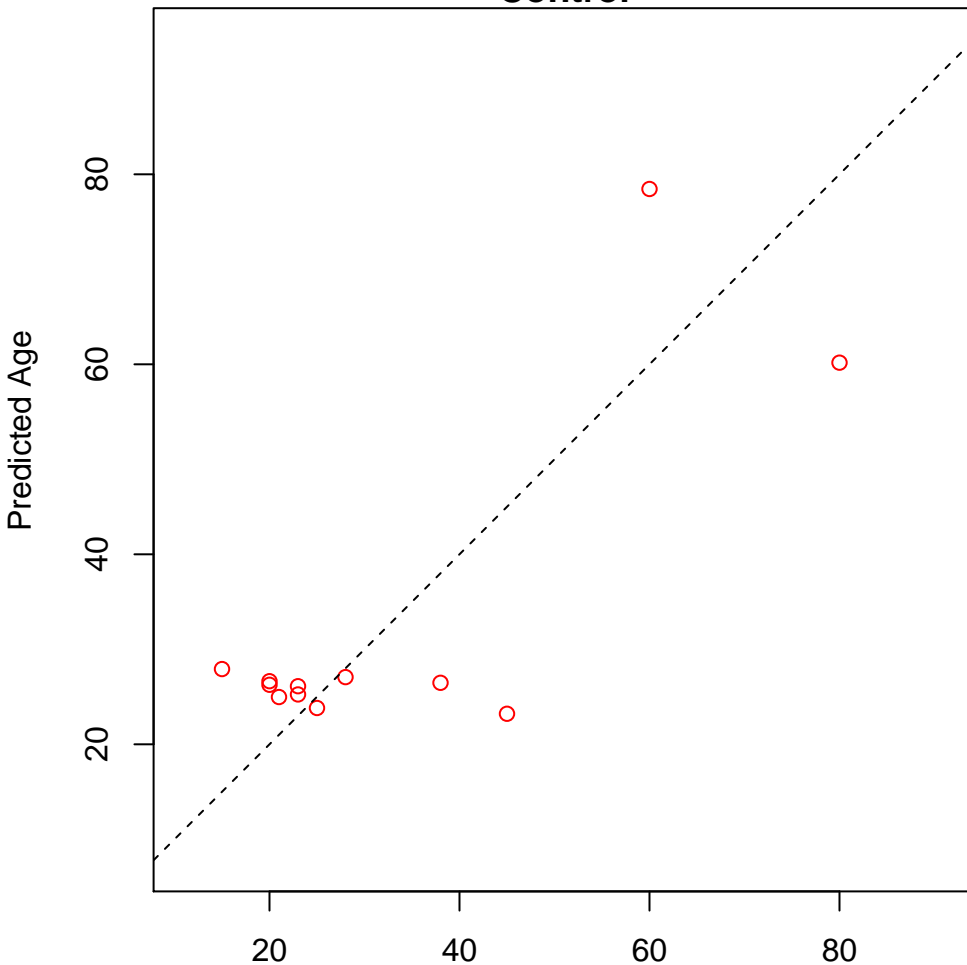


cellular response to decreased oxygen levels (Score: 6.602886)

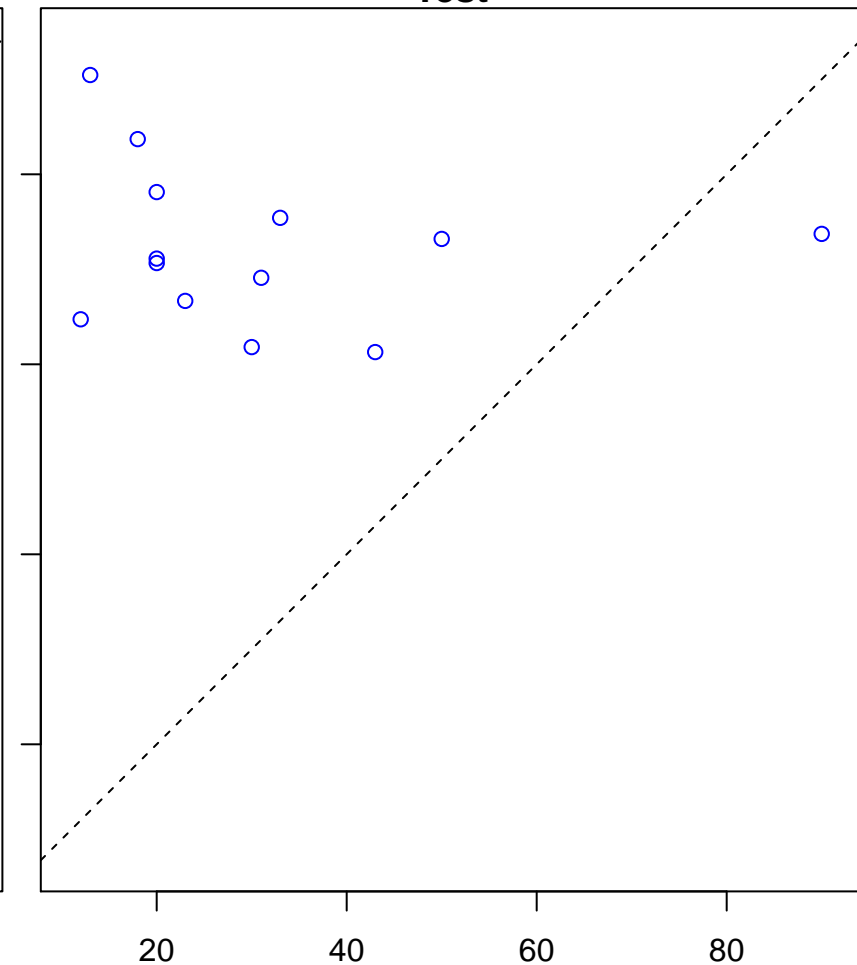


cellular response to oxygen levels (Score: 6.597048)

Control

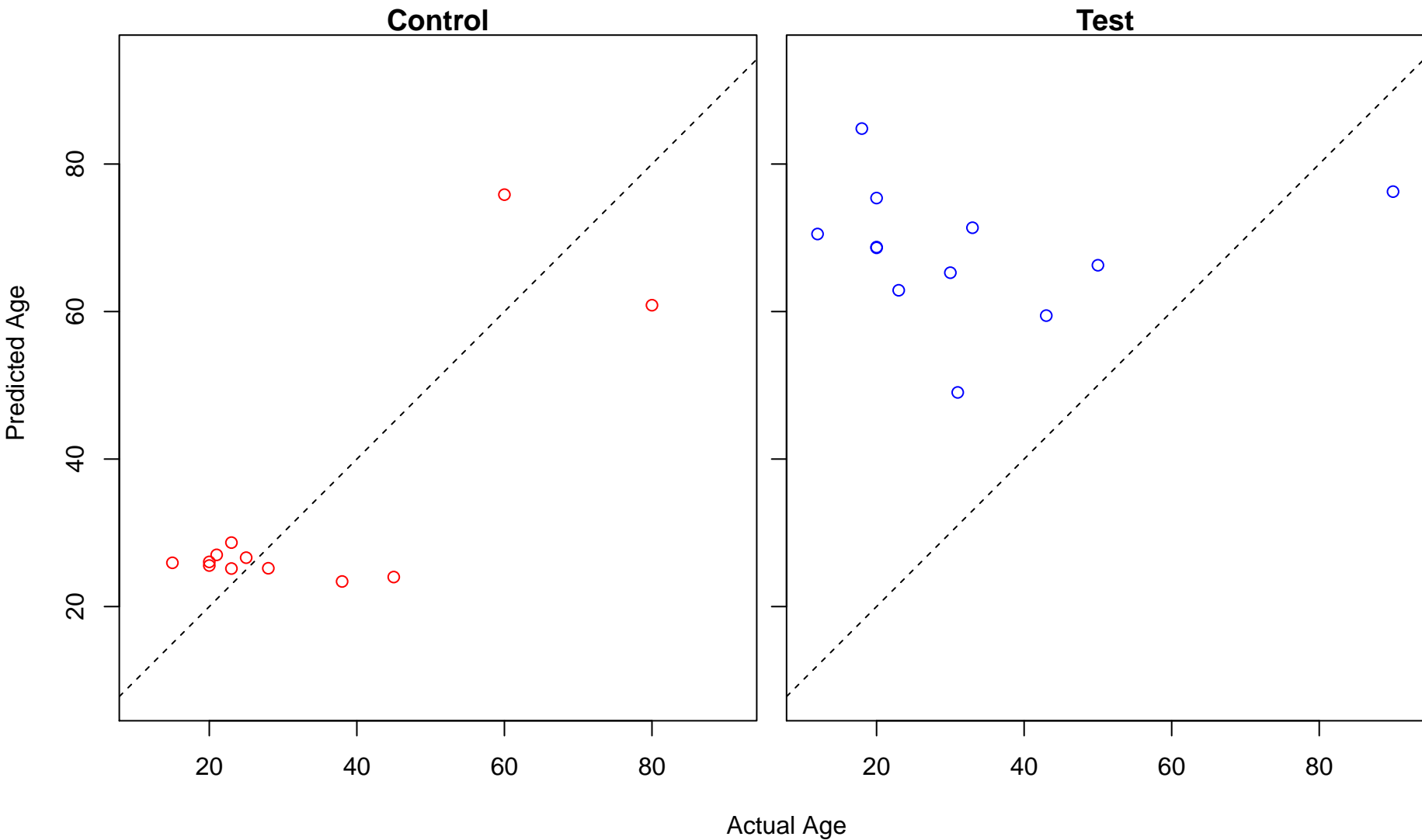


Test

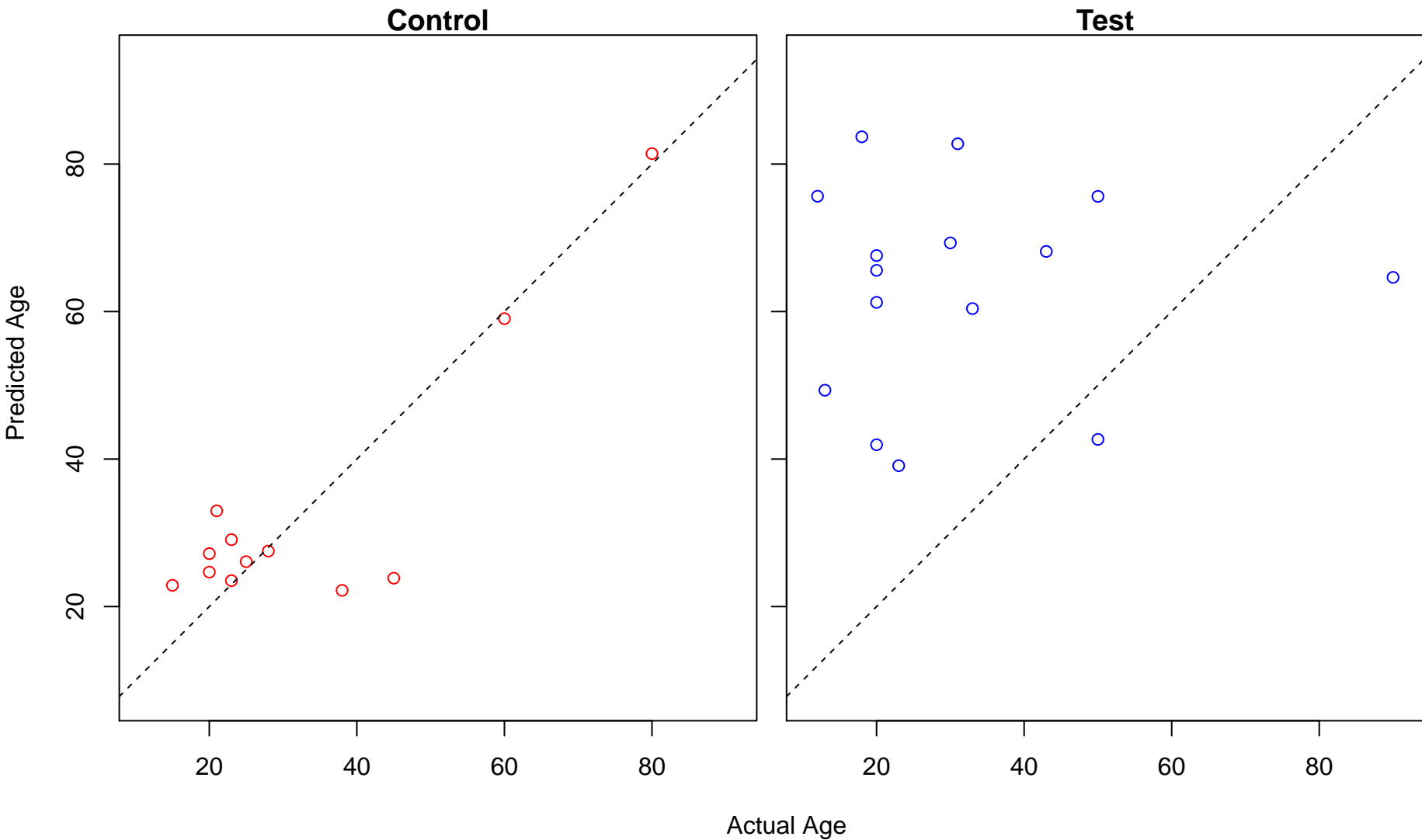


Actual Age

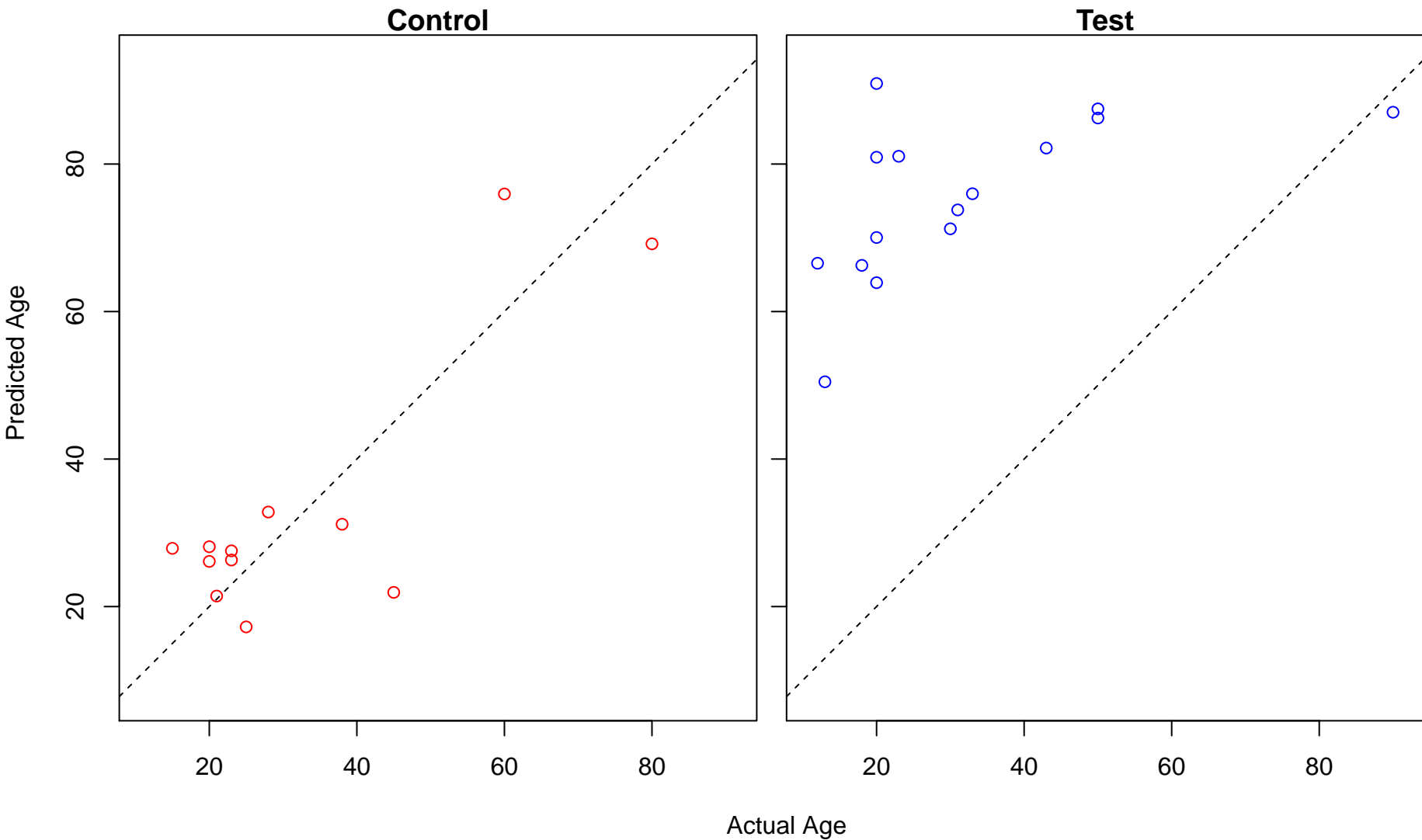
ribosome biogenesis (Score: 6.596974)



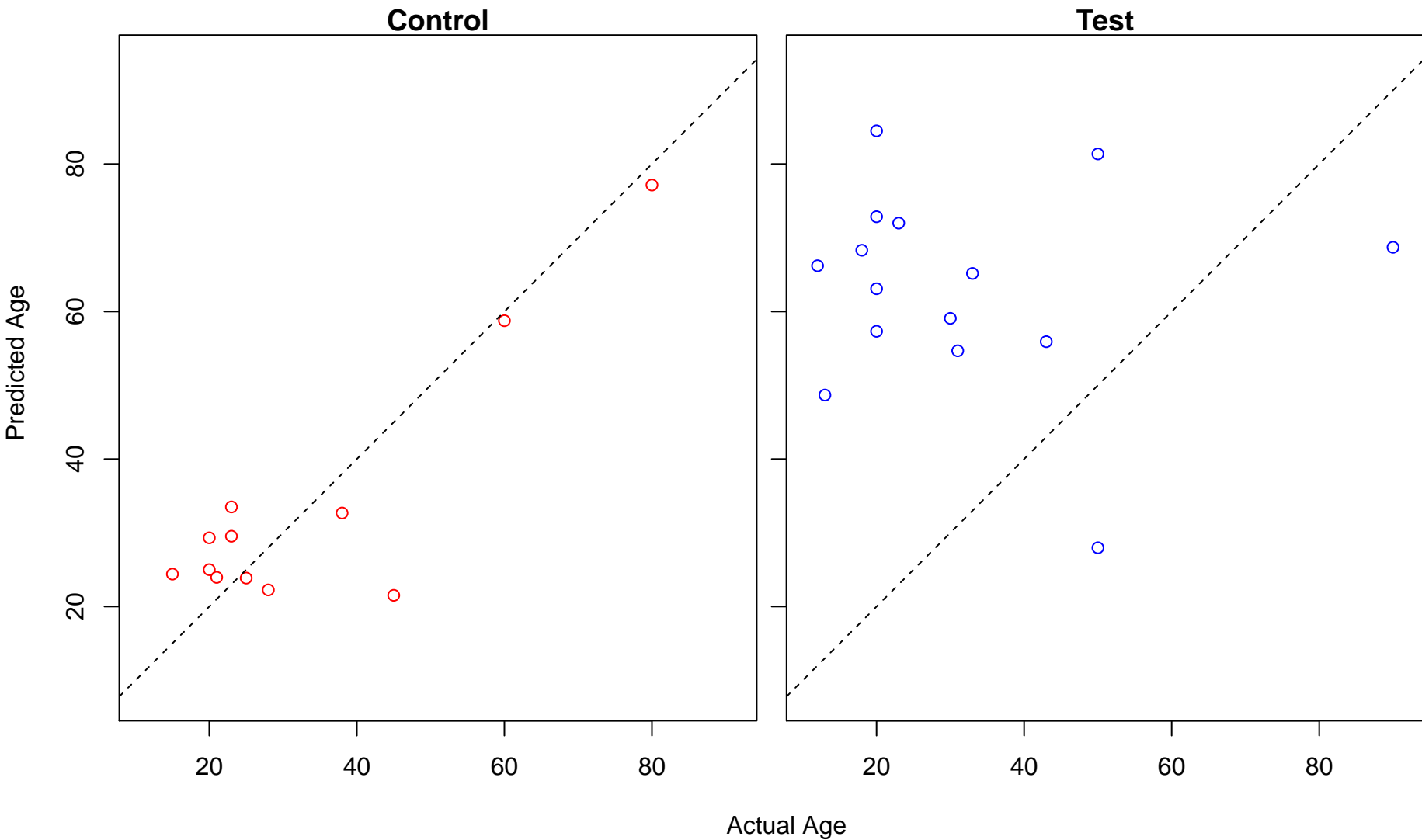
CRD-mediated mRNA stabilization (Score: 6.596901)



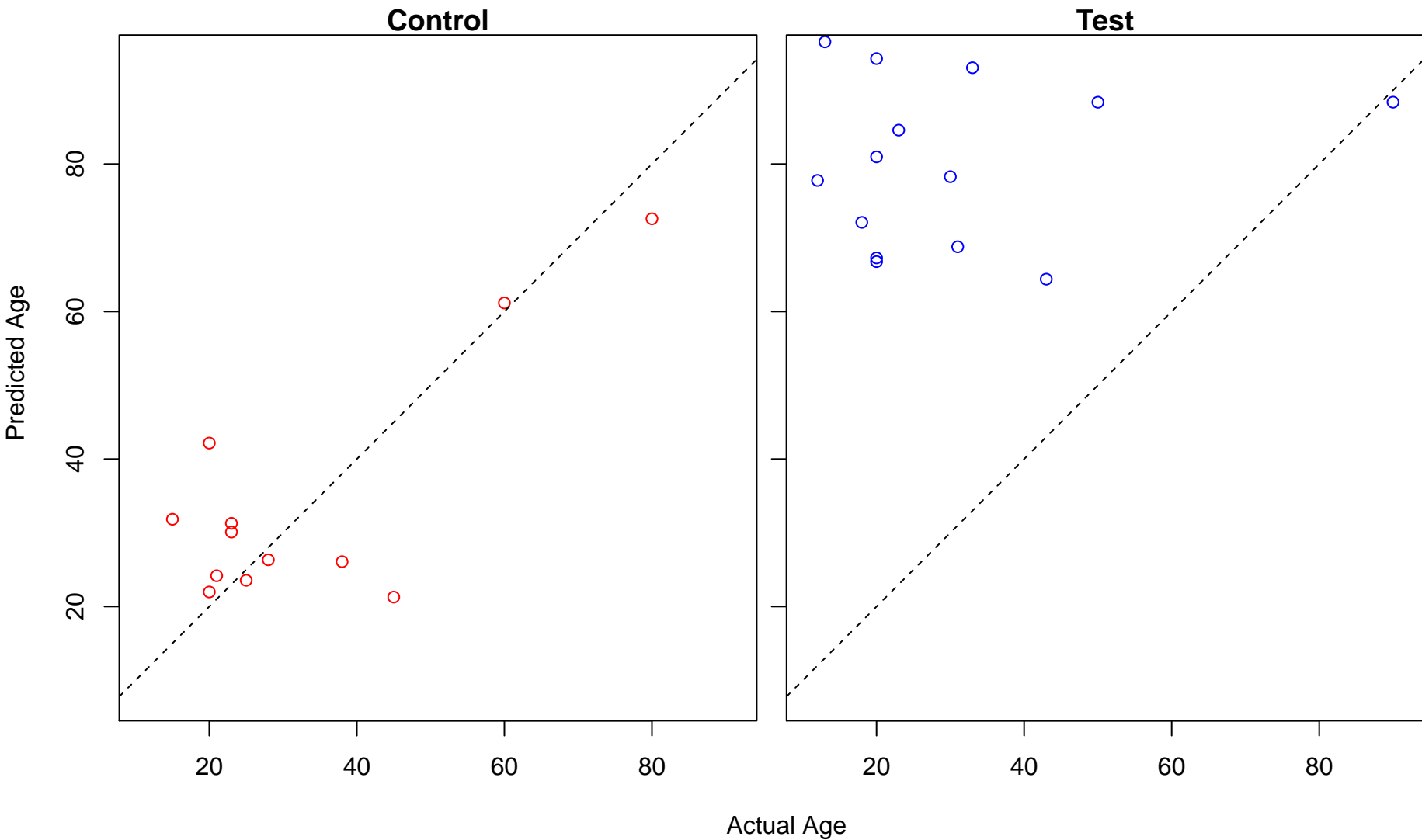
neural precursor cell proliferation (Score: 6.595993)



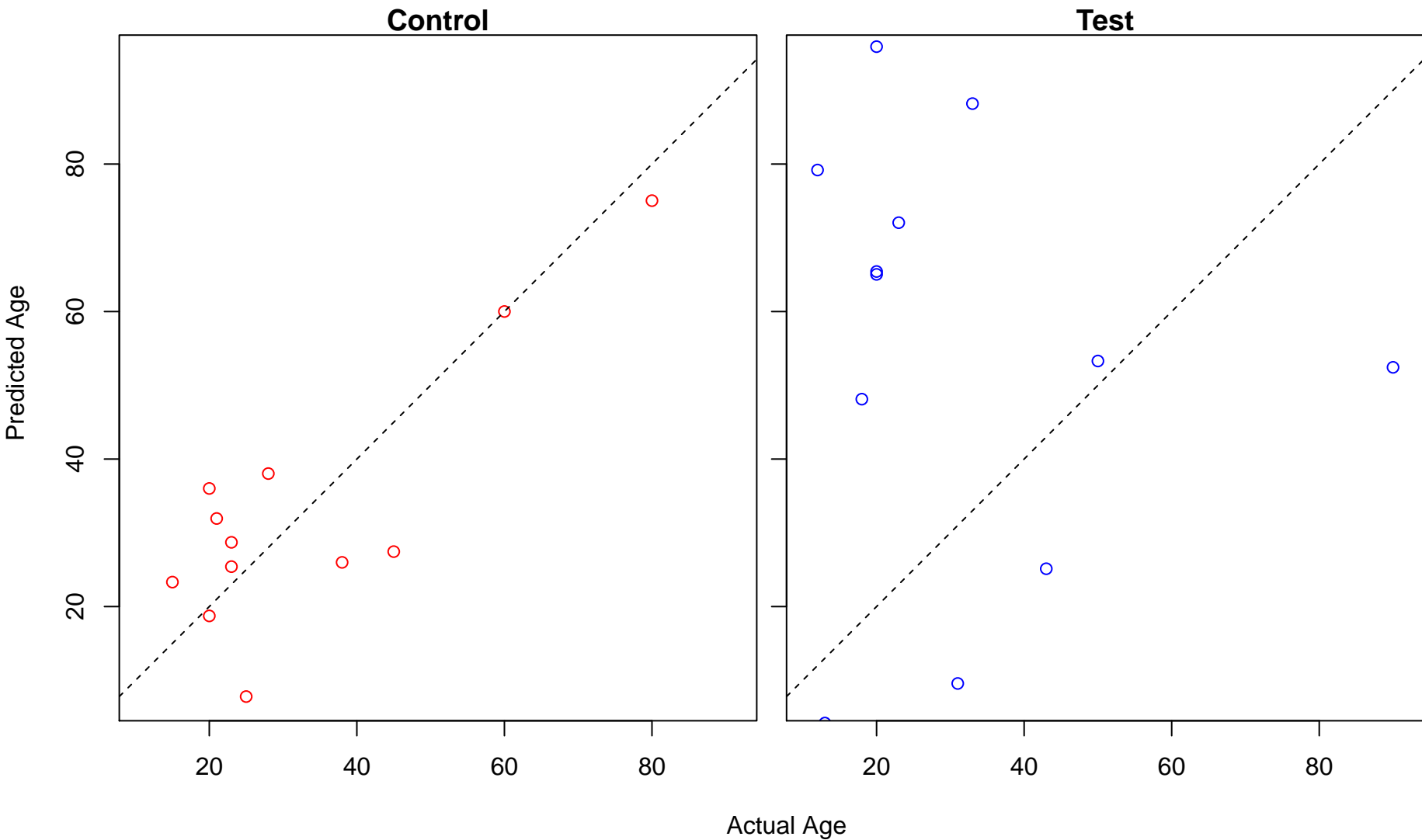
patterning of blood vessels (Score: 6.595865)



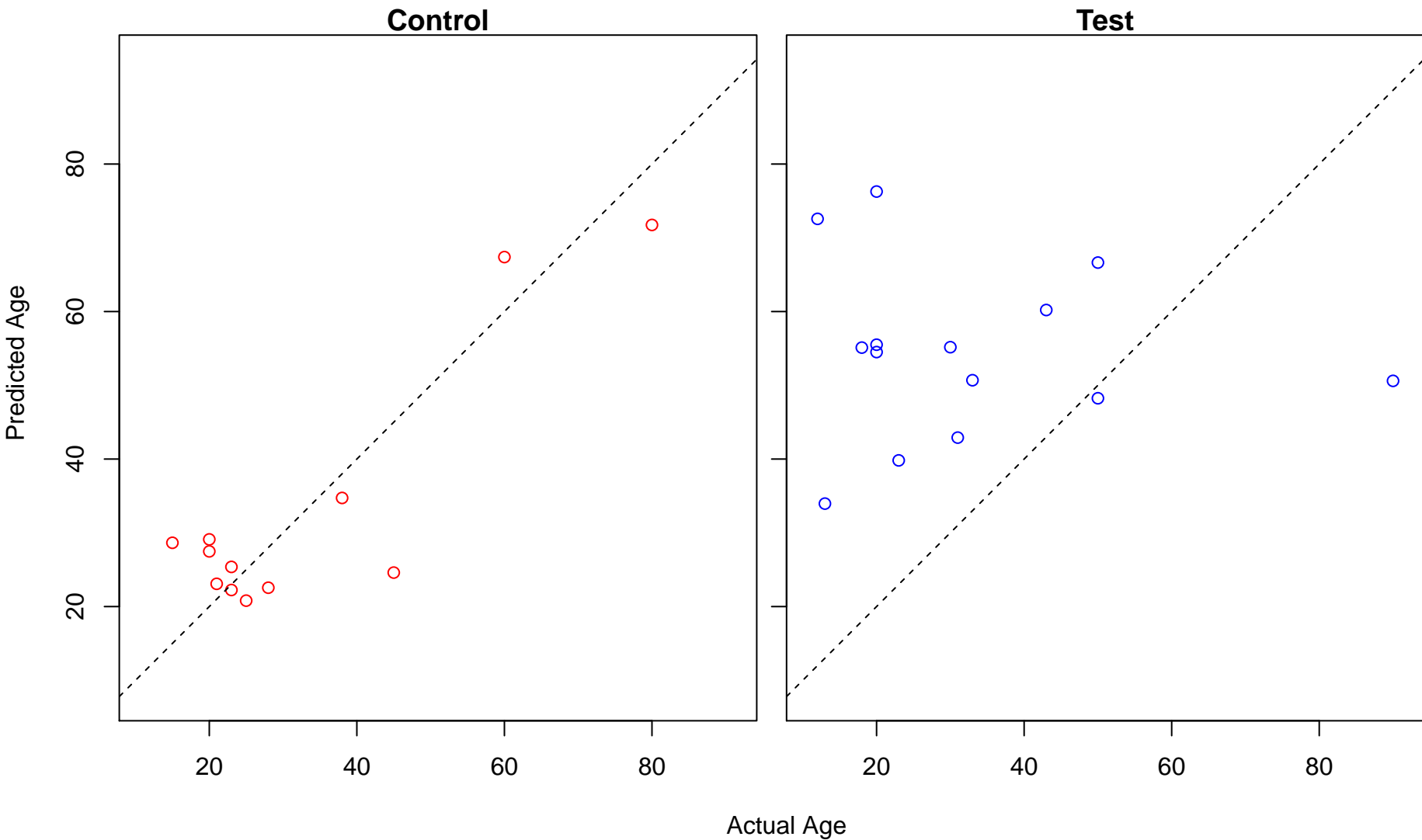
positive regulation of fatty acid oxidation (Score: 6.595683)



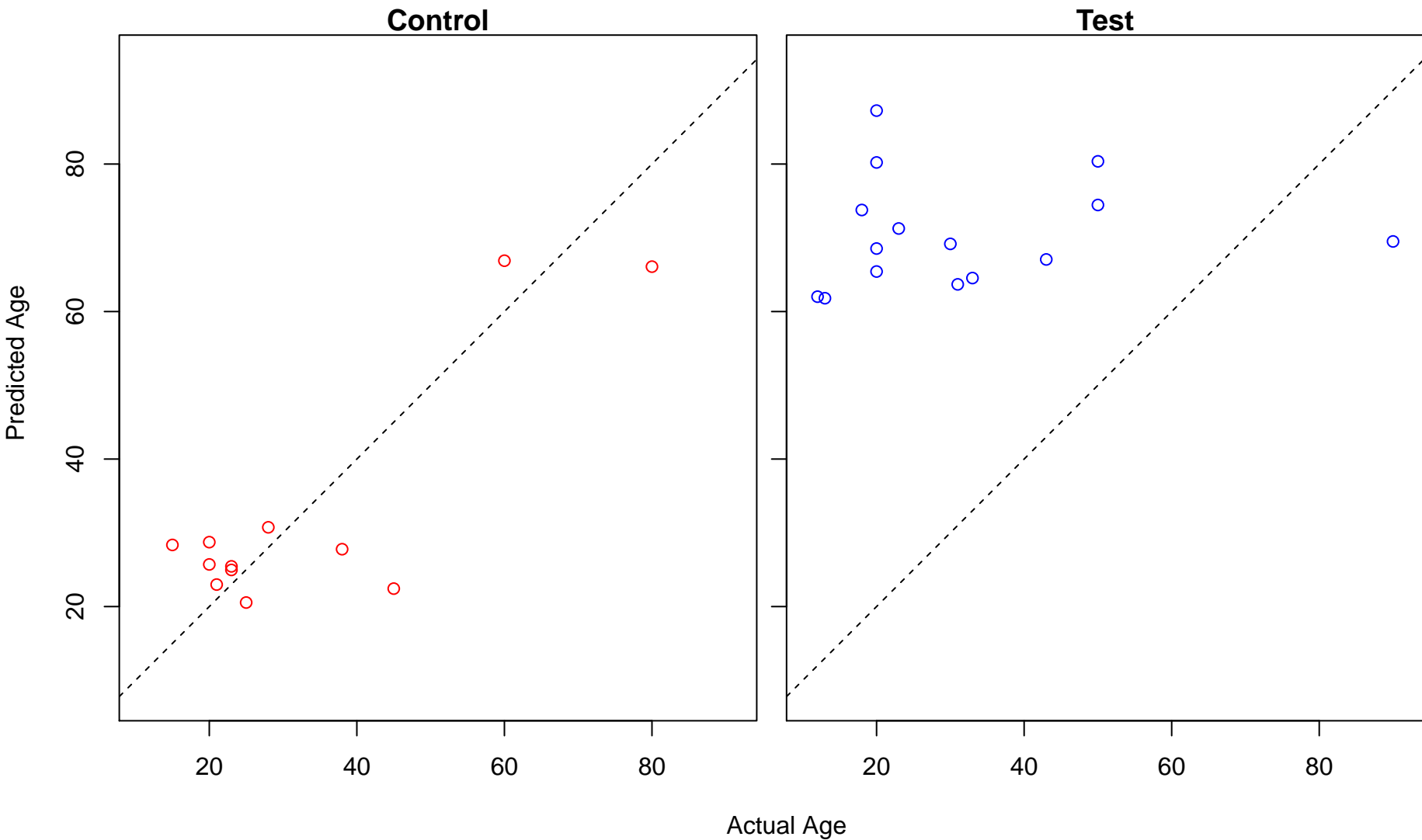
DNA duplex unwinding (Score: 6.594335)



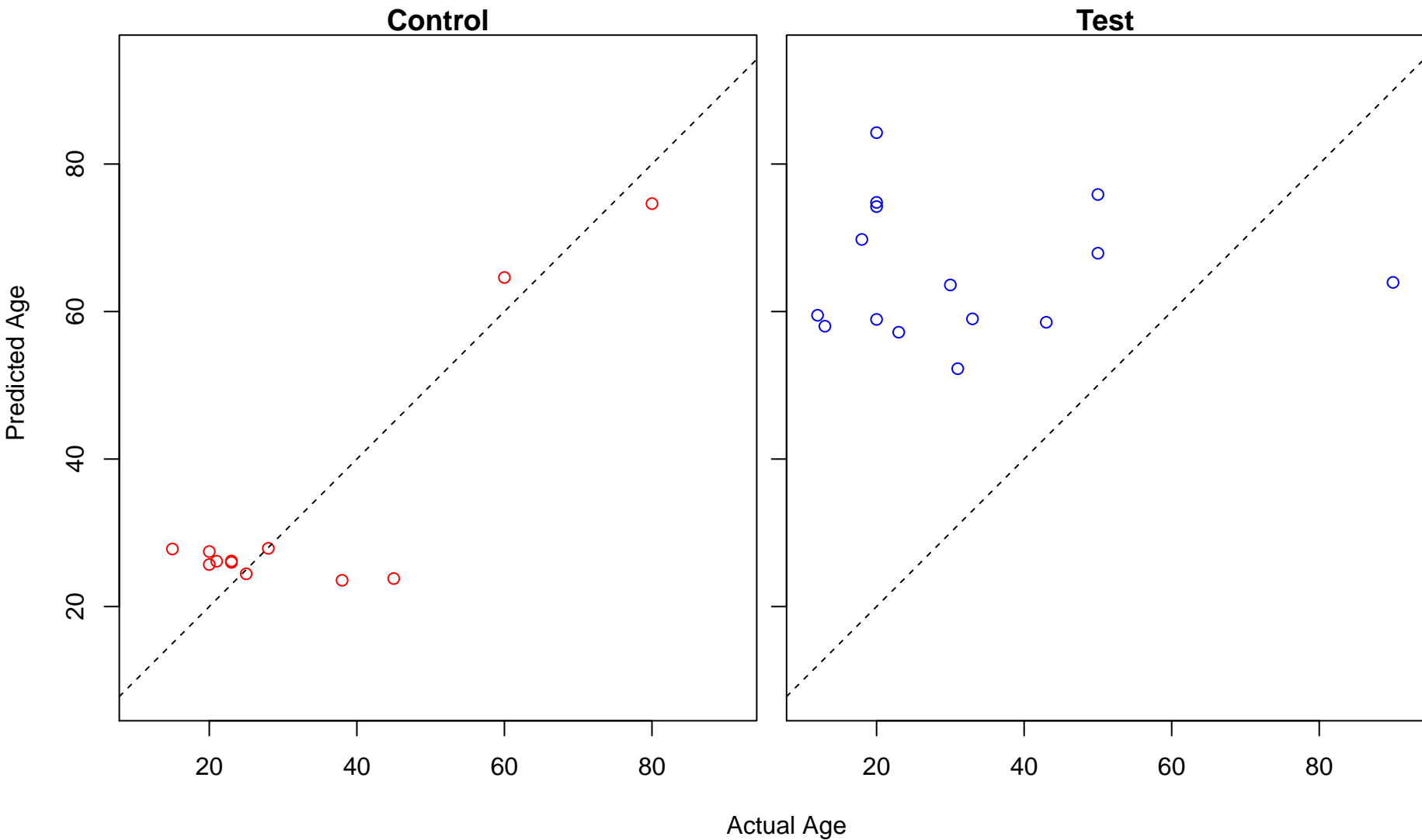
polyprenol metabolic process (Score: 6.594312)



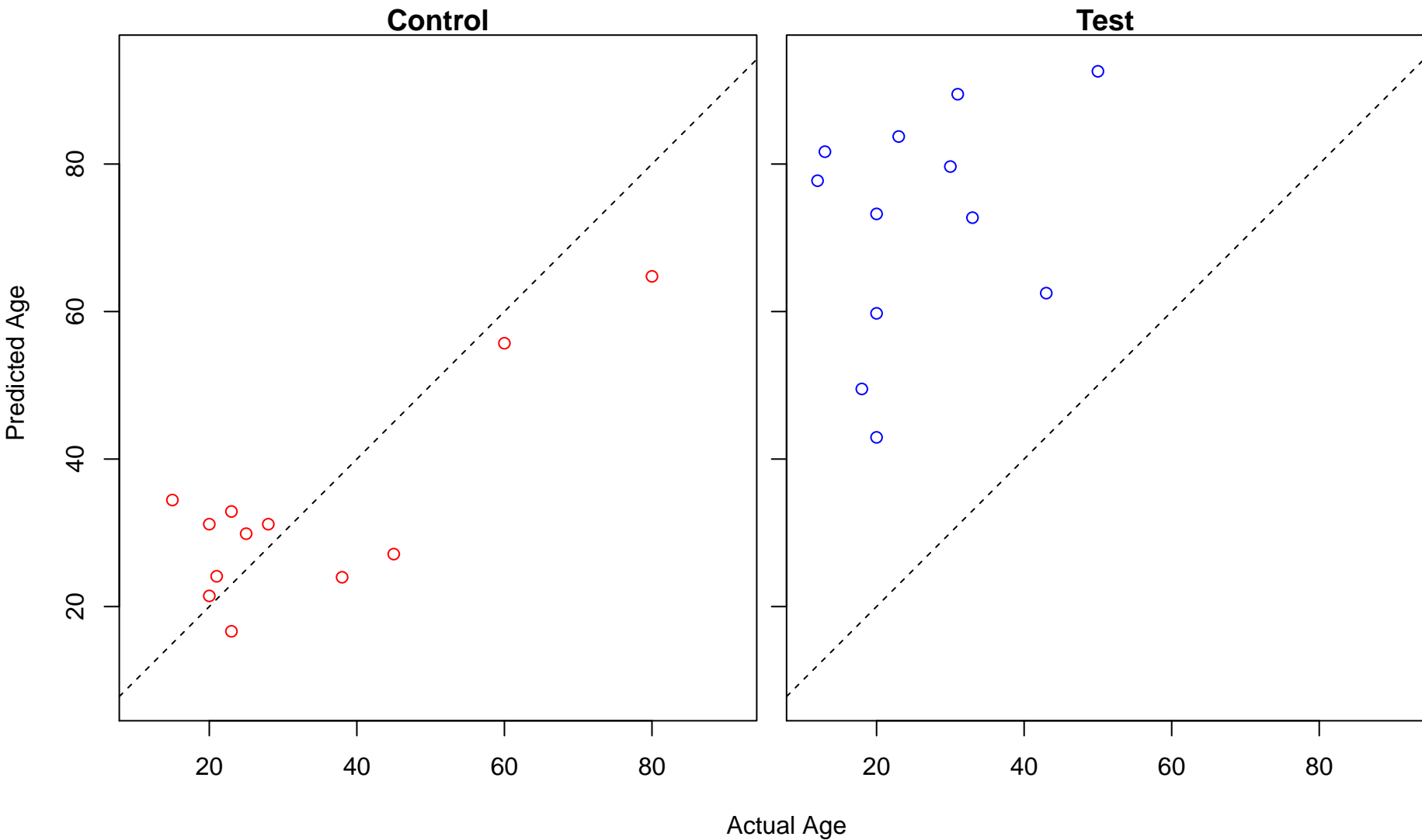
endoplasmic reticulum calcium ion homeostasis (Score: 6.591823)



organelle fission (Score: 6.591687)

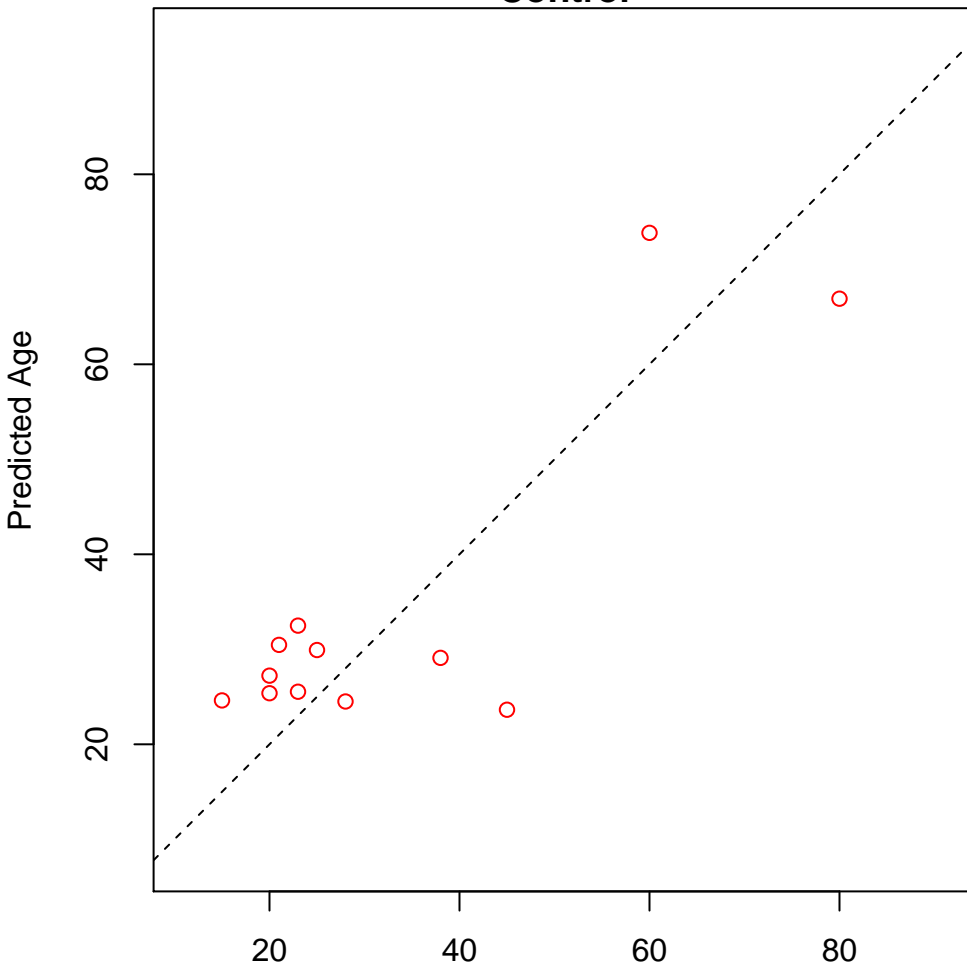


positive regulation of positive chemotaxis (Score: 6.591620)

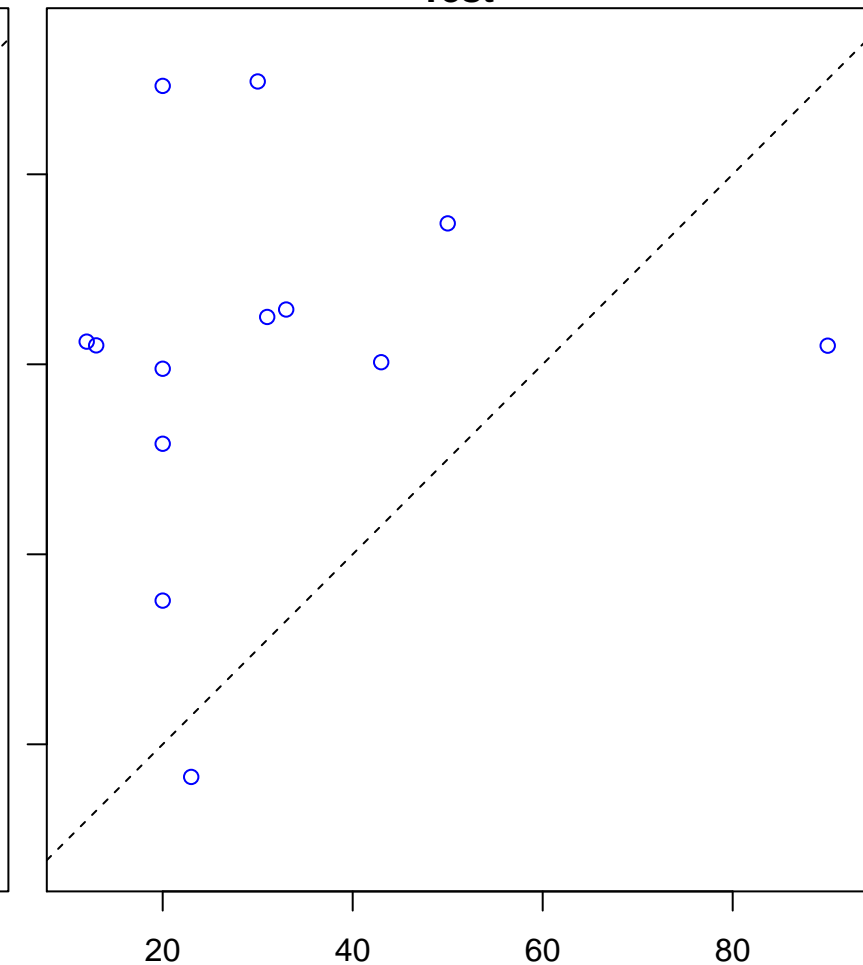


post-embryonic organ development (Score: 6.591305)

Control

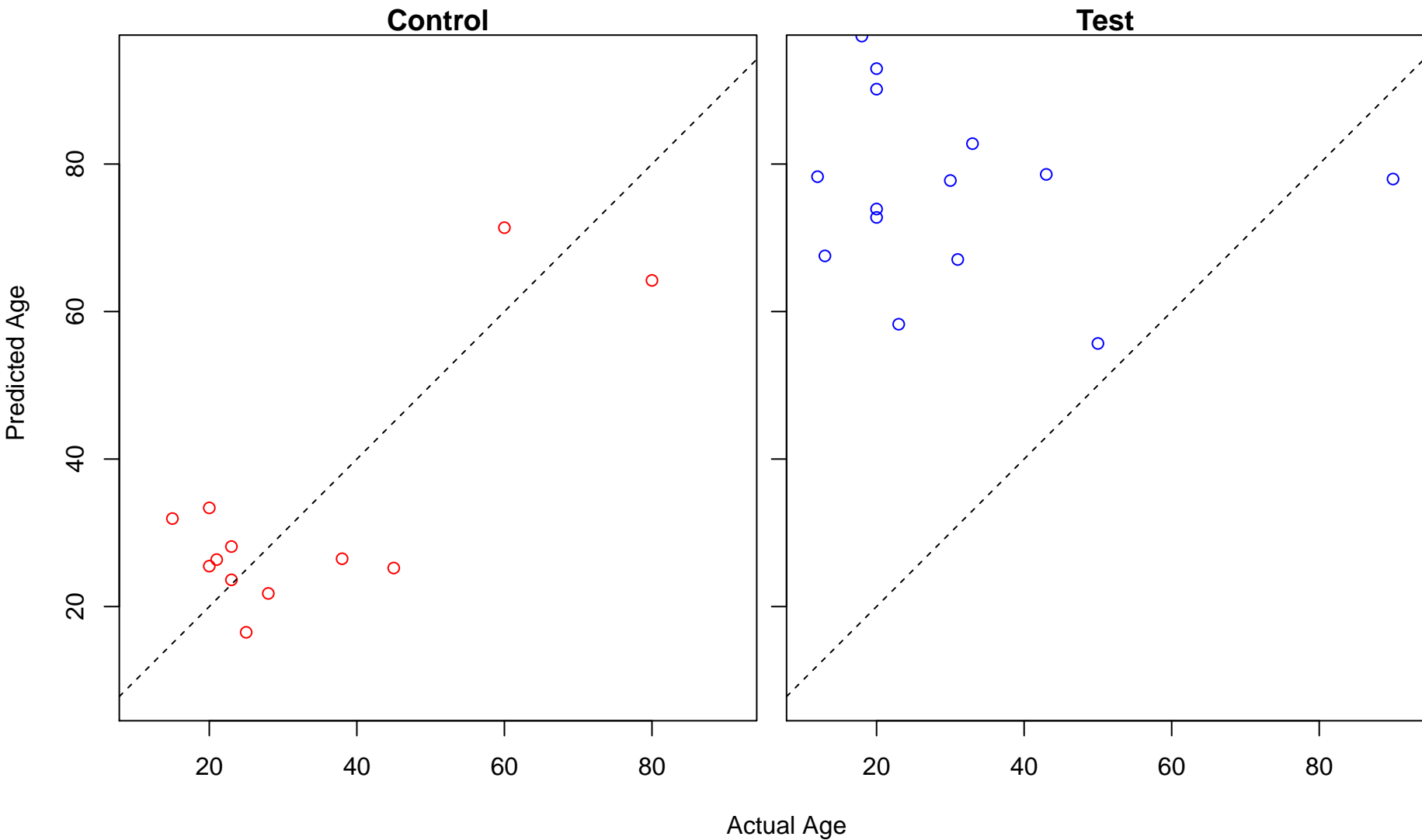


Test

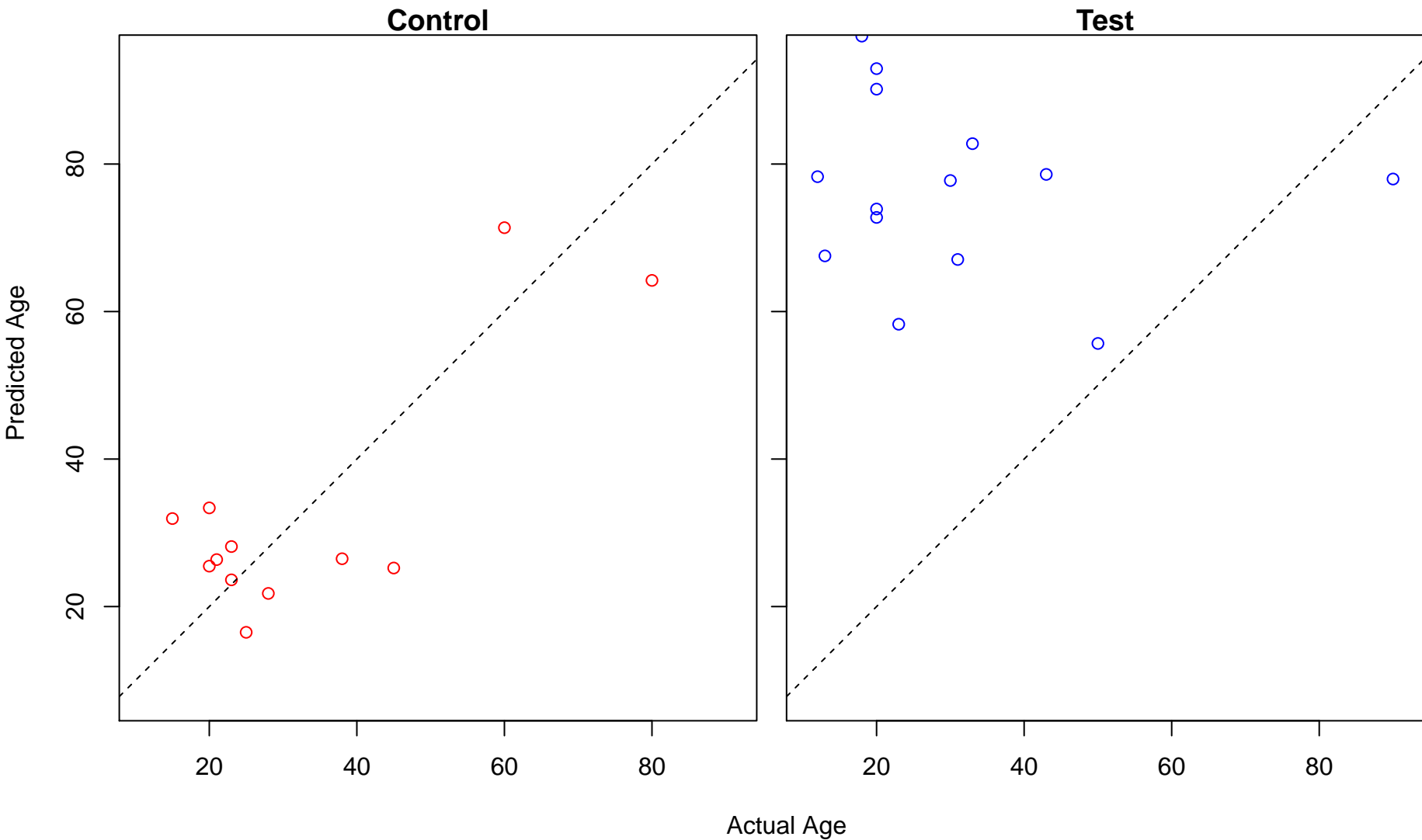


Actual Age

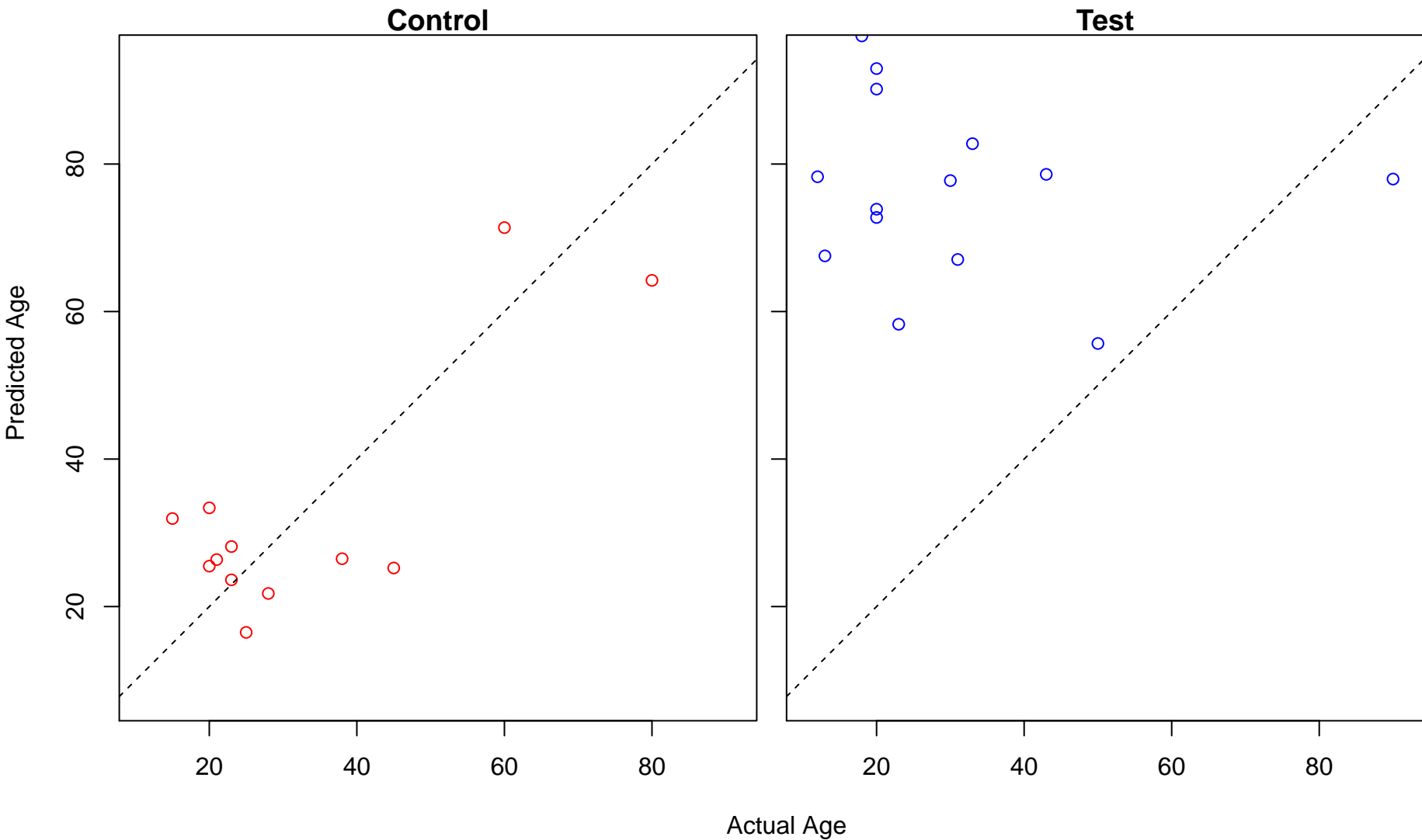
response to hexose (Score: 6.590217)



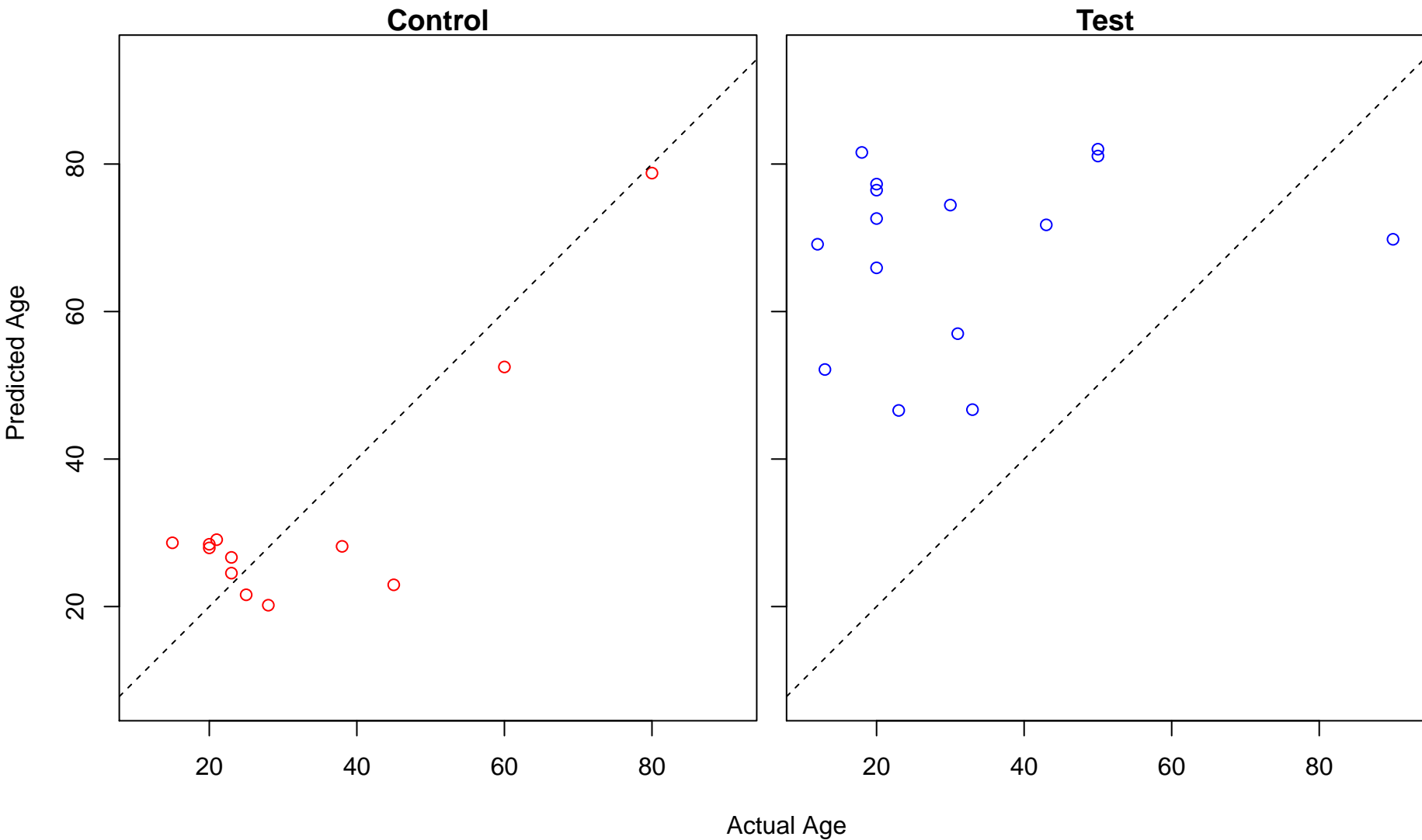
response to monosaccharide (Score: 6.590217)



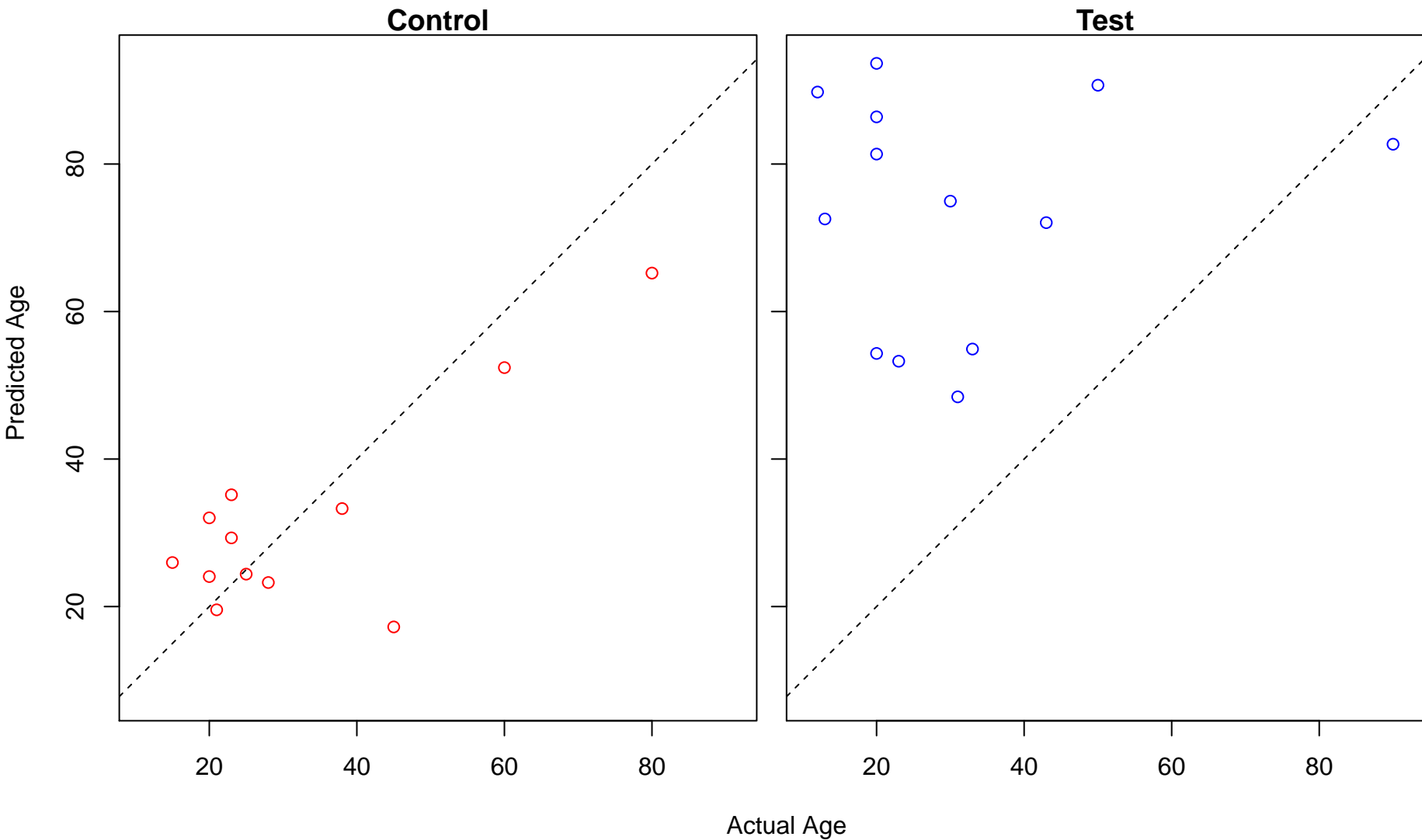
response to glucose (Score: 6.589373)



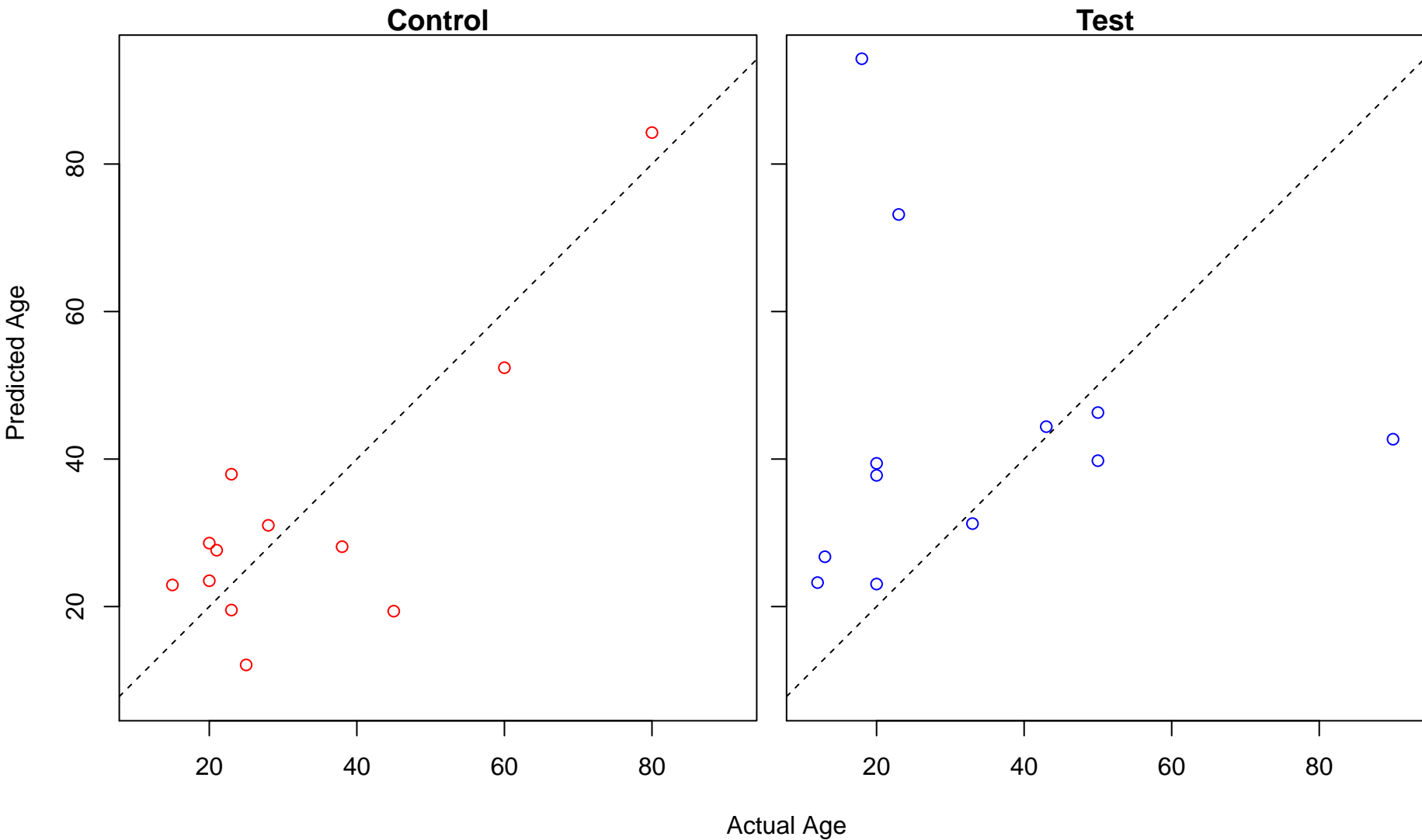
response to oxidative stress (Score: 6.587749)



hair follicle morphogenesis (Score: 6.584565)

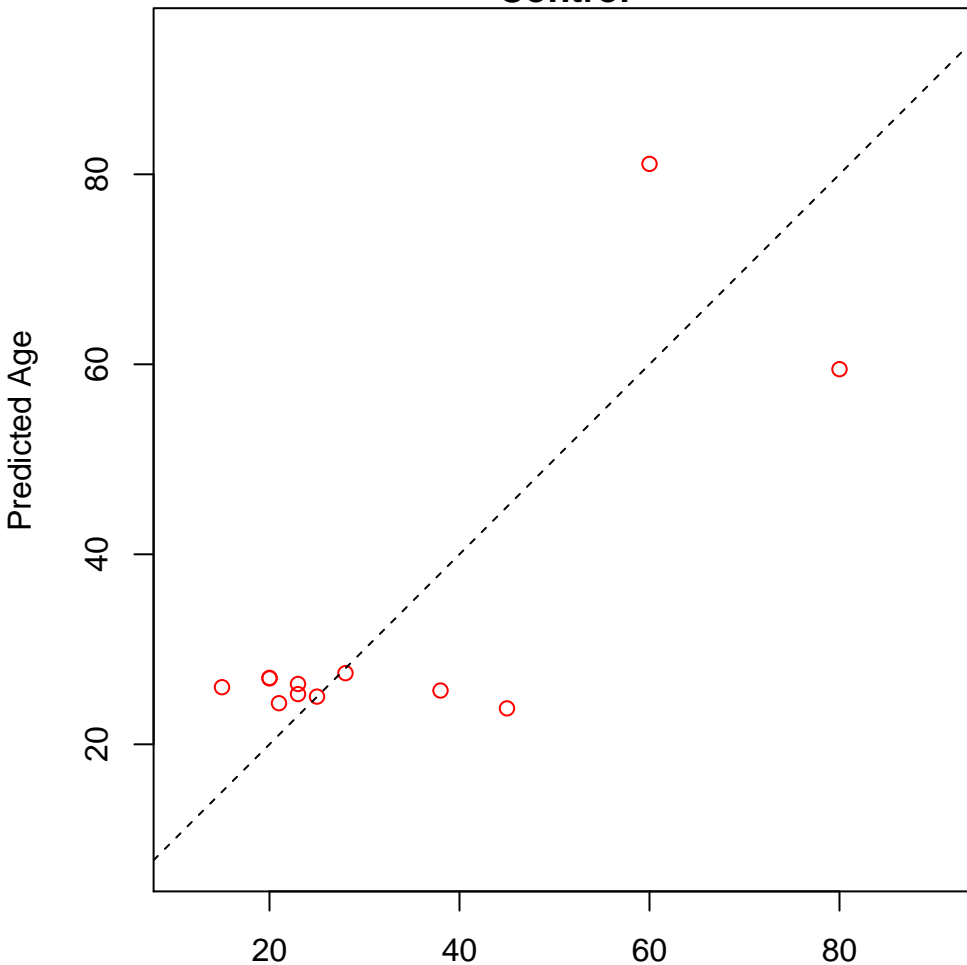


positive regulation of cell activation (Score: 6.583727)

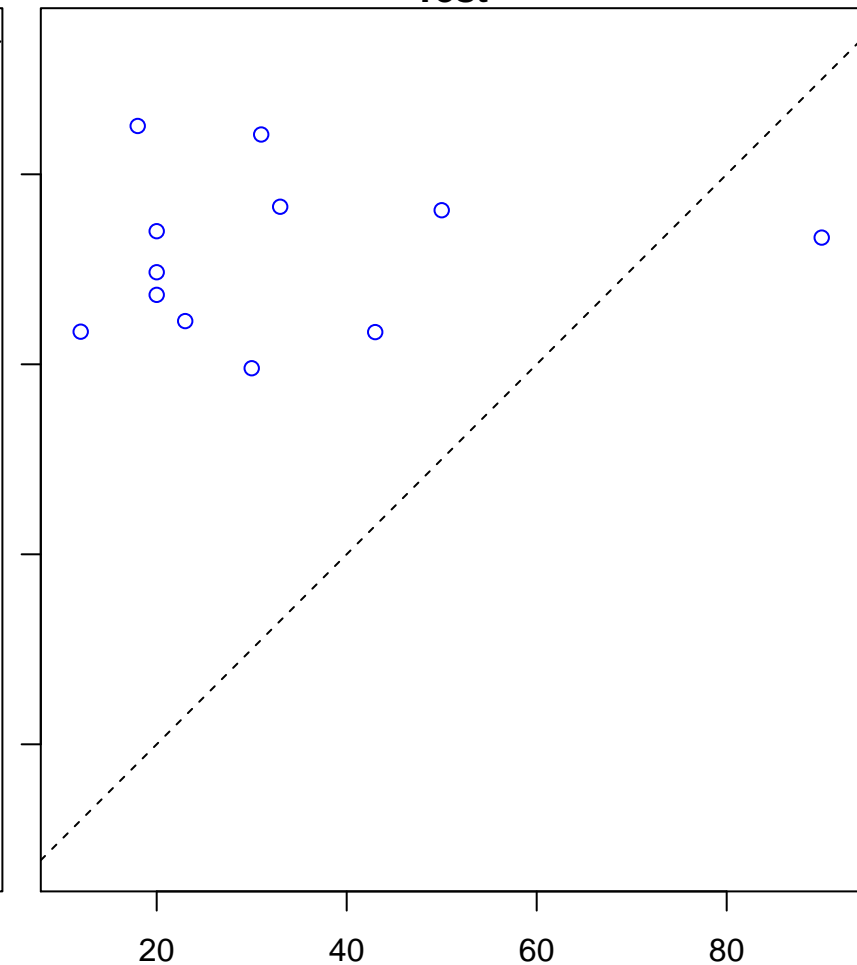


regulation of cell cycle phase transition (Score: 6.578913)

Control

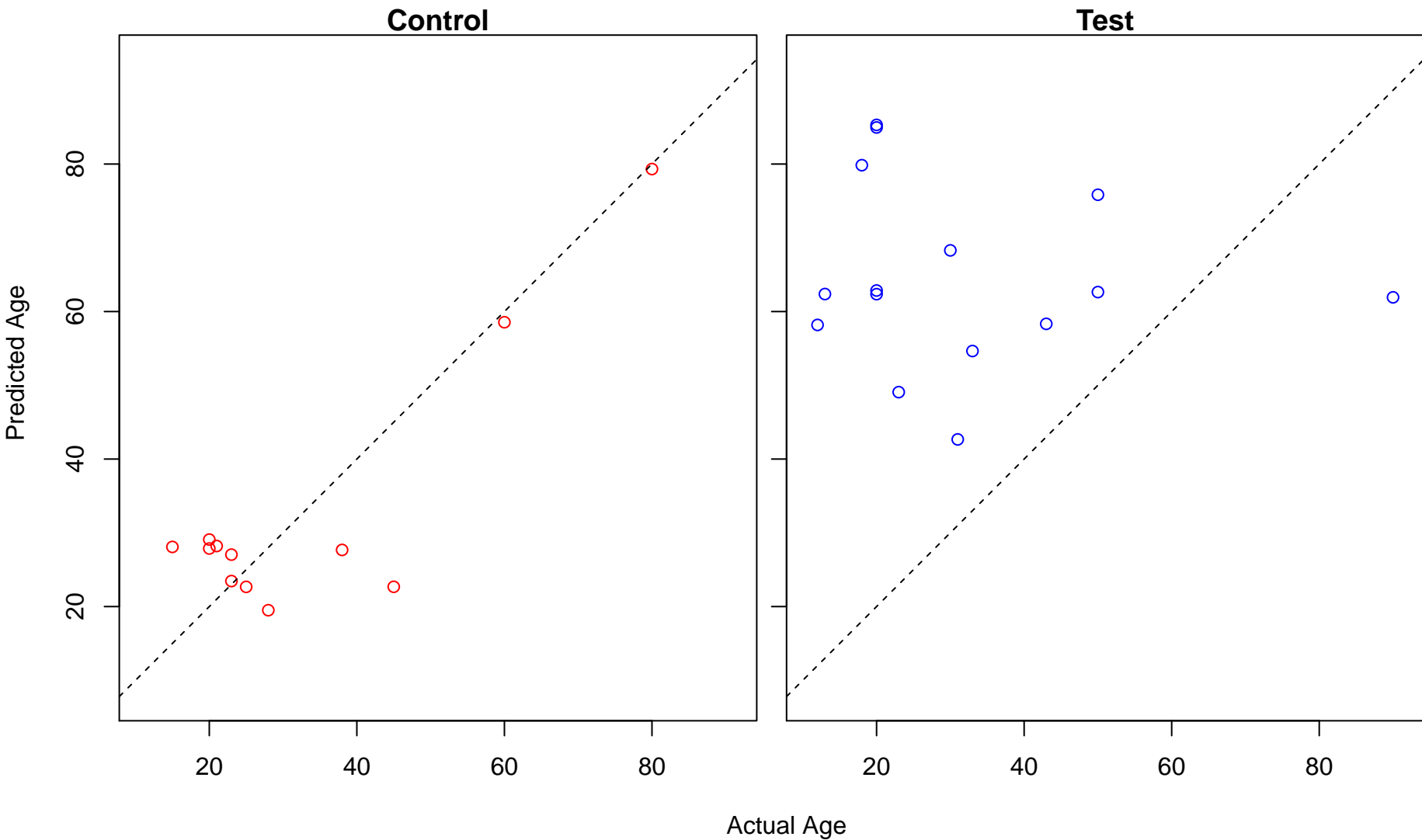


Test

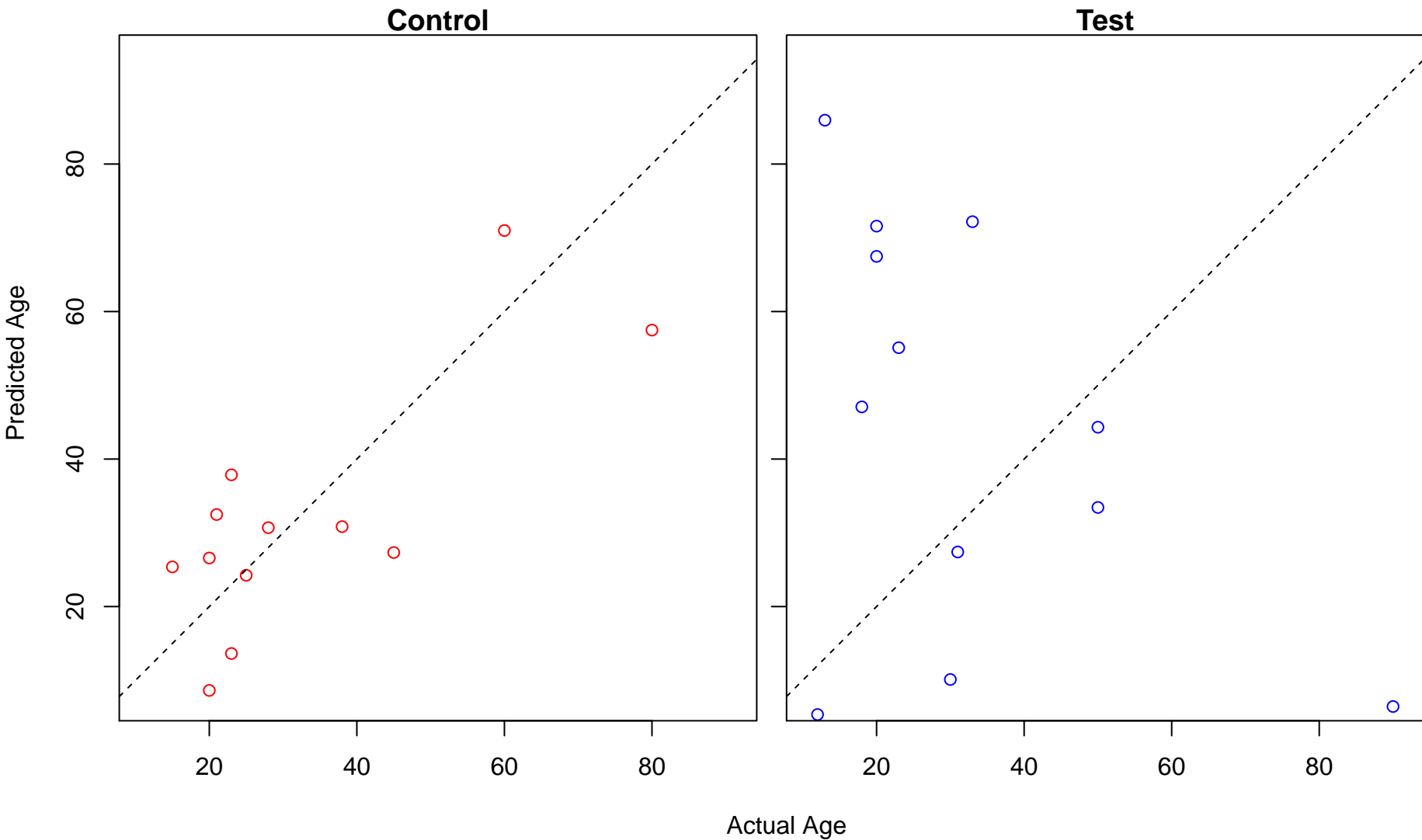


Actual Age

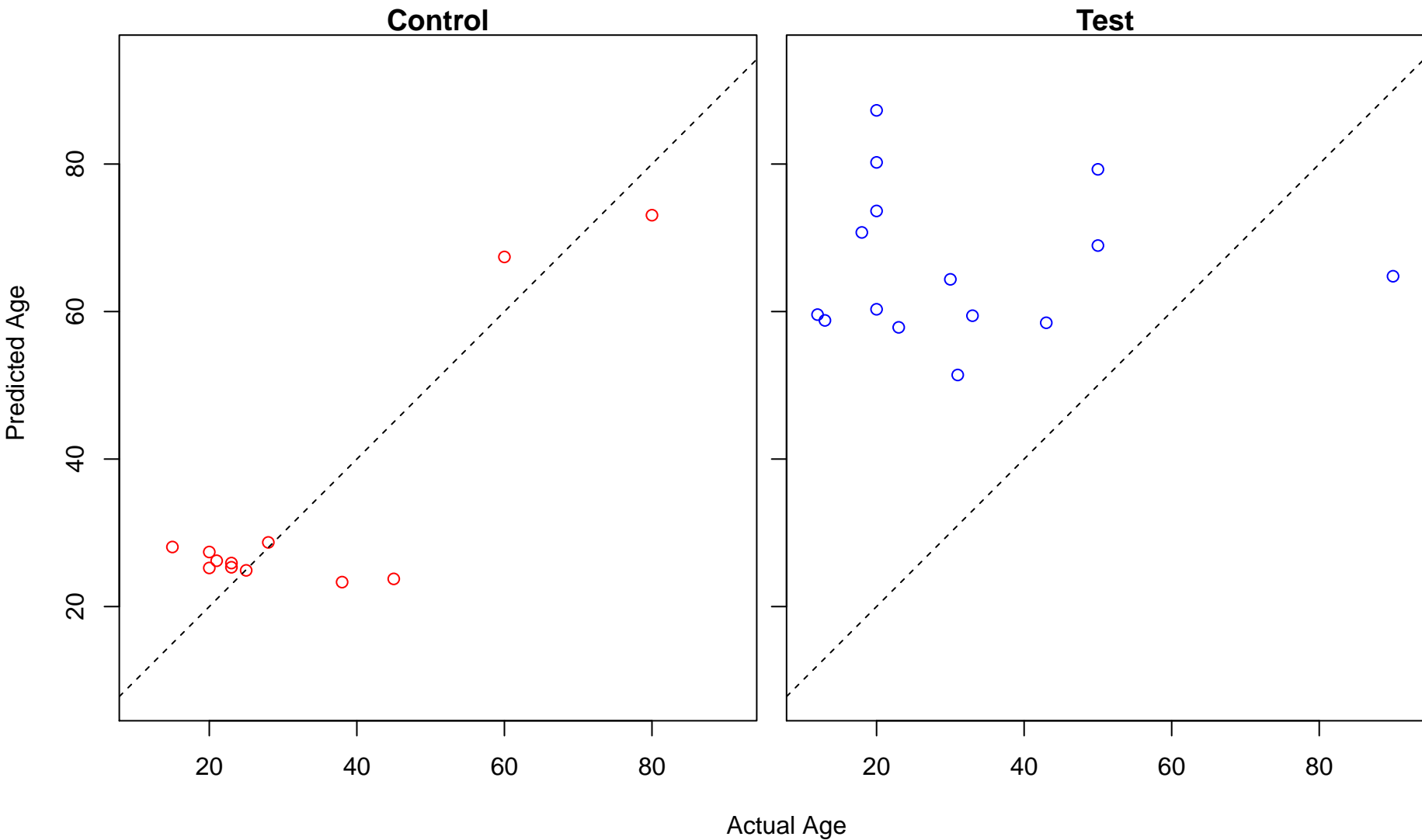
positive regulation of cell death (Score: 6.576775)



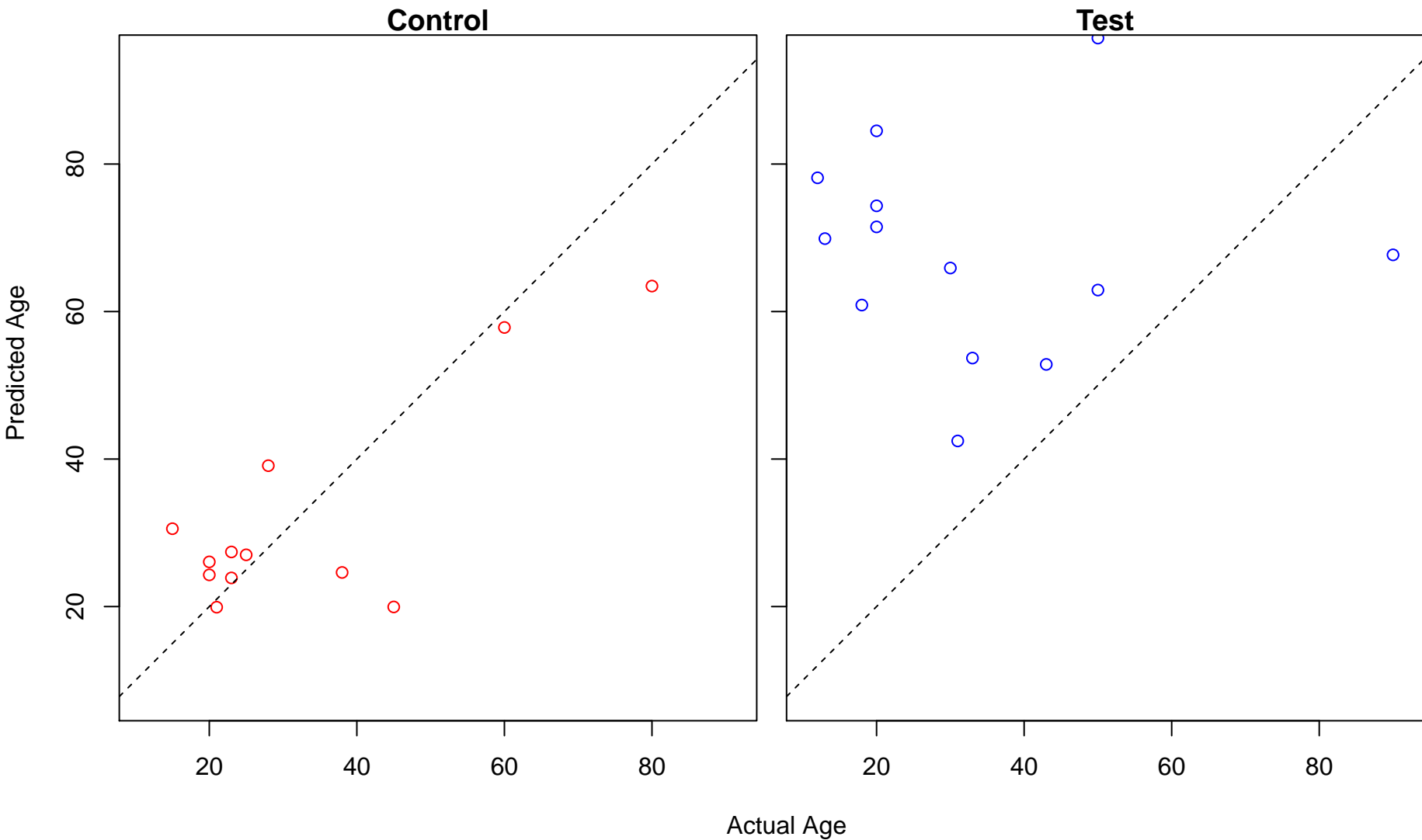
positive regulation of calcium ion transmembrane transport (Score: 6.576750)



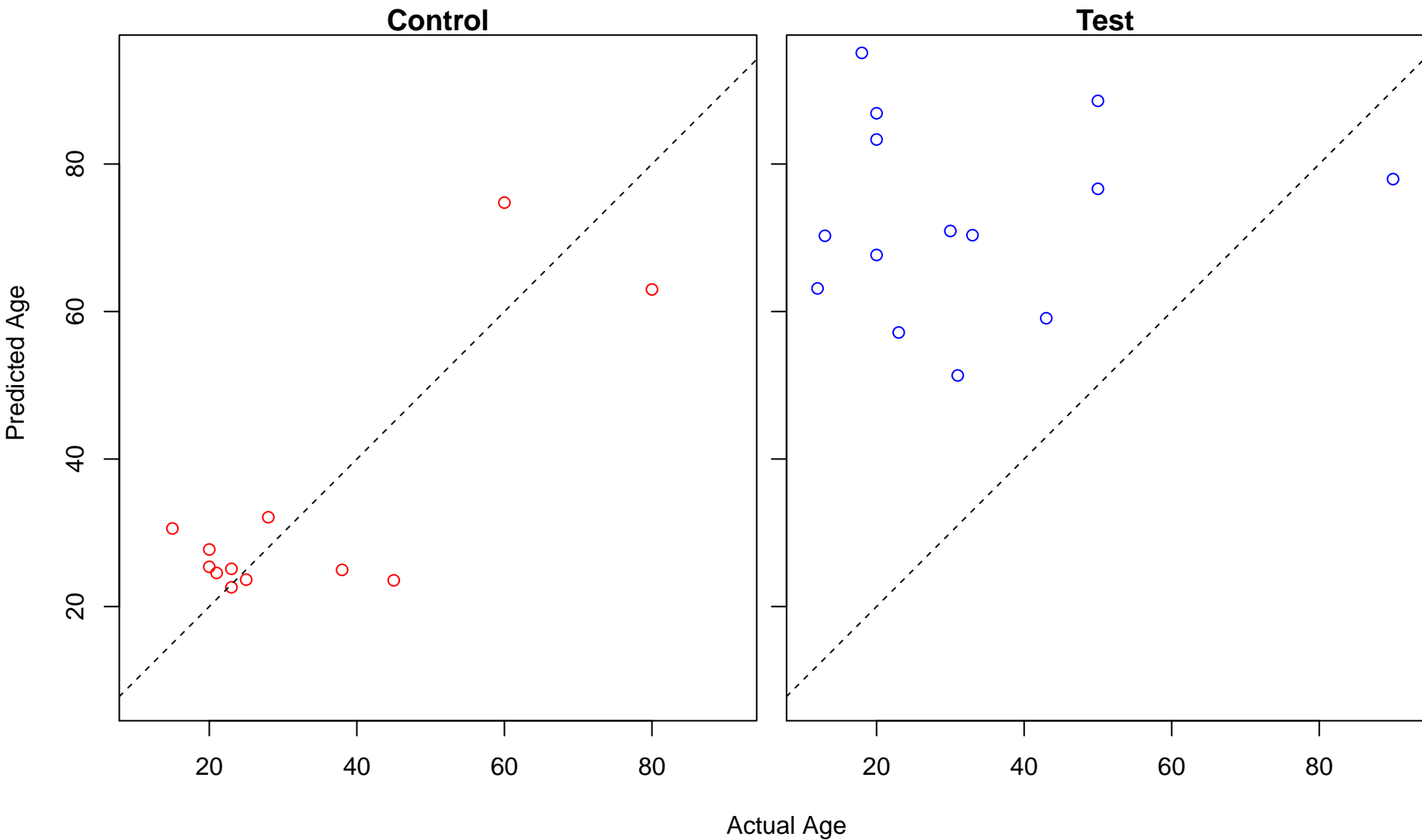
mitotic nuclear division (Score: 6.576727)



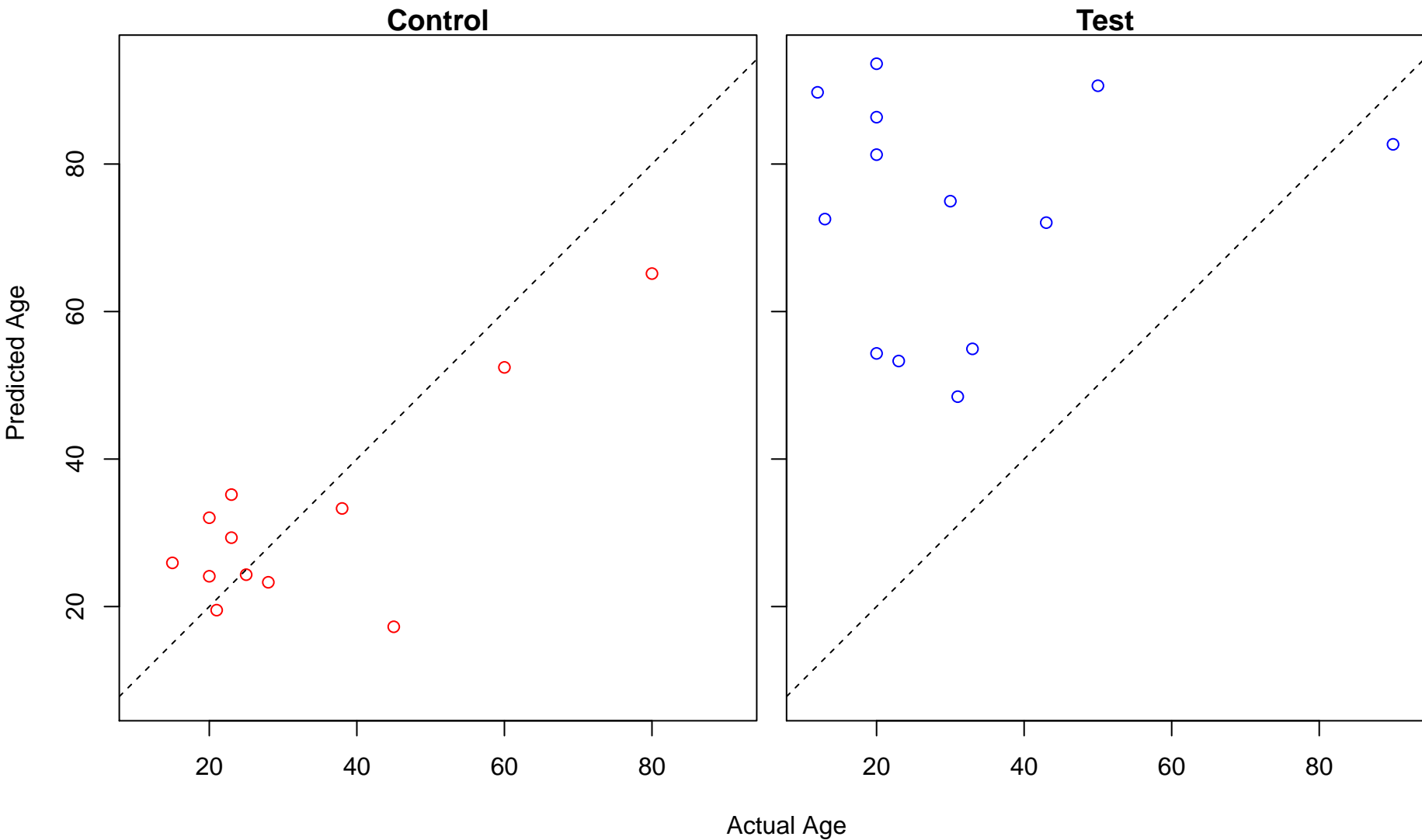
DNA dealkylation (Score: 6.575964)



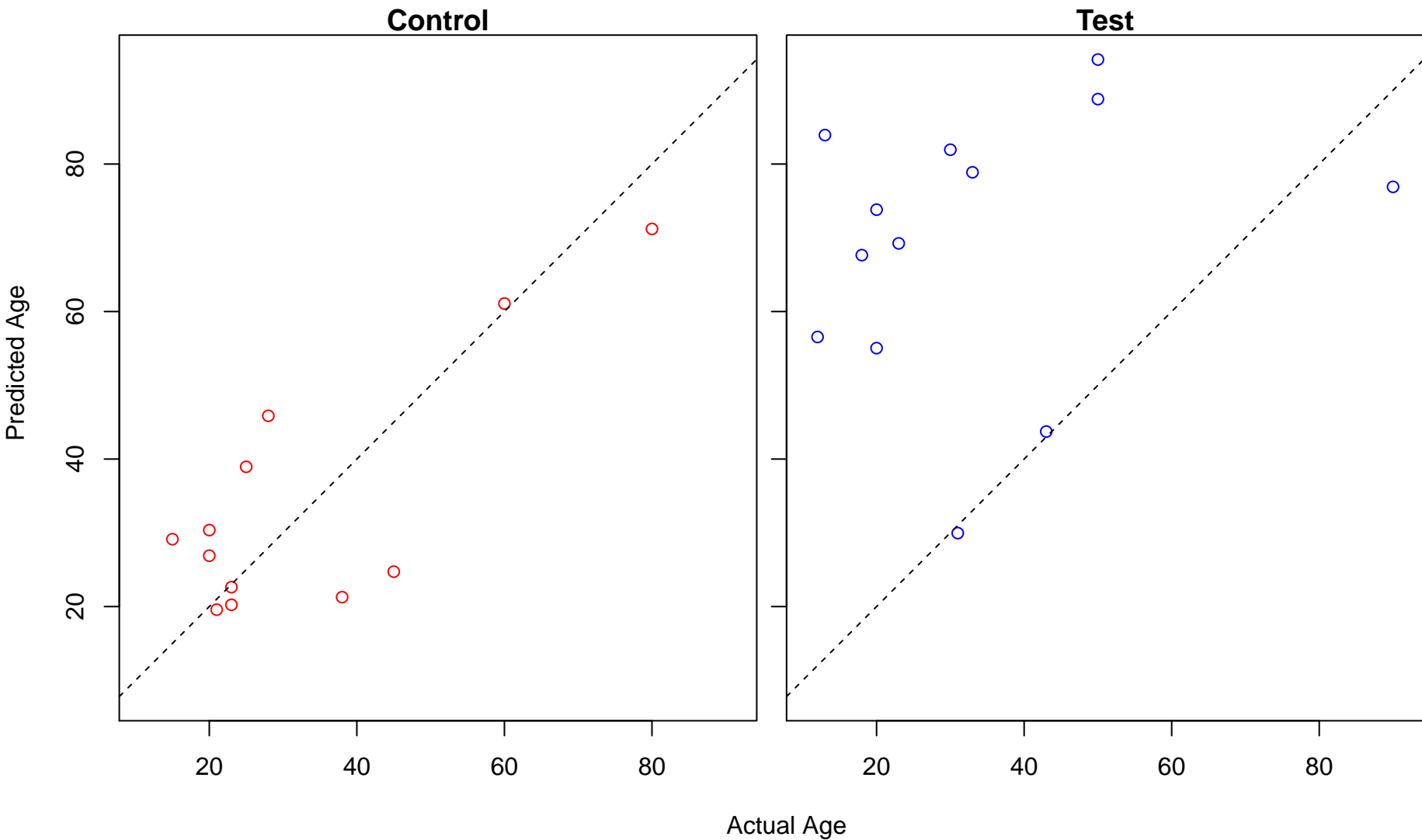
ruffle organization (Score: 6.574261)



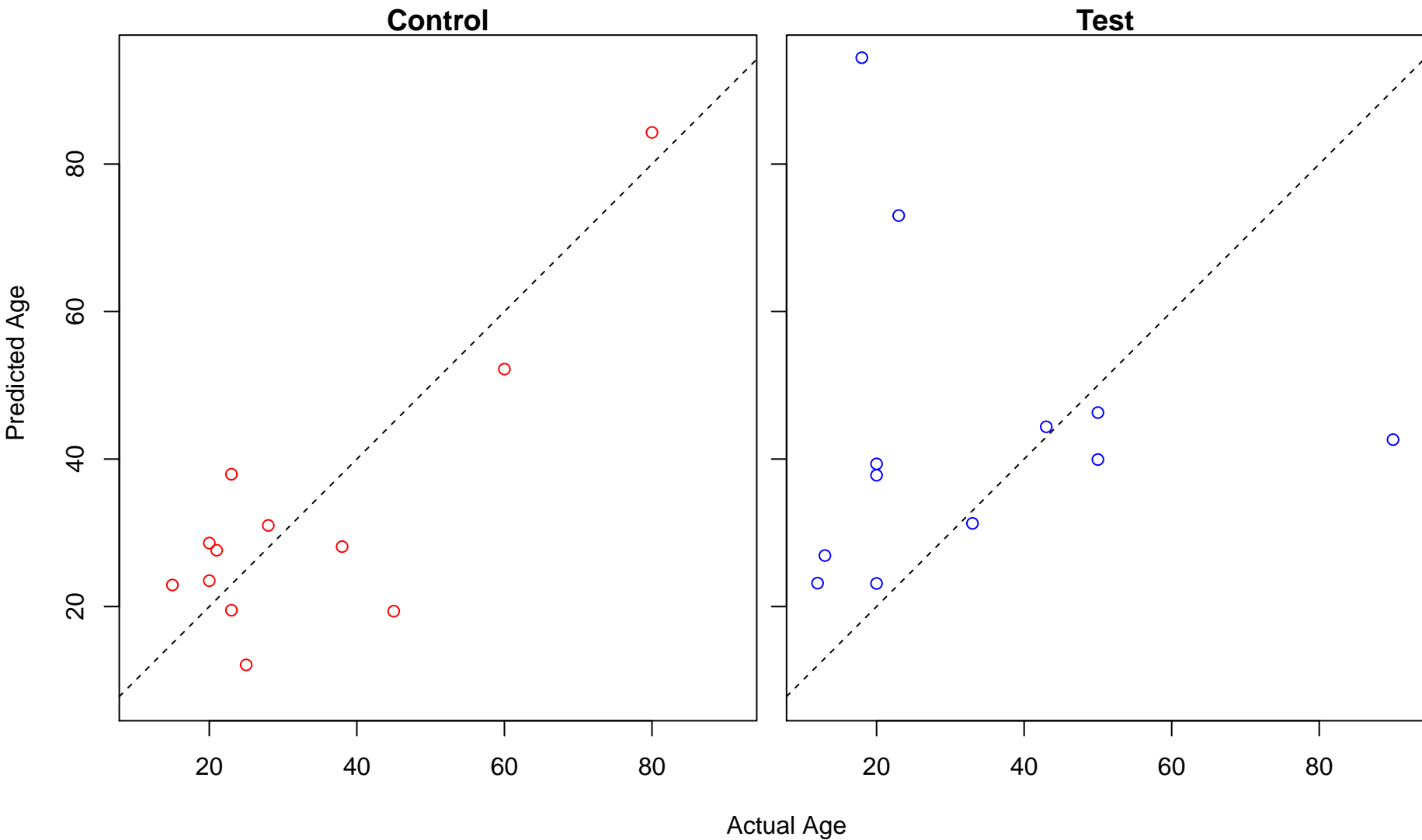
epidermis morphogenesis (Score: 6.572611)



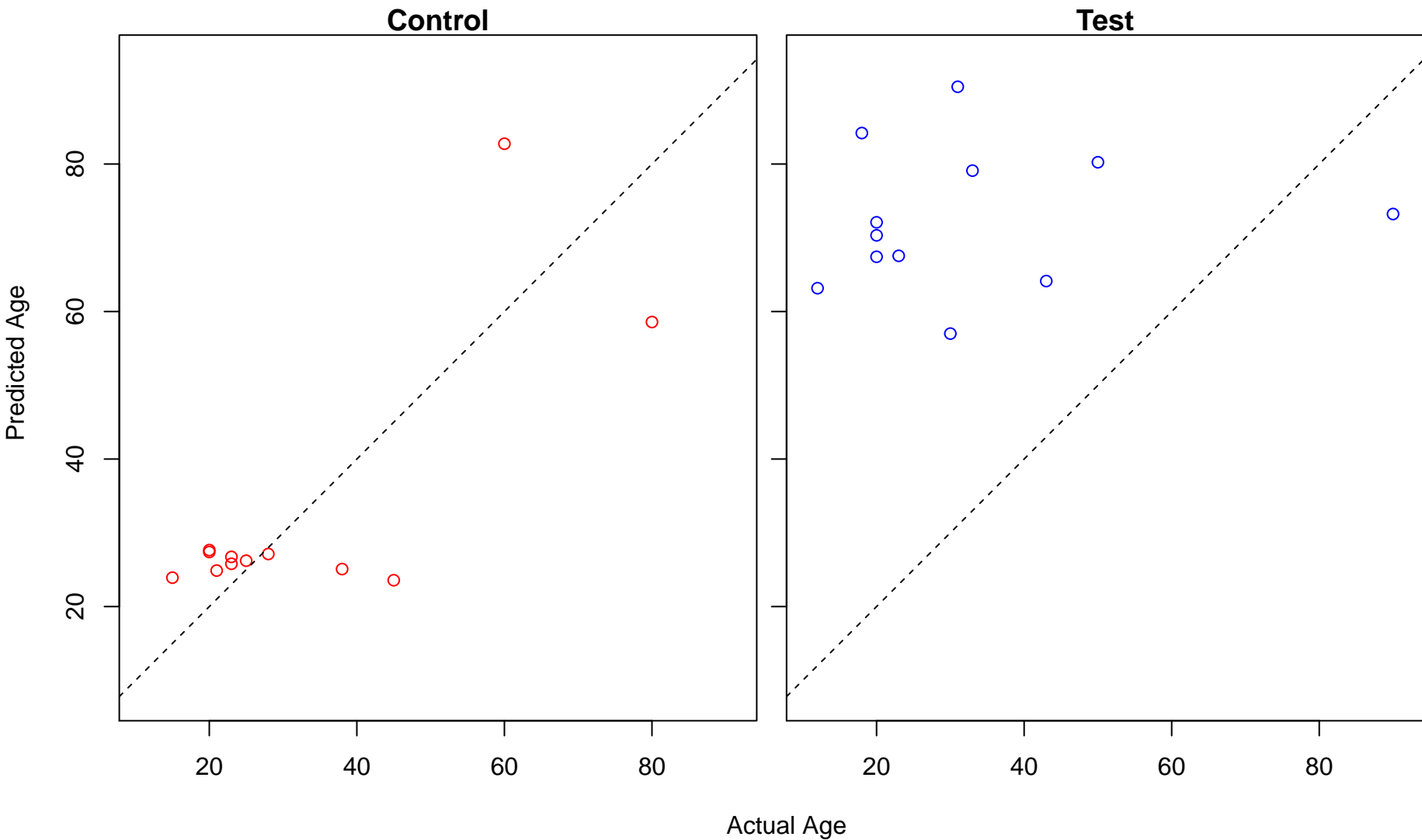
cell-cell junction maintenance (Score: 6.572578)



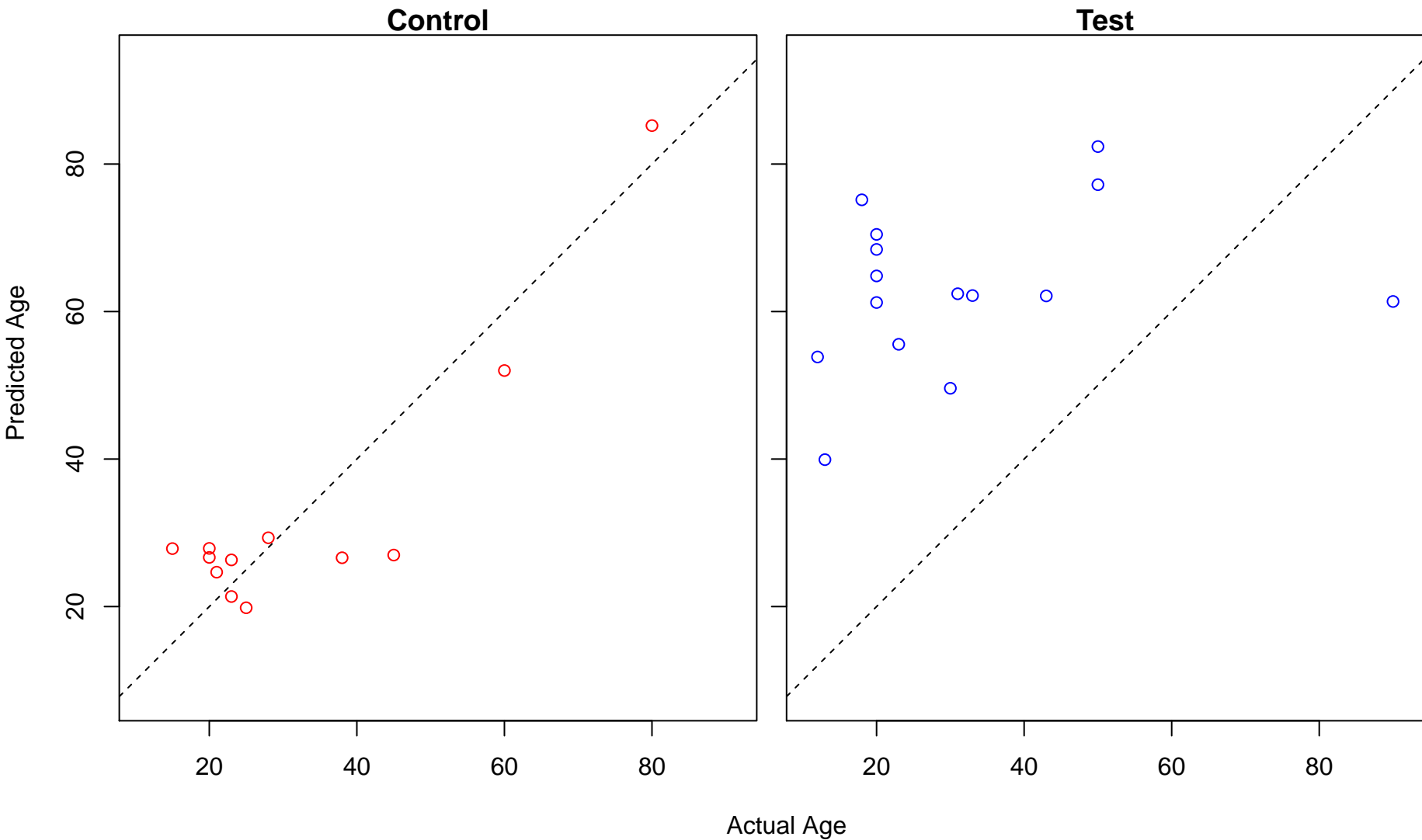
positive regulation of leukocyte activation (Score: 6.571655)



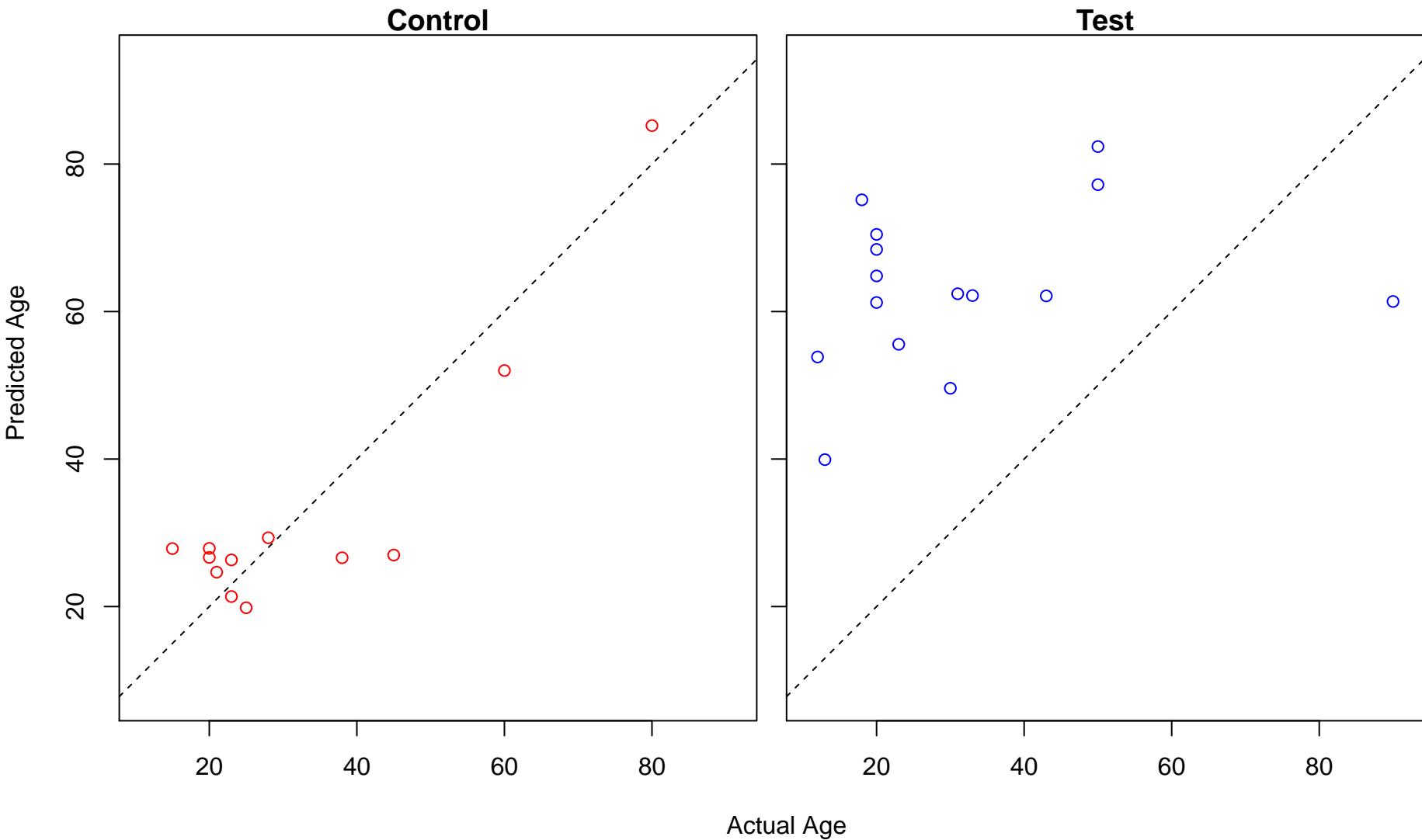
Notch signaling pathway (Score: 6.569392)



amino acid activation (Score: 6.566842)

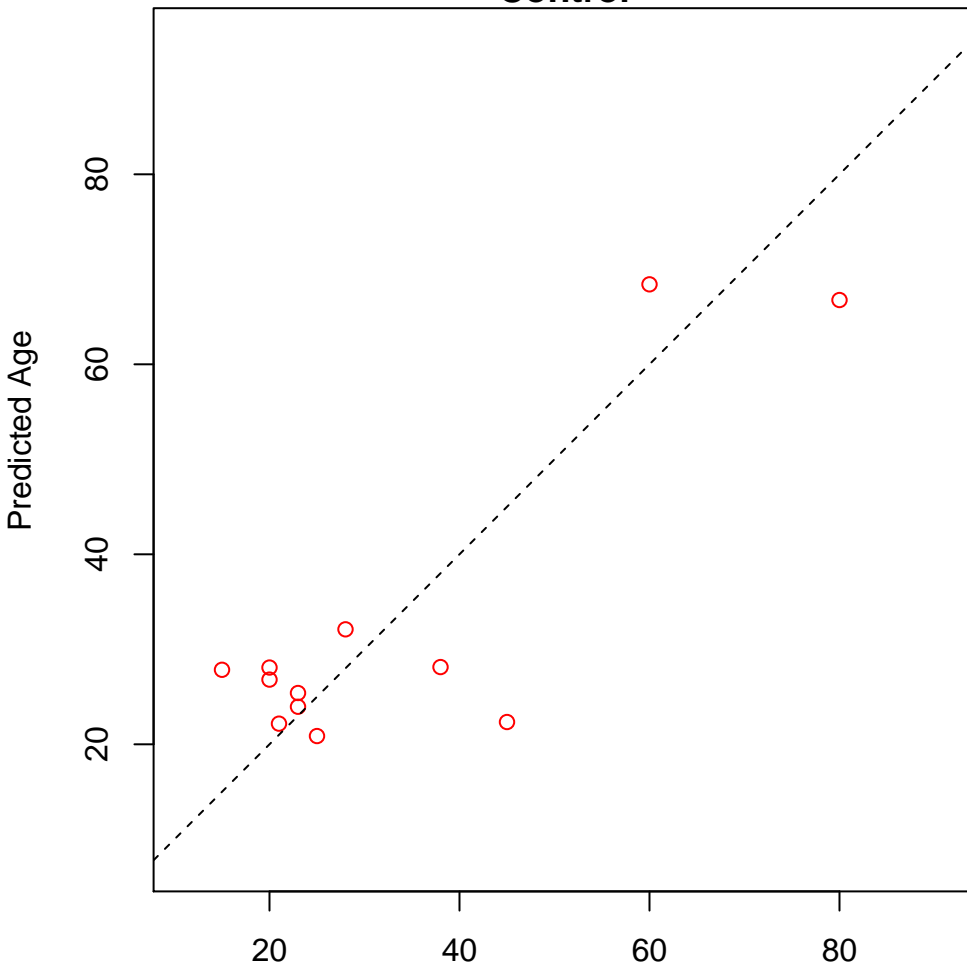


tRNA aminoacylation (Score: 6.566842)

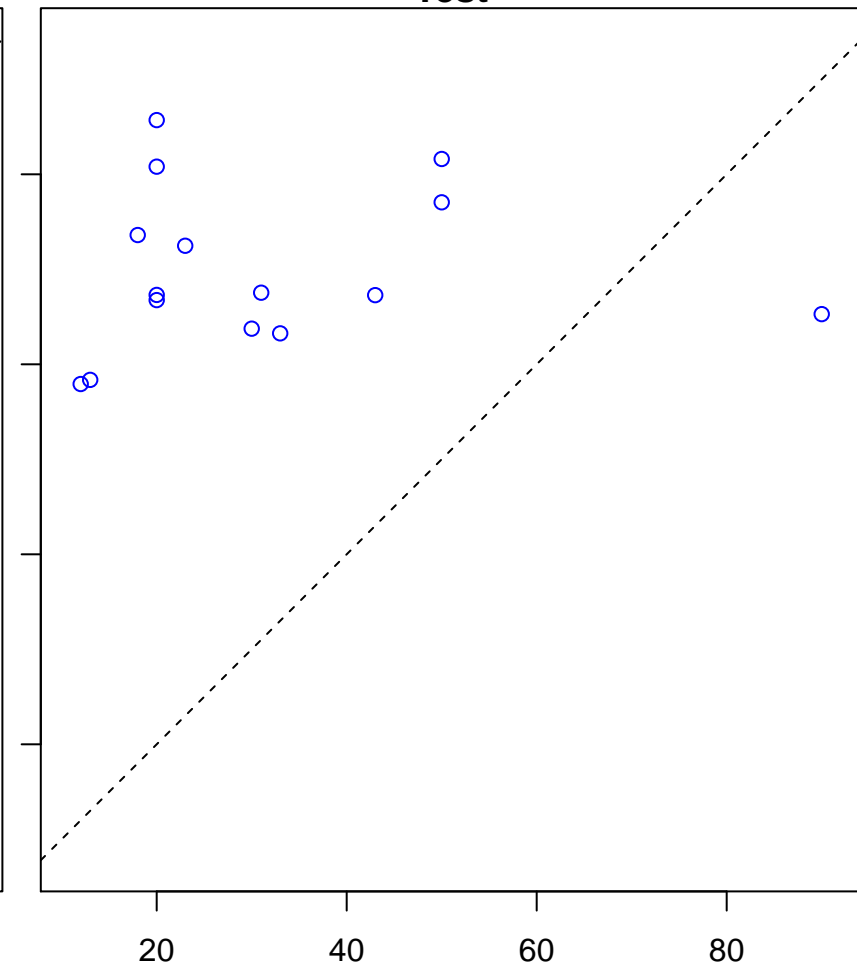


positive regulation of heart contraction (Score: 6.566821)

Control

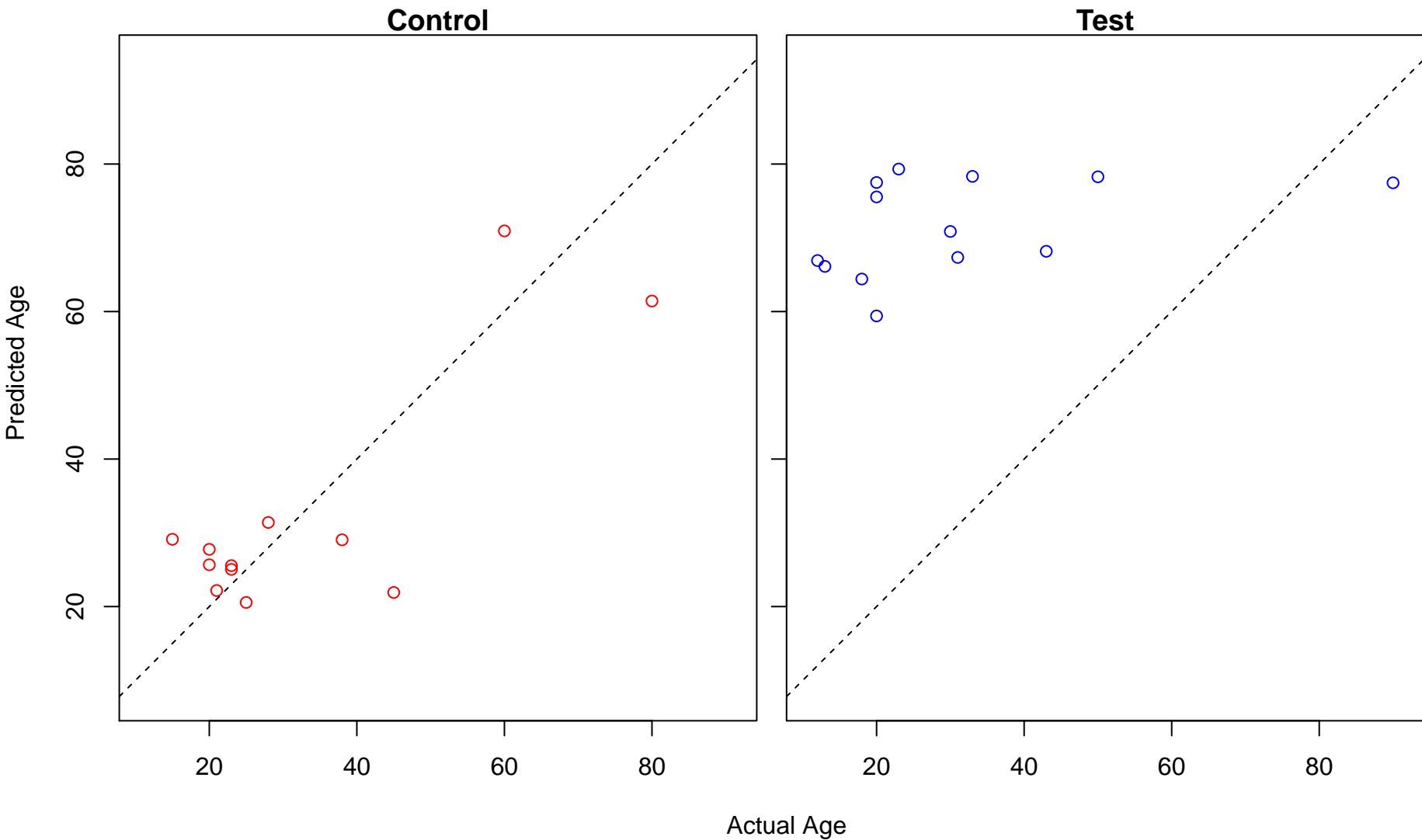


Test



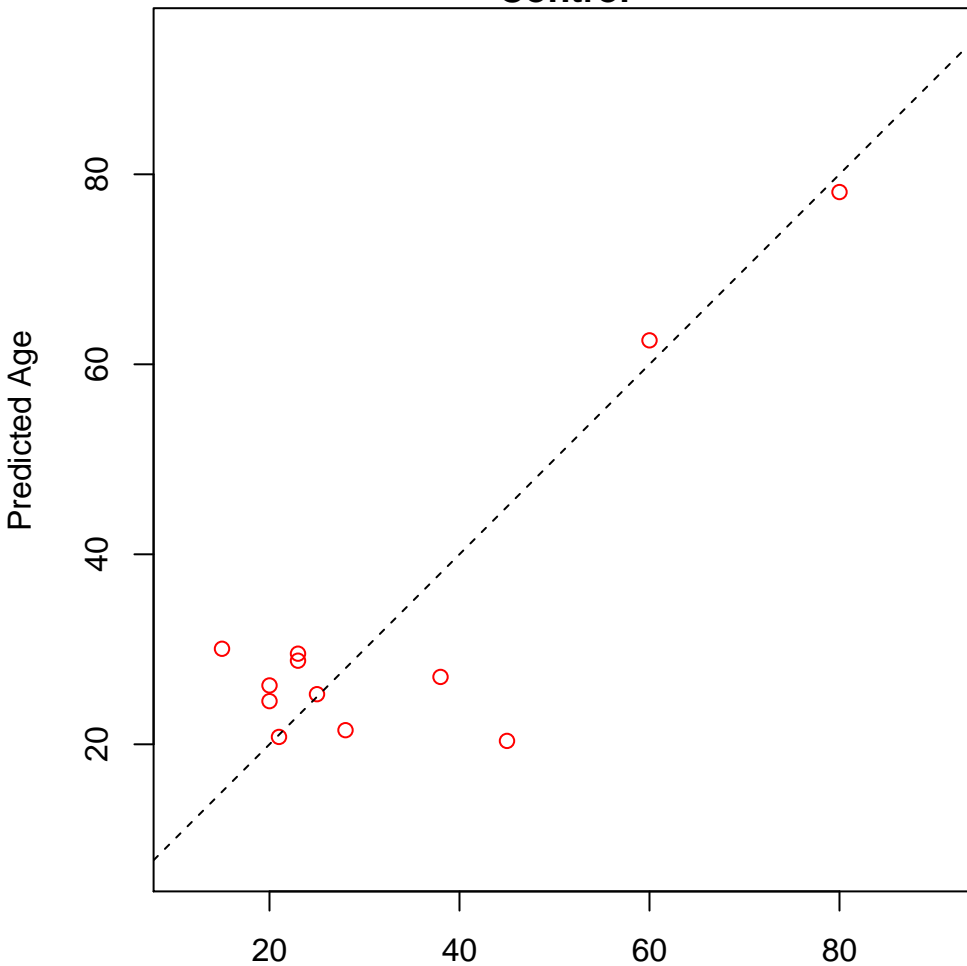
Actual Age

neural tube formation (Score: 6.565592)

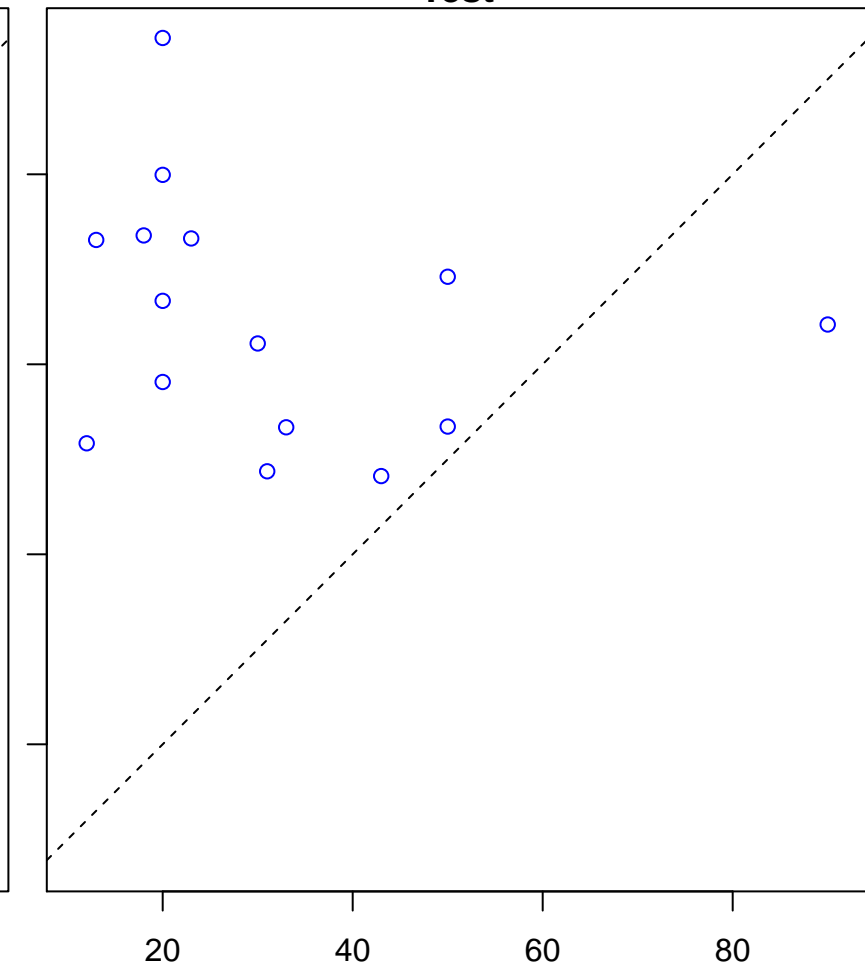


neuromuscular synaptic transmission (Score: 6.563265)

Control

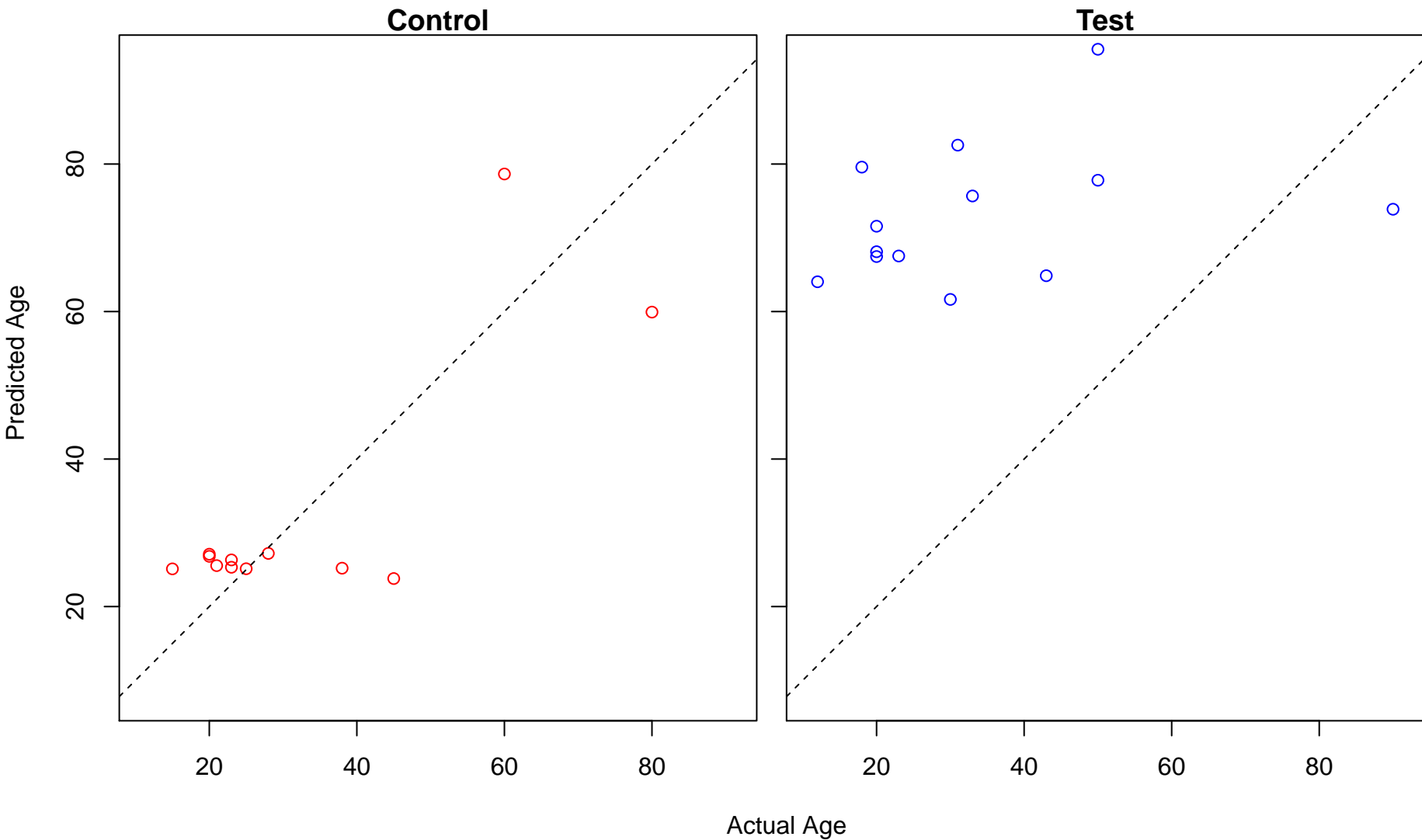


Test

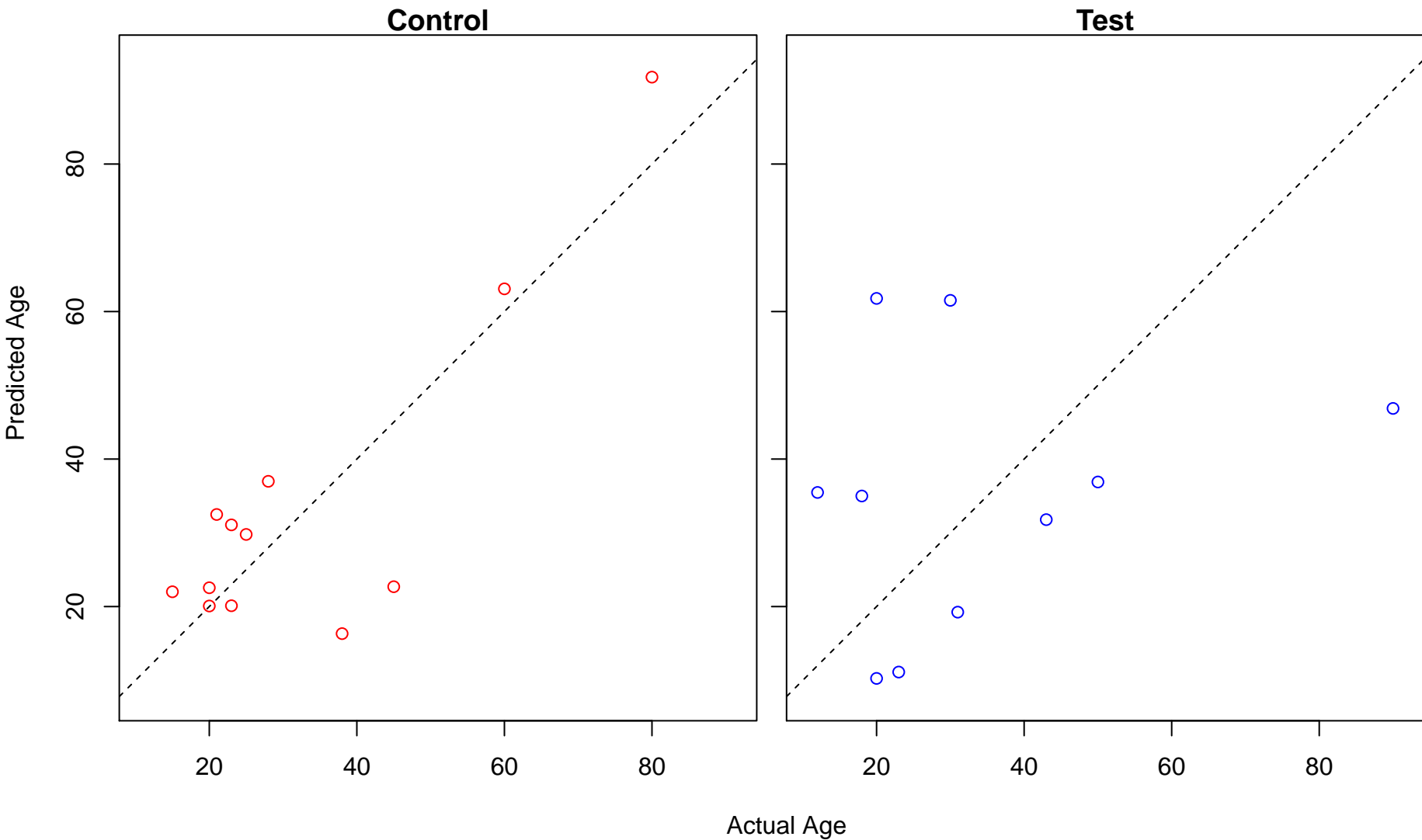


Actual Age

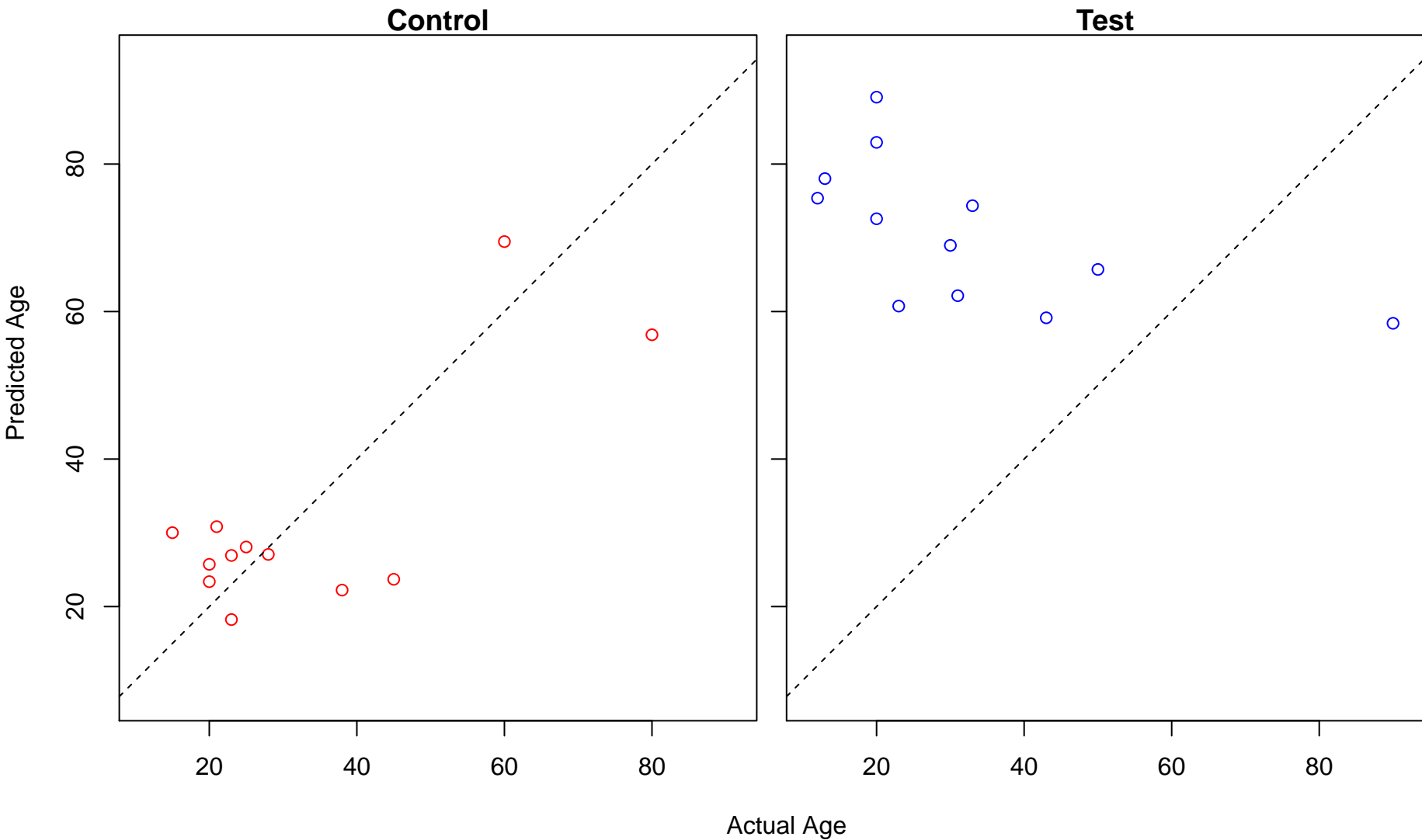
negative regulation of intracellular signal transduction (Score: 6.562803)



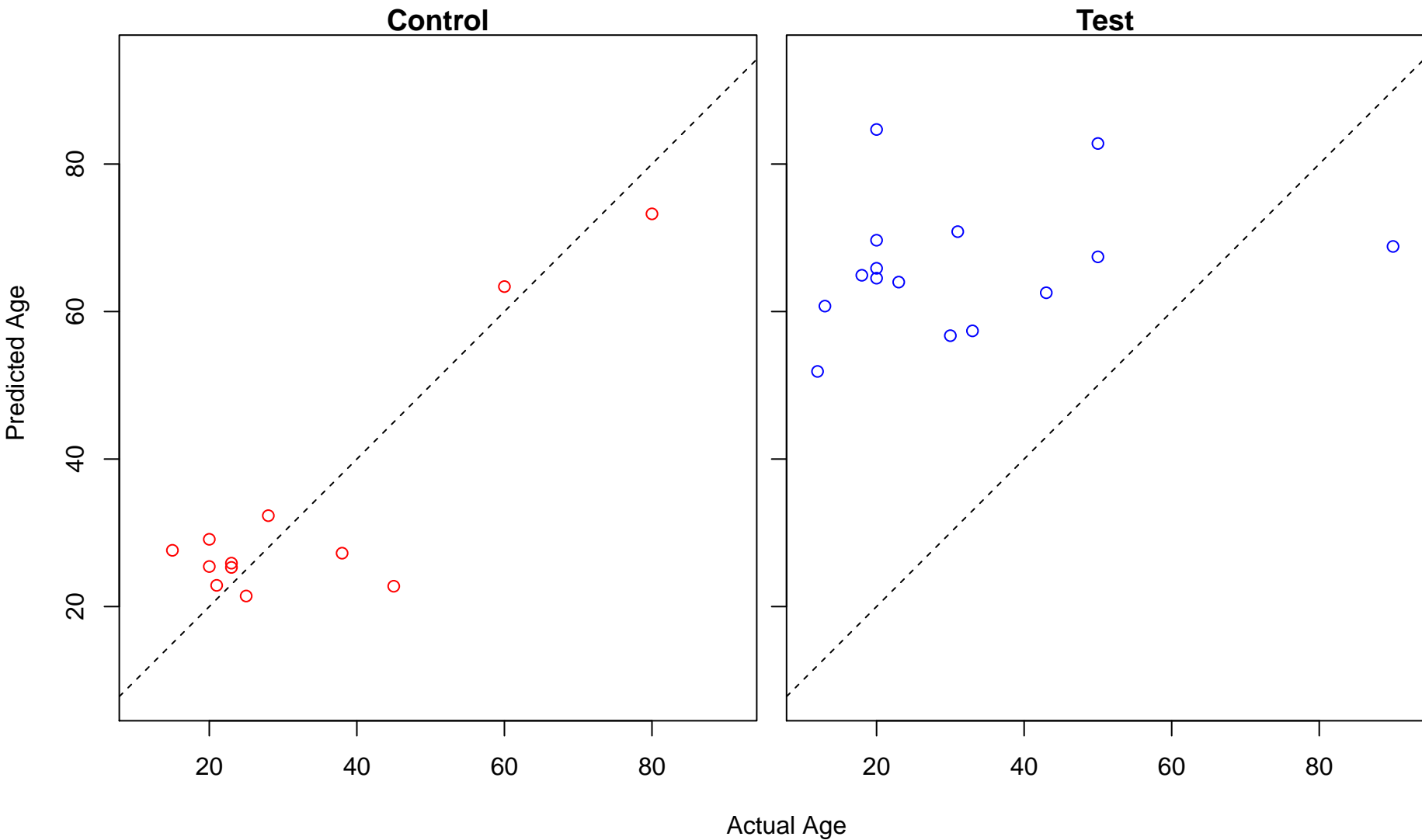
regulation of early endosome to late endosome transport (Score: 6.555373)



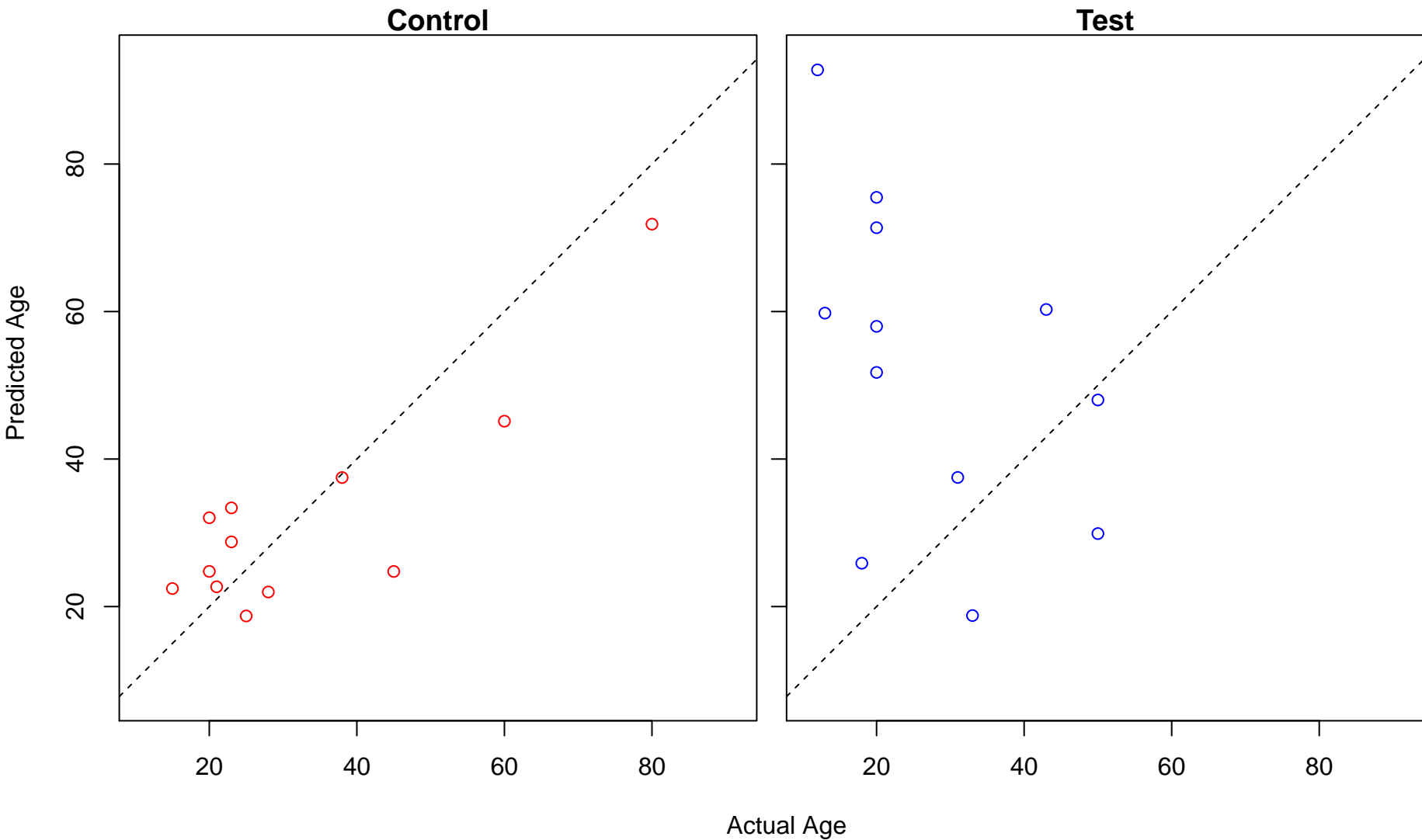
actin nucleation (Score: 6.555090)



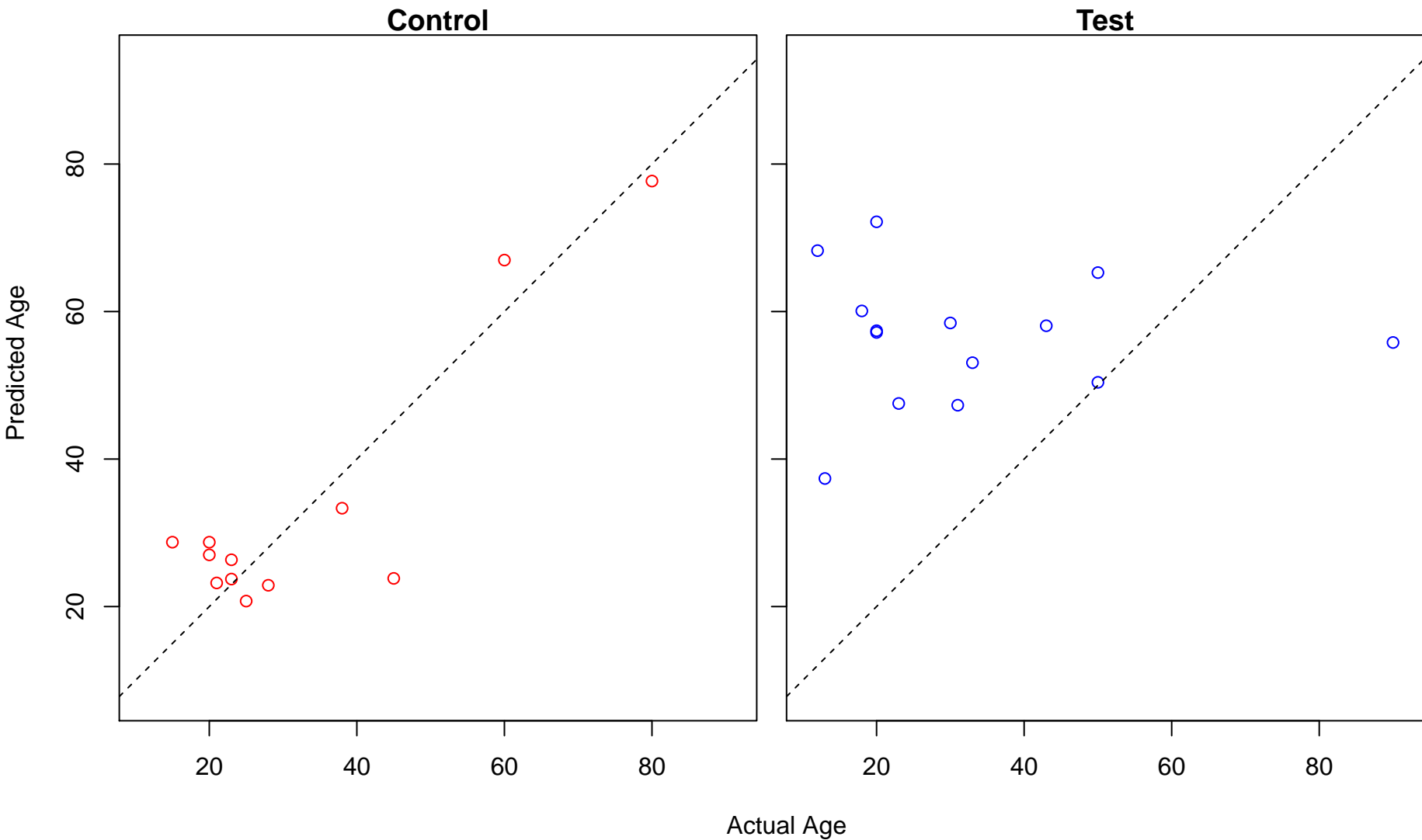
regulation of hormone secretion (Score: 6.553700)



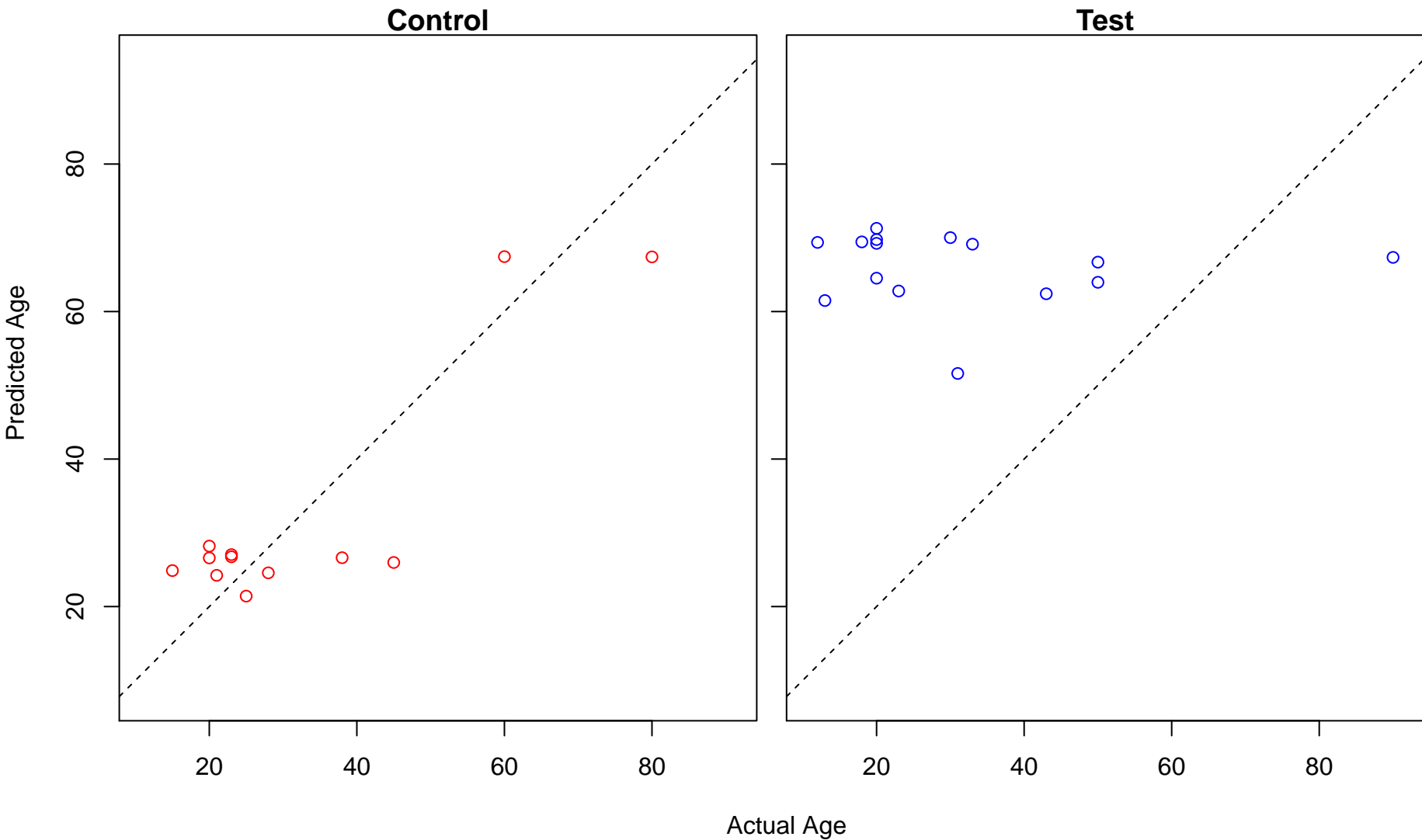
neuronal signal transduction (Score: 6.553611)



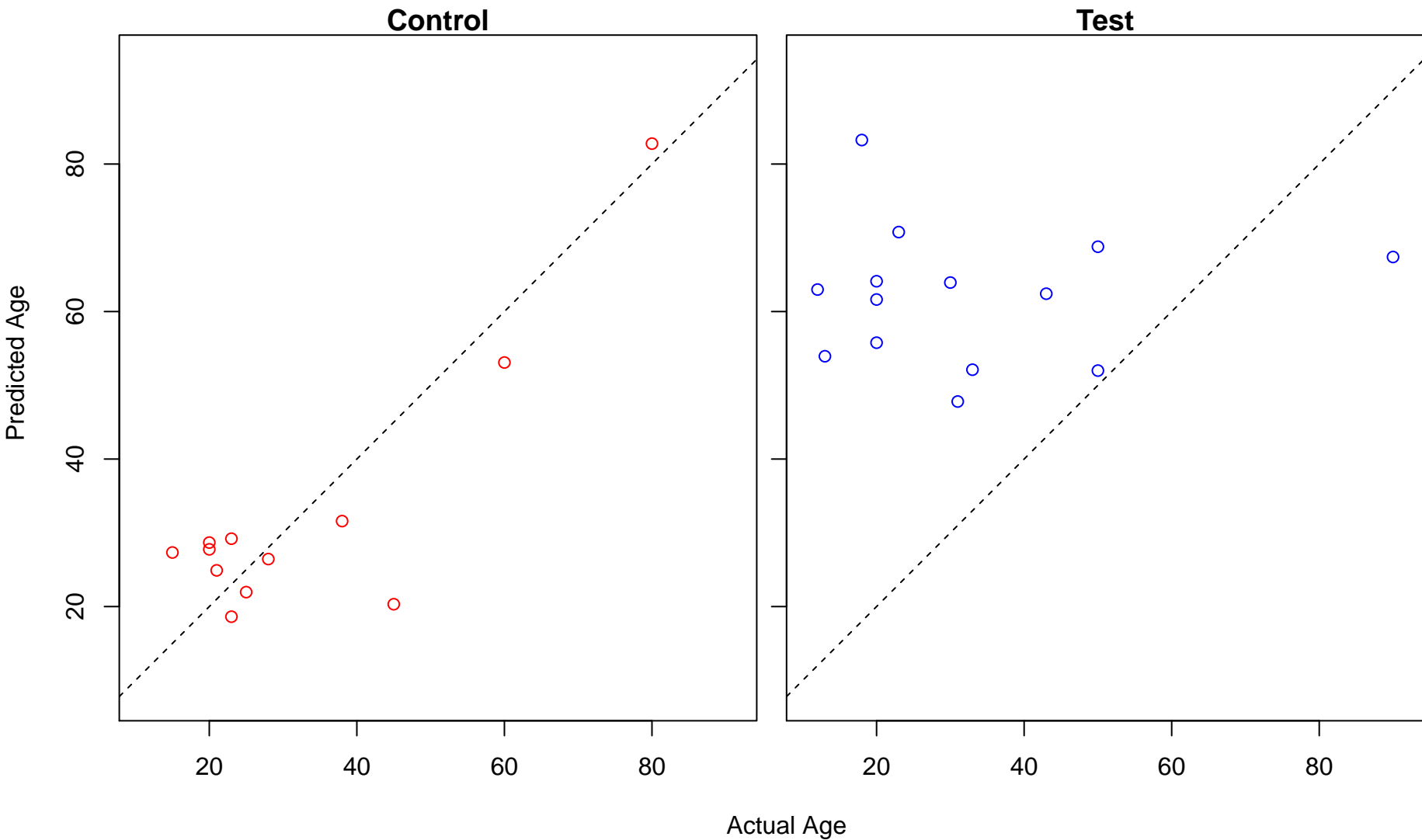
organic hydroxy compound catabolic process (Score: 6.553439)



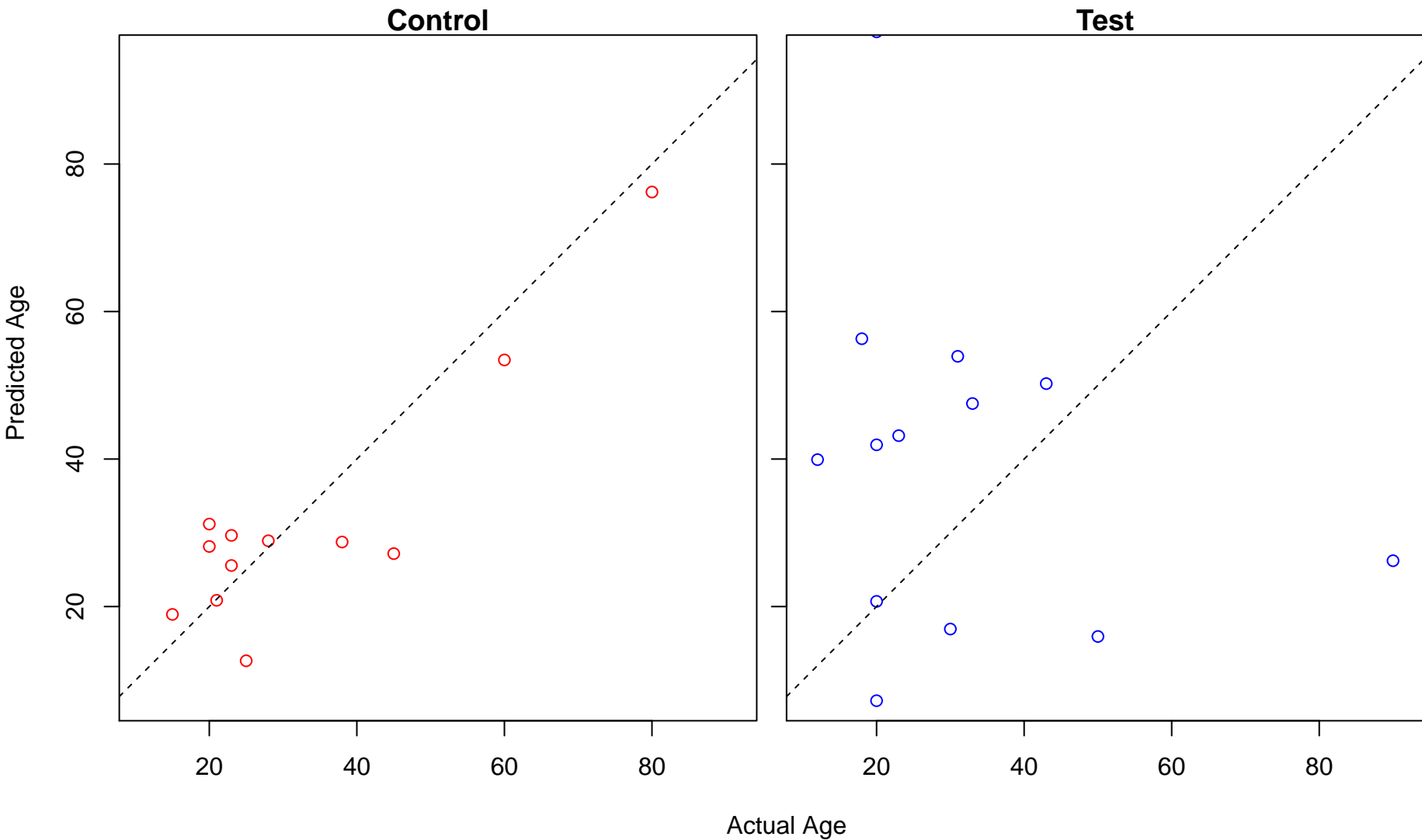
cardiocyte differentiation (Score: 6.551361)



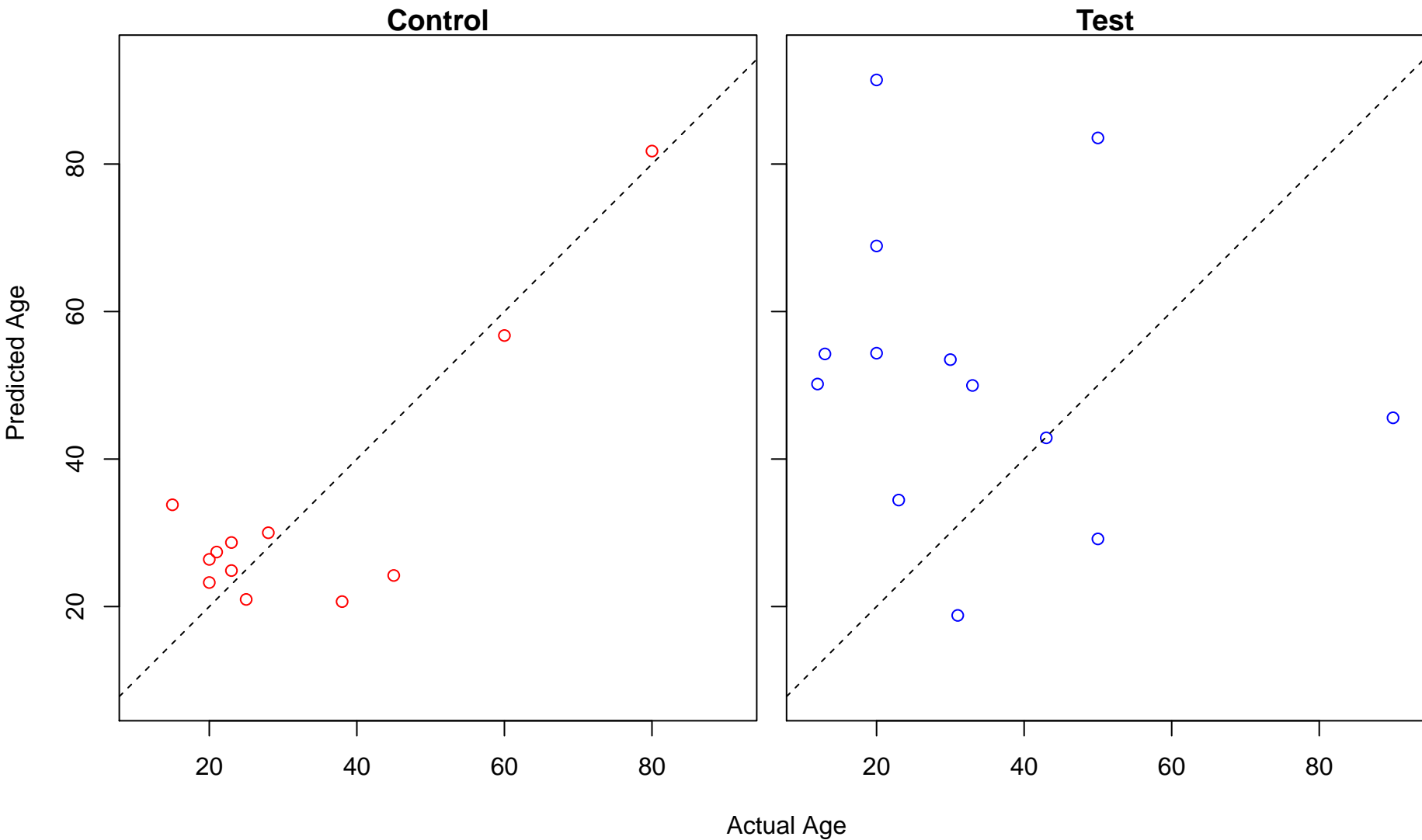
mesenchymal cell proliferation (Score: 6.550149)



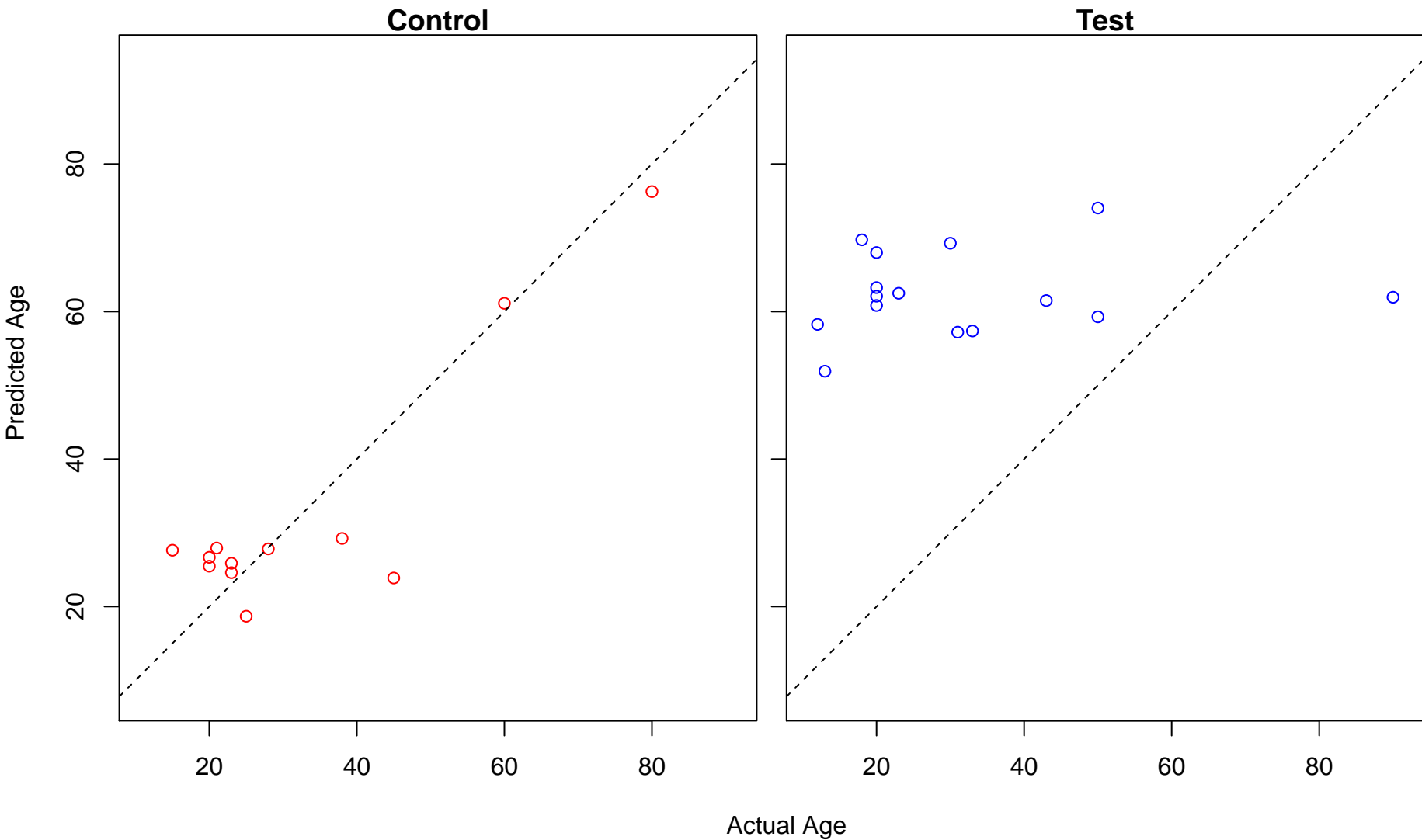
peptidyl-histidine modification (Score: 6.548917)



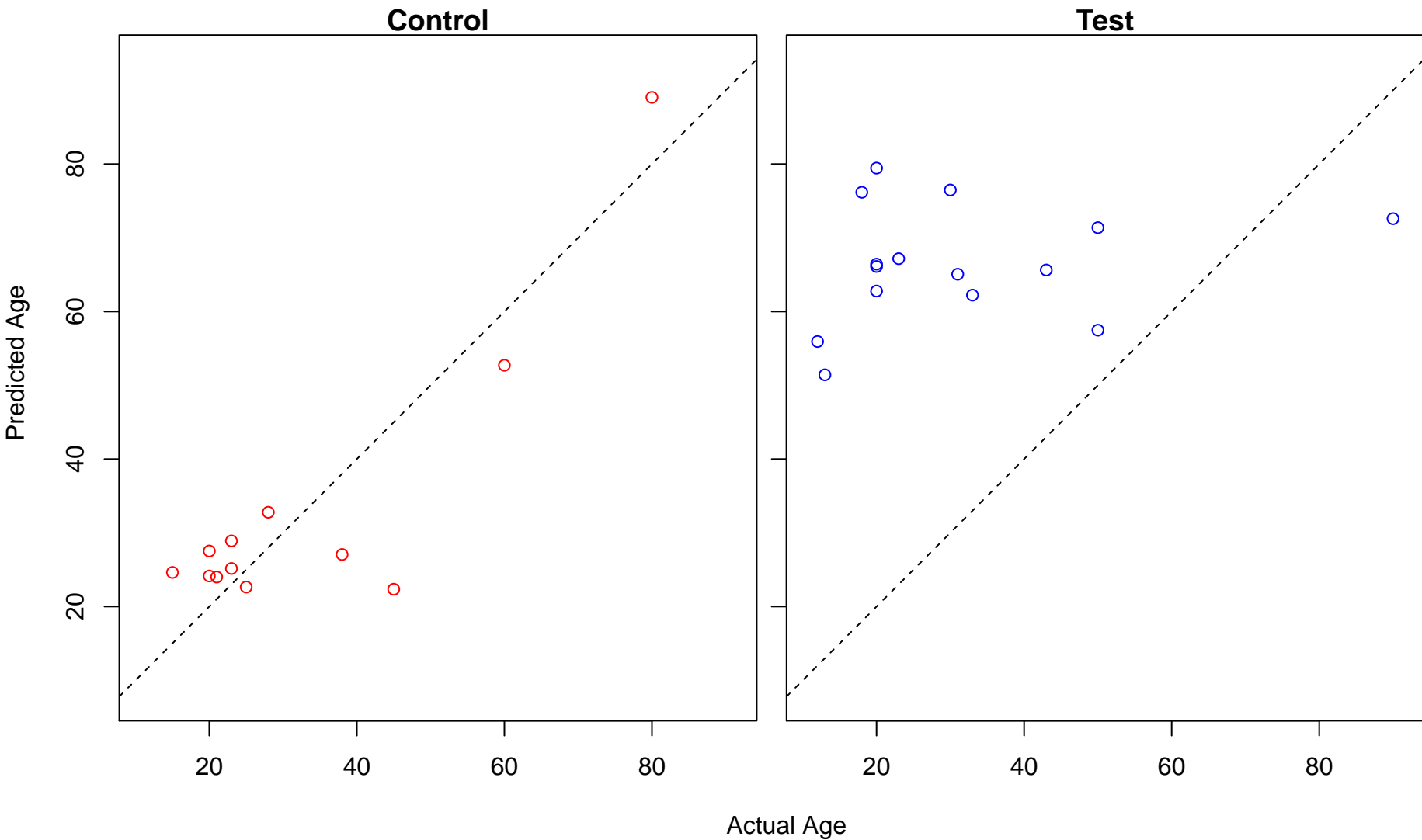
regulation of histone ubiquitination (Score: 6.546364)



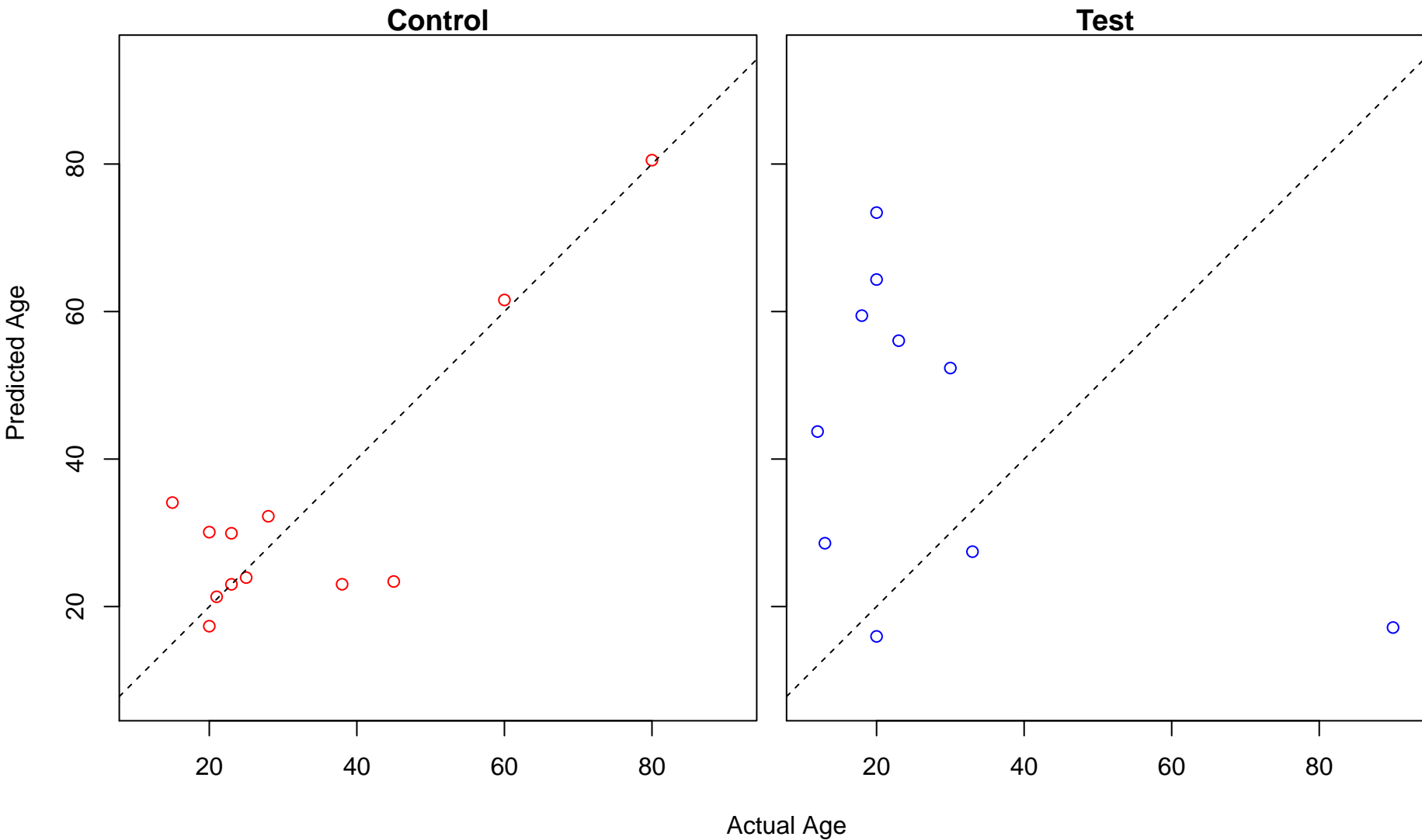
alcohol metabolic process (Score: 6.544504)



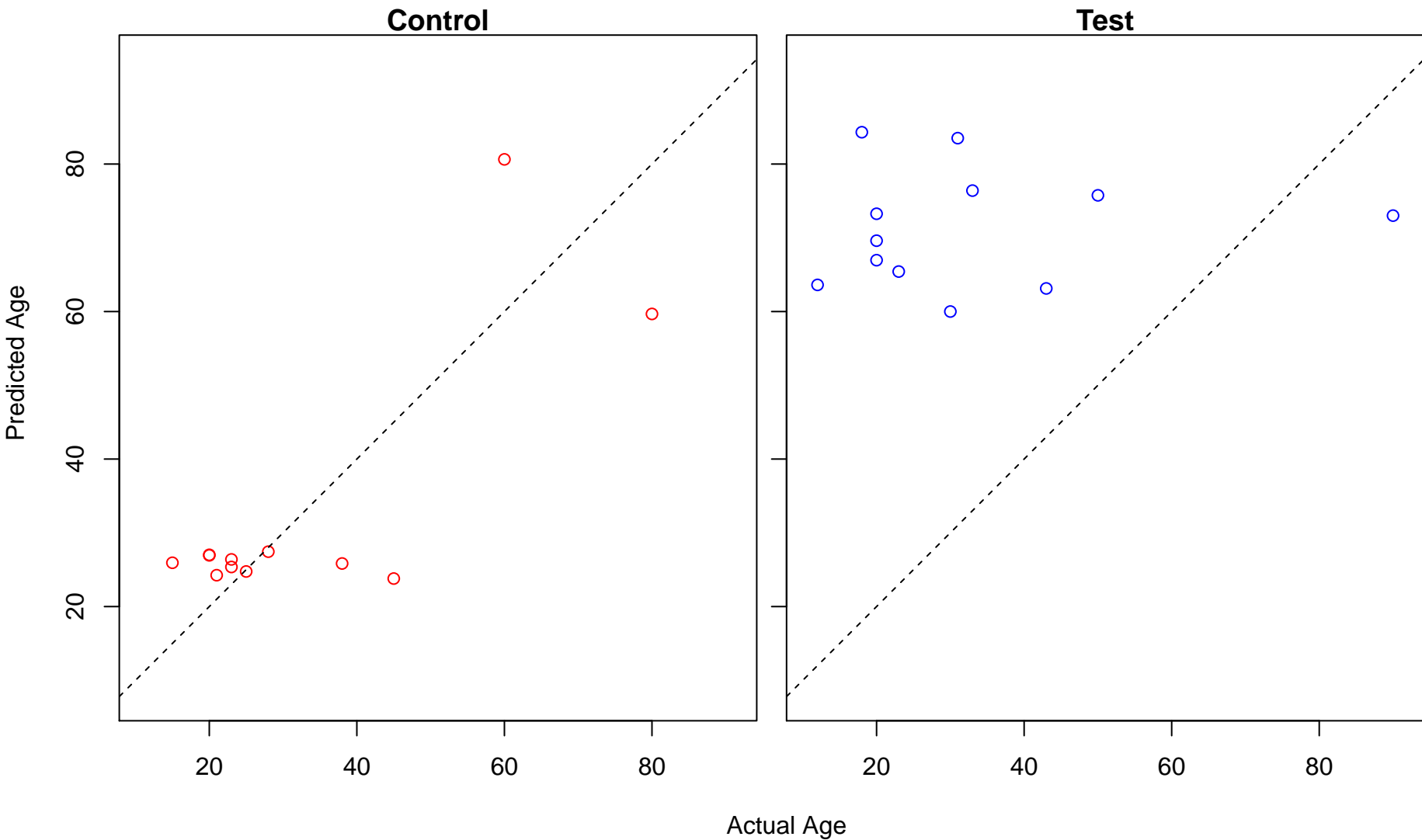
positive regulation of hemopoiesis (Score: 6.541138)



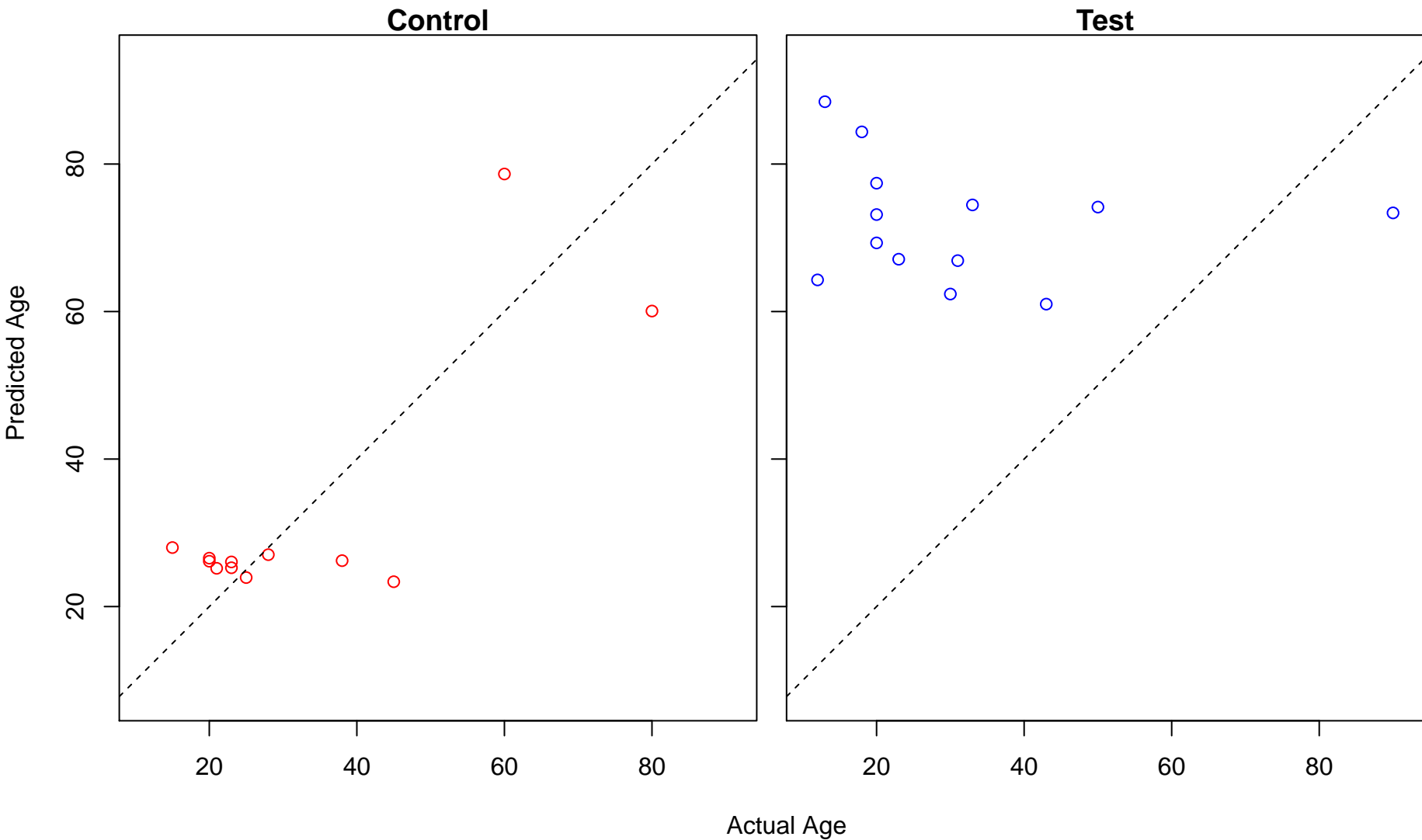
negative regulation of proteasomal ubiquitin-dependent protein catabolic process (Score: 6.53624)



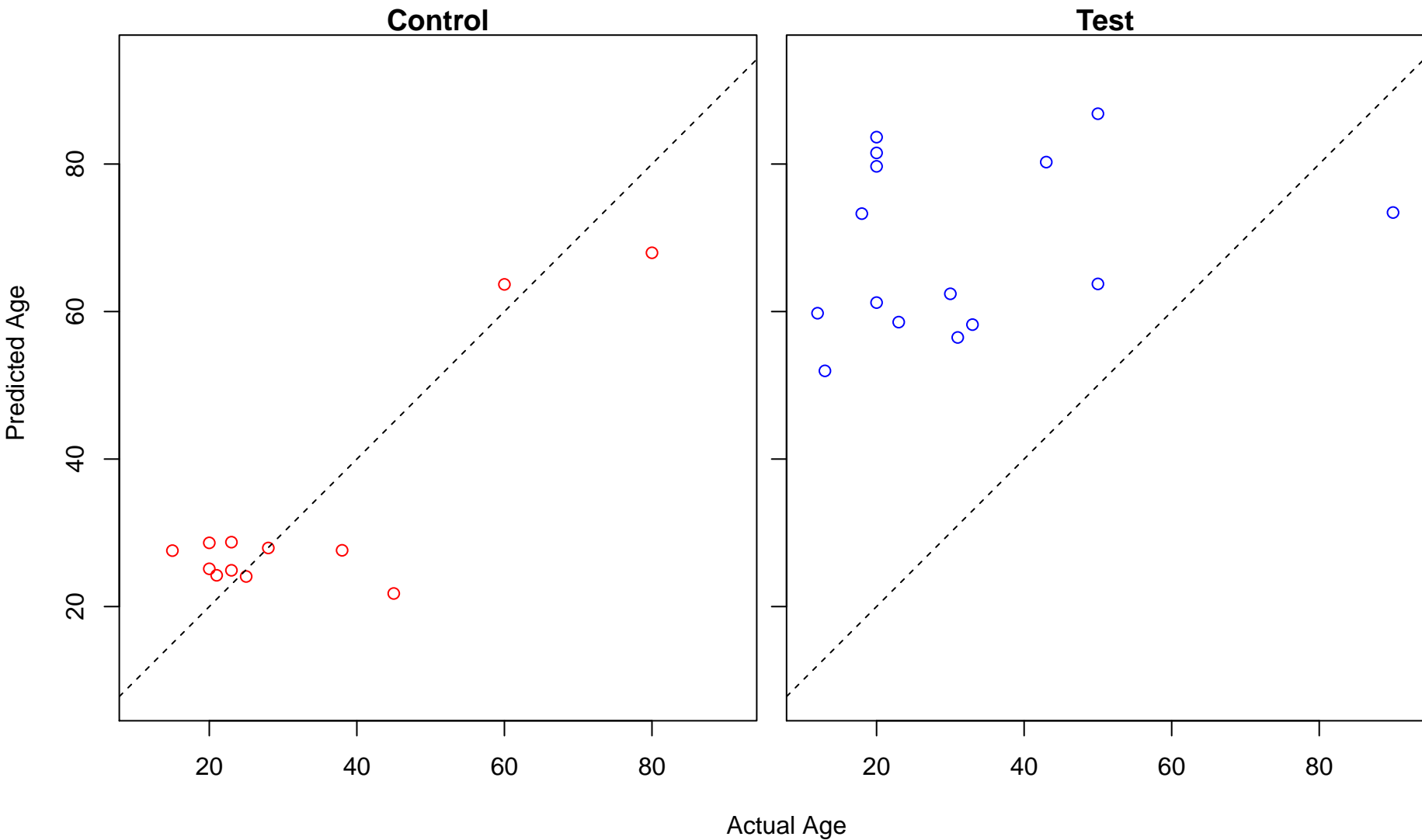
negative regulation of cell cycle (Score: 6.532224)



regulation of cell cycle arrest (Score: 6.531858)

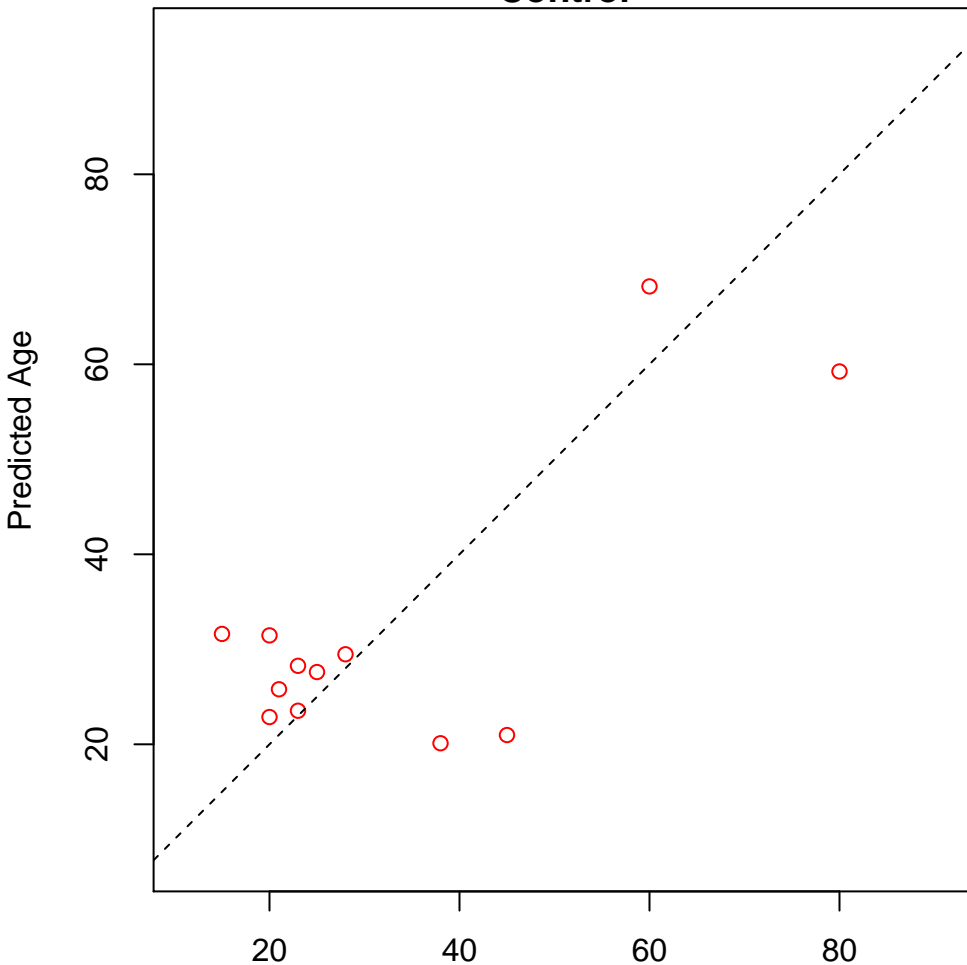


protein homooligomerization (Score: 6.530305)

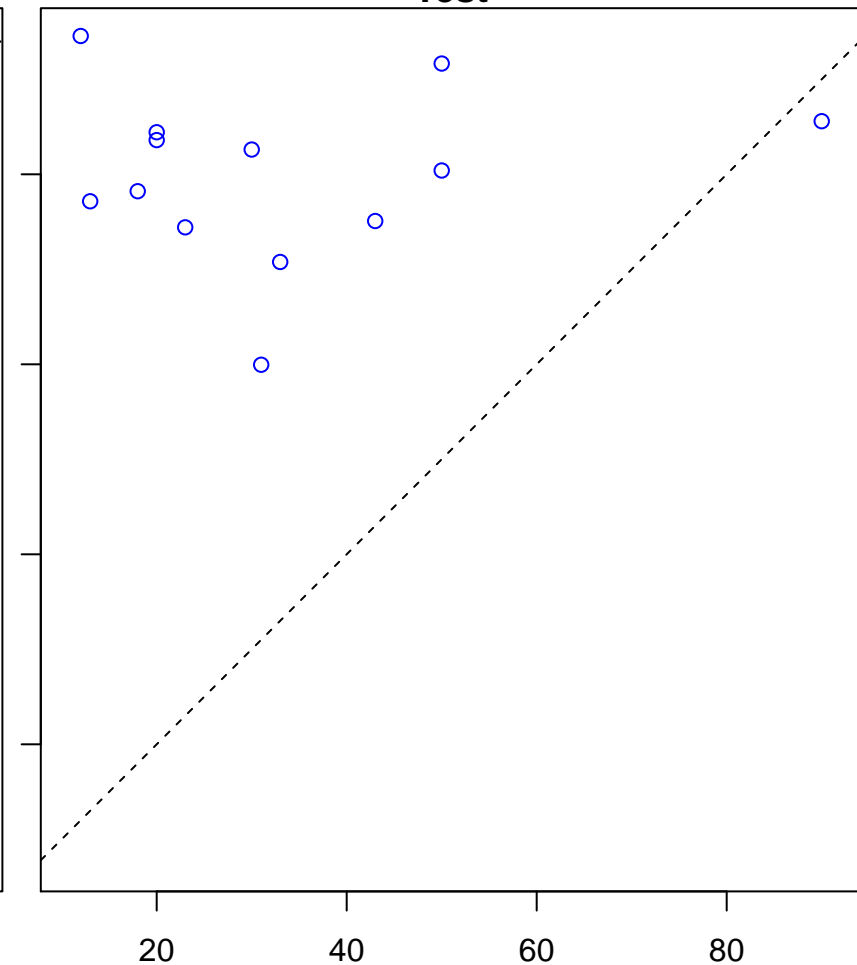


L-ascorbic acid metabolic process (Score: 6.530251)

Control

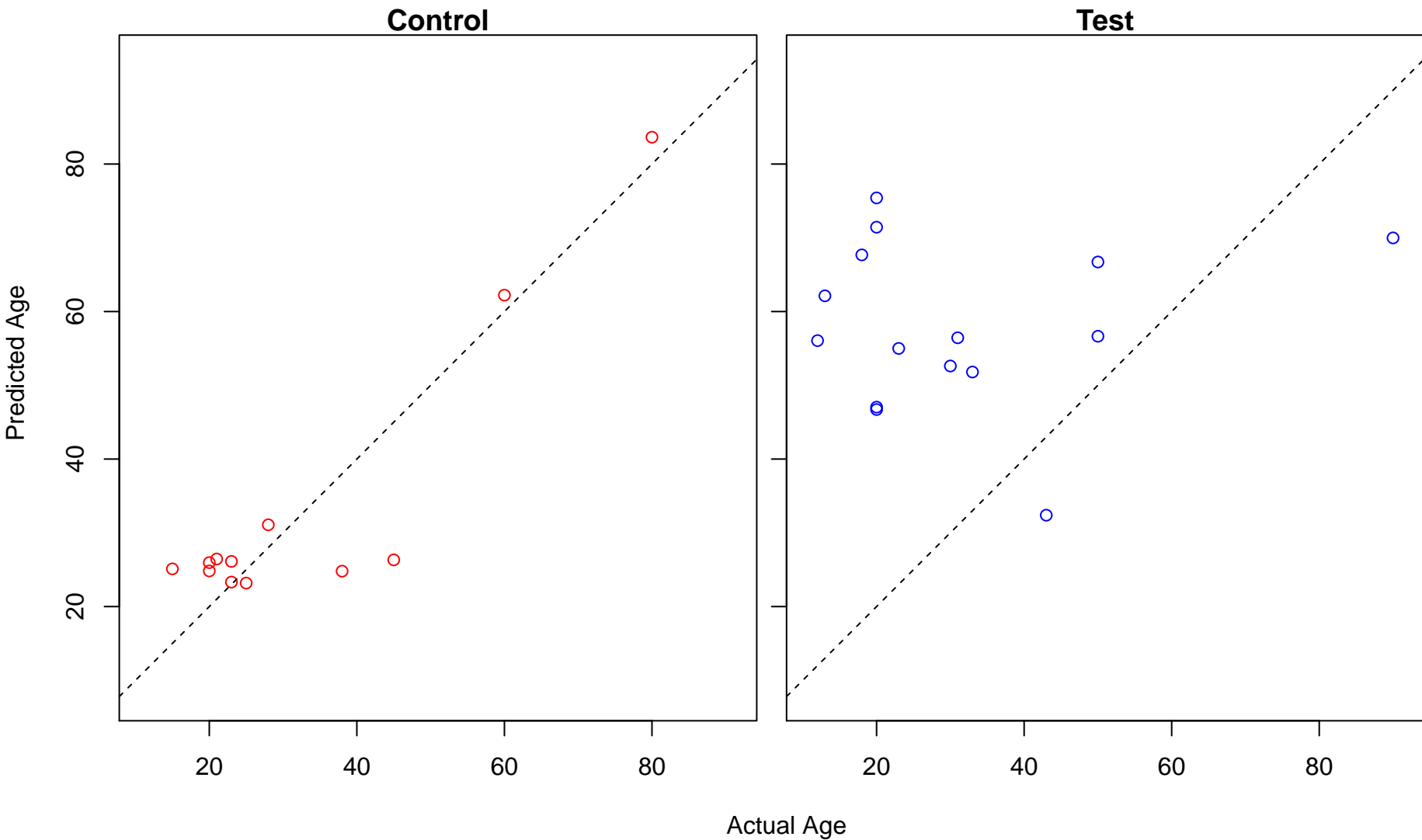


Test

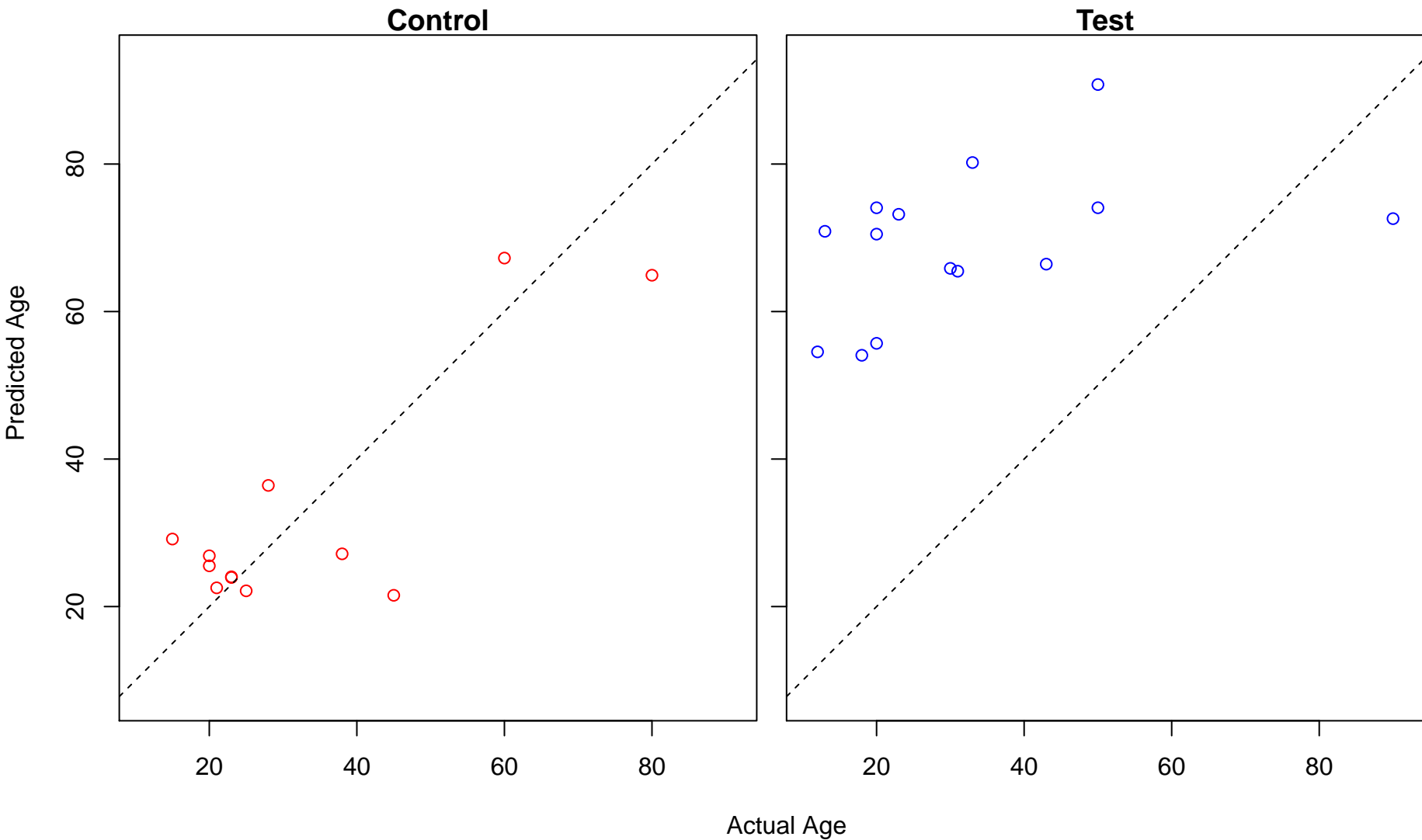


Actual Age

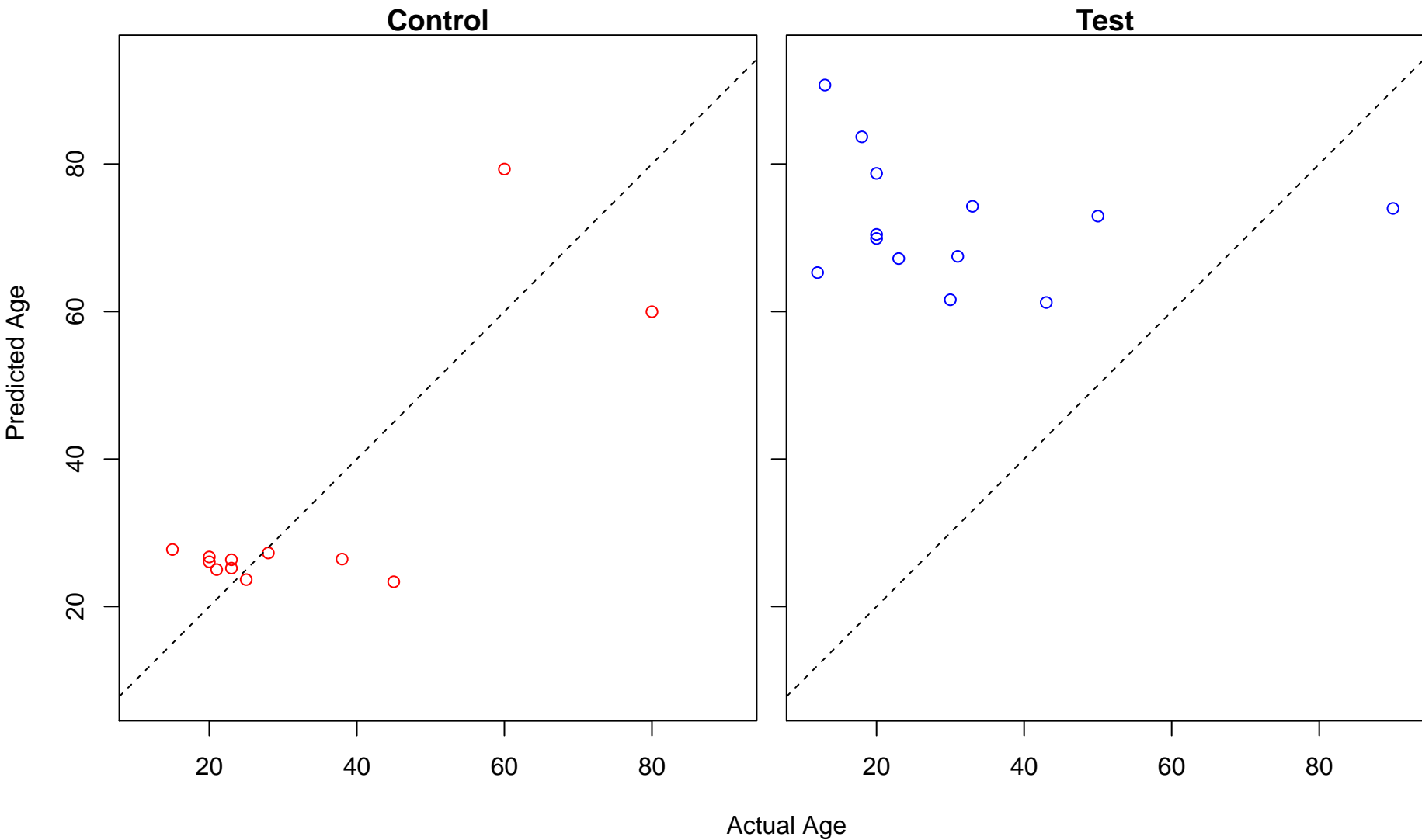
histone mRNA catabolic process (Score: 6.529615)



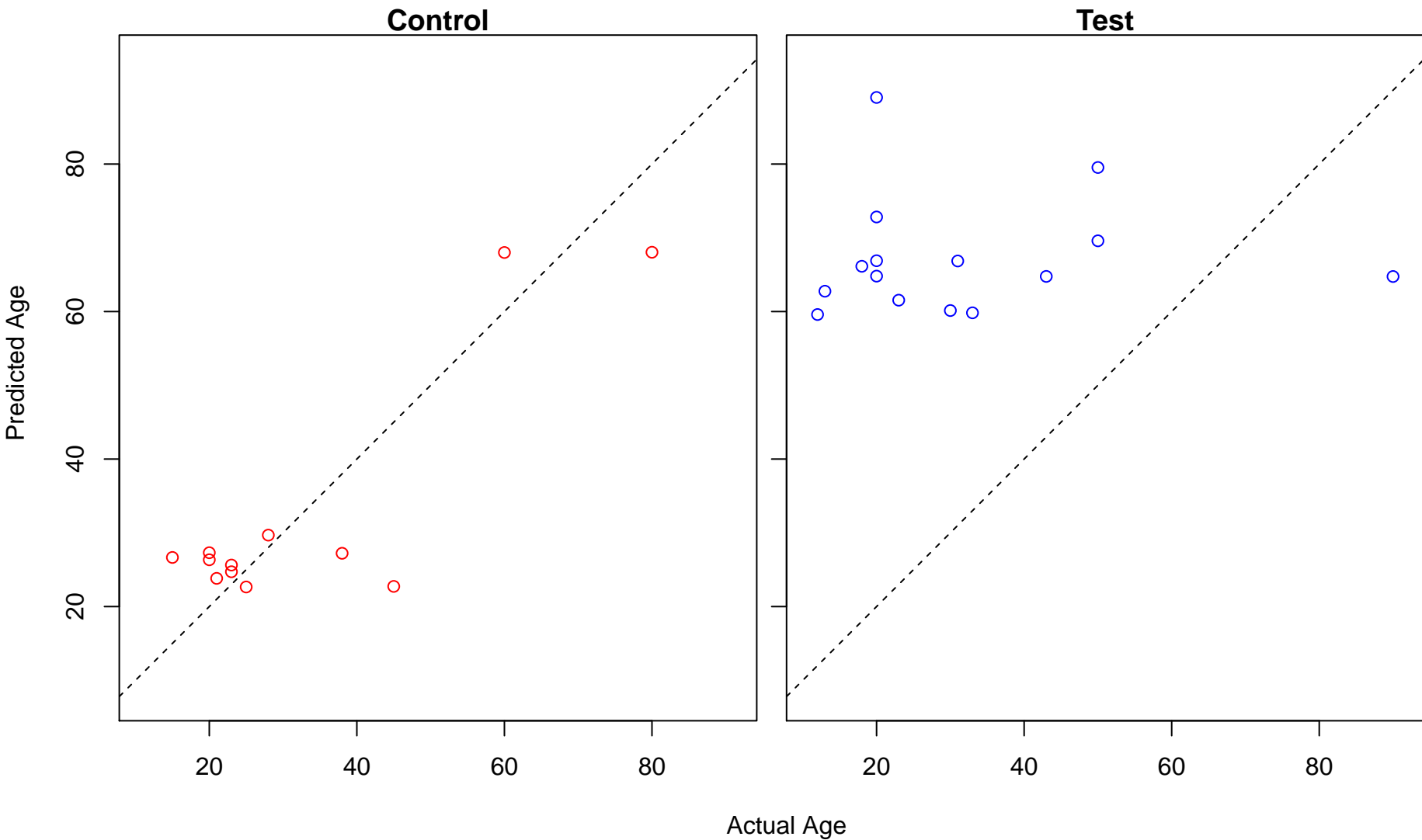
smooth muscle cell migration (Score: 6.529355)



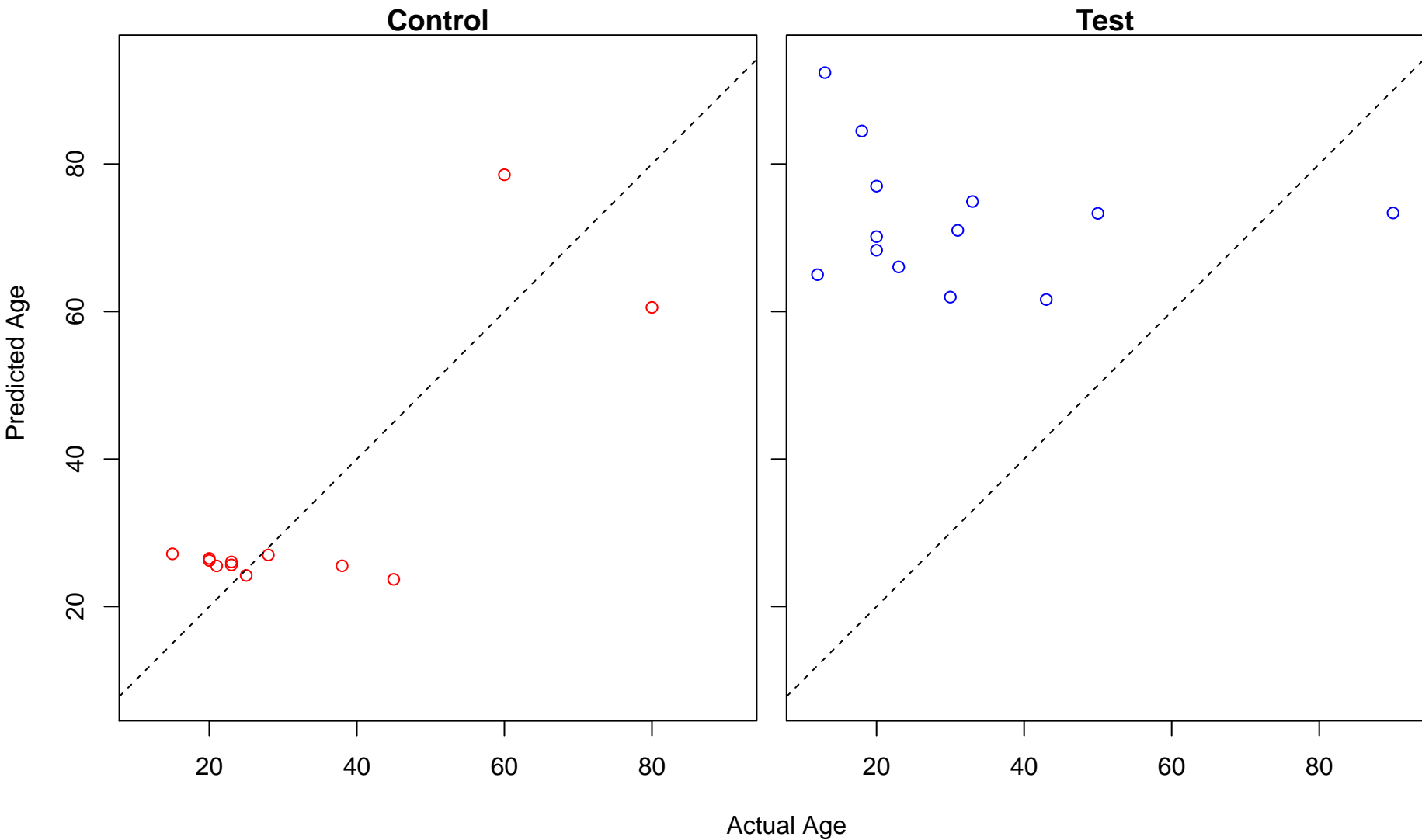
transcription-coupled nucleotide-excision repair (Score: 6.527632)



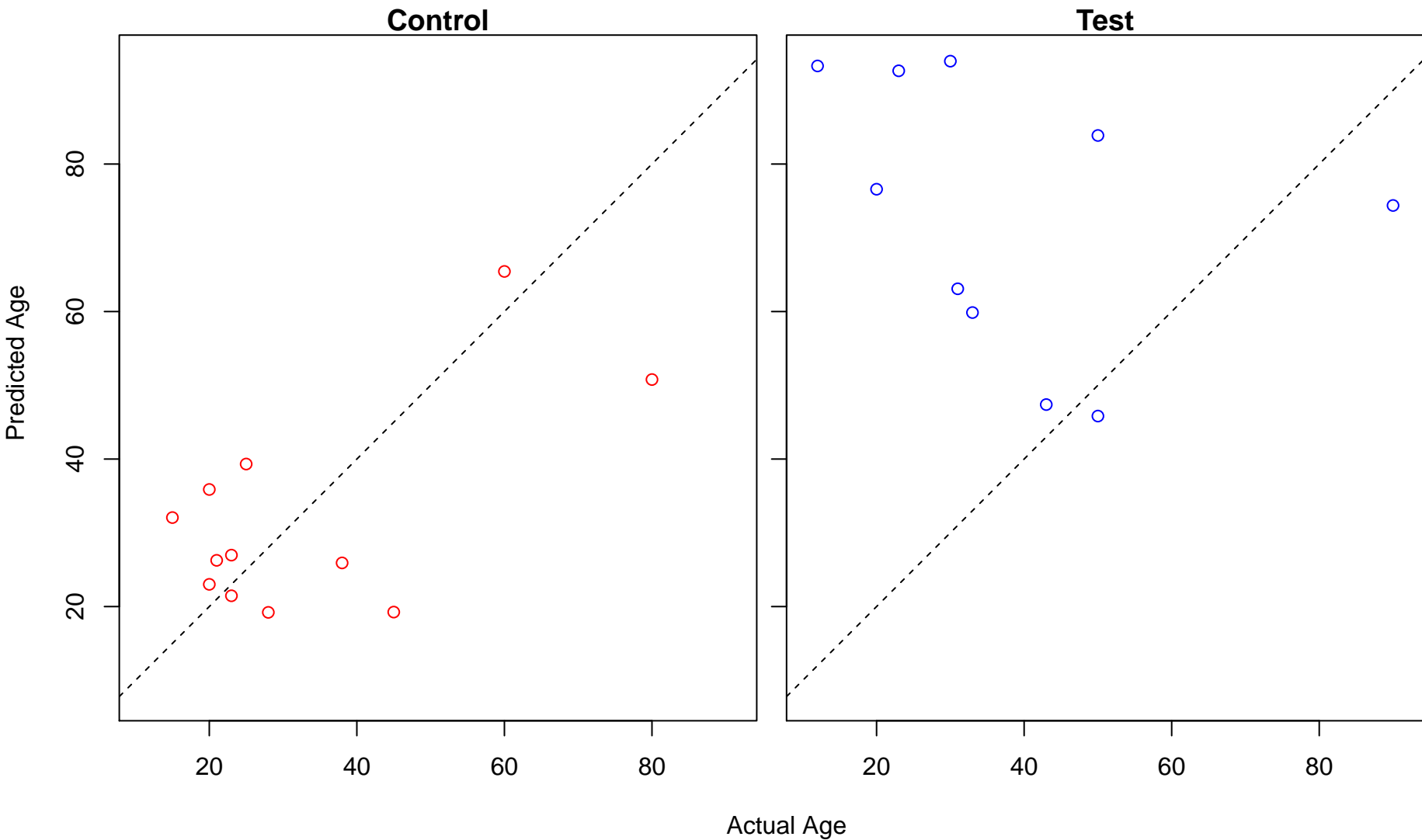
epidermis development (Score: 6.527279)



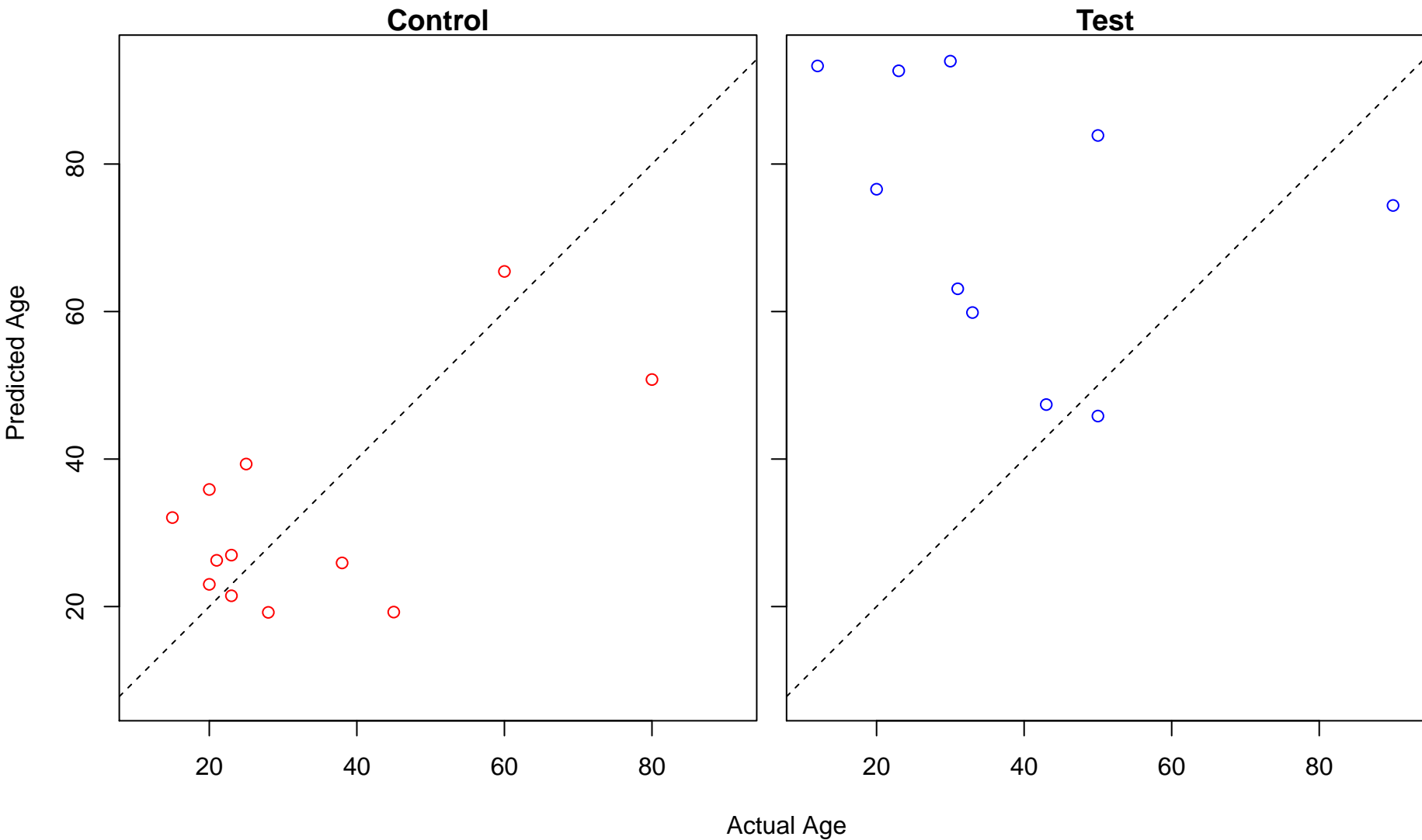
protein polyubiquitination (Score: 6.525287)



response to erythropoietin (Score: 6.524252)

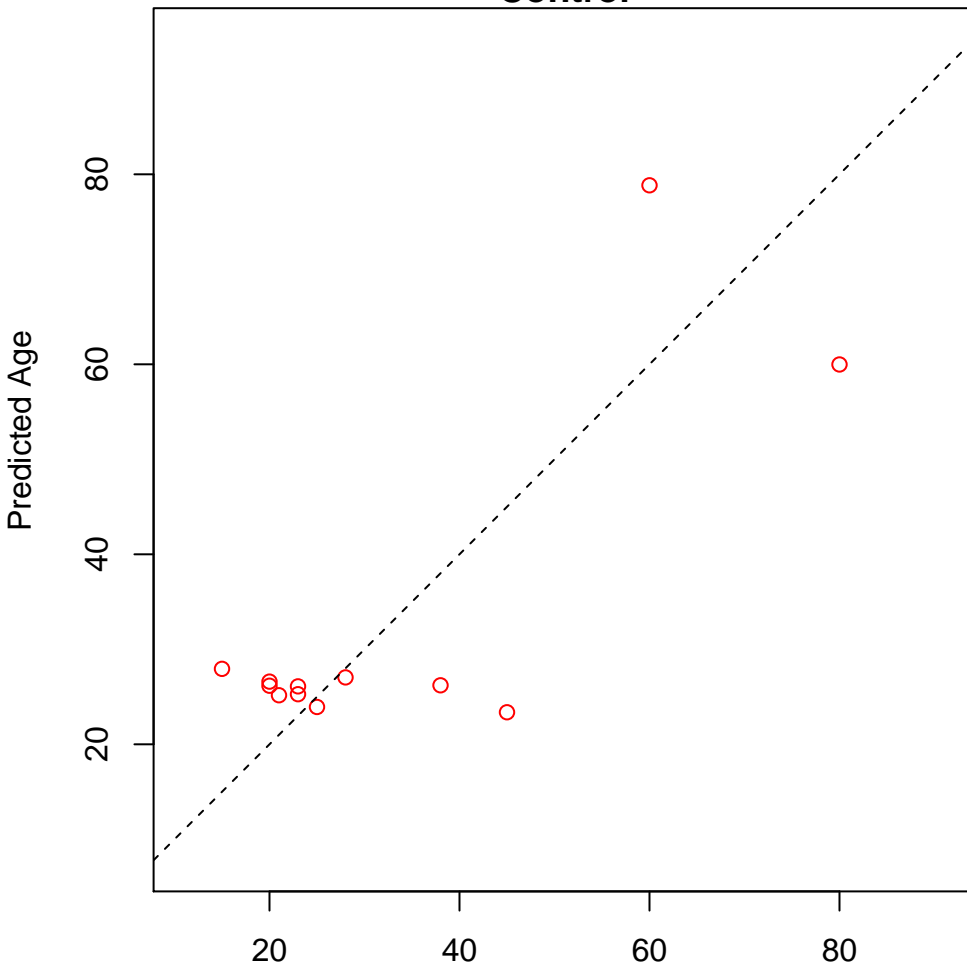


cellular response to erythropoietin (Score: 6.524252)

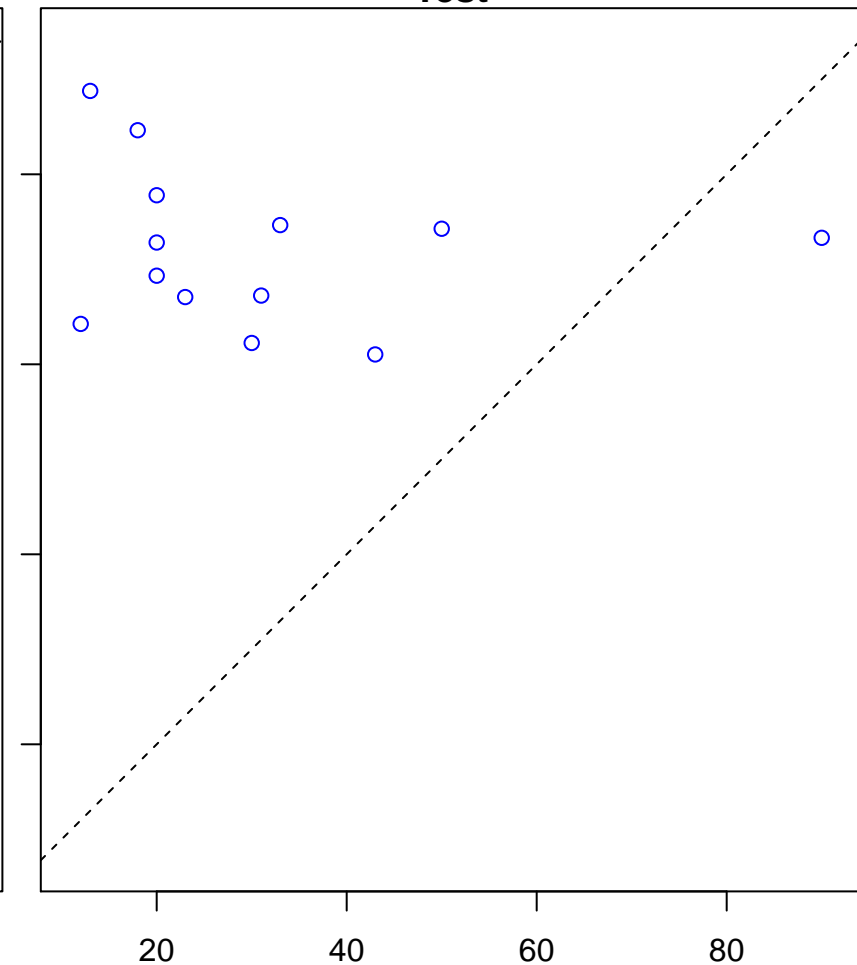


positive regulation of cell cycle arrest (Score: 6.523786)

Control

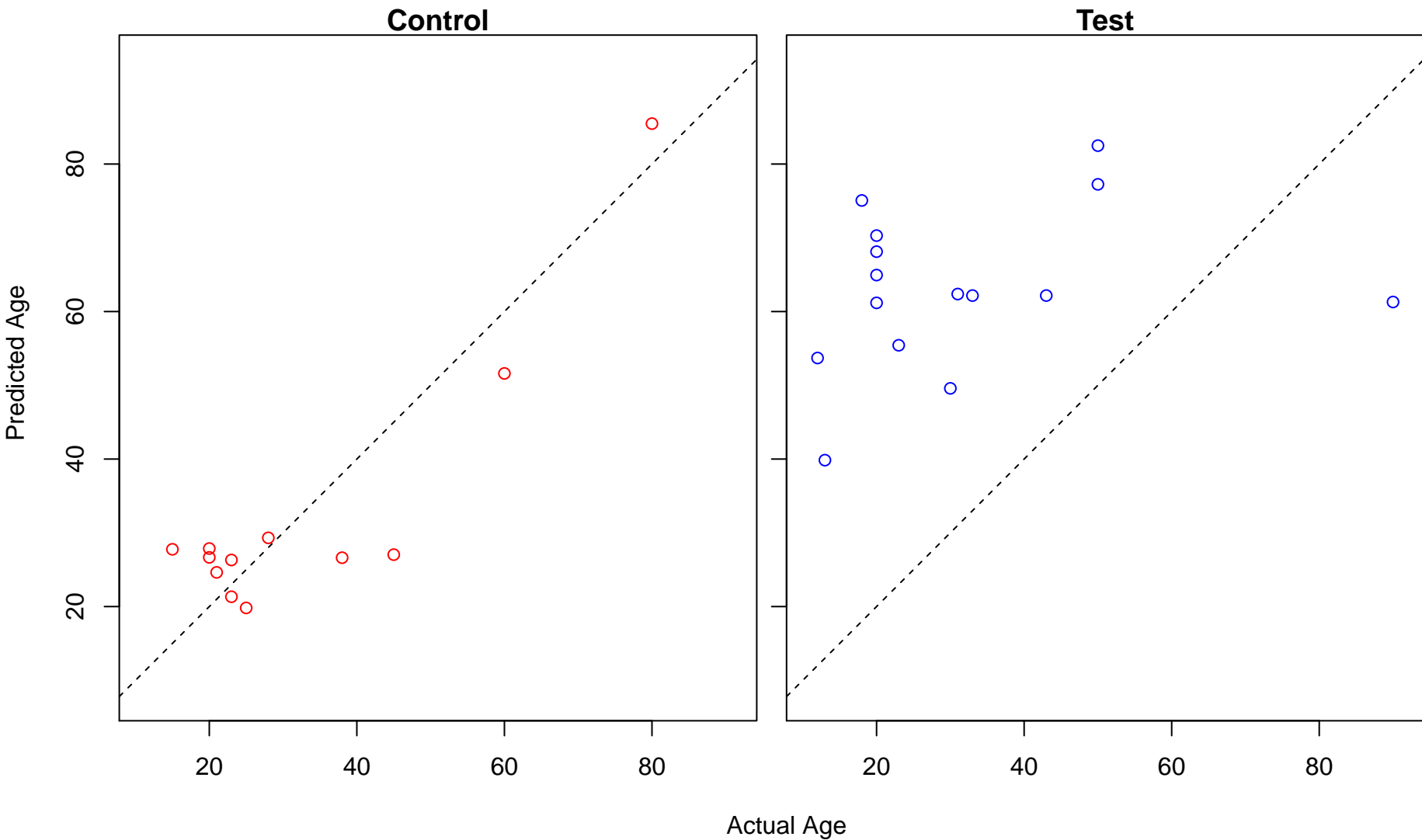


Test

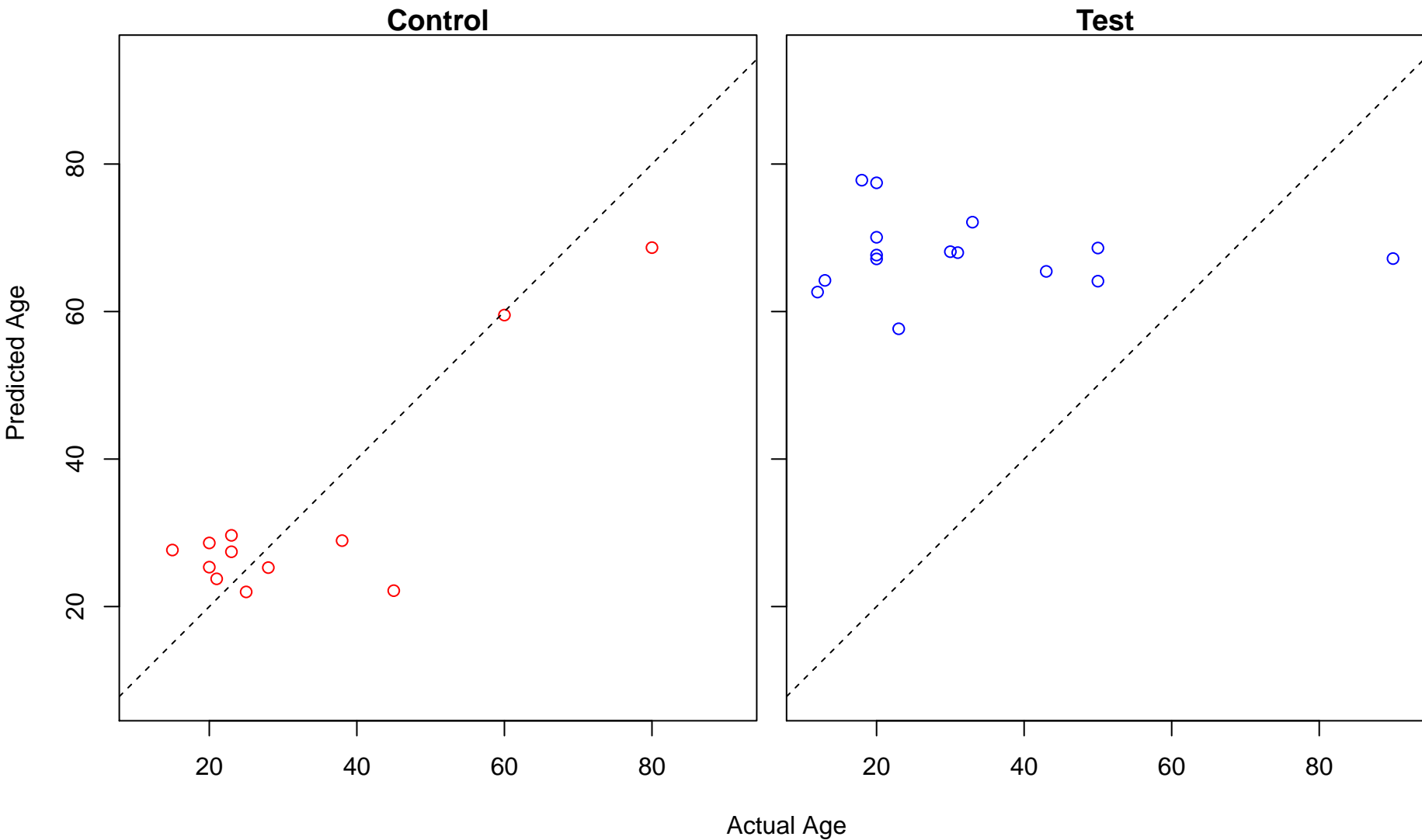


Actual Age

tRNA aminoacylation for protein translation (Score: 6.523699)

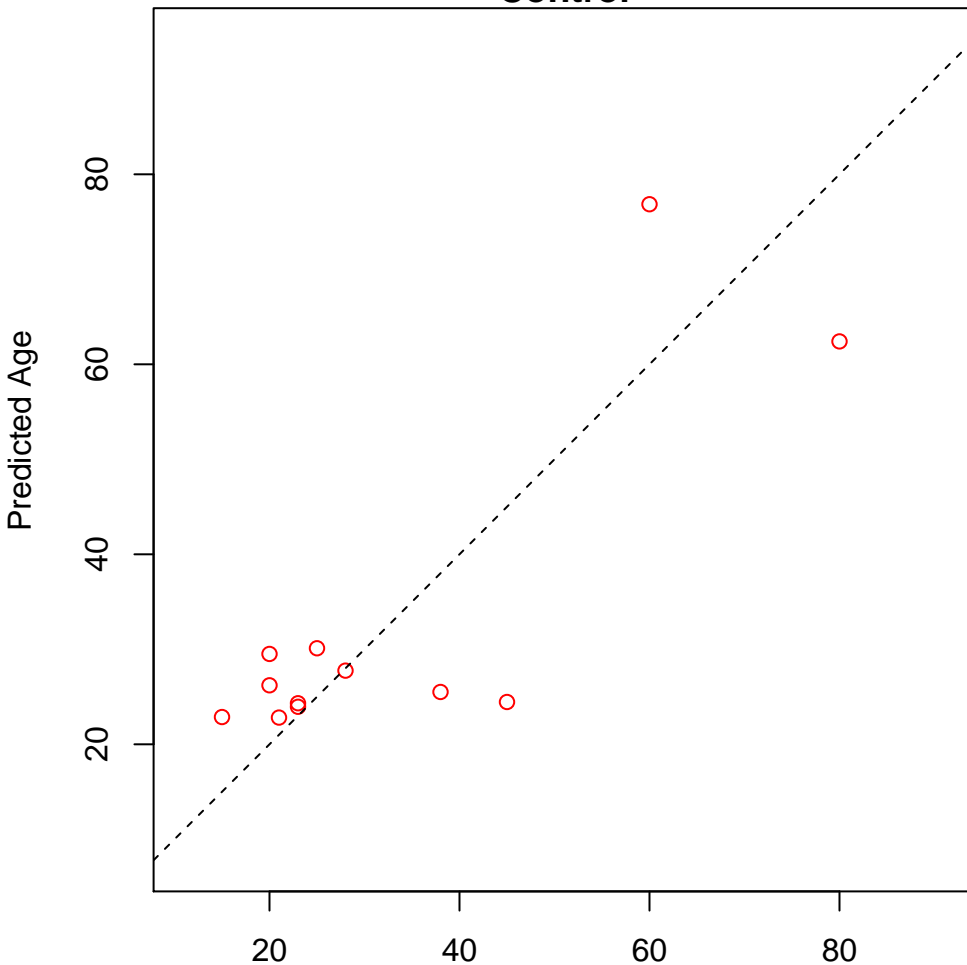


fat cell differentiation (Score: 6.523472)

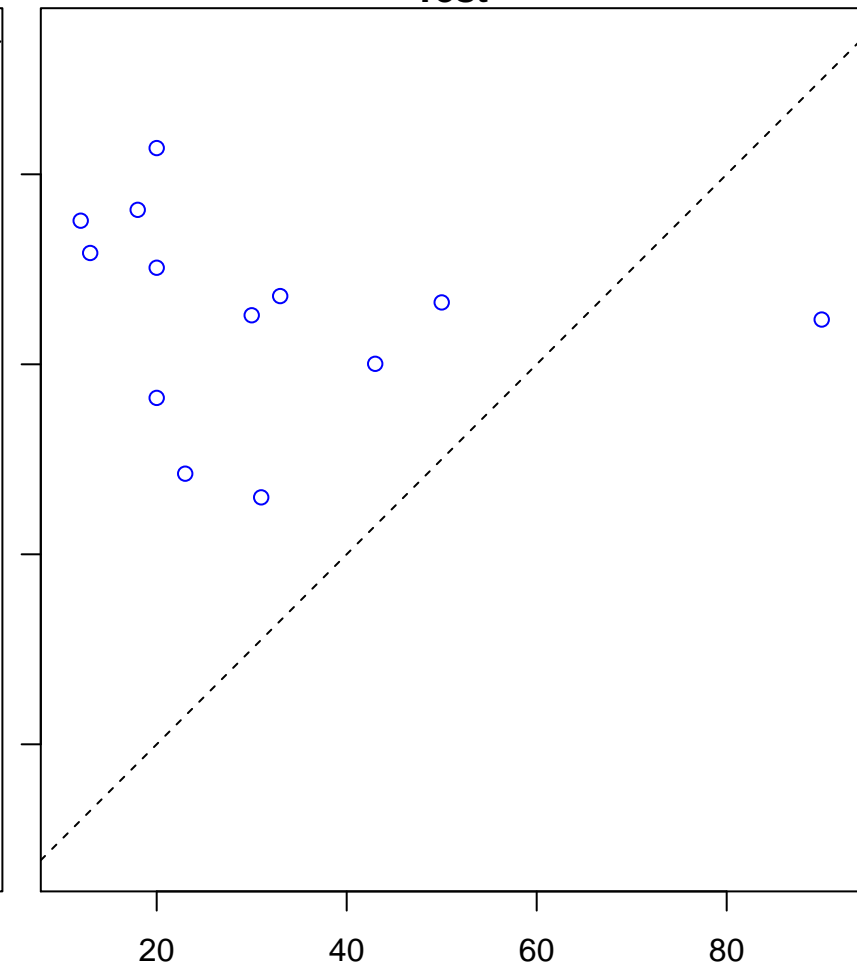


positive regulation of blood pressure (Score: 6.521481)

Control

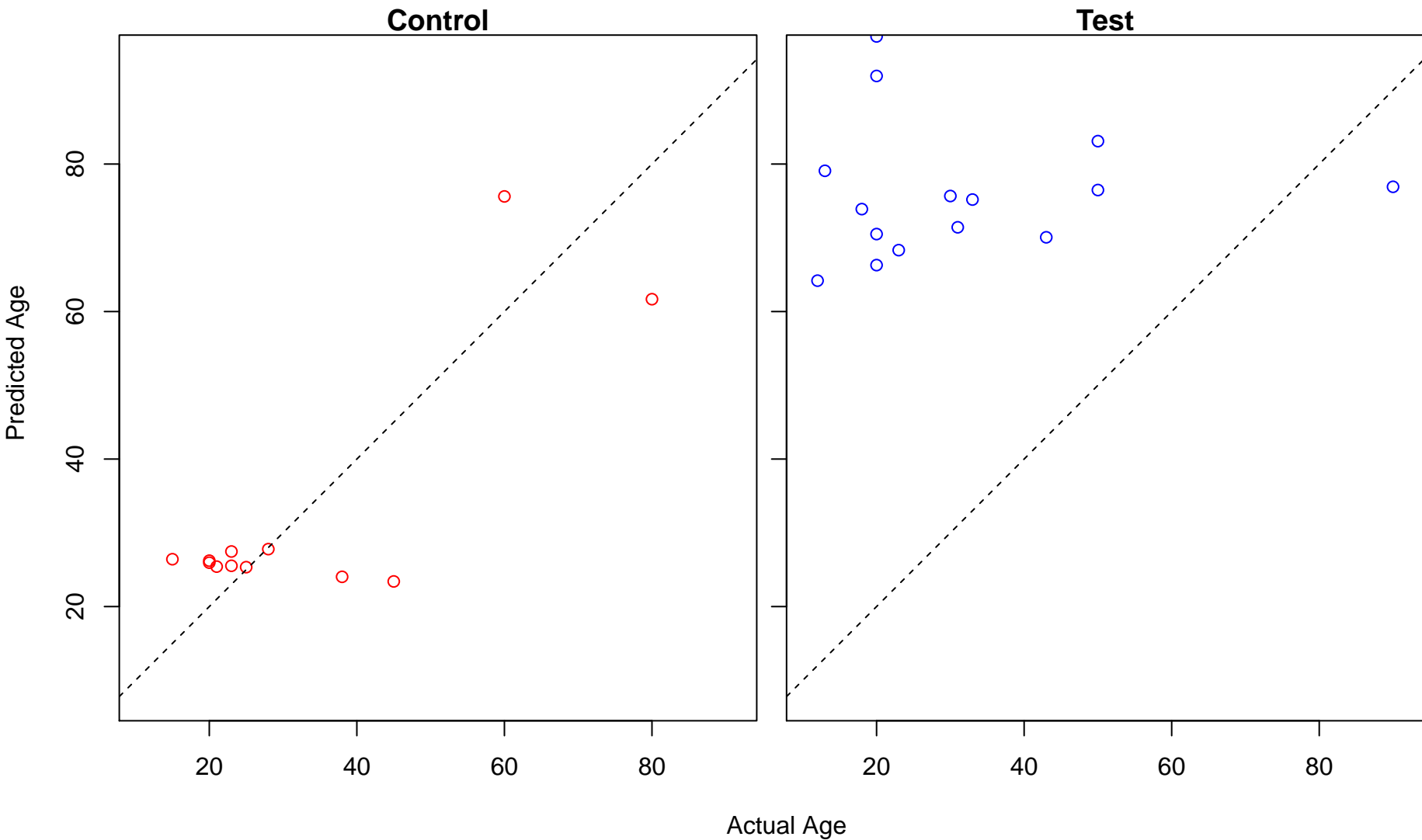


Test



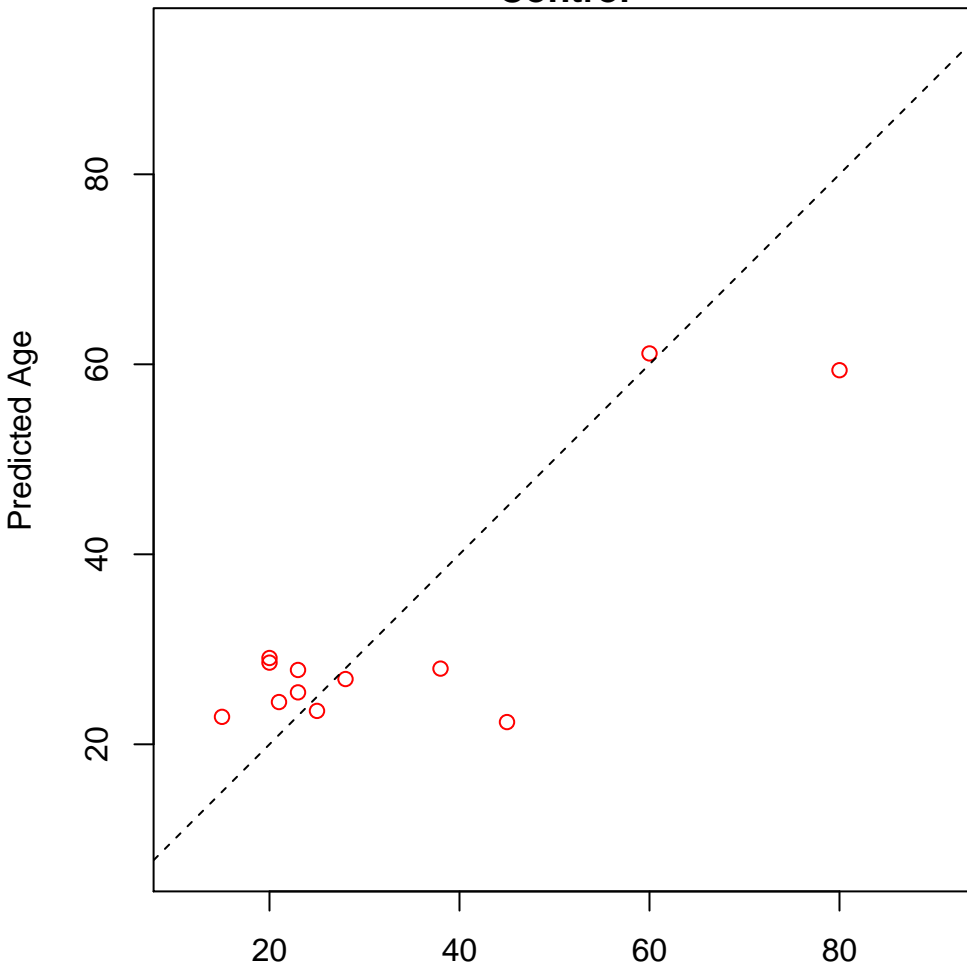
Actual Age

extrinsic apoptotic signaling pathway via death domain receptors (Score: 6.520821)

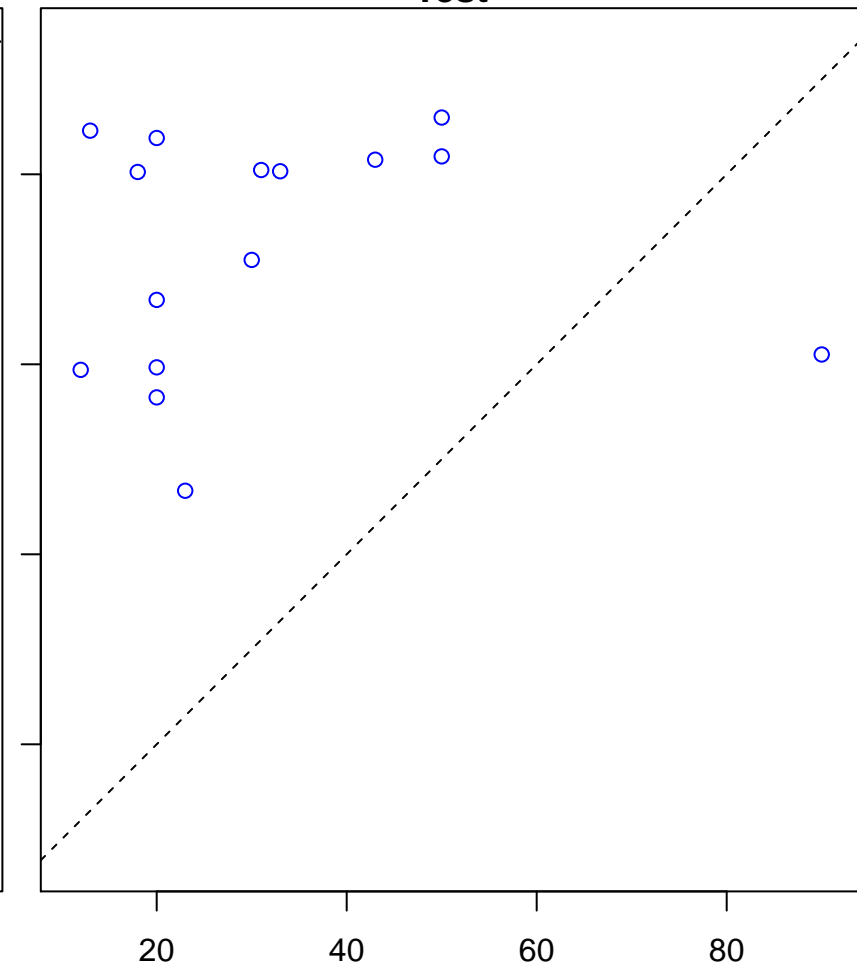


spinal cord dorsal/ventral patterning (Score: 6.517632)

Control

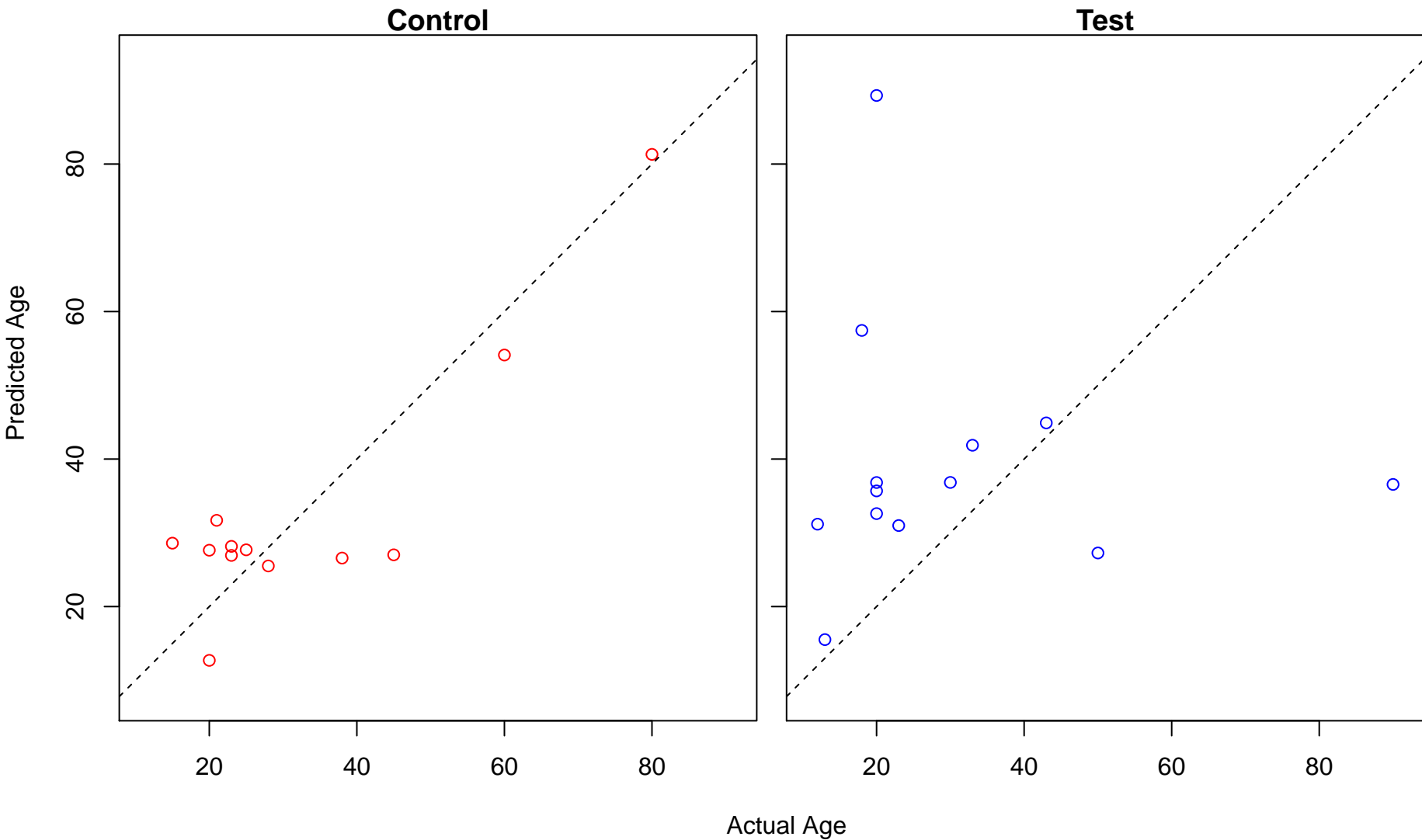


Test

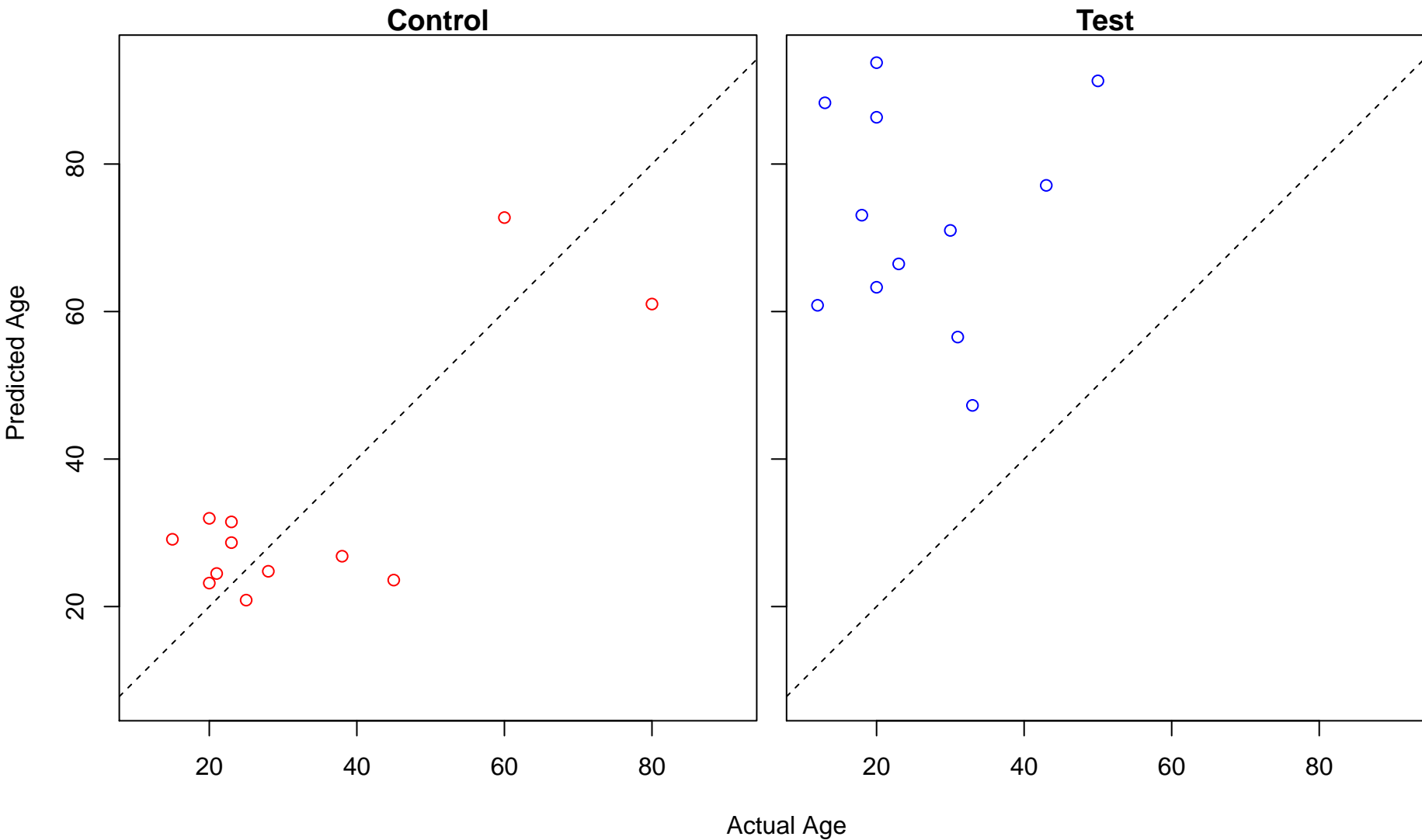


Actual Age

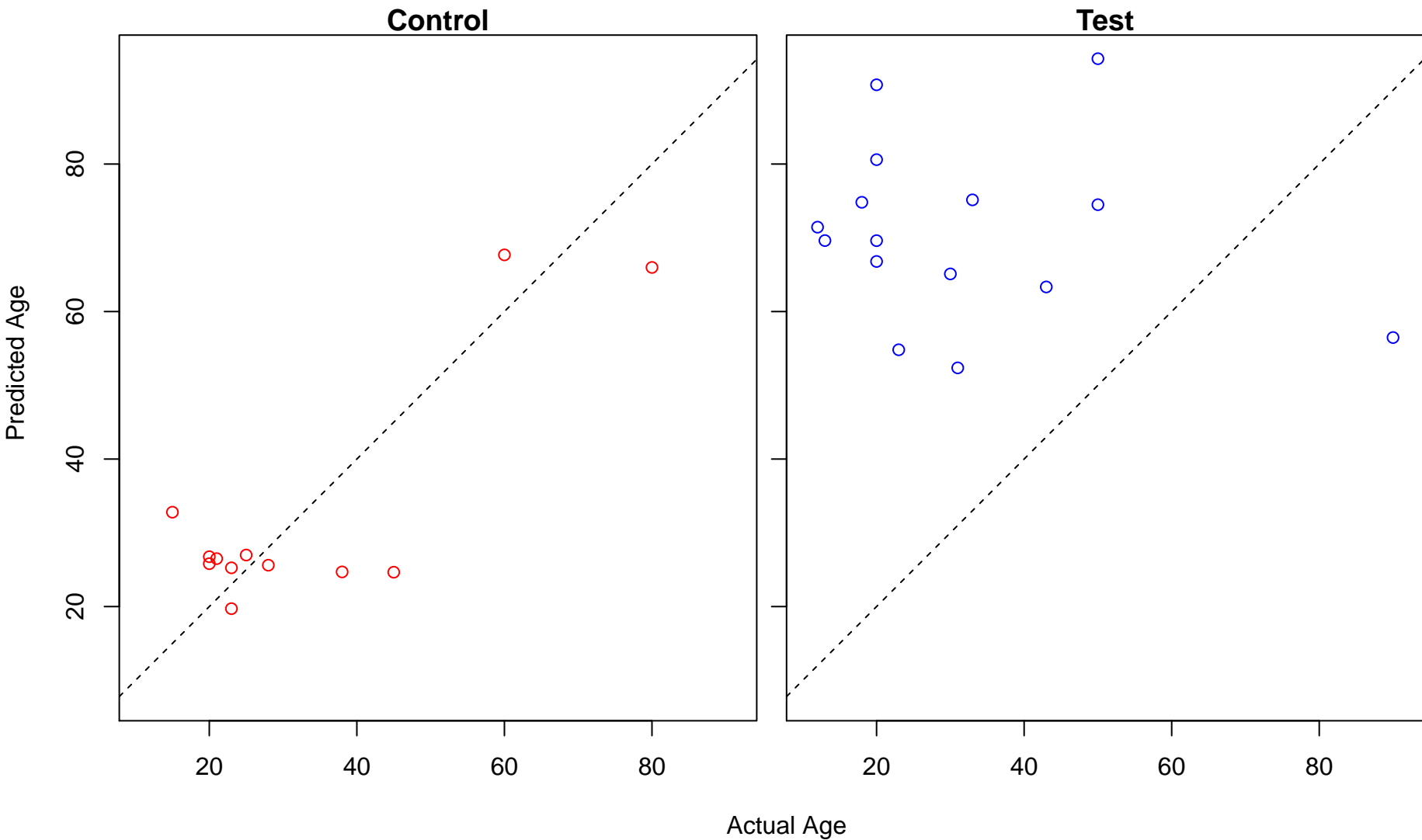
myeloid cell differentiation (Score: 6.514893)



negative regulation of response to wounding (Score: 6.513884)

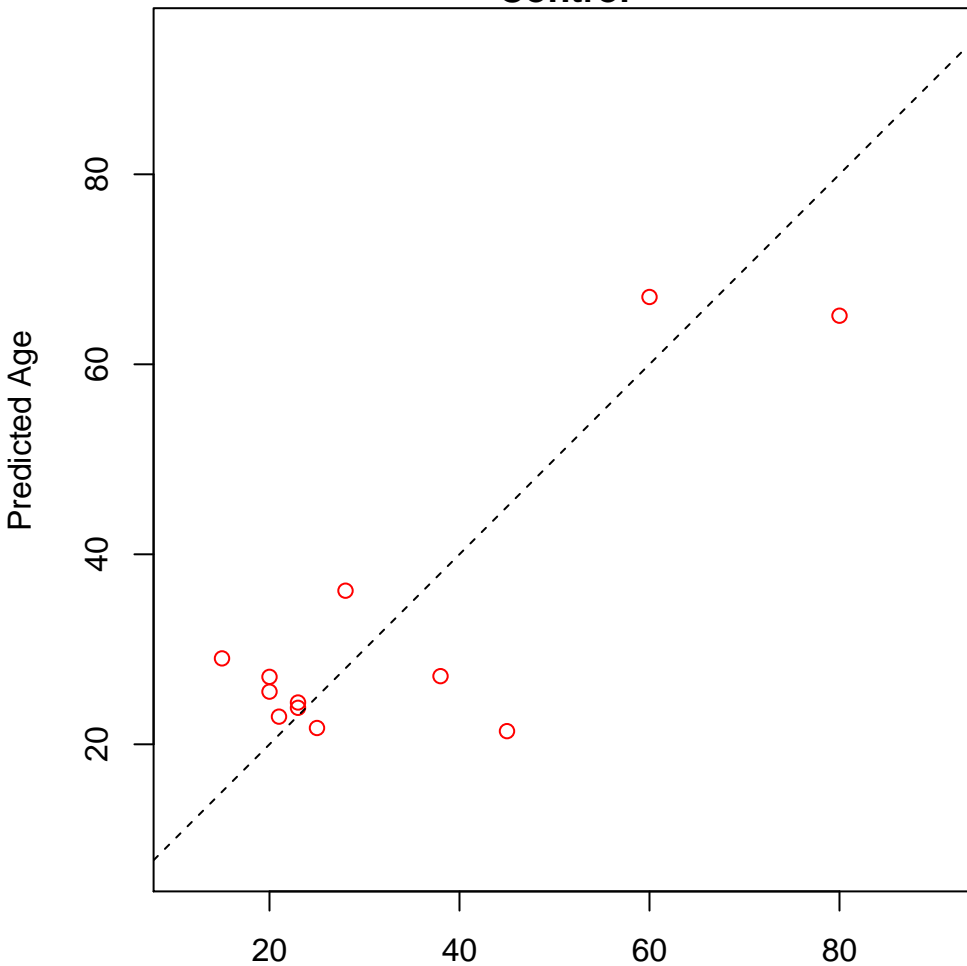


angiotensin-activated signaling pathway (Score: 6.513789)

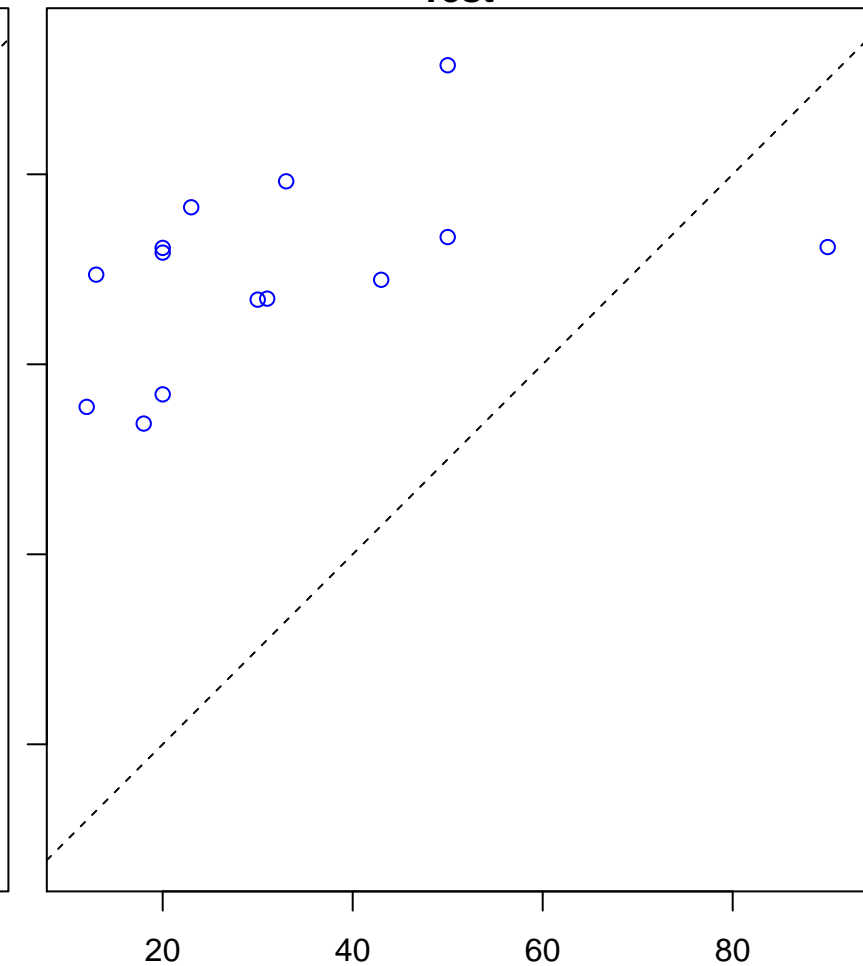


peptidyl-tyrosine autophosphorylation (Score: 6.511365)

Control

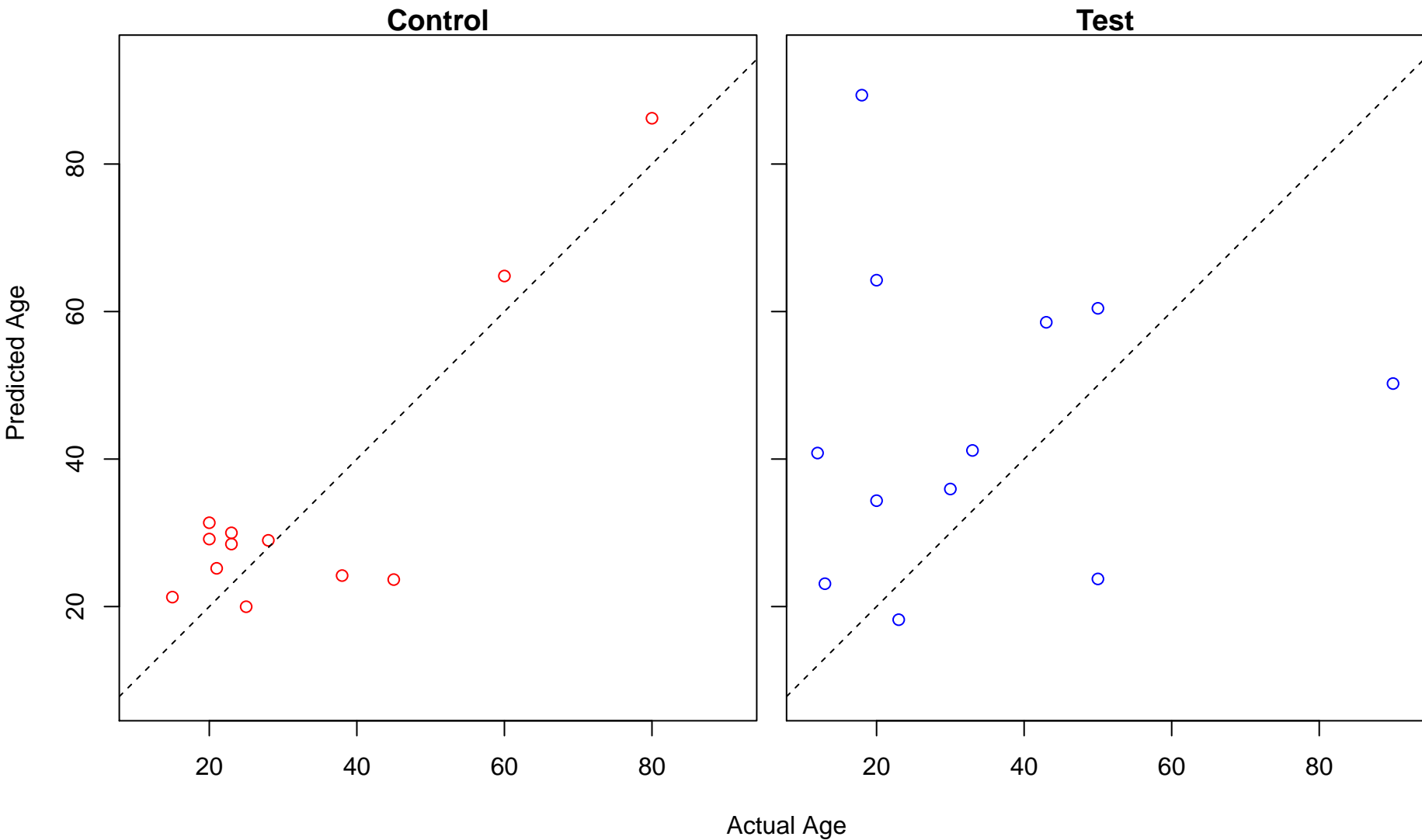


Test

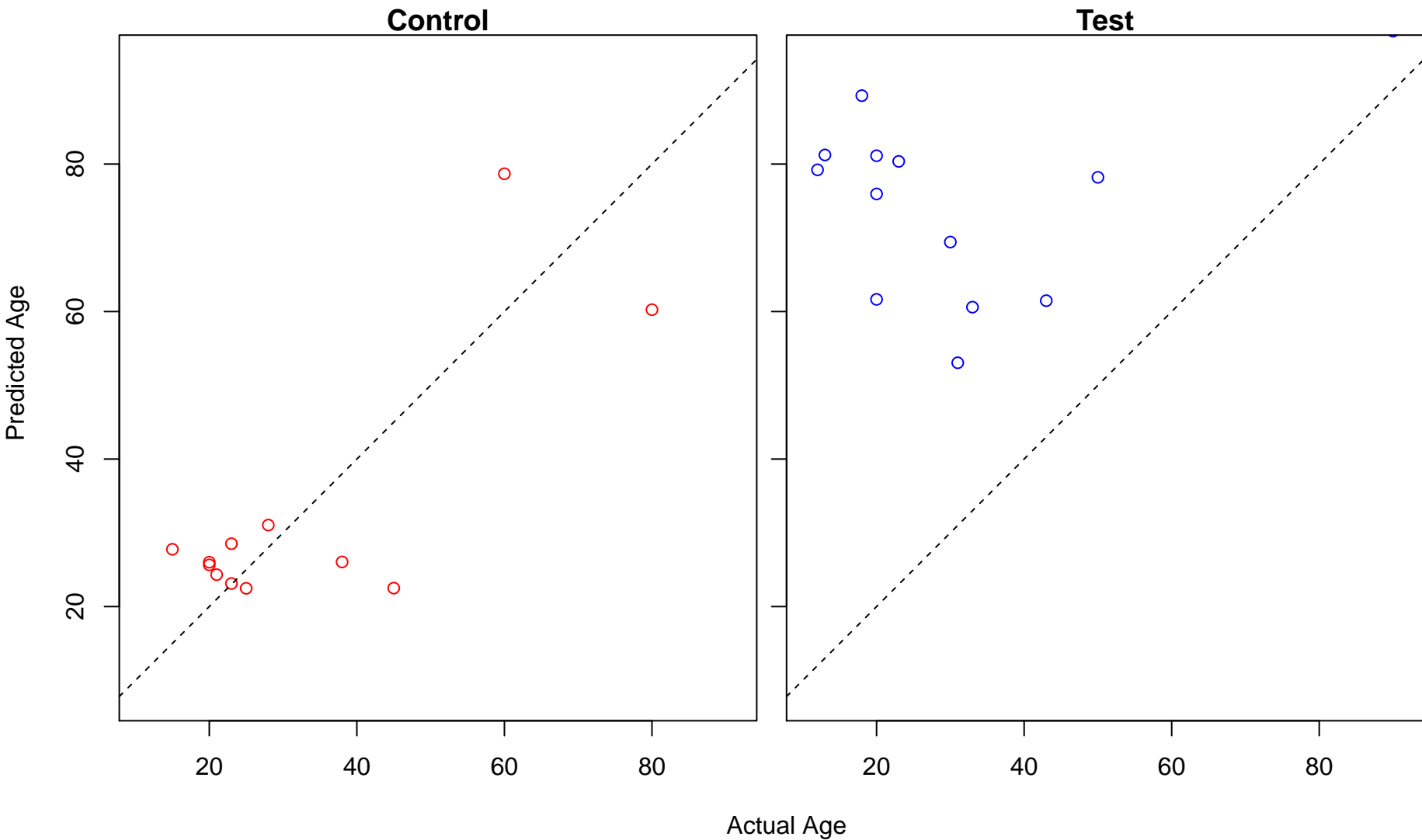


Actual Age

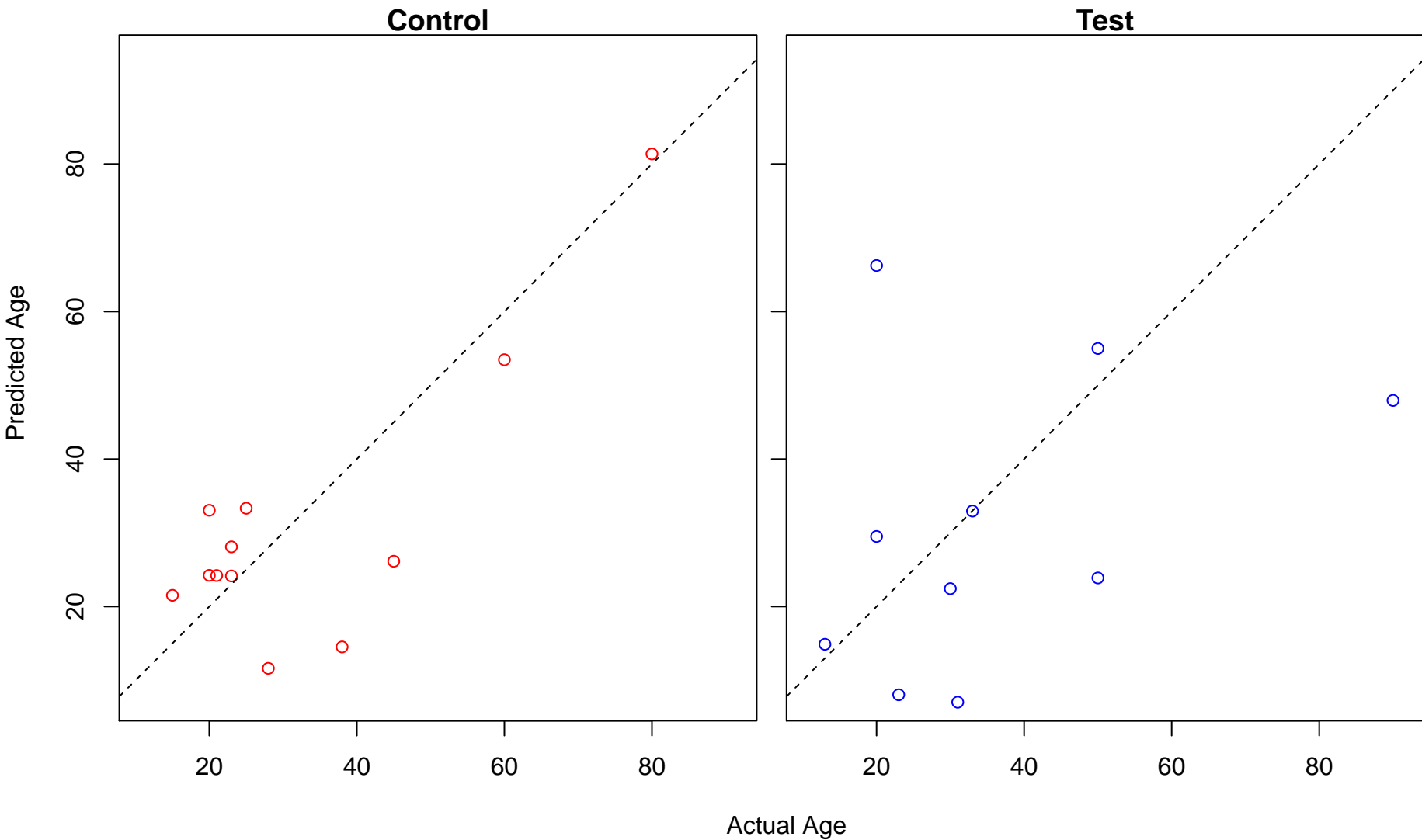
C-terminal protein amino acid modification (Score: 6.504385)



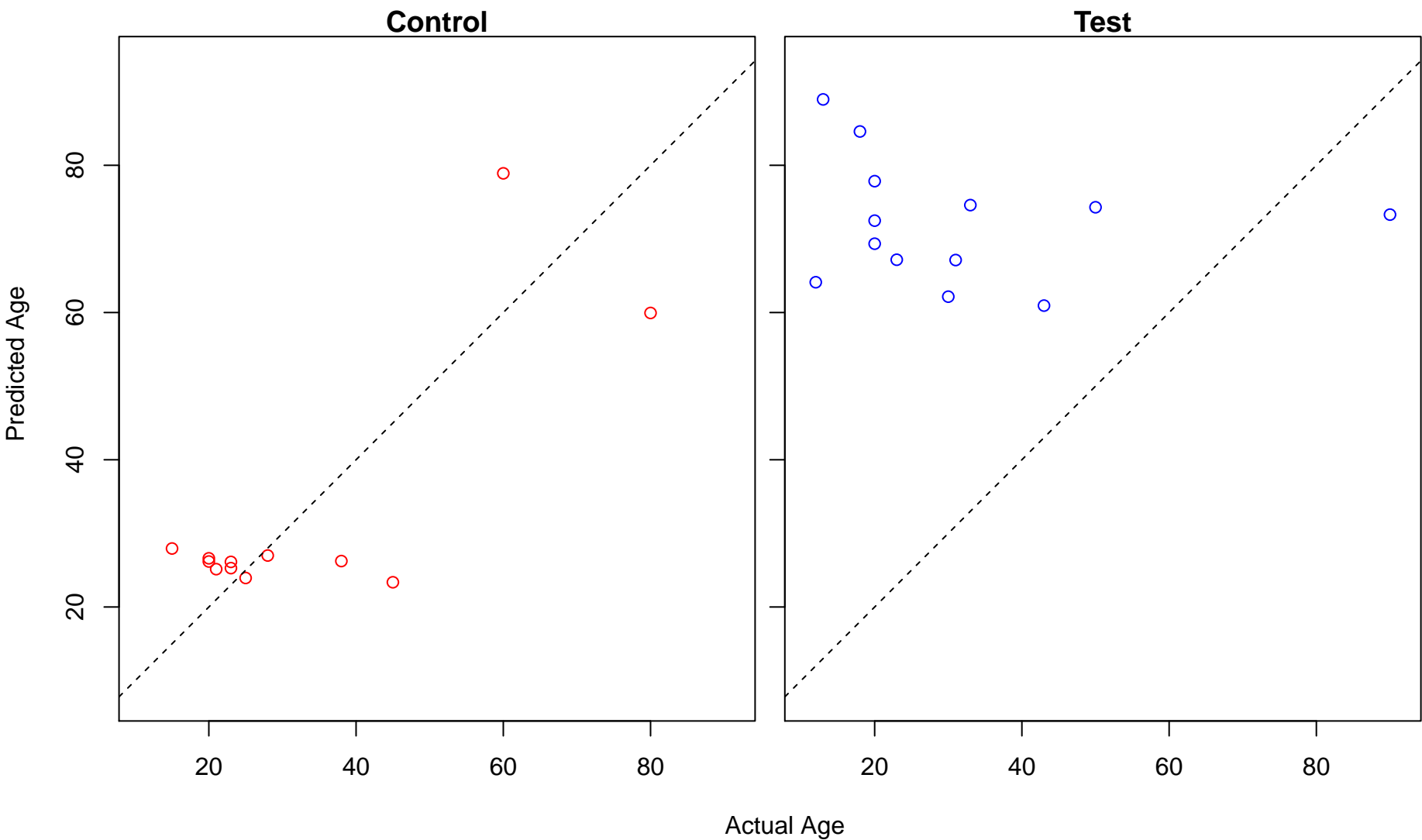
Notch receptor processing (Score: 6.504346)



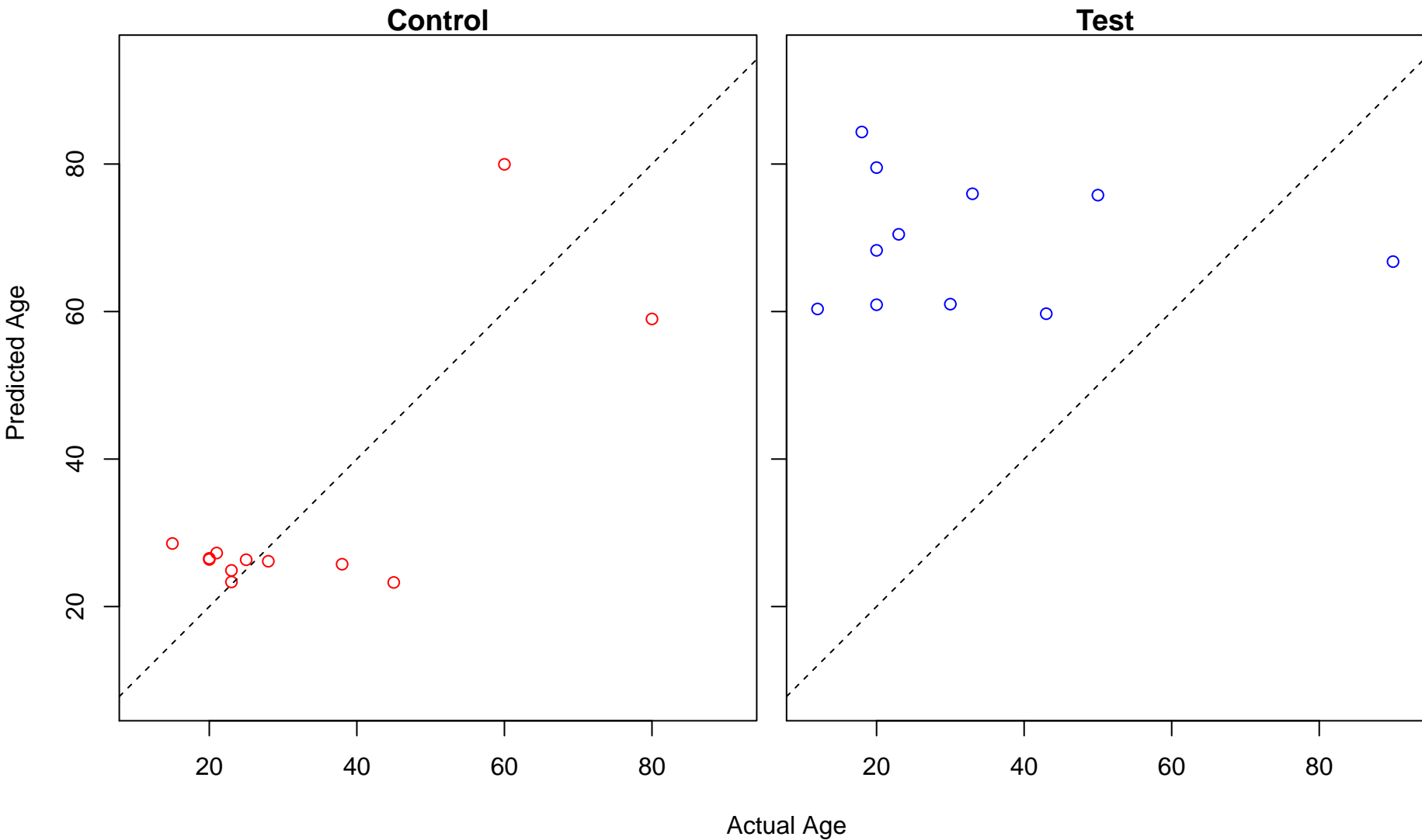
positive regulation of phospholipase A2 activity (Score: 6.502738)



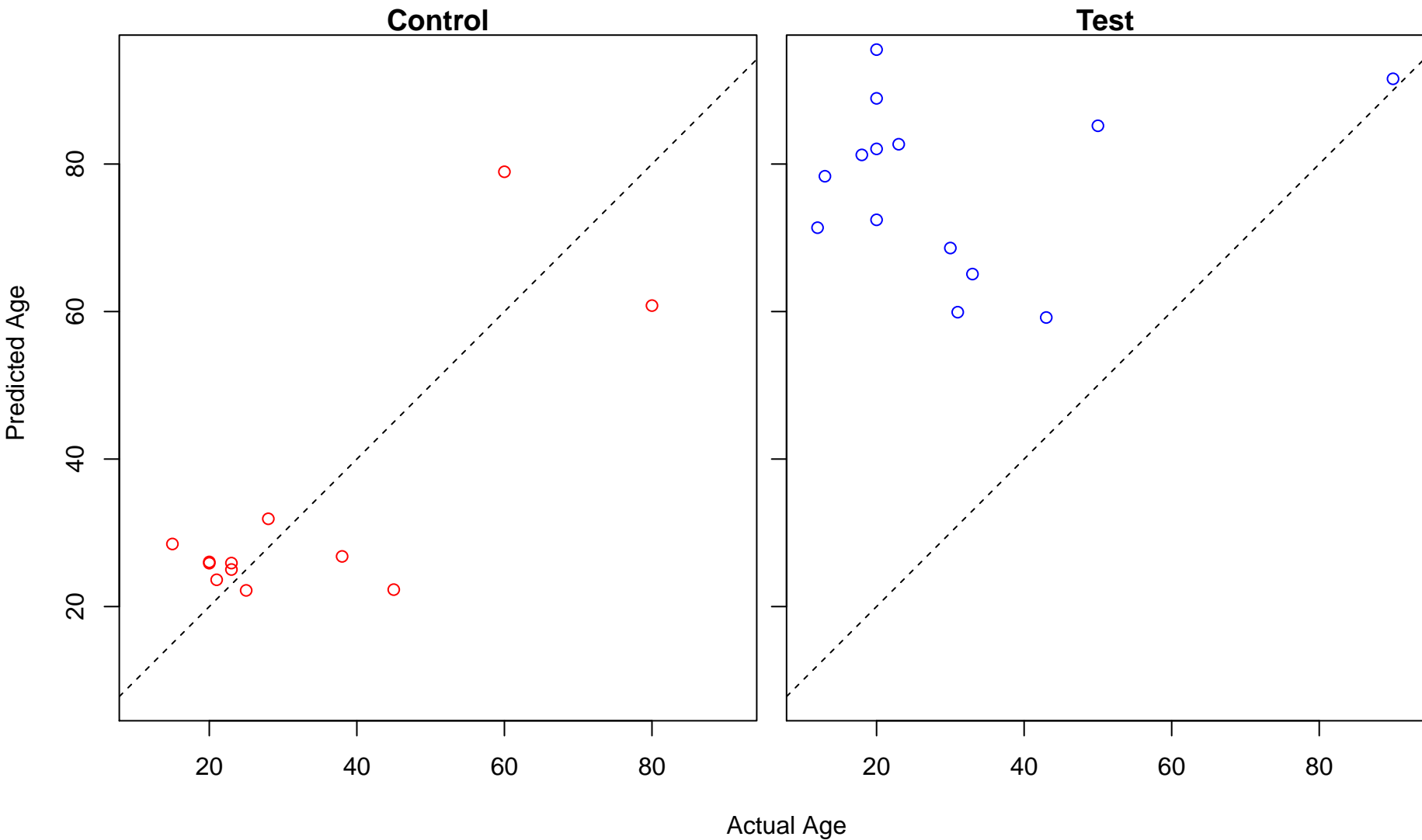
DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (Score: 6.



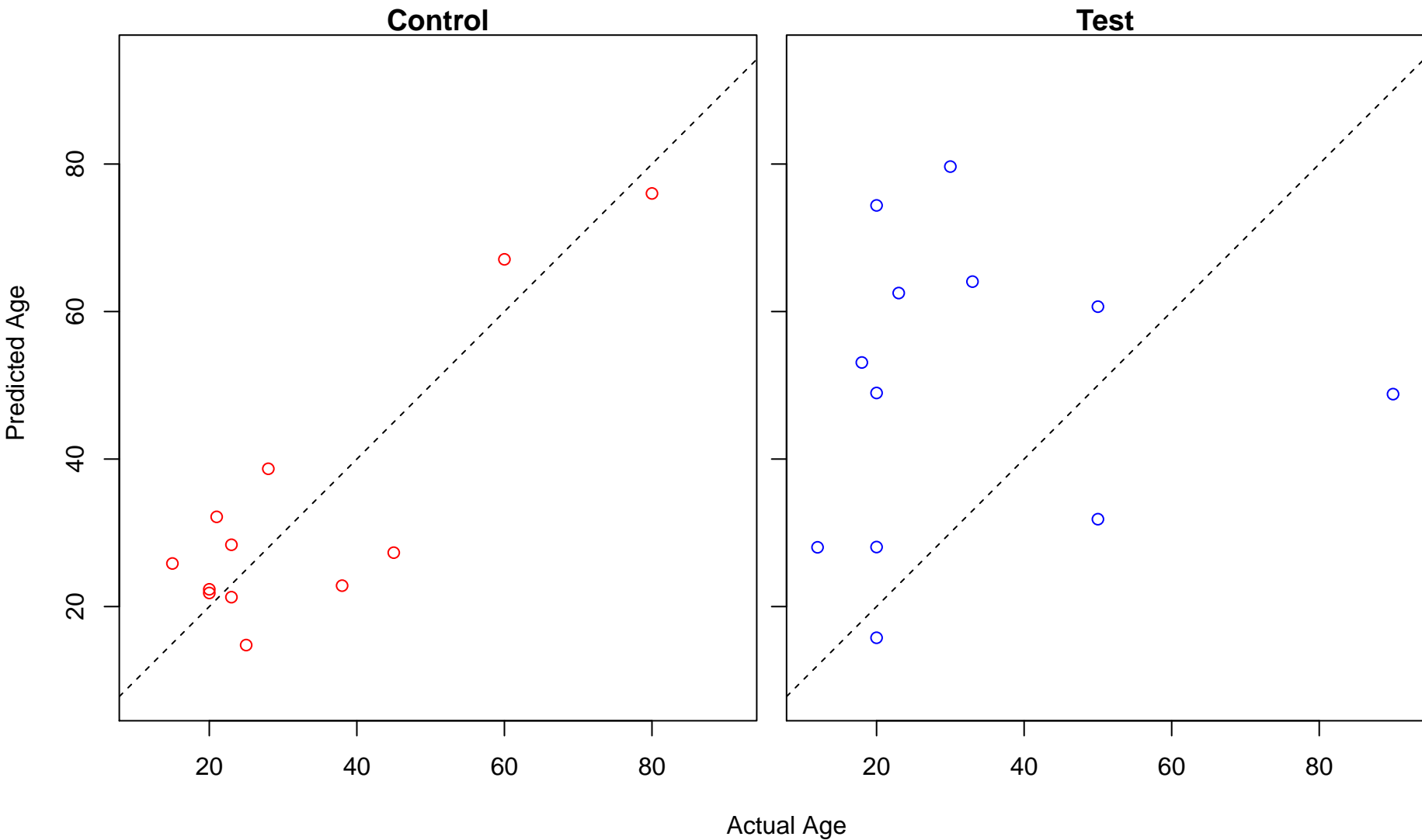
chromatin remodeling (Score: 6.501529)



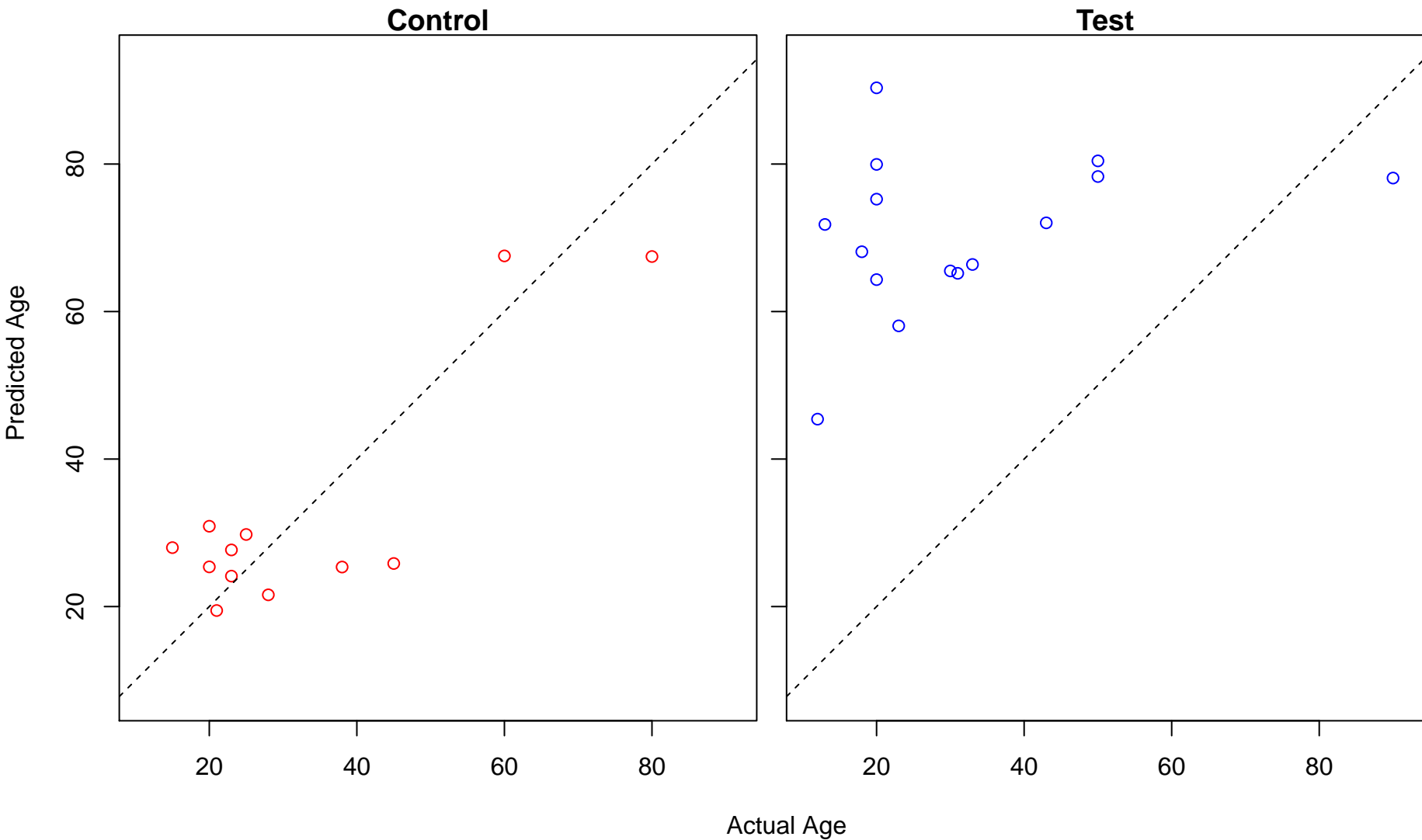
regulation of necrotic cell death (Score: 6.500884)



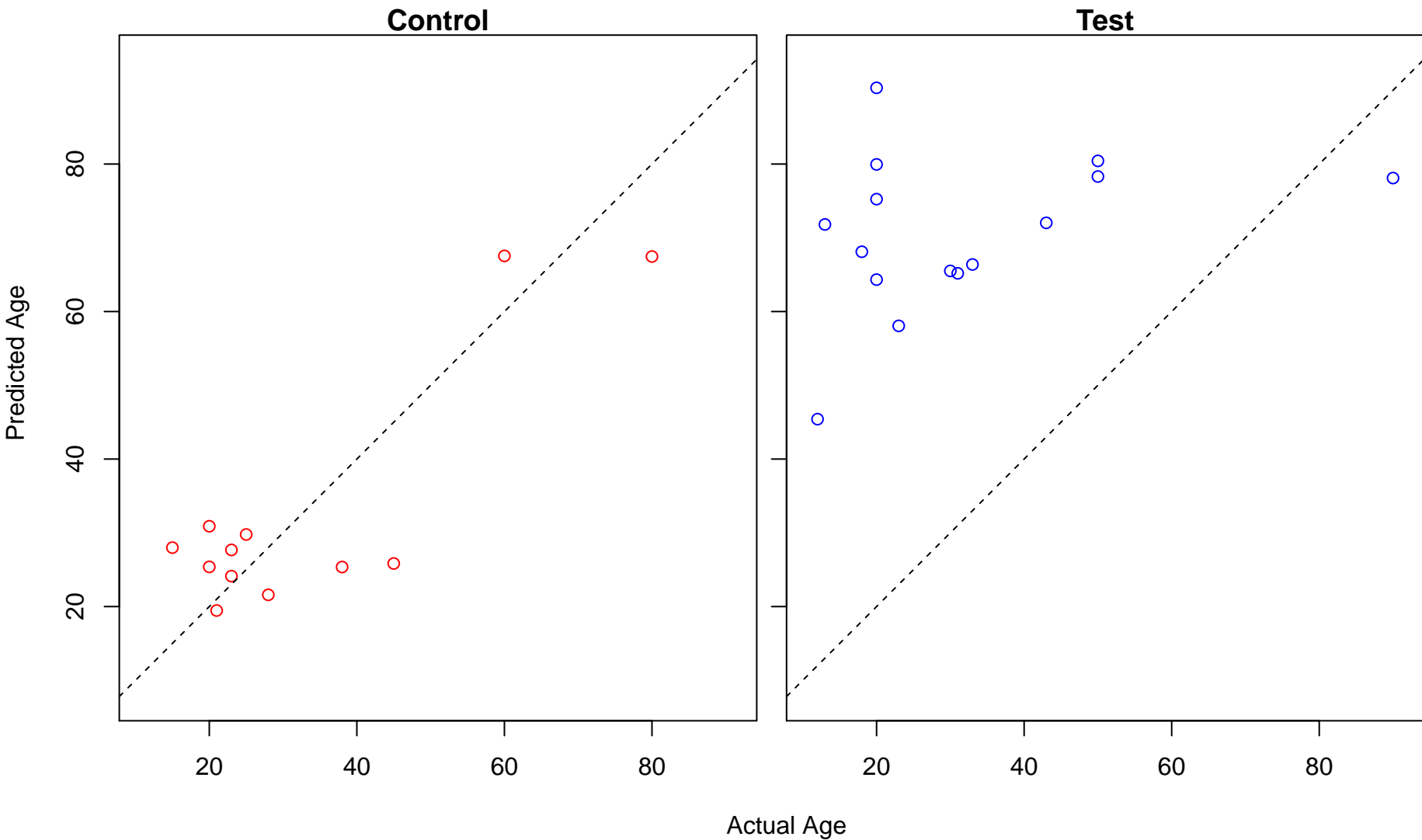
protein polymerization (Score: 6.499499)



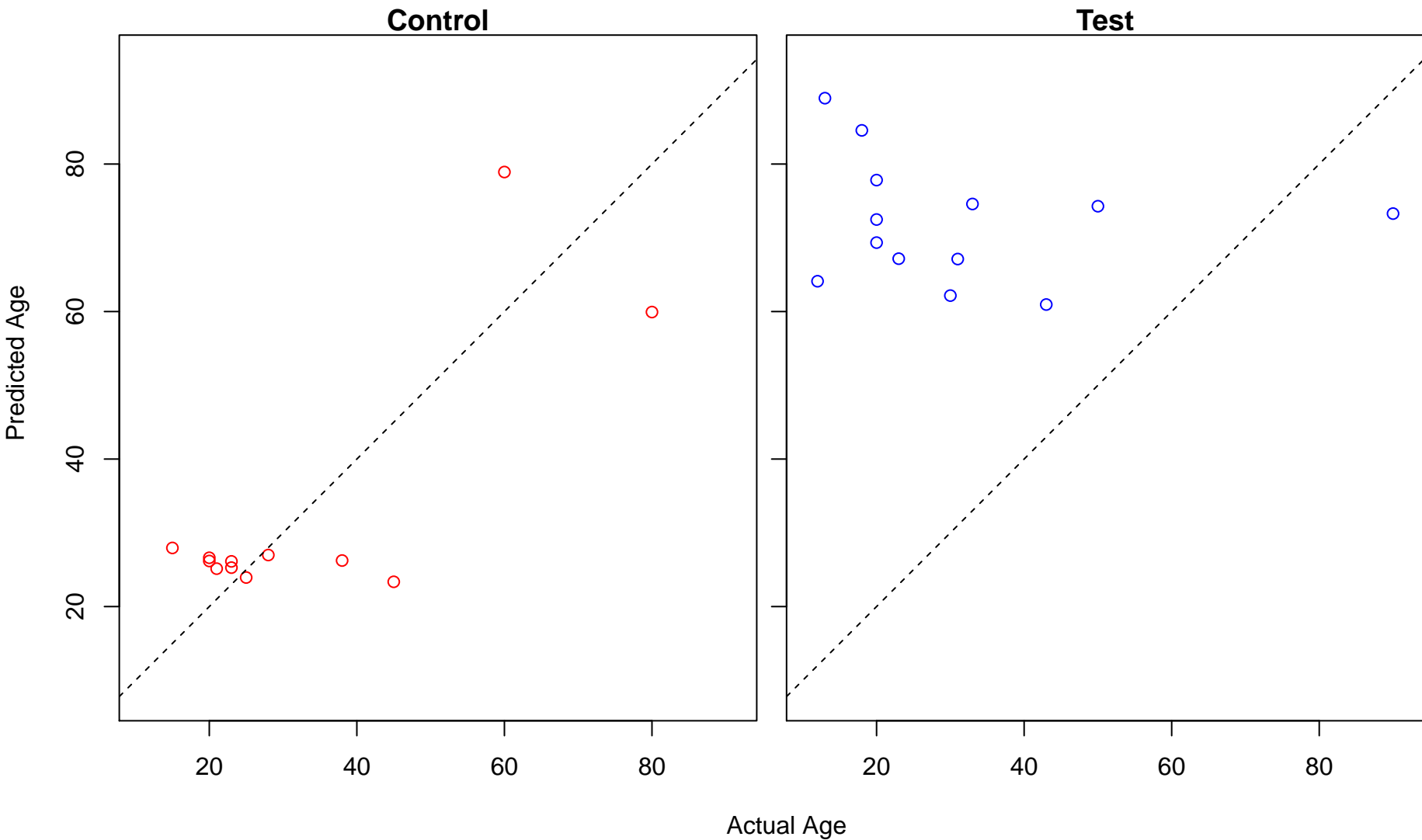
carnitine shuttle (Score: 6.497342)



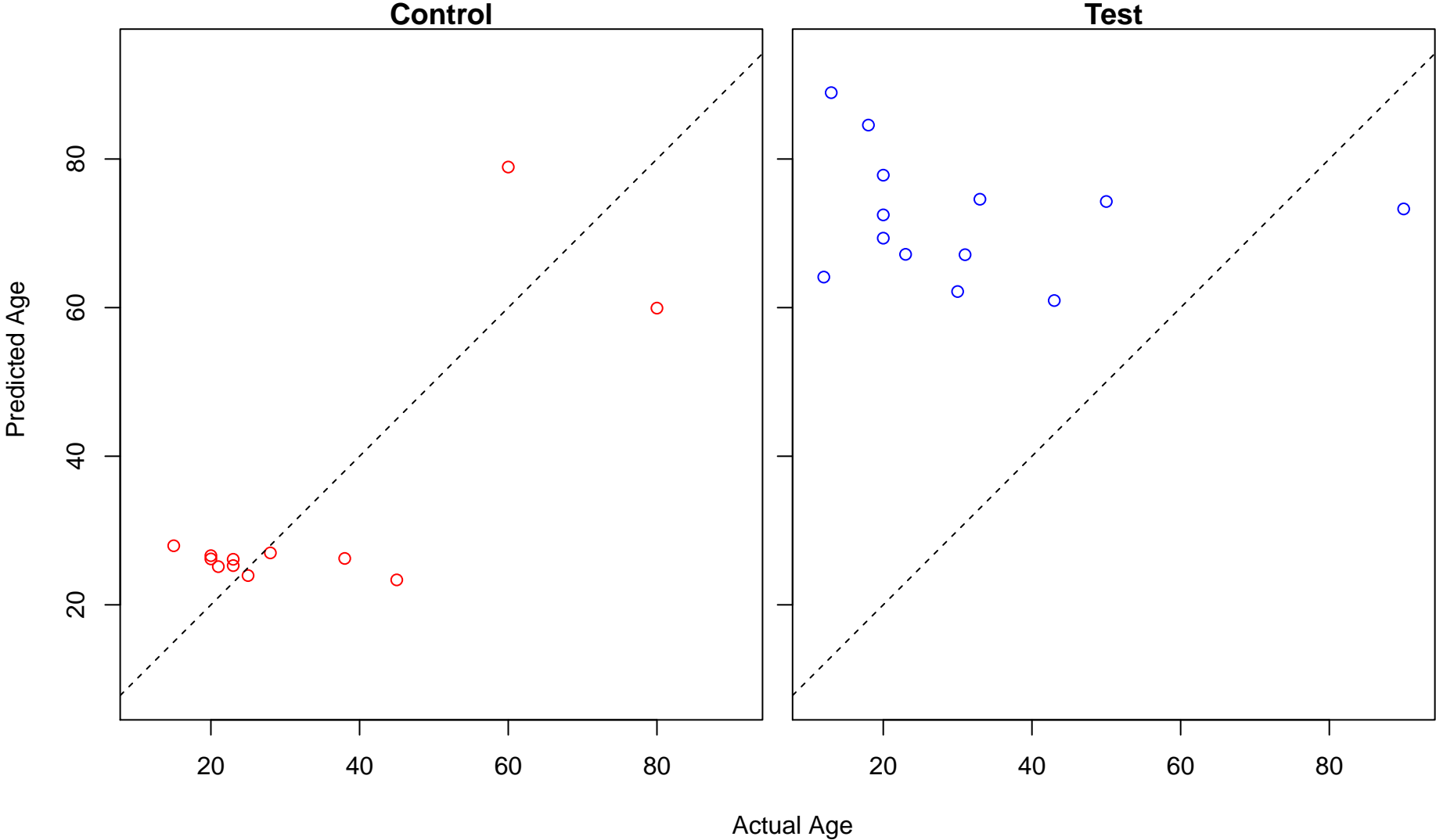
fatty acid transmembrane transport (Score: 6.497342)



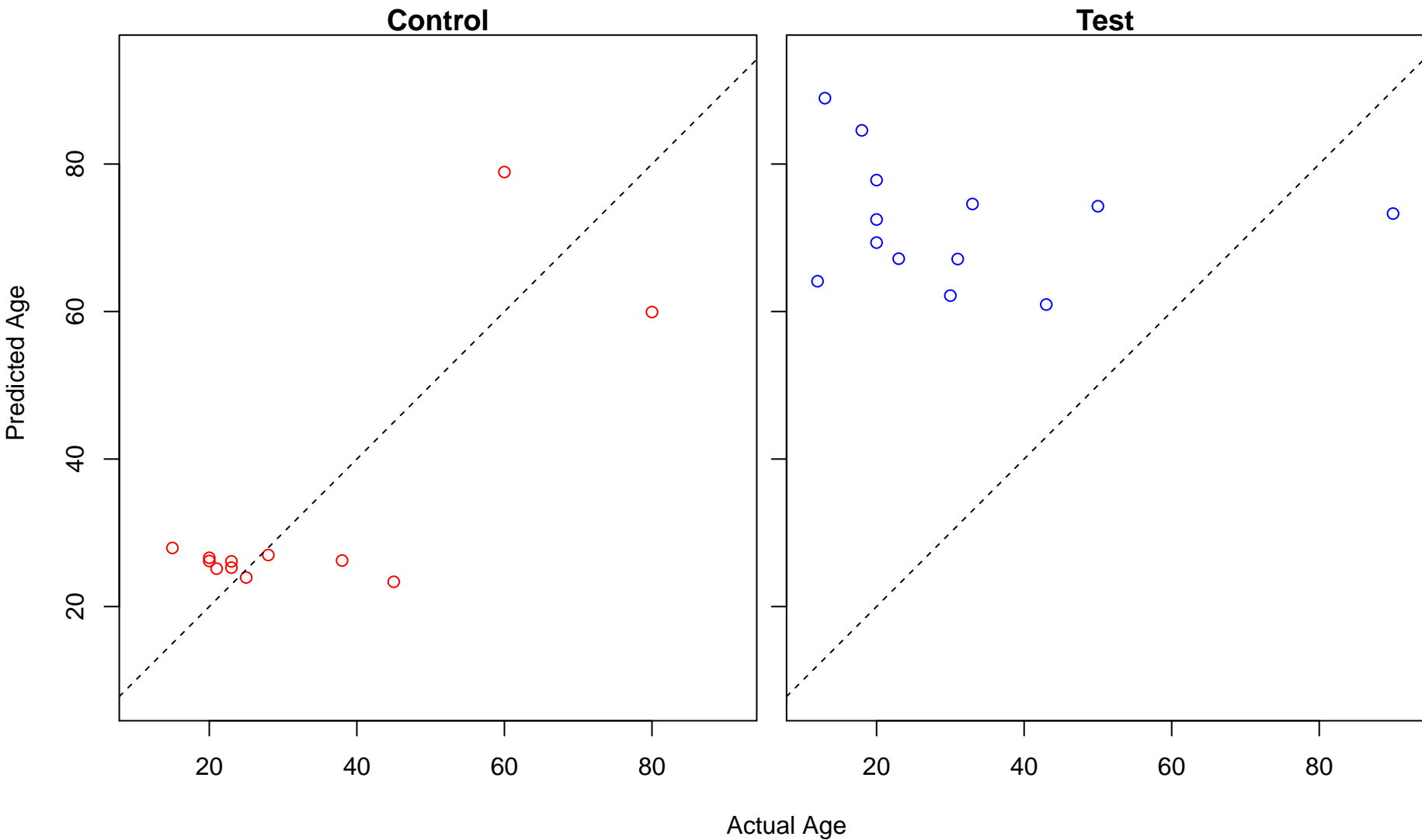
signal transduction involved in mitotic G1 DNA damage checkpoint (Score: 6.495805)



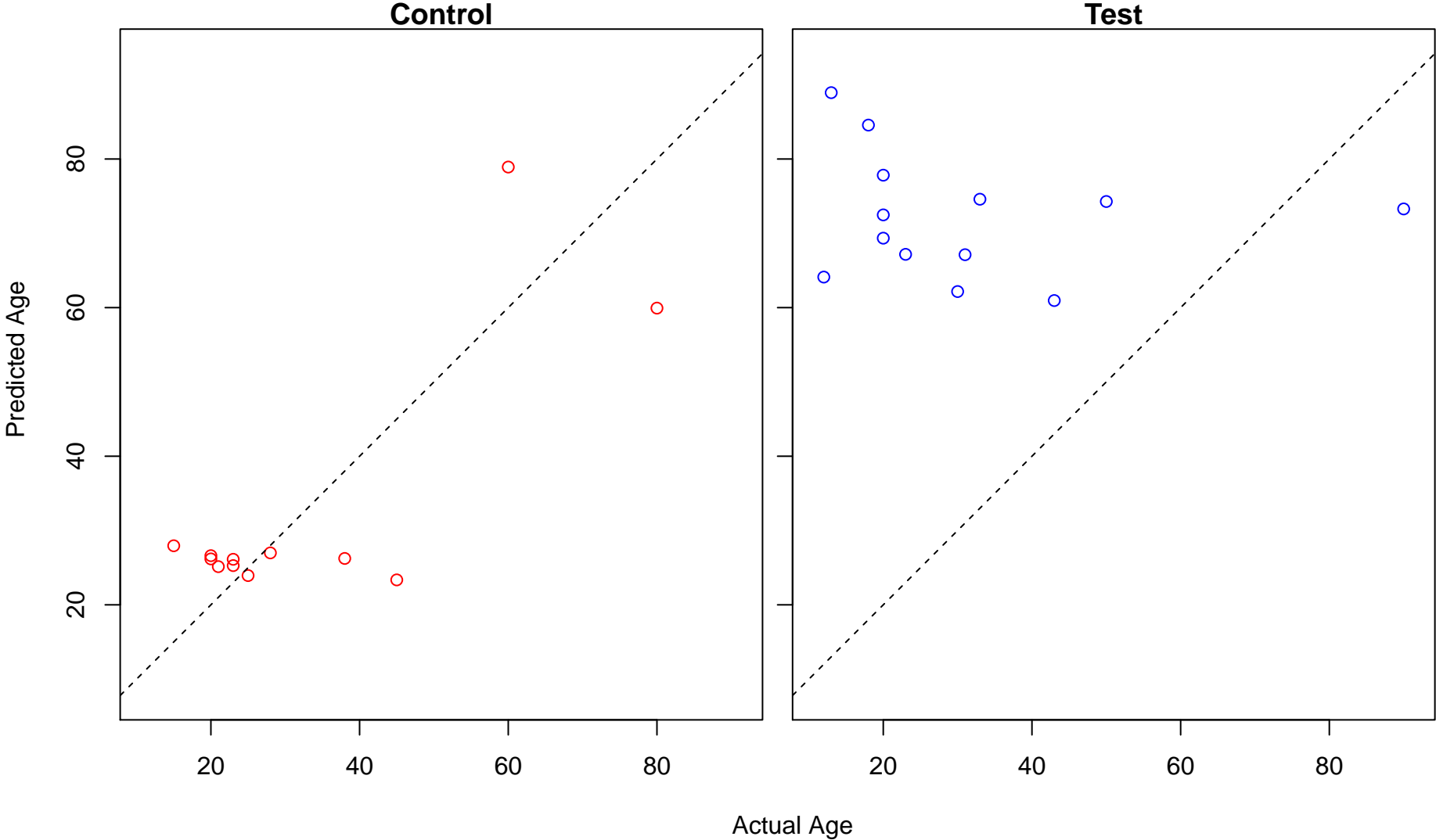
intracellular signal transduction involved in G1 DNA damage checkpoint (Score: 6.495805)



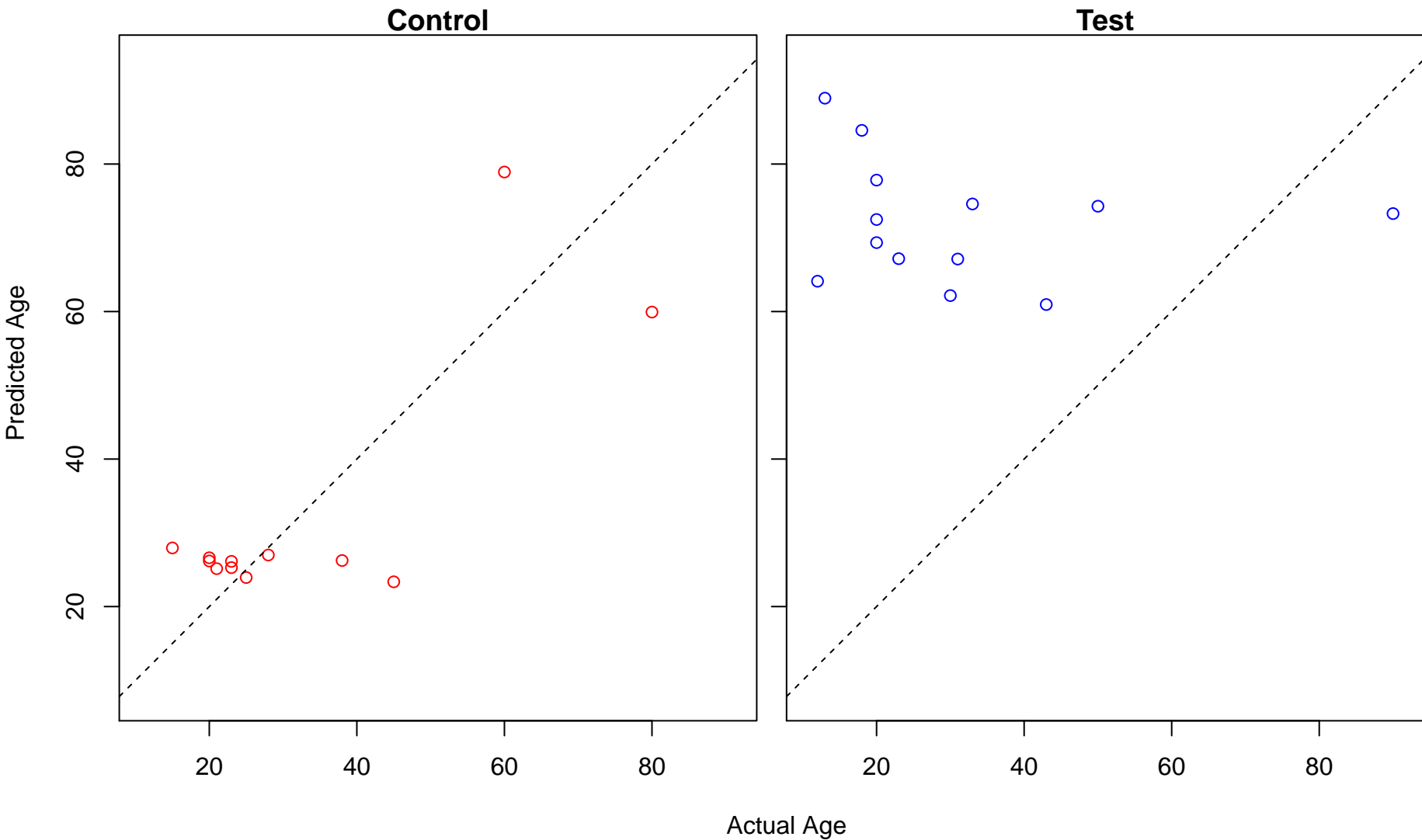
signal transduction involved in mitotic cell cycle checkpoint (Score: 6.495765)



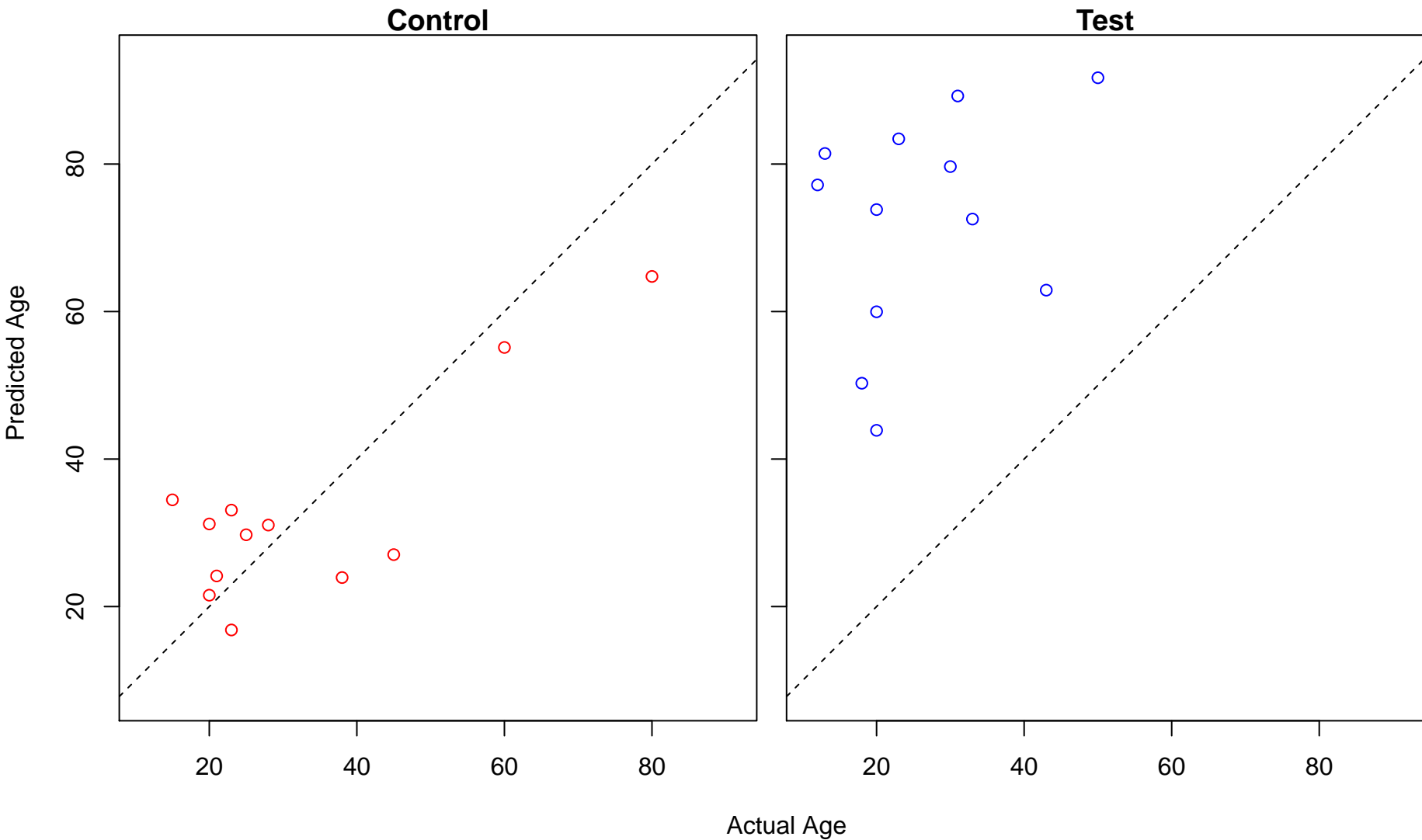
signal transduction involved in mitotic DNA damage checkpoint (Score: 6.495765)



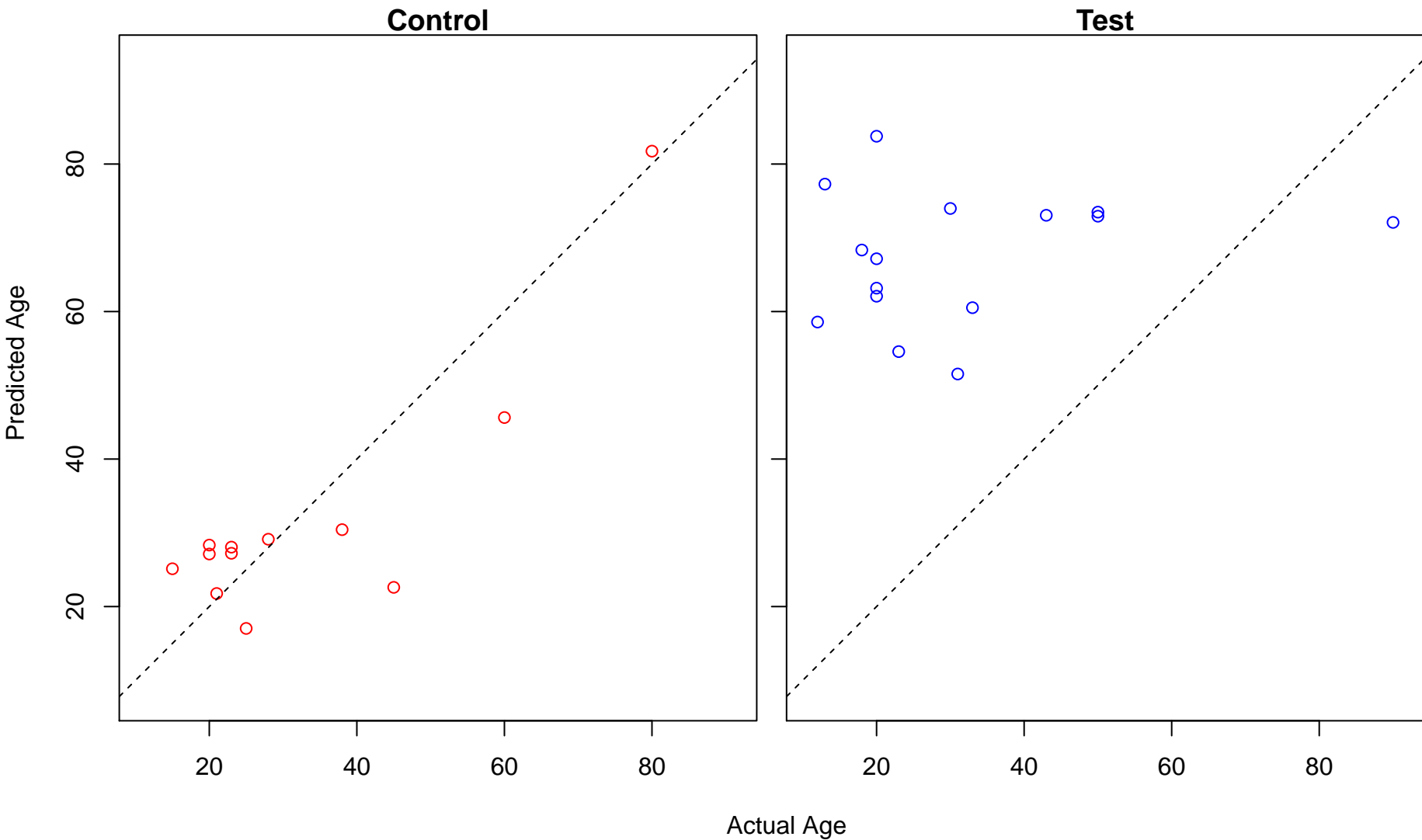
signal transduction involved in mitotic DNA integrity checkpoint (Score: 6.495765)



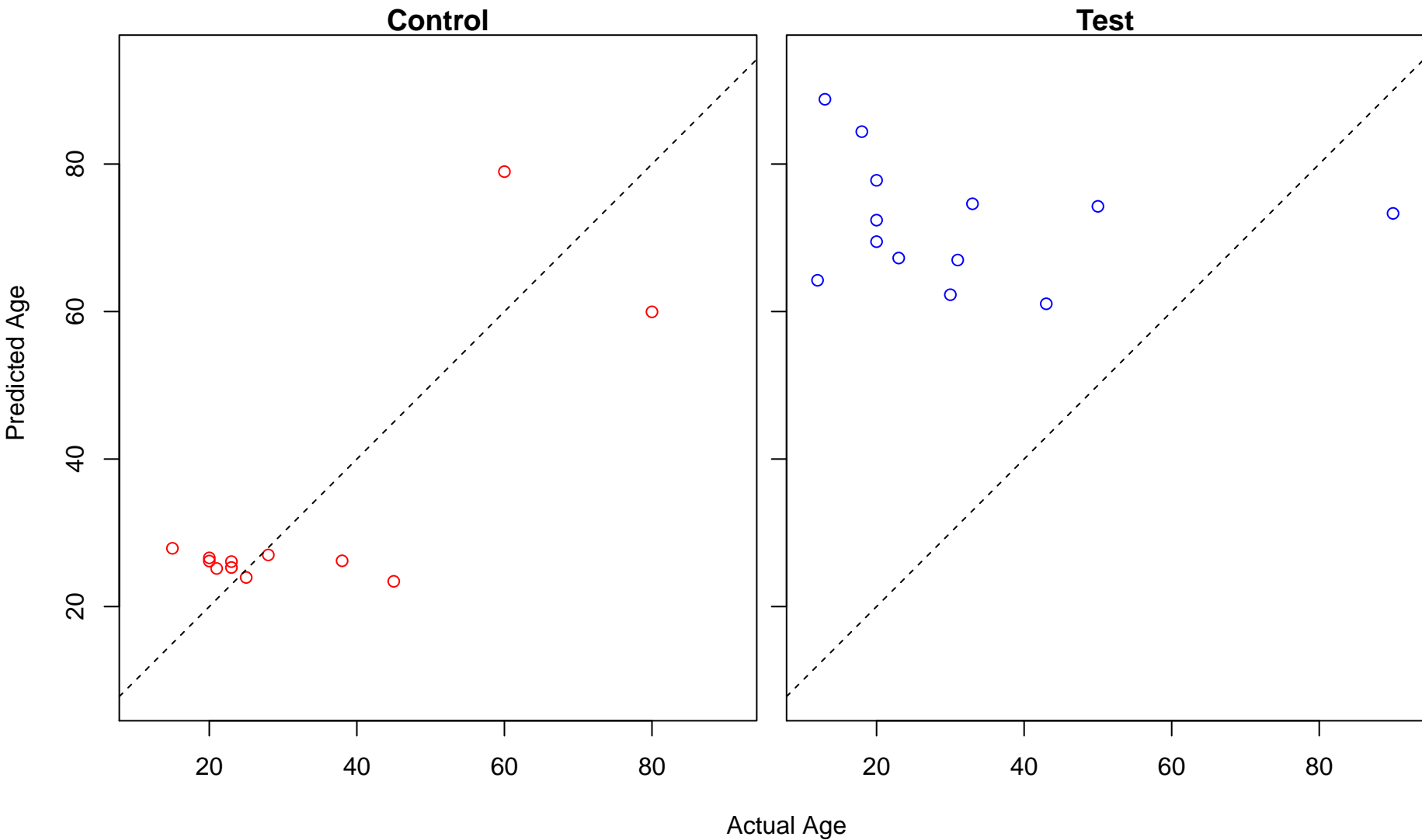
regulation of positive chemotaxis (Score: 6.494154)



adult behavior (Score: 6.493895)

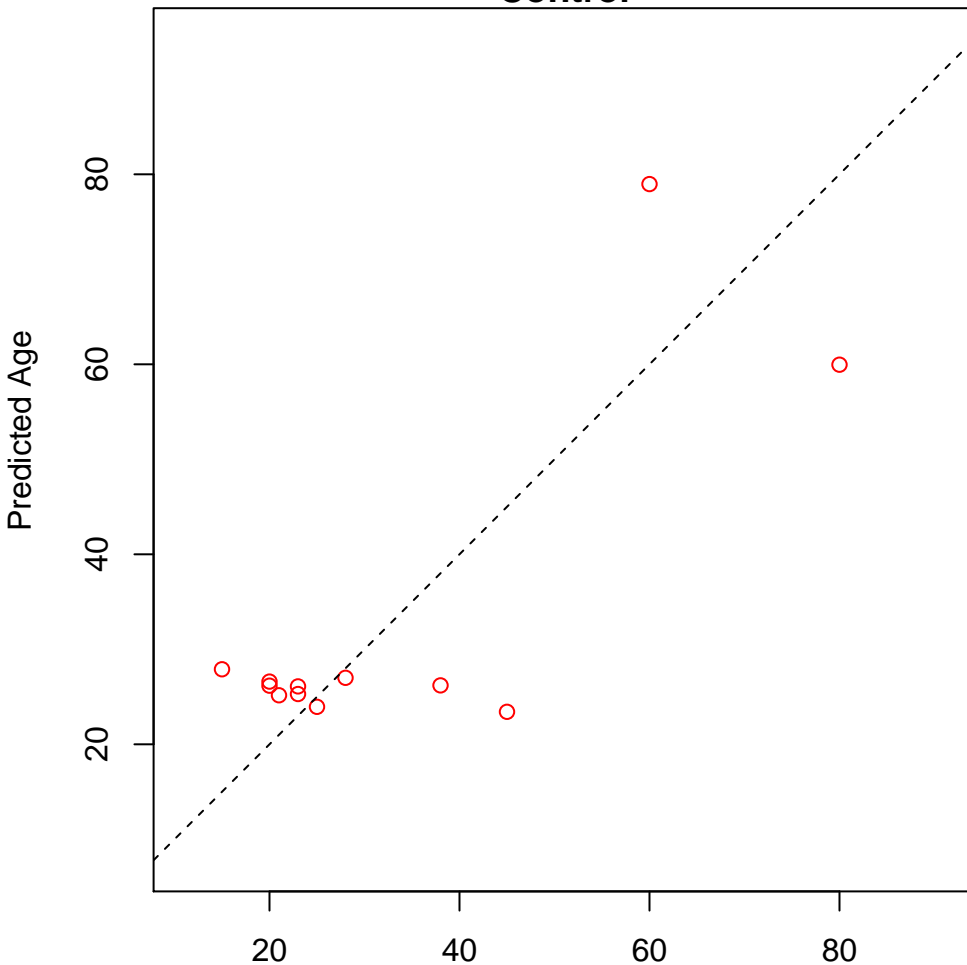


mitotic G1/S transition checkpoint (Score: 6.492273)

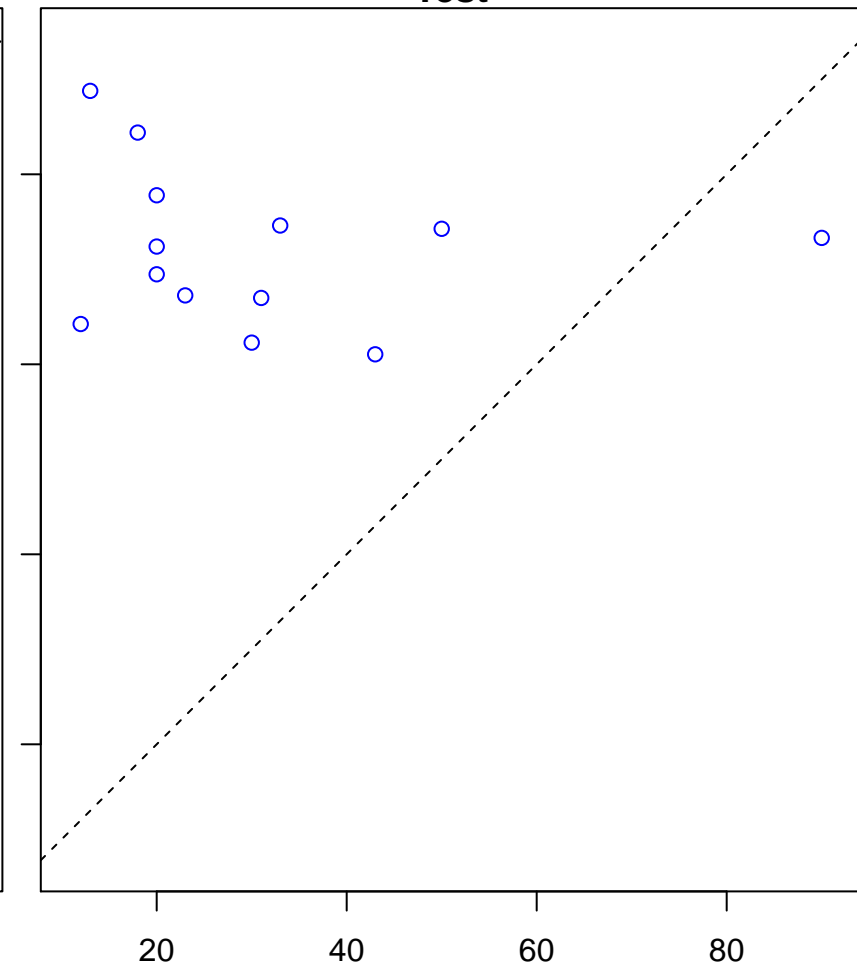


mitotic G1 DNA damage checkpoint (Score: 6.492264)

Control

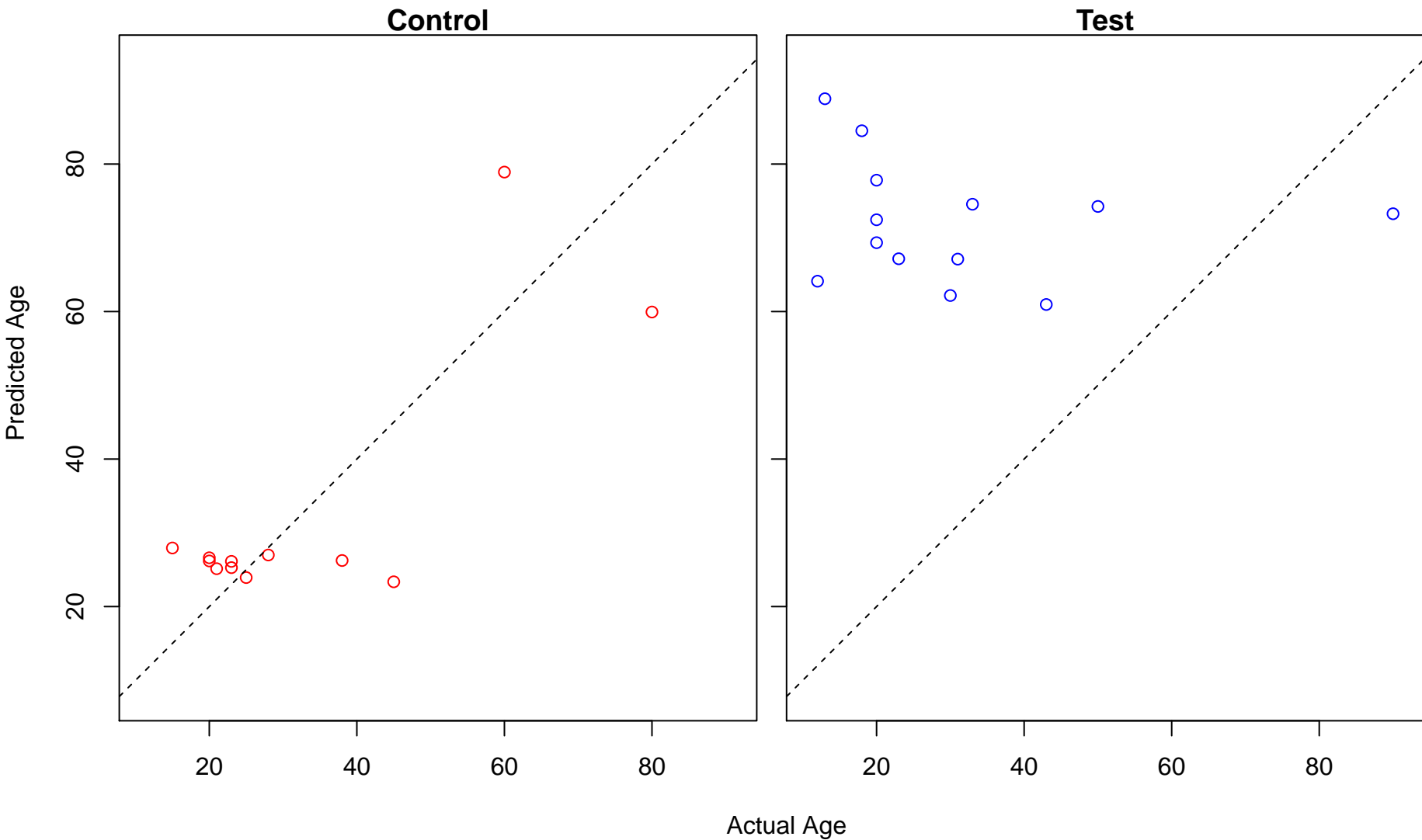


Test

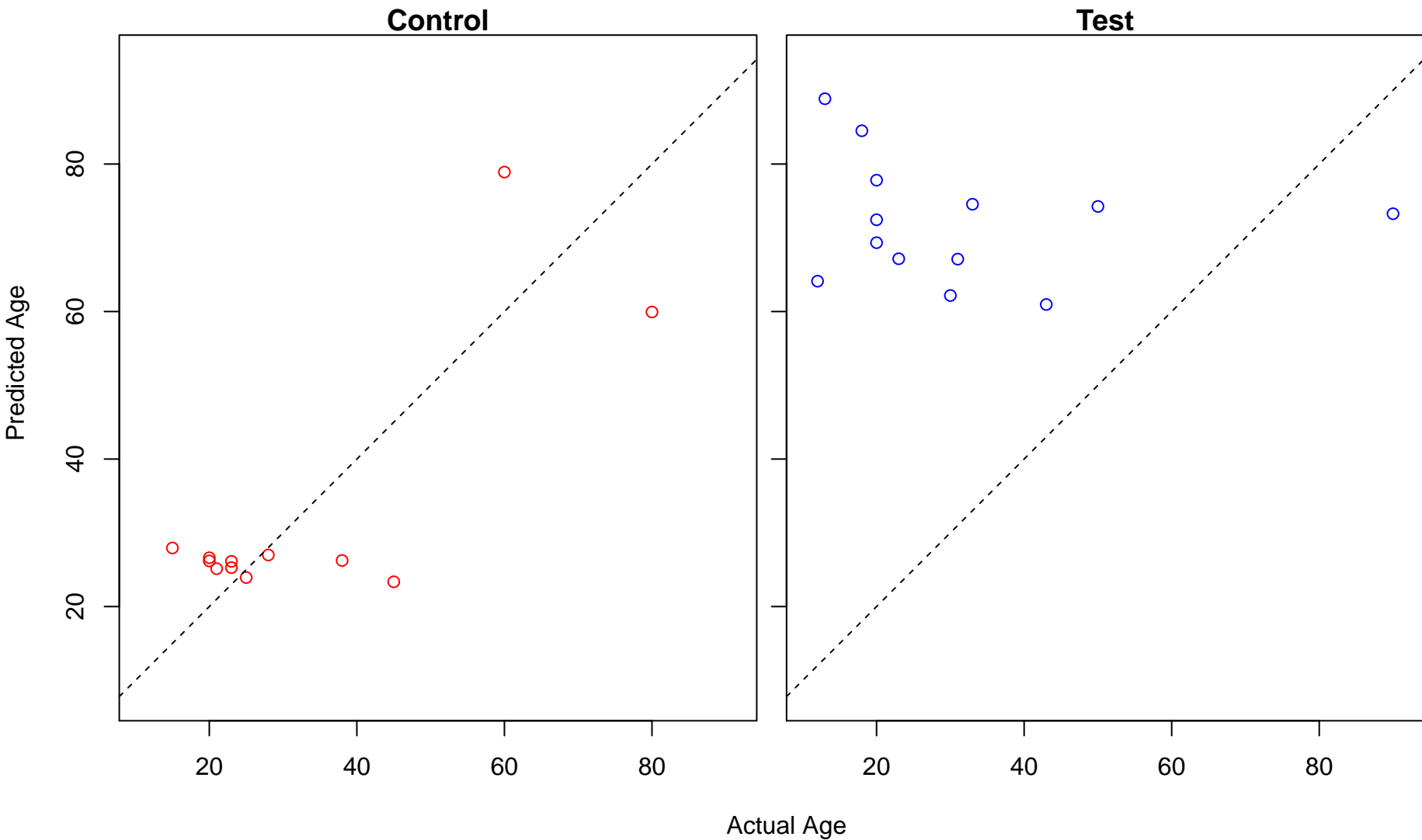


Actual Age

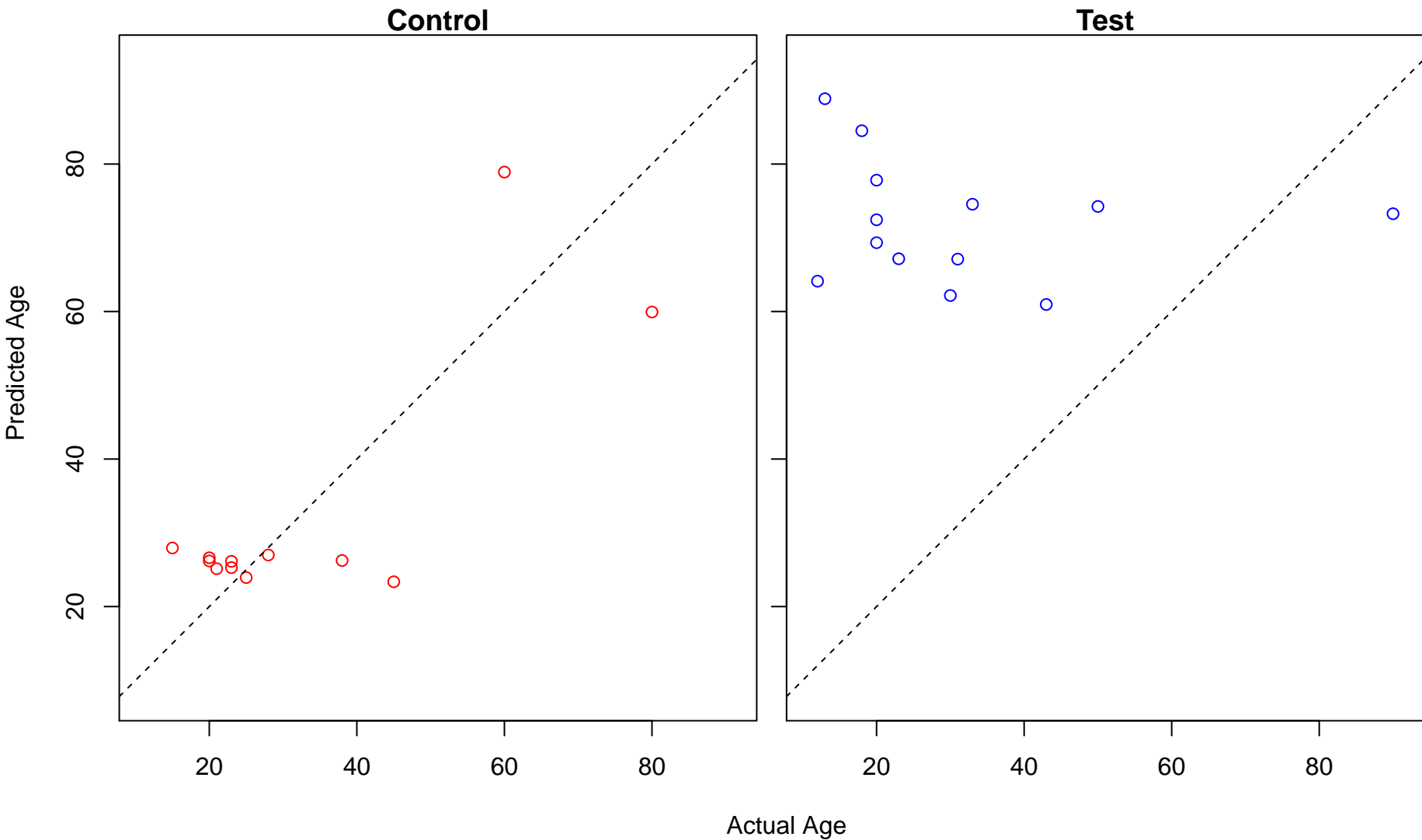
signal transduction involved in cell cycle checkpoint (Score: 6.490641)



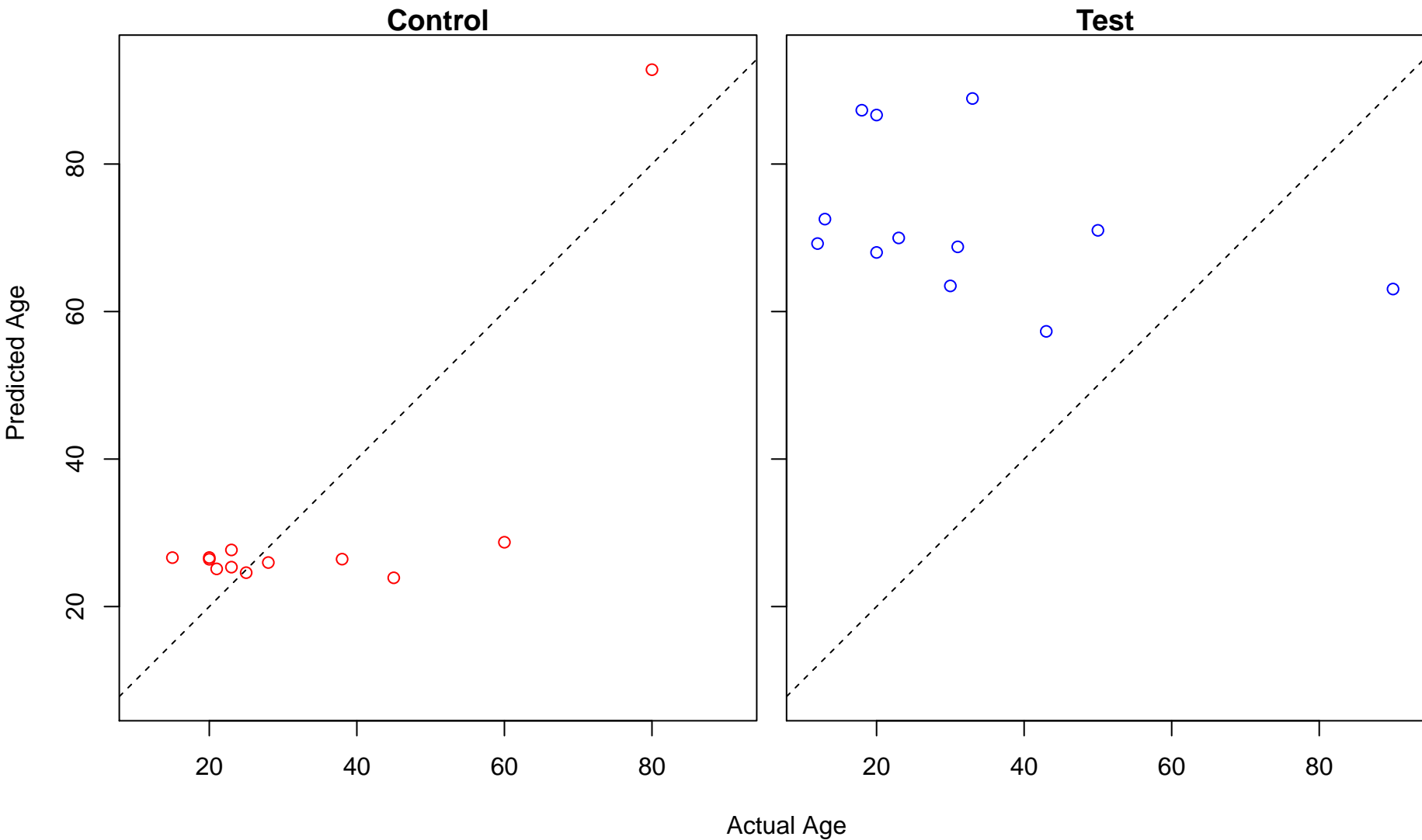
signal transduction involved in DNA integrity checkpoint (Score: 6.490640)



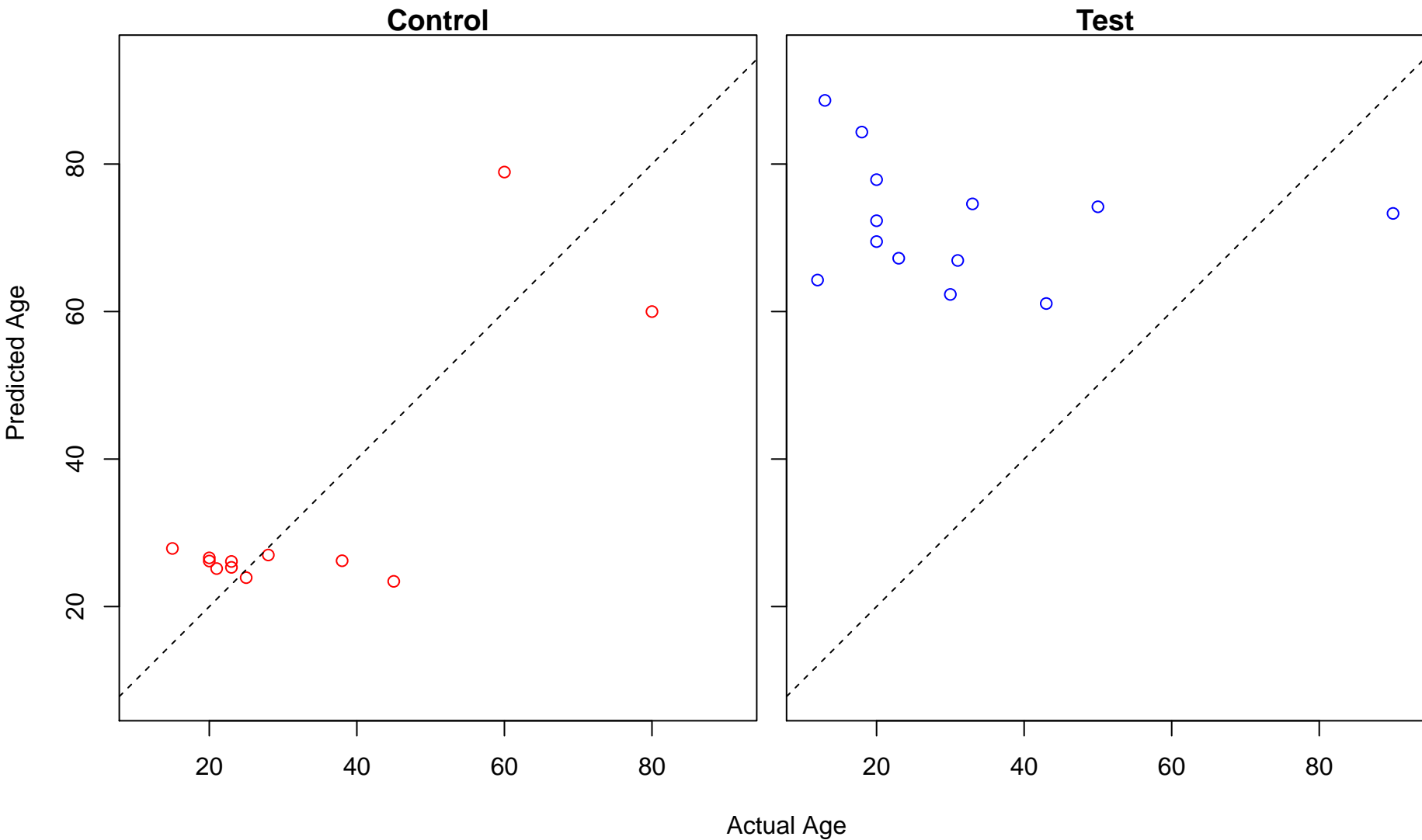
signal transduction involved in DNA damage checkpoint (Score: 6.490640)



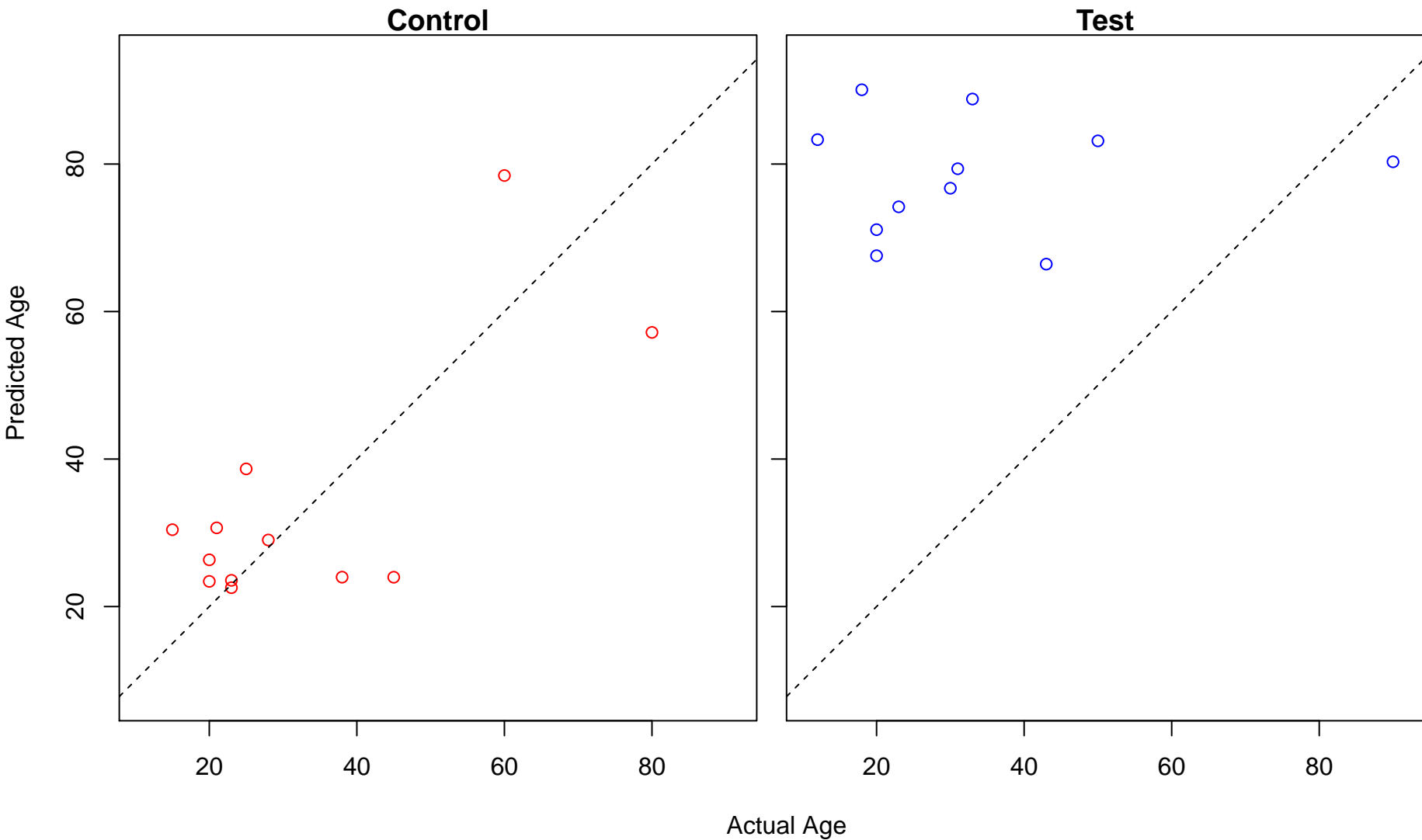
positive regulation of exocytosis (Score: 6.490460)



G1 DNA damage checkpoint (Score: 6.490291)

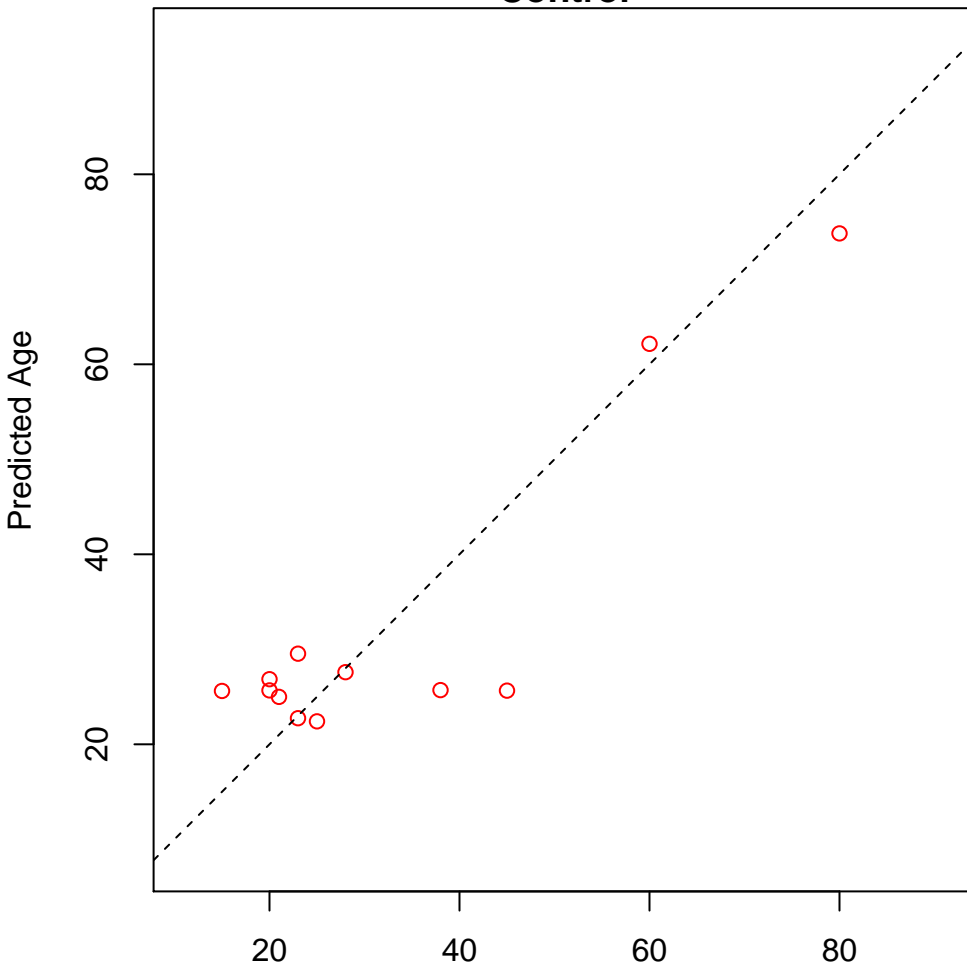


positive regulation of lymphocyte apoptotic process (Score: 6.487897)

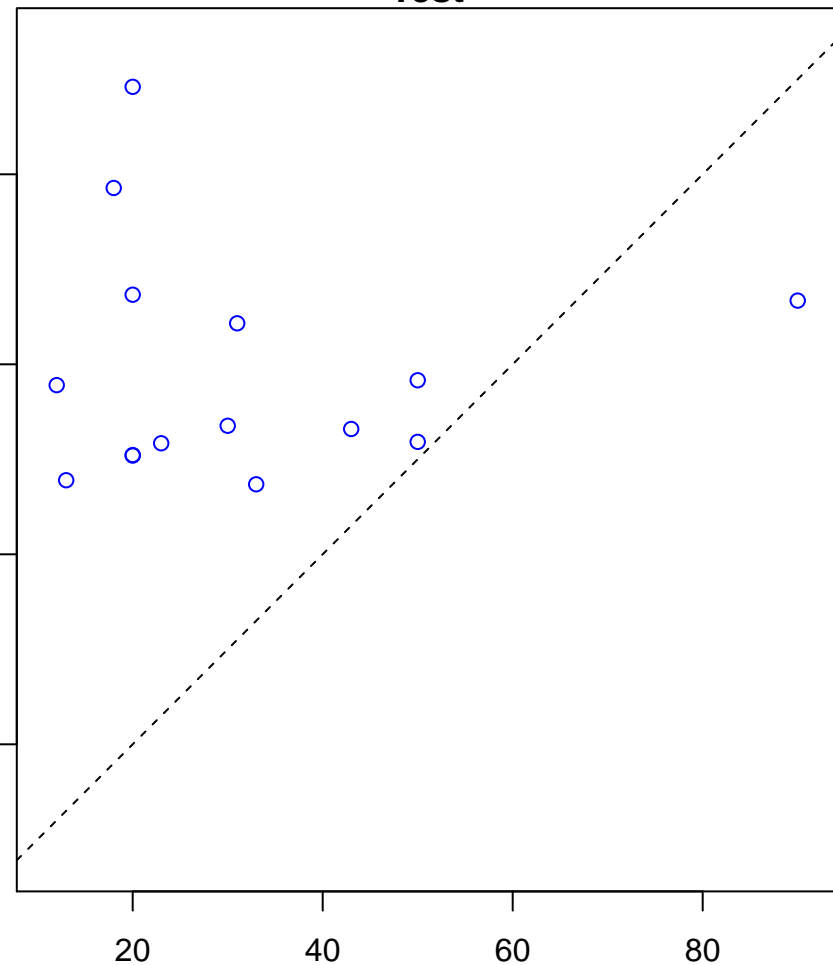


circadian regulation of gene expression (Score: 6.487416)

Control

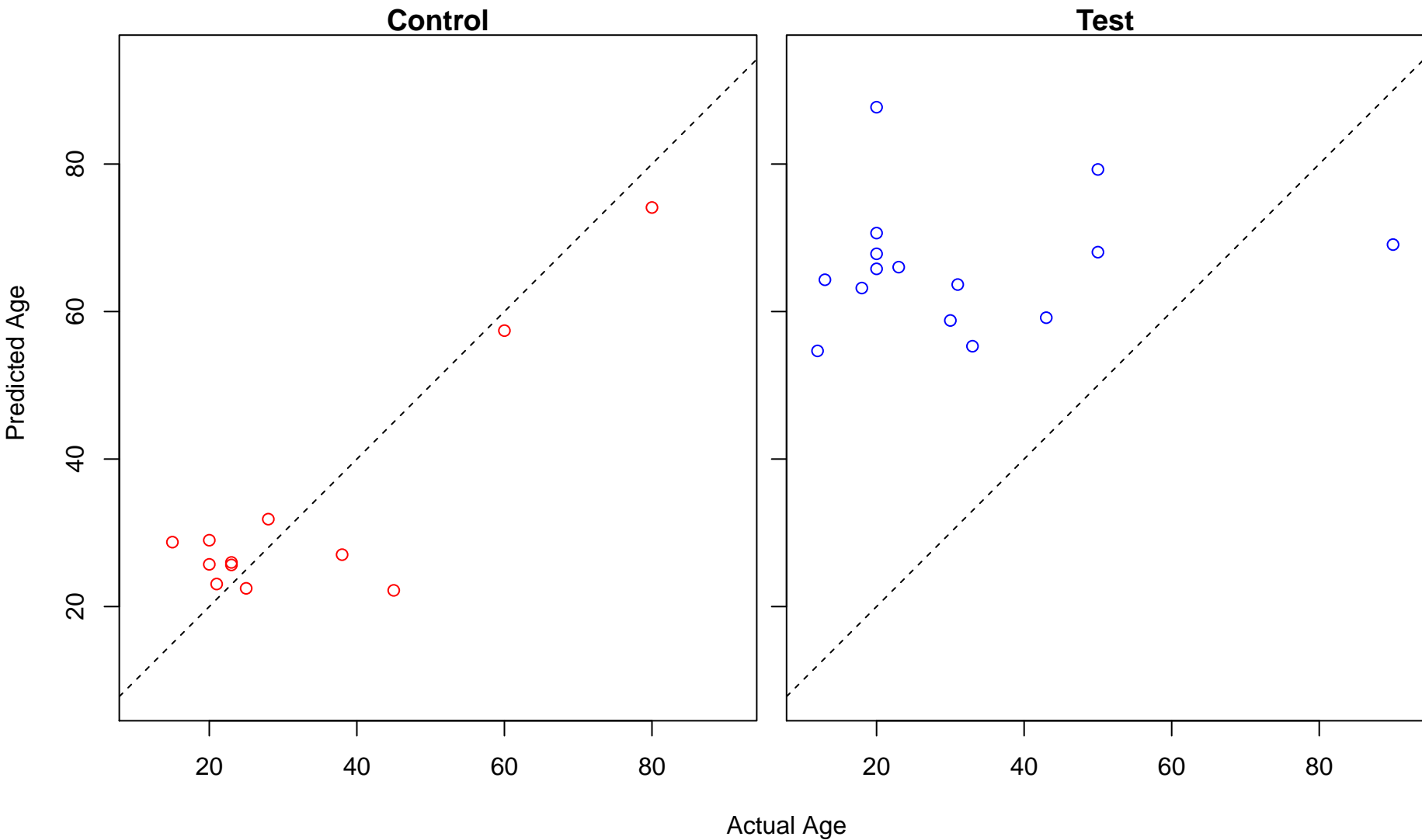


Test

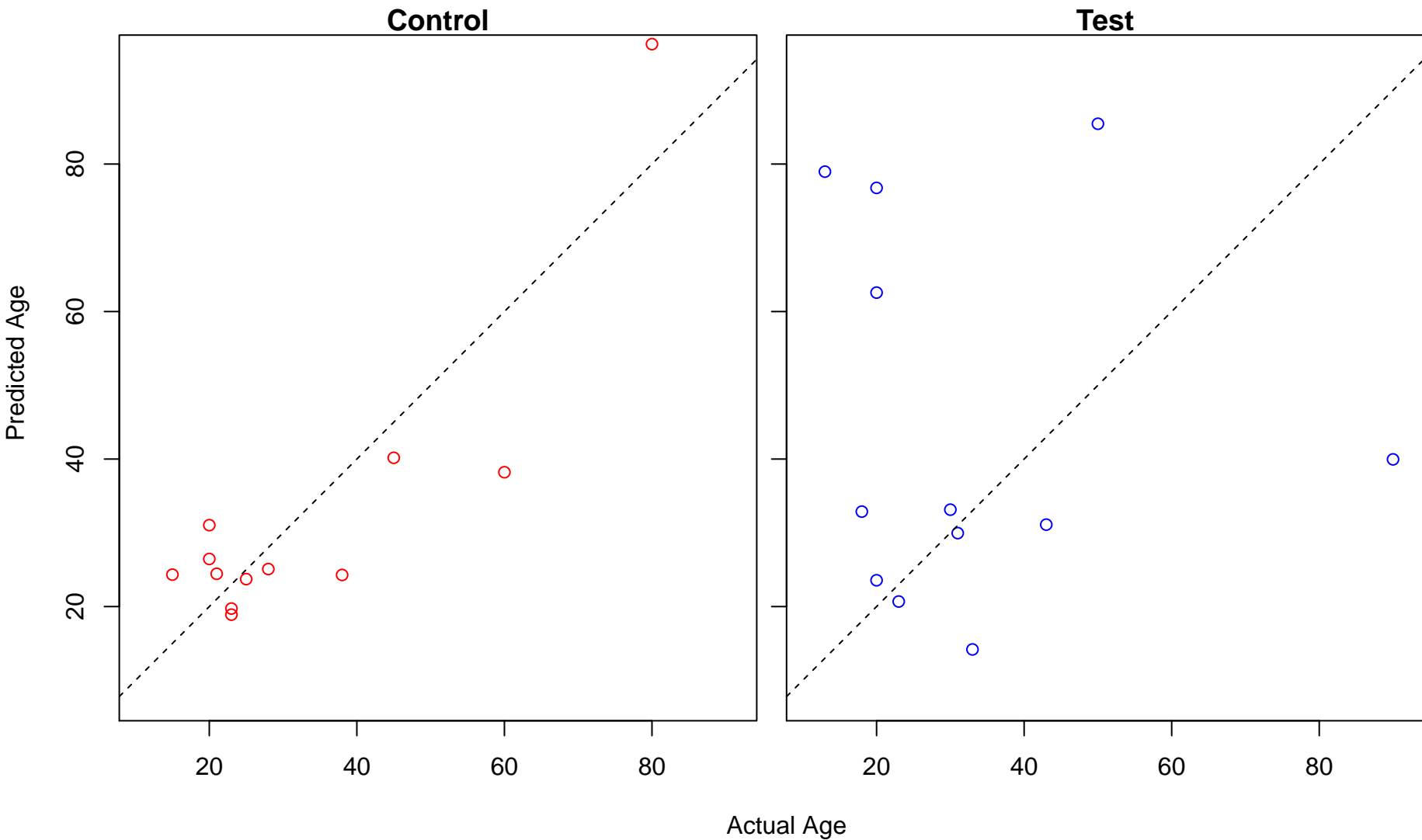


Actual Age

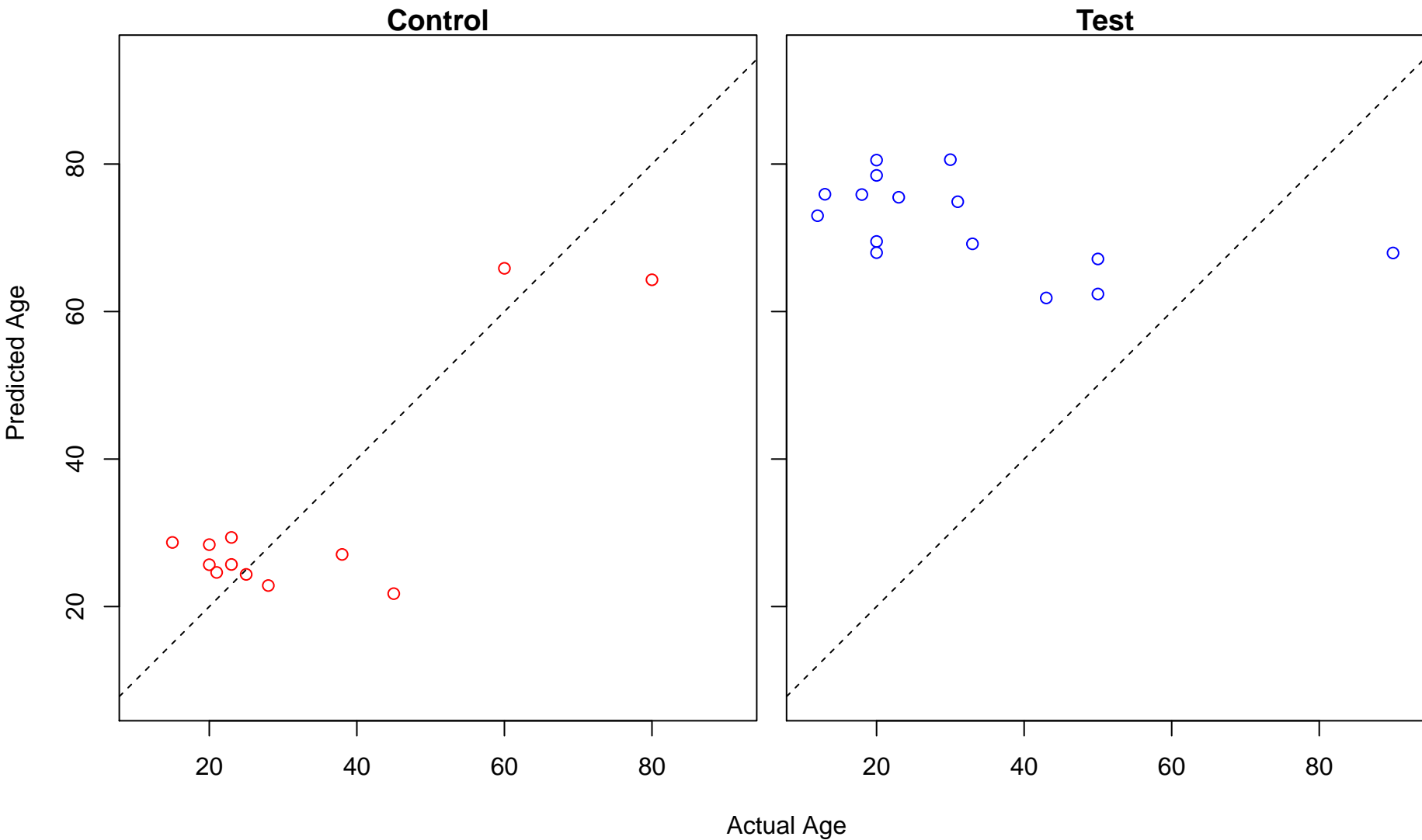
regulation of secretion by cell (Score: 6.487240)



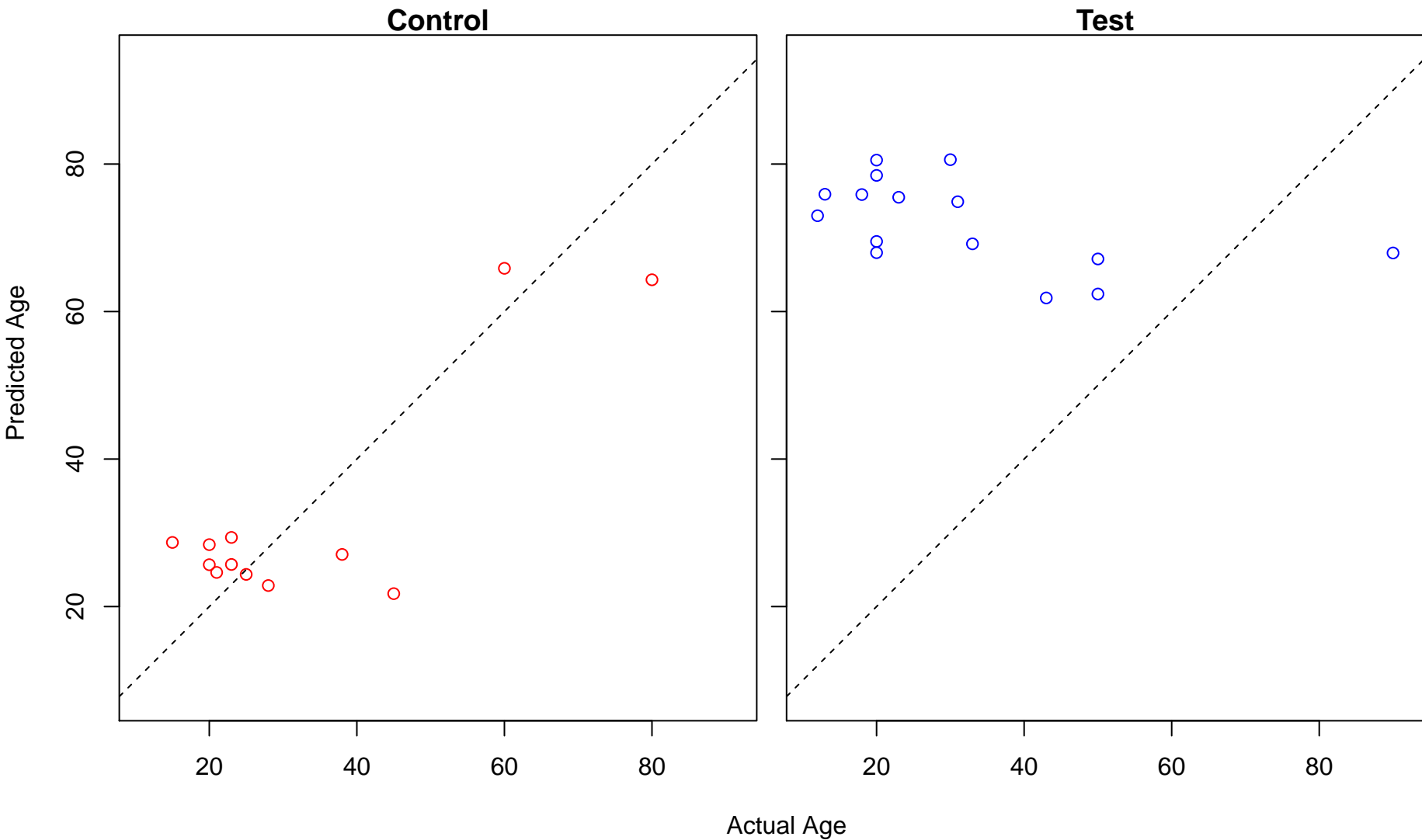
vocalization behavior (Score: 6.485995)



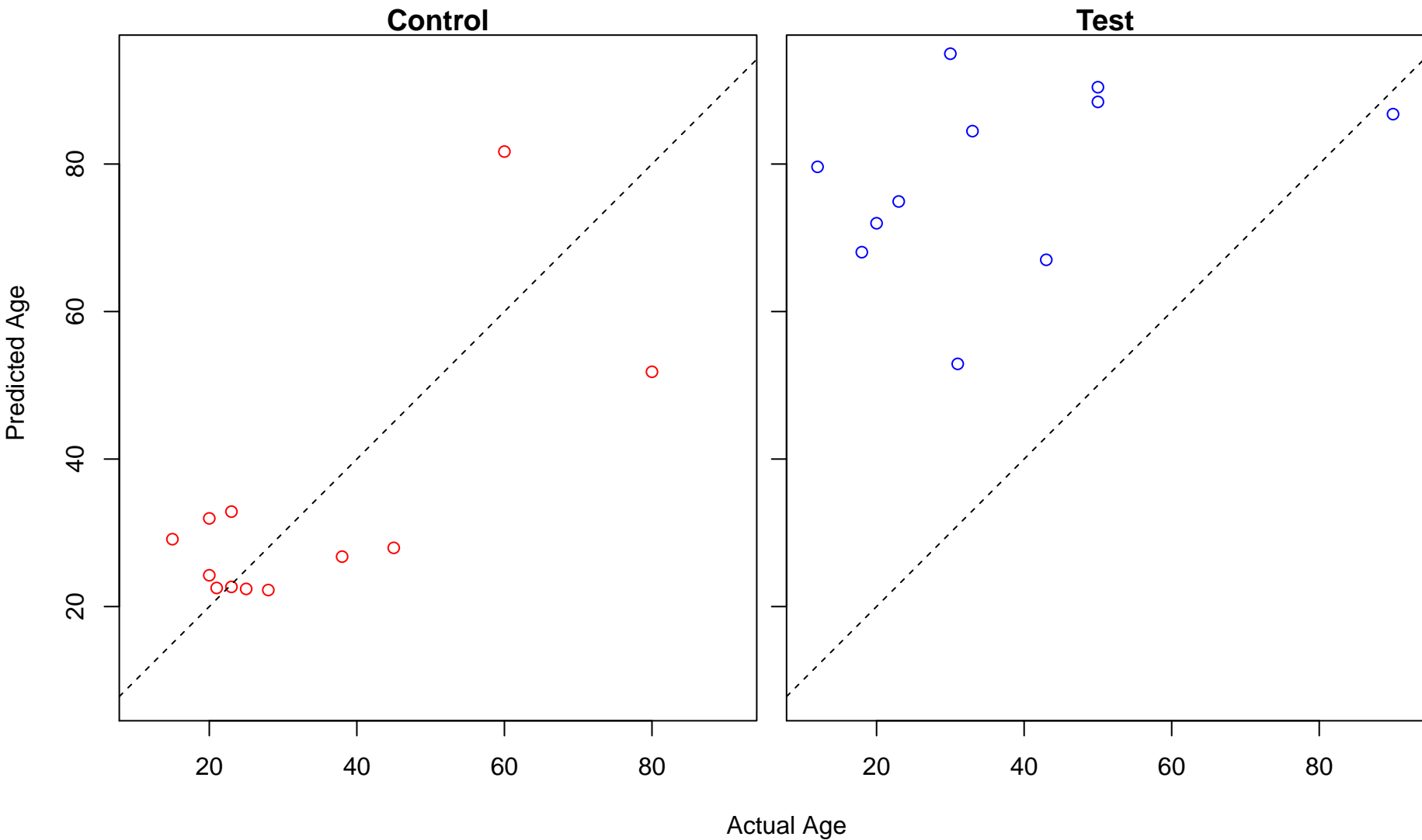
JAK-STAT cascade (Score: 6.481698)



STAT cascade (Score: 6.481698)

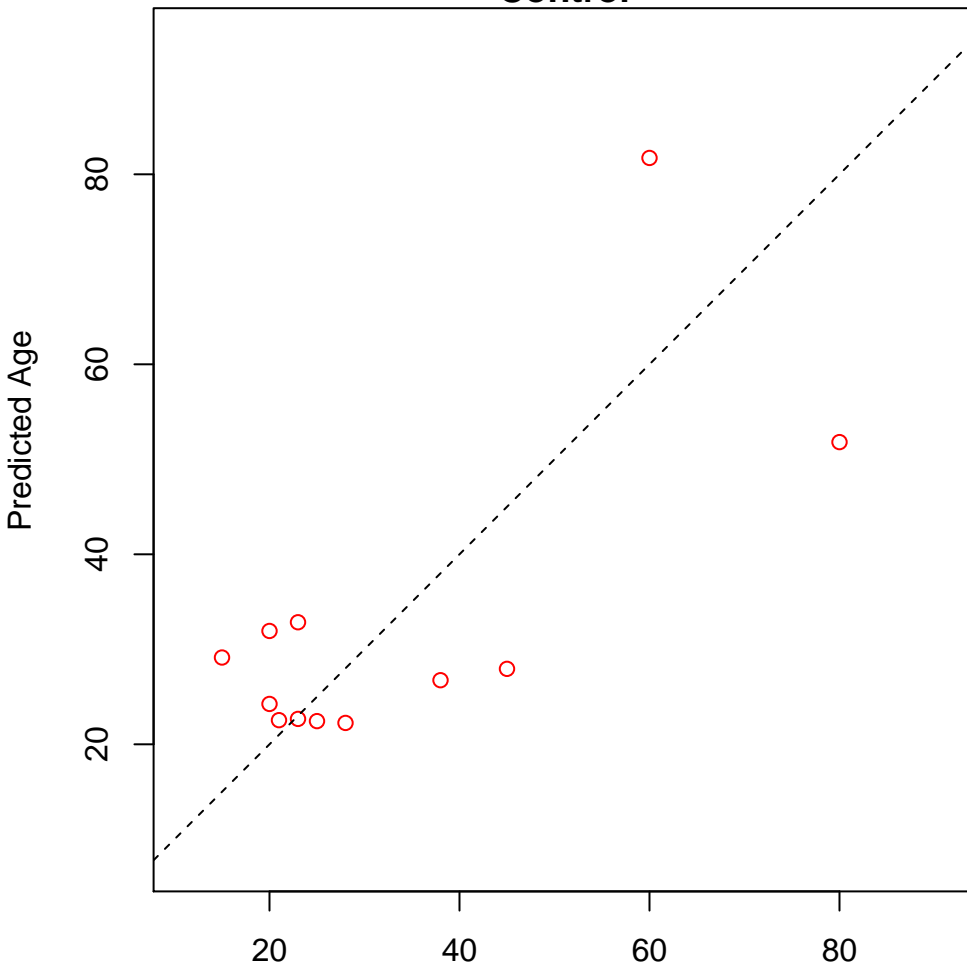


positive regulation of endothelial cell chemotaxis (Score: 6.480996)

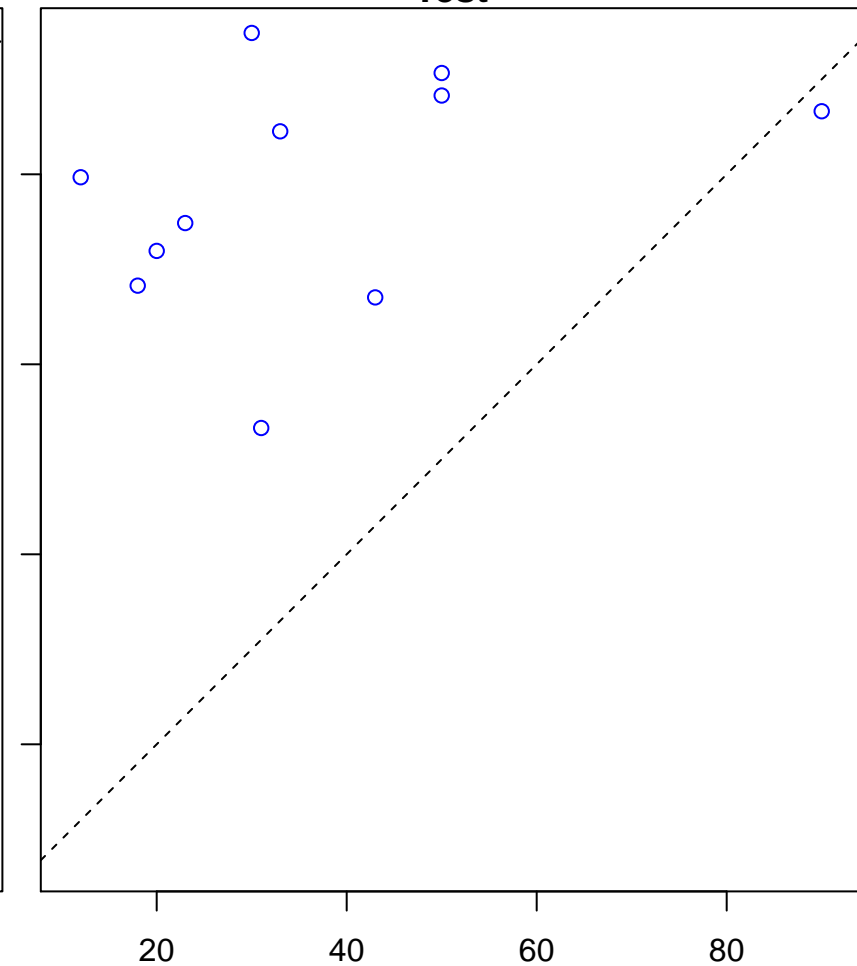


regulation of endothelial cell chemotaxis (Score: 6.480980)

Control

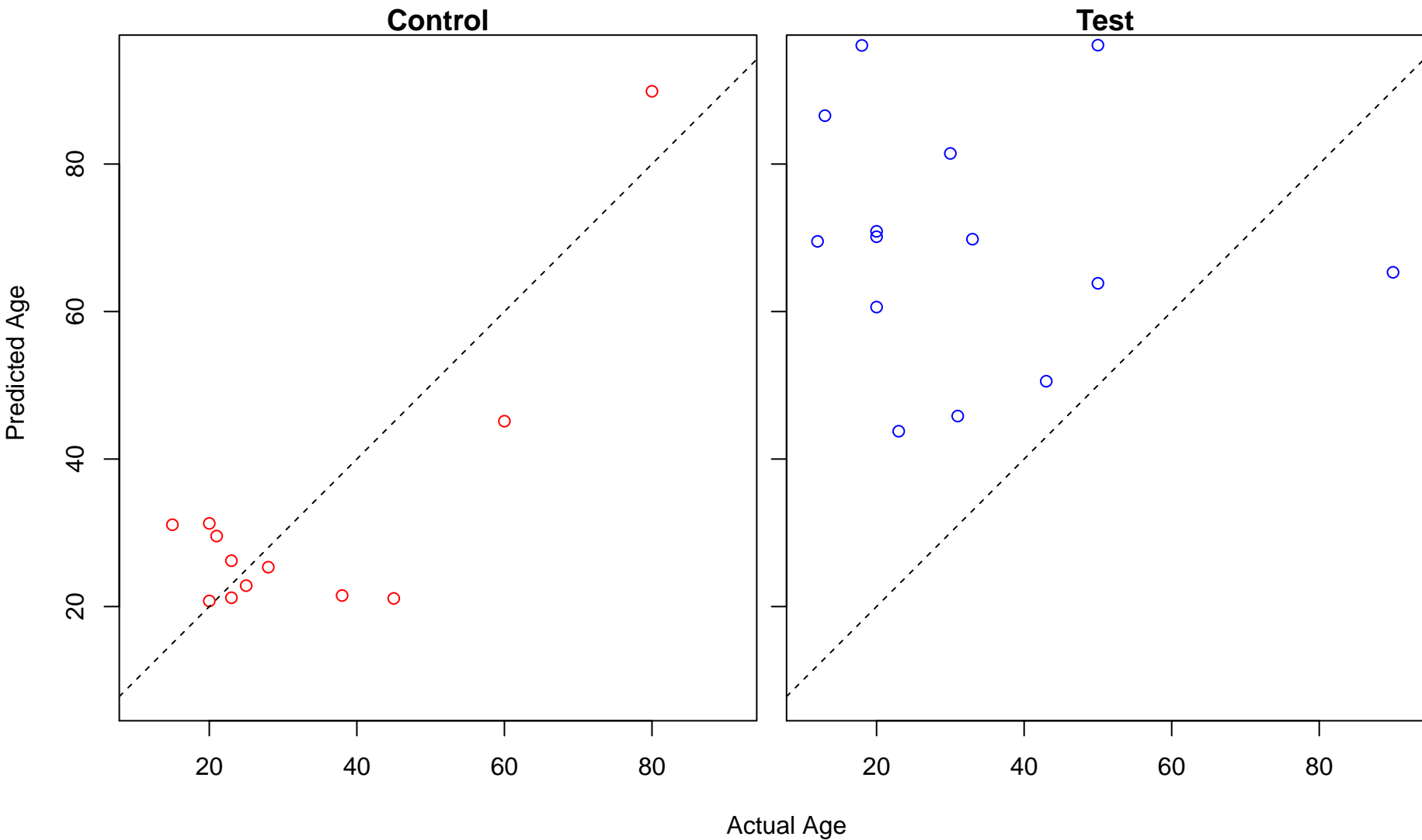


Test

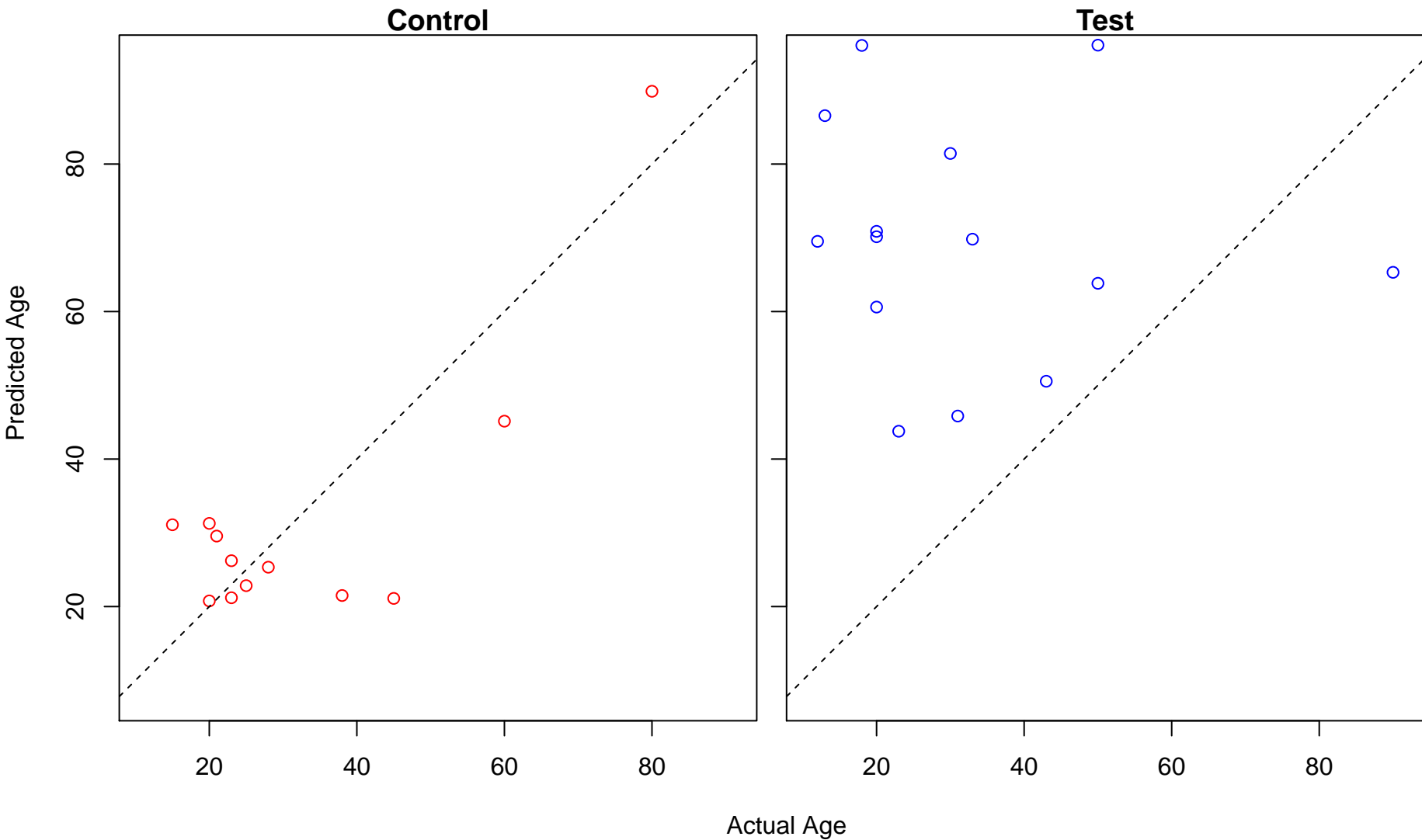


Actual Age

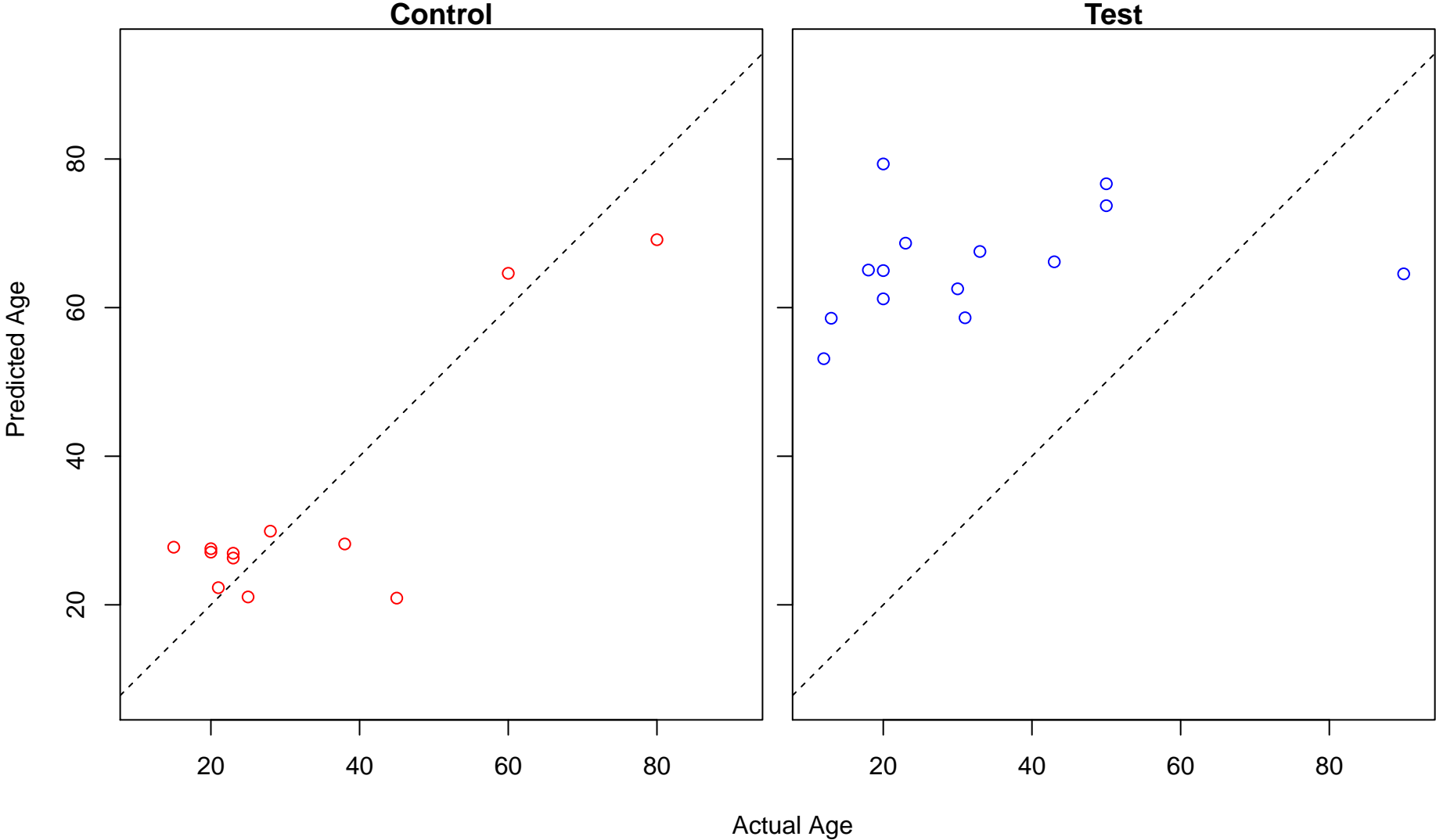
protein glycosylation (Score: 6.479953)



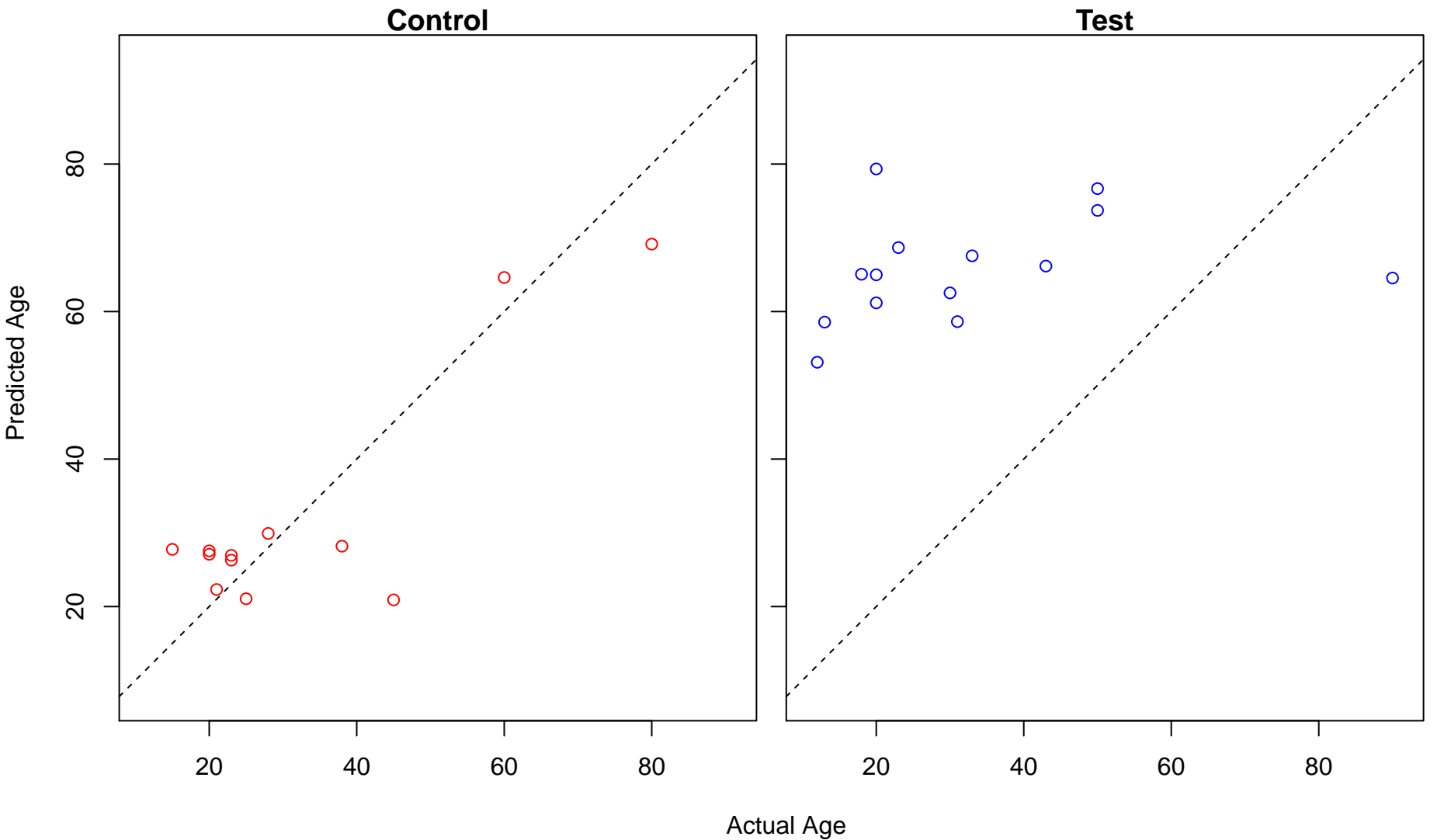
macromolecule glycosylation (Score: 6.479953)



regulation of basement membrane assembly involved in embryonic body morphogenesis (Score: 6.478)

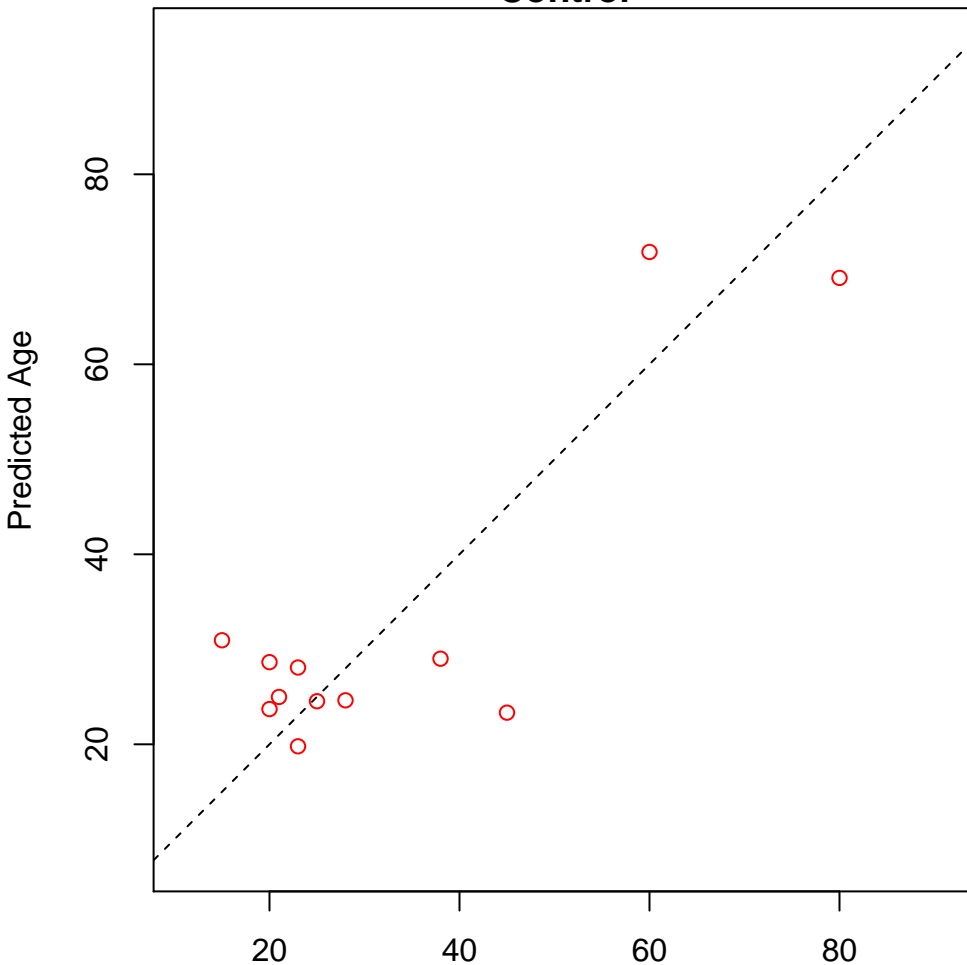


positive regulation of basement membrane assembly involved in embryonic body morphogenesis (Score: 0.0001)

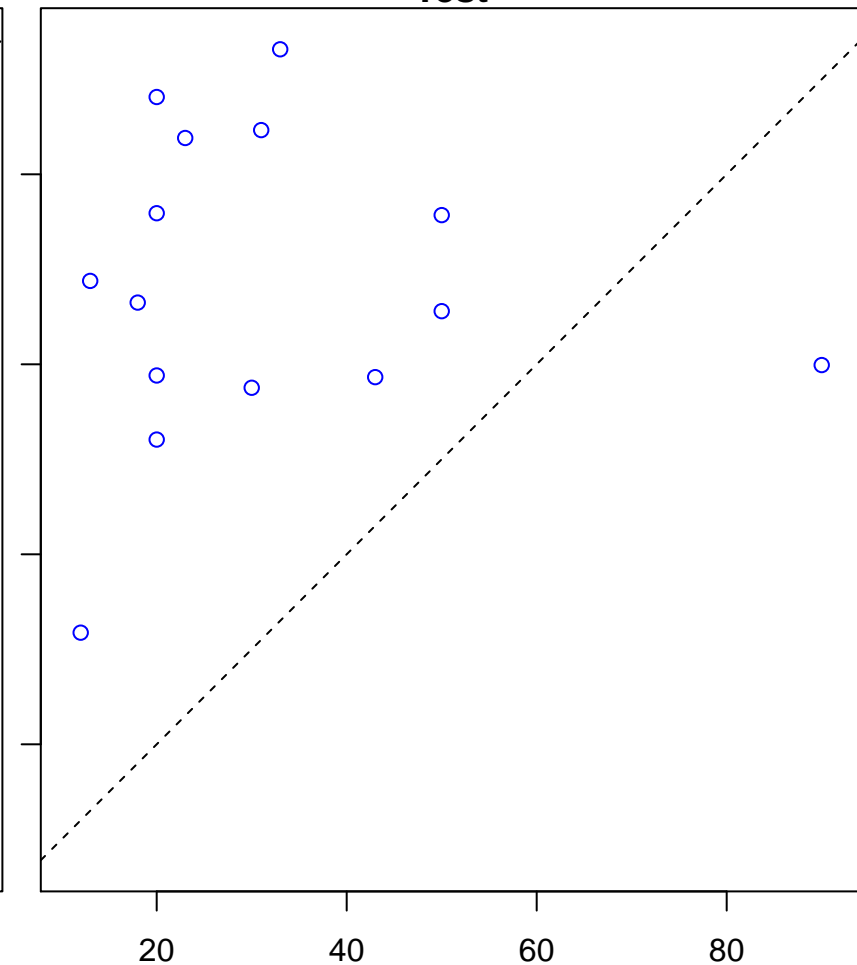


peptidyl-glutamic acid modification (Score: 6.477489)

Control

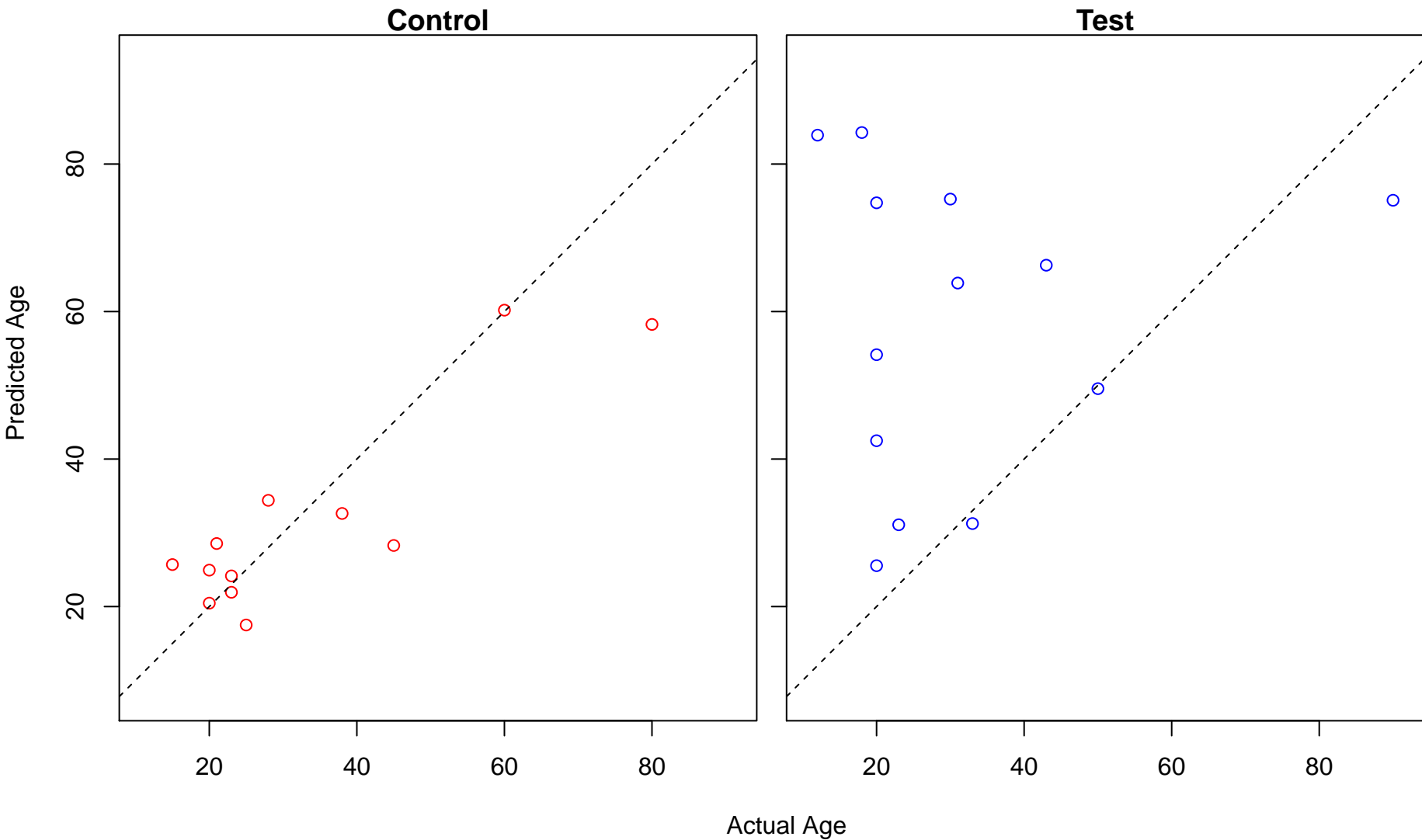


Test

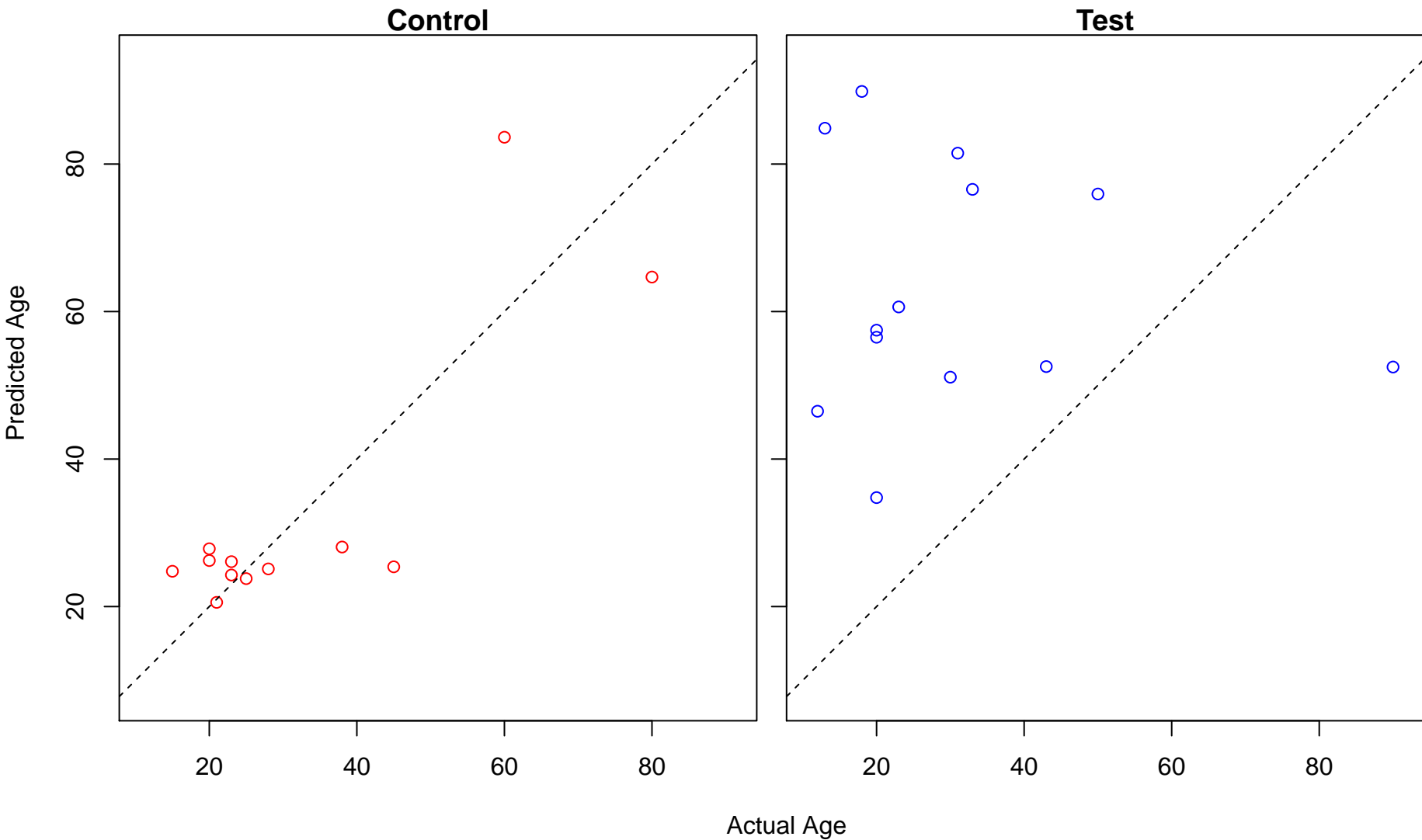


Actual Age

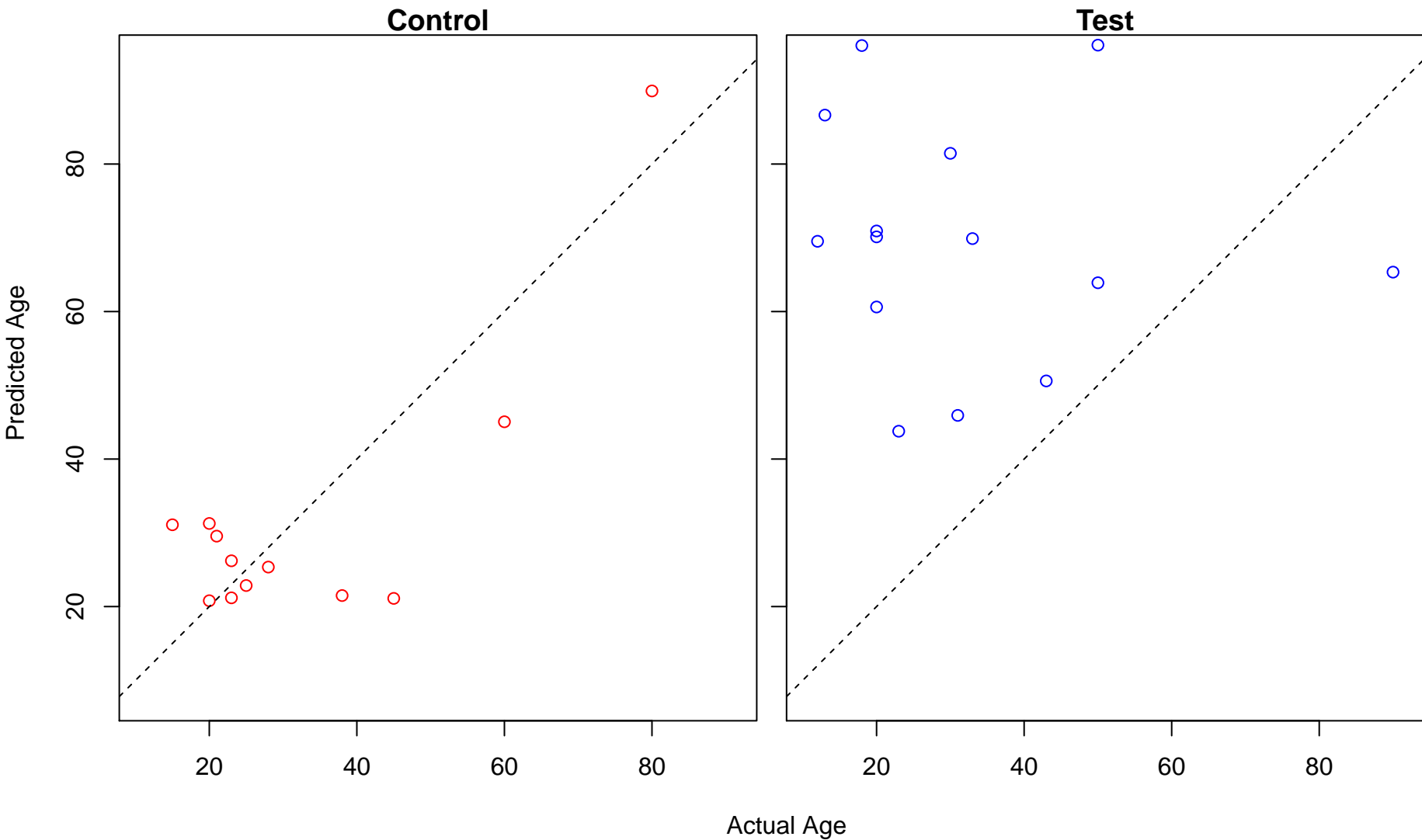
protein acylation (Score: 6.476324)



ATP transport (Score: 6.476270)

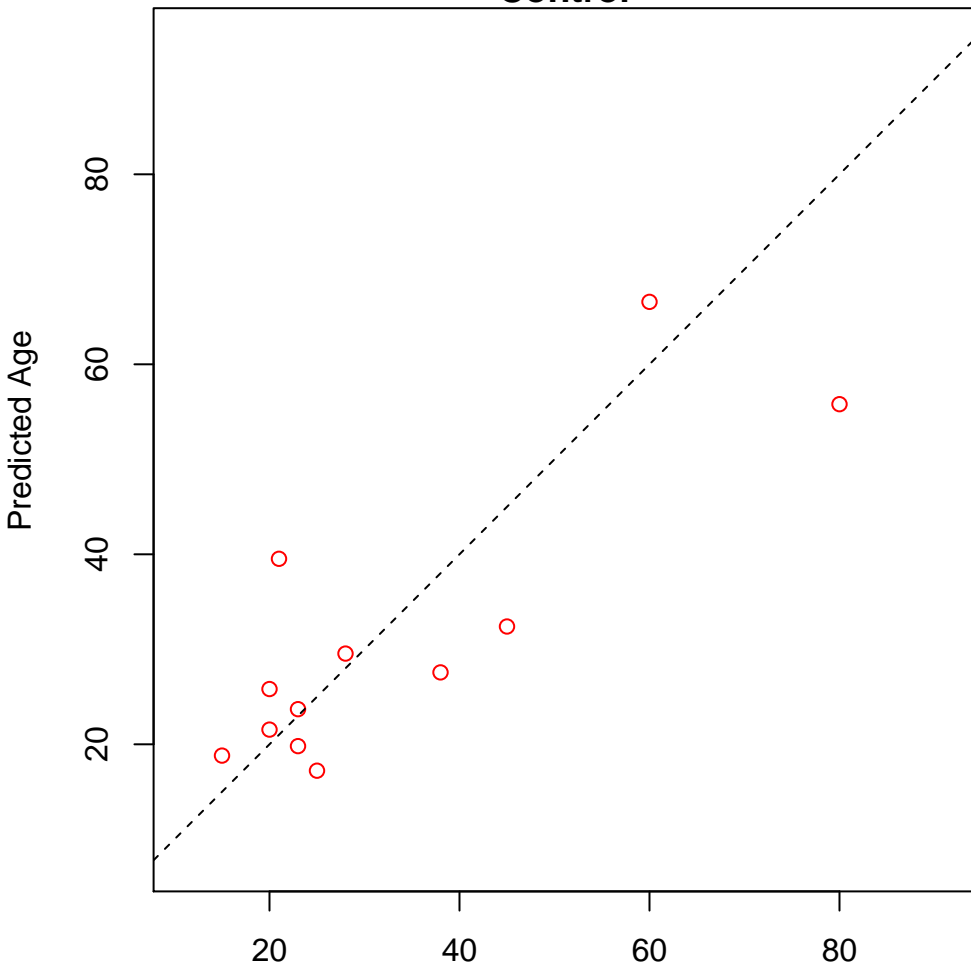


glycosylation (Score: 6.475625)

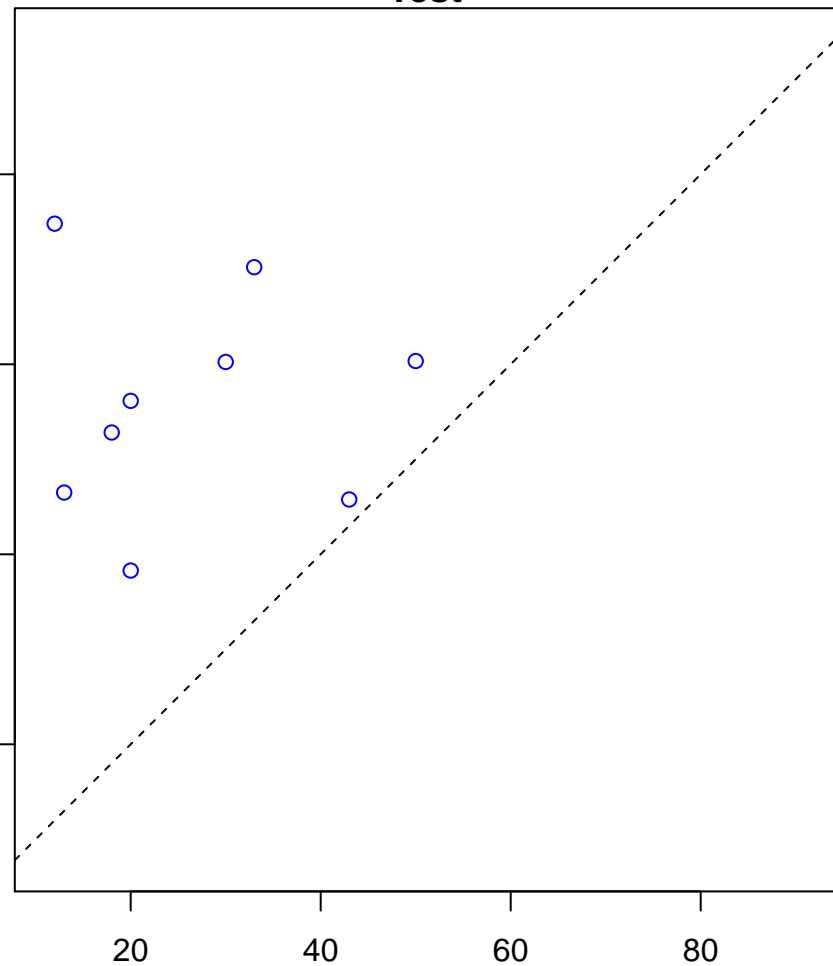


regulation of keratinocyte proliferation (Score: 6.472906)

Control

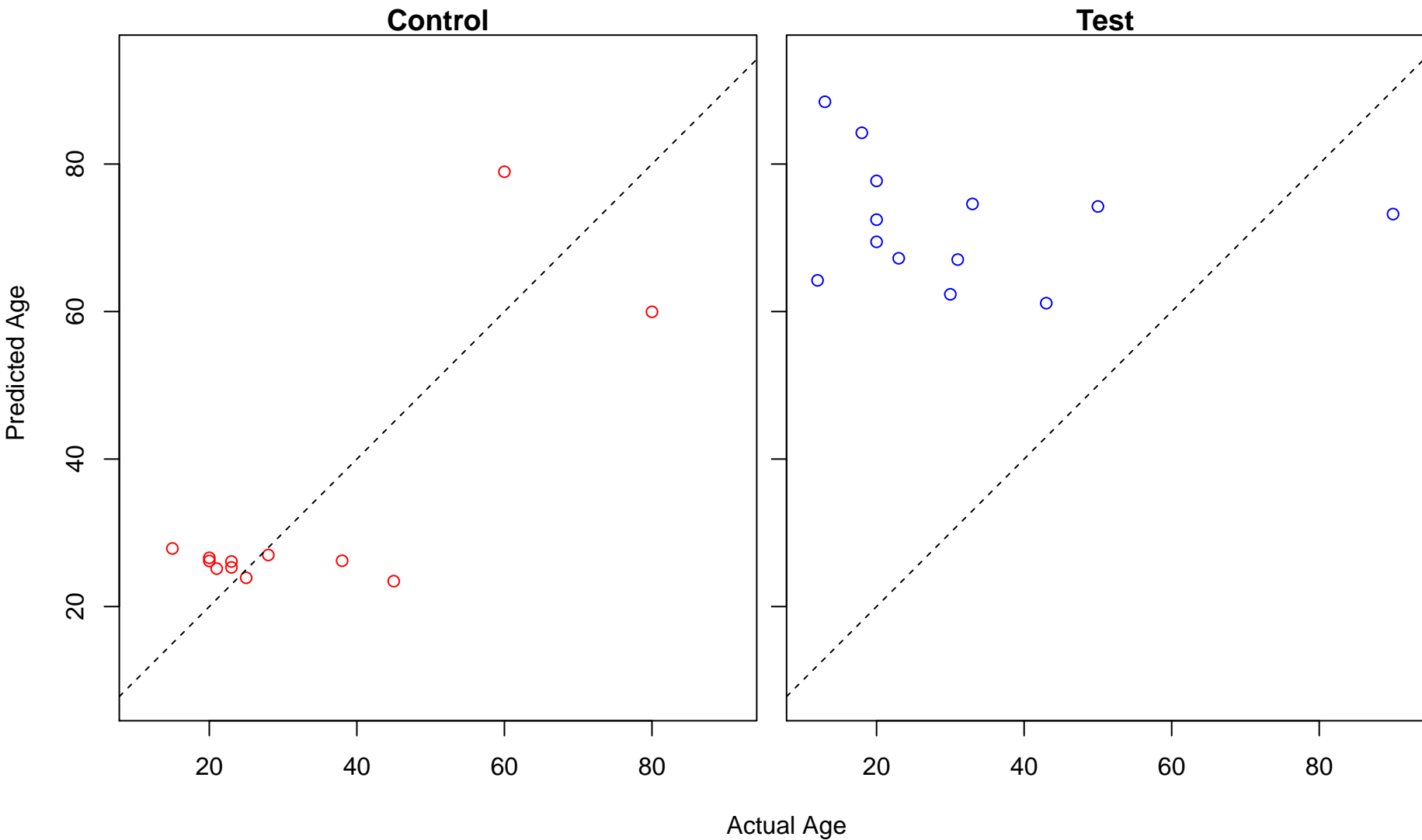


Test

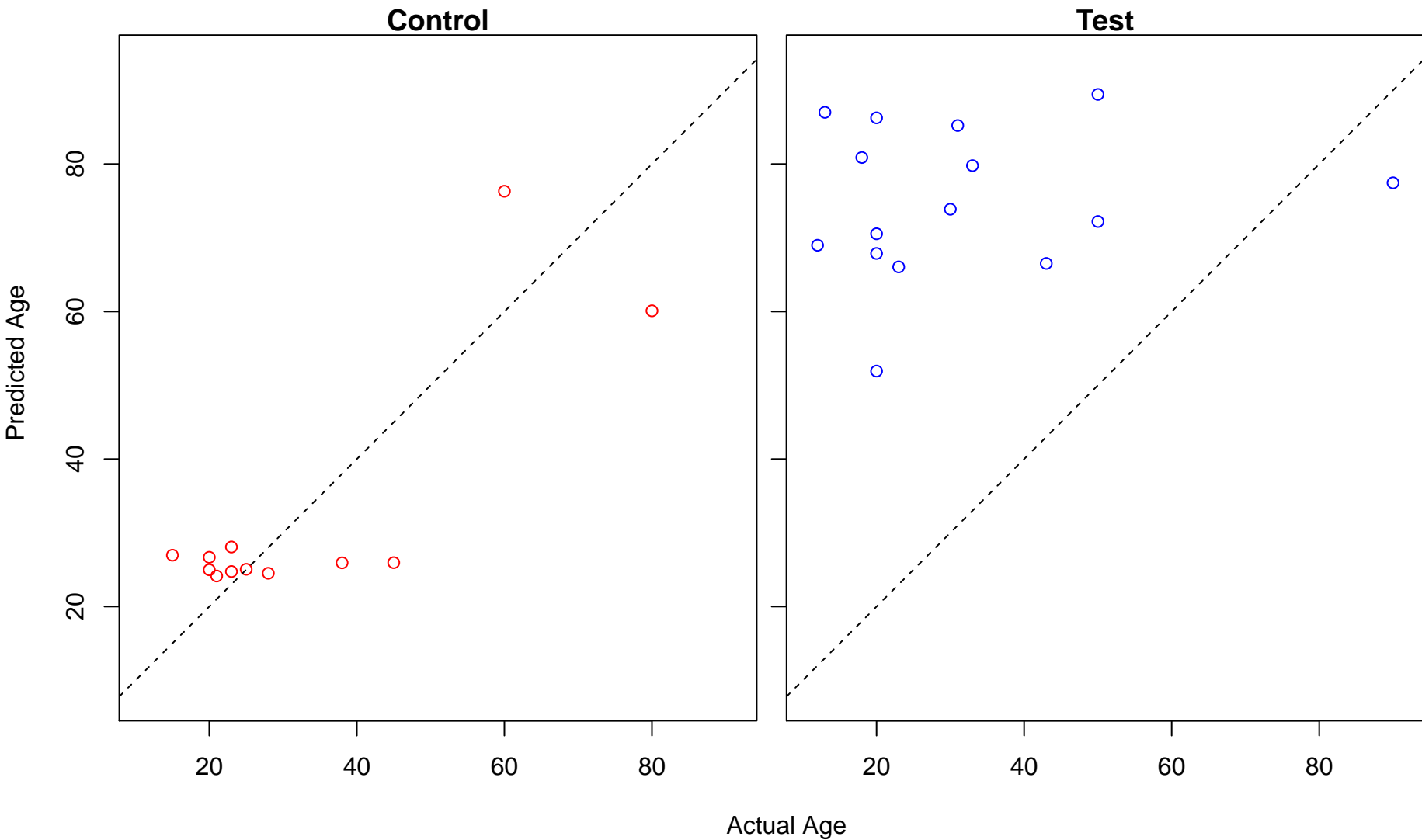


Actual Age

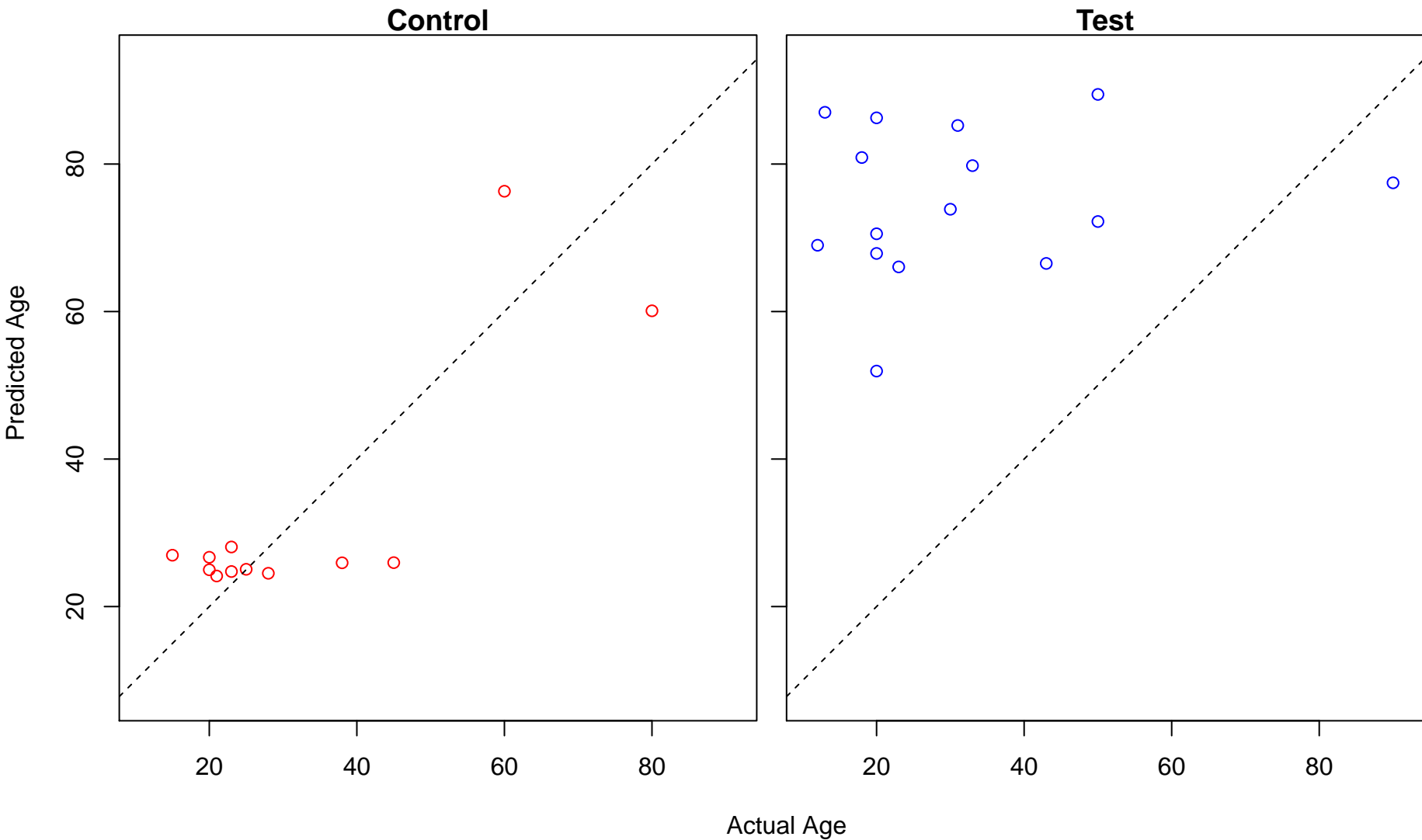
negative regulation of G1/S transition of mitotic cell cycle (Score: 6.471402)



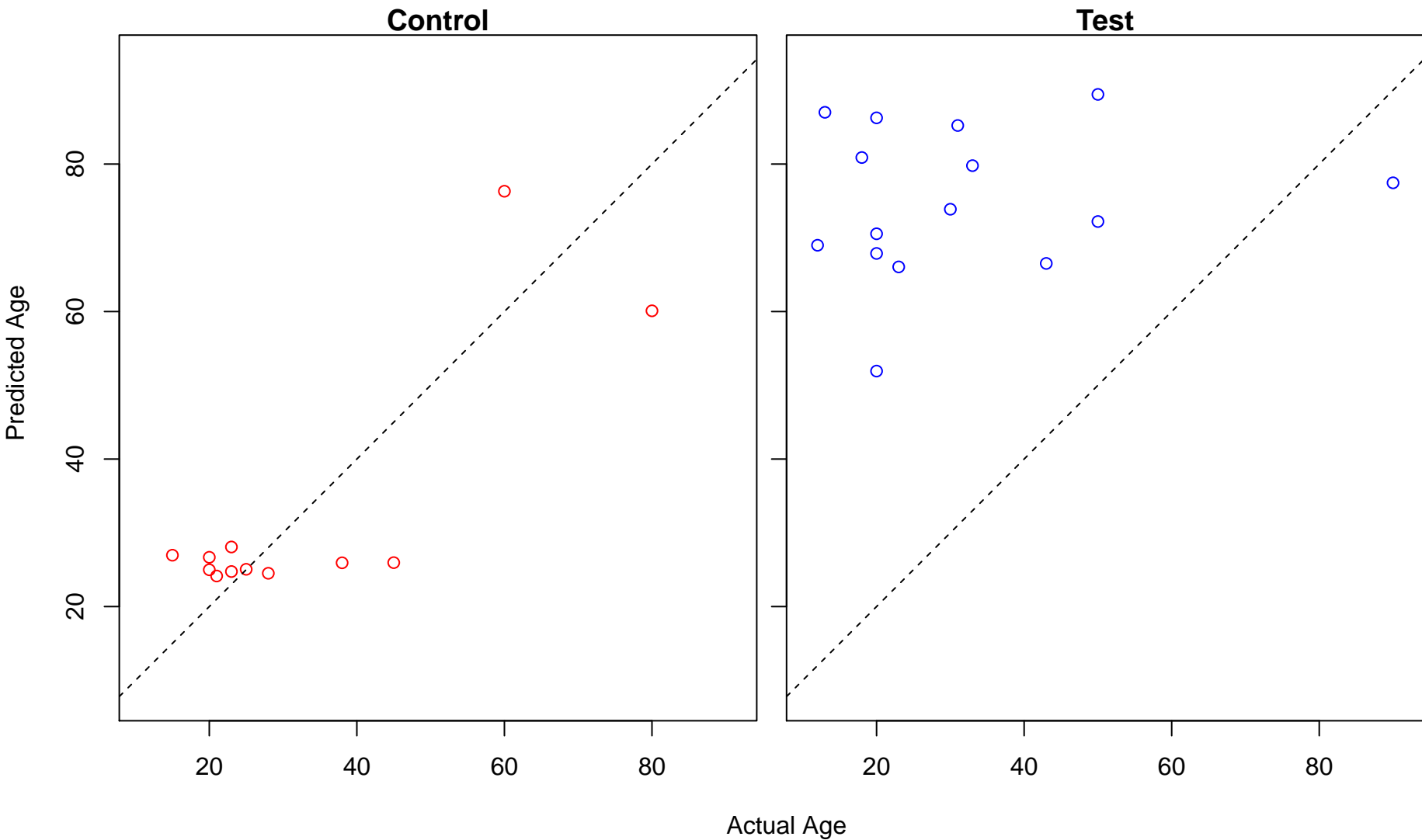
response to cell cycle checkpoint signaling (Score: 6.470478)



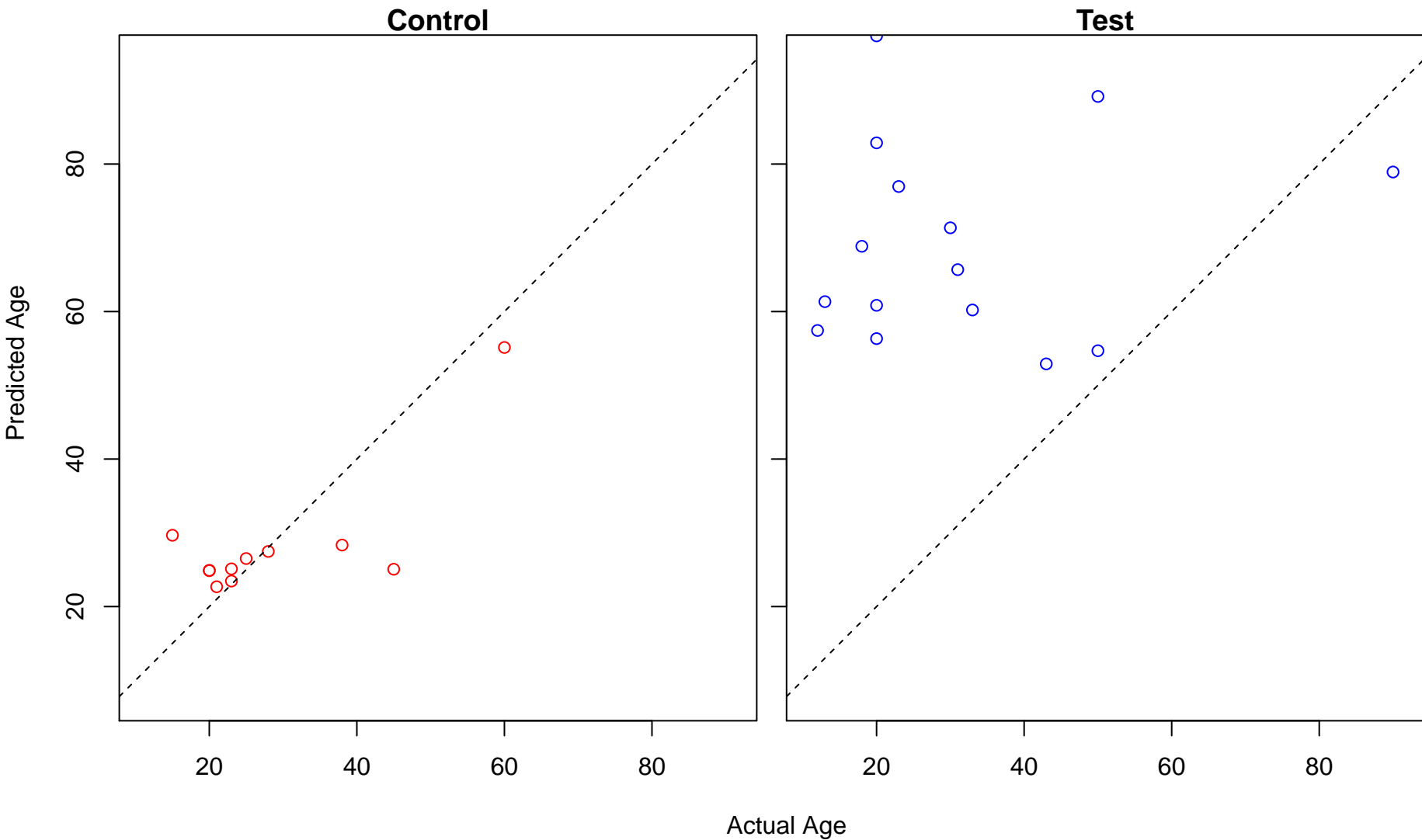
response to DNA integrity checkpoint signaling (Score: 6.470478)



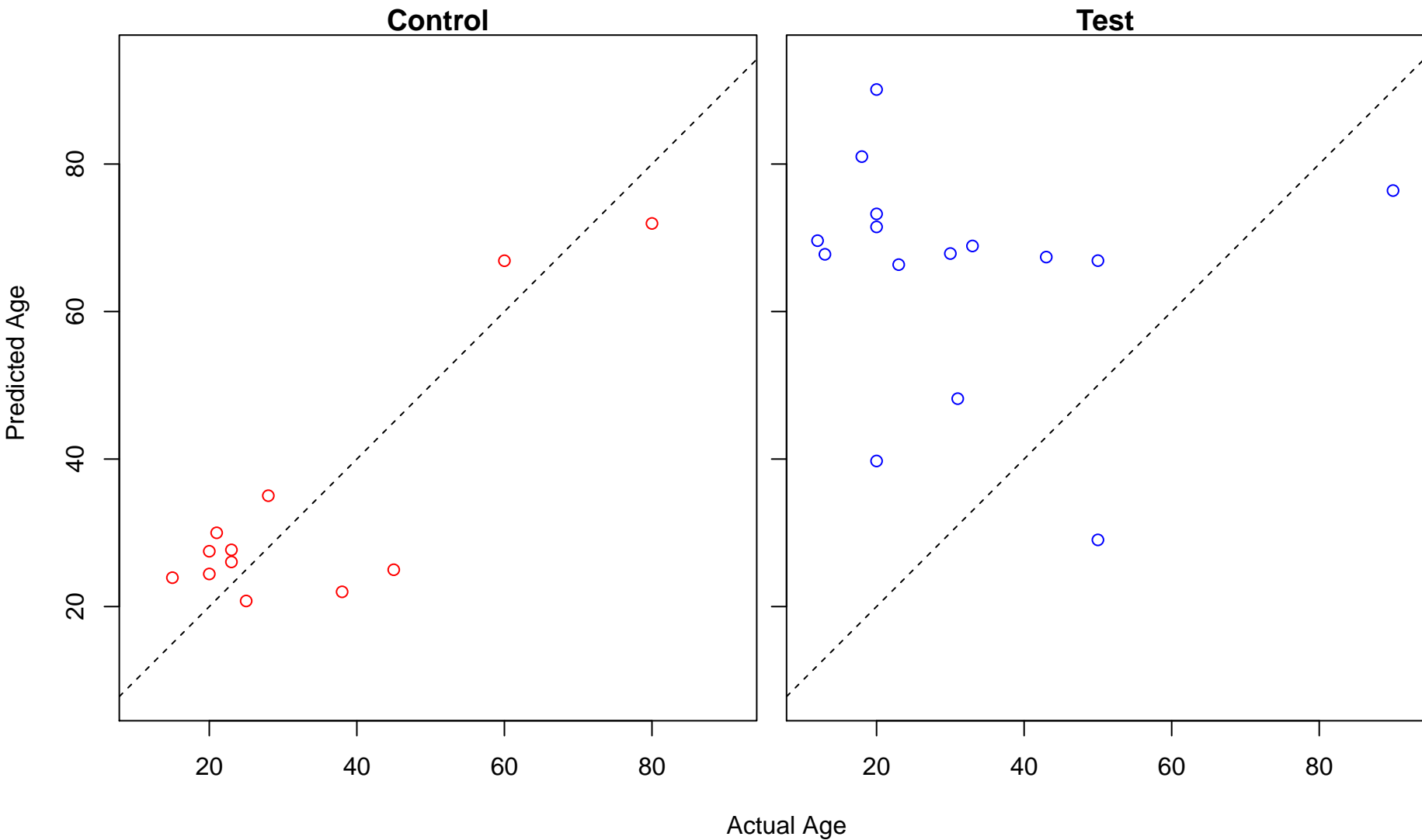
response to DNA damage checkpoint signaling (Score: 6.470478)



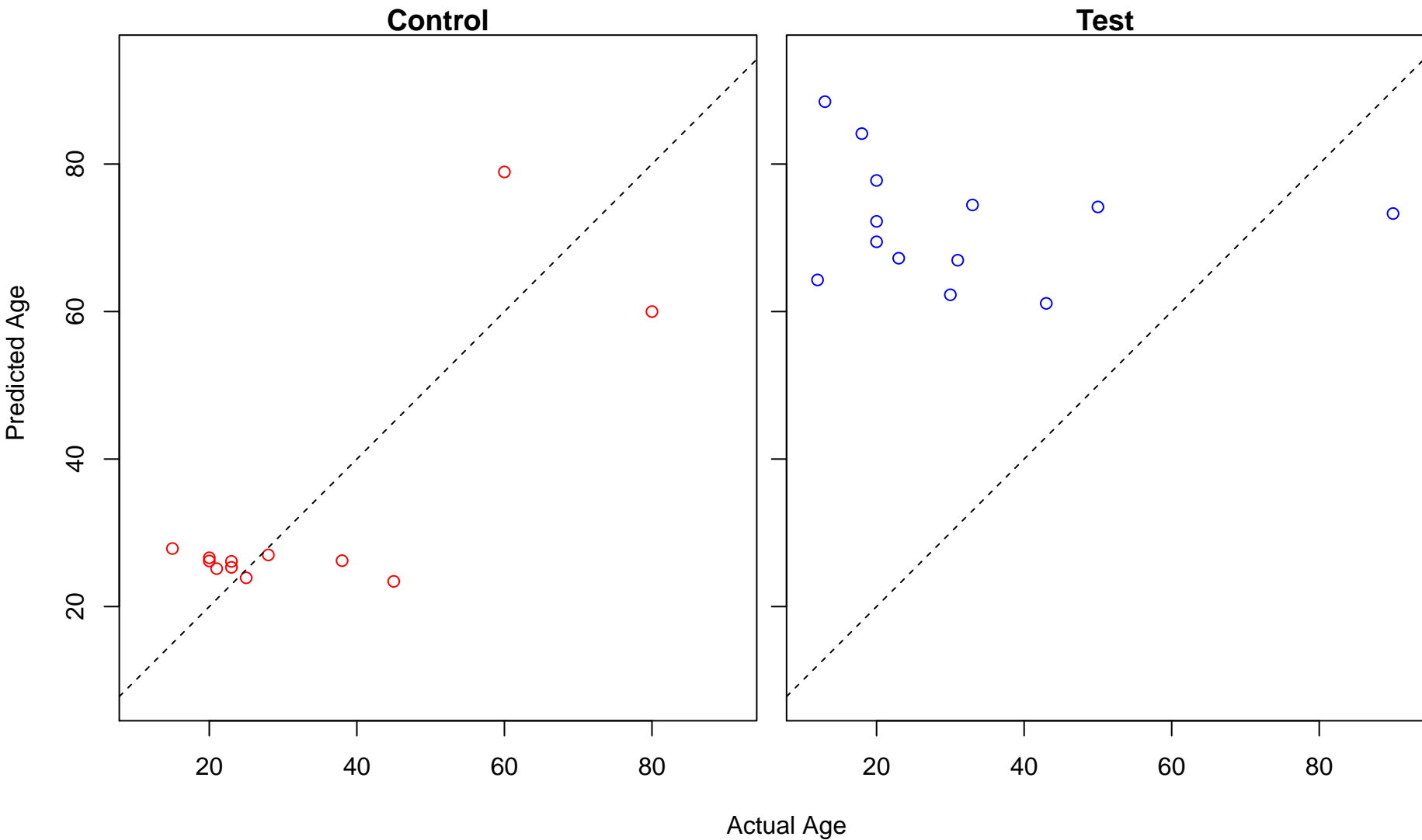
modulation of synaptic transmission (Score: 6.470144)



tRNA splicing, via endonucleolytic cleavage and ligation (Score: 6.469029)

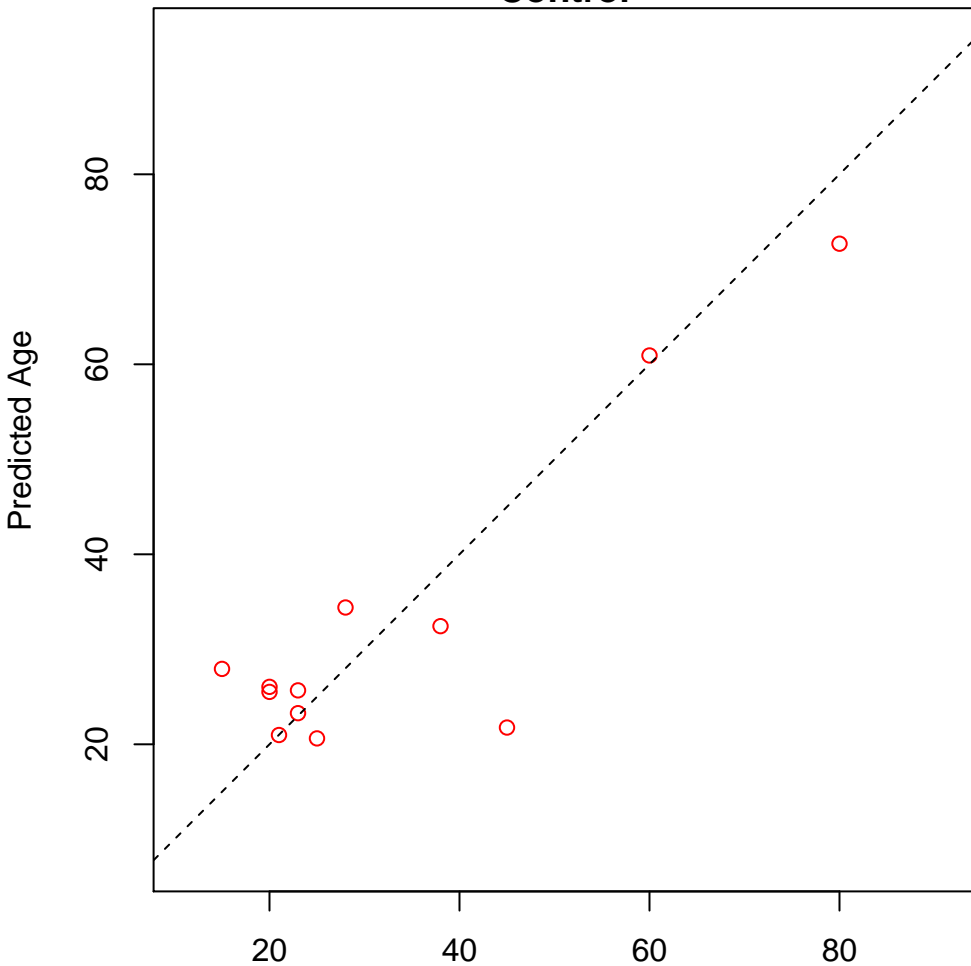


mitotic DNA damage checkpoint (Score: 6.468972)

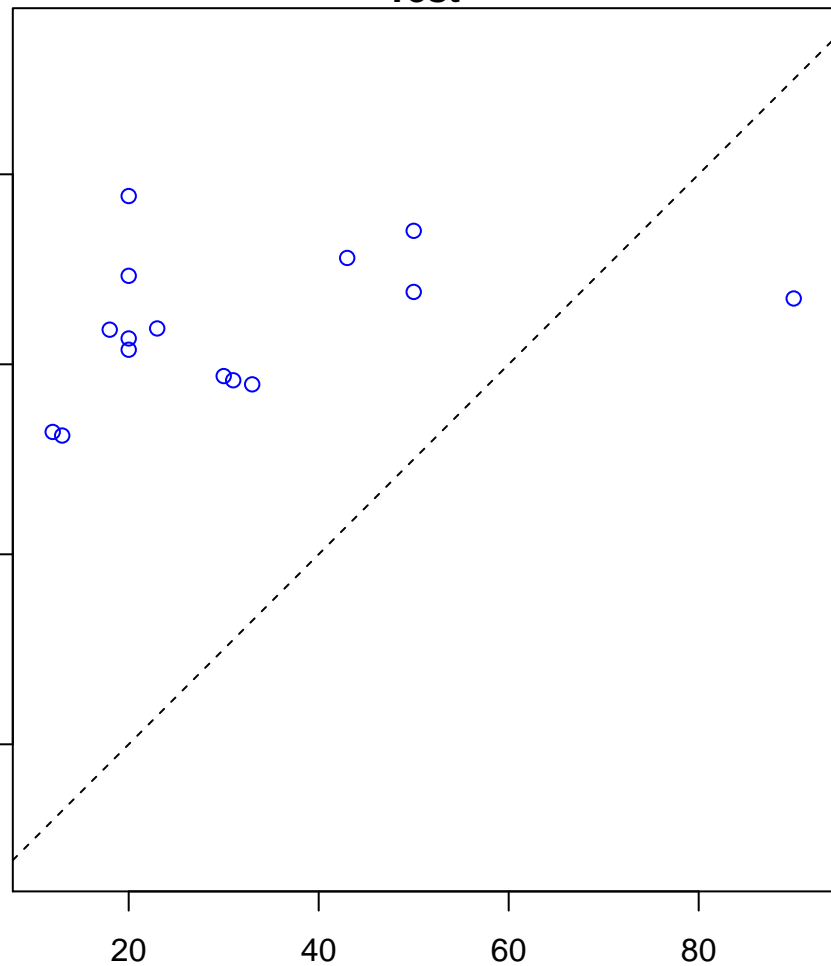


positive regulation of blood circulation (Score: 6.468808)

Control

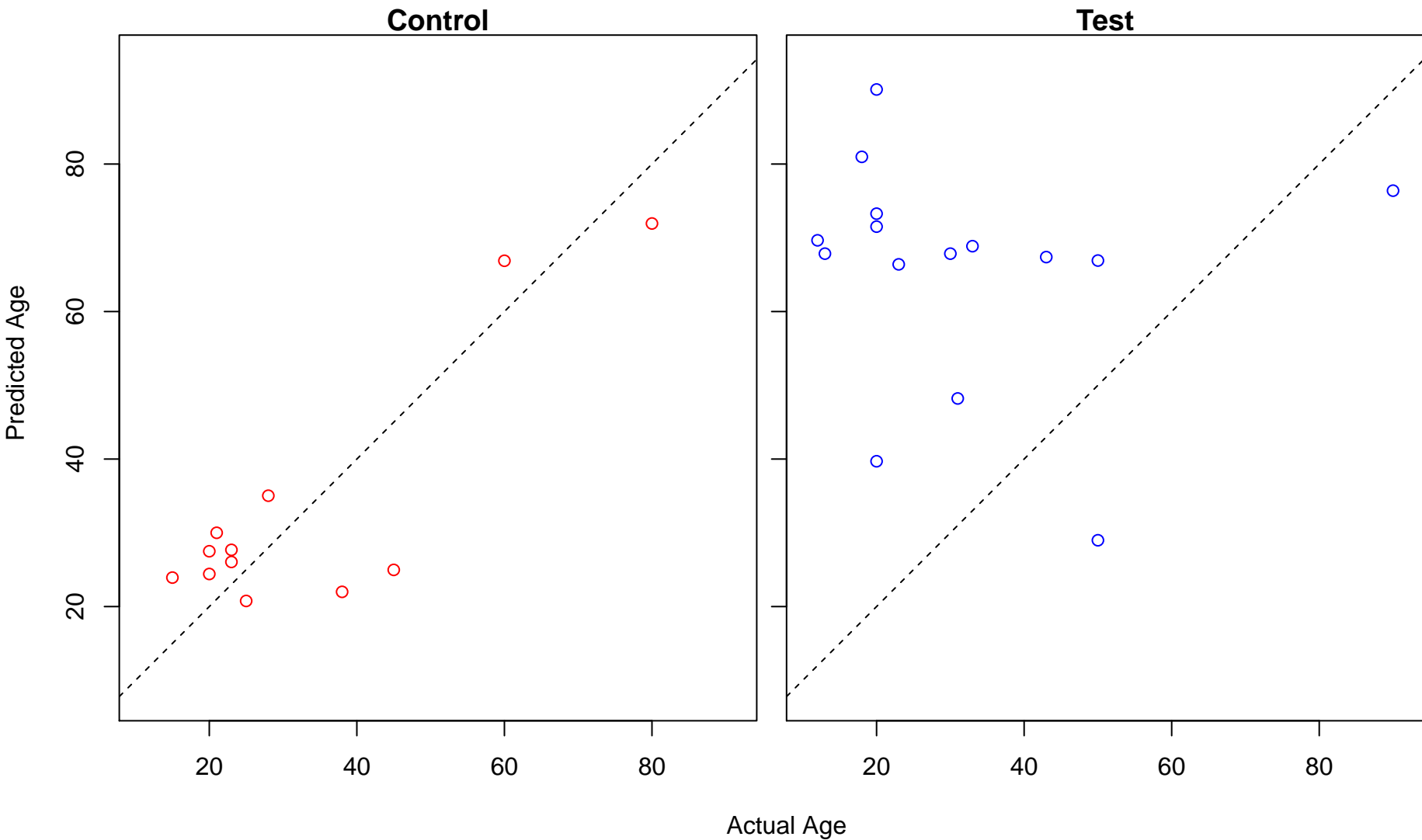


Test

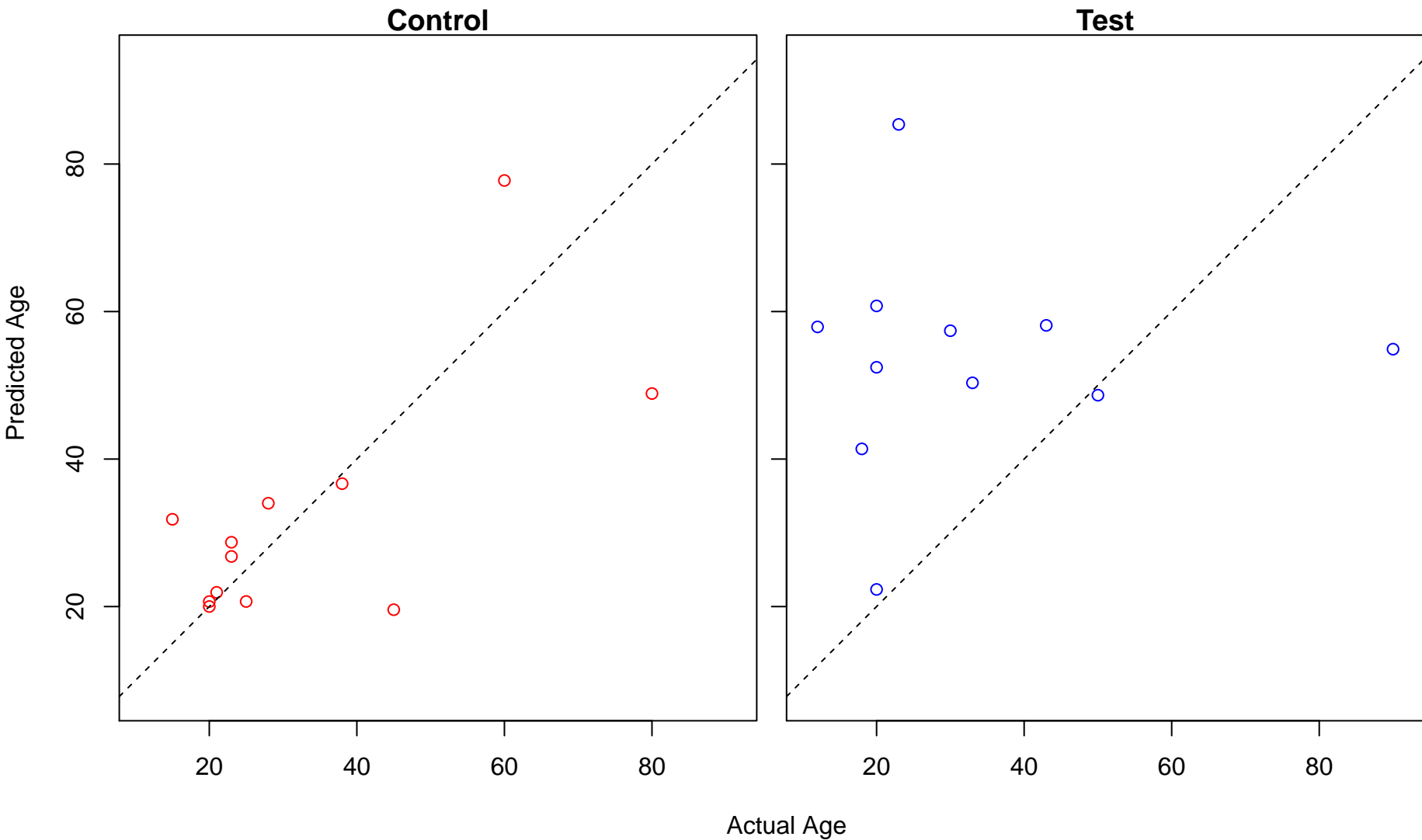


Actual Age

RNA splicing, via endonucleolytic cleavage and ligation (Score: 6.468380)

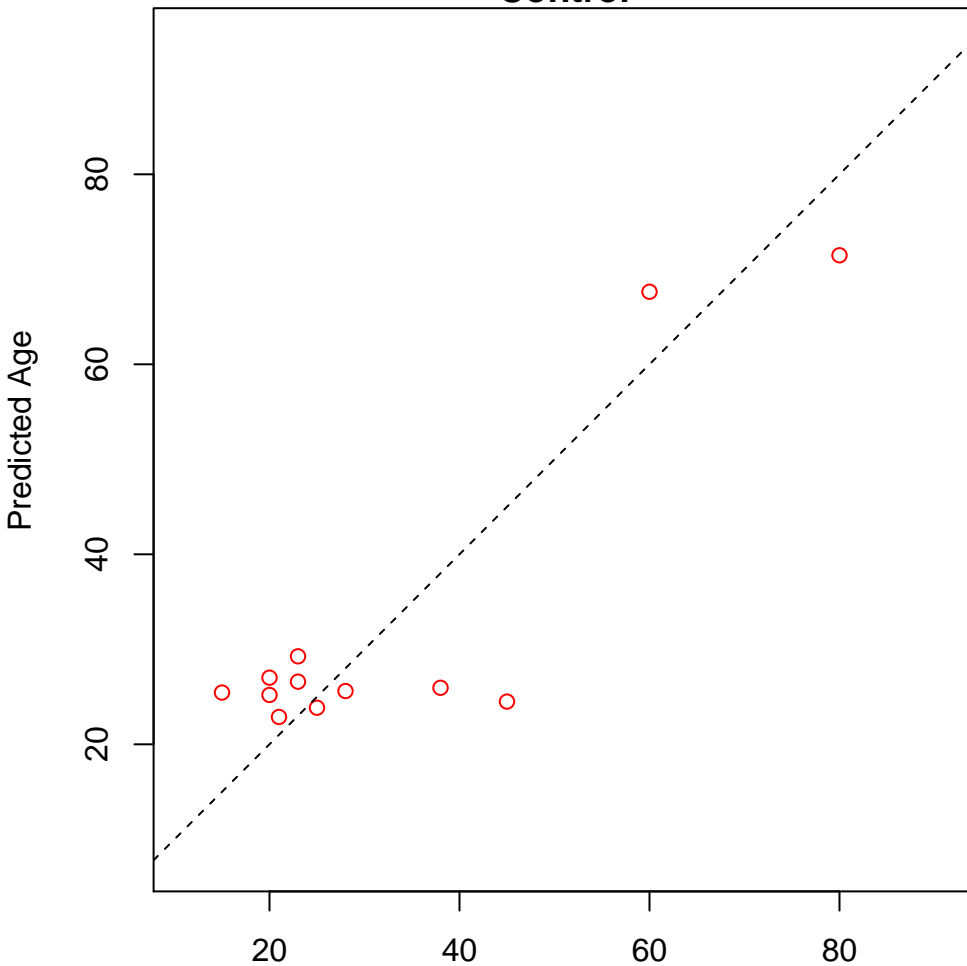


regulation of monocyte chemotaxis (Score: 6.466451)

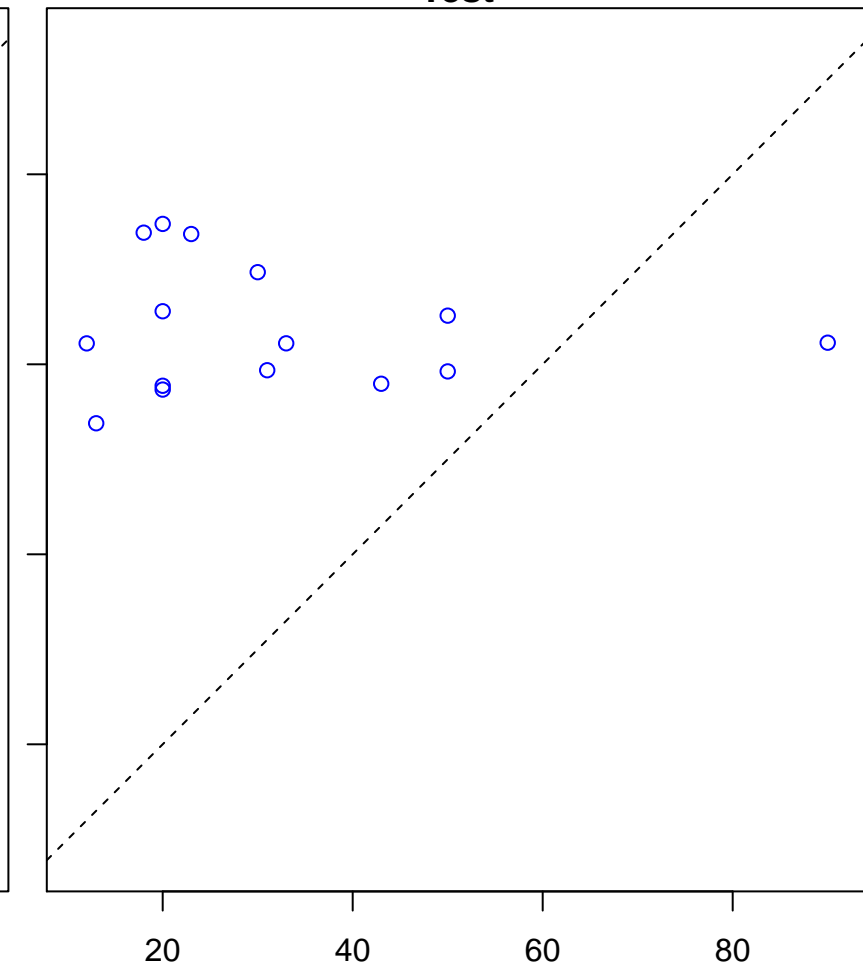


fatty acid elongation, unsaturated fatty acid (Score: 6.464875)

Control

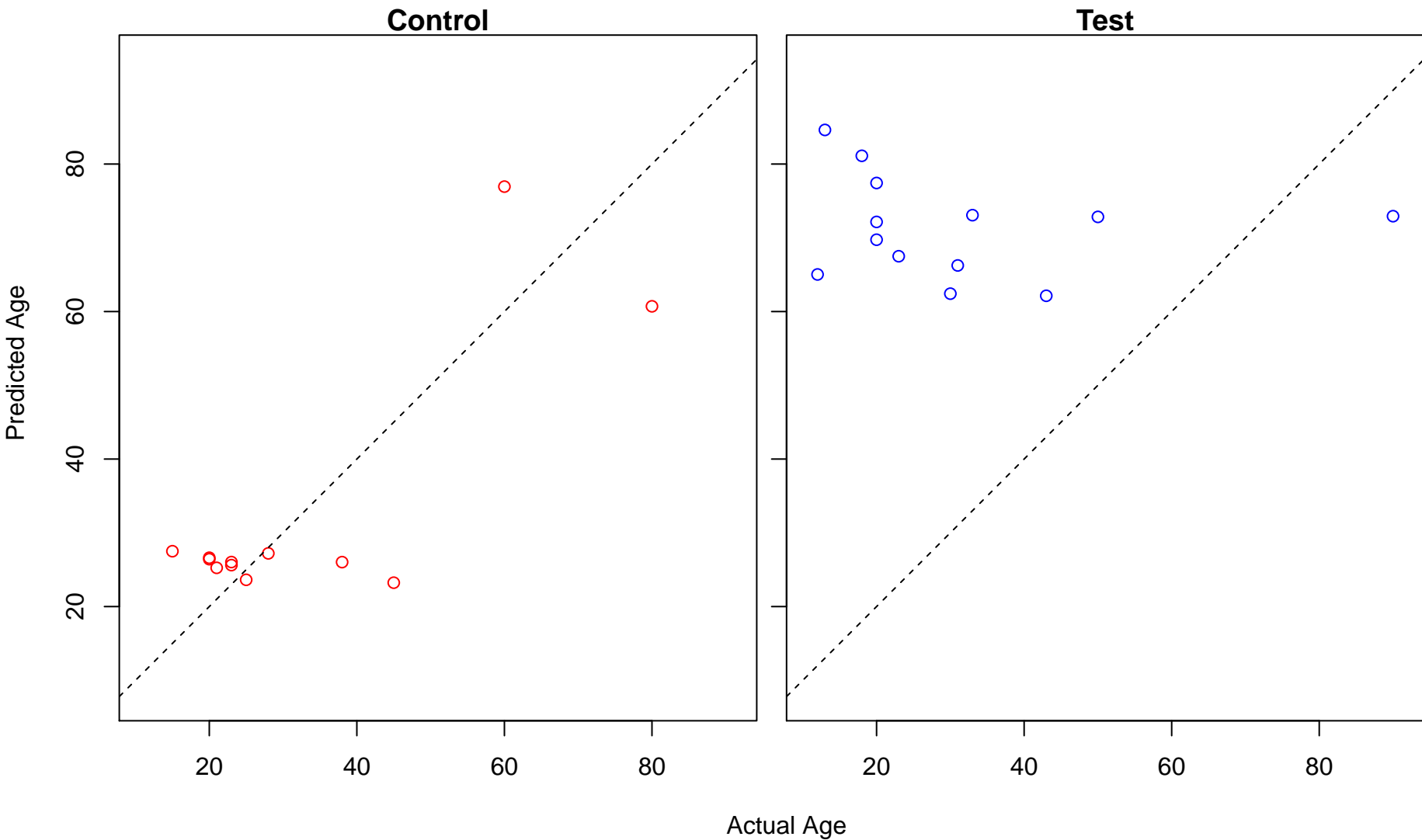


Test



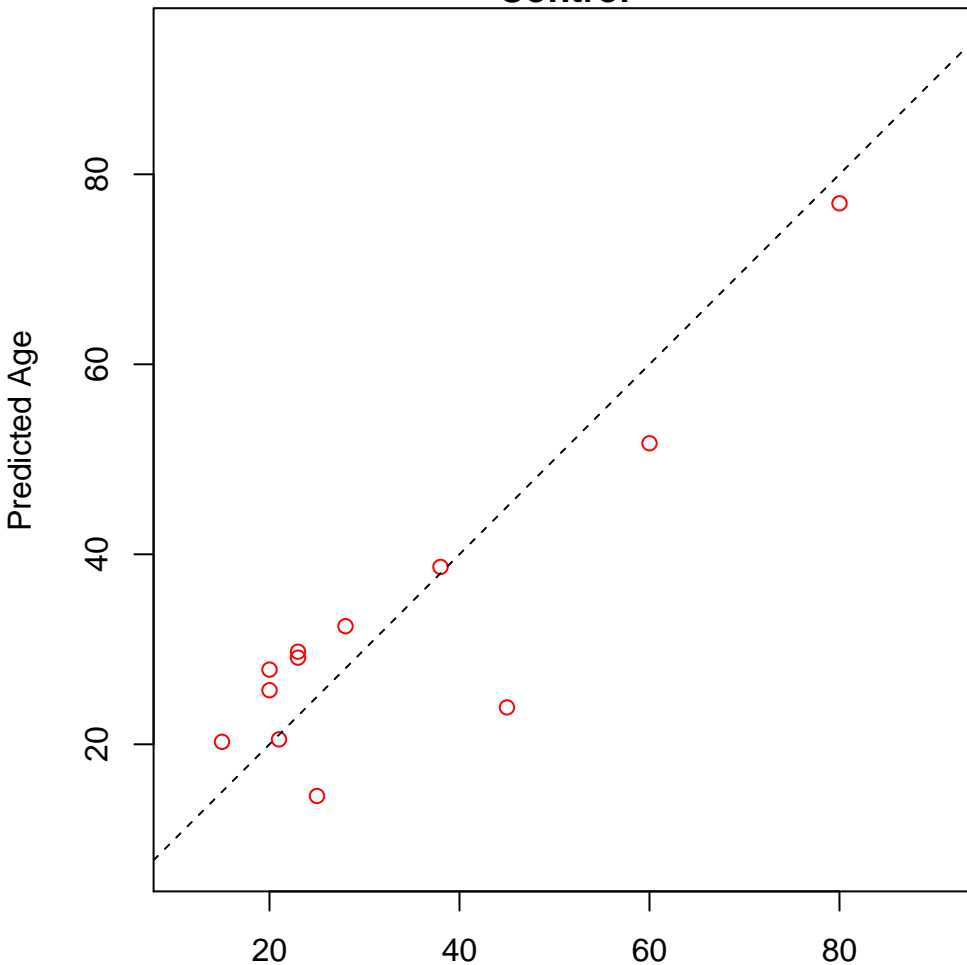
Actual Age

signal transduction by p53 class mediator (Score: 6.464212)

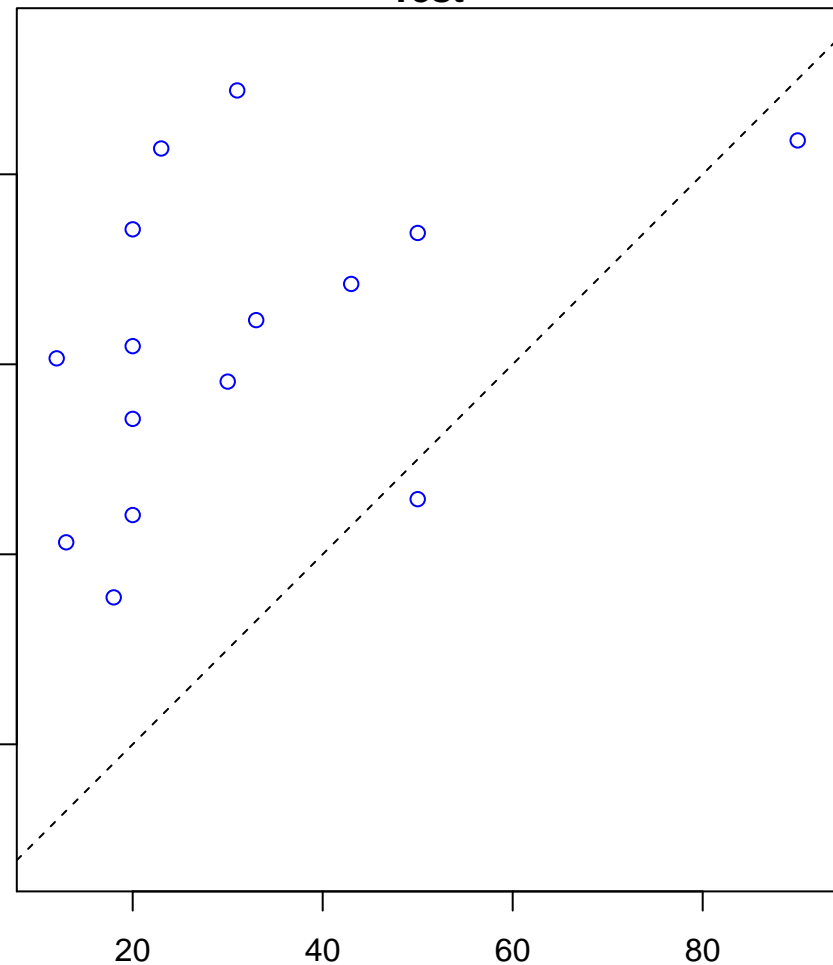


embryonic heart tube morphogenesis (Score: 6.459174)

Control

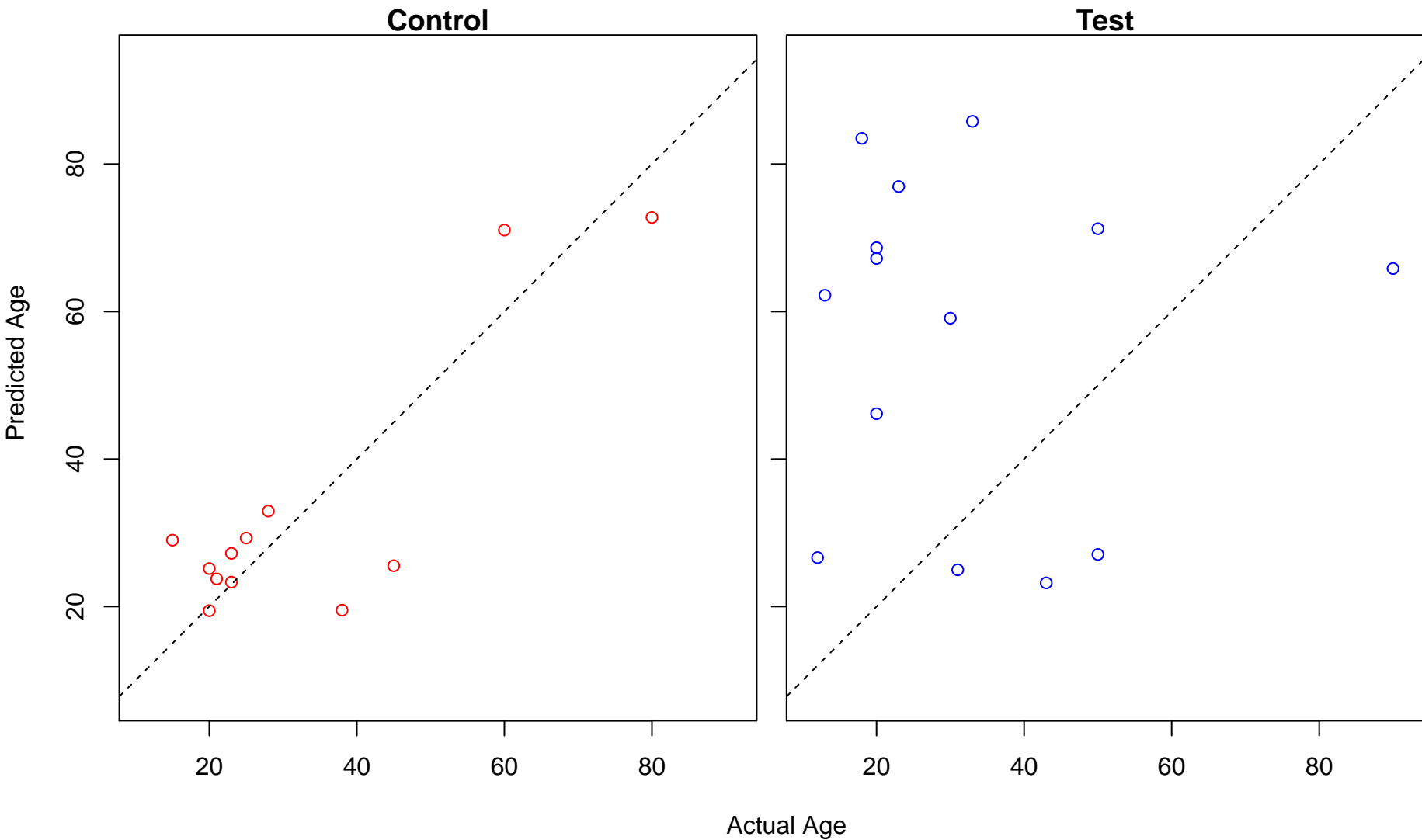


Test

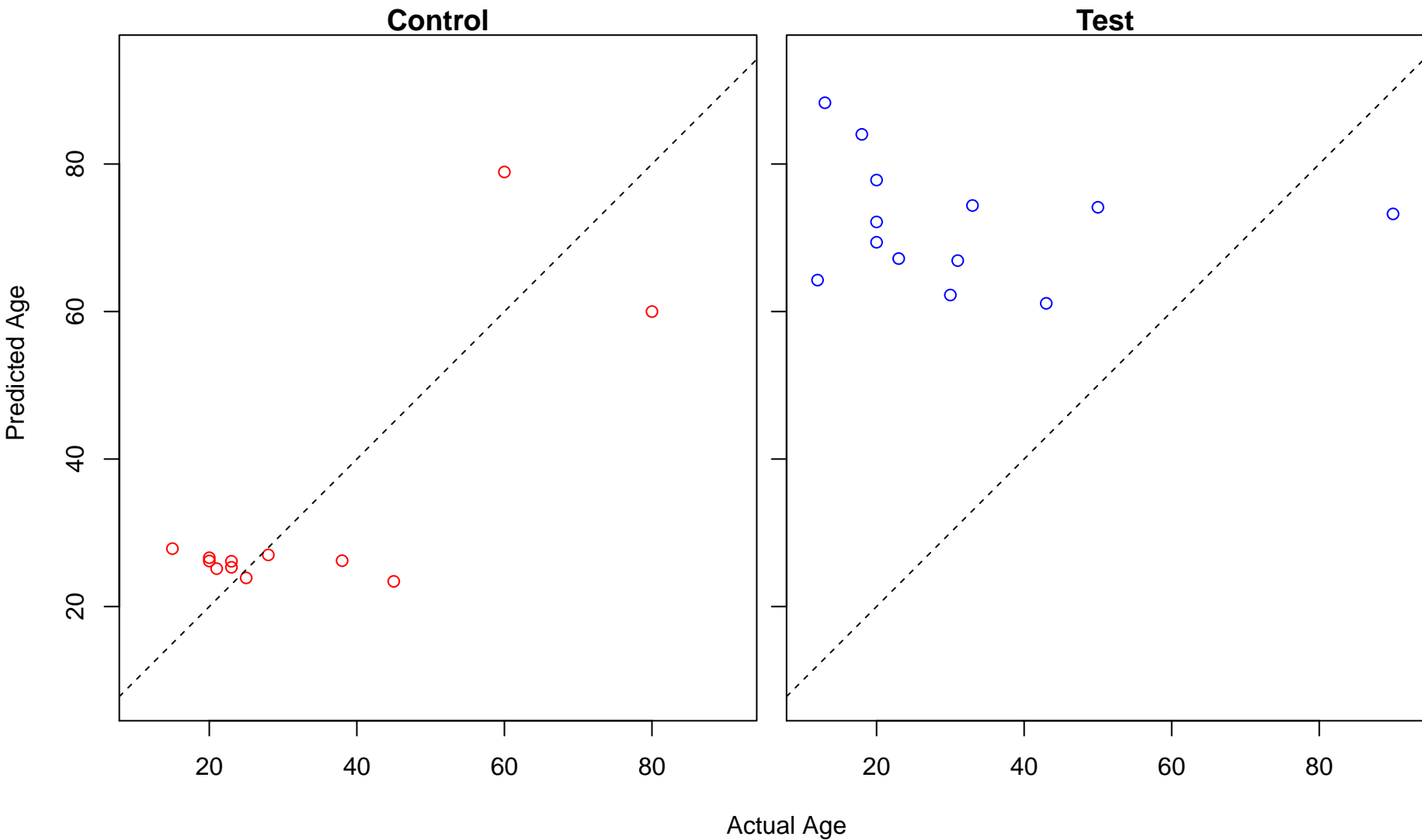


Actual Age

positive regulation of muscle cell apoptotic process (Score: 6.455474)

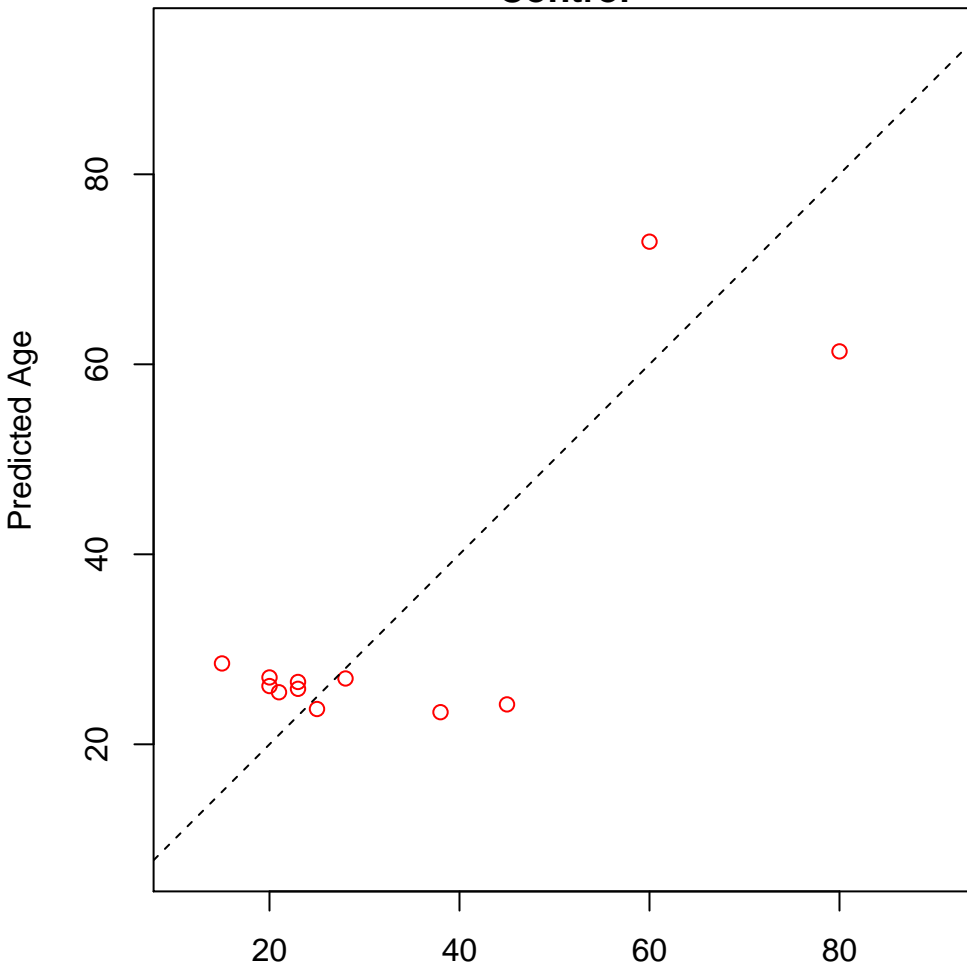


mitotic DNA integrity checkpoint (Score: 6.453758)

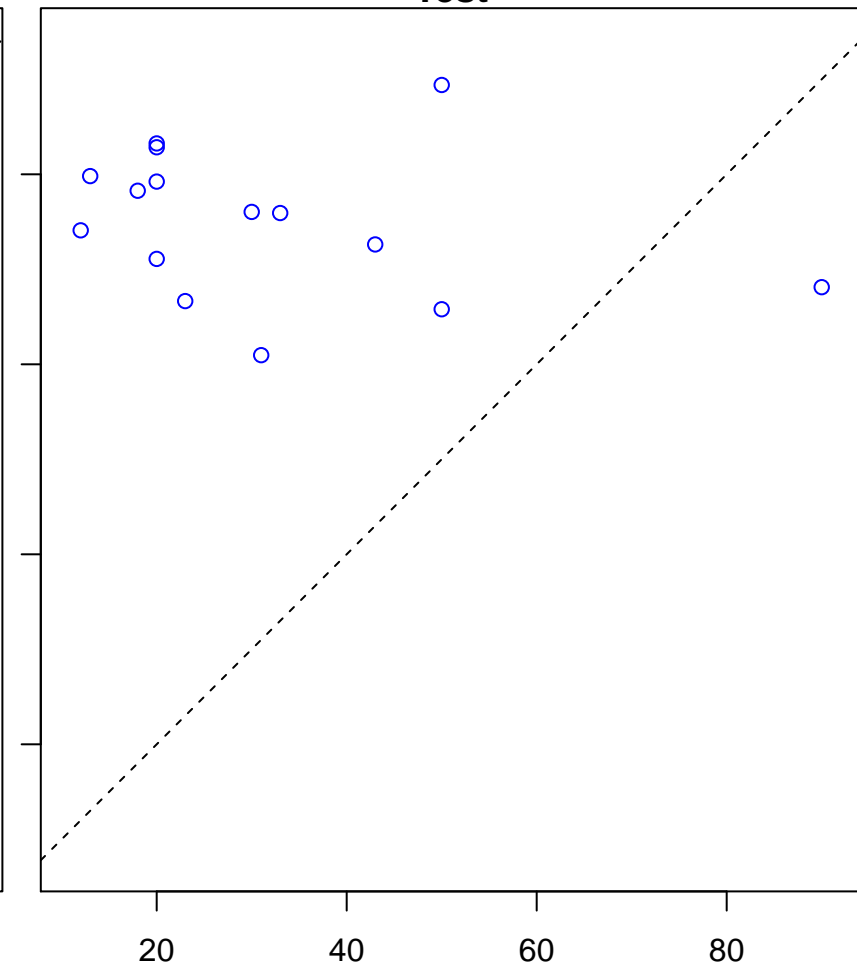


retinoic acid receptor signaling pathway (Score: 6.450929)

Control

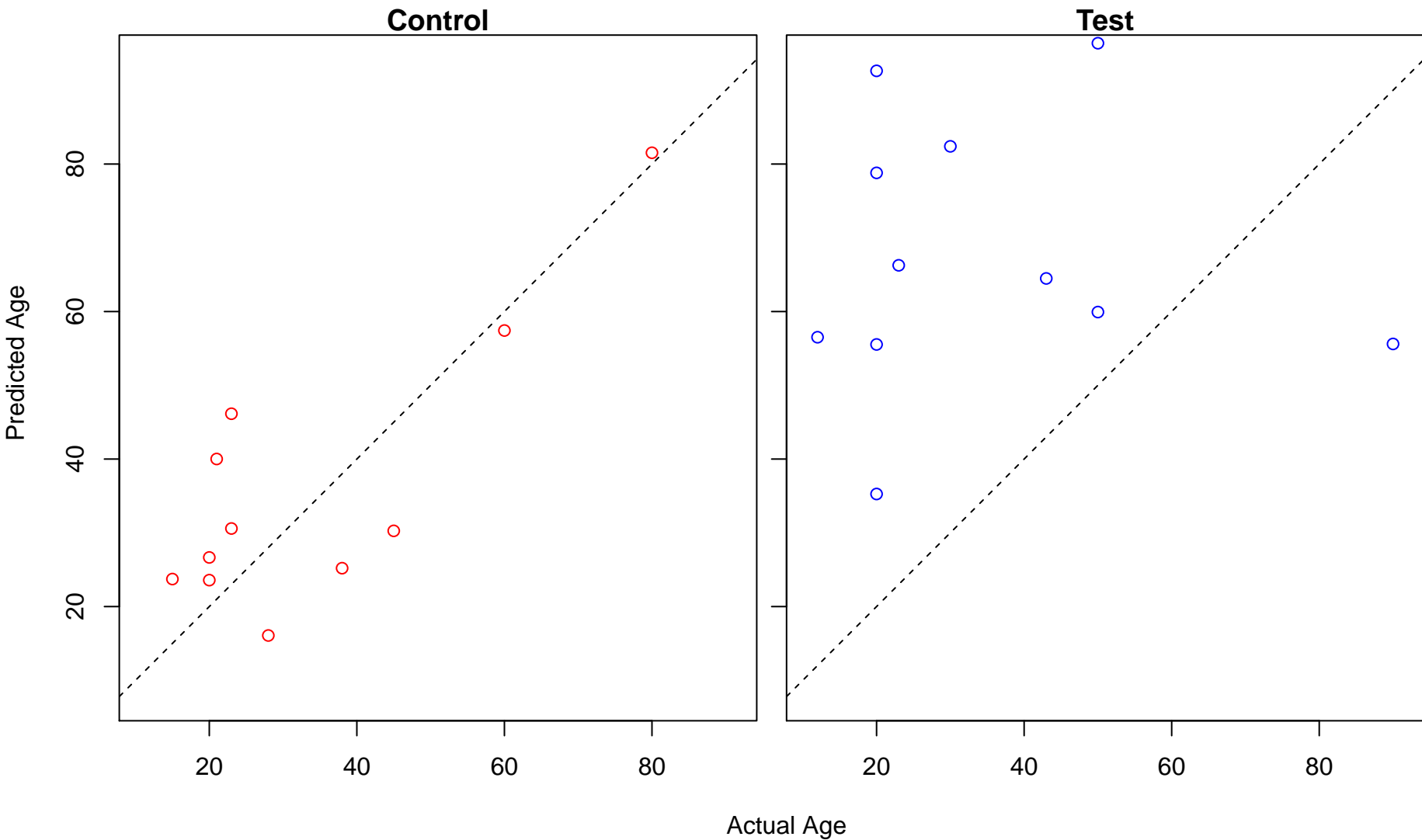


Test

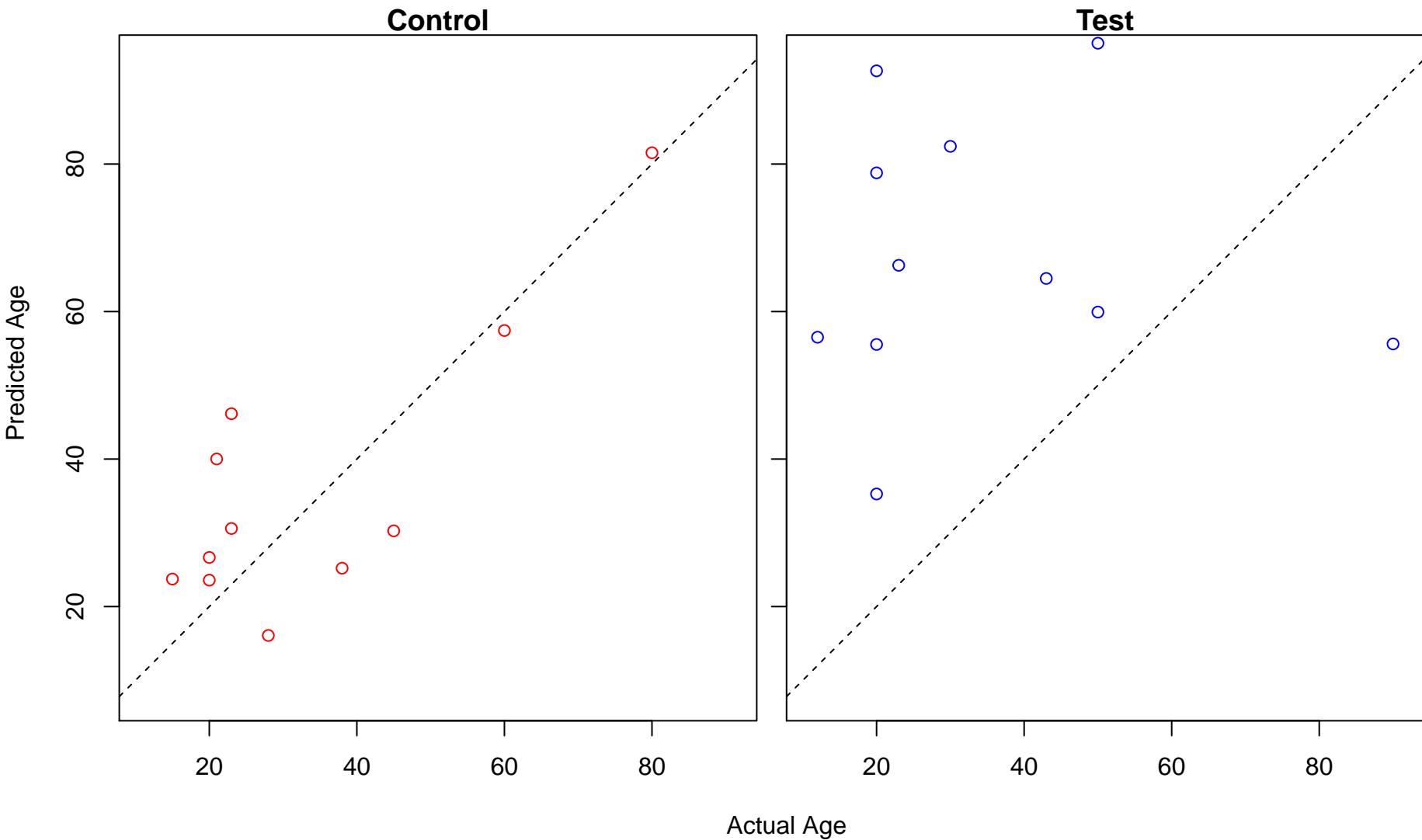


Actual Age

macromolecular complex remodeling (Score: 6.448492)

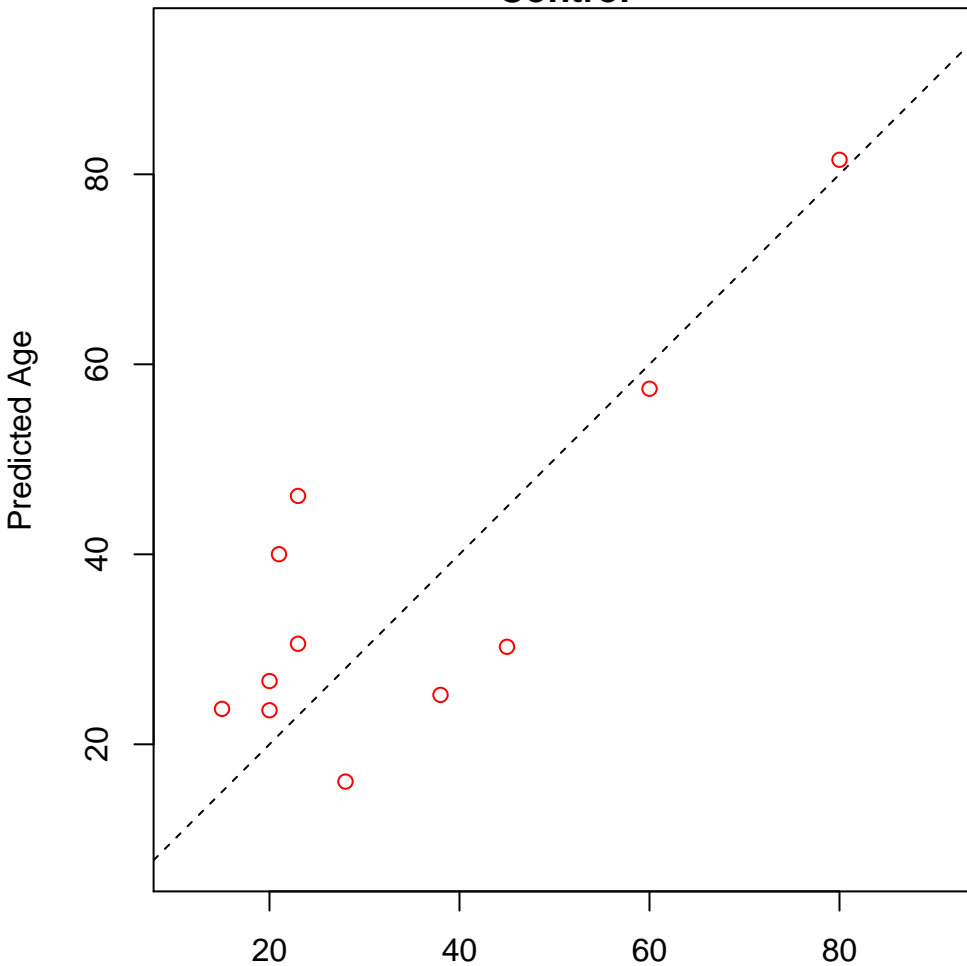


protein-lipid complex remodeling (Score: 6.448492)

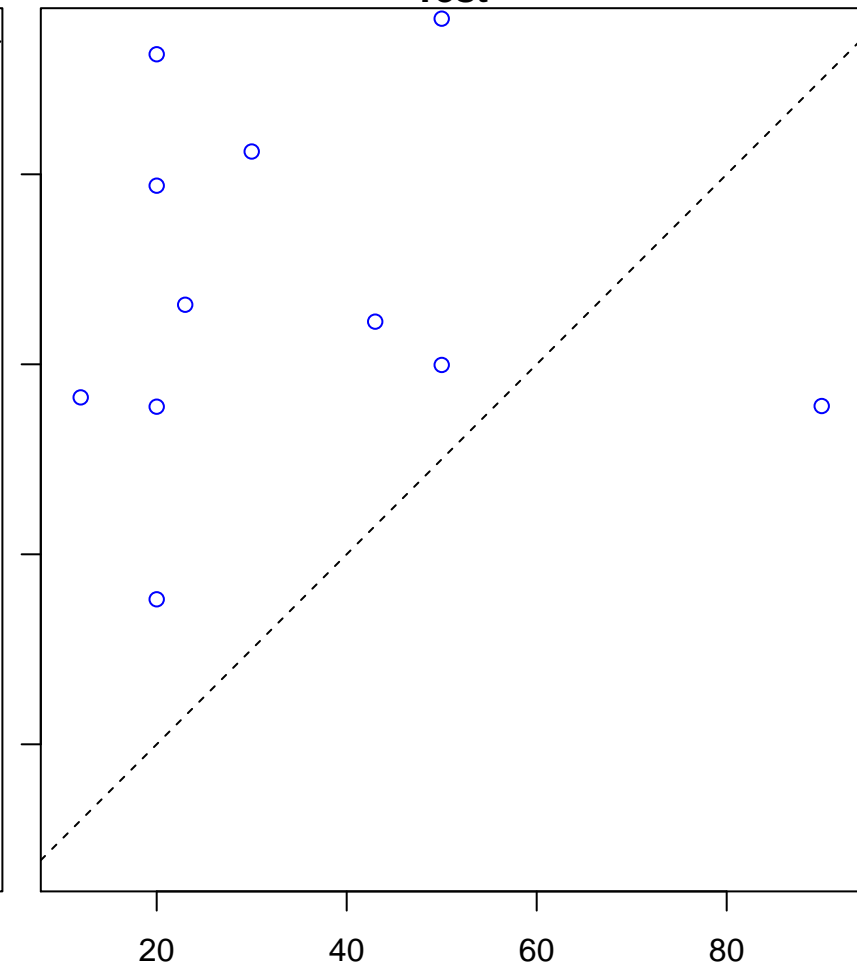


plasma lipoprotein particle remodeling (Score: 6.448492)

Control

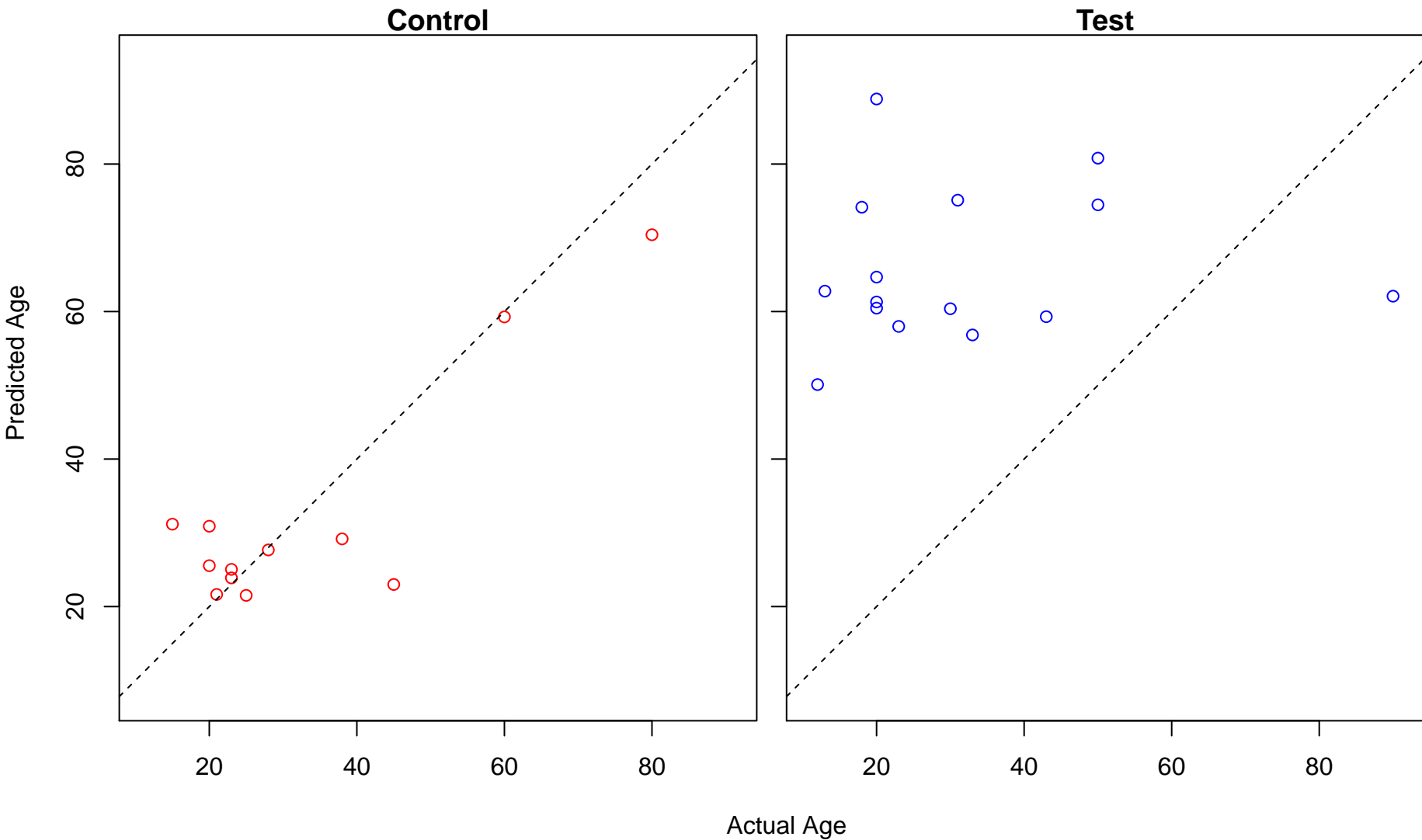


Test

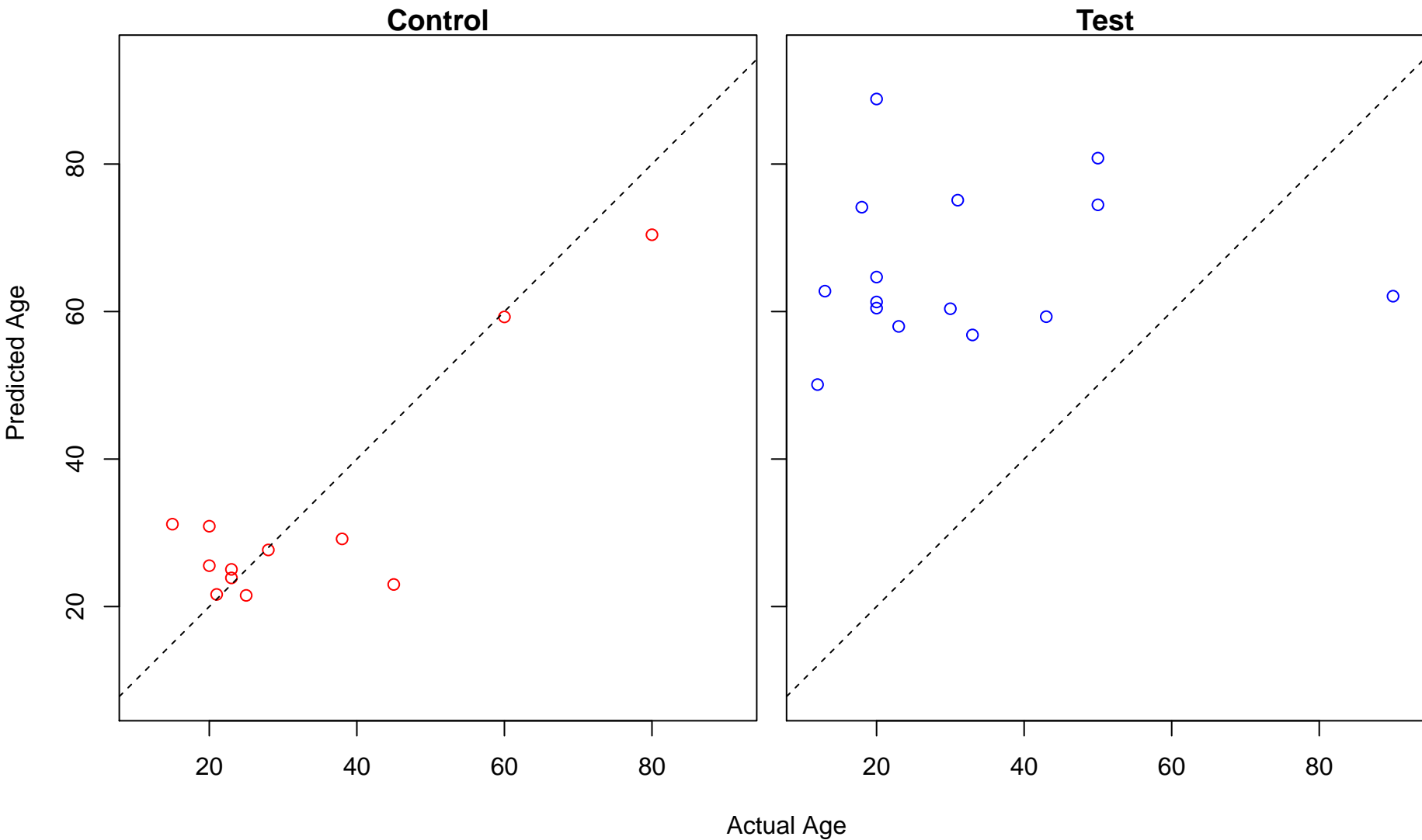


Actual Age

water homeostasis (Score: 6.447275)

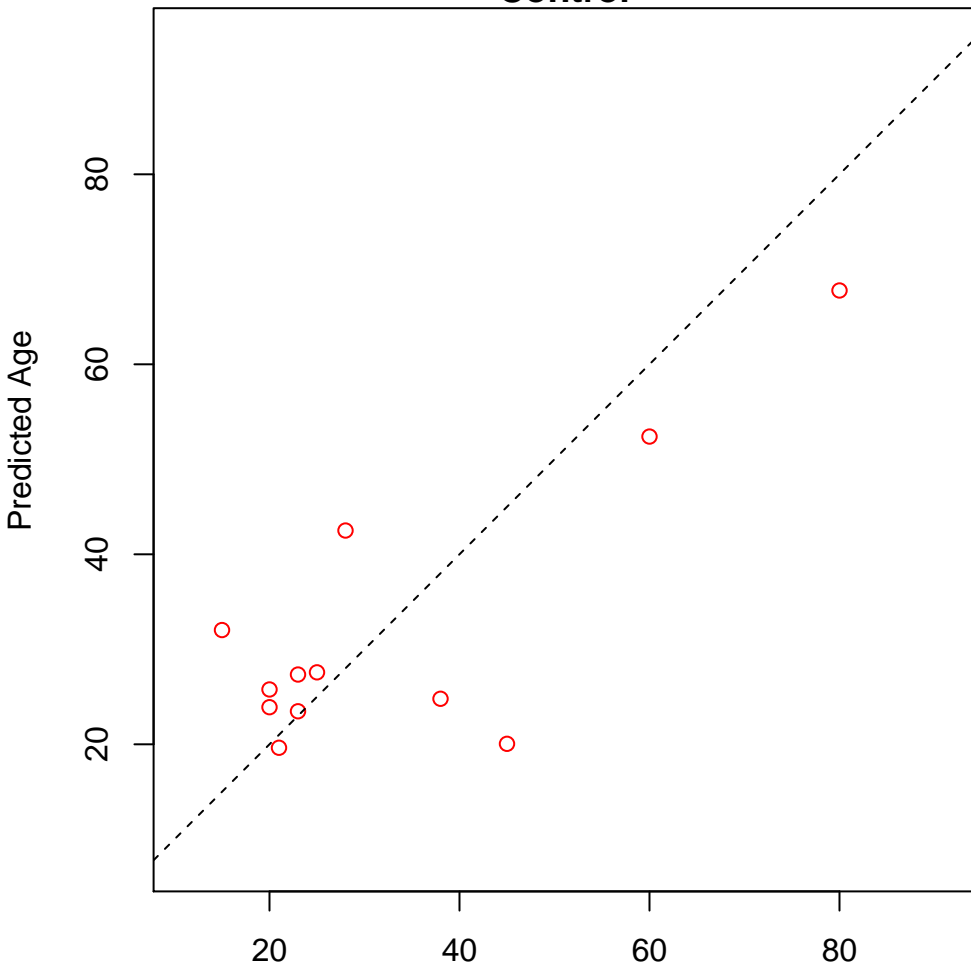


multicellular organismal water homeostasis (Score: 6.447275)

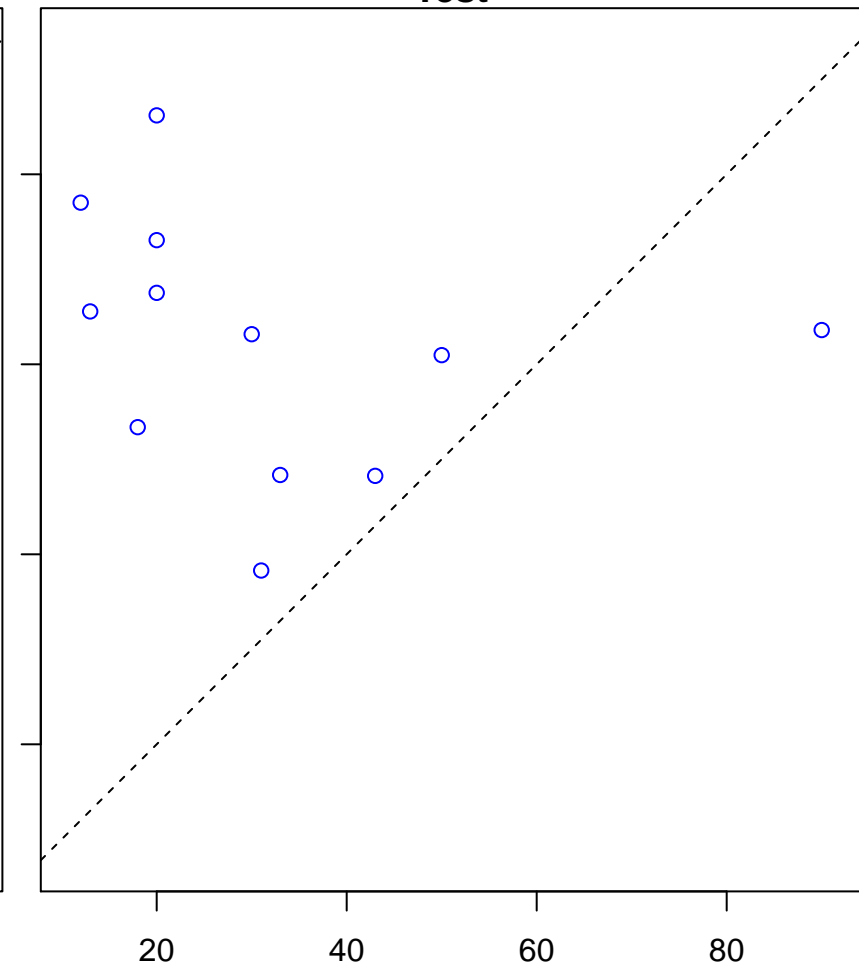


DNA dealkylation involved in DNA repair (Score: 6.445791)

Control

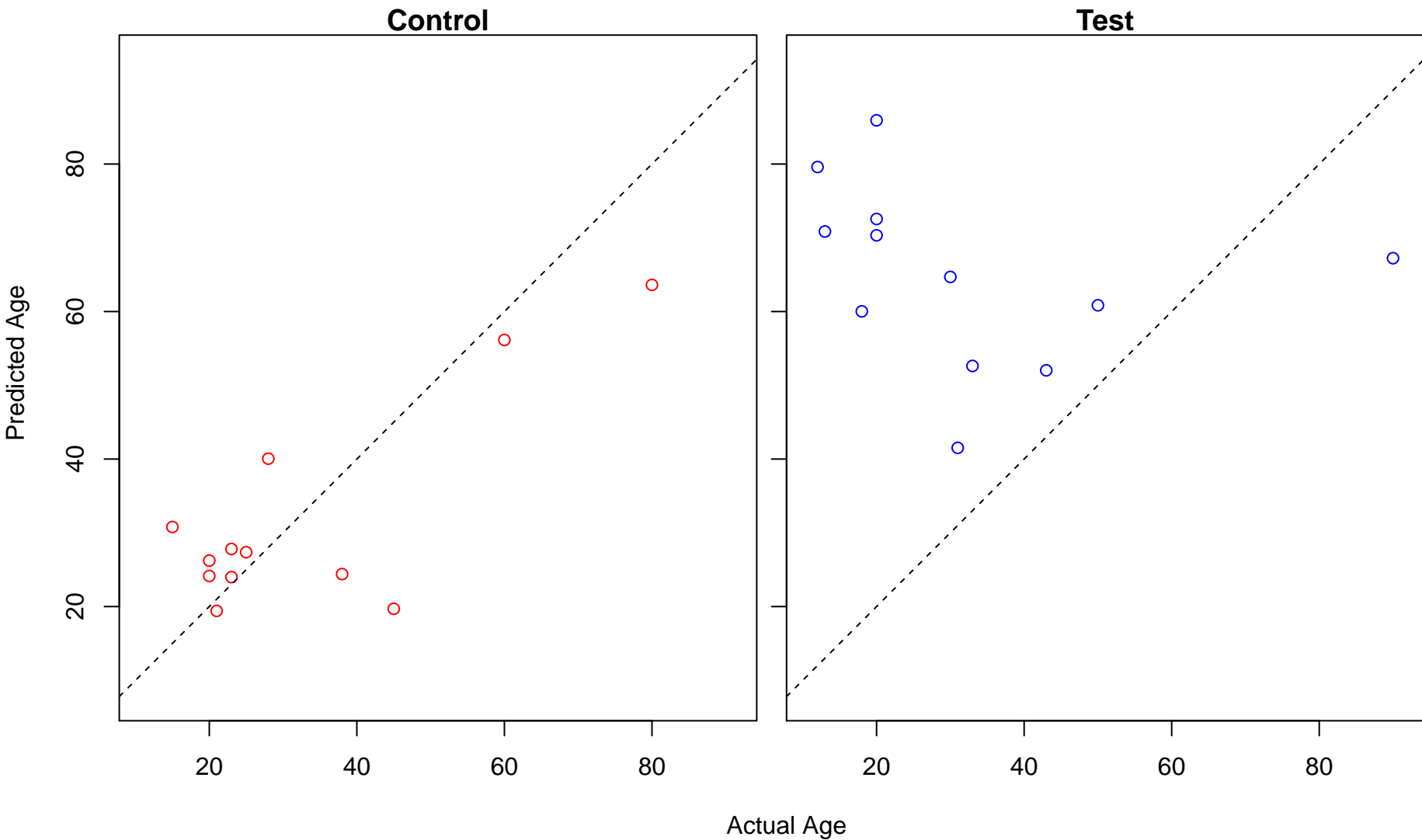


Test

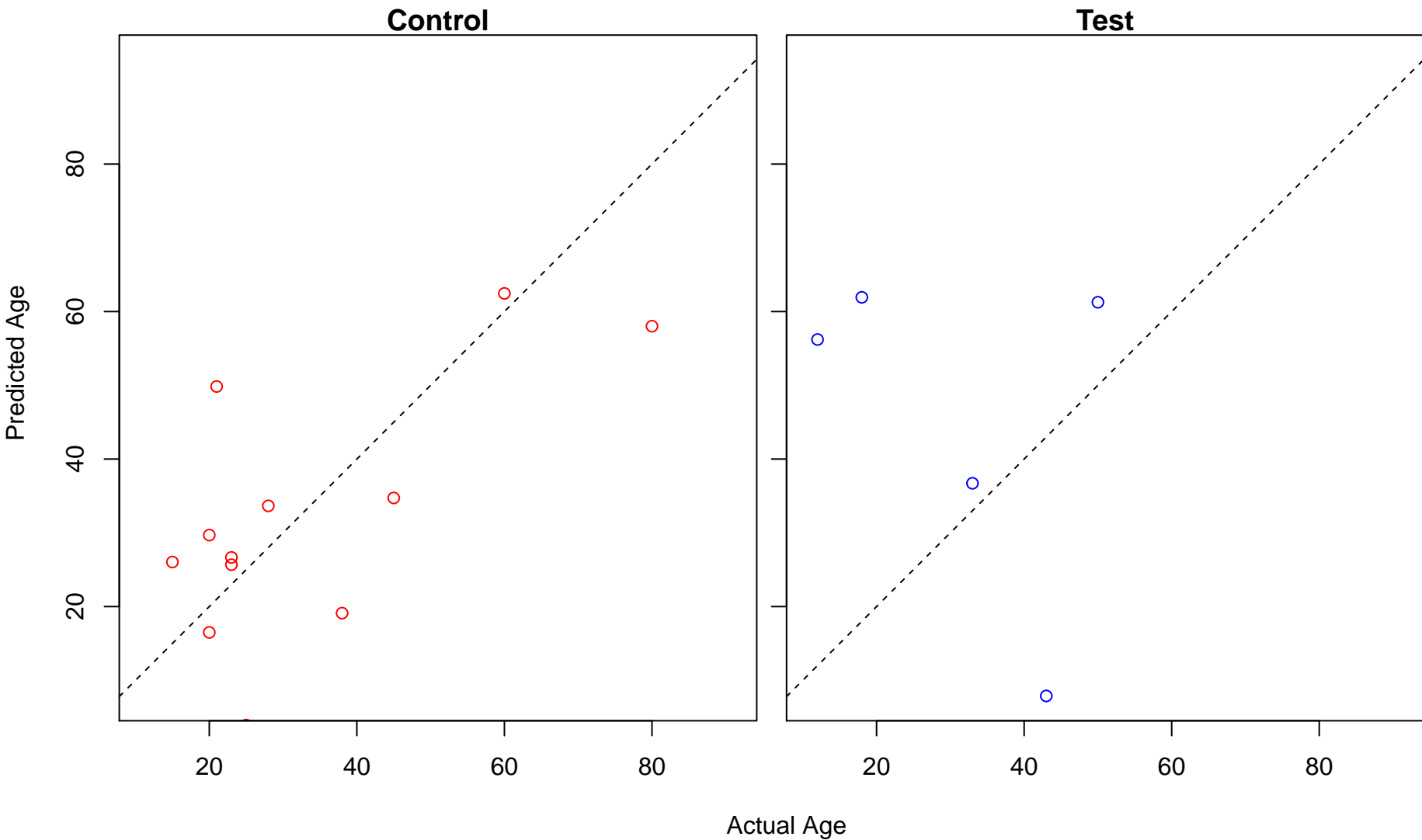


Actual Age

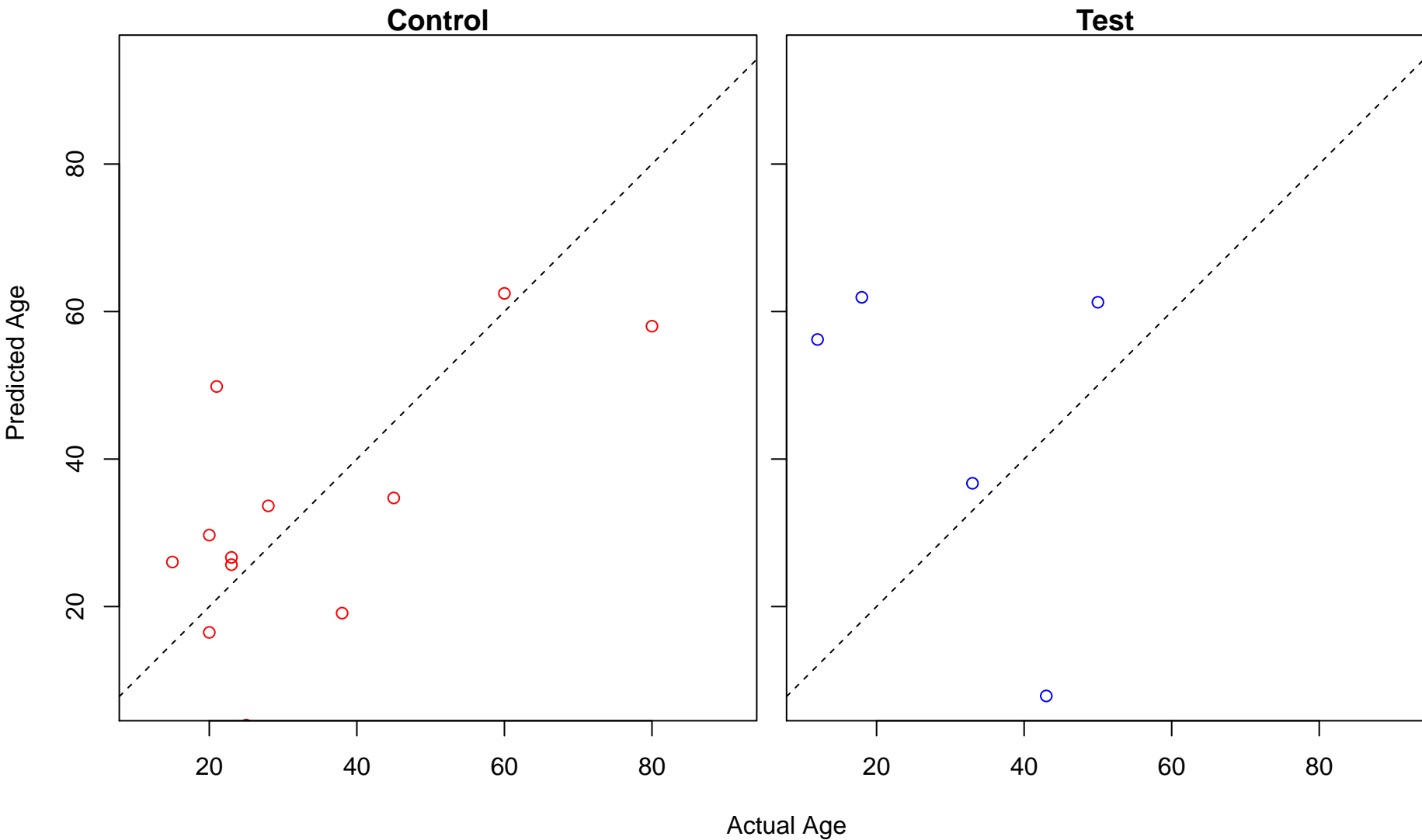
DNA demethylation (Score: 6.444227)



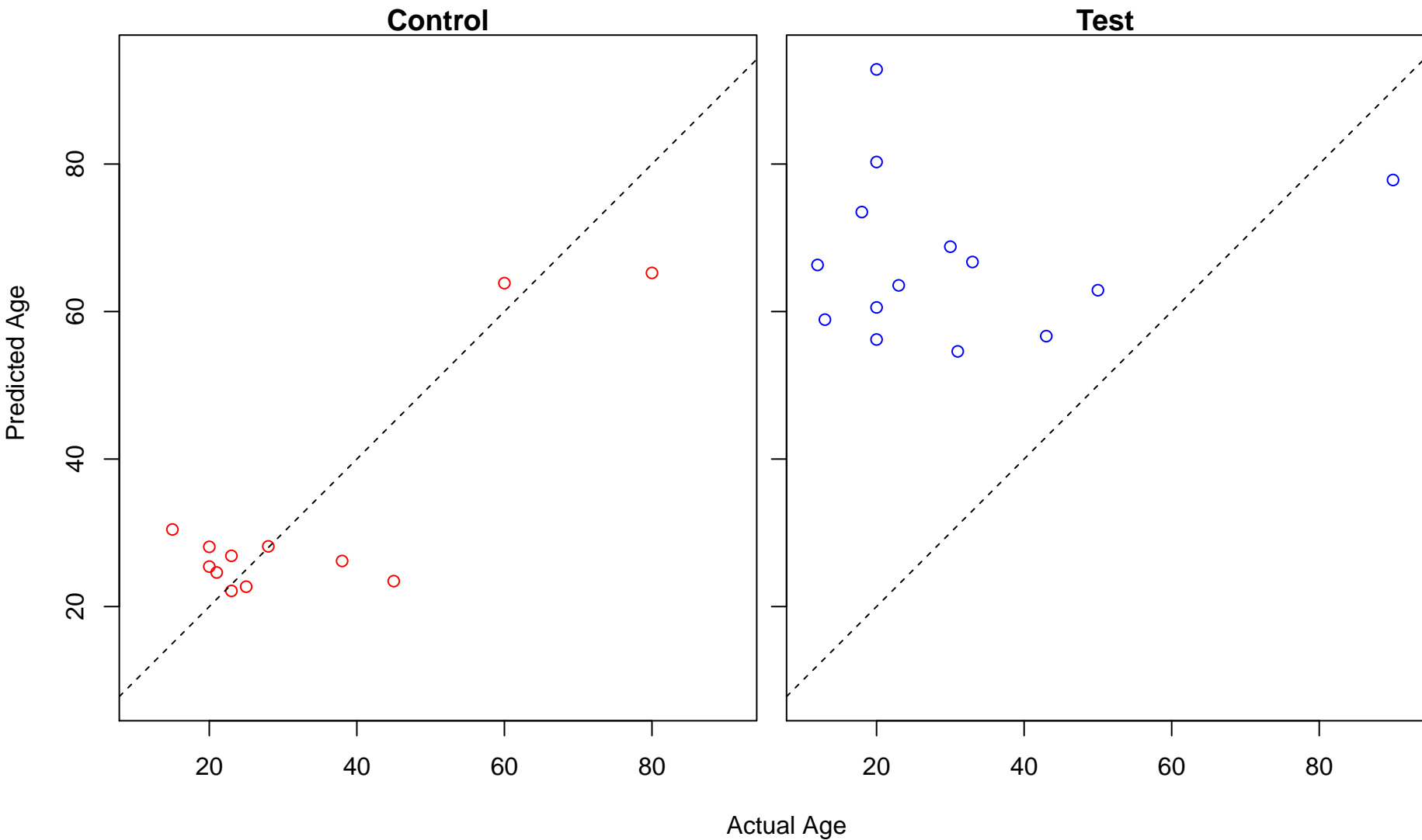
chylomicron remnant clearance (Score: 6.442790)



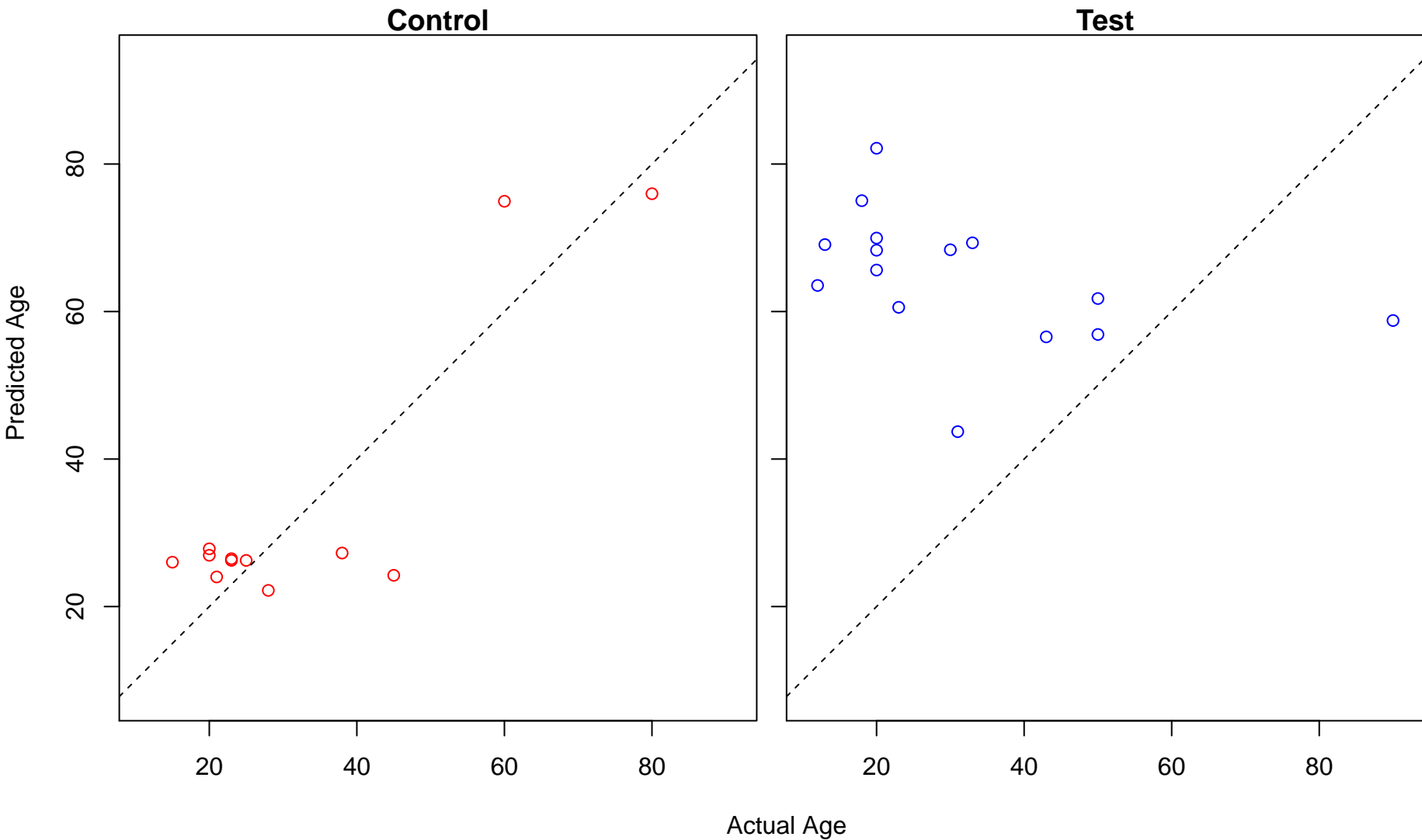
triglyceride-rich lipoprotein particle clearance (Score: 6.442790)



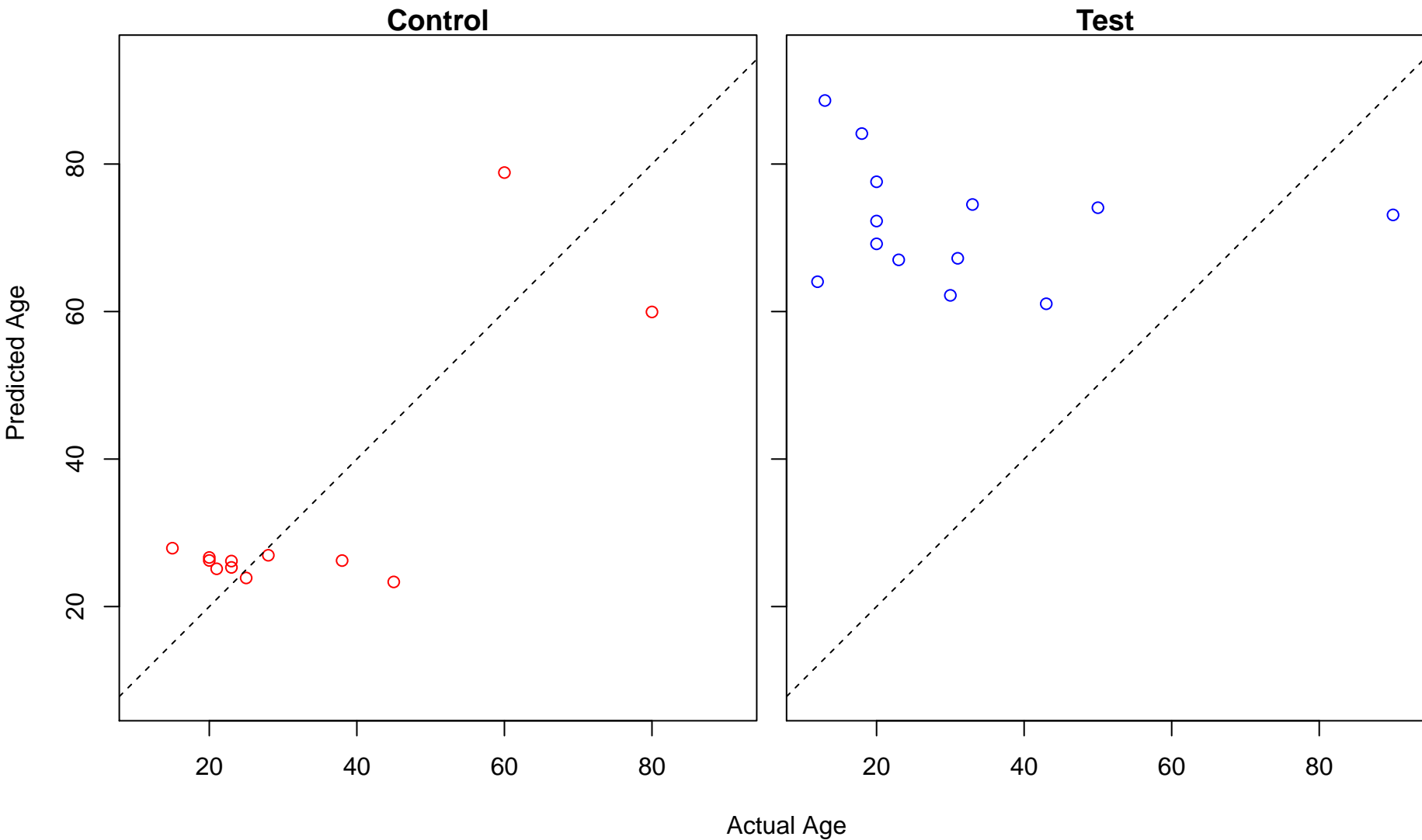
mammary gland development (Score: 6.441568)



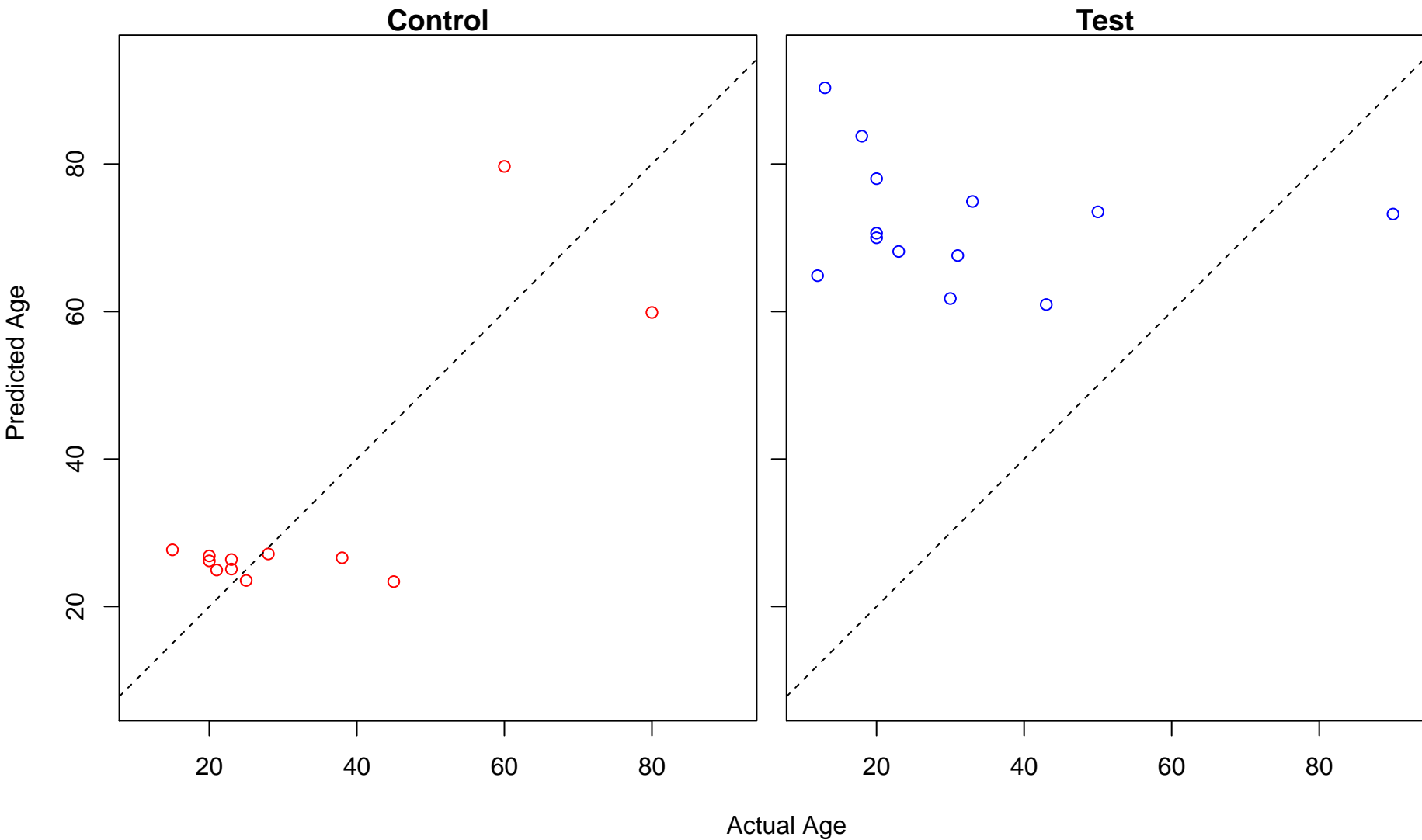
steroid hormone mediated signaling pathway (Score: 6.440735)



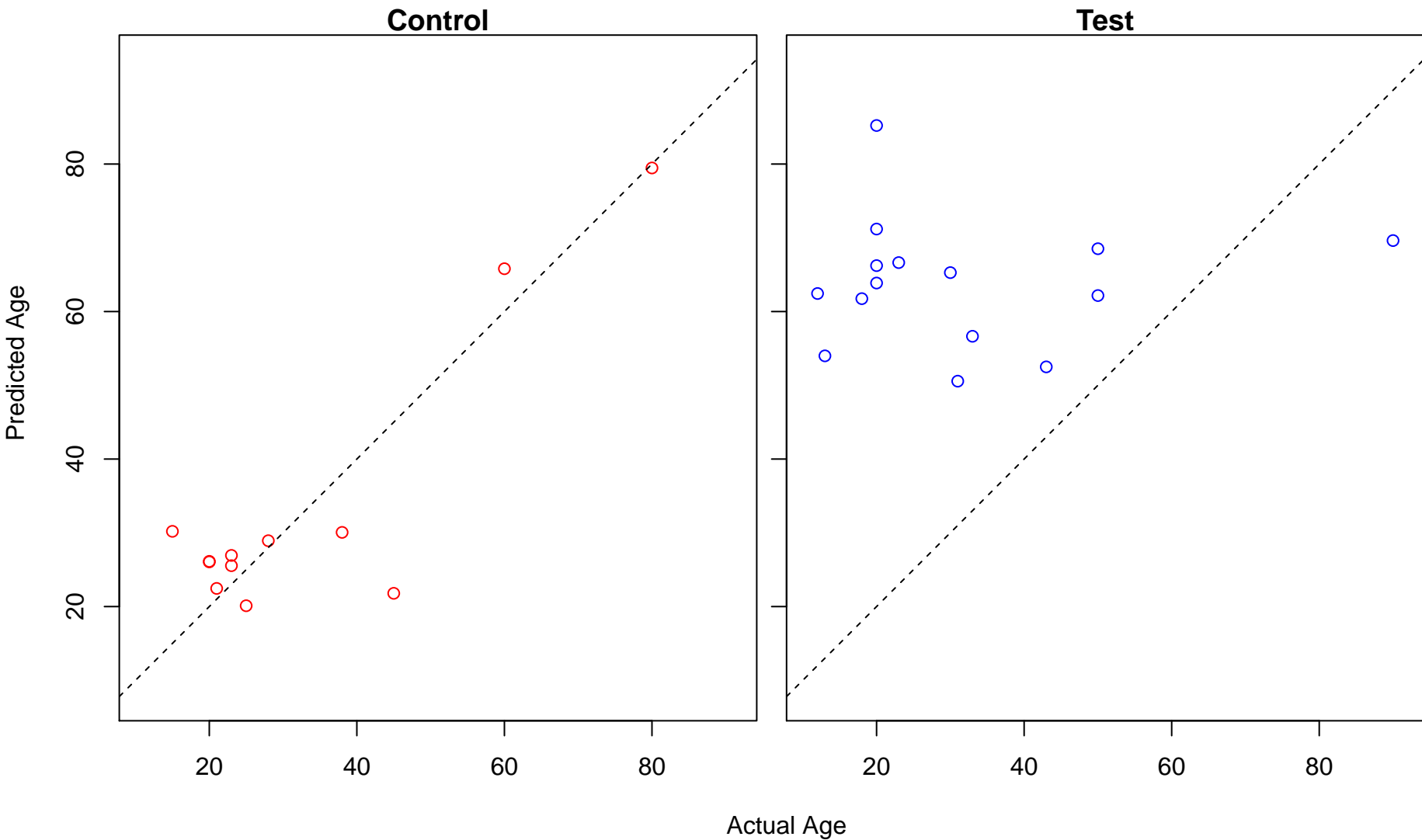
DNA damage response, signal transduction by p53 class mediator (Score: 6.437631)



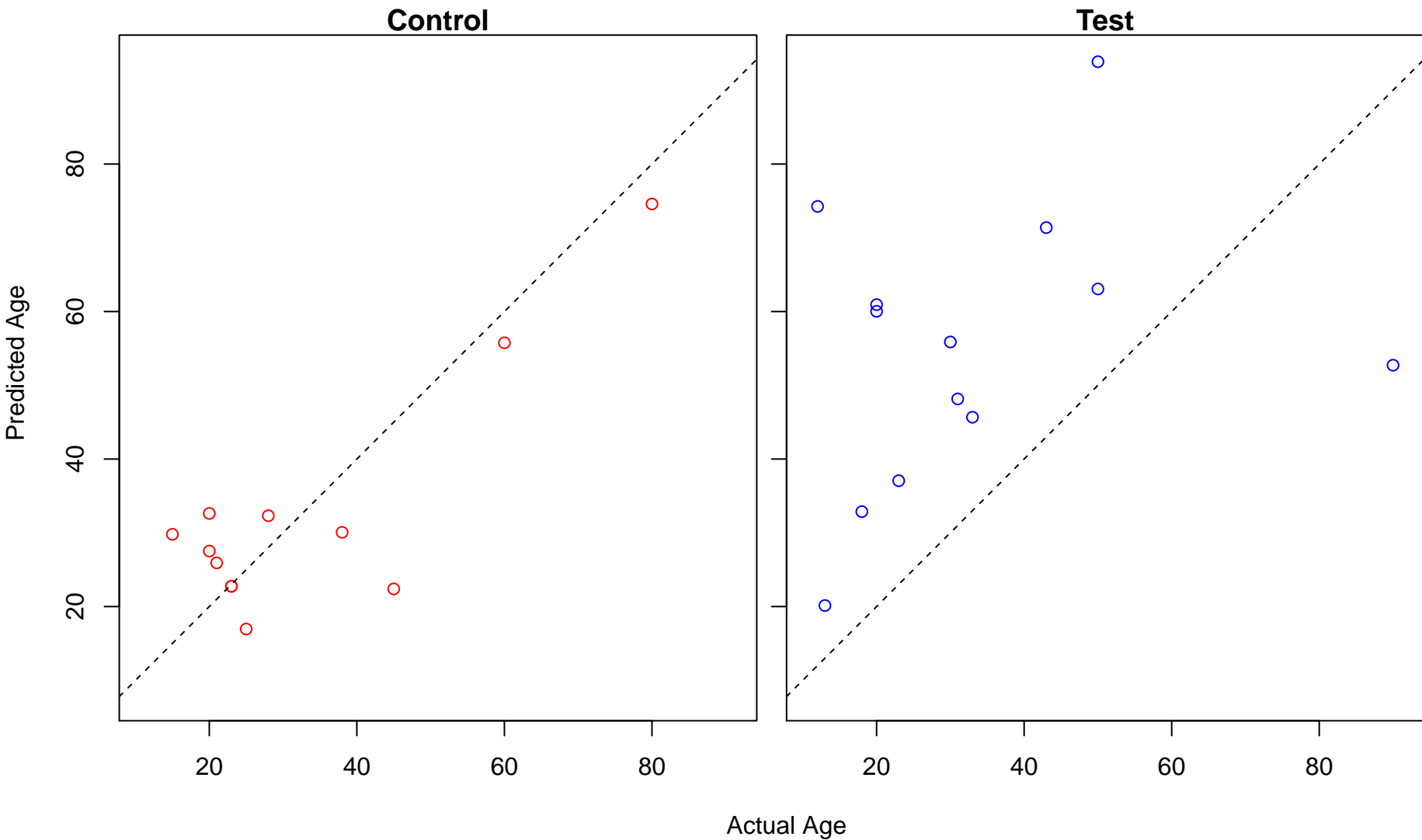
DNA biosynthetic process (Score: 6.437488)



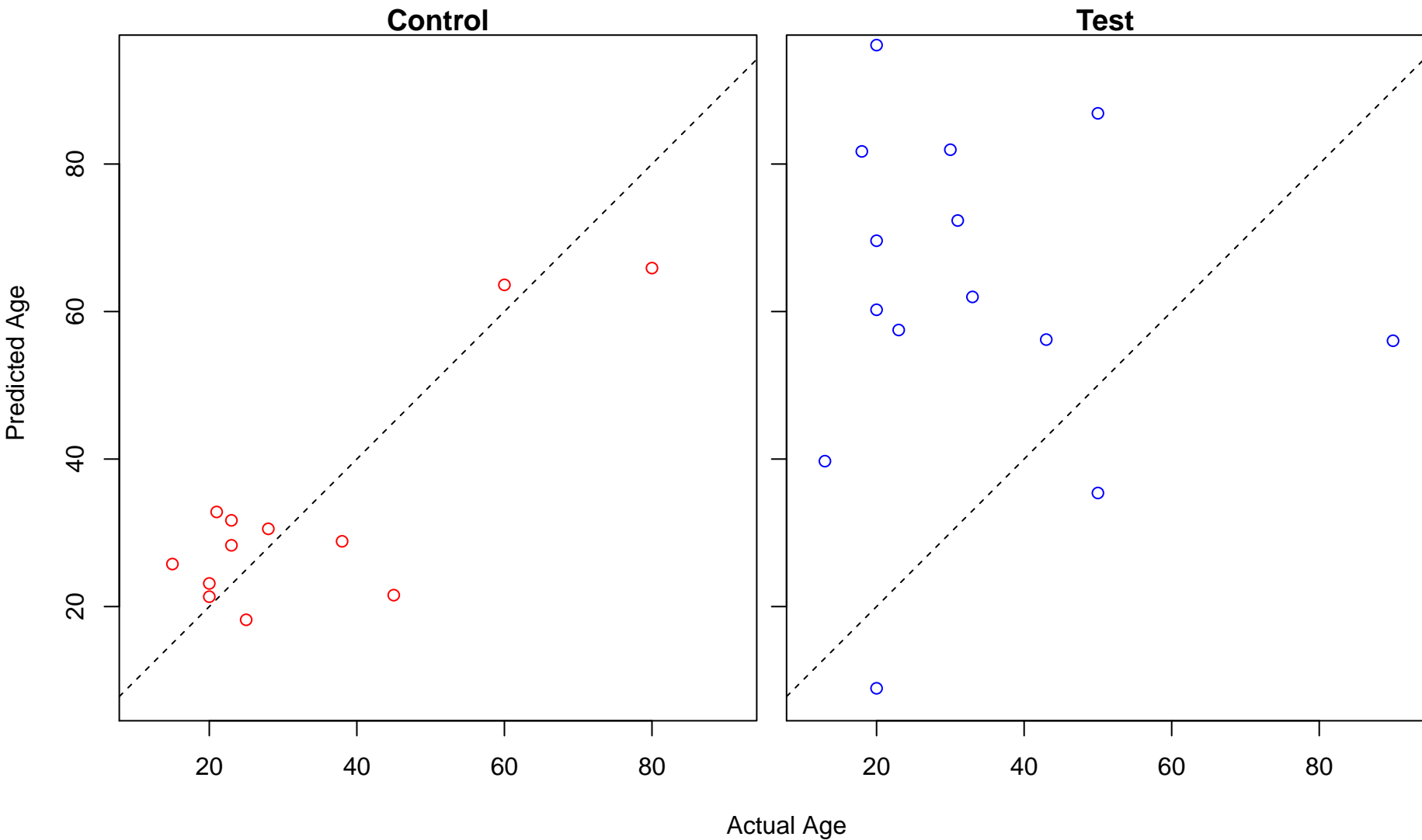
nitrogen compound transport (Score: 6.434753)



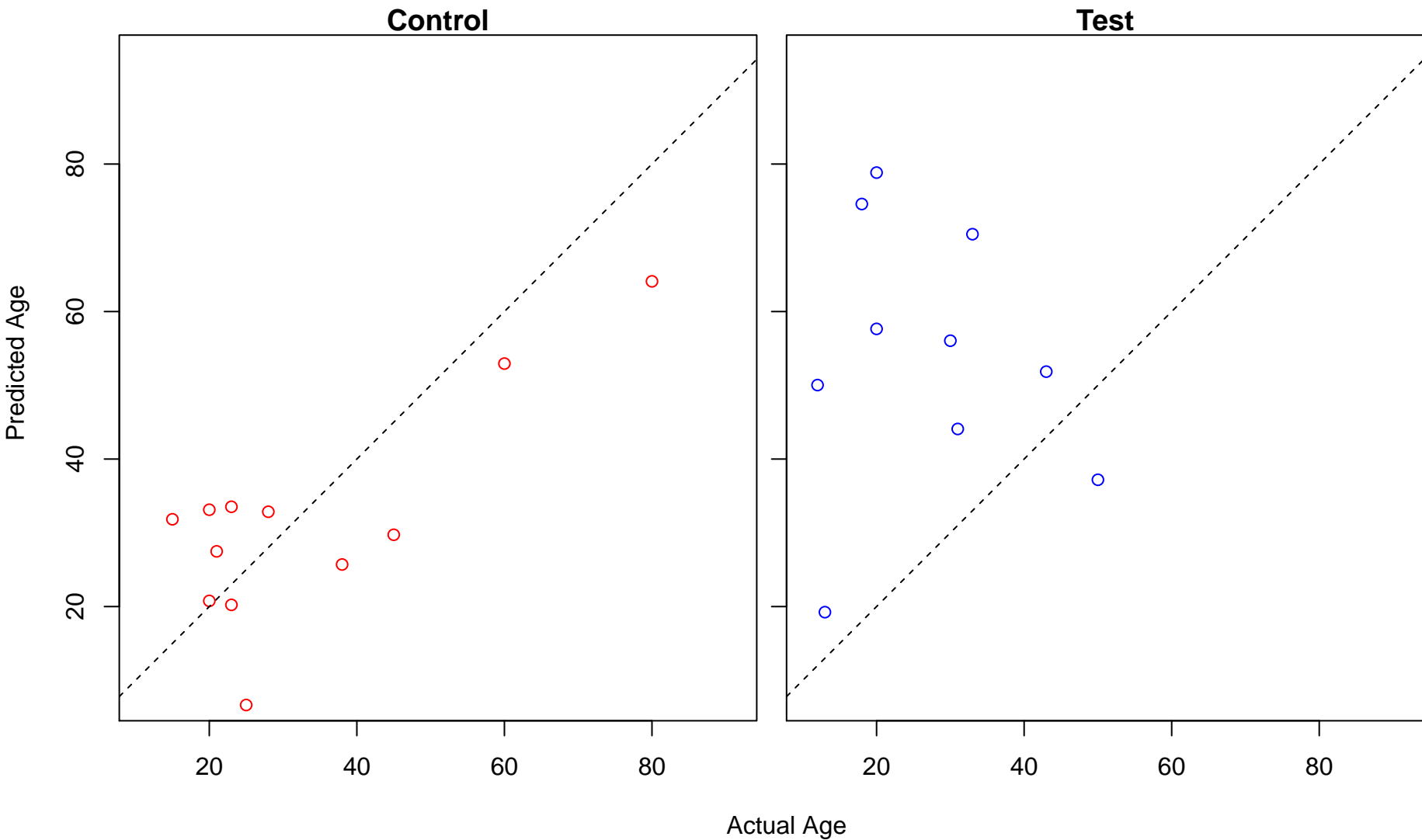
regulation of hormone metabolic process (Score: 6.430986)



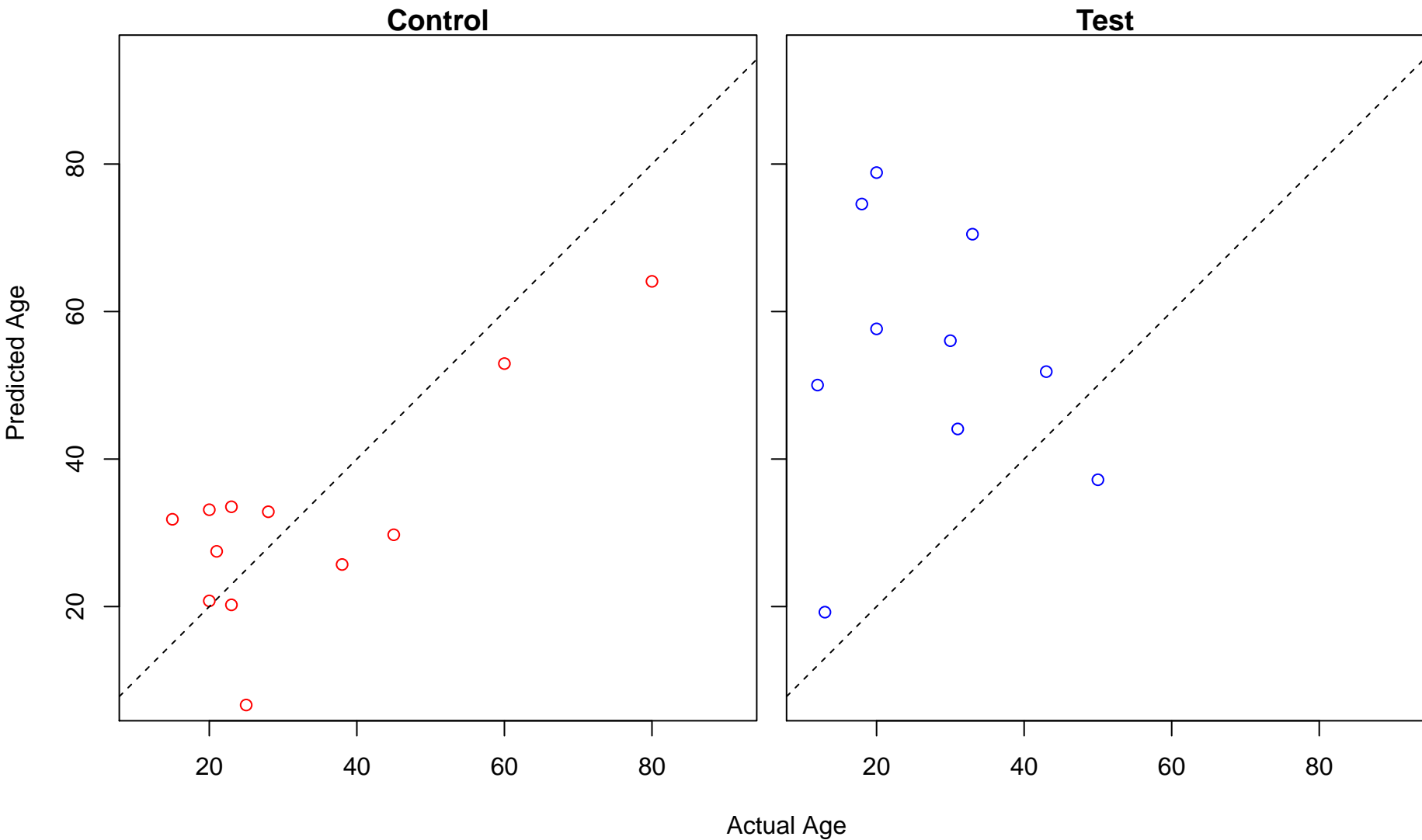
activin receptor signaling pathway (Score: 6.430613)



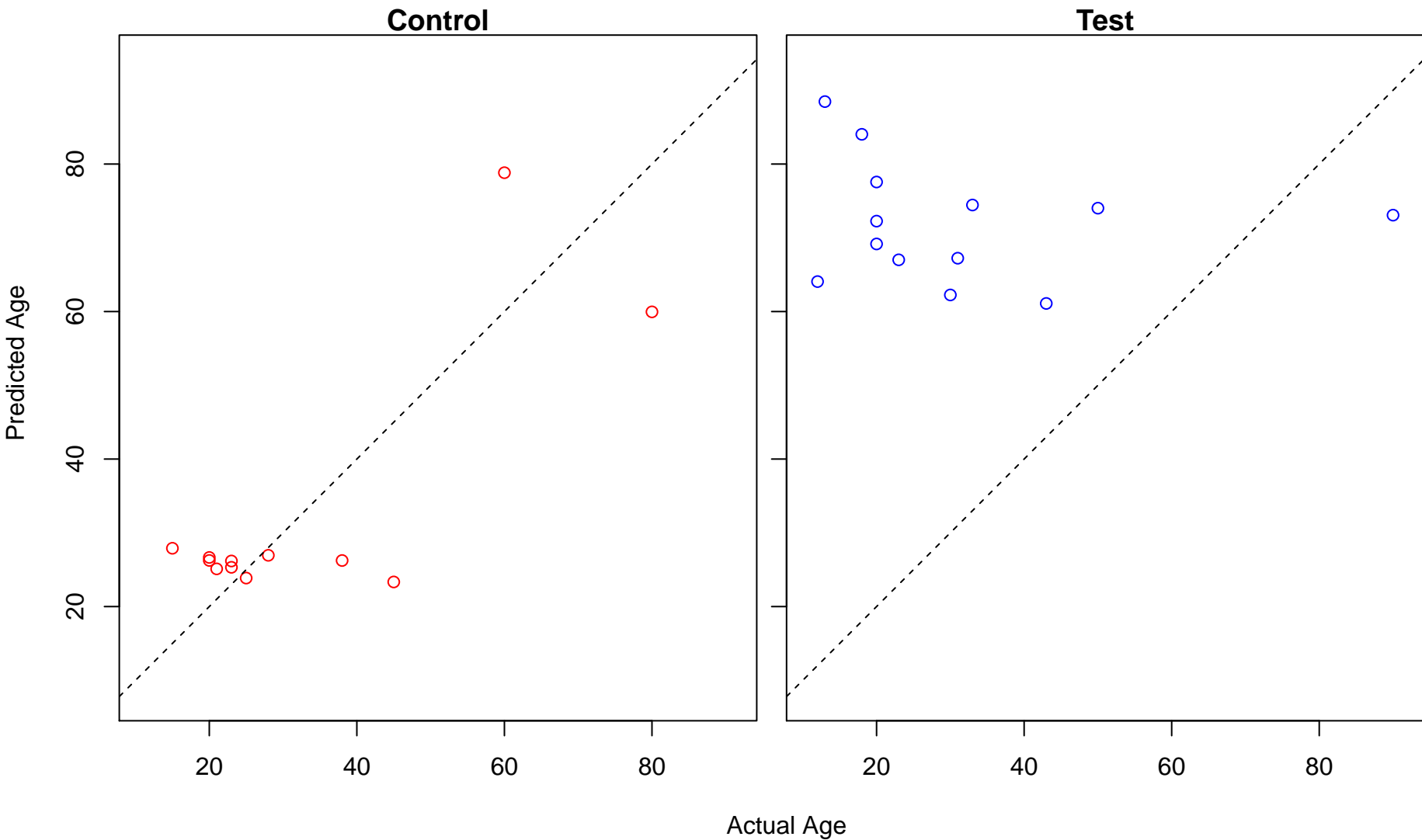
Purkinje myocyte to ventricular cardiac muscle cell signaling (Score: 6.429293)



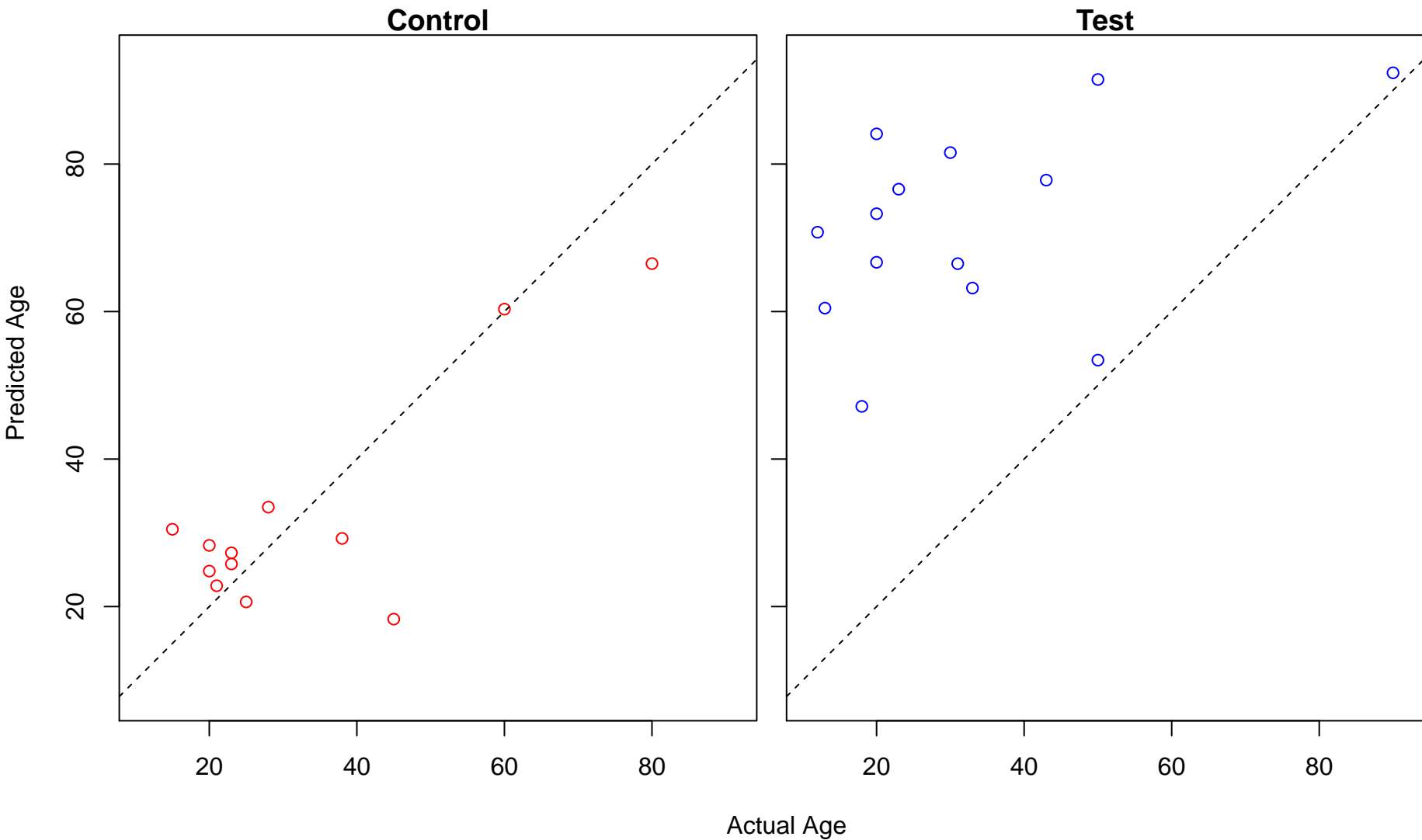
Purkinje myocyte to ventricular cardiac muscle cell communication (Score: 6.429293)



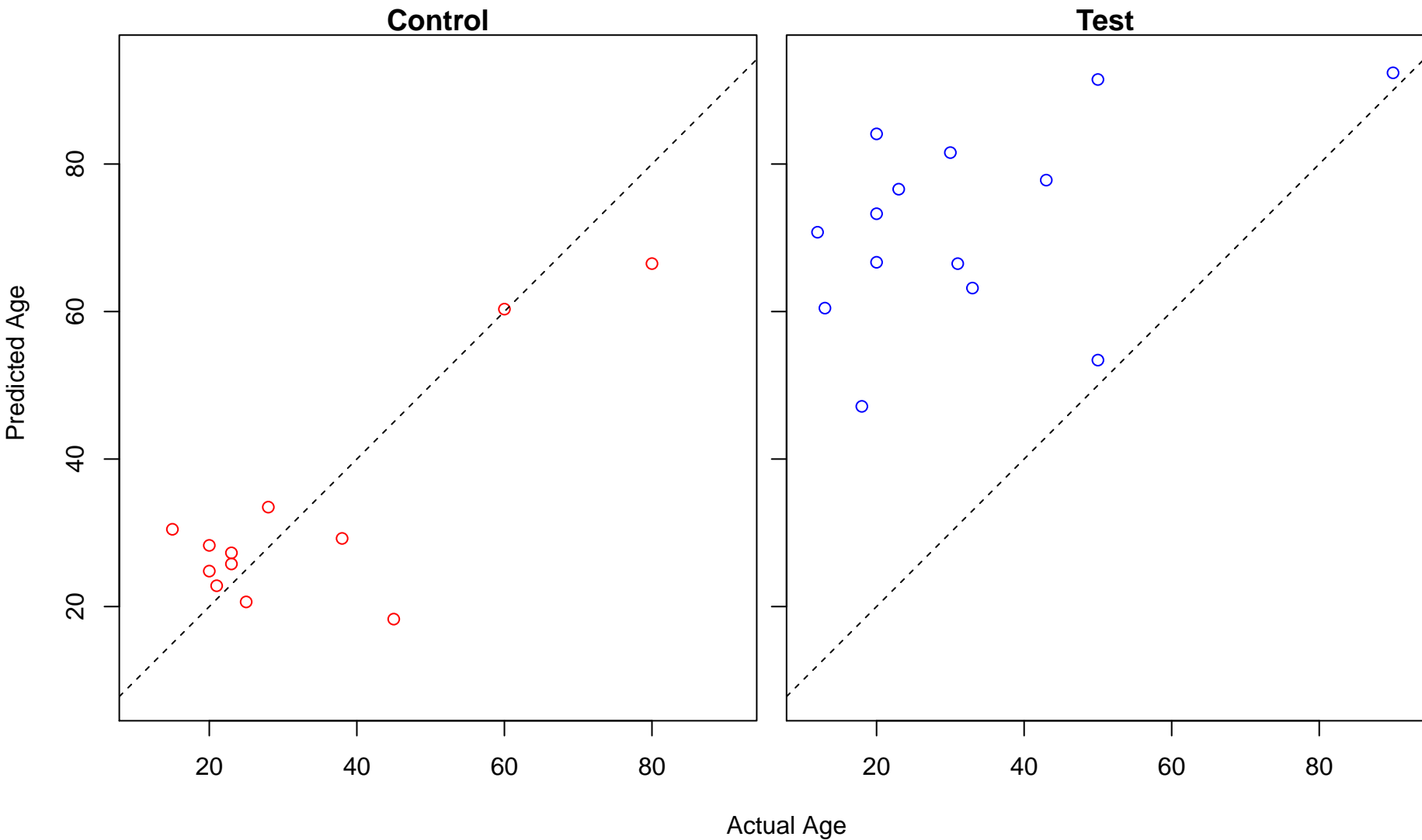
signal transduction in response to DNA damage (Score: 6.428115)



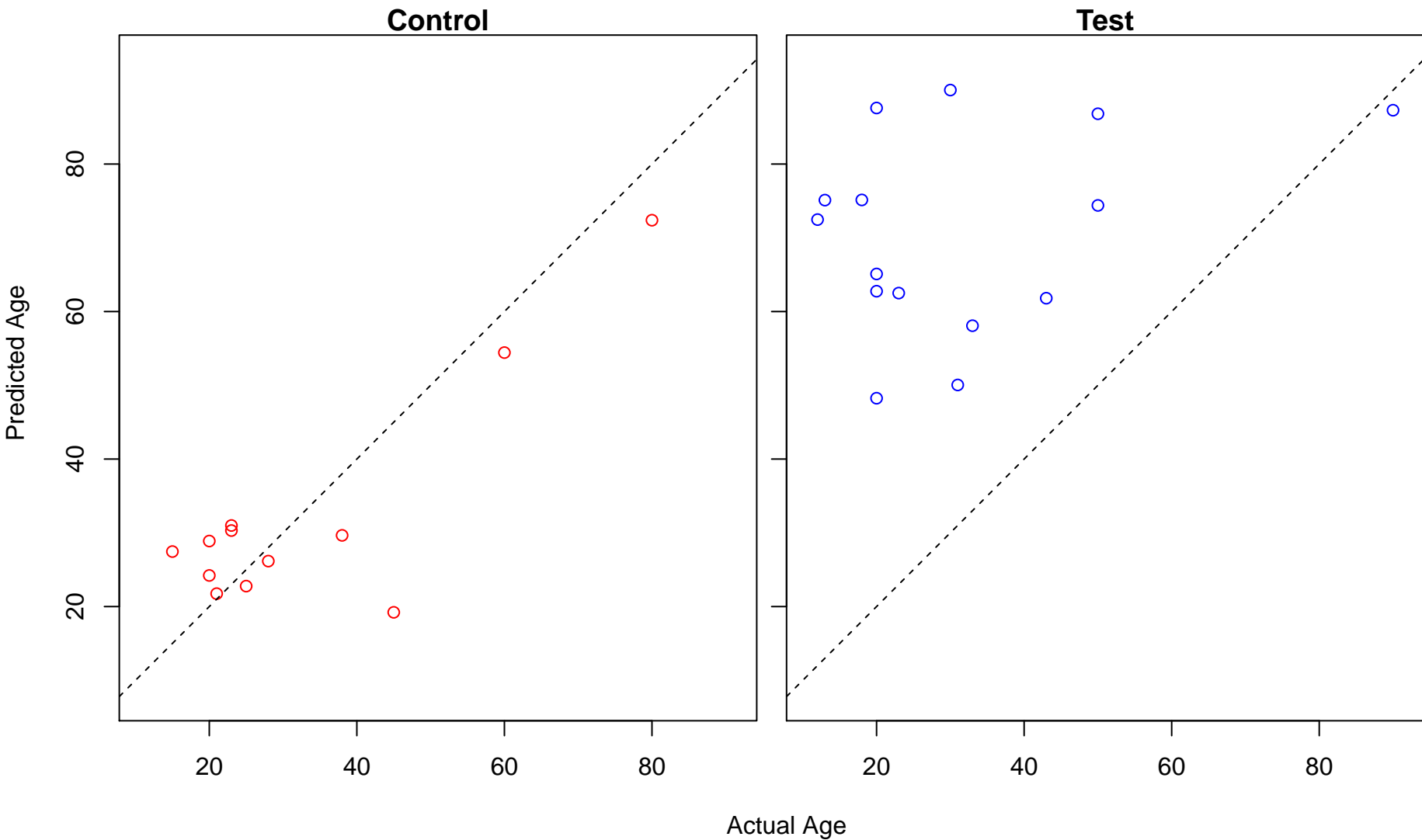
establishment or maintenance of apical/basal cell polarity (Score: 6.427999)



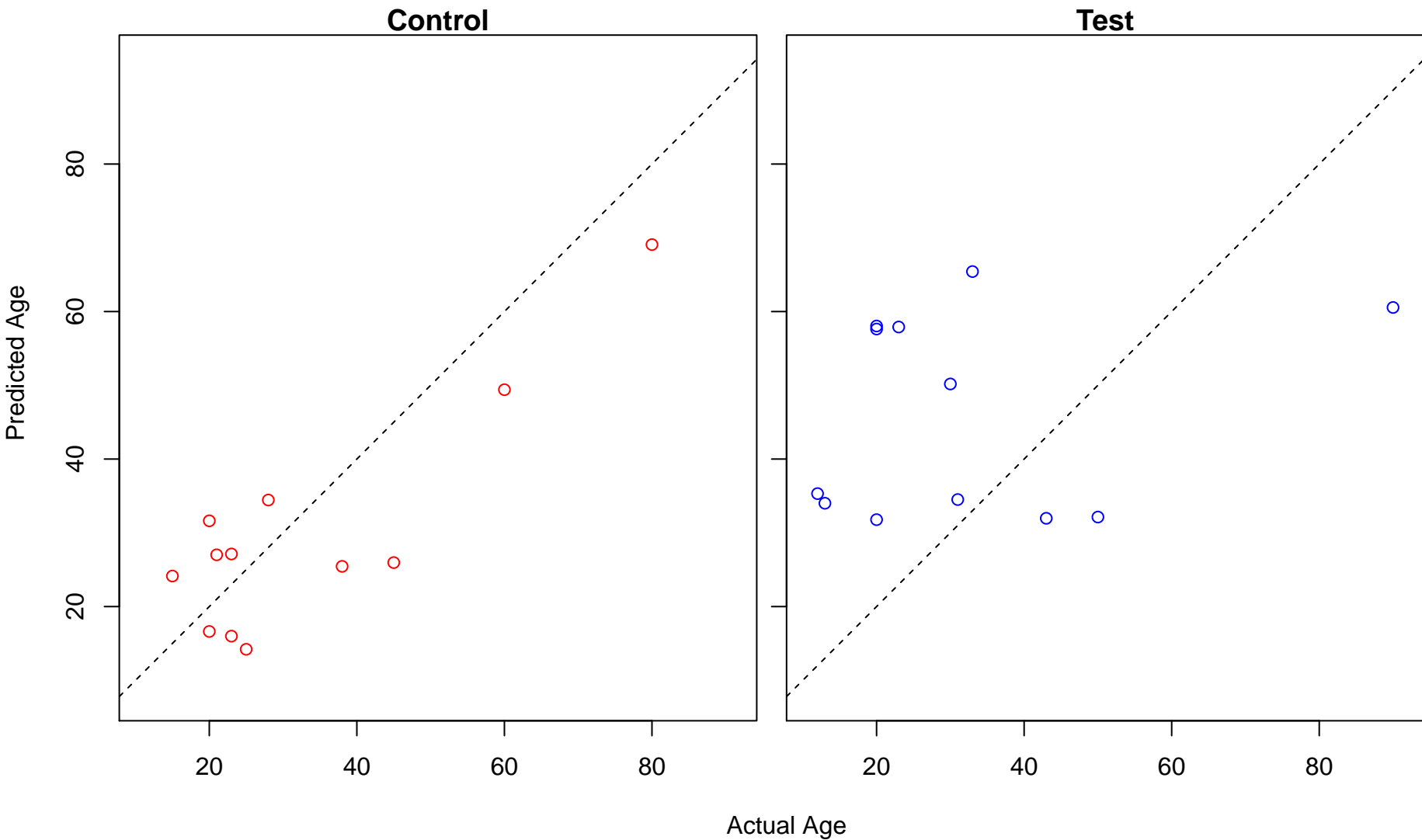
establishment or maintenance of bipolar cell polarity (Score: 6.427999)



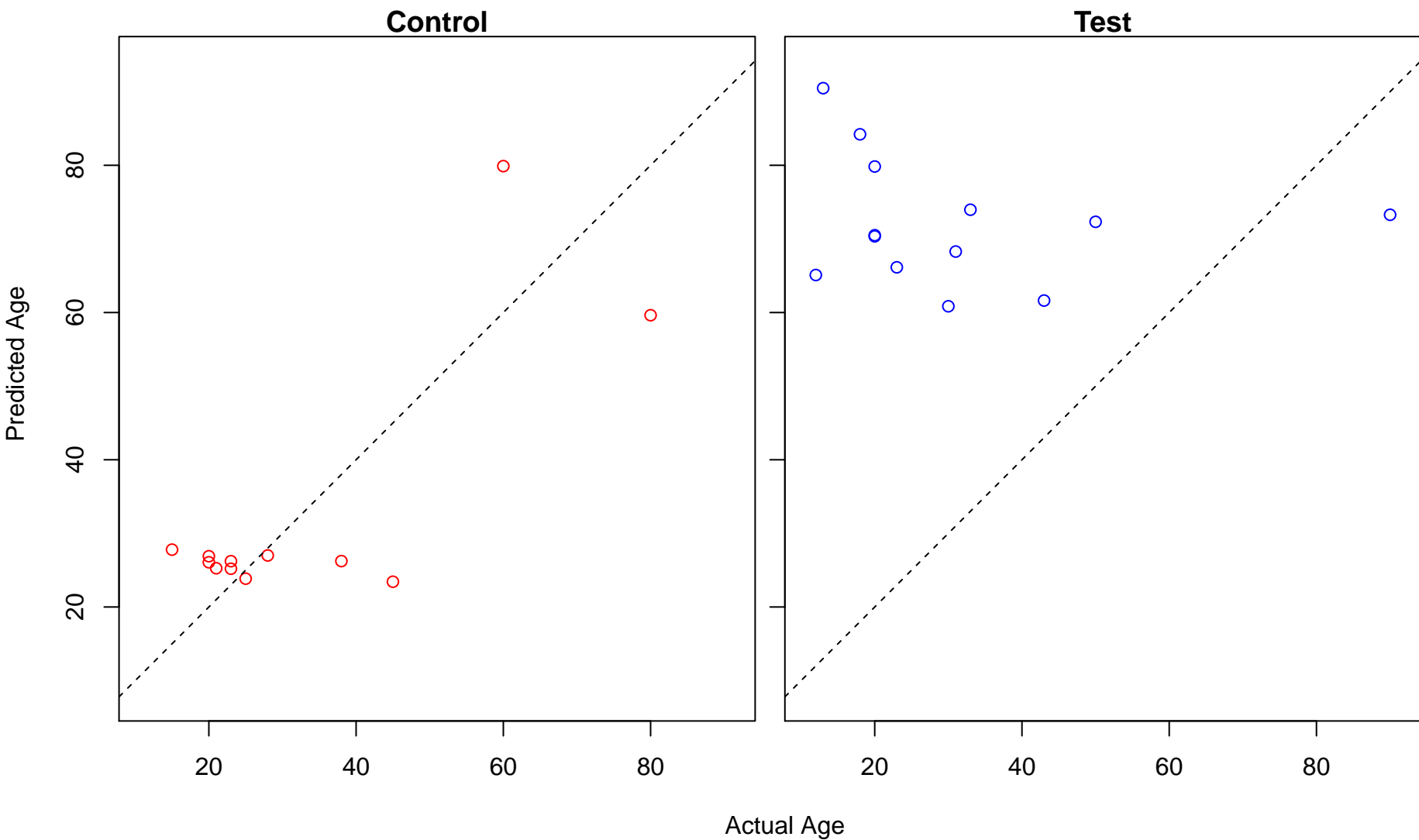
regulation of oligodendrocyte differentiation (Score: 6.423572)



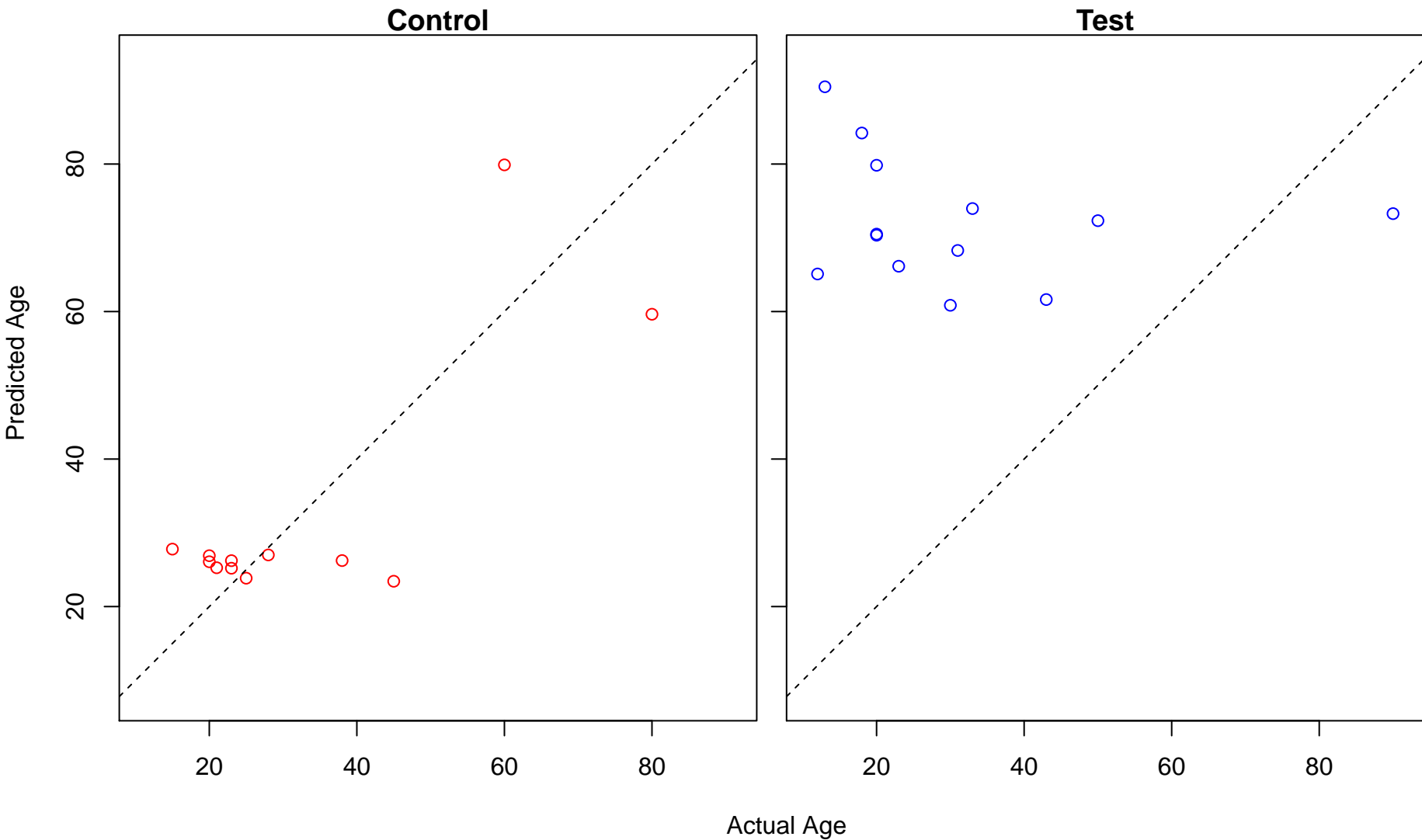
ribonucleoprotein complex export from nucleus (Score: 6.422400)



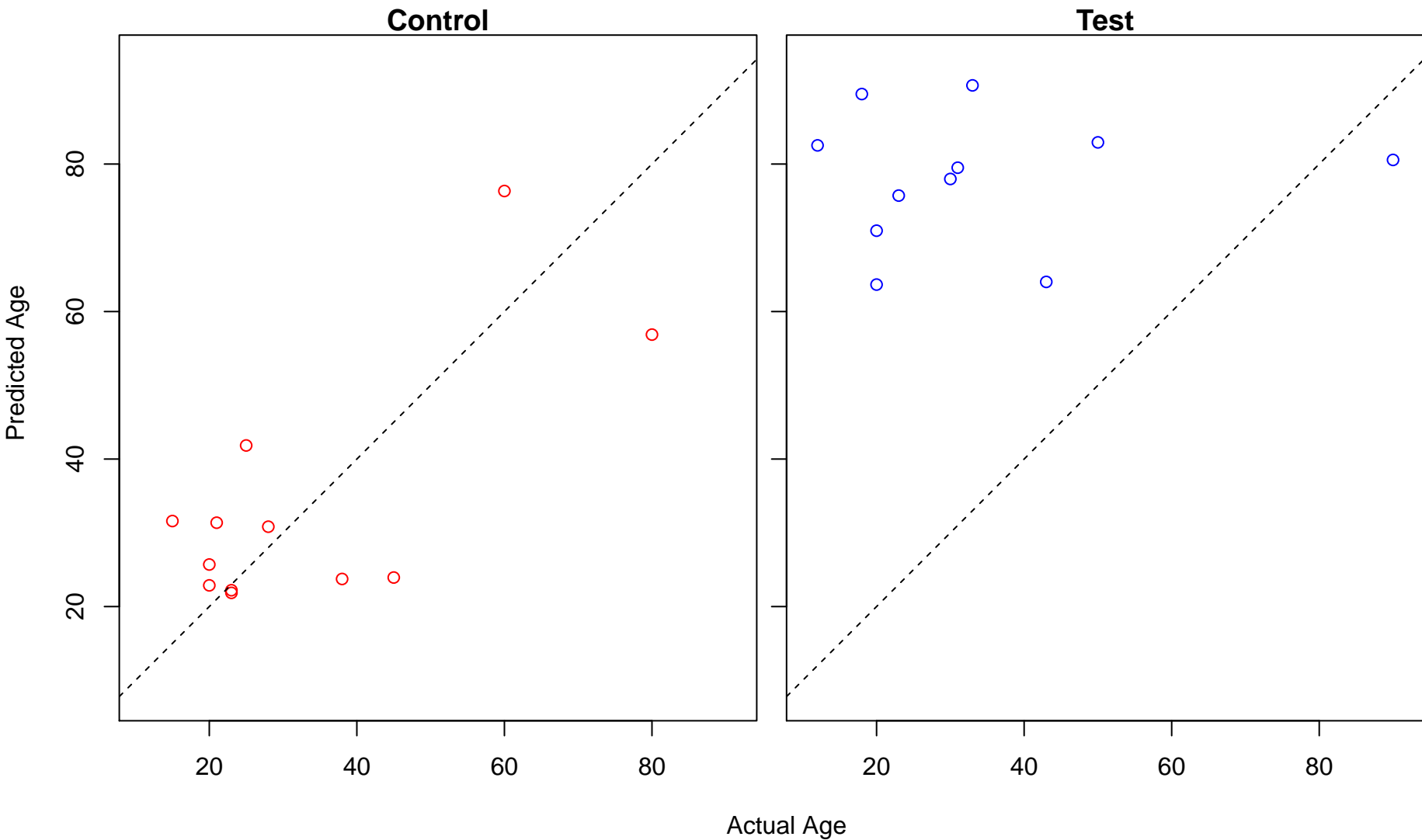
toll-like receptor 5 signaling pathway (Score: 6.422308)



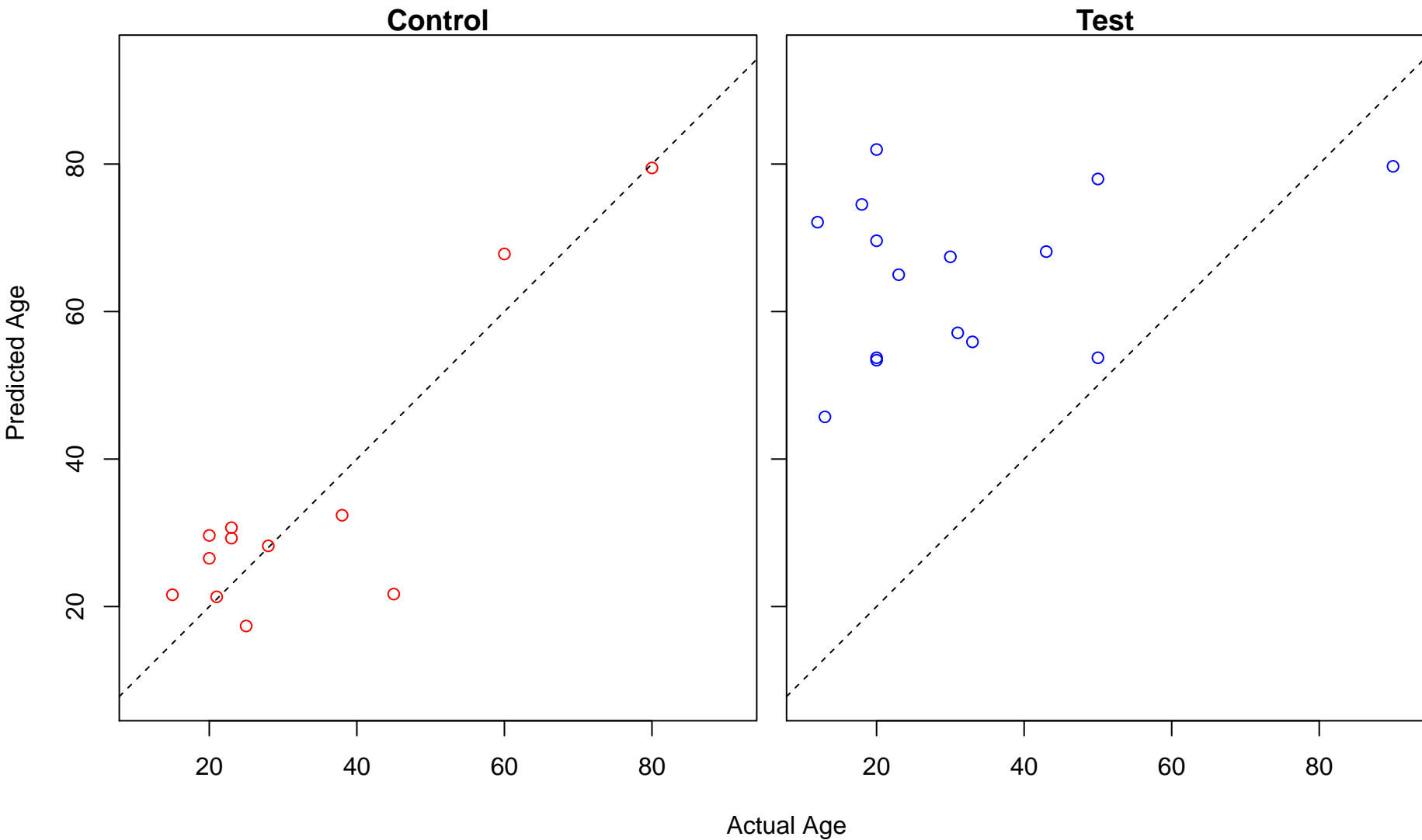
toll-like receptor 10 signaling pathway (Score: 6.422308)



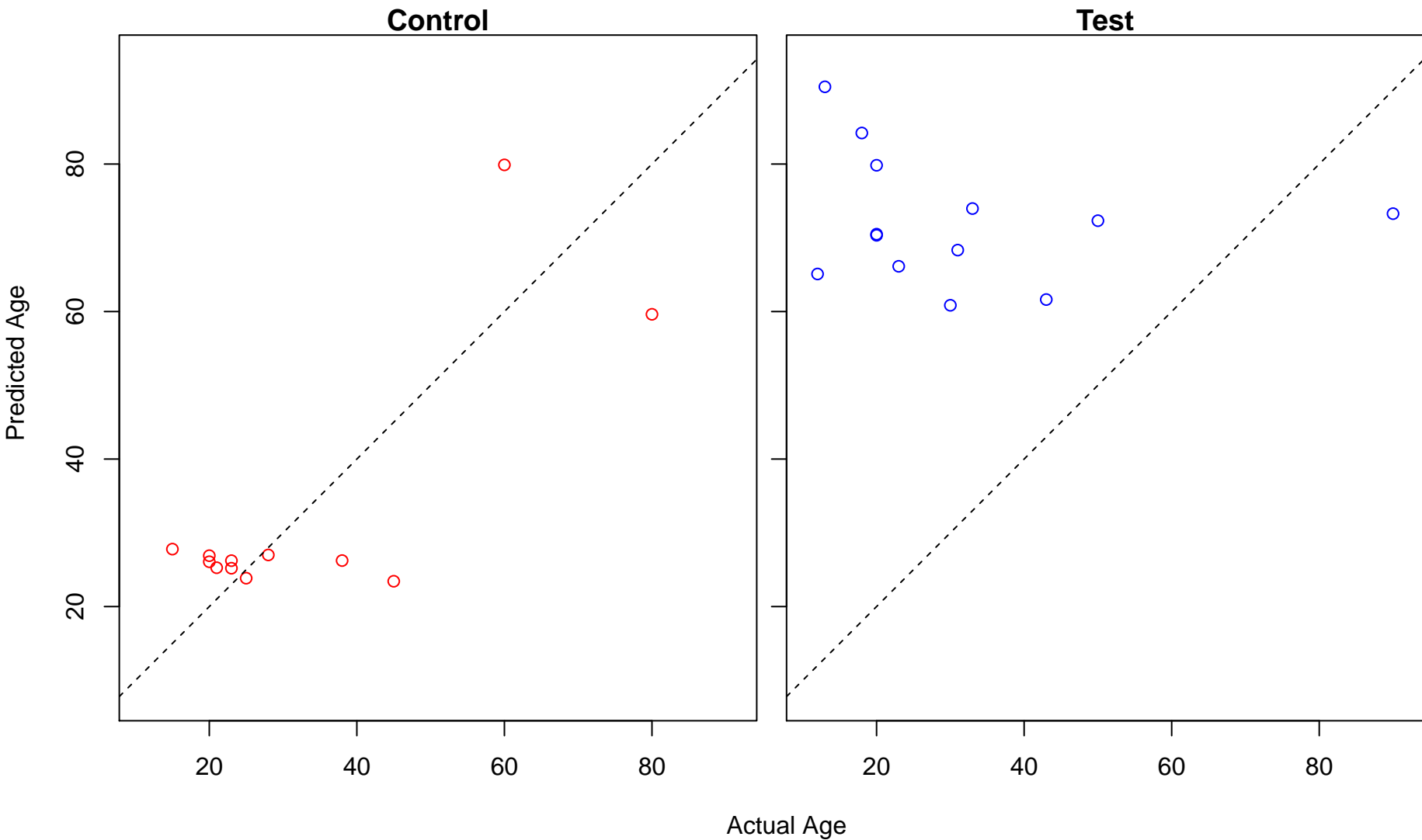
positive regulation of T cell apoptotic process (Score: 6.421882)



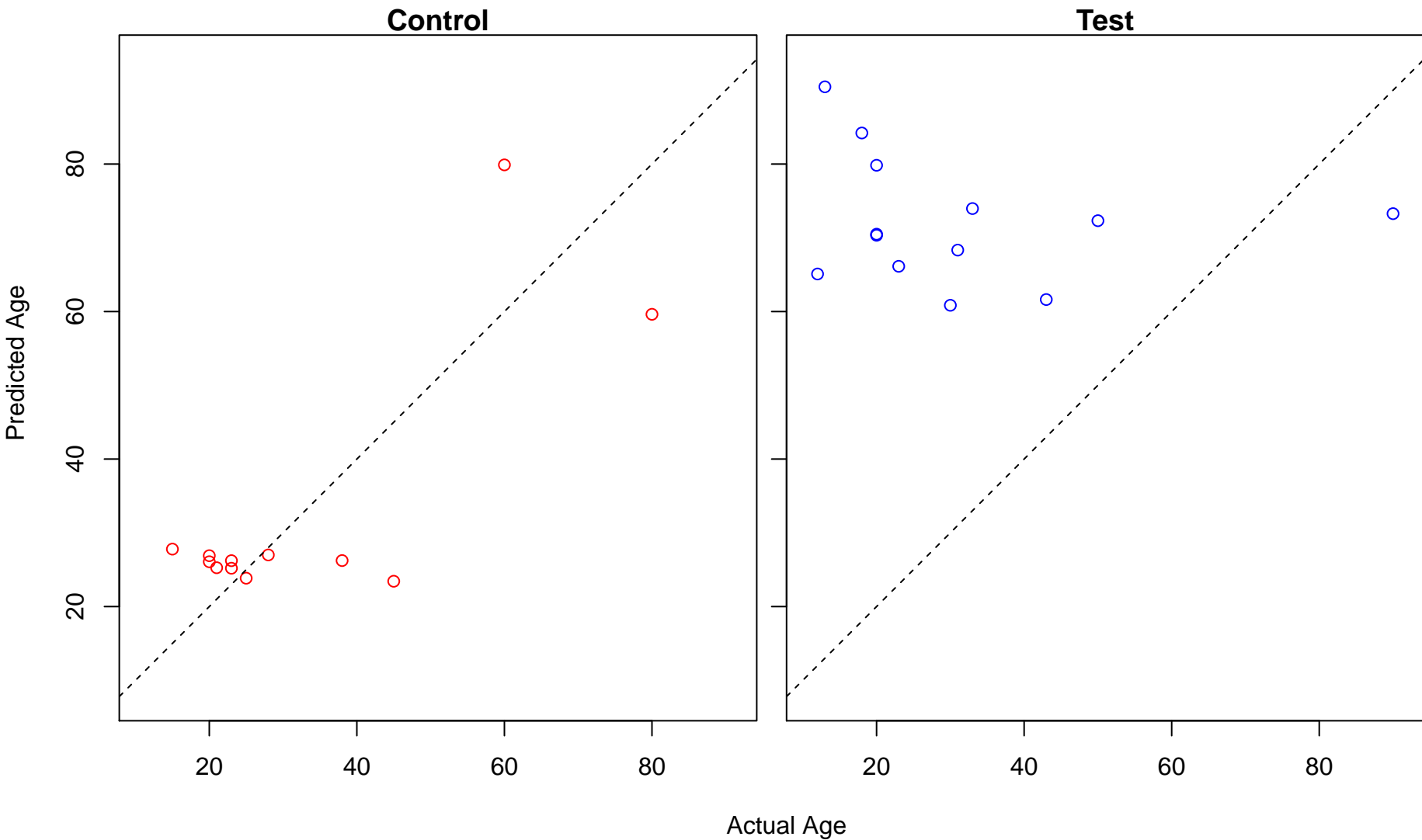
limbic system development (Score: 6.421258)



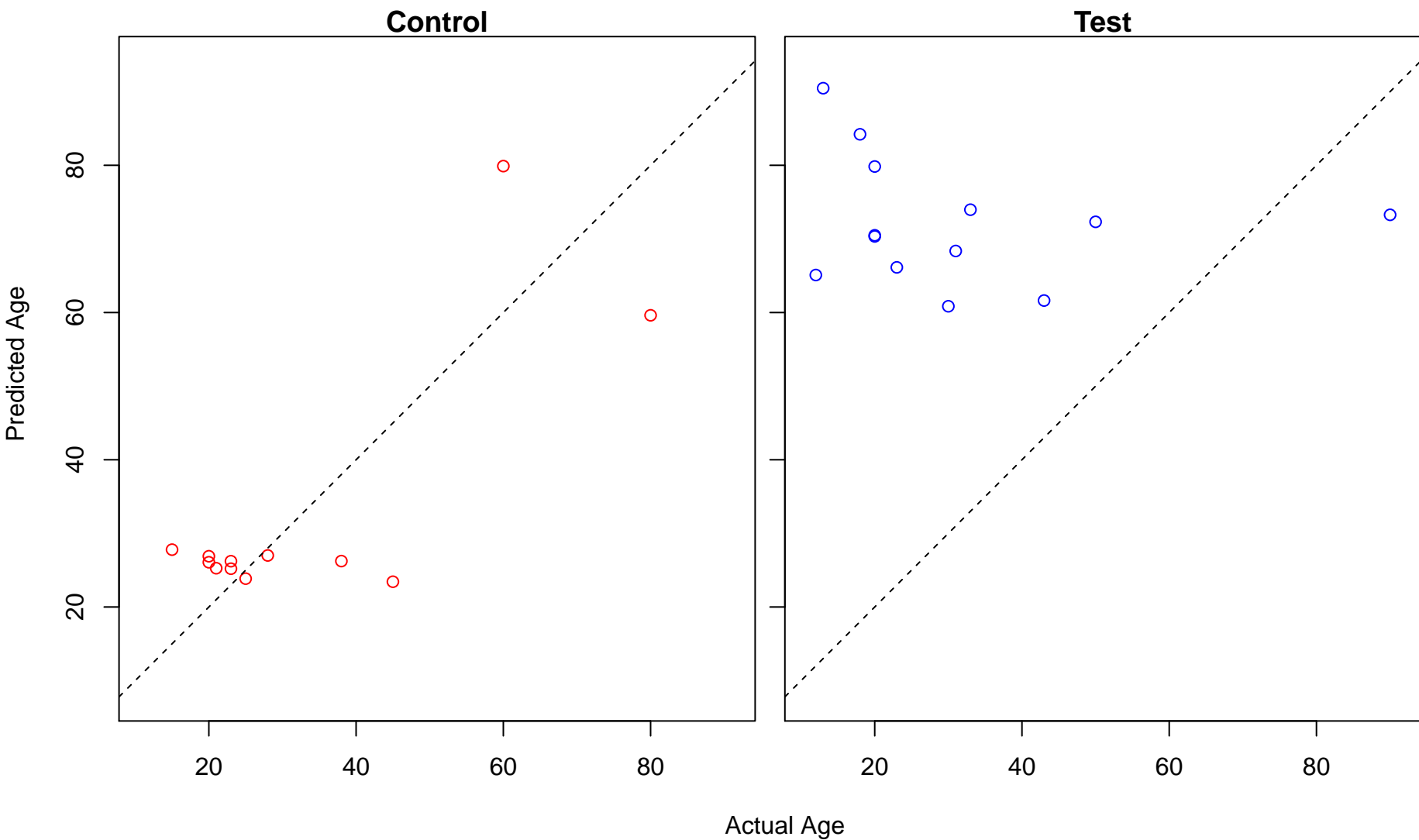
toll-like receptor TLR1:TLR2 signaling pathway (Score: 6.421018)



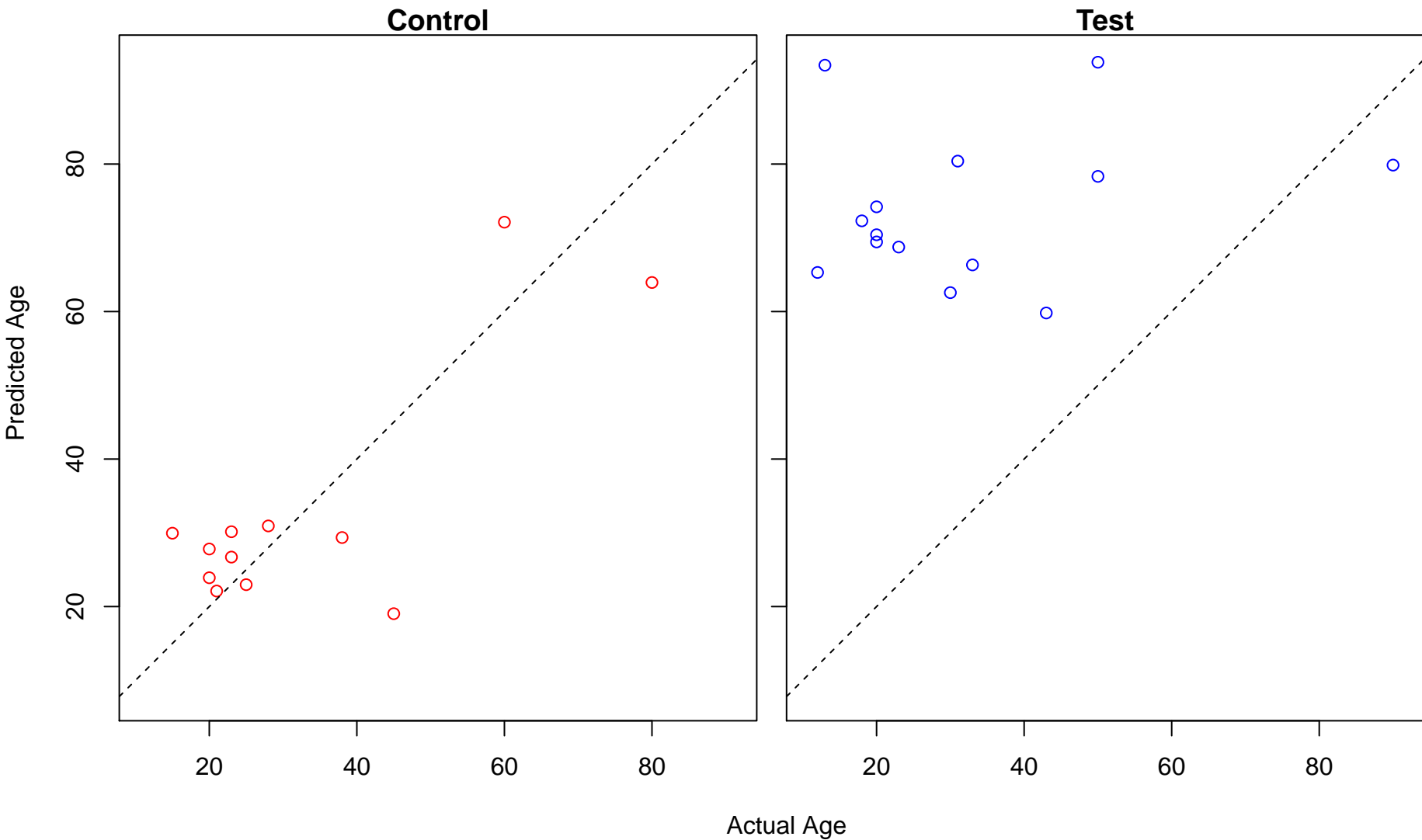
toll-like receptor TLR6:TLR2 signaling pathway (Score: 6.421018)



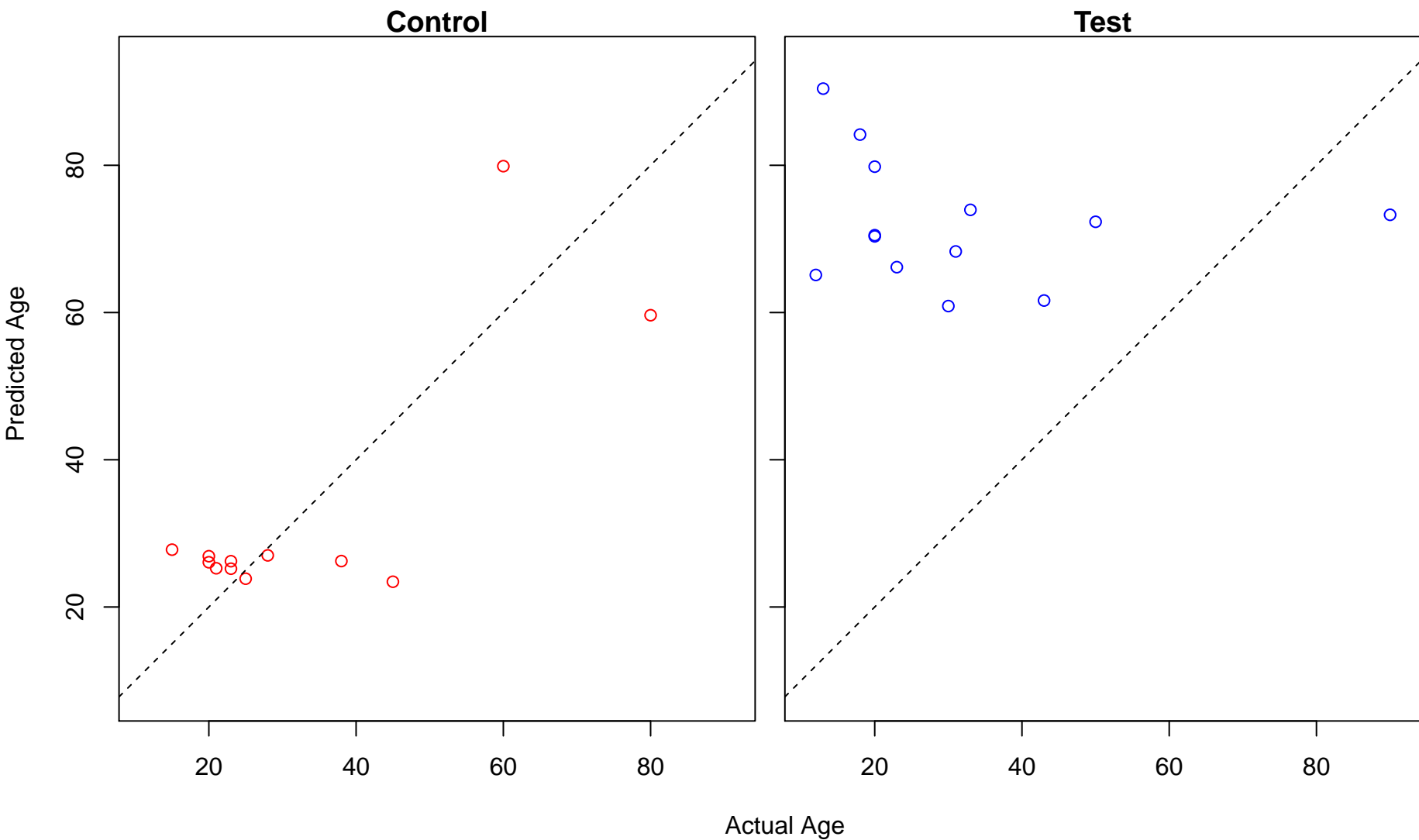
toll-like receptor 2 signaling pathway (Score: 6.420683)



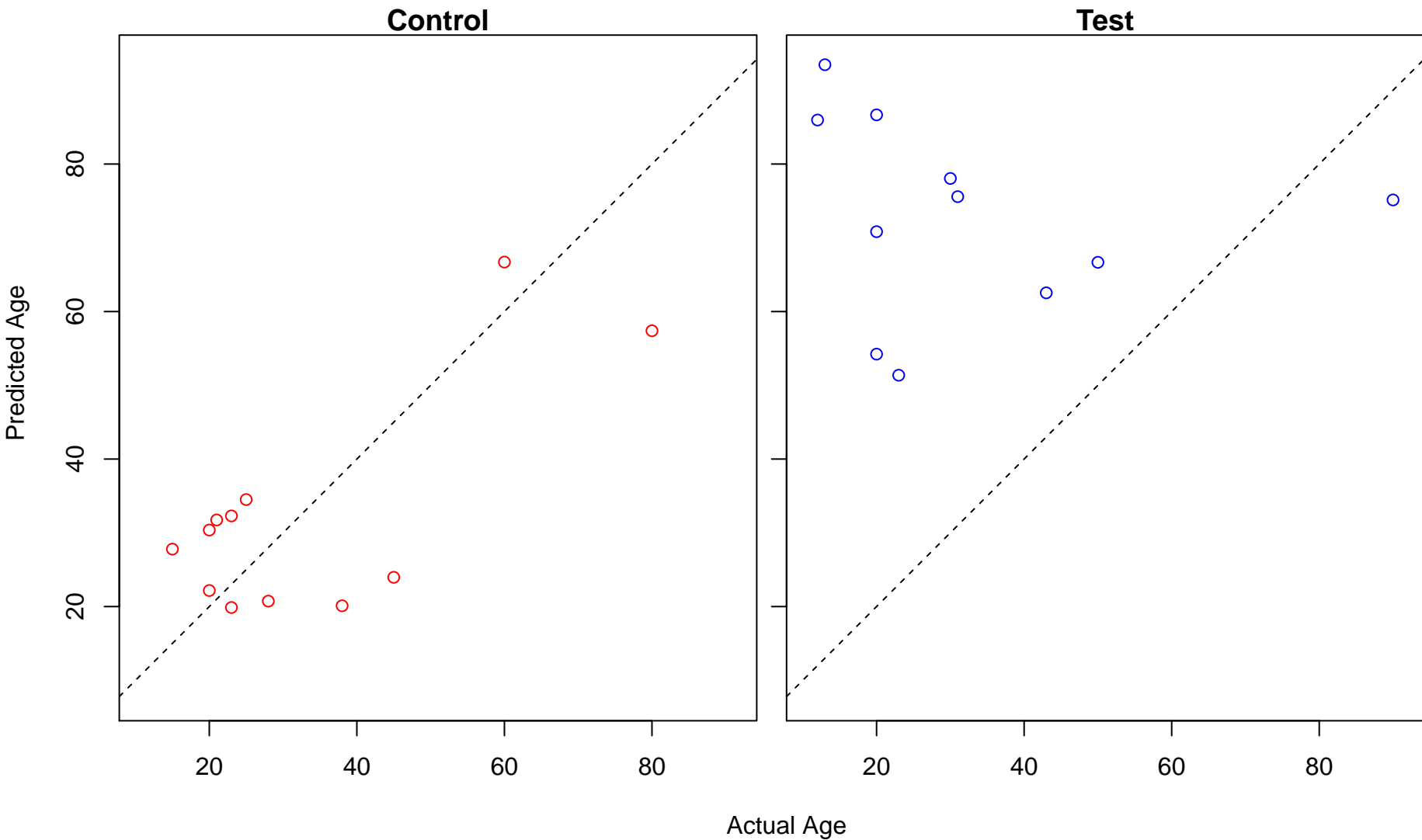
regulation of binding (Score: 6.420156)



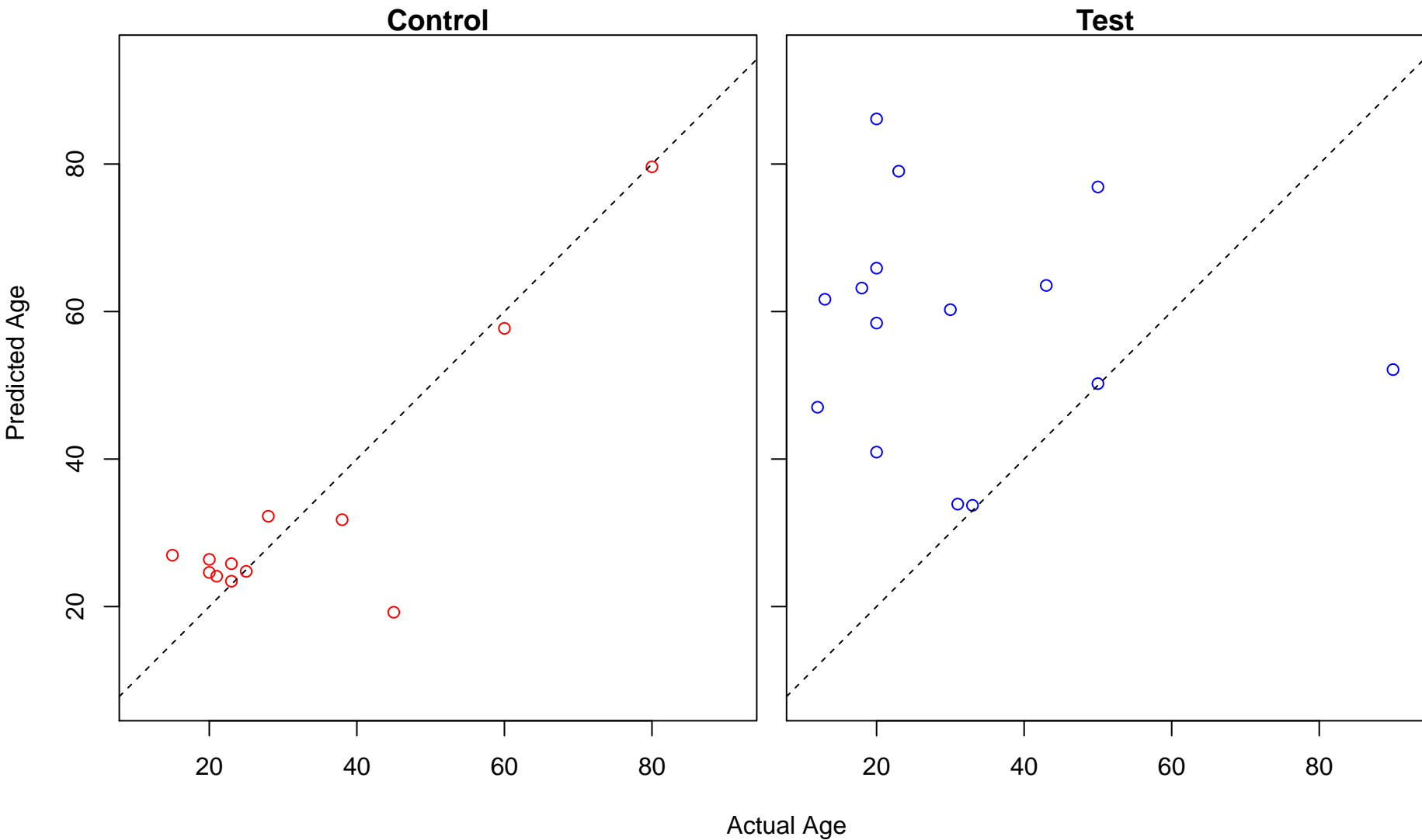
toll-like receptor 9 signaling pathway (Score: 6.419426)



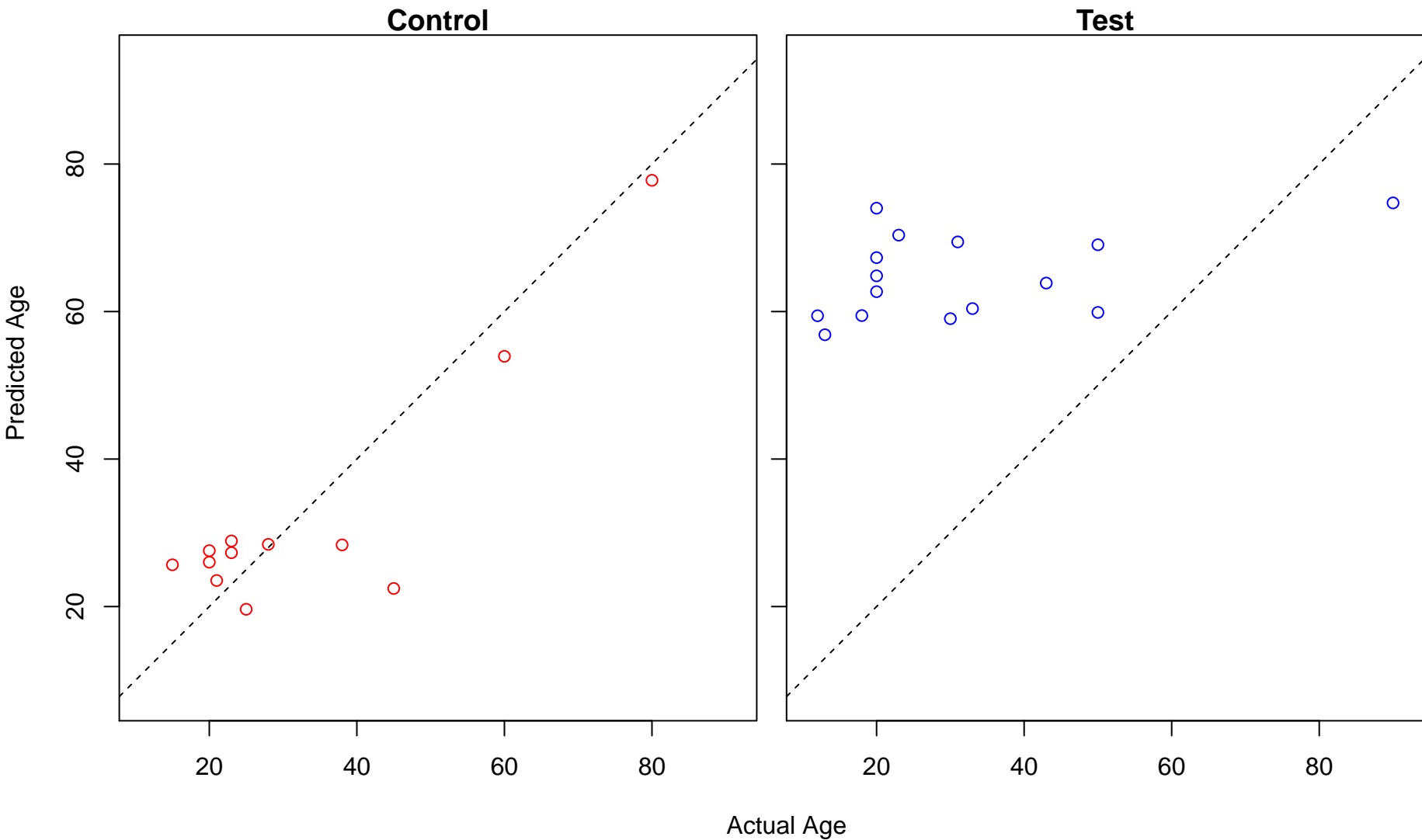
hydrogen sulfide metabolic process (Score: 6.418253)



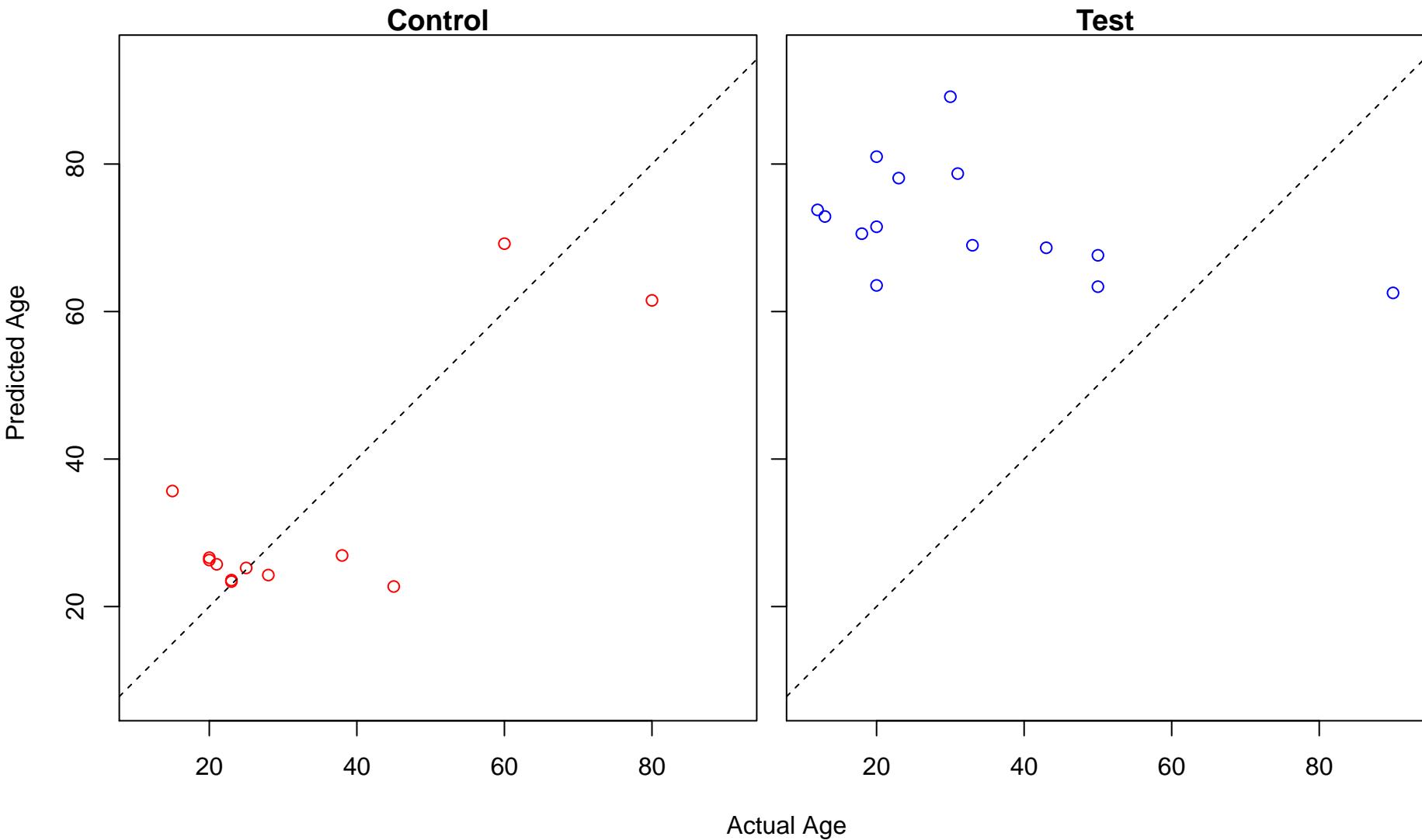
long-chain fatty acid biosynthetic process (Score: 6.417258)



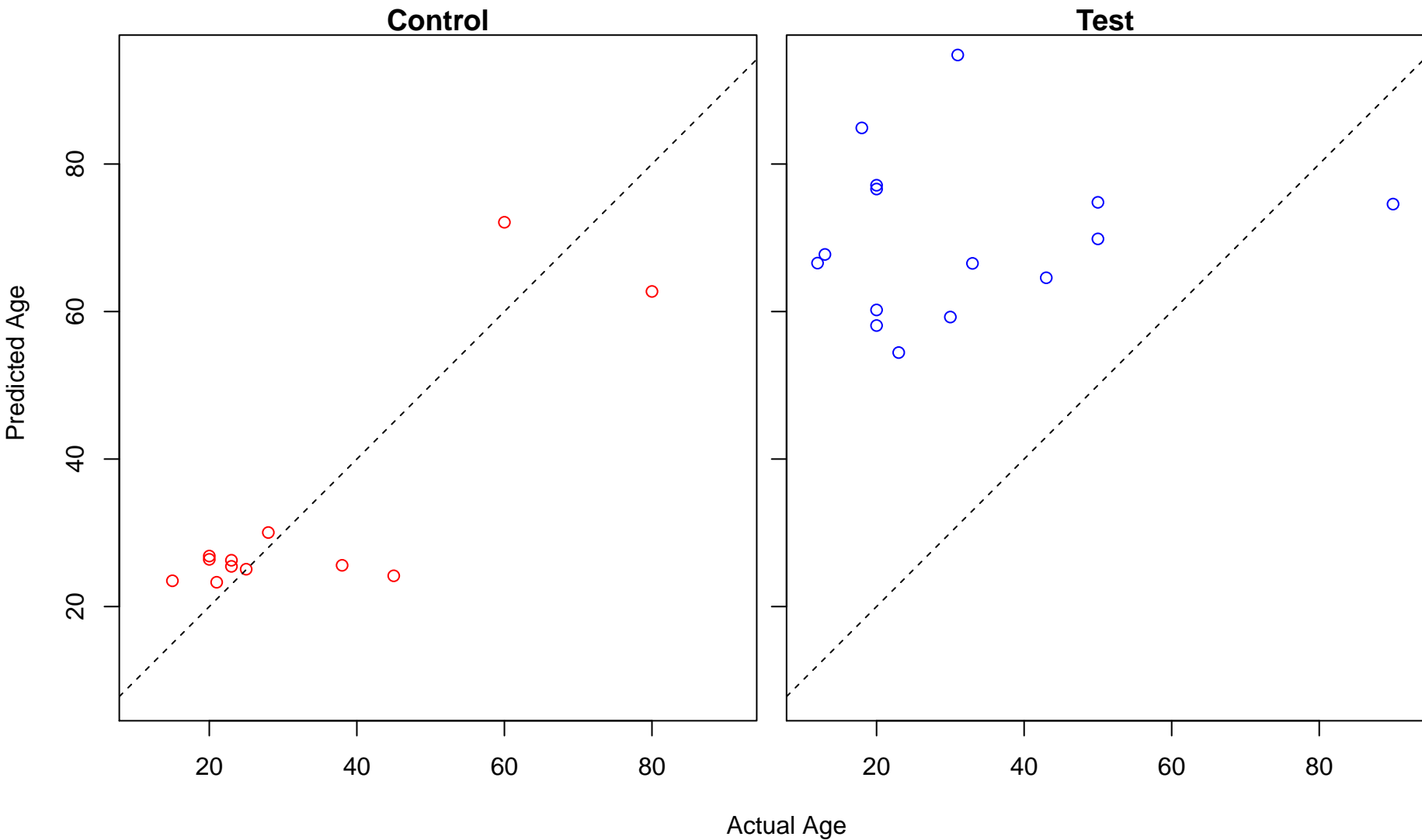
organelle assembly (Score: 6.408070)



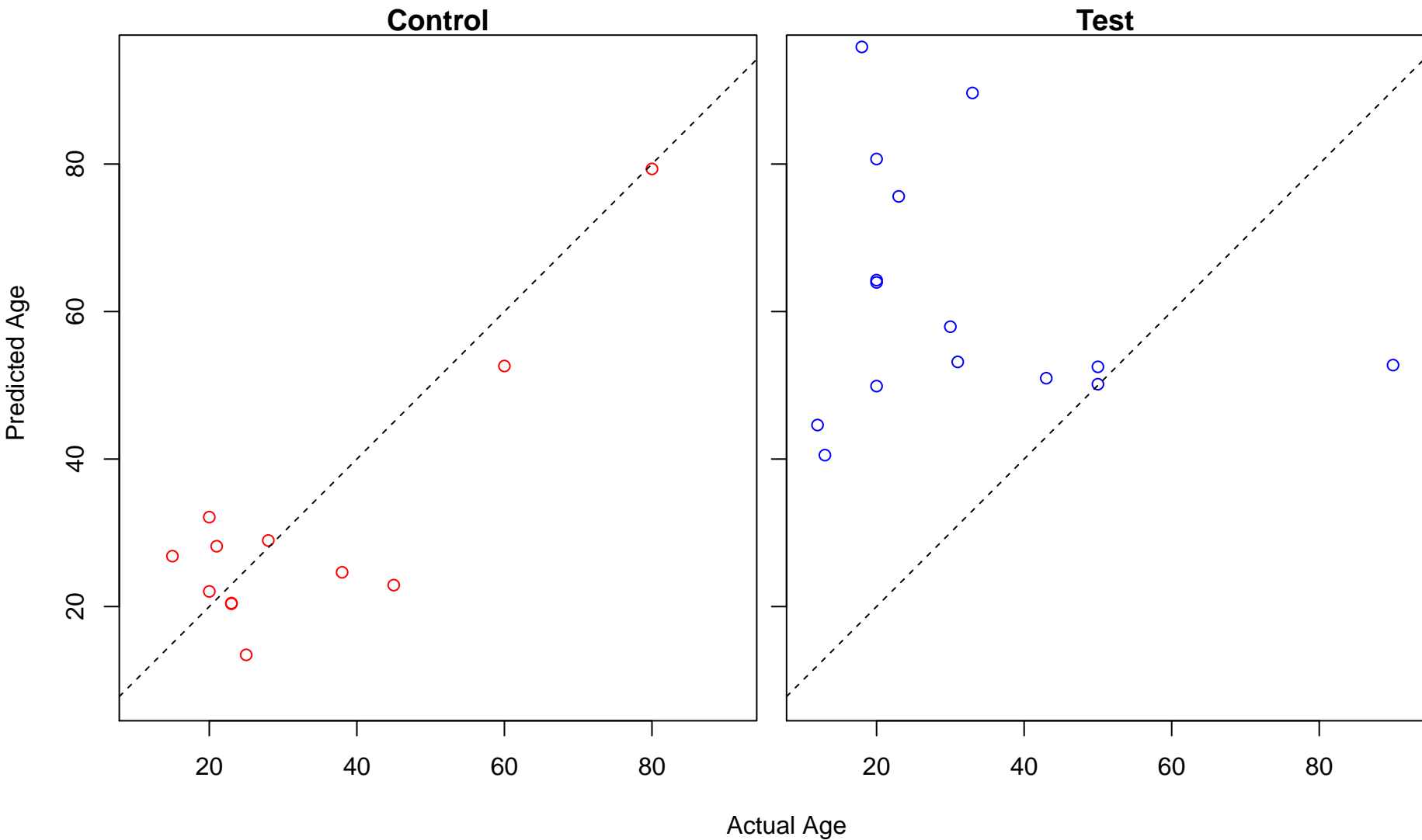
feeding behavior (Score: 6.401019)



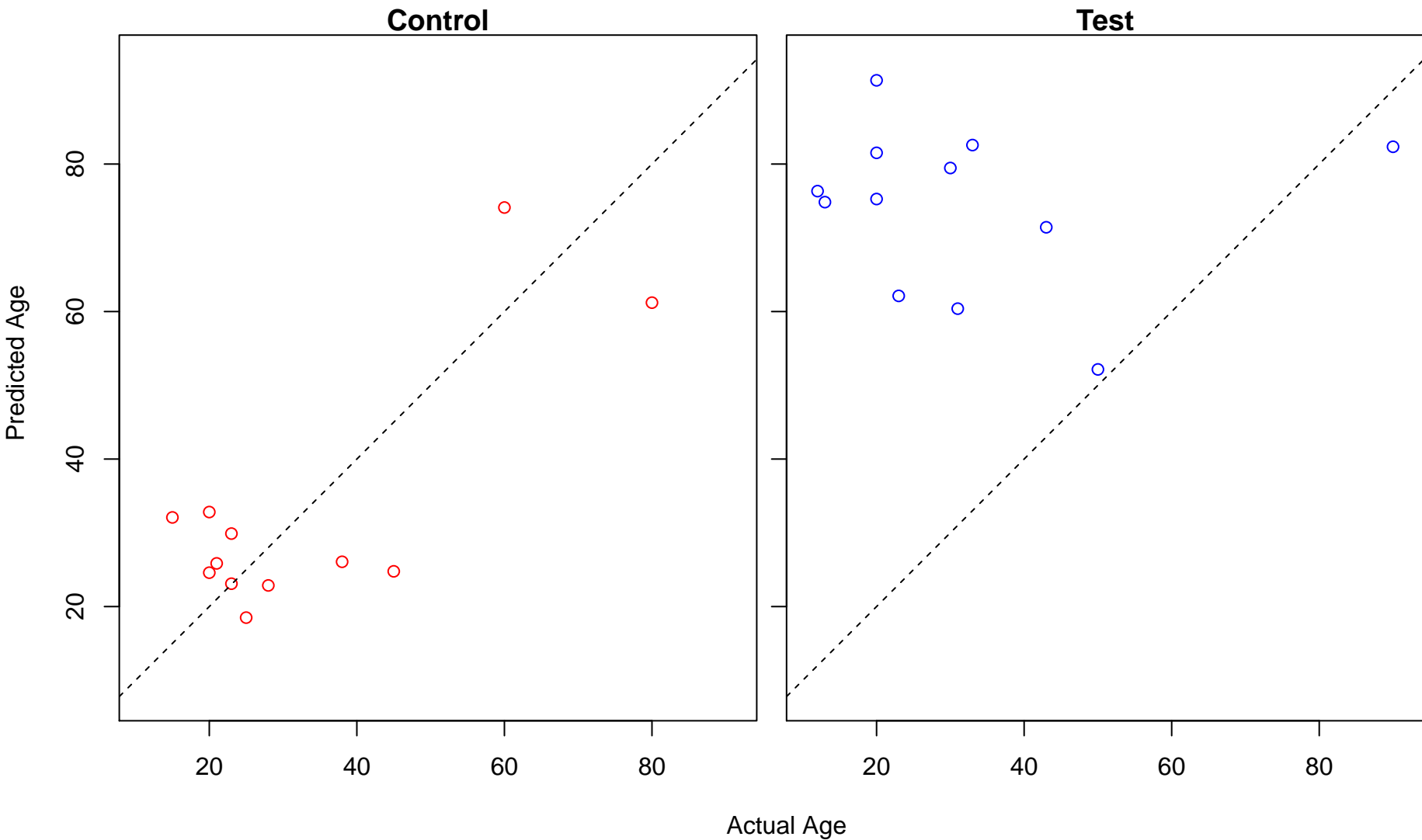
protein dephosphorylation (Score: 6.400281)



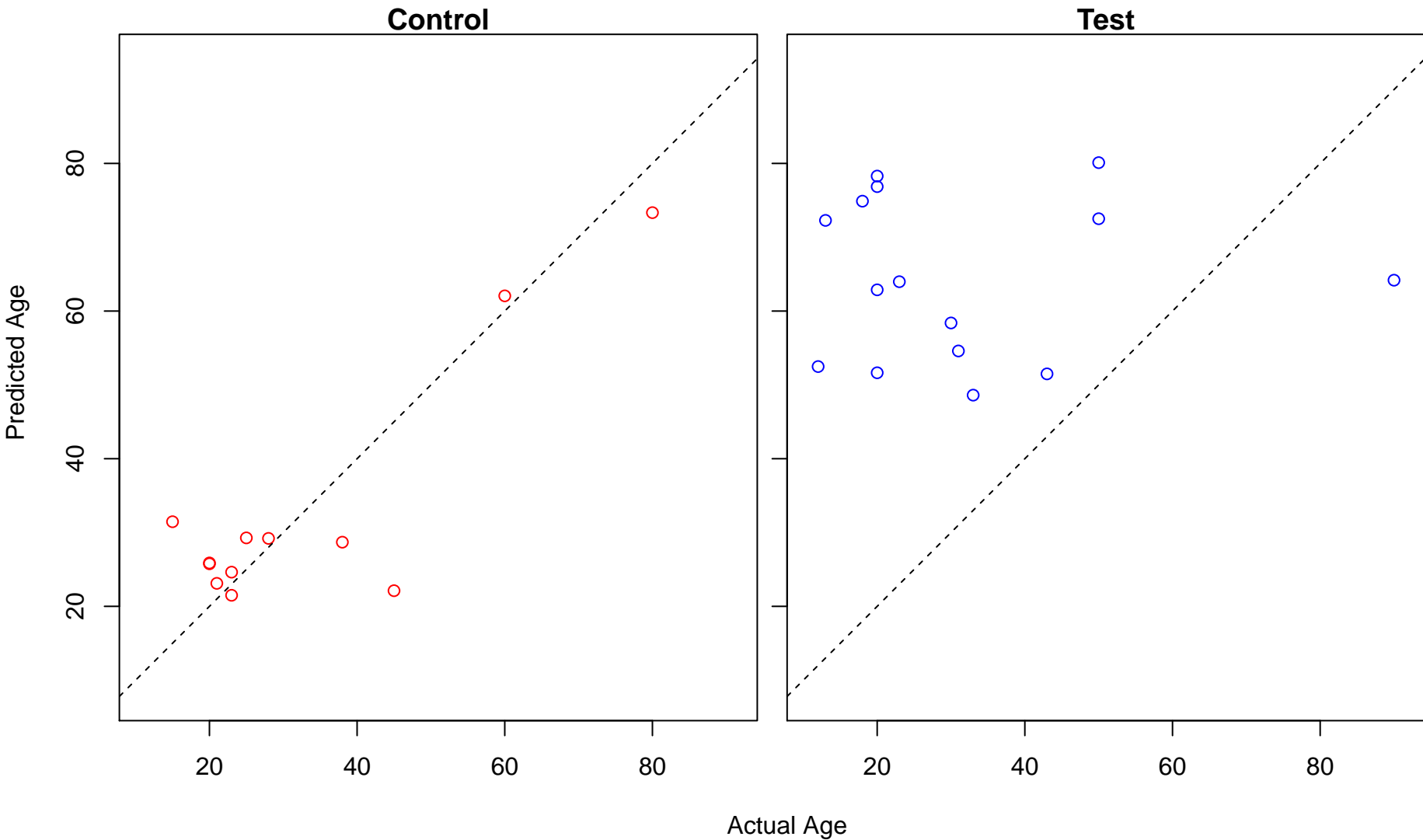
nuclear export (Score: 6.399463)



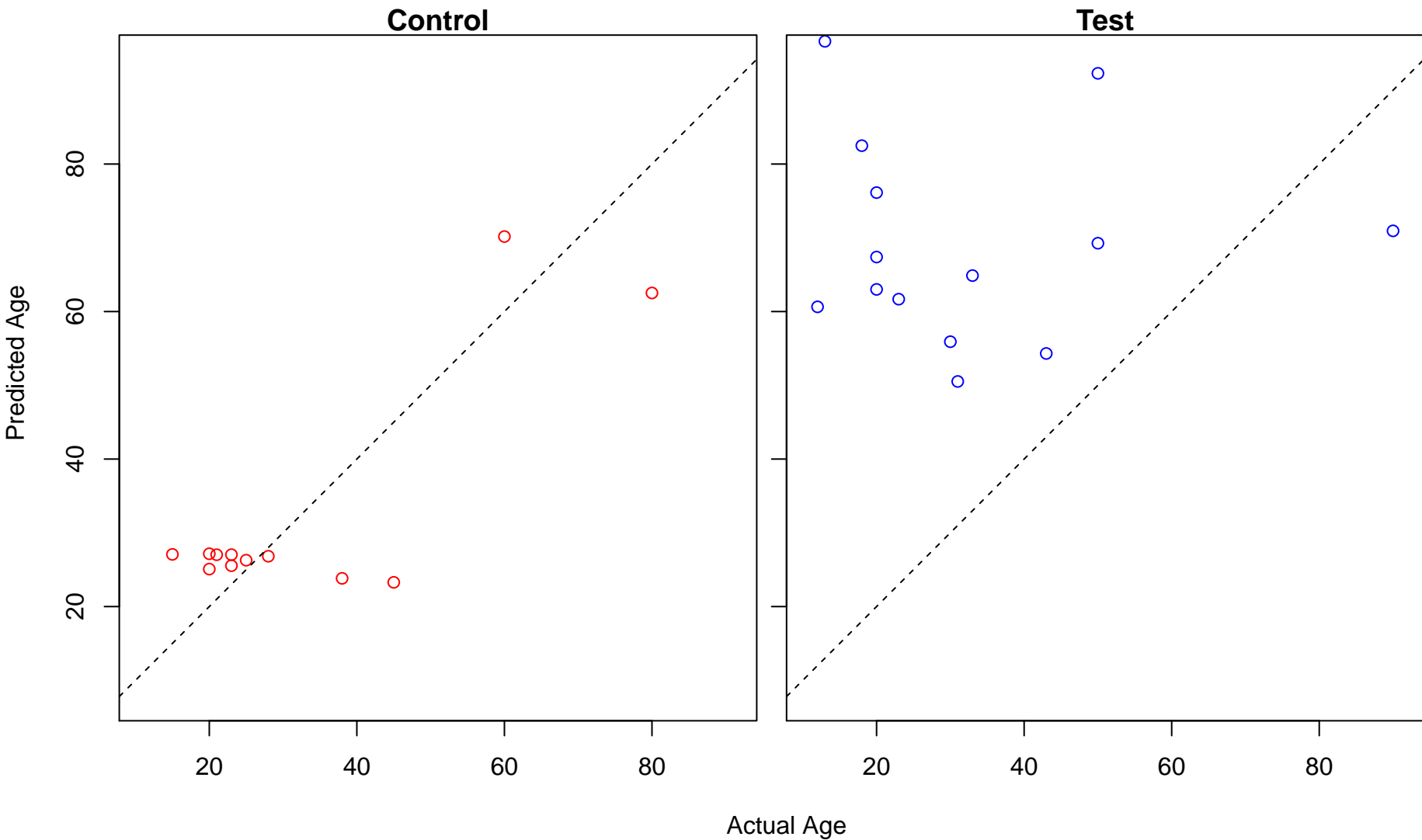
response to carbohydrate (Score: 6.396747)



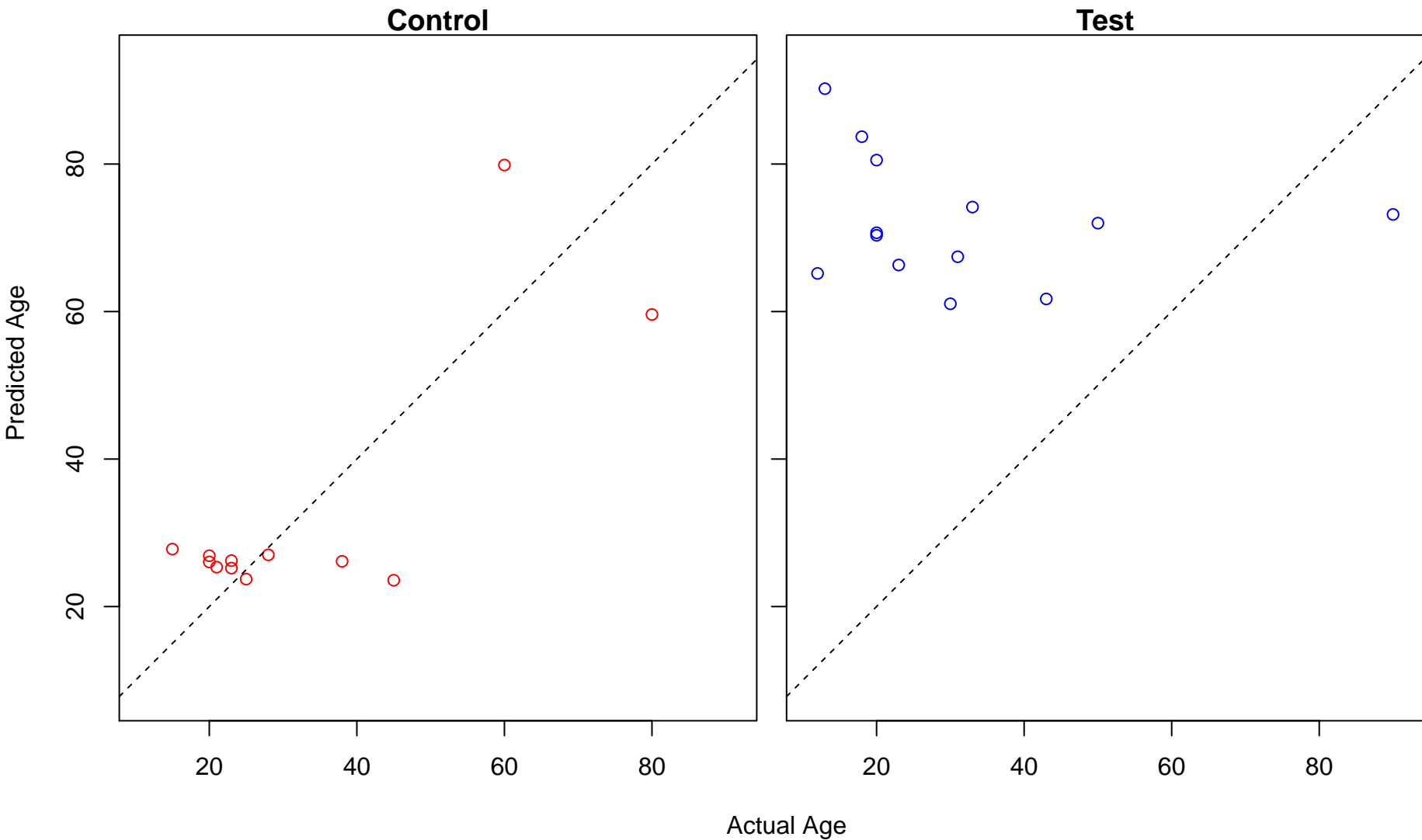
oxidoreduction coenzyme metabolic process (Score: 6.391449)



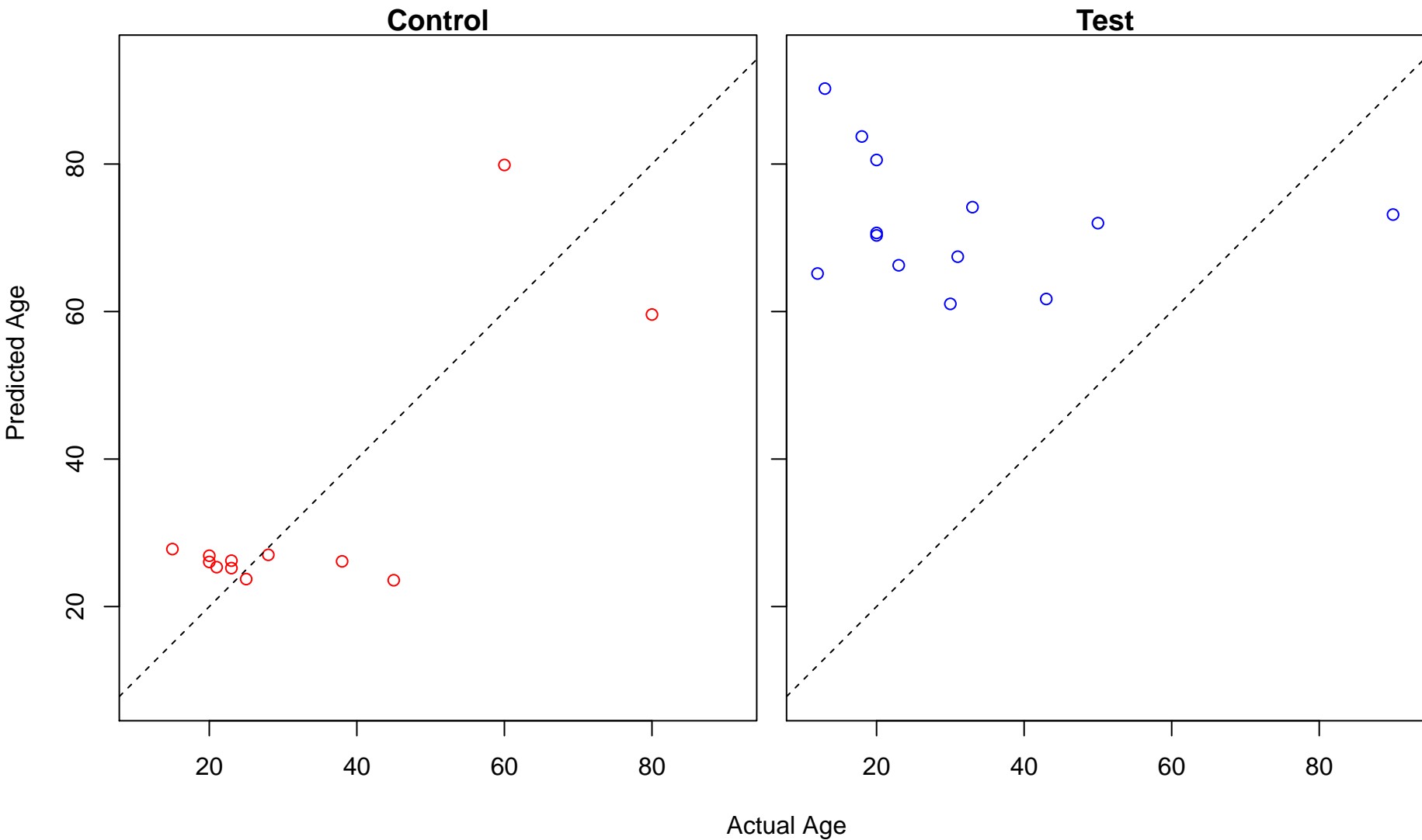
cellular modified amino acid metabolic process (Score: 6.390103)



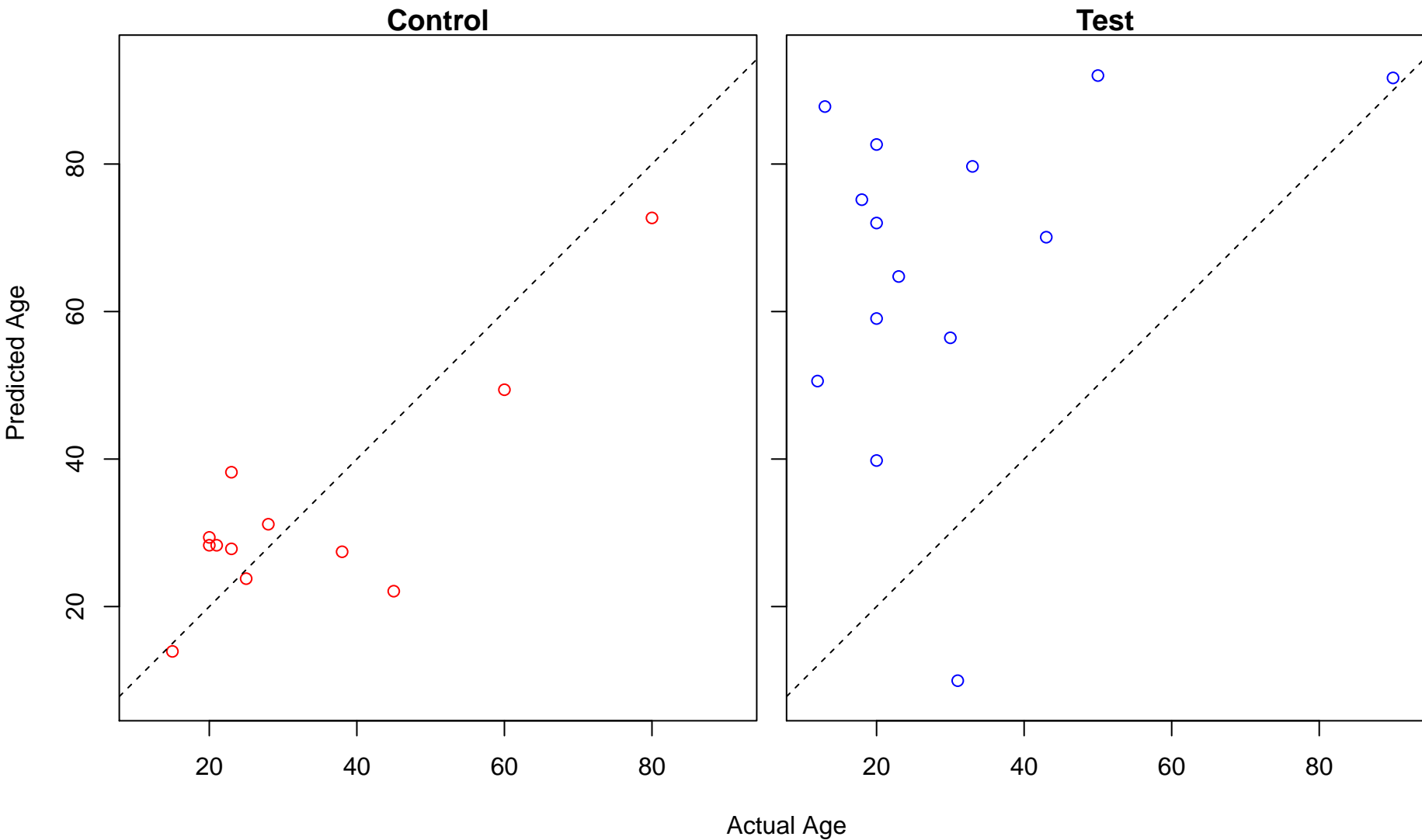
stress-activated protein kinase signaling cascade (Score: 6.388124)



stress-activated MAPK cascade (Score: 6.387163)

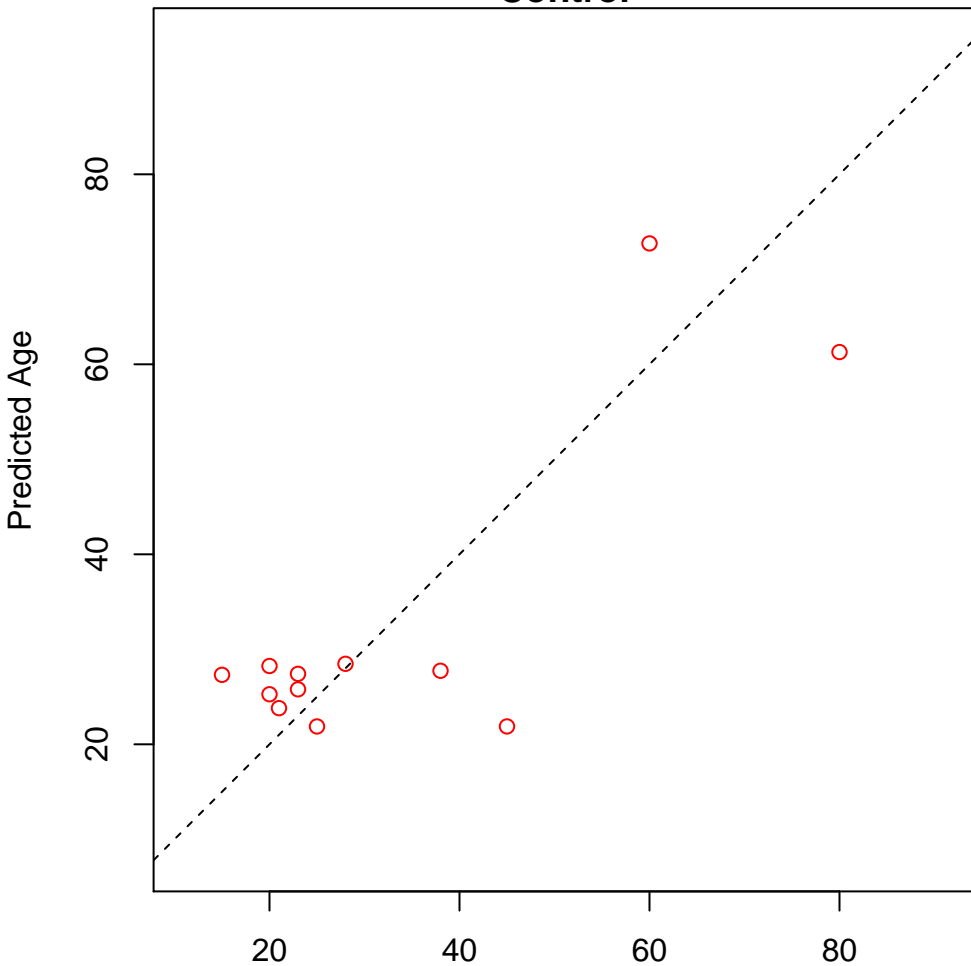


lung alveolus development (Score: 6.384167)

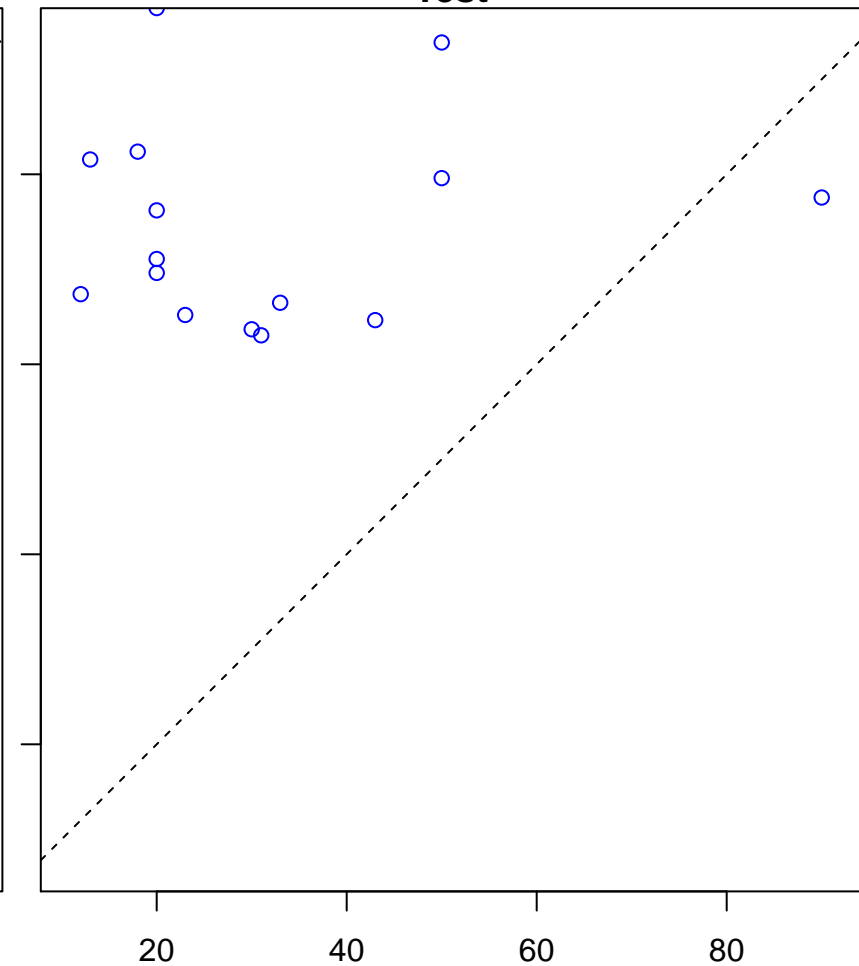


negative regulation of peptidase activity (Score: 6.378450)

Control

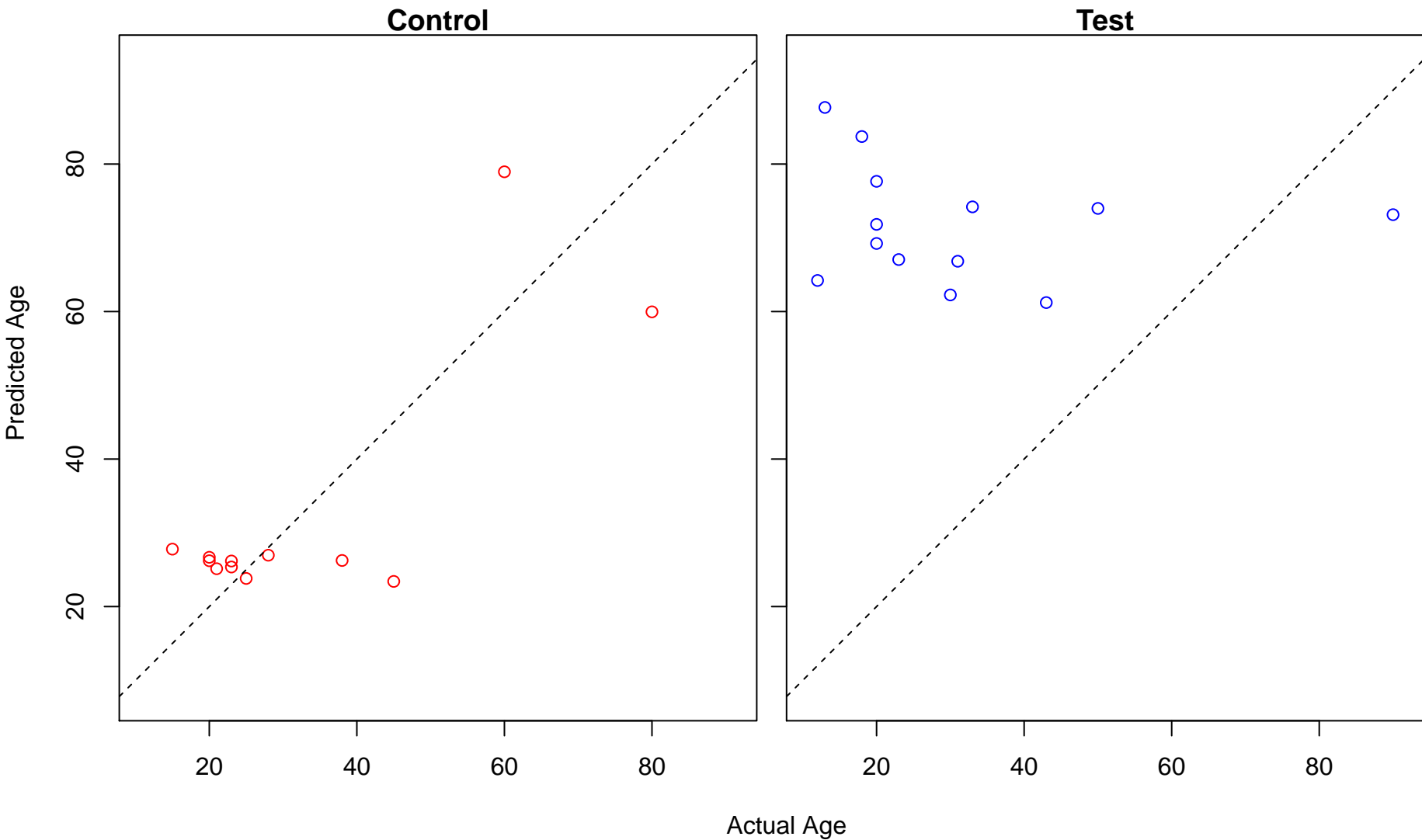


Test

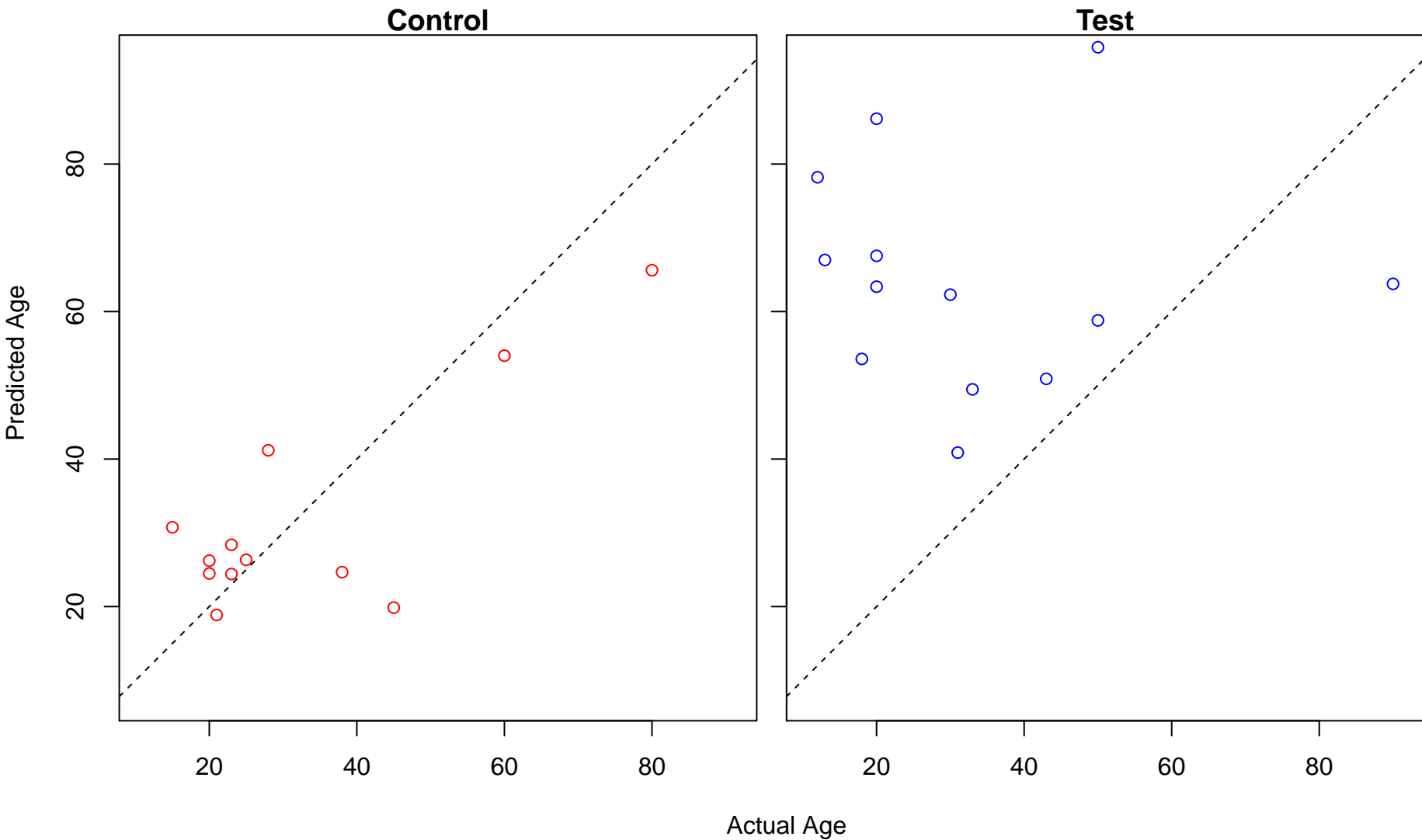


Actual Age

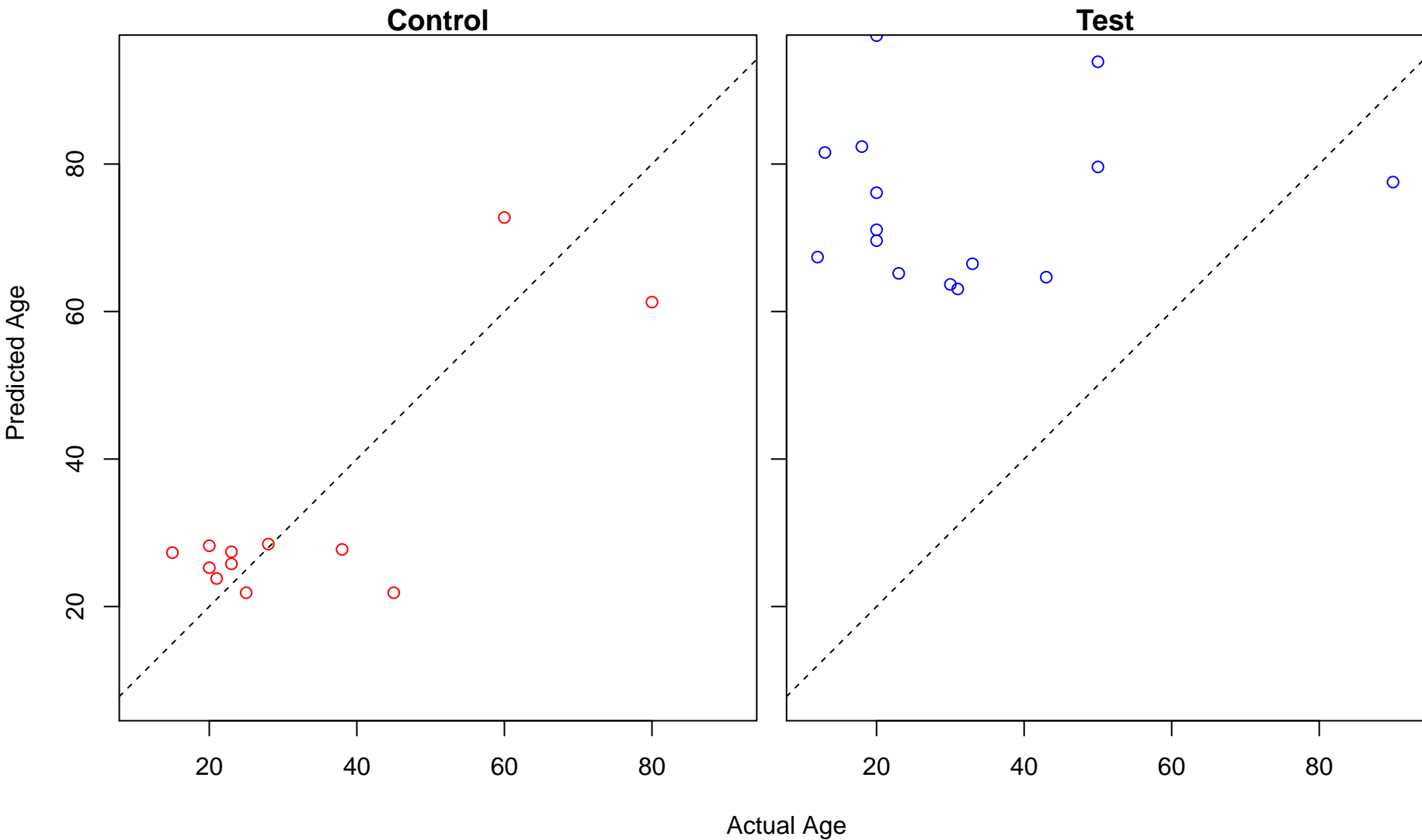
DNA damage checkpoint (Score: 6.373981)



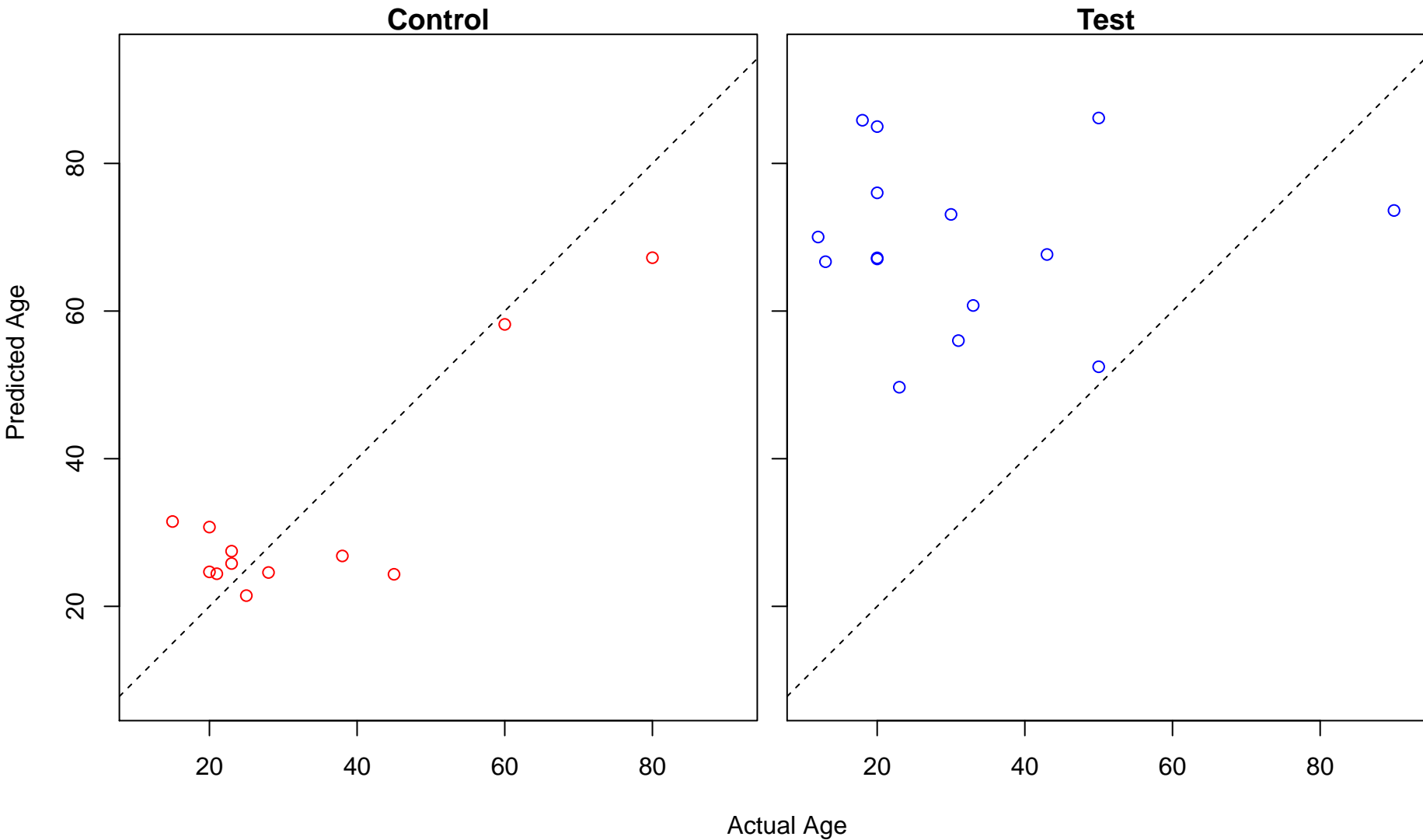
oxidative DNA demethylation (Score: 6.372855)



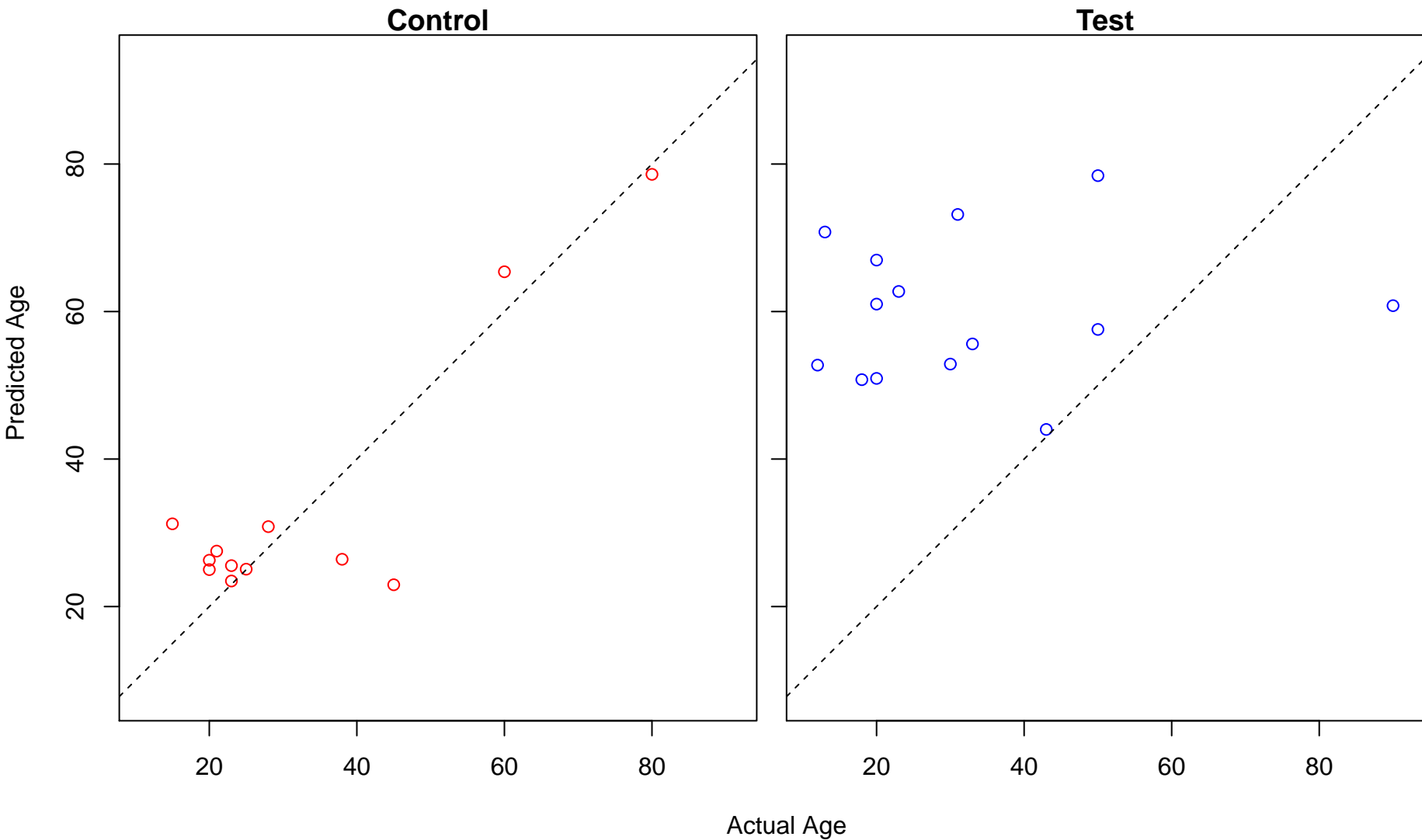
negative regulation of endopeptidase activity (Score: 6.369783)



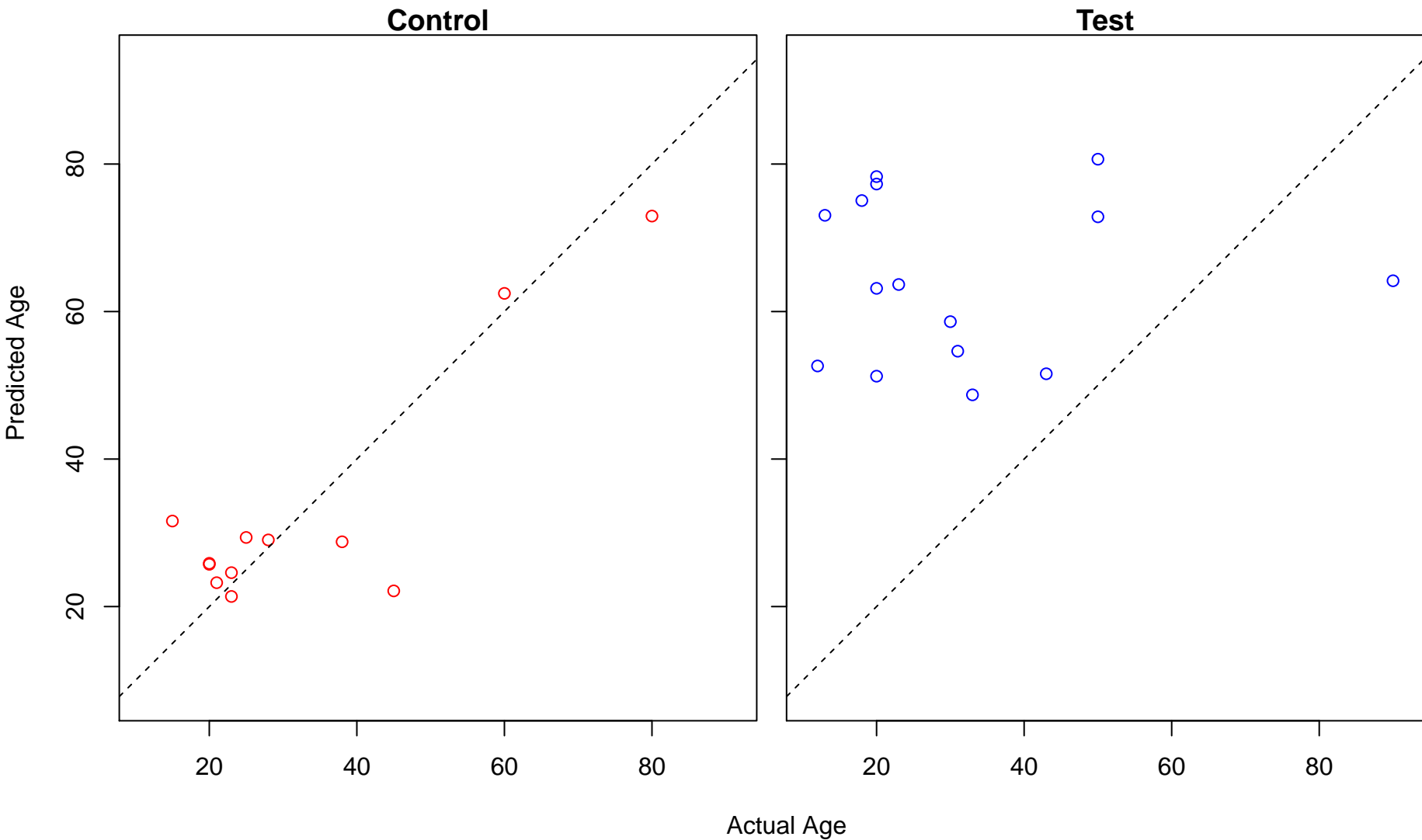
positive regulation of ERAD pathway (Score: 6.368417)



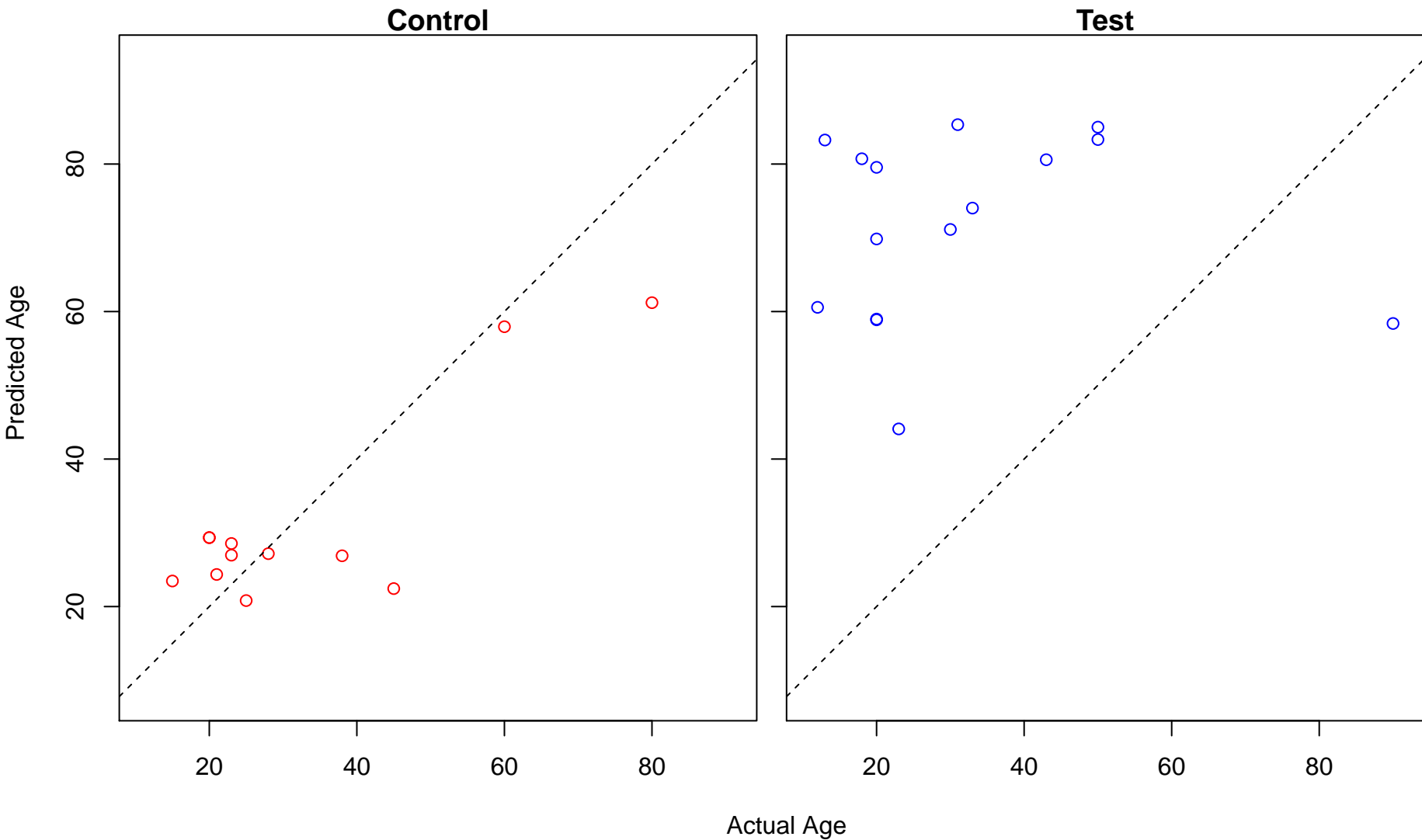
renal system process (Score: 6.368293)



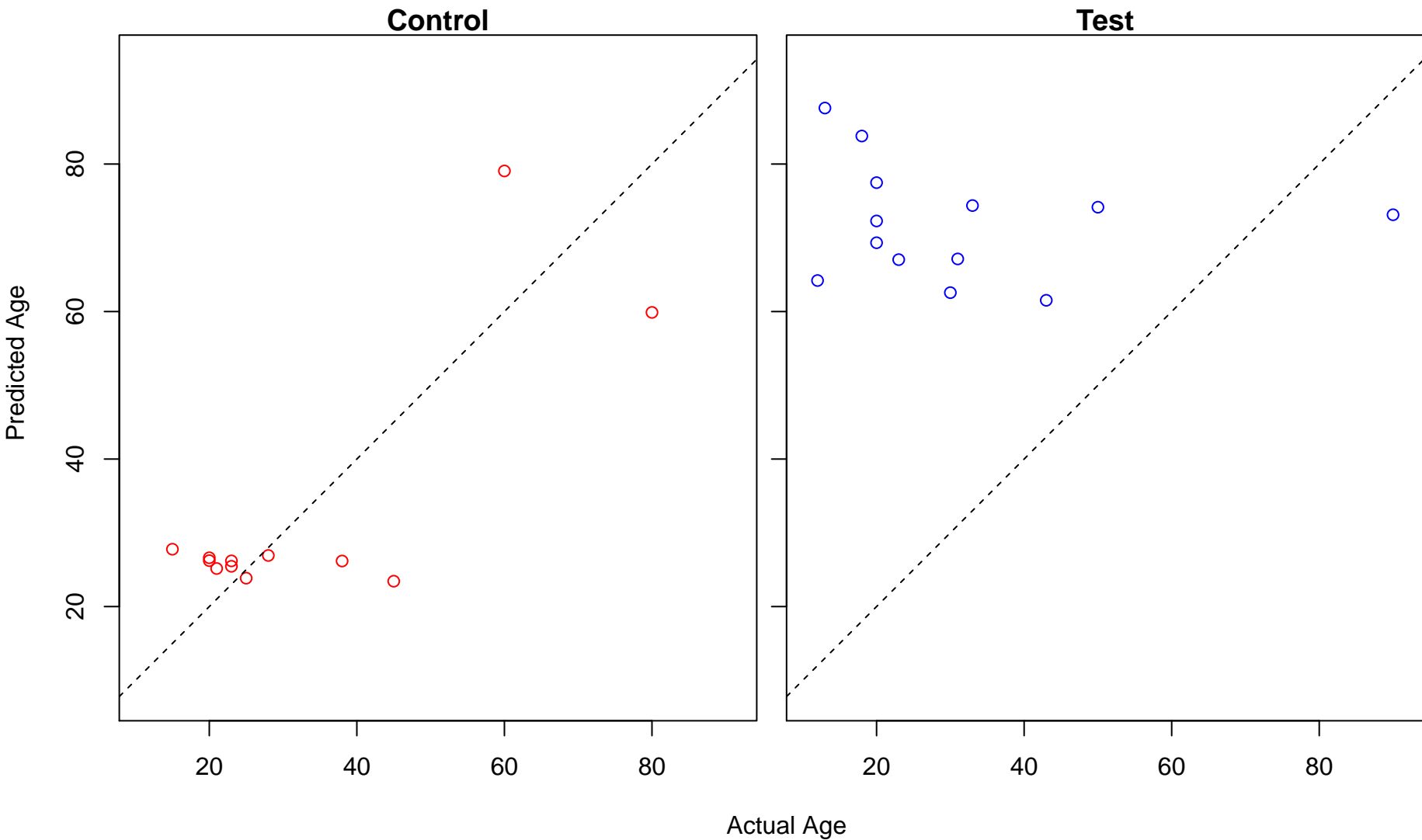
pyridine-containing compound metabolic process (Score: 6.368204)



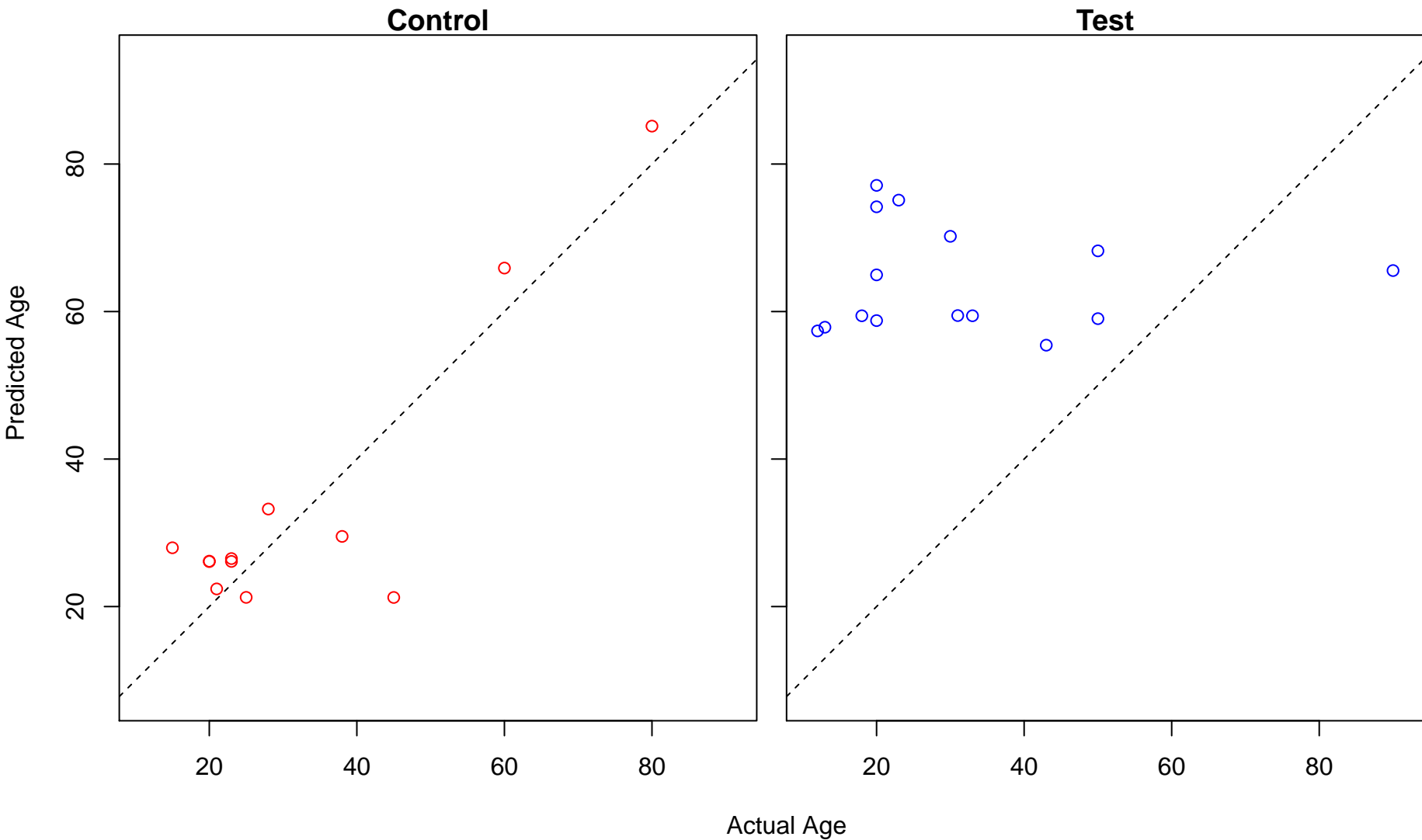
spinal cord patterning (Score: 6.365814)



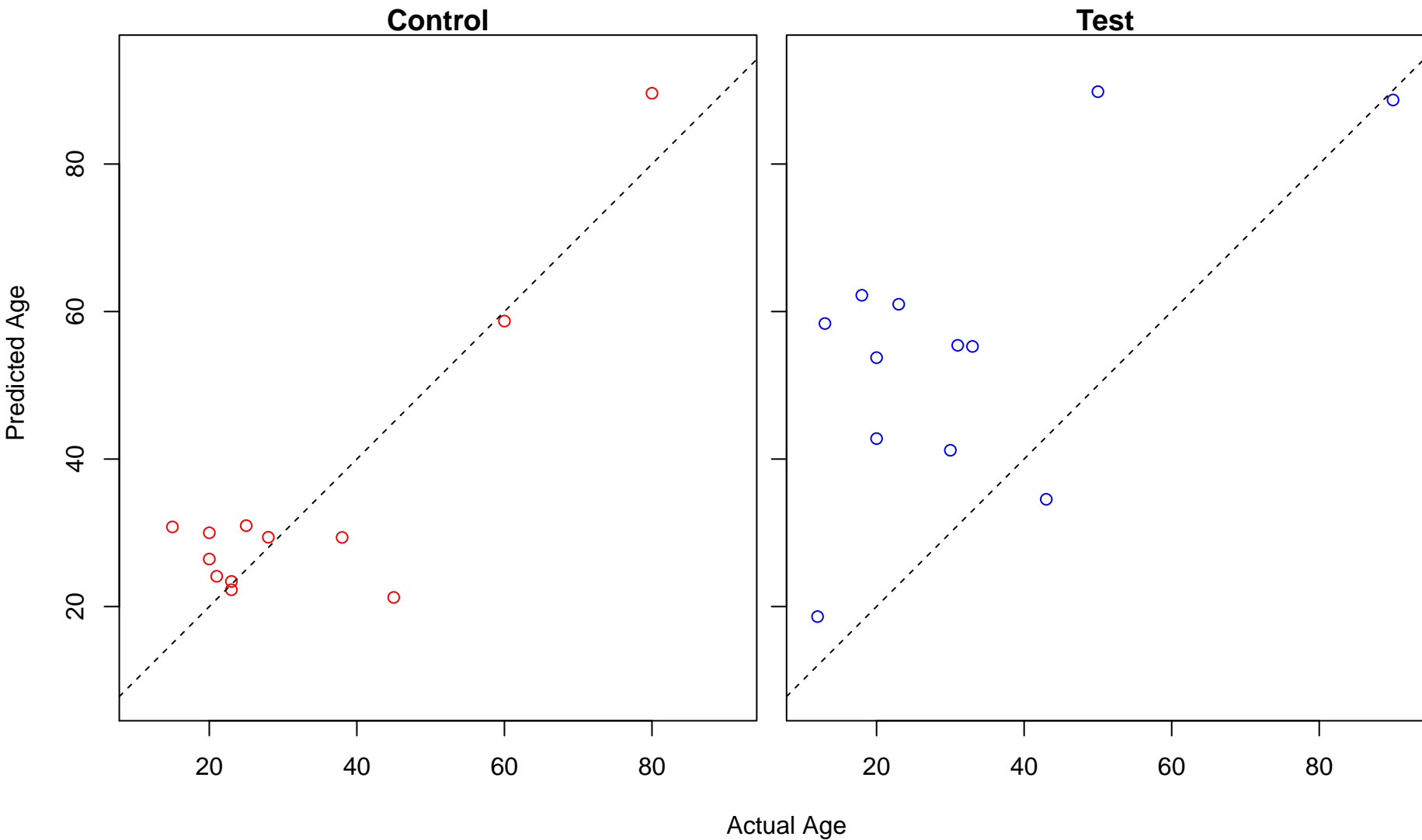
regulation of G1/S transition of mitotic cell cycle (Score: 6.364776)



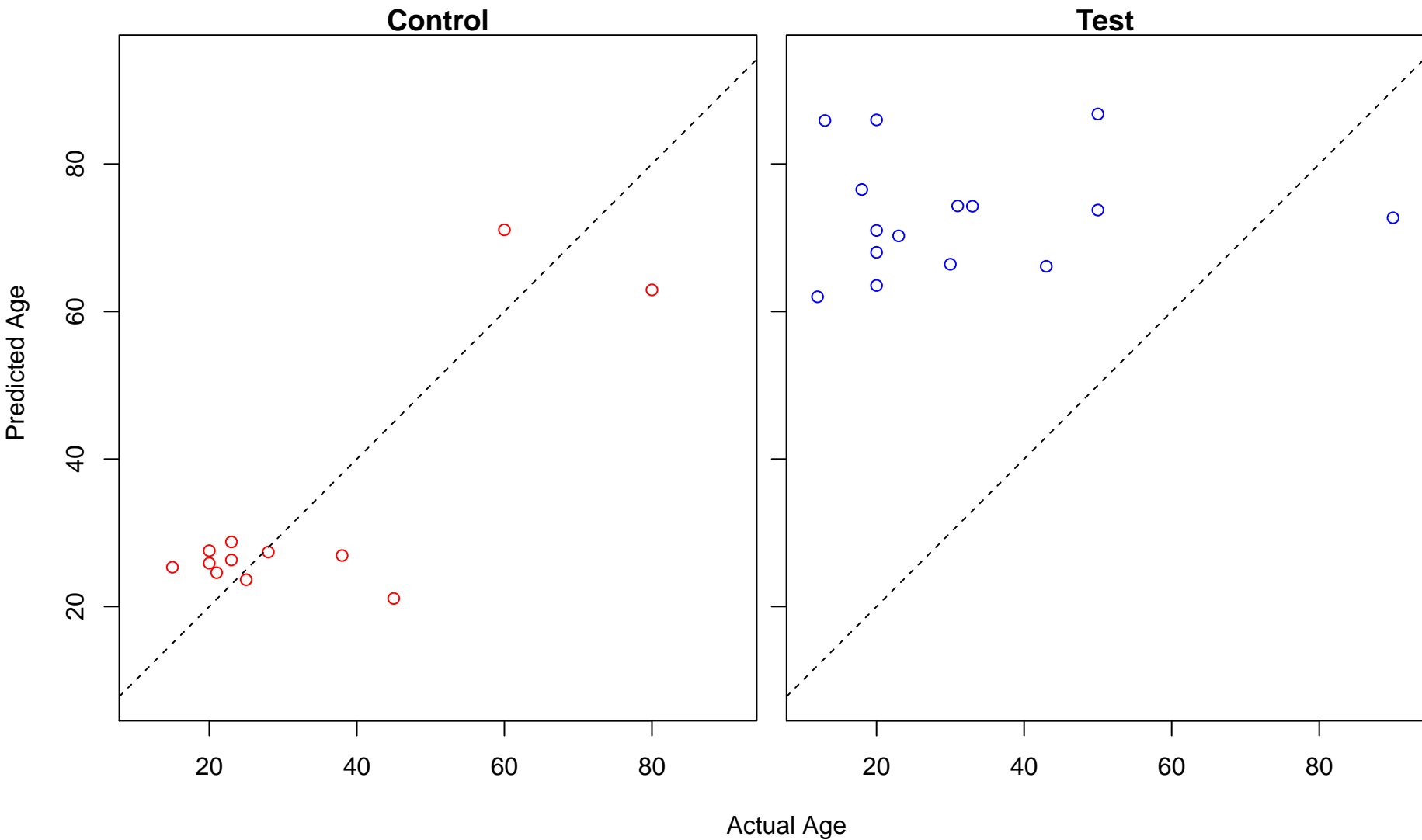
lipid biosynthetic process (Score: 6.364571)



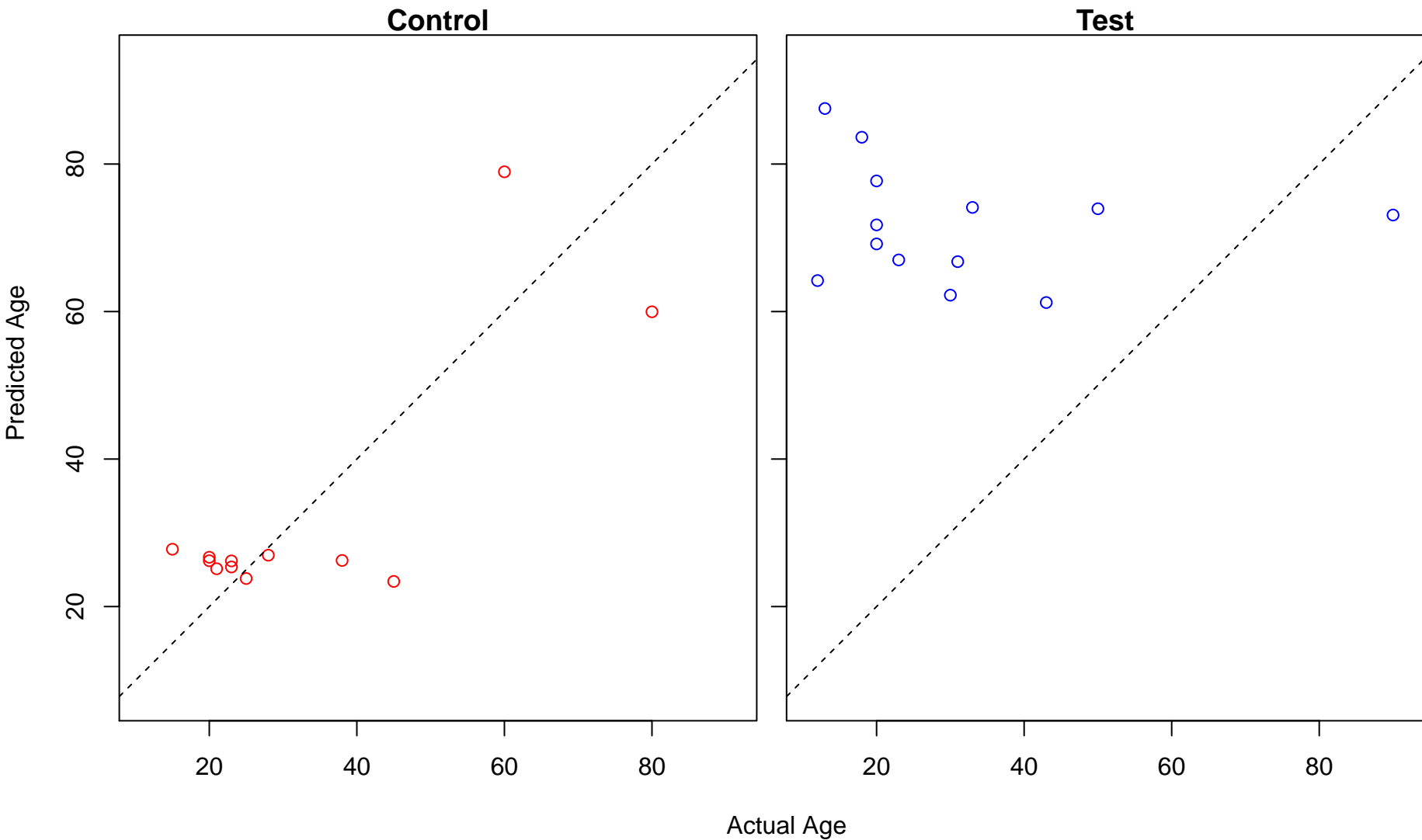
positive regulation of Rho protein signal transduction (Score: 6.363944)



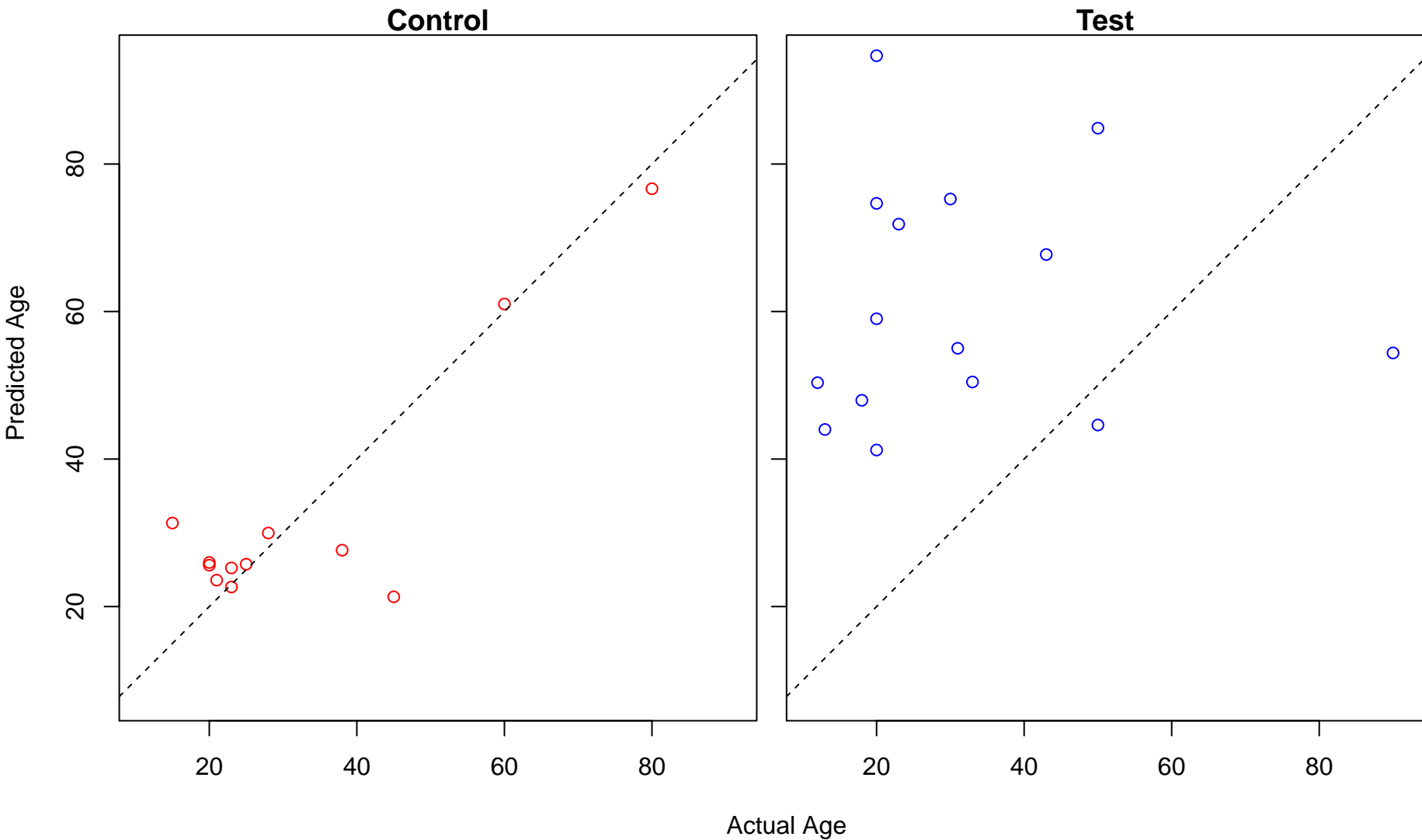
regulation of immune effector process (Score: 6.361220)



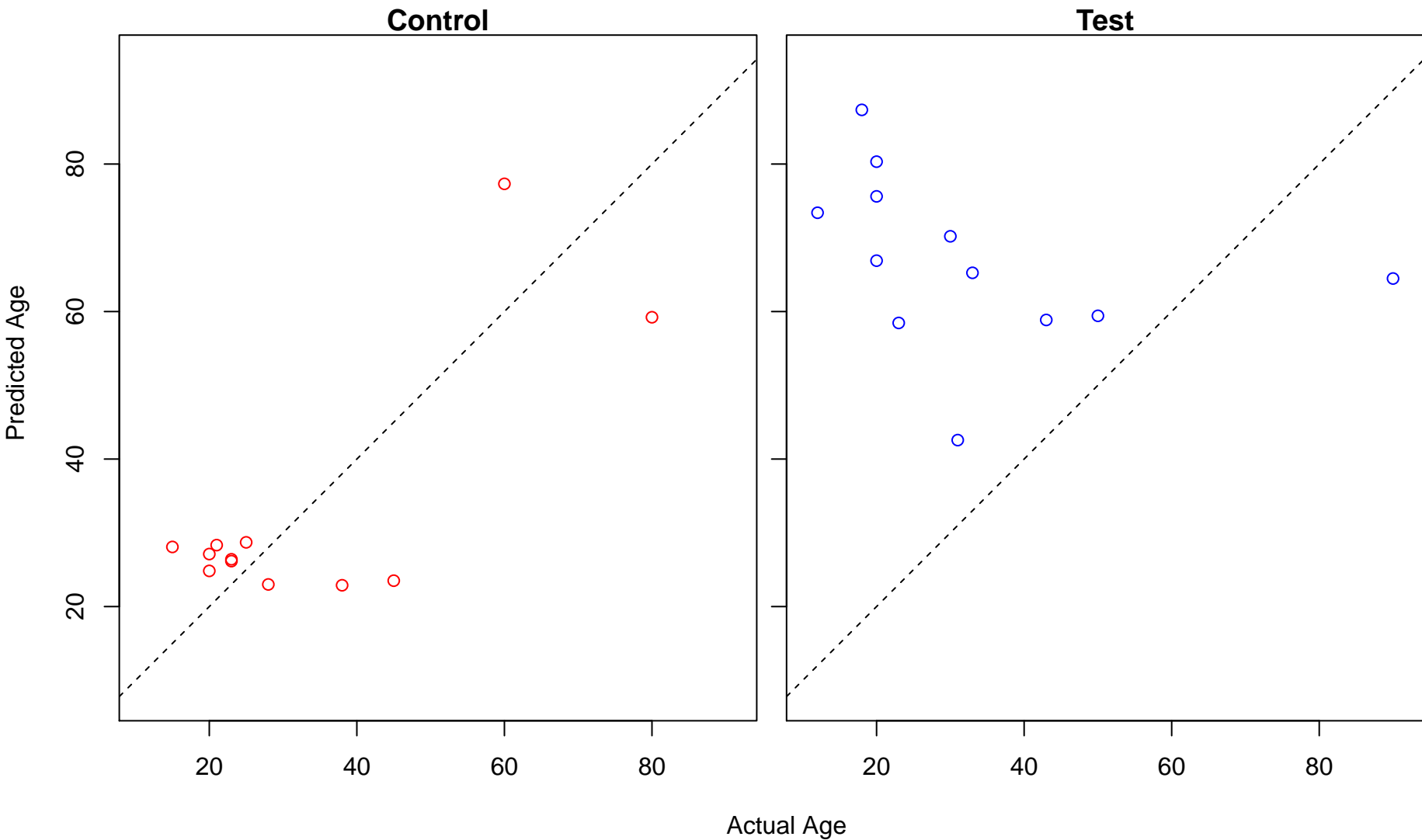
DNA integrity checkpoint (Score: 6.359615)



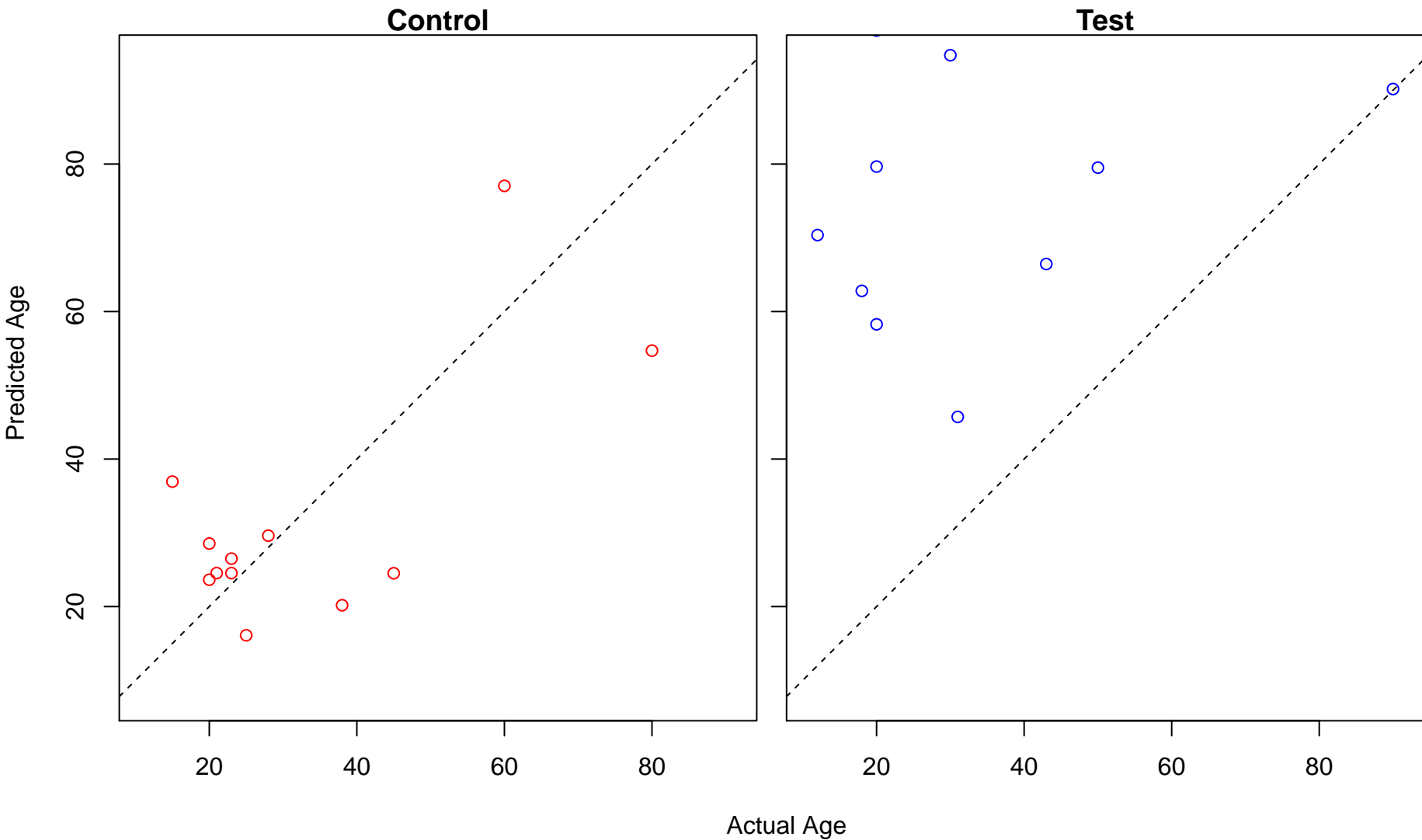
regulation of cellular respiration (Score: 6.355414)



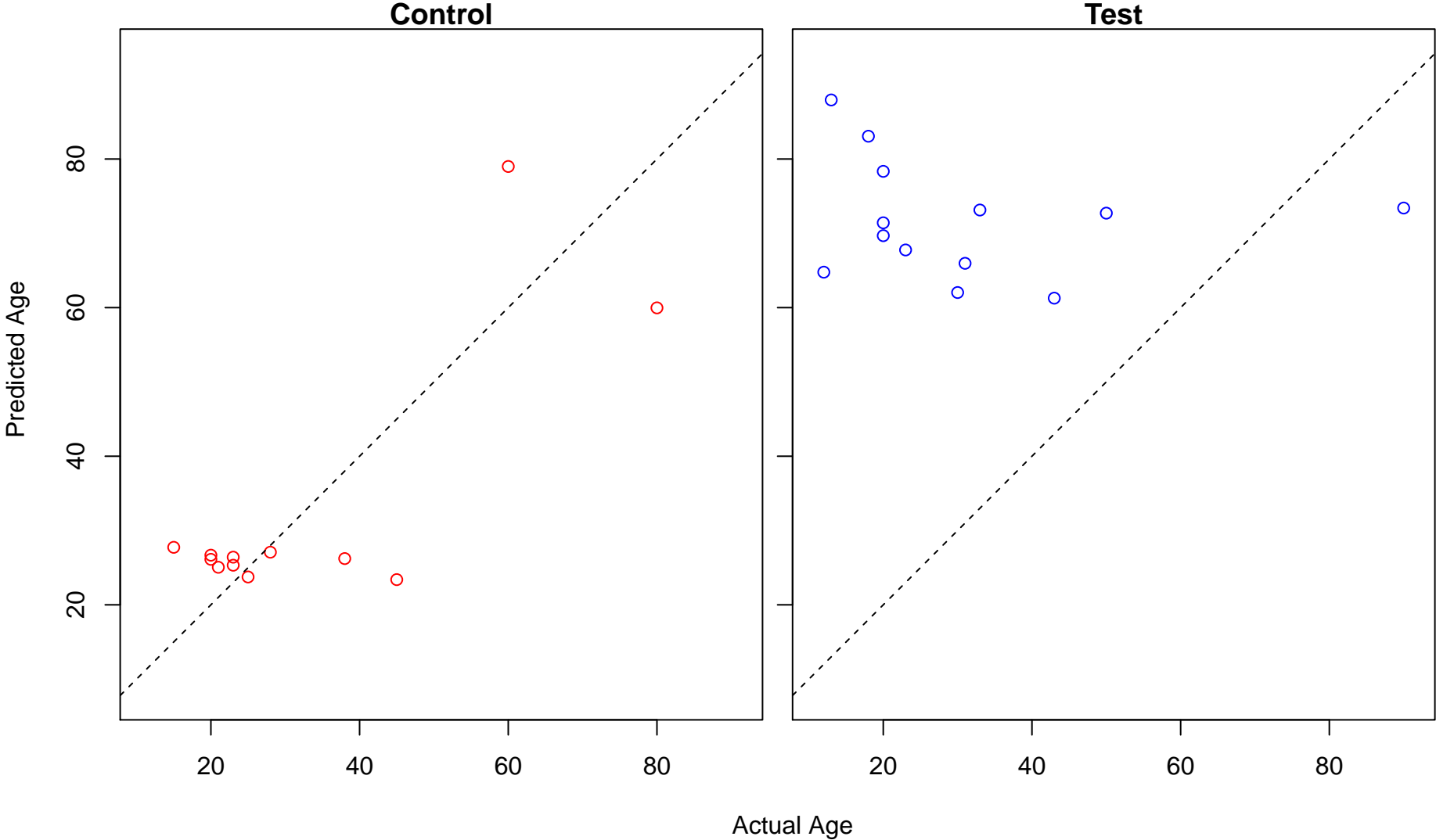
negative regulation of DNA repair (Score: 6.354600)



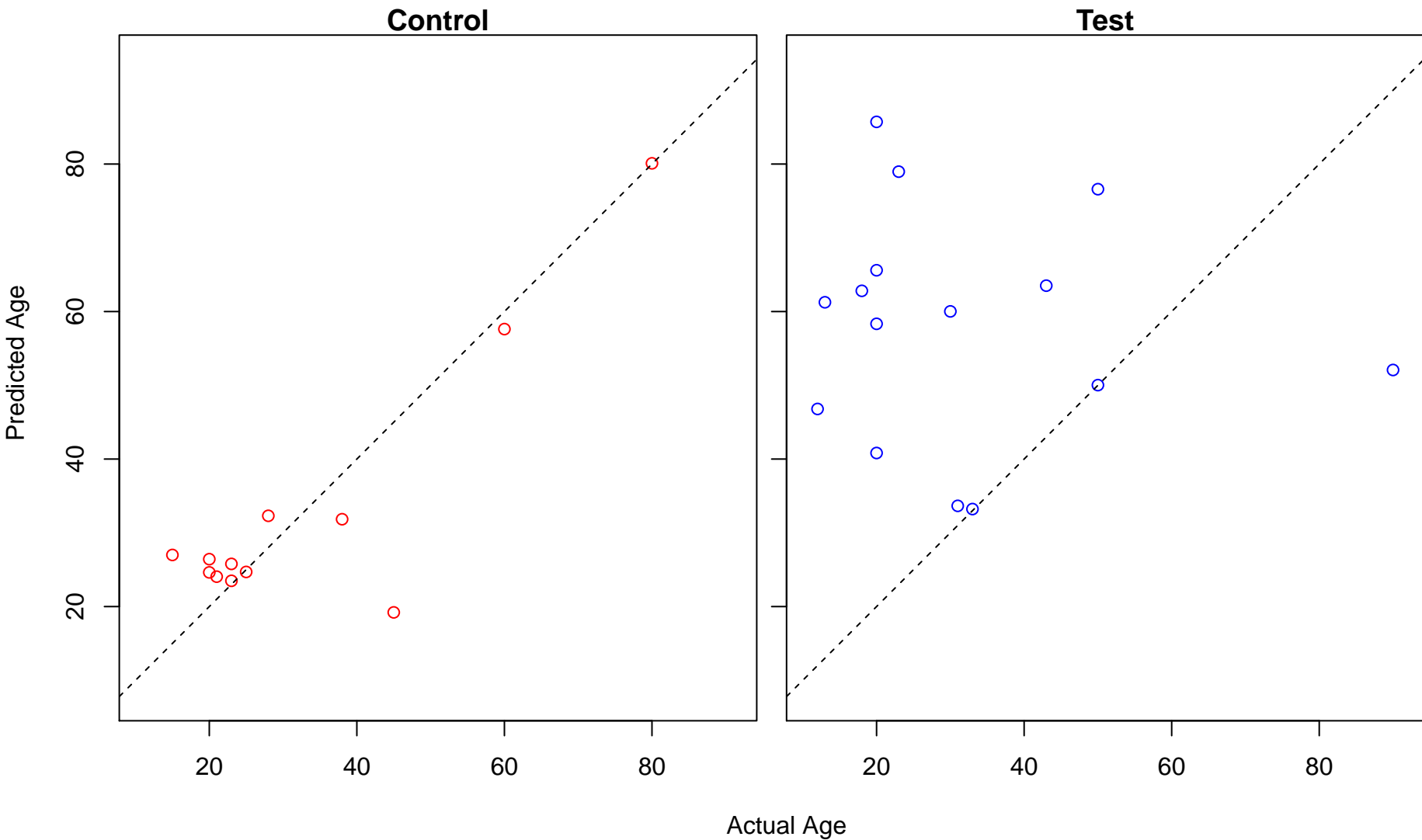
regulation of dopamine secretion (Score: 6.351866)



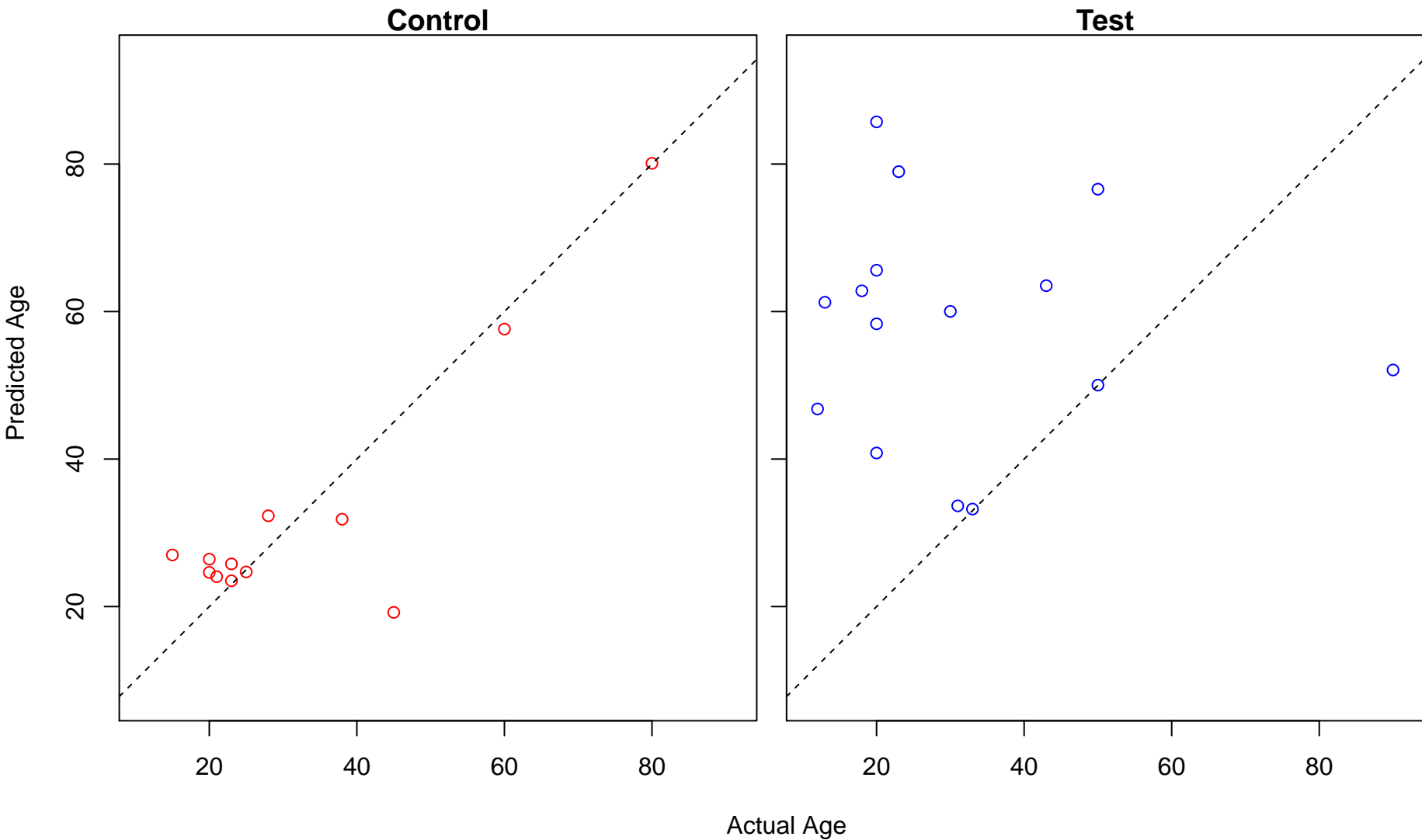
negative regulation of ubiquitin–protein ligase activity involved in mitotic cell cycle (Score: 6.35176)



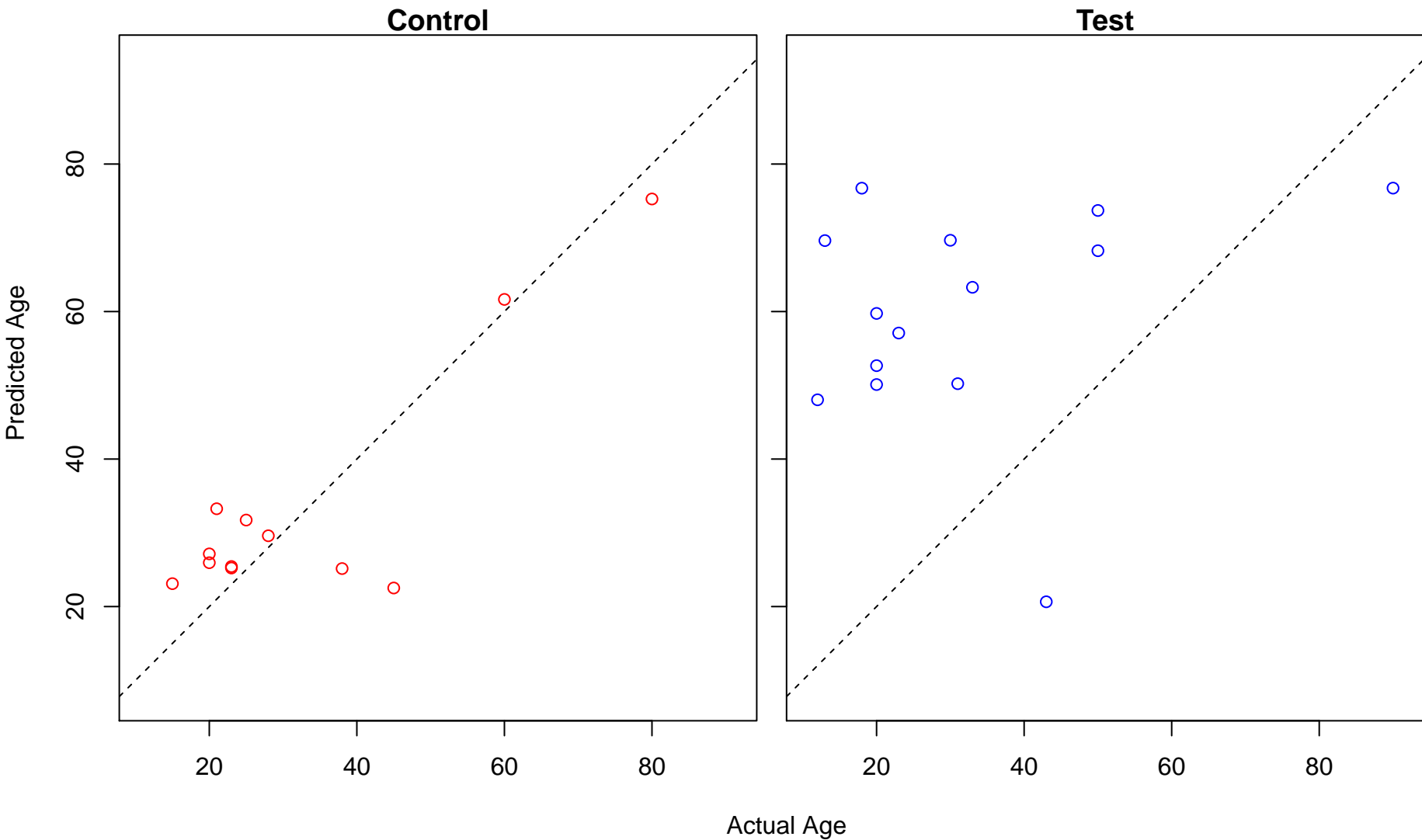
hepoxilin metabolic process (Score: 6.348304)



hepoxilin biosynthetic process (Score: 6.348304)

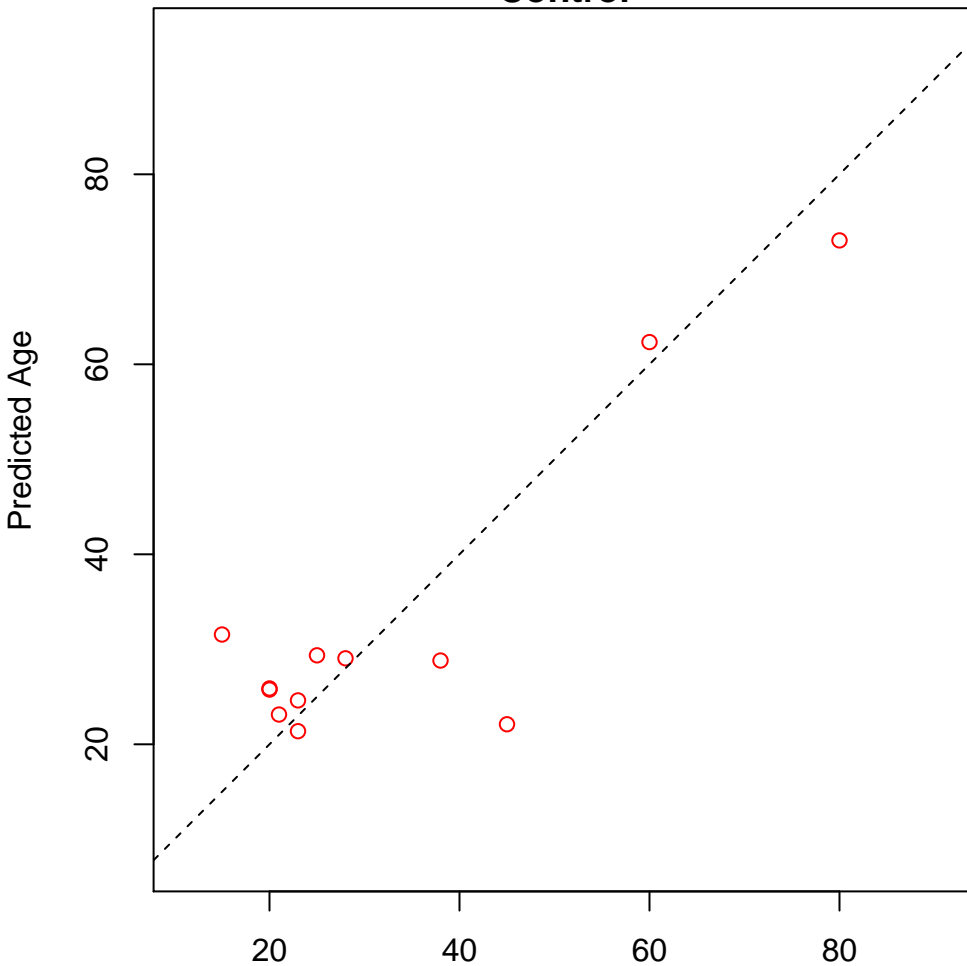


substrate adhesion-dependent cell spreading (Score: 6.346906)

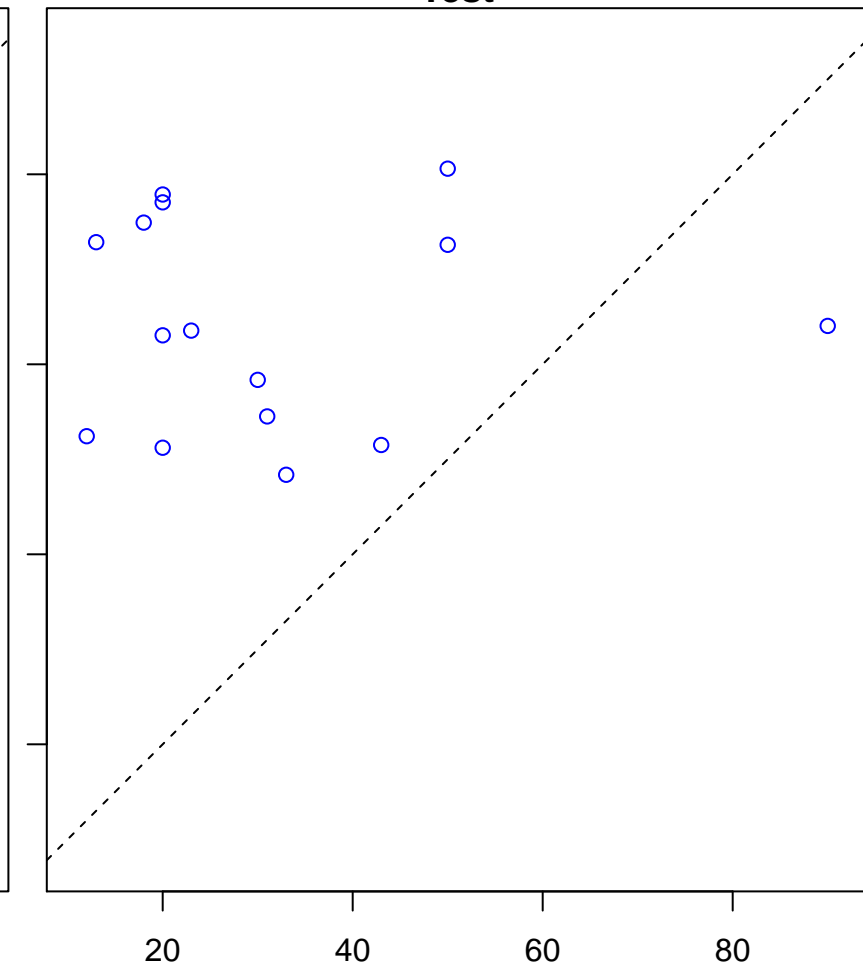


pyridine nucleotide metabolic process (Score: 6.346217)

Control

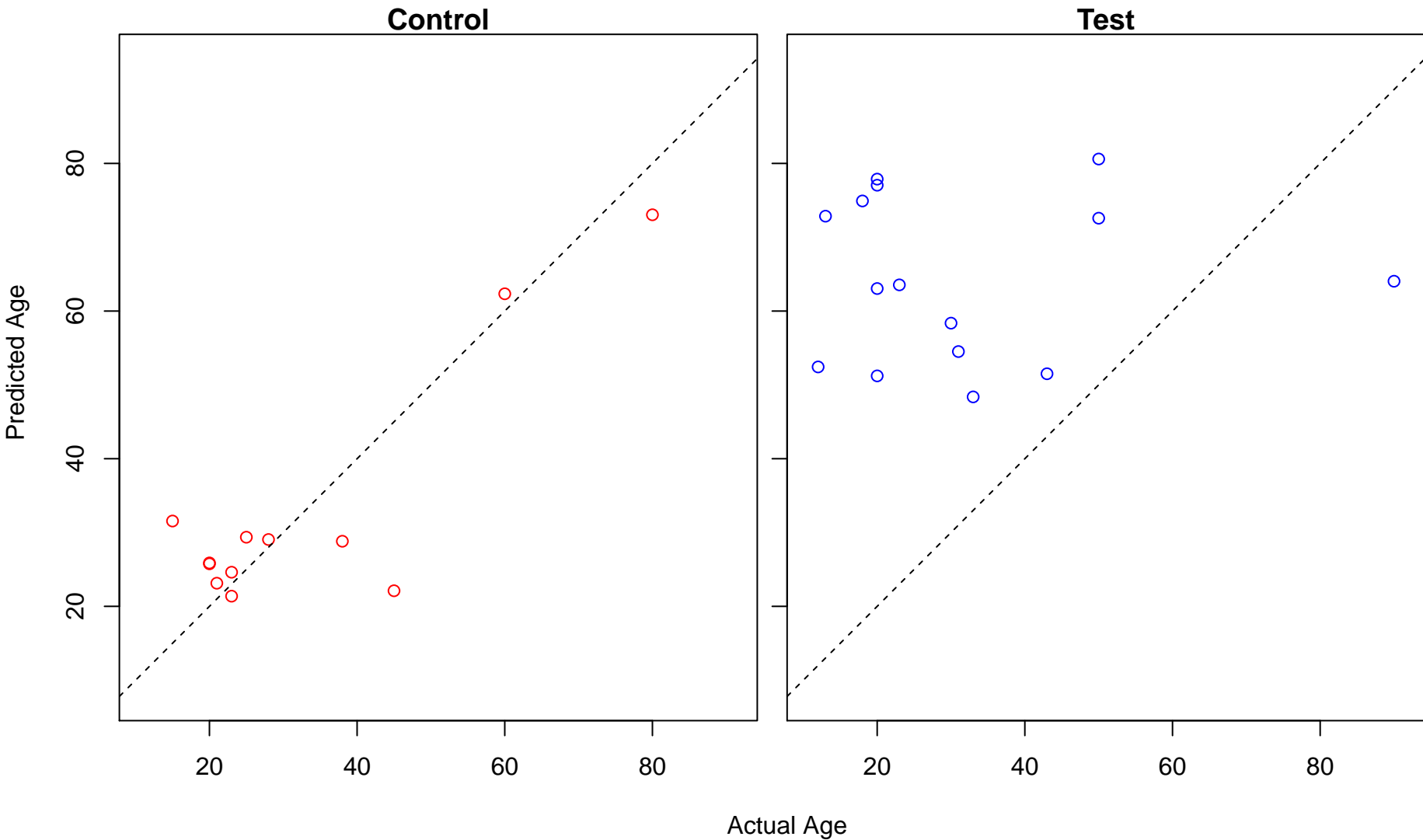


Test

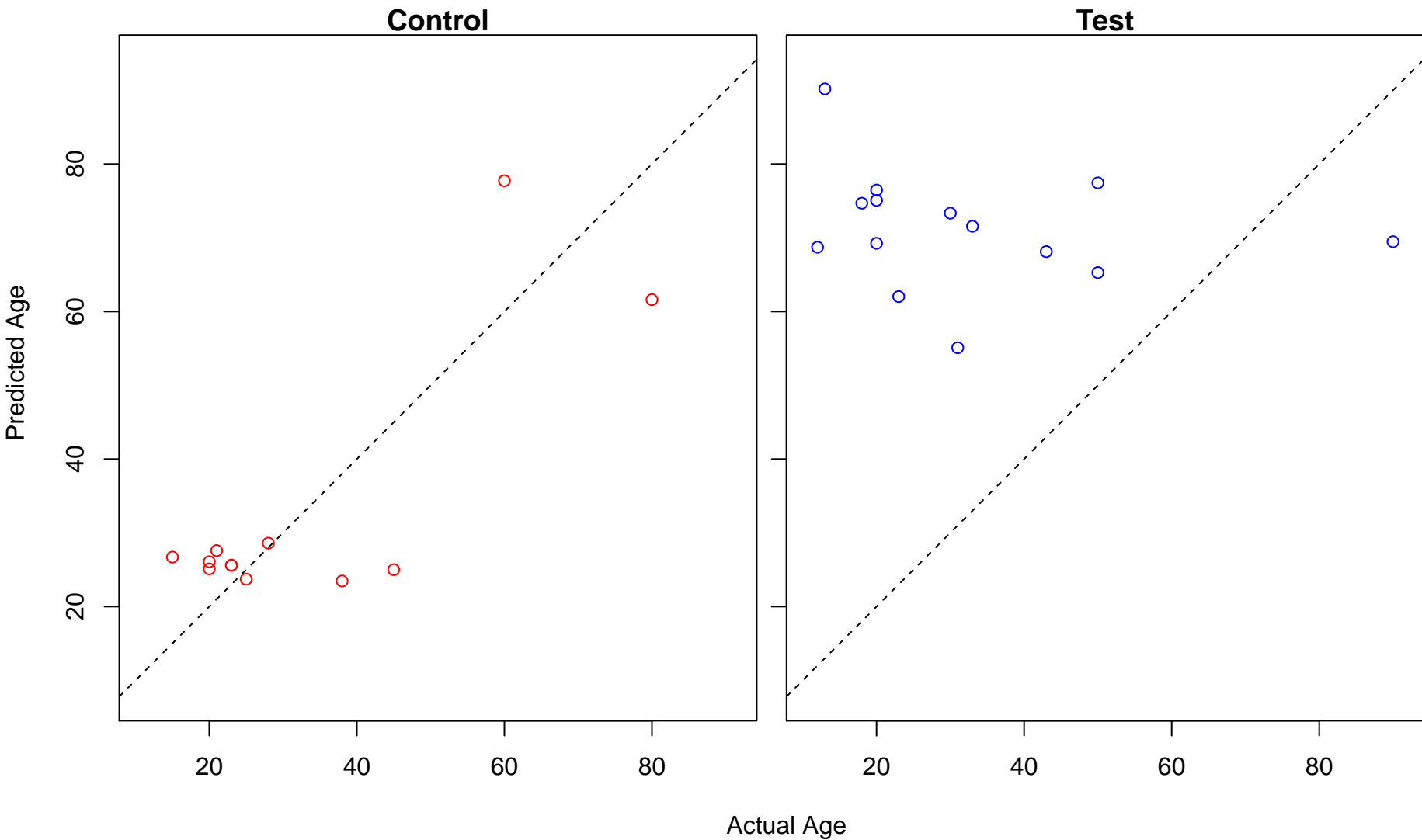


Actual Age

nicotinamide nucleotide metabolic process (Score: 6.346217)

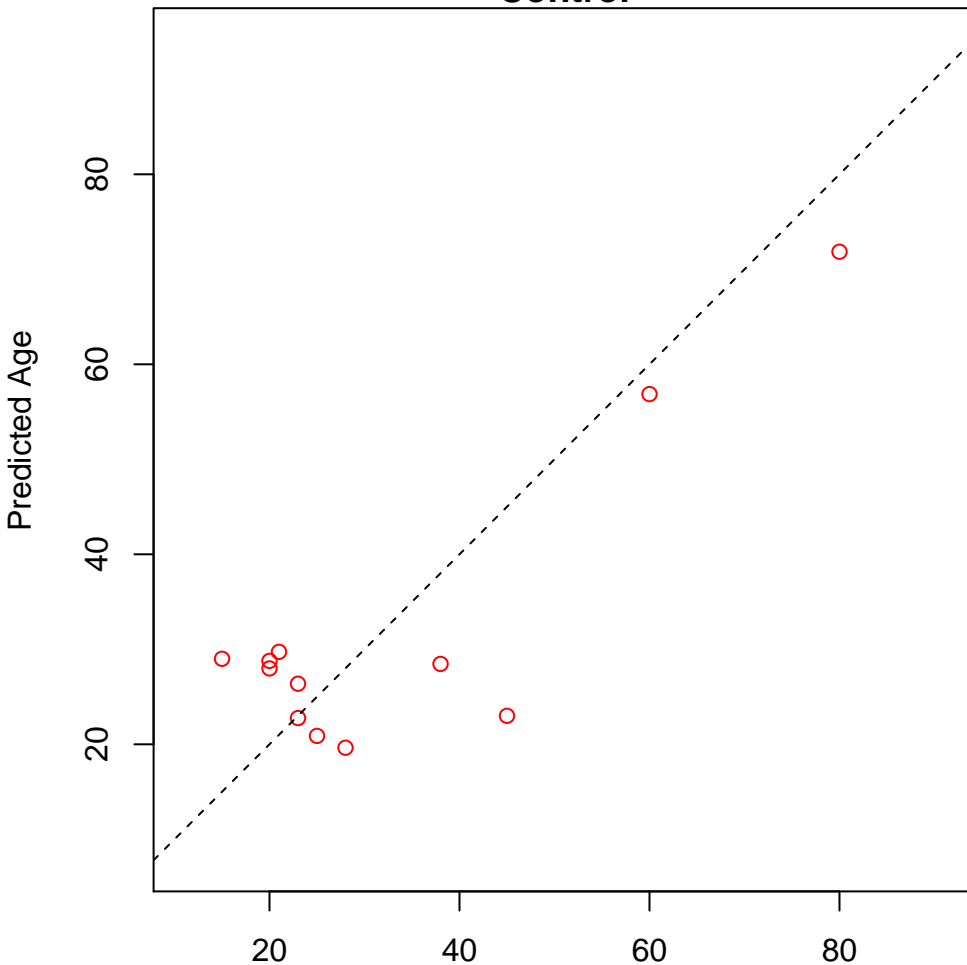


glyoxylate metabolic process (Score: 6.345634)

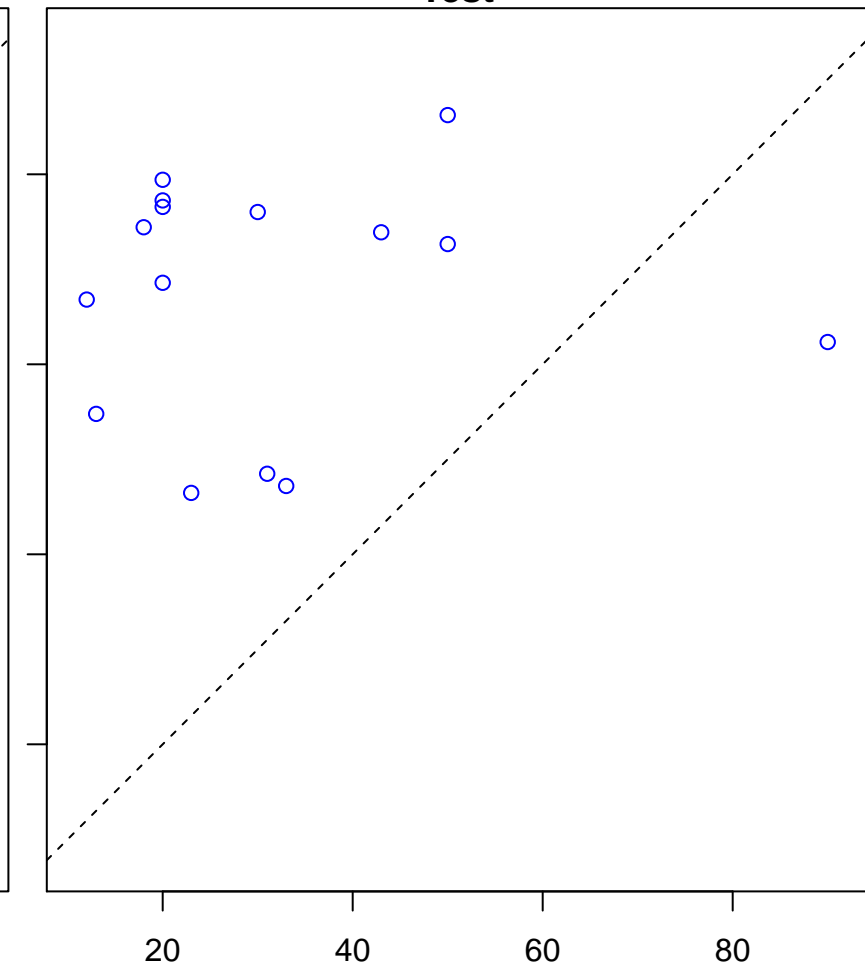


response to reactive oxygen species (Score: 6.344152)

Control

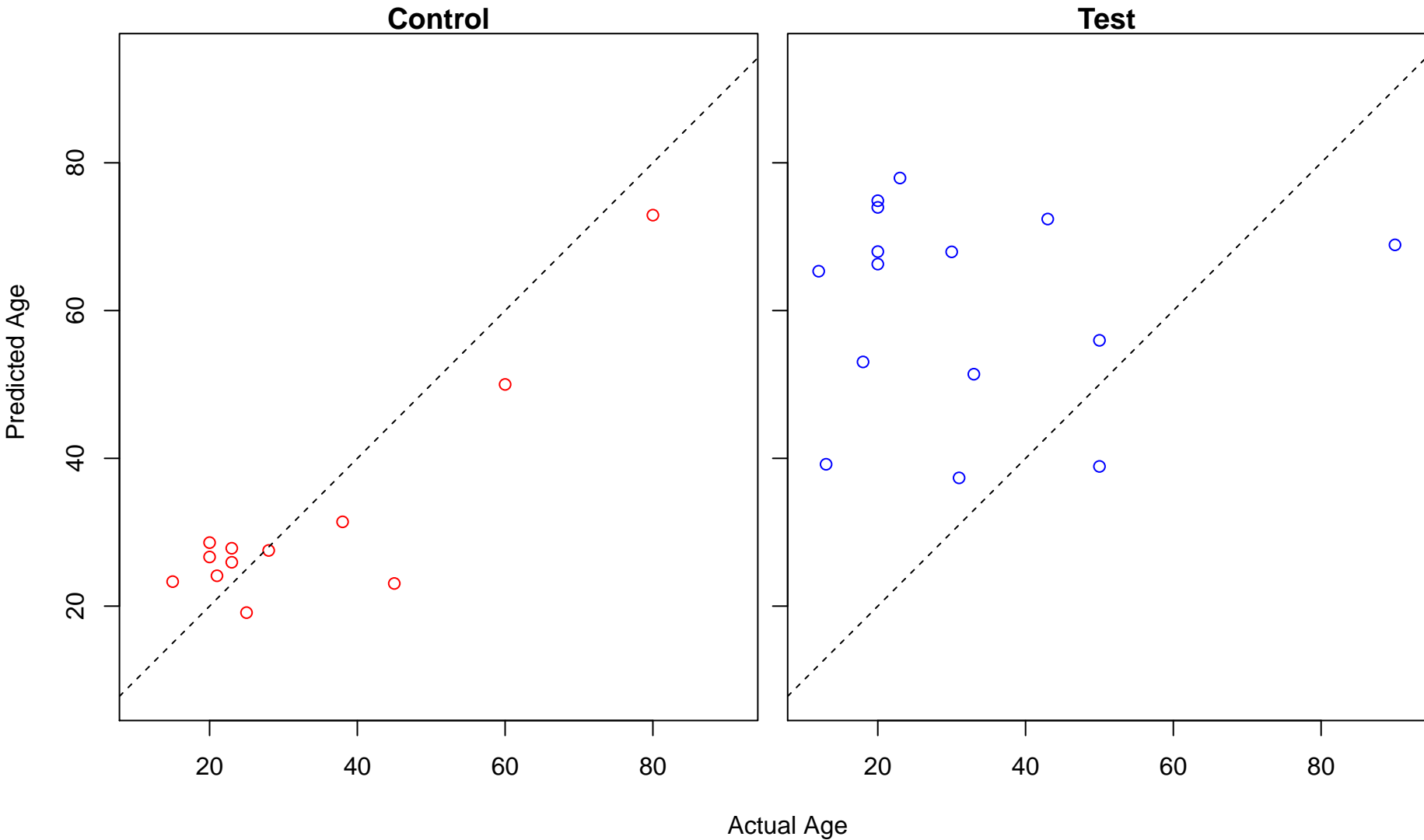


Test

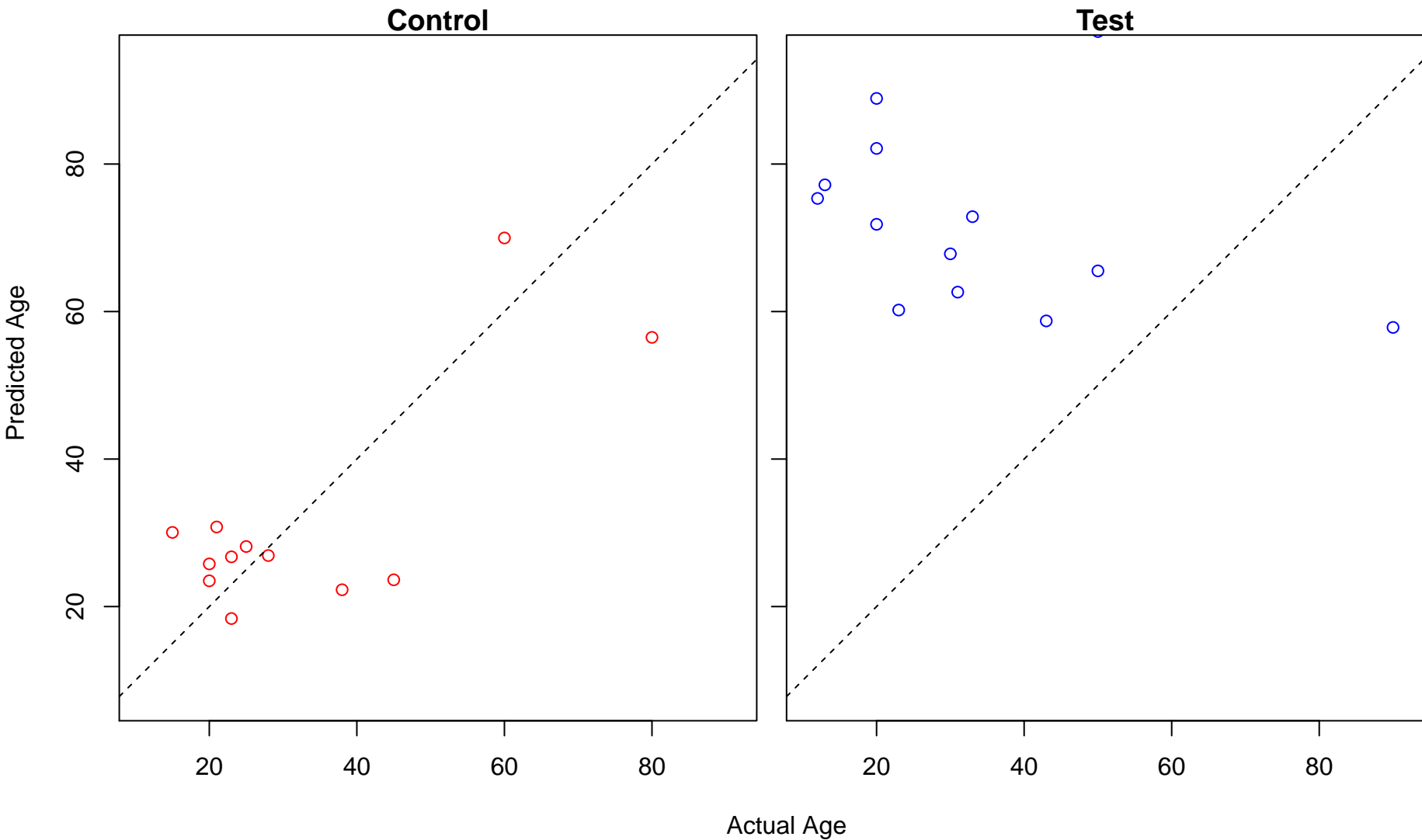


Actual Age

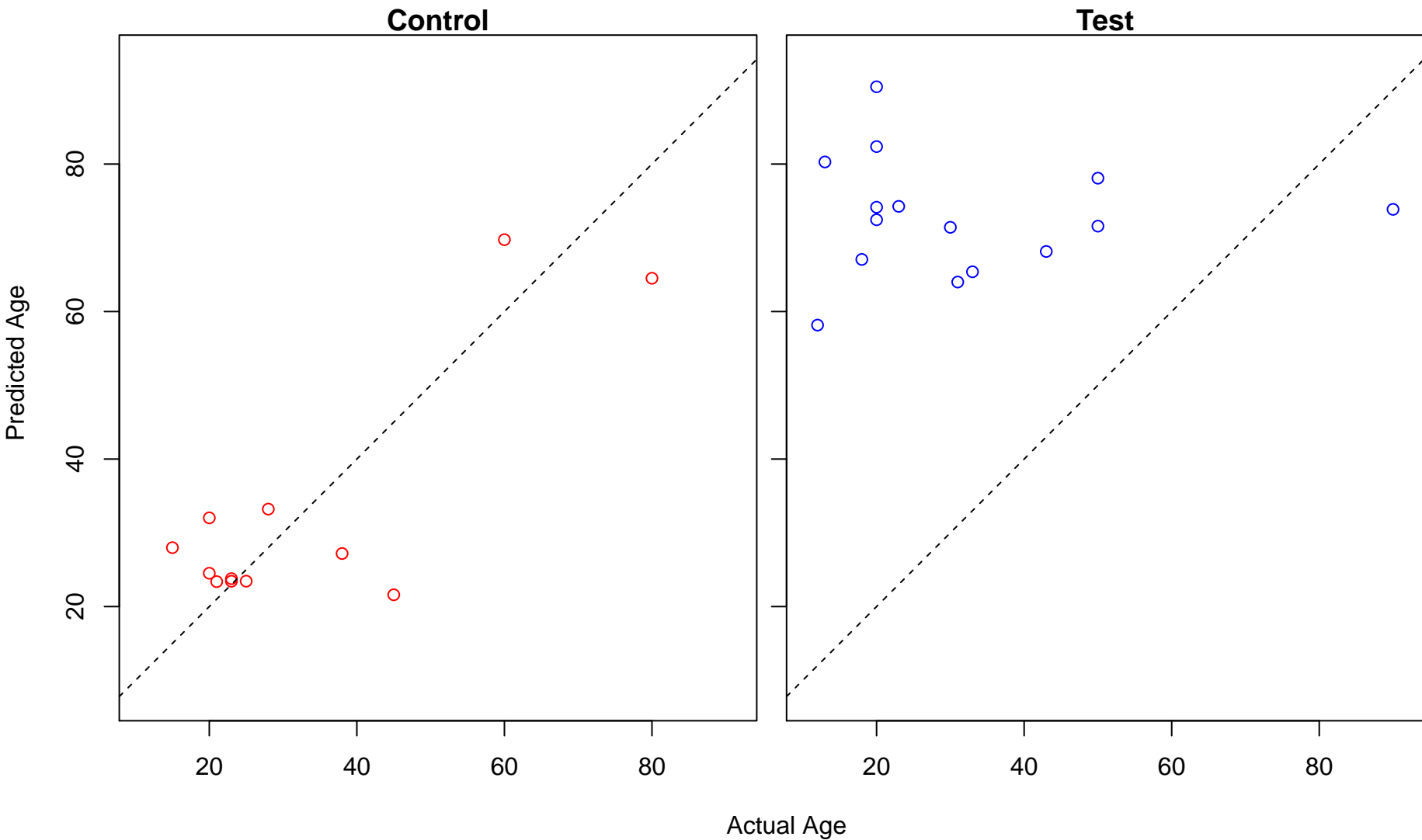
ventricular cardiac muscle cell development (Score: 6.341536)



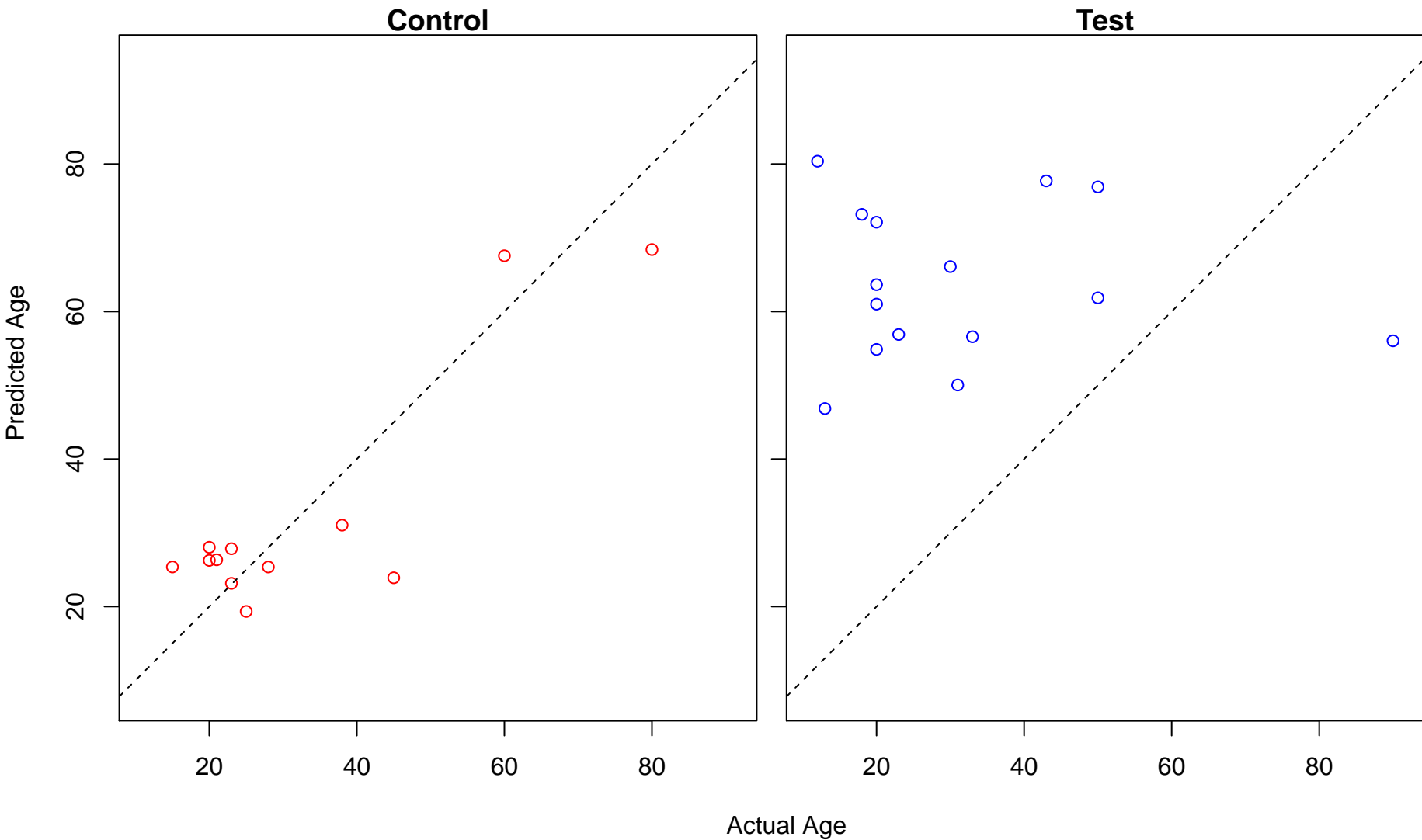
Arp2/3 complex-mediated actin nucleation (Score: 6.338880)



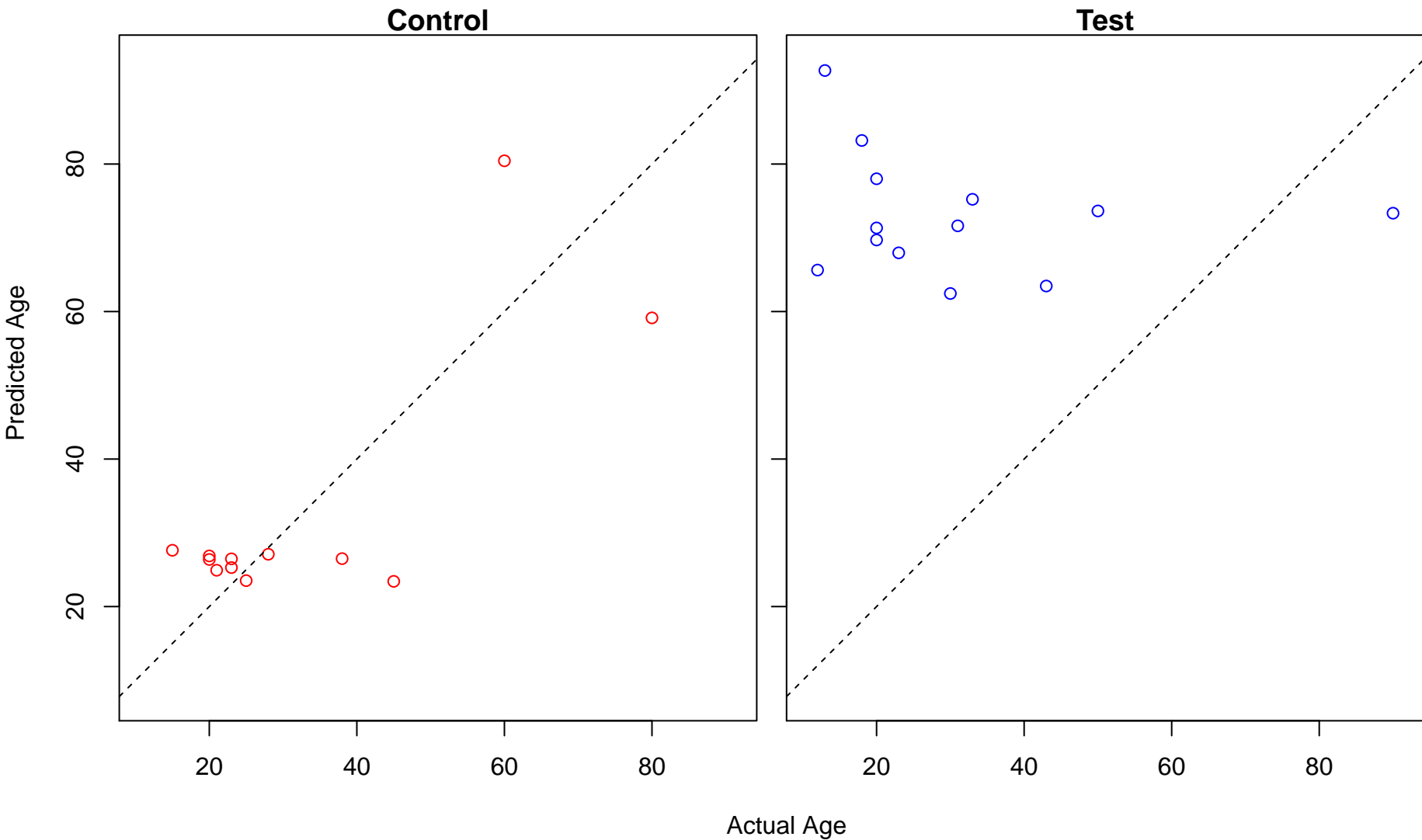
platelet activation (Score: 6.336076)



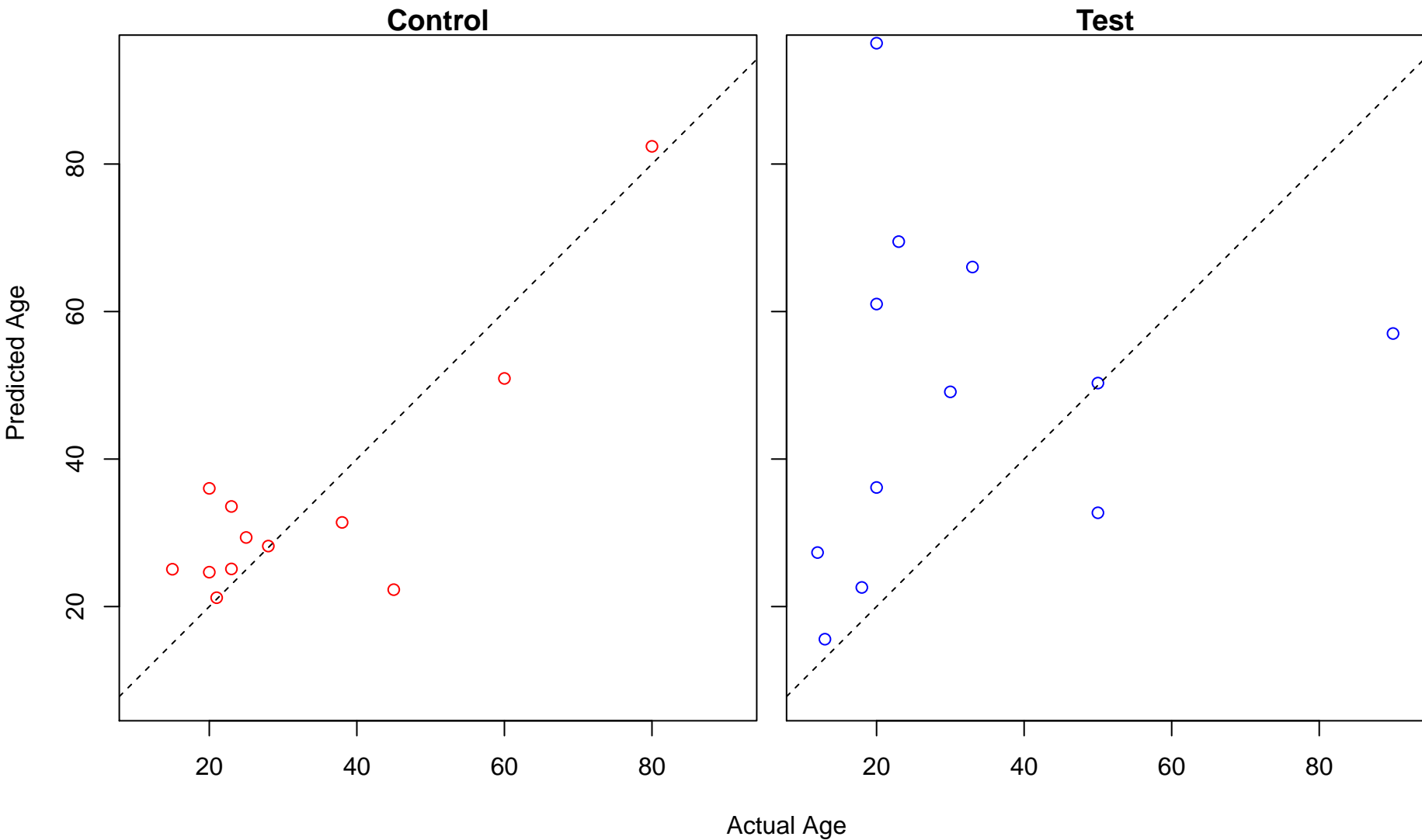
glutathione biosynthetic process (Score: 6.335350)



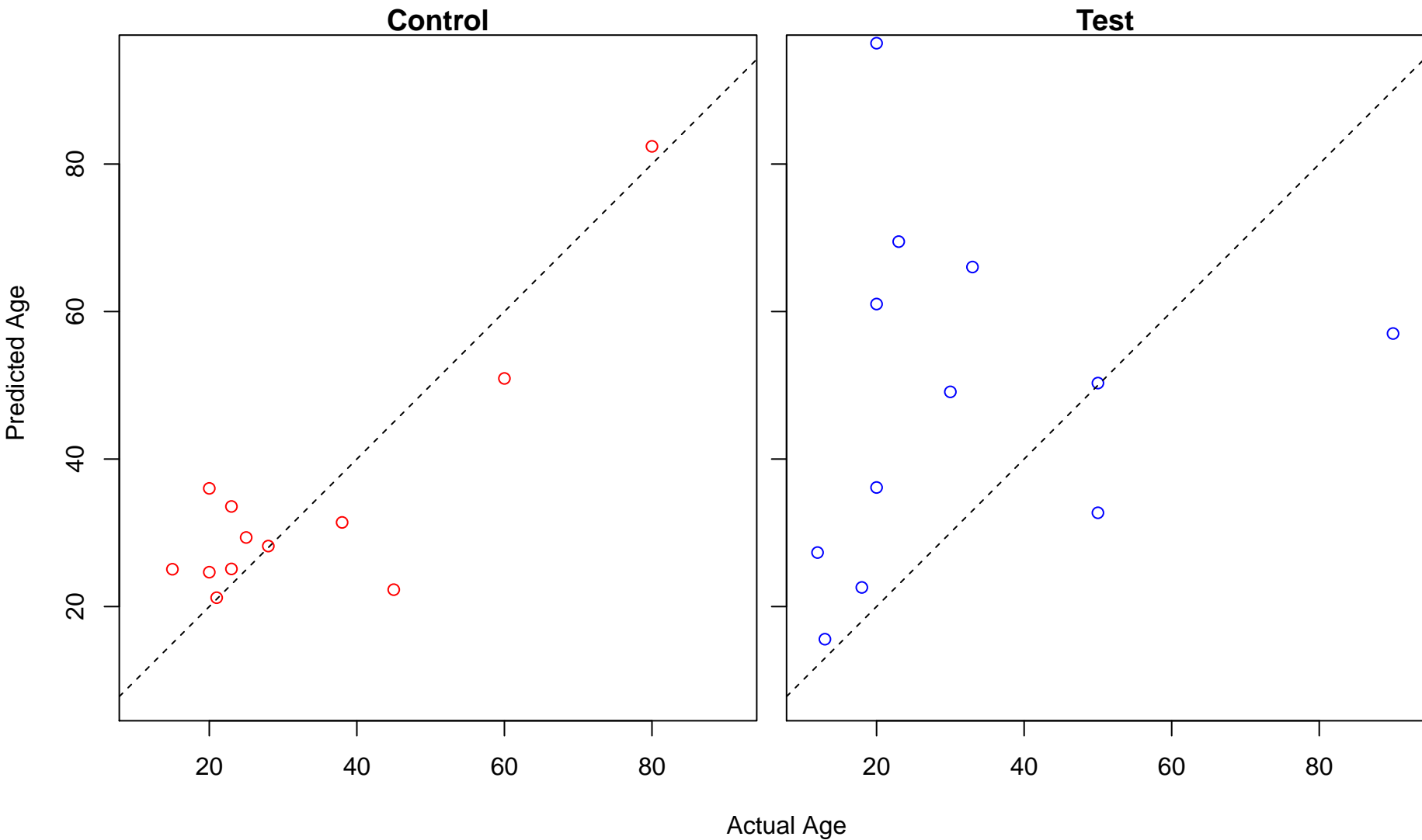
positive regulation of type I interferon production (Score: 6.334251)



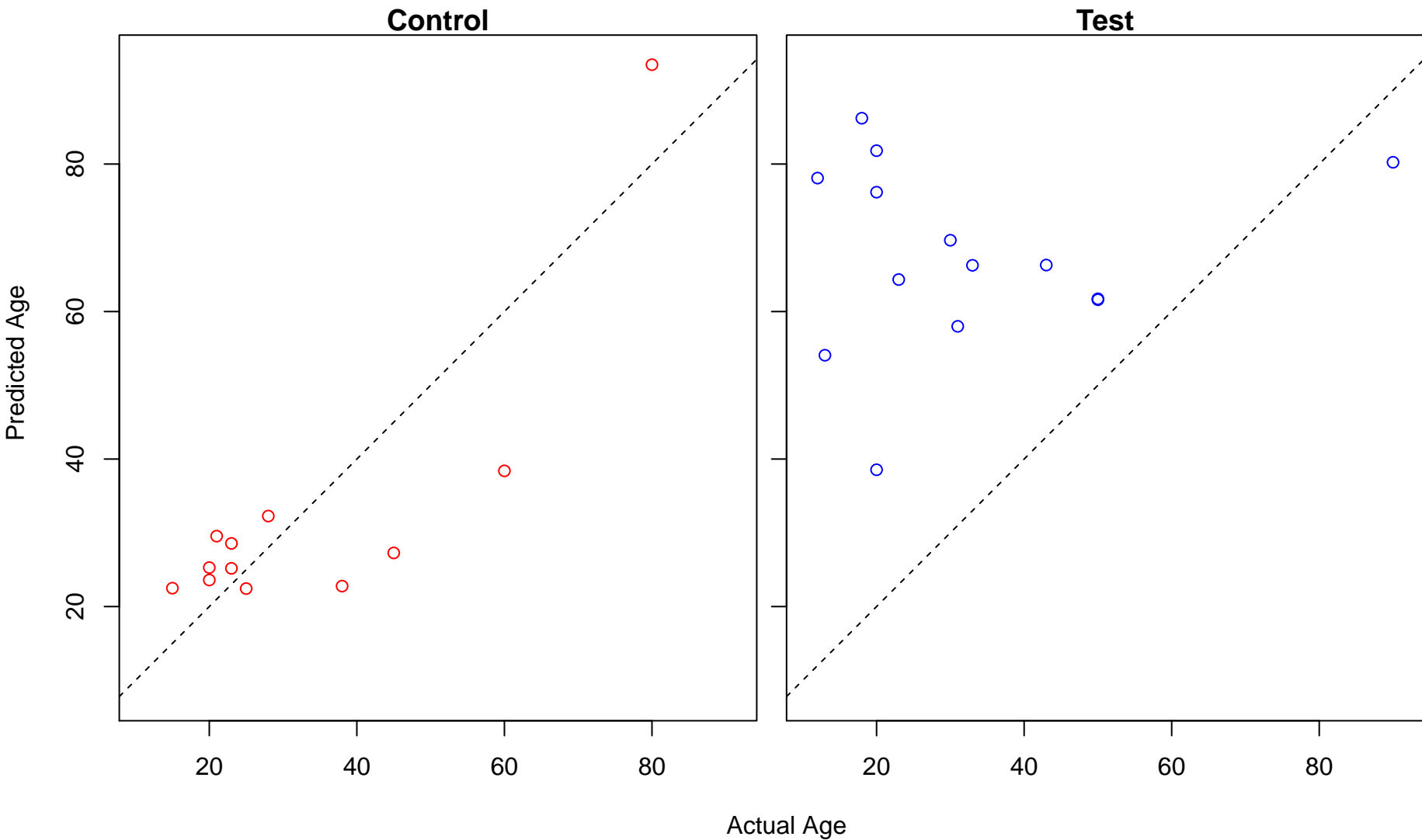
sphingosine metabolic process (Score: 6.332971)



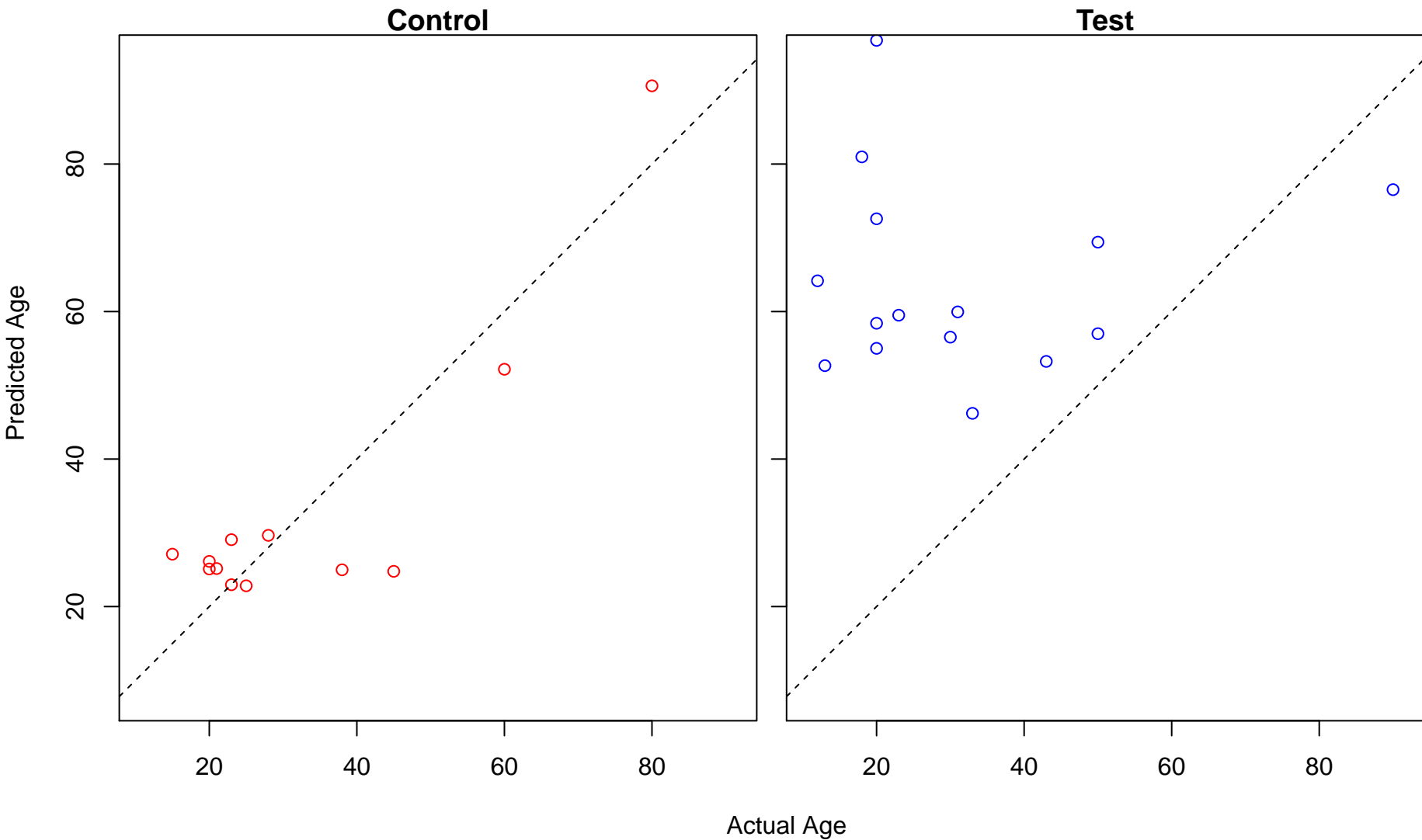
diol metabolic process (Score: 6.332971)



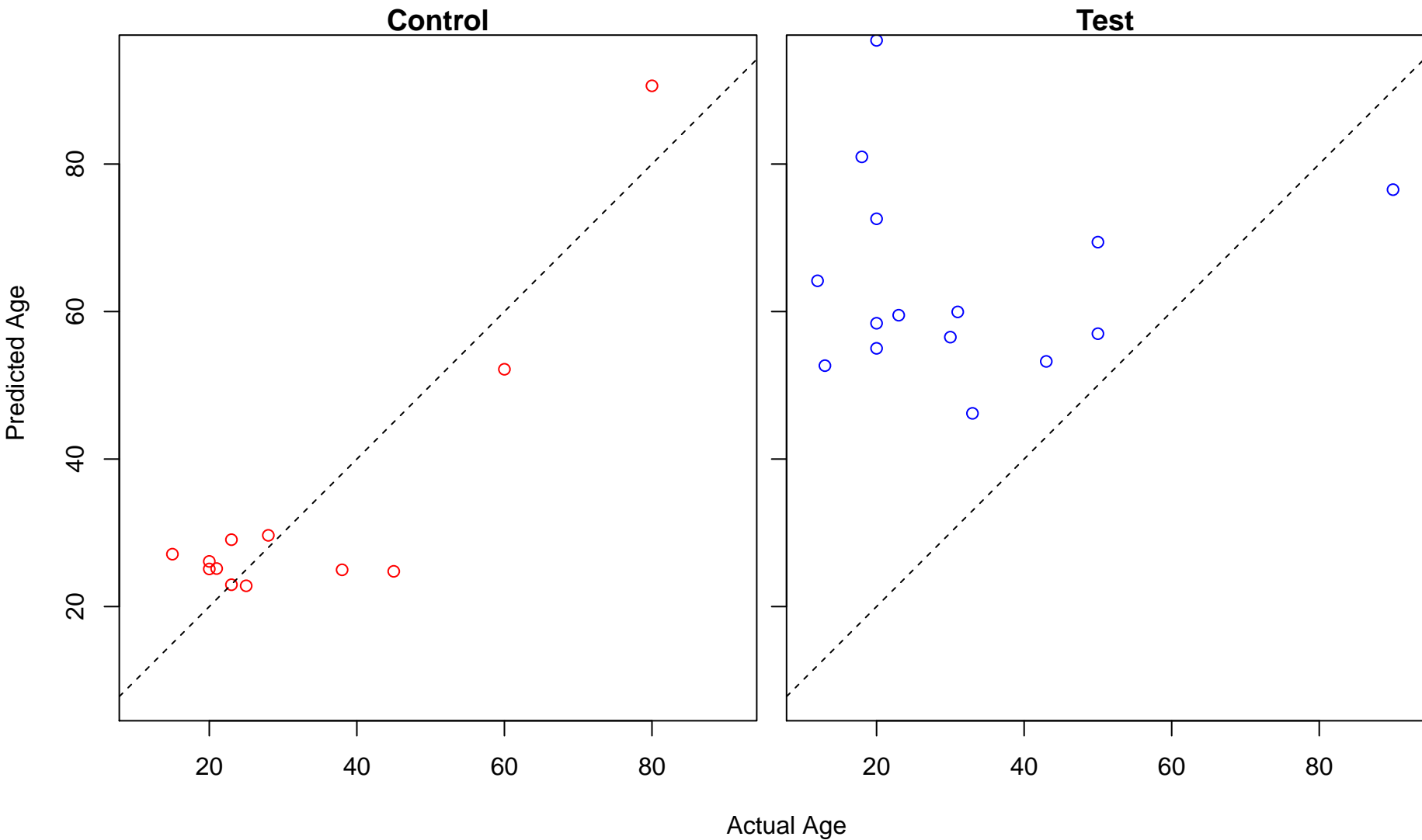
oxidative phosphorylation (Score: 6.331831)



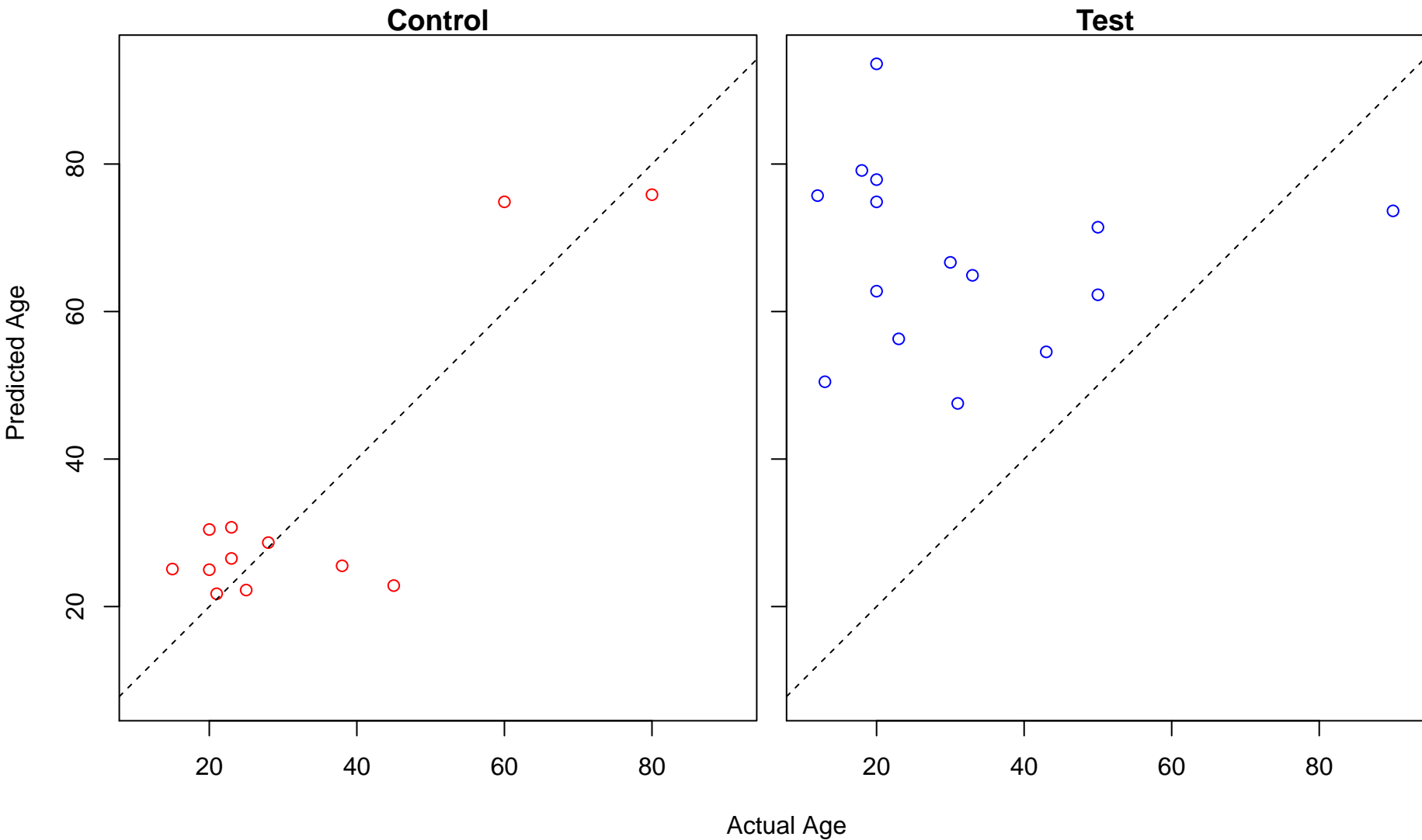
regulation of transforming growth factor beta receptor signaling pathway (Score: 6.328268)



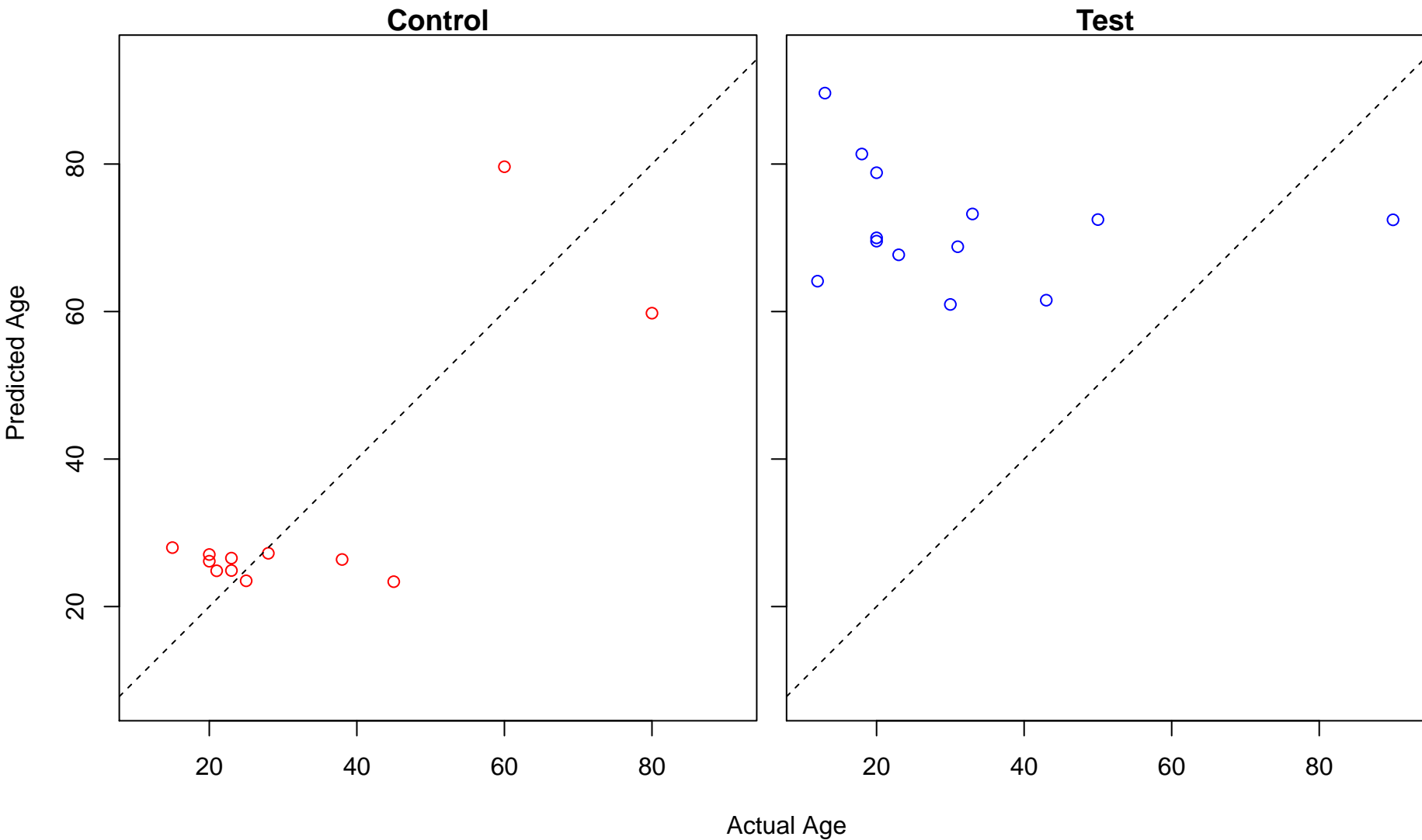
regulation of cellular response to transforming growth factor beta stimulus (Score: 6.328268)



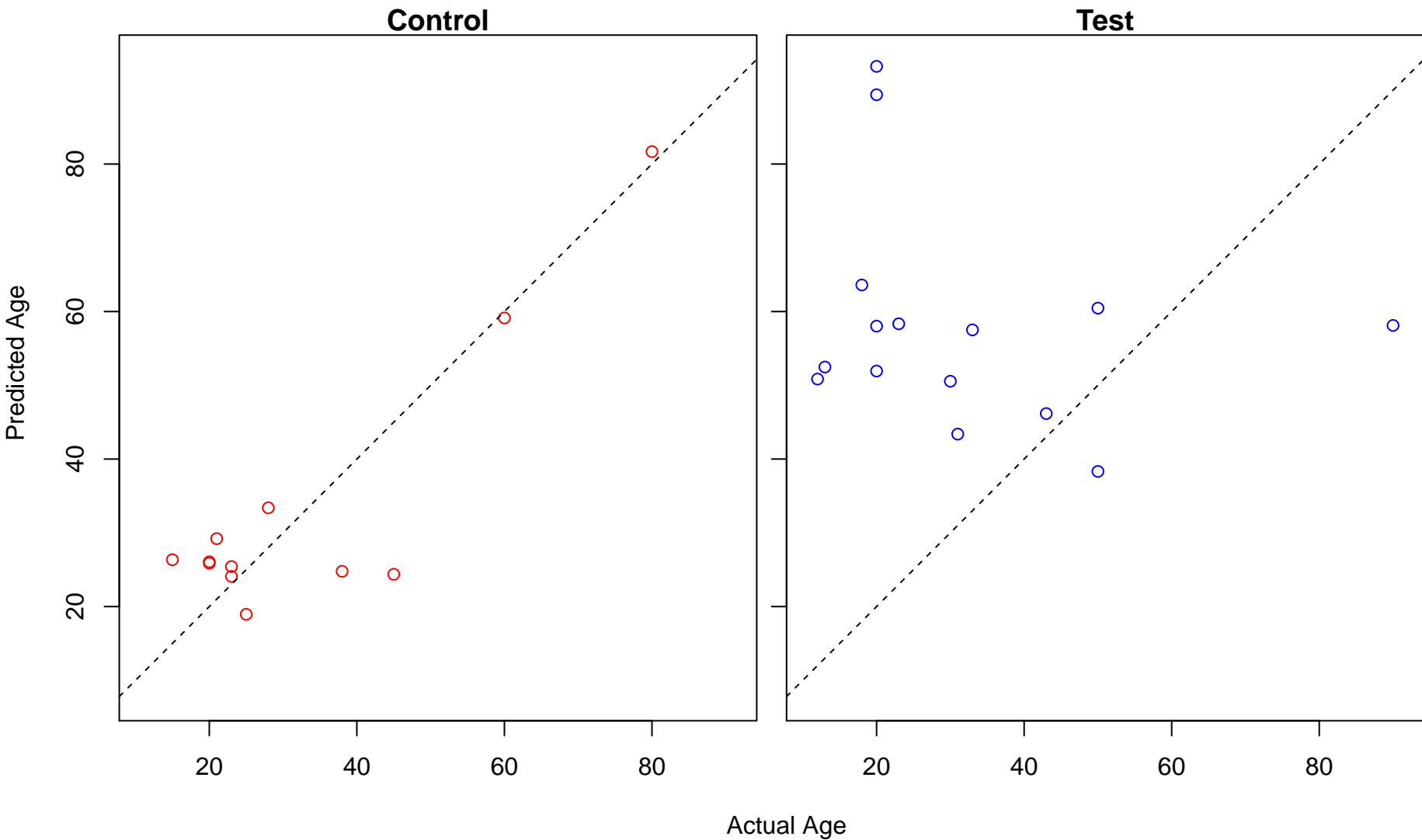
dicarboxylic acid transport (Score: 6.324748)



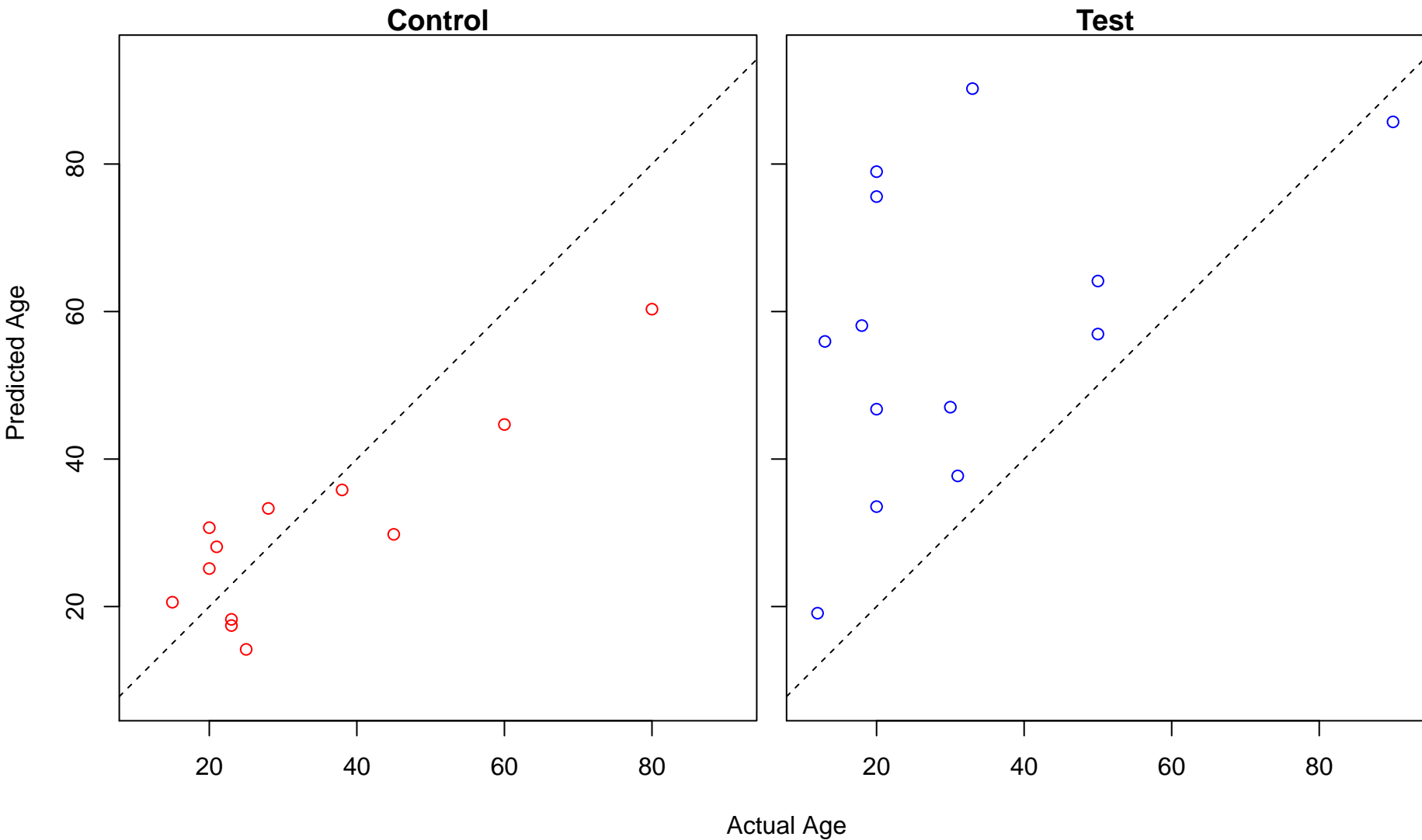
nucleotide-excision repair, DNA damage recognition (Score: 6.324145)



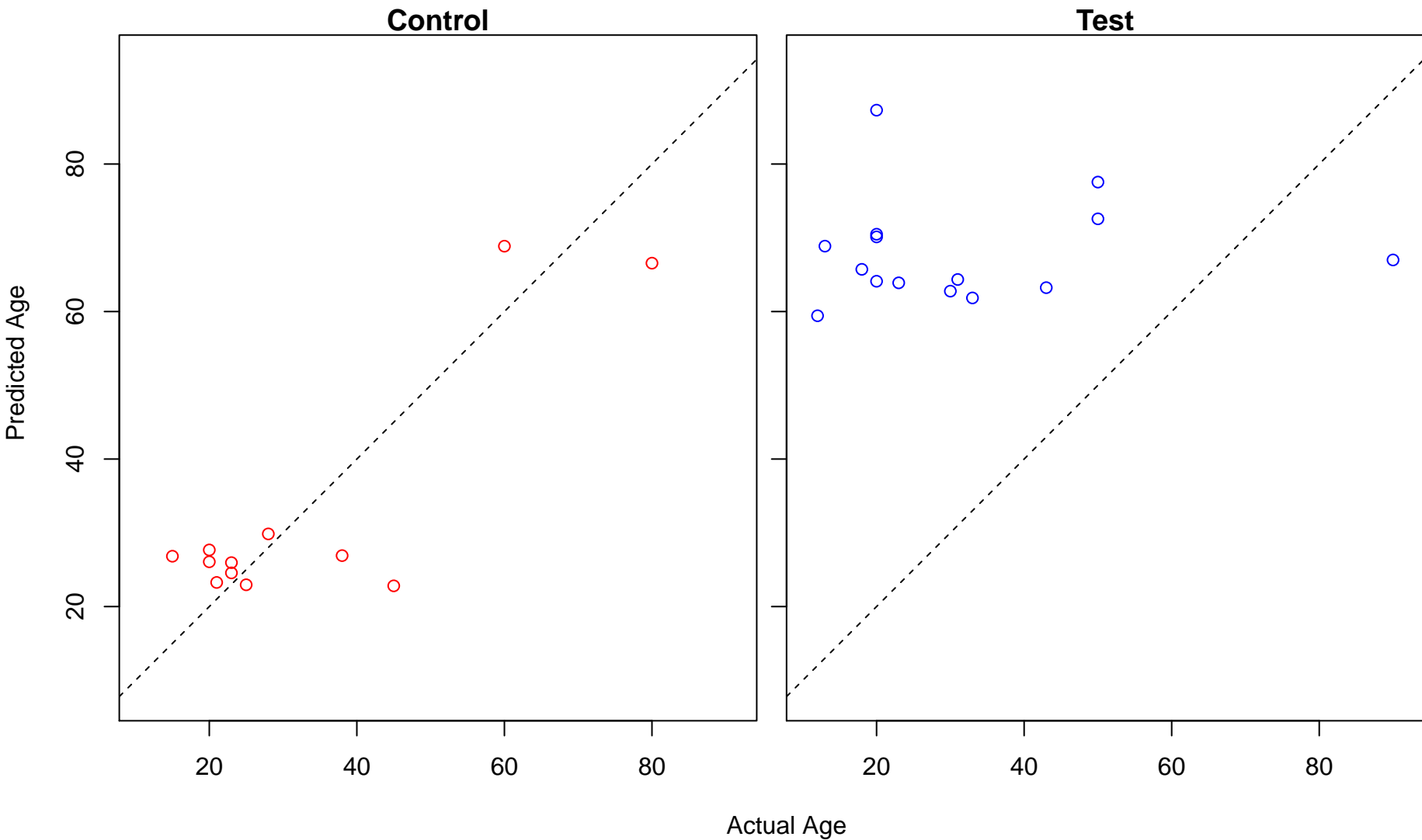
histone methylation (Score: 6.324110)



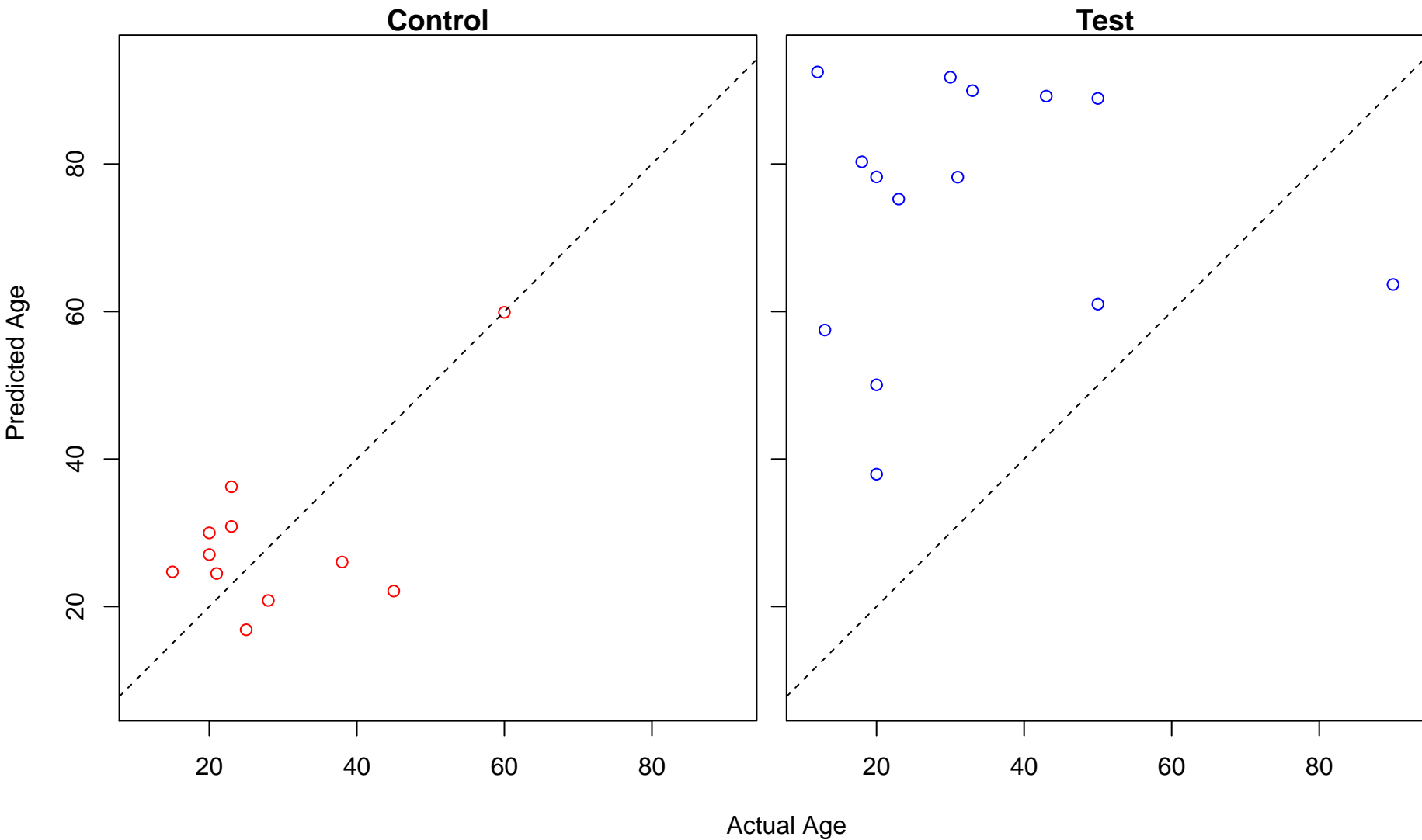
hindbrain development (Score: 6.323498)



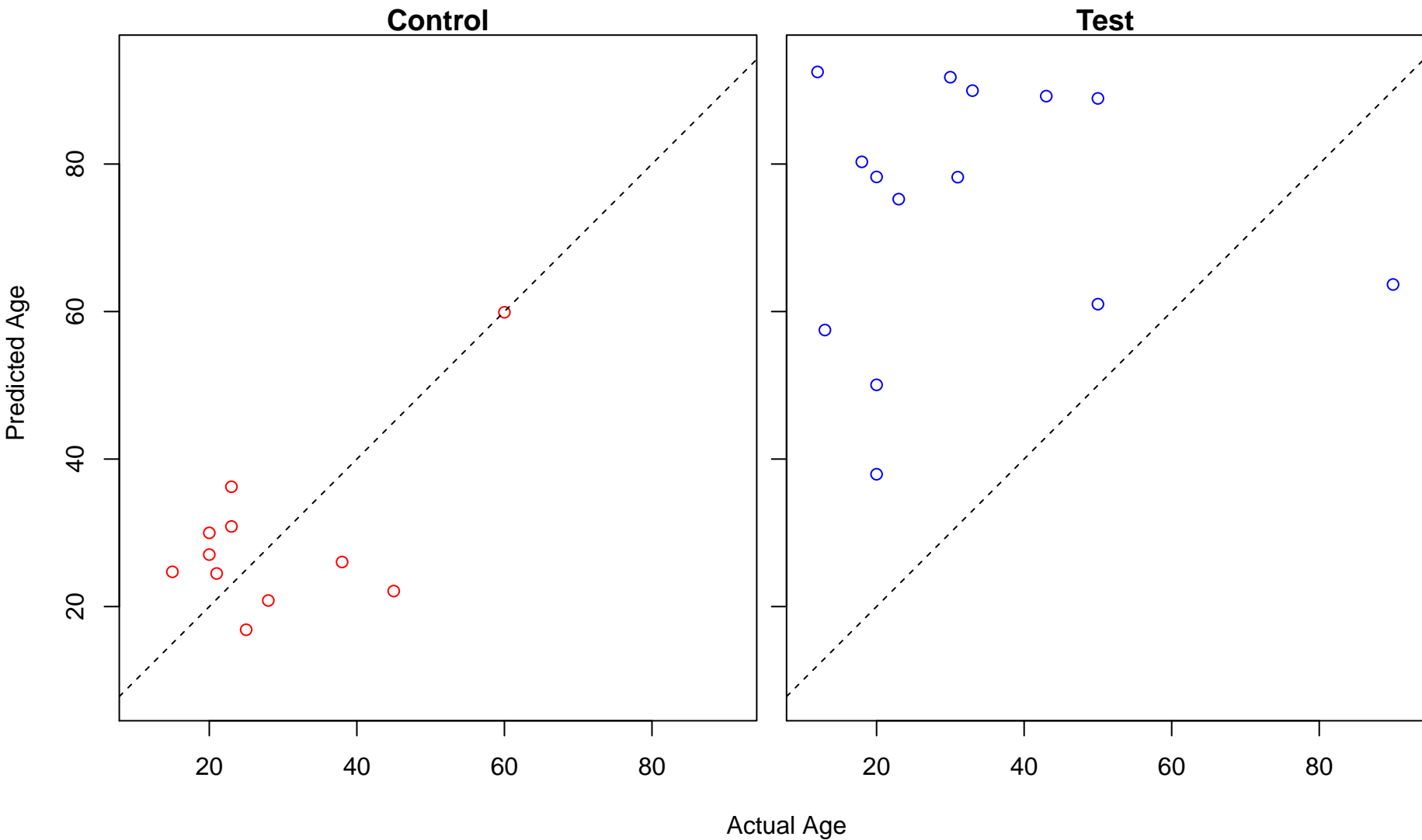
positive regulation of GTPase activity (Score: 6.321847)



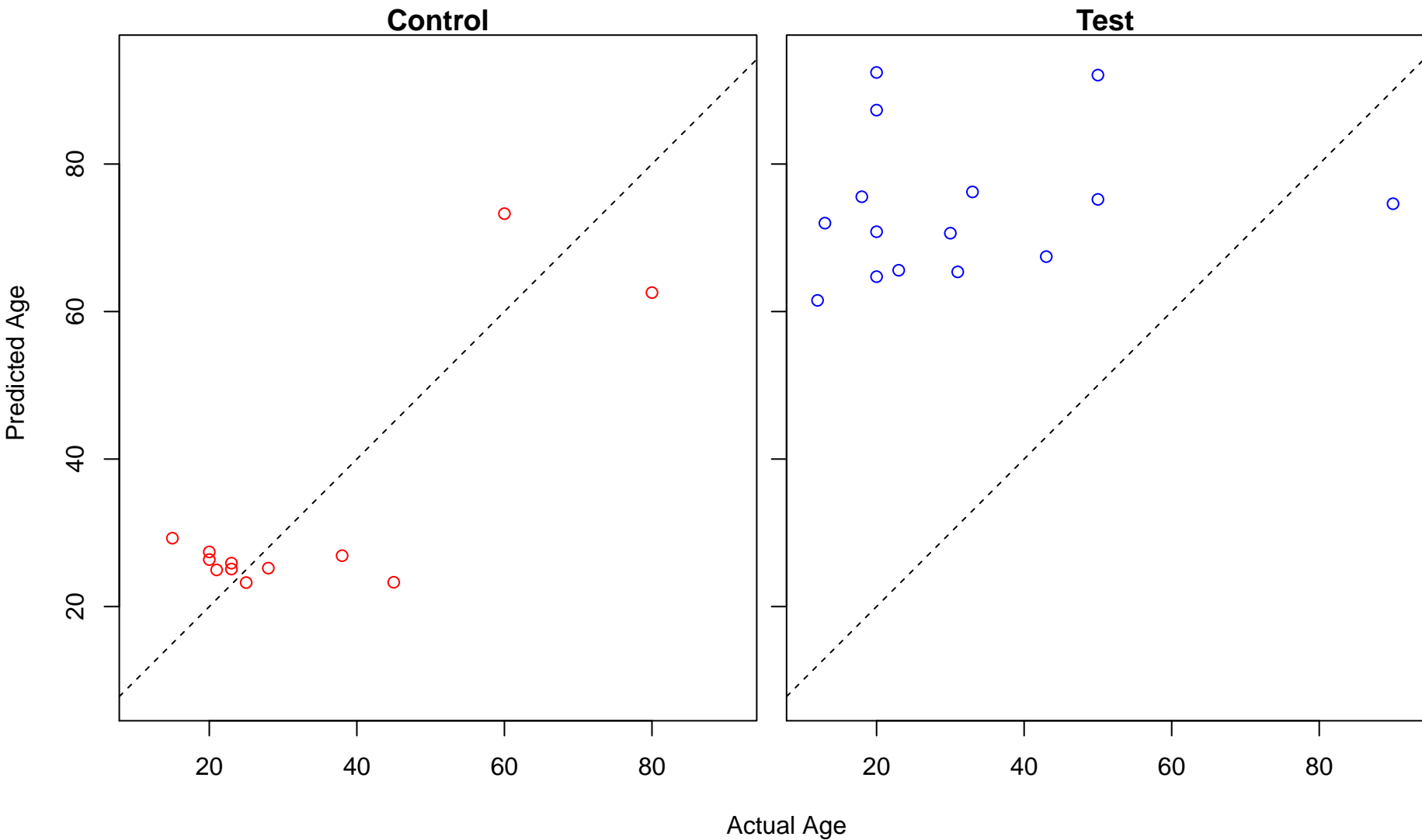
reciprocal meiotic recombination (Score: 6.320894)



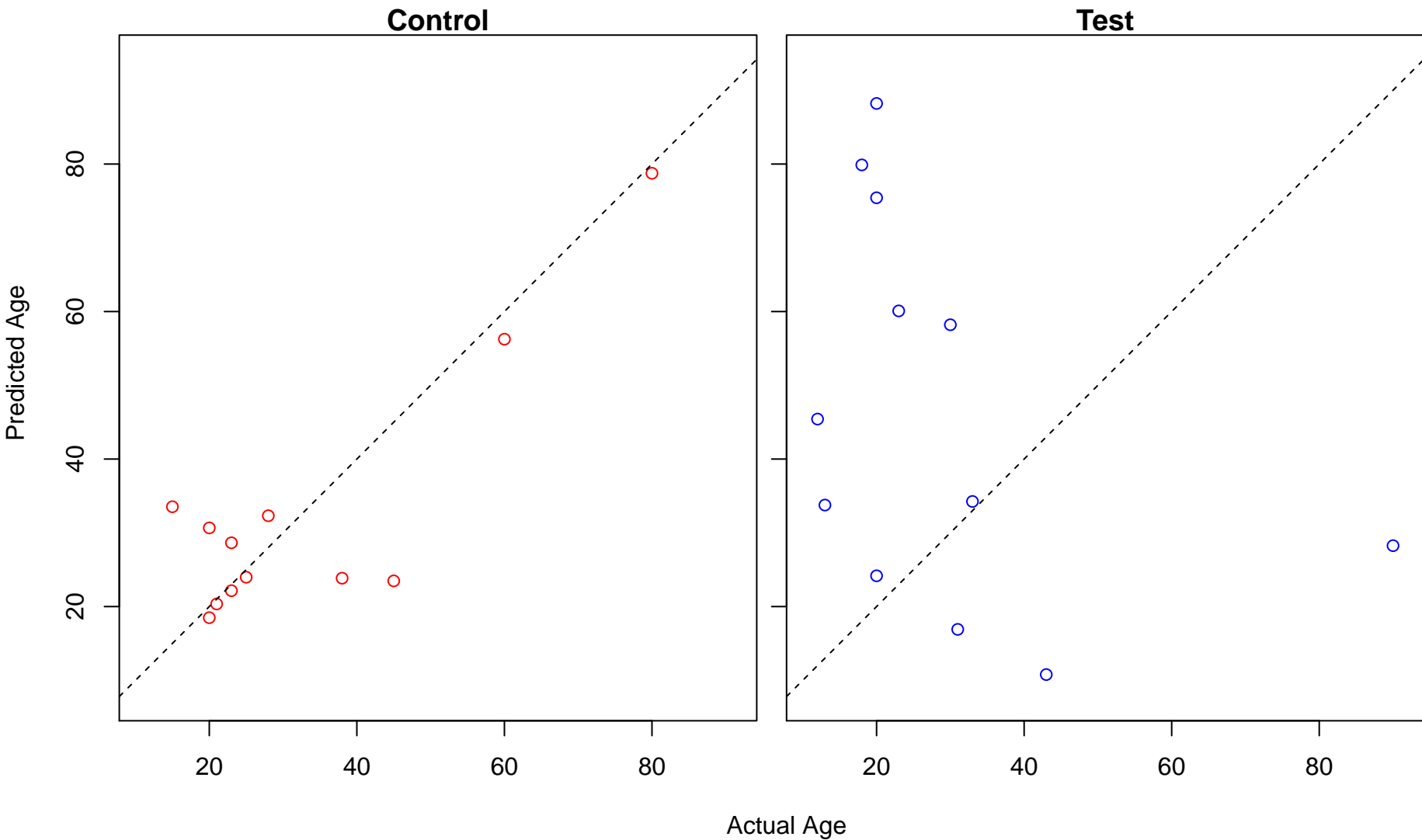
reciprocal DNA recombination (Score: 6.320894)



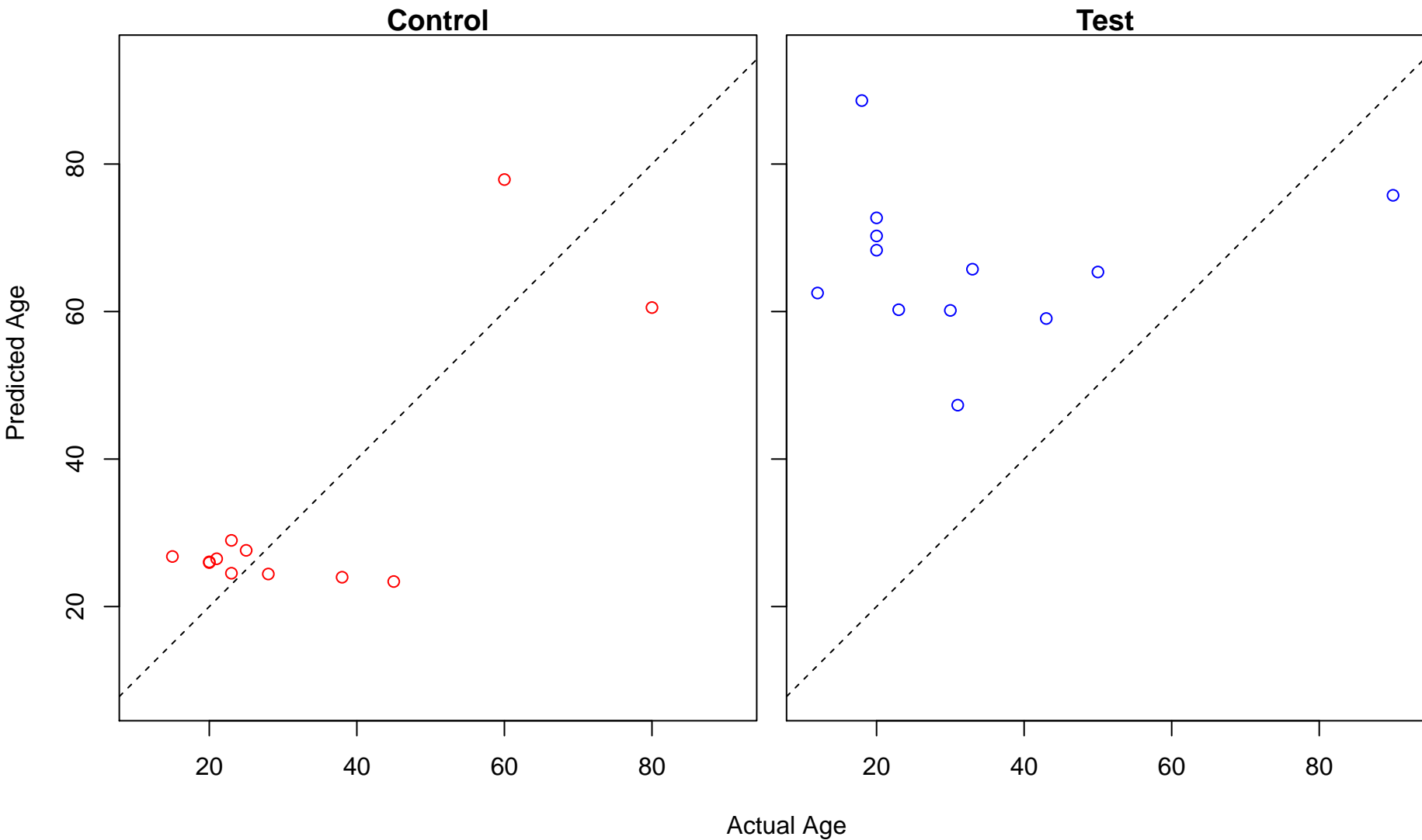
positive regulation of chromatin modification (Score: 6.319672)



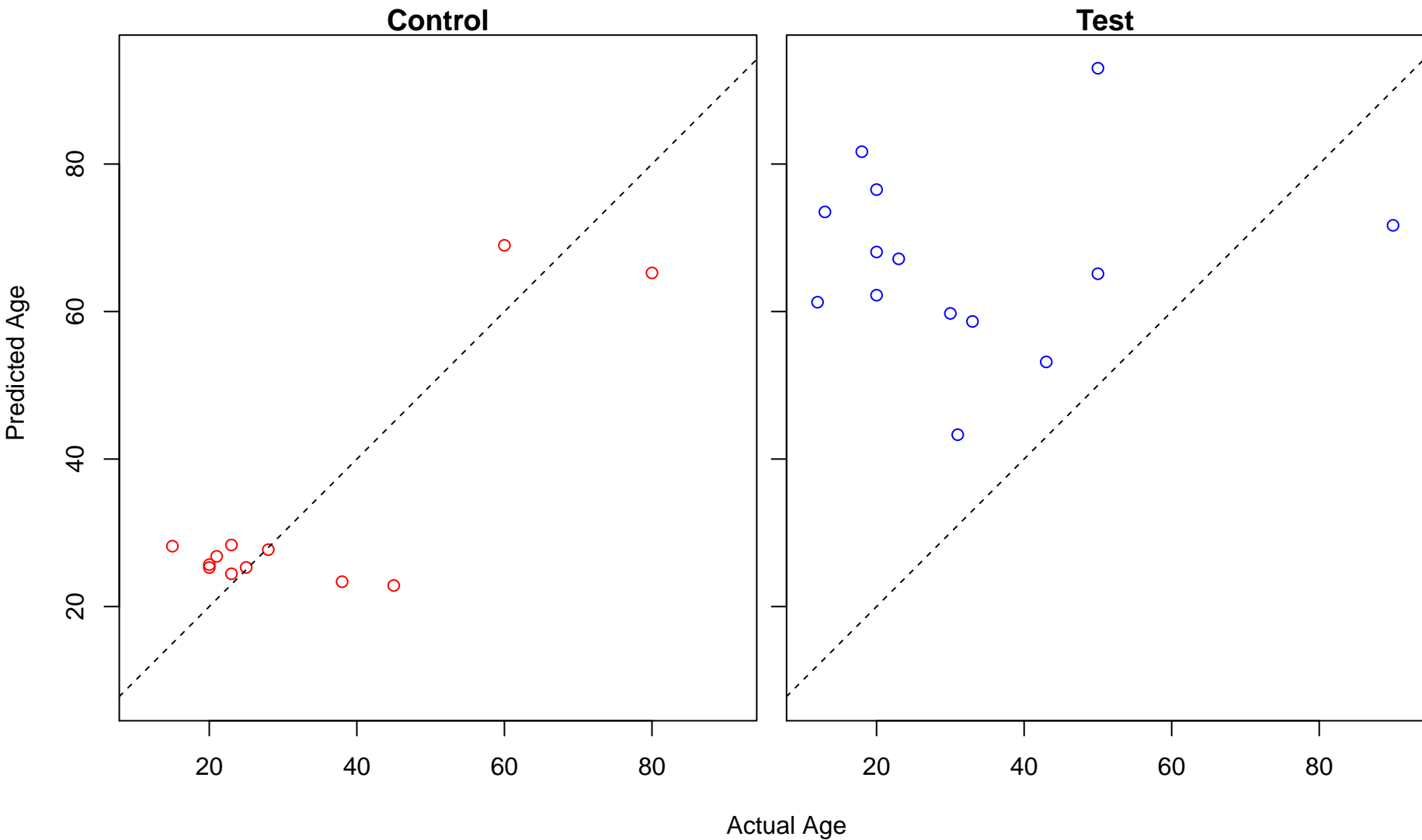
negative regulation of proteolysis involved in cellular protein catabolic process (Score: 6.314307)



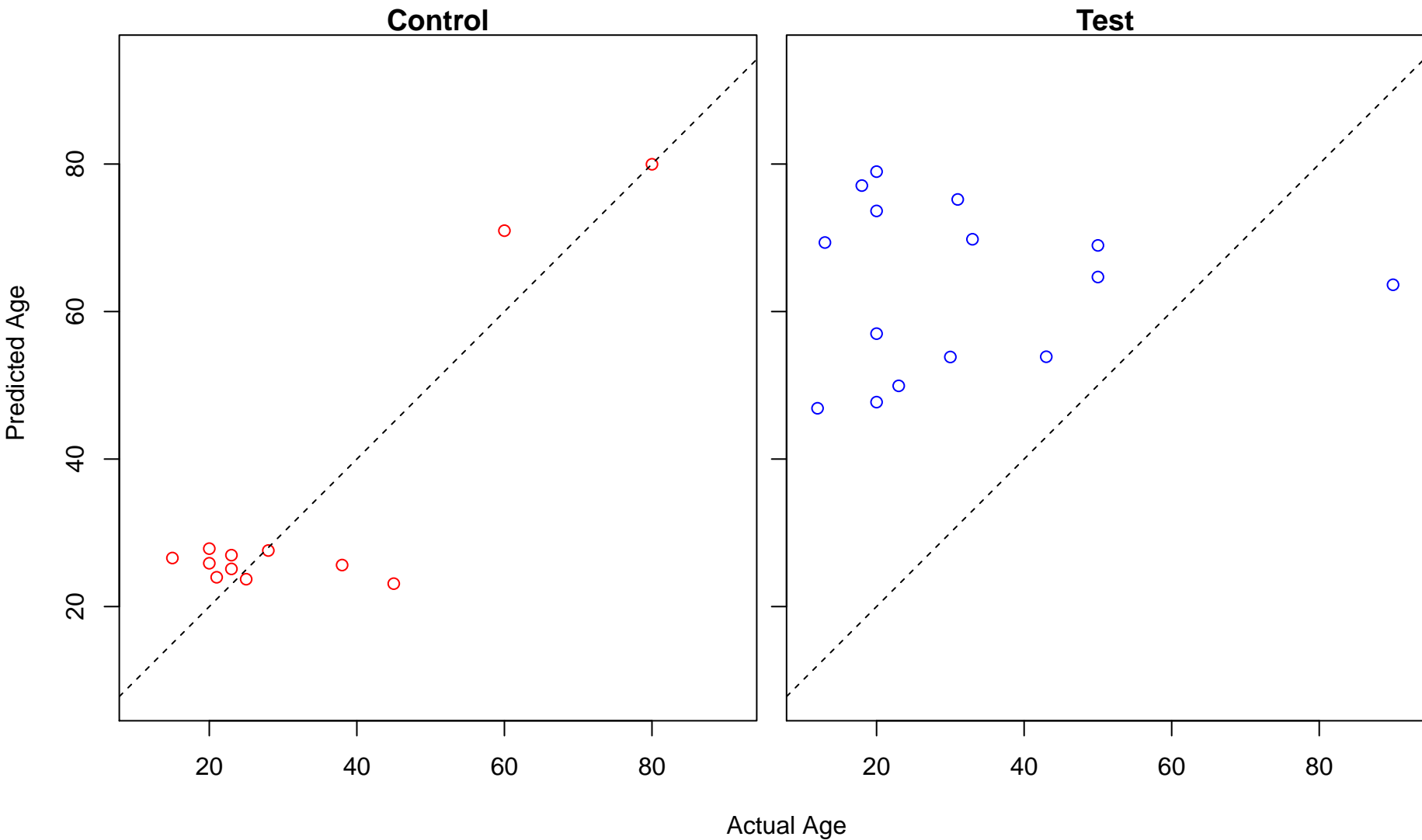
maturation of SSU-rRNA (Score: 6.314207)



ribonucleoprotein complex subunit organization (Score: 6.312807)

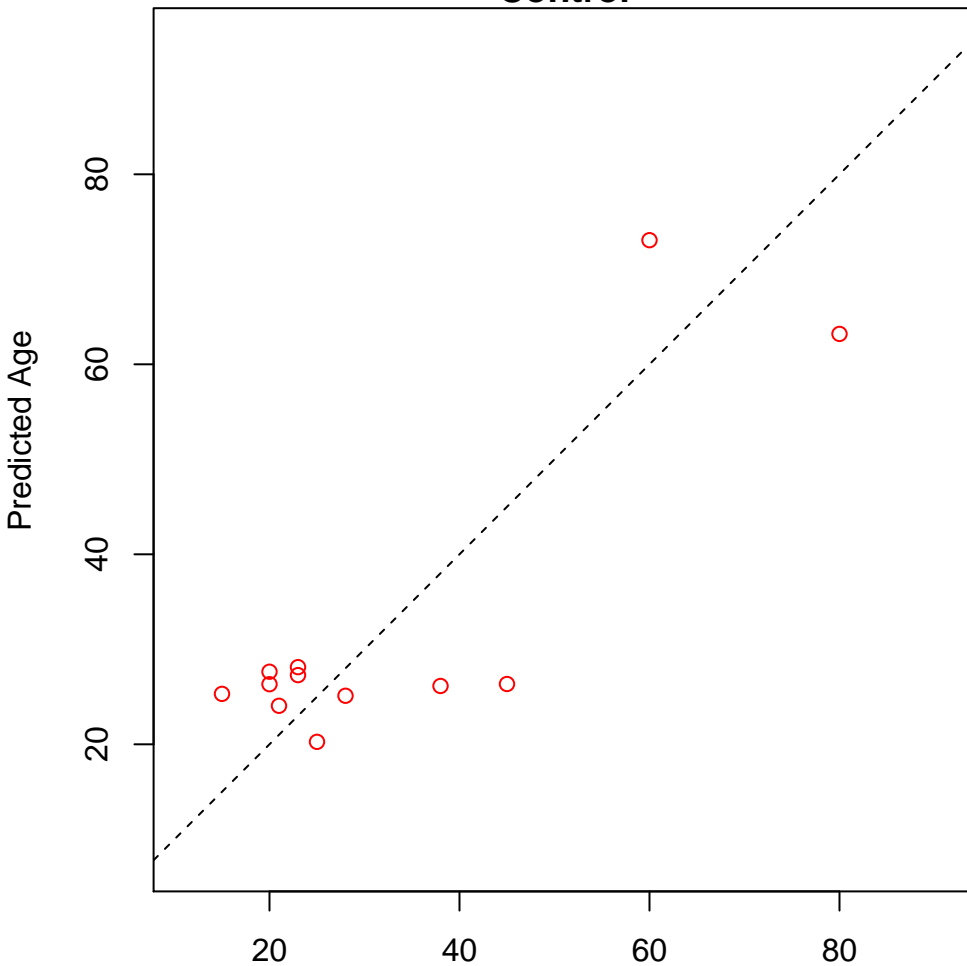


regulation of cellular protein localization (Score: 6.311860)

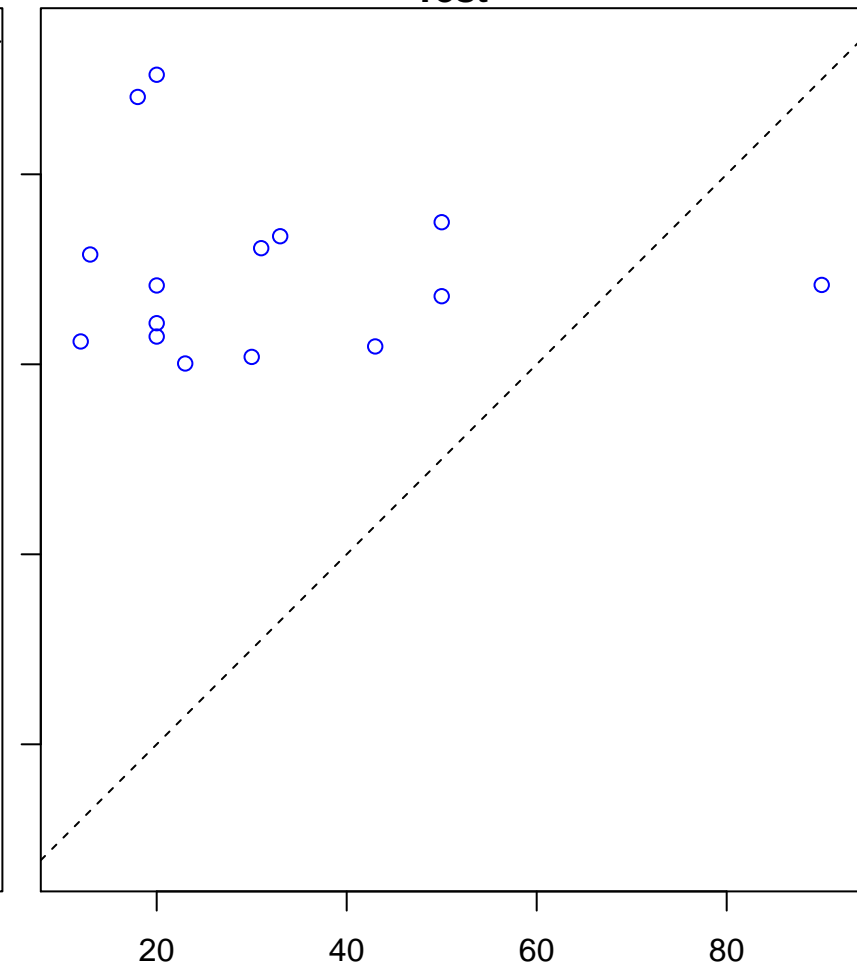


regulation of synaptic vesicle transport (Score: 6.311564)

Control

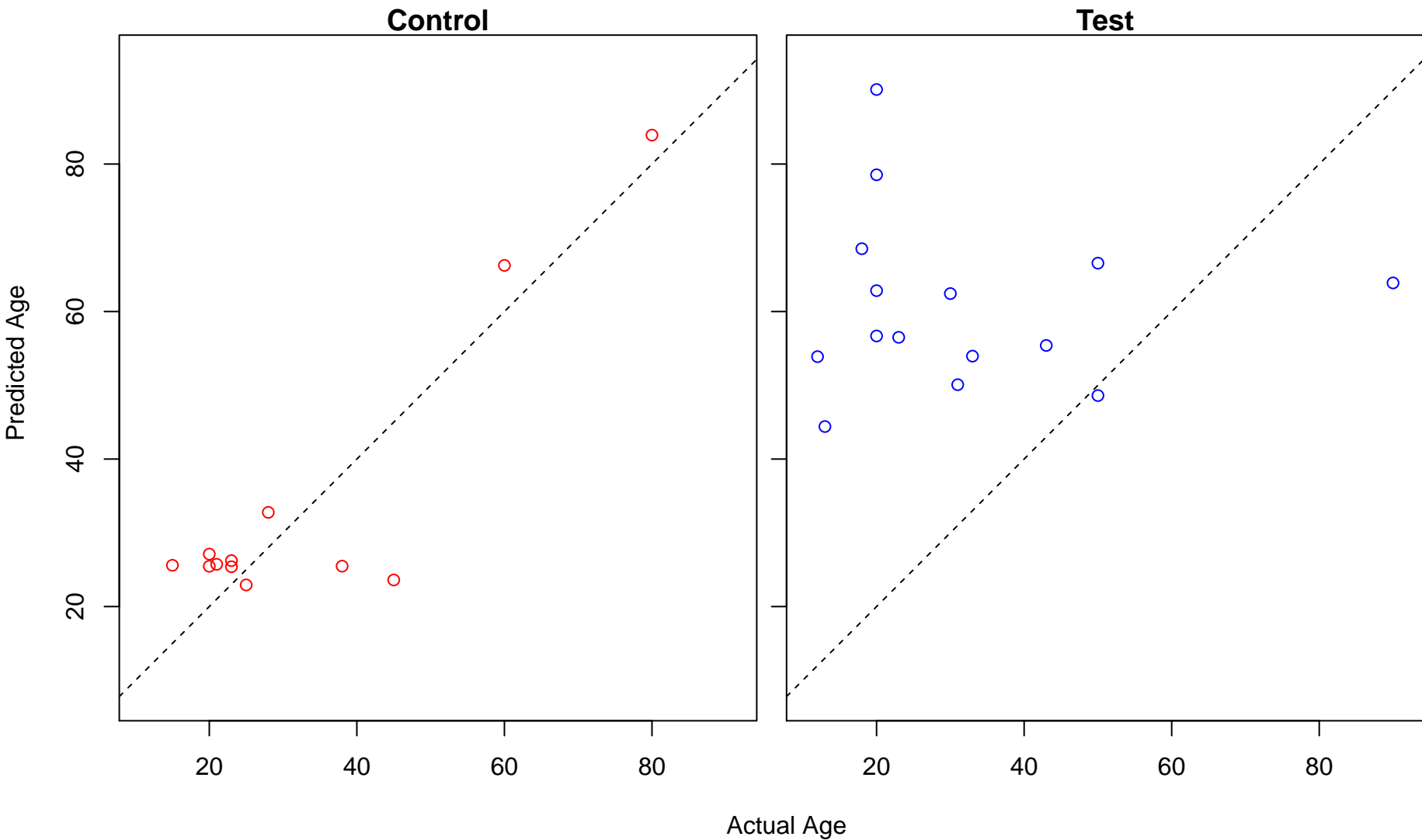


Test

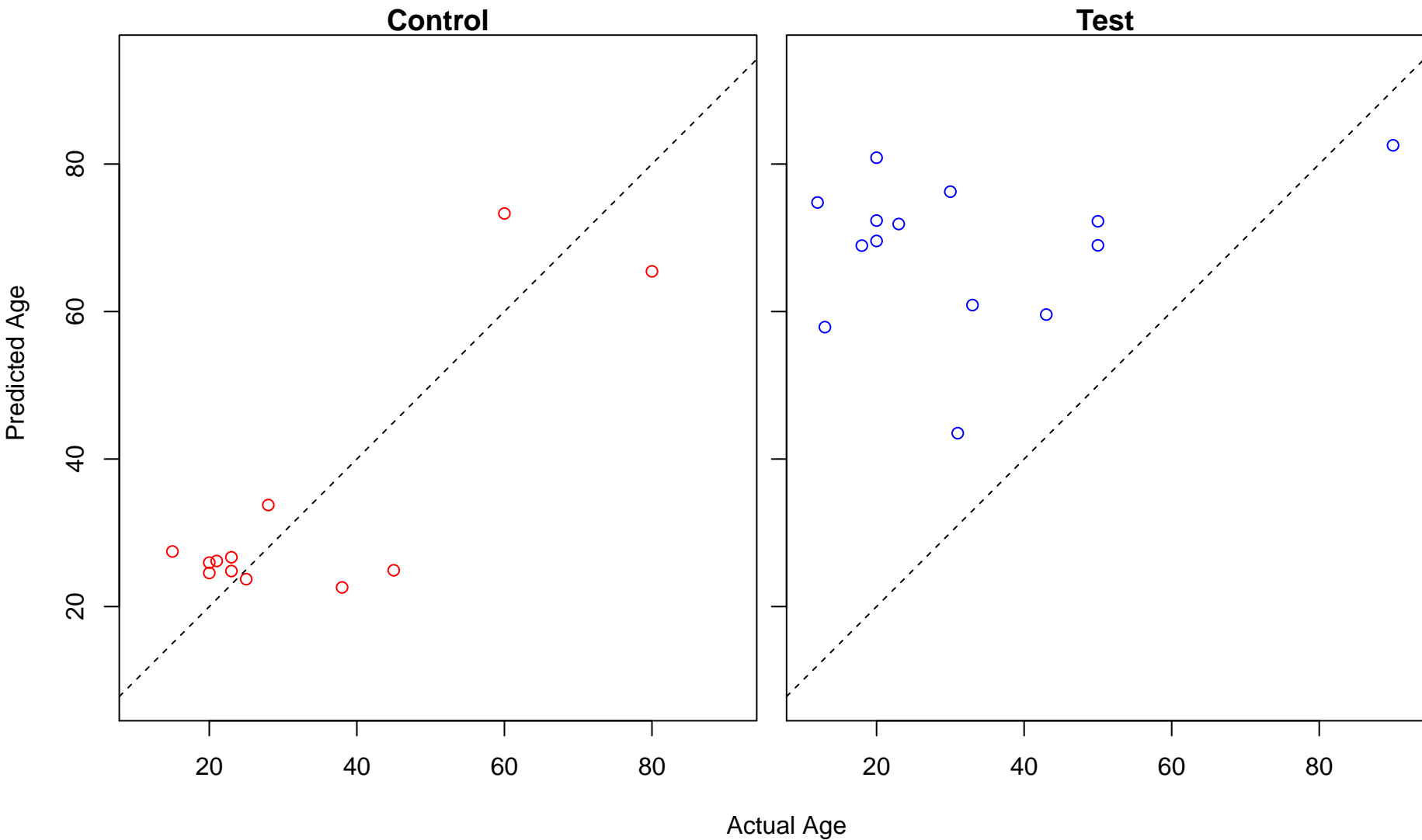


Actual Age

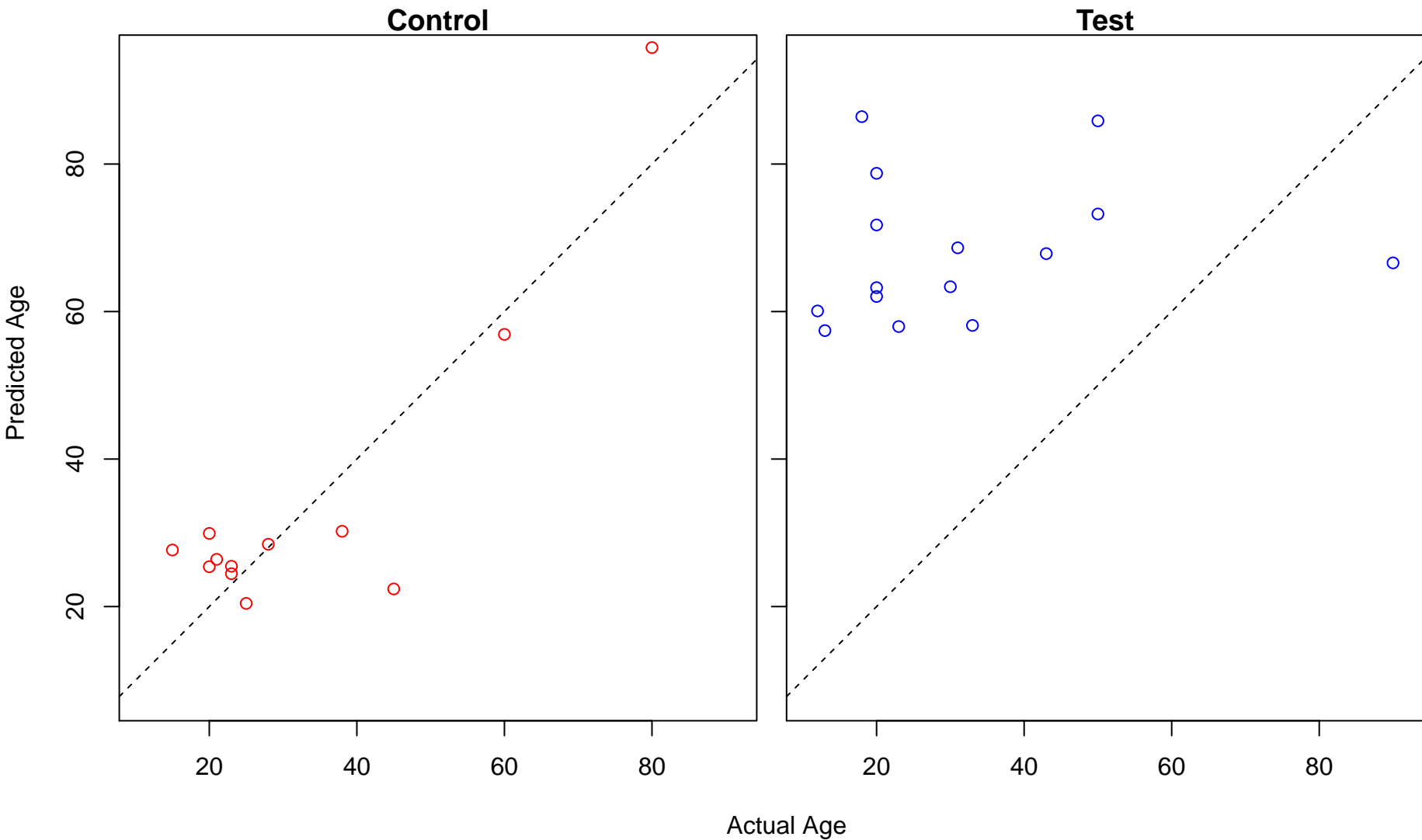
GPI anchor metabolic process (Score: 6.309826)



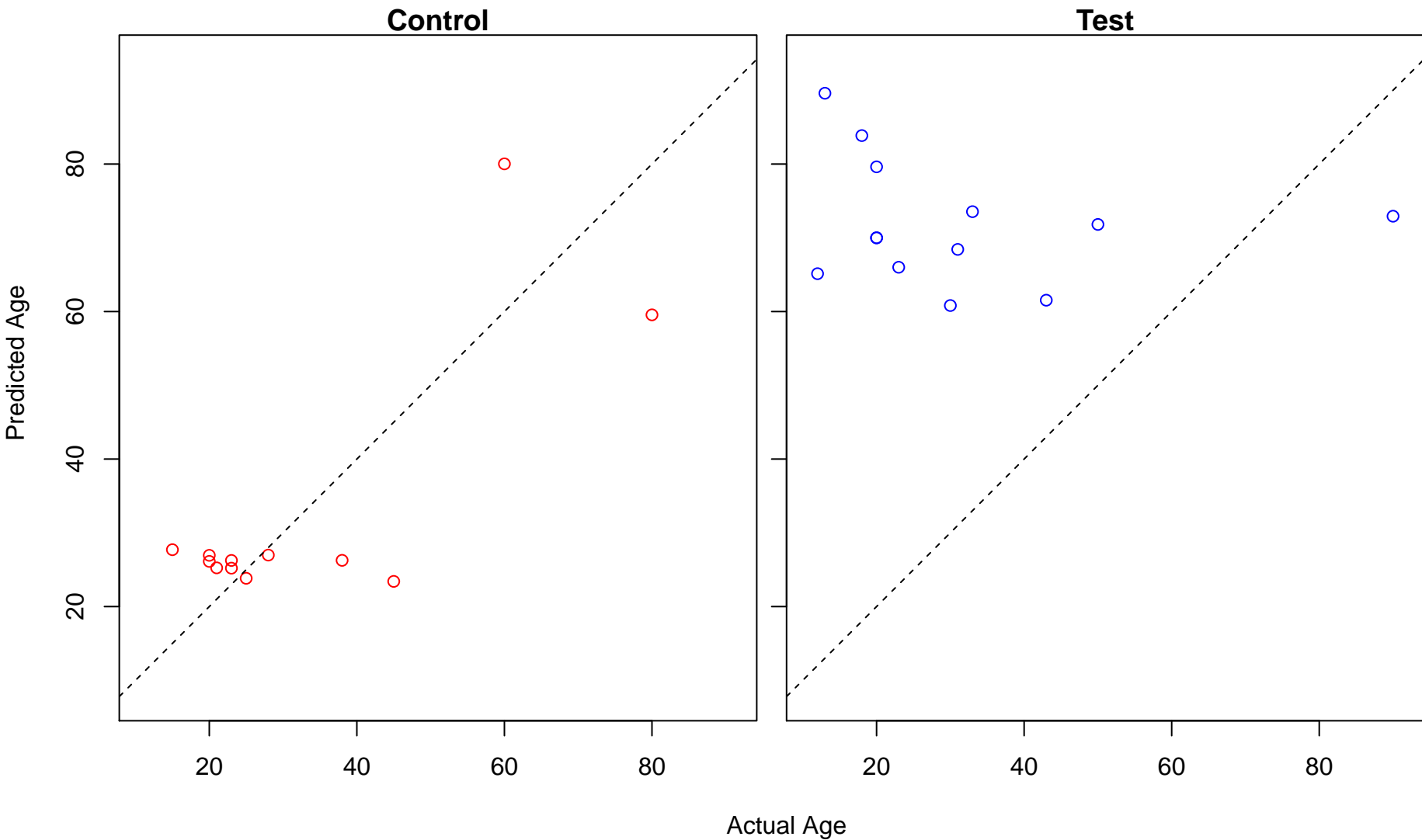
transcription from RNA polymerase I promoter (Score: 6.307970)



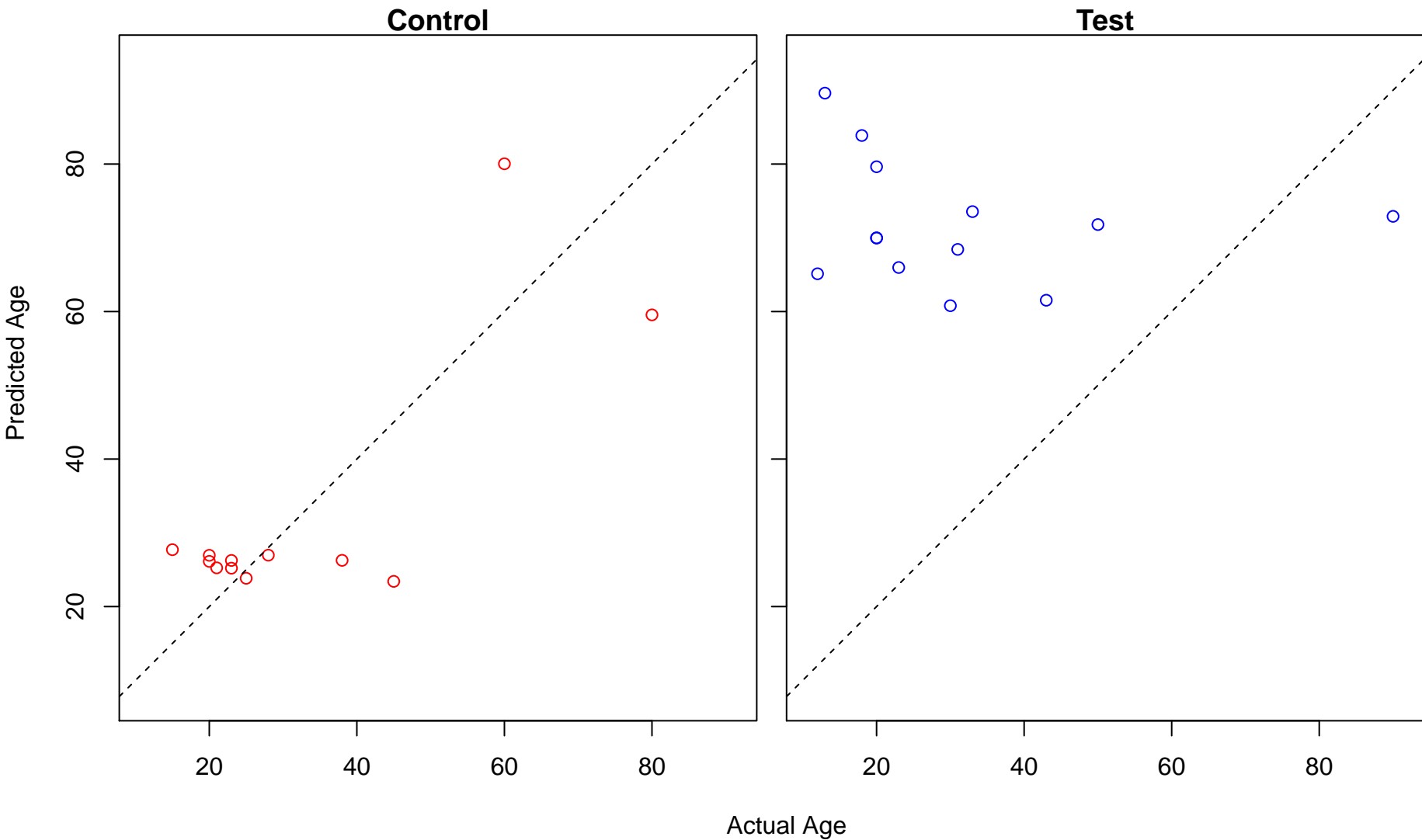
regulation of cell migration (Score: 6.307021)



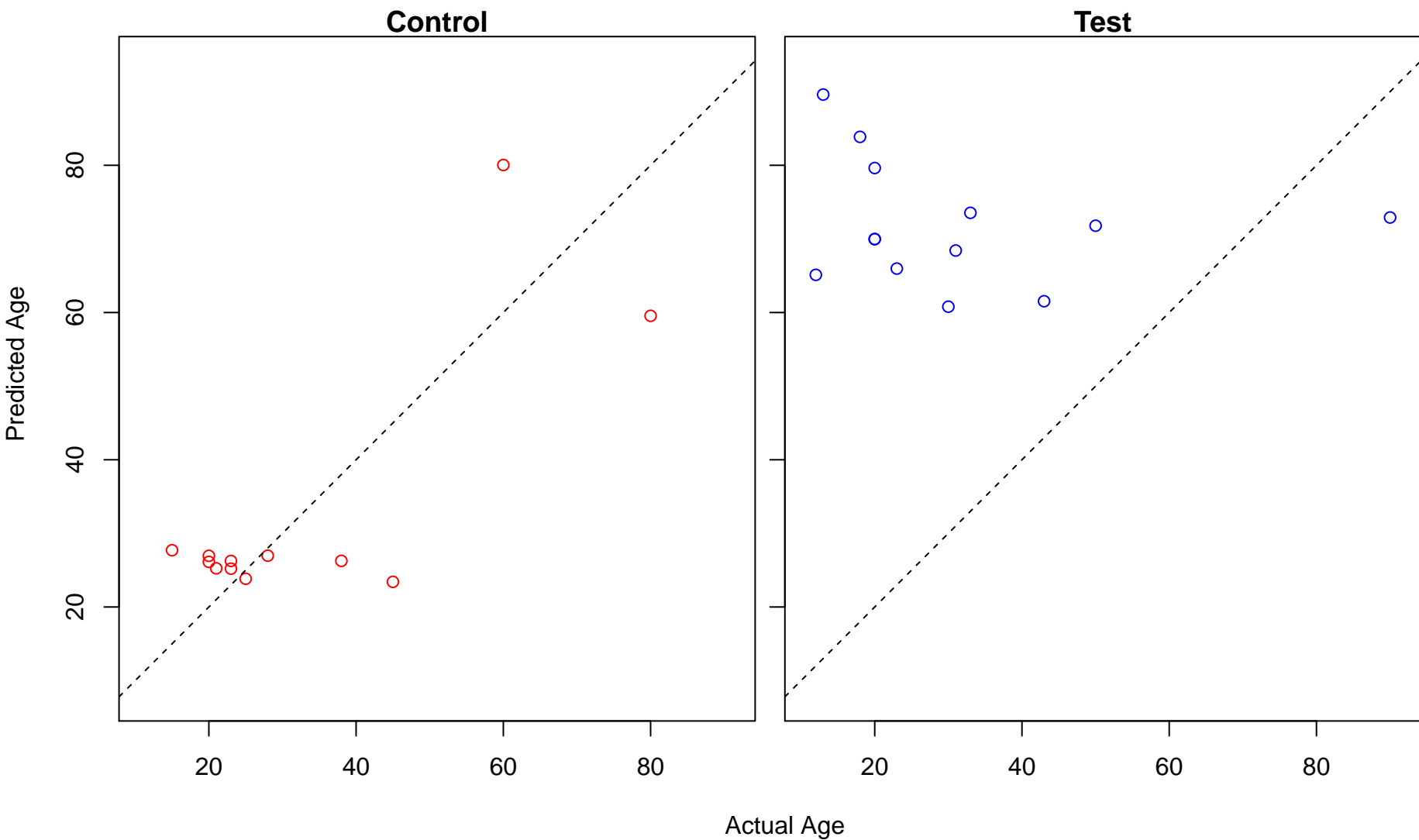
toll-like receptor 3 signaling pathway (Score: 6.306323)



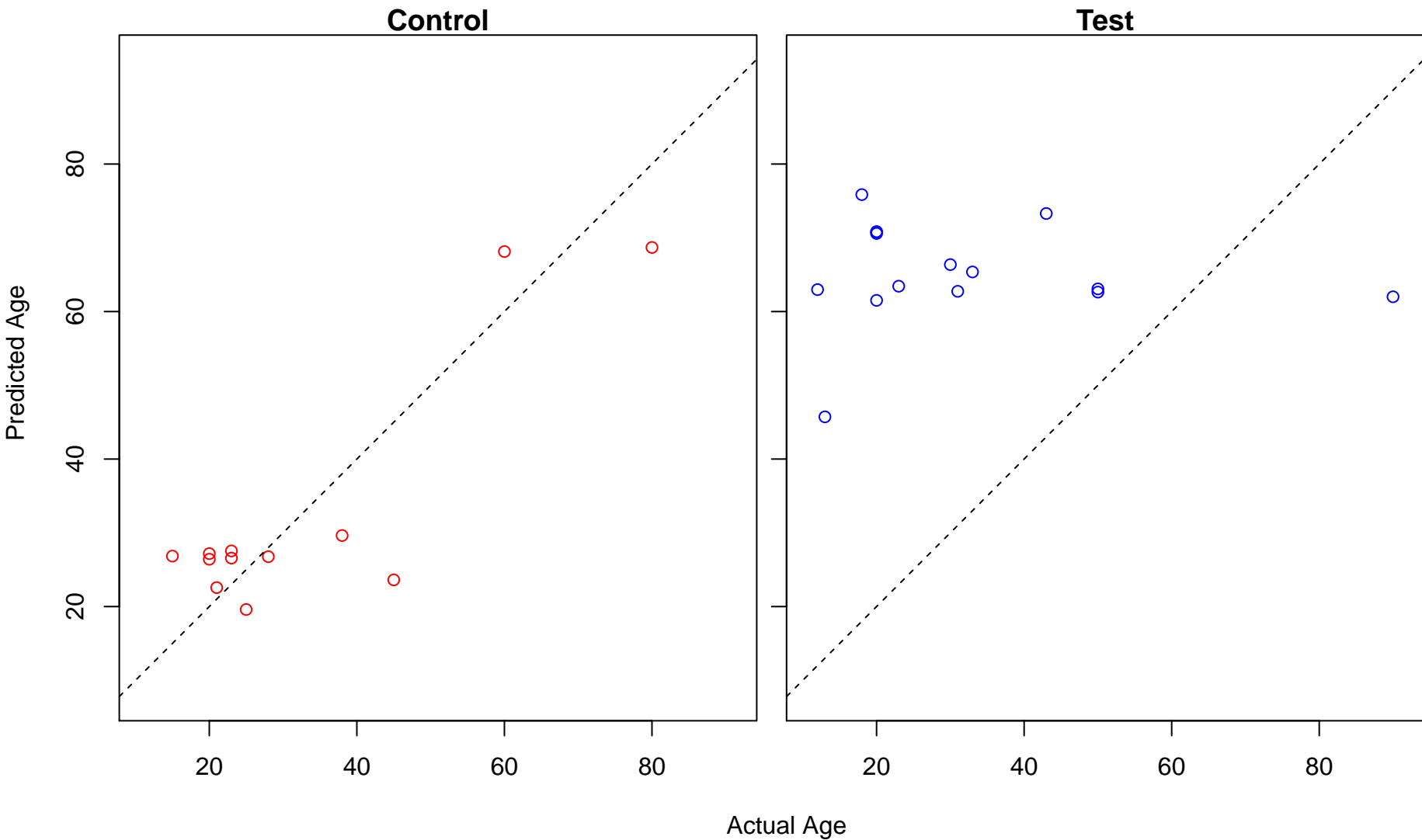
TRIF-dependent toll-like receptor signaling pathway (Score: 6.304504)



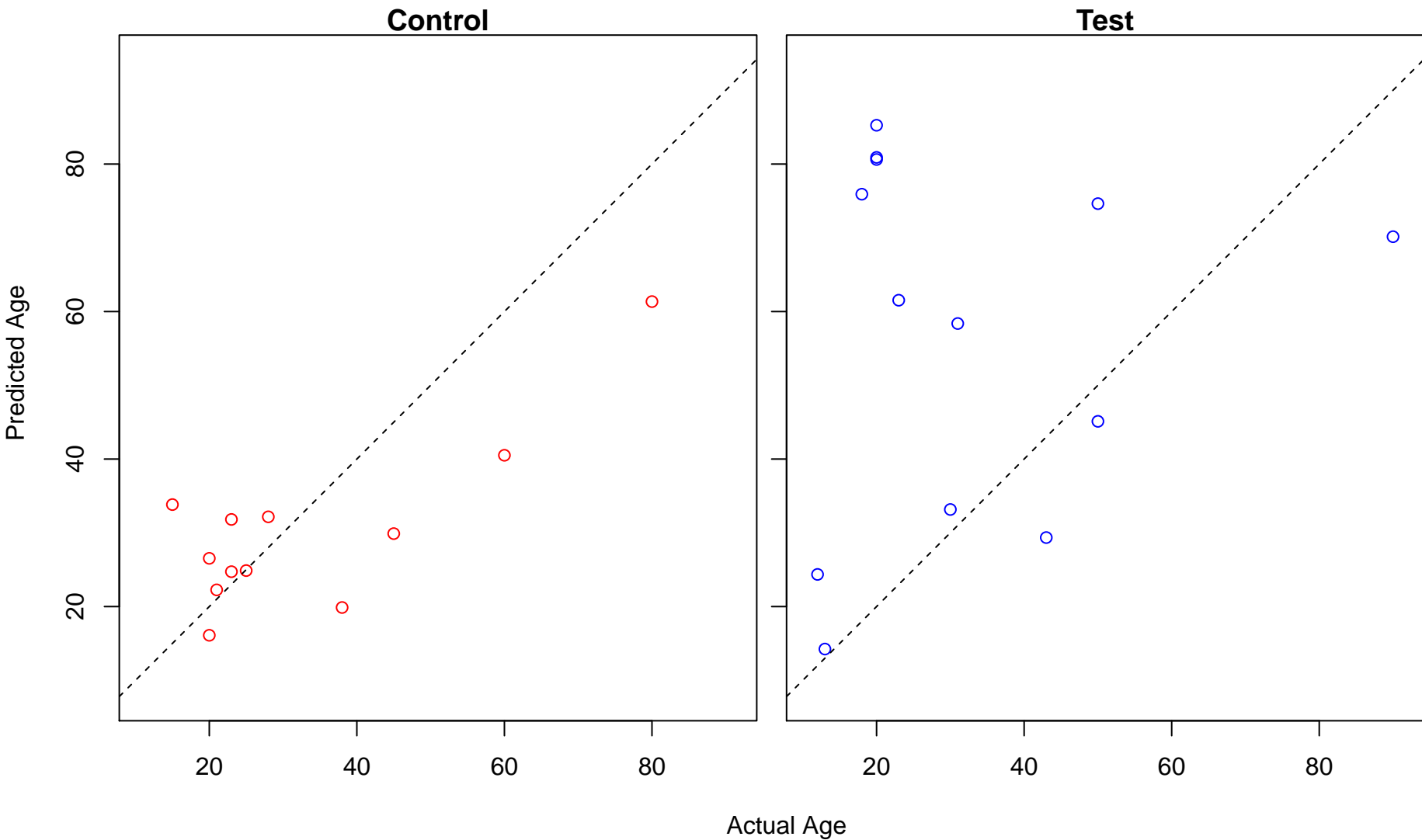
MyD88-independent toll-like receptor signaling pathway (Score: 6.302818)



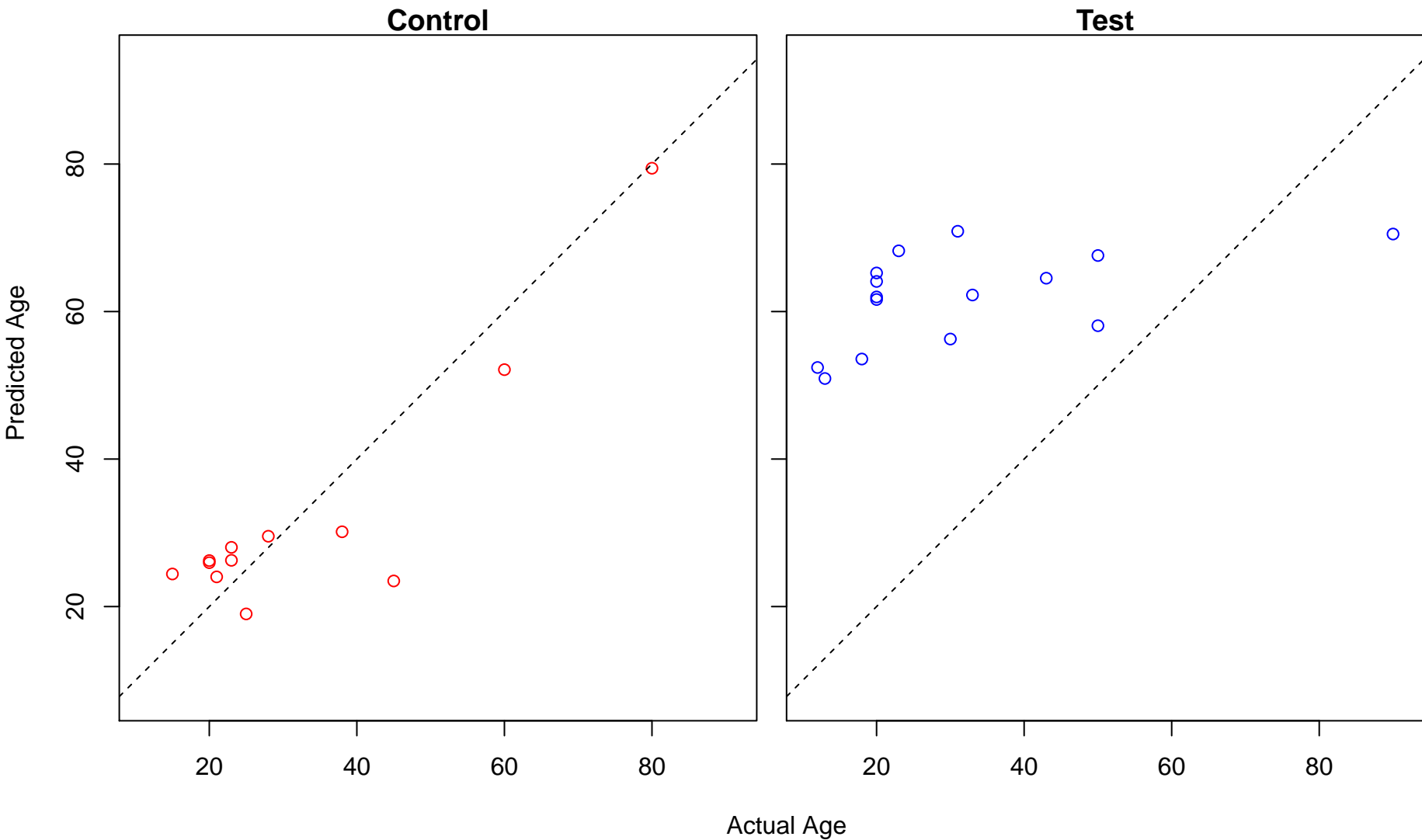
fatty acid transport (Score: 6.300898)



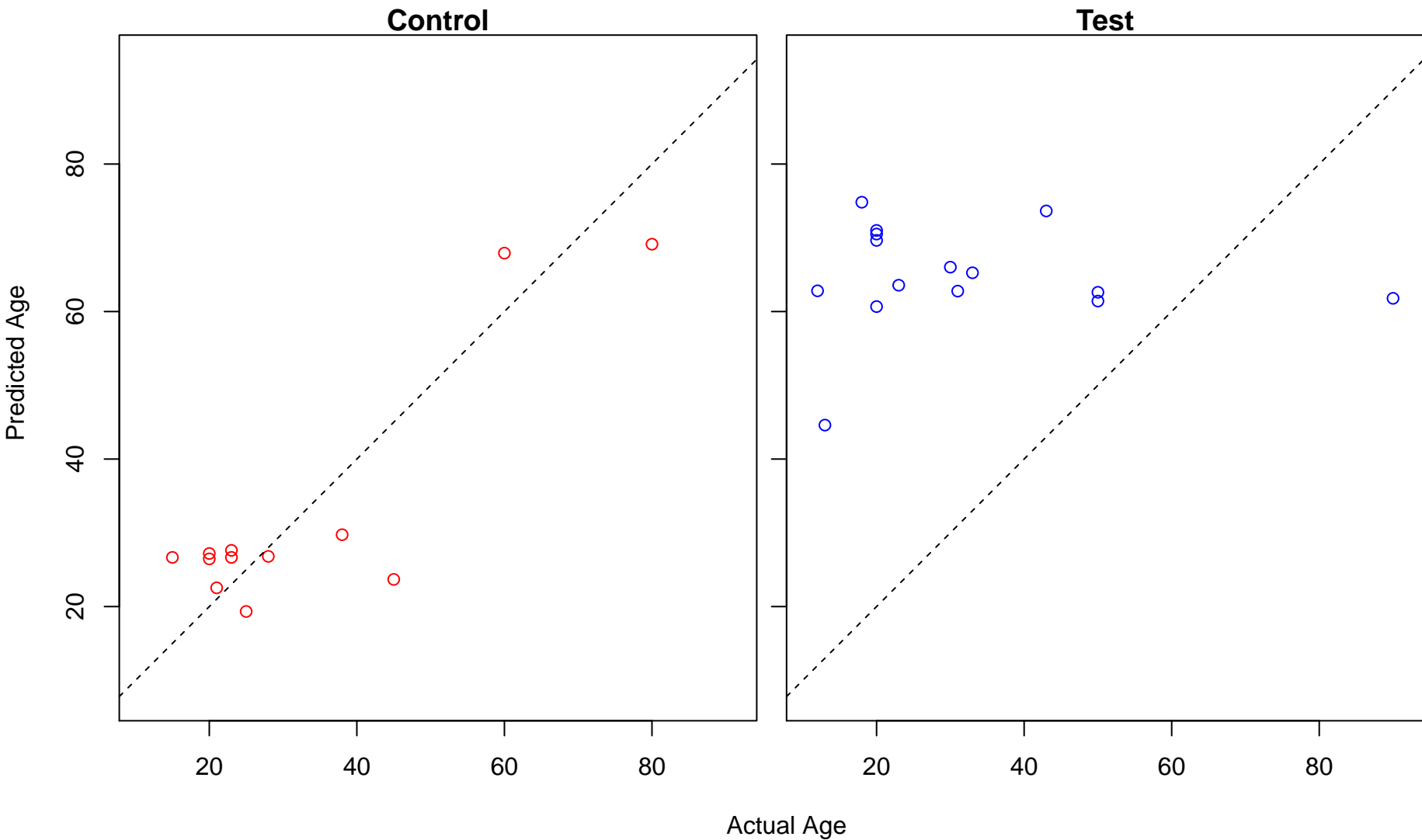
sensory perception of taste (Score: 6.299791)



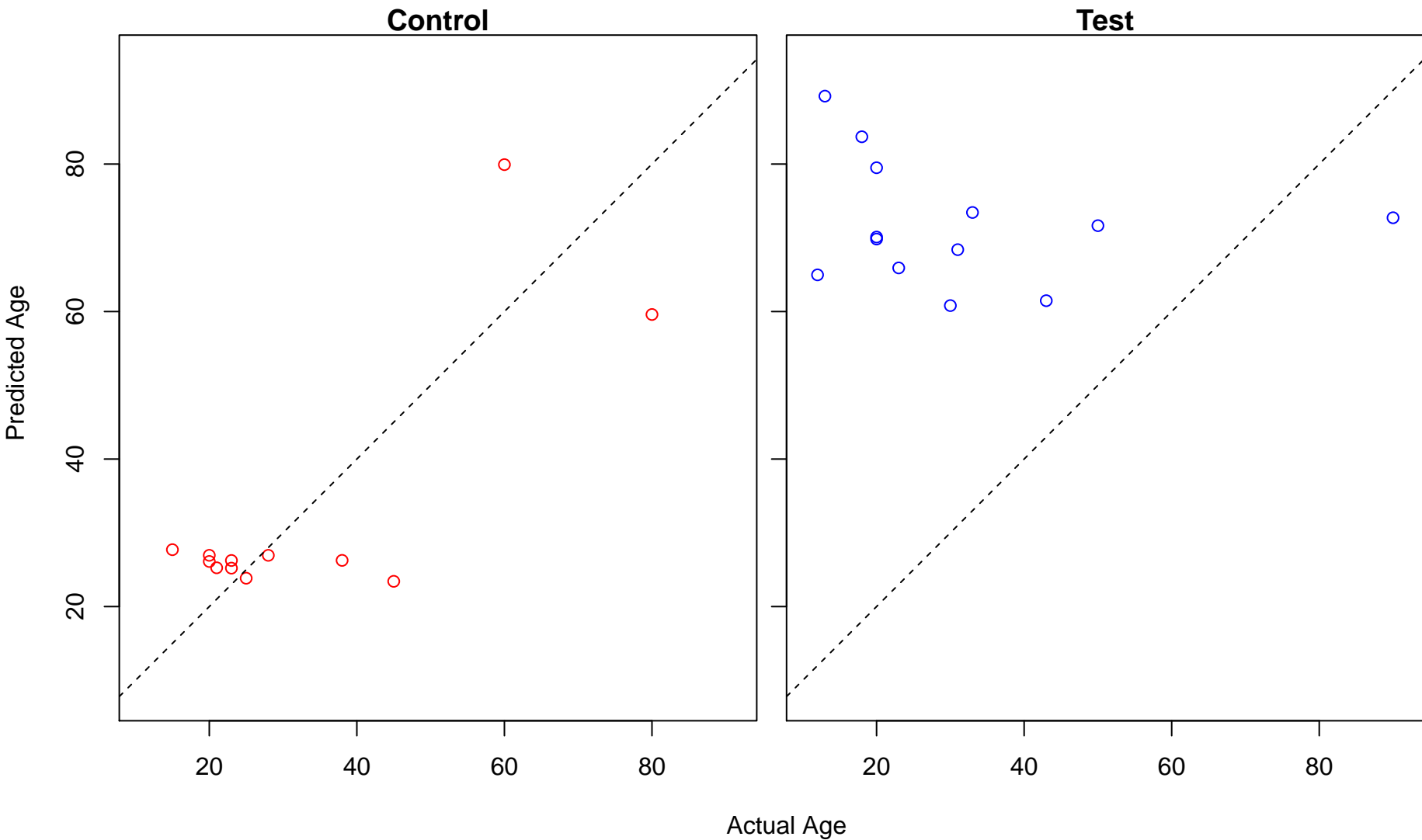
regulation of microtubule-based process (Score: 6.297509)



long-chain fatty acid transport (Score: 6.297231)

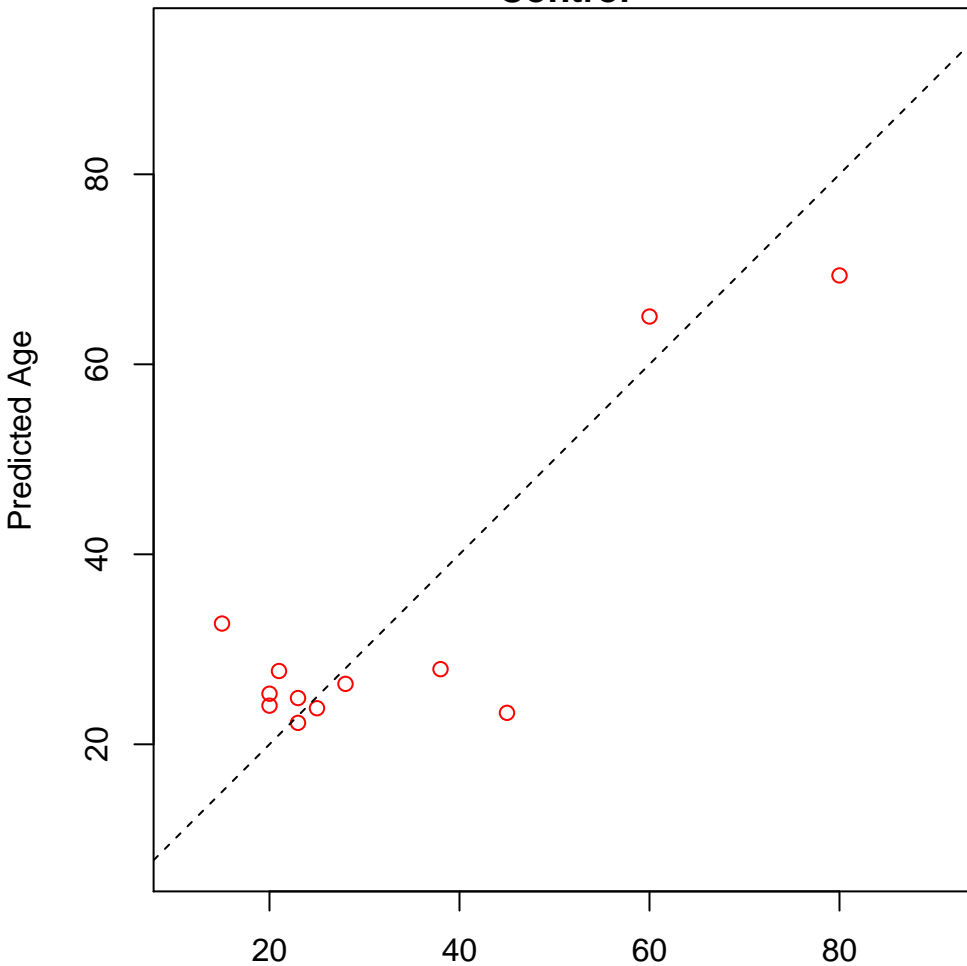


toll-like receptor 4 signaling pathway (Score: 6.290681)

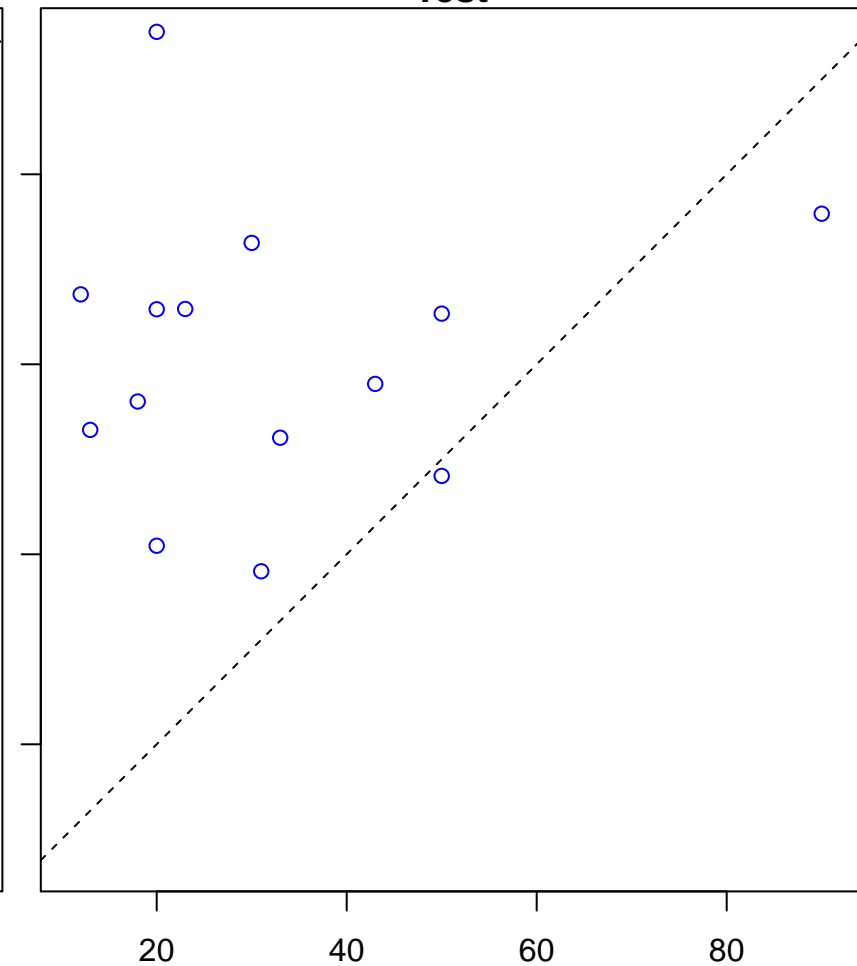


regulation of protein kinase A signaling (Score: 6.288333)

Control

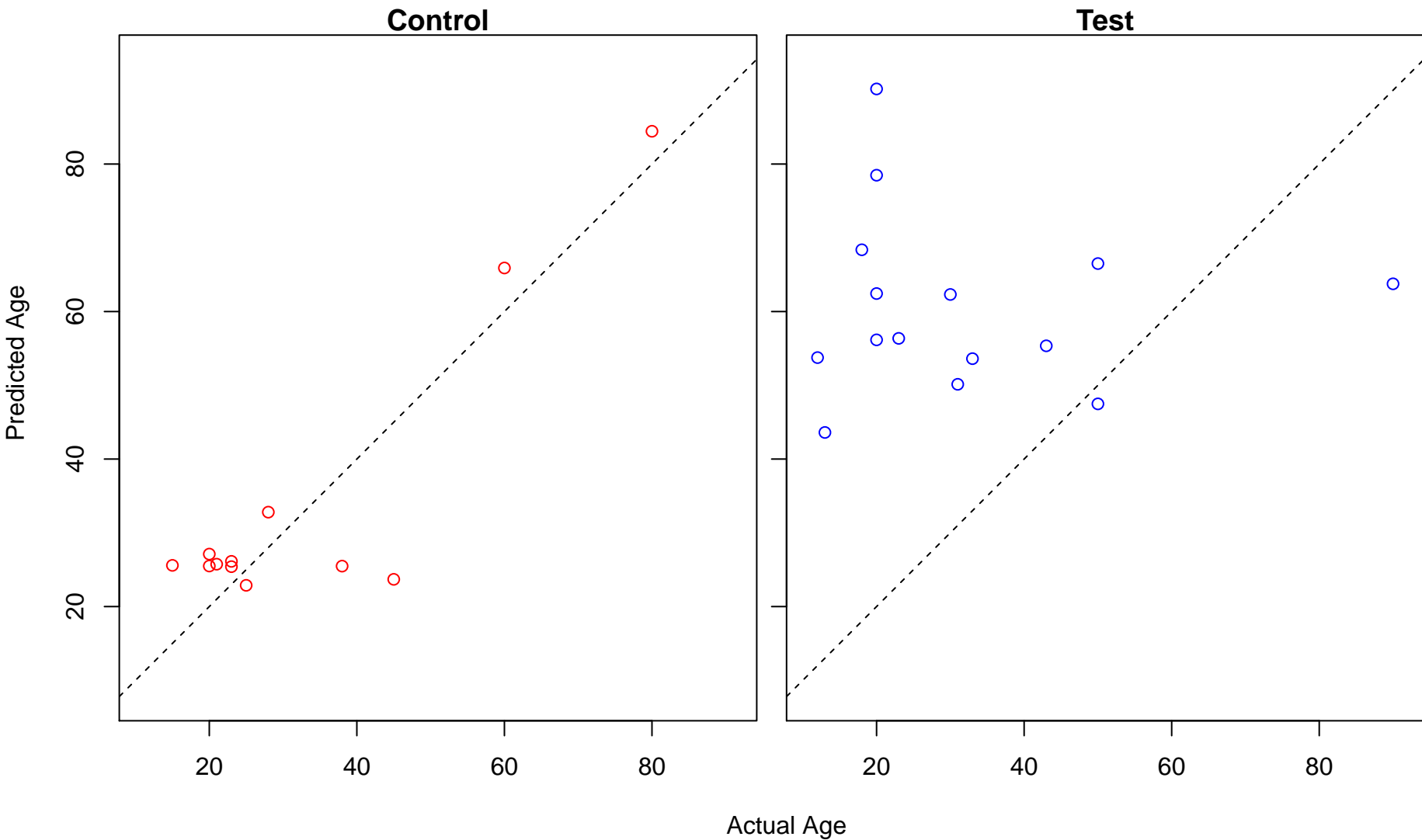


Test

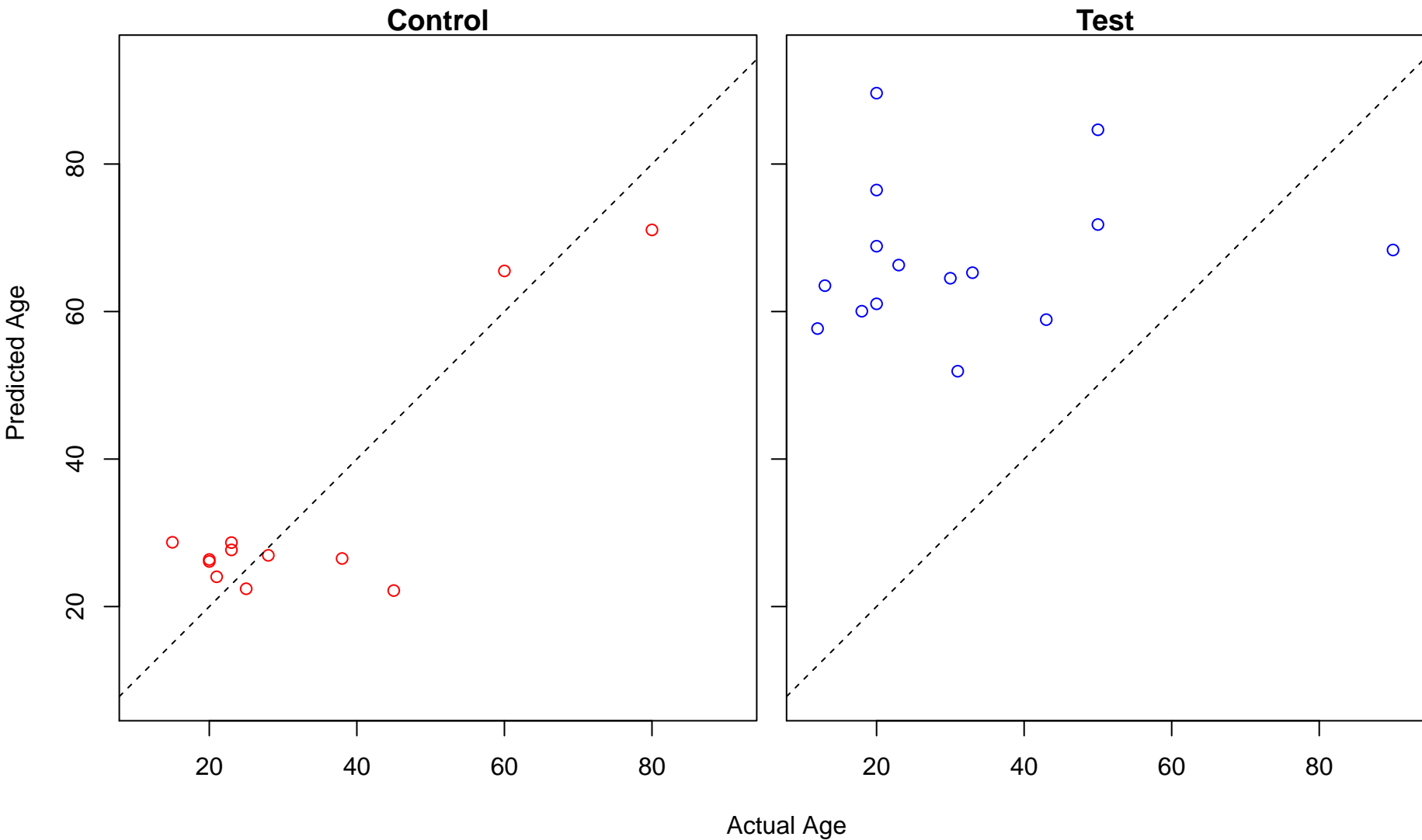


Actual Age

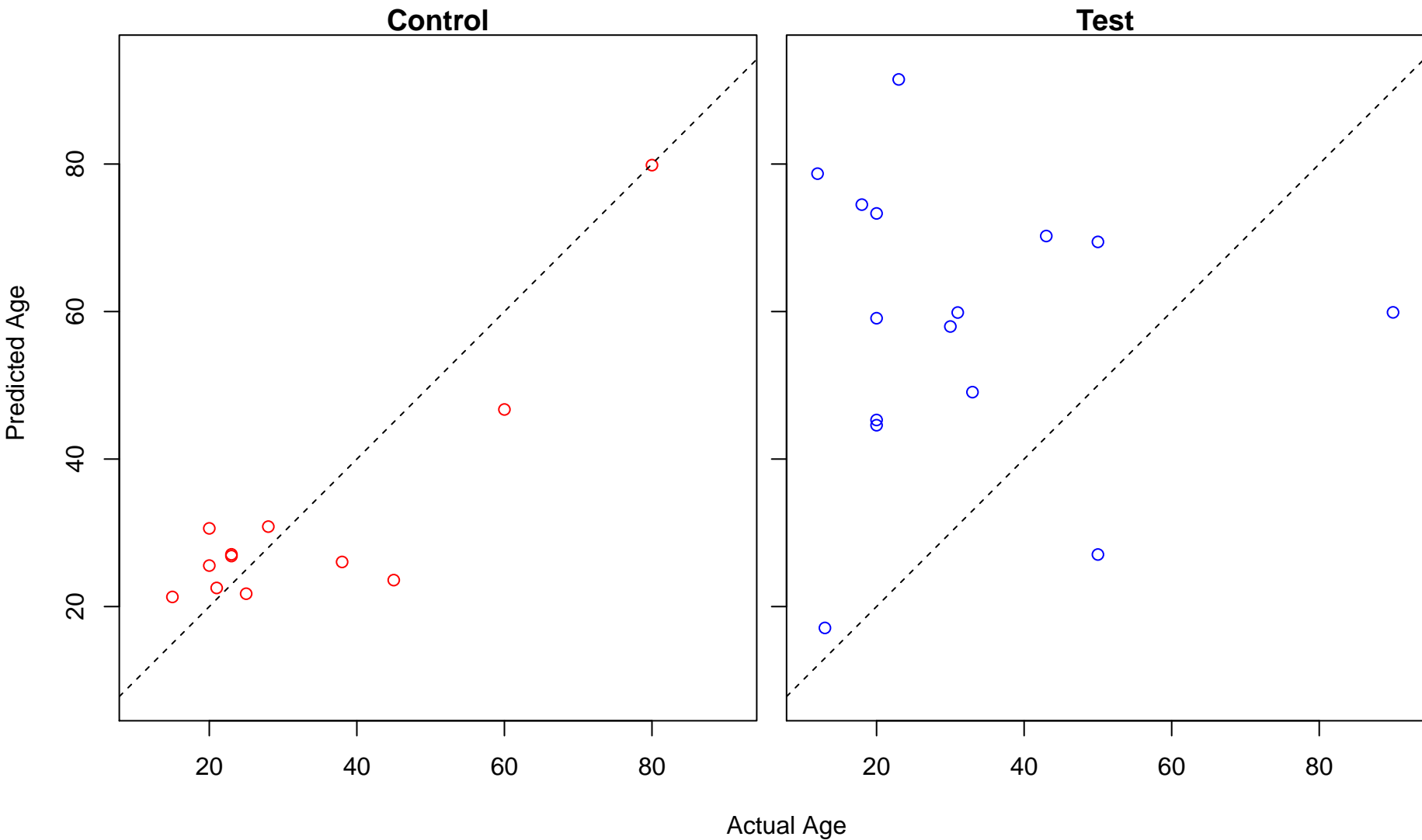
GPI anchor biosynthetic process (Score: 6.285793)



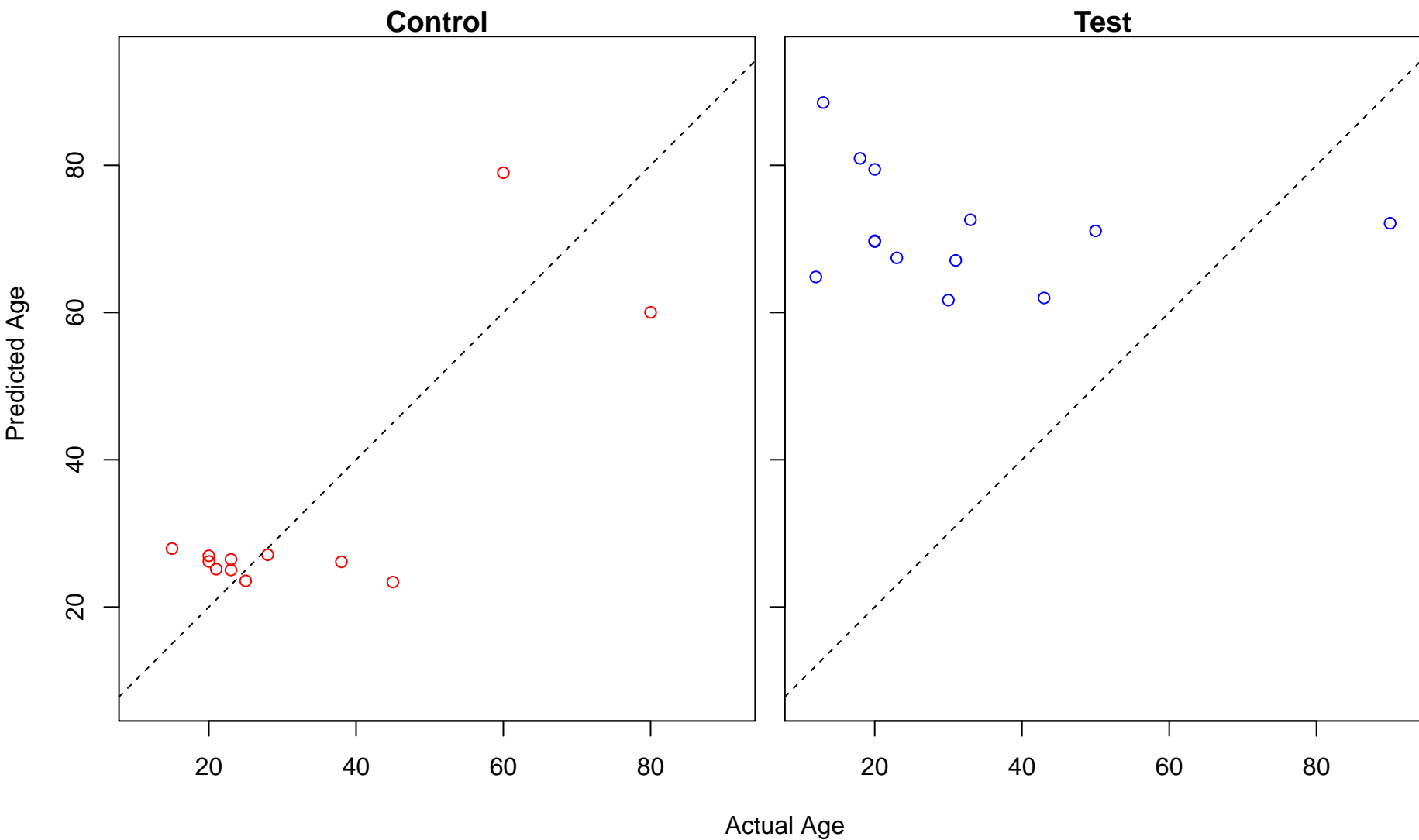
positive regulation of myeloid cell differentiation (Score: 6.285278)



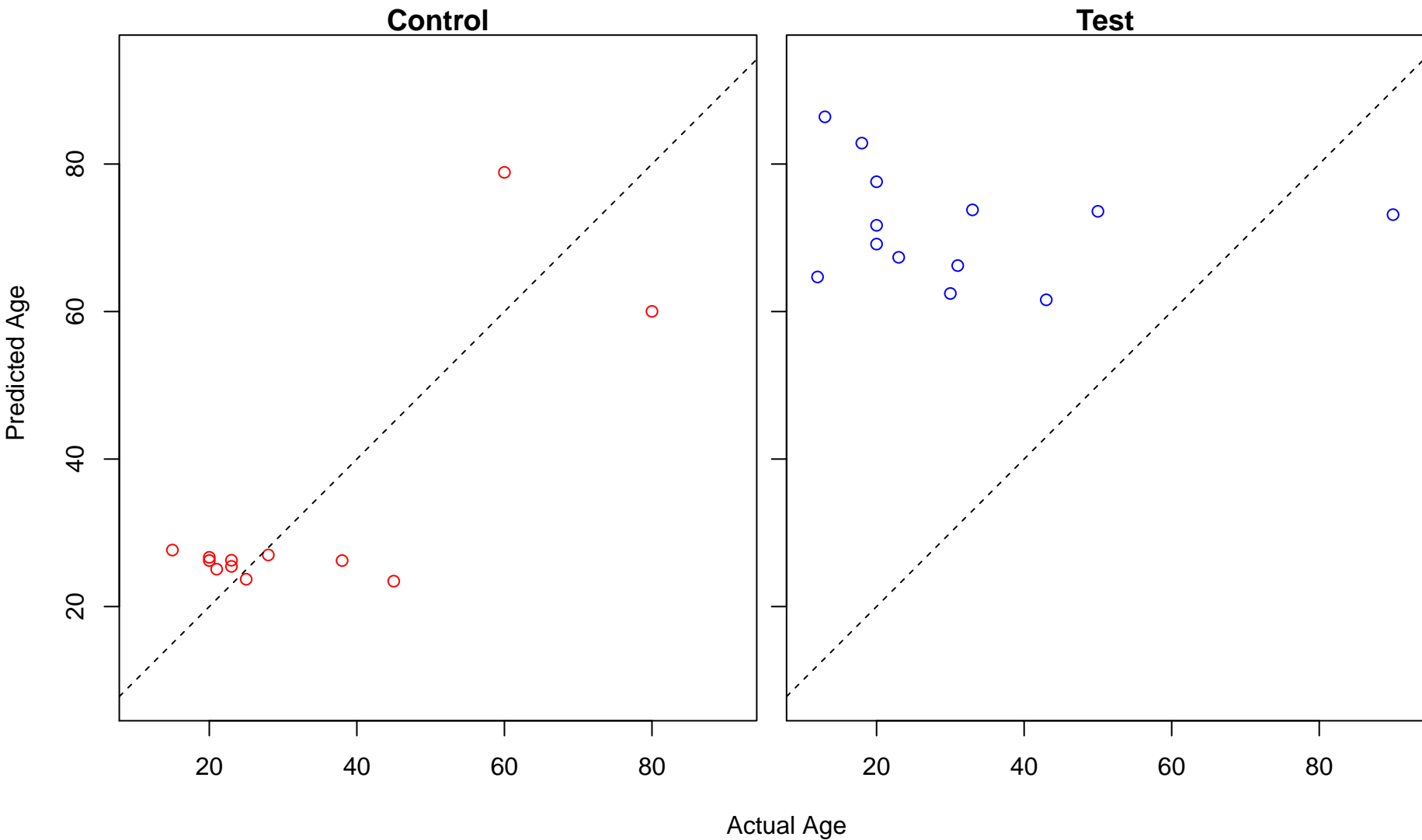
regulation of synaptic transmission, glutamatergic (Score: 6.279268)



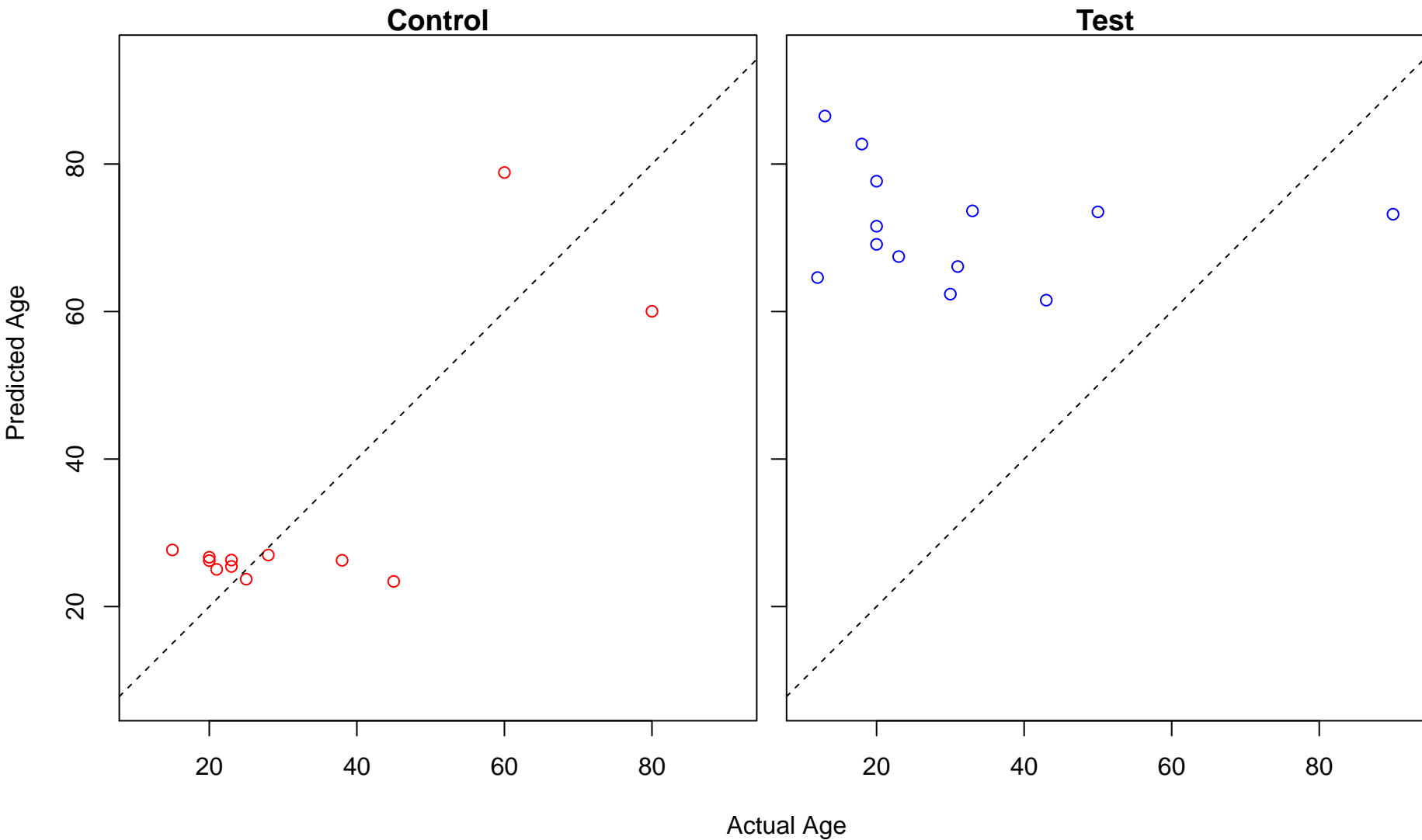
global genome nucleotide–excision repair (Score: 6.278337)



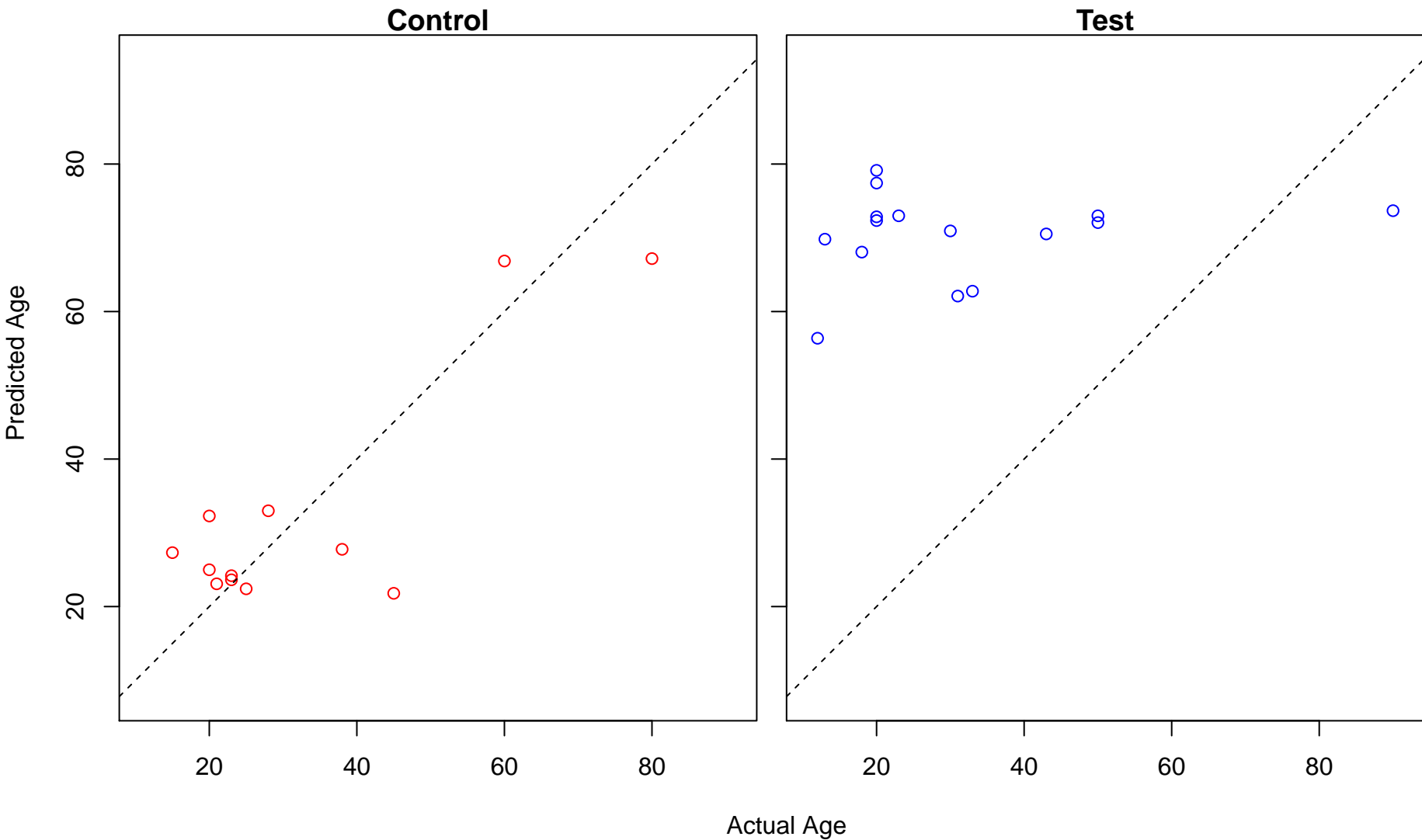
negative regulation of mitotic cell cycle phase transition (Score: 6.277297)



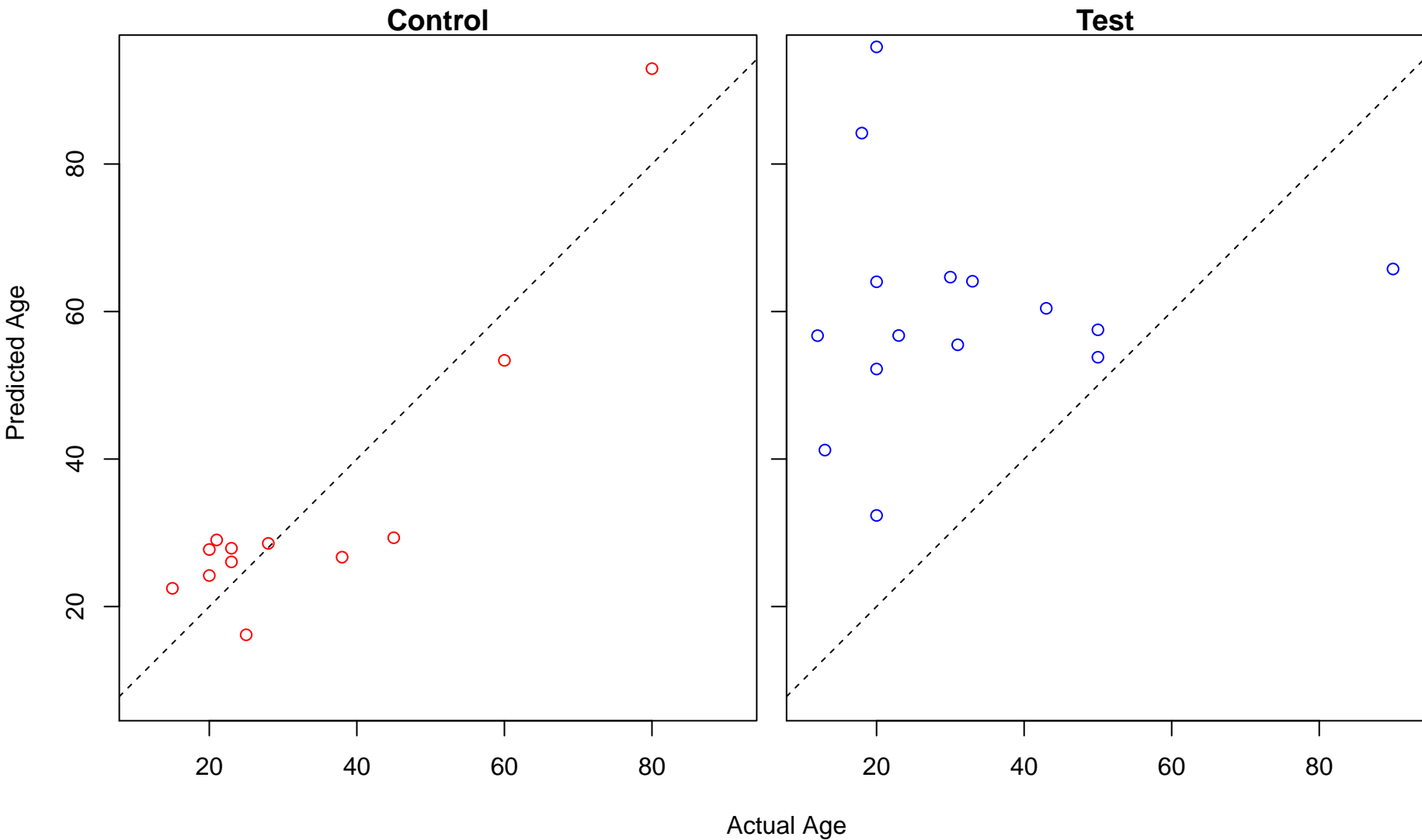
mitotic cell cycle checkpoint (Score: 6.273803)



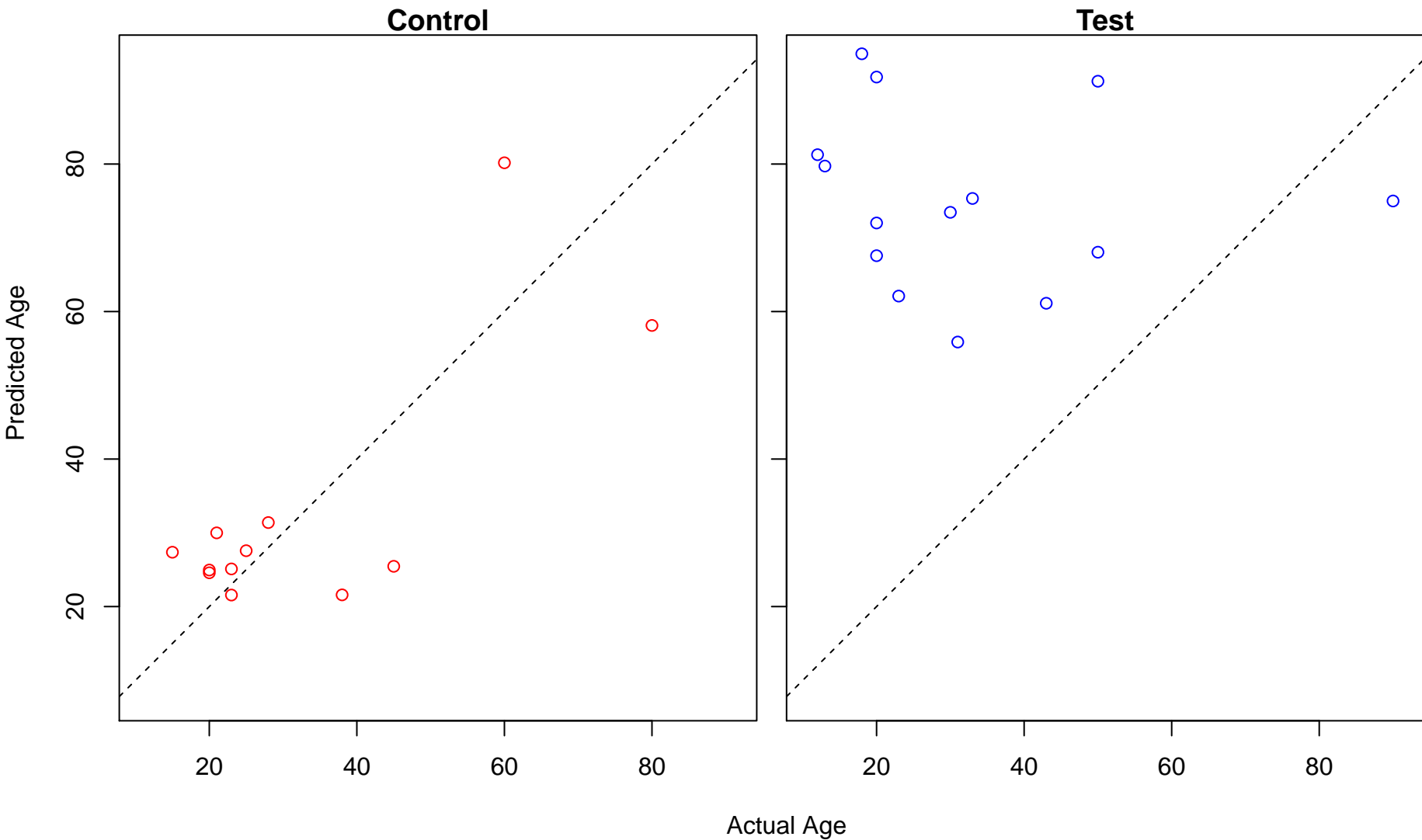
cell adhesion (Score: 6.273426)



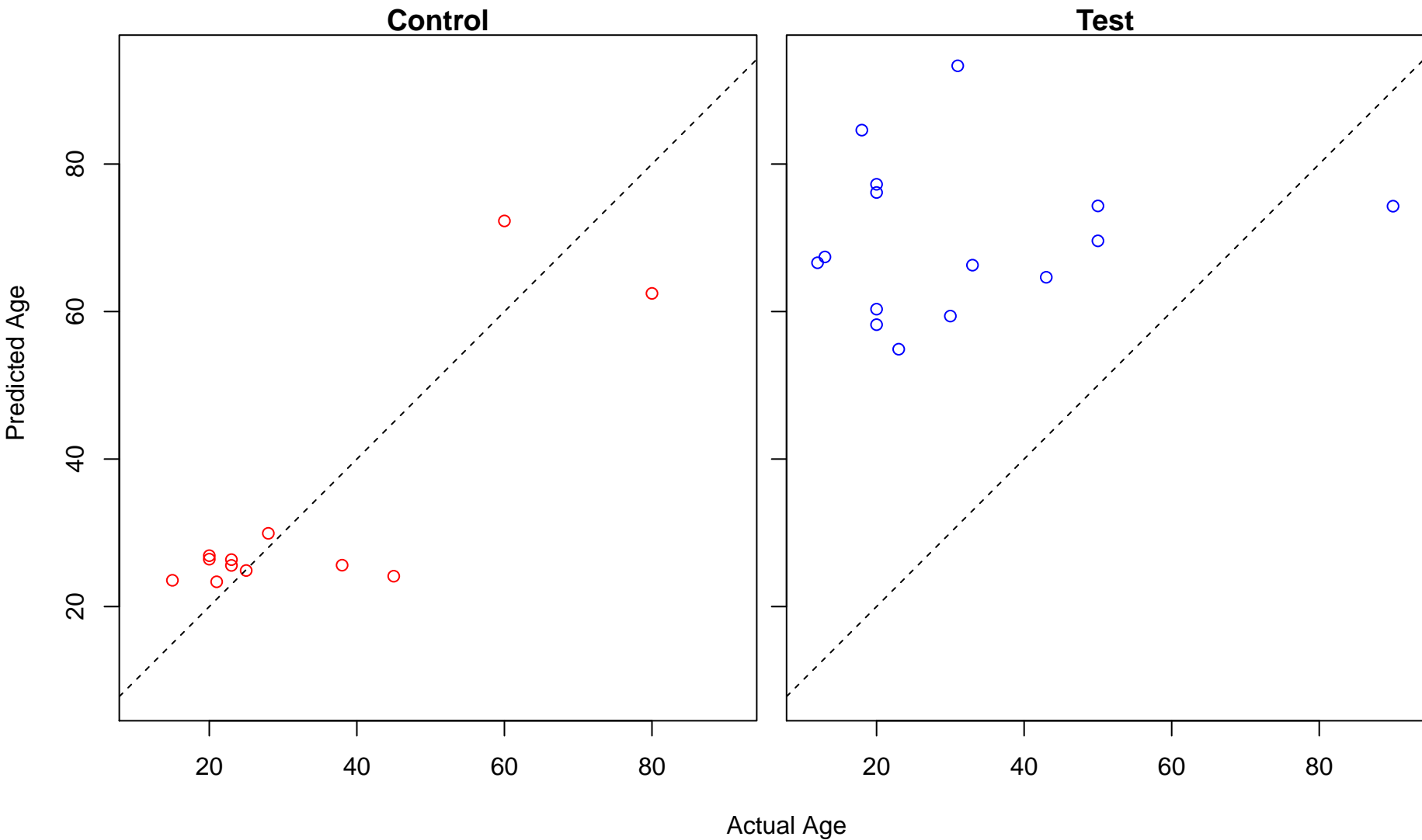
neuron cellular homeostasis (Score: 6.26951)



regulation of exit from mitosis (Score: 6.268696)

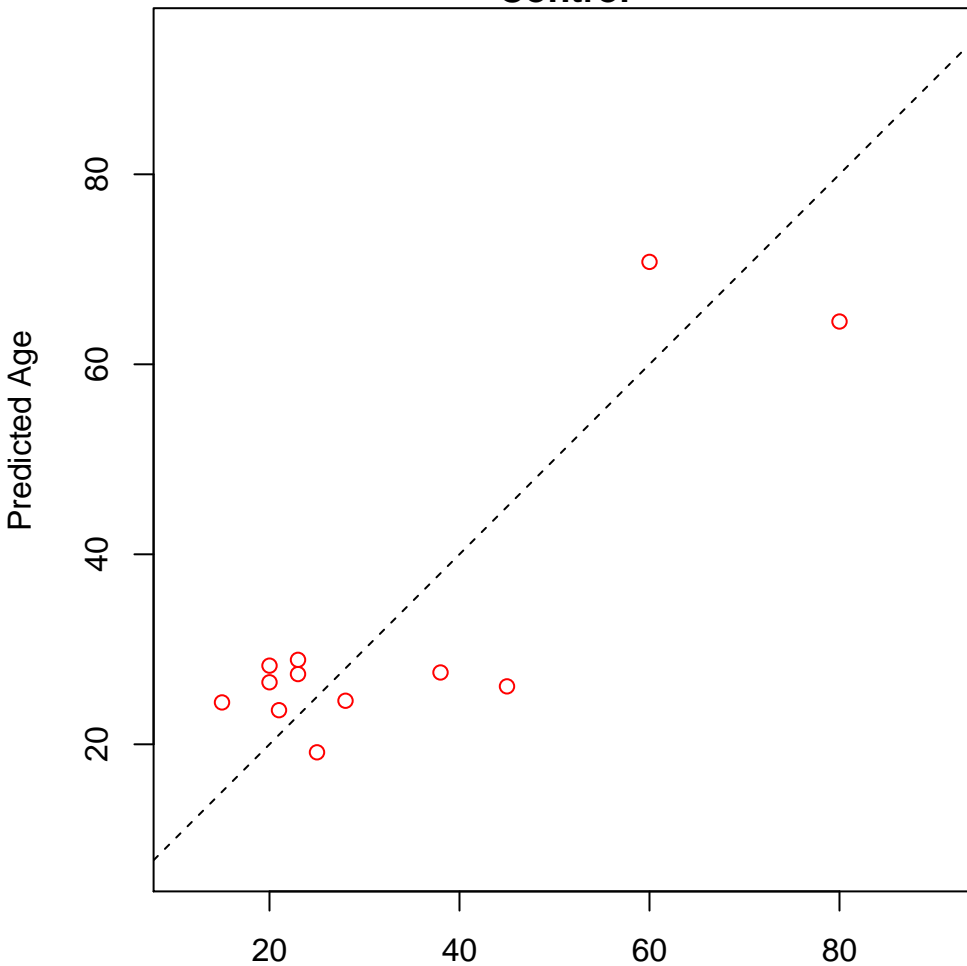


dephosphorylation (Score: 6.265742)

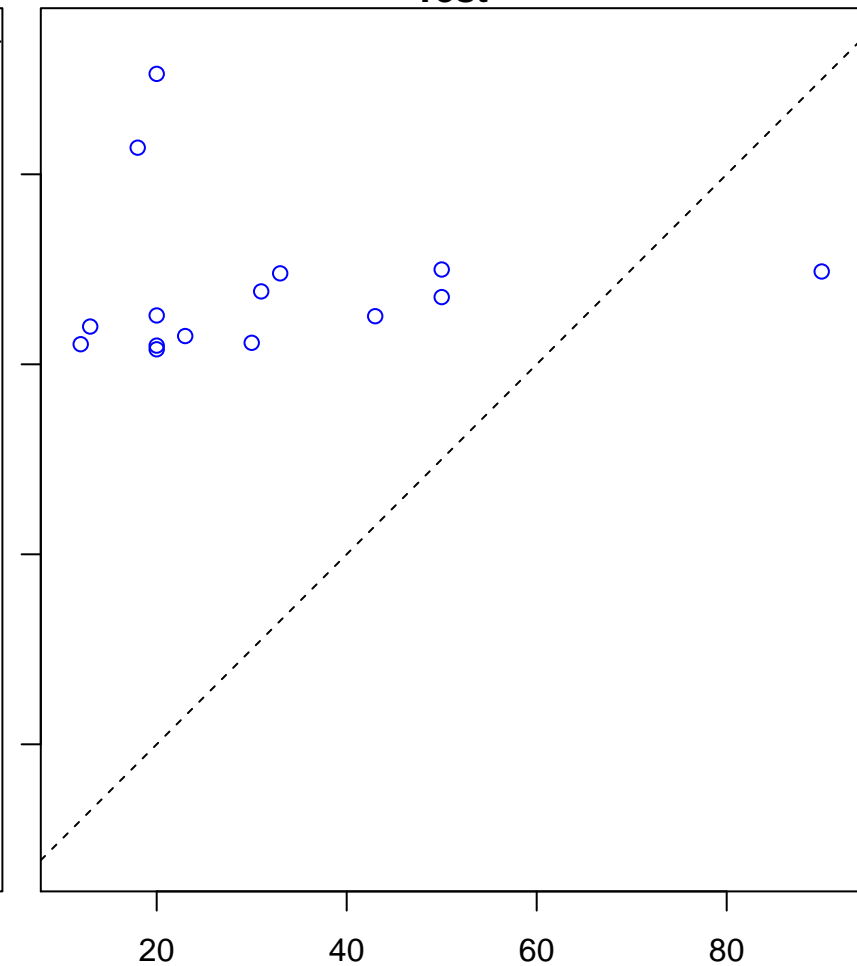


regulation of neurotransmitter secretion (Score: 6.264553)

Control

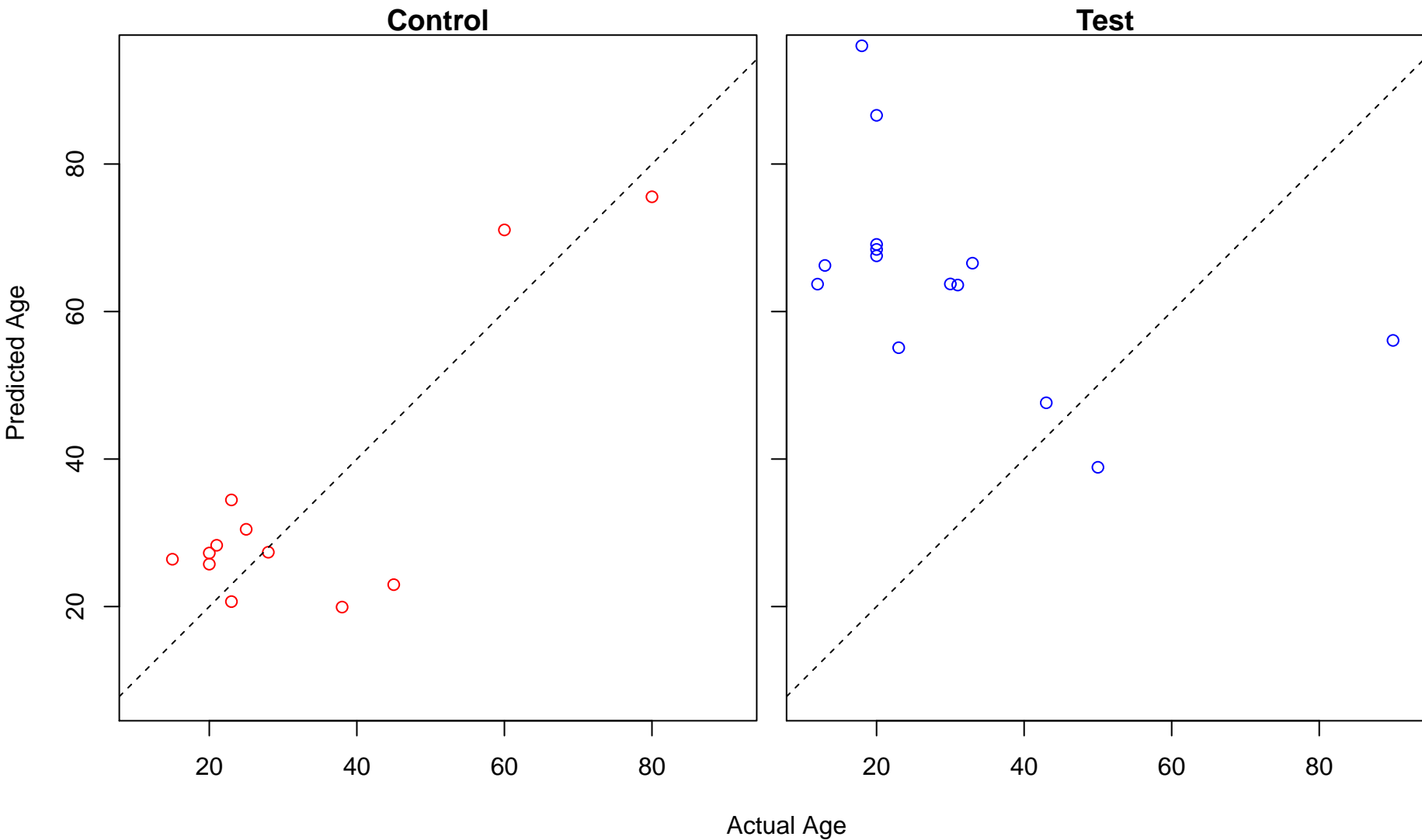


Test

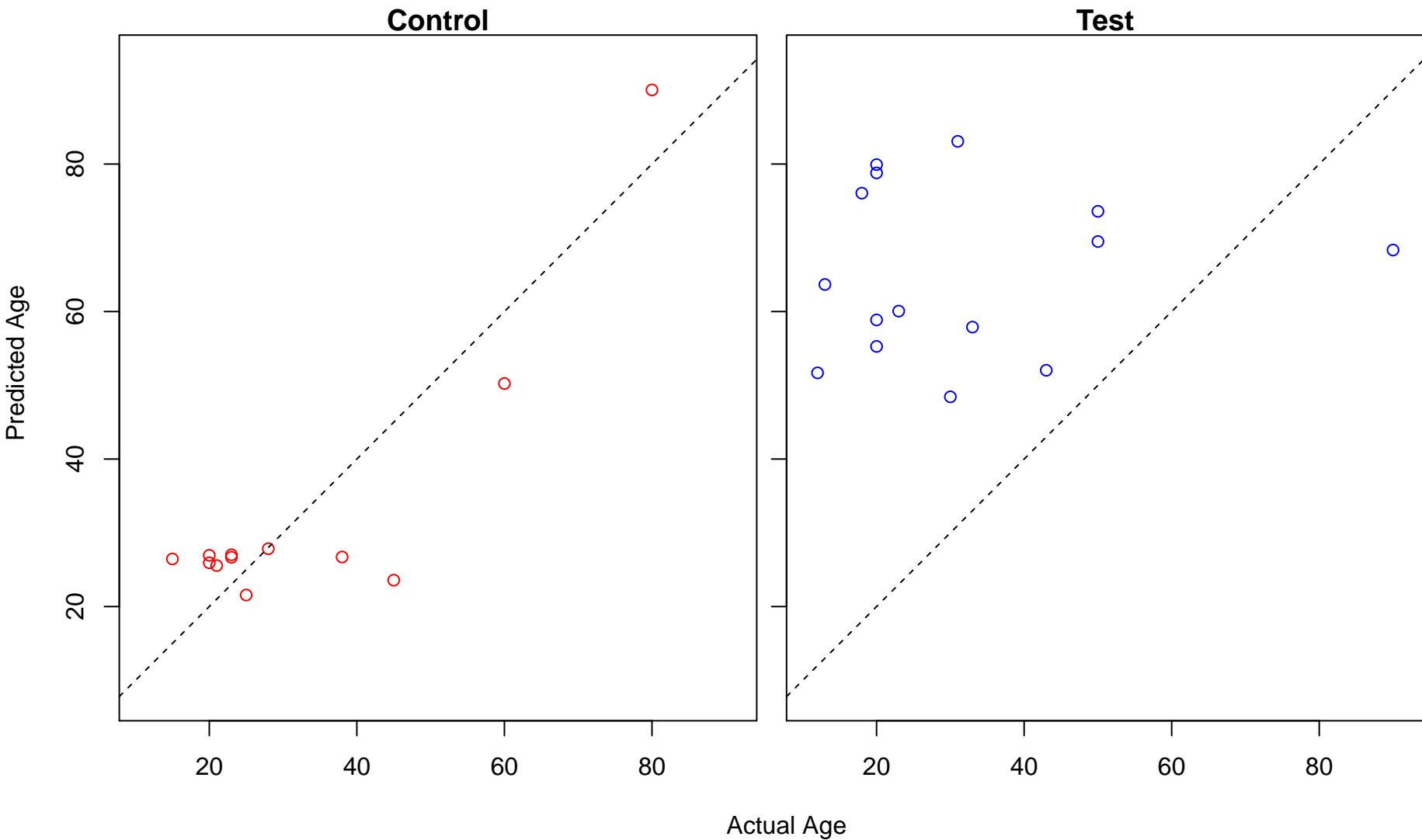


Actual Age

mitotic cell cycle arrest (Score: 6.264069)

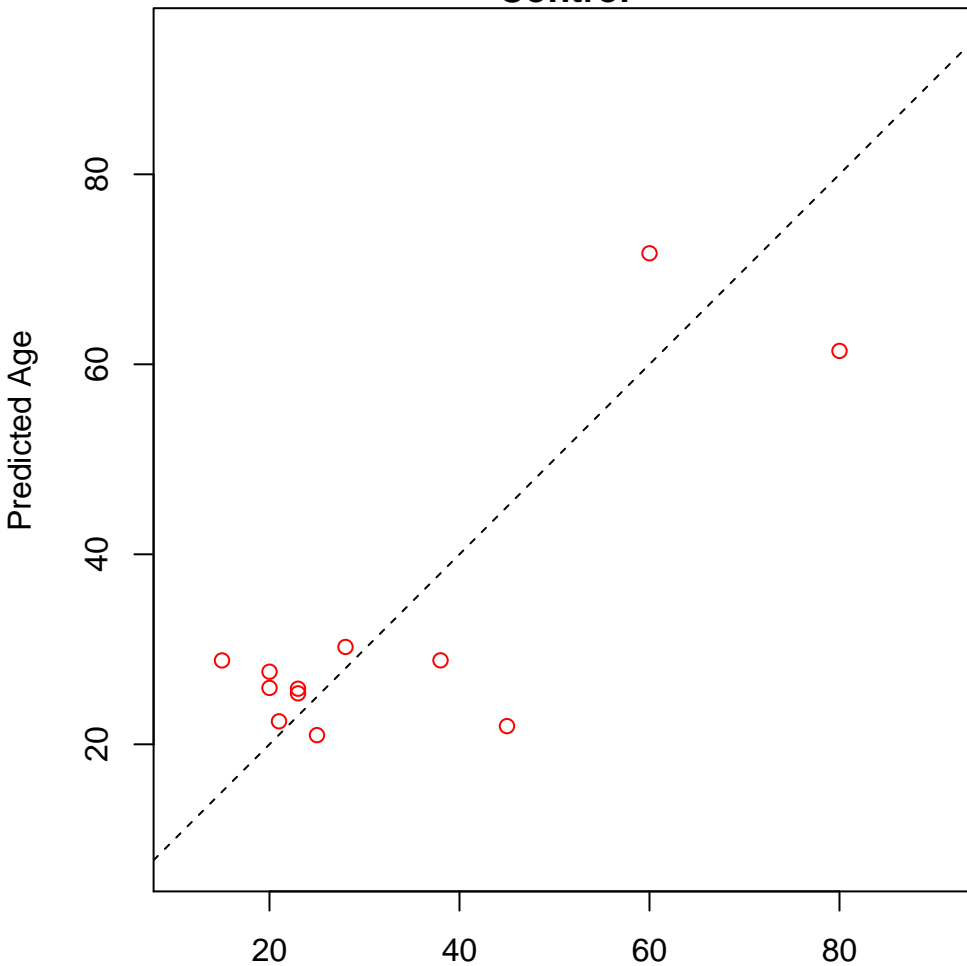


cellular macromolecular complex assembly (Score: 6.259082)

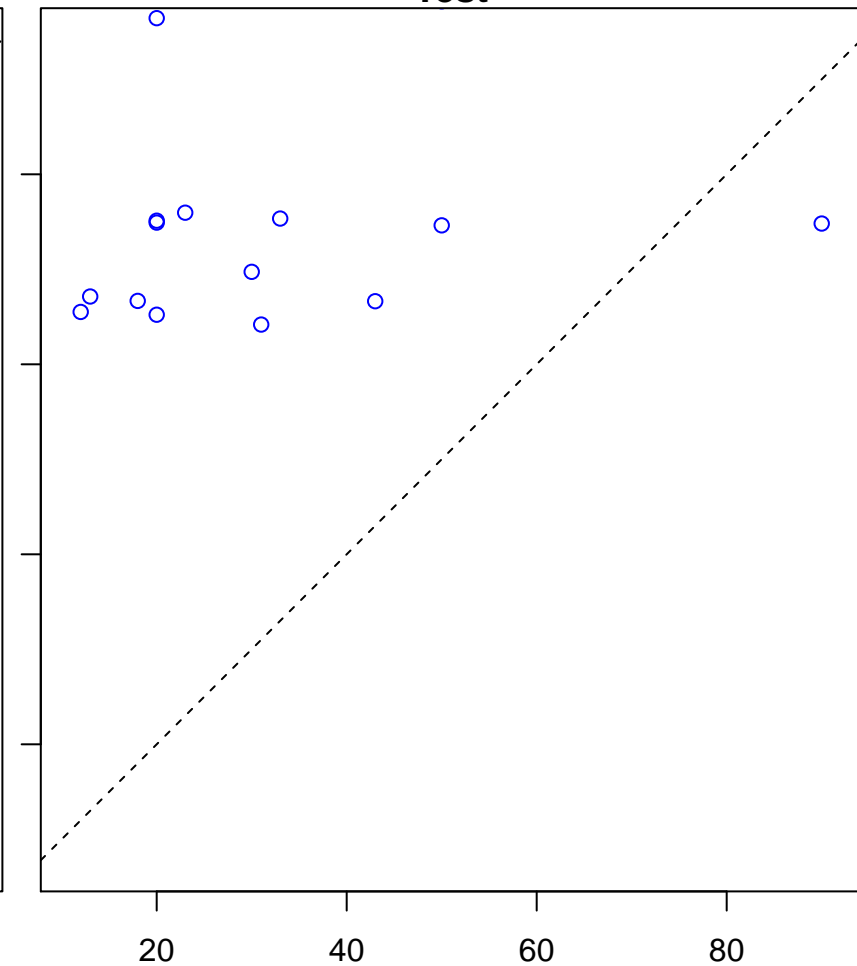


morphogenesis of embryonic epithelium (Score: 6.256989)

Control

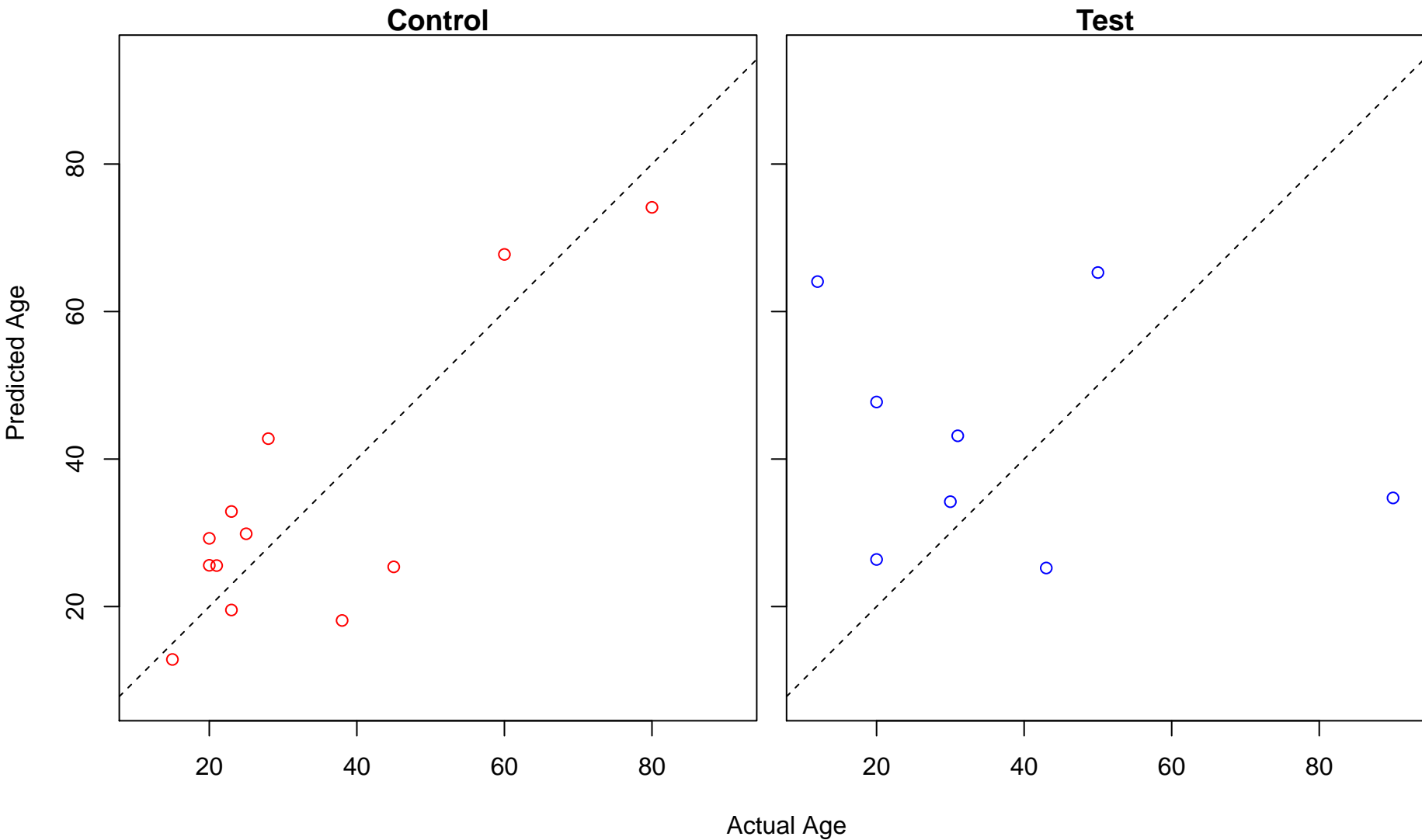


Test

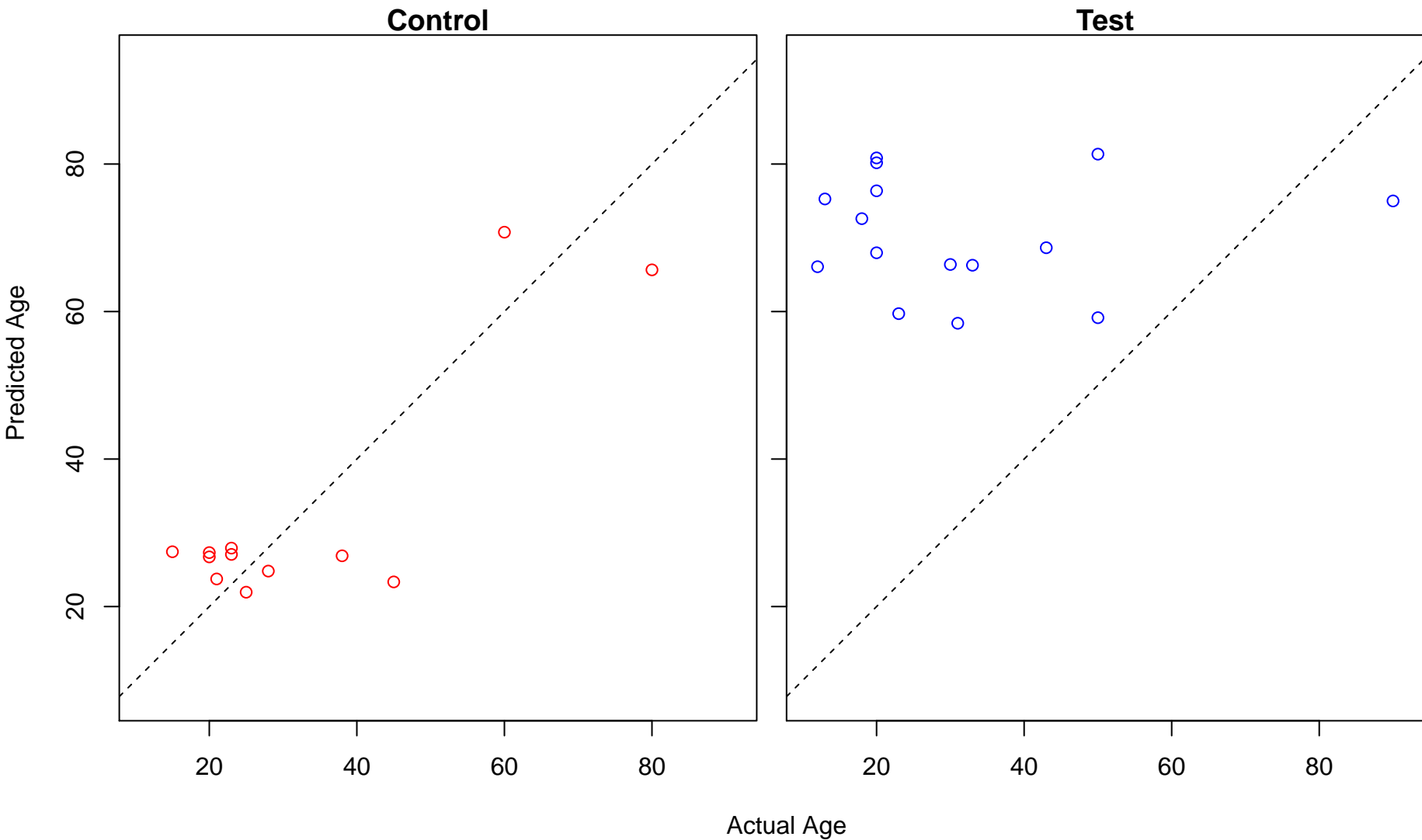


Actual Age

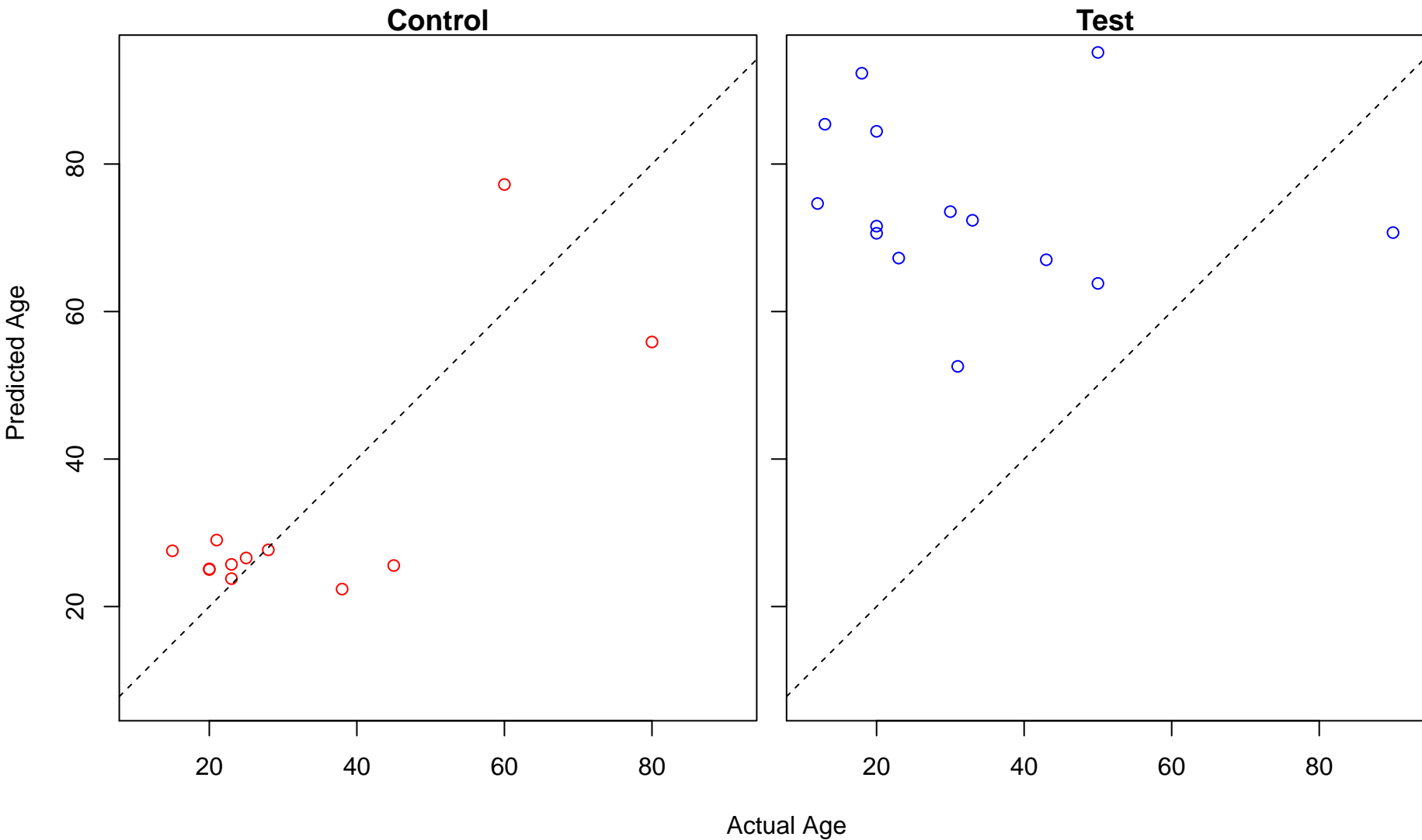
aldehyde catabolic process (Score: 6.251144)



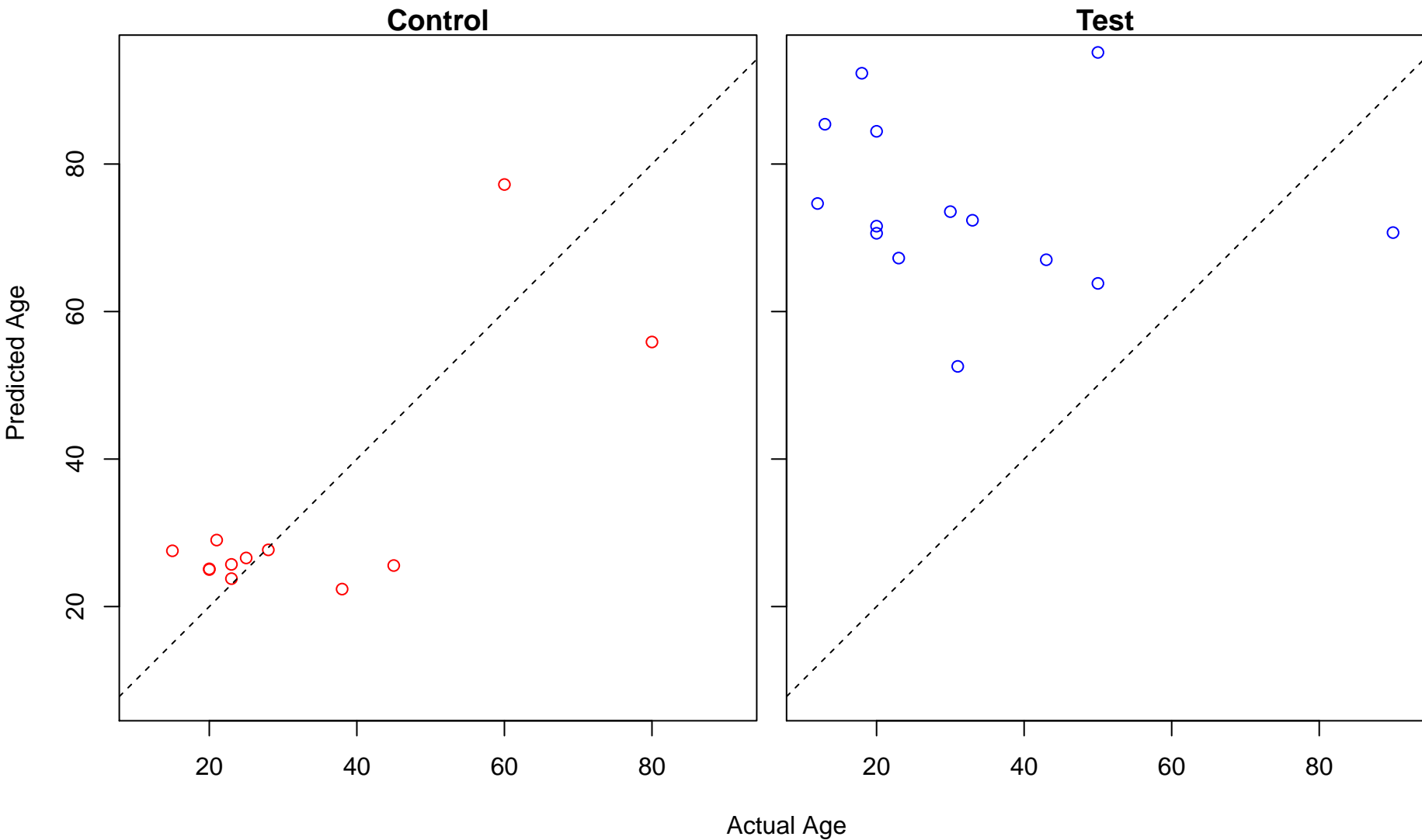
positive regulation of histone methylation (Score: 6.250259)



mitochondrial ATP synthesis coupled proton transport (Score: 6.248259)

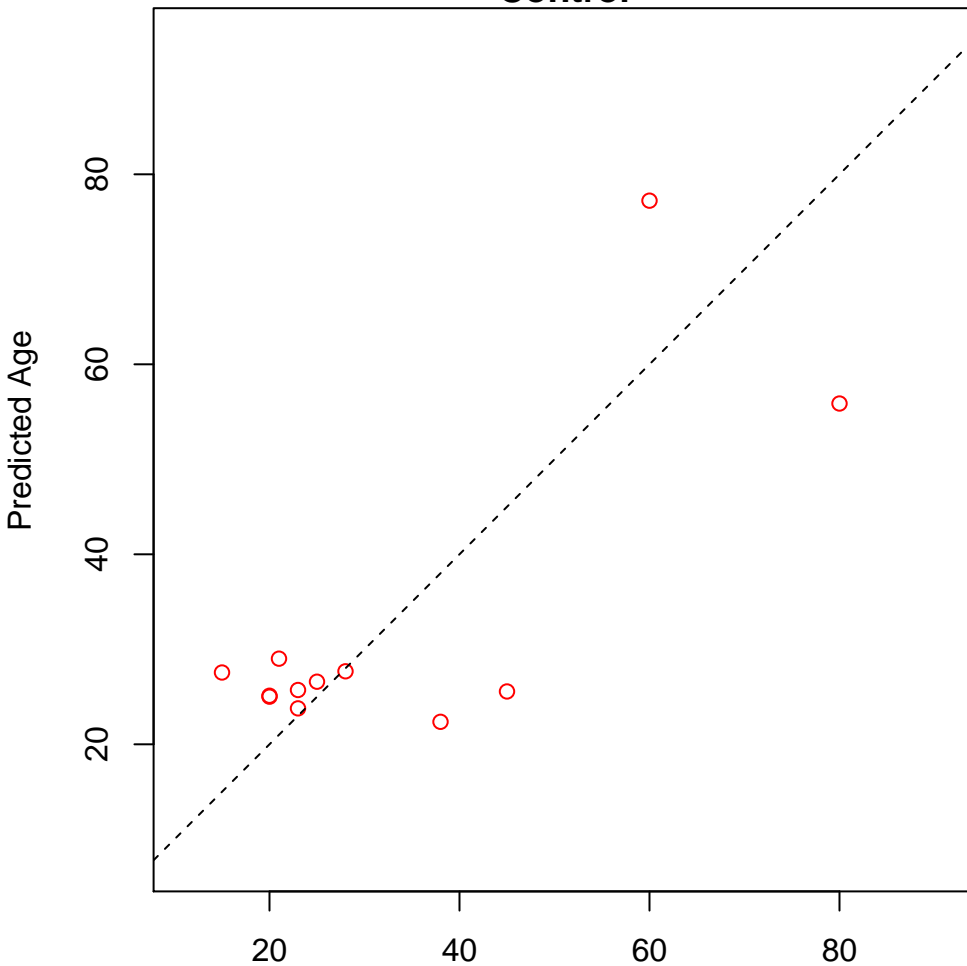


energy coupled proton transport, down electrochemical gradient (Score: 6.248251)

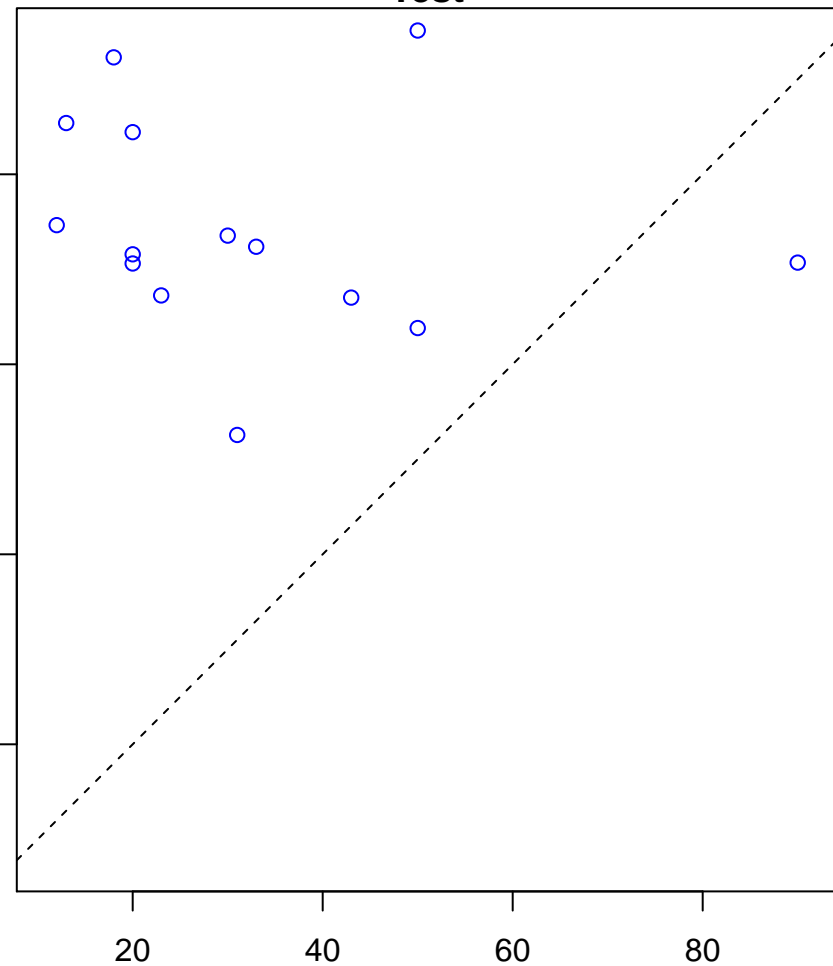


ATP synthesis coupled proton transport (Score: 6.248251)

Control

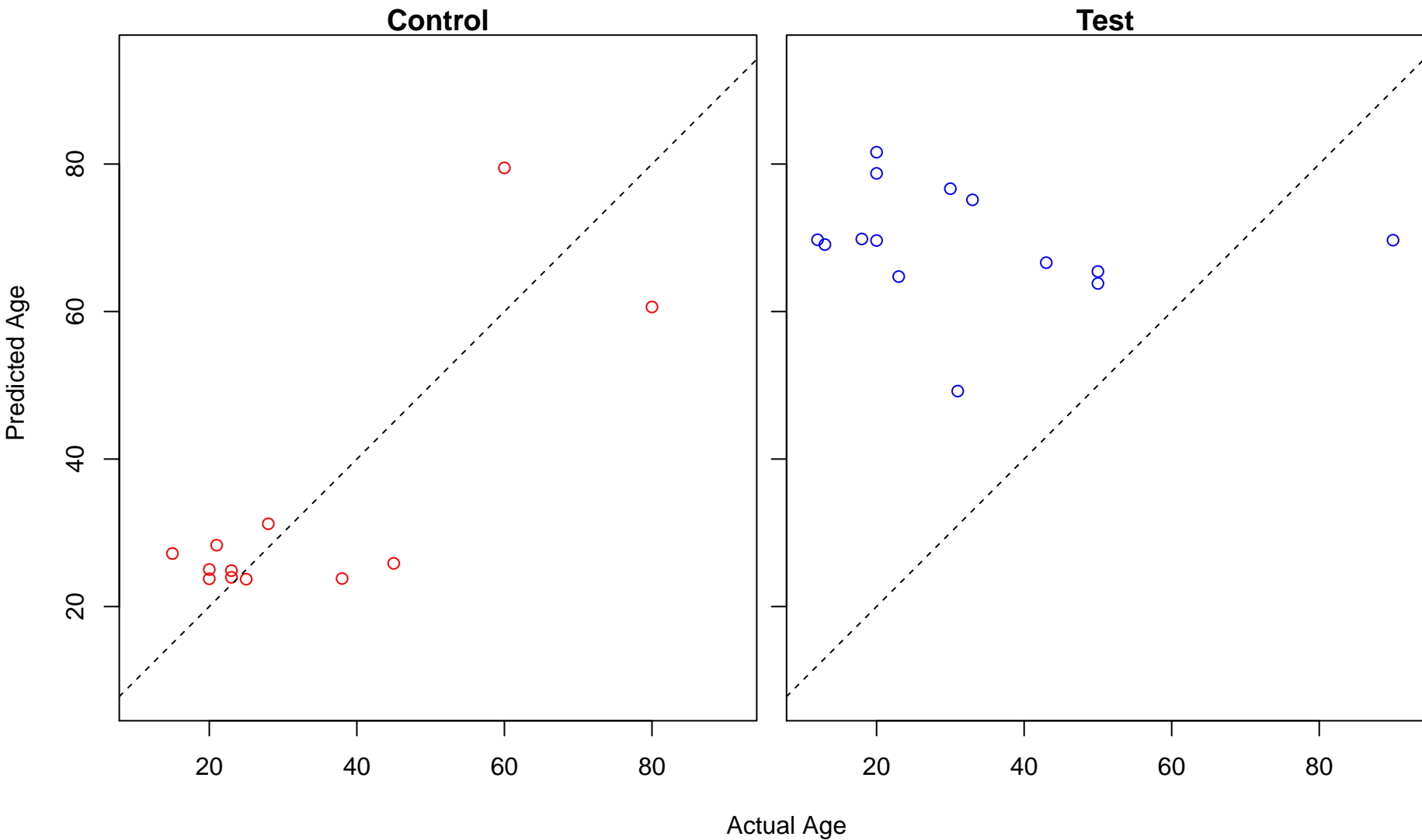


Test

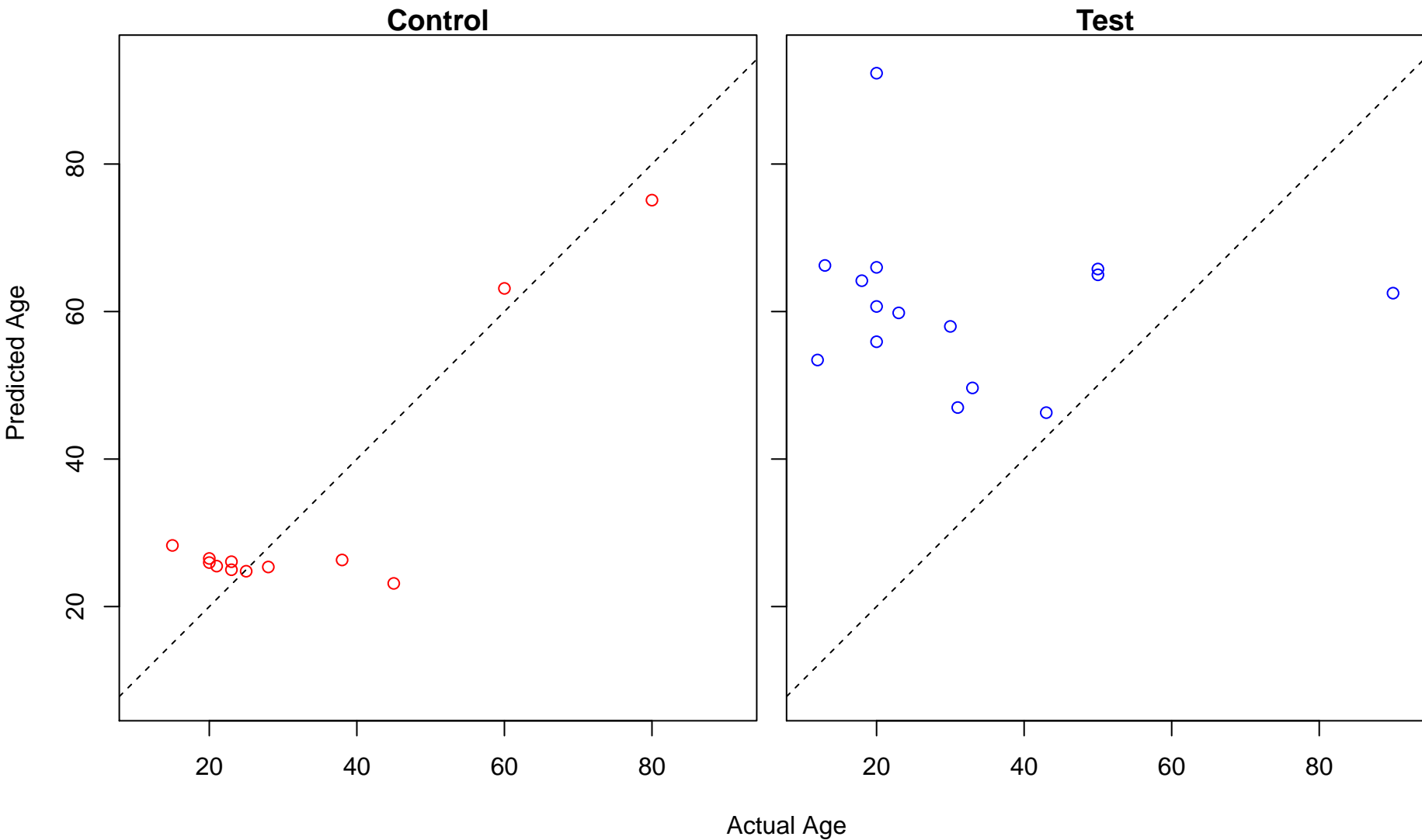


Actual Age

protein-cofactor linkage (Score: 6.247094)

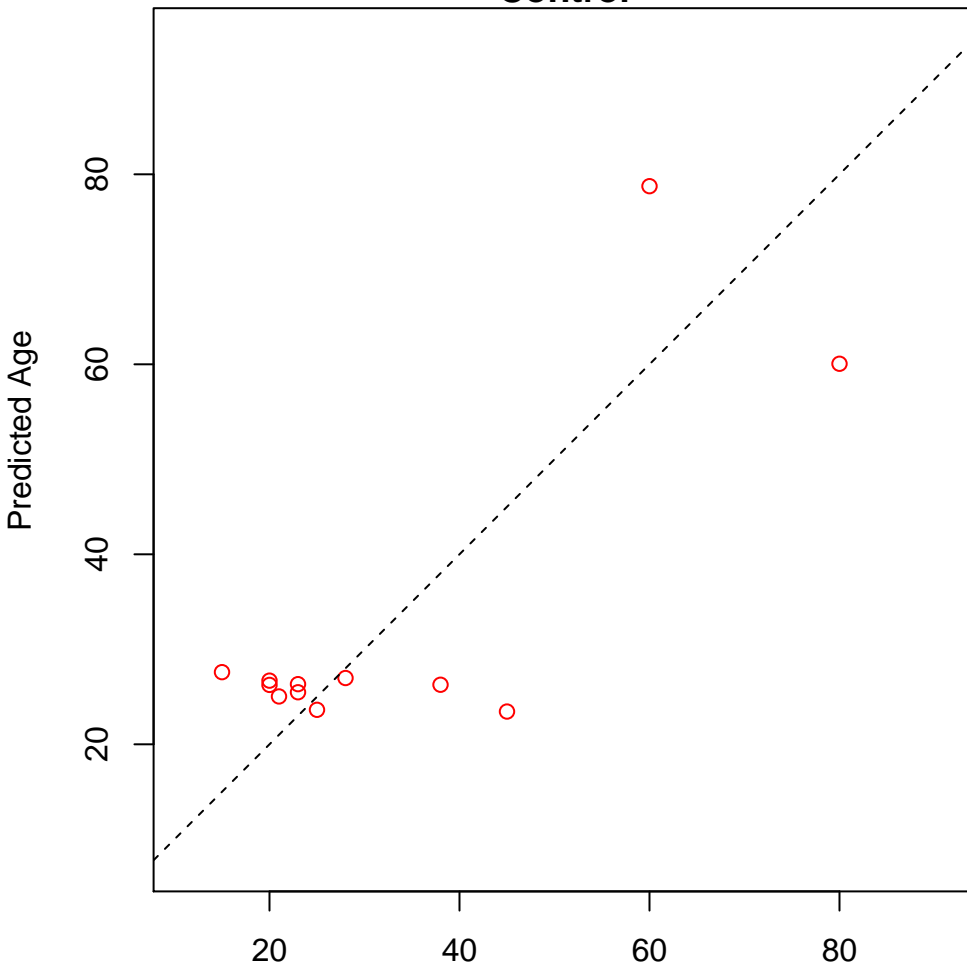


regulation of cellular component biogenesis (Score: 6.245573)

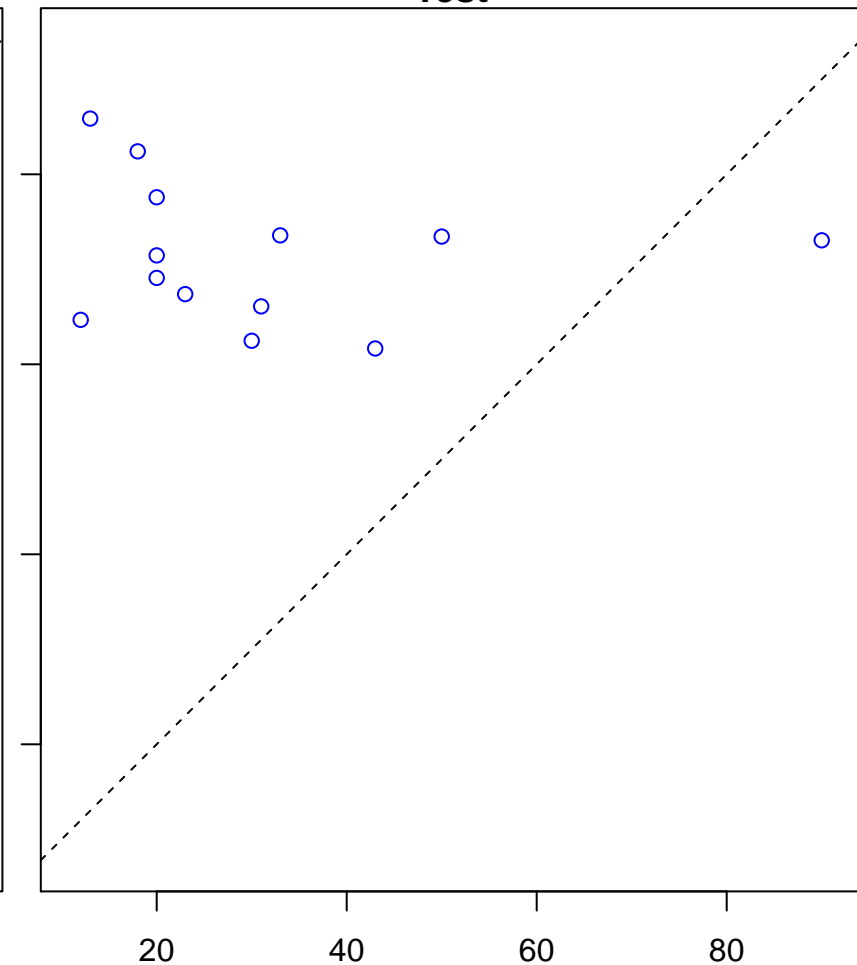


negative regulation of mitotic cell cycle (Score: 6.242968)

Control

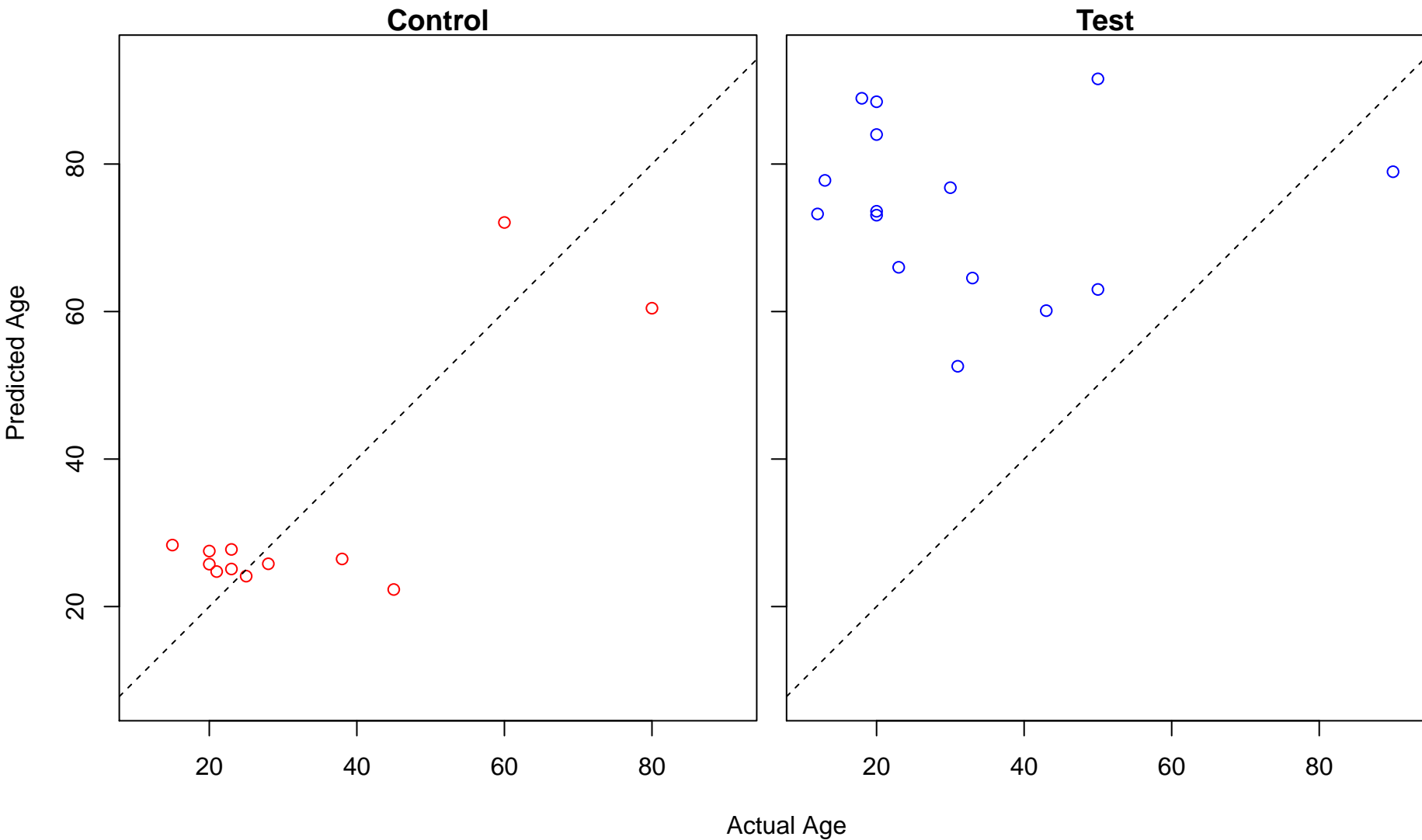


Test

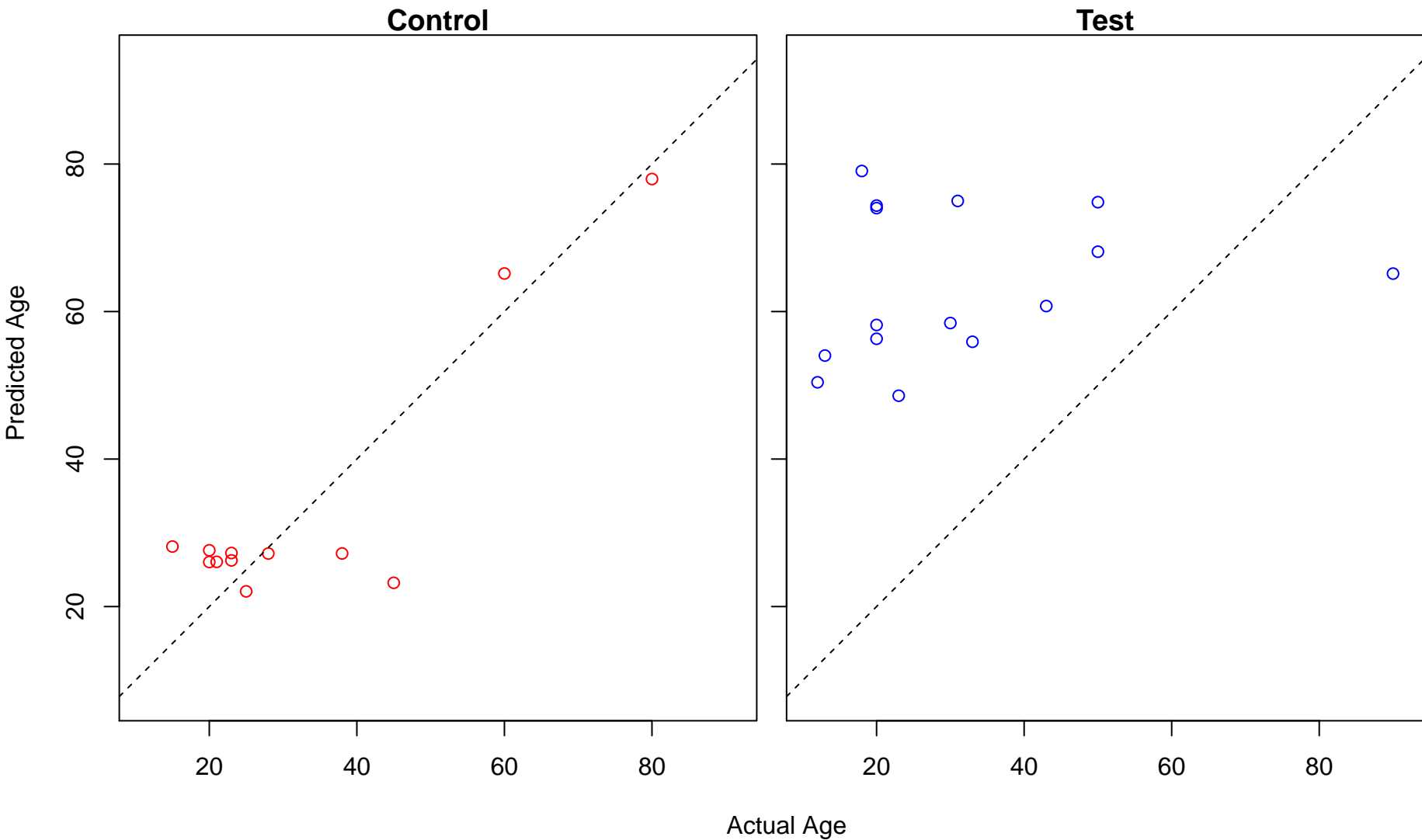


Actual Age

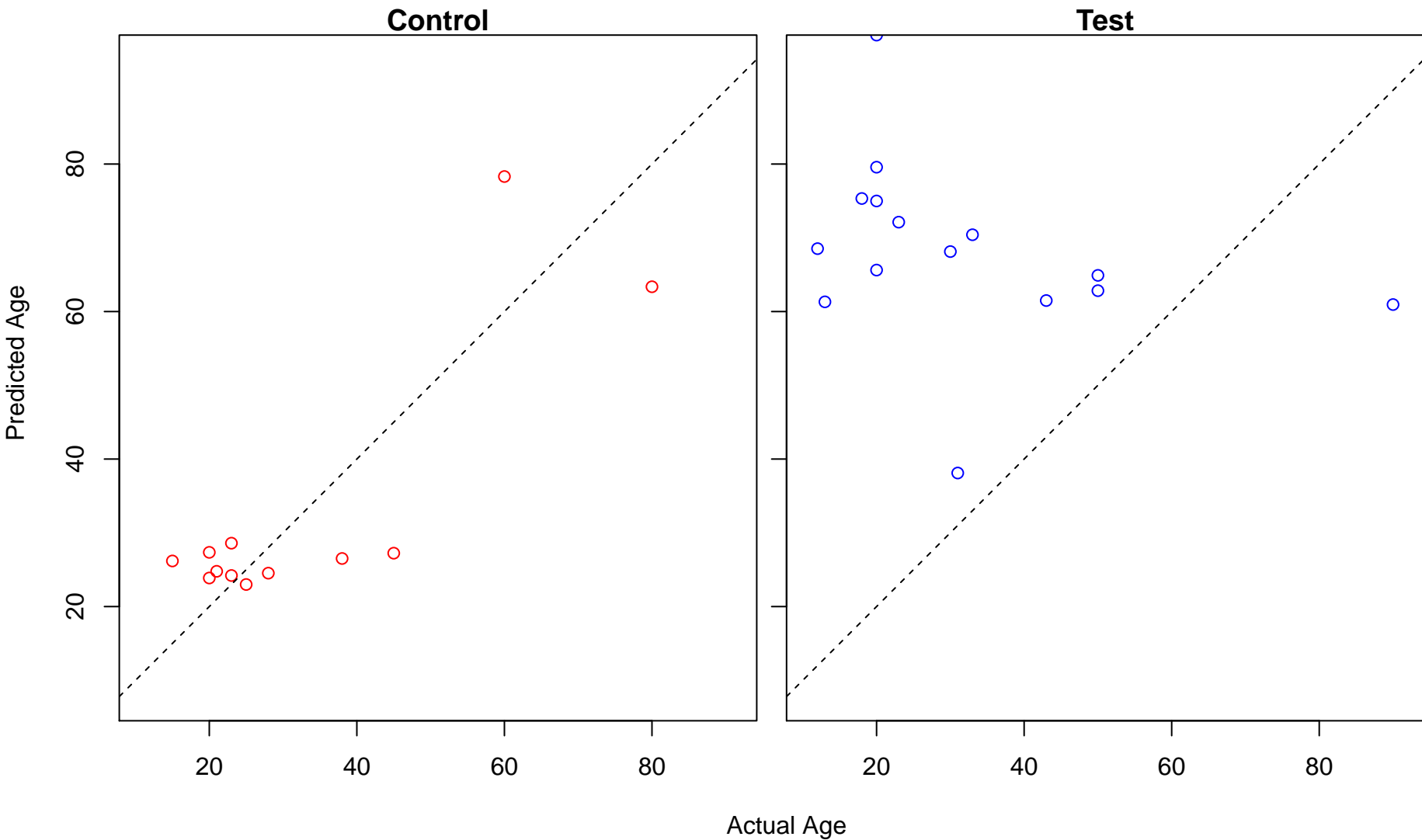
somatic stem cell population maintenance (Score: 6.240886)



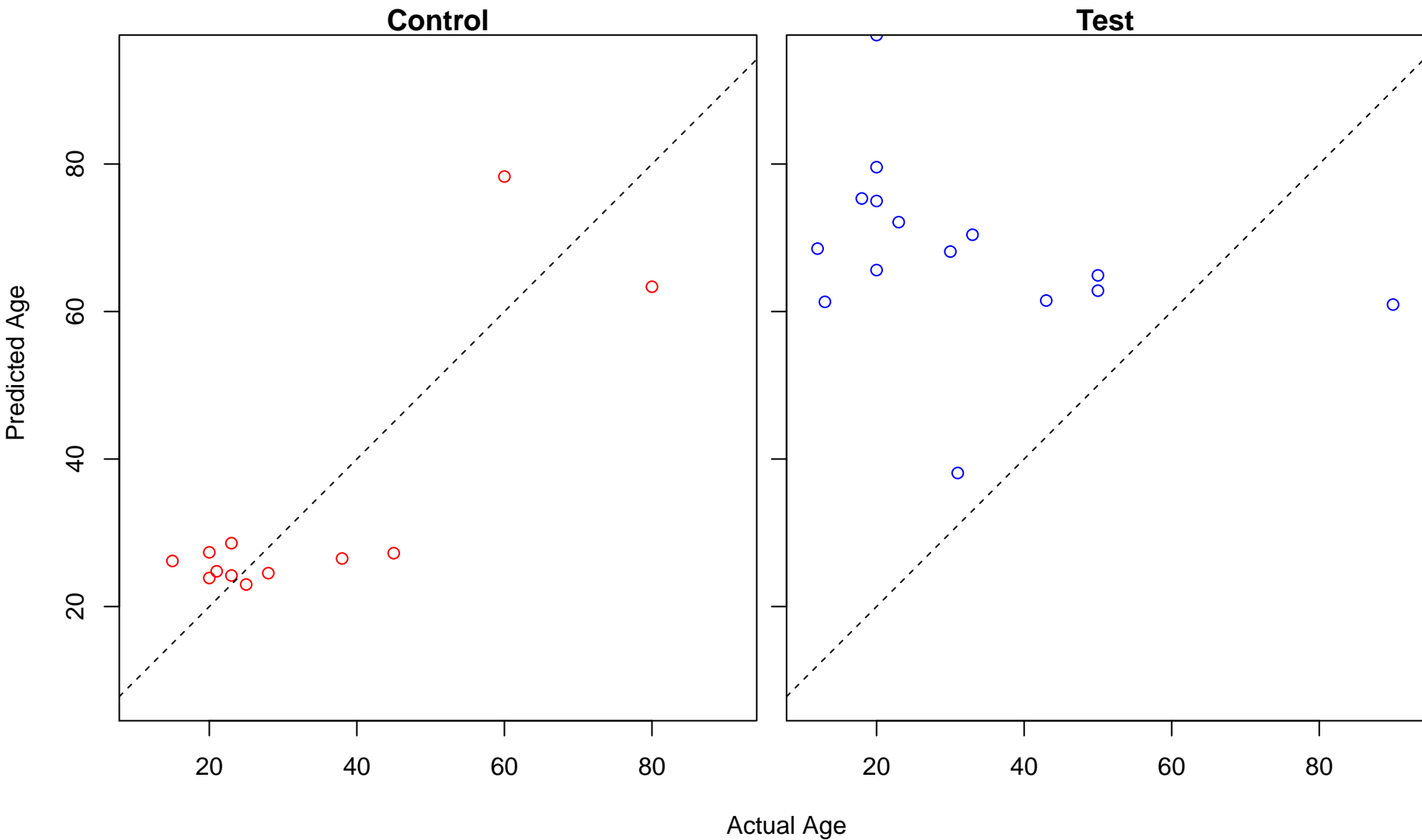
regulation of cell adhesion (Score: 6.240522)



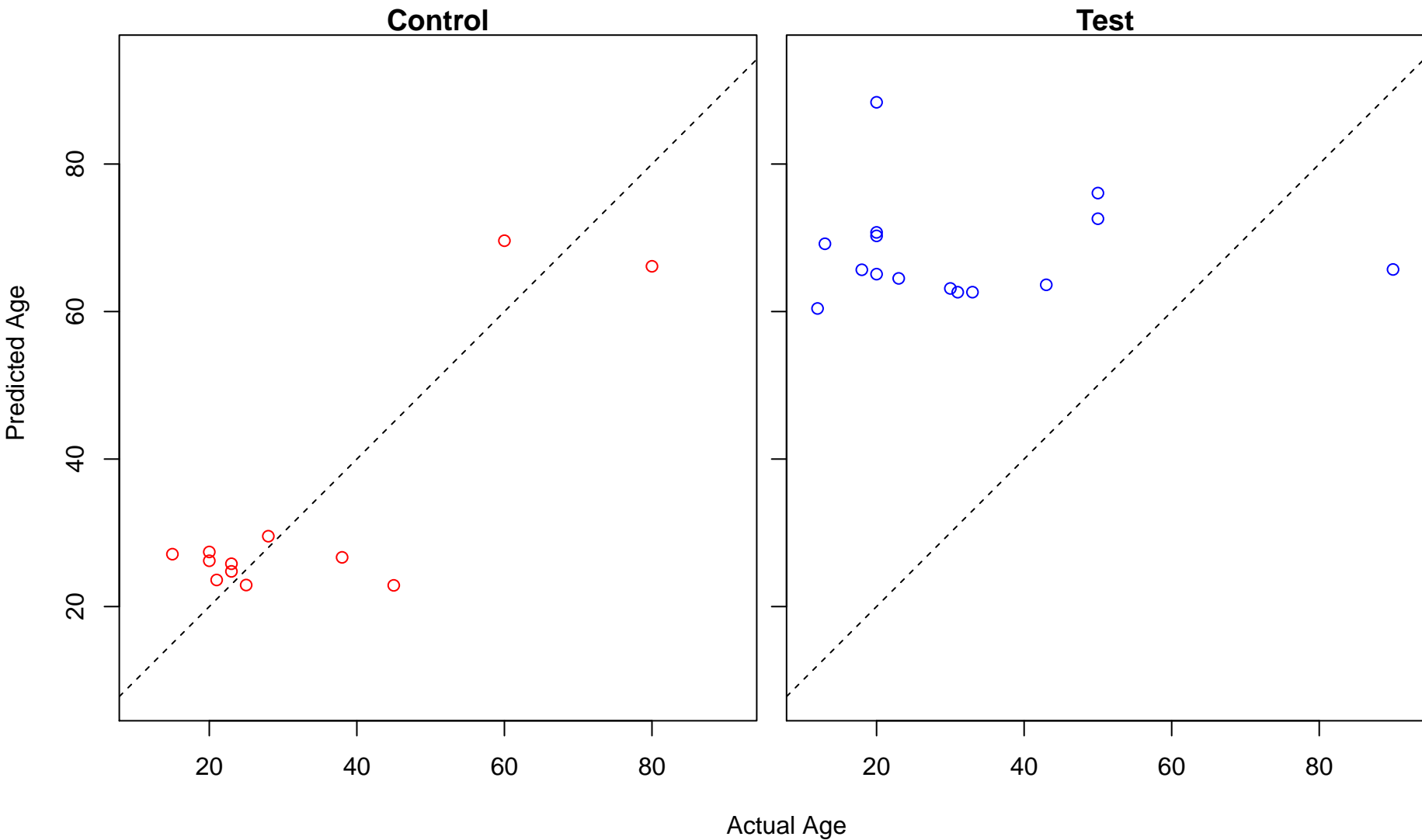
arginine metabolic process (Score: 6.238024)



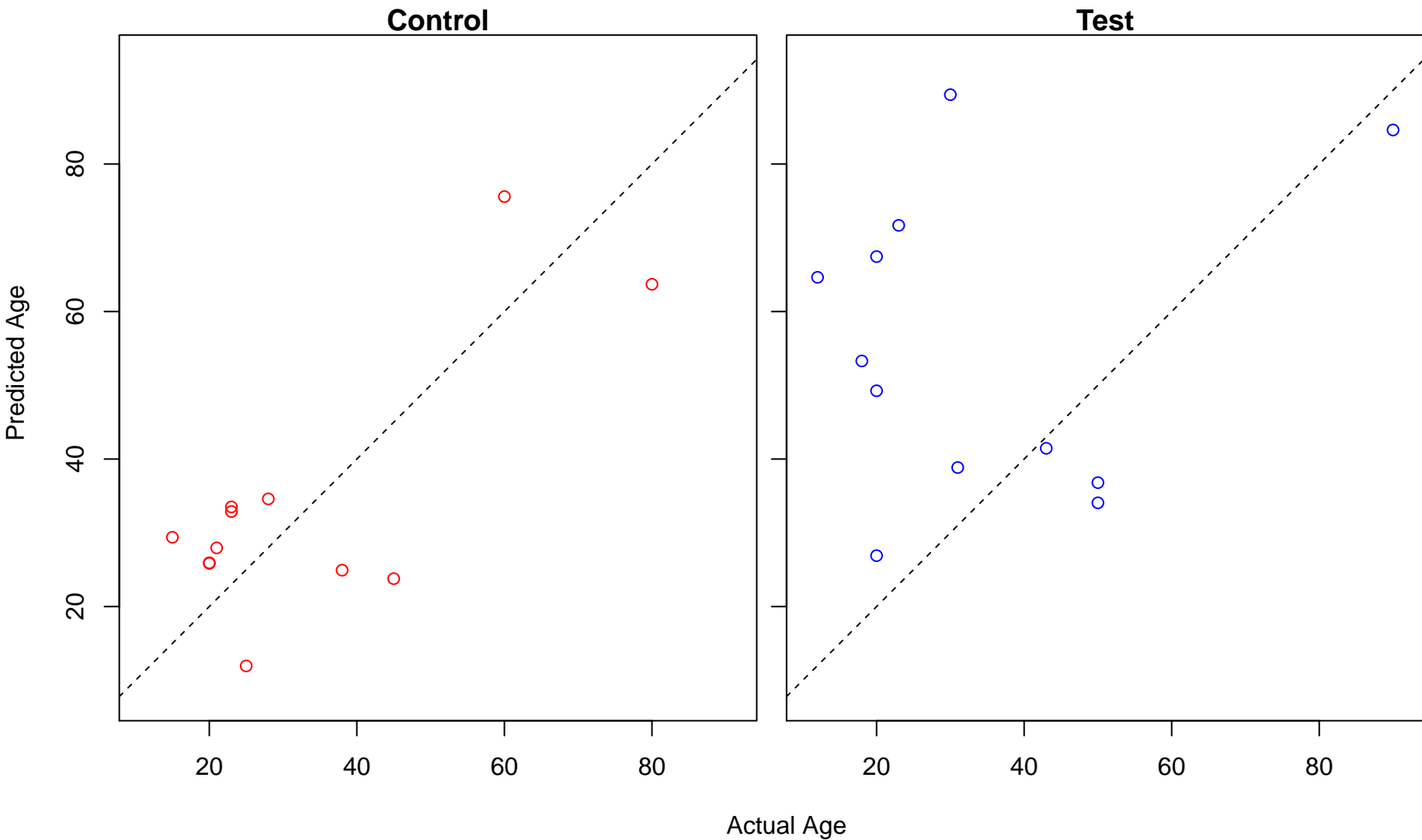
arginine catabolic process (Score: 6.238024)



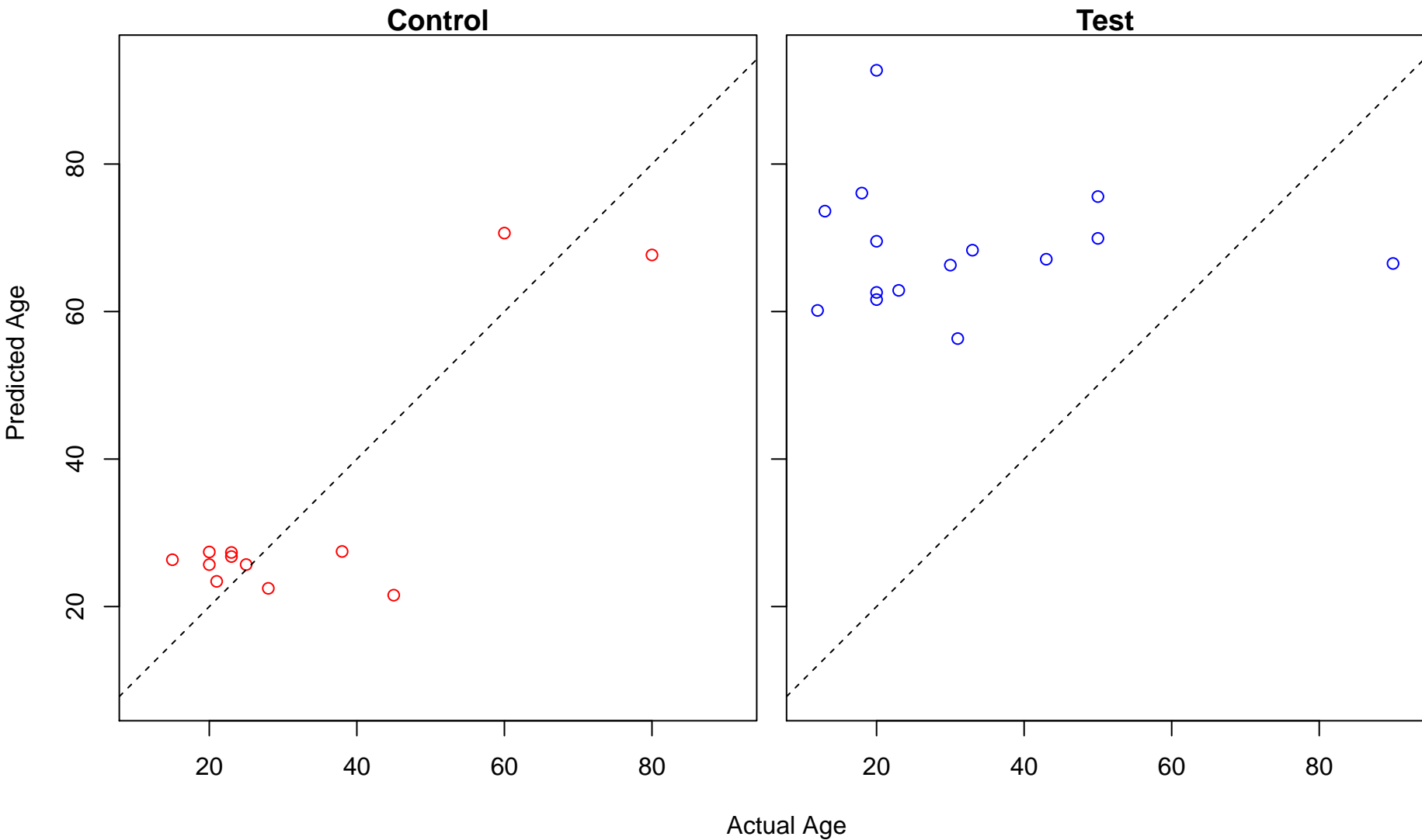
regulation of GTPase activity (Score: 6.237318)



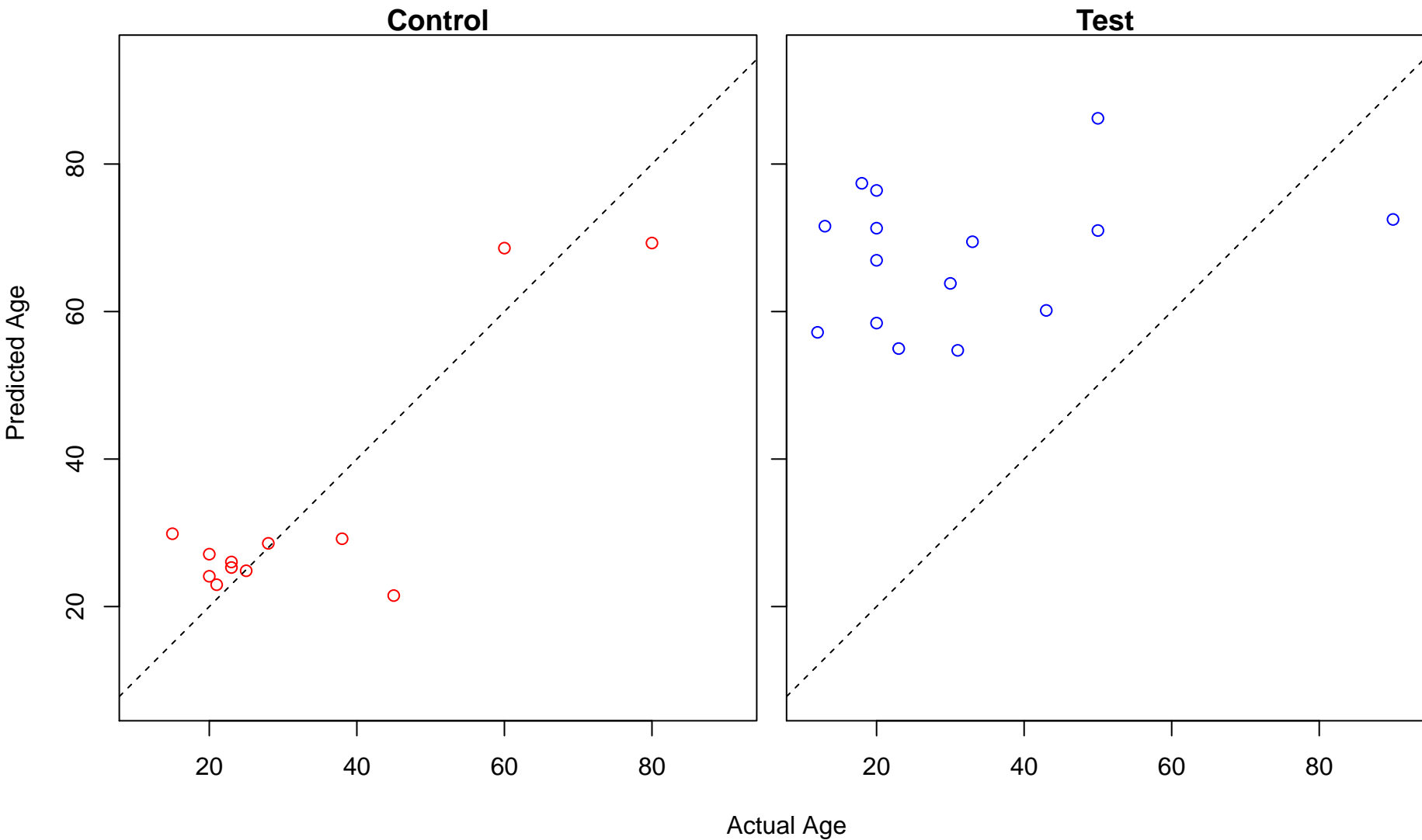
negative regulation of androgen receptor signaling pathway (Score: 6.236453)



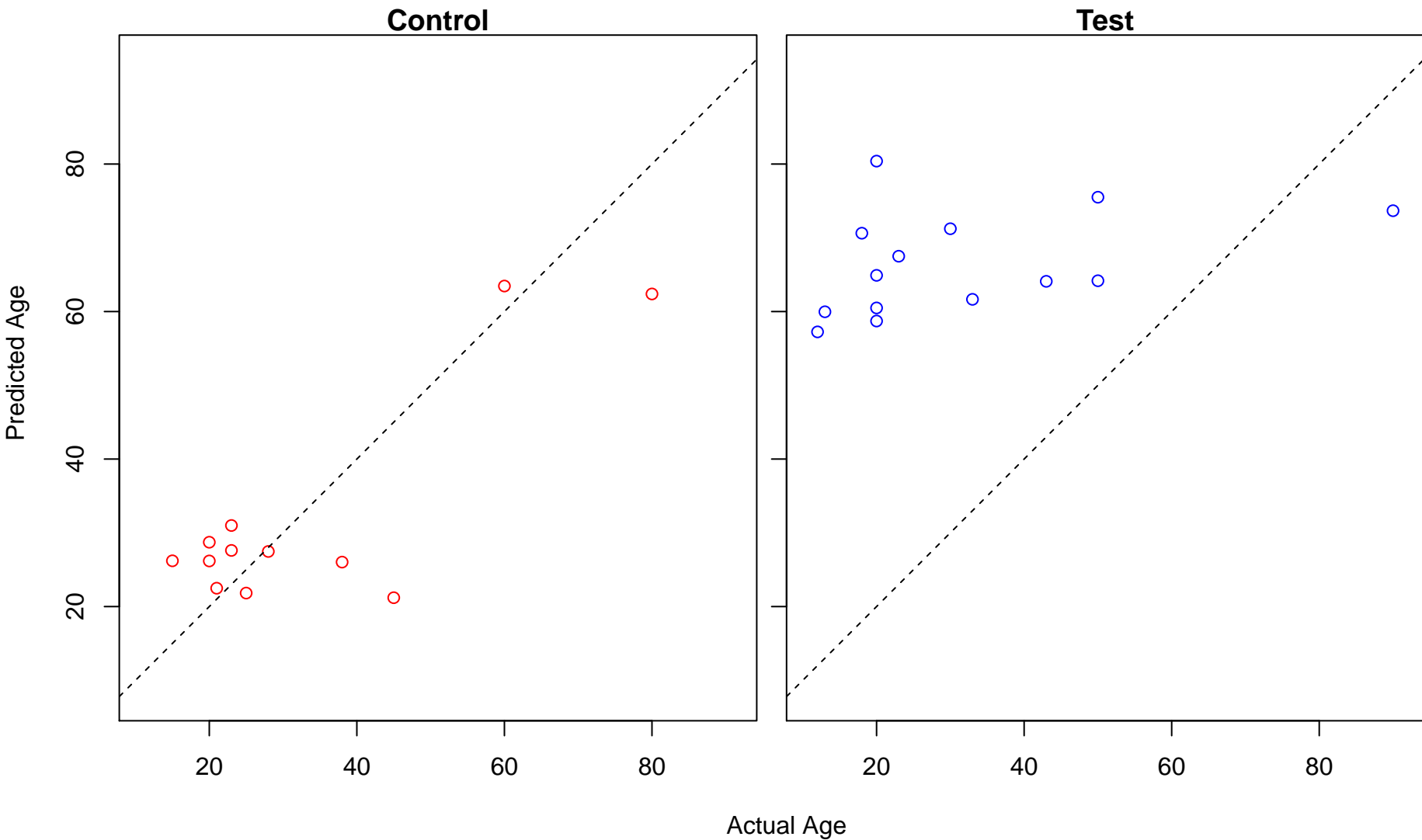
plasma membrane fusion (Score: 6.236176)



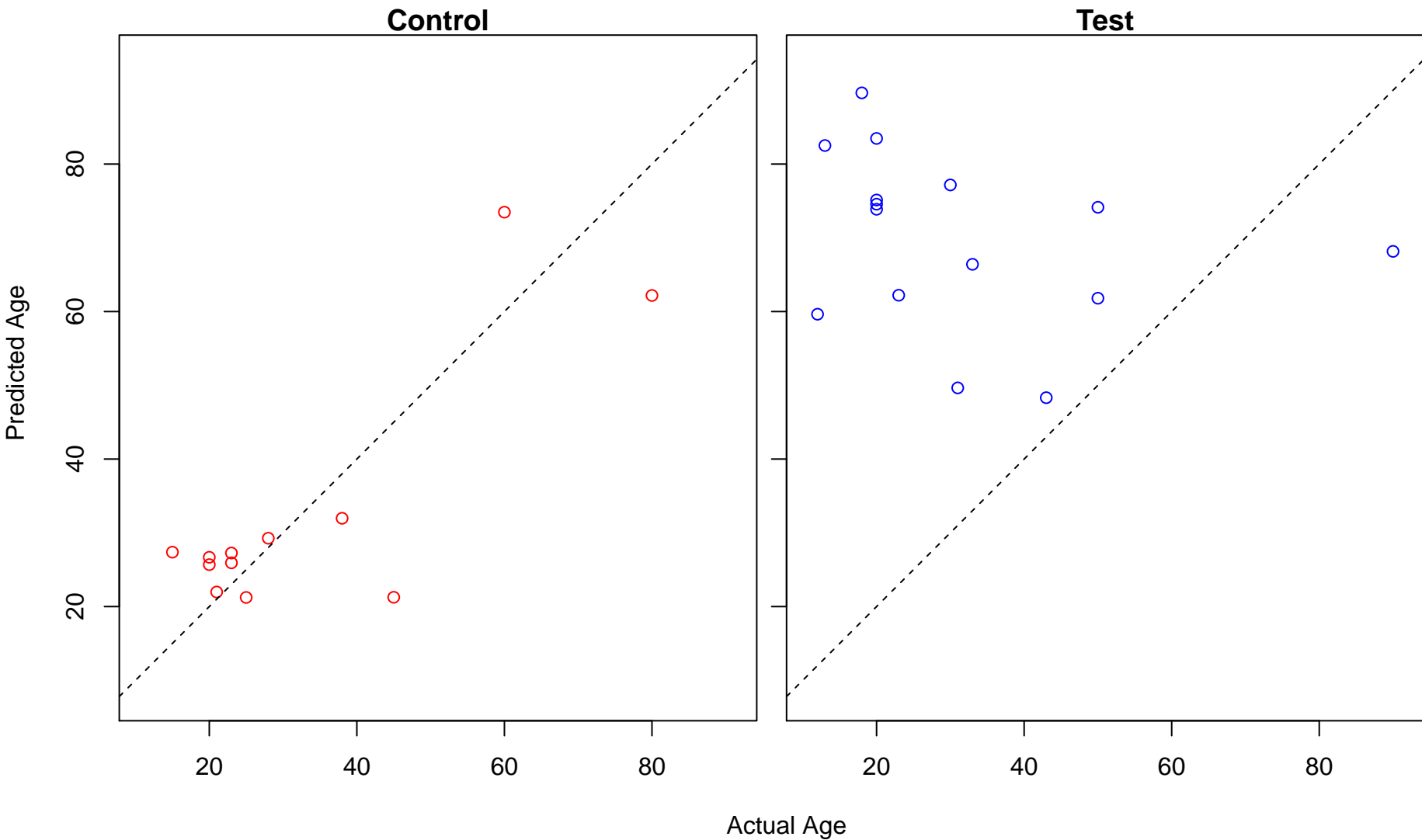
regulation of protein acetylation (Score: 6.235650)



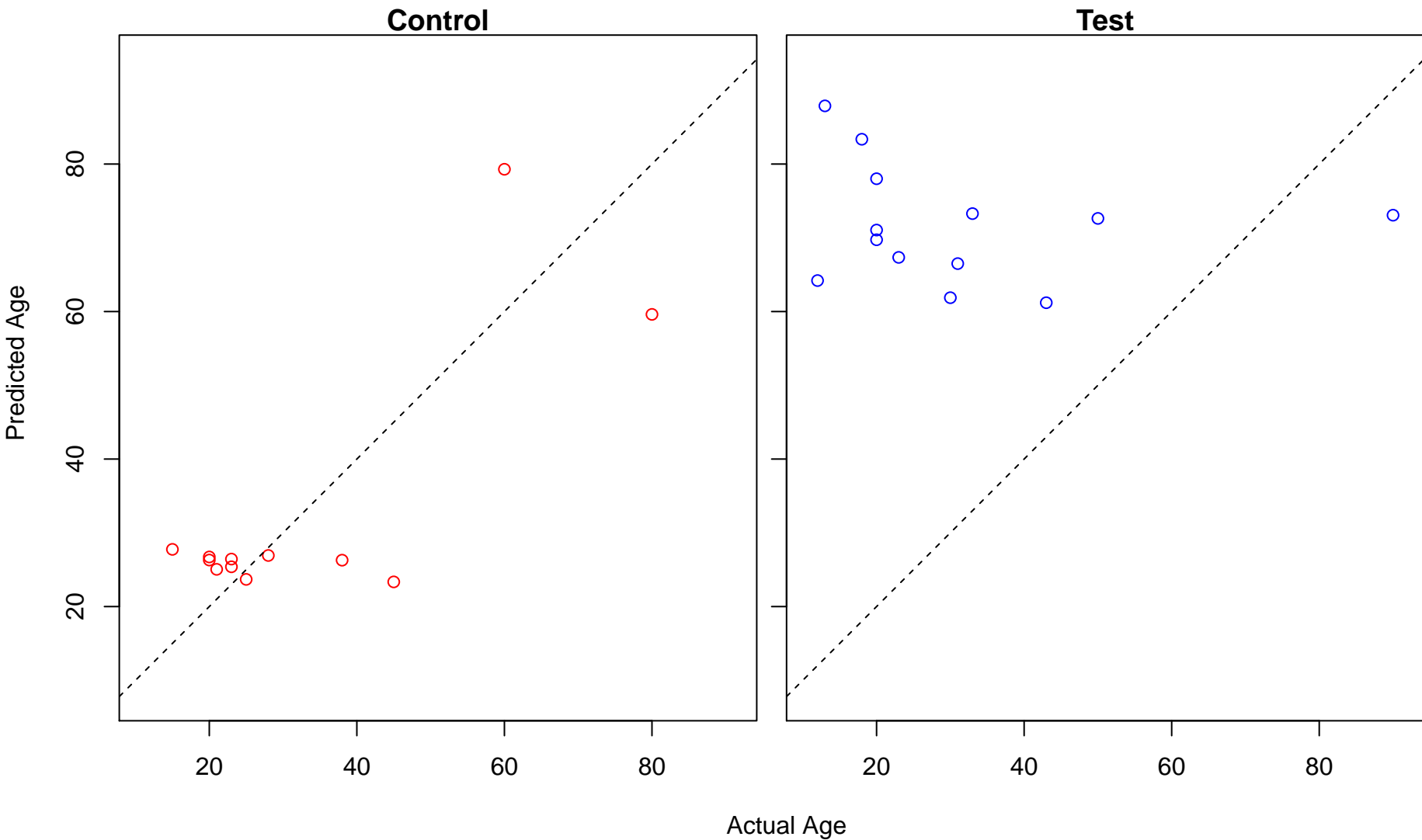
negative regulation of B cell activation (Score: 6.234434)



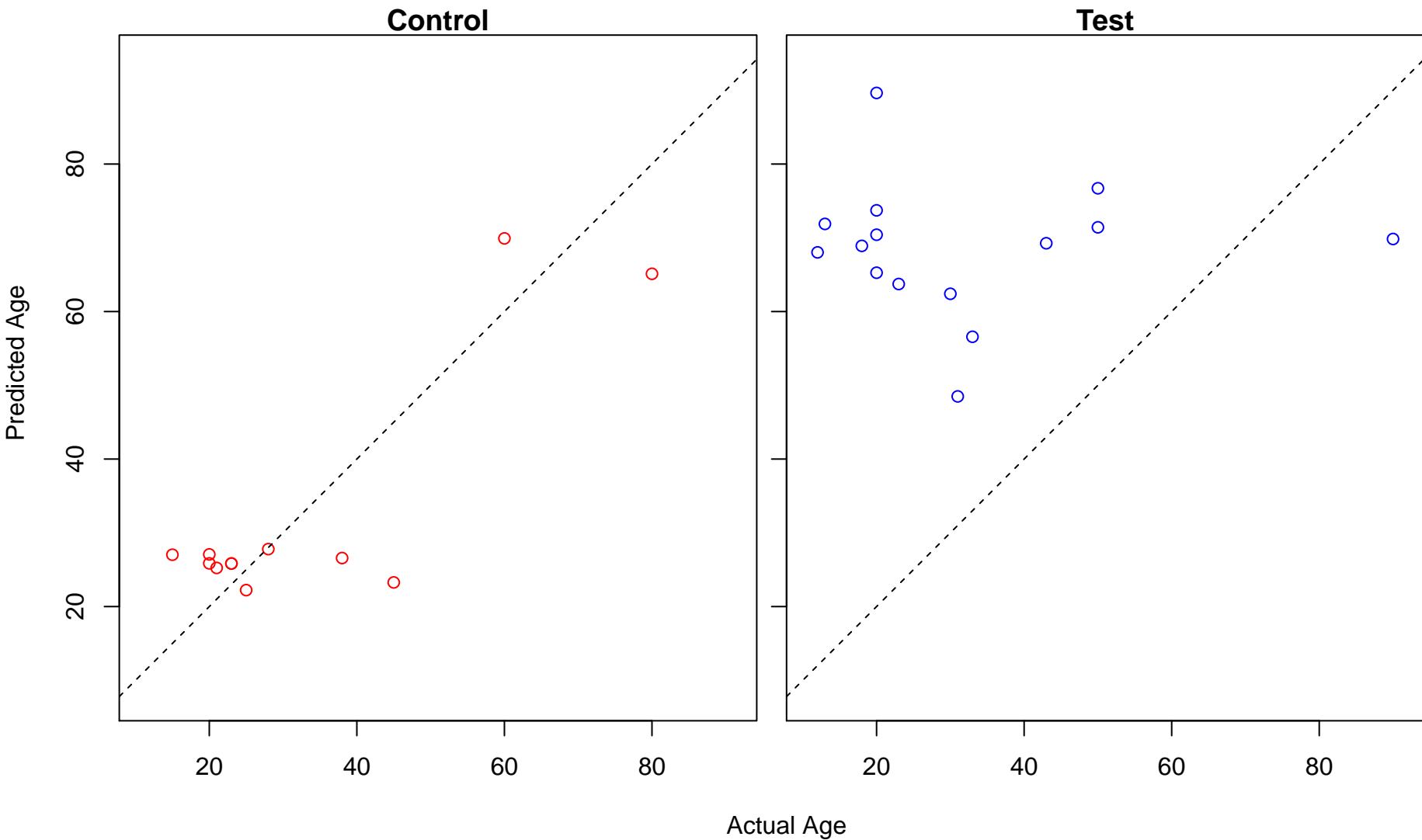
negative regulation of chromatin silencing (Score: 6.233009)



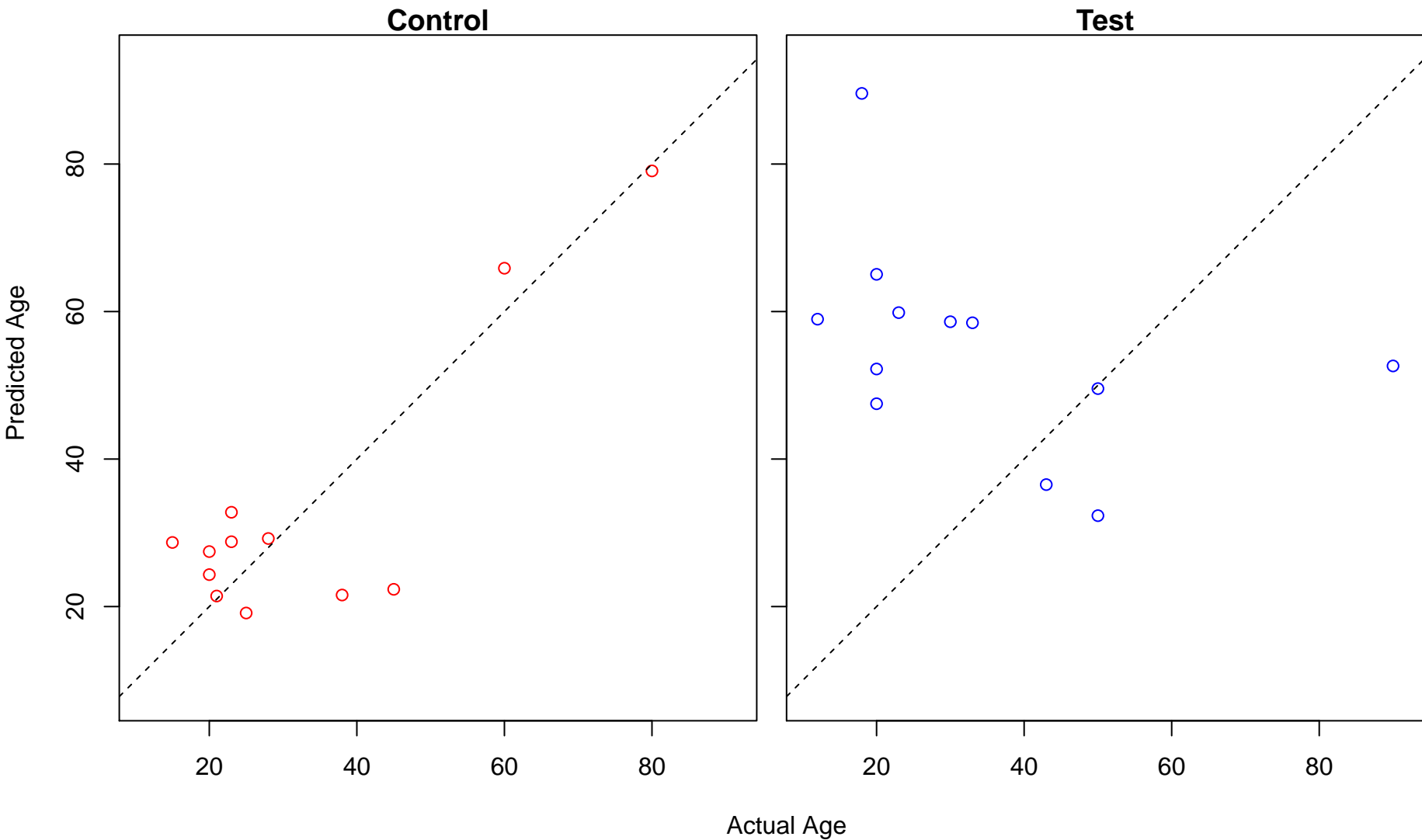
positive regulation of canonical Wnt signaling pathway (Score: 6.232634)



sulfur compound biosynthetic process (Score: 6.232385)

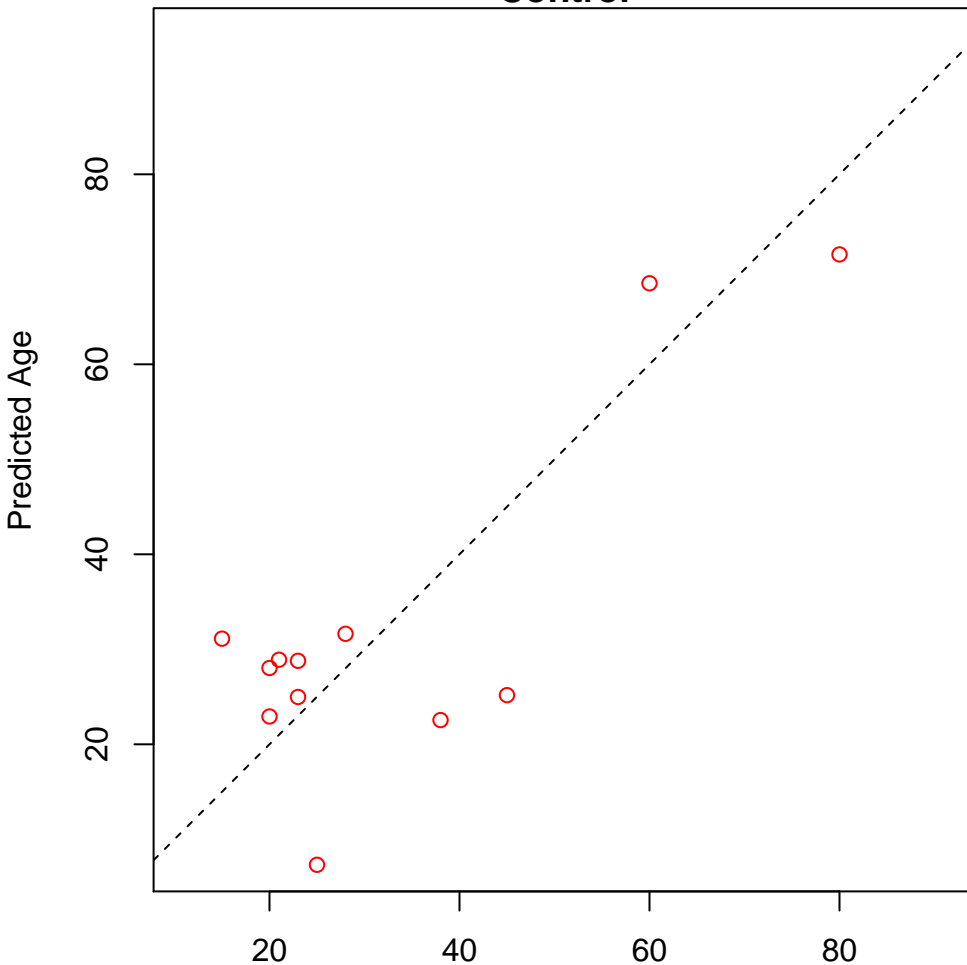


cellular amino acid catabolic process (Score: 6.230980)

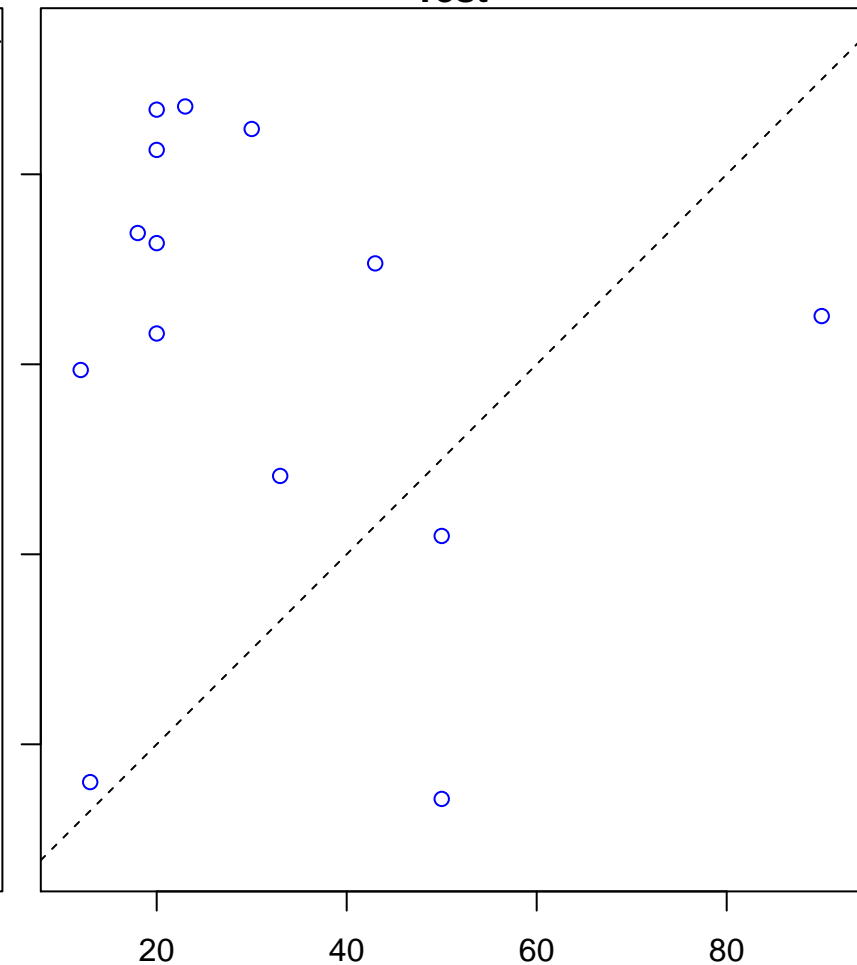


maintenance of protein location in cell (Score: 6.230635)

Control

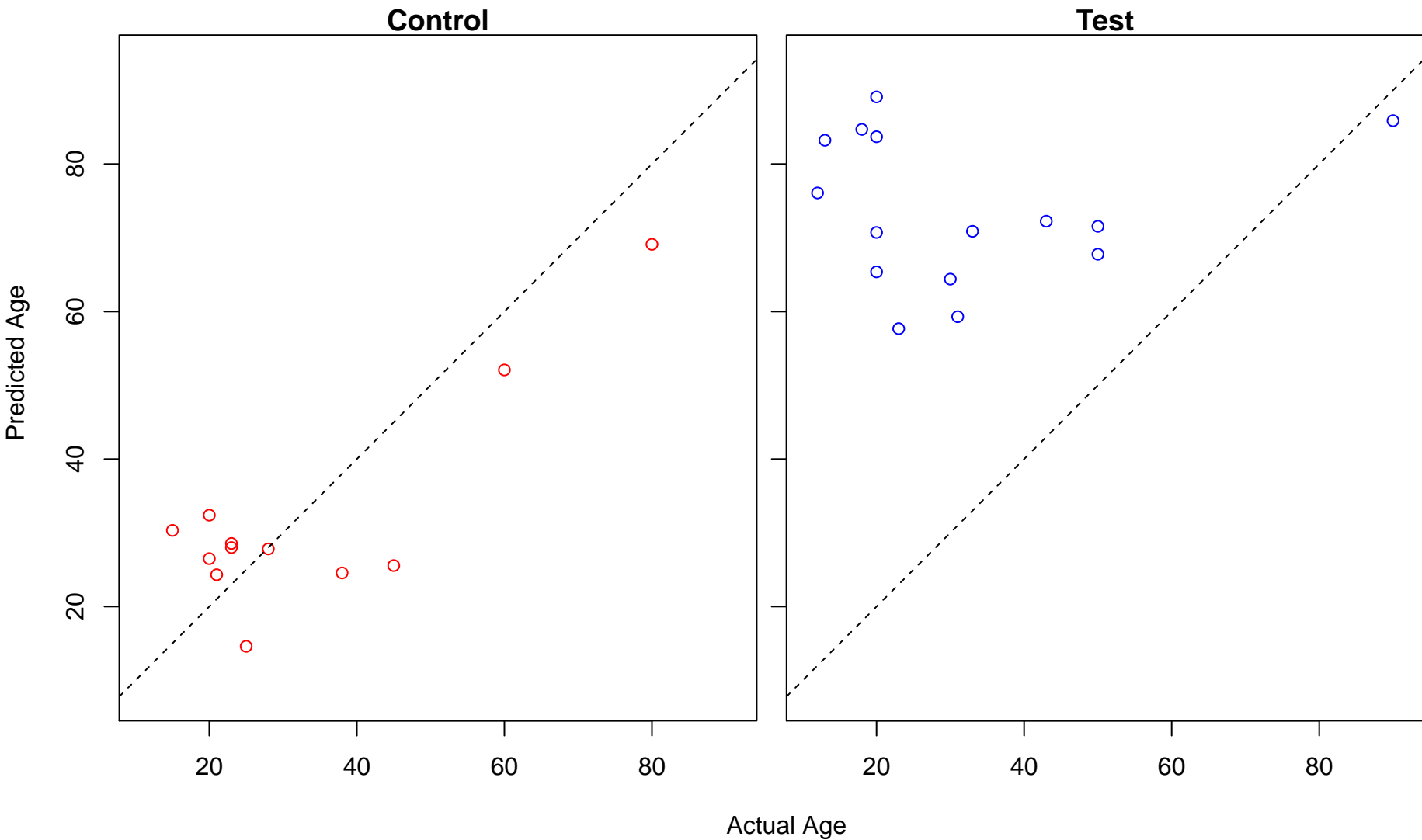


Test



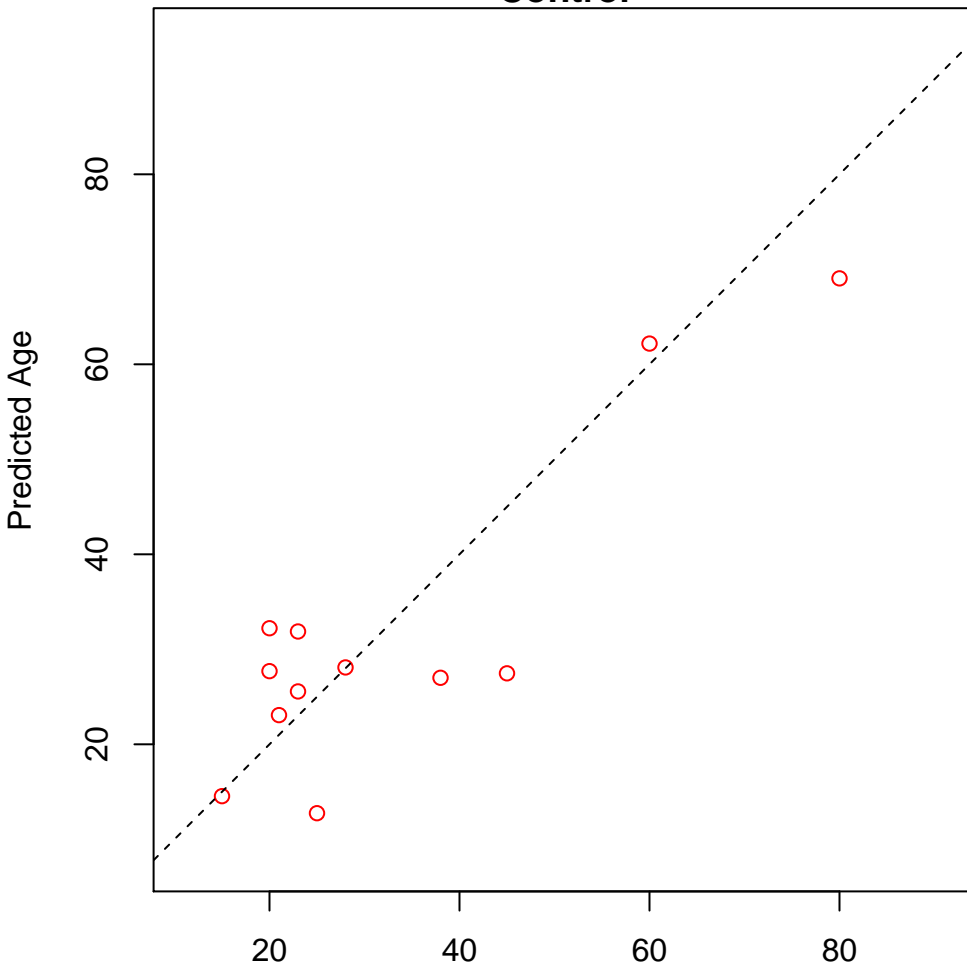
Actual Age

negative regulation of production of molecular mediator of immune response (Score: 6.225210)

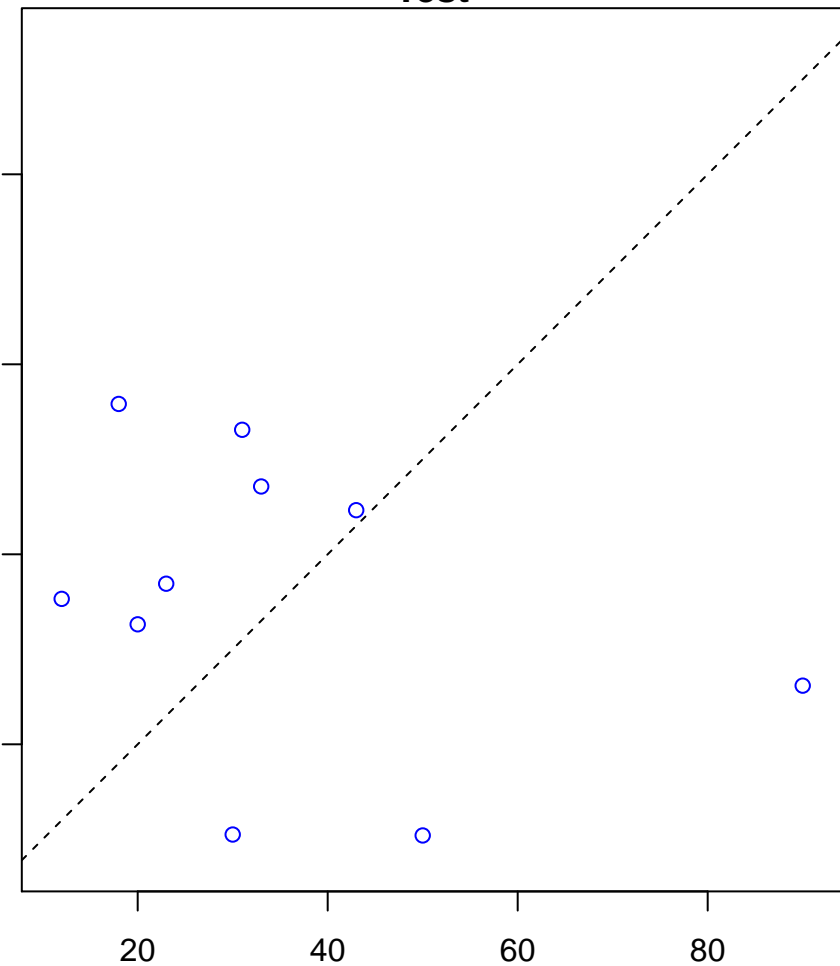


peptidyl-diphthamide metabolic process (Score: 6.223212)

Control

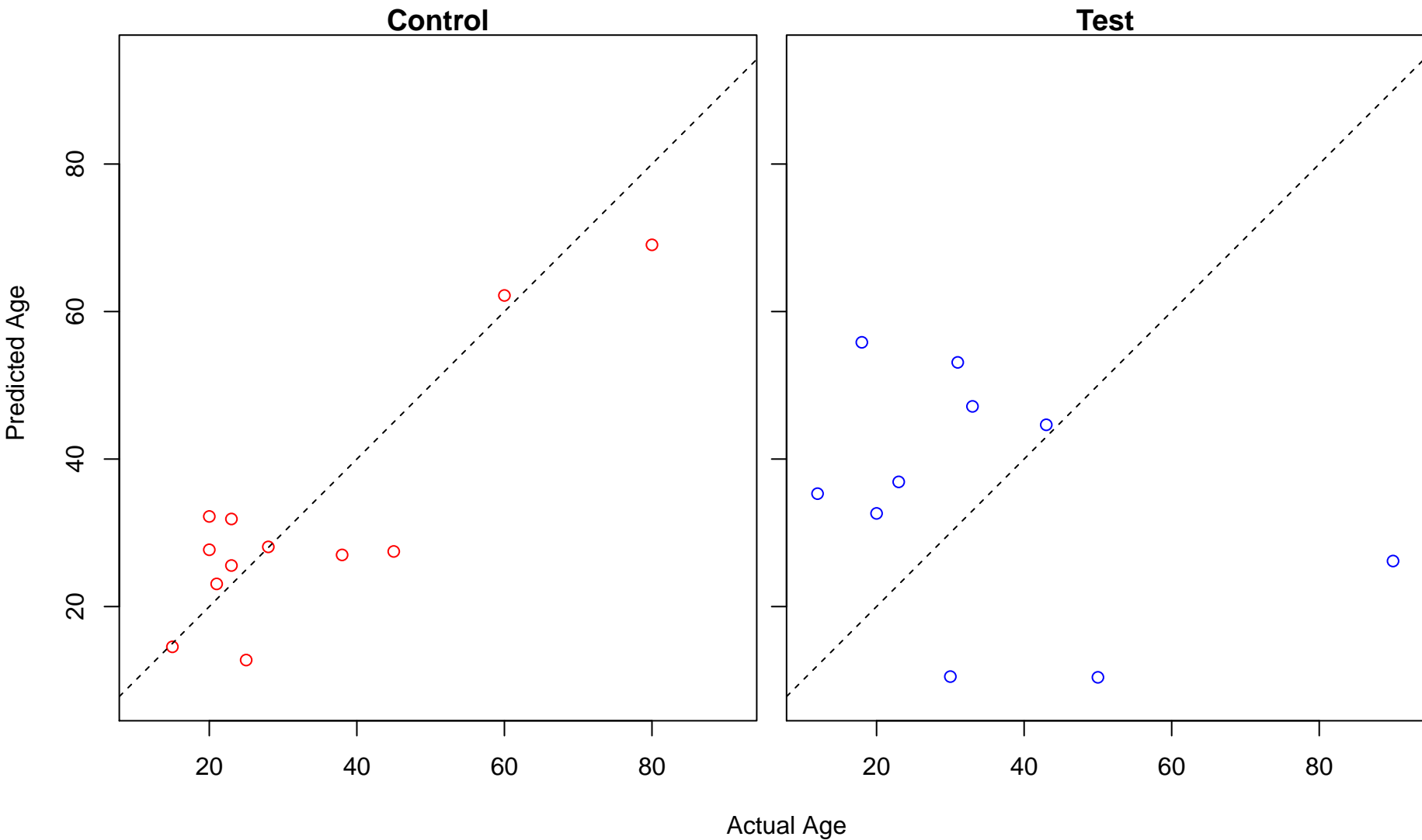


Test

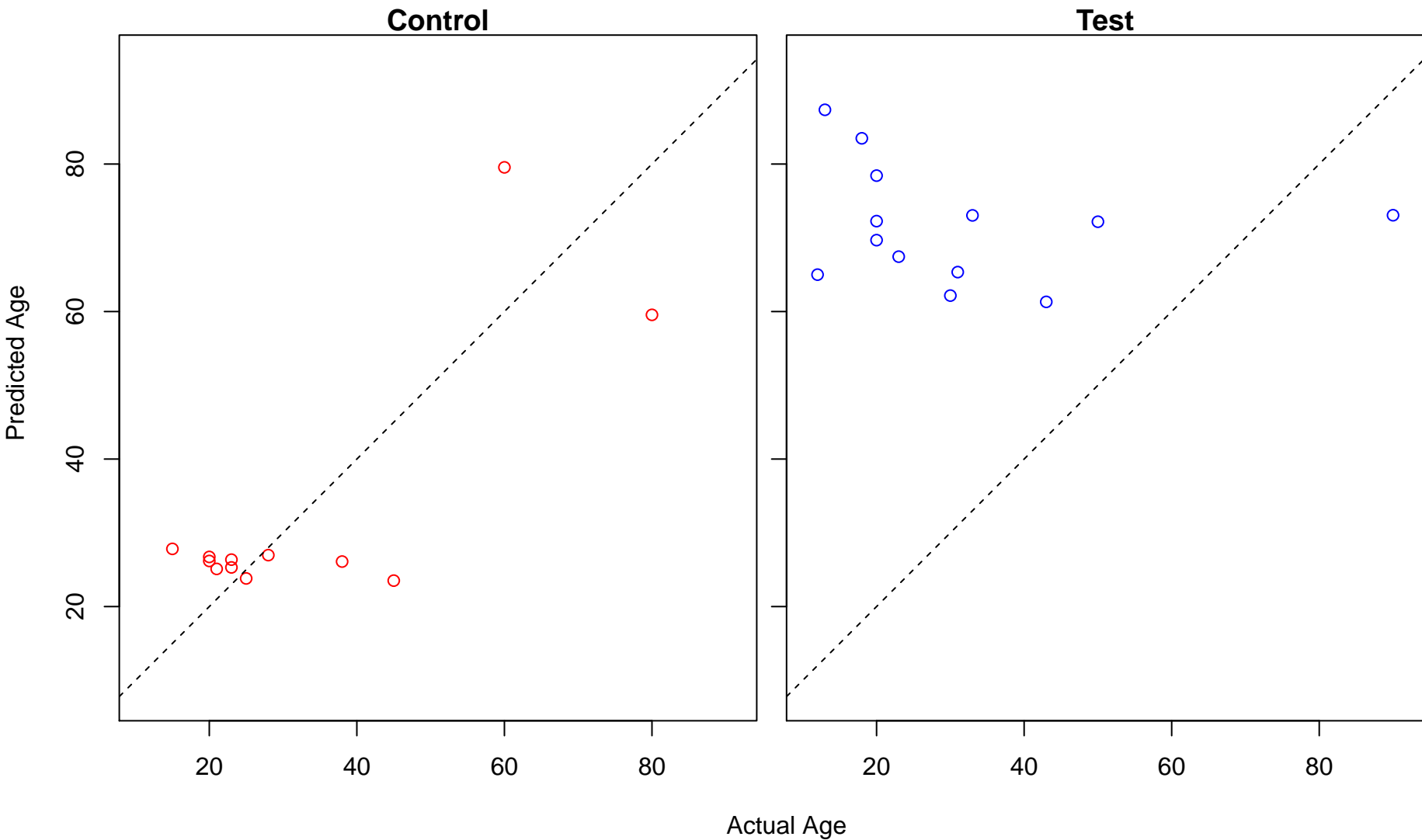


Actual Age

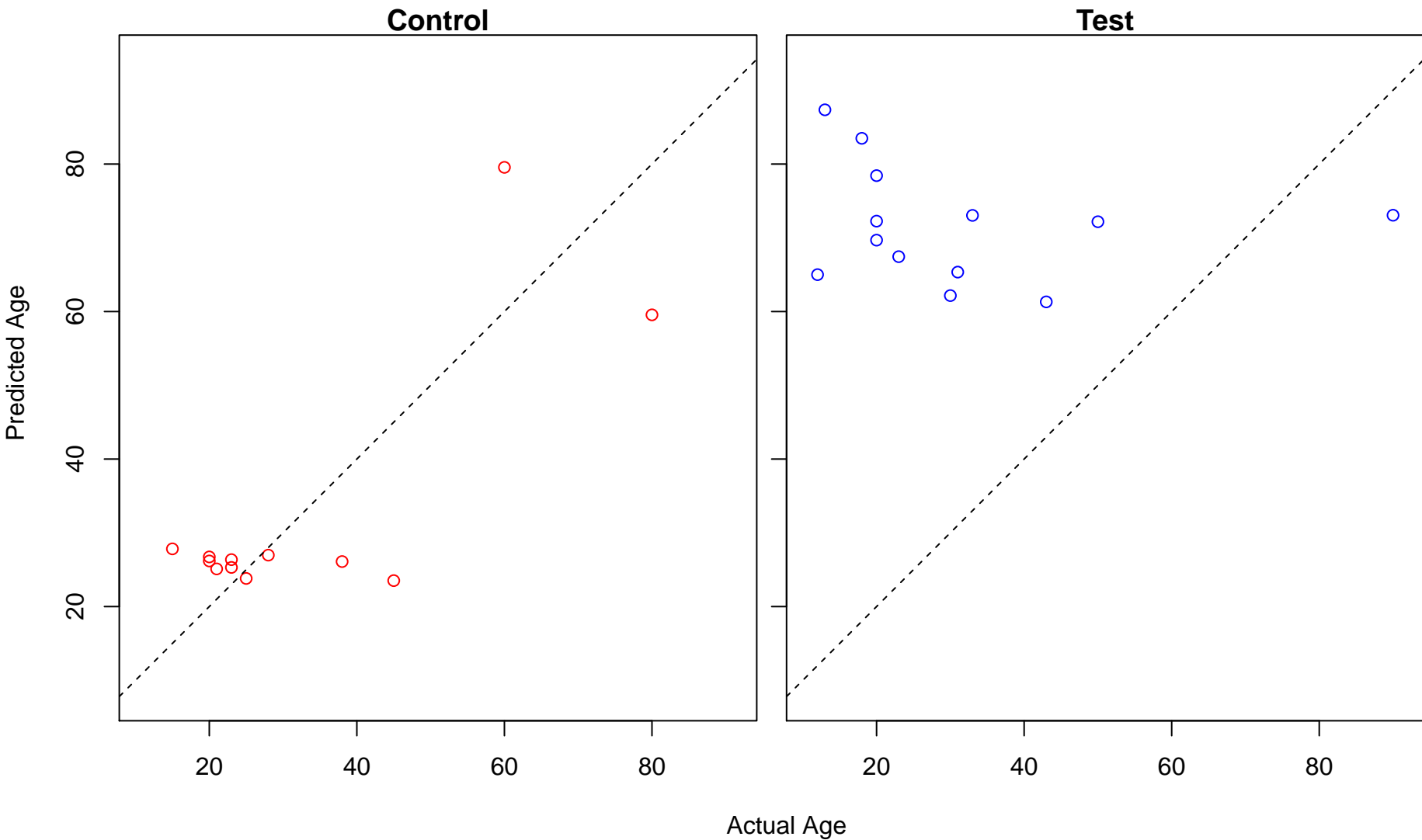
peptidyl-diphthamide biosynthetic process from peptidyl-histidine (Score: 6.223212)



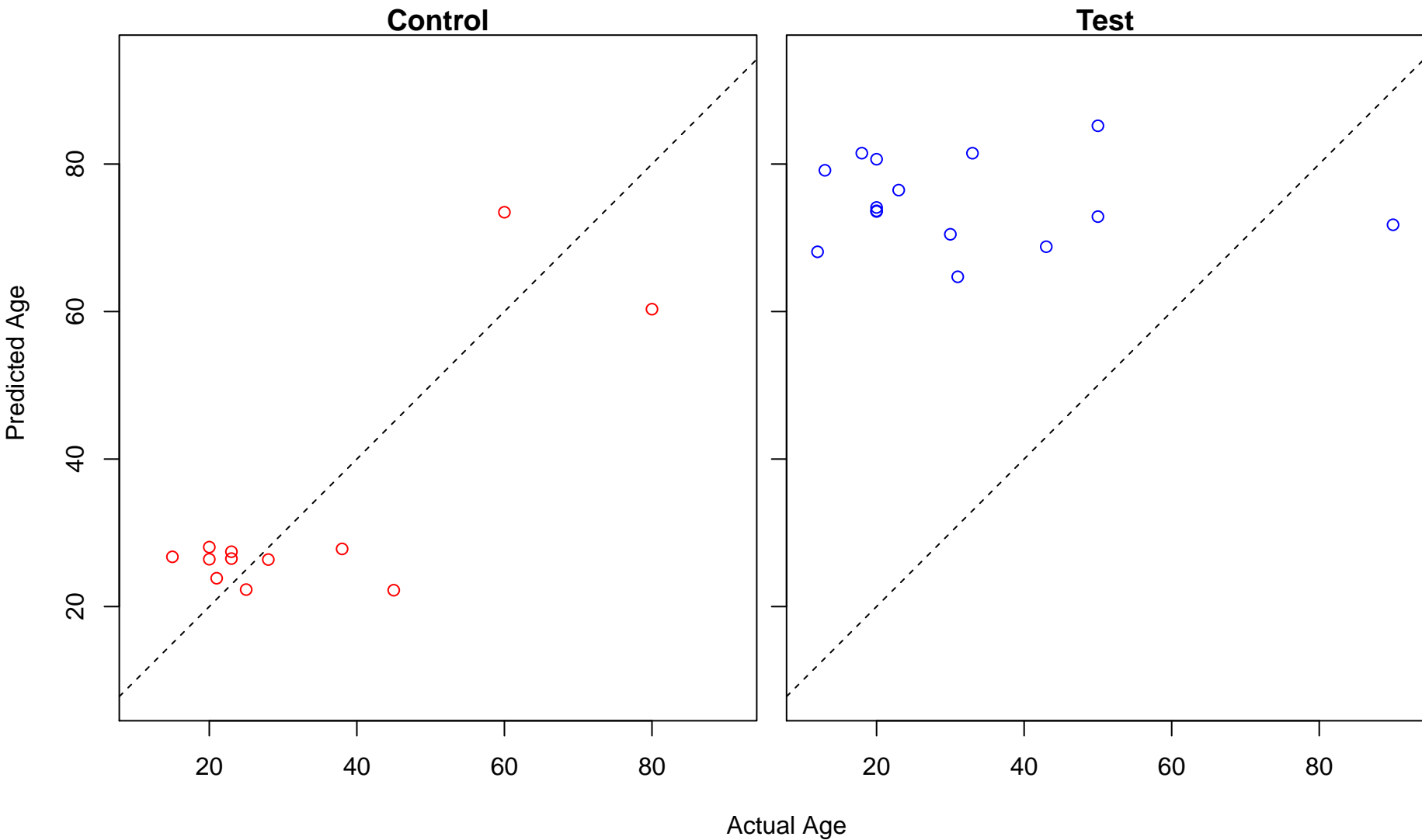
negative regulation of ligase activity (Score: 6.223166)



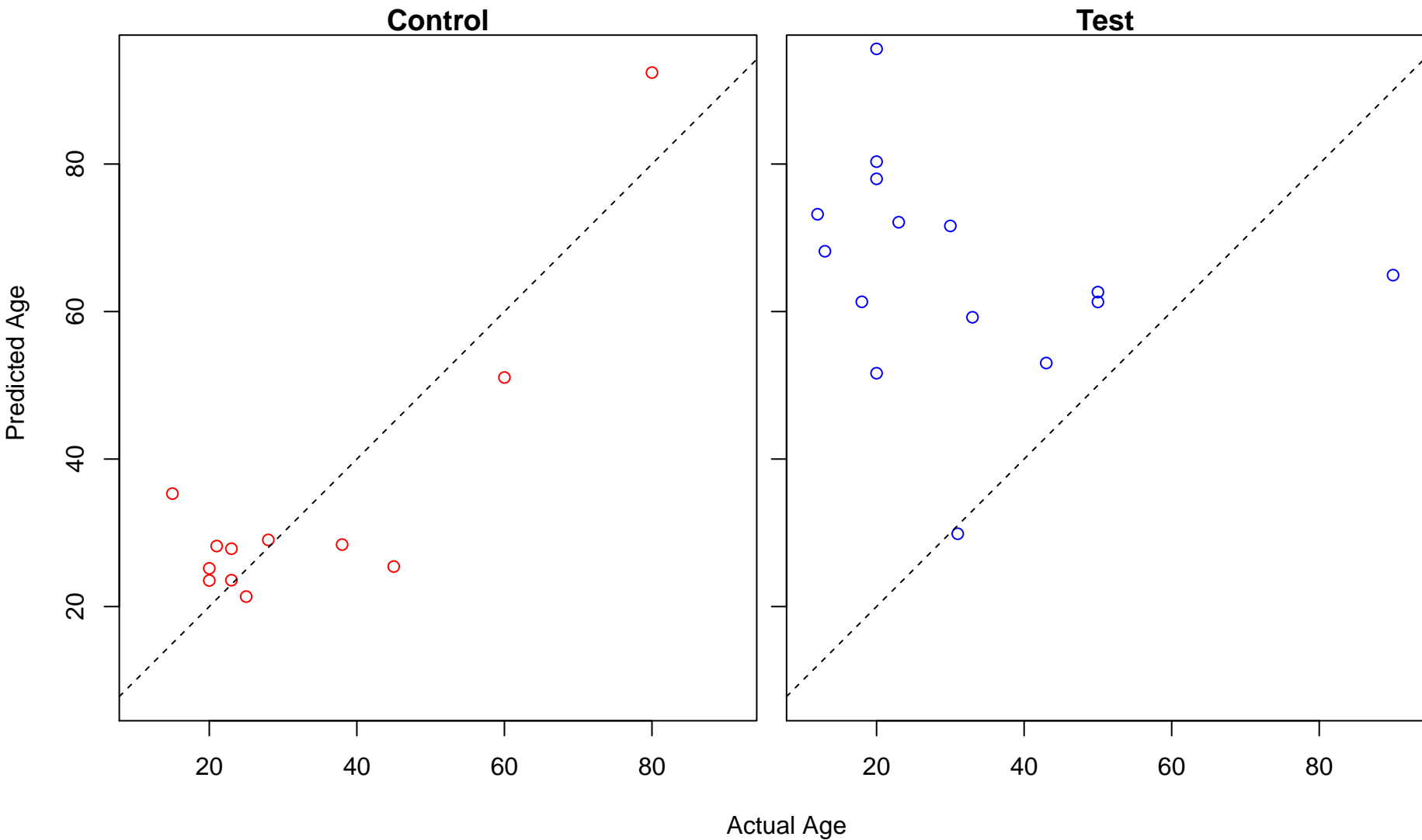
negative regulation of ubiquitin–protein transferase activity (Score: 6.223166)



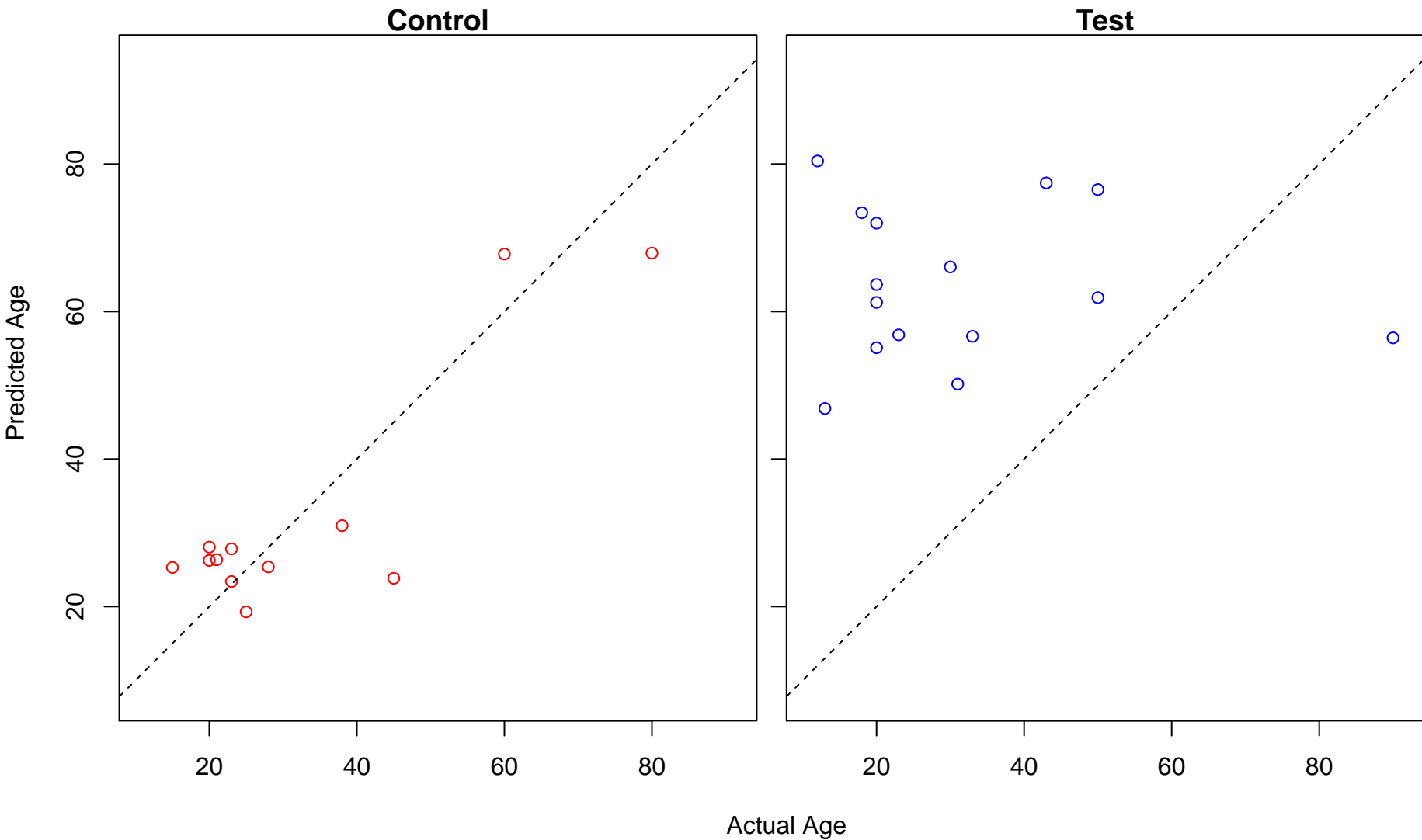
stem cell proliferation (Score: 6.223163)



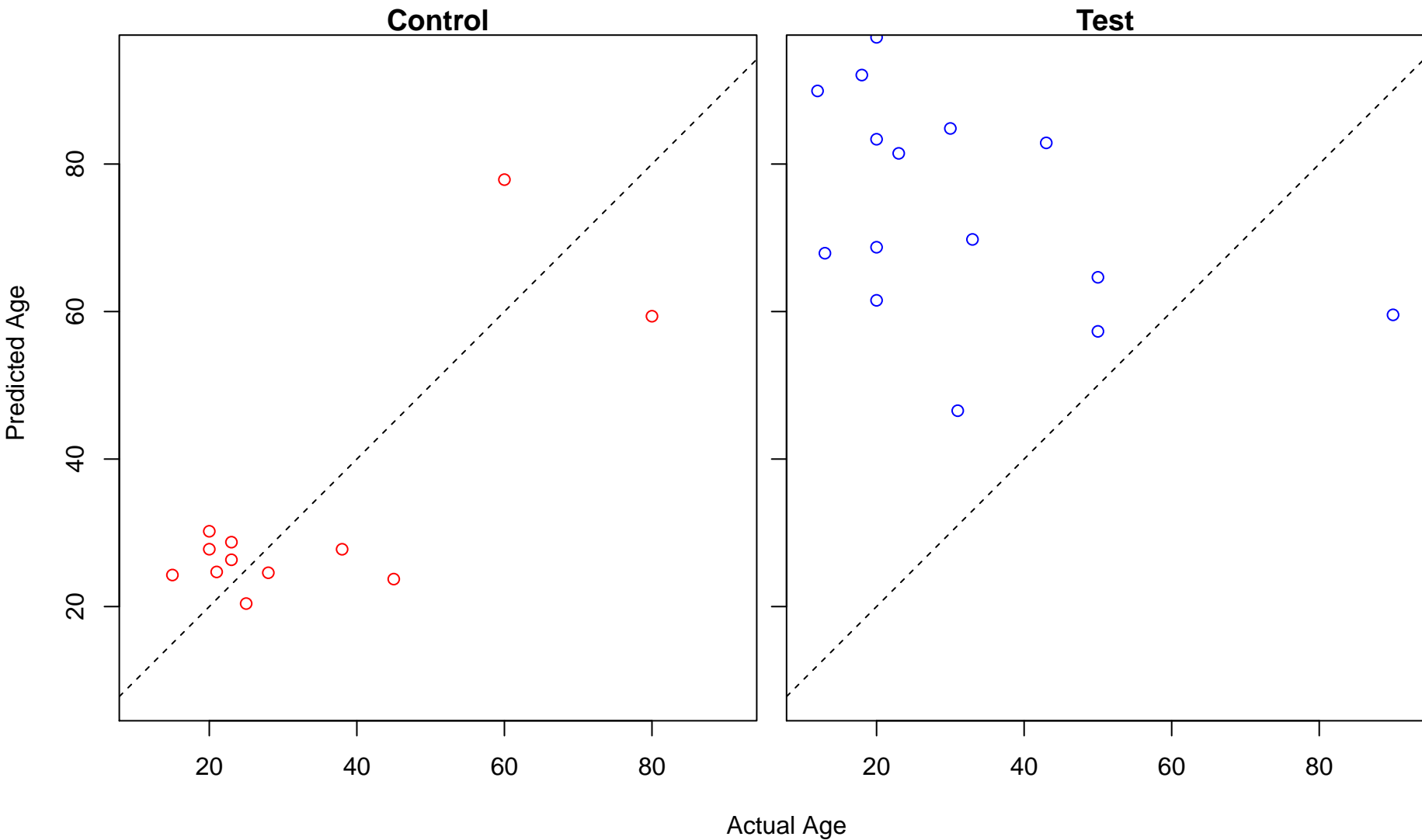
action potential (Score: 6.223064)



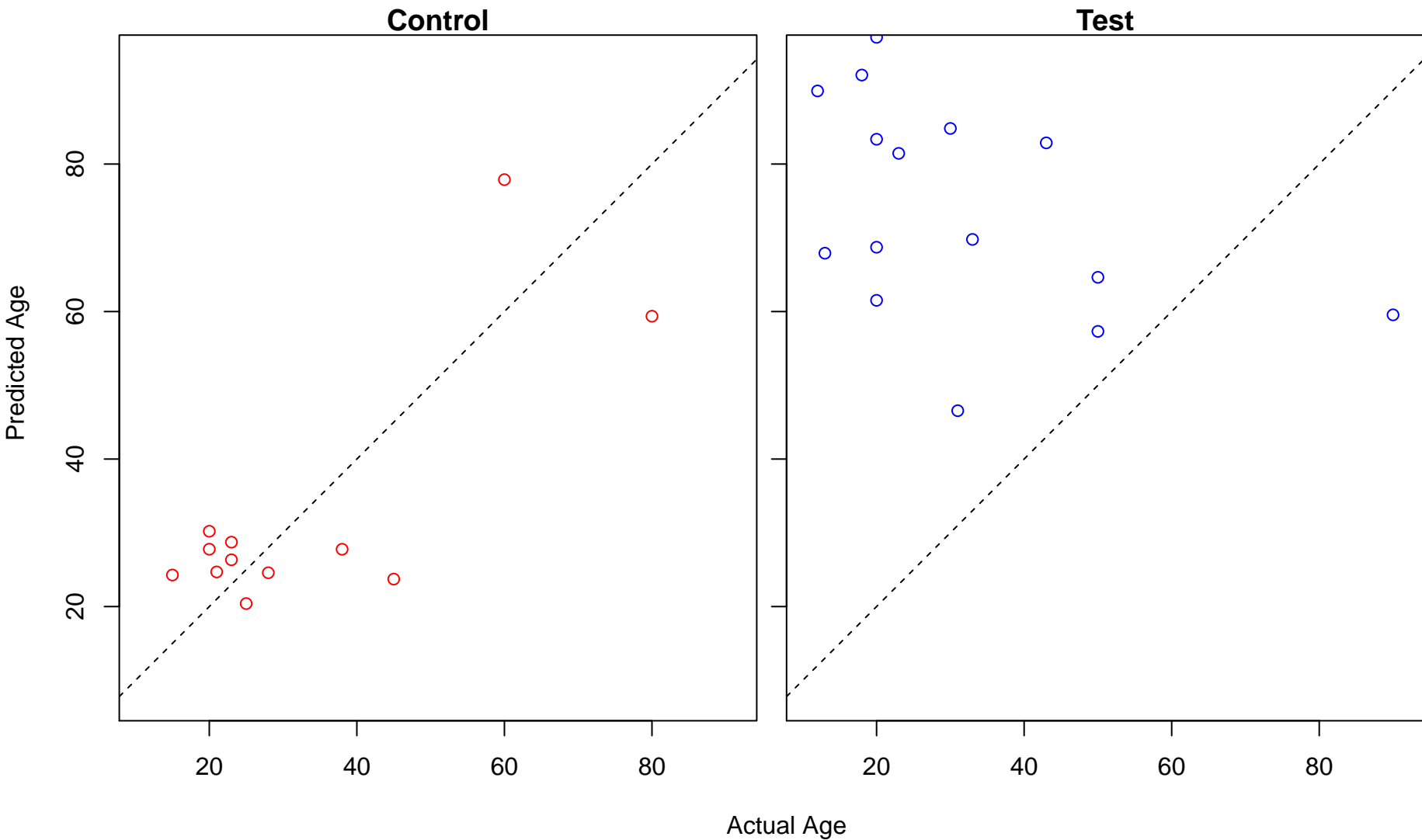
nonribosomal peptide biosynthetic process (Score: 6.222579)



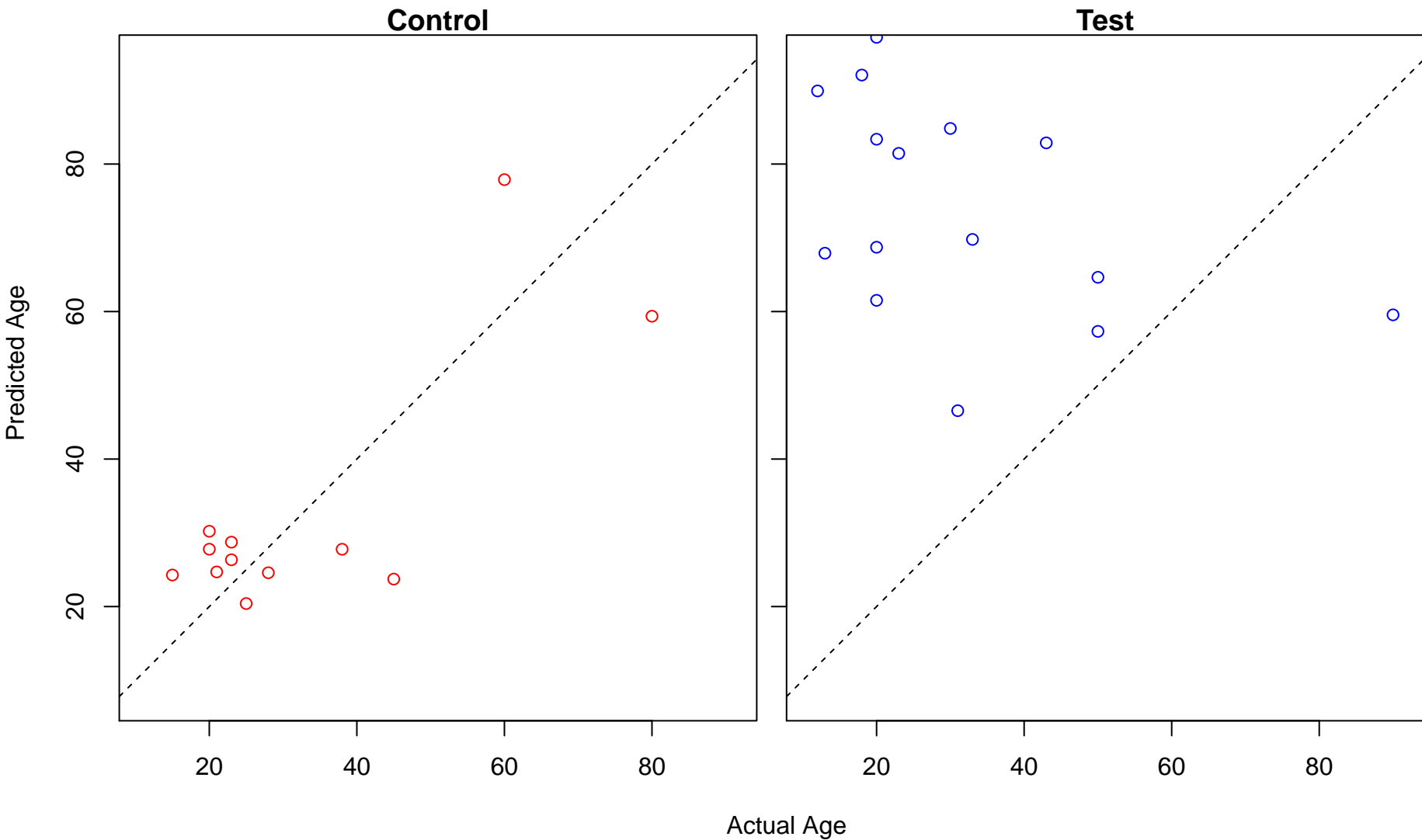
regulation of glucocorticoid biosynthetic process (Score: 6.215782)



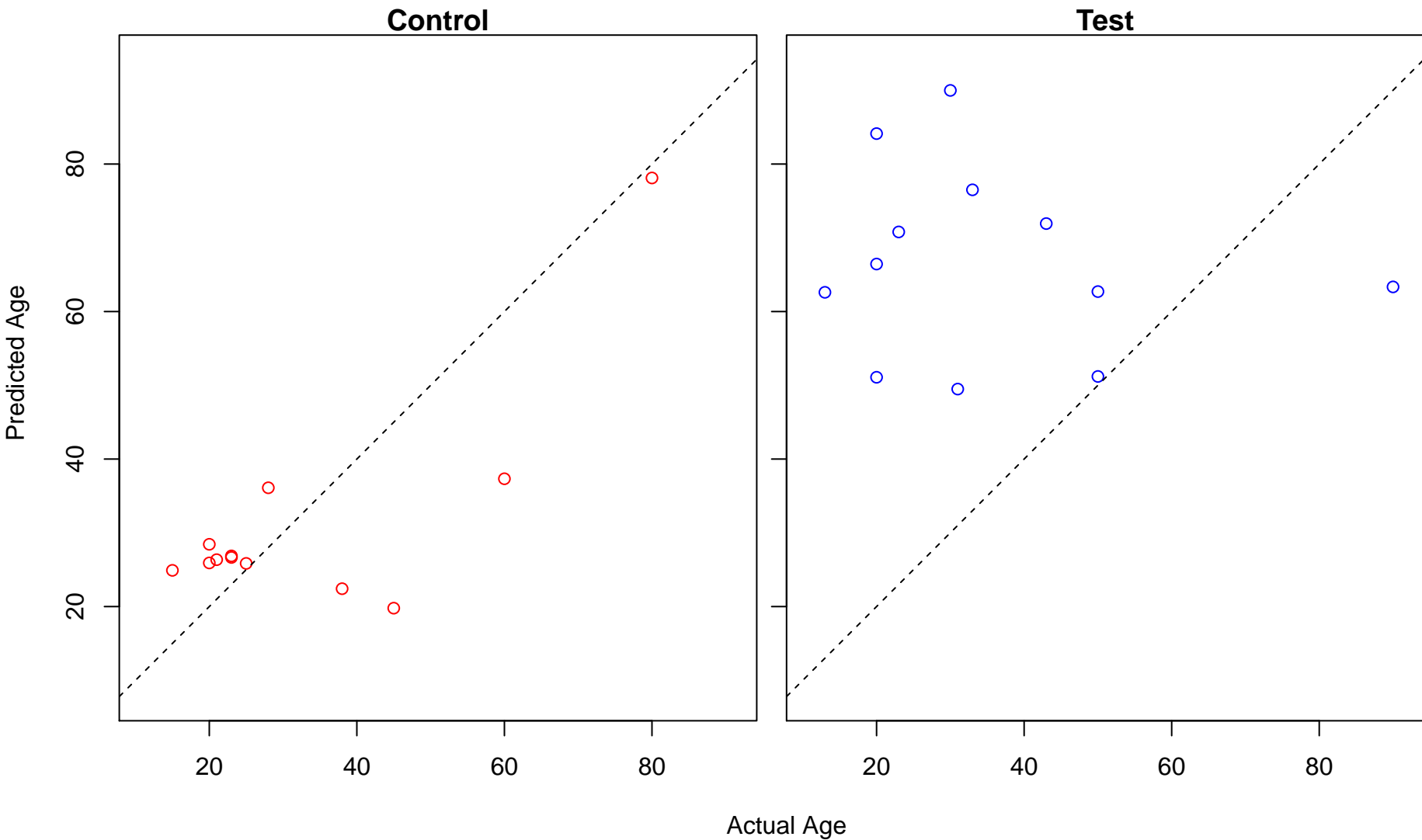
negative regulation of hormone biosynthetic process (Score: 6.215782)



regulation of cortisol biosynthetic process (Score: 6.215782)

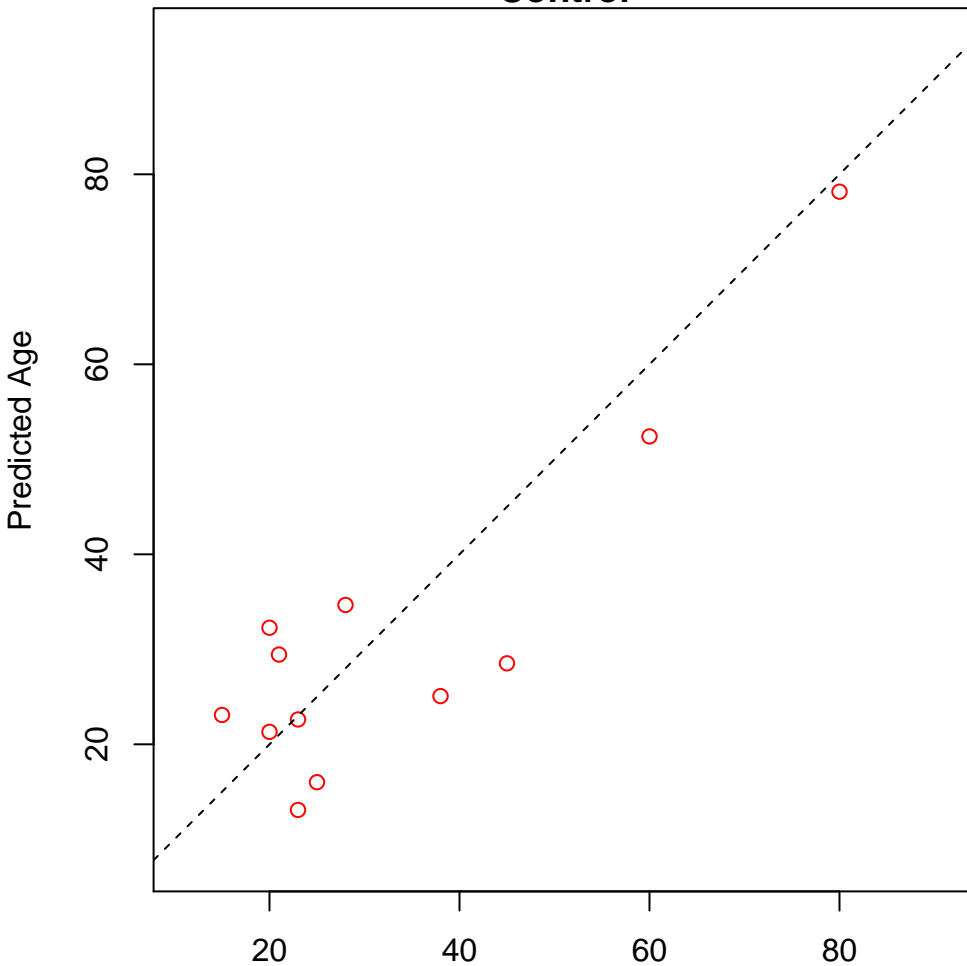


insulin secretion involved in cellular response to glucose stimulus (Score: 6.214479)

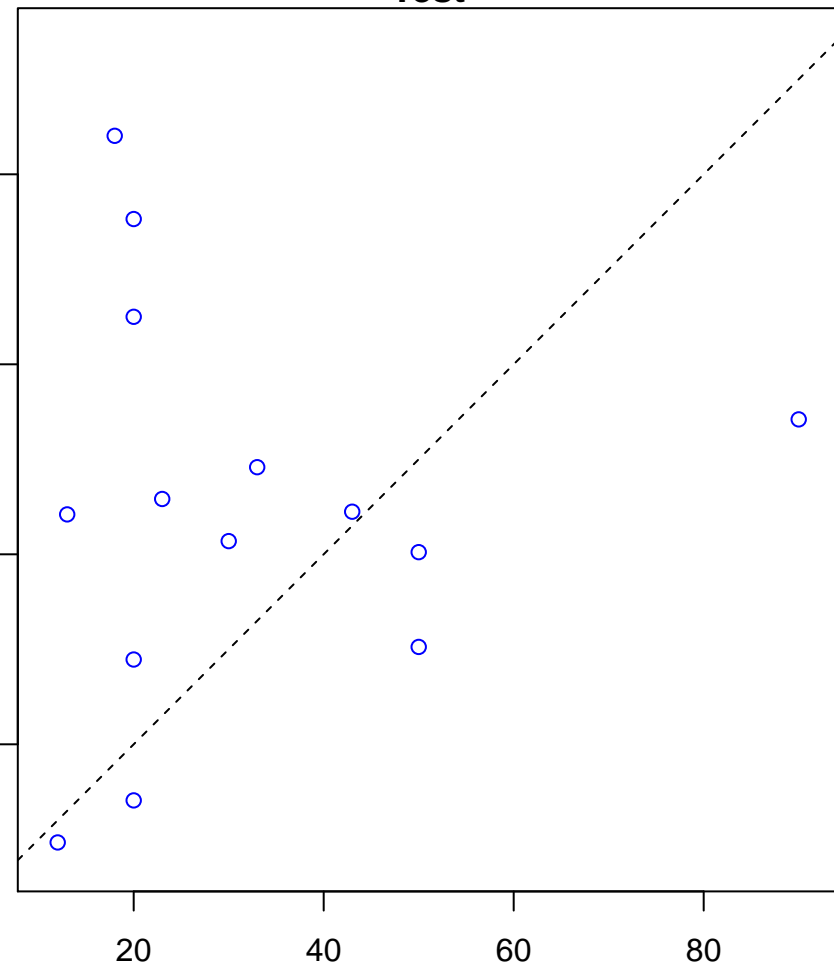


water-soluble vitamin metabolic process (Score: 6.214454)

Control

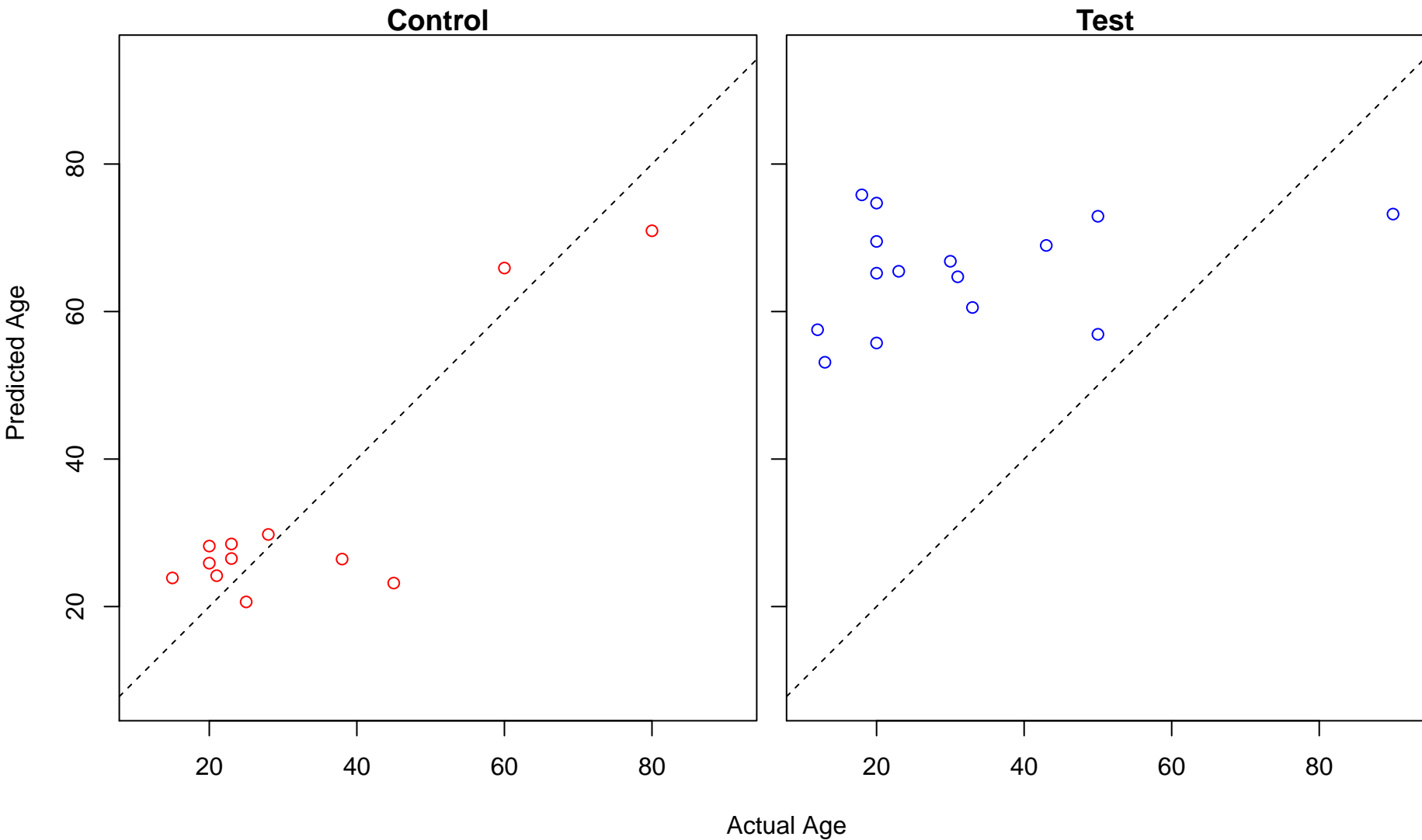


Test

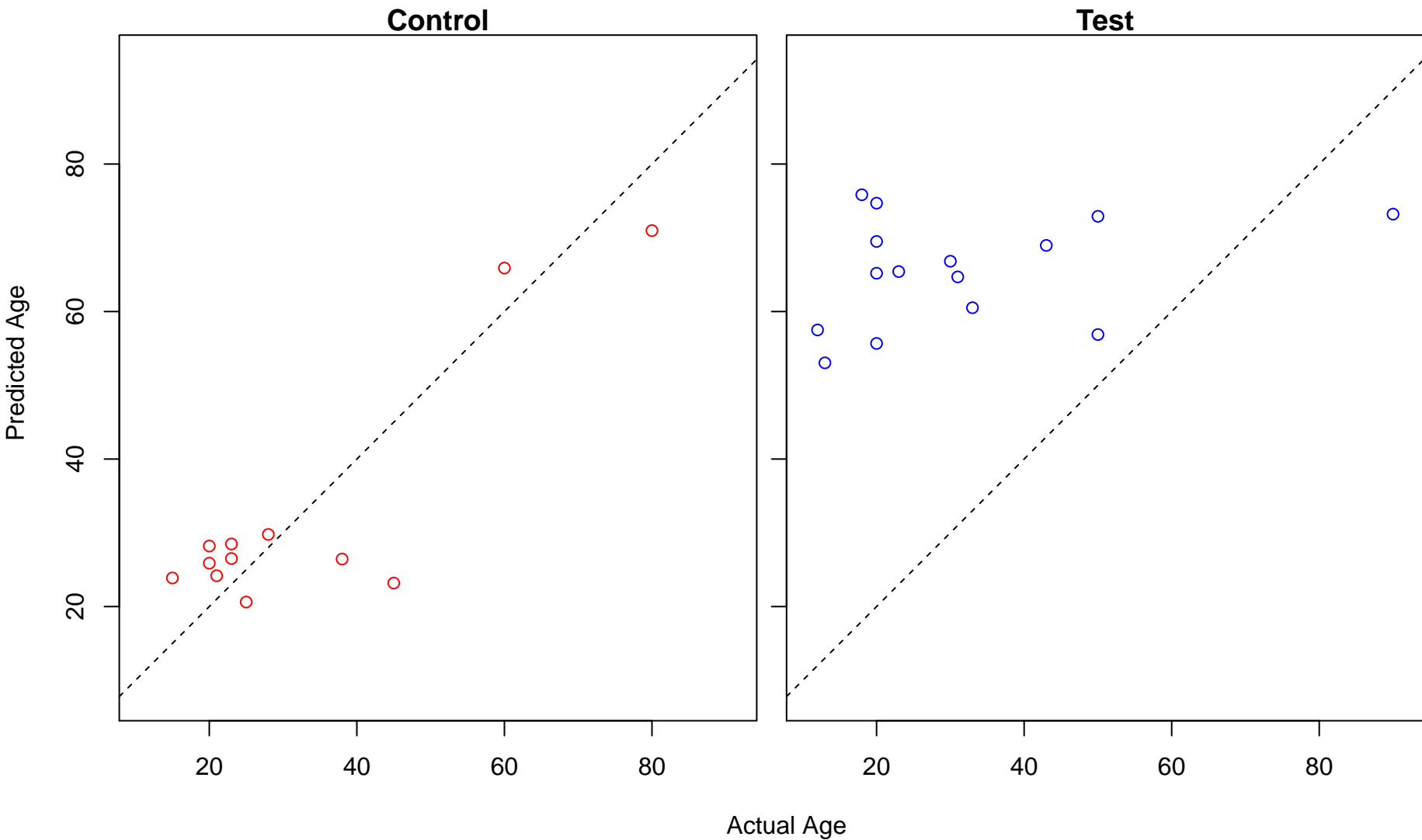


Actual Age

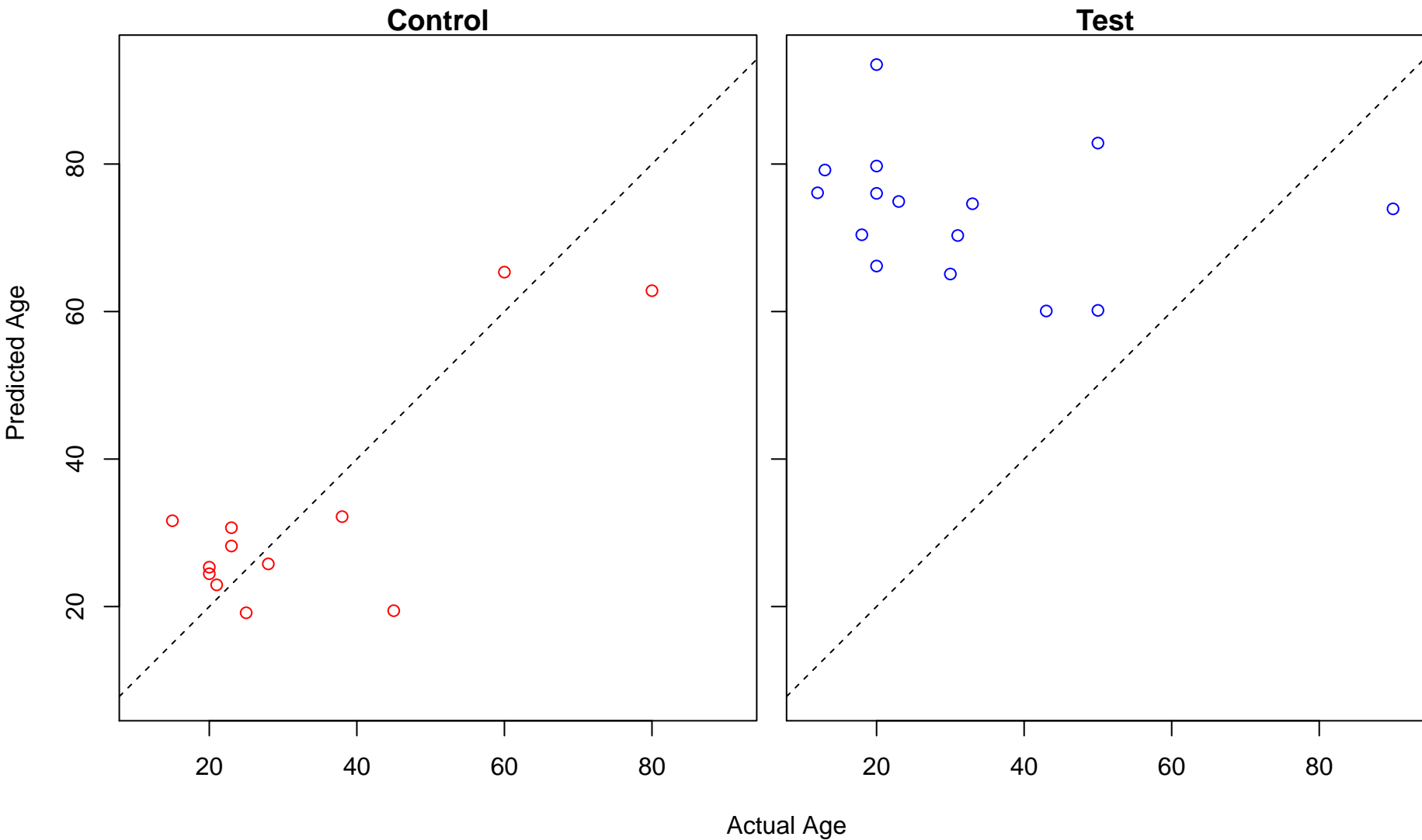
positive regulation of lymphocyte differentiation (Score: 6.212247)



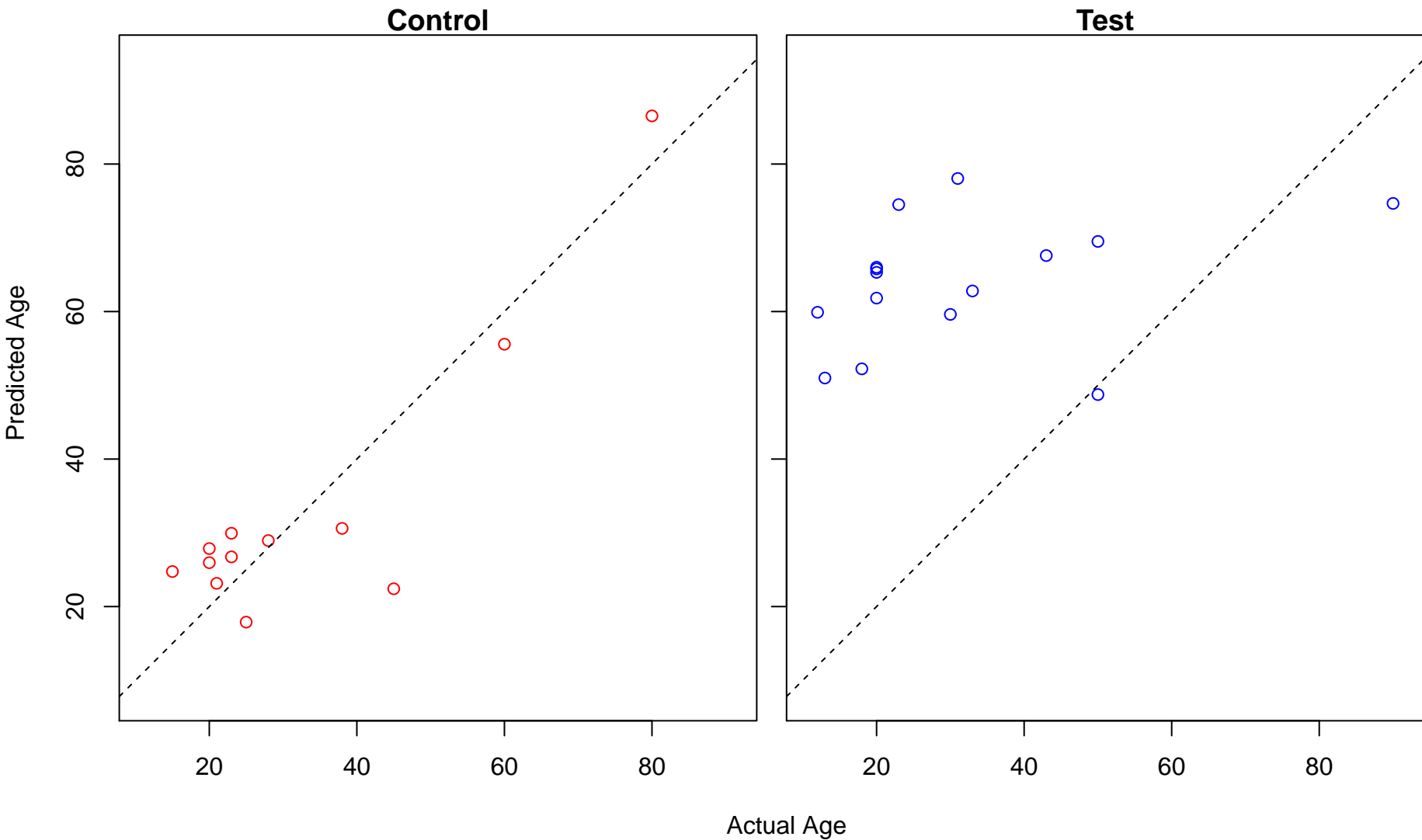
positive regulation of T cell differentiation (Score: 6.210689)



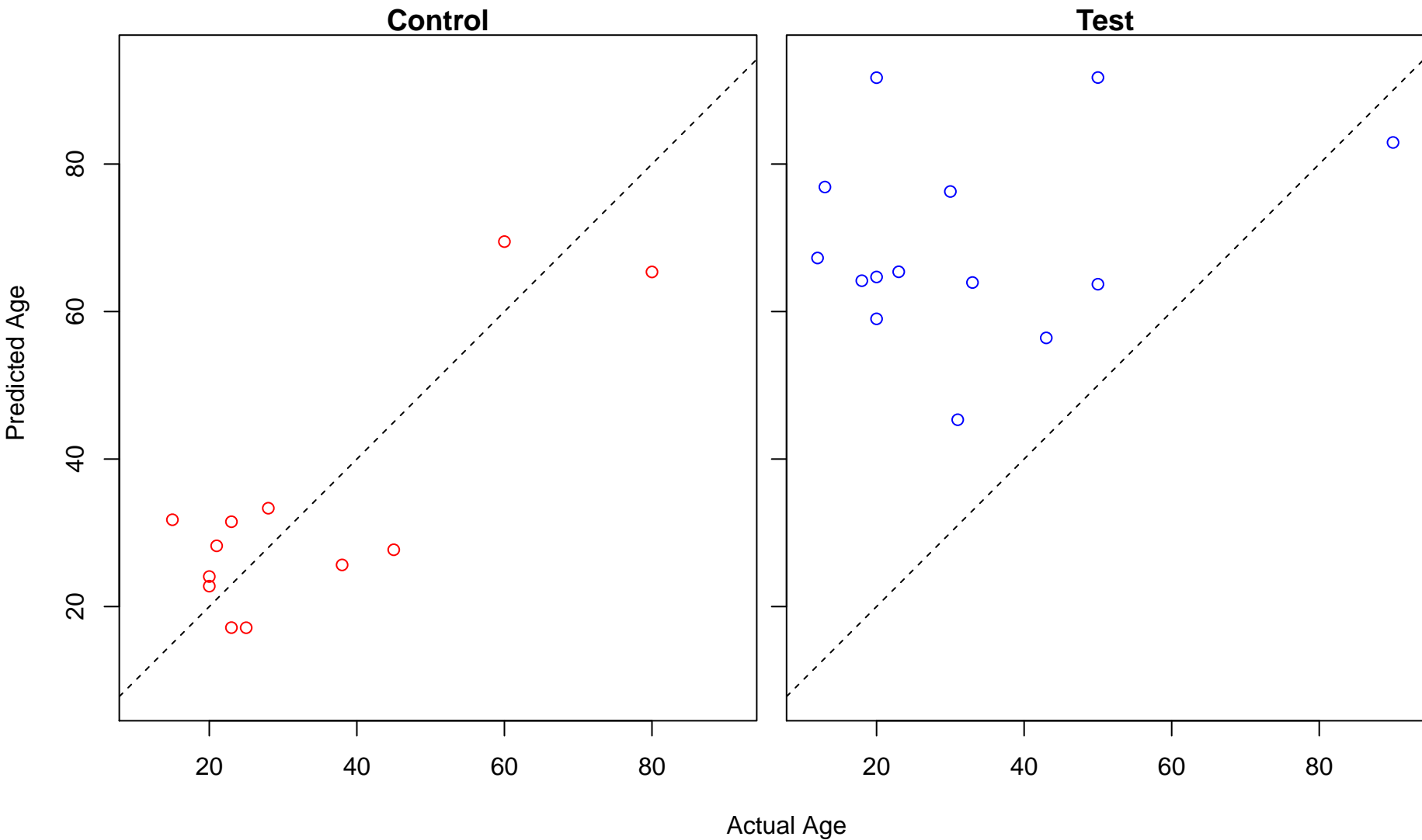
C-5 methylation of cytosine (Score: 6.209920)



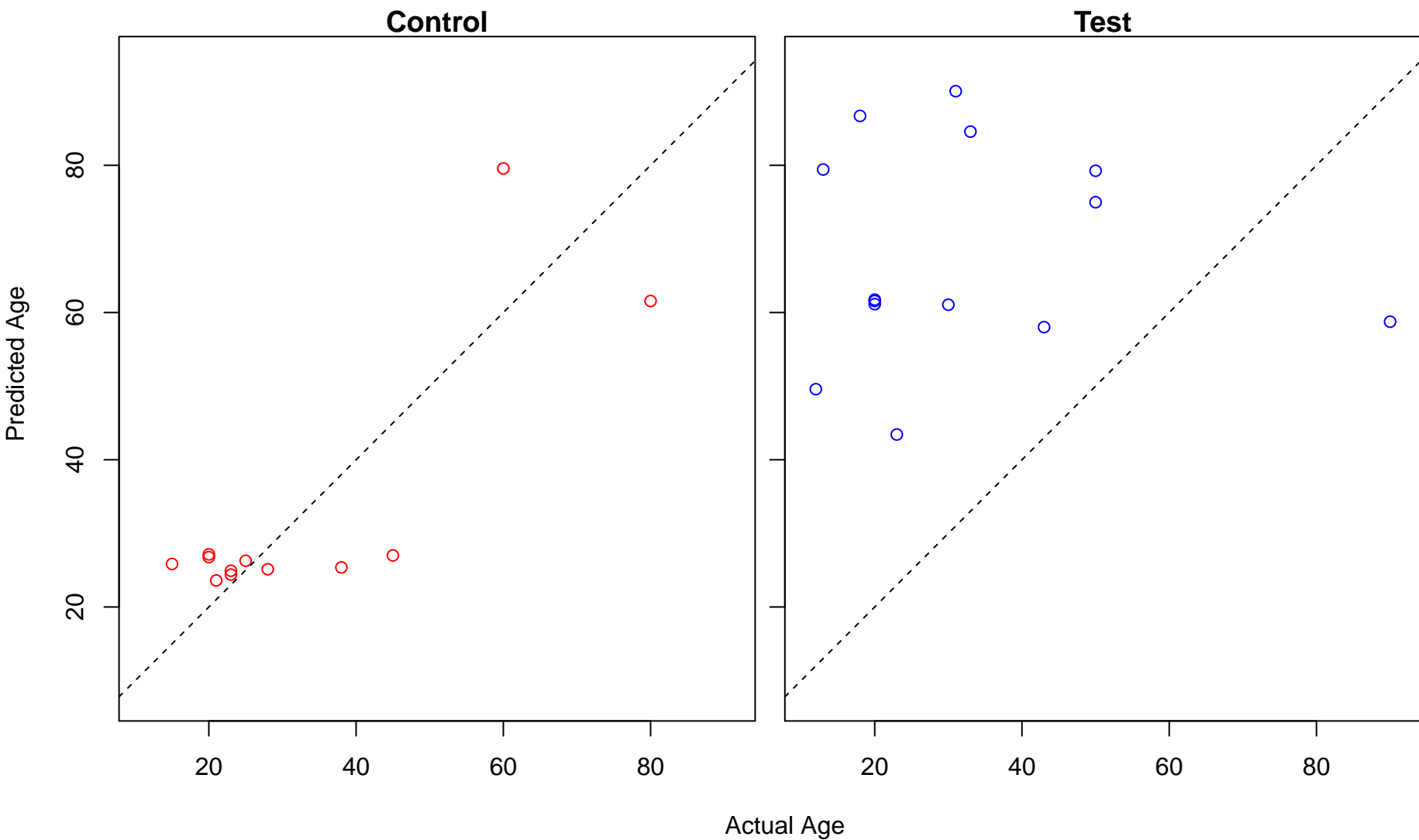
cilium morphogenesis (Score: 6.208542)



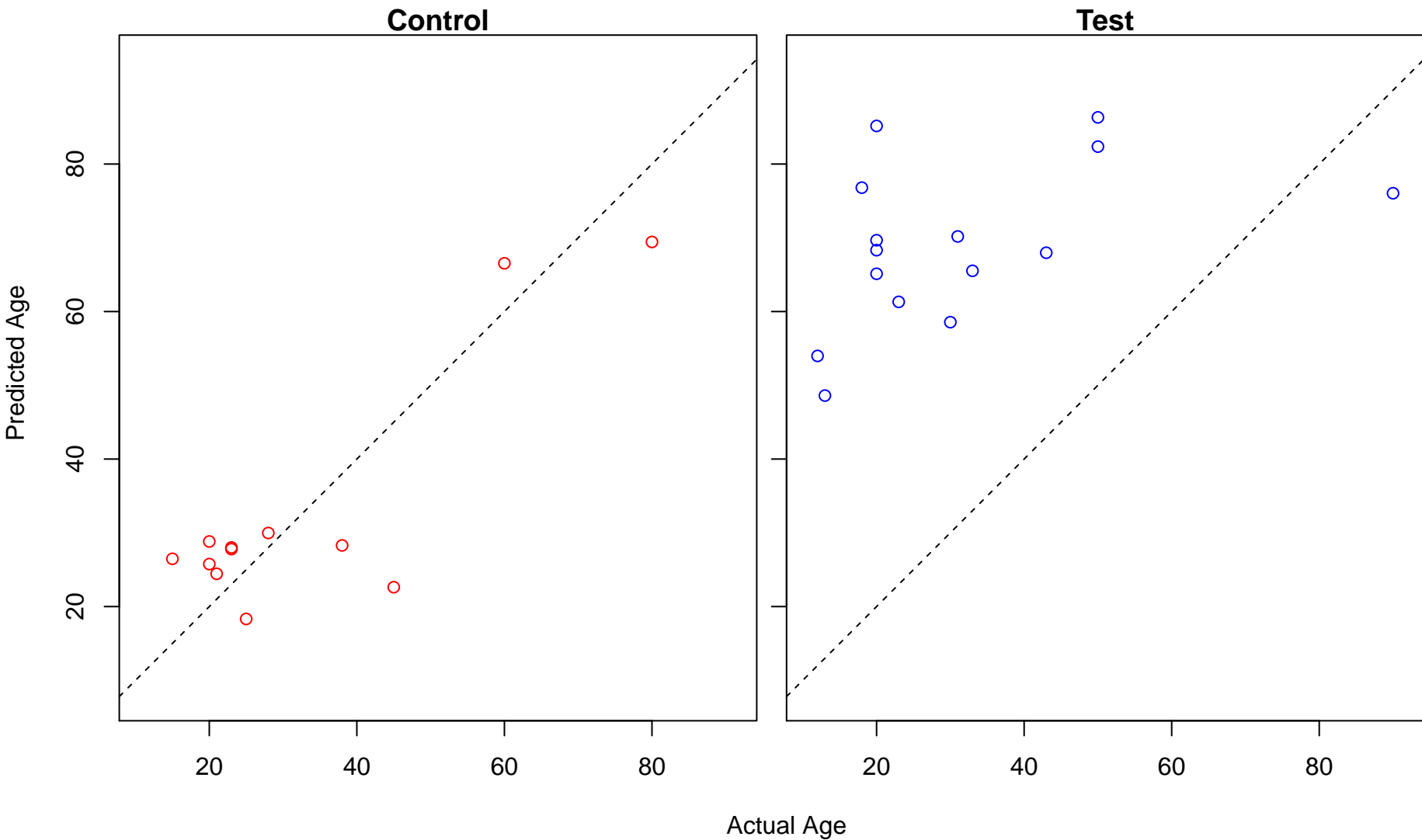
connective tissue development (Score: 6.208081)



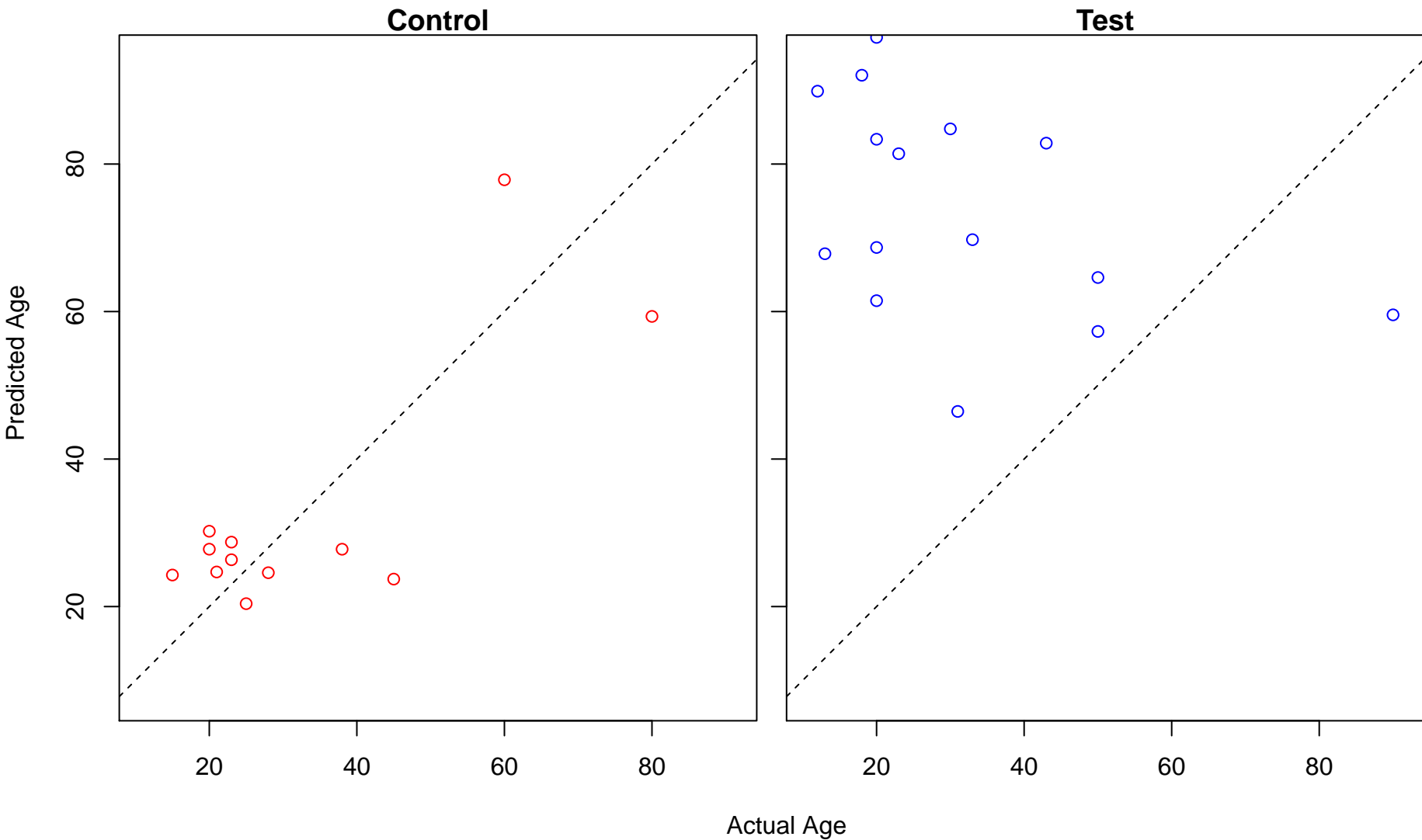
secretion by tissue (Score: 6.206752)



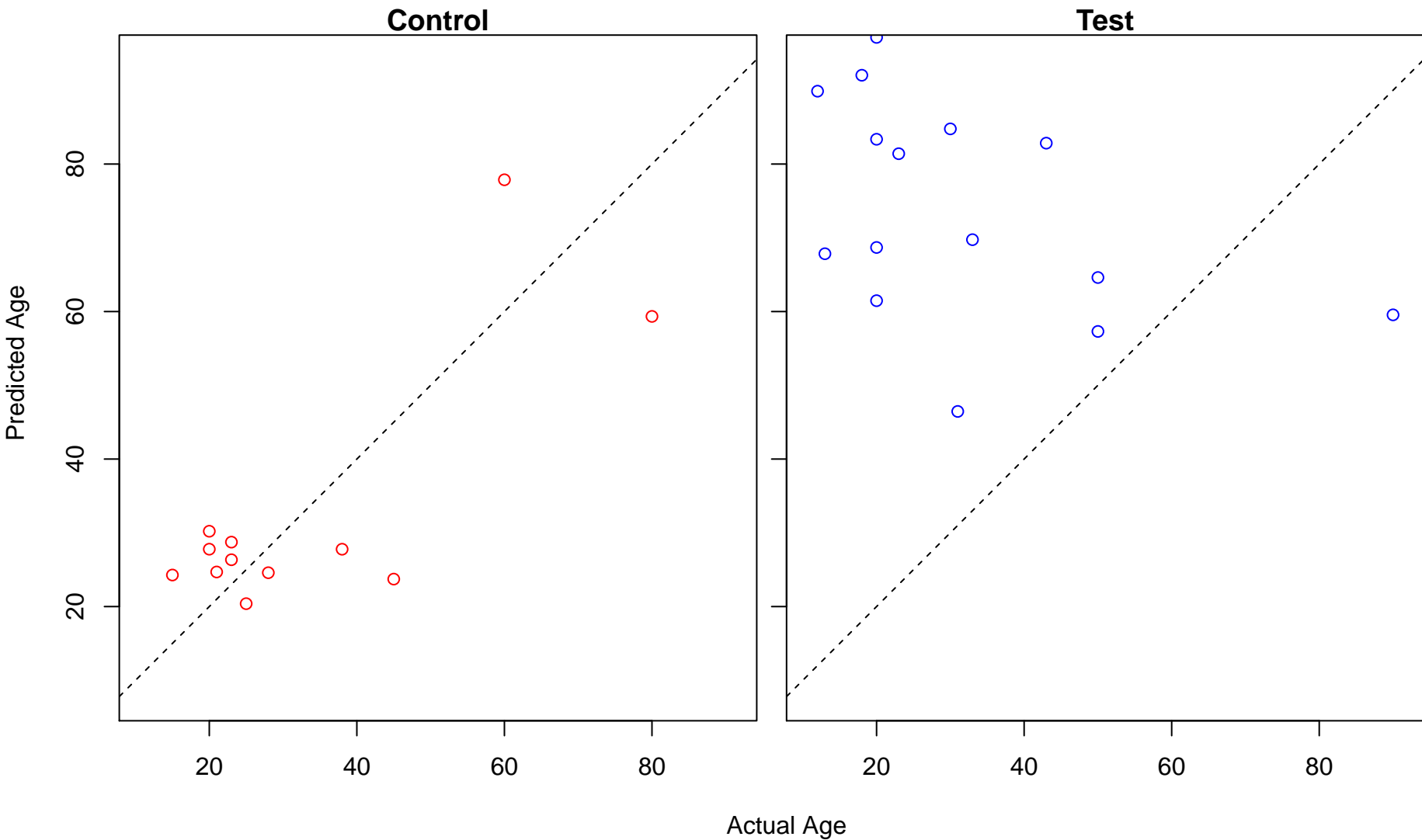
negative regulation of leukocyte cell-cell adhesion (Score: 6.206273)



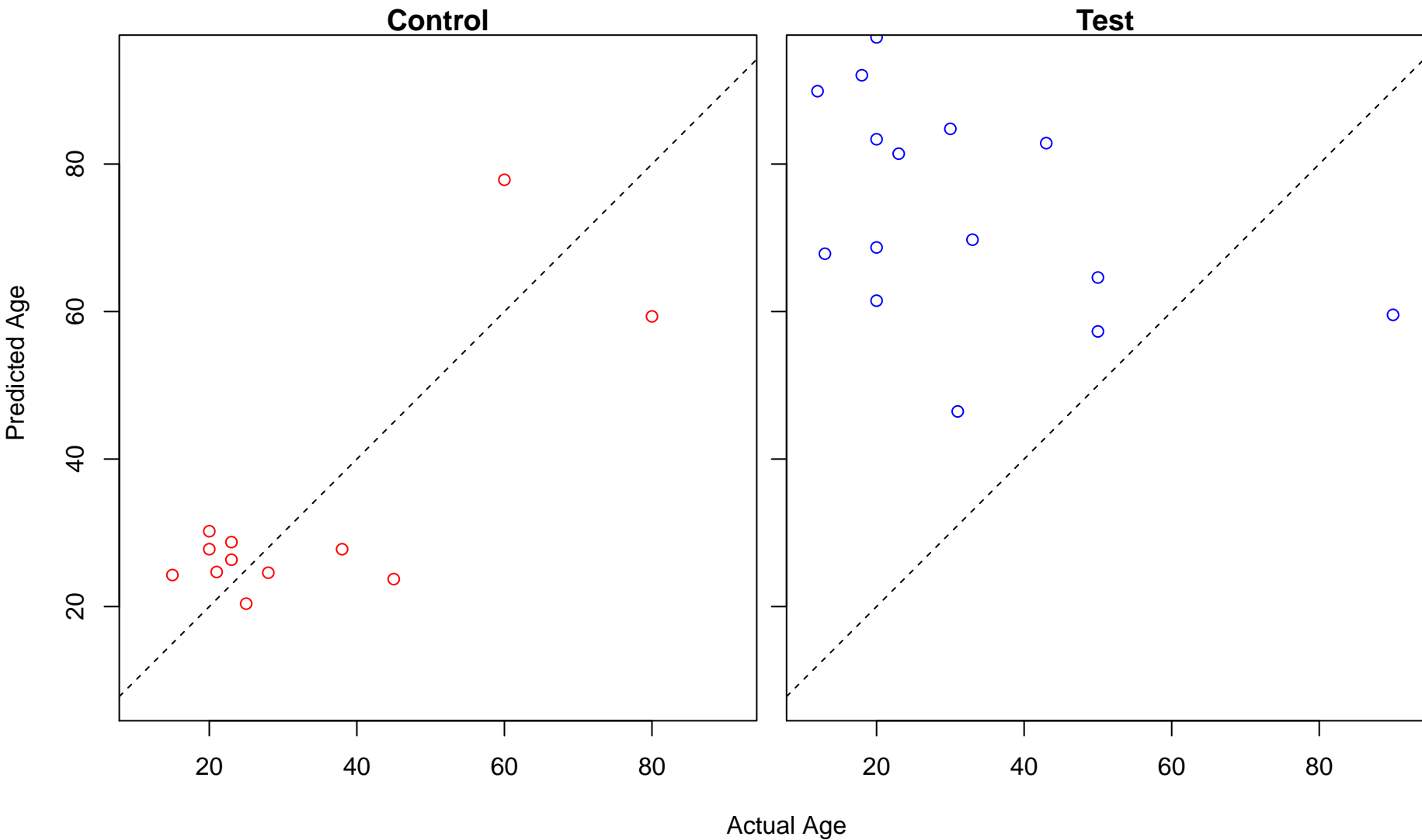
regulation of aldosterone metabolic process (Score: 6.206121)



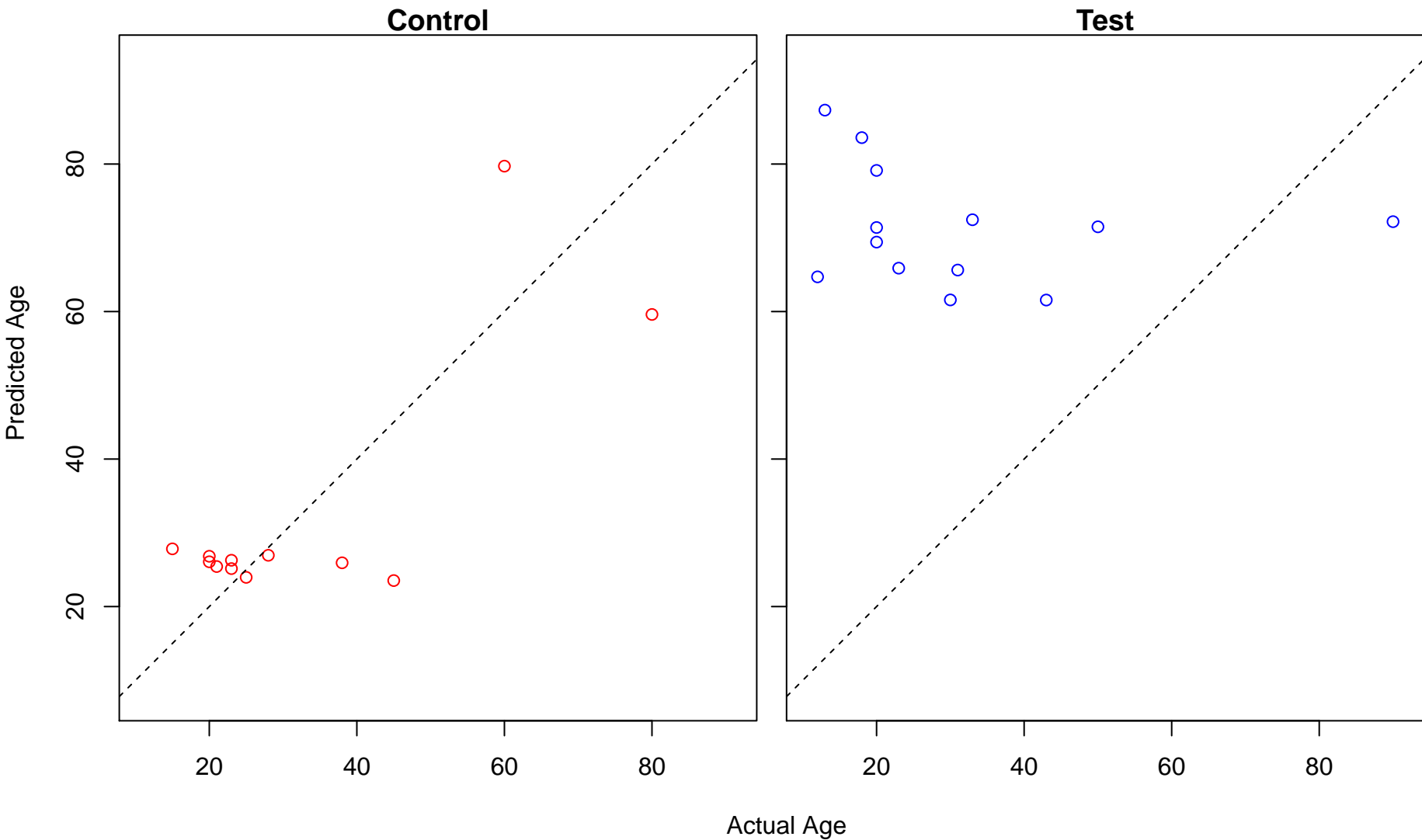
regulation of aldosterone biosynthetic process (Score: 6.206121)



regulation of steroid hormone biosynthetic process (Score: 6.206121)

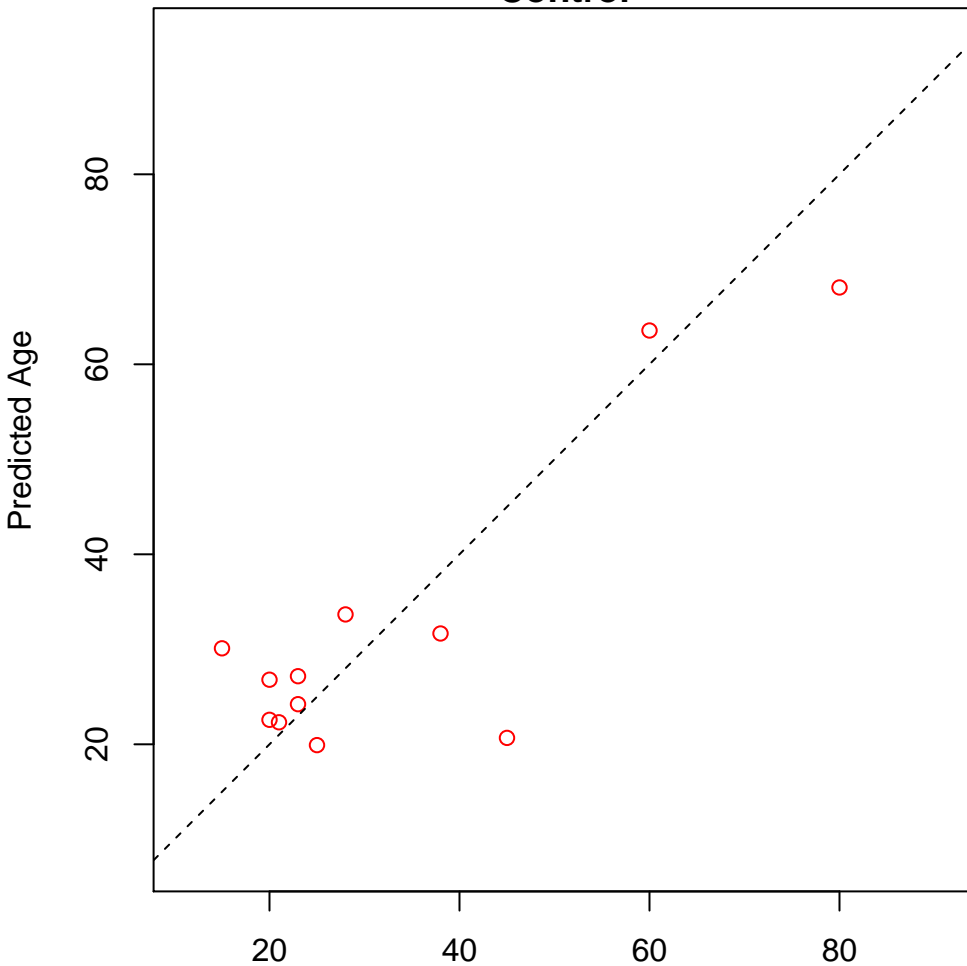


NIK/NF-kappaB signaling (Score: 6.206088)

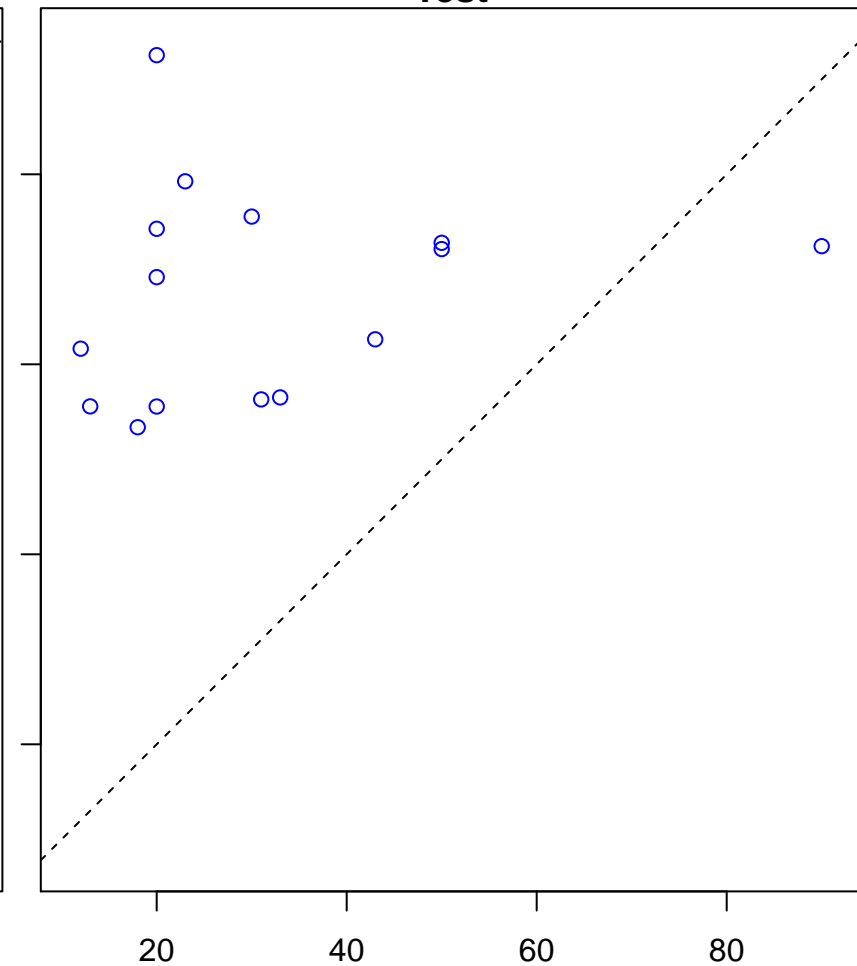


neurotransmitter biosynthetic process (Score: 6.205046)

Control

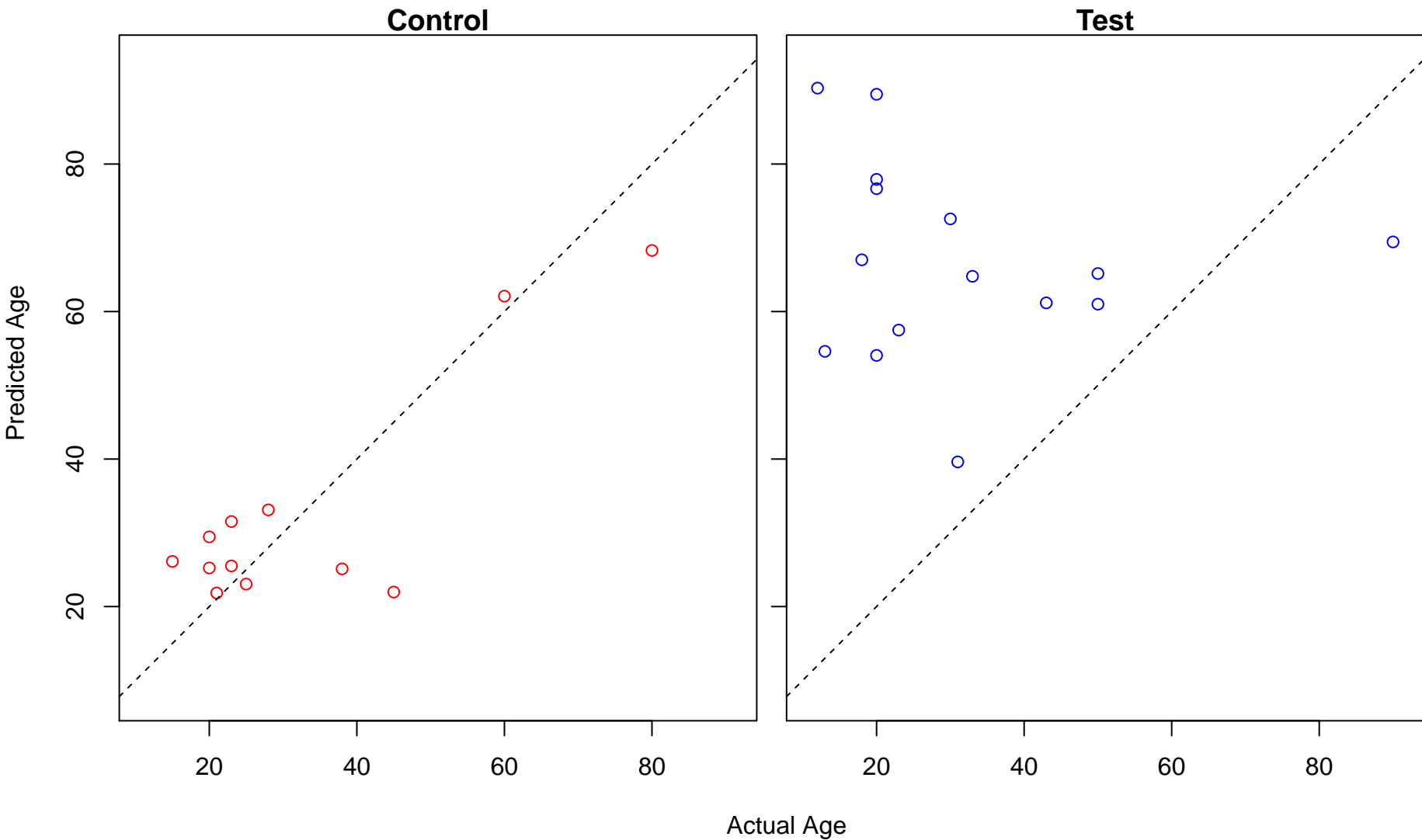


Test

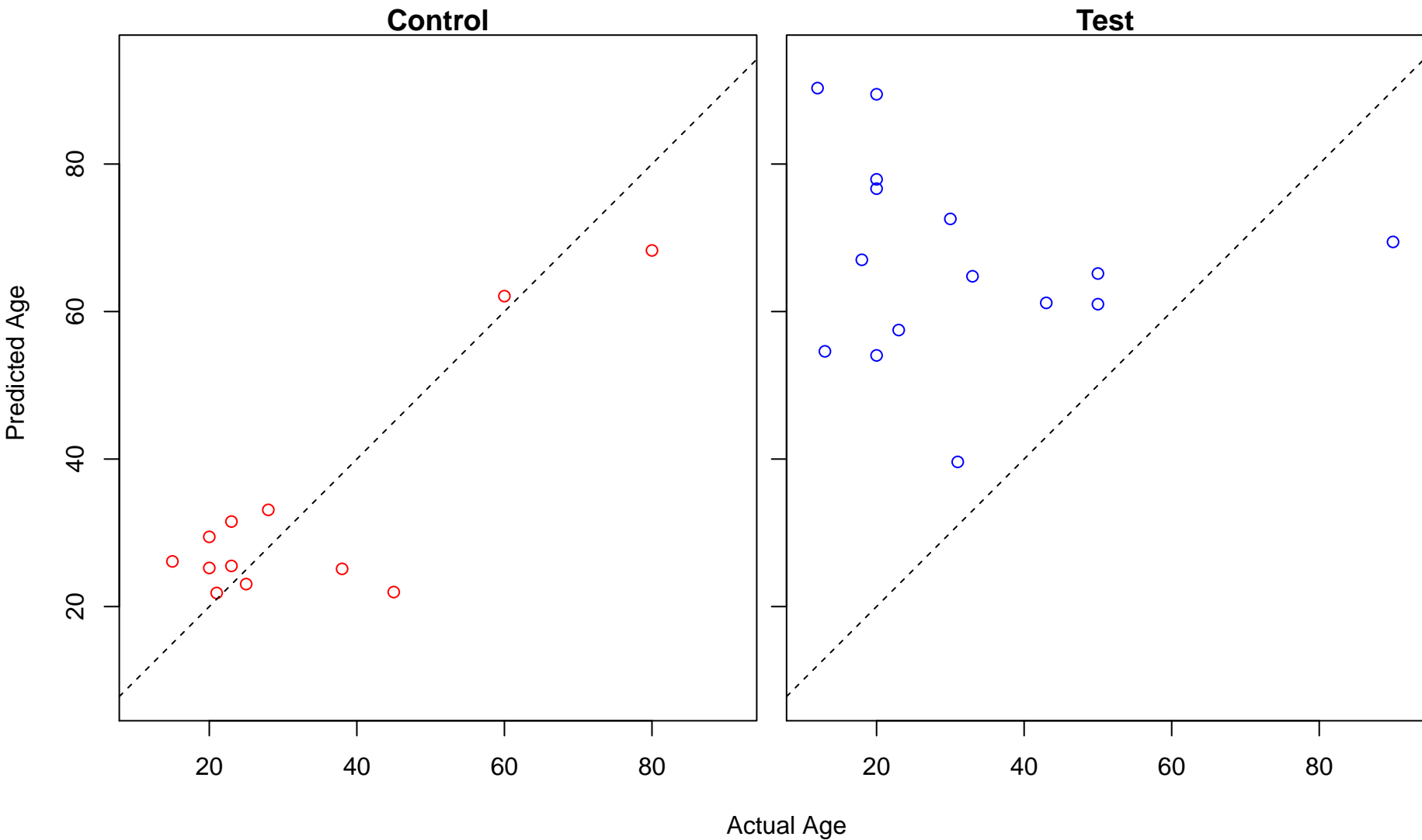


Actual Age

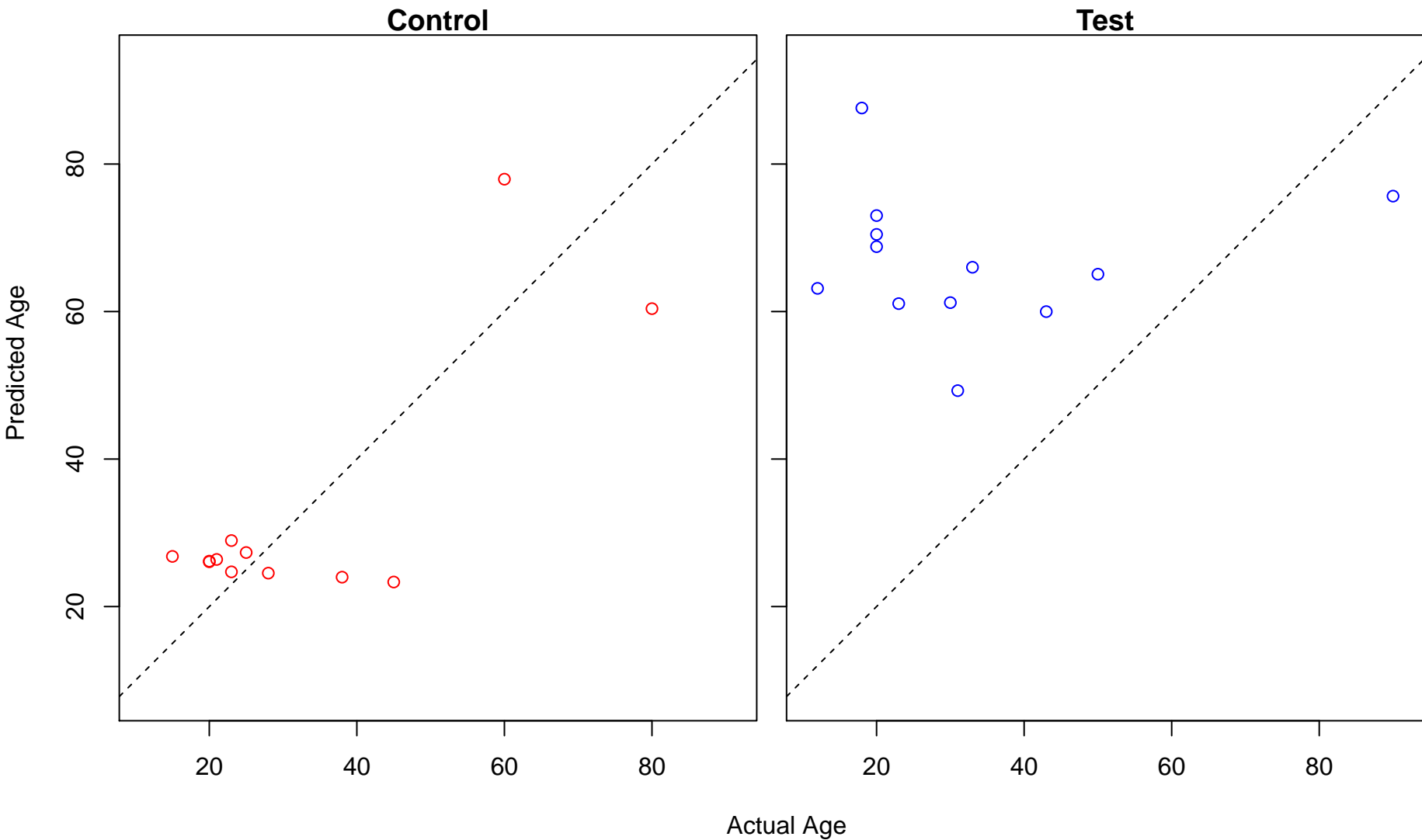
neuron projection regeneration (Score: 6.204936)



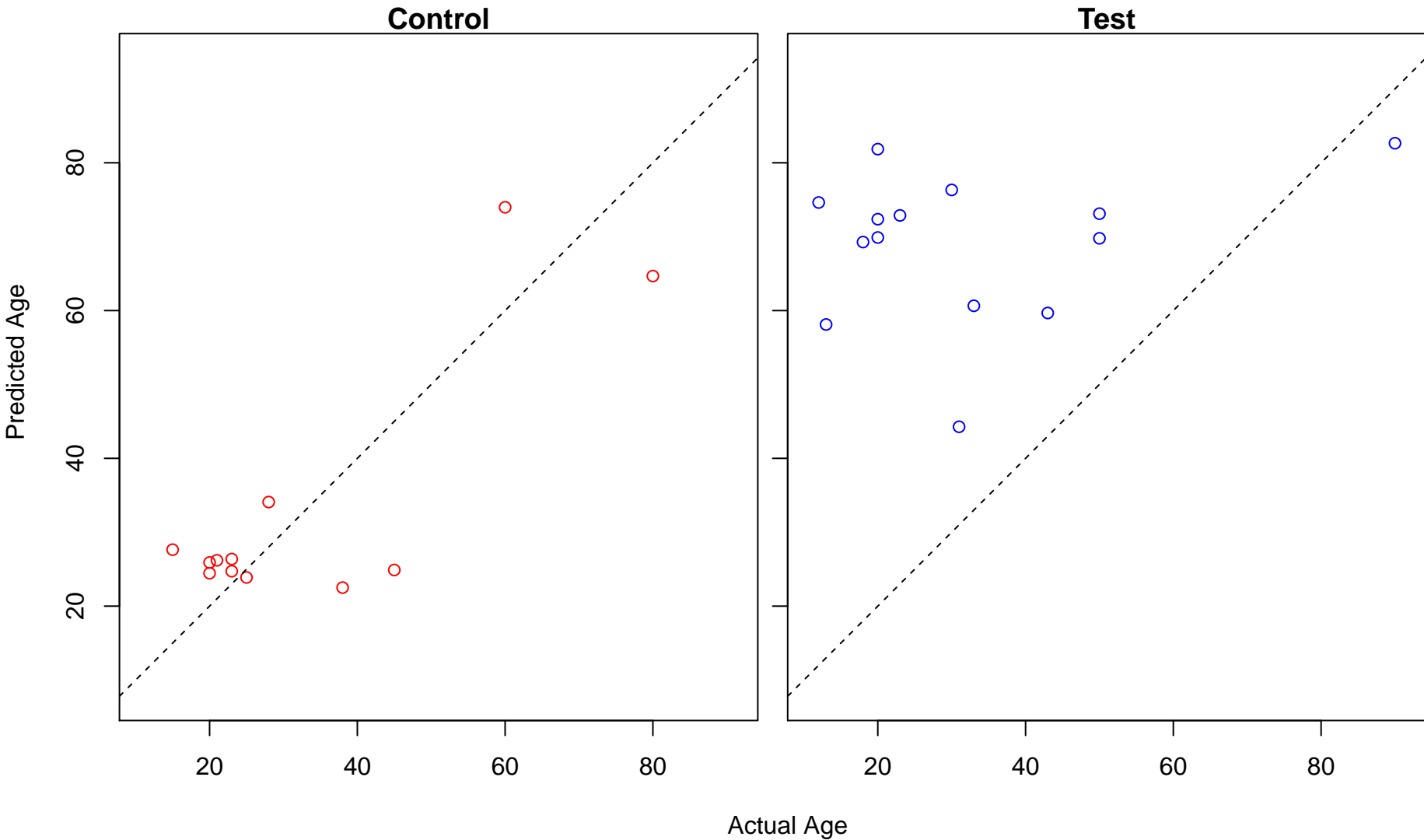
axon regeneration (Score: 6.204936)



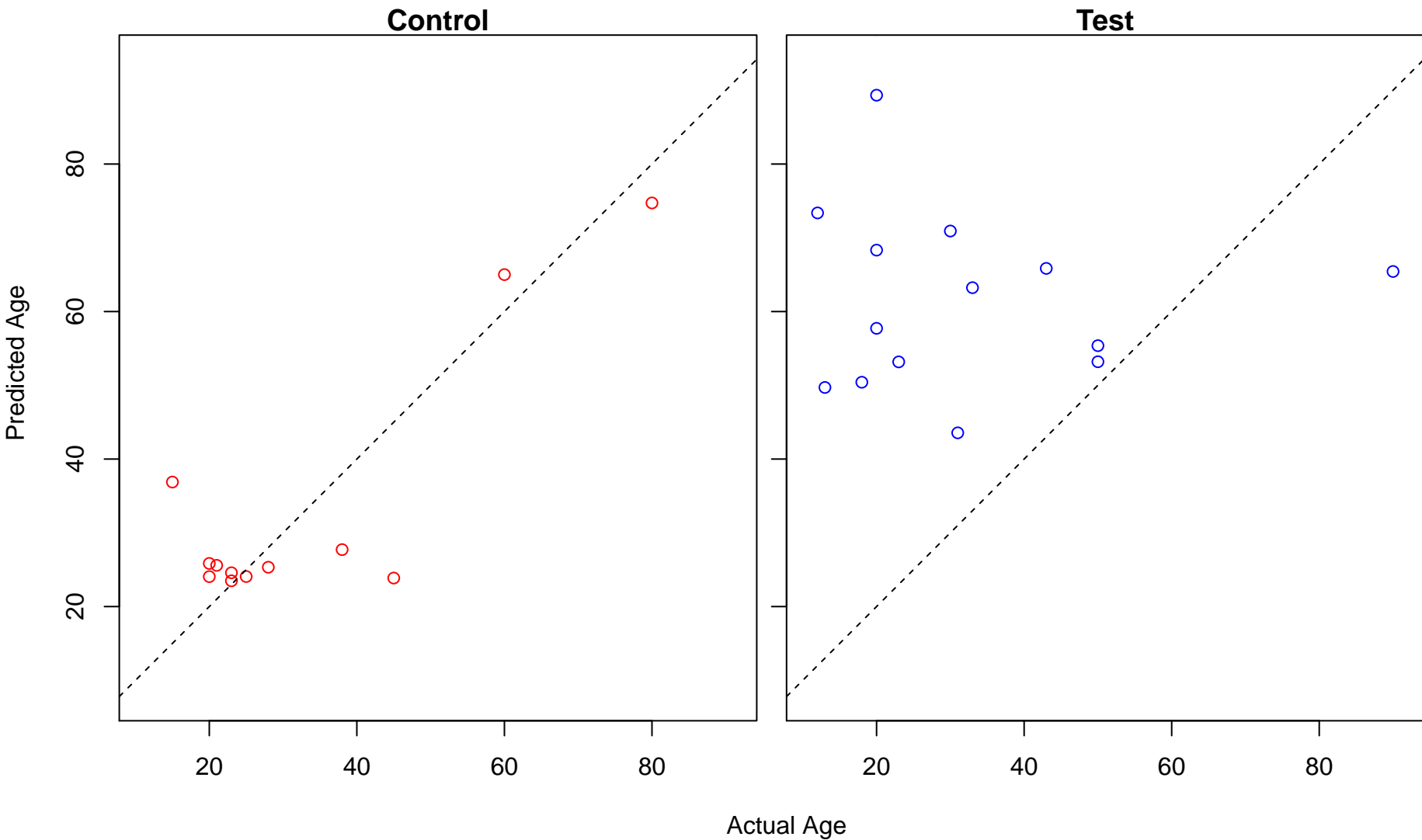
erythrocyte differentiation (Score: 6.204472)



termination of RNA polymerase I transcription (Score: 6.203449)

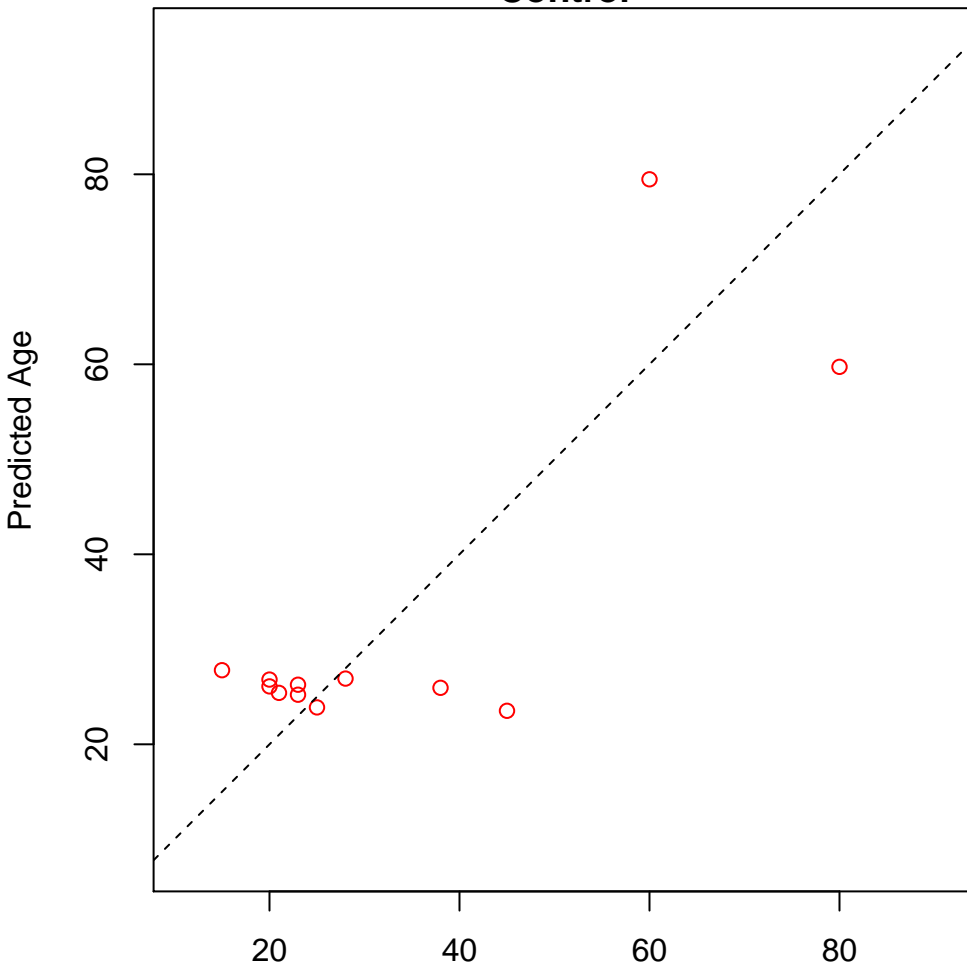


positive regulation of cytokine secretion (Score: 6.201284)

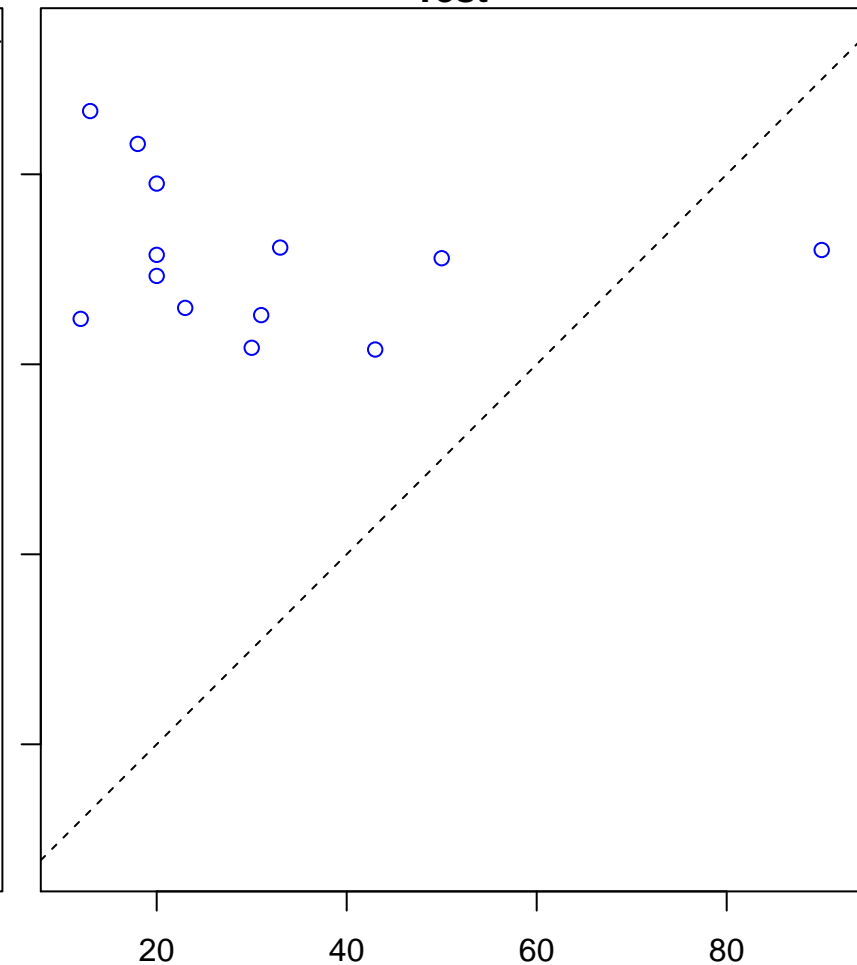


G1/S transition of mitotic cell cycle (Score: 6.198488)

Control



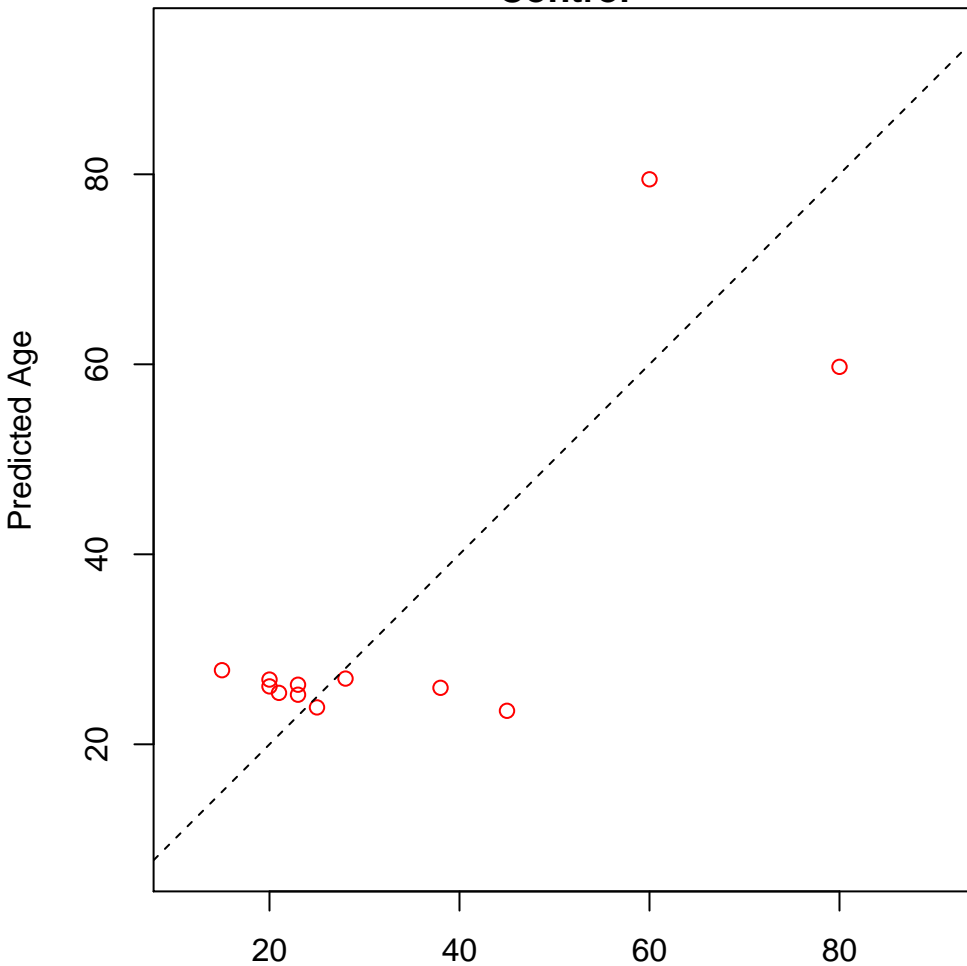
Test



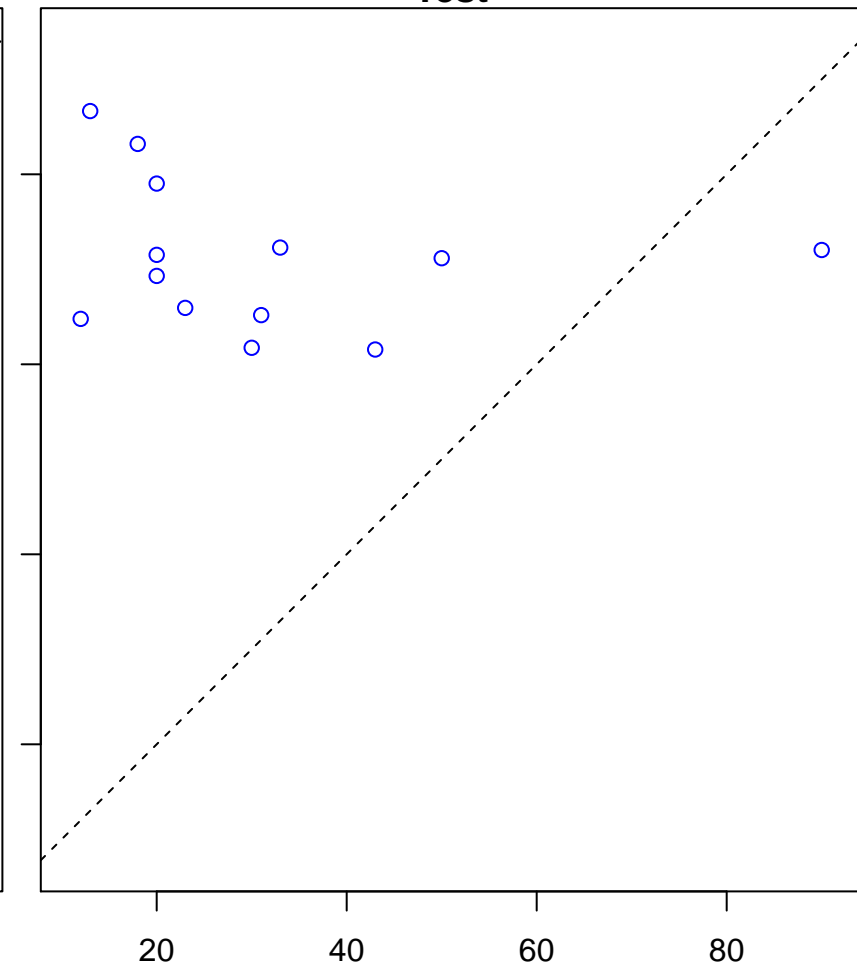
Actual Age

cell cycle G1/S phase transition (Score: 6.198488)

Control

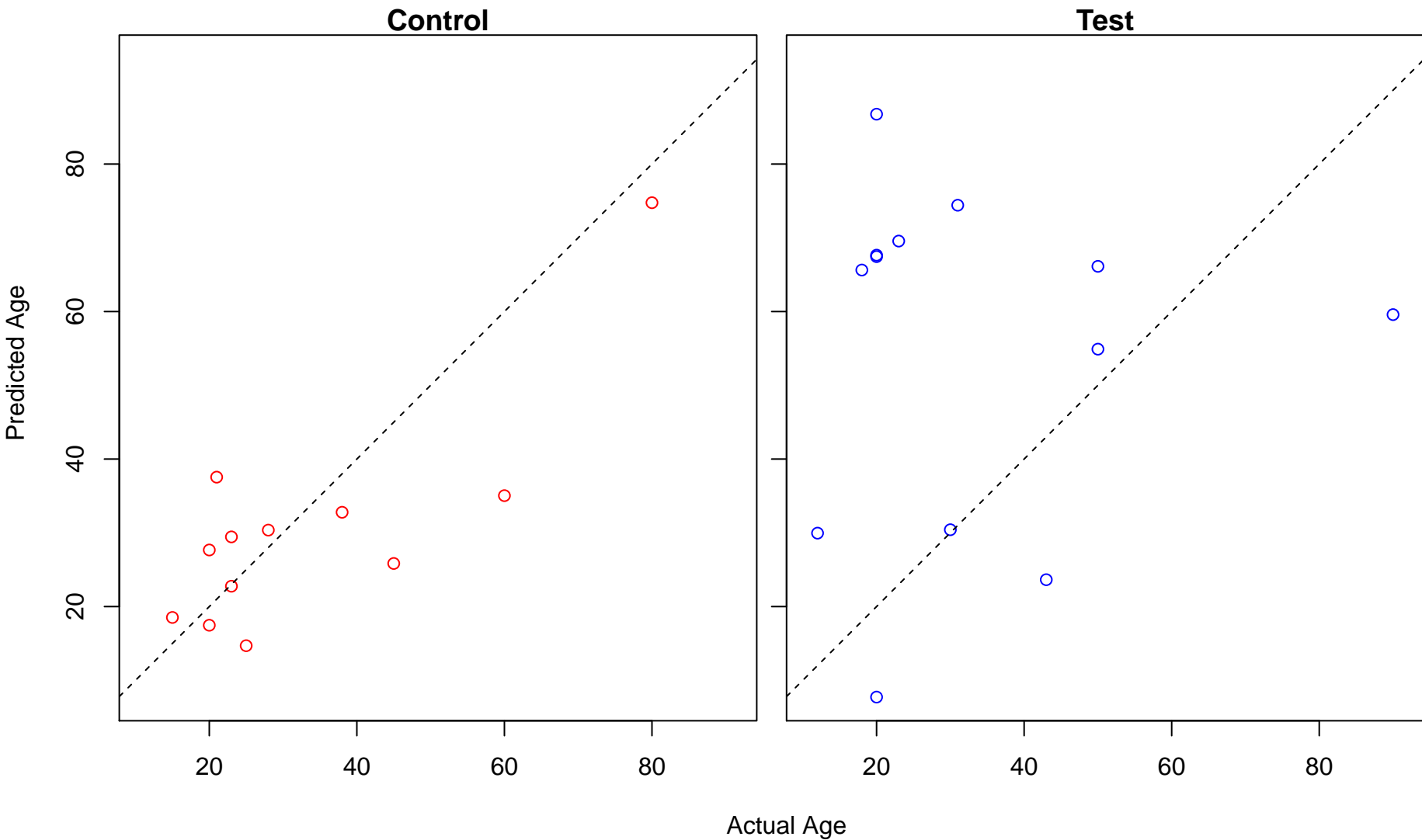


Test

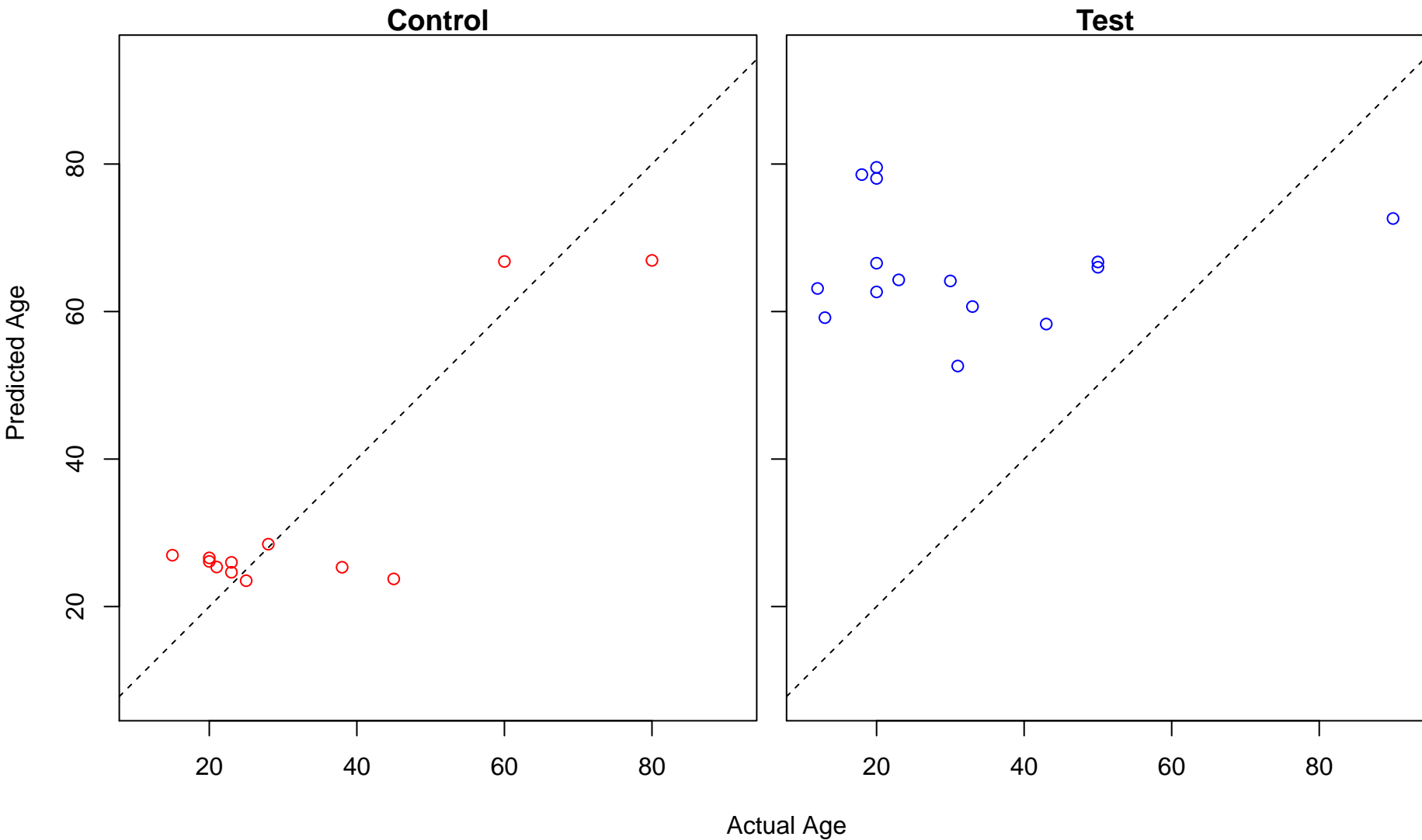


Actual Age

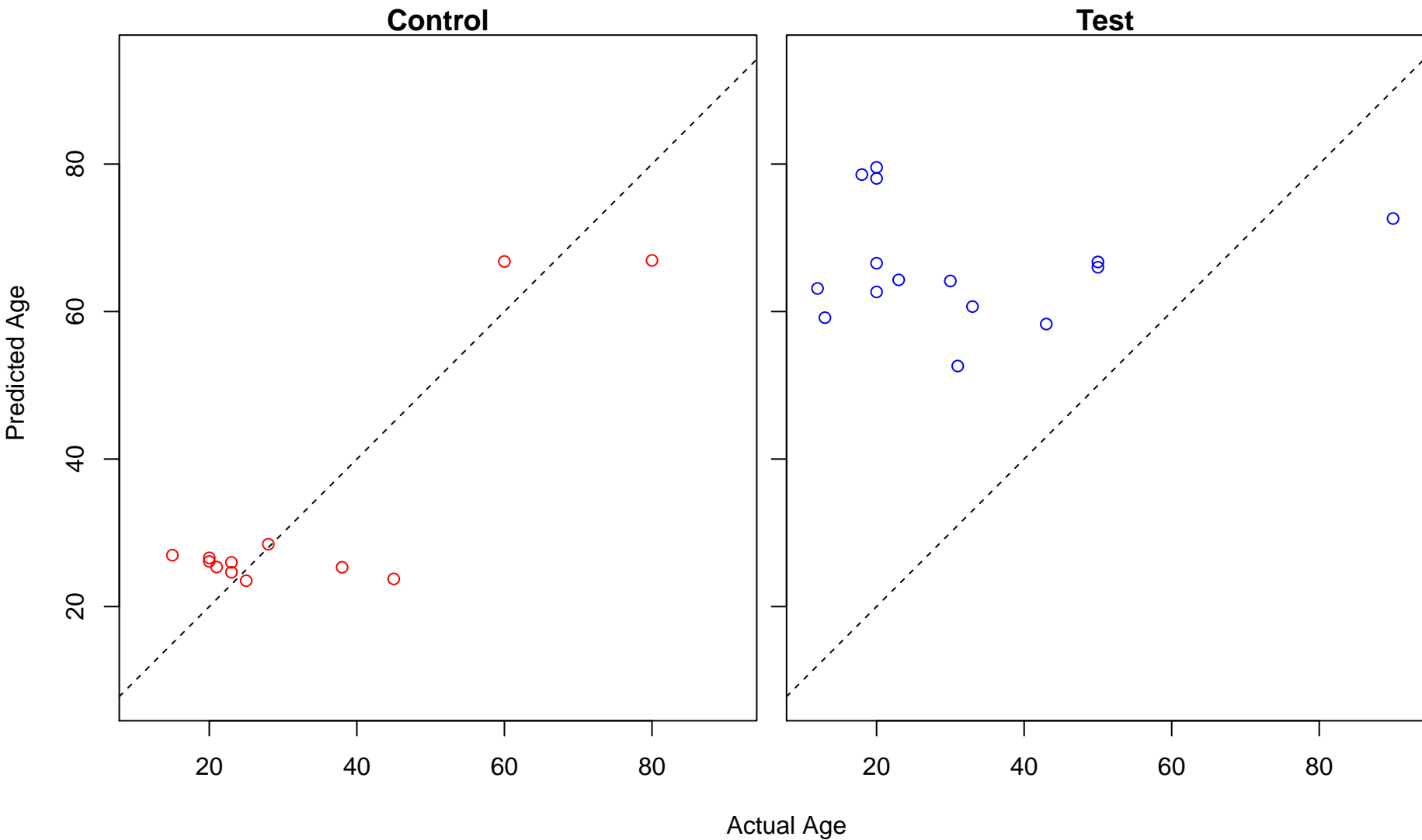
pallium development (Score: 6.194963)



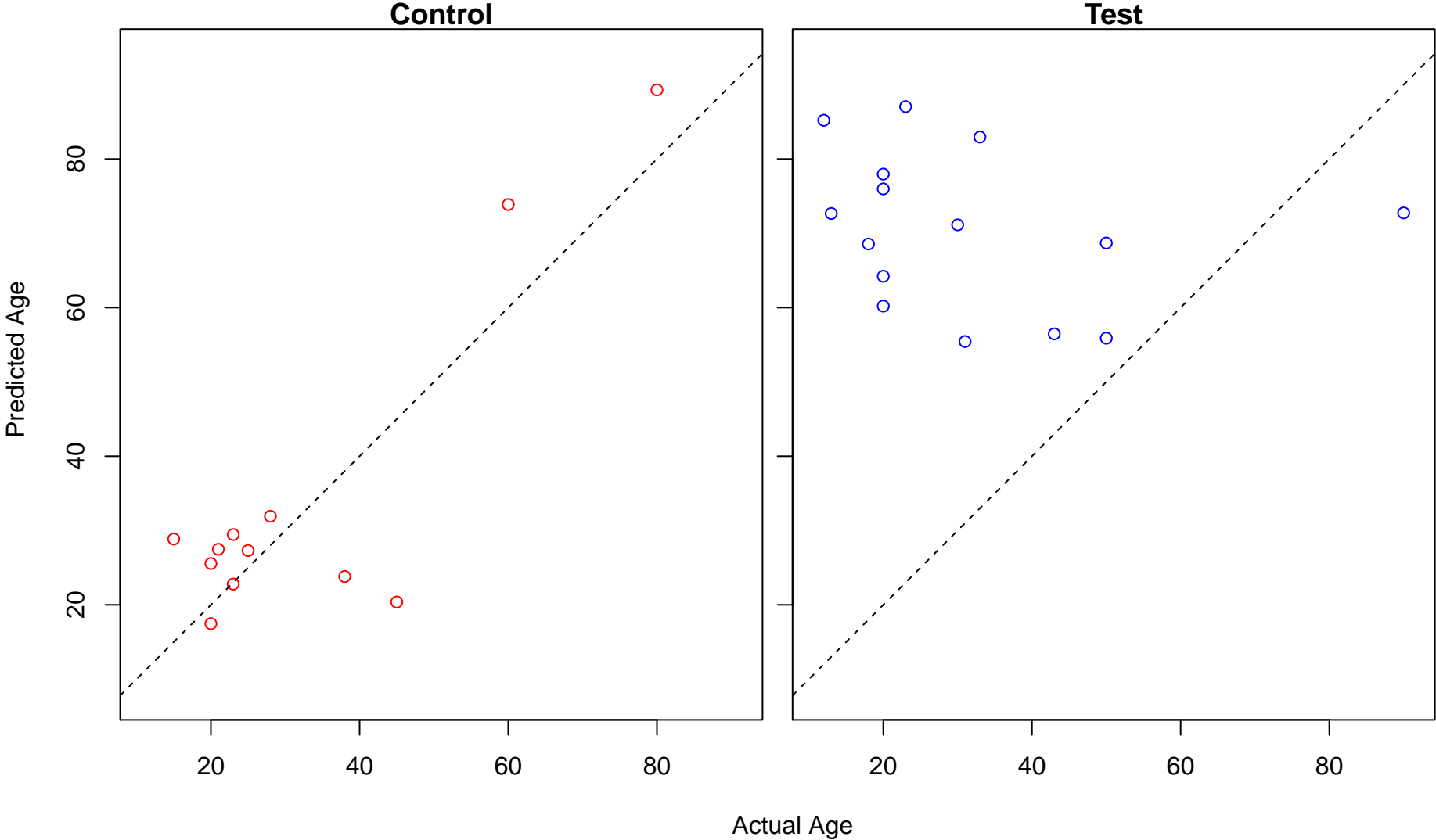
negative regulation of response to extracellular stimulus (Score: 6.194071)



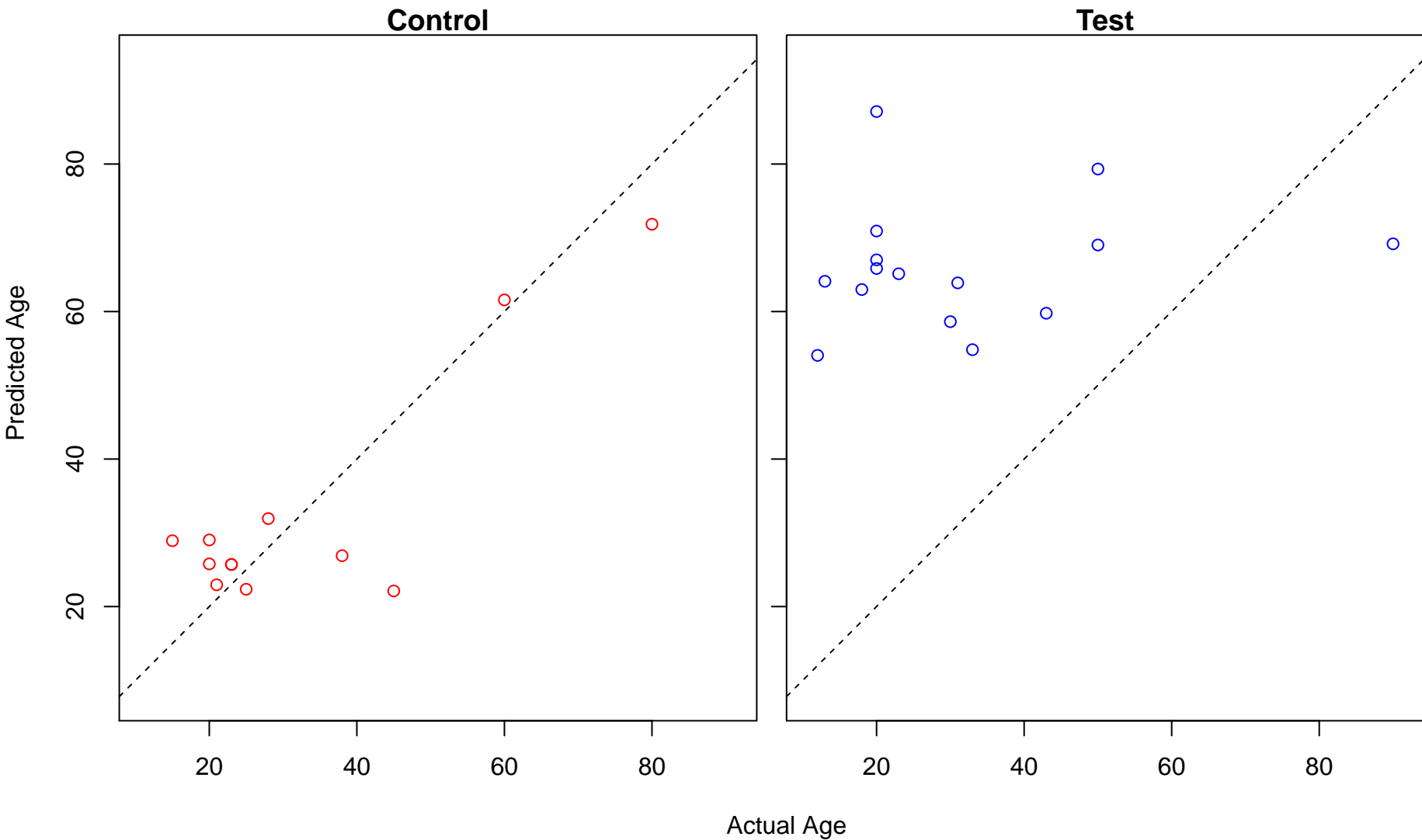
negative regulation of response to nutrient levels (Score: 6.194071)



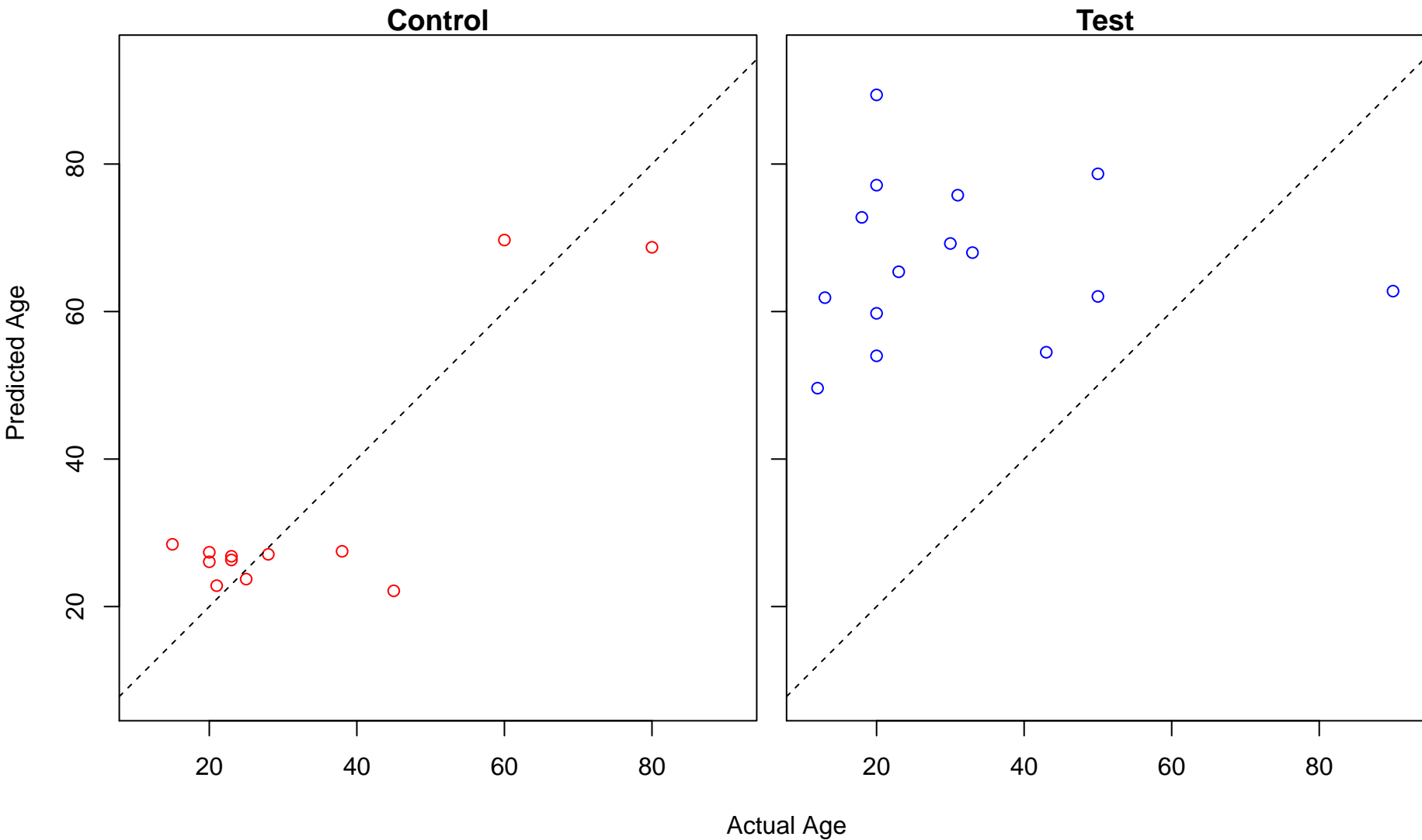
positive regulation of DNA damage response, signal transduction by p53 class mediator (Score: 6.193)



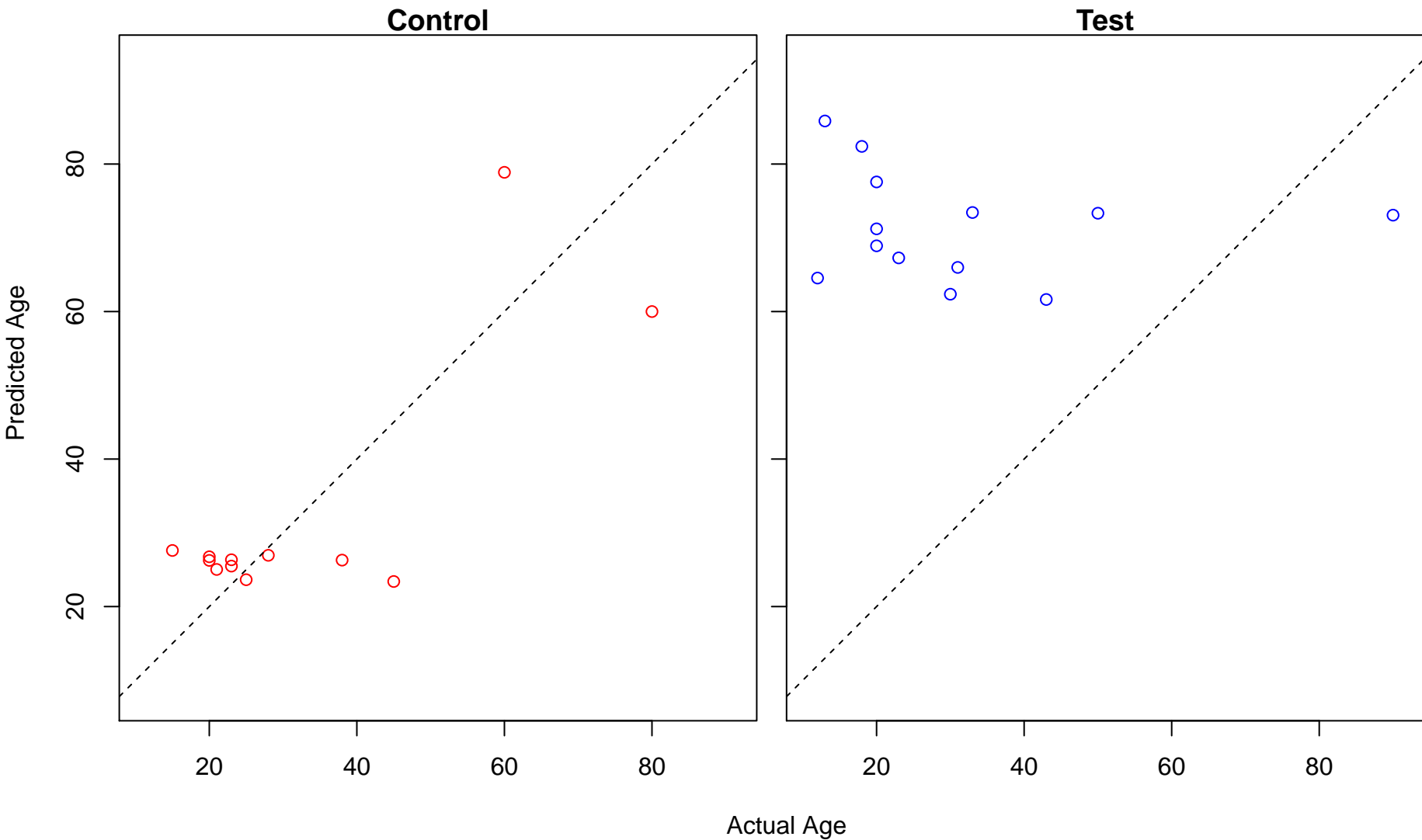
regulation of protein secretion (Score: 6.192868)



negative regulation of lipase activity (Score: 6.192303)

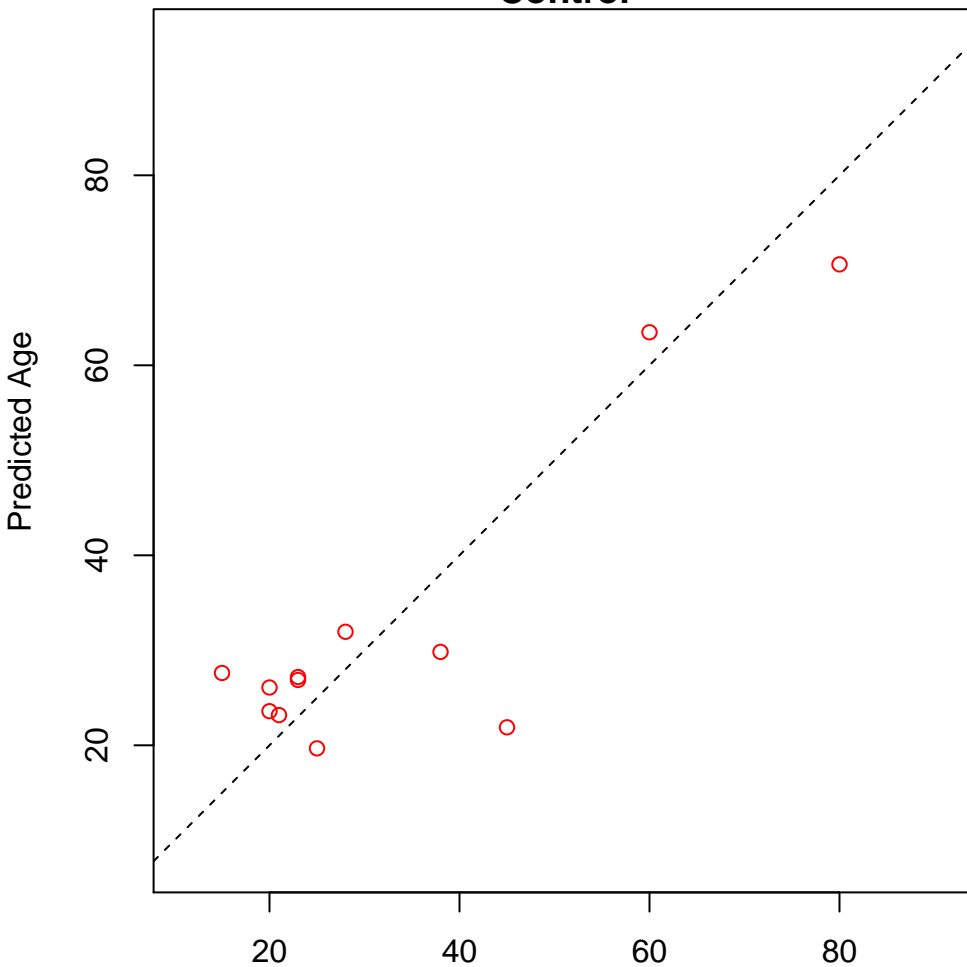


cell cycle checkpoint (Score: 6.191838)

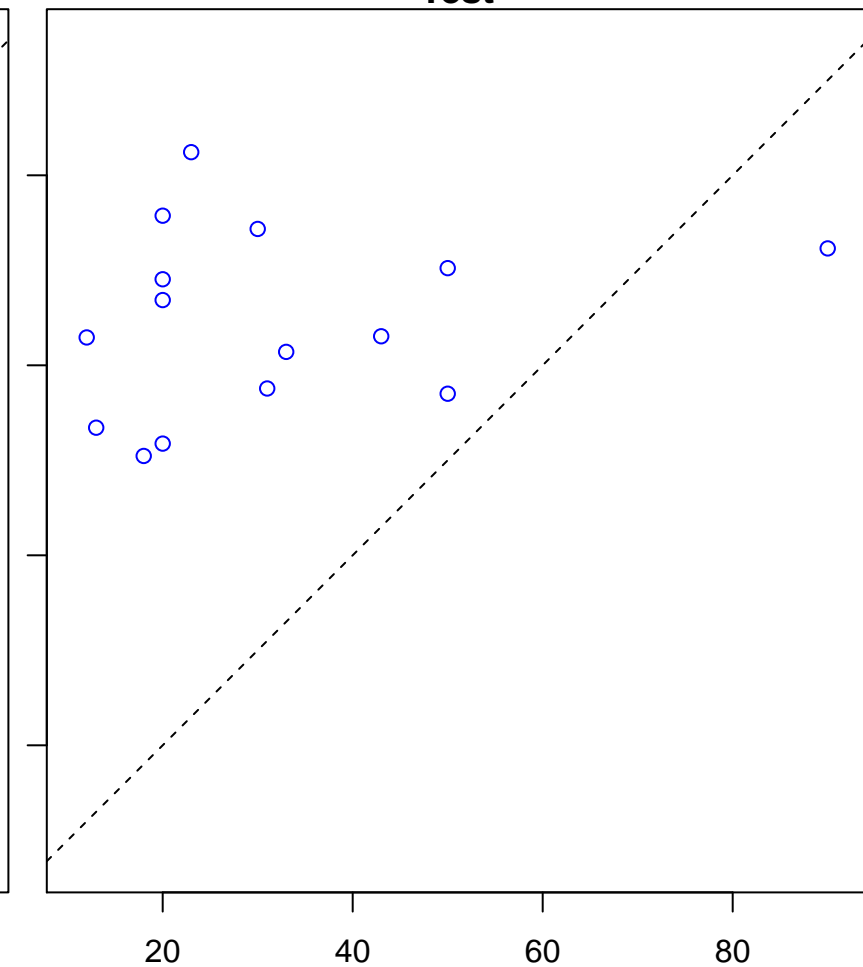


phosphatidylcholine metabolic process (Score: 6.191103)

Control

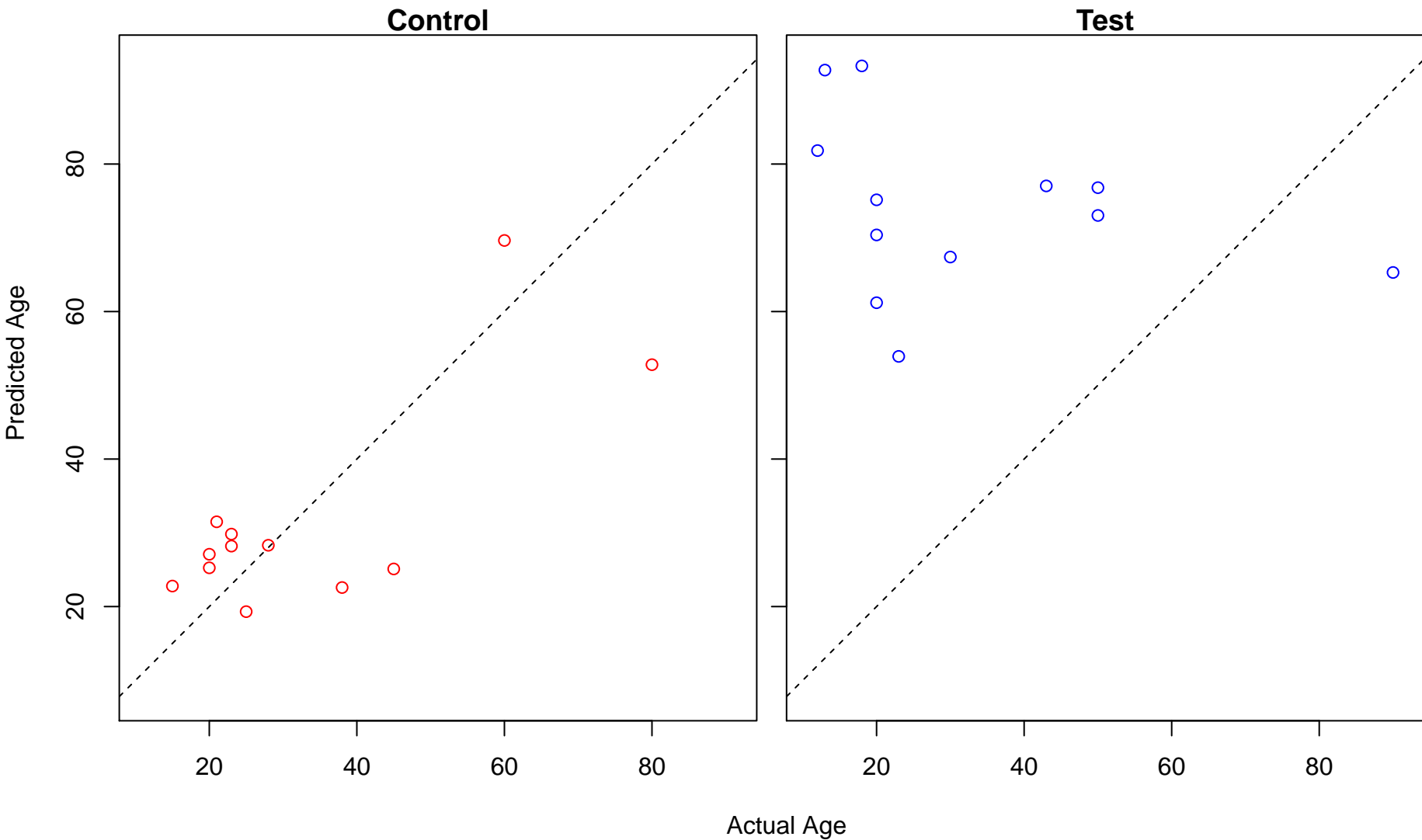


Test



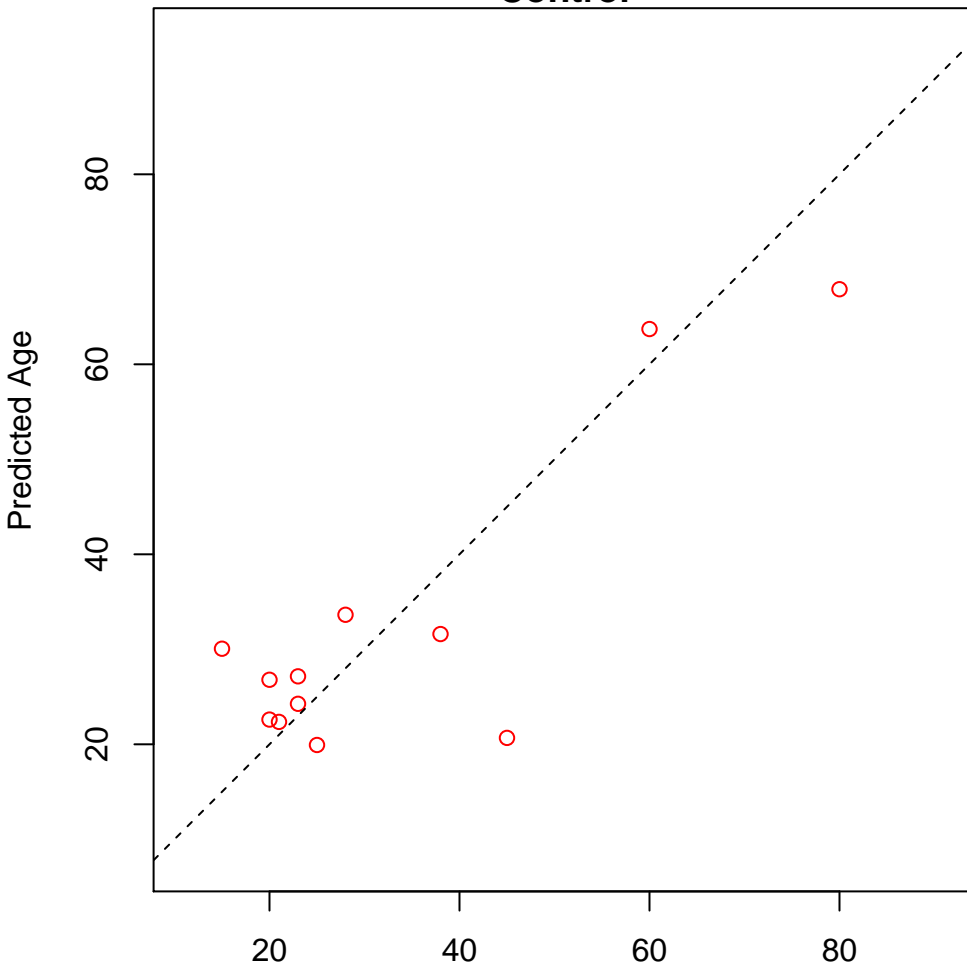
Actual Age

wound healing, spreading of epidermal cells (Score: 6.187117)

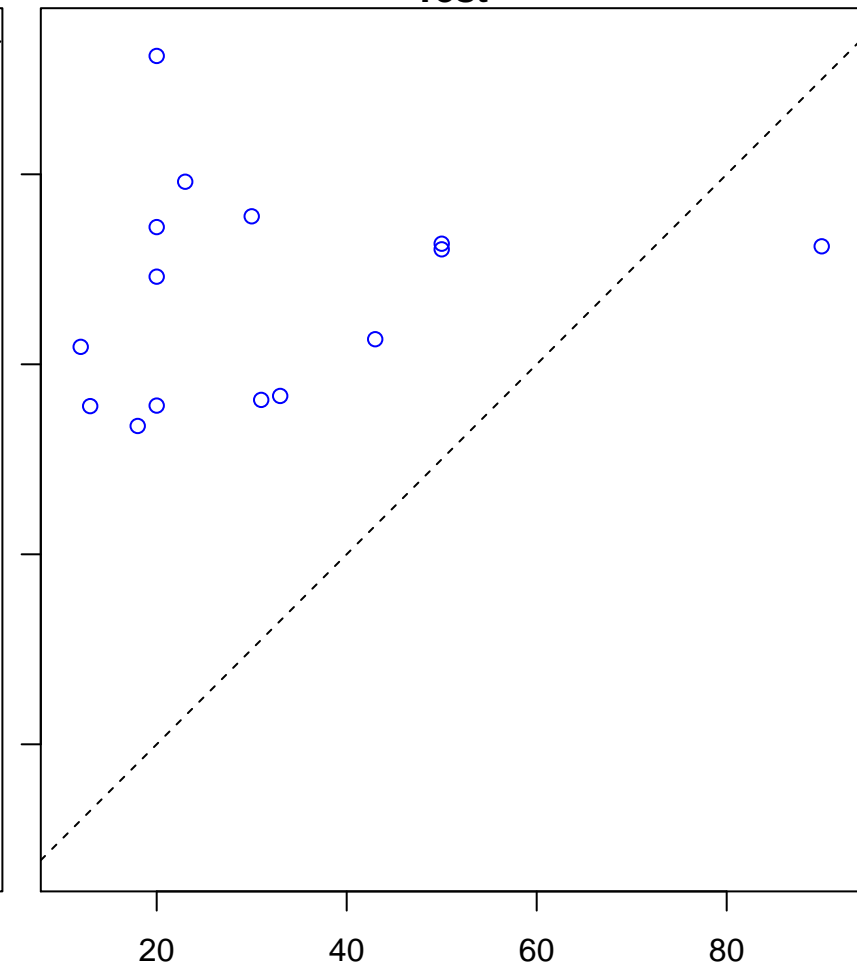


neurotransmitter metabolic process (Score: 6.186904)

Control

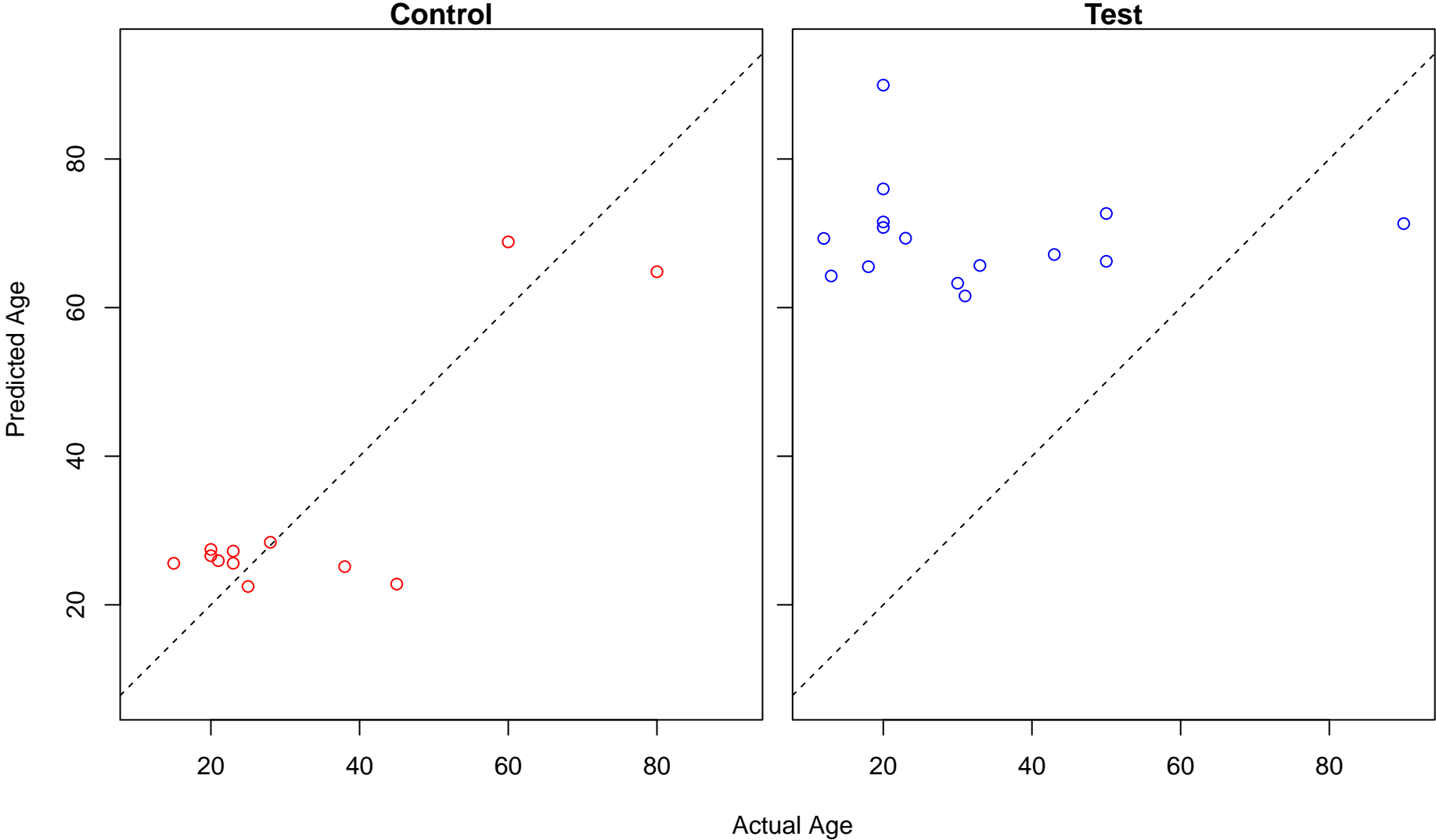


Test

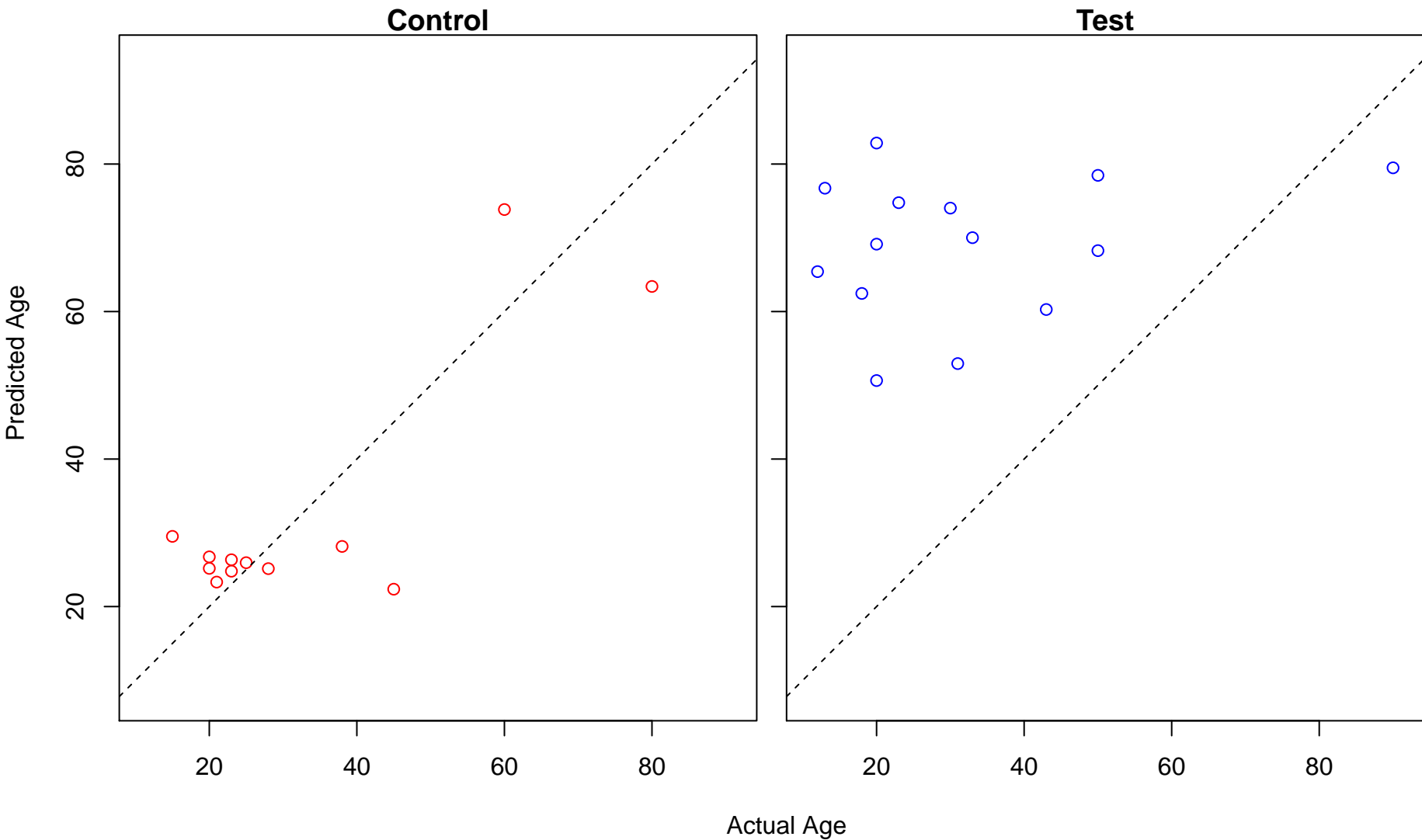


Actual Age

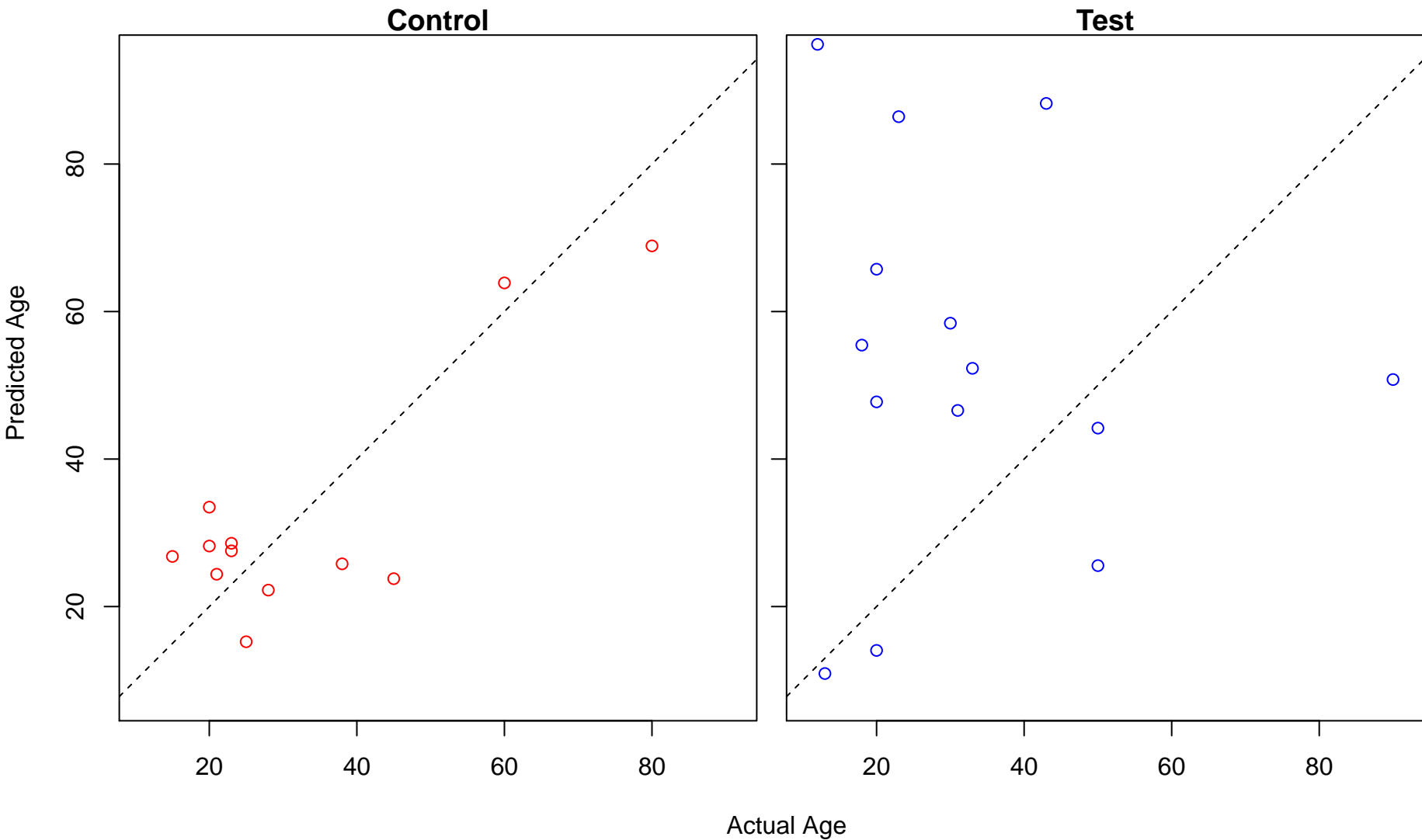
intrinsic apoptotic signaling pathway by p53 class mediator (Score: 6.186095)



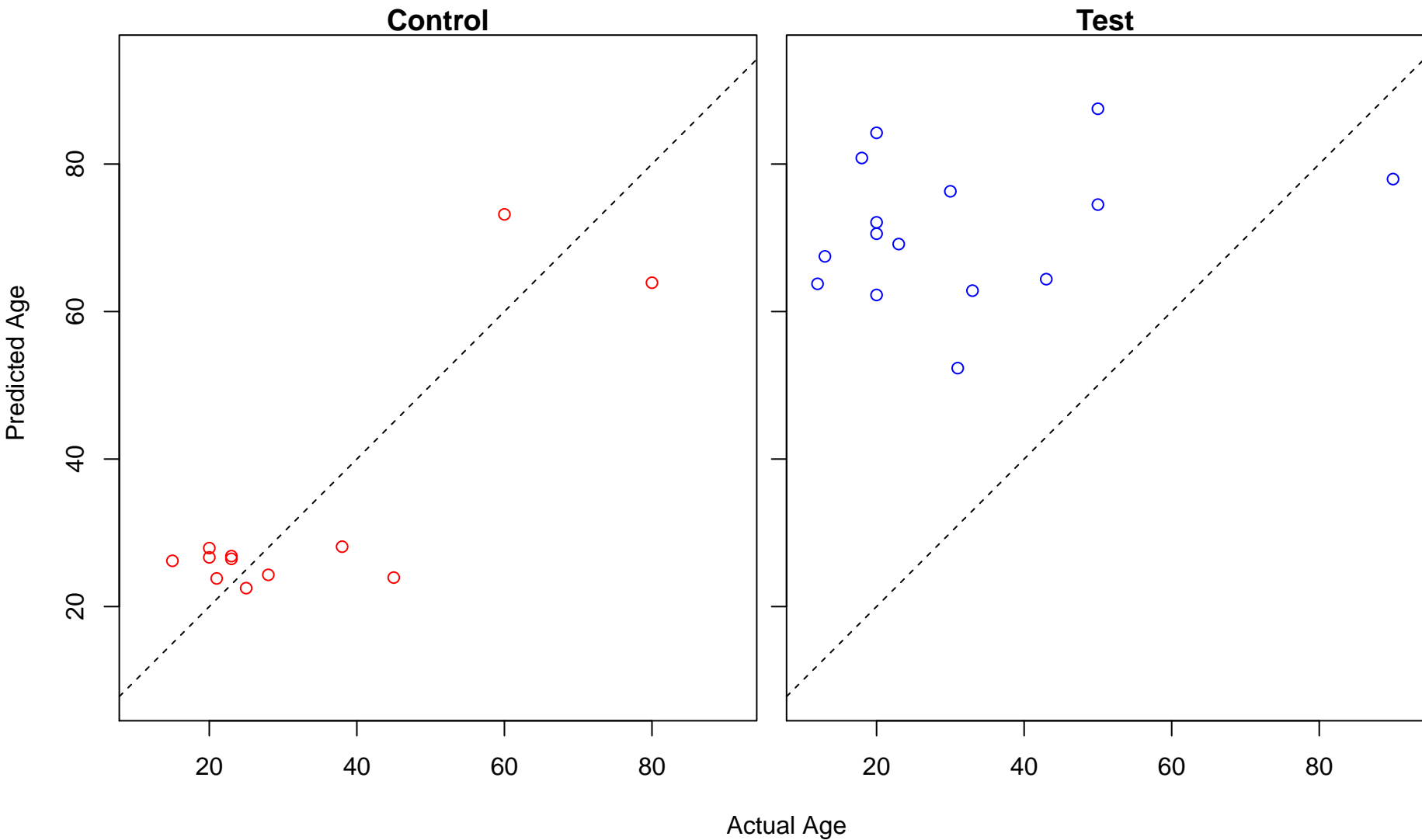
copper ion homeostasis (Score: 6.182961)



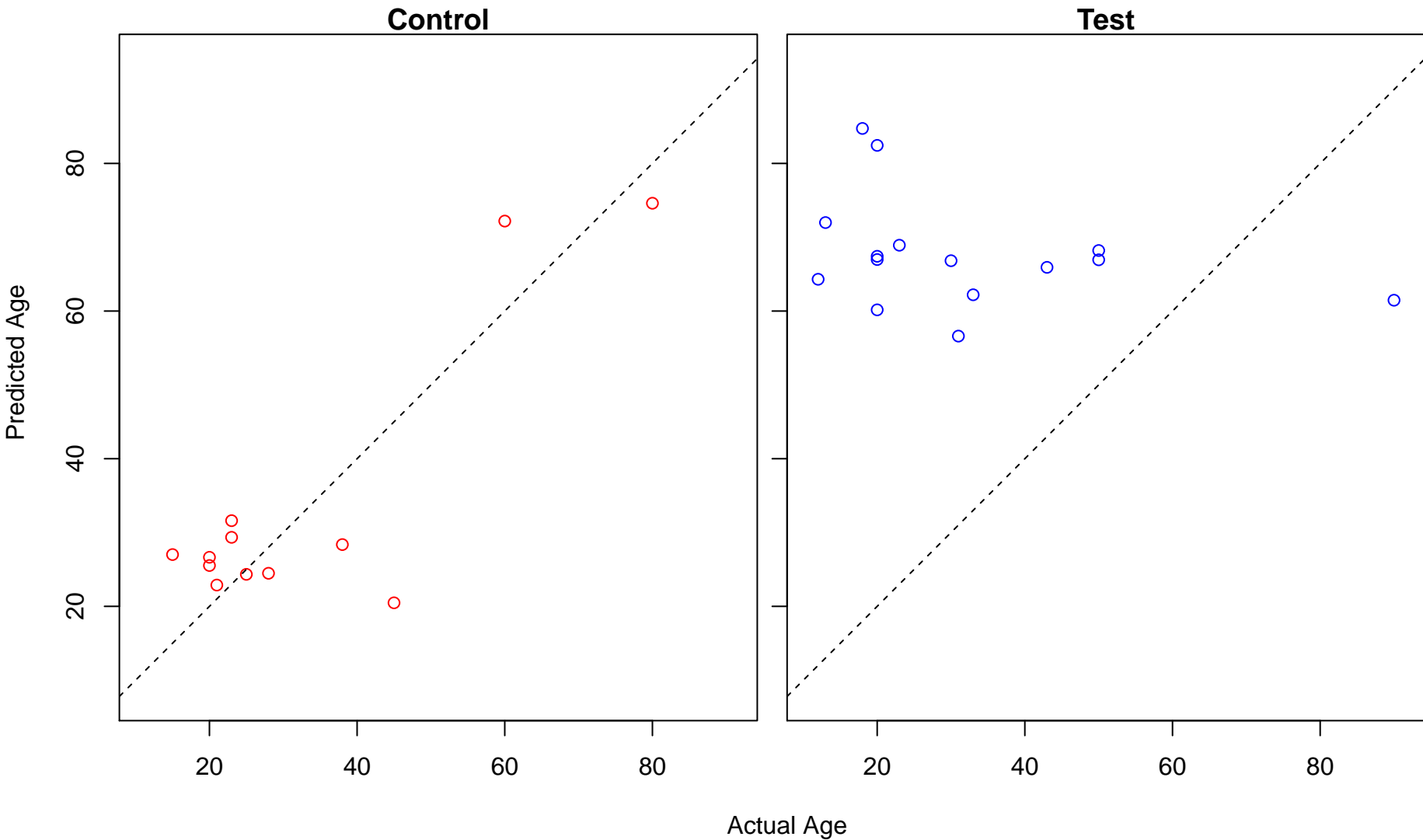
regulation of ketone biosynthetic process (Score: 6.182309)



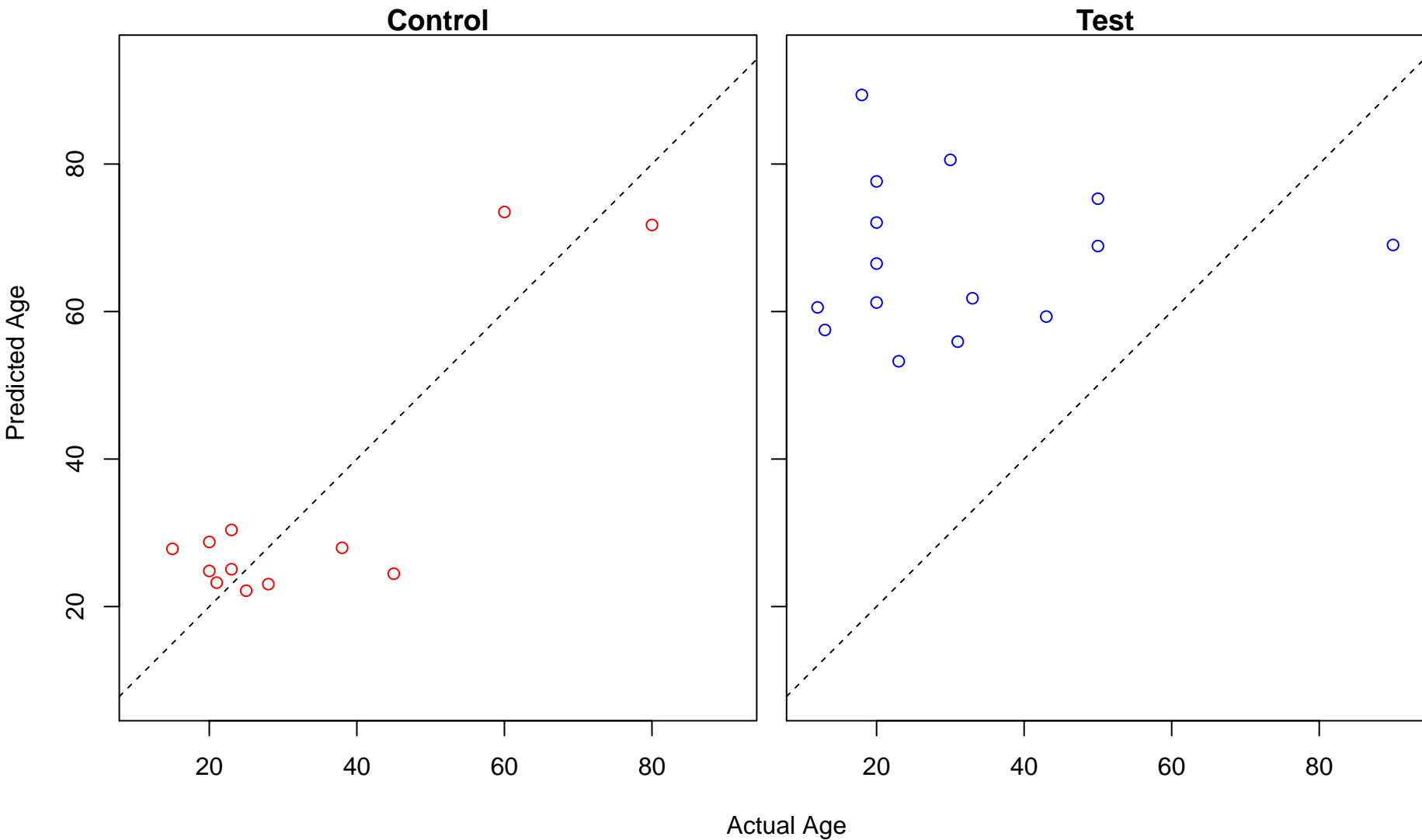
muscle cell development (Score: 6.182257)



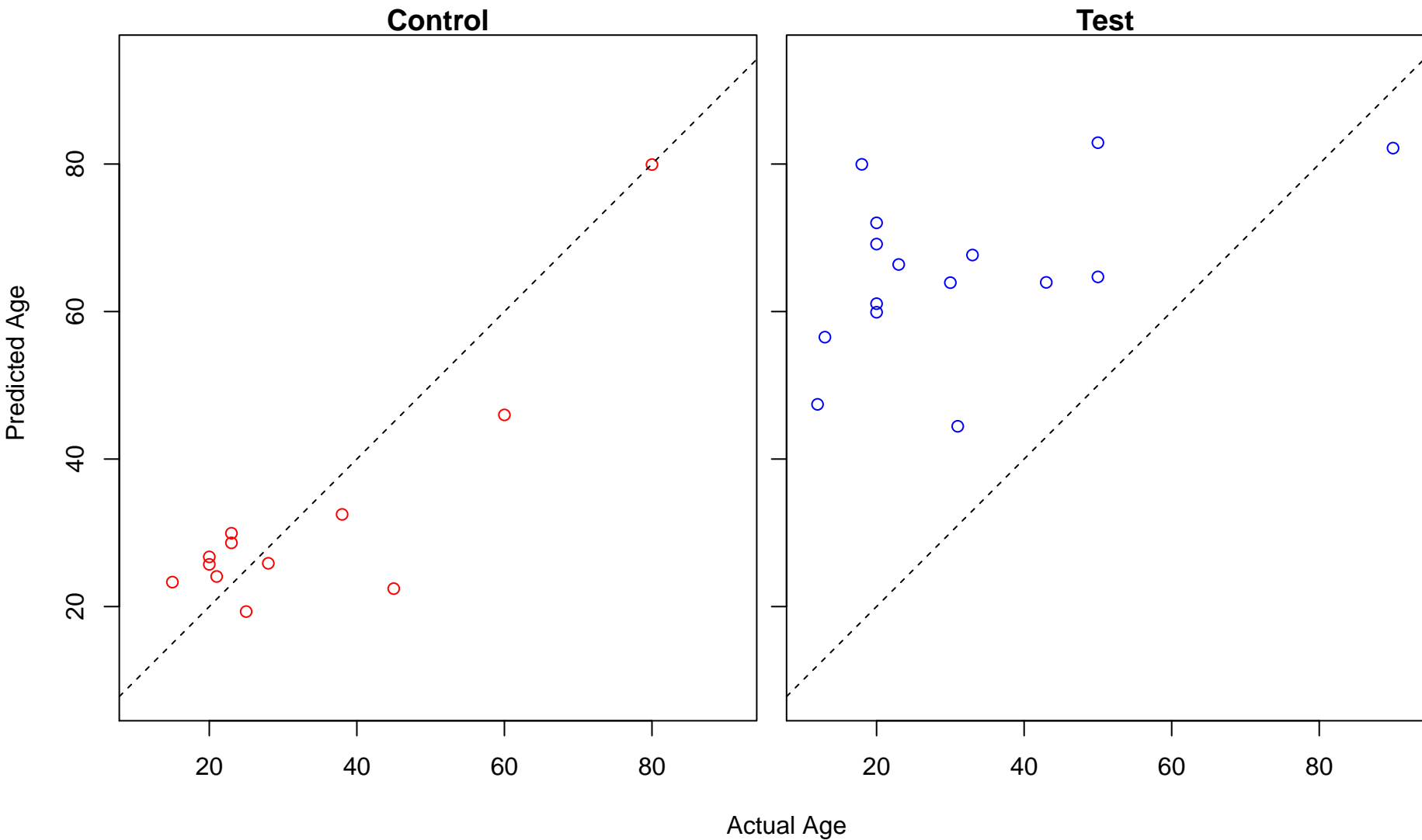
regulation of smooth muscle cell proliferation (Score: 6.181815)



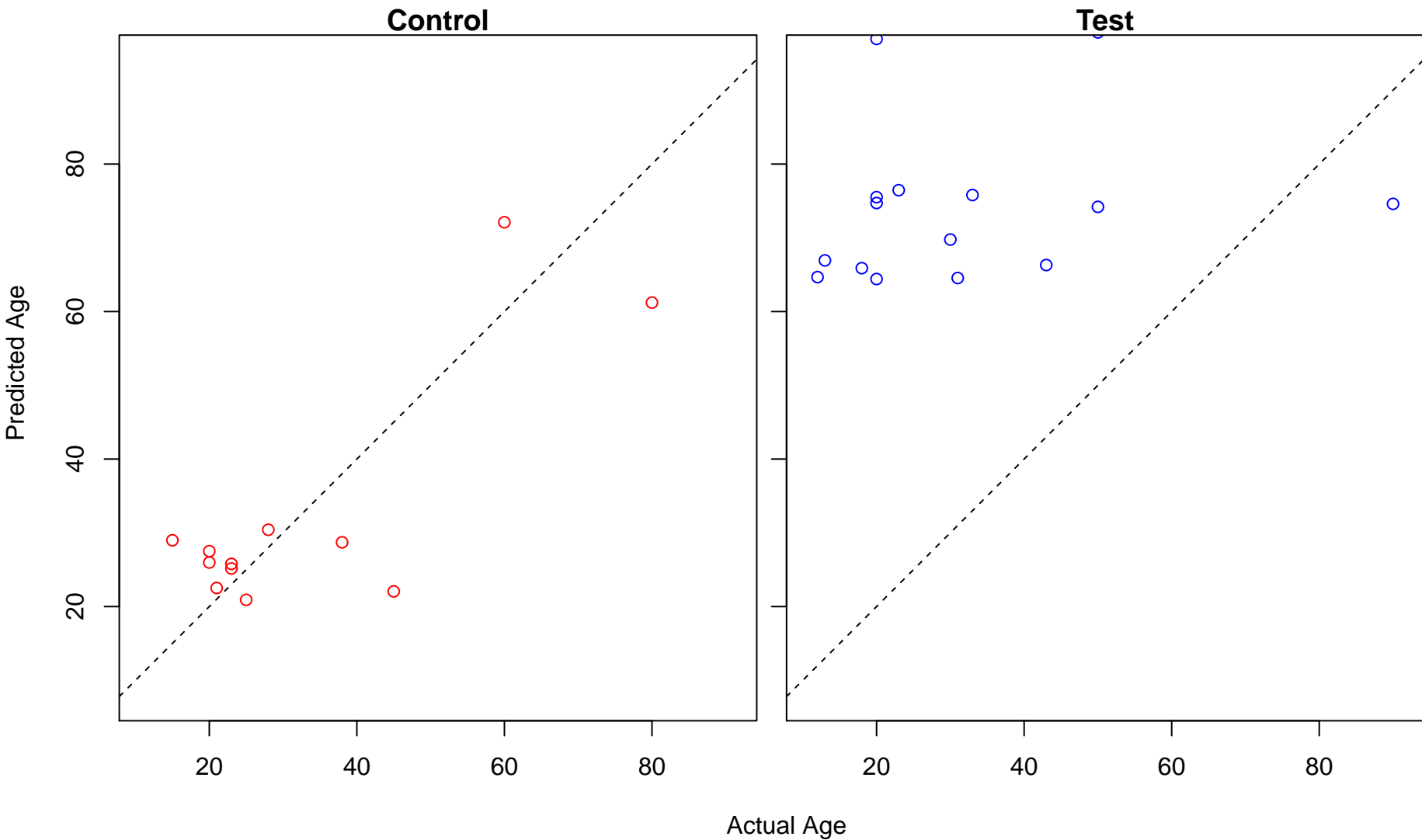
amino sugar metabolic process (Score: 6.181091)



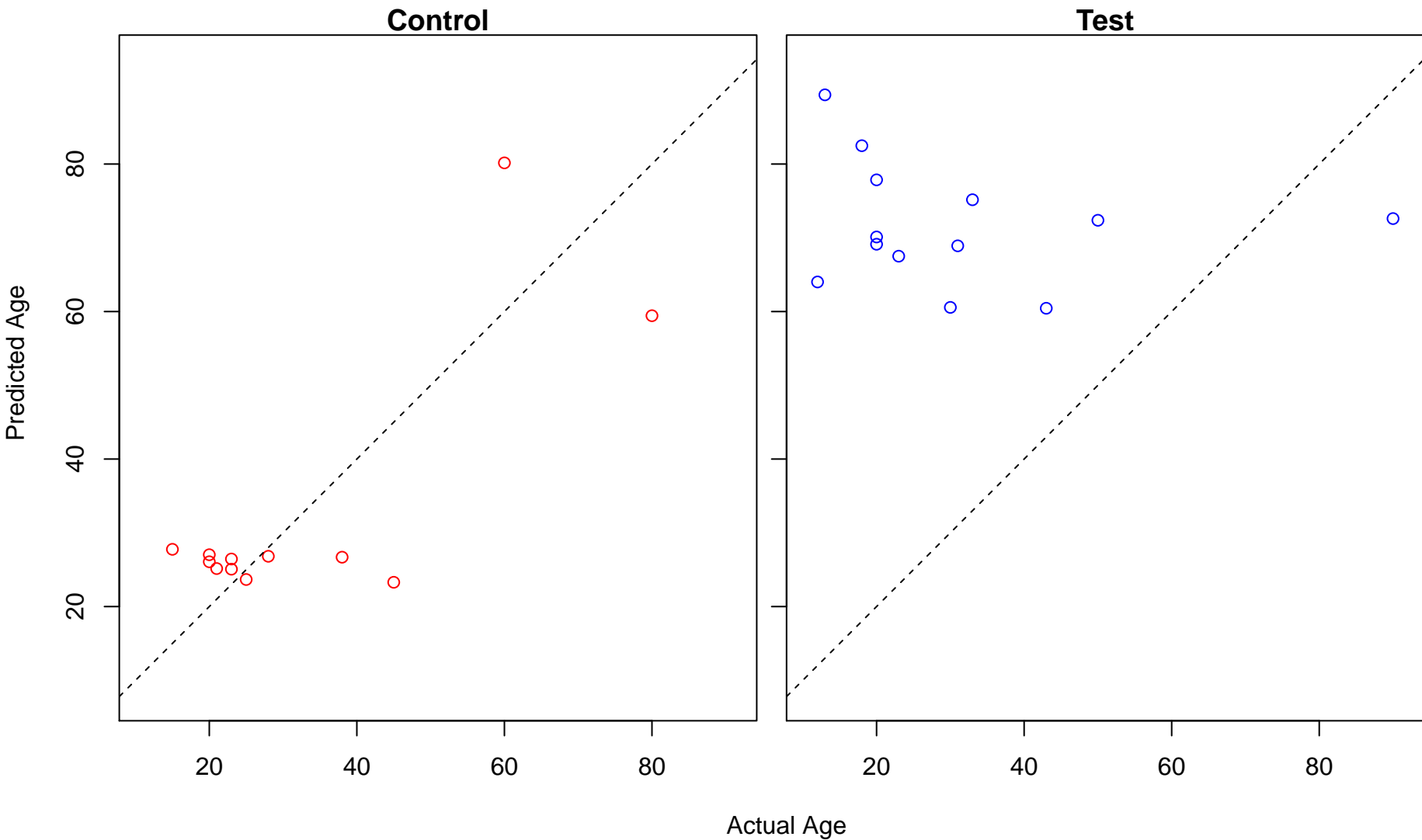
desmosome organization (Score: 6.178963)



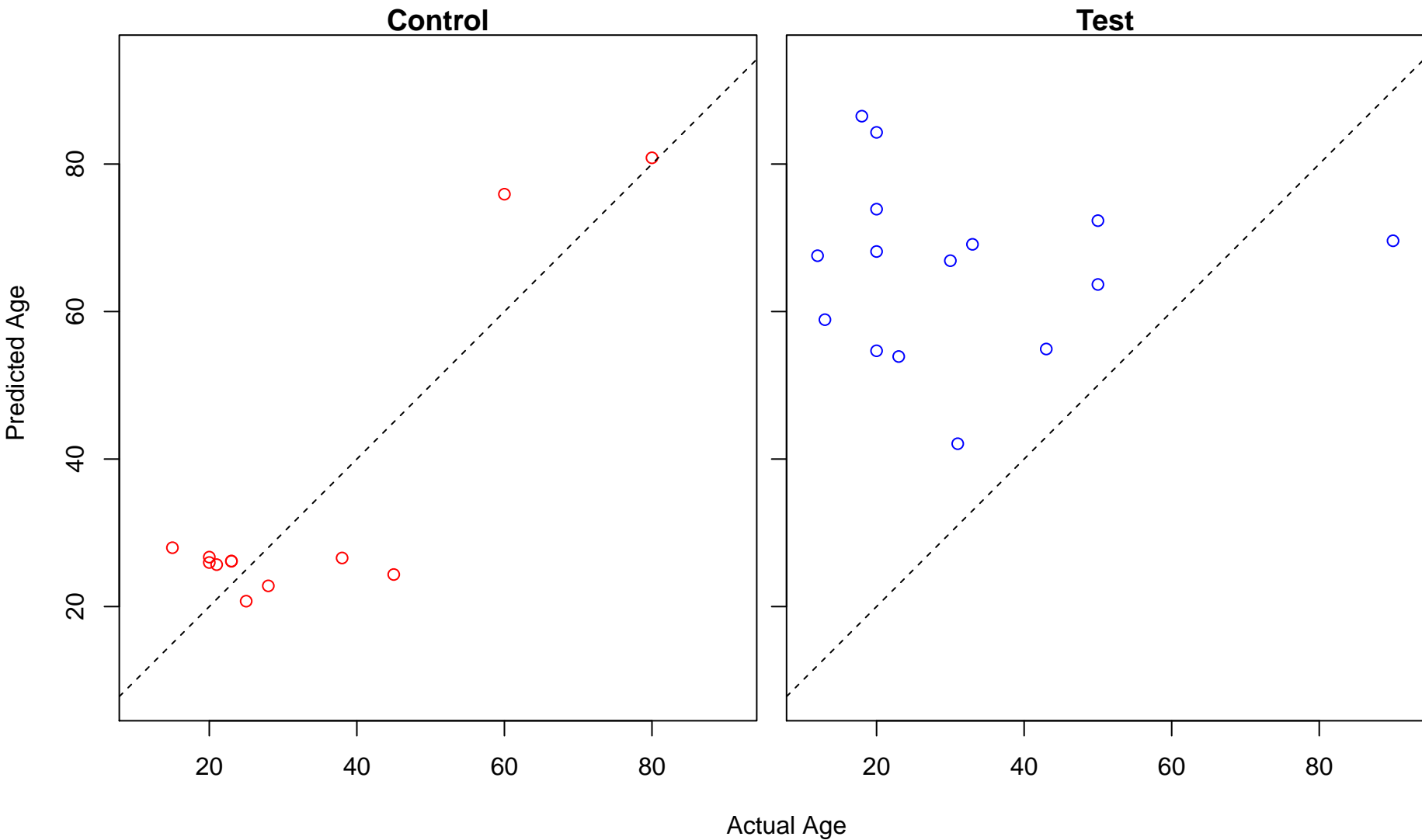
epithelial tube formation (Score: 6.177181)



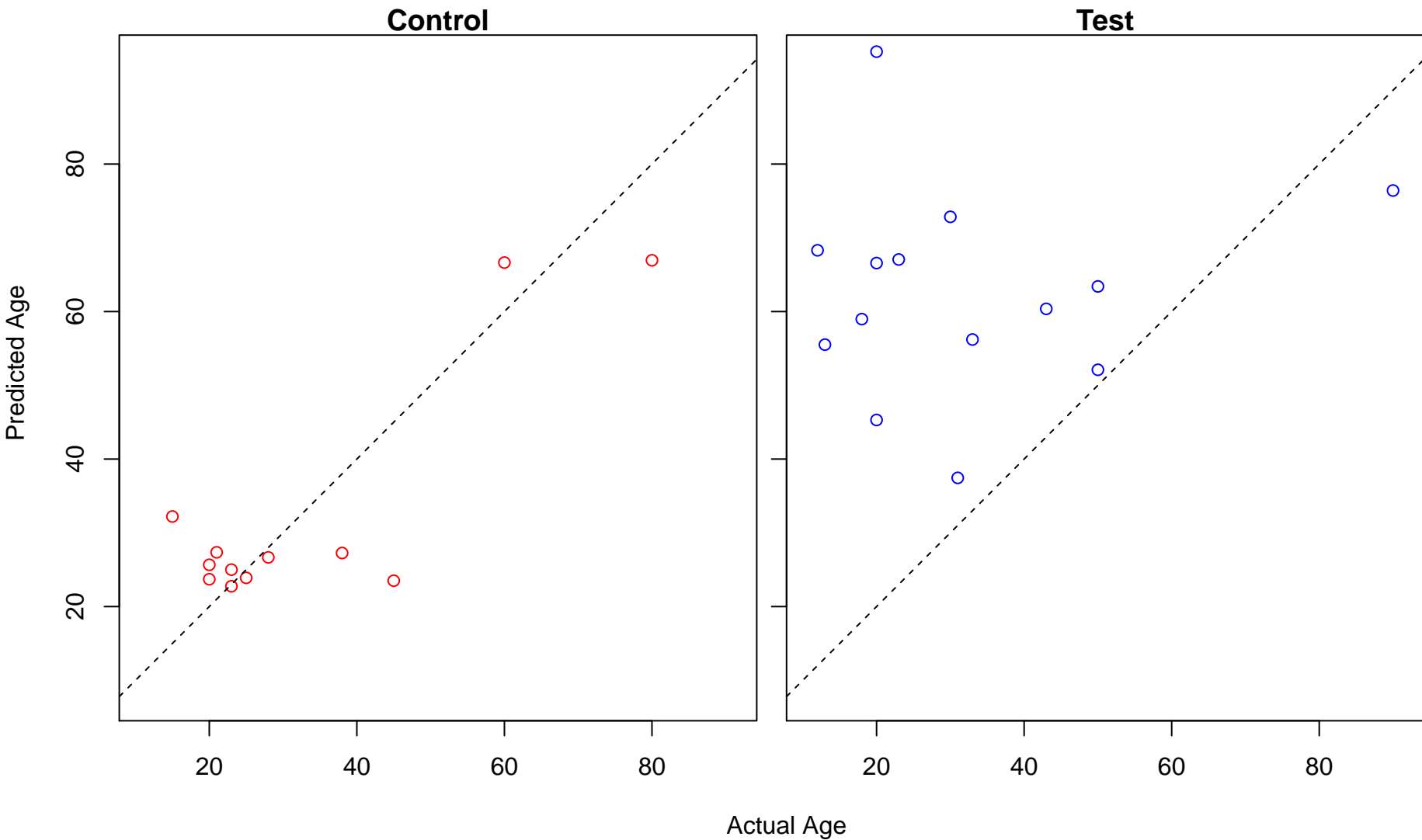
negative regulation of type I interferon production (Score: 6.176251)



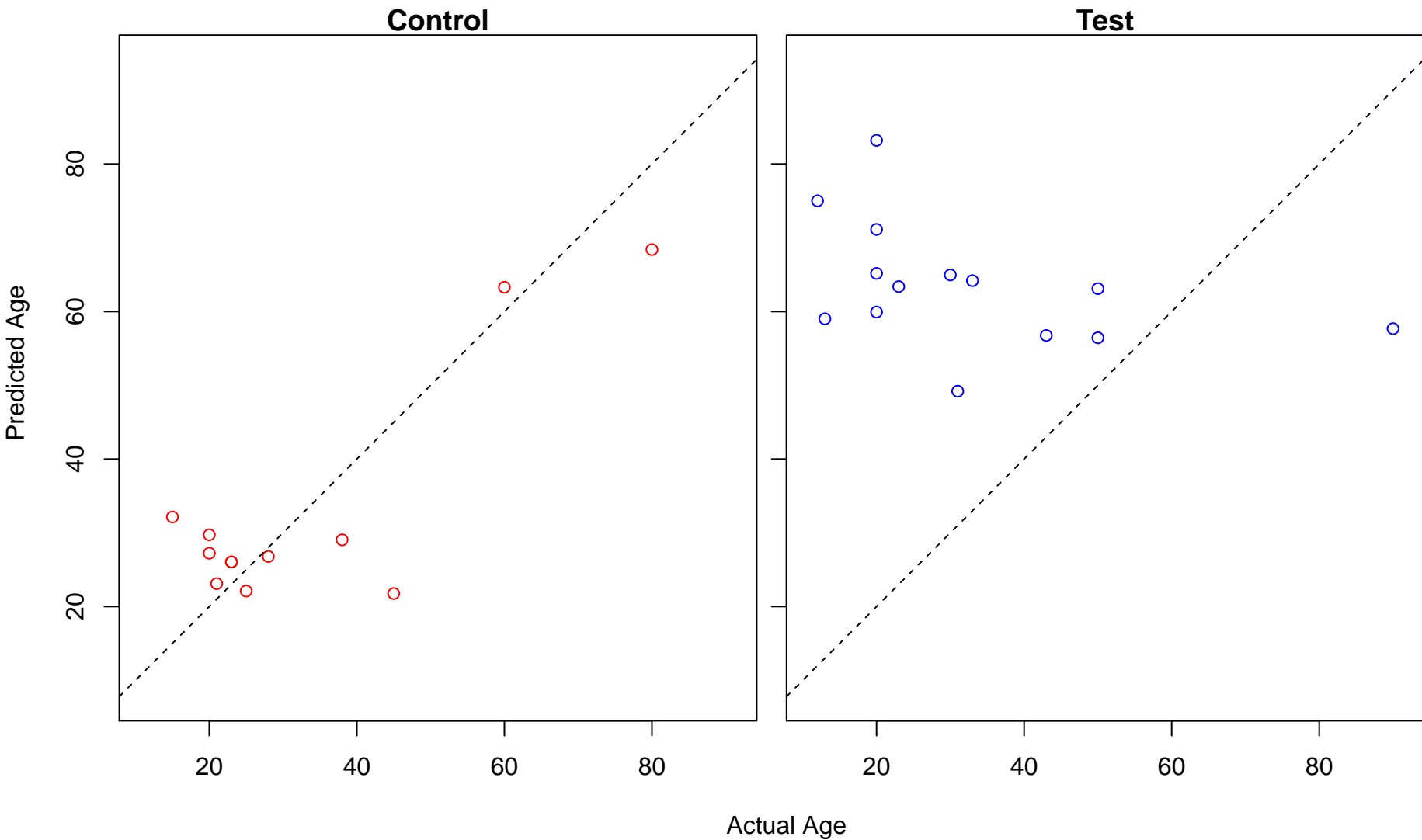
regulation of protein glycosylation (Score: 6.173455)



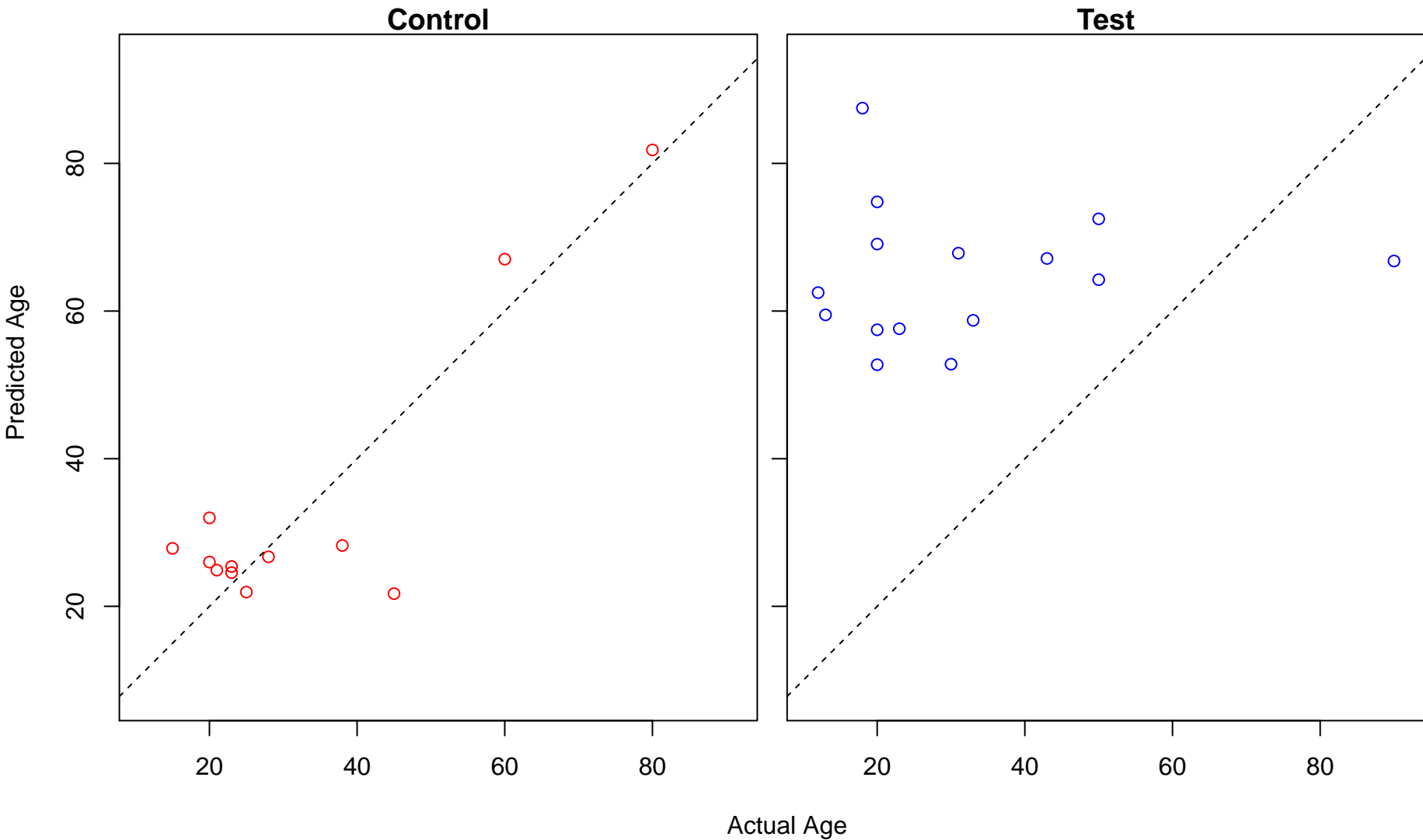
negative regulation of cell cycle arrest (Score: 6.173091)



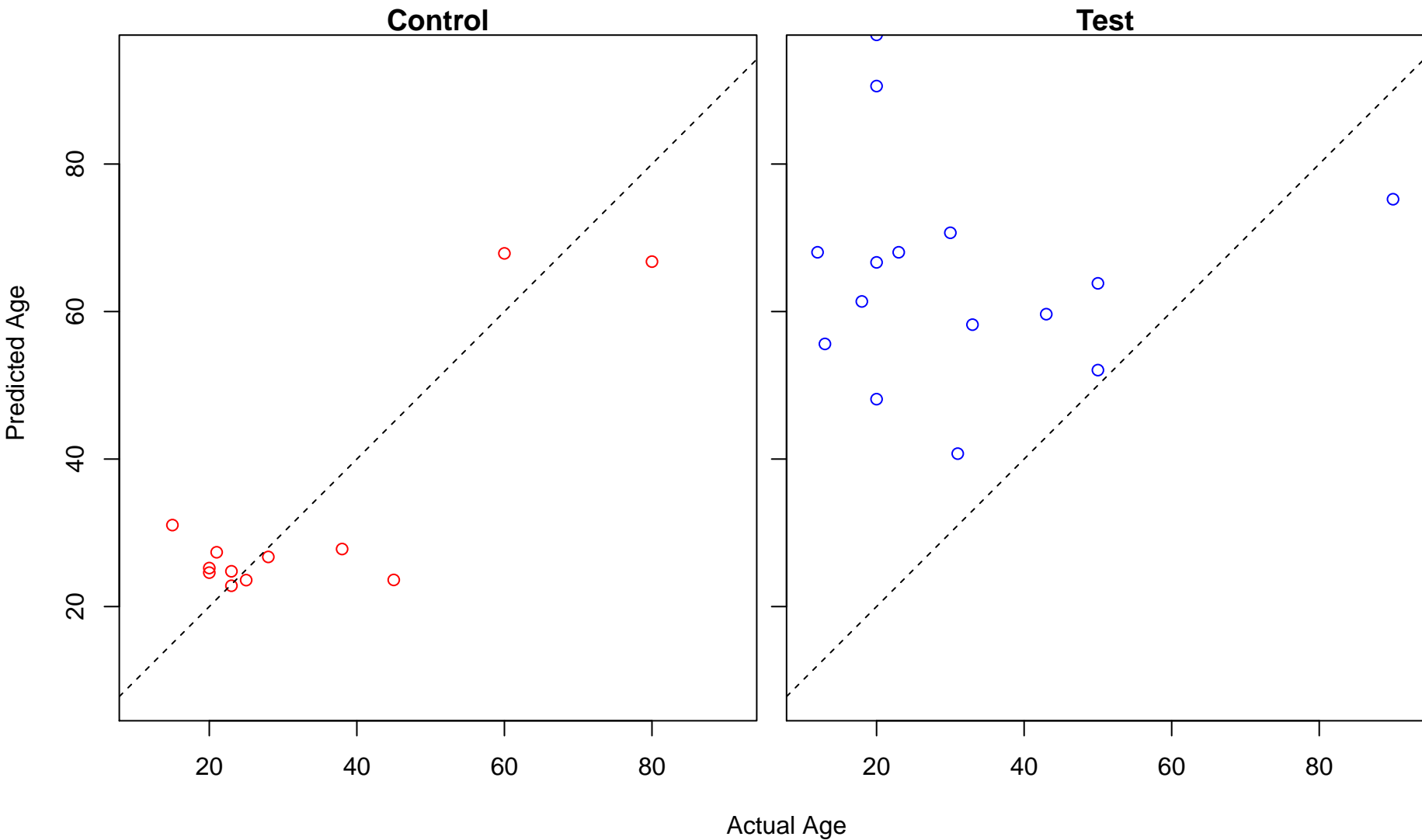
lymph vessel development (Score: 6.172979)



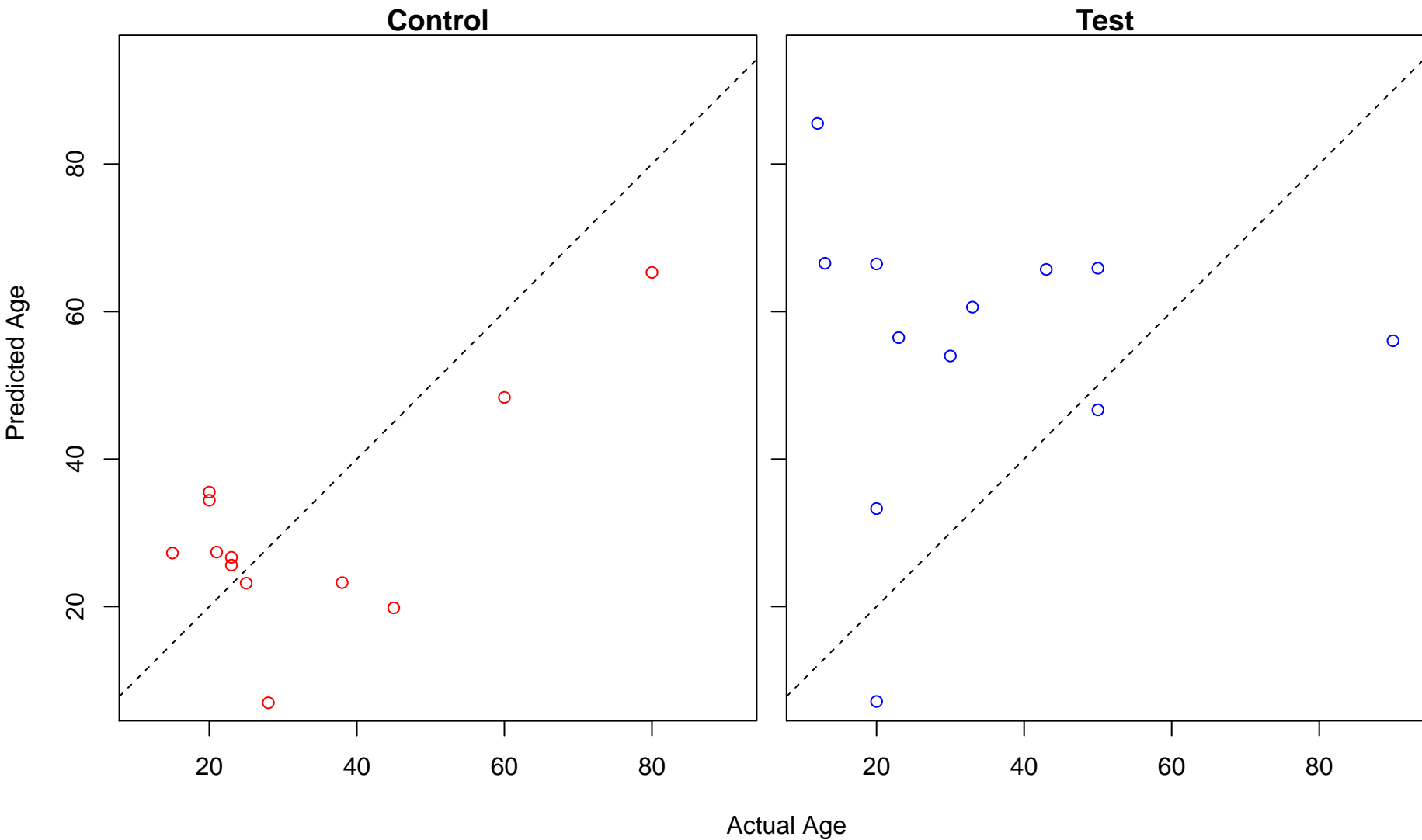
regulation of cell morphogenesis involved in differentiation (Score: 6.171541)



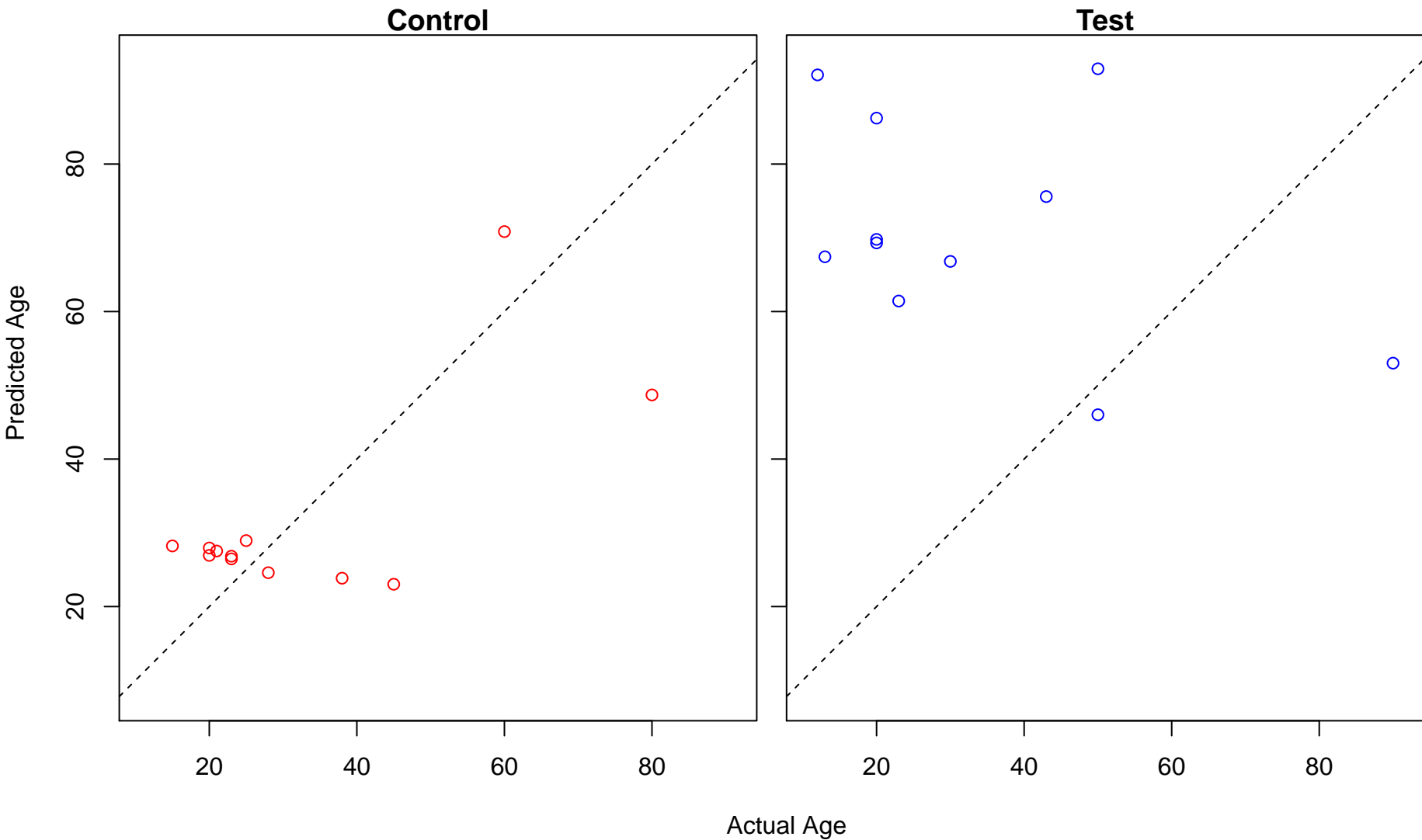
regulation of cell aging (Score: 6.171371)



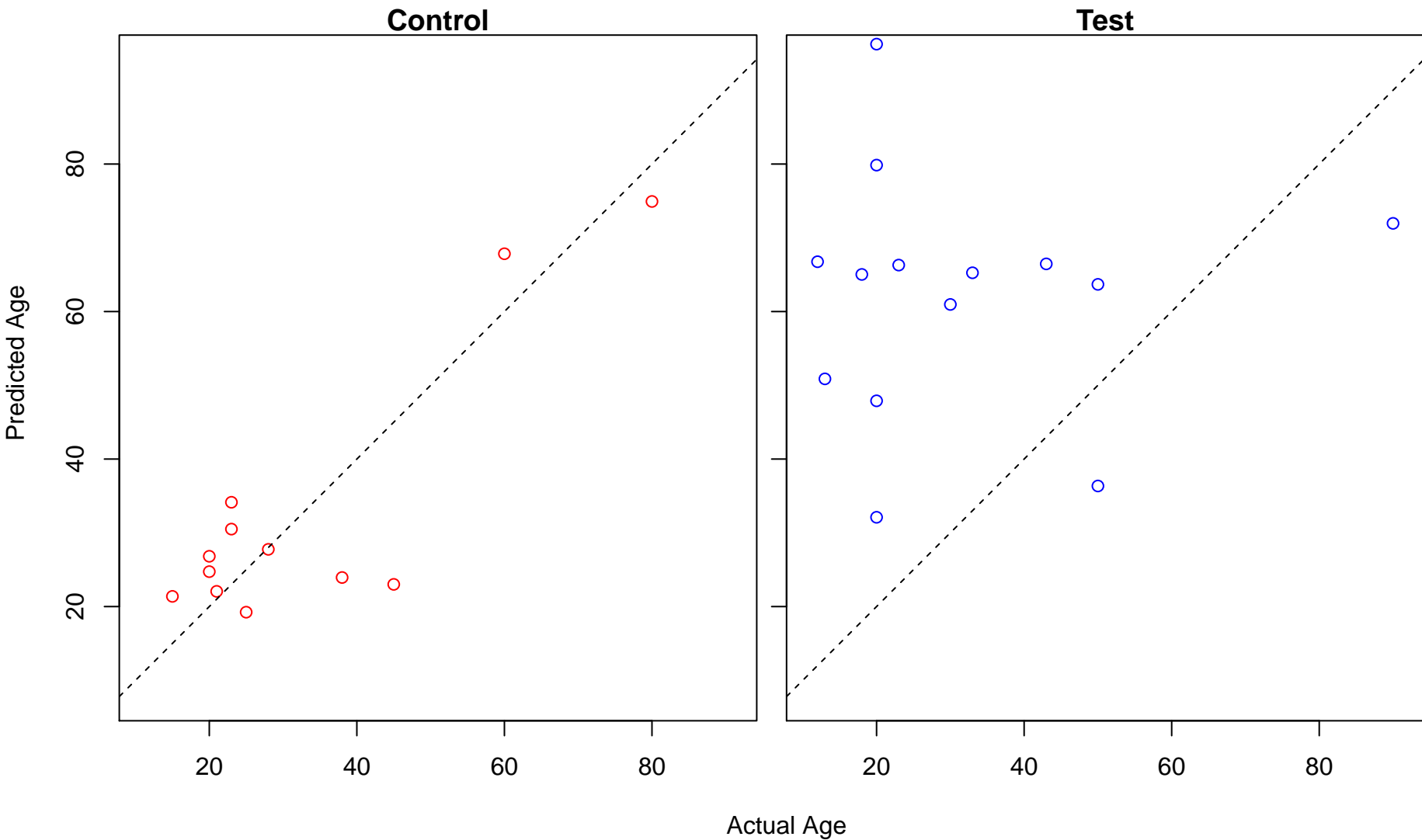
positive regulation of hormone metabolic process (Score: 6.167801)



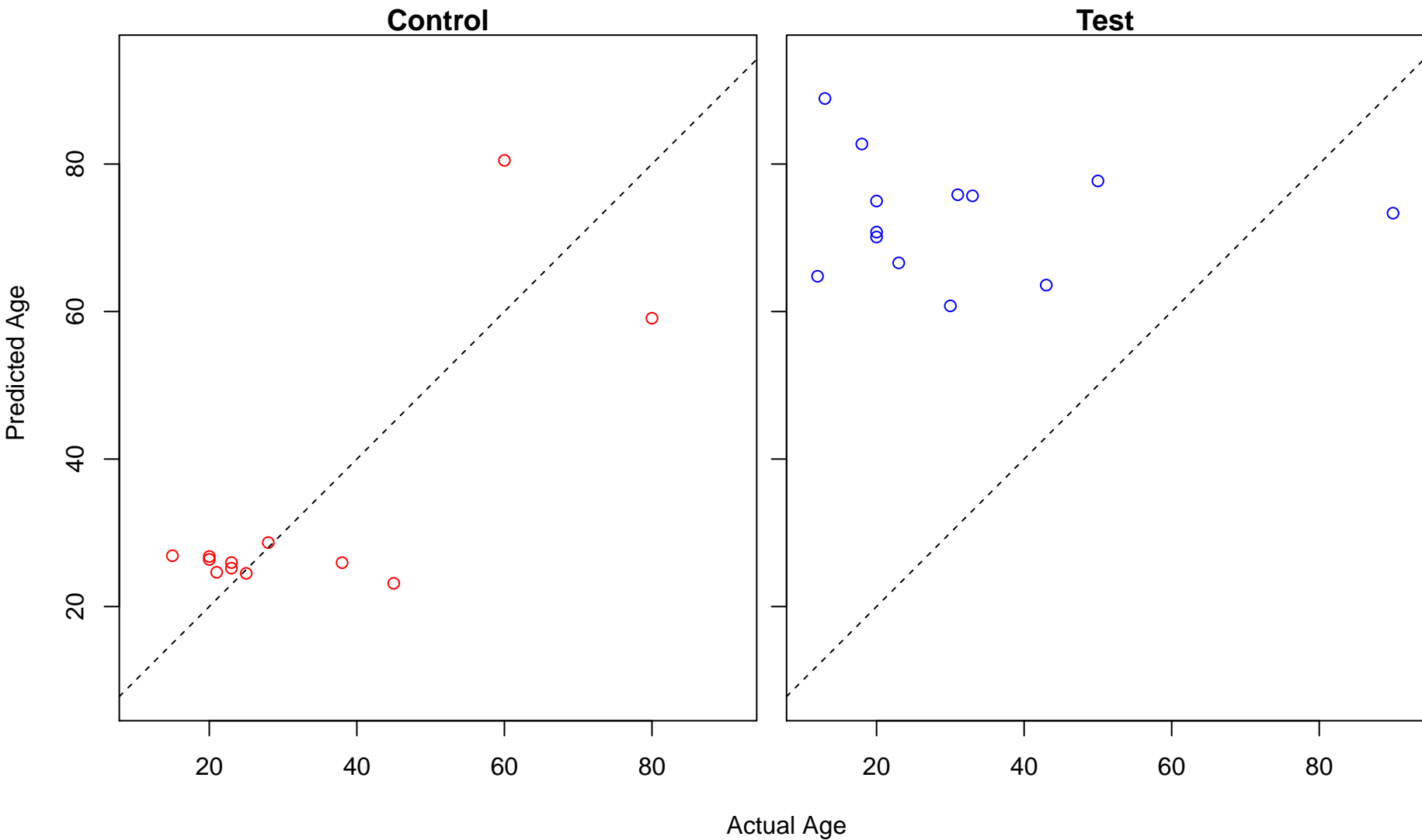
negative regulation of endothelial cell chemotaxis (Score: 6.167767)



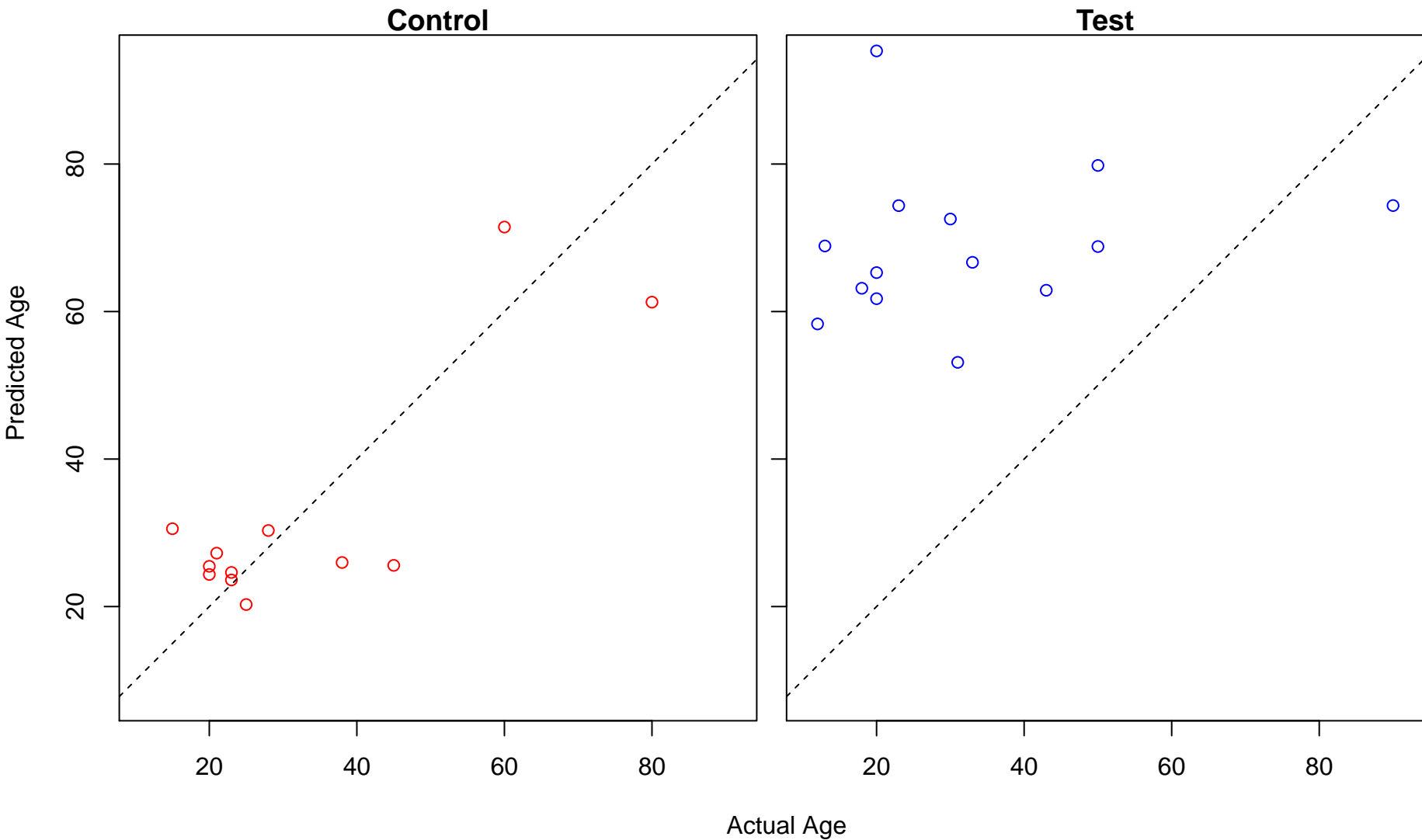
regulation of interferon-gamma biosynthetic process (Score: 6.167723)



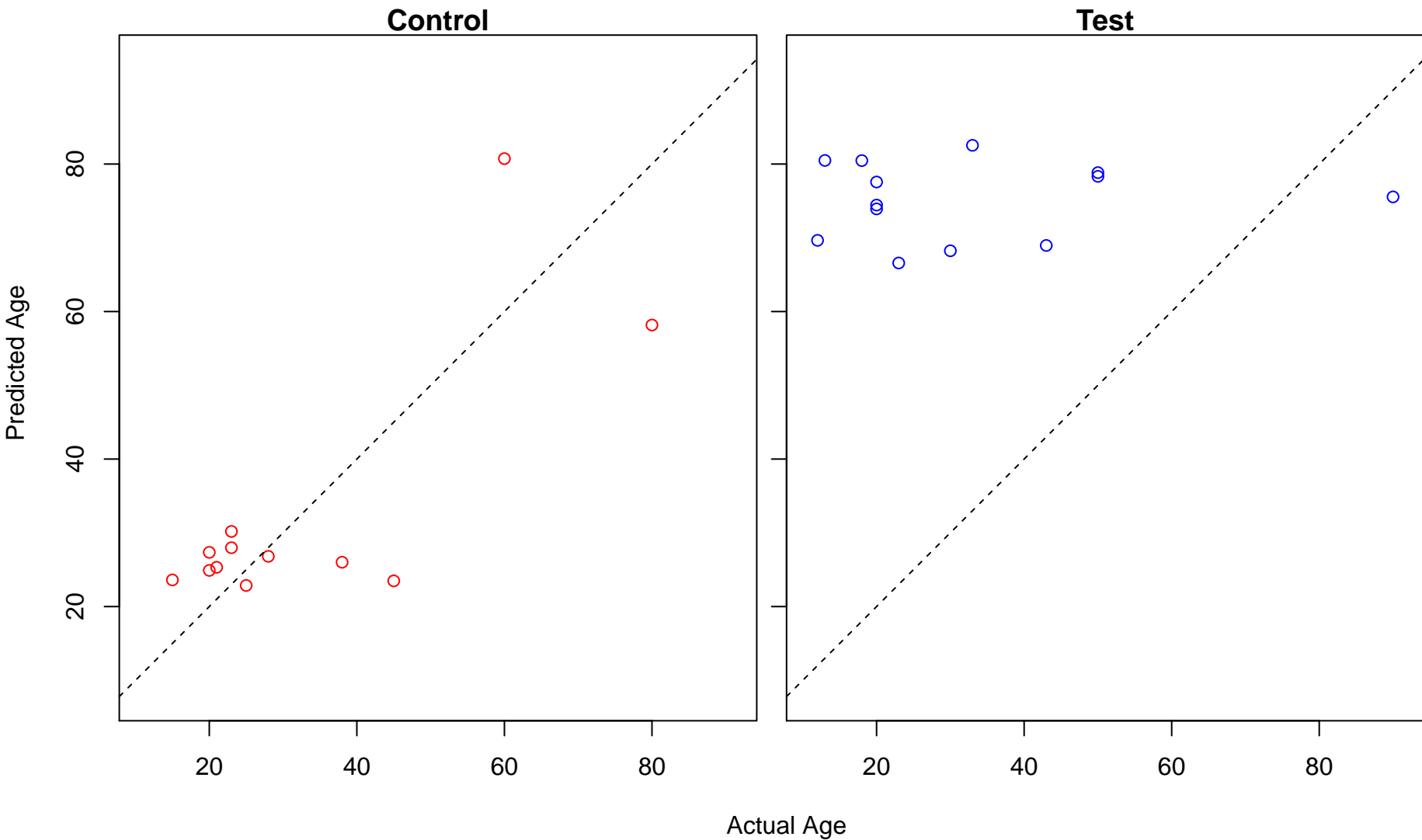
negative regulation of canonical Wnt signaling pathway (Score: 6.165826)



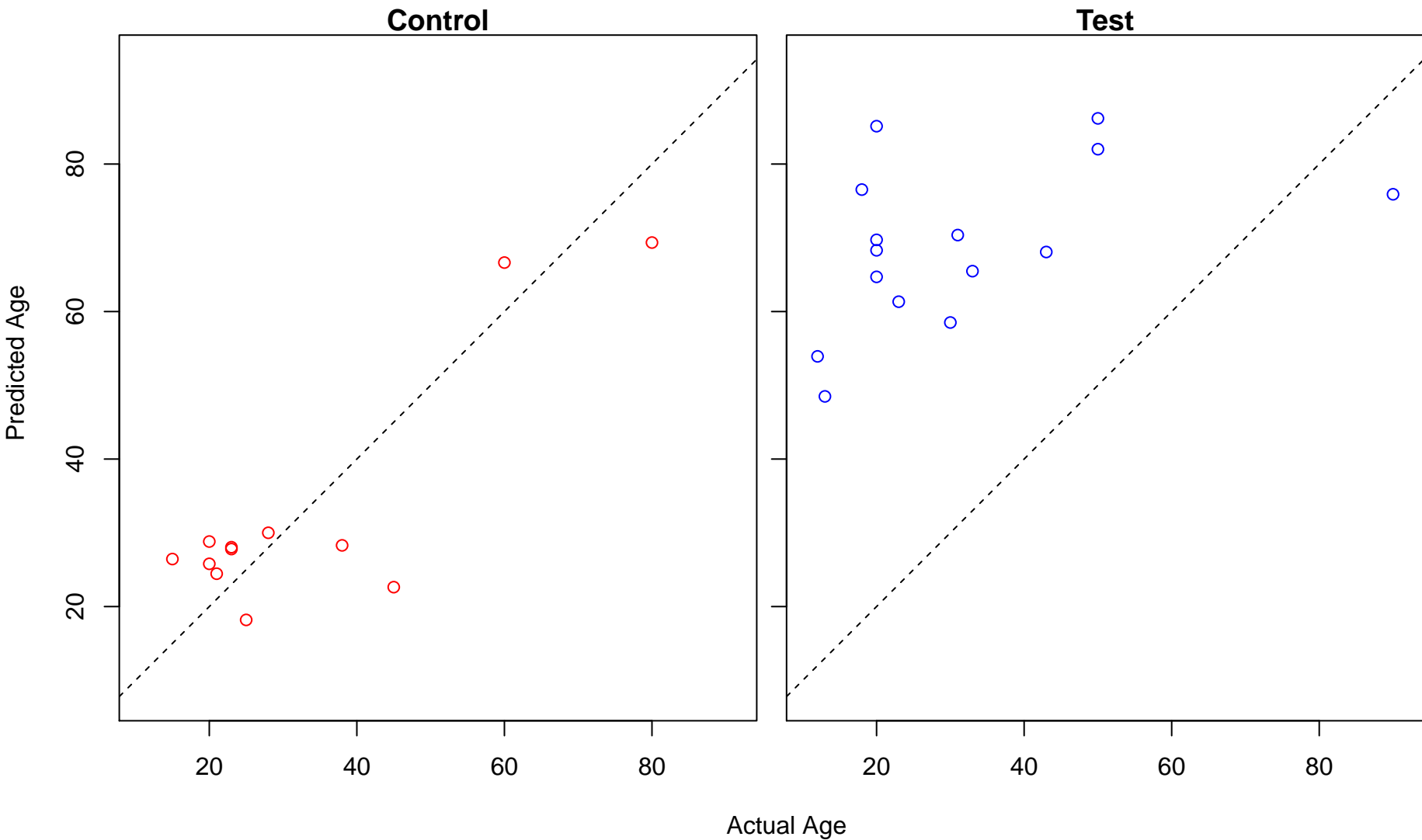
cellular response to UV (Score: 6.164415)



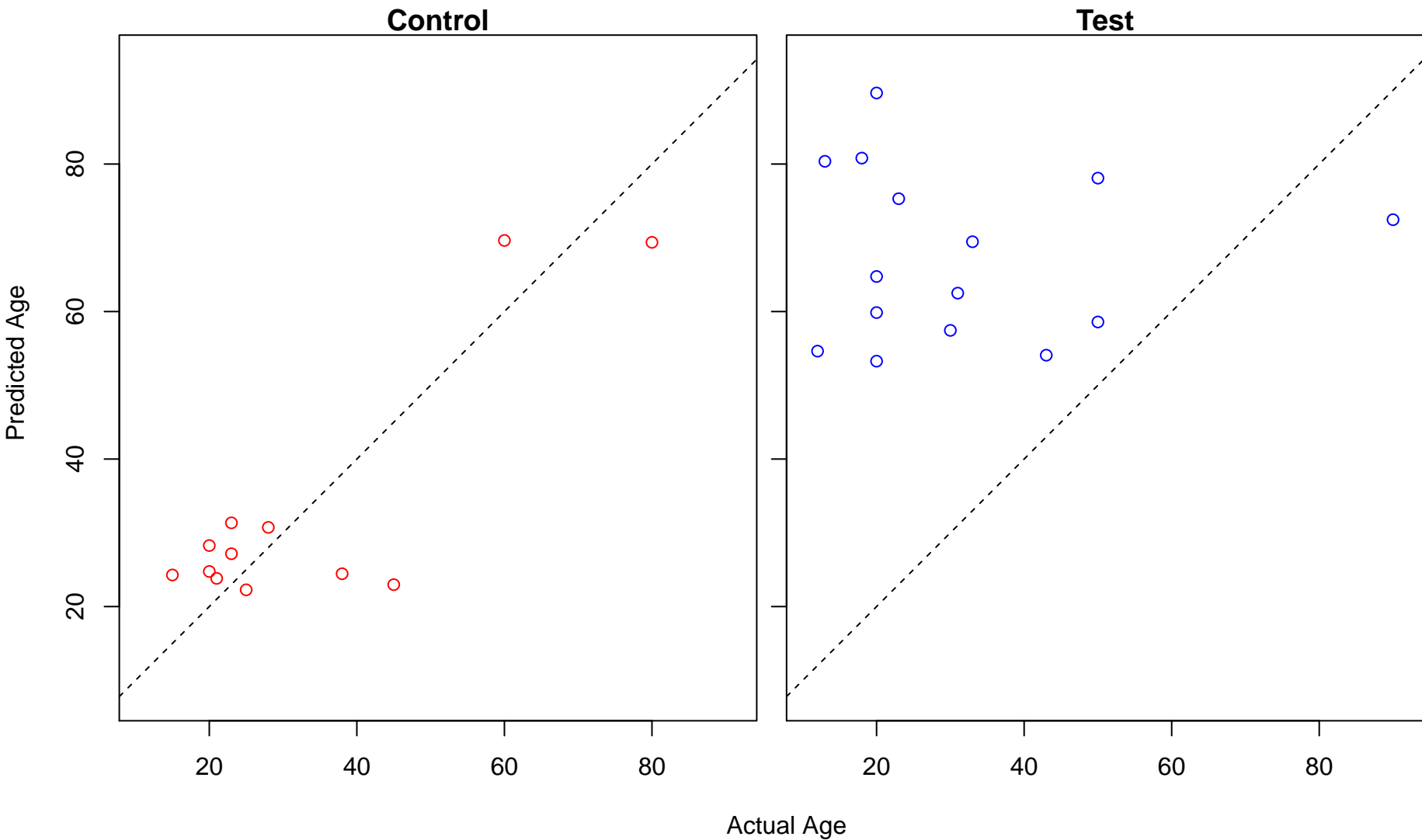
response to salt stress (Score: 6.163729)



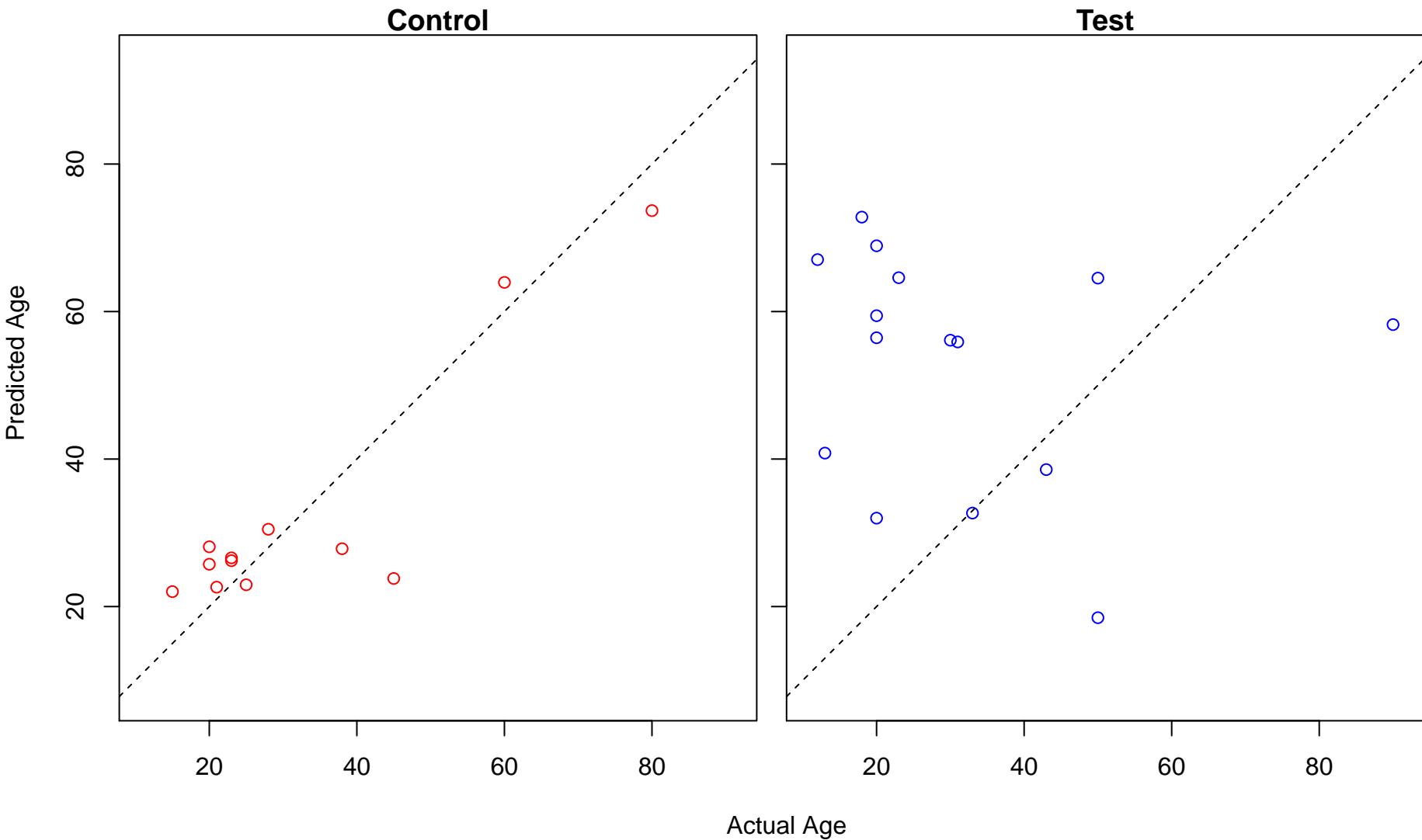
negative regulation of T cell activation (Score: 6.162757)



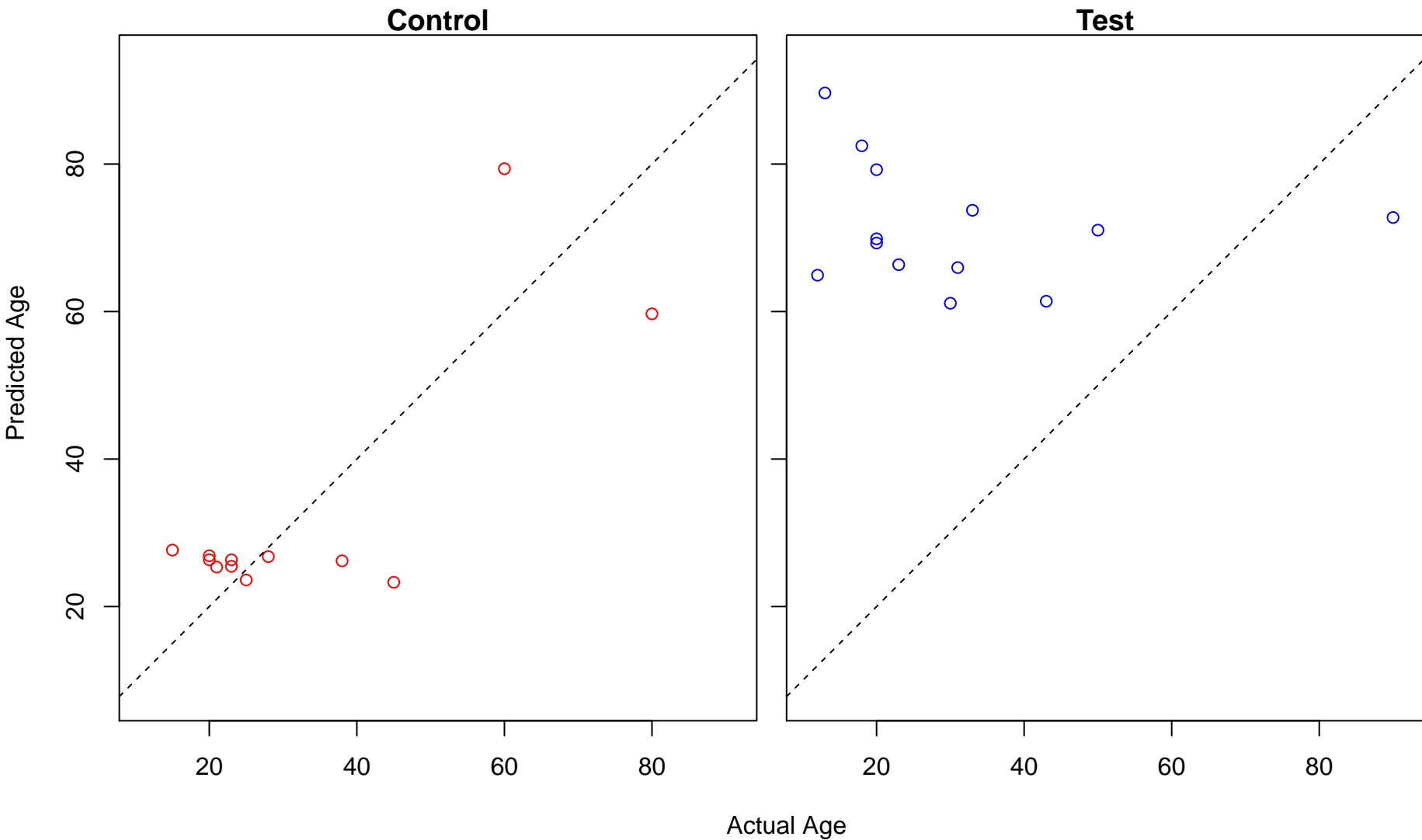
epithelial cell differentiation (Score: 6.162015)



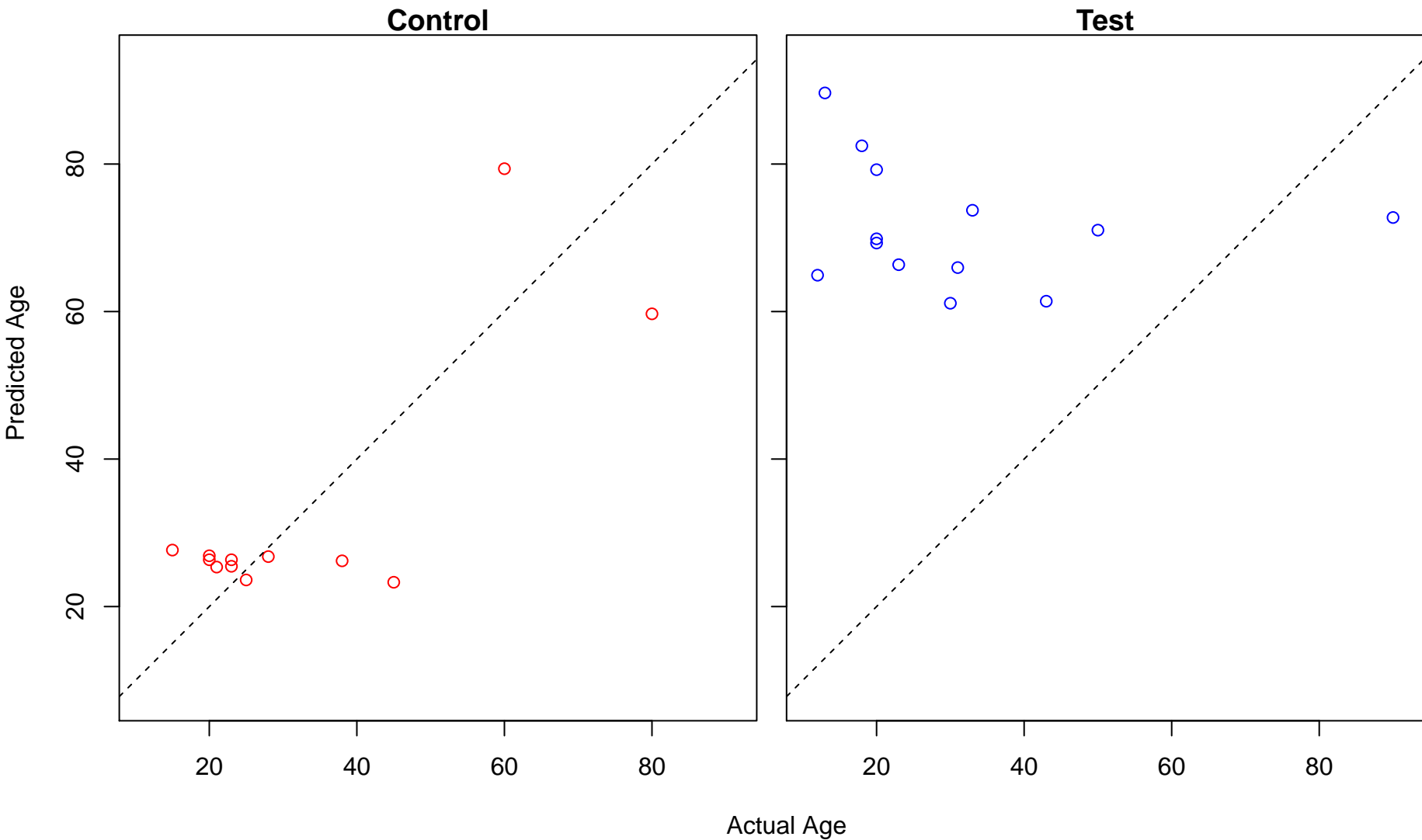
response to X-ray (Score: 6.159145)



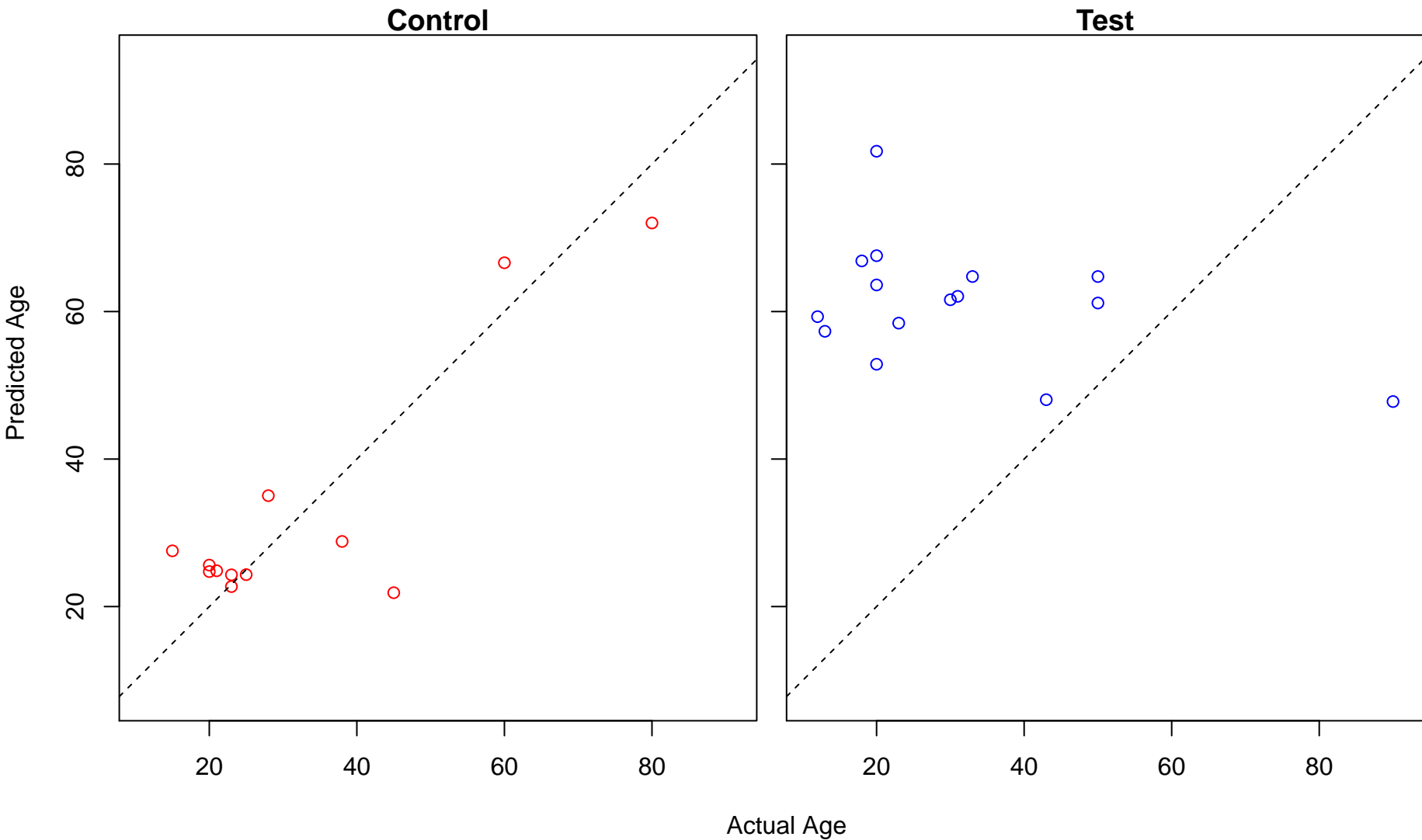
double-strand break repair via homologous recombination (Score: 6.158757)



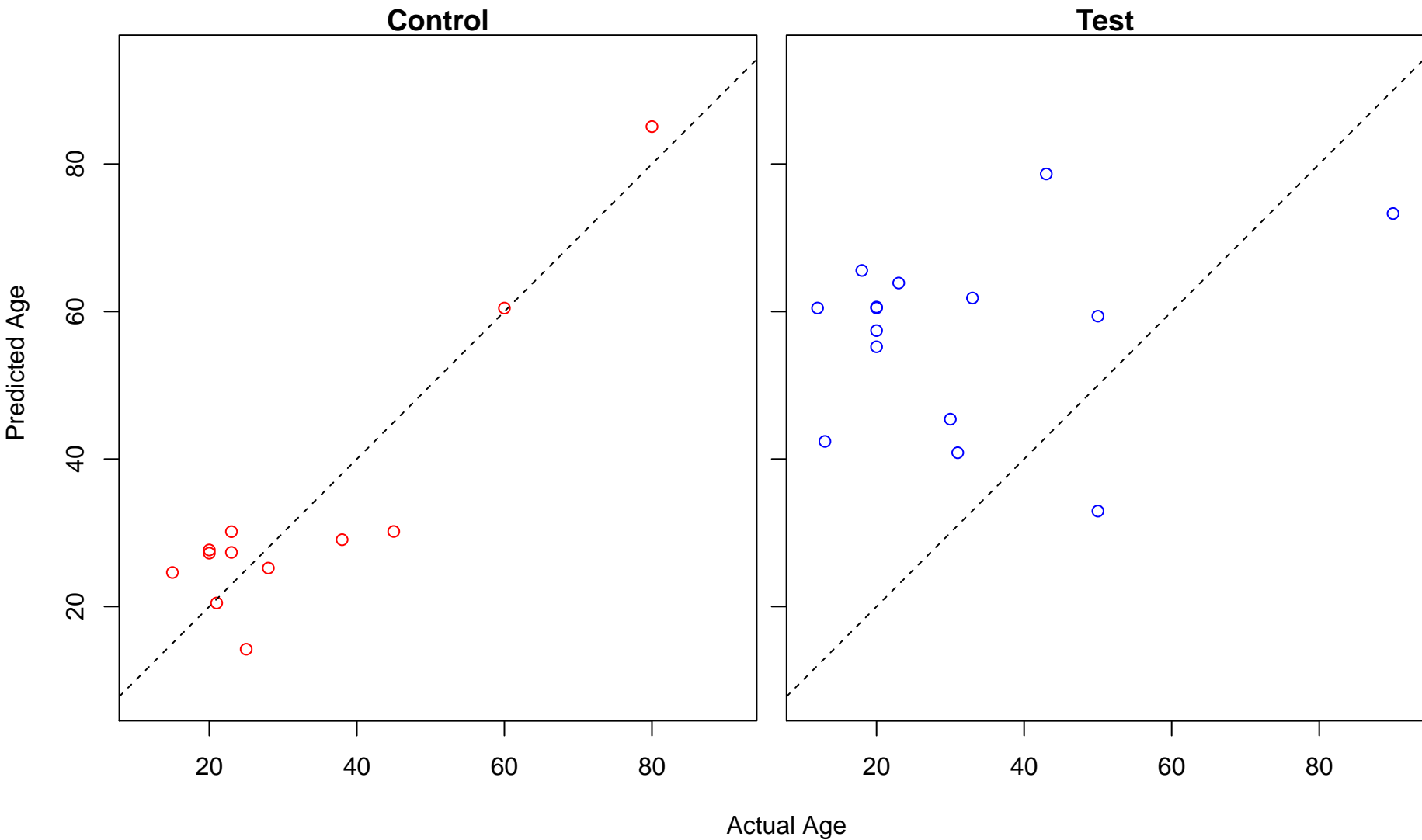
recombinational repair (Score: 6.158757)



trabecula formation (Score: 6.158213)

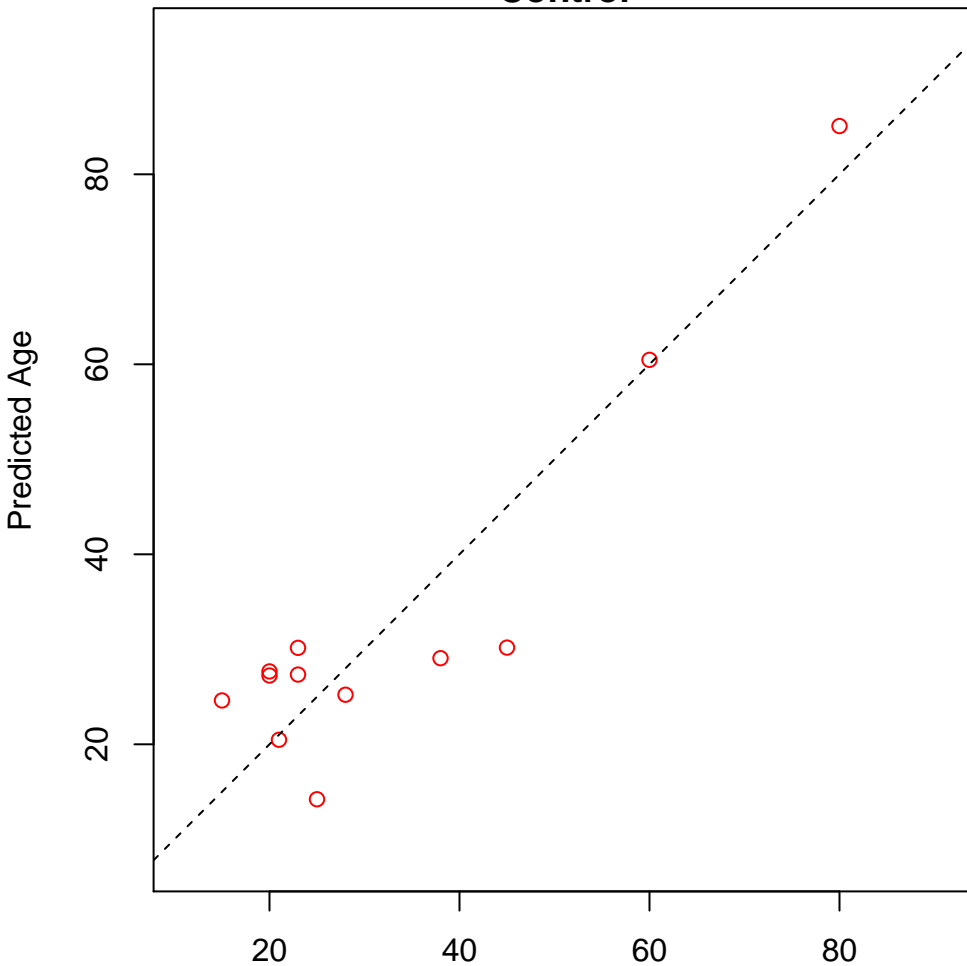


renal system vasculature morphogenesis (Score: 6.155783)

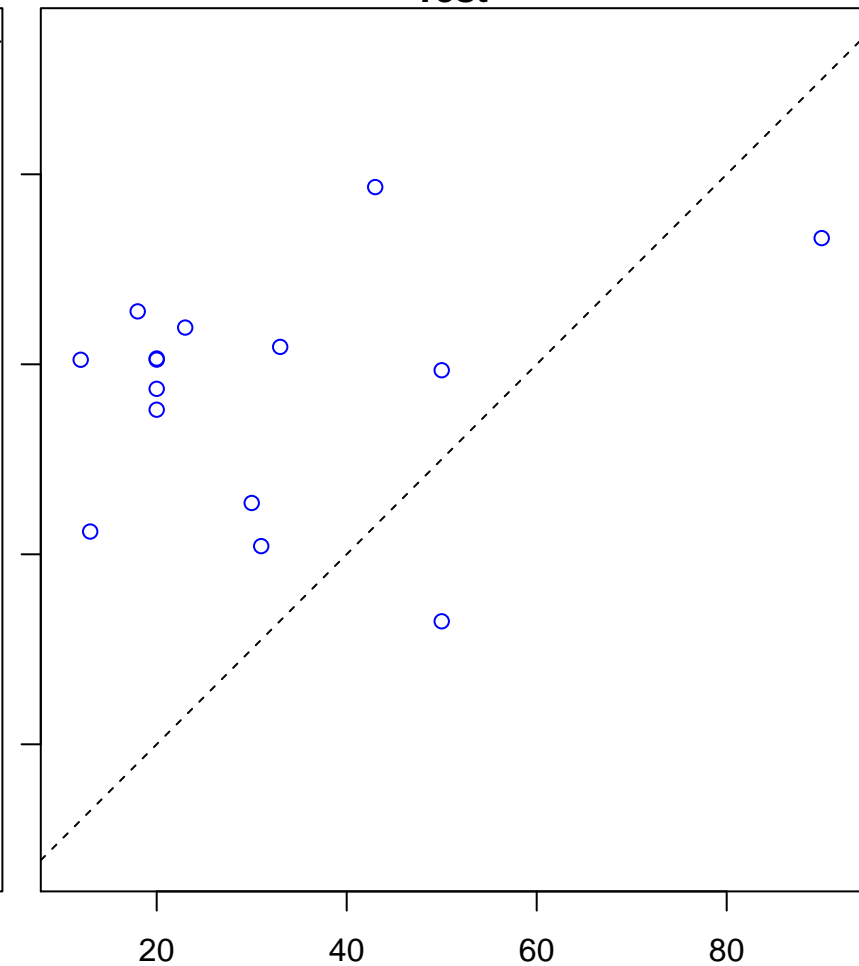


kidney vasculature morphogenesis (Score: 6.155783)

Control

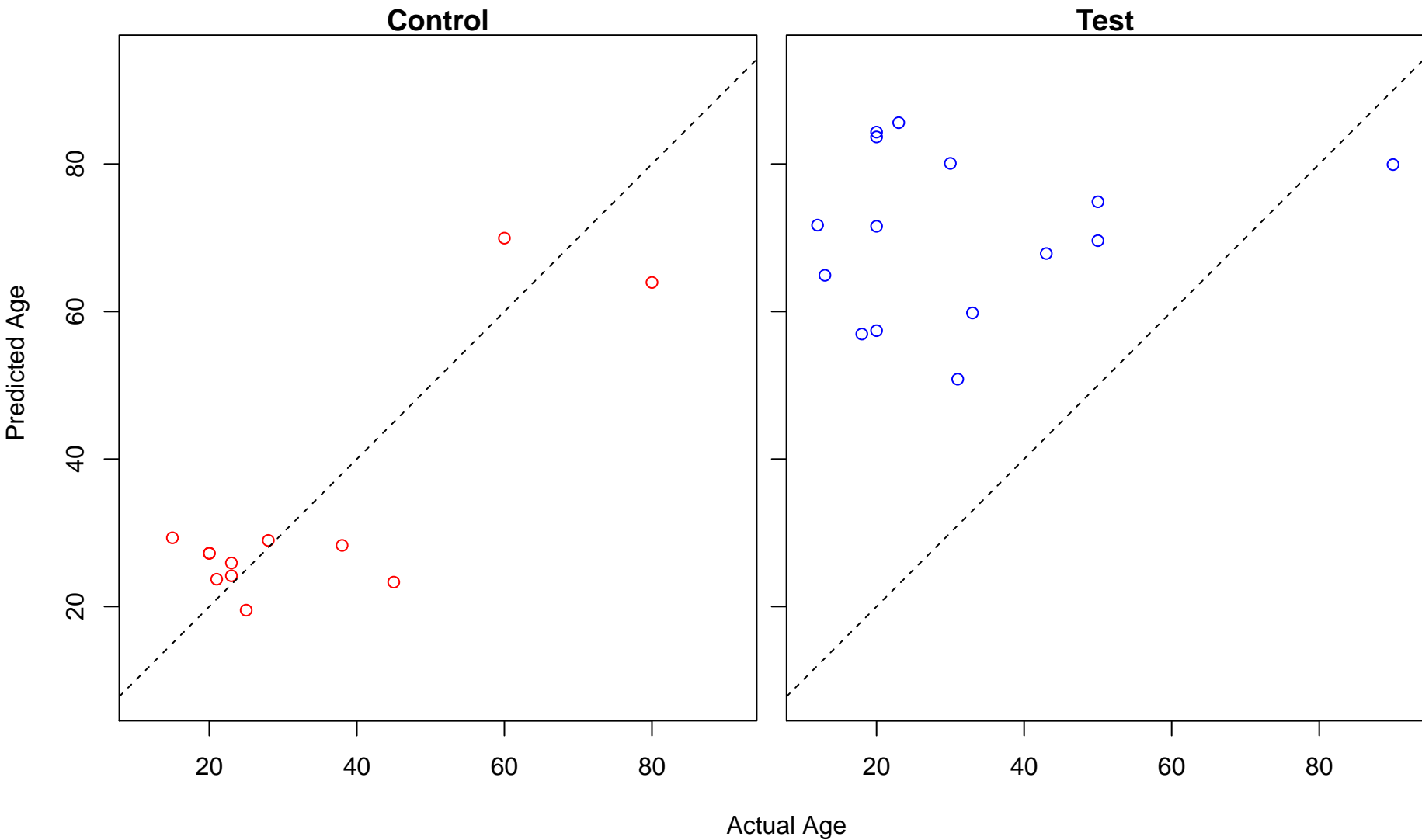


Test

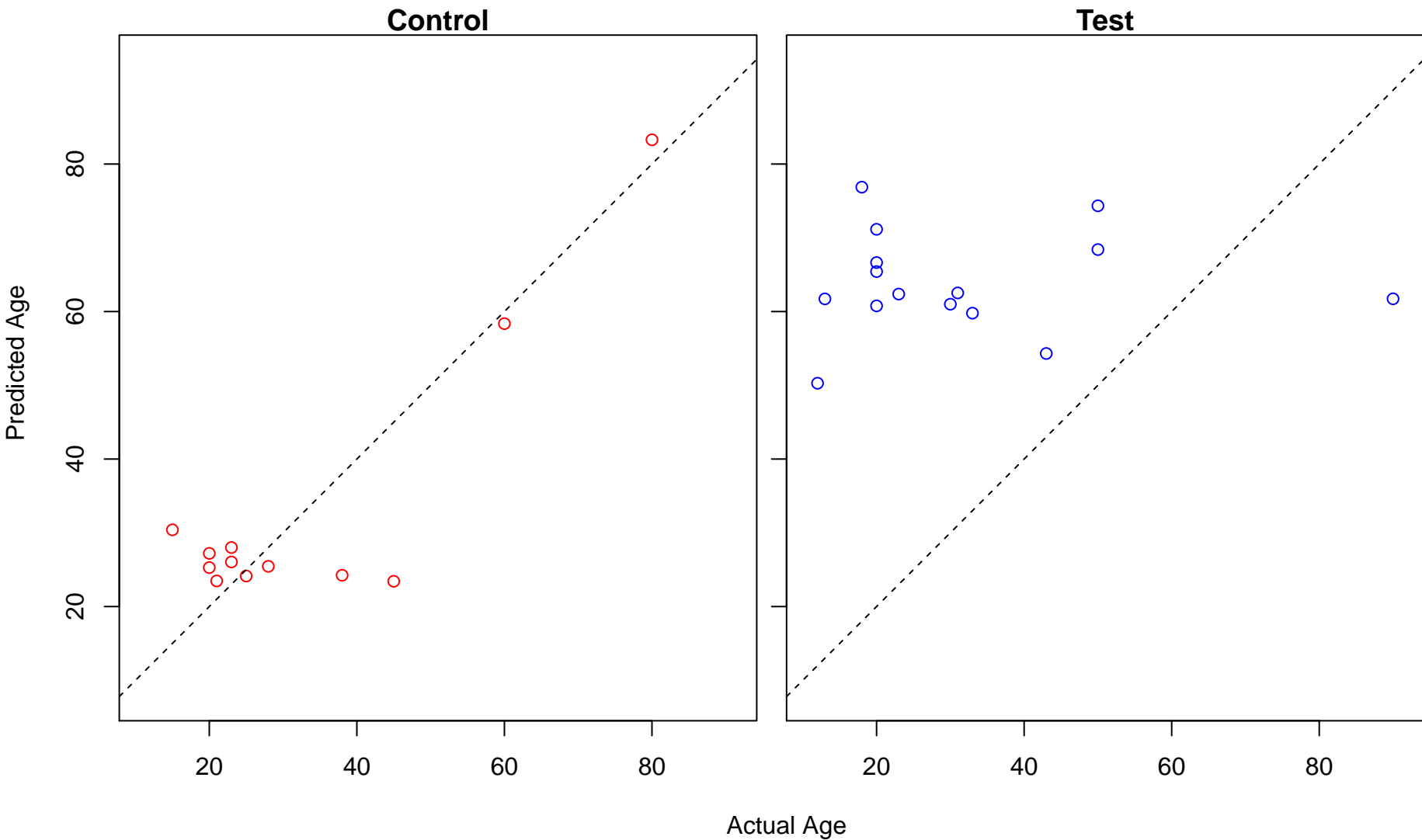


Actual Age

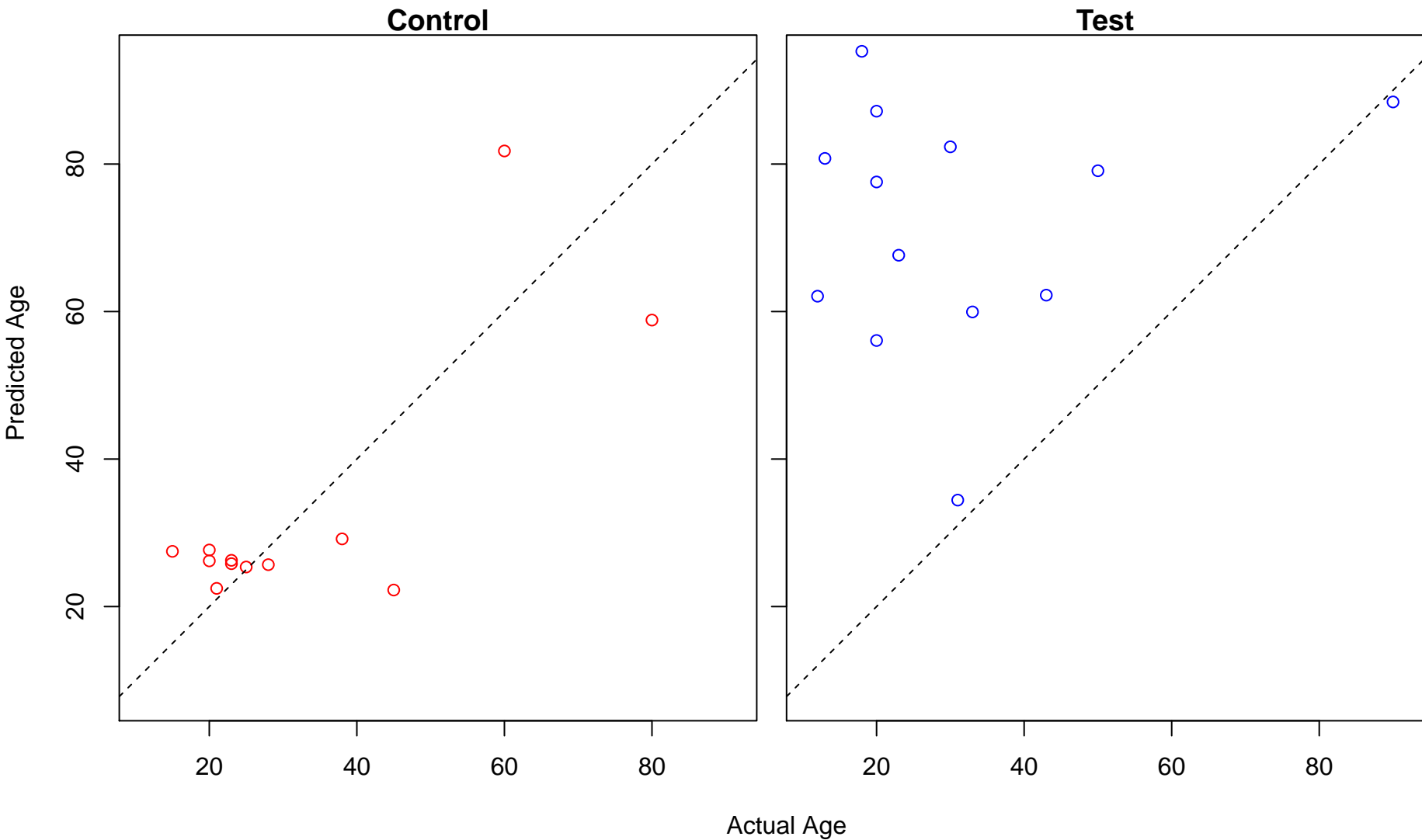
negative regulation of ERK1 and ERK2 cascade (Score: 6.154841)



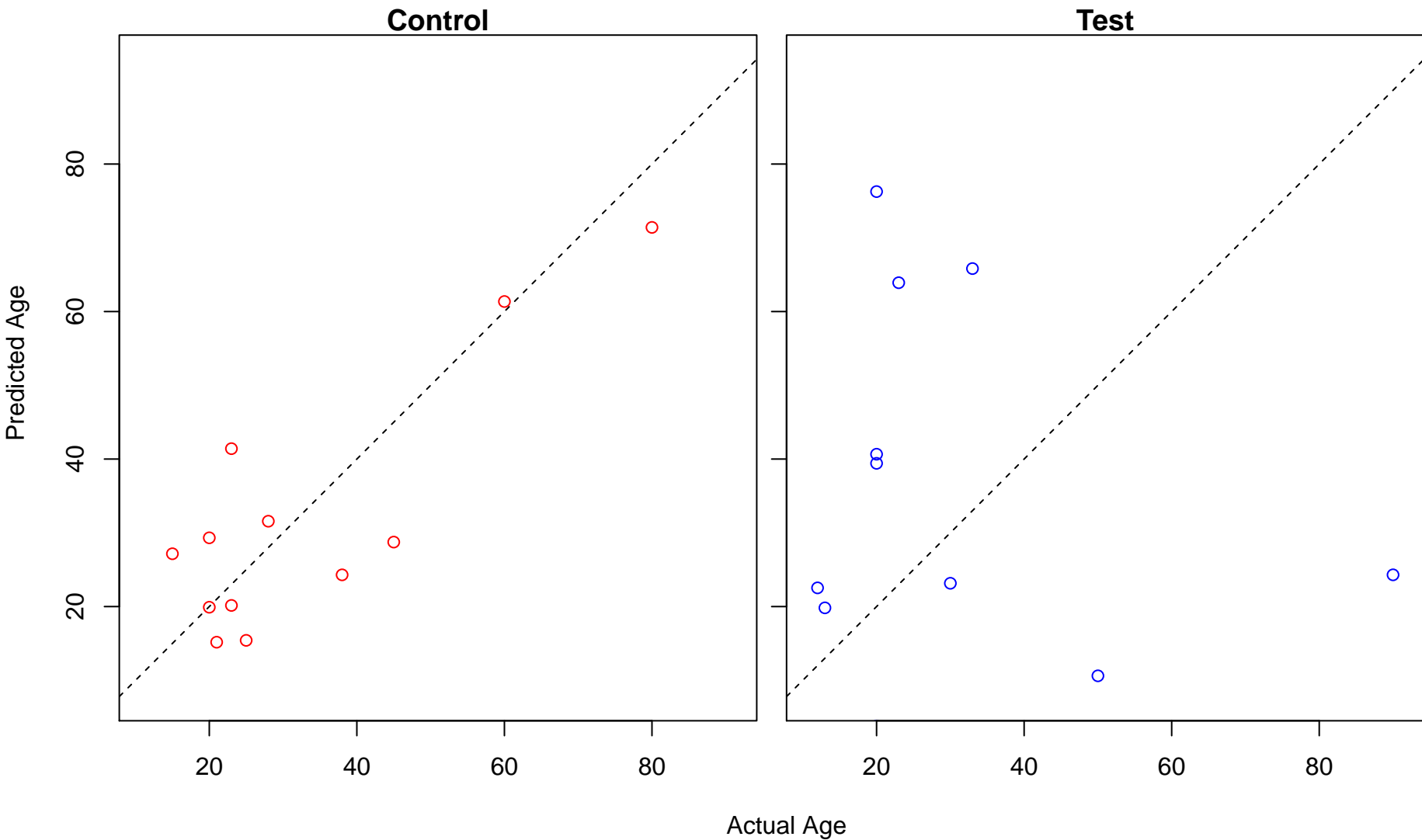
regulation of dendrite development (Score: 6.154155)



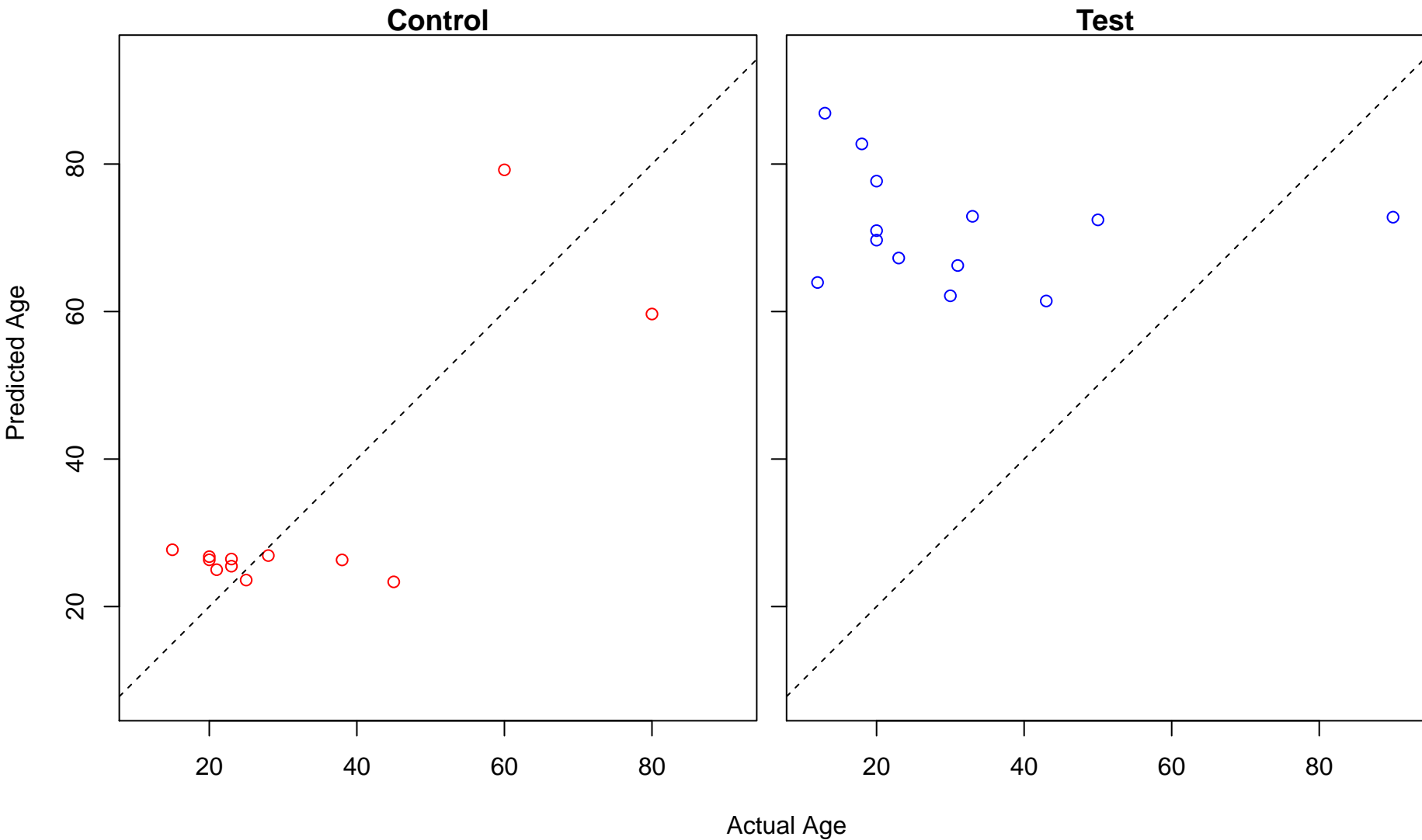
sarcomere organization (Score: 6.154001)



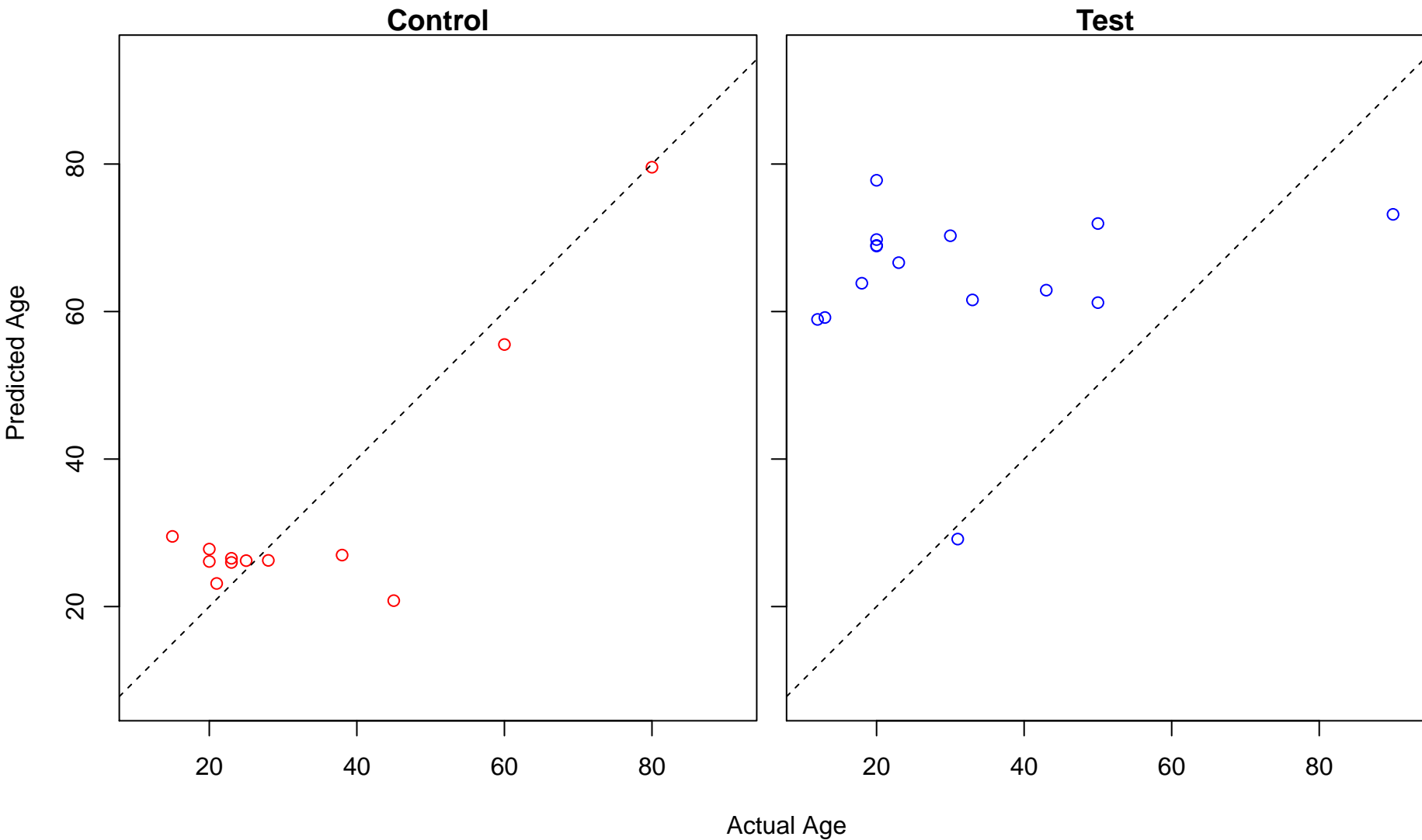
regulation of sister chromatid segregation (Score: 6.153227)



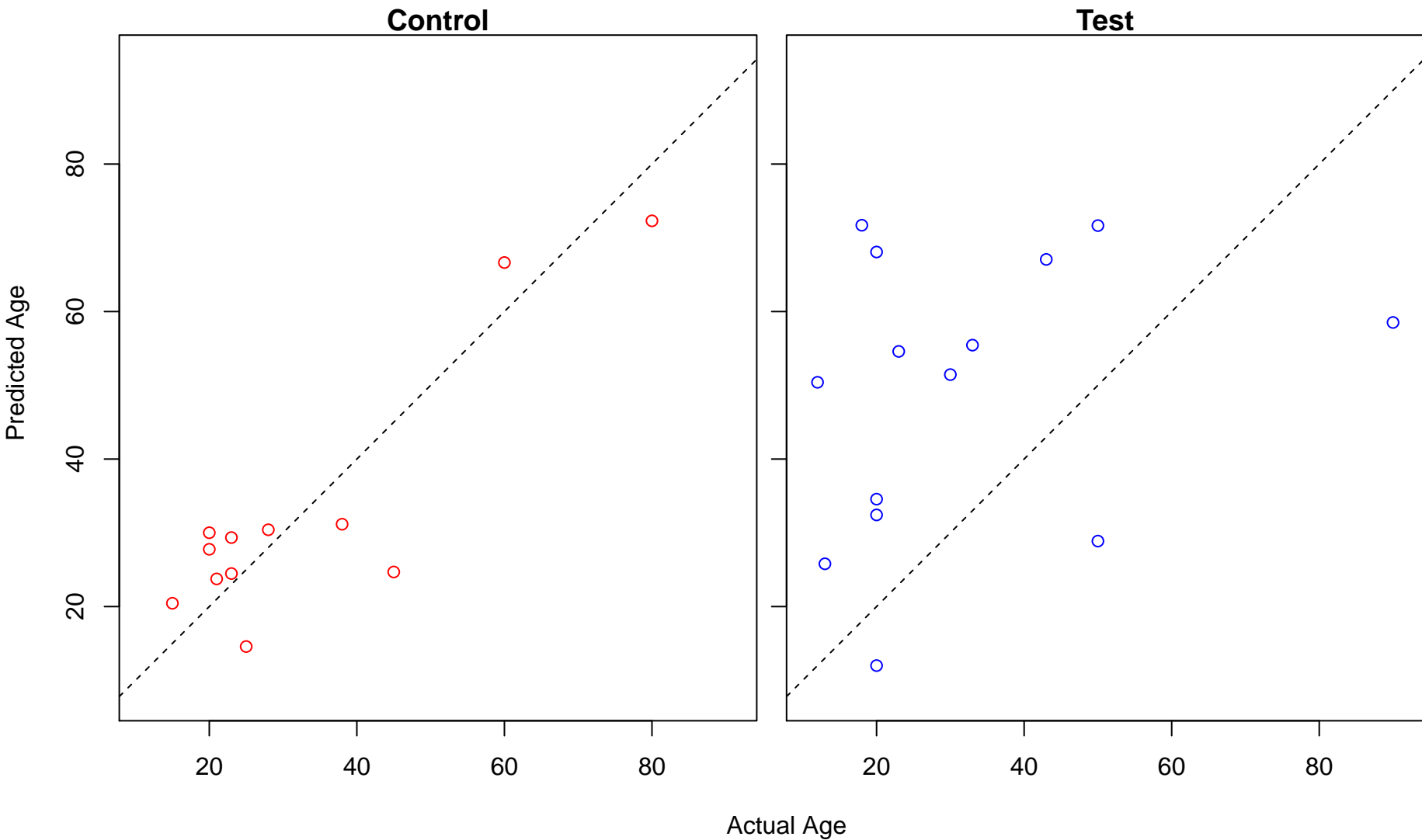
positive regulation of Wnt signaling pathway (Score: 6.148747)



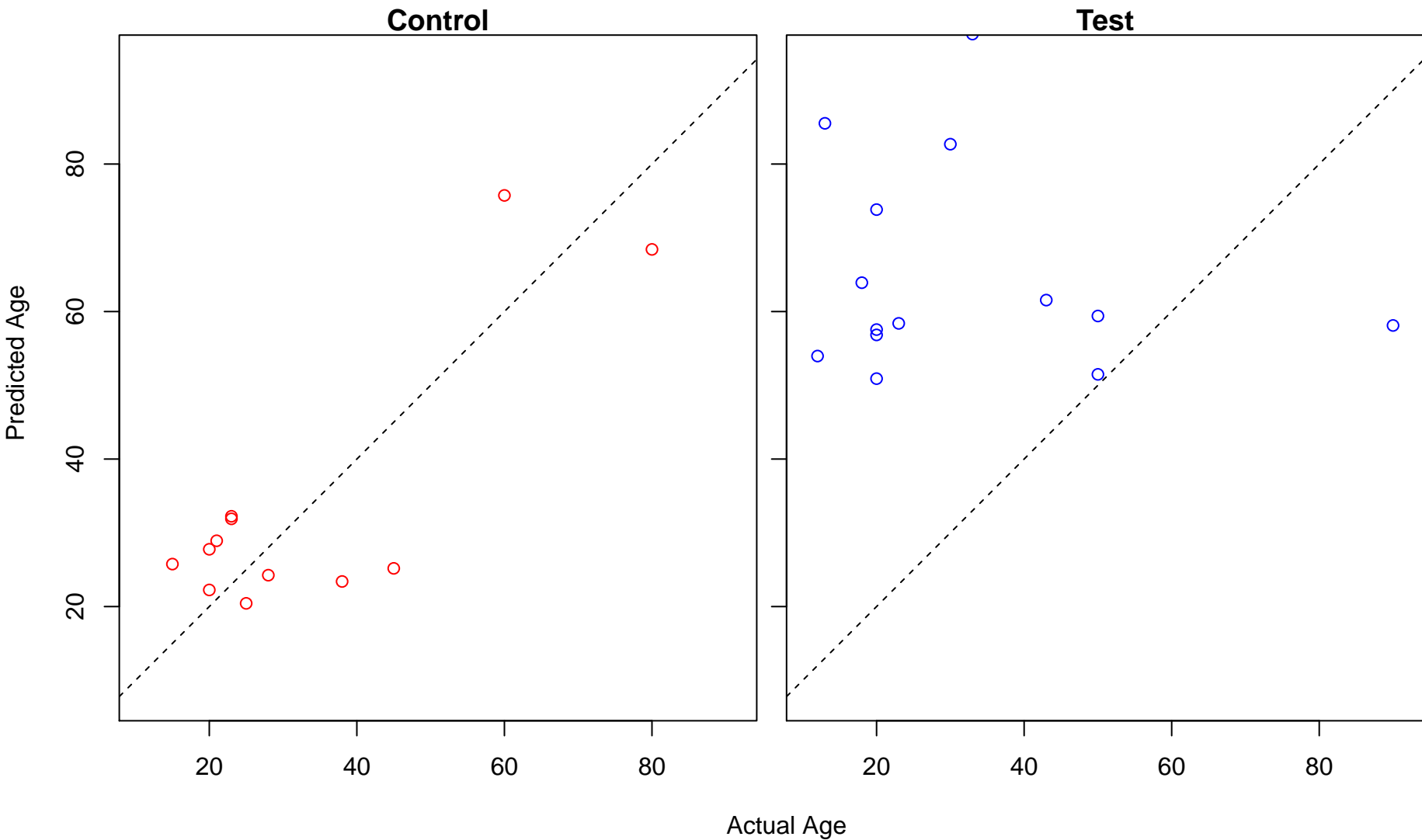
cardiac muscle cell action potential involved in contraction (Score: 6.147728)



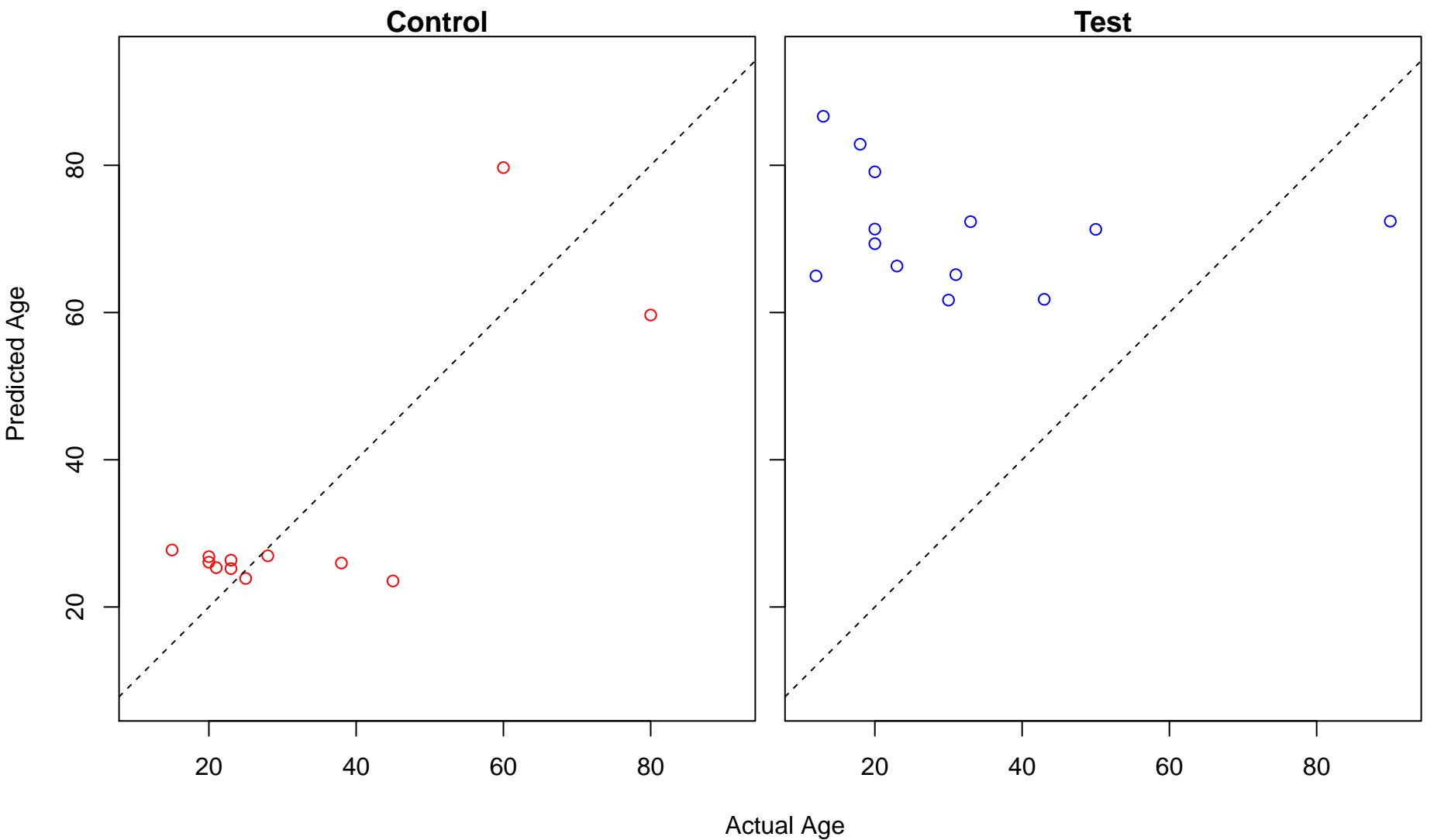
positive regulation of protein oligomerization (Score: 6.146988)



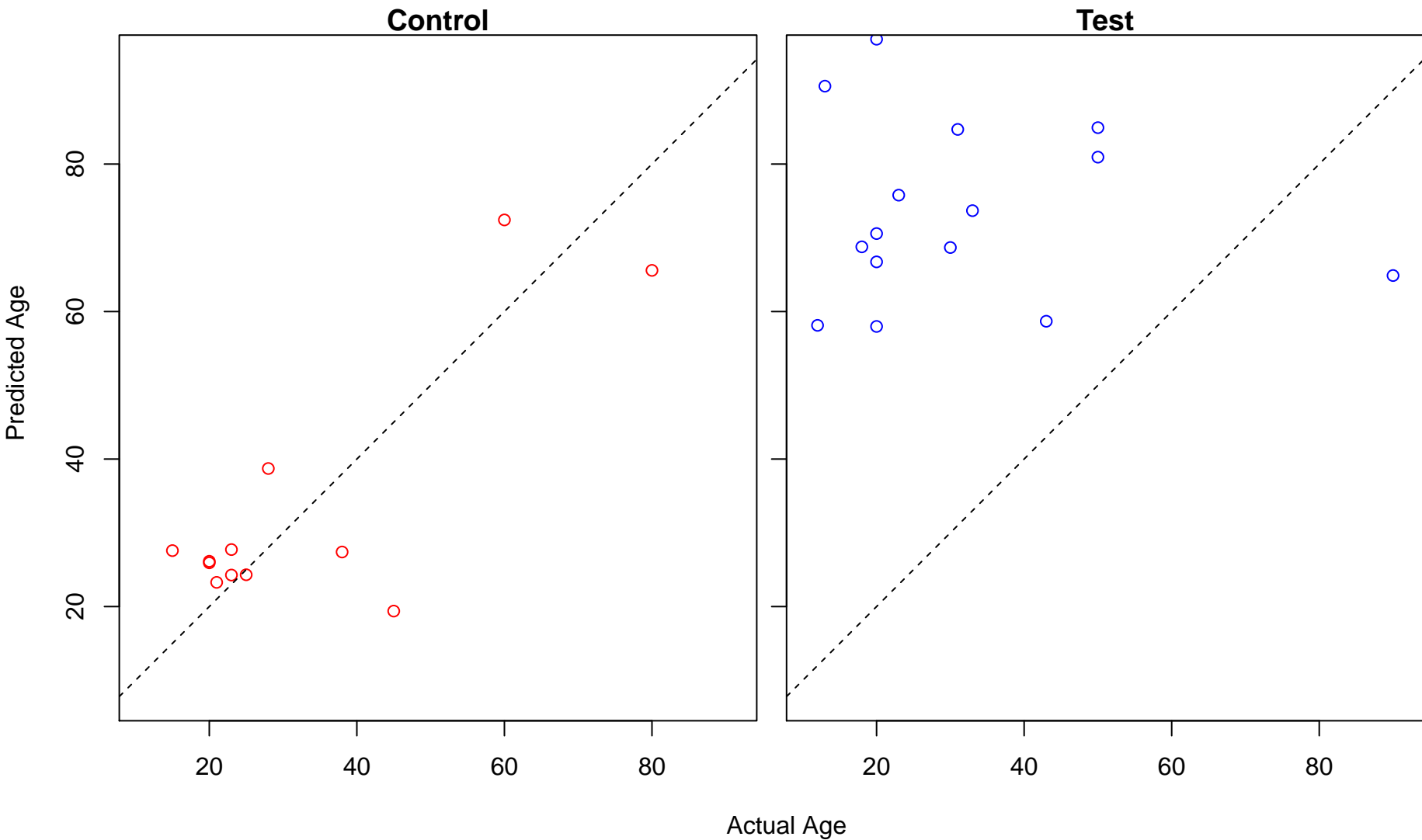
negative regulation of lipid storage (Score: 6.146309)



phase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process (Score

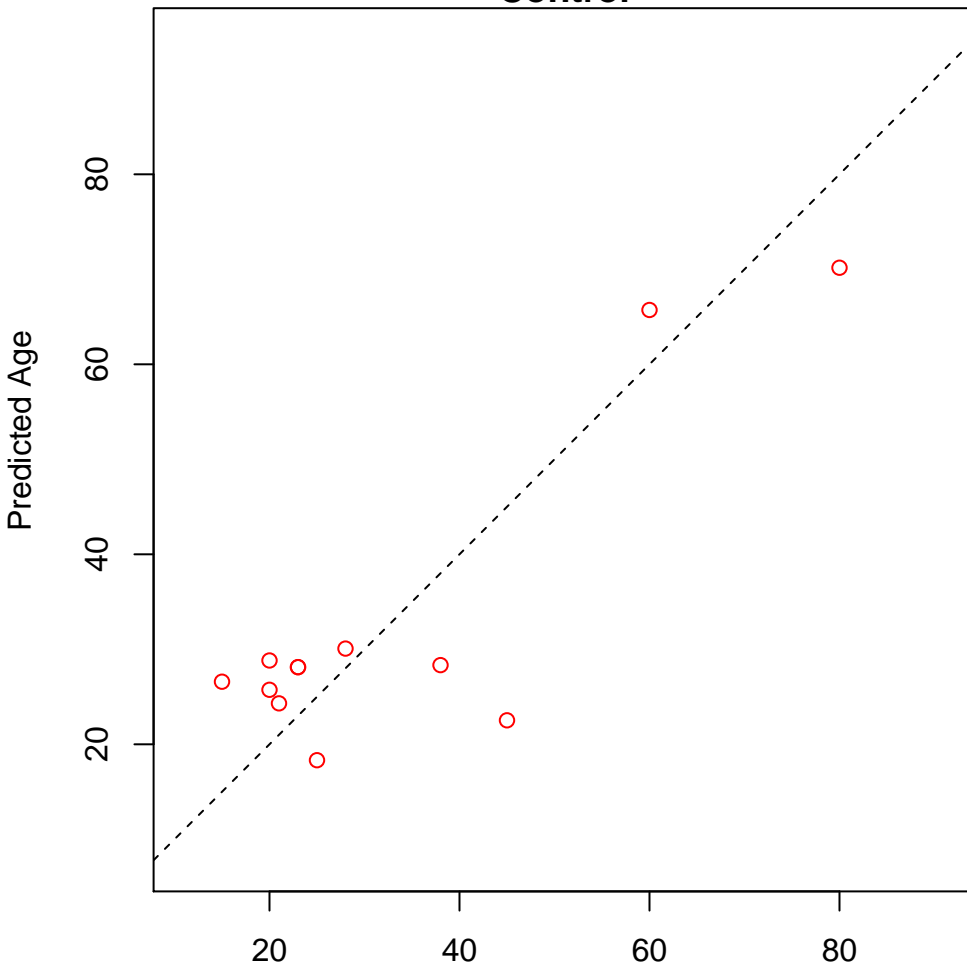


regulation of signal transduction by p53 class mediator (Score: 6.144583)

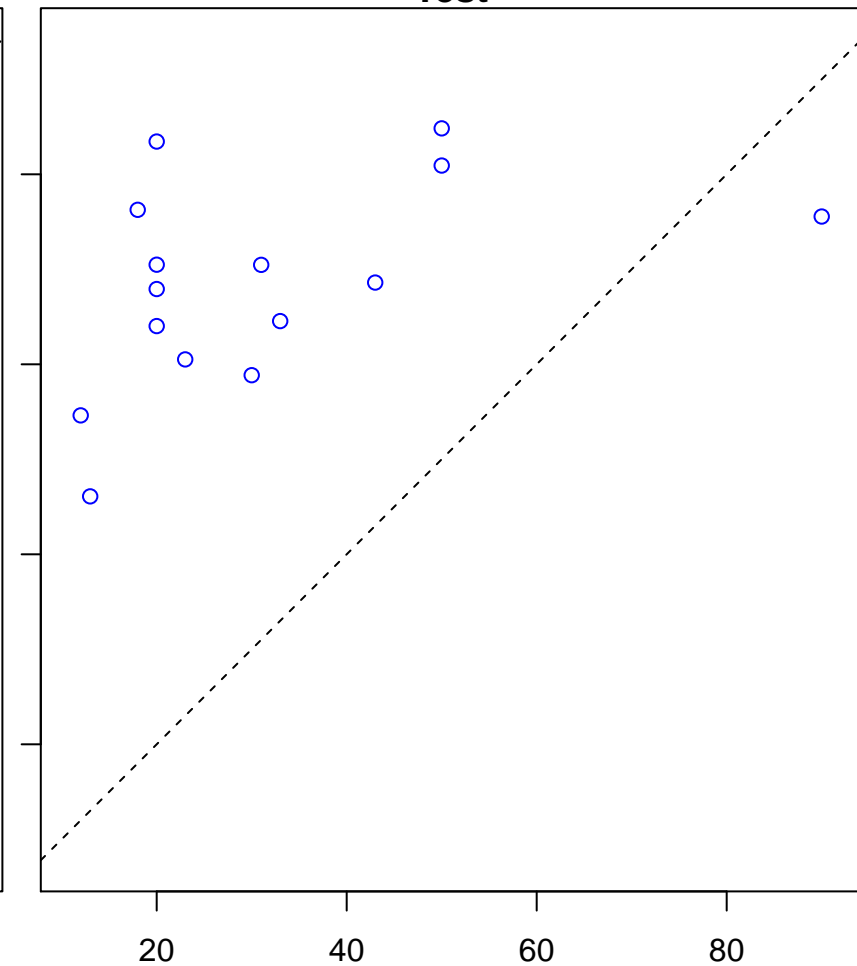


negative regulation of cell-cell adhesion (Score: 6.144474)

Control

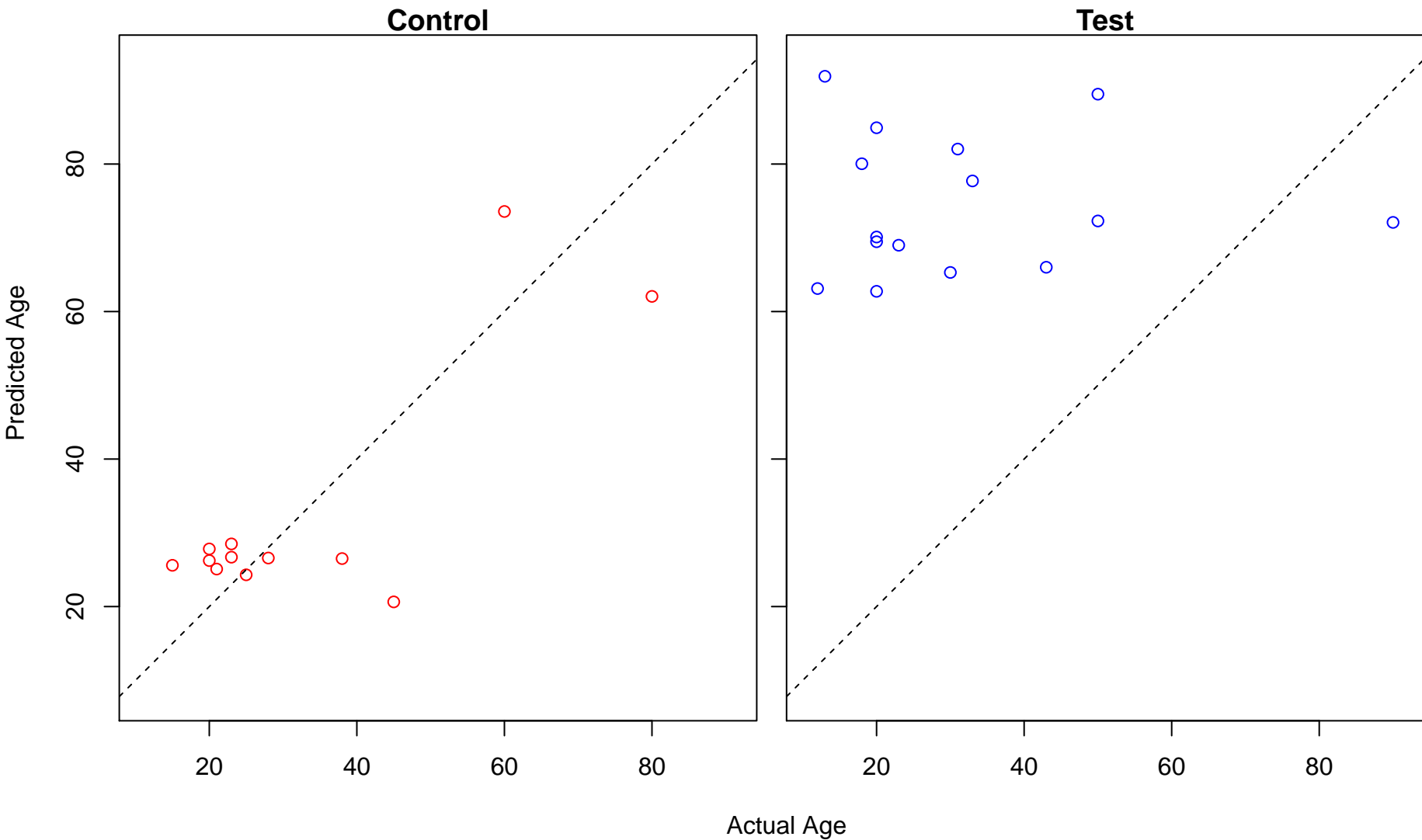


Test

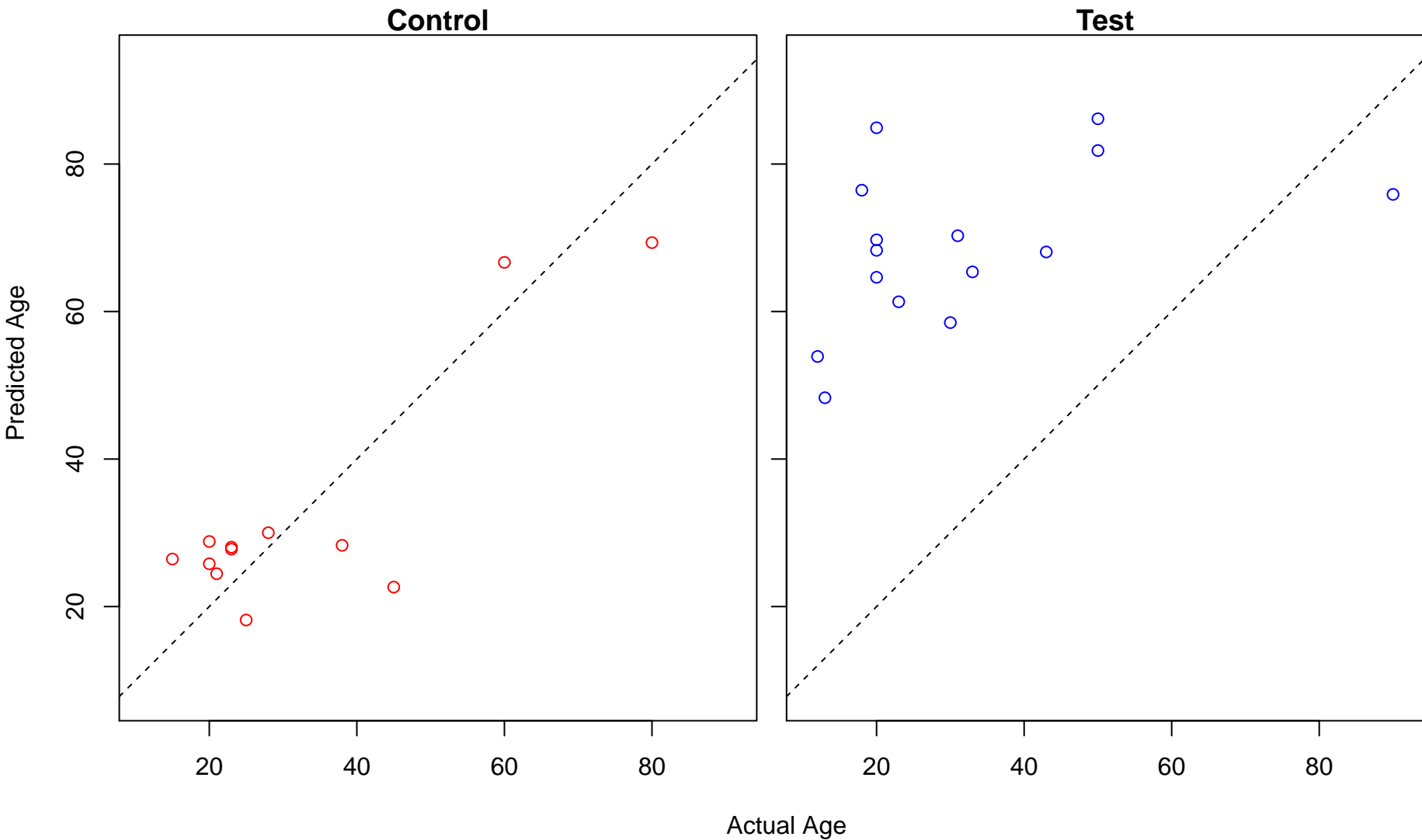


Actual Age

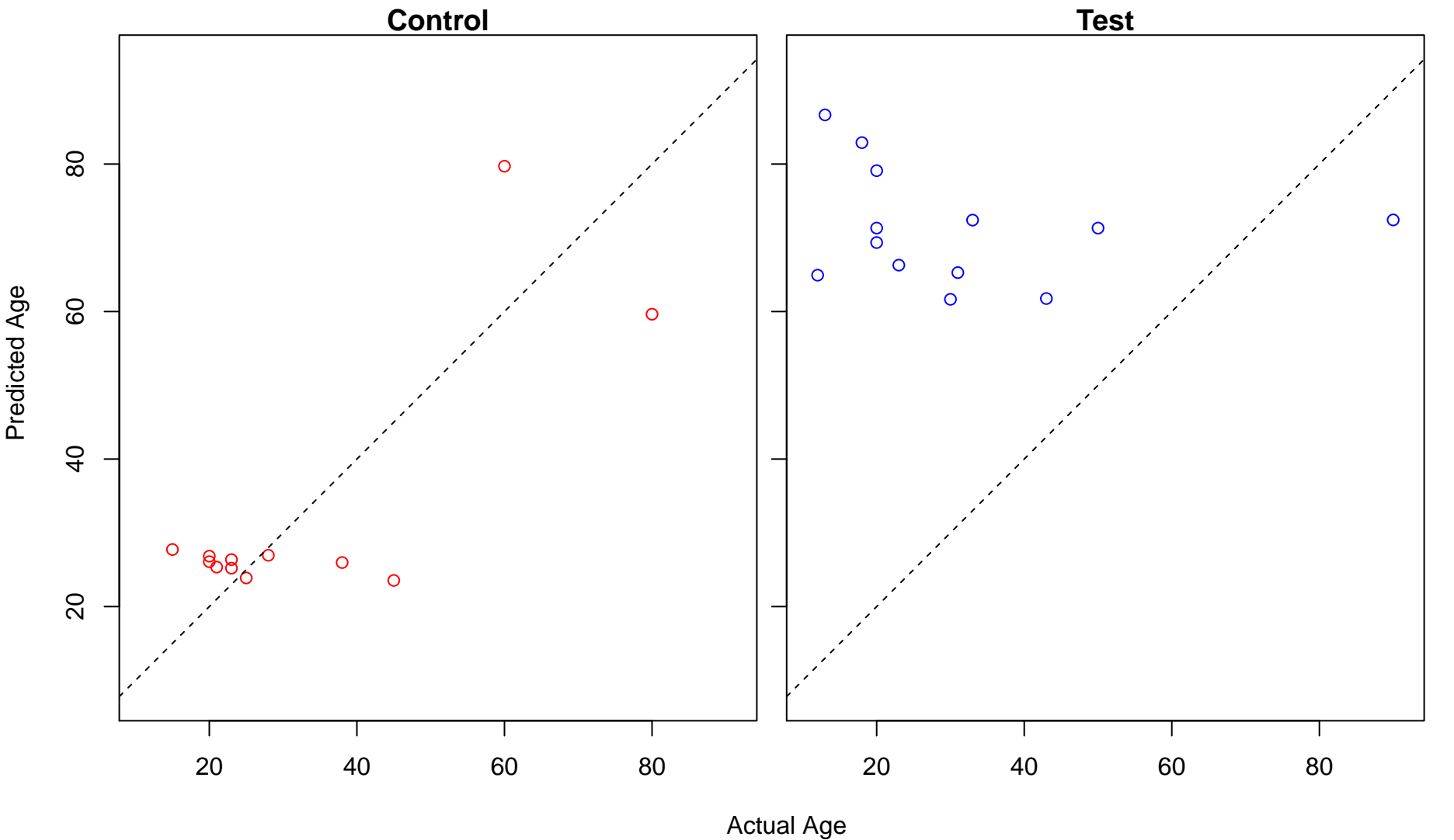
regulation of defense response to virus (Score: 6.143766)



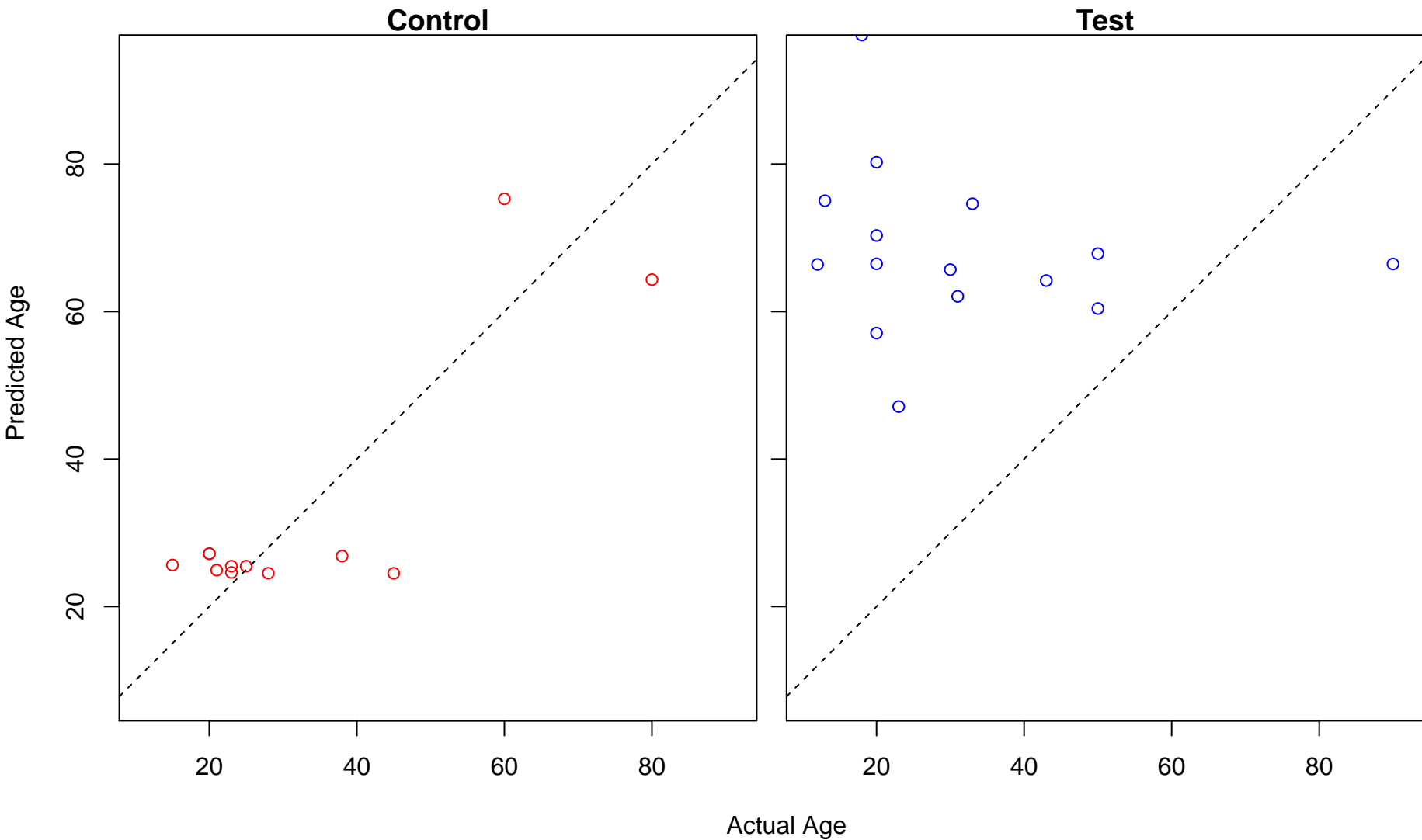
negative regulation of homotypic cell-cell adhesion (Score: 6.143637)



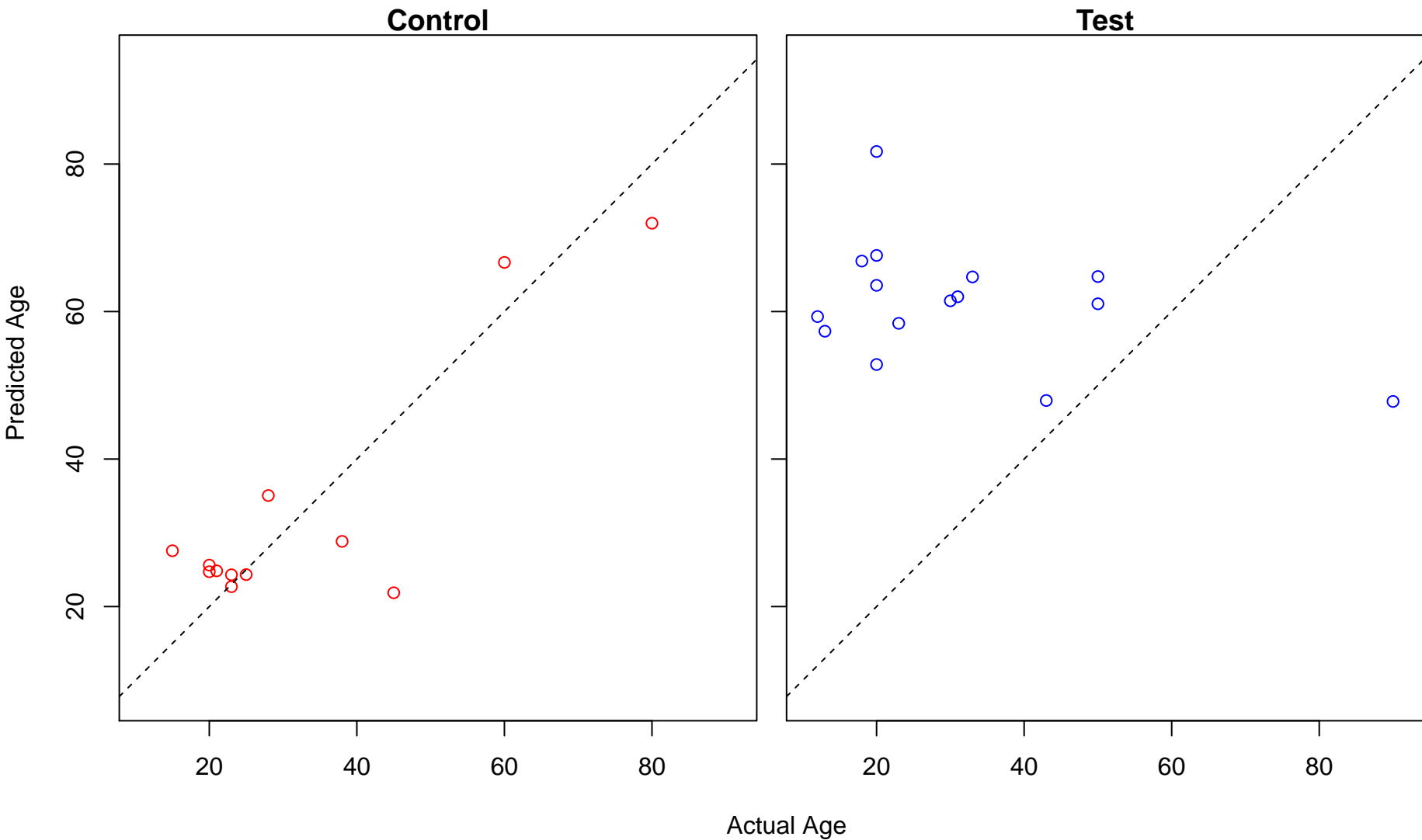
Regulation of ubiquitin–protein ligase activity involved in regulation of mitotic cell cycle transition (Sc



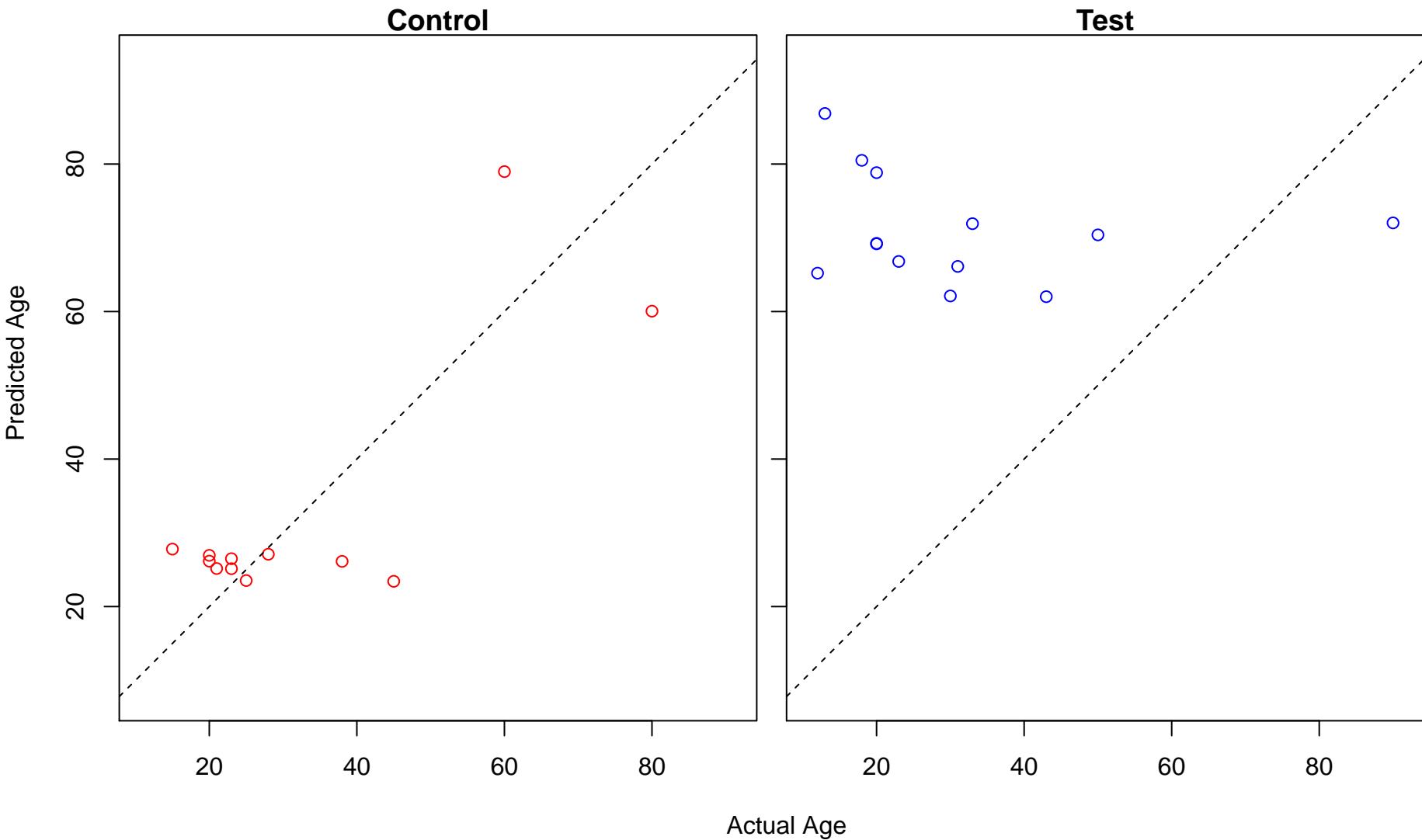
dendritic spine development (Score: 6.143252)



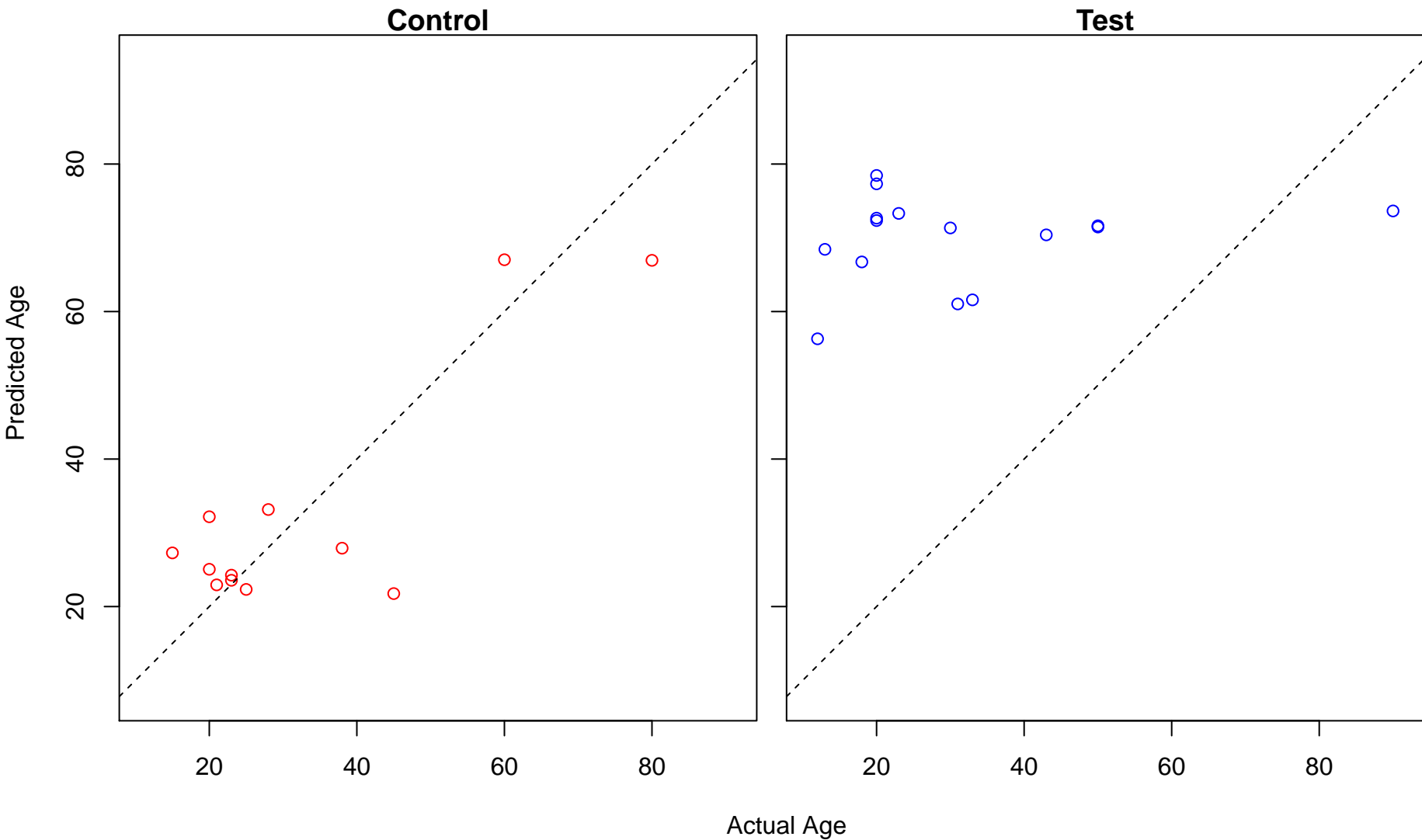
heart trabecula formation (Score: 6.142579)



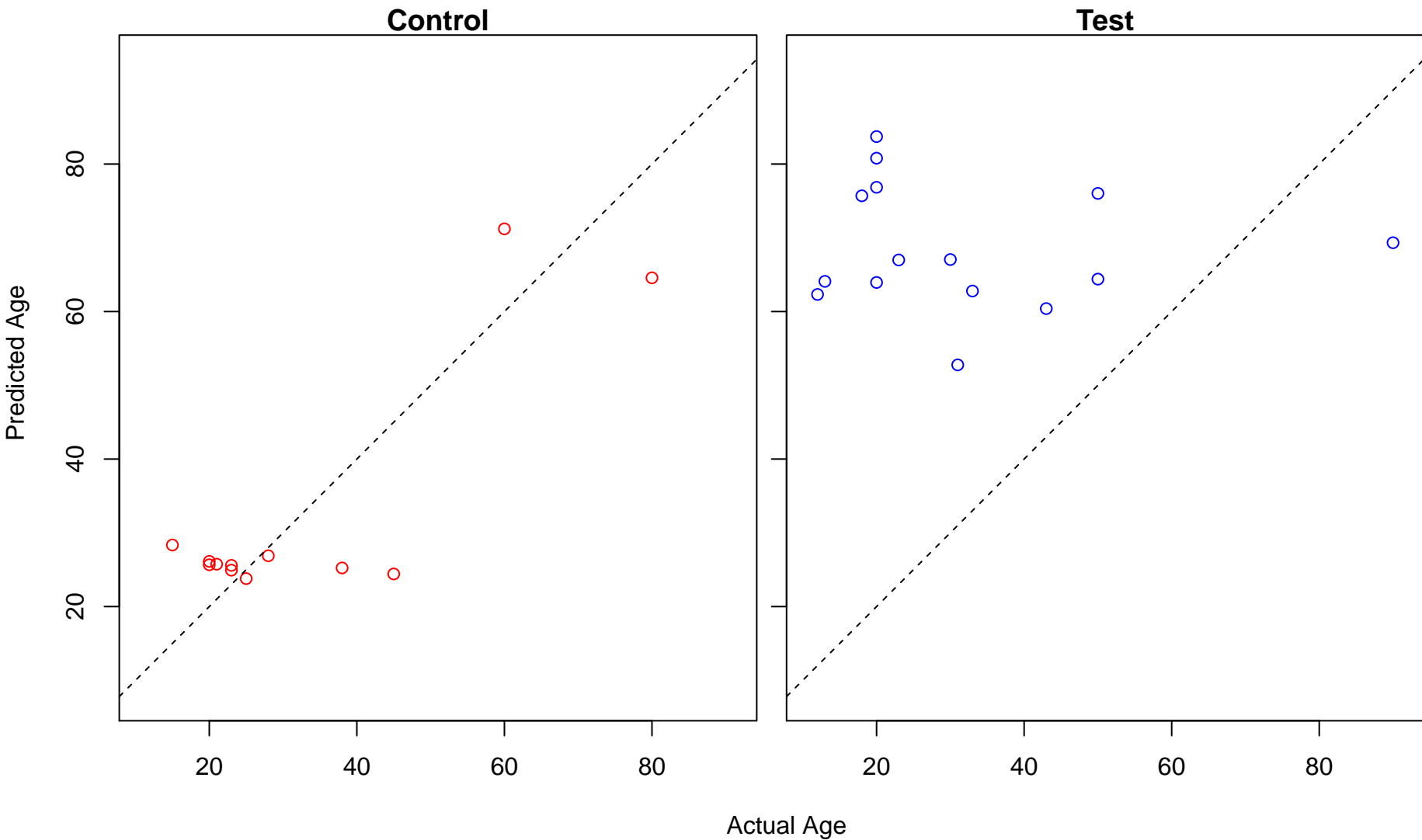
nucleotide-excision repair (Score: 6.142152)



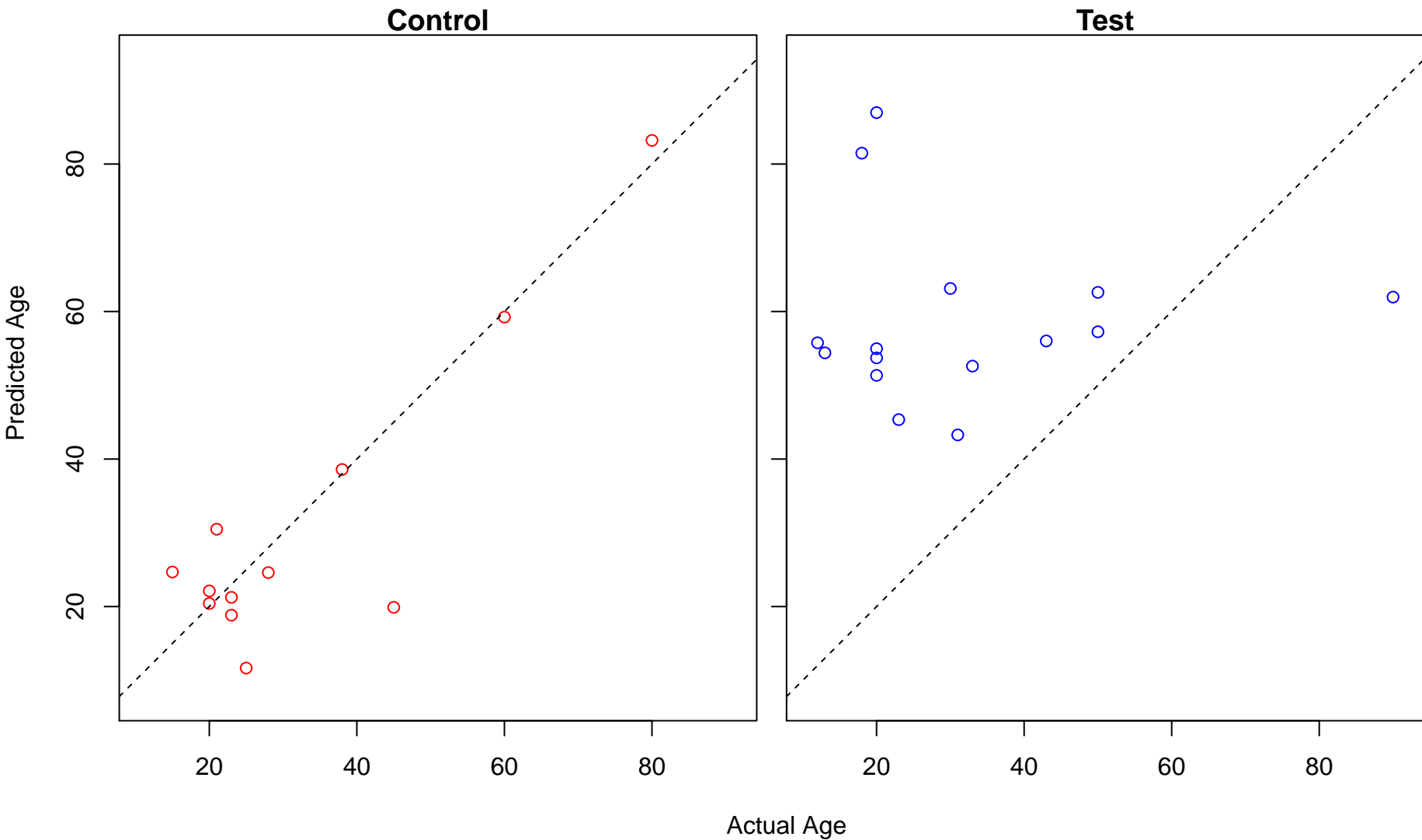
biological adhesion (Score: 6.139286)



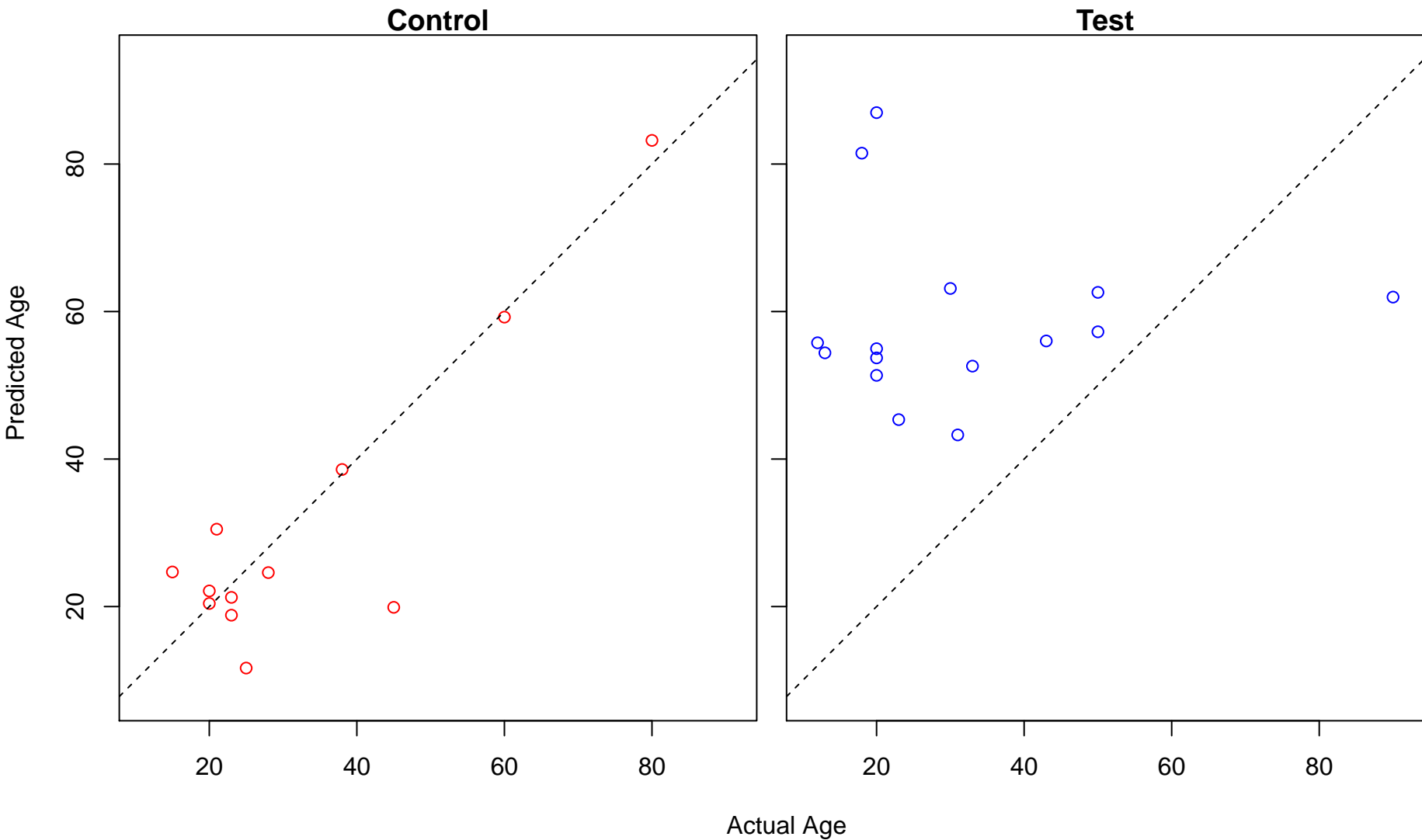
negative regulation of organelle assembly (Score: 6.137776)



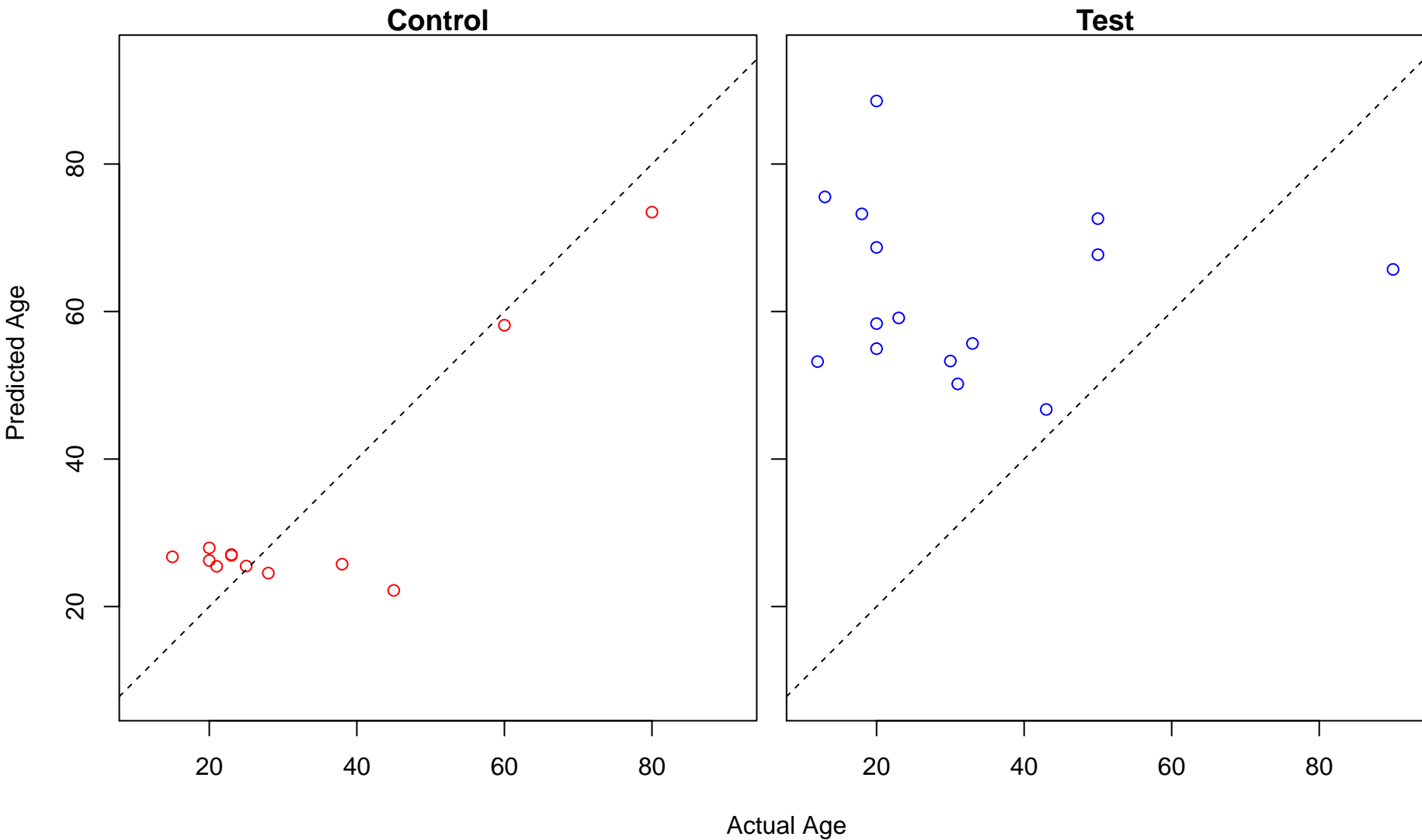
regulation of dopamine metabolic process (Score: 6.137166)



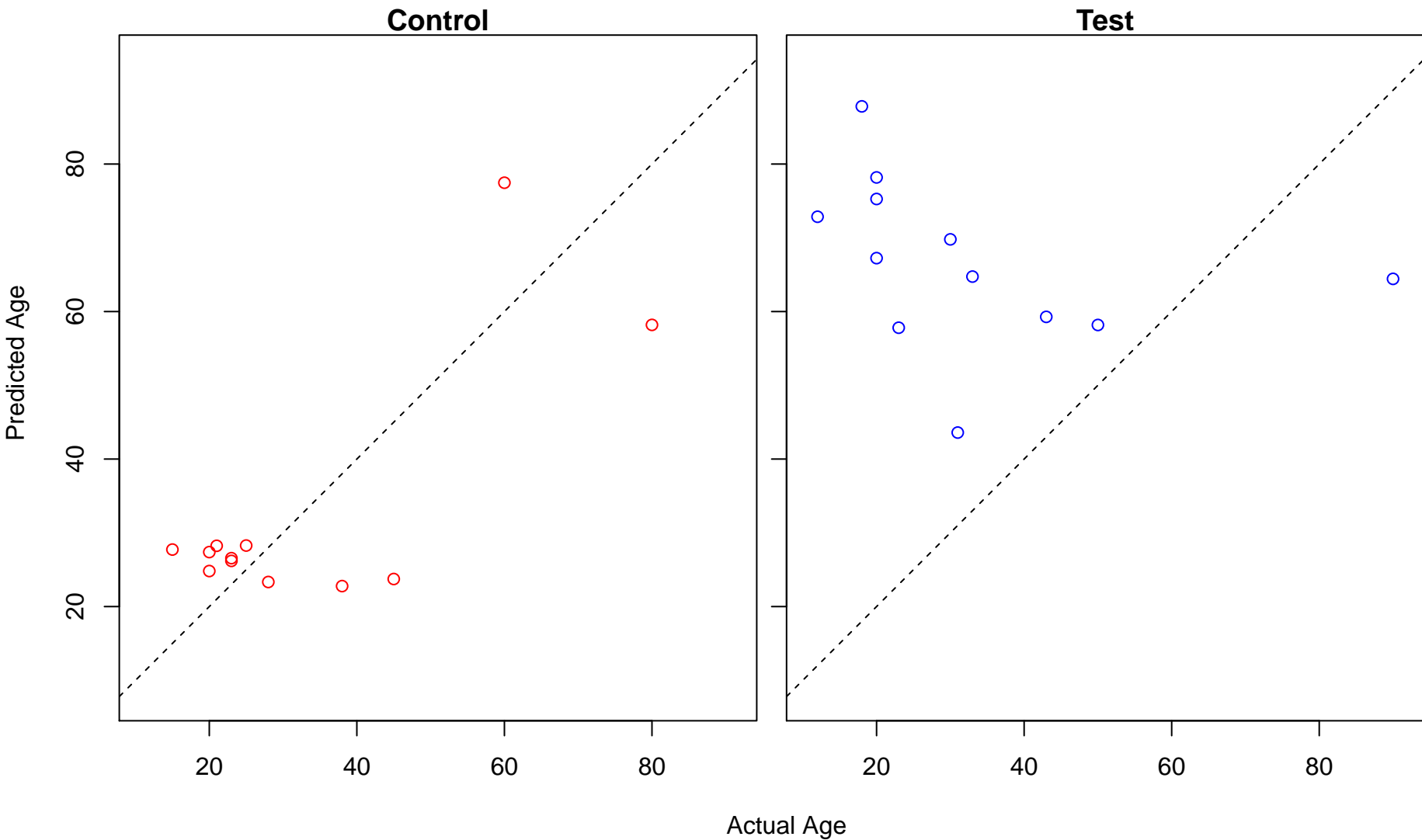
regulation of catecholamine metabolic process (Score: 6.137166)



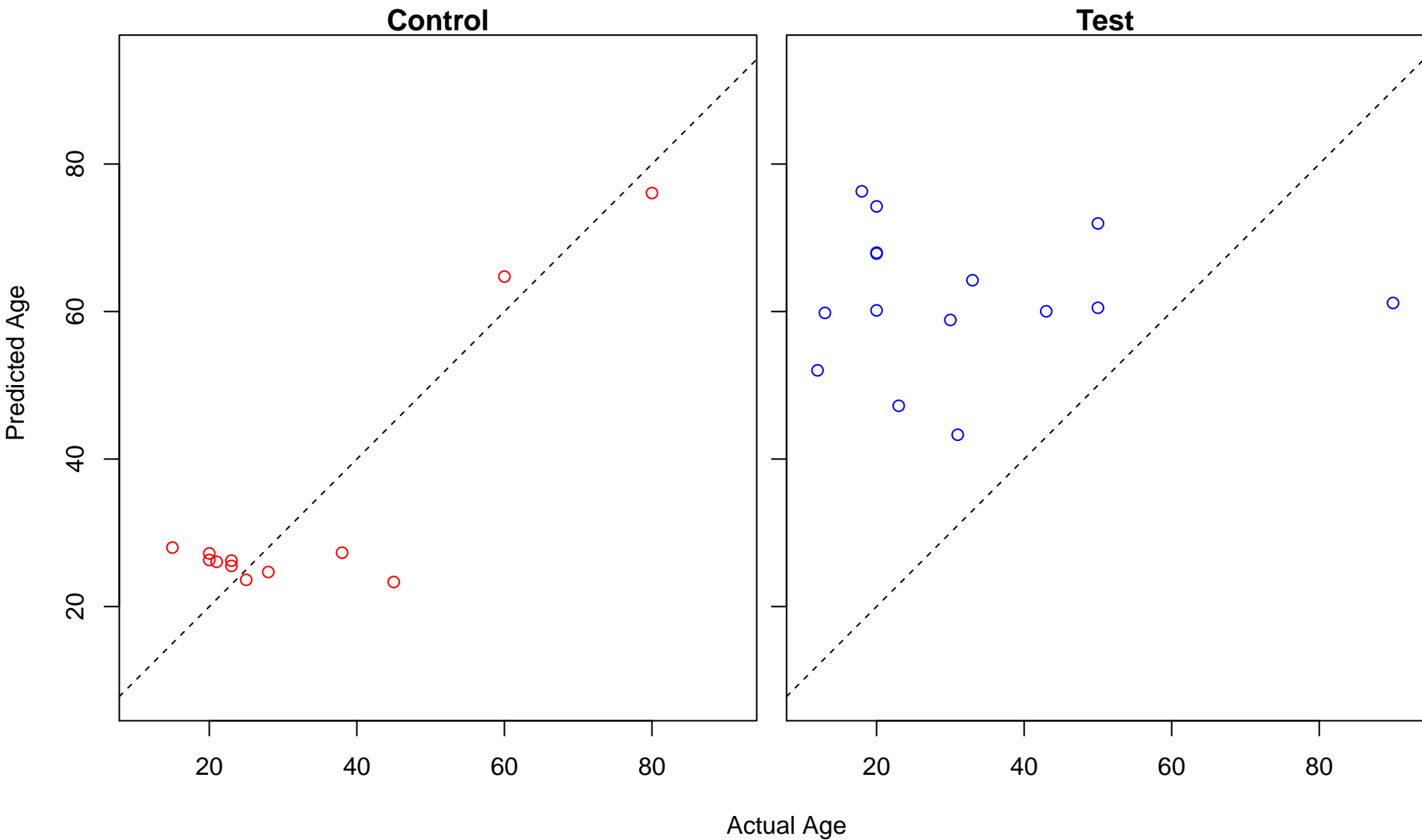
regulation of cellular amide metabolic process (Score: 6.13635)



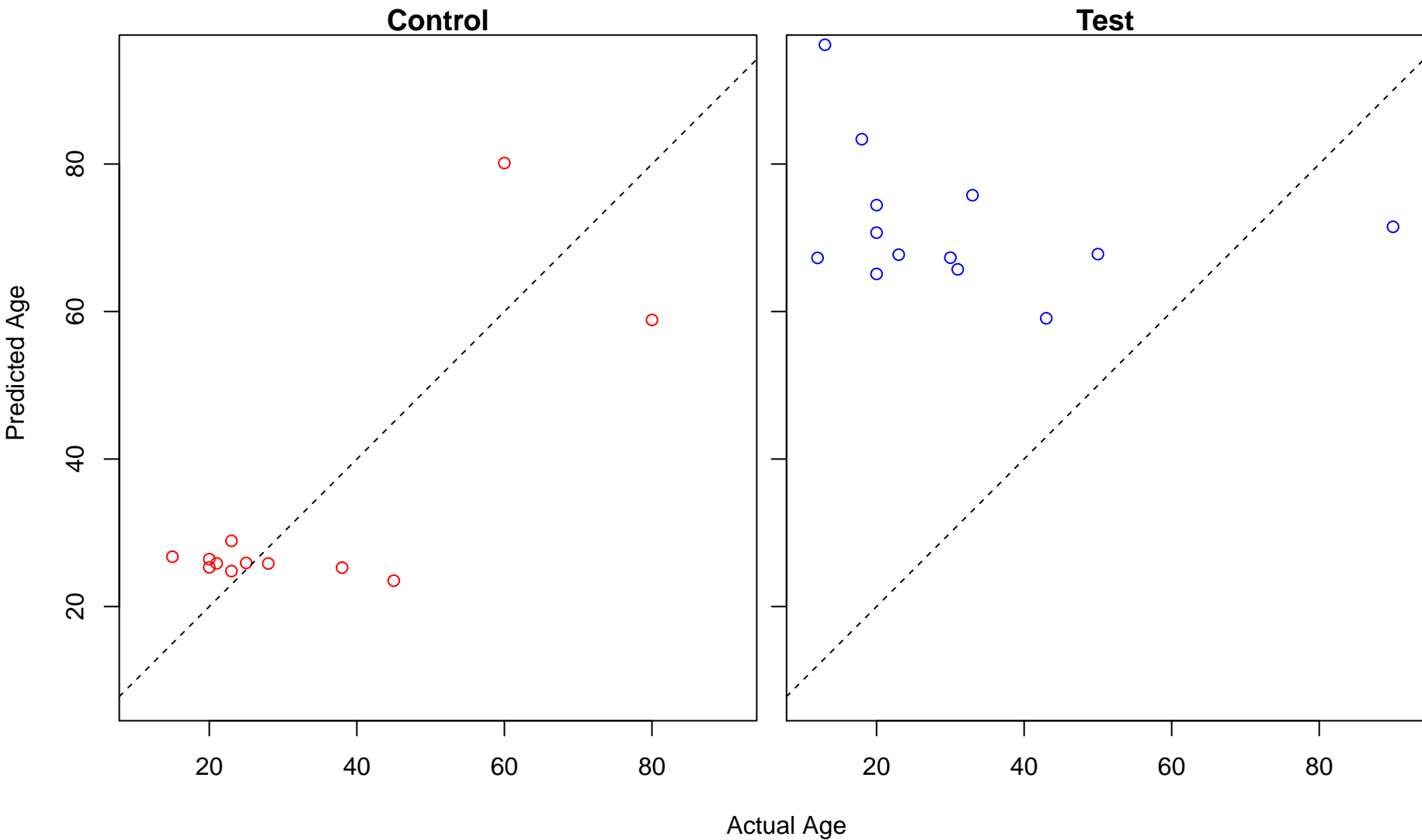
positive regulation of microtubule polymerization (Score: 6.132558)



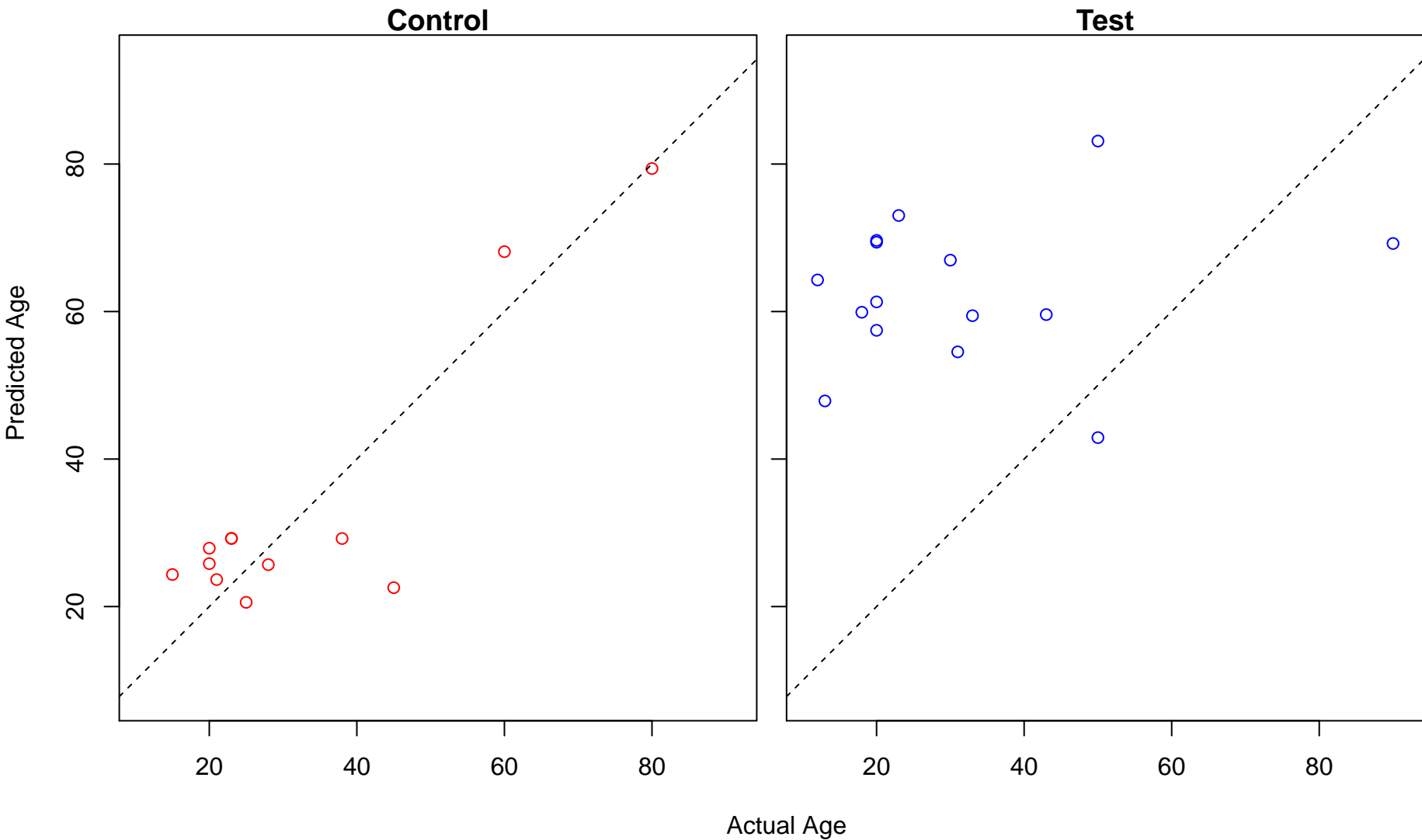
muscle cell differentiation (Score: 6.131617)



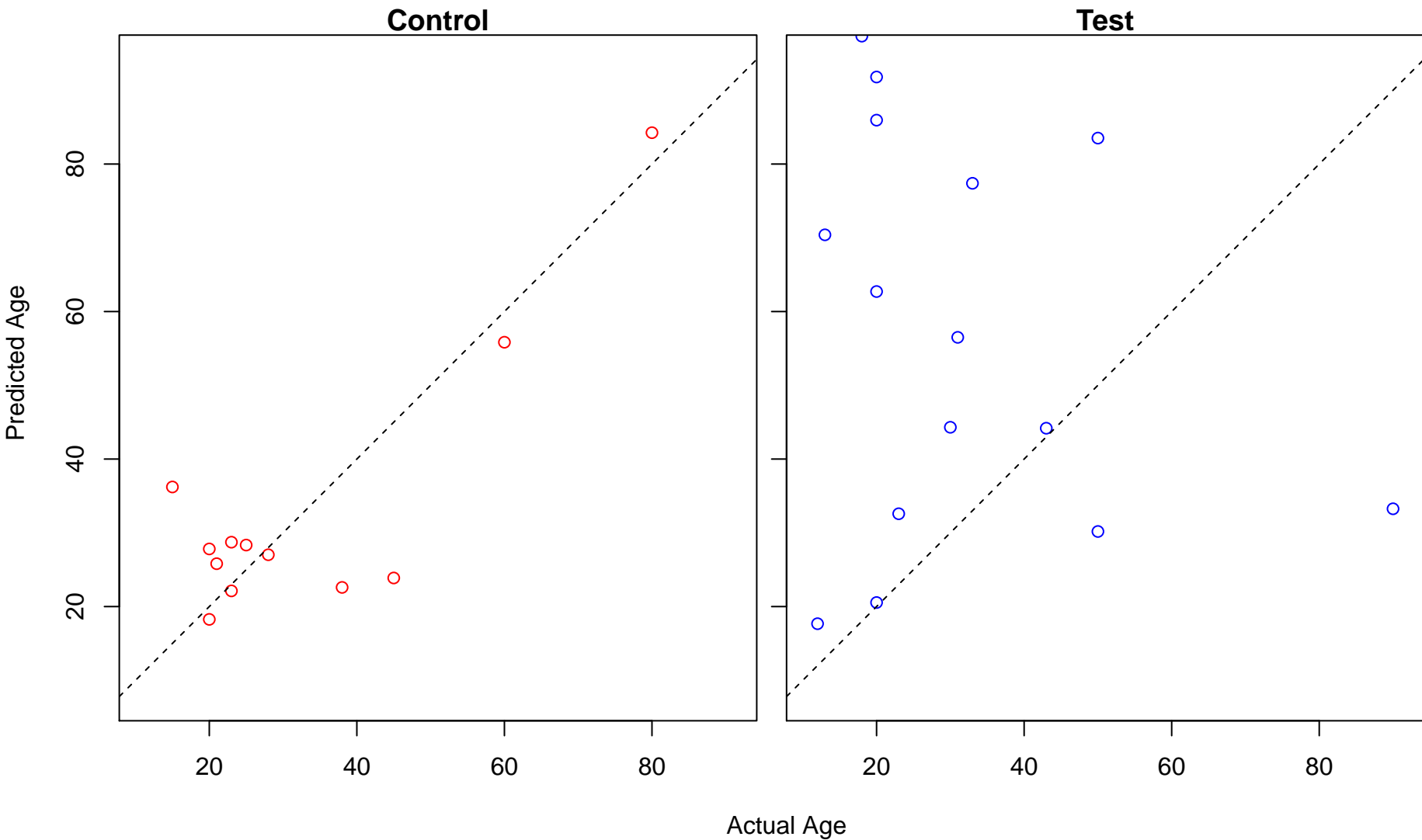
T cell receptor signaling pathway (Score: 6.129877)



response to sterol (Score: 6.129699)

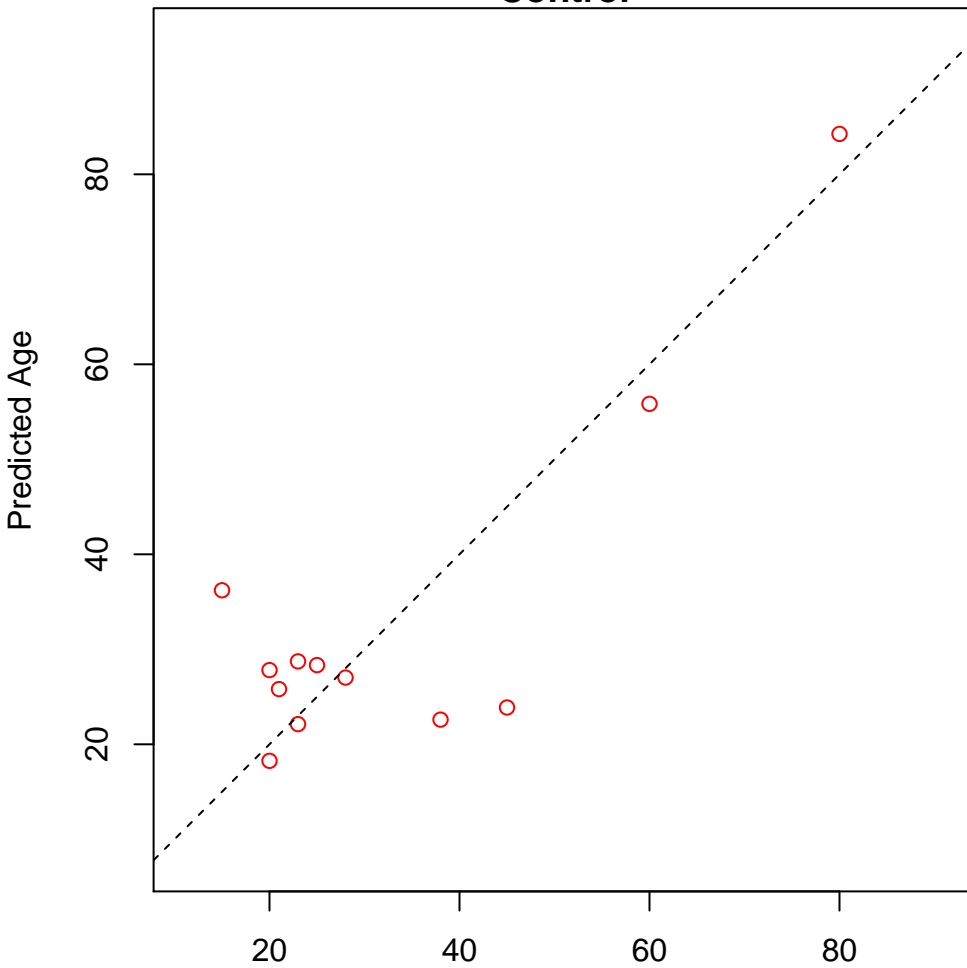


embryonic limb morphogenesis (Score: 6.128980)

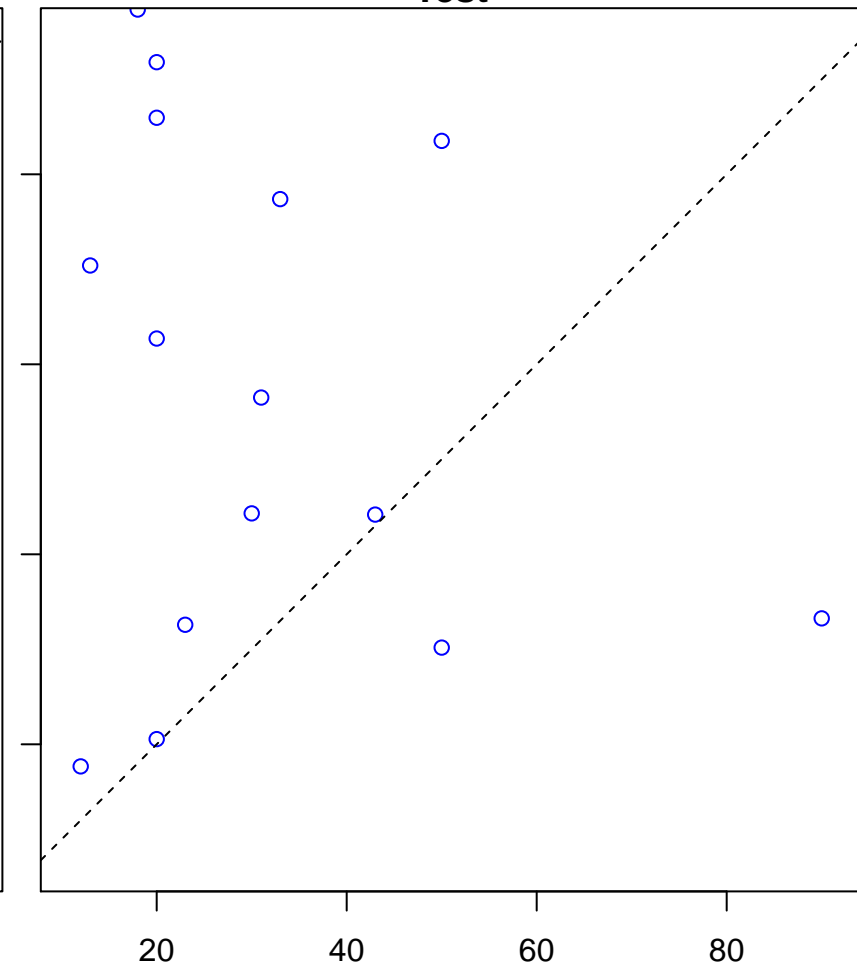


embryonic appendage morphogenesis (Score: 6.128980)

Control

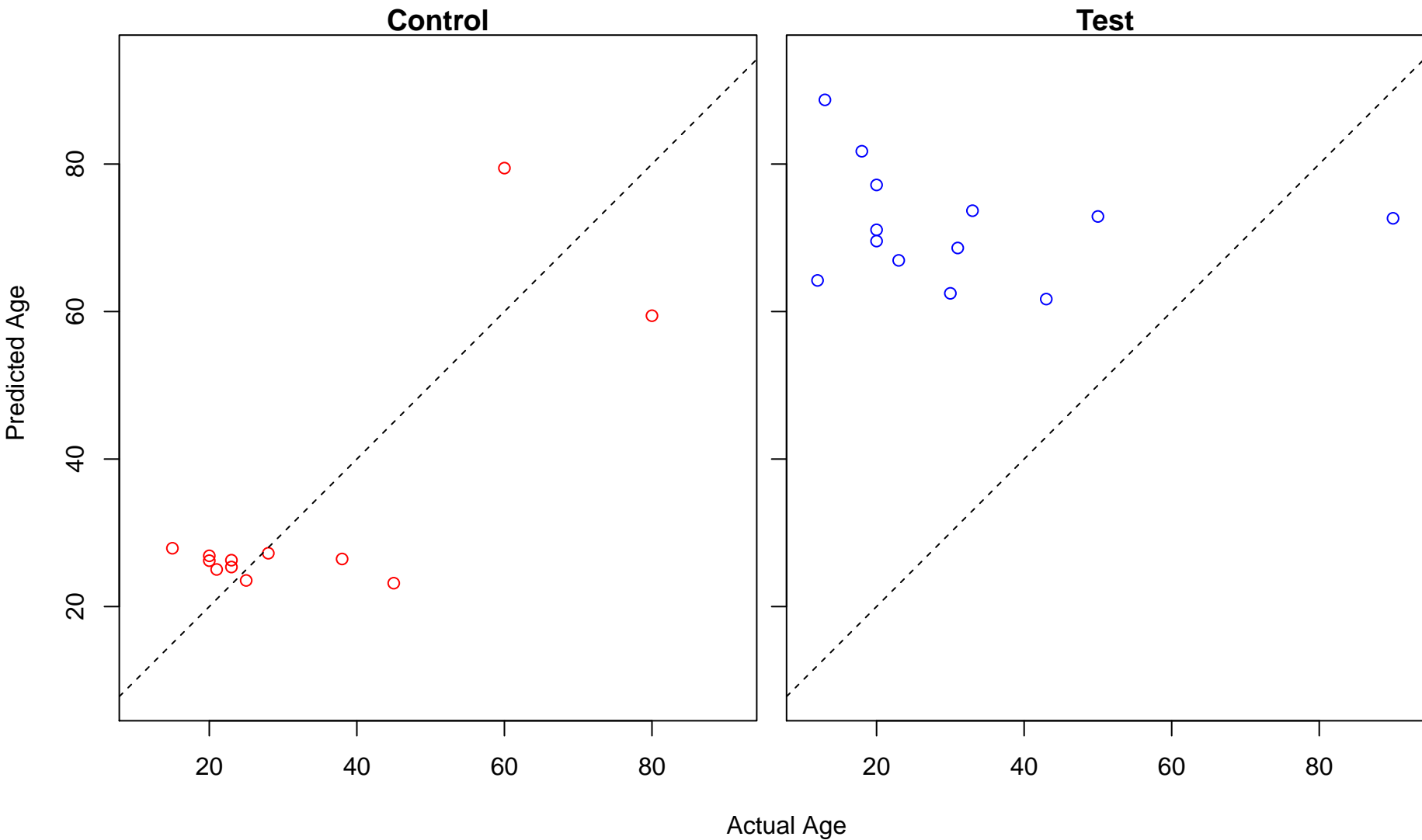


Test

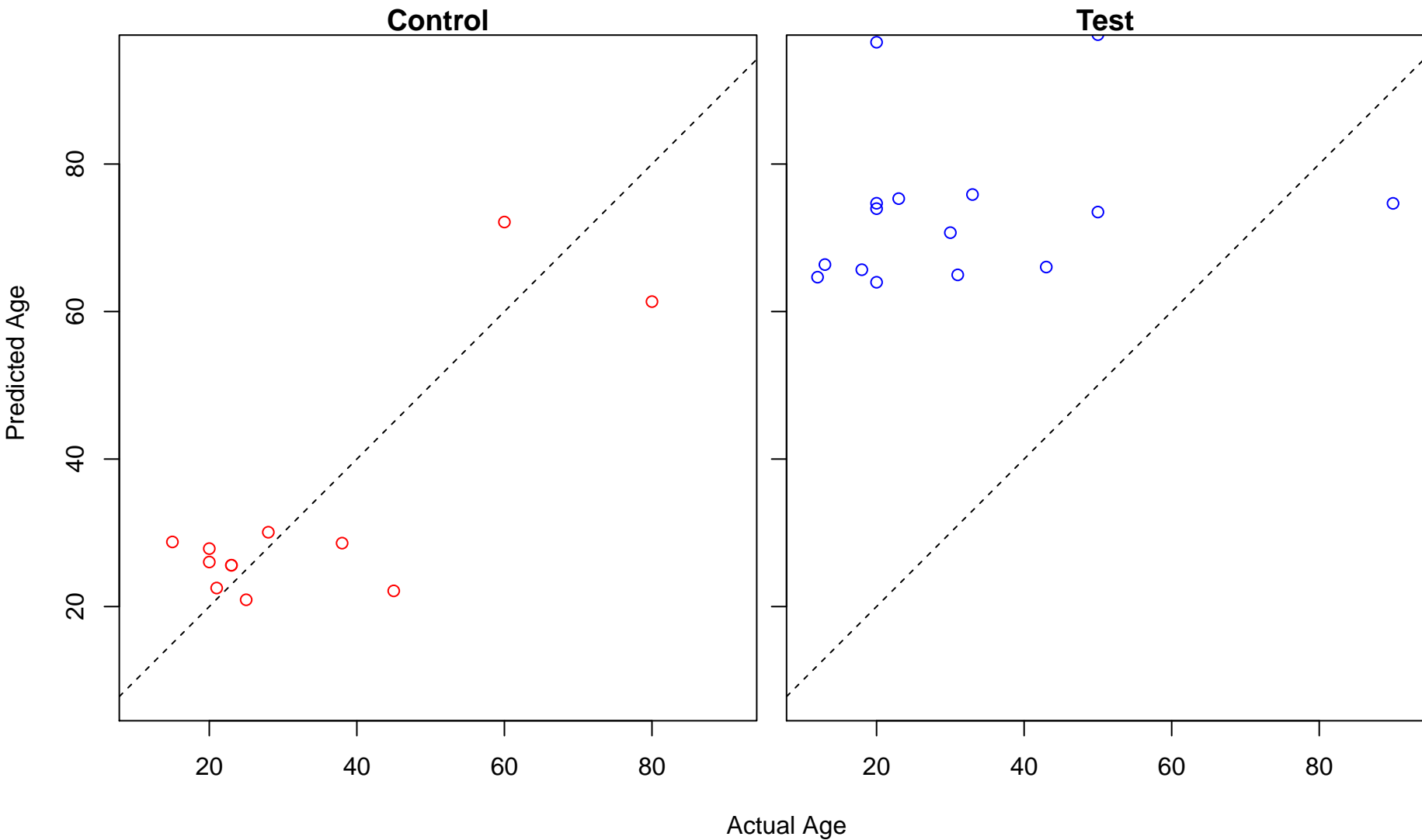


Actual Age

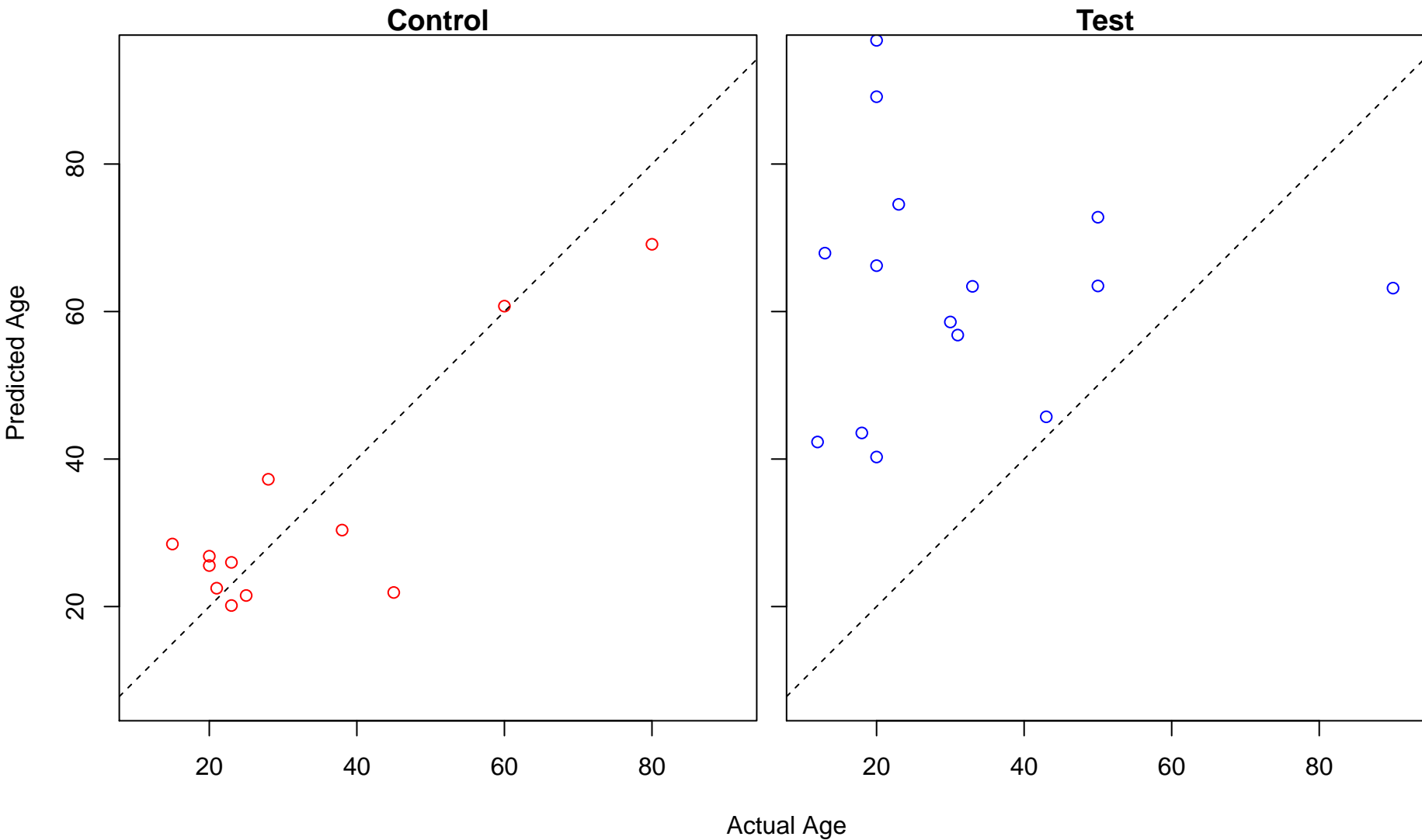
positive regulation of I-kappaB kinase/NF-kappaB signaling (Score: 6.127186)



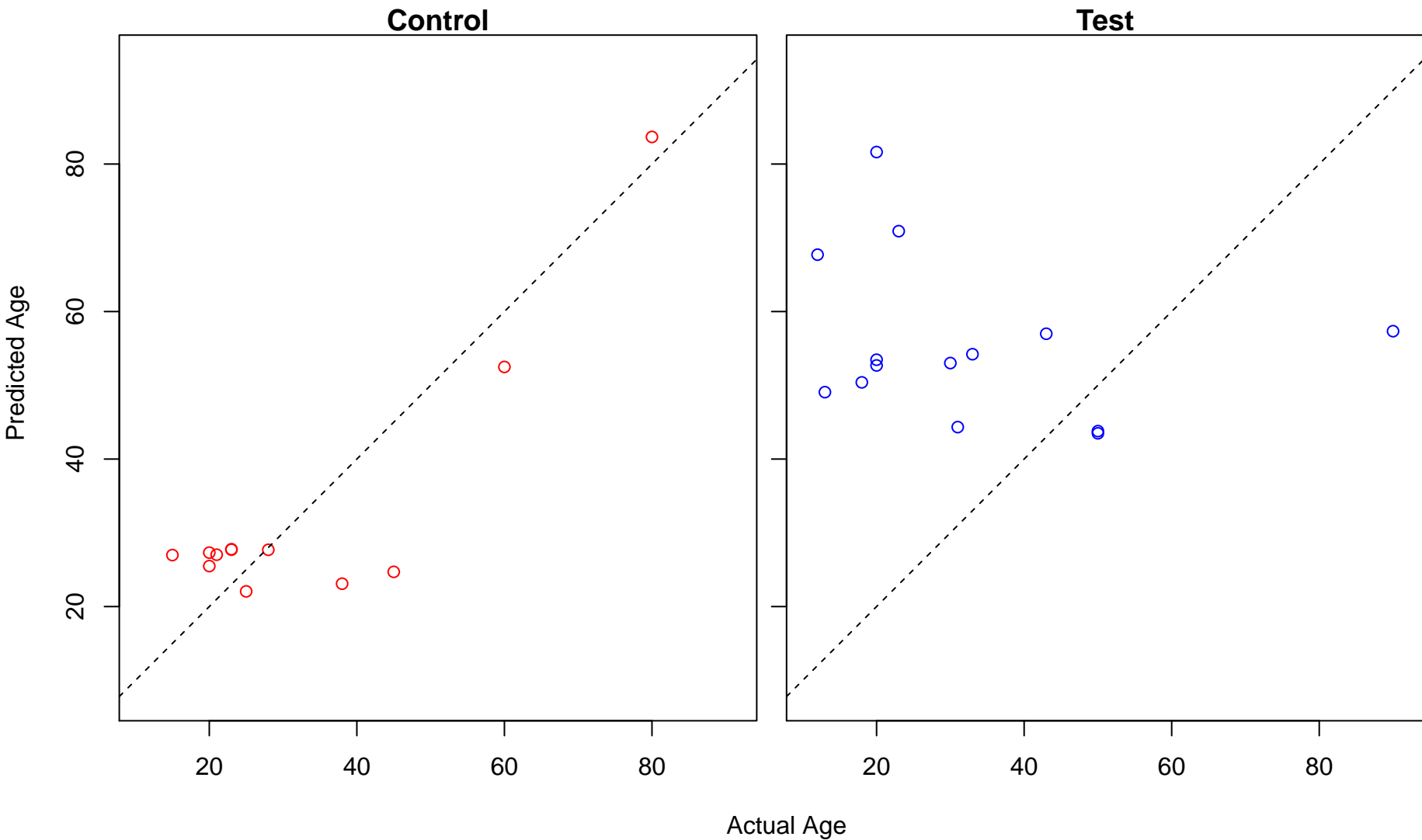
tube formation (Score: 6.125647)



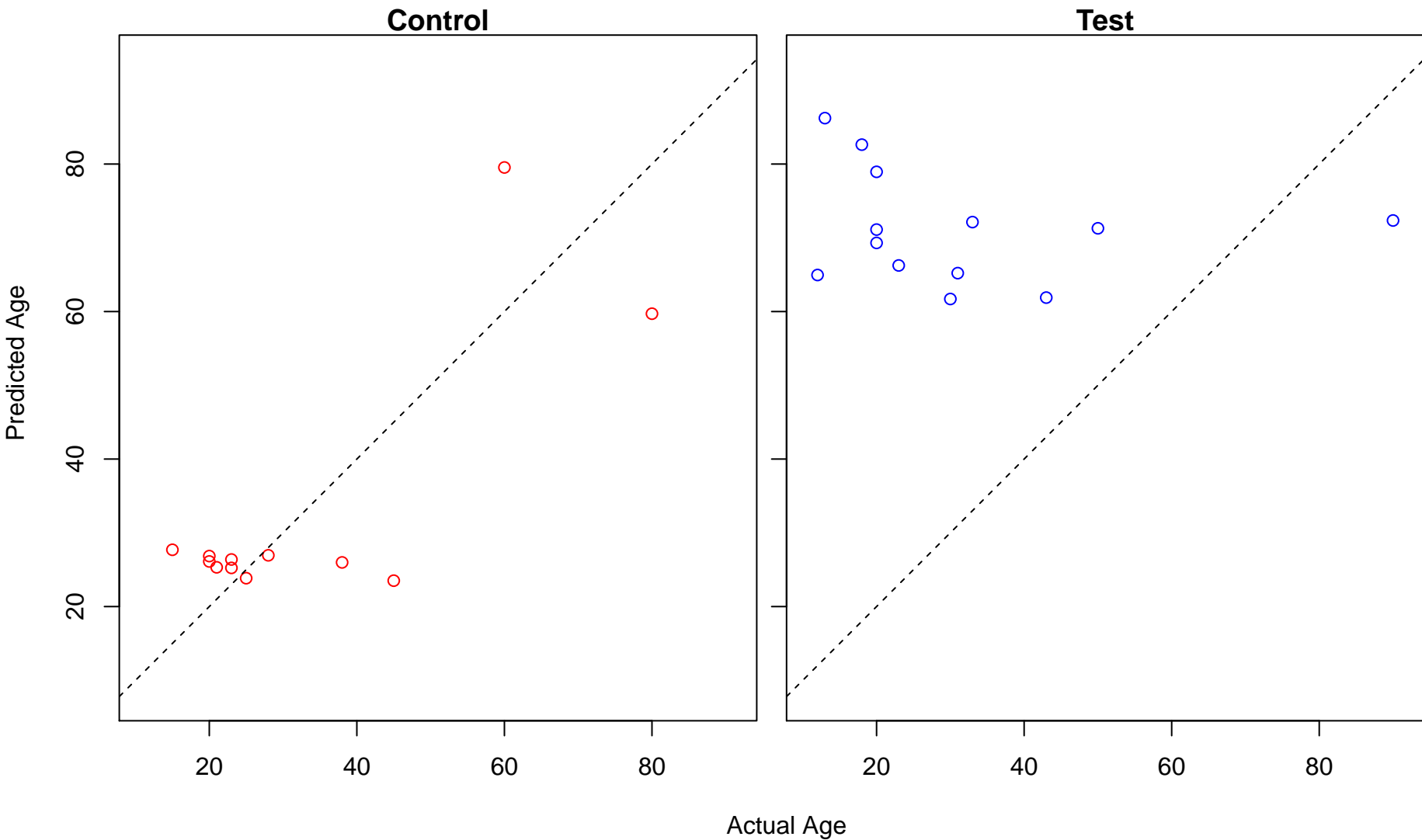
'de novo' posttranslational protein folding (Score: 6.124928)



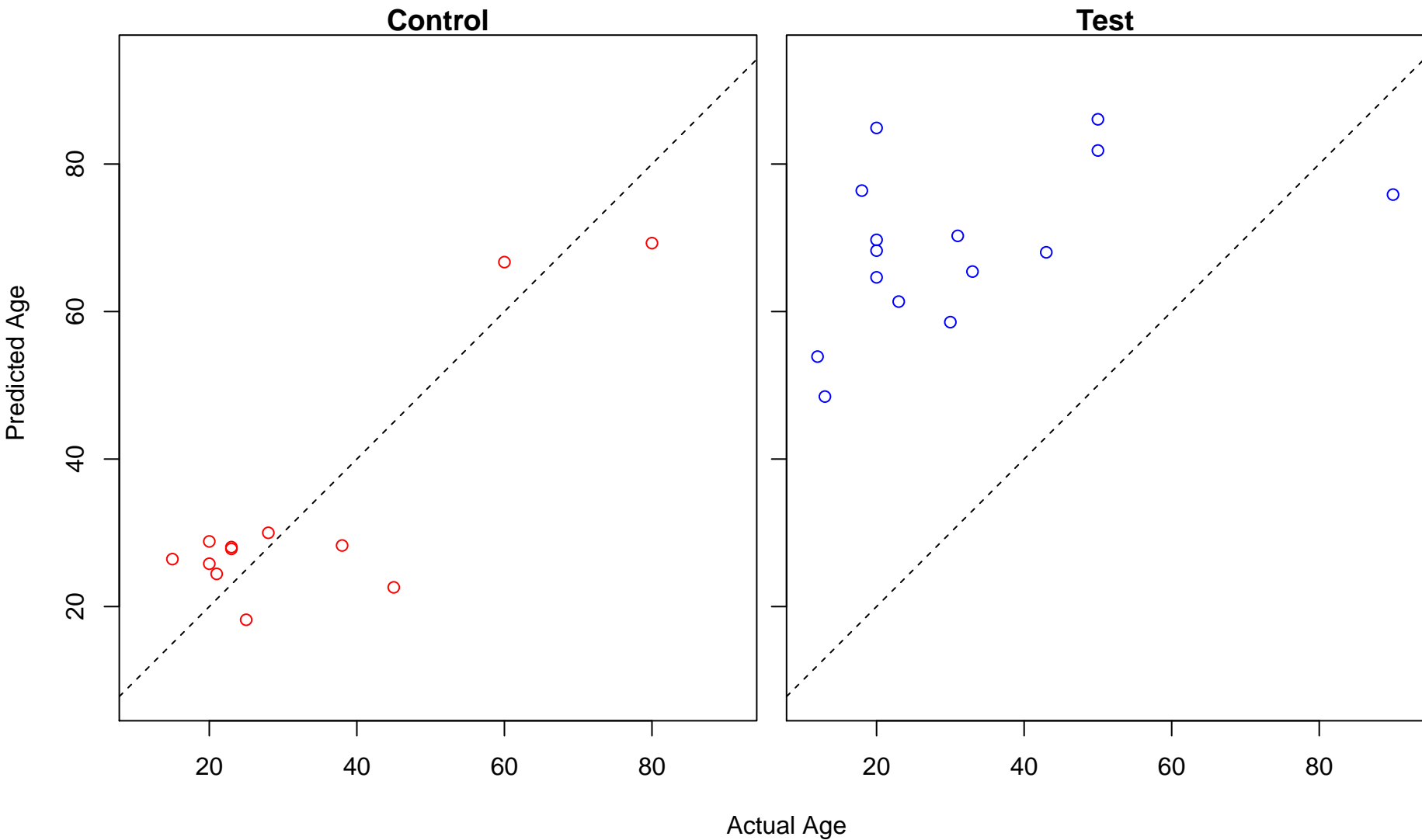
telomere maintenance via recombination (Score: 6.124307)



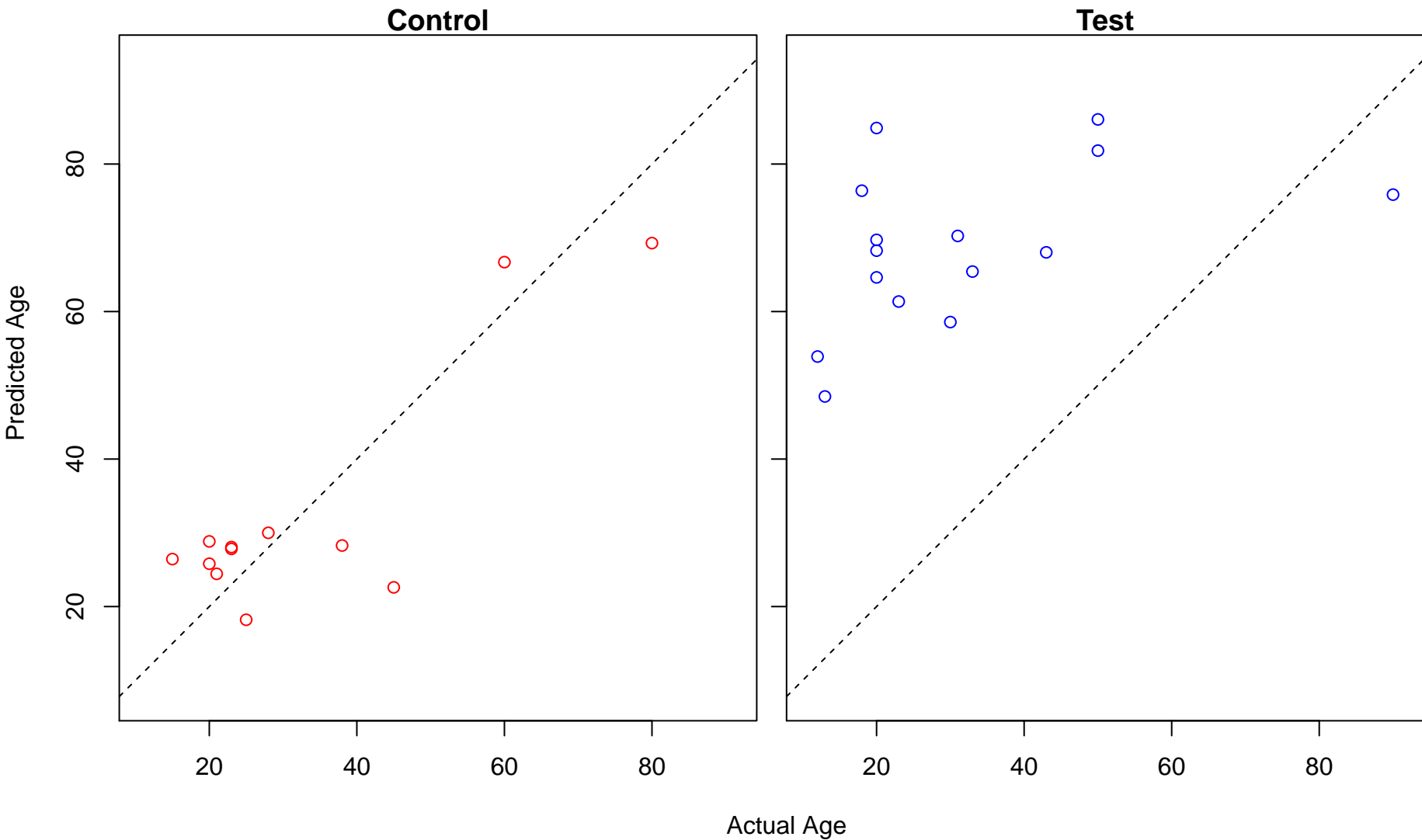
regulation of ubiquitin–protein ligase activity involved in mitotic cell cycle (Score: 6.123694)



negative regulation of lymphocyte activation (Score: 6.123506)

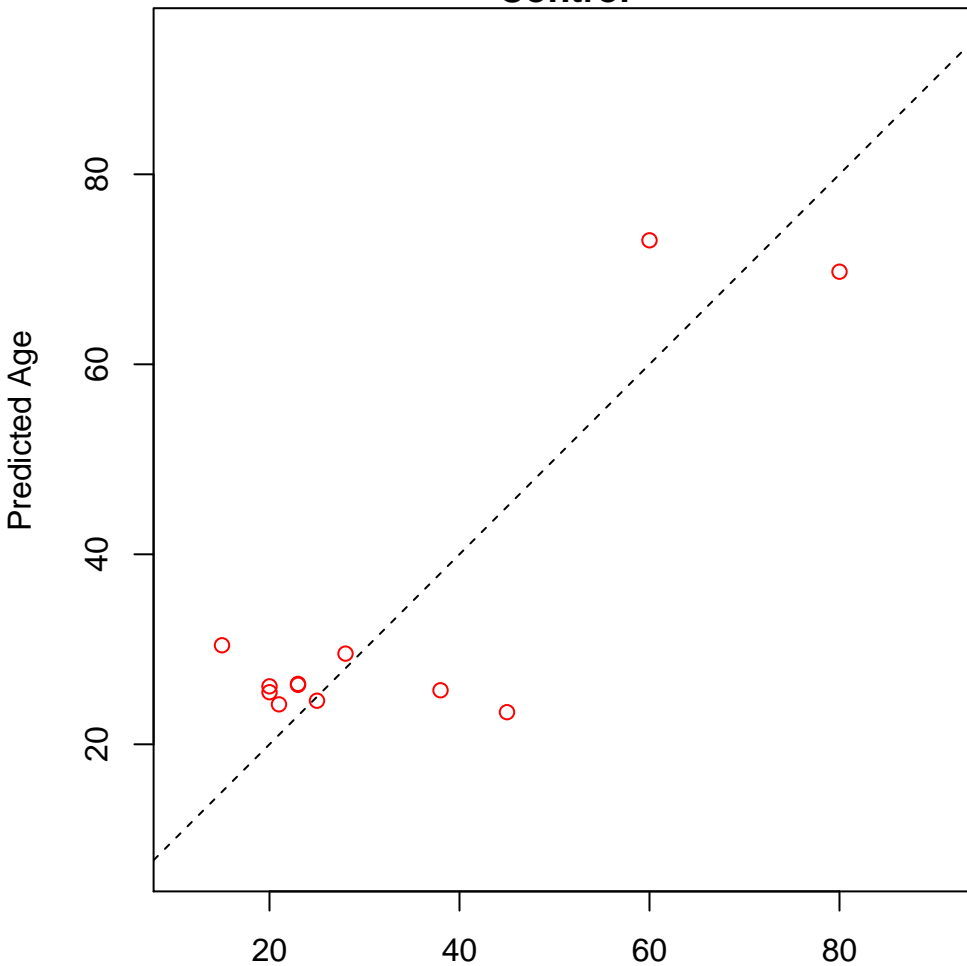


negative regulation of leukocyte activation (Score: 6.122820)

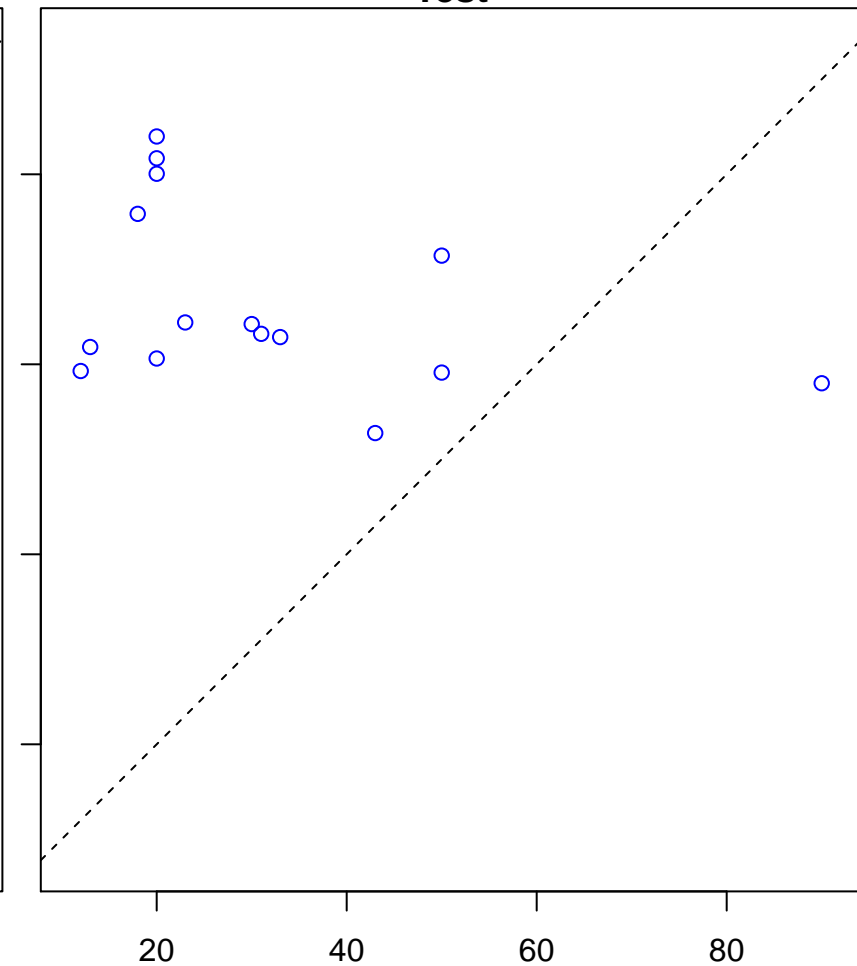


protein K63-linked ubiquitination (Score: 6.121838)

Control

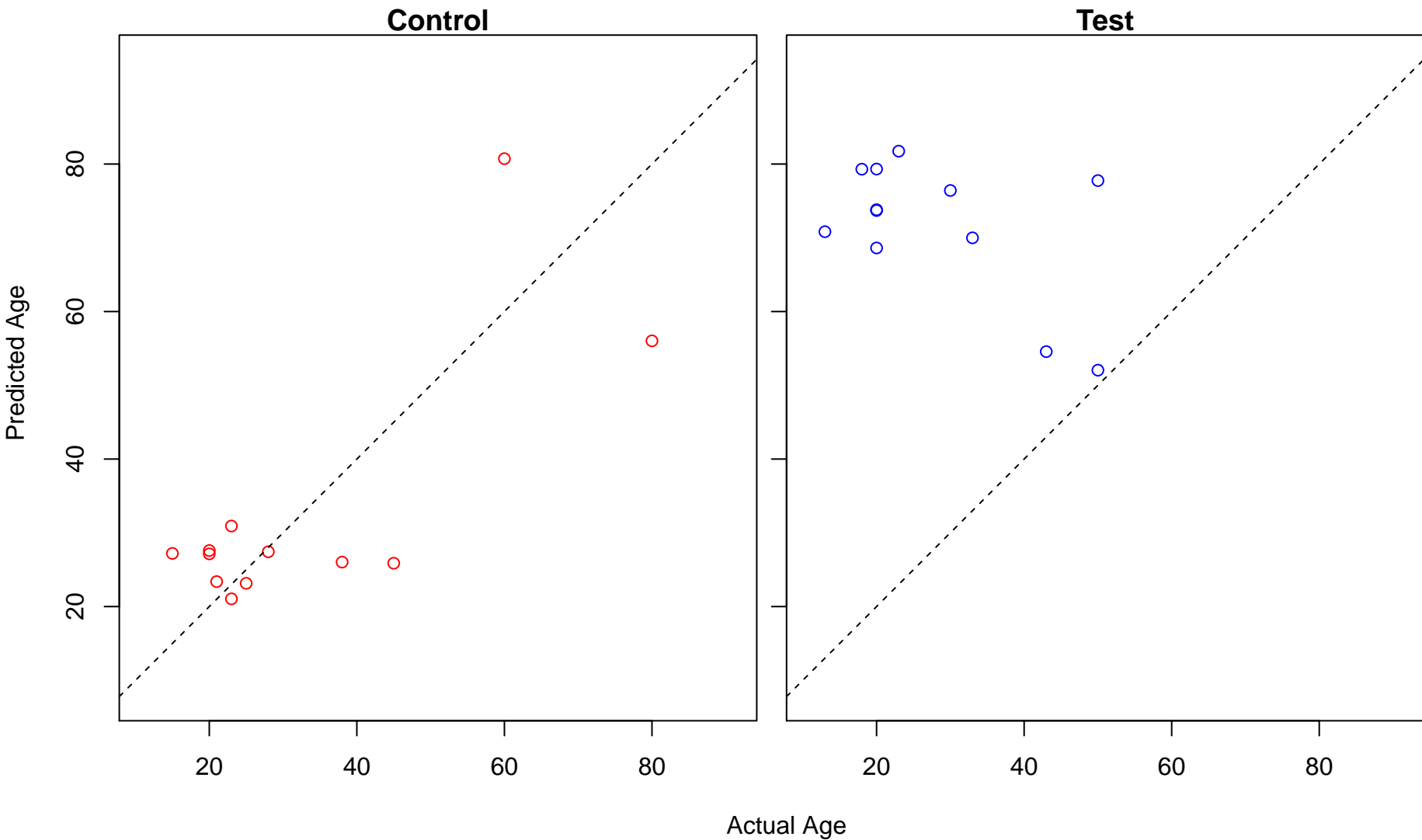


Test

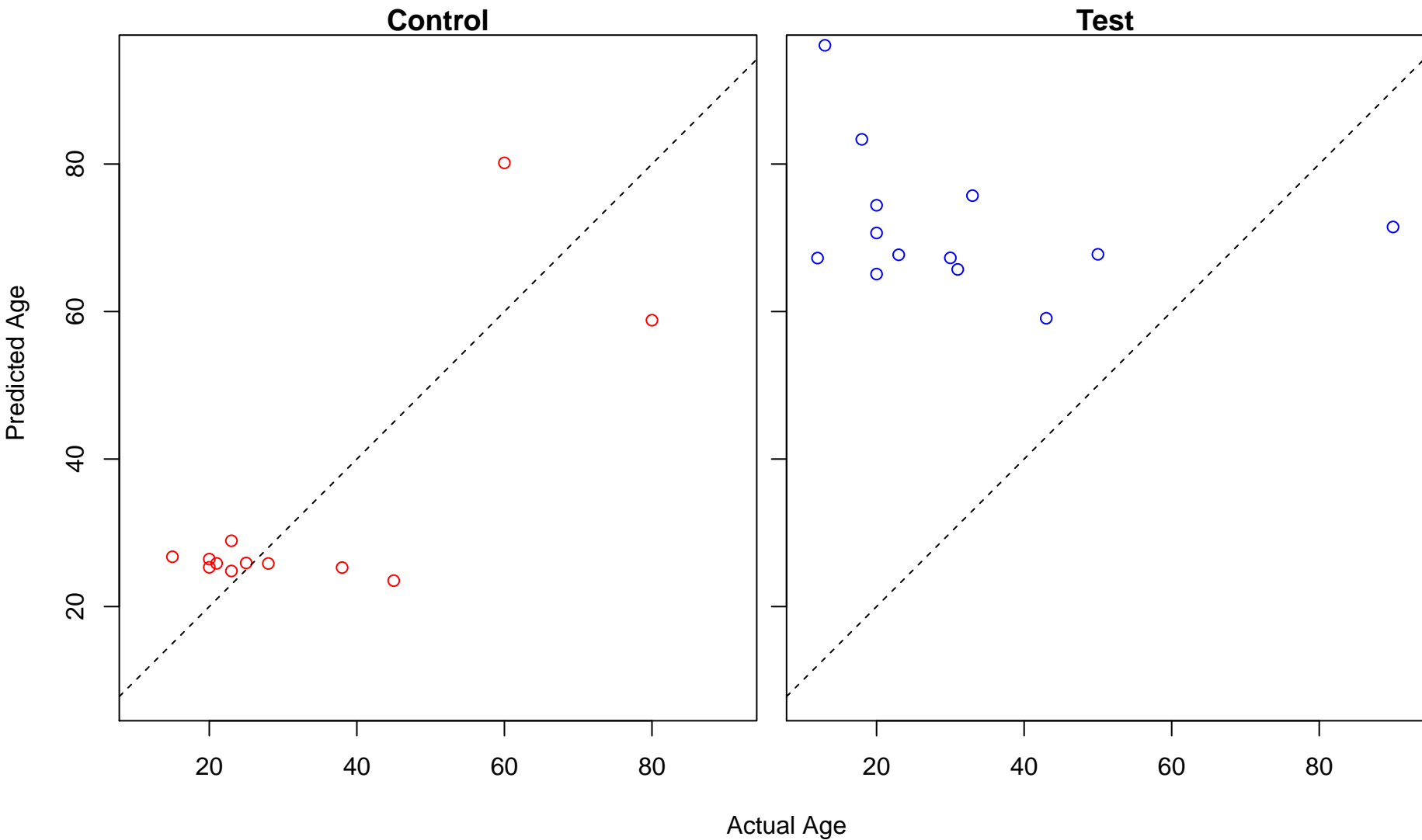


Actual Age

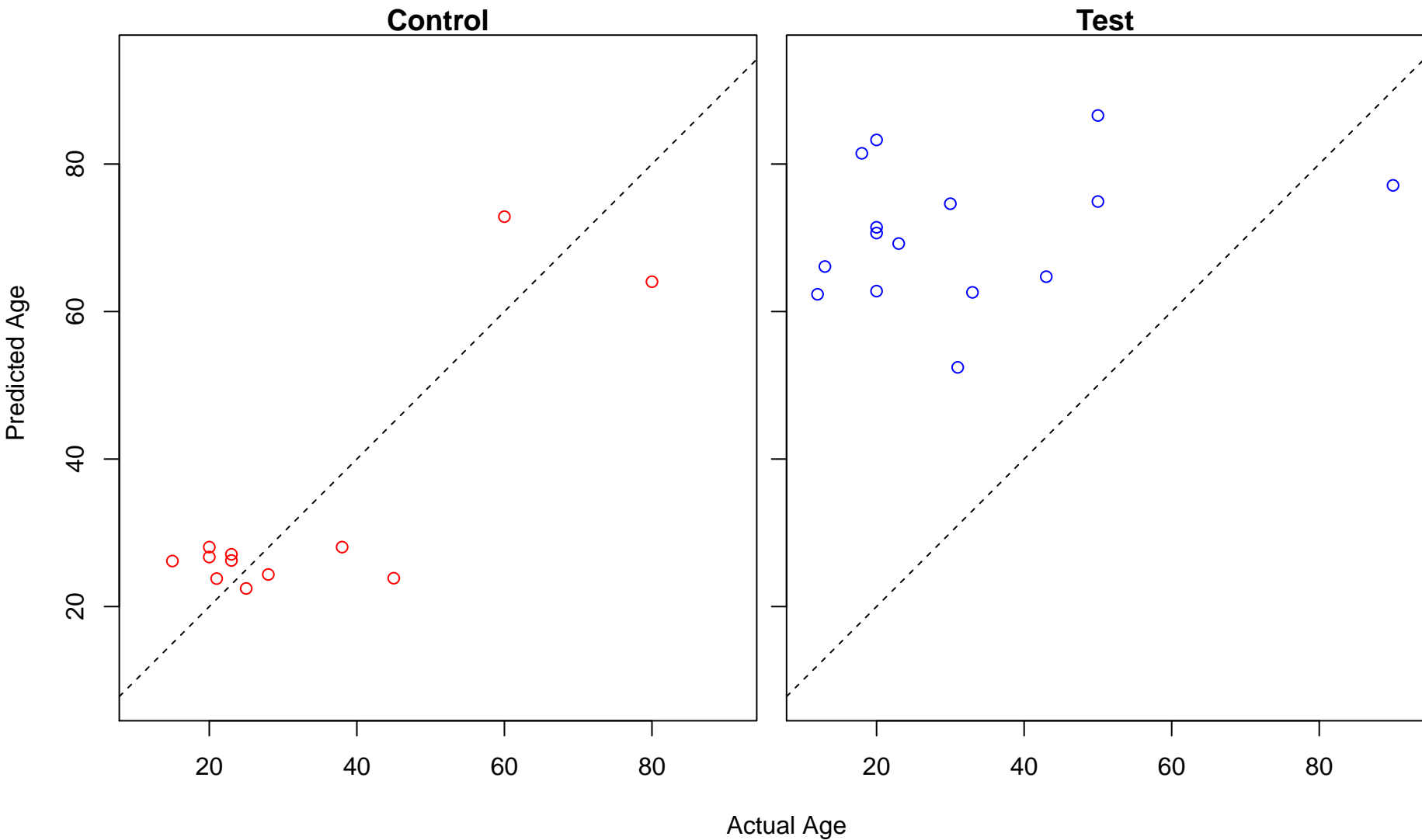
activation of MAPKKK activity (Score: 6.120034)



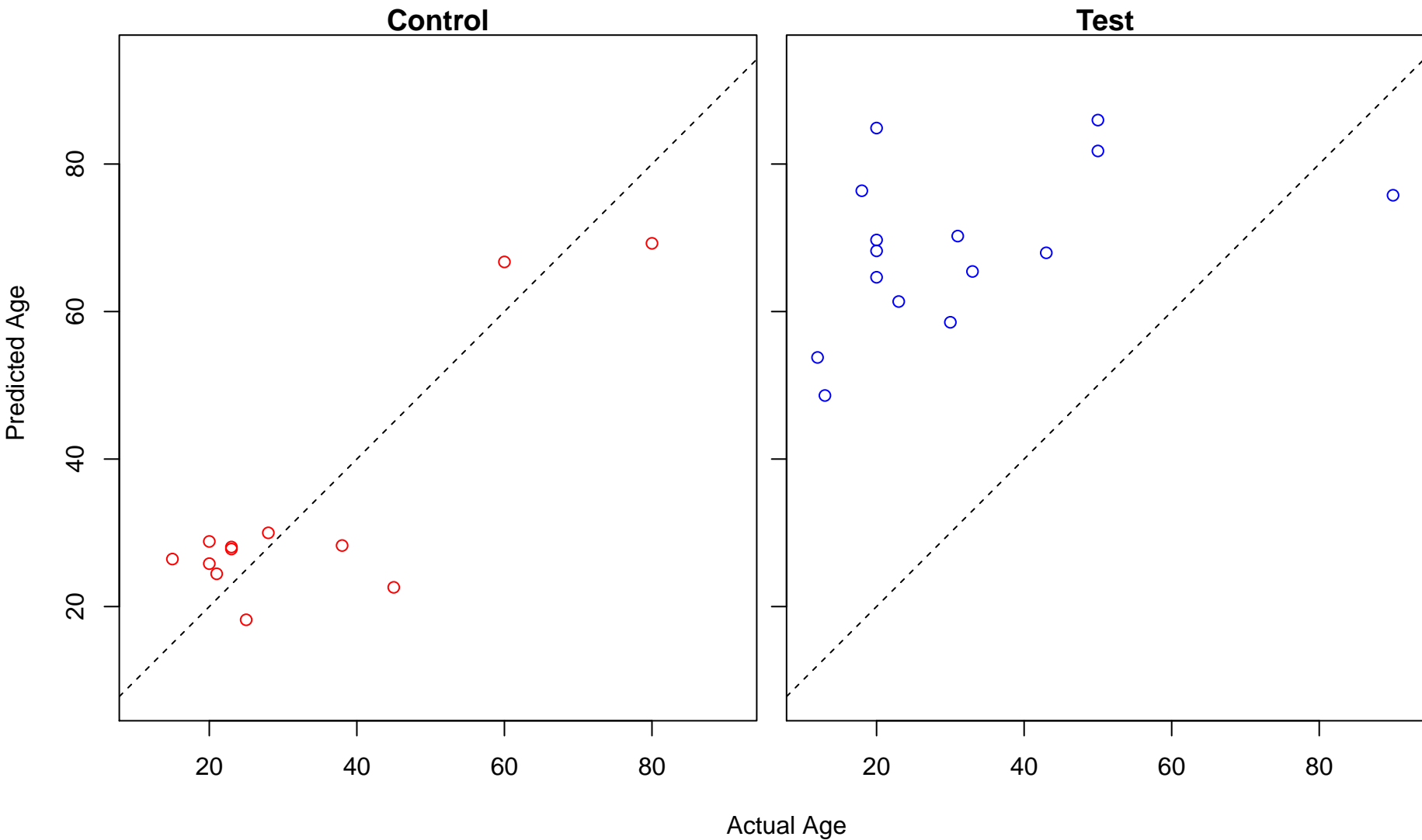
antigen receptor-mediated signaling pathway (Score: 6.114248)



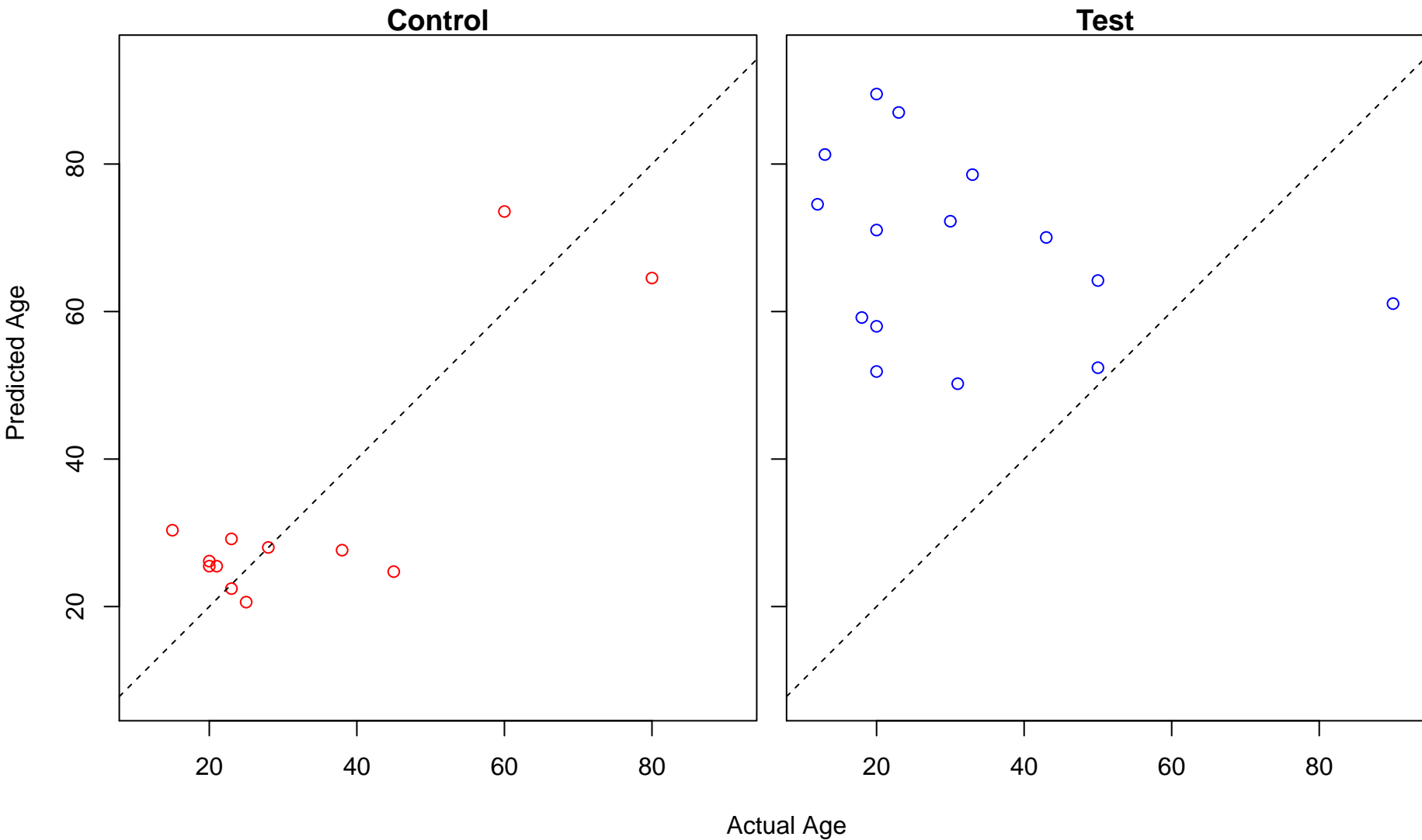
striated muscle cell development (Score: 6.114175)



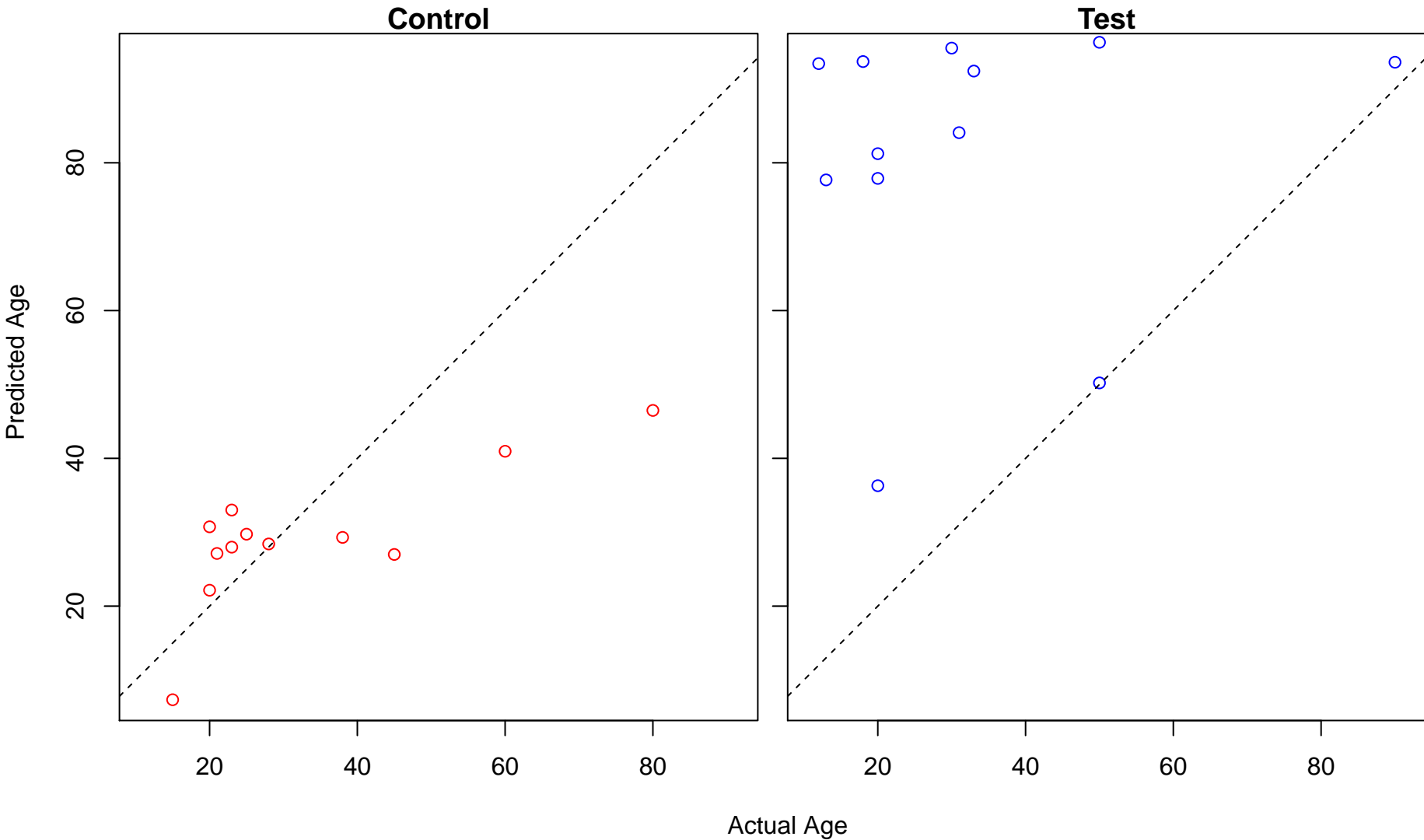
negative regulation of cell activation (Score: 6.112832)



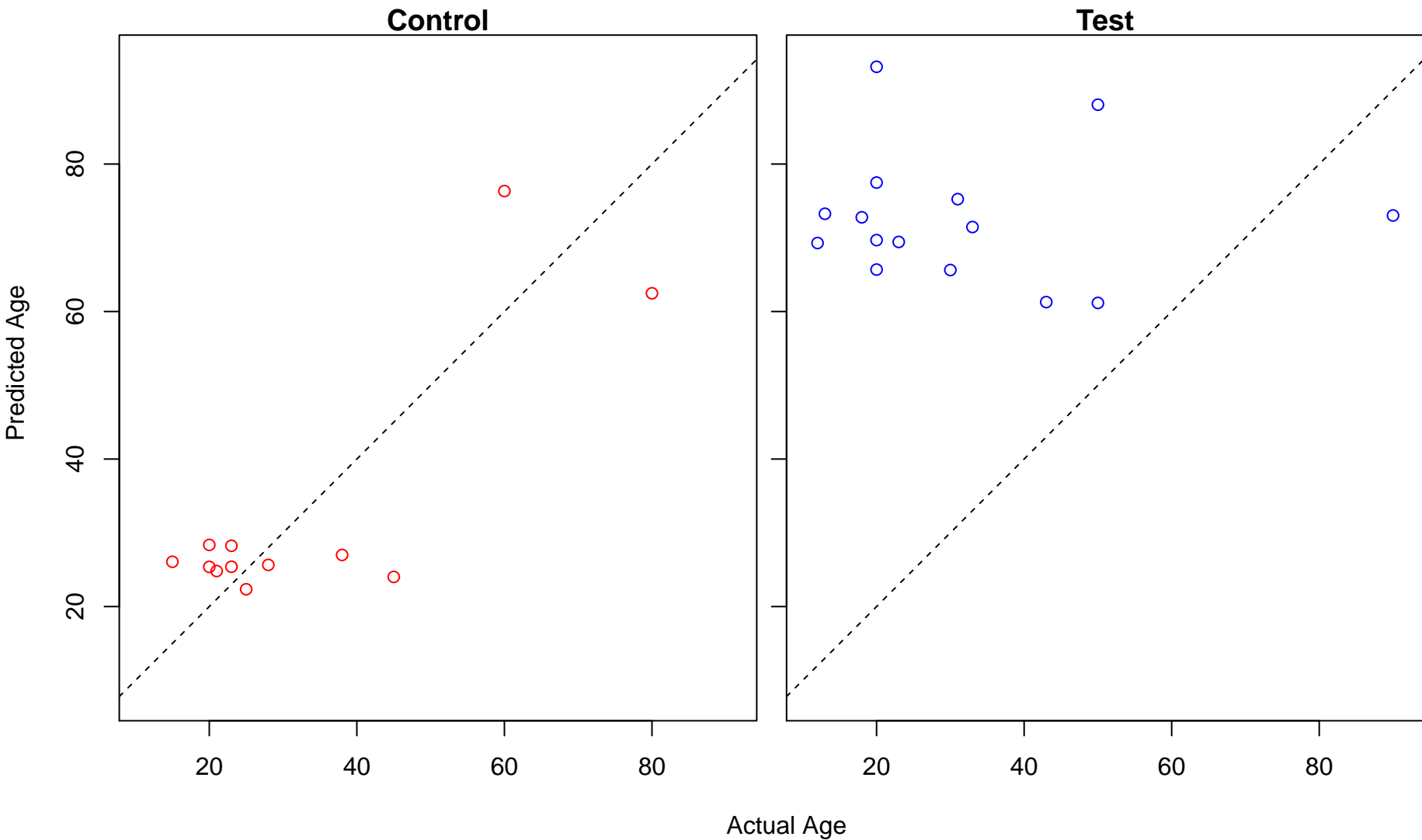
commissural neuron axon guidance (Score: 6.112649)



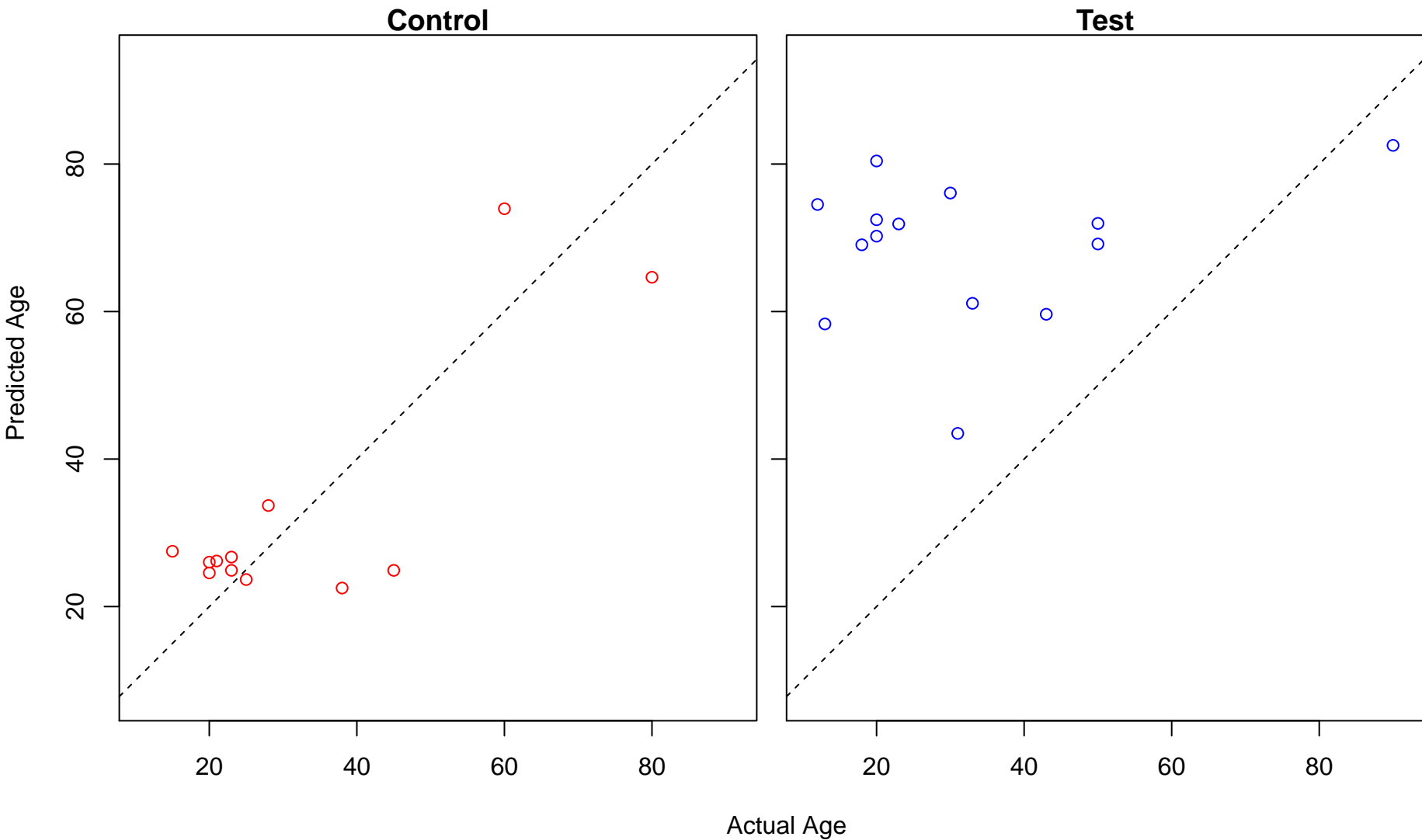
opioid receptor signaling pathway (Score: 6.110596)



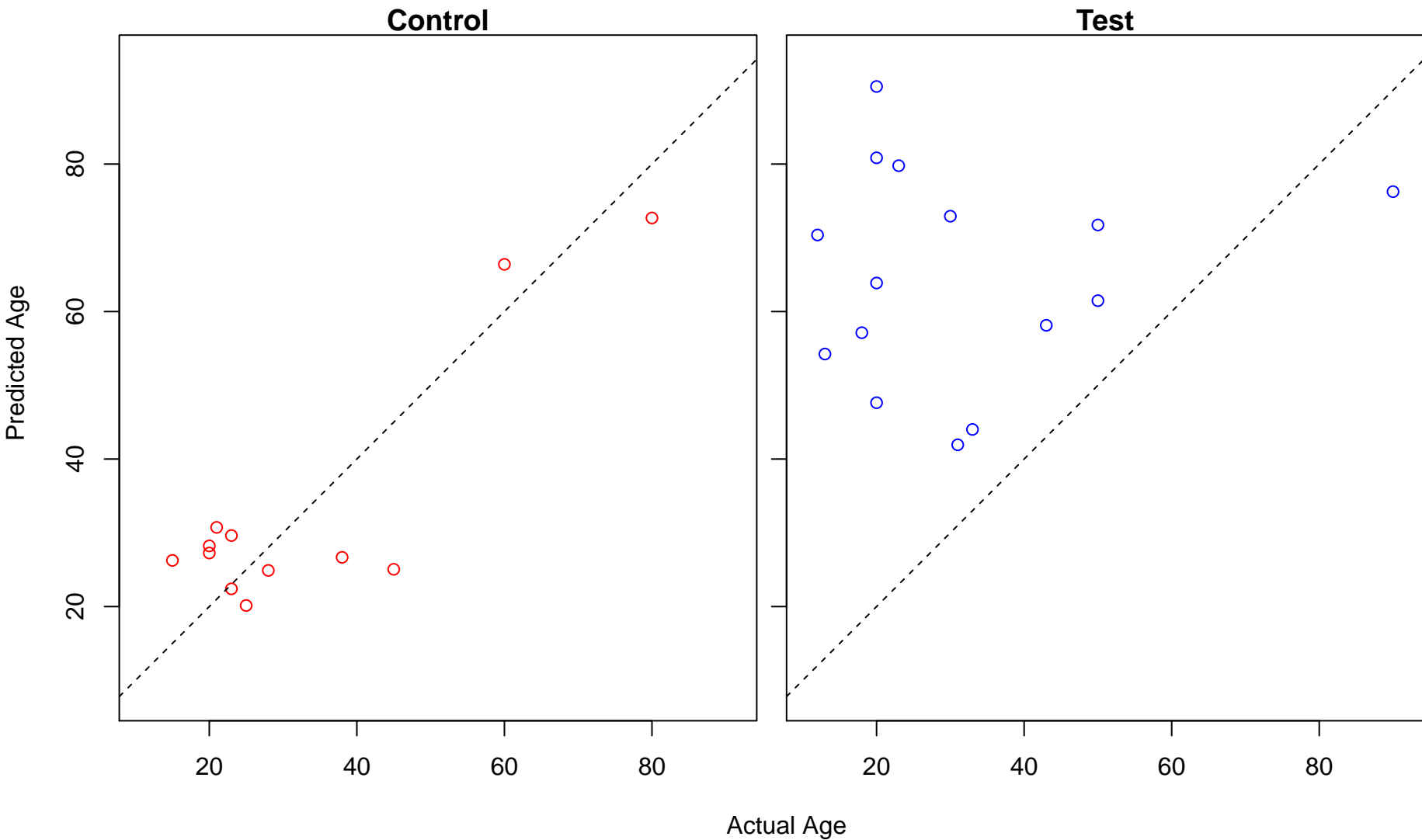
T cell mediated immunity (Score: 6.109091)



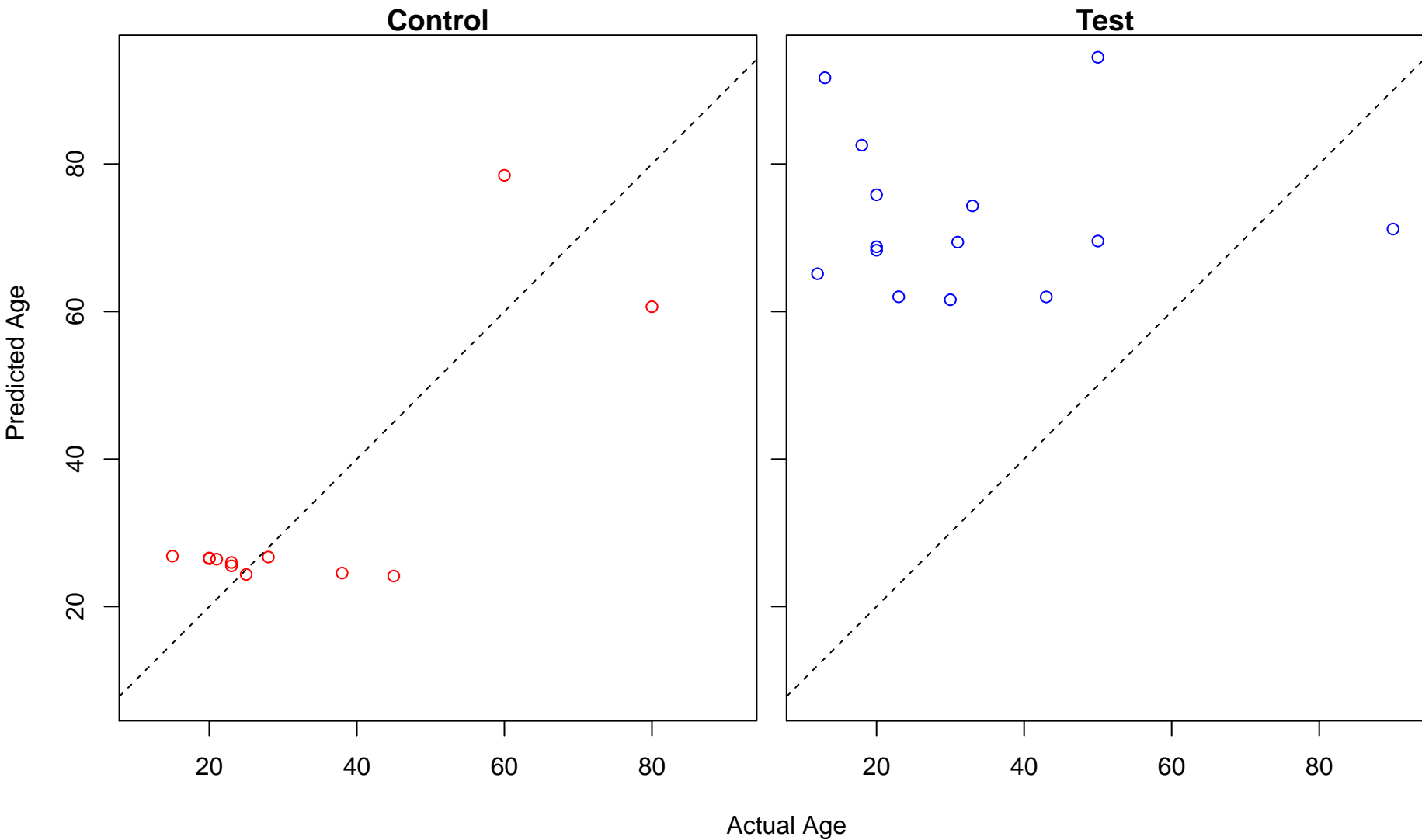
transcription initiation from RNA polymerase I promoter (Score: 6.107746)



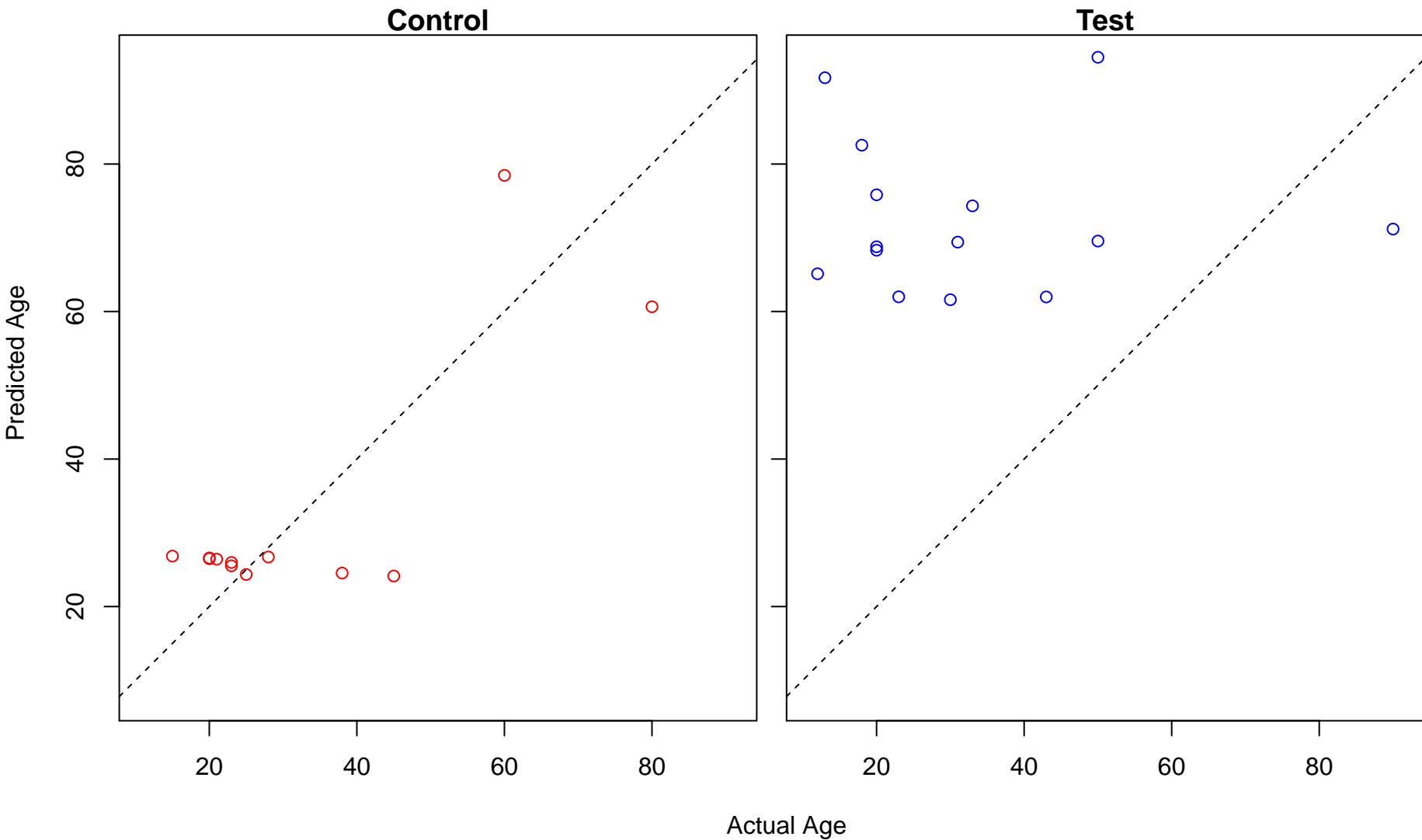
lens fiber cell differentiation (Score: 6.104993)



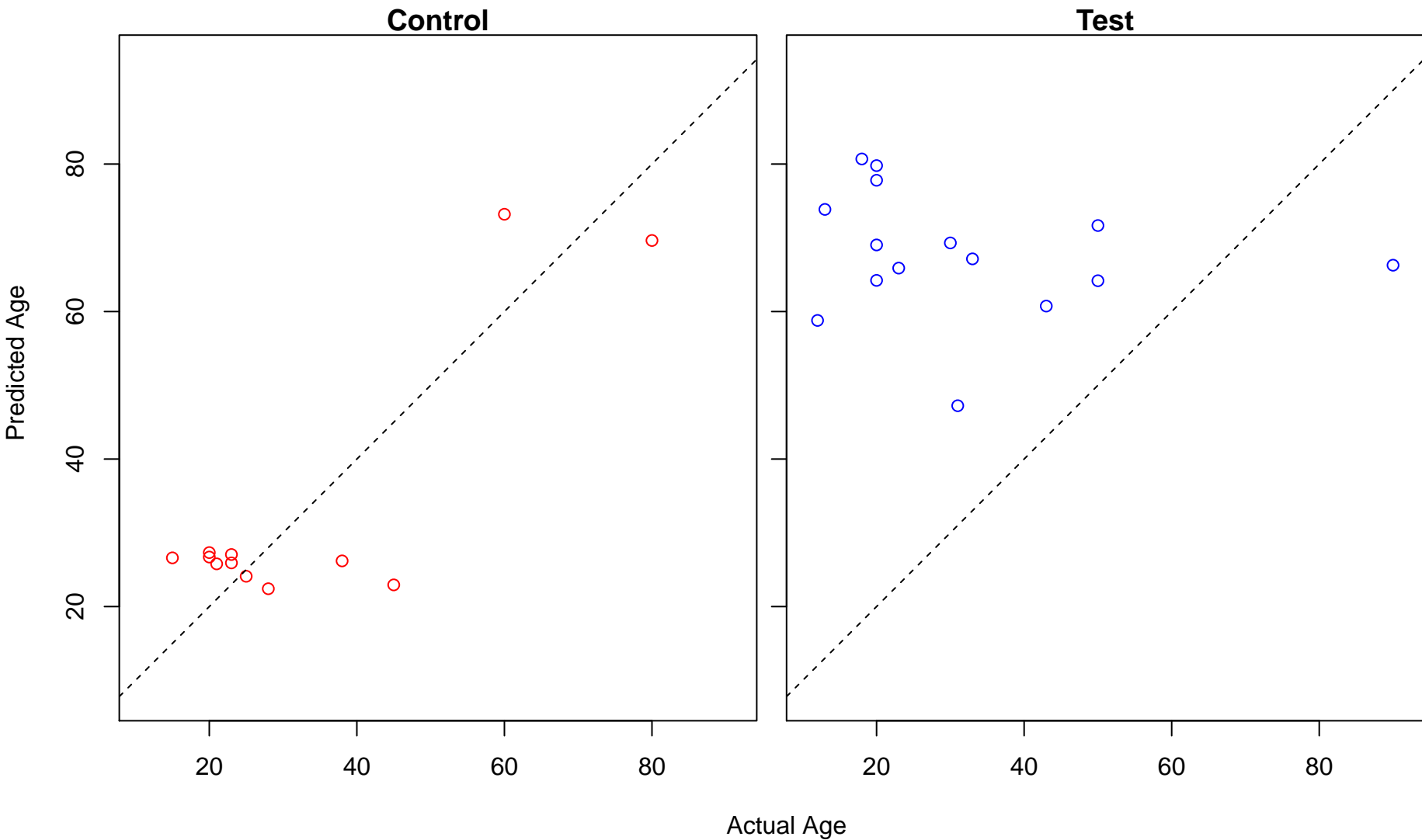
covalent chromatin modification (Score: 6.103751)



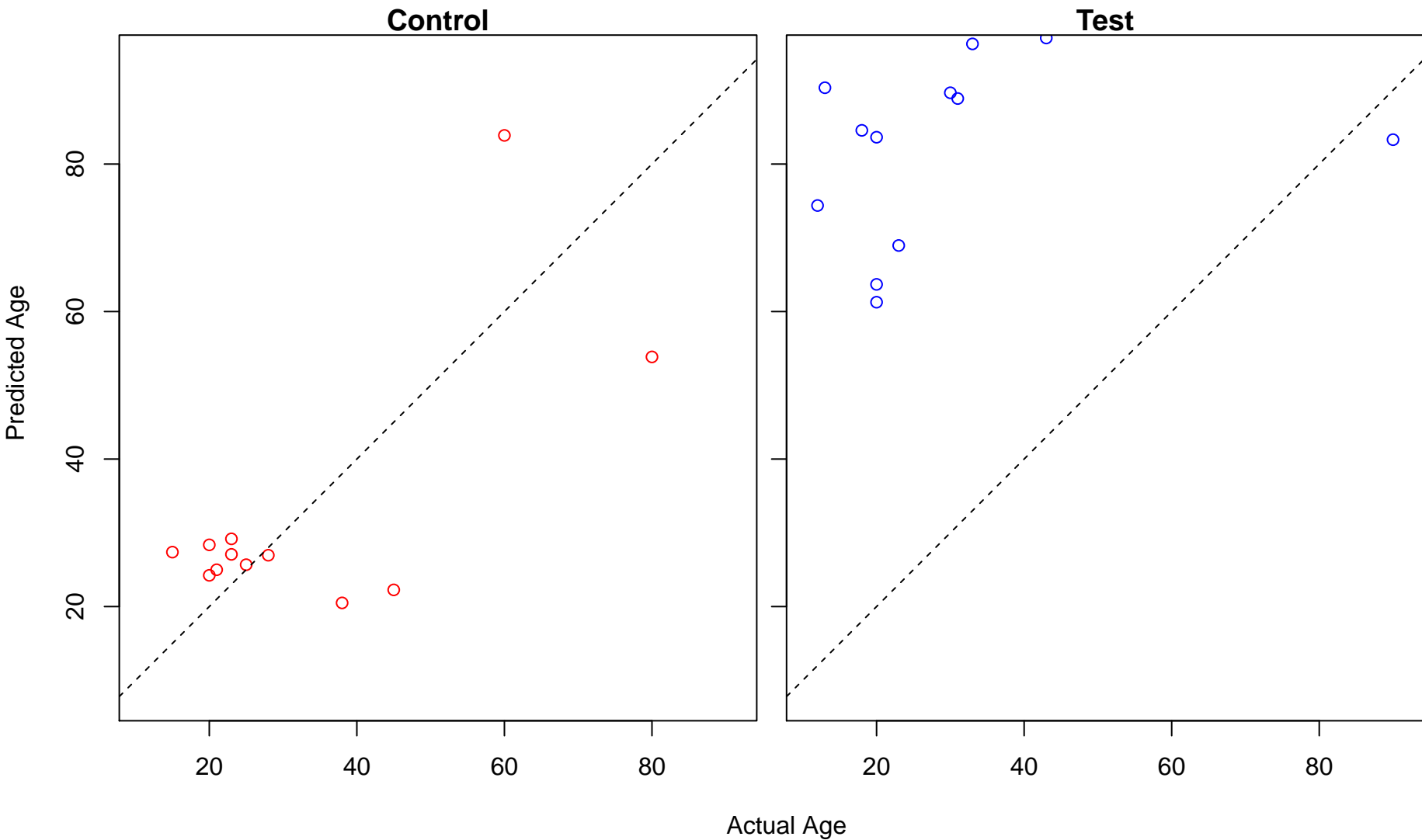
histone modification (Score: 6.103716)



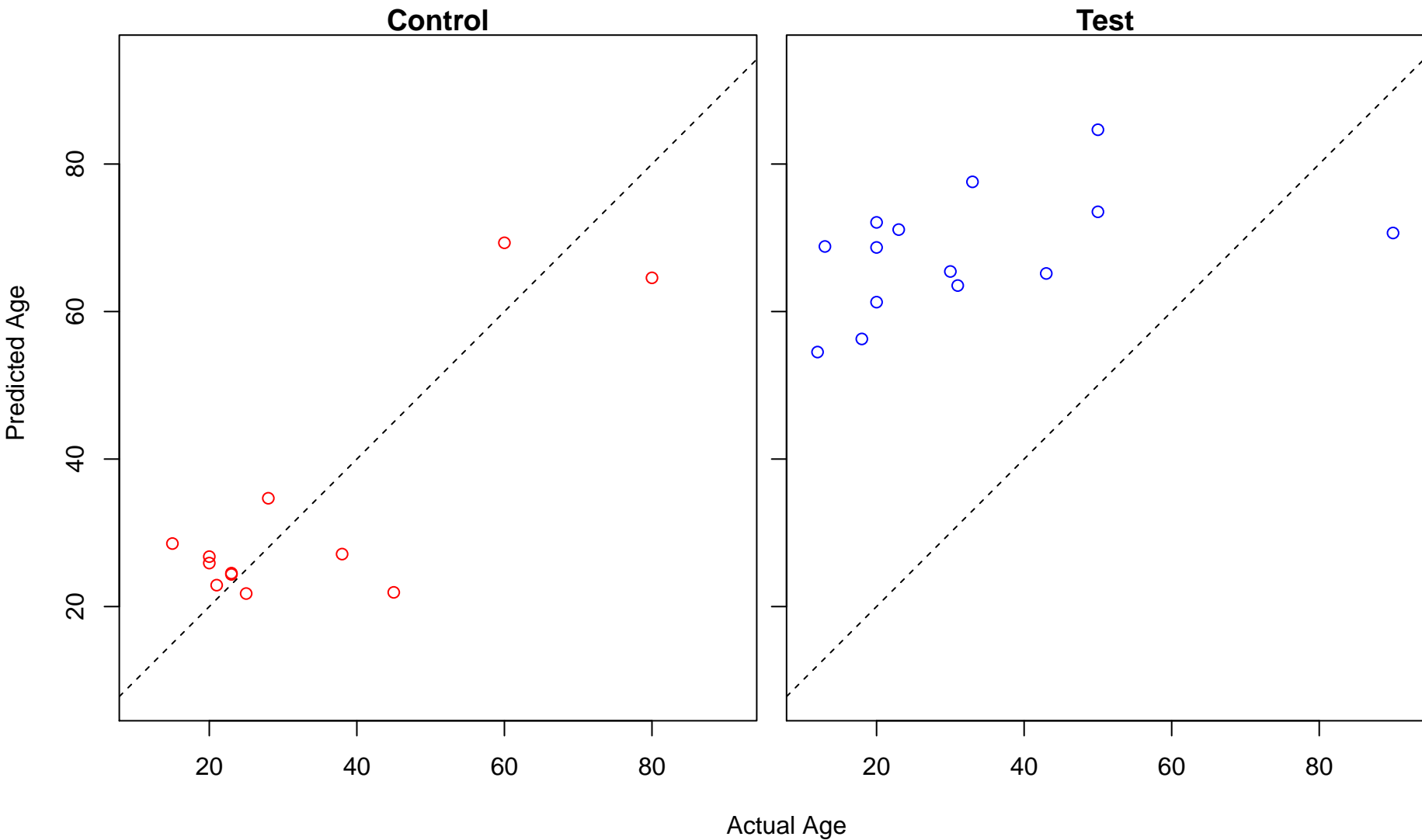
regulated exocytosis (Score: 6.103595)



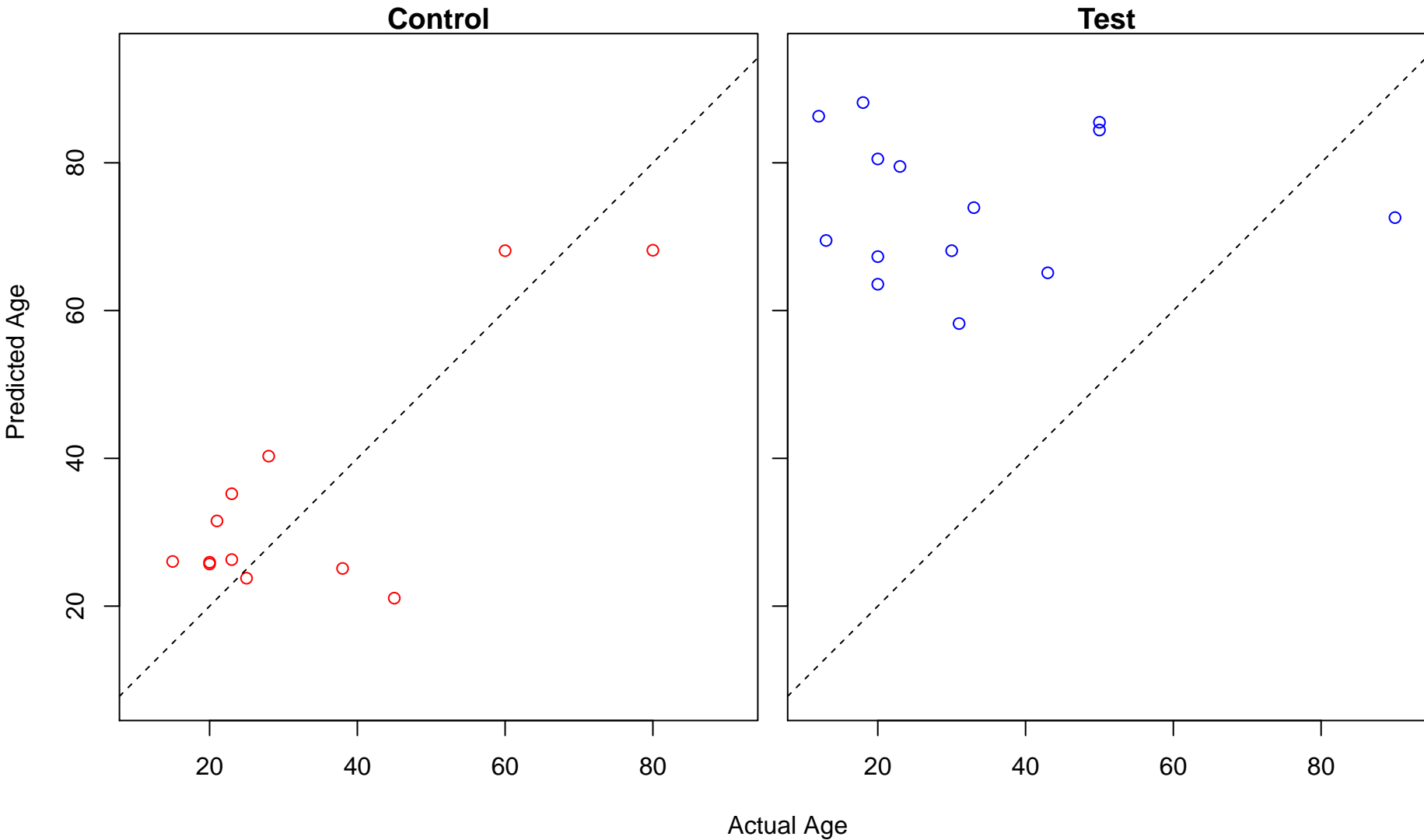
sulfation (Score: 6.100637)



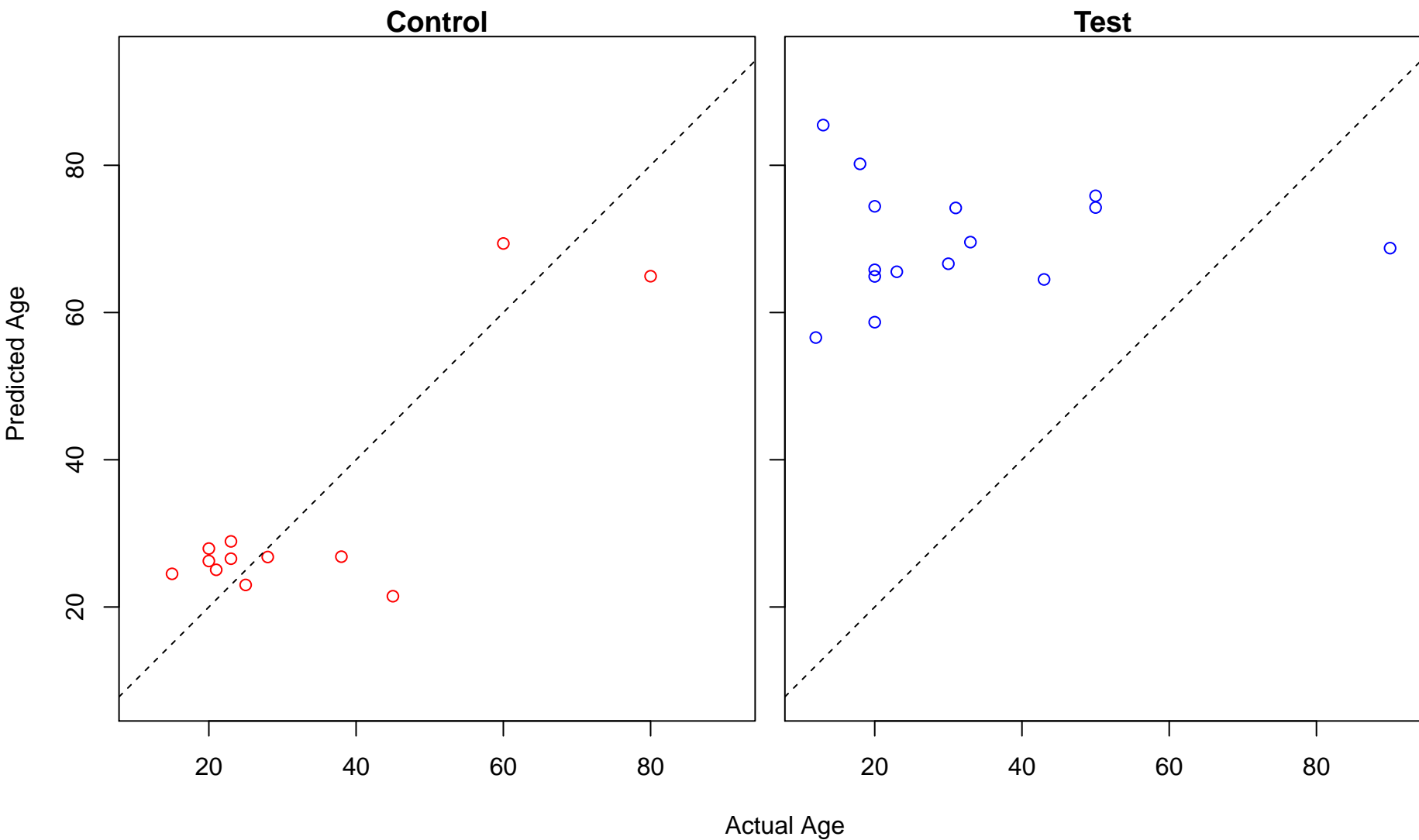
muscle cell migration (Score: 6.100109)



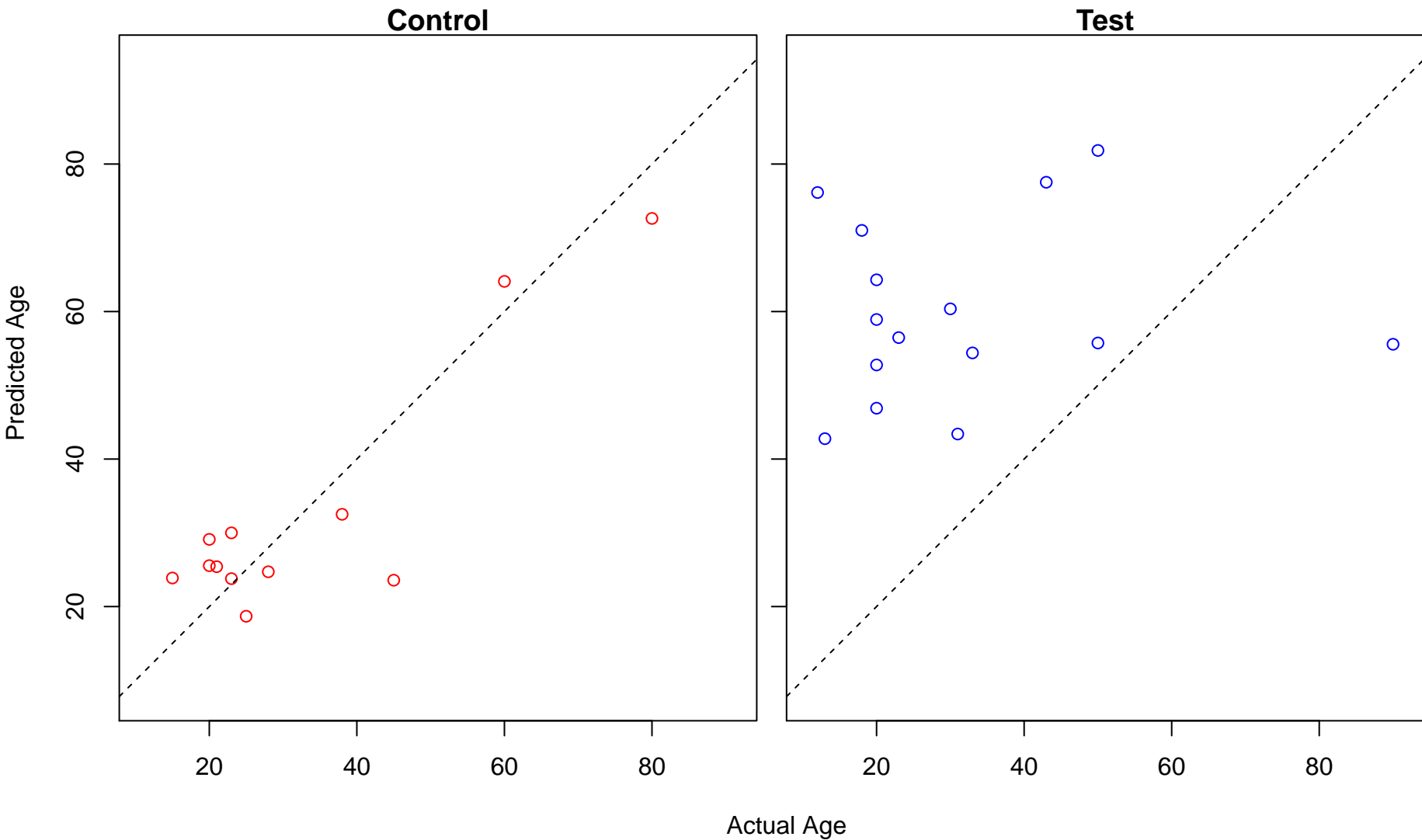
regulation of fatty acid biosynthetic process (Score: 6.098521)



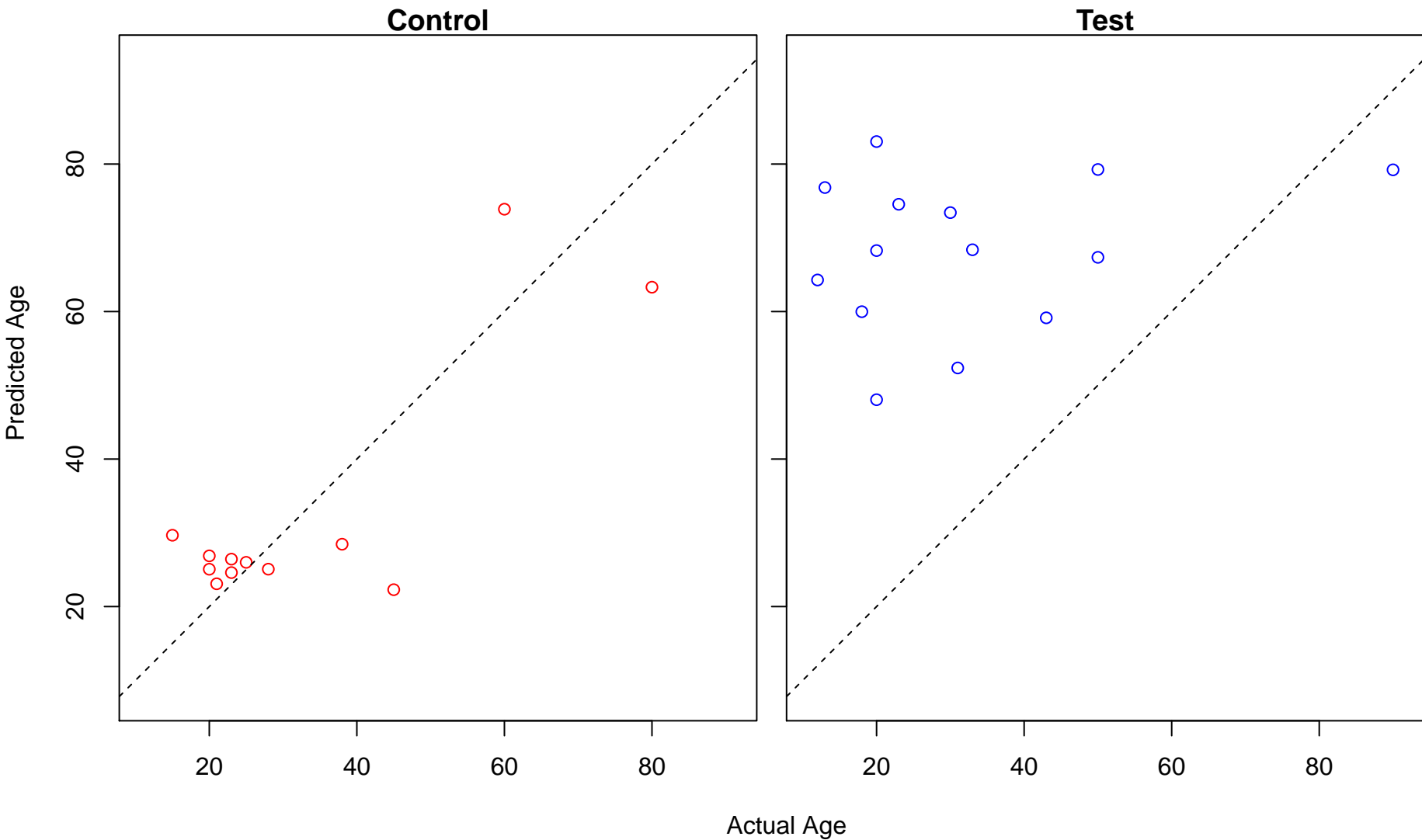
regulation of alpha-beta T cell activation (Score: 6.096309)



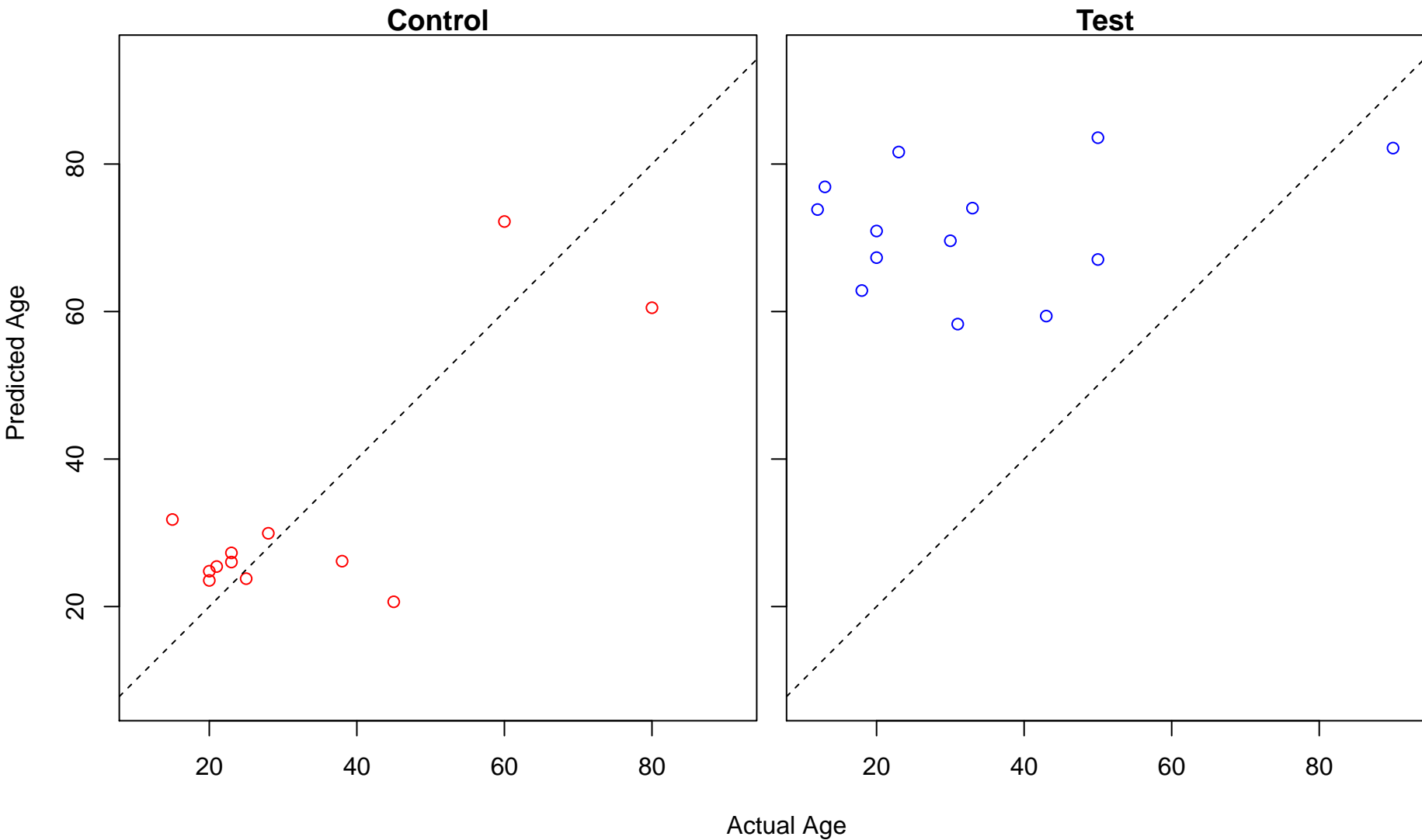
cysteine metabolic process (Score: 6.094503)



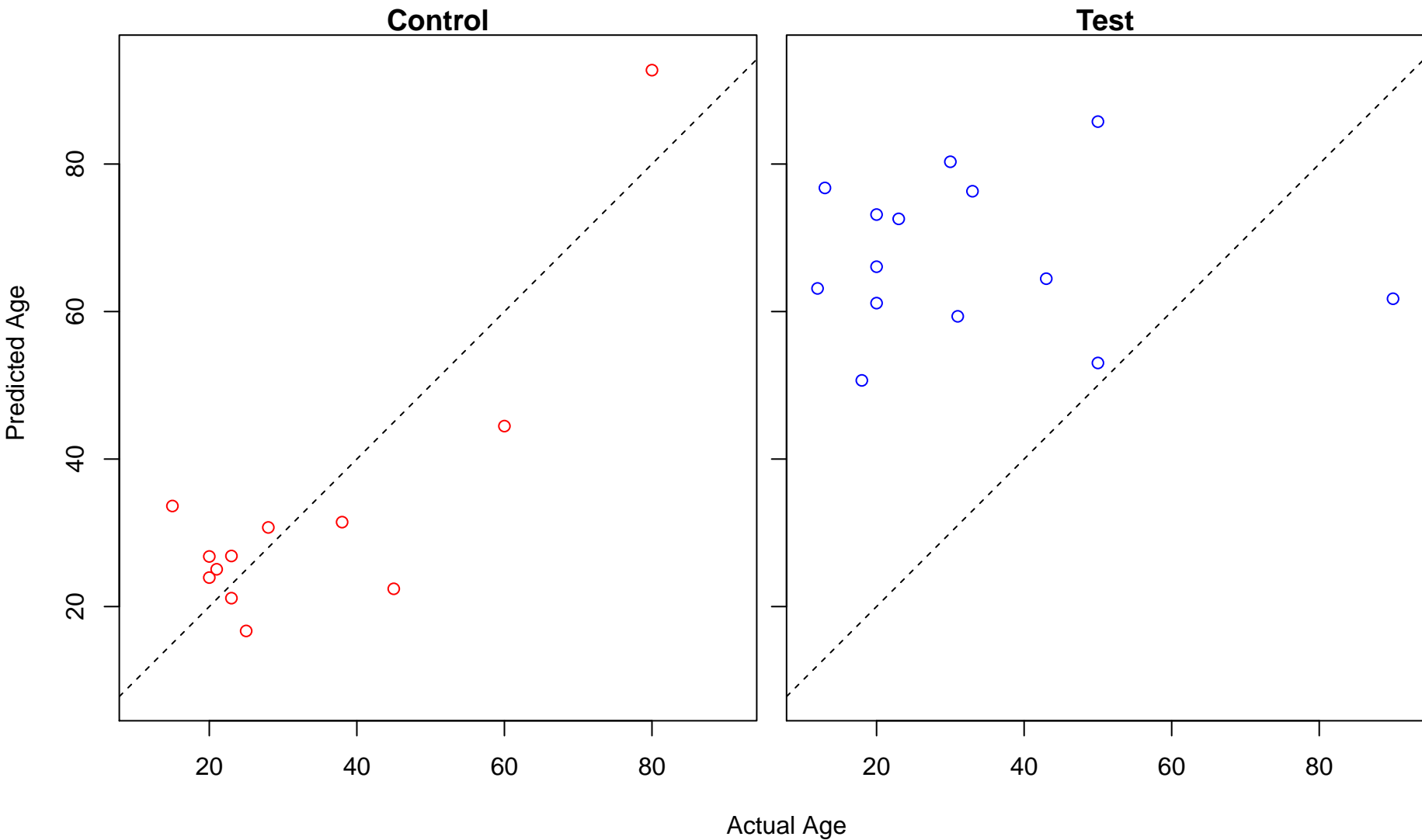
cellular copper ion homeostasis (Score: 6.093250)



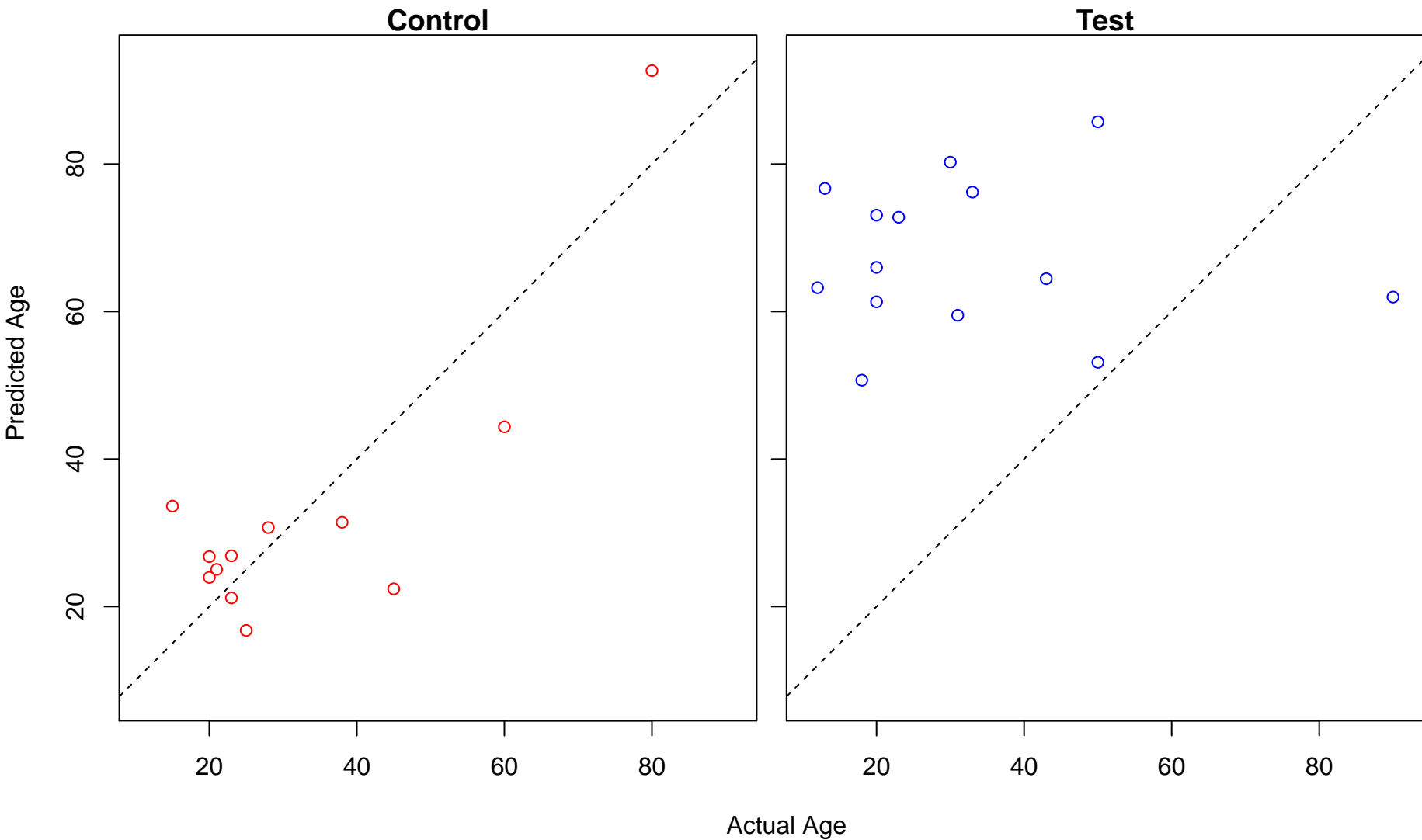
negative regulation of histone H3-K9 methylation (Score: 6.092139)



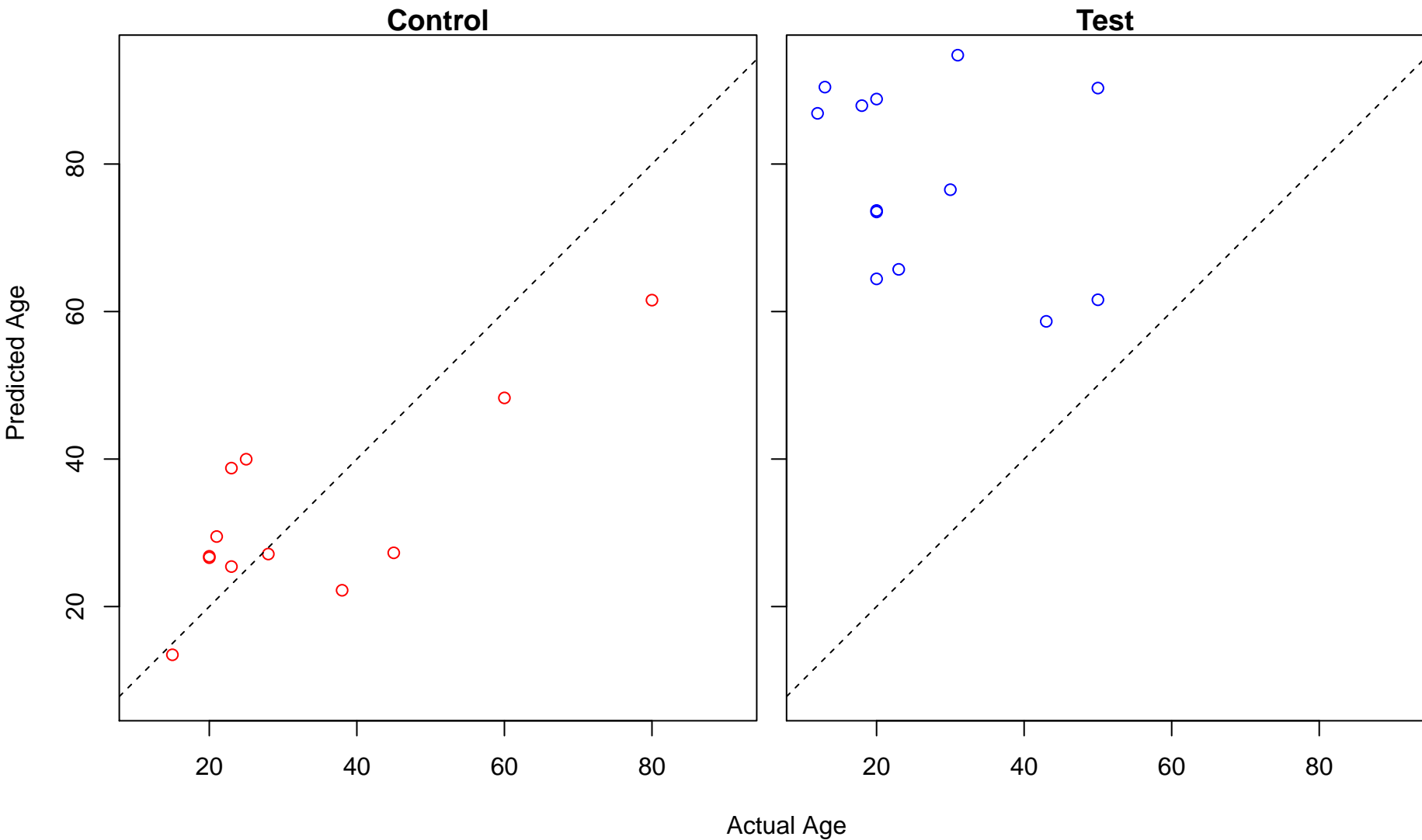
negative regulation of stress fiber assembly (Score: 6.089658)



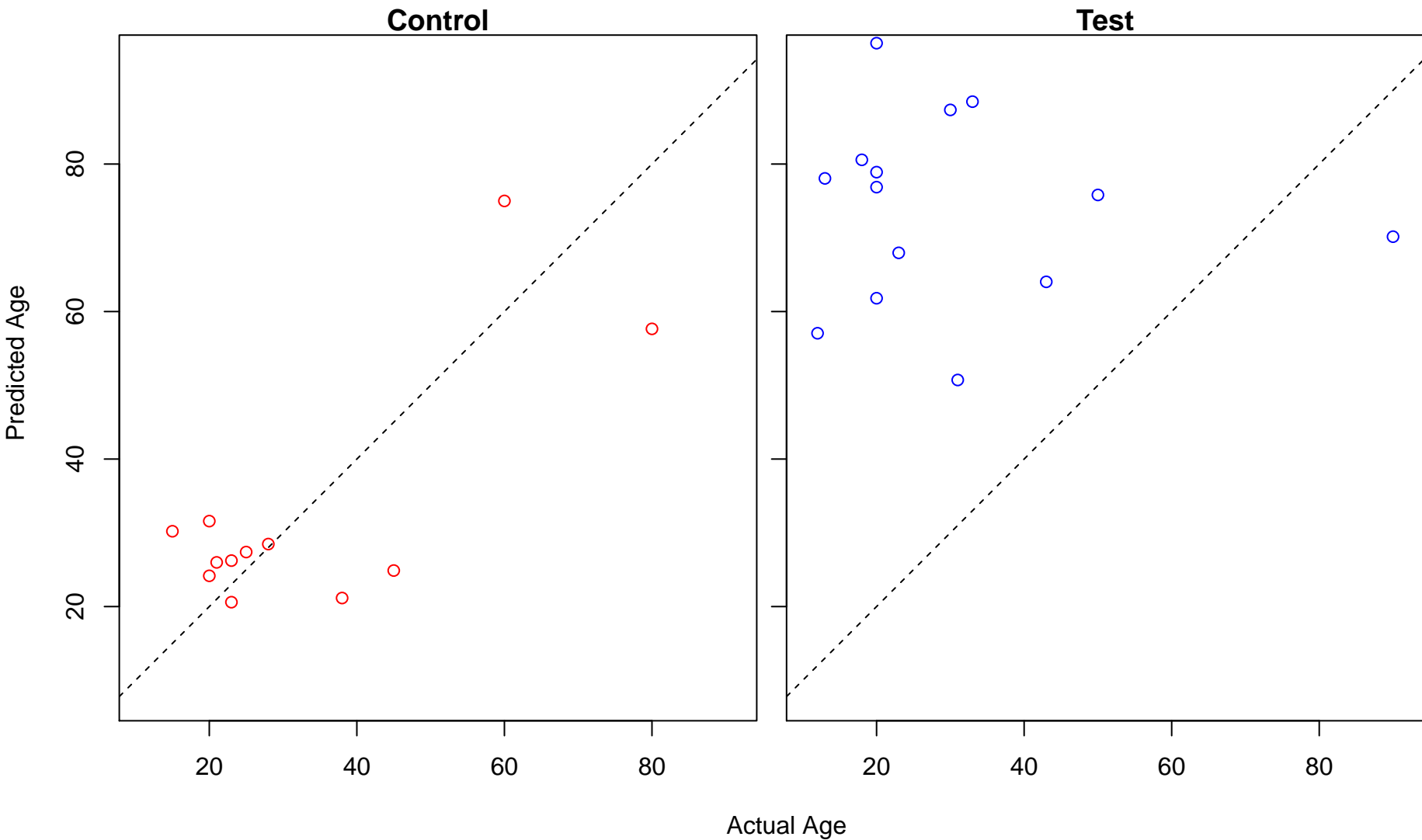
negative regulation of actin filament bundle assembly (Score: 6.088393)



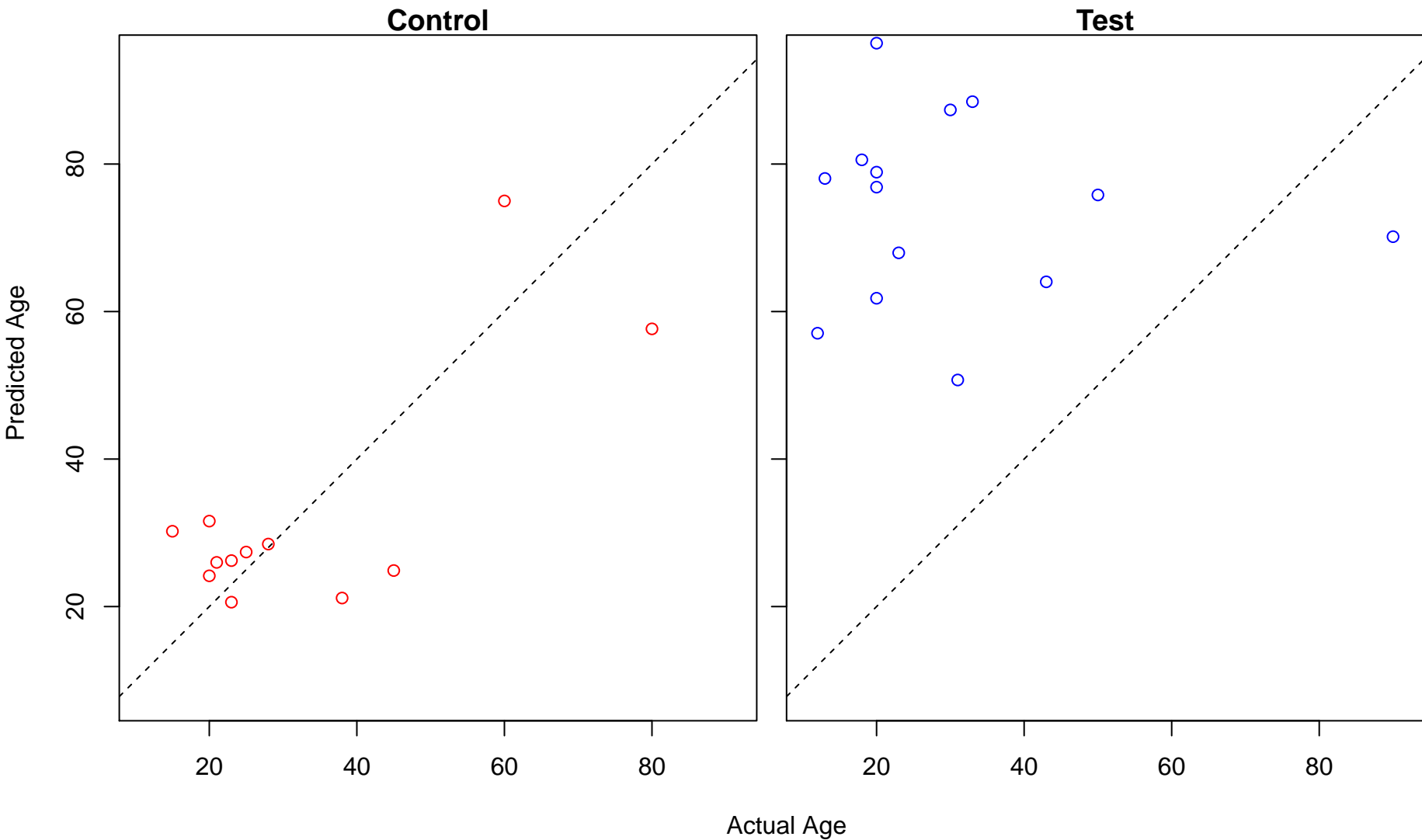
regulation of glutamate receptor signaling pathway (Score: 6.088223)



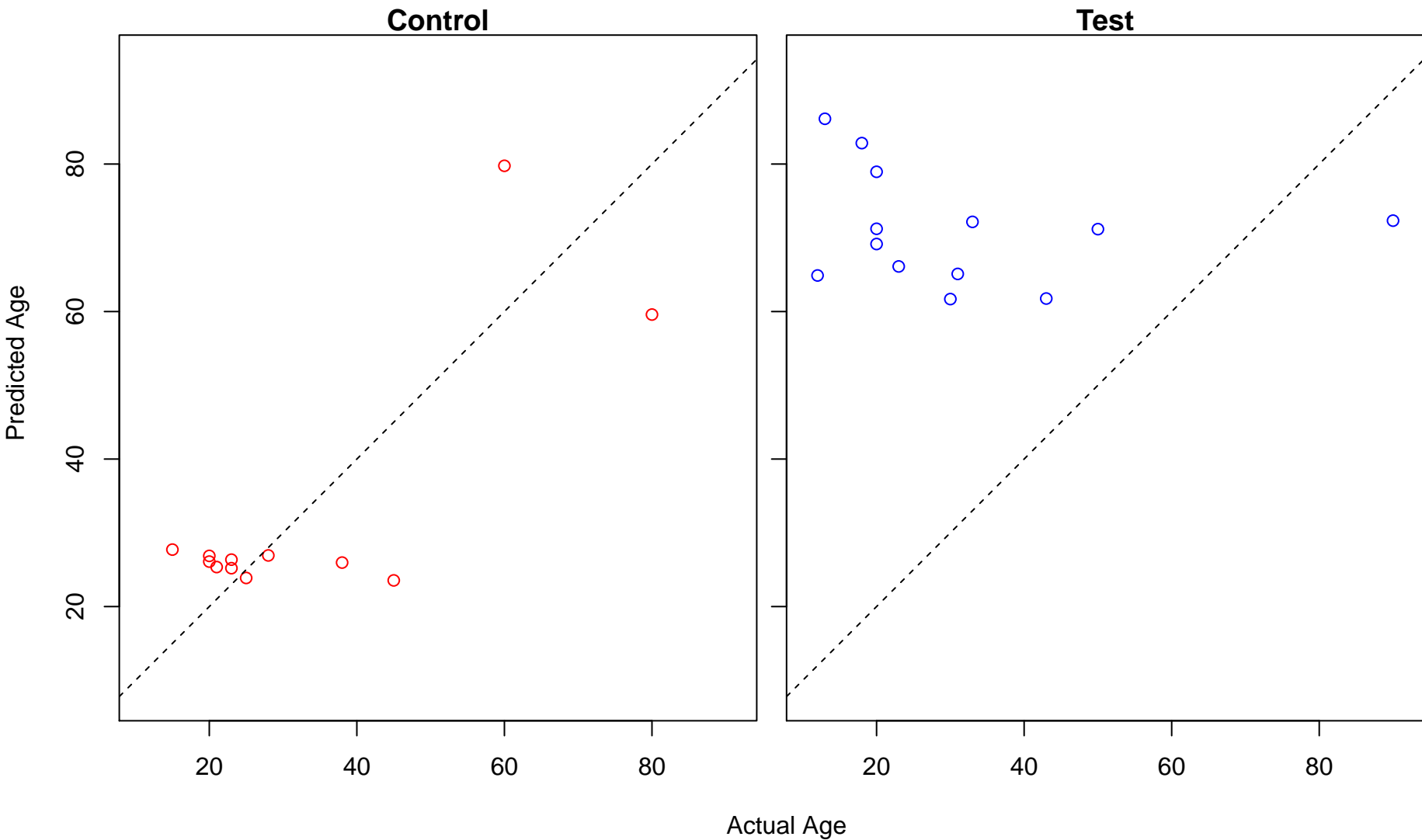
negative regulation of peptide hormone secretion (Score: 6.087281)



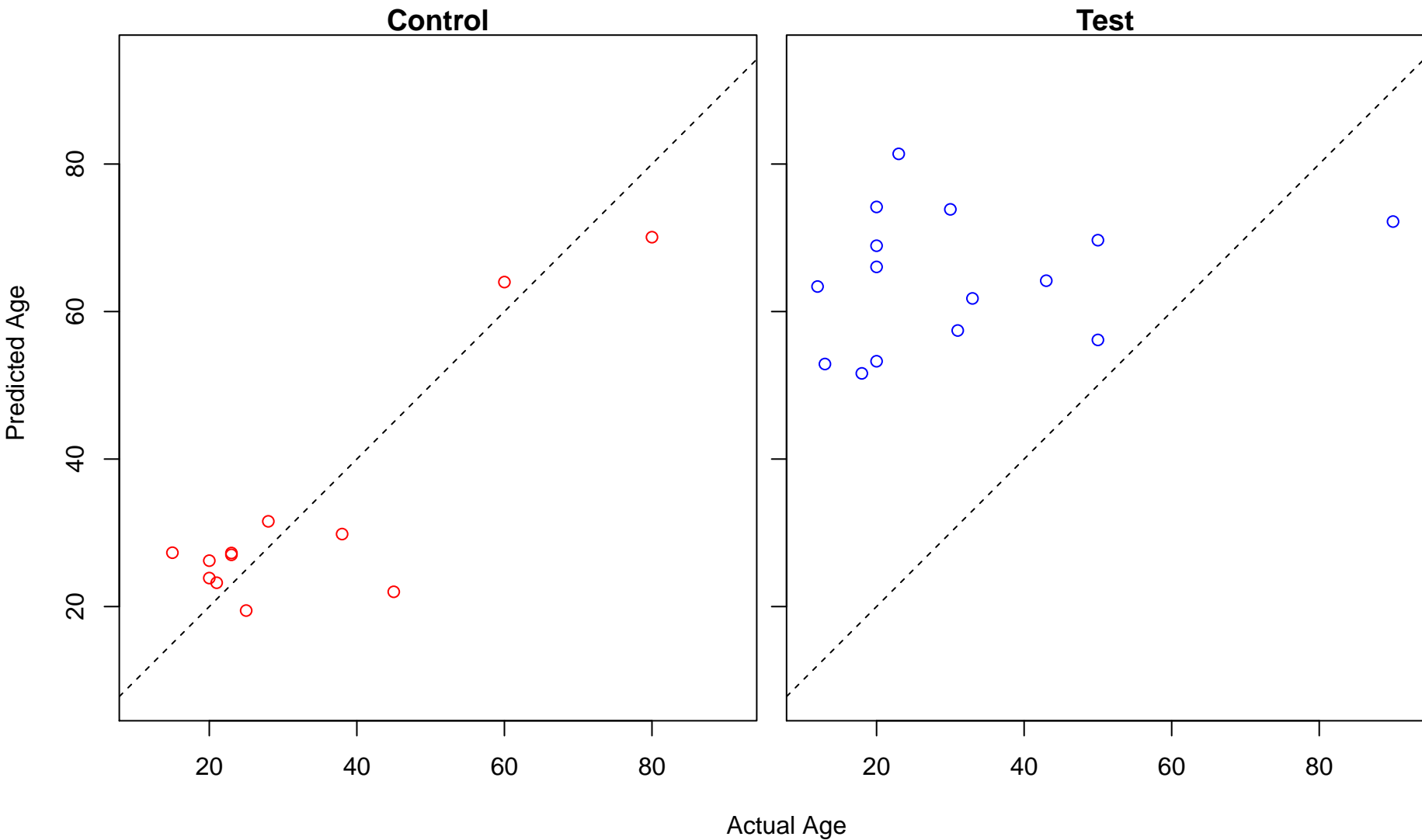
negative regulation of insulin secretion (Score: 6.087108)



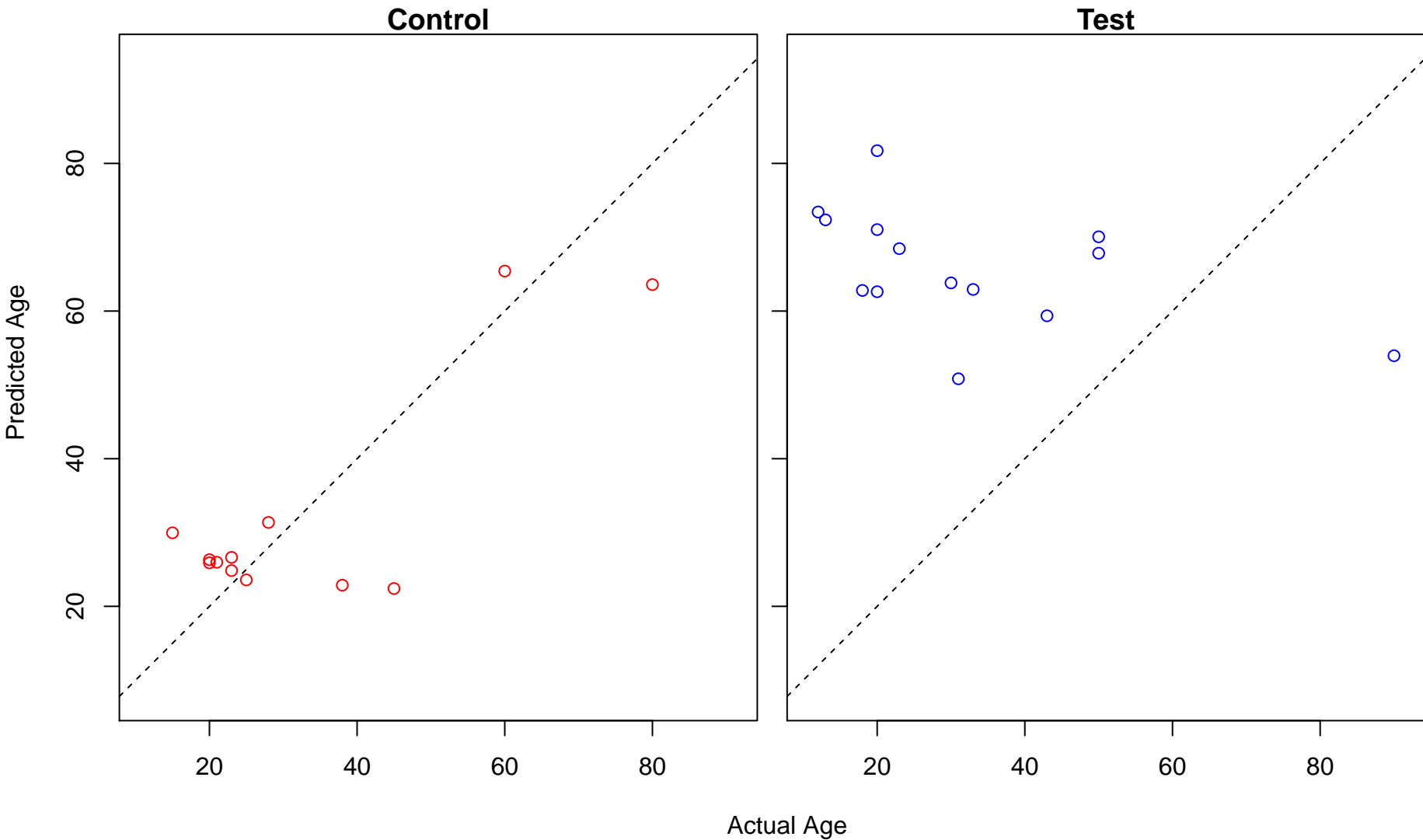
positive regulation of ligase activity (Score: 6.085031)



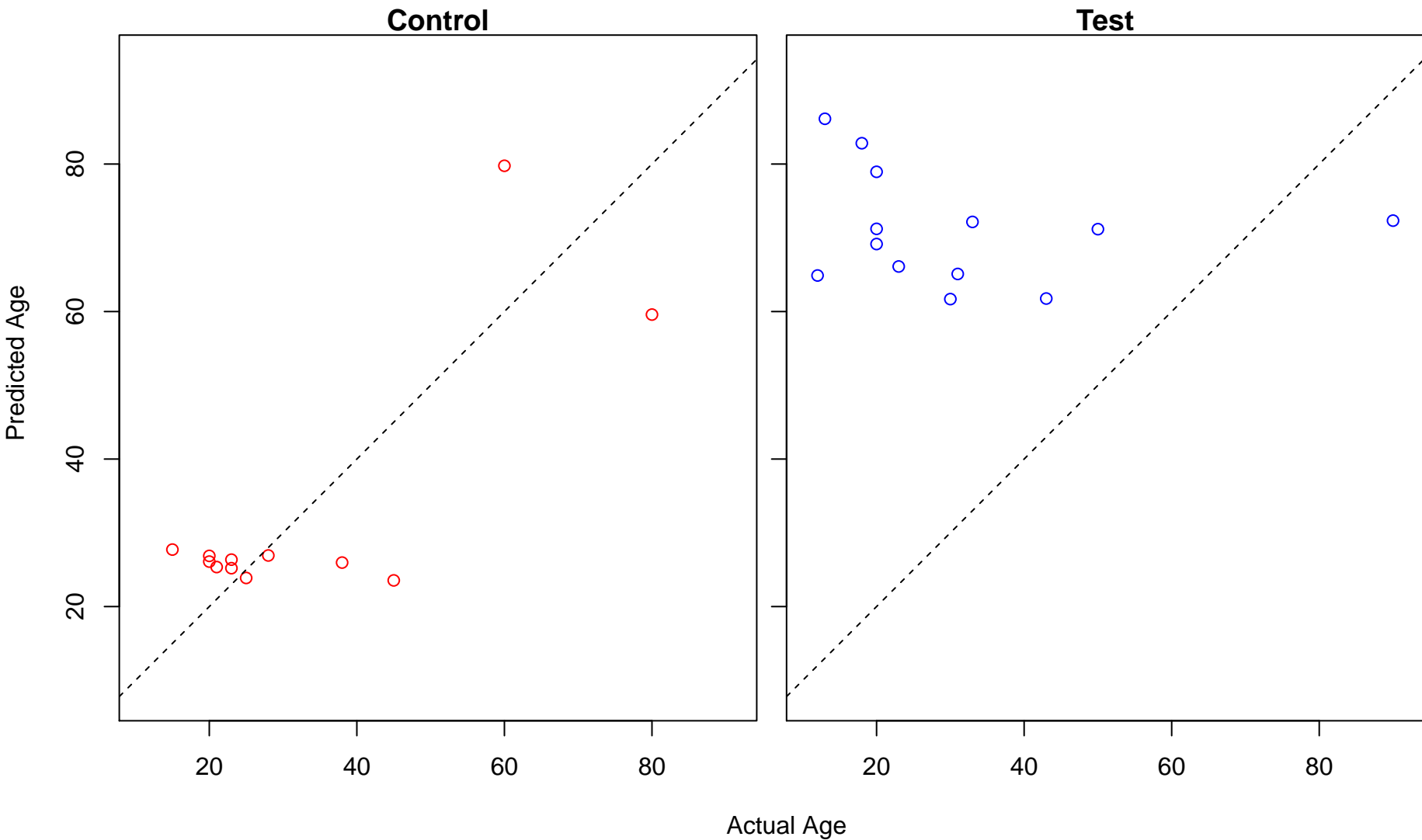
ethanolamine-containing compound metabolic process (Score: 6.084971)



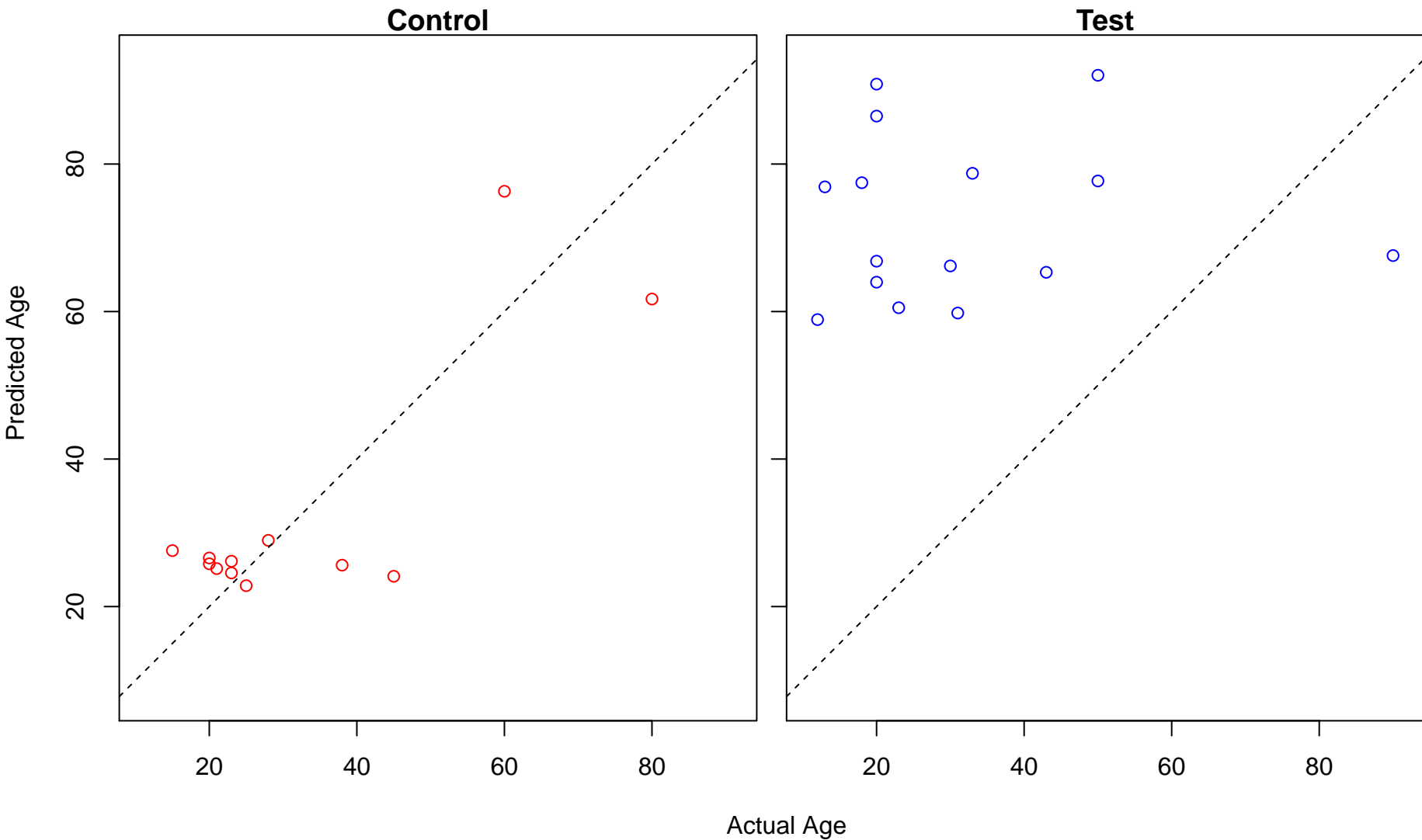
sensory perception of mechanical stimulus (Score: 6.083567)



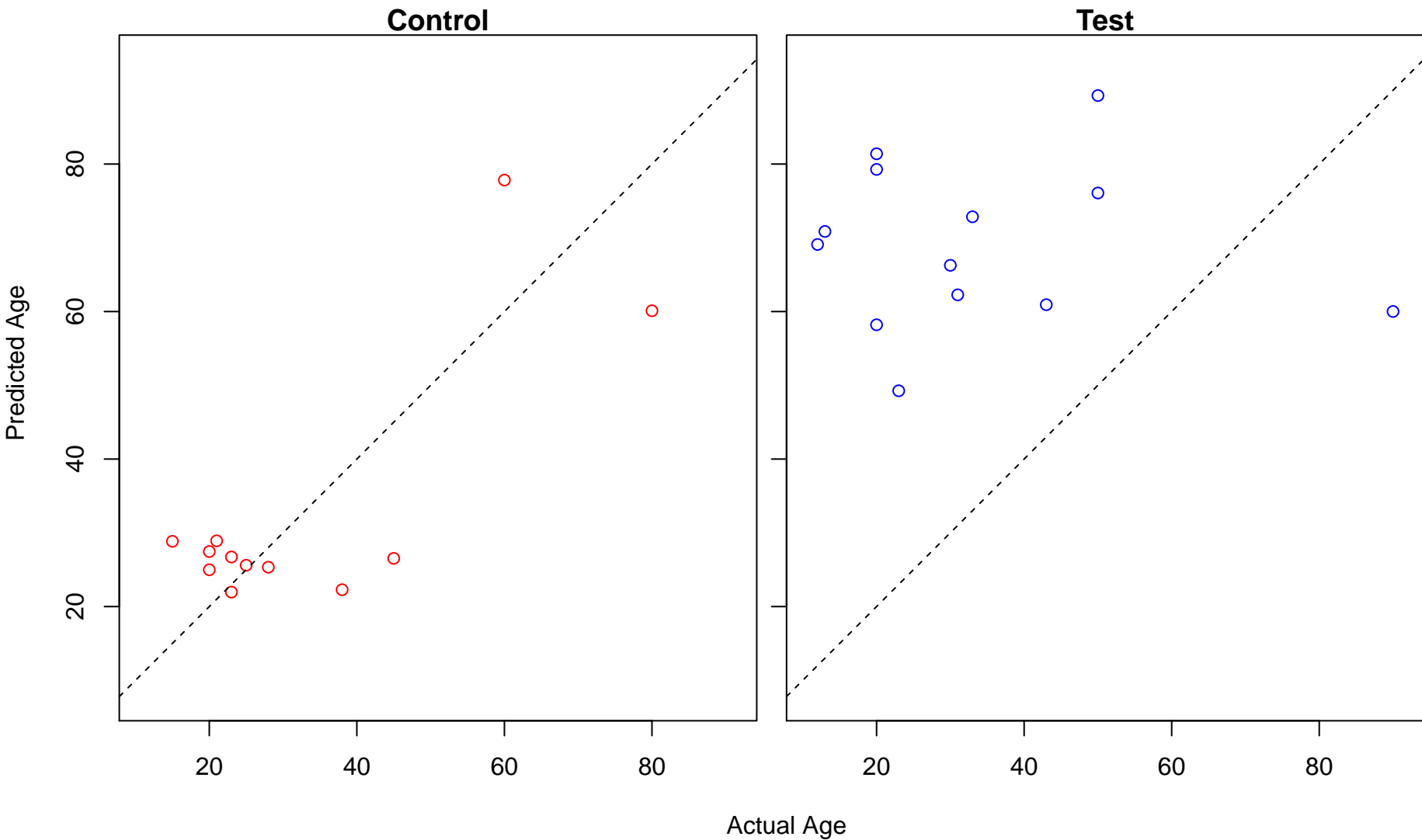
positive regulation of ubiquitin–protein transferase activity (Score: 6.083112)



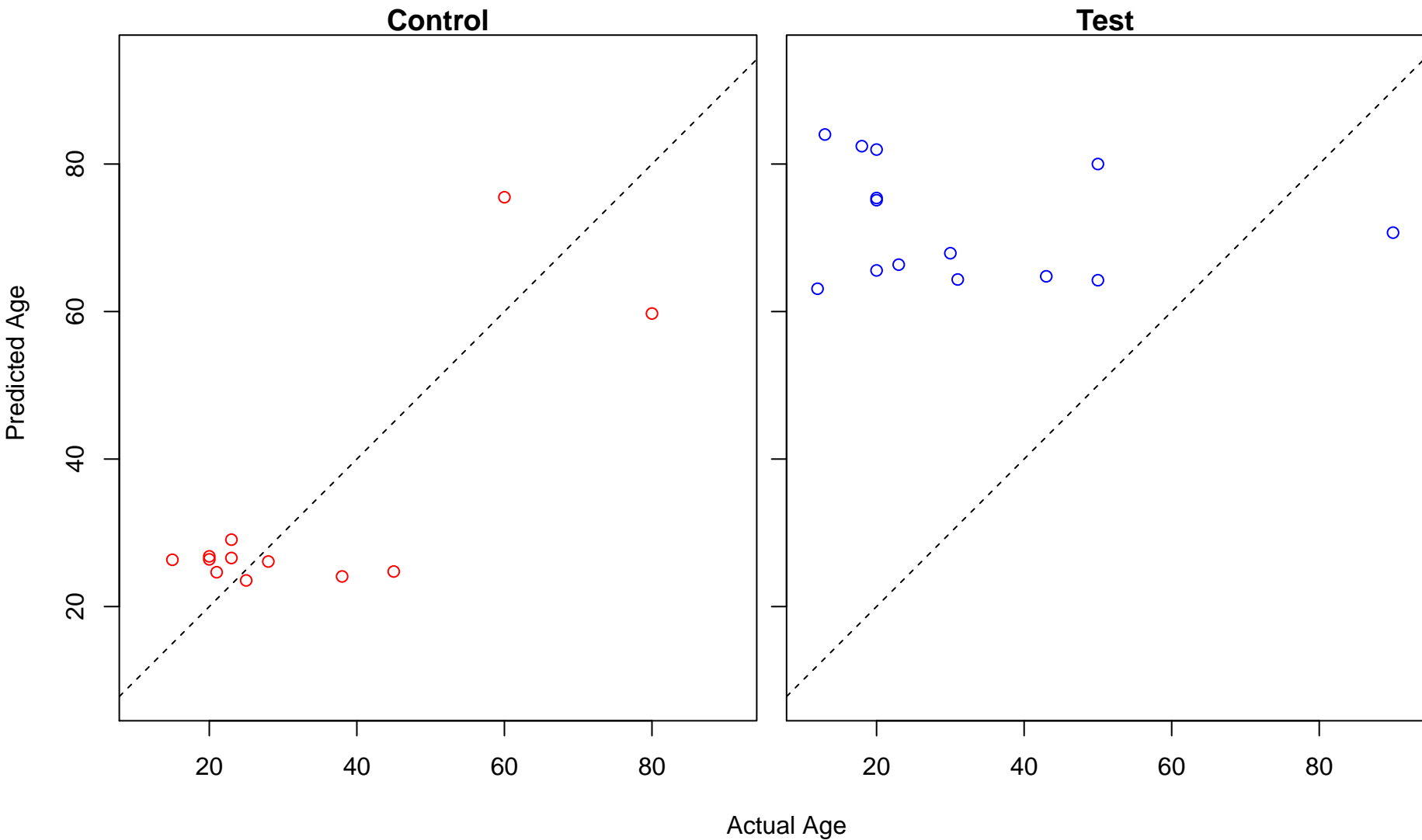
cell-matrix adhesion (Score: 6.082356)



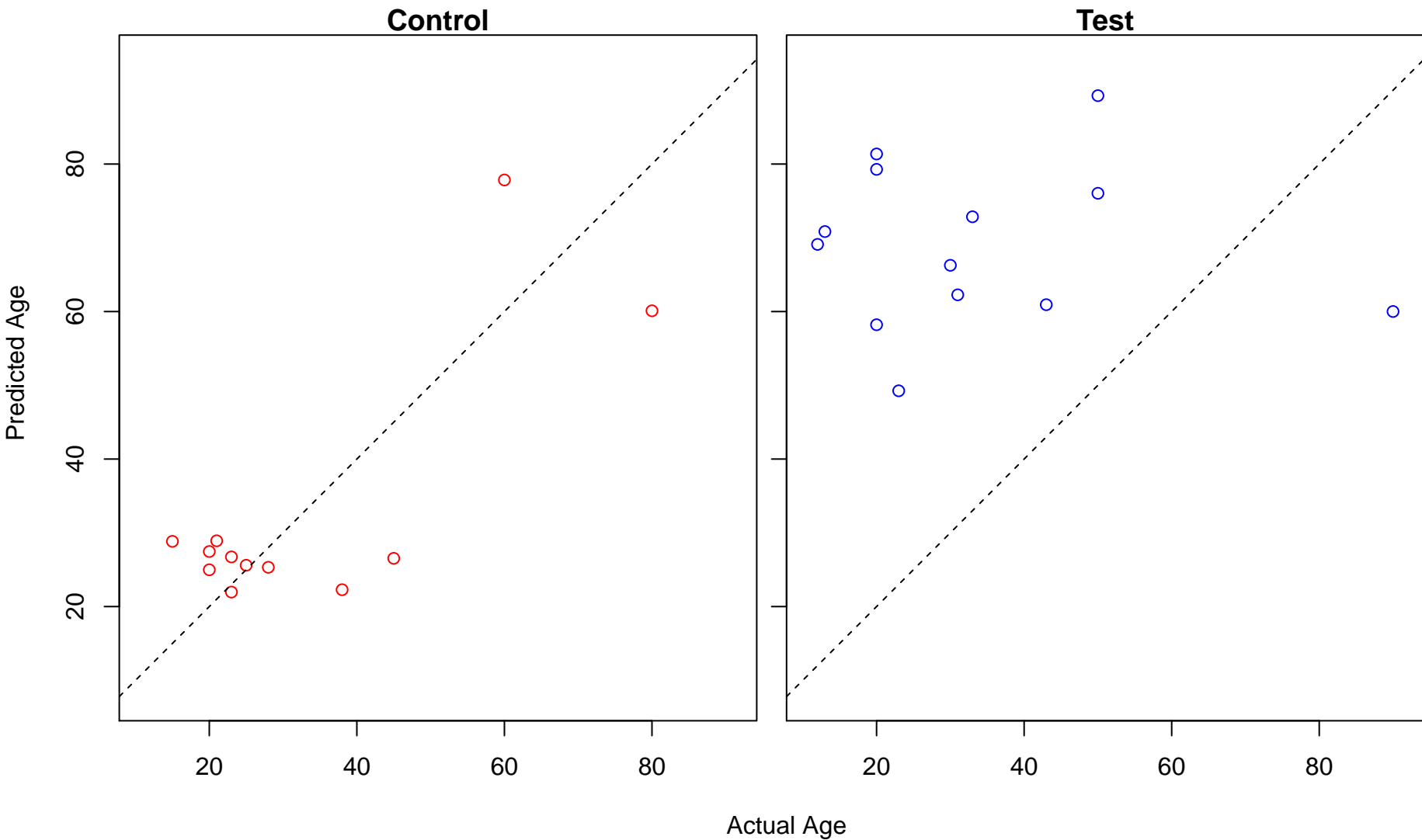
positive regulation of adherens junction organization (Score: 6.081168)



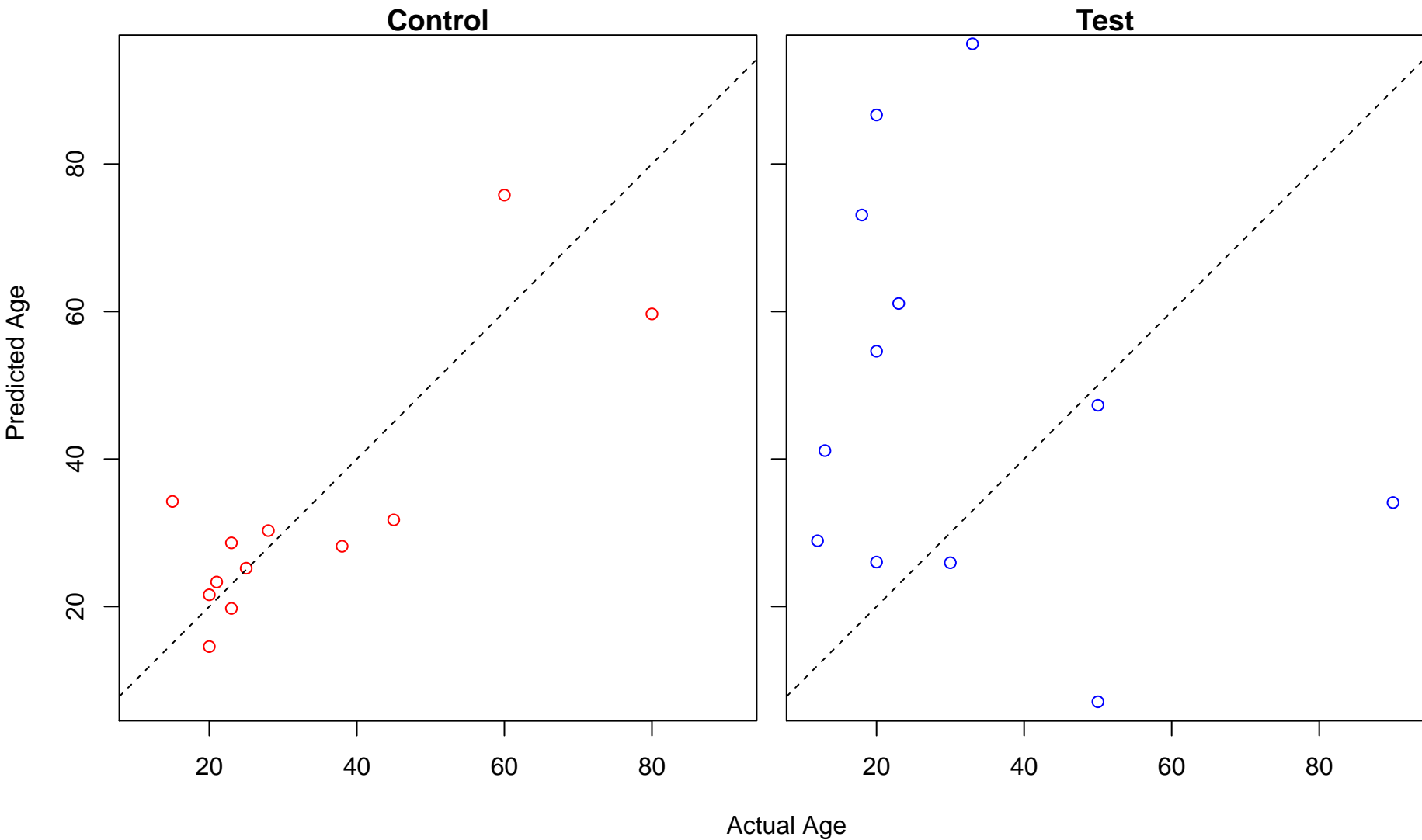
negative regulation of lymphocyte apoptotic process (Score: 6.078938)



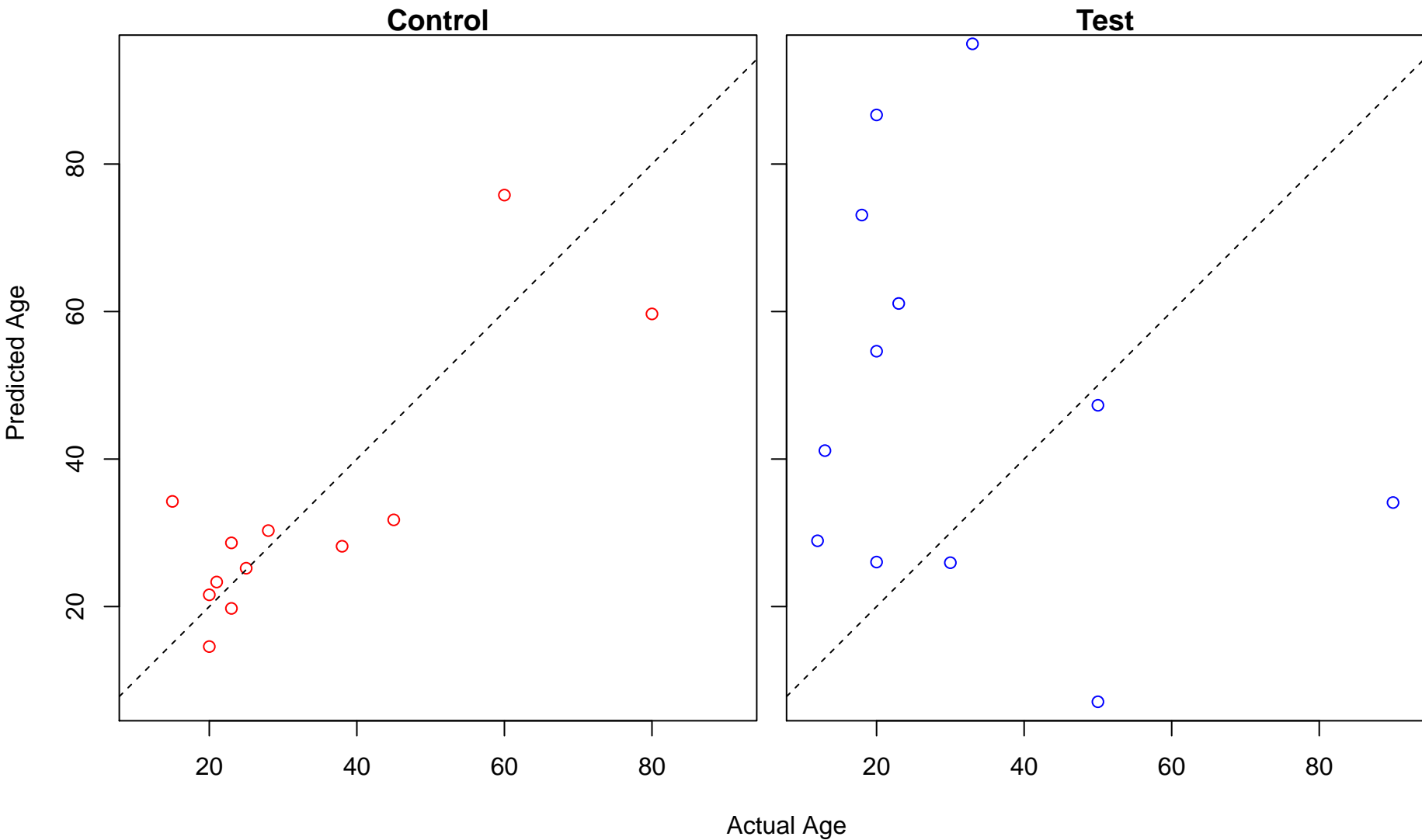
positive regulation of focal adhesion assembly (Score: 6.077468)



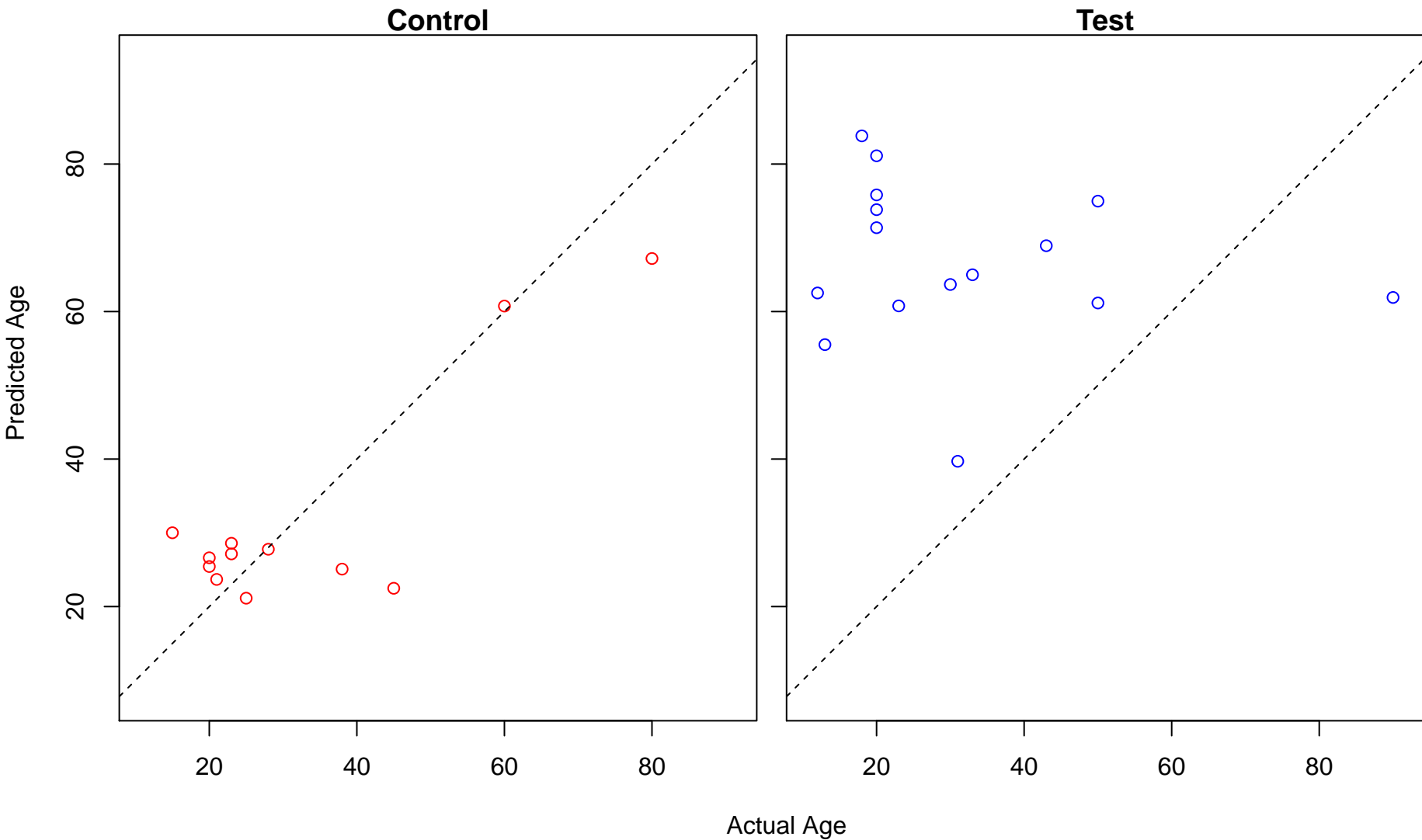
appendage development (Score: 6.077235)



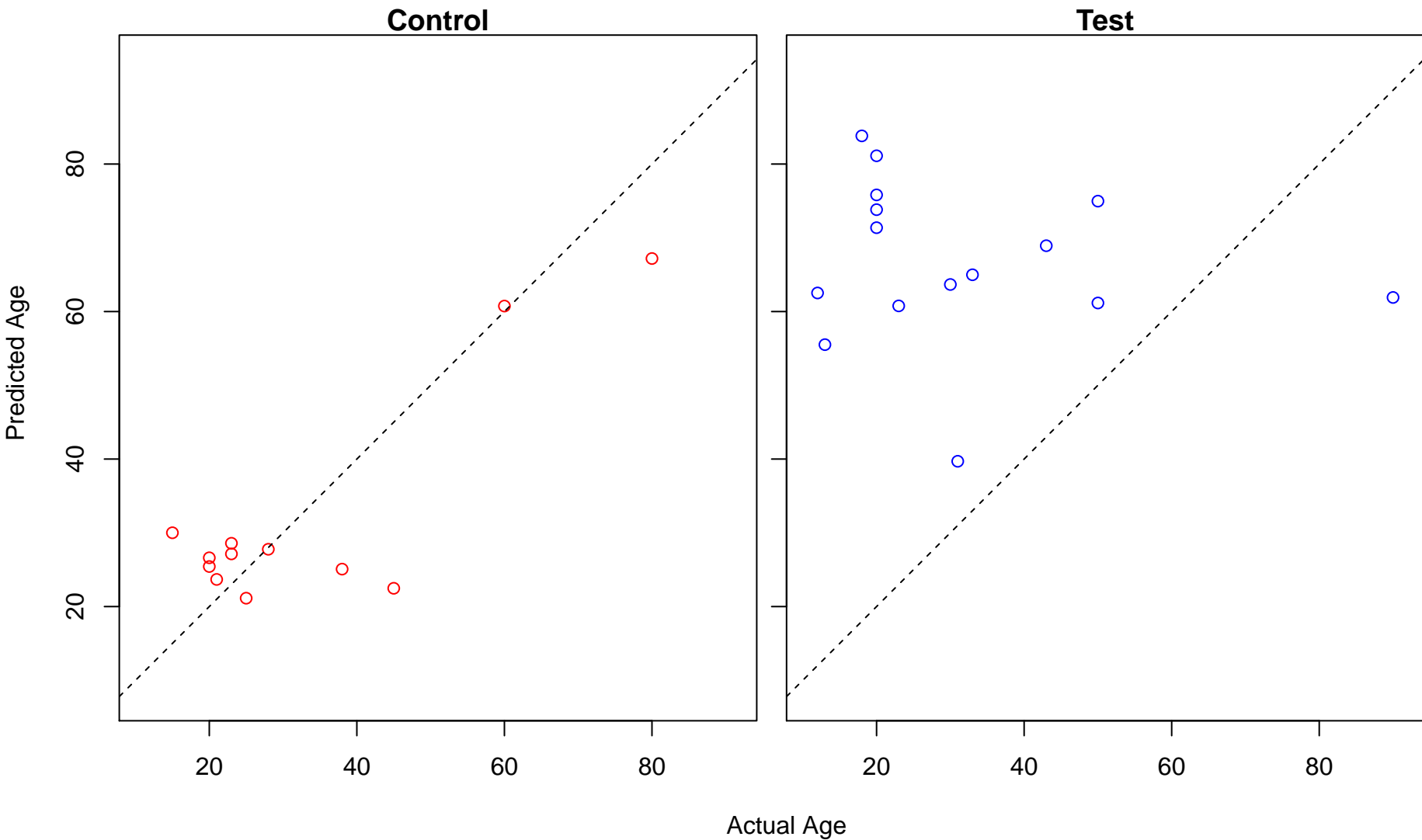
limb development (Score: 6.077235)



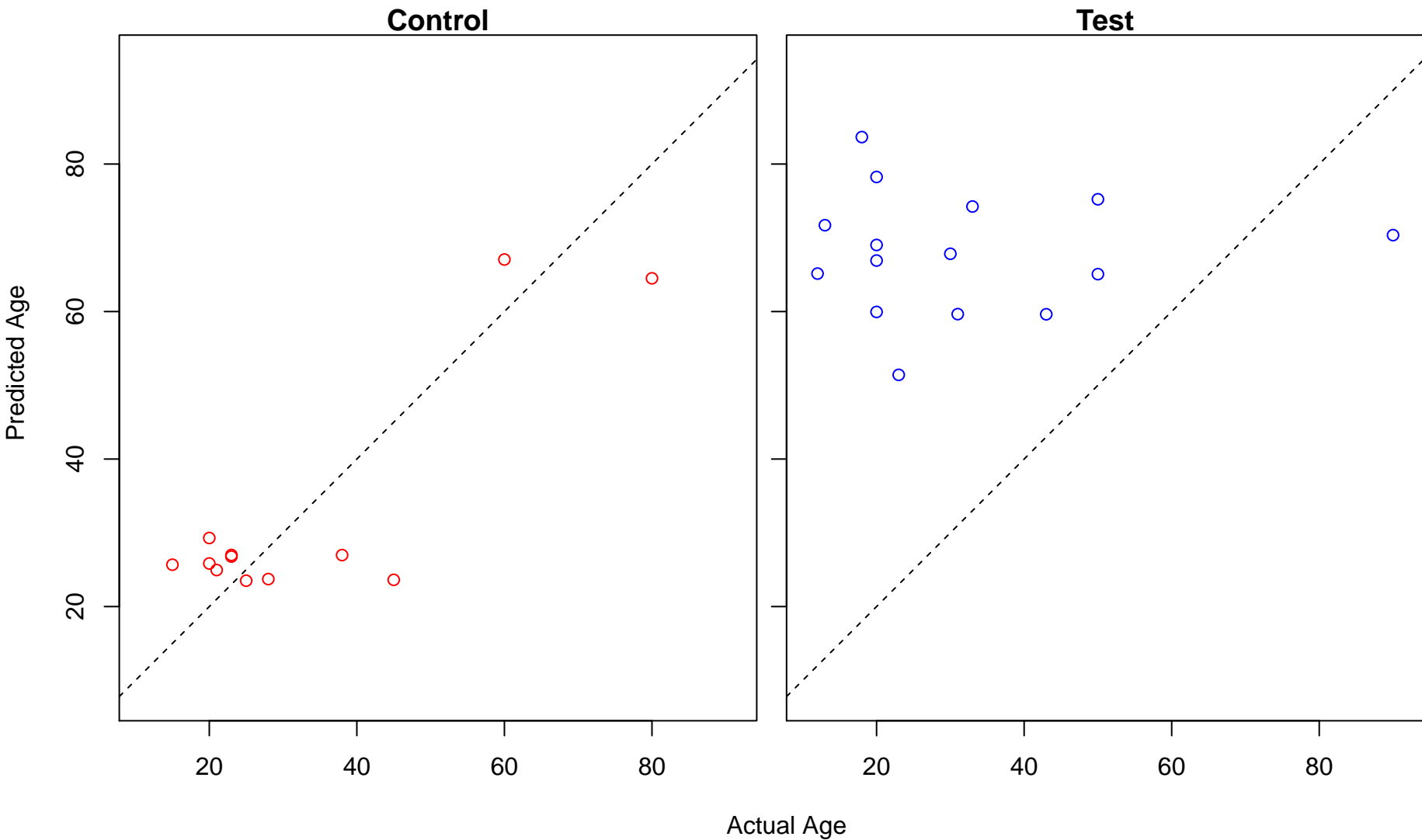
organic acid catabolic process (Score: 6.074042)



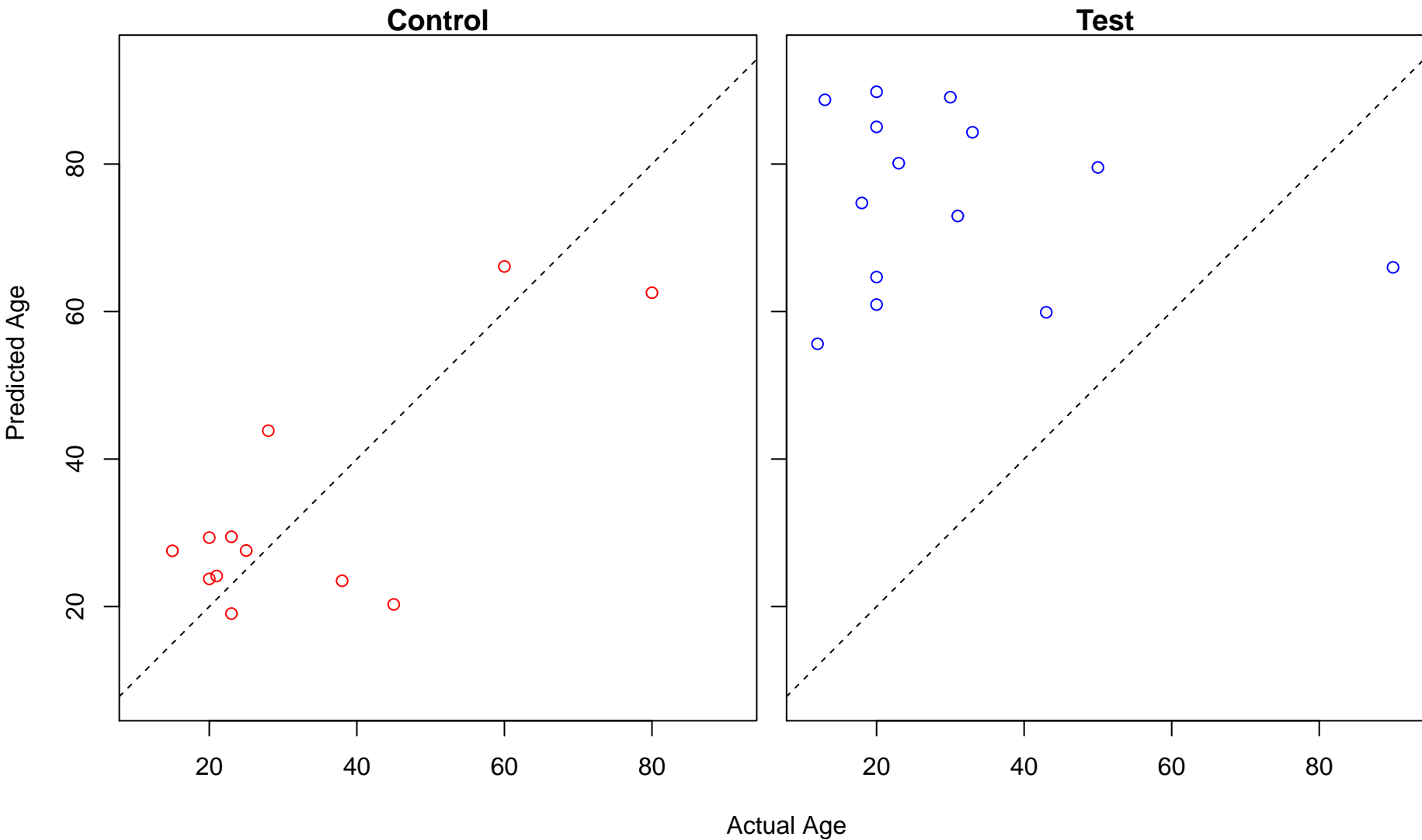
carboxylic acid catabolic process (Score: 6.074042)



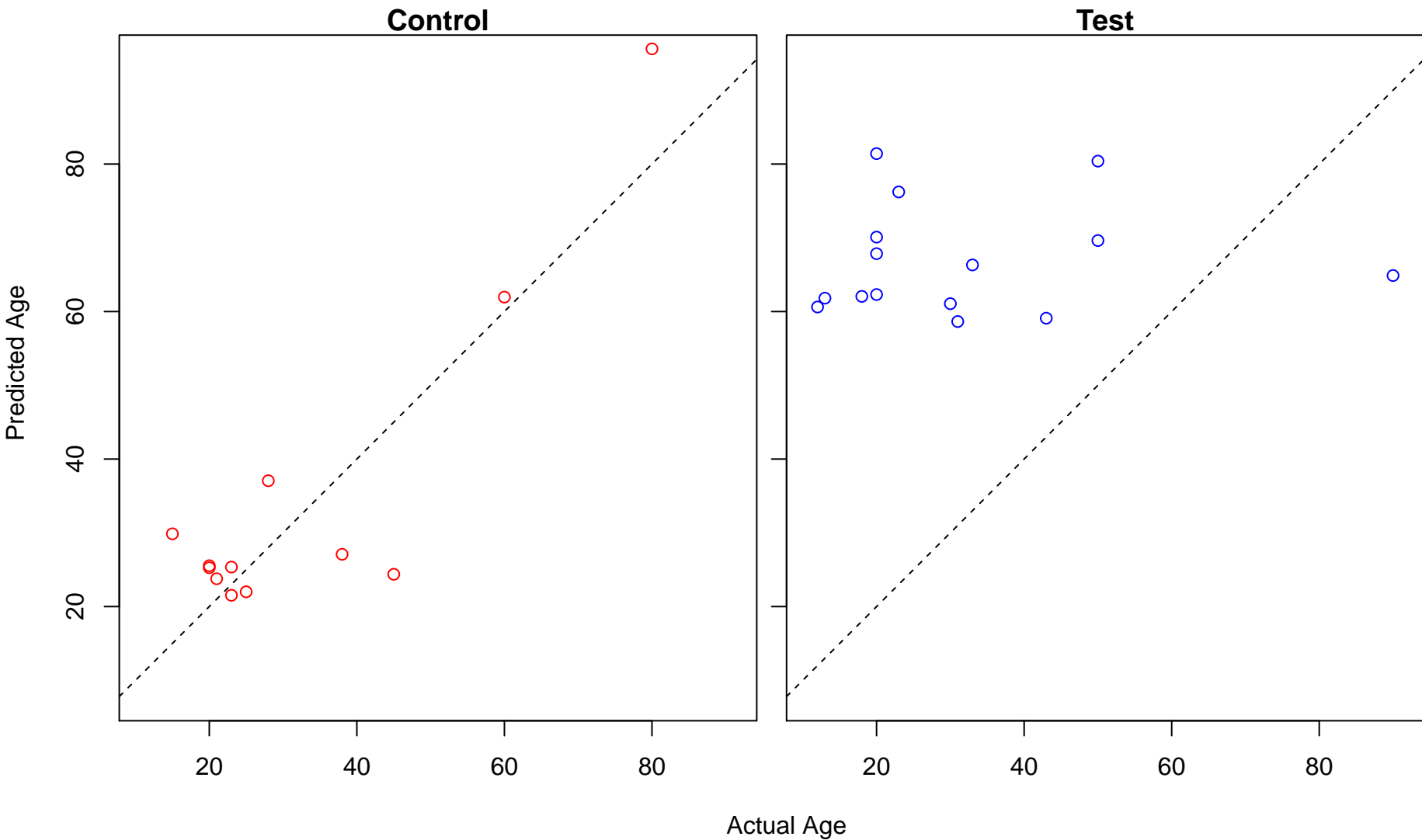
positive regulation of carbohydrate metabolic process (Score: 6.073073)



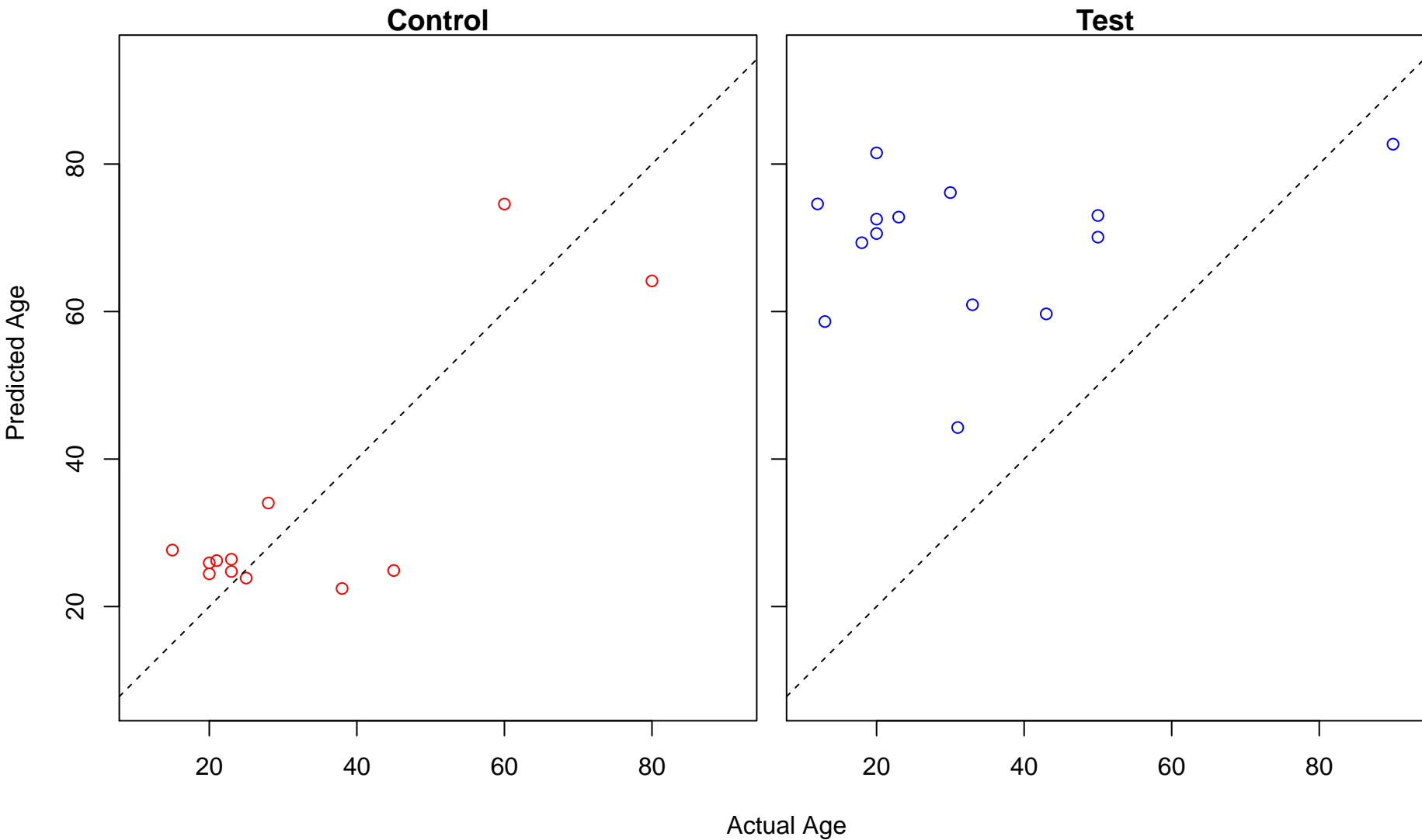
negative regulation of peptide secretion (Score: 6.071872)



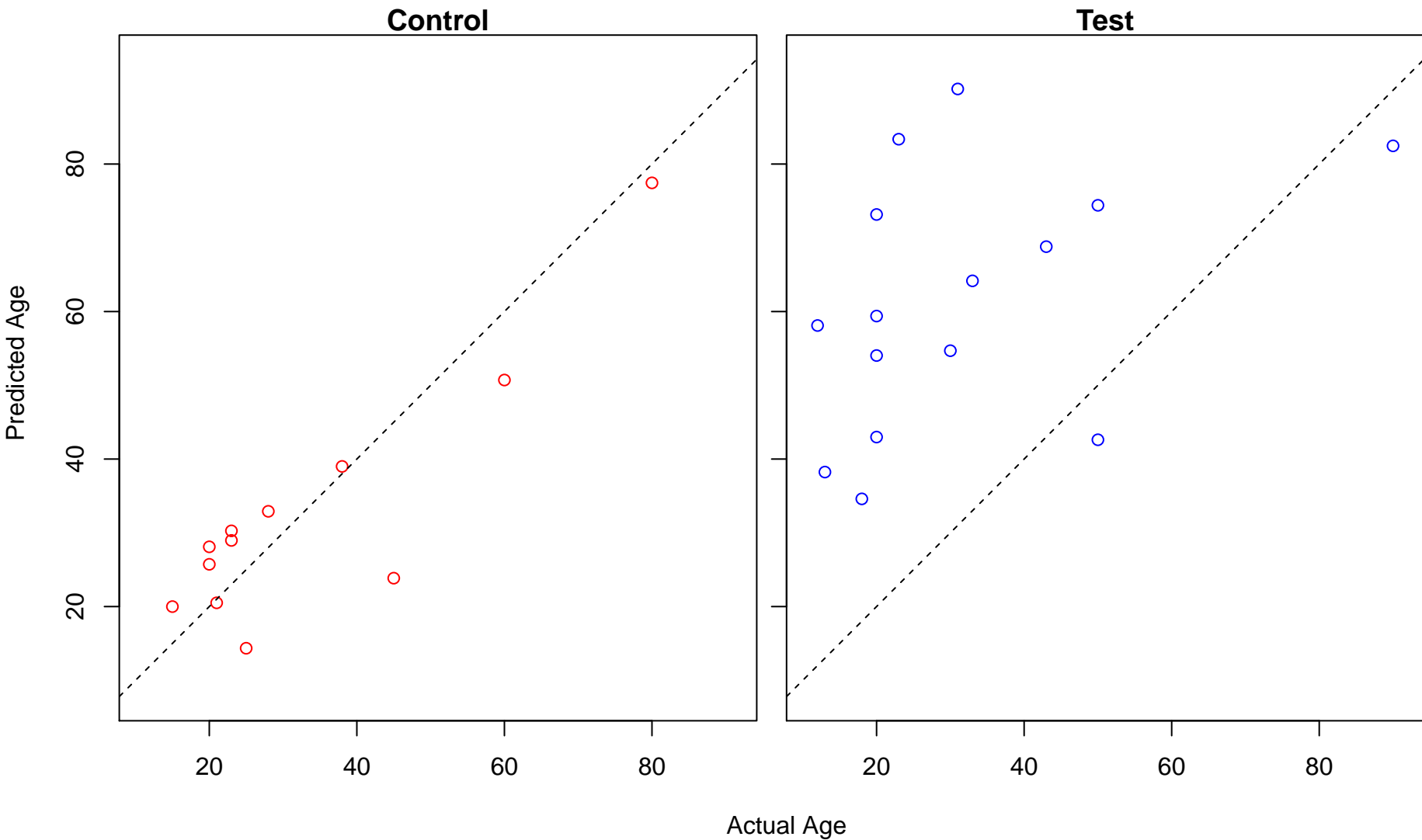
embryonic pattern specification (Score: 6.069219)



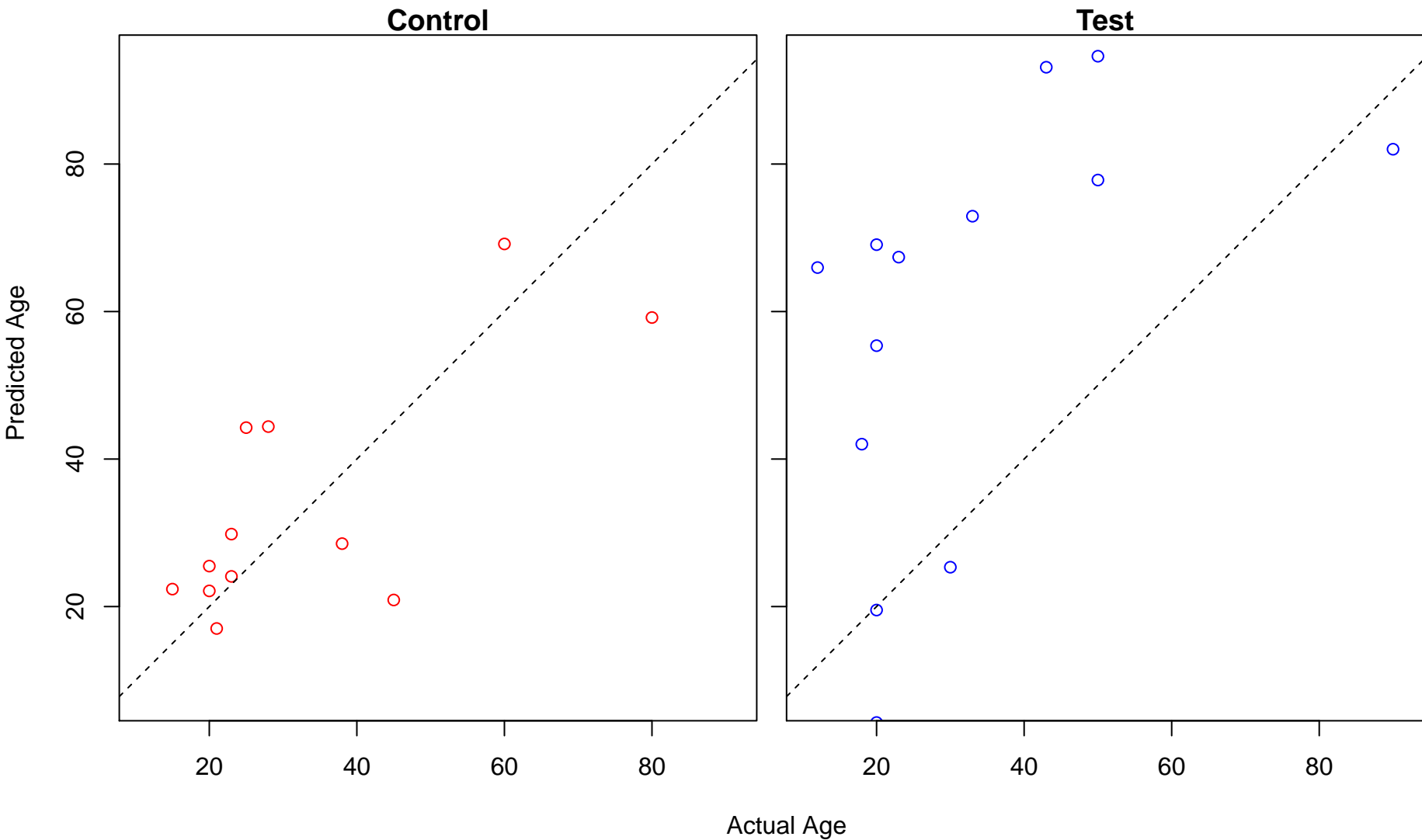
transcription elongation from RNA polymerase I promoter (Score: 6.068967)



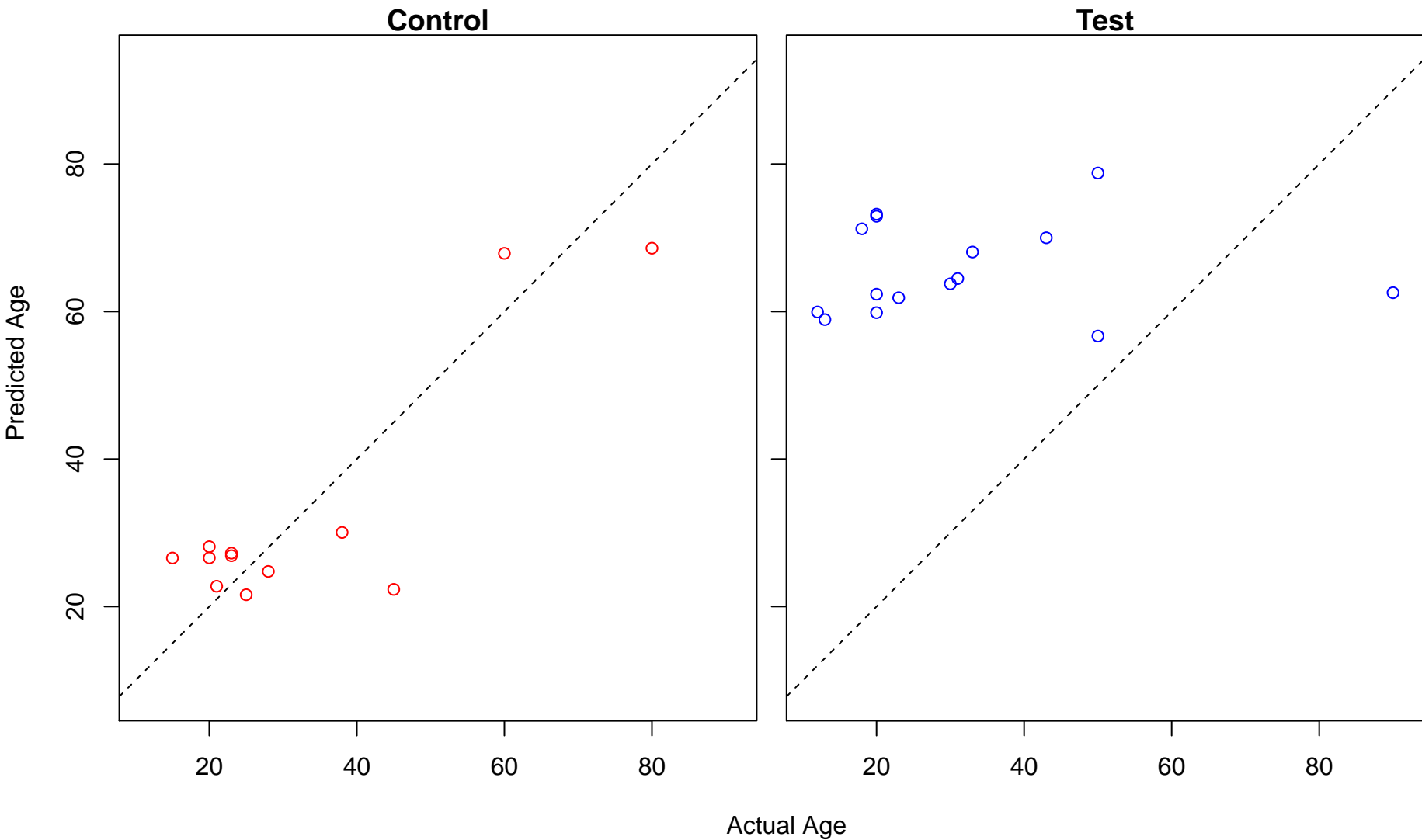
determination of heart left/right asymmetry (Score: 6.068060)



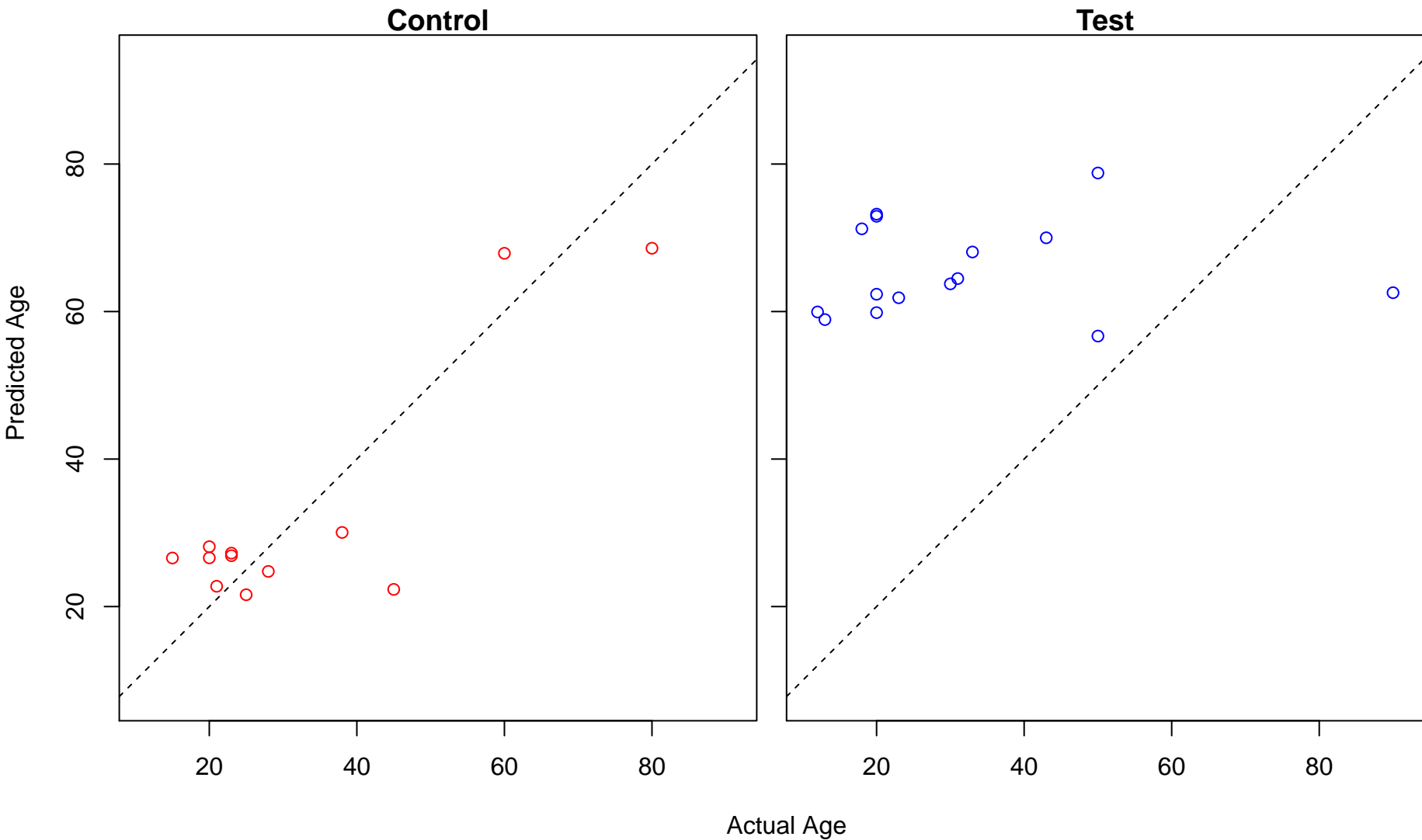
interleukin-1 beta secretion (Score: 6.067080)



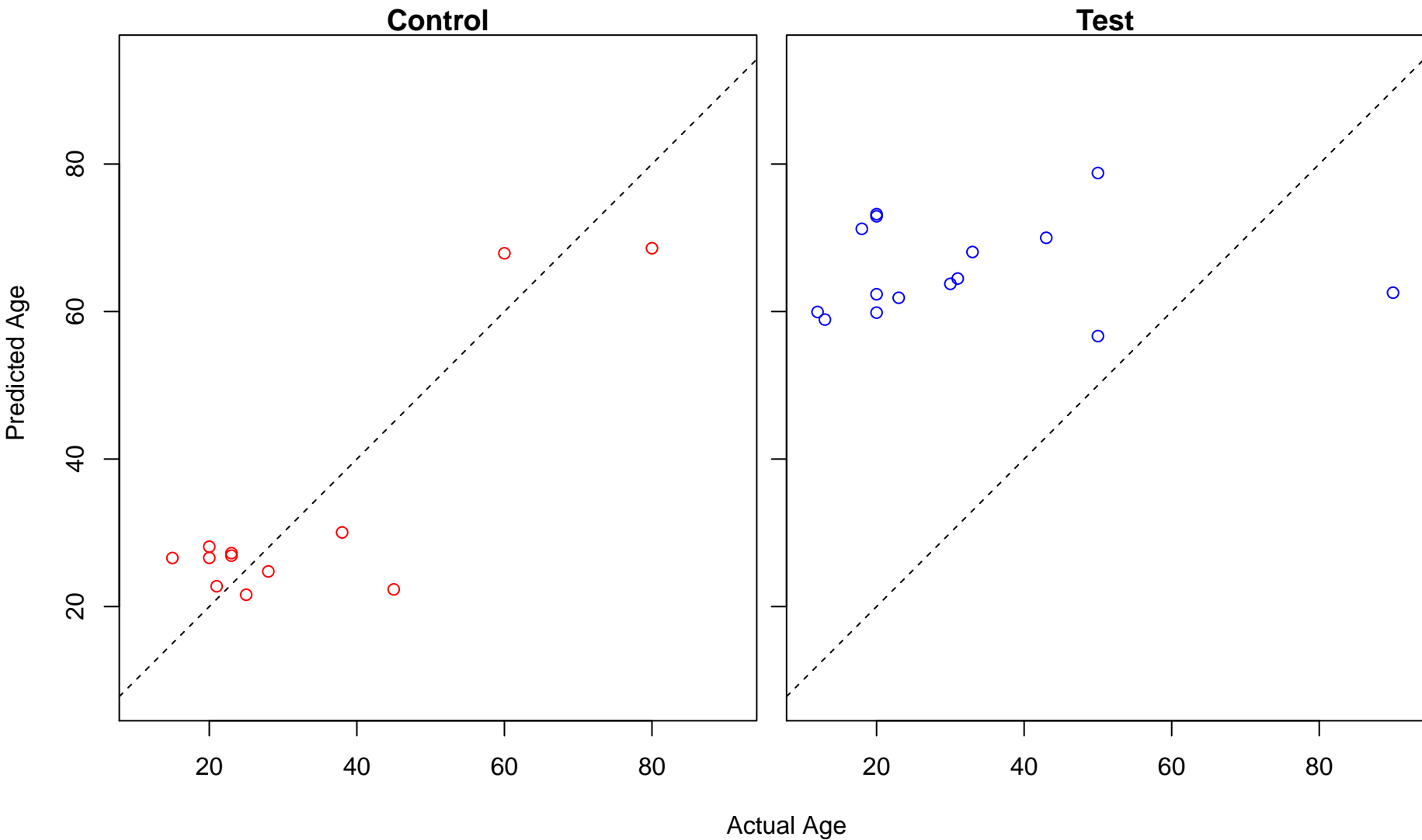
synaptic vesicle localization (Score: 6.065701)



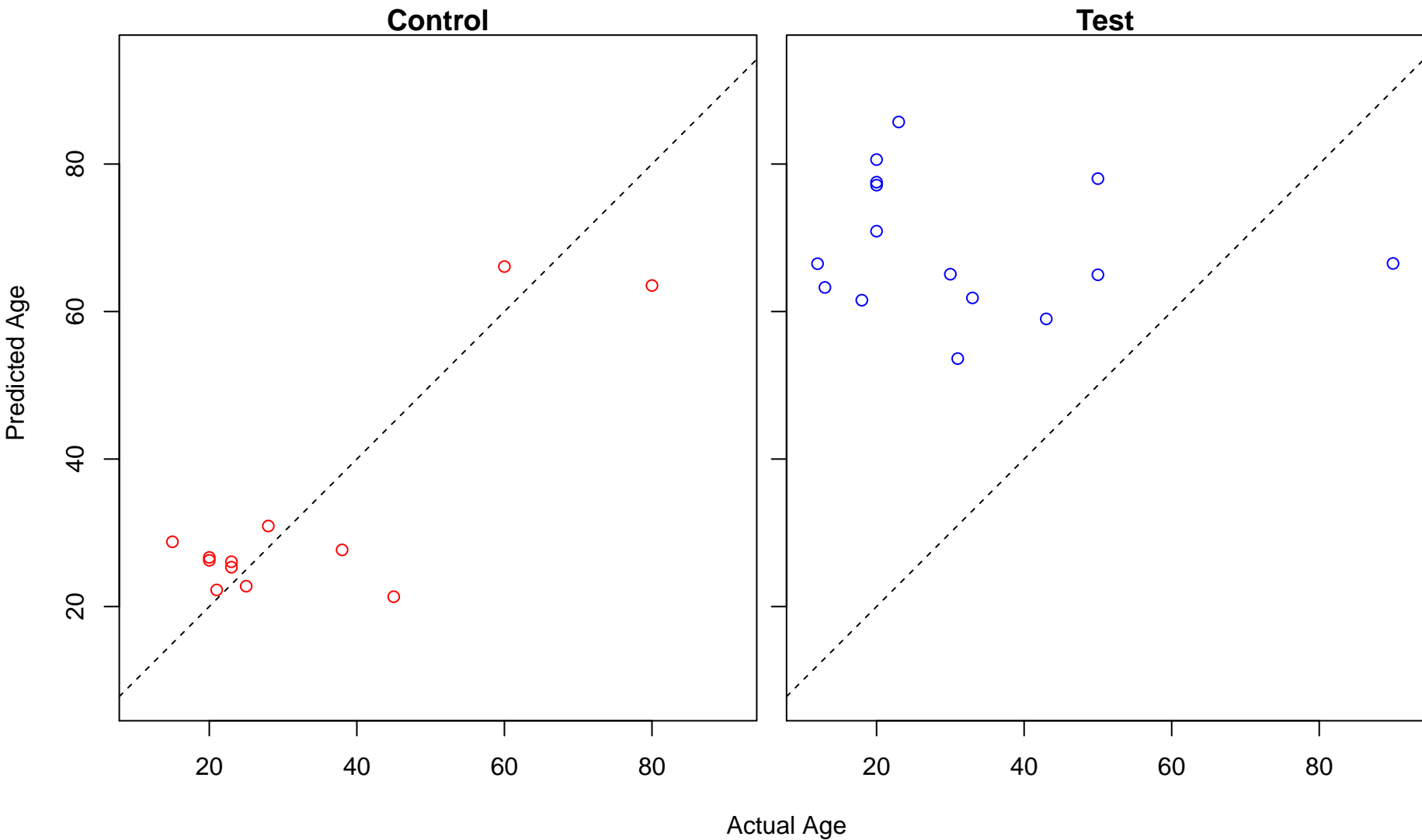
synaptic vesicle transport (Score: 6.065700)



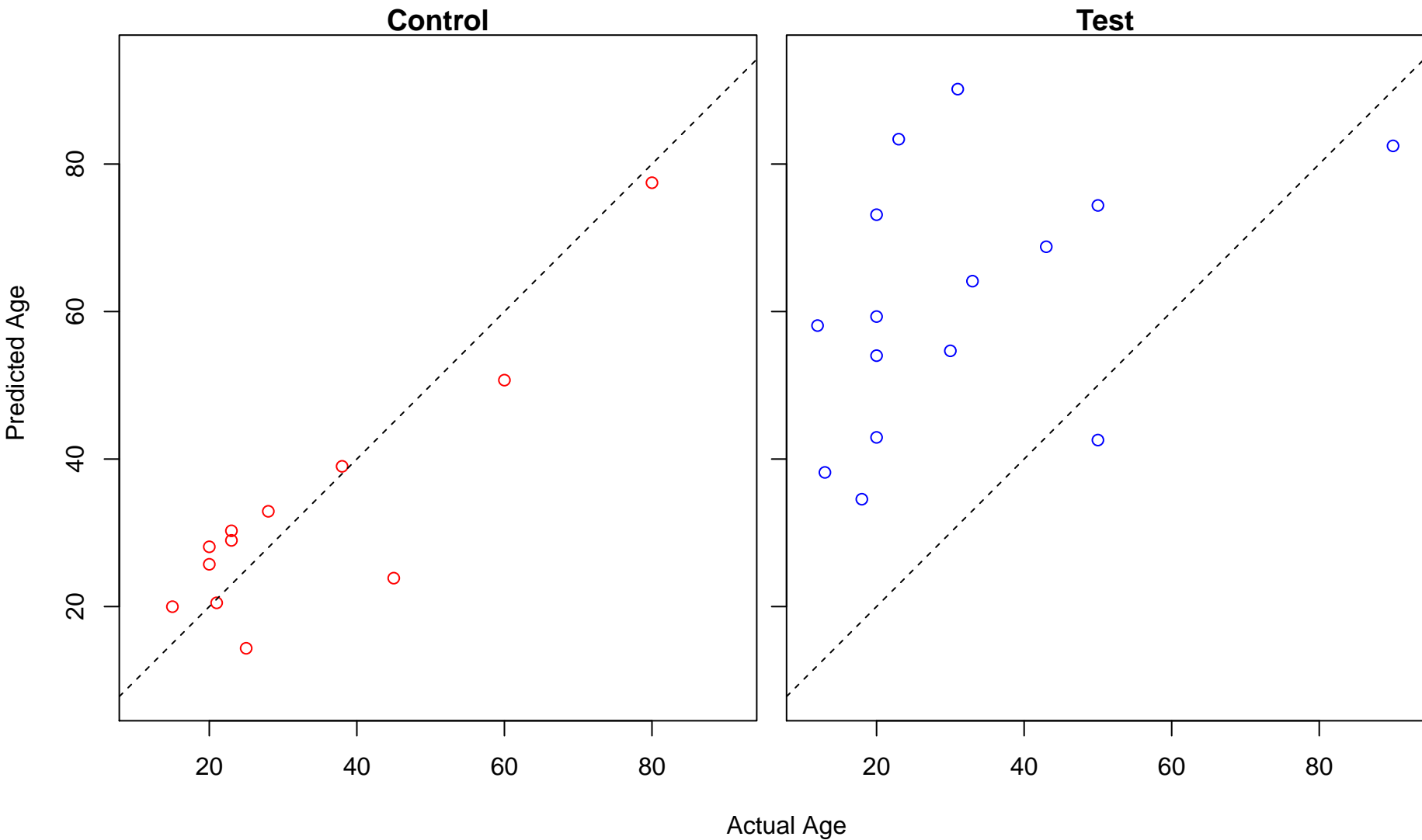
establishment of synaptic vesicle localization (Score: 6.065700)



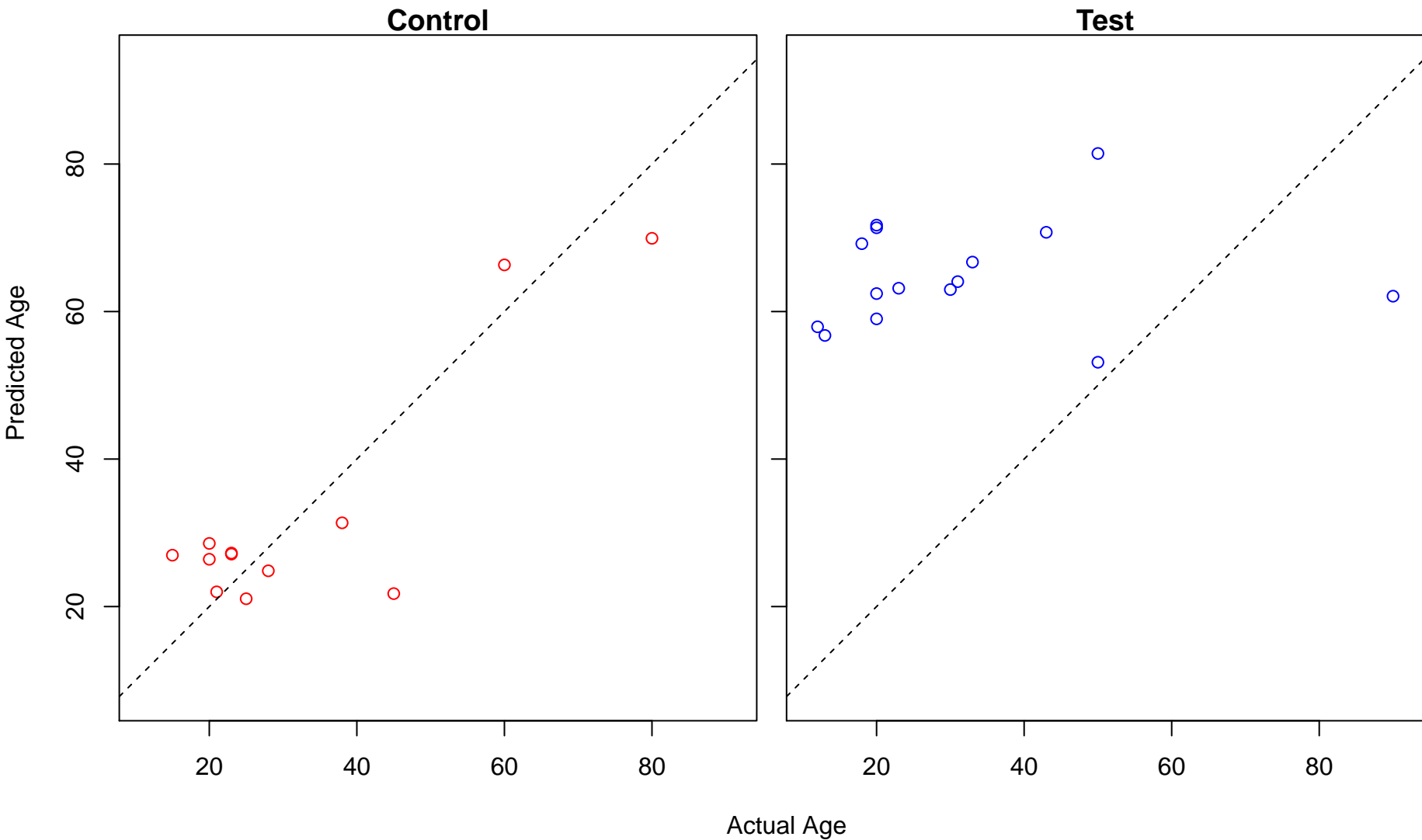
demethylation (Score: 6.061763)



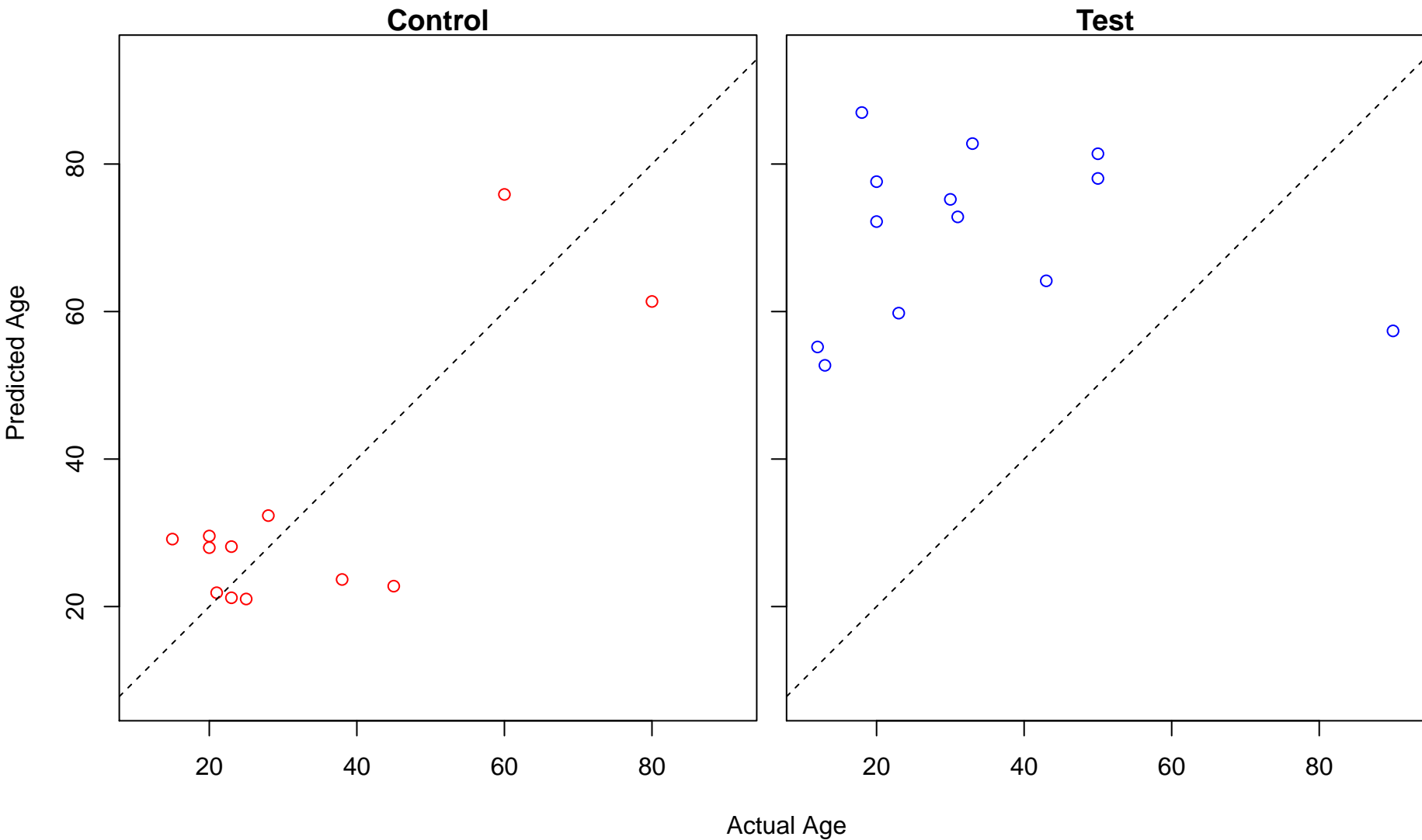
heart looping (Score: 6.059830)



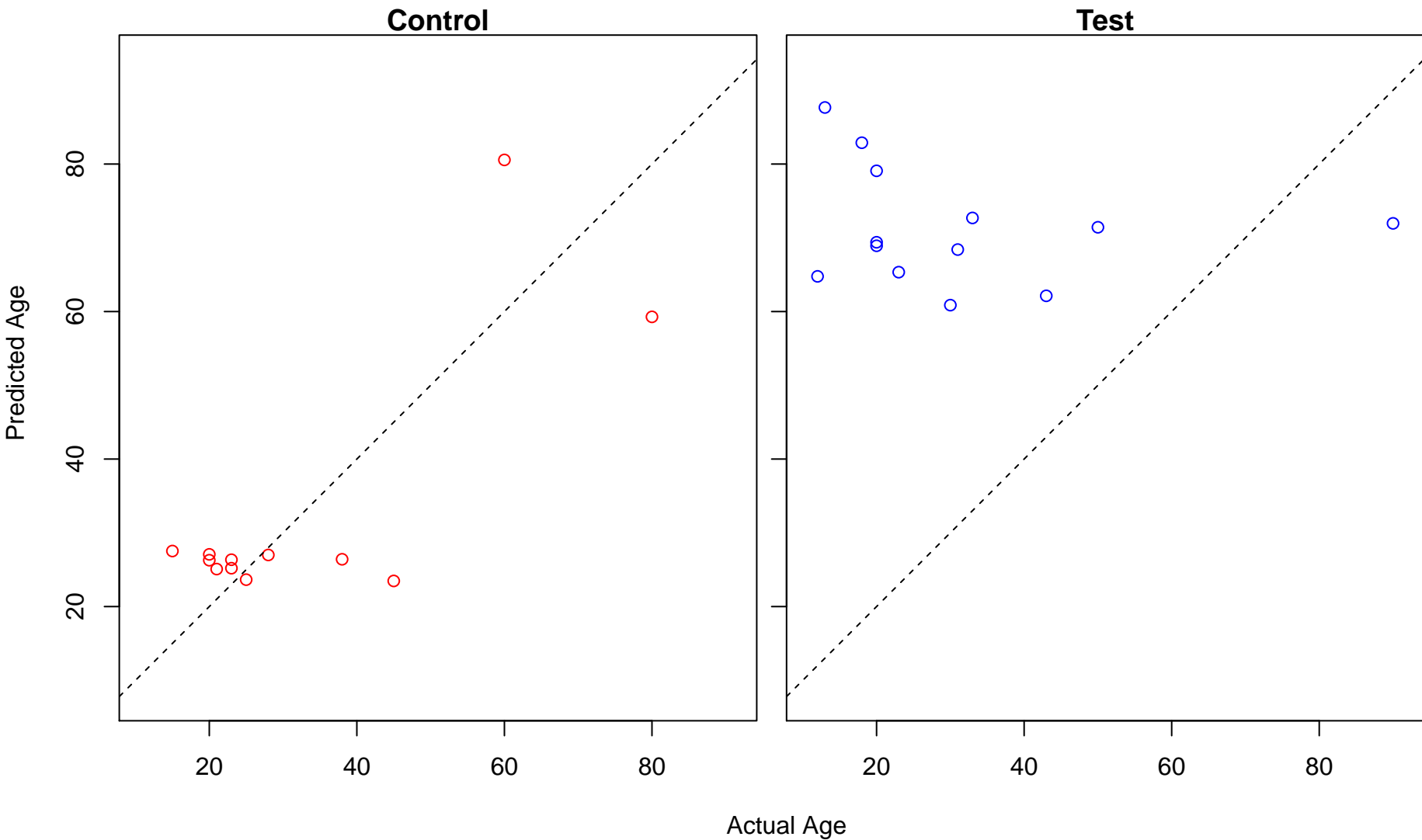
synaptic vesicle cycle (Score: 6.057993)



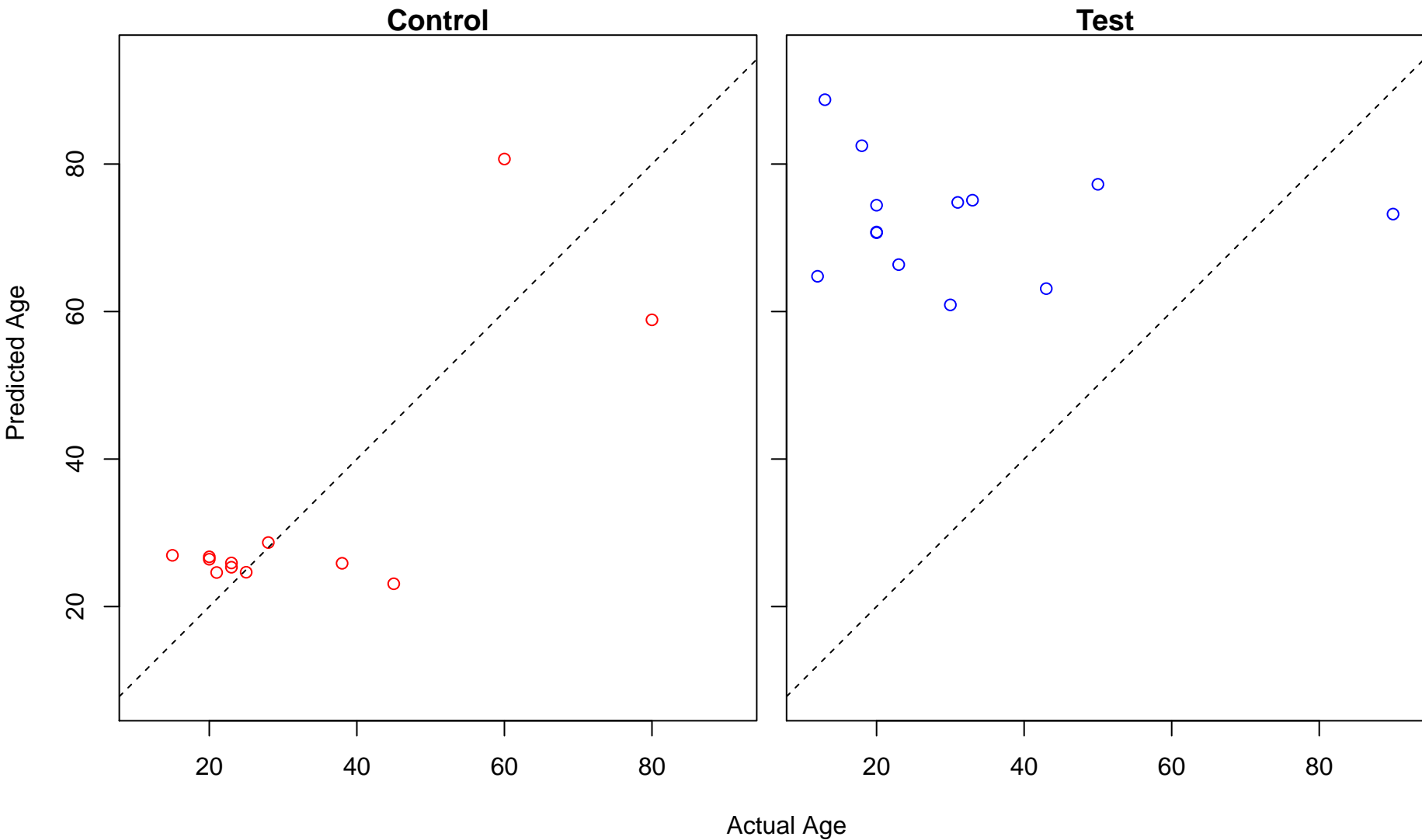
regulation of trophoblast cell migration (Score: 6.055995)



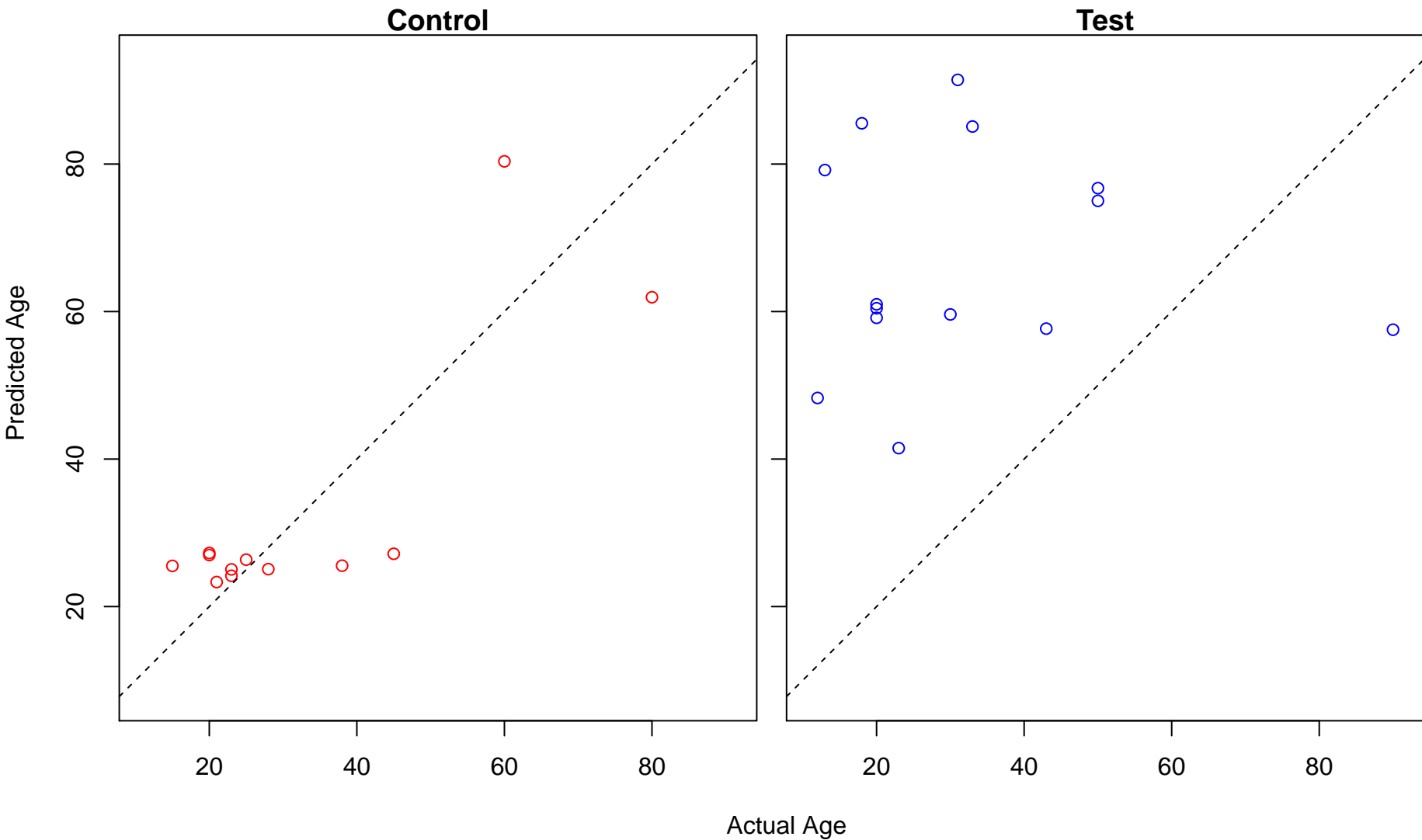
MyD88-dependent toll-like receptor signaling pathway (Score: 6.054575)



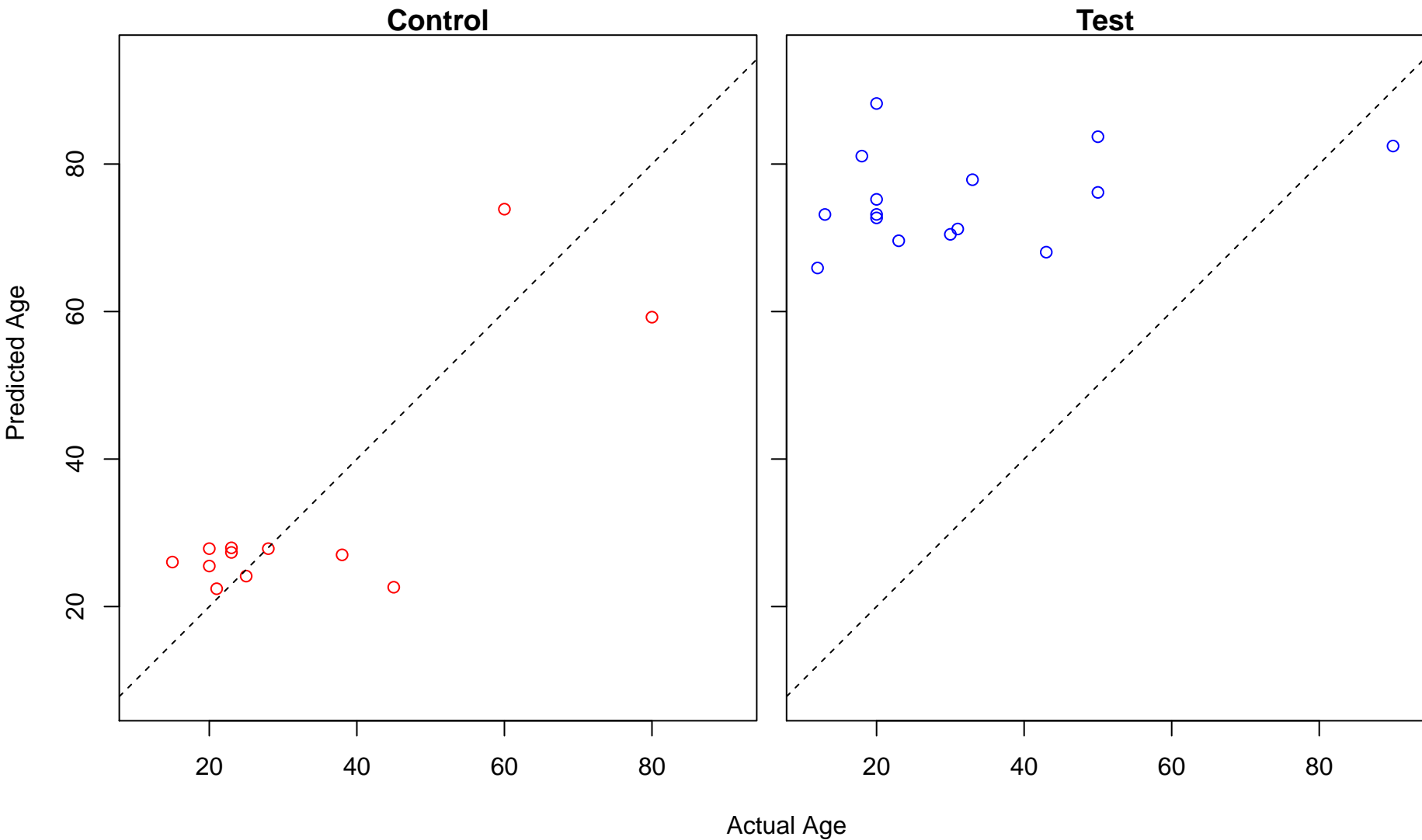
negative regulation of Wnt signaling pathway (Score: 6.054529)



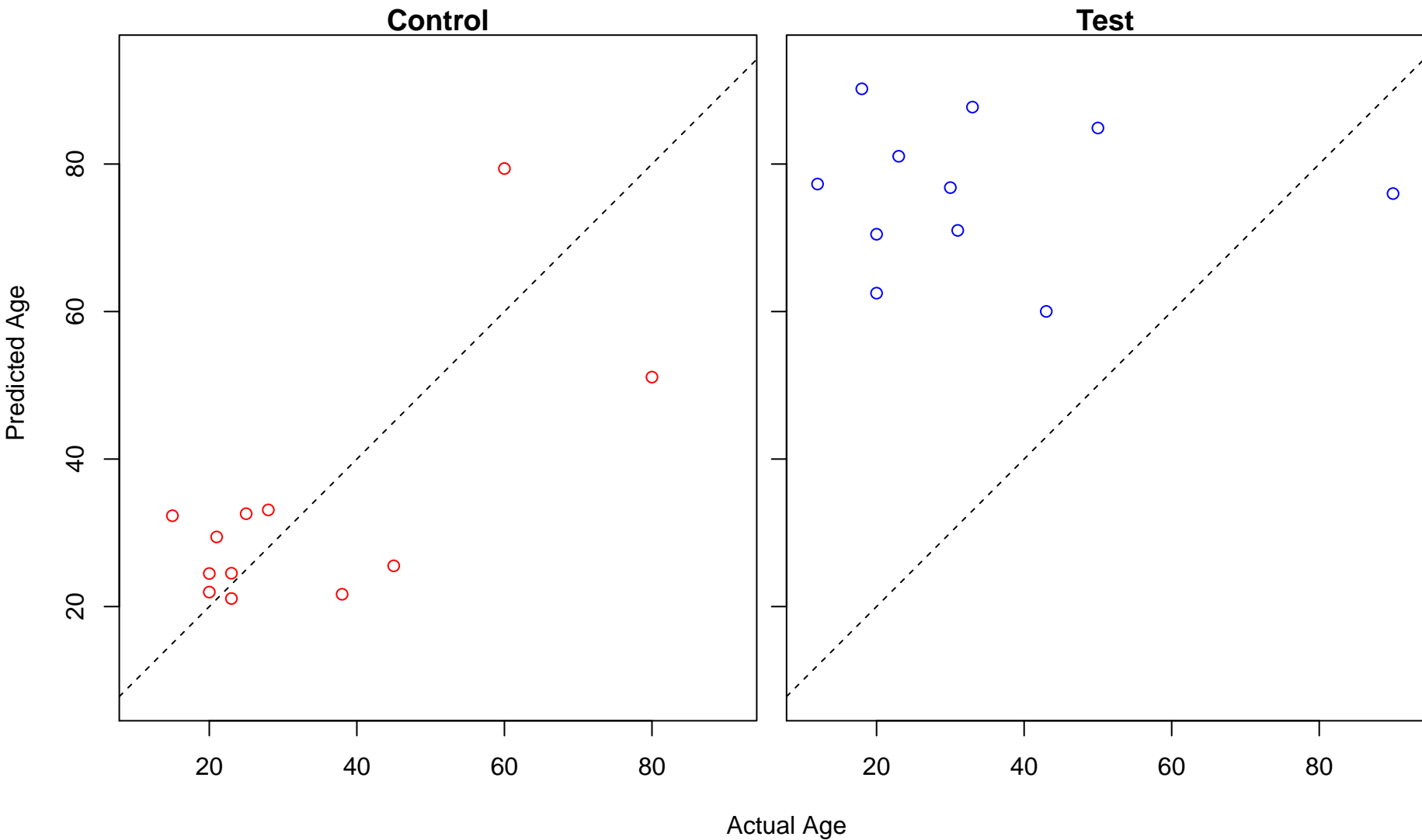
positive regulation of epidermal growth factor receptor signaling pathway (Score: 6.054159)



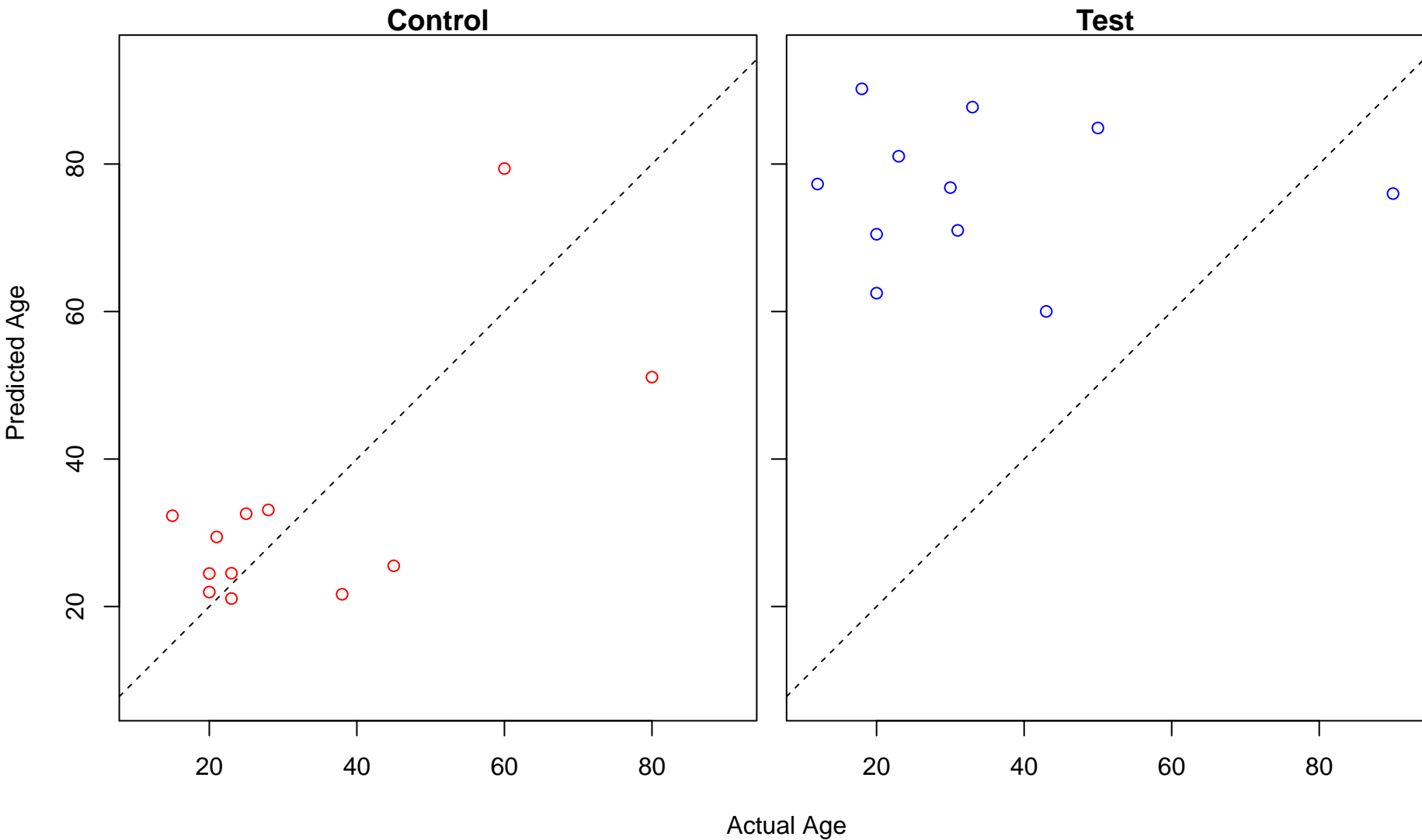
regulation of phosphatidylinositol 3-kinase signaling (Score: 6.051296)



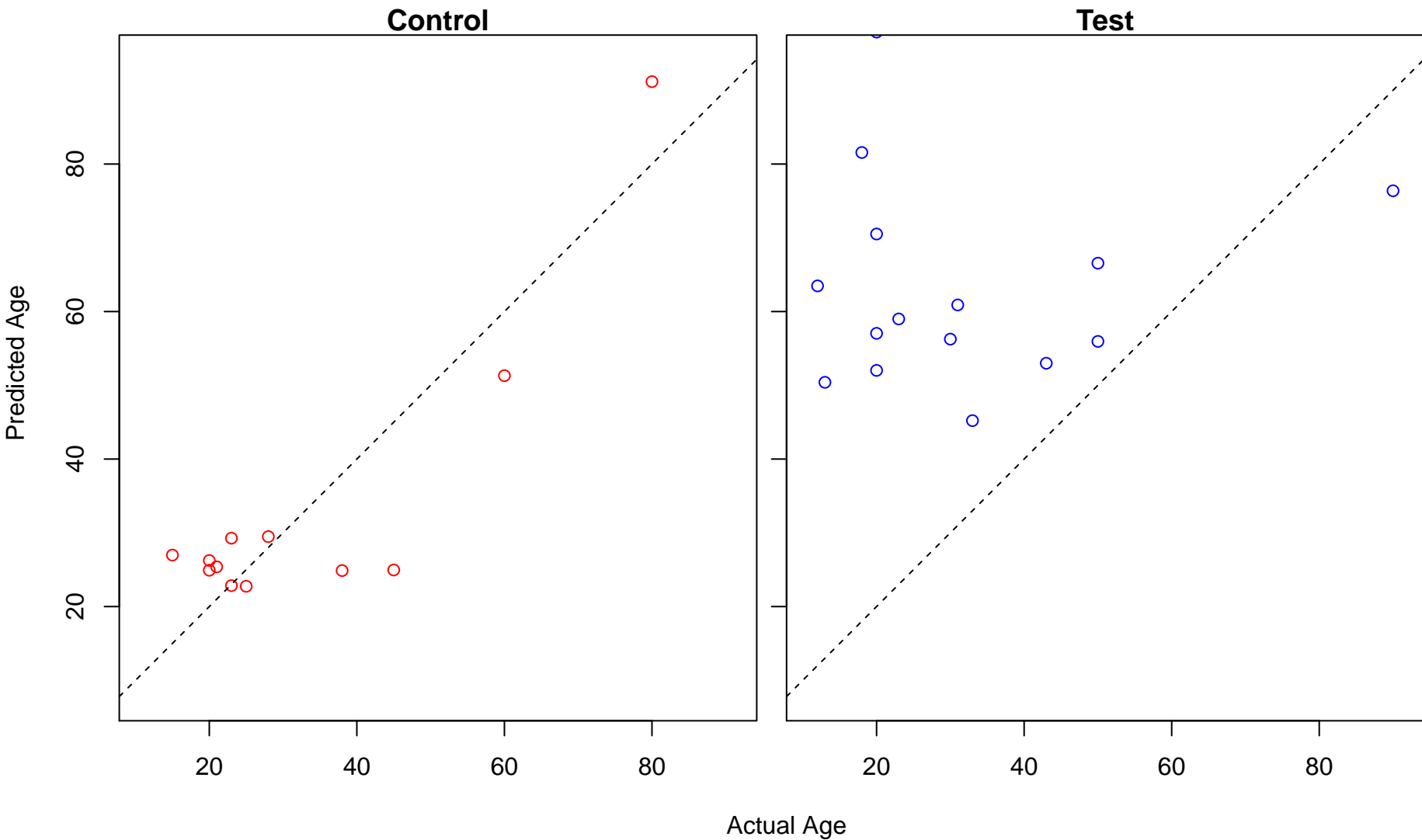
regulation of phospholipid transport (Score: 6.050106)



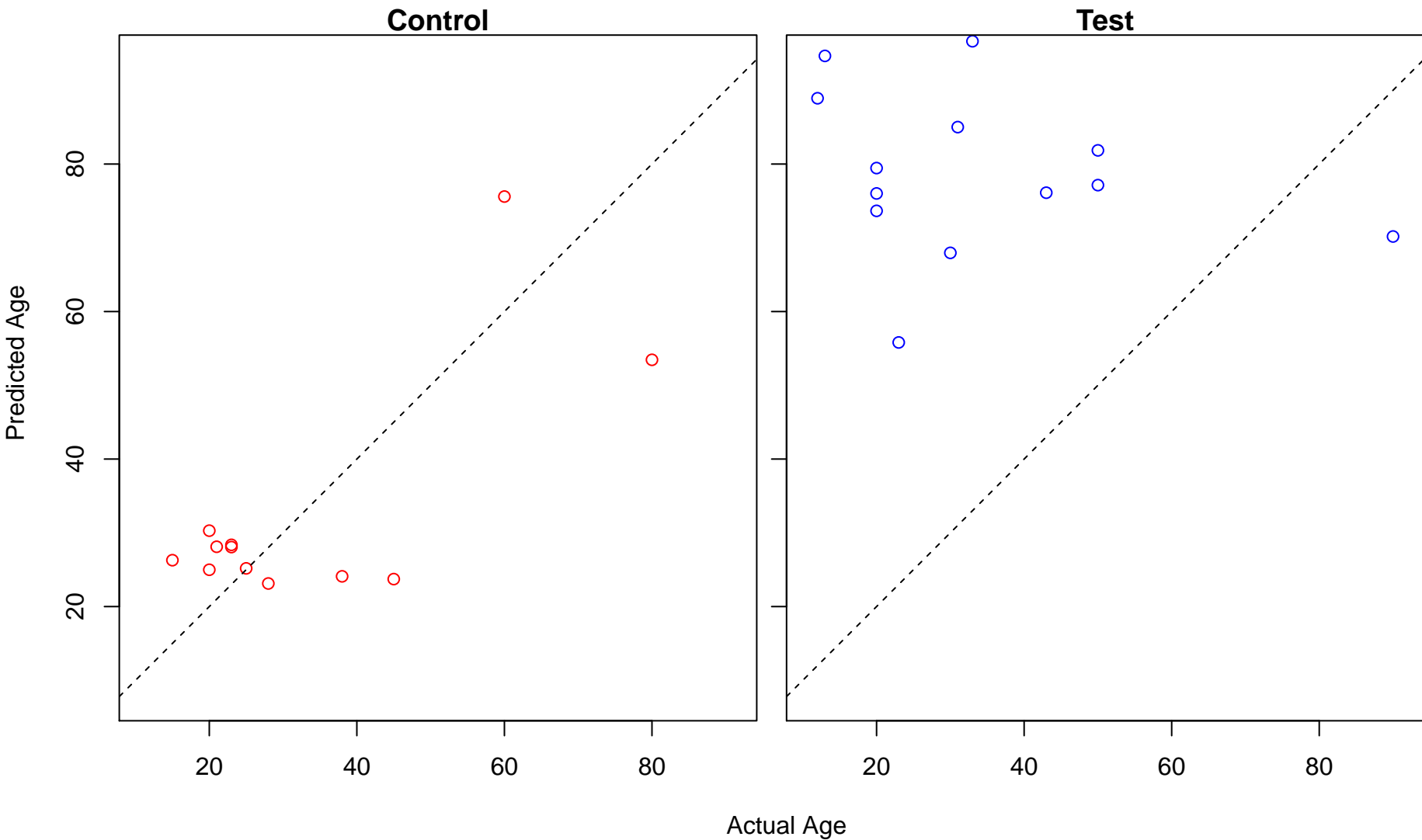
positive regulation of phospholipid transport (Score: 6.050106)



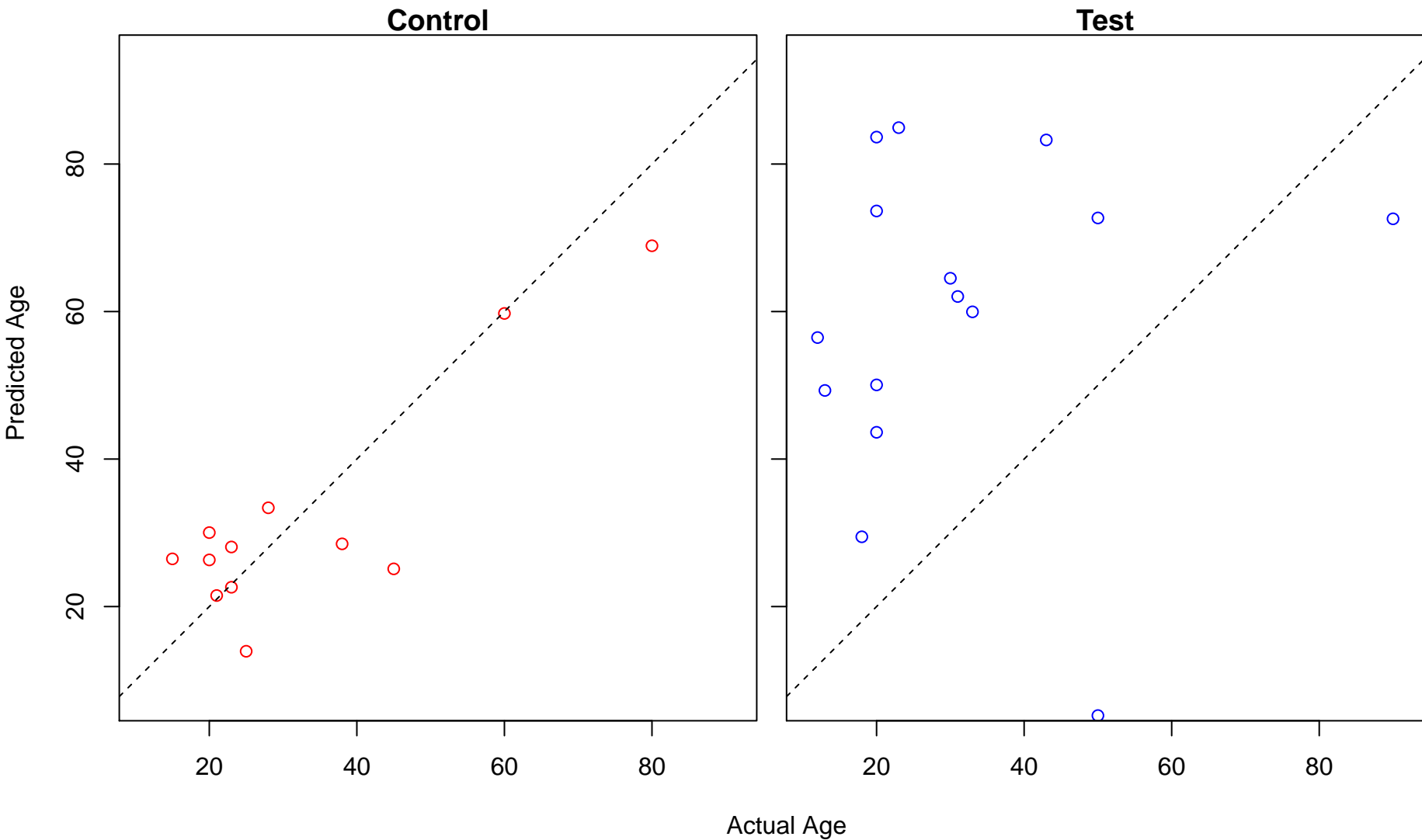
Negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 1)



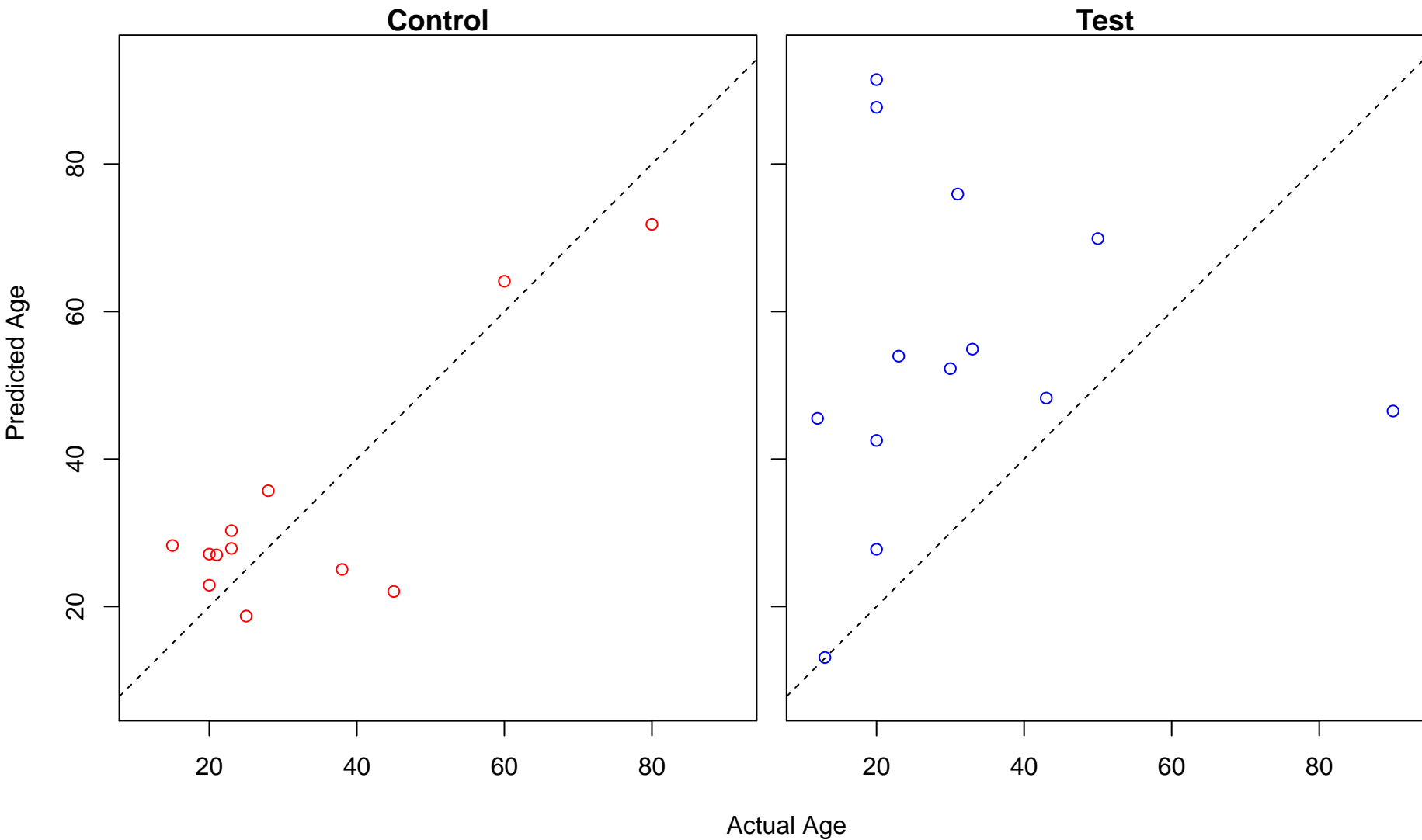
tryptophan metabolic process (Score: 6.048605)



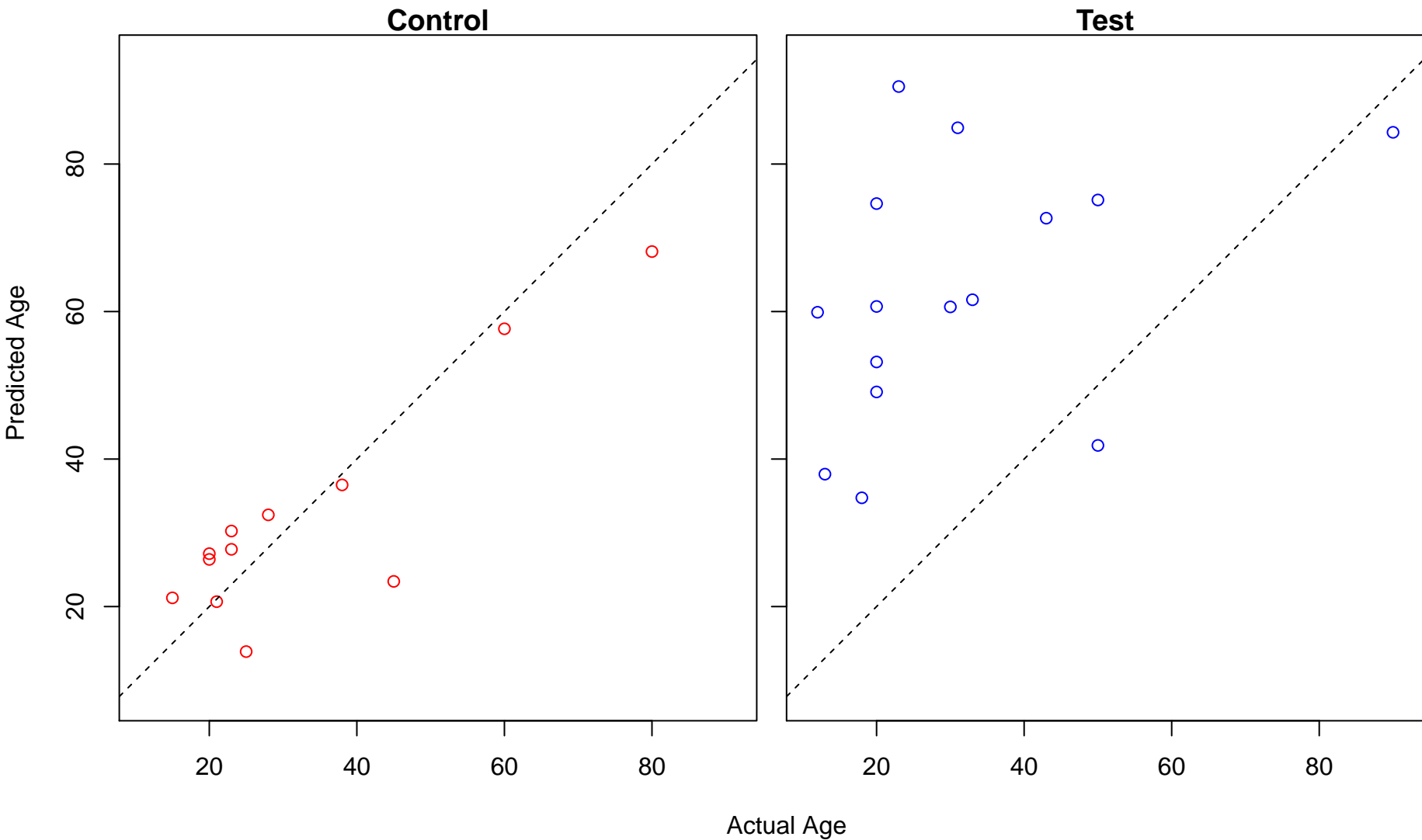
spinal cord development (Score: 6.046430)



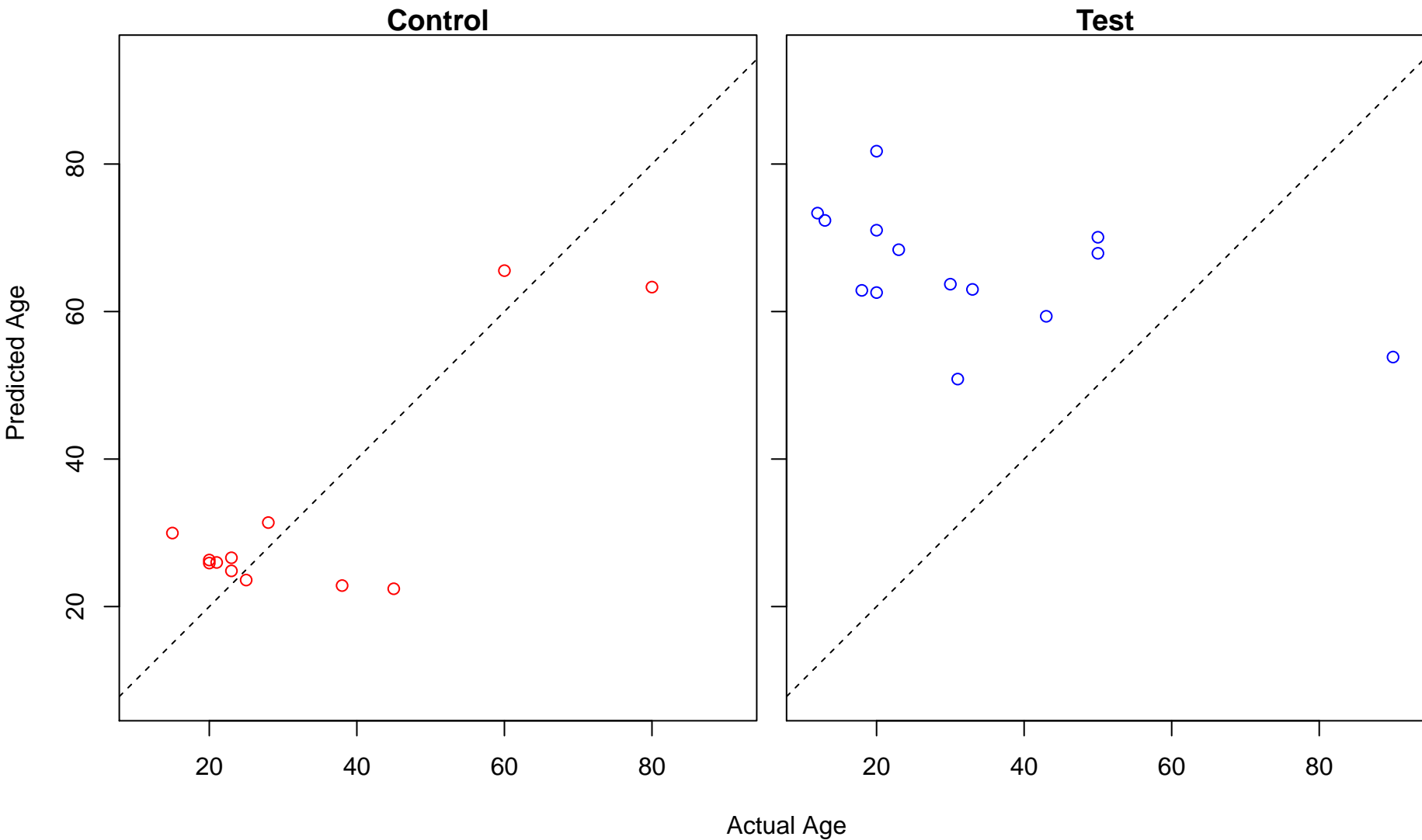
cell-cell adhesion (Score: 6.042590)



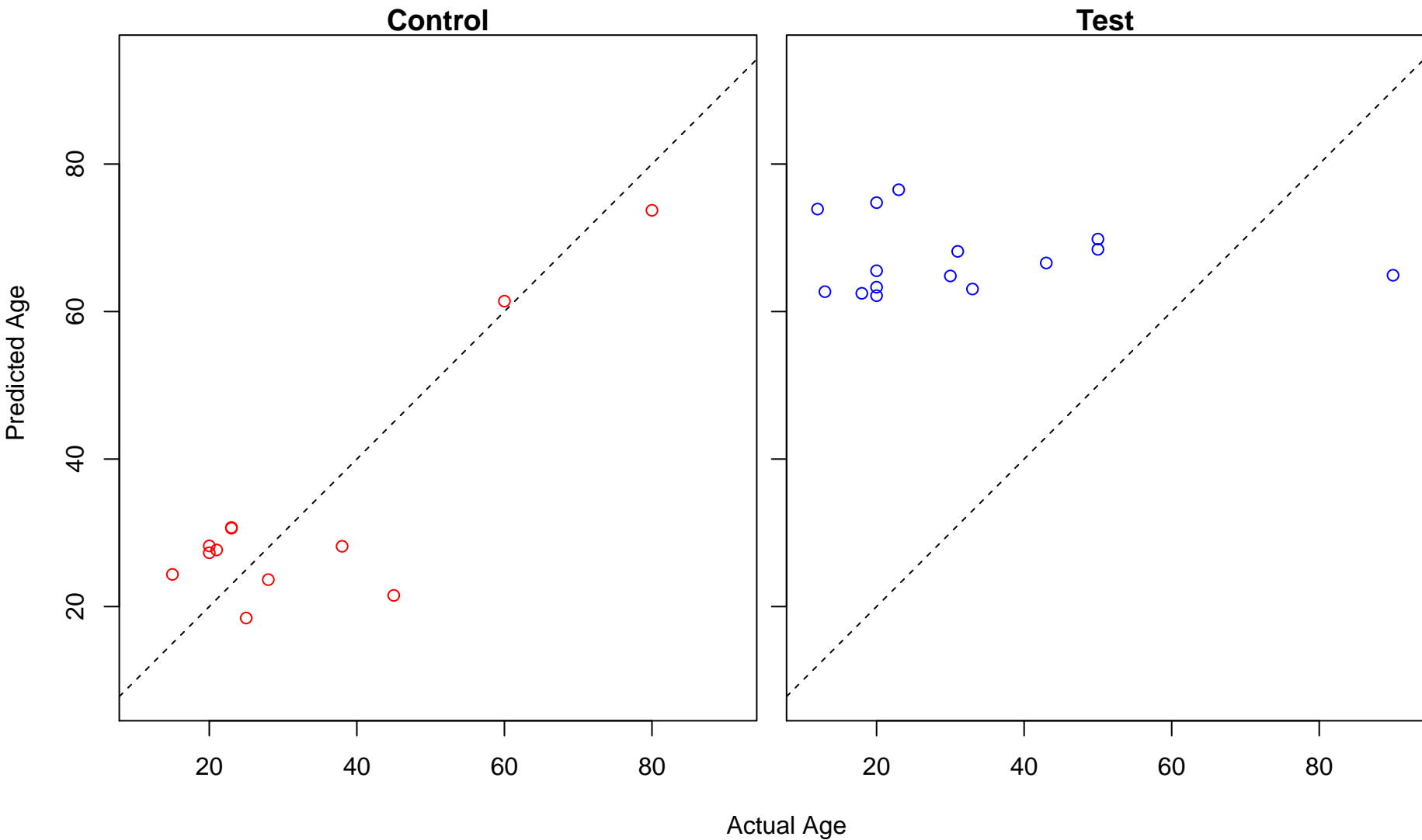
inner dynein arm assembly (Score: 6.042298)



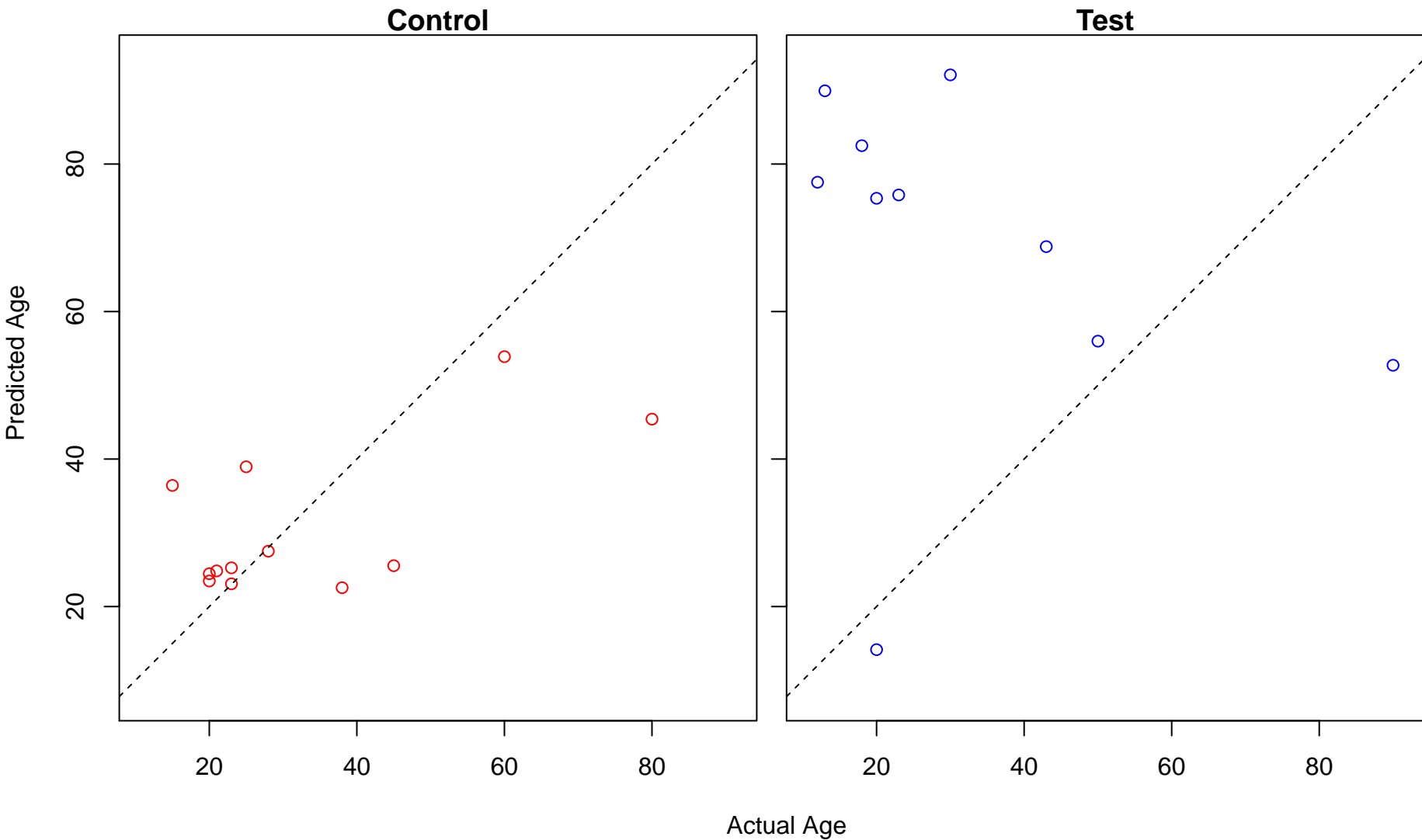
sensory perception of sound (Score: 6.036972)



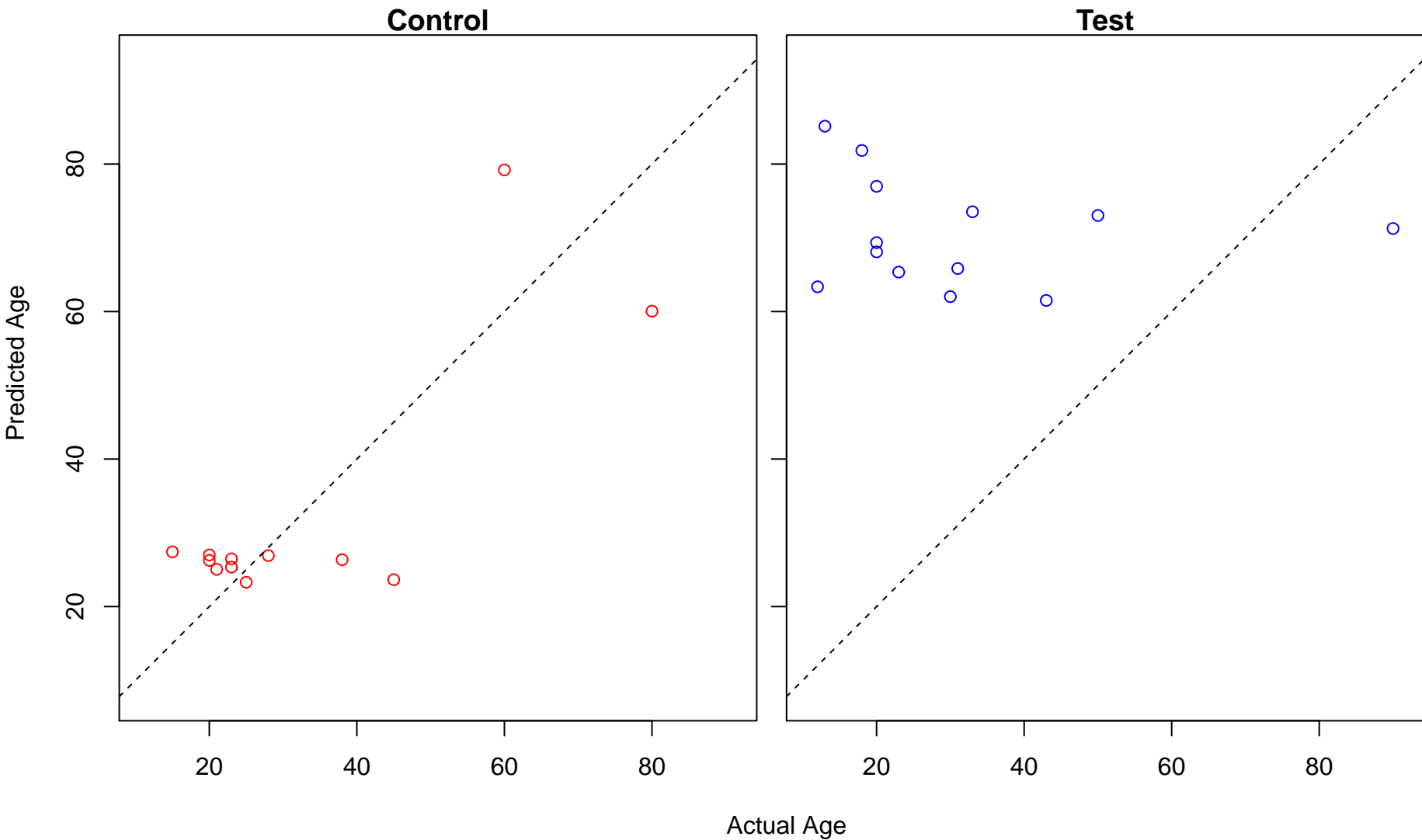
negative regulation of neural precursor cell proliferation (Score: 6.035453)



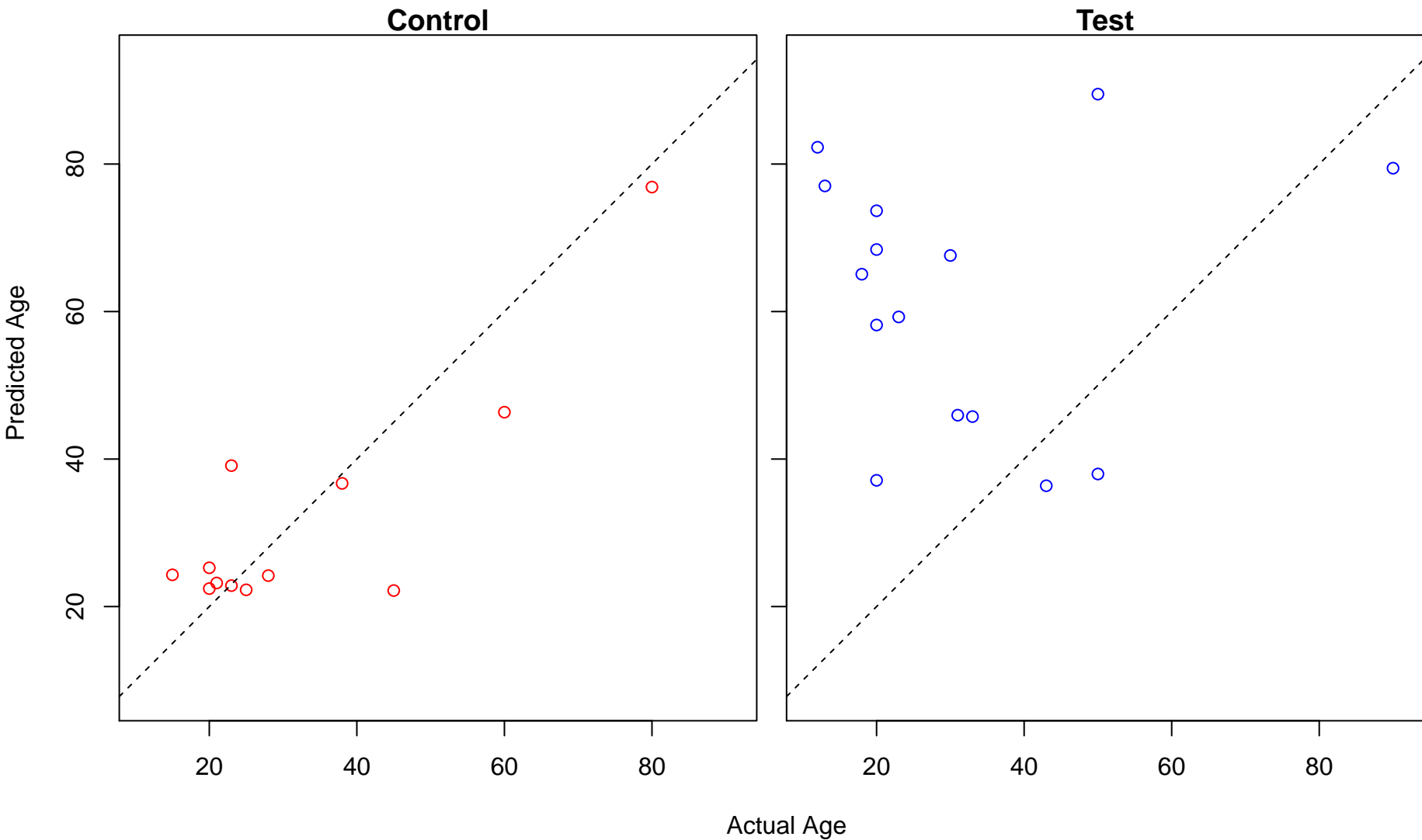
T cell migration (Score: 6.032772)



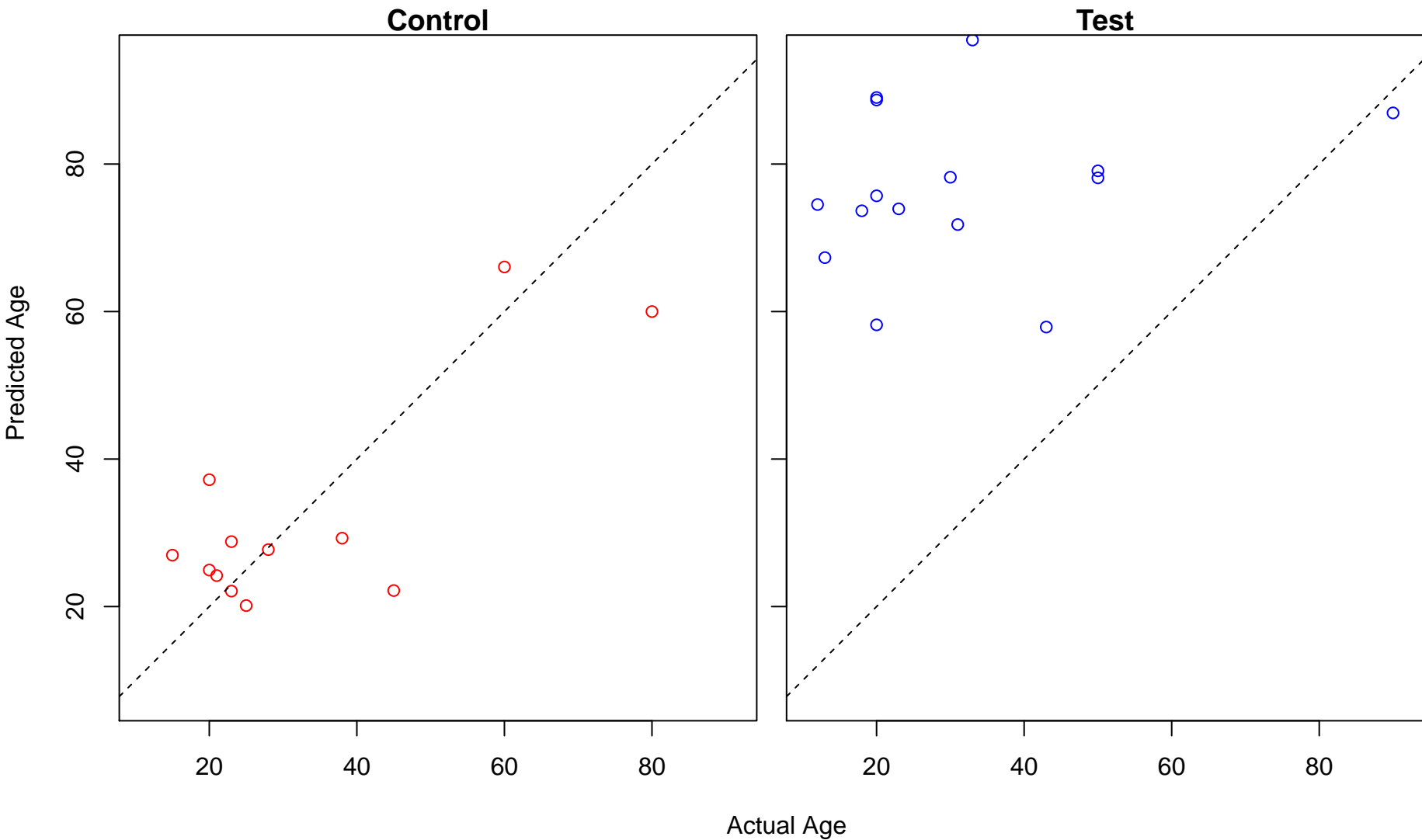
endosomal transport (Score: 6.031201)



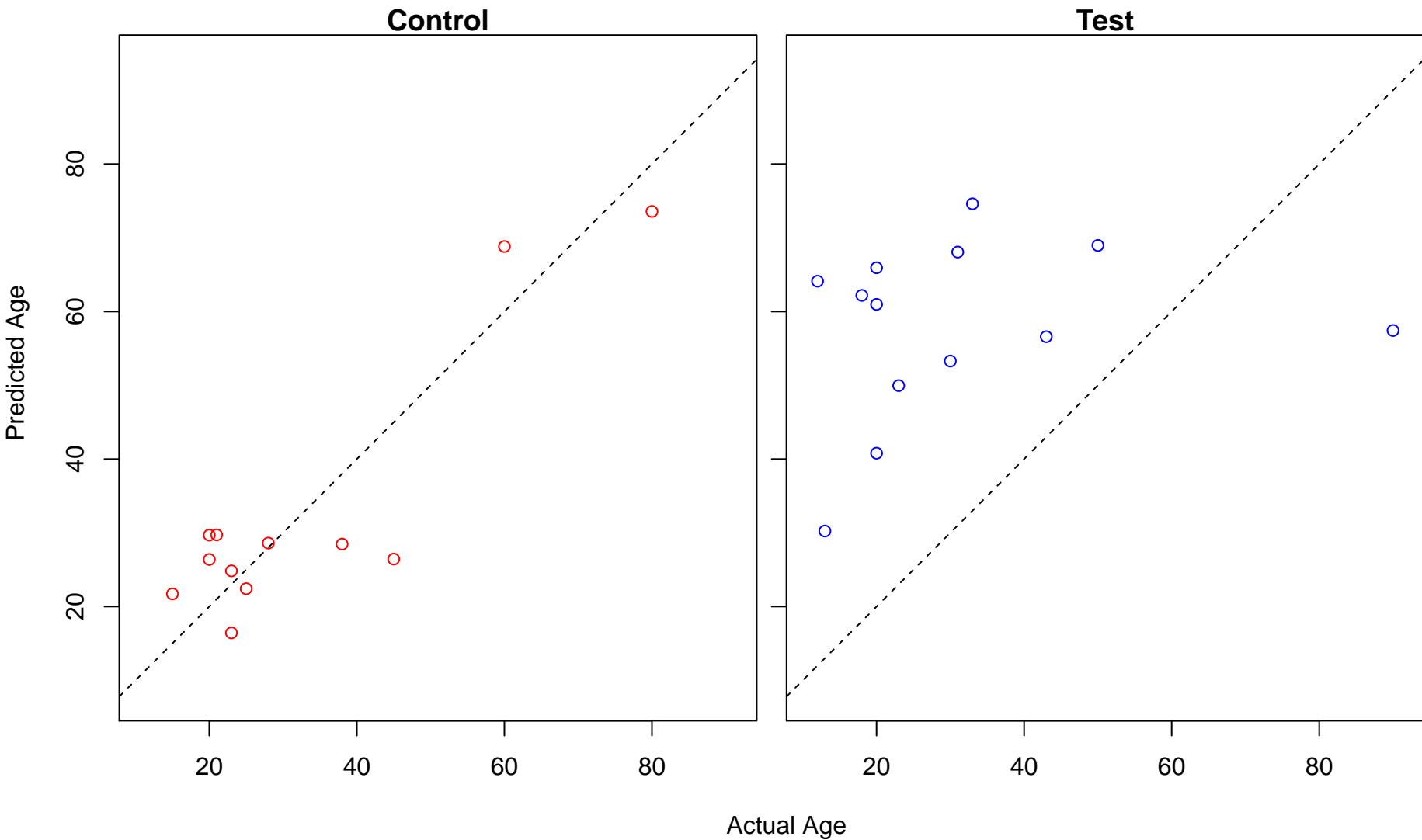
cellular response to heparin (Score: 6.030573)



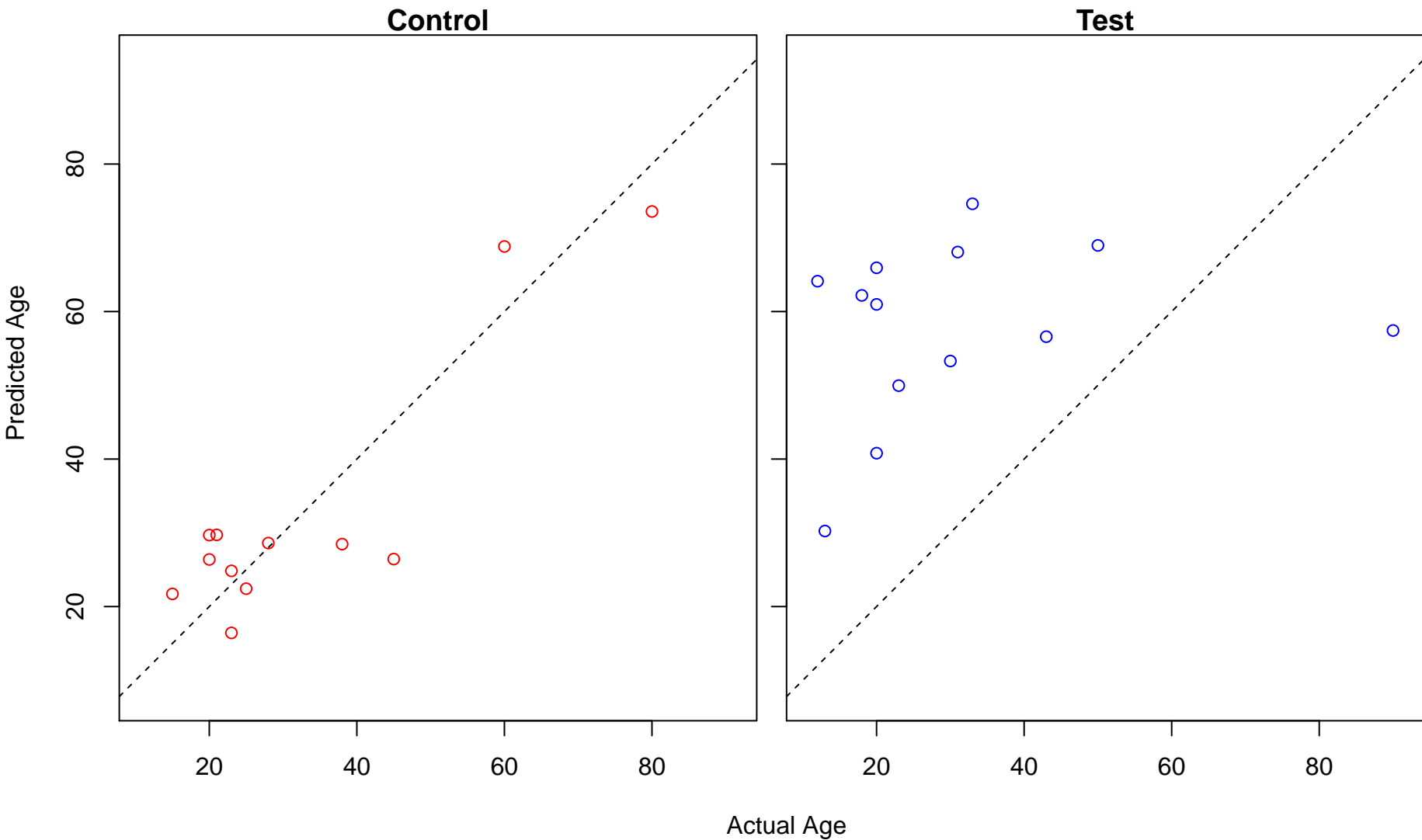
negative regulation of organic acid transport (Score: 6.029480)



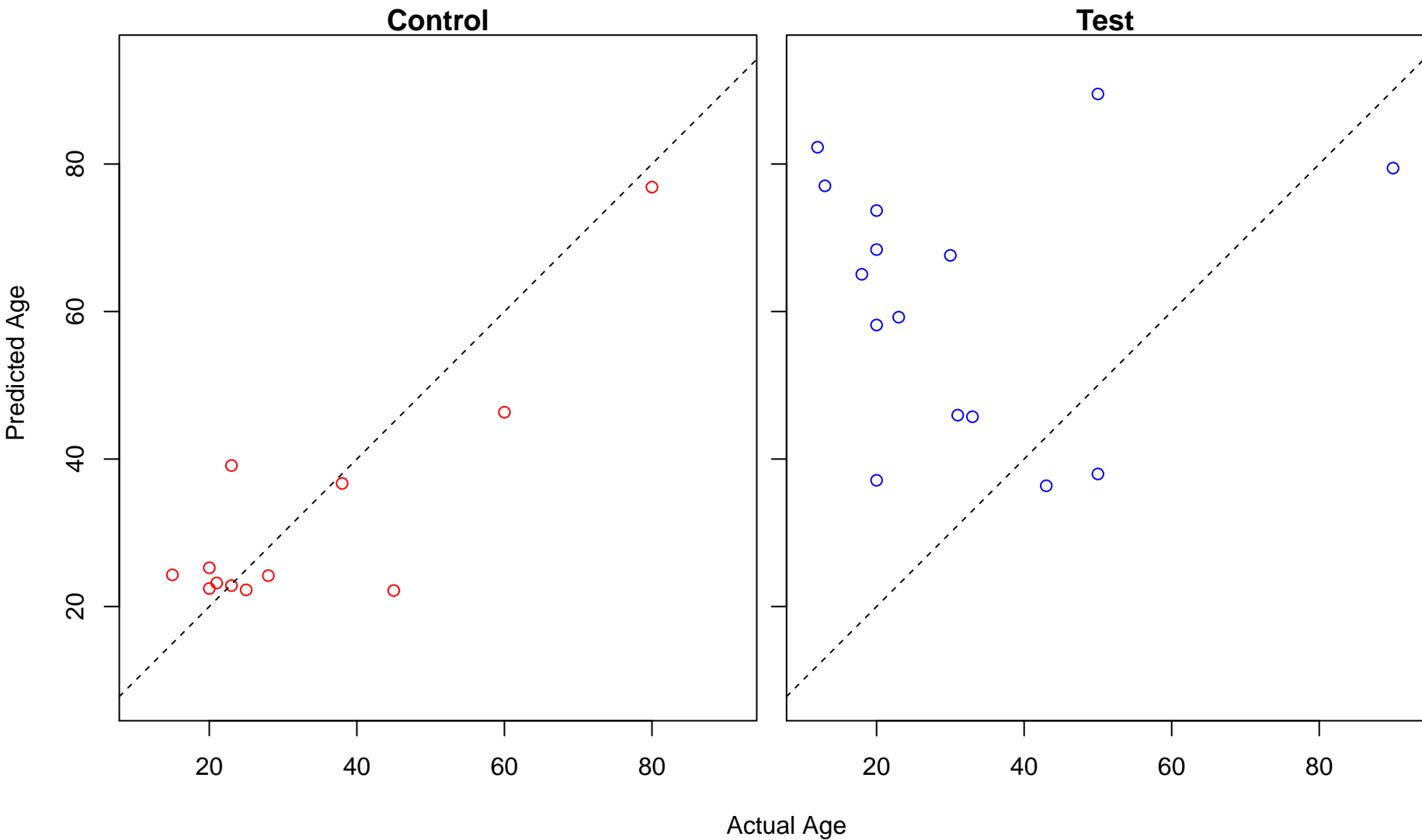
contractile actin filament bundle assembly (Score: 6.029397)



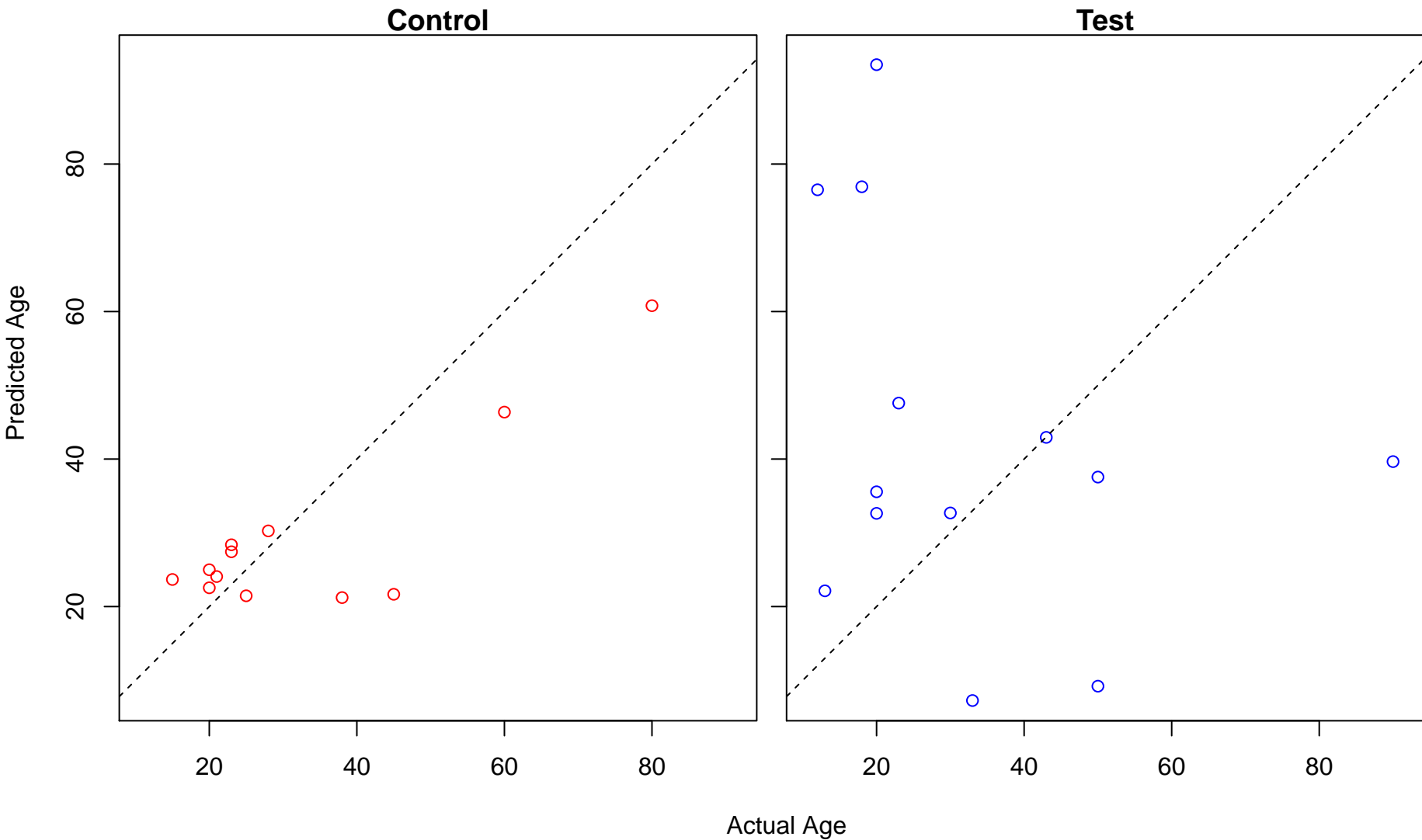
stress fiber assembly (Score: 6.029397)



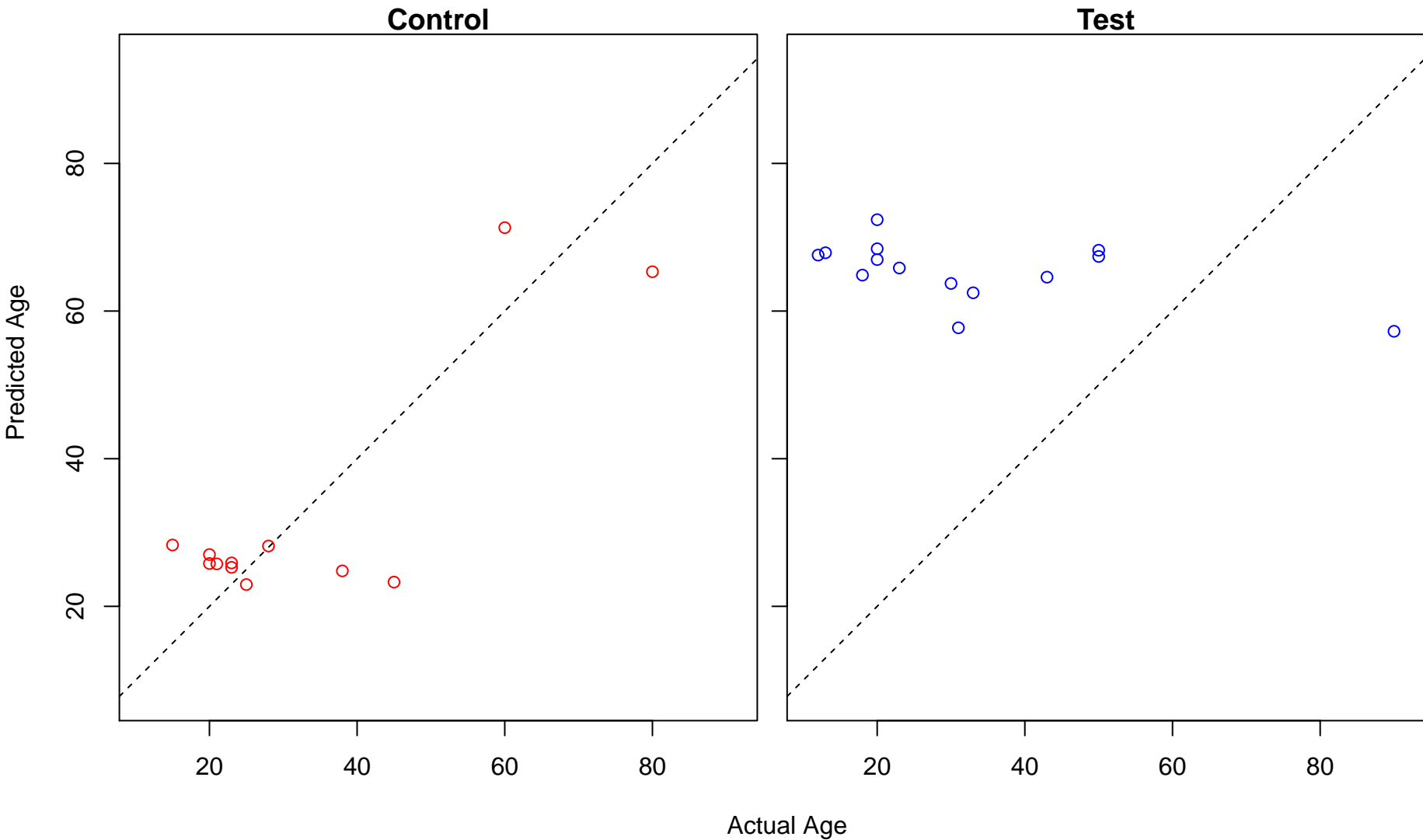
response to heparin (Score: 6.027242)



behavioral response to nicotine (Score: 6.026646)

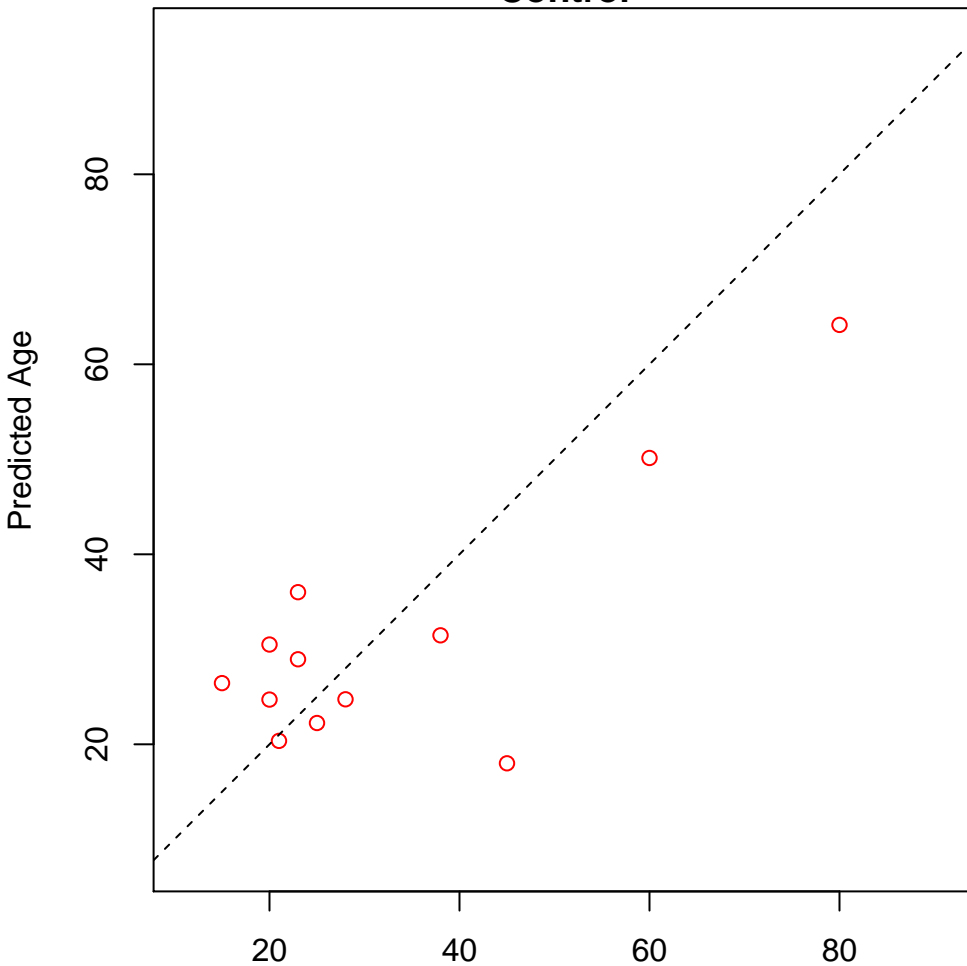


positive regulation of oxidative stress-induced cell death (Score: 6.022621)

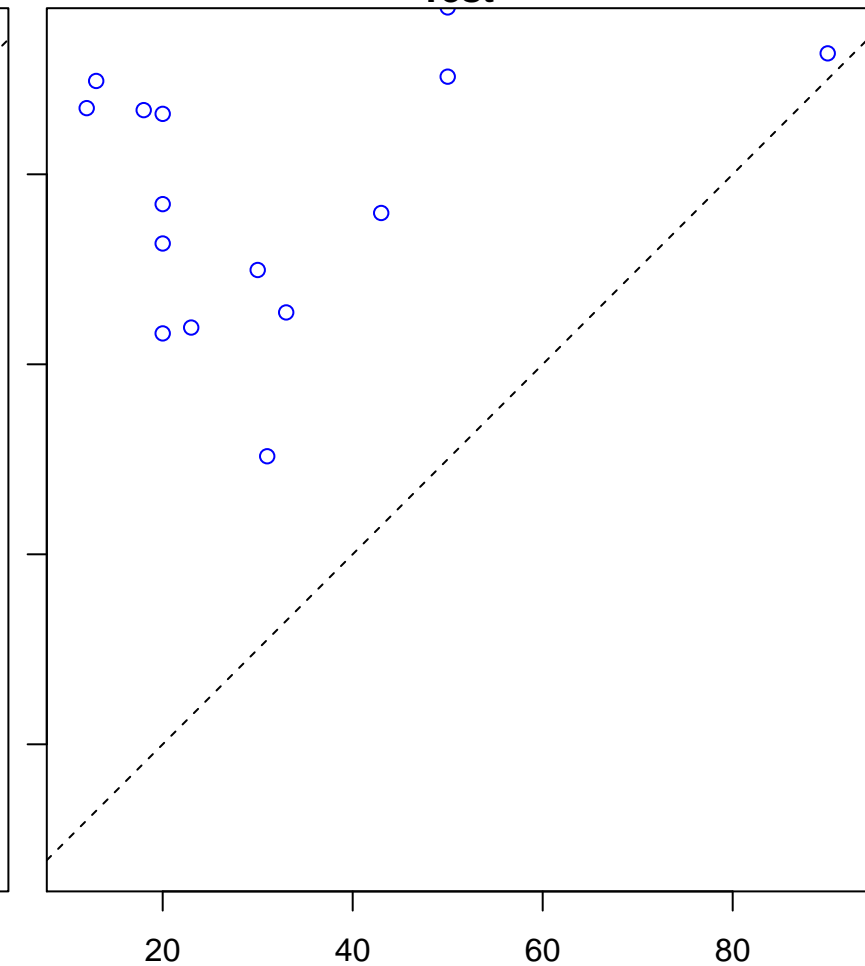


outflow tract septum morphogenesis (Score: 6.021768)

Control

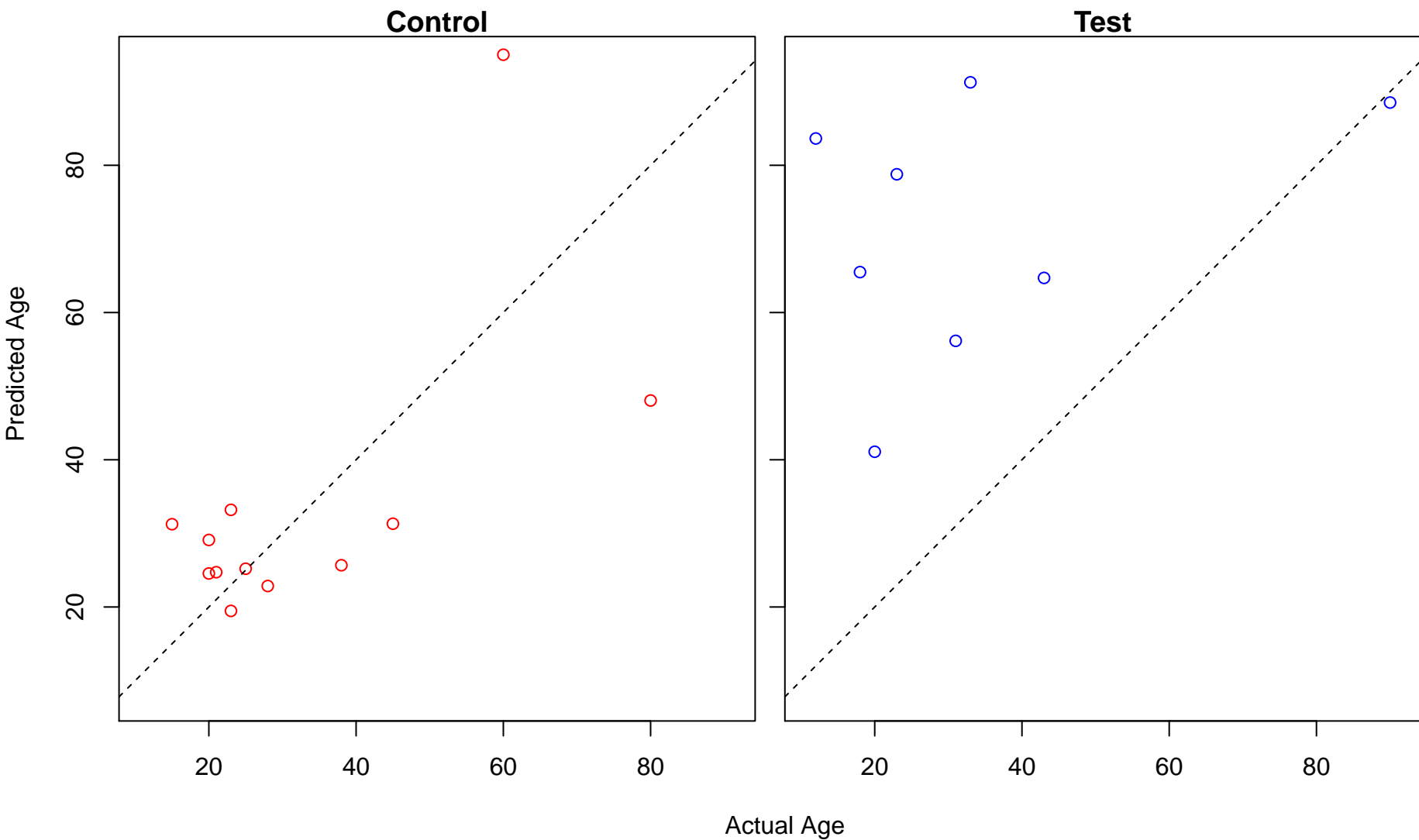


Test

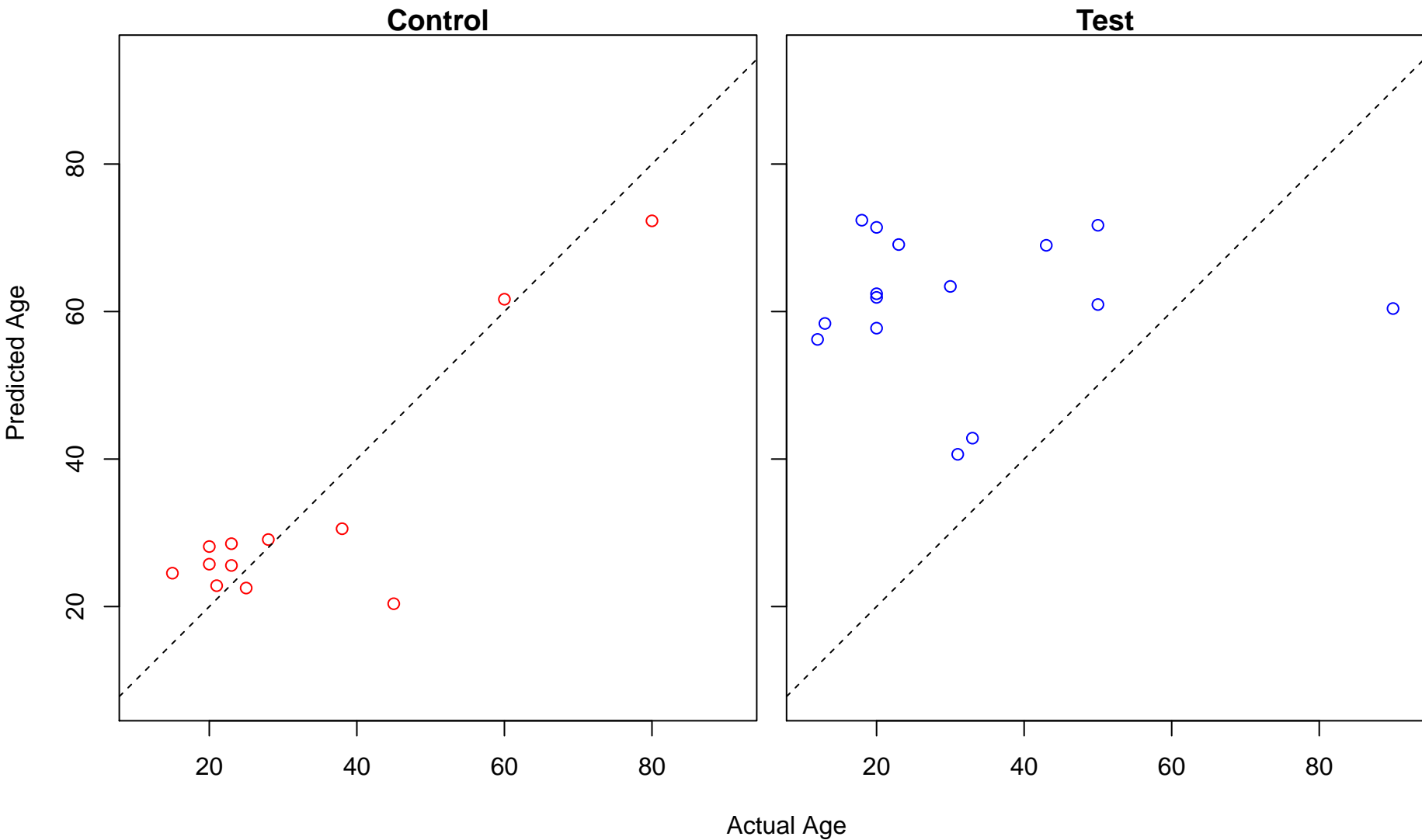


Actual Age

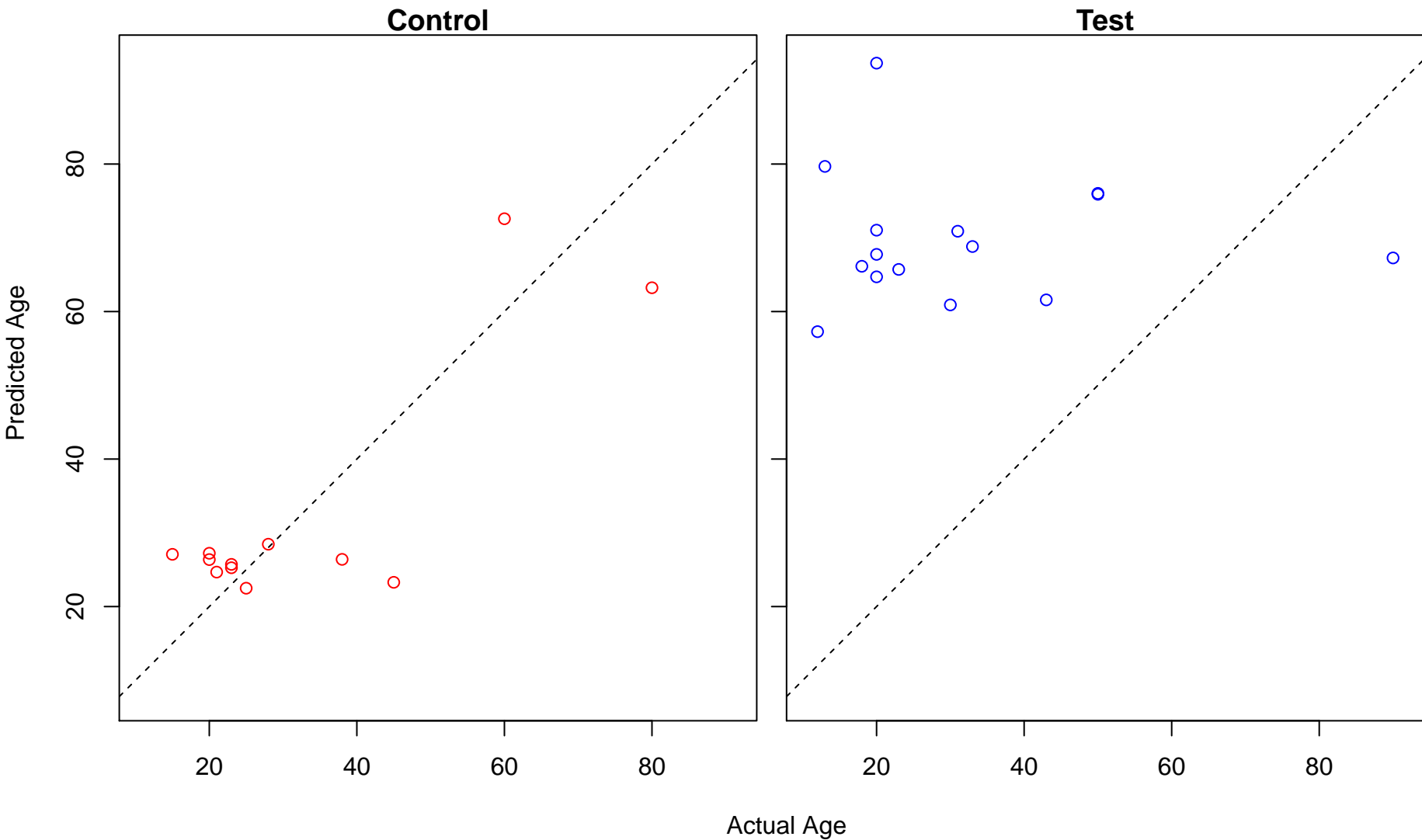
positive regulation of cell migration by vascular endothelial growth factor signaling pathway (Score: 6.0)



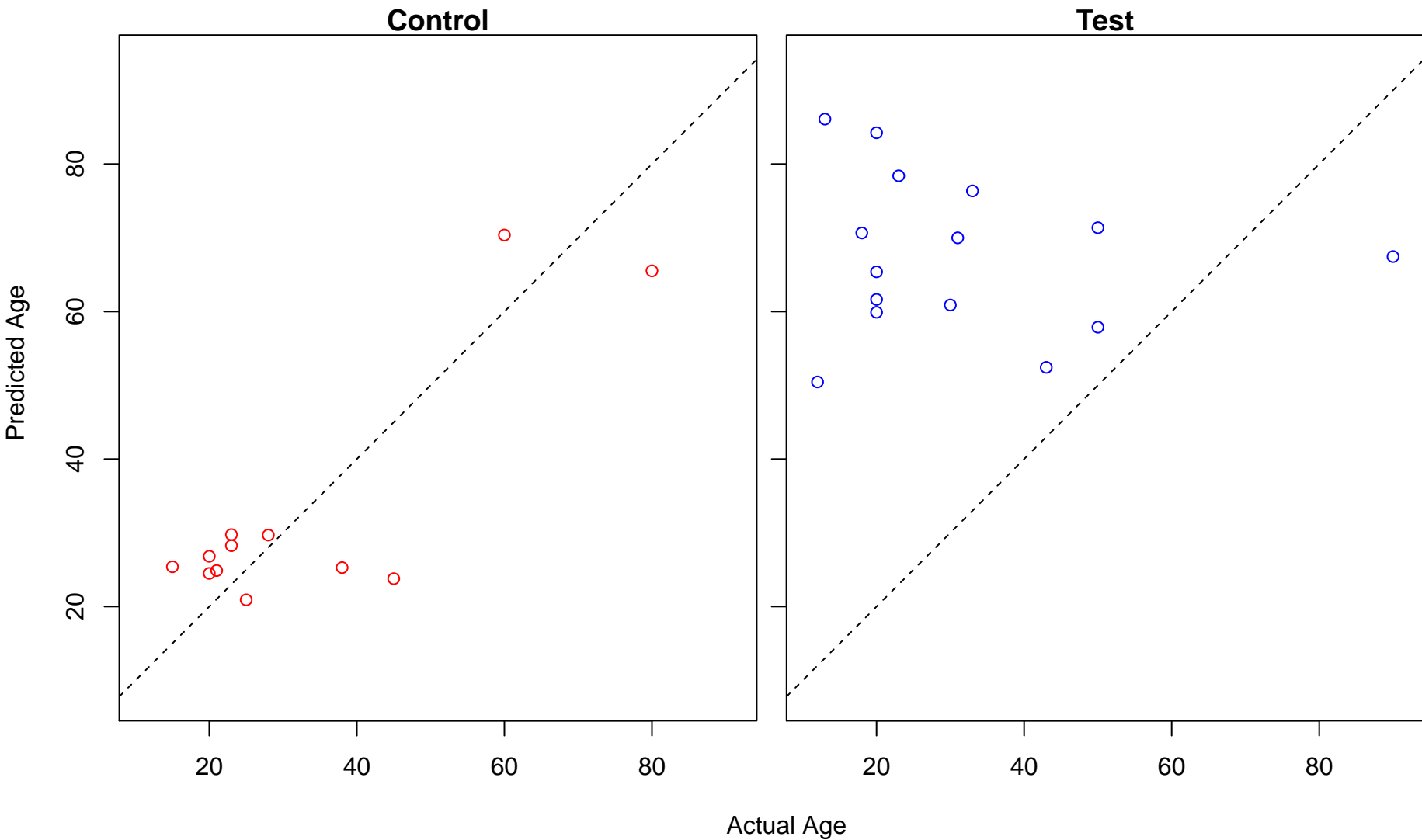
biomineral tissue development (Score: 6.018893)



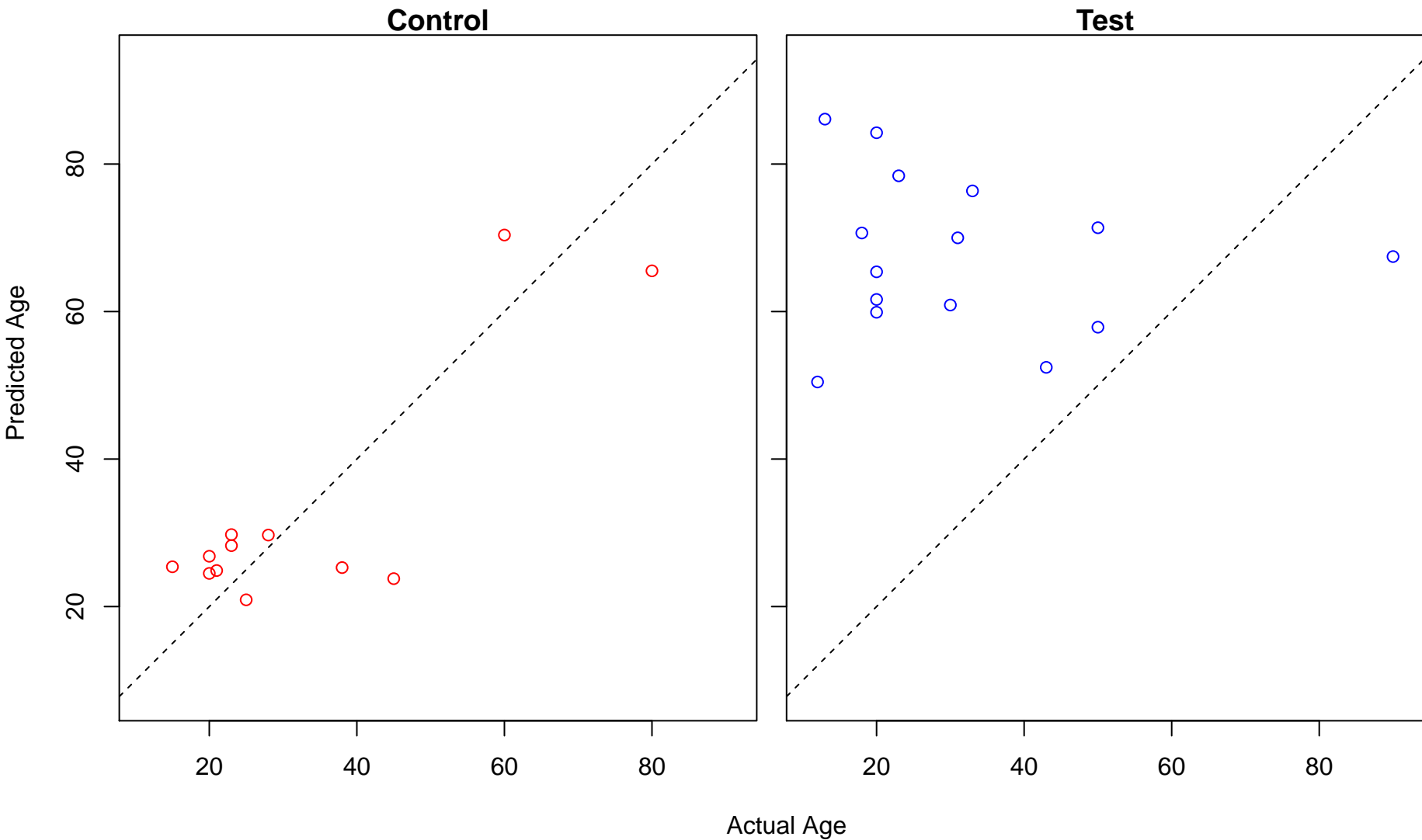
regulation of nucleotide metabolic process (Score: 6.017358)



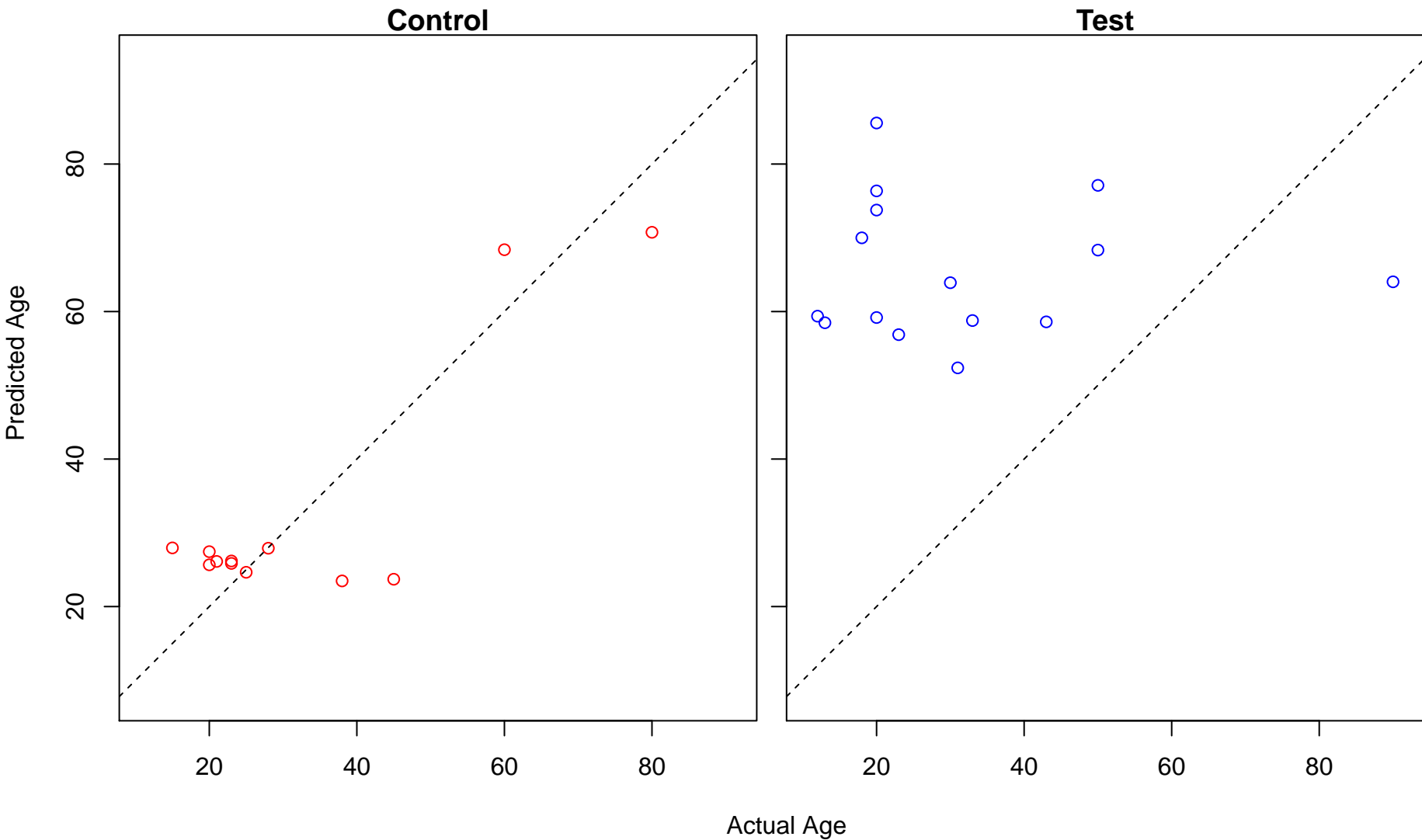
detection of light stimulus (Score: 6.016931)



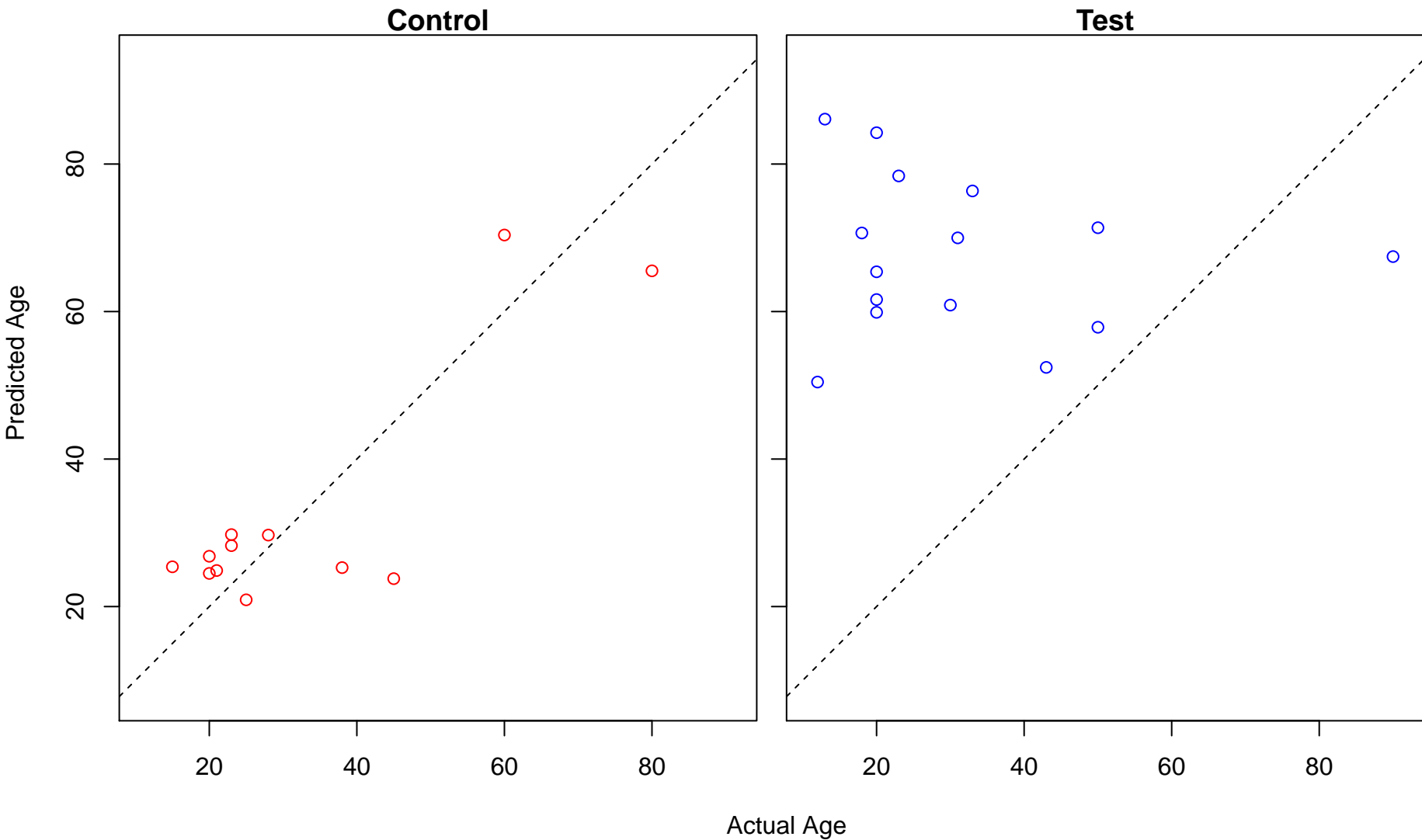
phototransduction (Score: 6.016887)



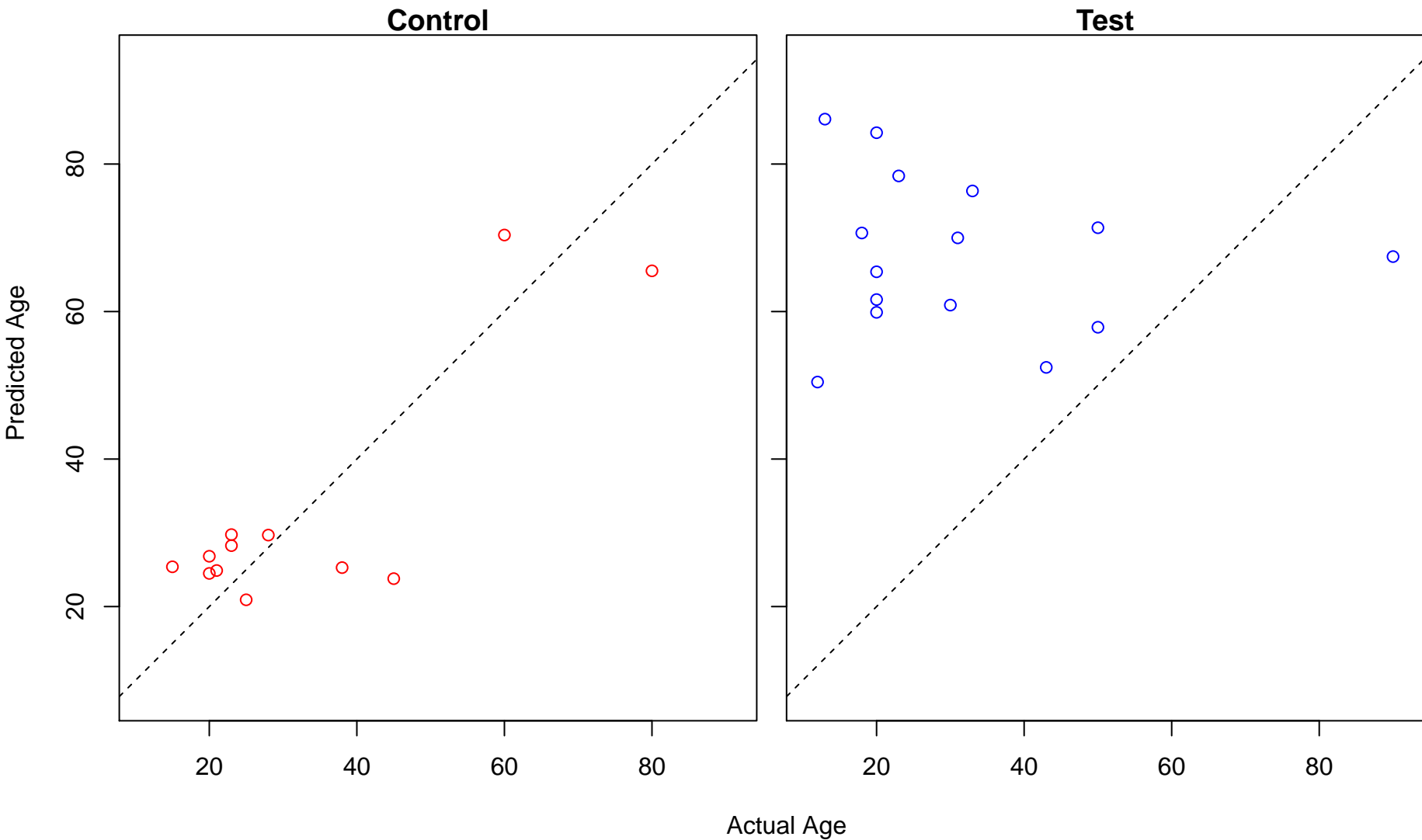
nuclear division (Score: 6.016387)



detection of visible light (Score: 6.016381)

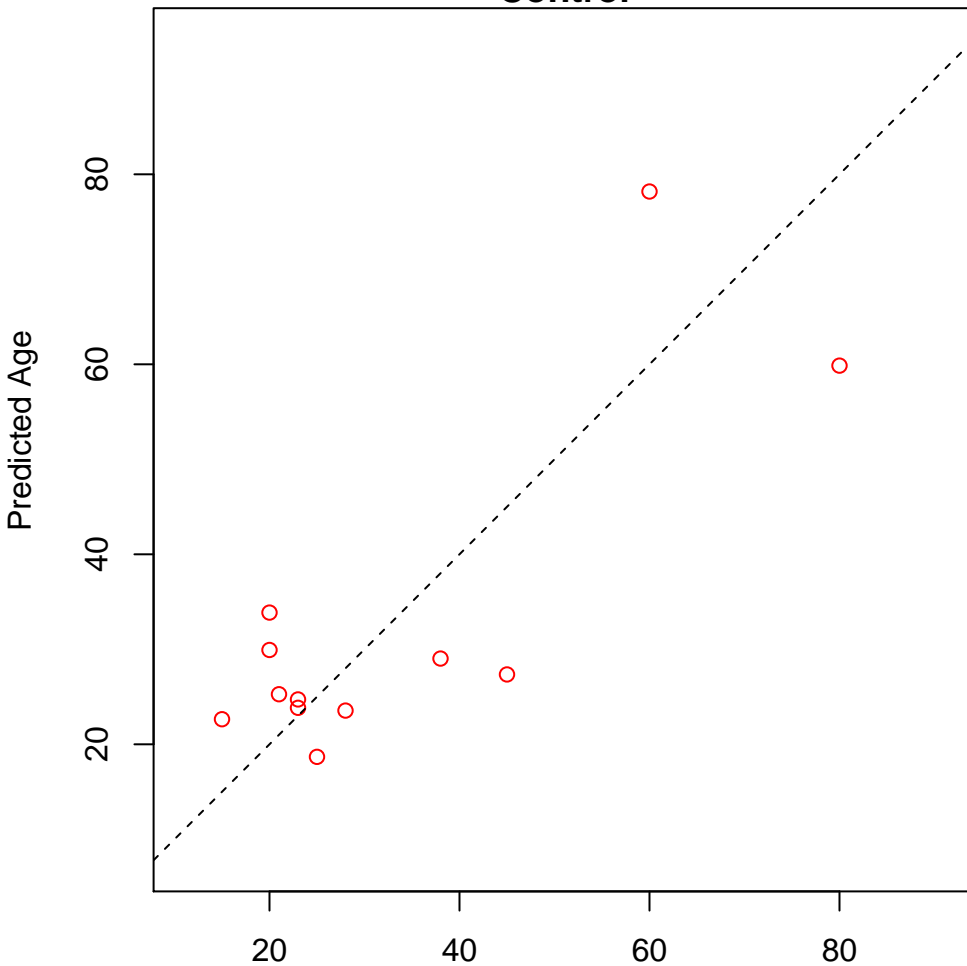


phototransduction, visible light (Score: 6.016369)

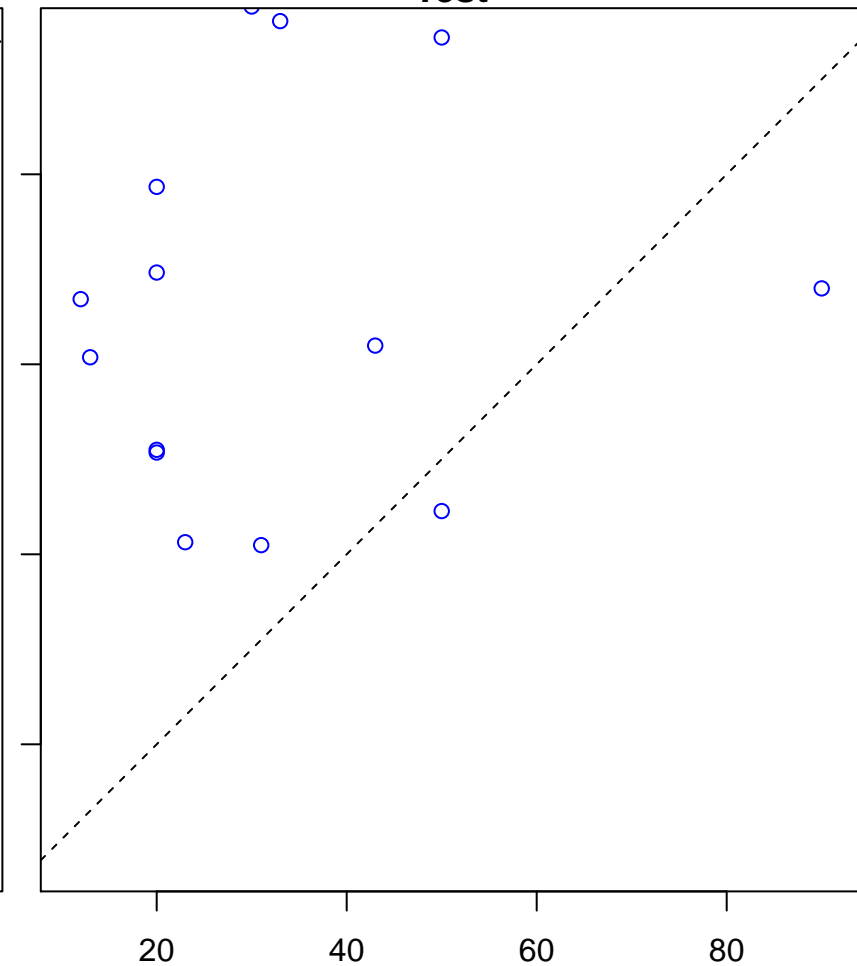


blood coagulation, extrinsic pathway (Score: 6.014743)

Control

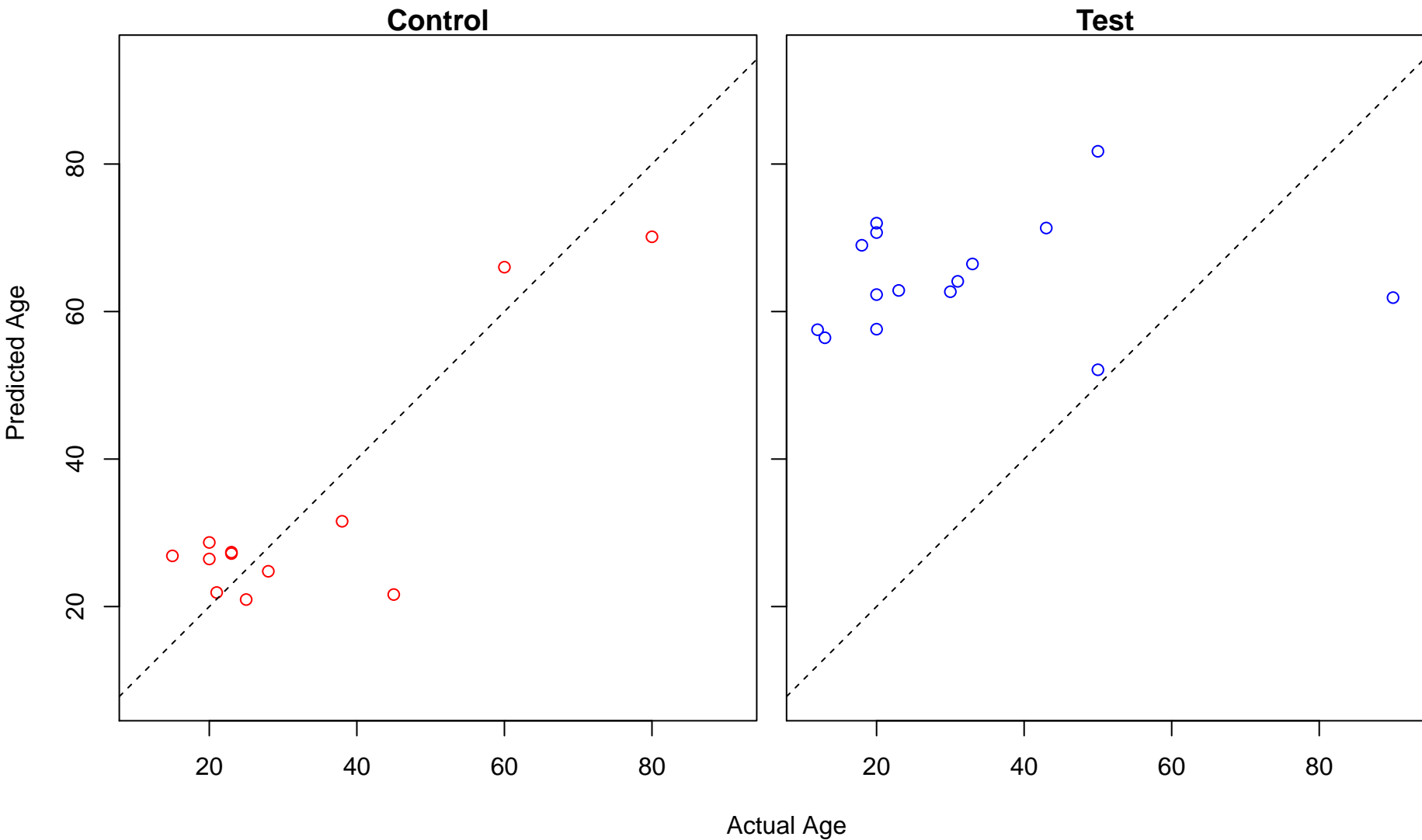


Test

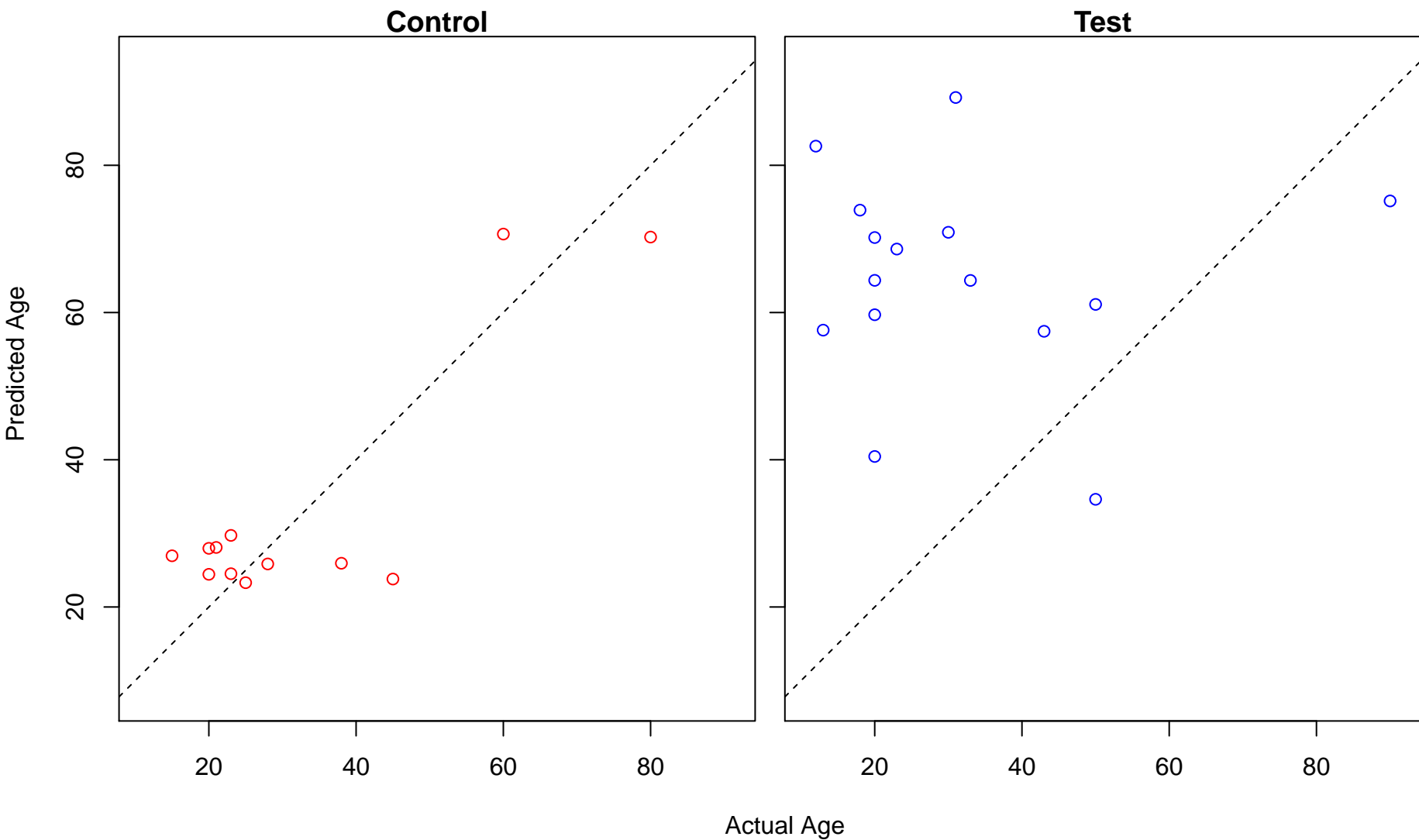


Actual Age

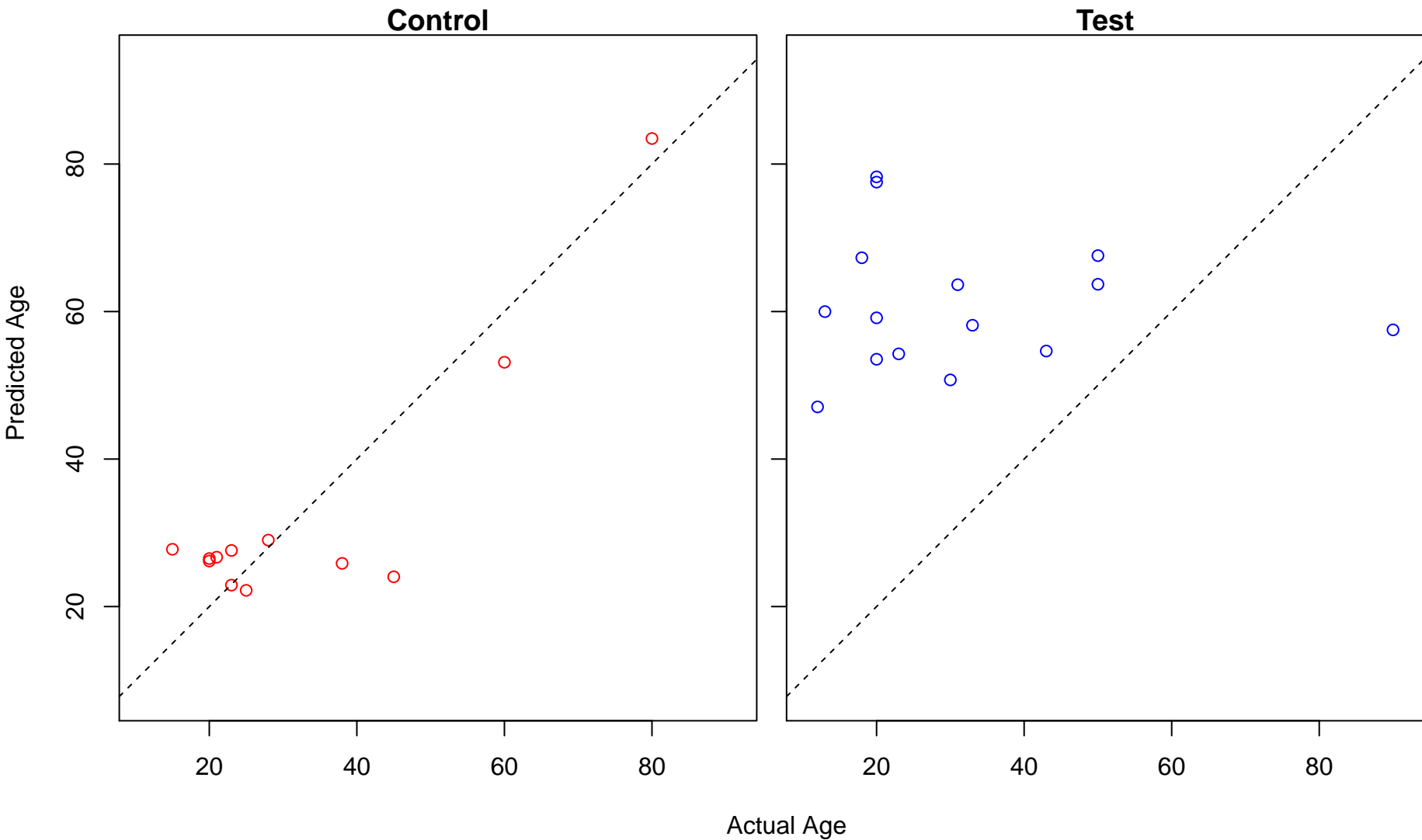
synaptic vesicle recycling (Score: 6.014215)



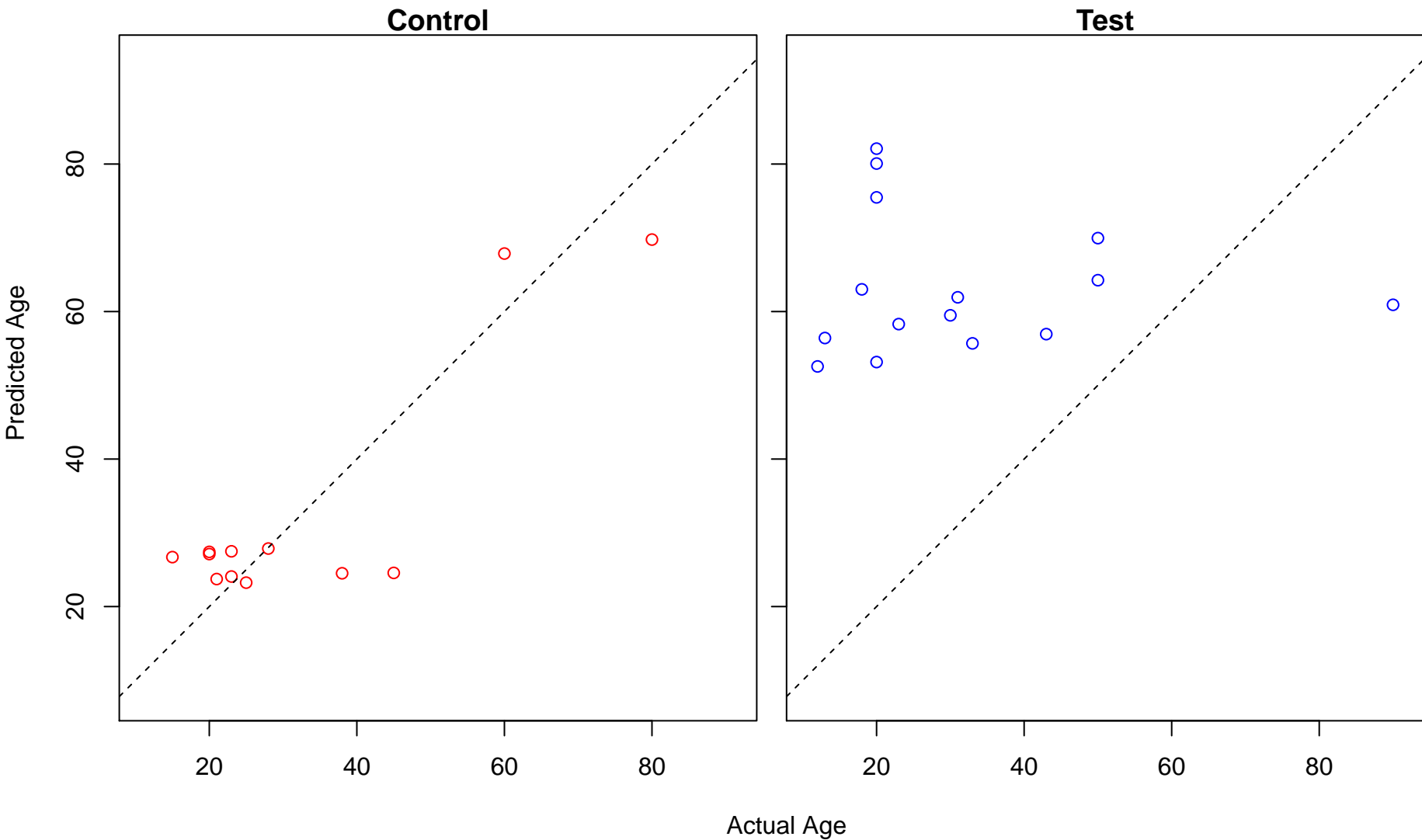
response to nitric oxide (Score: 6.012173)



regulation of cytokines (Score: 6.008492)

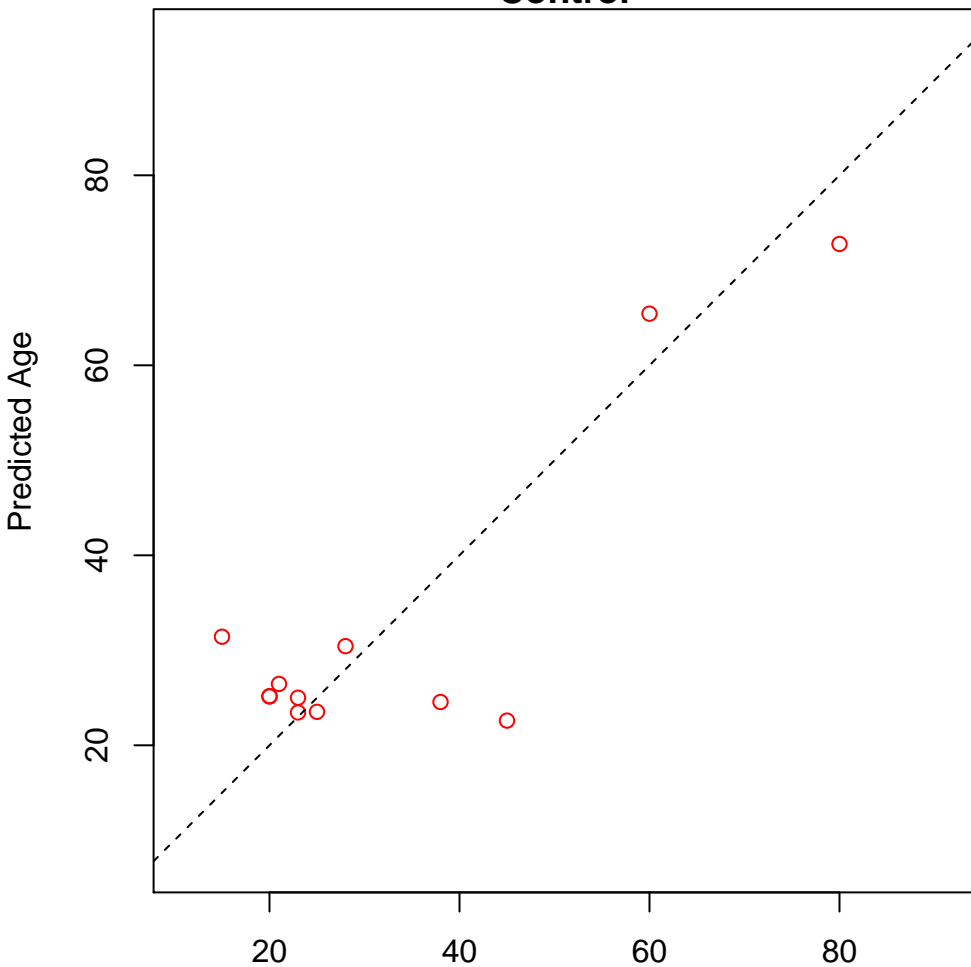


nucleobase-containing small molecule catabolic process (Score: 6.007278)

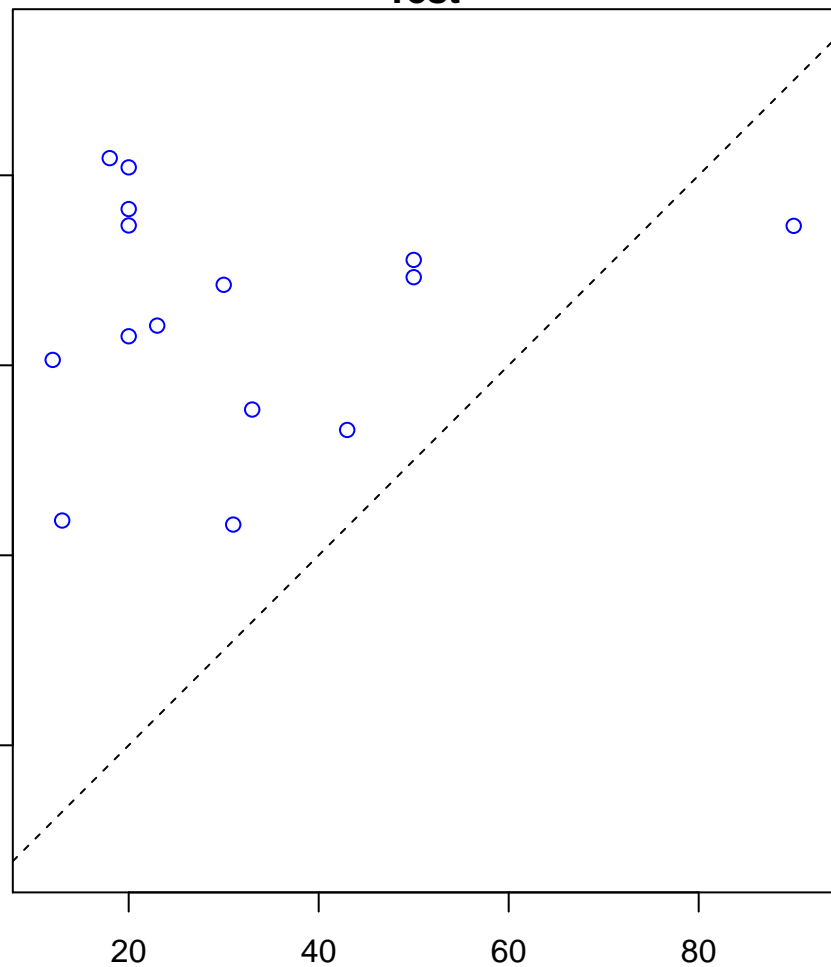


regulation of viral release from host cell (Score: 6.006620)

Control

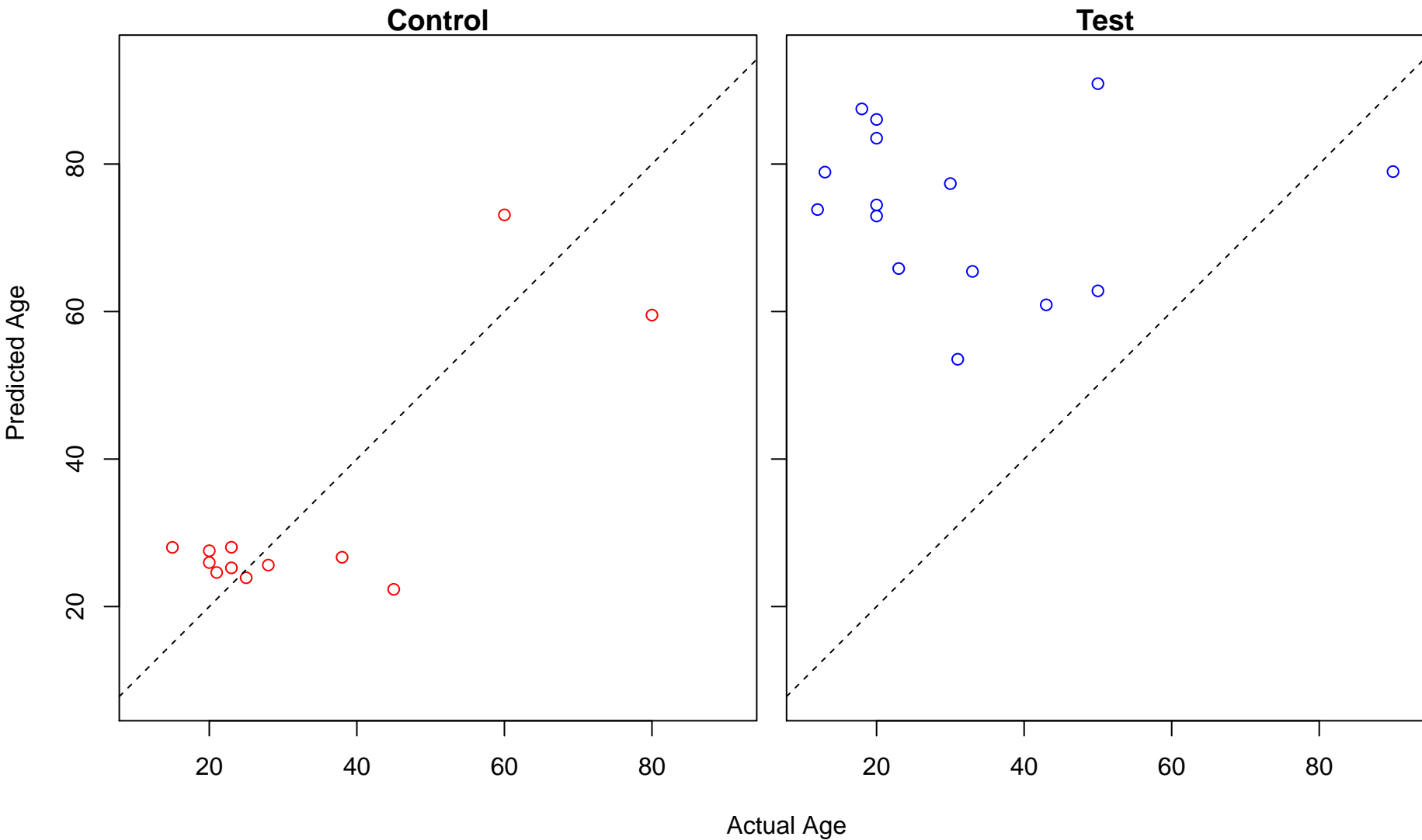


Test

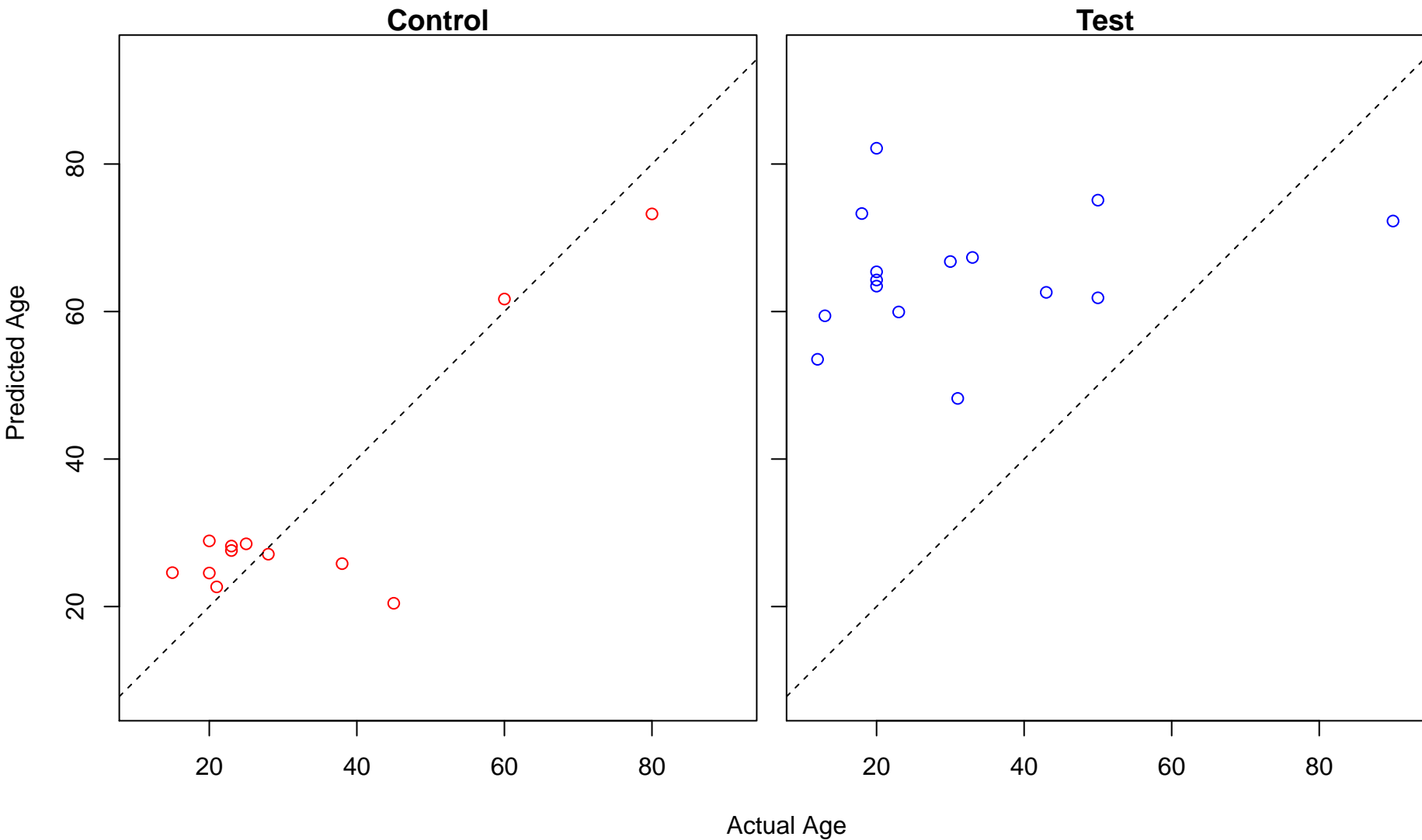


Actual Age

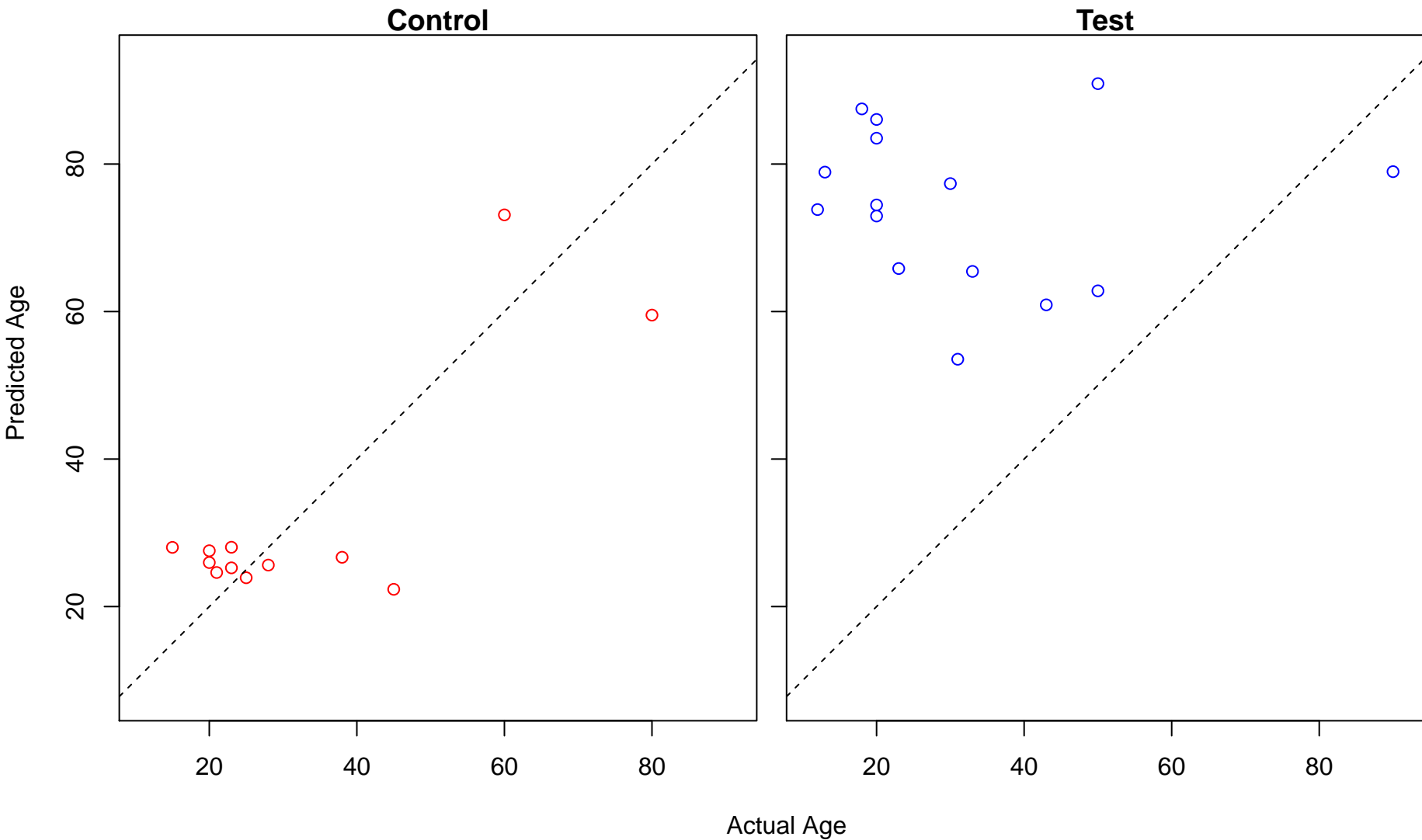
stem cell population maintenance (Score: 6.006301)



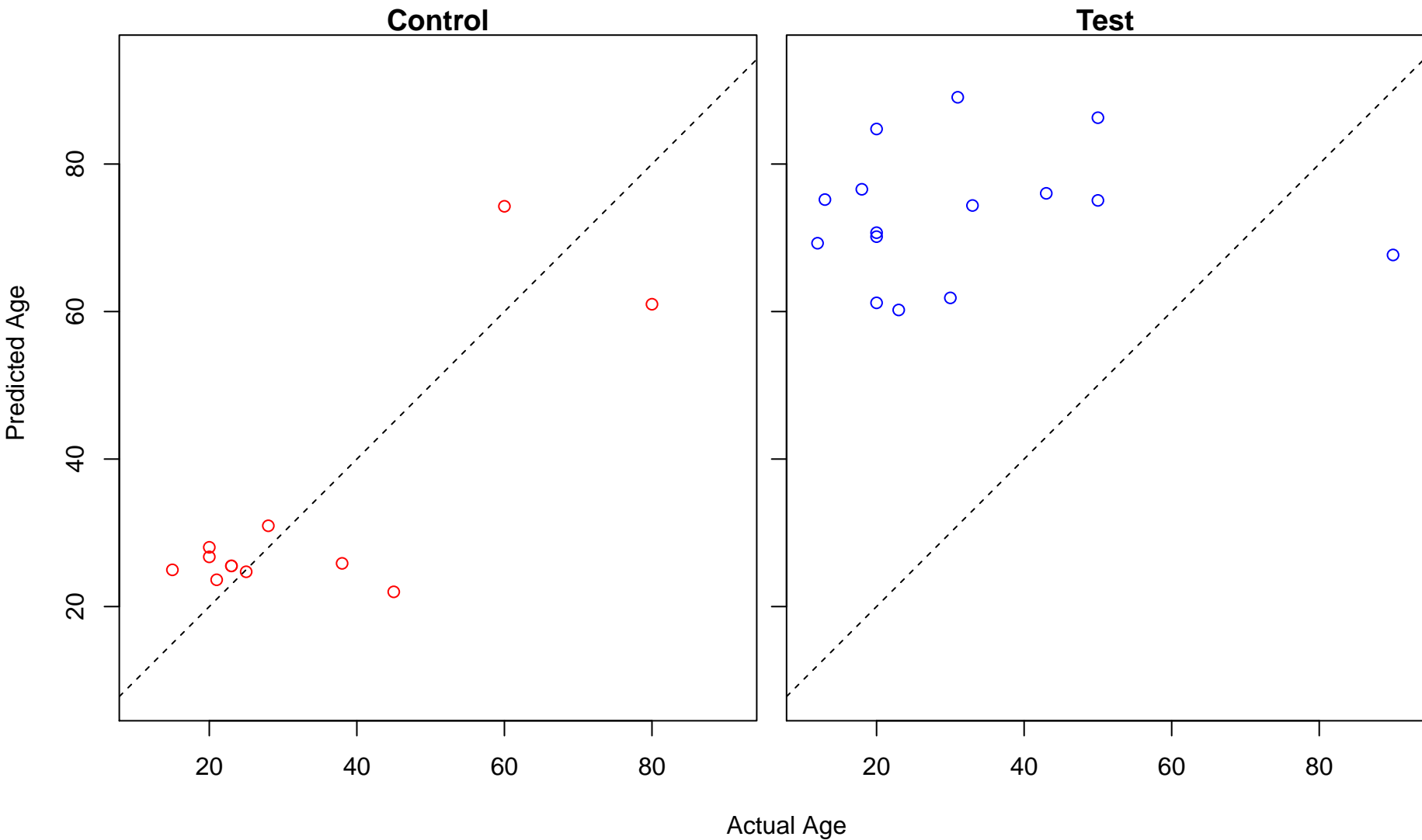
positive regulation of protein localization to cell surface (Score: 6.006242)



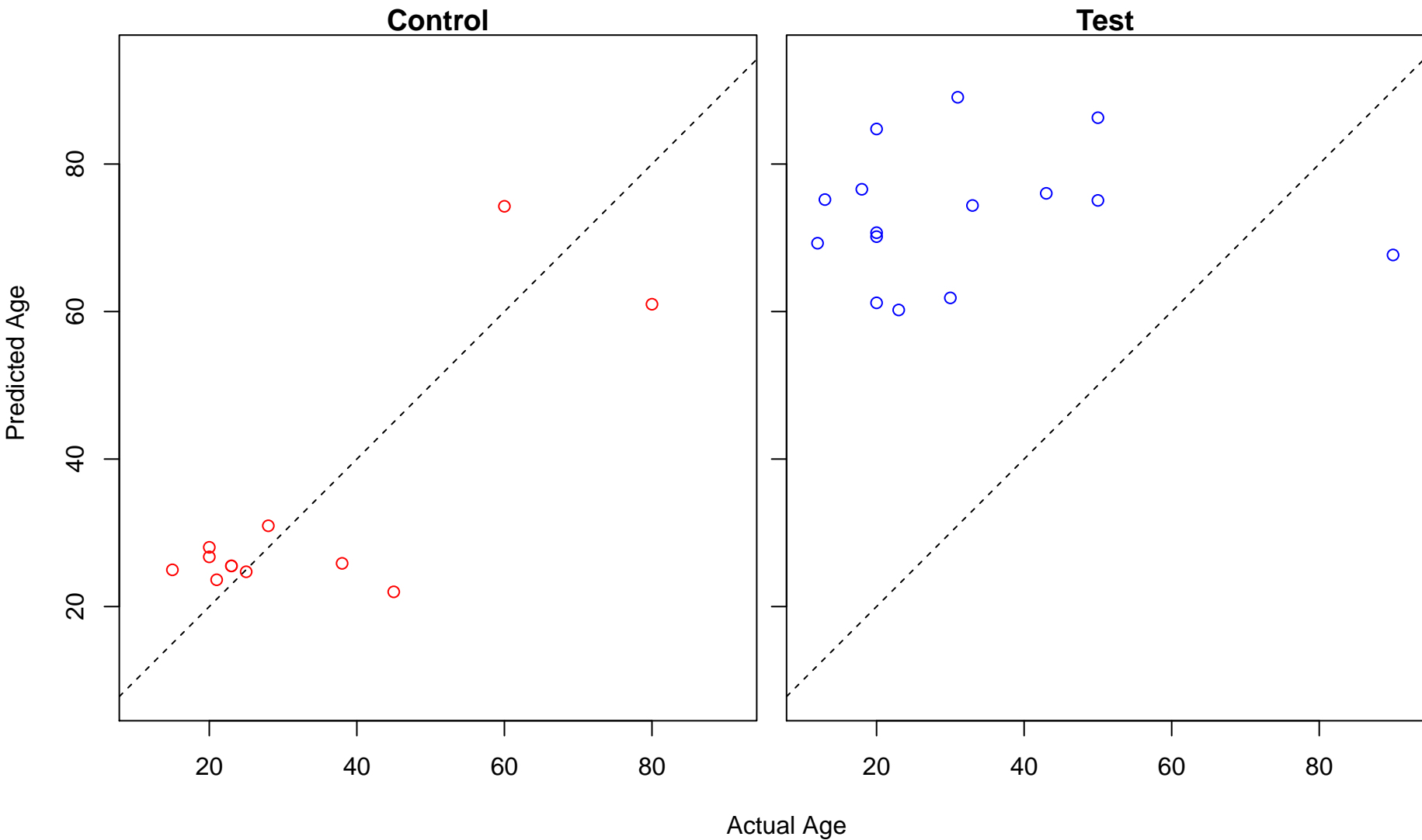
maintenance of cell number (Score: 6.005854)



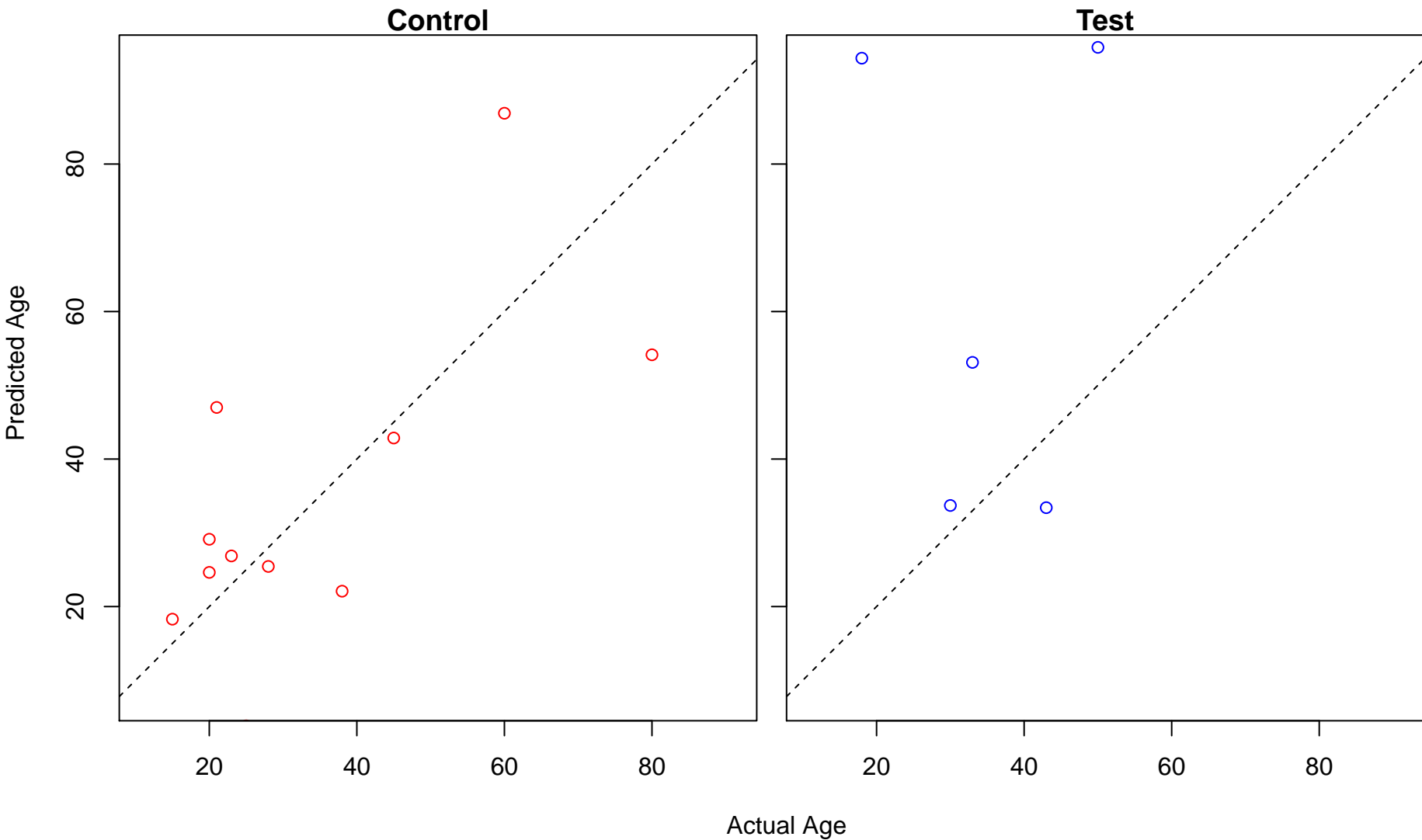
blood circulation (Score: 6.005518)



circulatory system process (Score: 6.005518)

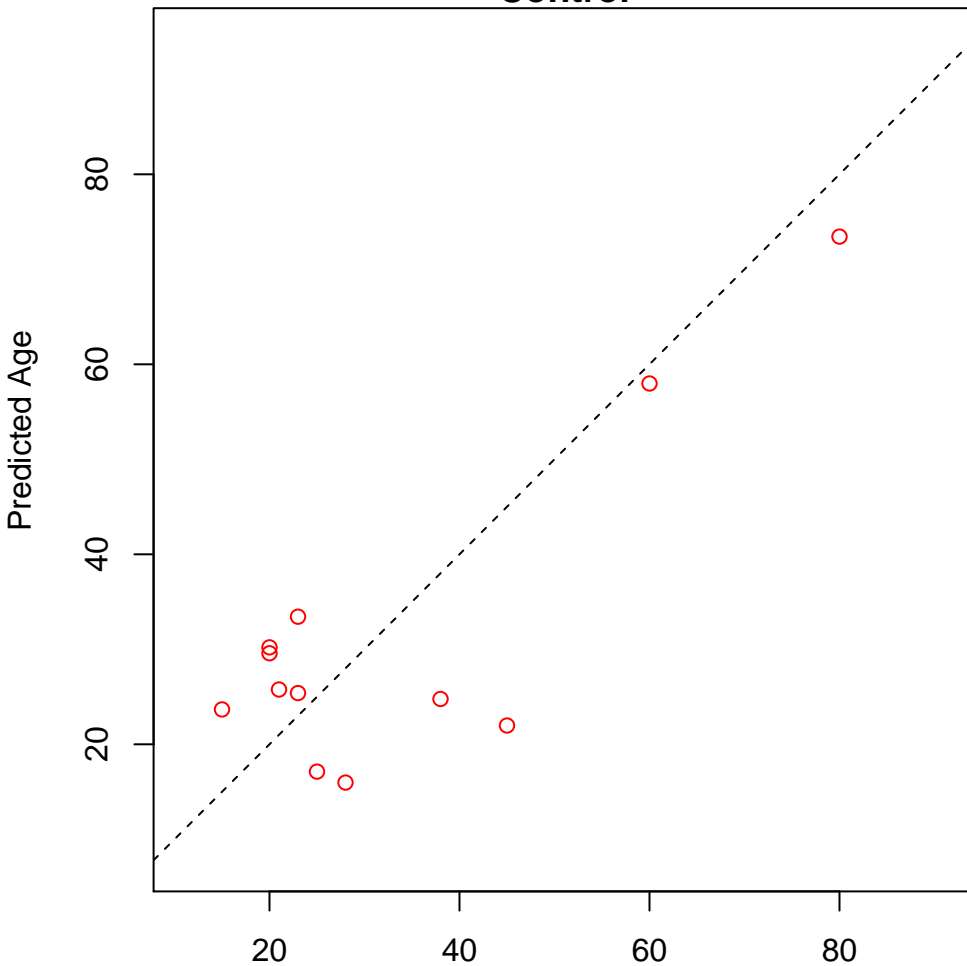


very-low-density lipoprotein particle remodeling (Score: 6.005471)

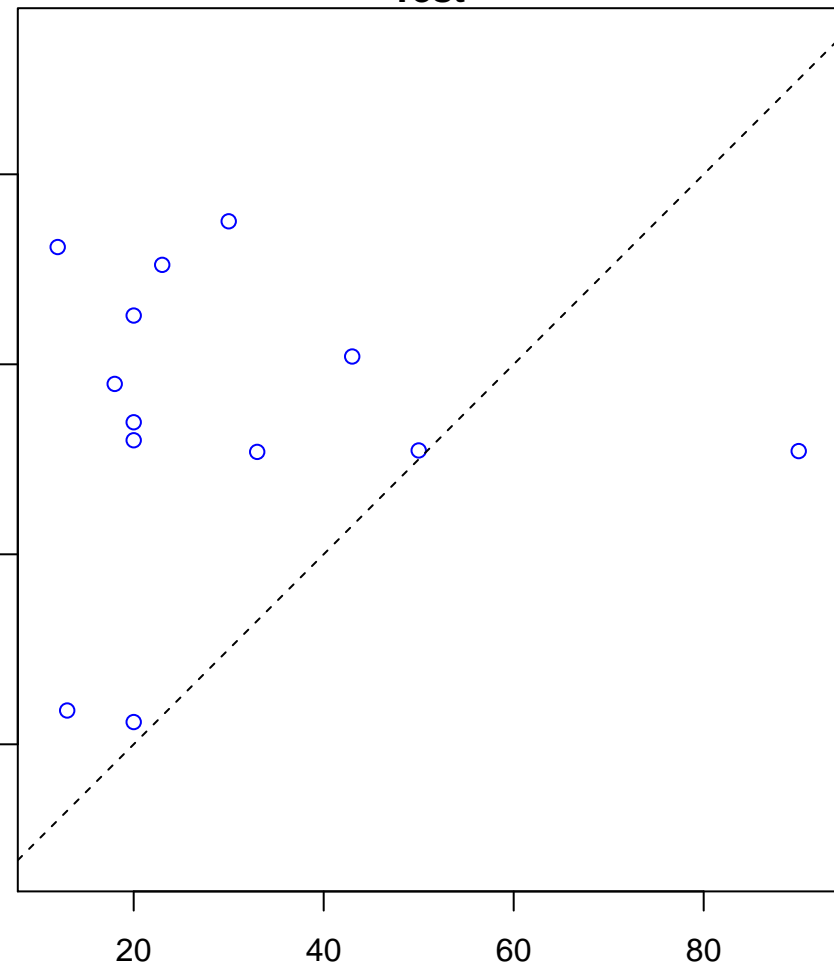


alditol phosphate metabolic process (Score: 6.004367)

Control



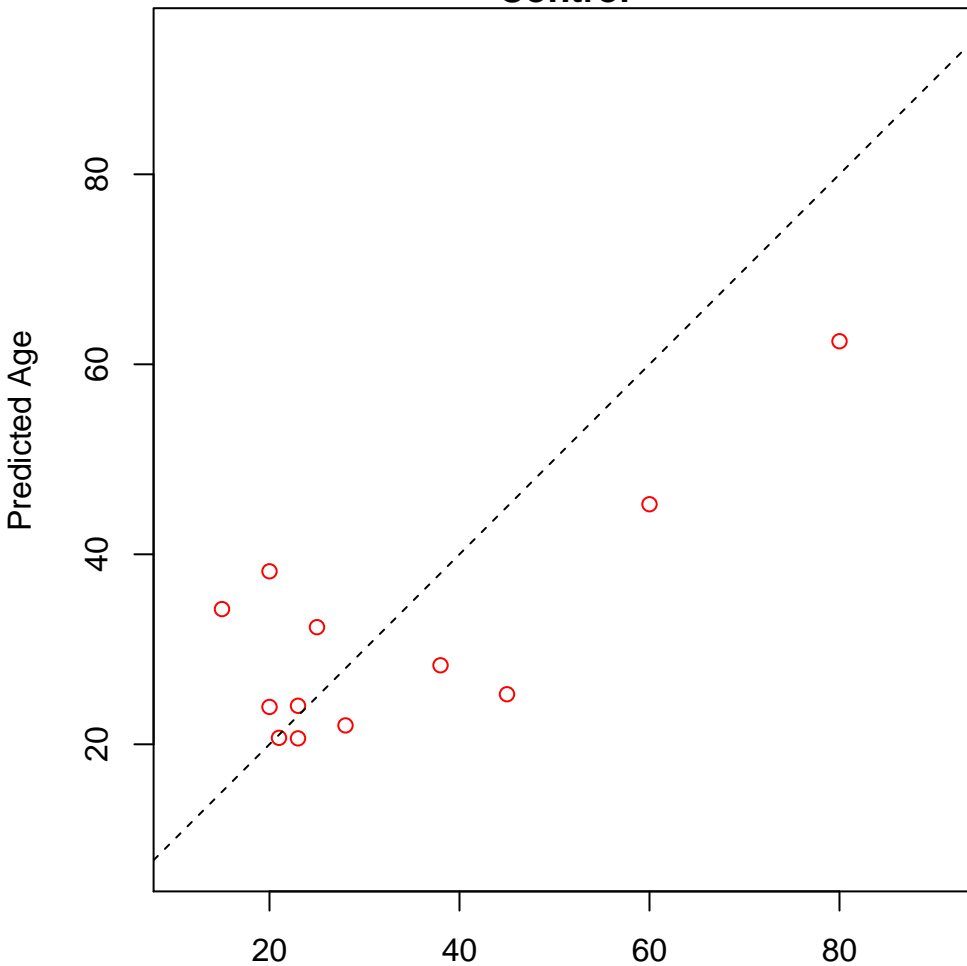
Test



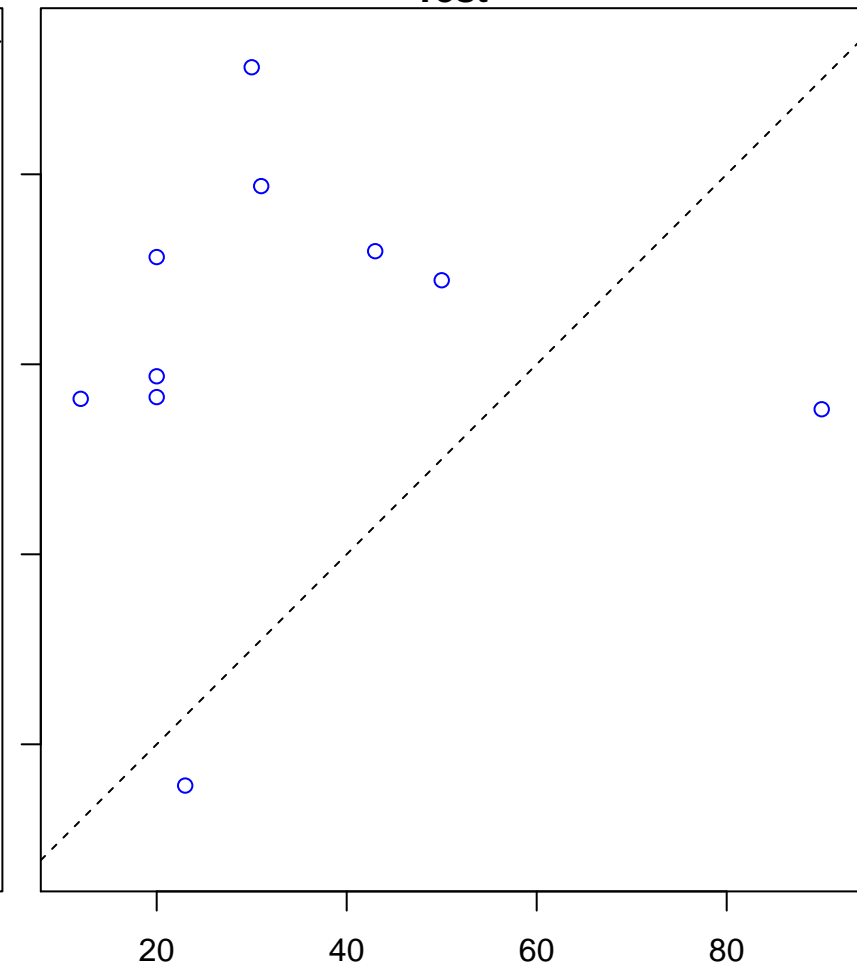
Actual Age

long-chain fatty acid catabolic process (Score: 6.002240)

Control



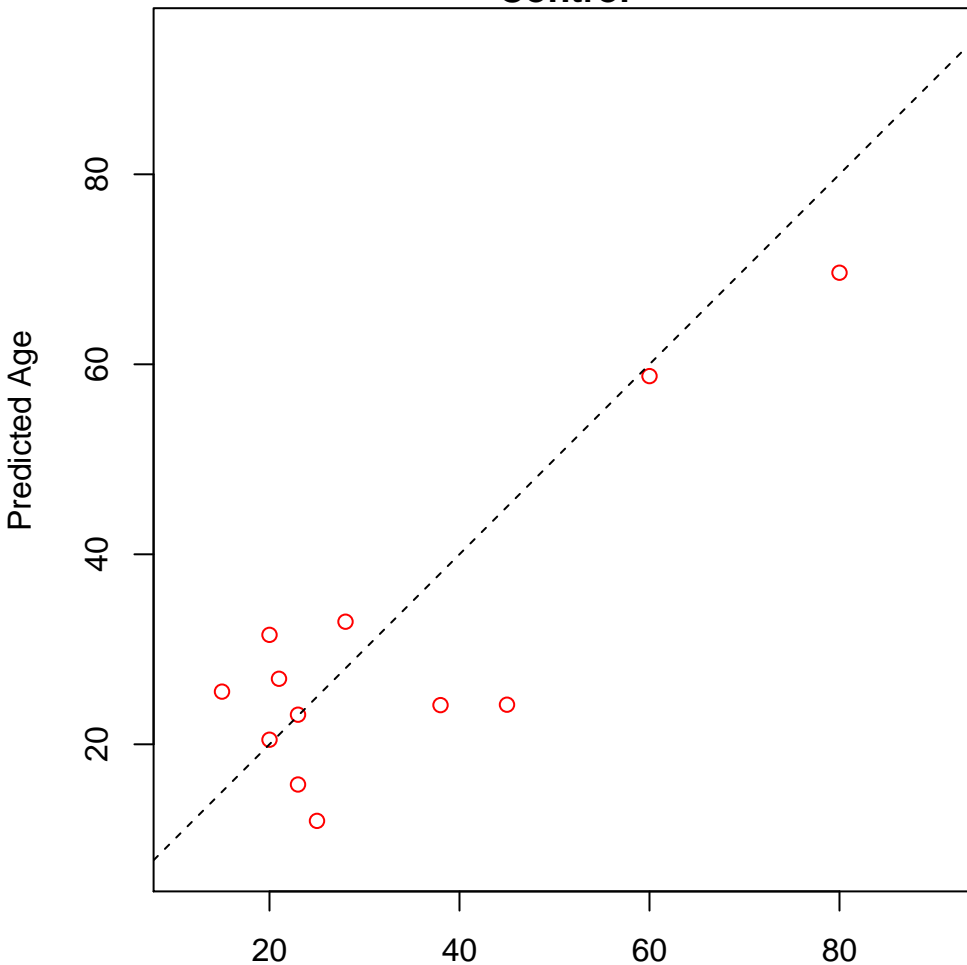
Test



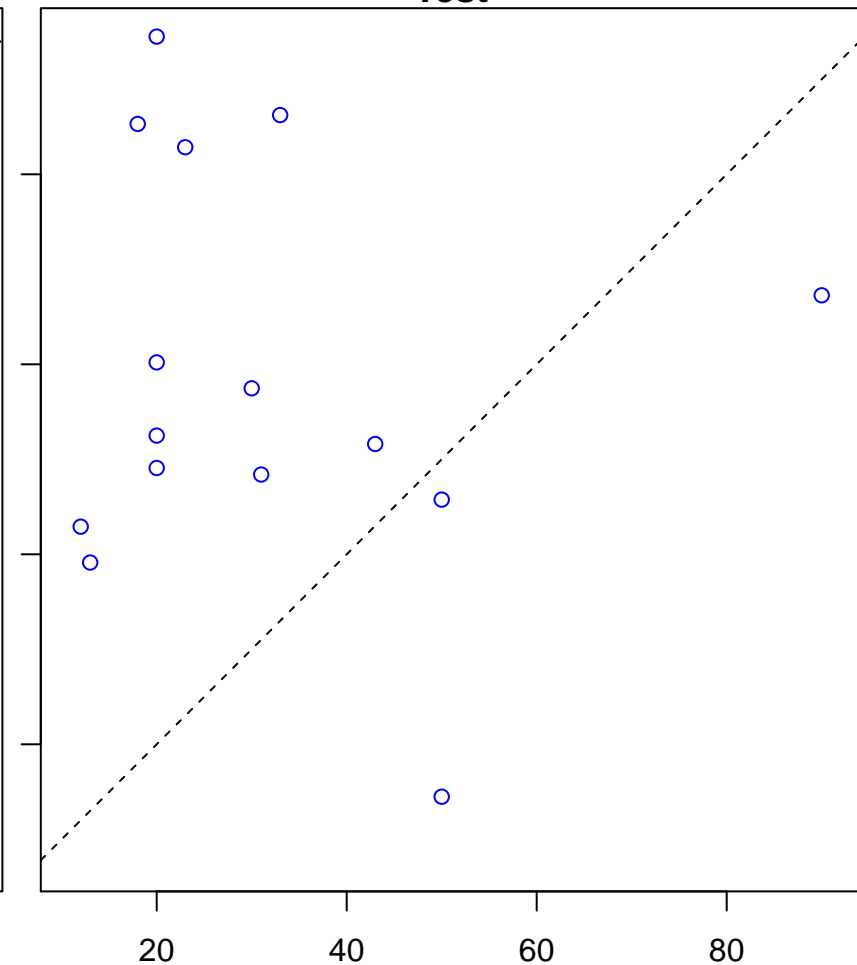
Actual Age

ribonucleoprotein complex localization (Score: 6.000982)

Control

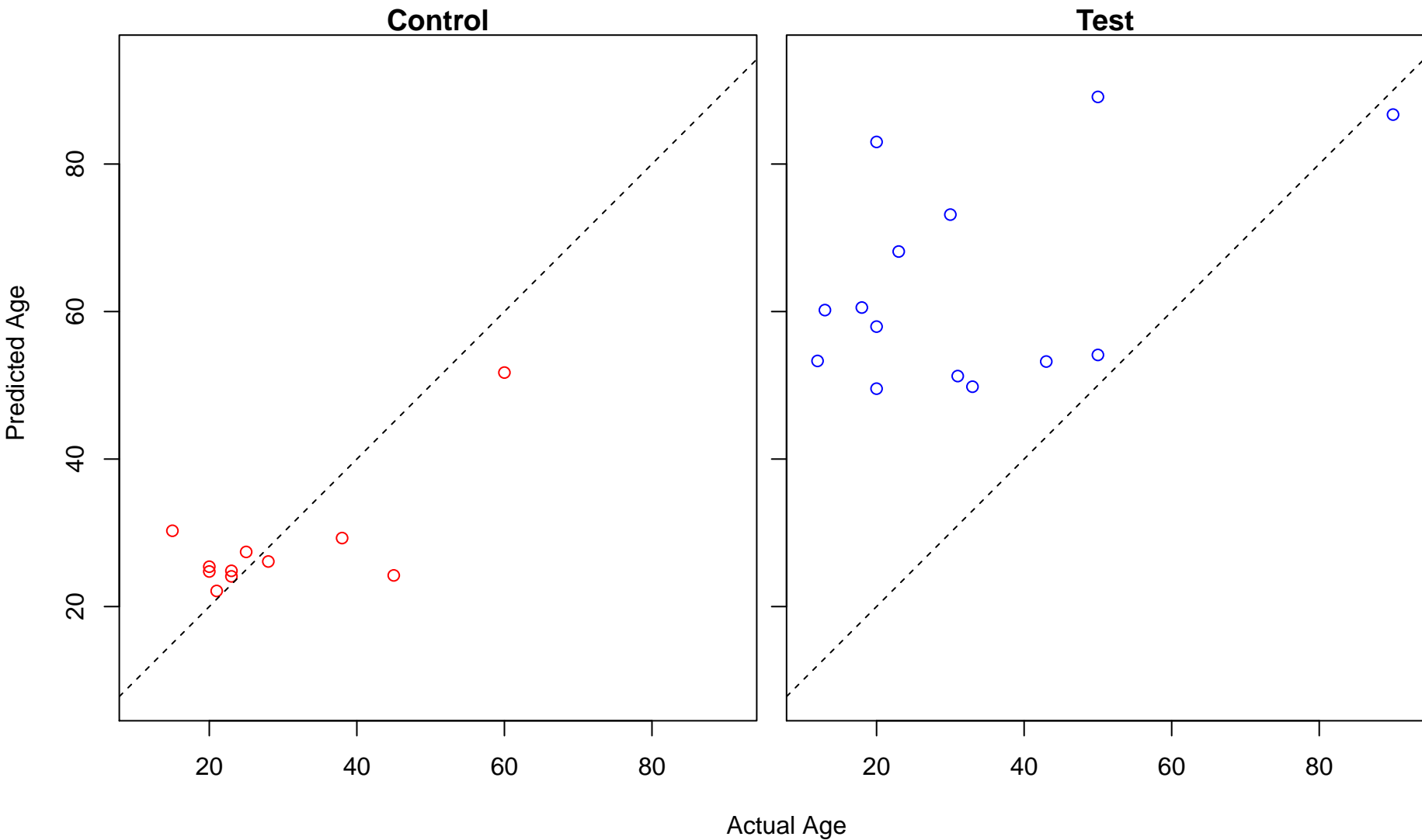


Test

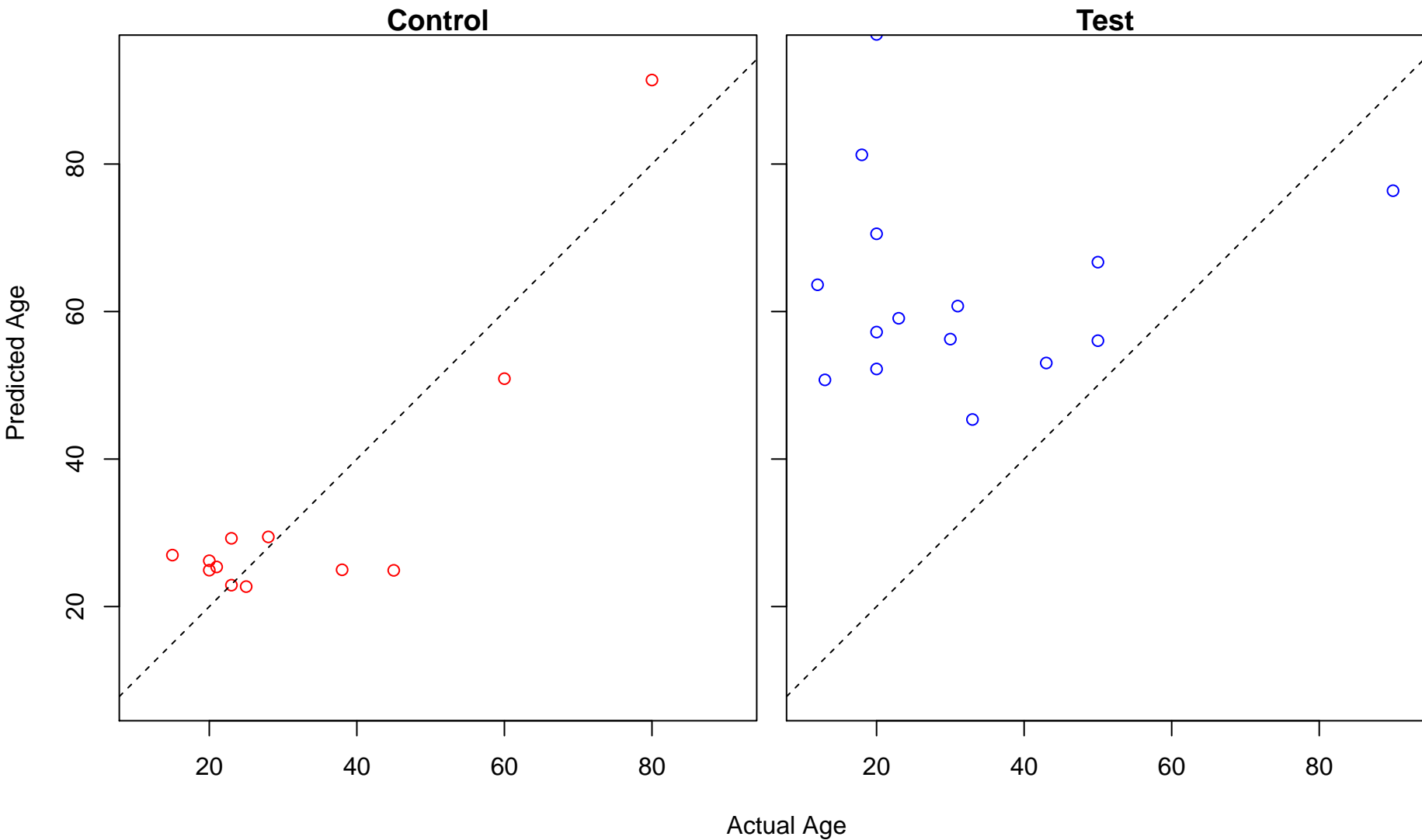


Actual Age

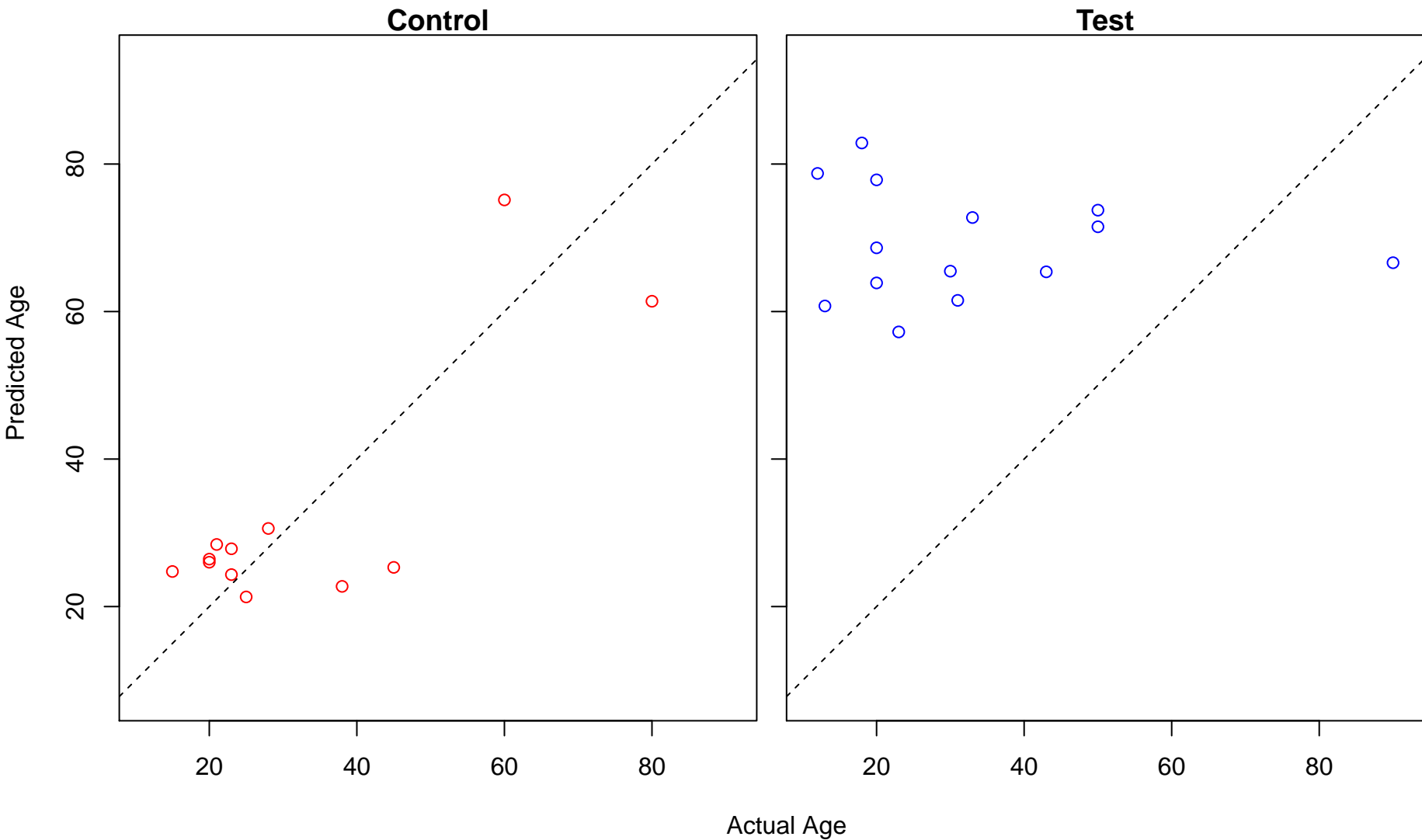
negative regulation of synaptic transmission (Score: 6.000268)



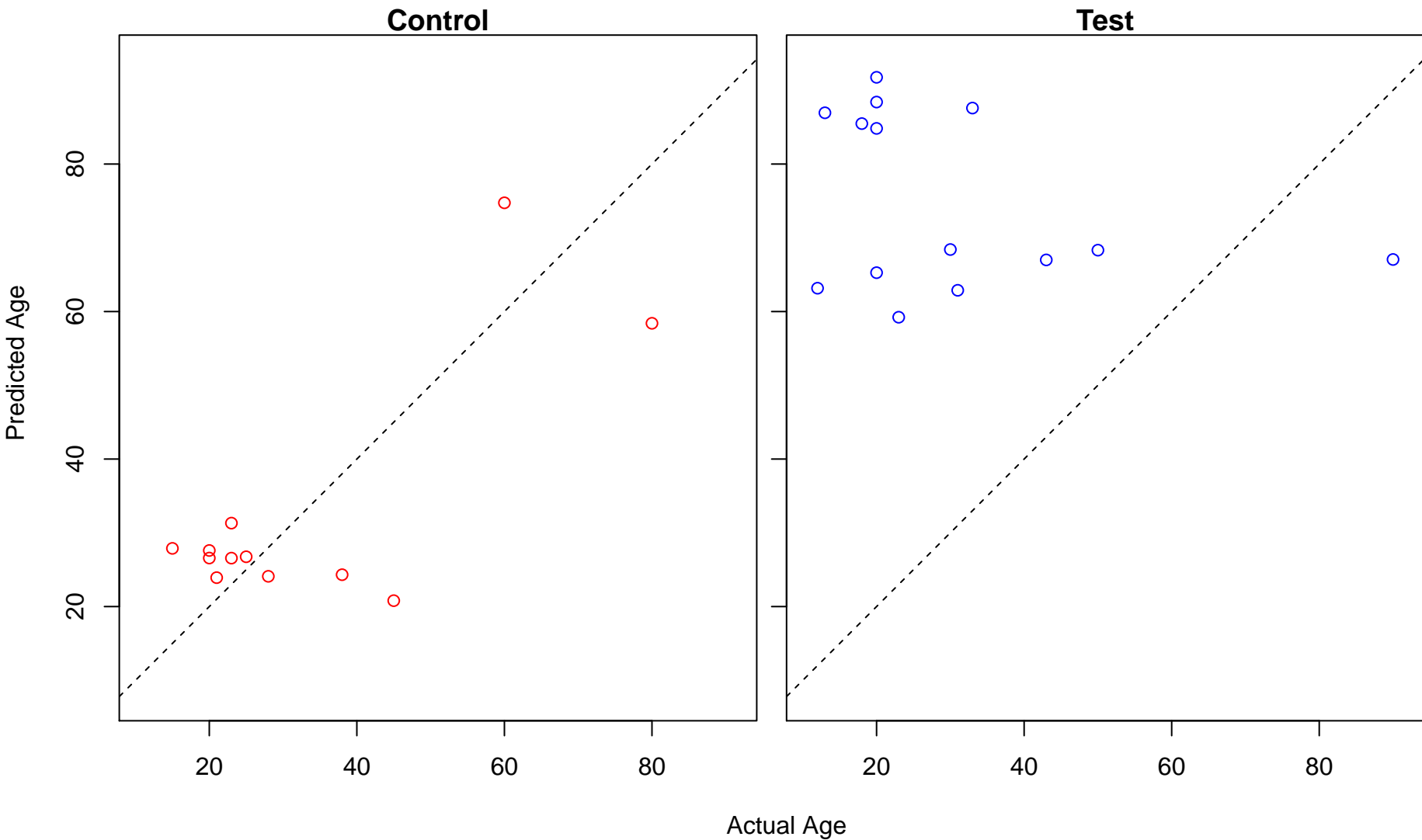
negative regulation of cellular response to growth factor stimulus (Score: 5.999384)



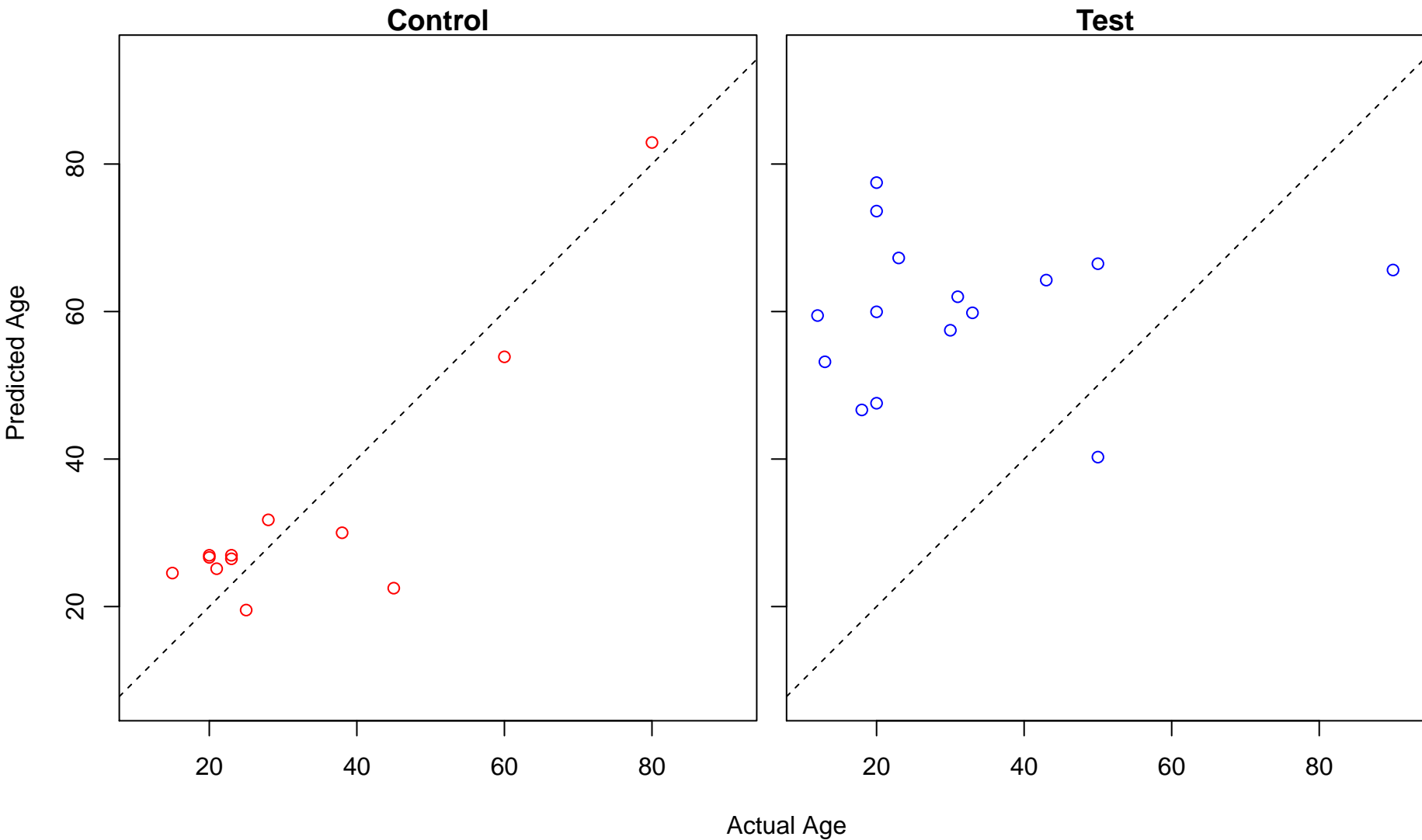
regulation of extracellular matrix assembly (Score: 5.998991)



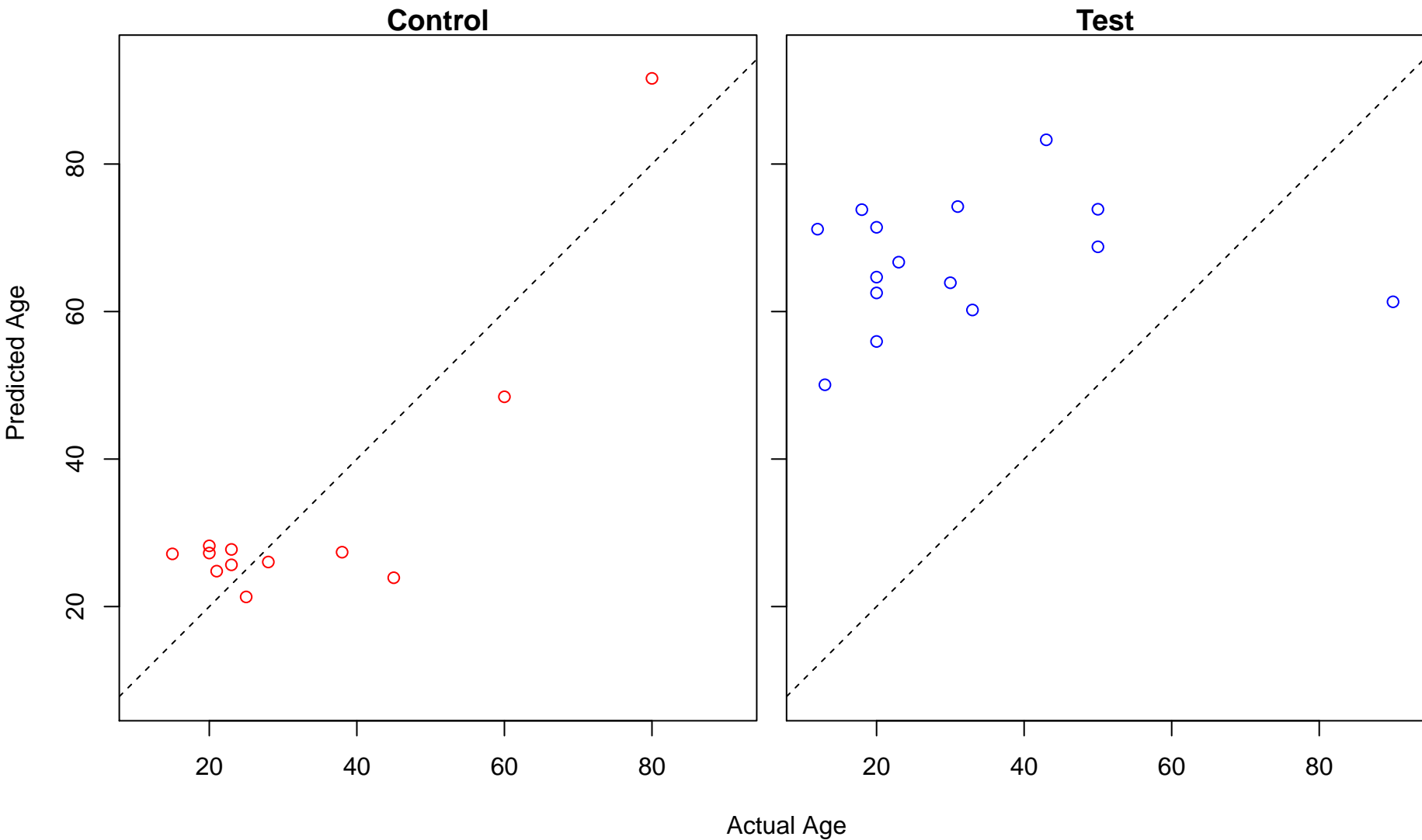
positive regulation of natural killer cell mediated immunity (Score: 5.998186)



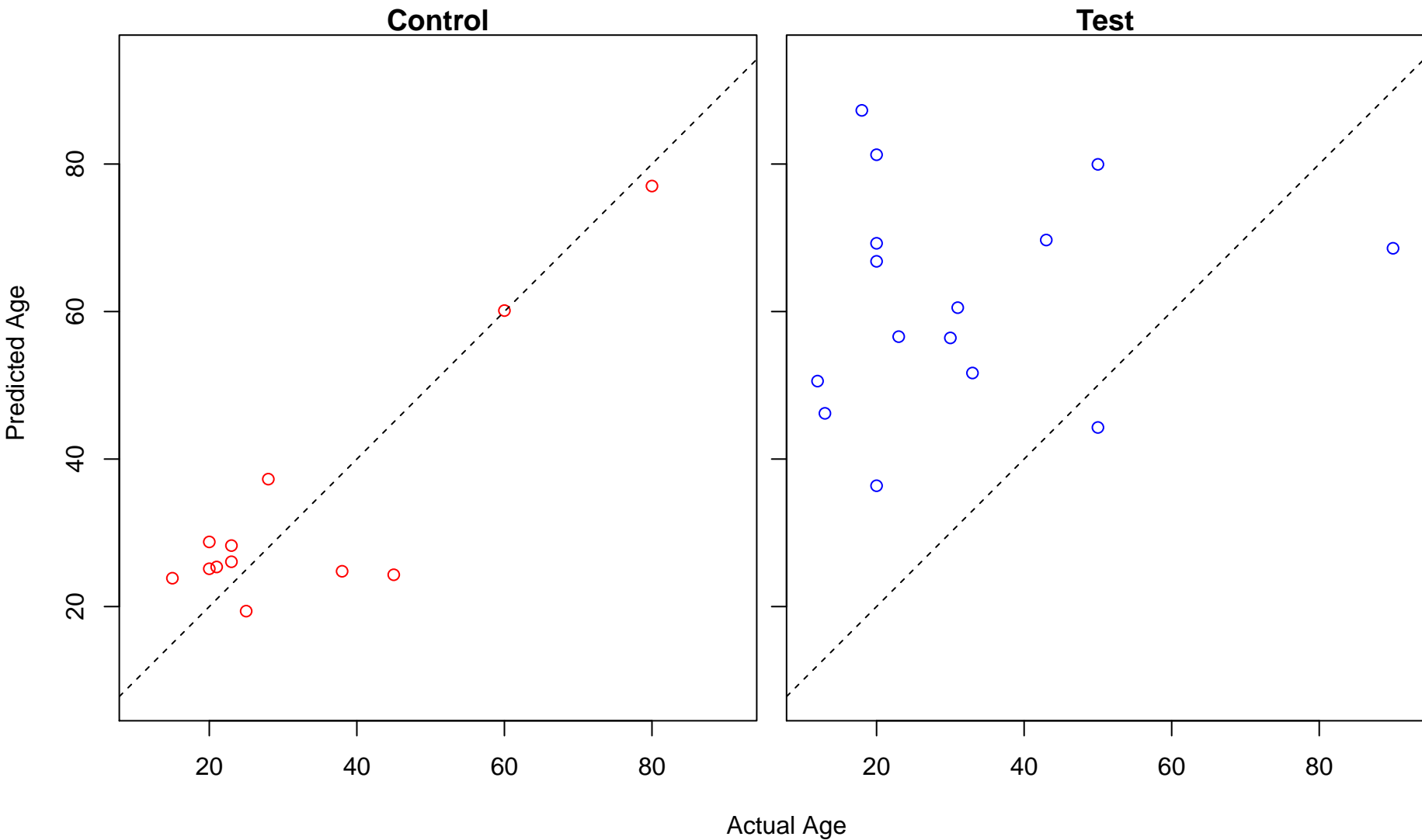
cytoplasmic mRNA processing body assembly (Score: 5.996851)



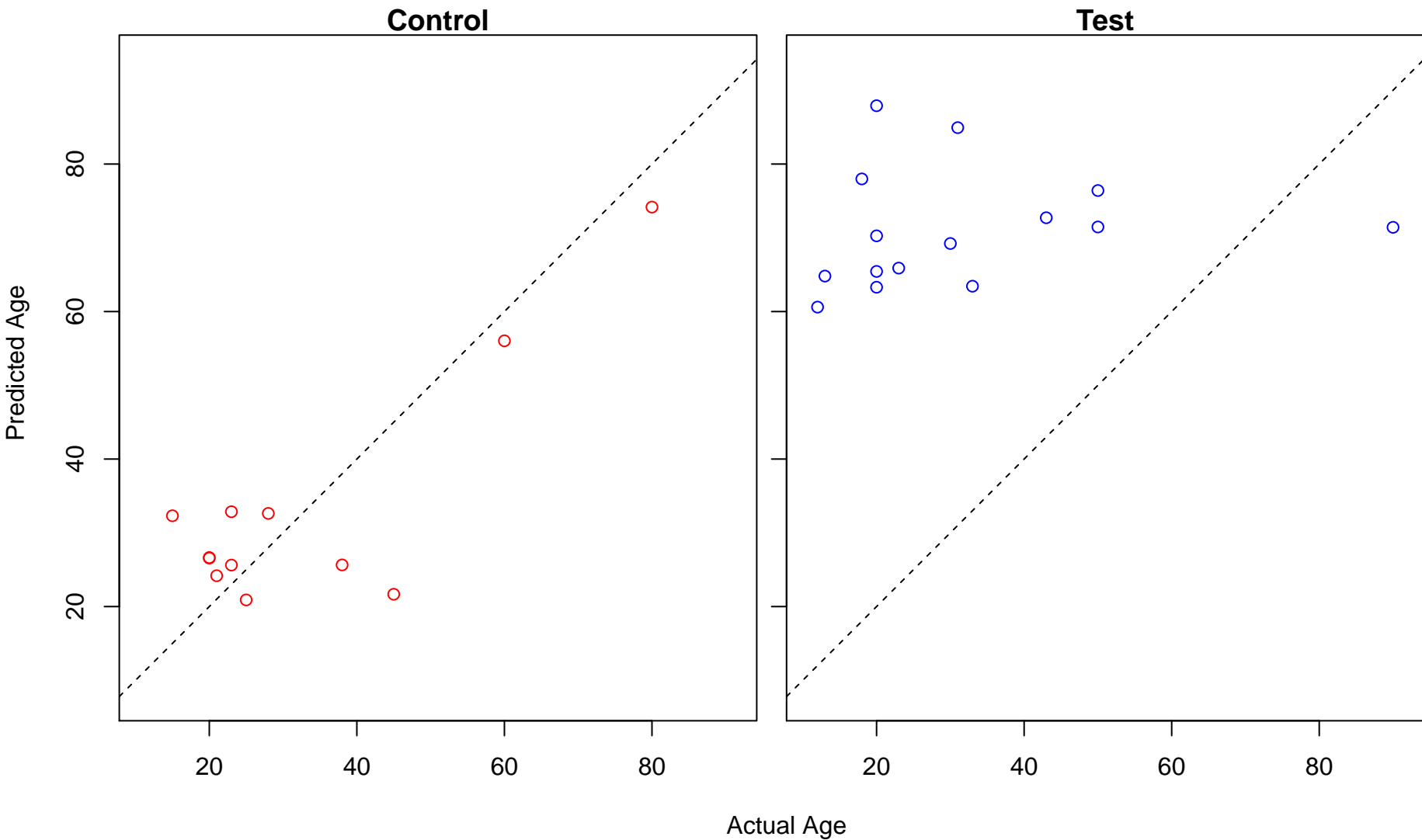
negative regulation of circadian rhythm (Score: 5.996524)



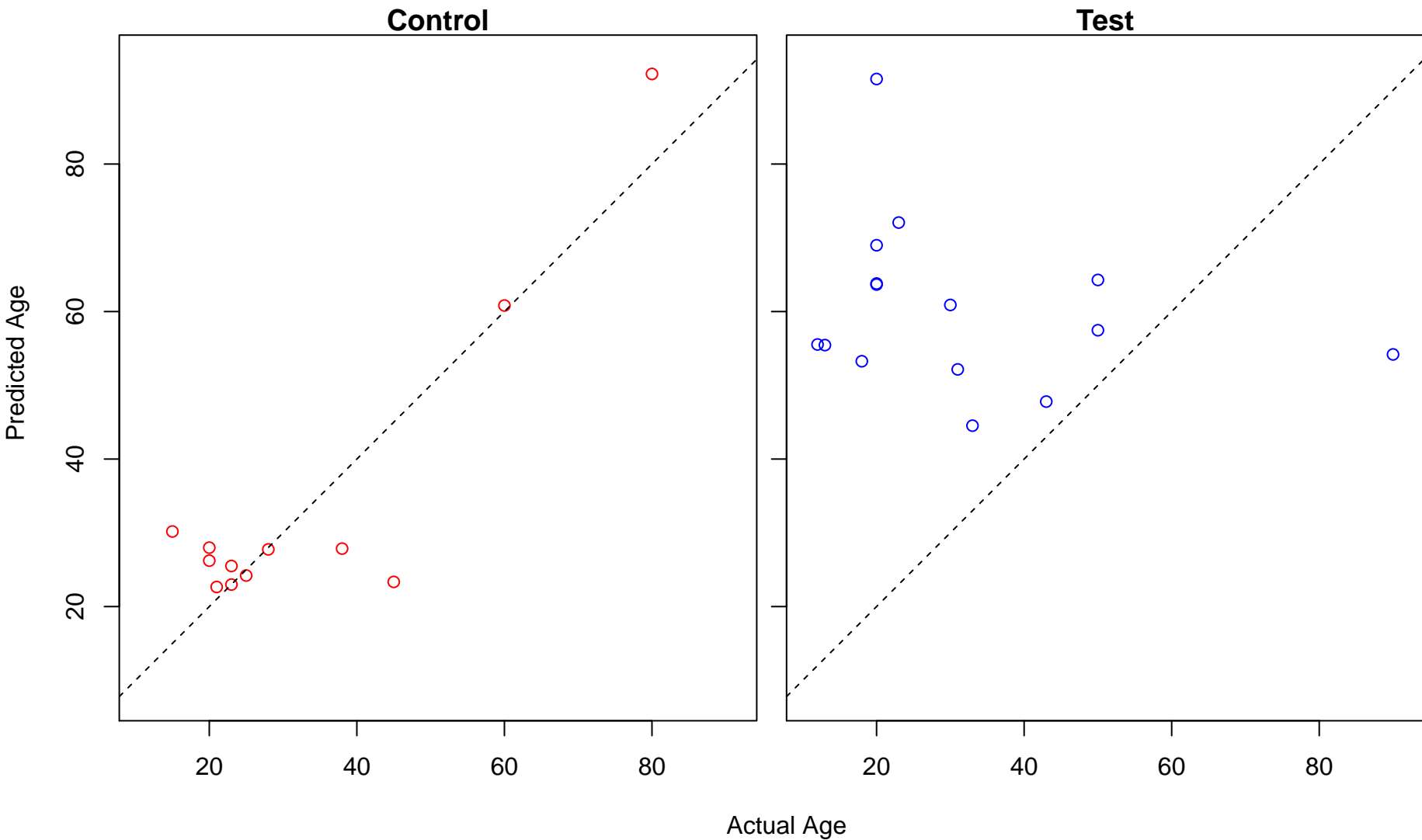
regulation of T-helper cell differentiation (Score: 5.995979)



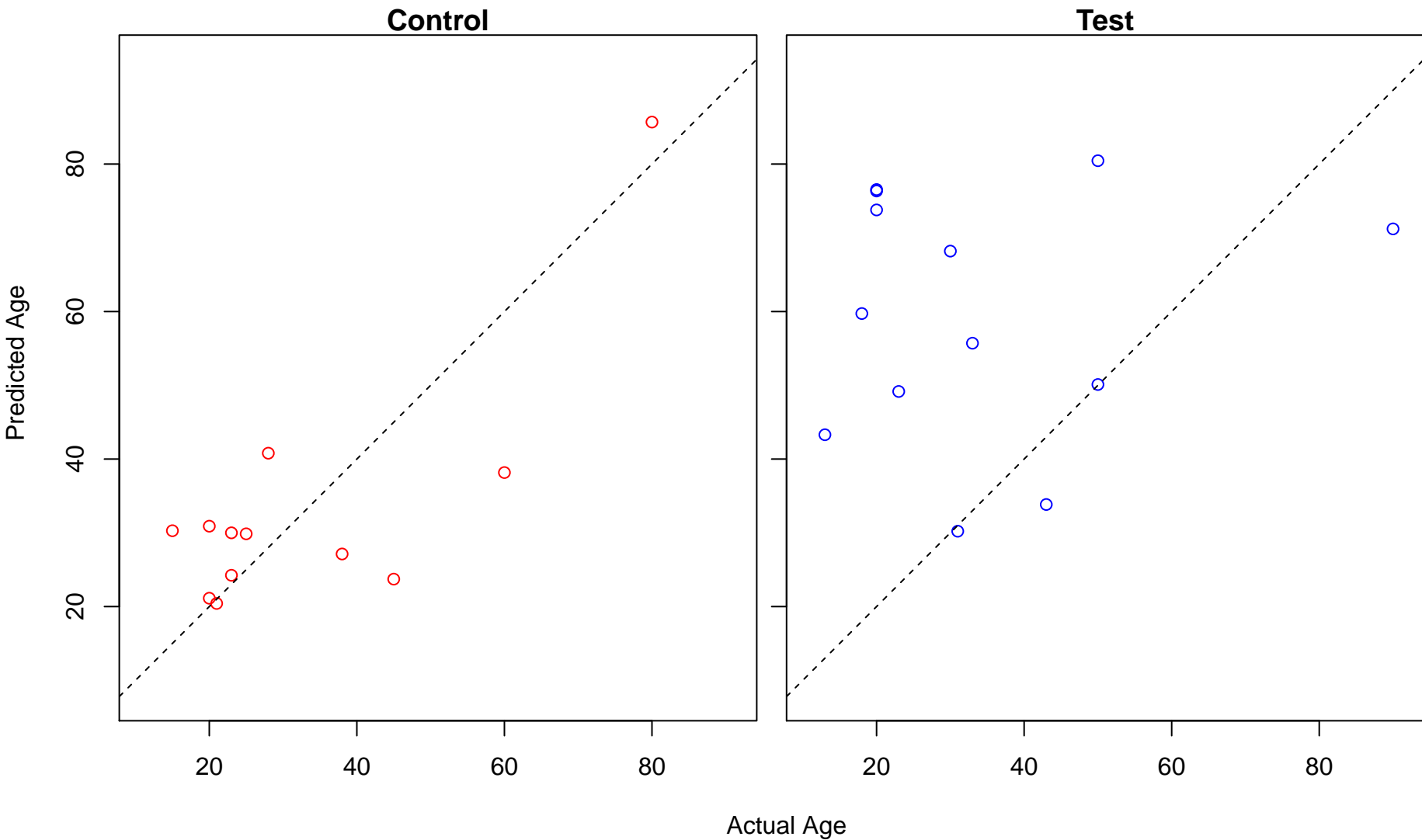
regulation of interleukin-6 biosynthetic process (Score: 5.994586)



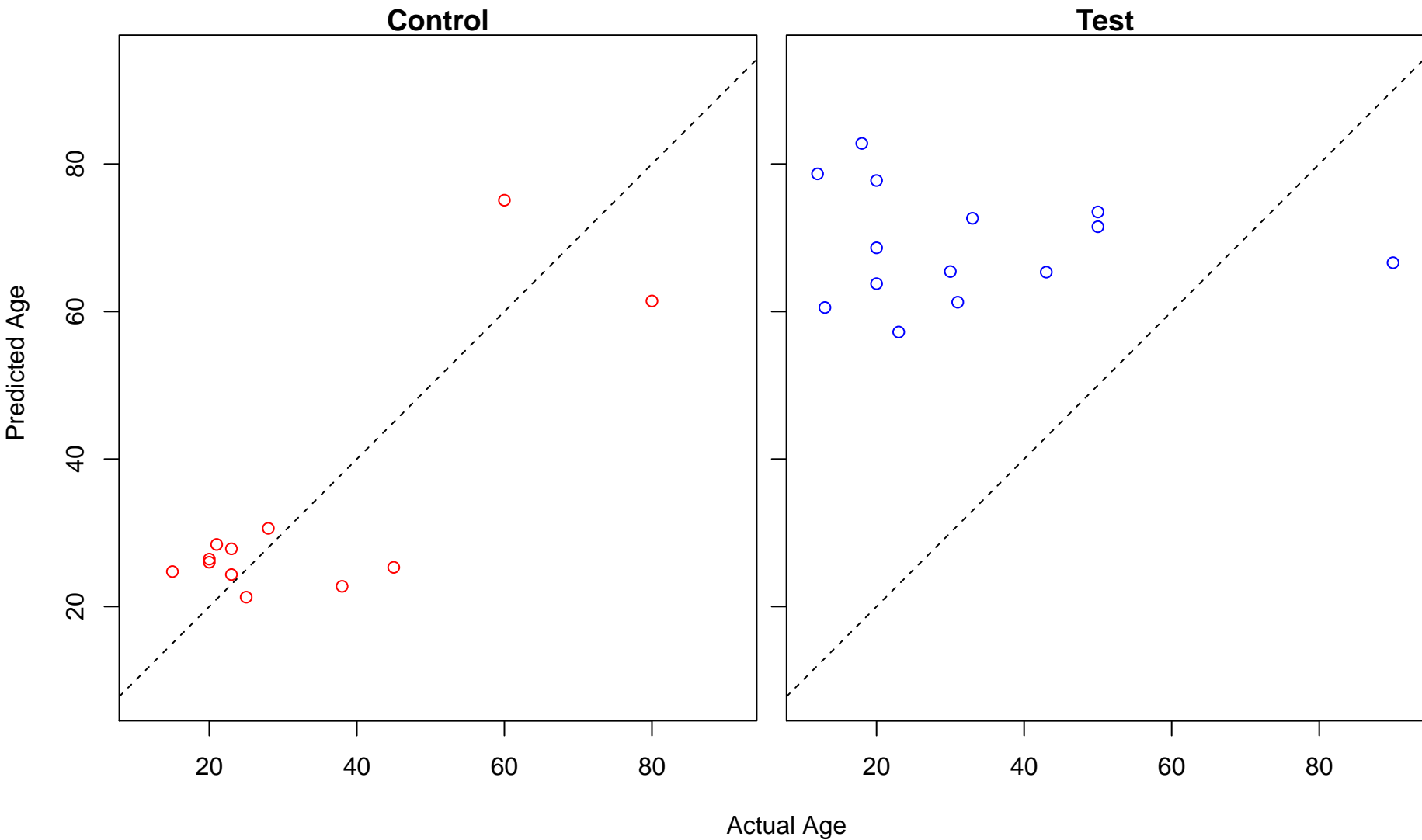
negative regulation of intracellular estrogen receptor signaling pathway (Score: 5.992955)



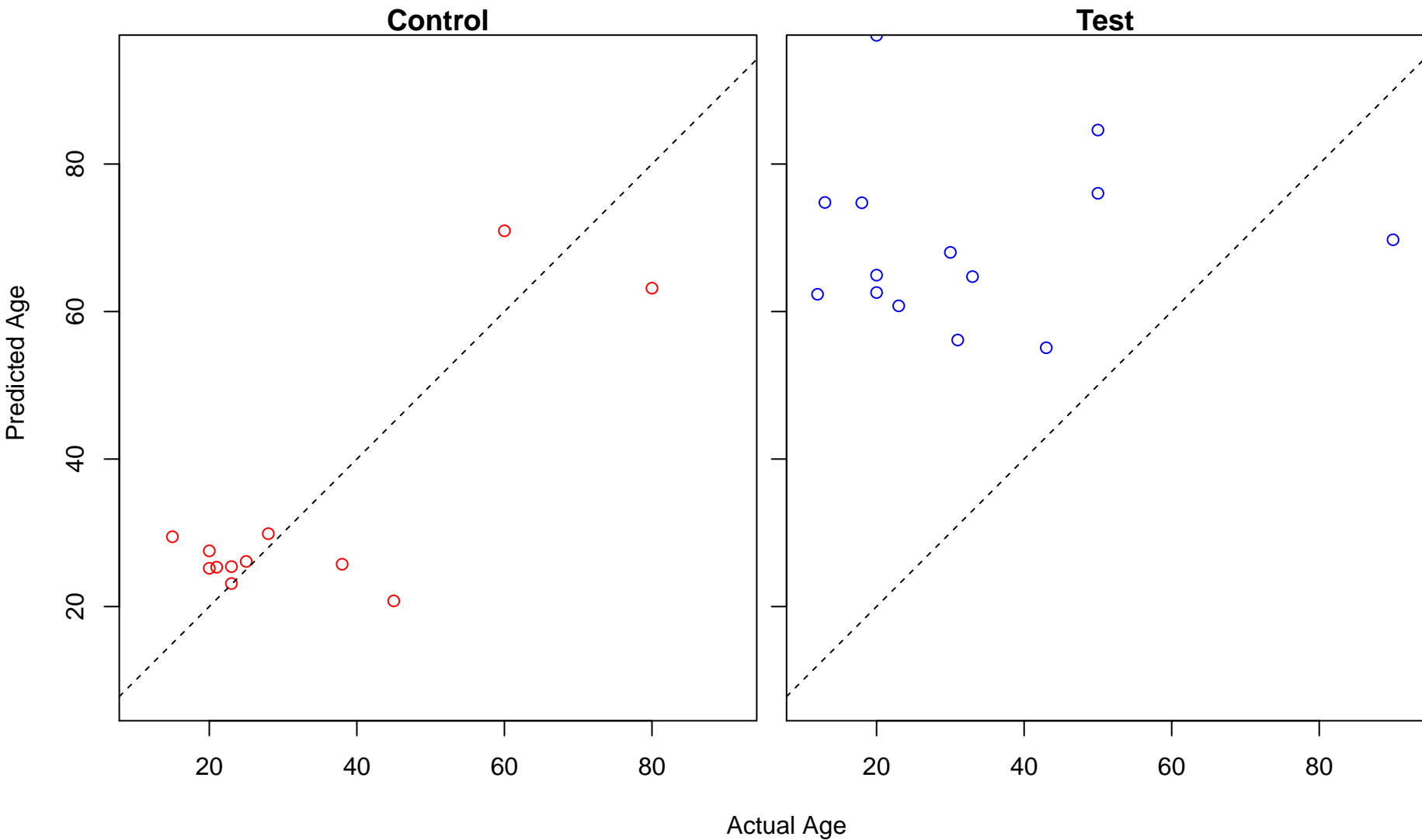
heart formation (Score: 5.992596)



positive regulation of extracellular matrix assembly (Score: 5.990973)

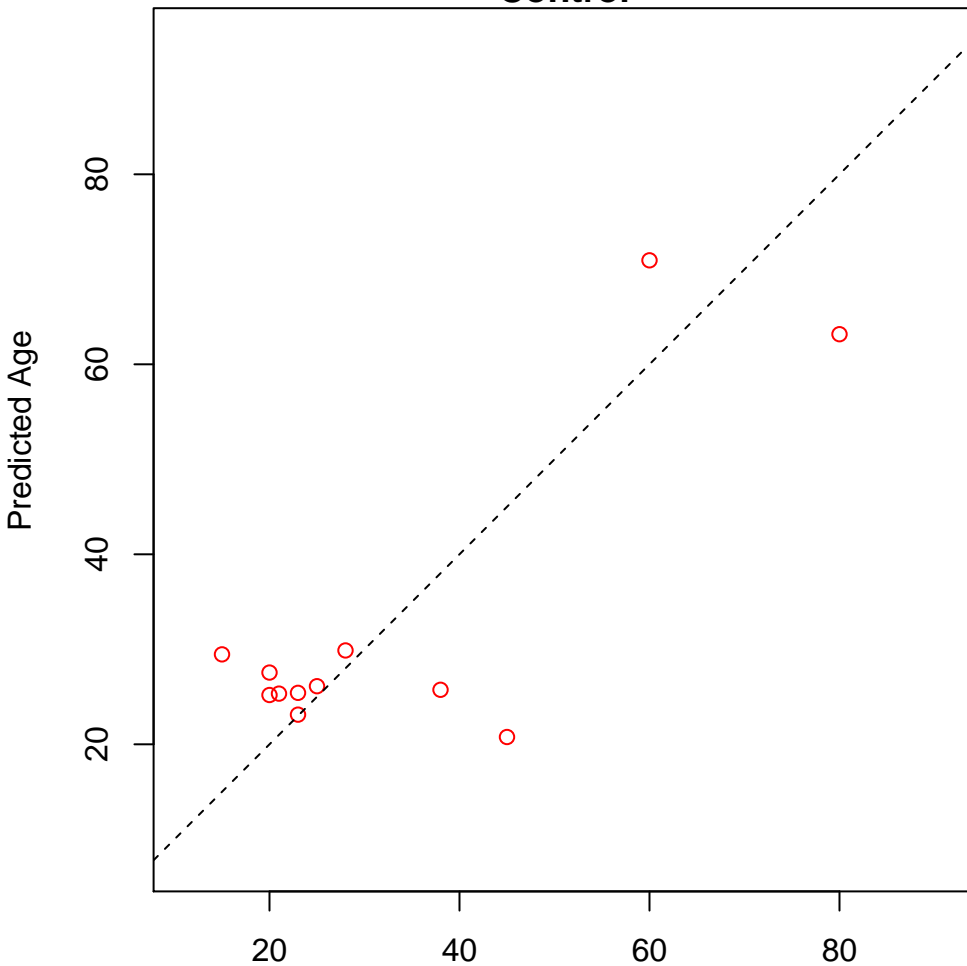


phosphate ion transport (Score: 5.989727)

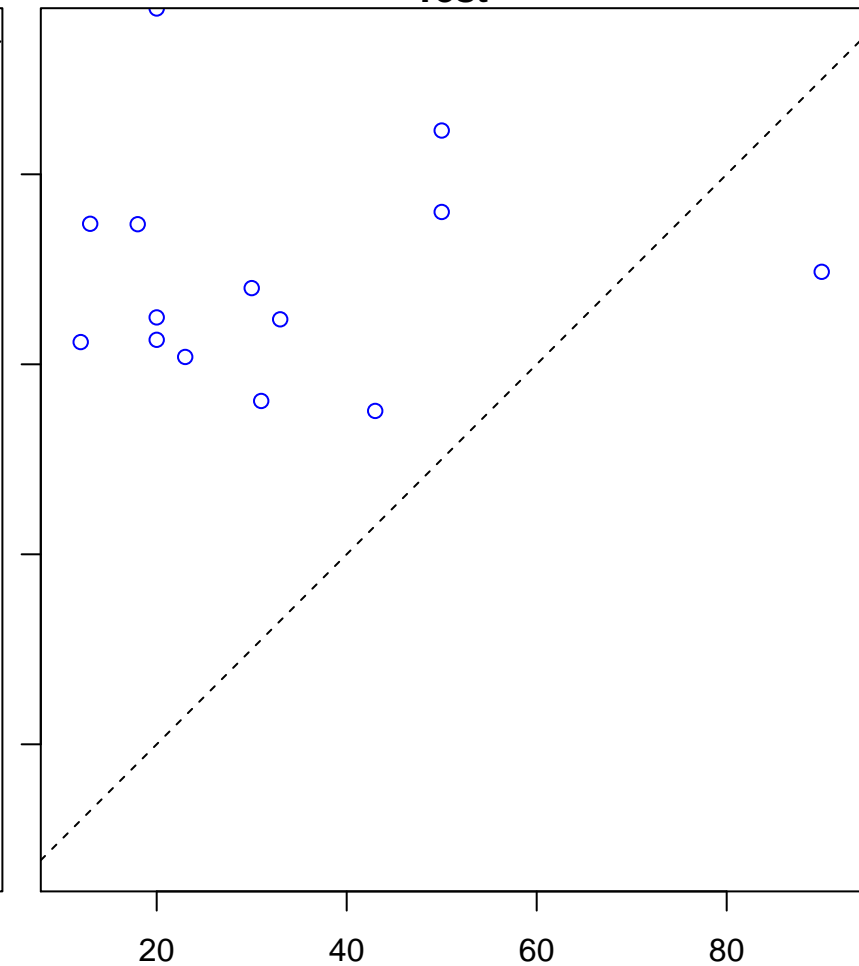


phosphate ion transmembrane transport (Score: 5.989727)

Control

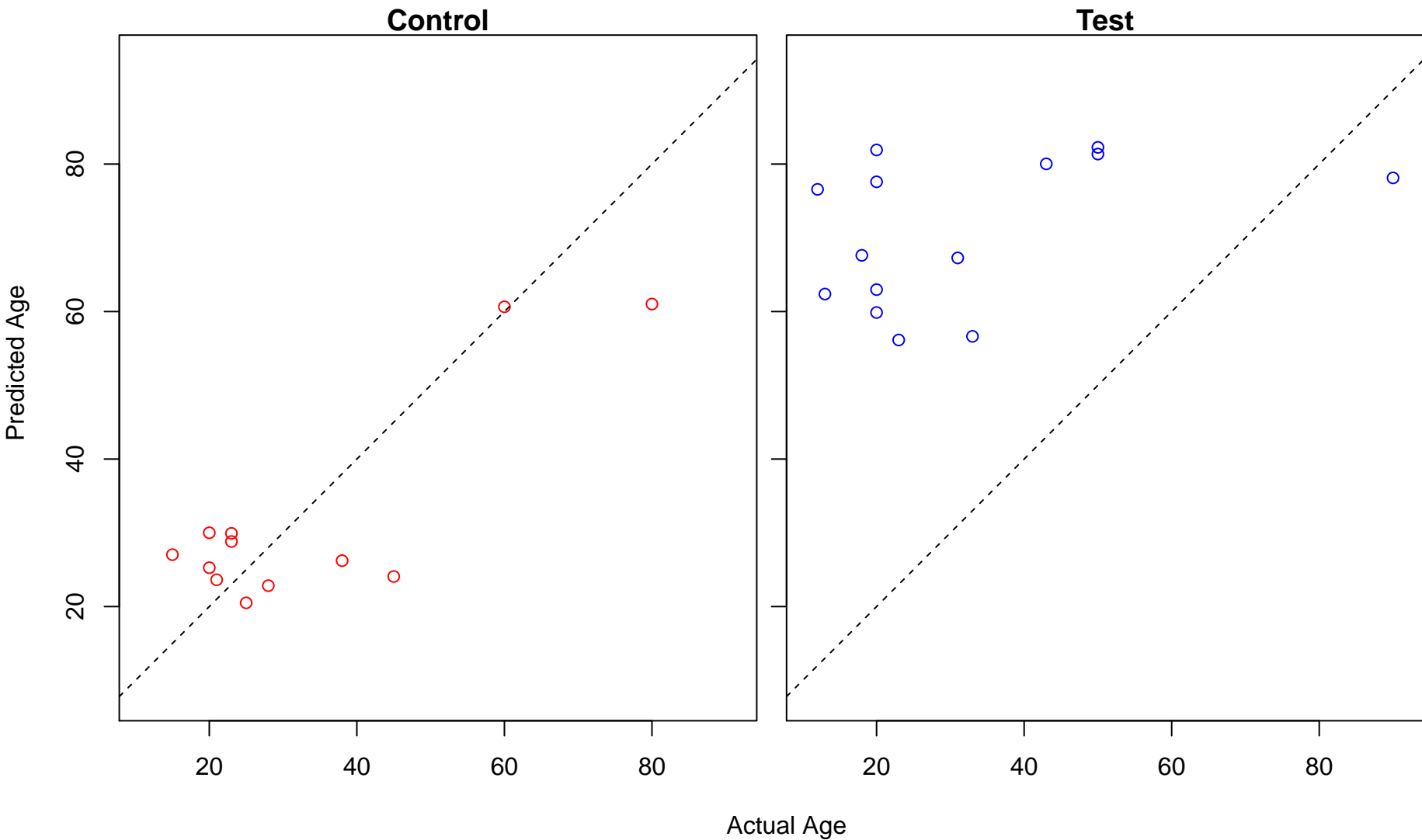


Test

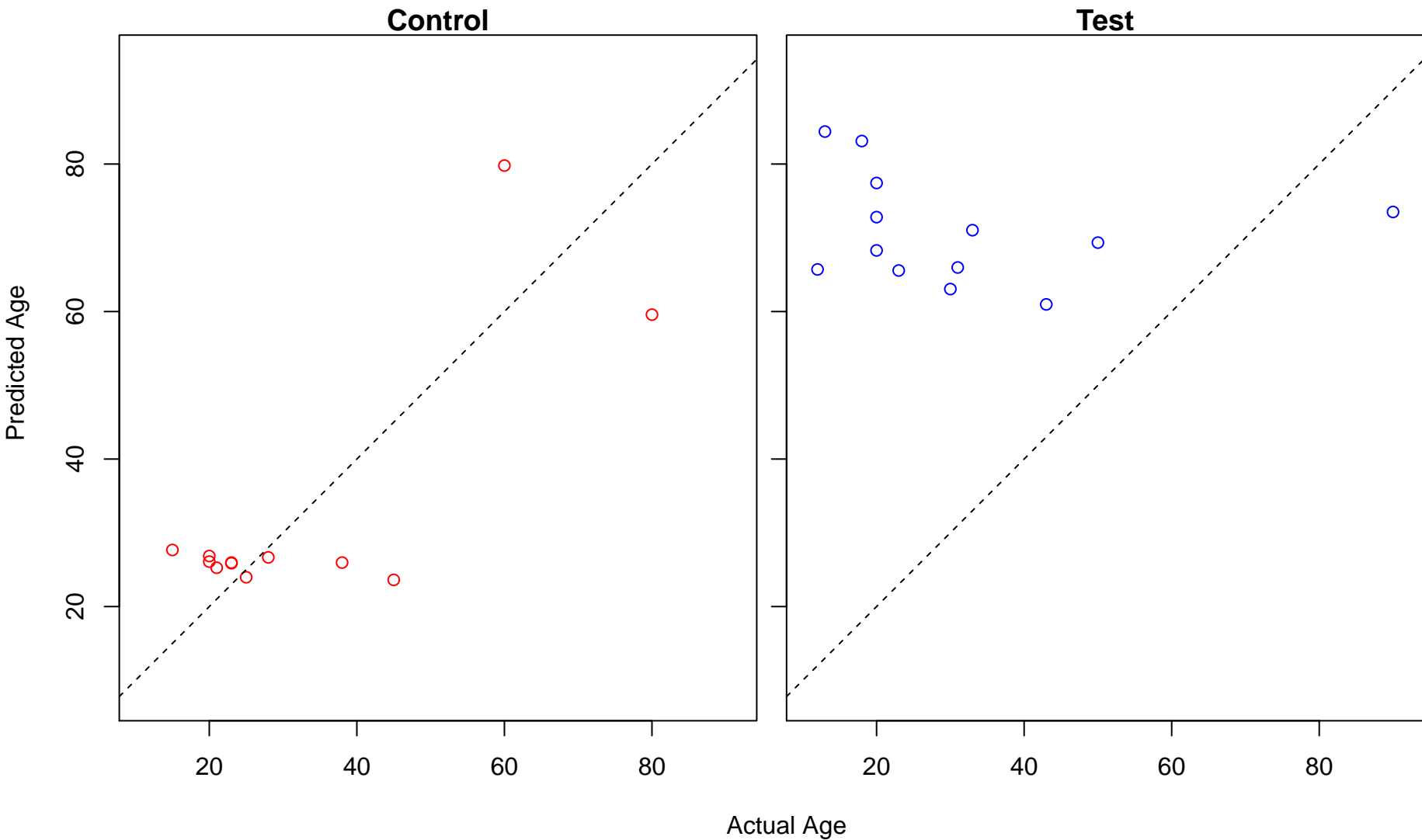


Actual Age

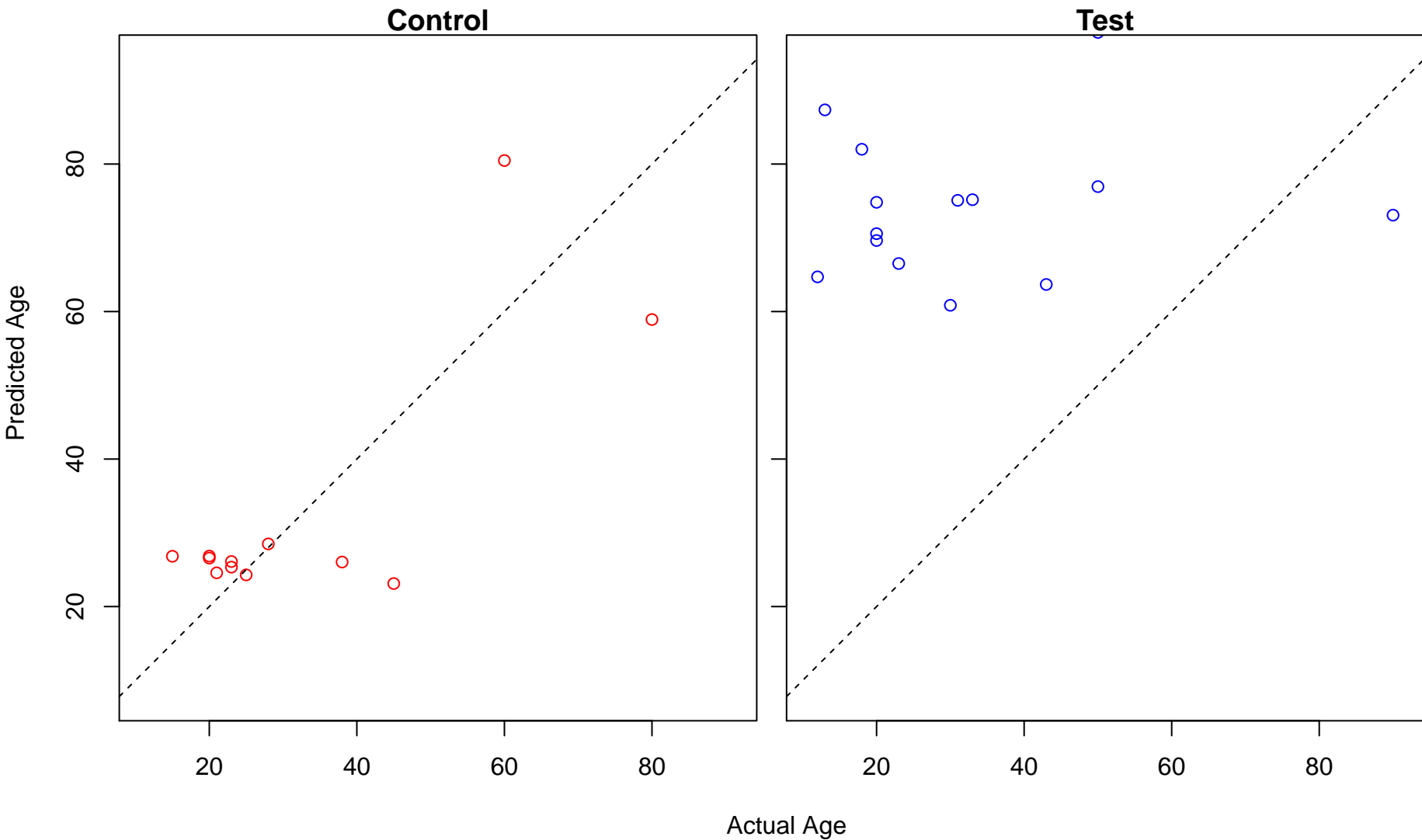
copper ion transmembrane transport (Score: 5.988593)



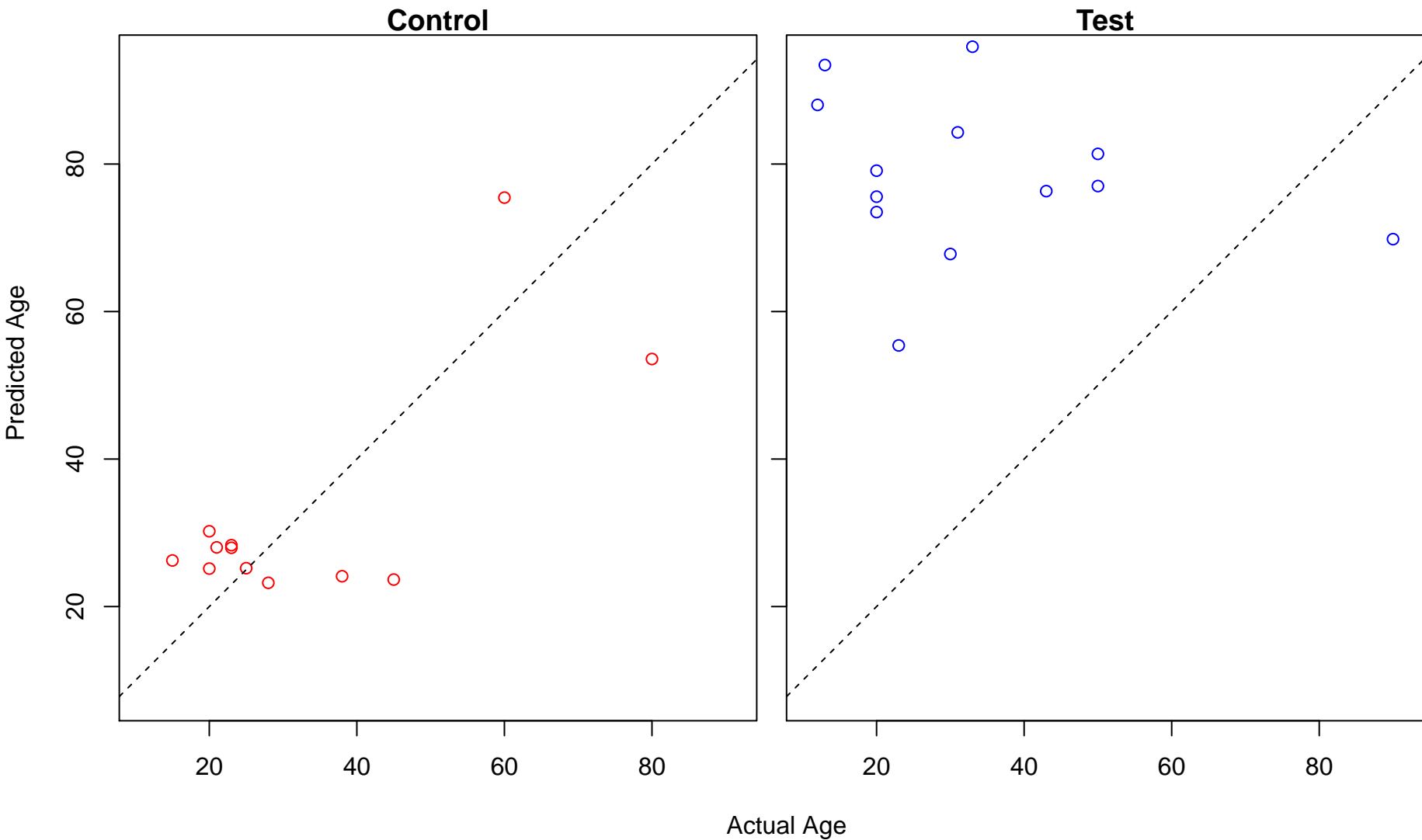
regulation of ligase activity (Score: 5.986141)



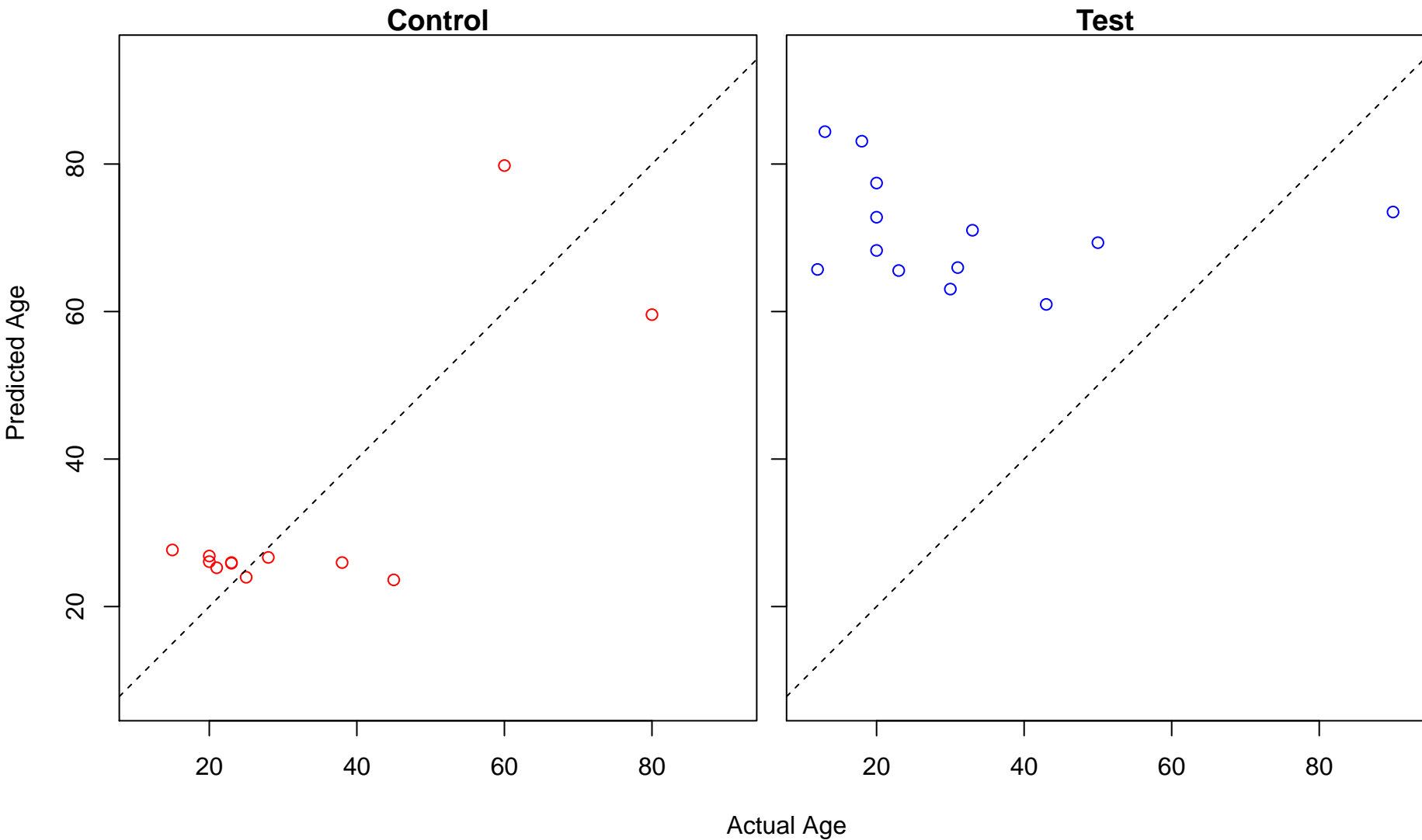
regulation of canonical Wnt signaling pathway (Score: 5.985627)



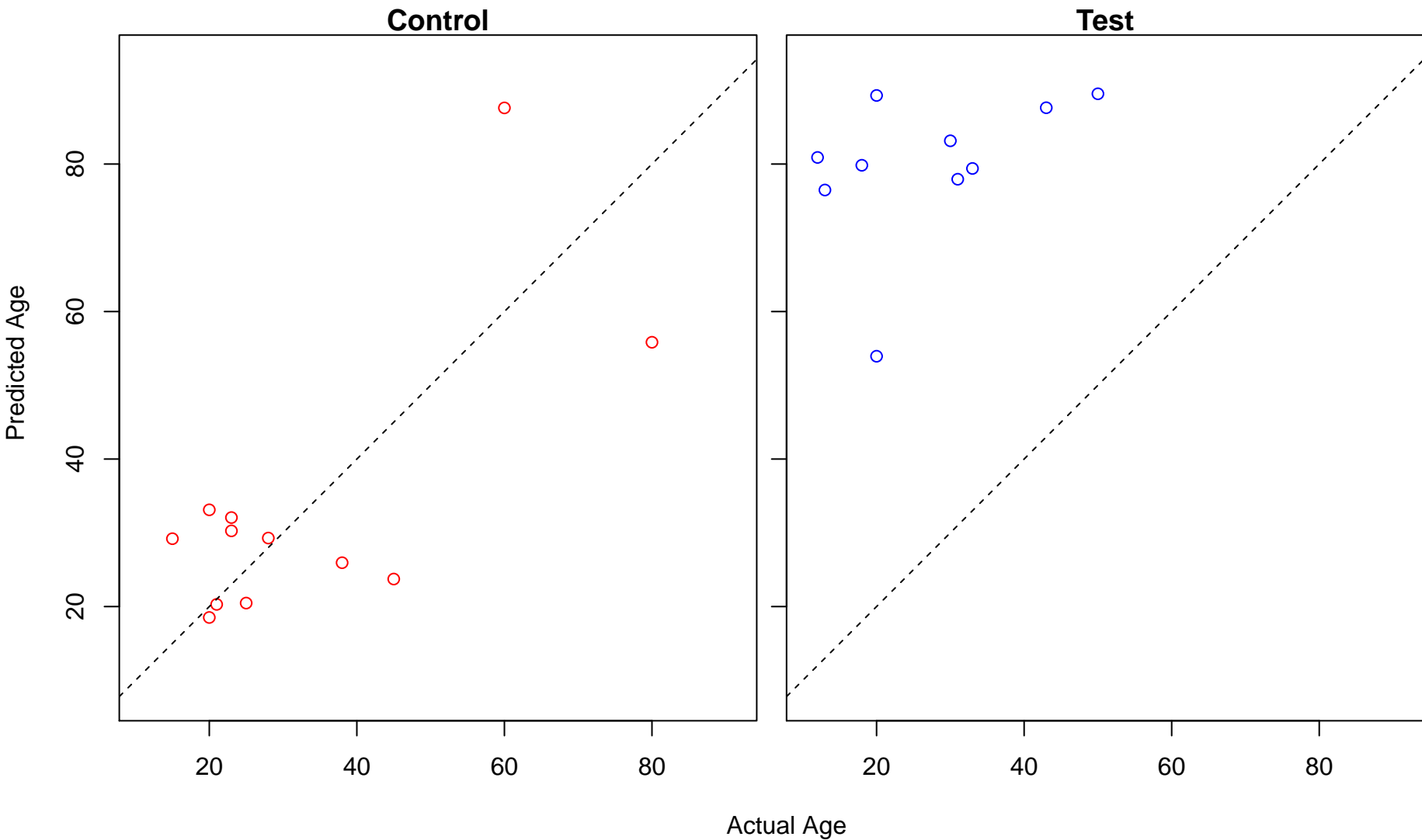
indole-containing compound metabolic process (Score: 5.985236)



regulation of ubiquitin–protein transferase activity (Score: 5.983418)

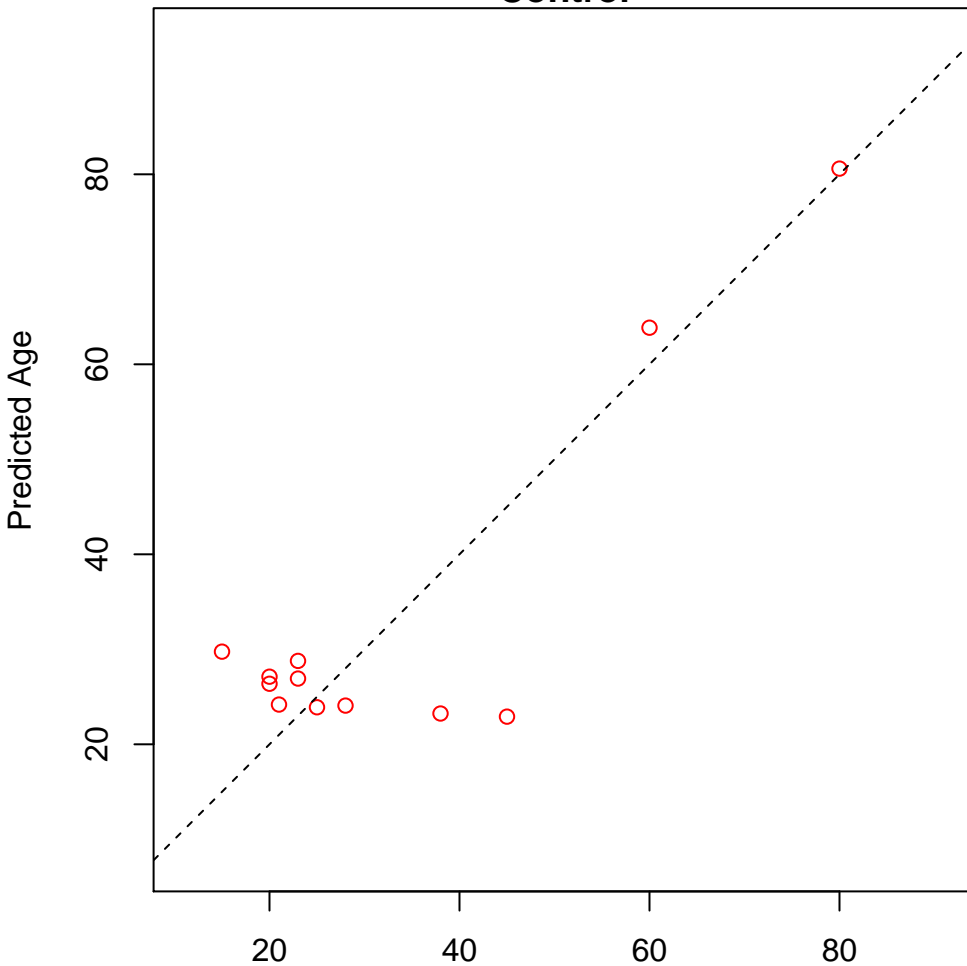


RNA surveillance (Score: 5.982165)

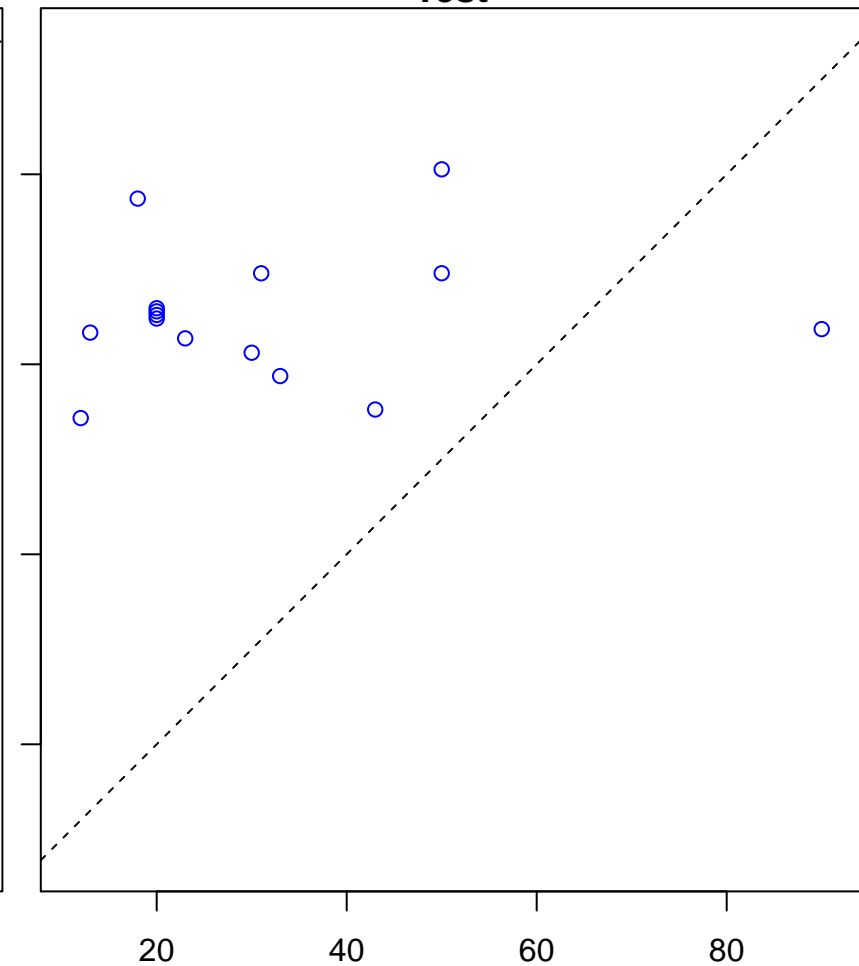


regulation of dendritic spine development (Score: 5.980644)

Control



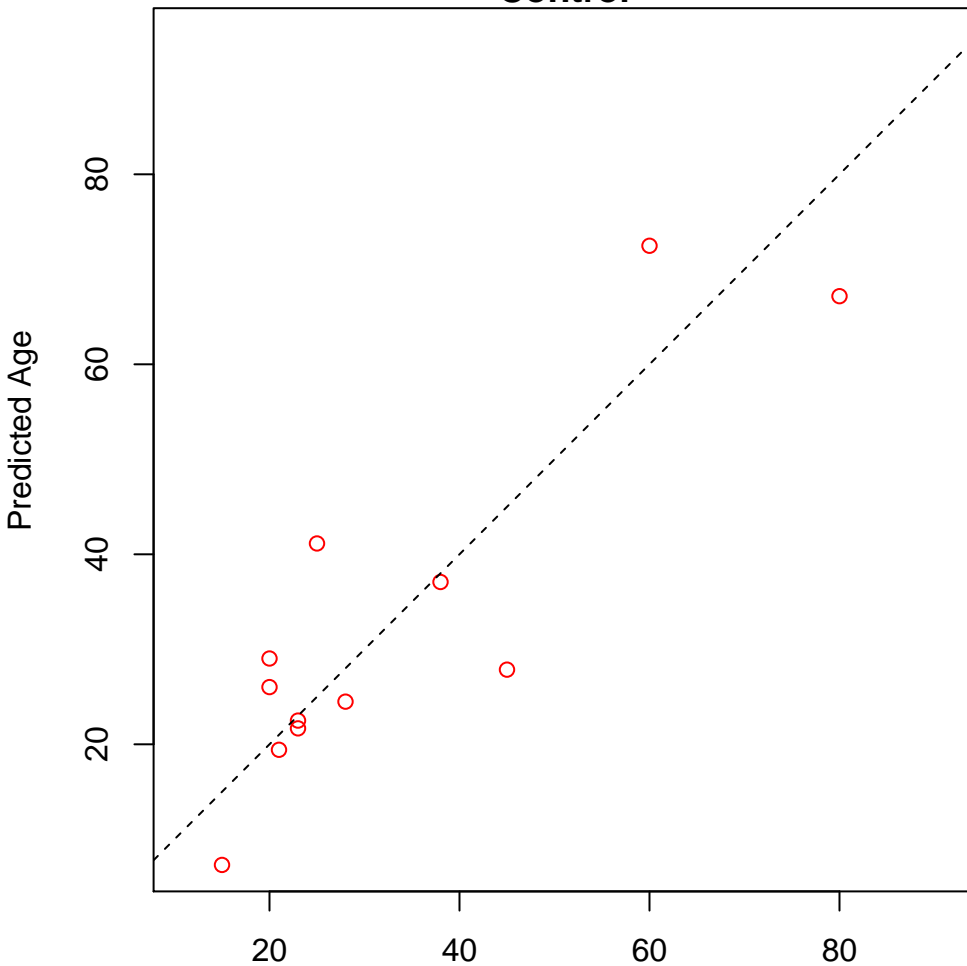
Test



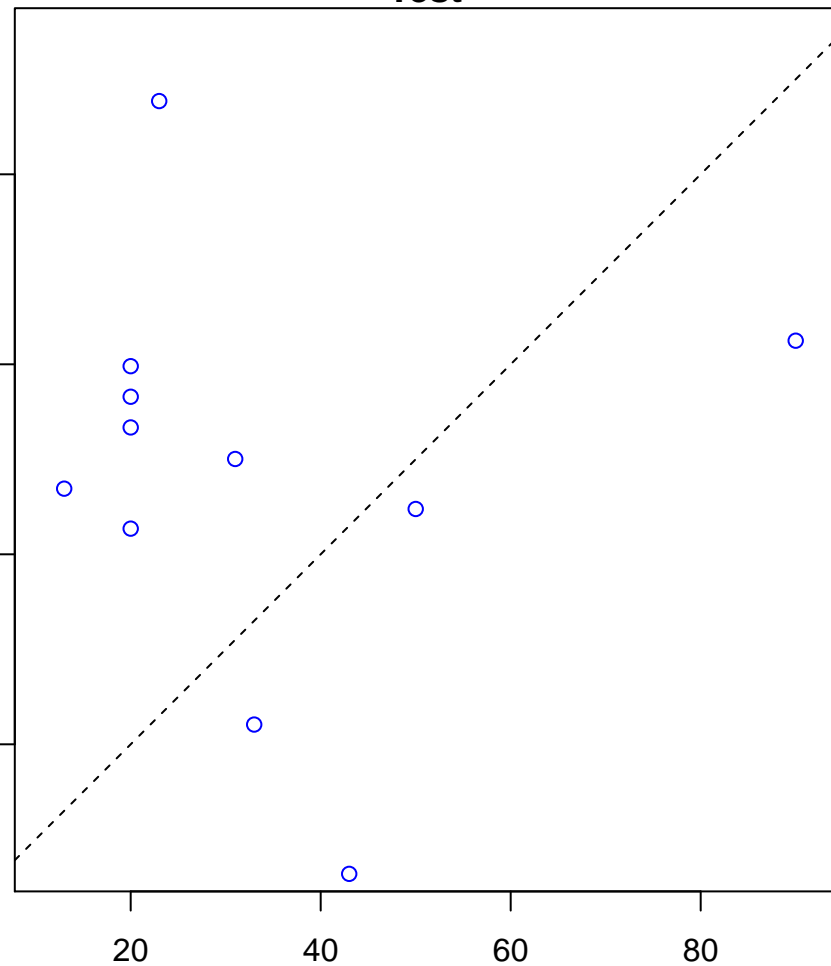
Actual Age

short-chain fatty acid catabolic process (Score: 5.978167)

Control

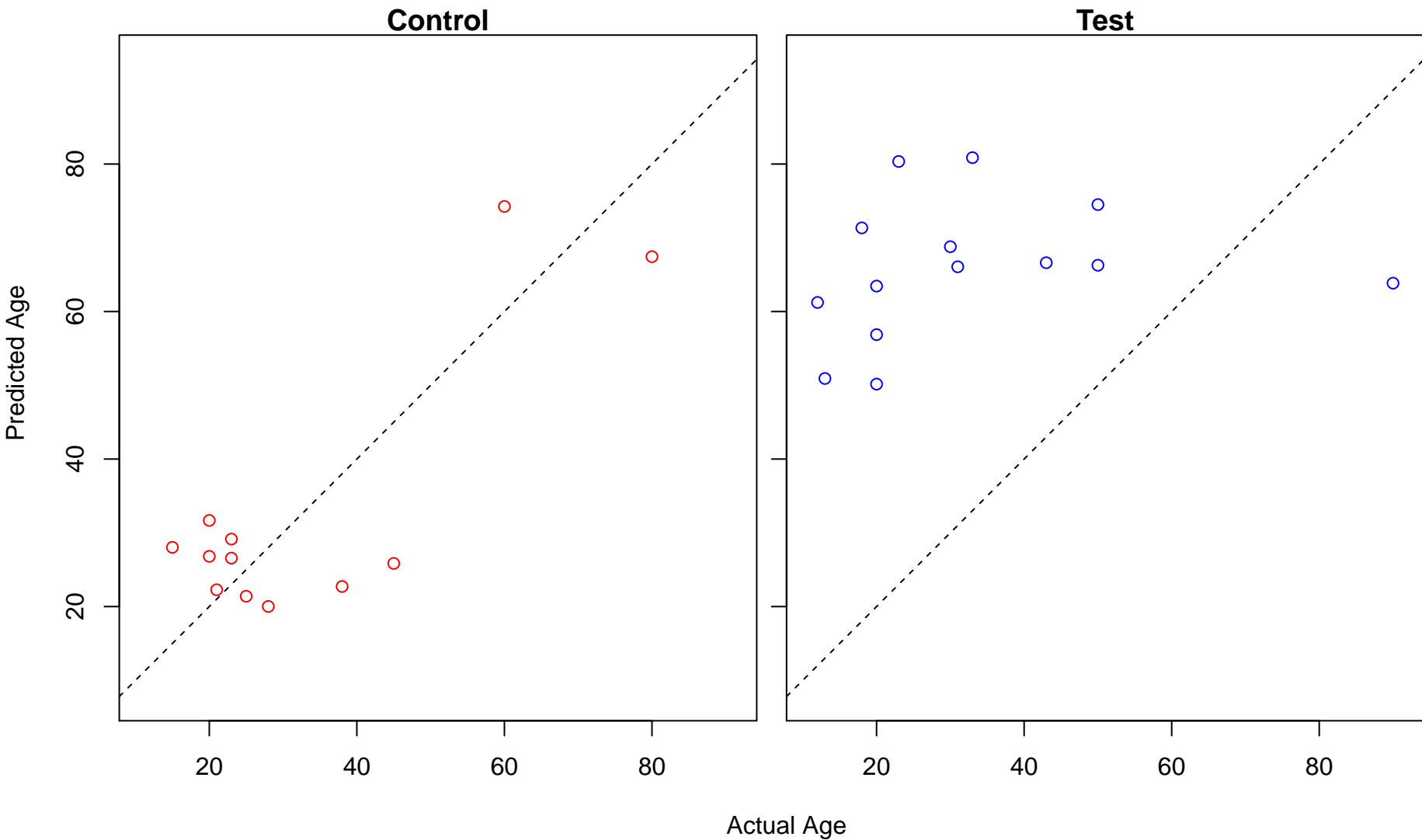


Test

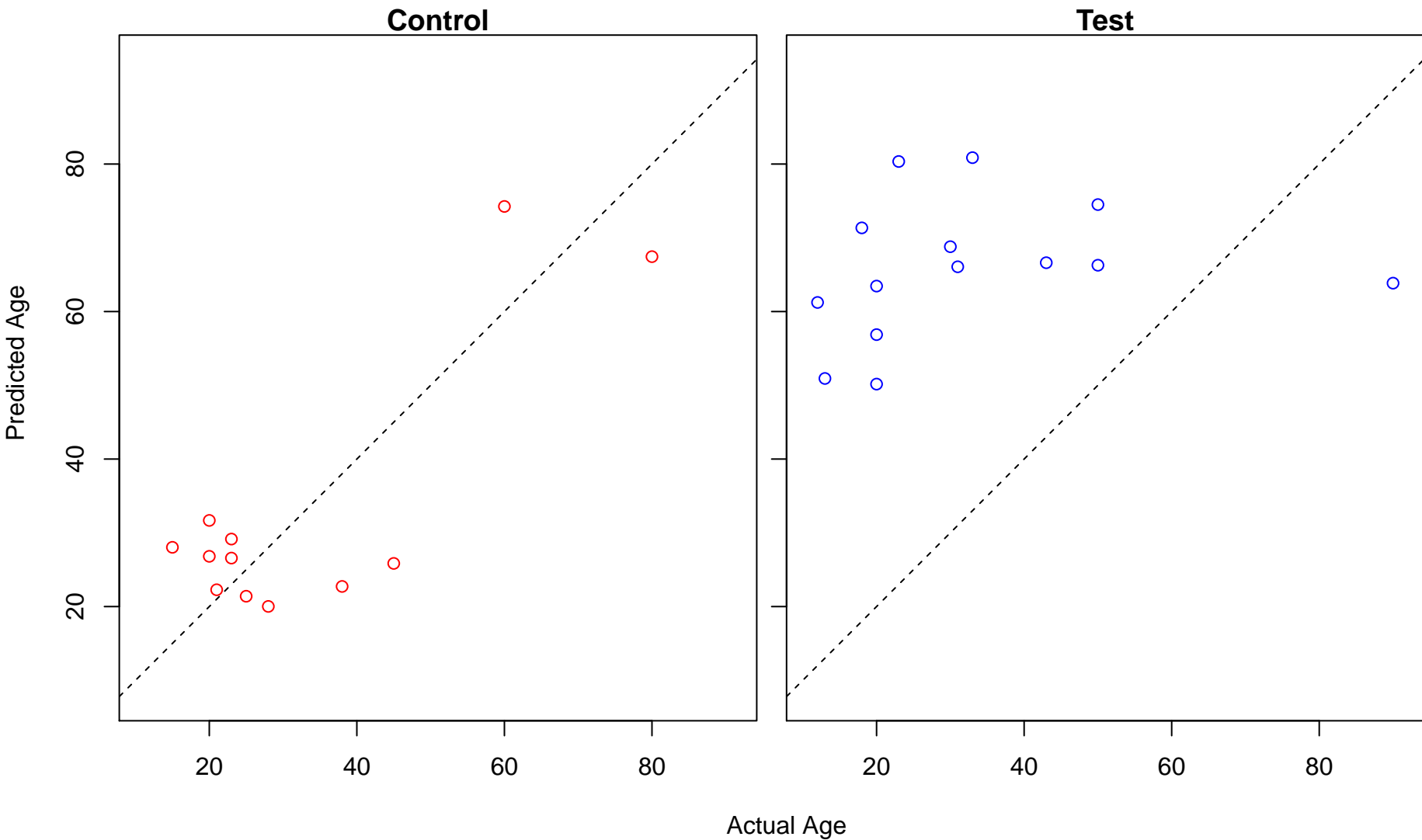


Actual Age

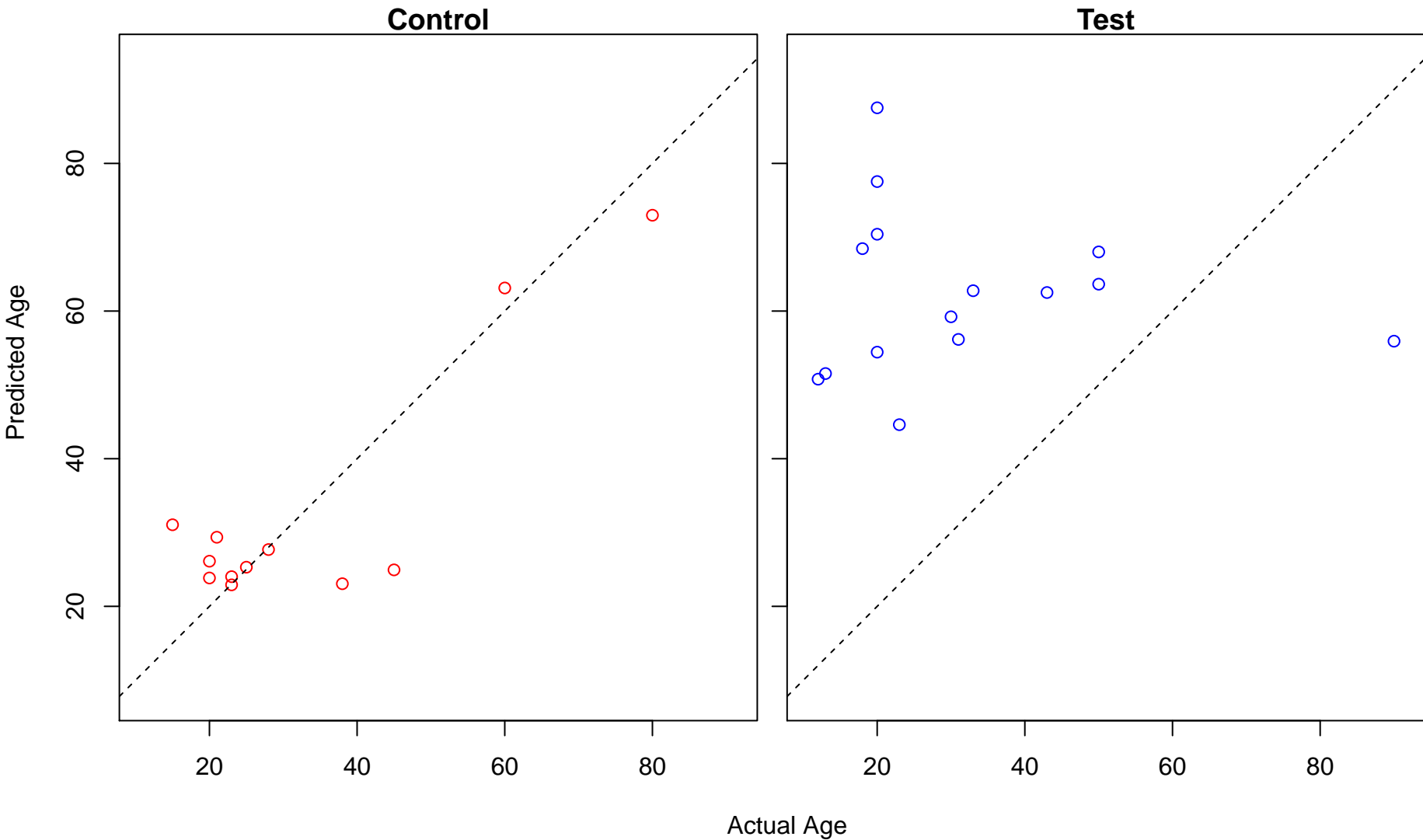
regulation of immature T cell proliferation (Score: 5.977744)



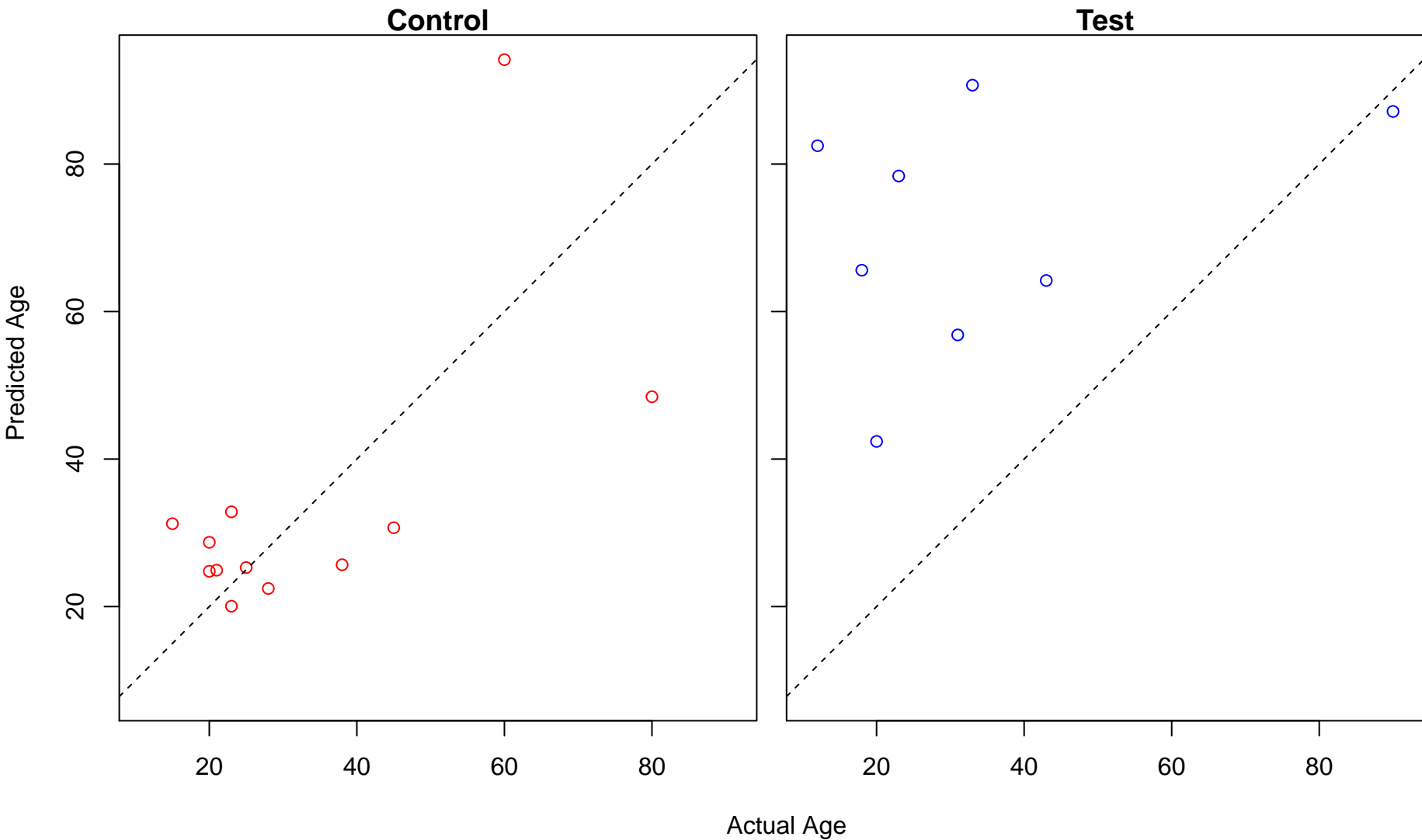
regulation of immature T cell proliferation in thymus (Score: 5.977744)



regulation of substrate adhesion-dependent cell spreading (Score: 5.976197)

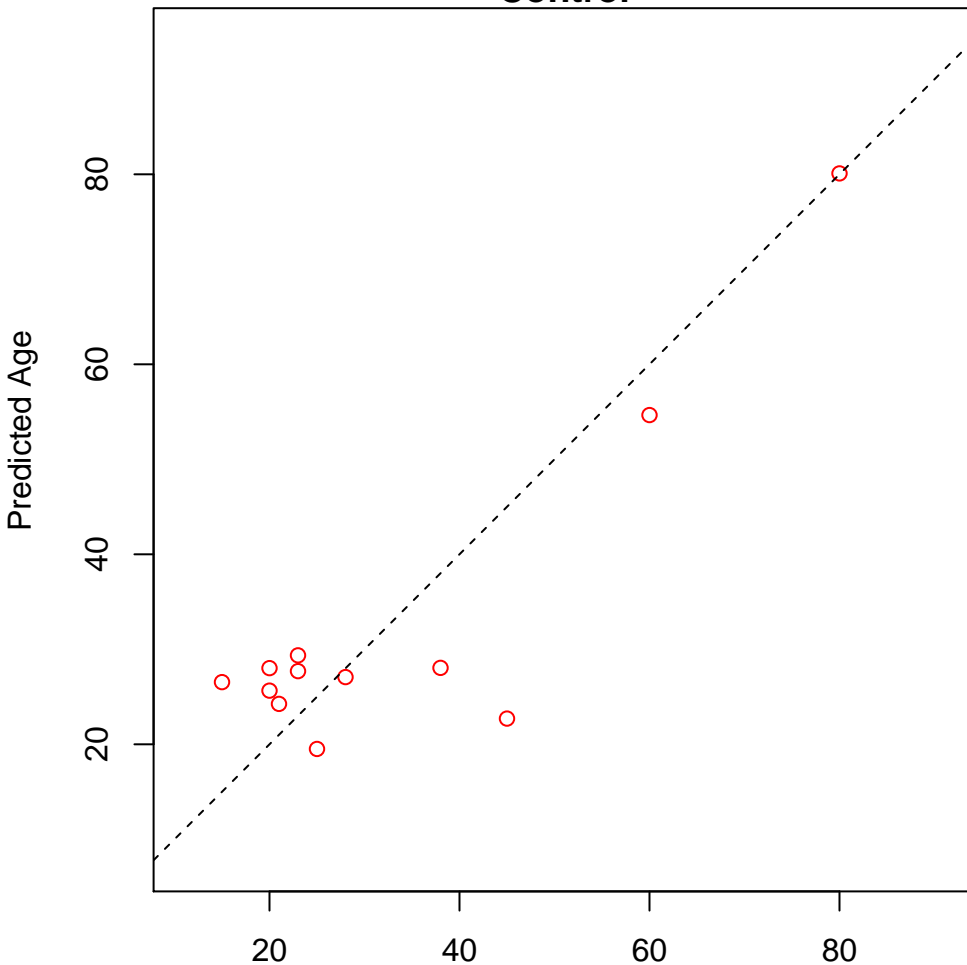


vascular endothelial growth factor signaling pathway (Score: 5.973617)

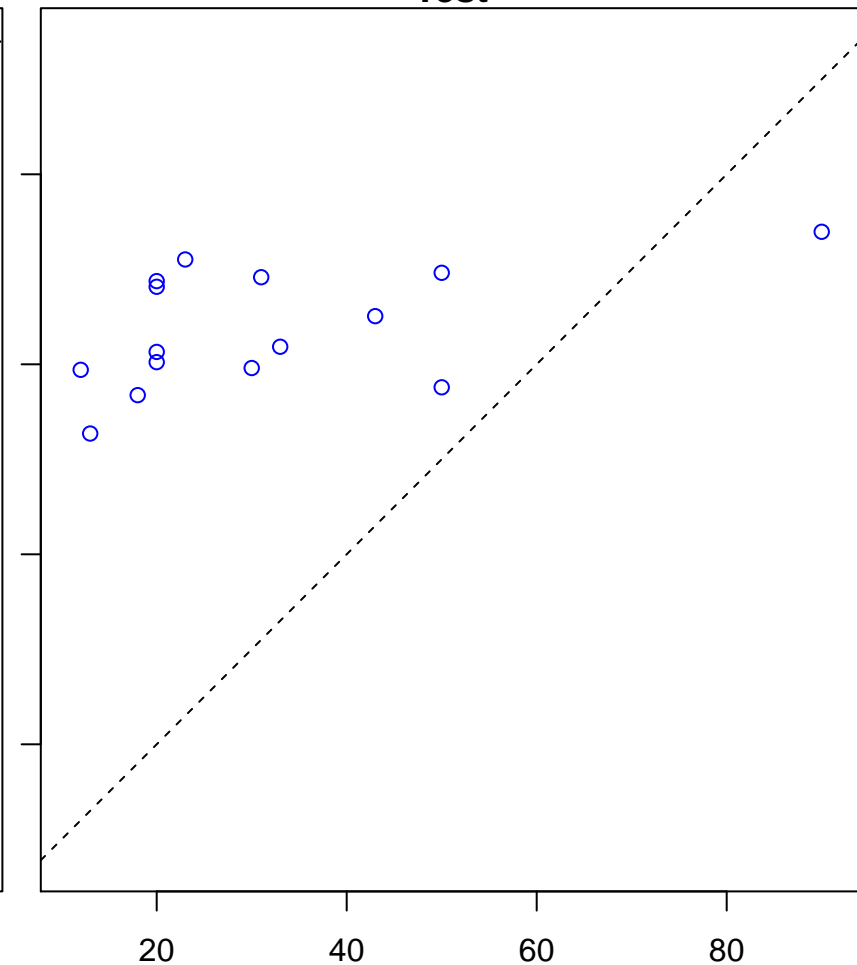


microtubule cytoskeleton organization (Score: 5.970234)

Control

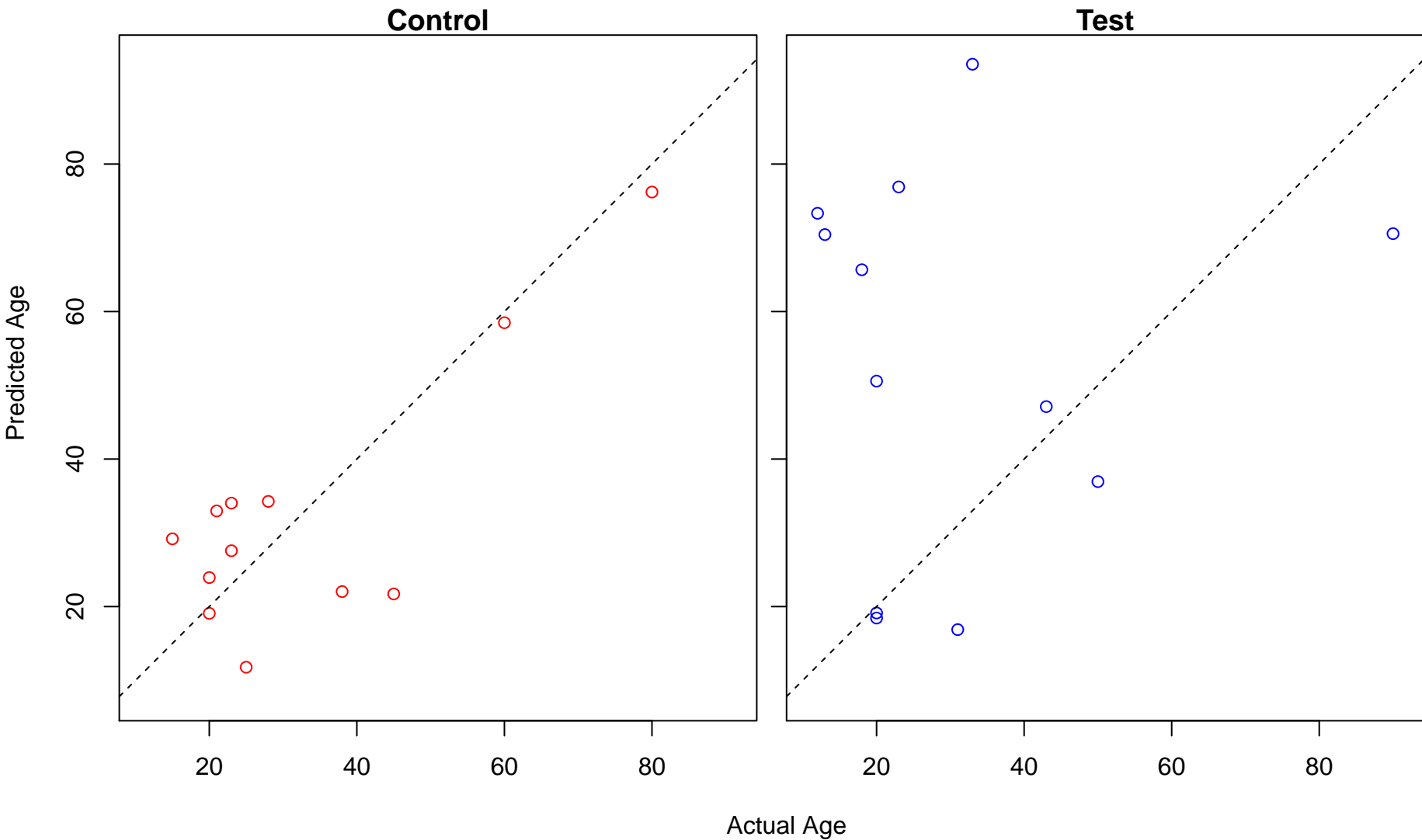


Test

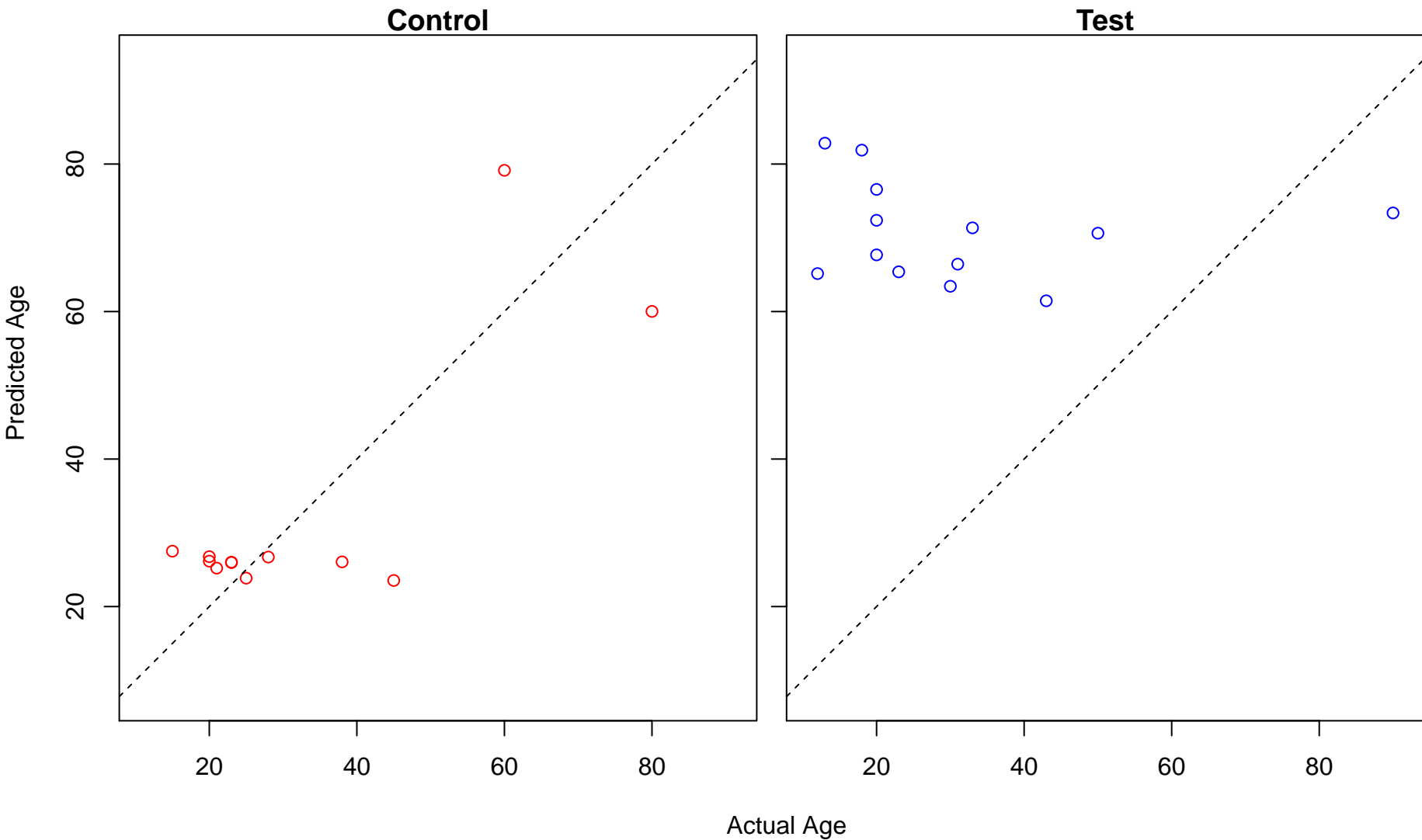


Actual Age

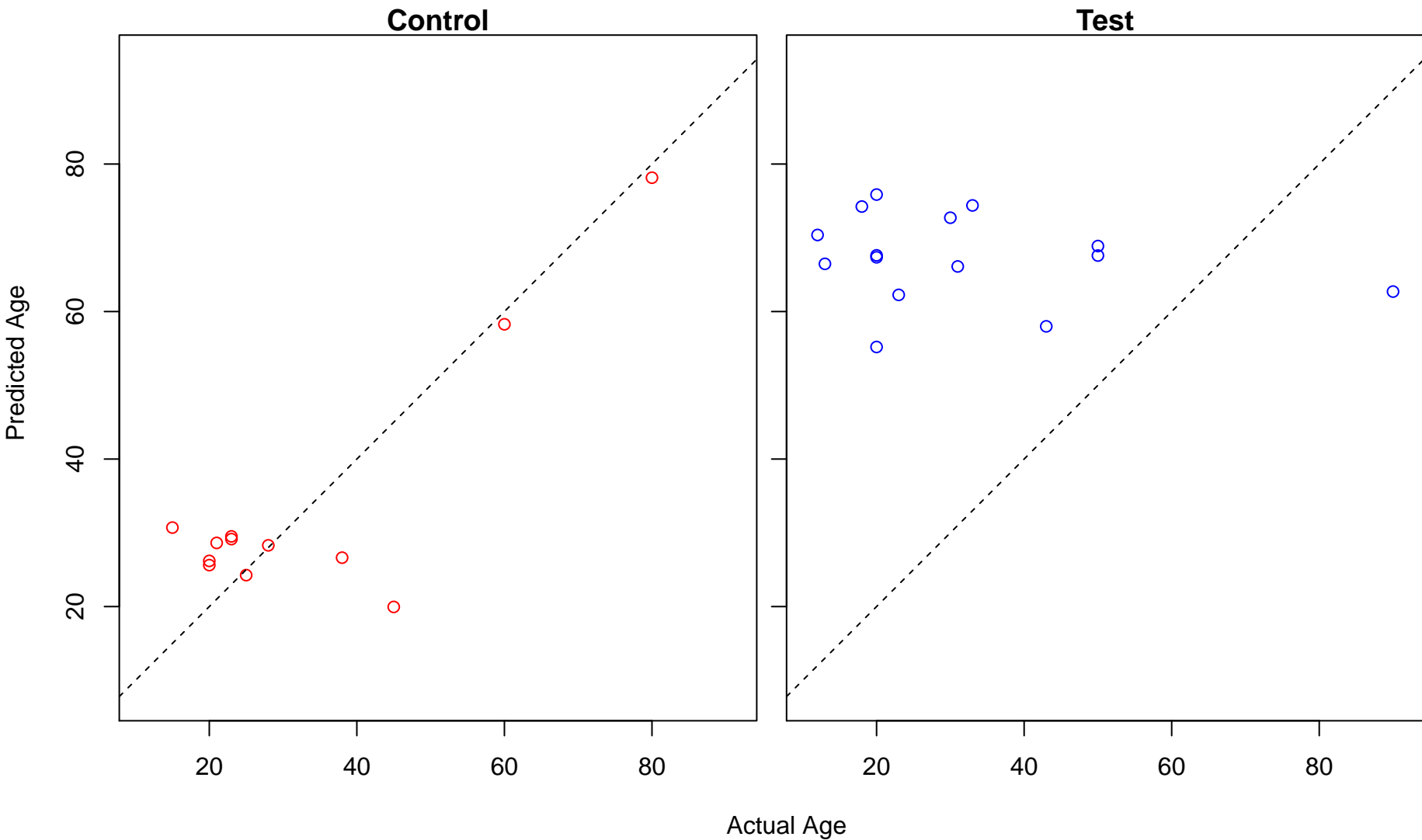
regulation of androgen receptor signaling pathway (Score: 5.967586)



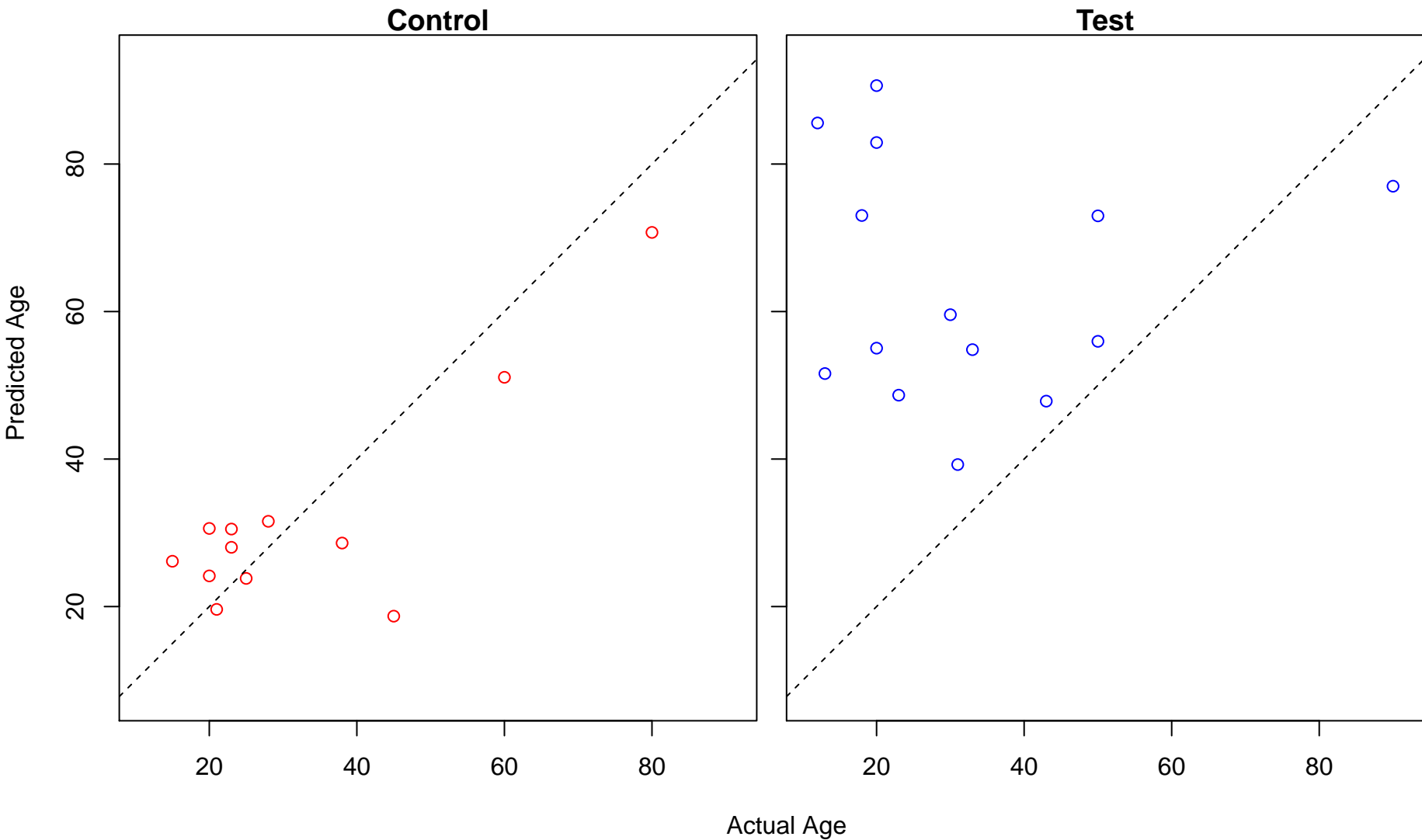
regulation of mitotic cell cycle phase transition (Score: 5.967501)



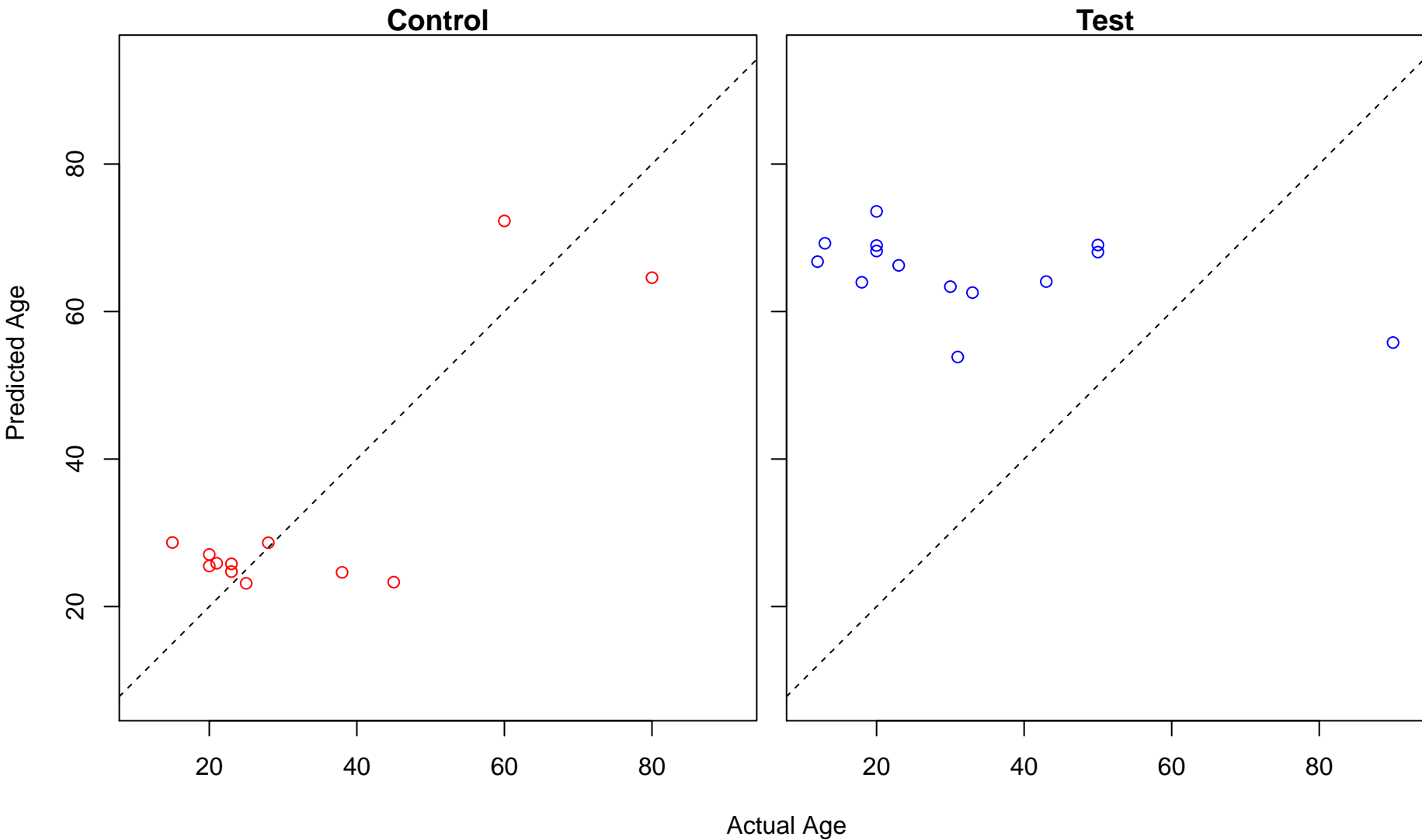
positive regulation of SMAD protein import into nucleus (Score: 5.966072)



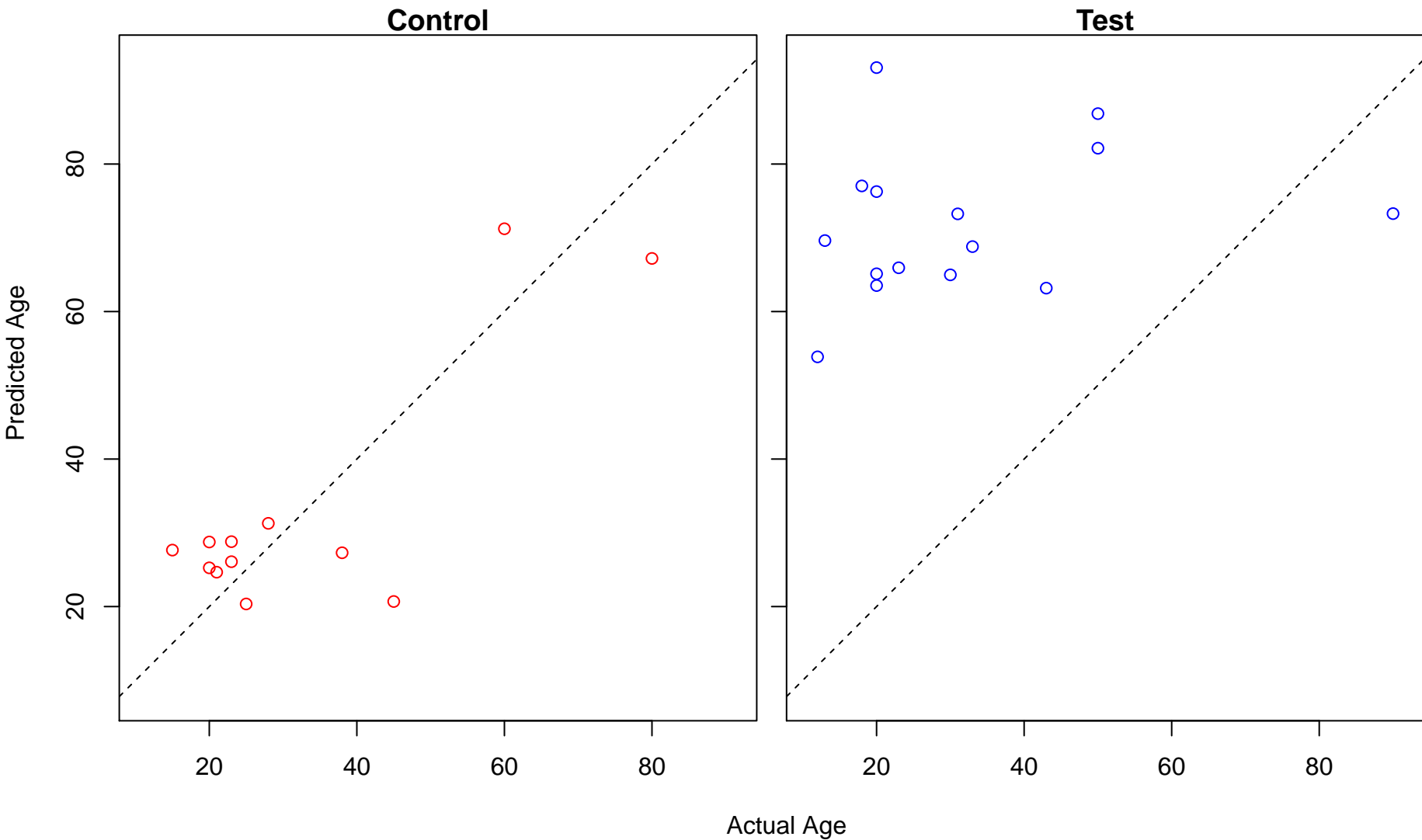
cell migration involved in heart development (Score: 5.964552)



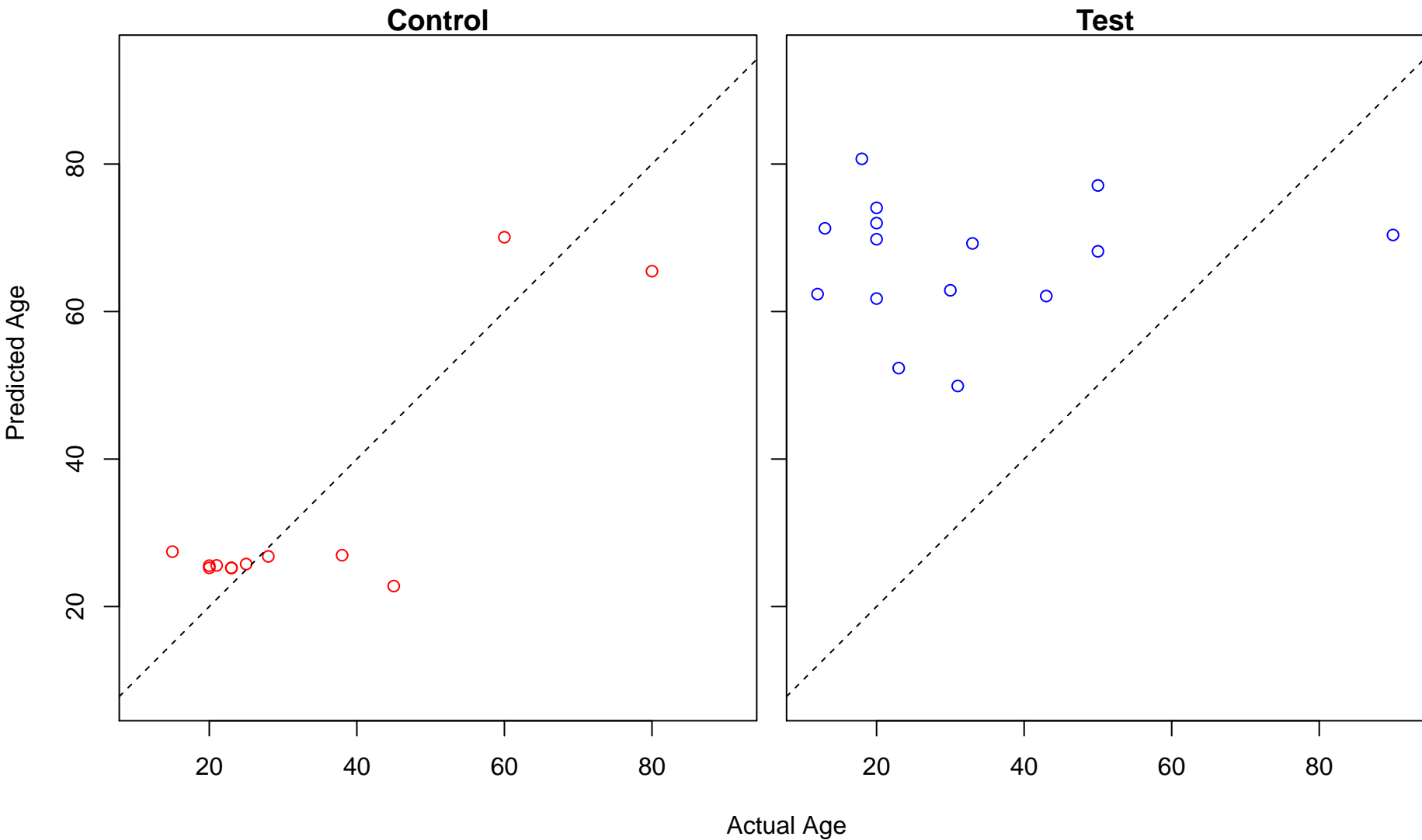
negative regulation of muscle contraction (Score: 5.958523)



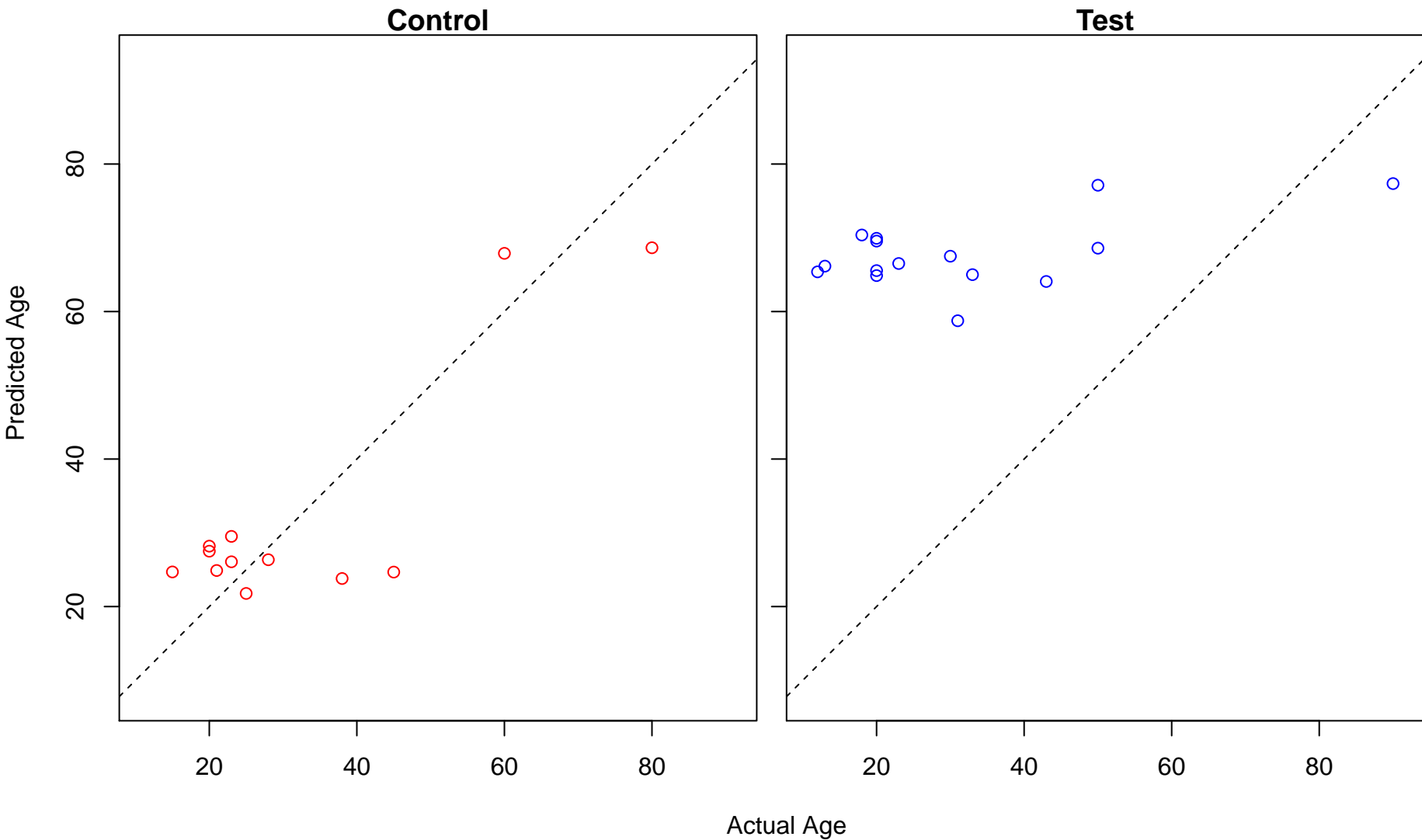
regulation of leukocyte proliferation (Score: 5.958509)



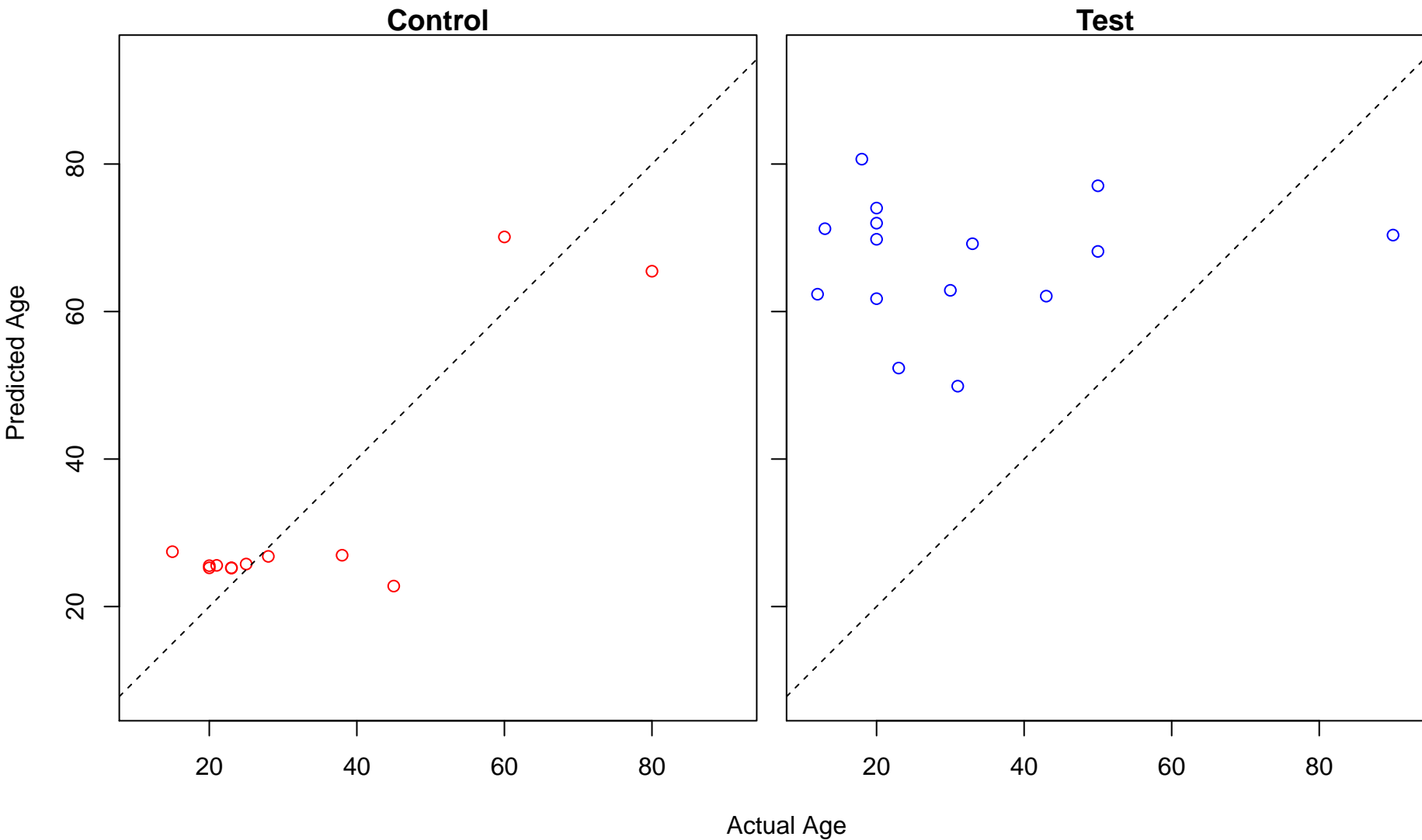
negative regulation of peptidyl-lysine acetylation (Score: 5.956495)



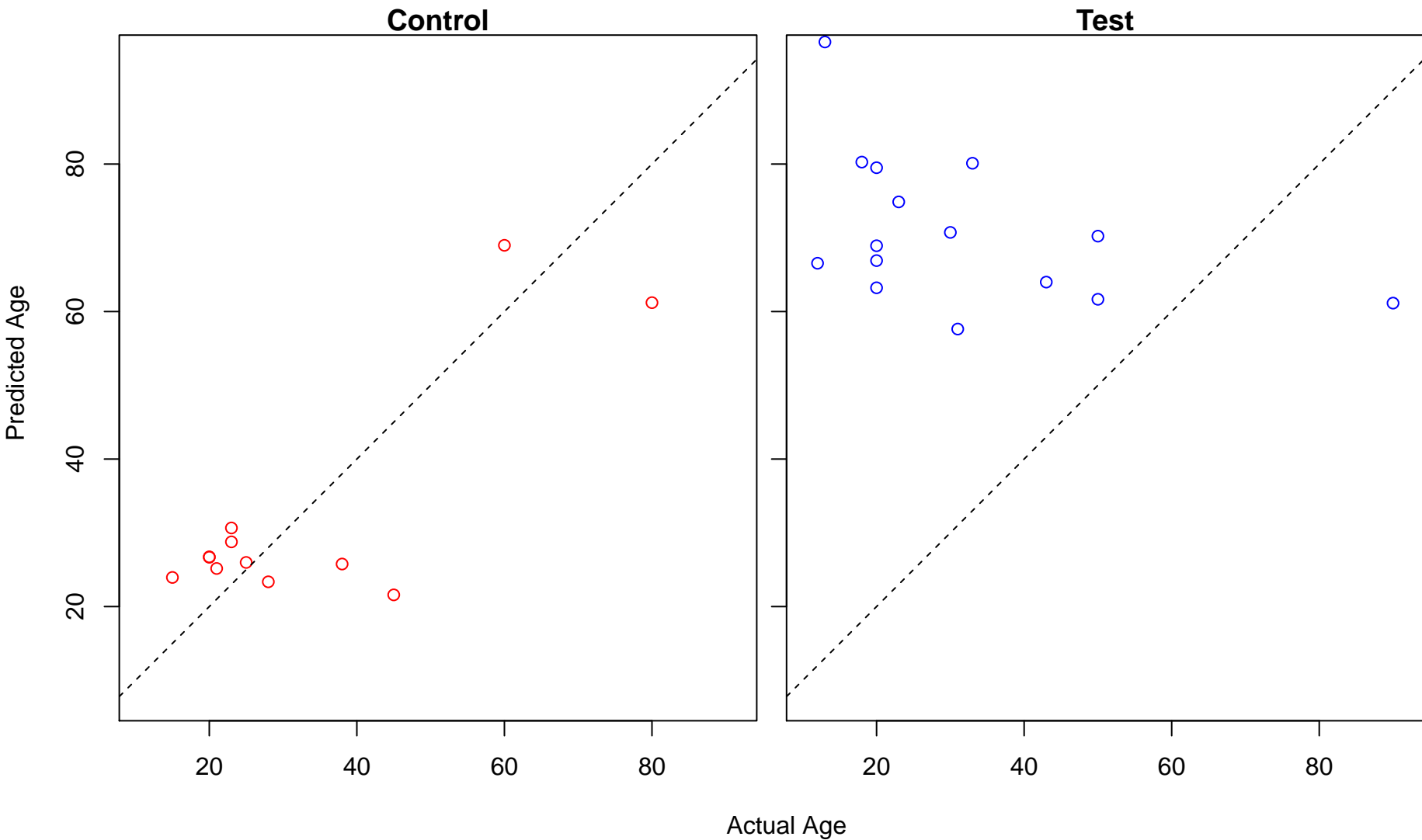
positive regulation of deacetylase activity (Score: 5.951912)



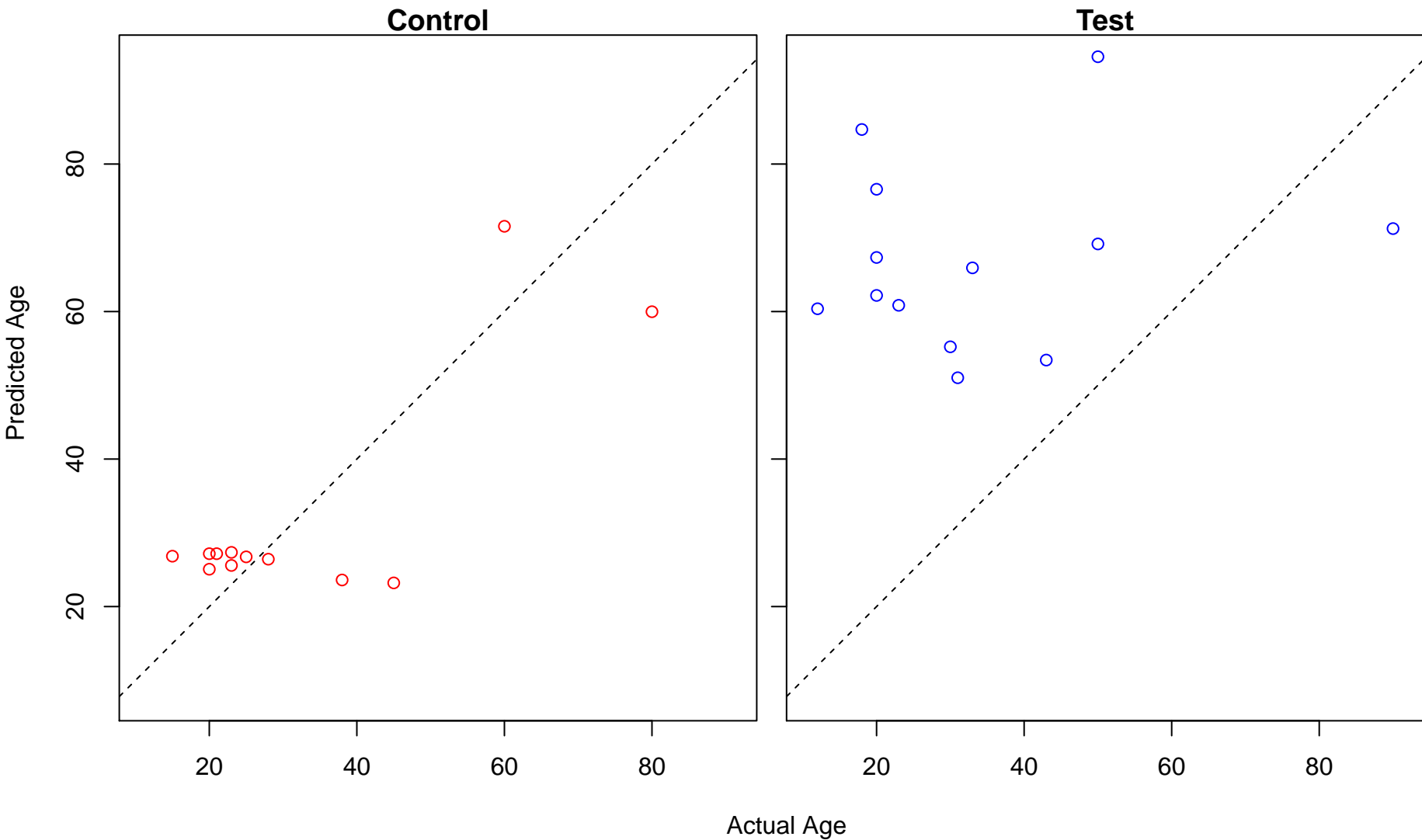
negative regulation of histone acetylation (Score: 5.948396)



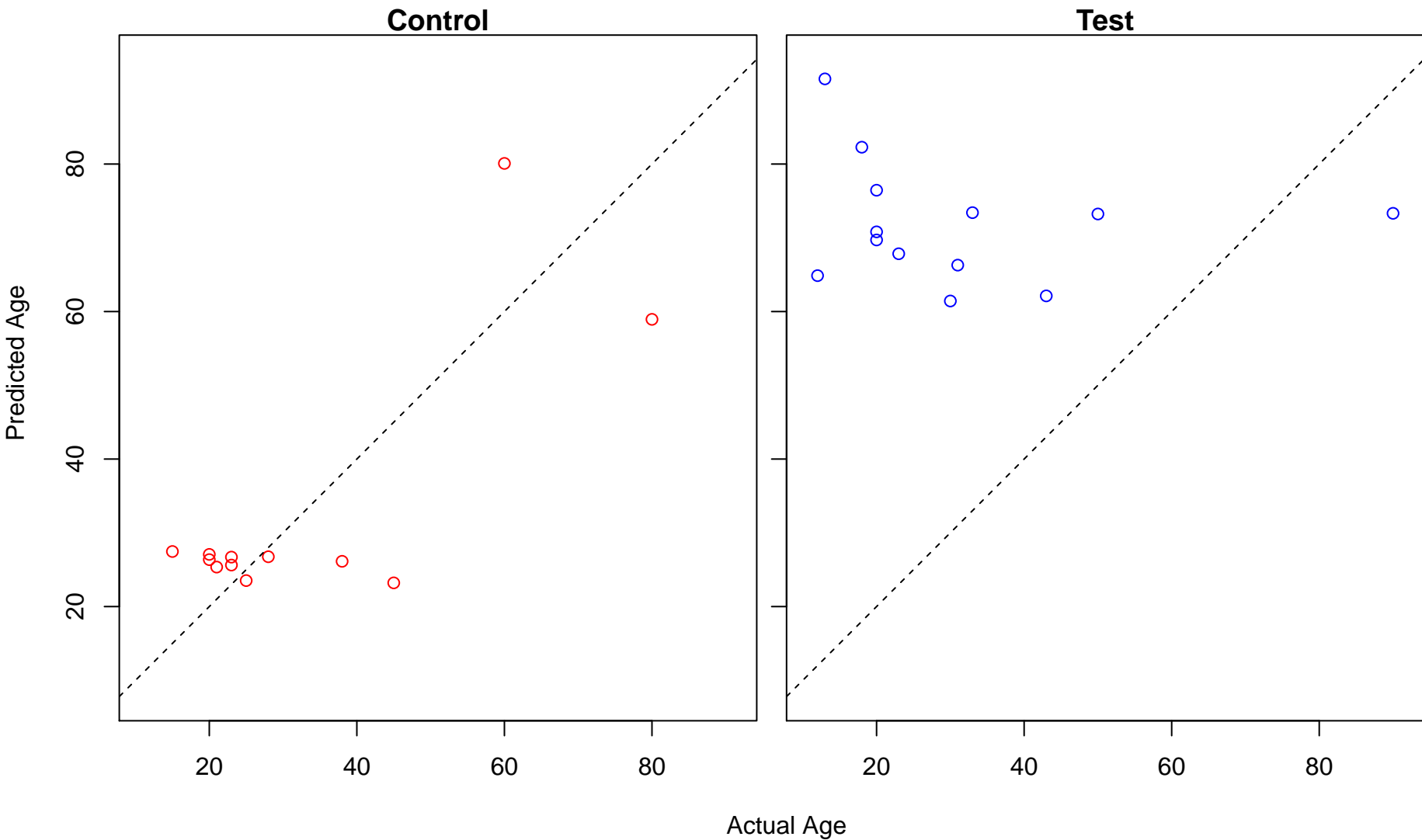
positive regulation of smooth muscle cell proliferation (Score: 5.947600)



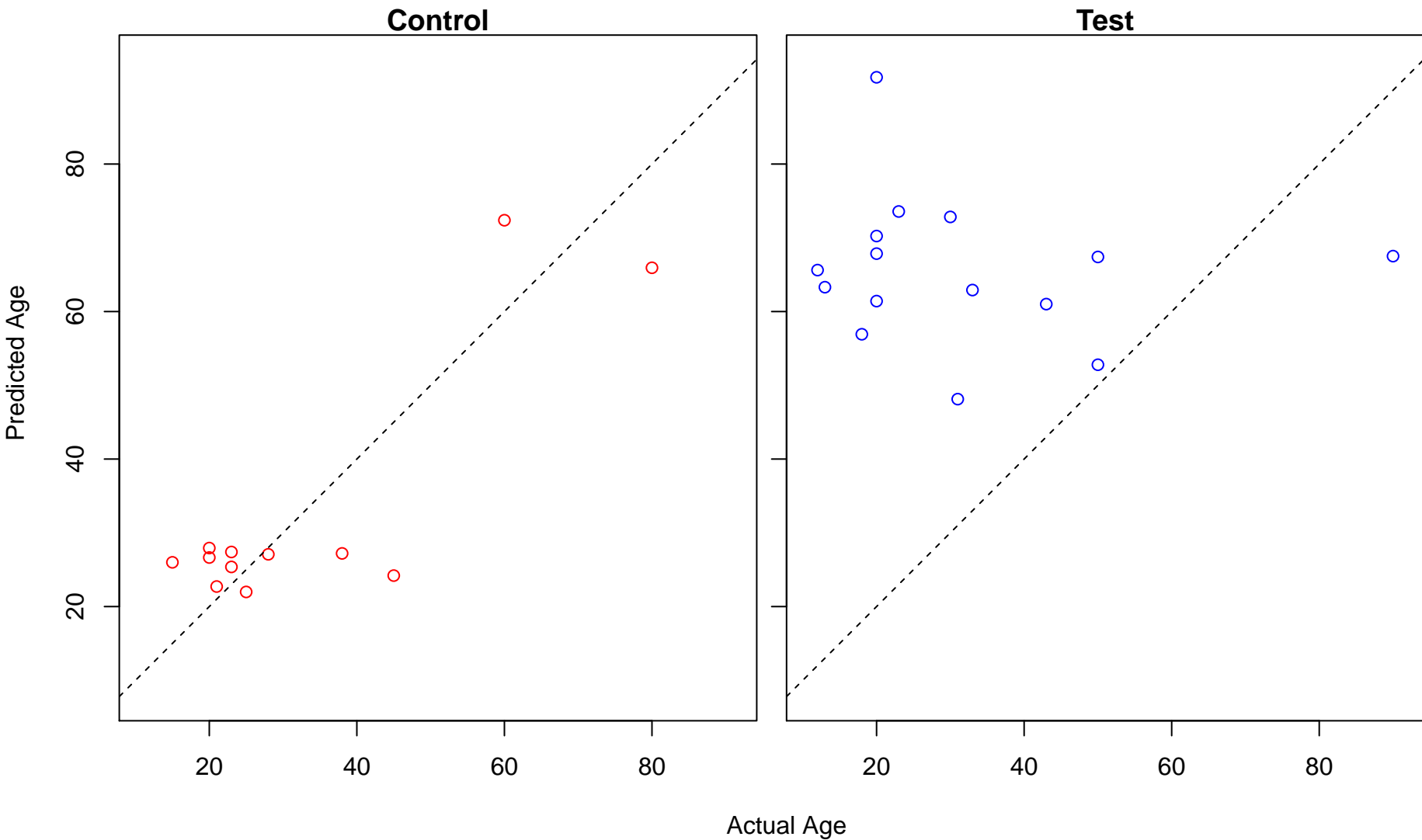
alpha-amino acid metabolic process (Score: 5.947226)



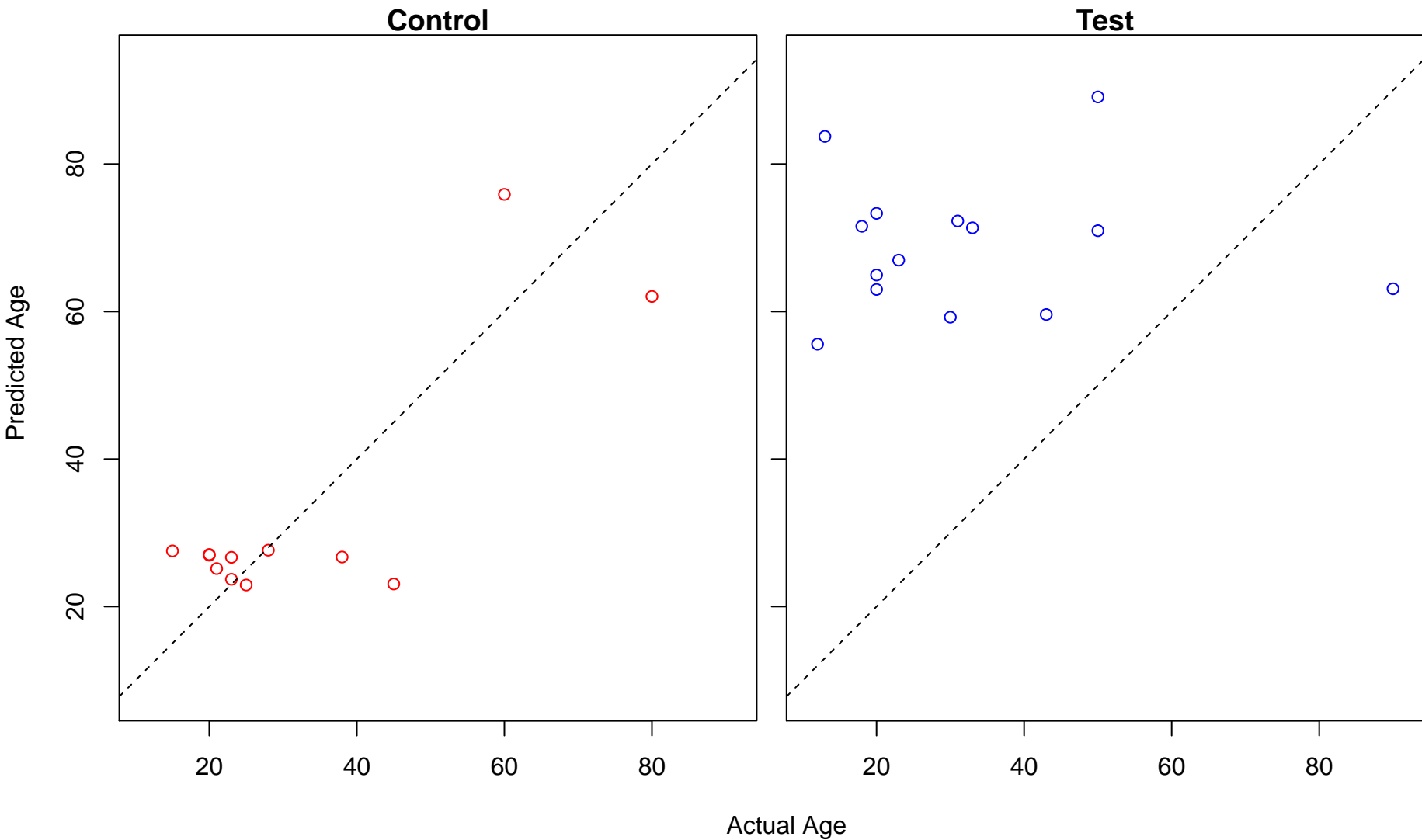
nucleic acid phosphodiester bond hydrolysis (Score: 5.945742)



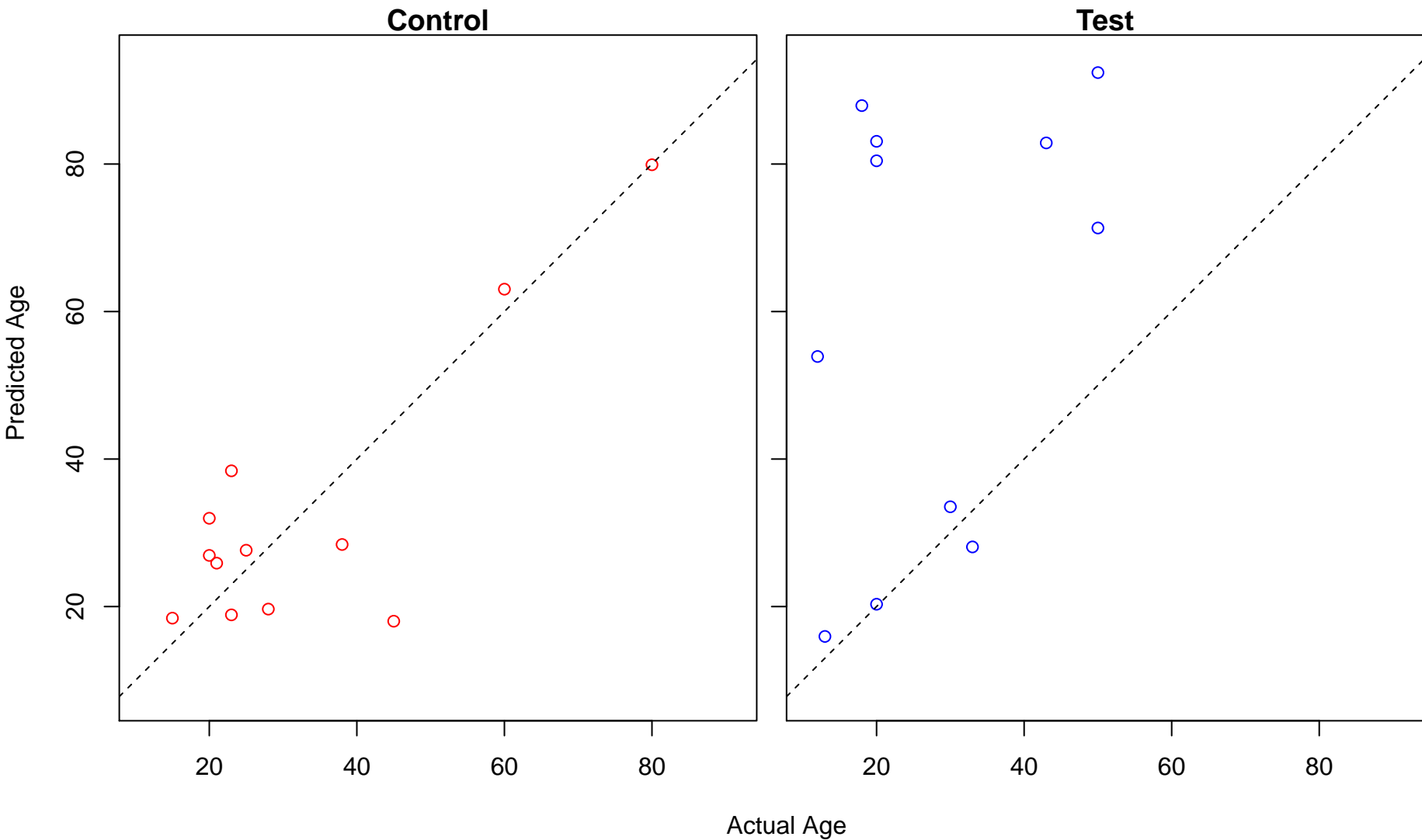
regulation of translational initiation by eIF2 alpha phosphorylation (Score: 5.943104)



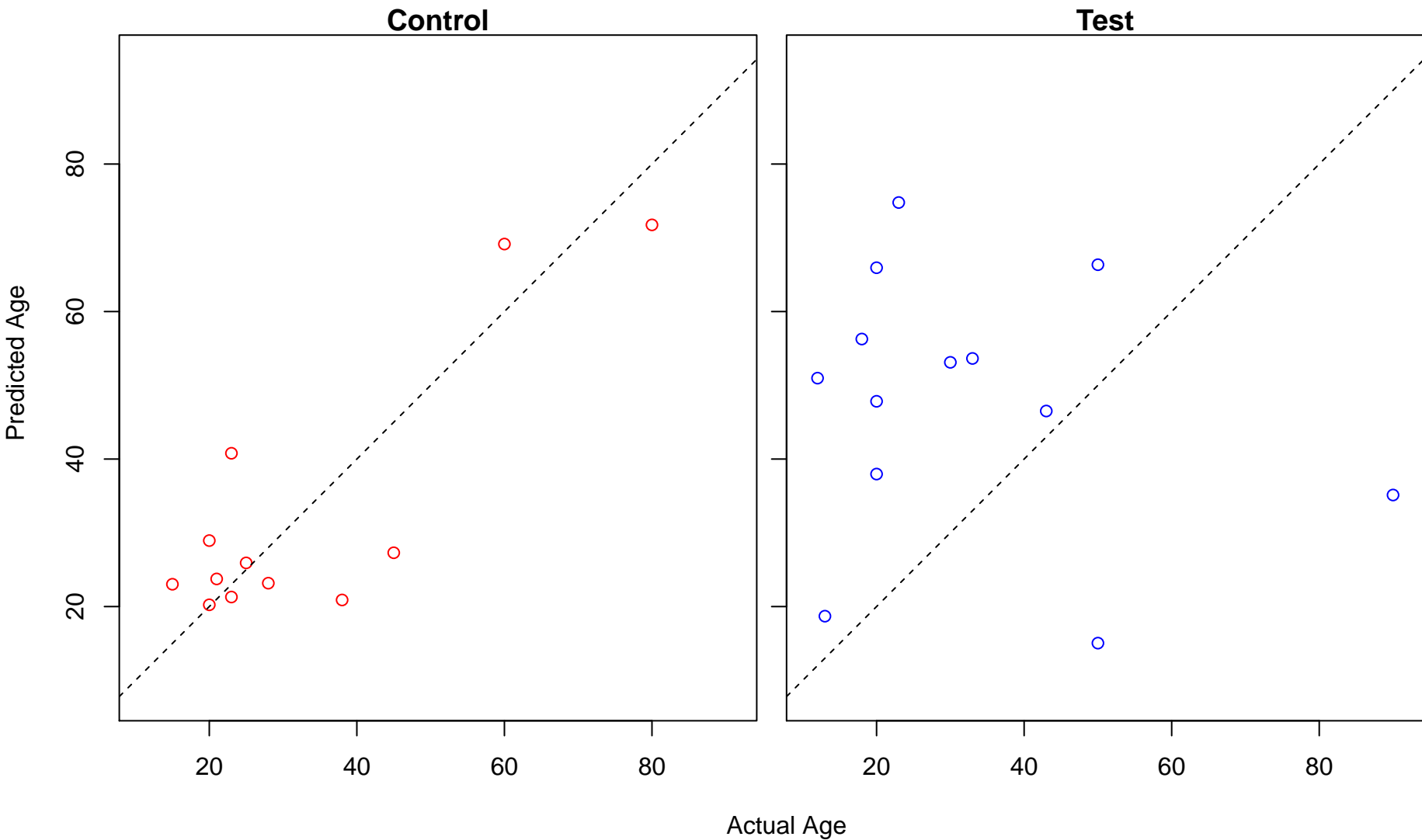
cytoskeleton-dependent intracellular transport (Score: 5.942395)



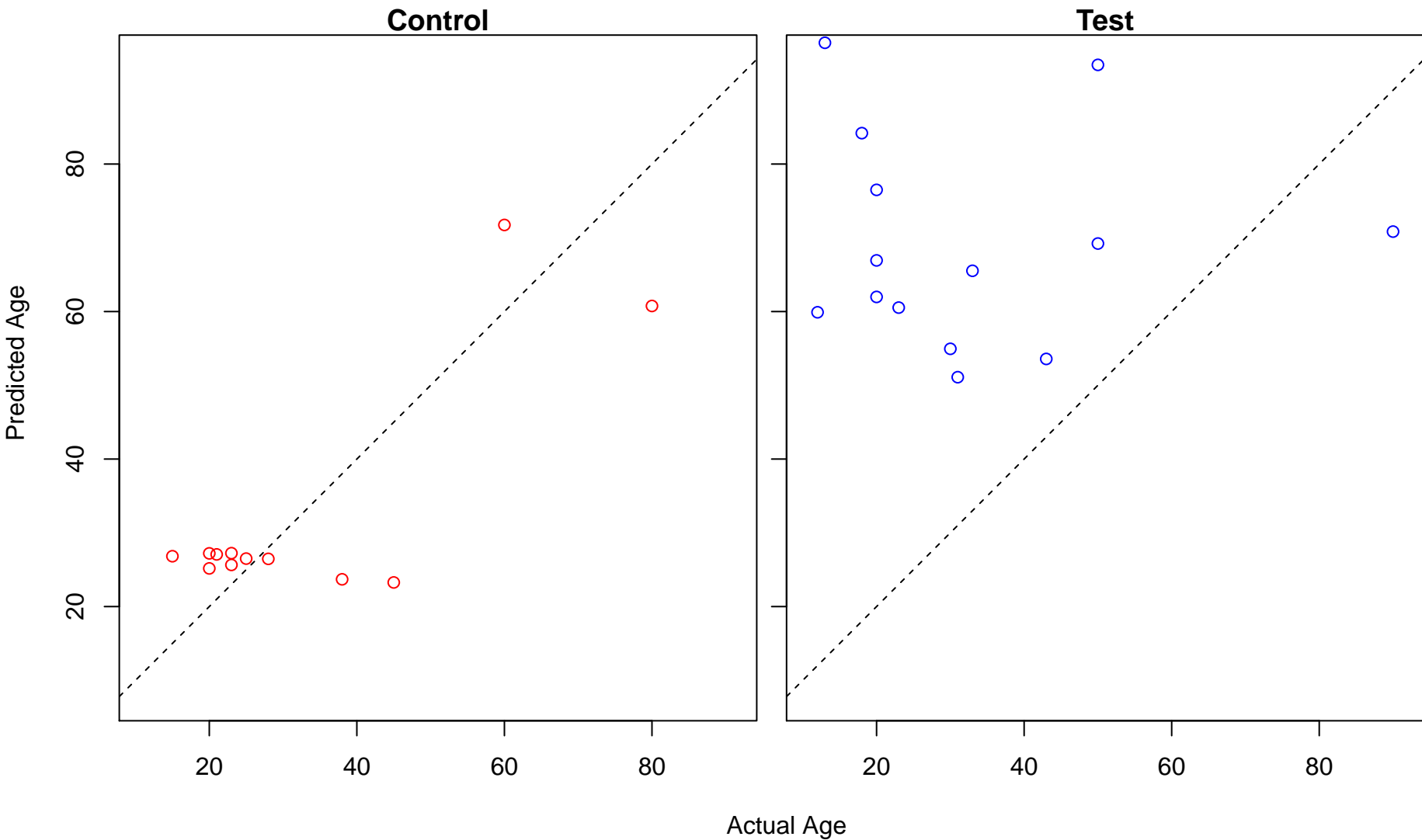
somatic diversification of immunoglobulins (Score: 5.941094)



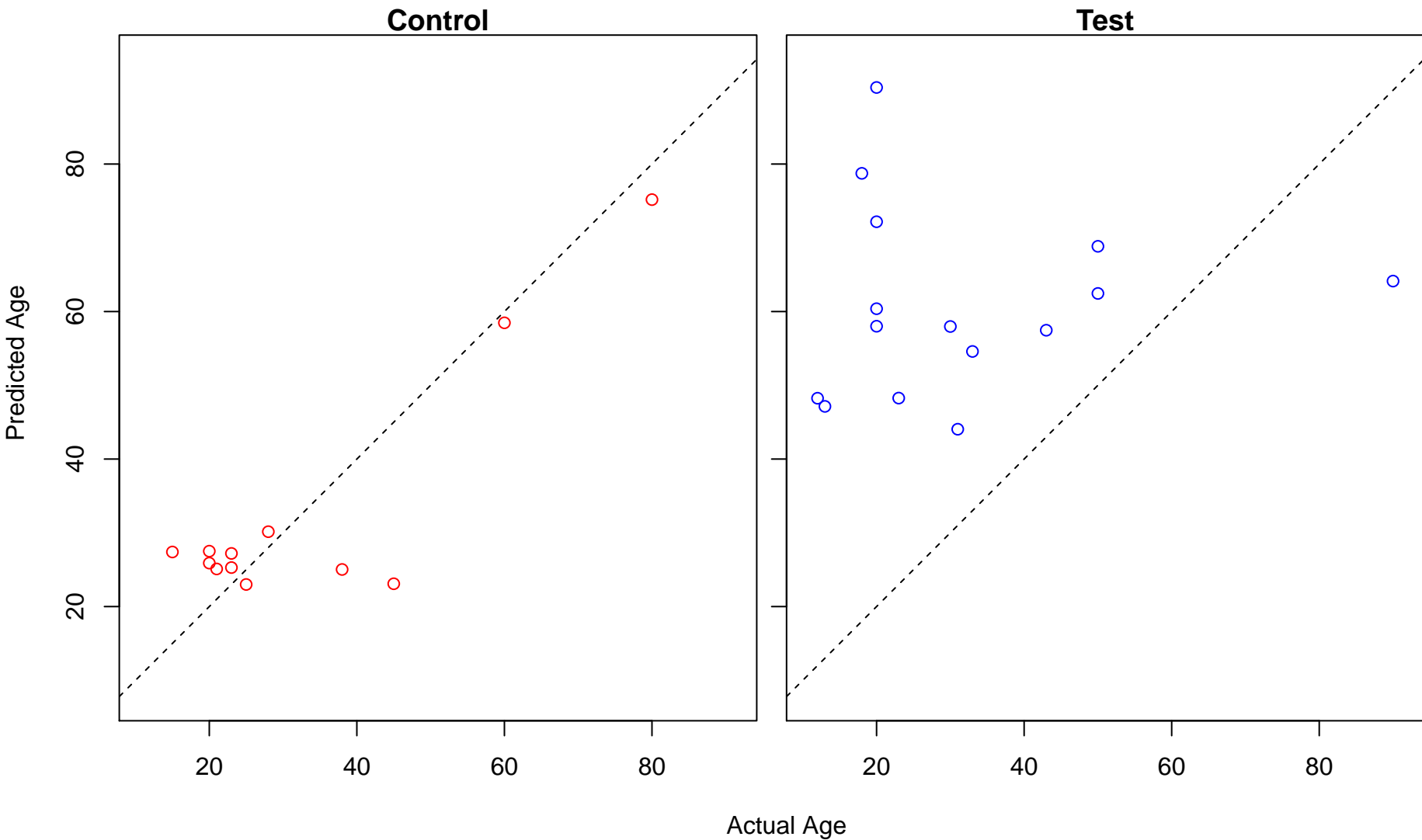
glutamine family amino acid catabolic process (Score: 5.940737)



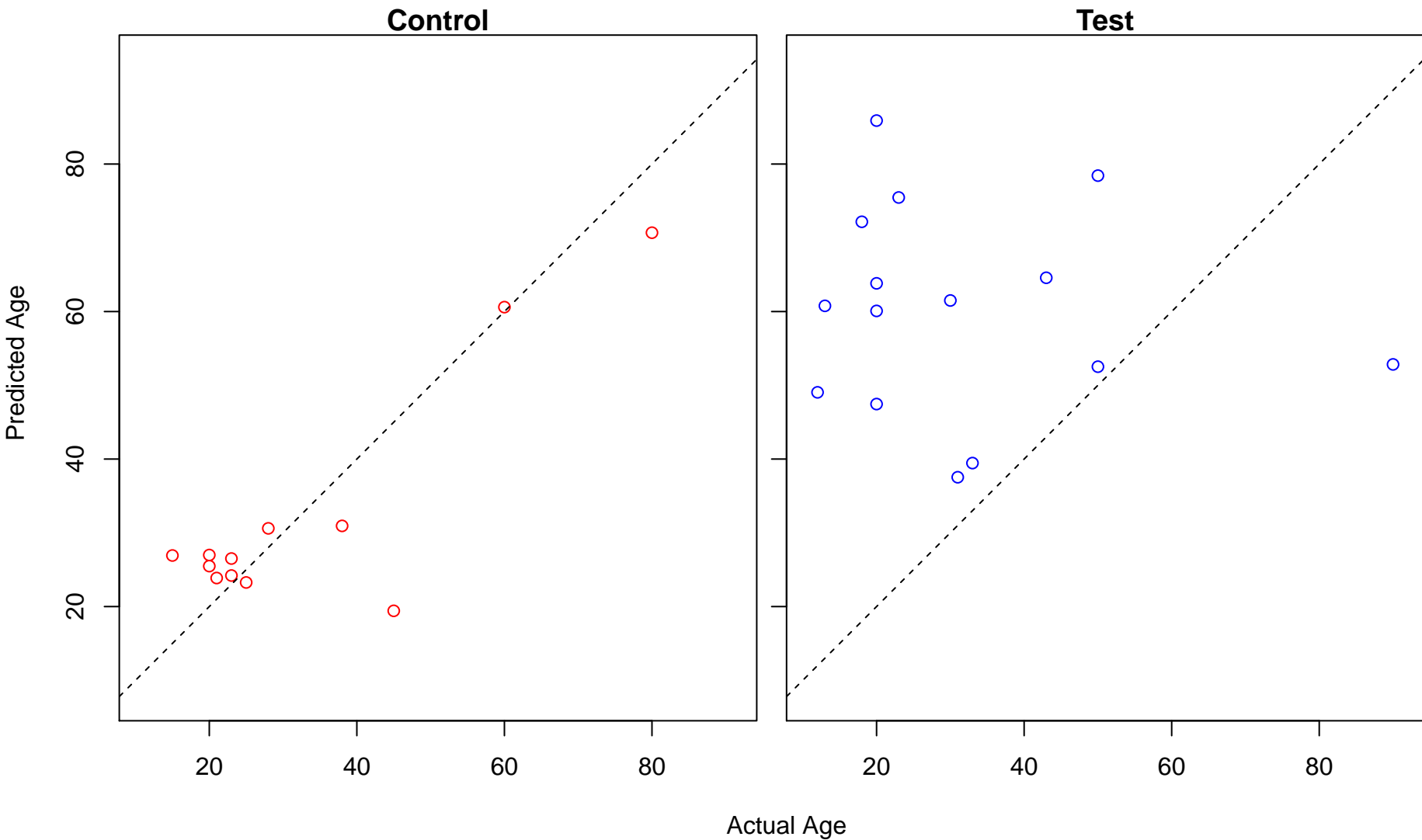
cellular amino acid metabolic process (Score: 5.939537)



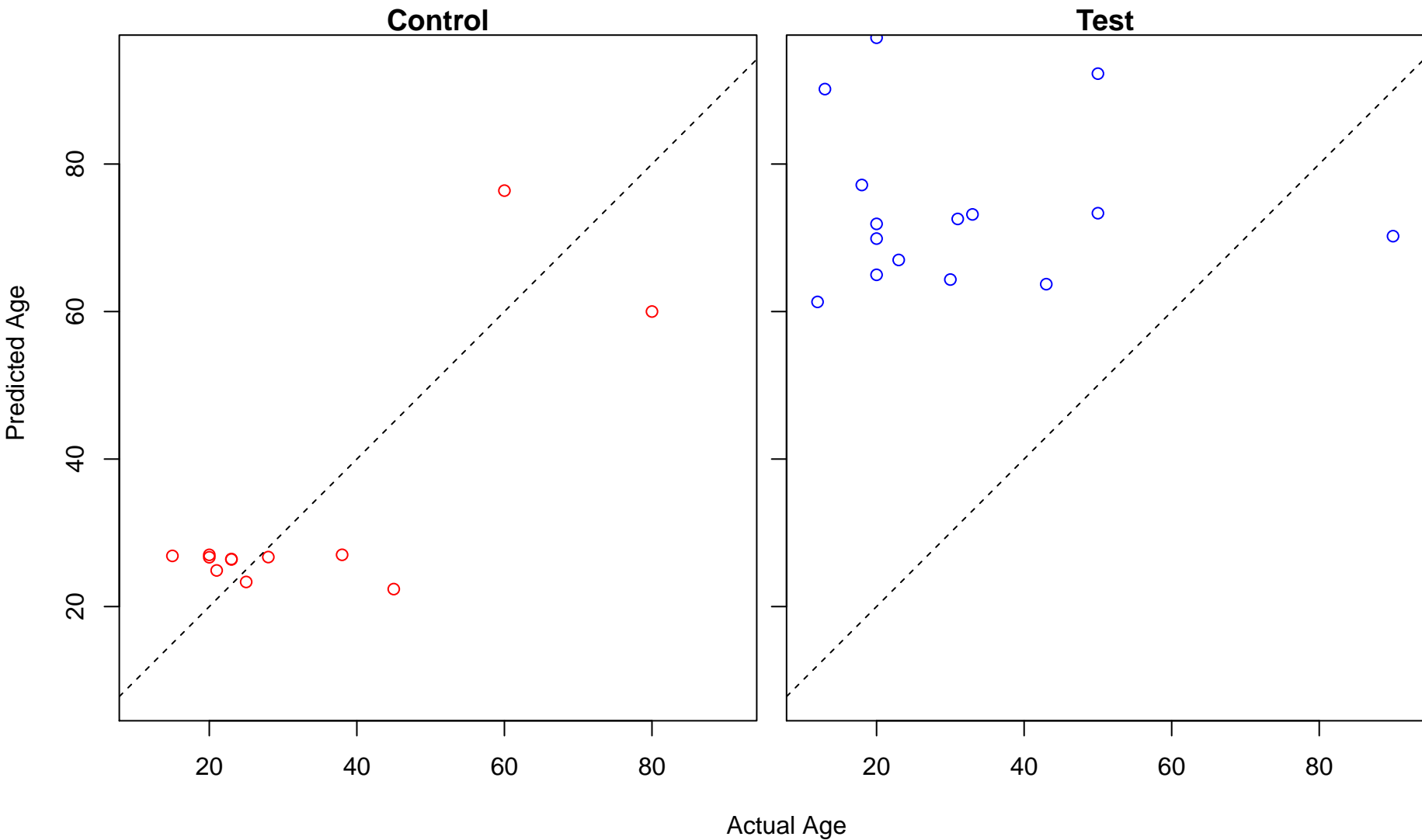
immune system development (Score: 5.939204)



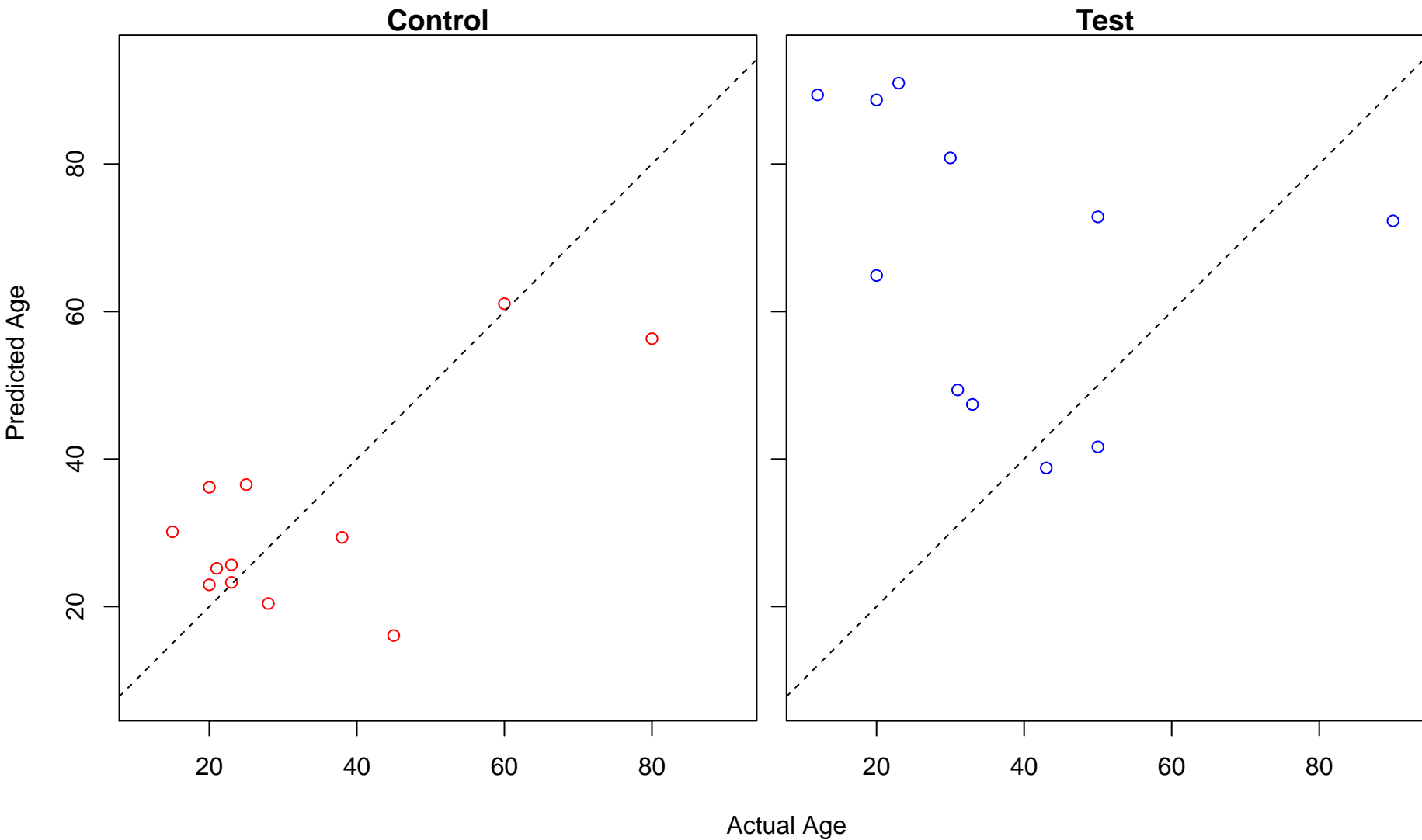
regulation of phagocytosis, engulfment (Score: 5.937202)



regulation of innate immune response (Score: 5.935572)

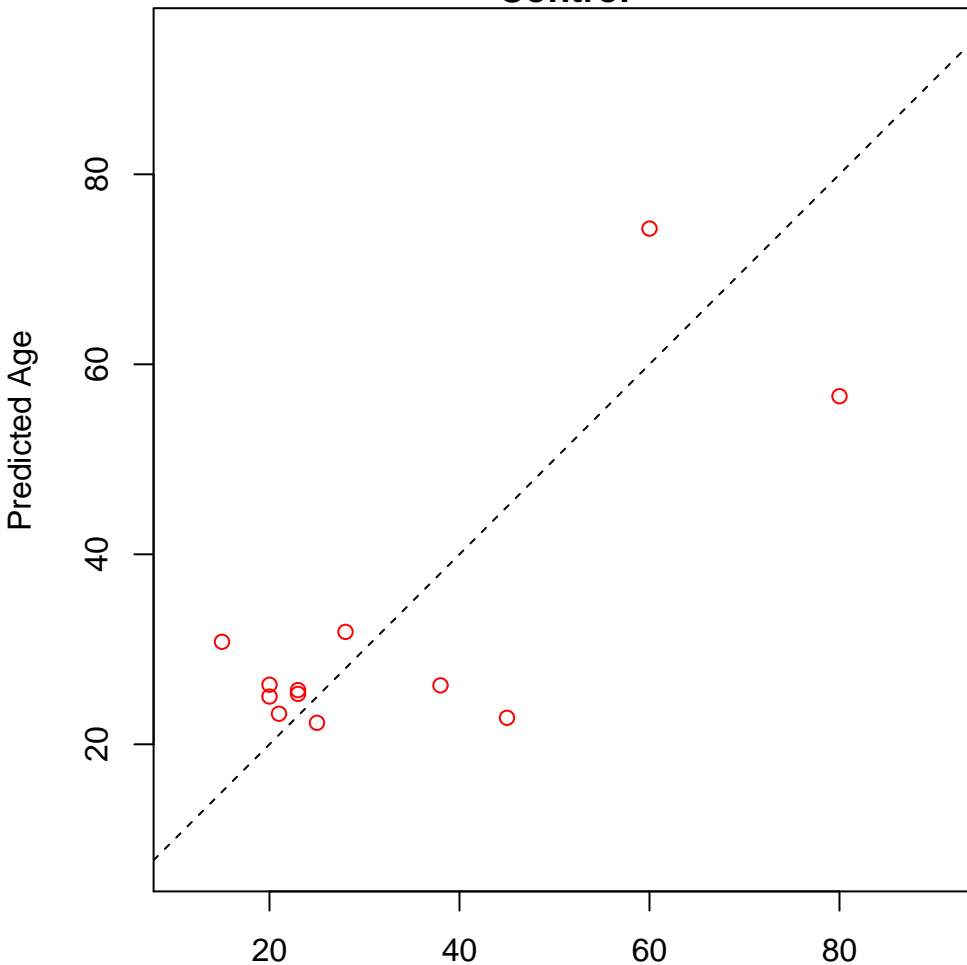


cellular response to zinc ion (Score: 5.934838)

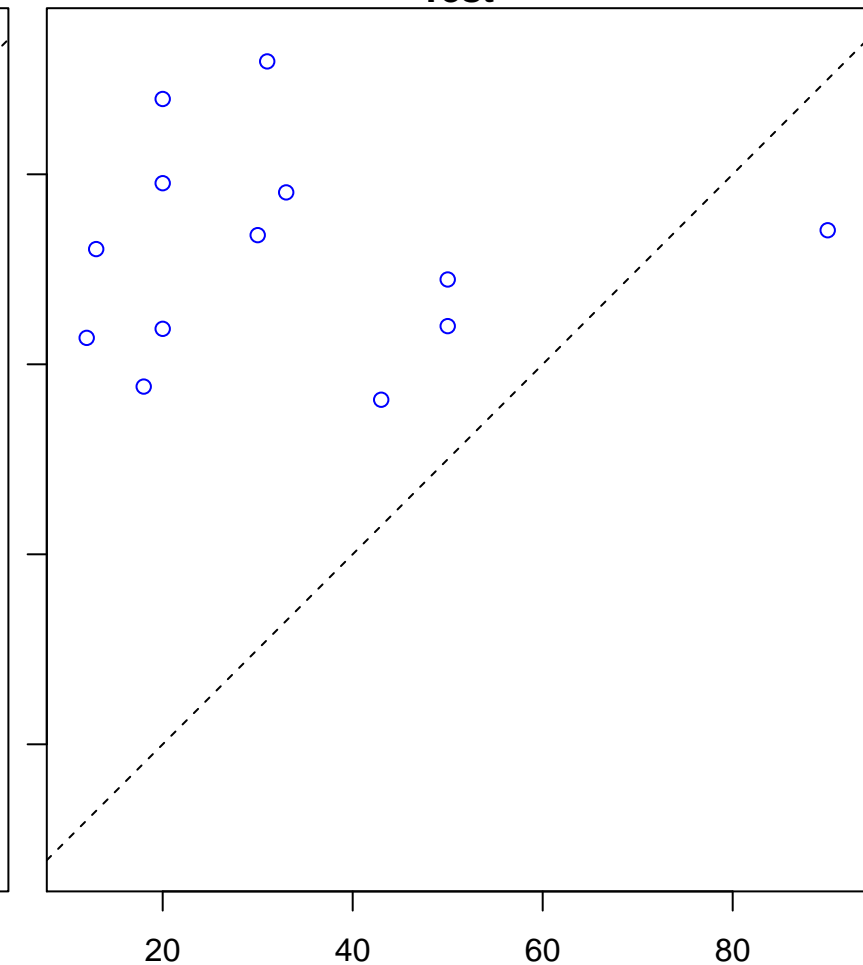


cellular response to exogenous dsRNA (Score: 5.931317)

Control

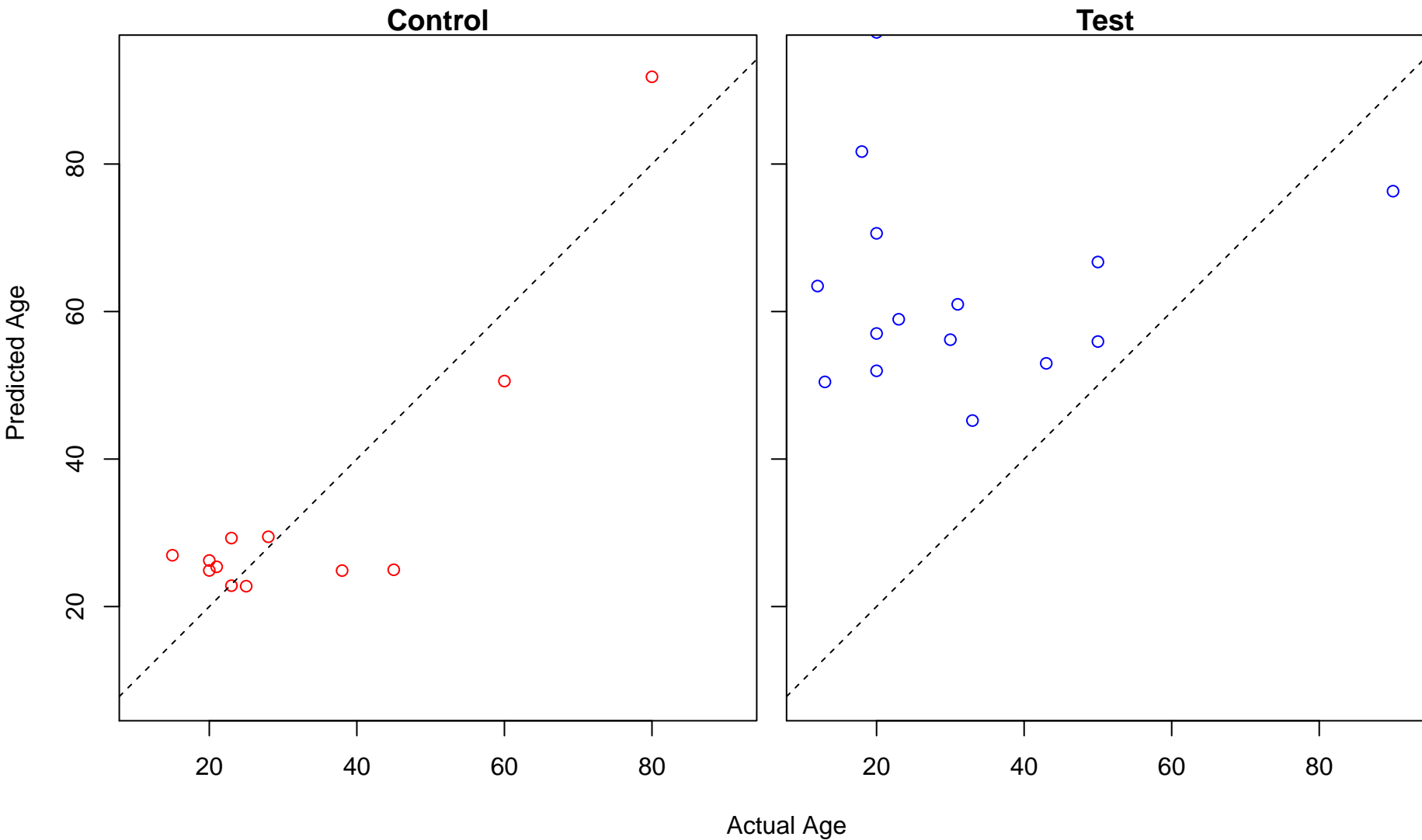


Test

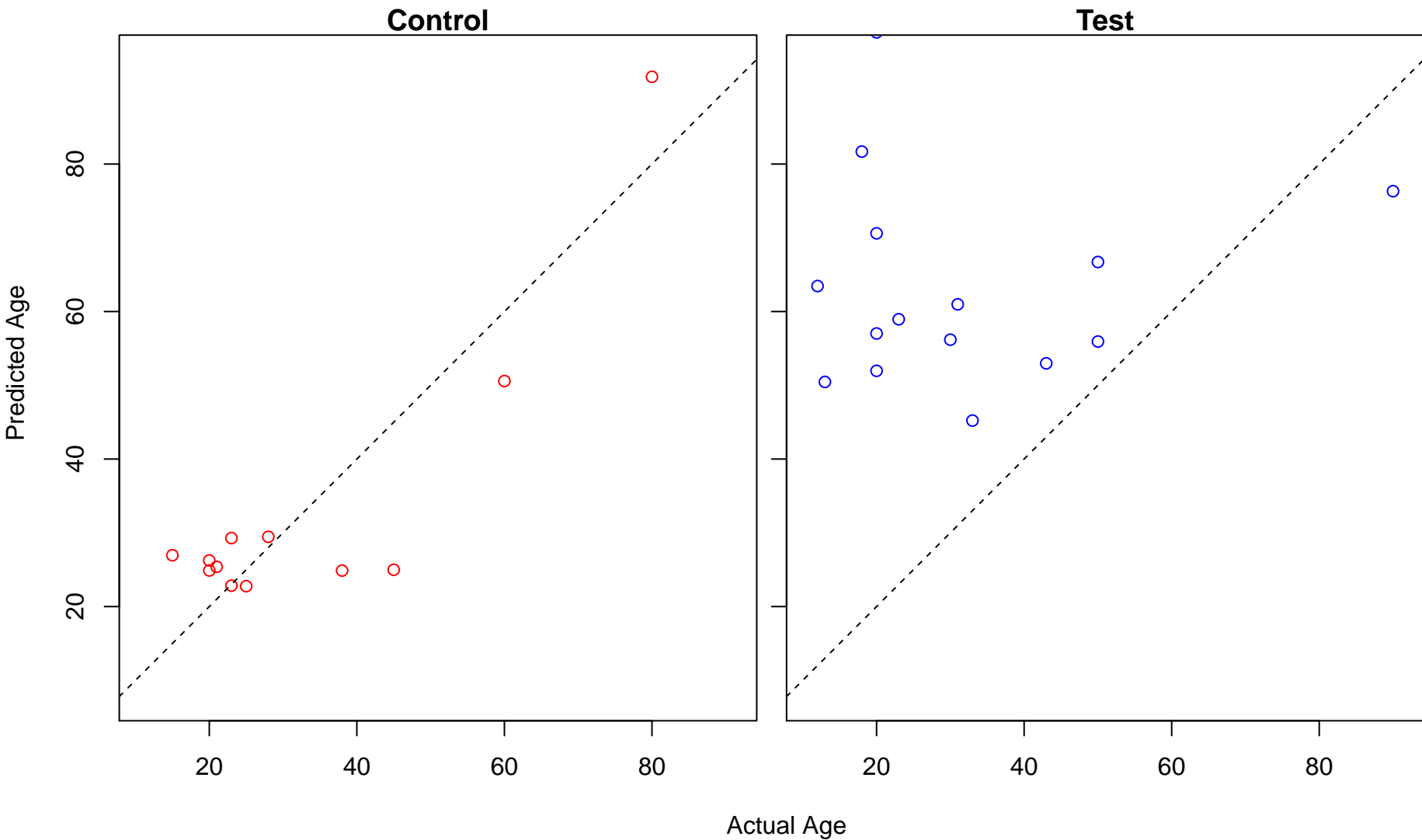


Actual Age

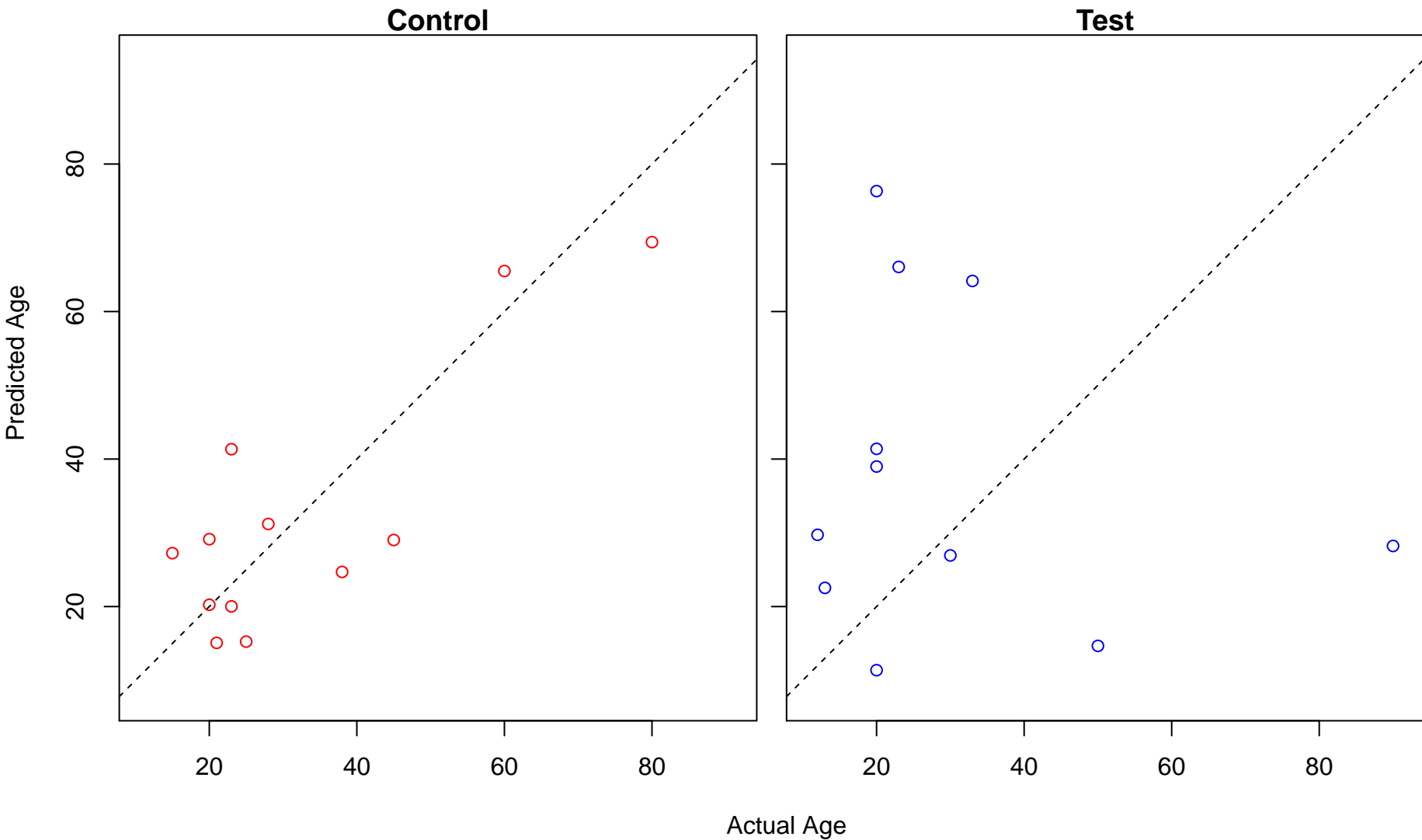
negative regulation of transforming growth factor beta receptor signaling pathway (Score: 5.930203)



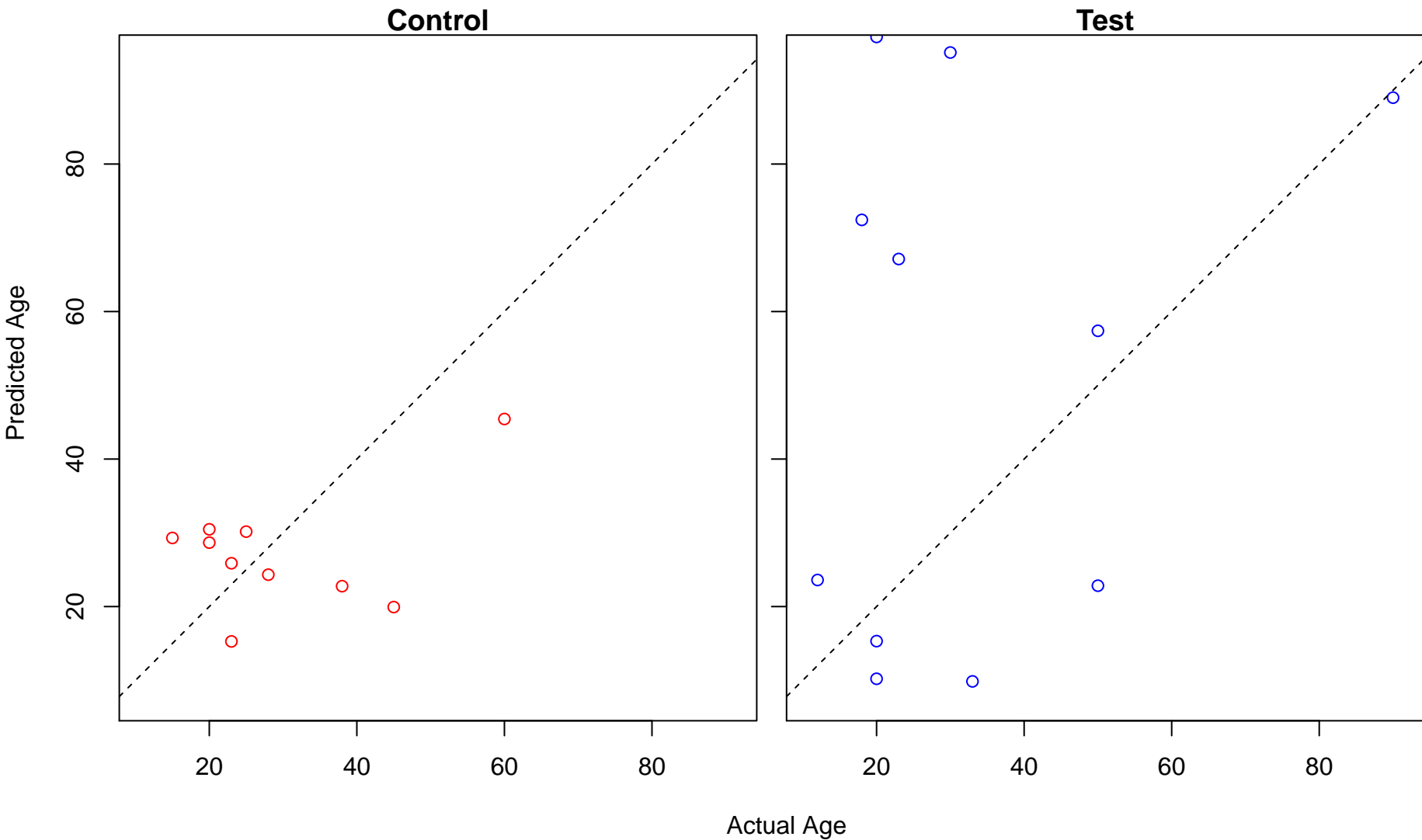
negative regulation of cellular response to transforming growth factor beta stimulus (Score: 5.93020)



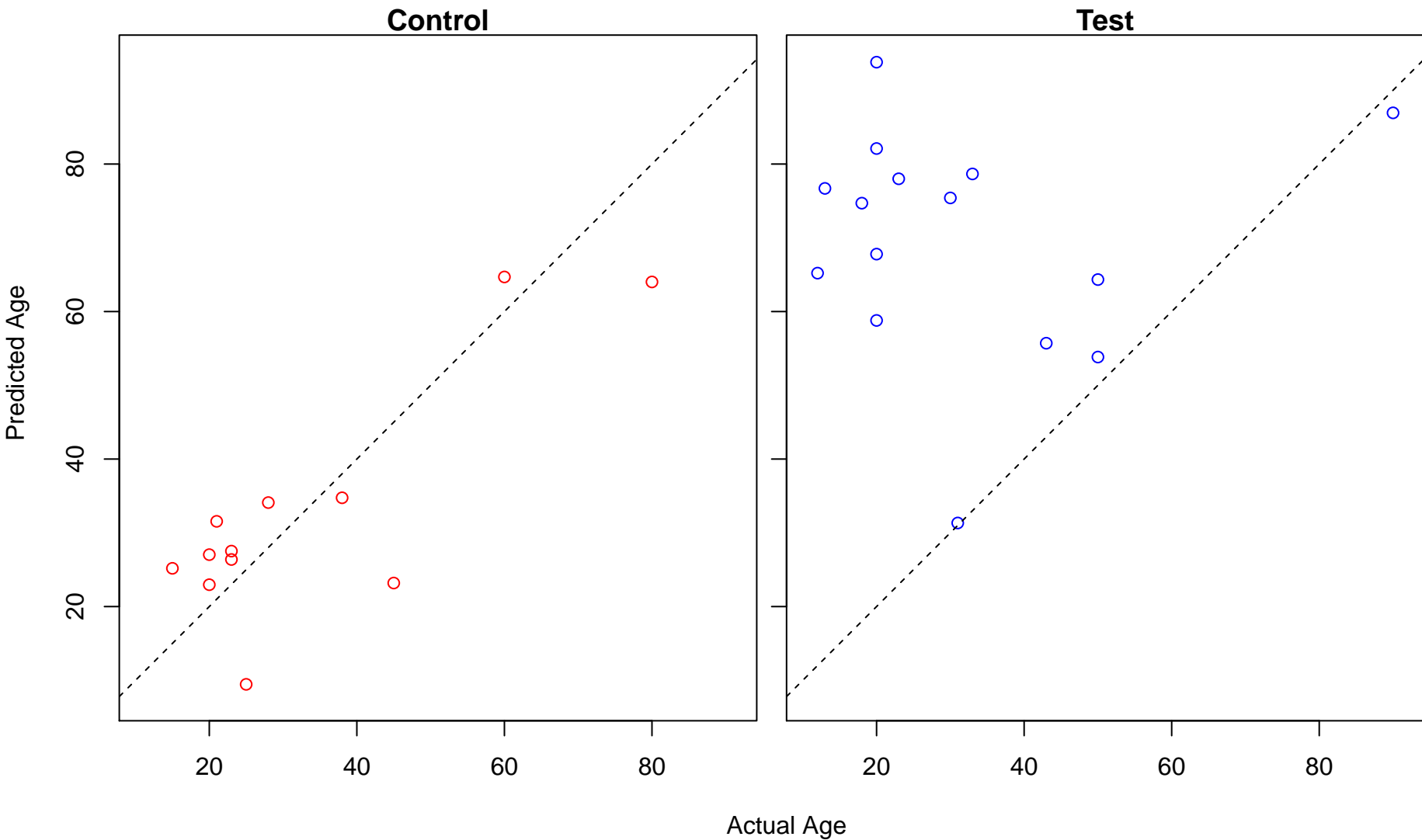
regulation of mitotic sister chromatid segregation (Score: 5.928388)



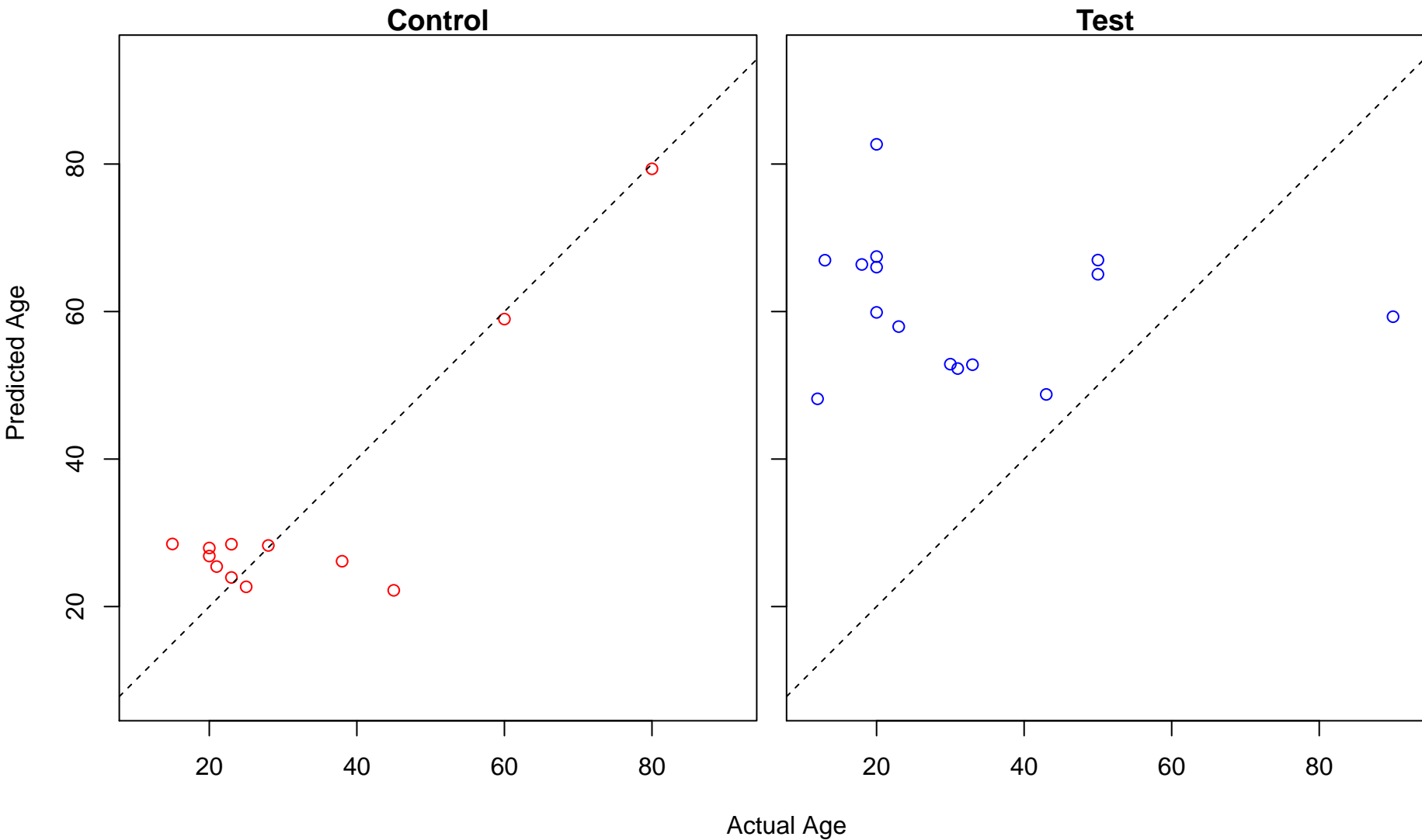
negative regulation of gluconeogenesis (Score: 5.923207)



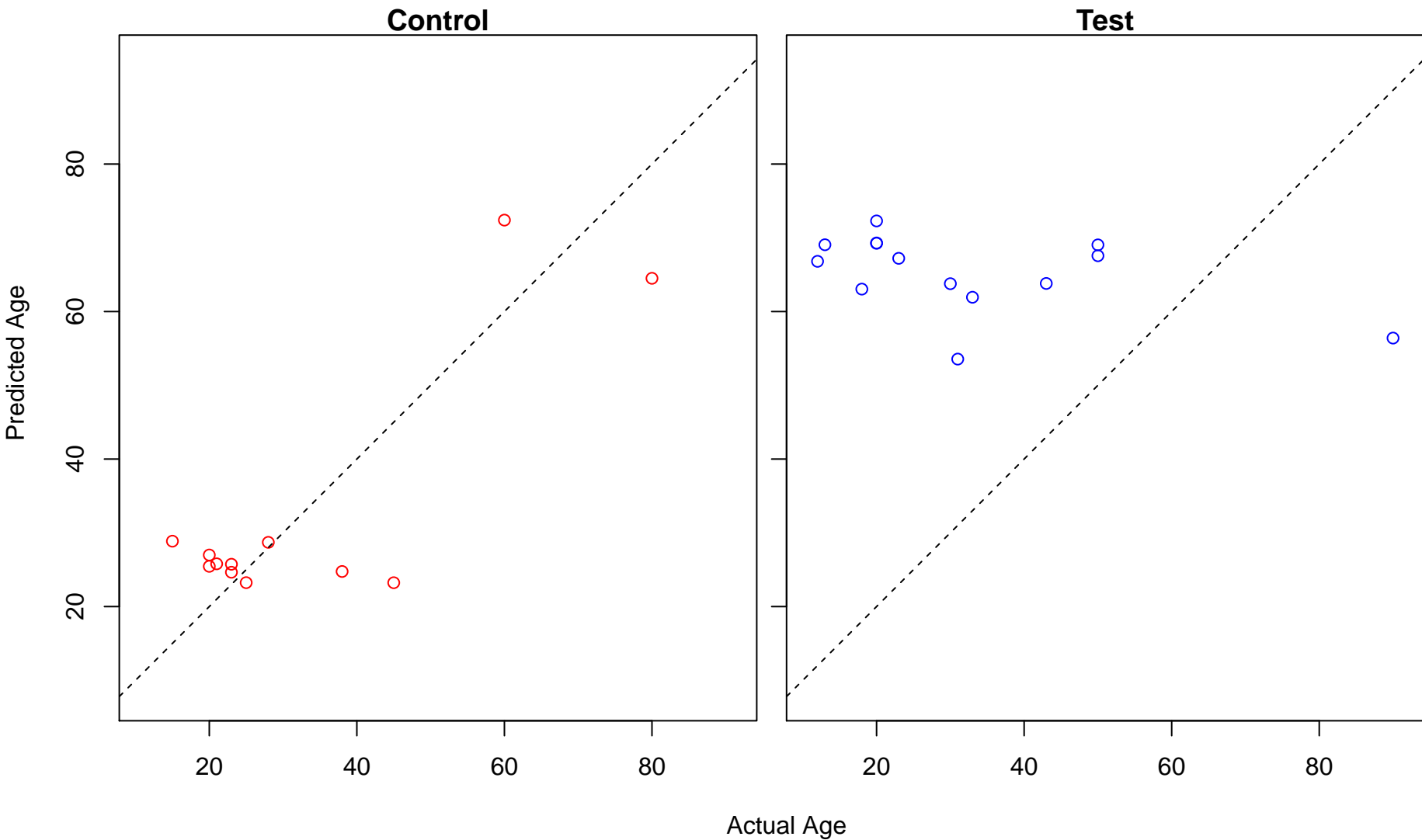
erythrocyte development (Score: 5.922768)



exocytosis (Score: 5.921334)

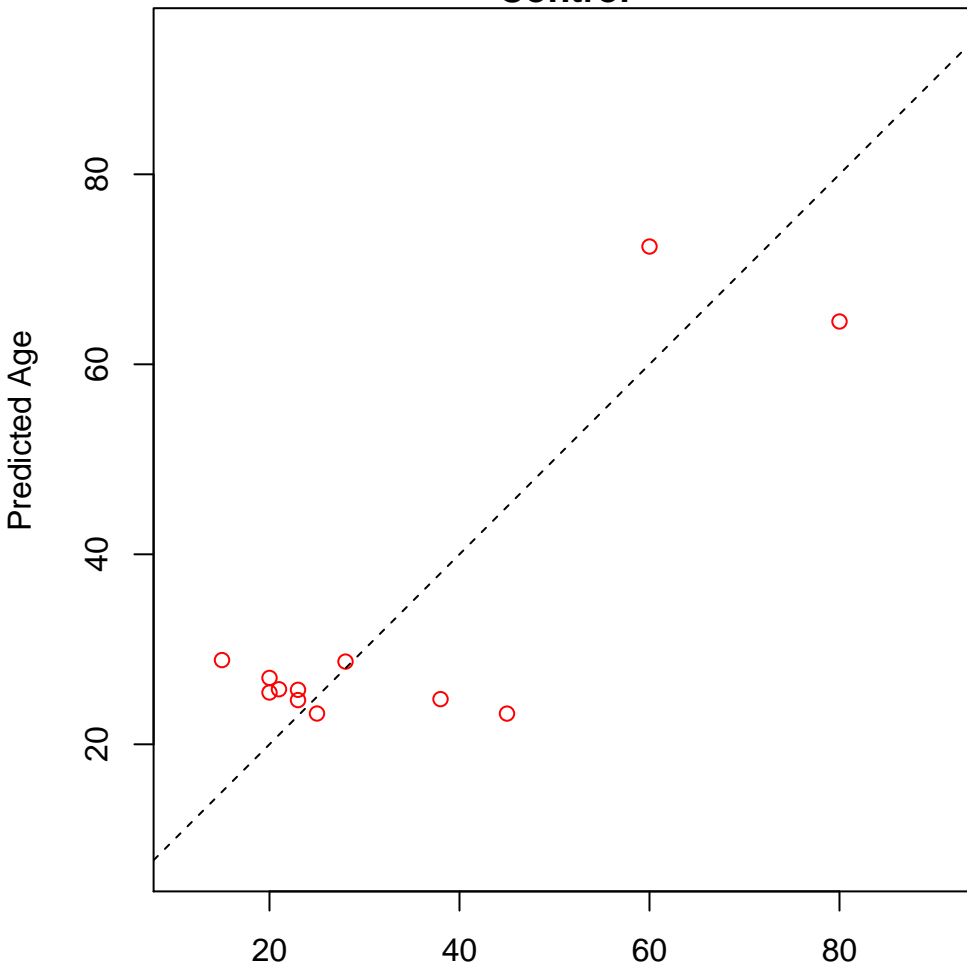


mechanoreceptor differentiation (Score: 5.917448)

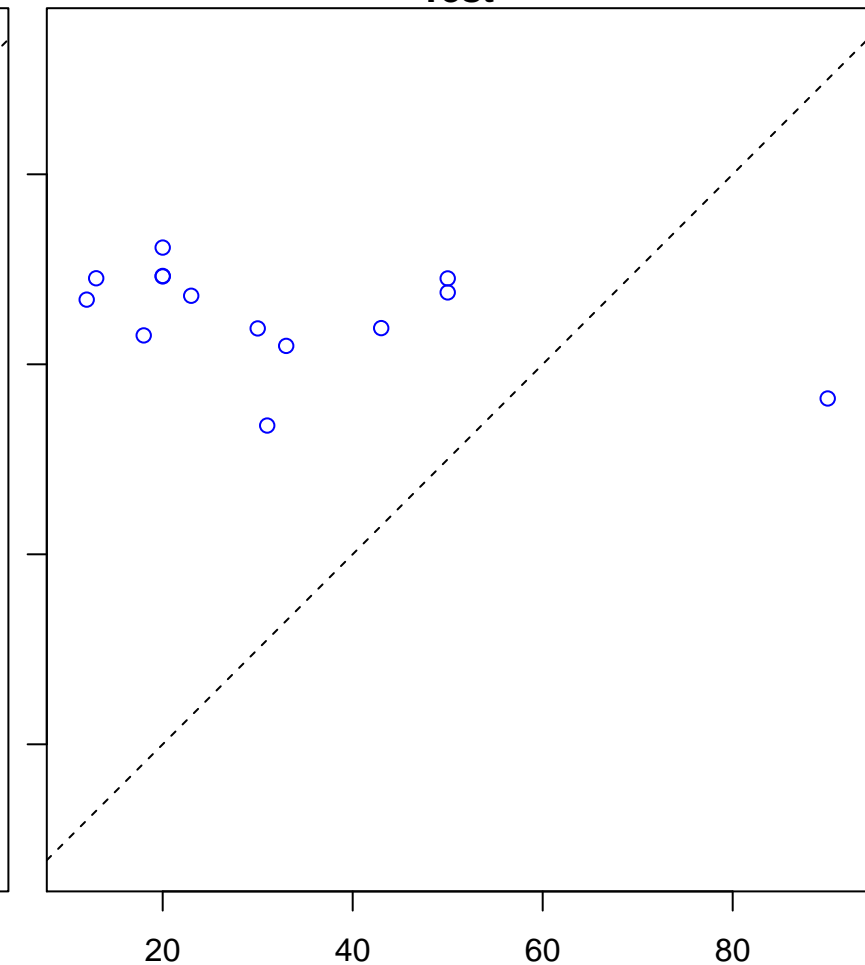


inner ear receptor cell differentiation (Score: 5.917448)

Control

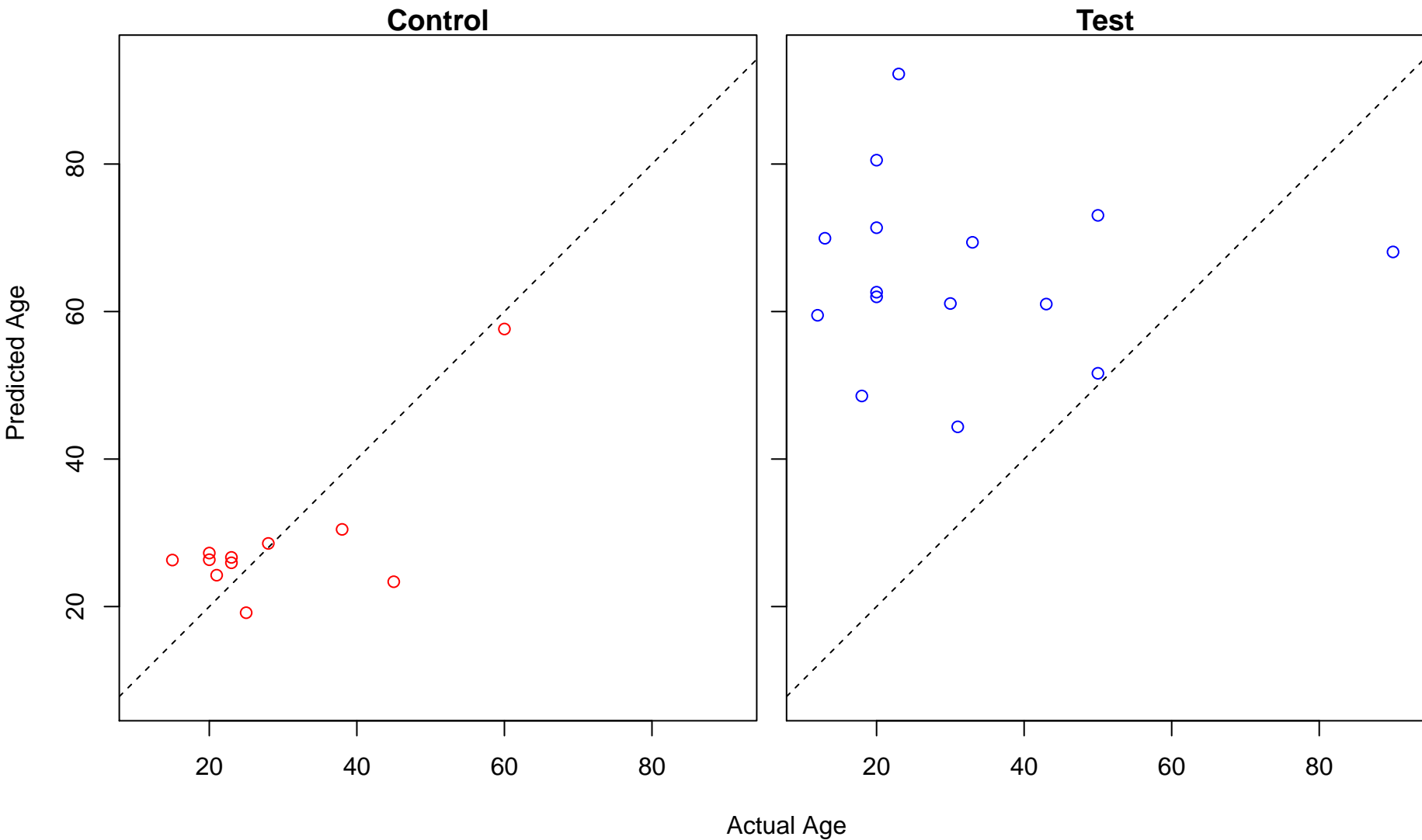


Test



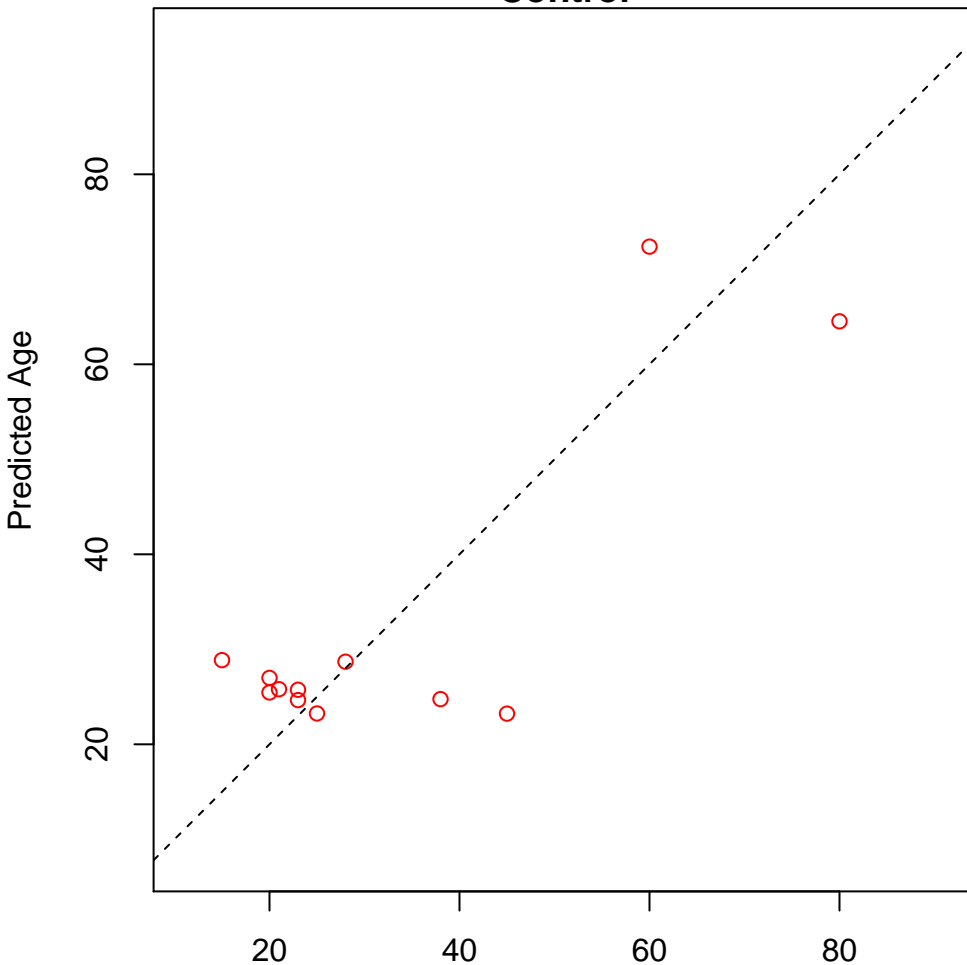
Actual Age

regulation of lipid kinase activity (Score: 5.917311)

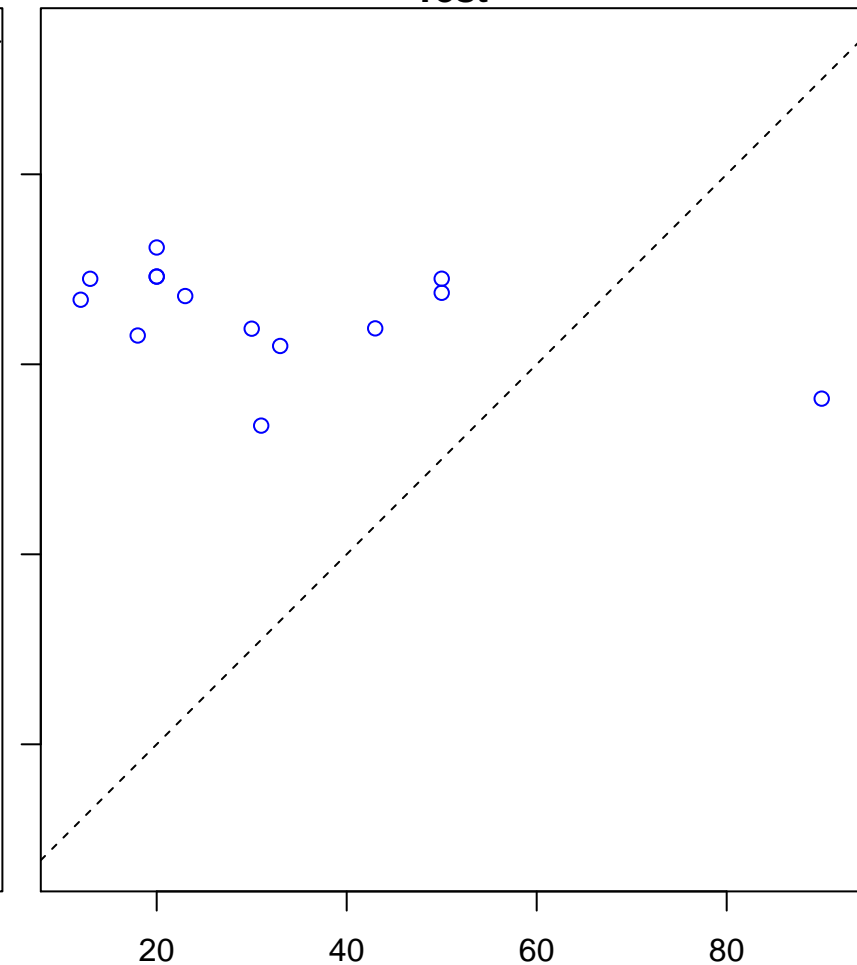


inner ear receptor cell development (Score: 5.916522)

Control

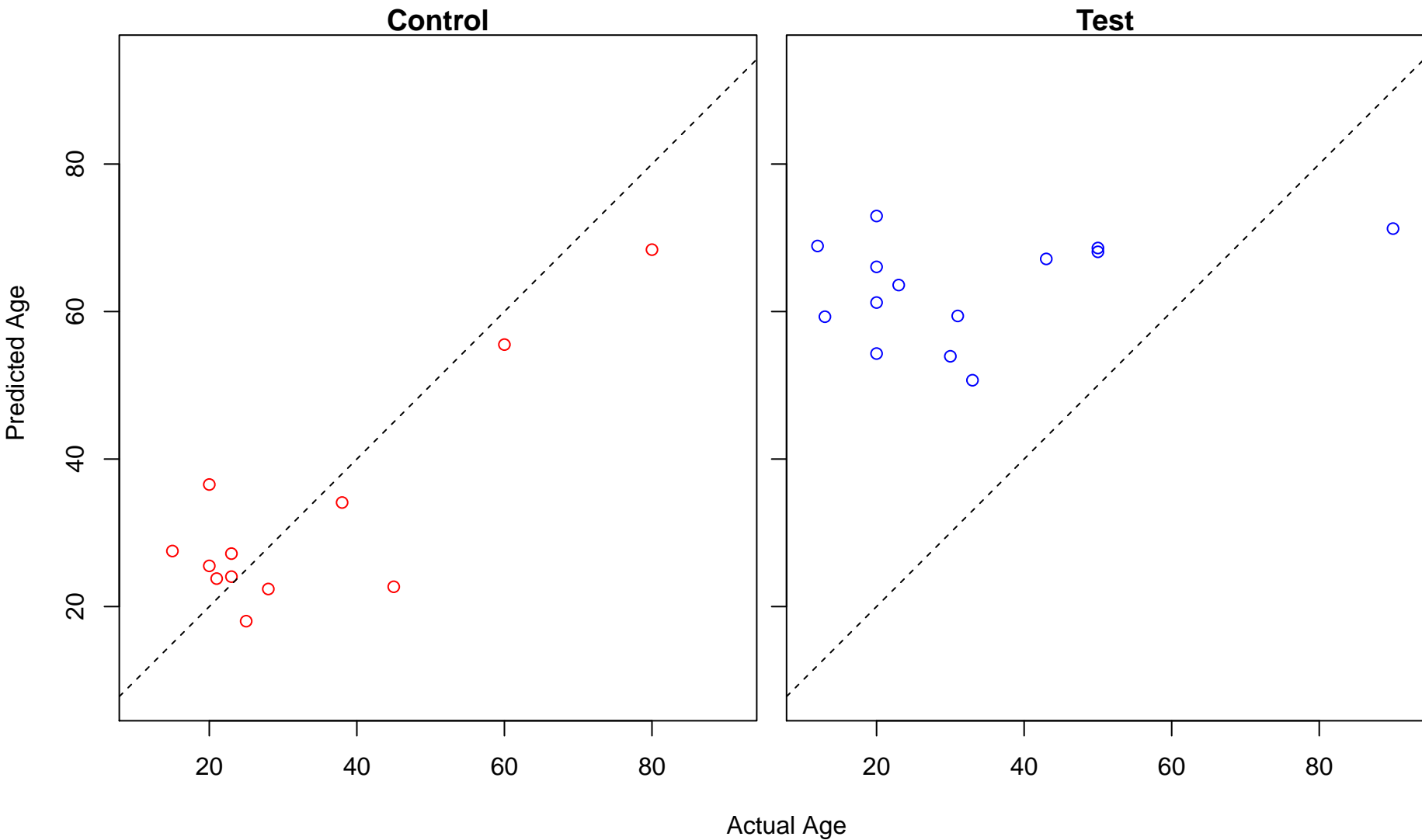


Test

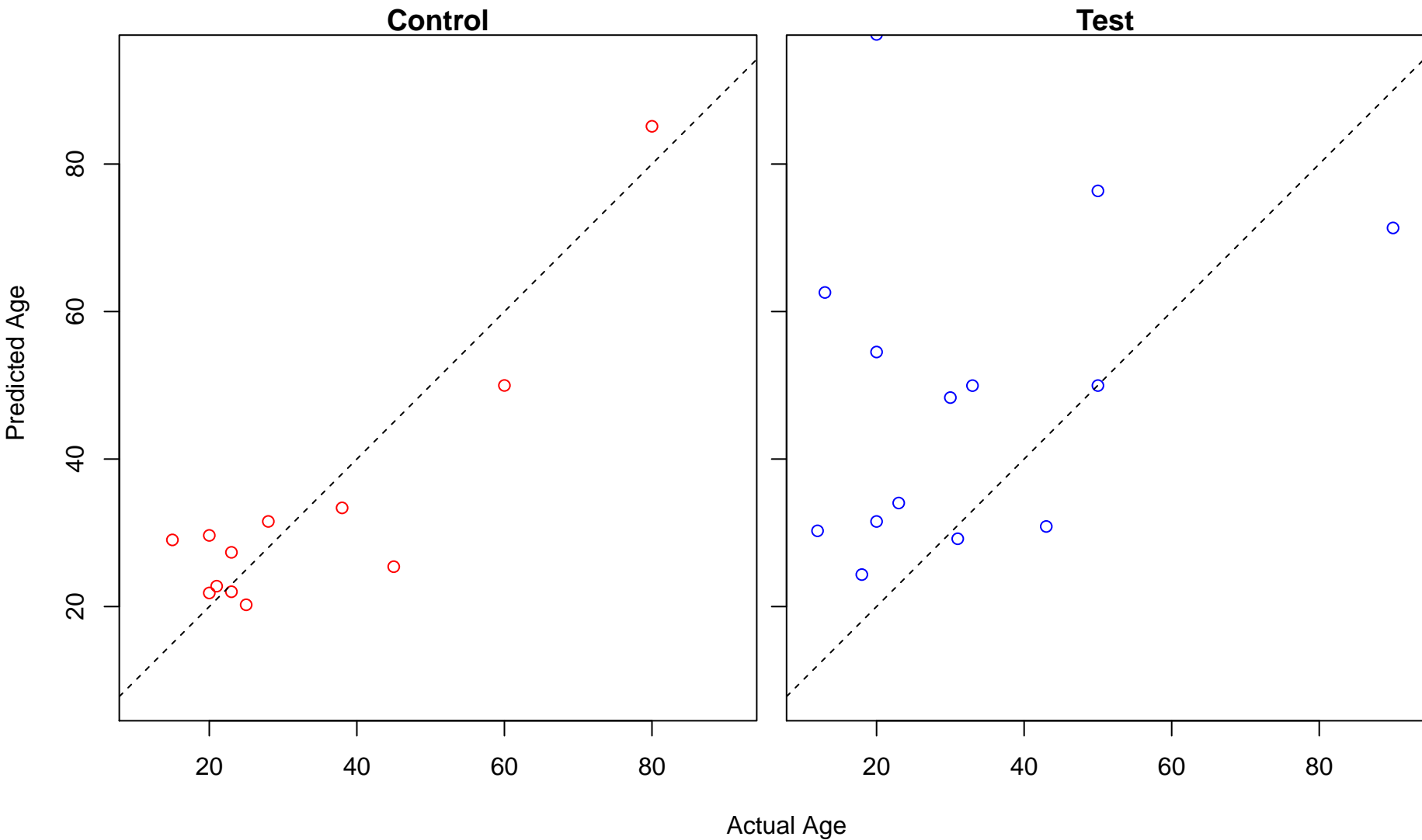


Actual Age

viral entry into host cell (Score: 5.915179)

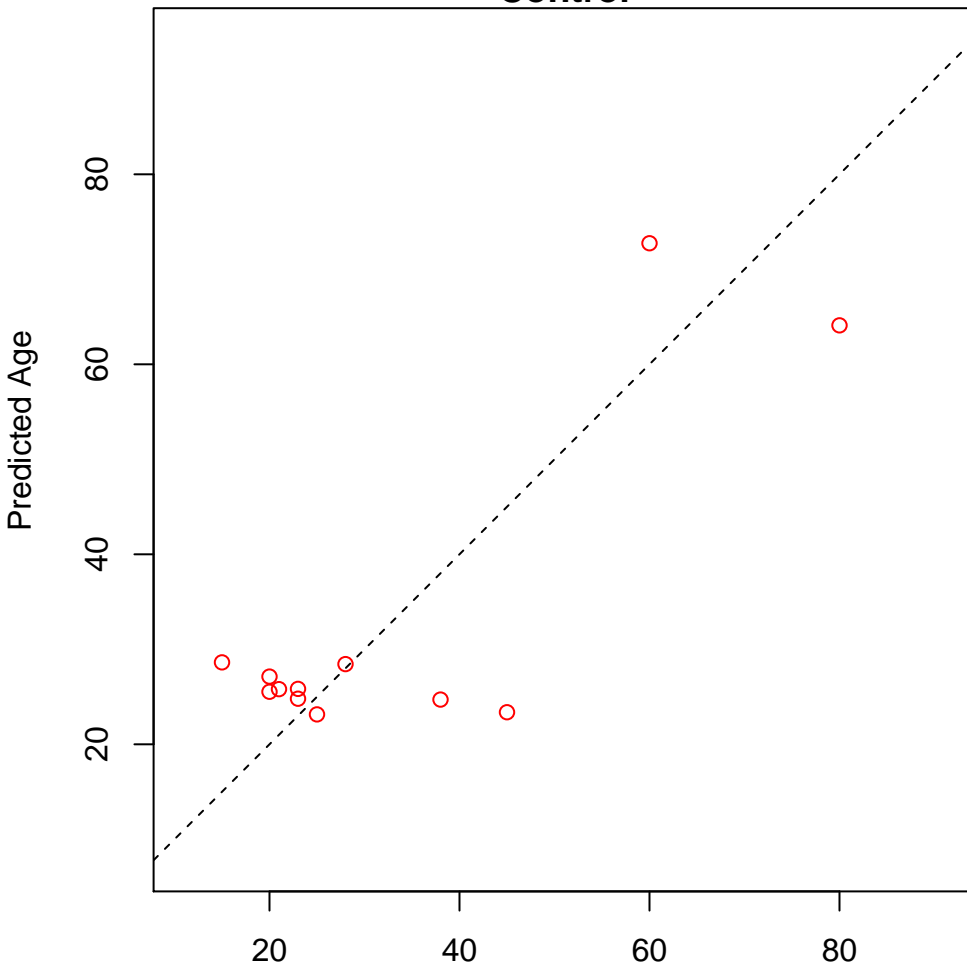


negative regulation of DNA recombination (Score: 5.914250)

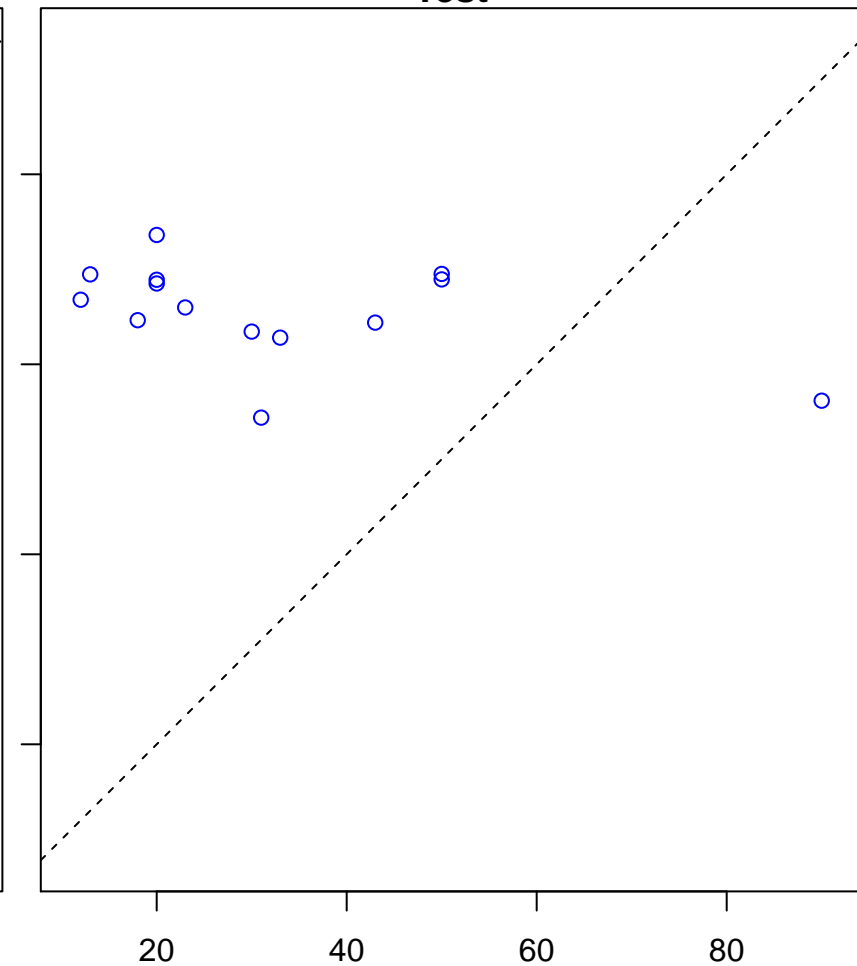


regulation of smooth muscle contraction (Score: 5.910201)

Control



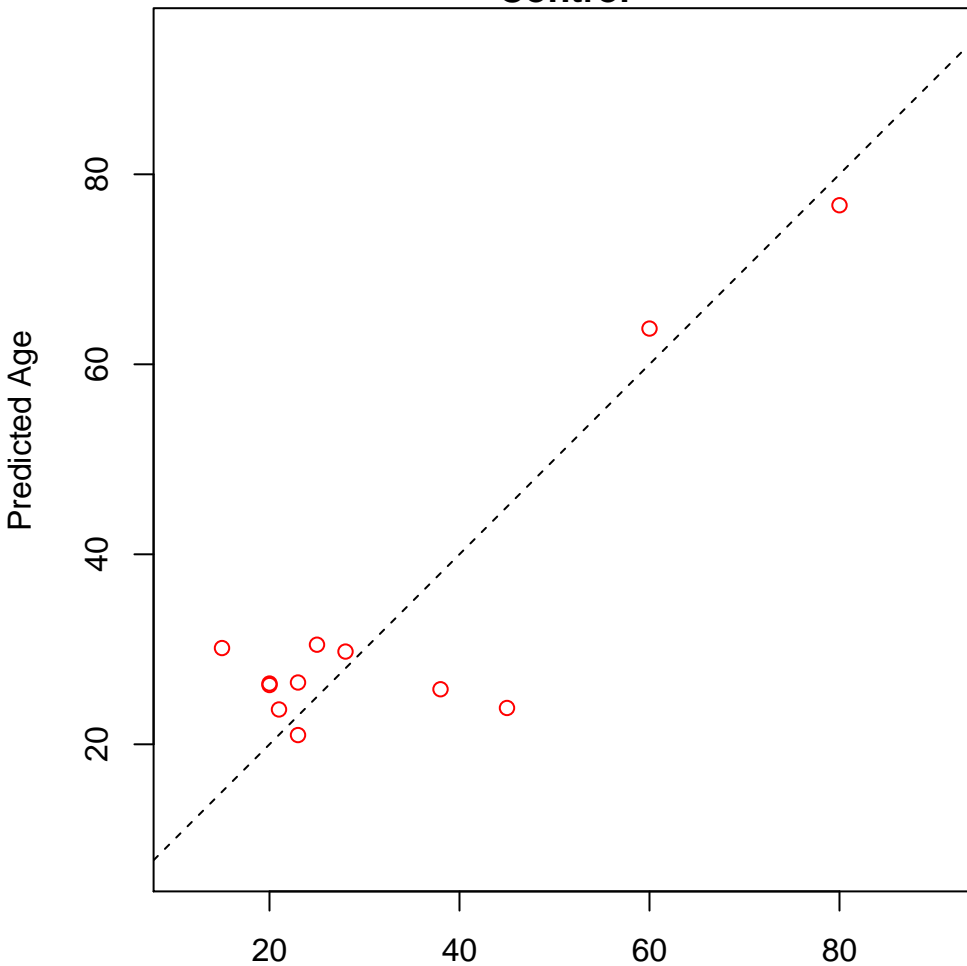
Test



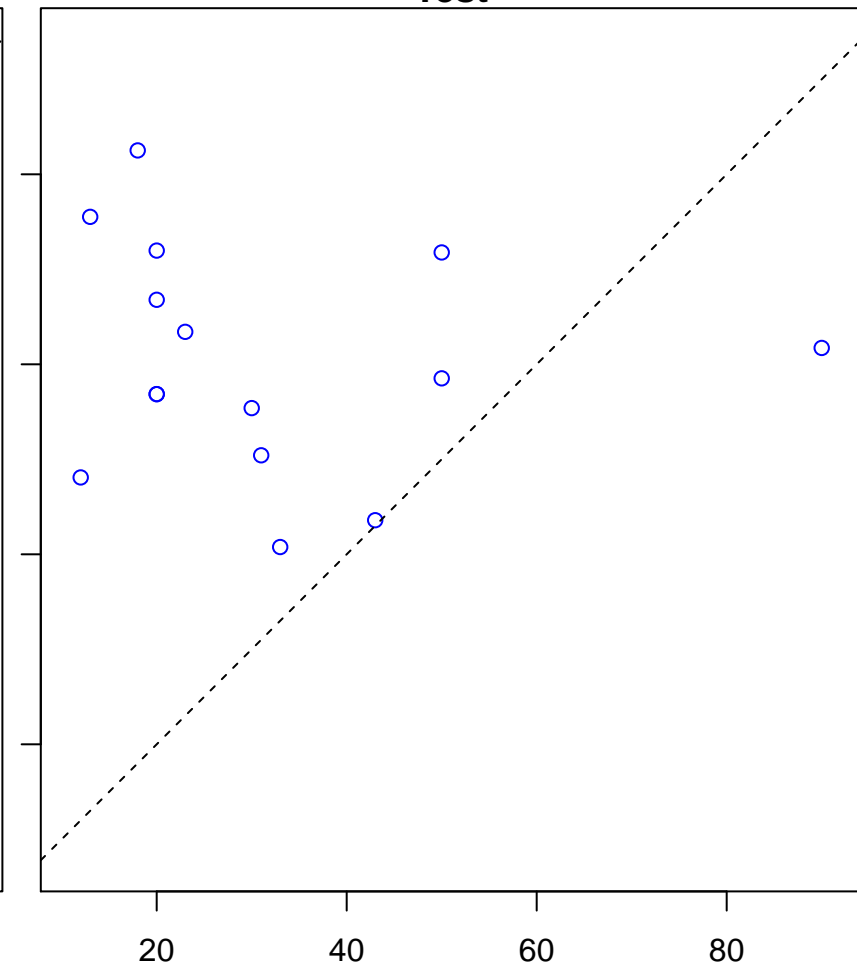
Actual Age

monosaccharide biosynthetic process (Score: 5.910194)

Control

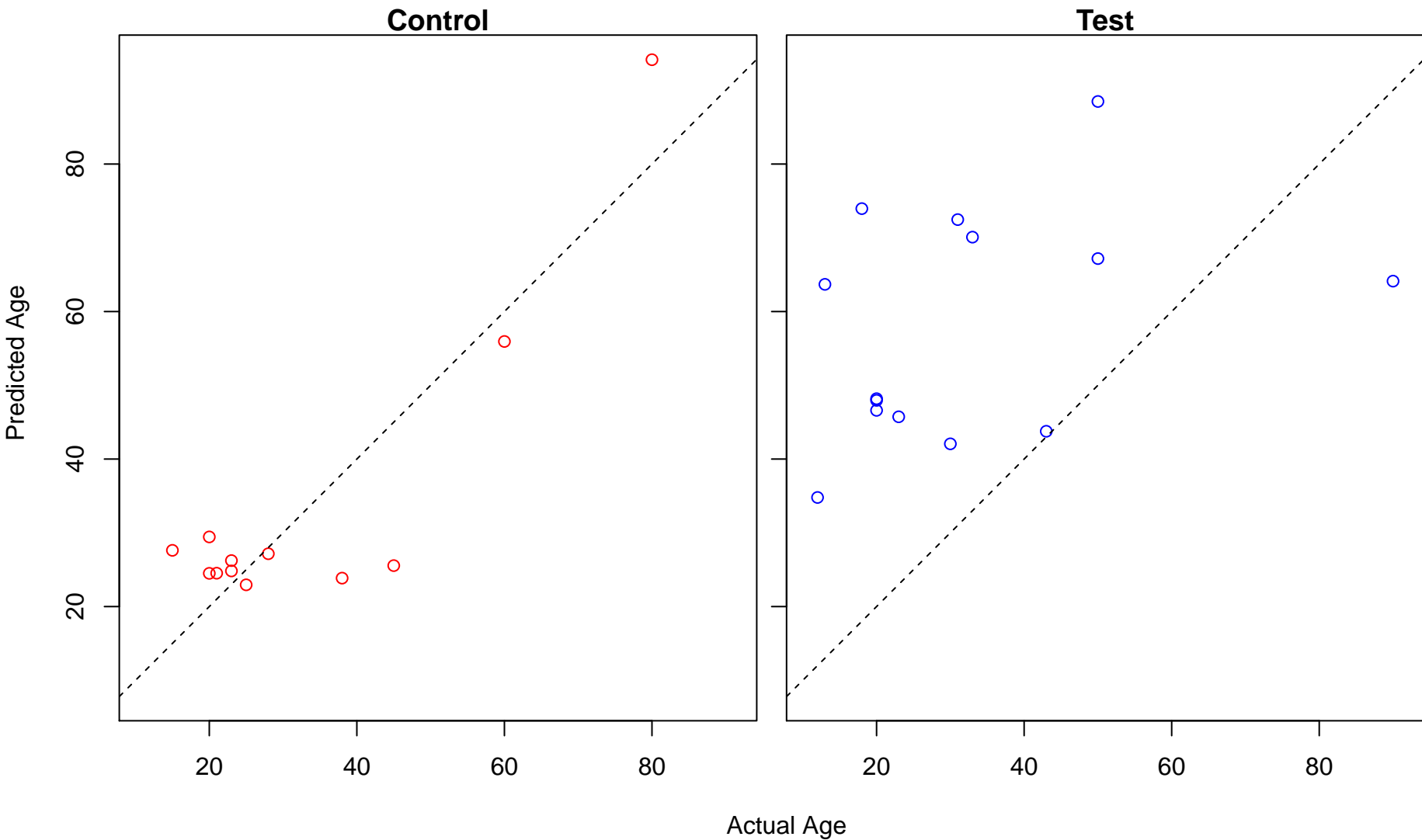


Test

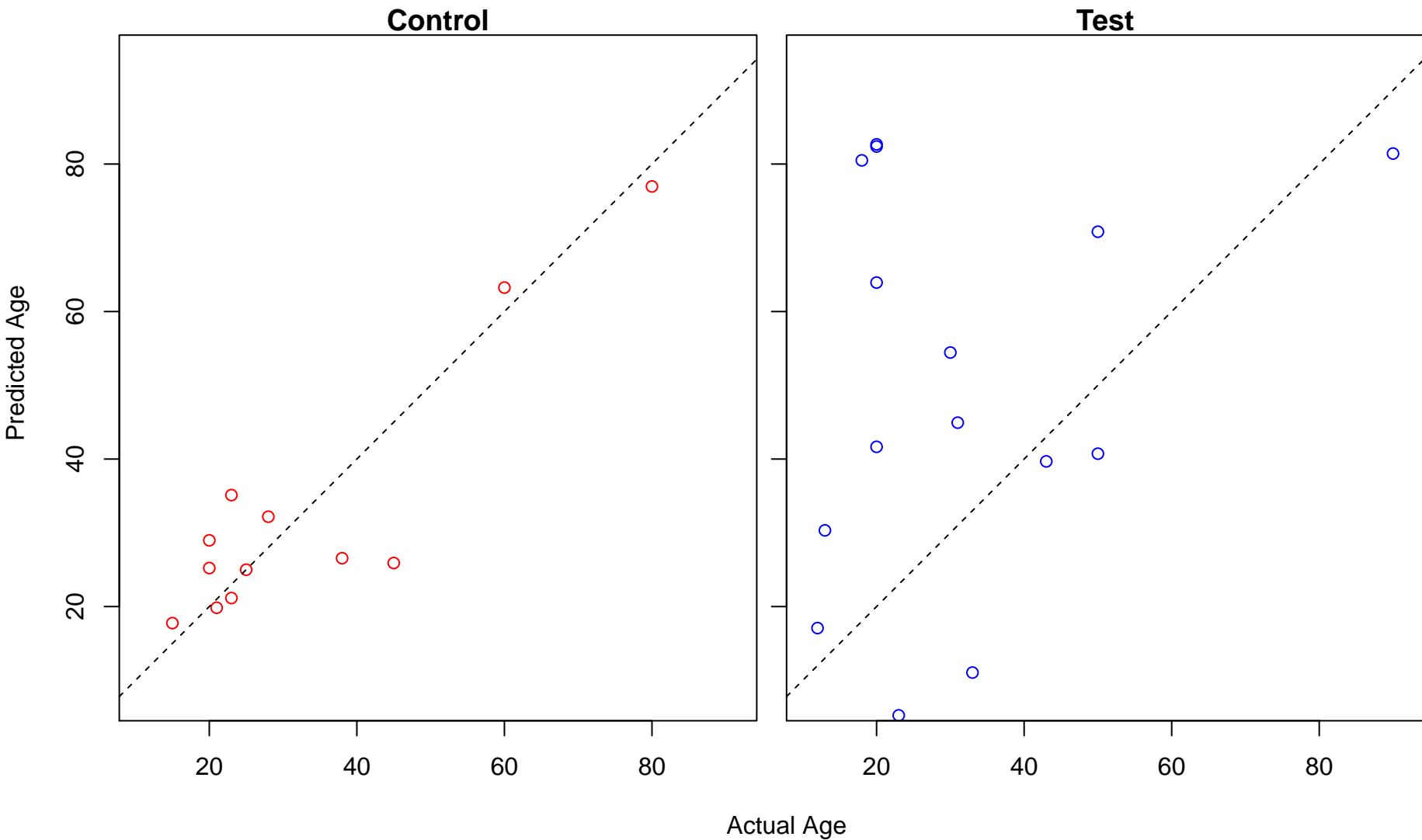


Actual Age

regulation of cytosolic calcium ion concentration (Score: 5.909927)

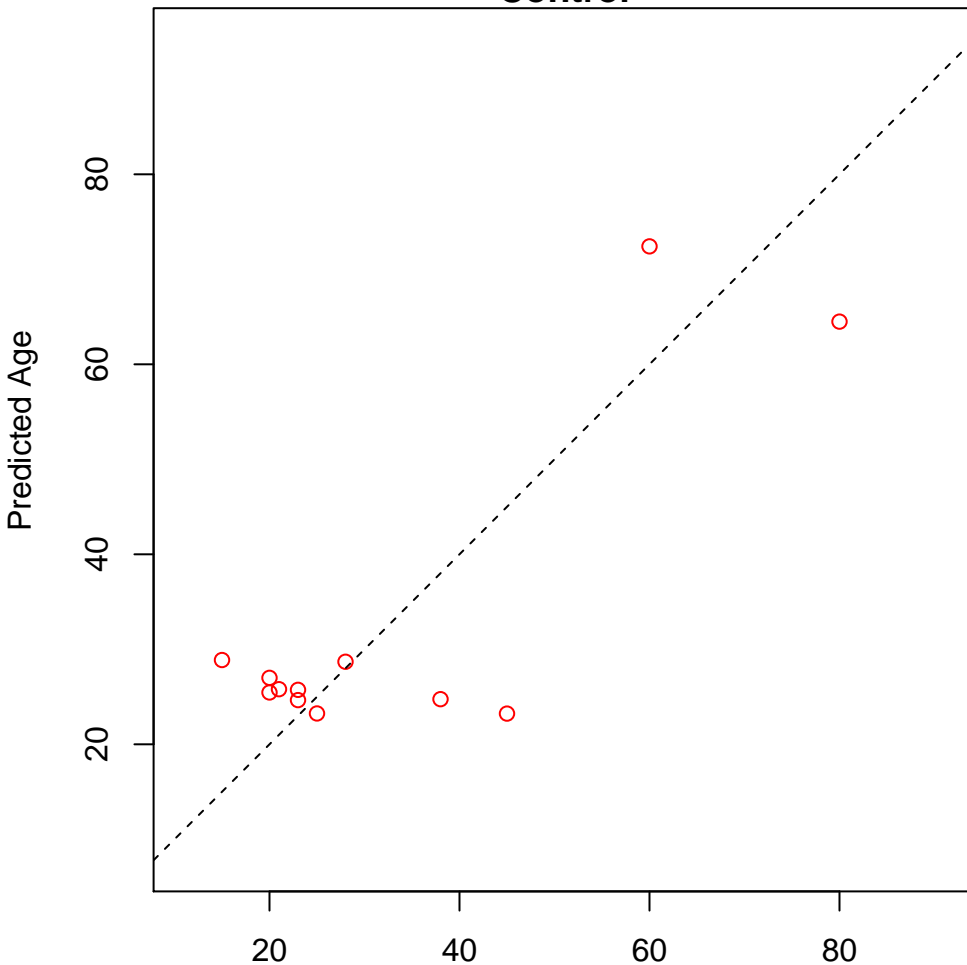


long-term synaptic potentiation (Score: 5.909893)

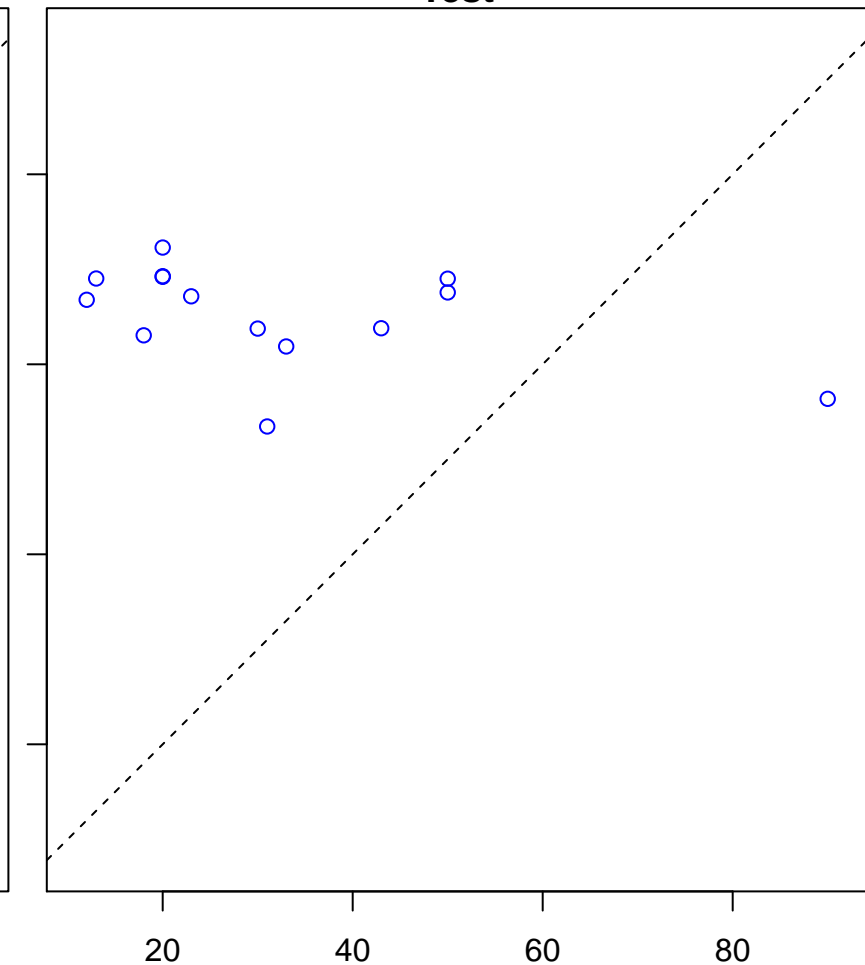


auditory receptor cell differentiation (Score: 5.908895)

Control

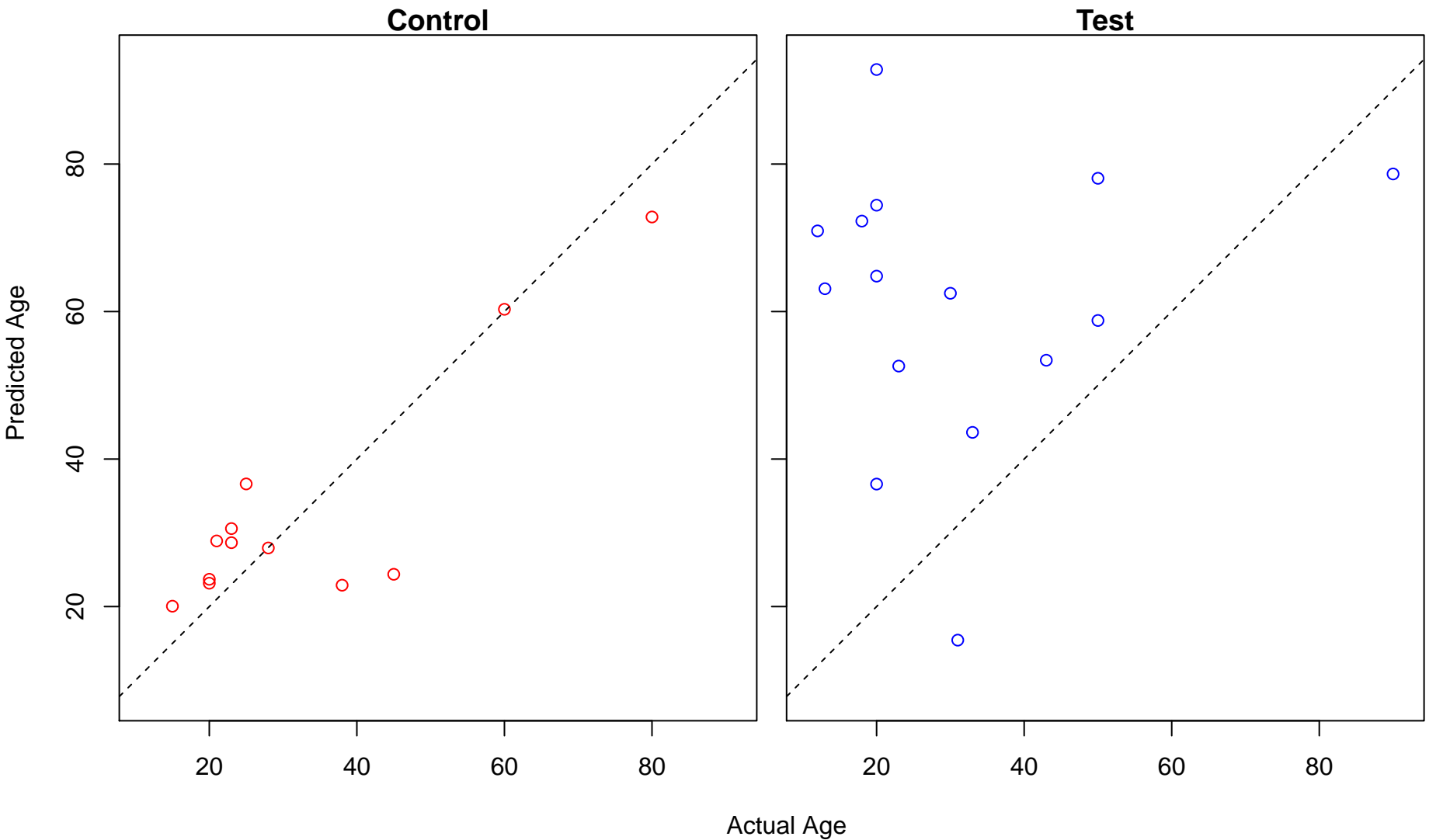


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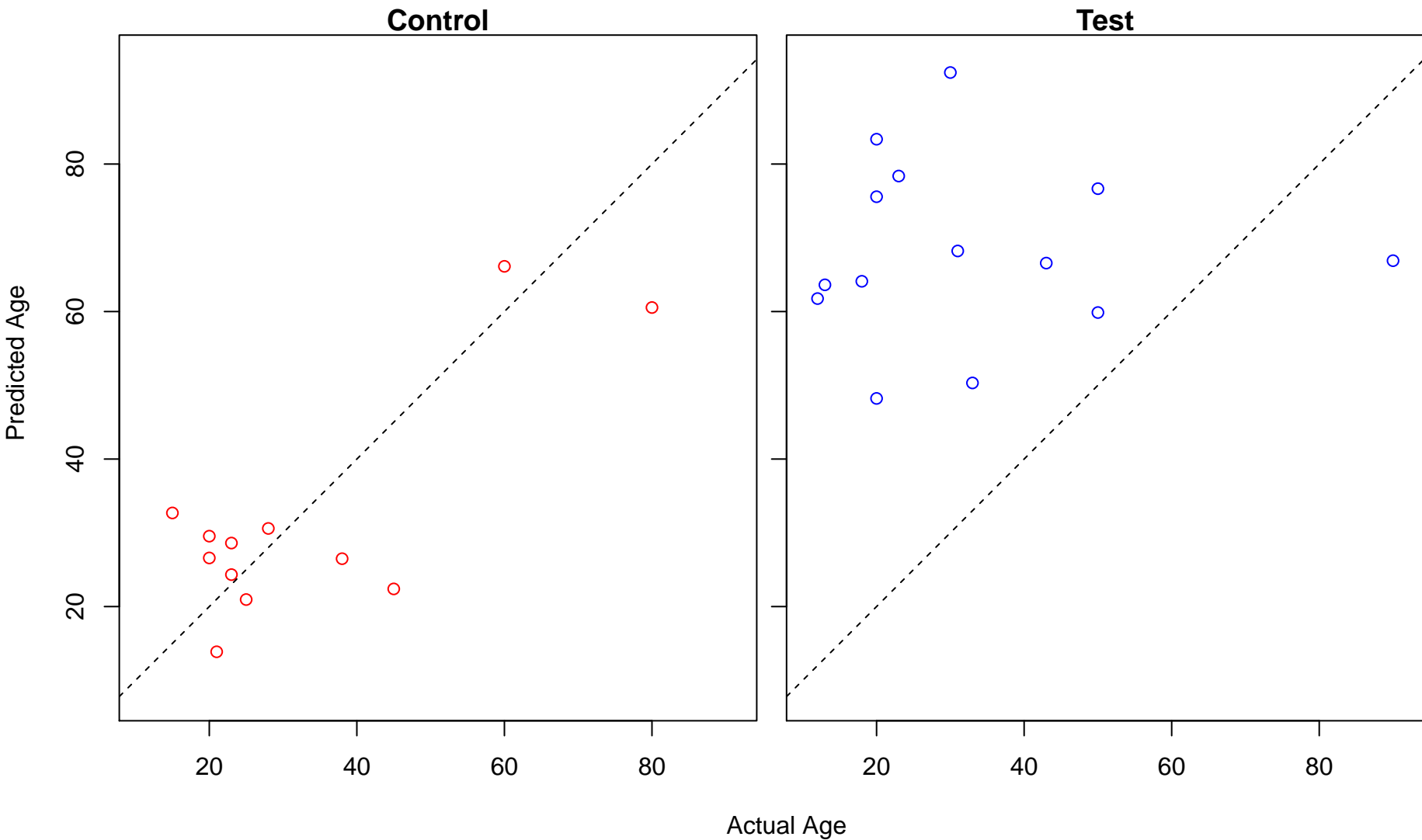


Actual Age

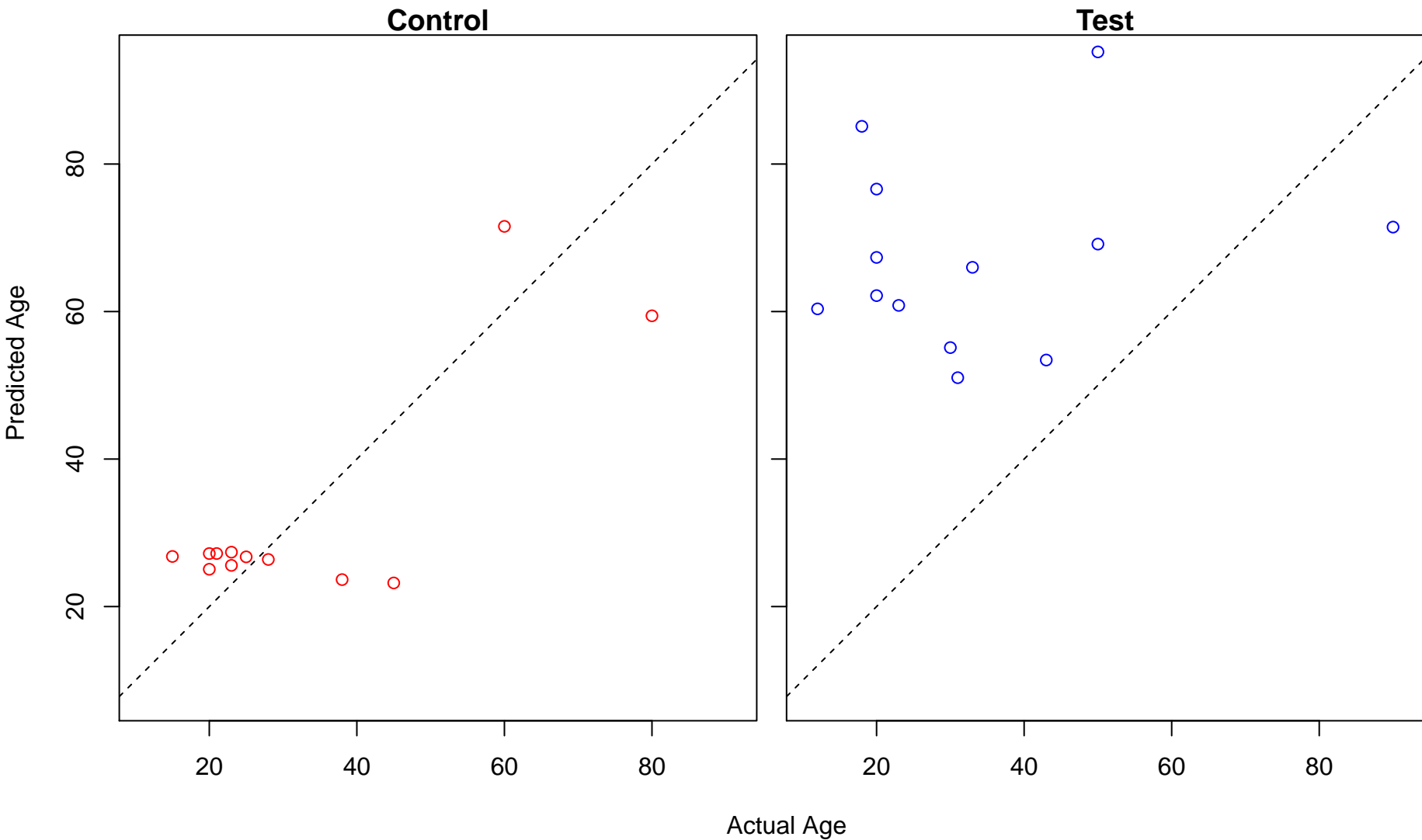
Positive regulation of transcription from RNA polymerase II promoter involved in heart development (Score: 100)



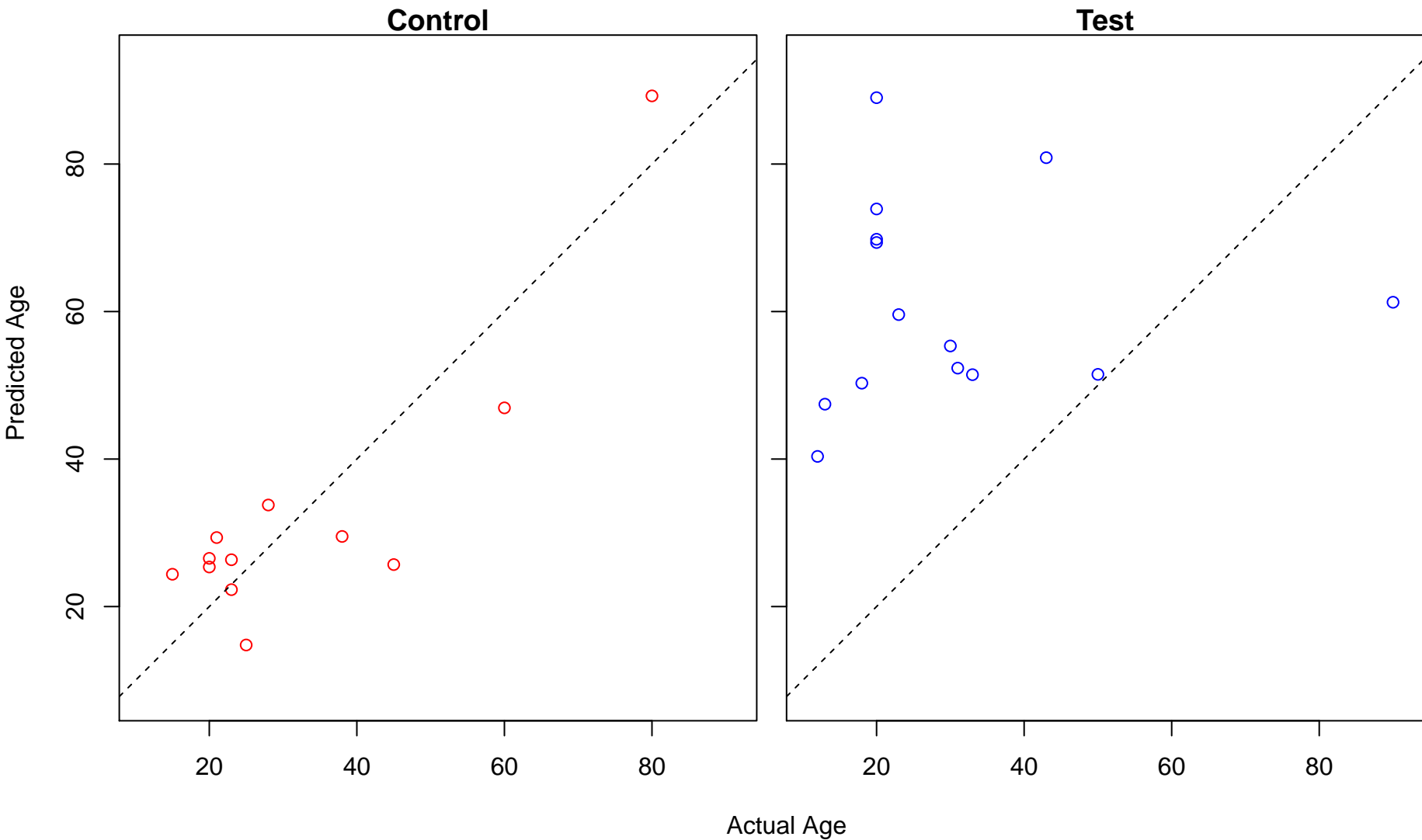
positive regulation of humoral immune response (Score: 5.902386)



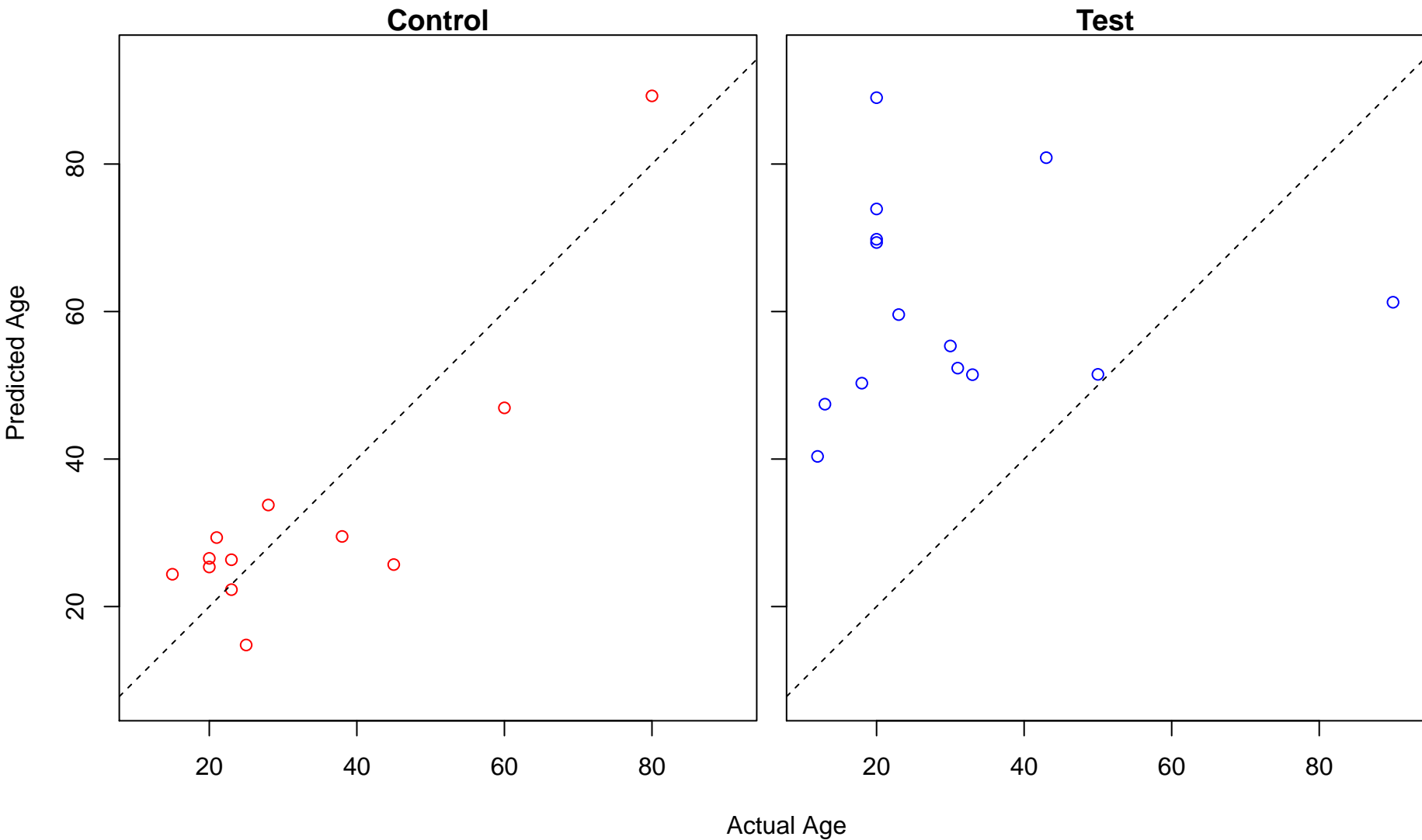
serine family amino acid metabolic process (Score: 5.900872)



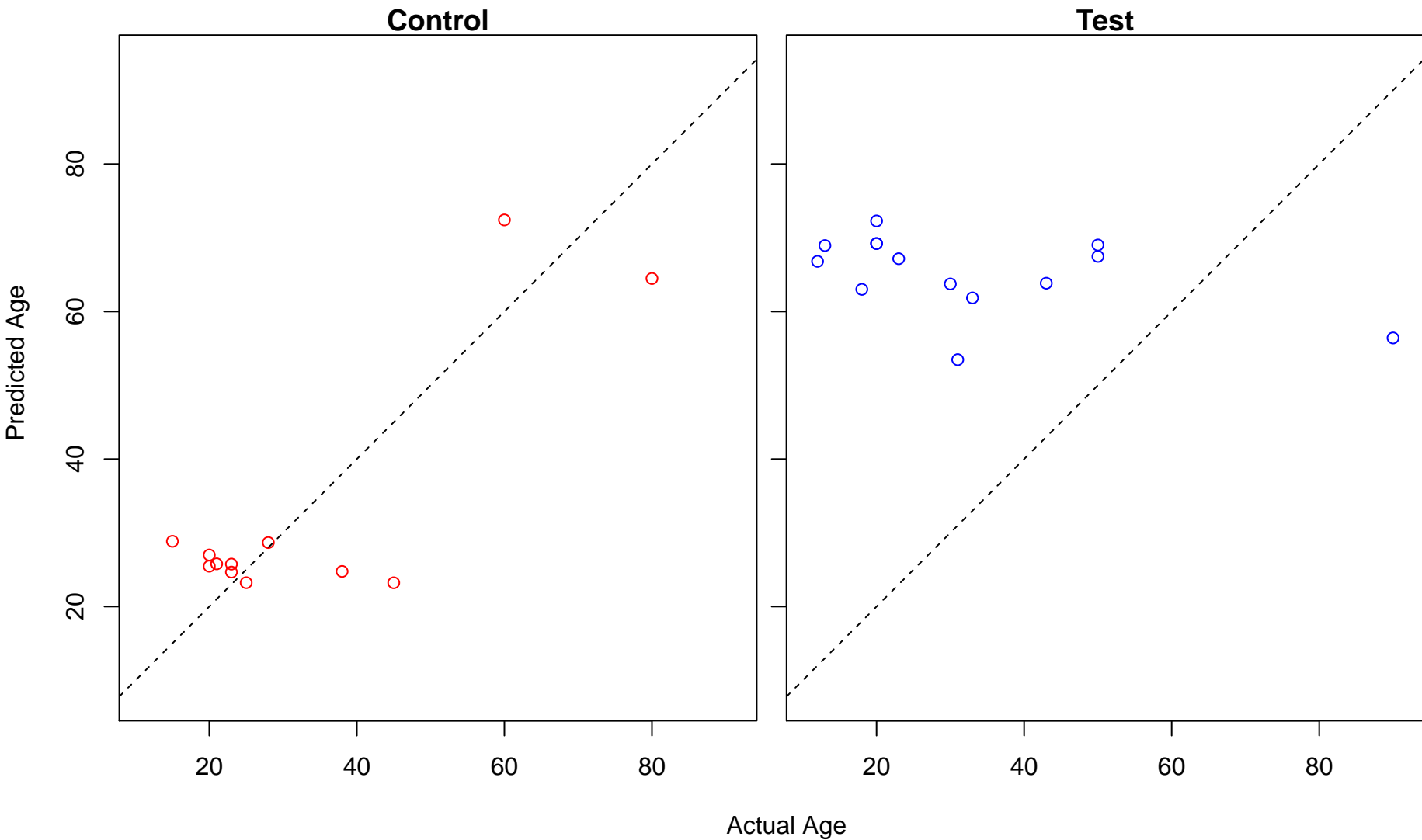
ethanol metabolic process (Score: 5.899649)



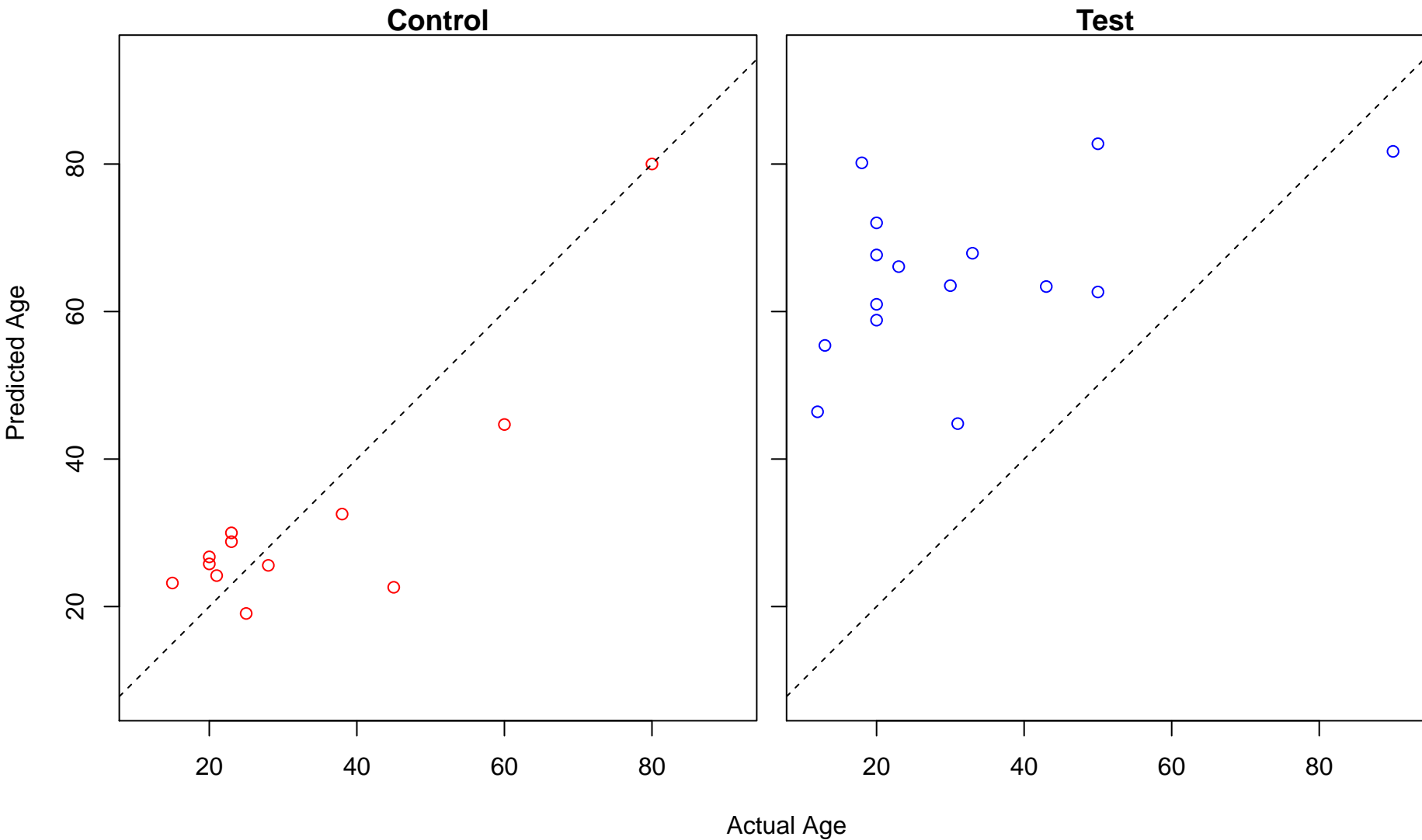
ethanol oxidation (Score: 5.899649)



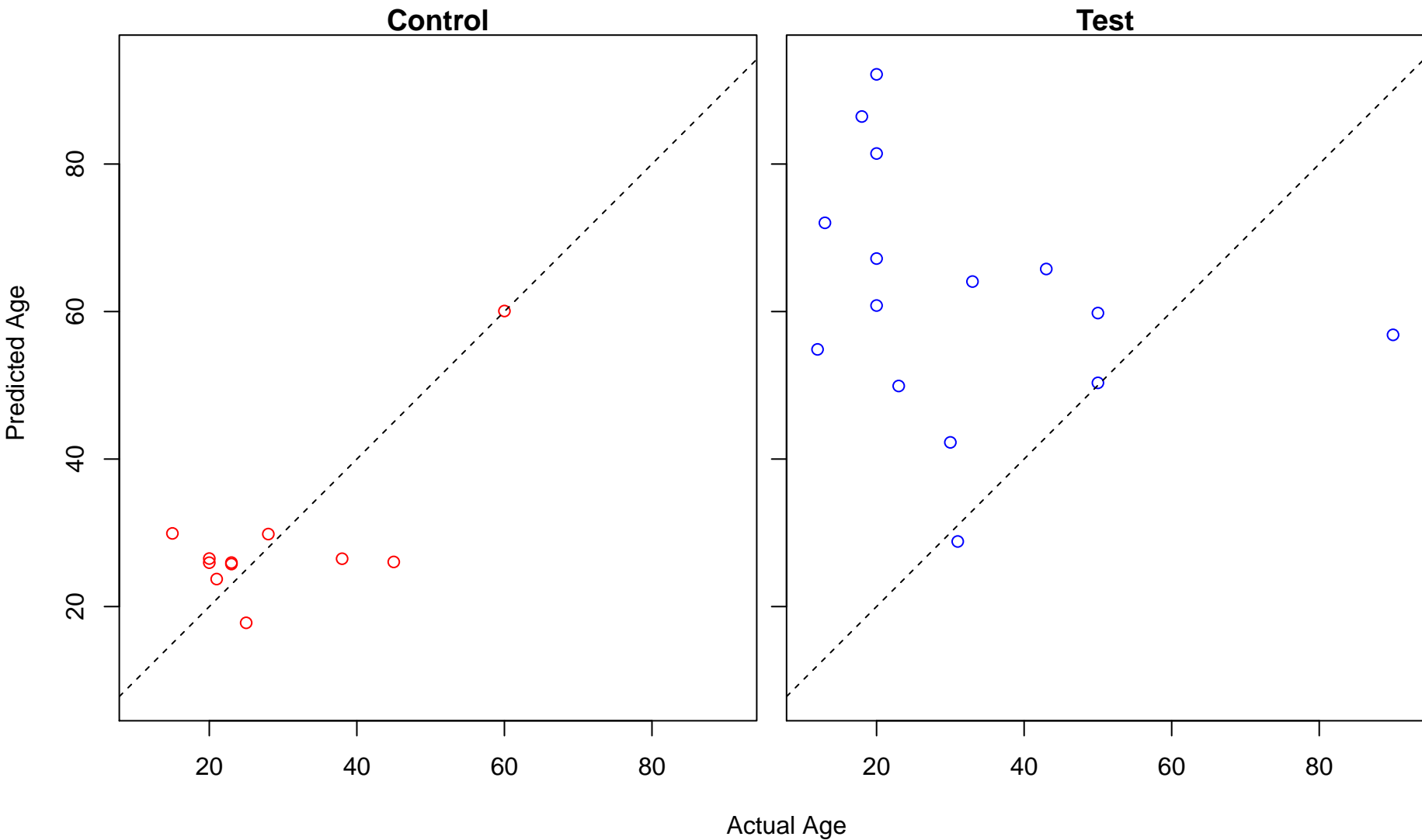
columnar/cuboidal epithelial cell development (Score: 5.898838)



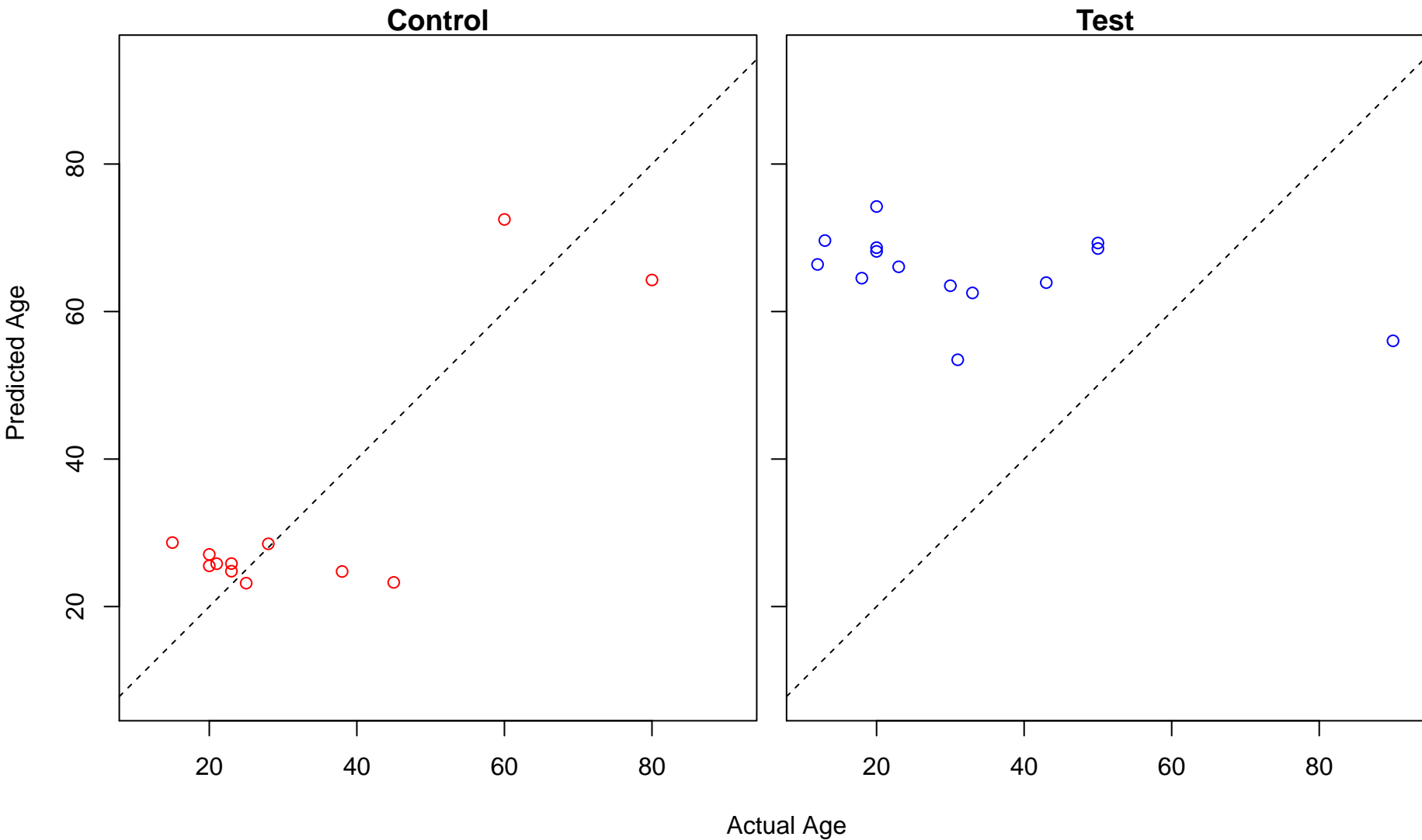
bundle of His cell to Purkinje myocyte communication (Score: 5.897539)



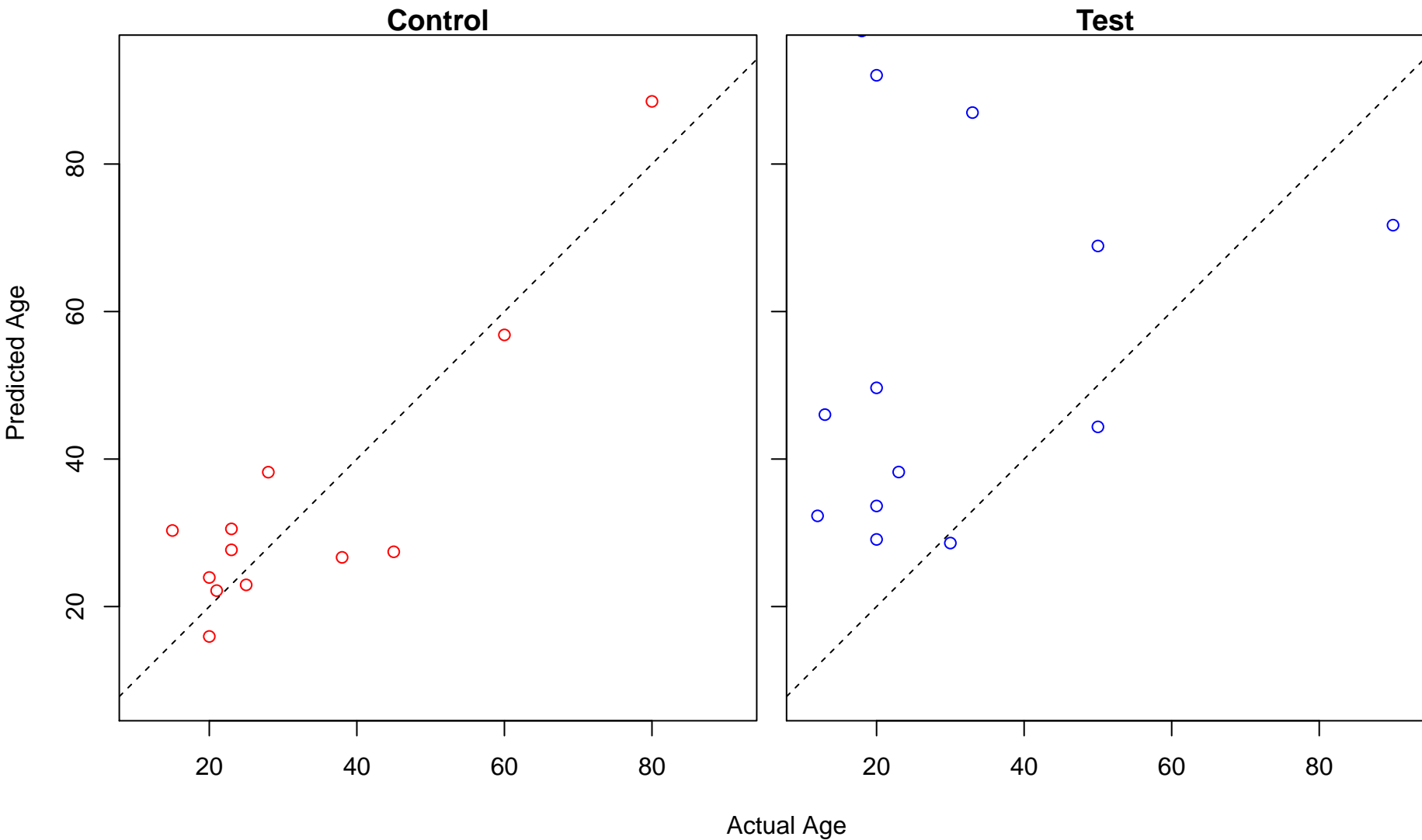
negative regulation of DNA-templated transcription, elongation (Score: 5.894497)



inner ear morphogenesis (Score: 5.894113)

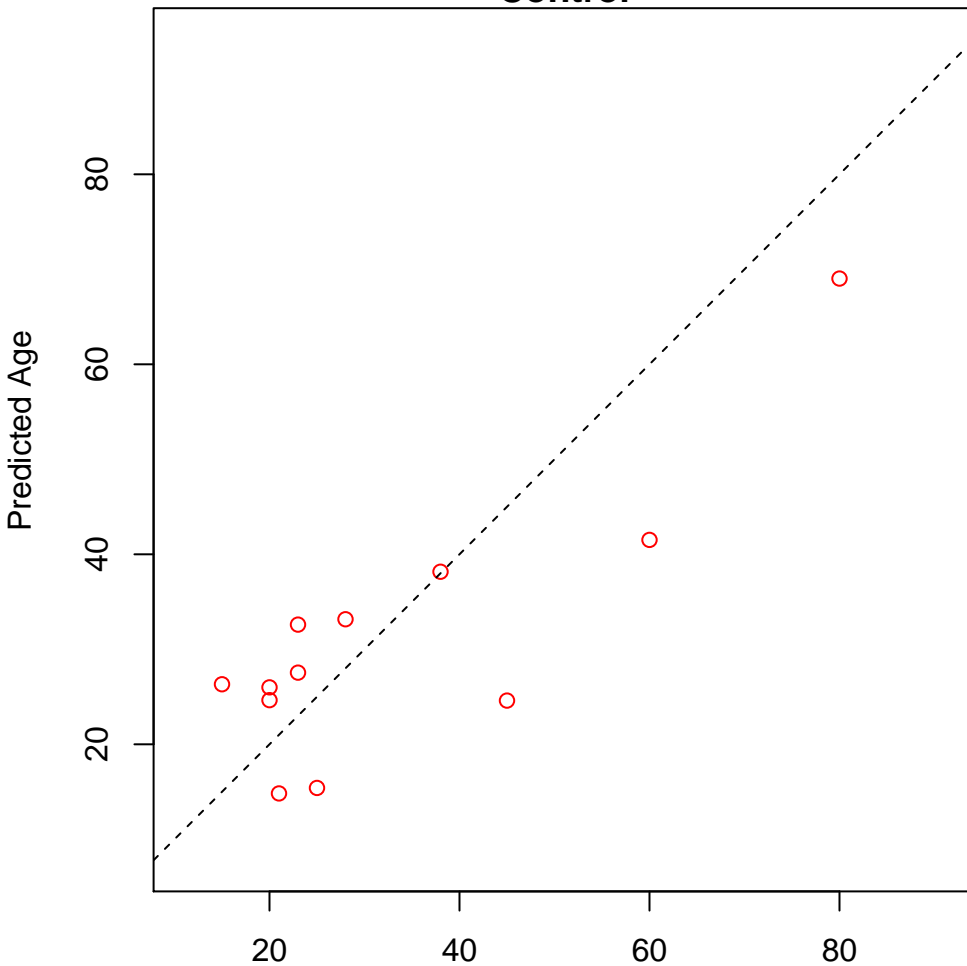


growth (Score: 5.891793)

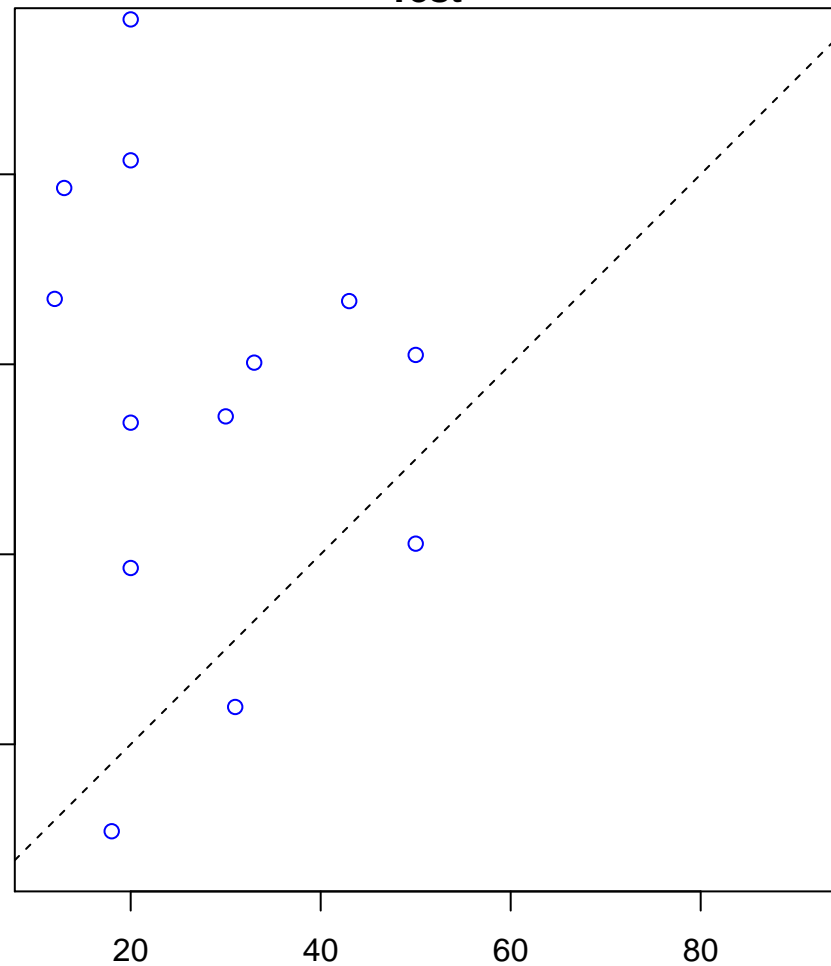


glandular epithelial cell development (Score: 5.889706)

Control

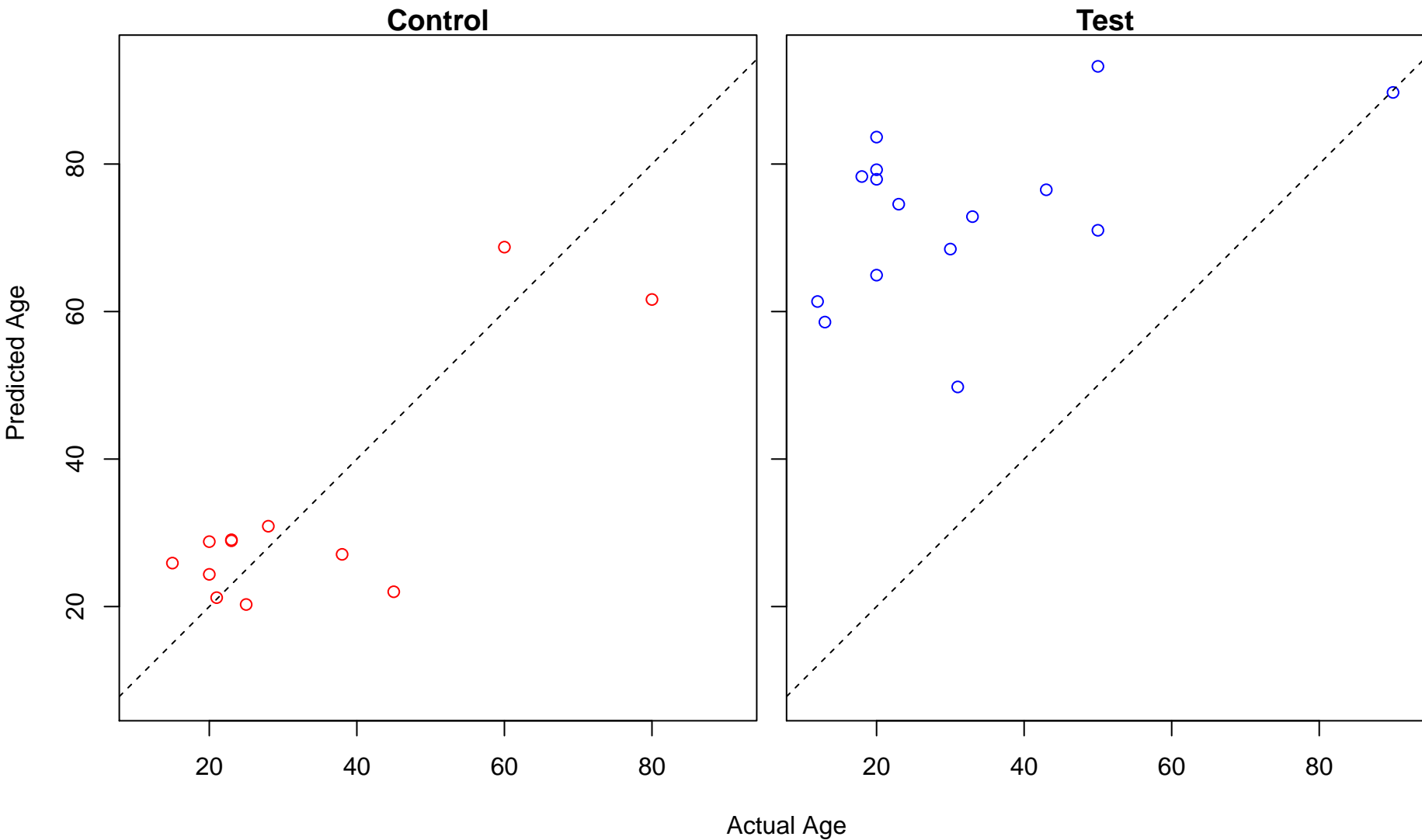


Test

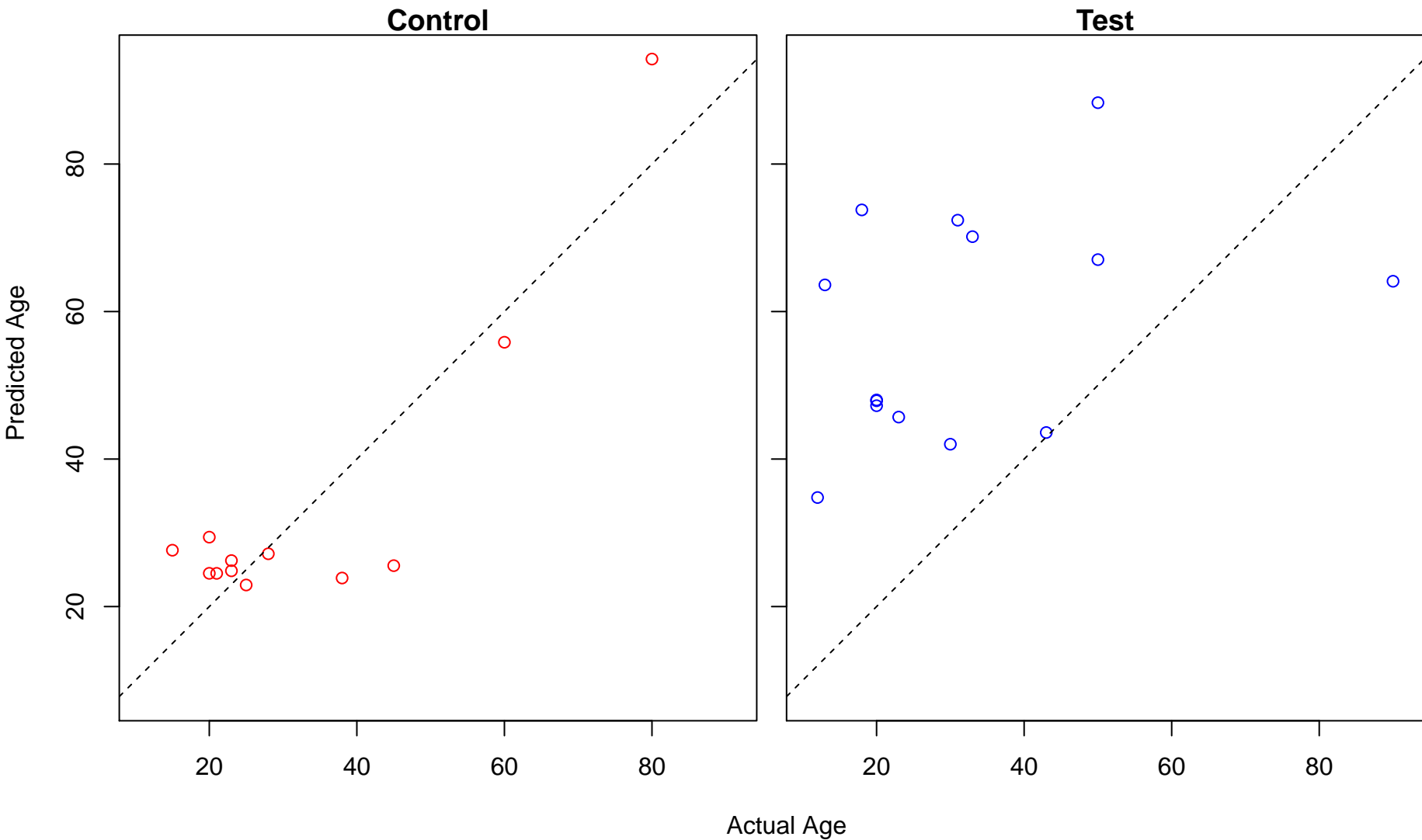


Actual Age

cranial nerve development (Score: 5.889293)

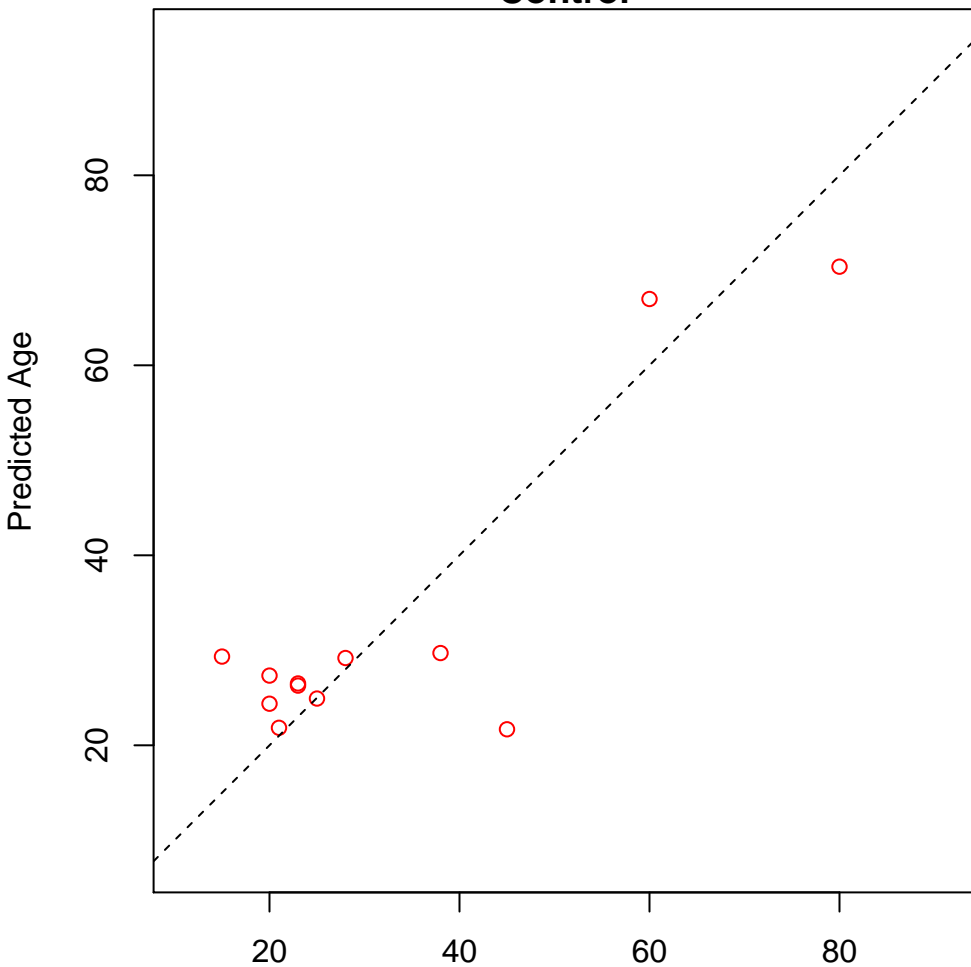


positive regulation of cytosolic calcium ion concentration (Score: 5.888202)

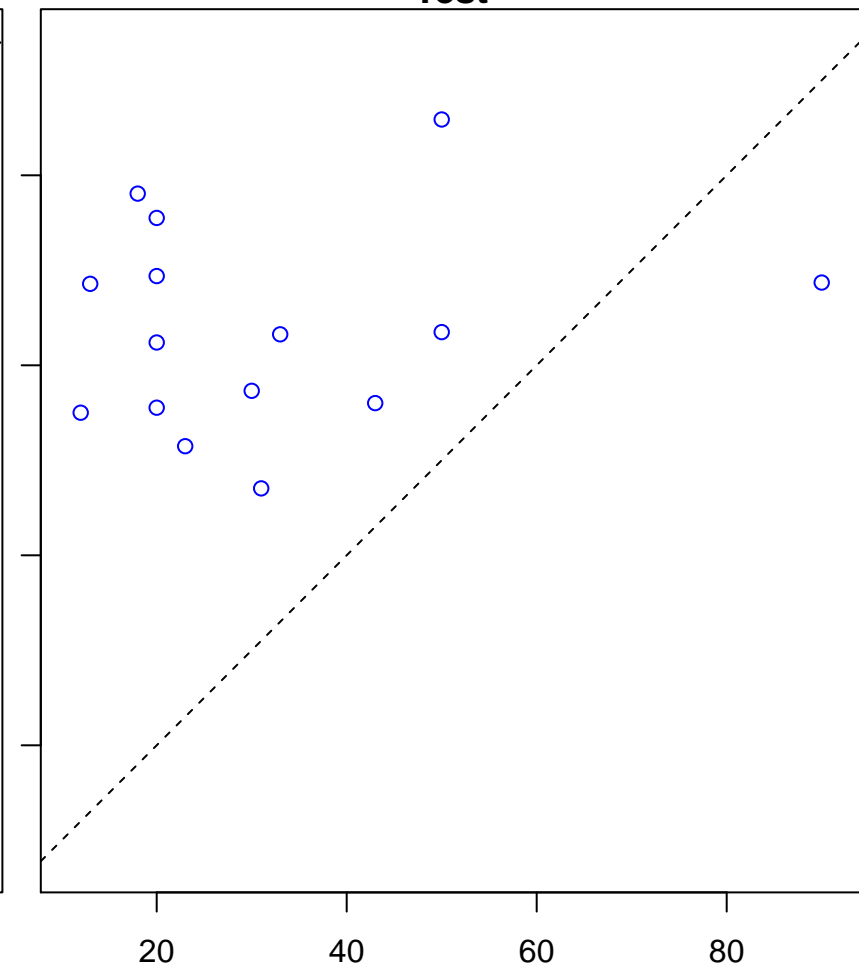


regulation of peptidyl-lysine acetylation (Score: 5.887295)

Control

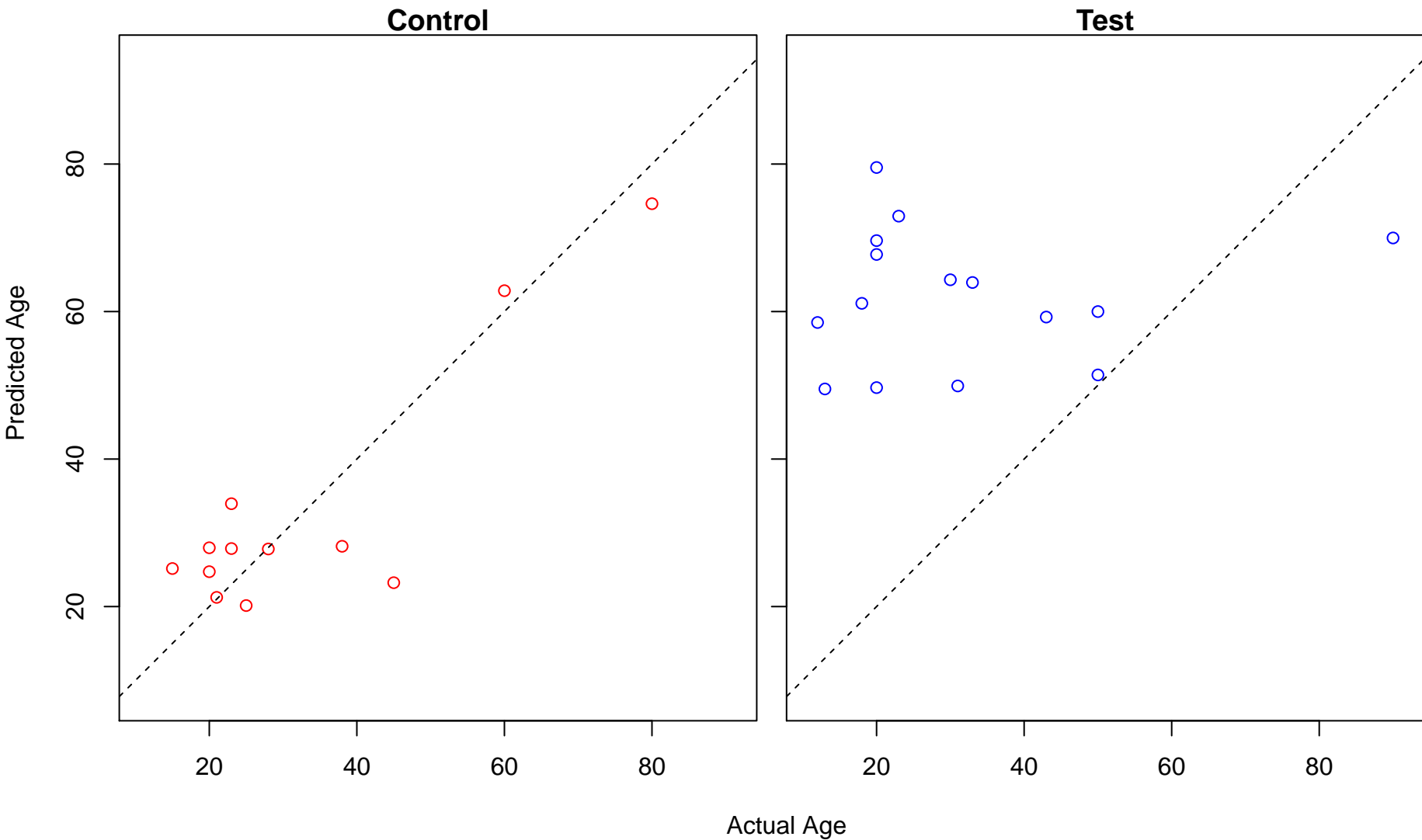


Test

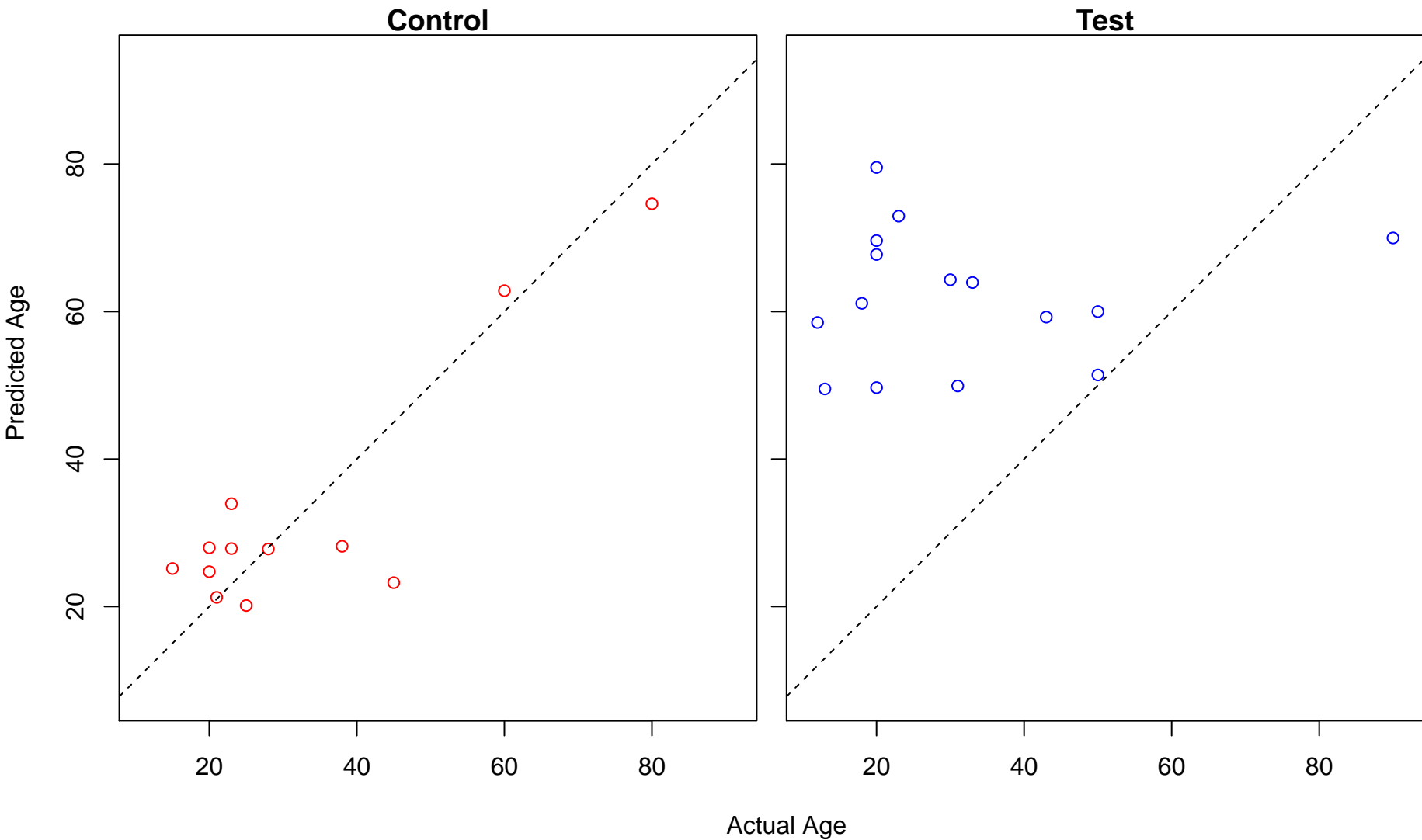


Actual Age

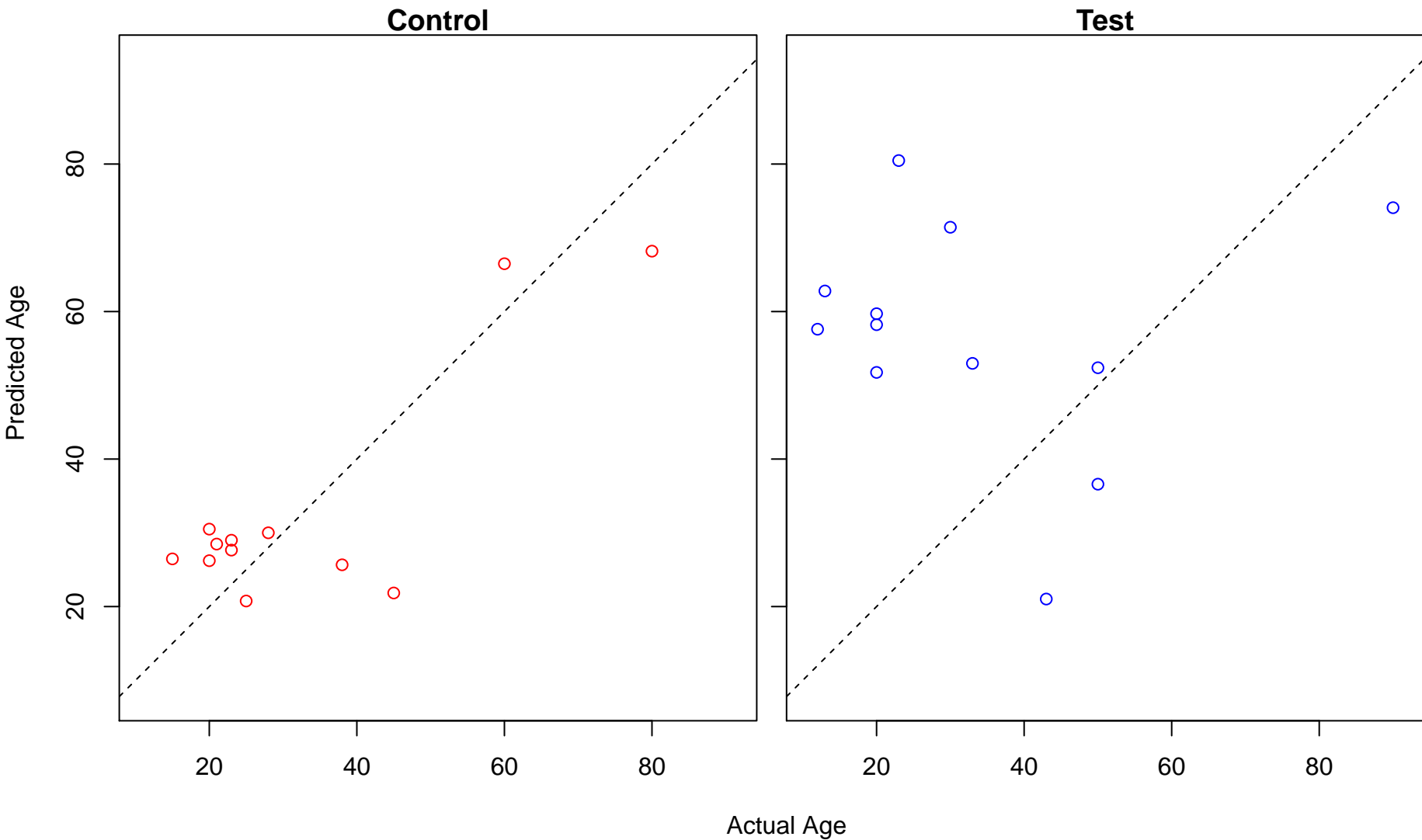
organic acid transport (Score: 5.885065)



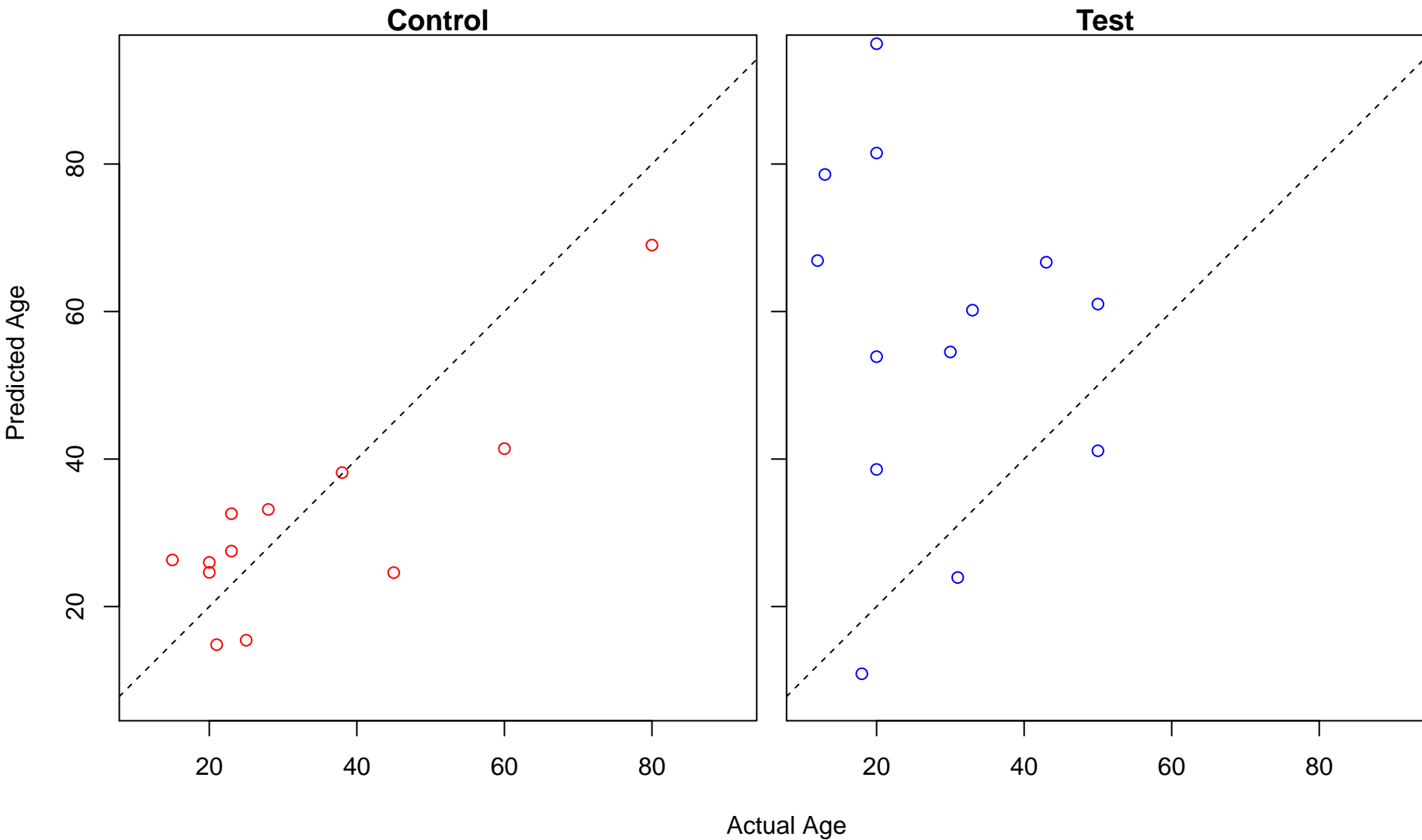
carboxylic acid transport (Score: 5.884962)



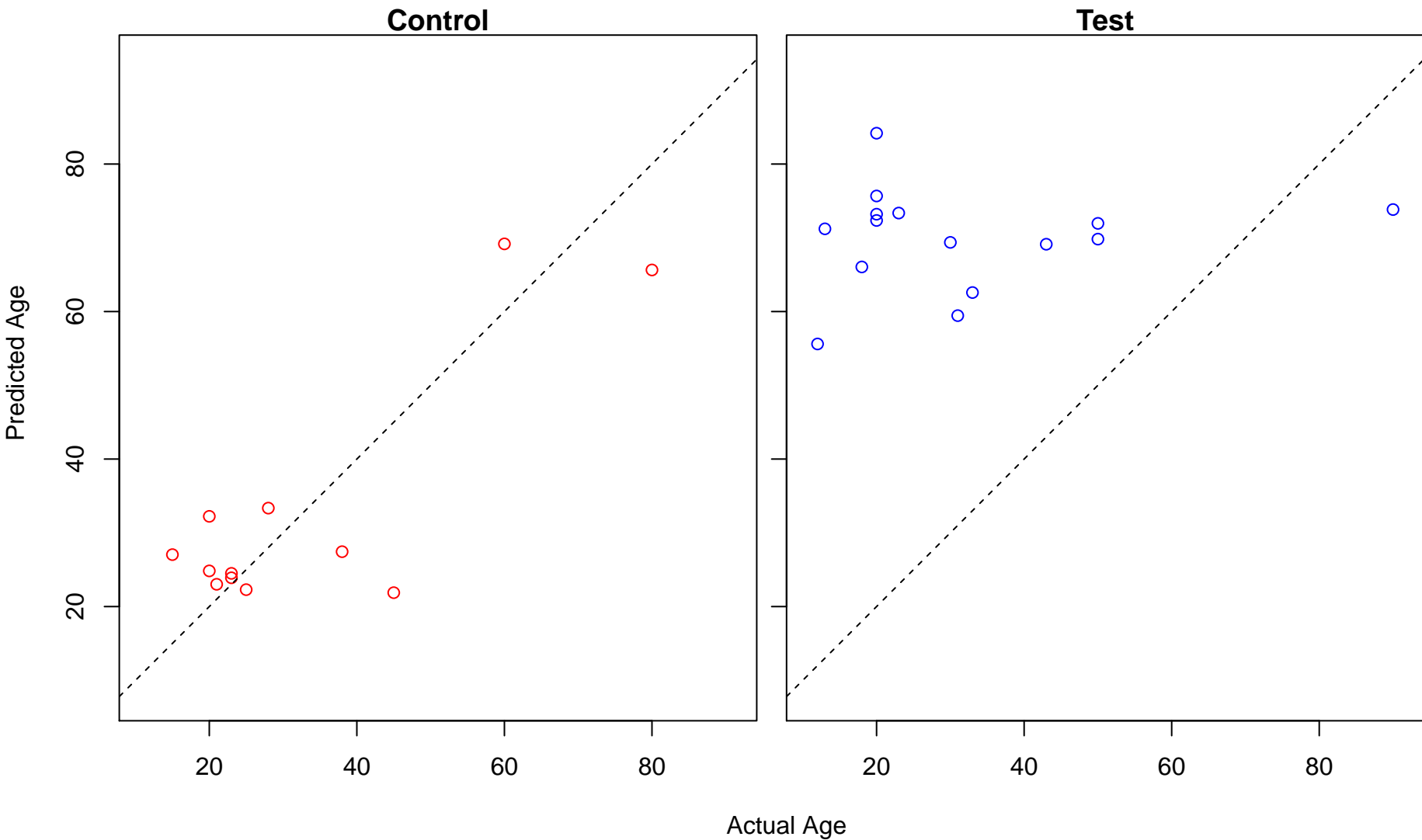
positive regulation of cell migration involved in sprouting angiogenesis (Score: 5.884959)



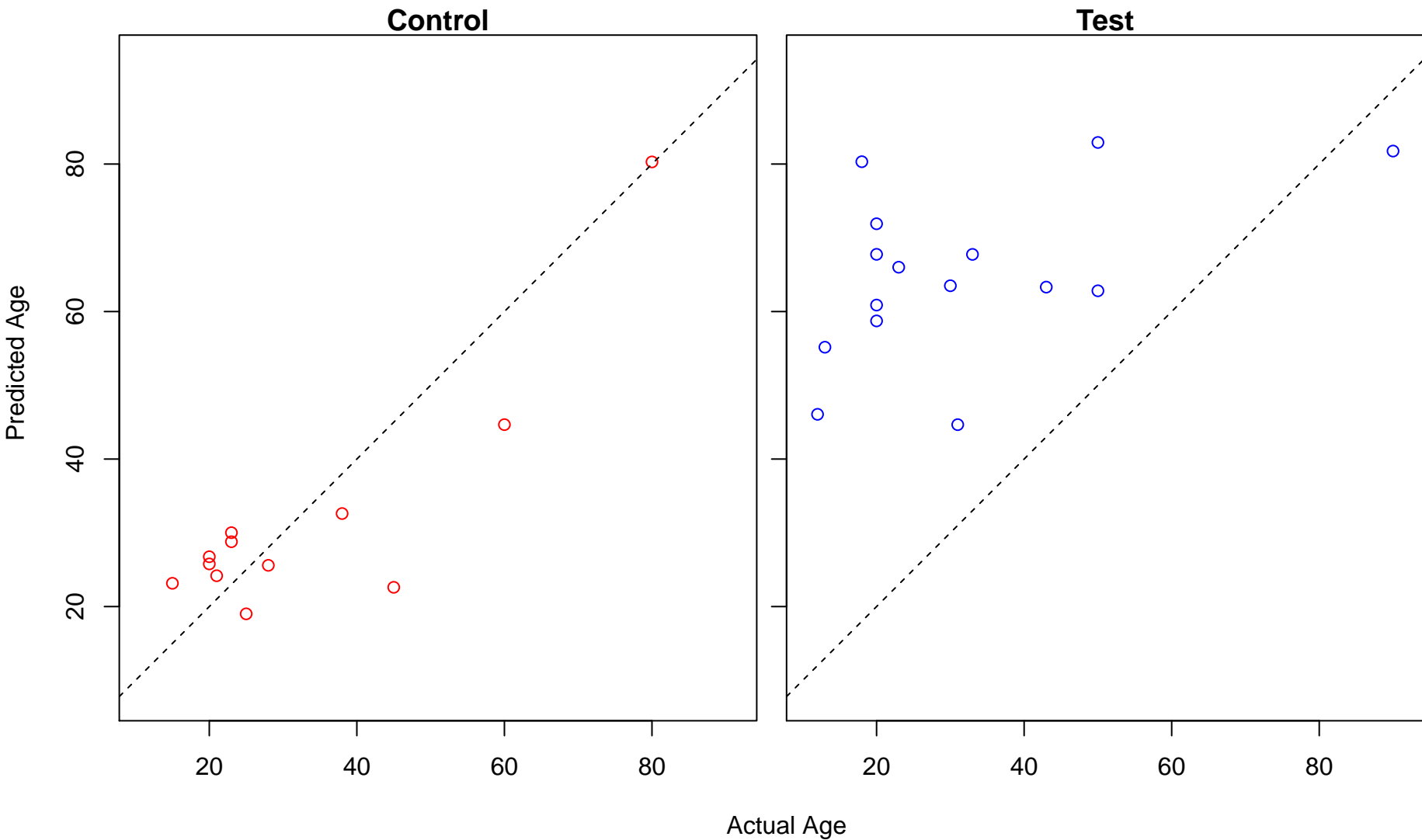
type B pancreatic cell development (Score: 5.883384)



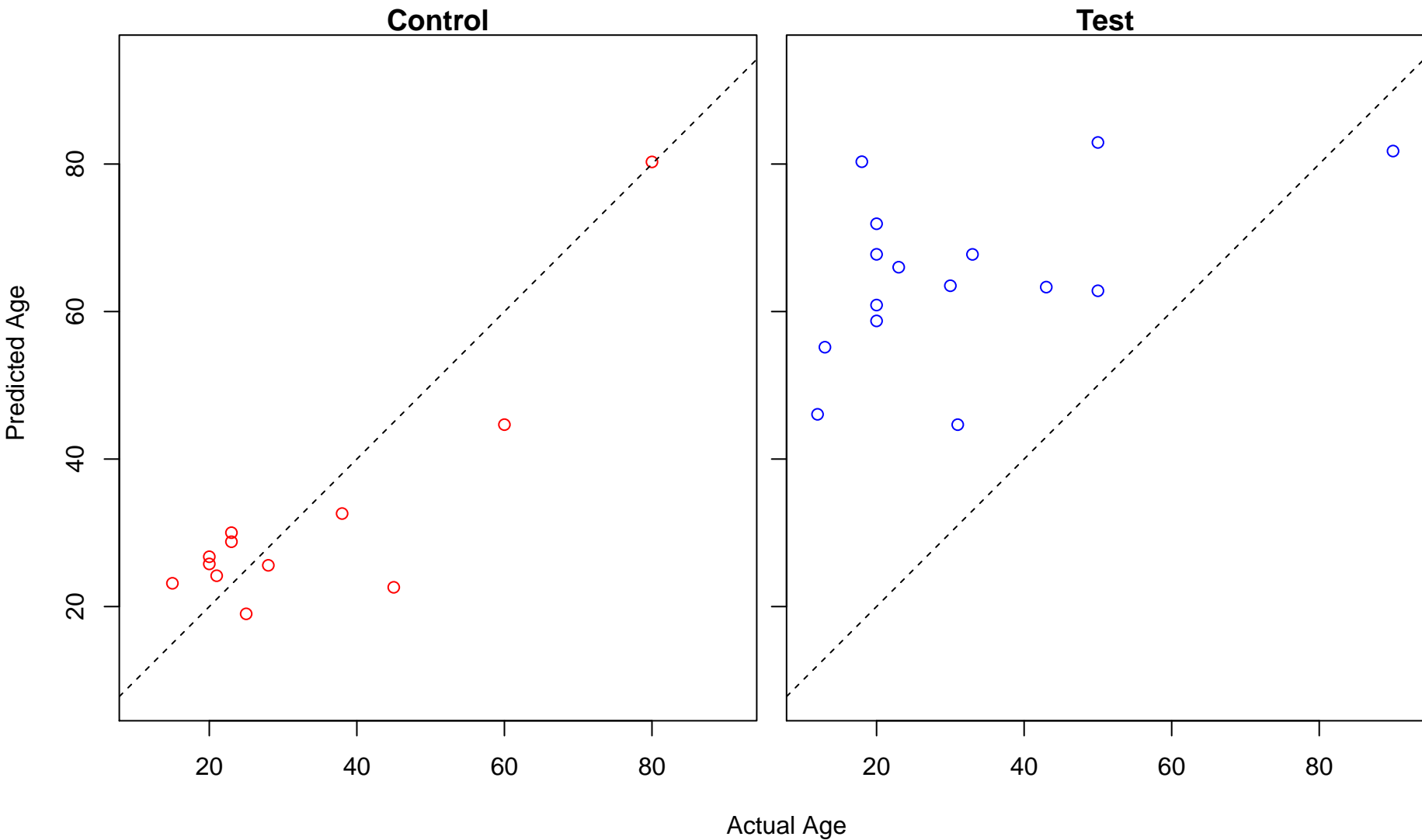
cell activation (Score: 5.883226)



cardiac muscle cell-cardiac muscle cell adhesion (Score: 5.878401)

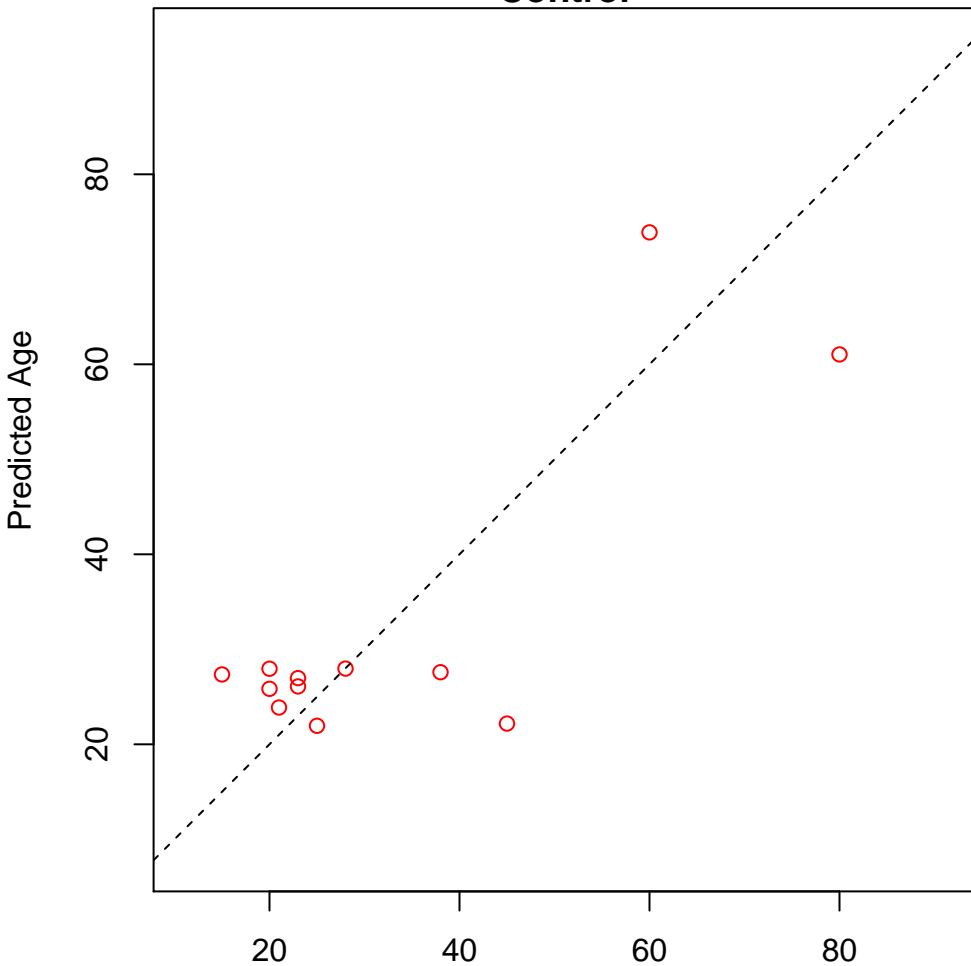


bundle of His cell–Purkinje myocyte adhesion involved in cell communication (Score: 5.878401)

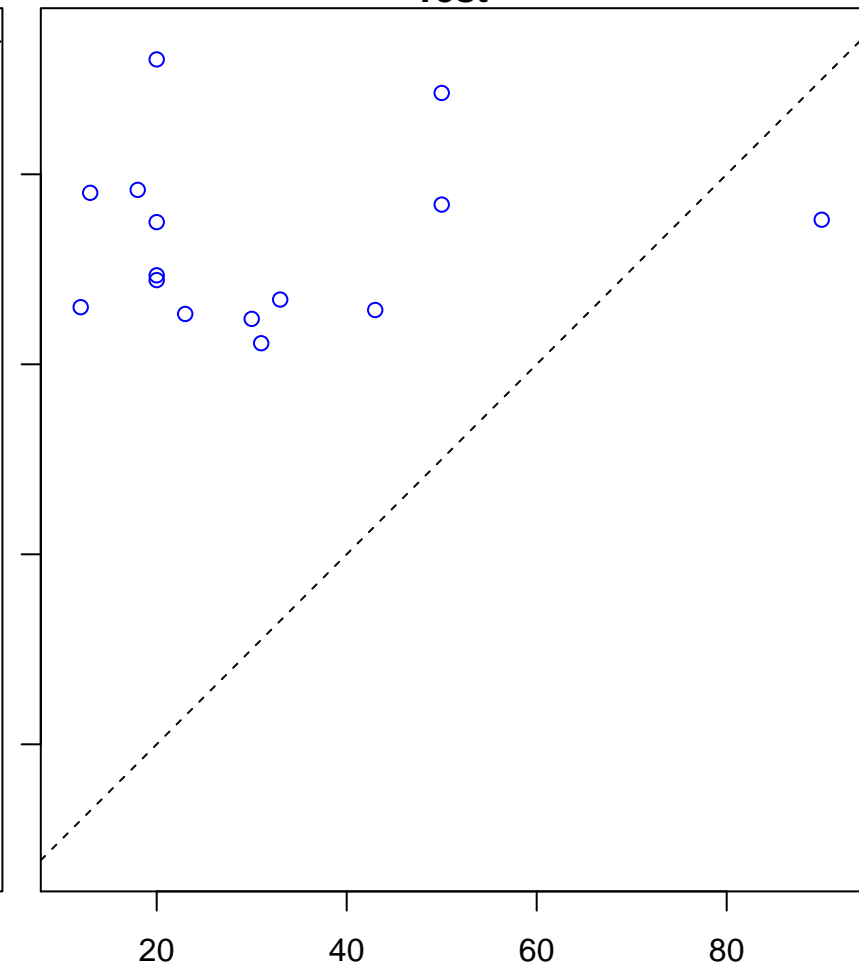


negative regulation of hydrolase activity (Score: 5.875841)

Control

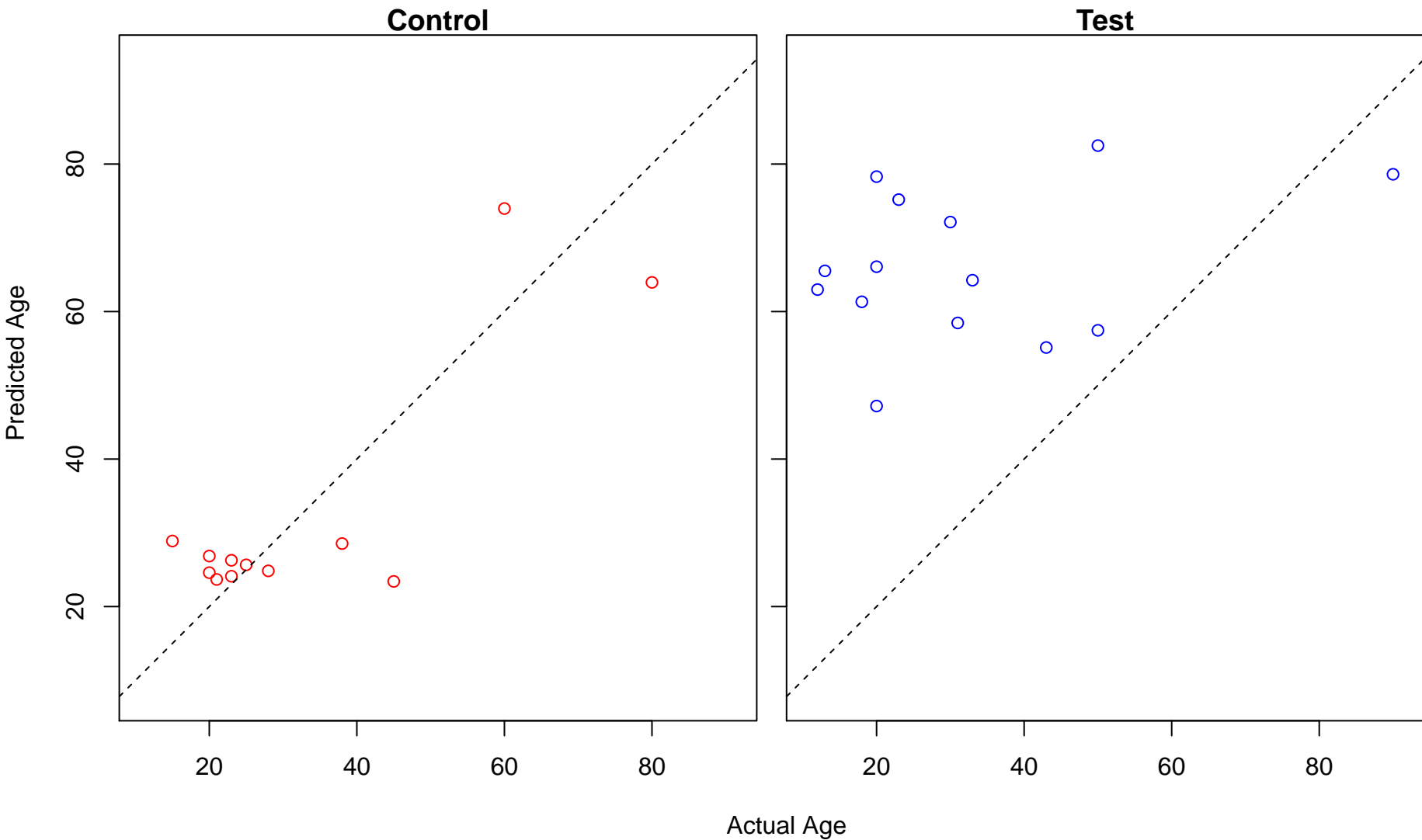


Test

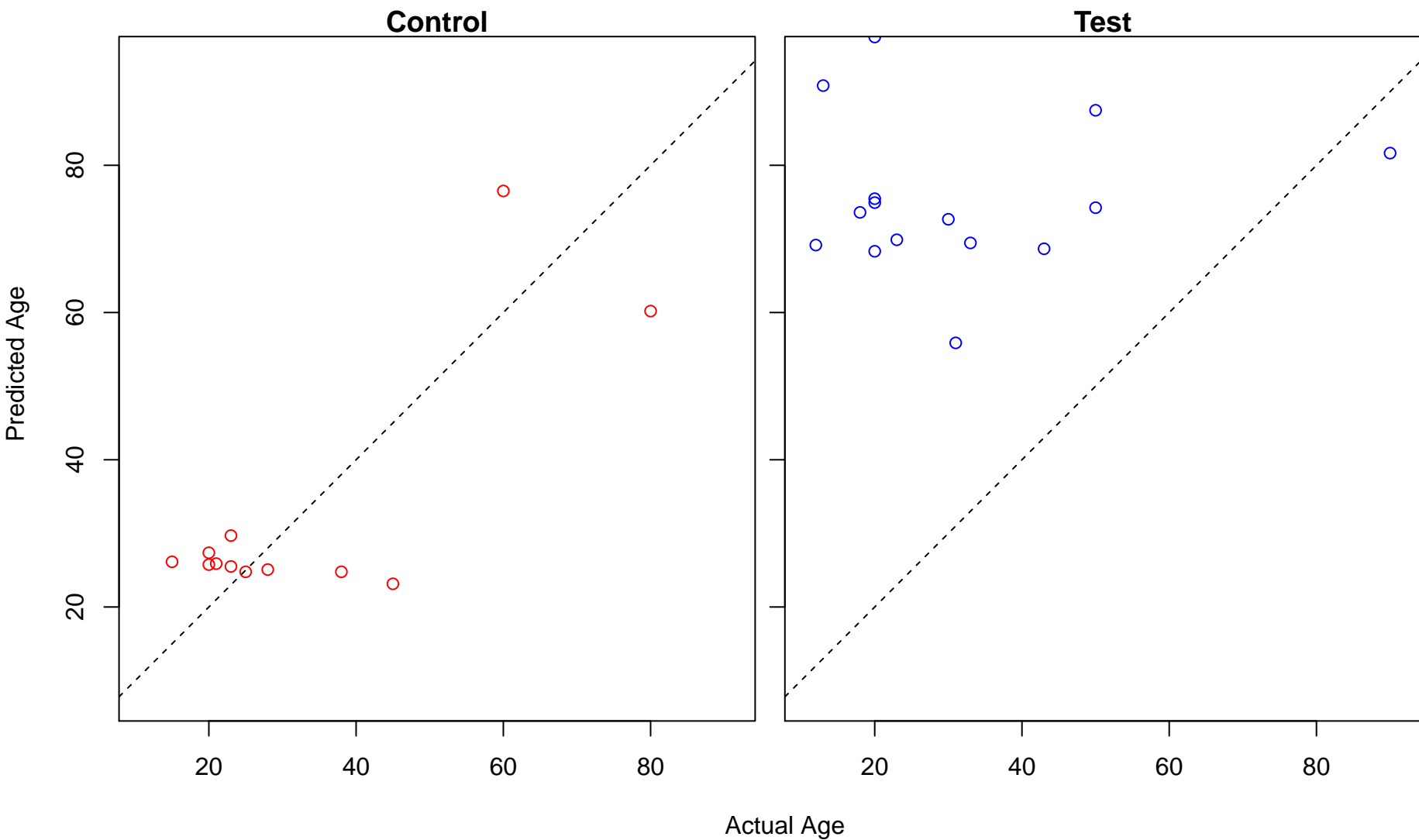


Actual Age

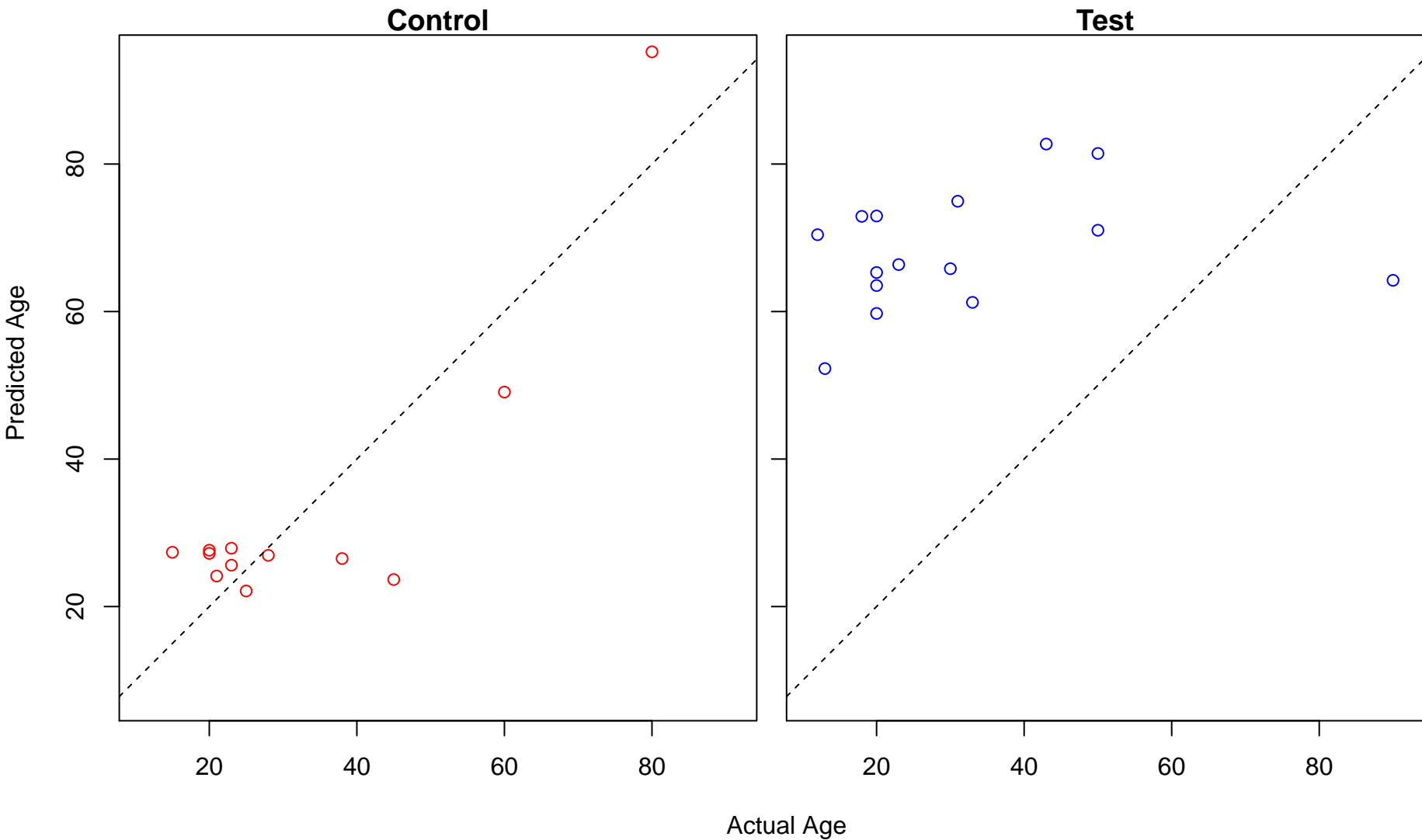
dendritic spine organization (Score: 5.875541)



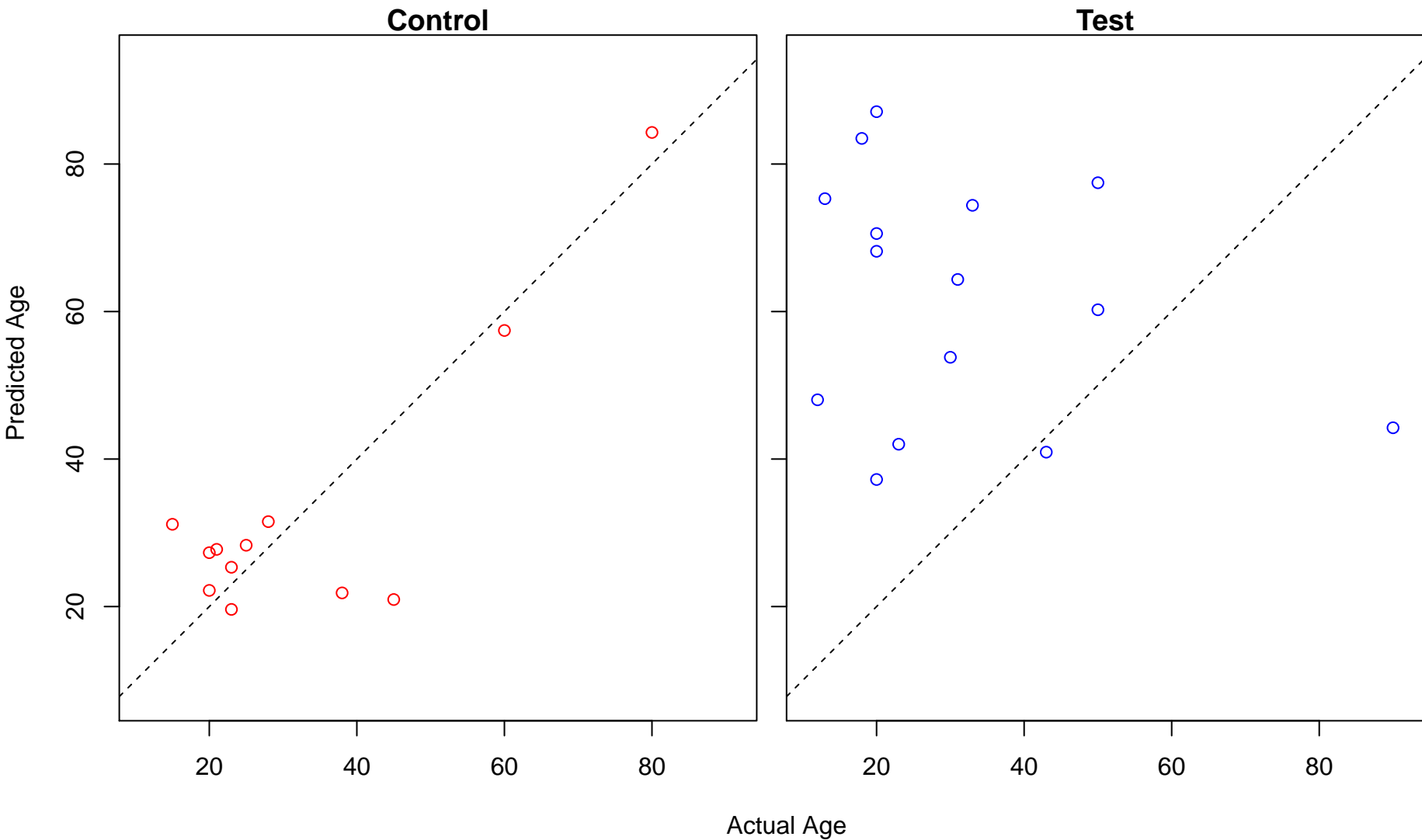
nucleus organization (Score: 5.874777)



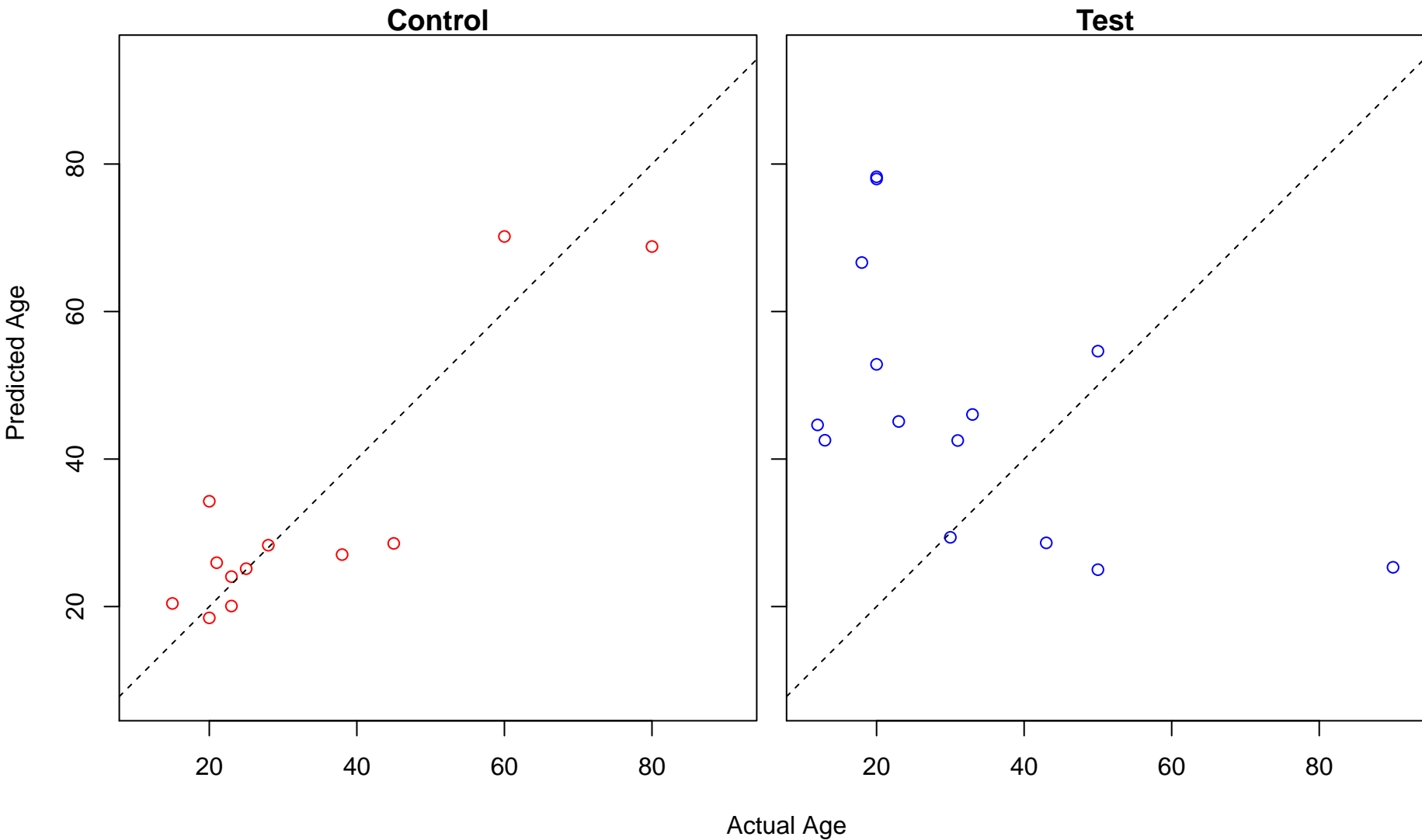
histone H3 deacetylation (Score: 5.873374)



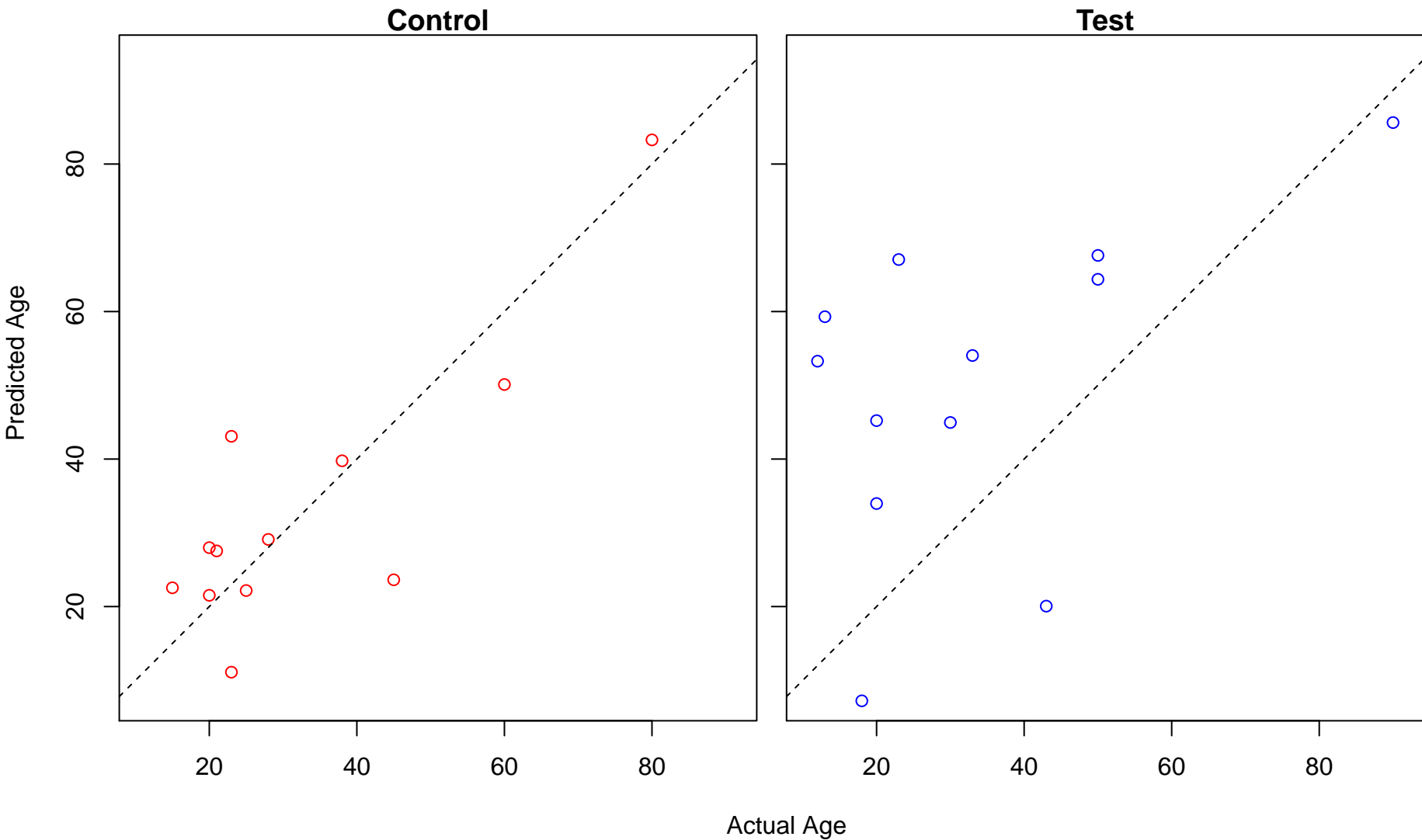
regulation of lipase activity (Score: 5.872367)



positive regulation of catenin import into nucleus (Score: 5.870225)

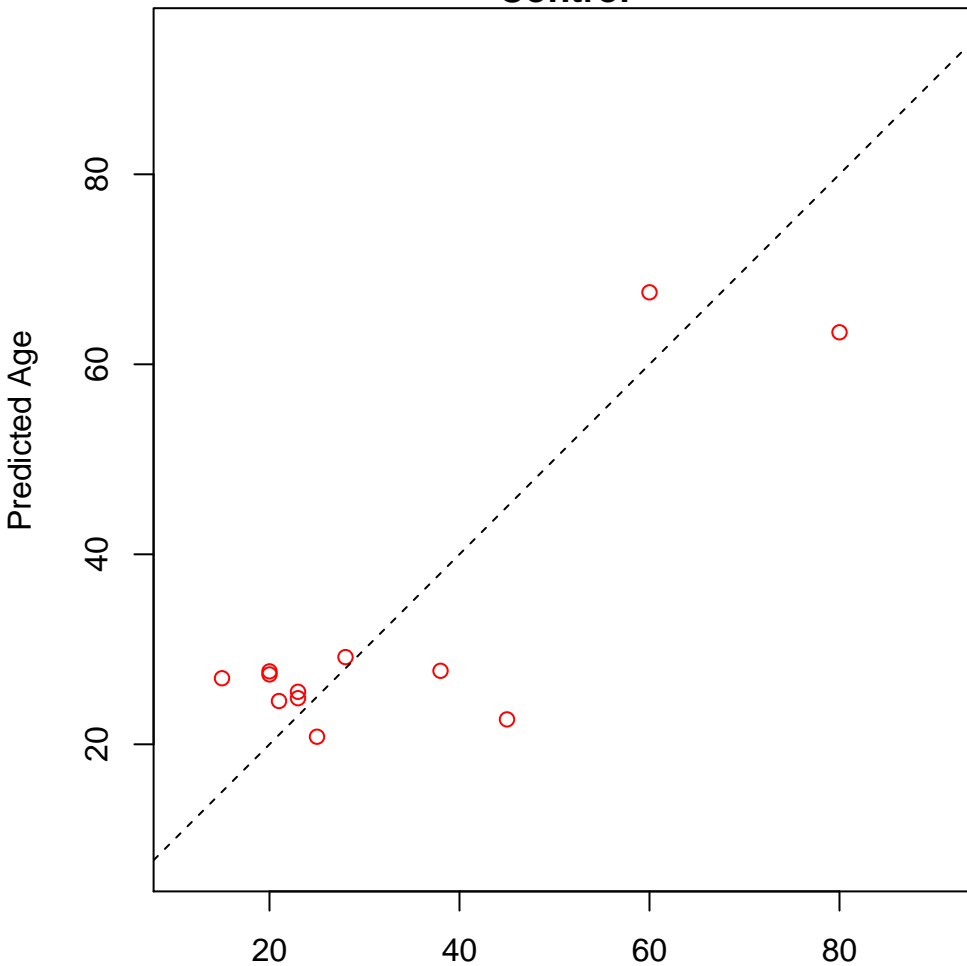


ERK1 and ERK2 cascade (Score: 5.867995)

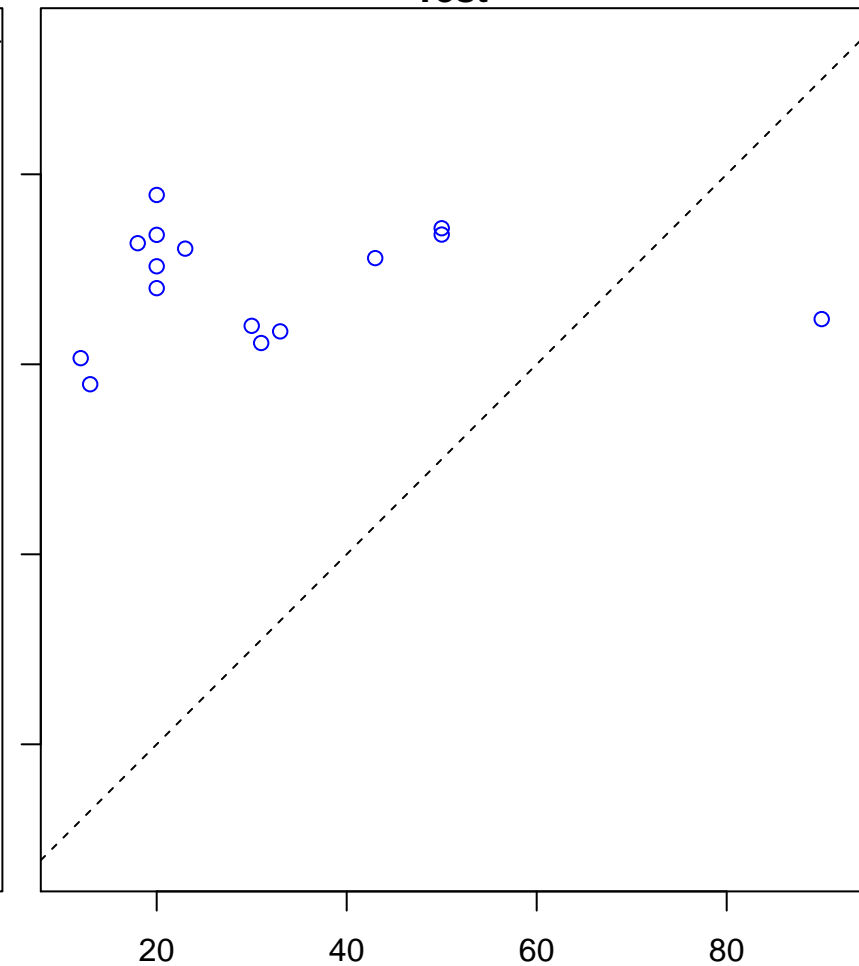


calcium ion transmembrane transport (Score: 5.866430)

Control

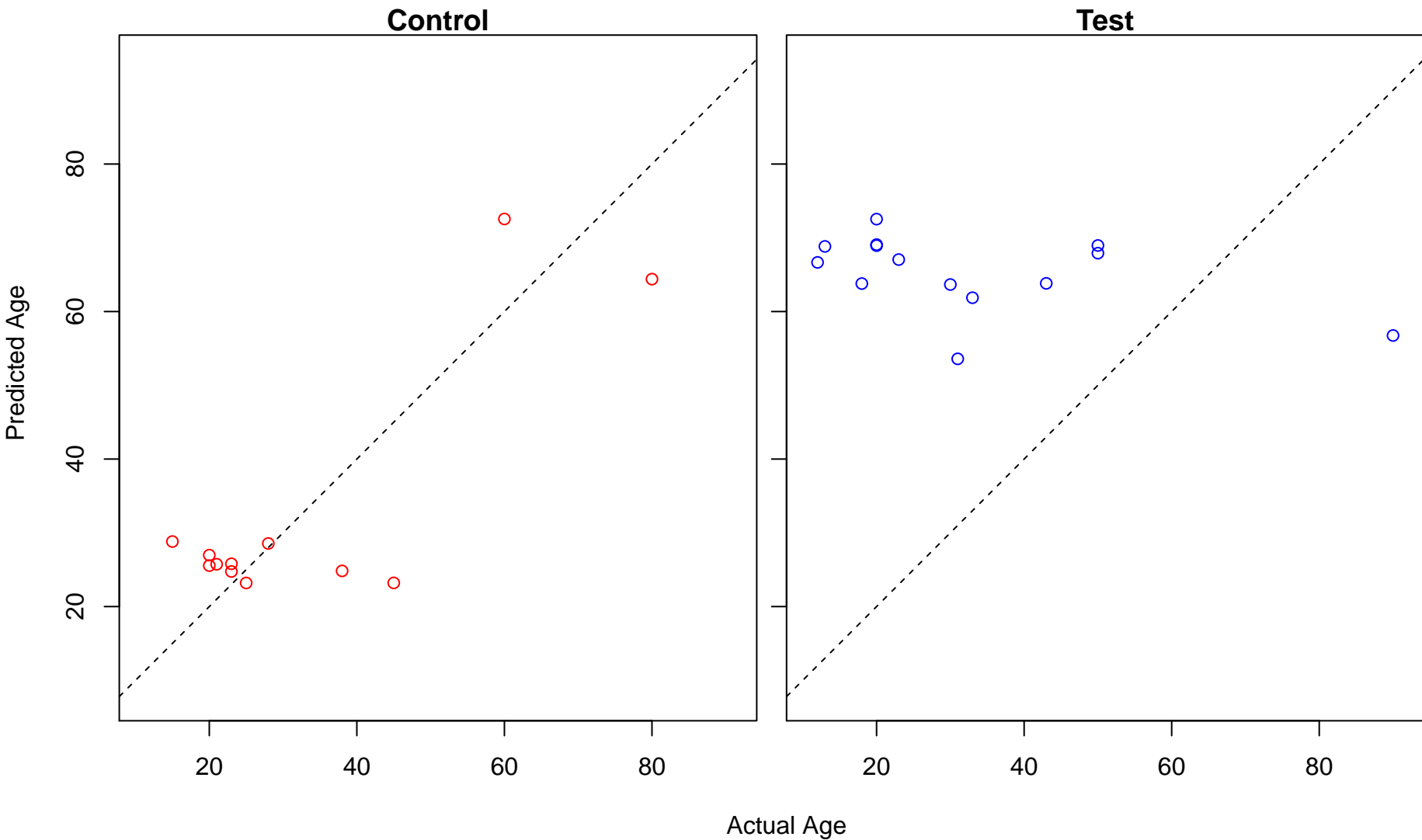


Test

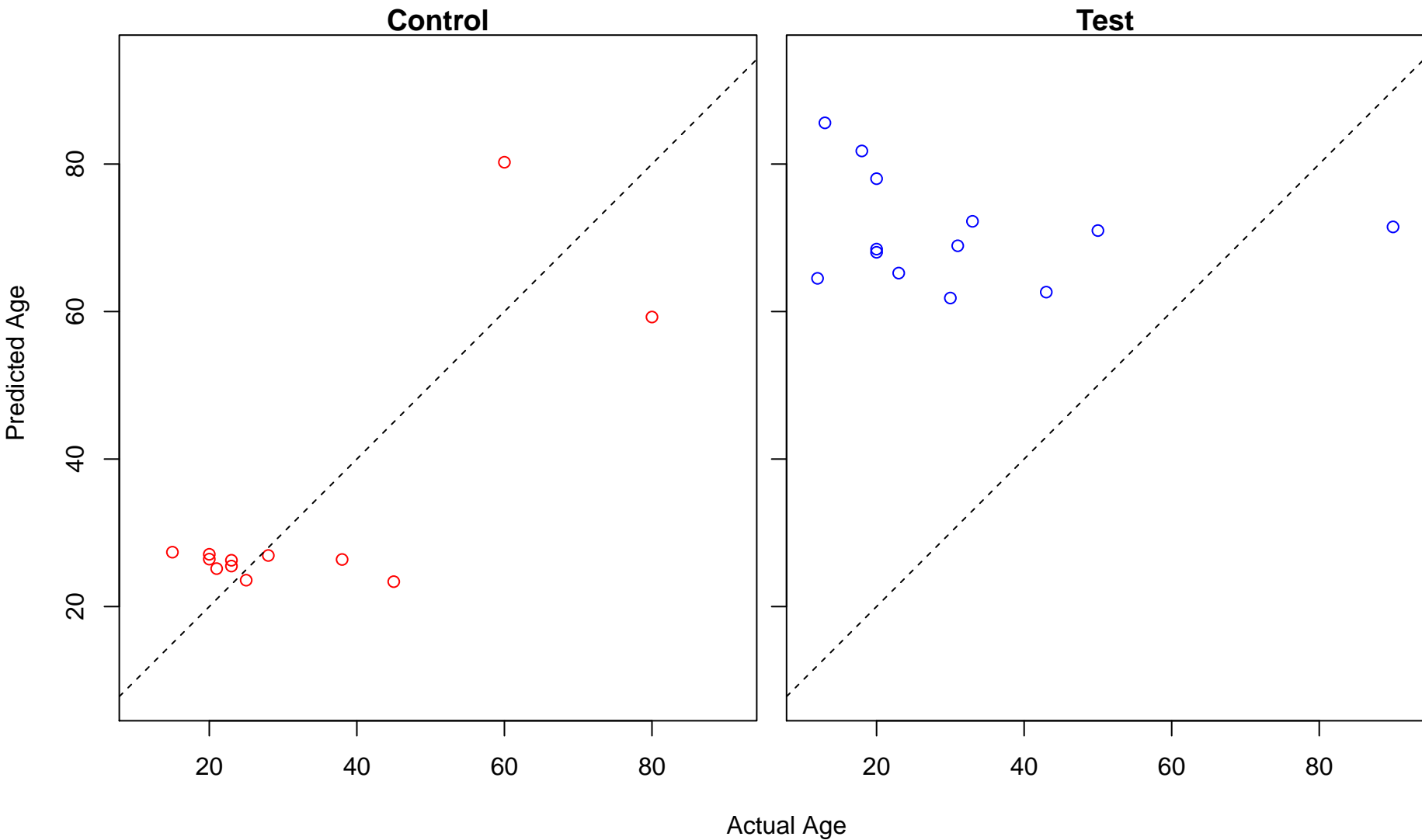


Actual Age

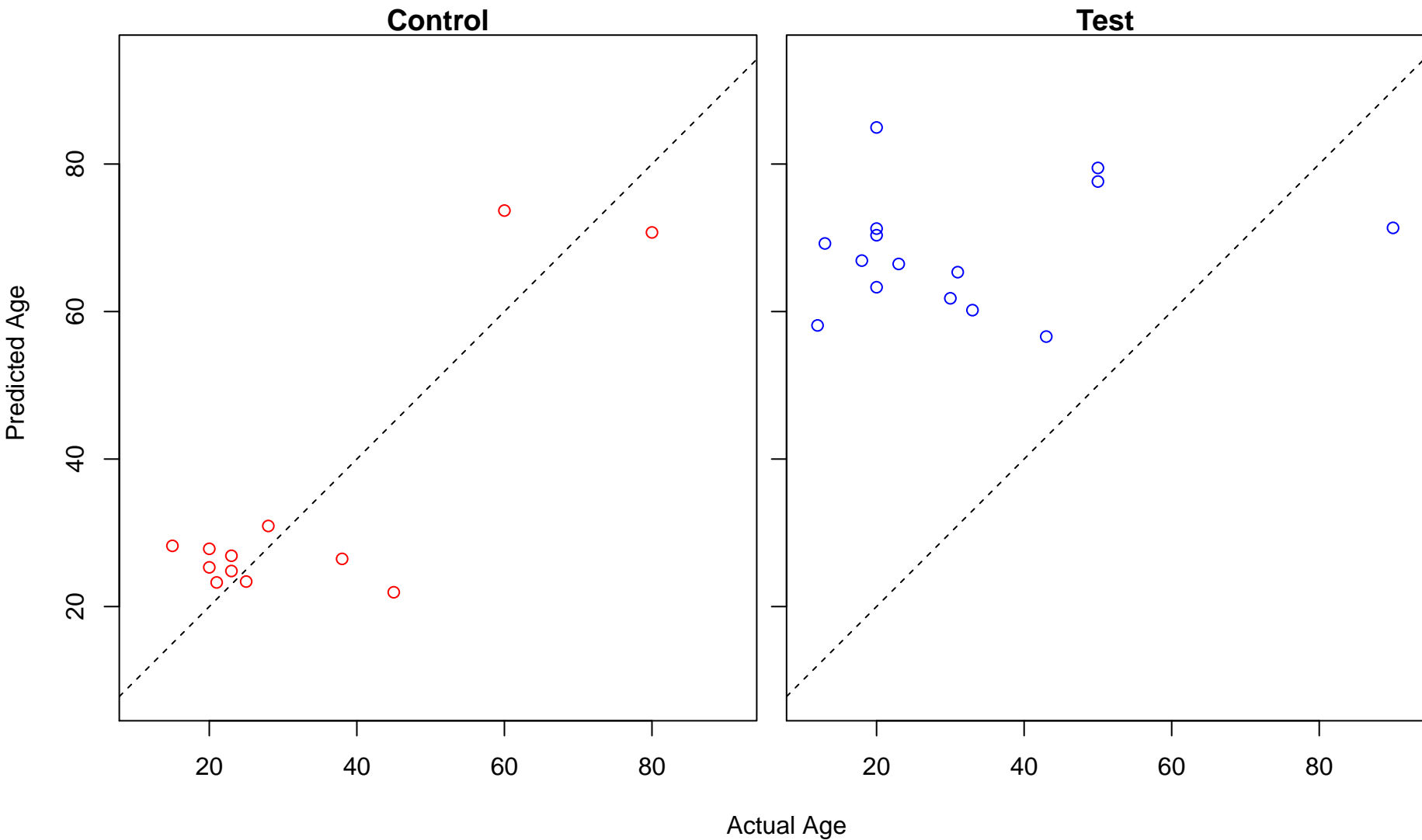
neuroepithelial cell differentiation (Score: 5.865264)



toll-like receptor signaling pathway (Score: 5.864878)

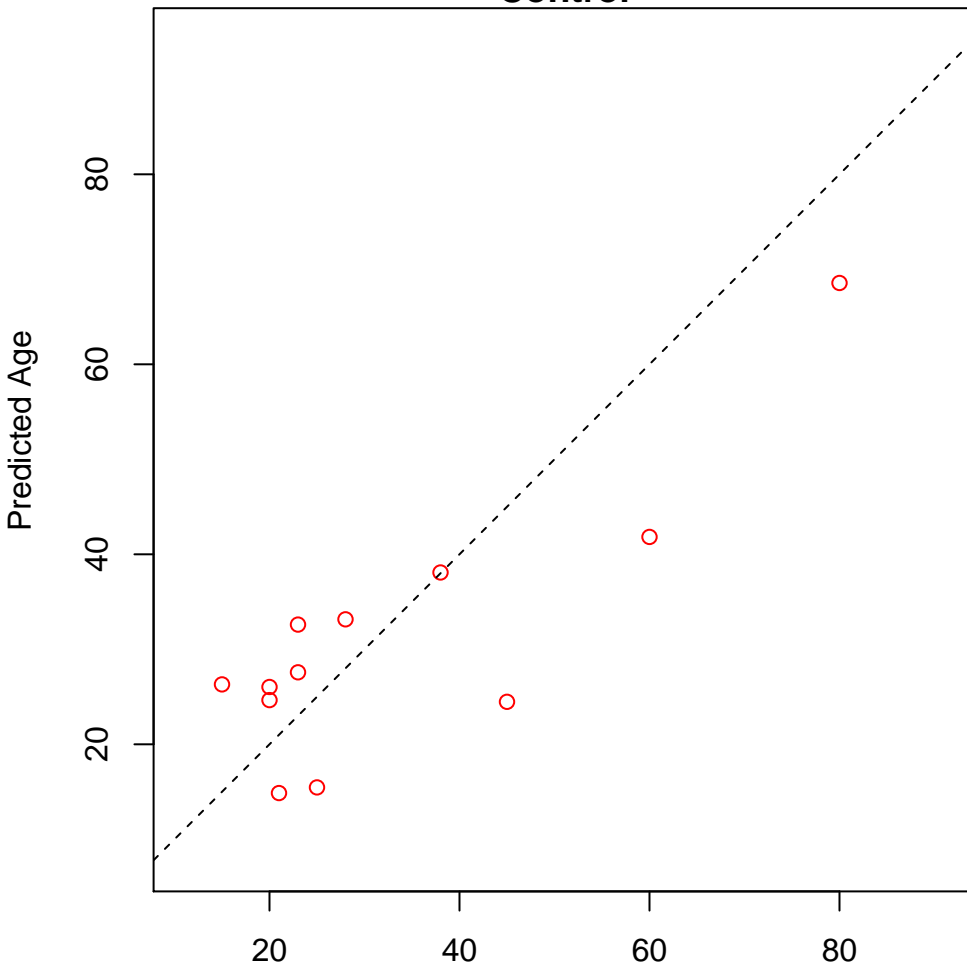


cellular response to organonitrogen compound (Score: 5.862065)

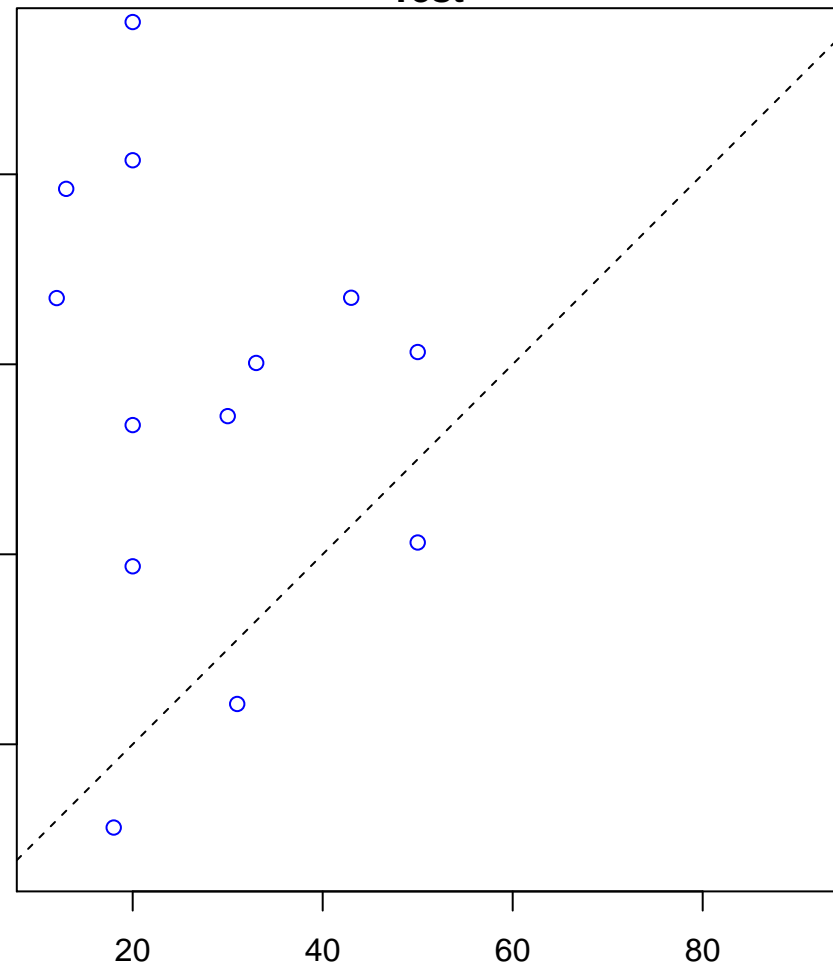


type B pancreatic cell differentiation (Score: 5.860577)

Control

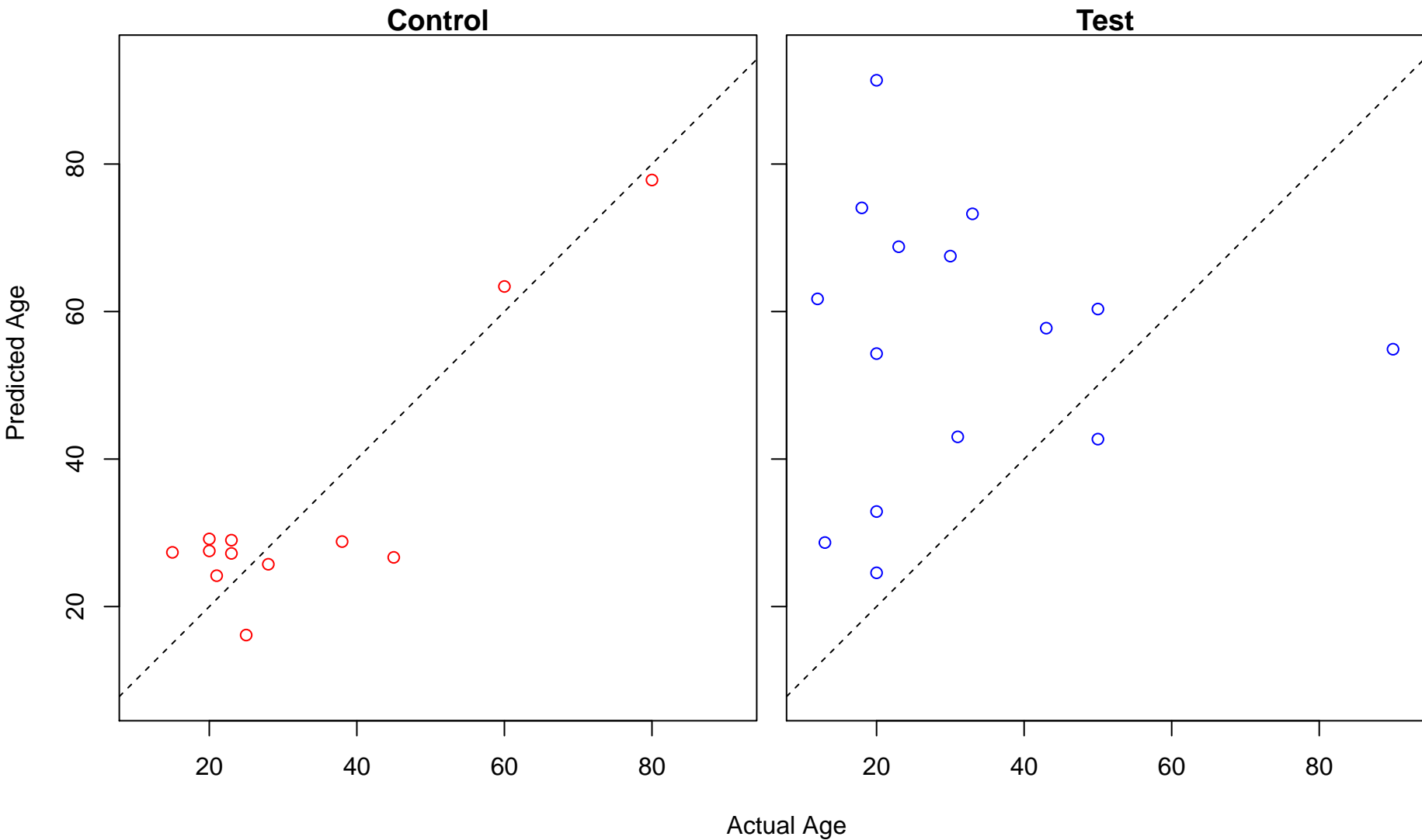


Test

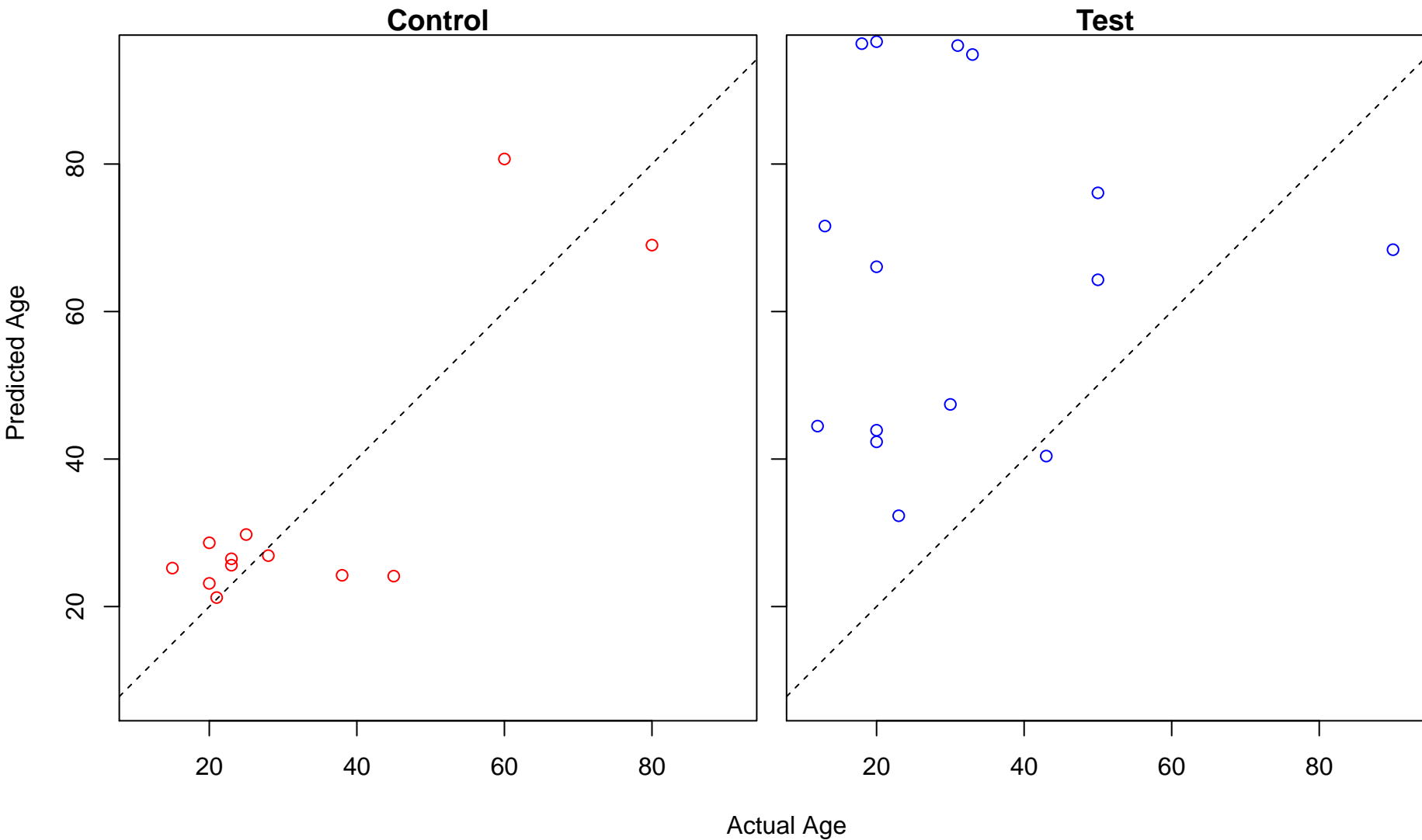


Actual Age

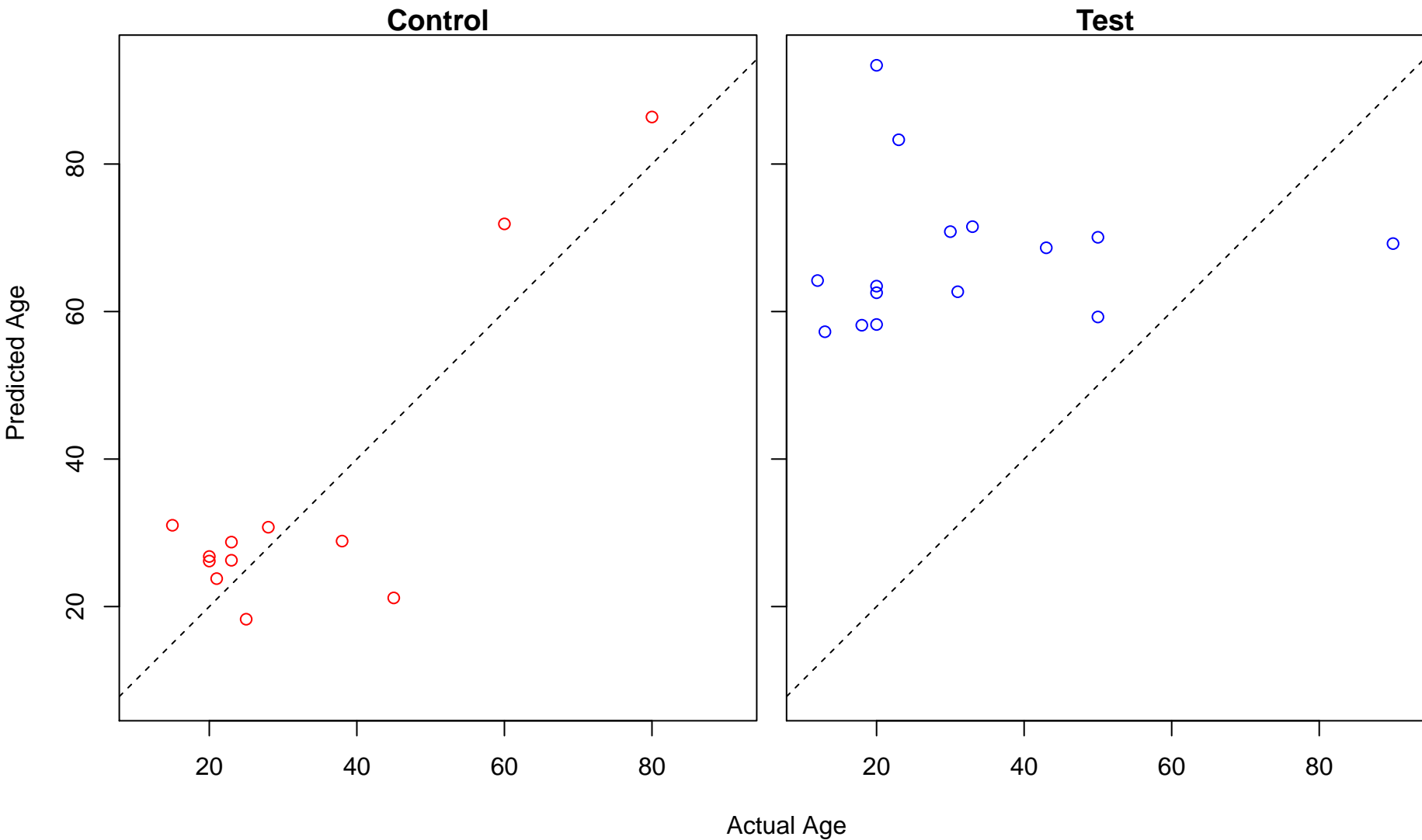
positive regulation of phospholipid metabolic process (Score: 5.859265)



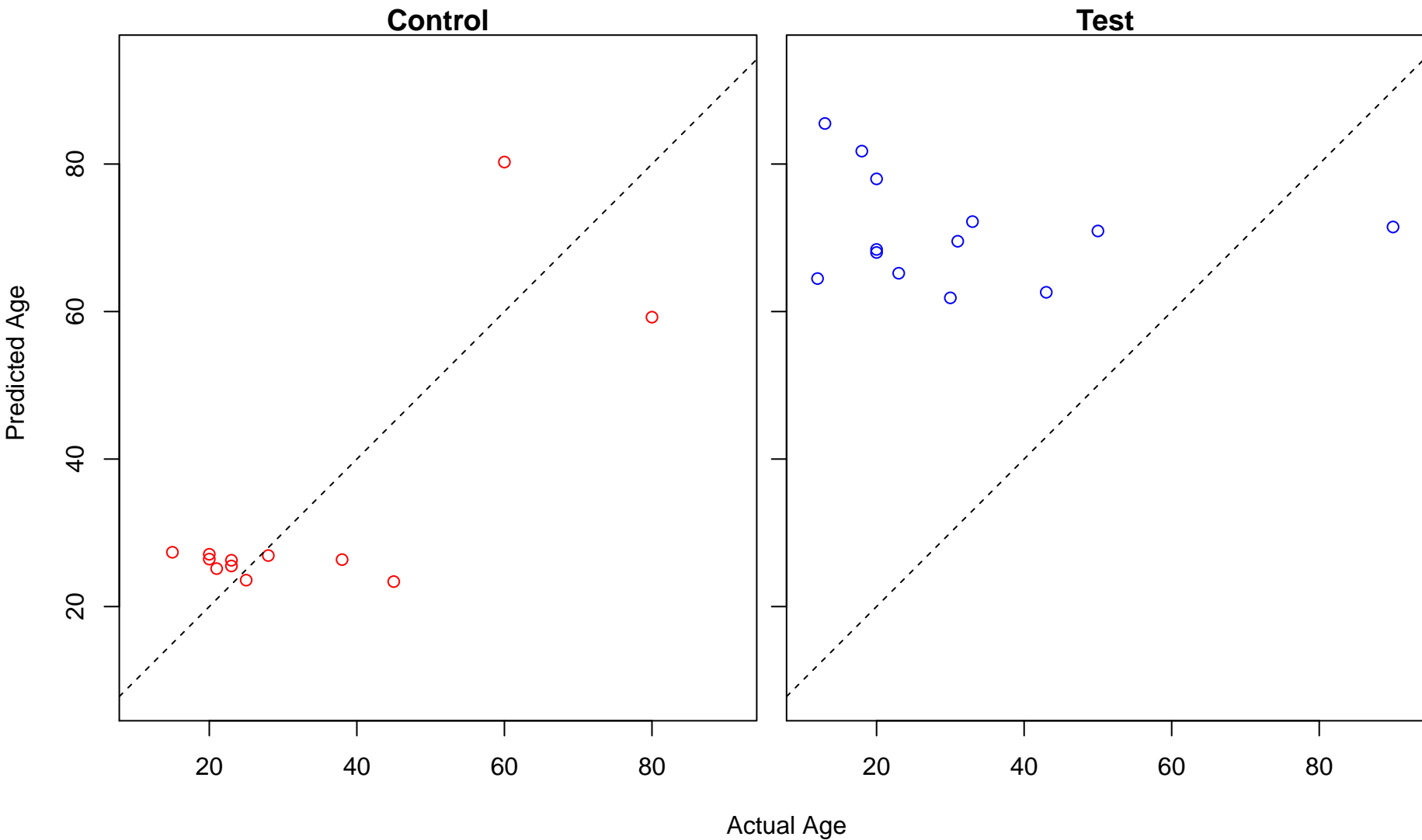
regulation of IRE1-mediated unfolded protein response (Score: 5.858593)



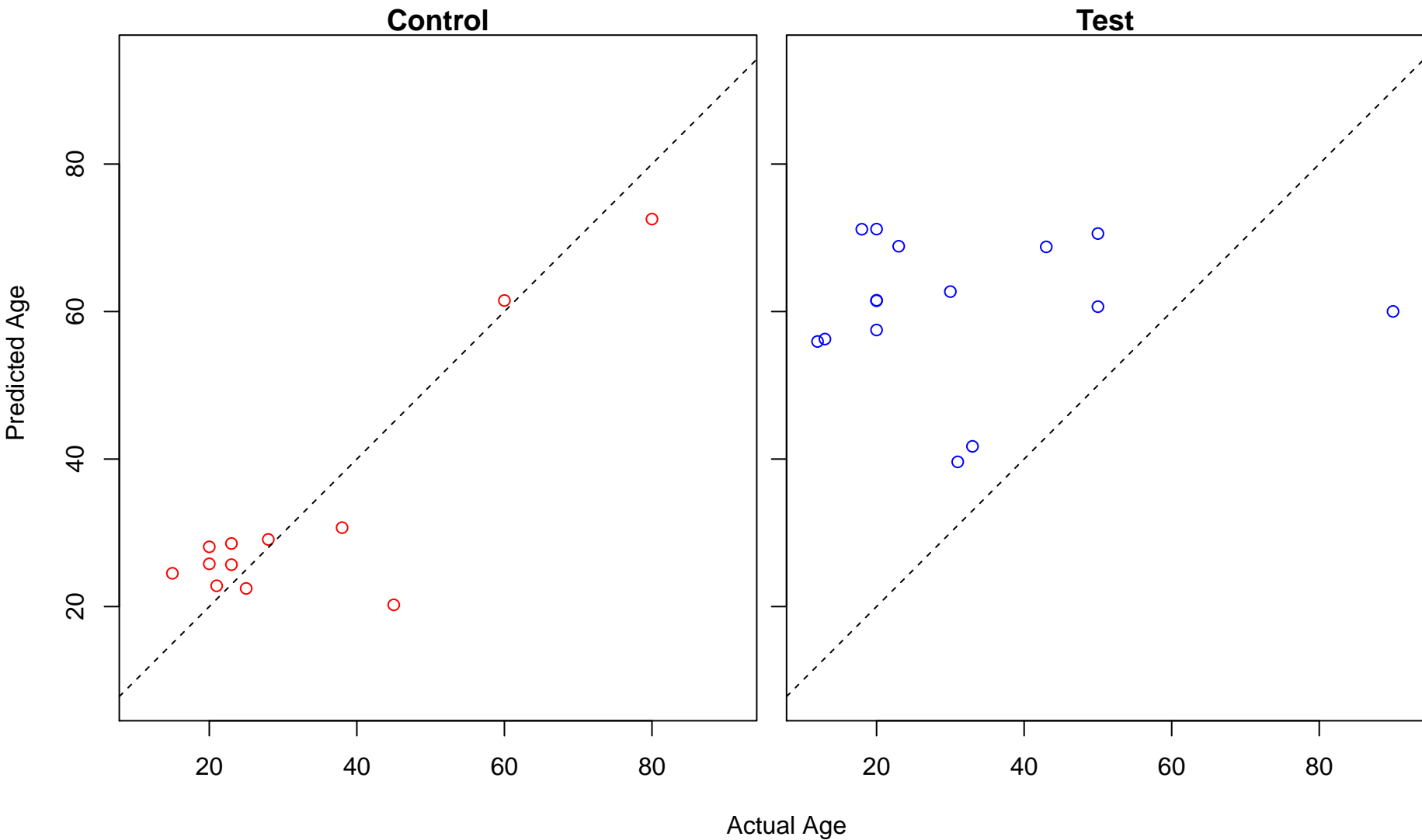
sphingomyelin metabolic process (Score: 5.858080)



pattern recognition receptor signaling pathway (Score: 5.855327)

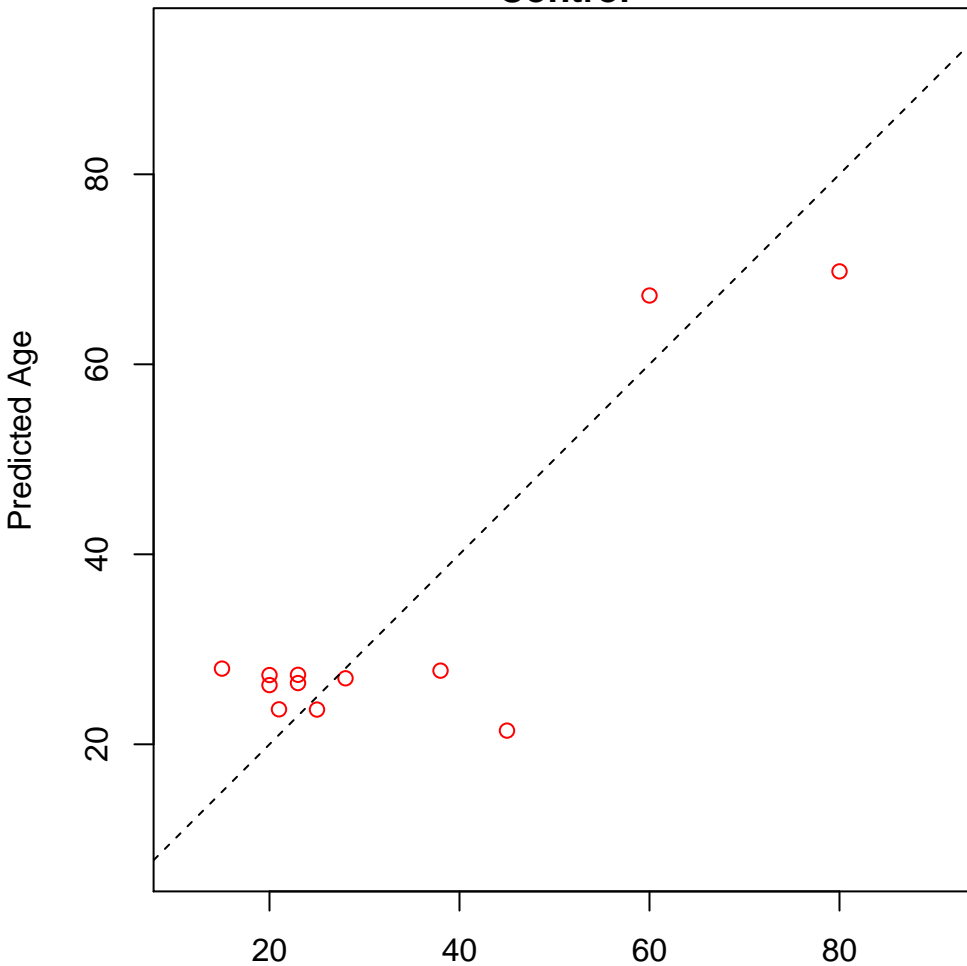


bone mineralization (Score: 5.854886)

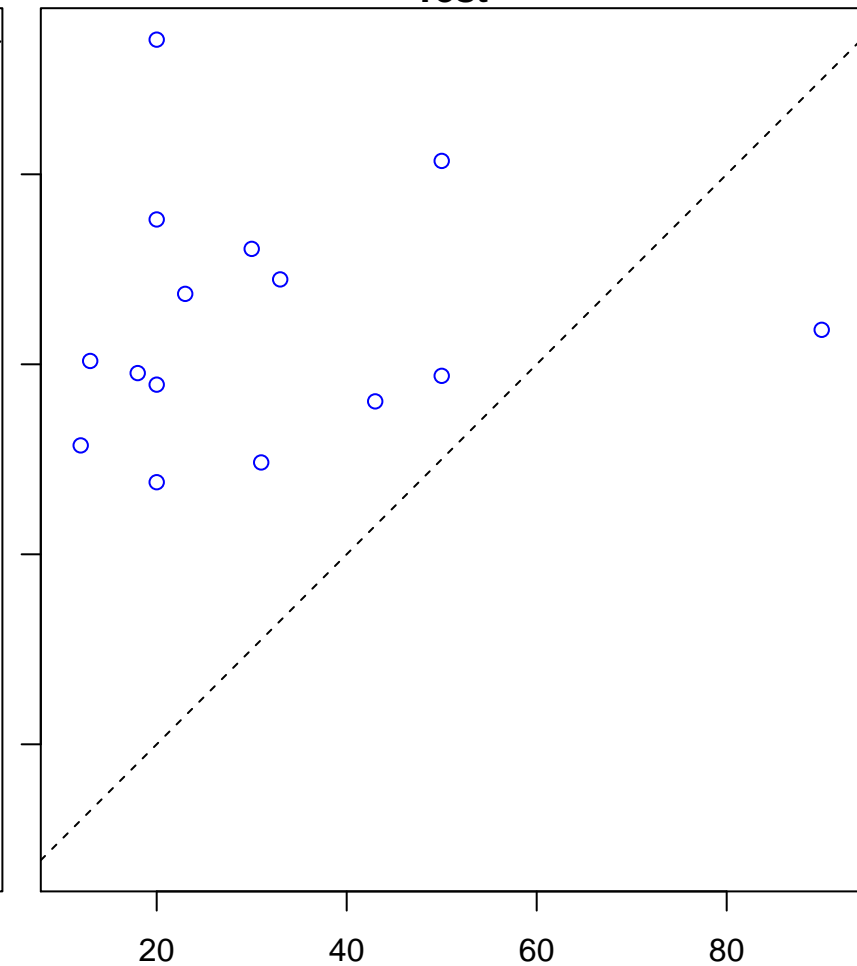


regulation of lipoprotein lipase activity (Score: 5.852975)

Control

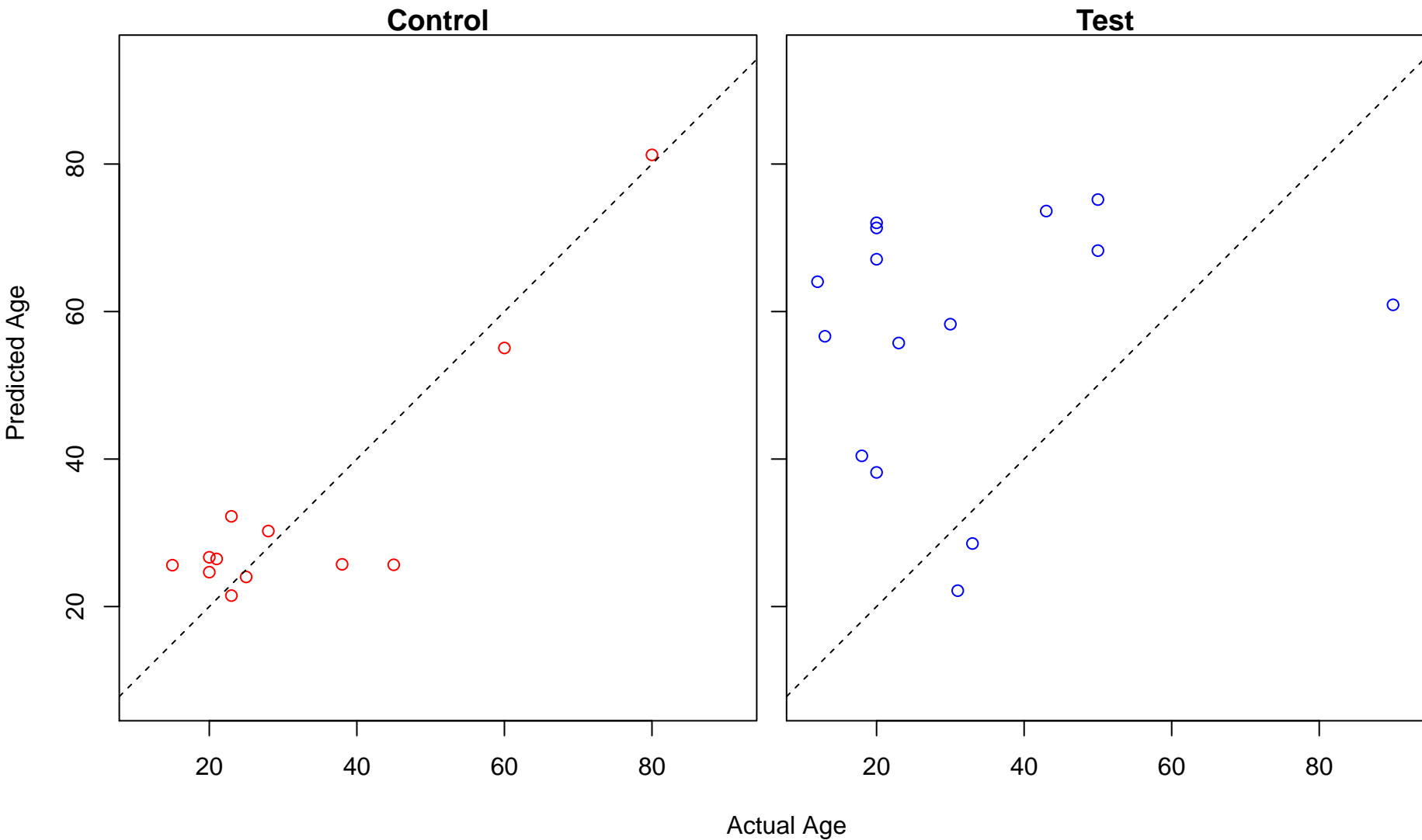


Test

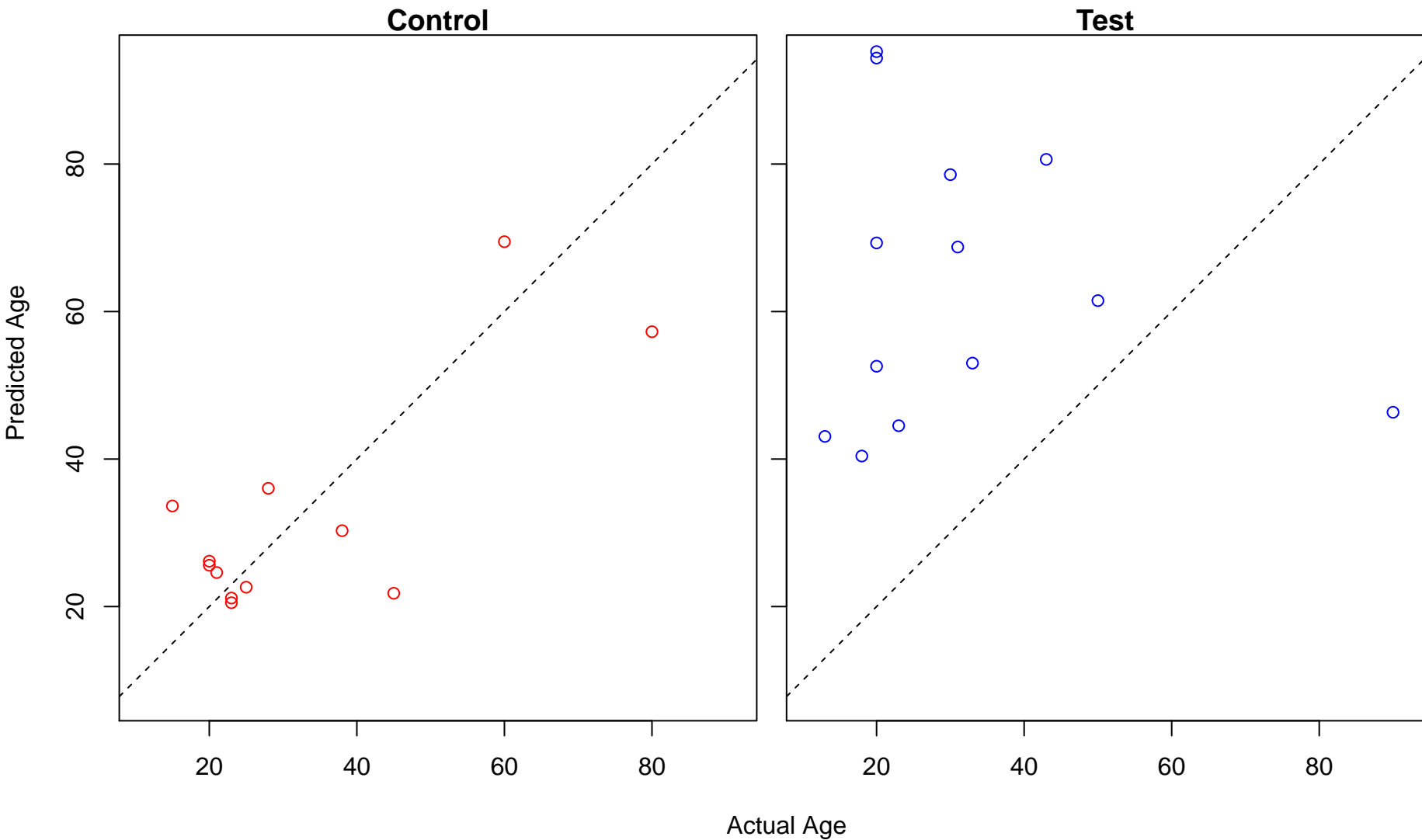


Actual Age

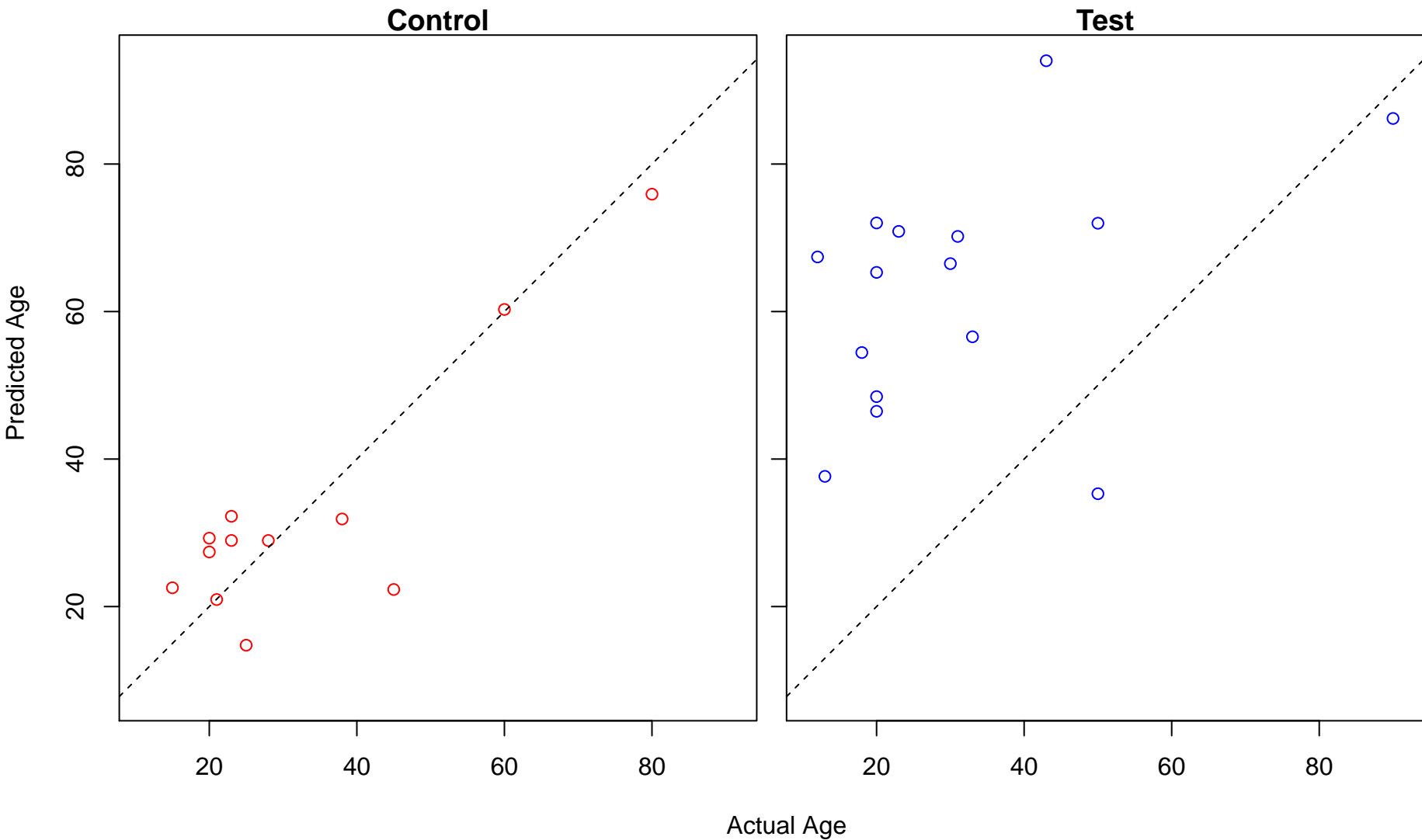
positive regulation of epithelial cell proliferation involved in wound healing (Score: 5.852945)



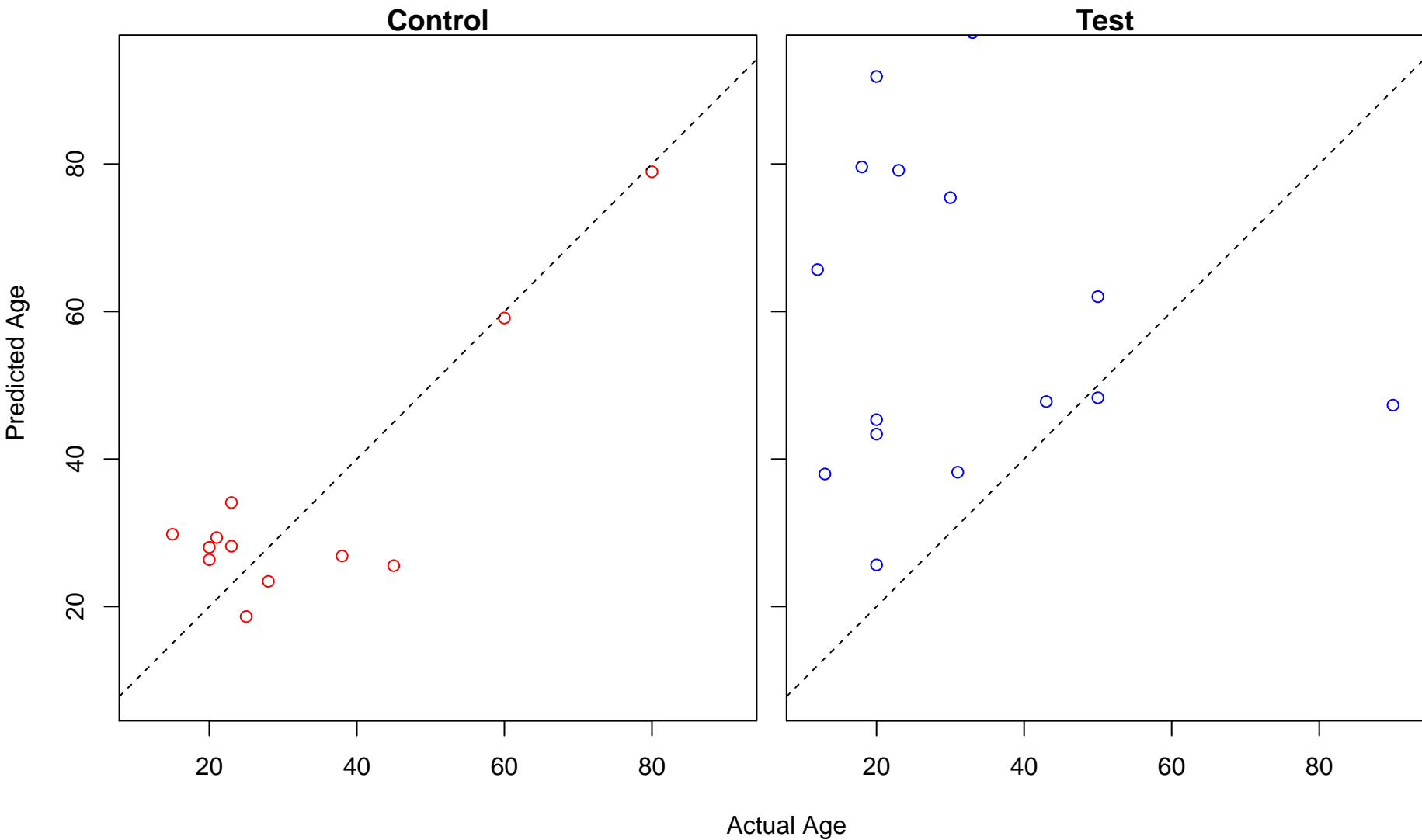
pentose metabolic process (Score: 5.852242)



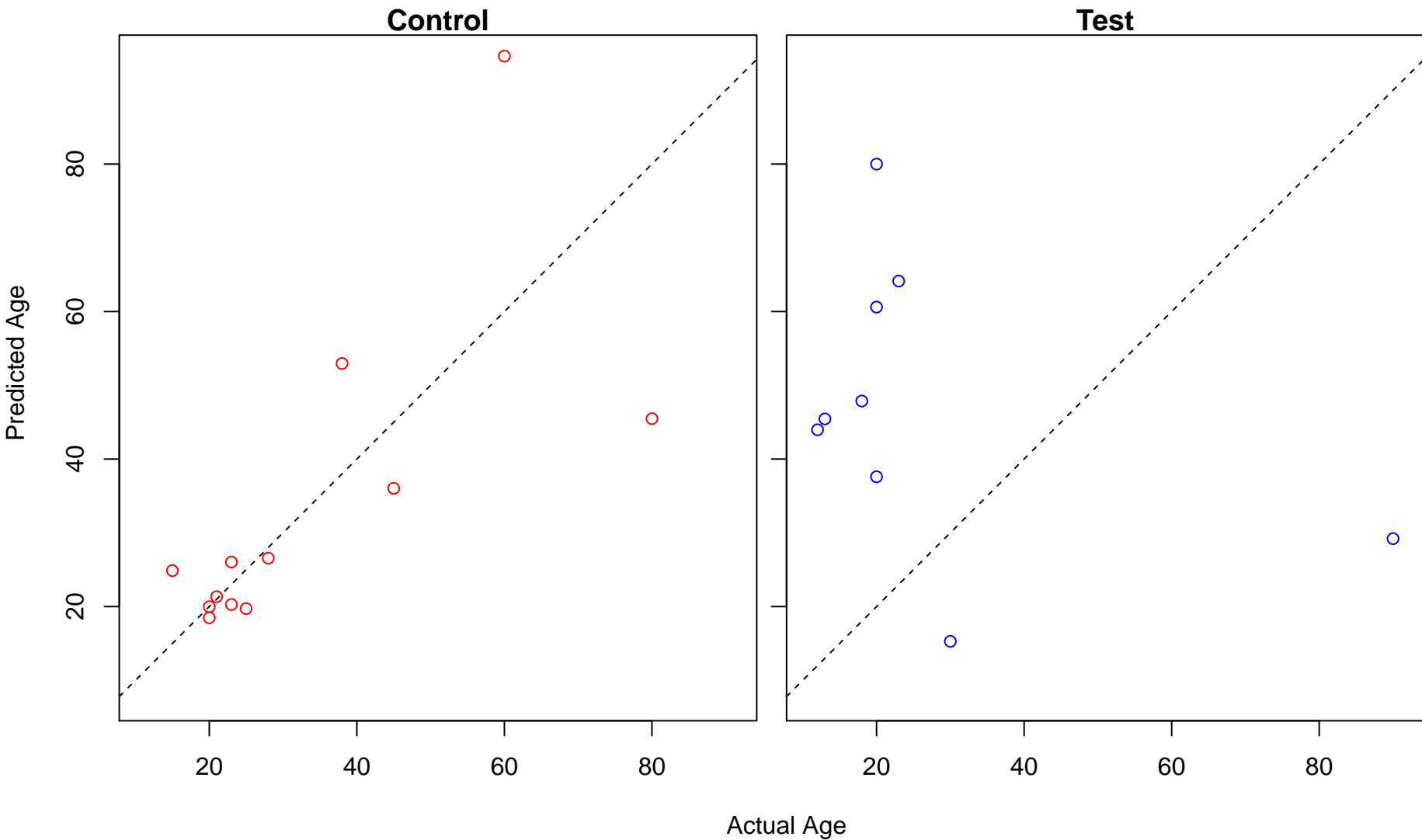
nucleus localization (Score: 5.847871)



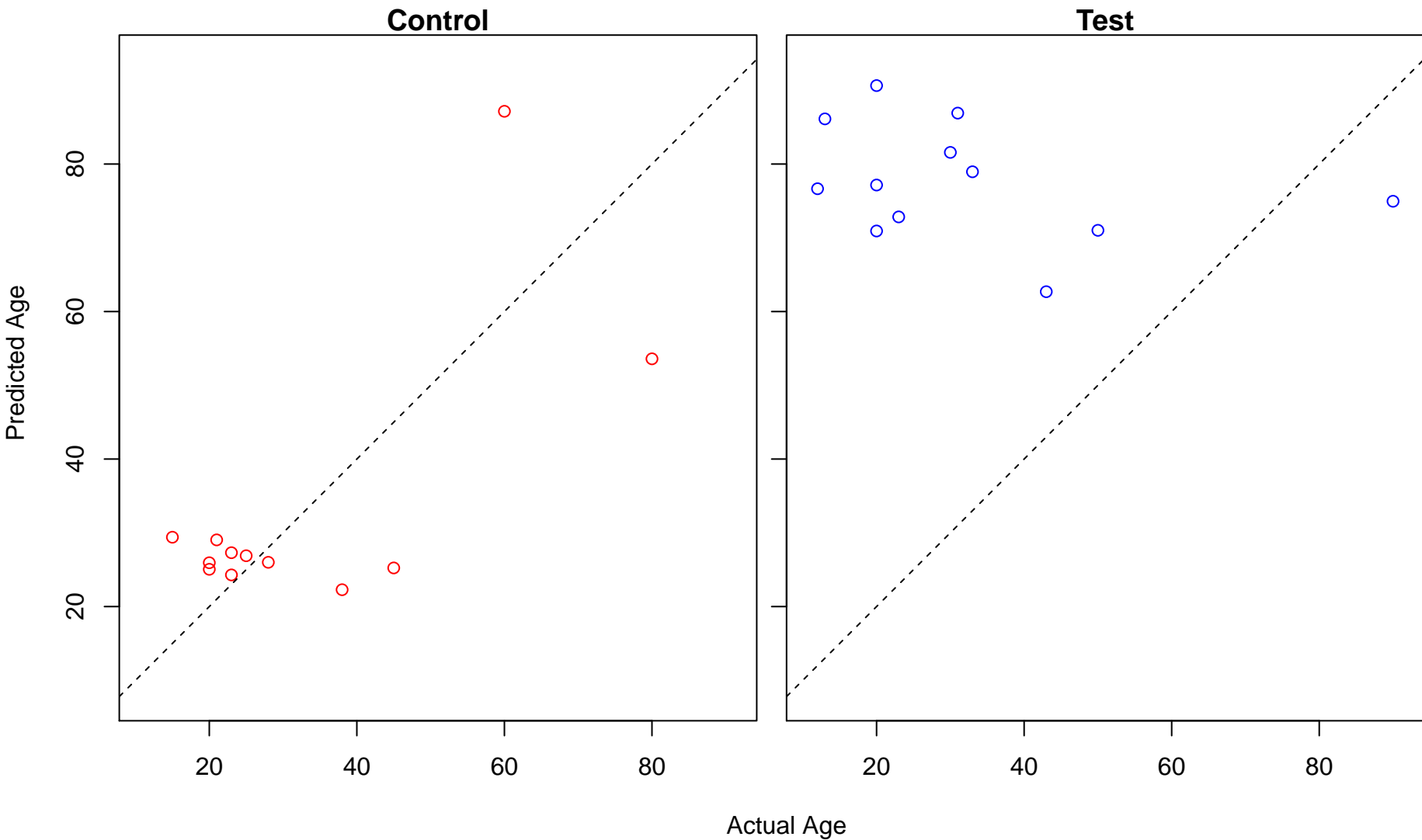
regulation of phospholipid metabolic process (Score: 5.846506)



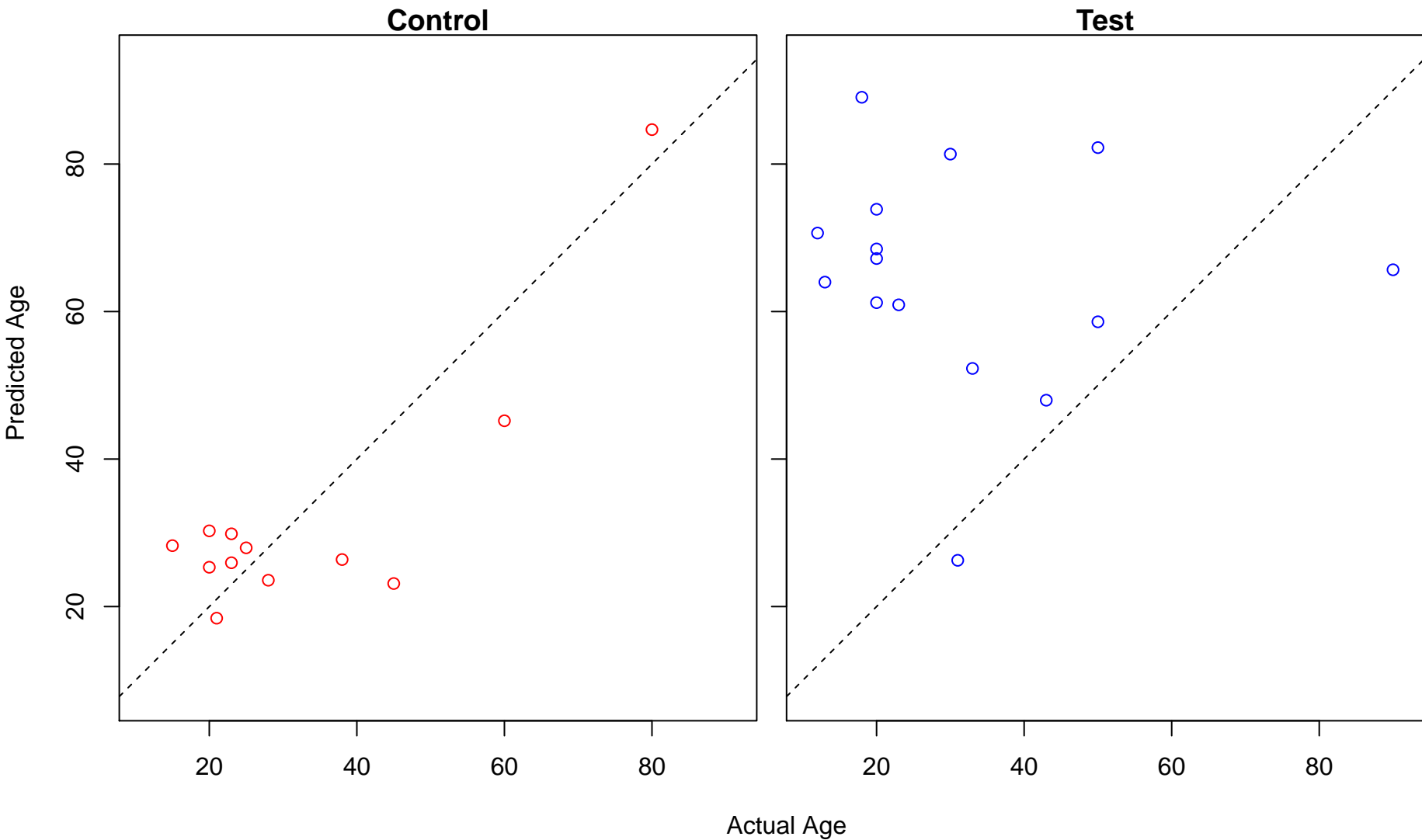
positive regulation of chondrocyte differentiation (Score: 5.846364)



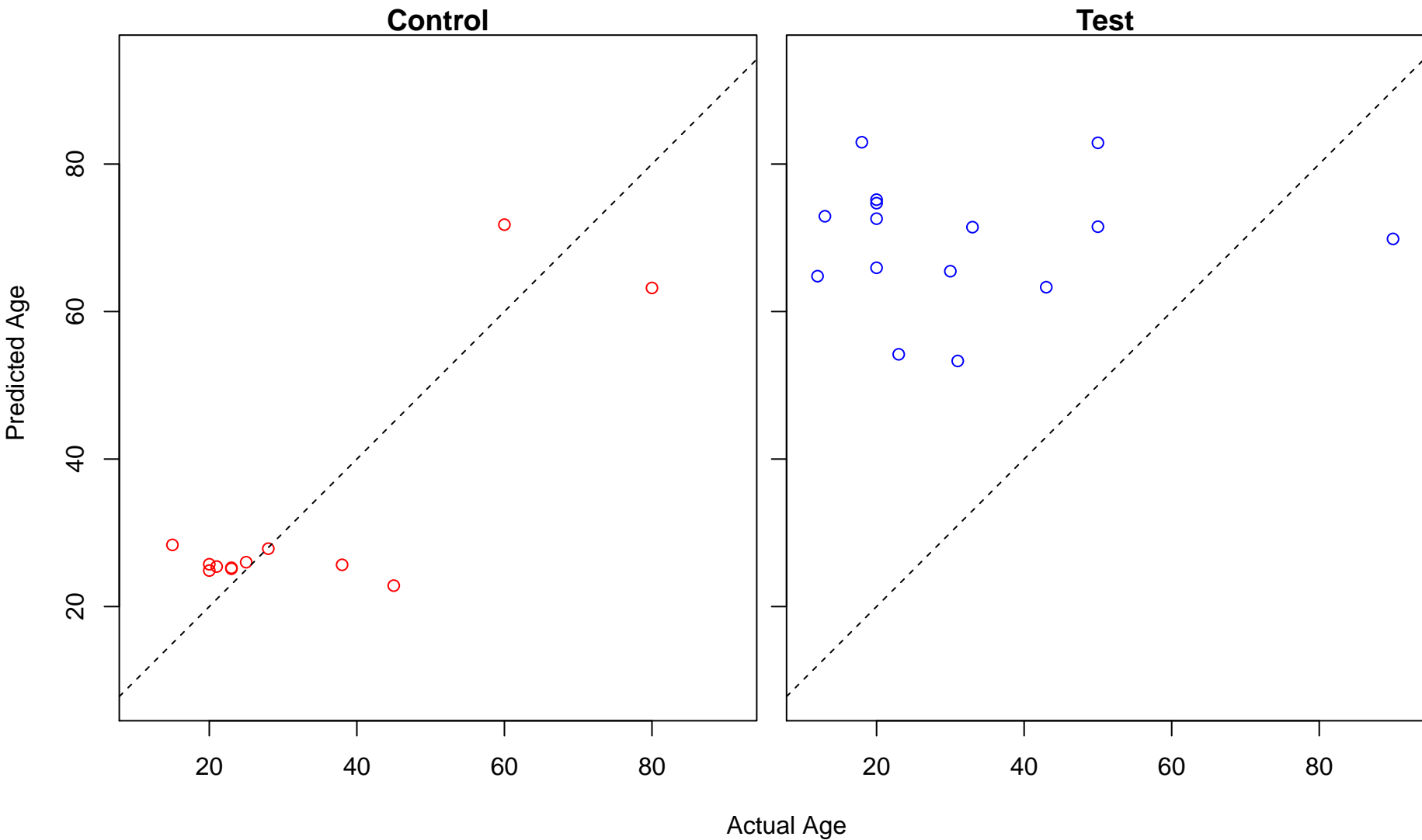
regulation of mast cell activation (Score: 5.845480)



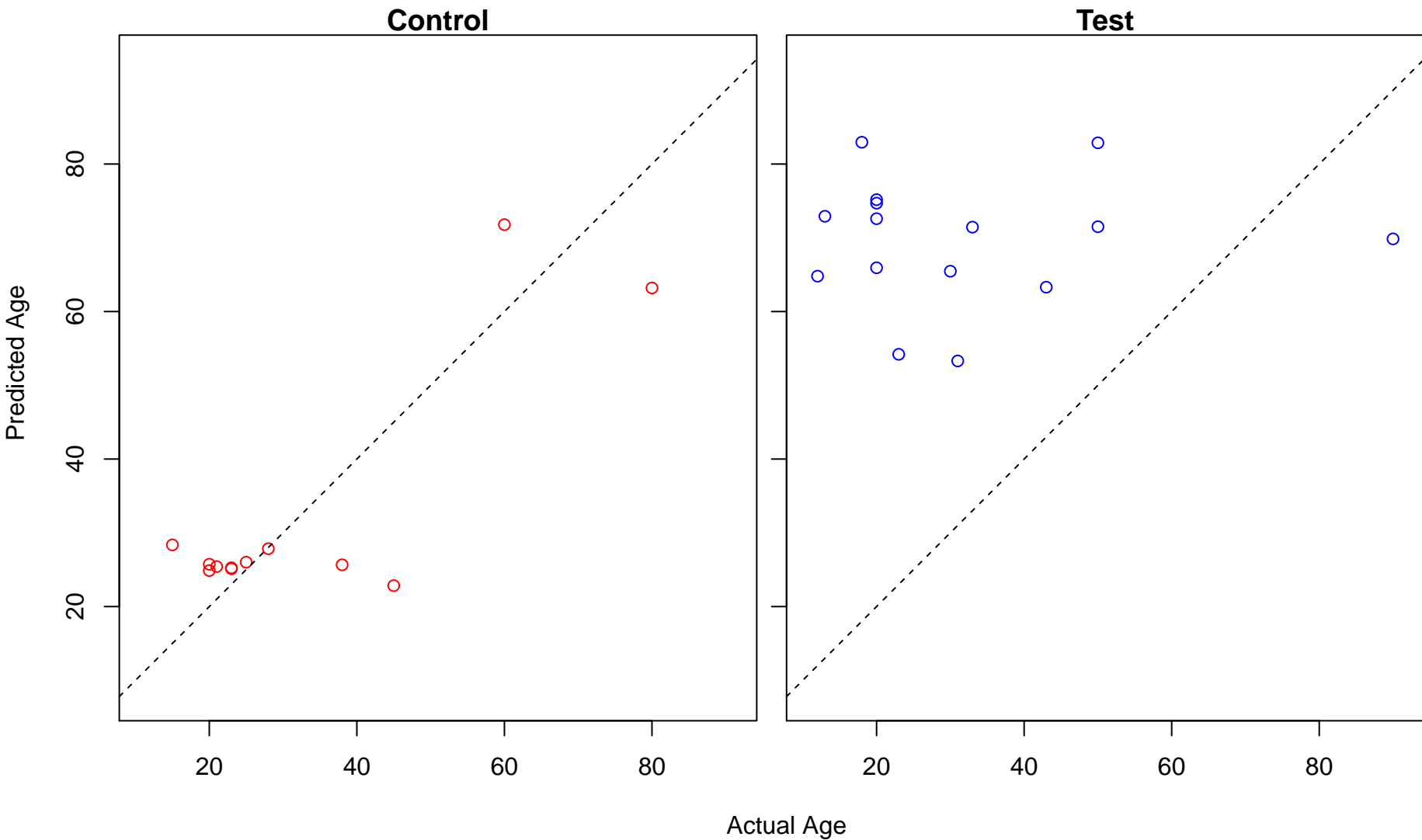
negative regulation of transcription regulatory region DNA binding (Score: 5.845362)



nucleosome disassembly (Score: 5.845307)

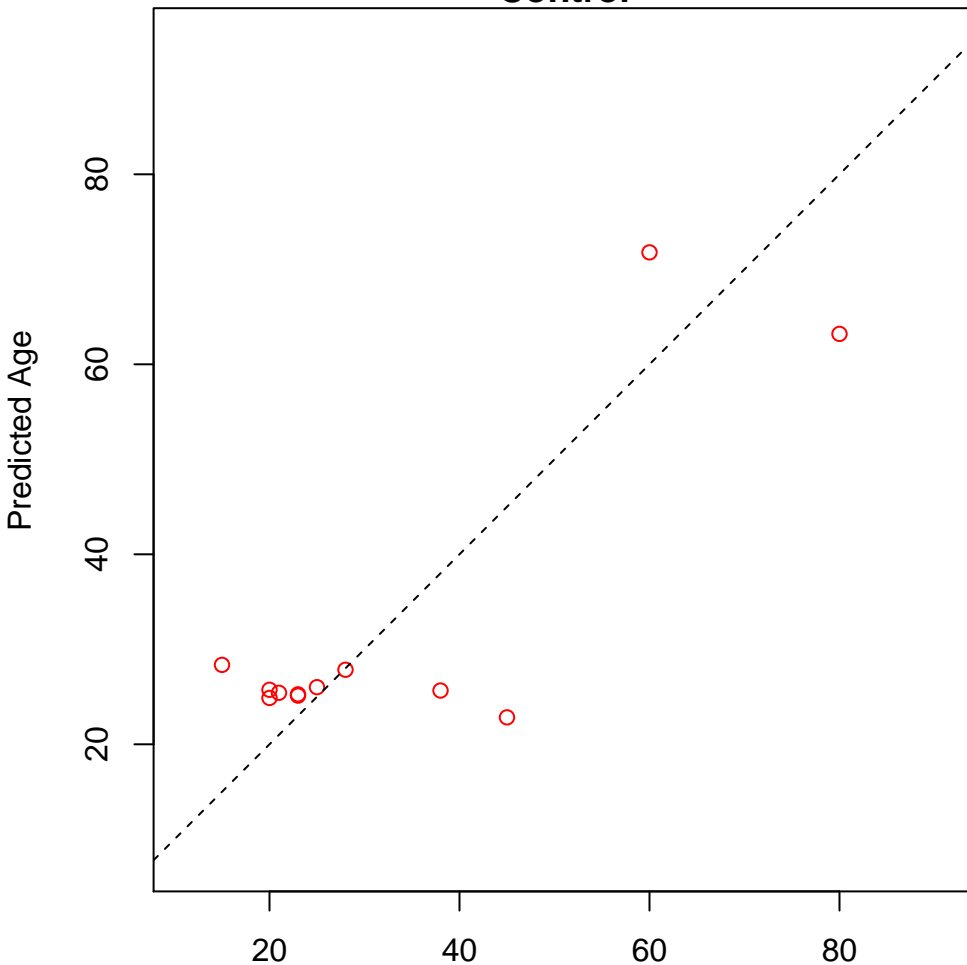


chromatin disassembly (Score: 5.845307)

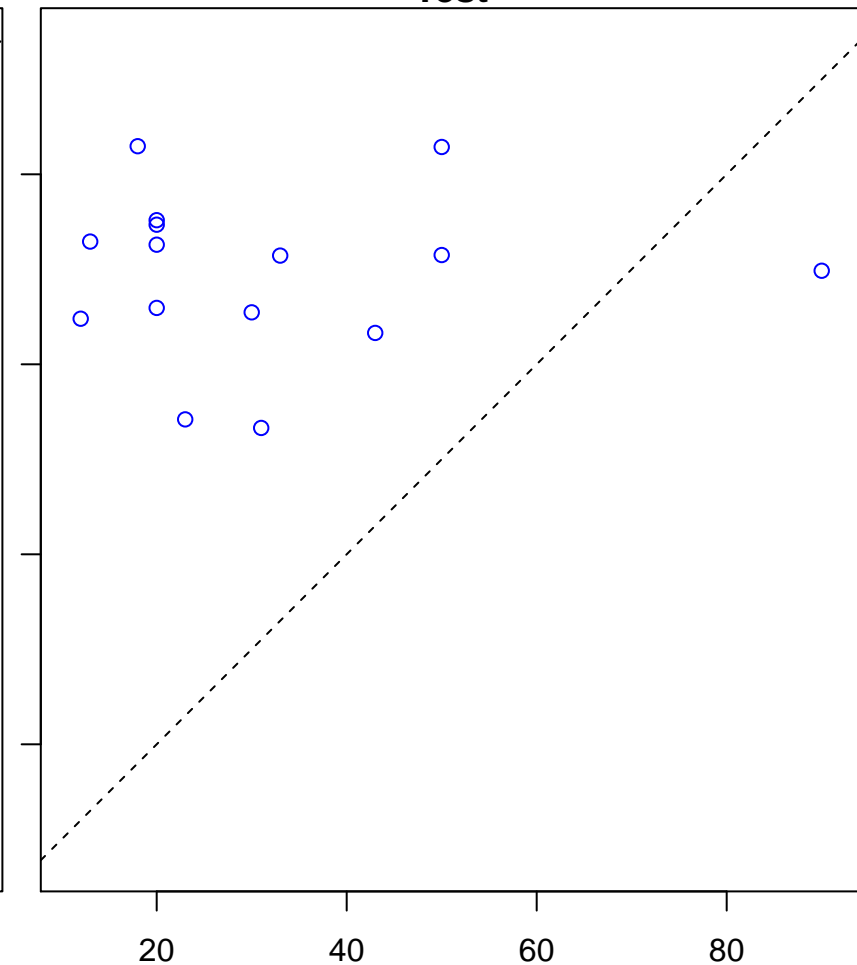


protein-DNA complex disassembly (Score: 5.845307)

Control

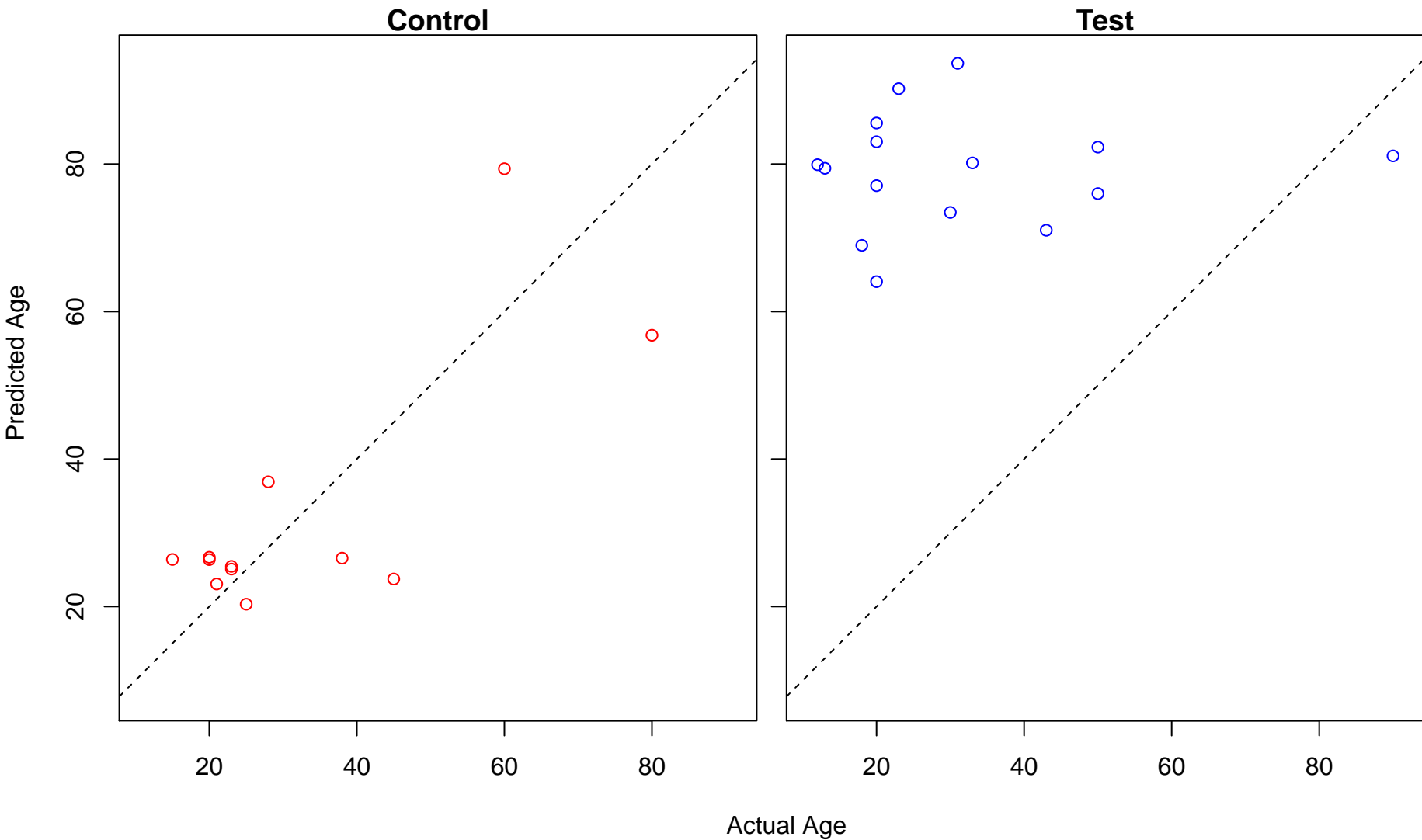


Test

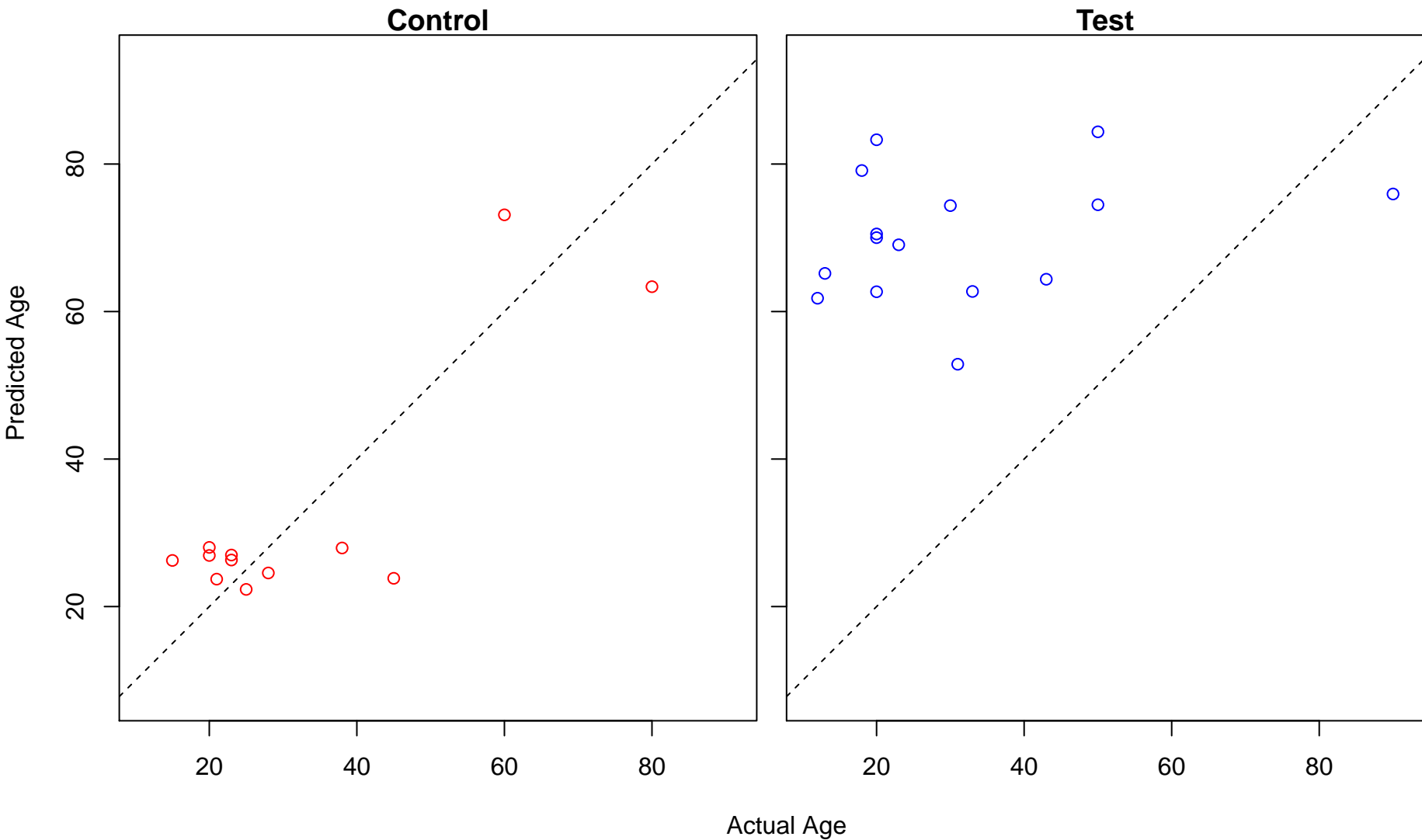


Actual Age

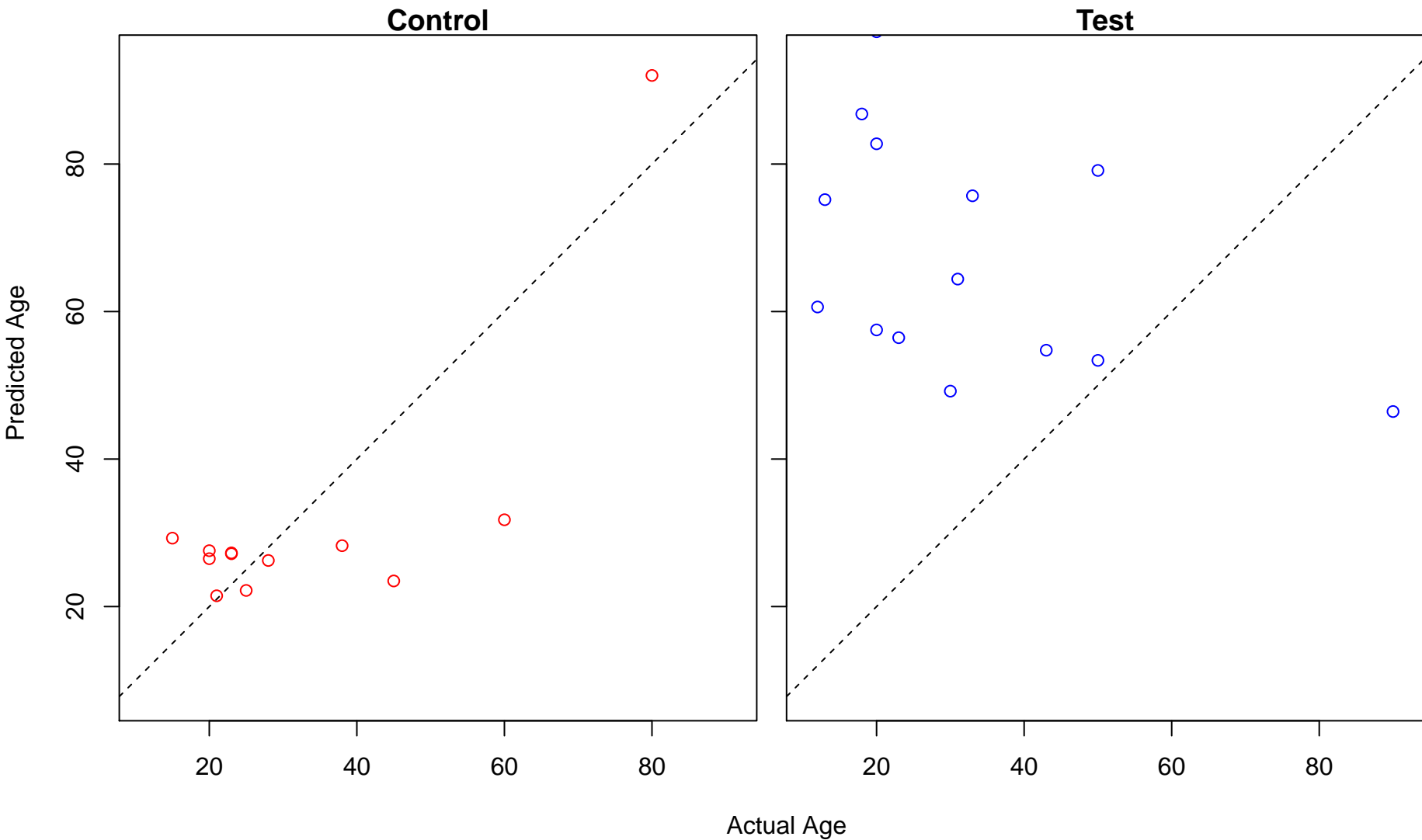
viral mRNA export from host cell nucleus (Score: 5.842548)



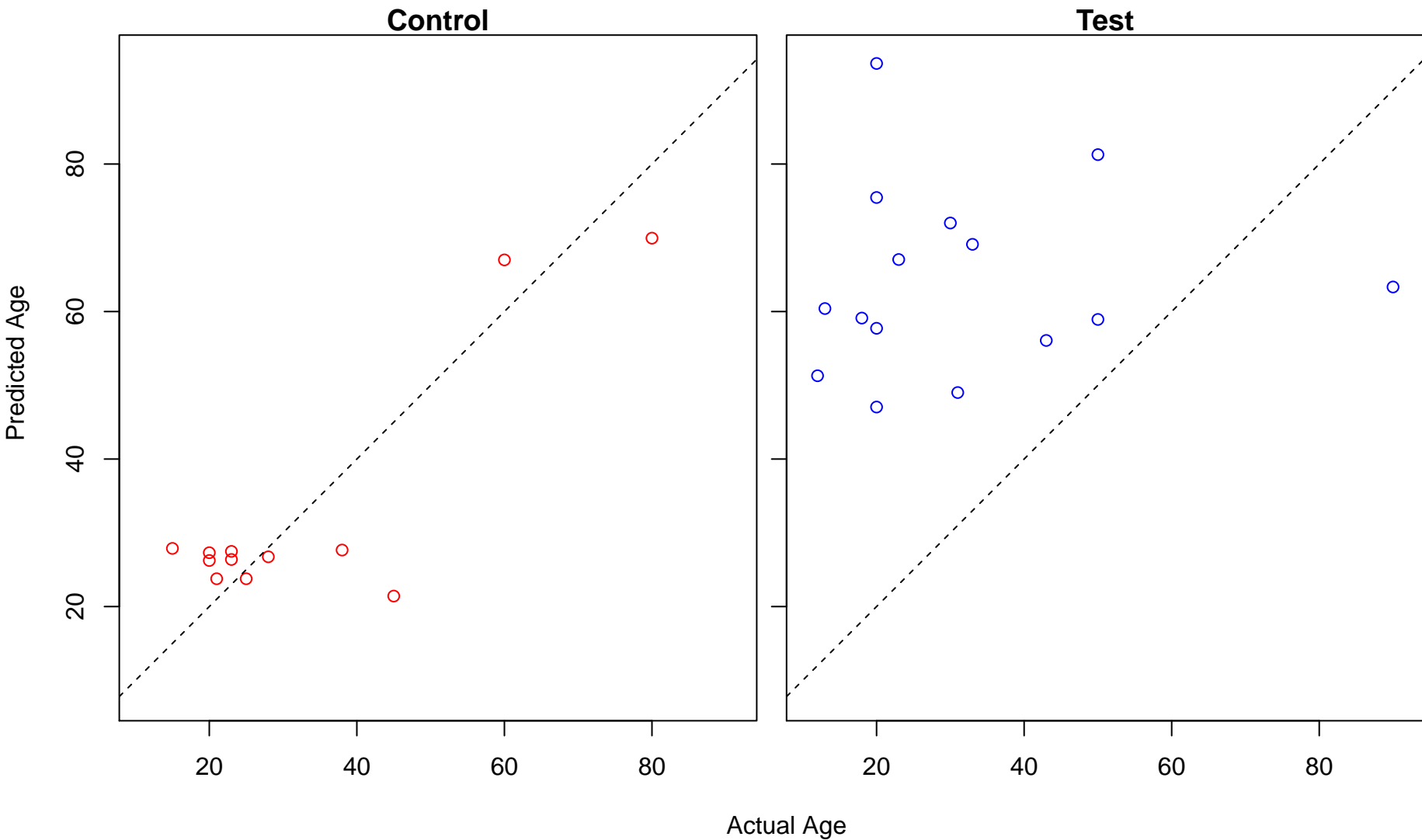
striated muscle cell differentiation (Score: 5.842015)



heparan sulfate proteoglycan biosynthetic process (Score: 5.841972)

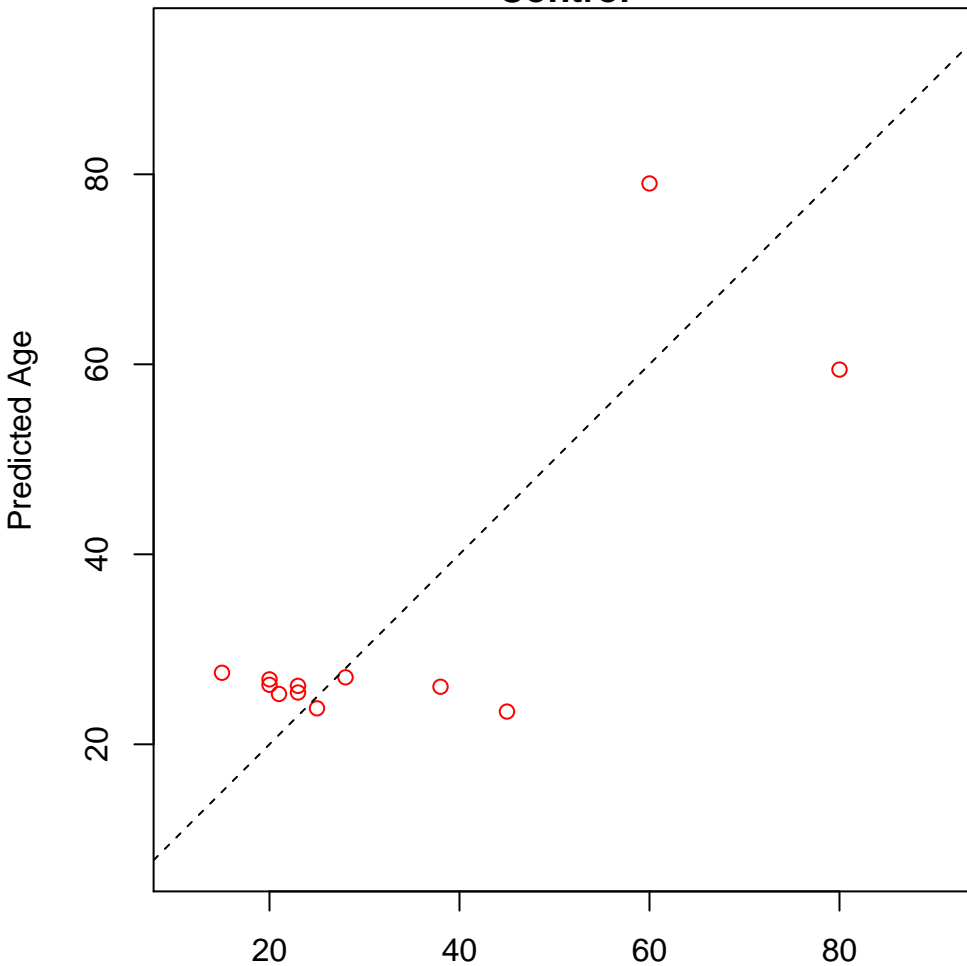


negative regulation of lipoprotein lipase activity (Score: 5.840330)

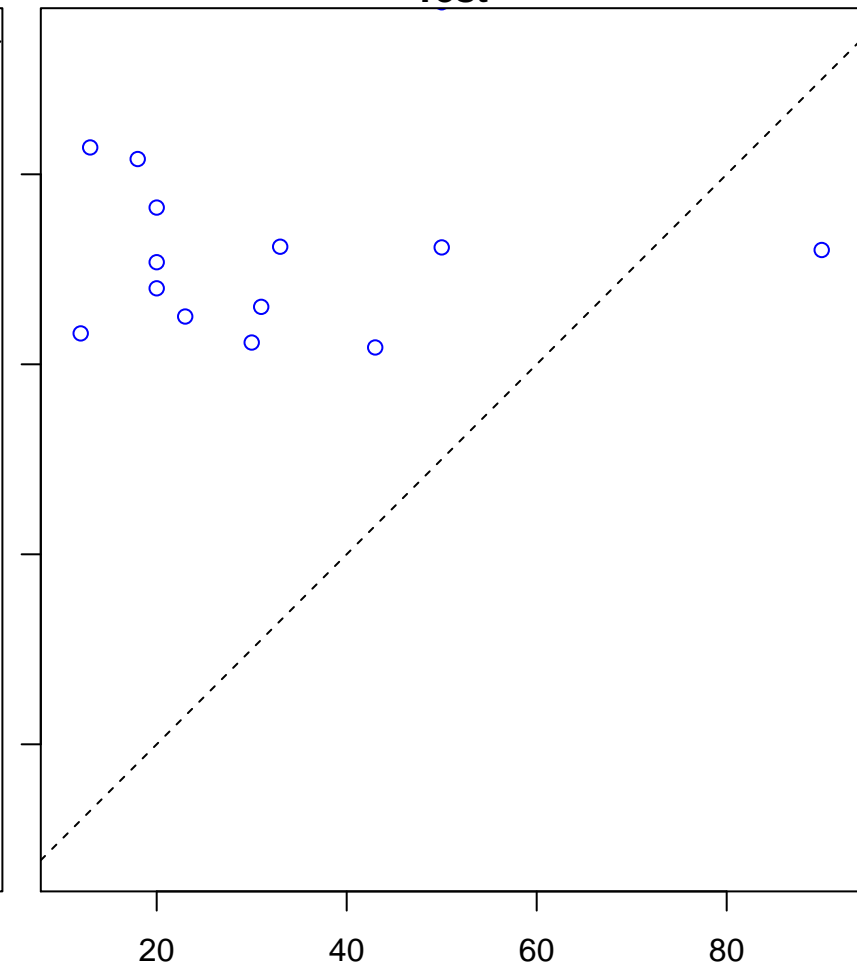


positive regulation of cell cycle process (Score: 5.839523)

Control

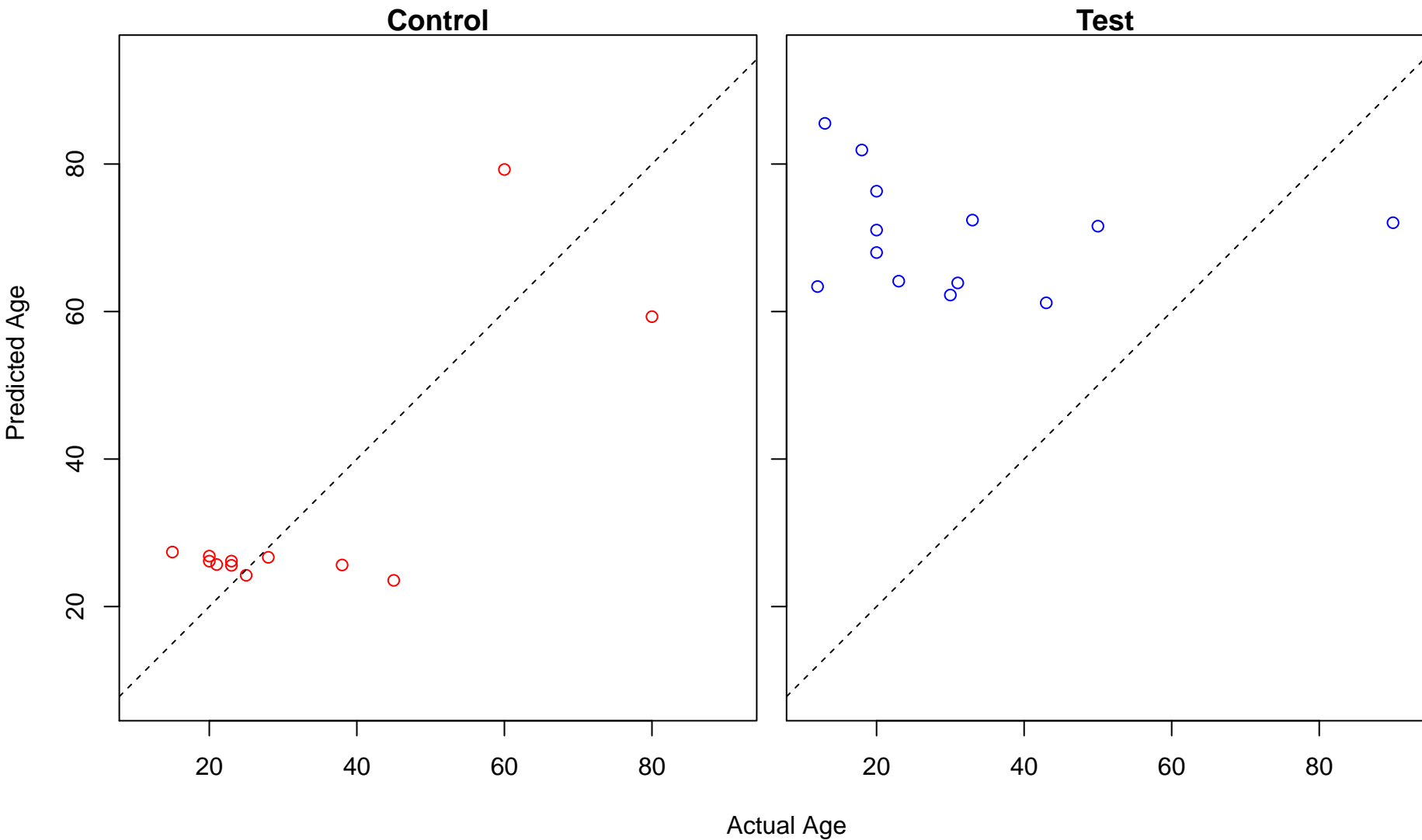


Test

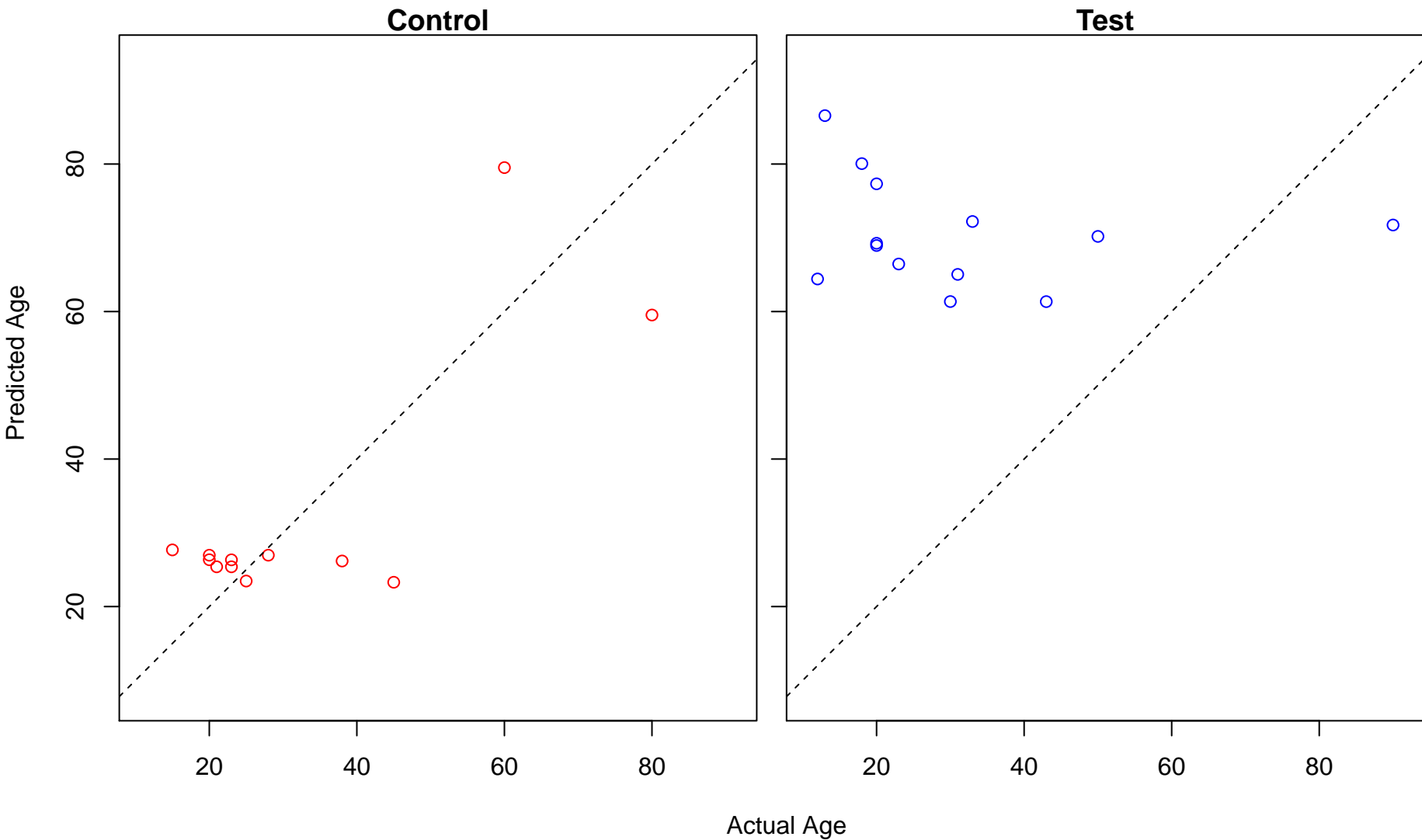


Actual Age

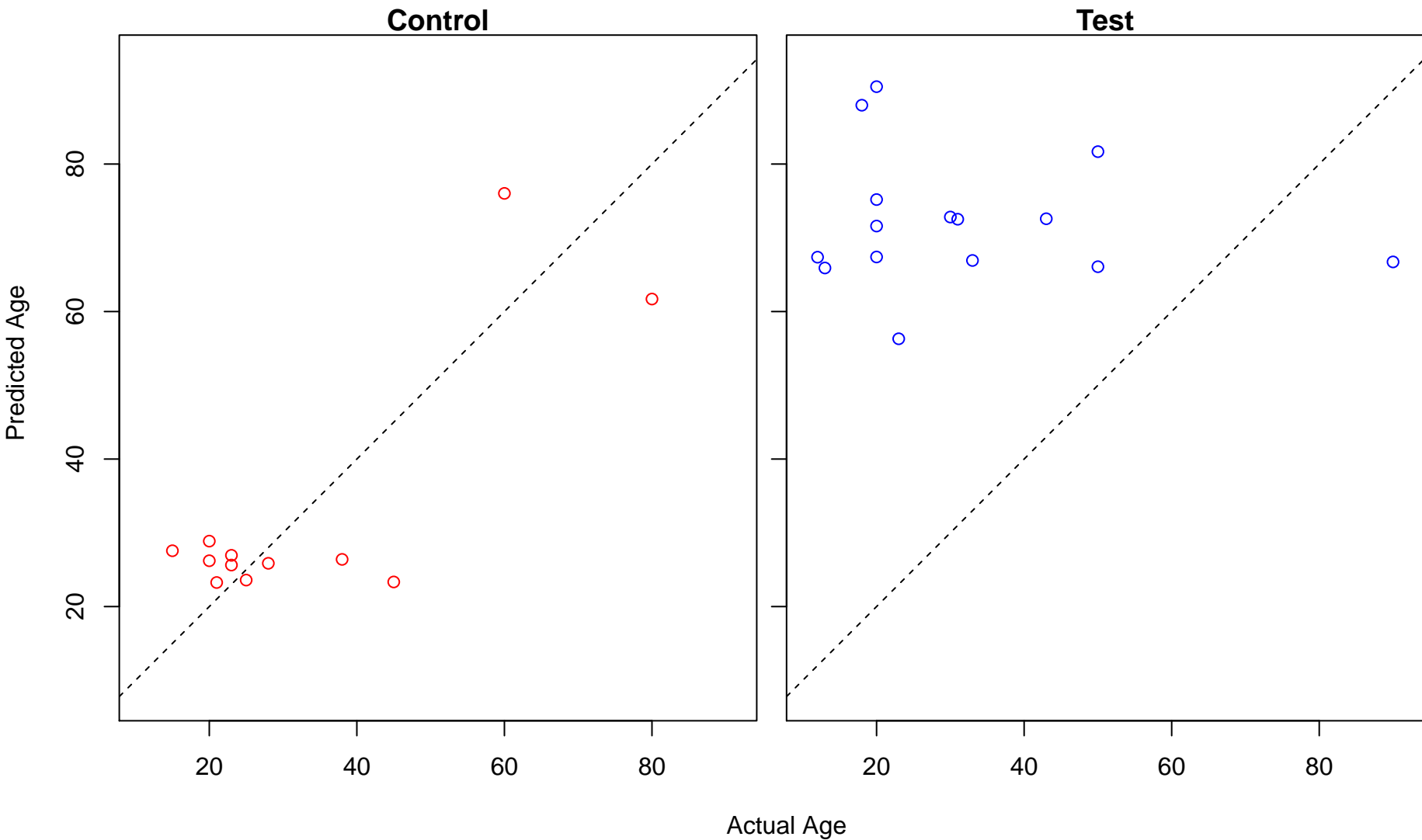
positive regulation of cell cycle (Score: 5.838702)



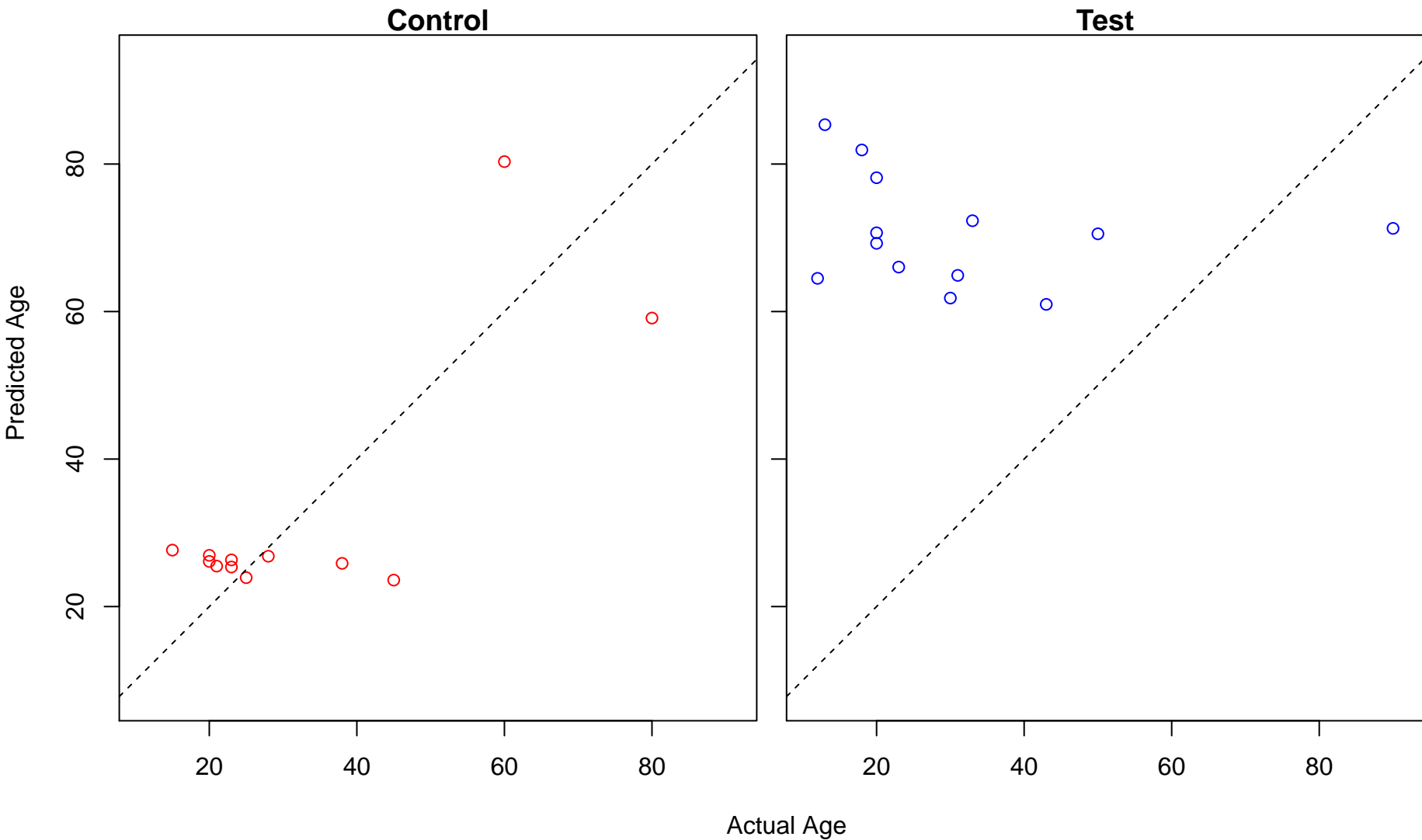
double-strand break repair (Score: 5.837804)



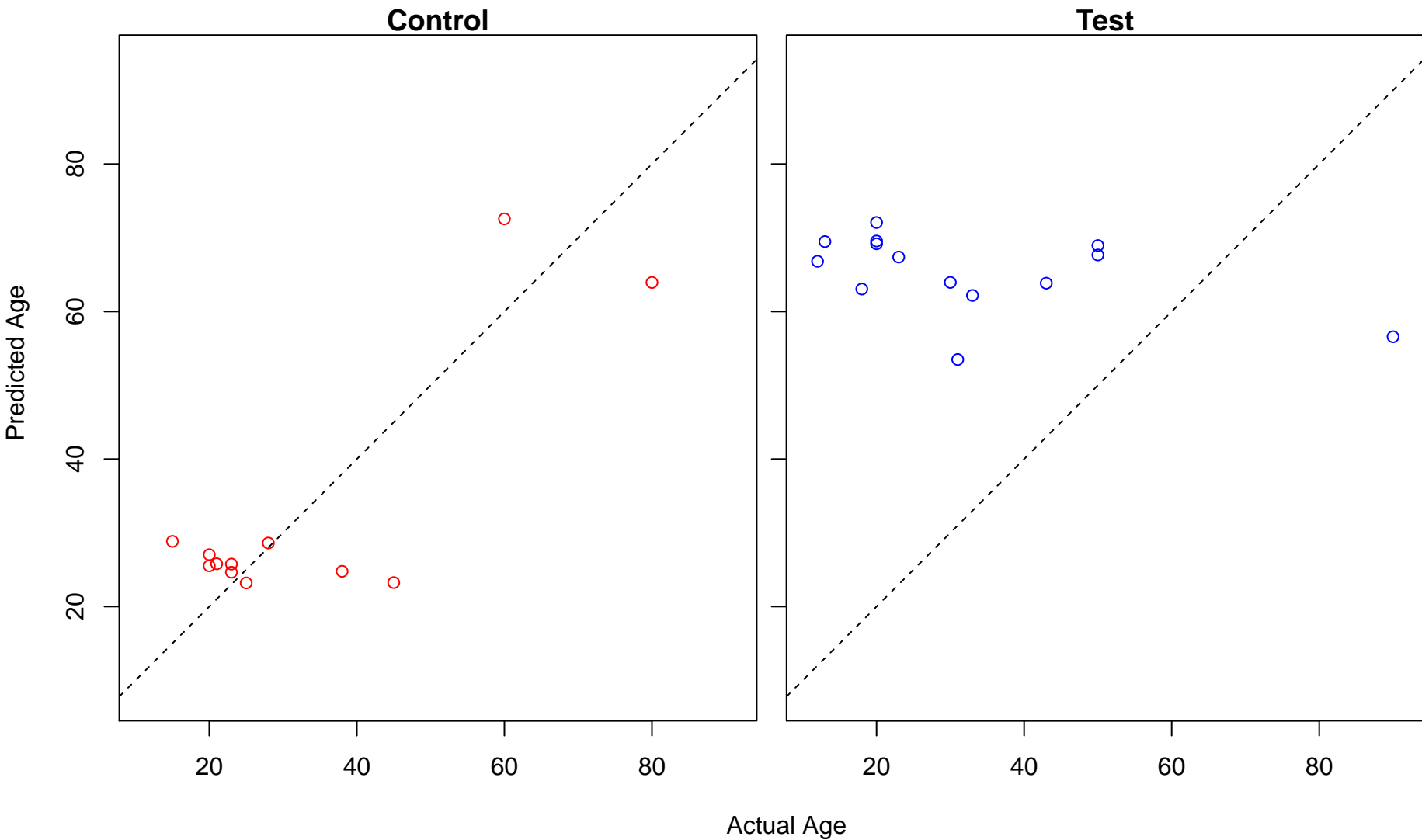
cellular response to glucose starvation (Score: 5.837683)



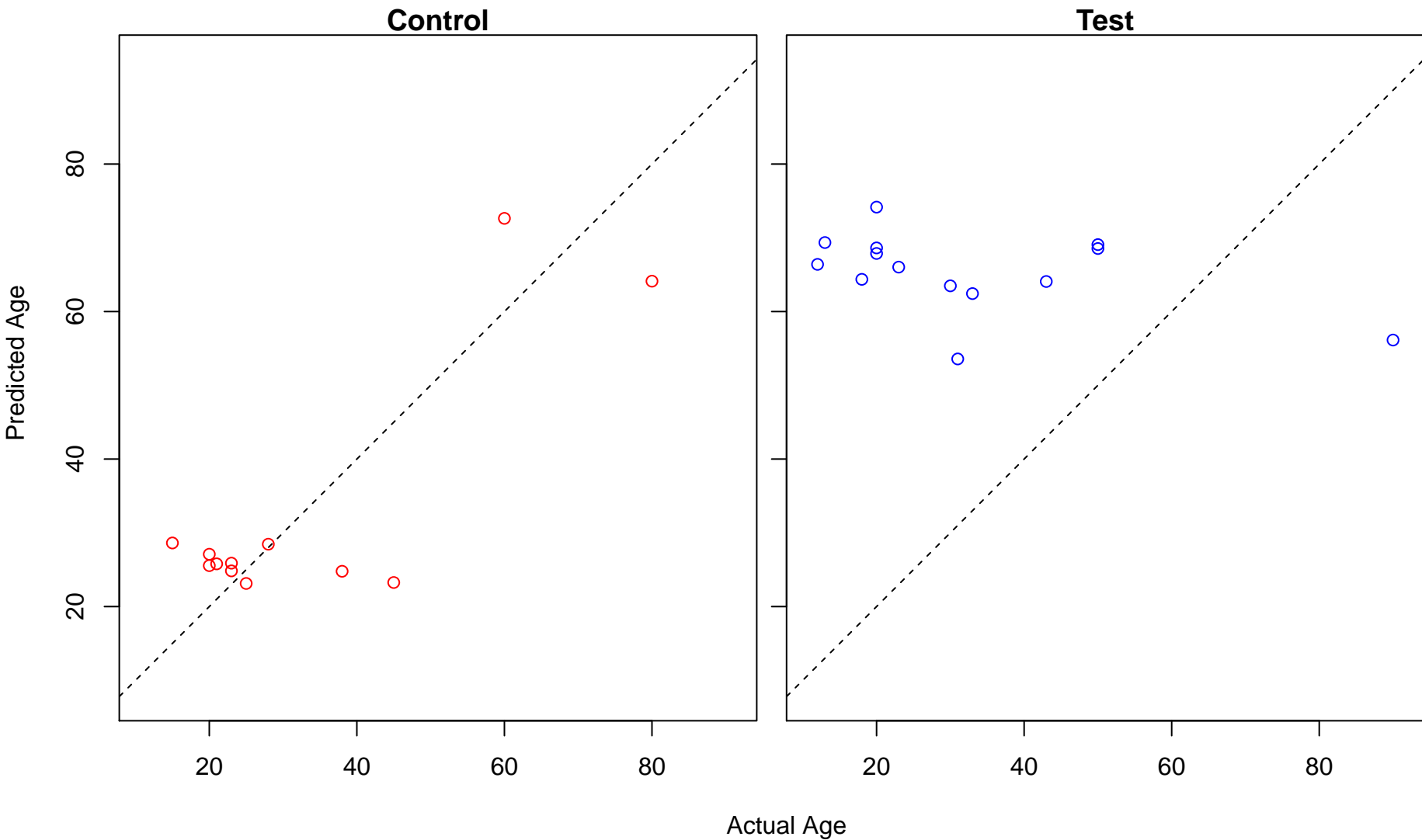
tumor necrosis factor-mediated signaling pathway (Score: 5.835348)



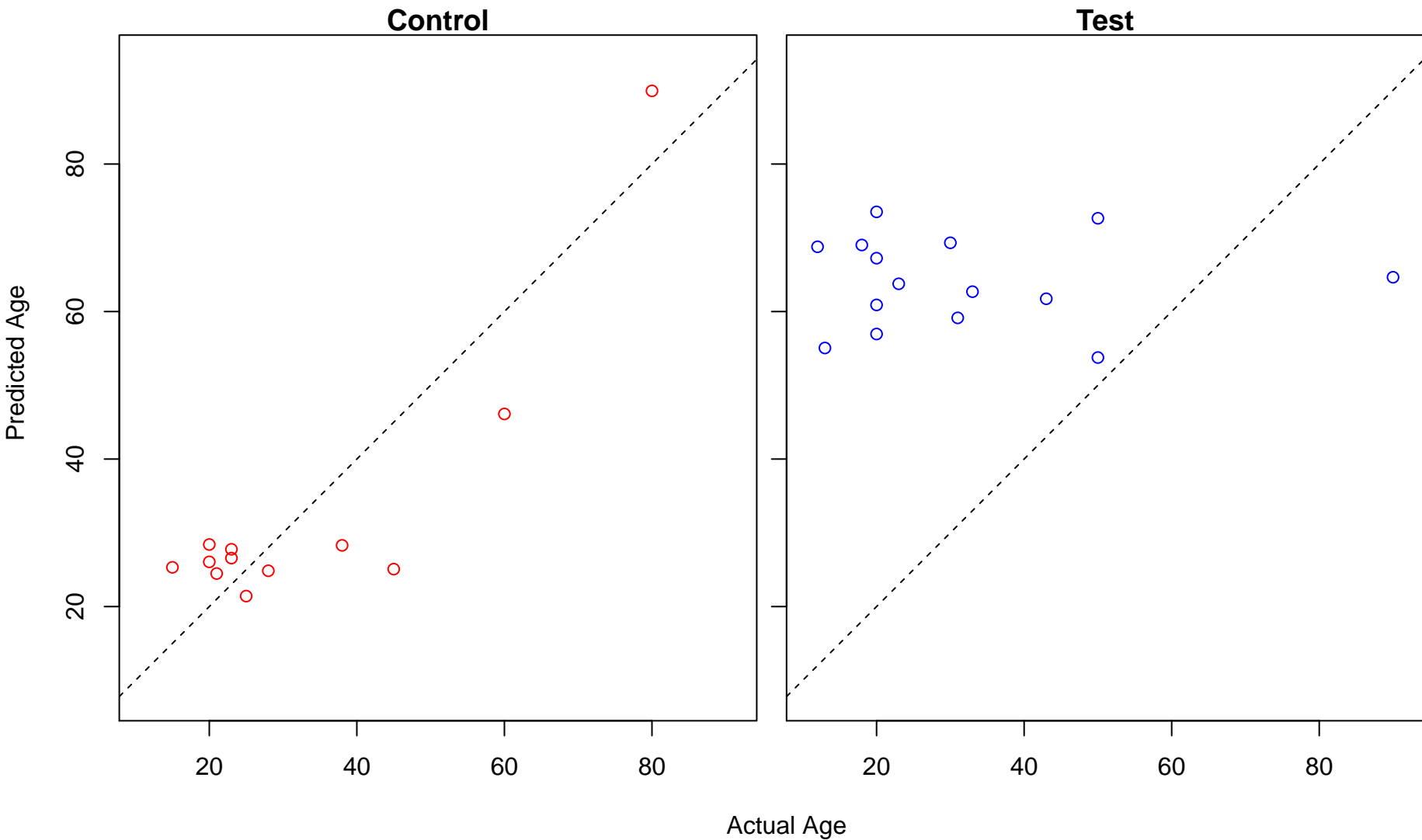
hair cell differentiation (Score: 5.832805)



ear morphogenesis (Score: 5.832122)

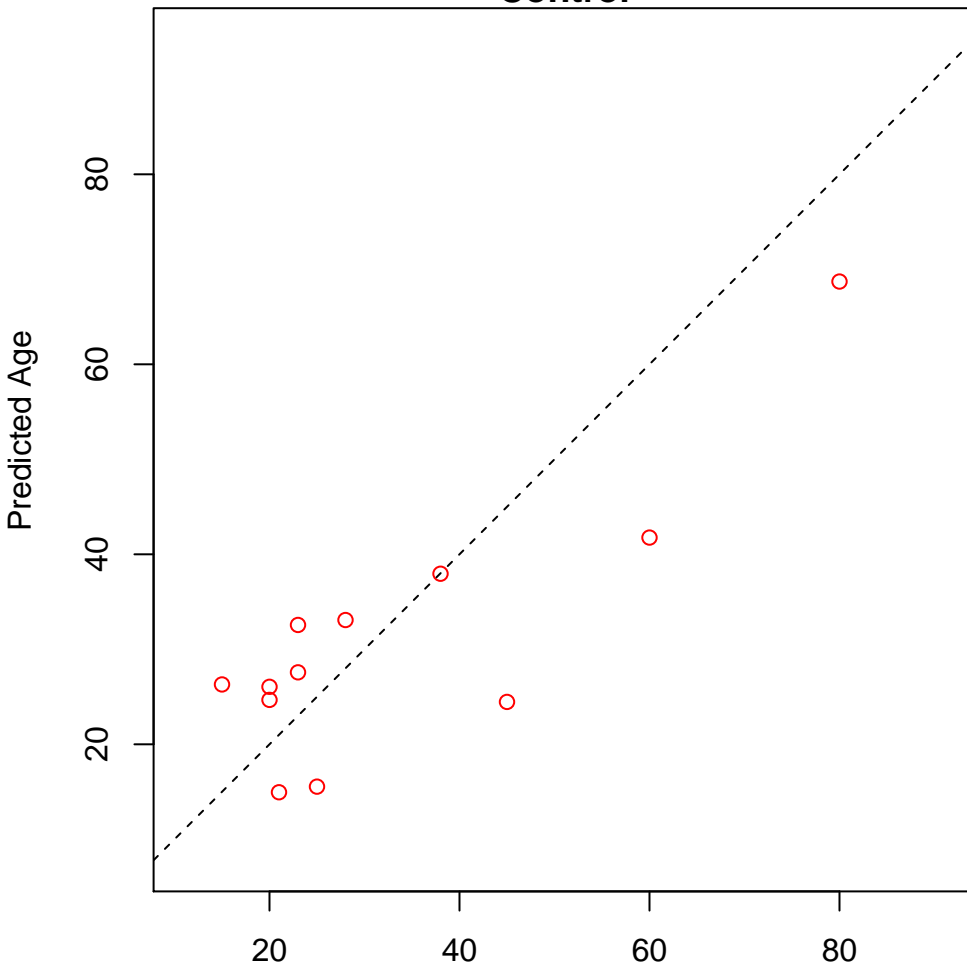


muscle tissue development (Score: 5.831262)

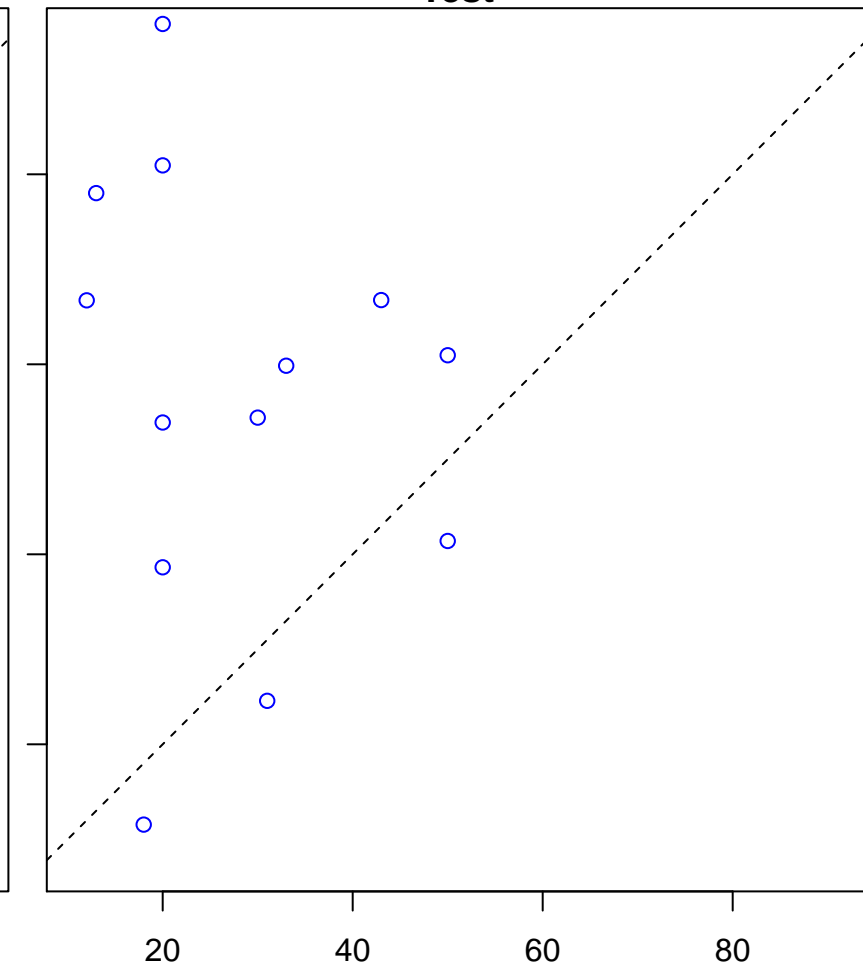


enteroendocrine cell differentiation (Score: 5.831179)

Control

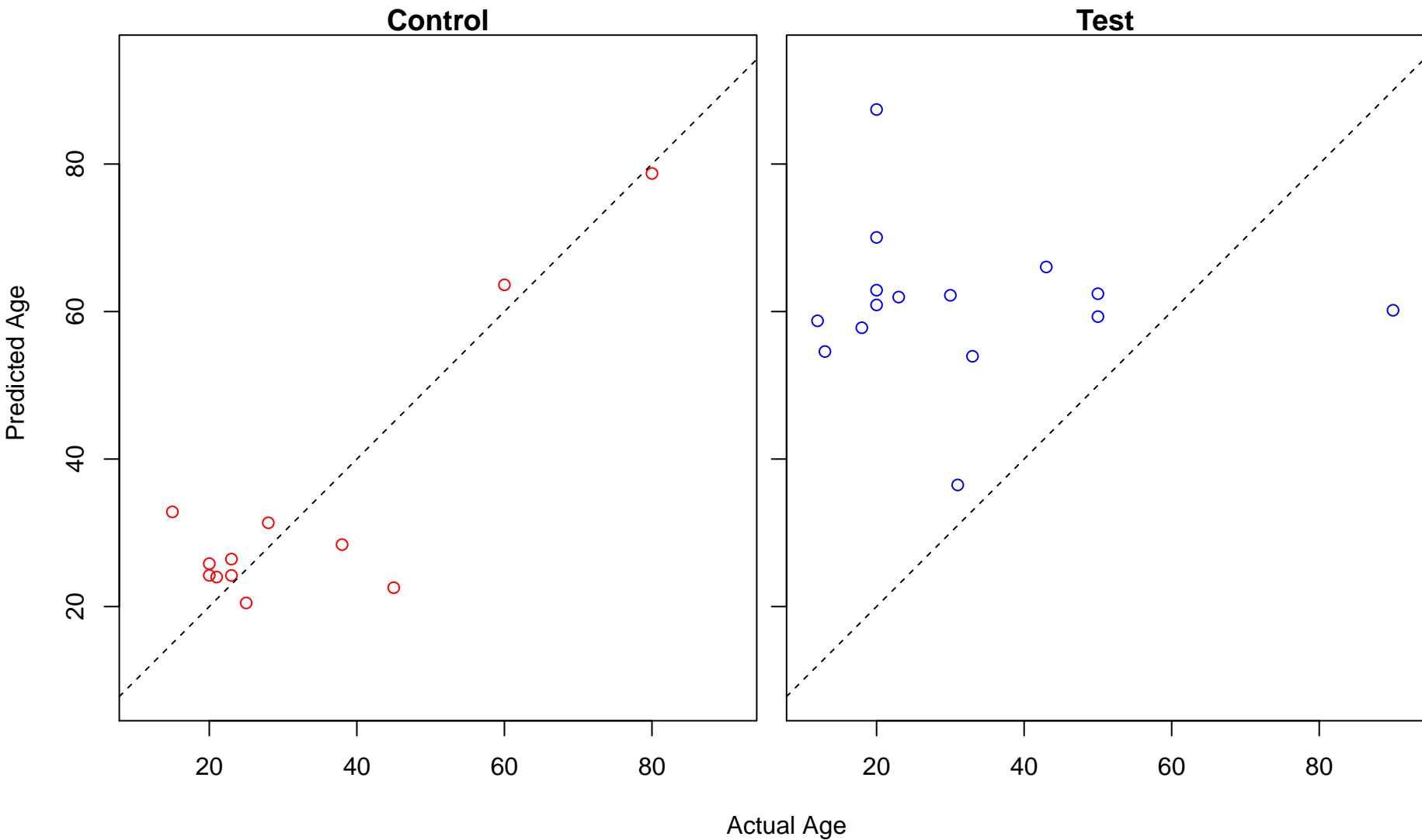


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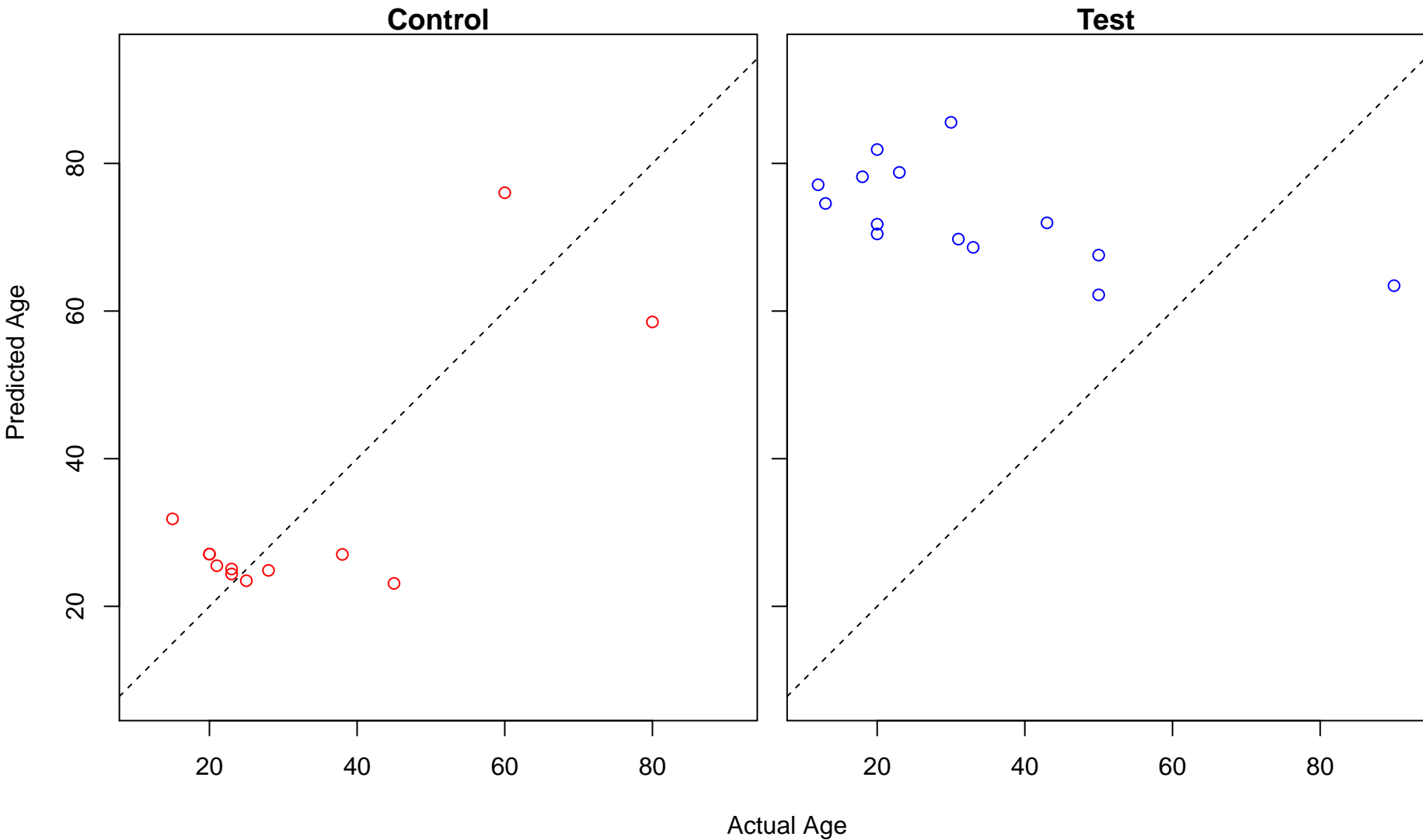


Actual Age

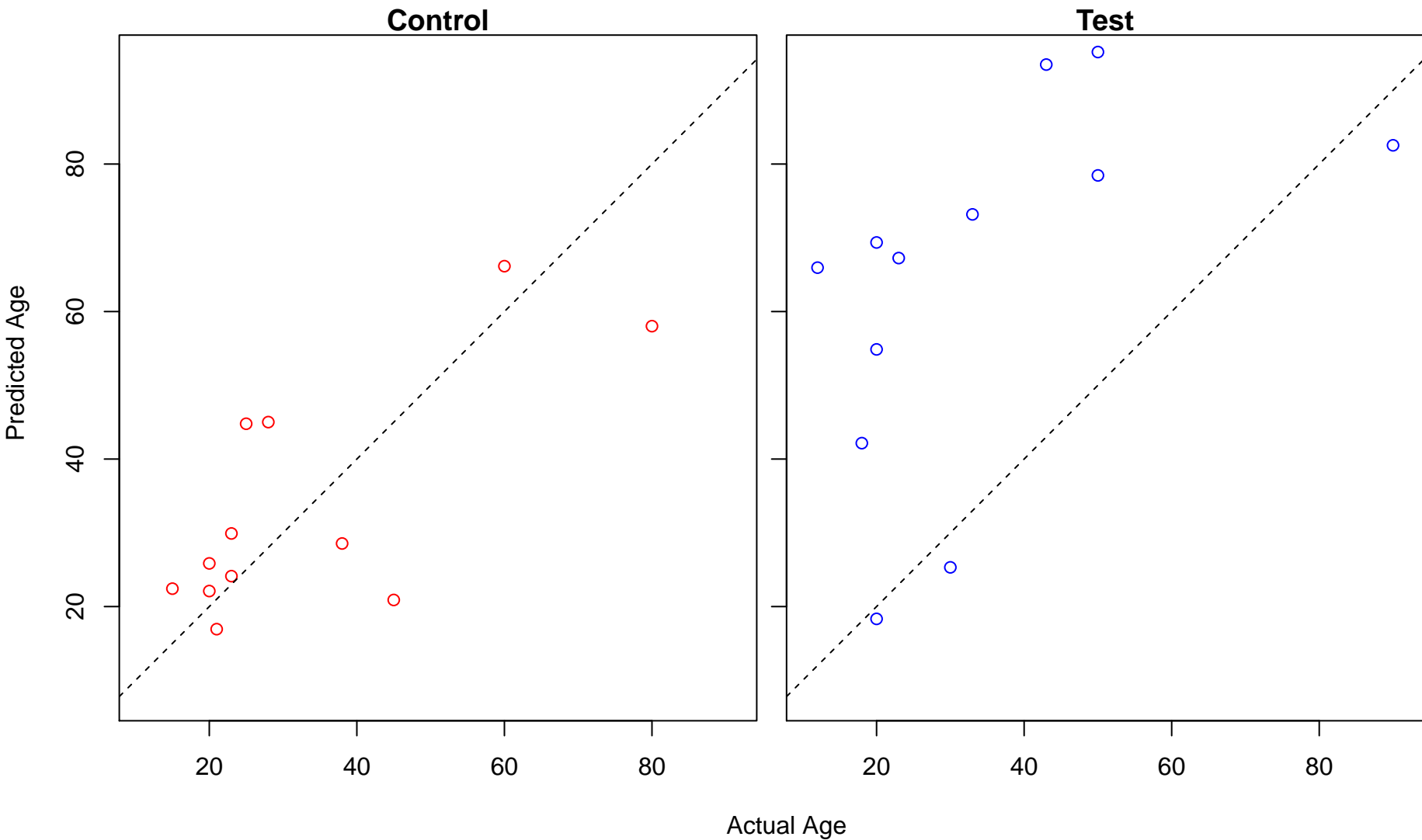
regulation of blood pressure (Score: 5.827317)



positive regulation of Notch signaling pathway (Score: 5.826592)

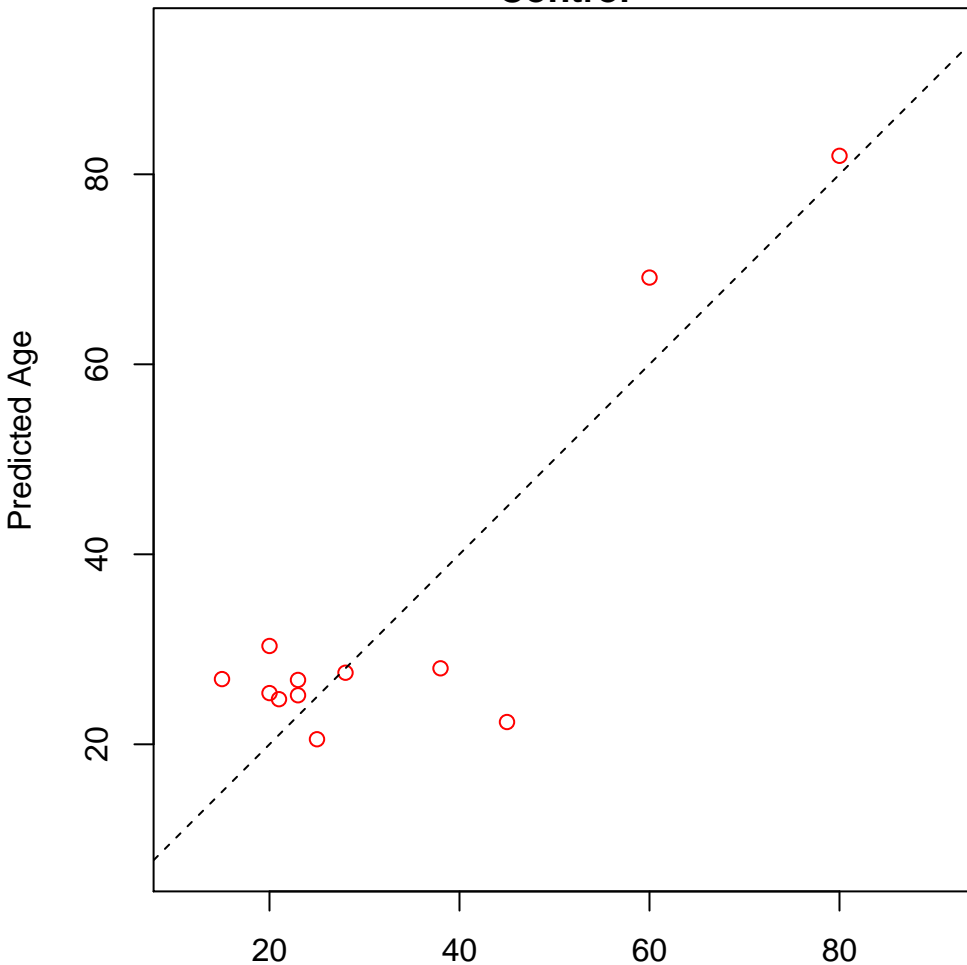


interleukin-1 beta production (Score: 5.824526)

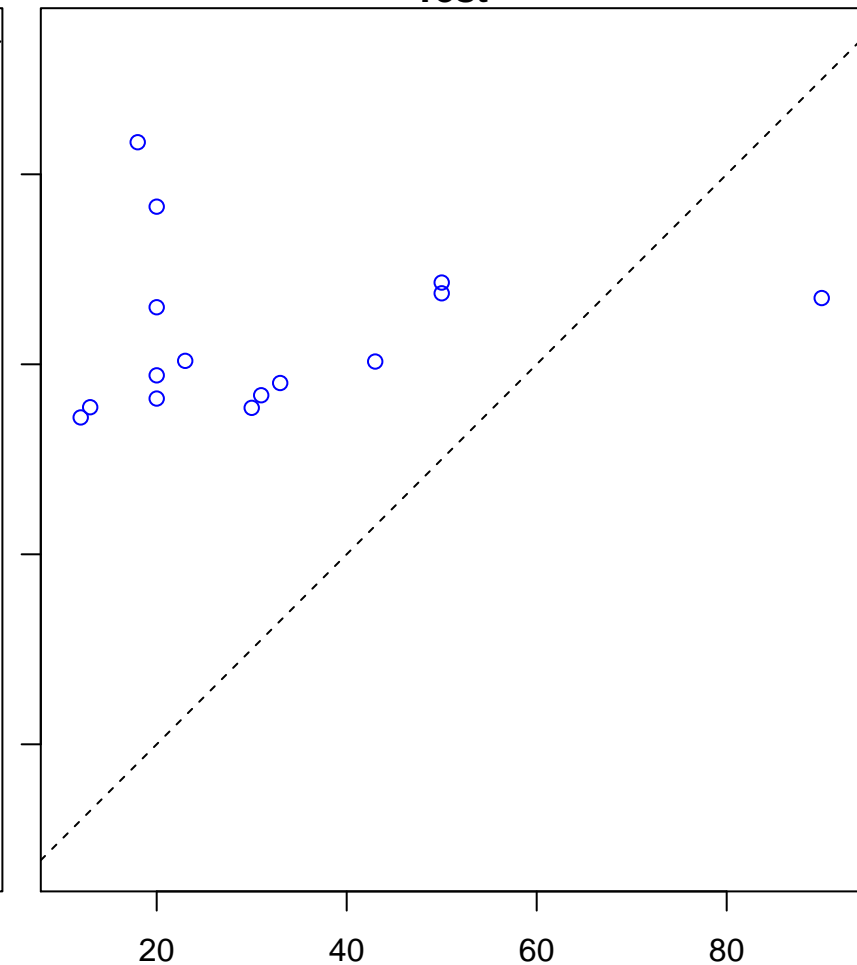


positive regulation of cell differentiation (Score: 5.822396)

Control

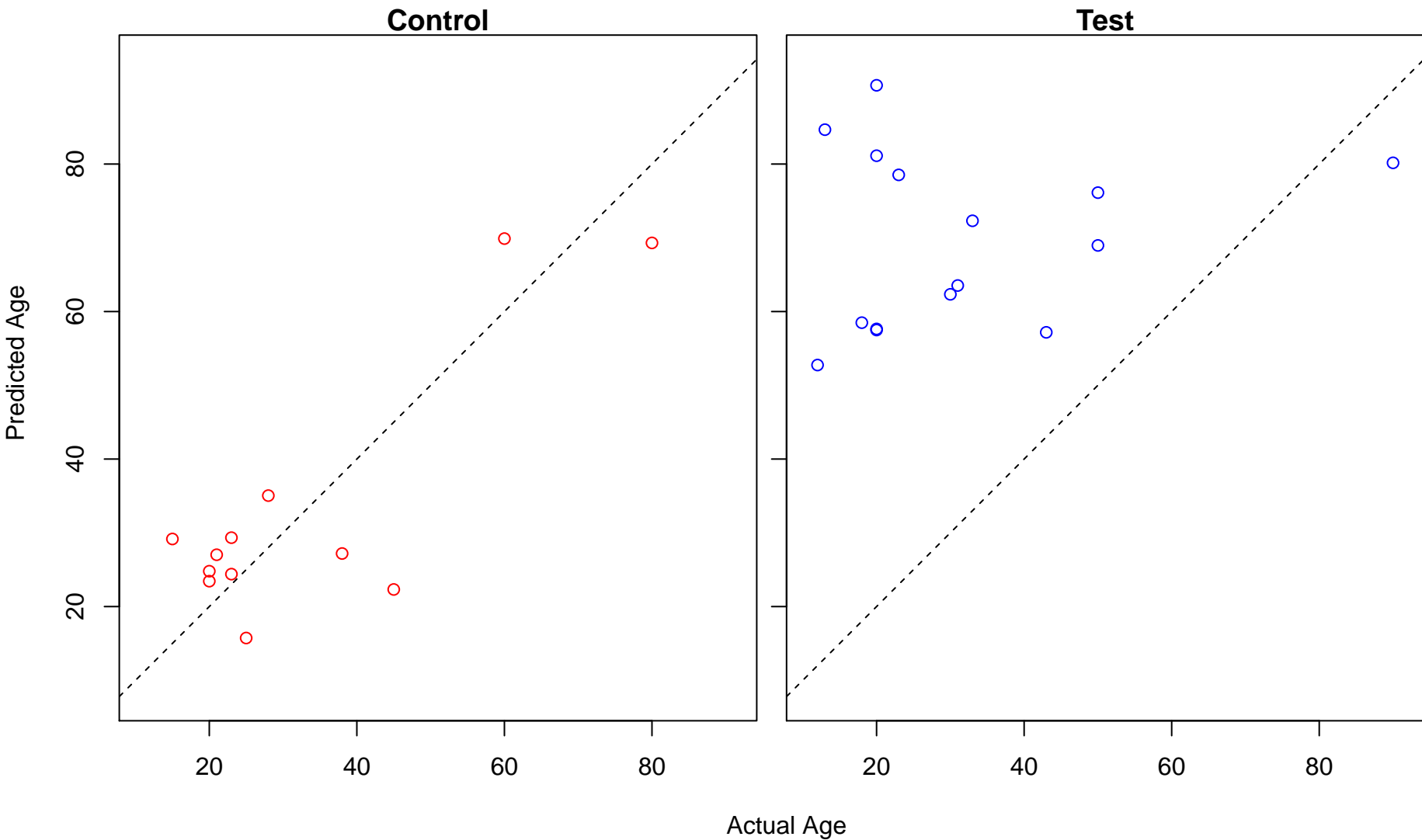


Test

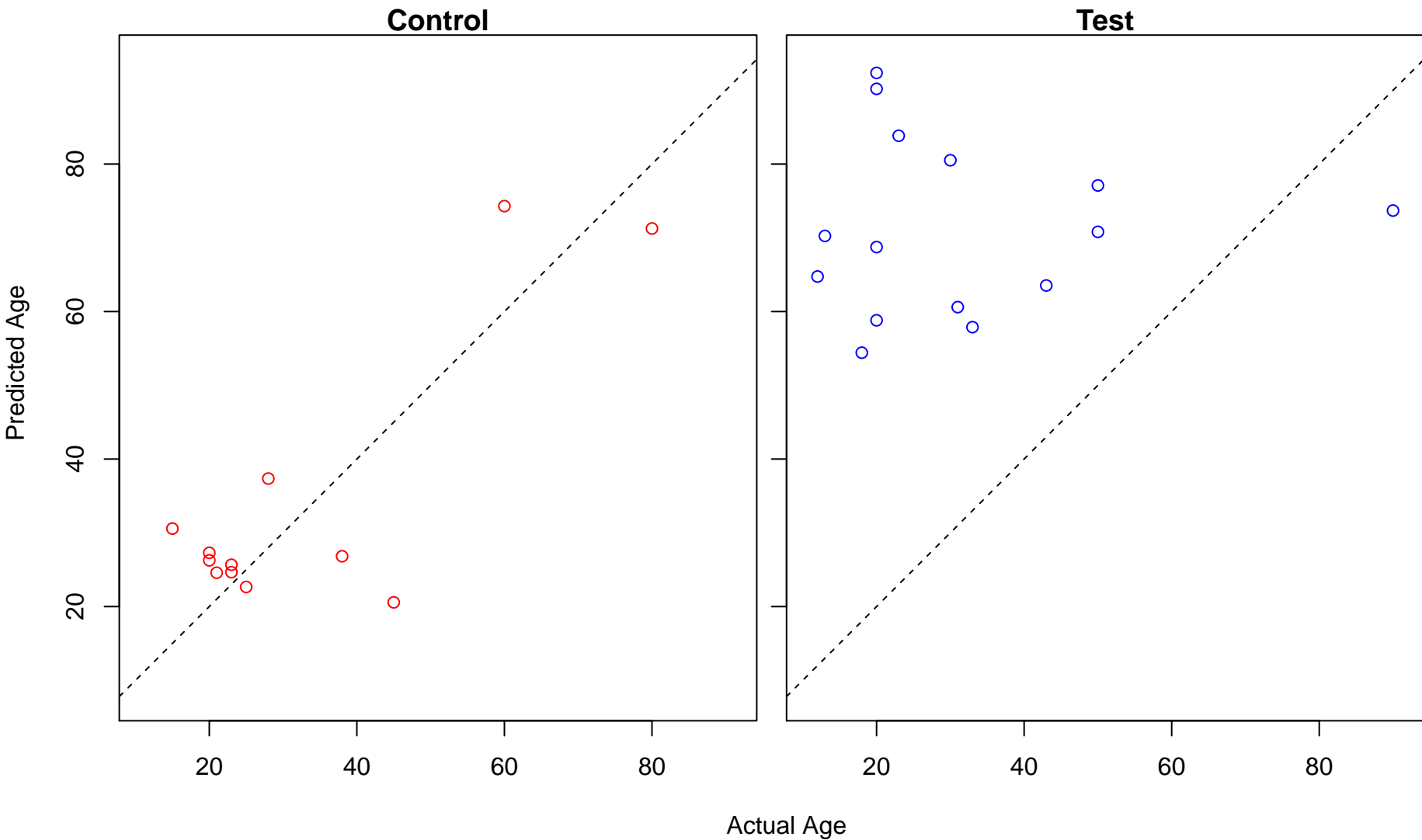


Actual Age

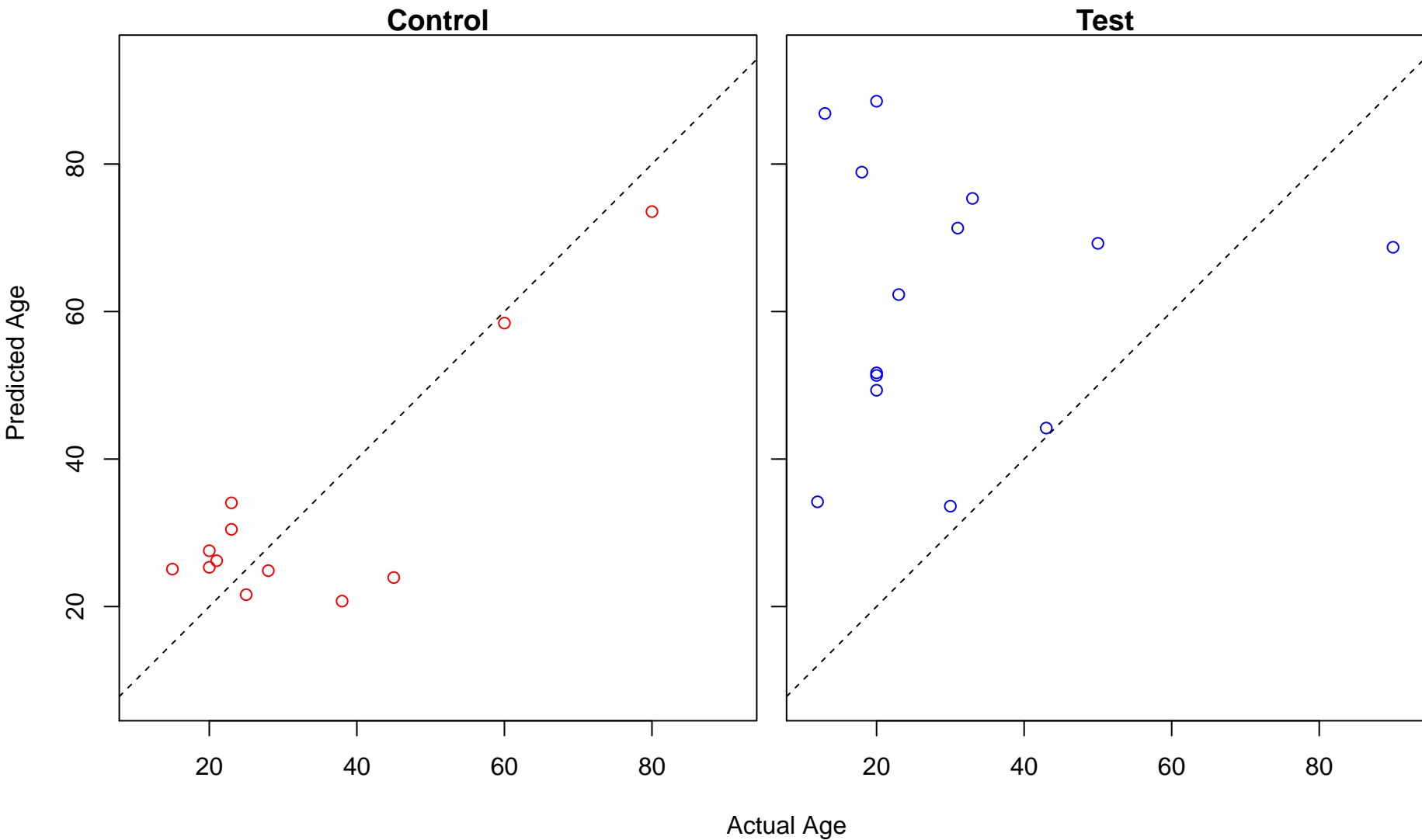
response to transition metal nanoparticle (Score: 5.821426)



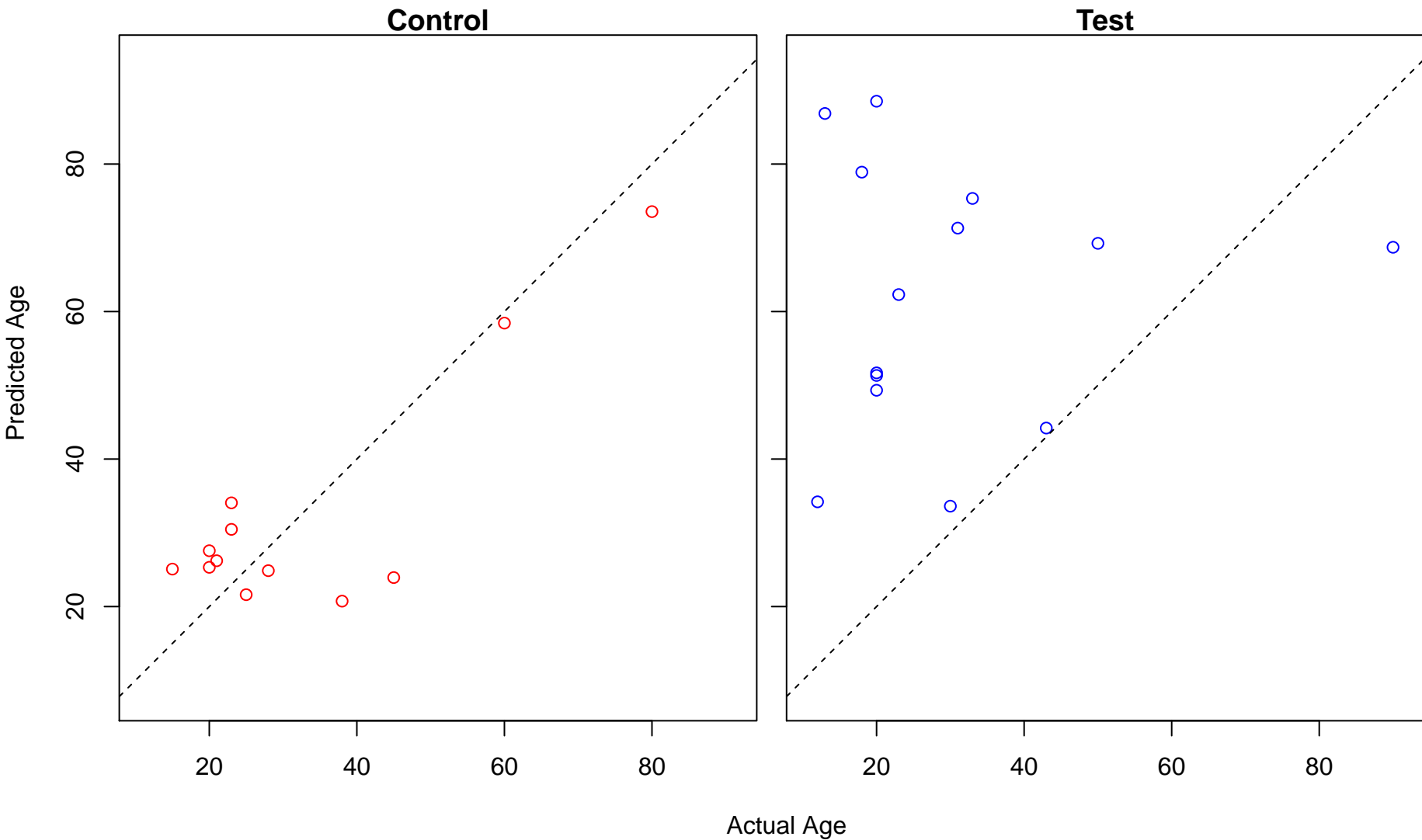
regulation of ERK1 and ERK2 cascade (Score: 5.815916)



cholesterol homeostasis (Score: 5.815218)

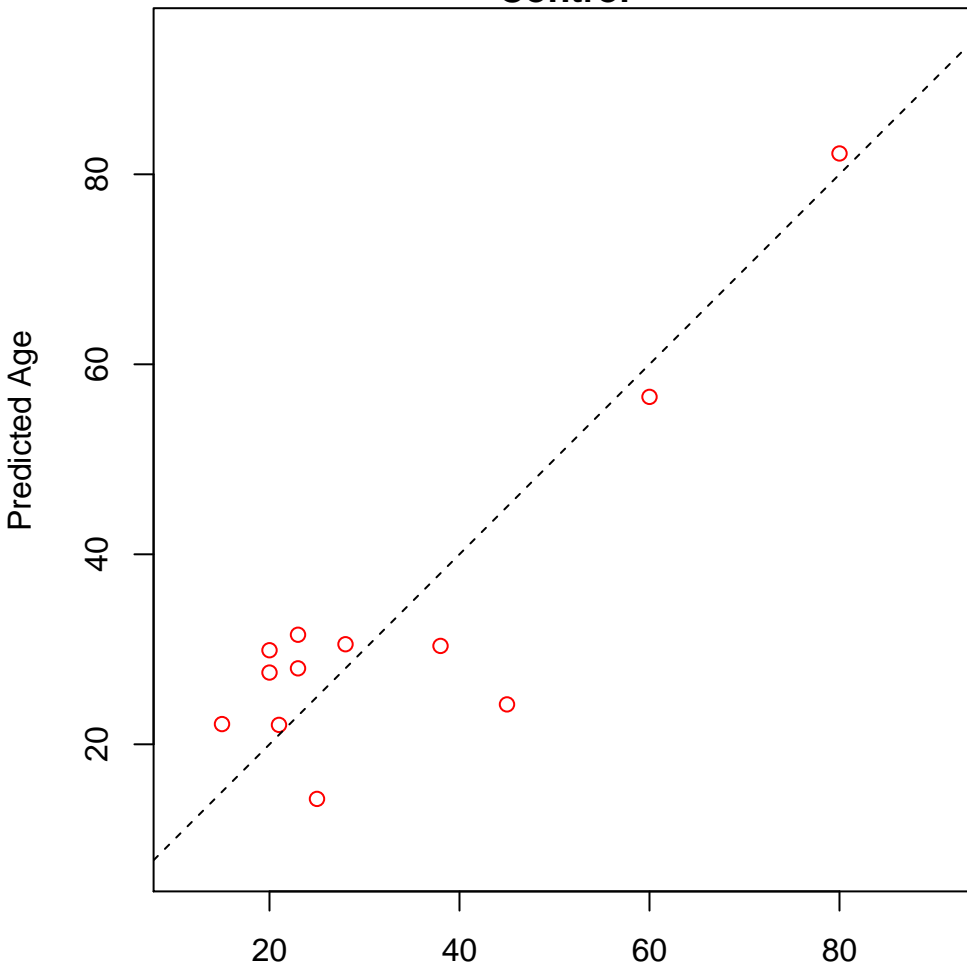


sterol homeostasis (Score: 5.815218)

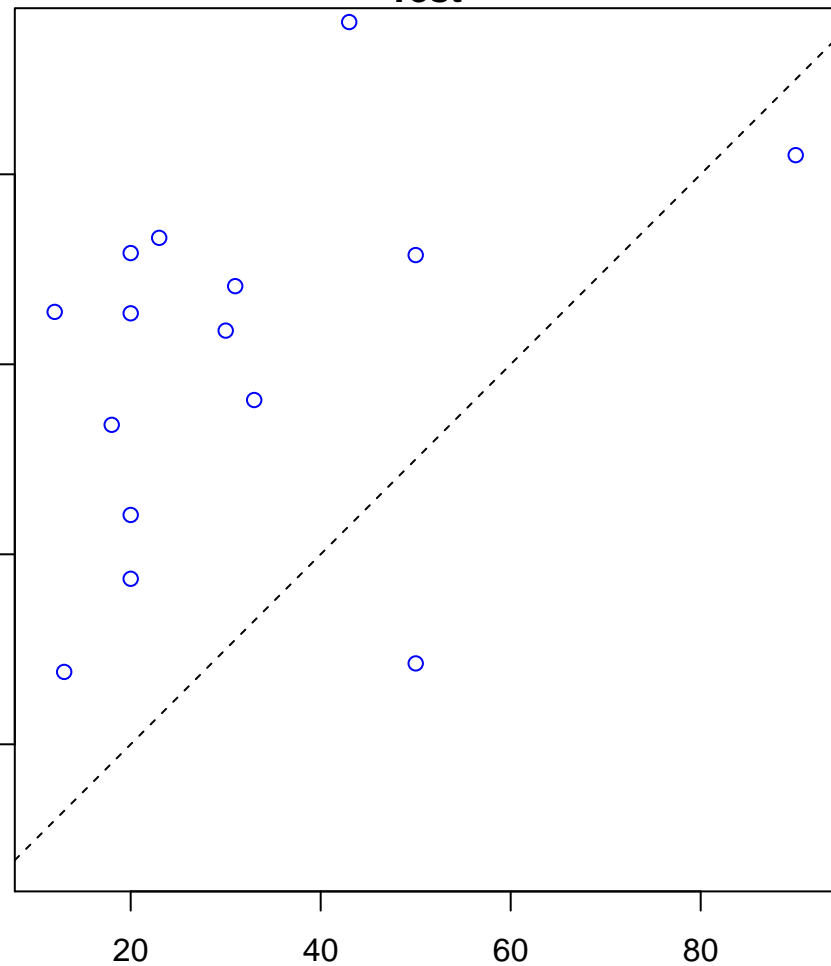


protein localization to centrosome (Score: 5.812173)

Control



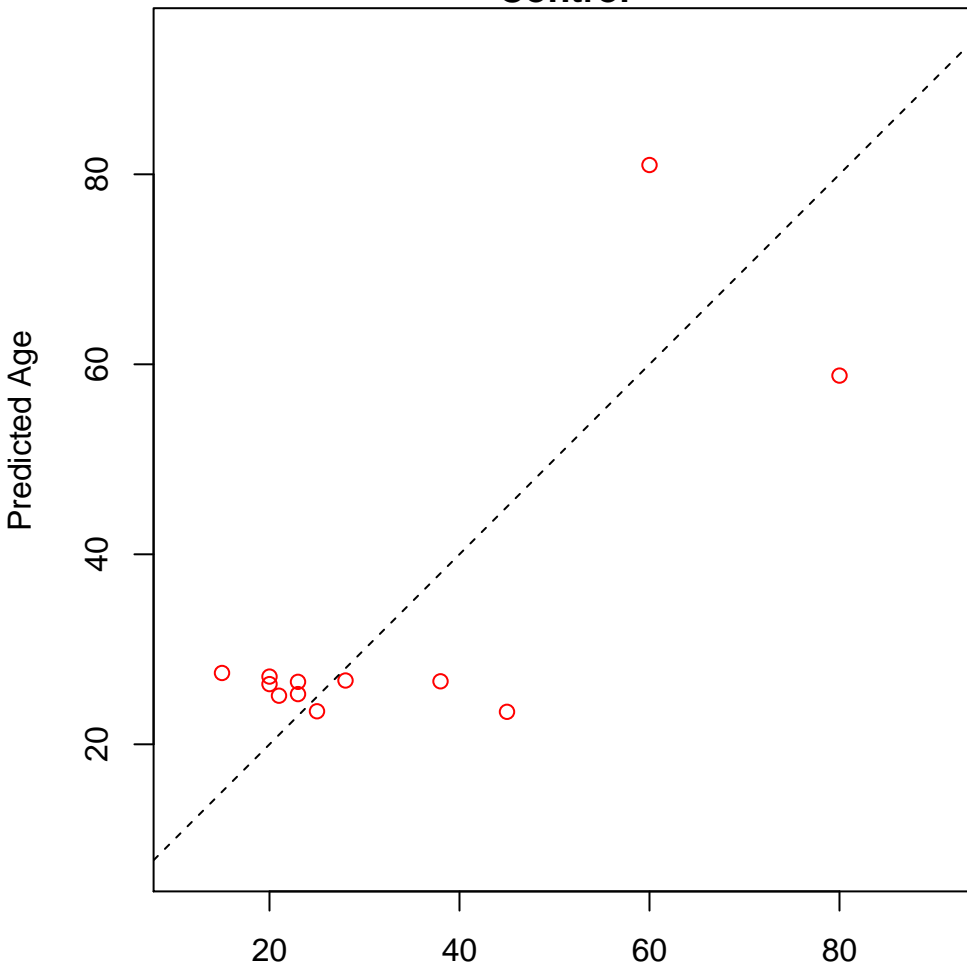
Test



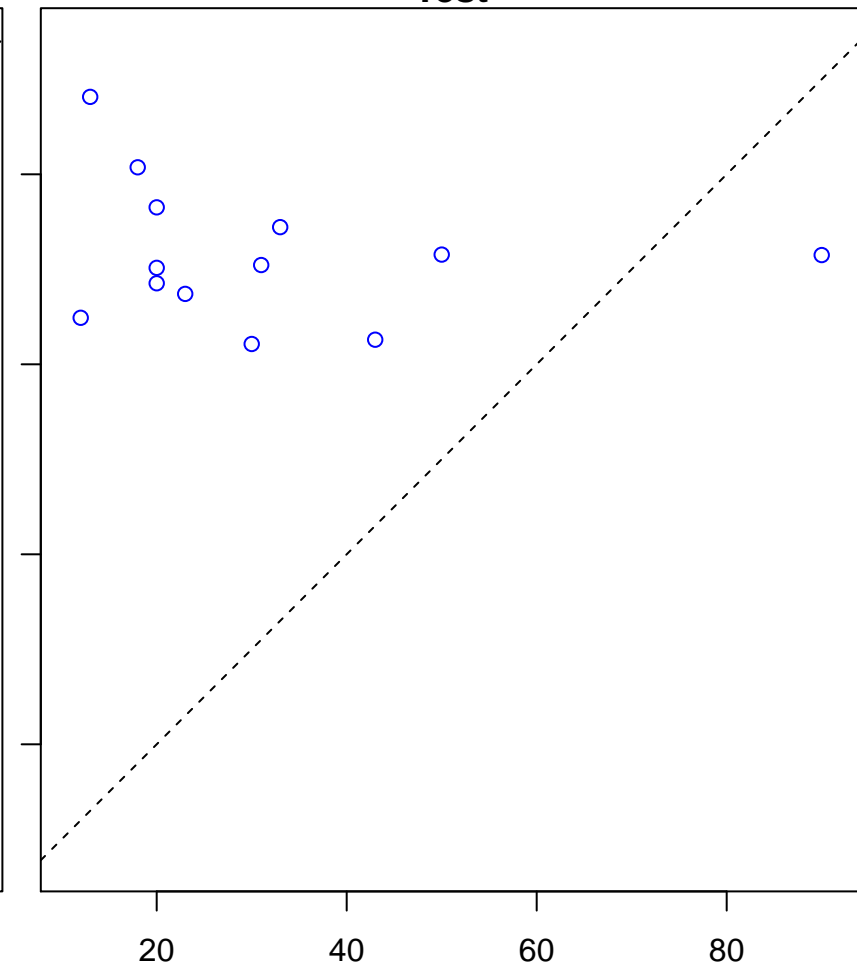
Actual Age

regulation of type I interferon production (Score: 5.811464)

Control

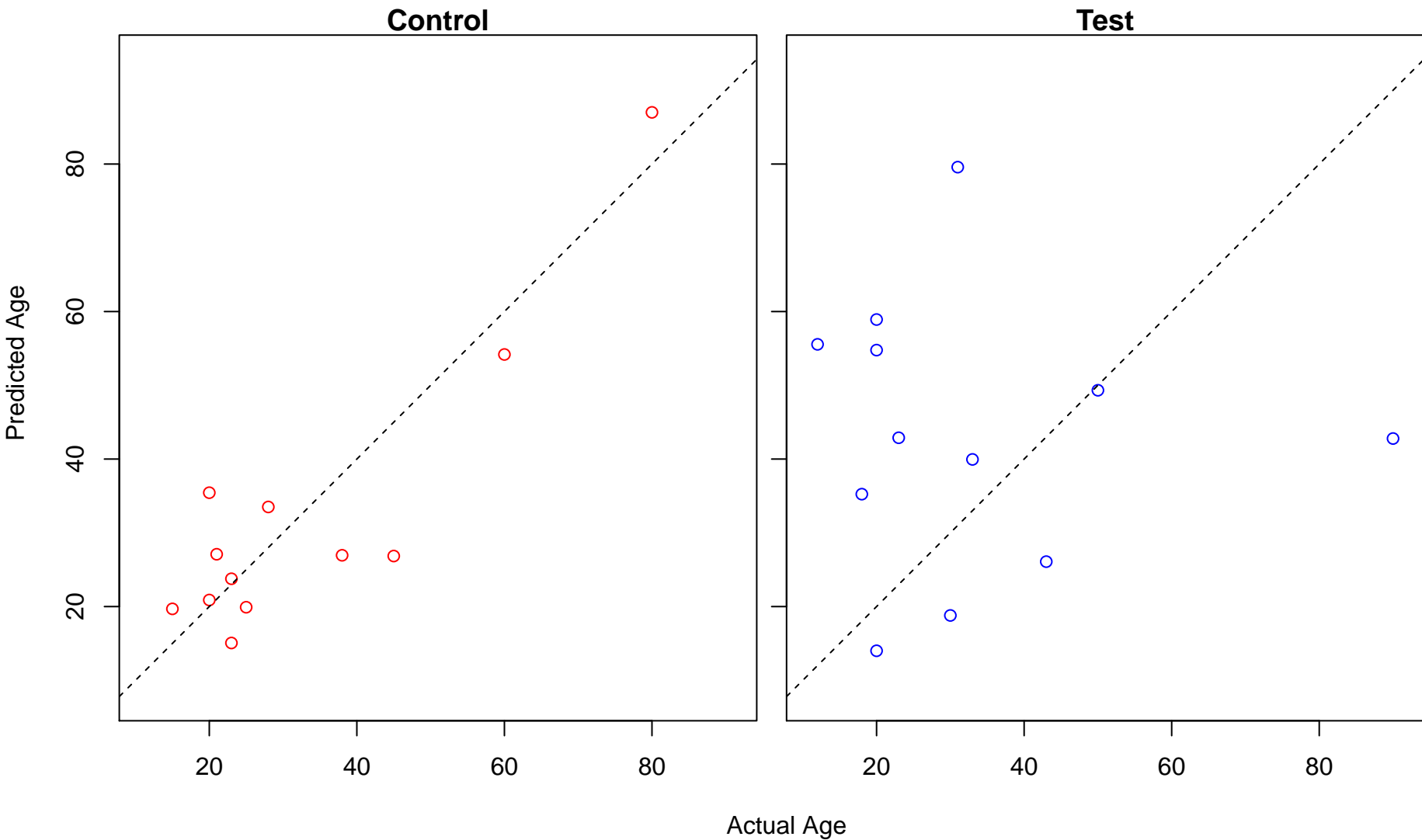


Test

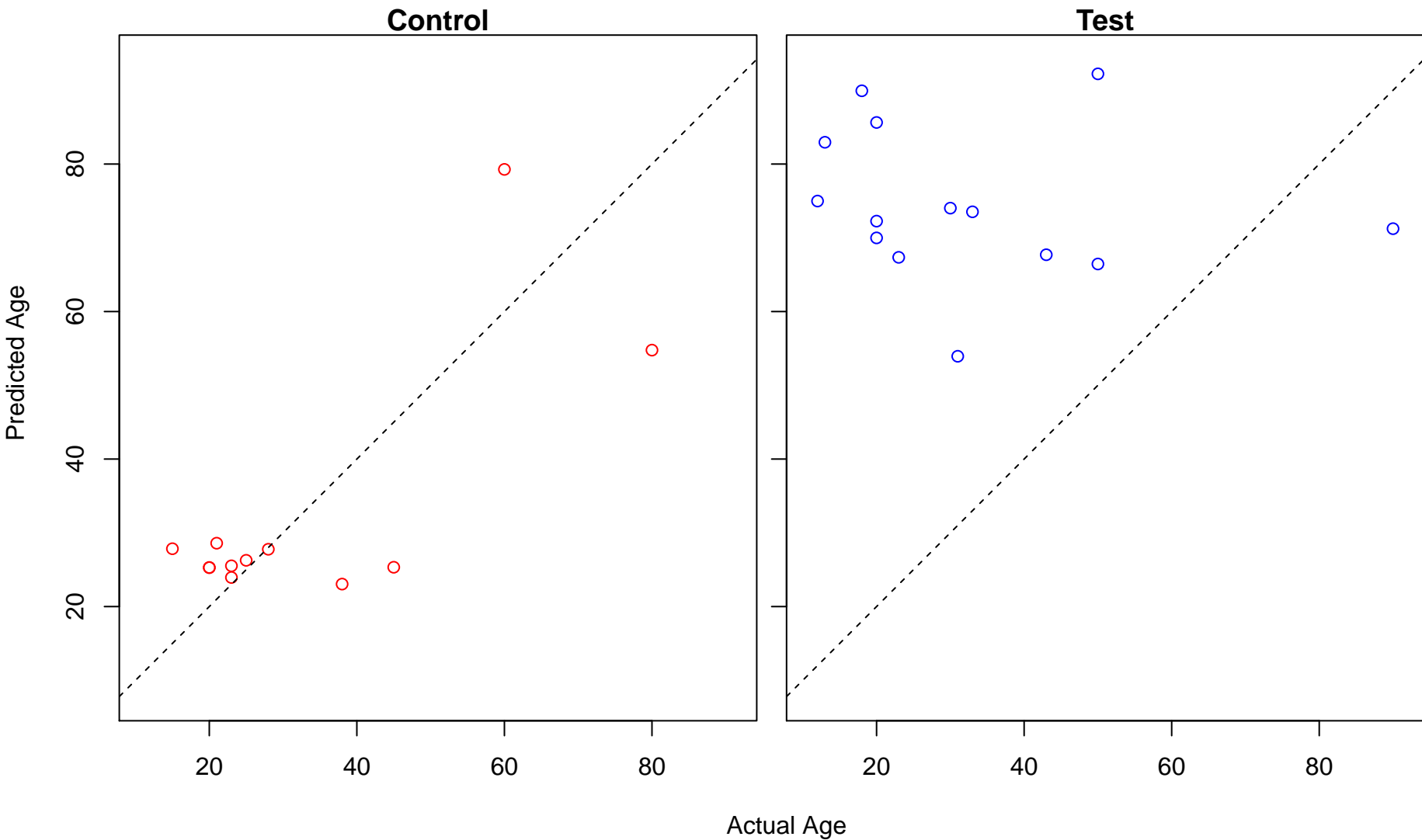


Actual Age

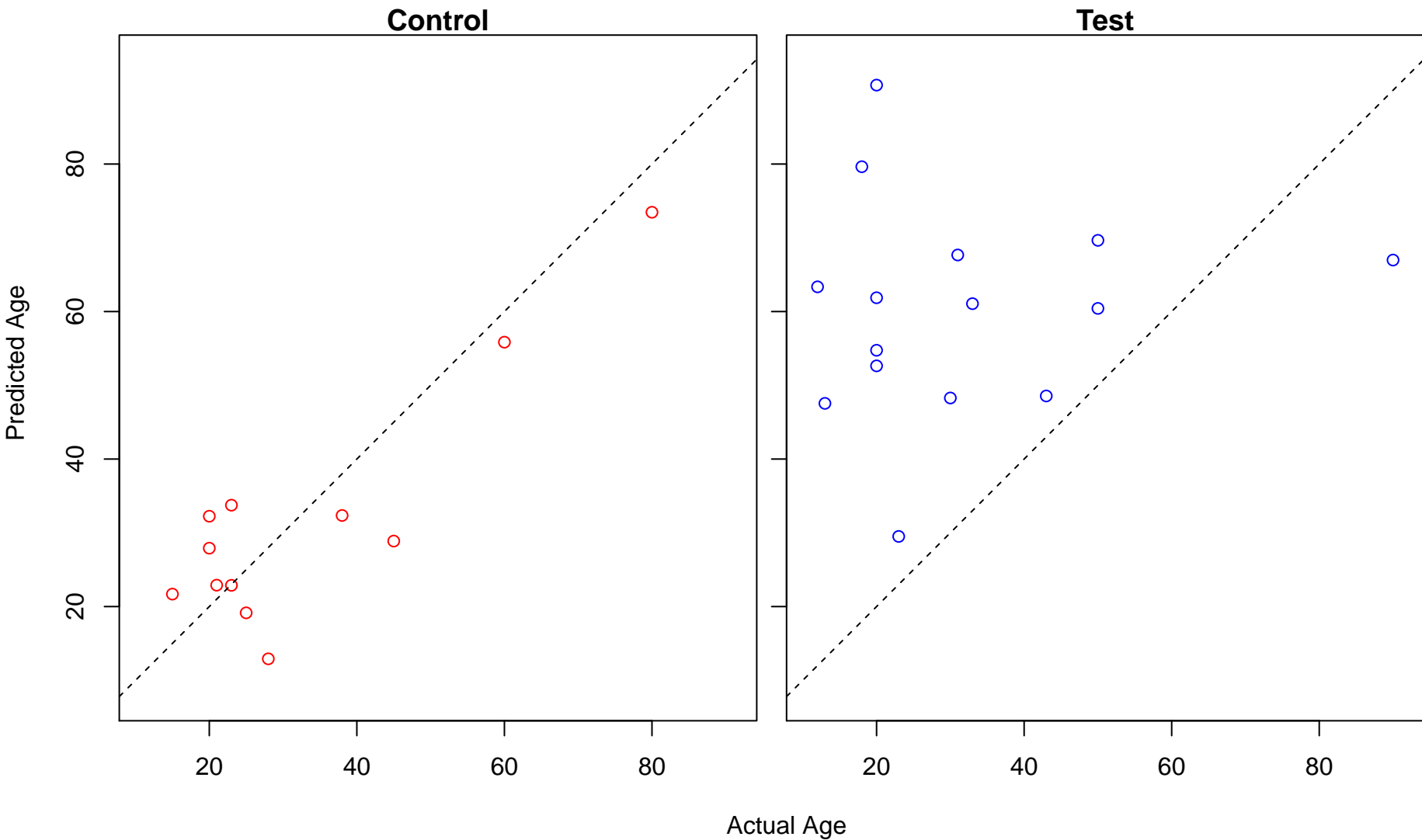
regulation of cyclin-dependent protein serine/threonine kinase activity (Score: 5.810253)



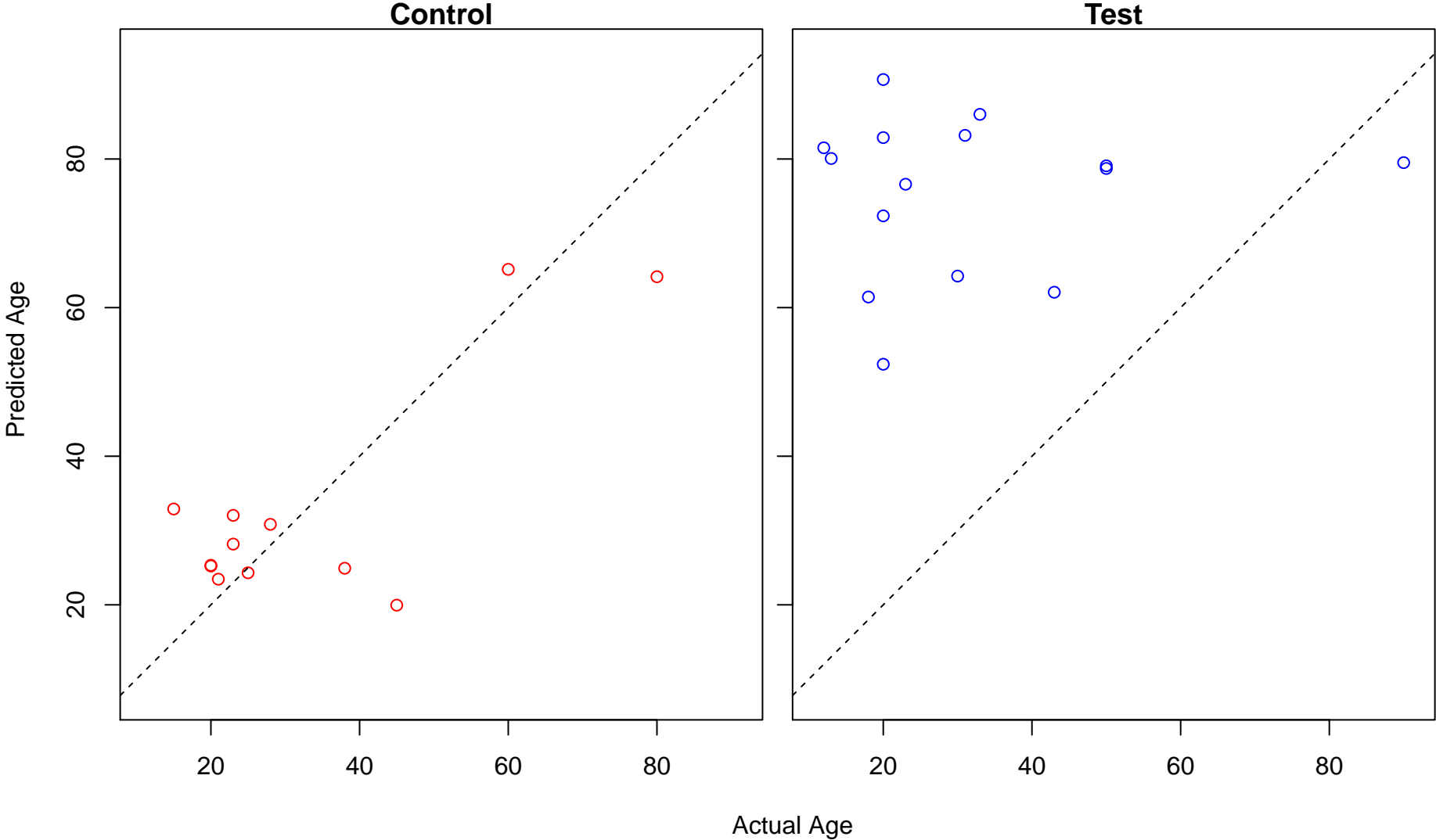
nucleoside triphosphate biosynthetic process (Score: 5.808405)



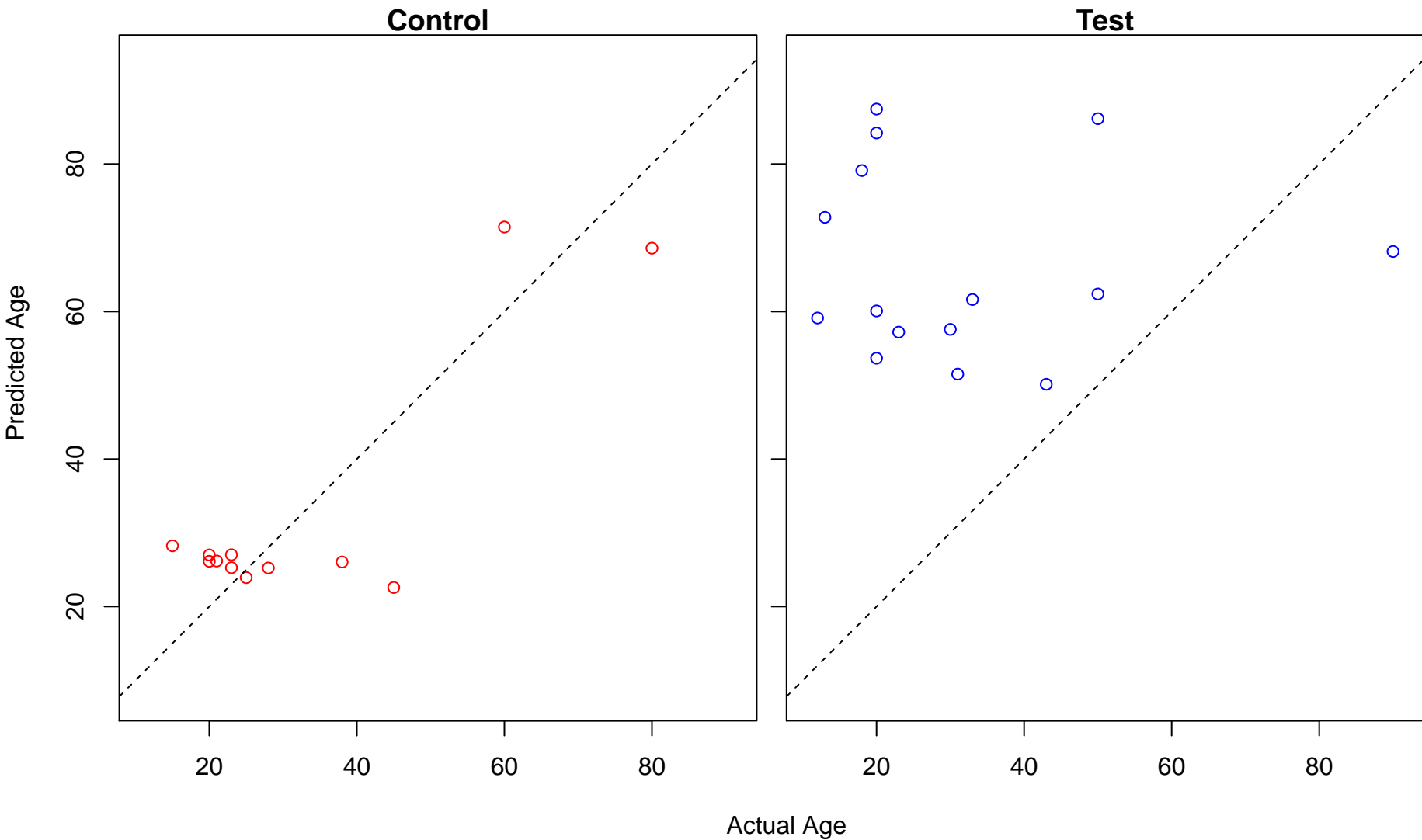
acid secretion (Score: 5.806738)



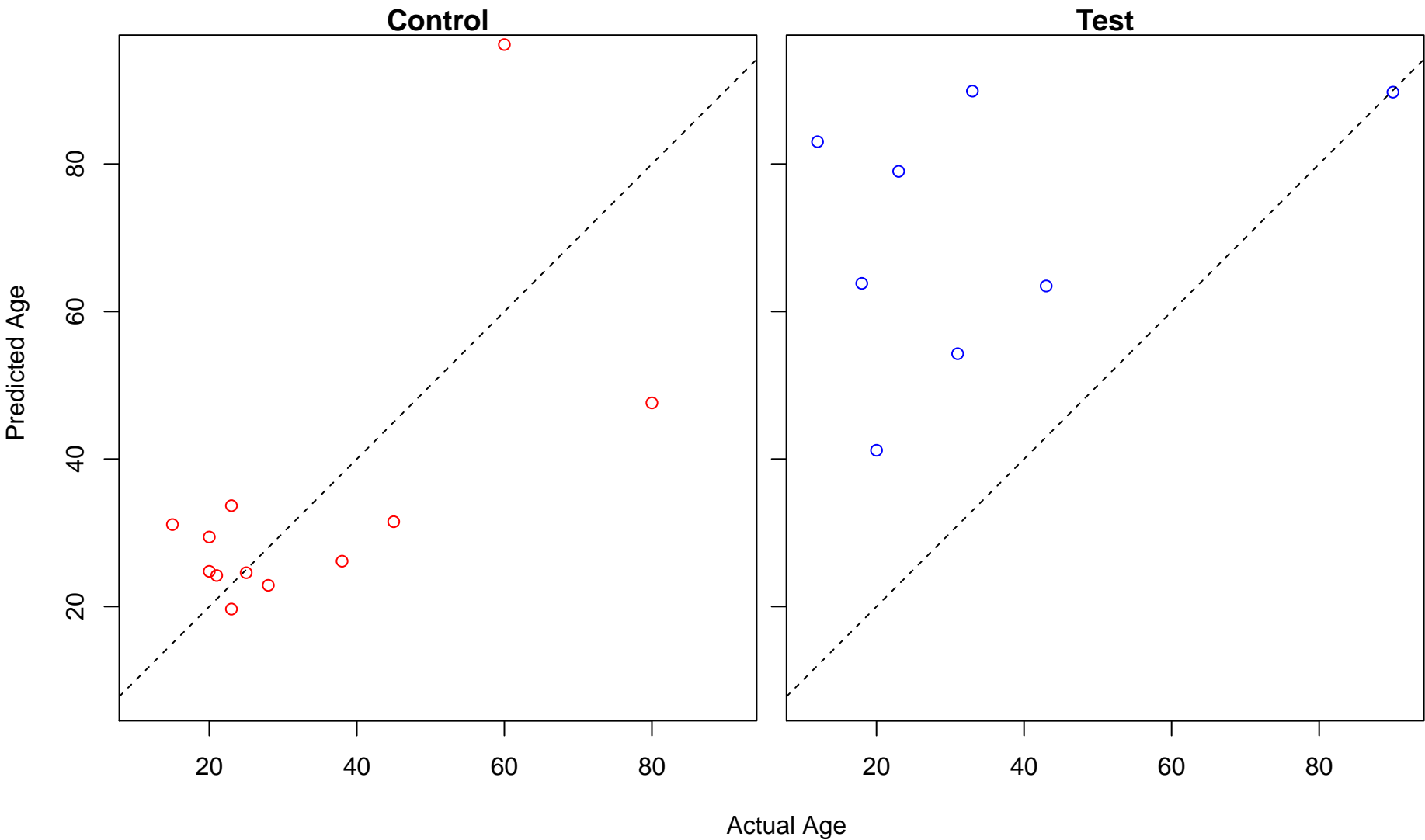
positive regulation of signal transduction by p53 class mediator (Score: 5.804651)



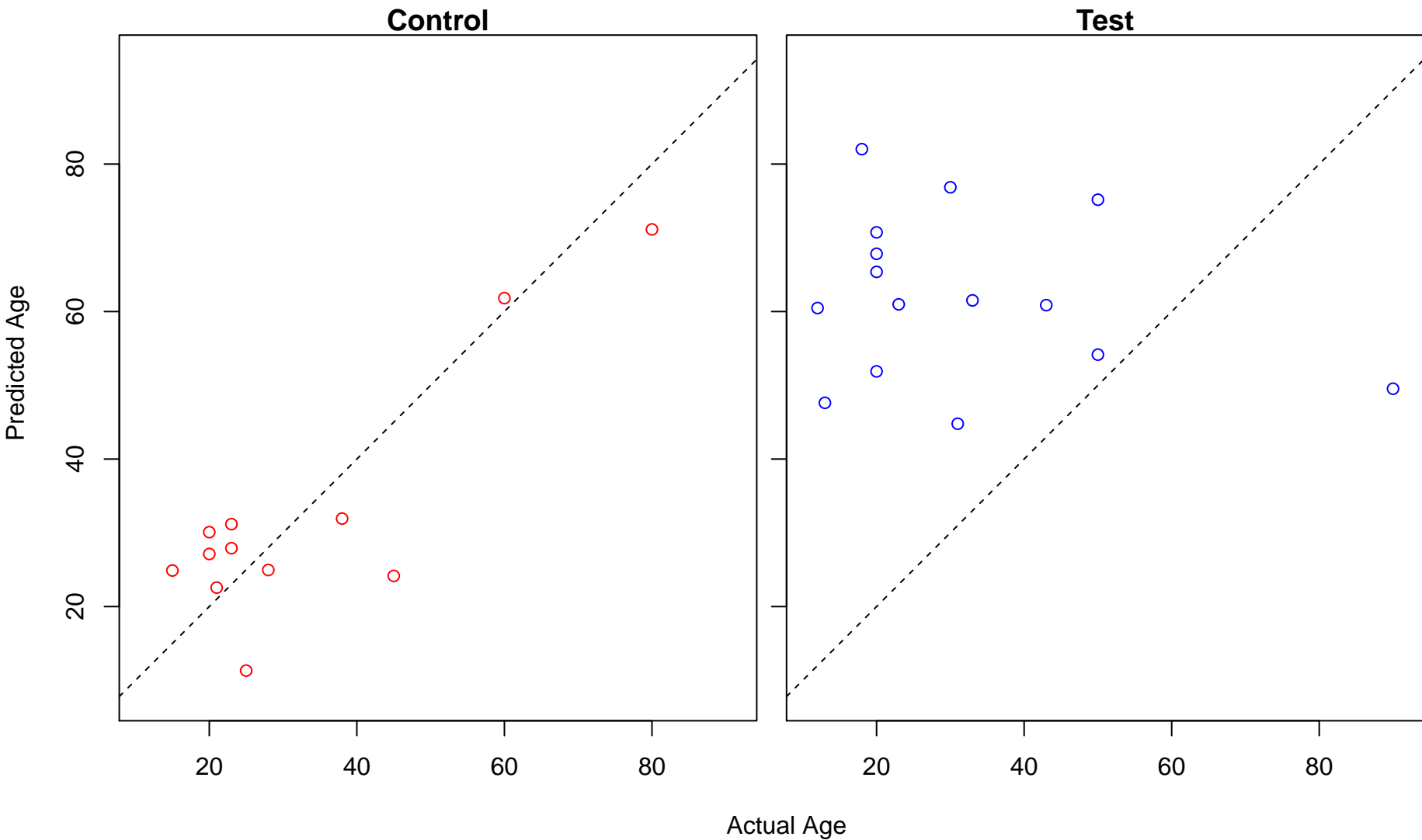
positive regulation of proteolysis involved in cellular protein catabolic process (Score: 5.804382)



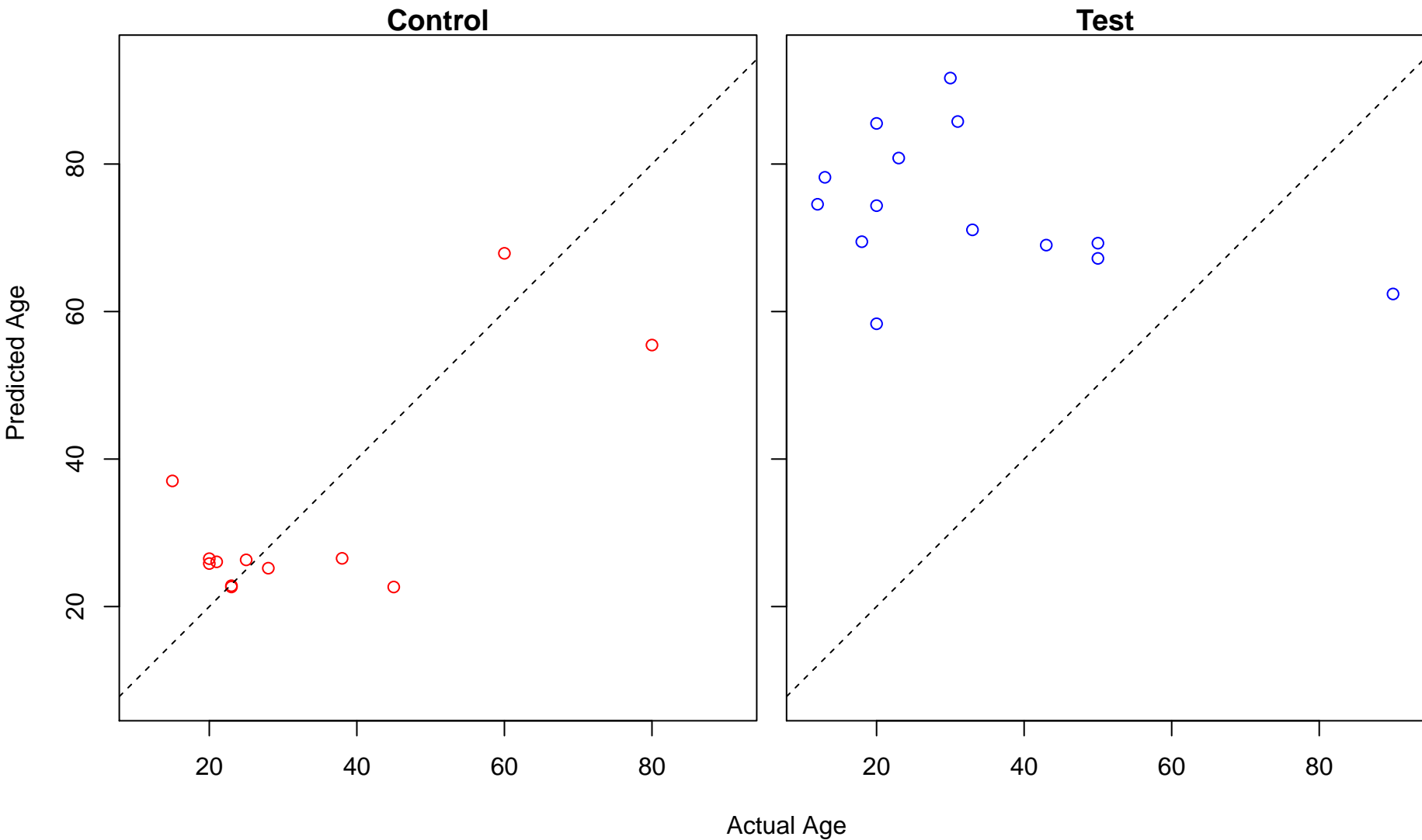
n of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling



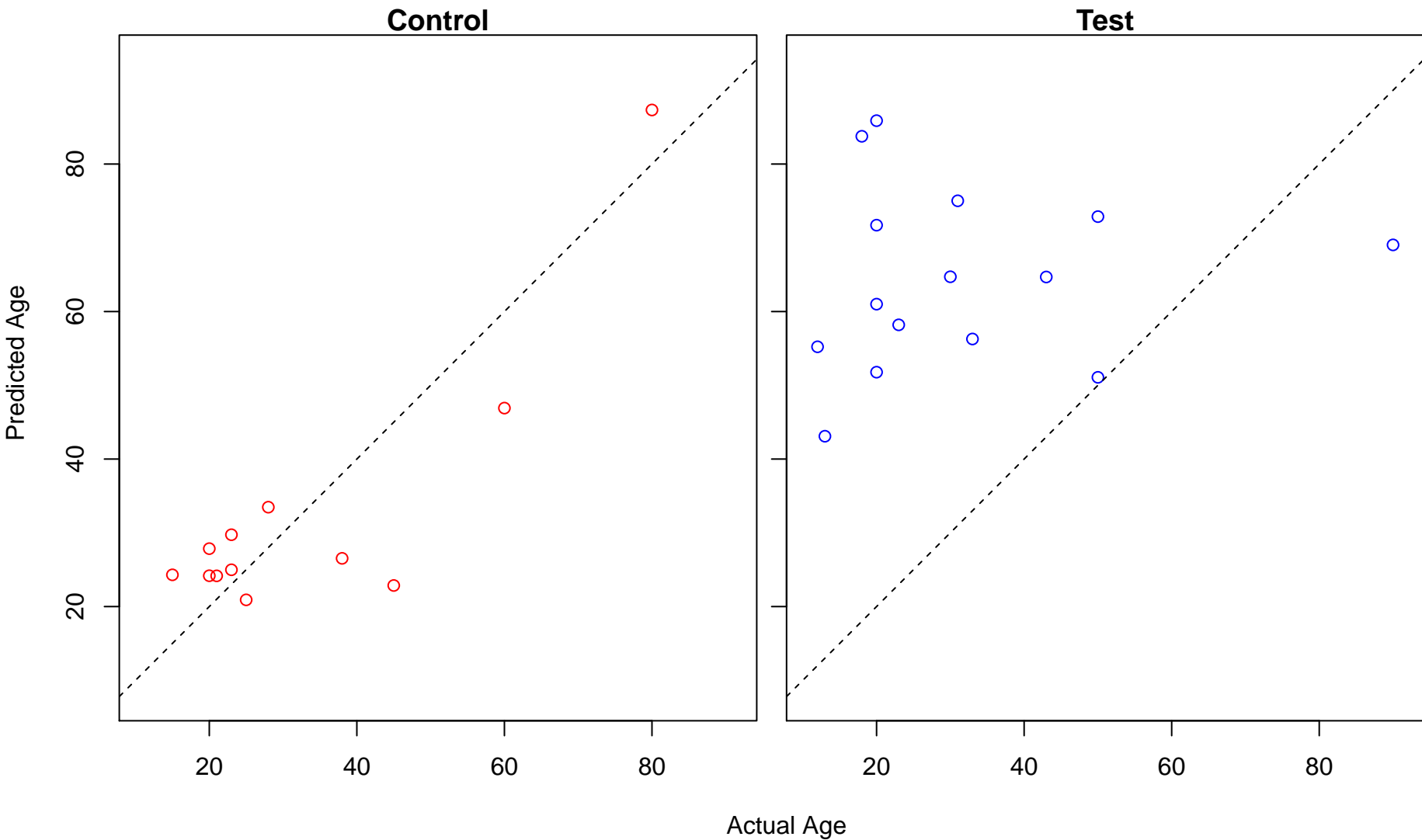
phagolysosome assembly (Score: 5.799772)



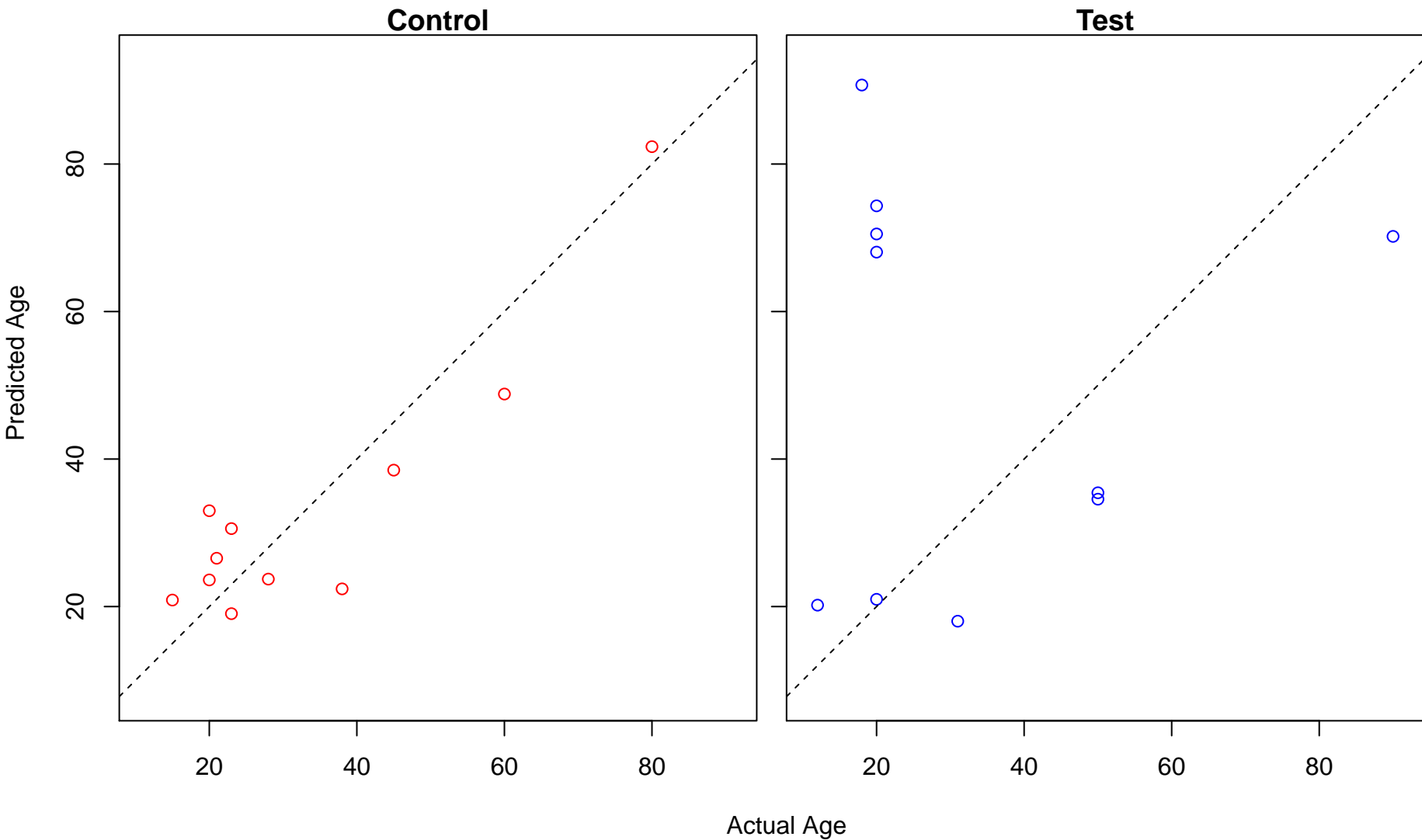
temperature homeostasis (Score: 5.797995)



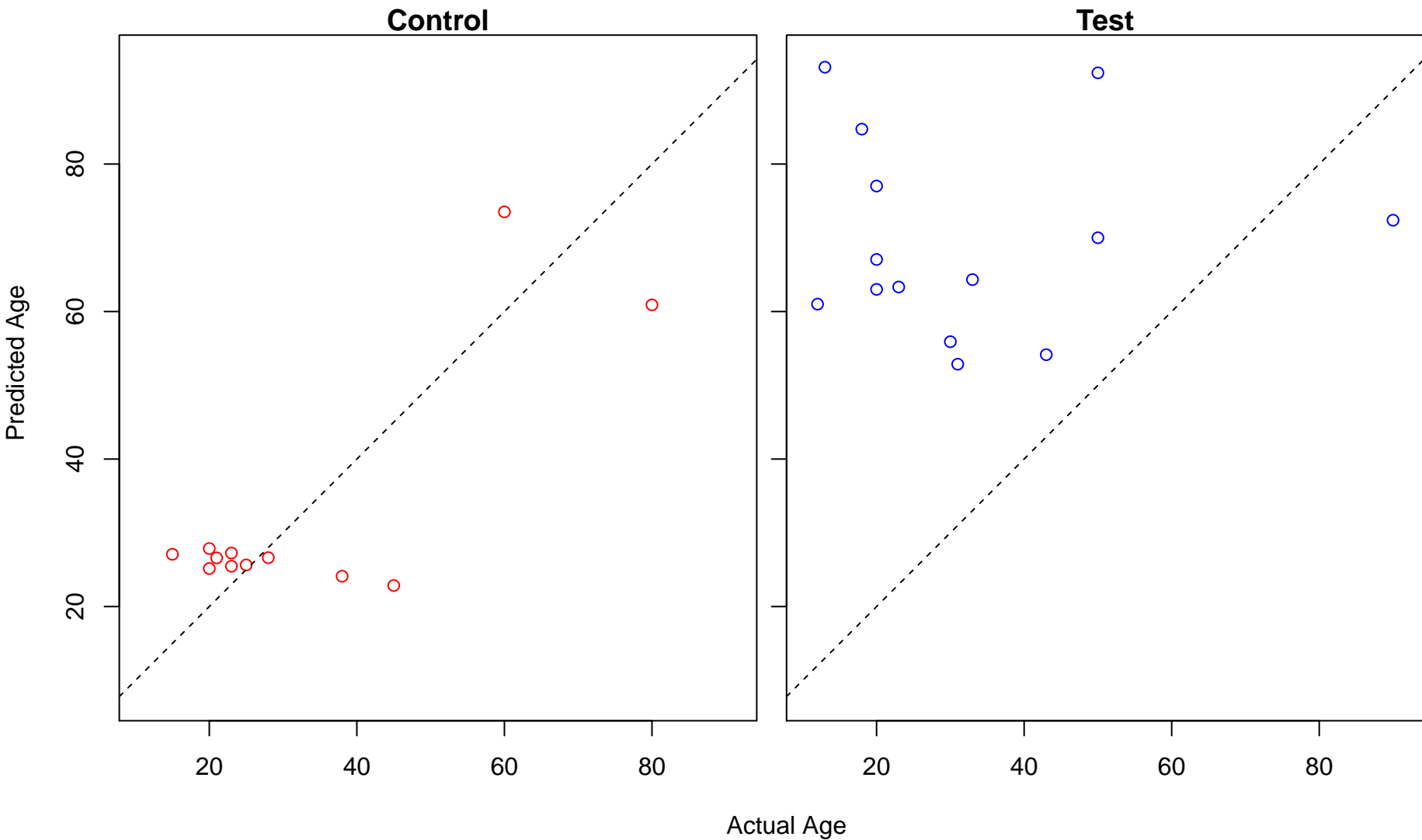
alpha-beta T cell activation (Score: 5.797312)



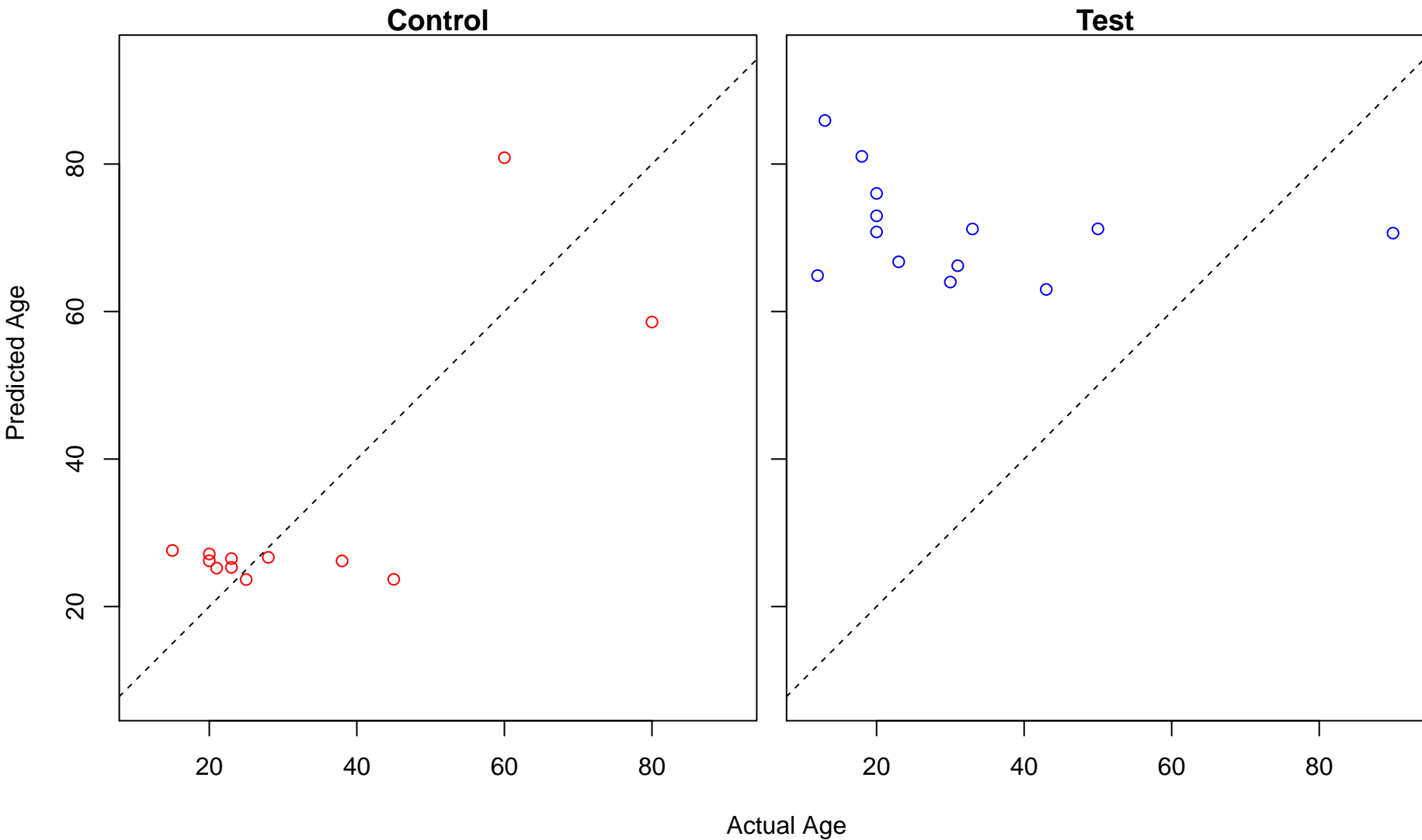
regulation of bile acid biosynthetic process (Score: 5.796999)



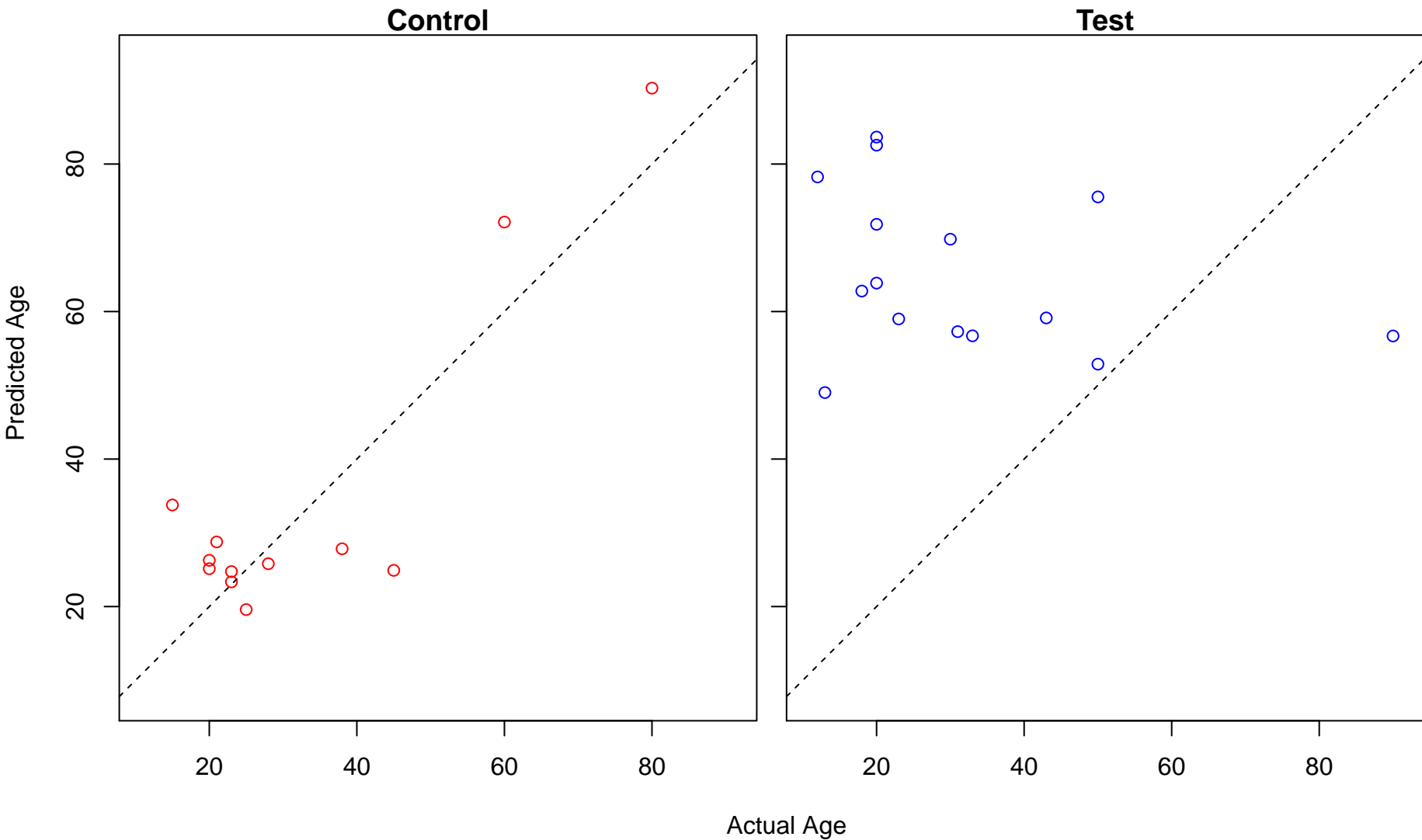
viral life cycle (Score: 5.791547)



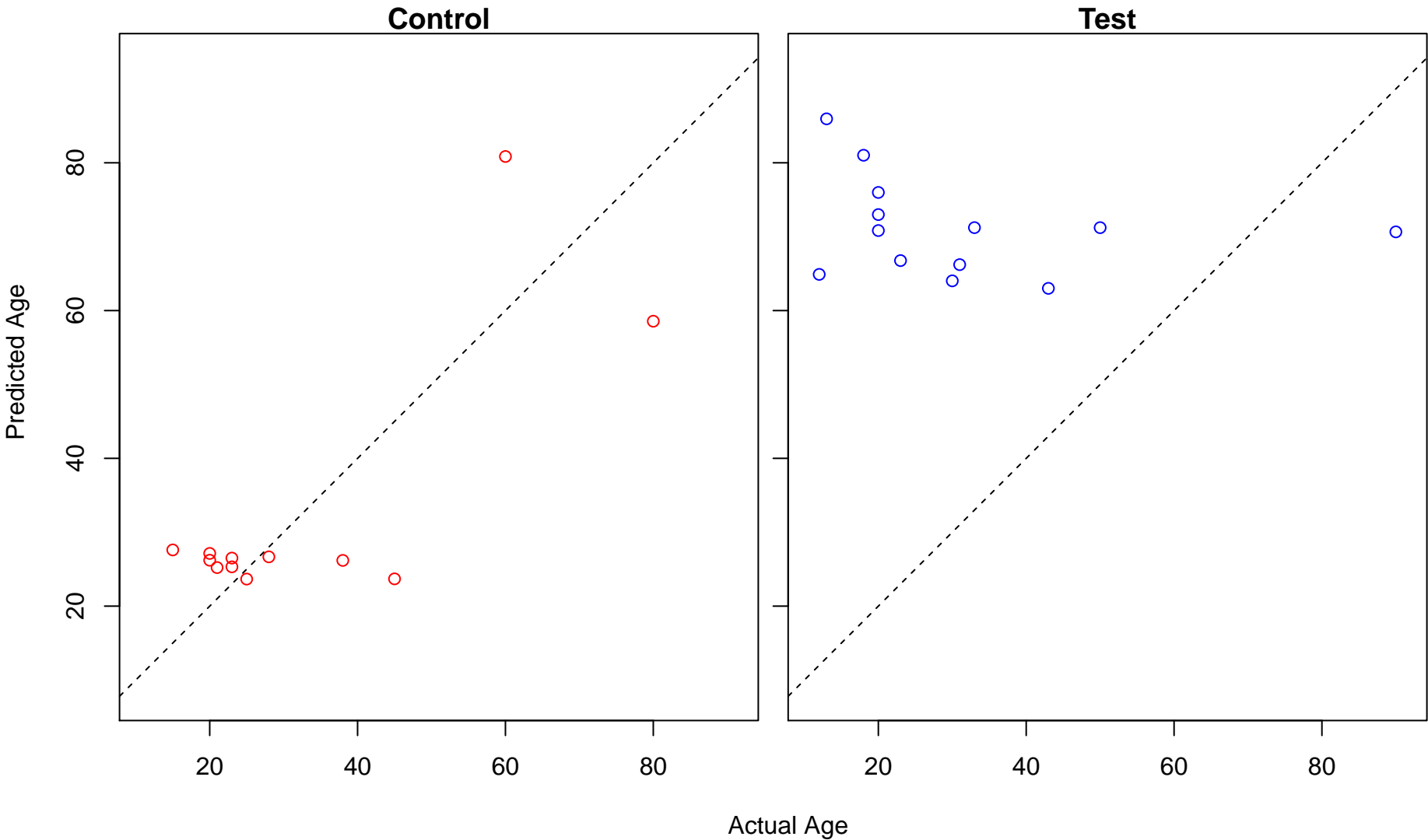
negative regulation of protein ubiquitination (Score: 5.788121)



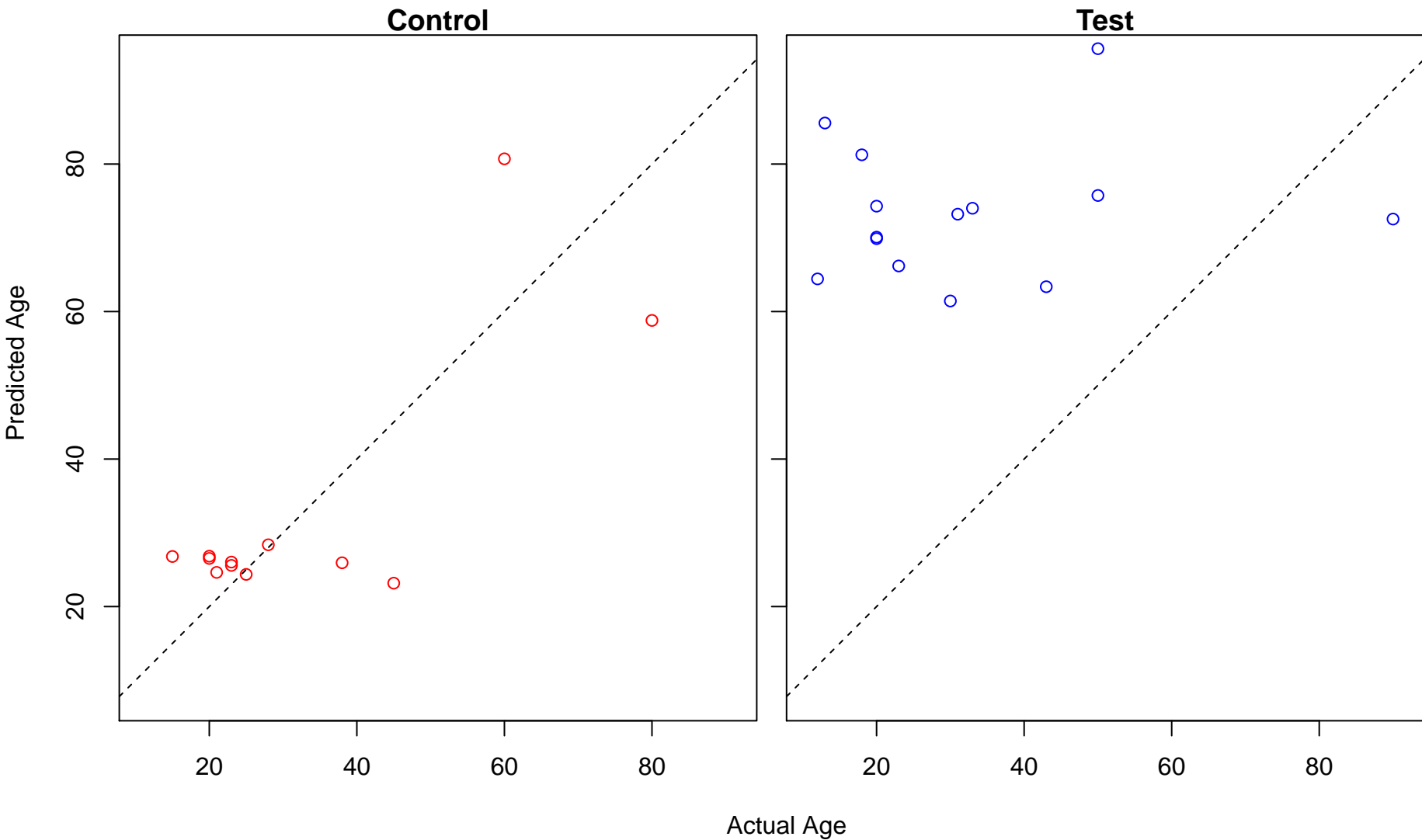
histone H3 acetylation (Score: 5.787788)



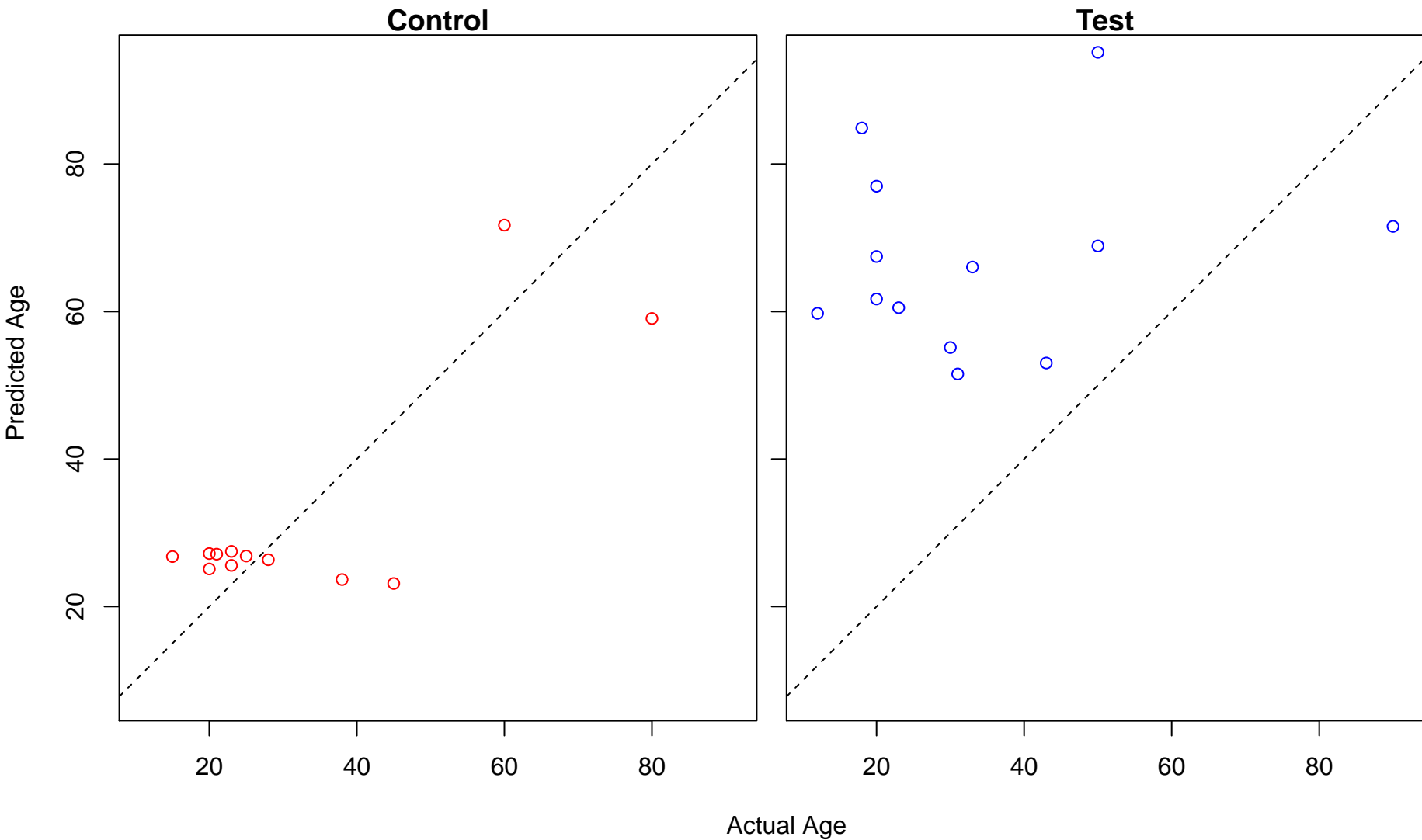
negative regulation of protein modification by small protein conjugation or removal (Score: 5.78611)



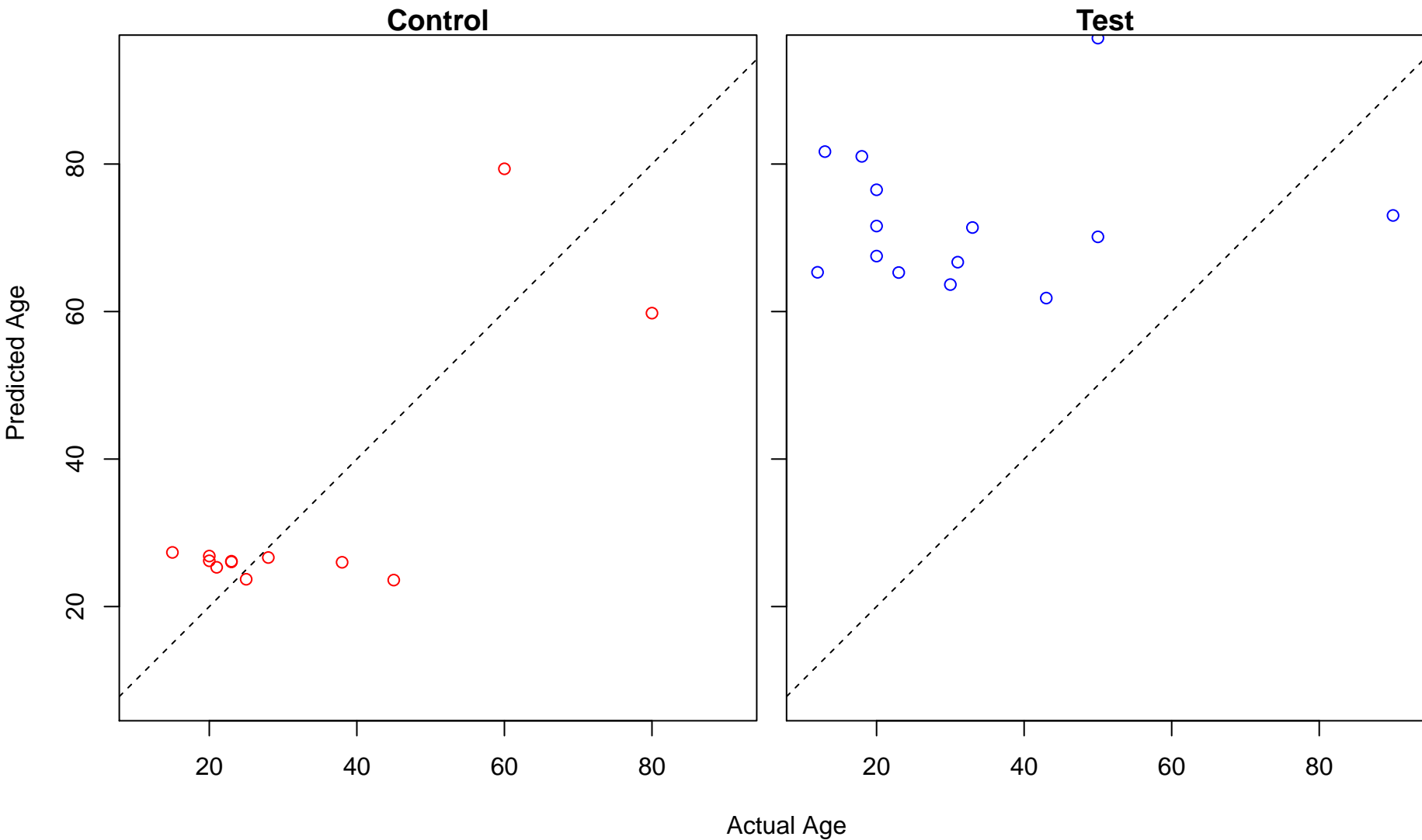
regulation of Wnt signaling pathway (Score: 5.785746)



nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (Score: 5.782671)

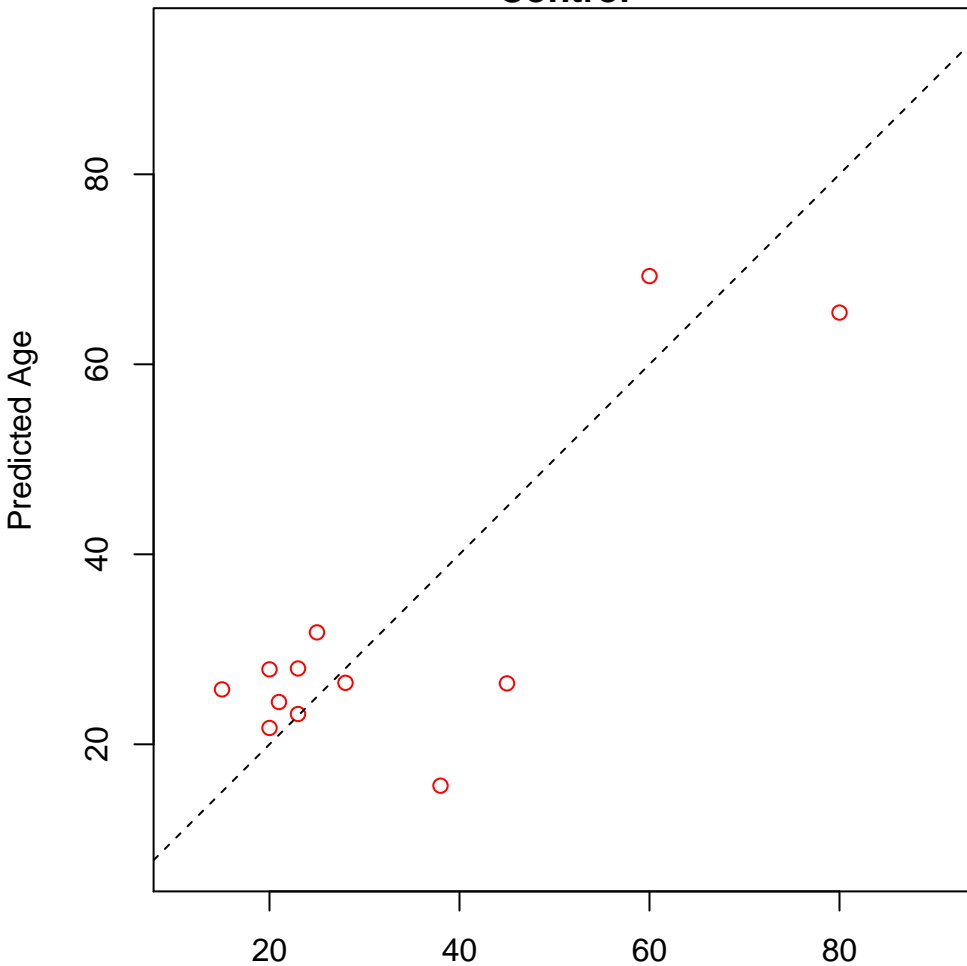


regulation of mitotic cell cycle (Score: 5.782472)

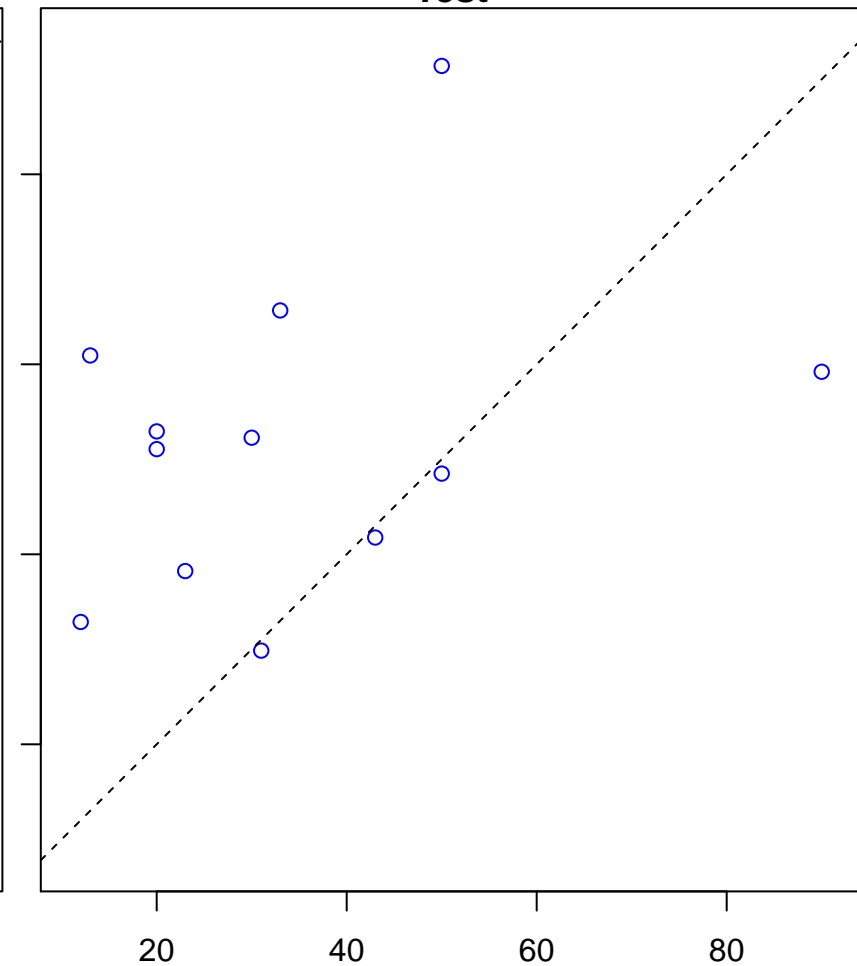


regulation of phospholipase A2 activity (Score: 5.778858)

Control

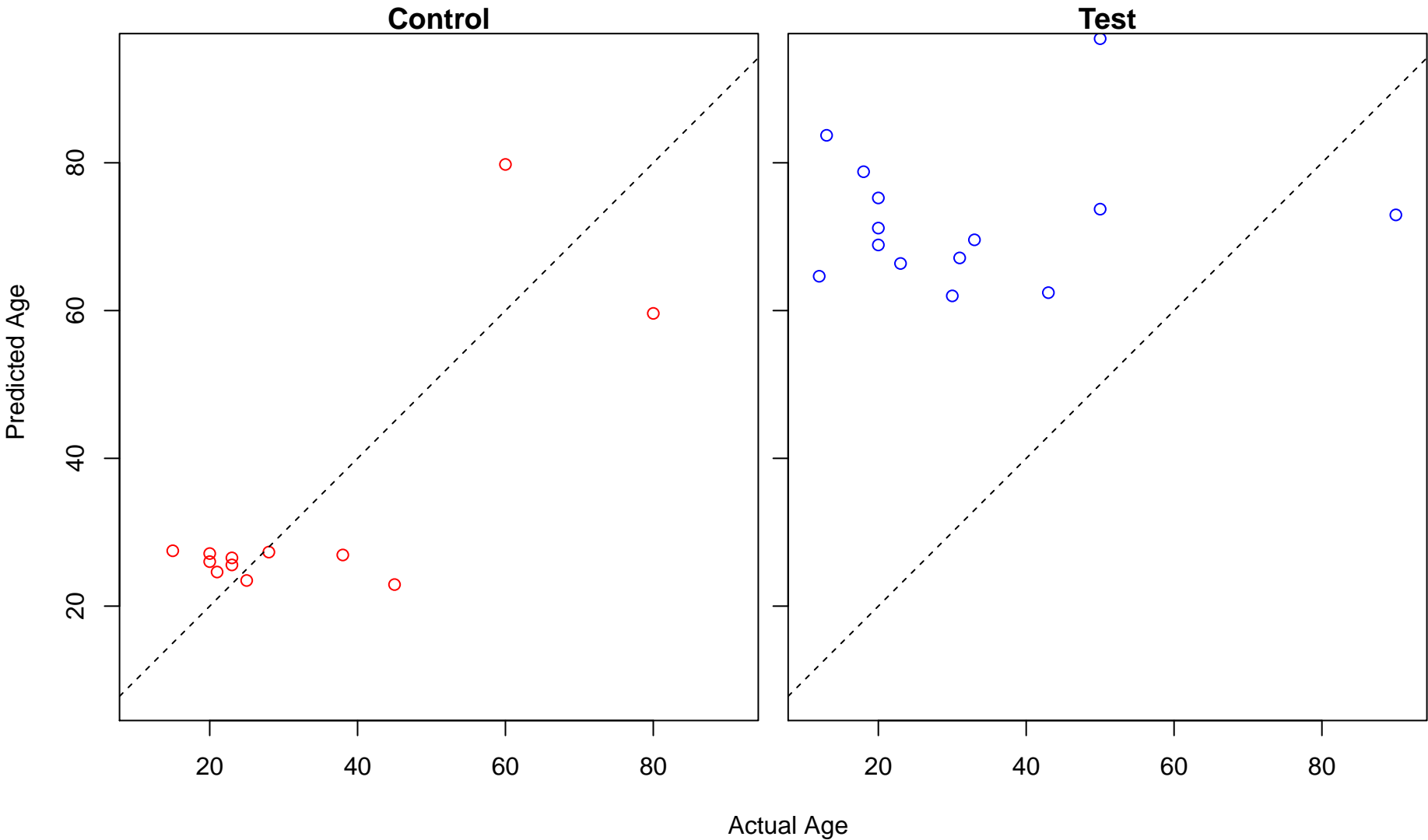


Test

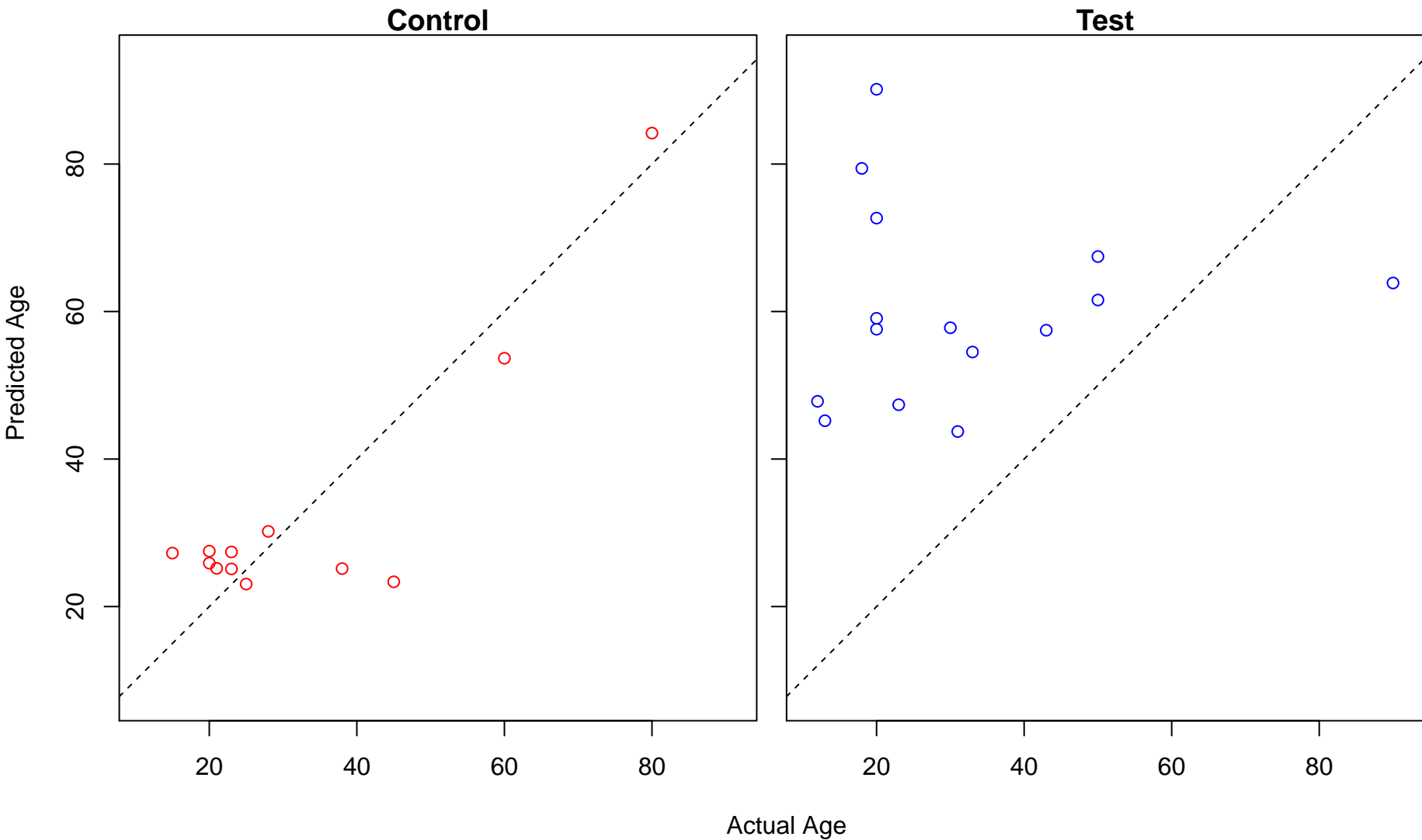


Actual Age

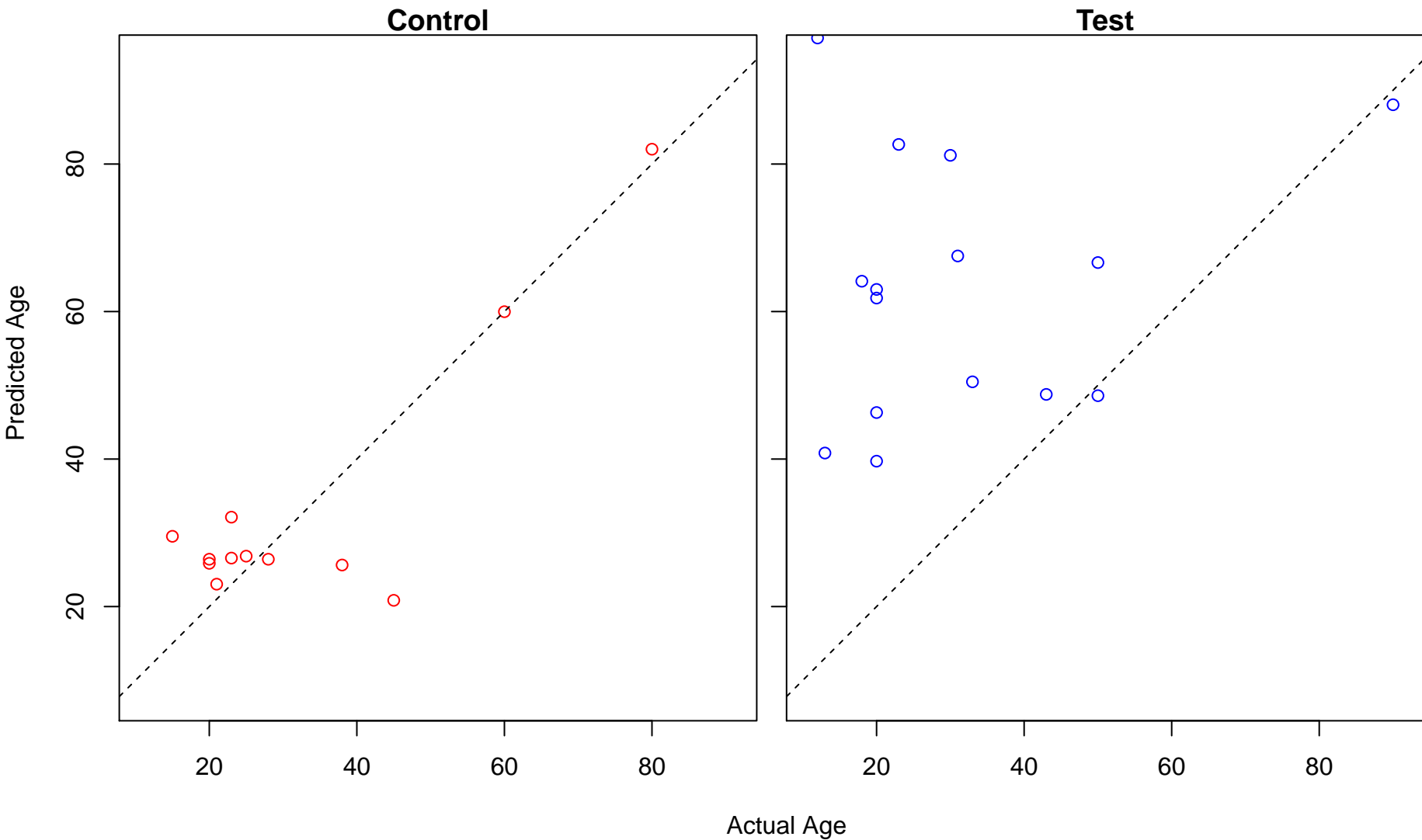
nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway (Score: 5.7773)



hematopoietic or lymphoid organ development (Score: 5.771383)

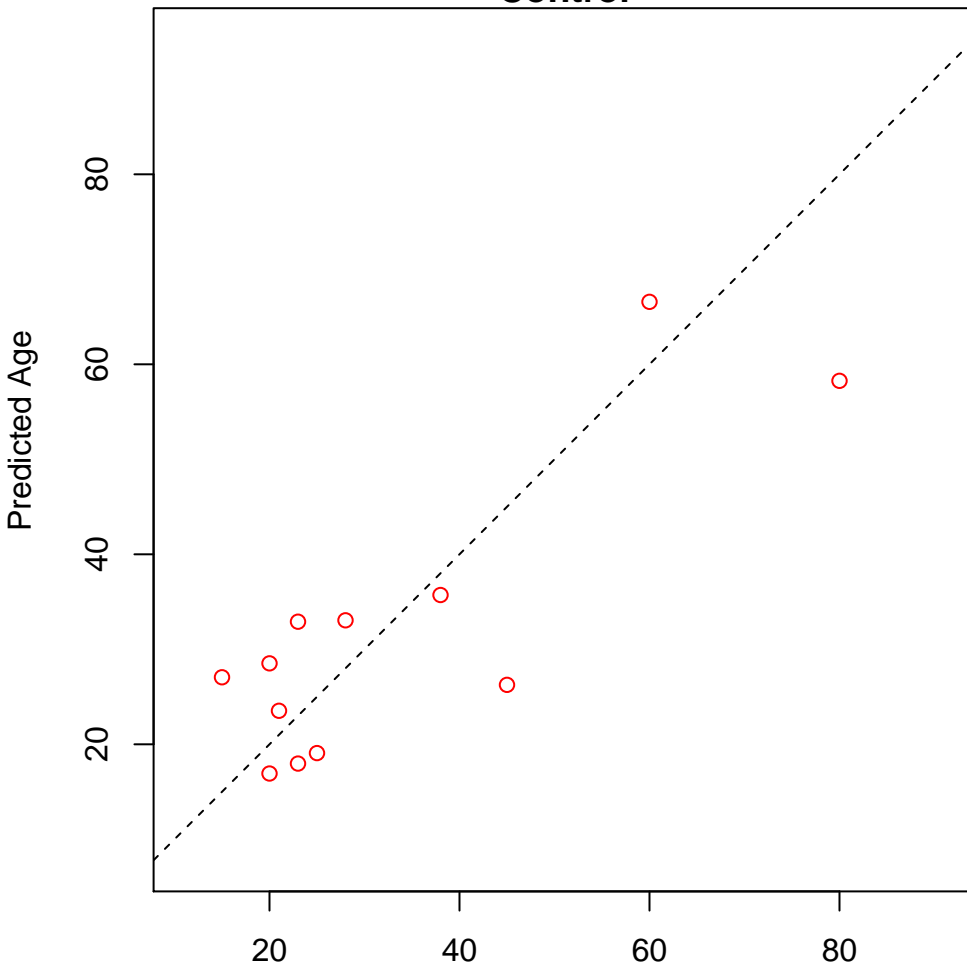


positive regulation of dendritic spine development (Score: 5.768507)

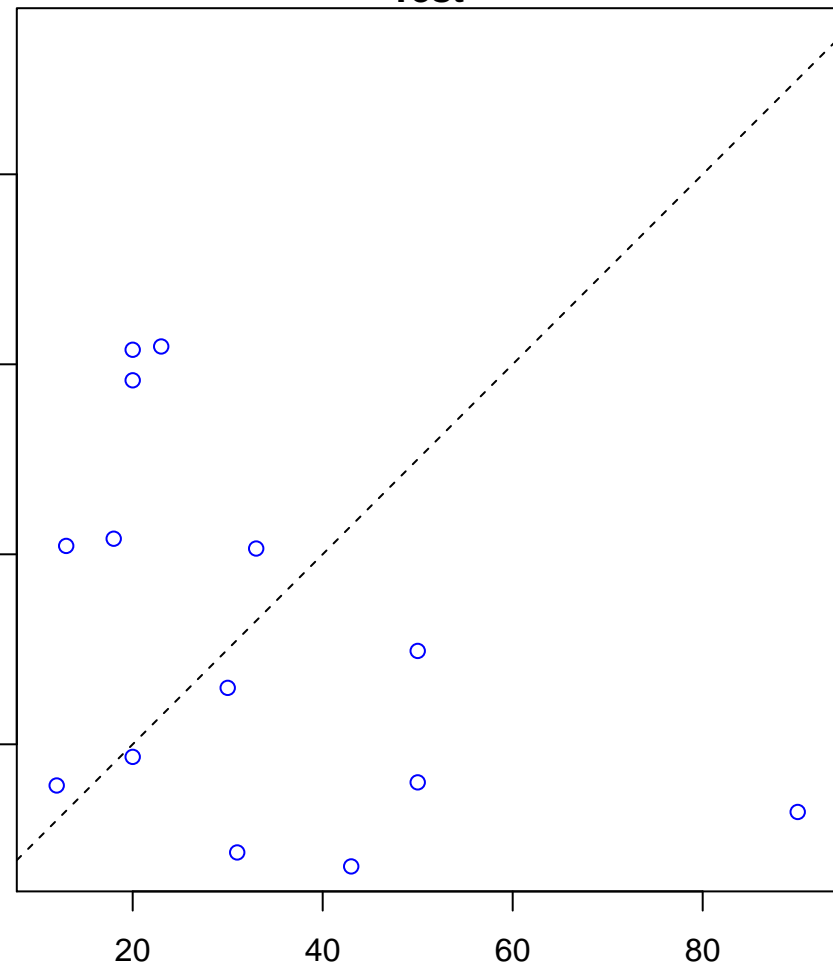


regulation of muscle system process (Score: 5.767736)

Control

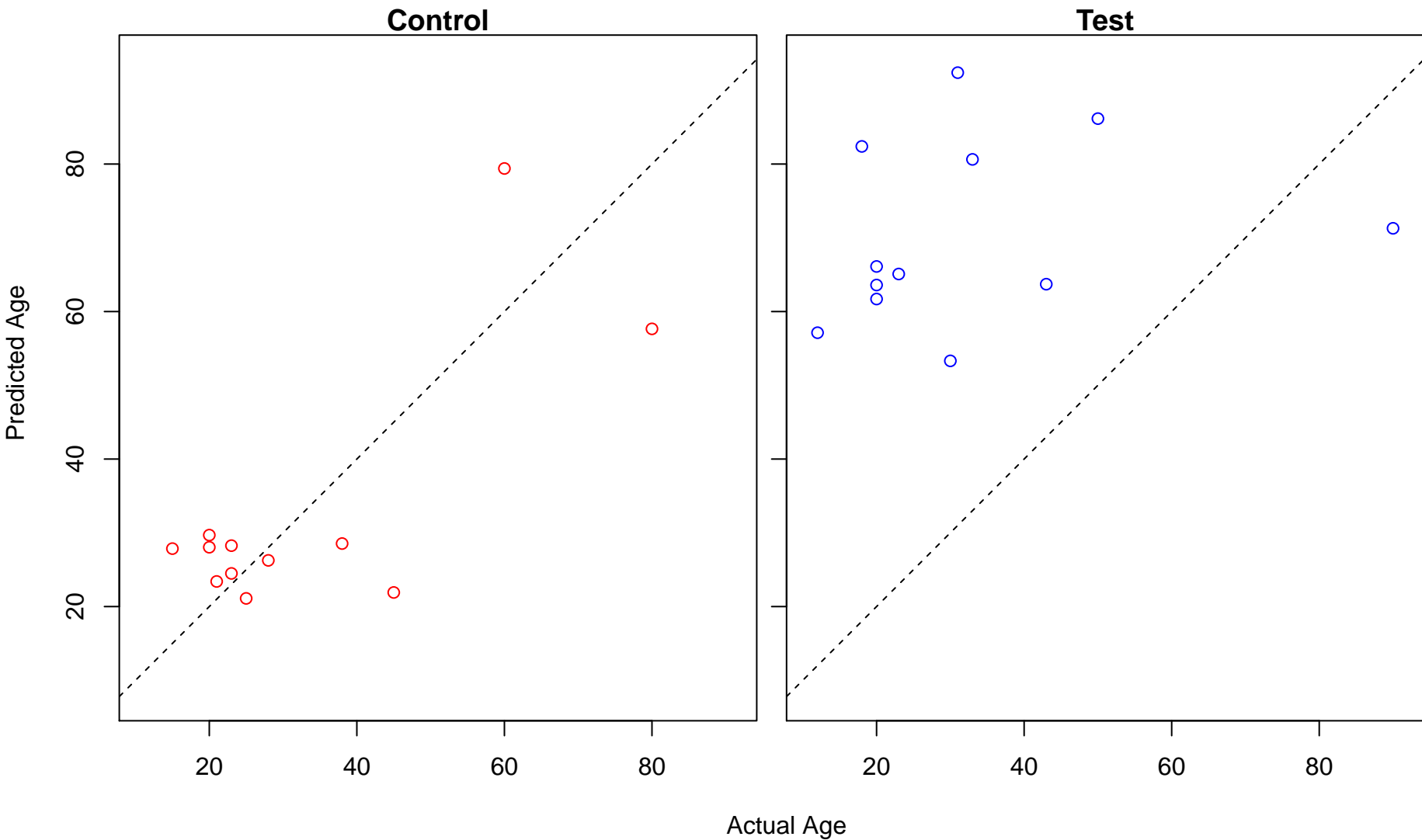


Test

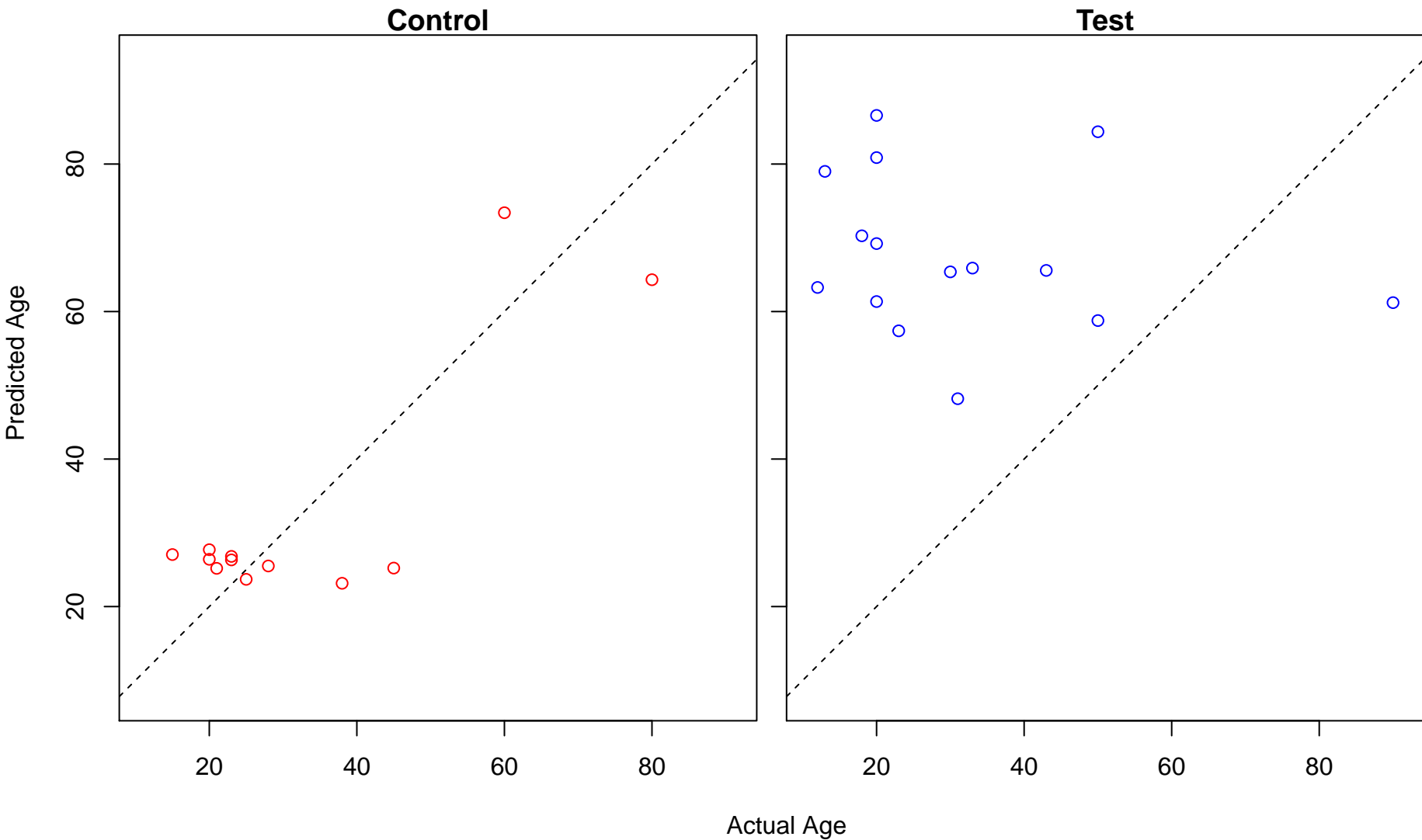


Actual Age

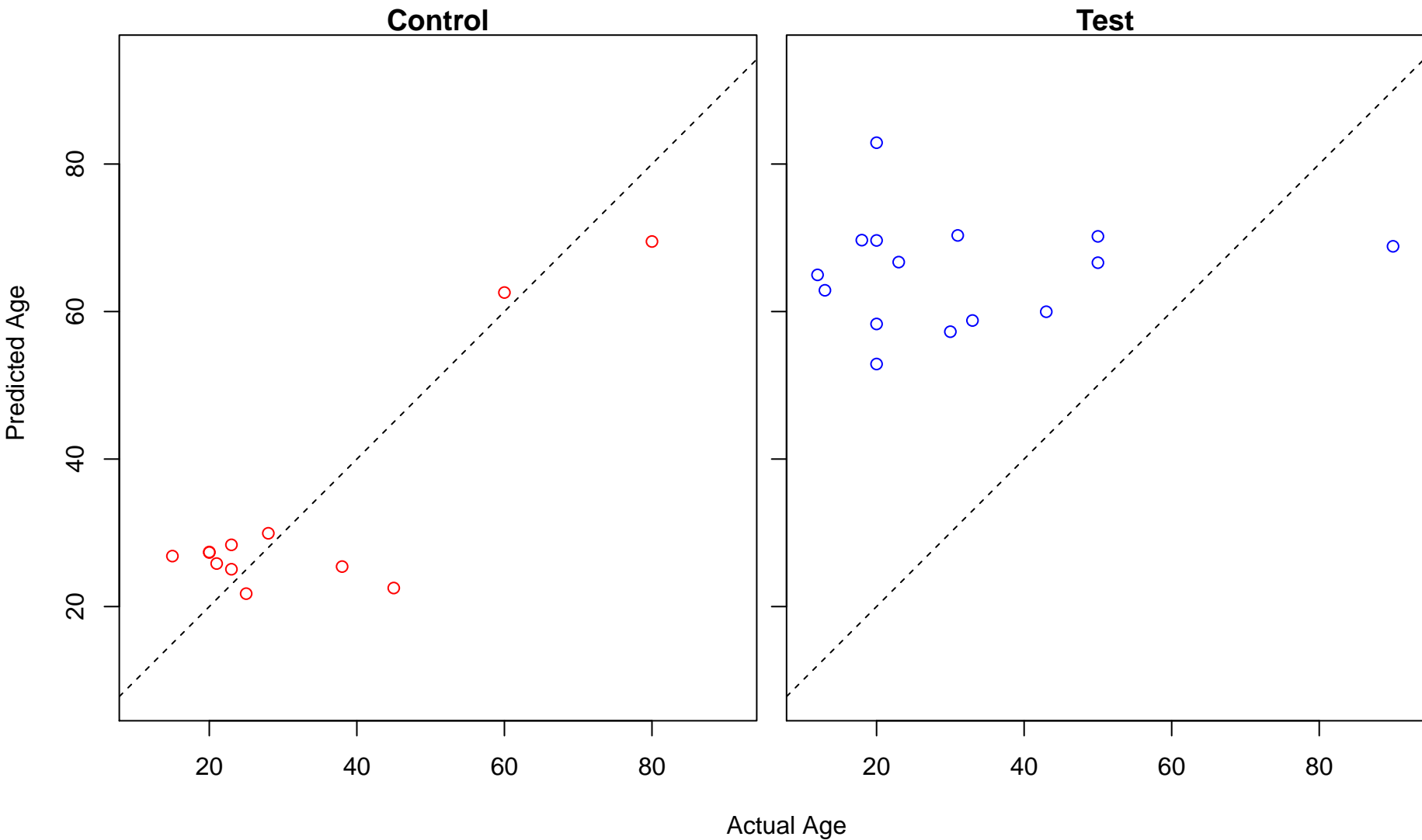
regulation of toll-like receptor signaling pathway (Score: 5.767646)

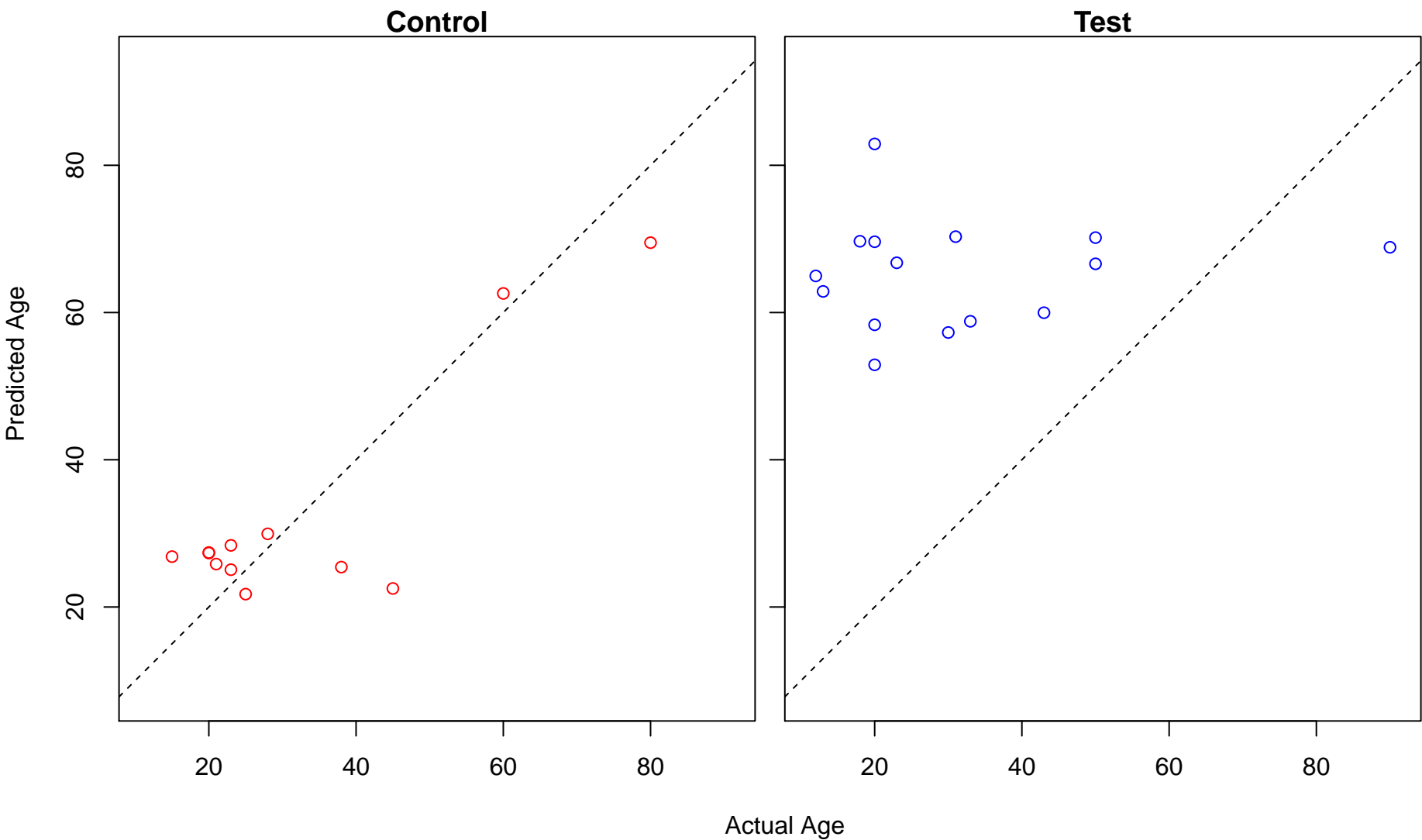


regulation of response to alcohol (Score: 5.766889)

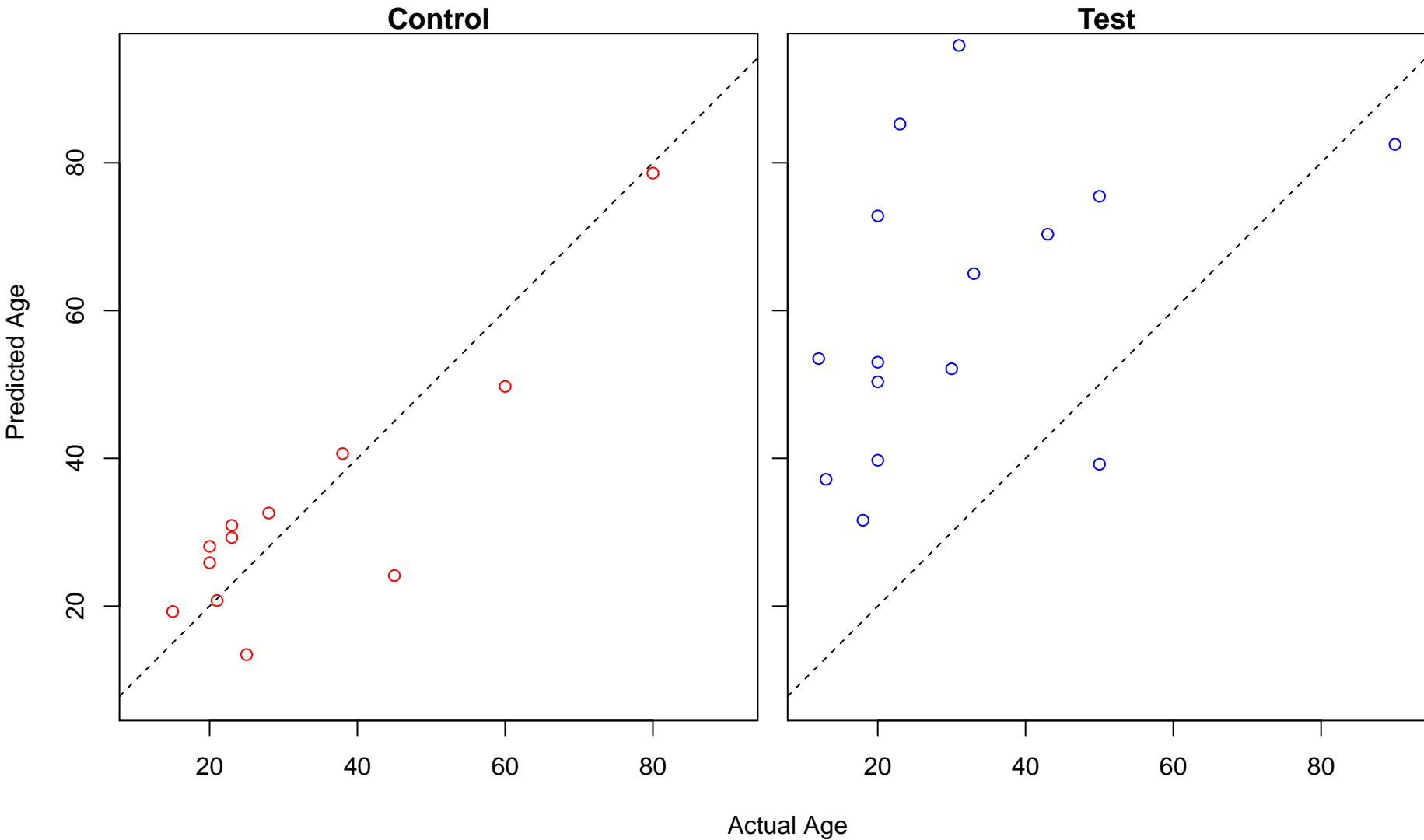


modification of morphology or physiology of other organism (Score: 5.763247)

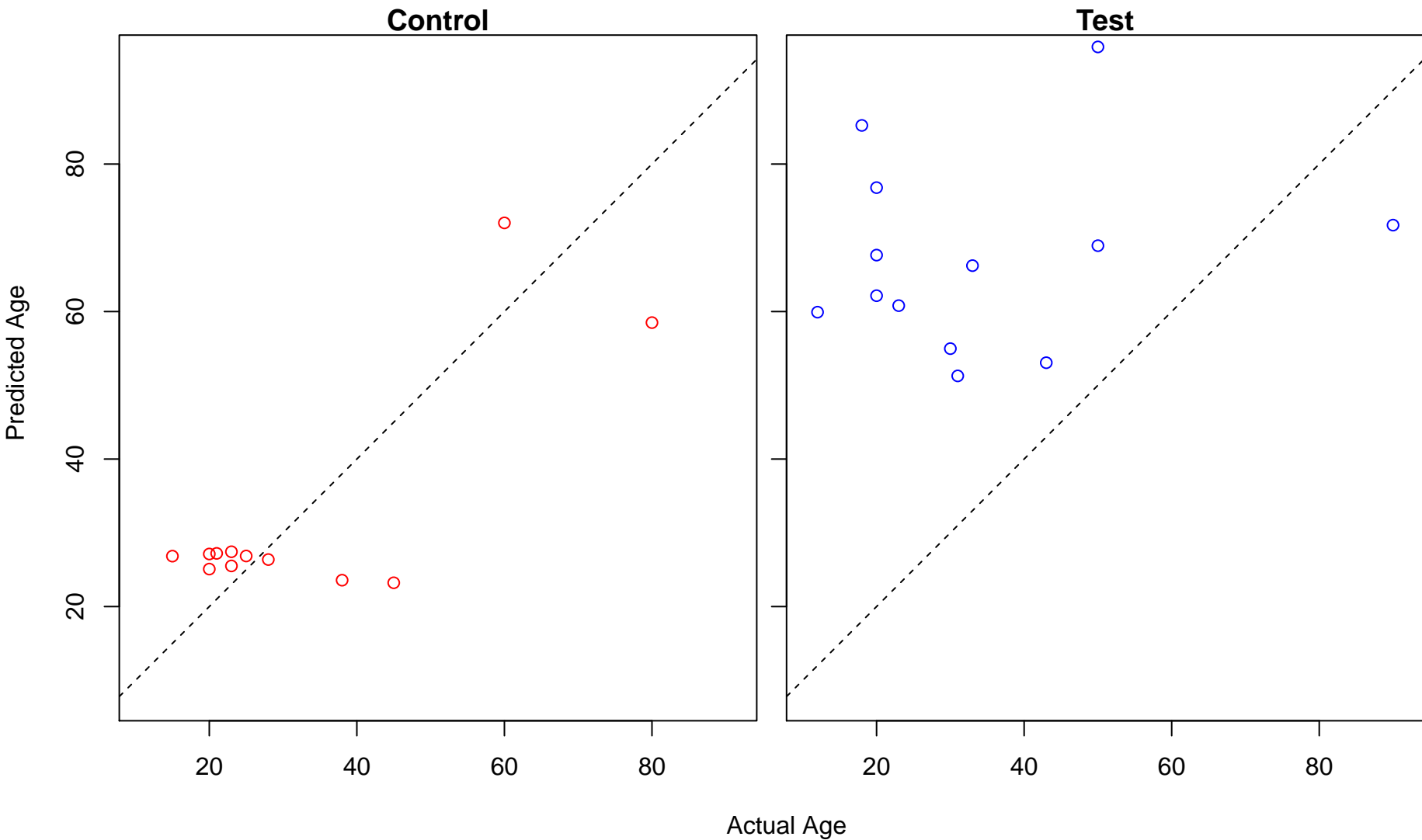




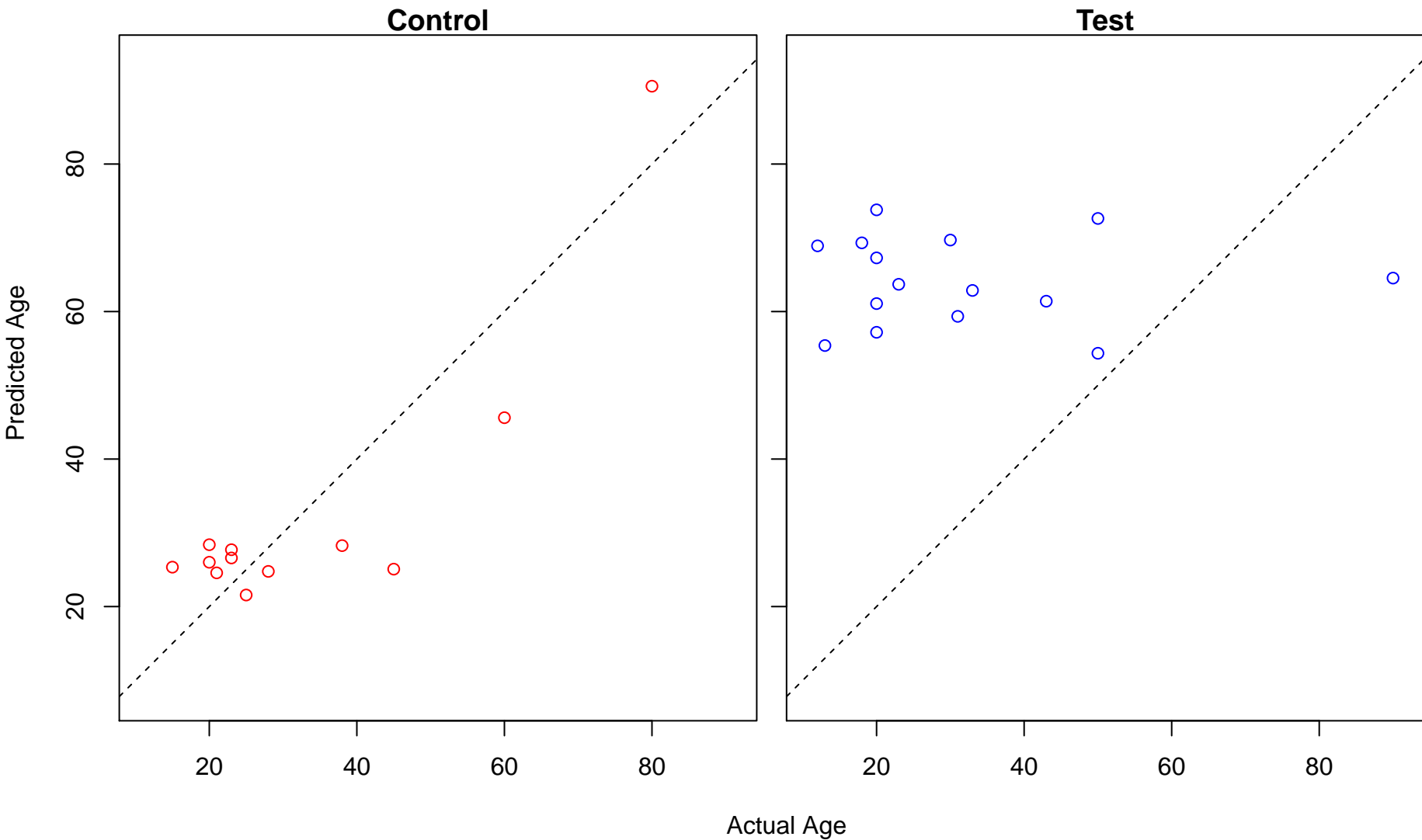
determination of liver left/right asymmetry (Score: 5.761015)



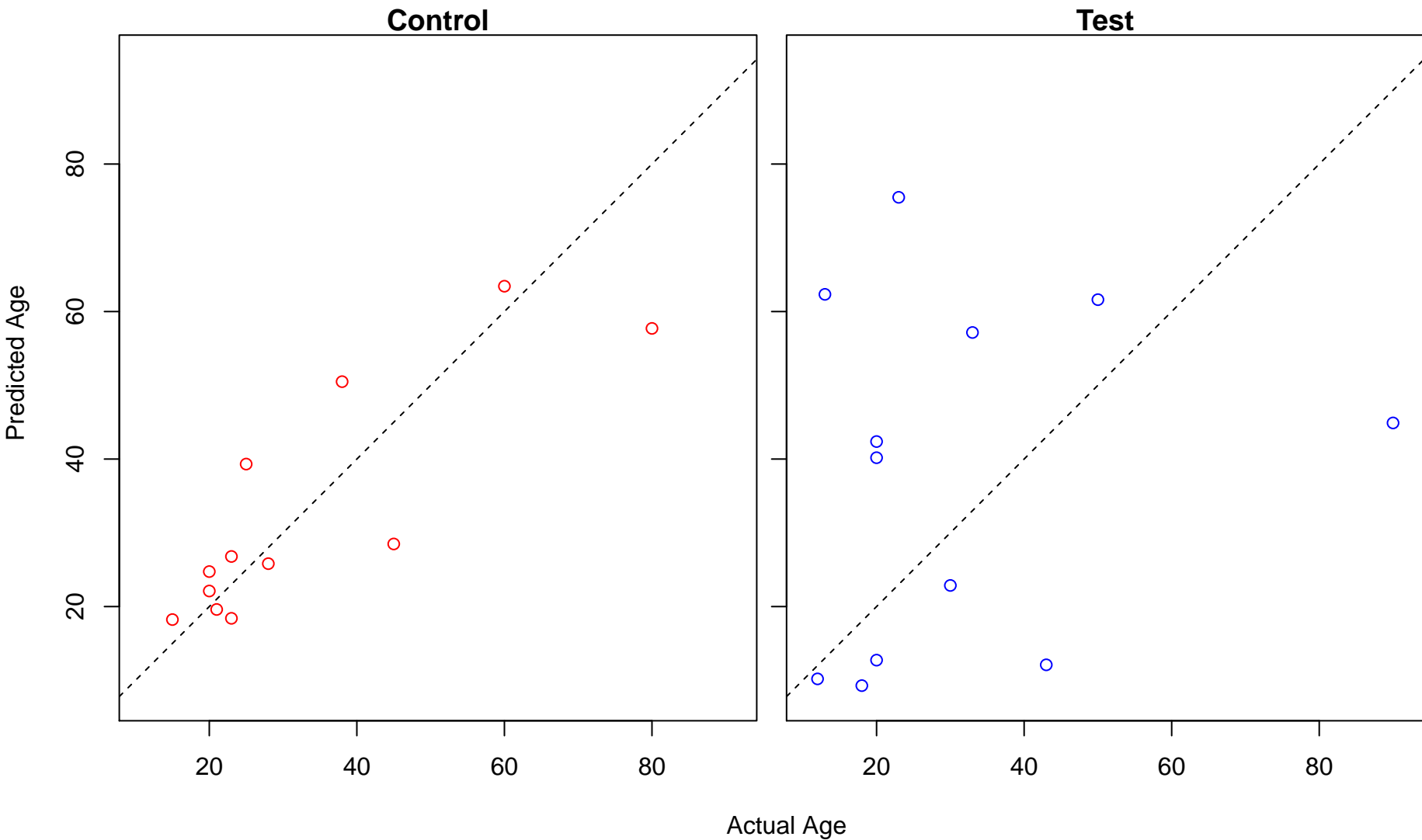
viral transcription (Score: 5.755994)



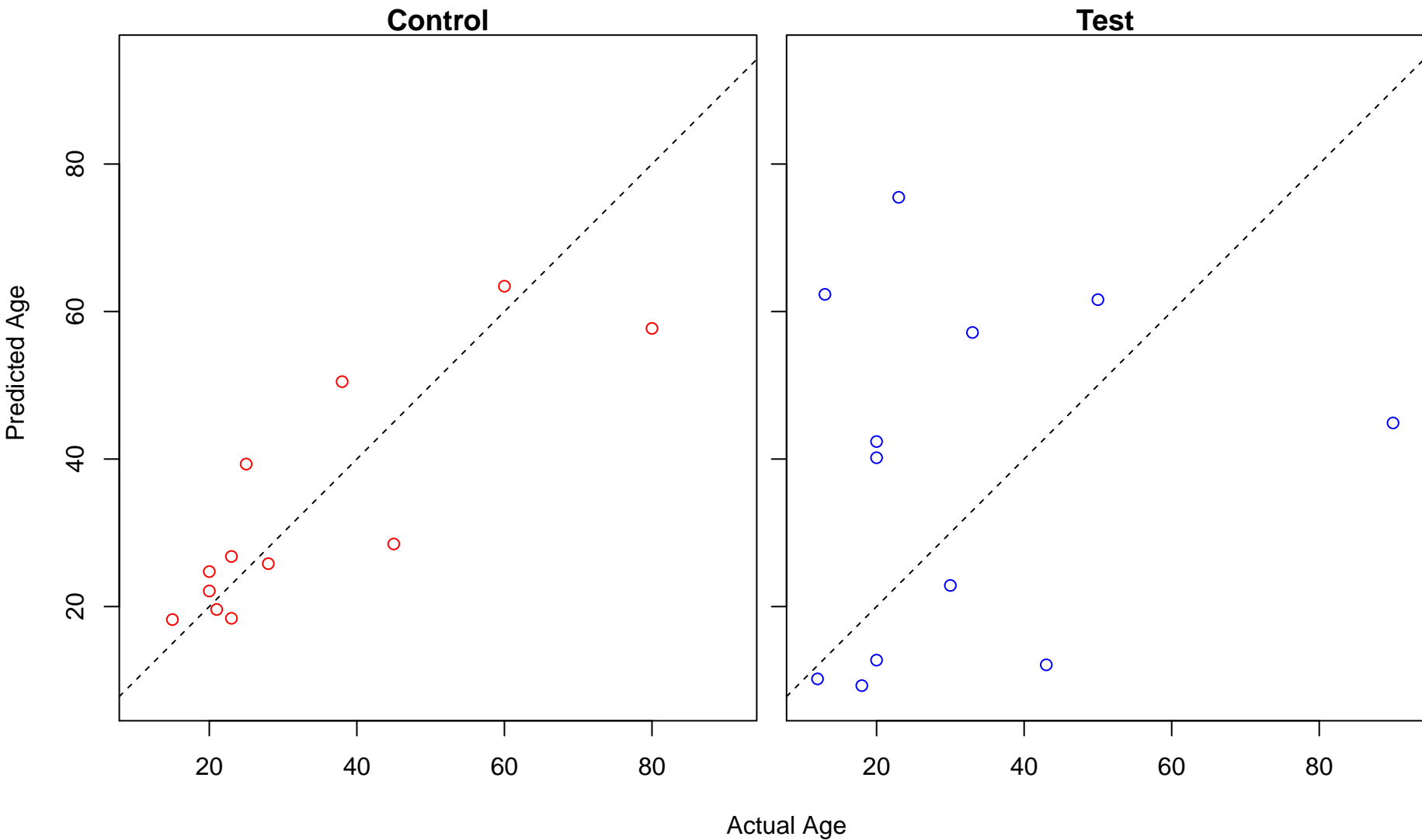
striated muscle tissue development (Score: 5.754293)



cartilage condensation (Score: 5.754093)

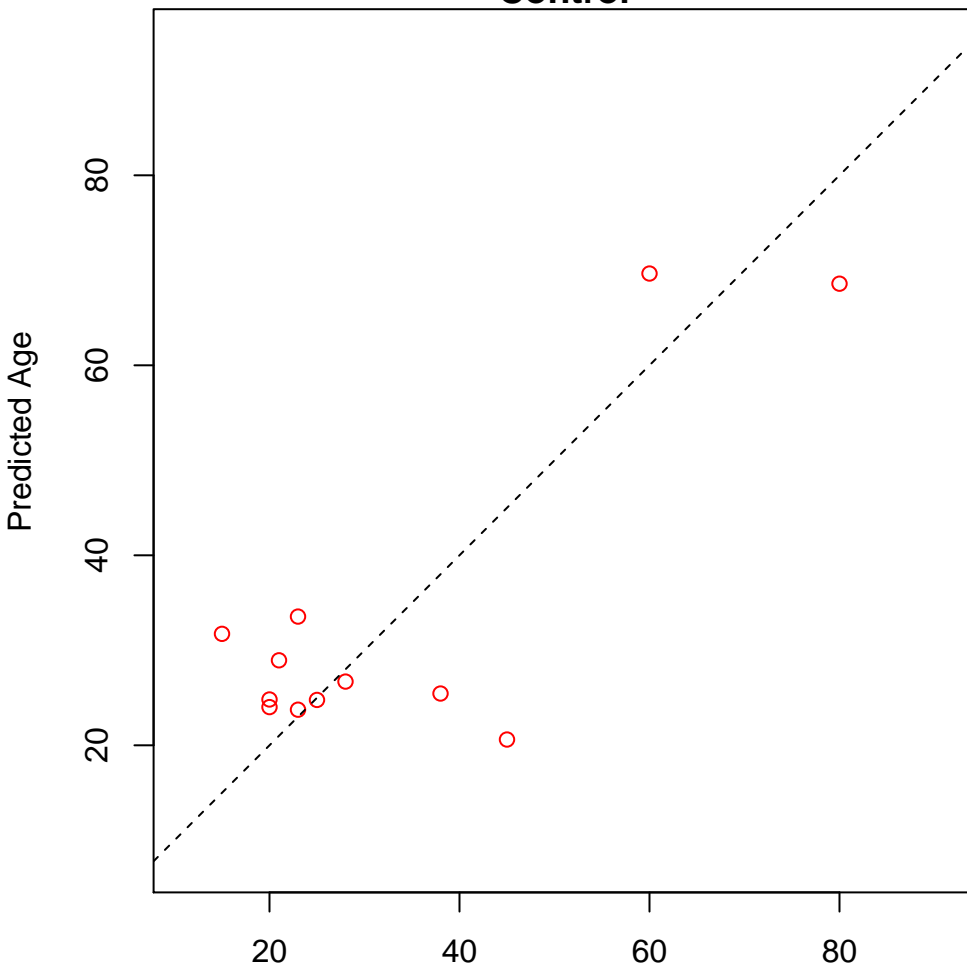


cell aggregation (Score: 5.754093)

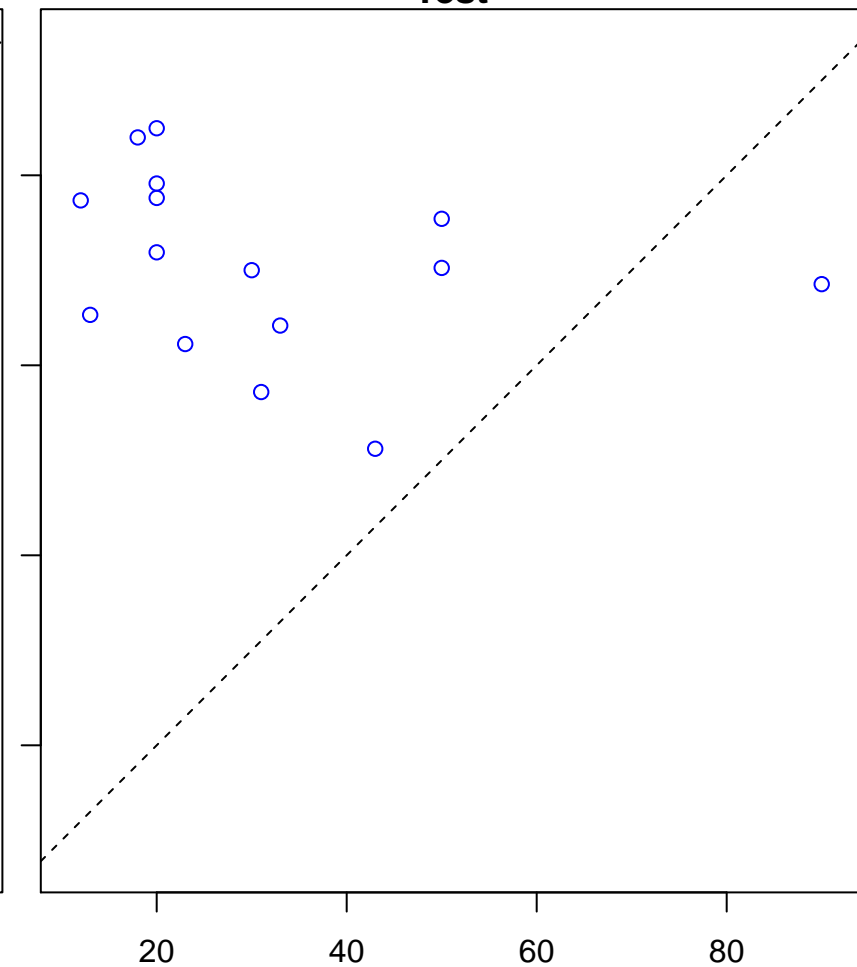


regulation of lamellipodium organization (Score: 5.753601)

Control

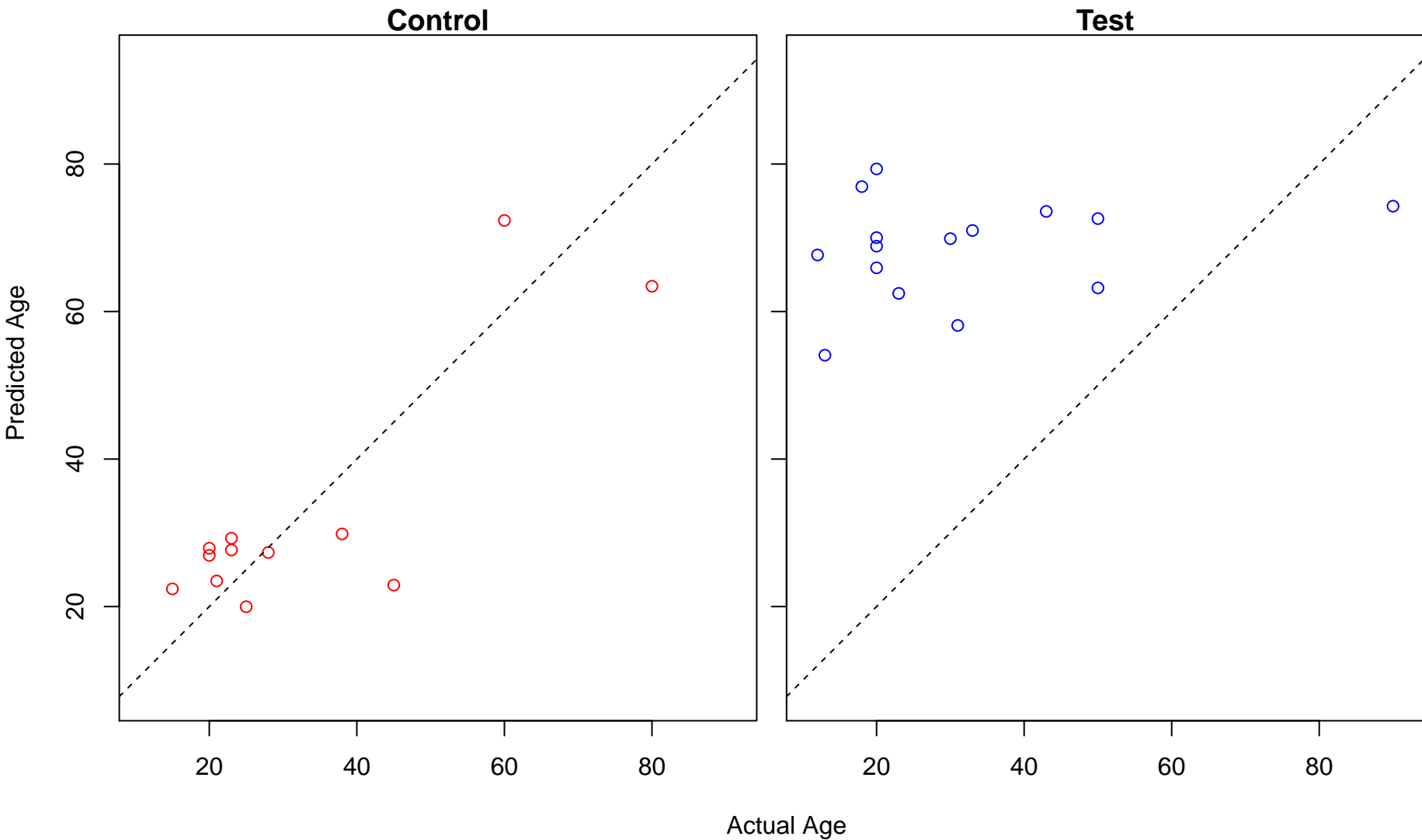


Test

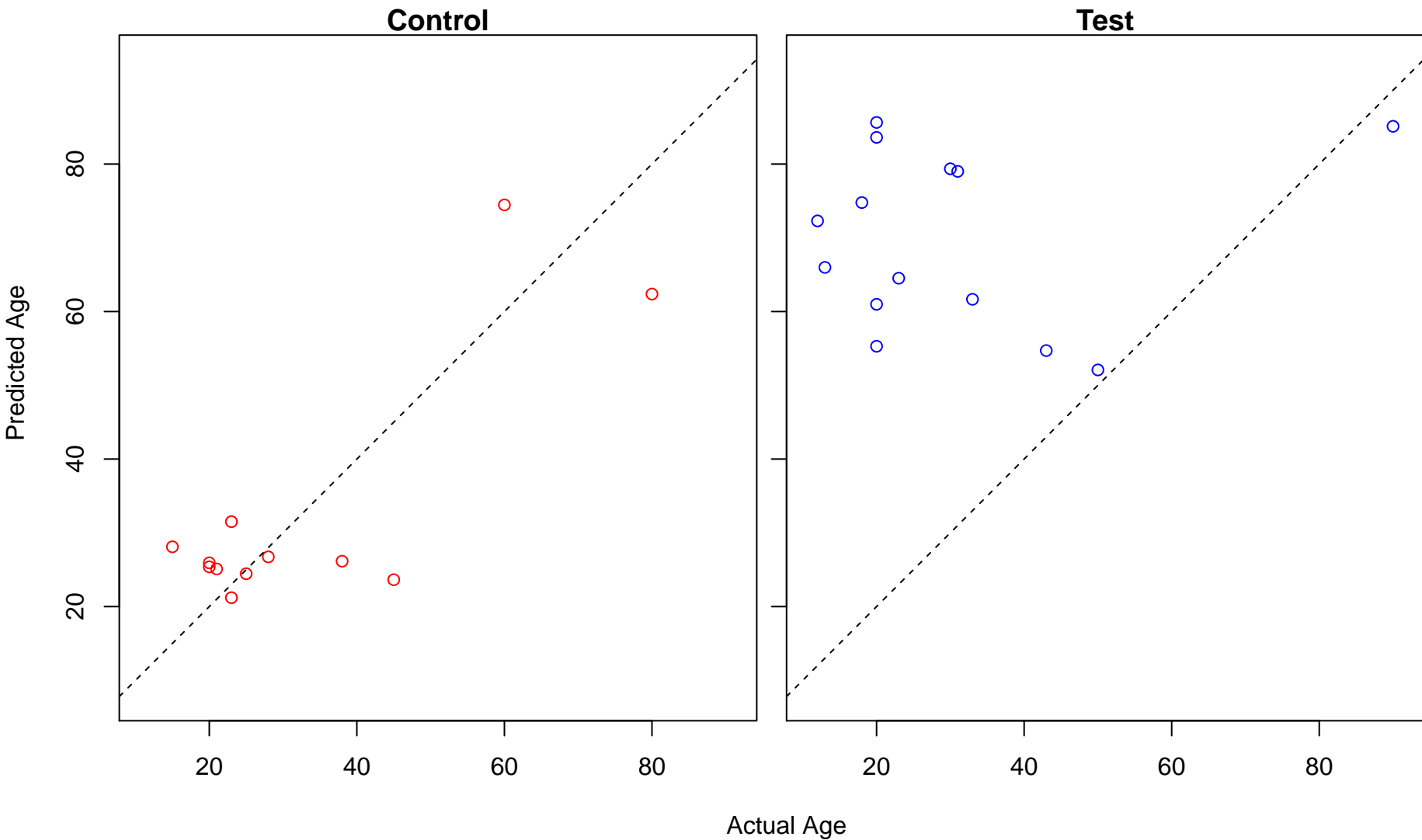


Actual Age

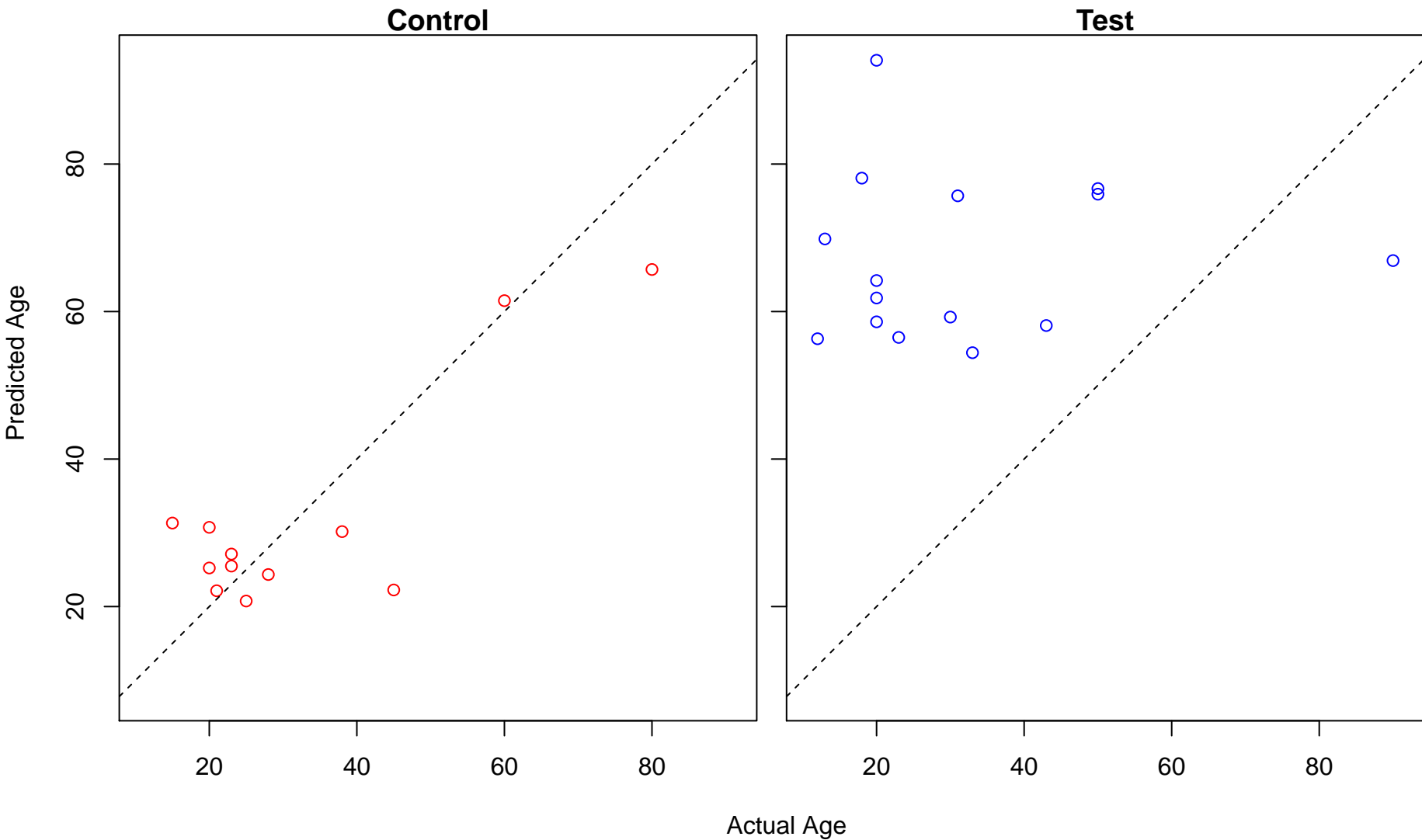
neuromuscular process controlling balance (Score: 5.751876)



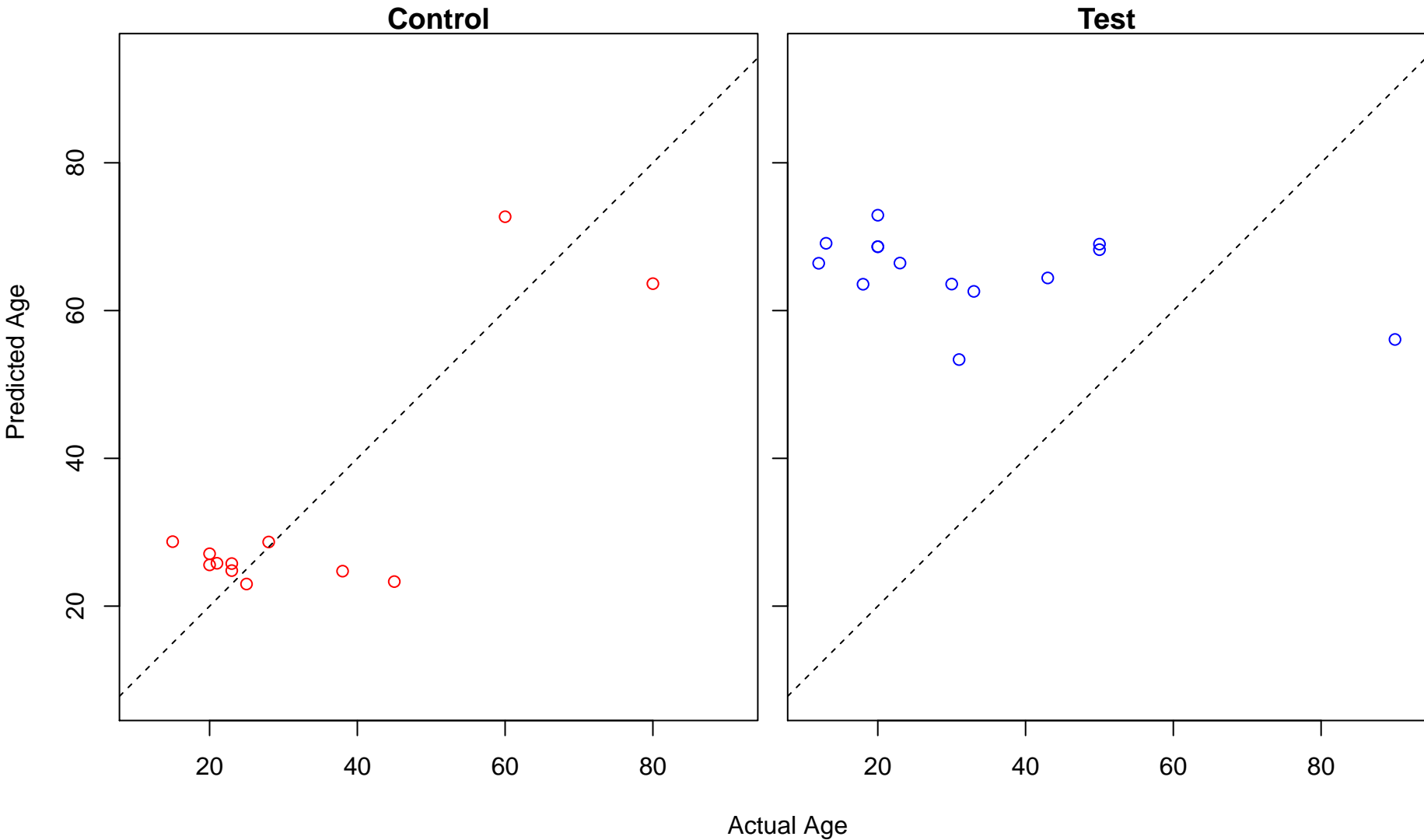
regulation of reproductive process (Score: 5.749746)



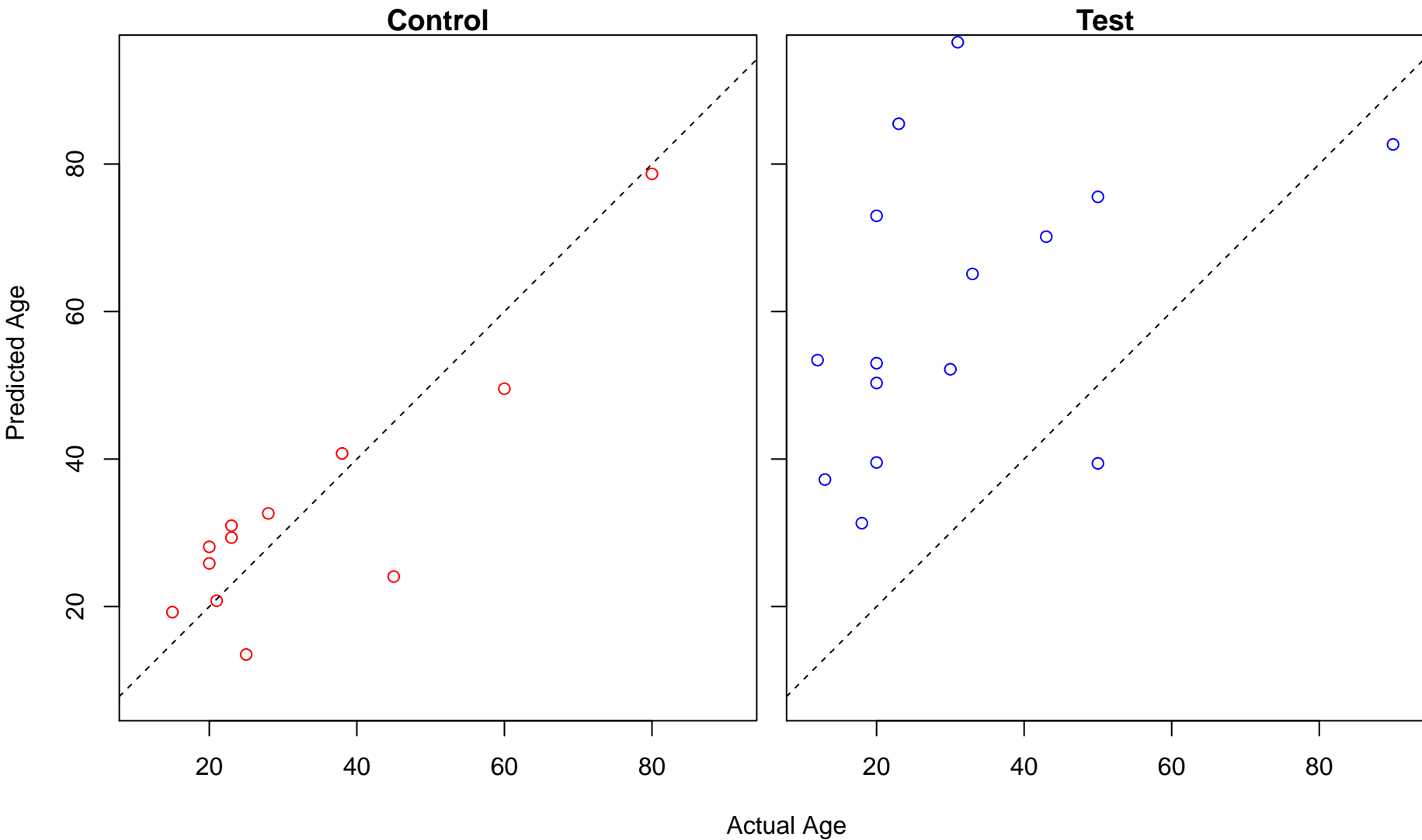
negative regulation of multi-organism process (Score: 5.748002)



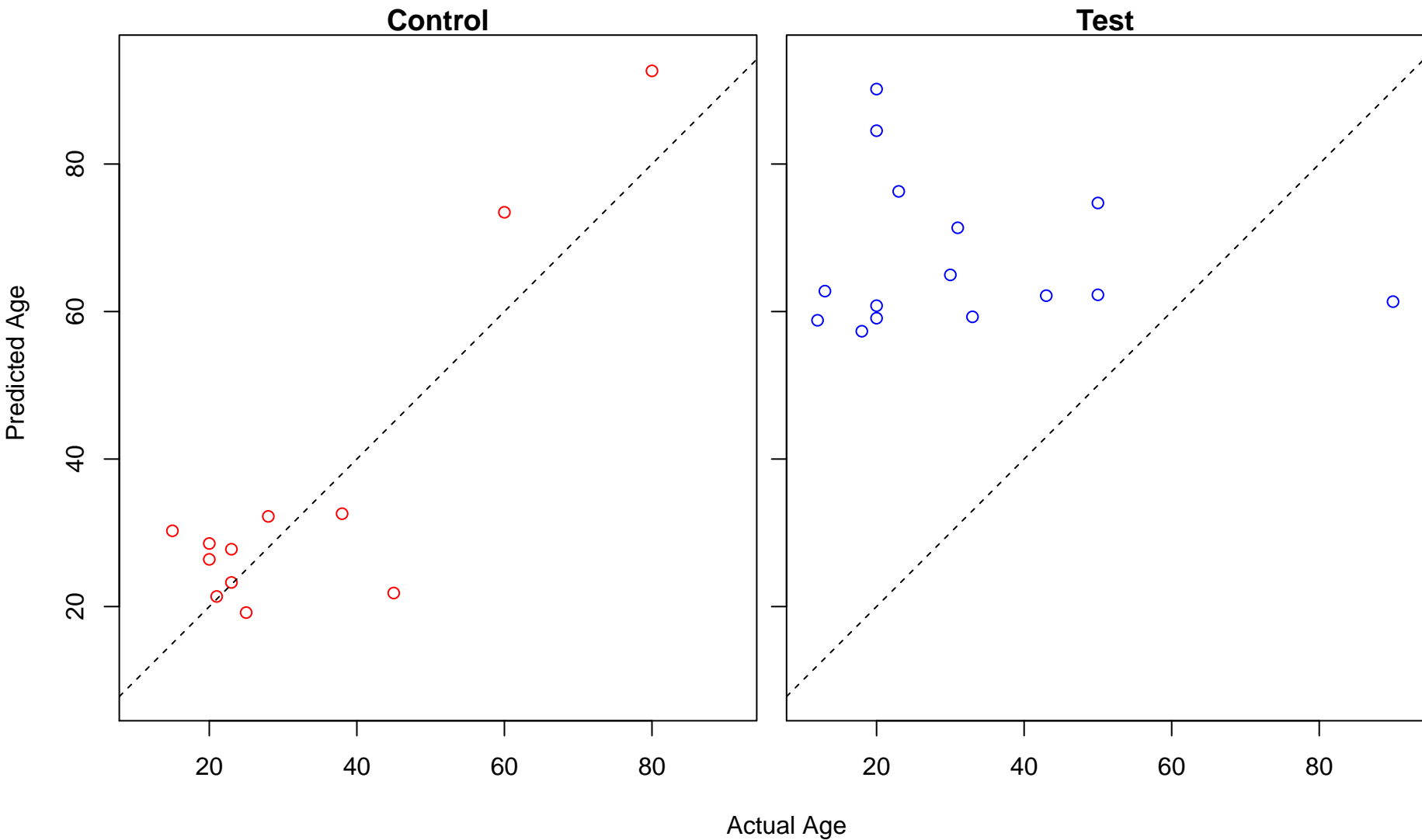
regulation of cholesterol metabolic process (Score: 5.746796)



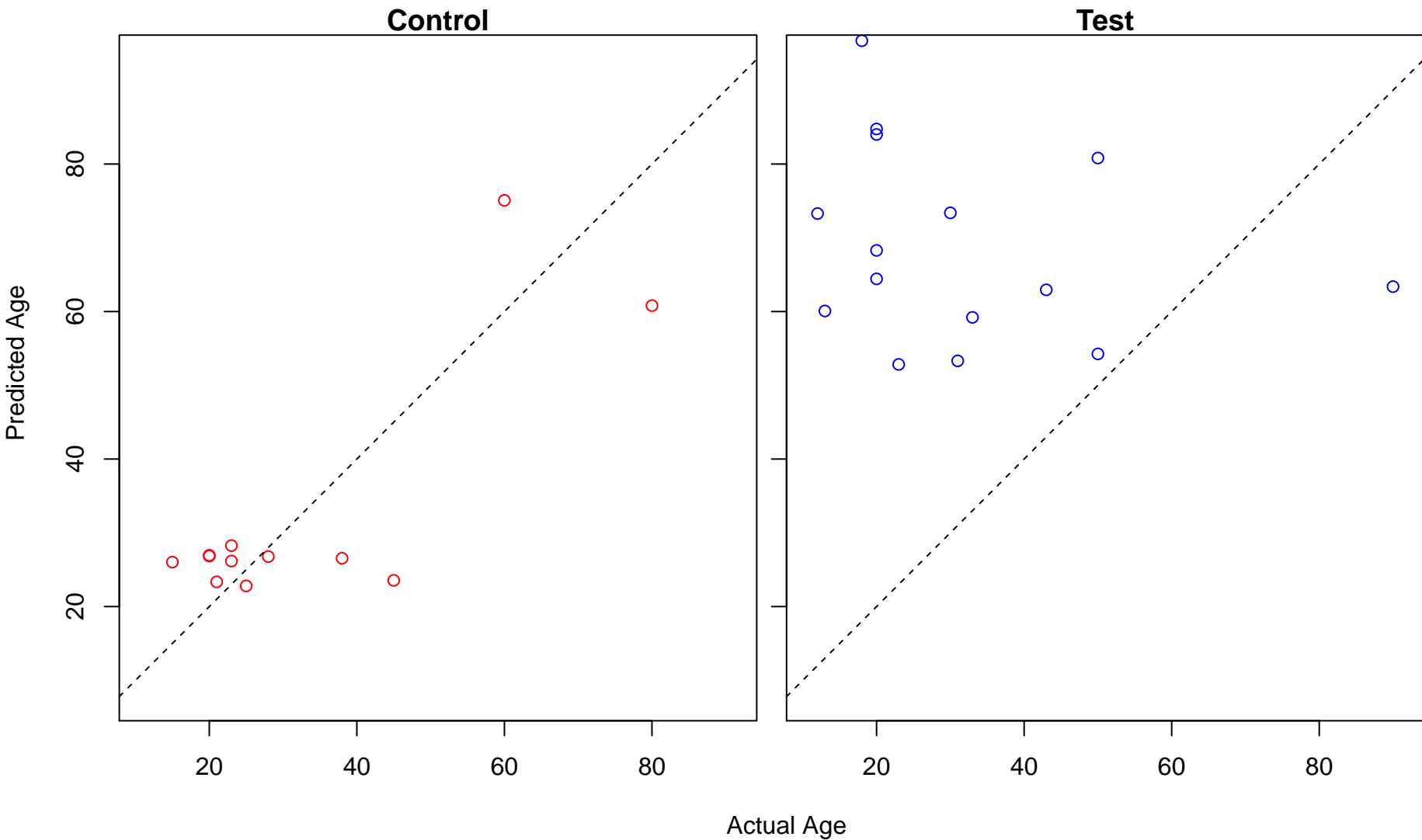
determination of digestive tract left/right asymmetry (Score: 5.742243)



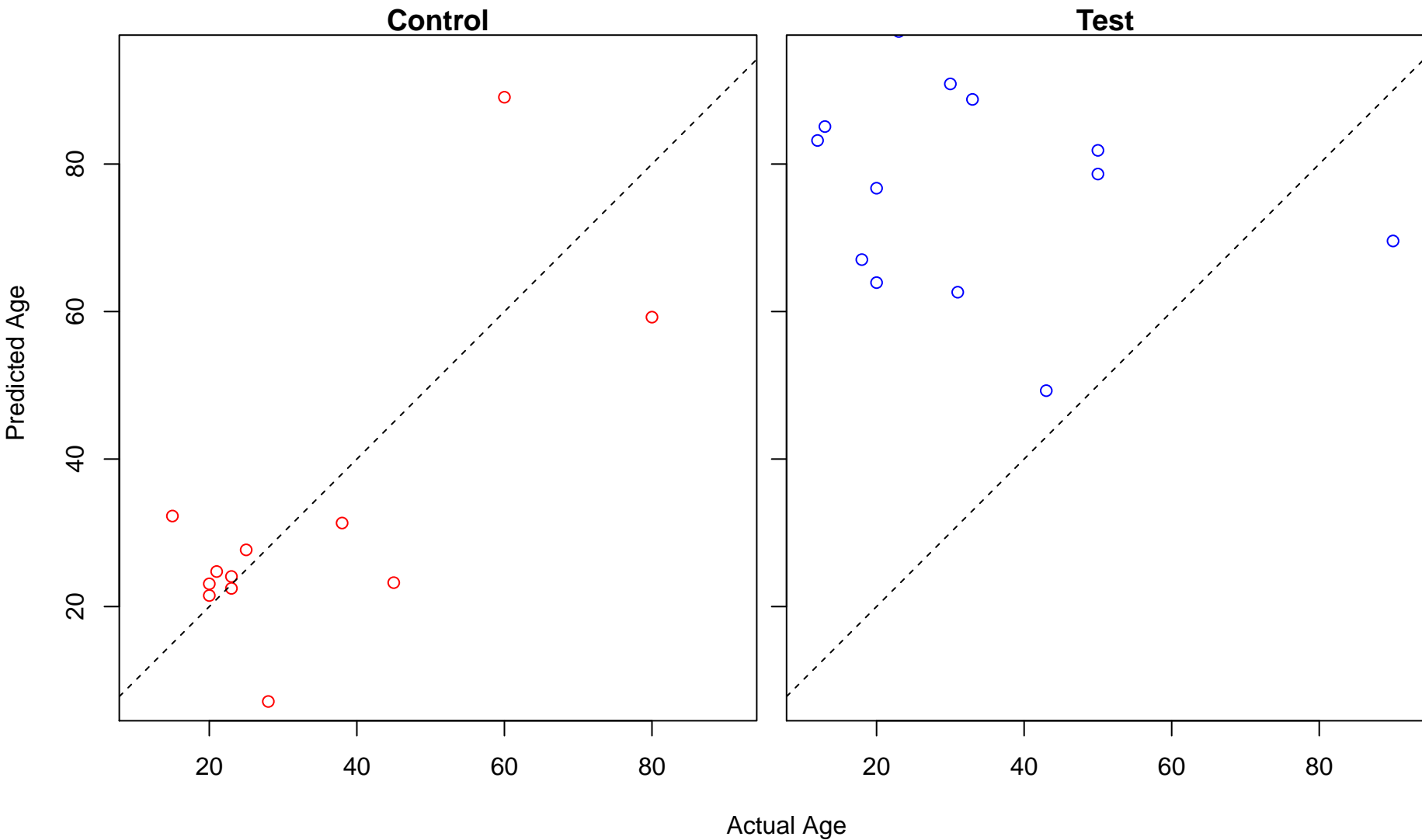
meiosis I (Score: 5.741409)



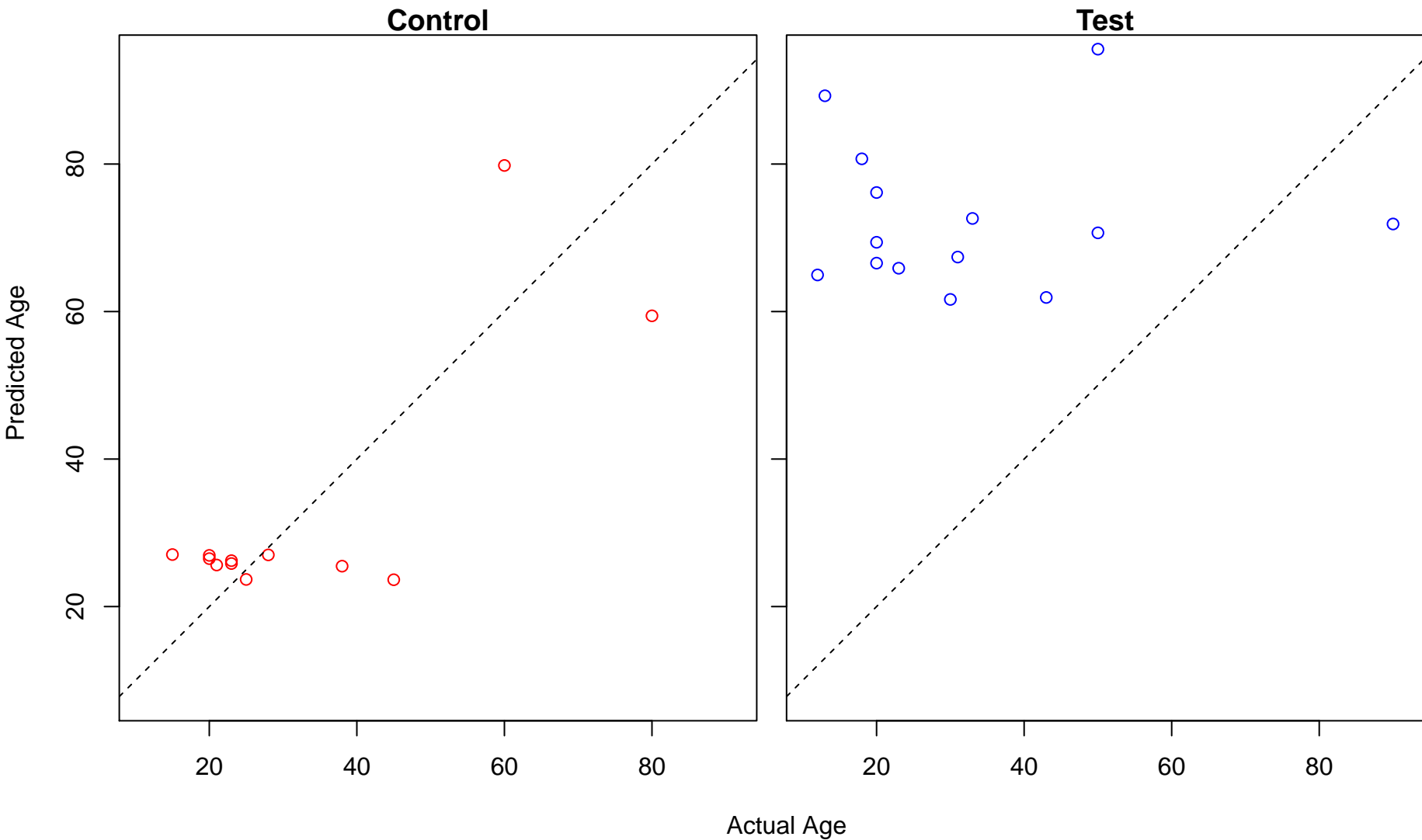
amide transport (Score: 5.741361)



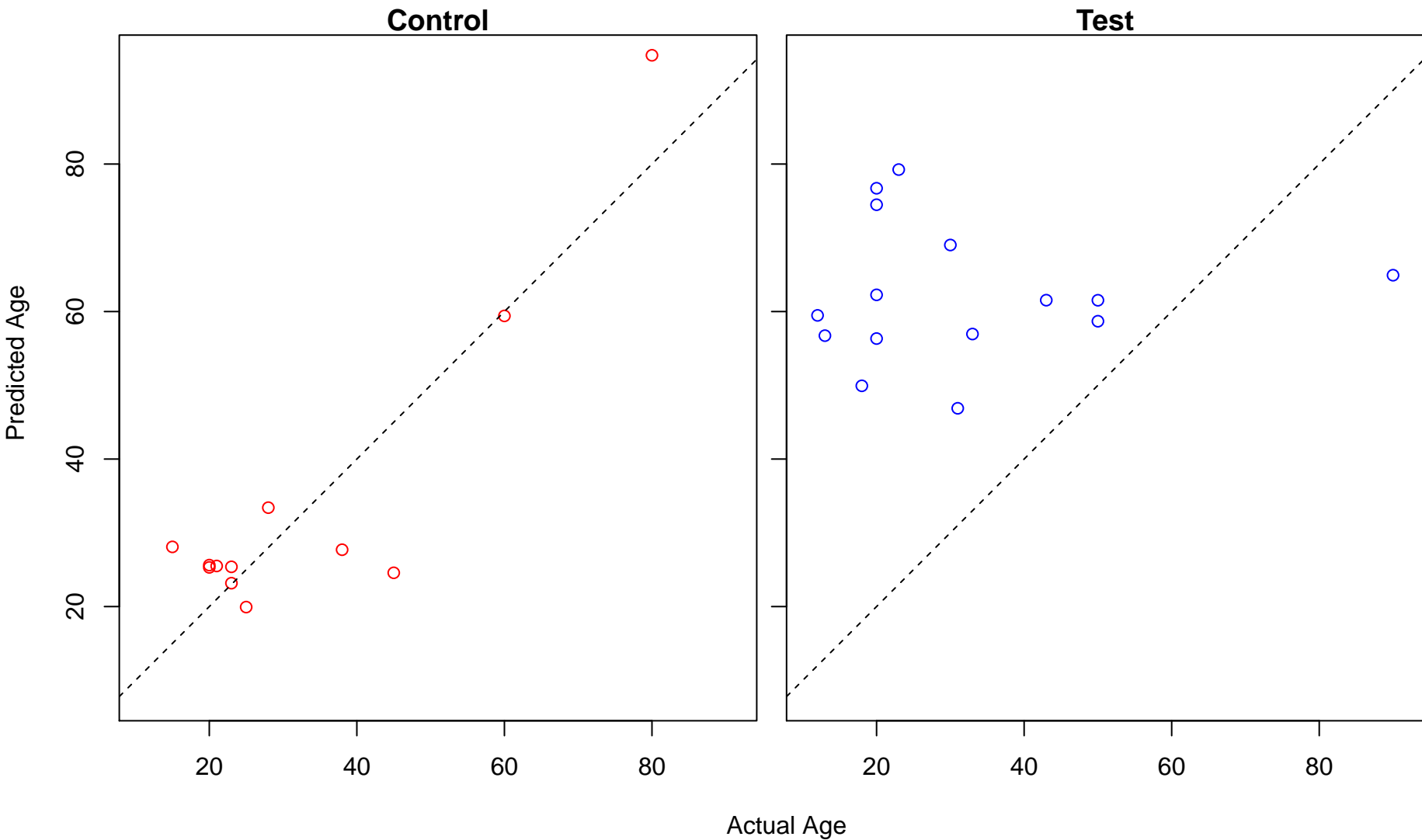
extracellular fibril organization (Score: 5.741259)



DNA repair (Score: 5.741168)

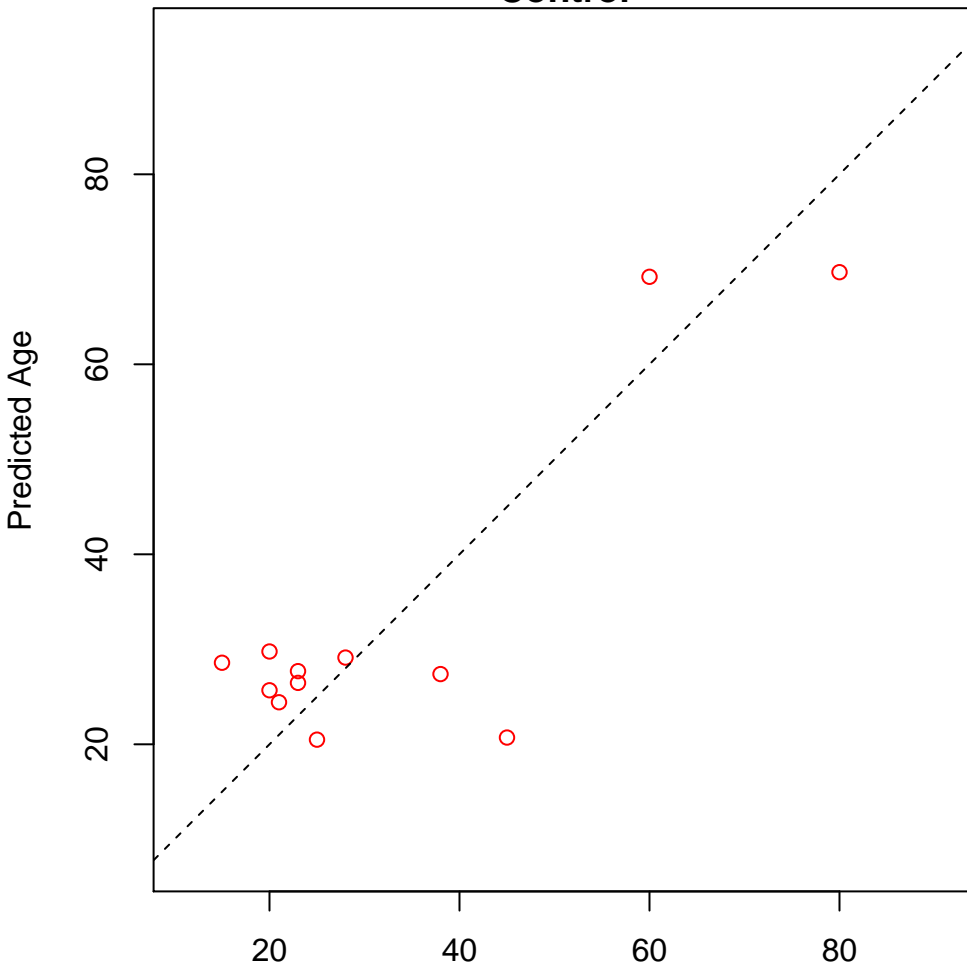


microtubule nucleation (Score: 5.740667)

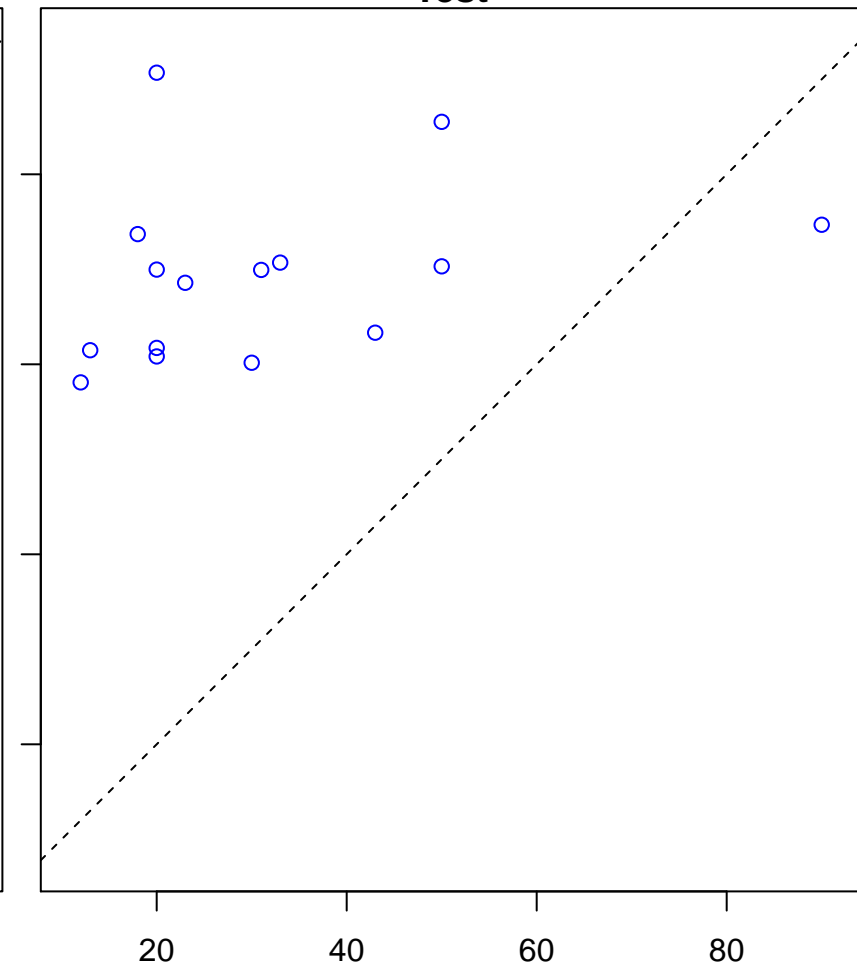


regulation of vesicle-mediated transport (Score: 5.739321)

Control

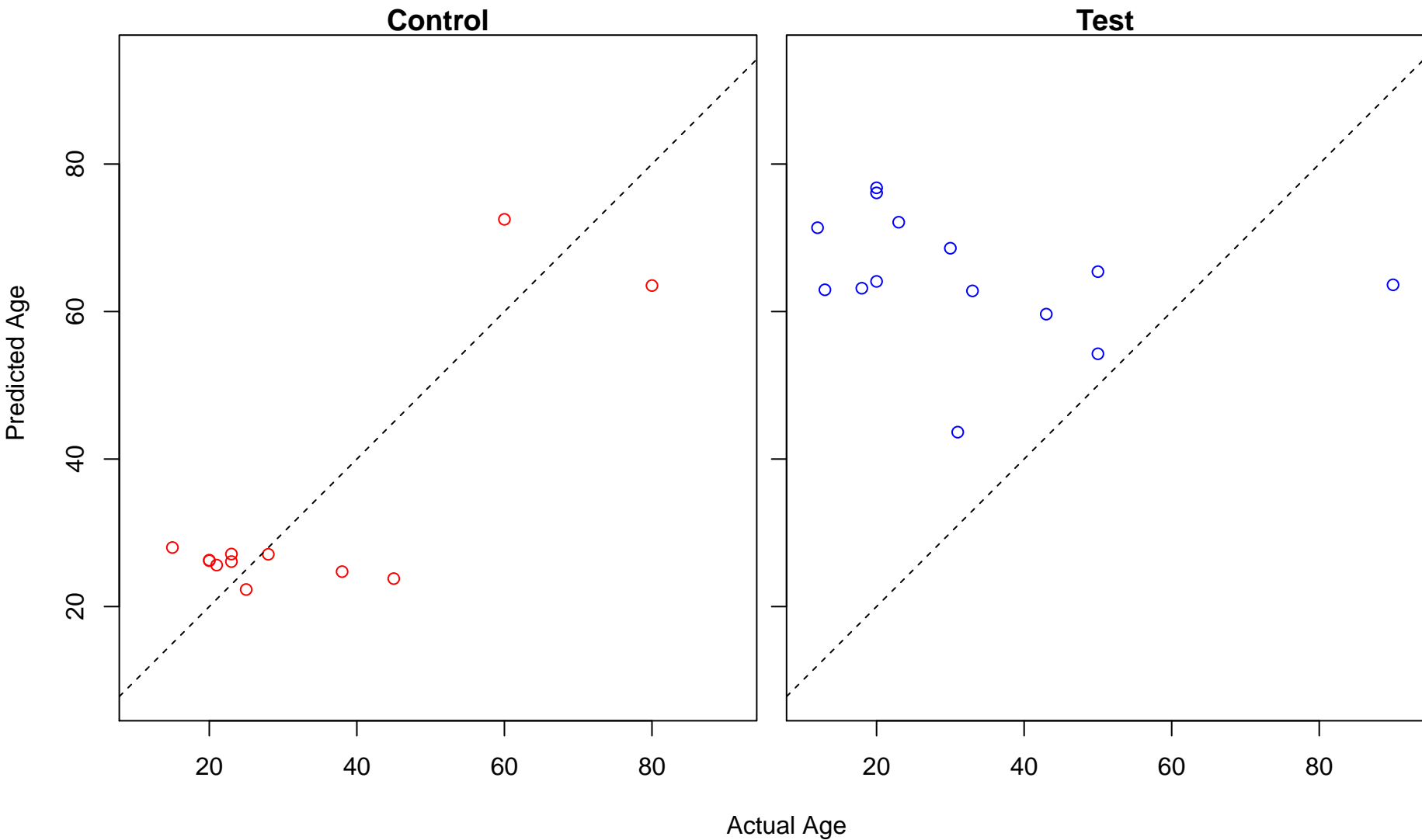


Test

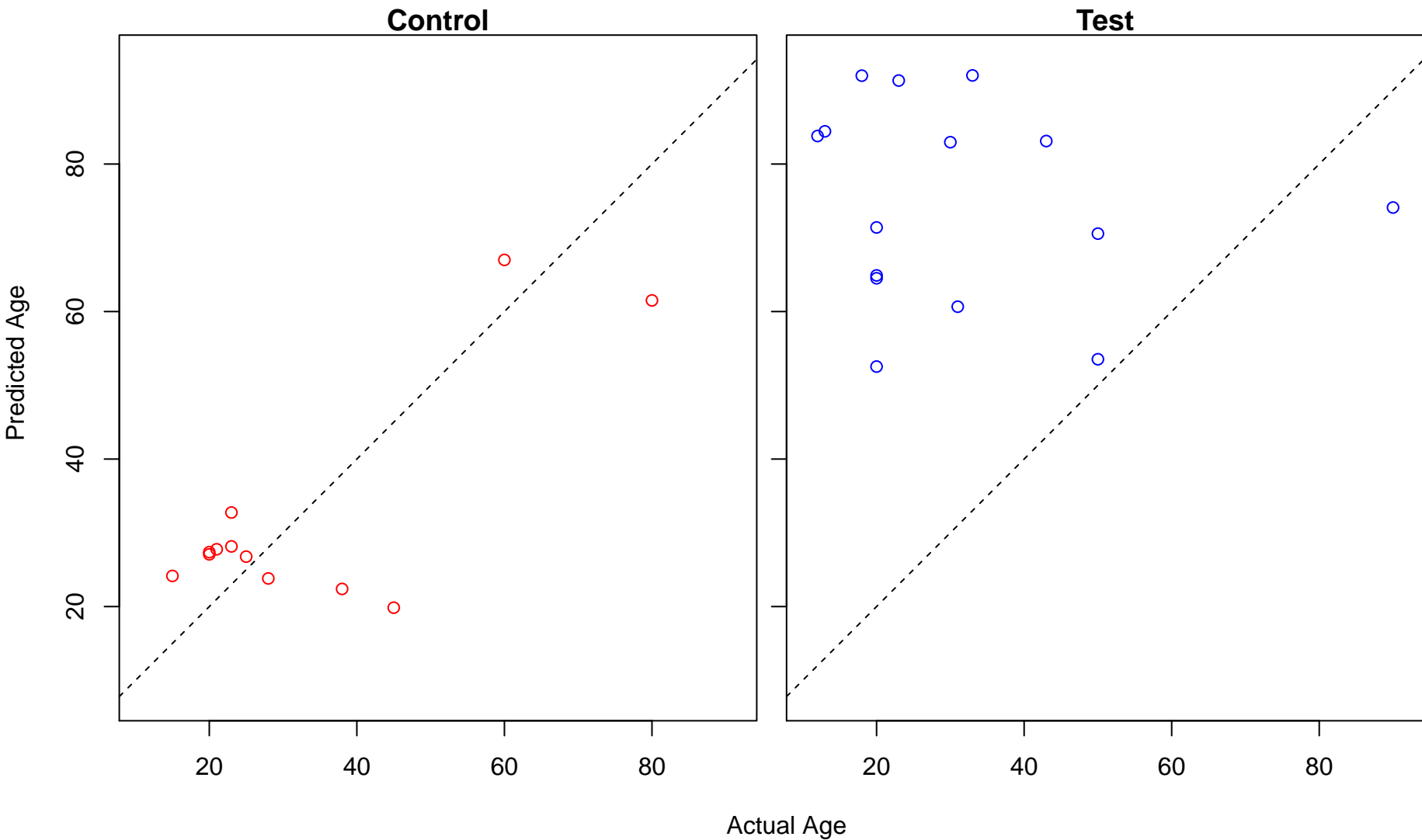


Actual Age

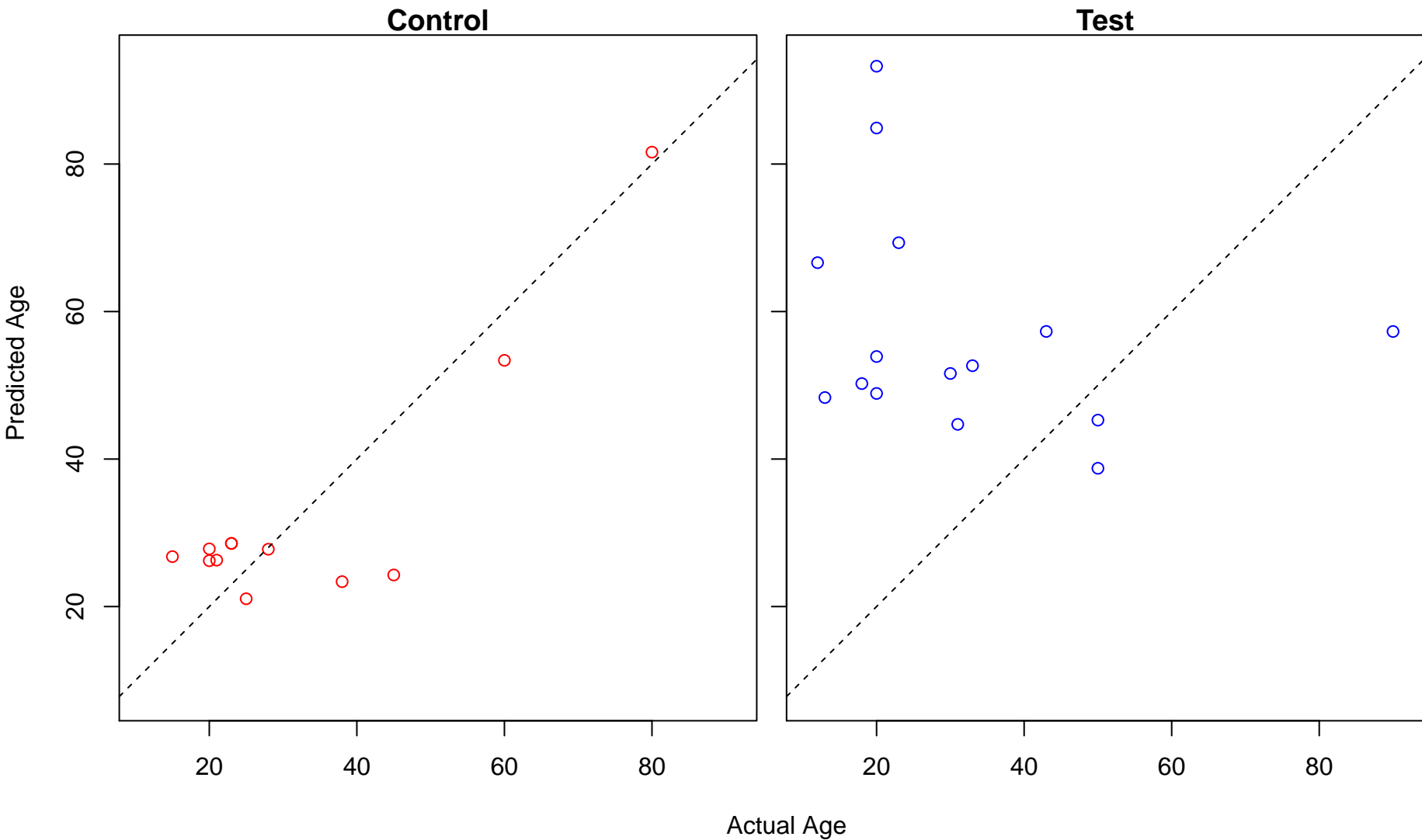
telomere maintenance via semi-conservative replication (Score: 5.737028)



purine deoxyribonucleotide metabolic process (Score: 5.736997)

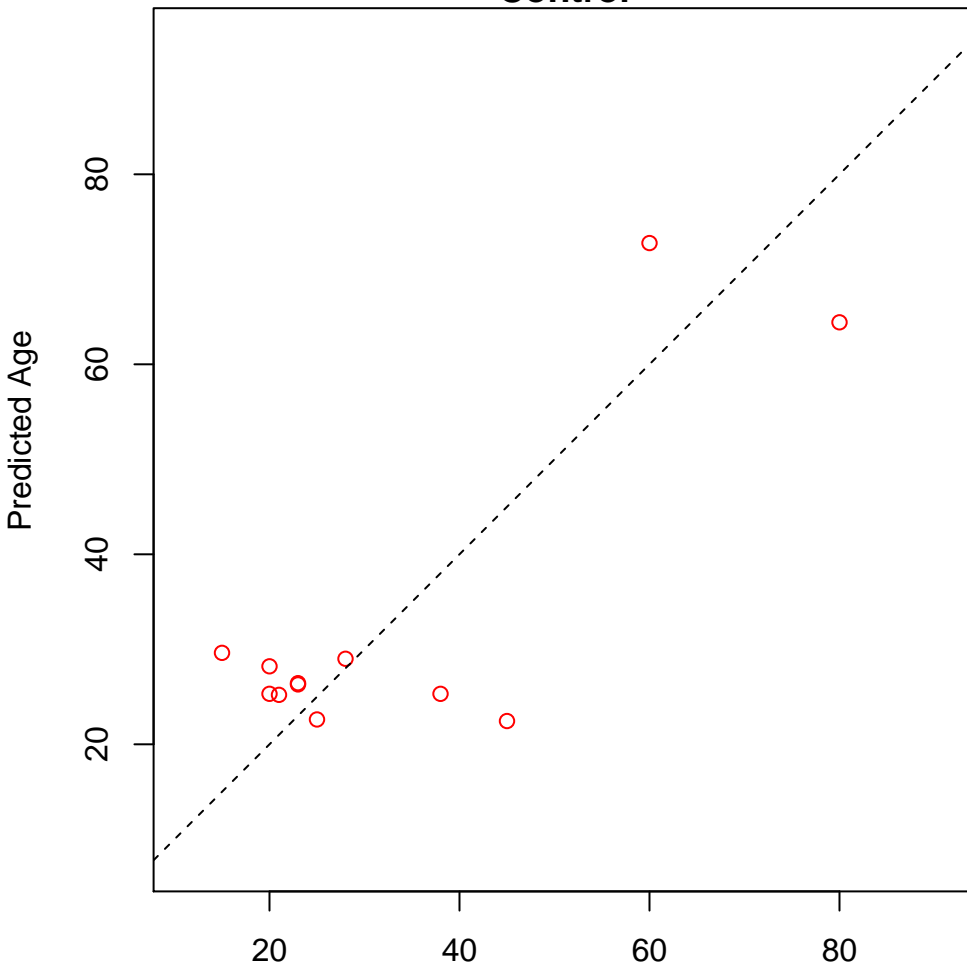


mitotic recombination (Score: 5.734835)

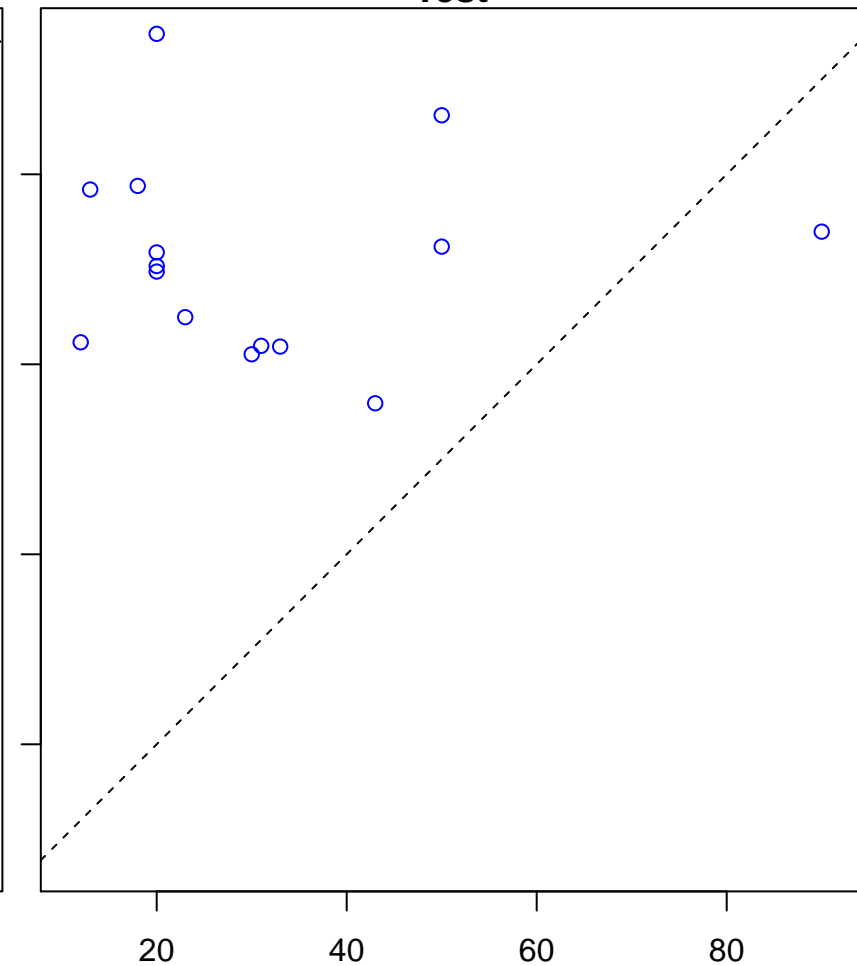


positive regulation of protein transport (Score: 5.733838)

Control

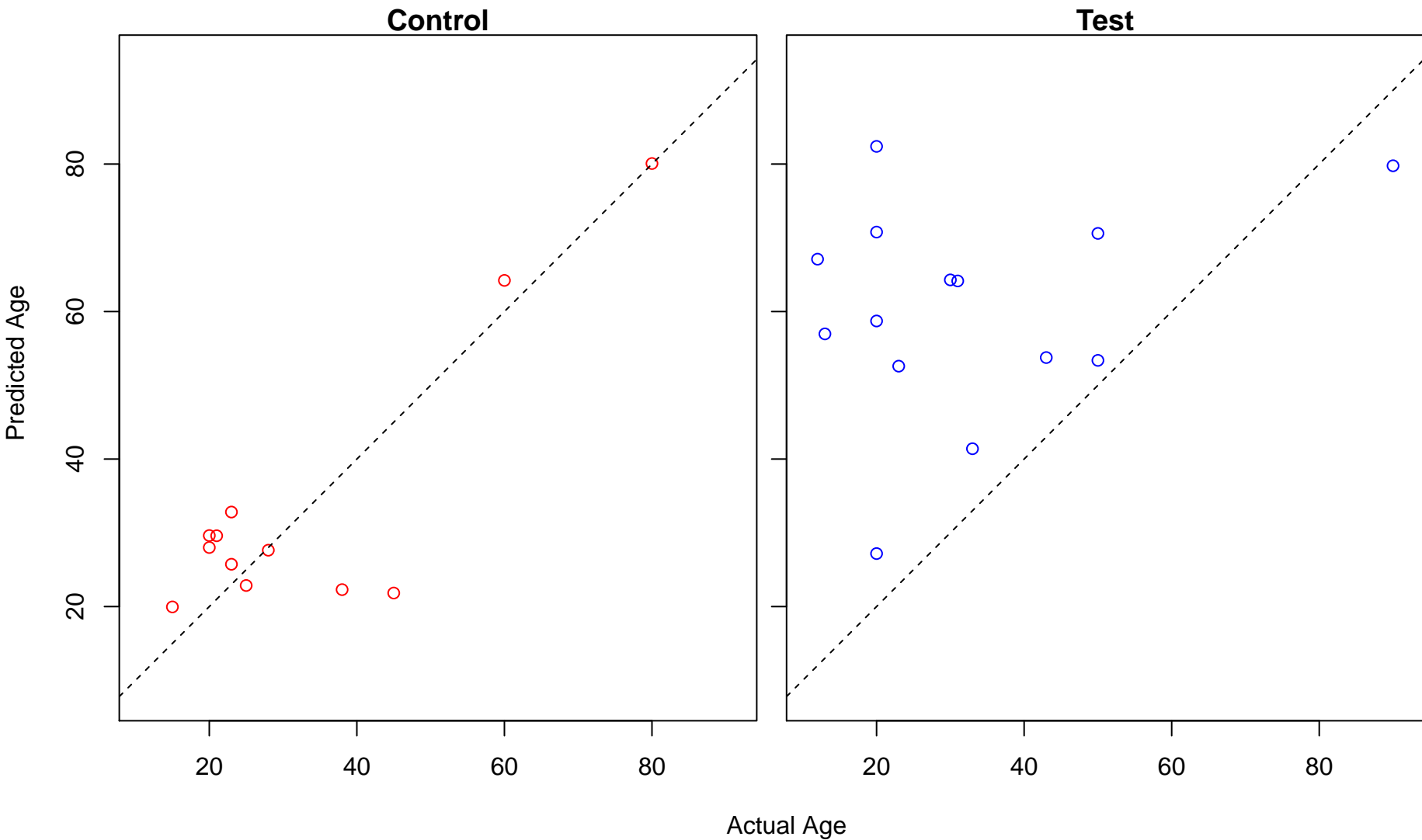


Test



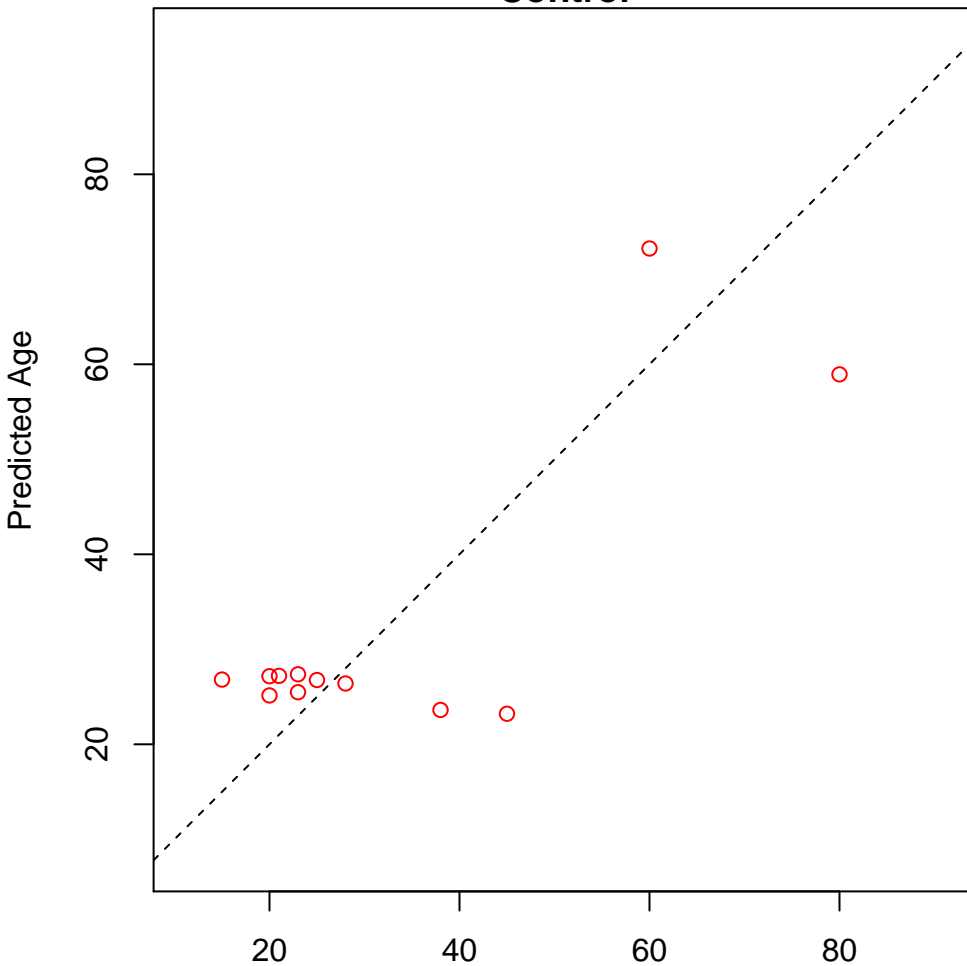
Actual Age

positive regulation of mitochondrial calcium ion concentration (Score: 5.732127)

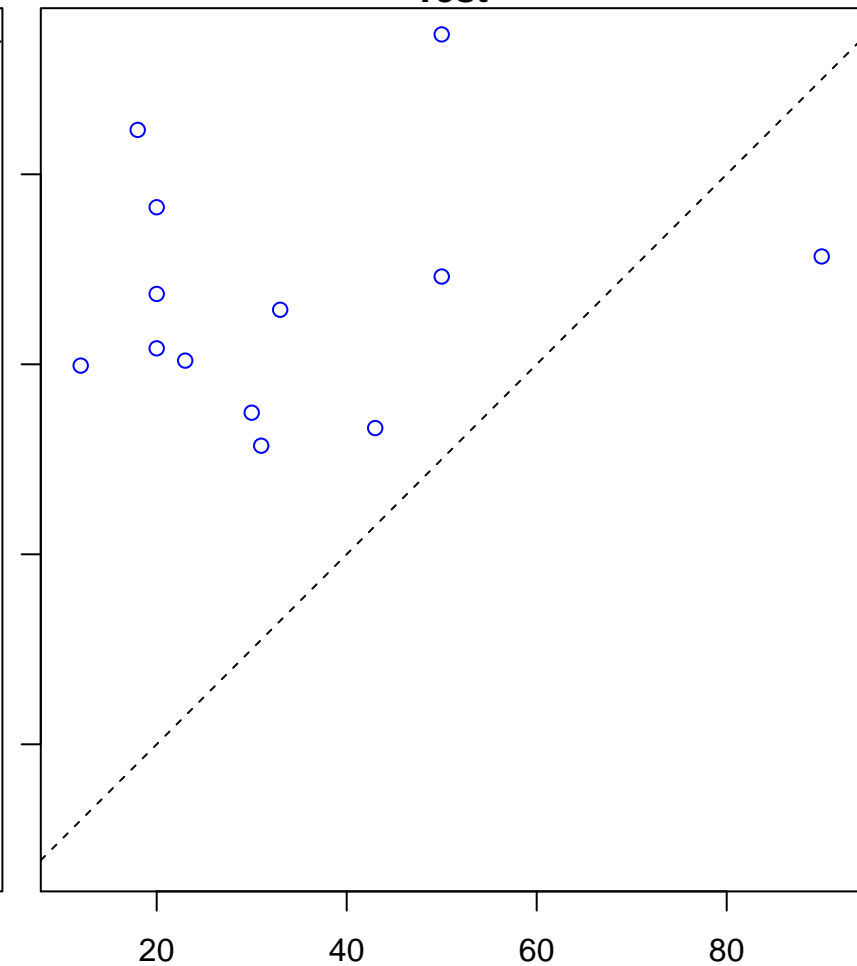


selenium compound metabolic process (Score: 5.731881)

Control

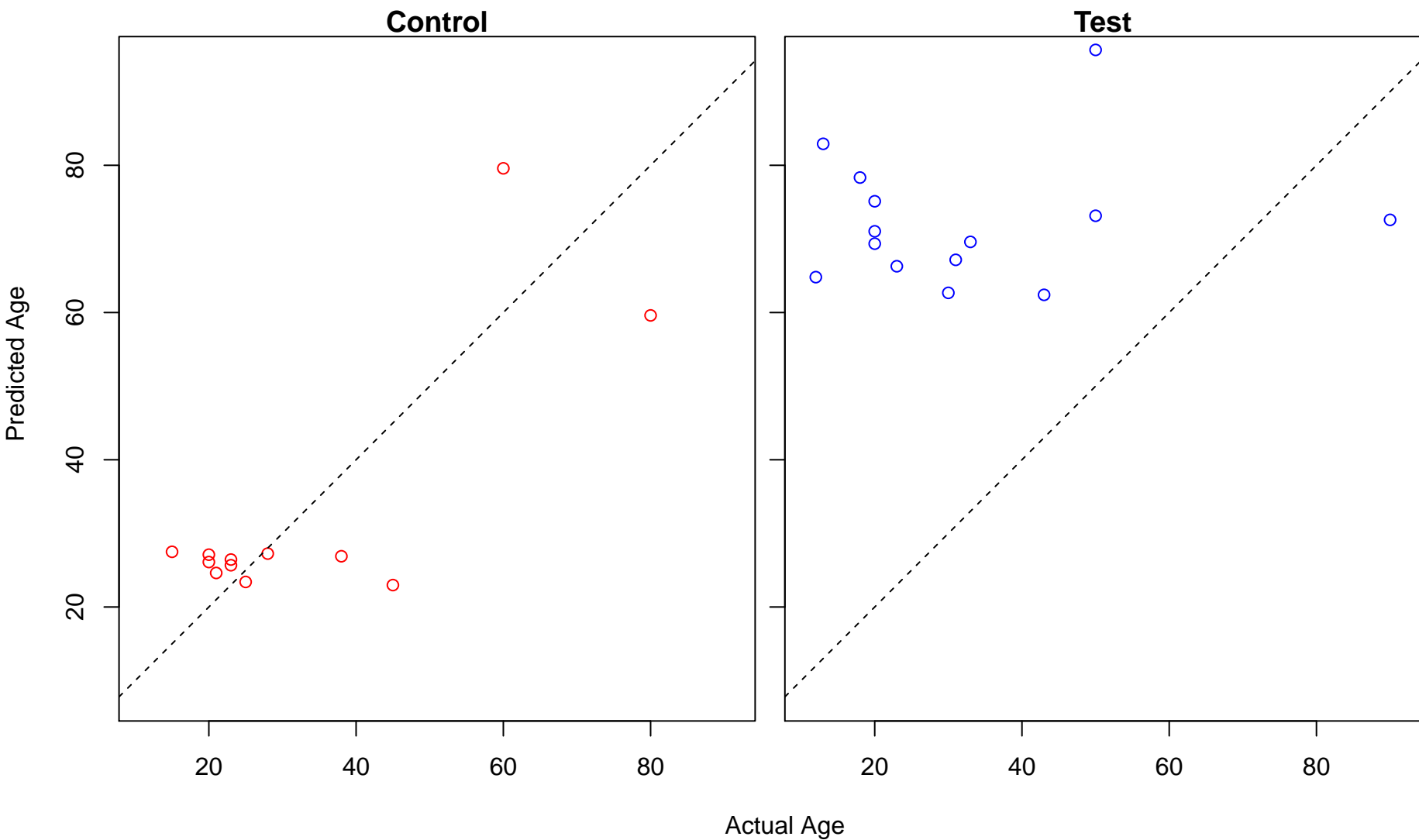


Test

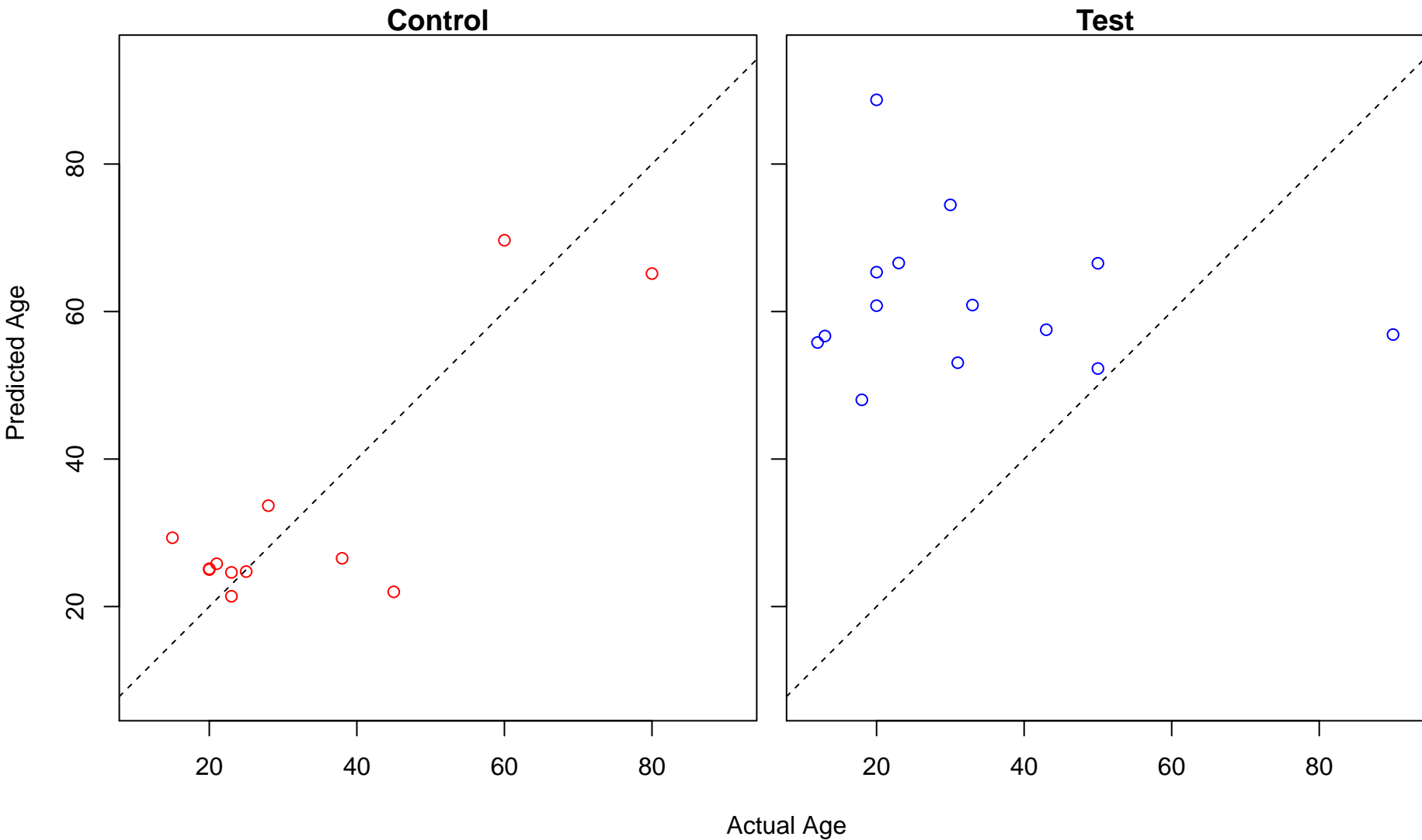


Actual Age

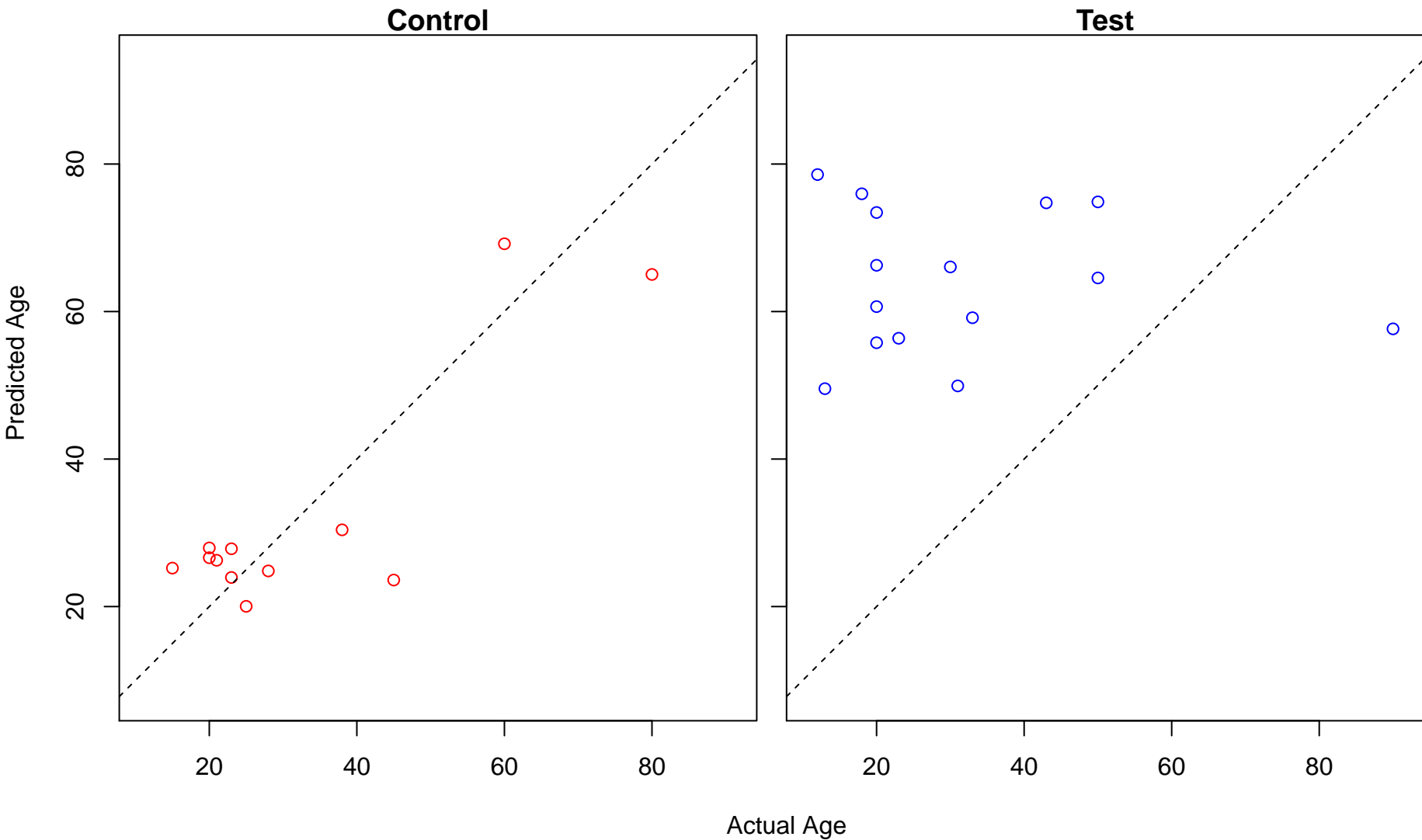
intracellular receptor signaling pathway (Score: 5.730922)



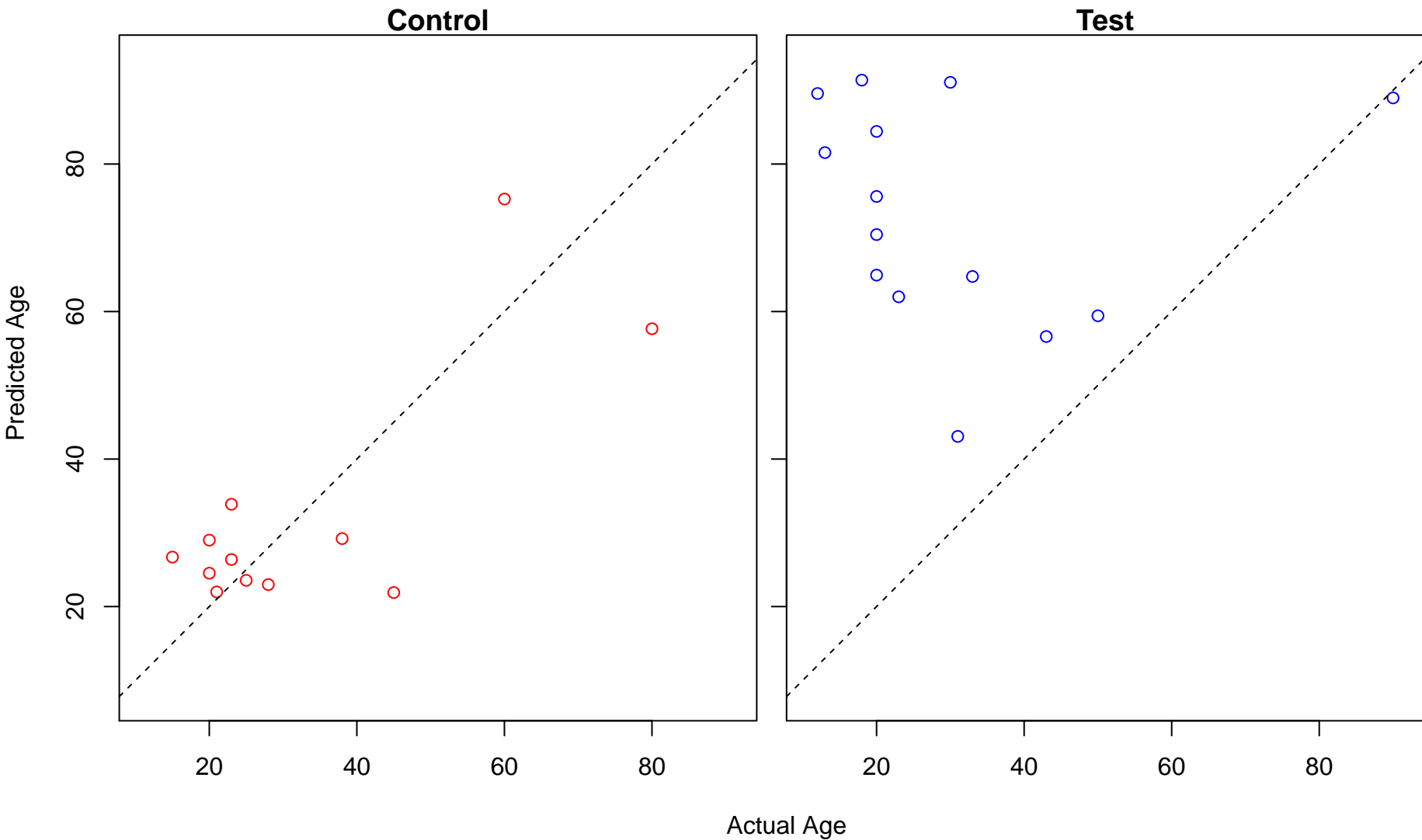
regulation of TORC1 signaling (Score: 5.729835)



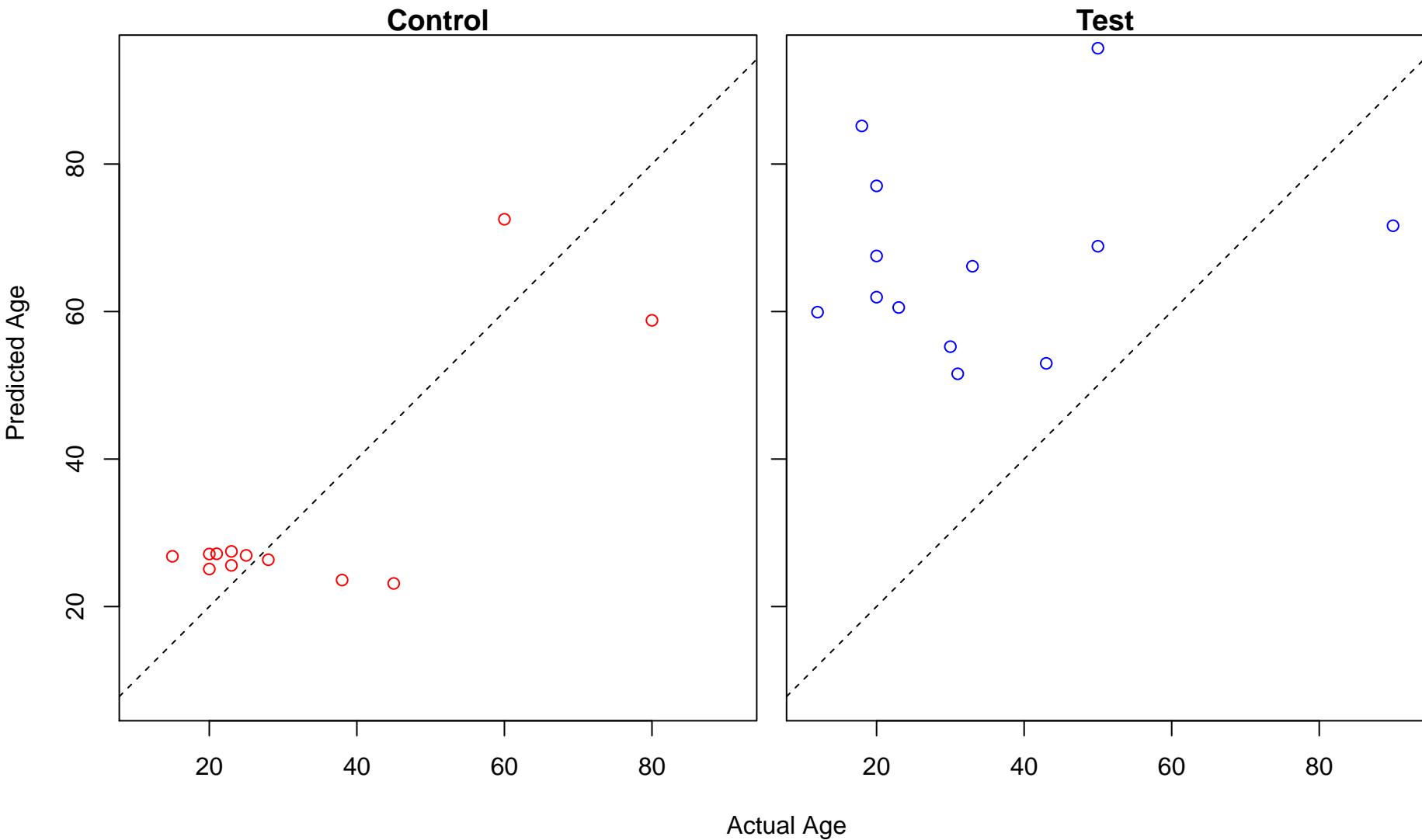
sulfur amino acid metabolic process (Score: 5.727849)



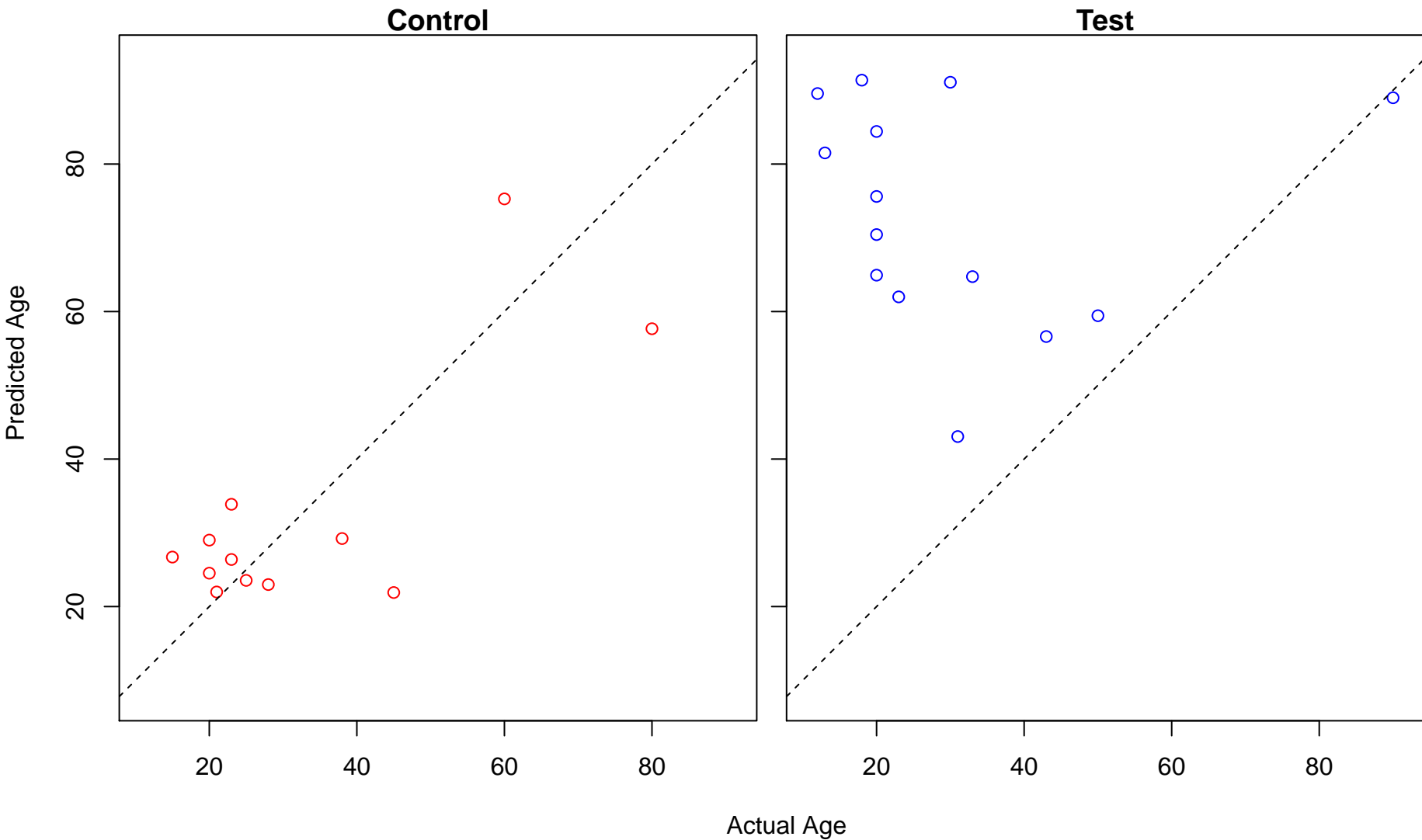
ventricular septum development (Score: 5.726510)



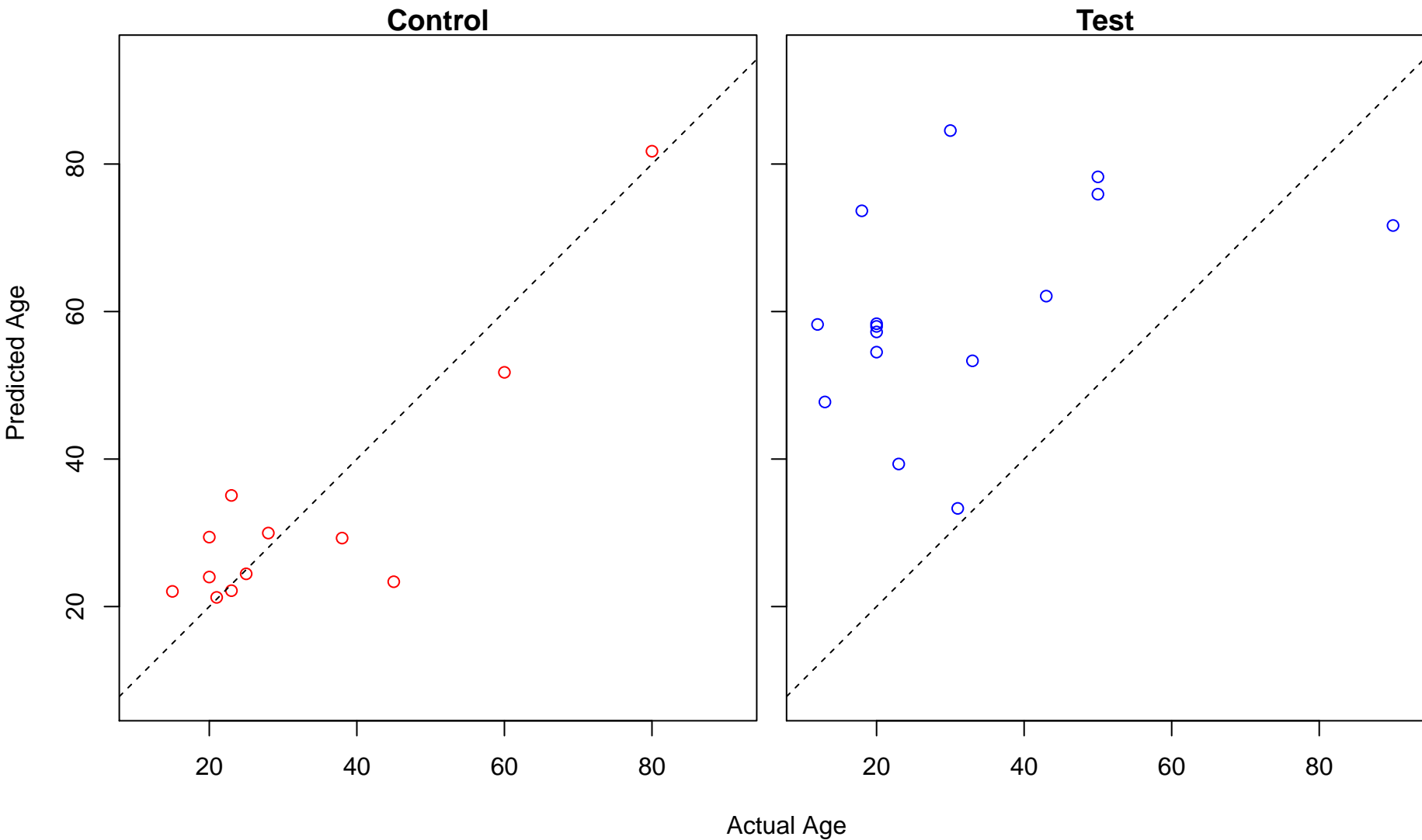
RNA catabolic process (Score: 5.724543)



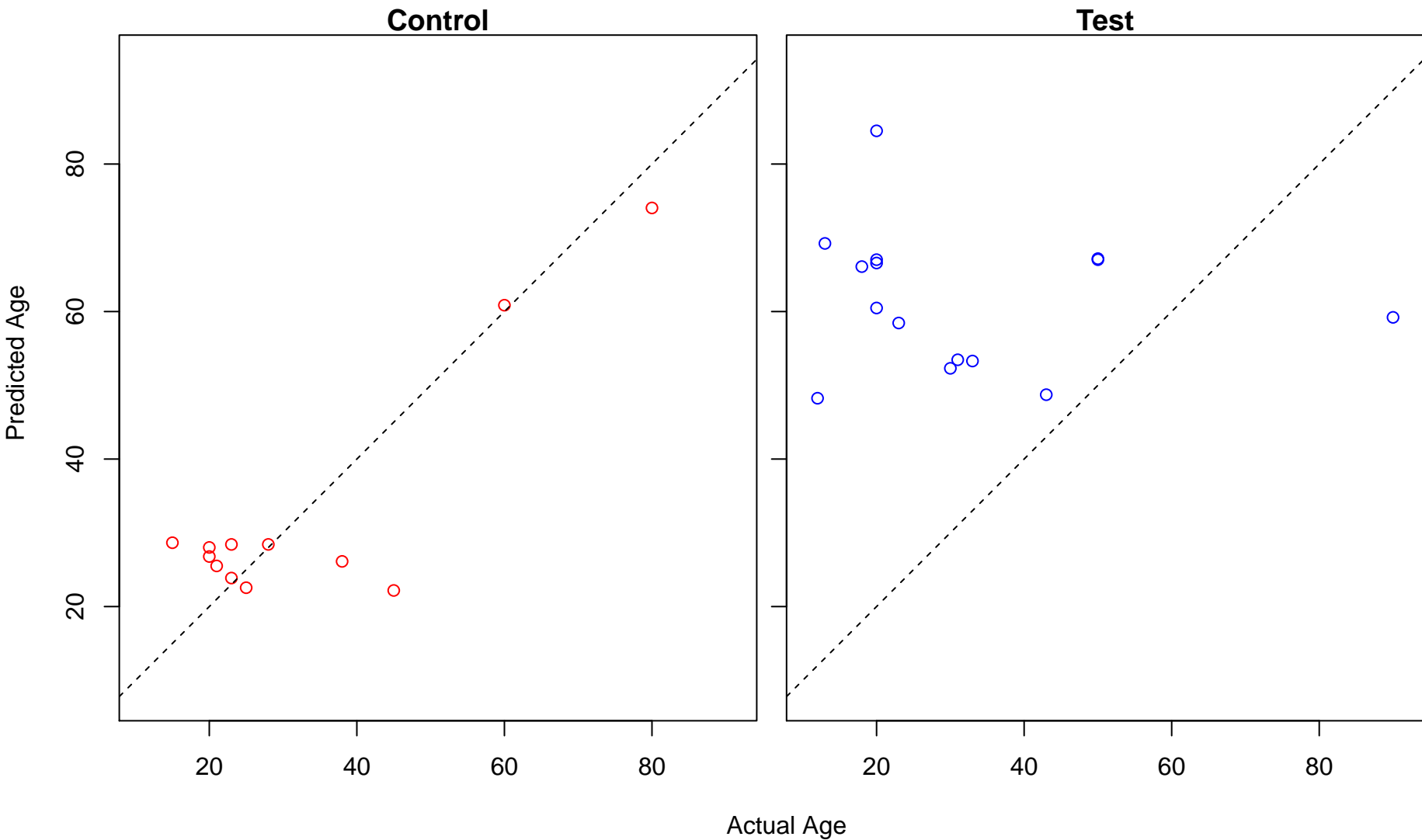
ventricular septum morphogenesis (Score: 5.724496)



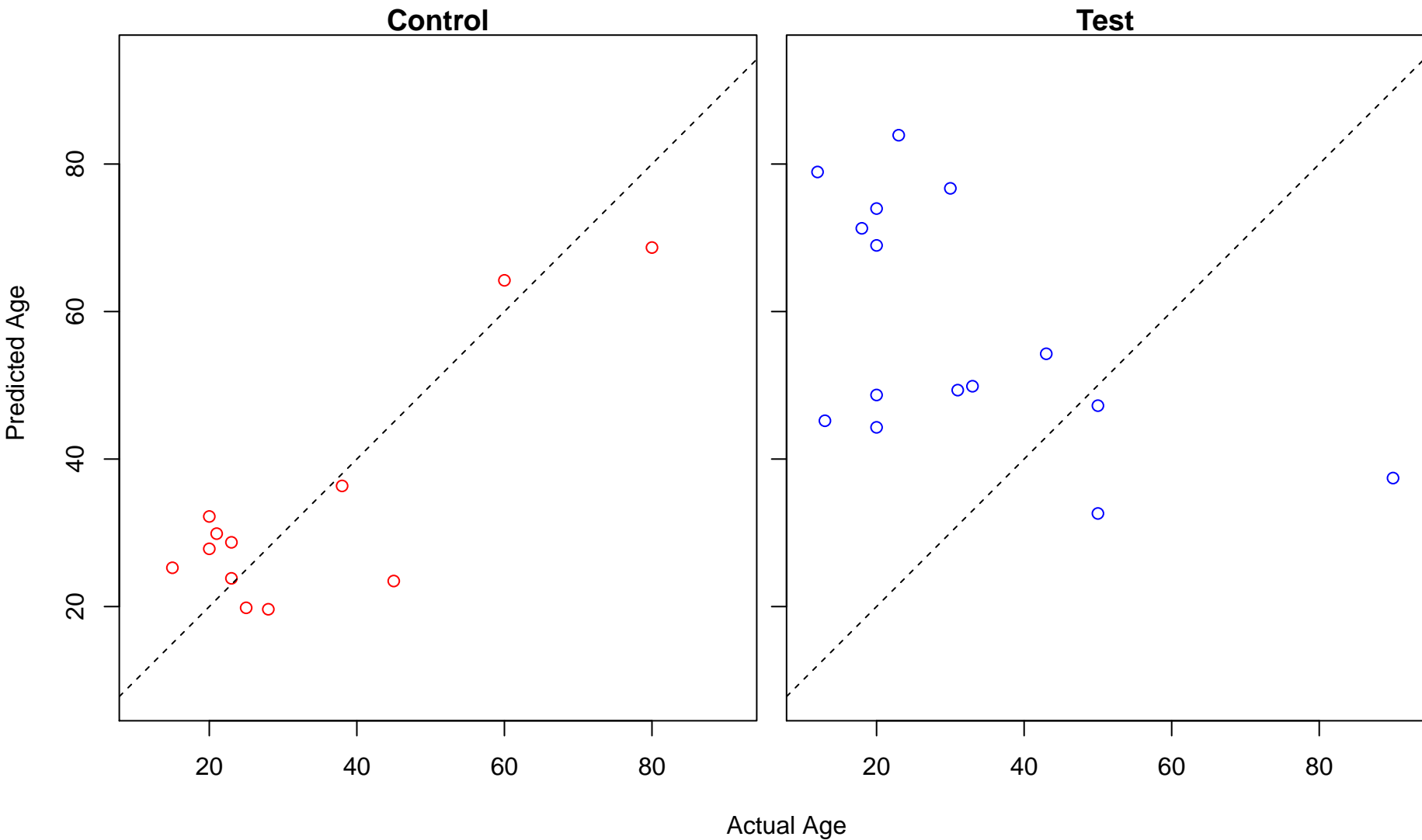
regulation of interleukin-8 biosynthetic process (Score: 5.723562)



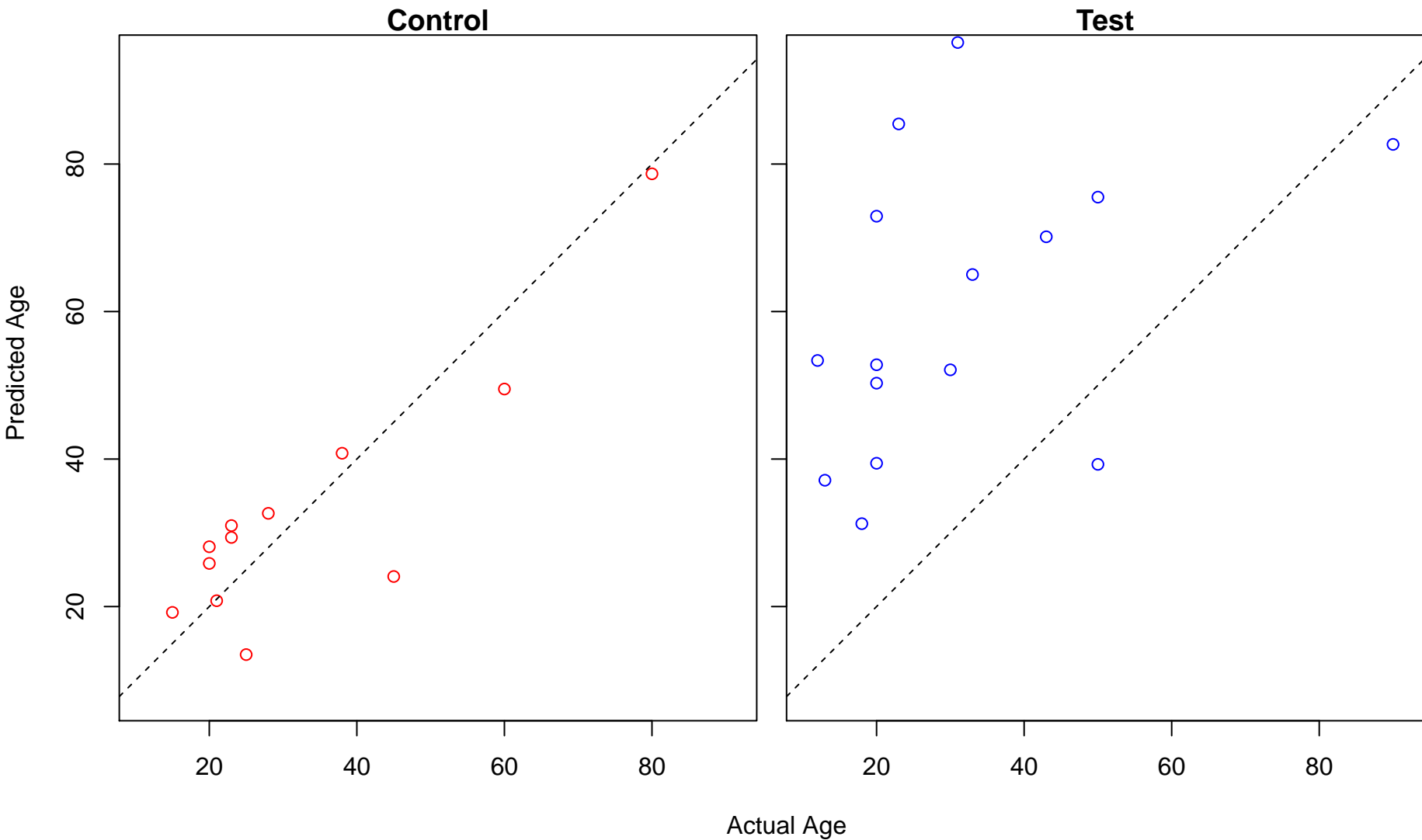
platelet degranulation (Score: 5.722817)



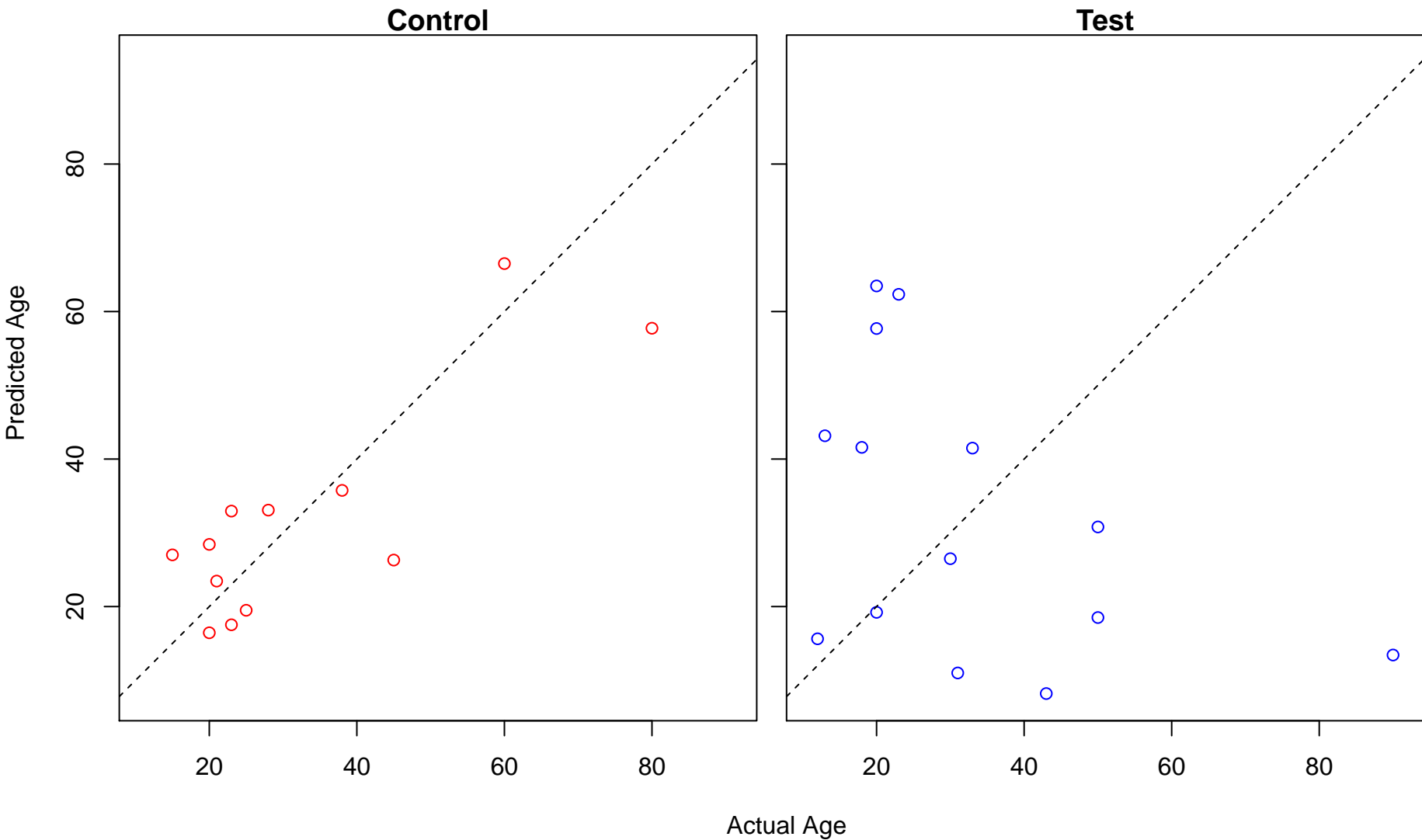
muscle fiber development (Score: 5.722026)



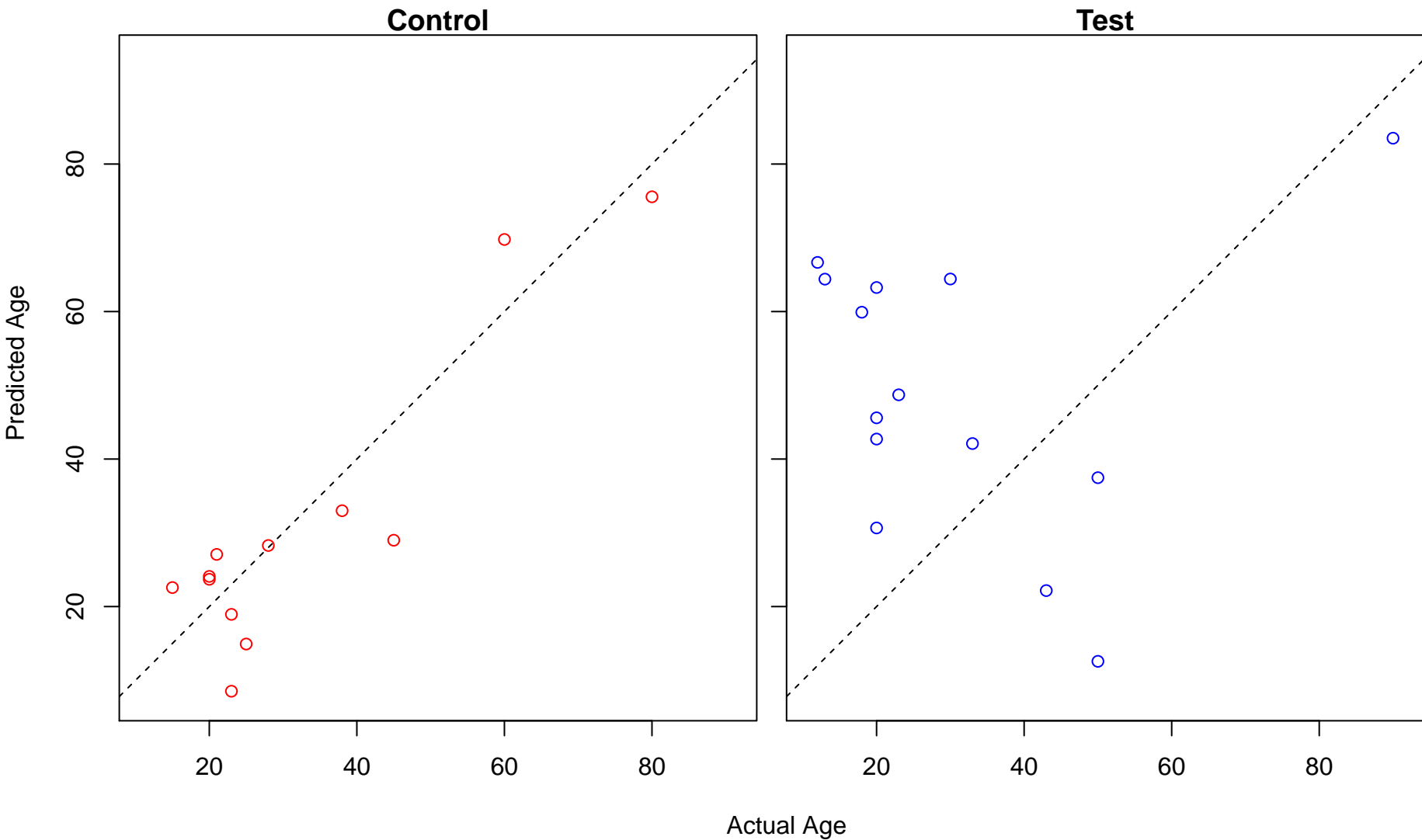
determination of pancreatic left/right asymmetry (Score: 5.720605)



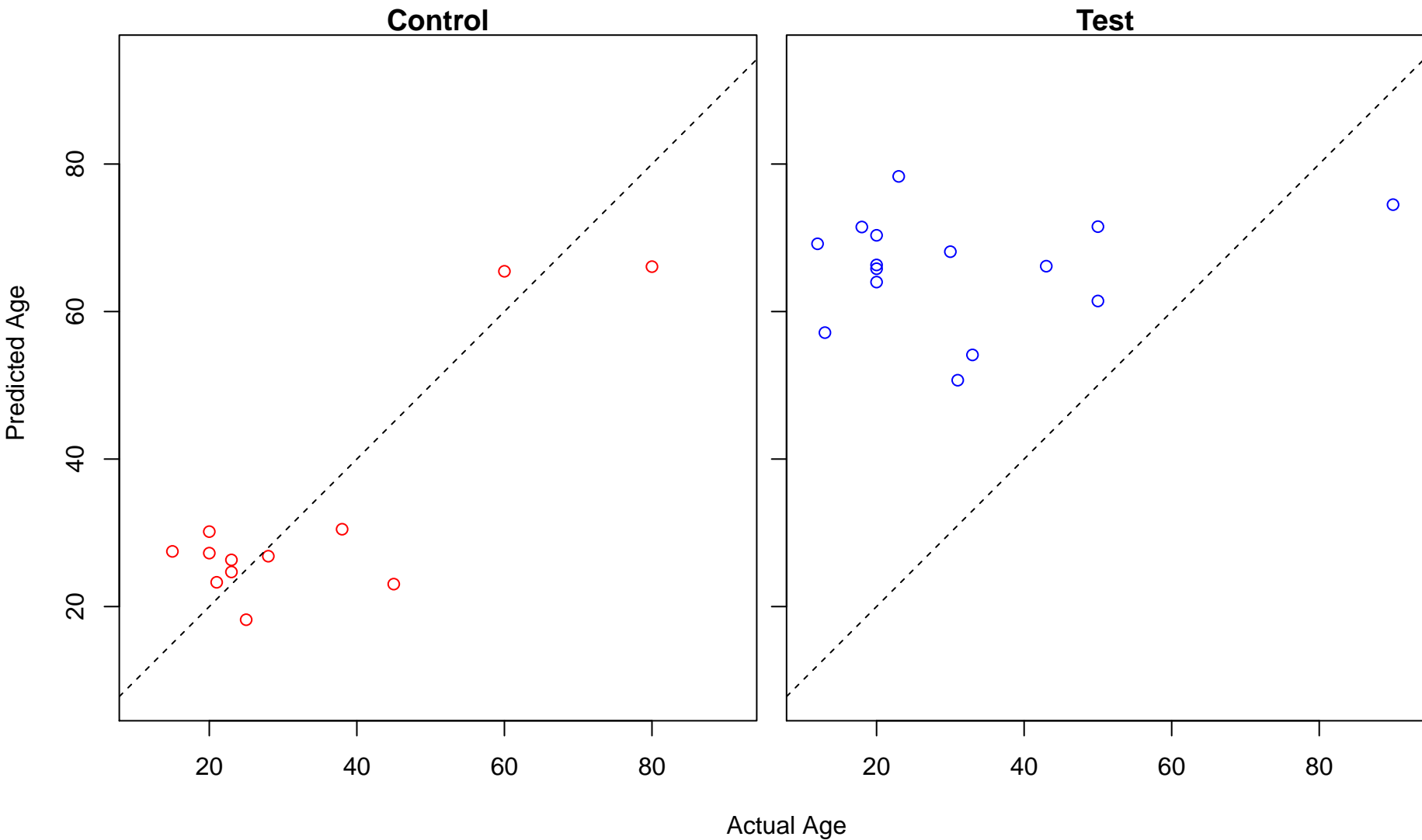
regulation of muscle contraction (Score: 5.720576)



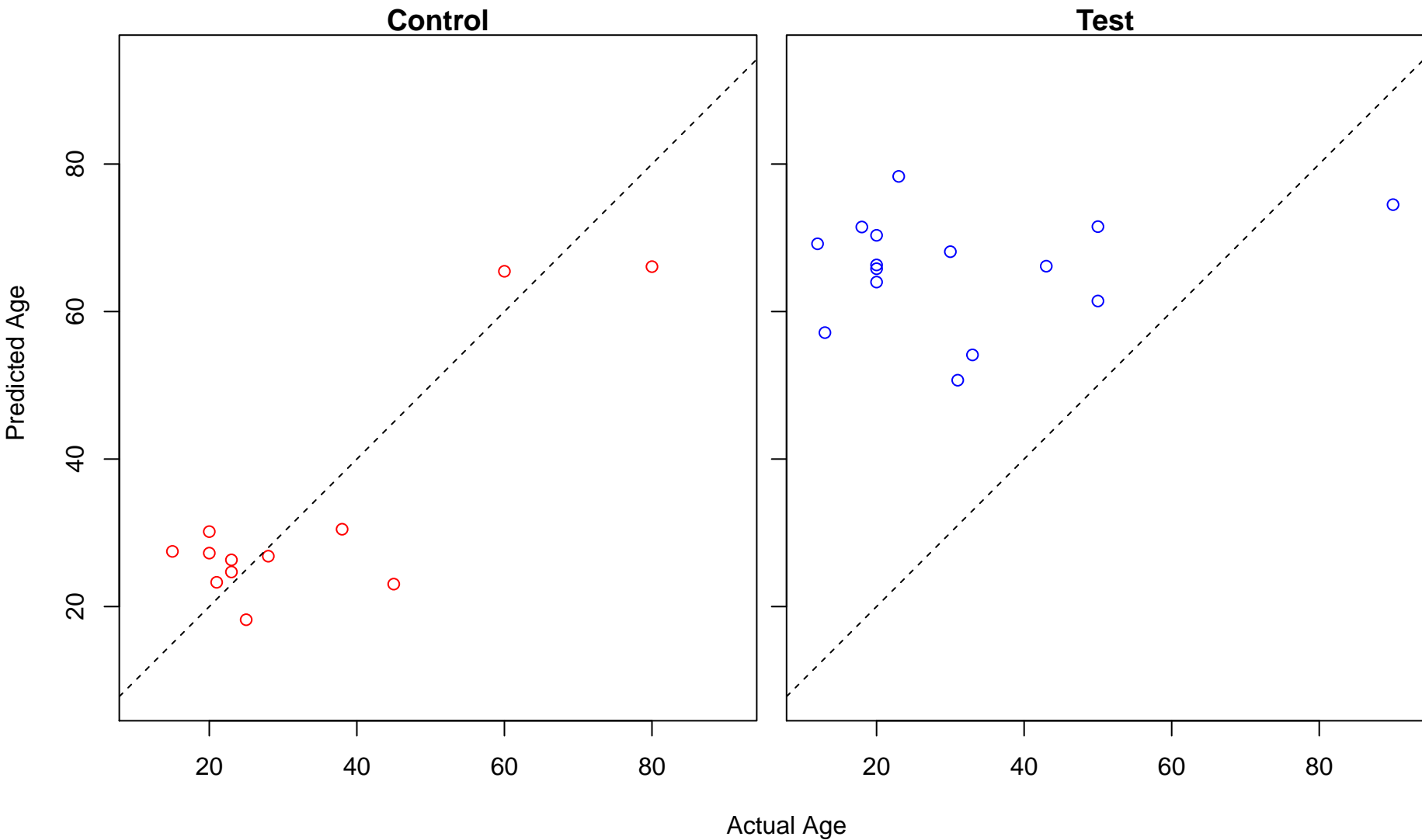
endosome to lysosome transport (Score: 5.719080)



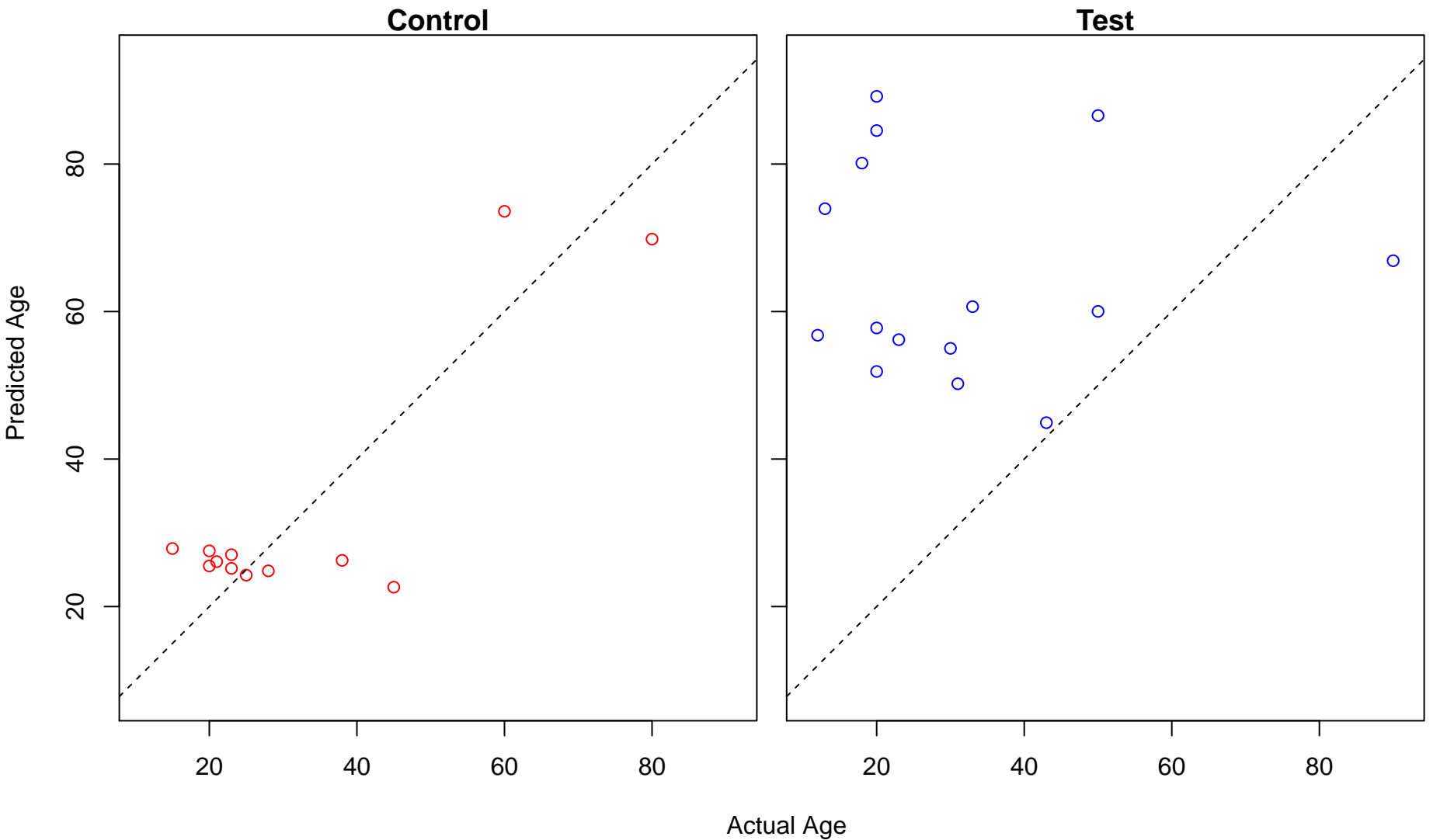
negative regulation of stress-activated MAPK cascade (Score: 5.718512)



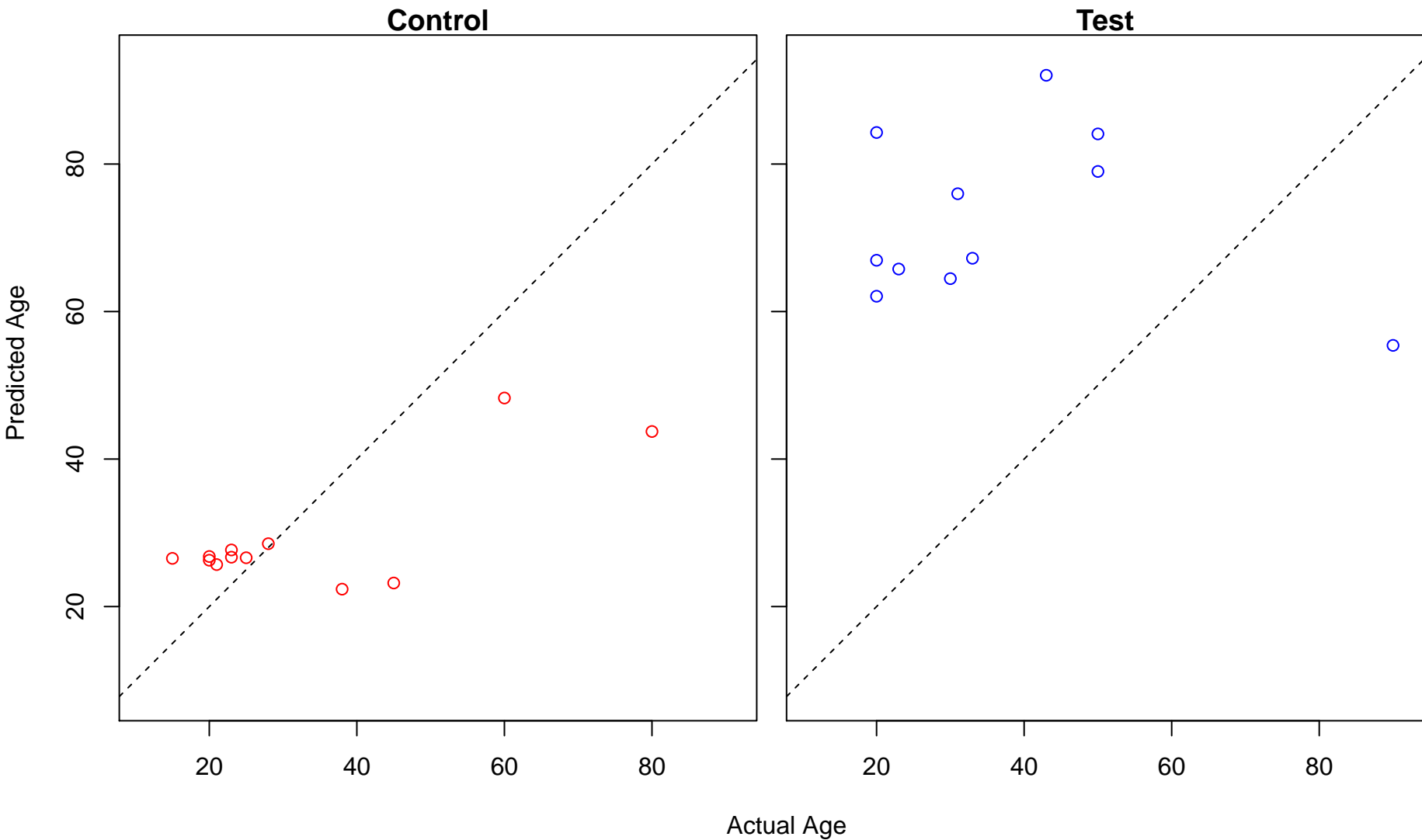
negative regulation of stress-activated protein kinase signaling cascade (Score: 5.718512)



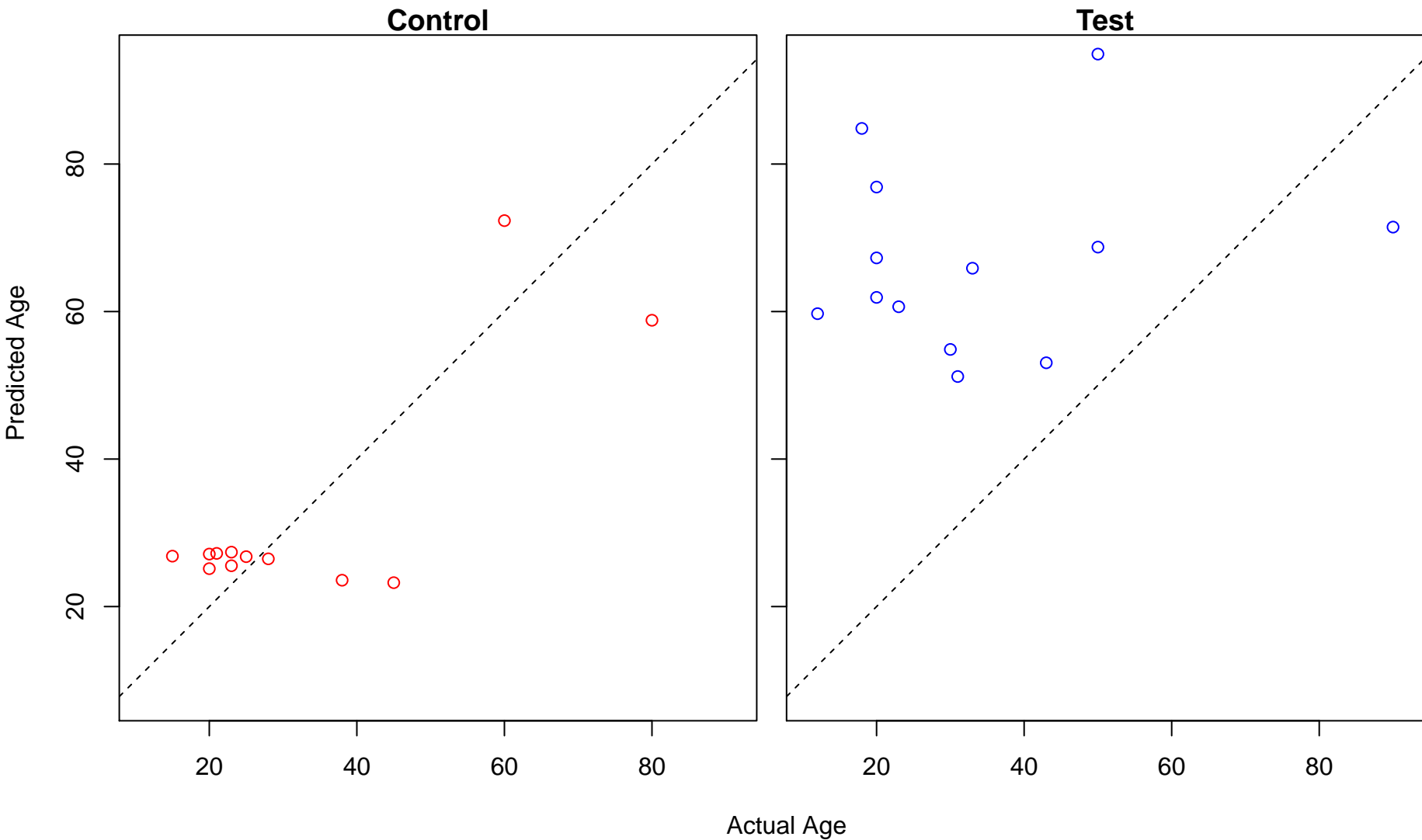
Positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score



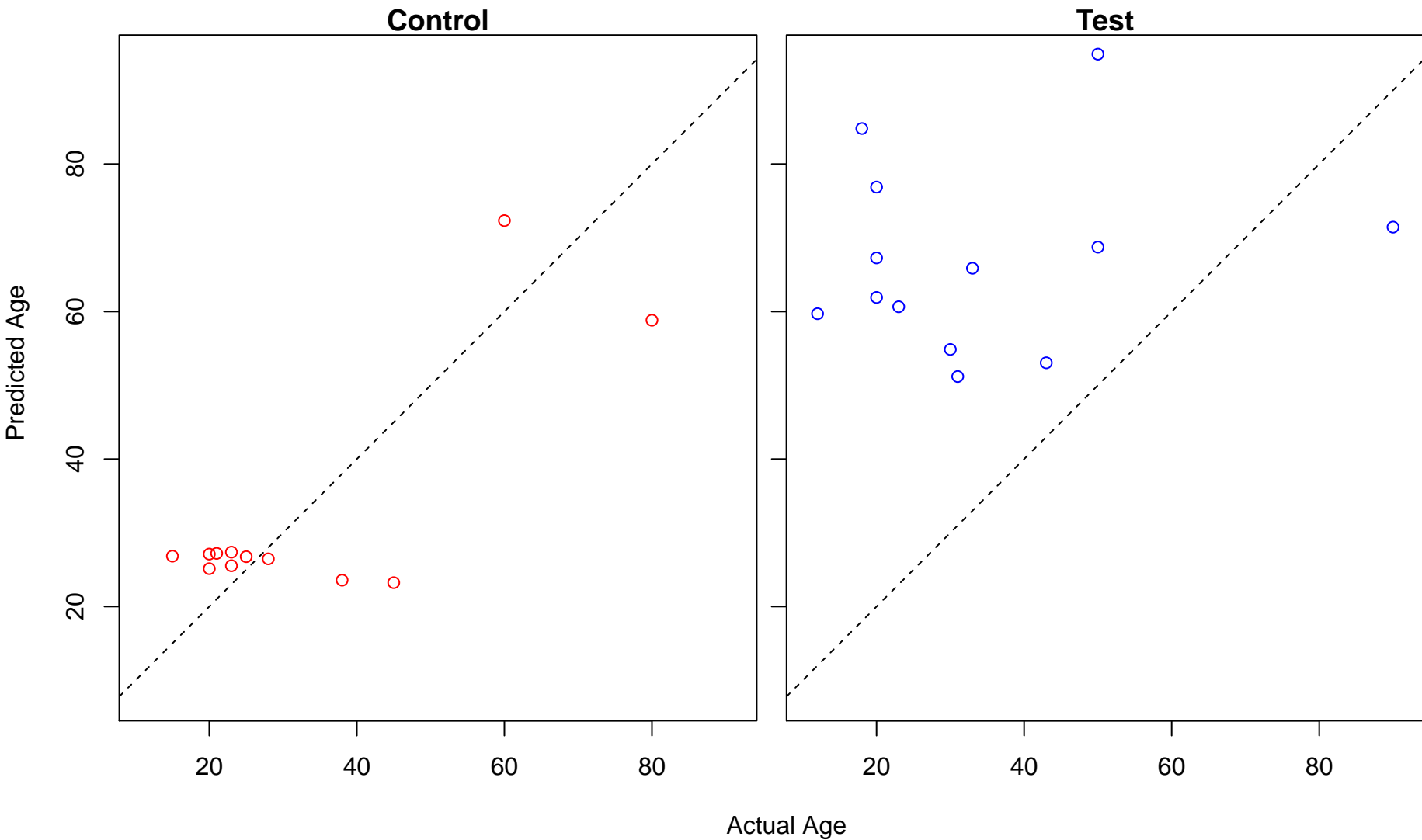
negative regulation of cardiac muscle cell apoptotic process (Score: 5.717469)



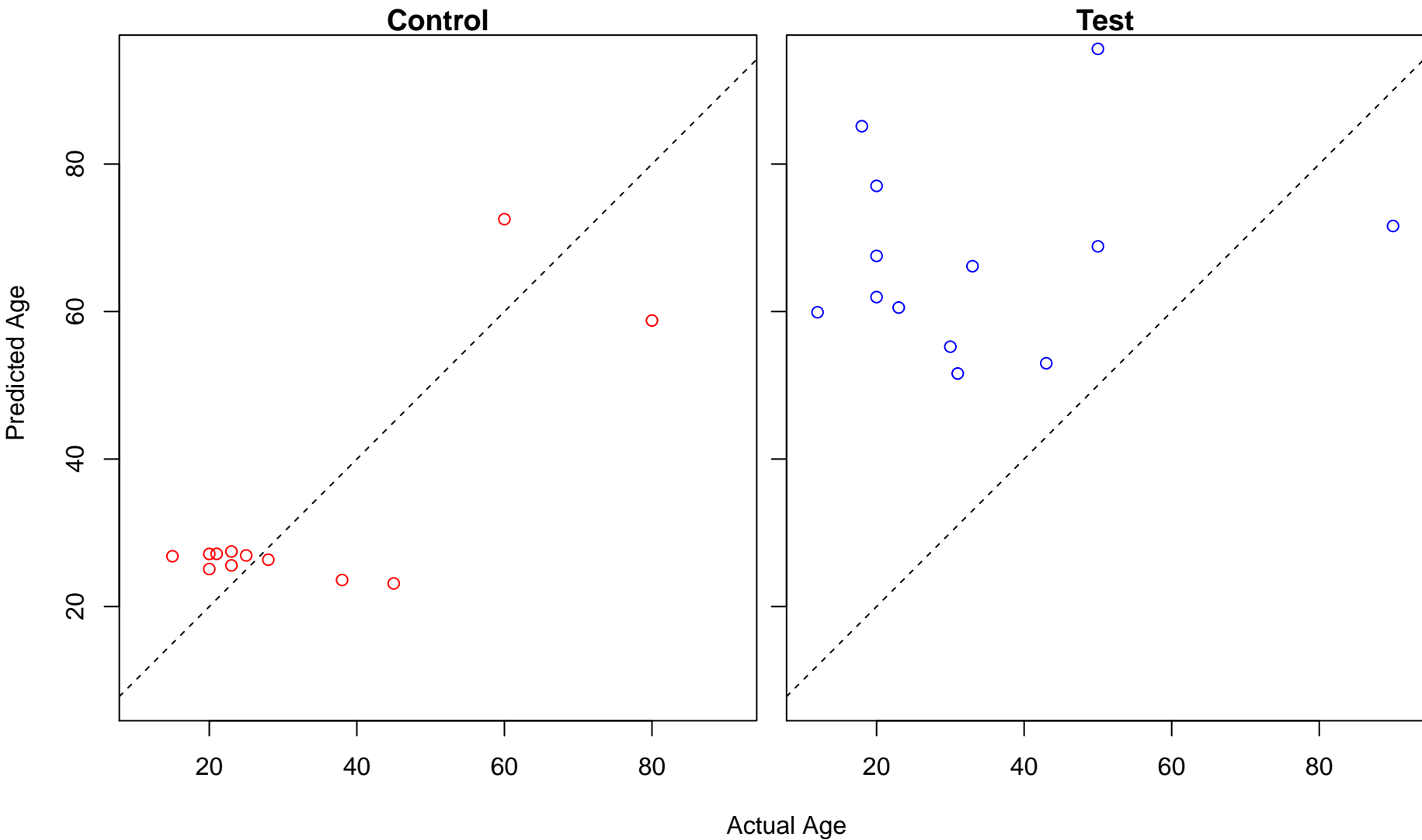
translational termination (Score: 5.716822)



cellular protein complex disassembly (Score: 5.716396)

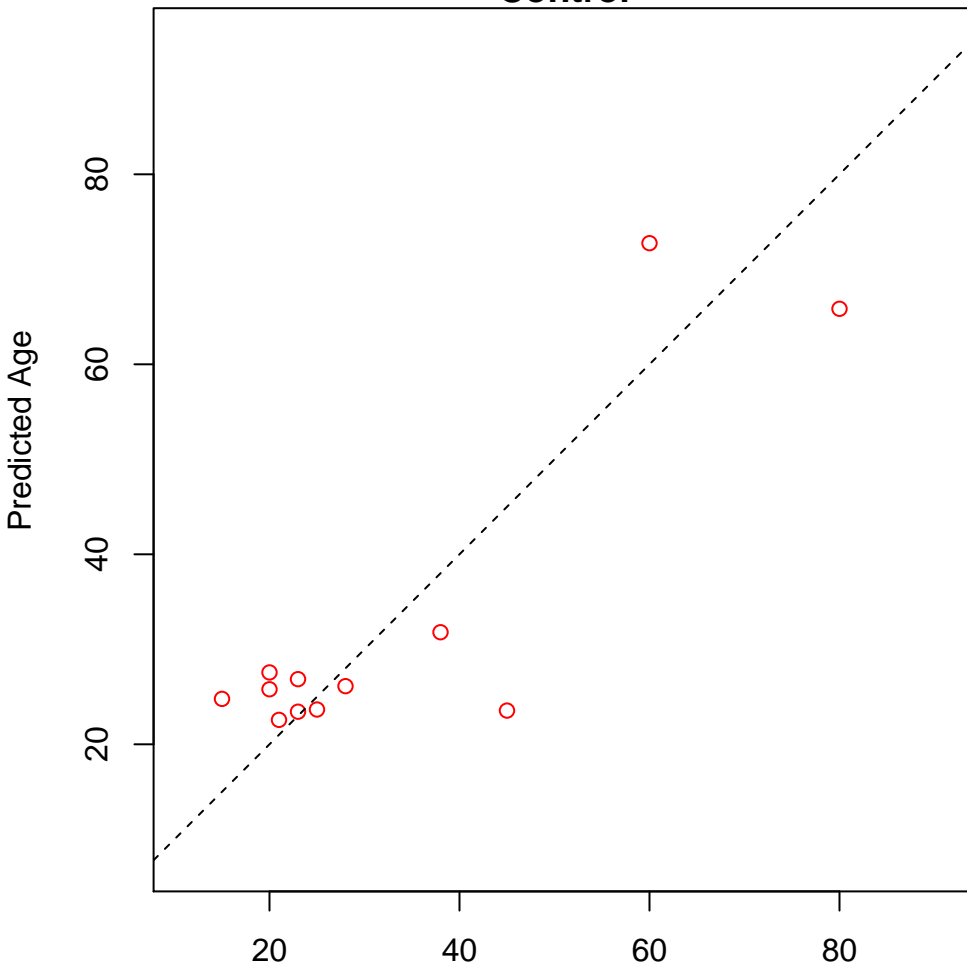


nuclear-transcribed mRNA catabolic process (Score: 5.715914)

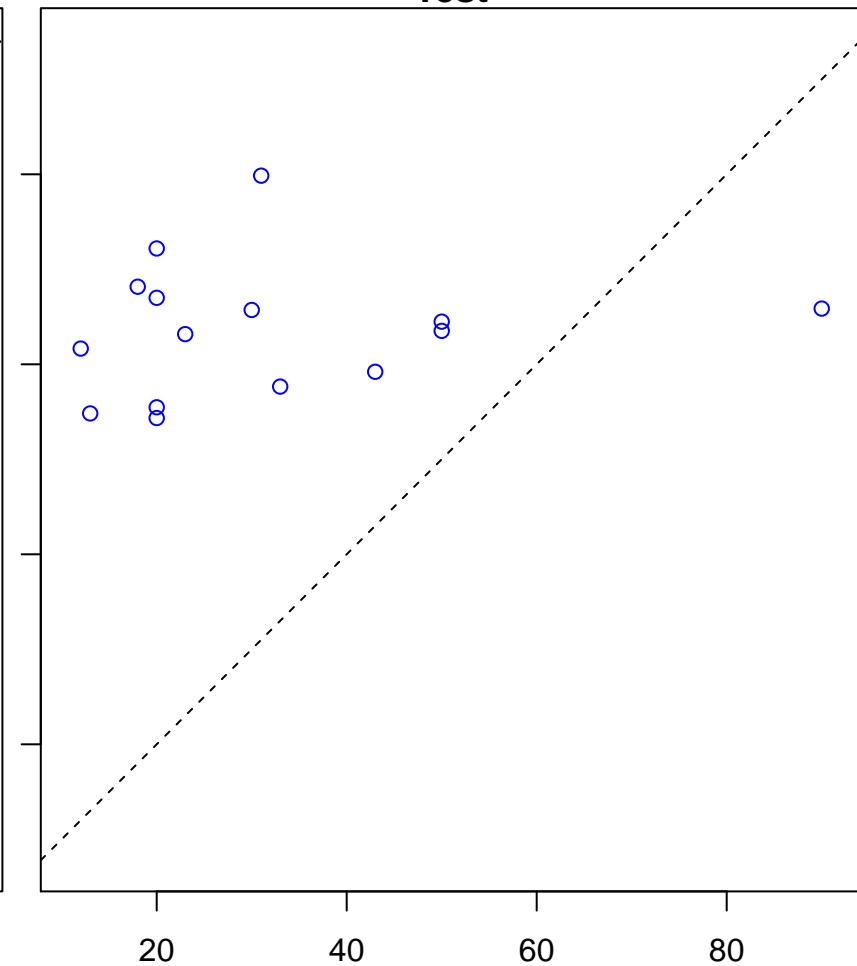


stress-induced premature senescence (Score: 5.714790)

Control

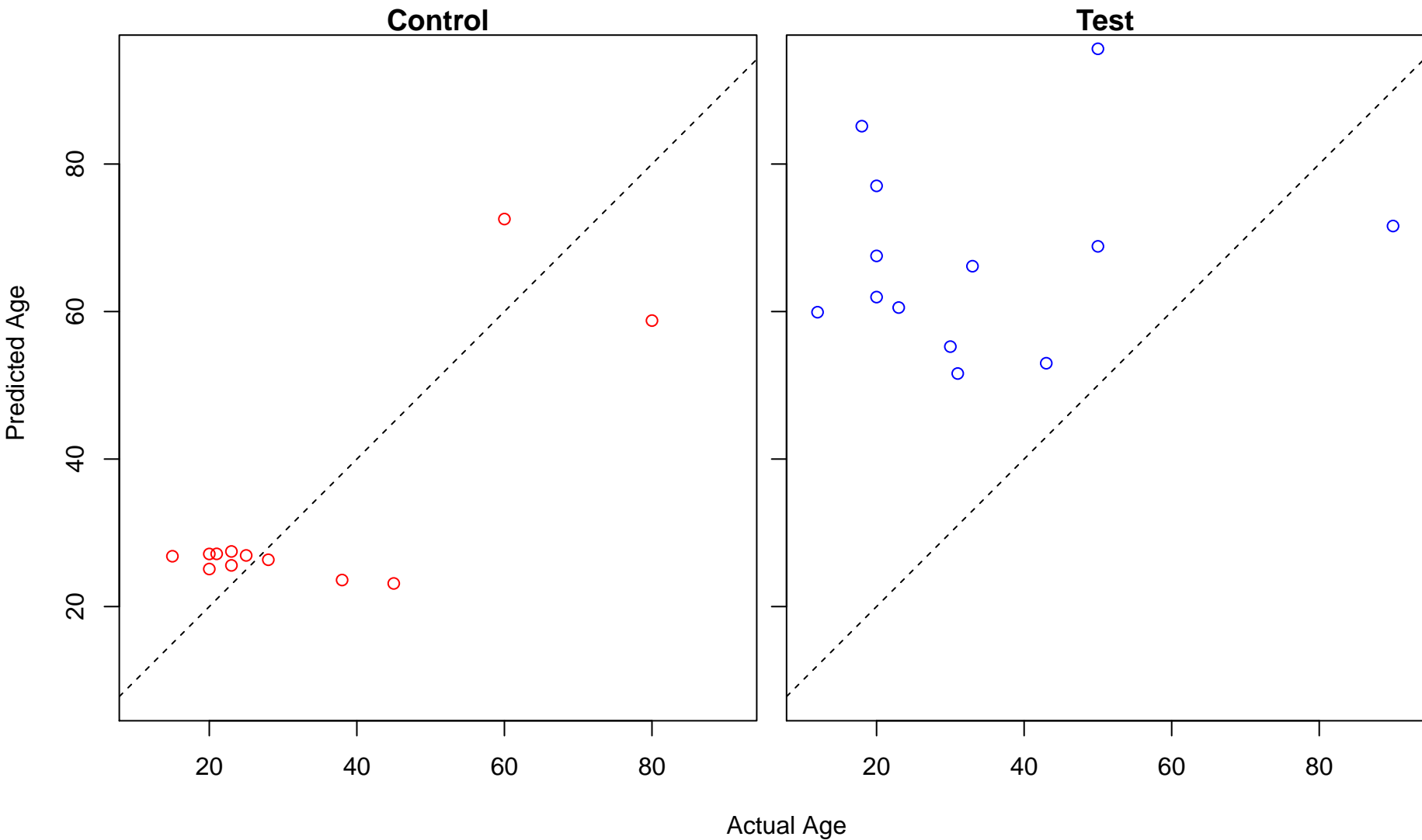


Test

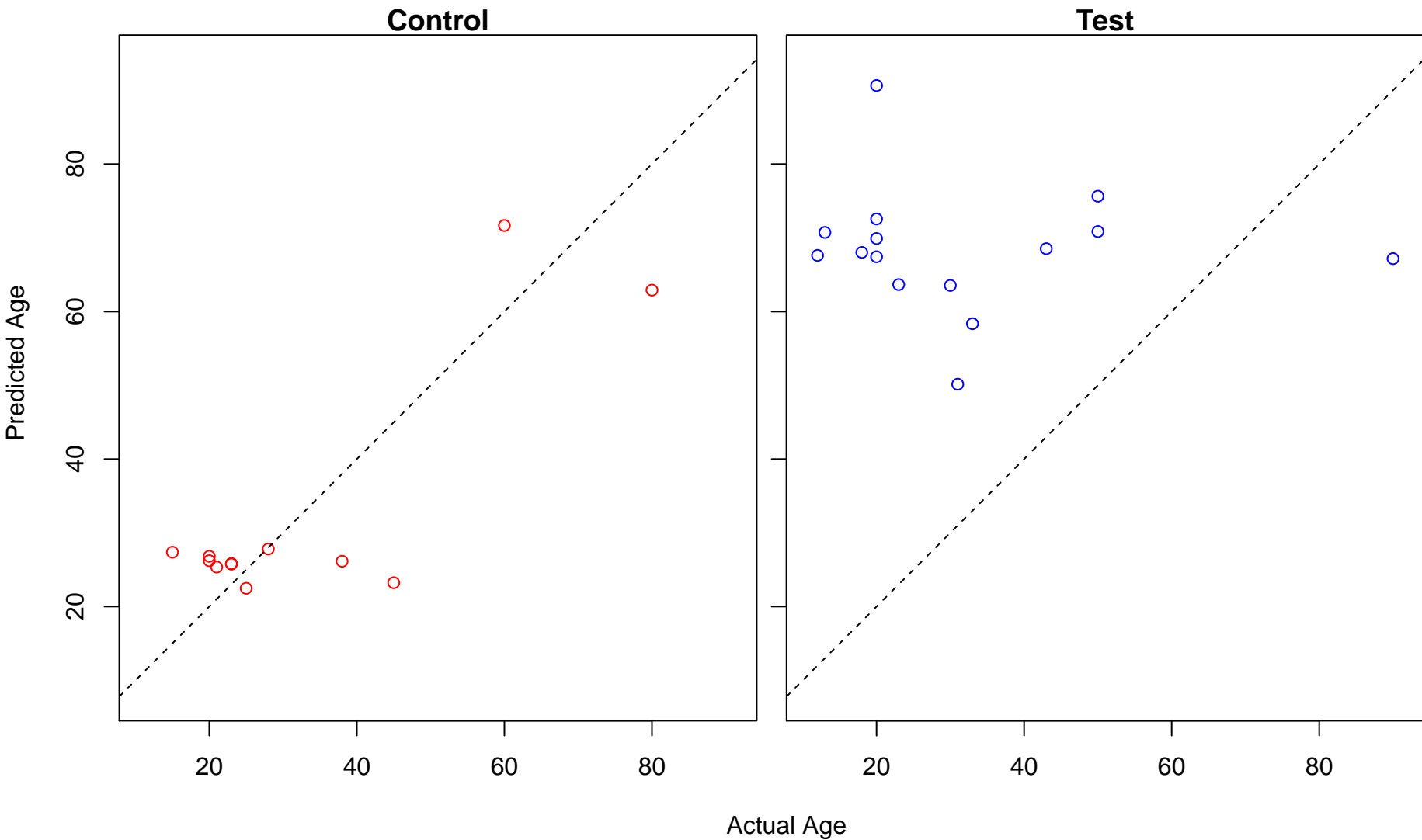


Actual Age

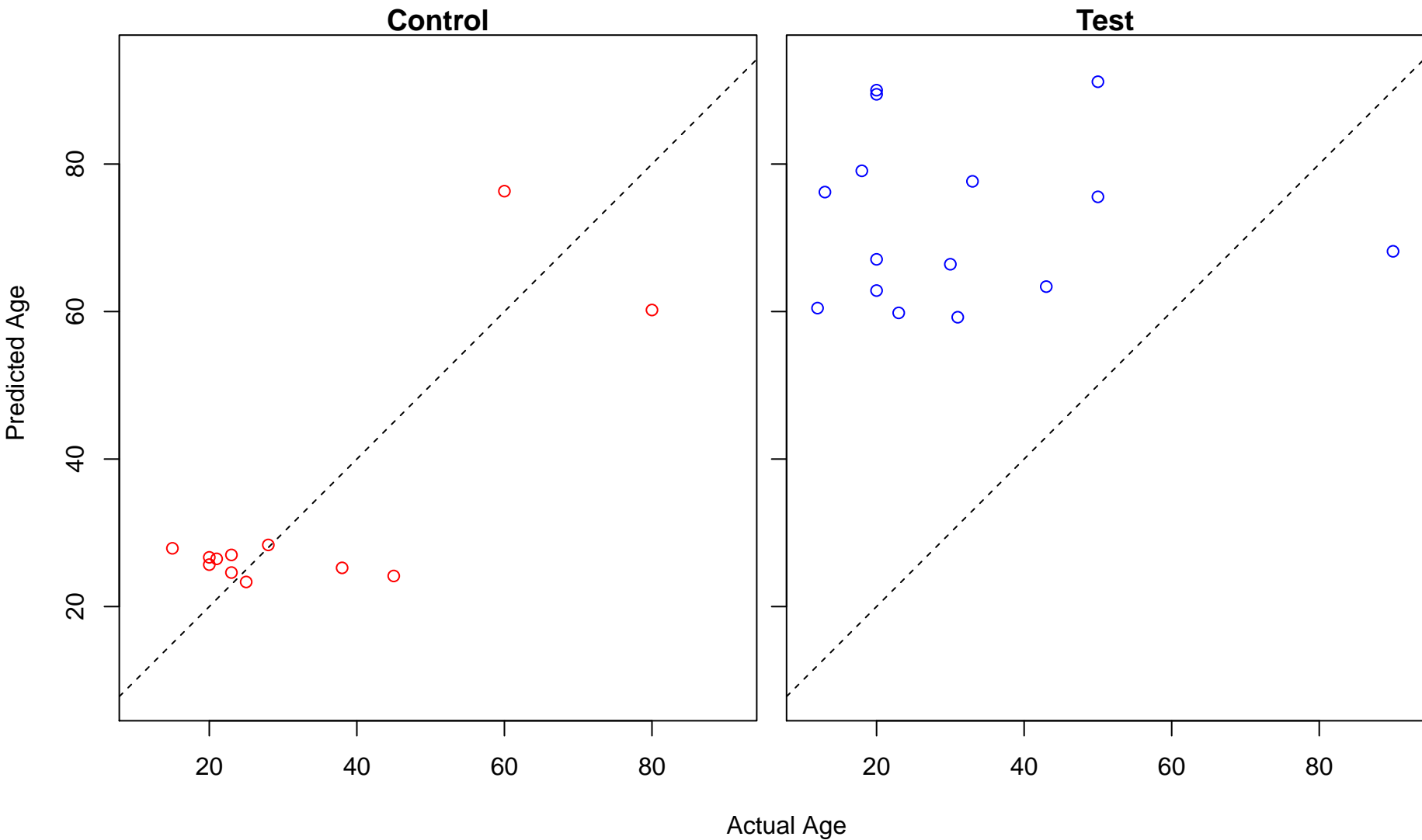
mRNA catabolic process (Score: 5.713345)



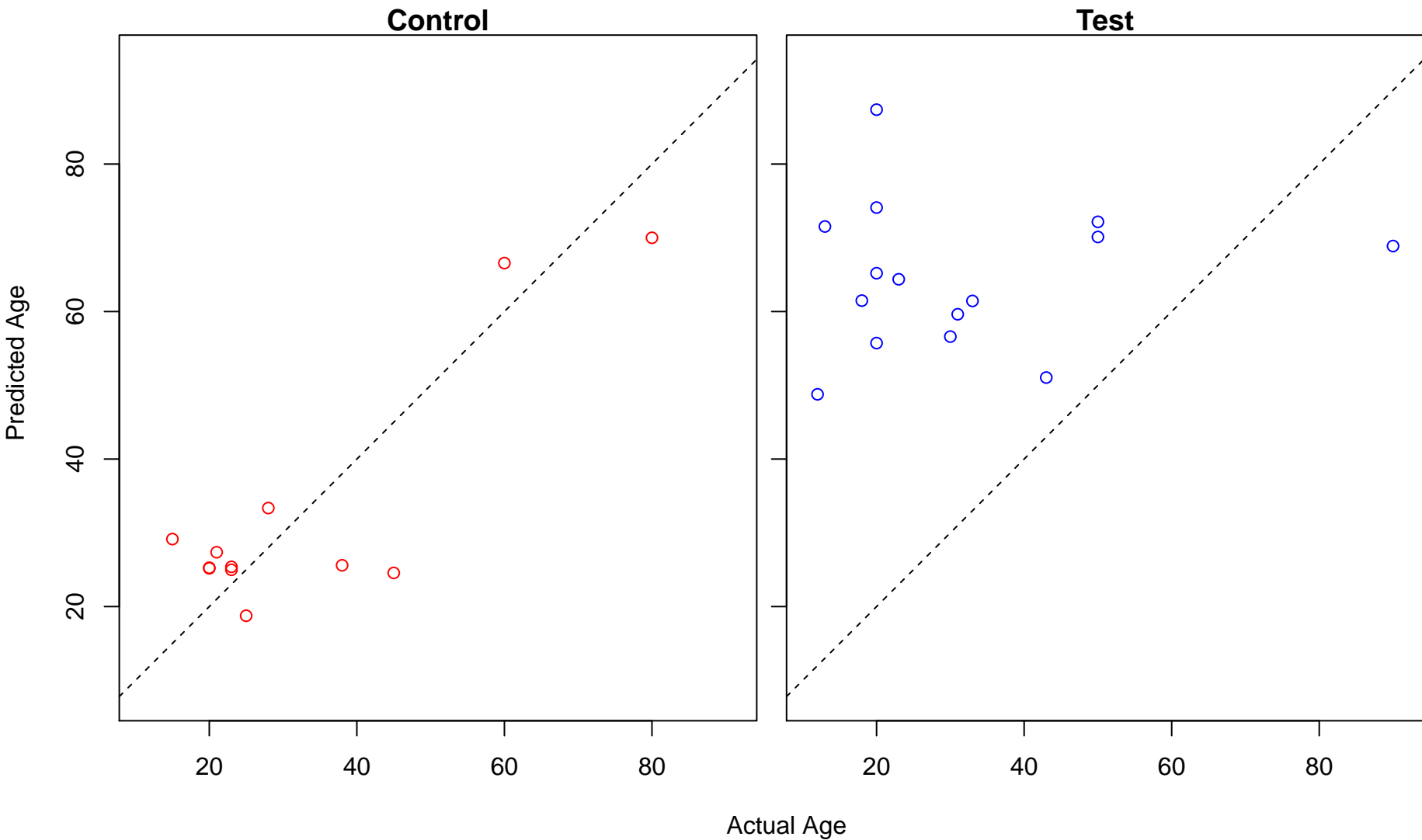
sulfur compound metabolic process (Score: 5.712690)



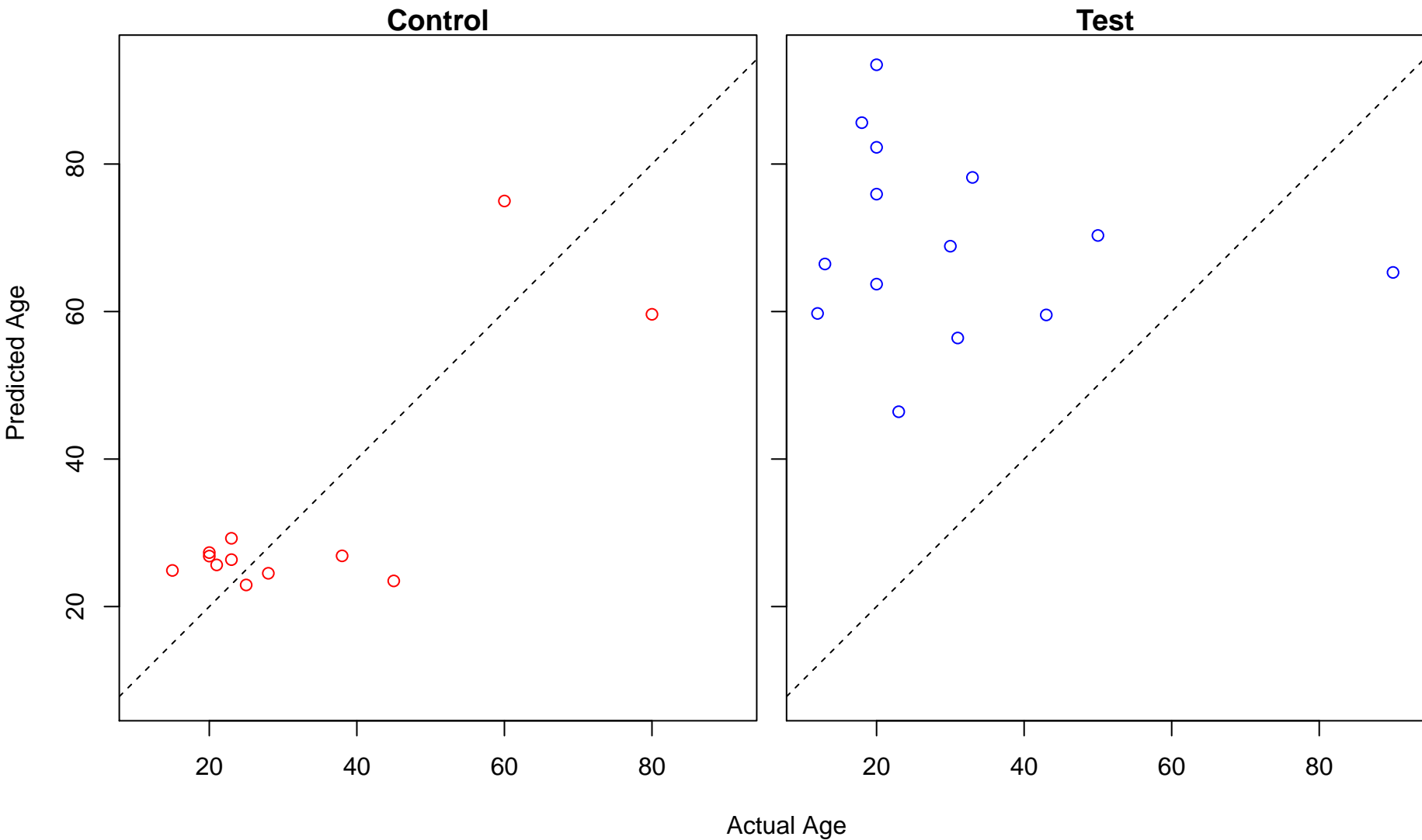
cell-substrate adhesion (Score: 5.712114)



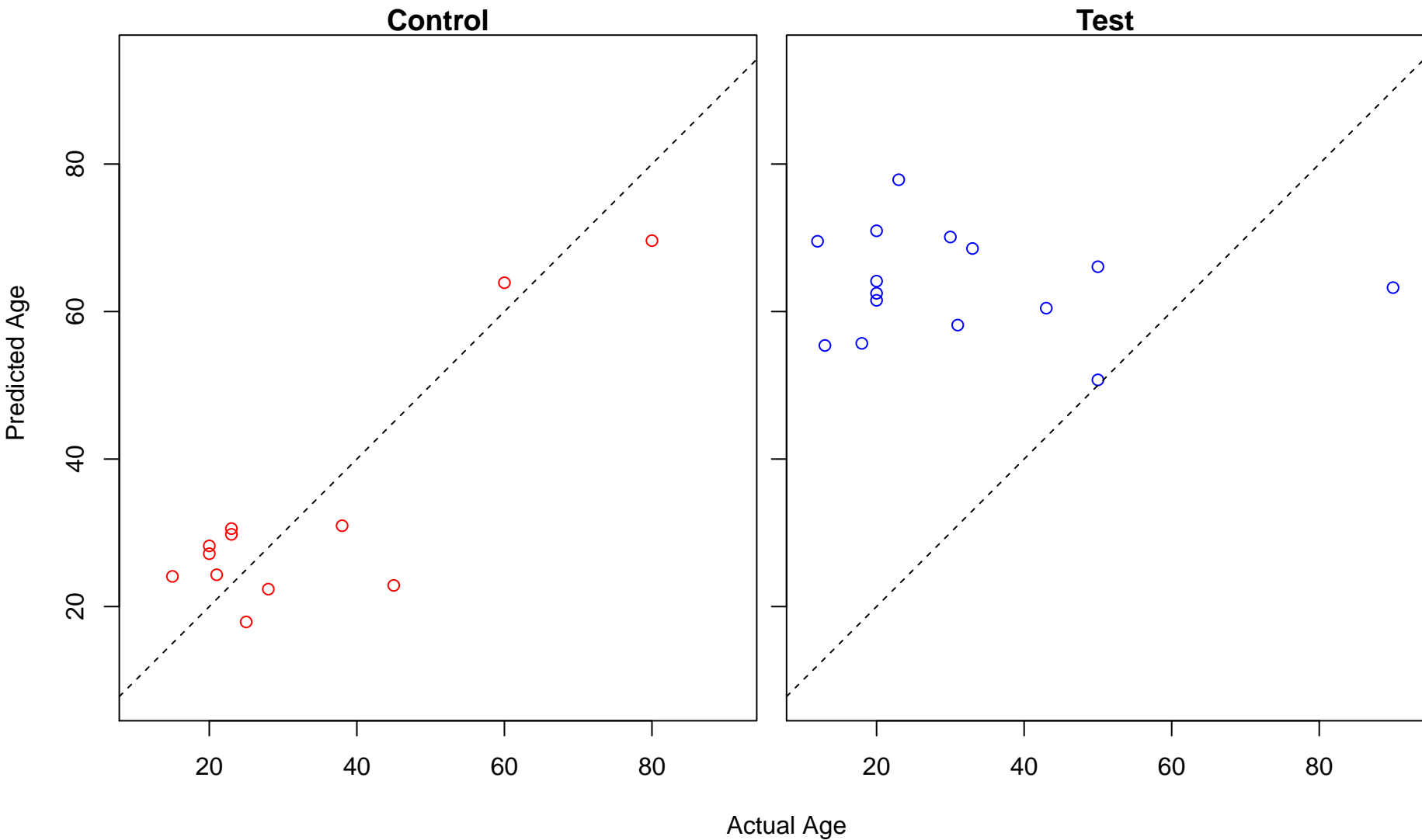
cellular response to radiation (Score: 5.710475)



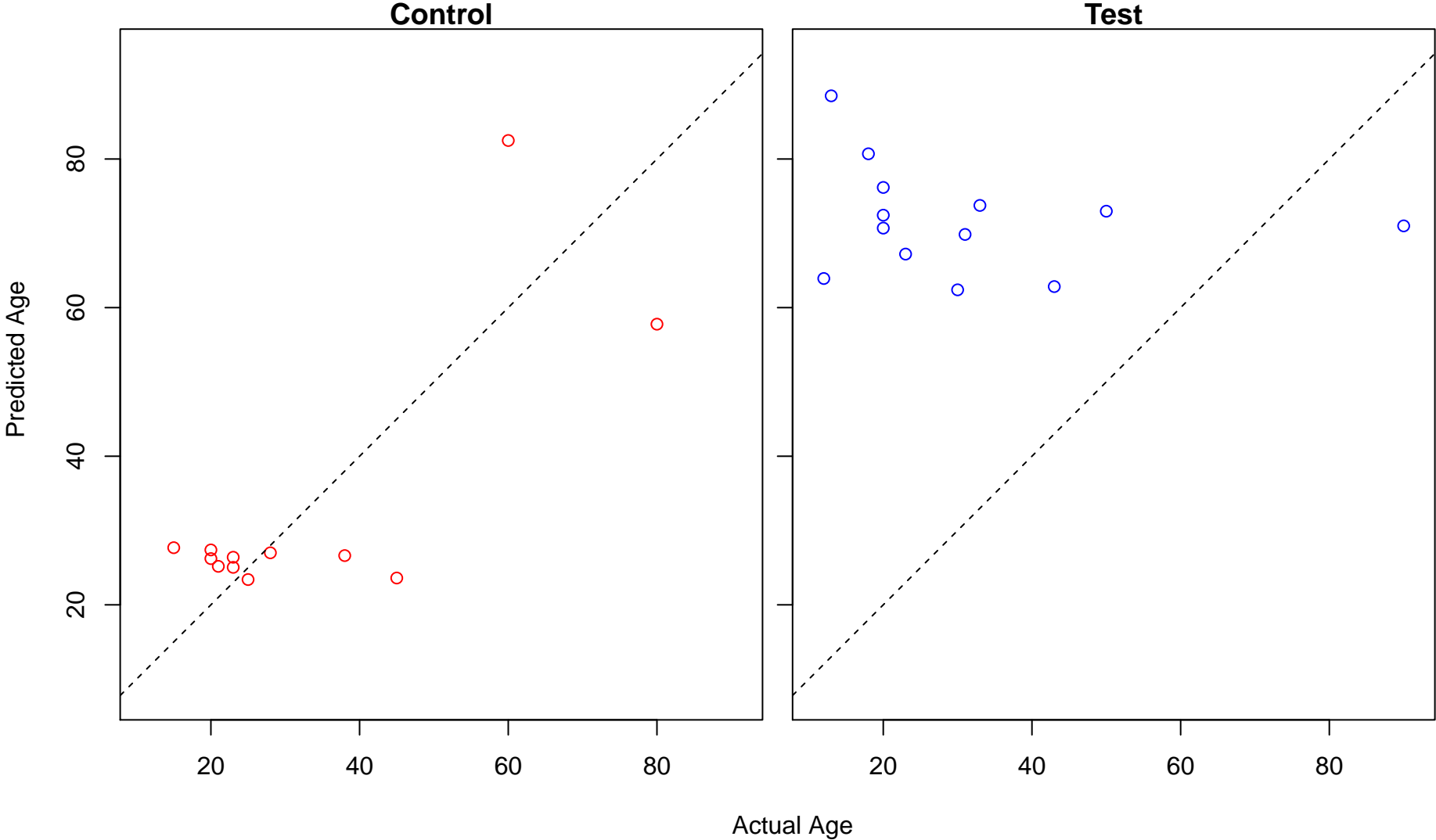
positive regulation of lamellipodium morphogenesis (Score: 5.710464)



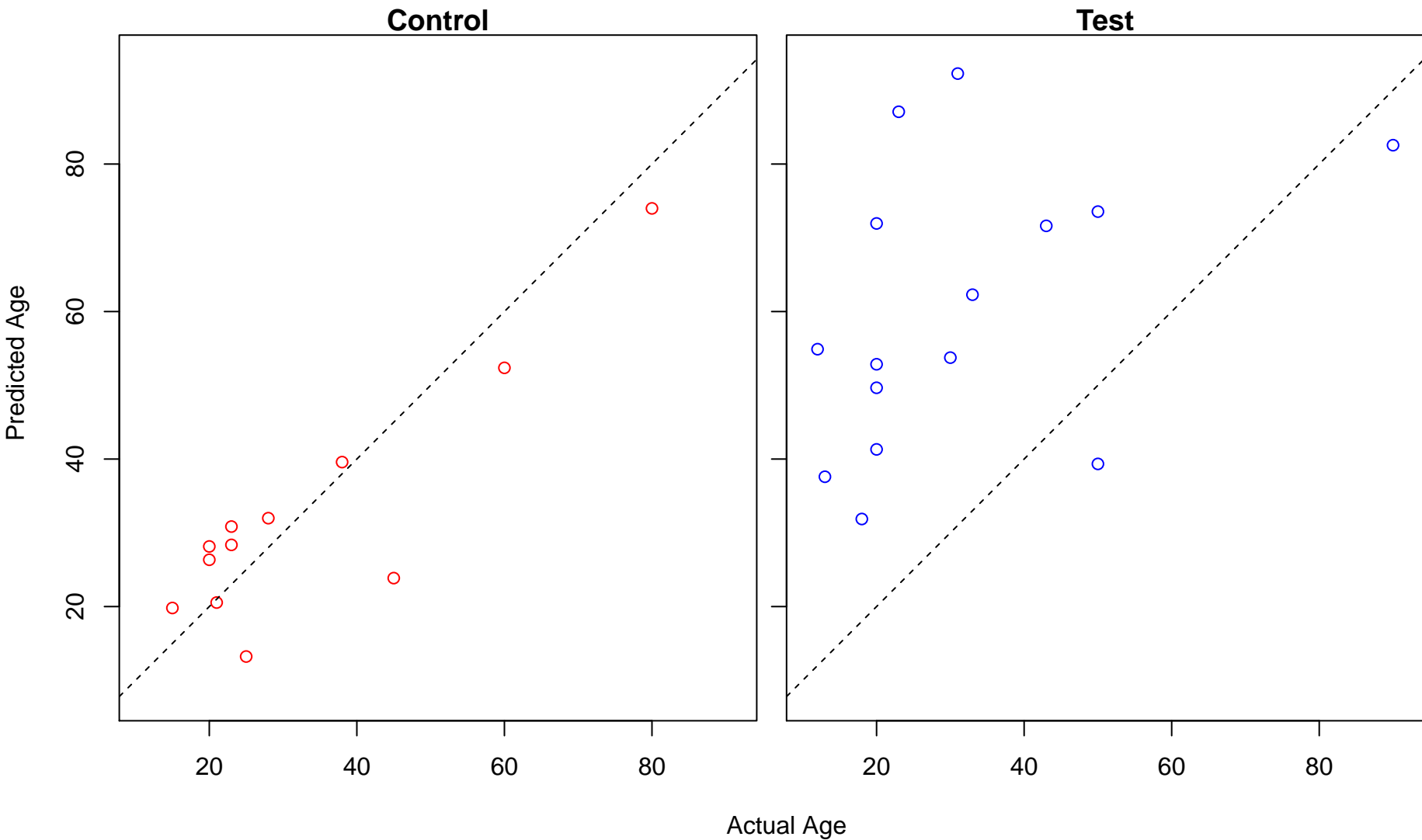
female meiotic division (Score: 5.709277)



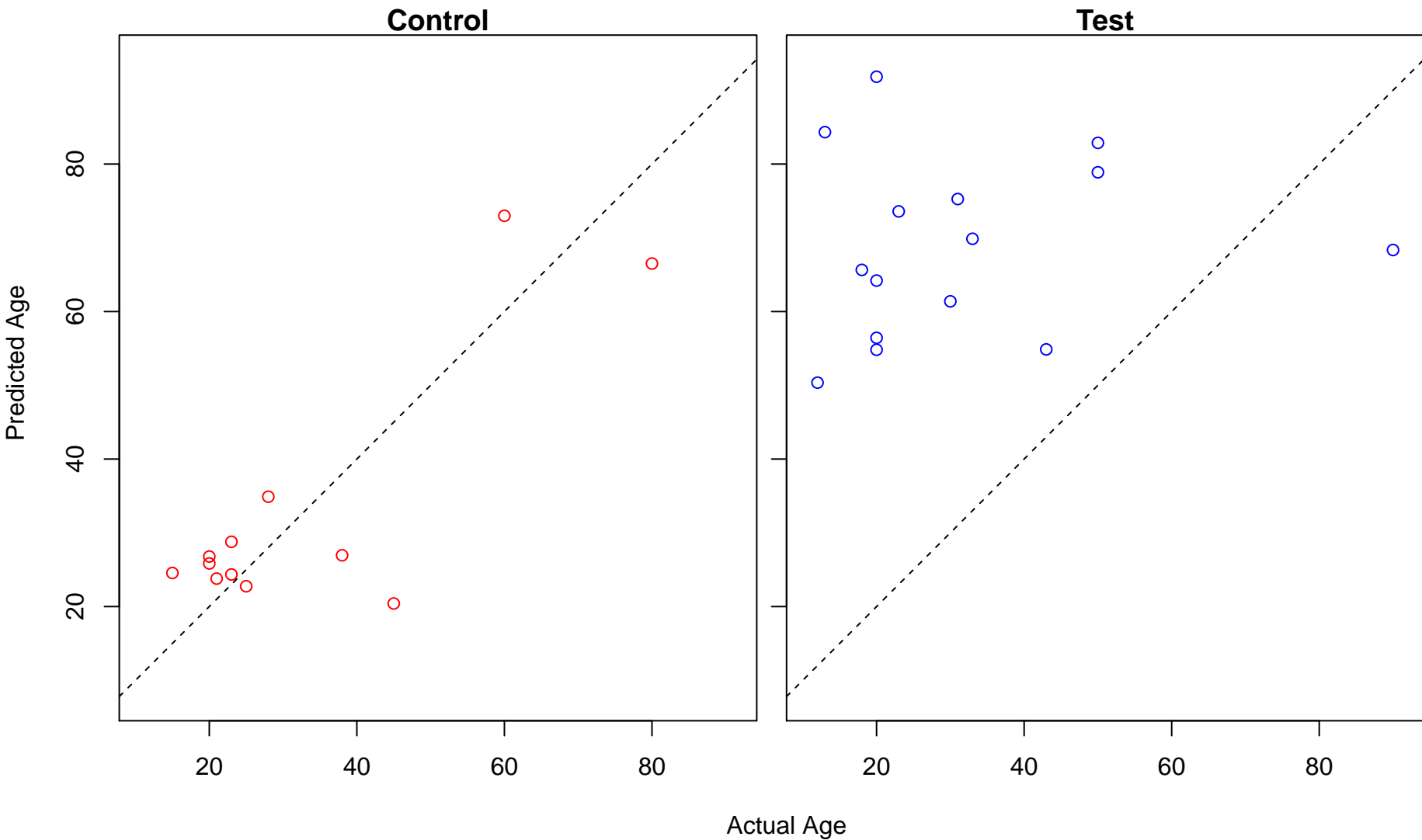
regulation of tumor necrosis factor-mediated signaling pathway (Score: 5.703207)



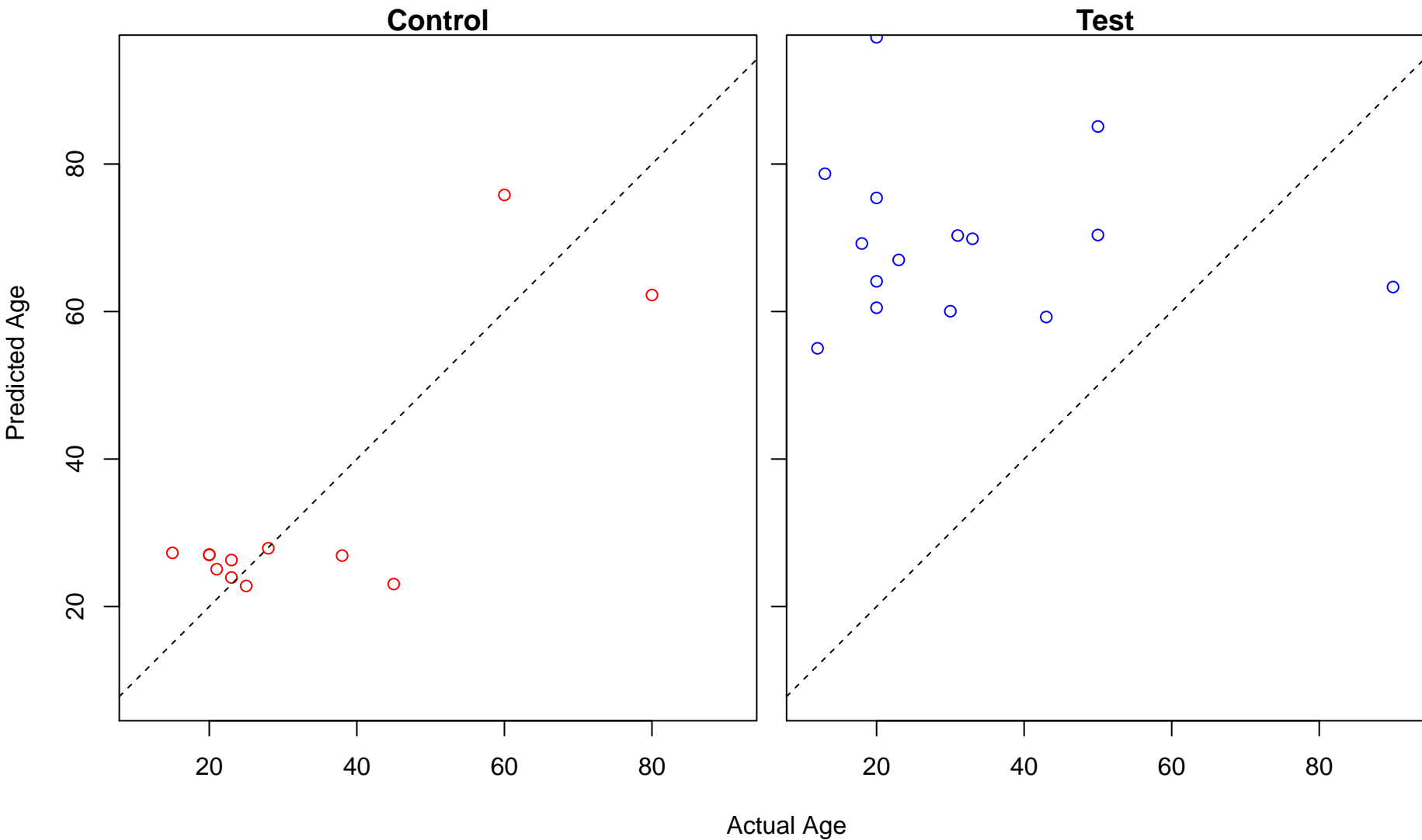
regulation of cilium beat frequency (Score: 5.696301)



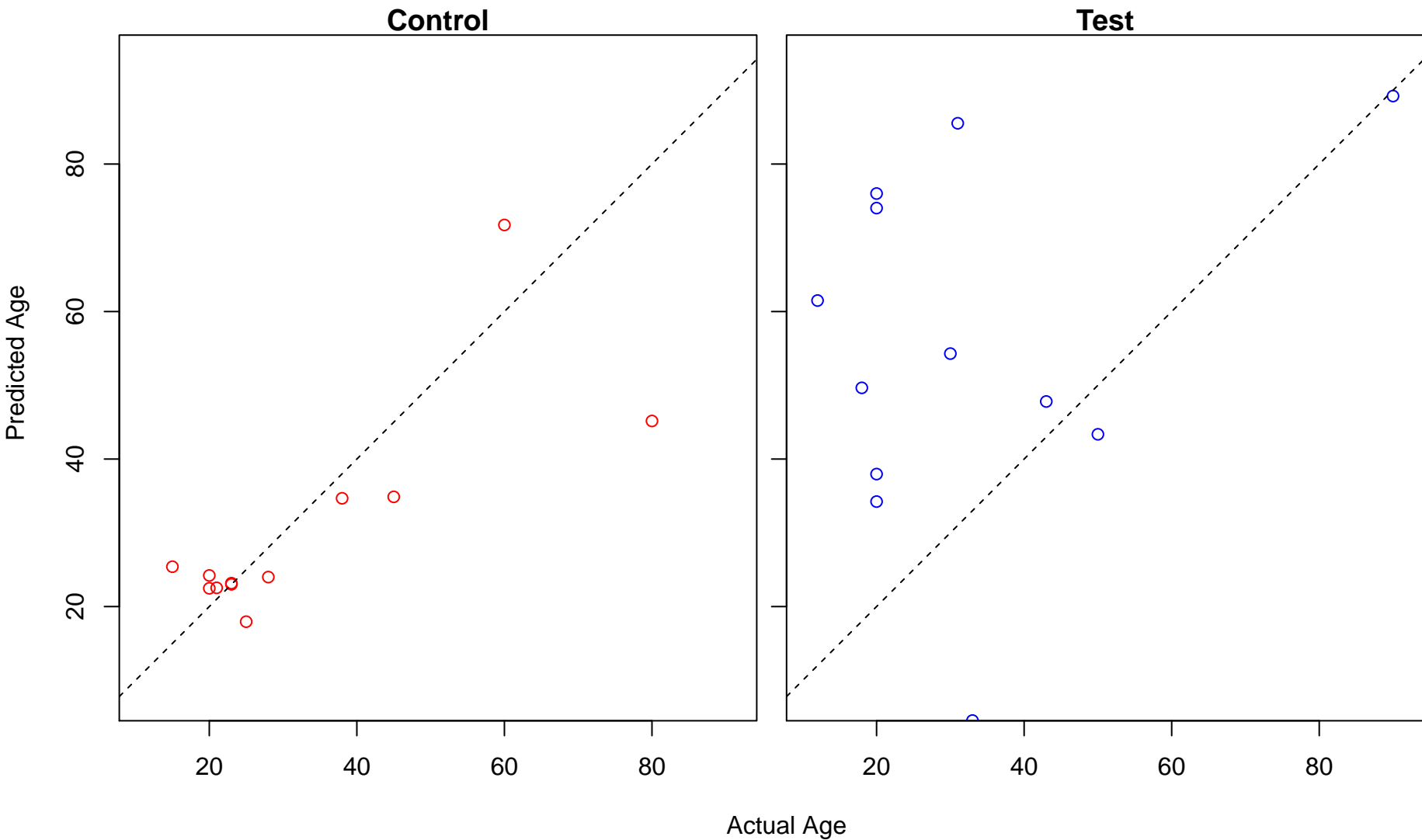
positive regulation of peptidyl-tyrosine phosphorylation (Score: 5.695011)



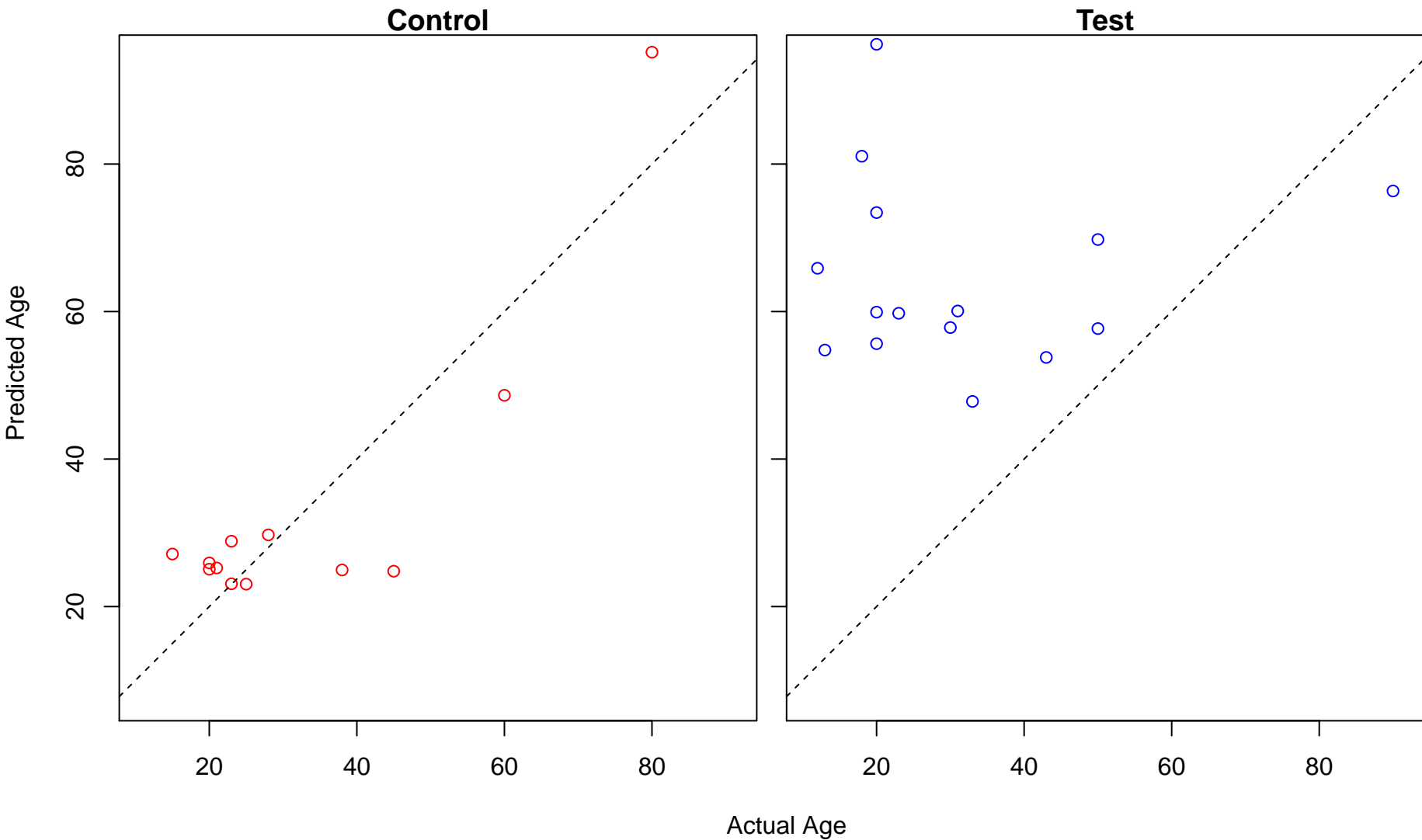
cell division (Score: 5.694294)



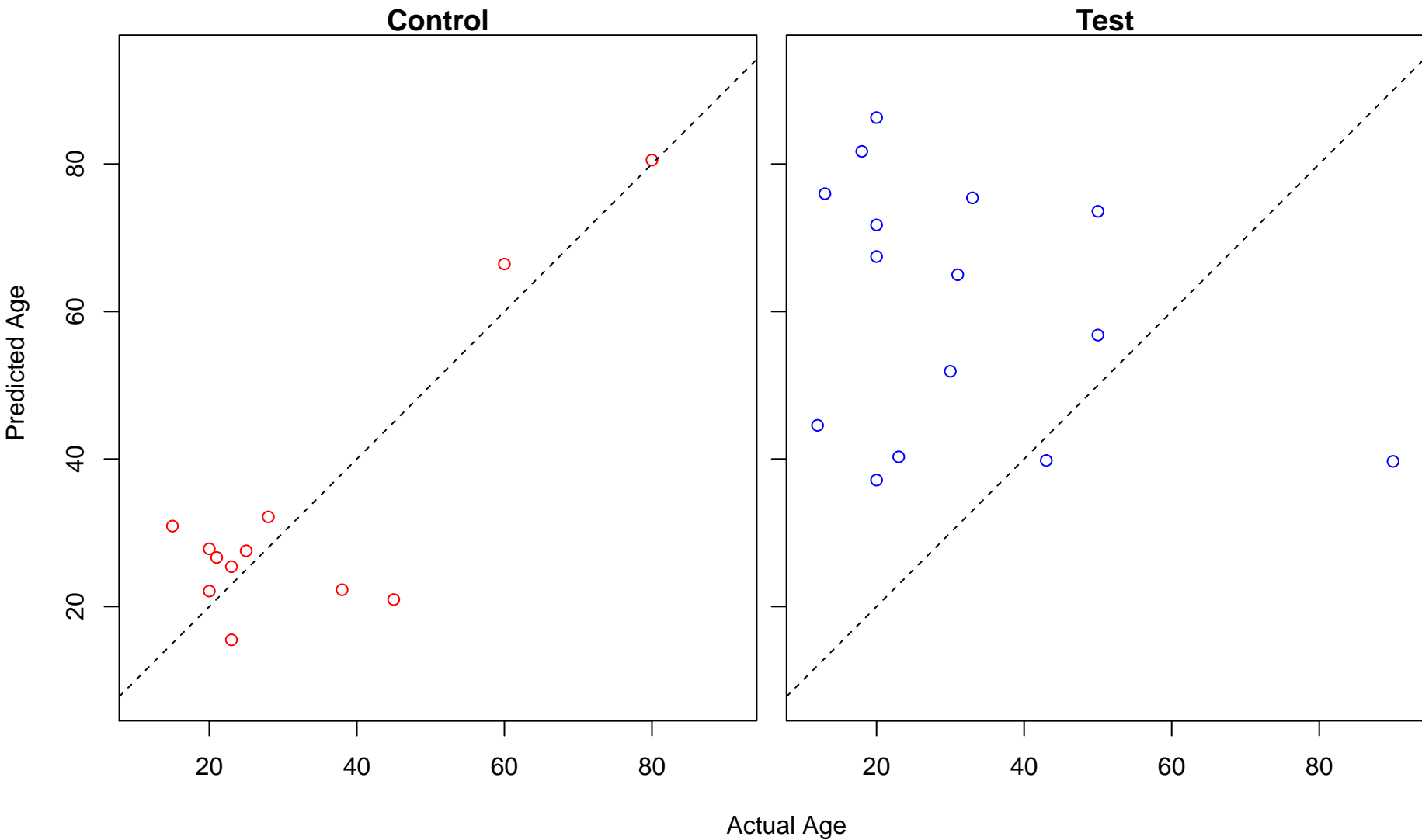
histone H4 acetylation (Score: 5.691490)



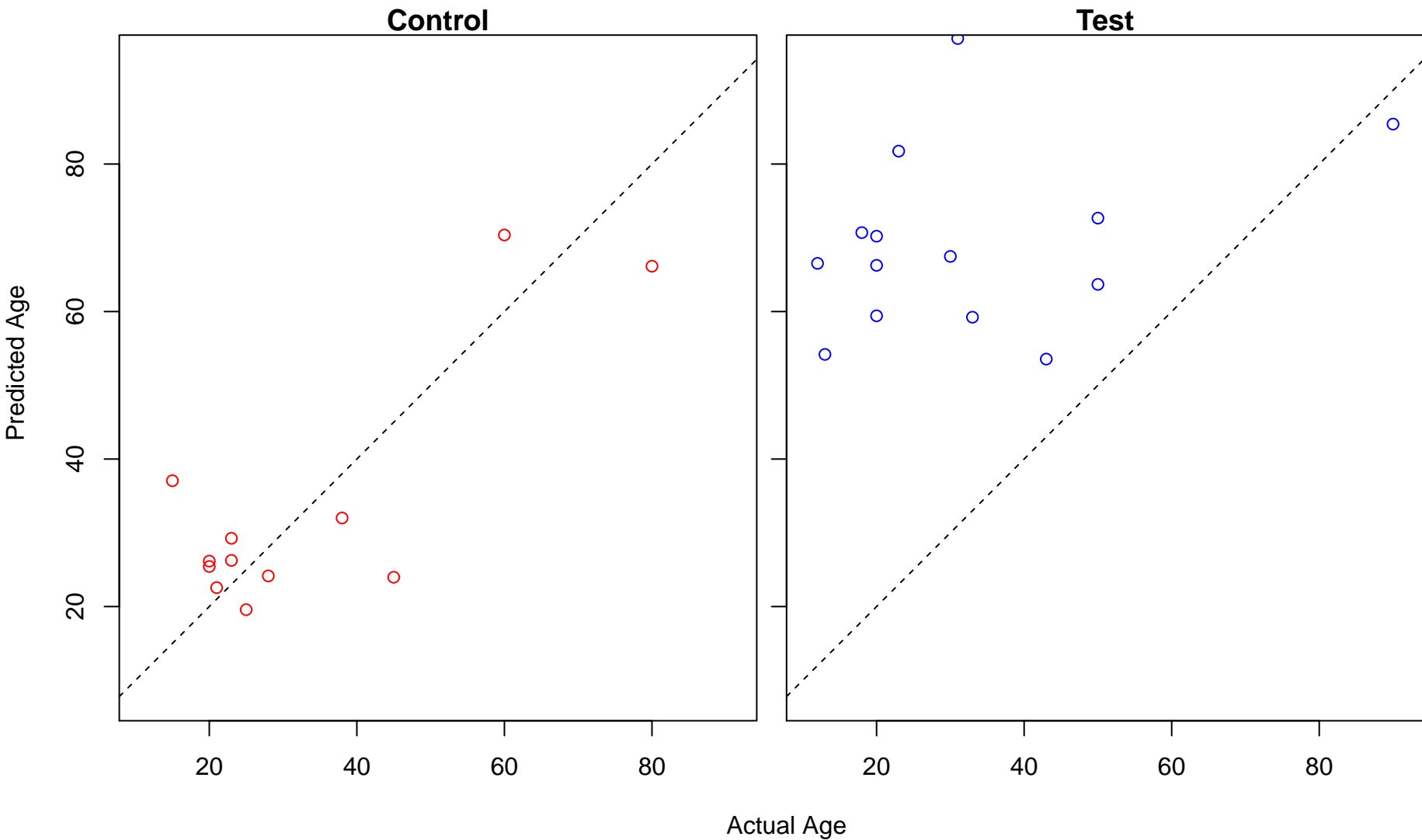
regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 5.691)



regulation of phospholipase activity (Score: 5.683979)

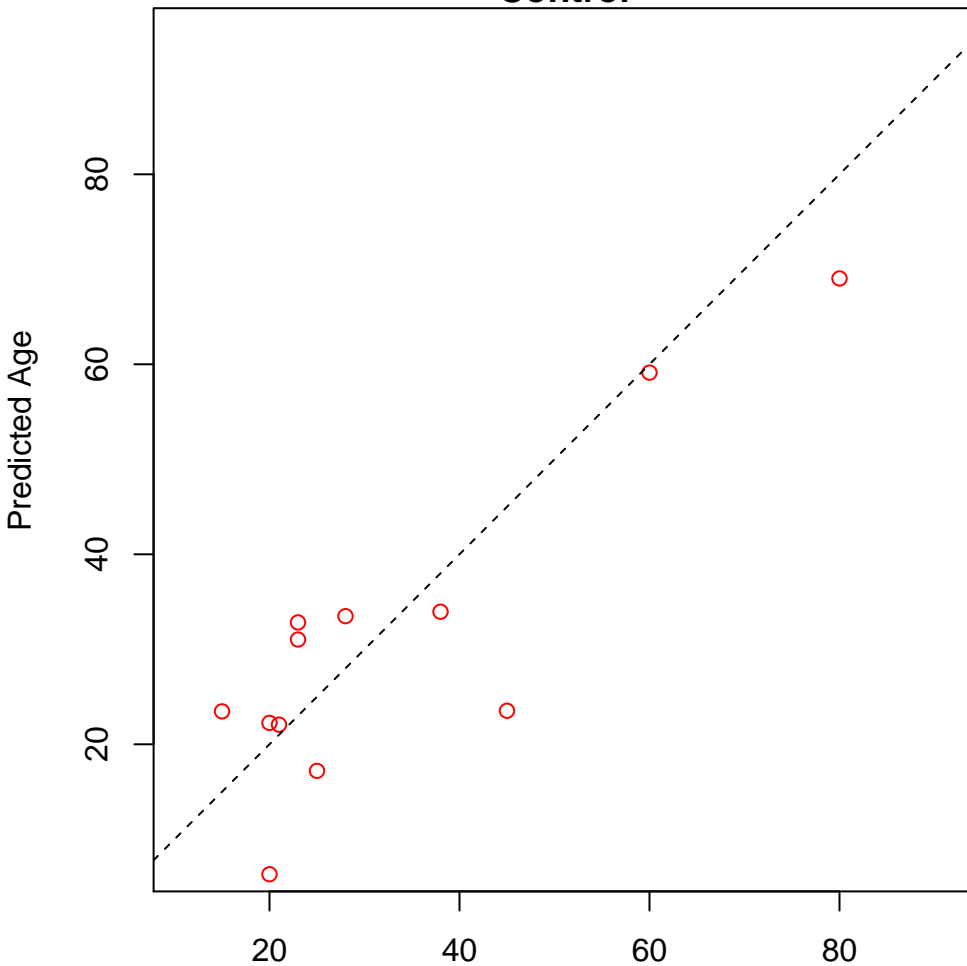


regulation of cytokine production involved in inflammatory response (Score: 5.683472)

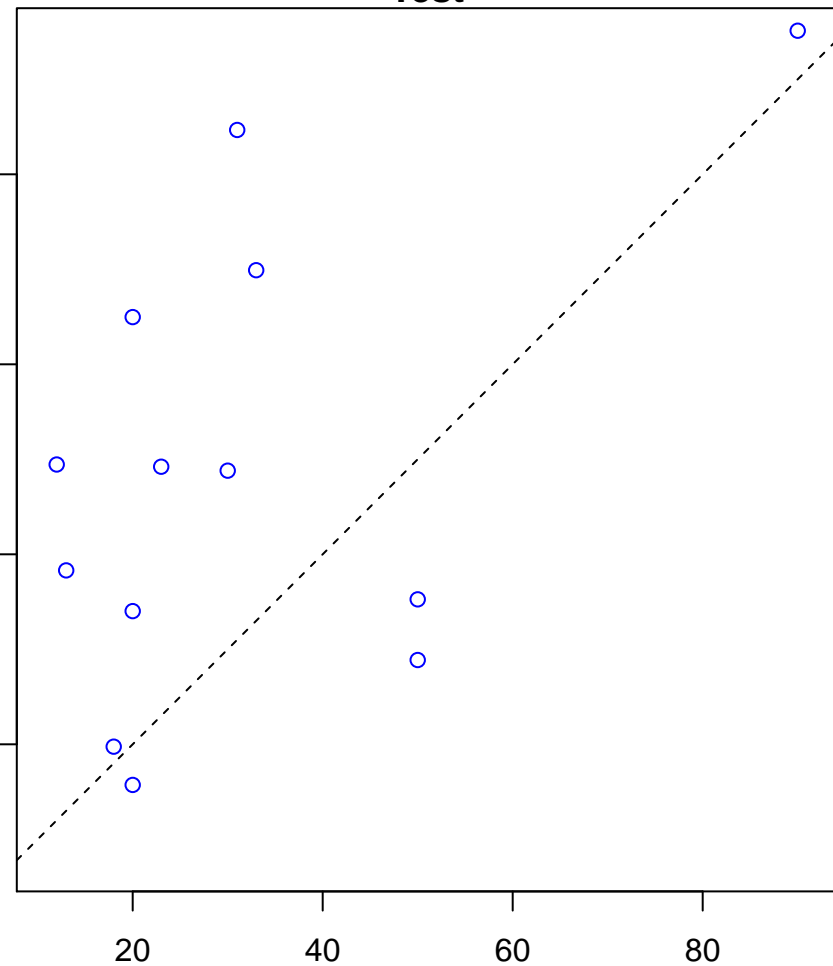


regulation of interleukin-12 secretion (Score: 5.681923)

Control

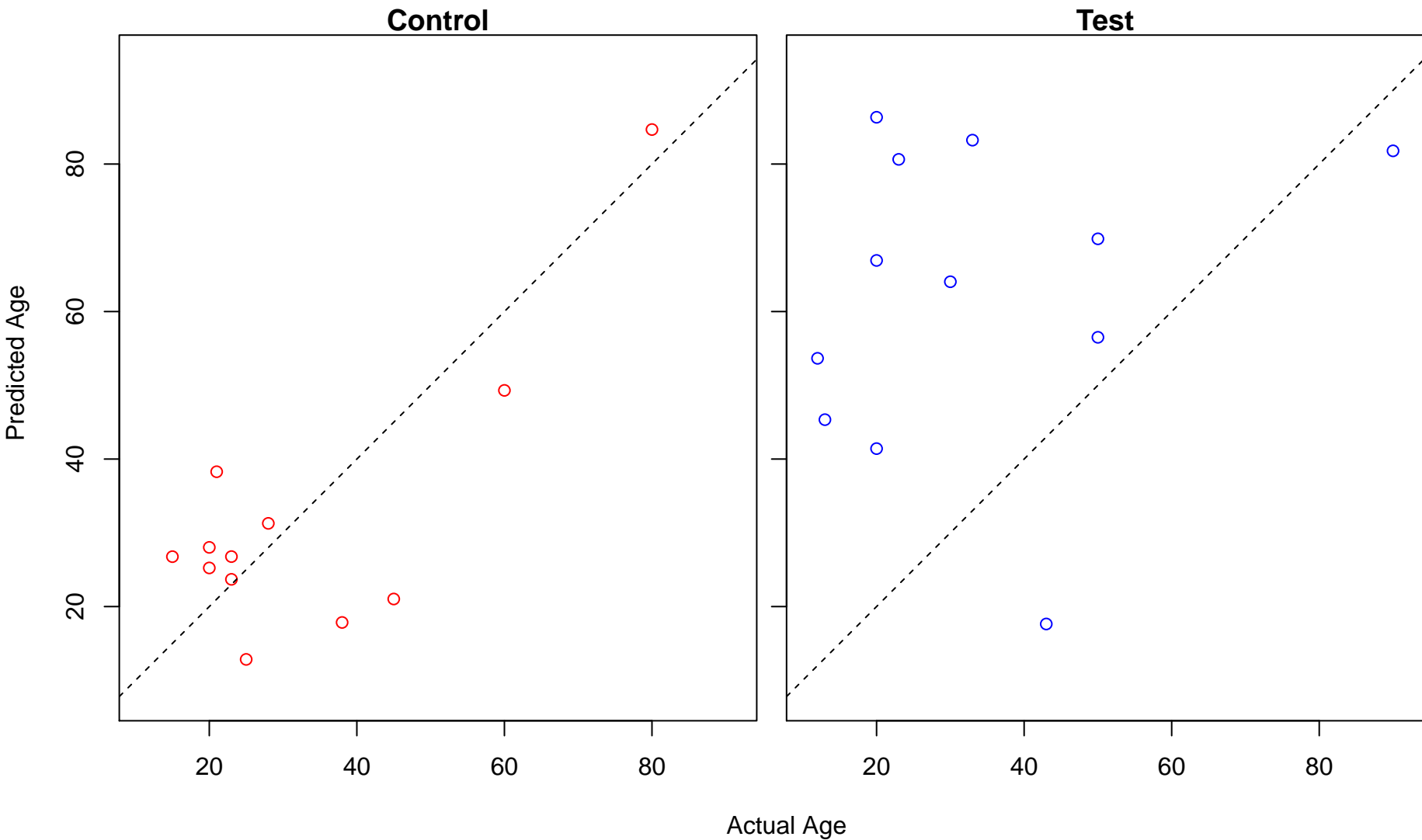


Test

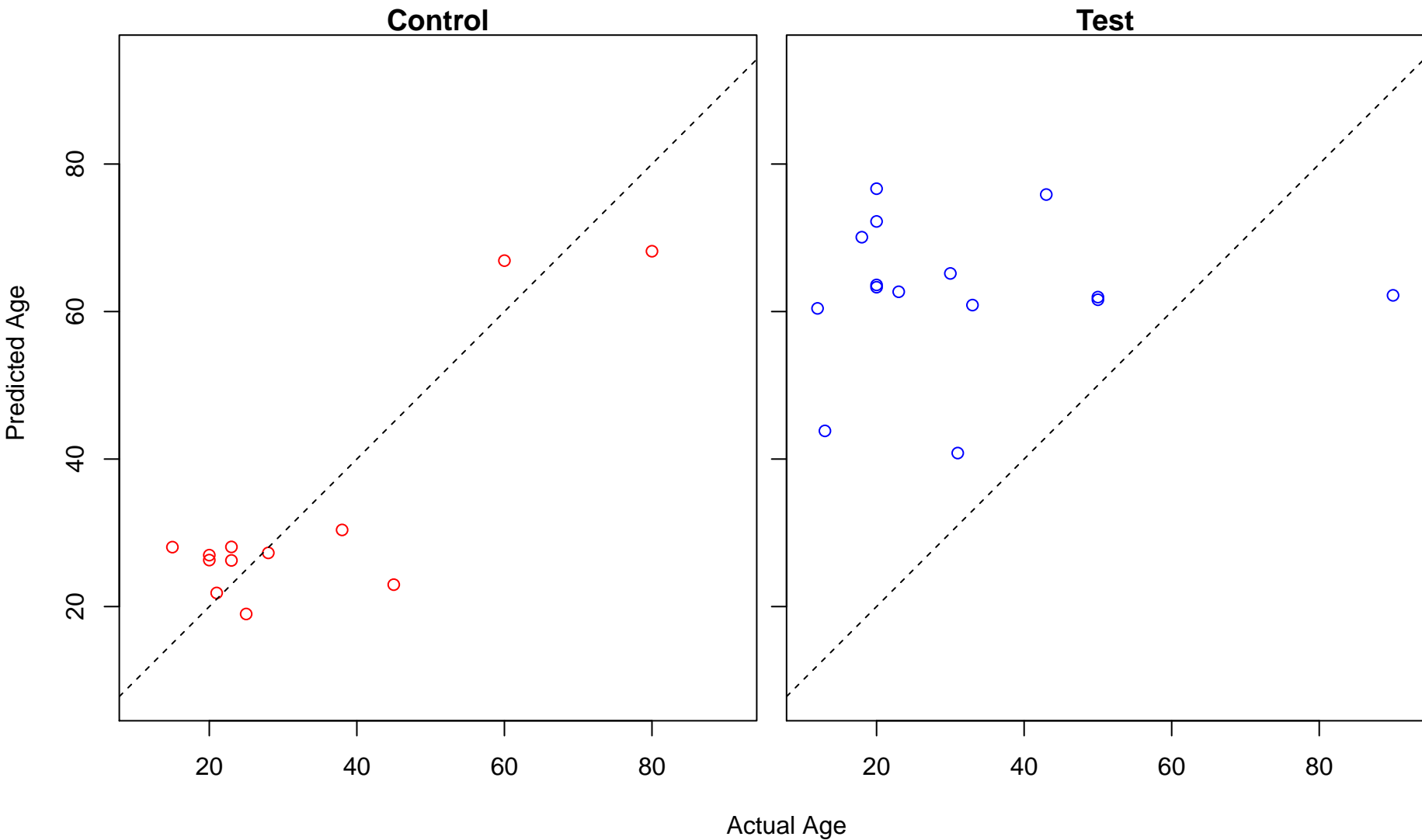


Actual Age

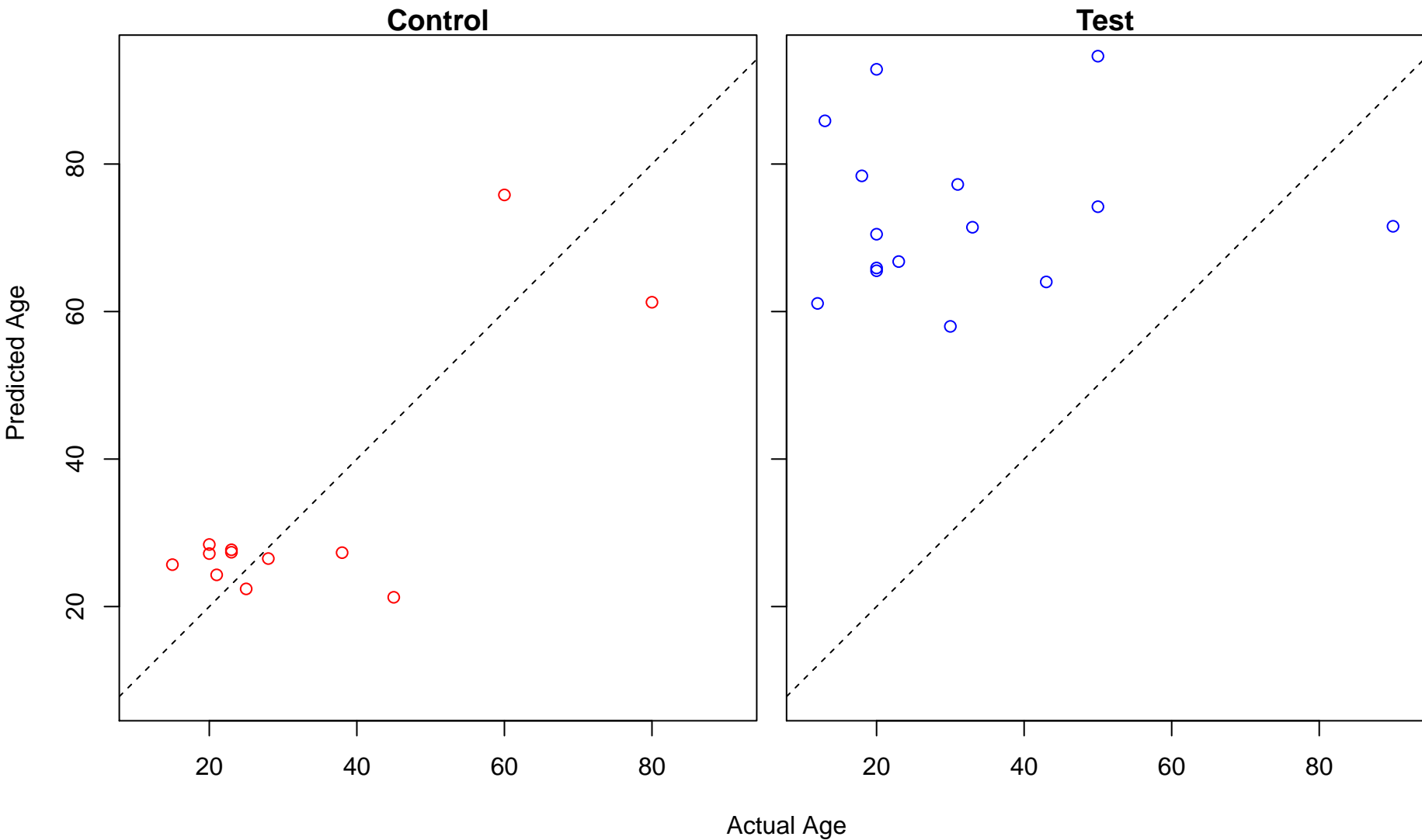
double-strand break repair via nonhomologous end joining (Score: 5.680583)



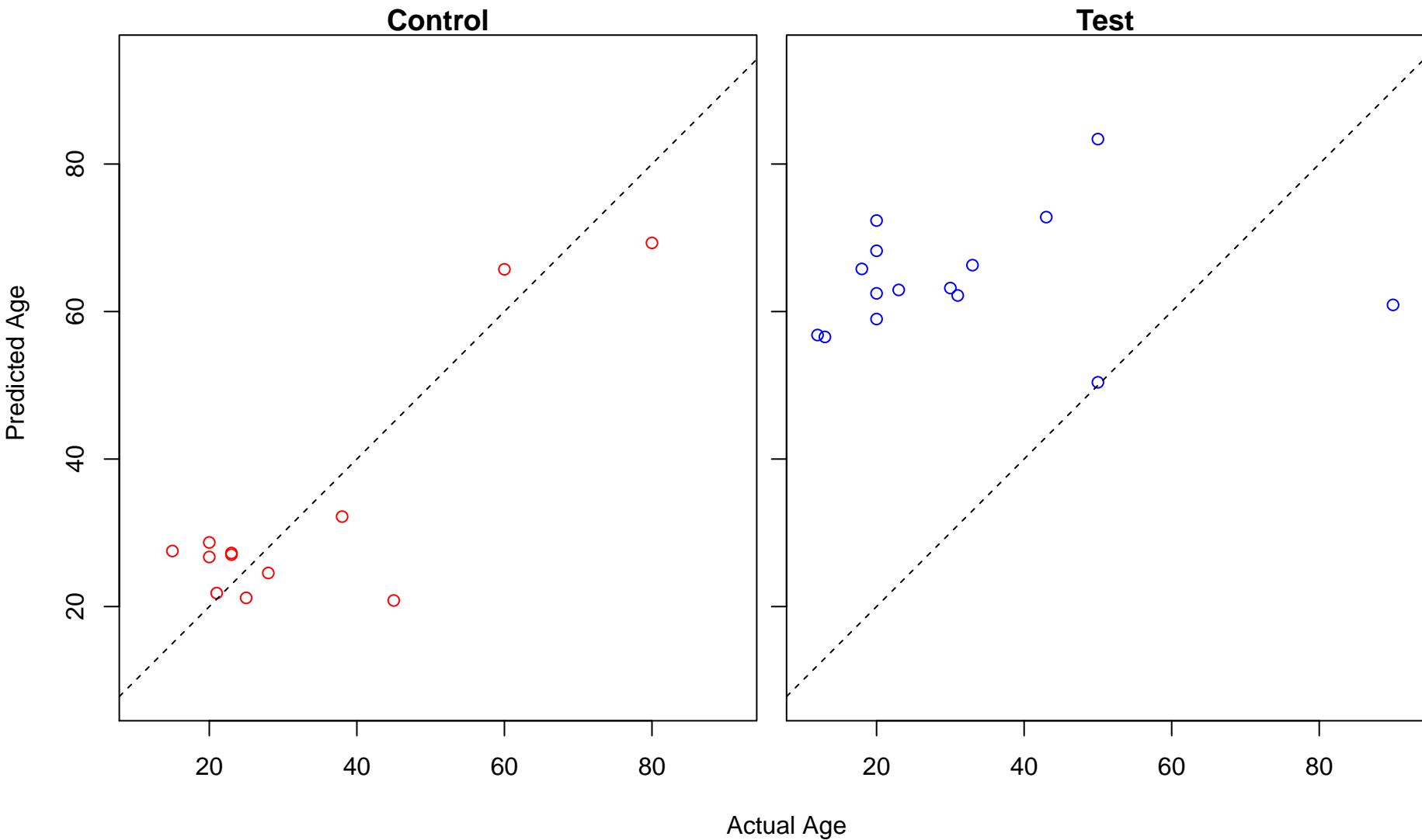
fatty acid alpha-oxidation (Score: 5.679390)



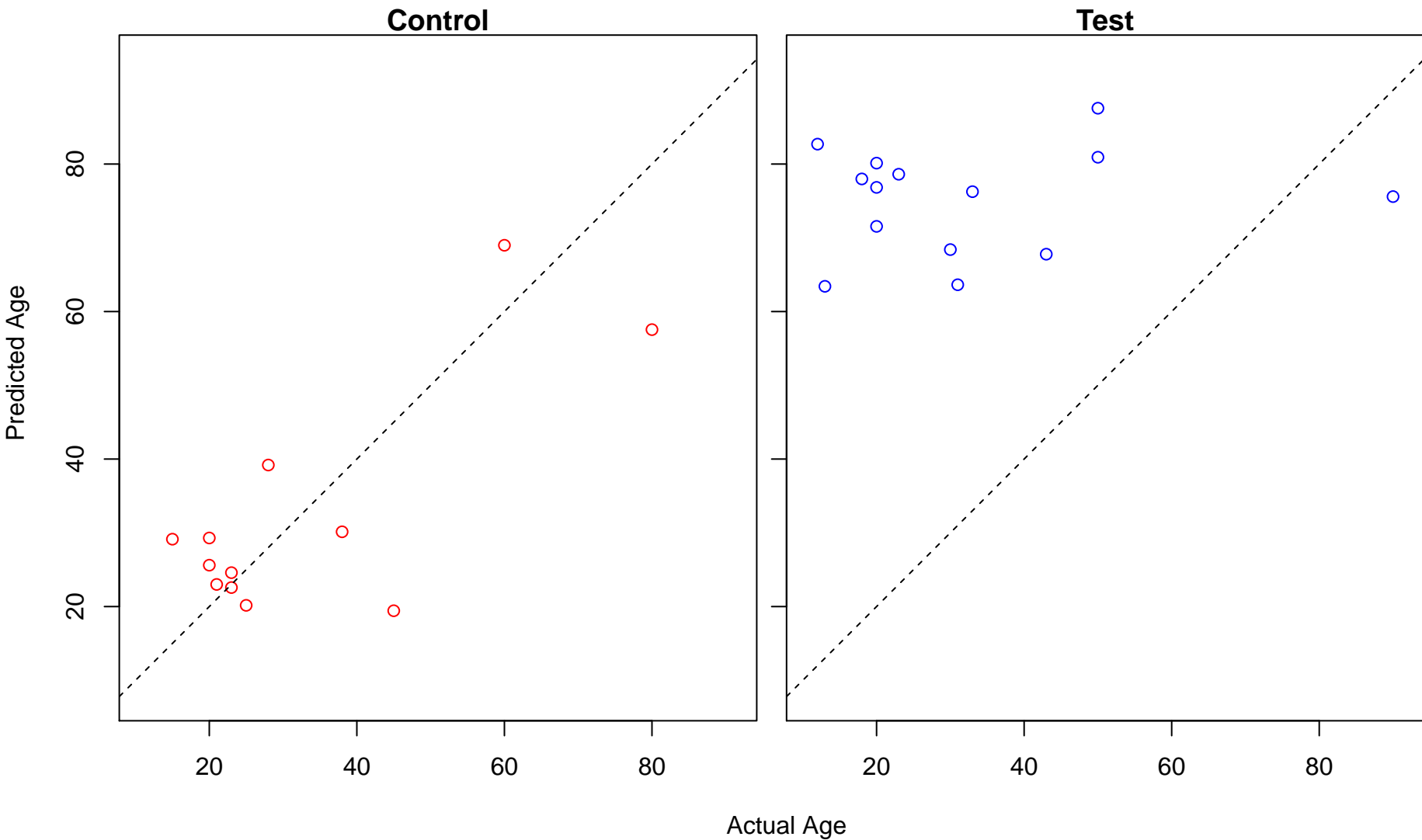
negative regulation of protein binding (Score: 5.677703)



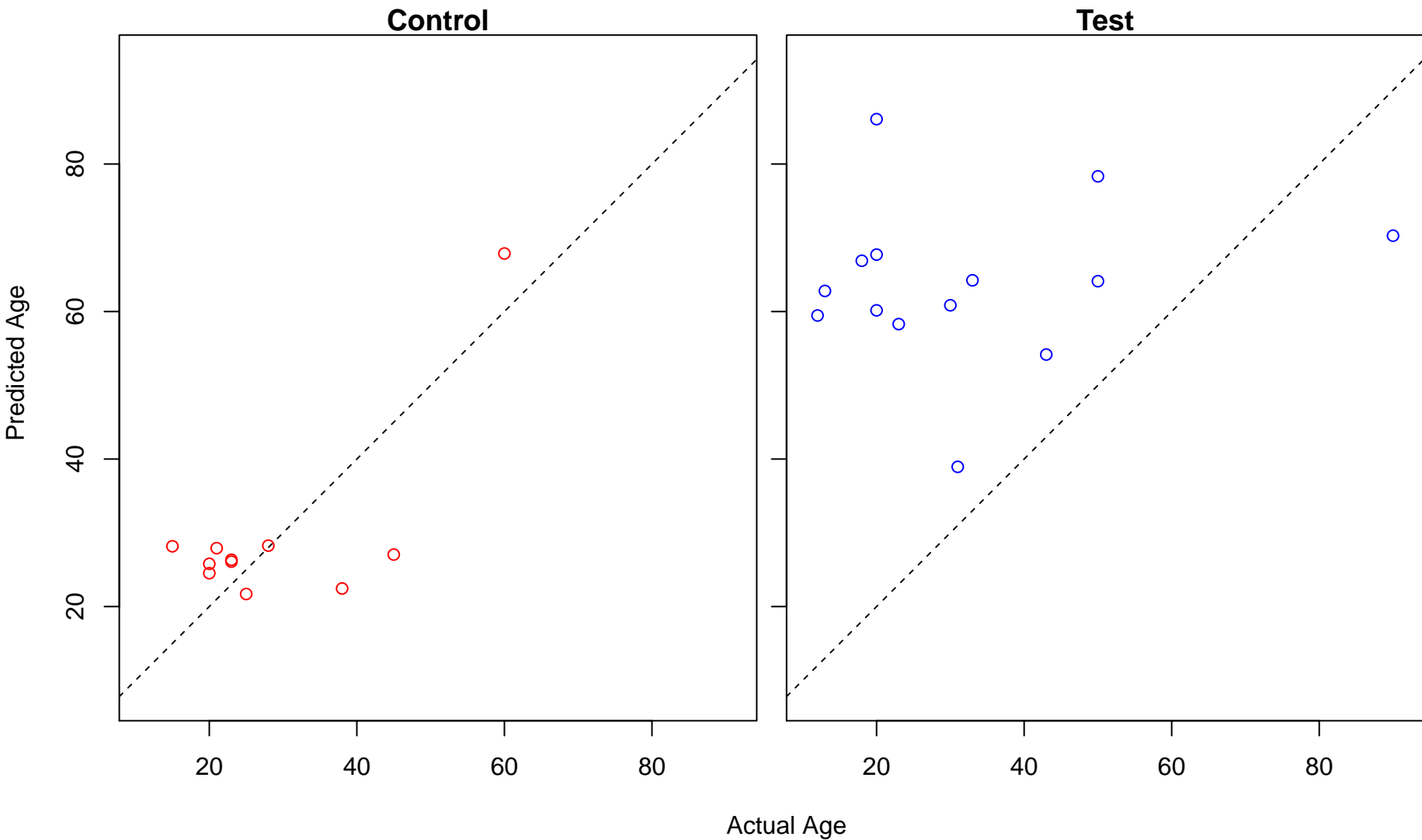
synaptic vesicle endocytosis (Score: 5.677233)



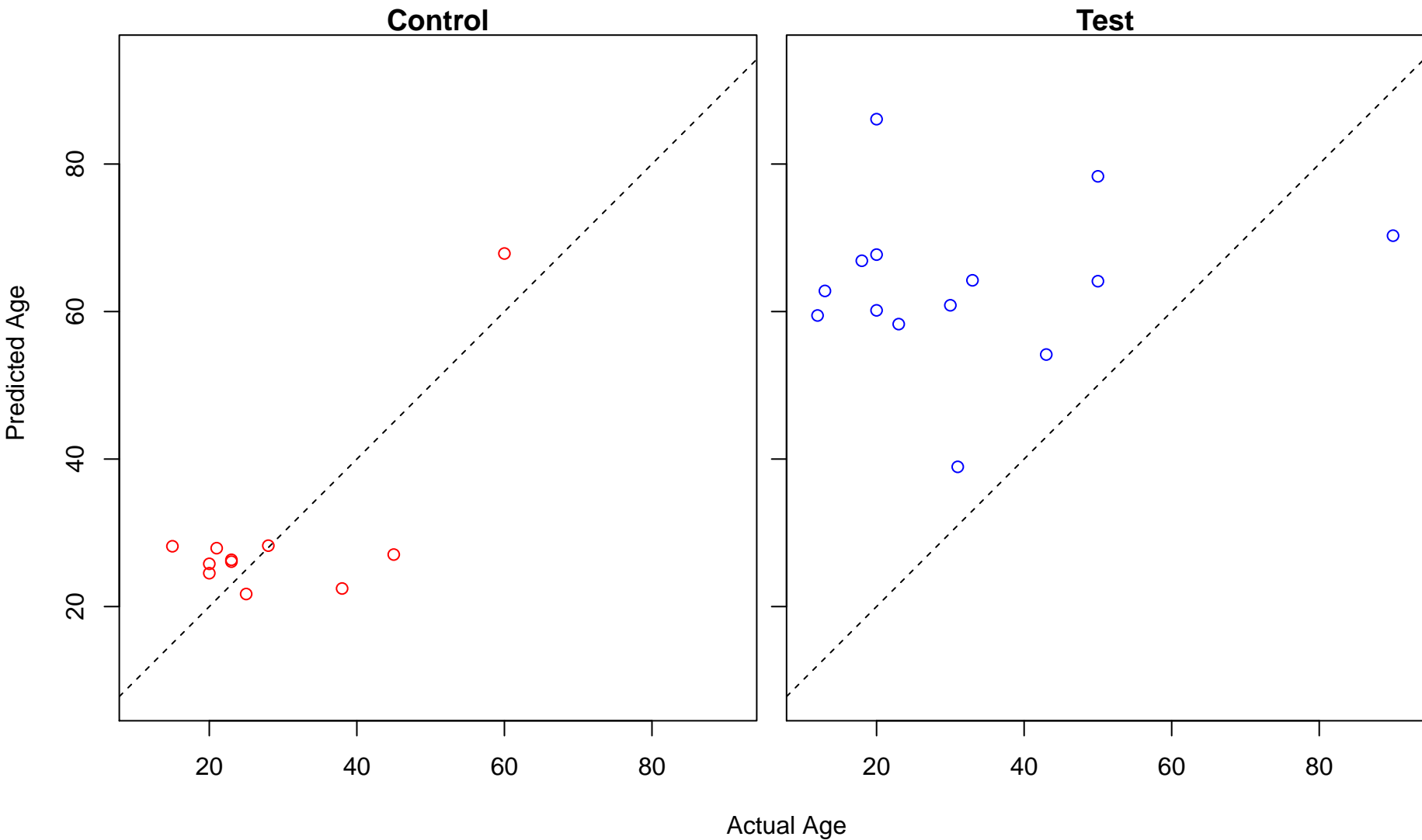
regulation of chemokine biosynthetic process (Score: 5.675802)



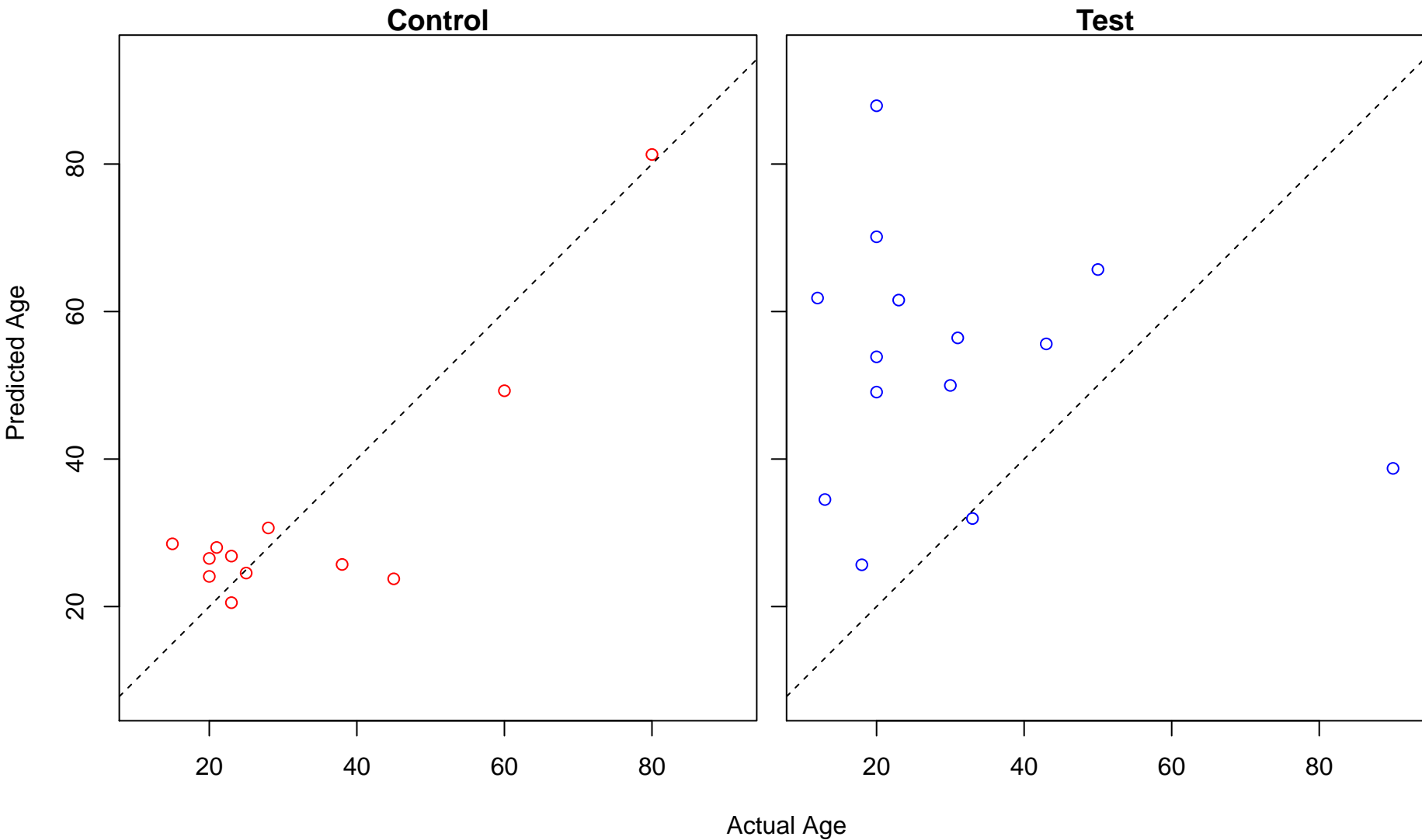
iron-sulfur cluster assembly (Score: 5.672539)



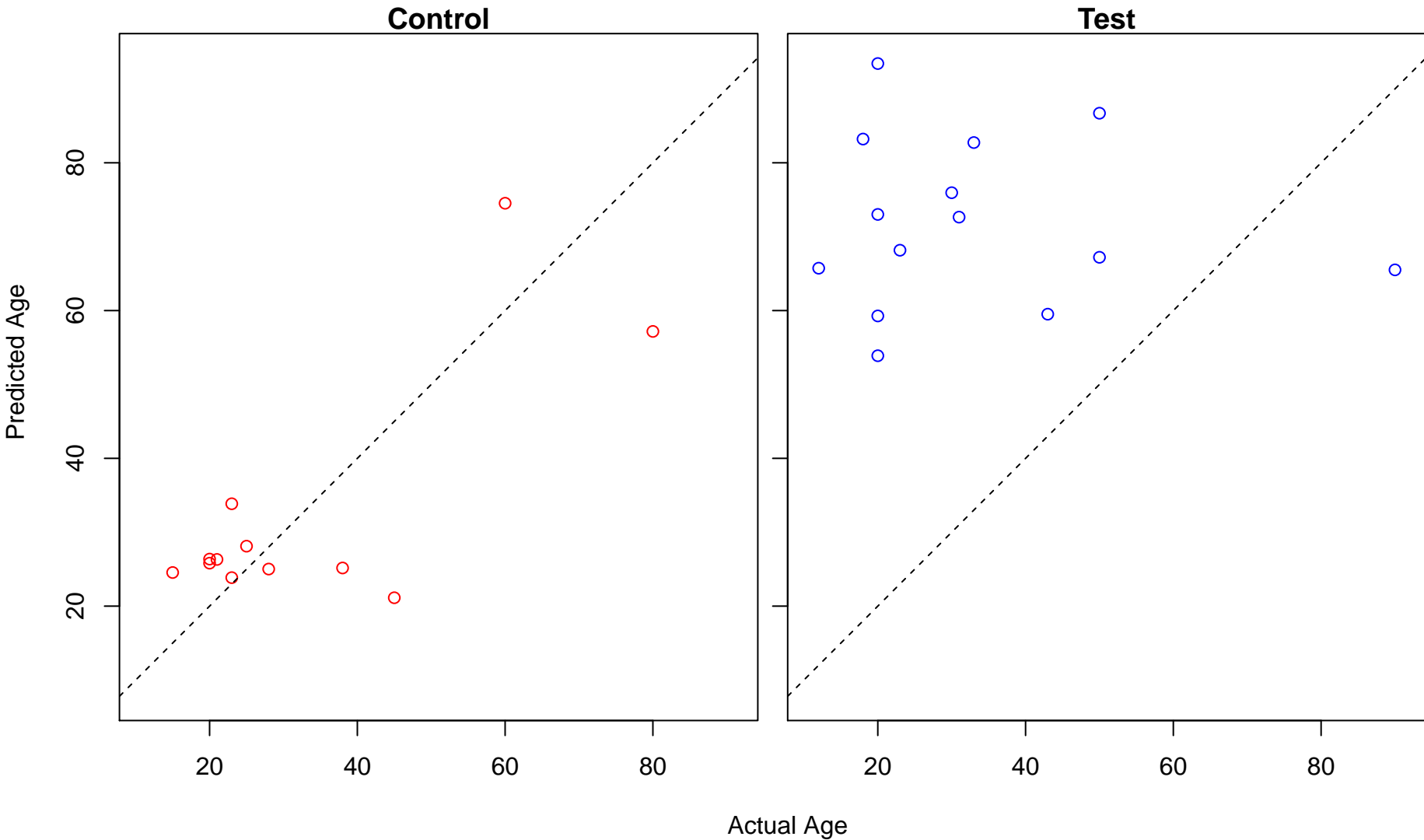
metallo-sulfur cluster assembly (Score: 5.672539)



response to alcohol (Score: 5.667940)

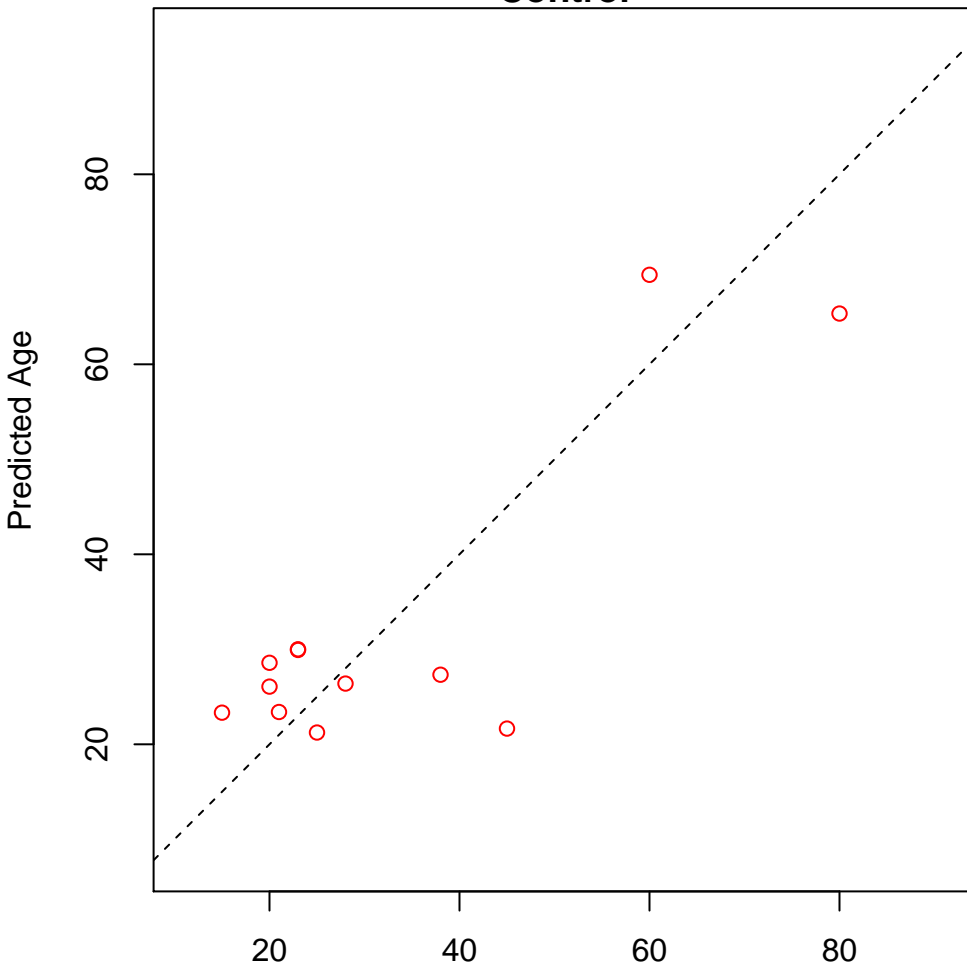


regulation of interferon- γ production (Score: 5.666901)

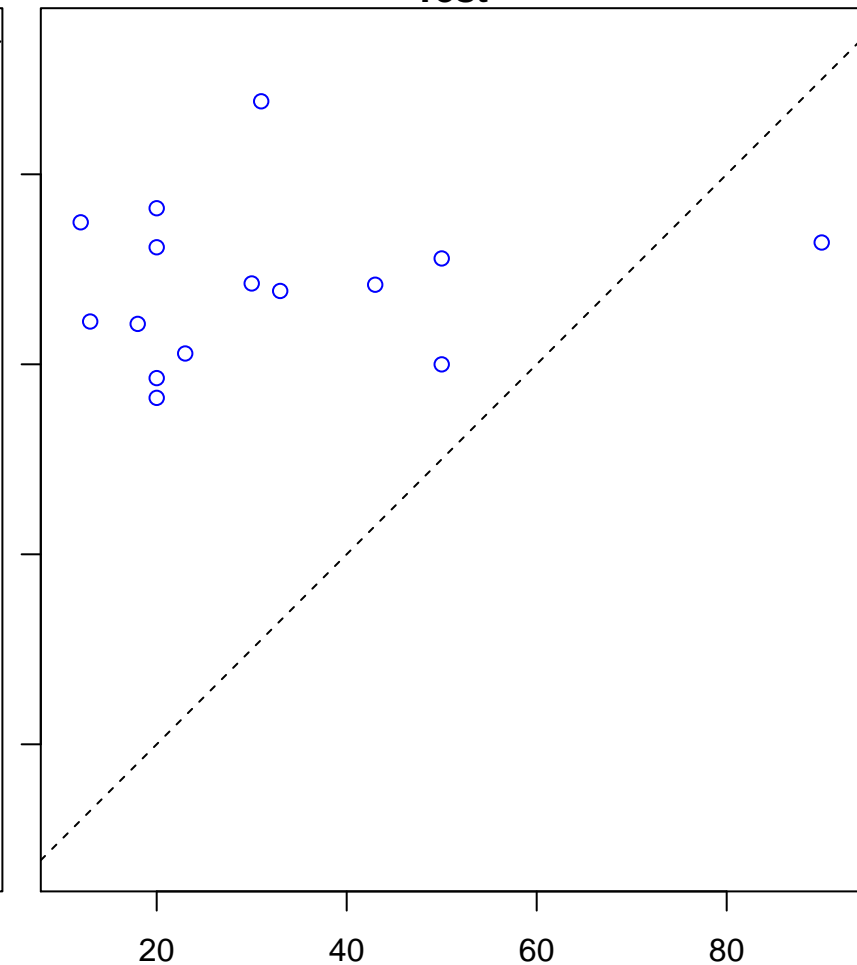


mitotic G2 DNA damage checkpoint (Score: 5.665672)

Control

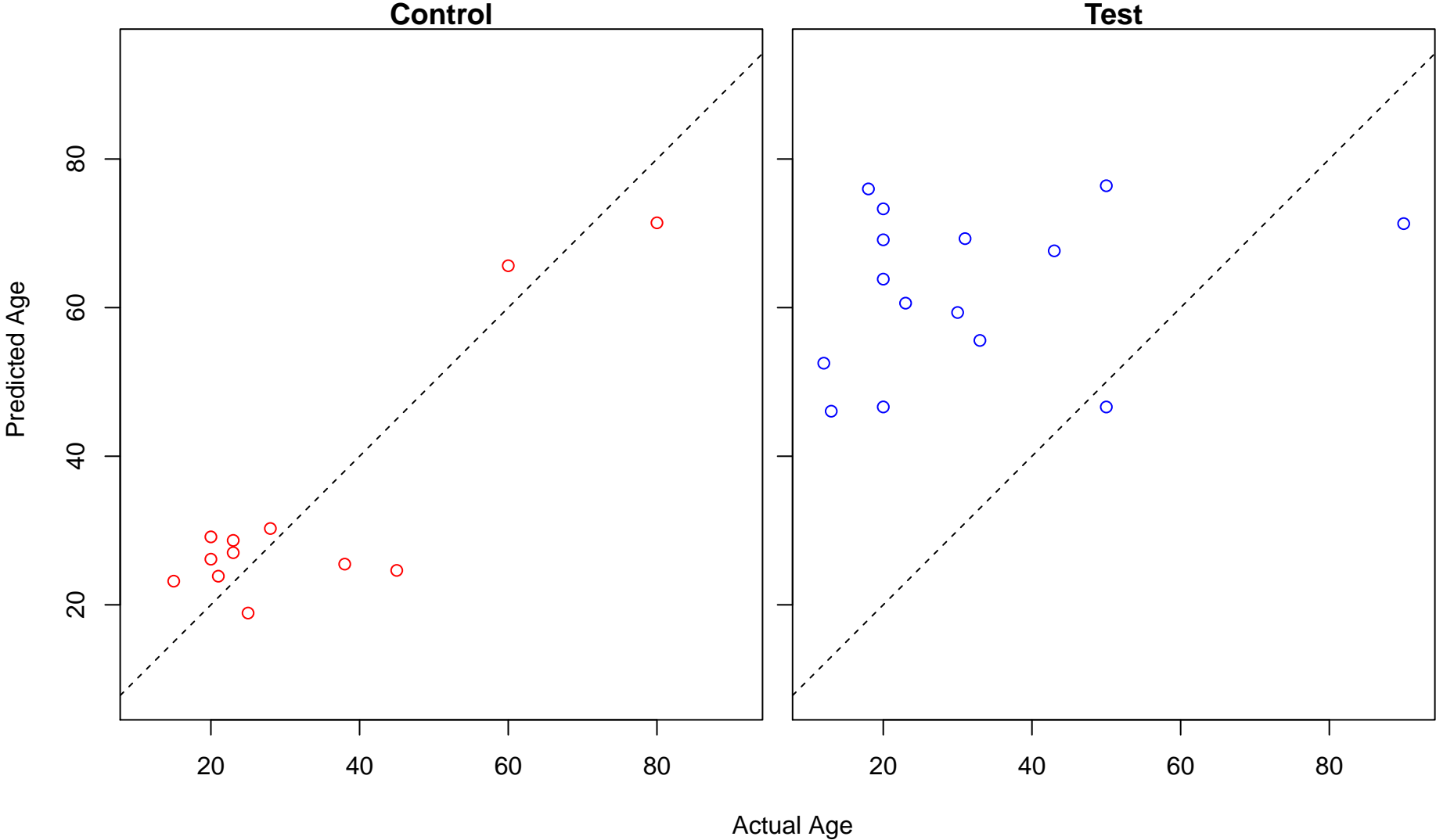


Test

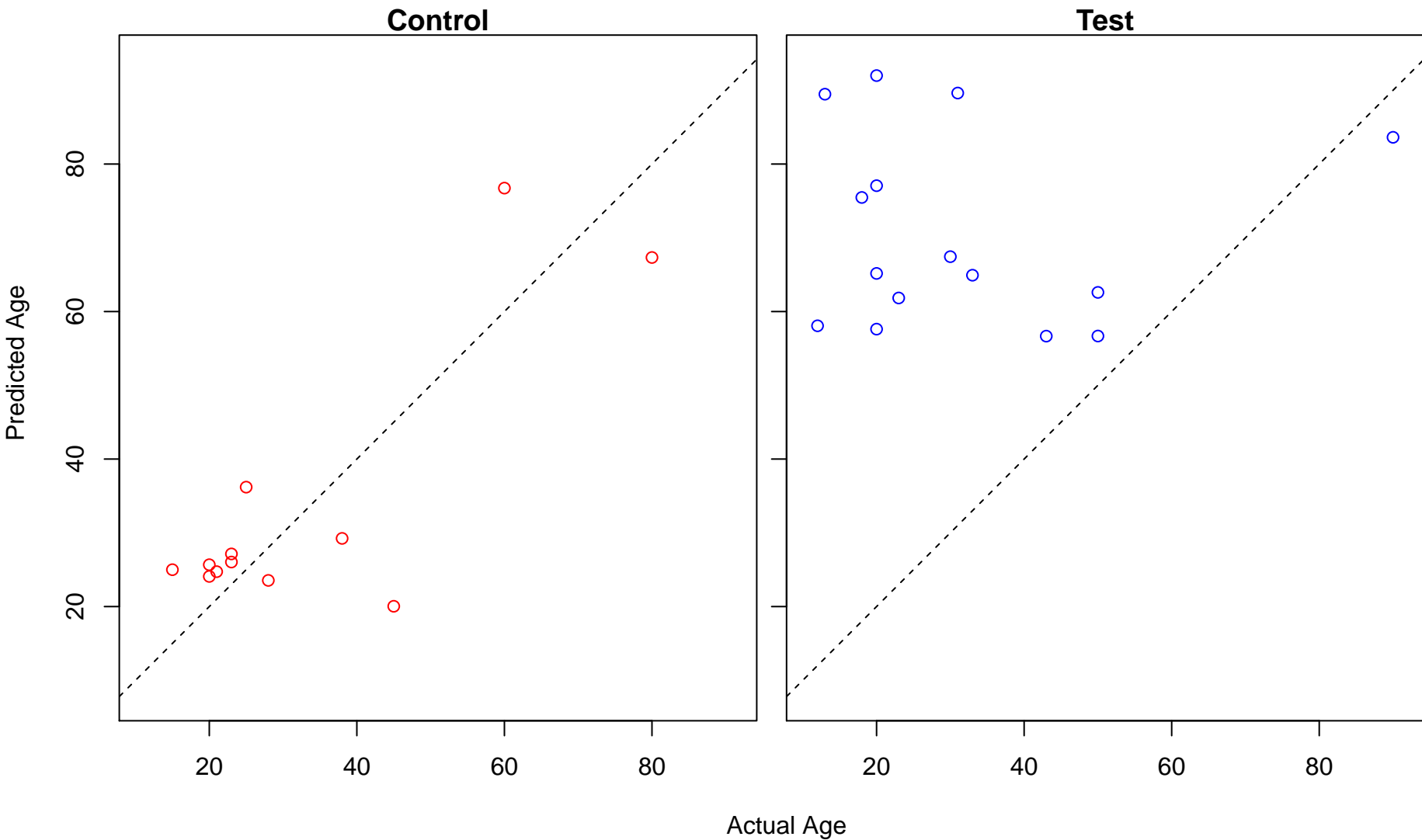


Actual Age

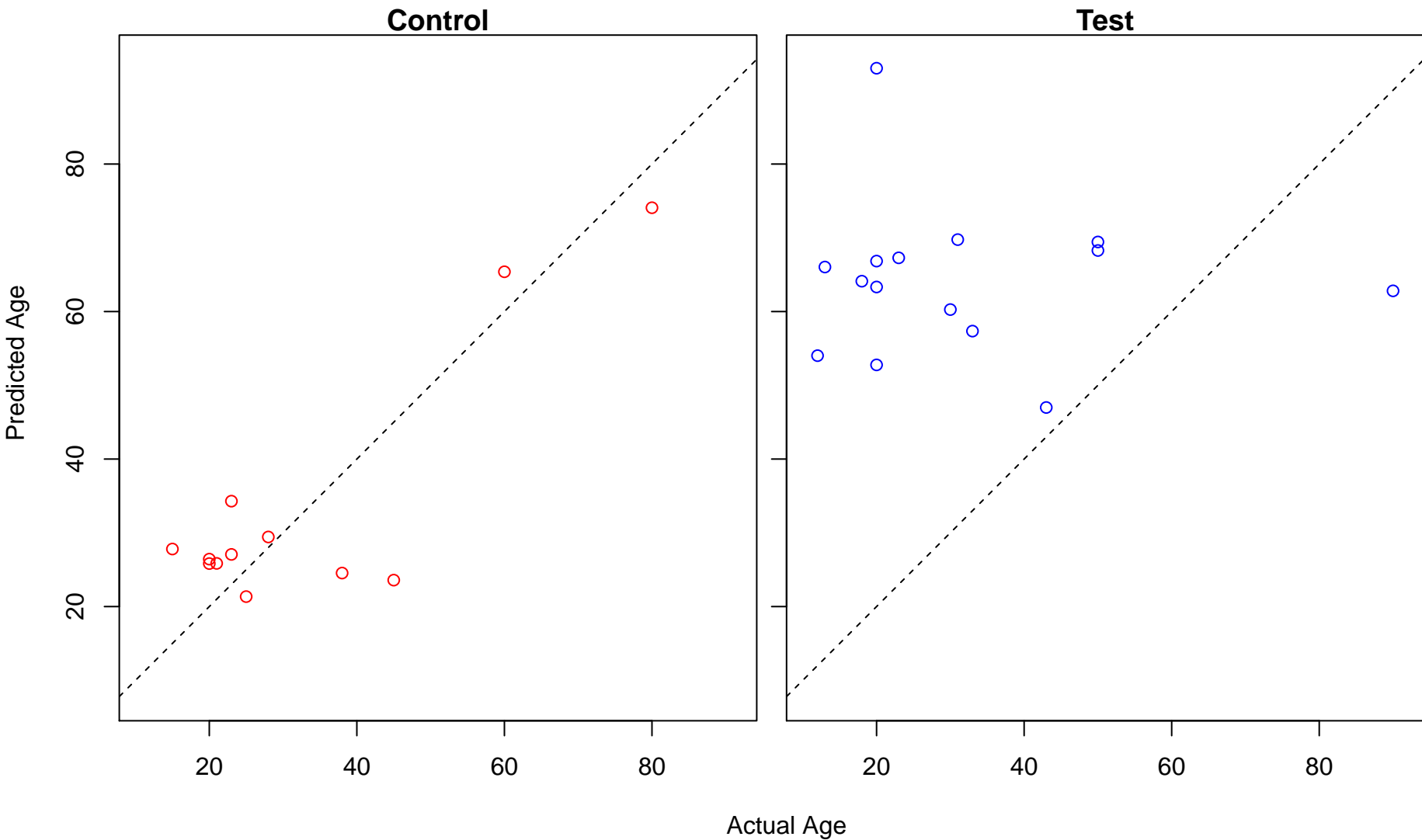
positive regulation of CD4-positive, alpha-beta T cell activation (Score: 5.665198)



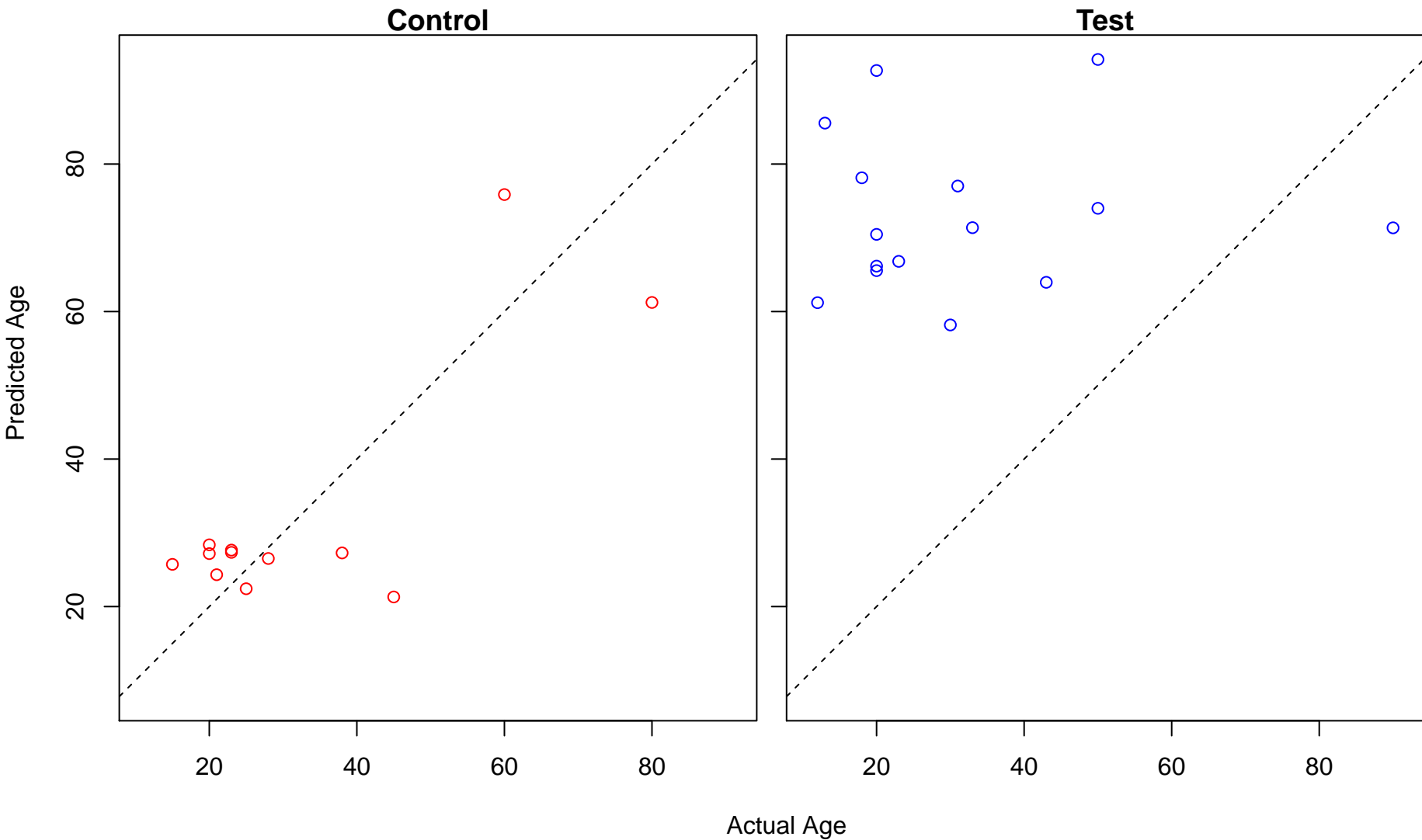
histone-threonine phosphorylation (Score: 5.664937)



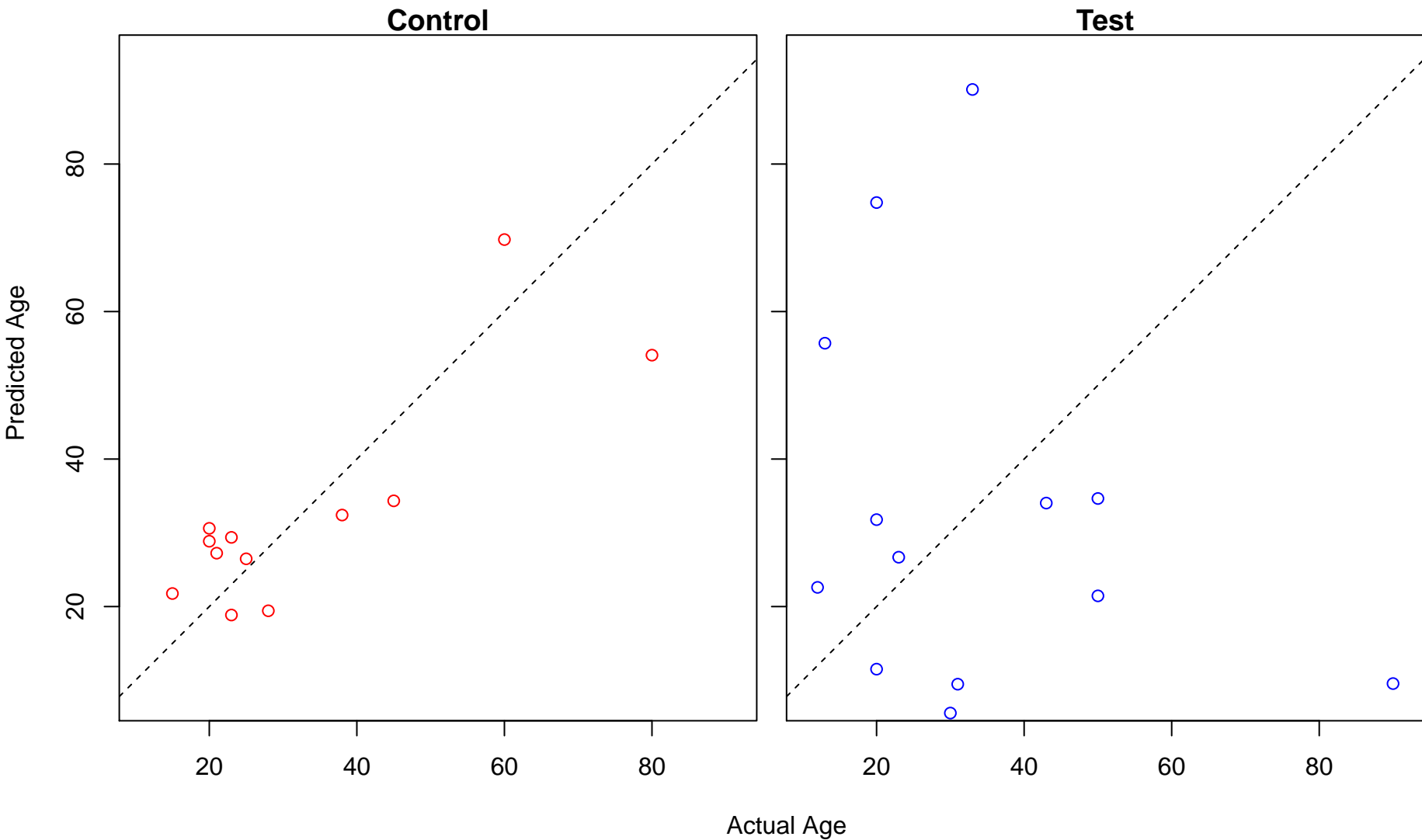
positive regulation of homeostatic process (Score: 5.661005)



regulation of protein binding (Score: 5.659024)

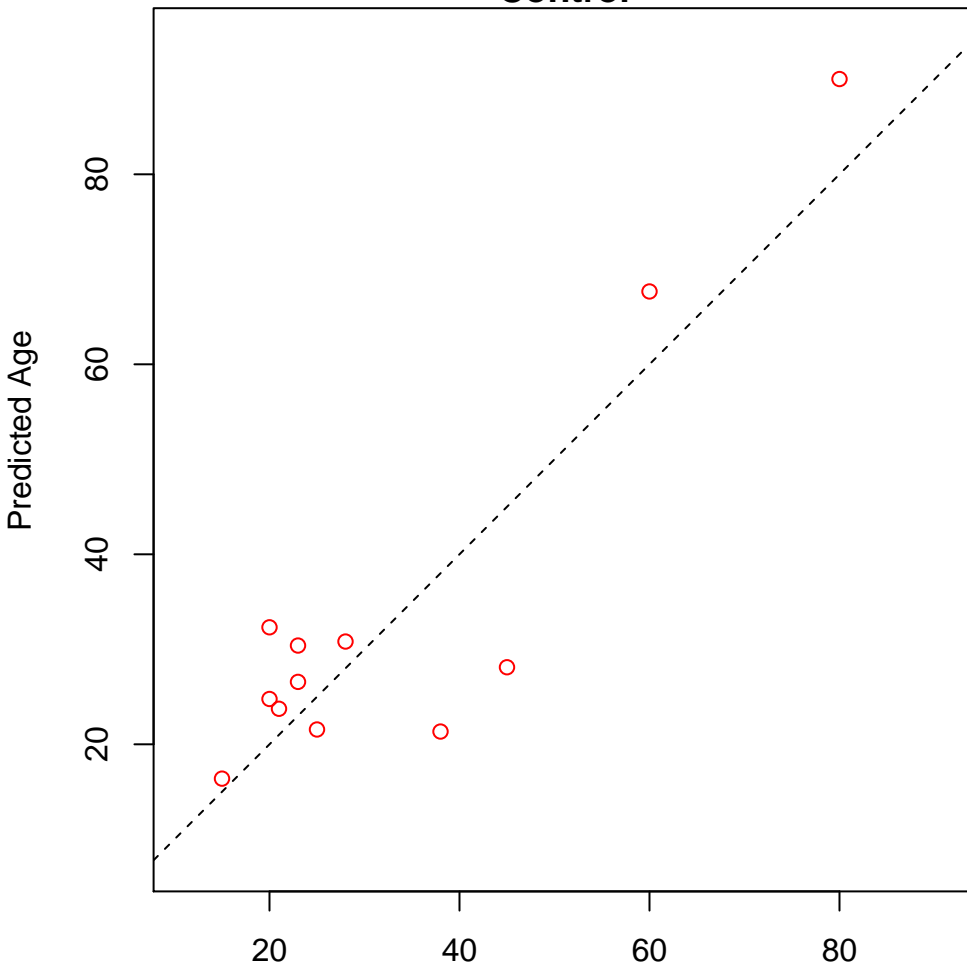


sulfate transport (Score: 5.657646)

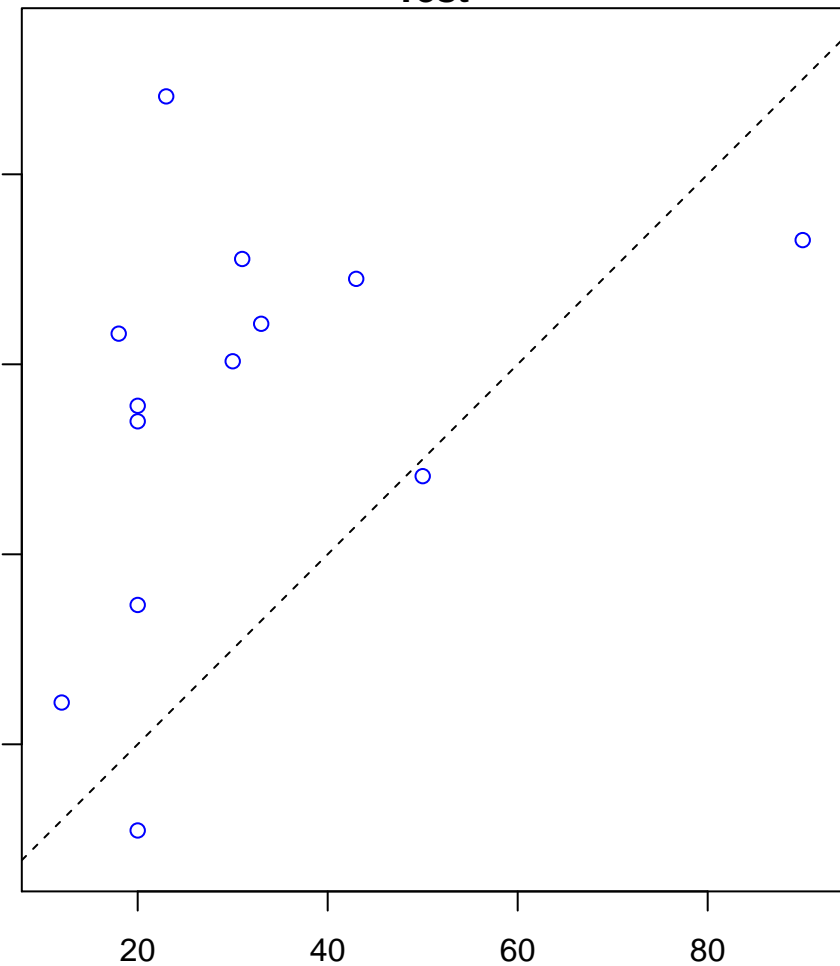


cerebellar Purkinje cell layer development (Score: 5.656931)

Control

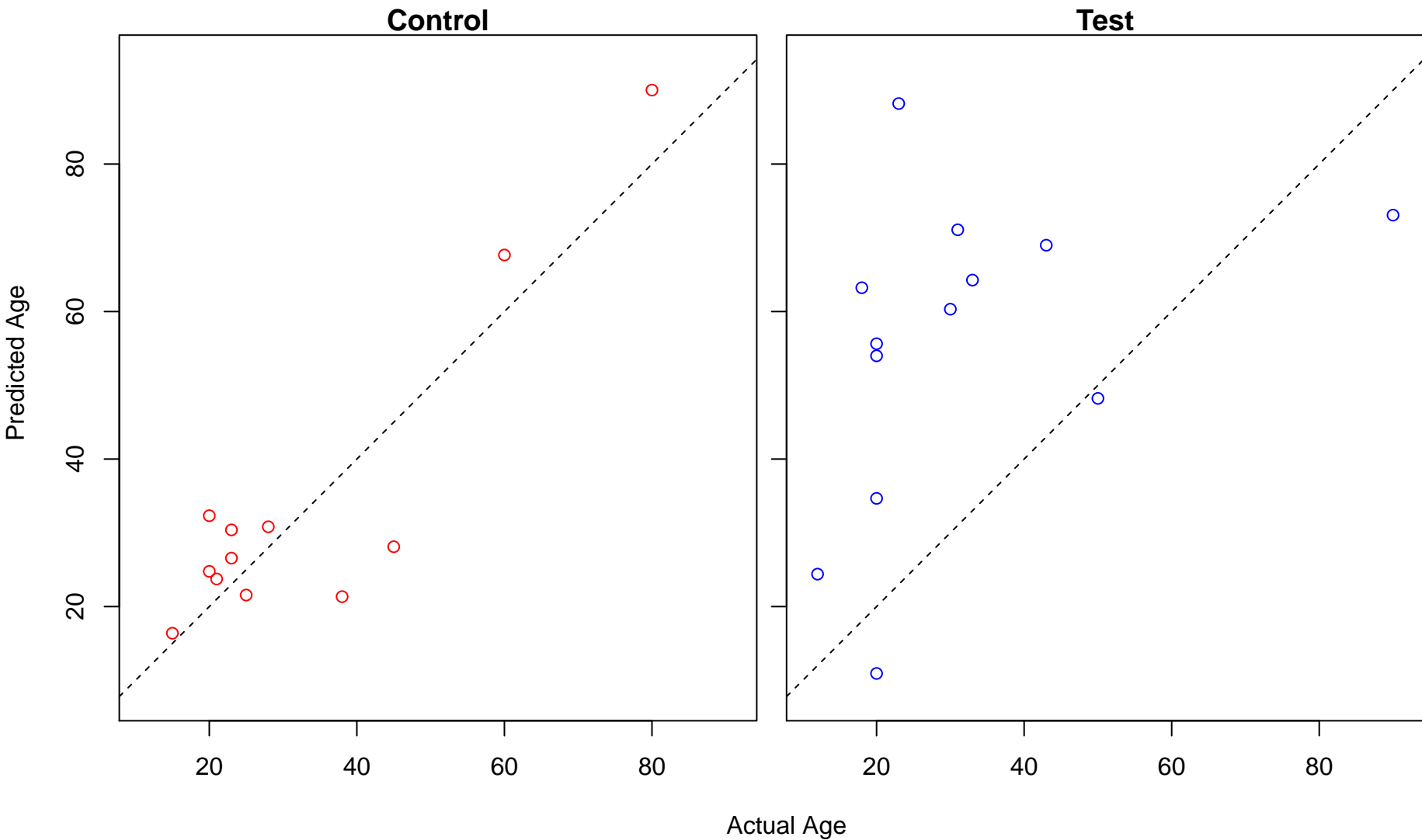


Test

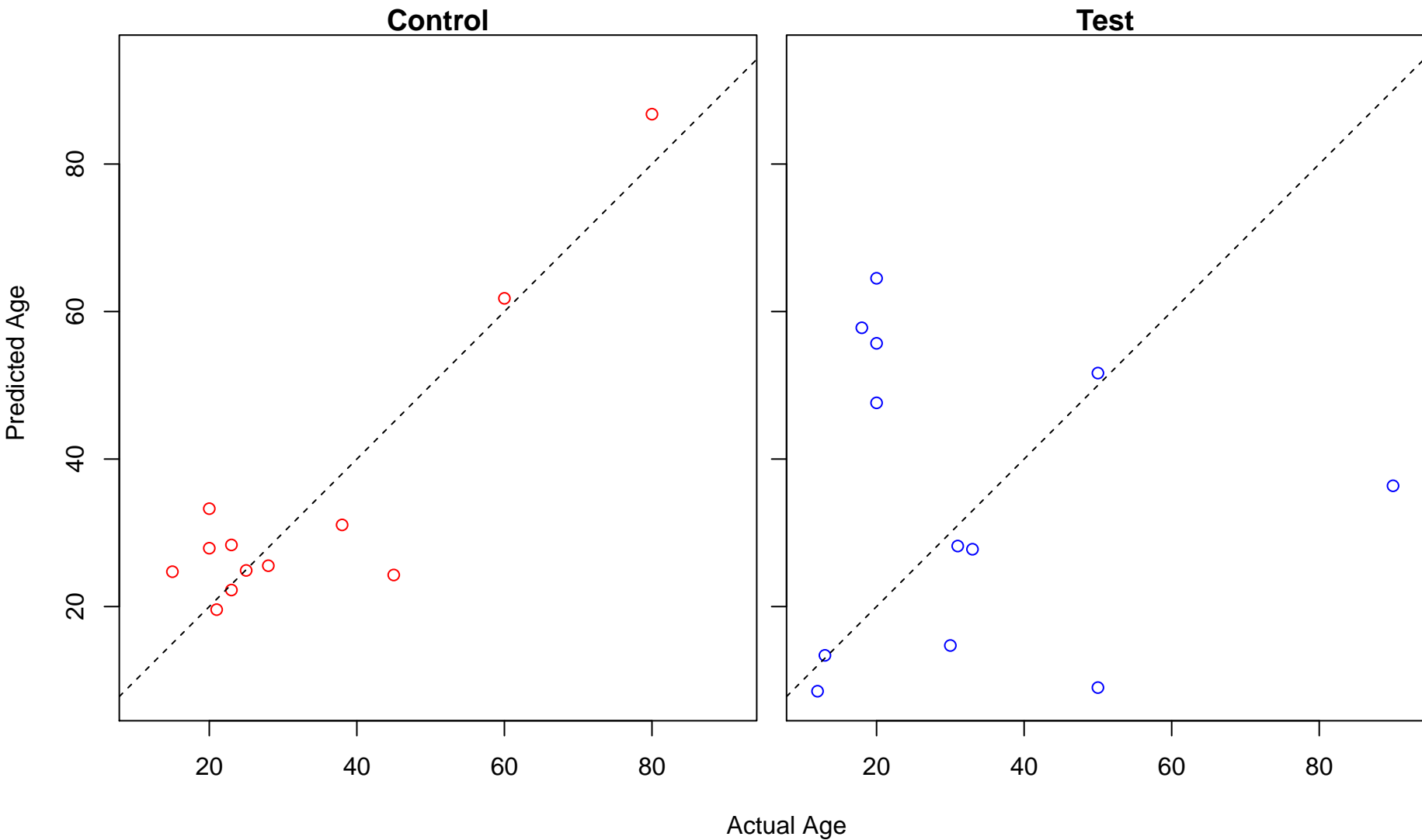


Actual Age

cerebellar Purkinje cell layer morphogenesis (Score: 5.656931)

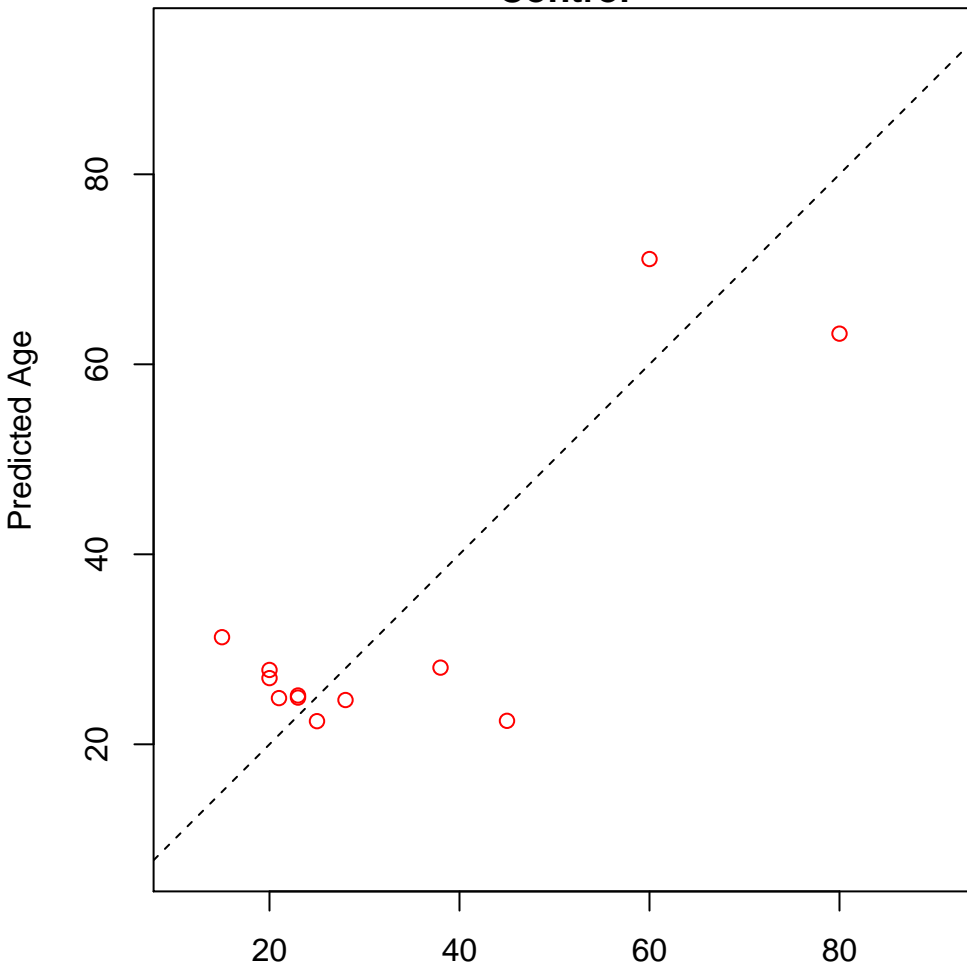


UDP-N-acetylglucosamine metabolic process (Score: 5.651319)

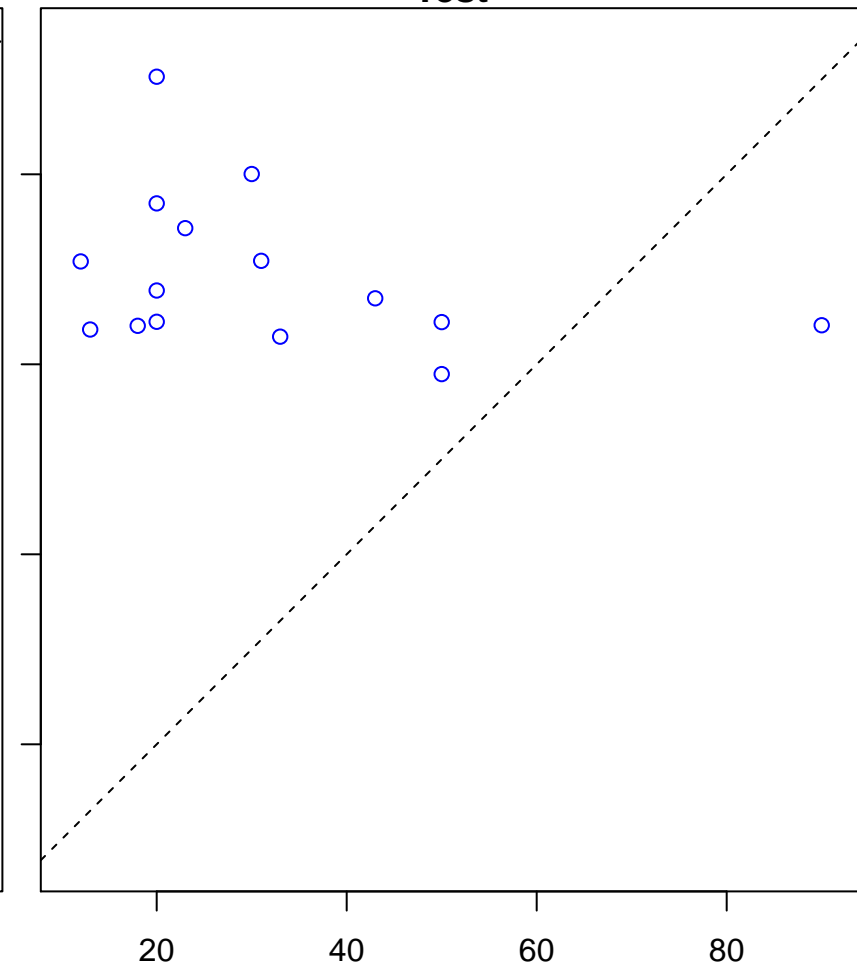


cellular response to interleukin-6 (Score: 5.651298)

Control

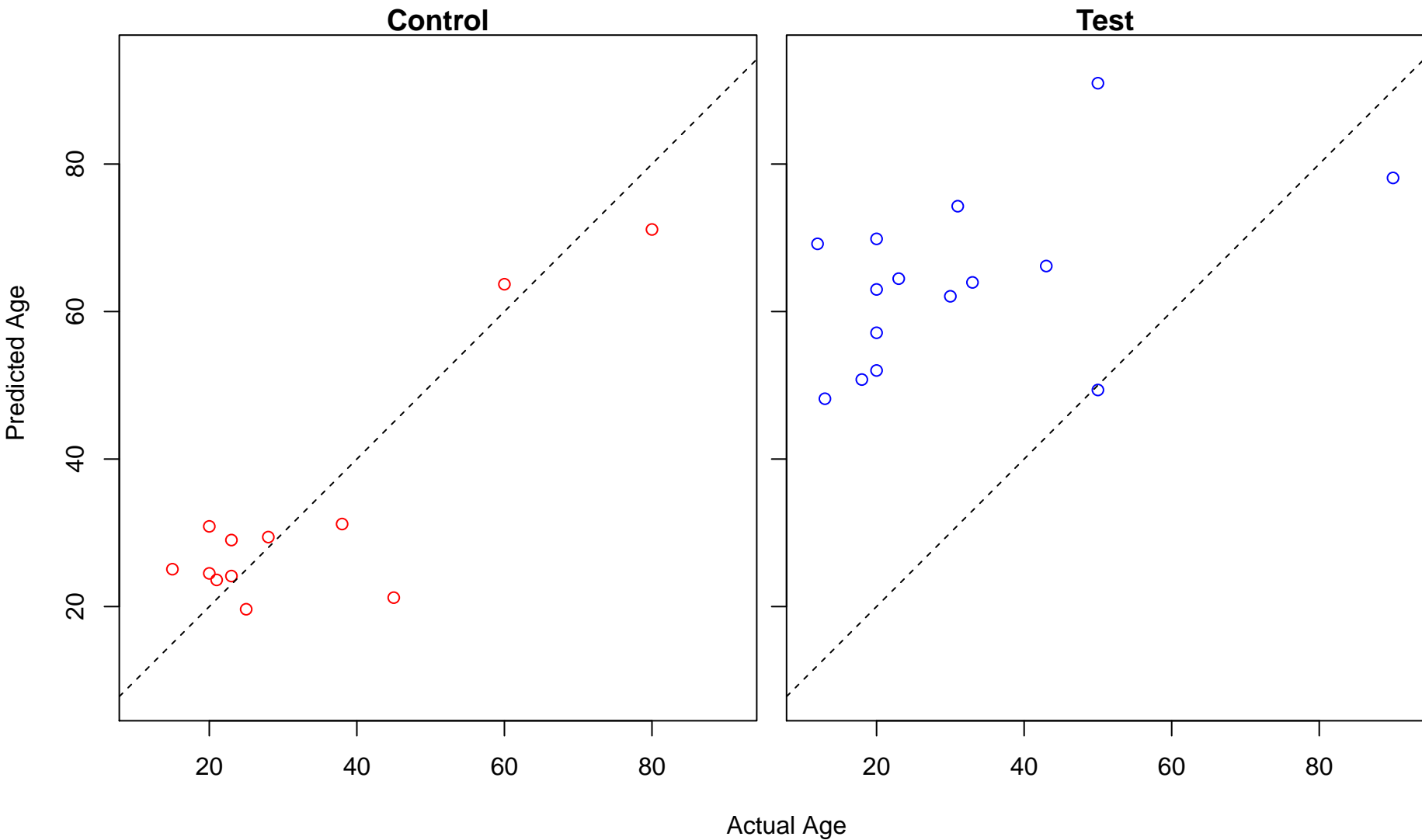


Test

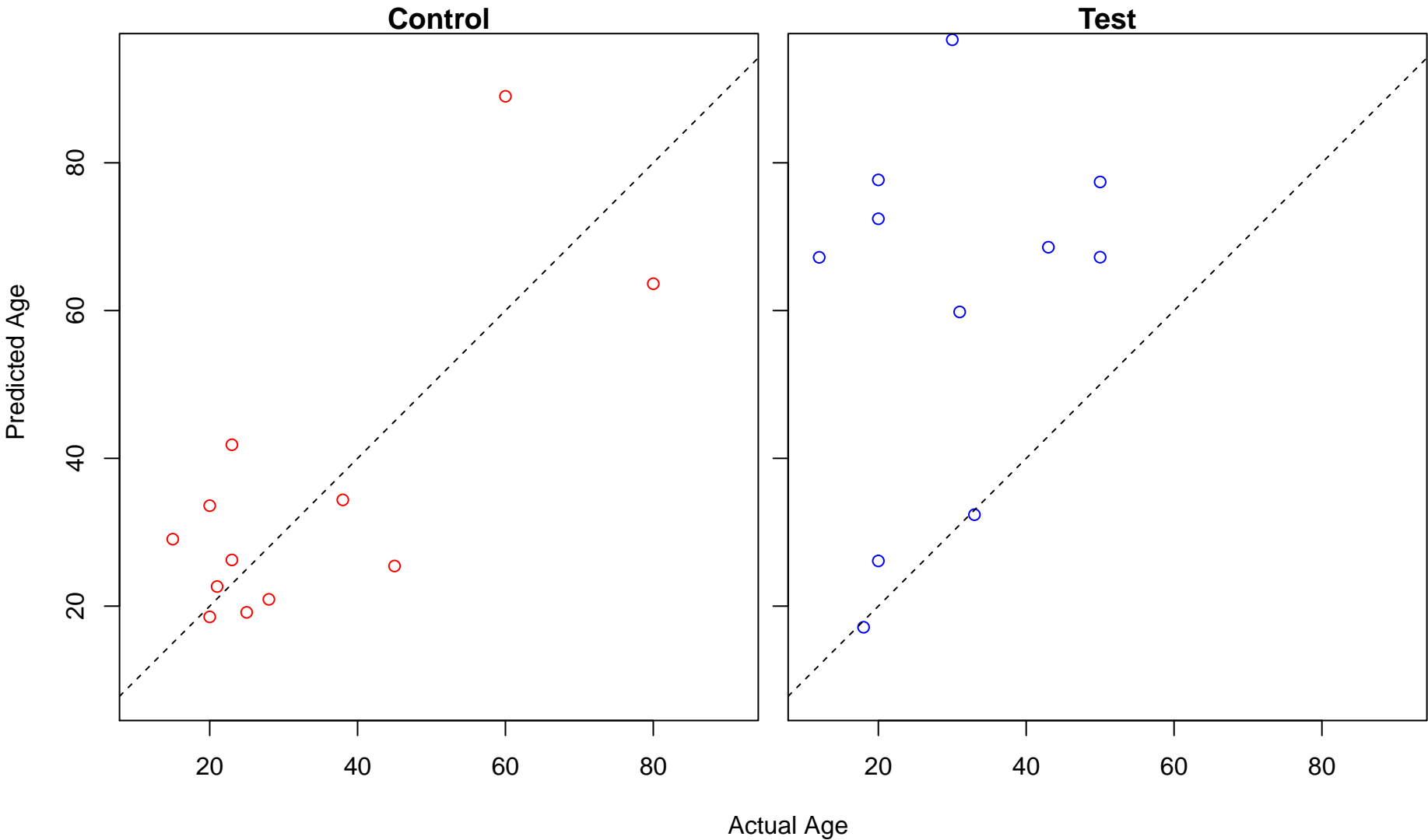


Actual Age

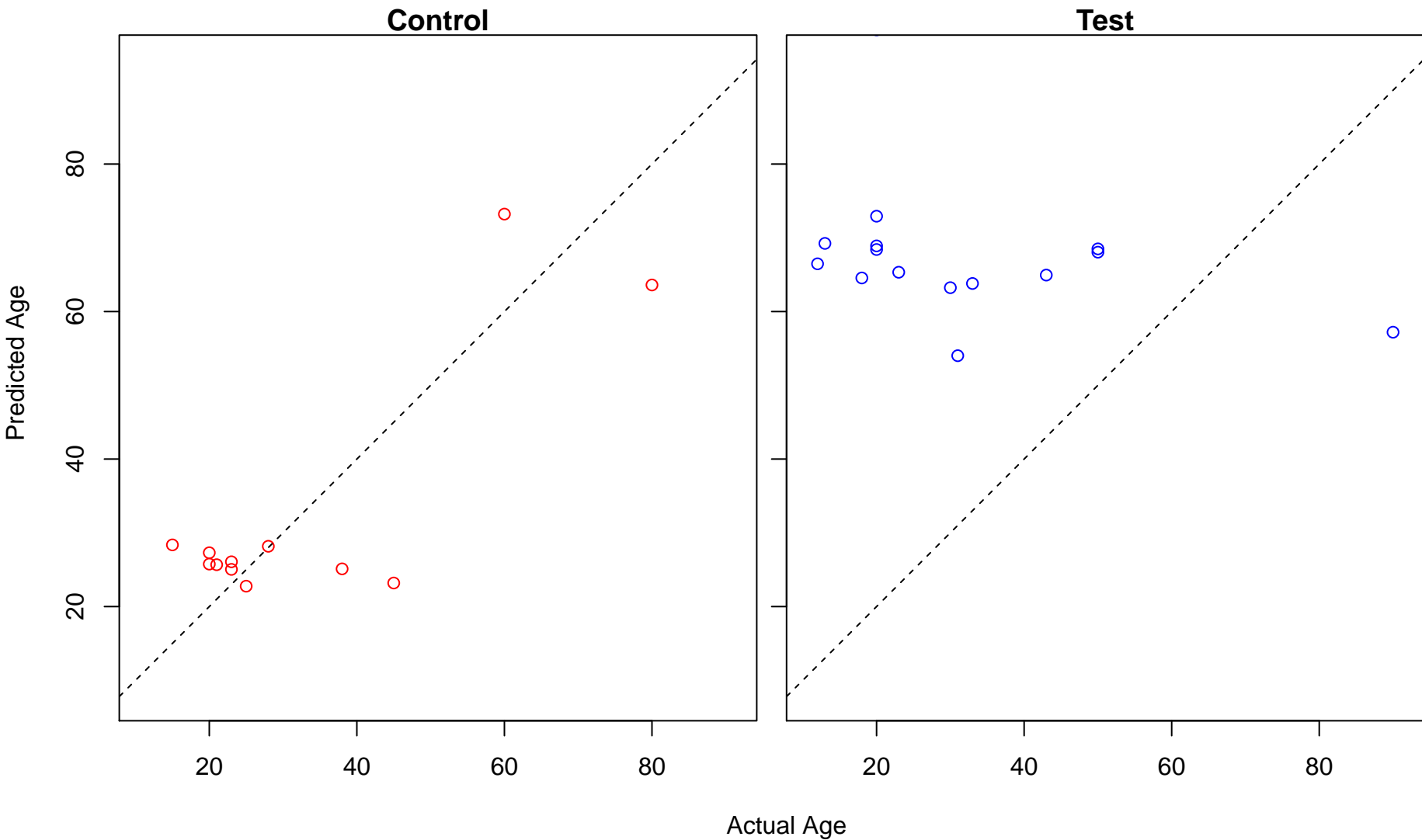
regulation of lysosomal lumen pH (Score: 5.648019)



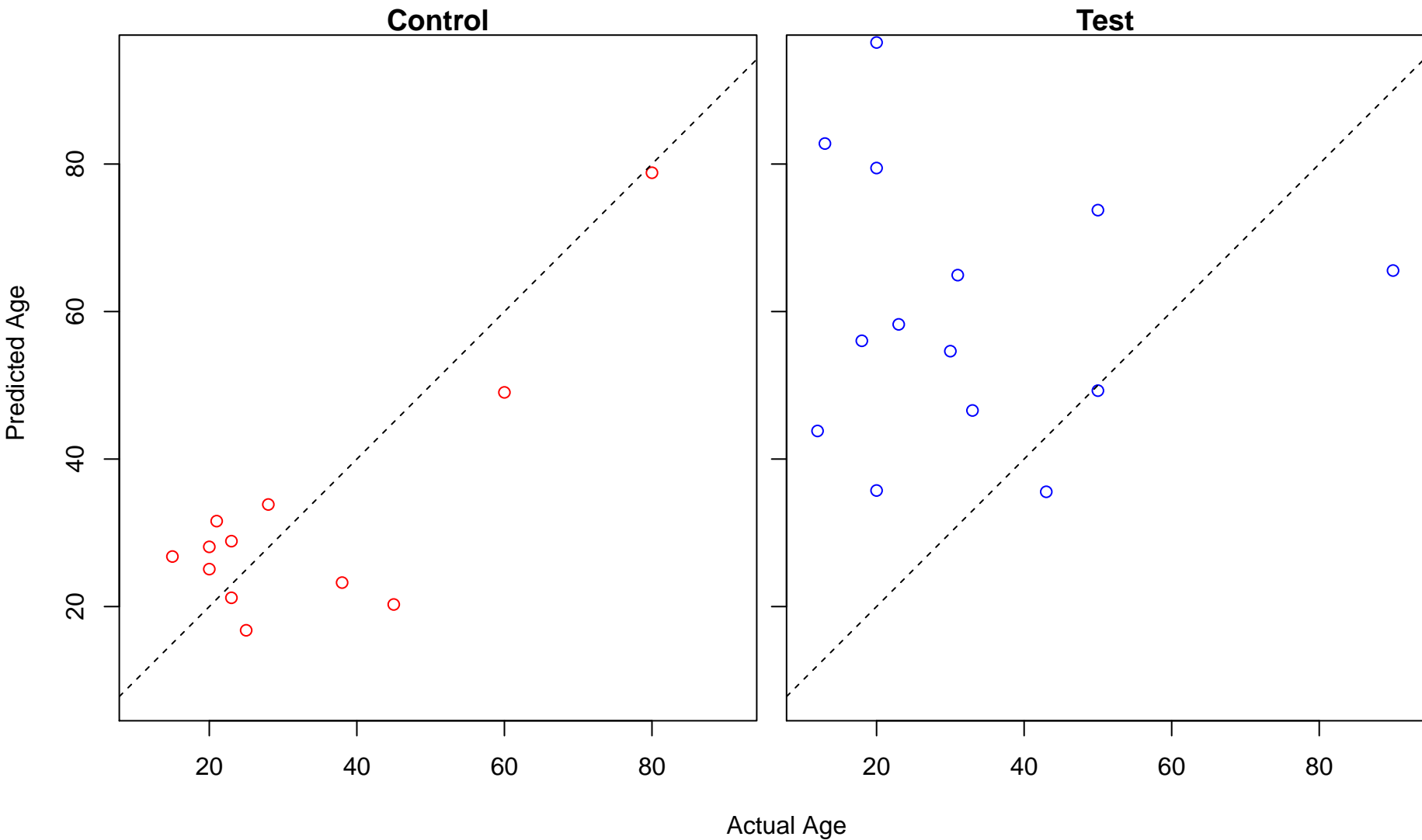
regulation of insulin secretion involved in cellular response to glucose stimulus (Score: 5.646723)



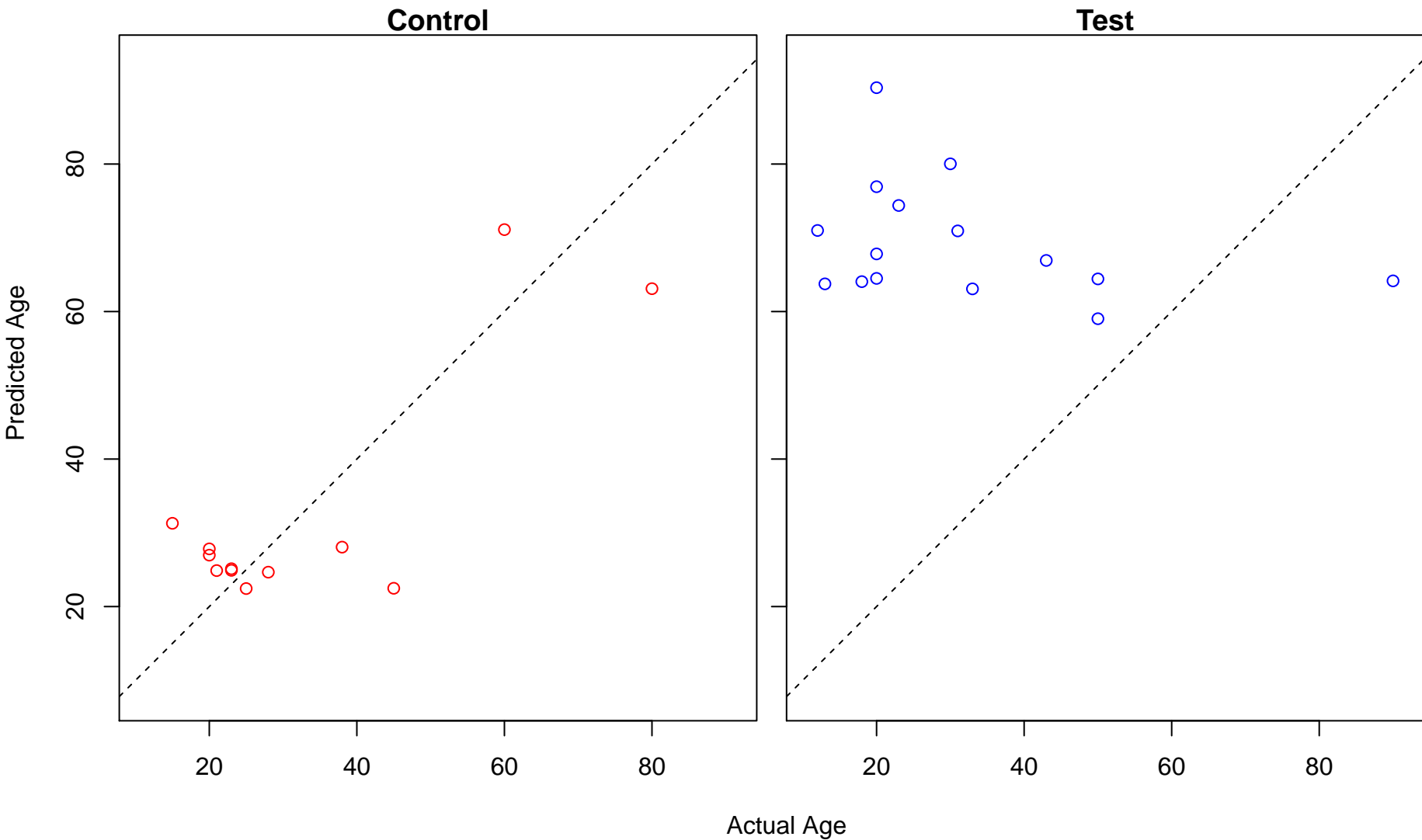
locomotory behavior (Score: 5.645533)



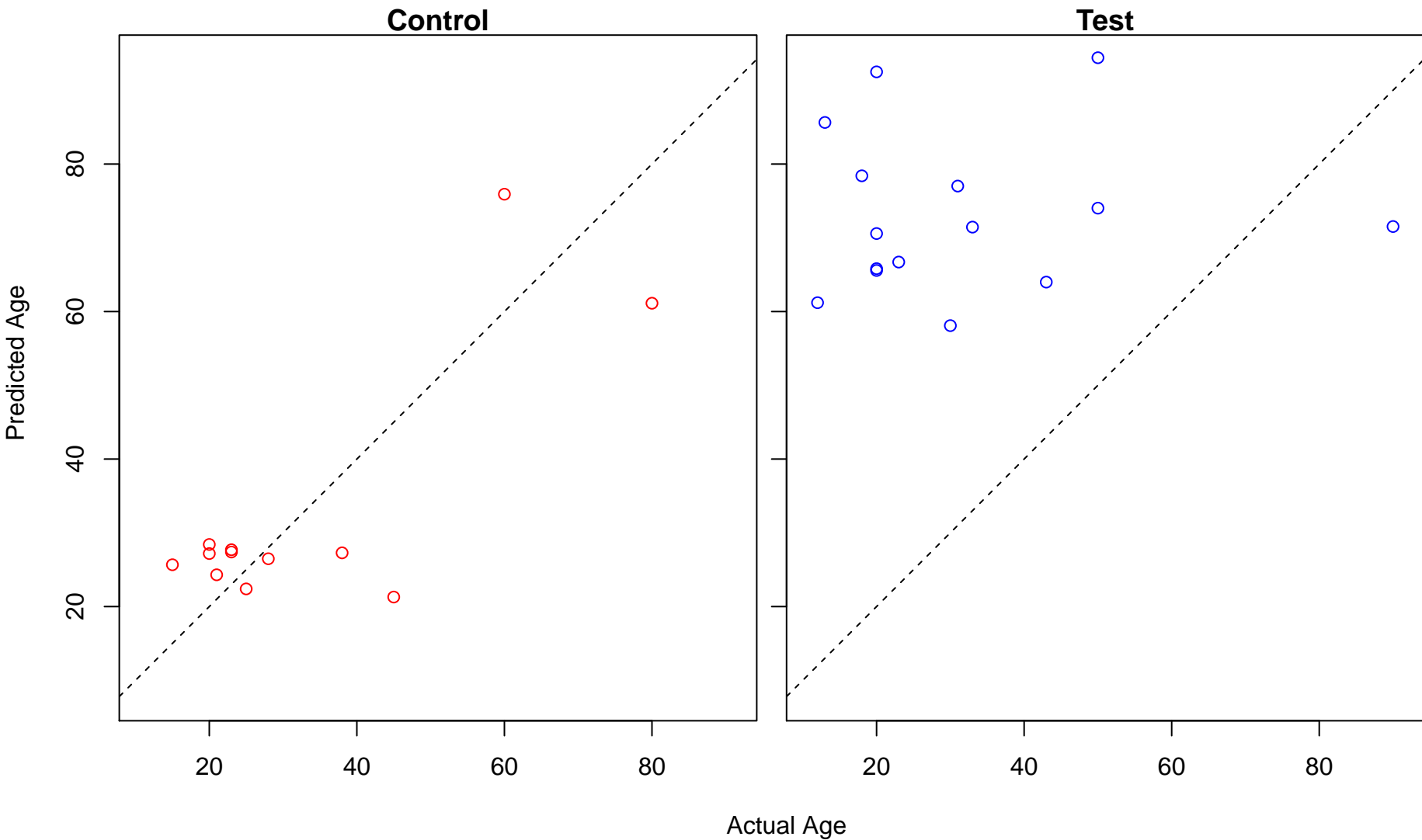
negative regulation of mitochondrial fusion (Score: 5.641367)



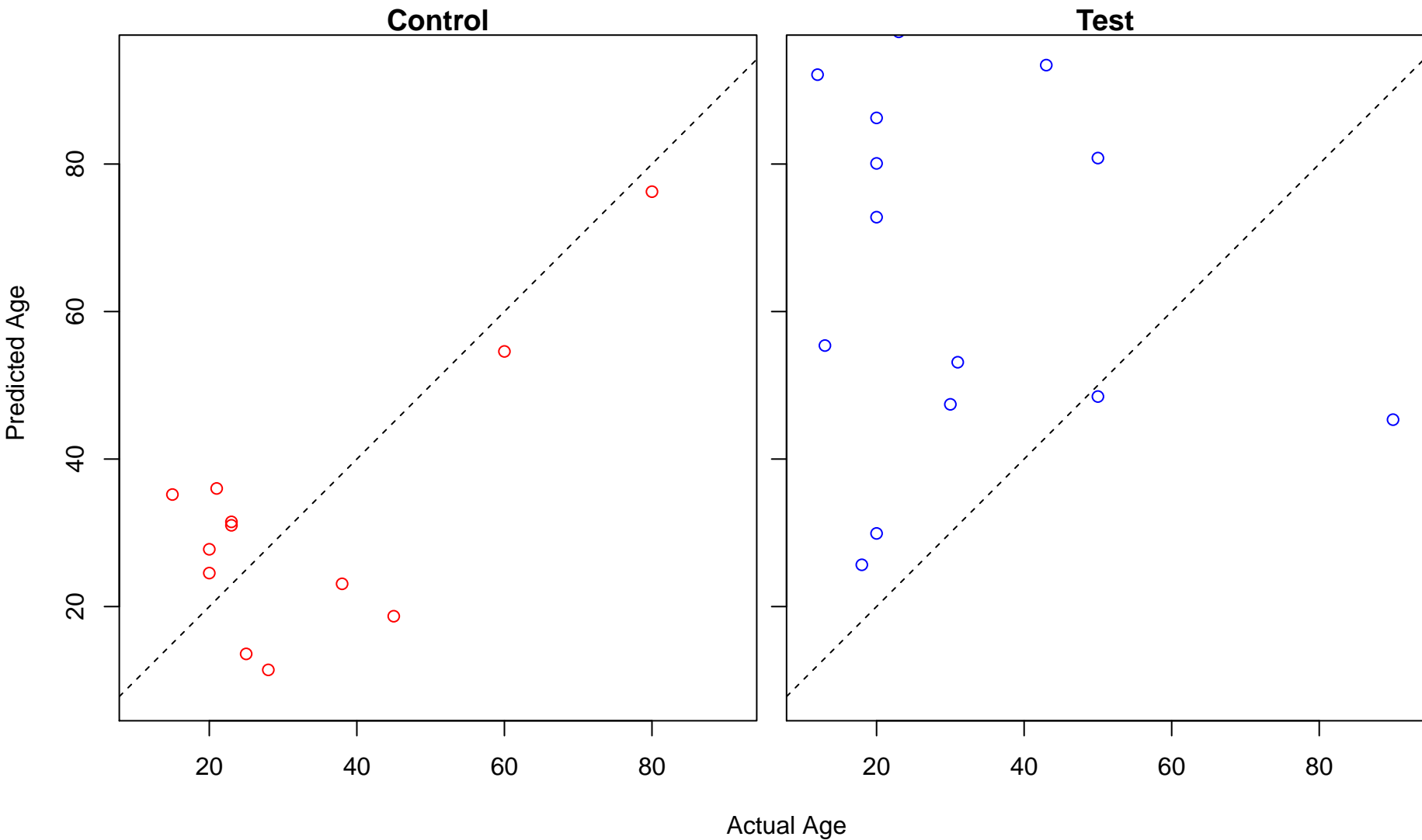
response to interleukin-6 (Score: 5.641069)



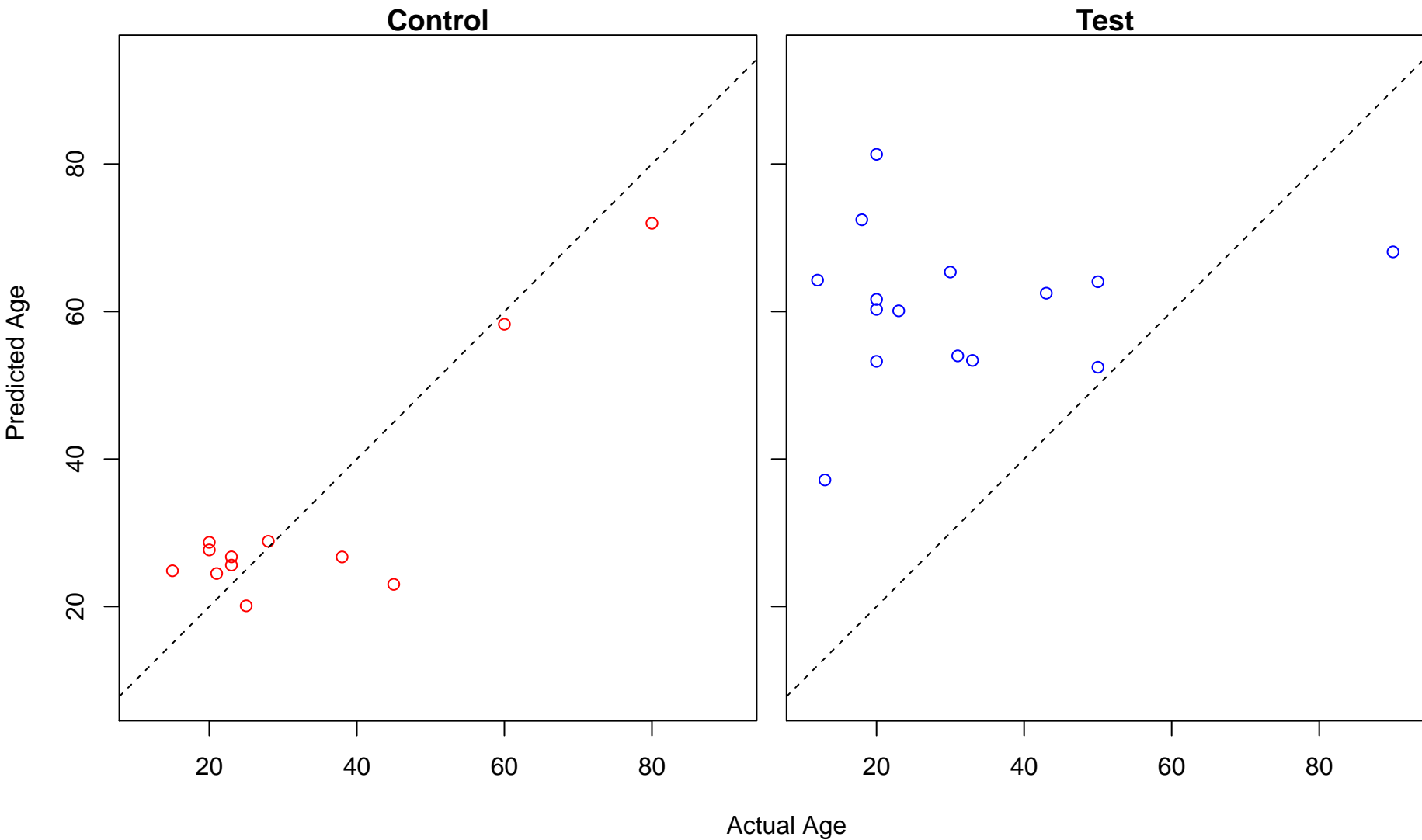
negative regulation of binding (Score: 5.637367)



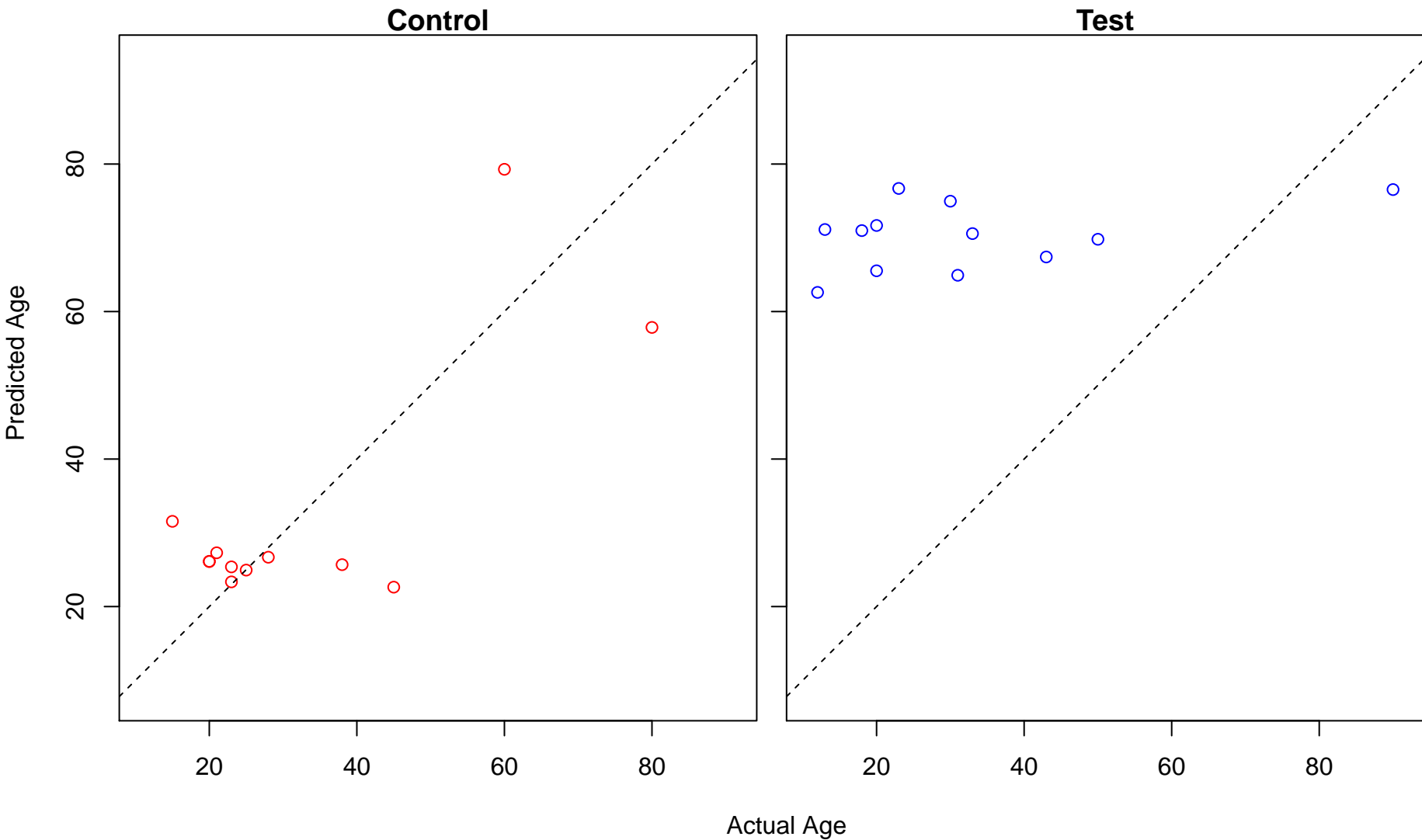
azole transport (Score: 5.635375)



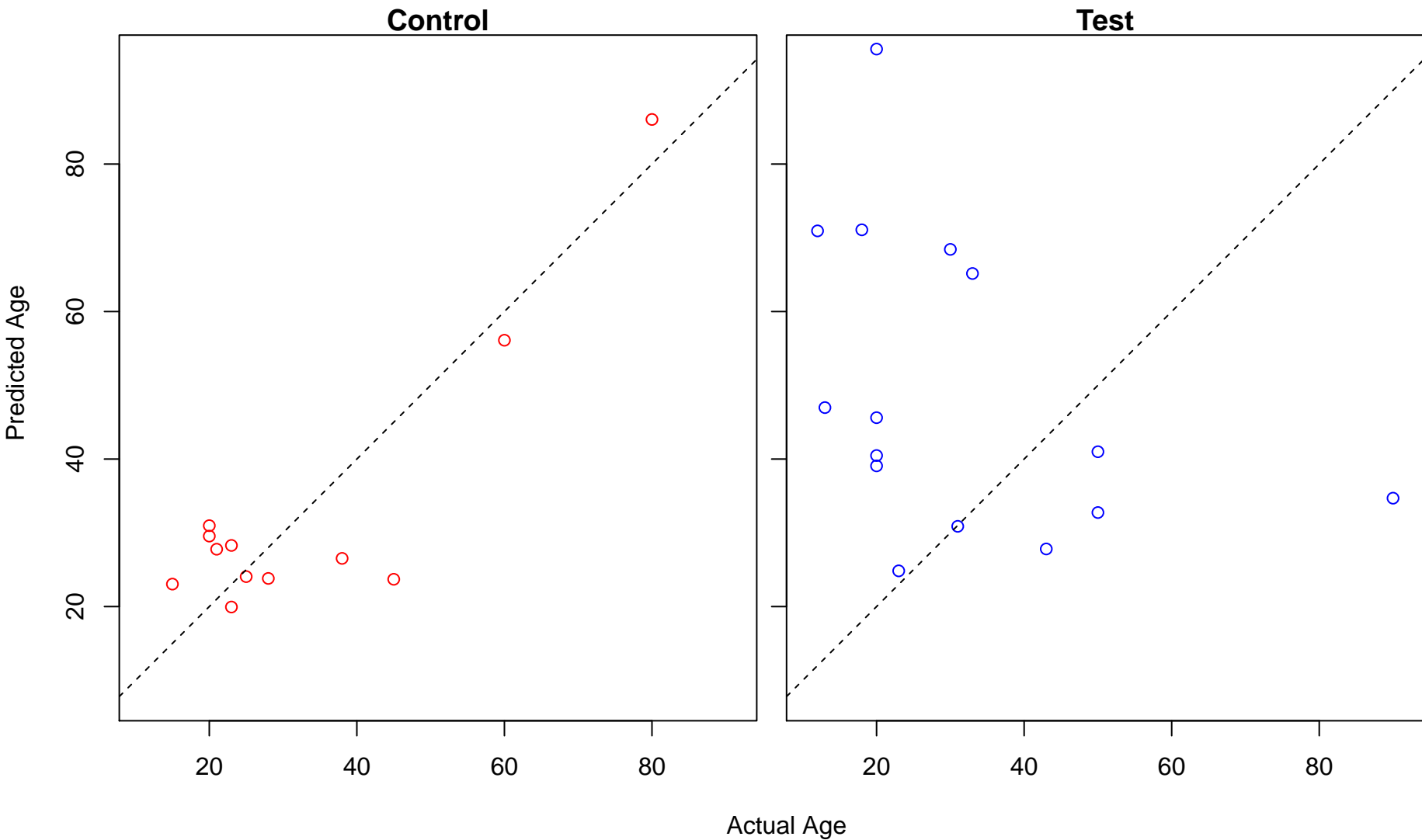
regulation of store-operated calcium channel activity (Score: 5.635323)



establishment of protein localization to chromatin (Score: 5.633128)

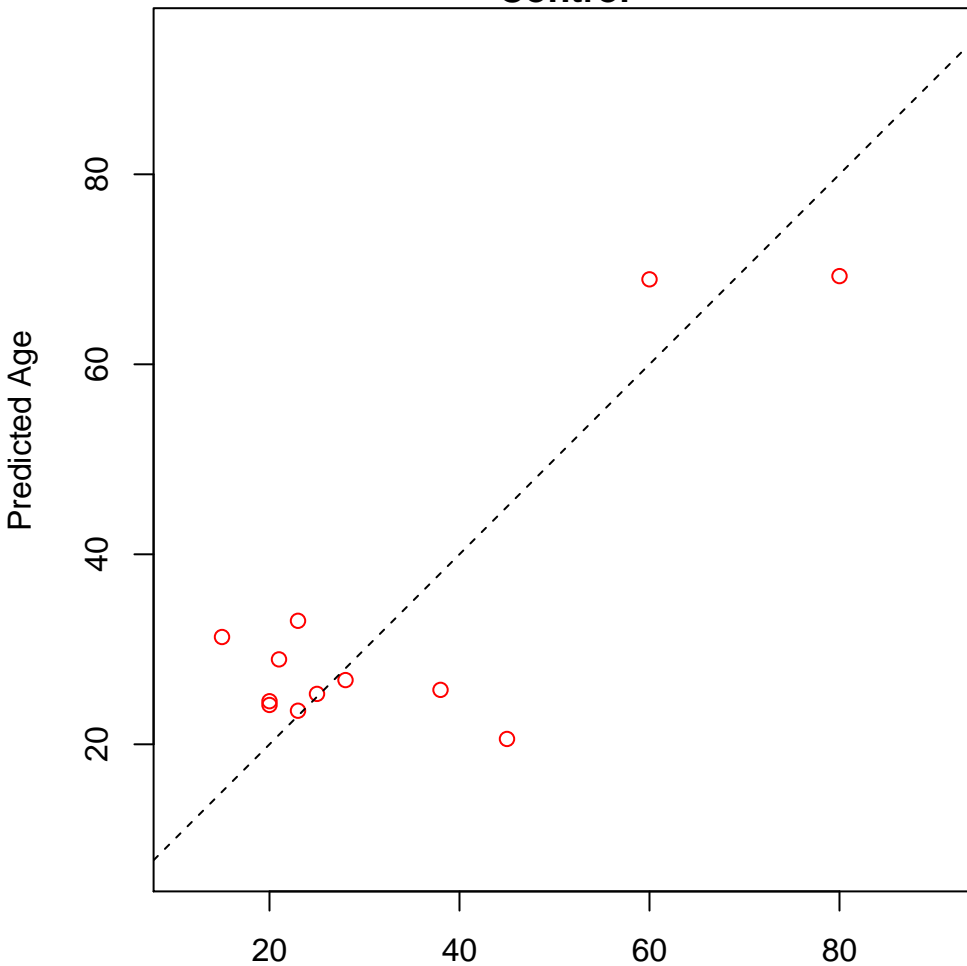


protein localization to chromosome, telomeric region (Score: 5.632331)

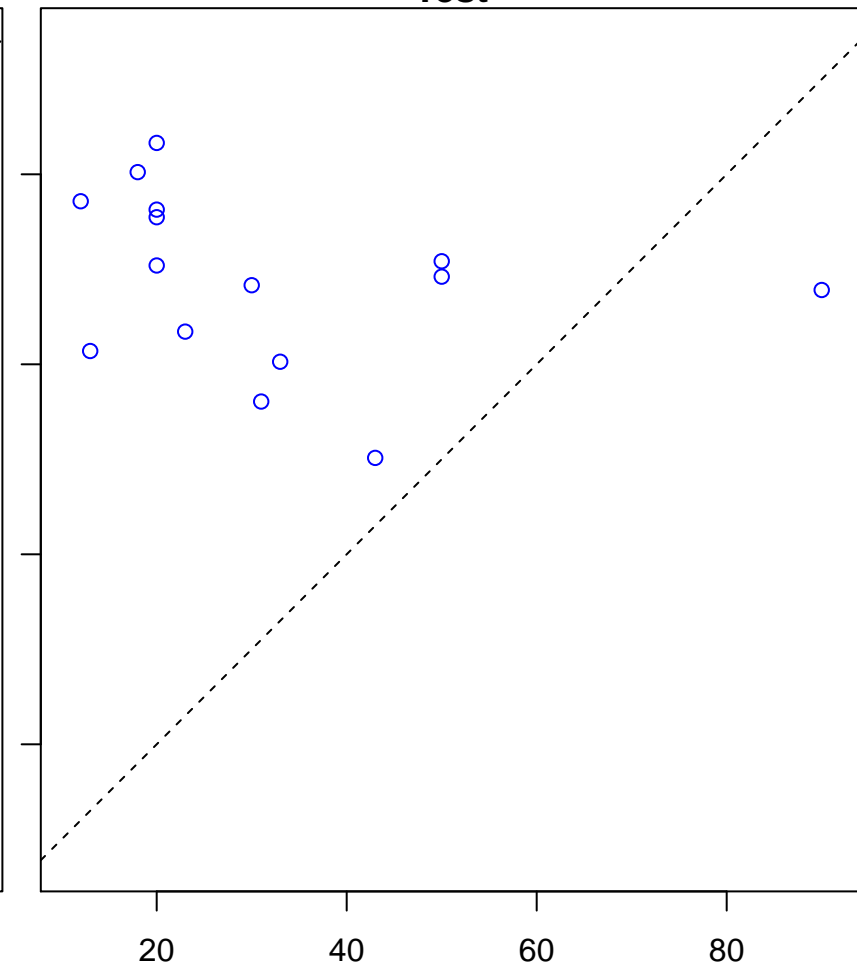


regulation of lamellipodium assembly (Score: 5.628211)

Control

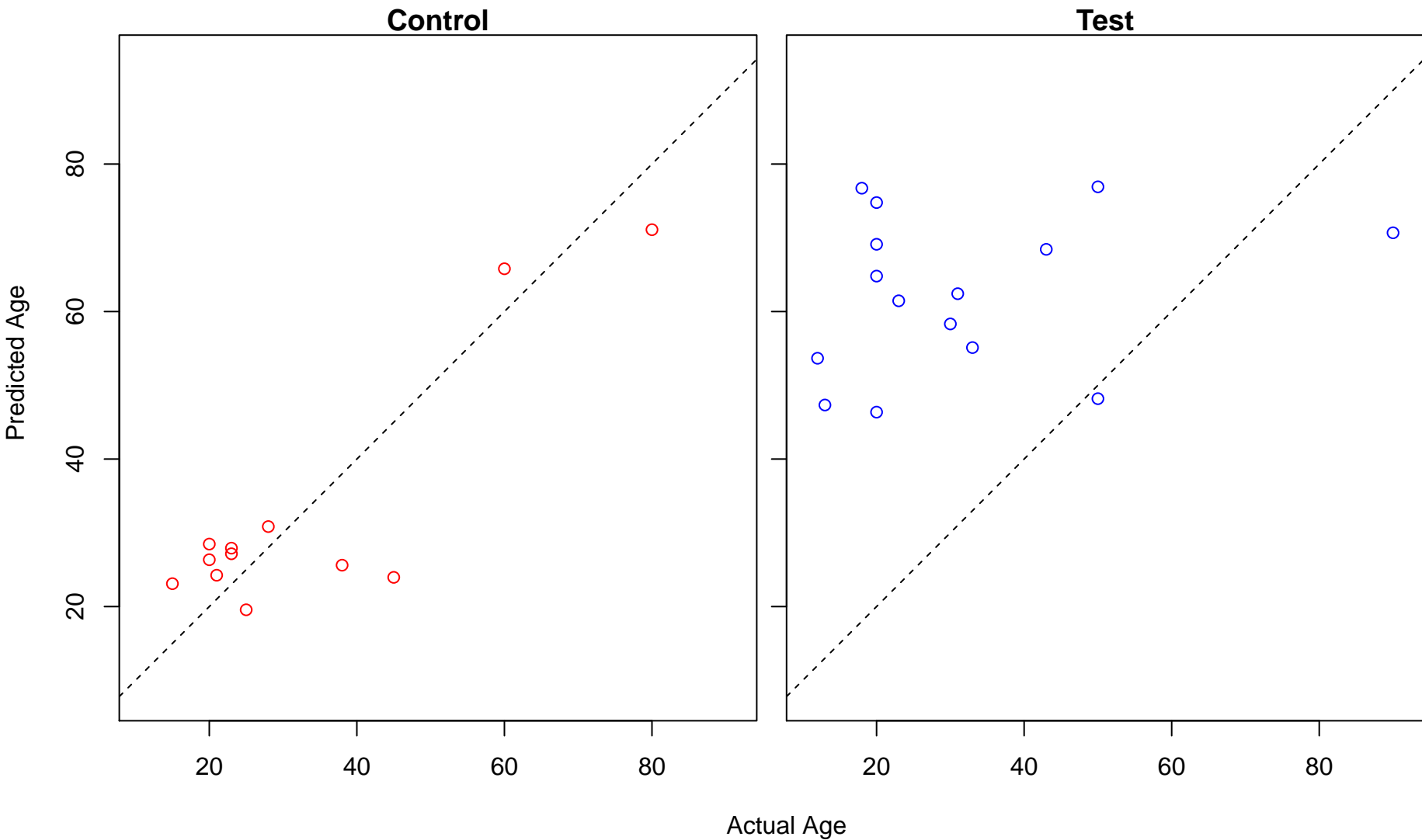


Test

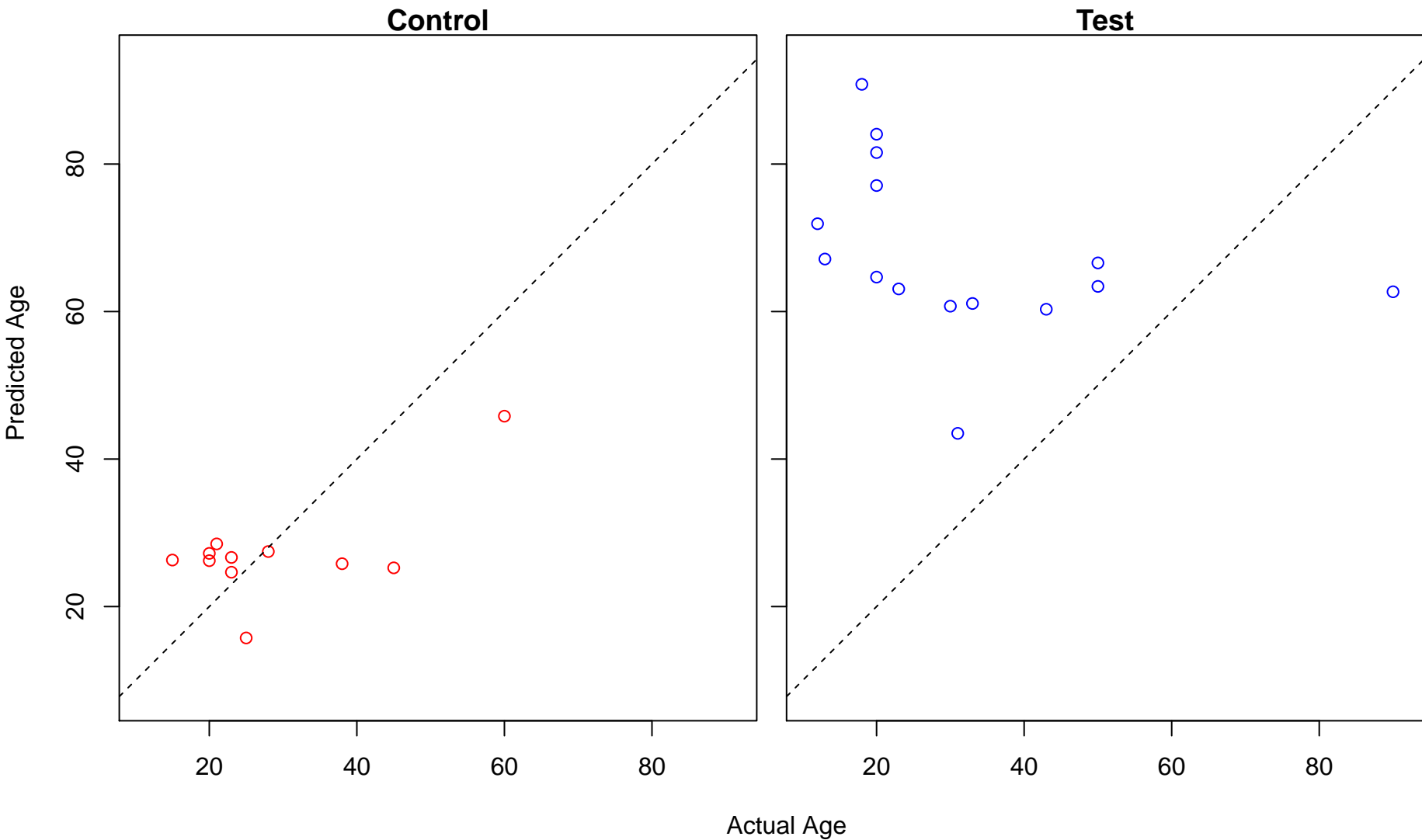


Actual Age

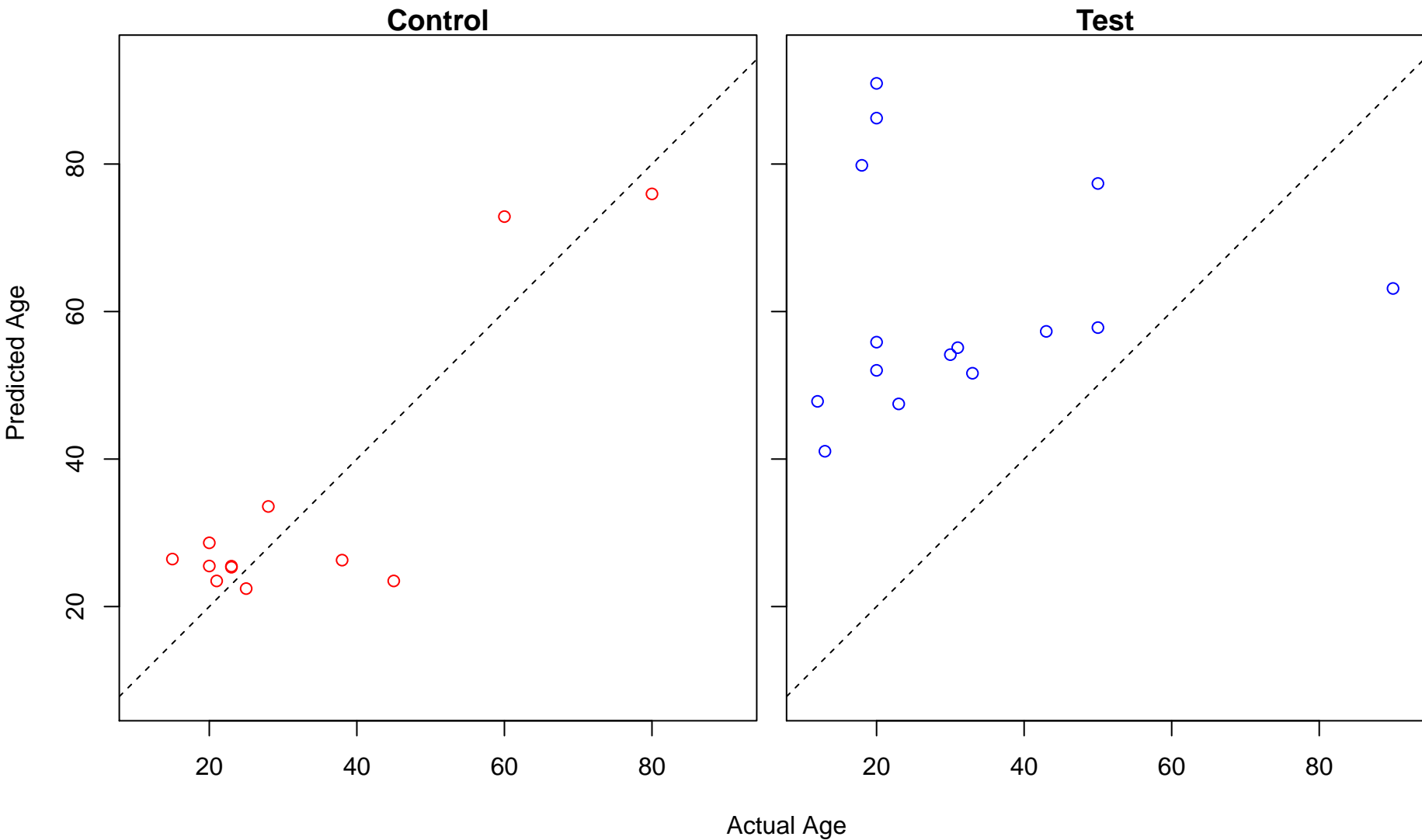
cellular response to glucocorticoid stimulus (Score: 5.622600)



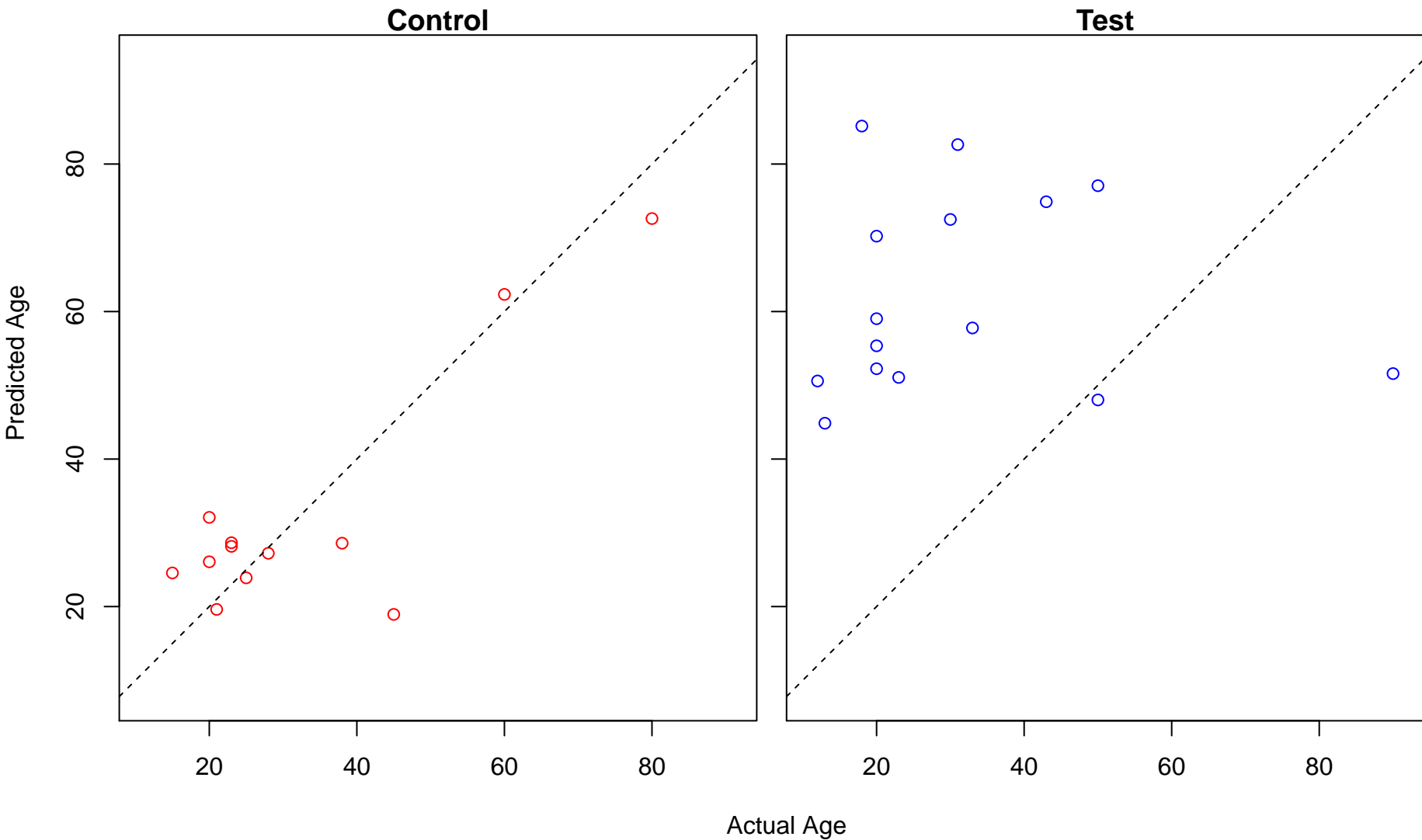
negative regulation of glucose import (Score: 5.621723)



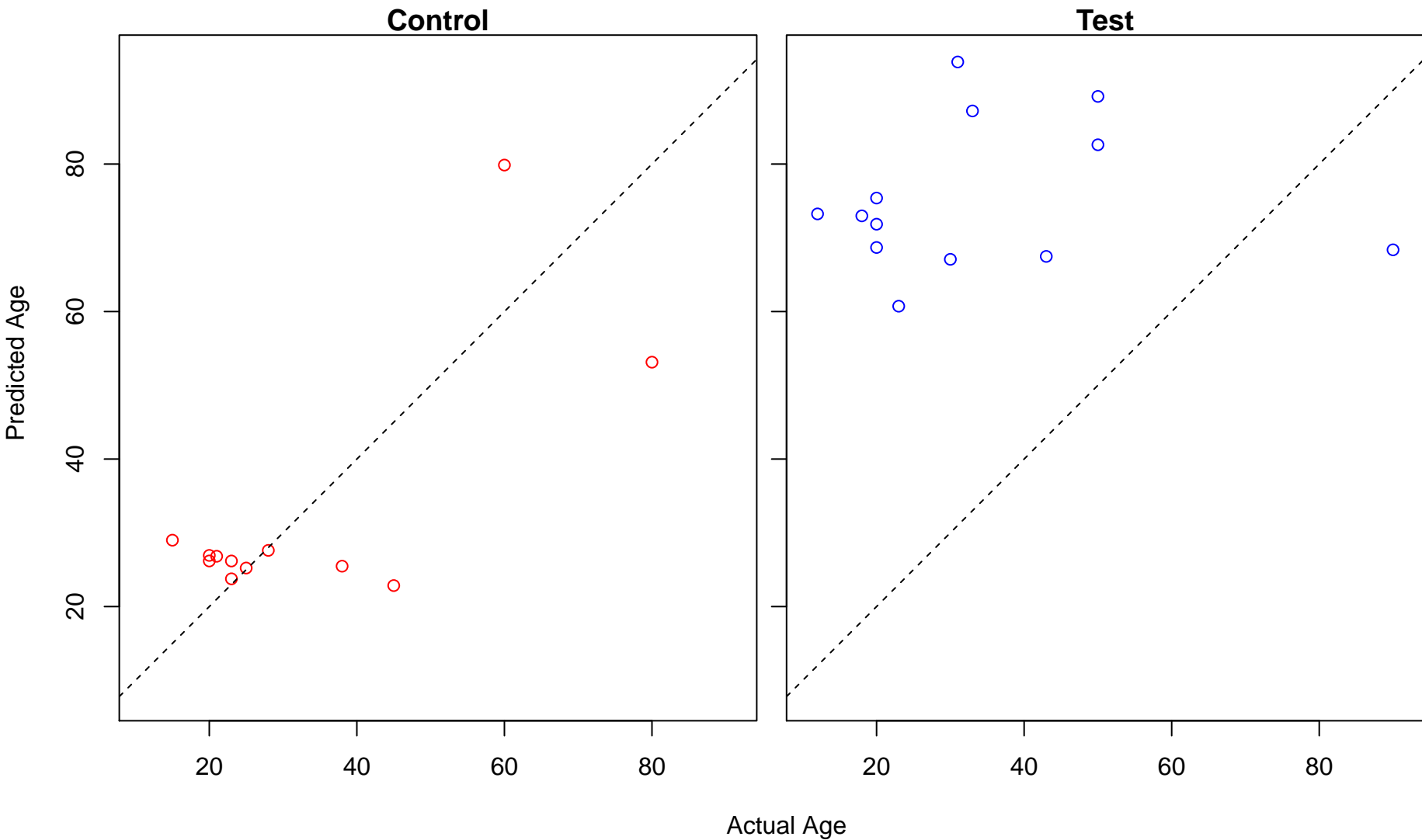
C-terminal protein lipidation (Score: 5.617883)



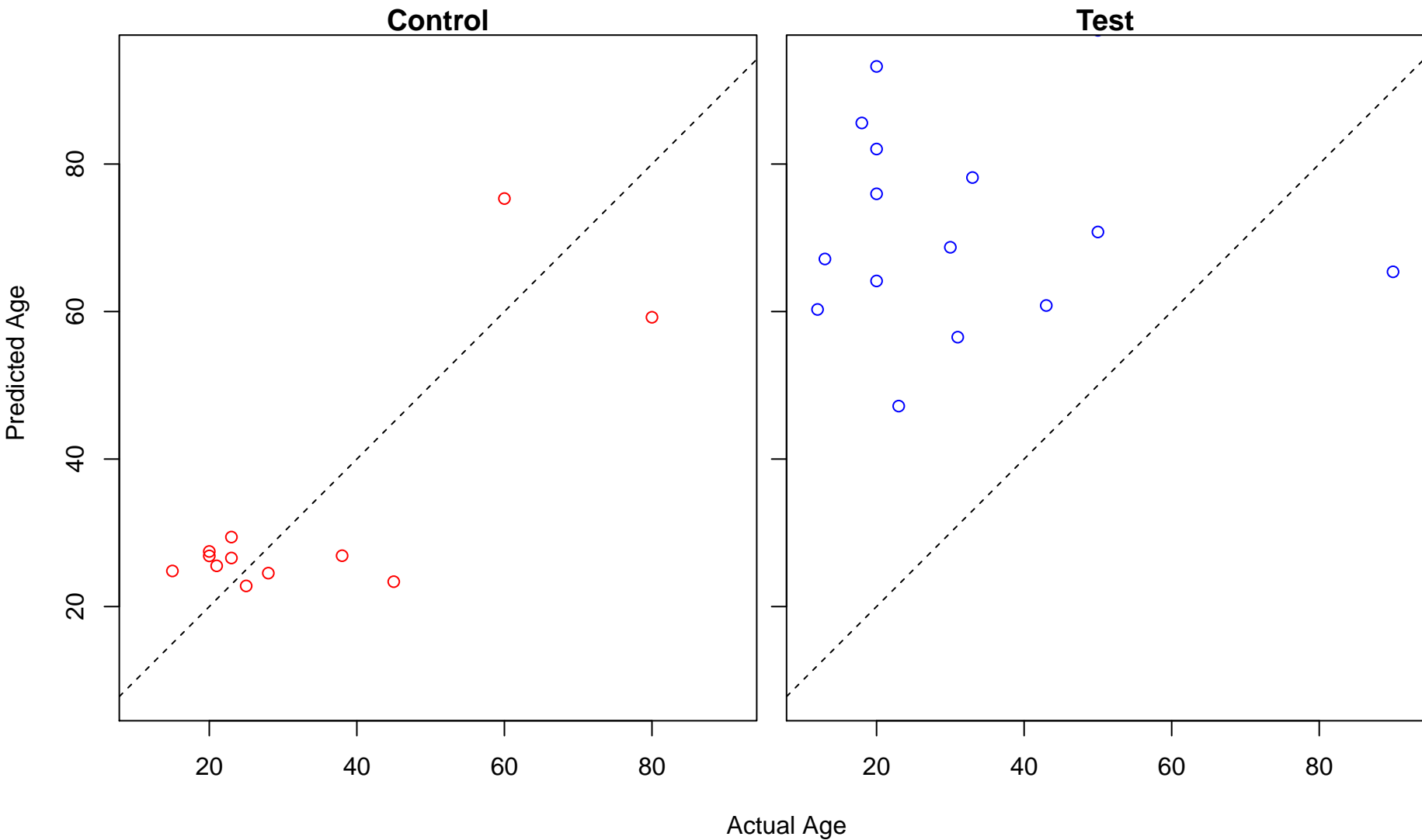
regulation of protein homodimerization activity (Score: 5.617731)



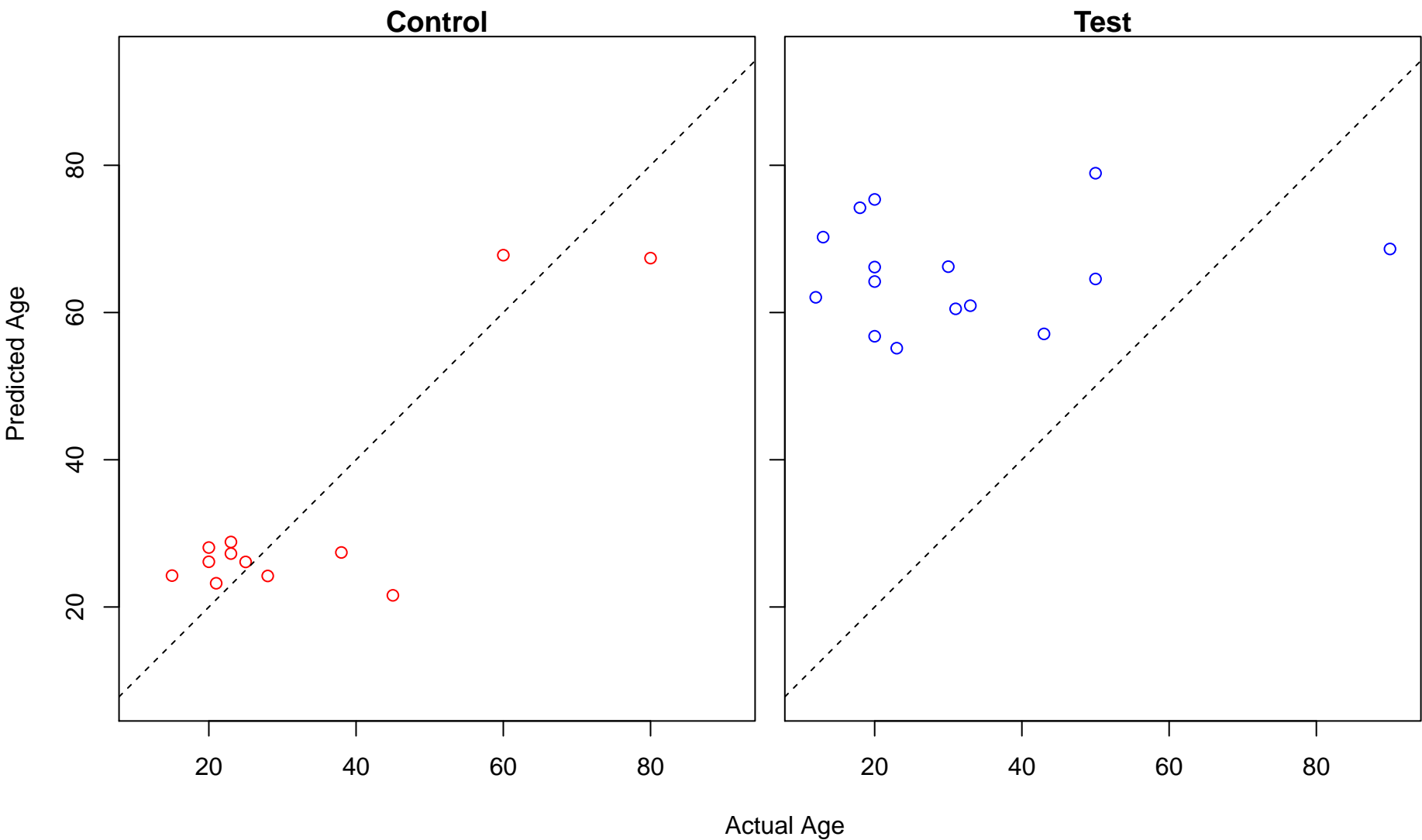
cellular transition metal ion homeostasis (Score: 5.617105)



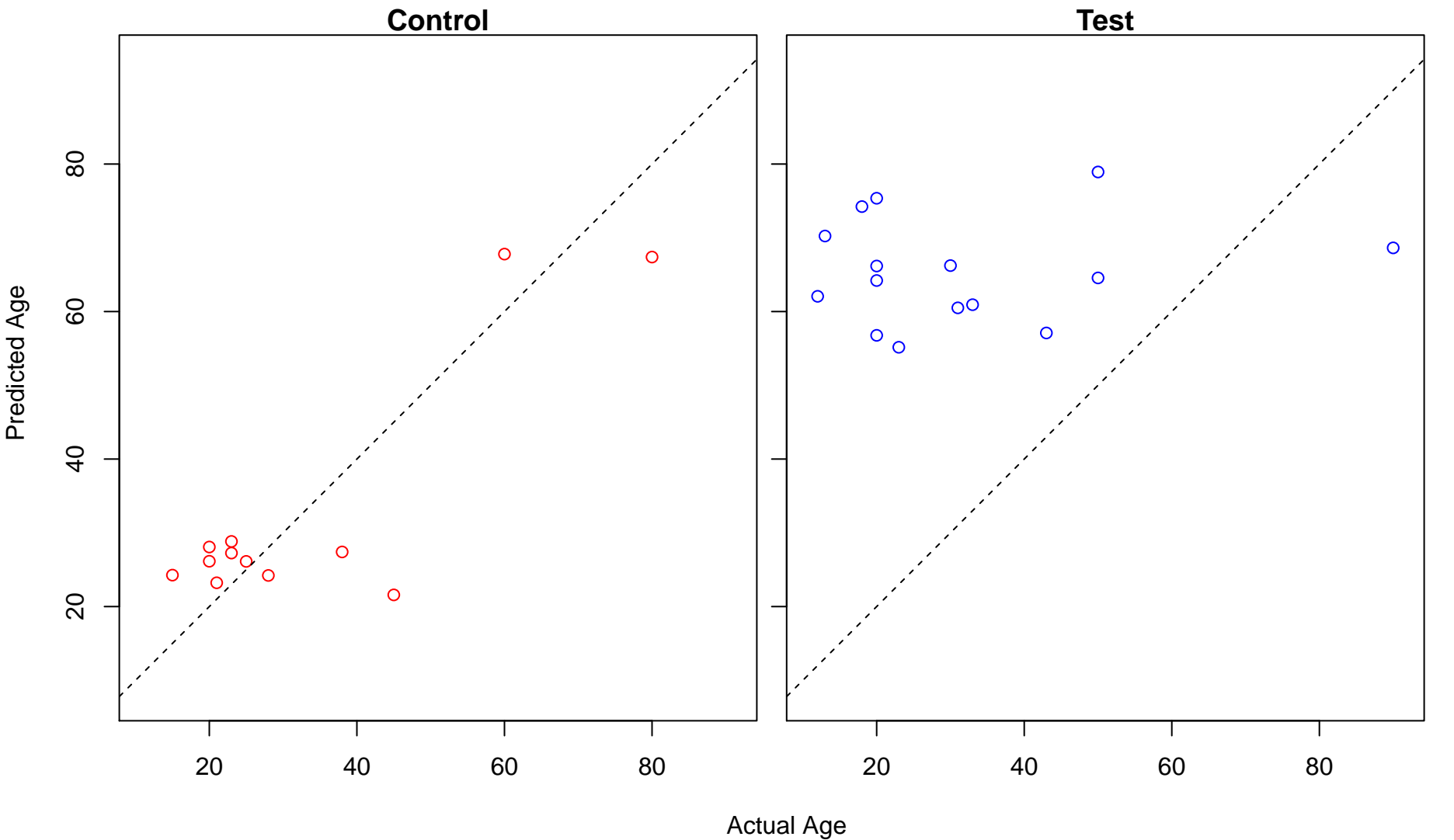
regulation of lamellipodium morphogenesis (Score: 5.615138)



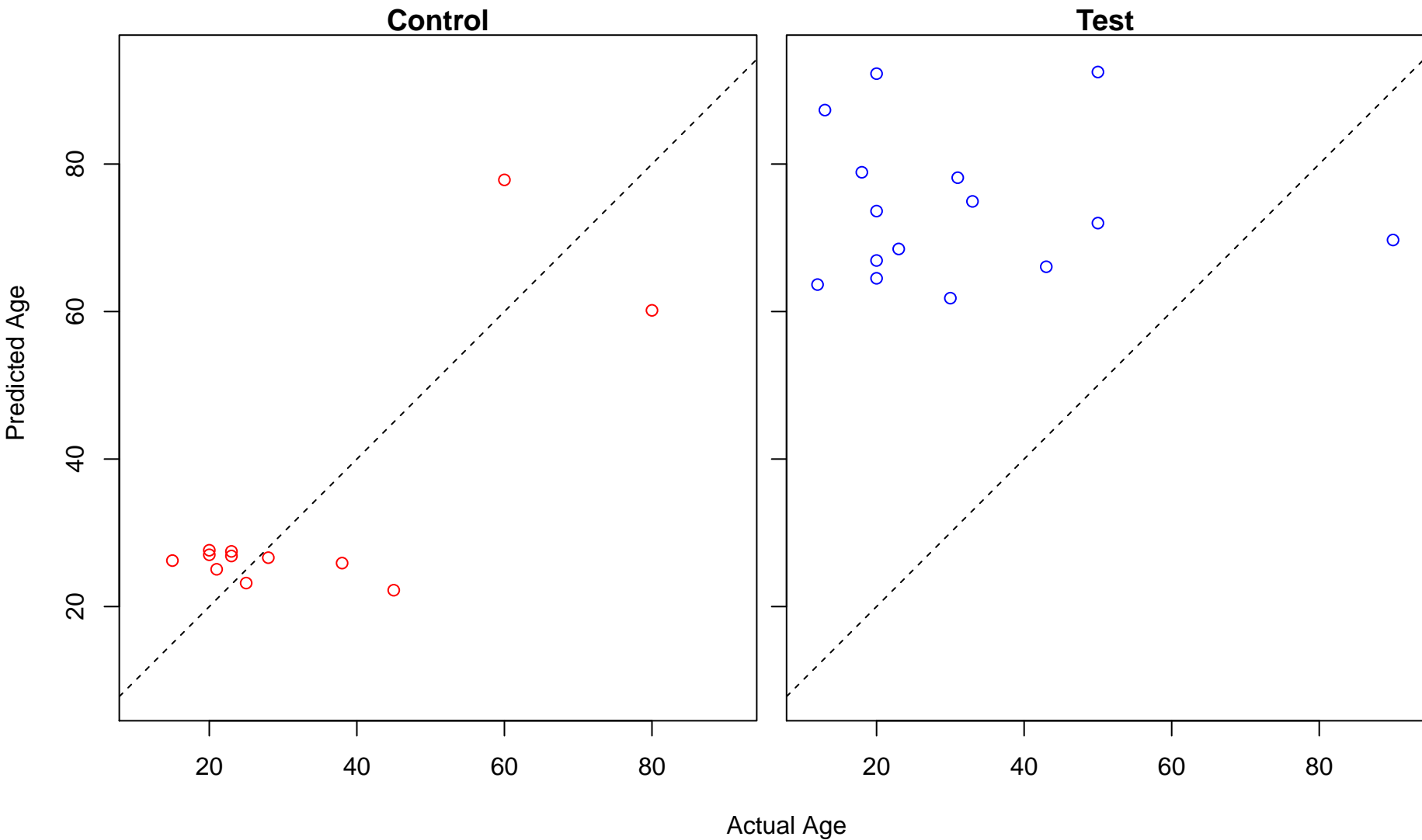
regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay (Score: 5.6)



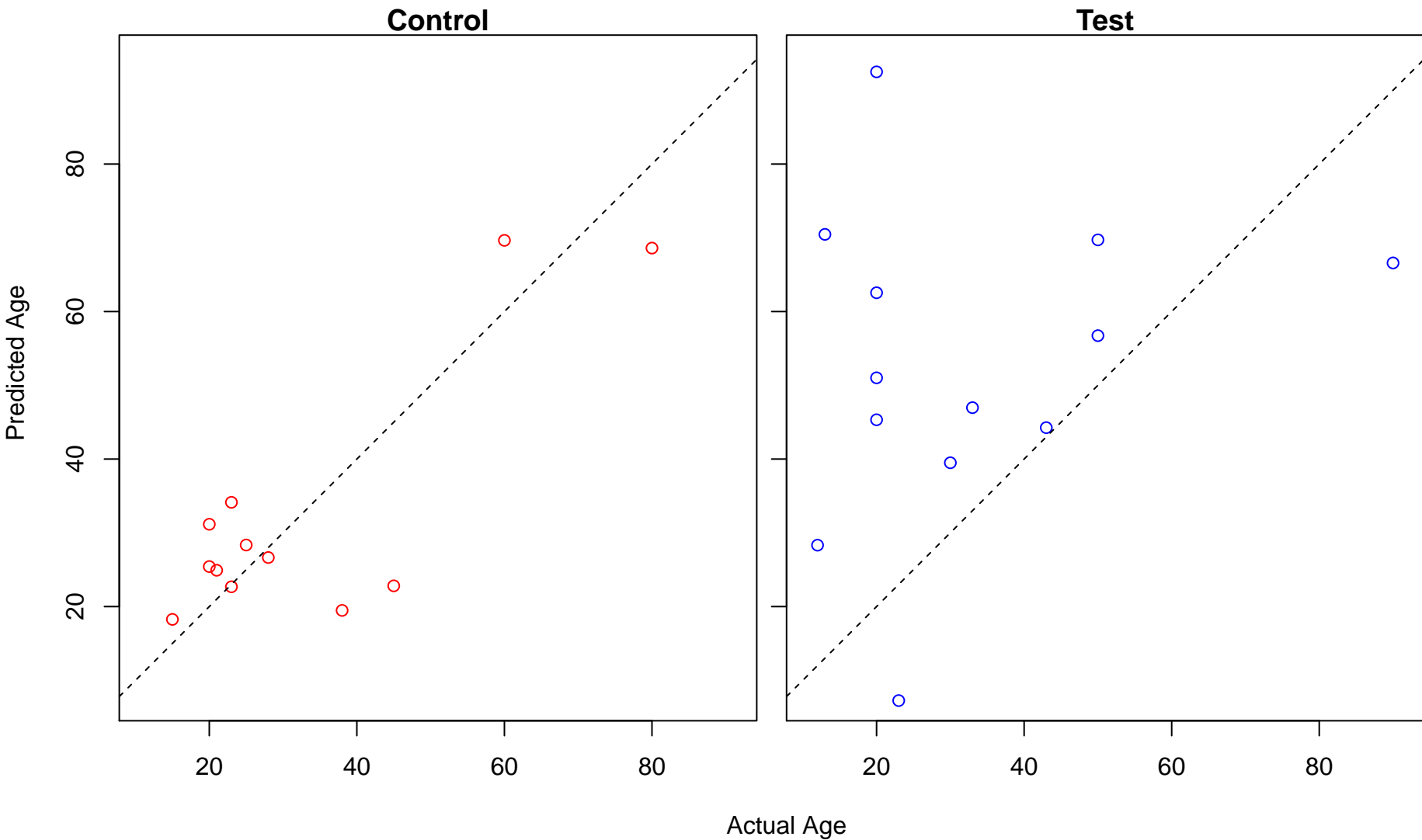
positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay (Score



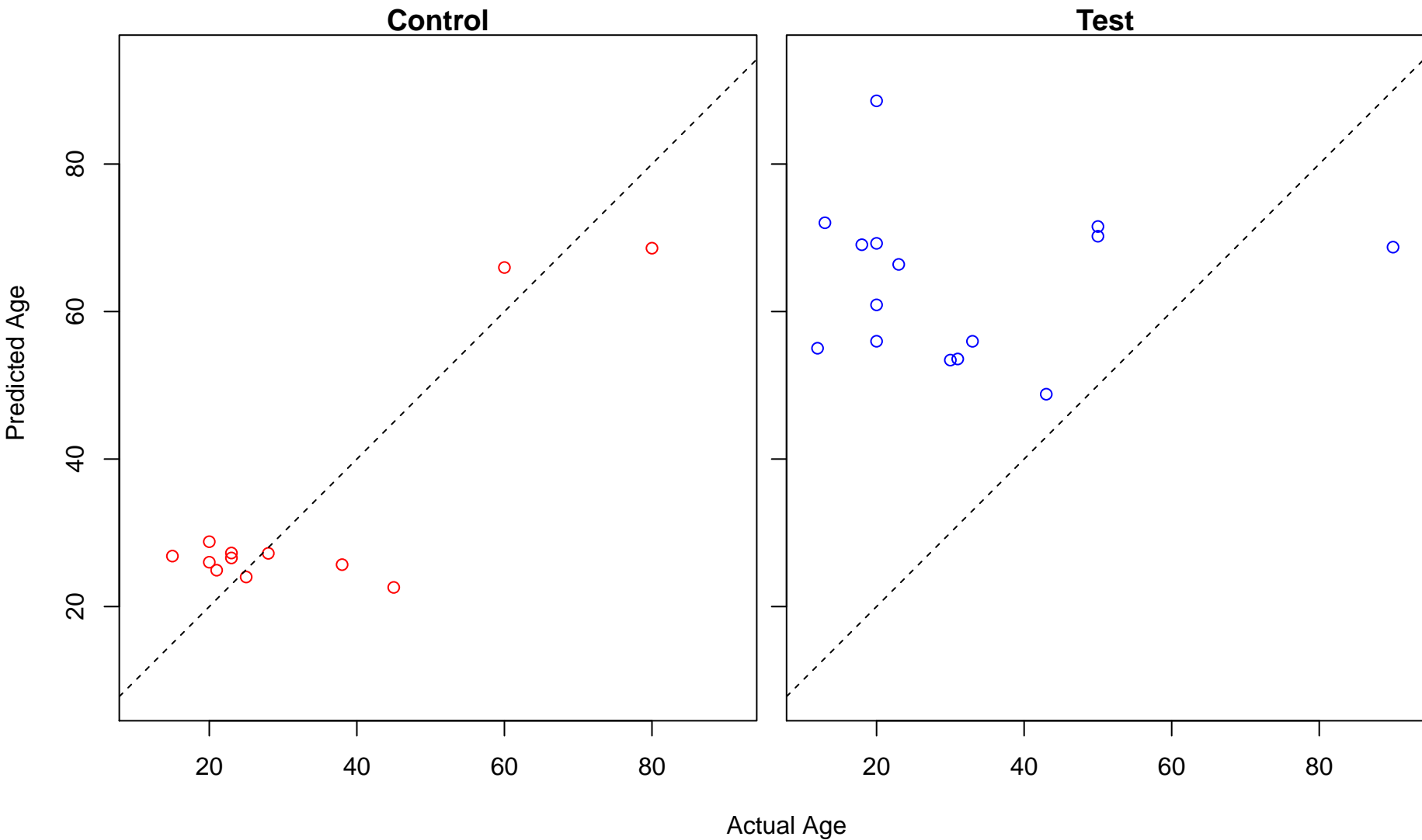
regulation of membrane potential (Score: 5.613660)



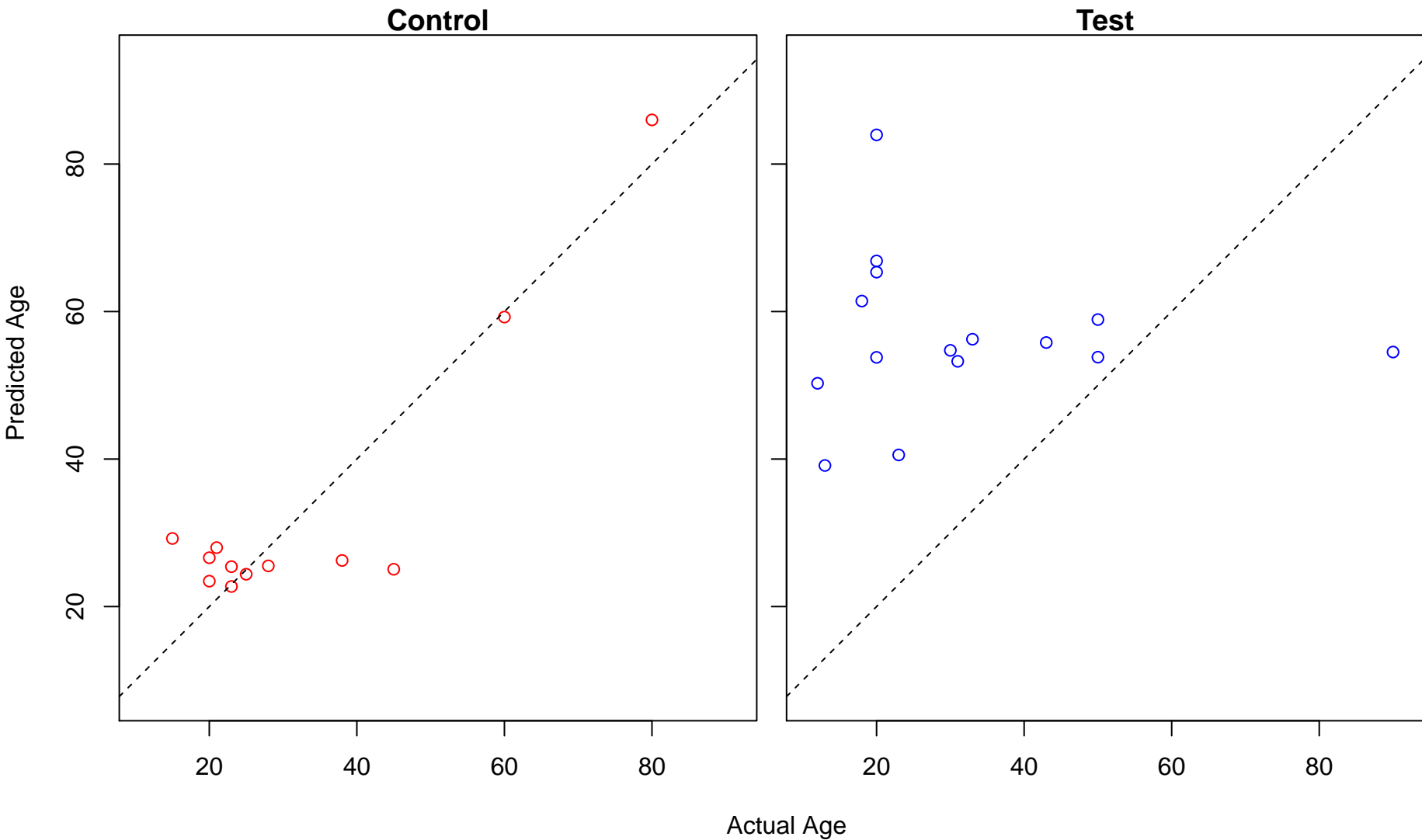
multi-organism behavior (Score: 5.612861)



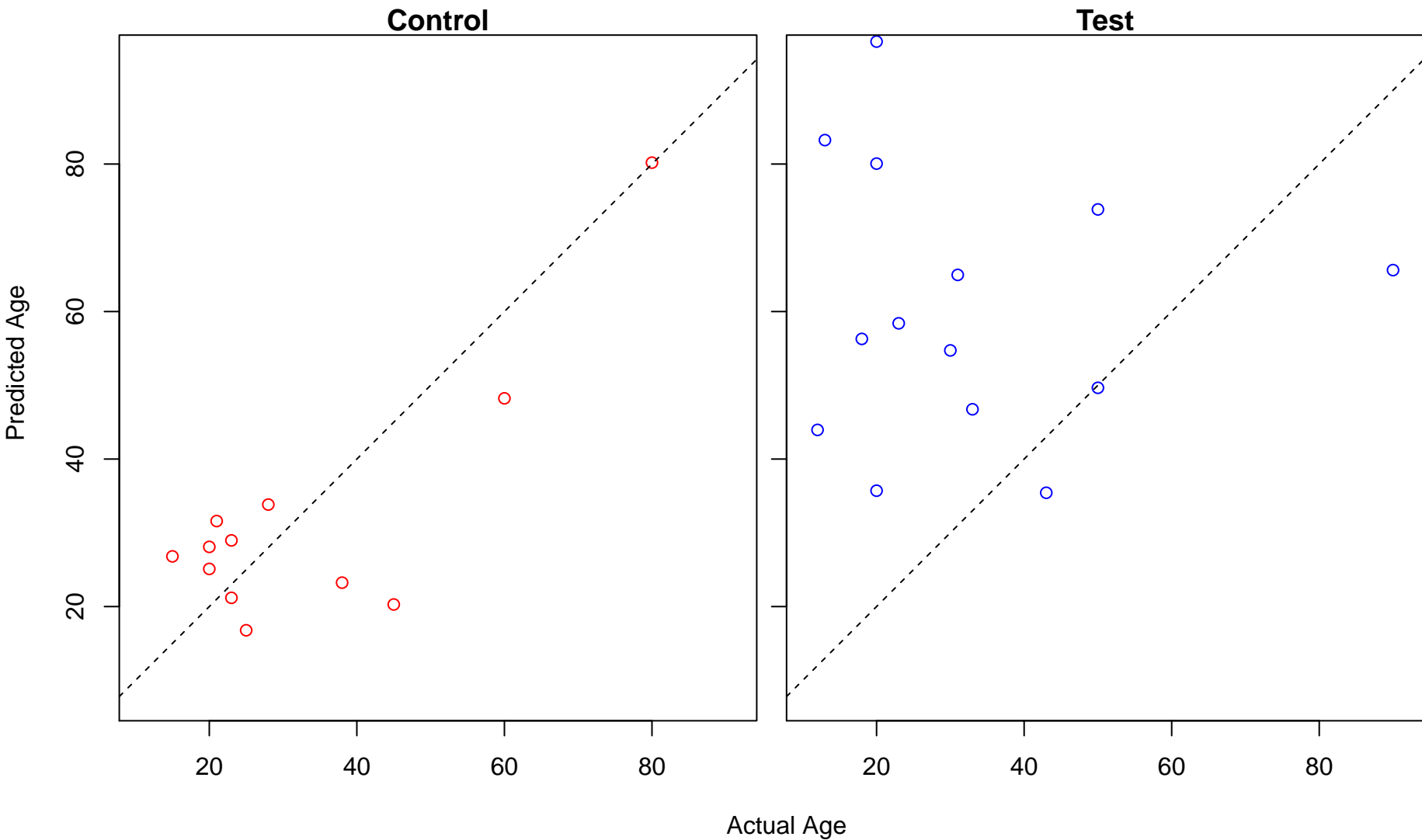
regulation of translation (Score: 5.612301)



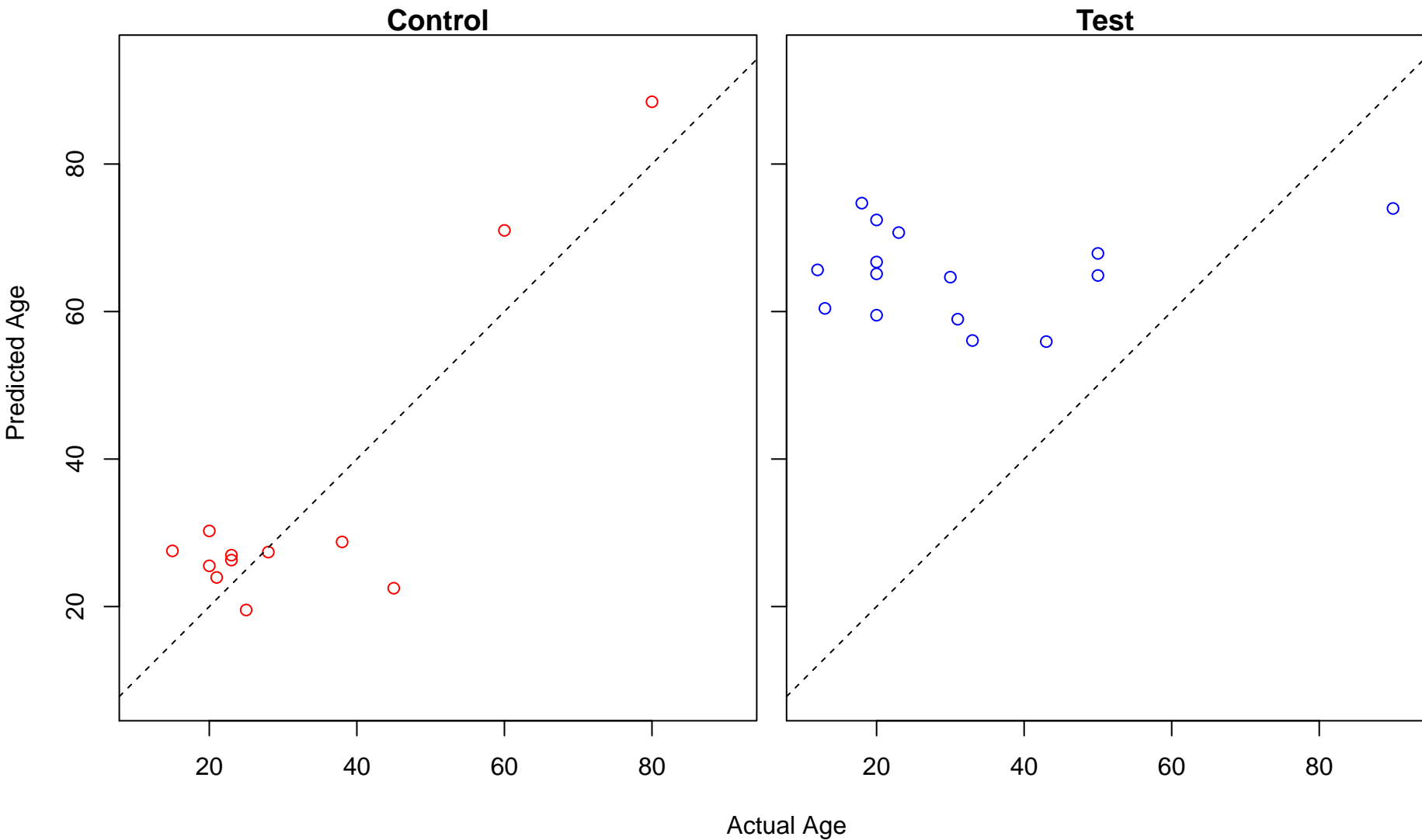
regulation of cell projection assembly (Score: 5.61696)



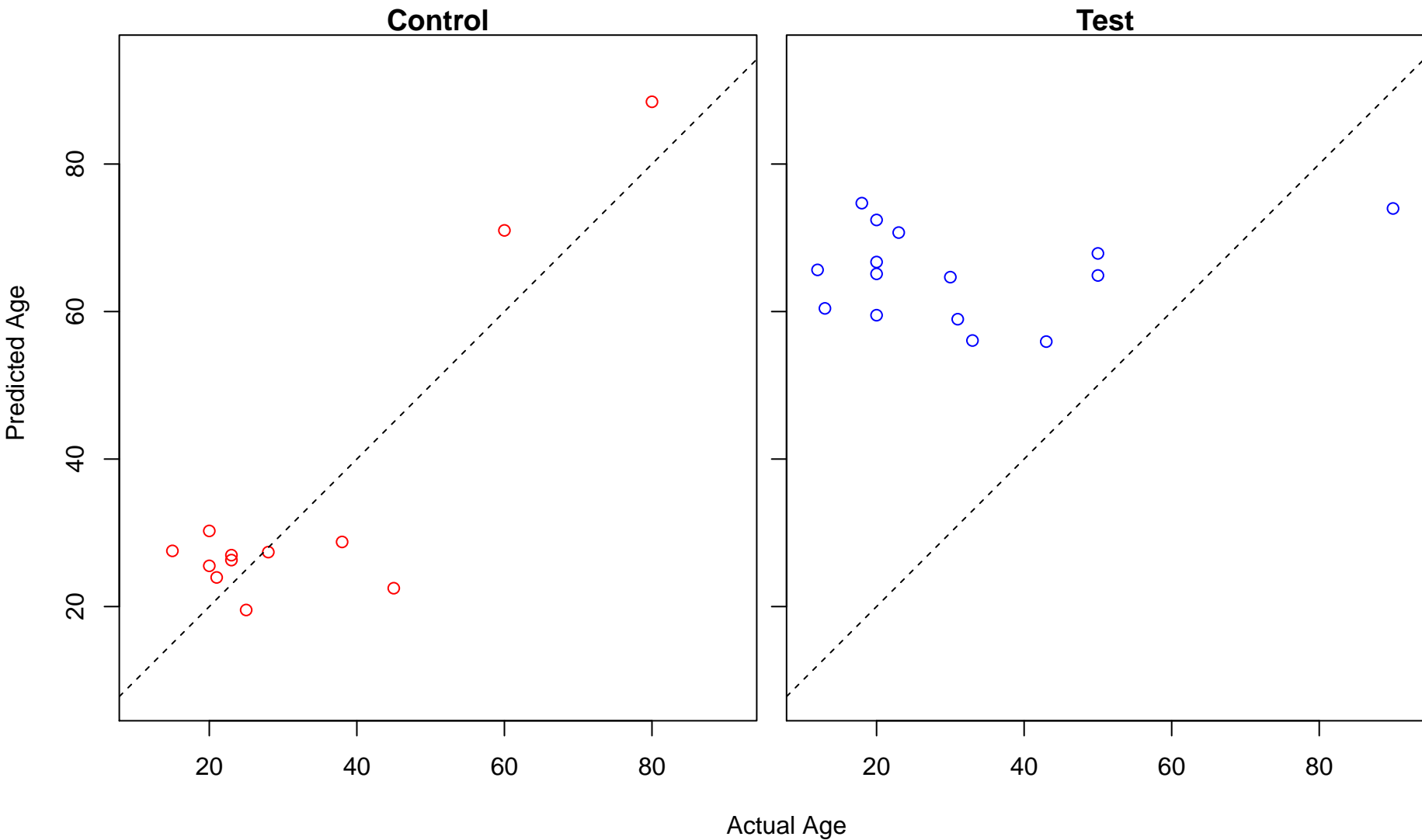
regulation of mitochondrial fusion (Score: 5.609895)



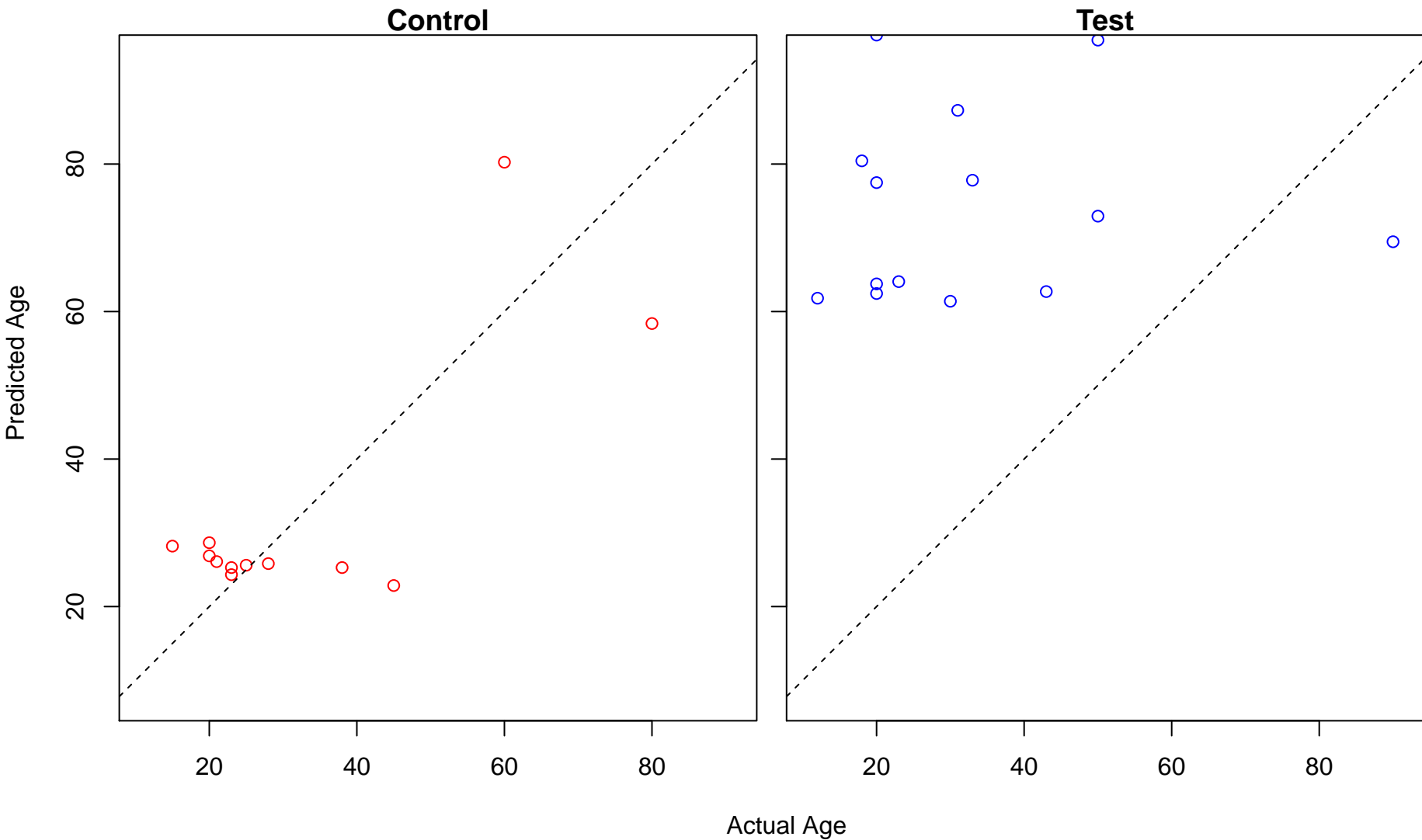
negative regulation of phosphorus metabolic process (Score: 5.609542)



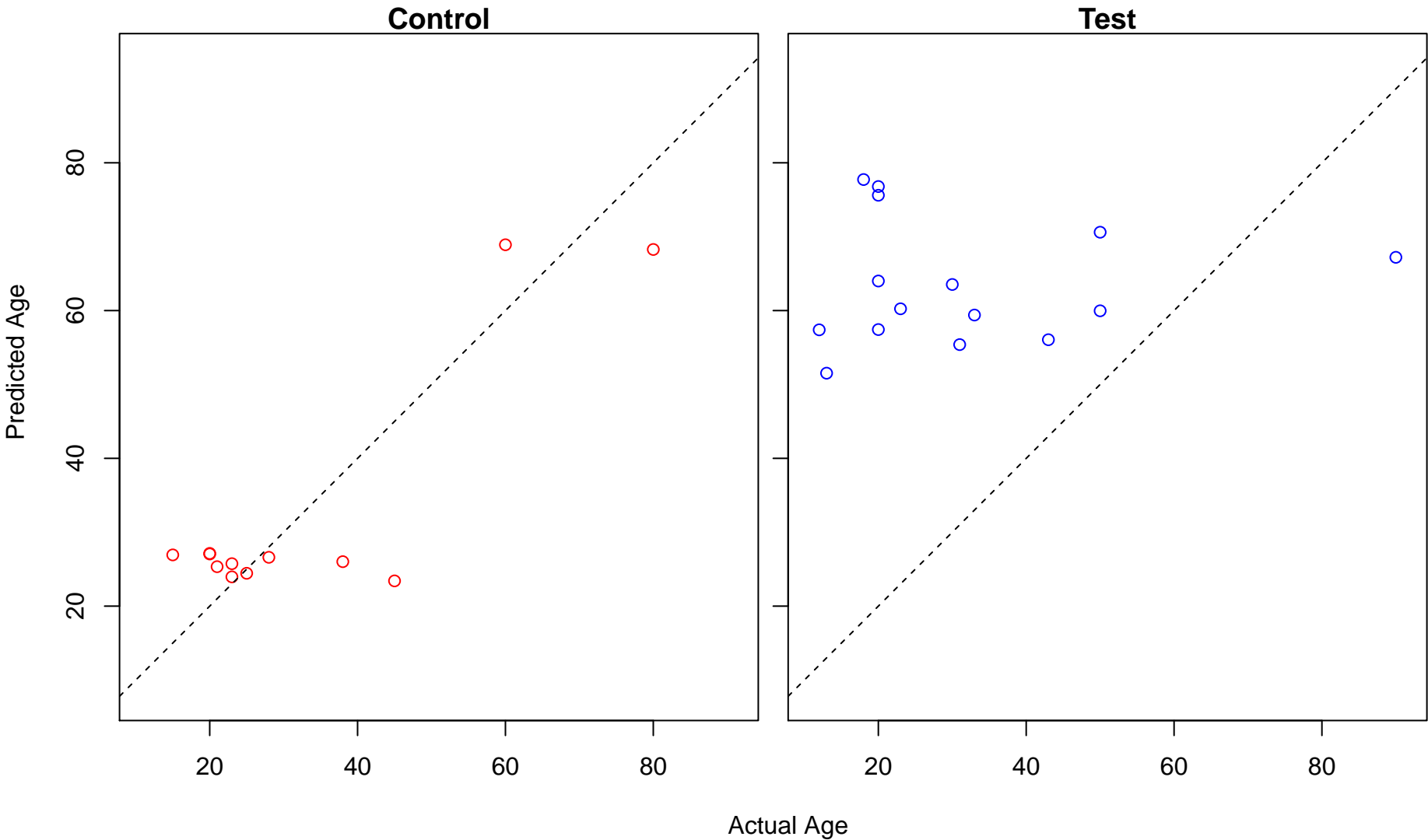
negative regulation of phosphate metabolic process (Score: 5.609542)



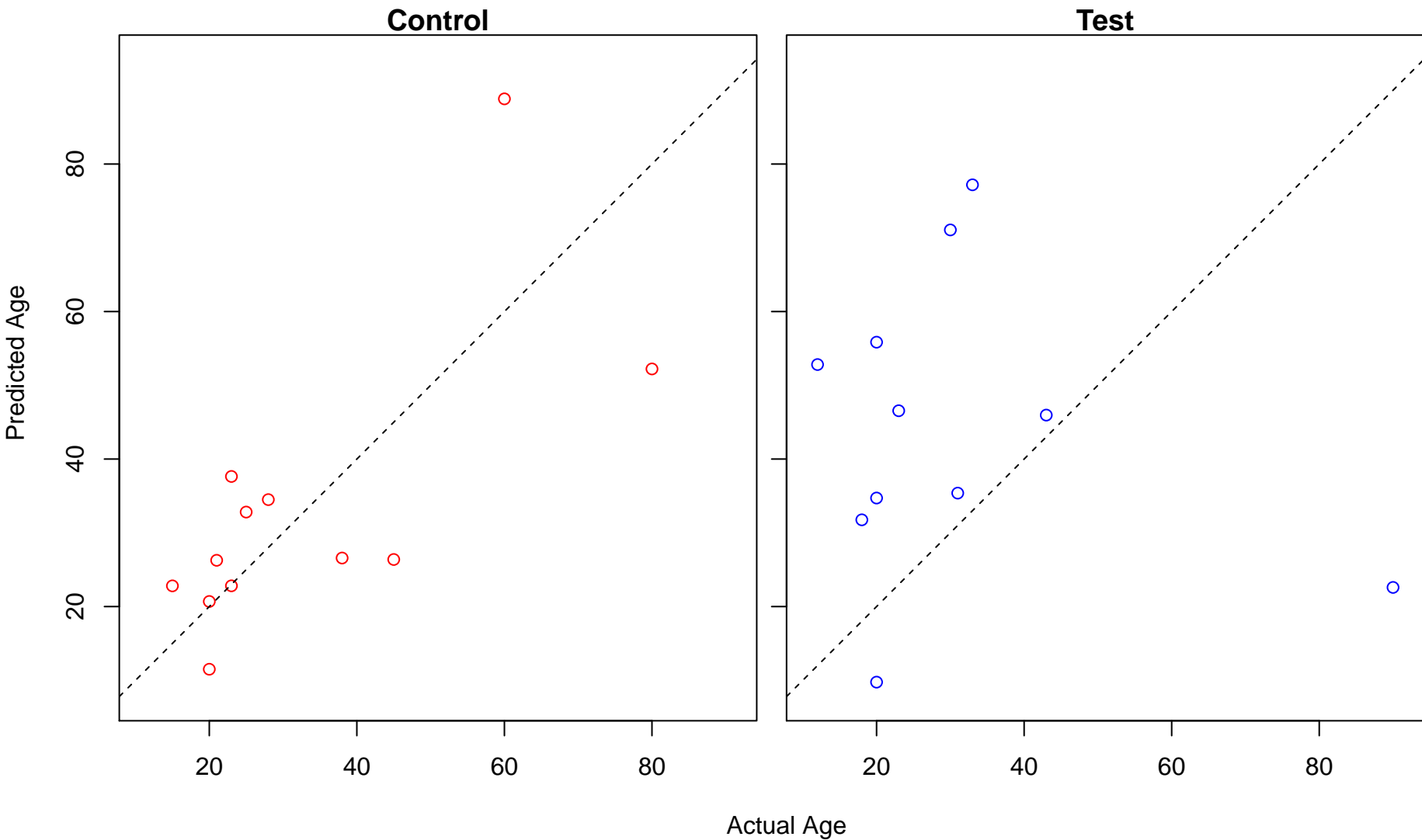
cell-cell junction organization (Score: 5.606936)



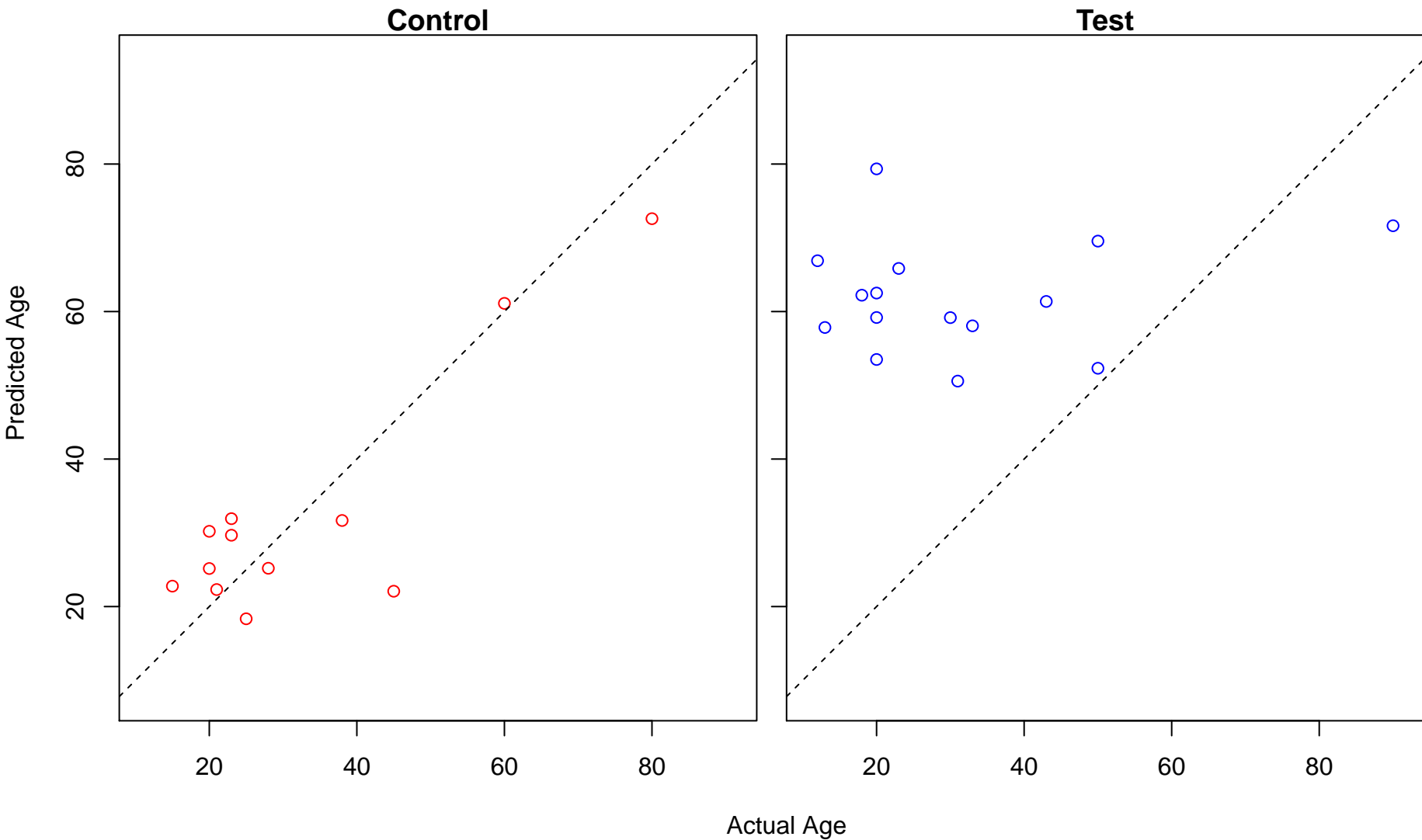
ubiquitin-independent protein catabolic process via the multivesicular body sorting pathway (Score: 5.6



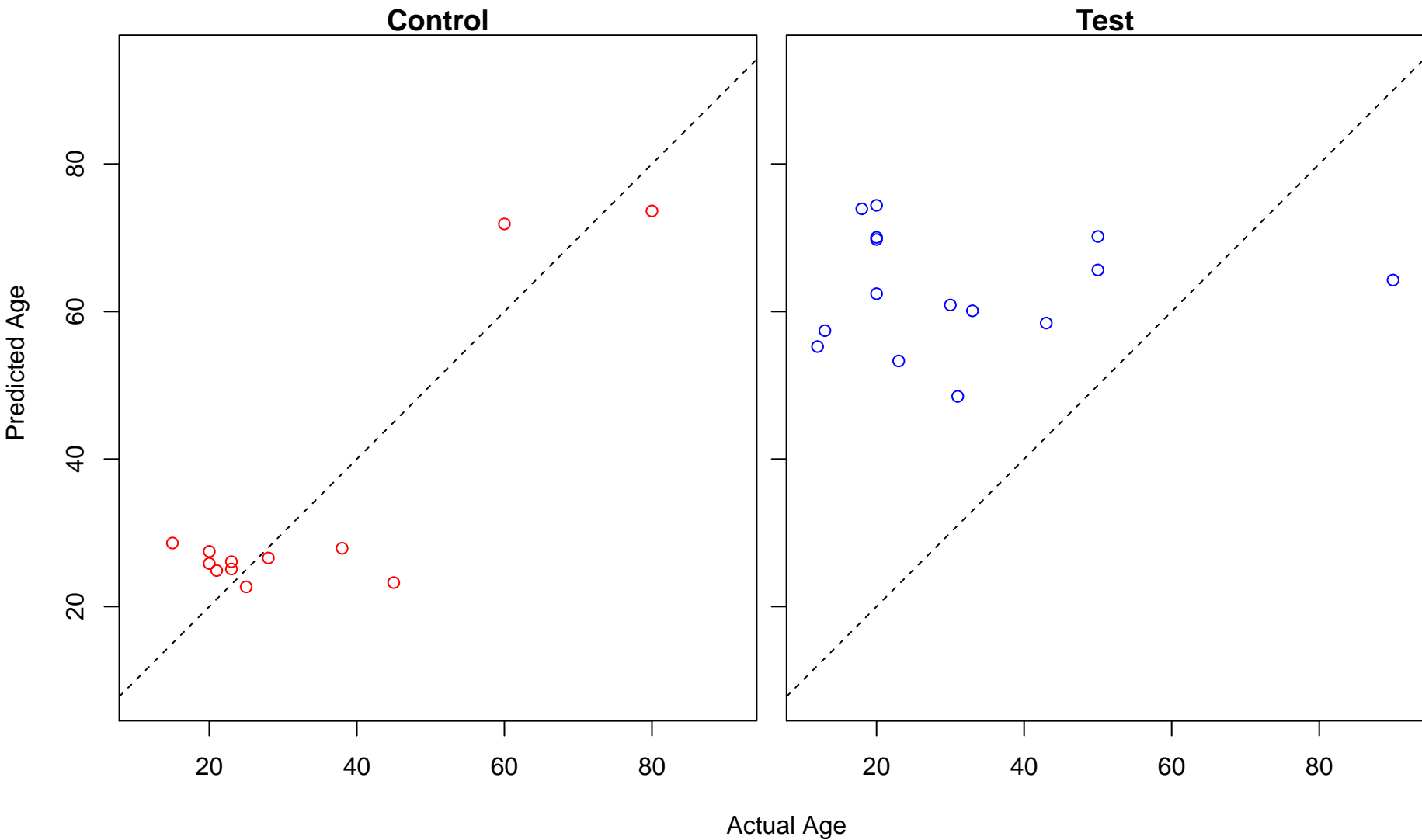
T cell activation involved in immune response (Score: 5.605343)



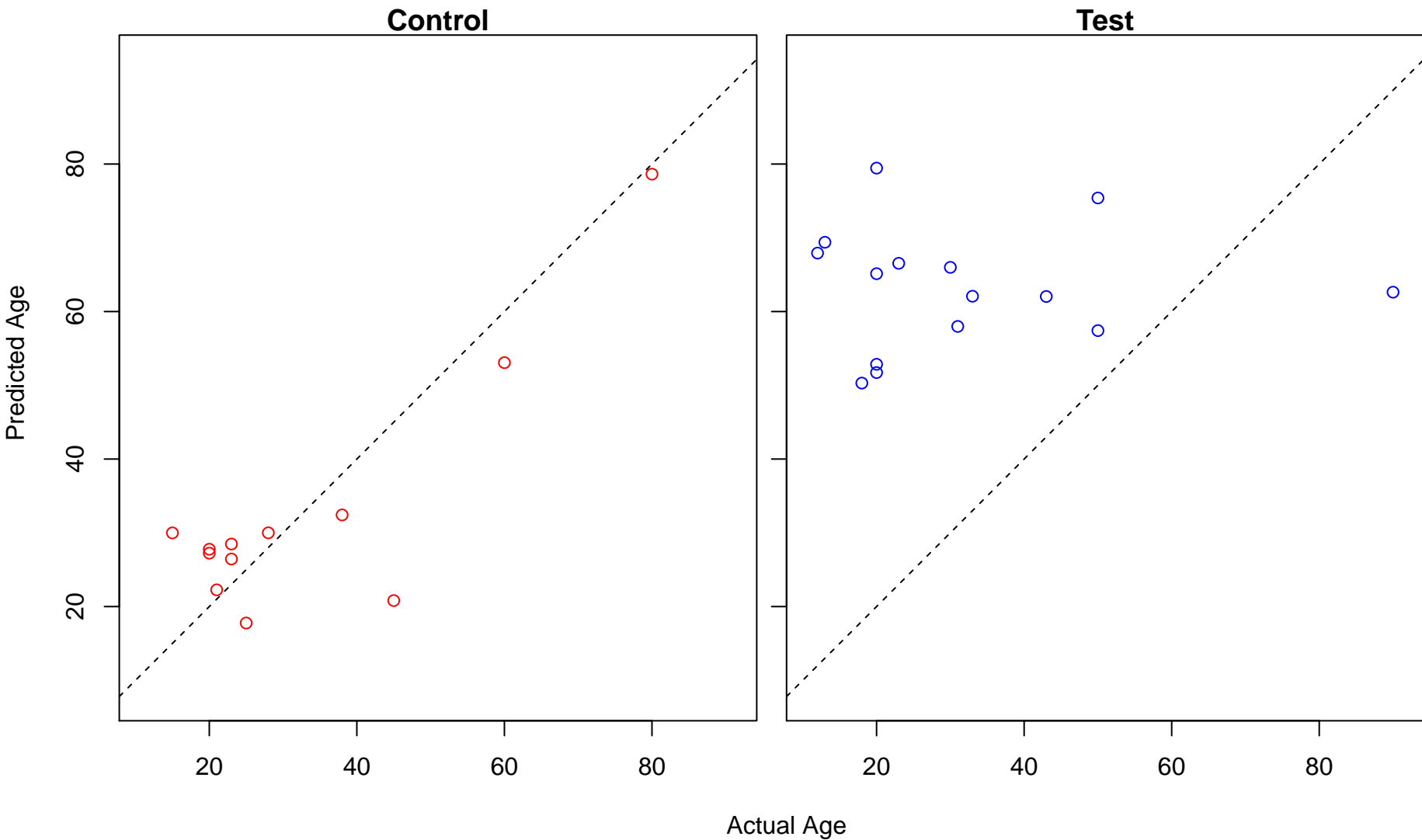
regulation of glycogen (starch) synthase activity (Score: 5.604544)



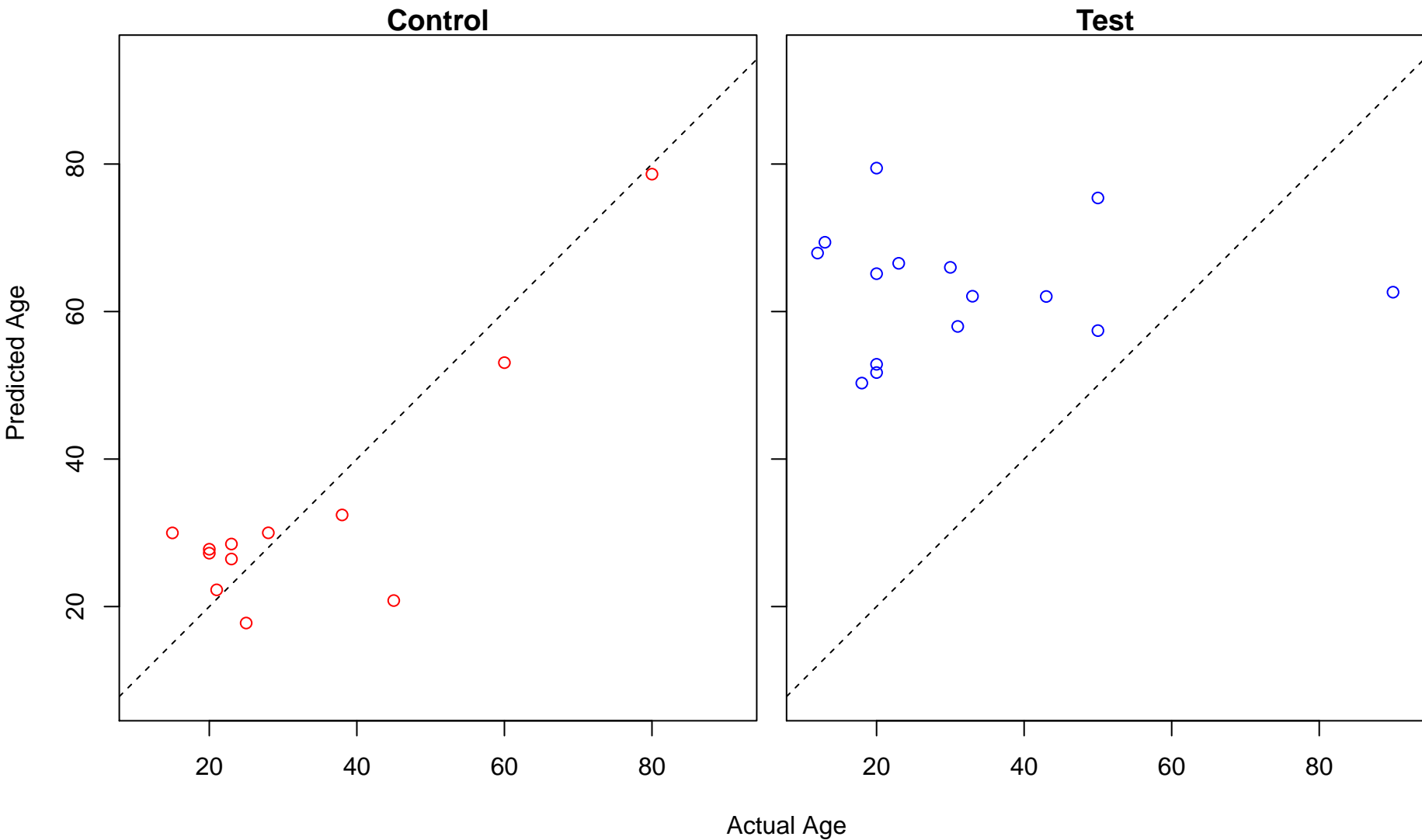
muscle structure development (Score: 5.602450)



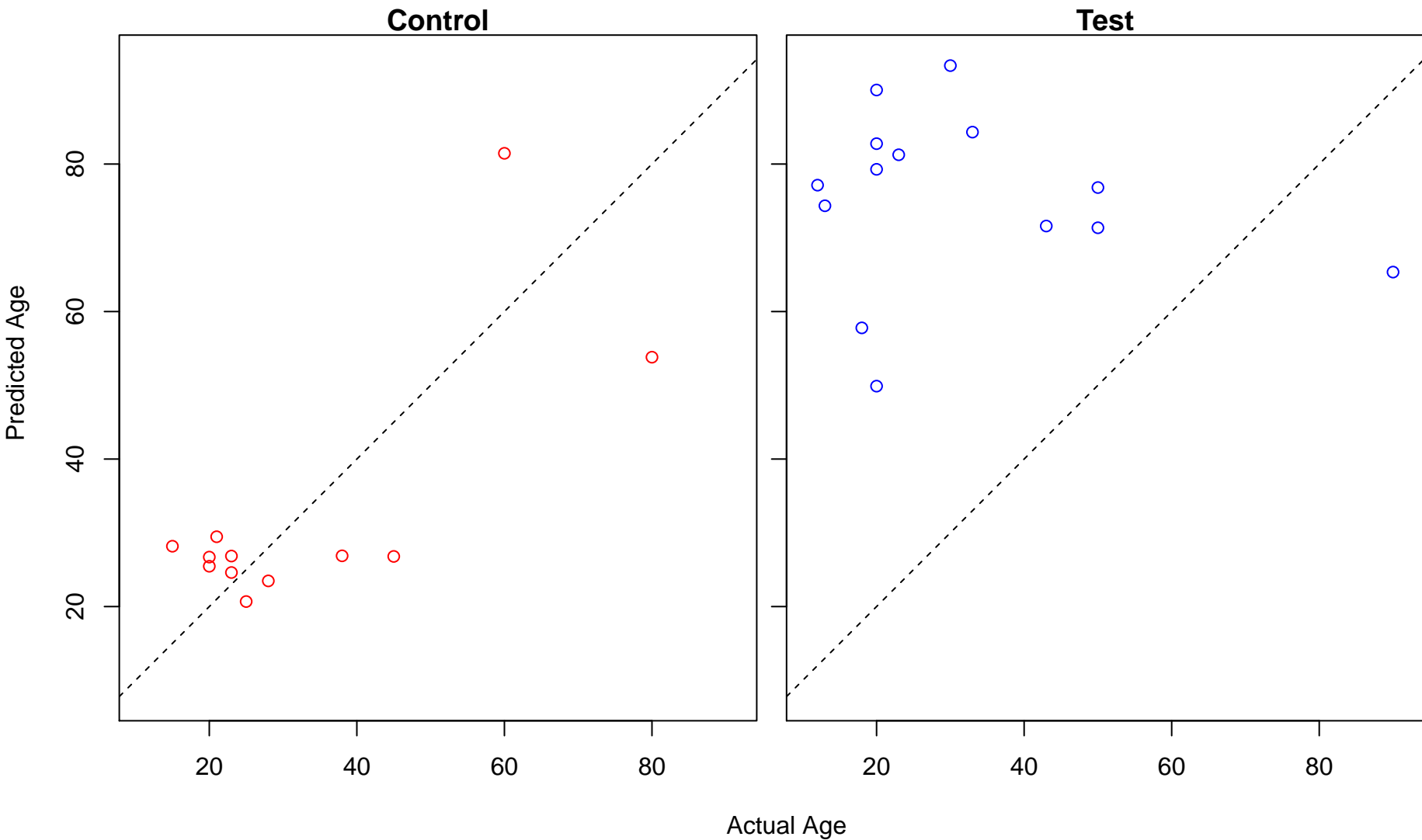
RNA destabilization (Score: 5.602351)



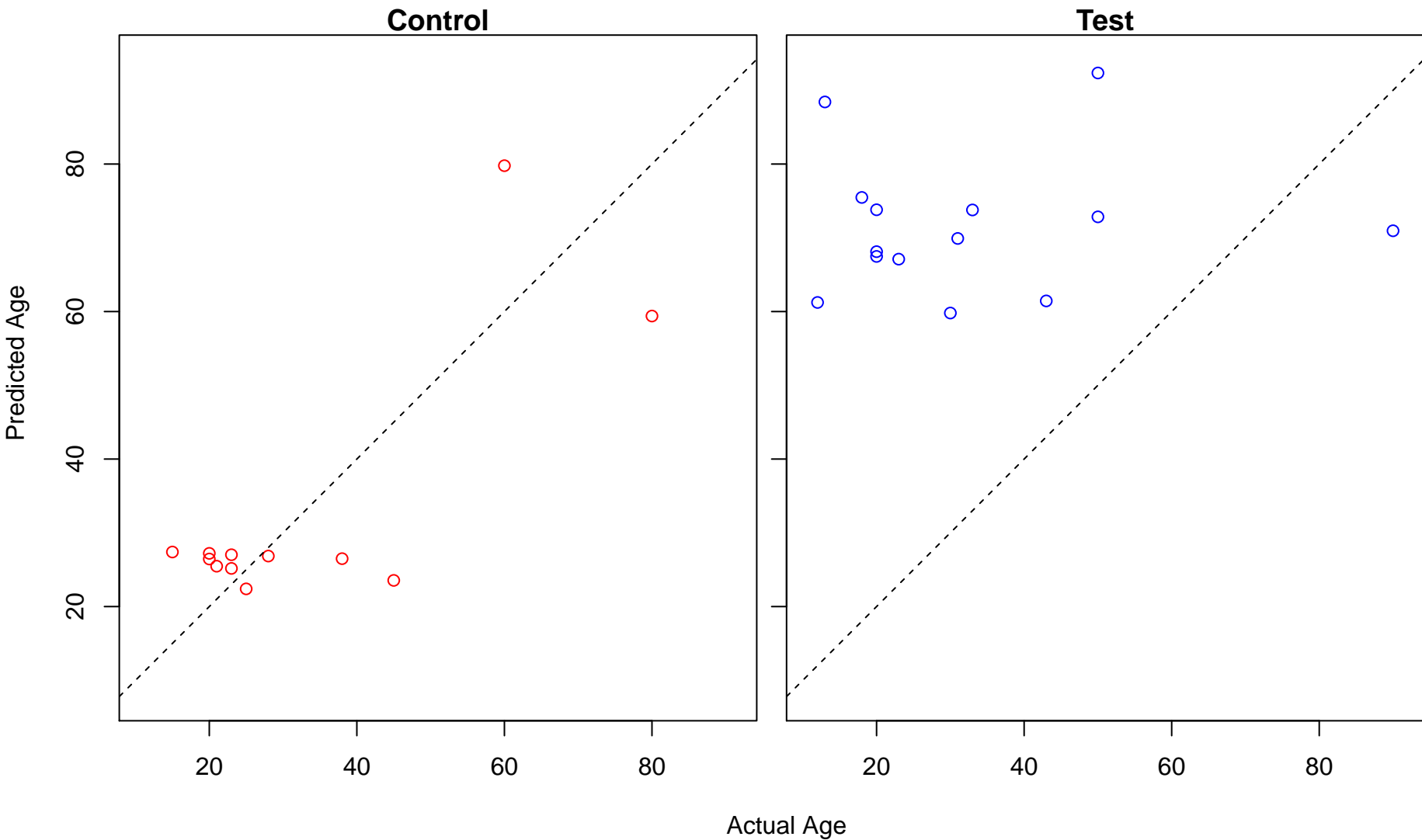
mRNA destabilization (Score: 5.602351)



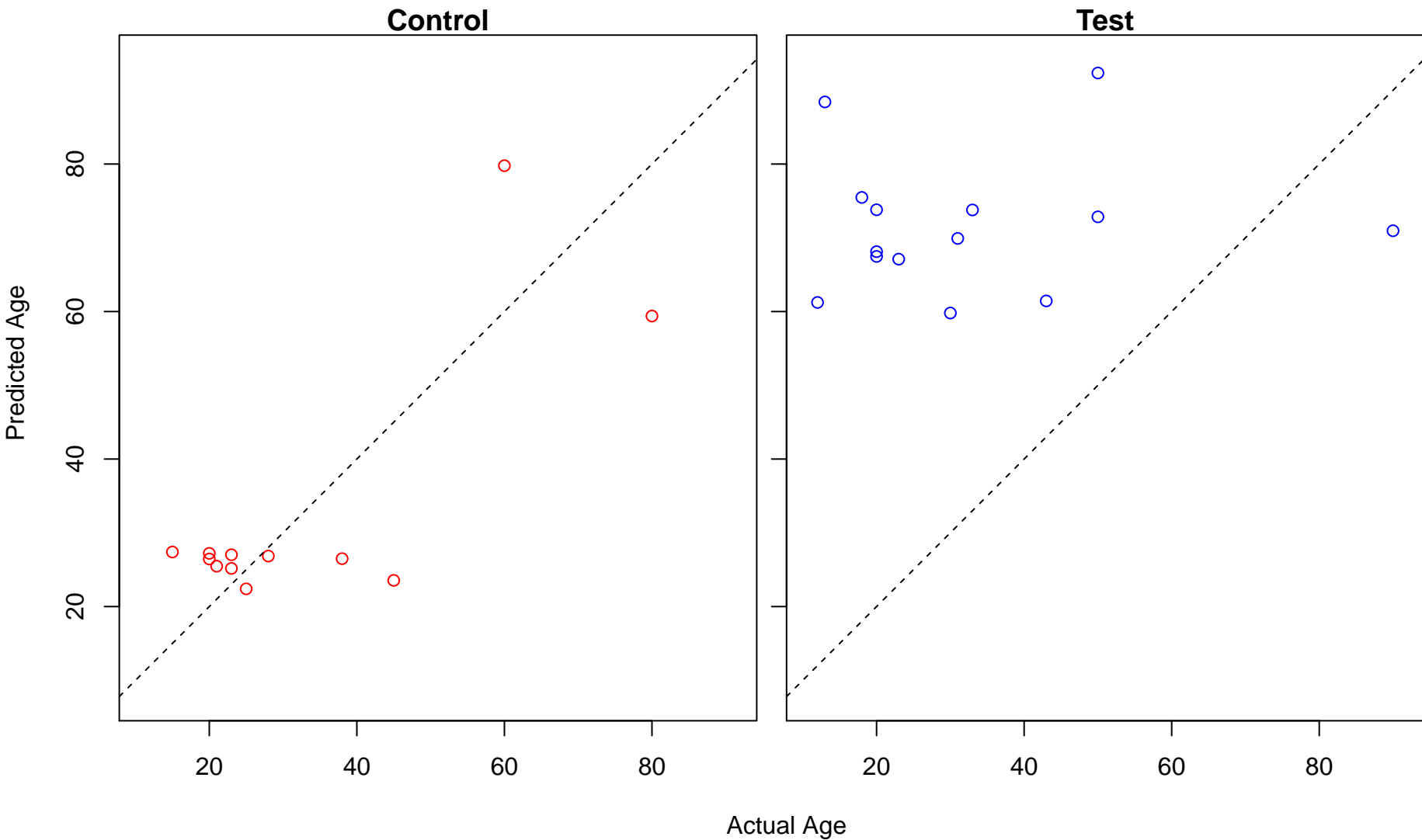
striated muscle adaptation (Score: 5.602348)



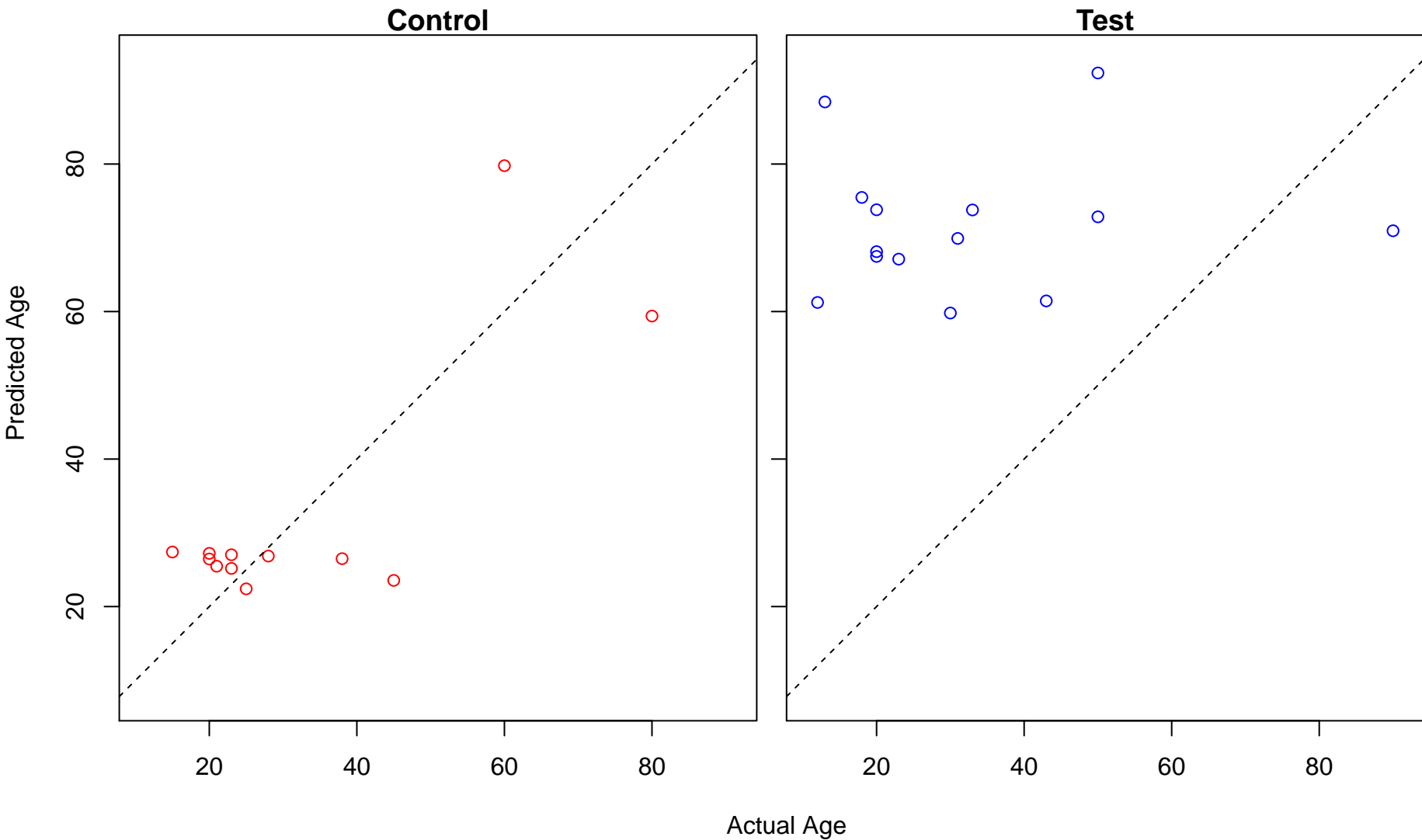
glycogen metabolic process (Score: 5.602055)



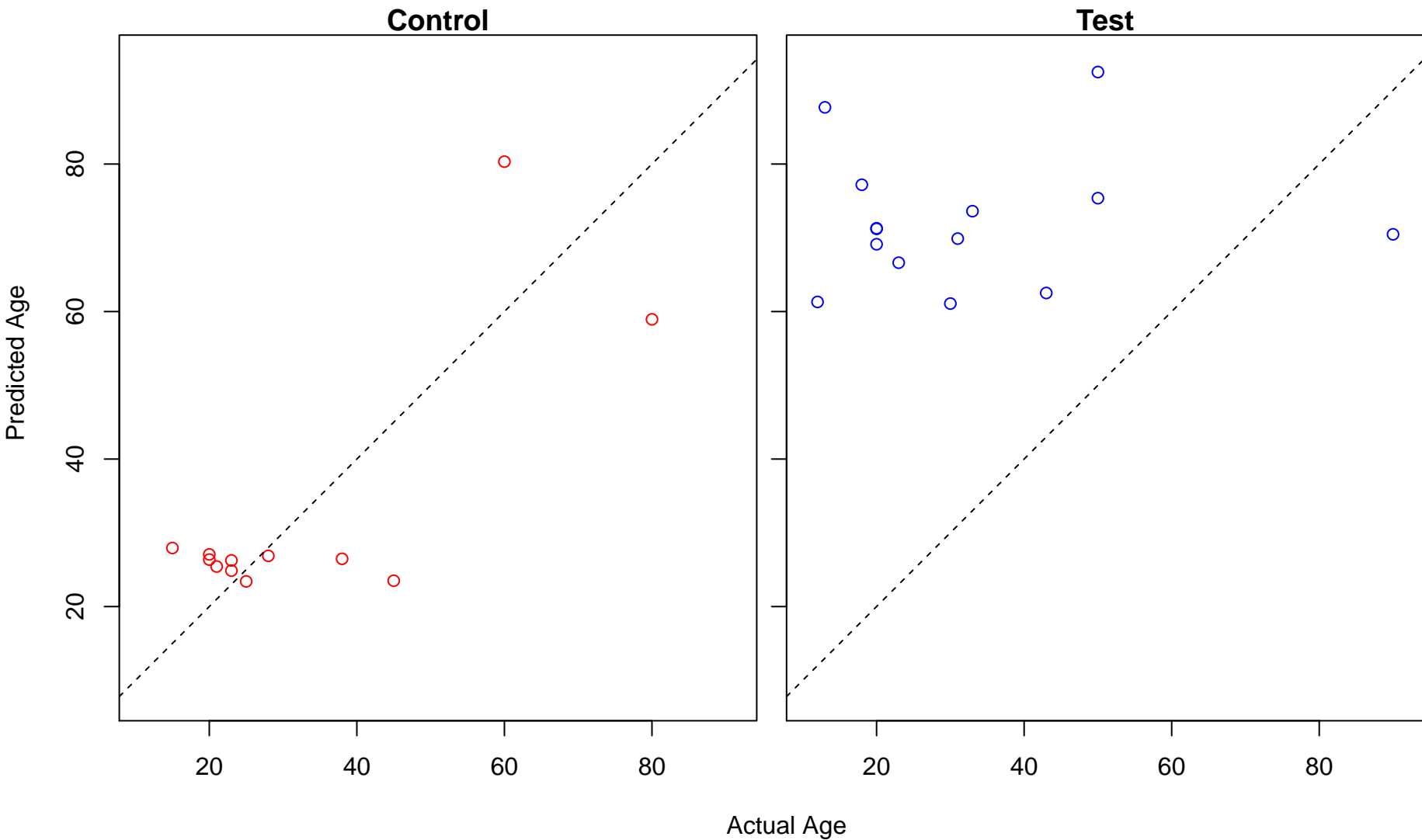
cellular glucan metabolic process (Score: 5.602048)



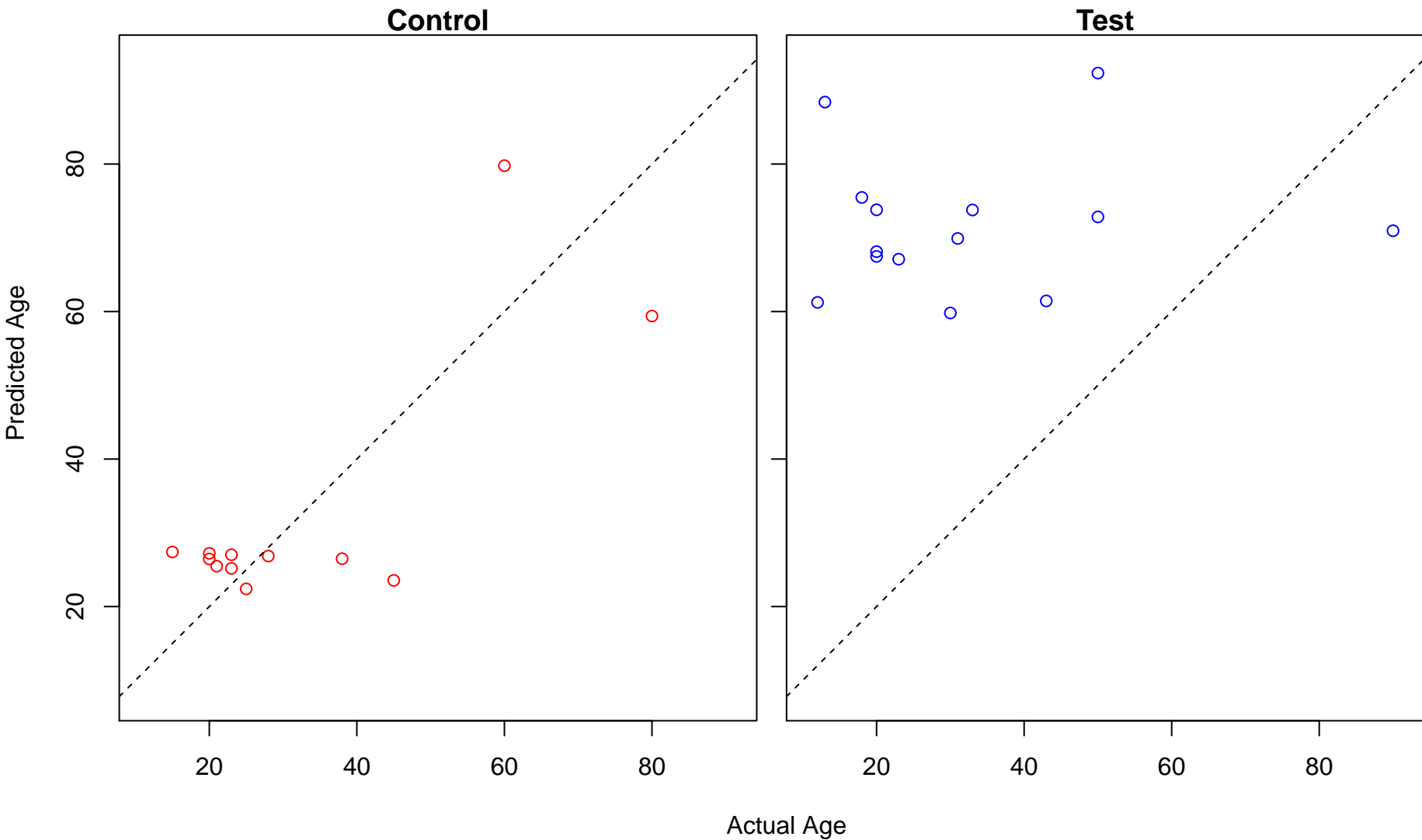
glucan metabolic process (Score: 5.602048)



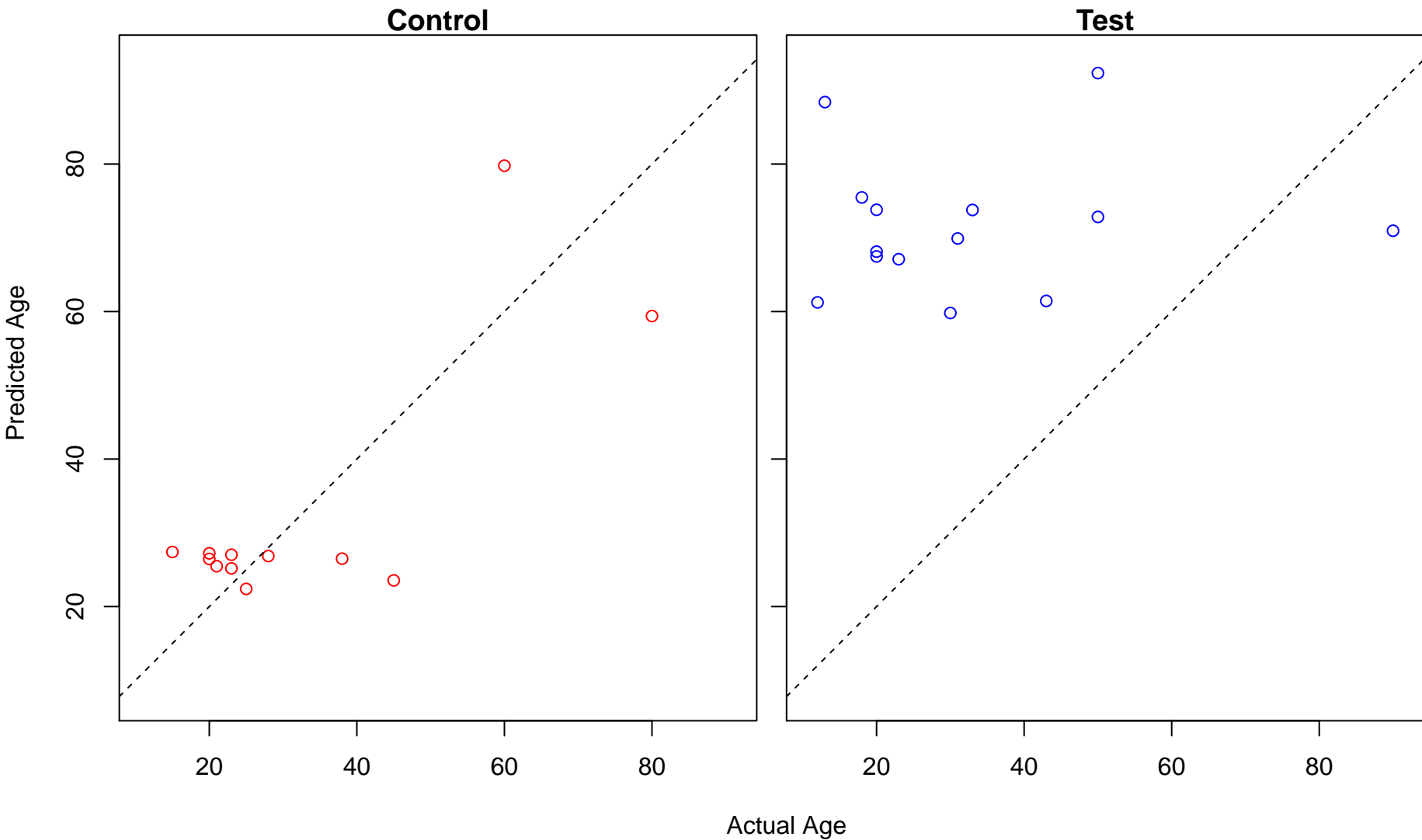
glucose metabolic process (Score: 5.601838)



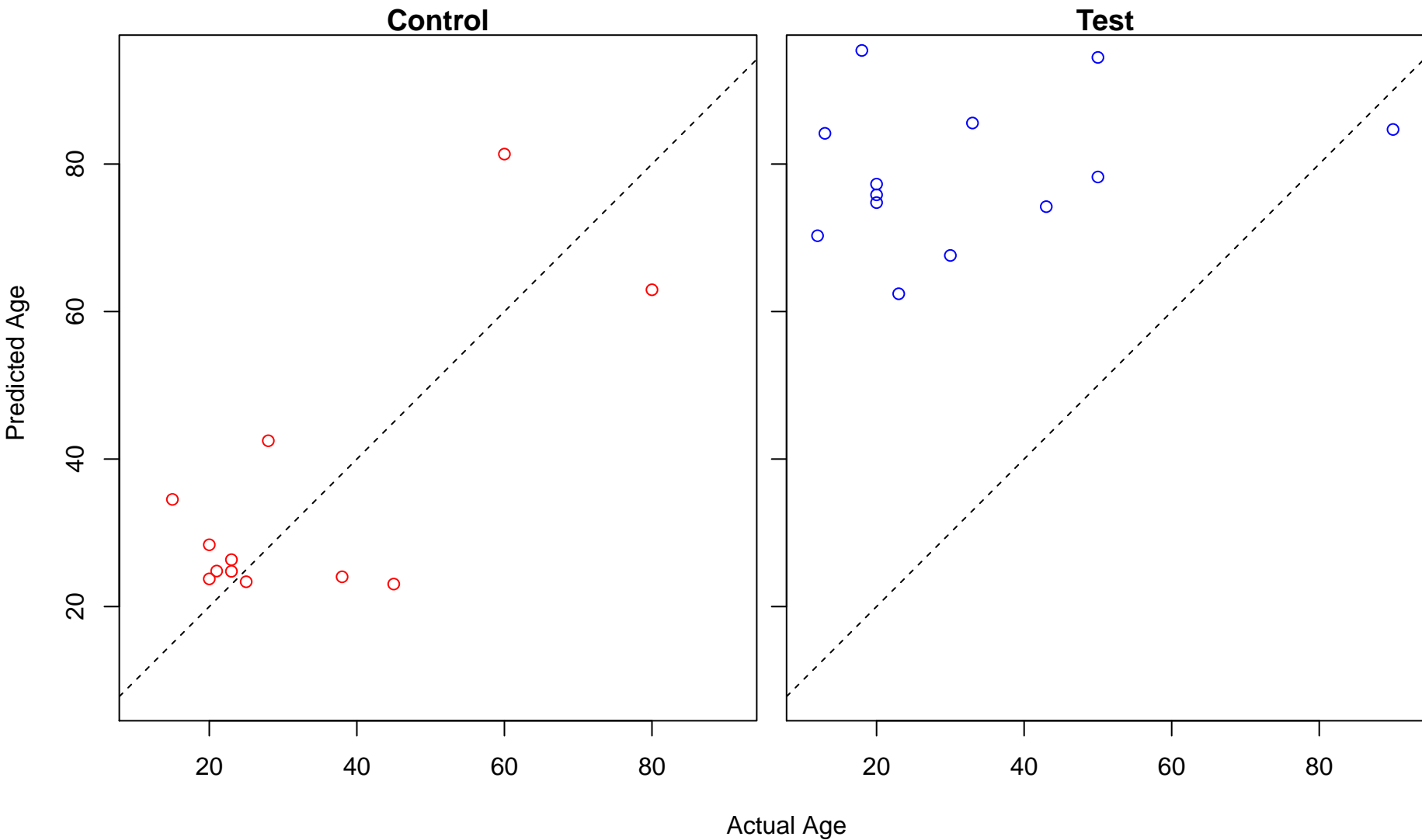
polysaccharide metabolic process (Score: 5.599744)



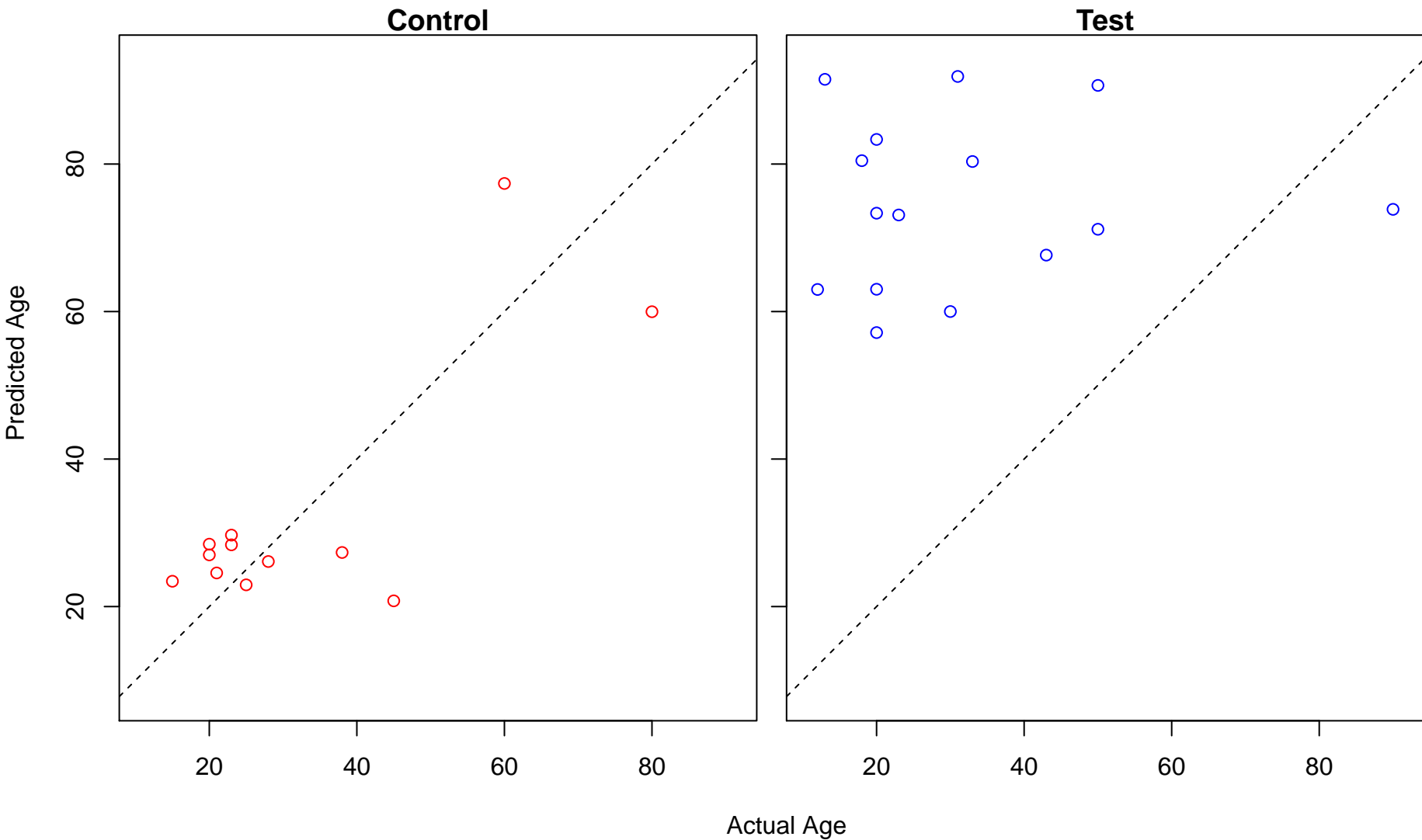
cellular polysaccharide metabolic process (Score: 5.599701)



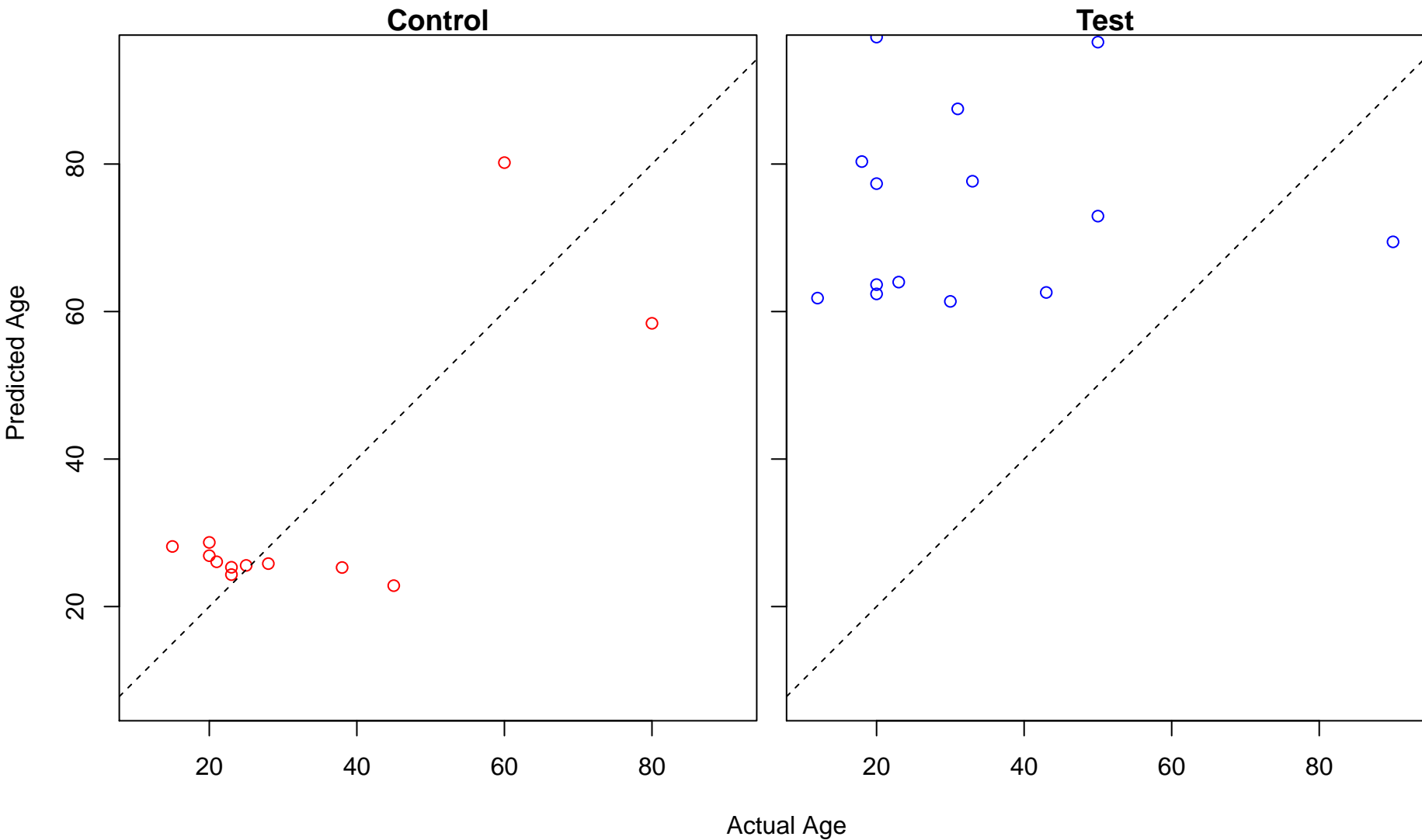
lamellipodium organization (Score: 5.598502)



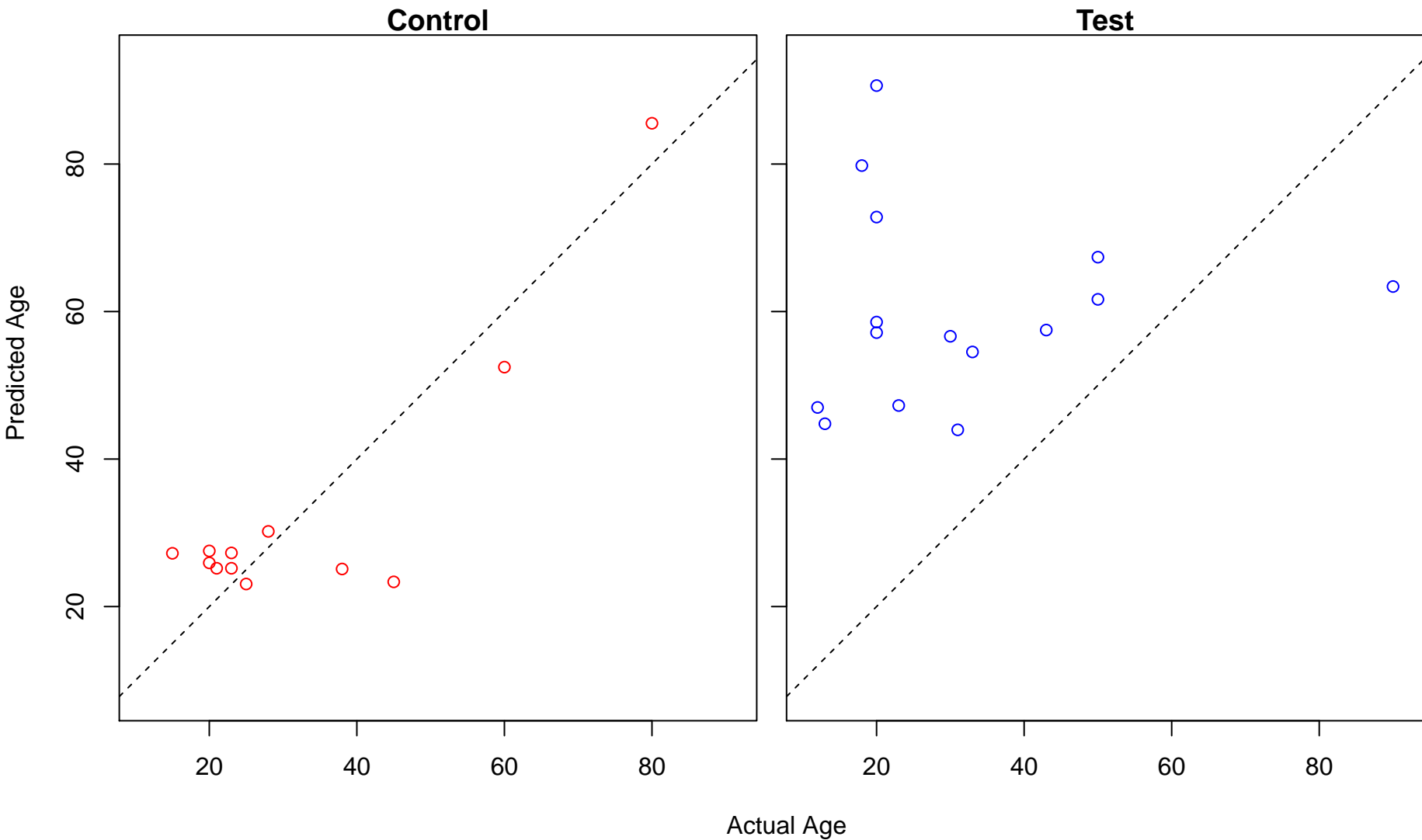
defense response to Gram-negative bacterium (Score: 5.597506)



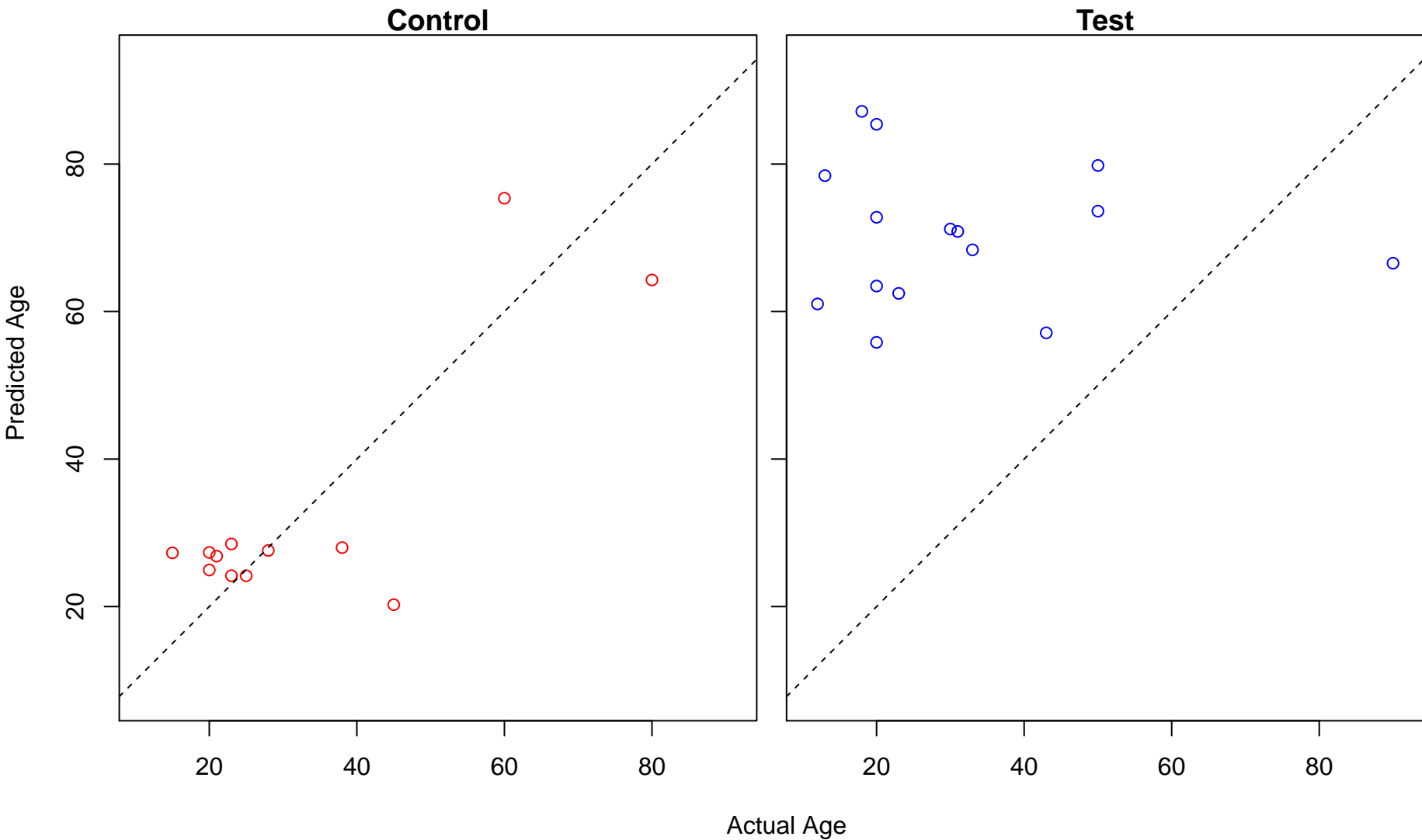
cell junction assembly (Score: 5.595171)



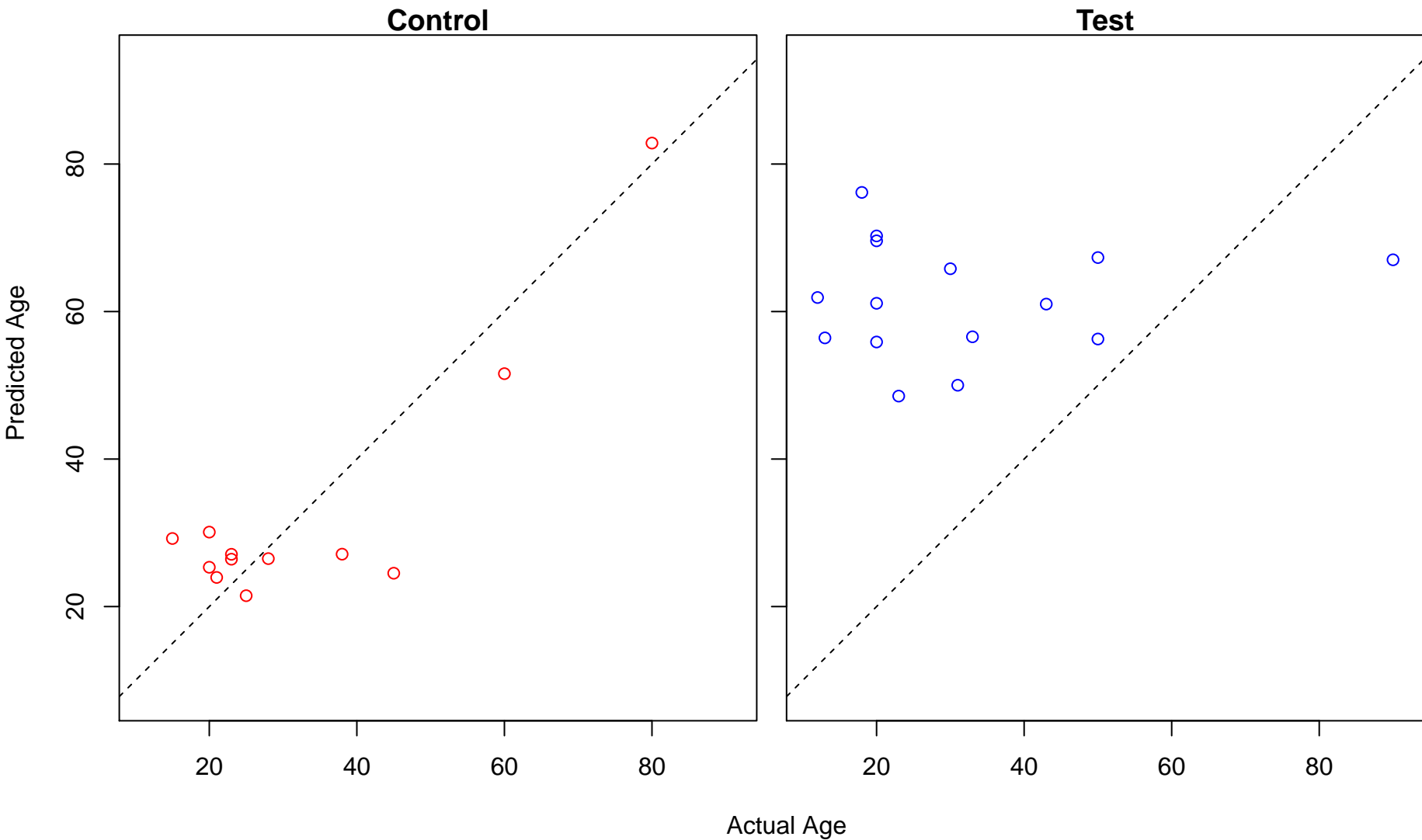
hemopoiesis (Score: 5.593427)



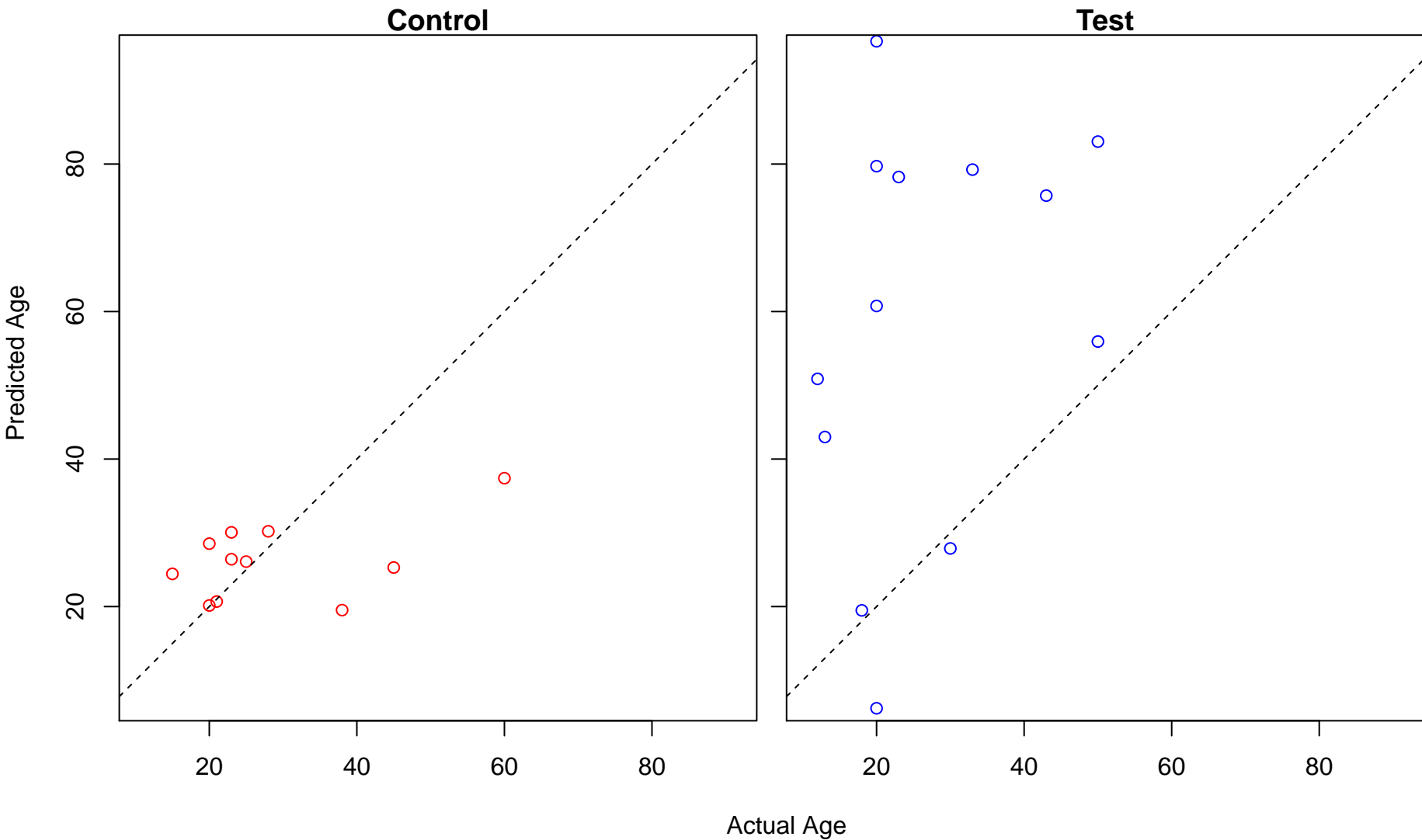
positive regulation of cytokine production (Score: 5.593421)



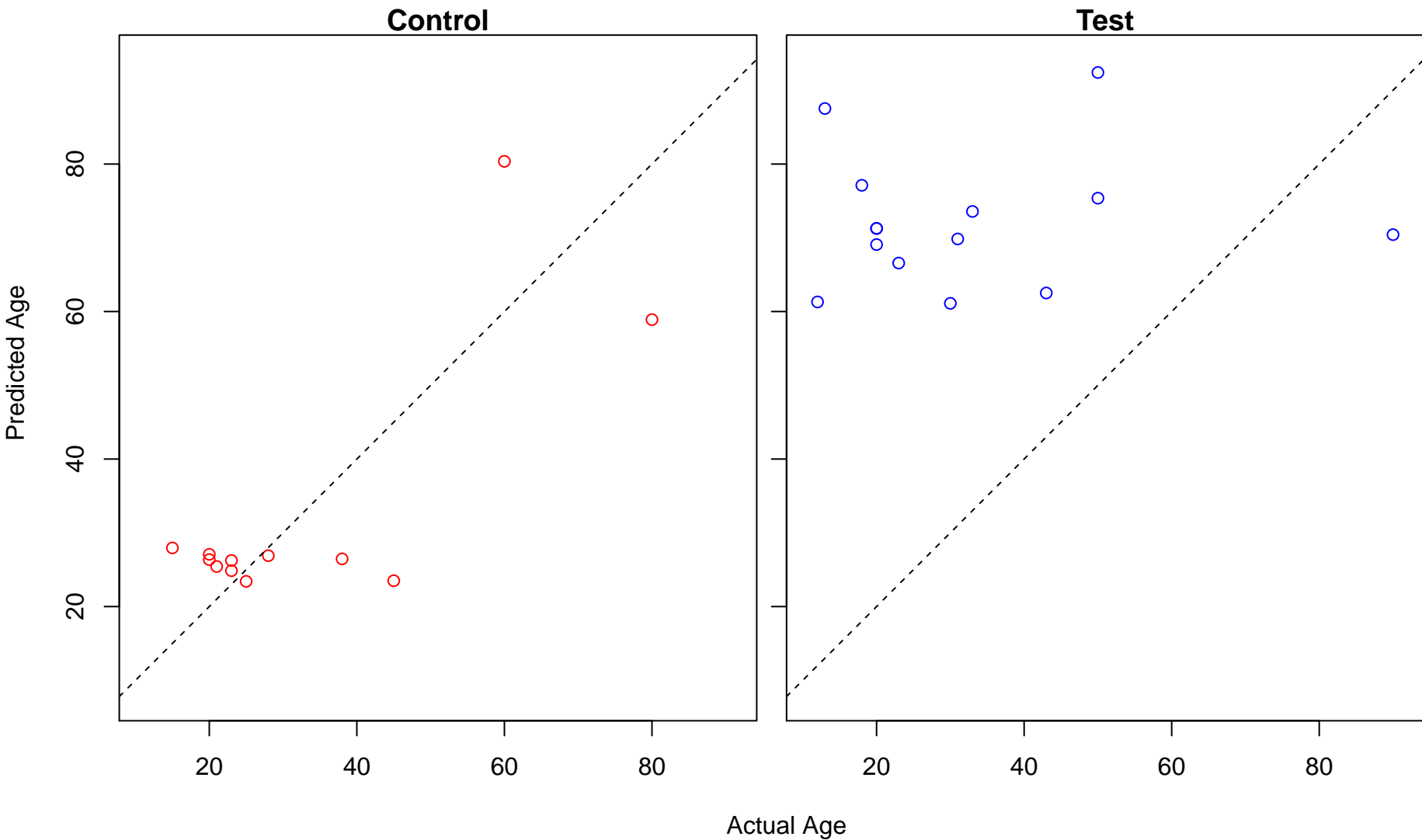
regulation of ERAD pathway (Score: 5.590054)



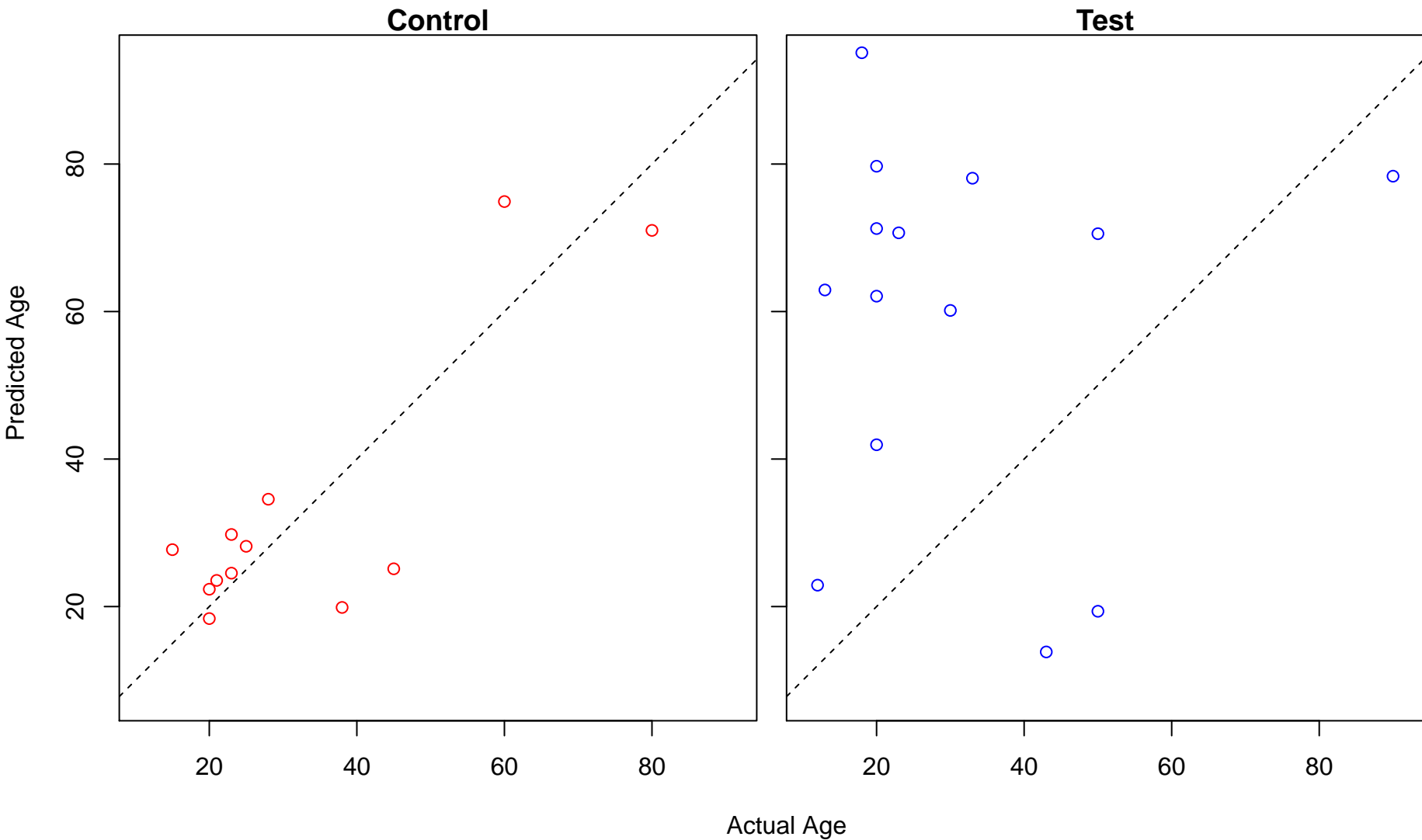
Notch signaling involved in heart development (Score: 5.587334)



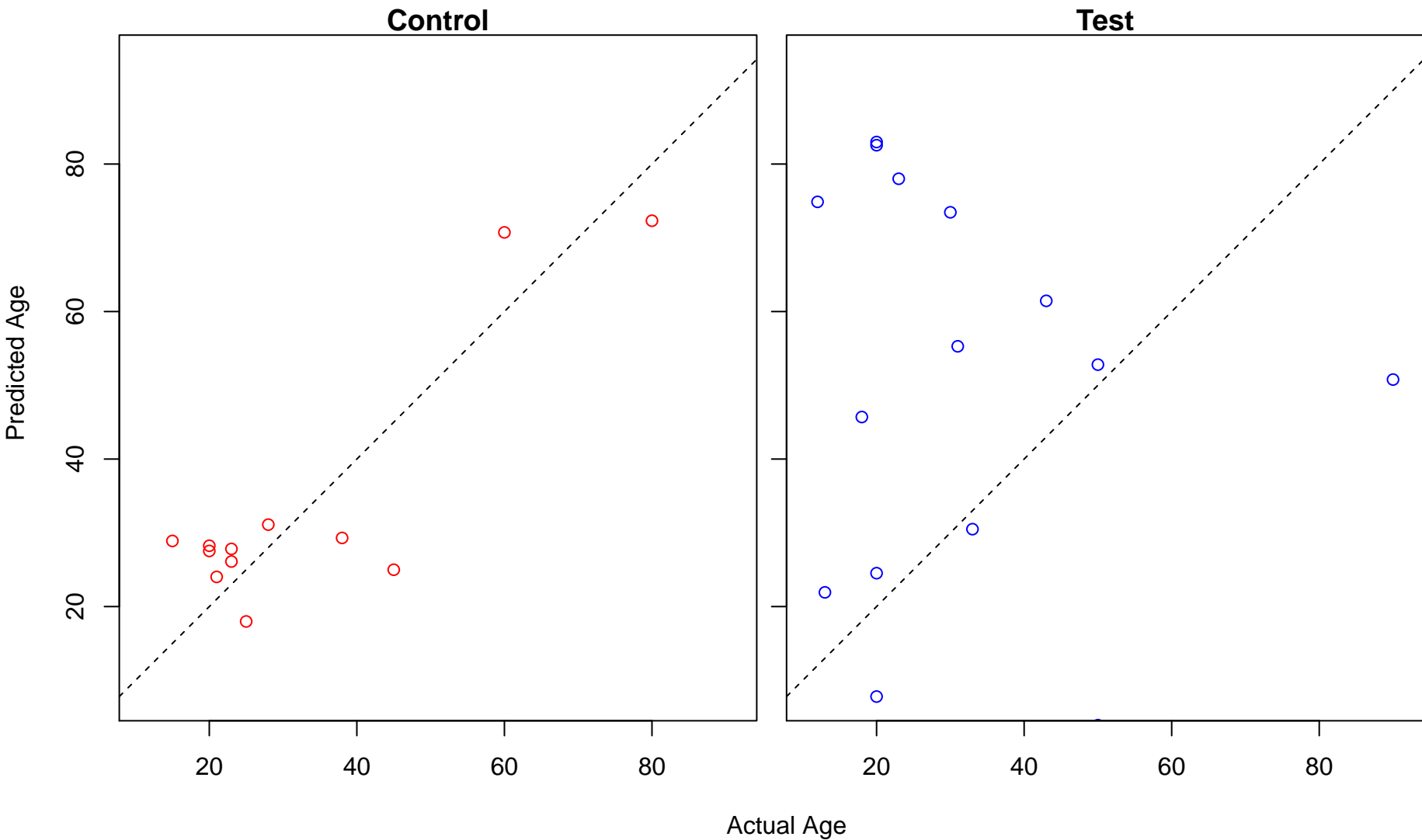
hexose metabolic process (Score: 5.584419)



regulation of cardiac muscle cell apoptotic process (Score: 5.584295)

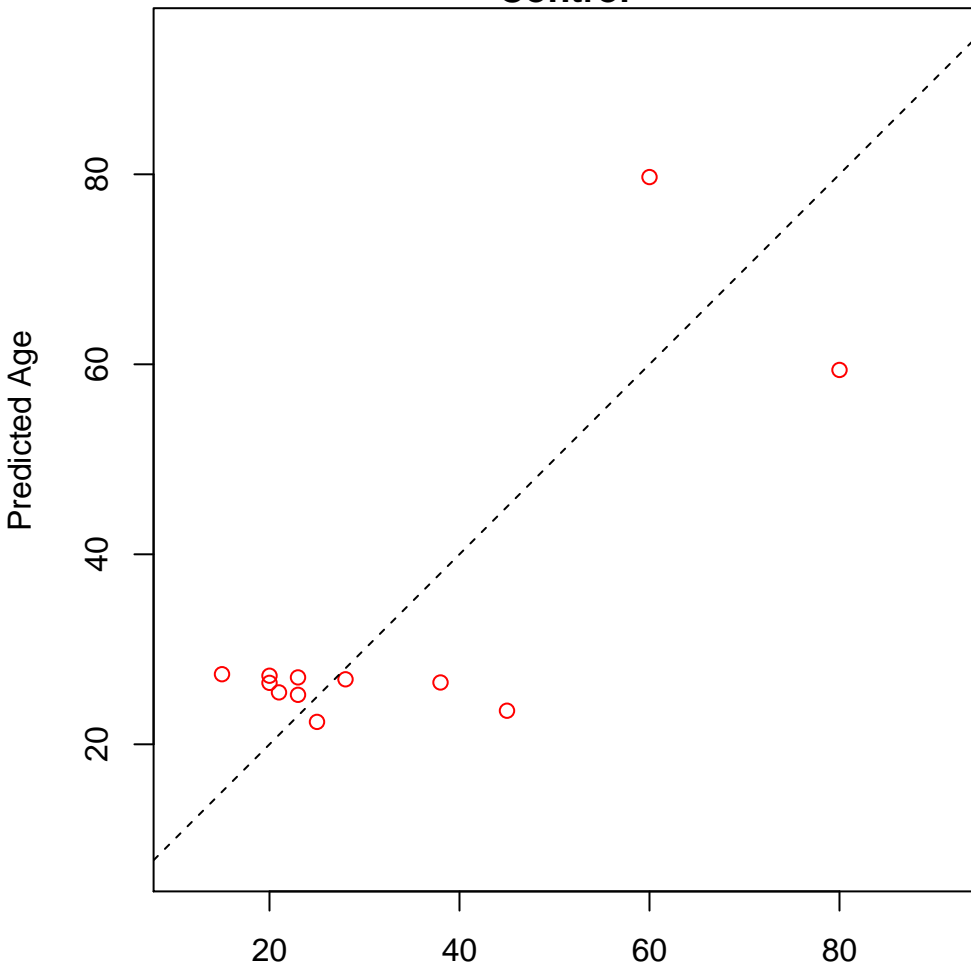


regulation of cell communication by electrical coupling (Score: 5.582786)

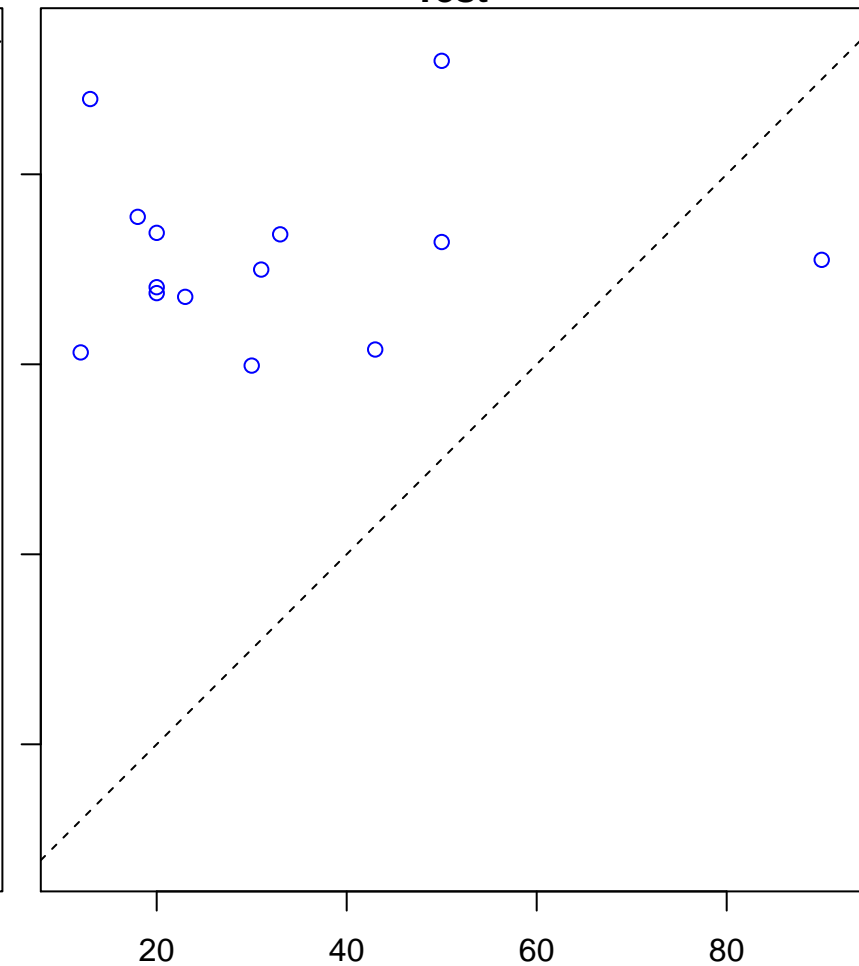


cellular carbohydrate metabolic process (Score: 5.58218)

Control

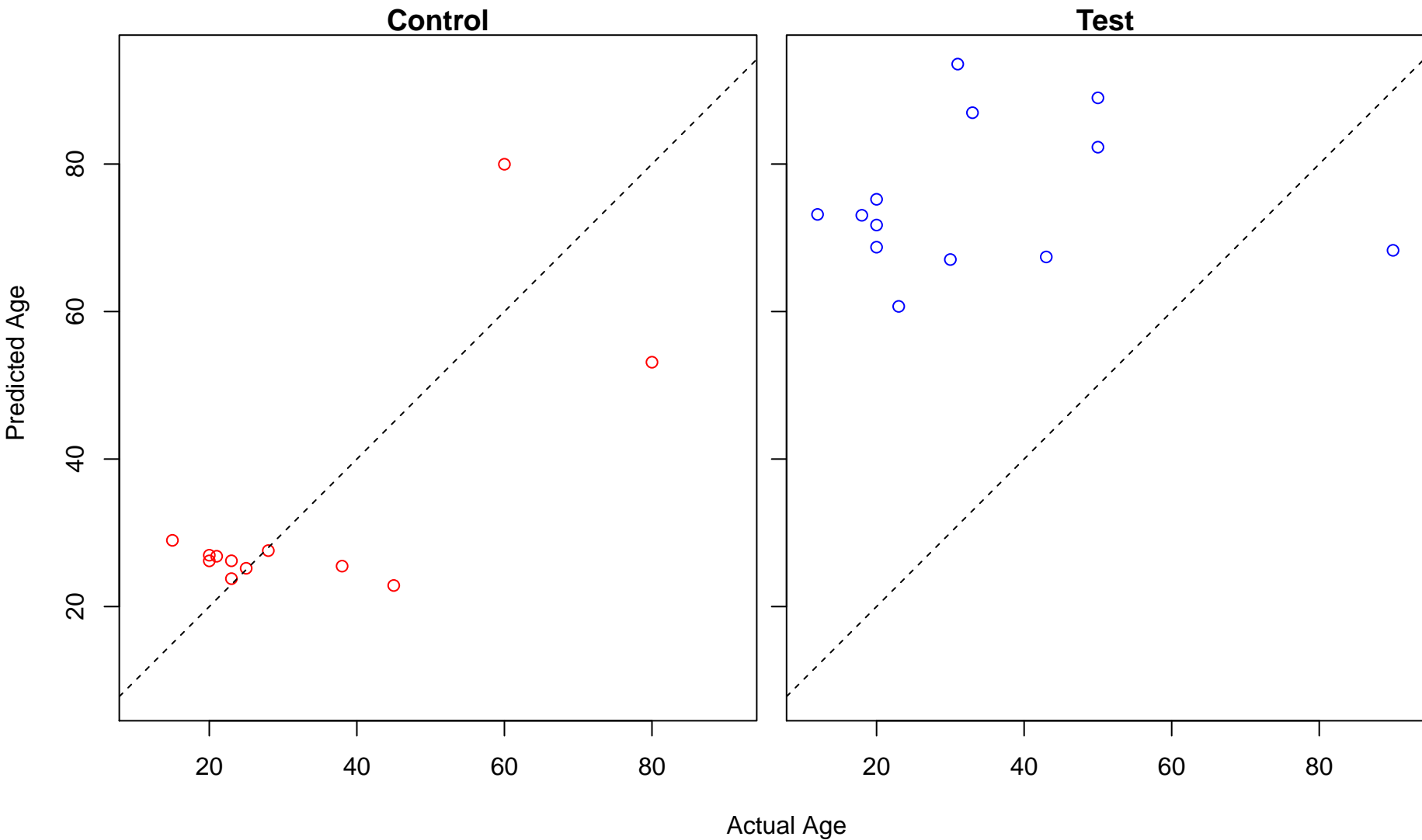


Test

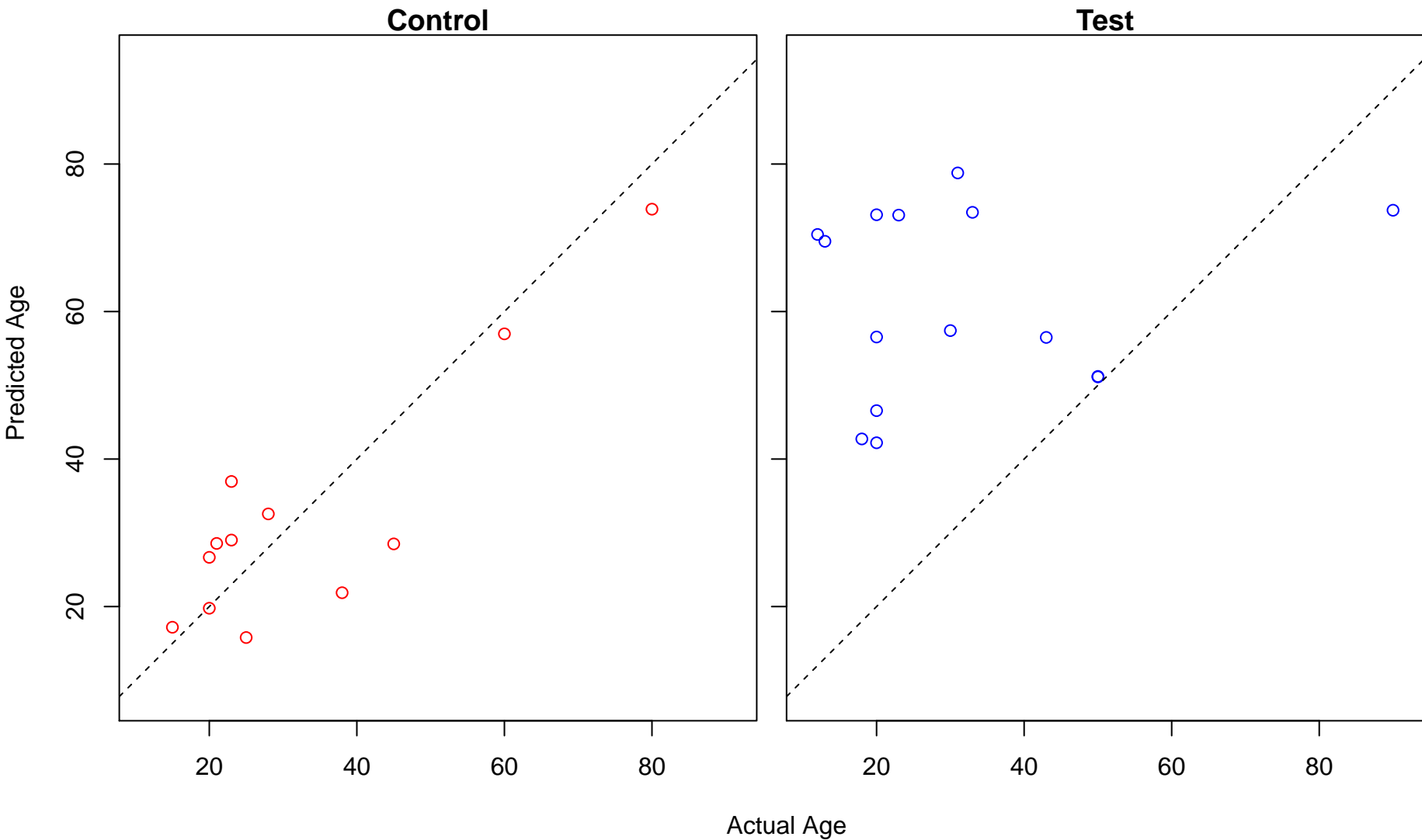


Actual Age

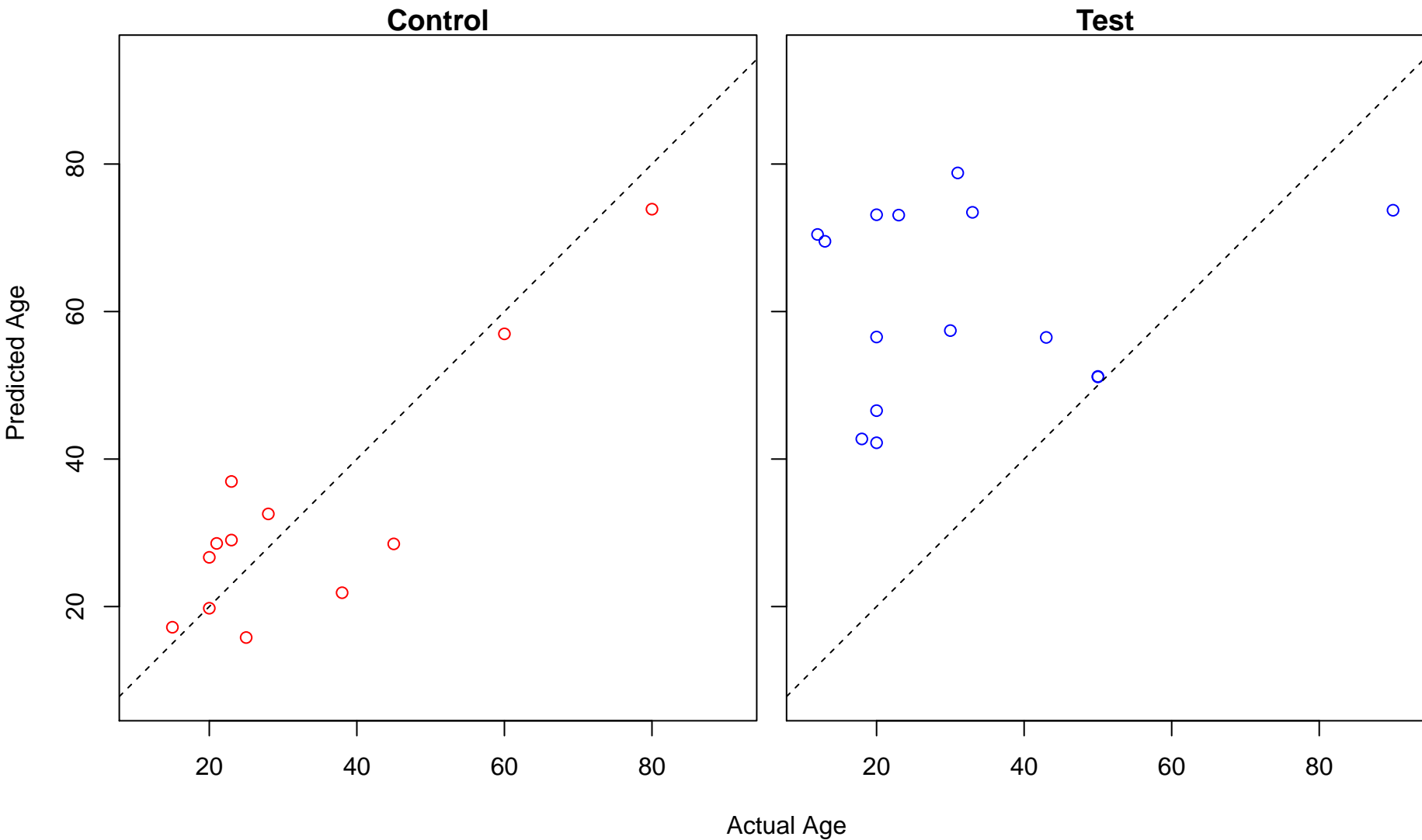
transition metal ion homeostasis (Score: 5.582003)



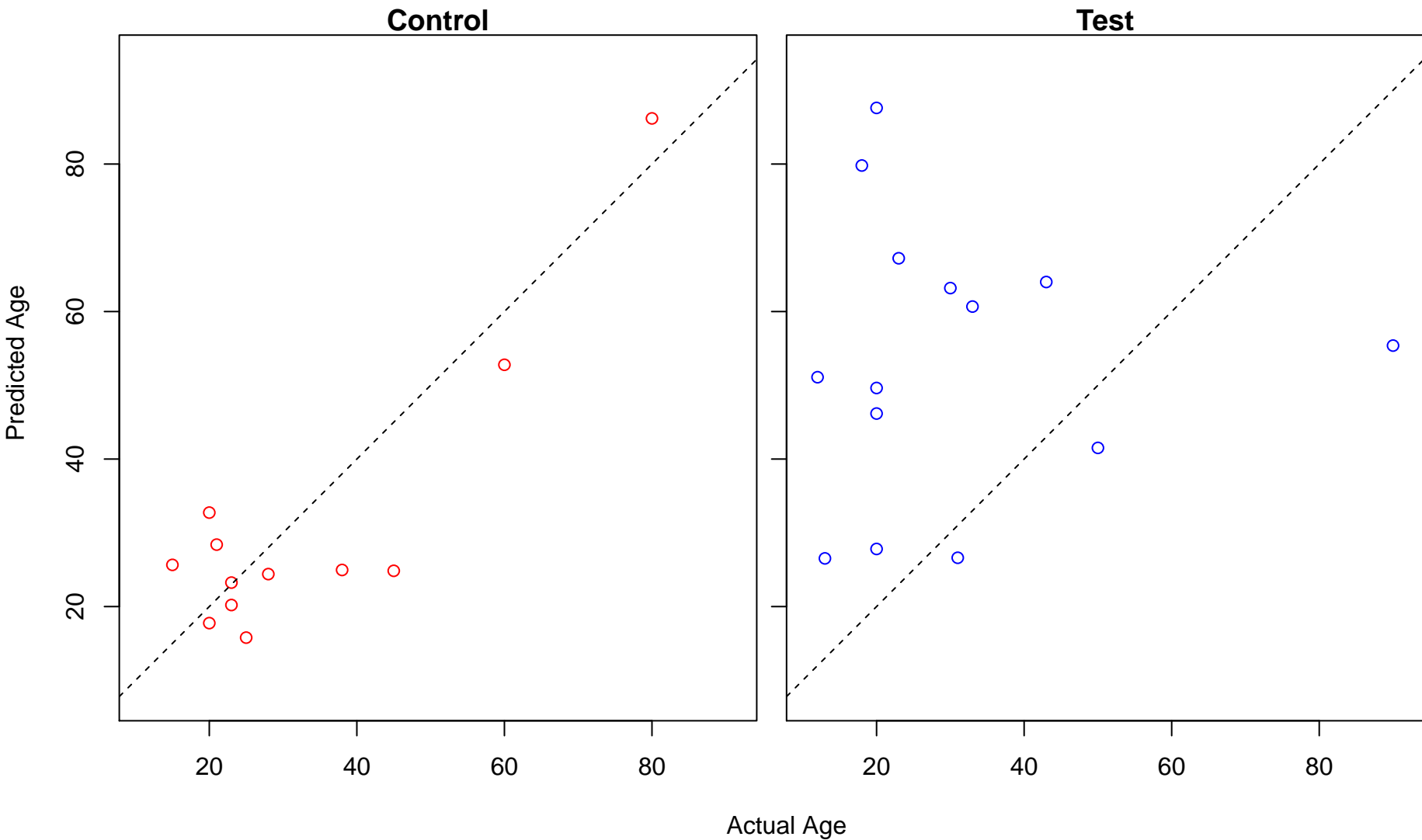
regulation of blood coagulation (Score: 5.580813)



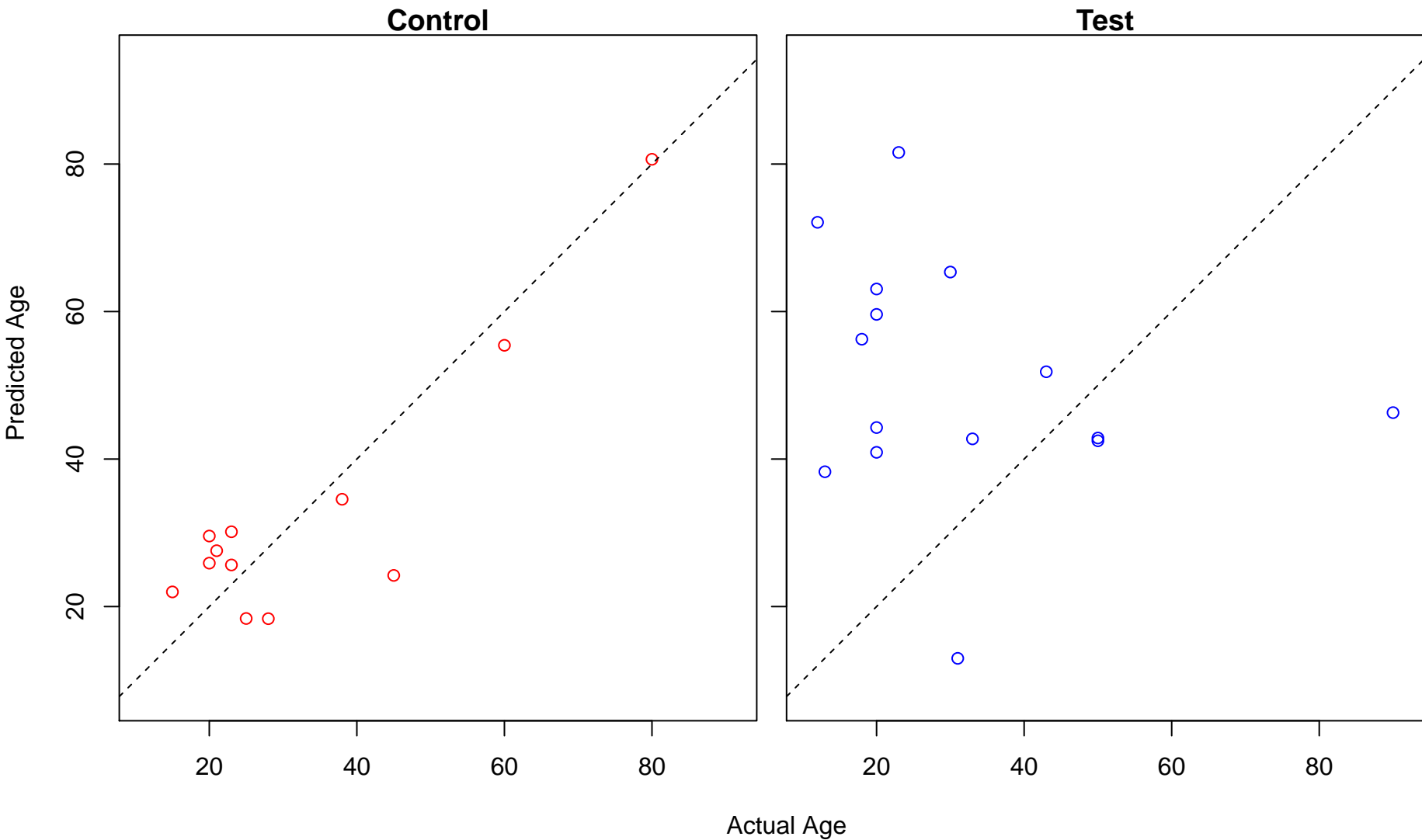
regulation of hemostasis (Score: 5.580813)



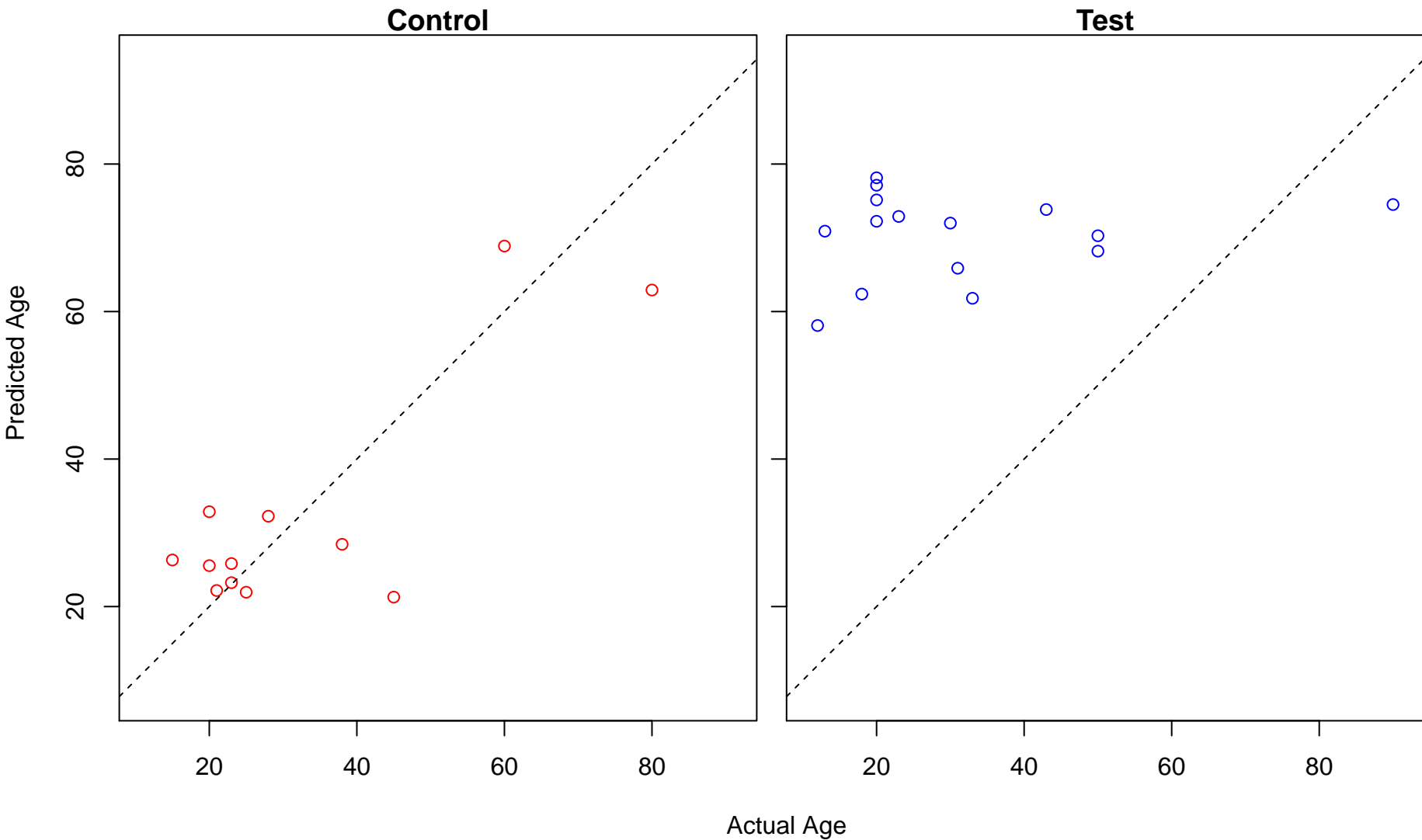
termination of RNA polymerase II transcription (Score: 5.579860)



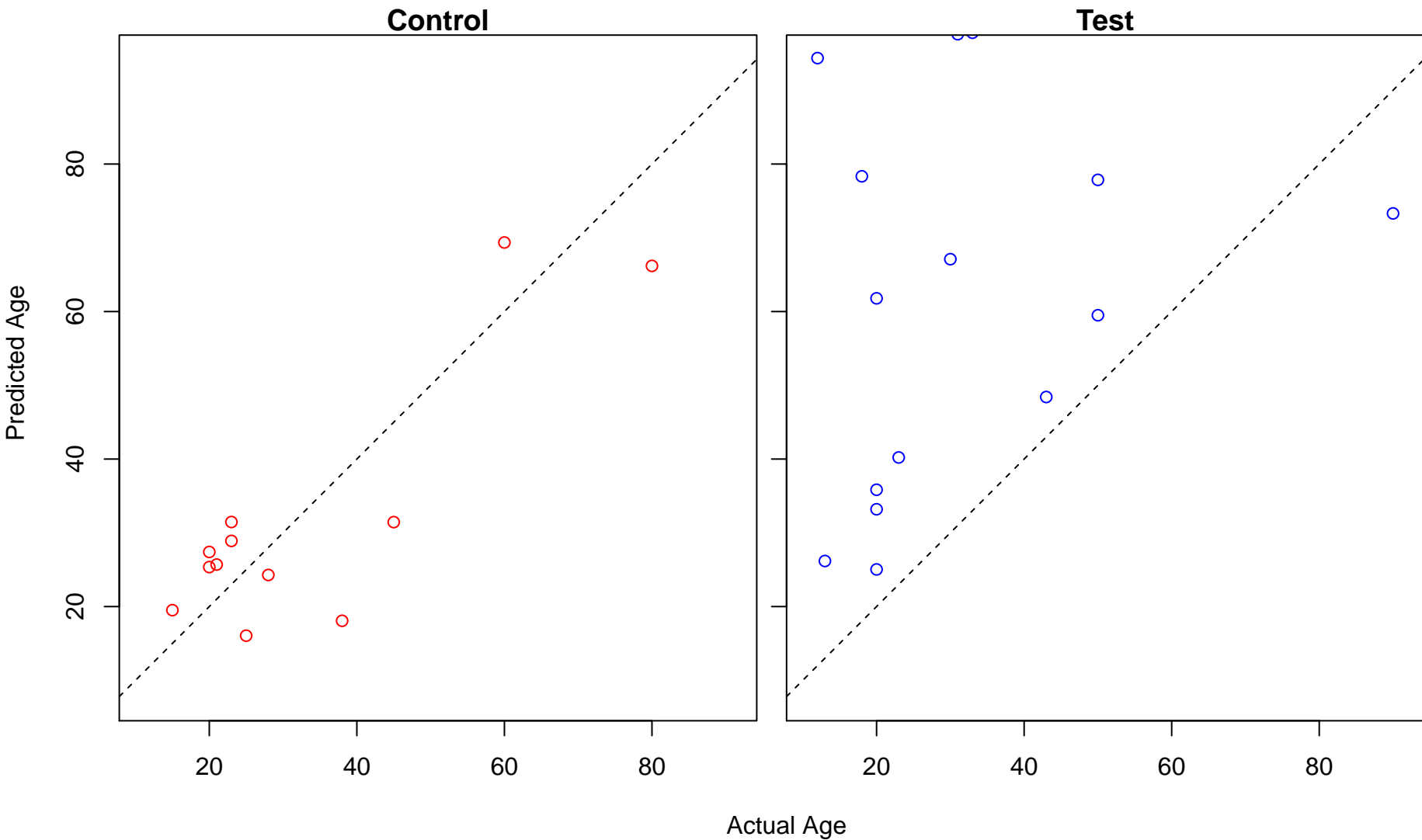
regulation of skeletal muscle contraction (Score: 5.579204)



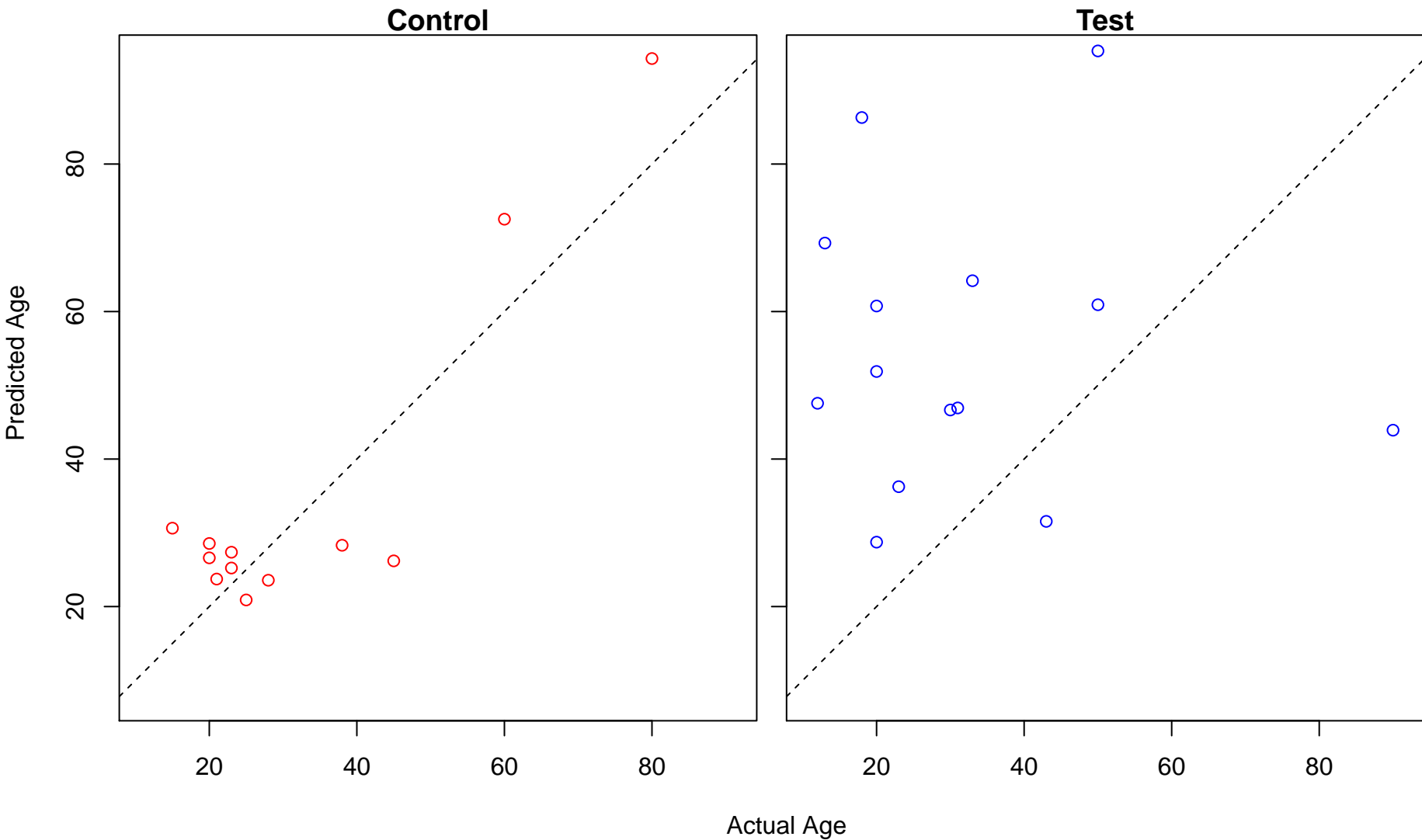
endocytosis (Score: 5.577100)



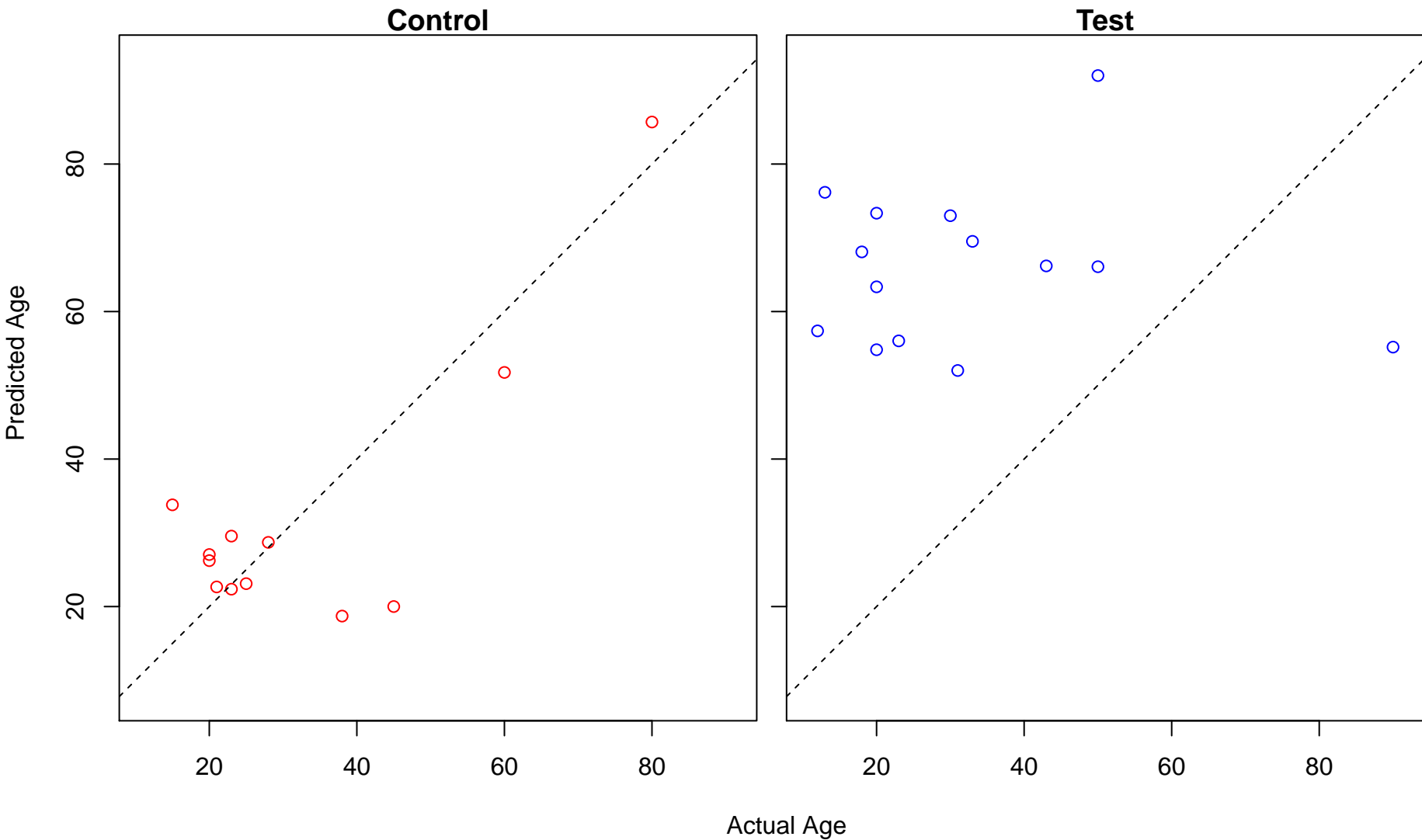
negative regulation of macrophage differentiation (Score: 5.577074)



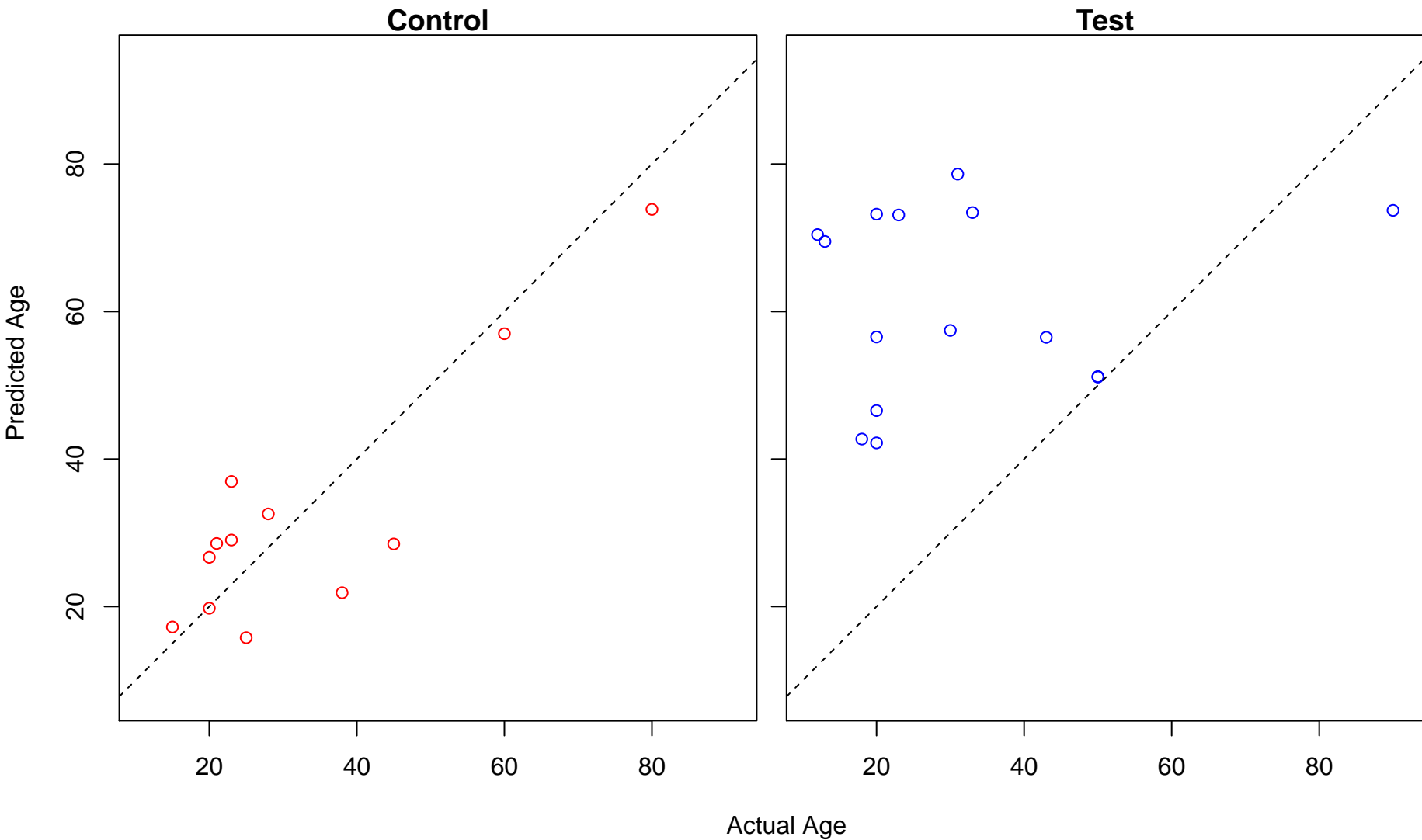
purine nucleoside transmembrane transport (Score: 5.573822)



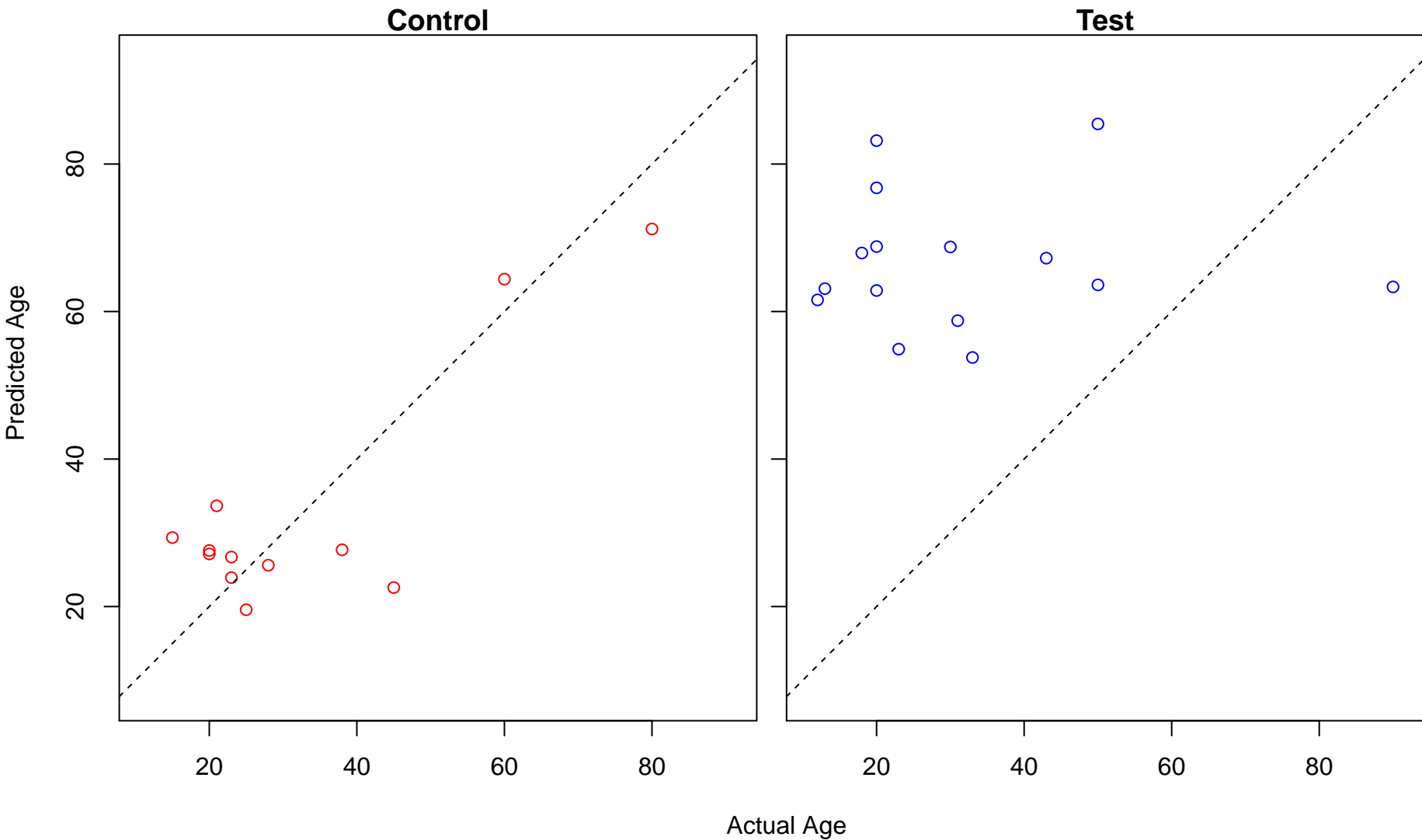
glutamine family amino acid biosynthetic process (Score: 5.573307)



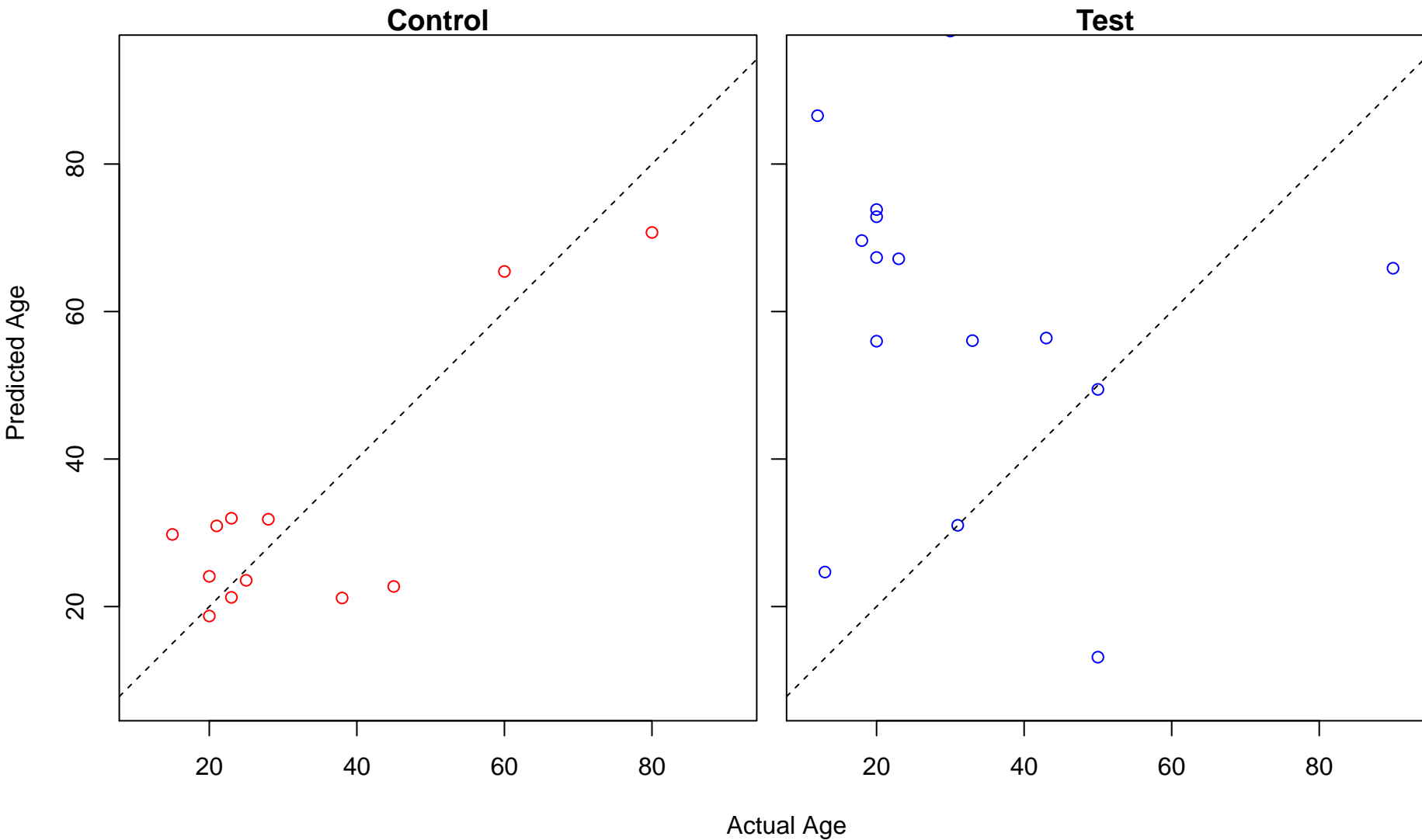
regulation of coagulation (Score: 5.572729)



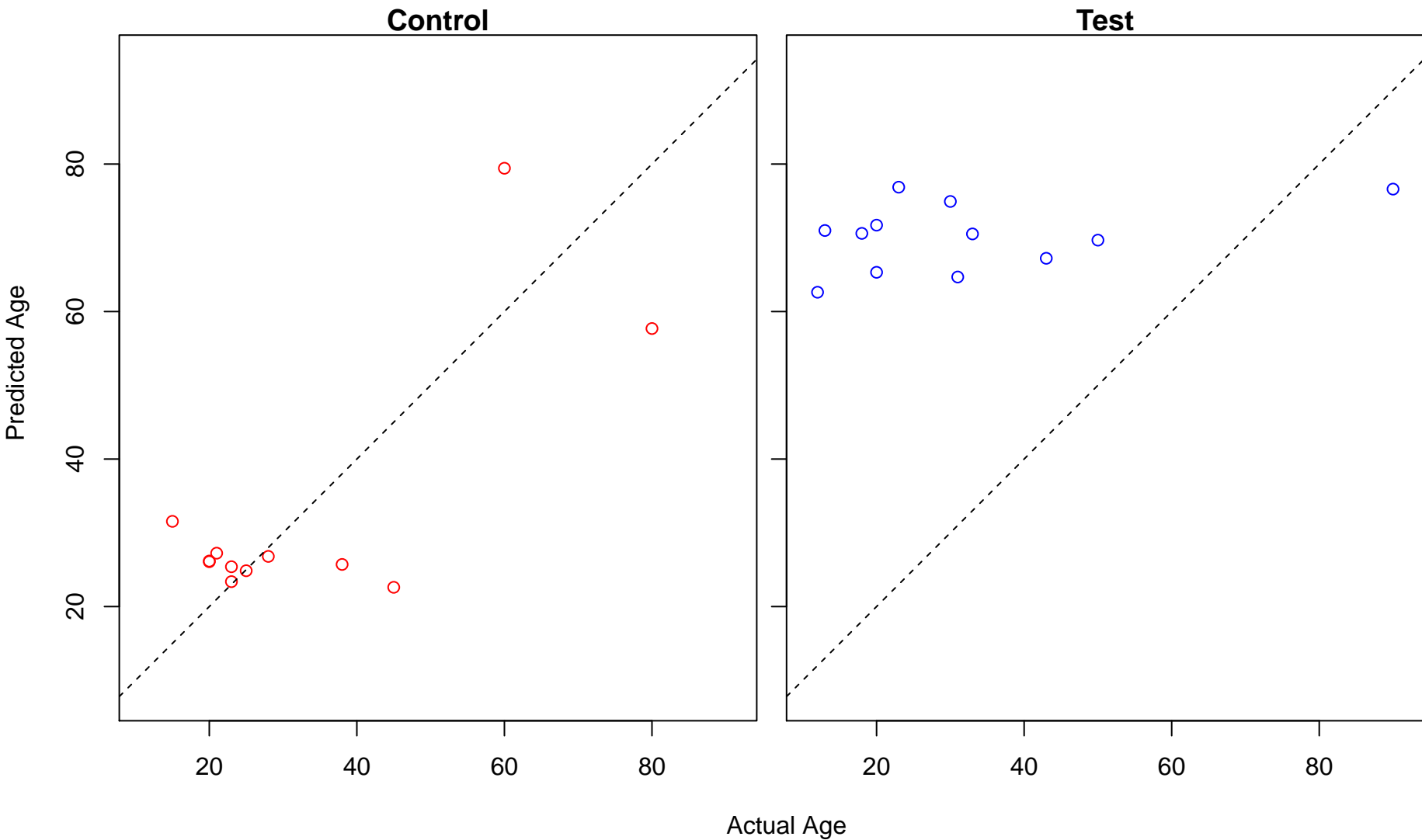
response to inorganic substance (Score: 5.572567)



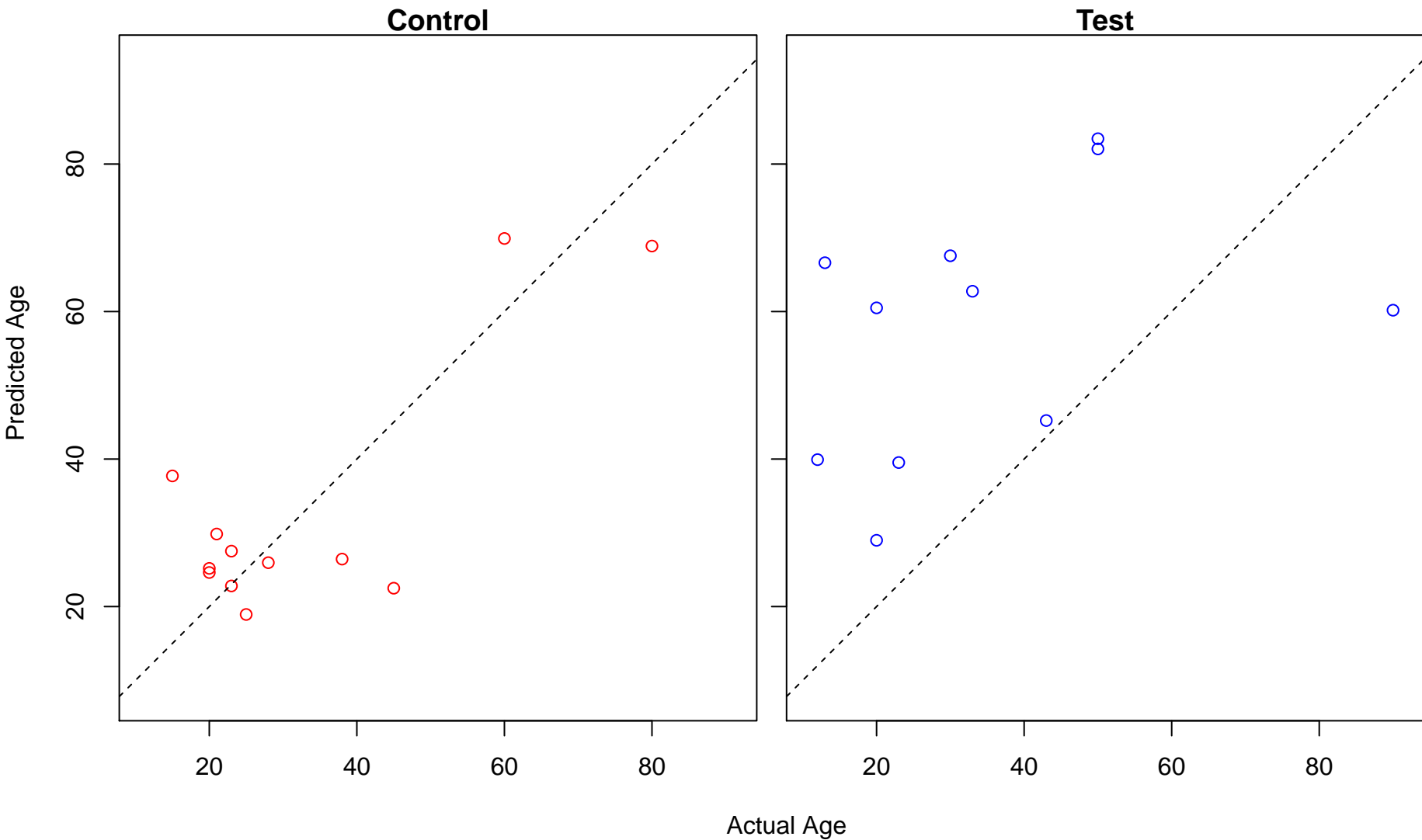
vesicle organization (Score: 5.572047)



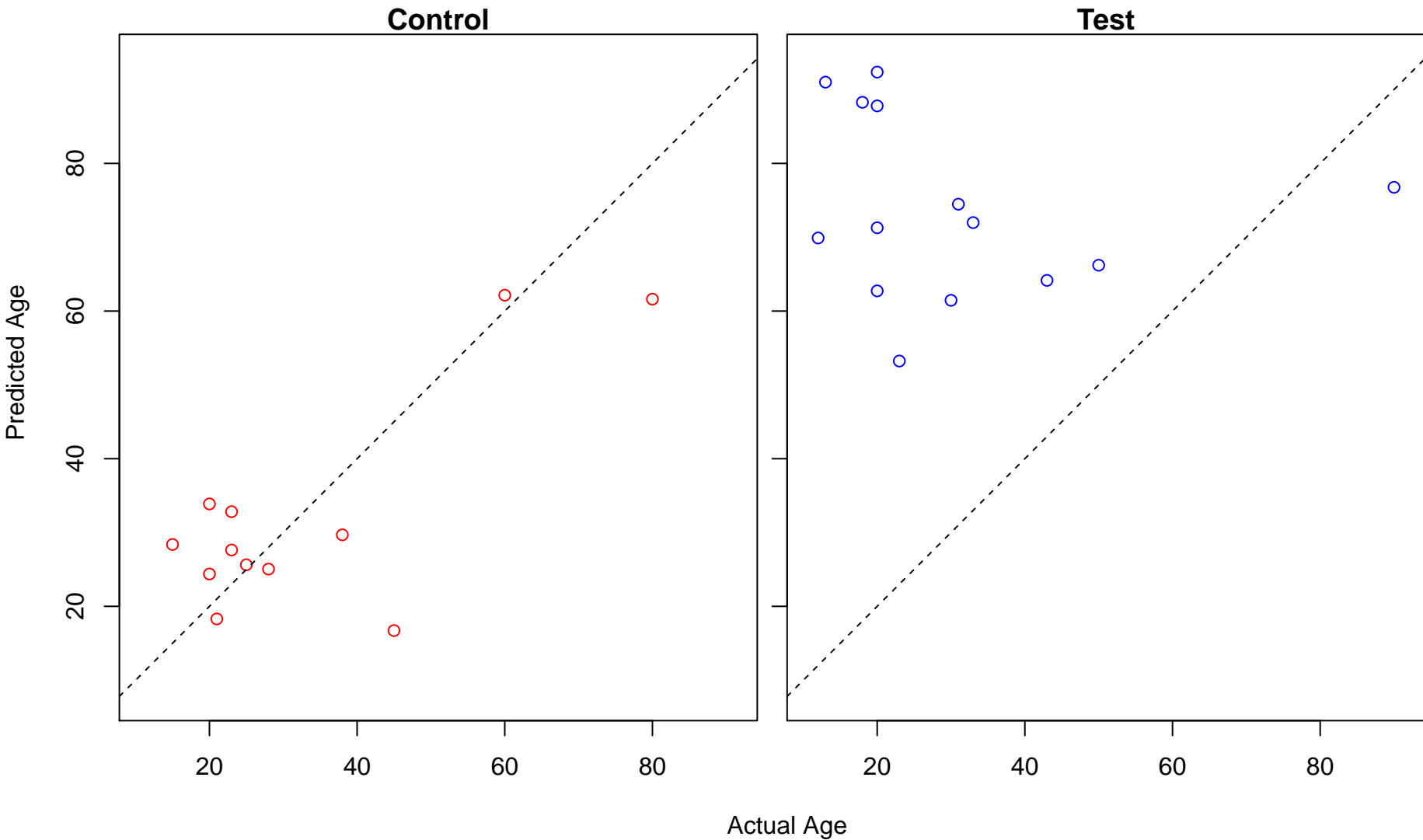
establishment of protein localization to chromosome (Score: 5.570245)



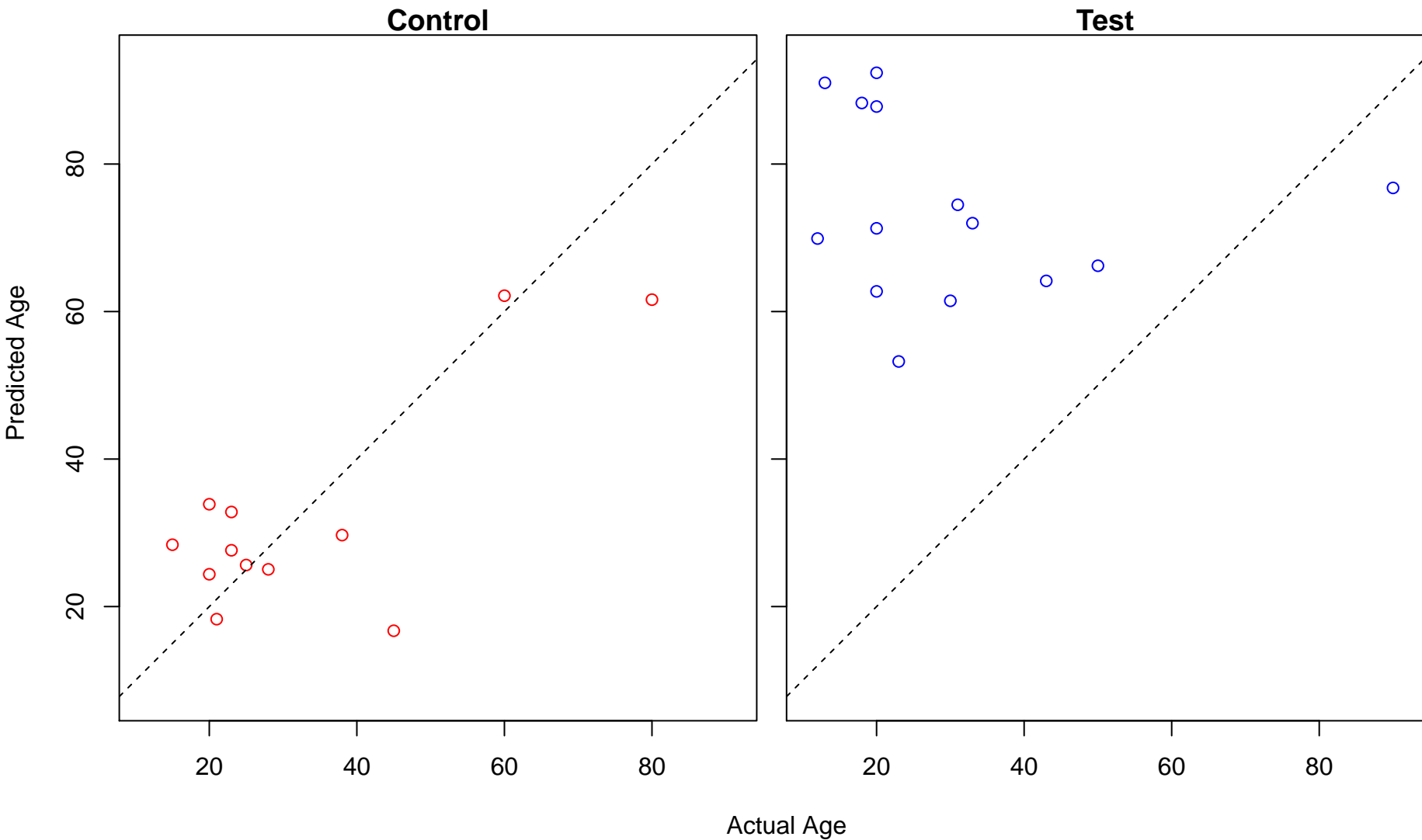
positive regulation of receptor-mediated endocytosis (Score: 5.569610)



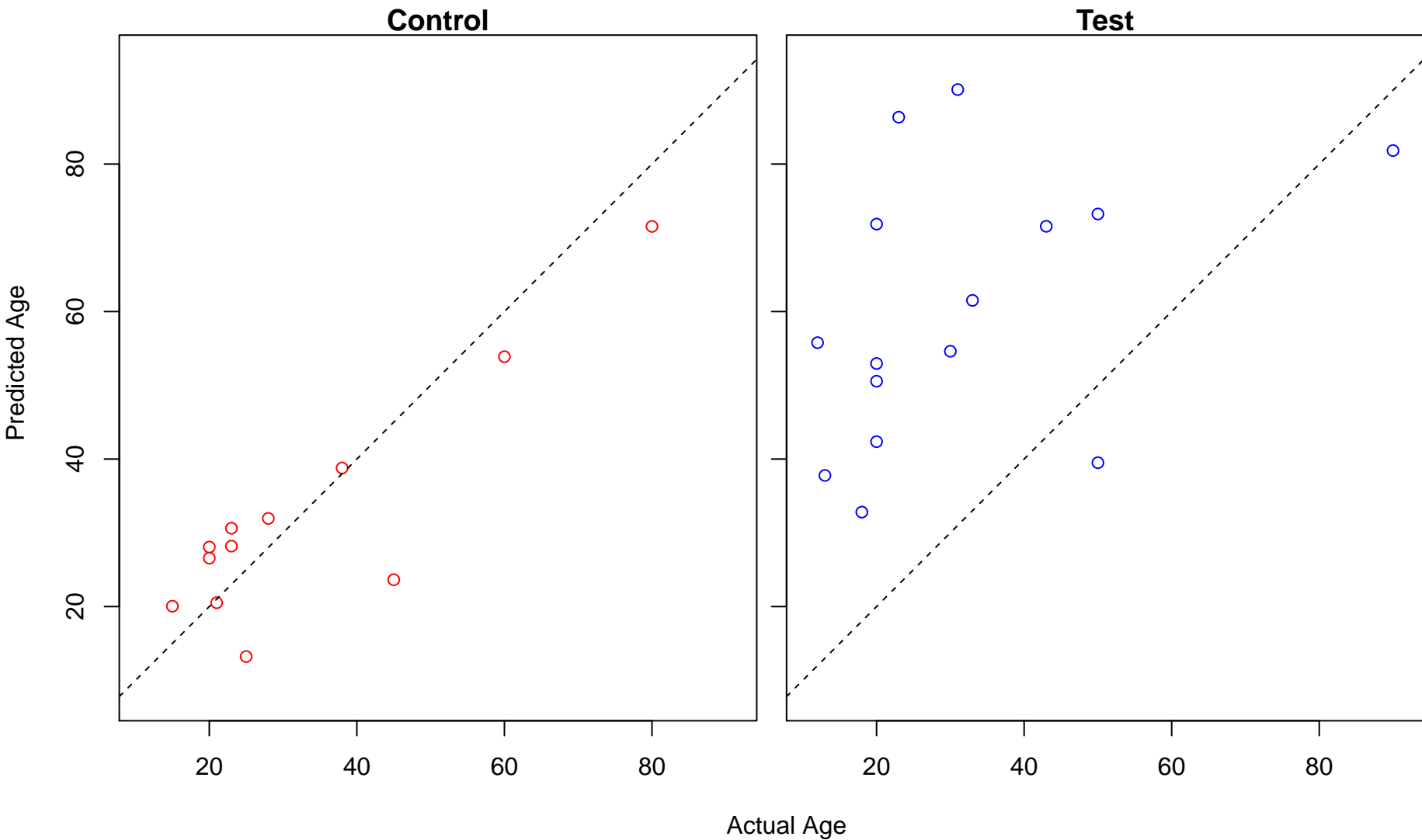
mature B cell differentiation involved in immune response (Score: 5.569417)



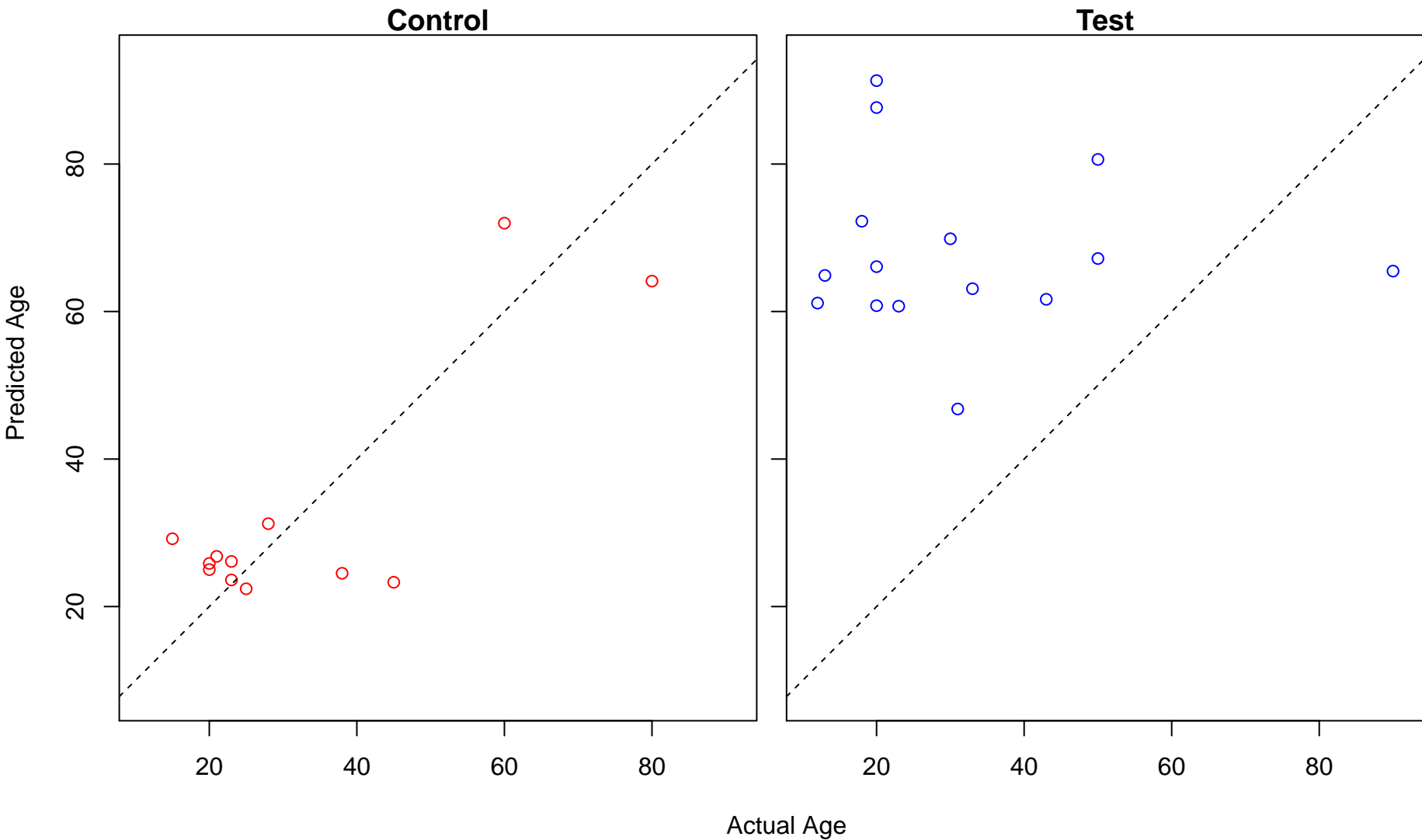
mature B cell differentiation (Score: 5.569417)



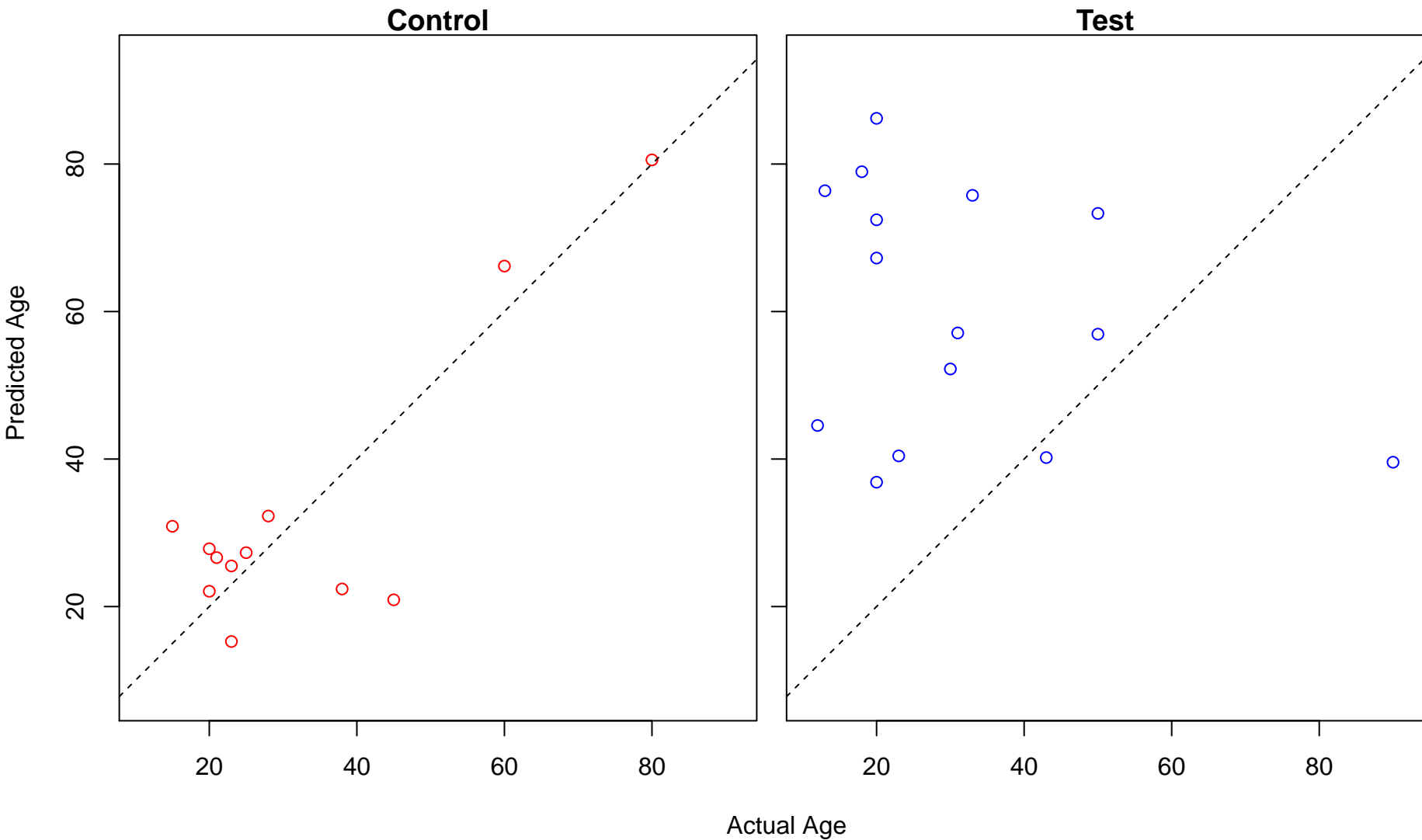
regulation of cilium movement (Score: 5.567971)



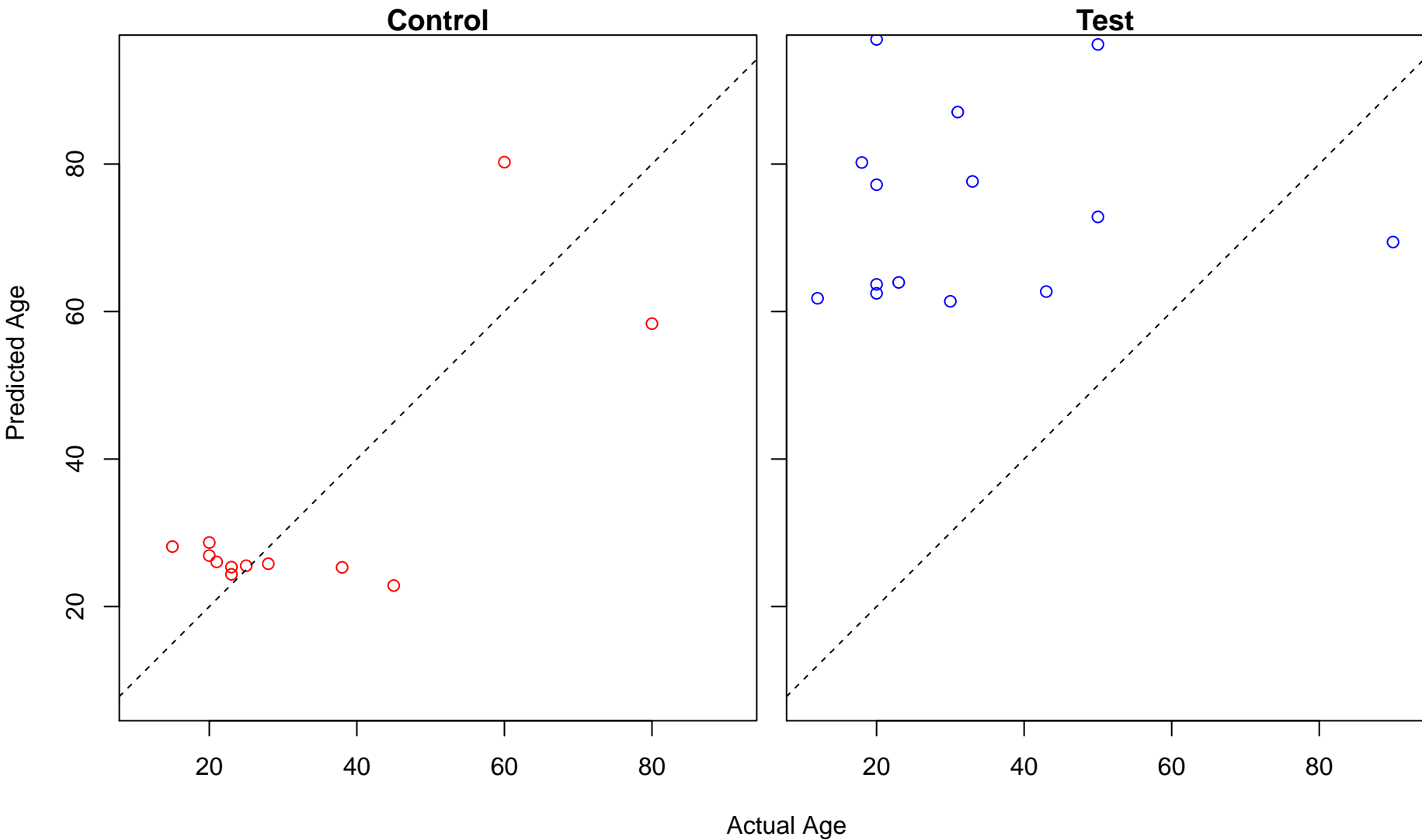
negative regulation of osteoblast proliferation (Score: 5.565718)



positive regulation of phospholipase activity (Score: 5.564264)

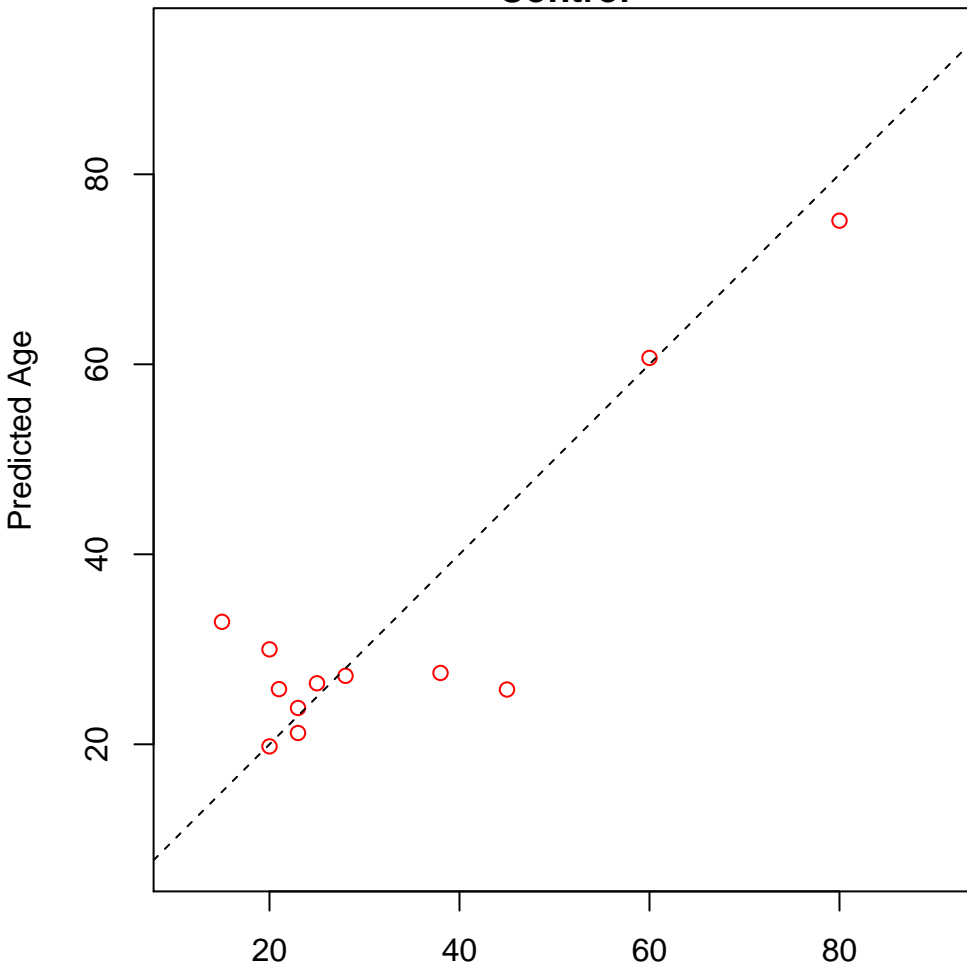


cell junction organization (Score: 5.561997)

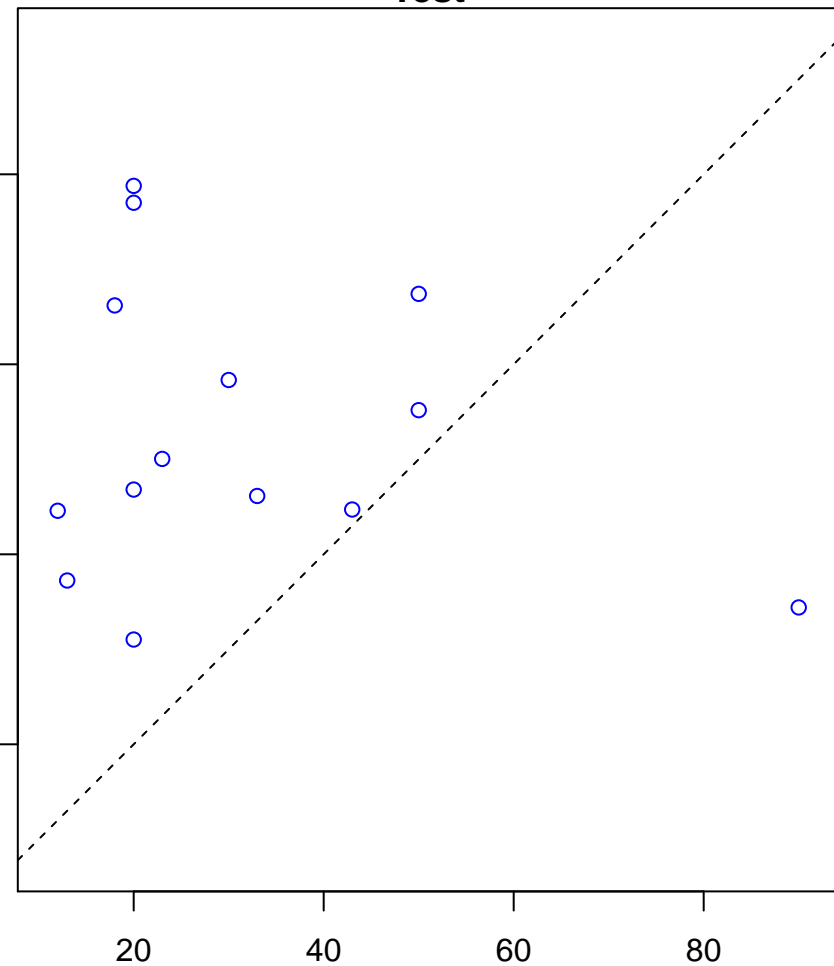


regulation of ATP biosynthetic process (Score: 5.561890)

Control

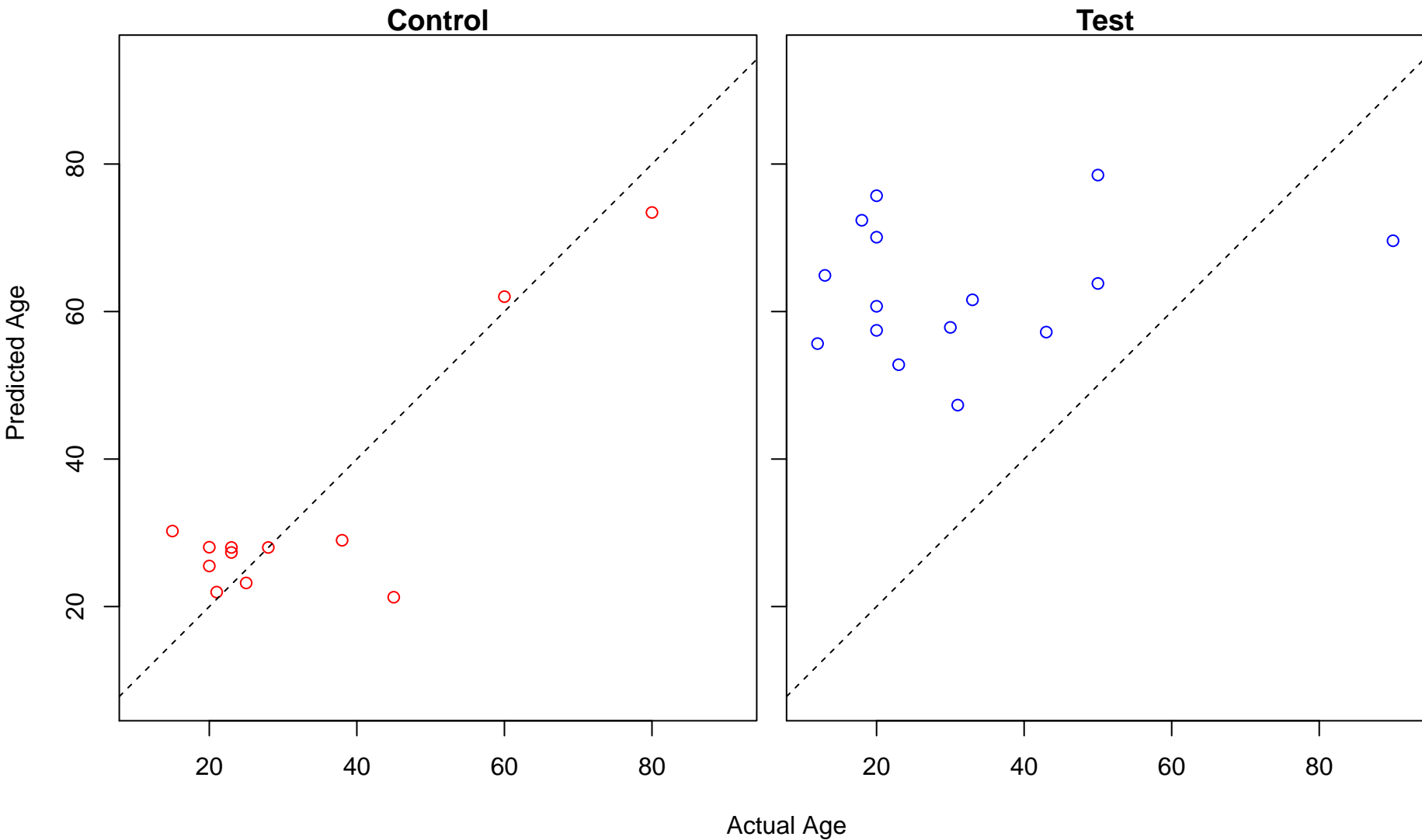


Test

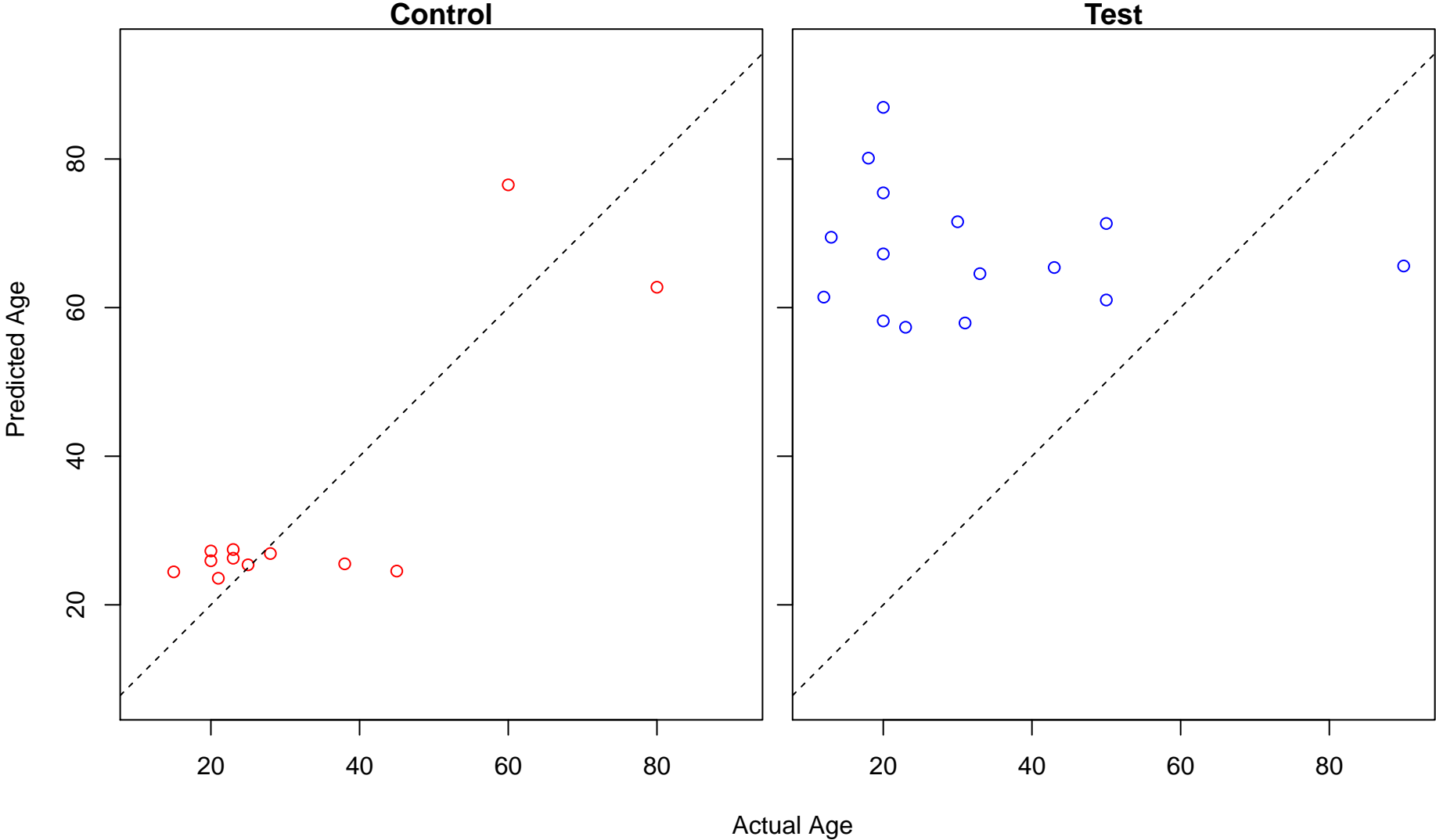


Actual Age

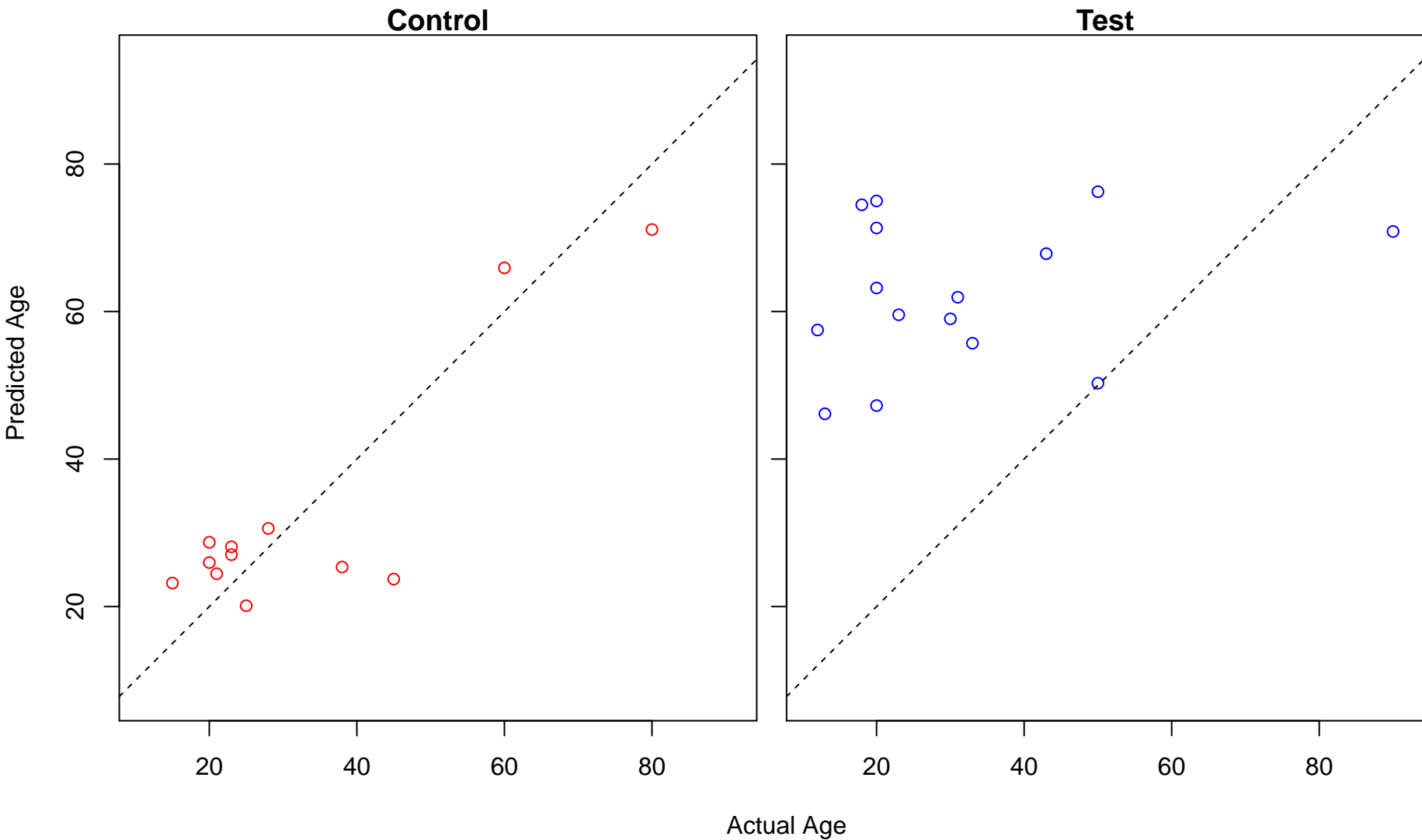
regulation of histone modification (Score: 5.560221)



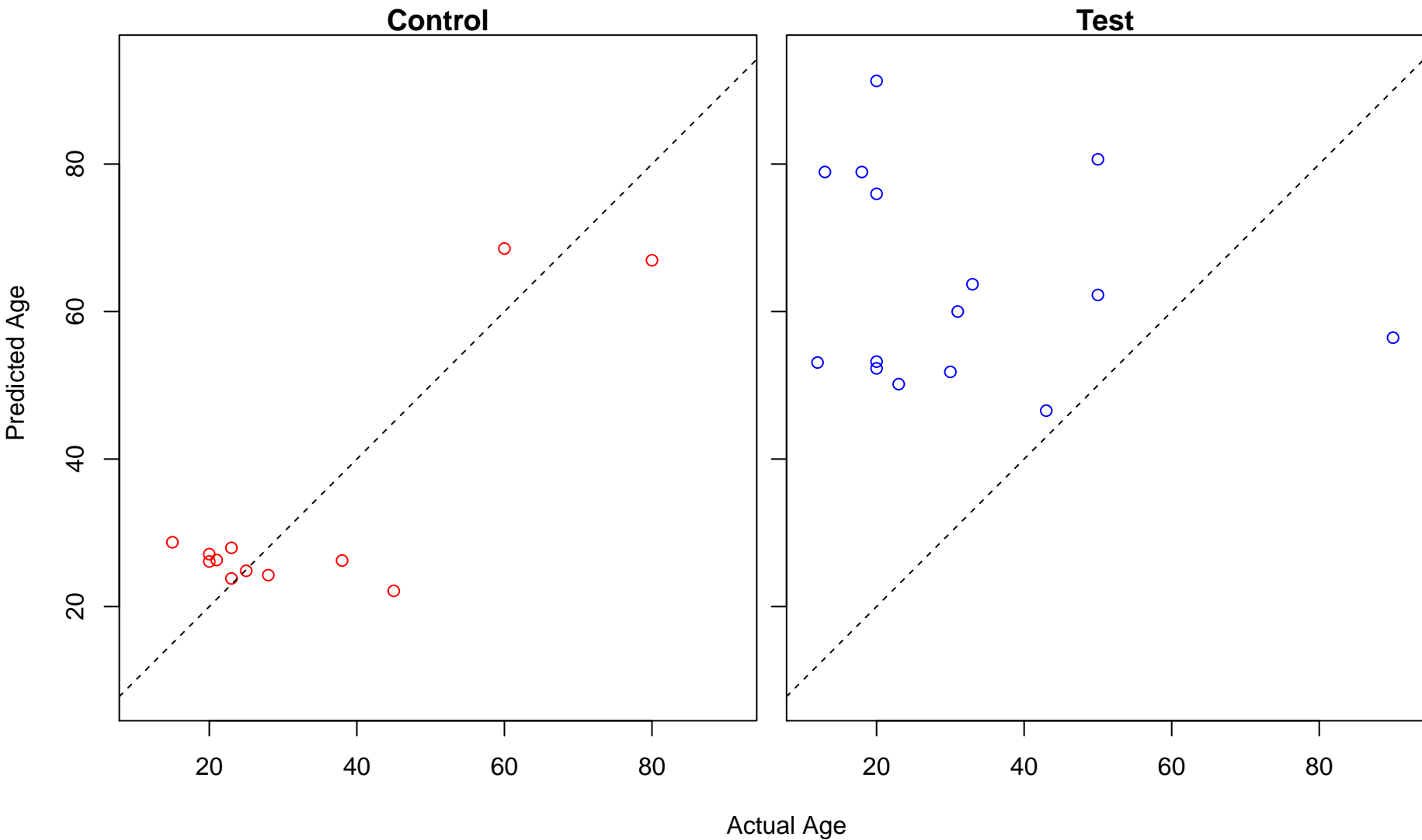
regulation of systemic arterial blood pressure mediated by a chemical signal (Score: 5.559964)



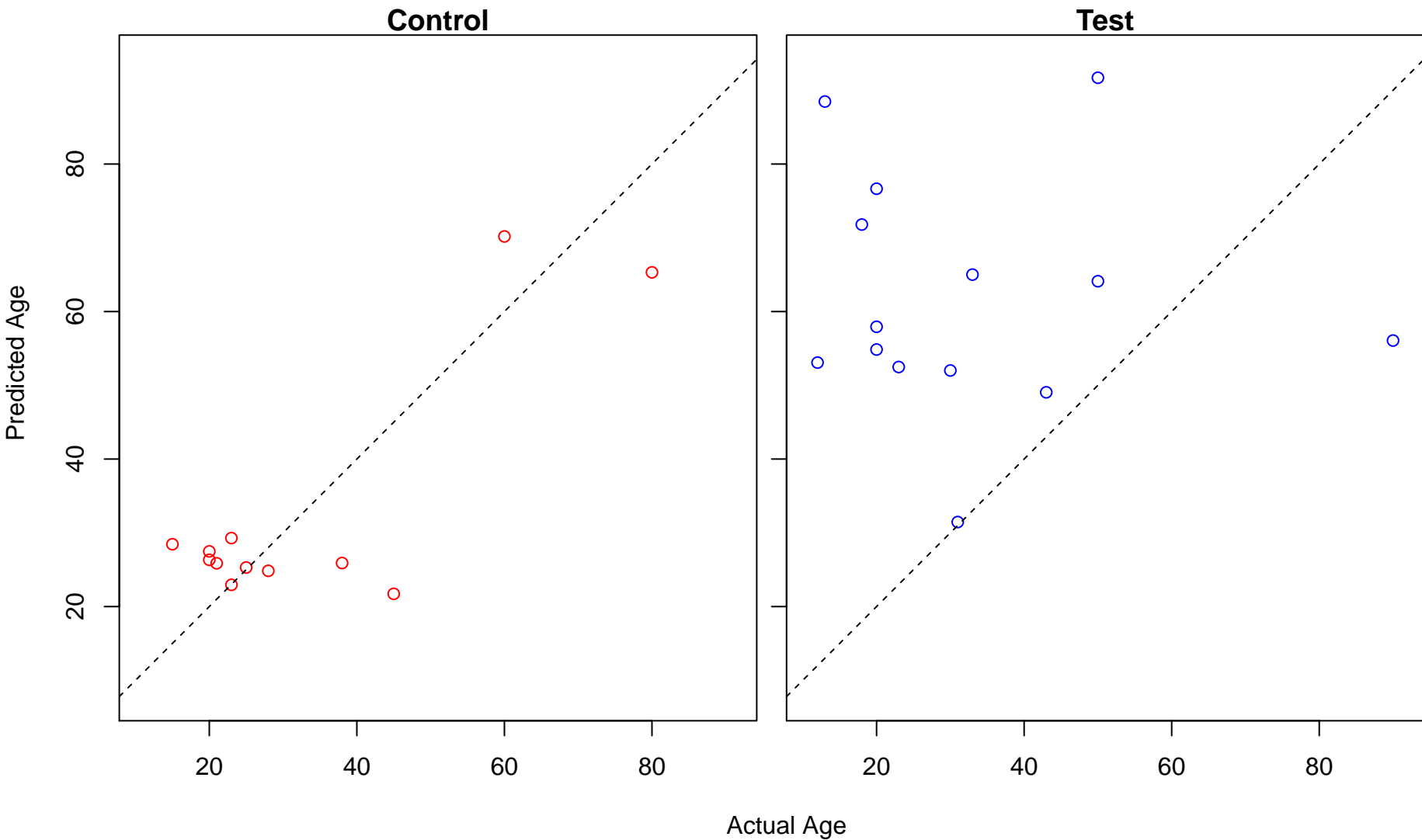
negative regulation of interleukin-8 production (Score: 5.559782)



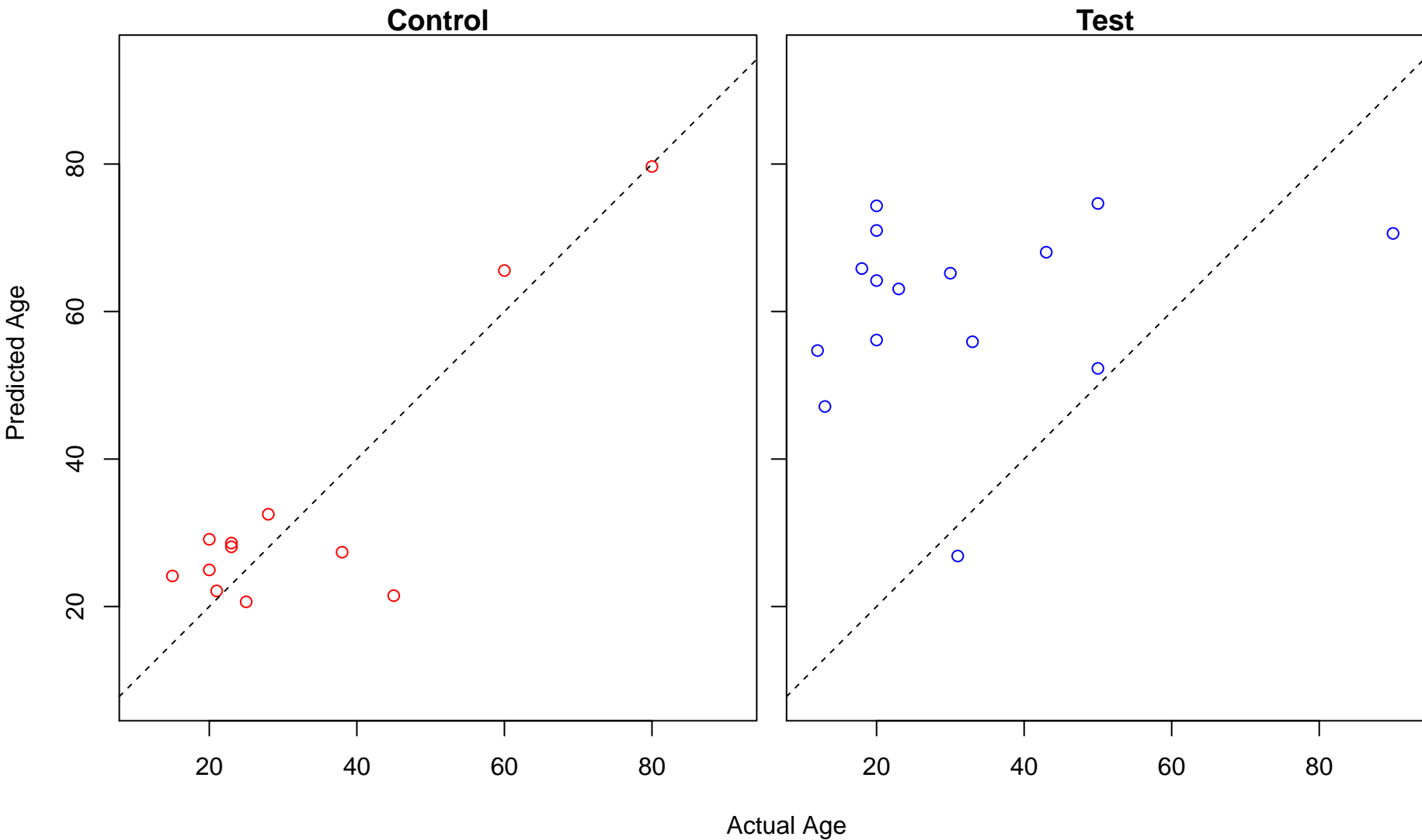
regulation of neuron death (Score: 5.558694)



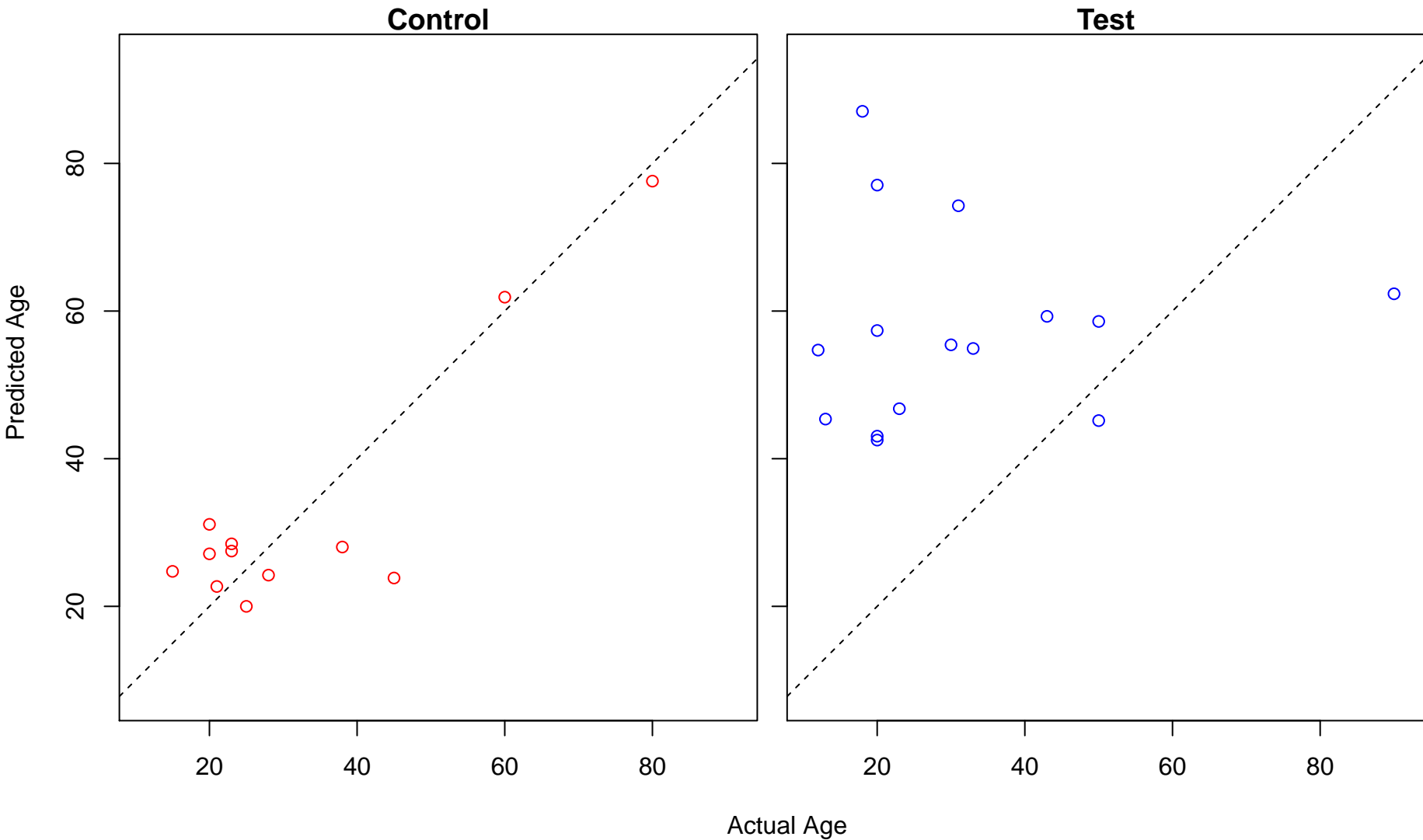
positive regulation of intrinsic apoptotic signaling pathway (Score: 5.558600)



leukocyte aggregation (Score: 5.556839)

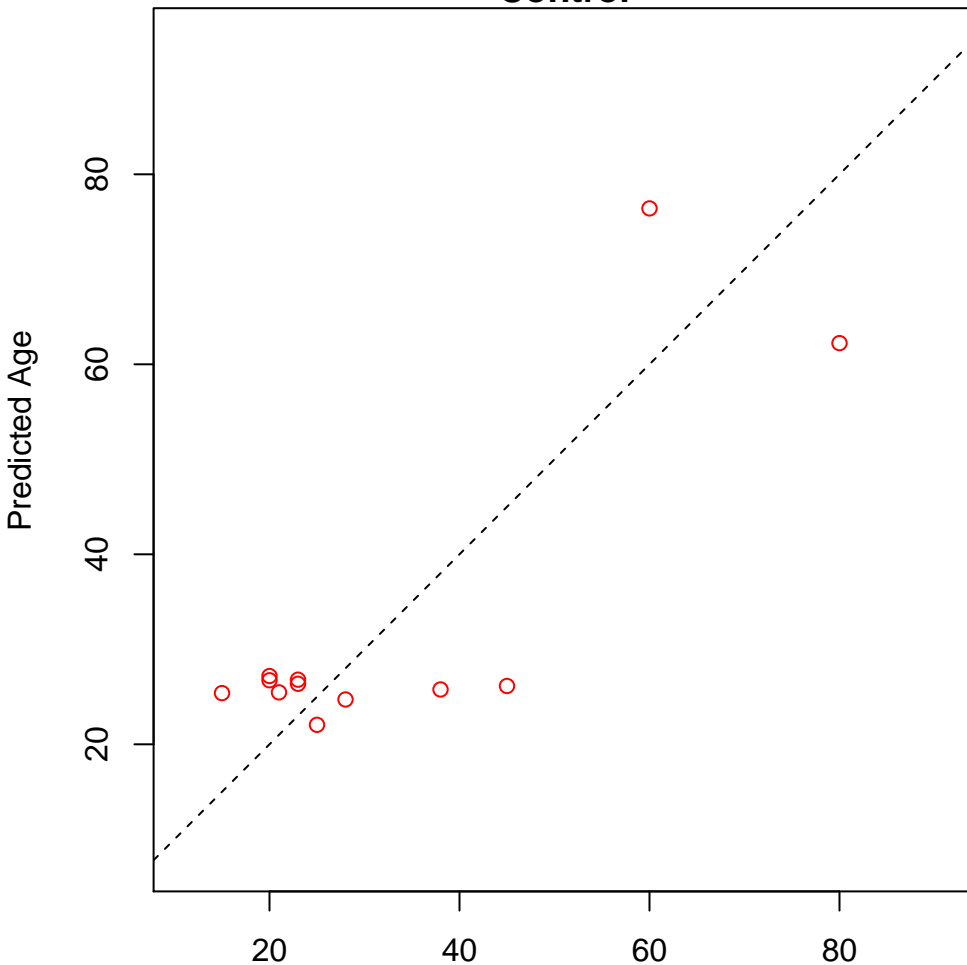


positive regulation of protein exit from endoplasmic reticulum (Score: 5.555286)

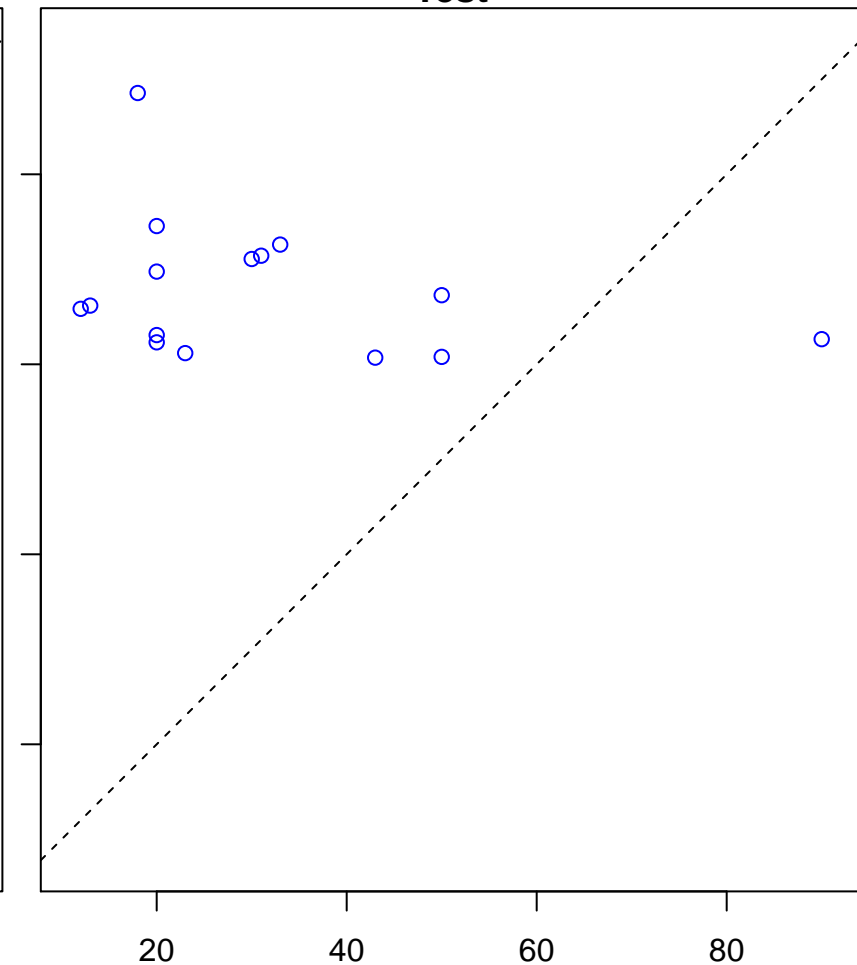


protein localization to Golgi apparatus (Score: 5.551036)

Control



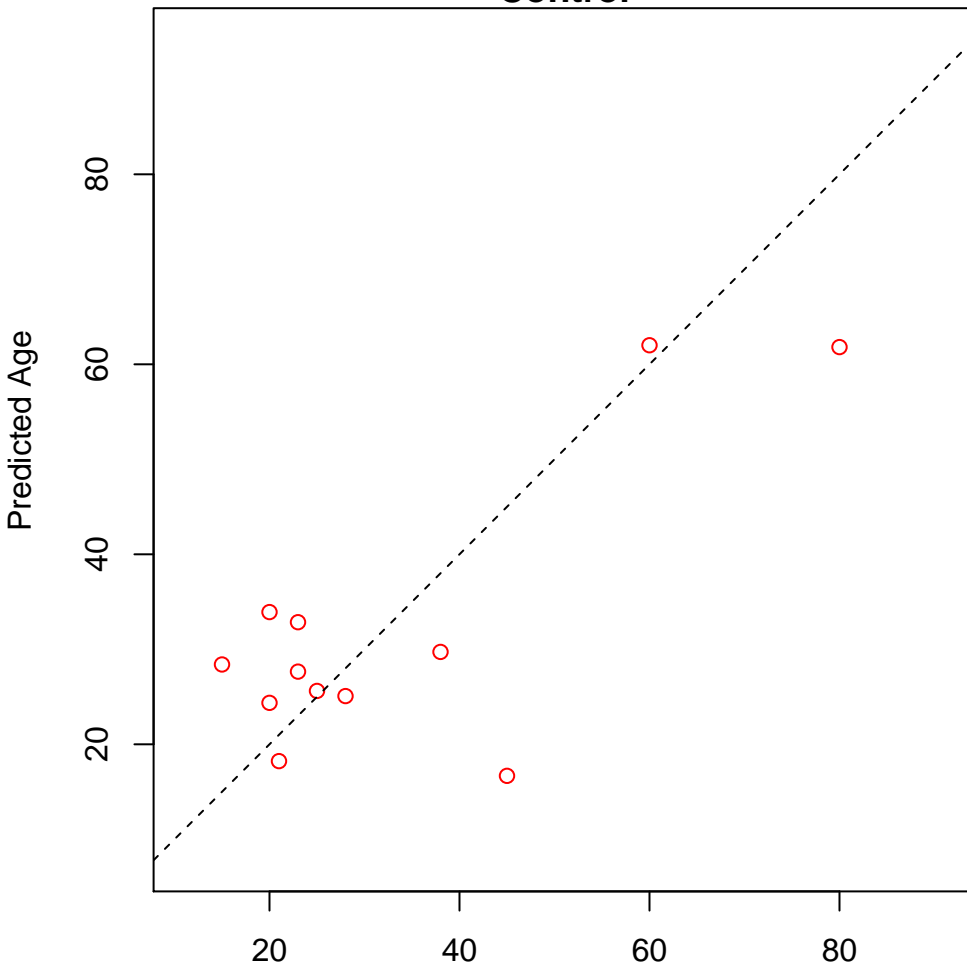
Test



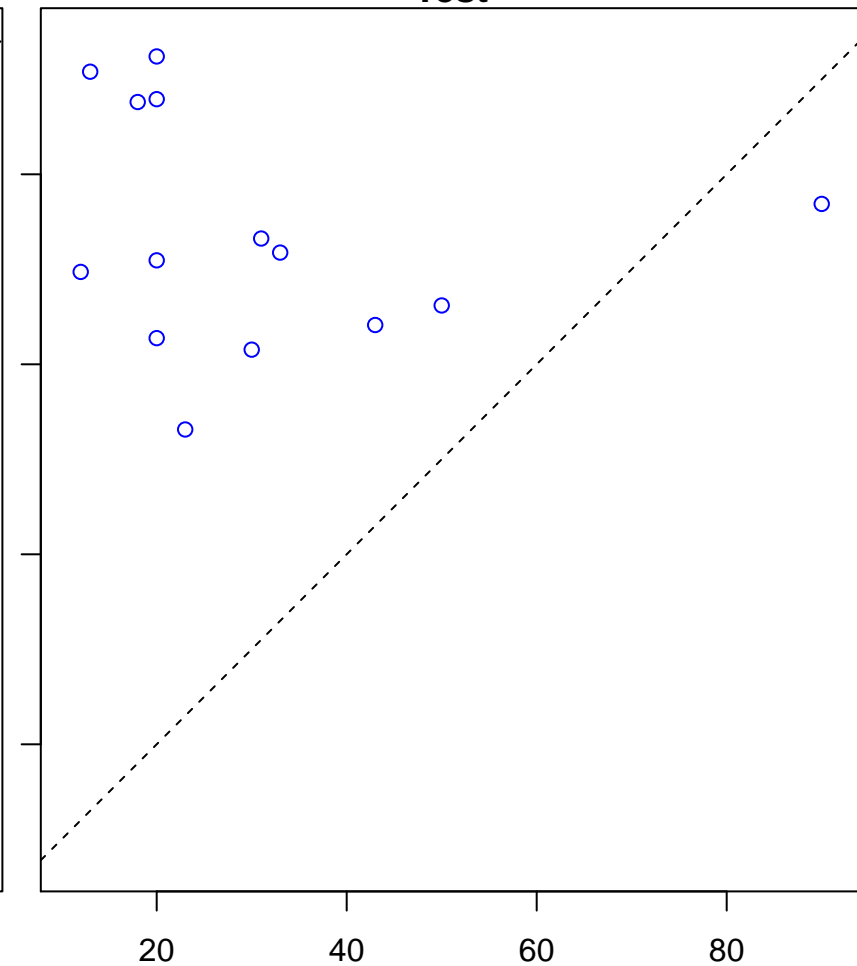
Actual Age

marginal zone B cell differentiation (Score: 5.550839)

Control

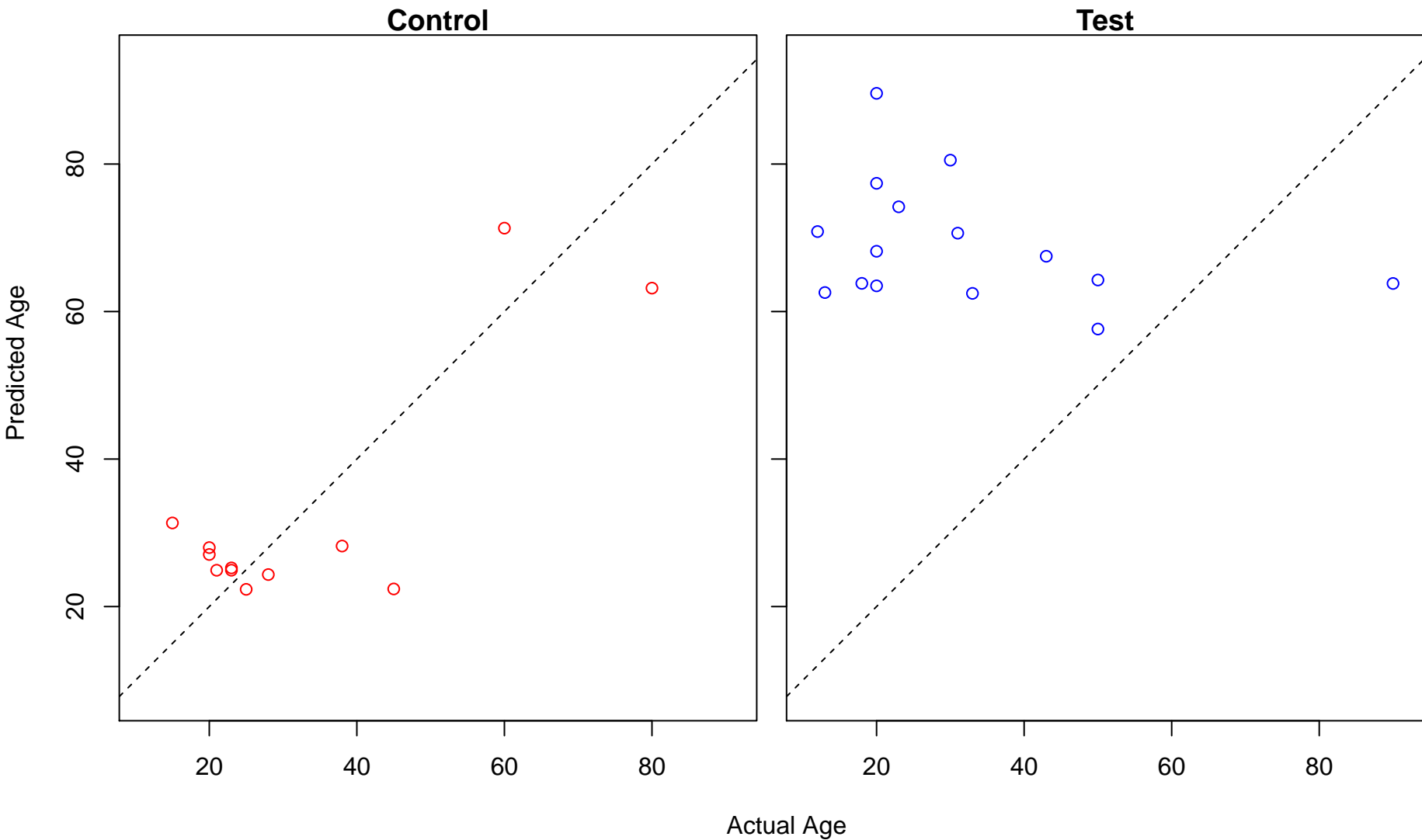


Test

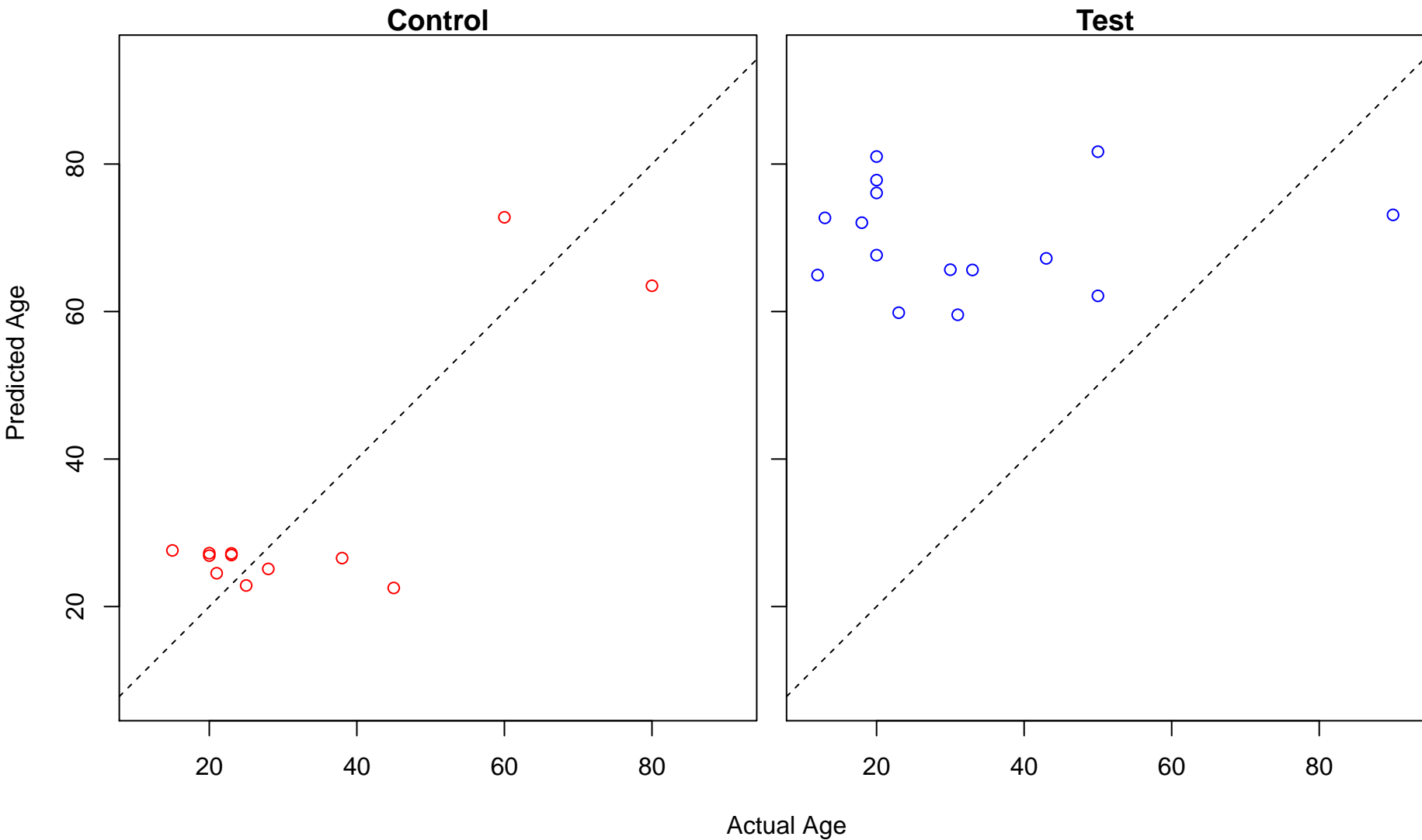


Actual Age

interleukin-6-mediated signaling pathway (Score: 5.545027)

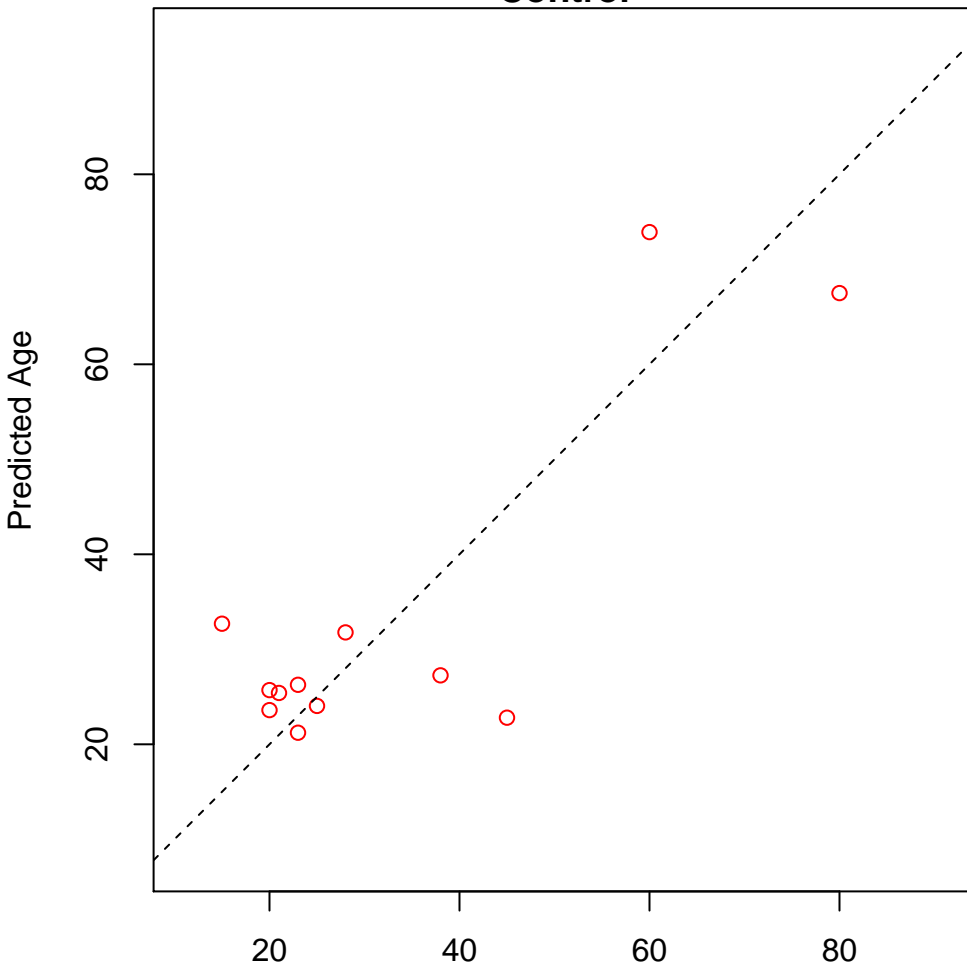


regulation of histone methylation (Score: 5.544718)

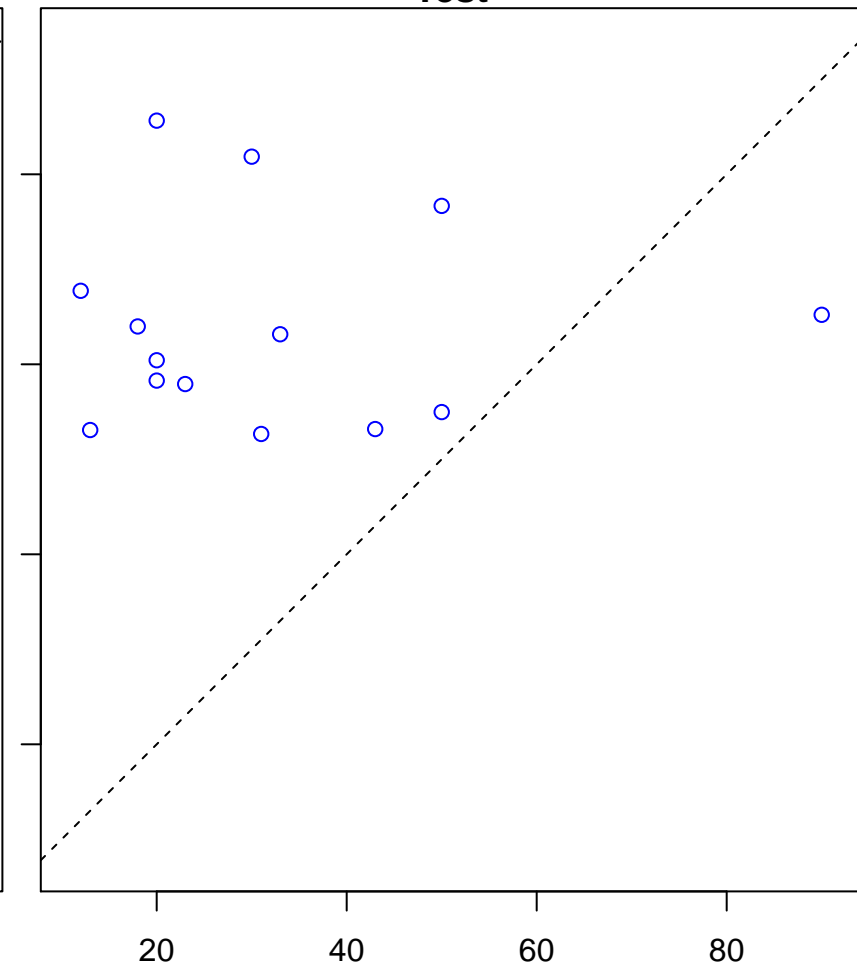


regulation of endothelial cell migration (Score: 5.543779)

Control

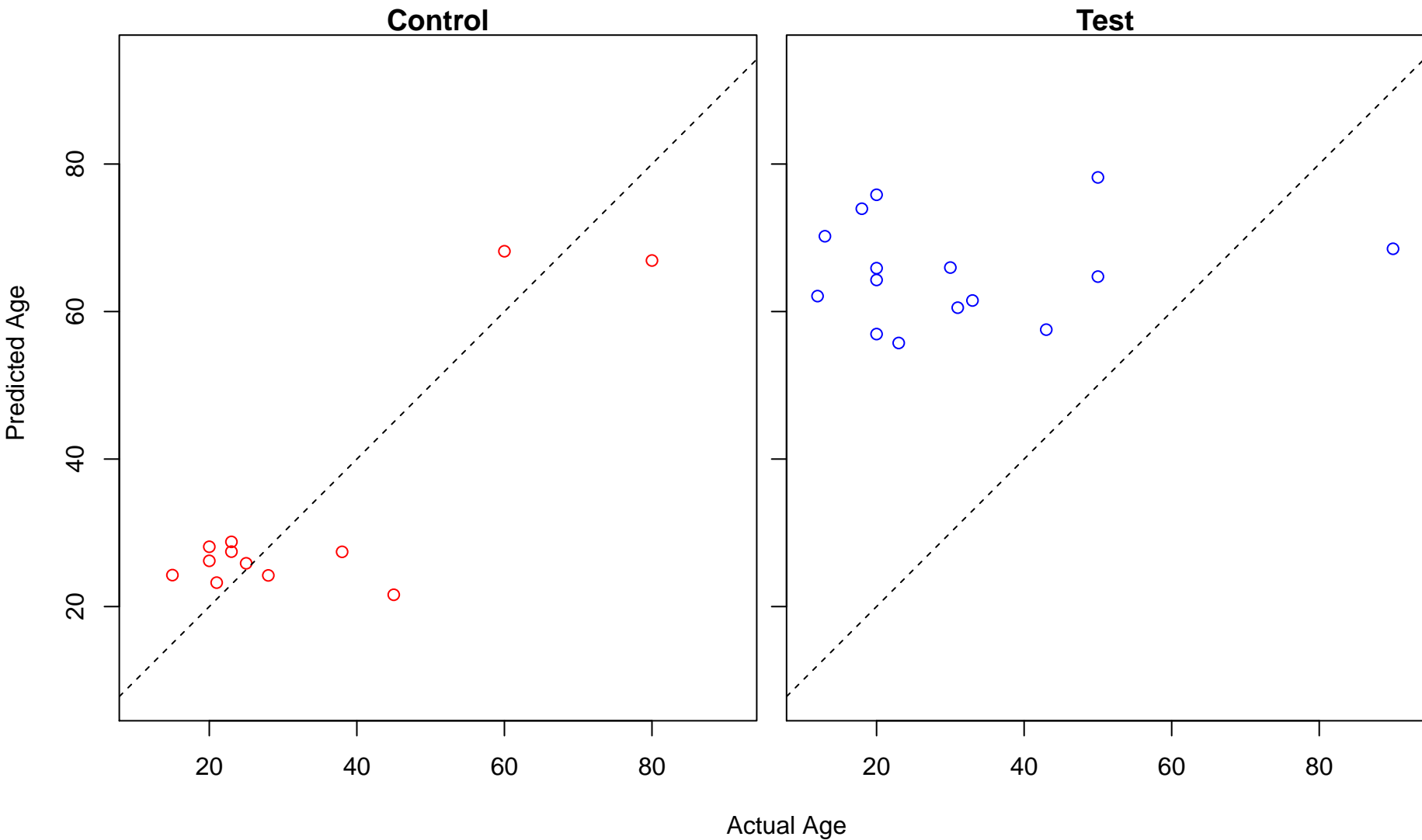


Test

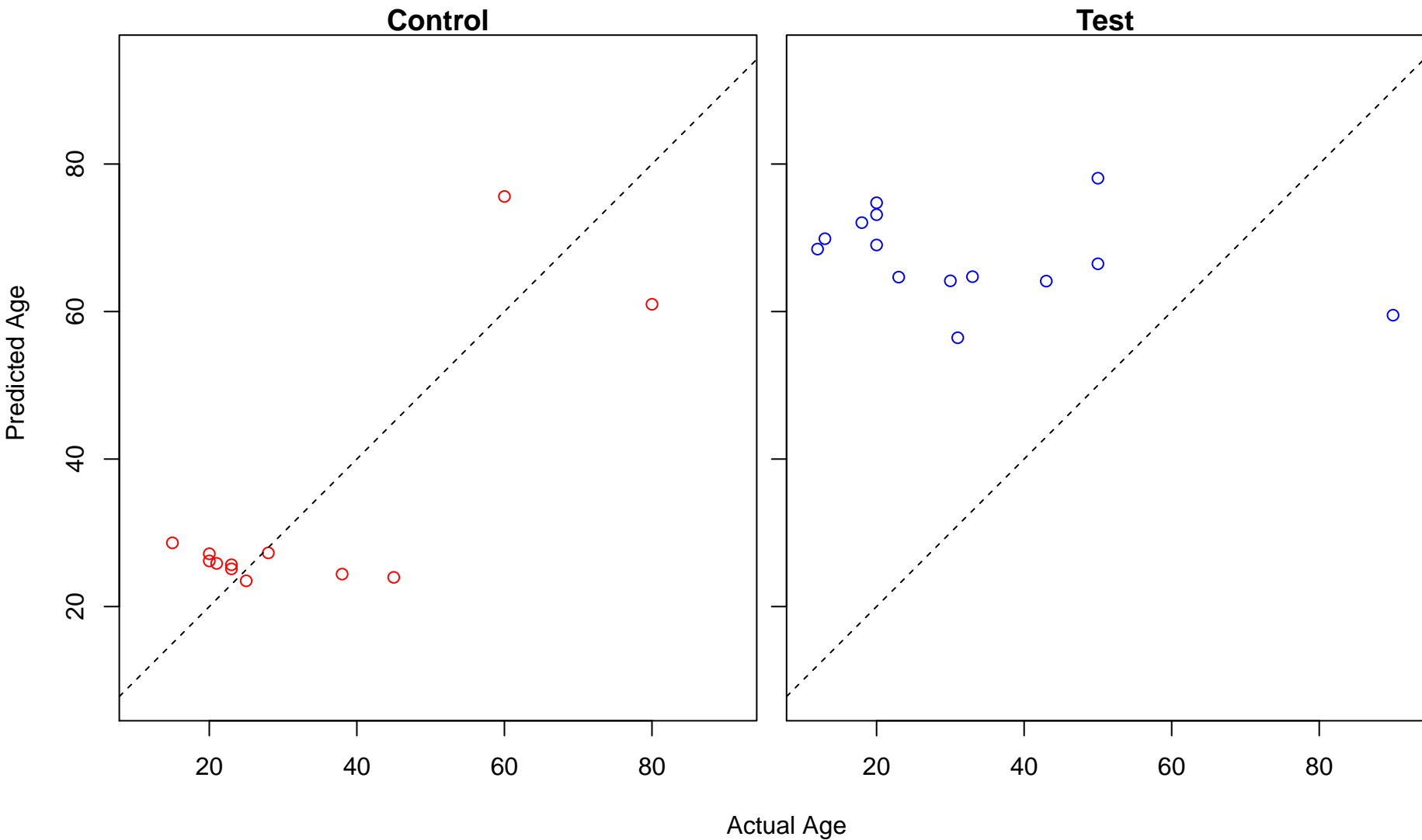


Actual Age

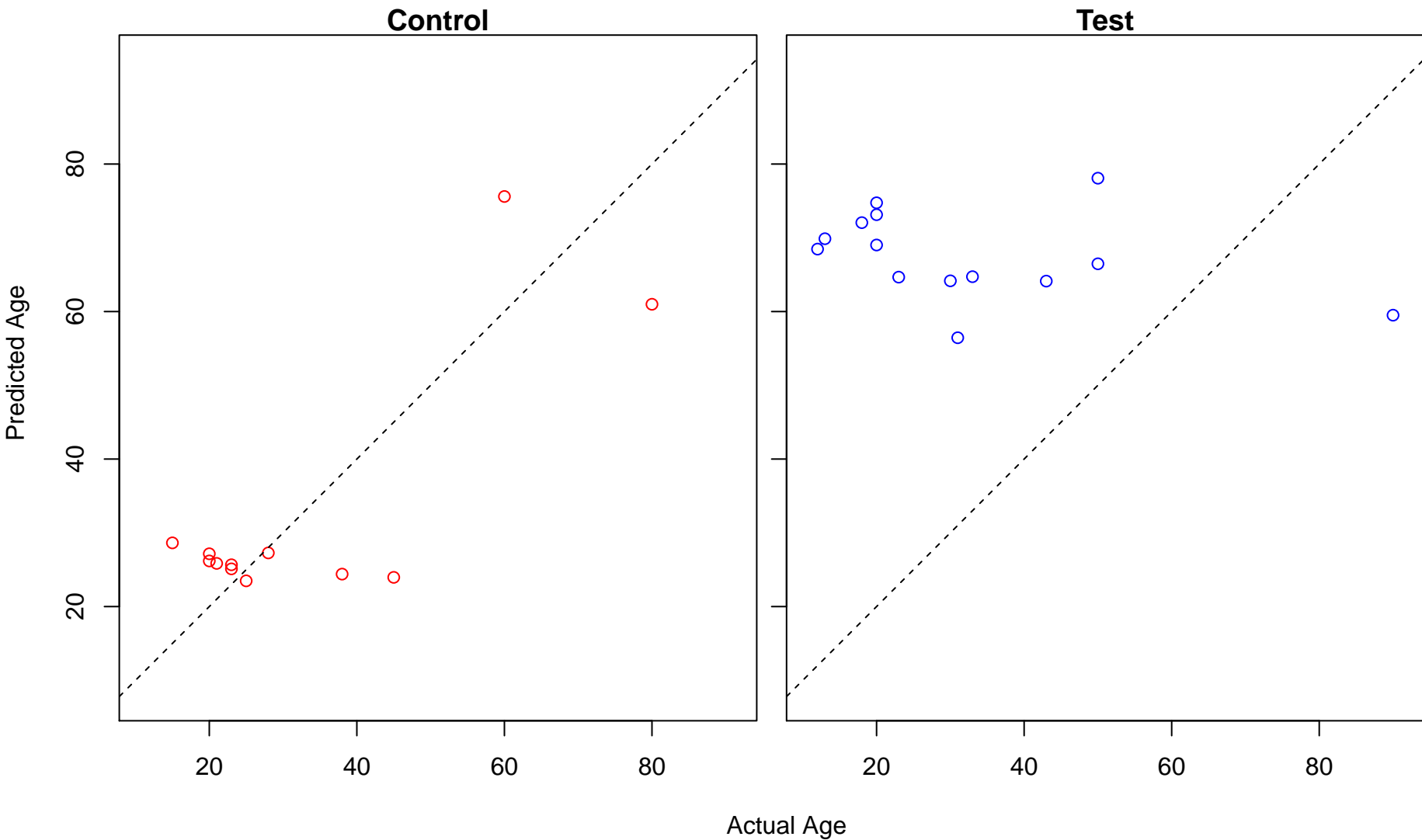
positive regulation of mRNA catabolic process (Score: 5.543775)



positive regulation of cellular response to oxidative stress (Score: 5.543239)

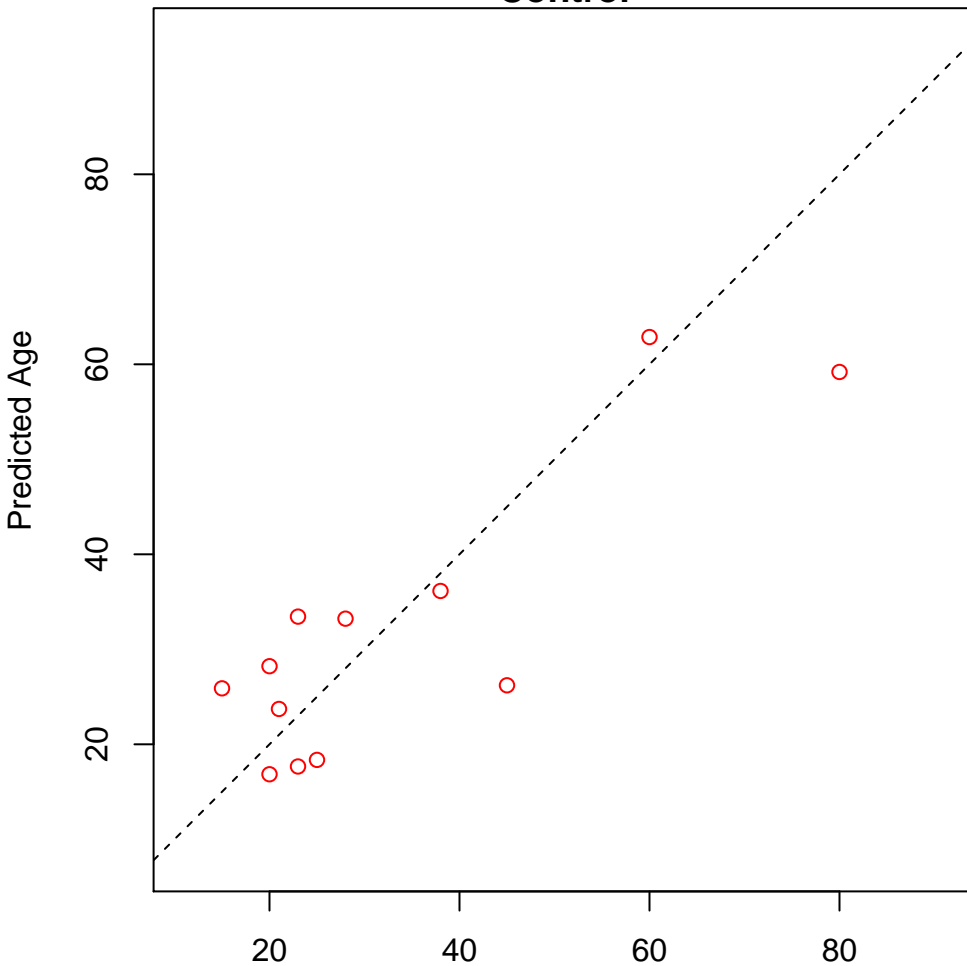


positive regulation of response to oxidative stress (Score: 5.543239)

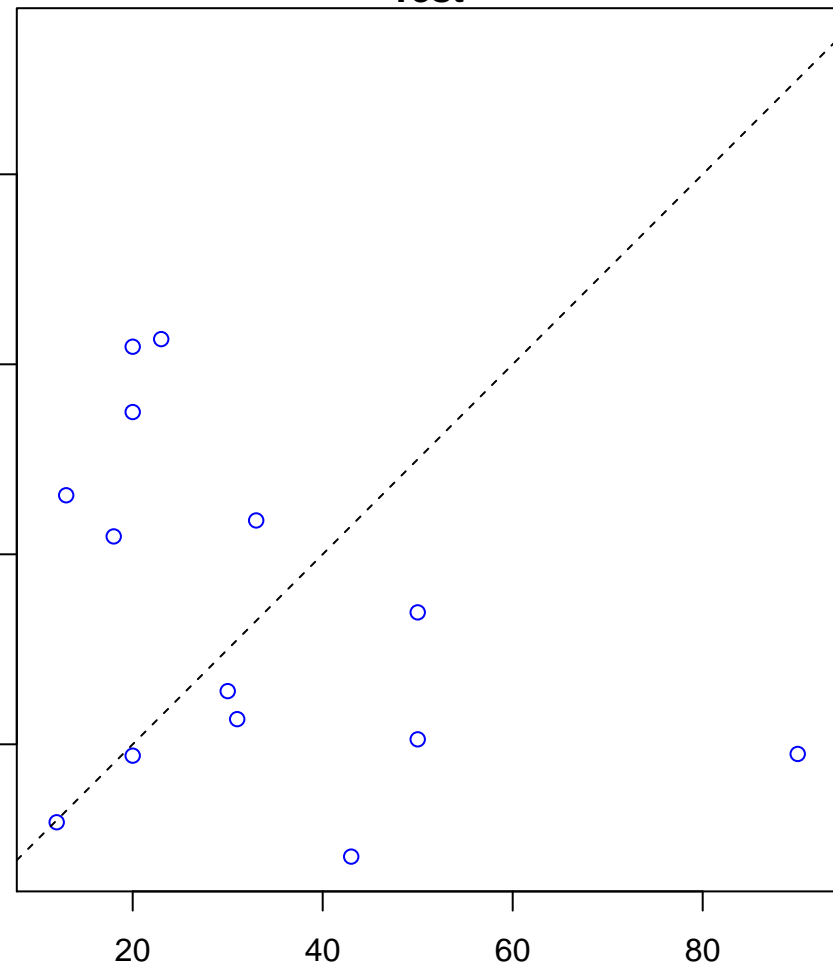


regulation of striated muscle contraction (Score: 5.542387)

Control

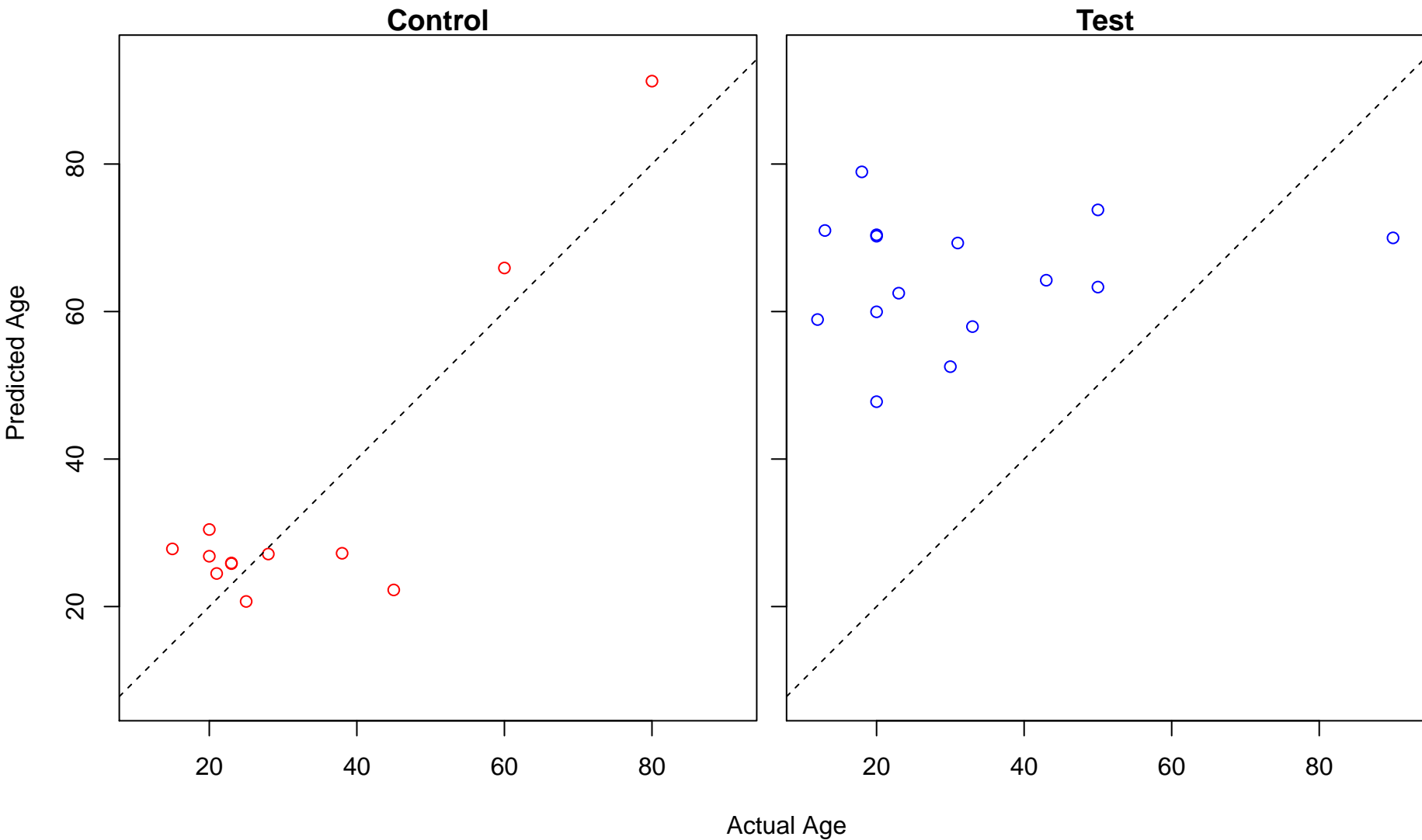


Test

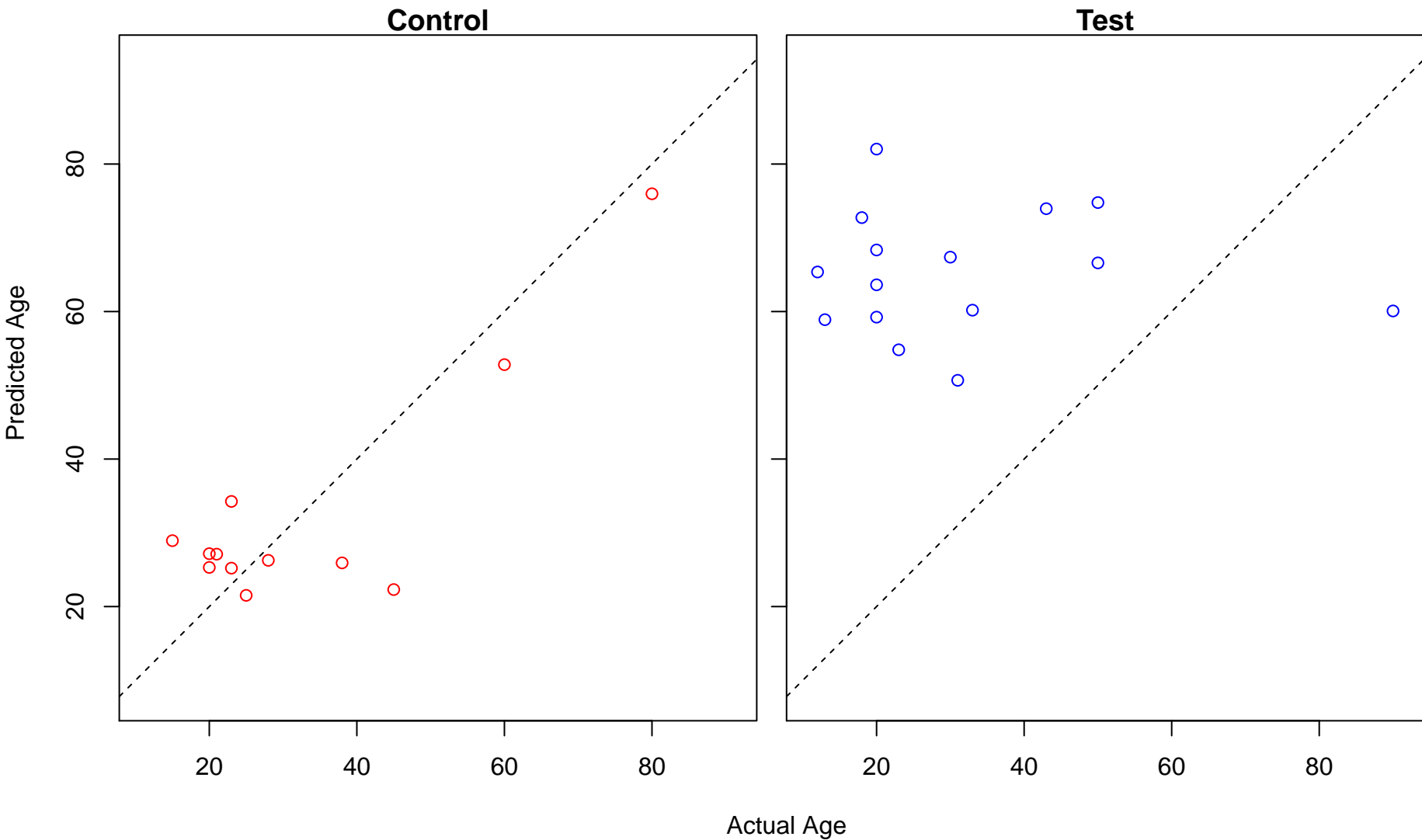


Actual Age

regulation of cell morphogenesis (Score: 5.539485)

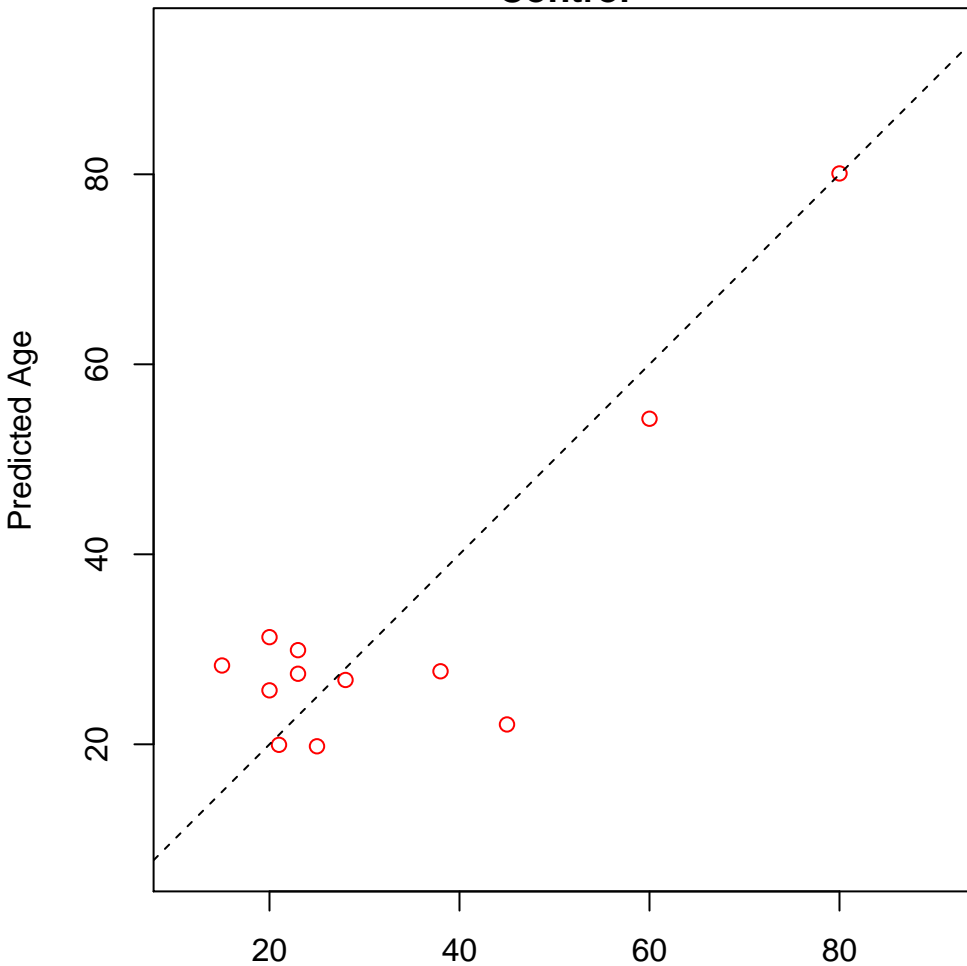


lipid modification (Score: 5.538910)

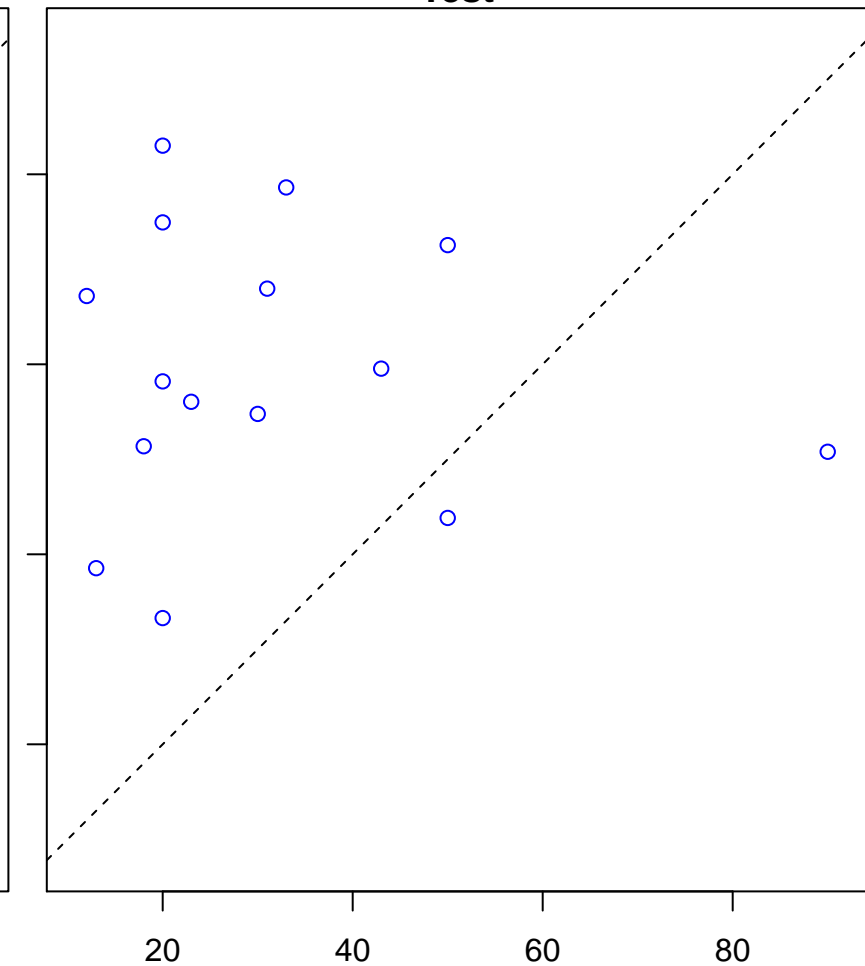


apoptotic chromosome condensation (Score: 5.538294)

Control

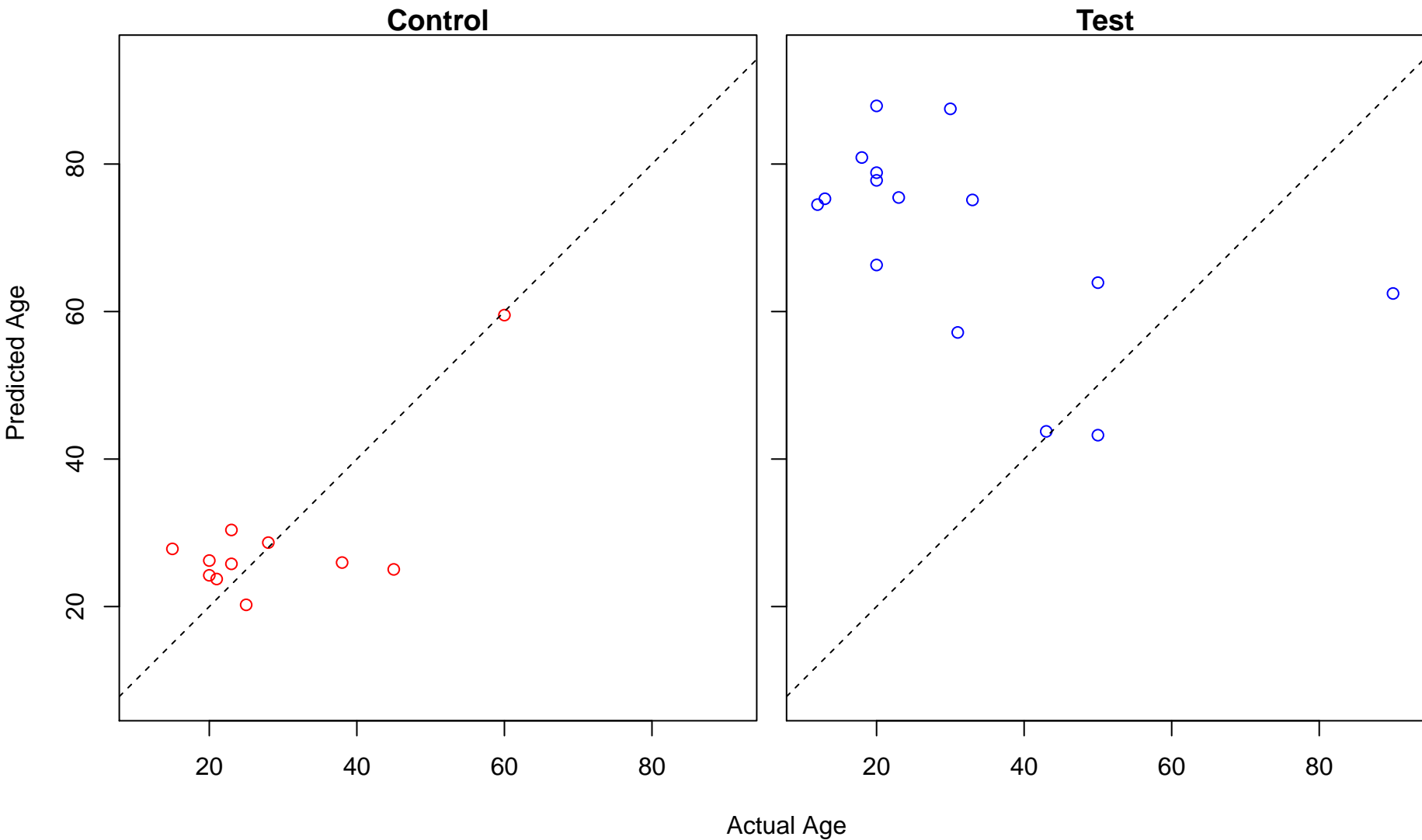


Test

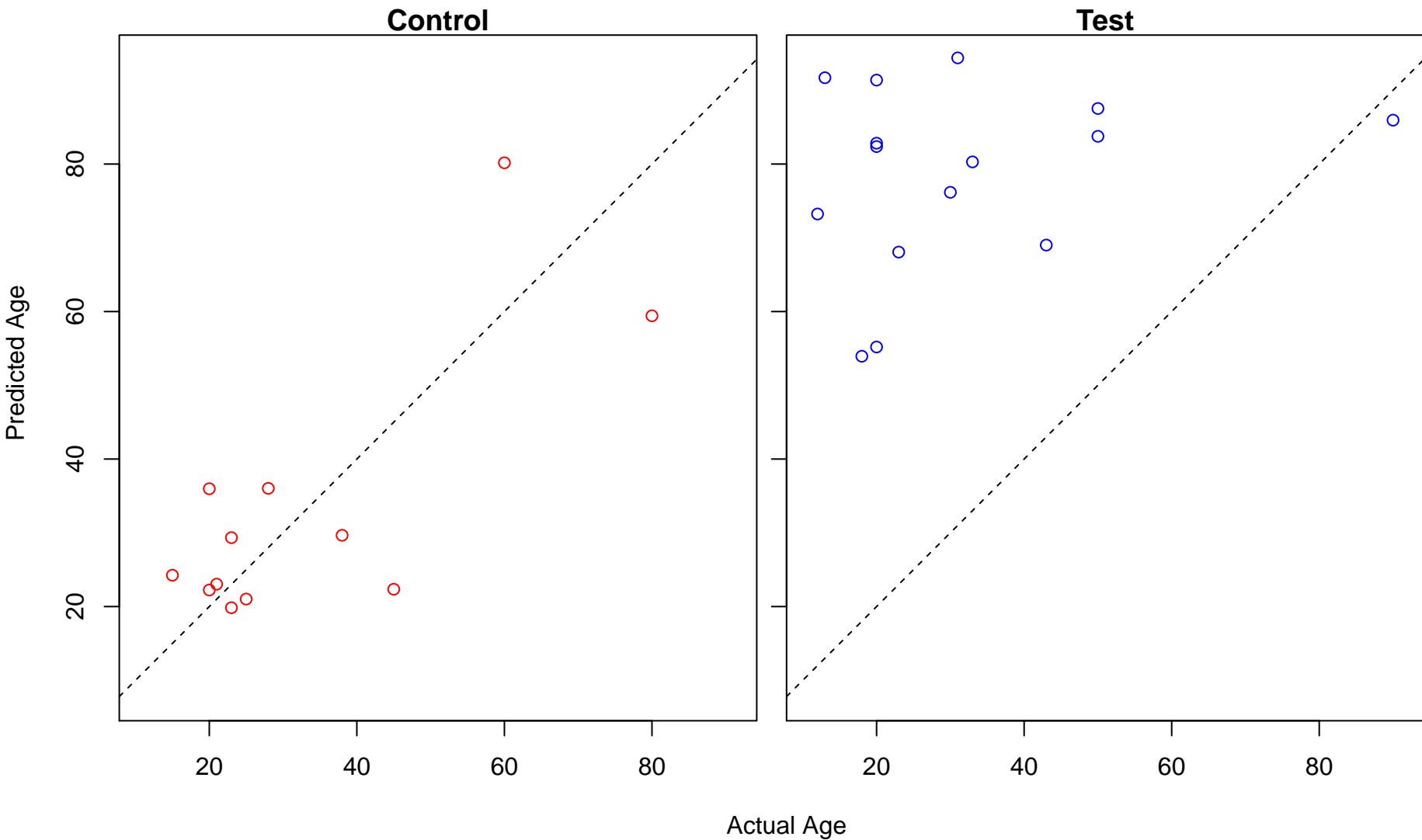


Actual Age

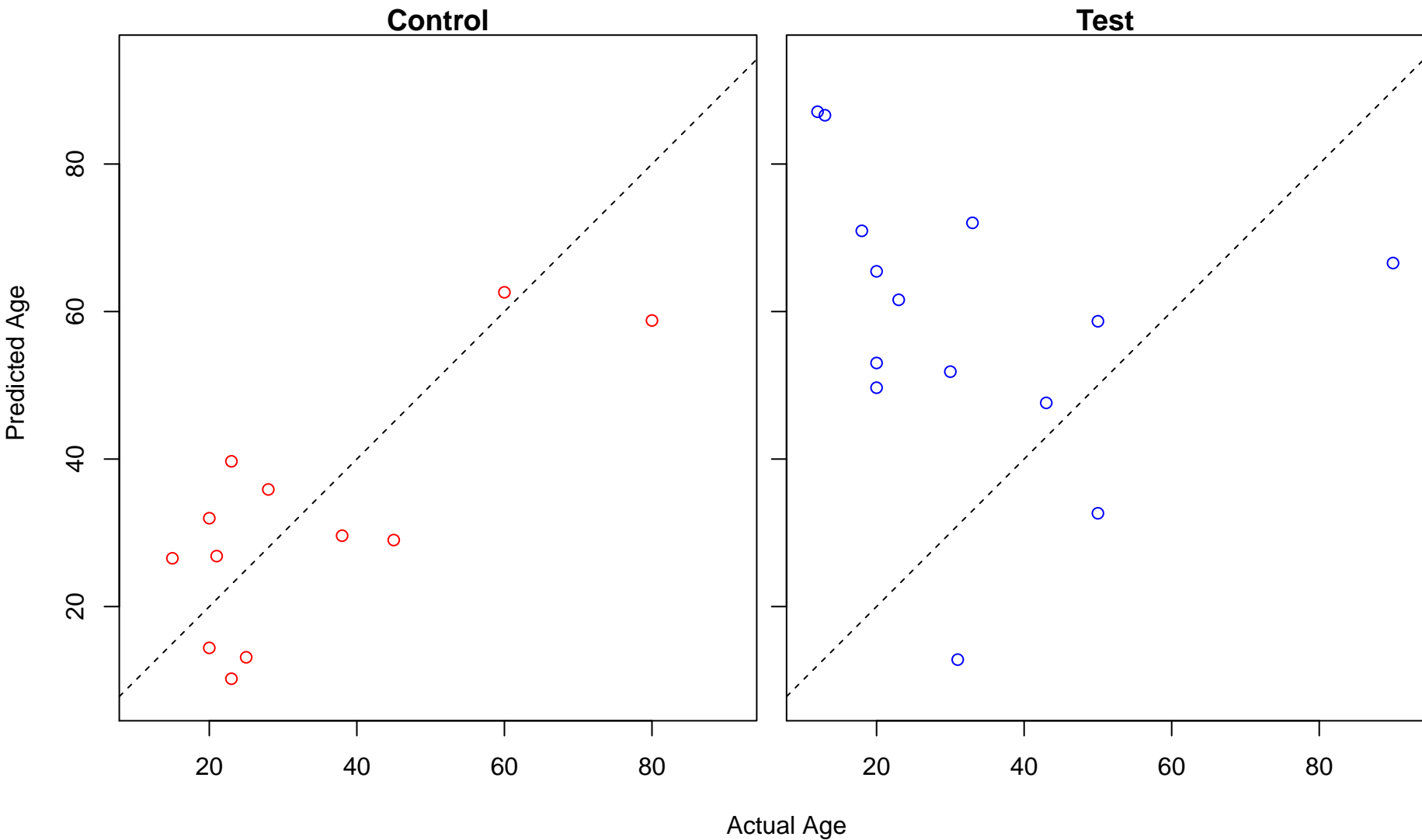
L-alpha-amino acid transmembrane transport (Score: 5.536633)



elastic fiber assembly (Score: 5.536328)

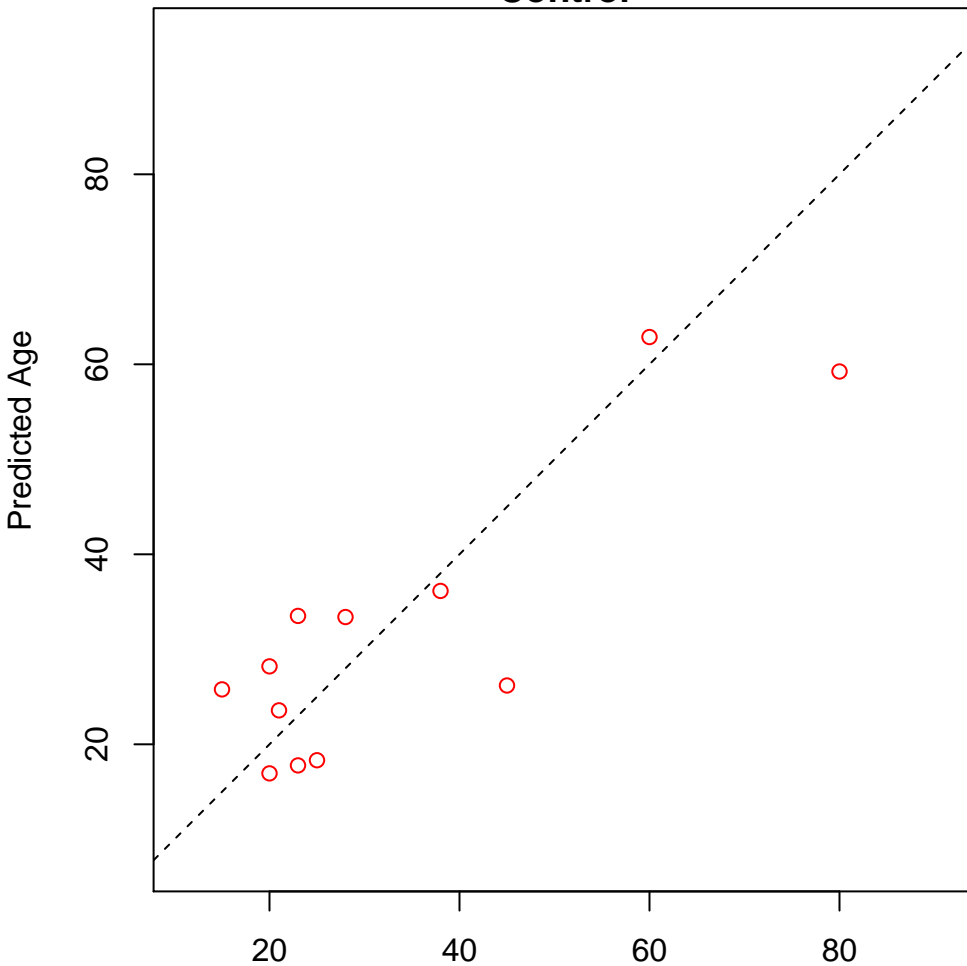


protein localization to nucleus (Score: 5.536258)

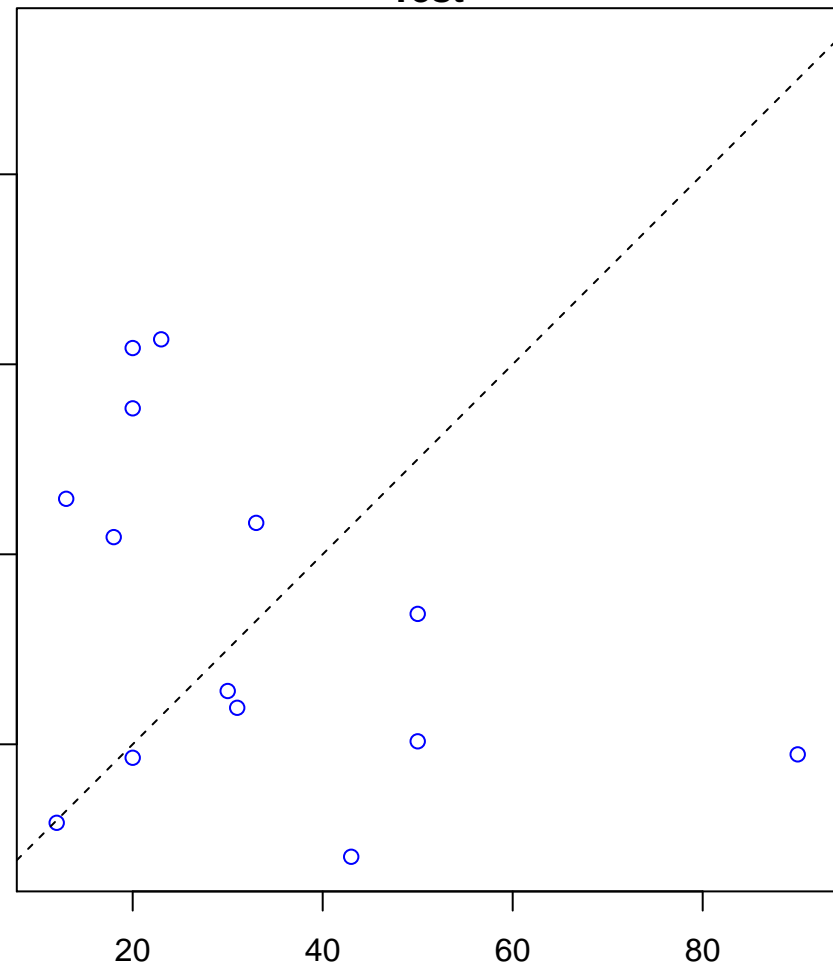


regulation of cardiac muscle contraction (Score: 5.533915)

Control

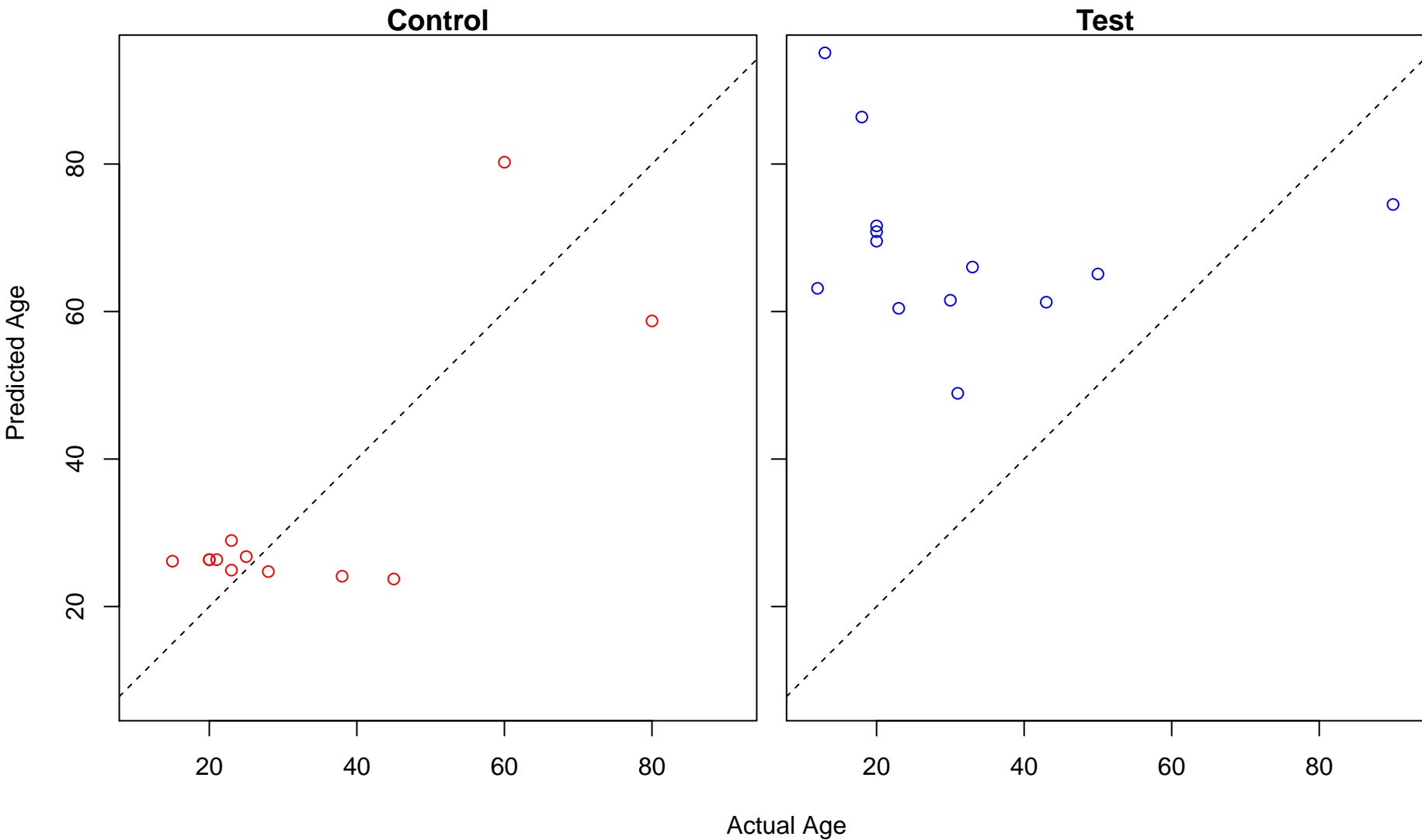


Test

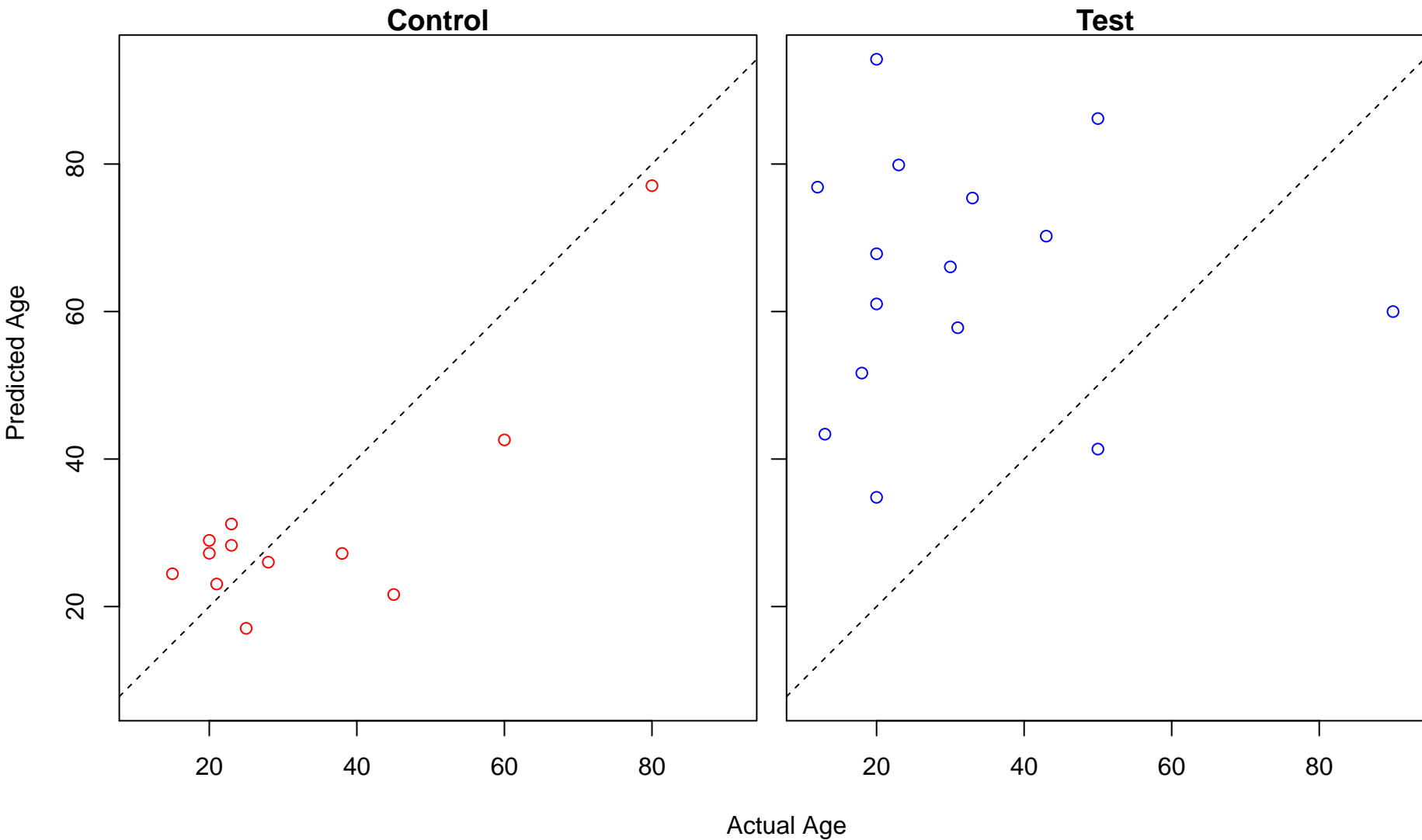


Actual Age

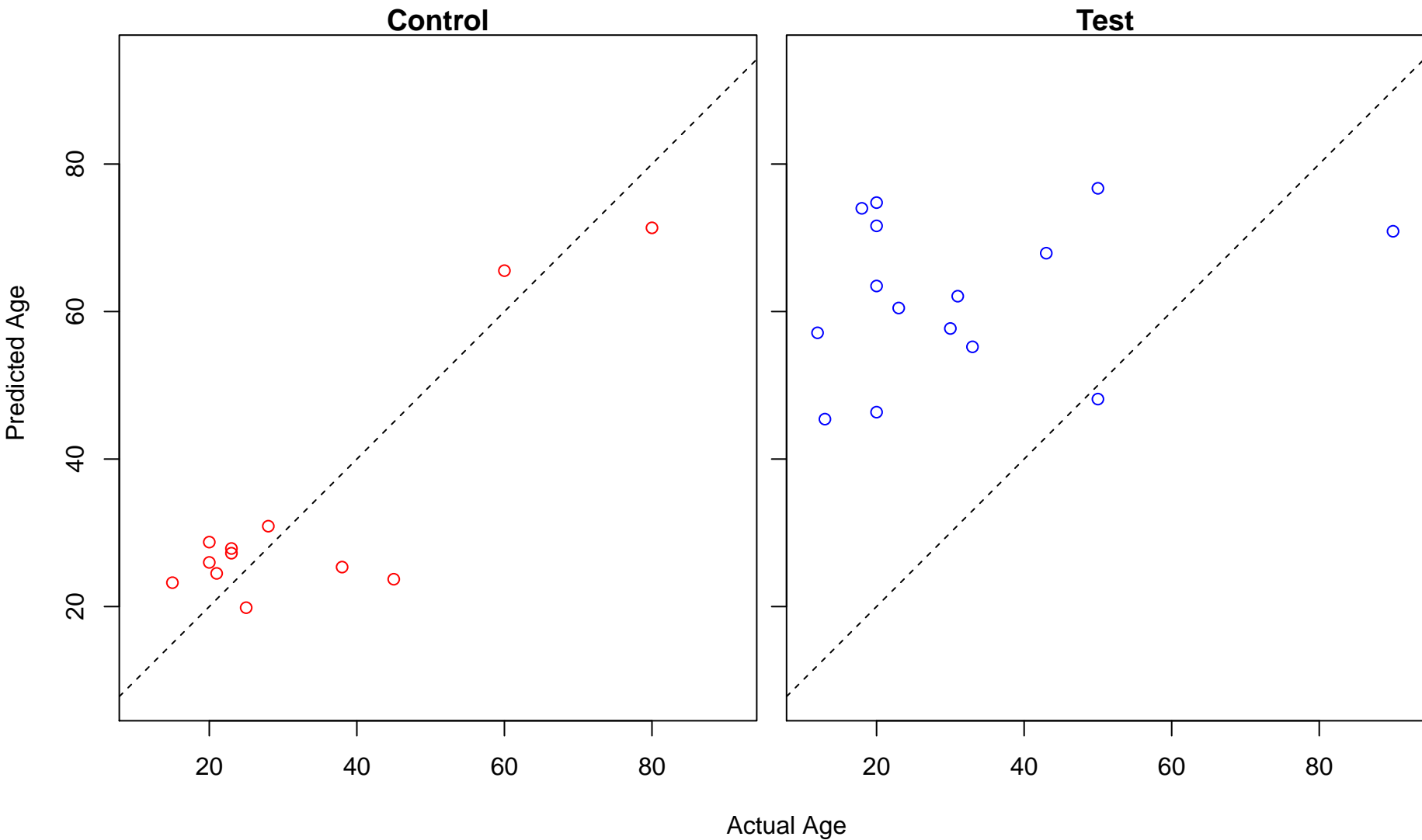
ribosome assembly (Score: 5.533828)



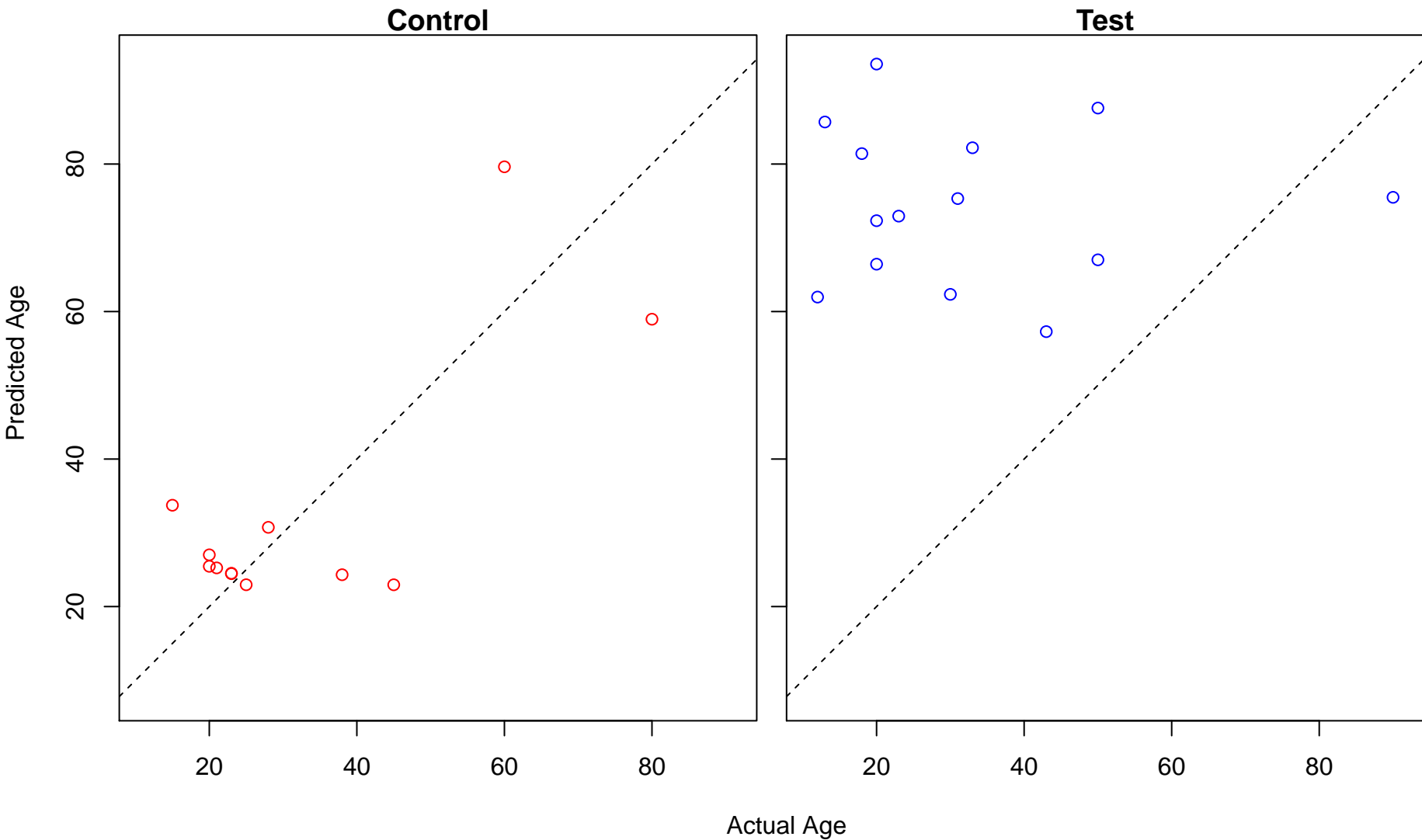
ear development (Score: 5.53534)



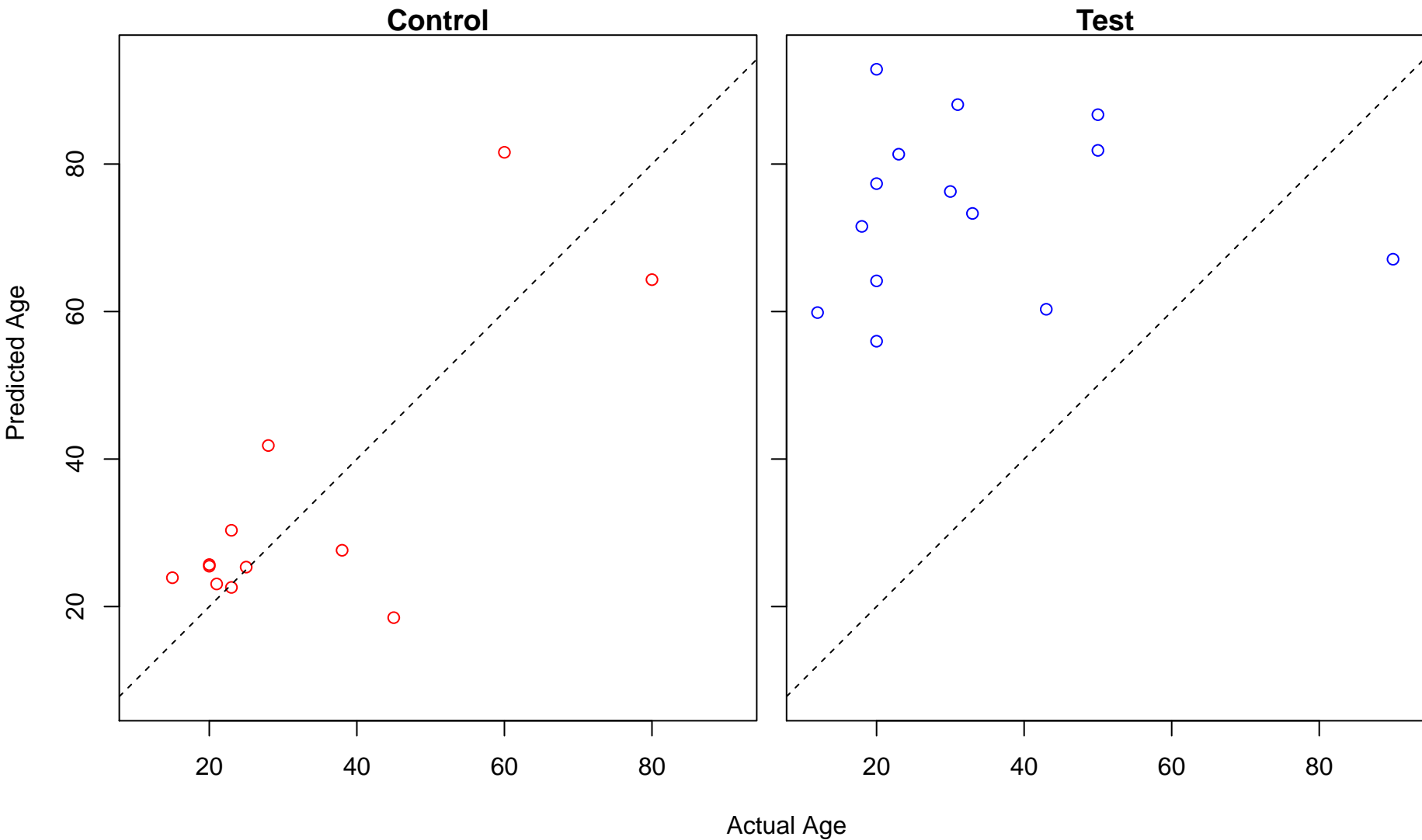
regulation of interleukin-8 secretion (Score: 5.533201)



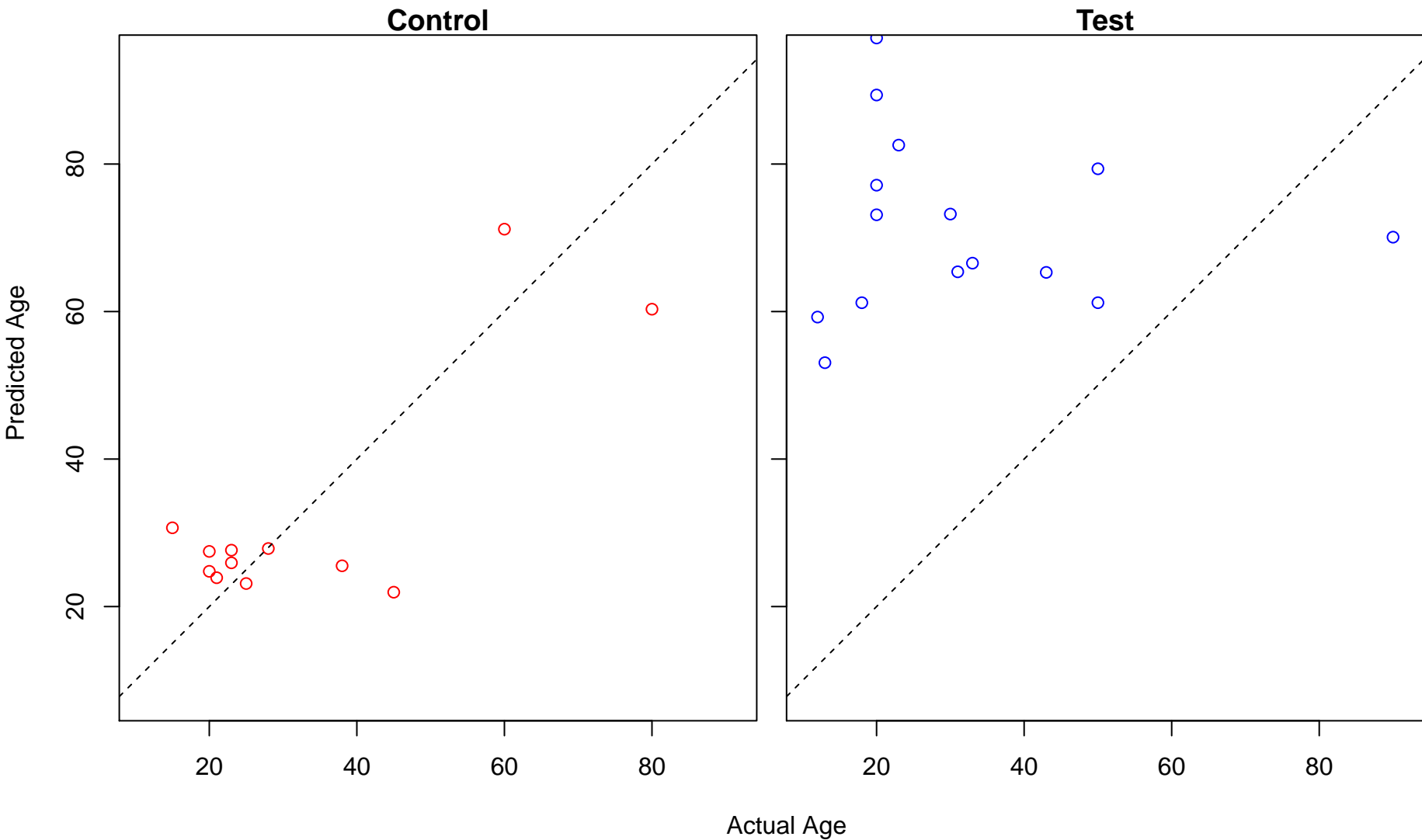
positive regulation of interferon-beta production (Score: 5.532968)



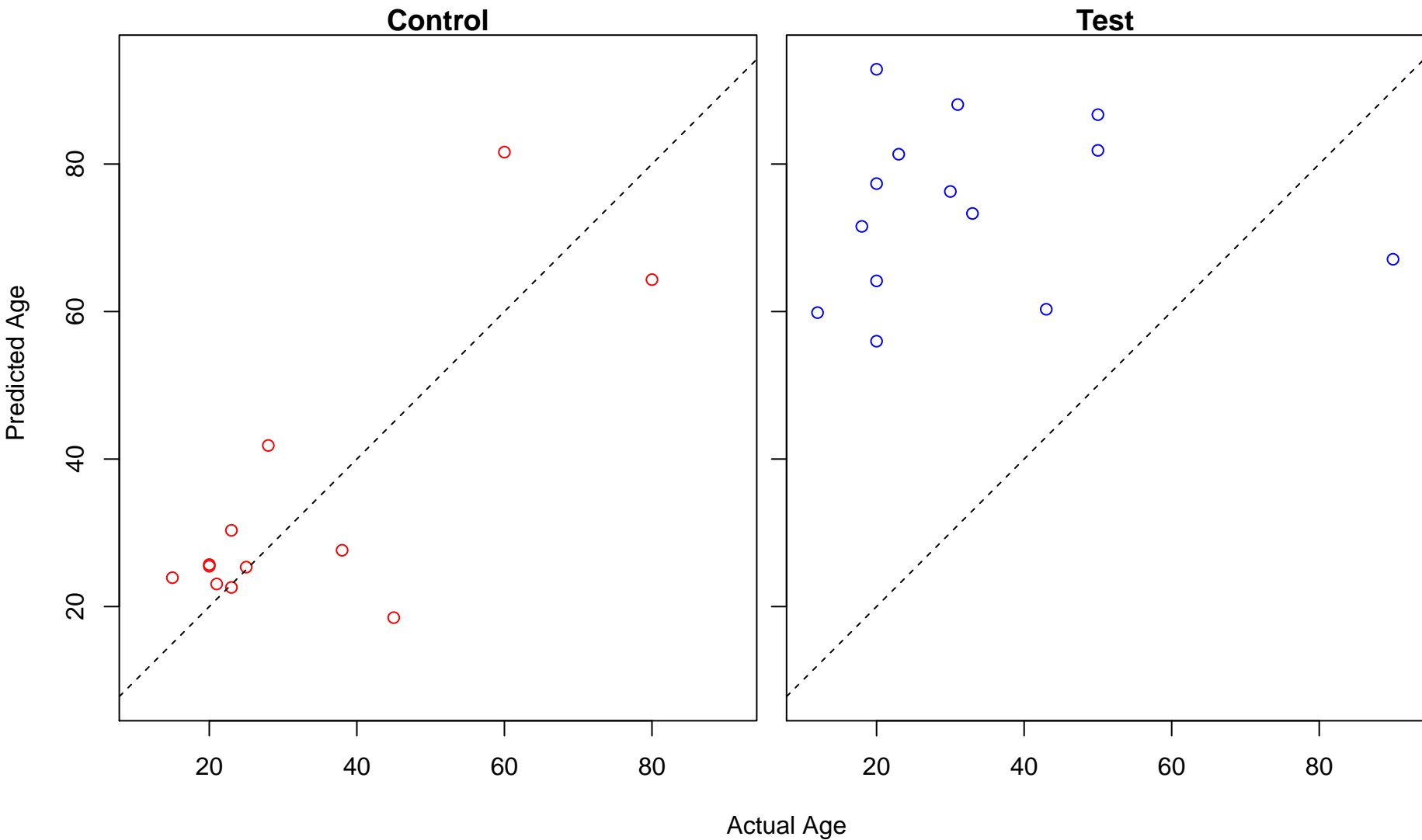
positive regulation of behavior (Score: 5.532343)



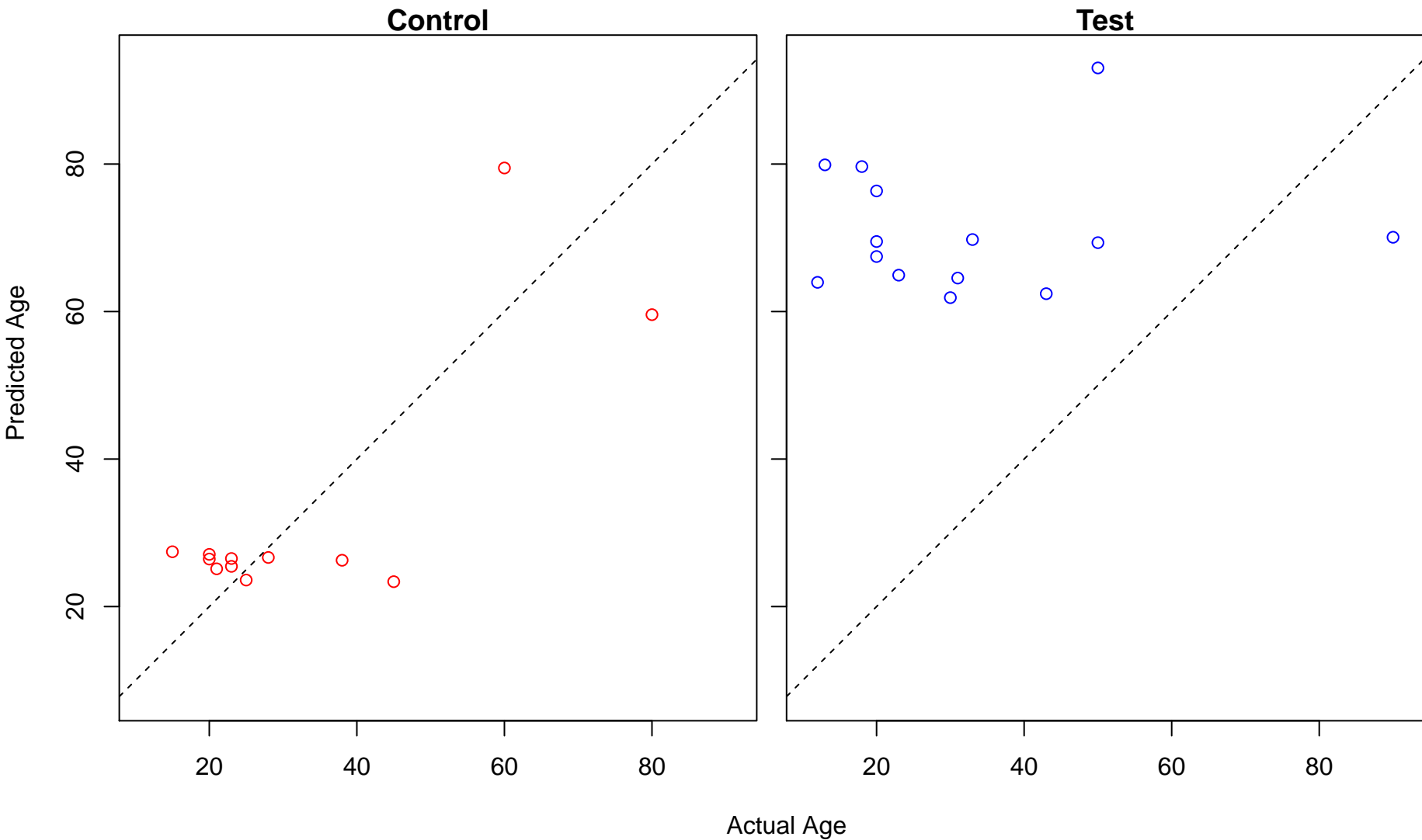
positive regulation of actin cytoskeleton reorganization (Score: 5.530401)



positive regulation of chemotaxis (Score: 5.529765)

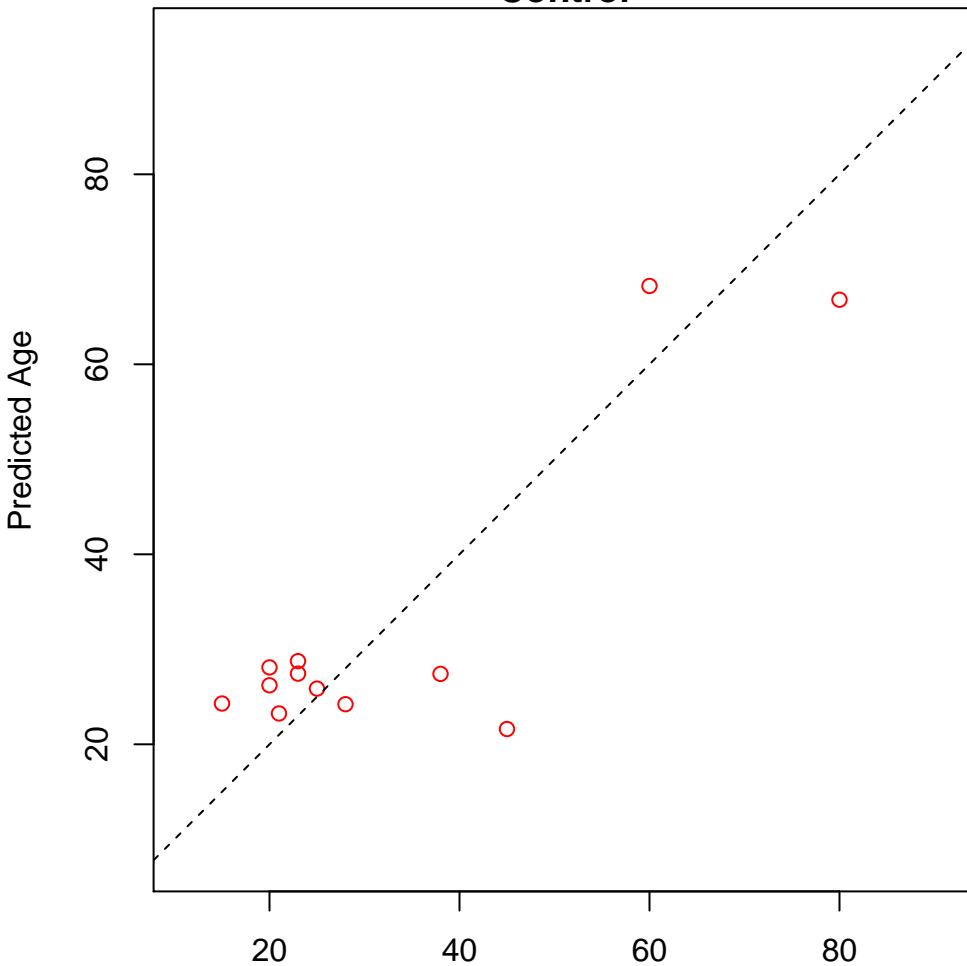


proteasome-mediated ubiquitin-dependent protein catabolic process (Score: 5.529603)

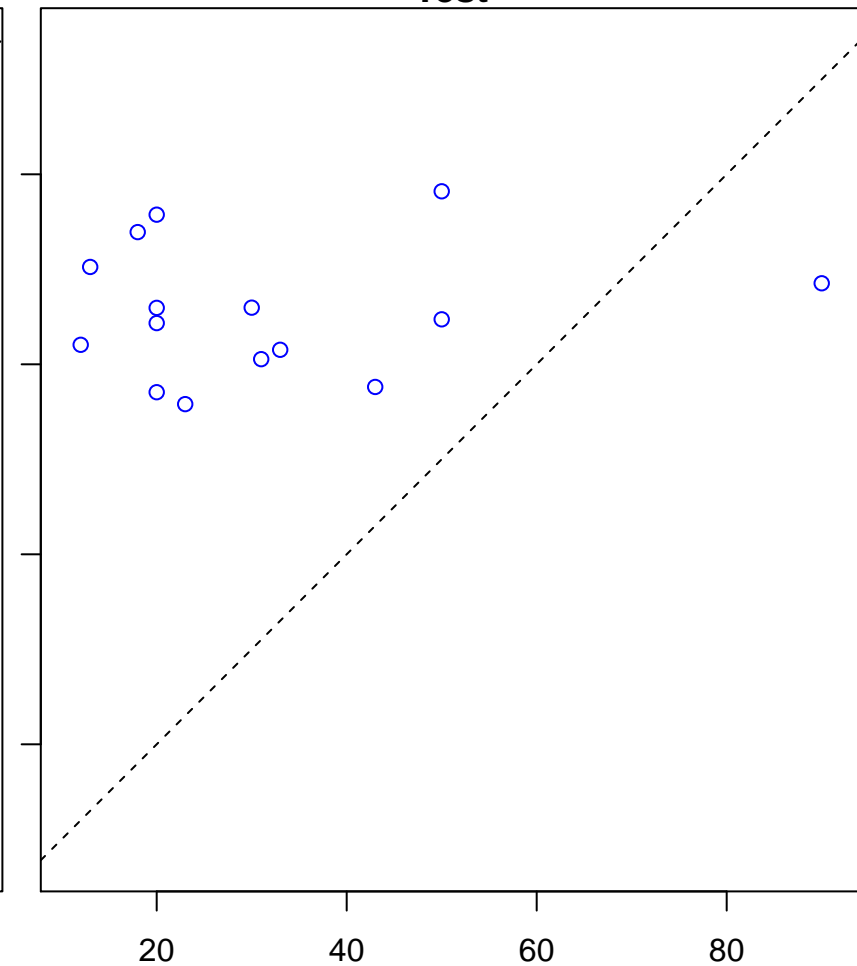


regulation of mRNA catabolic process (Score: 5.528317)

Control

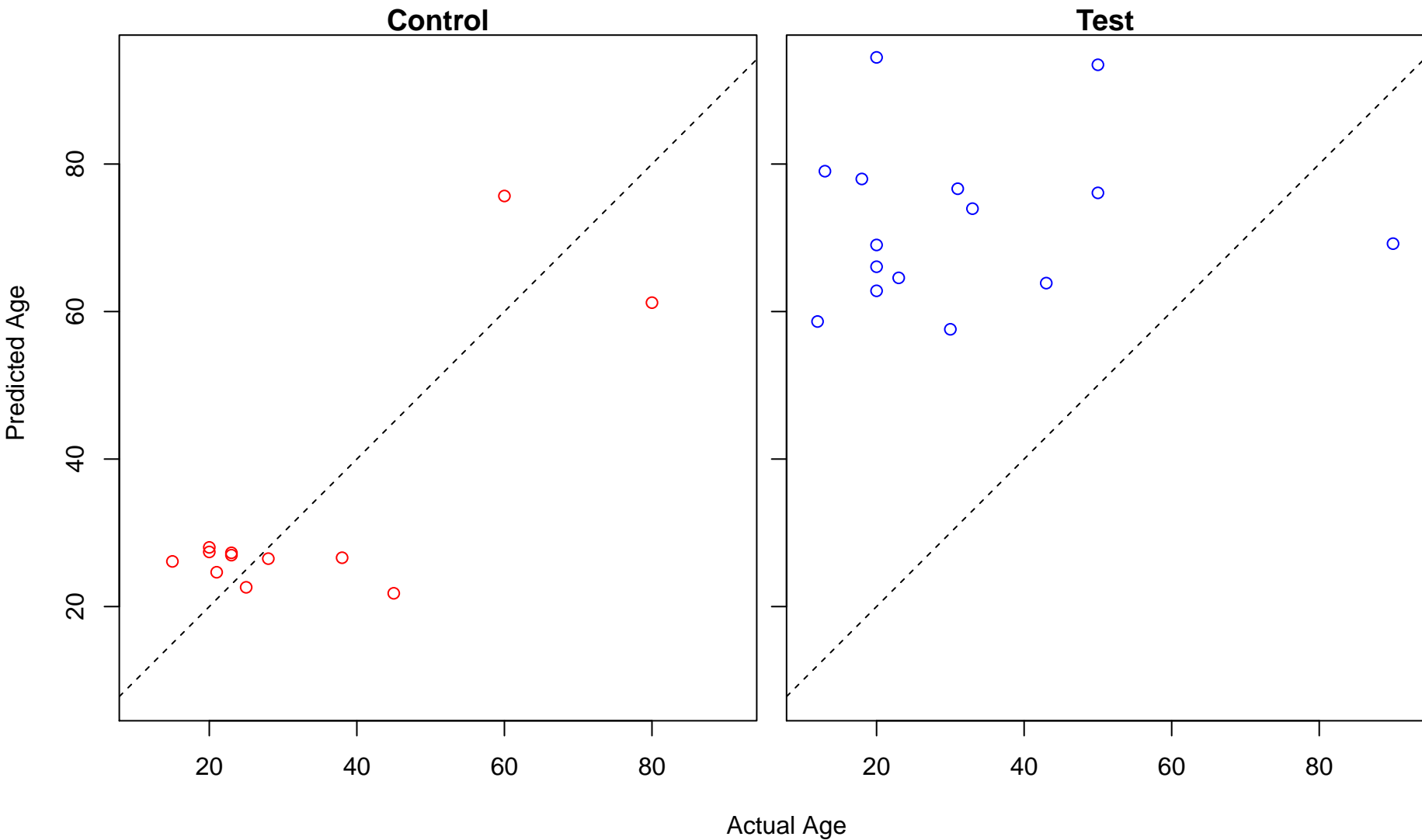


Test

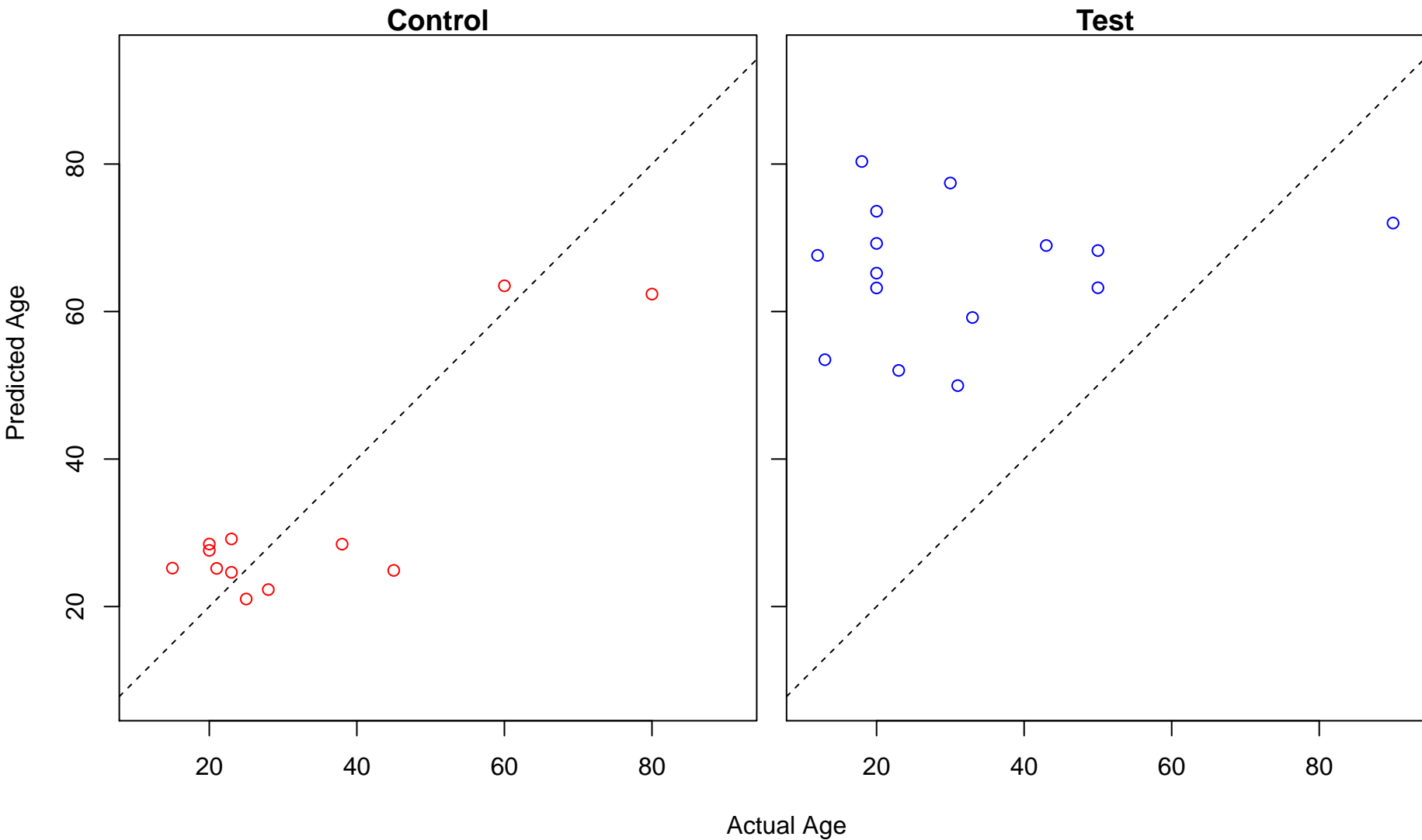


Actual Age

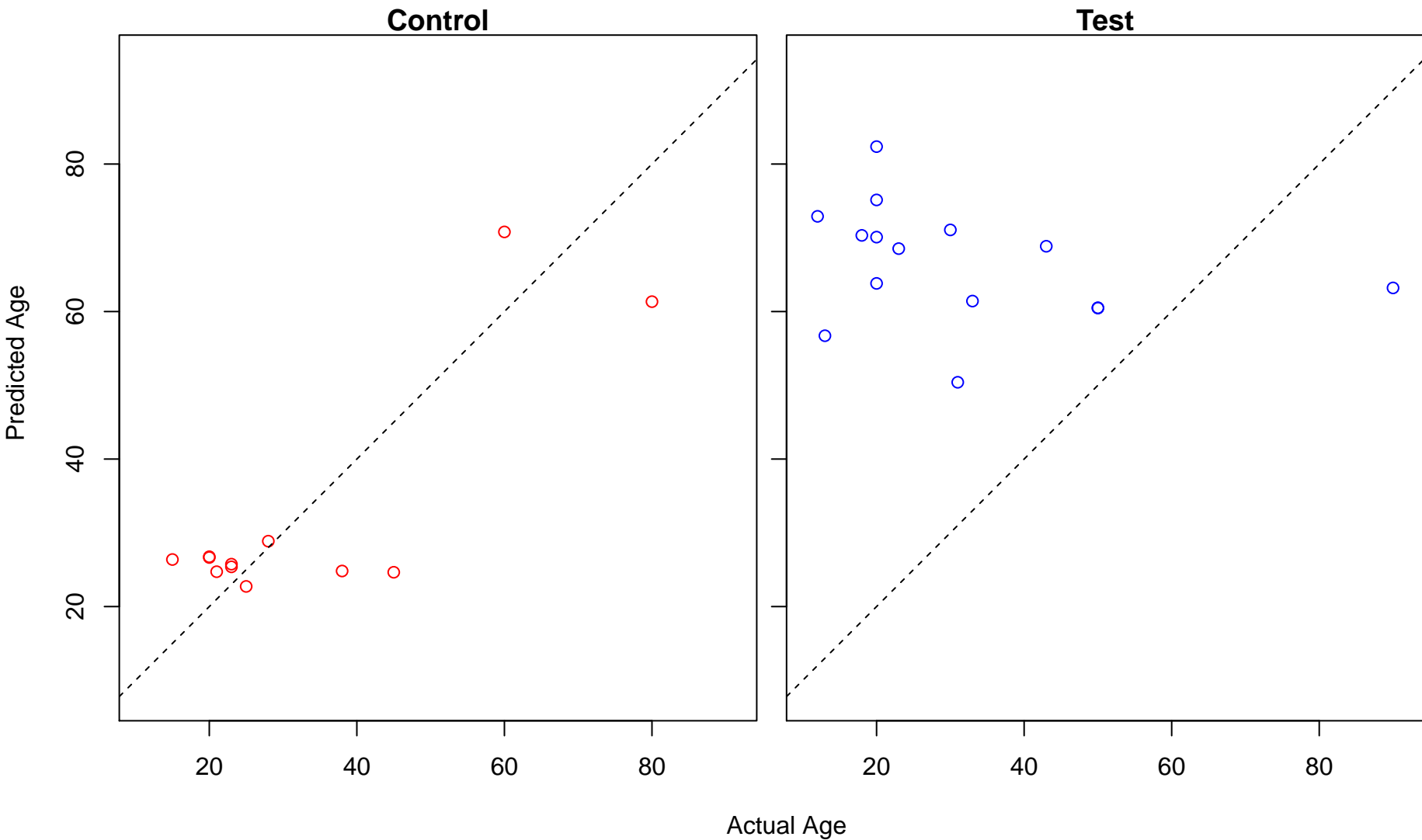
regulation of endocytosis (Score: 5.527438)



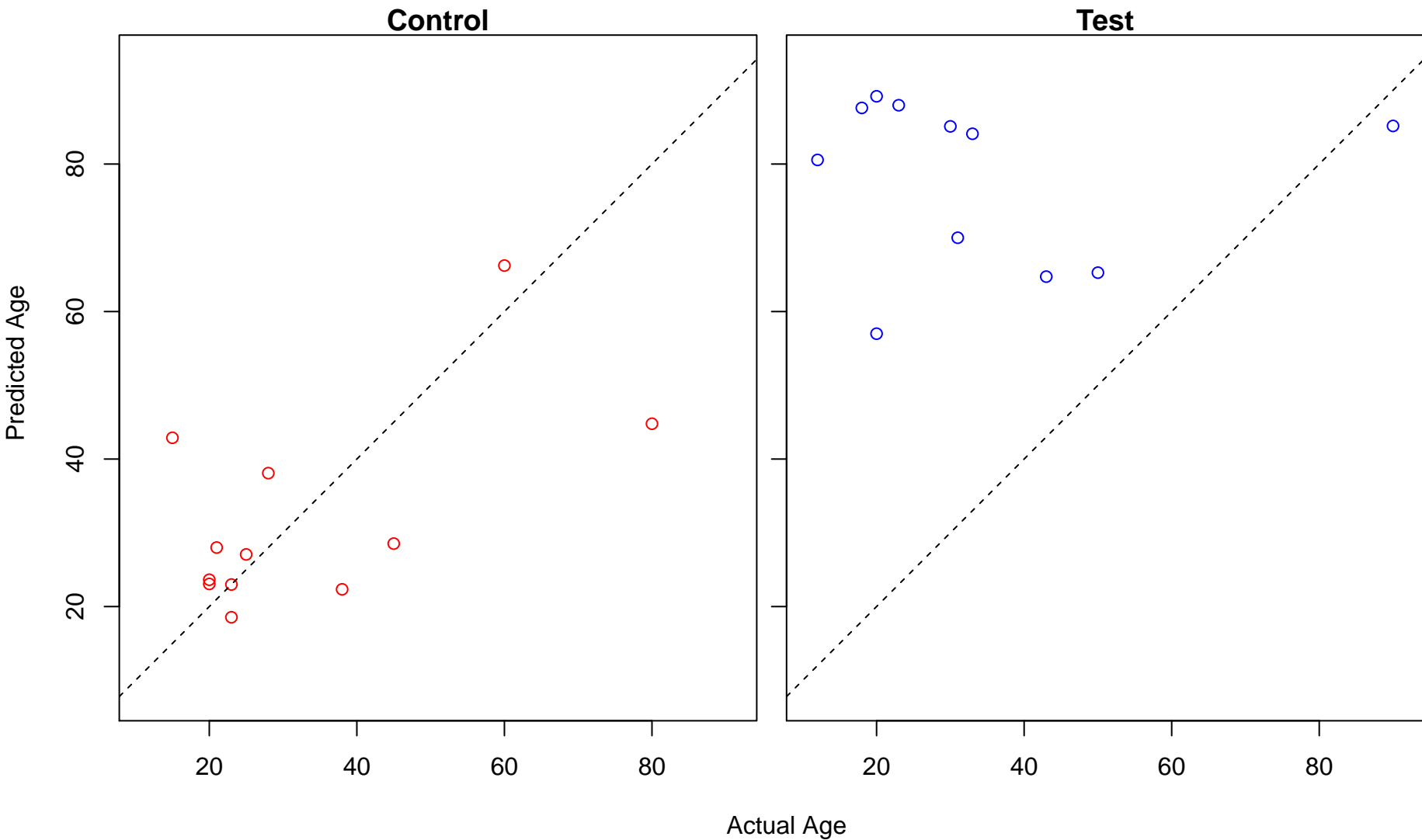
sialylation (Score: 5.527282)



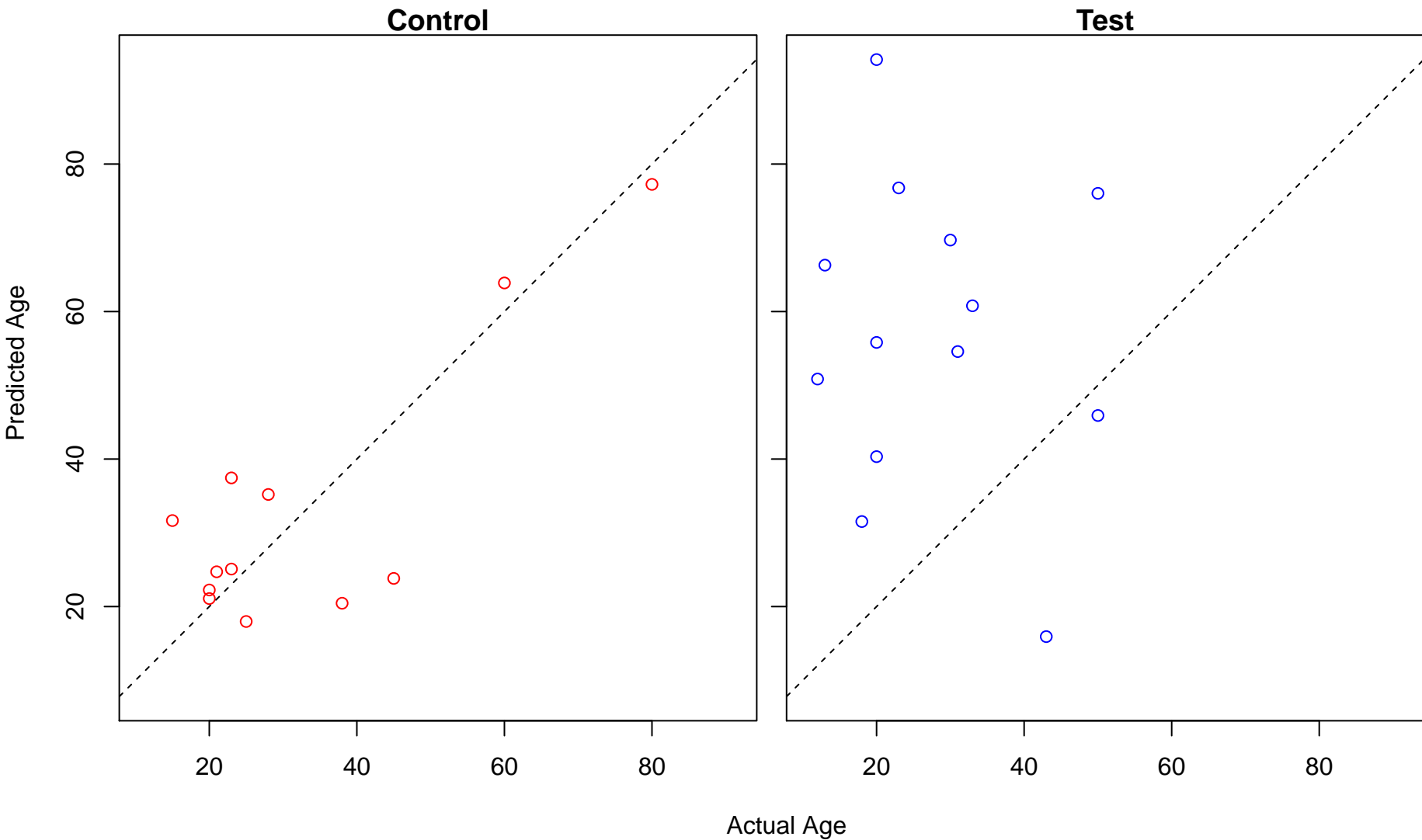
regulation of helicase activity (Score: 5.527262)



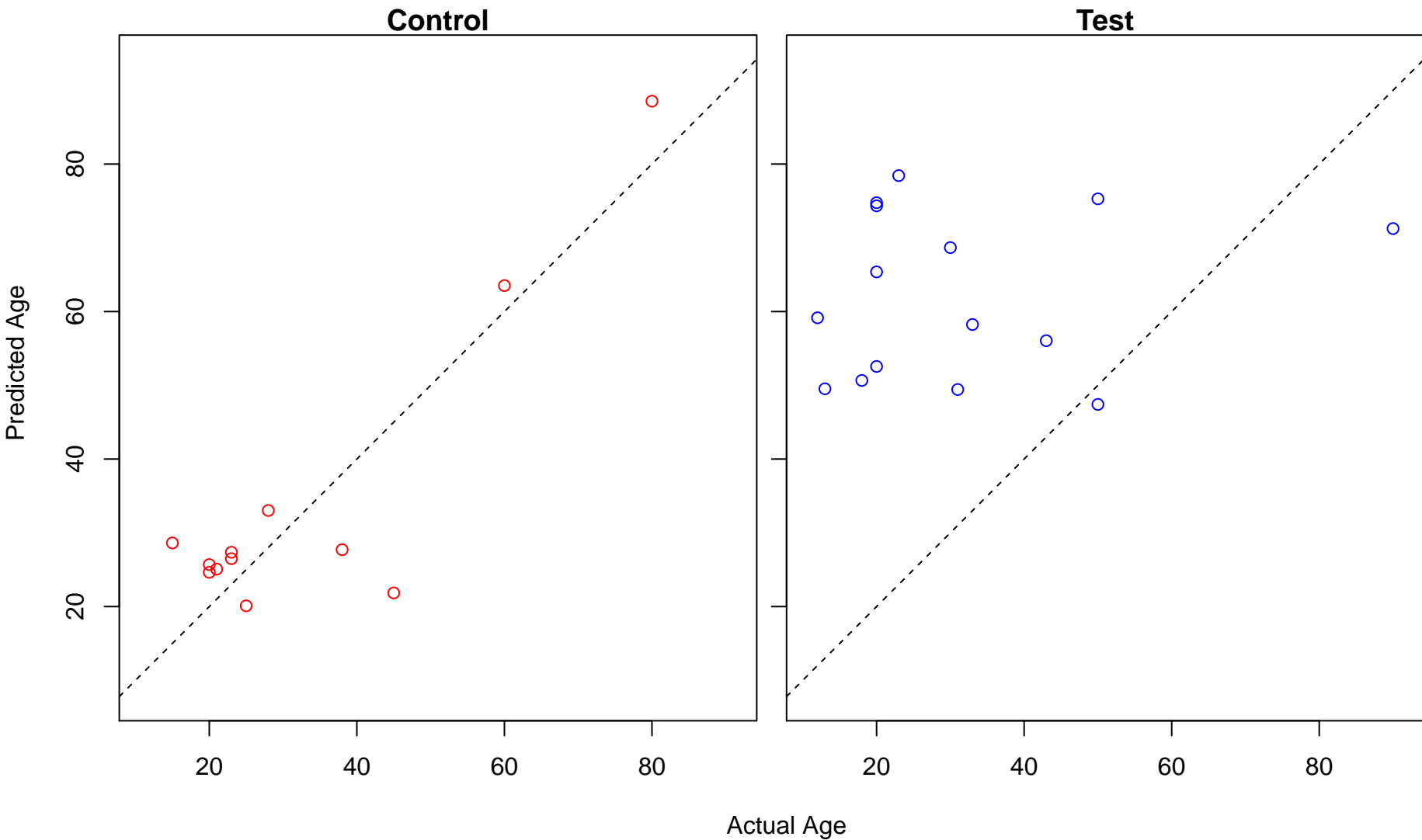
negative regulation of cytokine production involved in inflammatory response (Score: 5.525525)



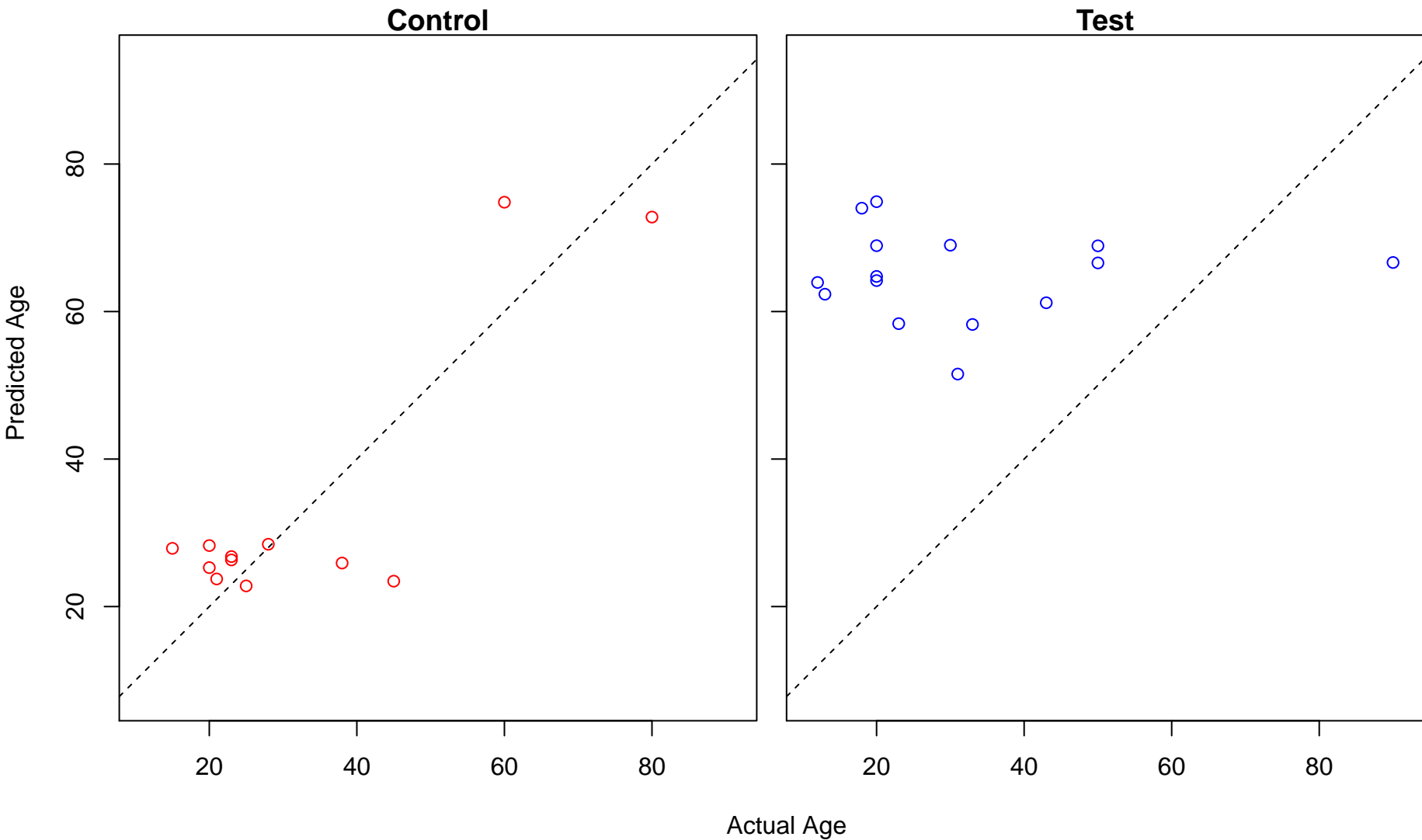
positive regulation of mitochondrial translation (Score: 5.523230)



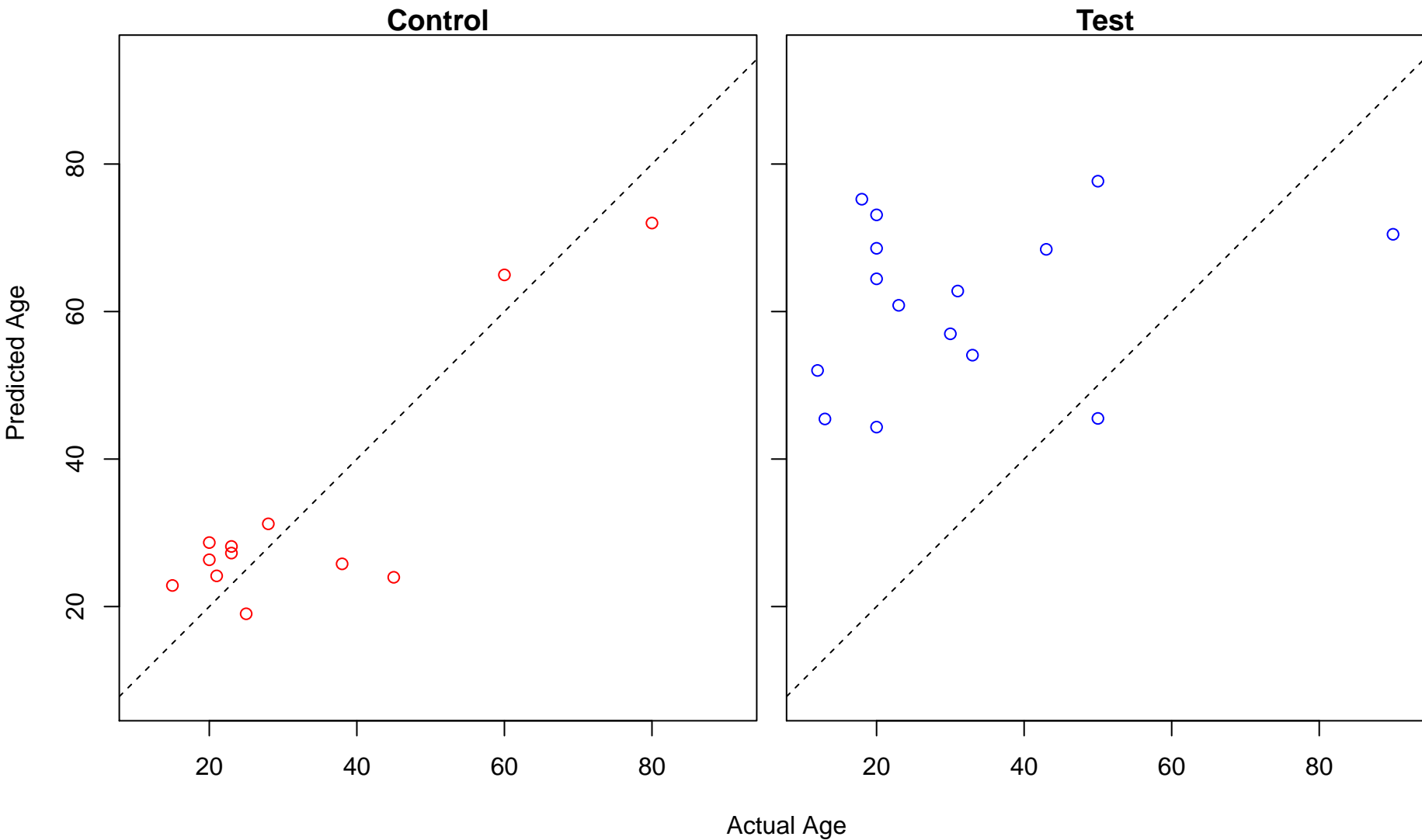
phospholipid metabolic process (Score: 5.520633)



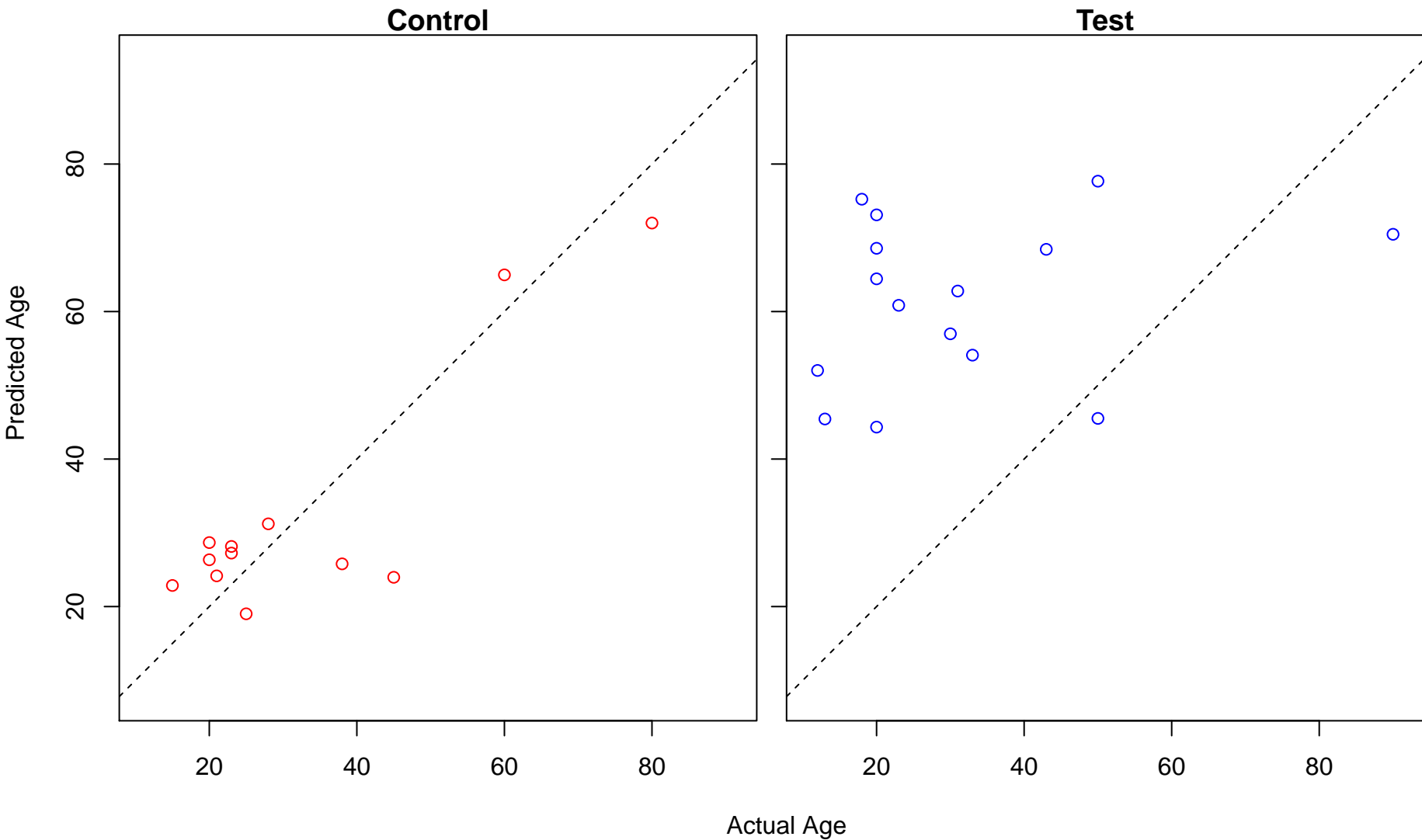
cellular response to topologically incorrect protein (Score: 5.519279)



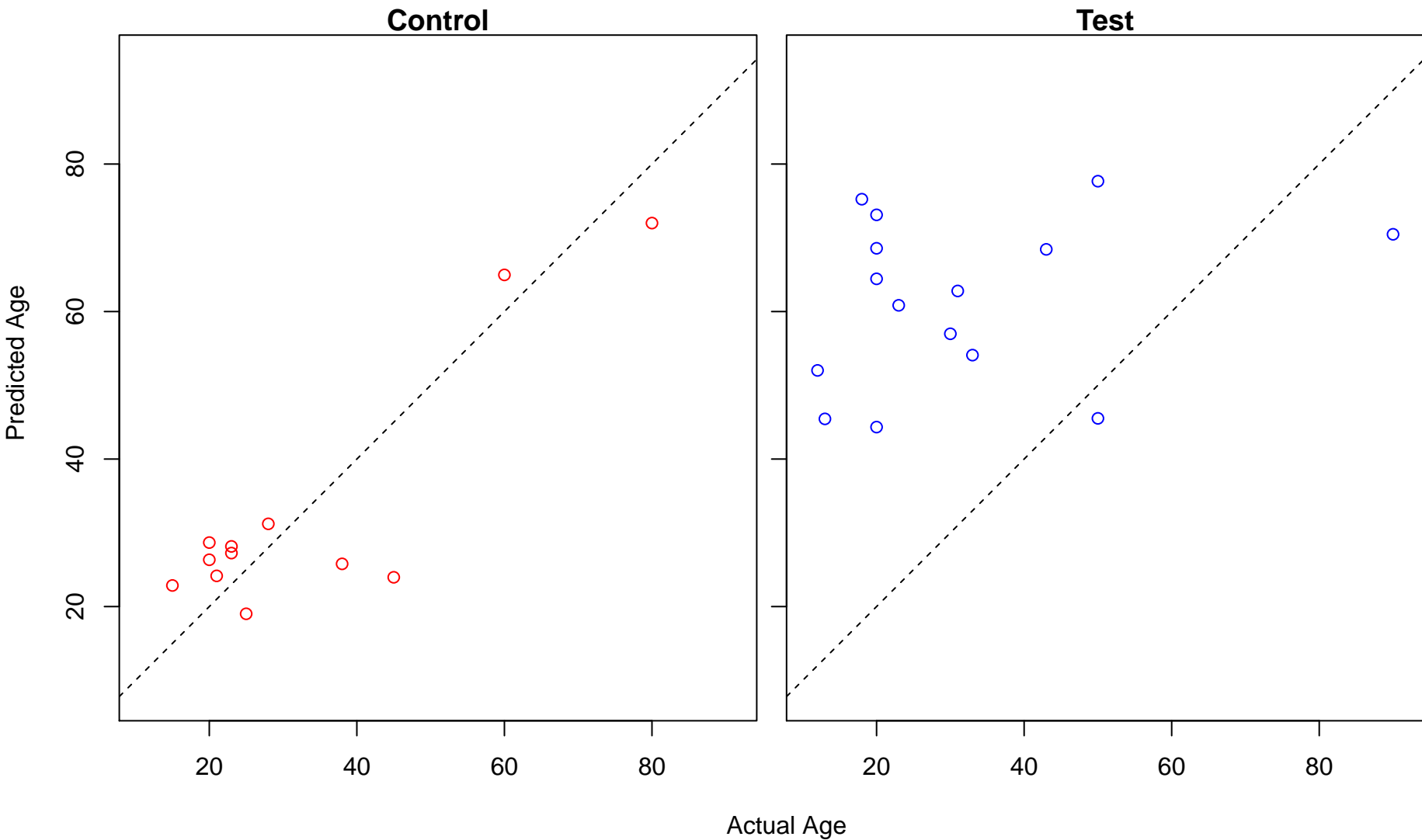
regulation of T-helper 1 cell differentiation (Score: 5.518355)



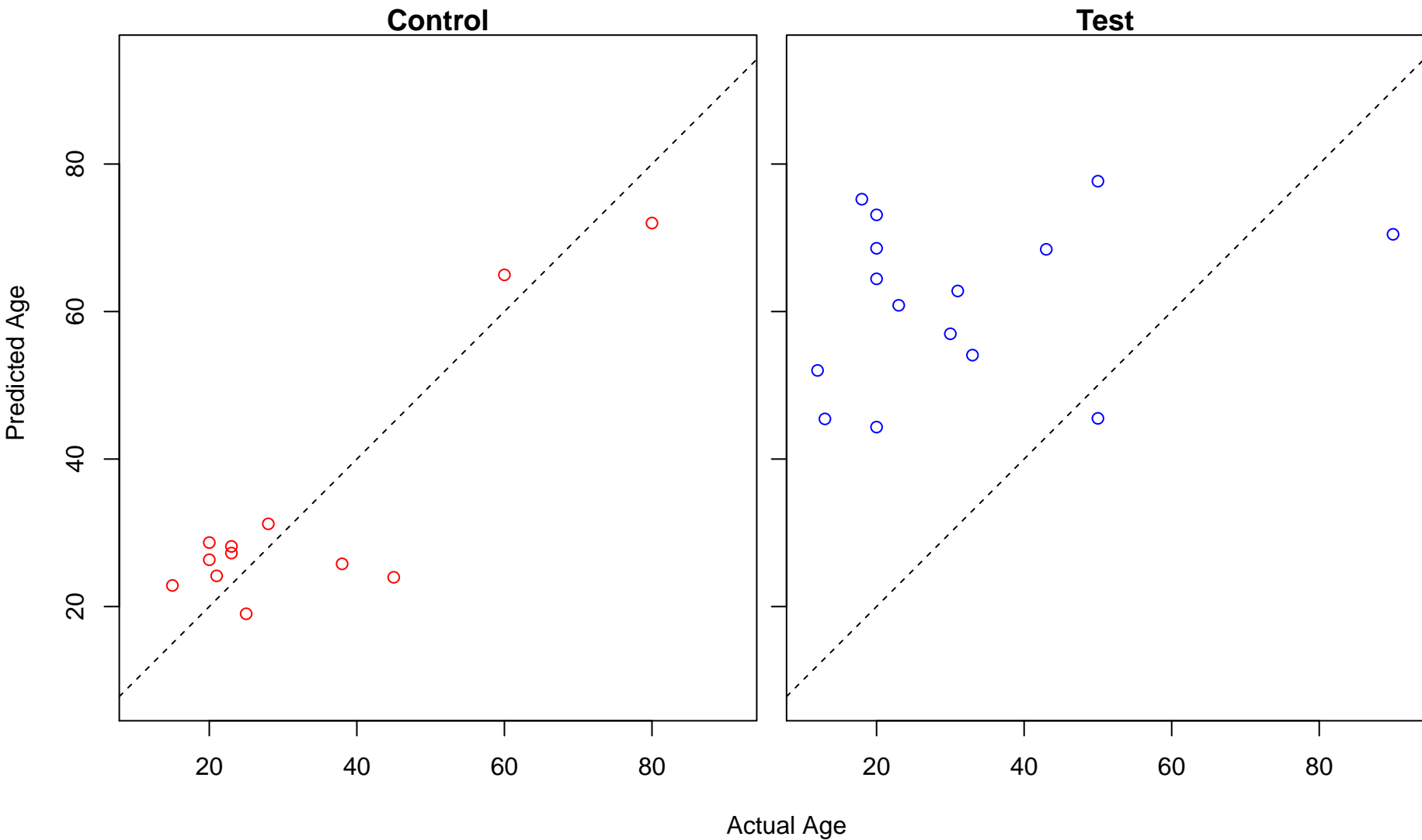
negative regulation of type 2 immune response (Score: 5.518231)



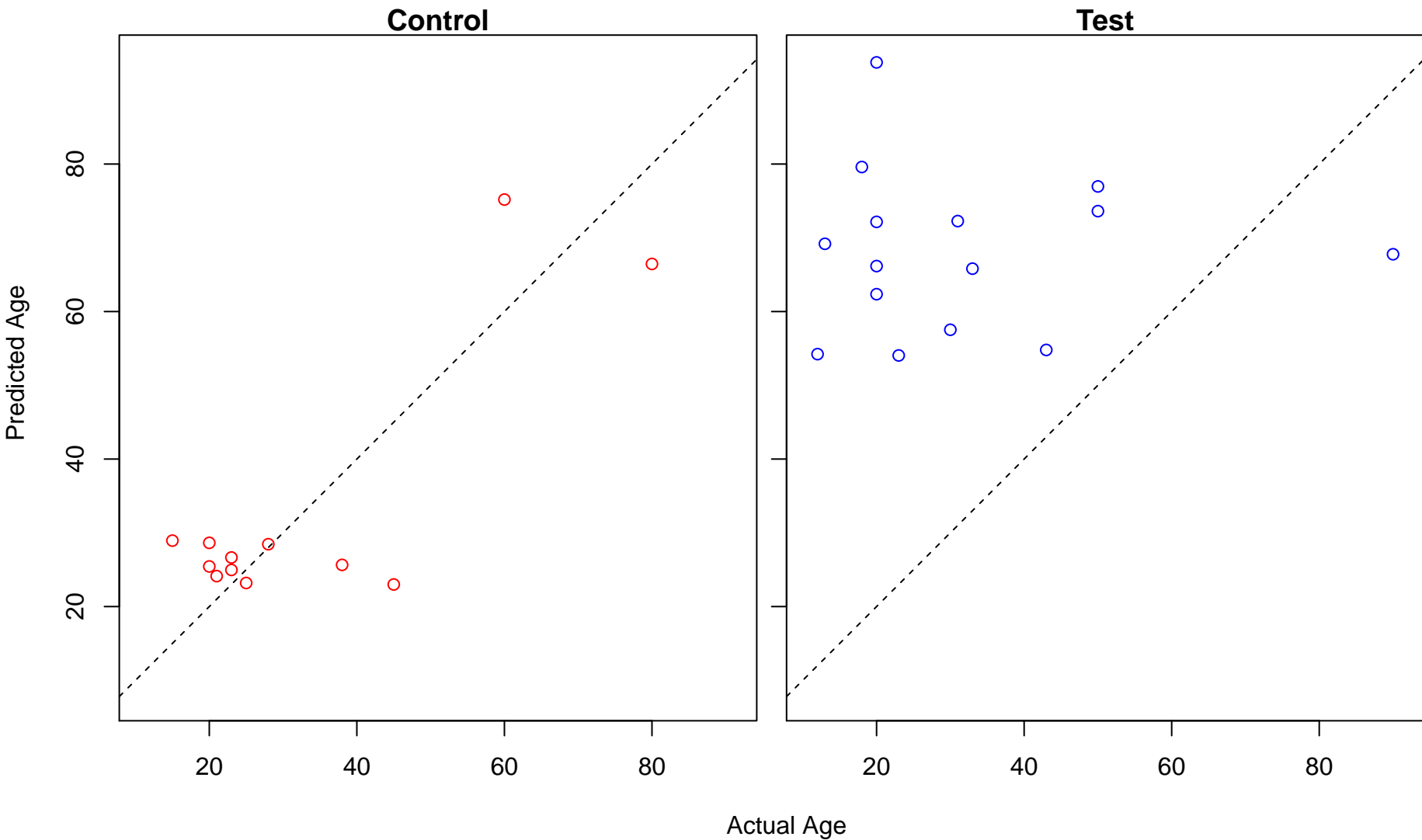
regulation of T-helper 1 type immune response (Score: 5.518218)



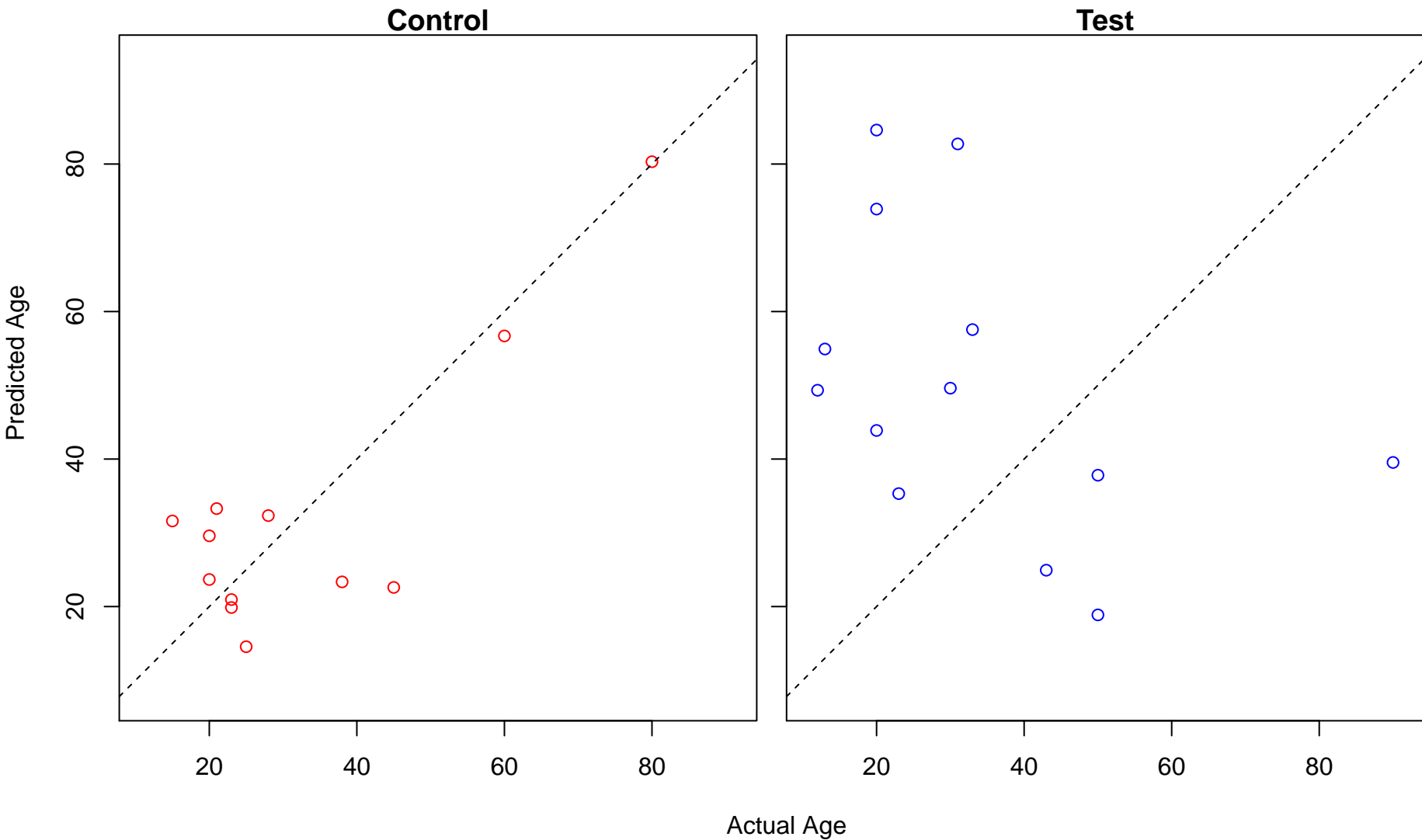
positive regulation of T-helper 1 type immune response (Score: 5.518060)



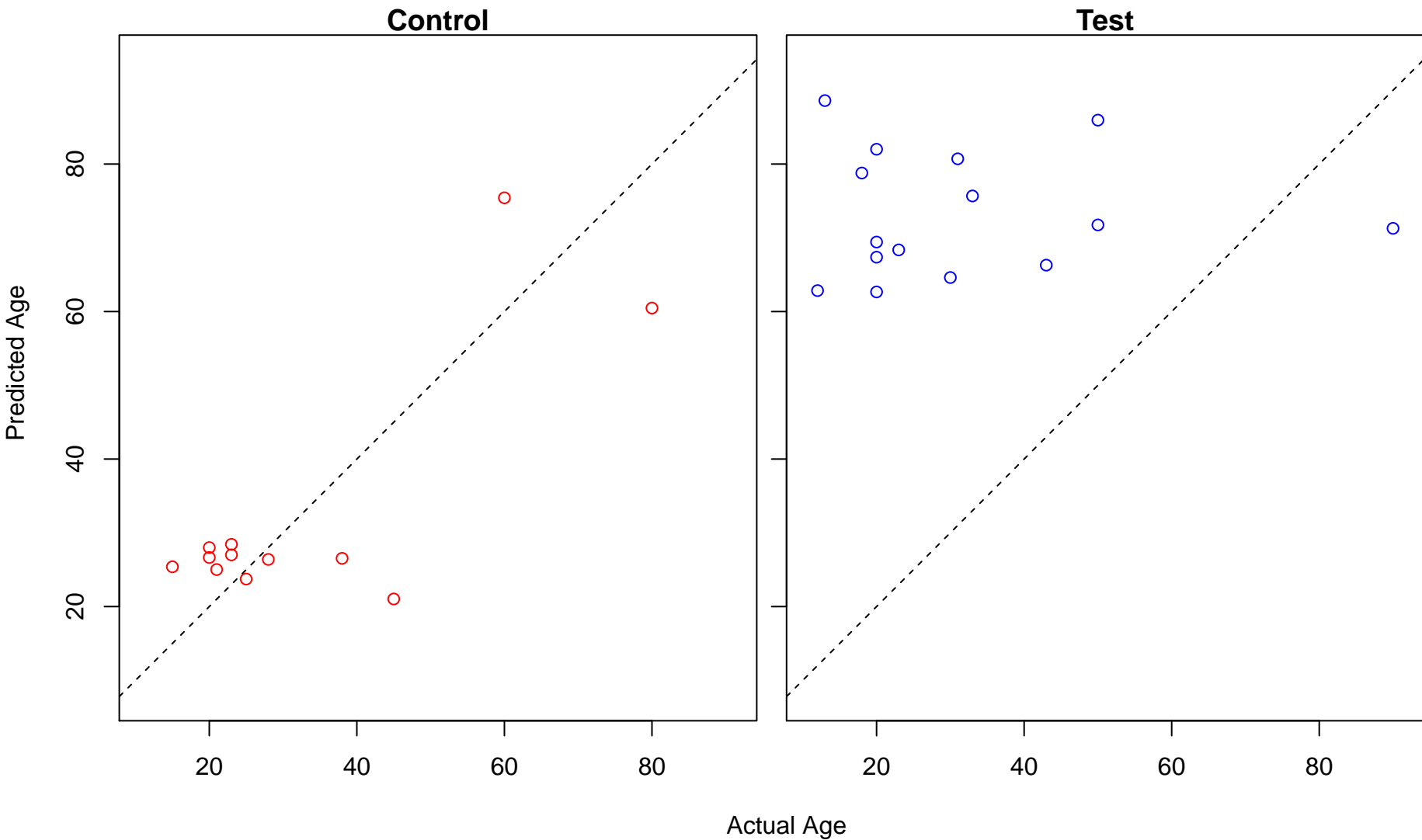
positive regulation of establishment of protein localization (Score: 5.516253)



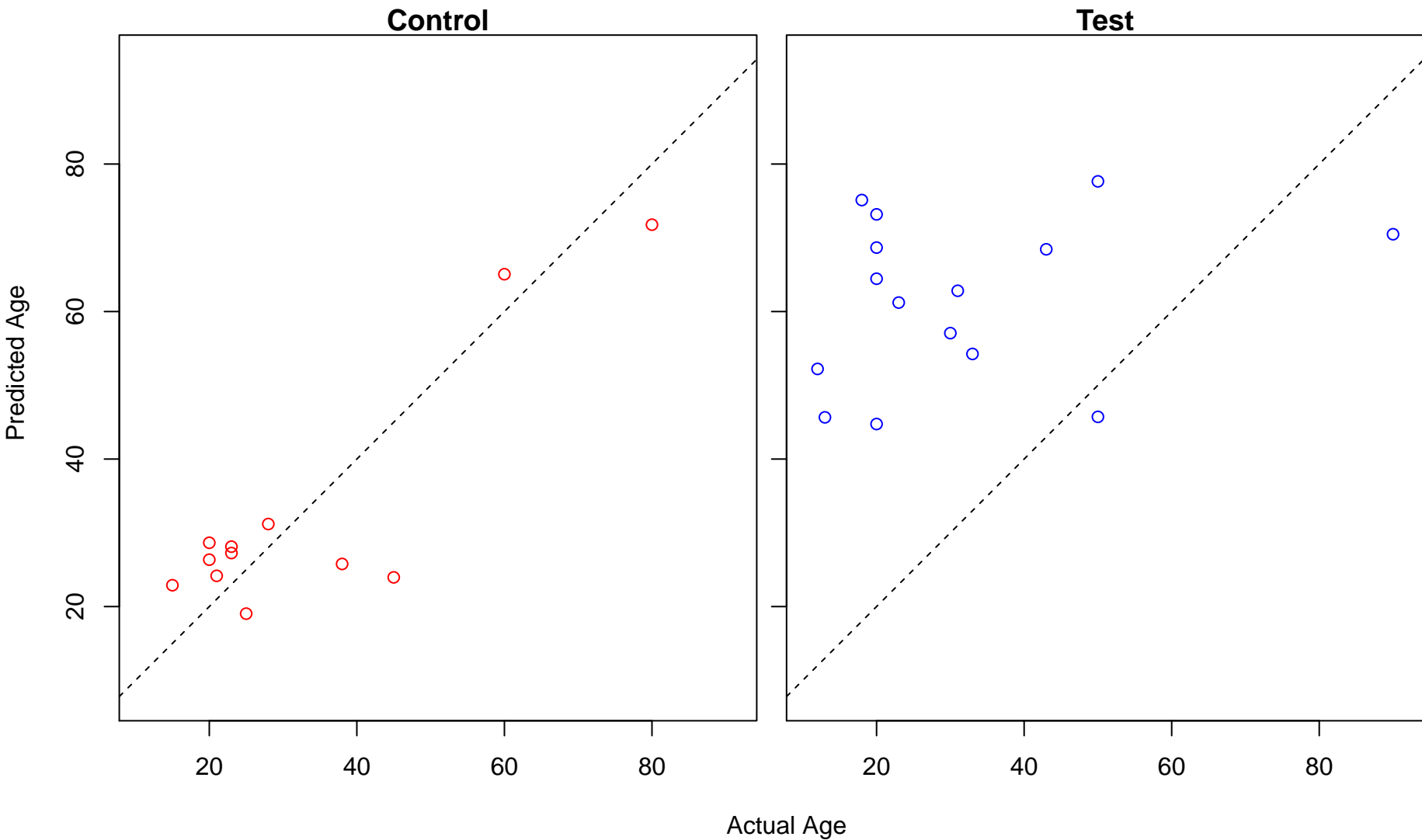
regulation of intracellular transport (Score: 5.514631)



regulation of response to biotic stimulus (Score: 5.514569)

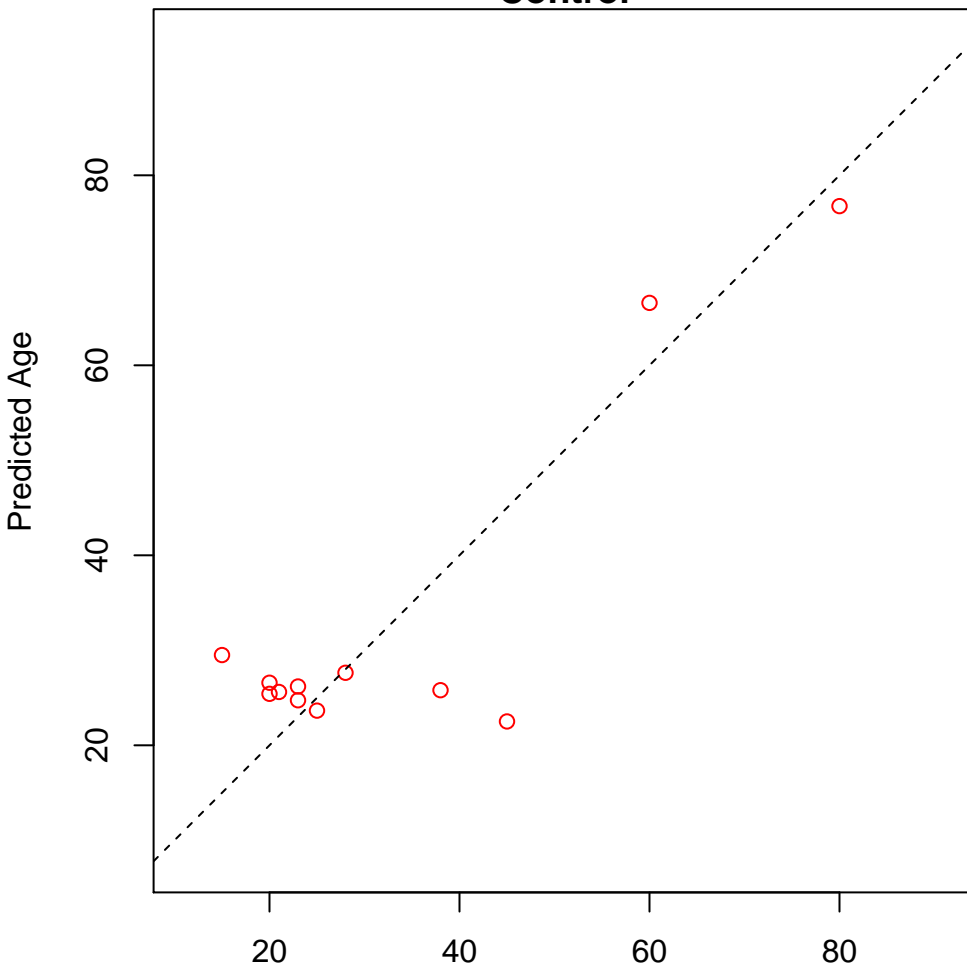


regulation of type 2 immune response (Score: 5.514530)

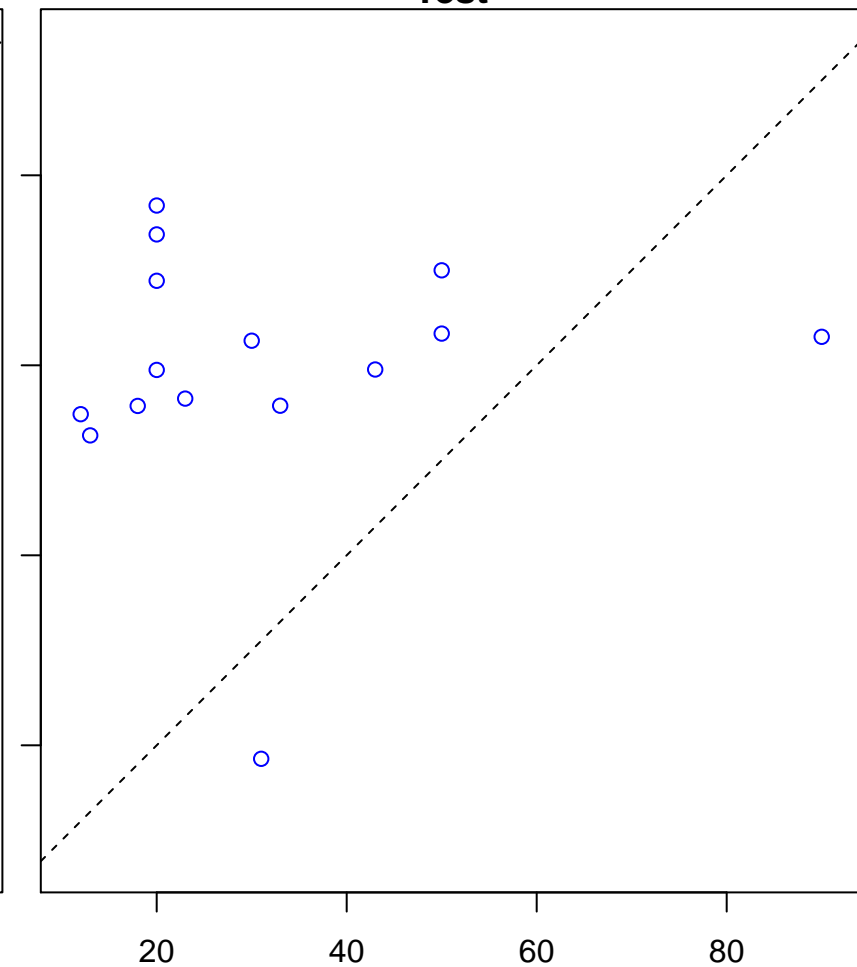


regulation of cytoskeleton organization (Score: 5.514031)

Control

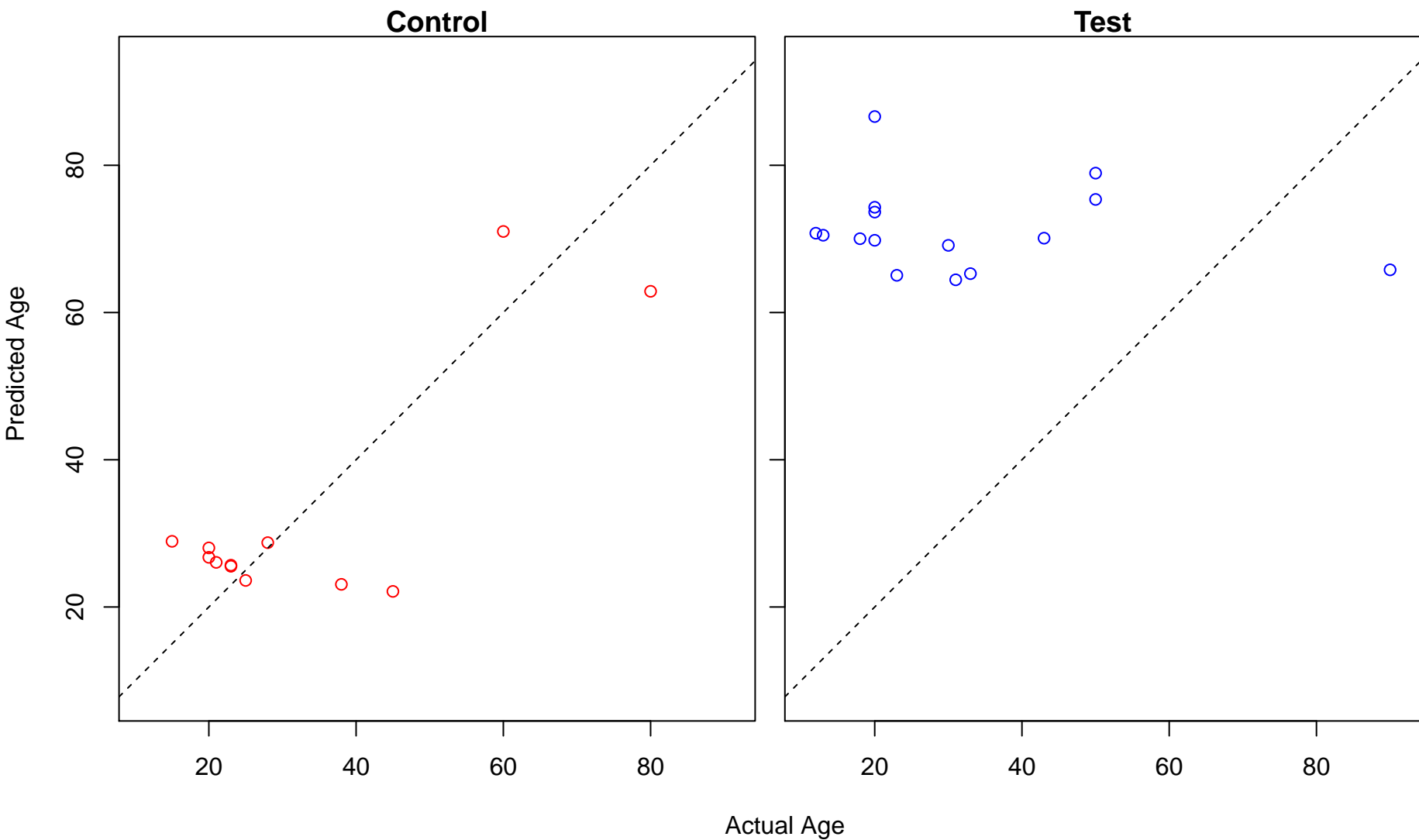


Test

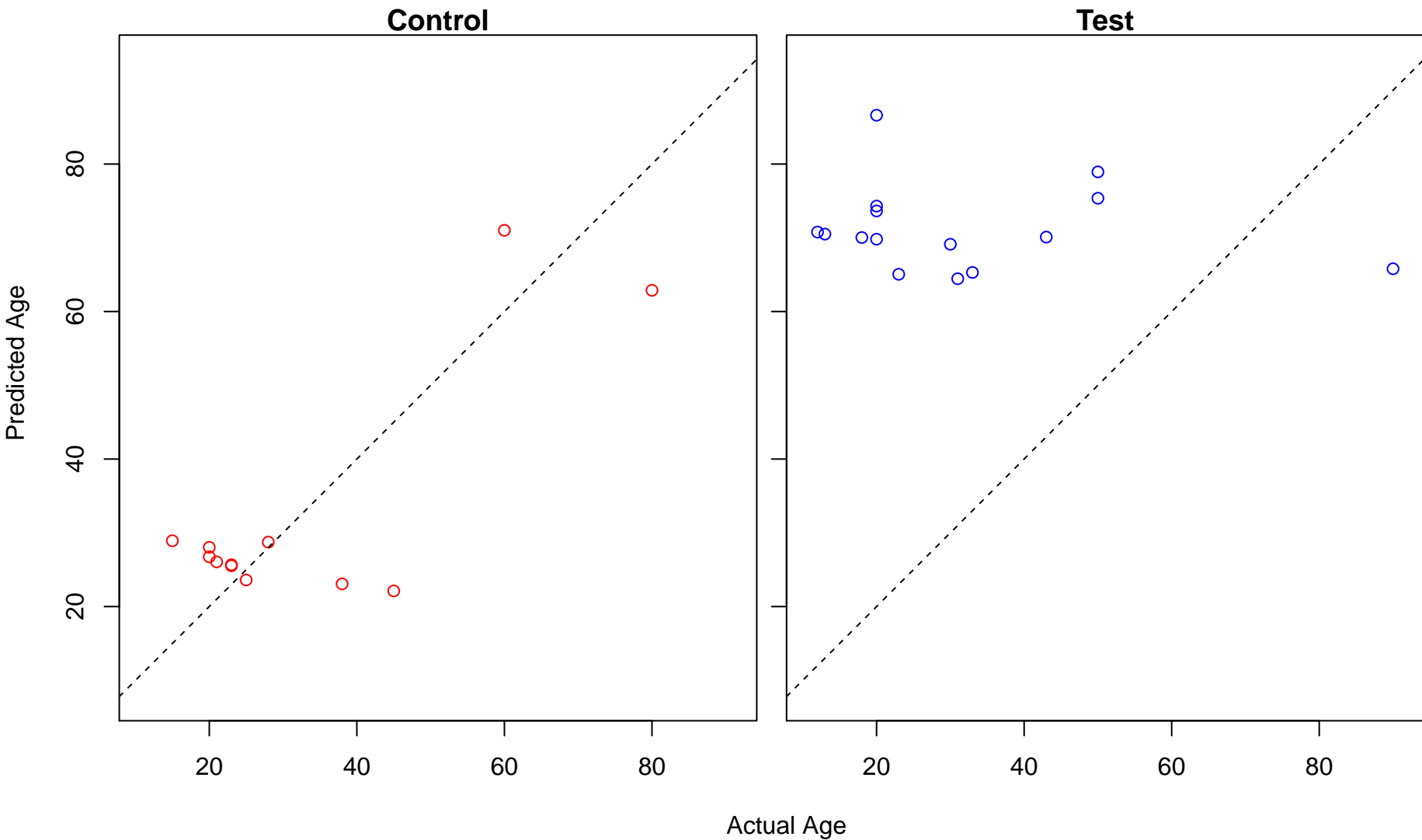


Actual Age

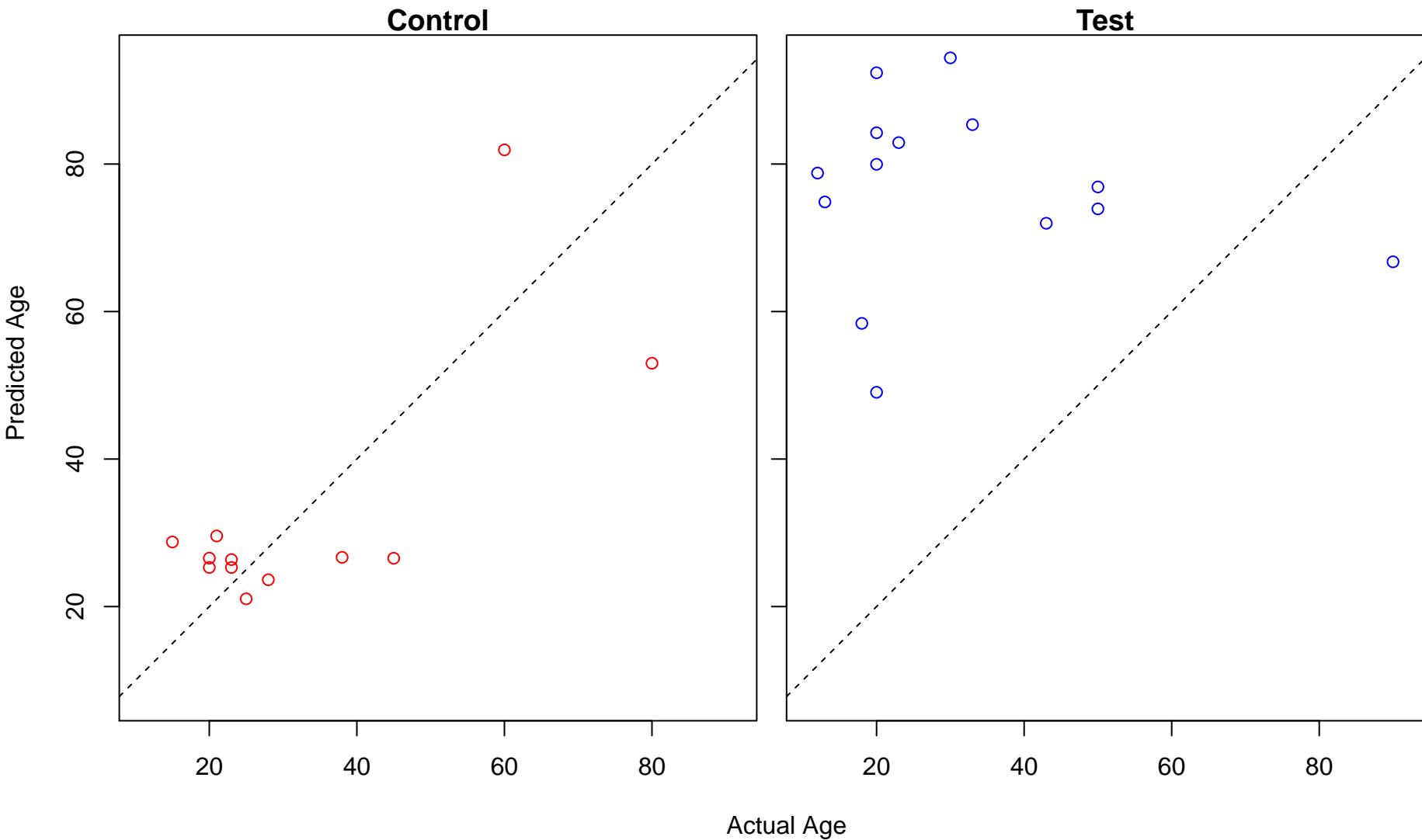
heart contraction (Score: 5.512216)



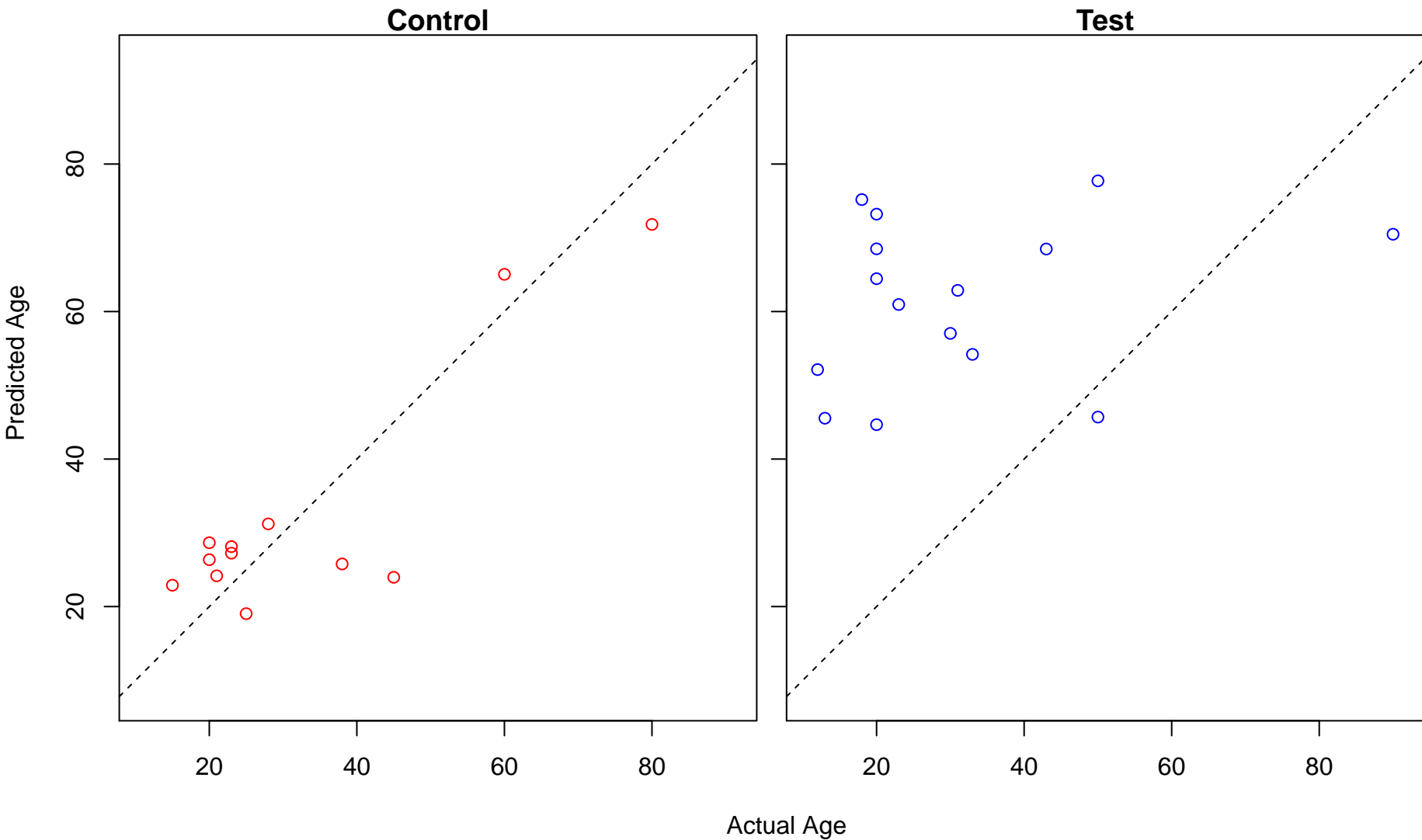
heart process (Score: 5.51915)



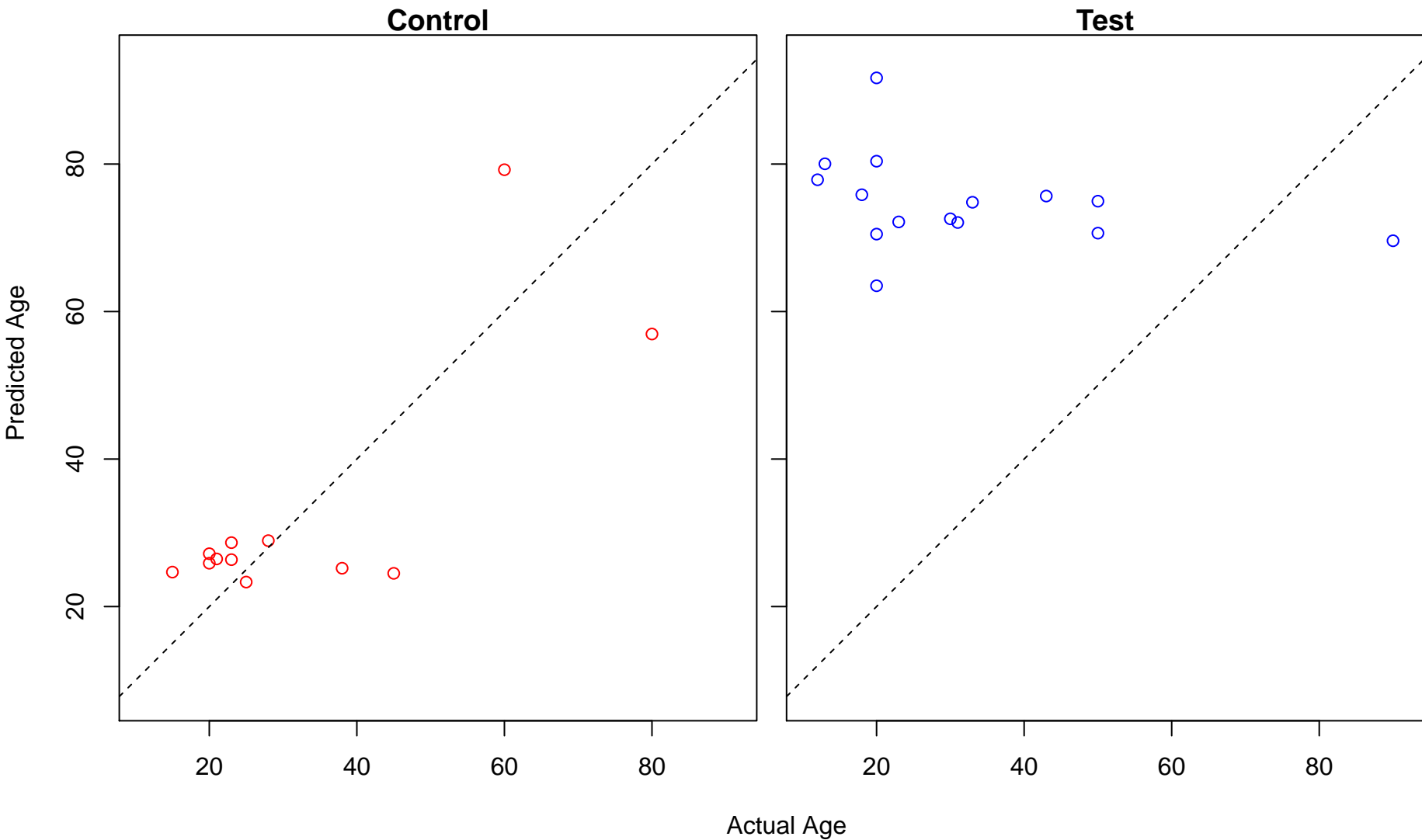
muscle adaptation (Score: 5.511243)



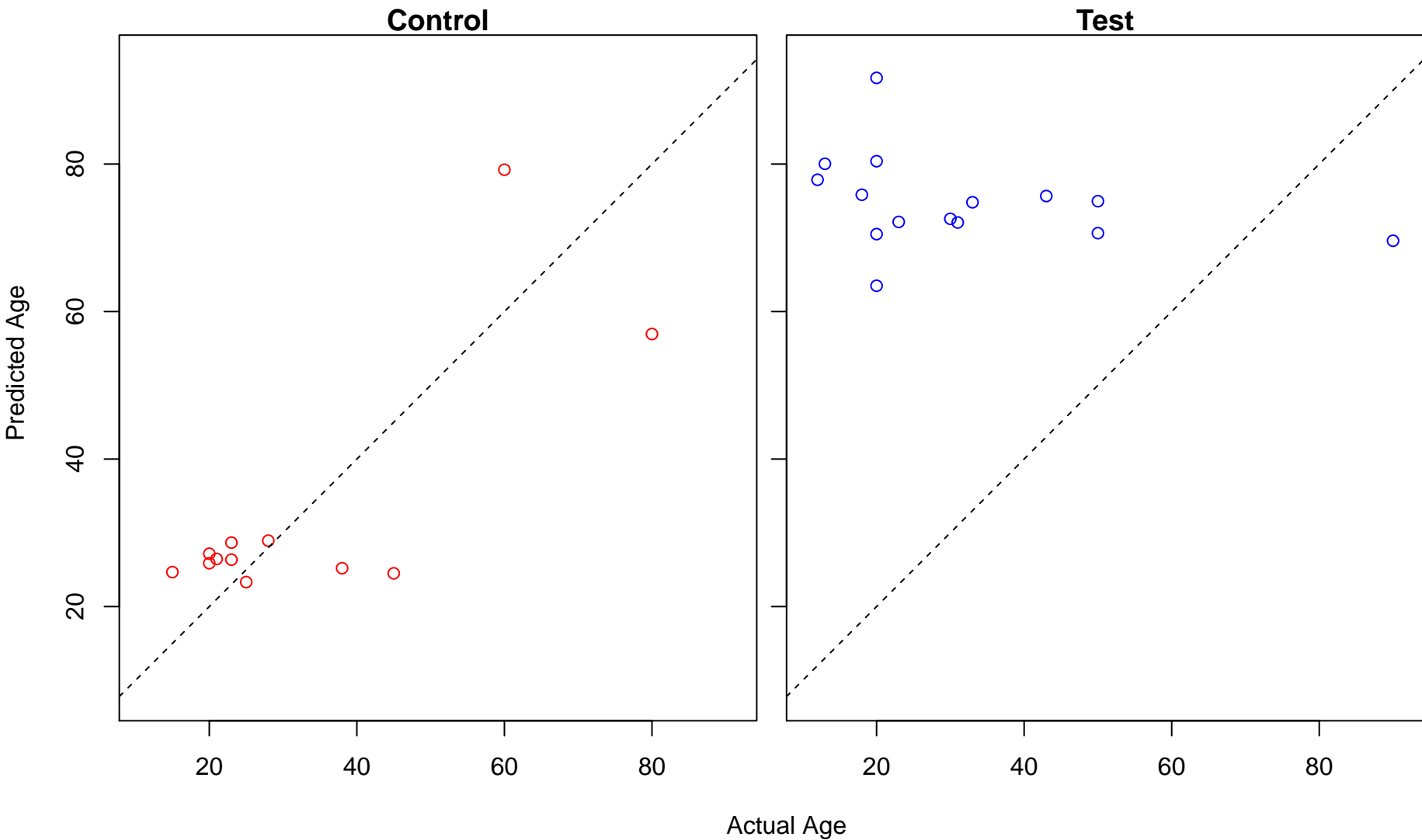
regulation of T-helper 2 cell differentiation (Score: 5.510998)



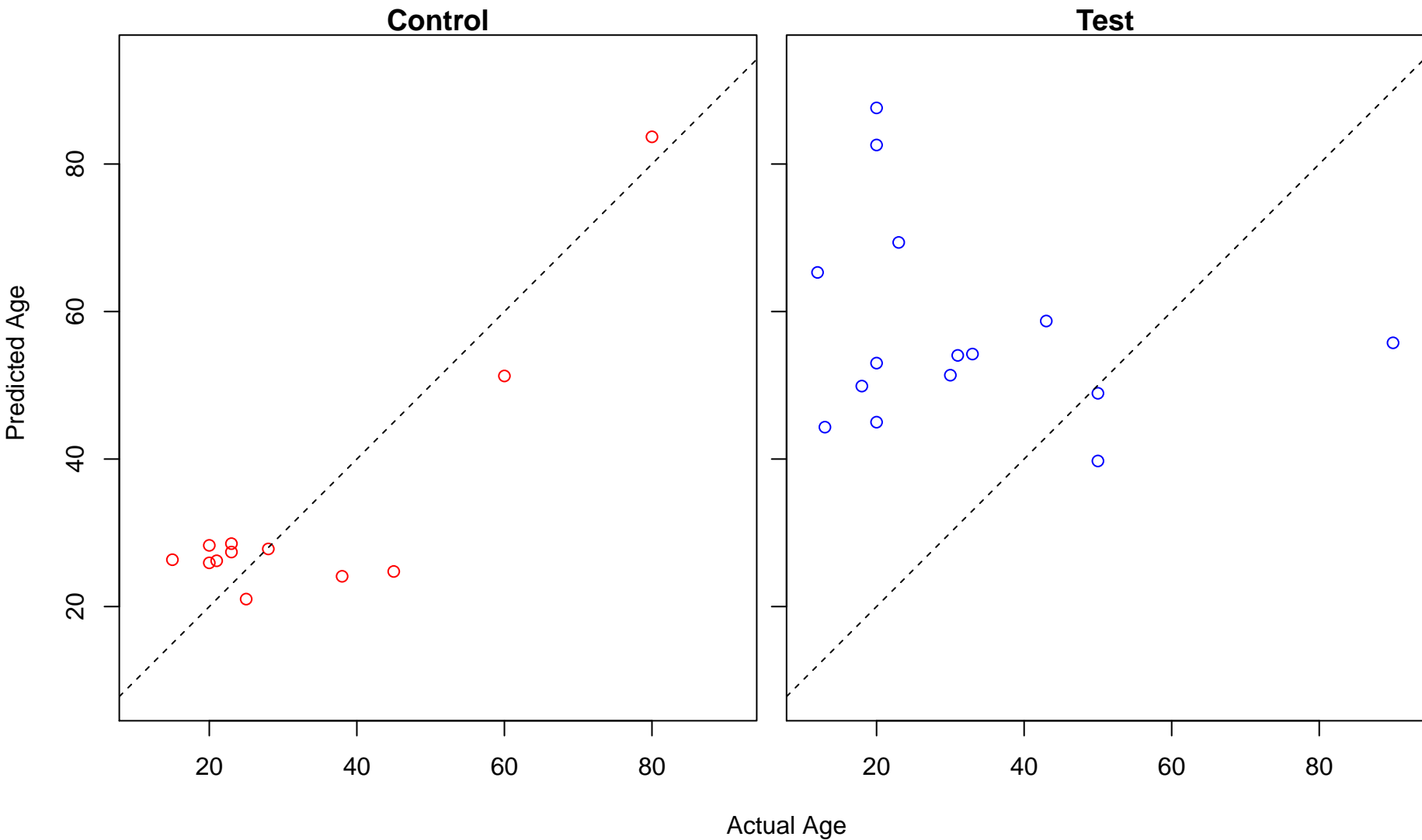
T cell differentiation in thymus (Score: 5.510978)



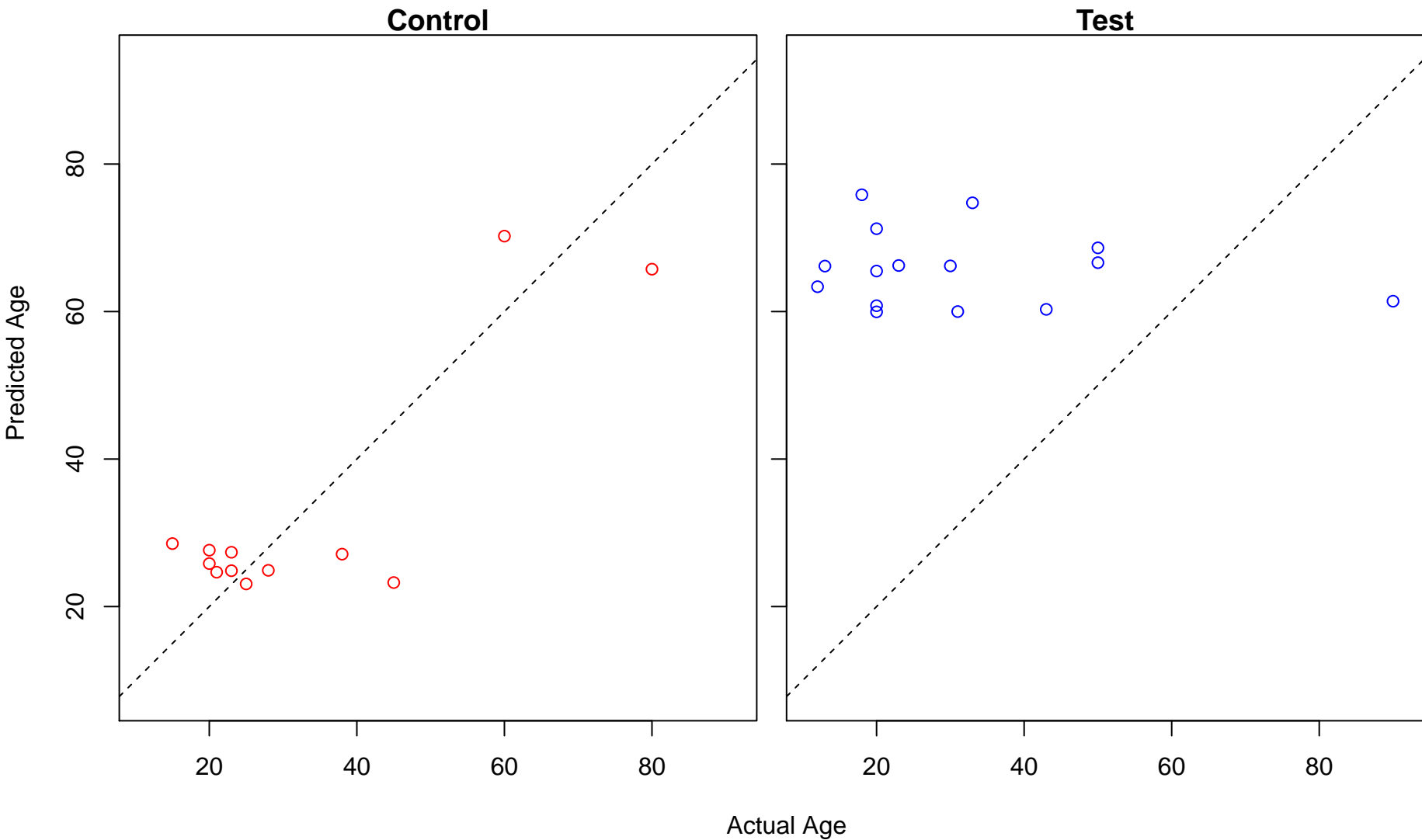
thymocyte aggregation (Score: 5.510978)



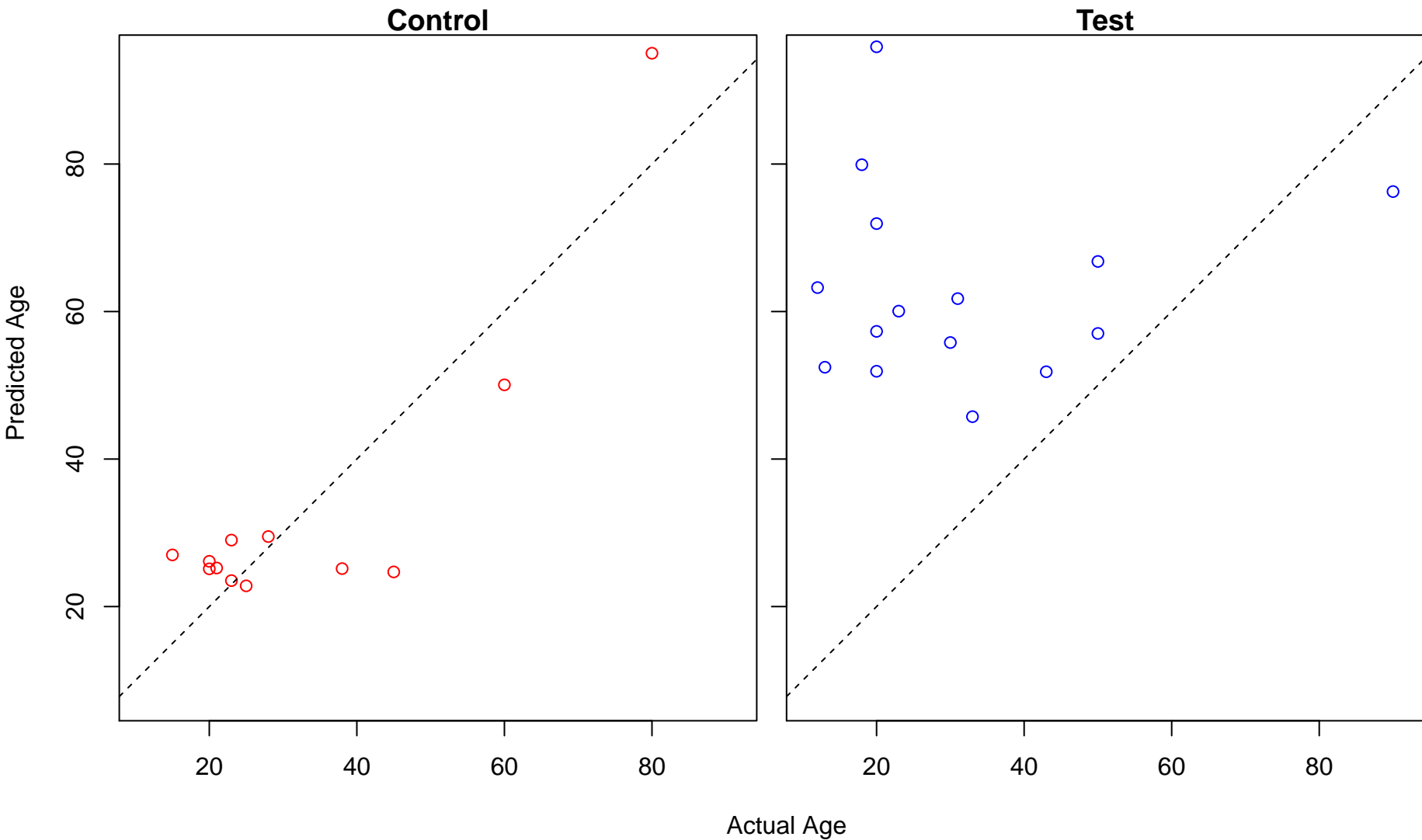
DNA strand elongation (Score: 5.509929)



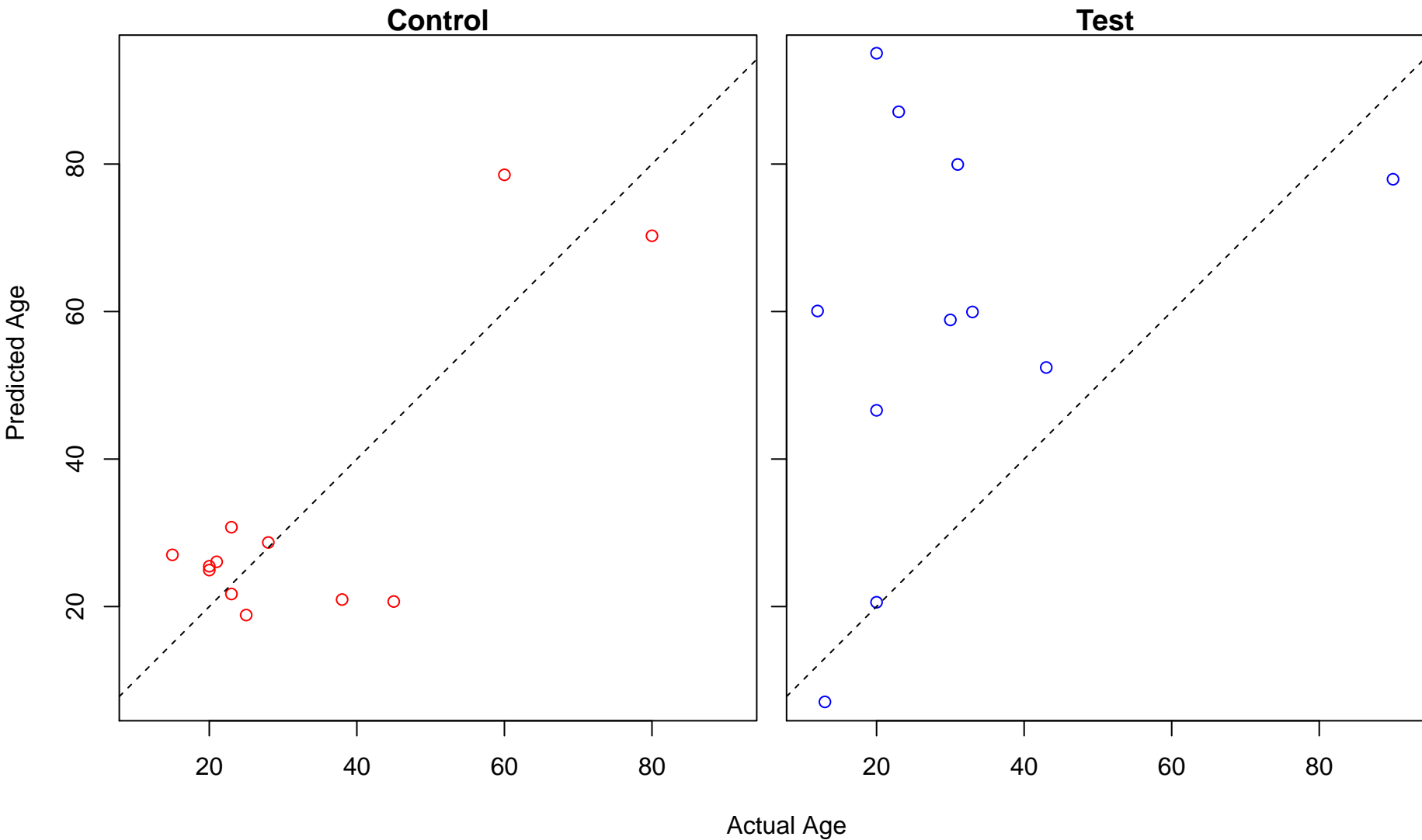
G-protein coupled acetylcholine receptor signaling pathway (Score: 5.509583)



transforming growth factor beta receptor signaling pathway (Score: 5.508657)

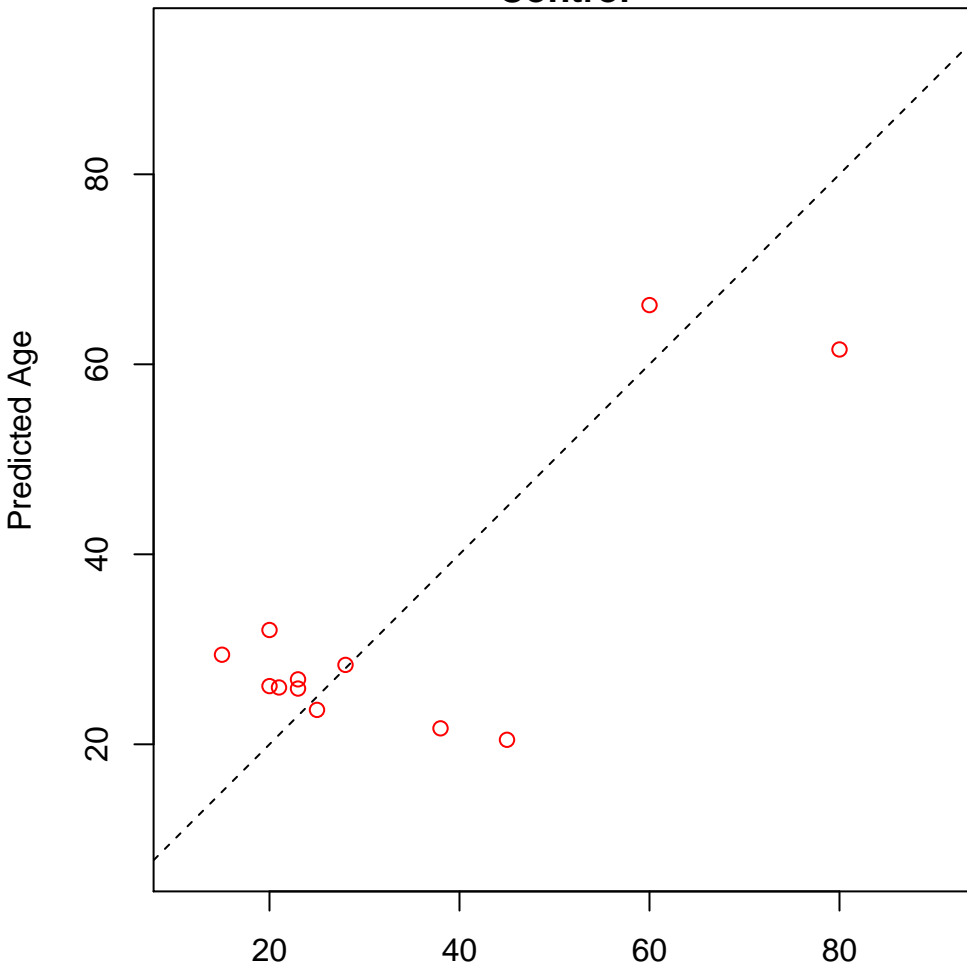


growth hormone secretion (Score: 5.508562)

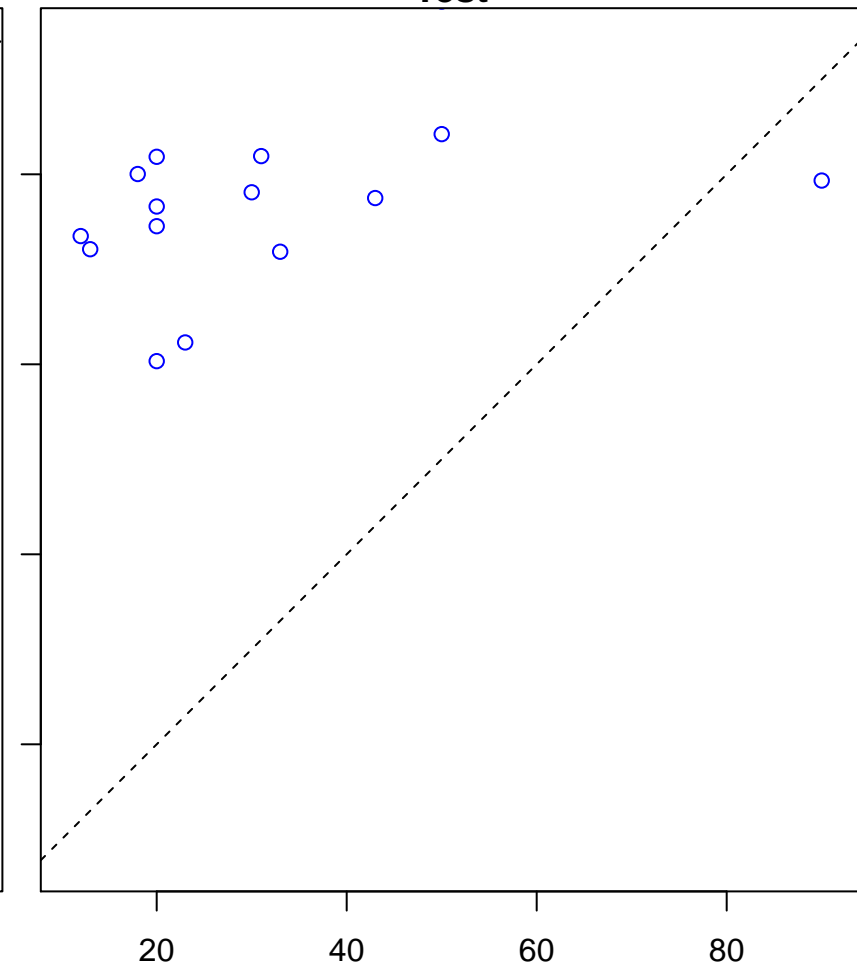


sodium ion transmembrane transport (Score: 5.507276)

Control

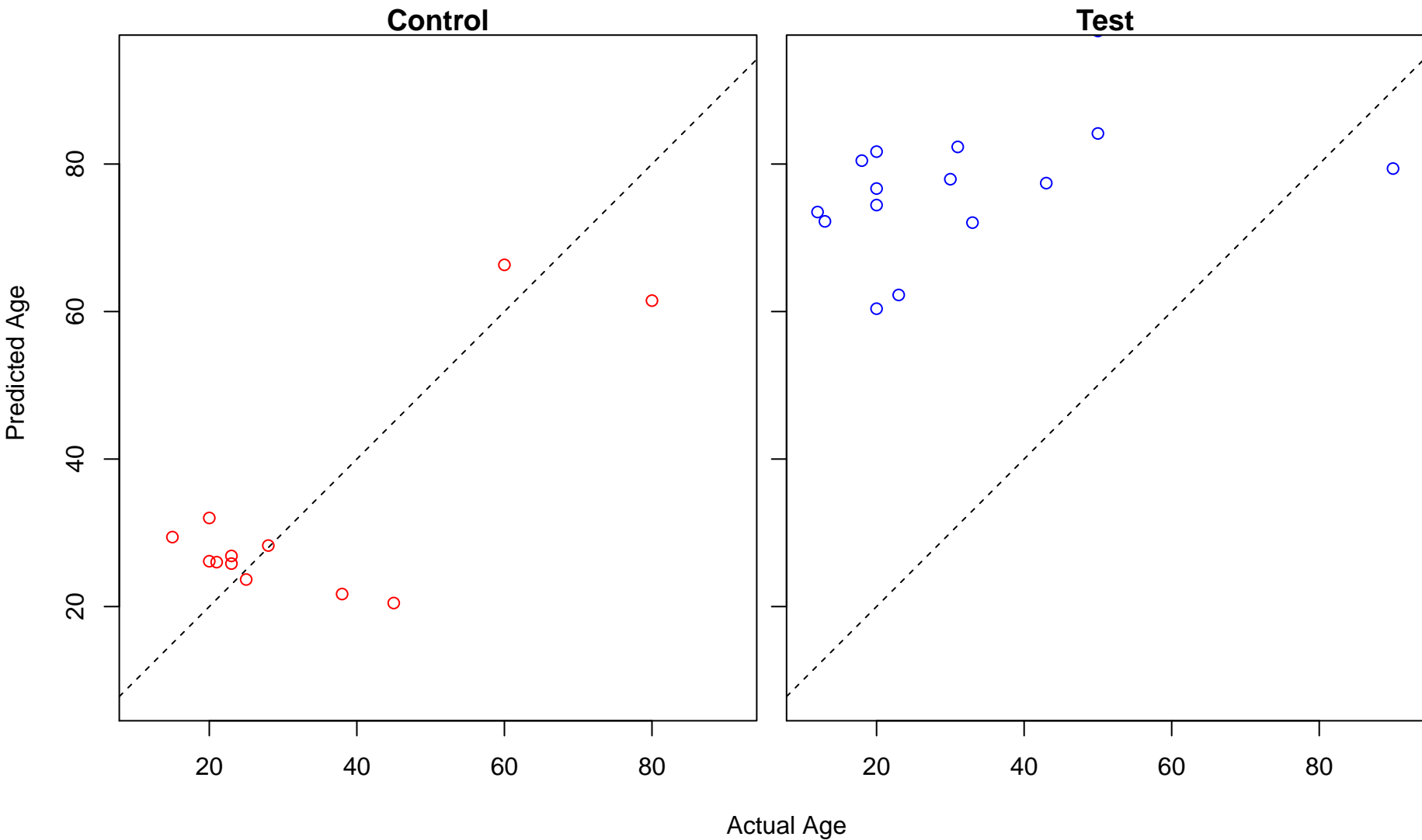


Test

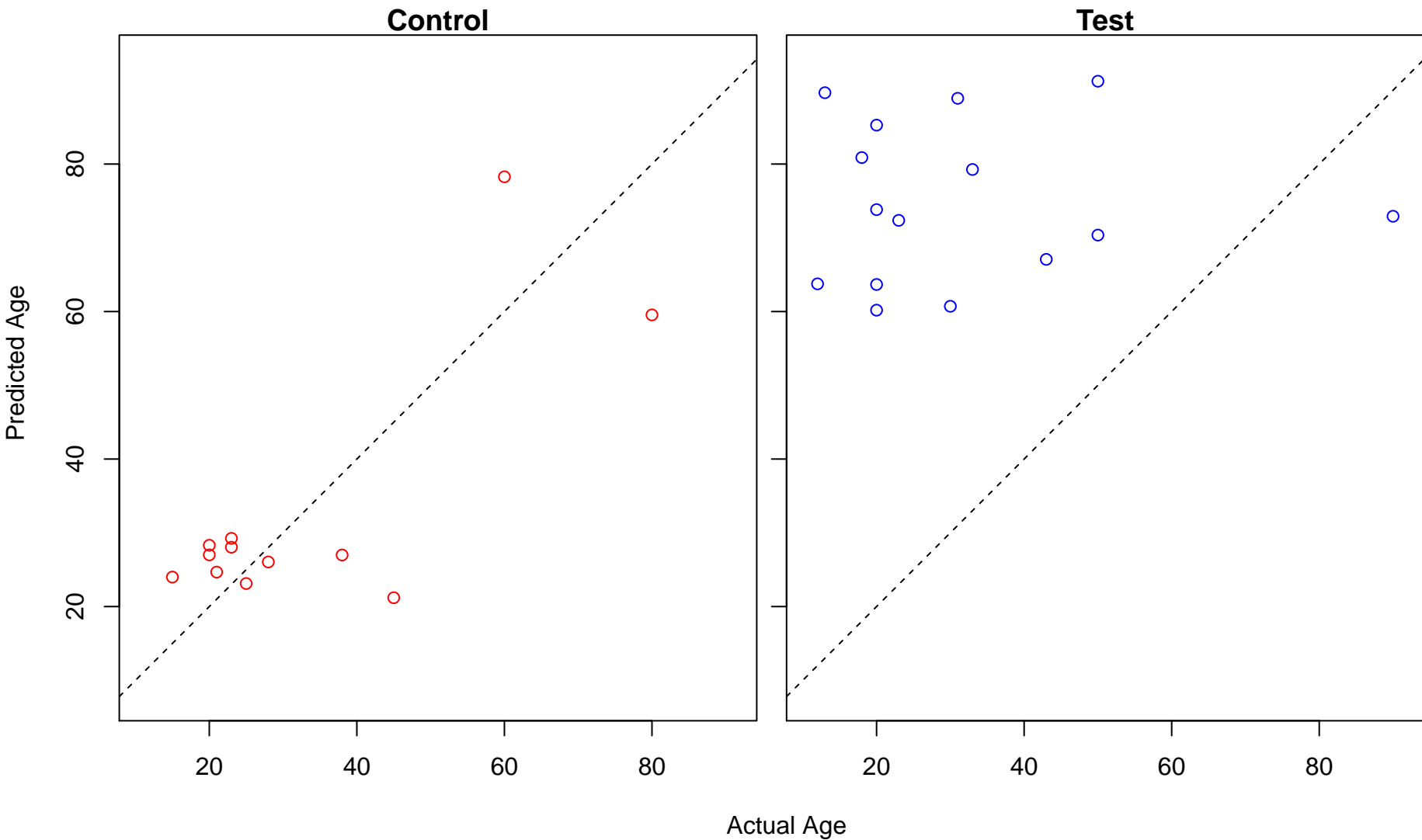


Actual Age

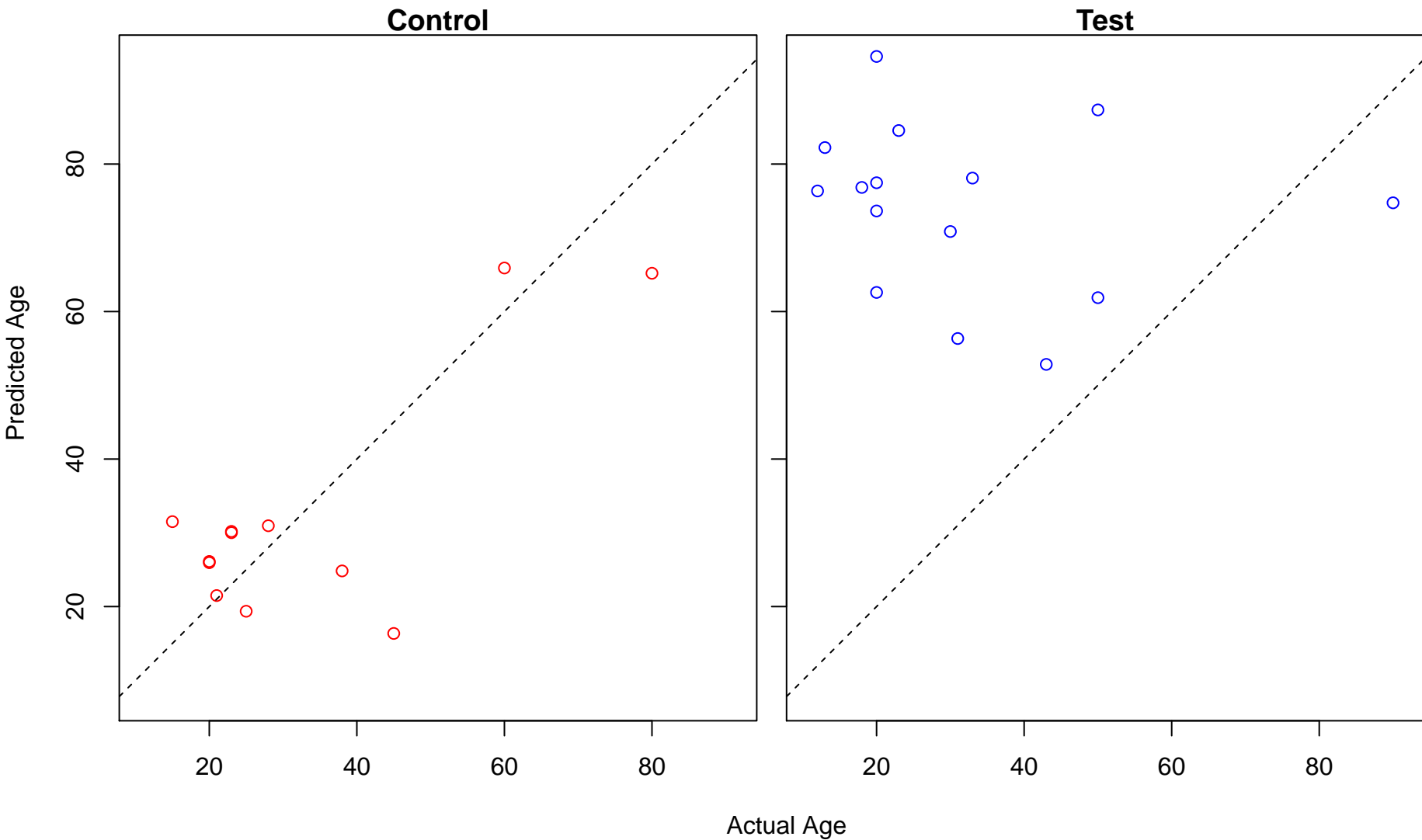
sodium ion transport (Score: 5.505248)



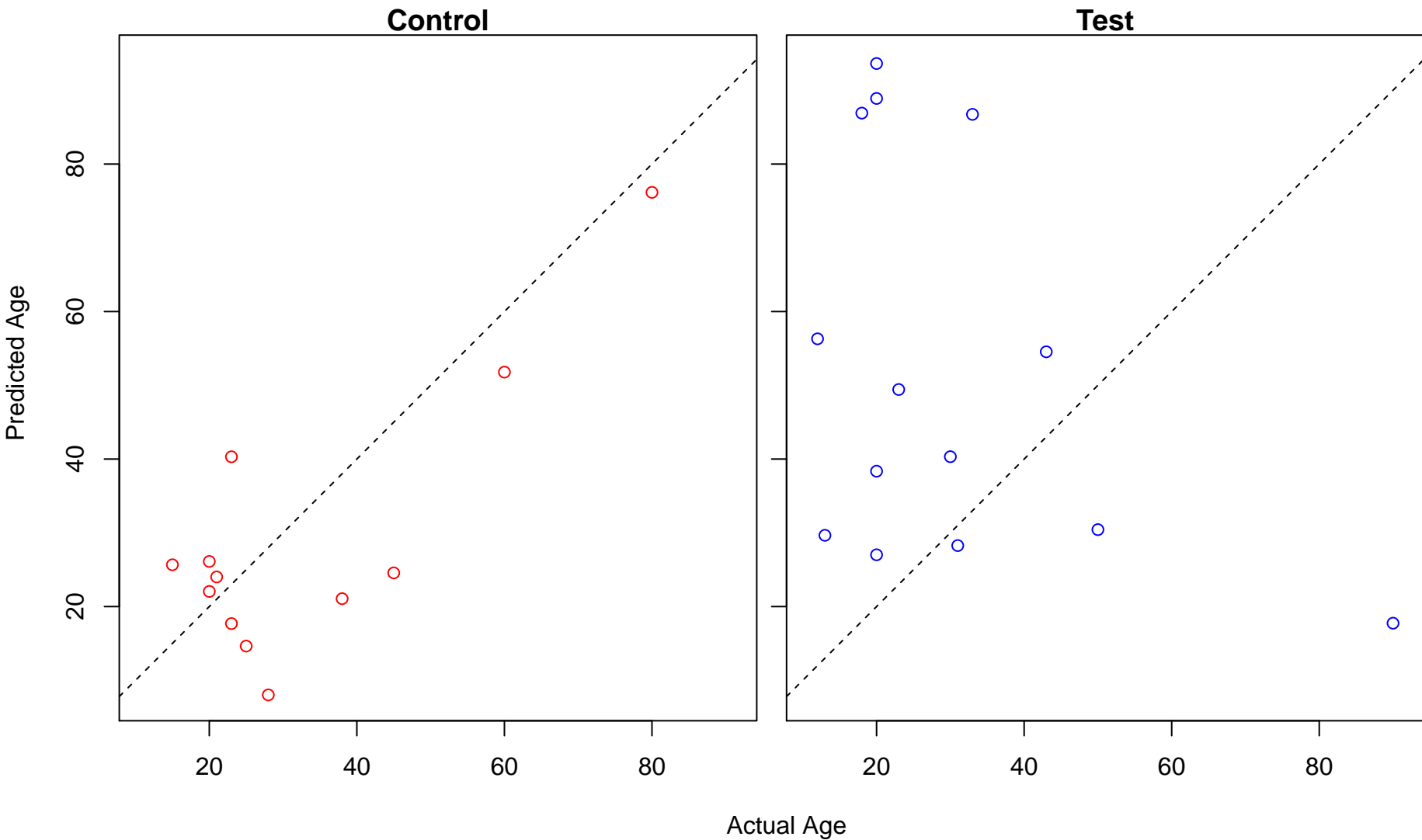
positive regulation of protein binding (Score: 5.505020)



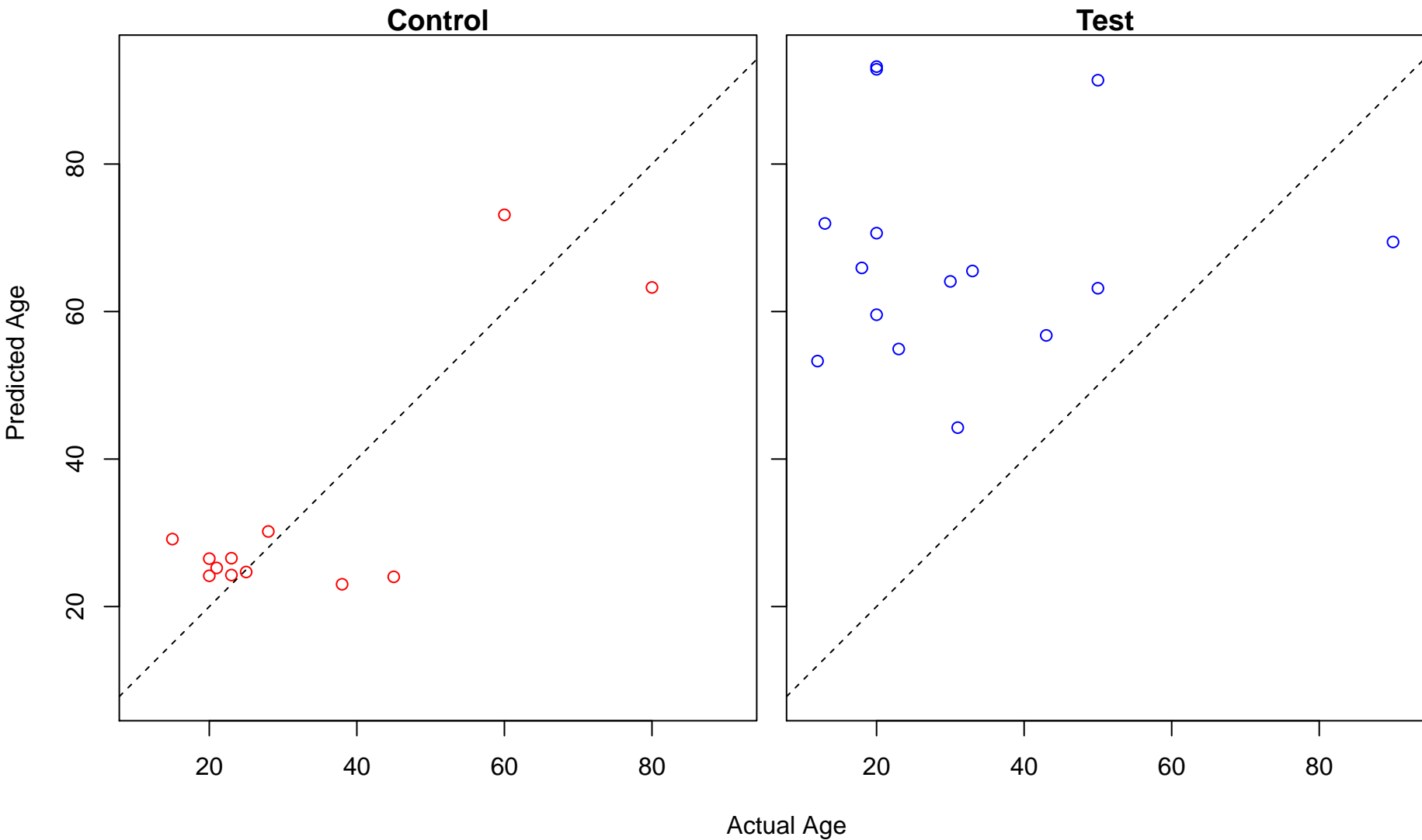
negative regulation of histone methylation (Score: 5.504690)



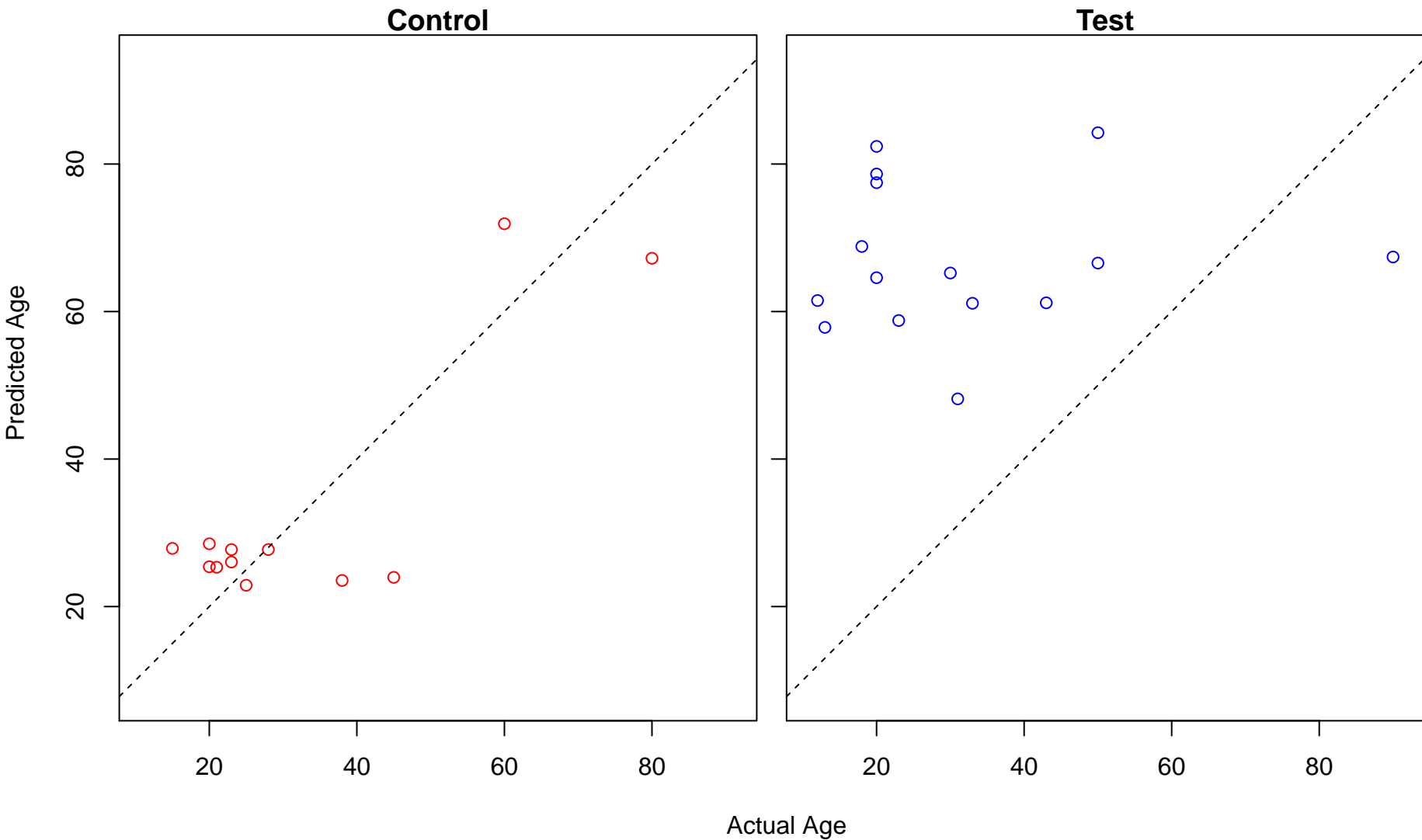
potassium ion transport (Score: 5.504136)



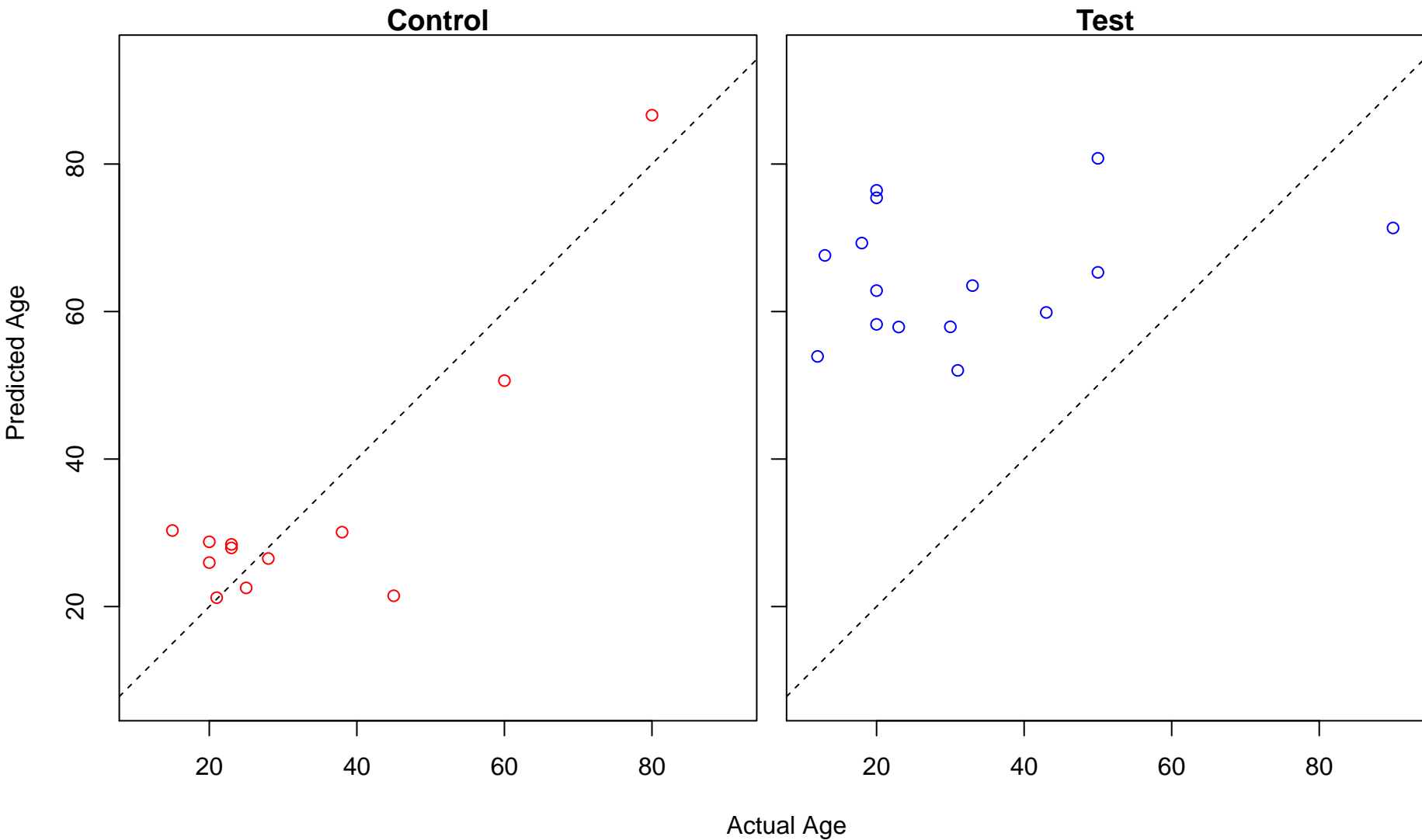
visual behavior (Score: 5.503786)



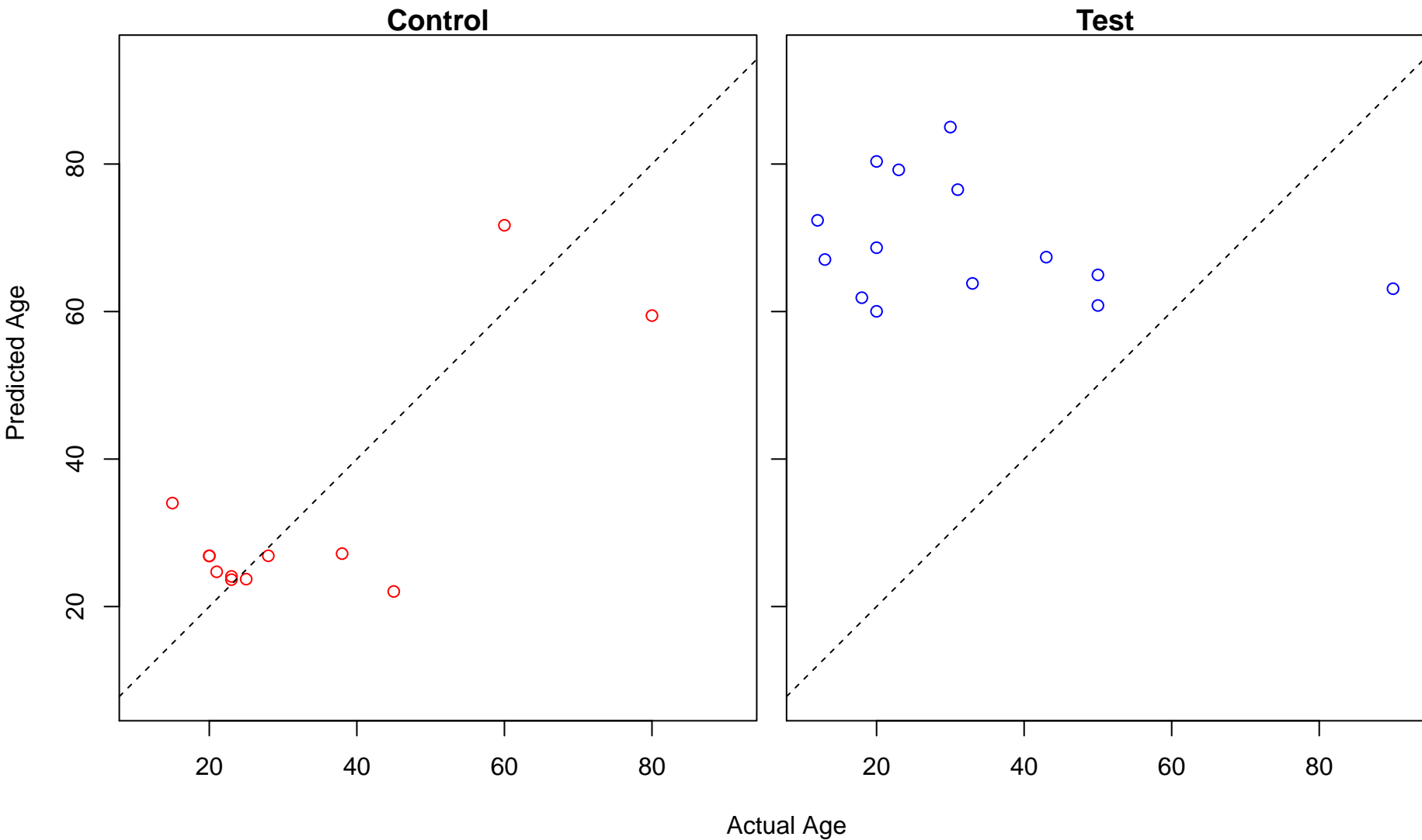
cytokinesis (Score: 5.502845)



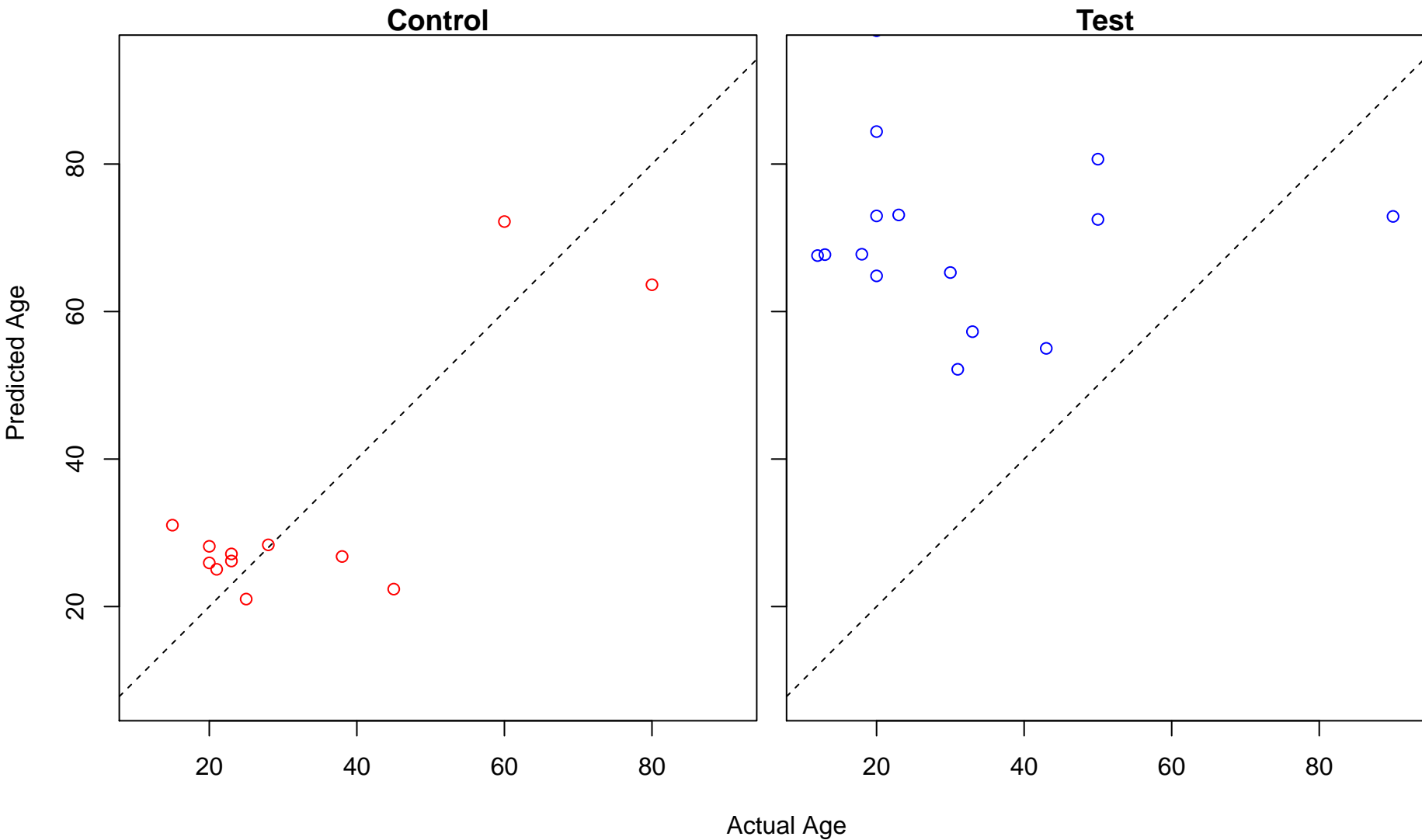
positive regulation of histone modification (Score: 5.496637)



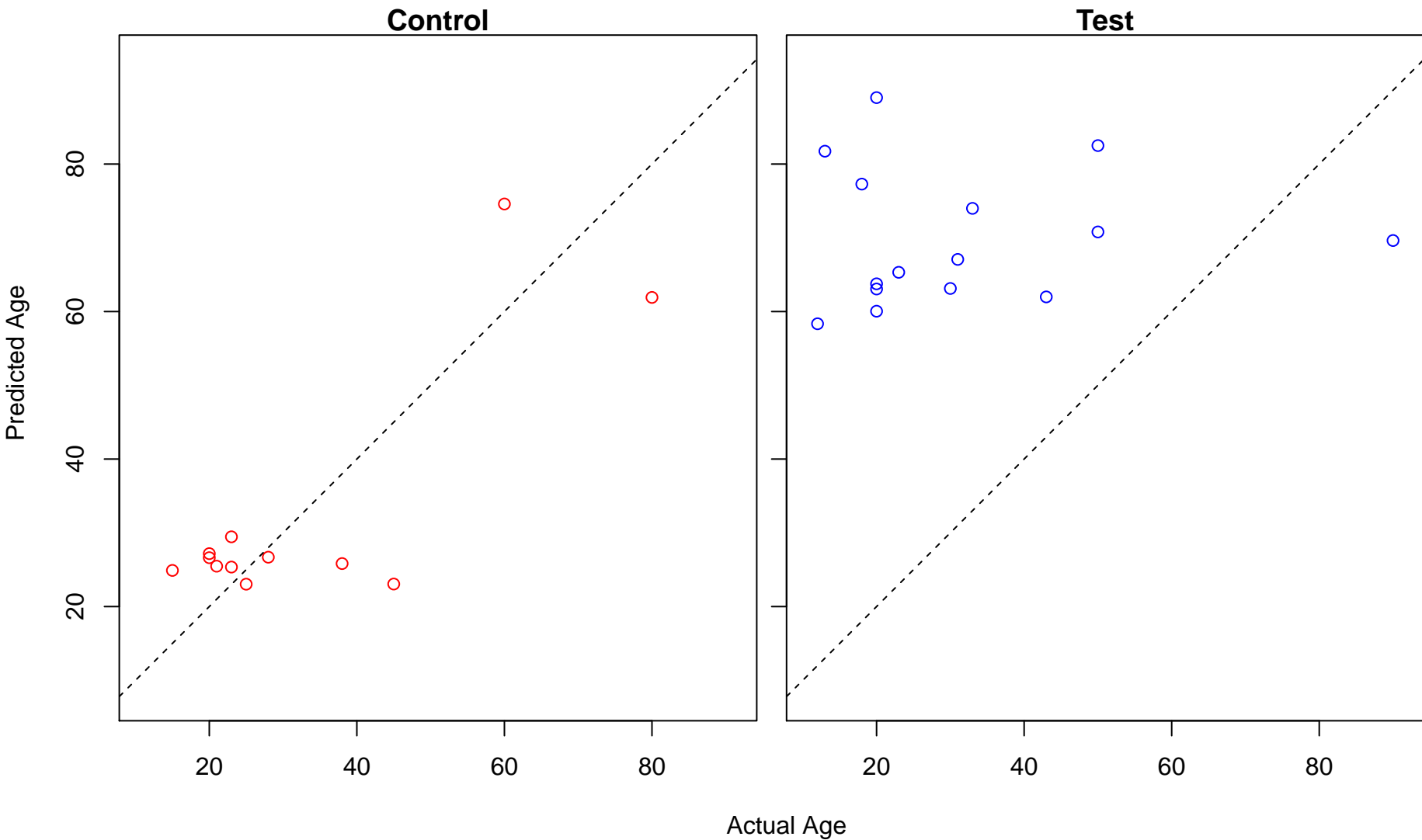
leptin-mediated signaling pathway (Score: 5.494063)



positive regulation of secretion (Score: 5.492869)

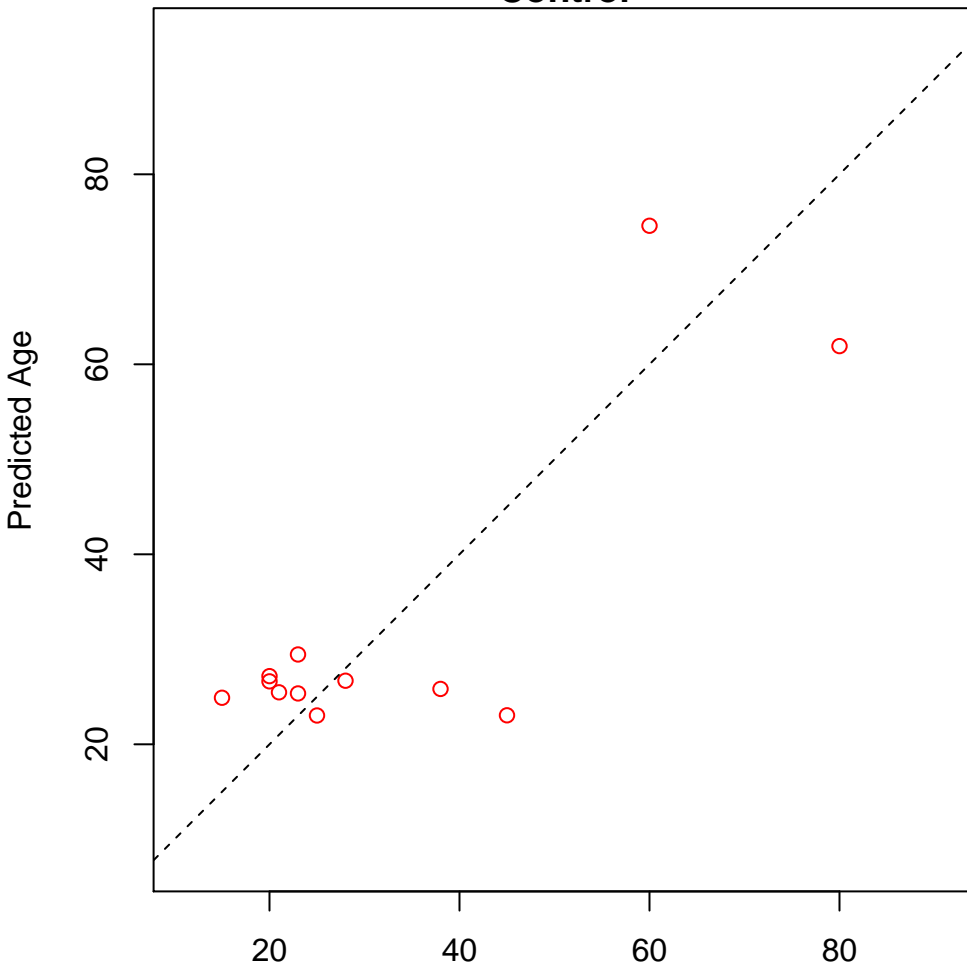


regulation of mononuclear cell proliferation (Score: 5.486816)

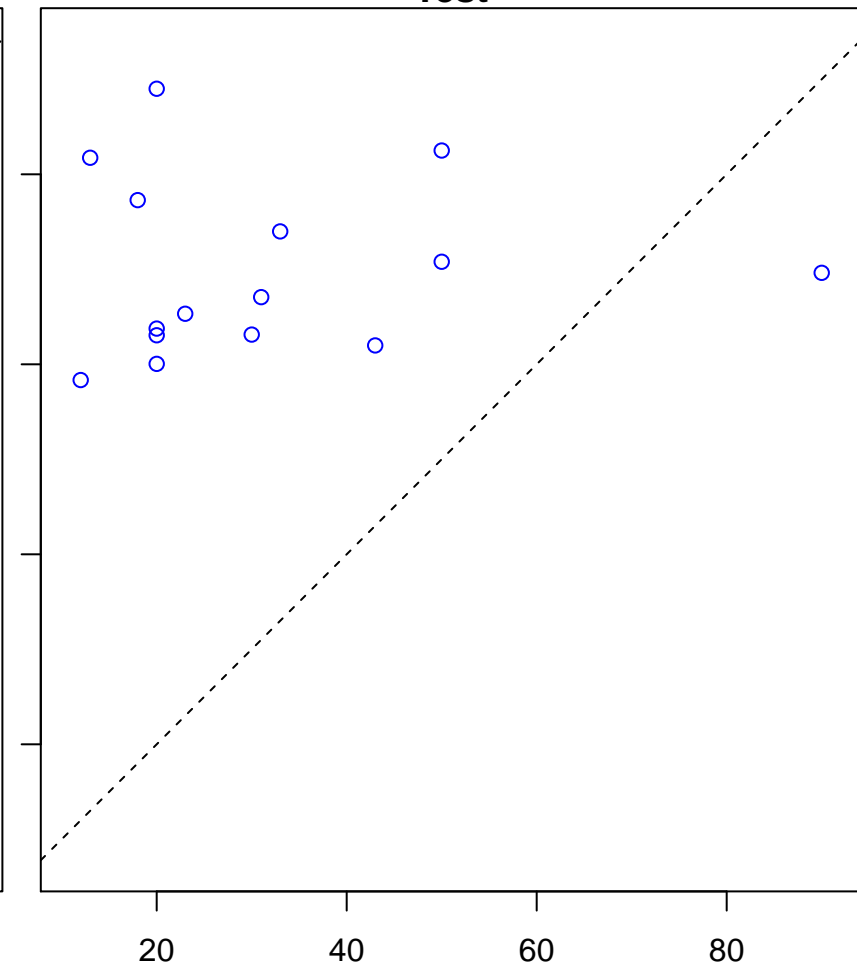


regulation of lymphocyte proliferation (Score: 5.486803)

Control

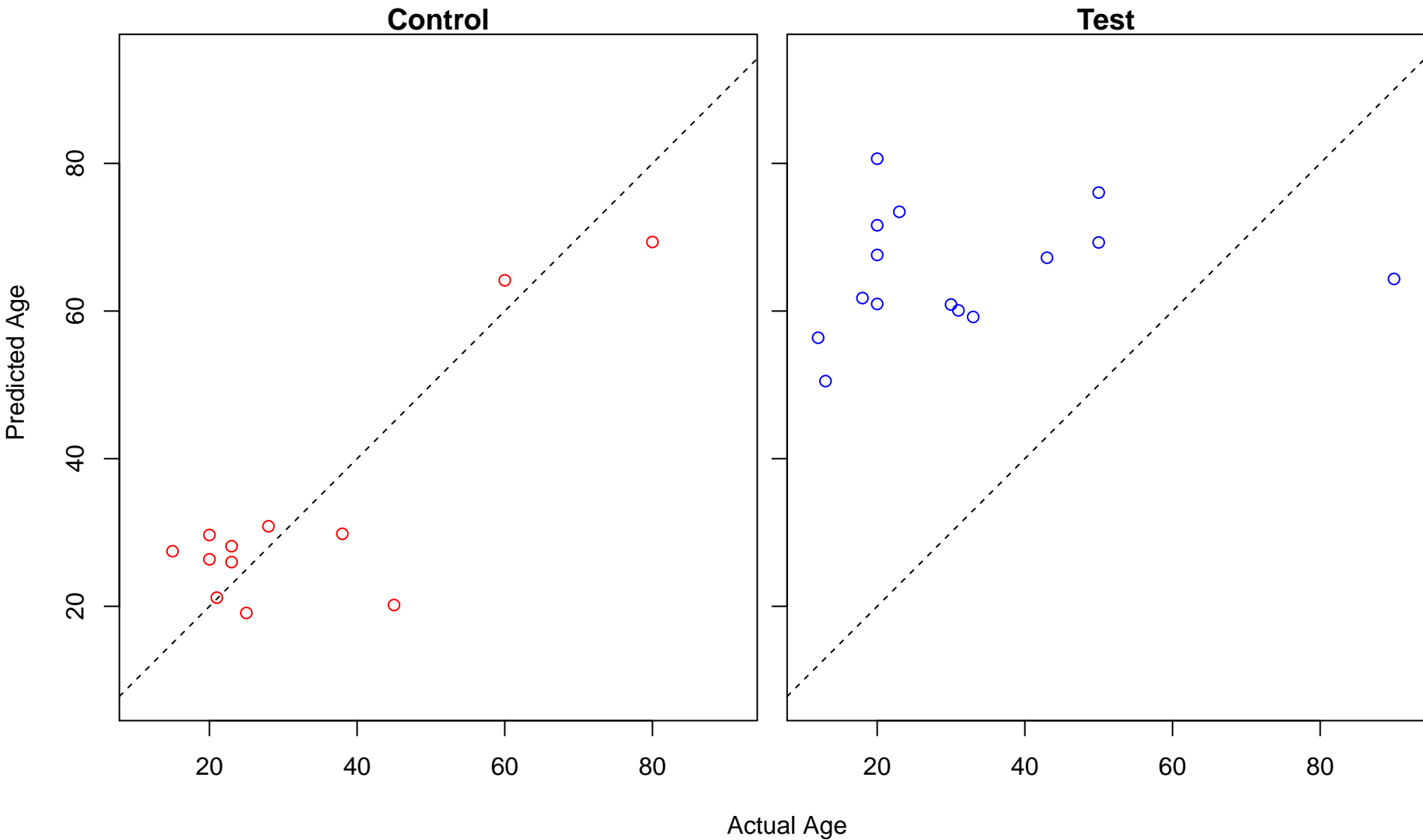


Test



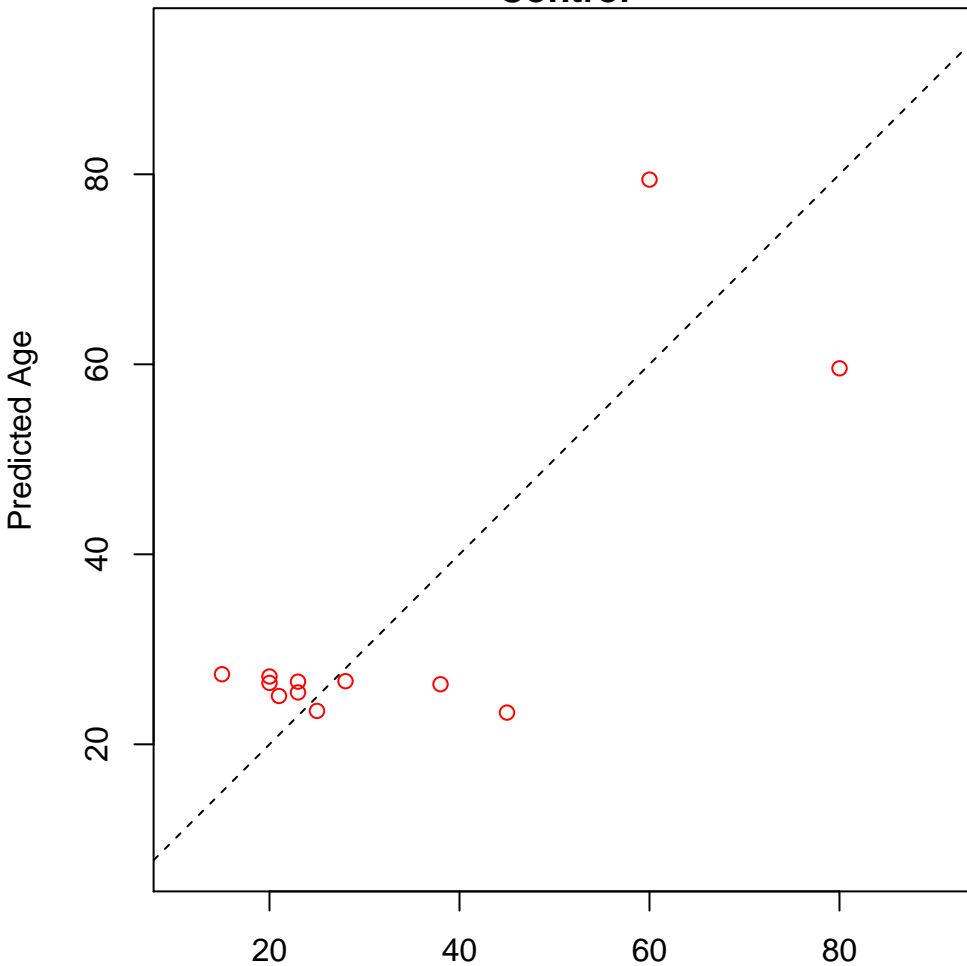
Actual Age

regulation of cardiac muscle cell membrane potential (Score: 5.485304)

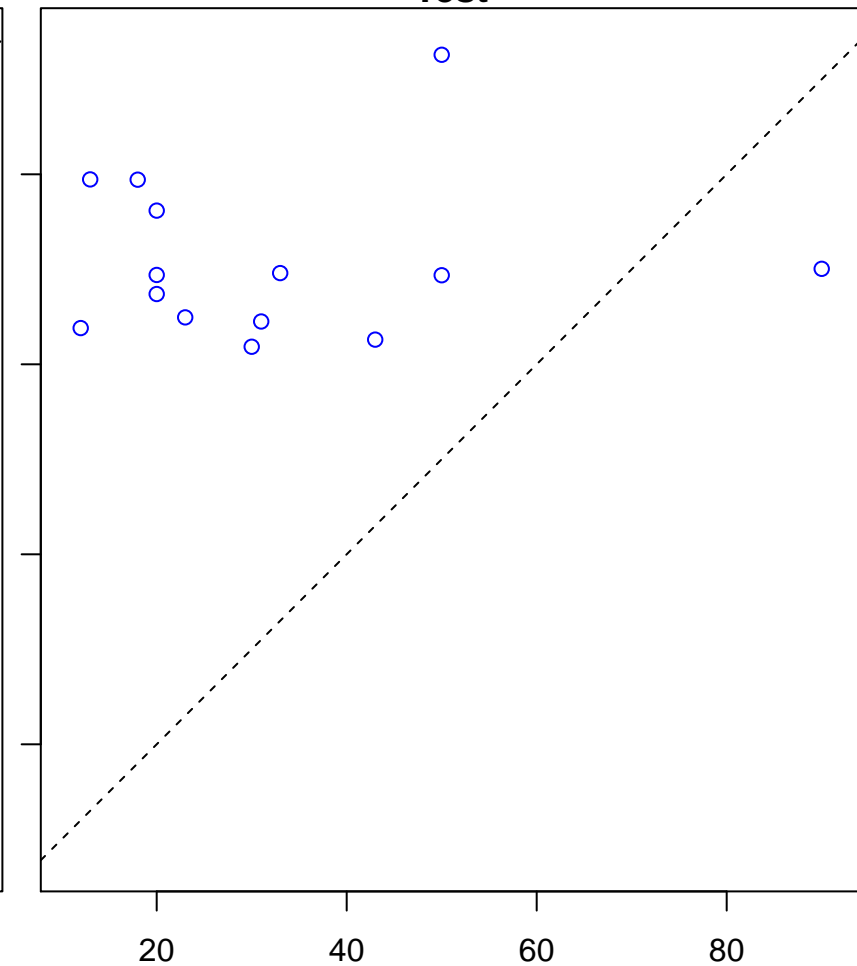


proteasomal protein catabolic process (Score: 5.485185)

Control

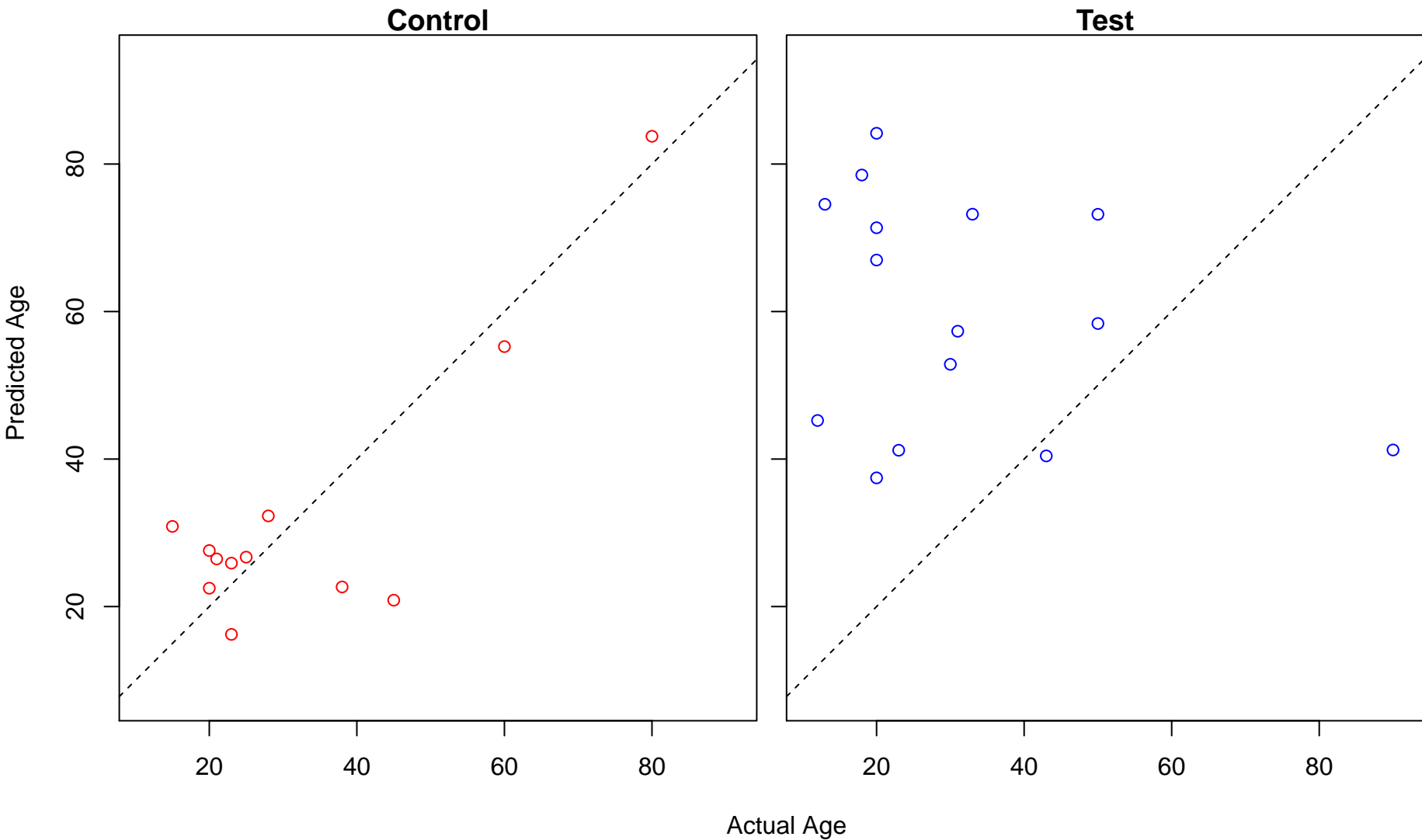


Test



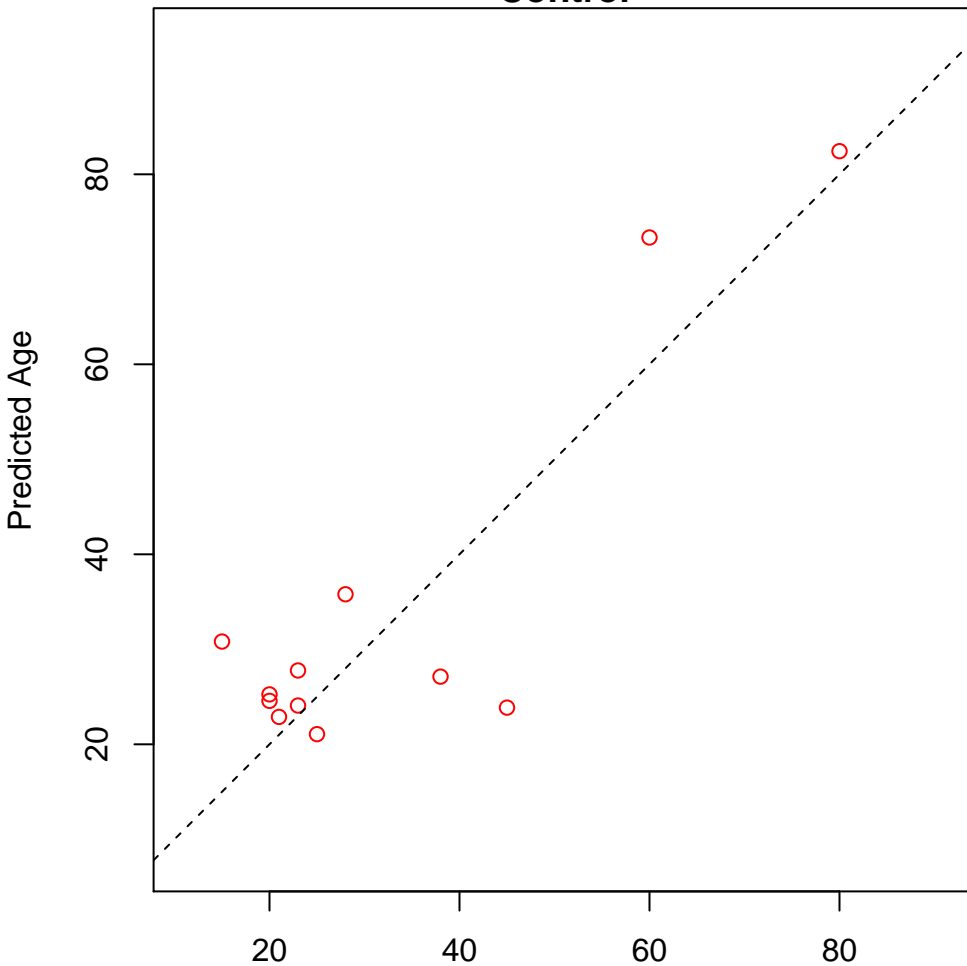
Actual Age

positive regulation of lipase activity (Score: 5.481482)

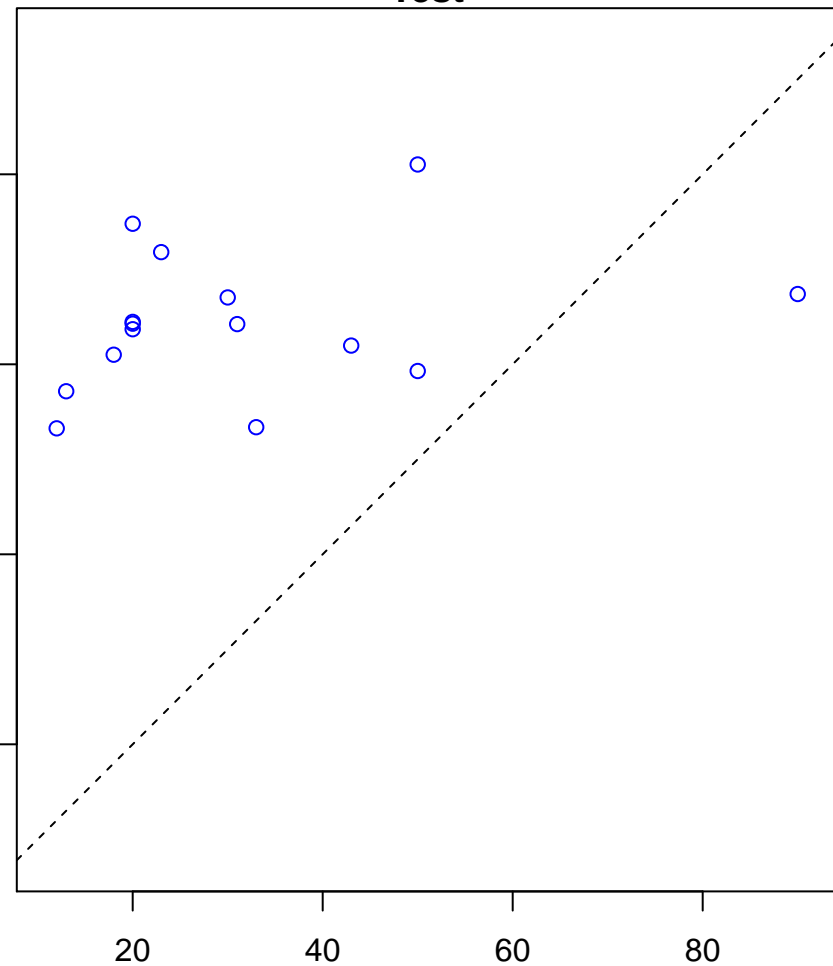


anterior/posterior pattern specification (Score: 5.481146)

Control

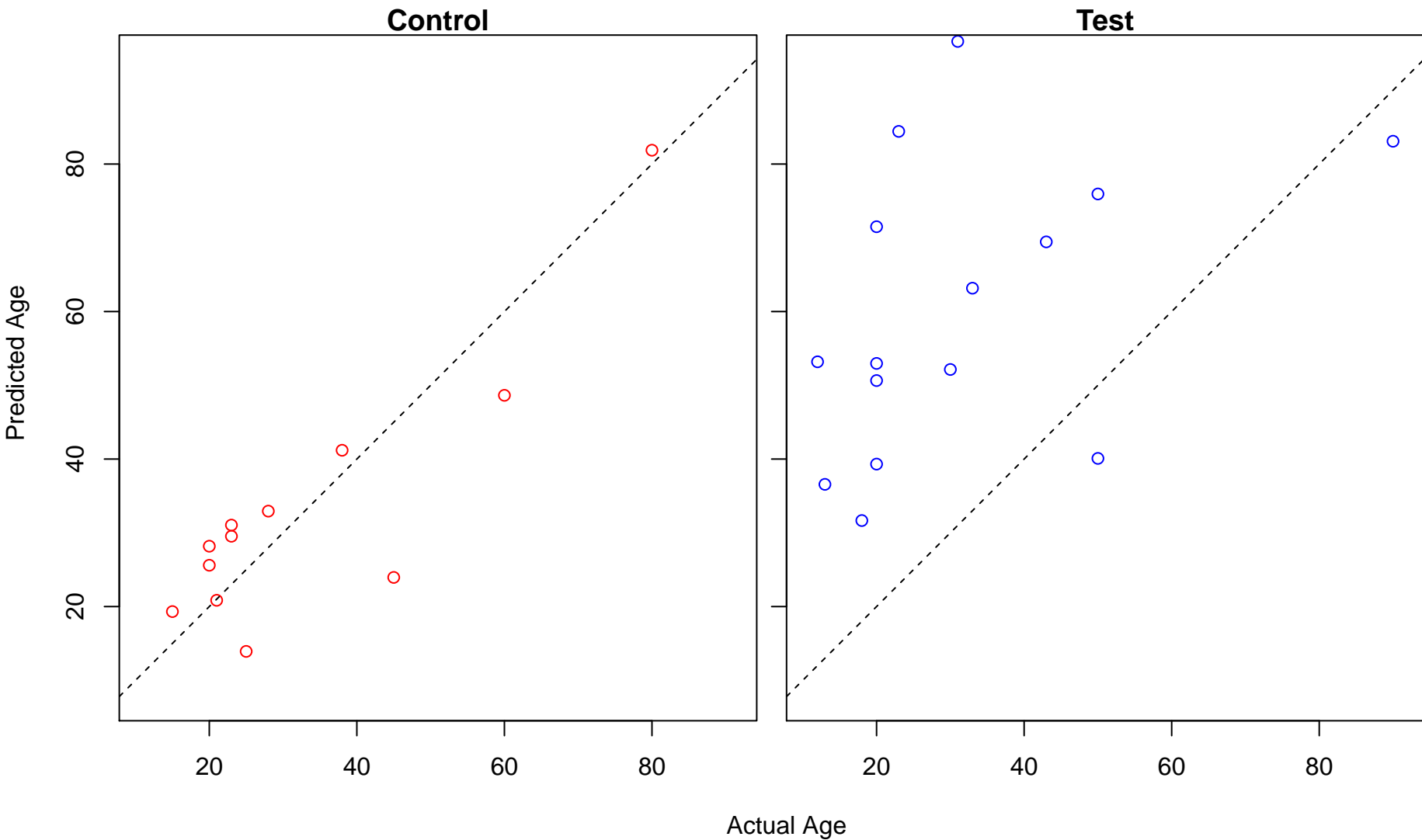


Test

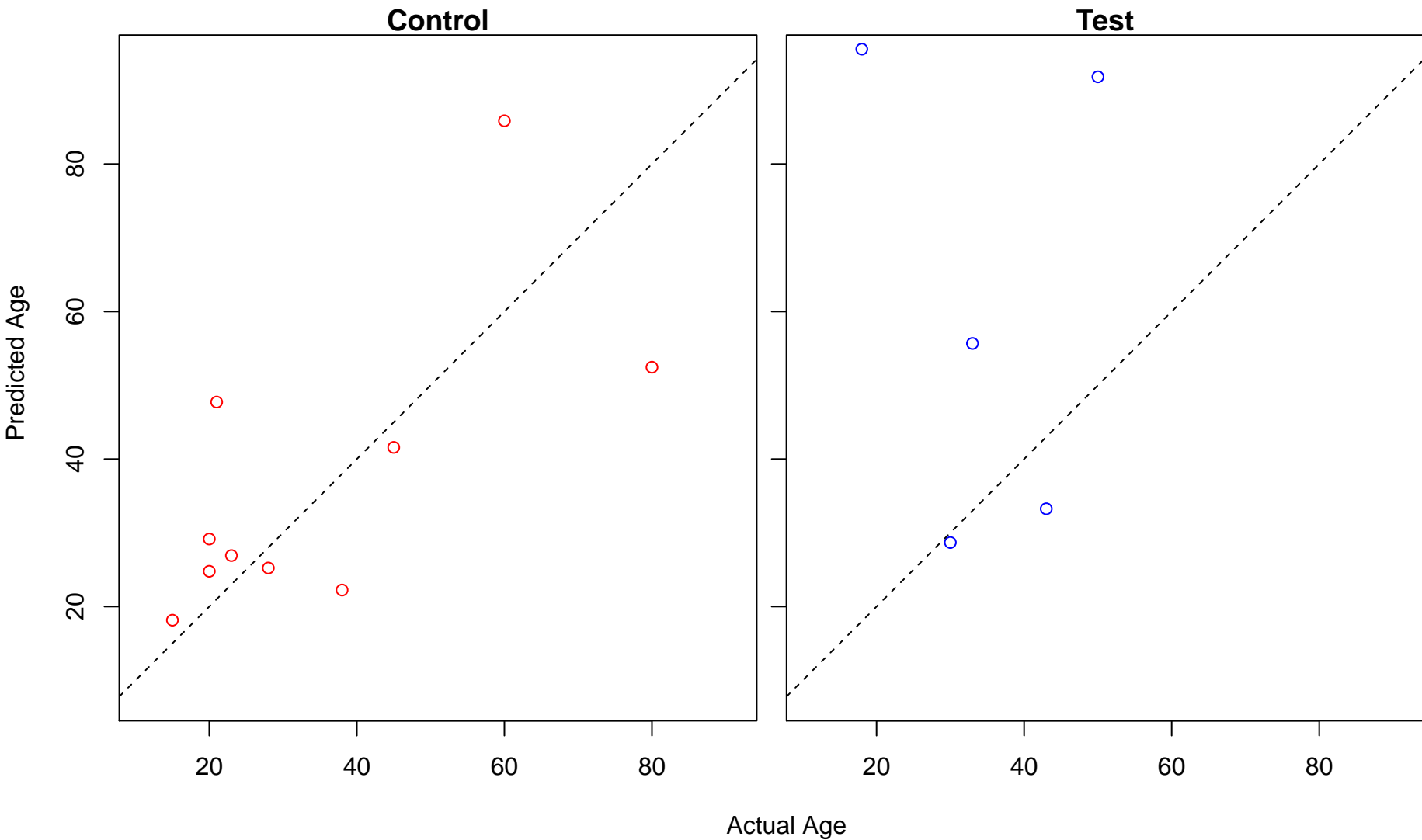


Actual Age

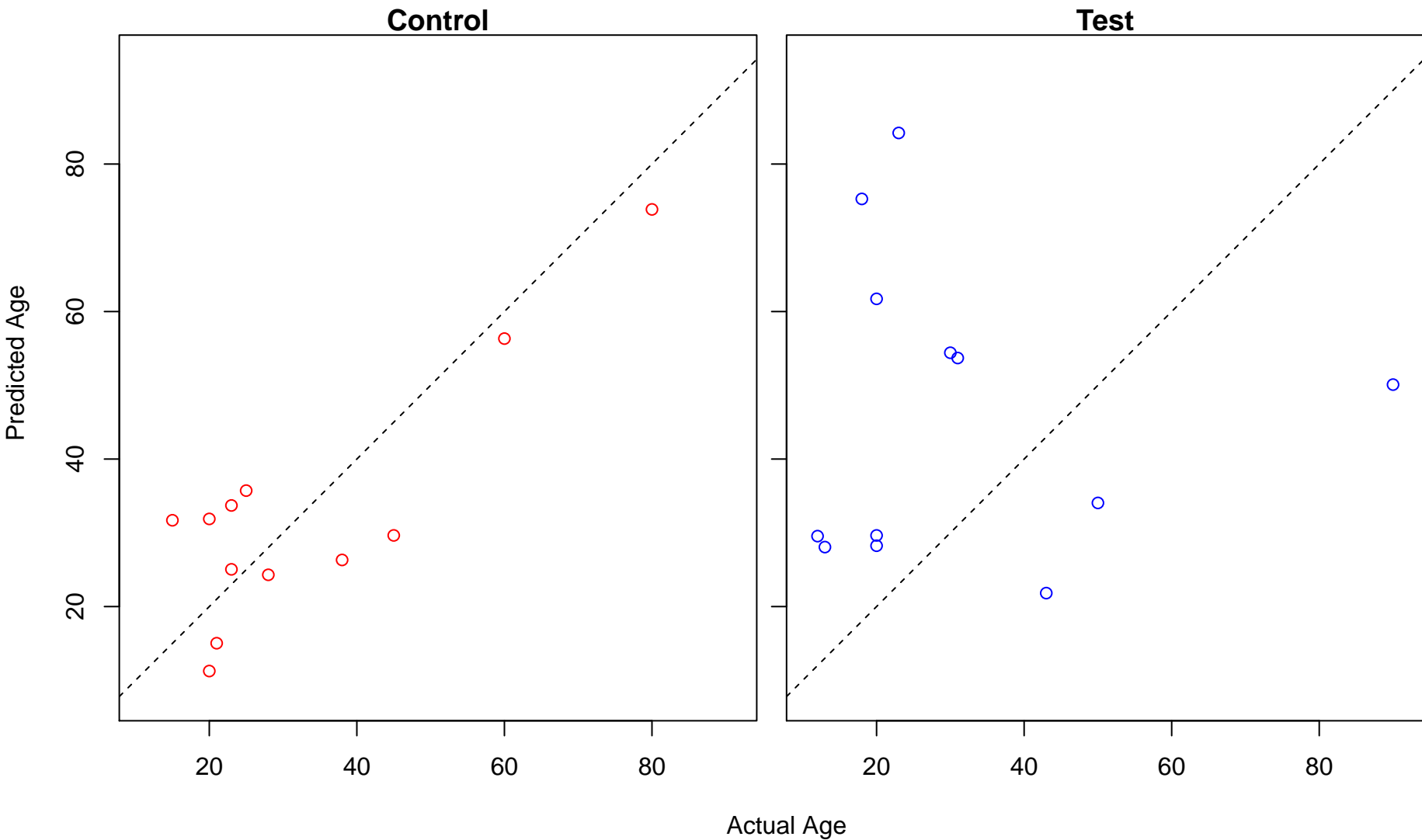
left/right pattern formation (Score: 5.479373)



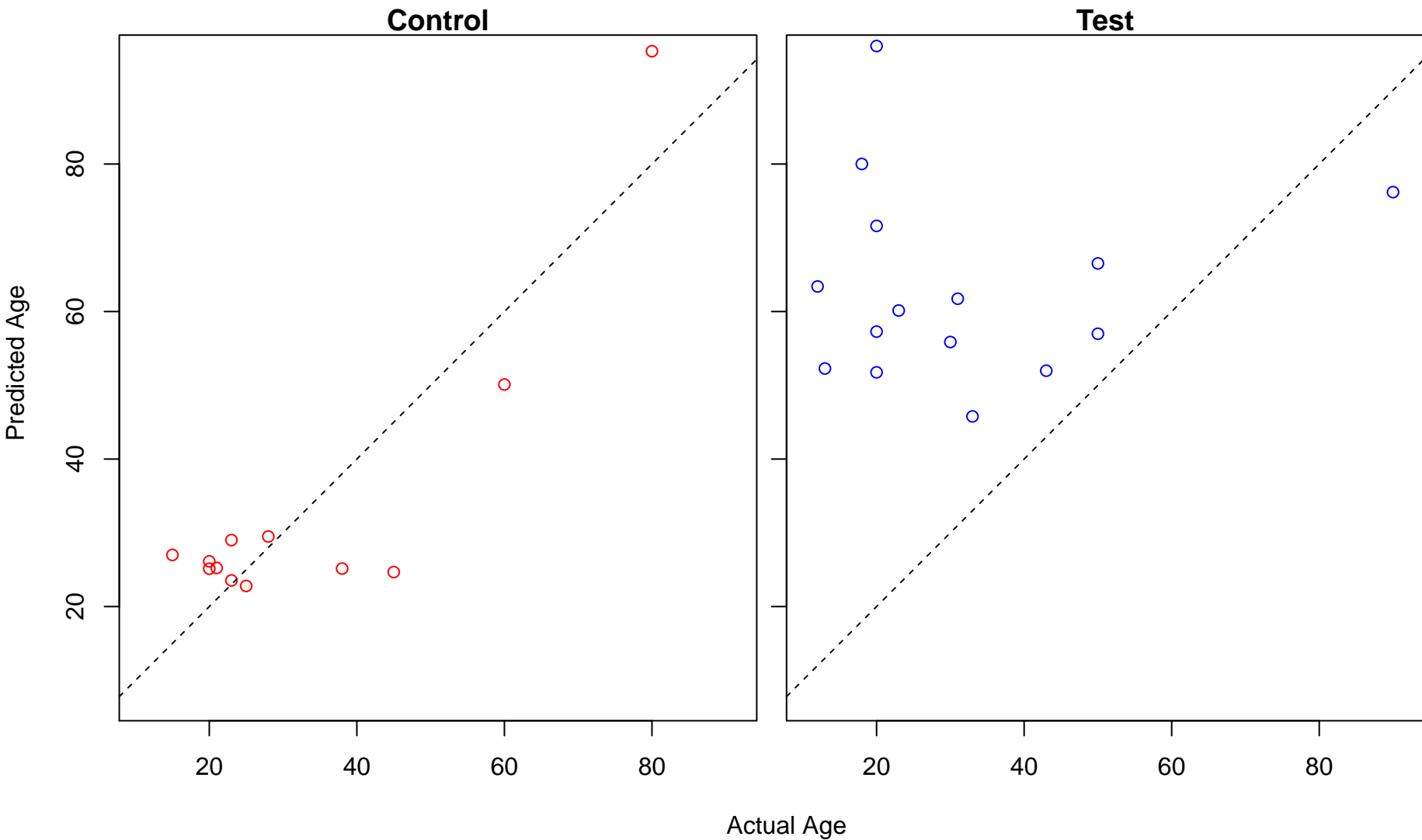
triglyceride-rich lipoprotein particle remodeling (Score: 5.477362)



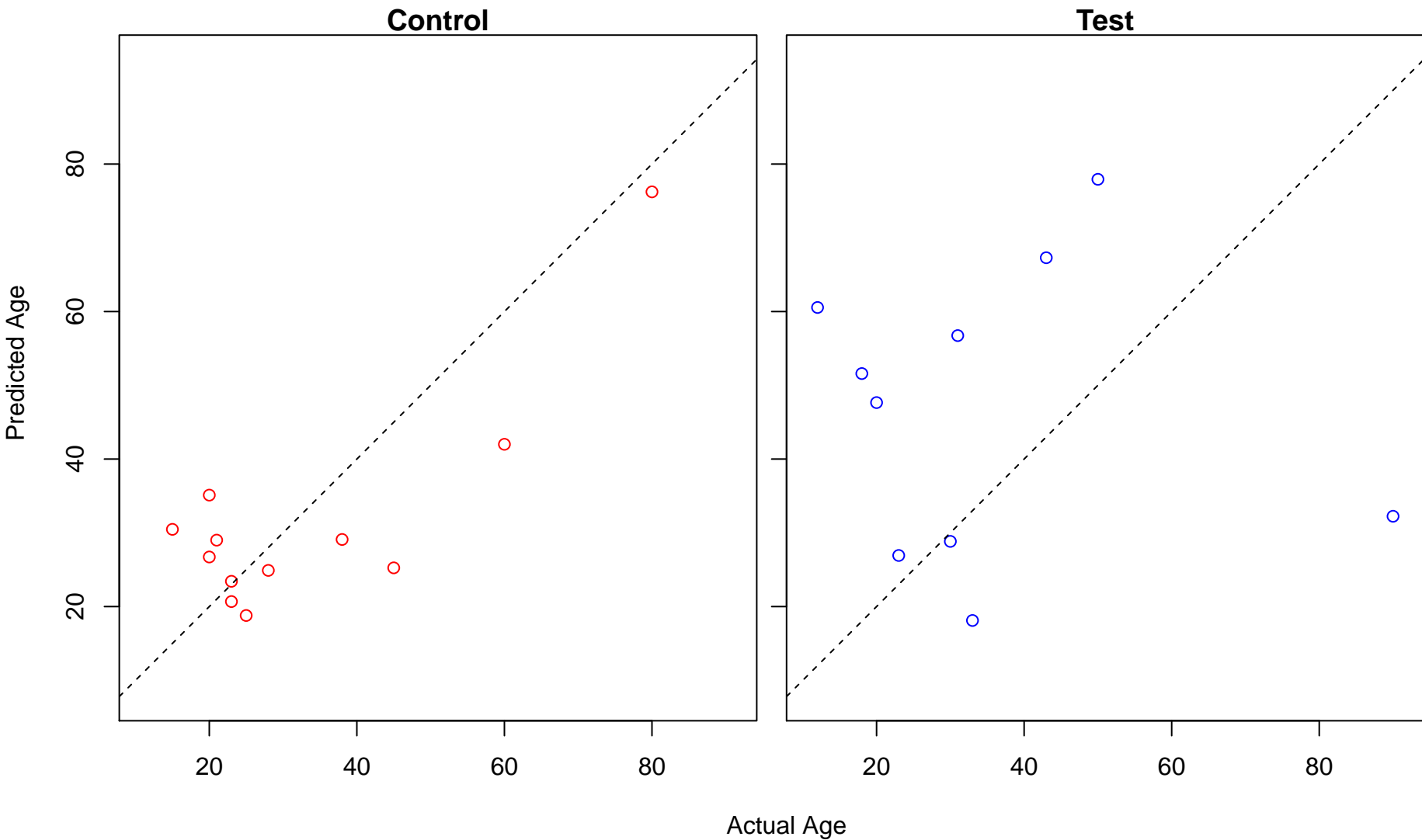
regulation of catenin import into nucleus (Score: 5.476382)



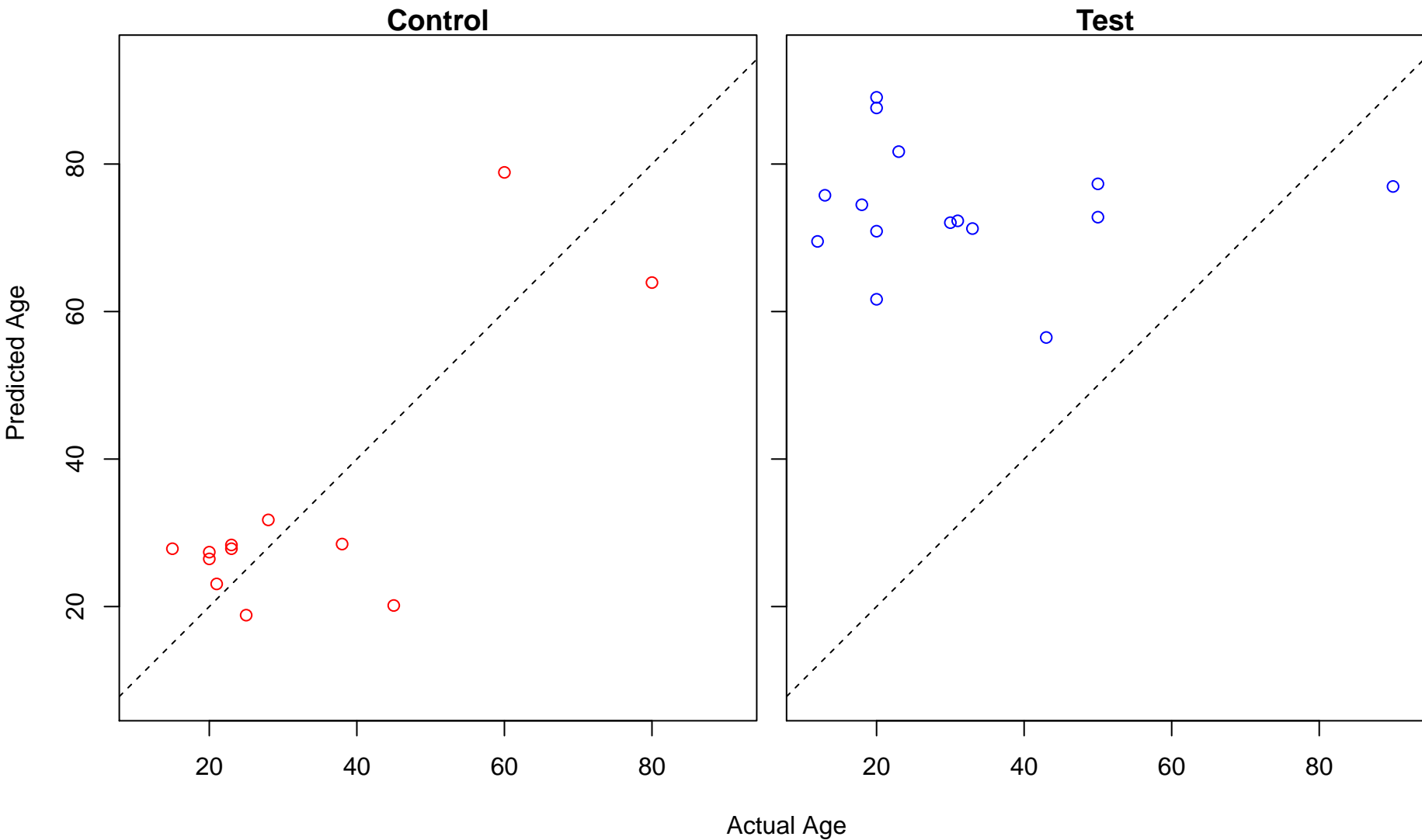
cellular response to transforming growth factor beta stimulus (Score: 5.475445)



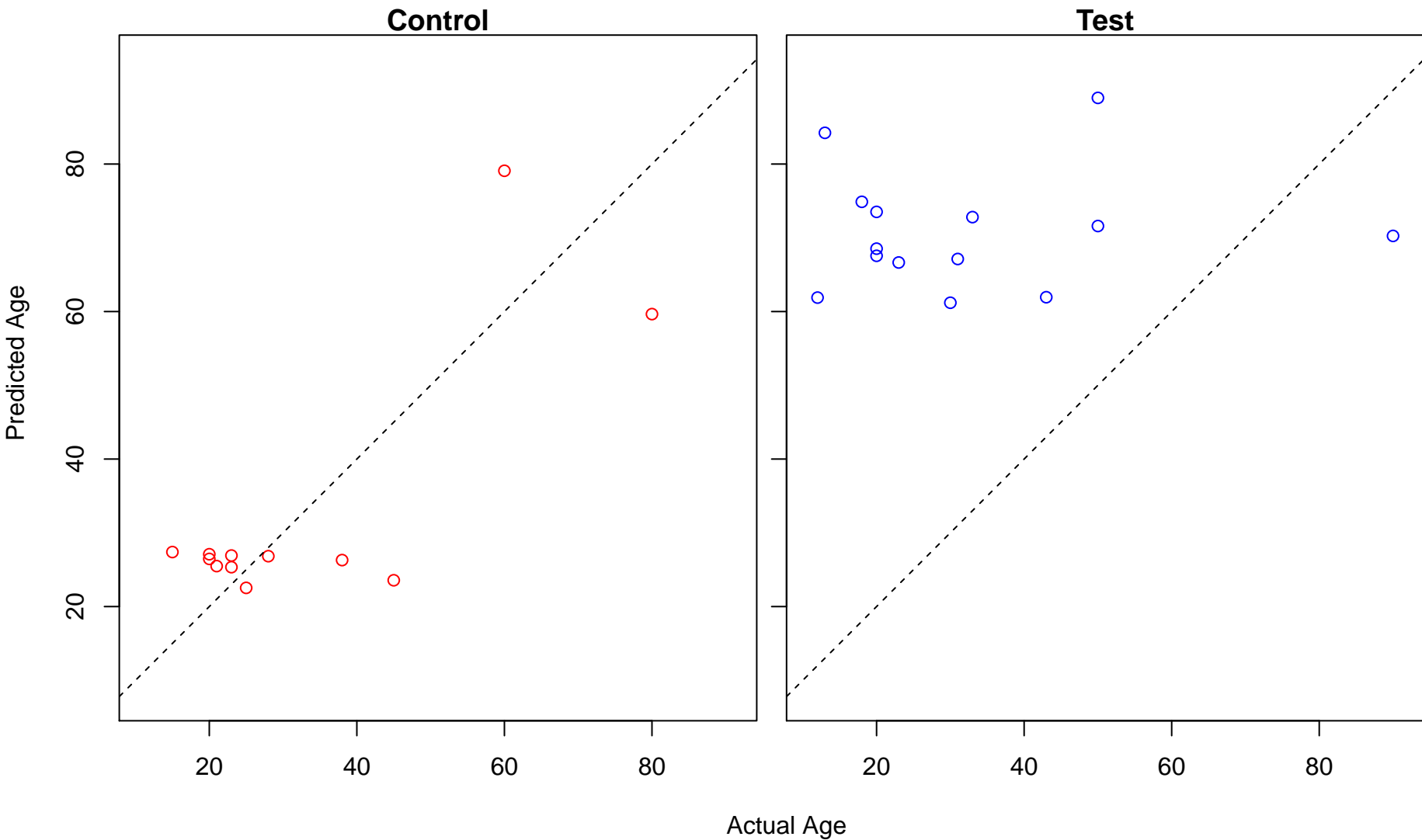
organic hydroxy compound biosynthetic process (Score: 5.472637)



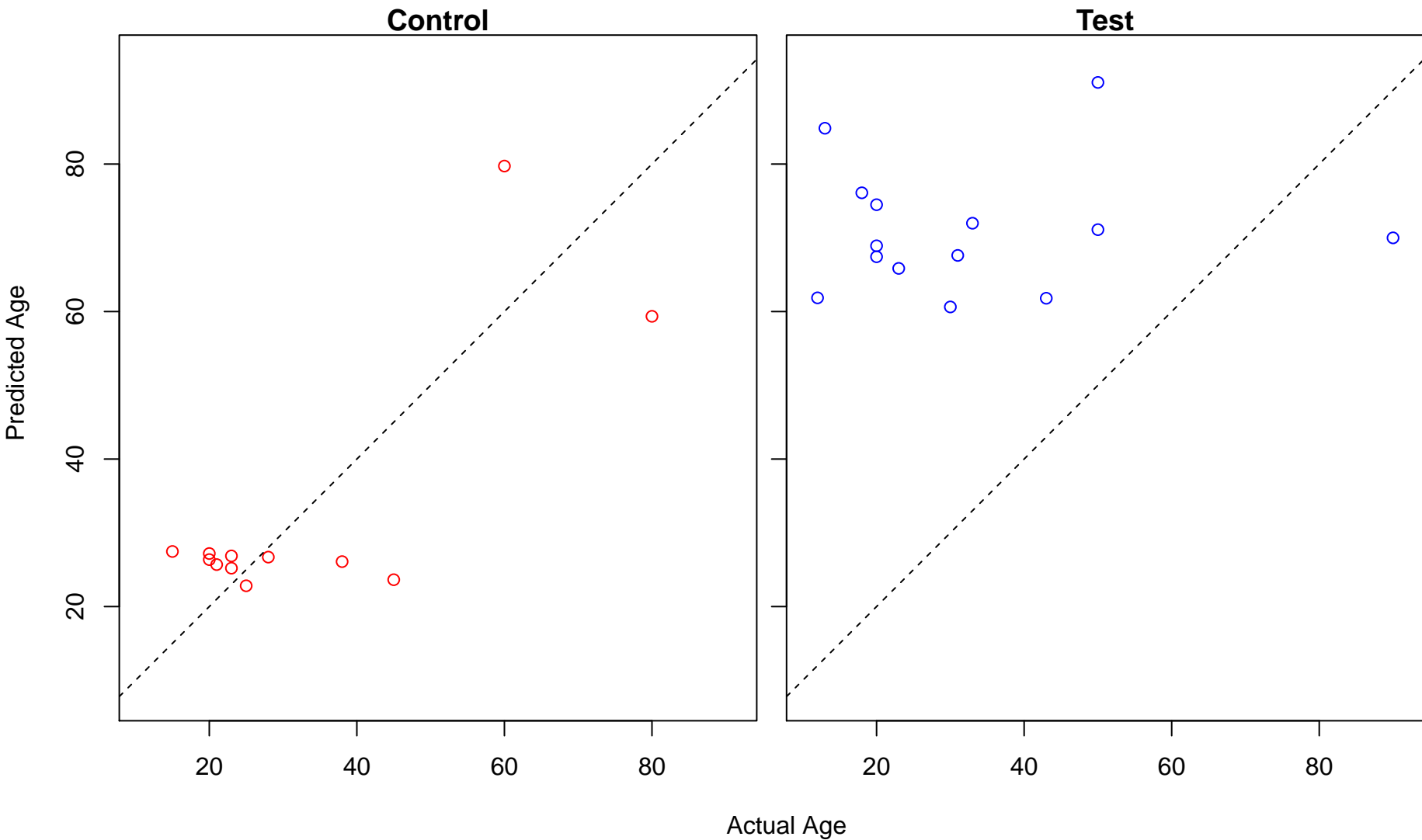
positive regulation of mitochondrial fission (Score: 5.472166)



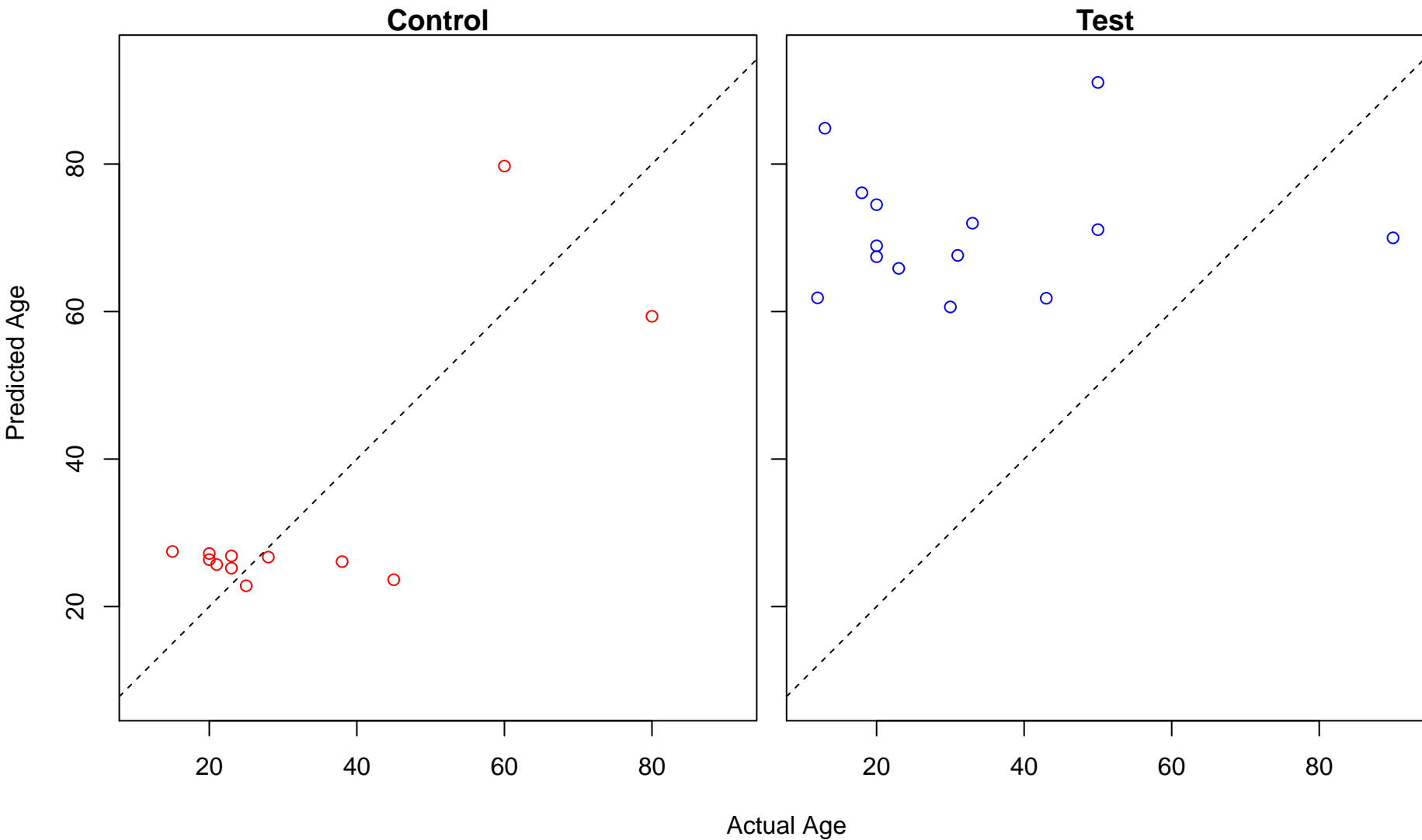
activation of MAPKK activity (Score: 5.470578)



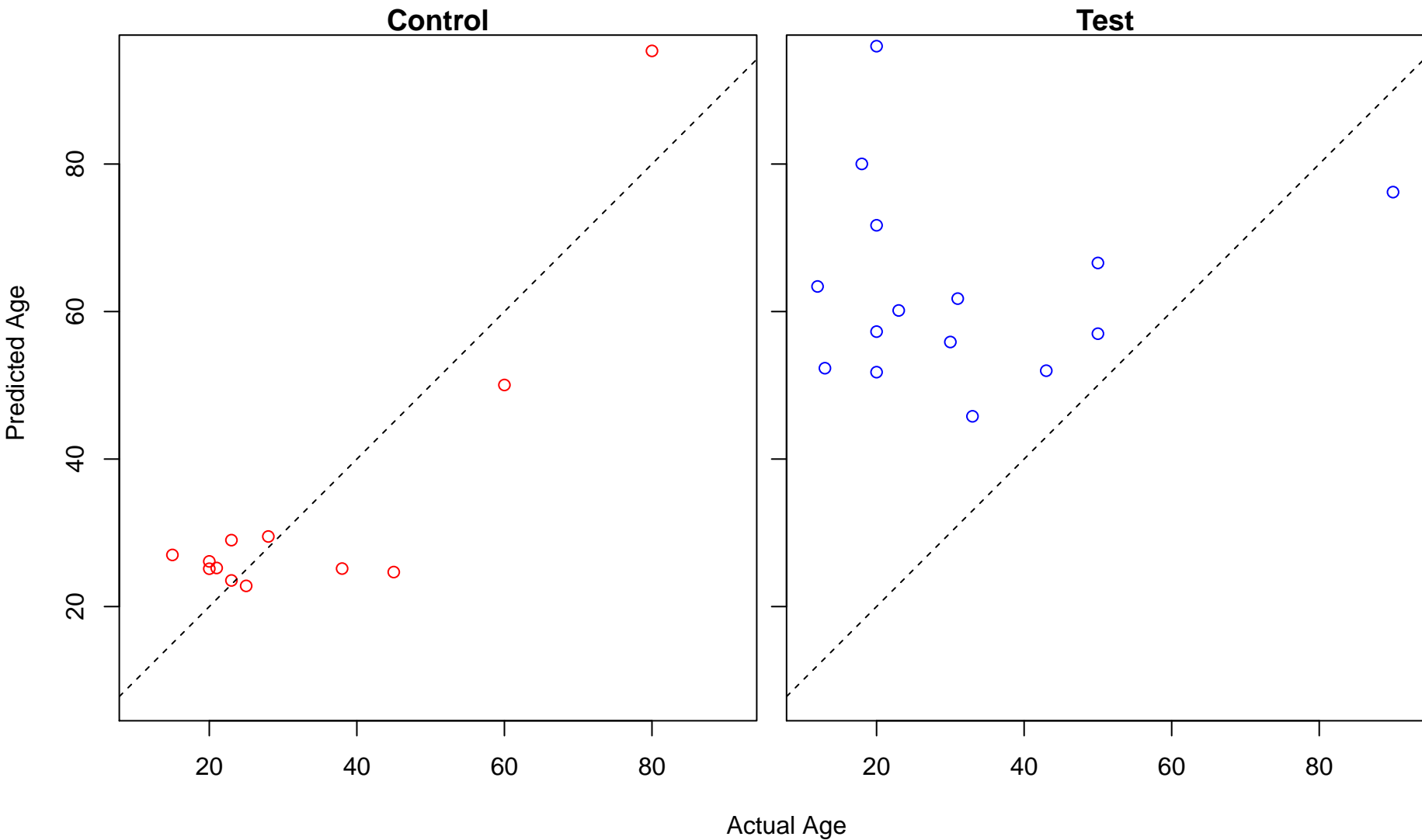
innate immune response activating cell surface receptor signaling pathway (Score: 5.470249)



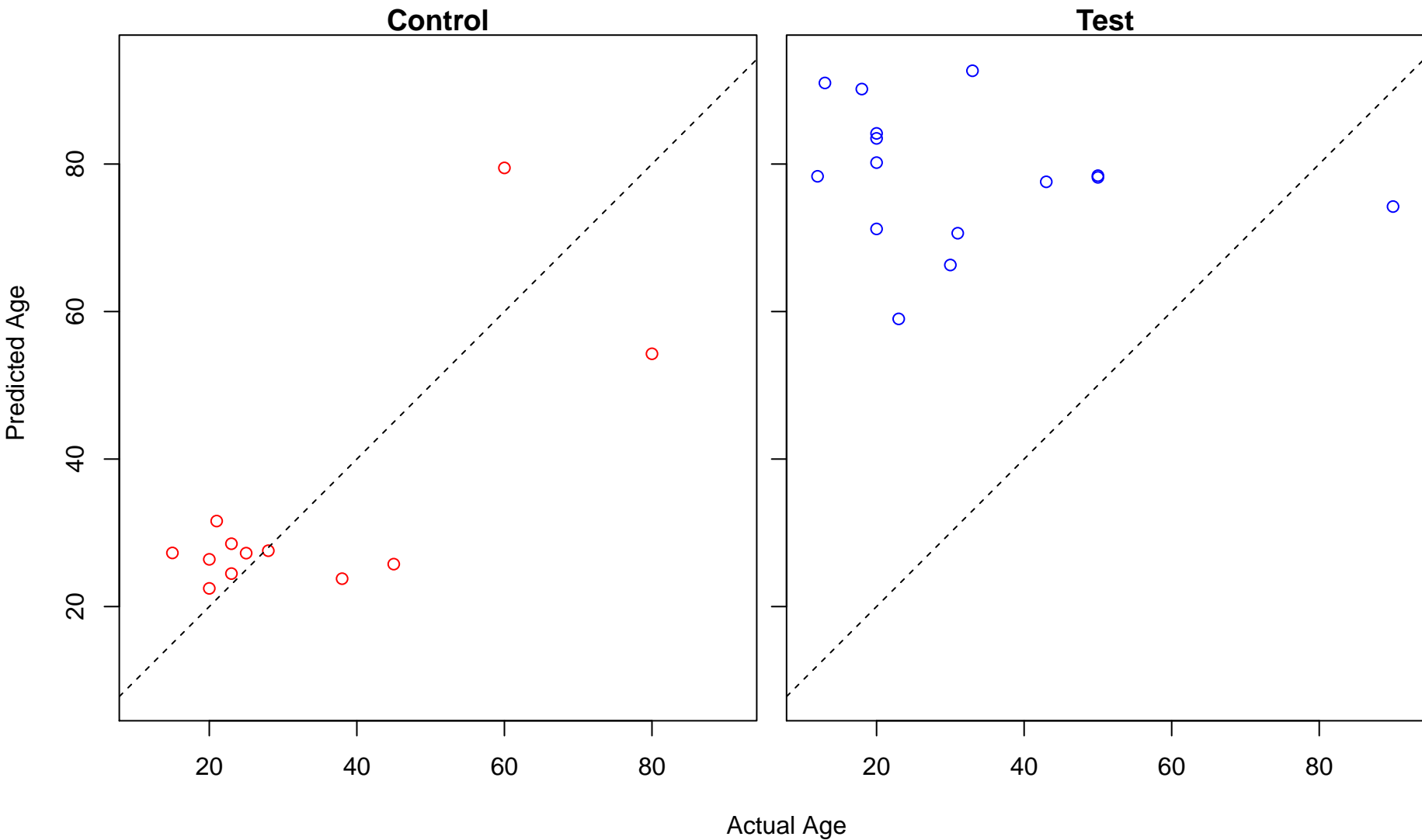
stimulatory C-type lectin receptor signaling pathway (Score: 5.470245)



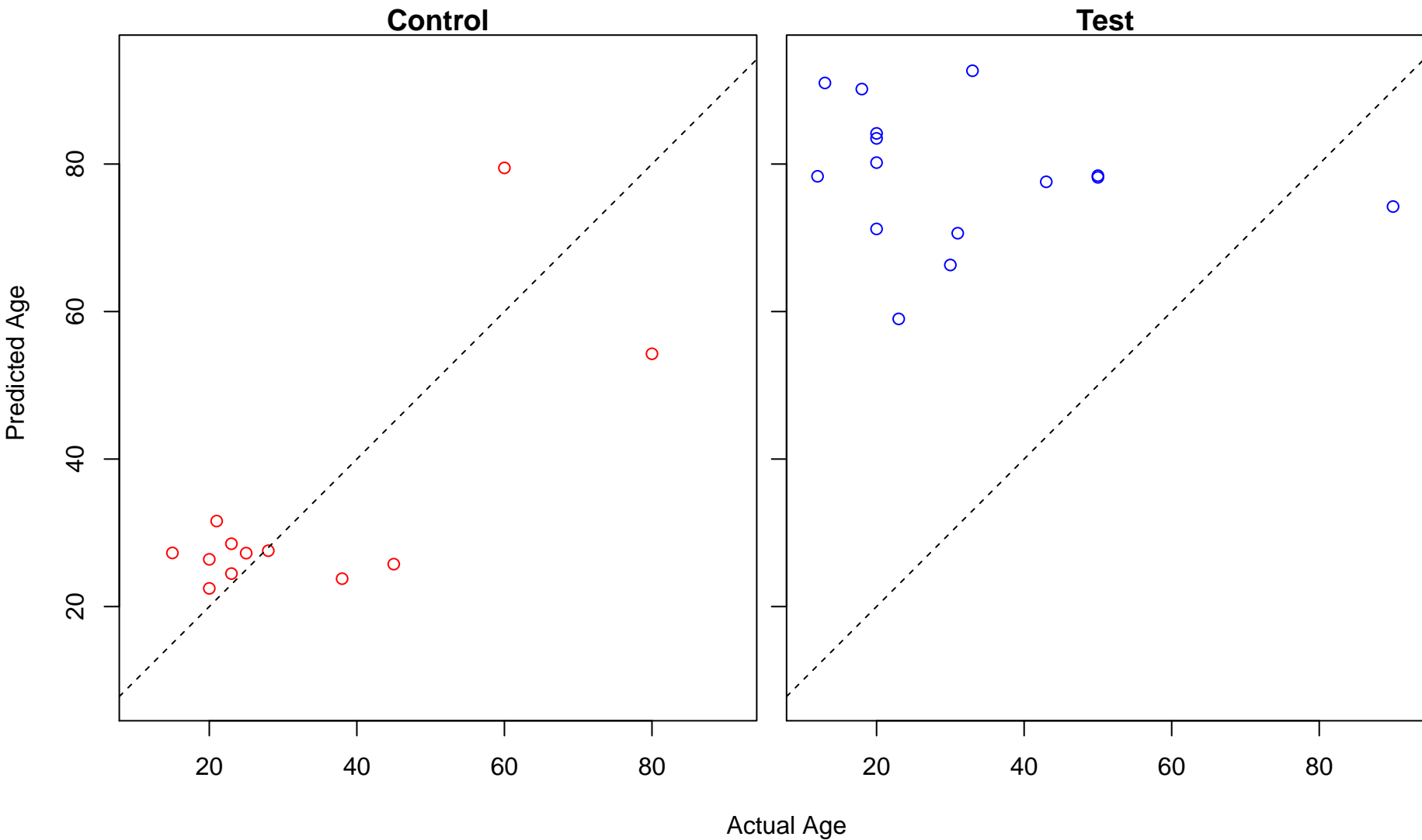
response to transforming growth factor beta (Score: 5.469495)



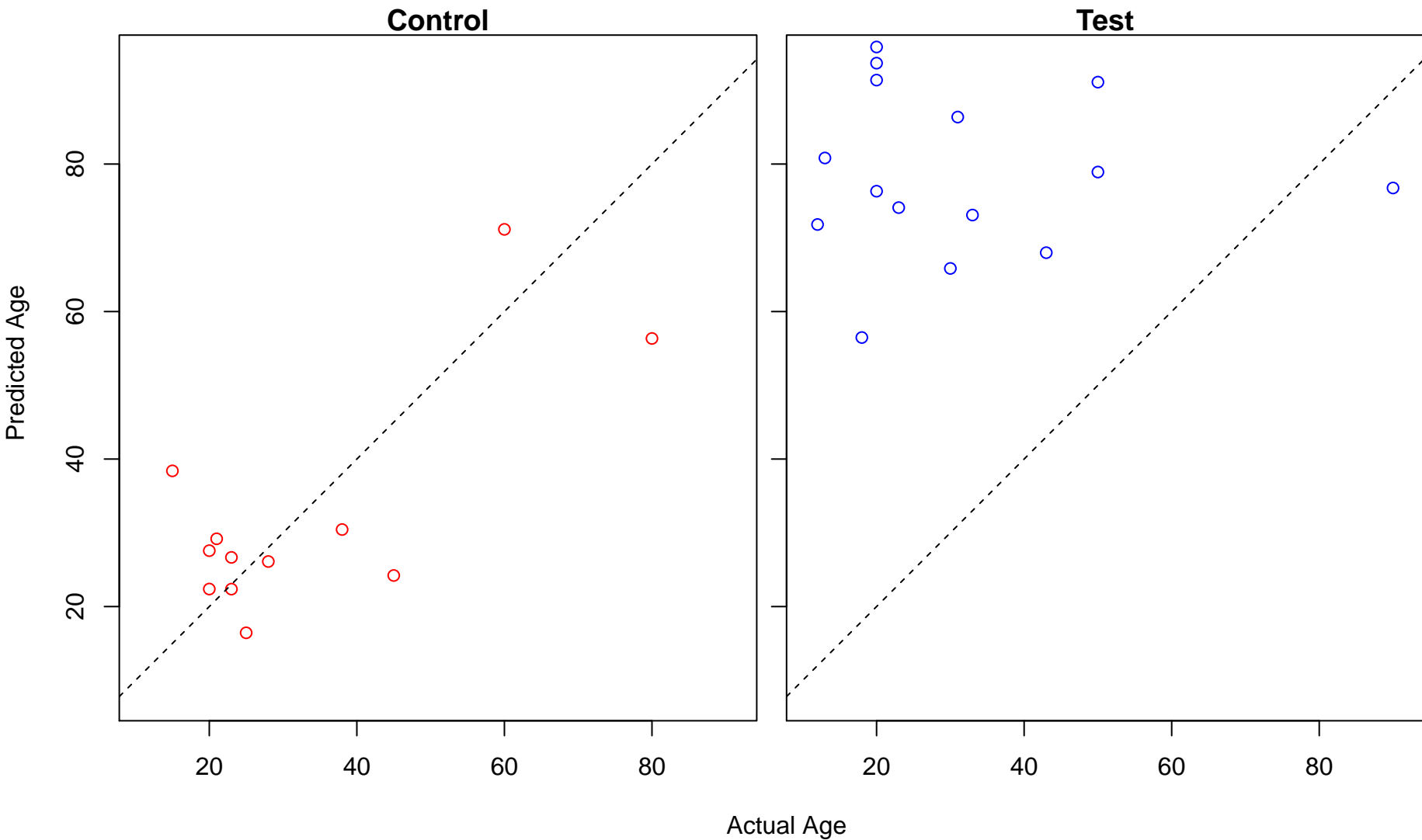
amine catabolic process (Score: 5.467793)



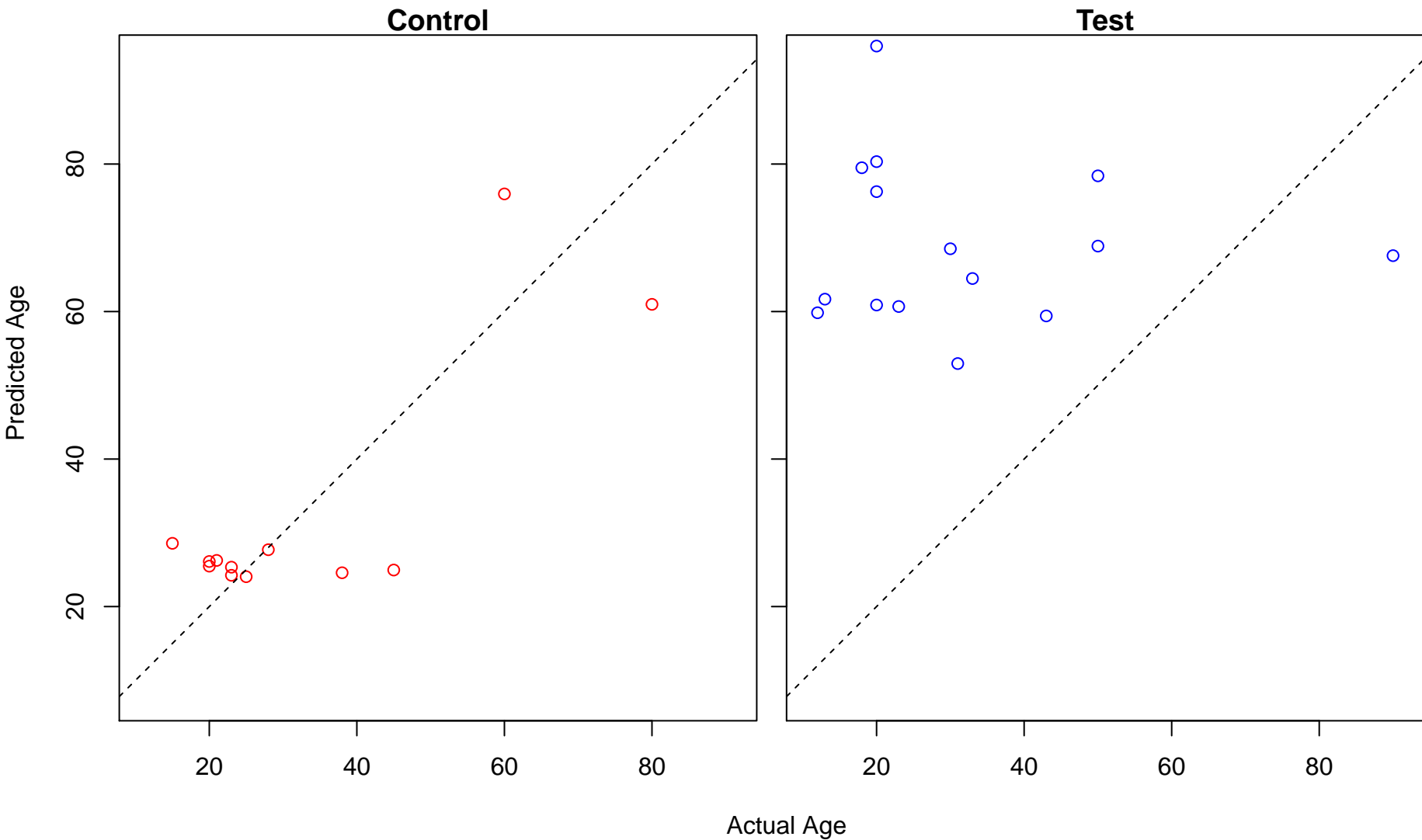
cellular biogenic amine catabolic process (Score: 5.467793)



negative regulation of insulin-like growth factor receptor signaling pathway (Score: 5.466306)

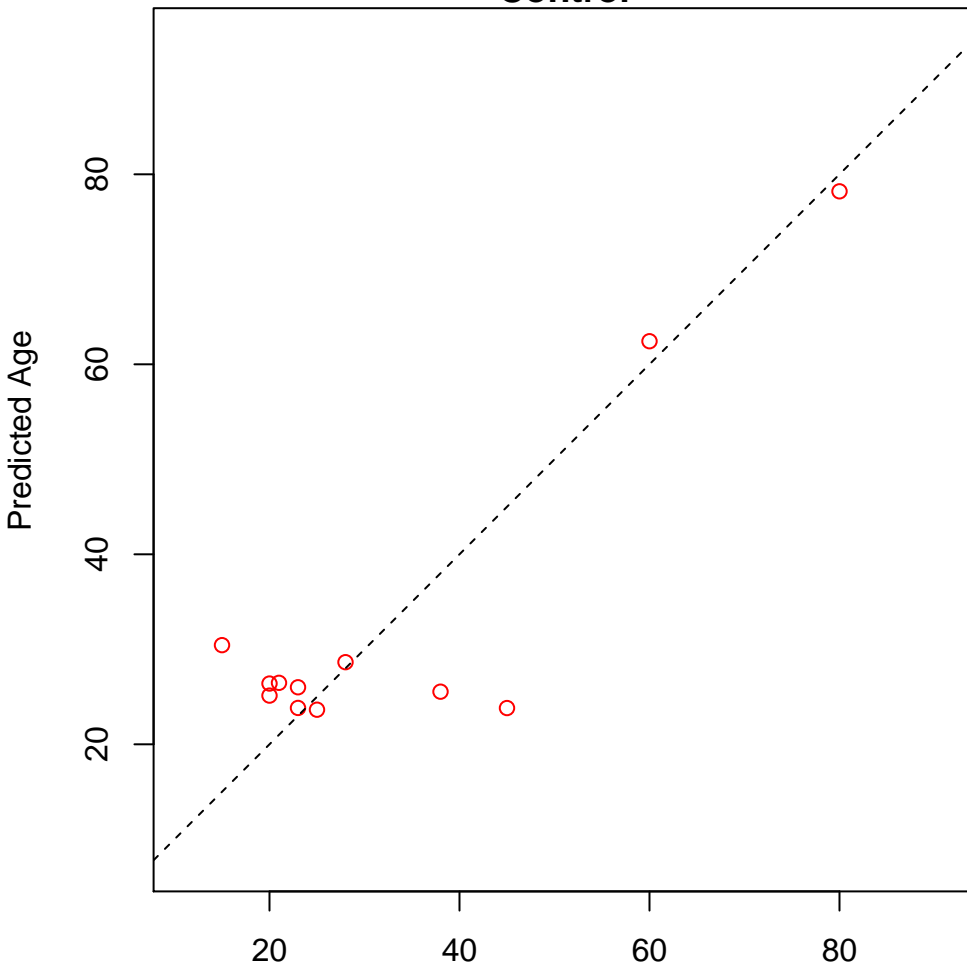


multivesicular body assembly (Score: 5.465322)

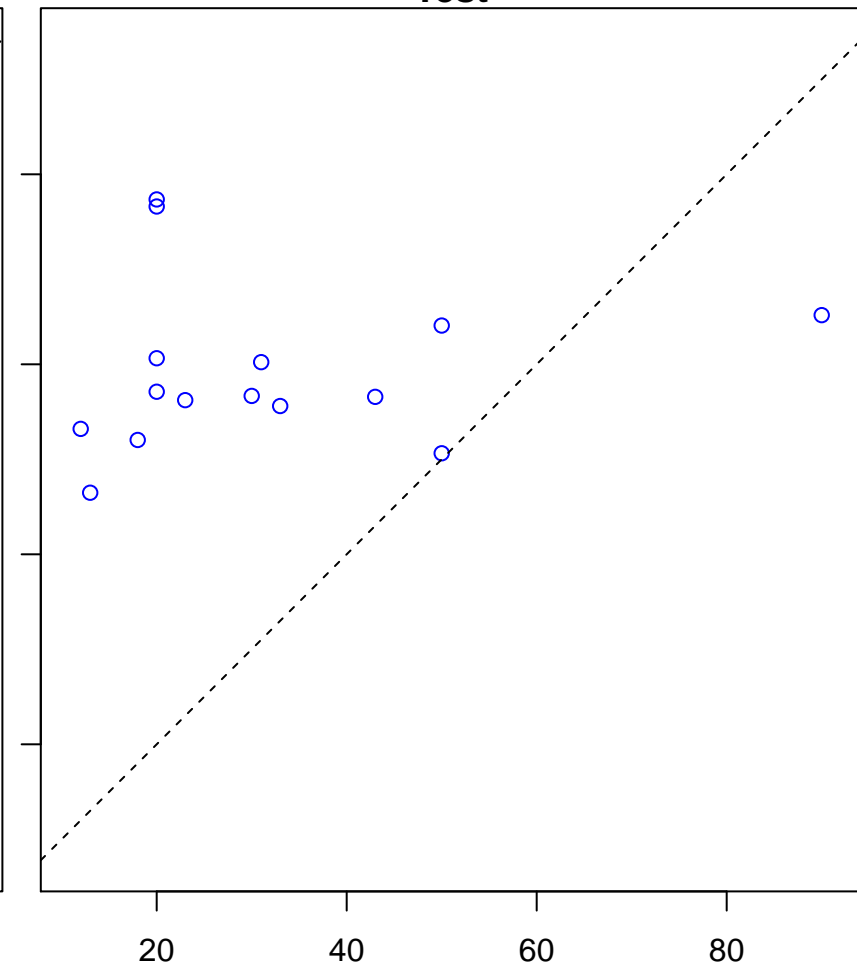


regulation of cell projection organization (Score: 5.464874)

Control

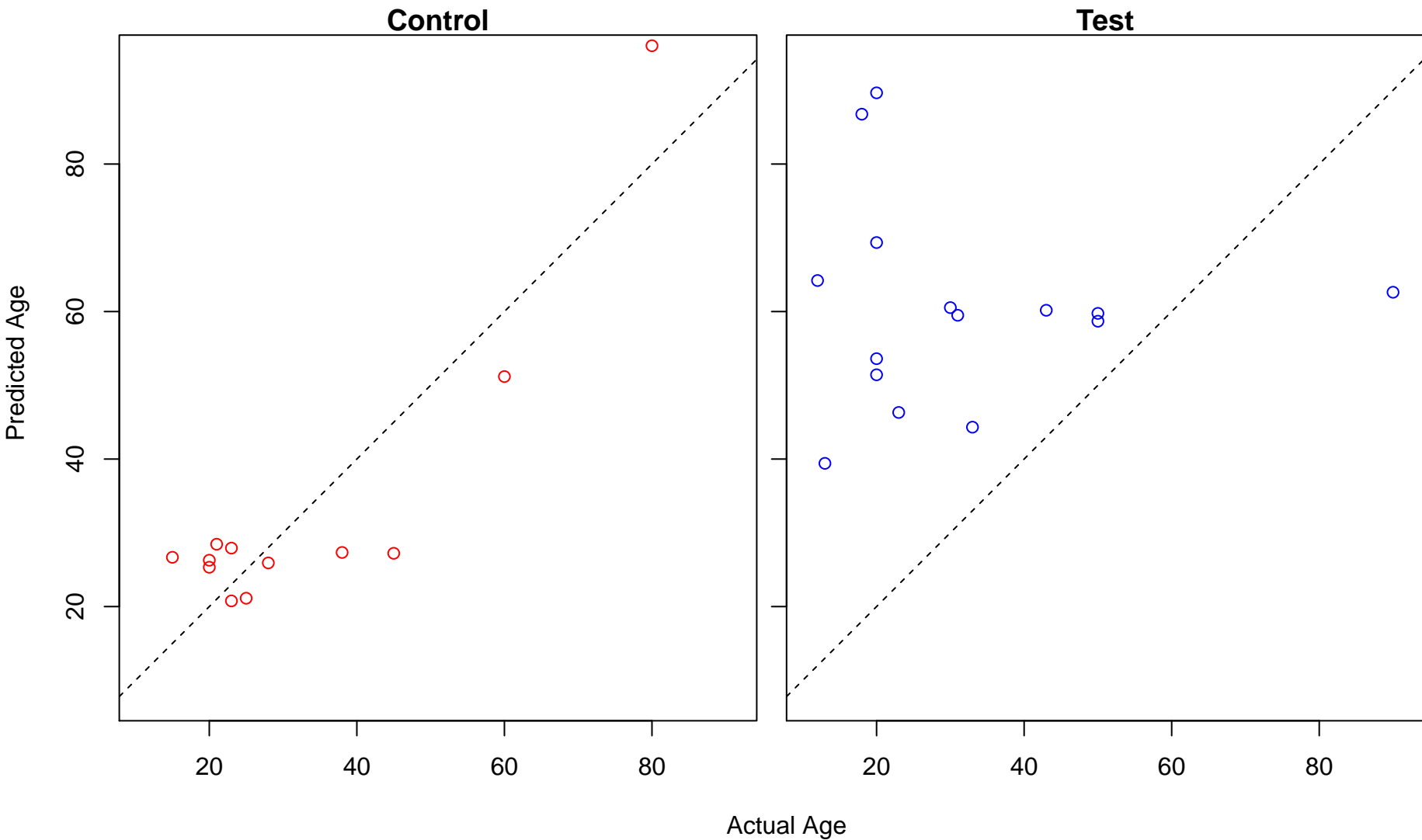


Test



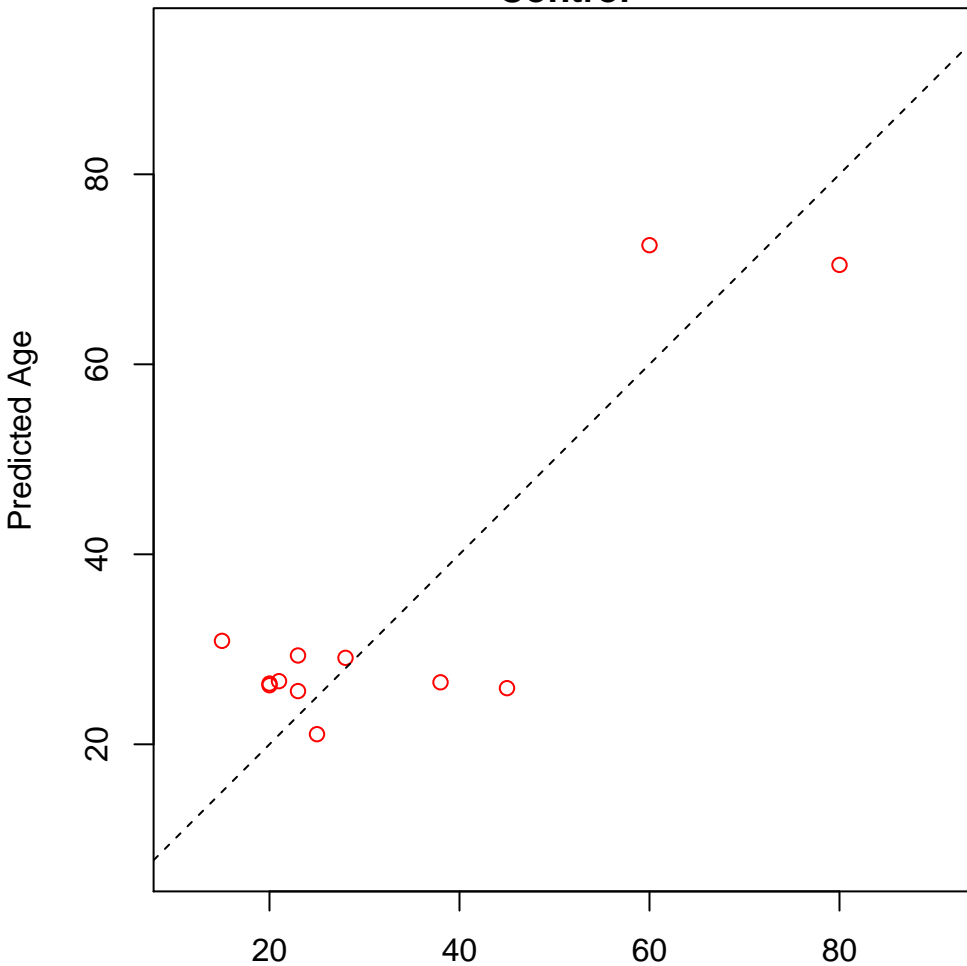
Actual Age

cellular lipid catabolic process (Score: 5.464780)

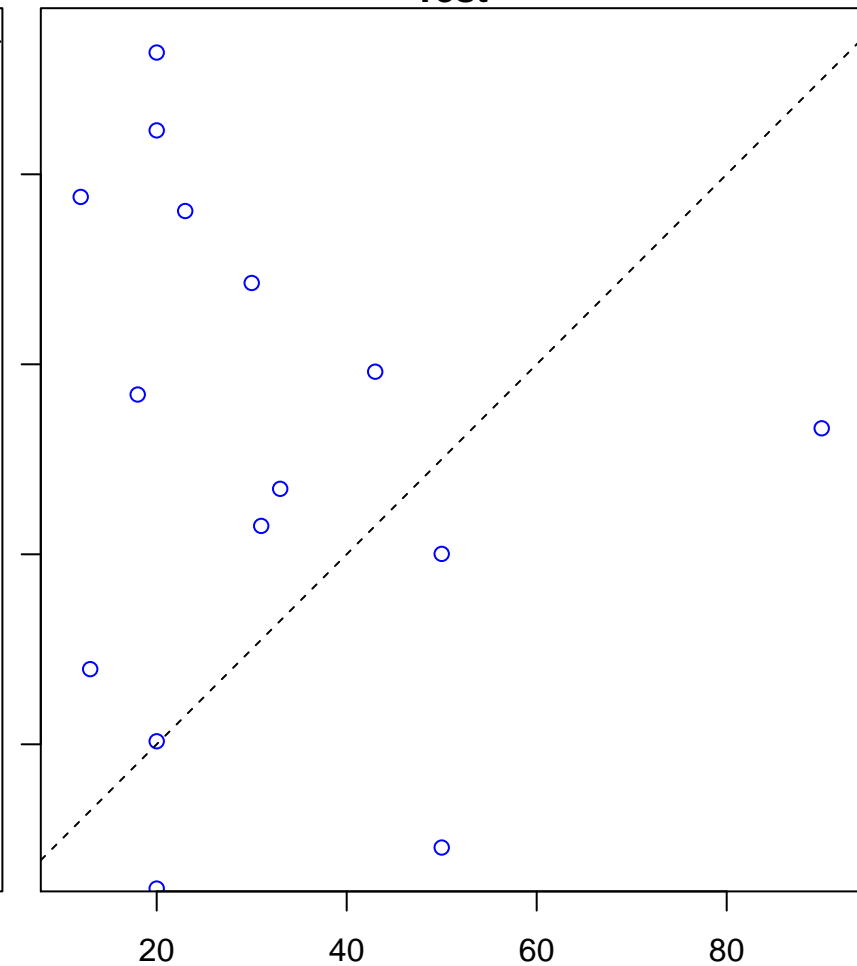


negative regulation of blood circulation (Score: 5.464586)

Control

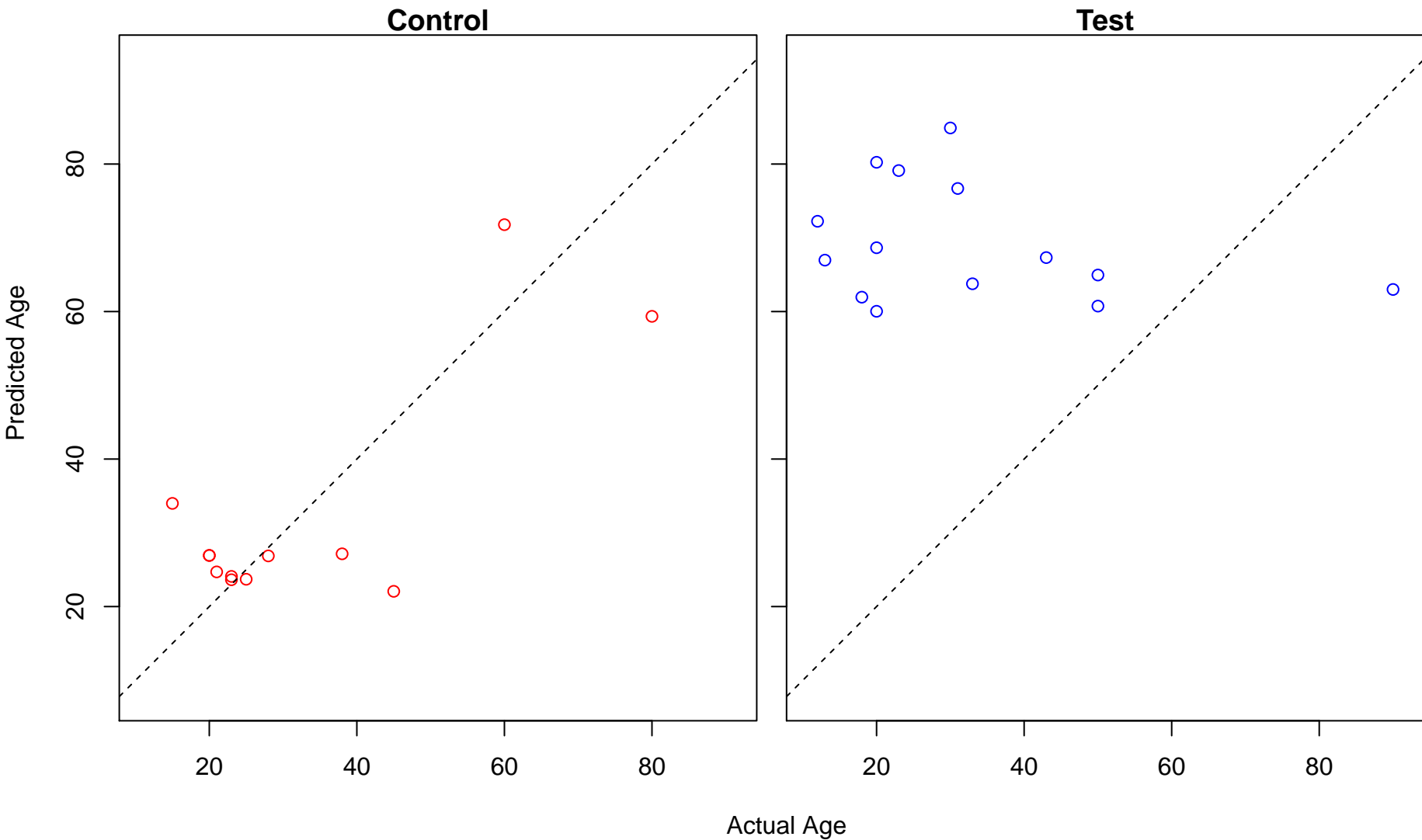


Test

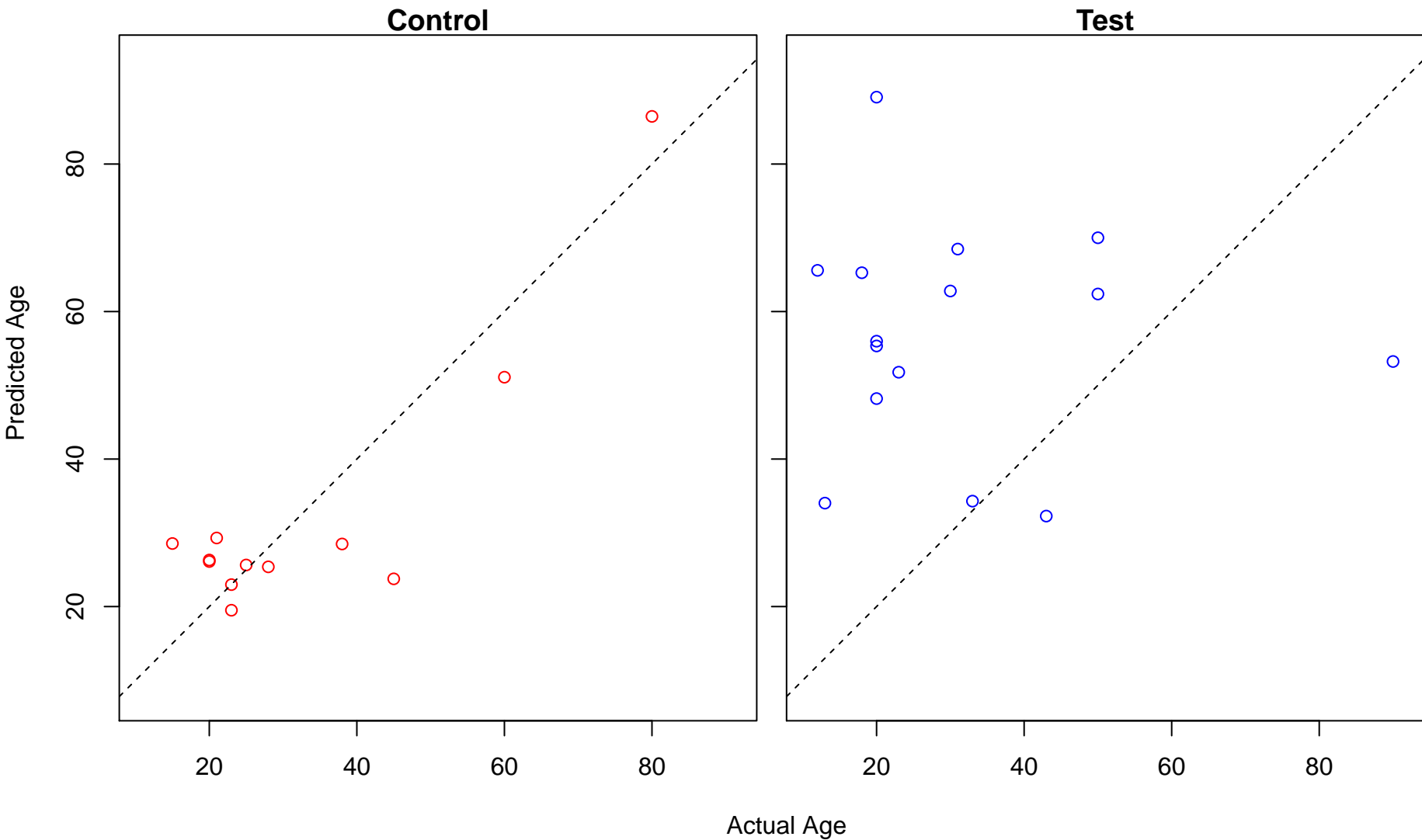


Actual Age

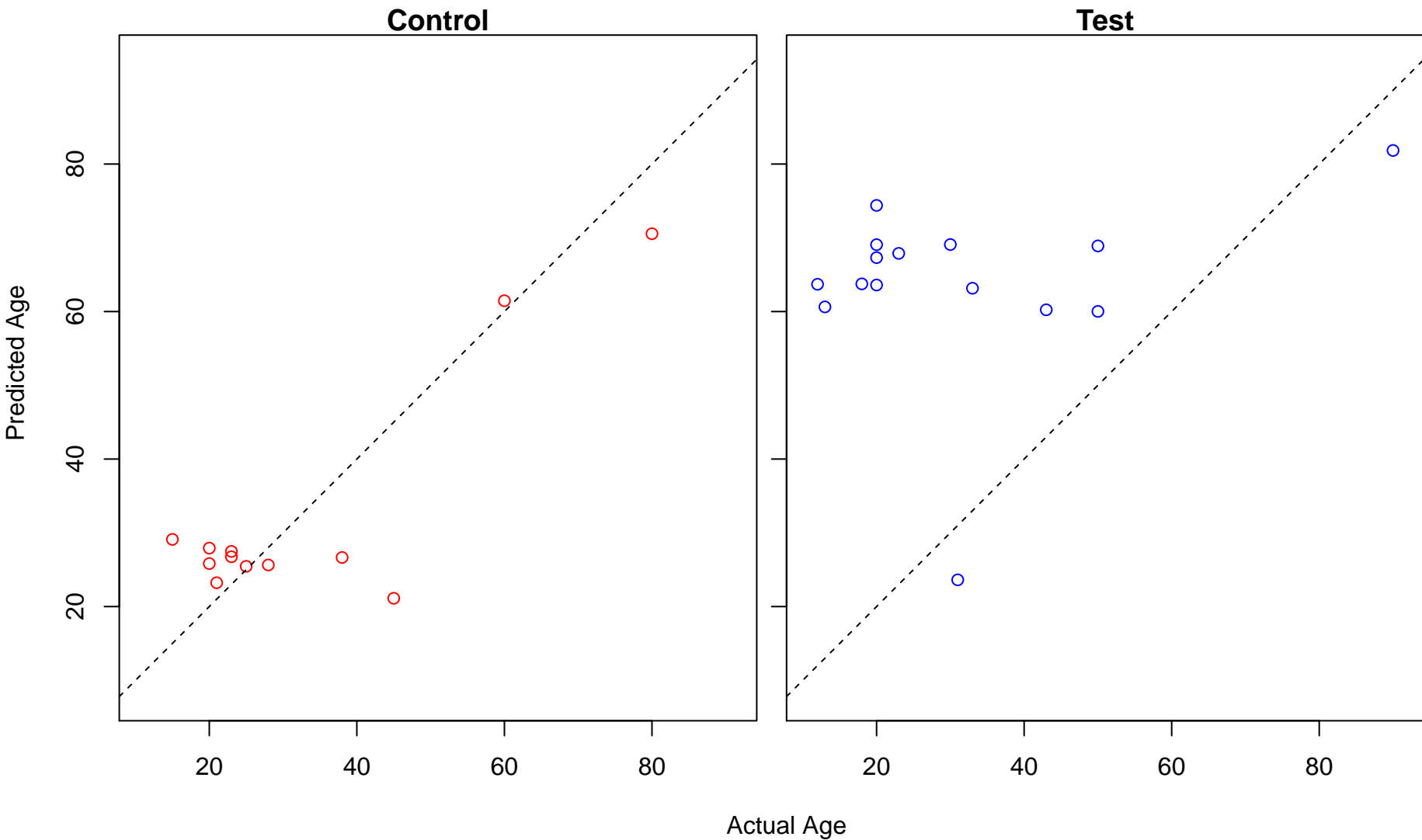
cellular response to leptin stimulus (Score: 5.463626)



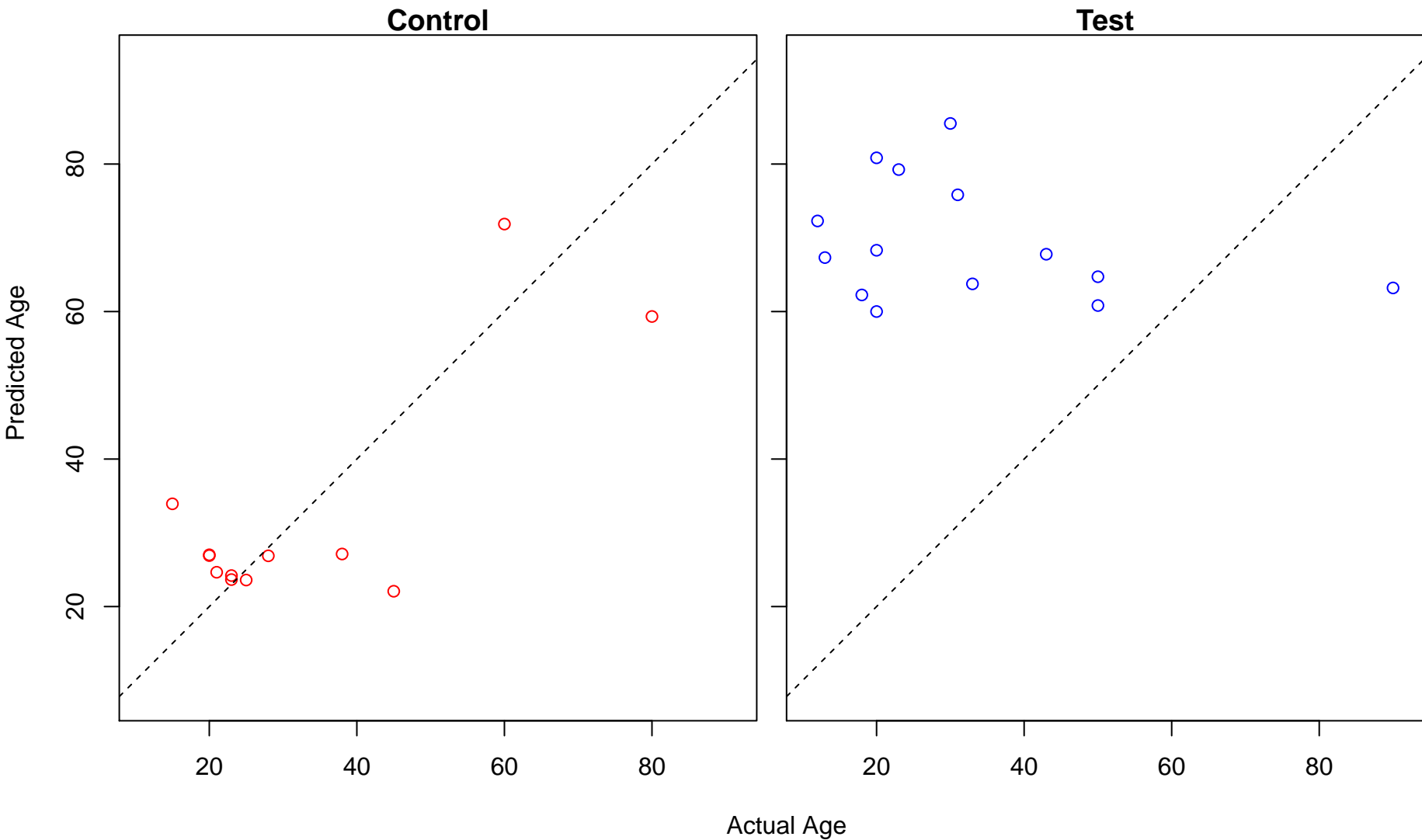
nucleobase-containing small molecule interconversion (Score: 5.462435)



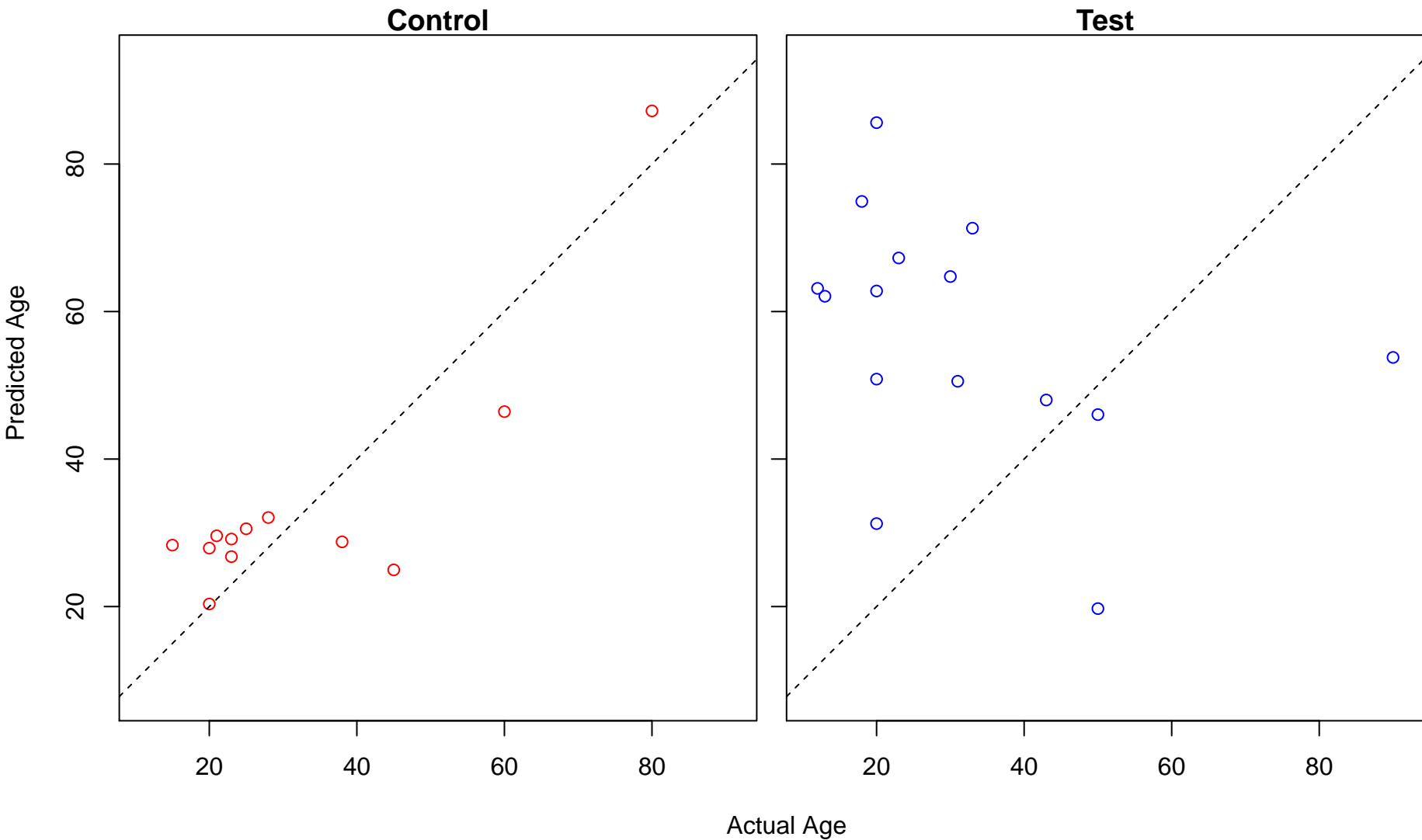
cardiac muscle cell contraction (Score: 5.461695)



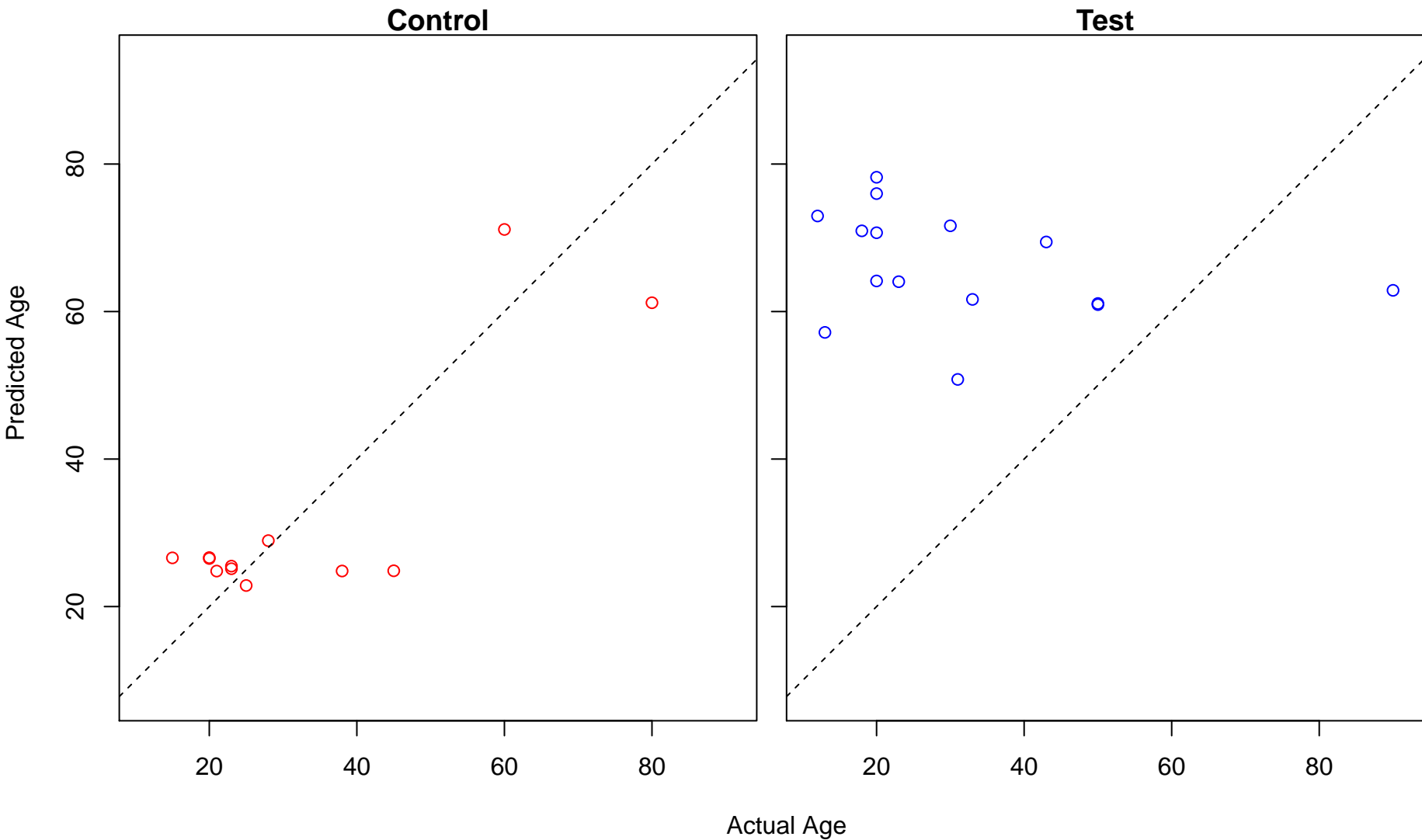
response to leptin (Score: 5.460654)



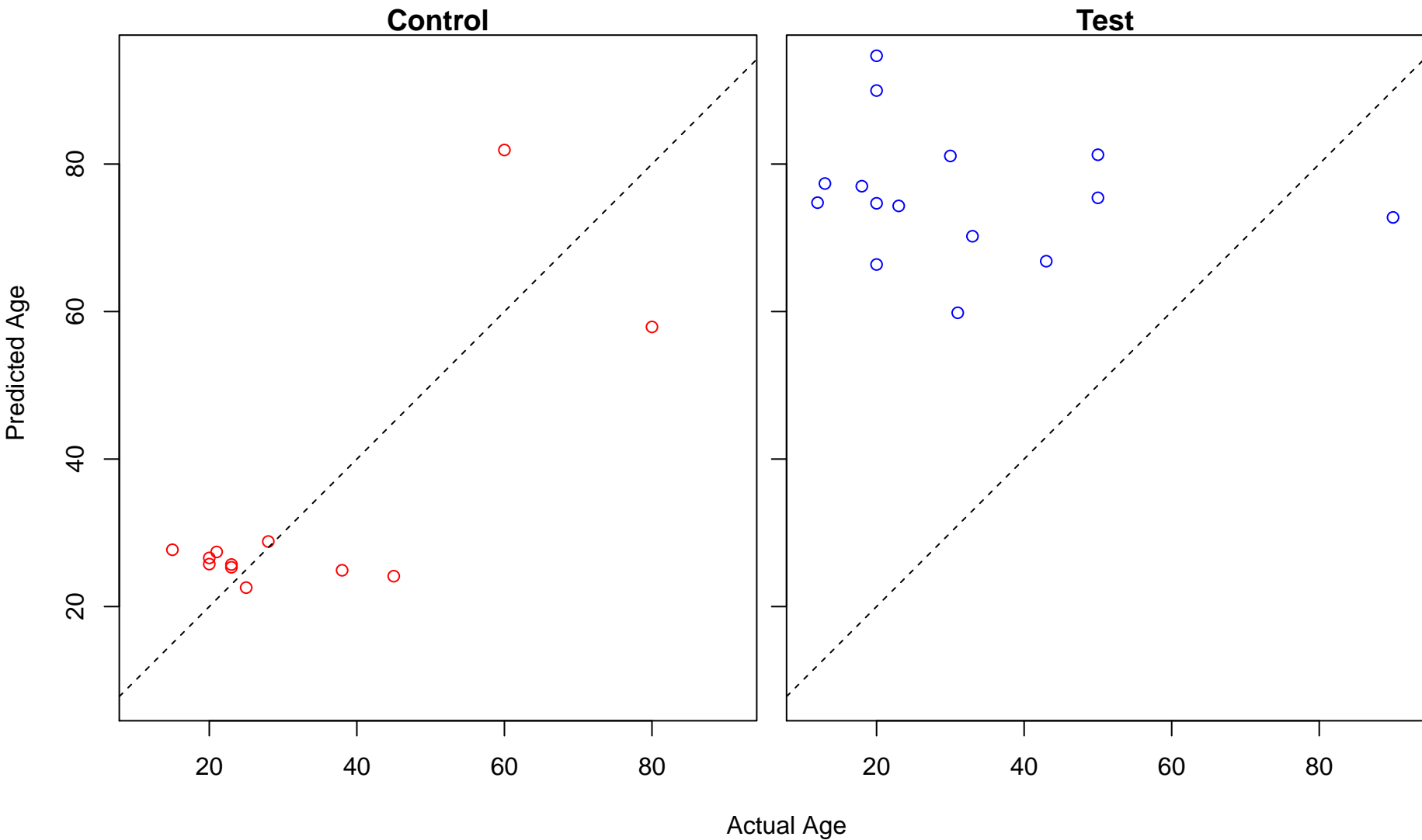
regulation of neuron differentiation (Score: 5.454555)



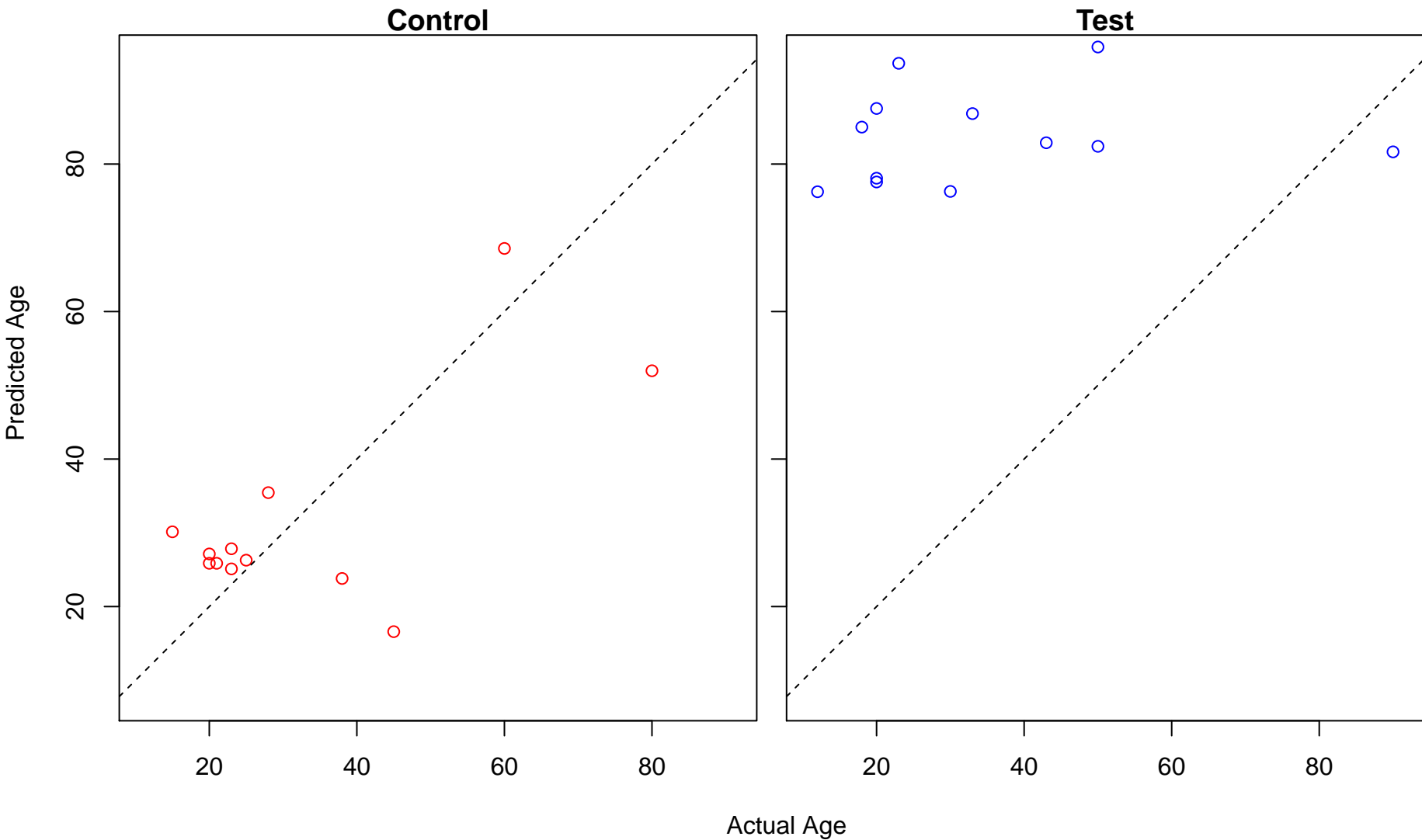
positive regulation of helicase activity (Score: 5.451985)



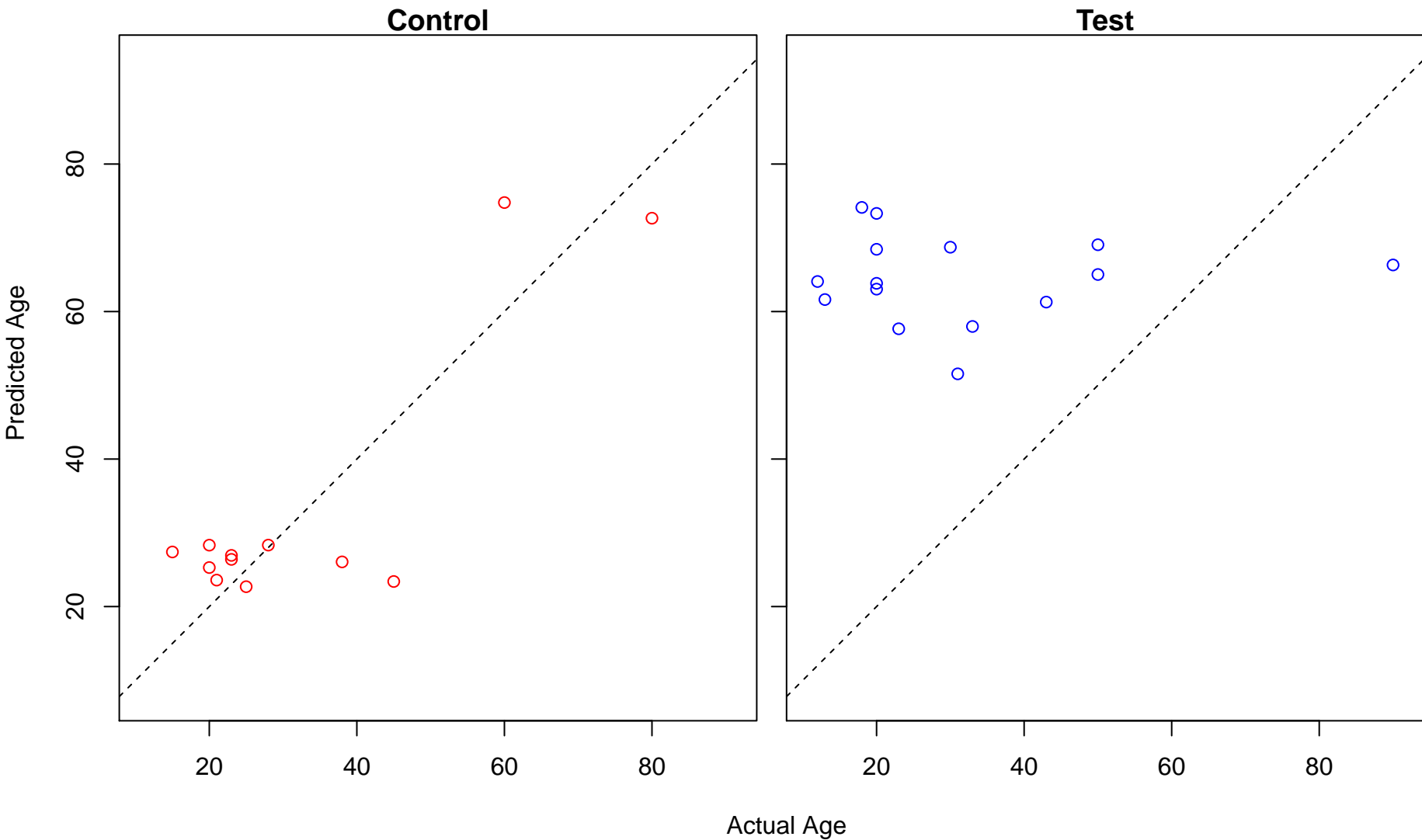
peroxisome fission (Score: 5.450943)



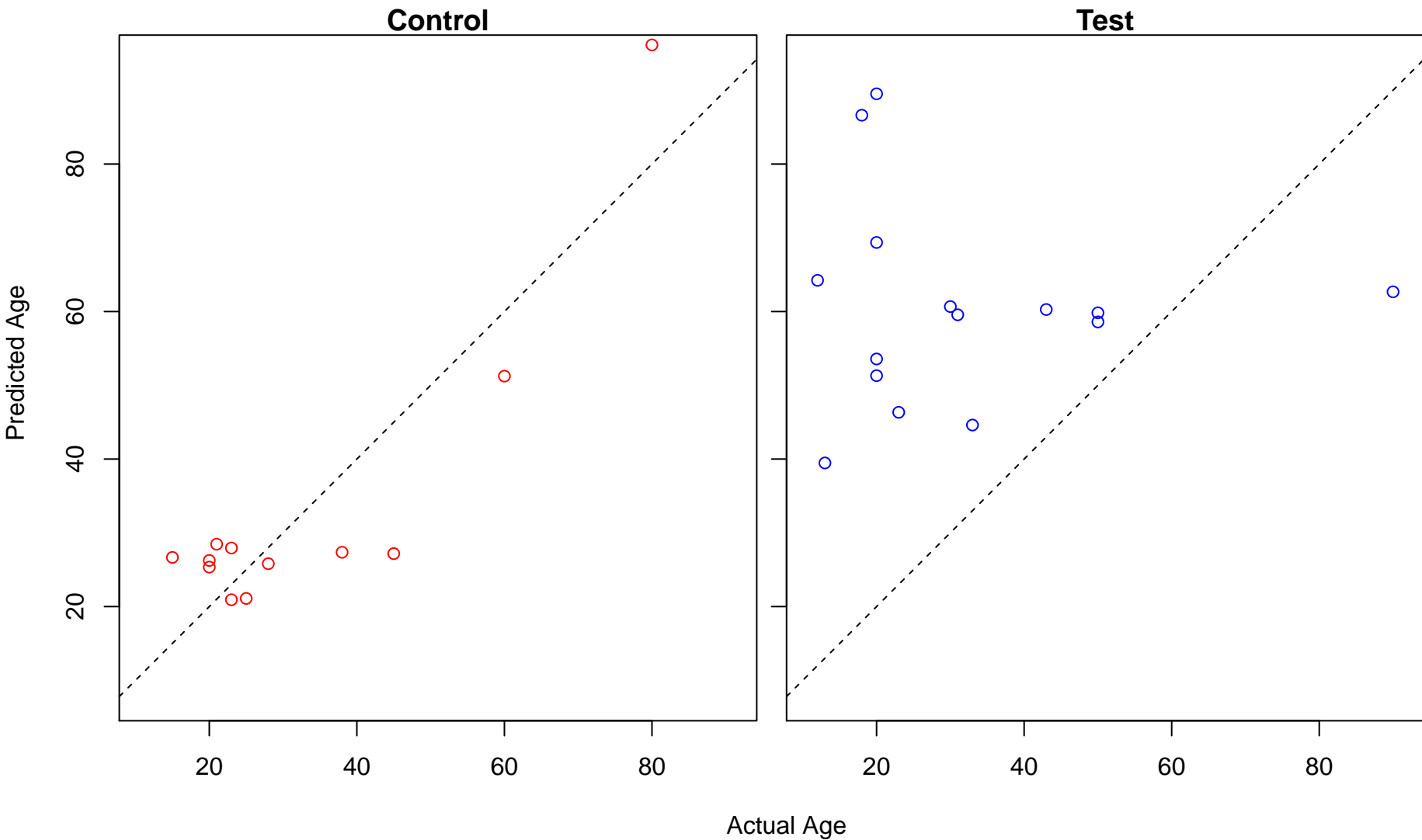
regulation of respiratory system process (Score: 5.450446)



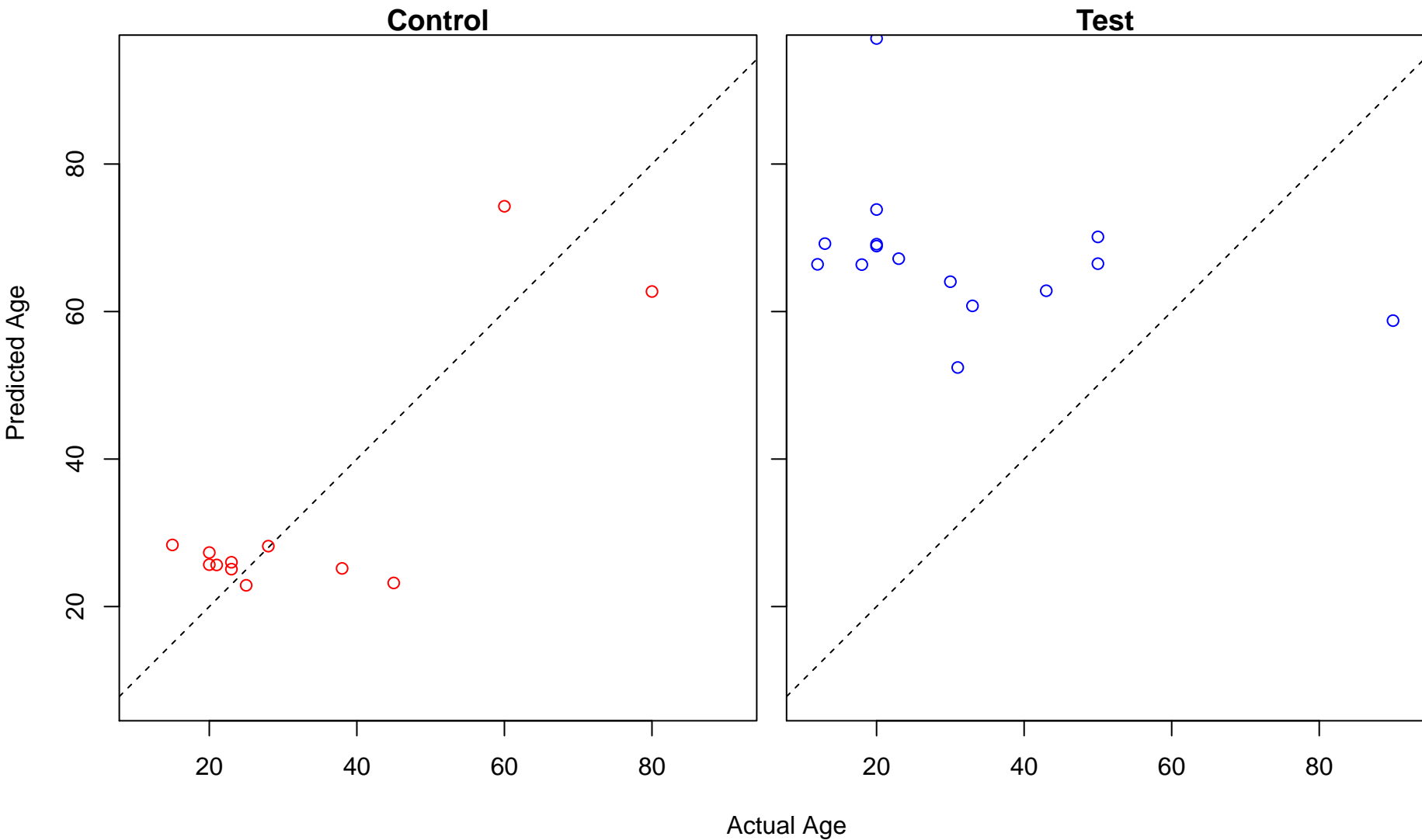
endoplasmic reticulum unfolded protein response (Score: 5.450161)



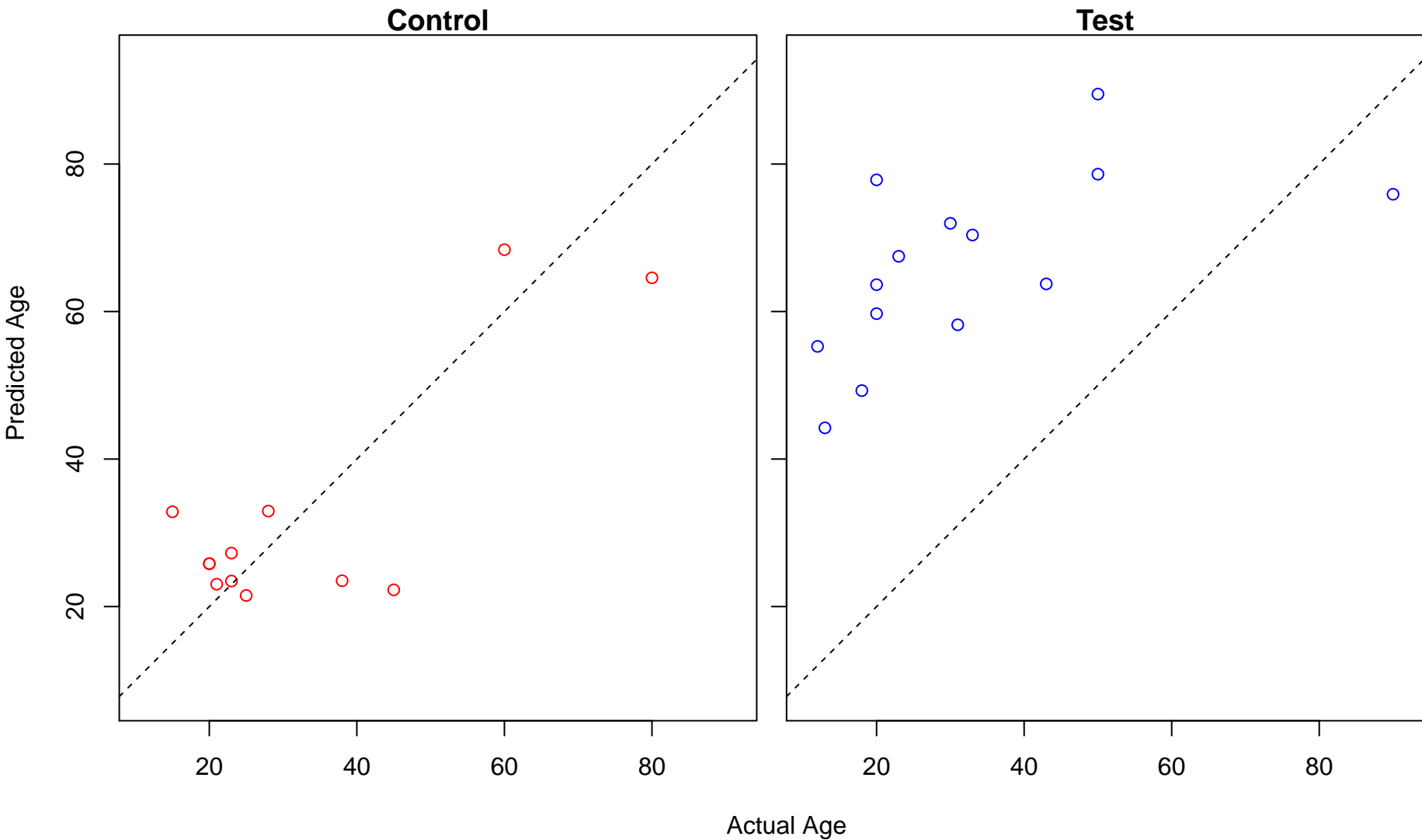
lipid catabolic process (Score: 5.449283)



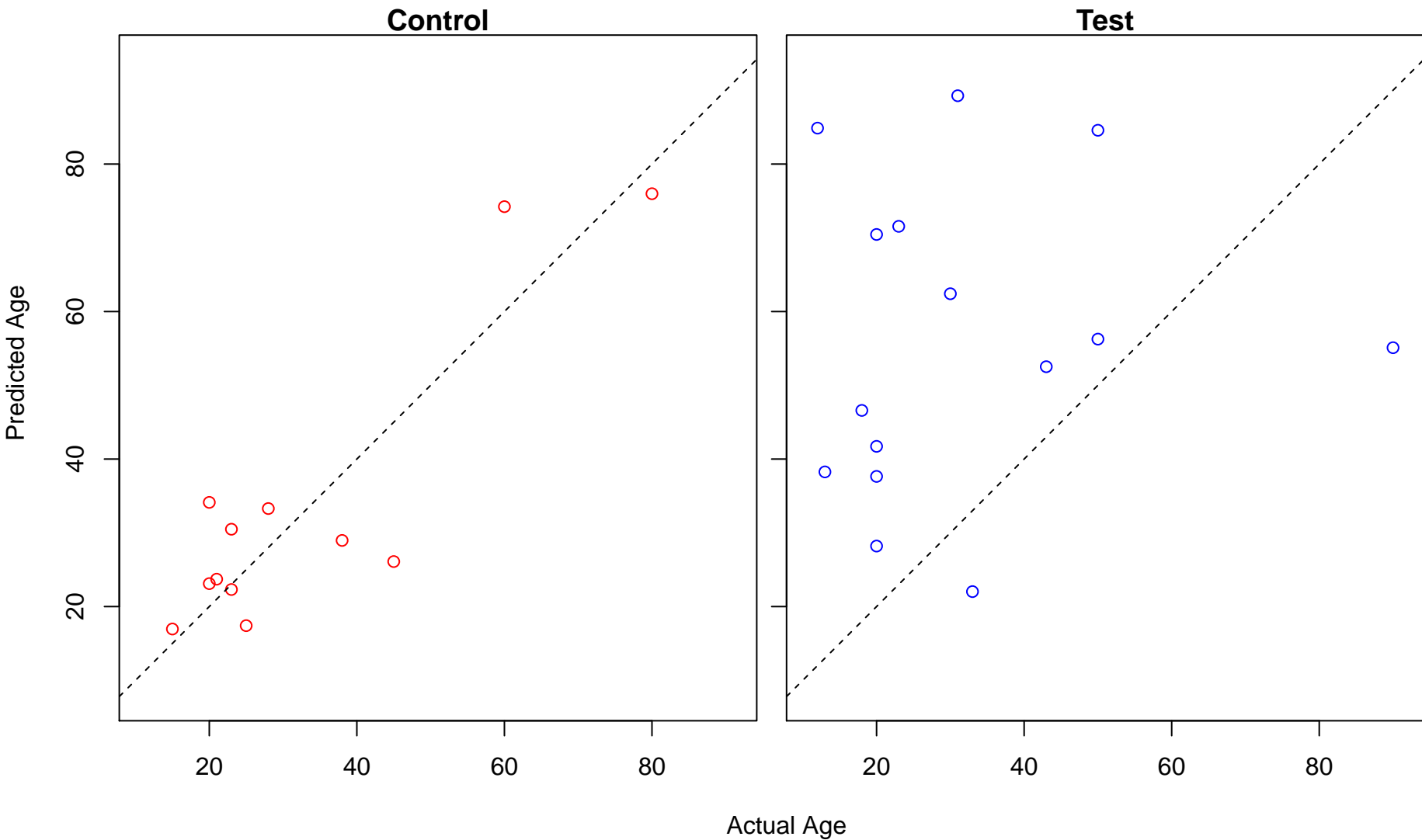
inner ear development (Score: 5.448618)



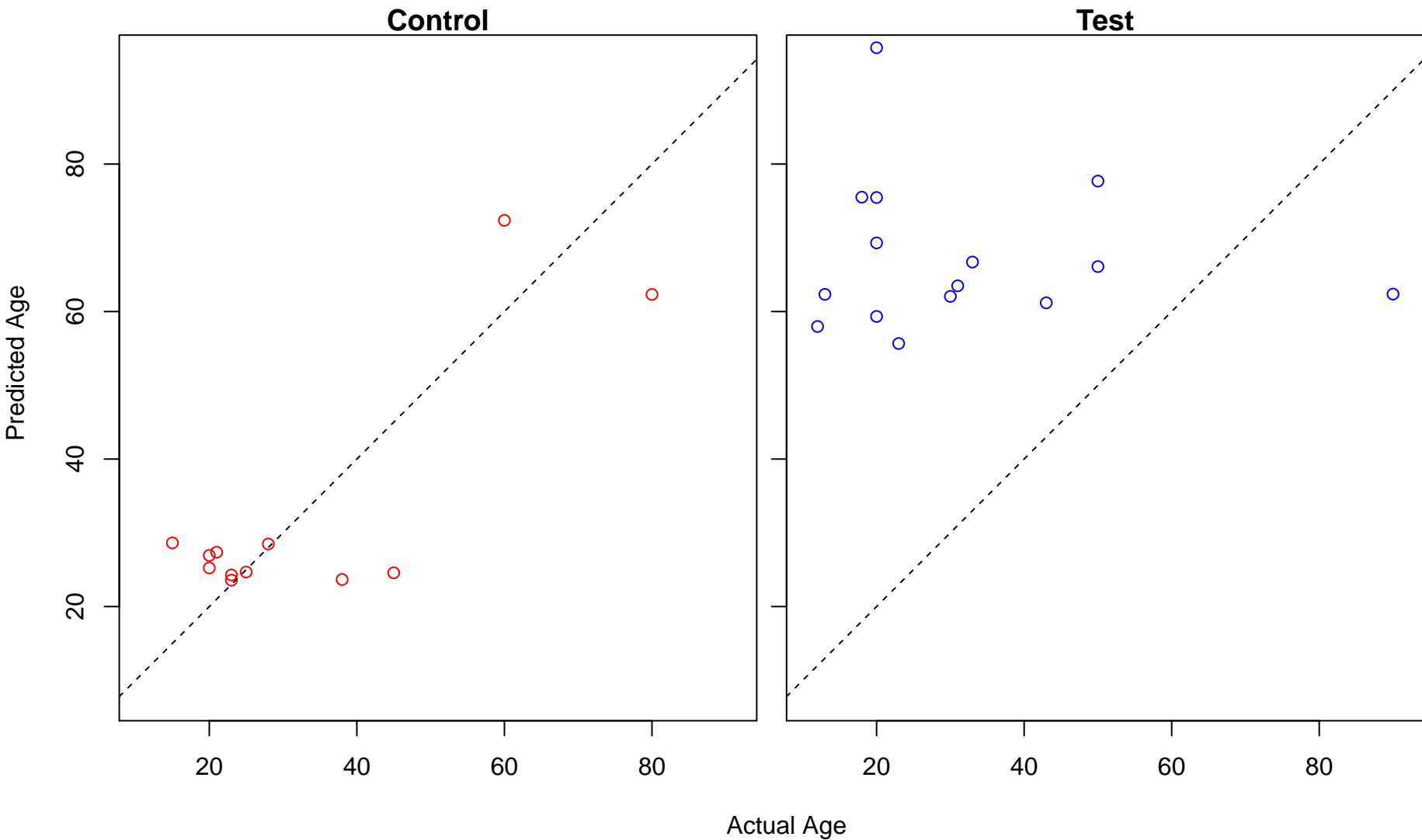
hemidesmosome assembly (Score: 5.444816)



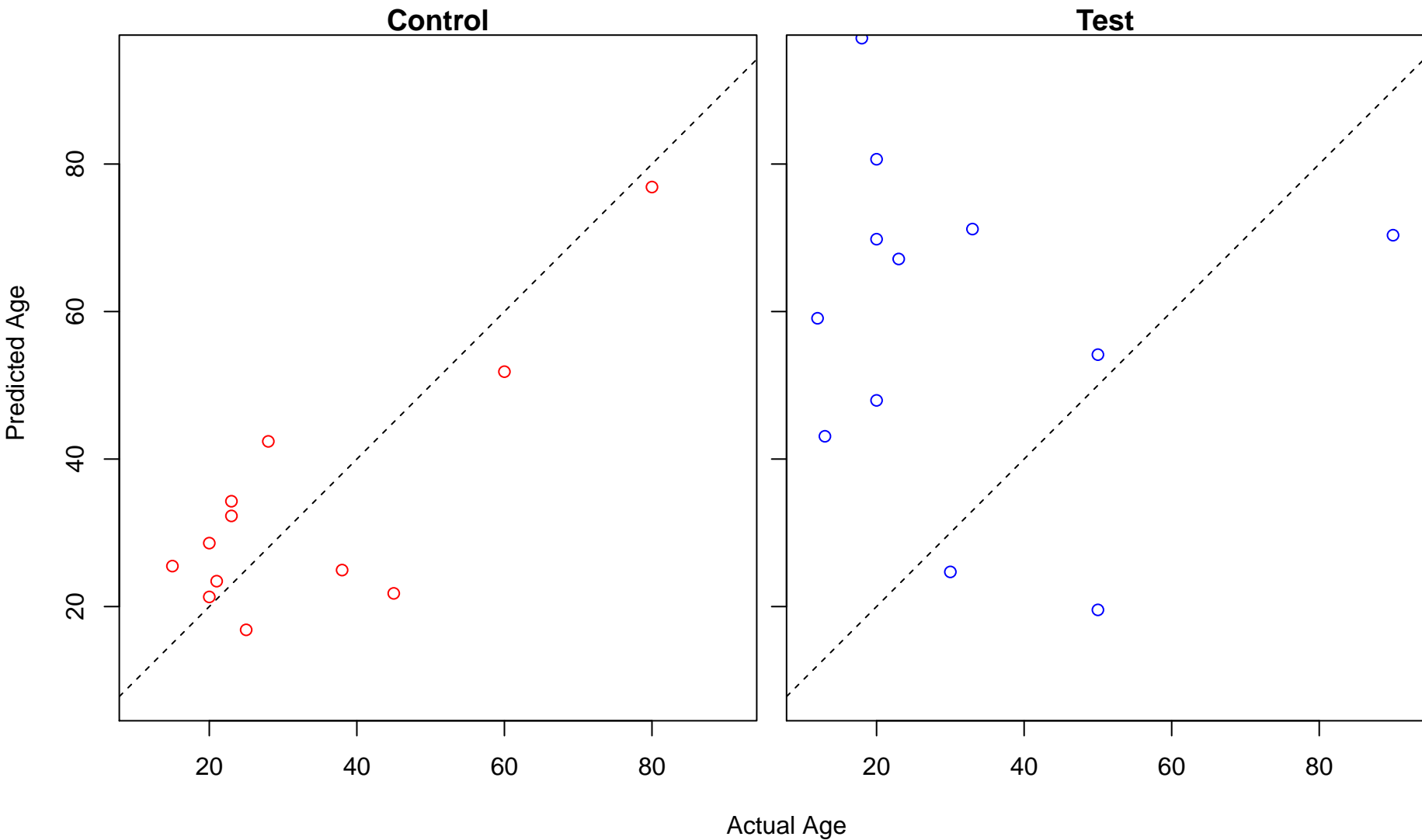
positive regulation of keratinocyte proliferation (Score: 5.442708)



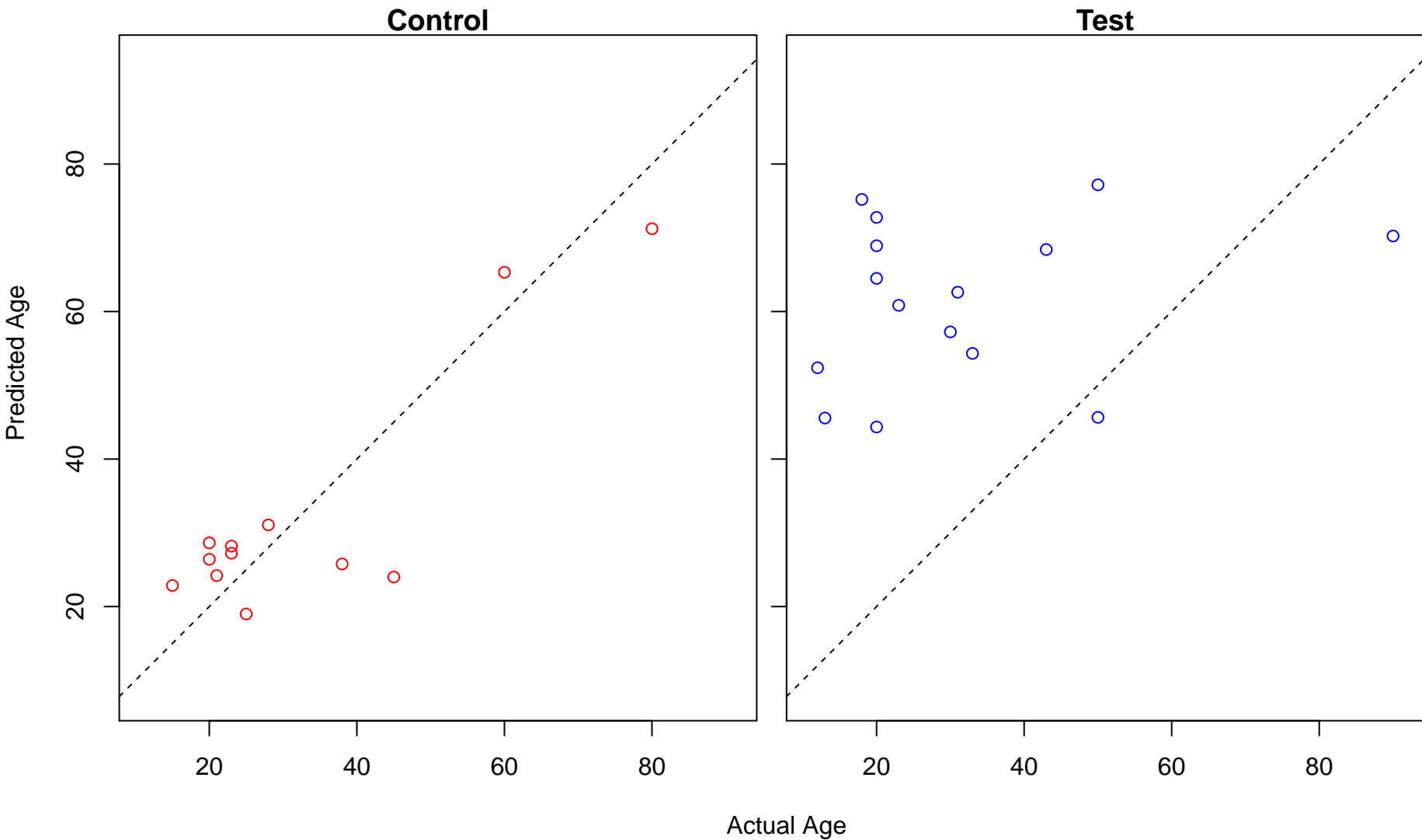
positive regulation of substrate adhesion–dependent cell spreading (Score: 5.442266)



regulation of axonogenesis (Score: 5.440873)

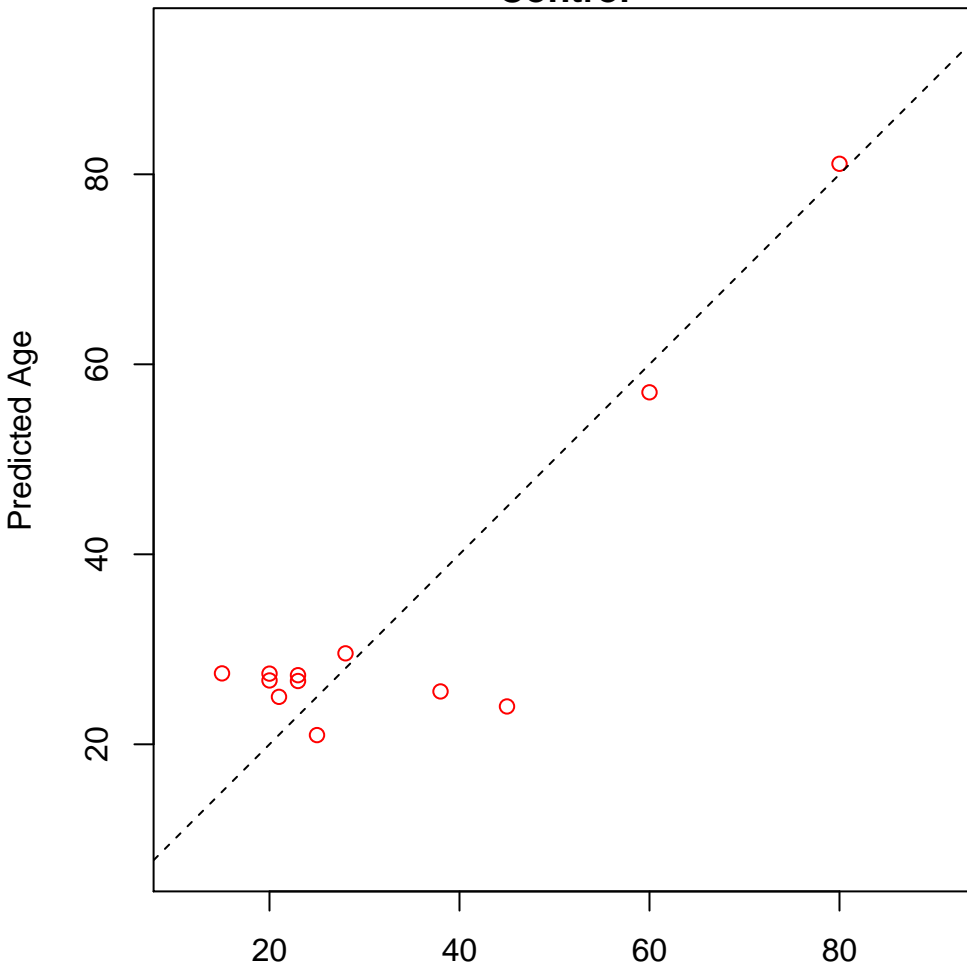


negative regulation of exocytosis (Score: 5.440455)

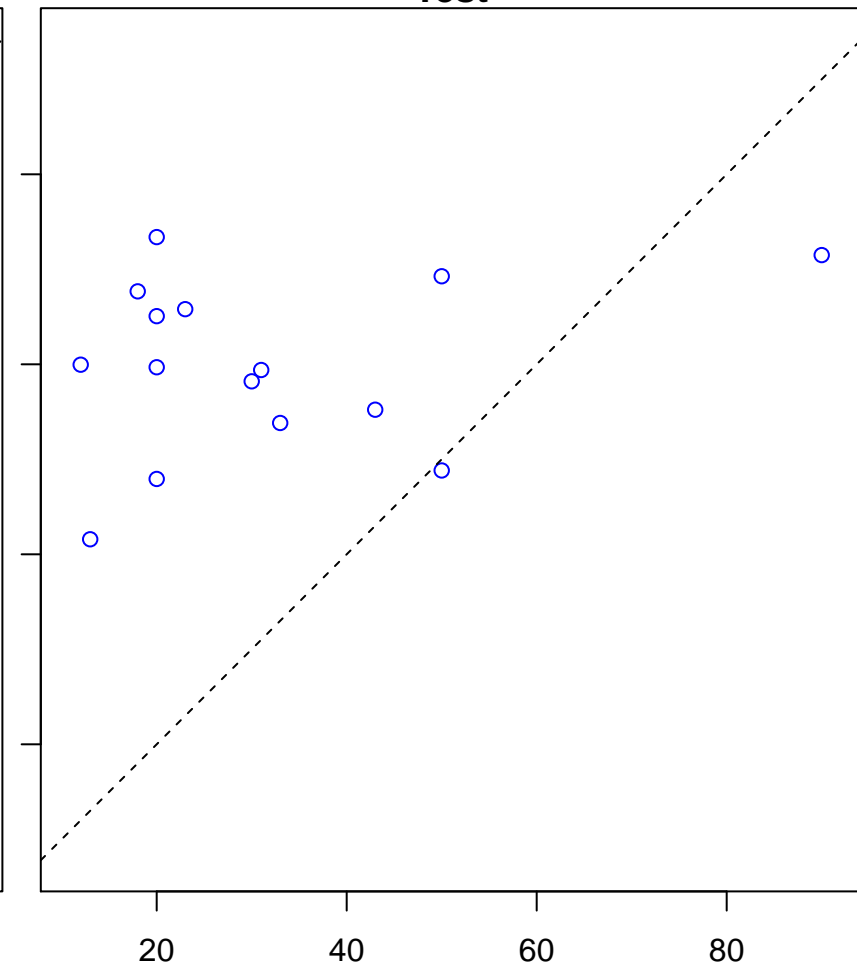


regulation of autophagosome assembly (Score: 5.439781)

Control

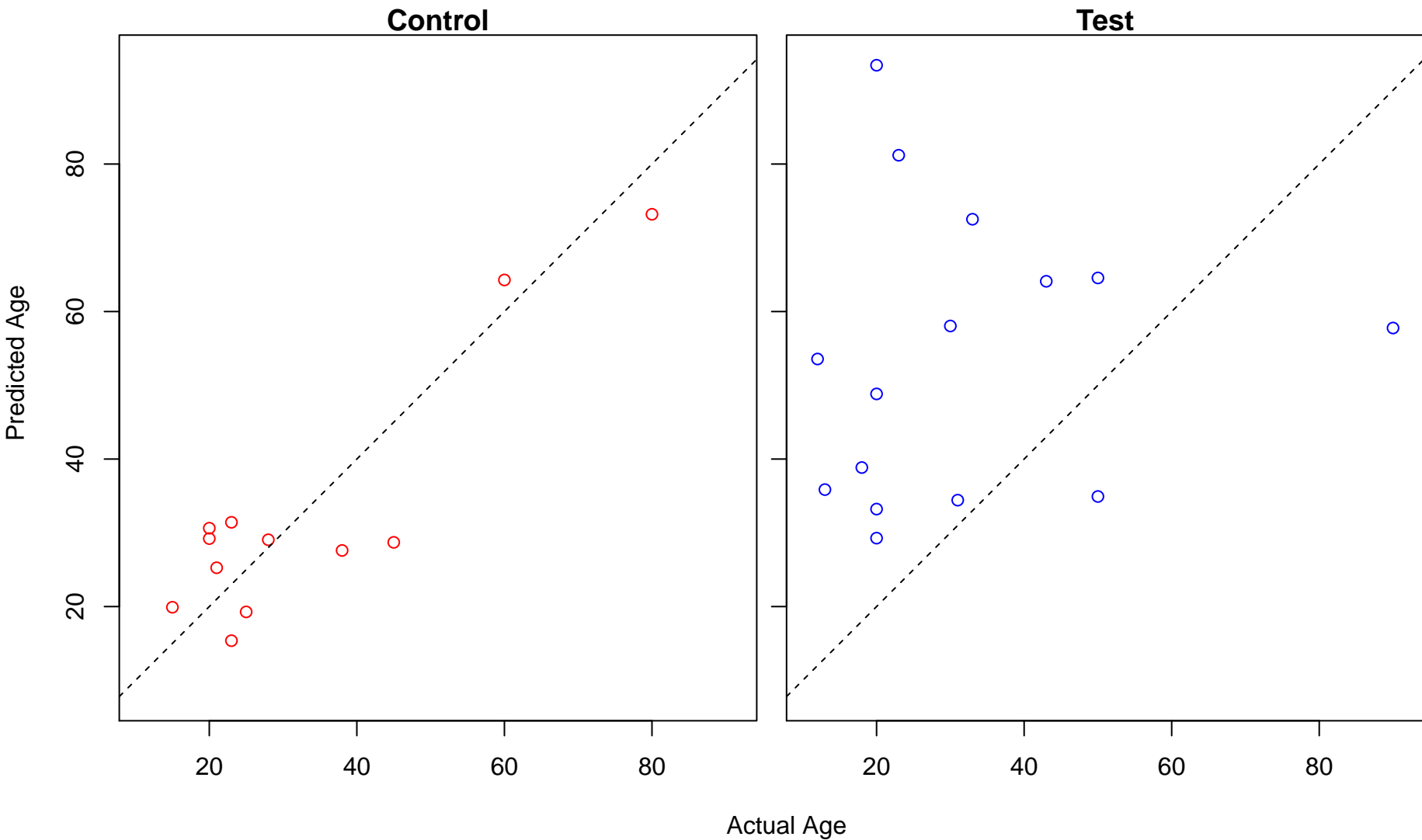


Test



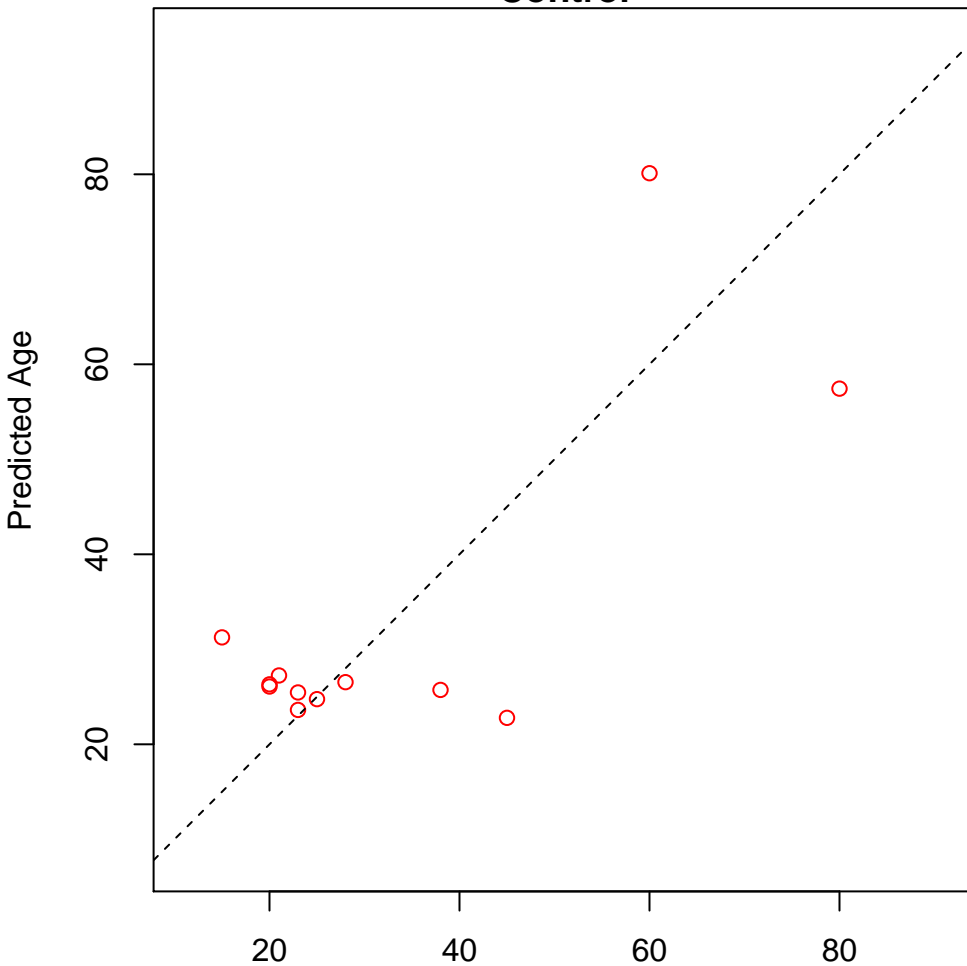
Actual Age

lactation (Score: 5.438919)

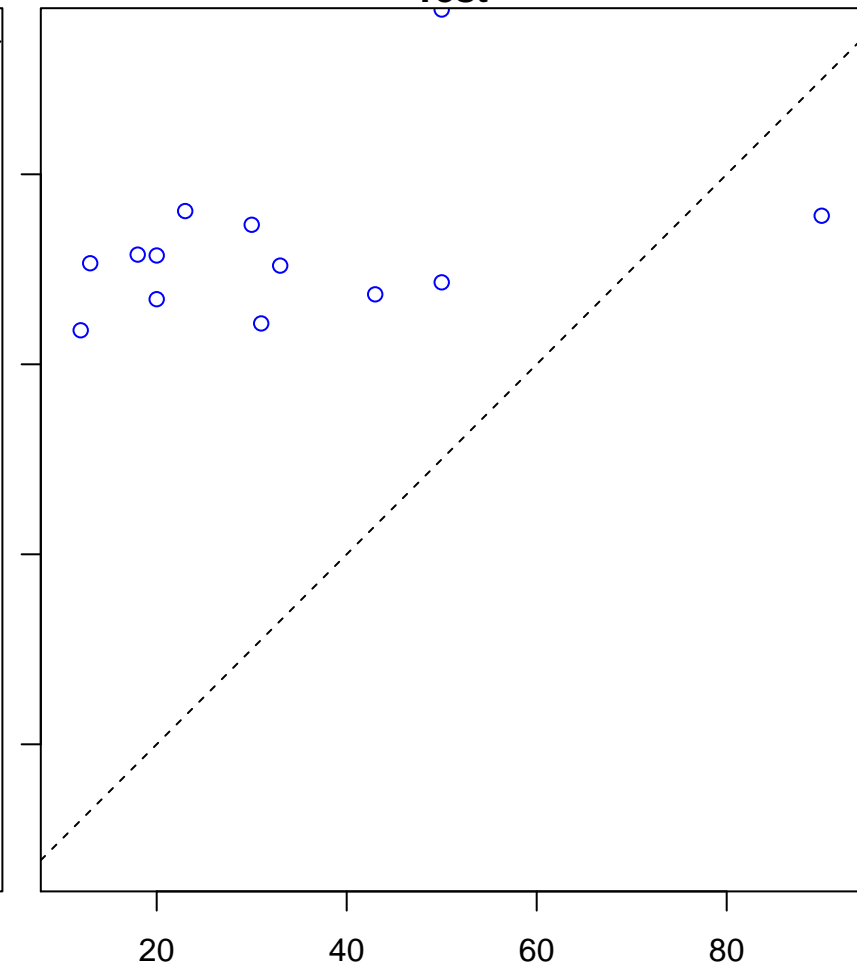


protein localization to chromatin (Score: 5.438831)

Control



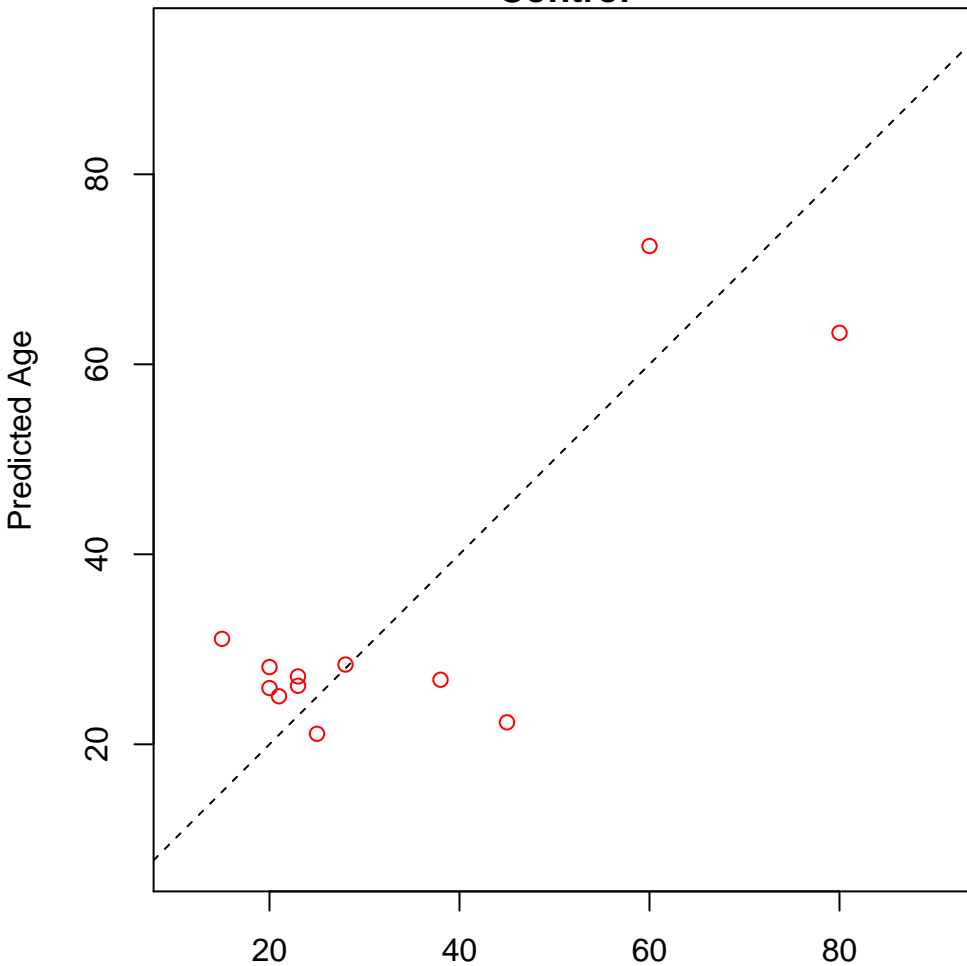
Test



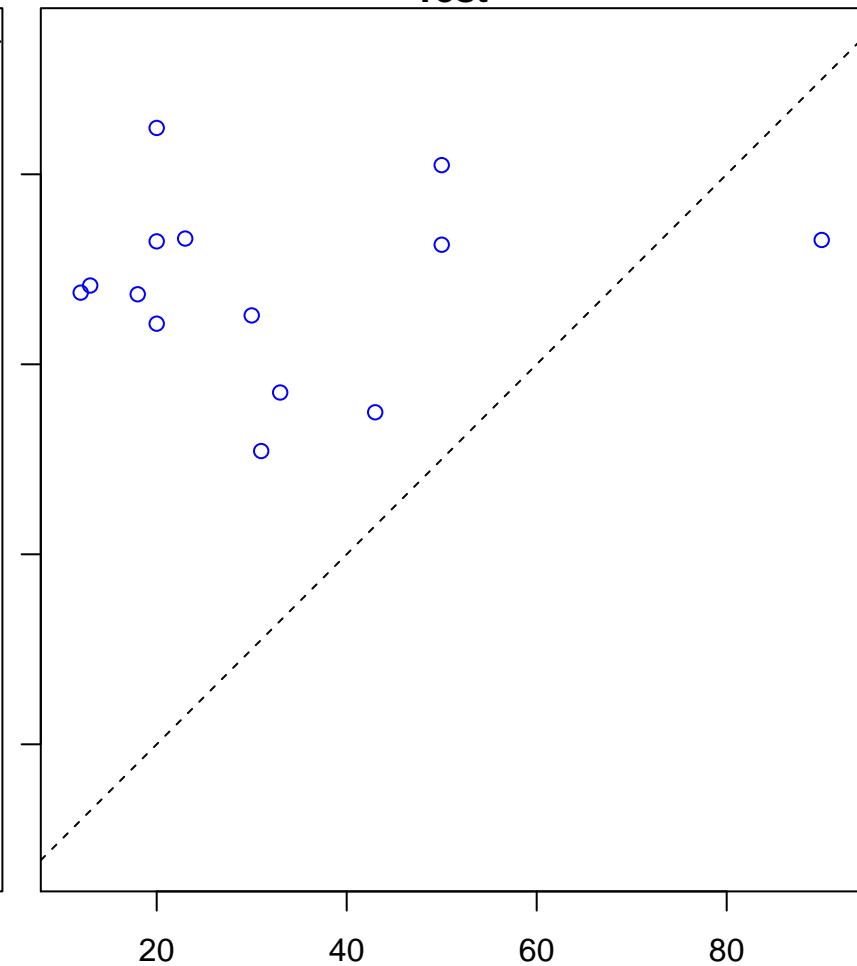
Actual Age

positive regulation of secretion by cell (Score: 5.437633)

Control

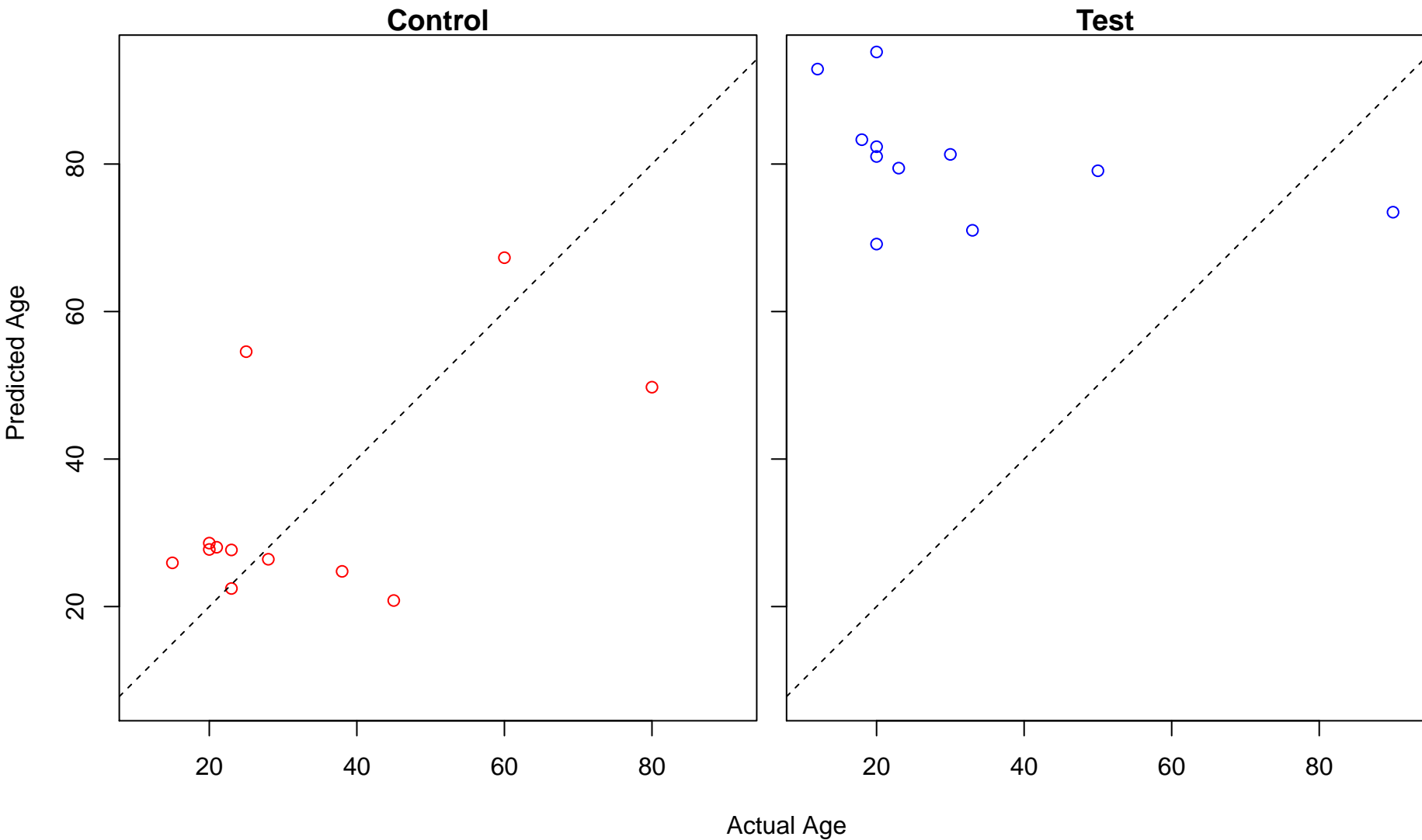


Test

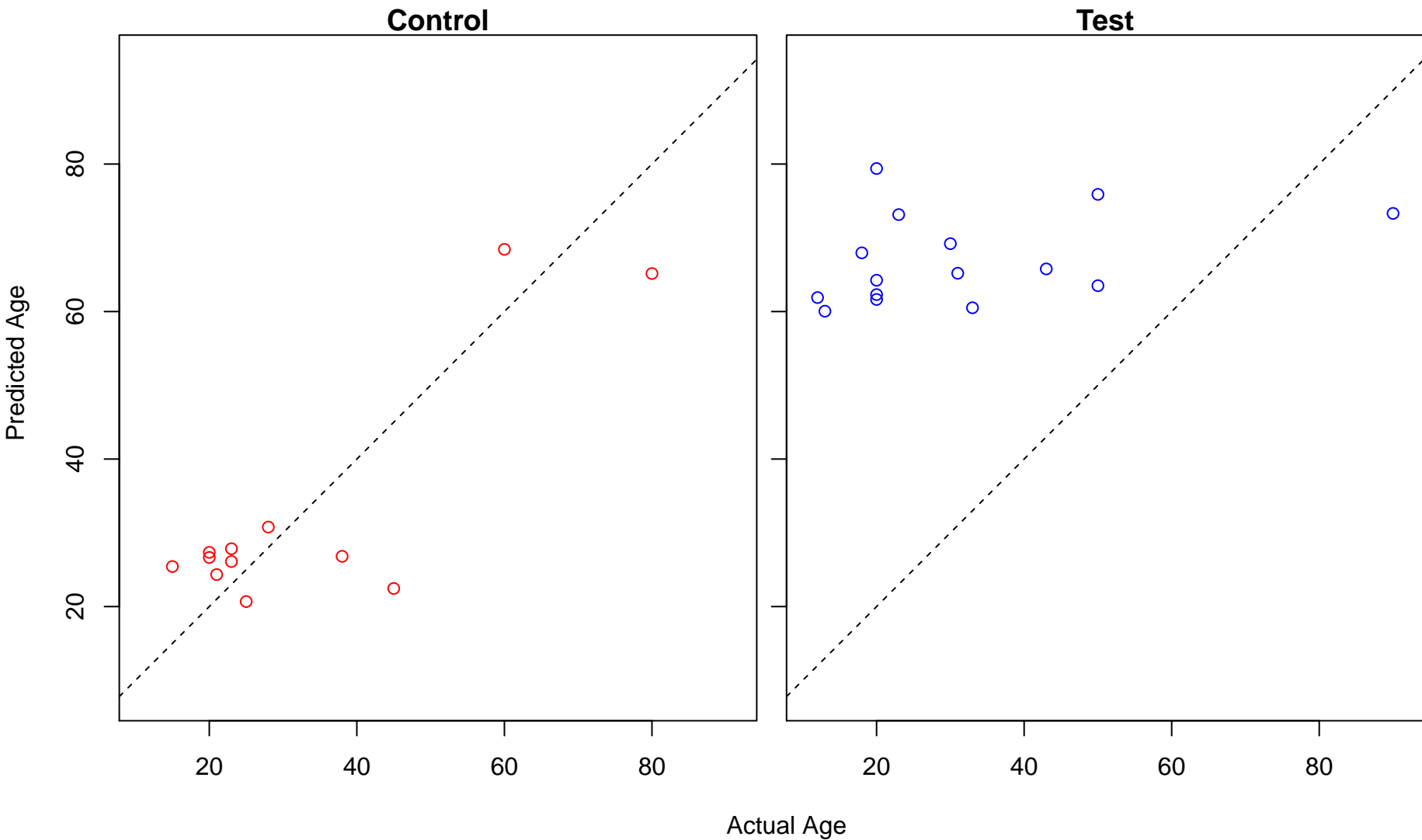


Actual Age

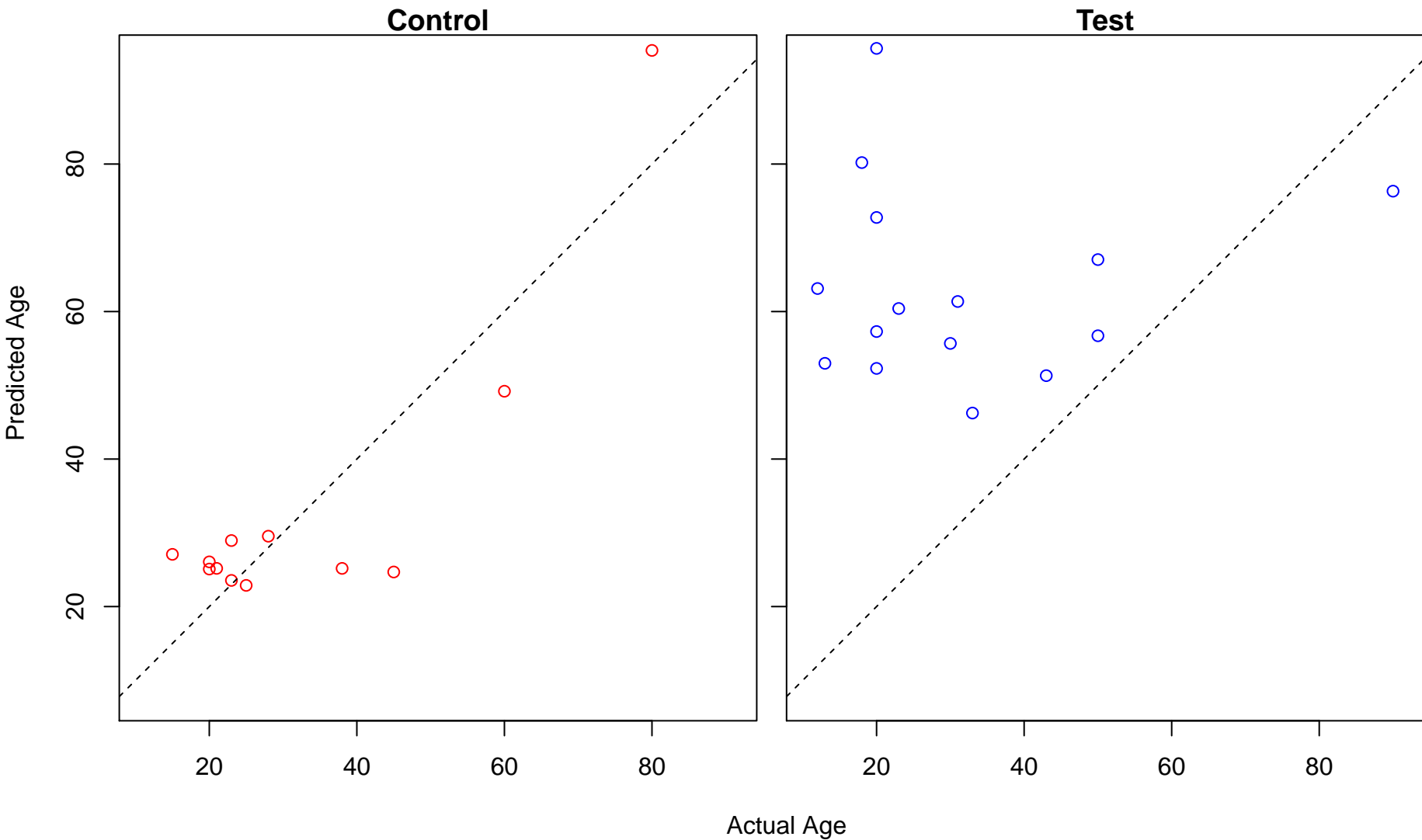
regulation of activation of Janus kinase activity (Score: 5.436668)



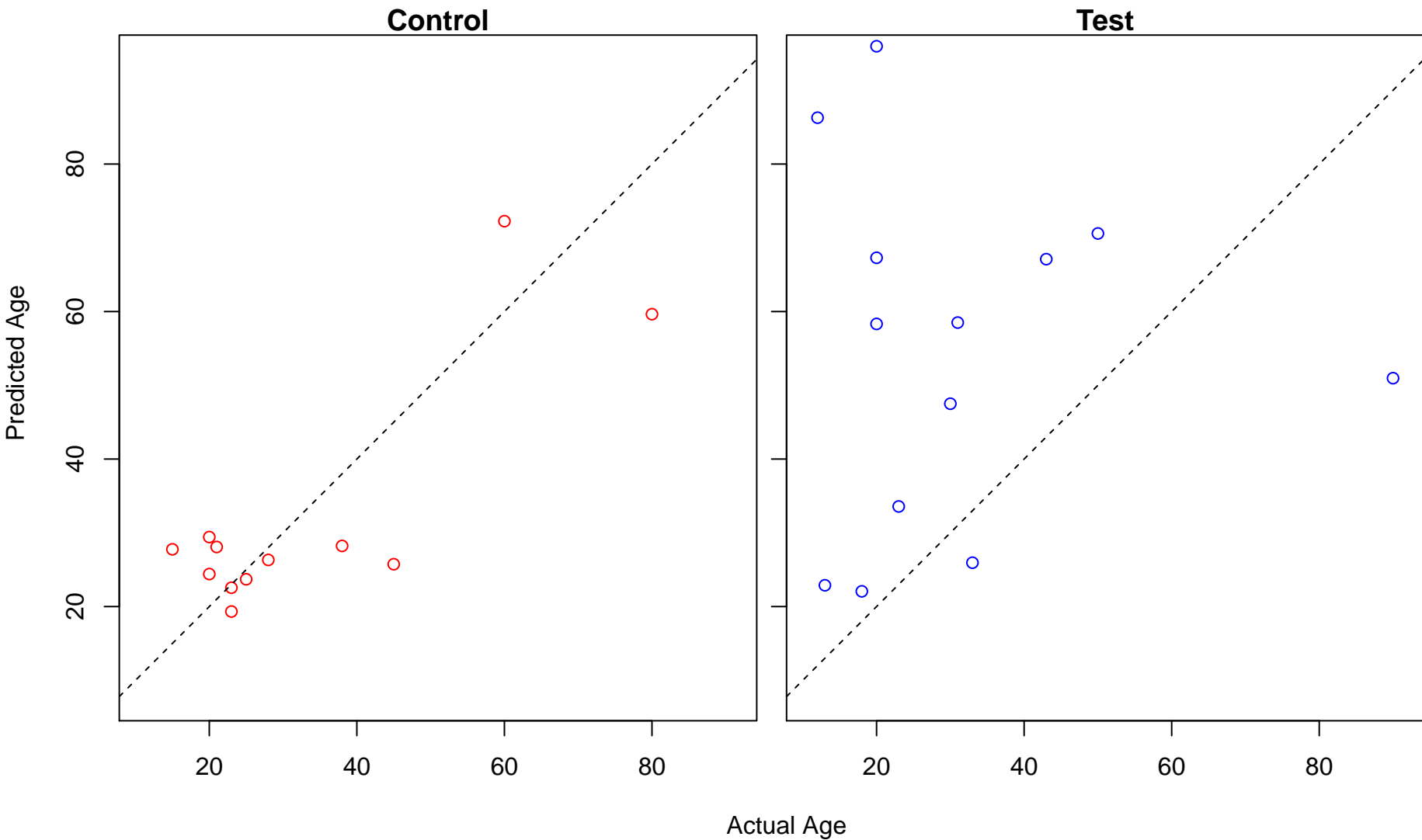
negative regulation of secretion (Score: 5.43172)



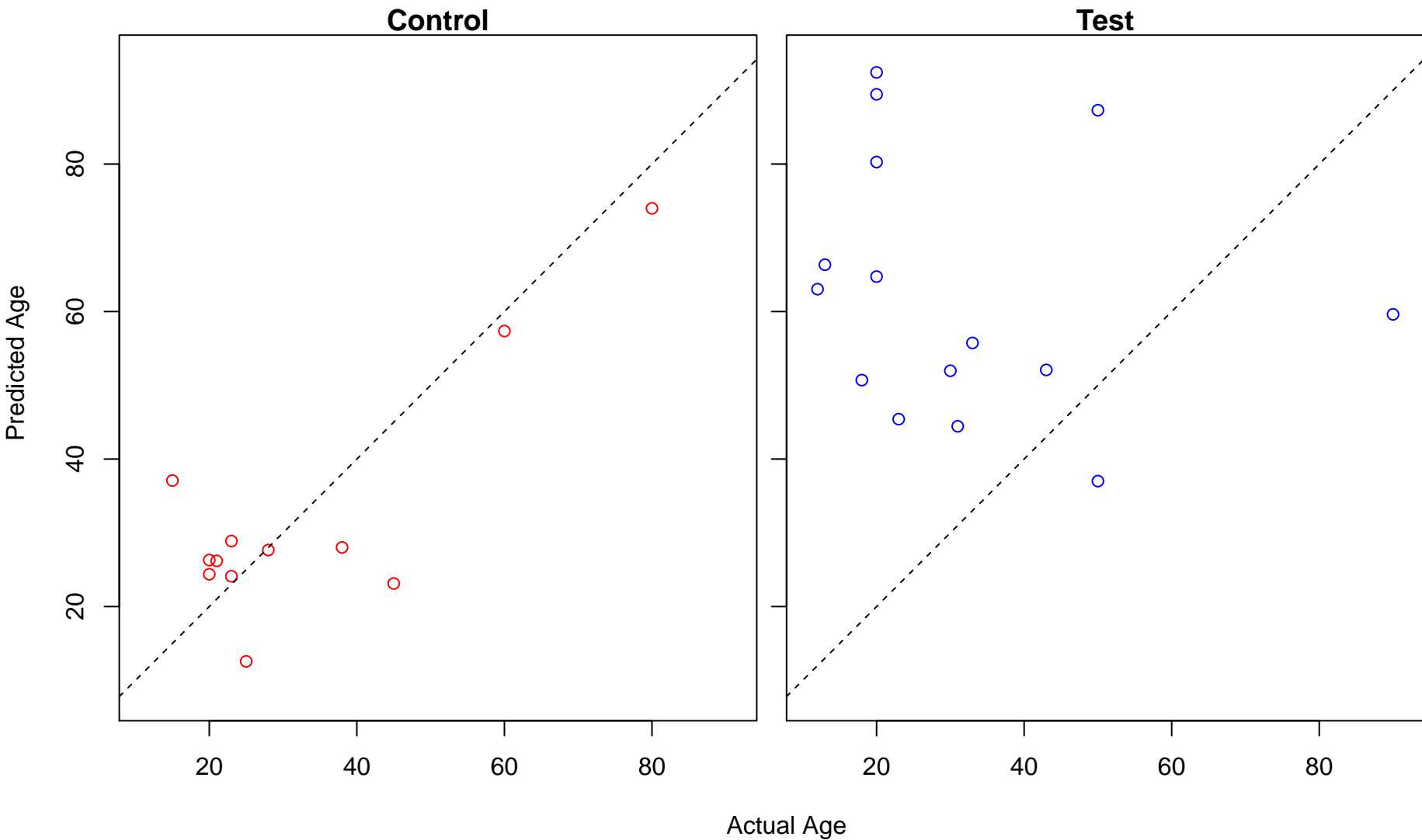
transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 5.432490)



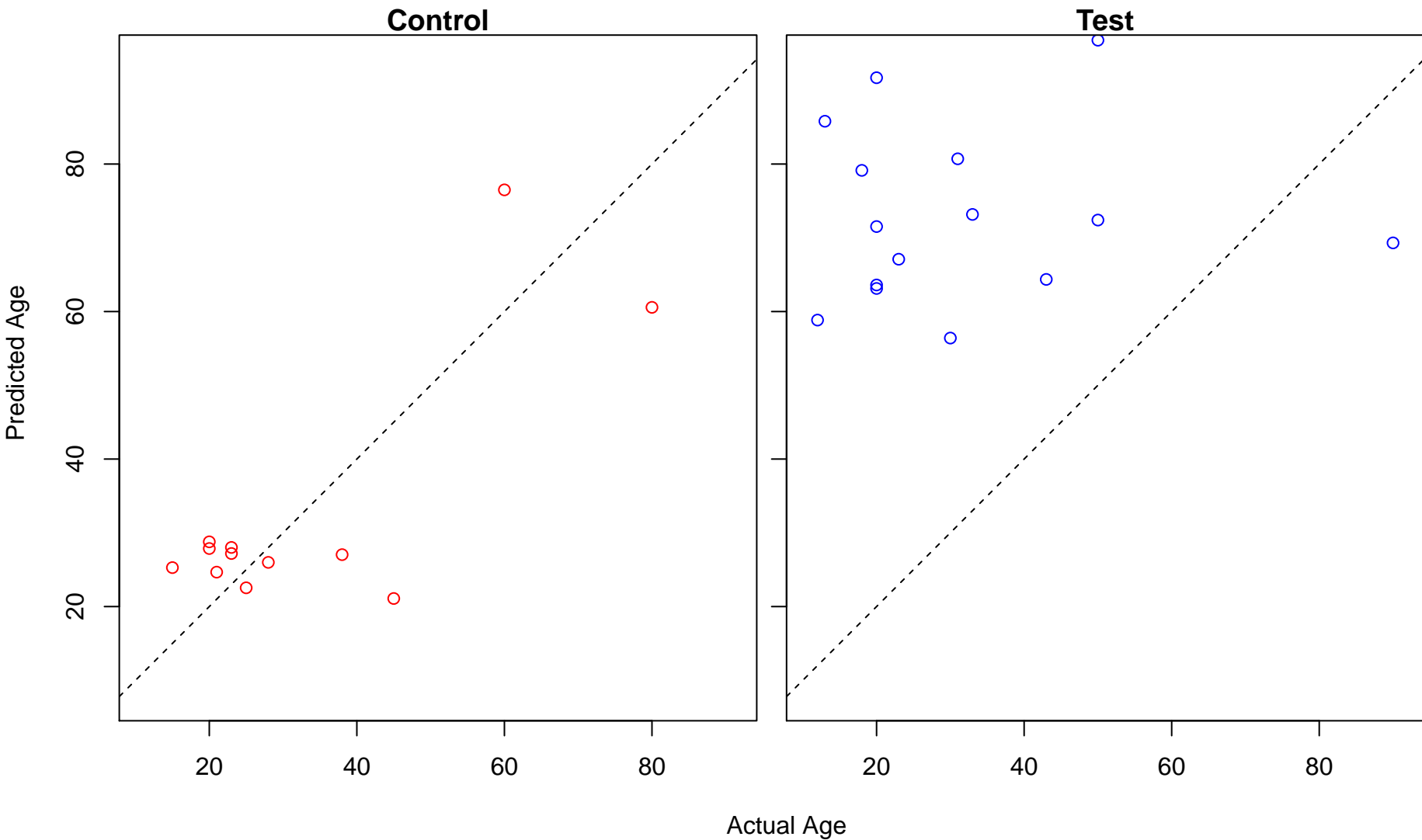
response to nutrient (Score: 5.431667)



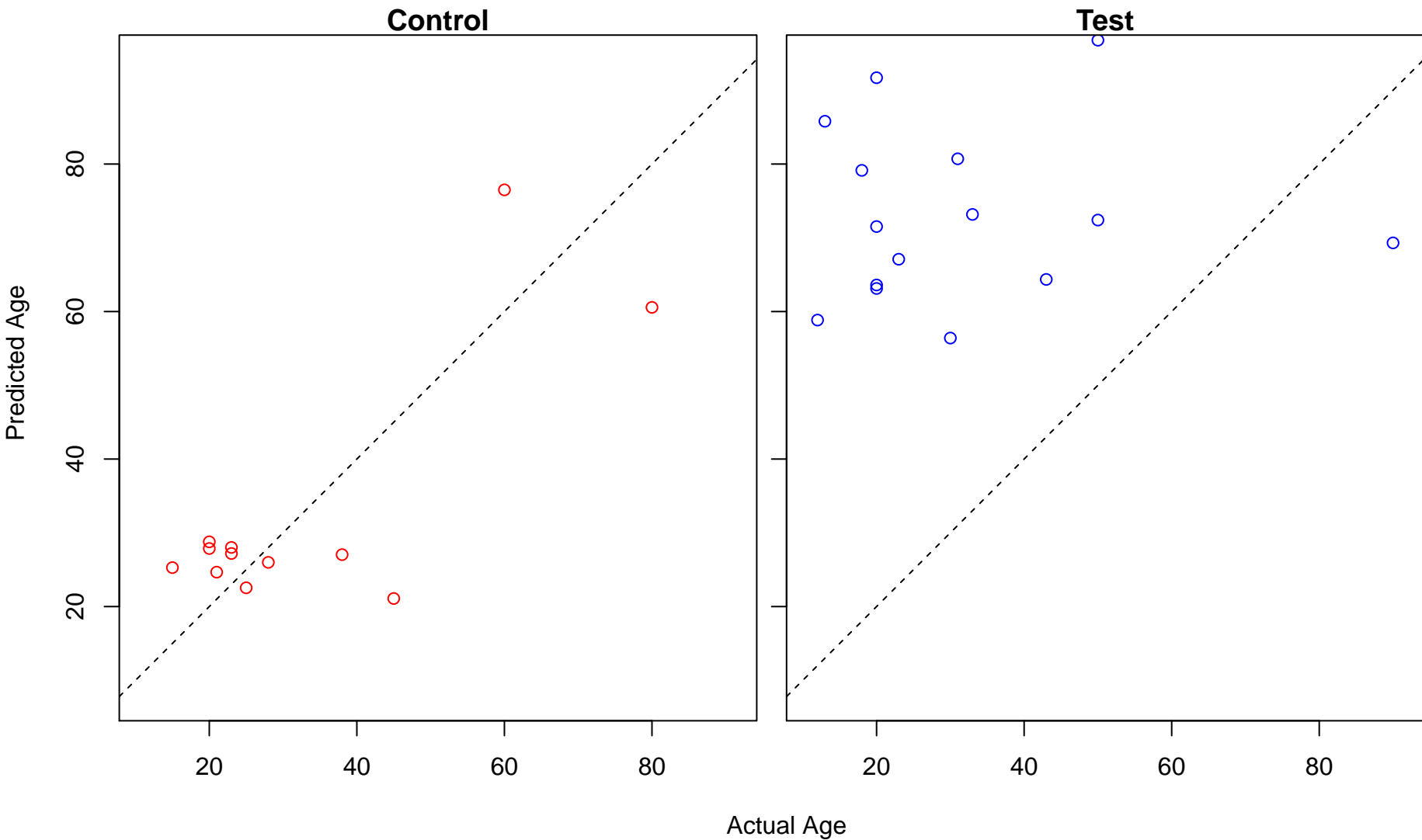
regulation of immunoglobulin production (Score: 5.431505)



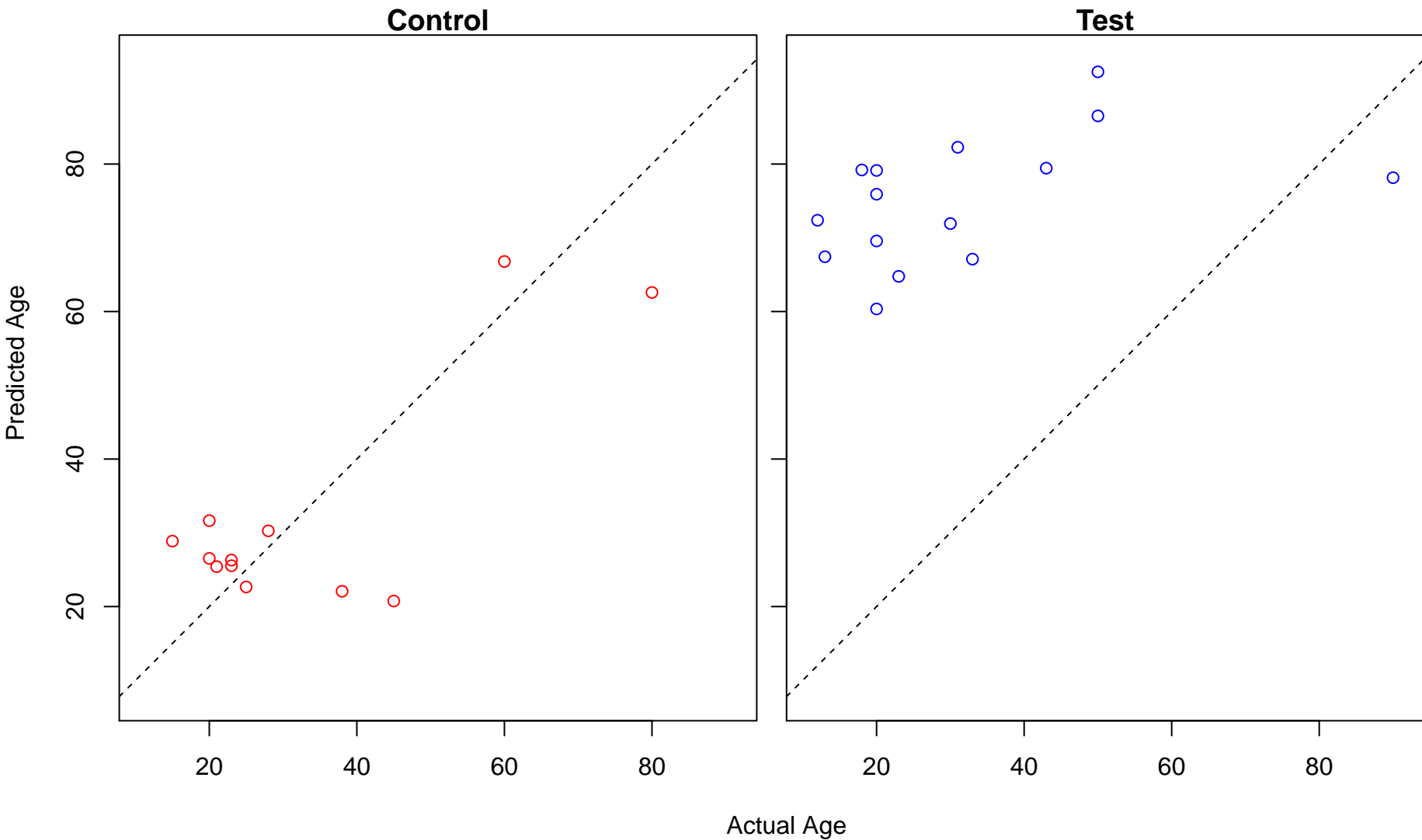
regulation of receptor binding (Score: 5.429838)



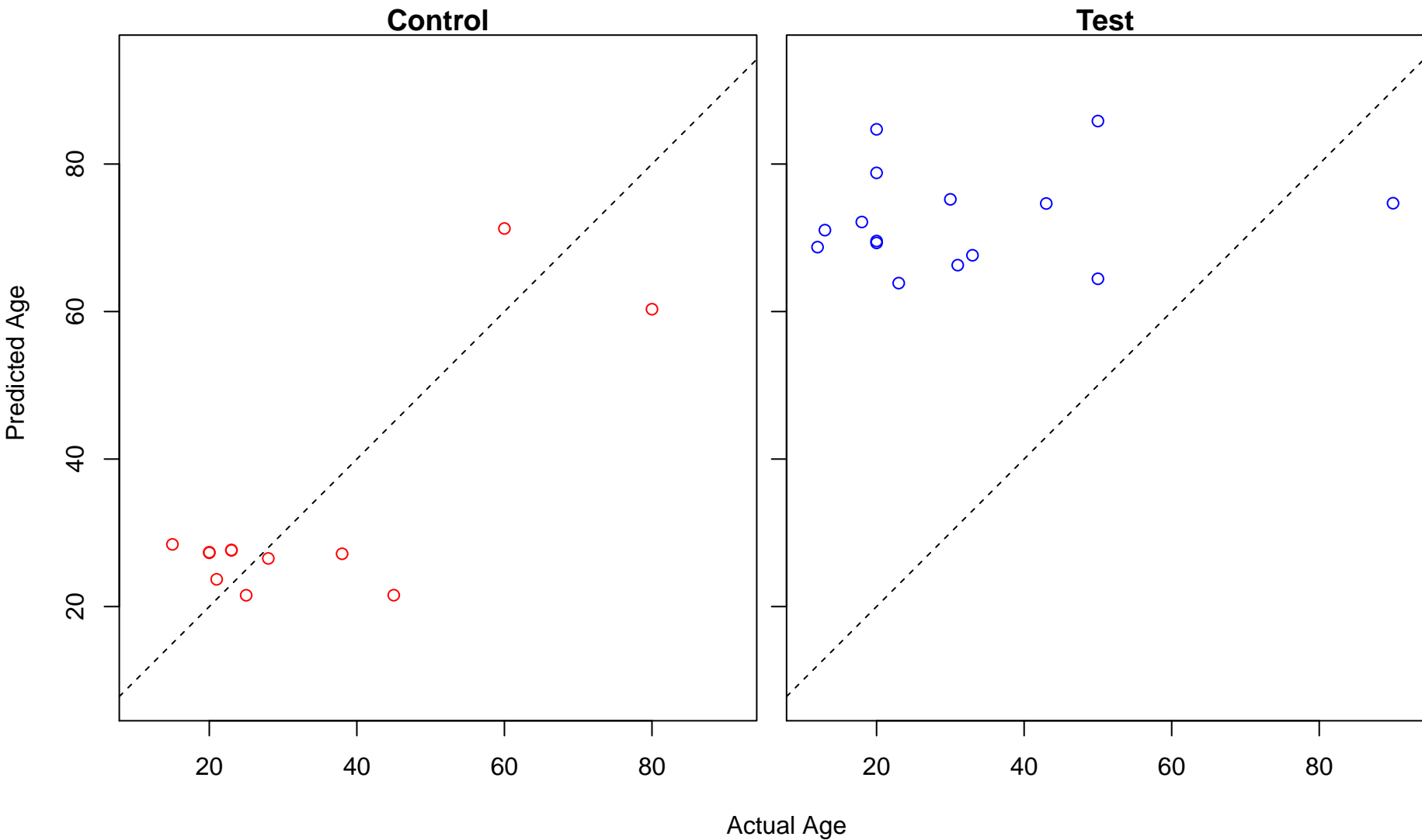
negative regulation of receptor binding (Score: 5.429793)



regulation of cardiac muscle contraction by calcium ion signaling (Score: 5.429260)

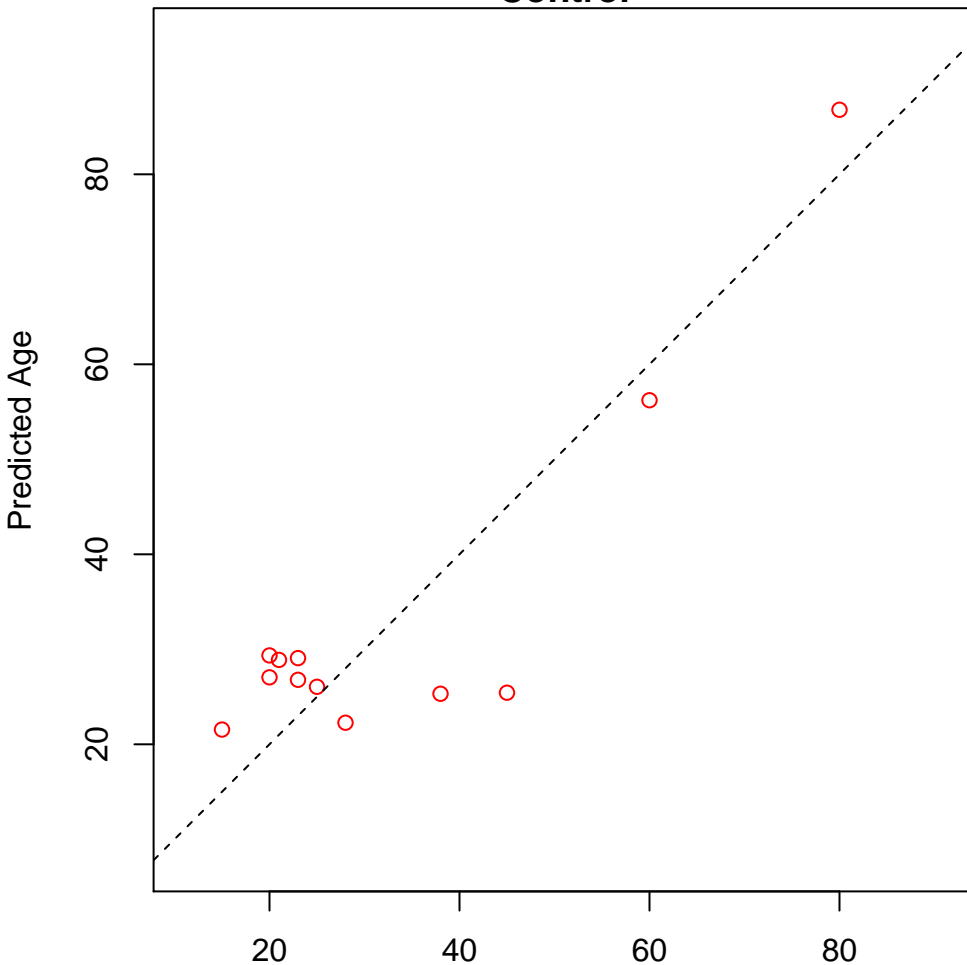


positive regulation of protein import (Score: 5.429052)

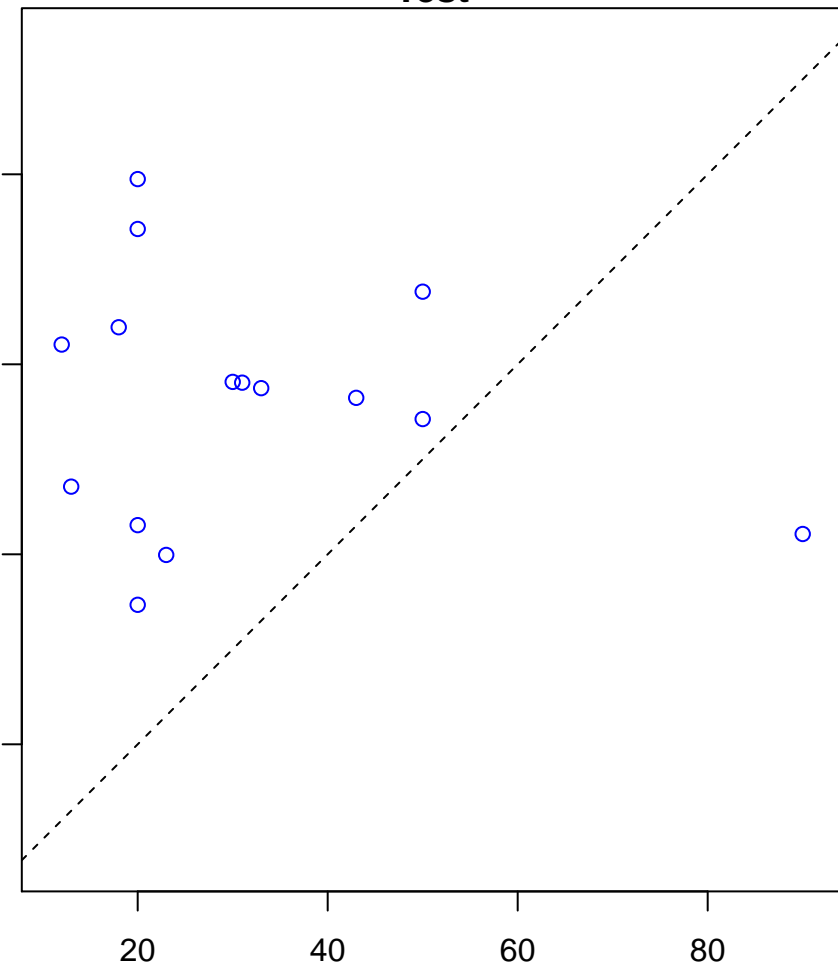


telomere maintenance via telomerase (Score: 5.428861)

Control

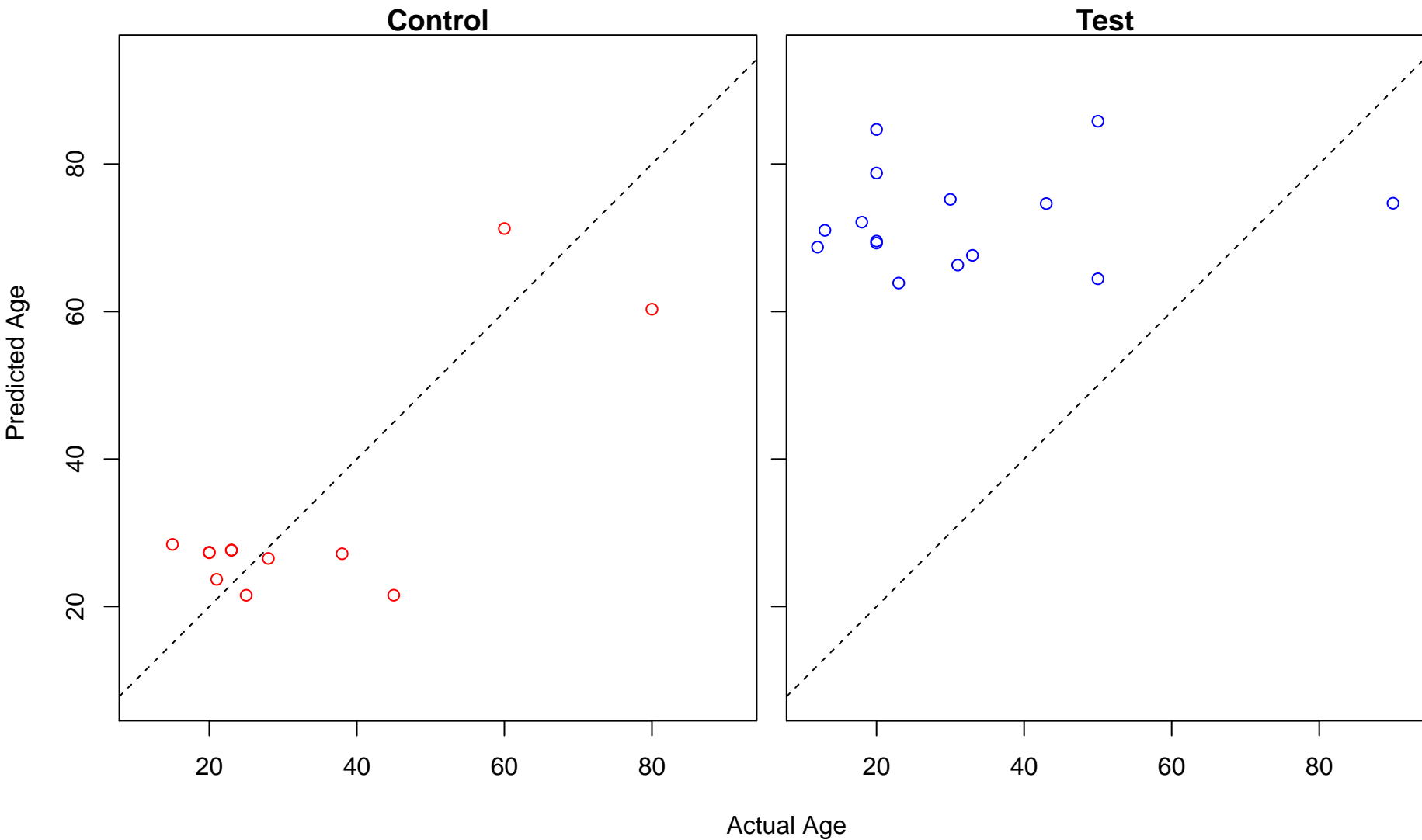


Test

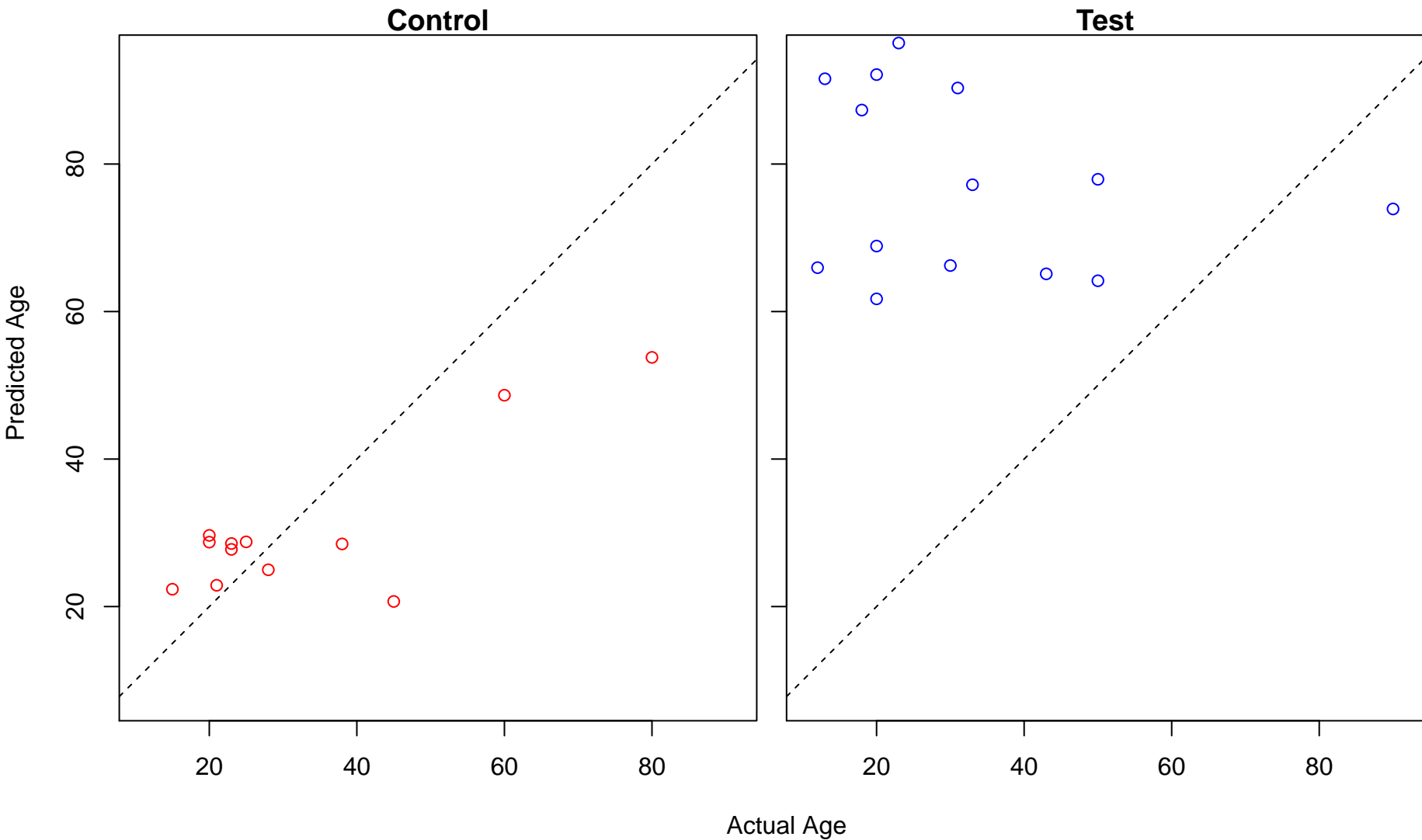


Actual Age

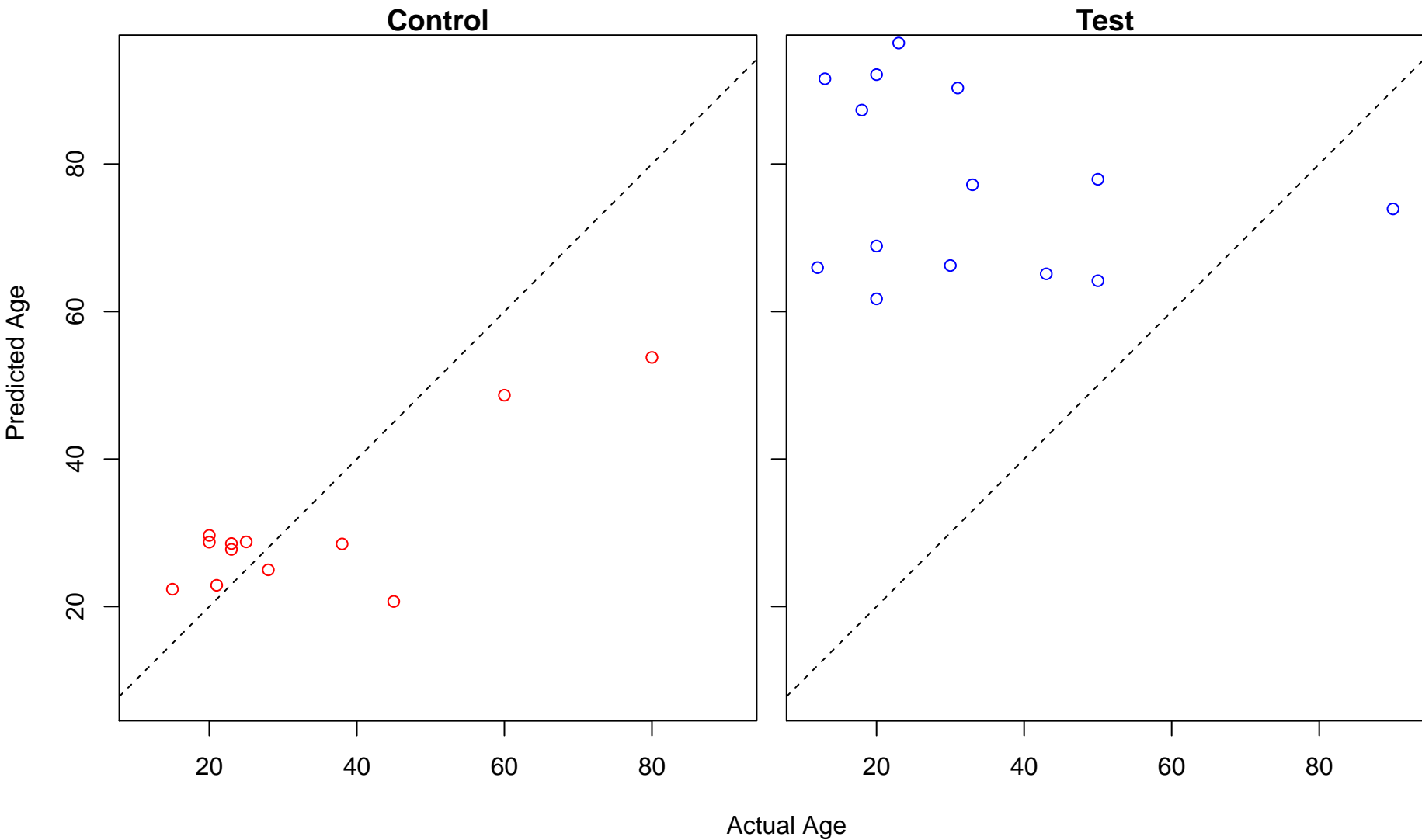
positive regulation of protein import into nucleus (Score: 5.426502)



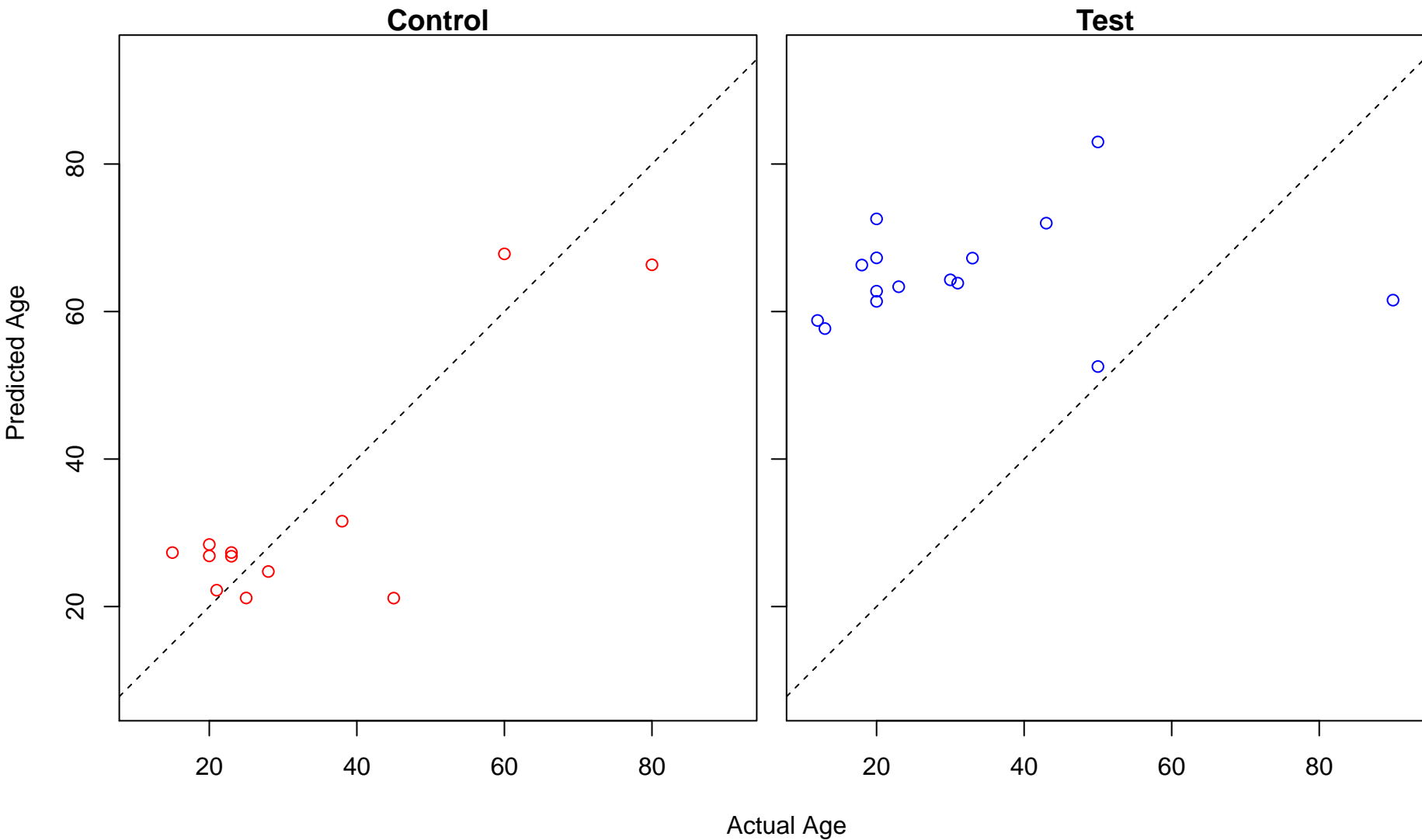
somatostatin receptor signaling pathway (Score: 5.425636)



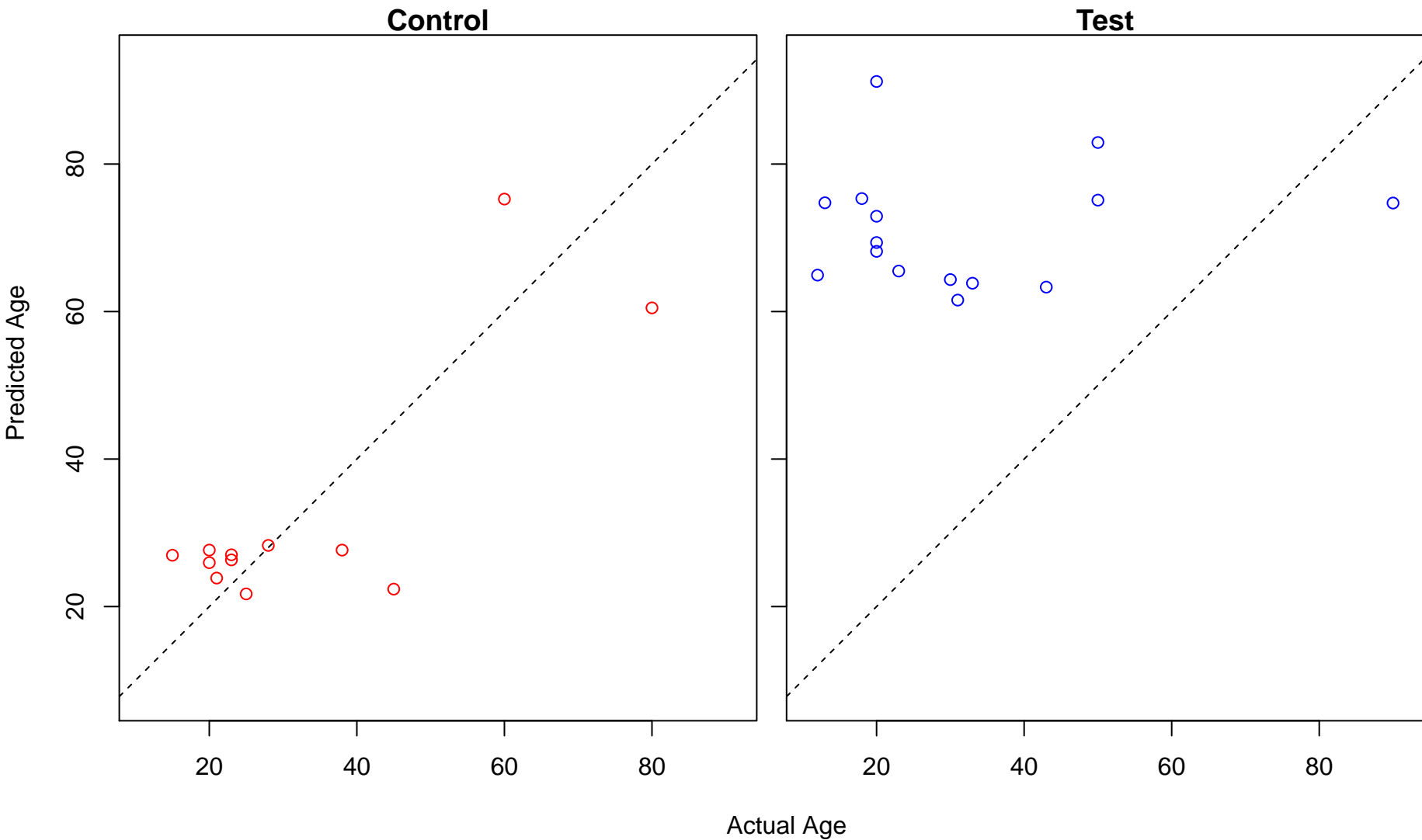
somatostatin signaling pathway (Score: 5.425636)



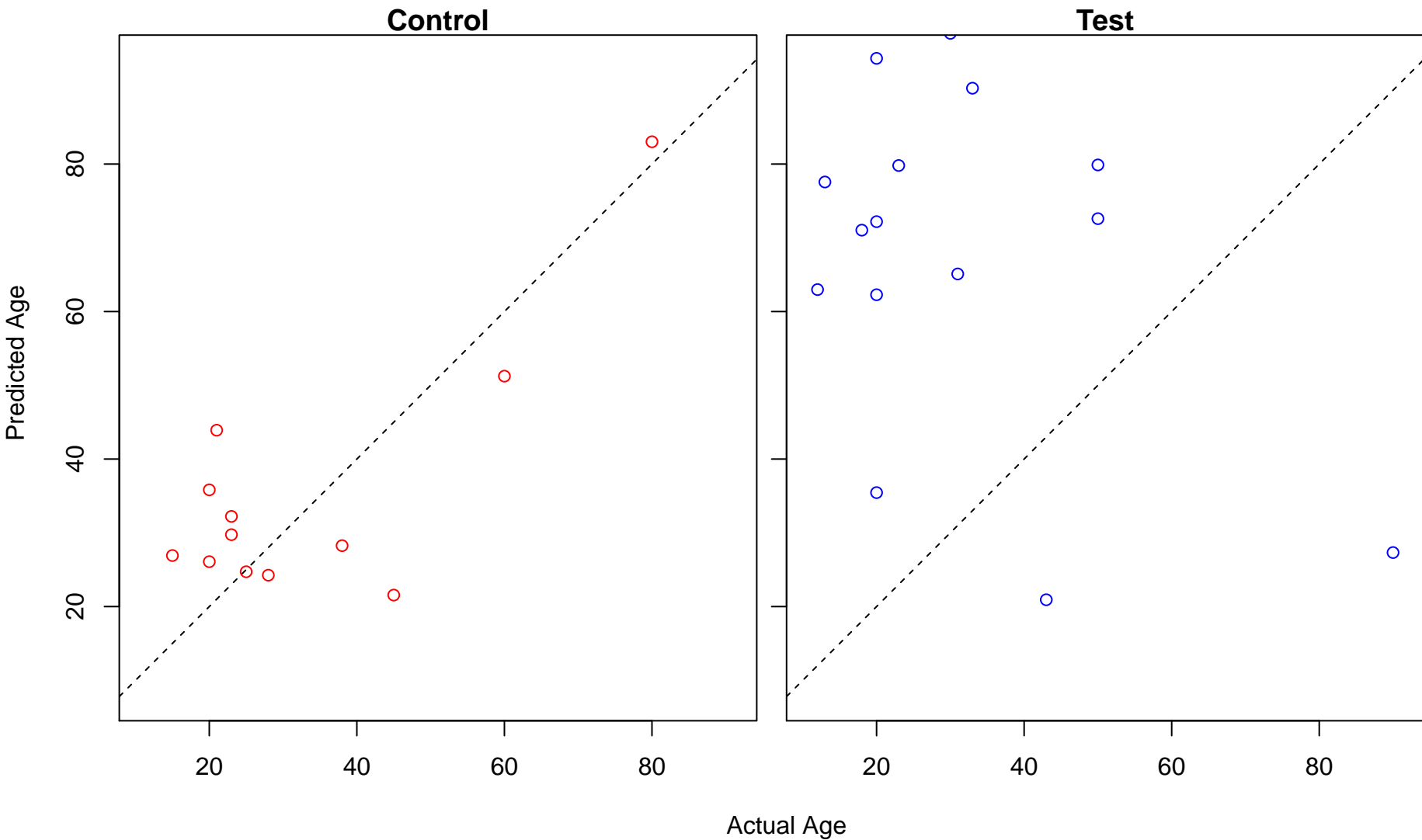
clathrin-mediated endocytosis (Score: 5.424078)



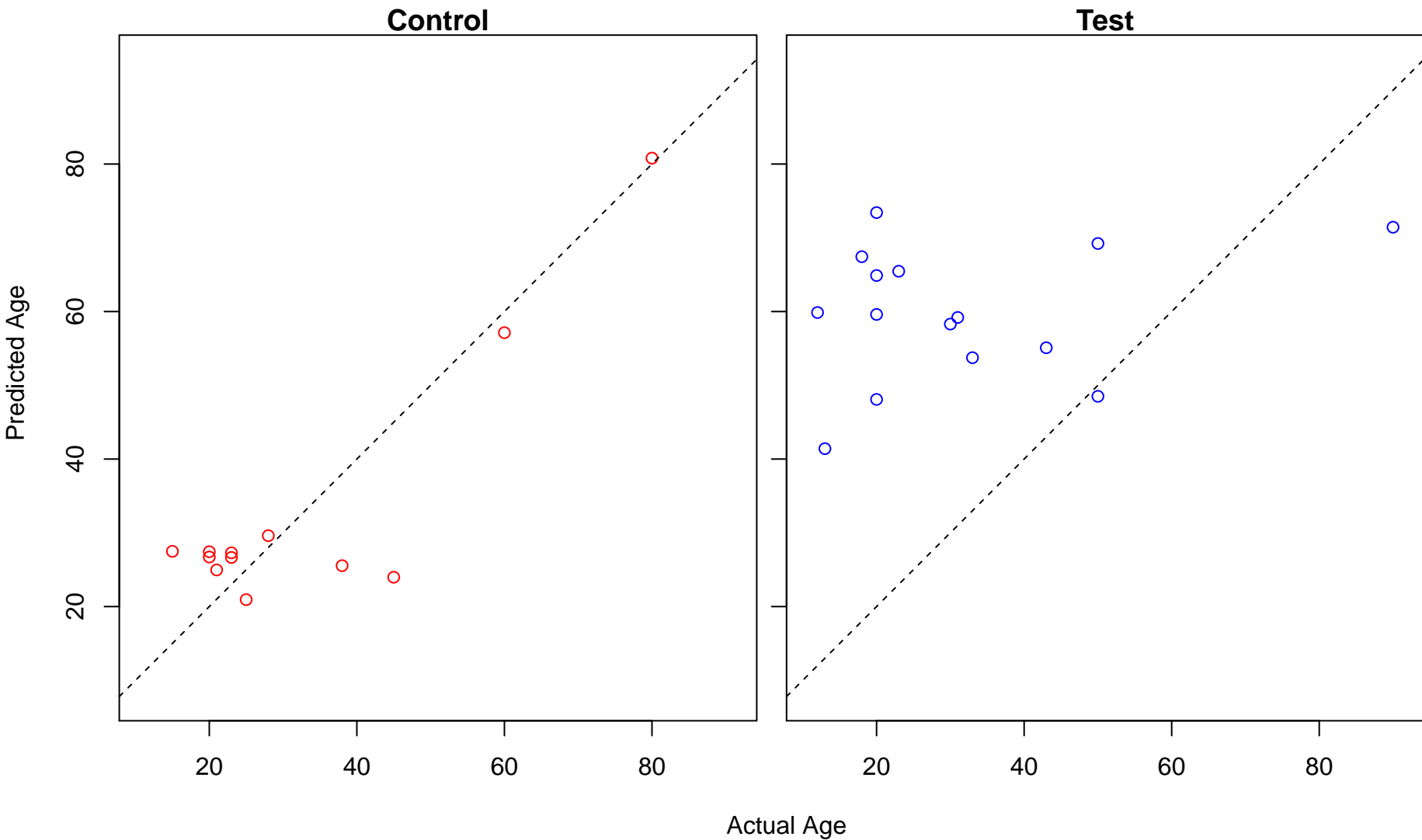
negative regulation of proteolysis (Score: 5.422292)



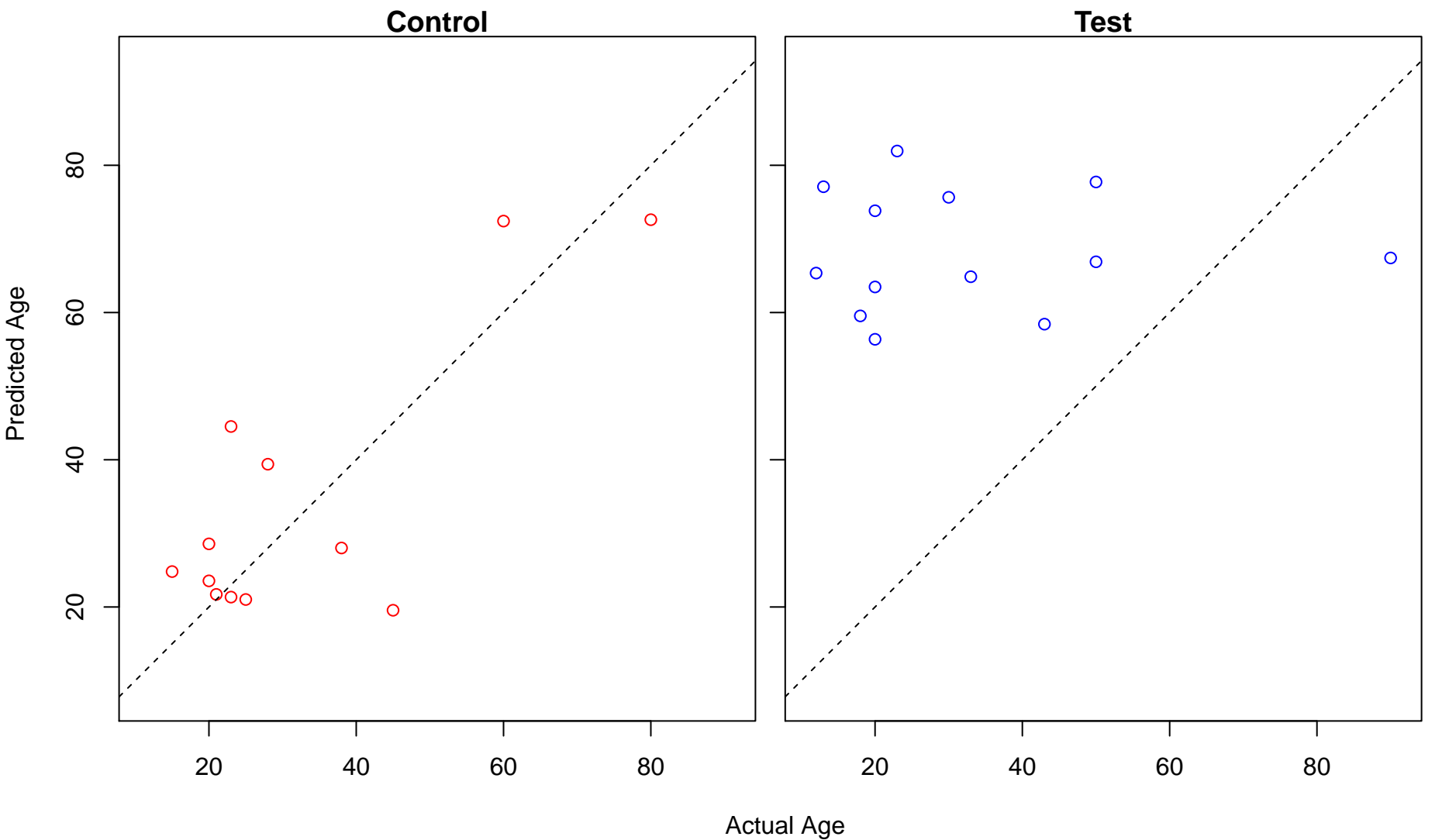
venous blood vessel morphogenesis (Score: 5.422246)



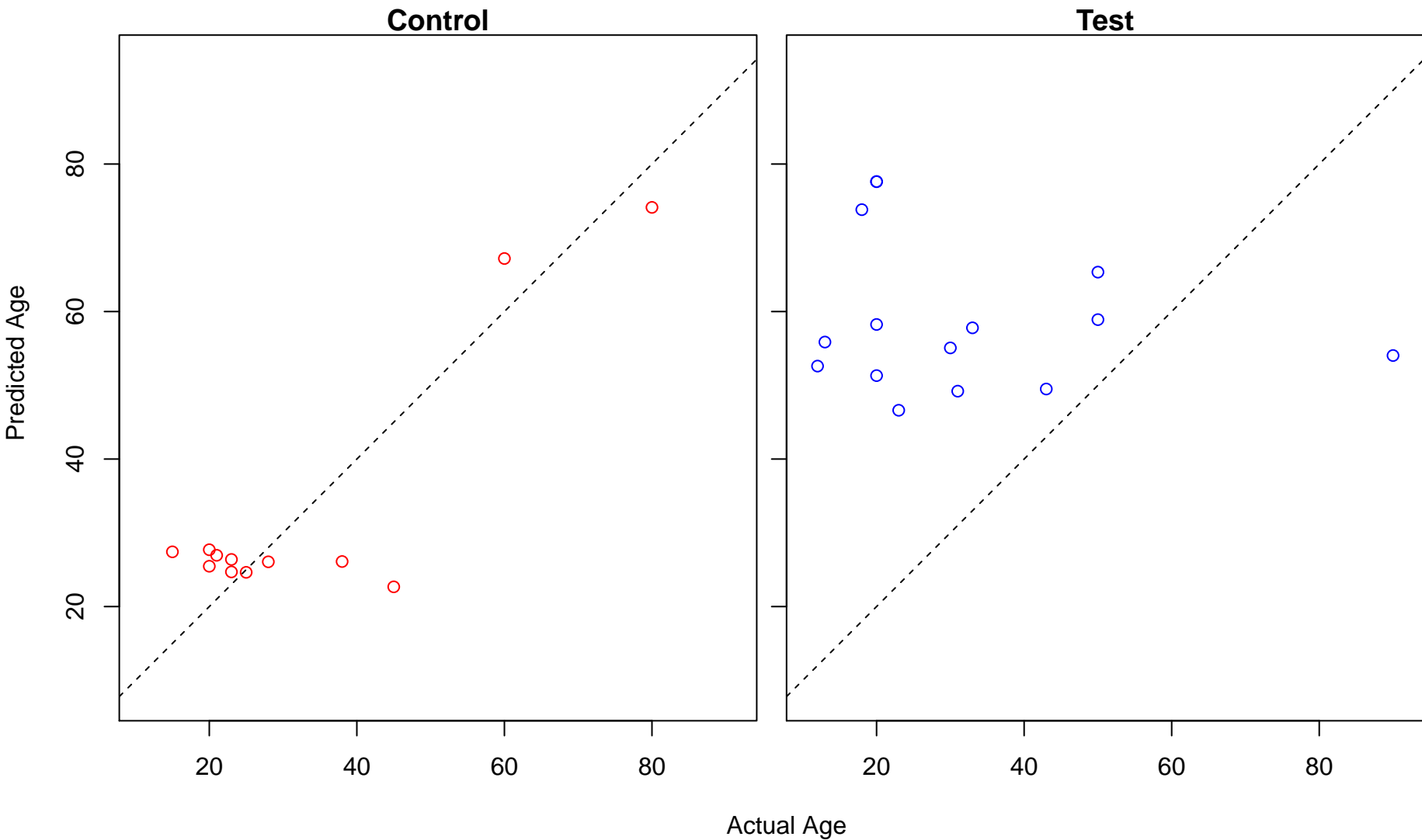
regulation of vacuole organization (Score: 5.421811)



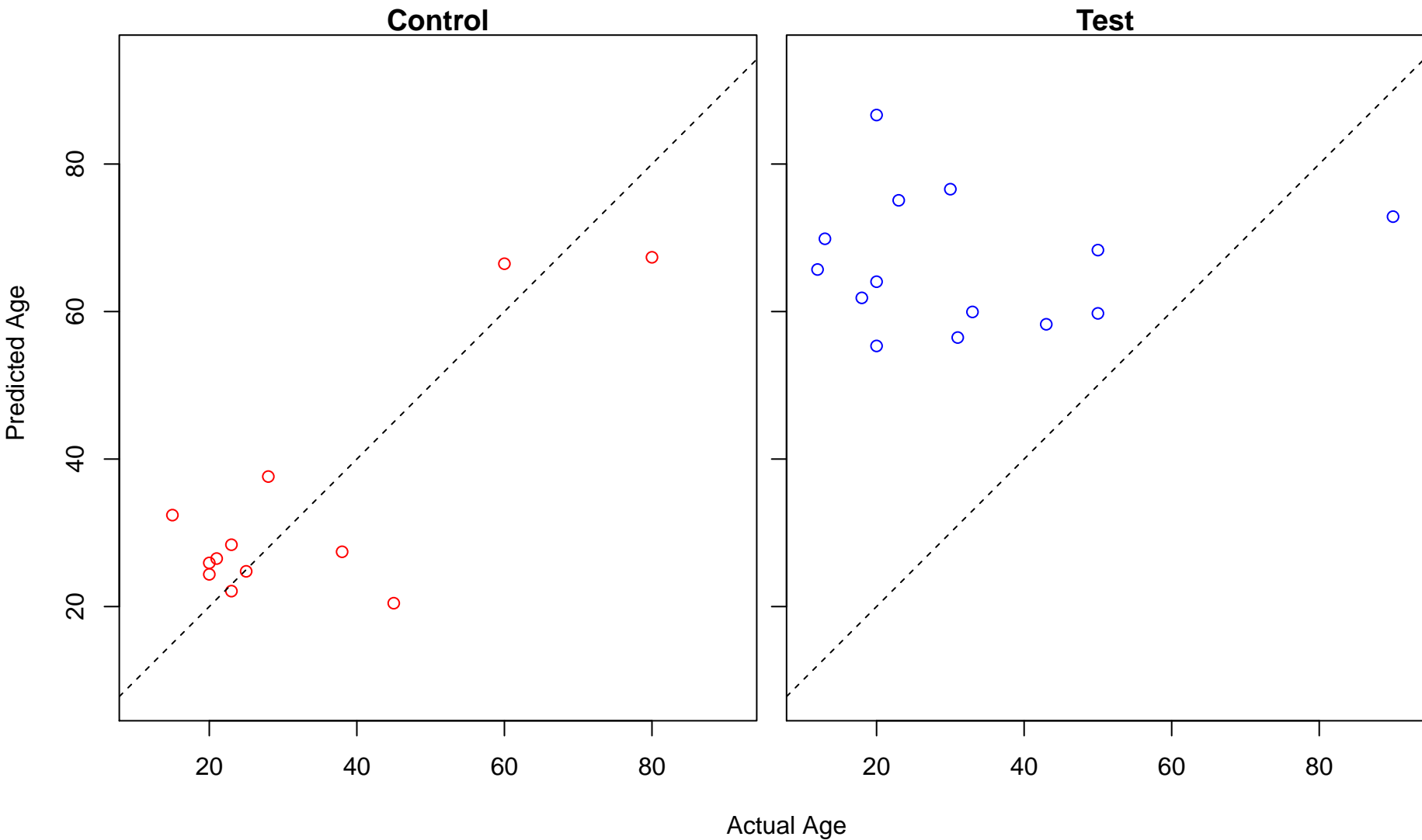
response based on somatic recombination of immune receptors built from immunoglobulin superfamily c



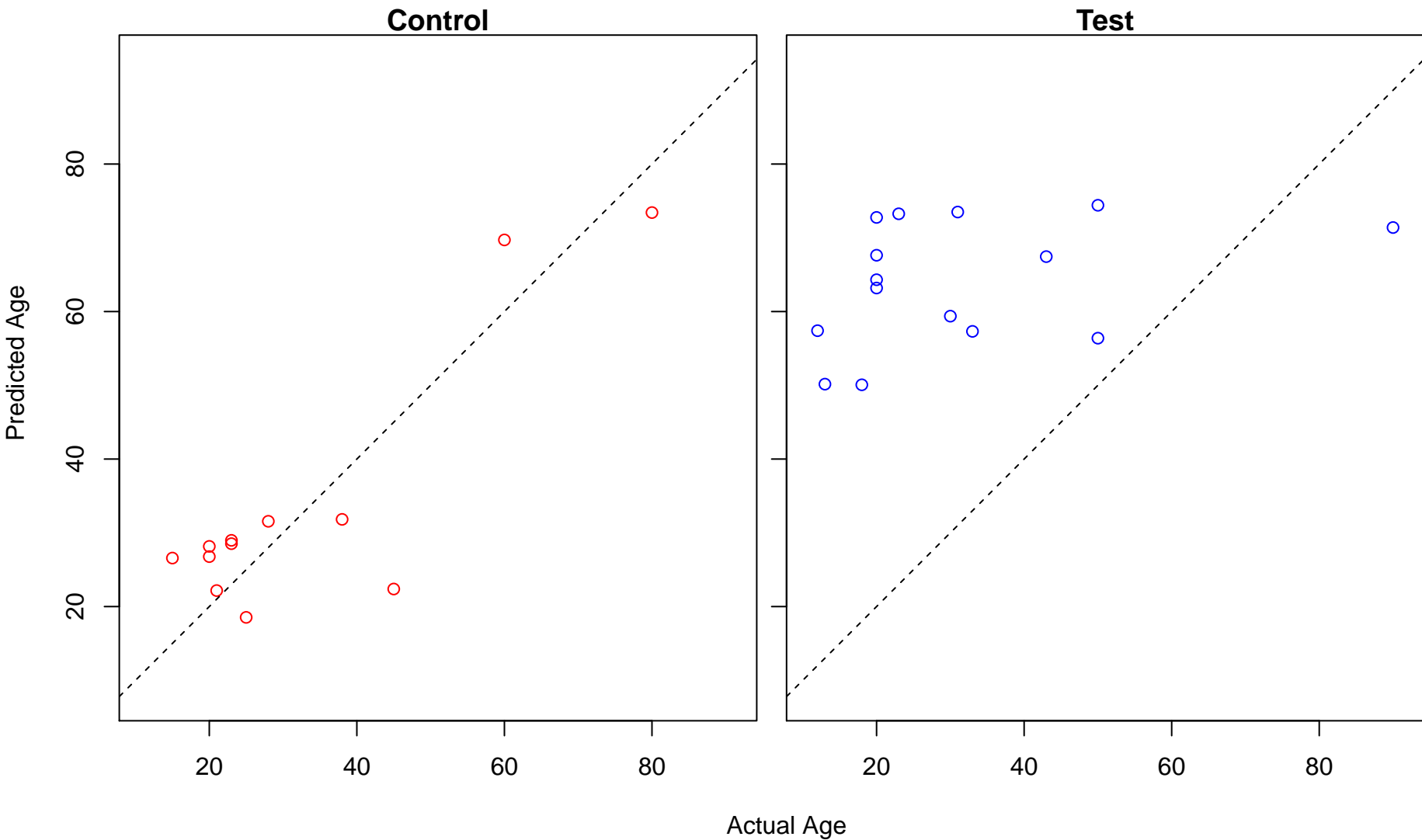
positive regulation of cellular component biogenesis (Score: 5.417481)



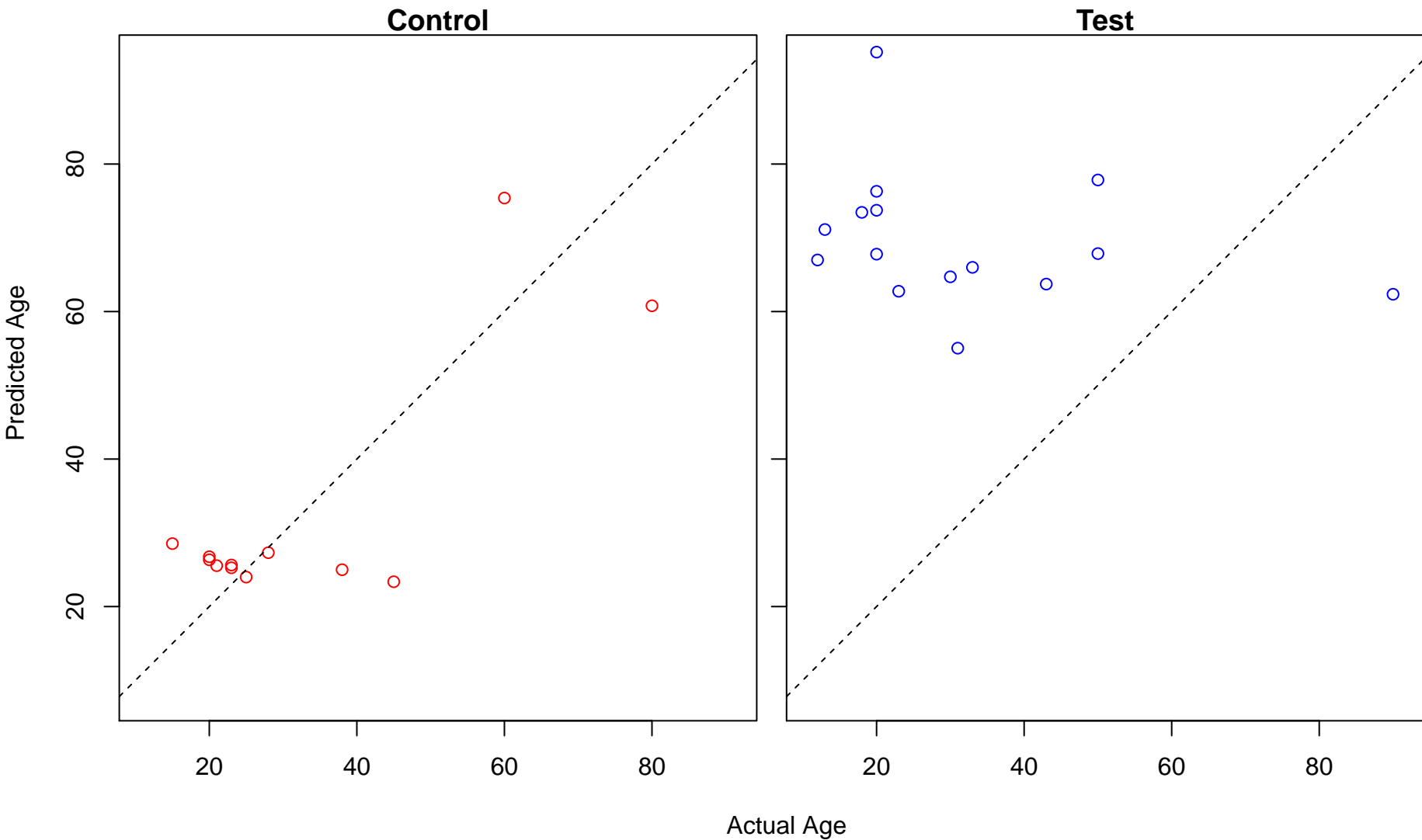
positive regulation of fibroblast proliferation (Score: 5.416304)



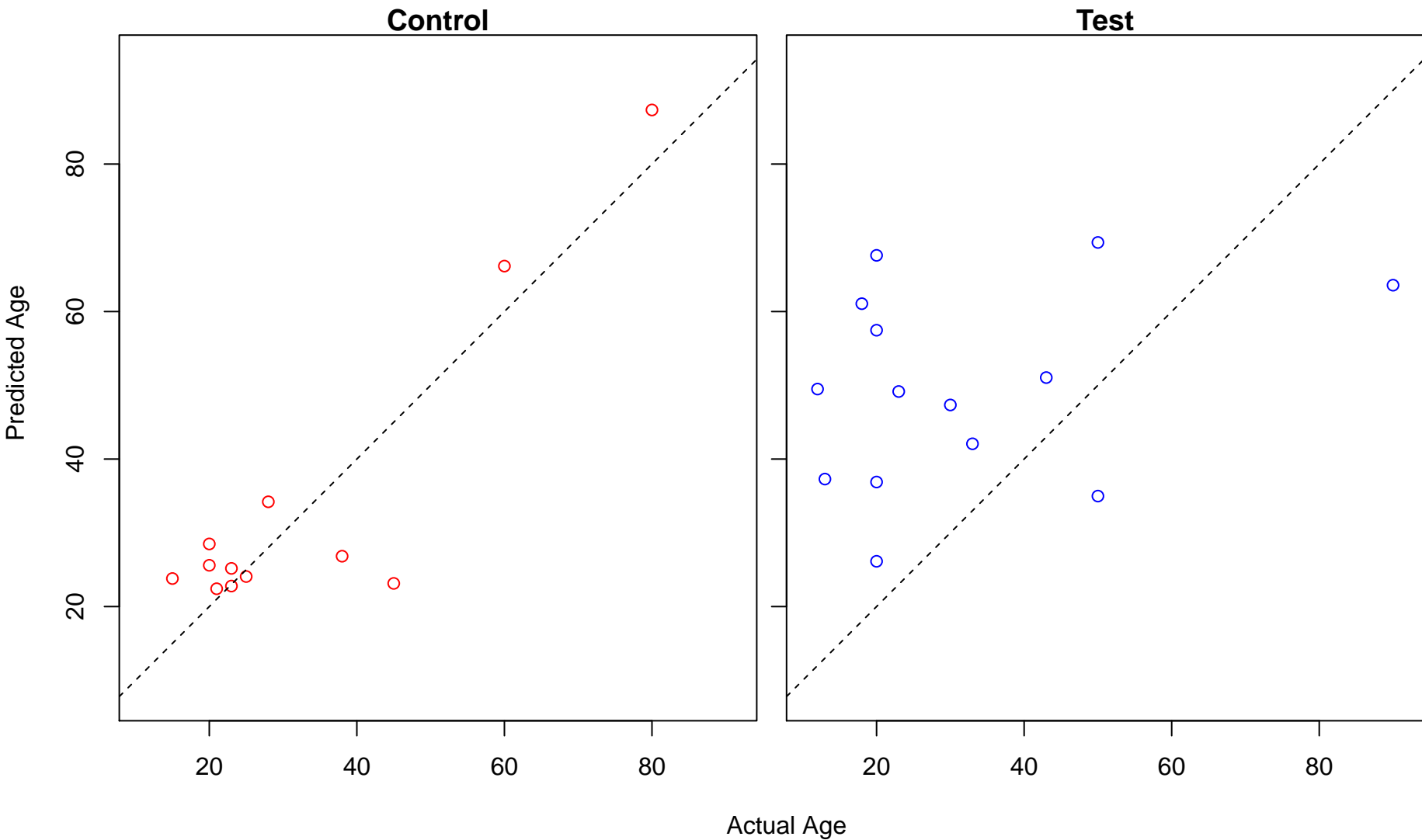
embryonic morphogenesis (Score: 5.416277)



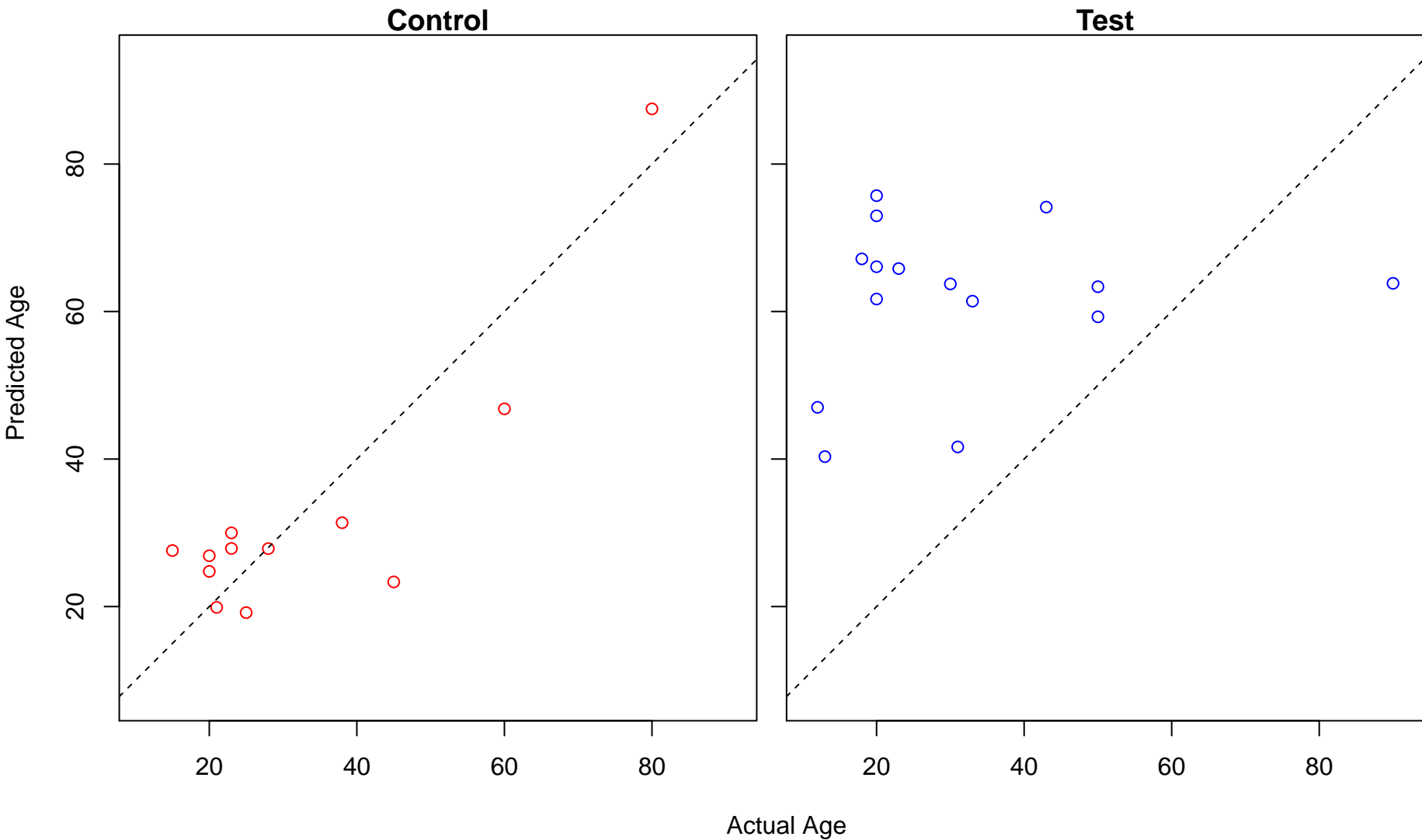
negative regulation of neuron apoptotic process (Score: 5.415215)



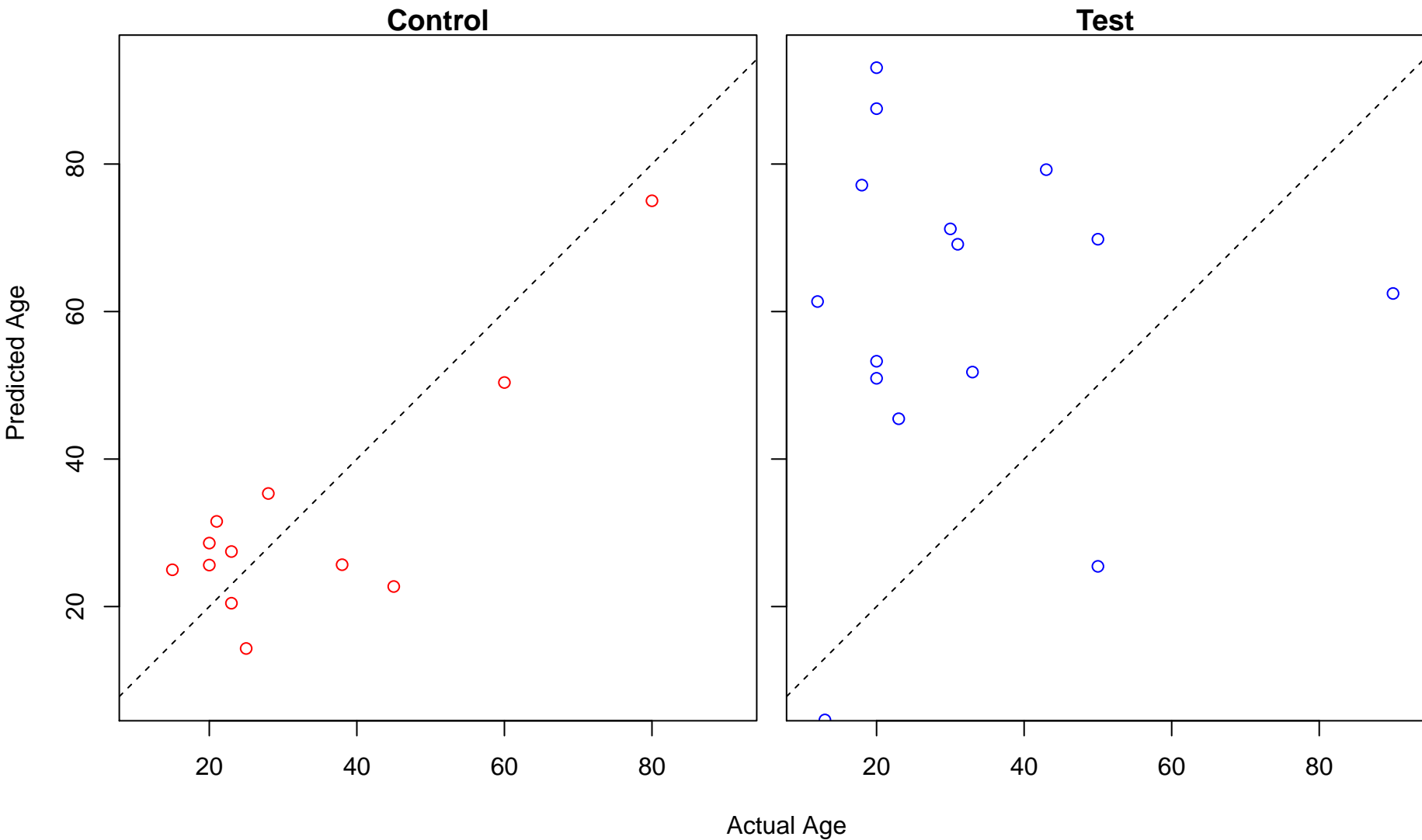
receptor catabolic process (Score: 5.413695)



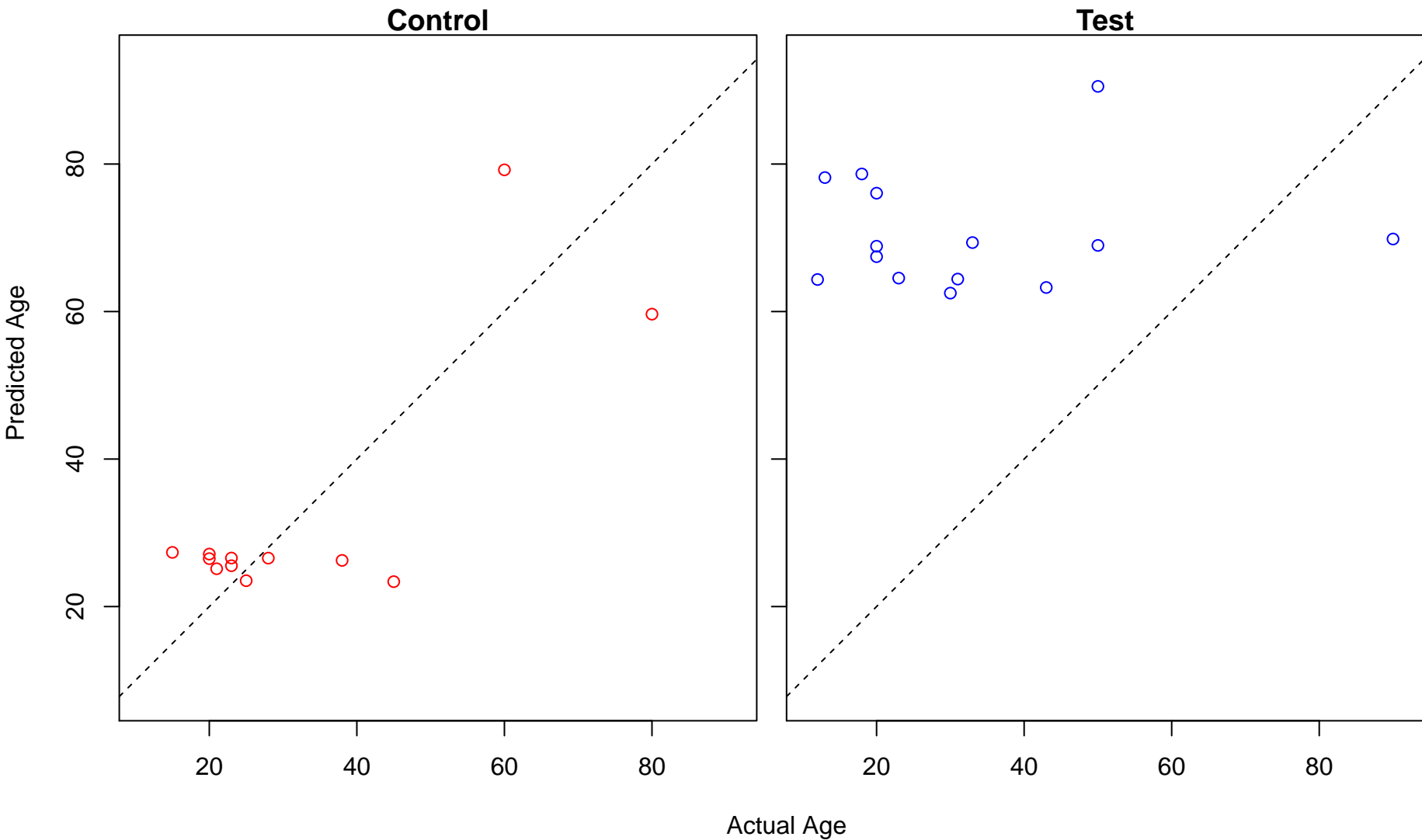
bile acid biosynthetic process (Score: 5.410529)



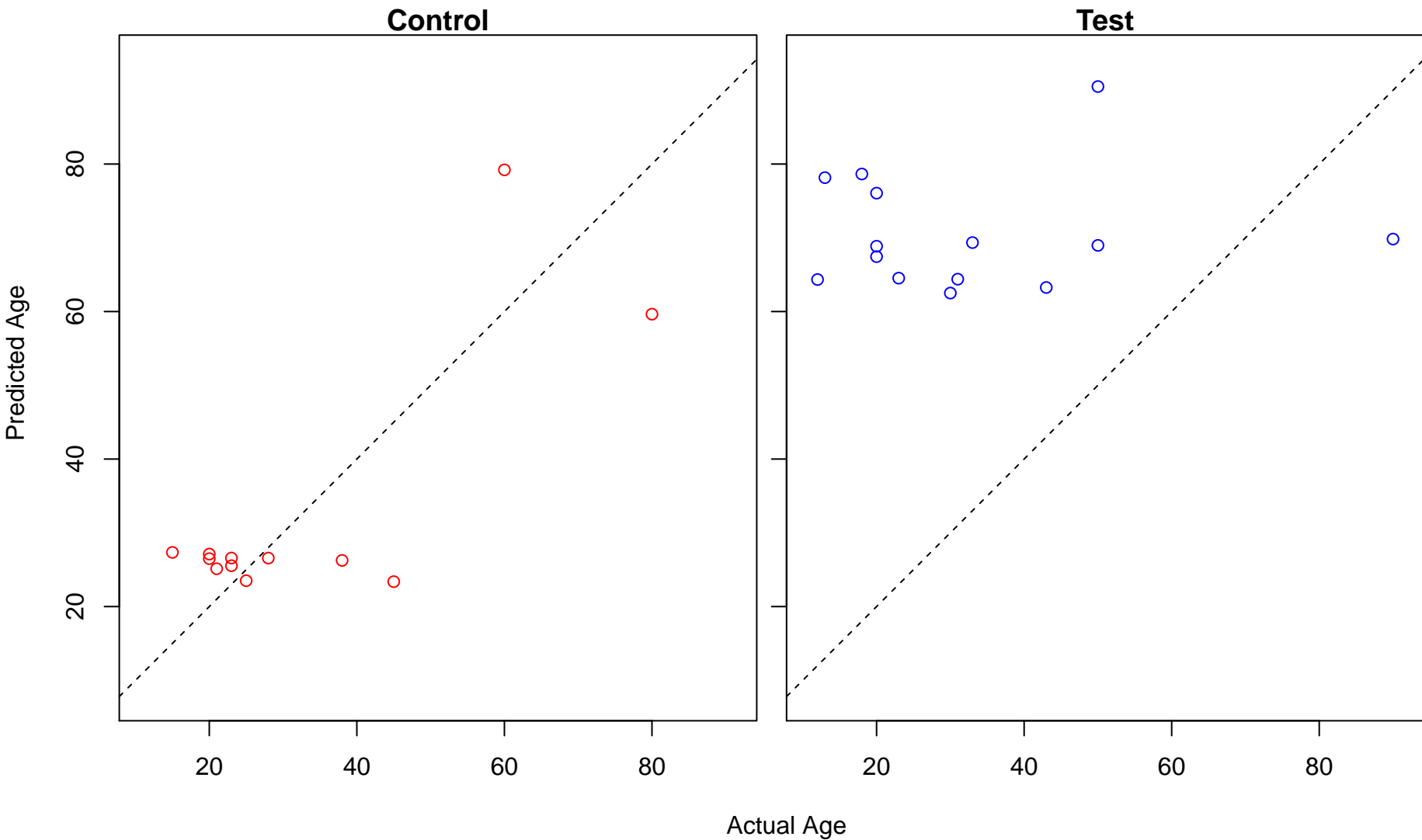
osteoblast differentiation (Score: 5.410438)



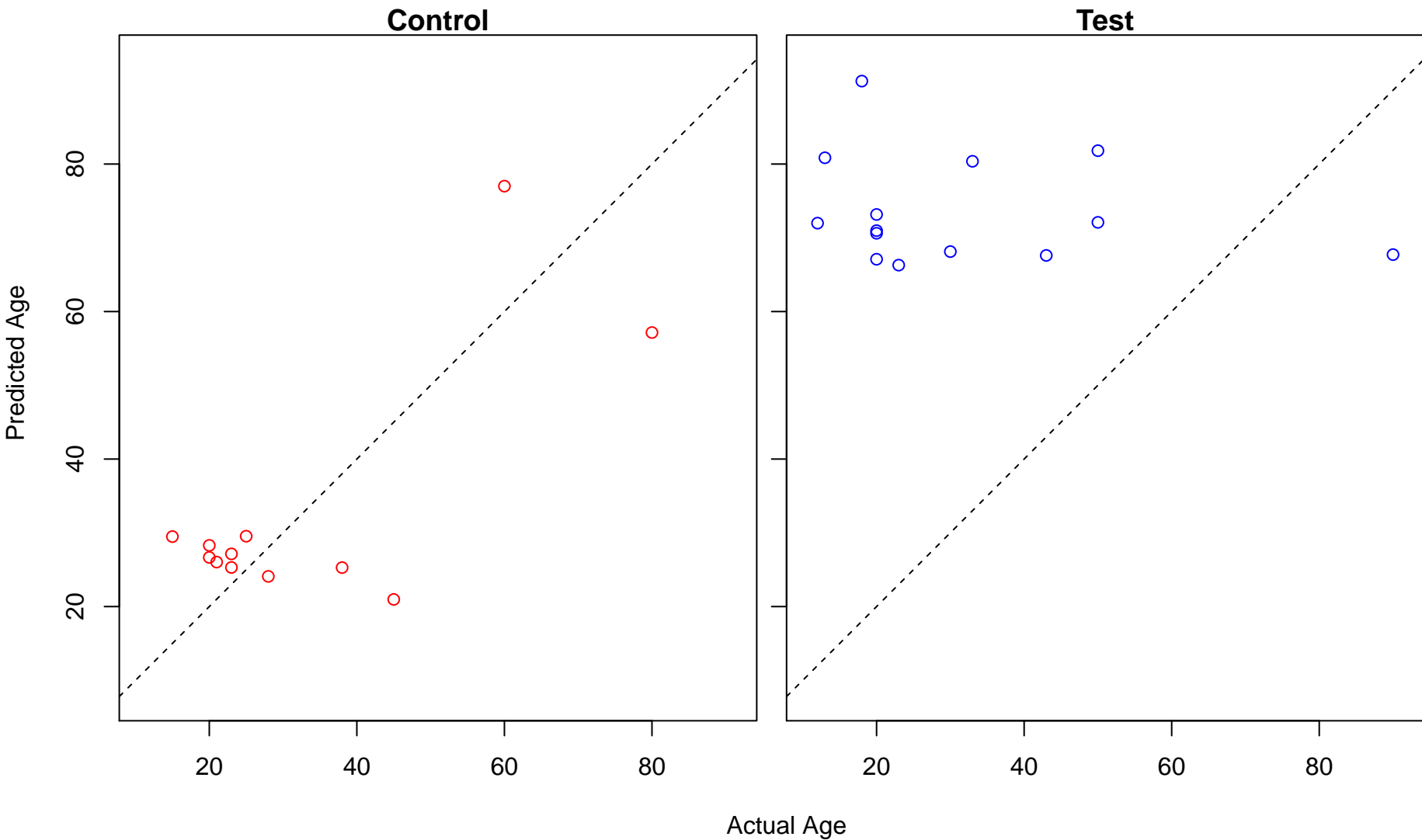
ubiquitin-dependent protein catabolic process (Score: 5.410259)



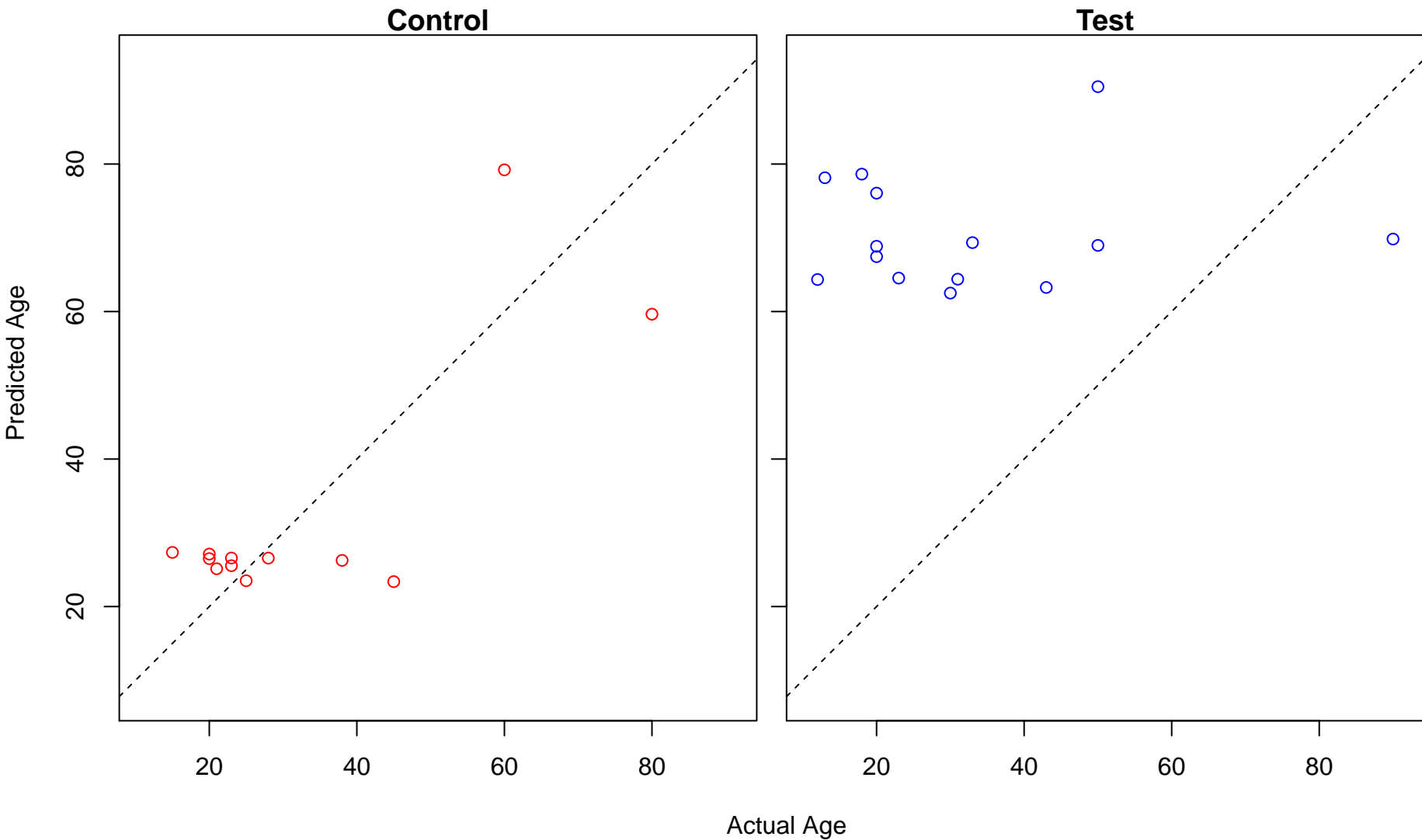
modification-dependent protein catabolic process (Score: 5.409414)



positive regulation of leukocyte apoptotic process (Score: 5.407843)

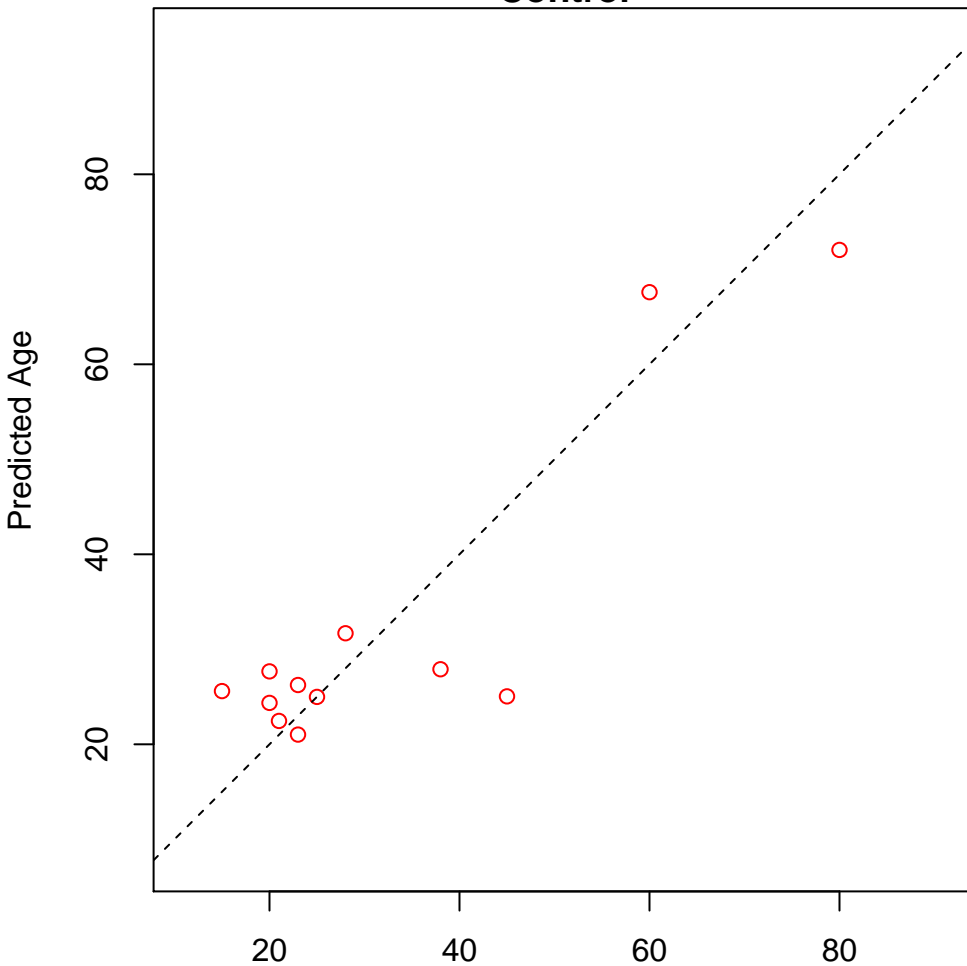


modification-dependent macromolecule catabolic process (Score: 5.407323)

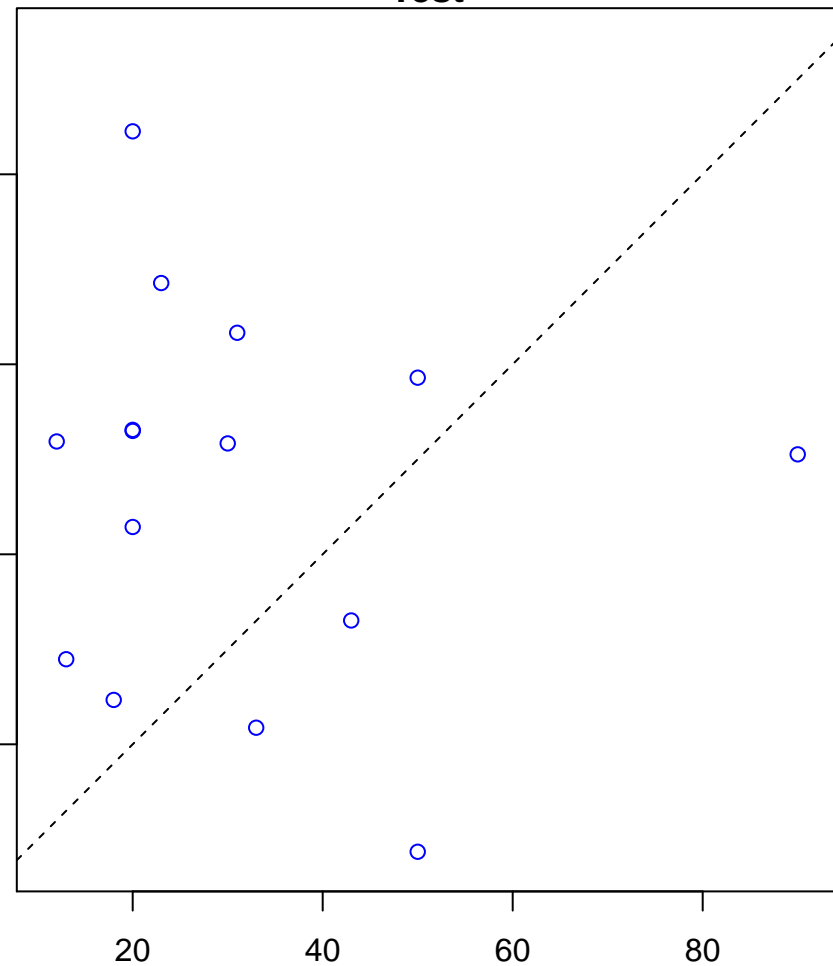


response to extracellular stimulus (Score: 5.406906)

Control

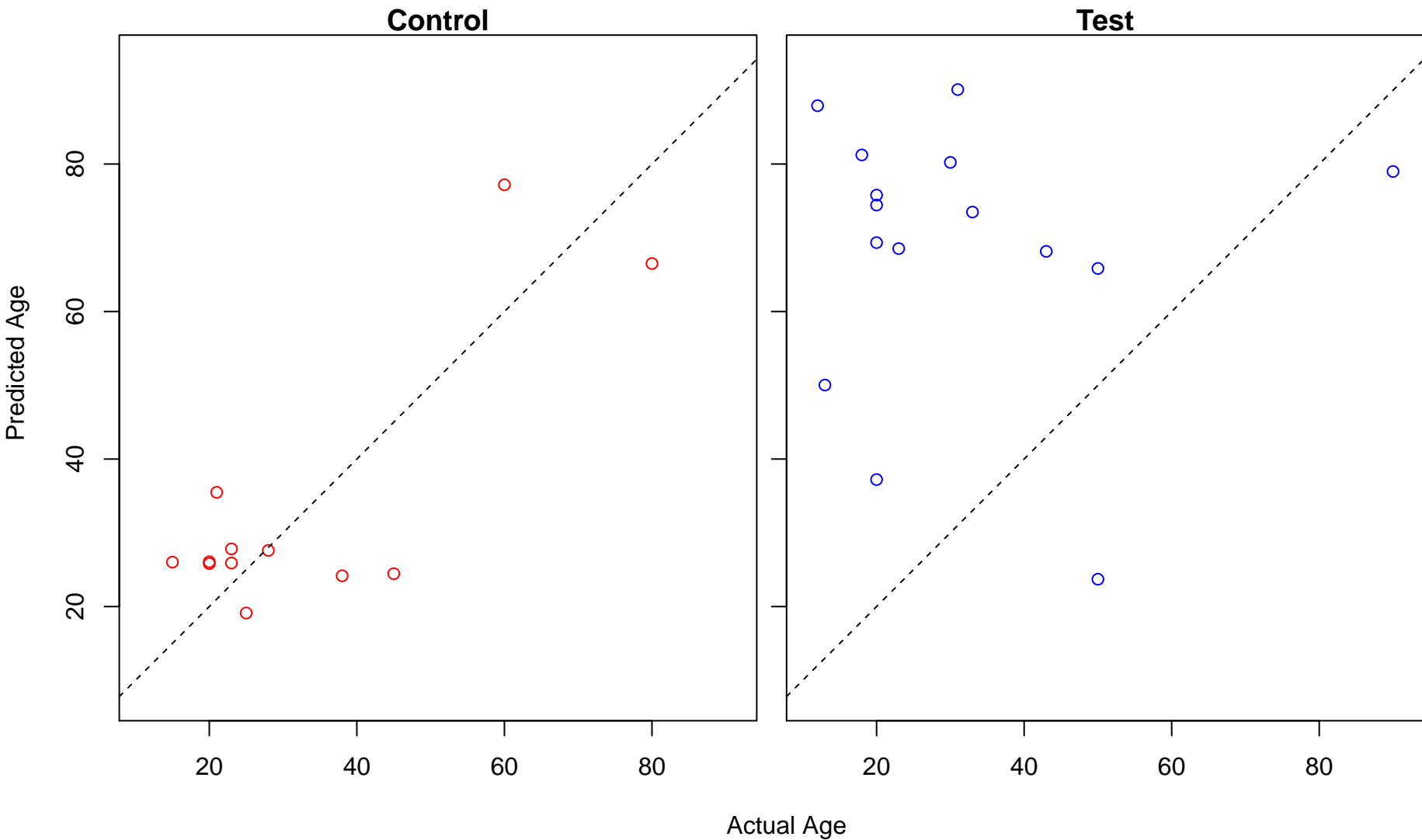


Test

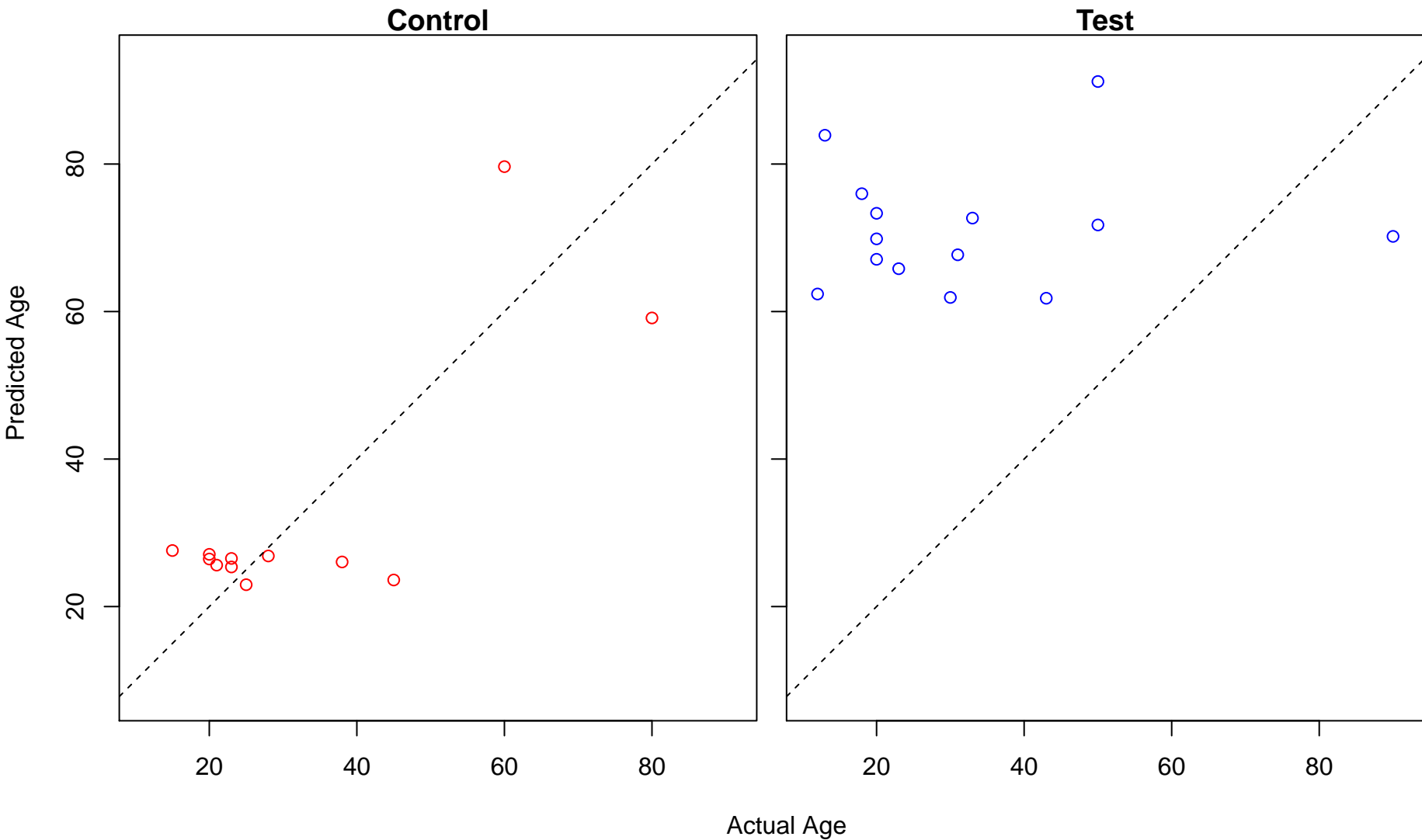


Actual Age

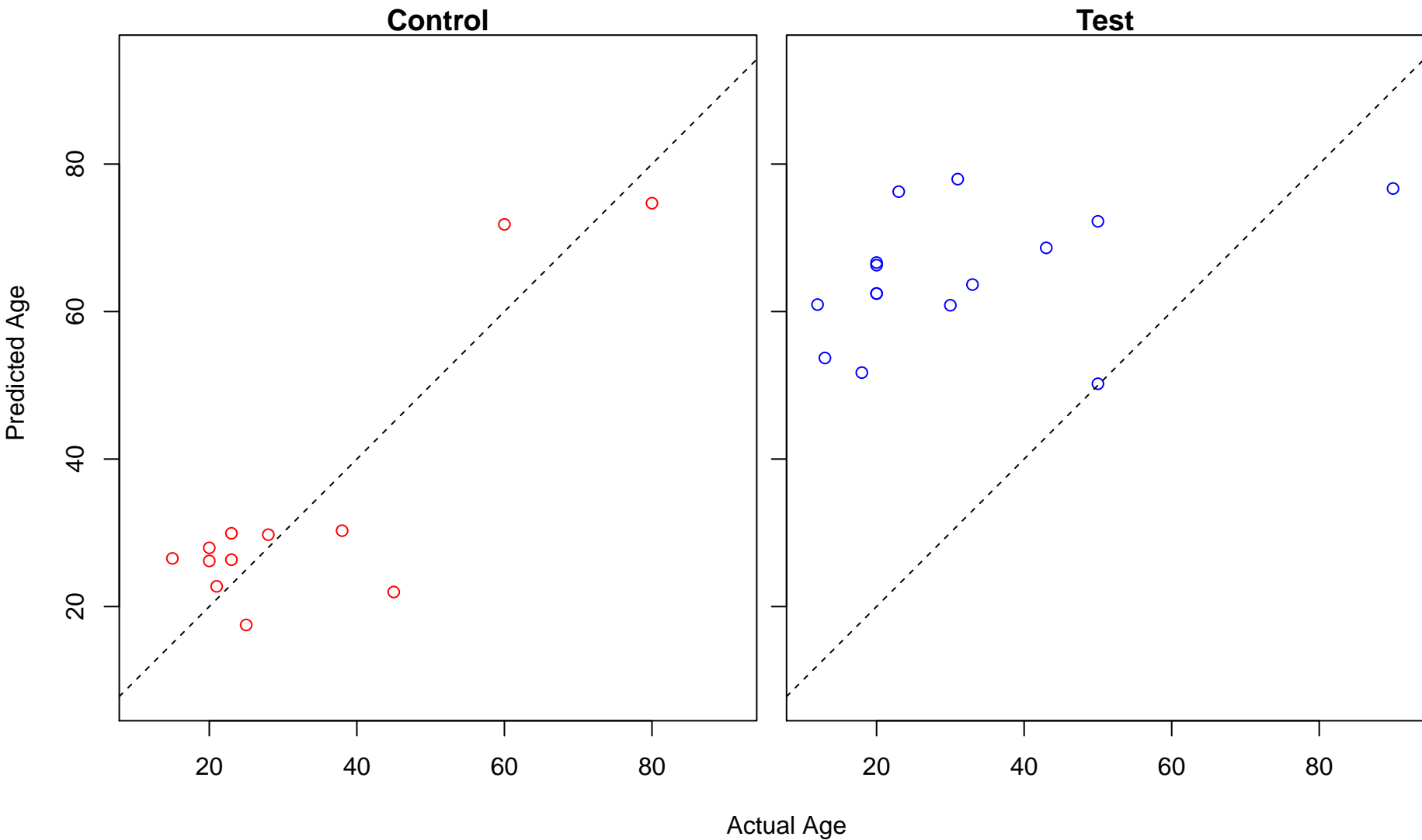
negative regulation of nucleotide catabolic process (Score: 5.406502)



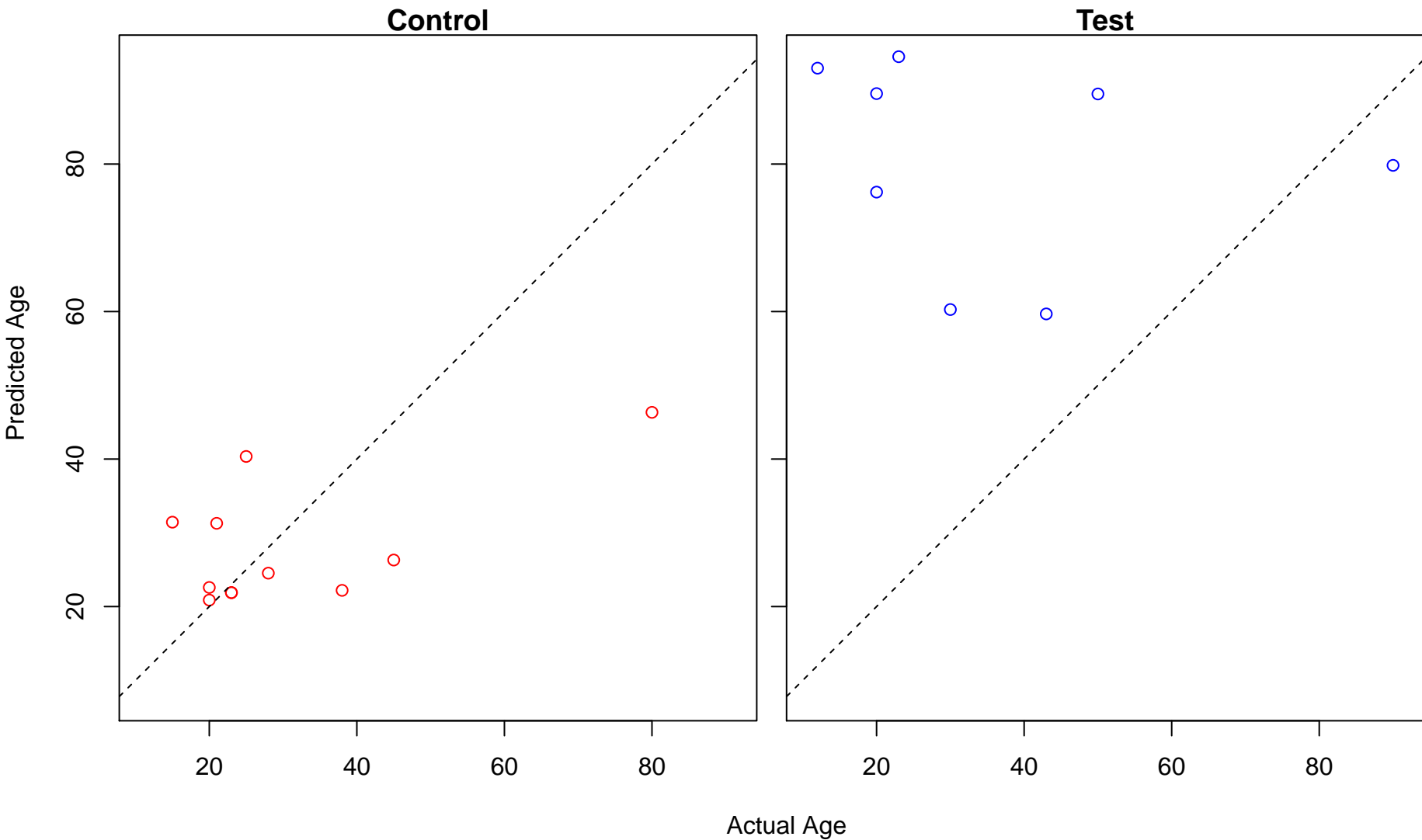
Ras protein signal transduction (Score: 5.405713)



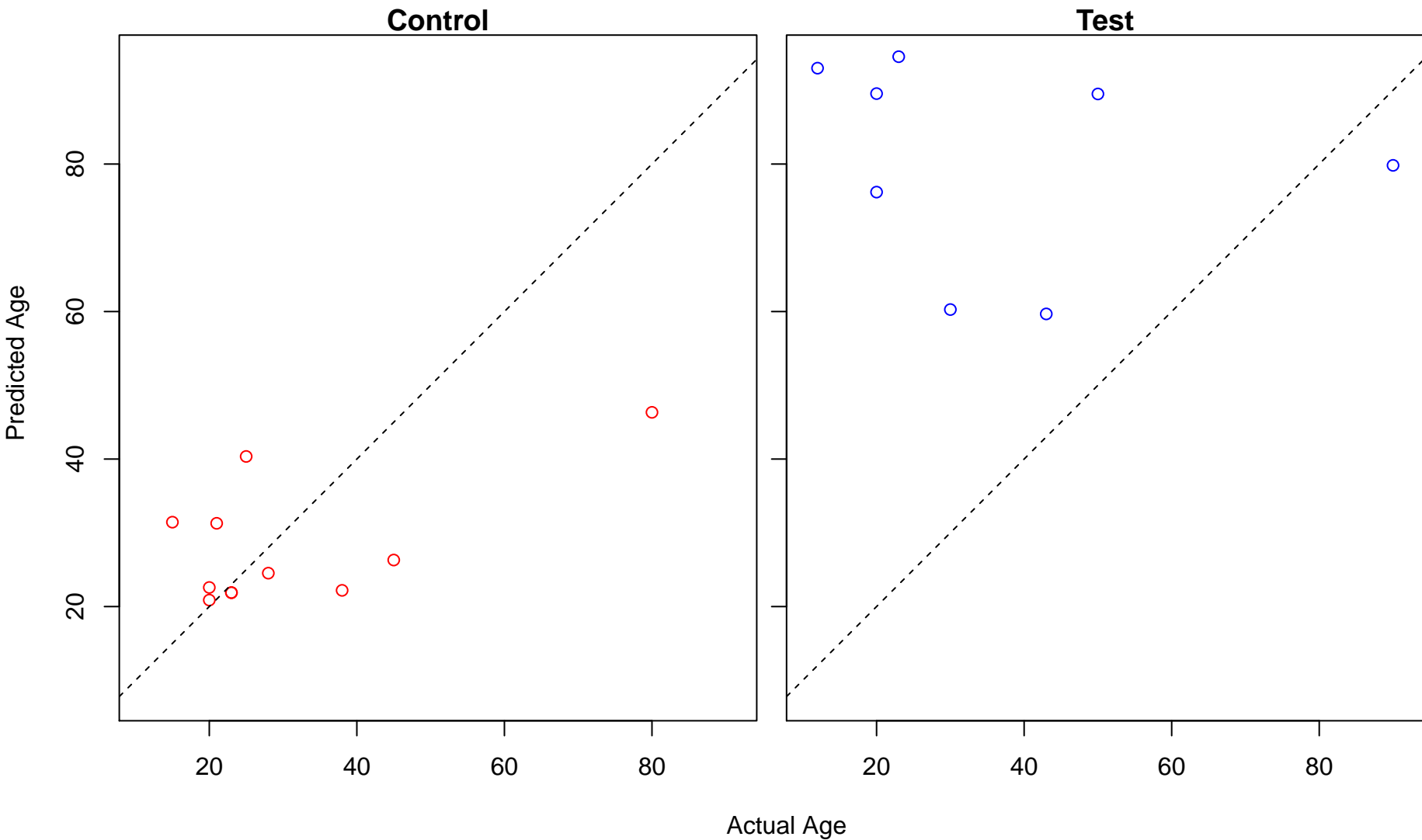
cell projection assembly (Score: 5.405485)



spindle midzone assembly (Score: 5.405129)

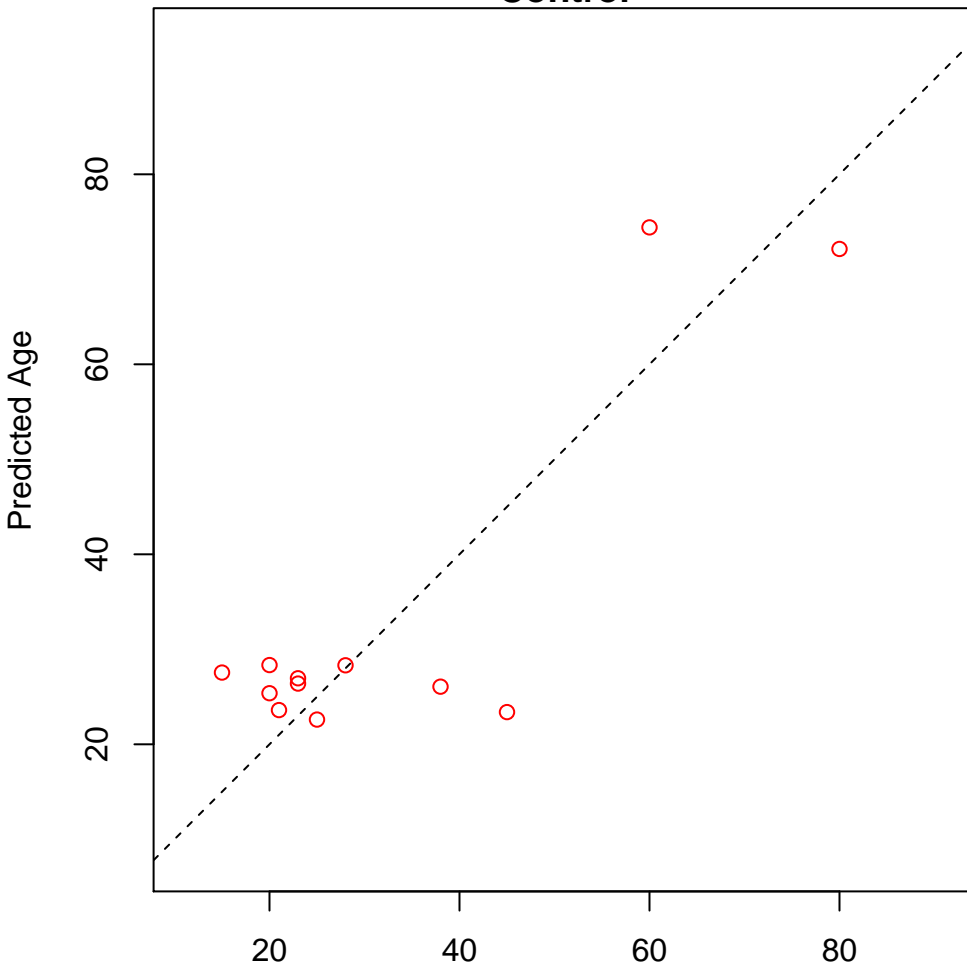


mitotic spindle midzone assembly (Score: 5.405129)

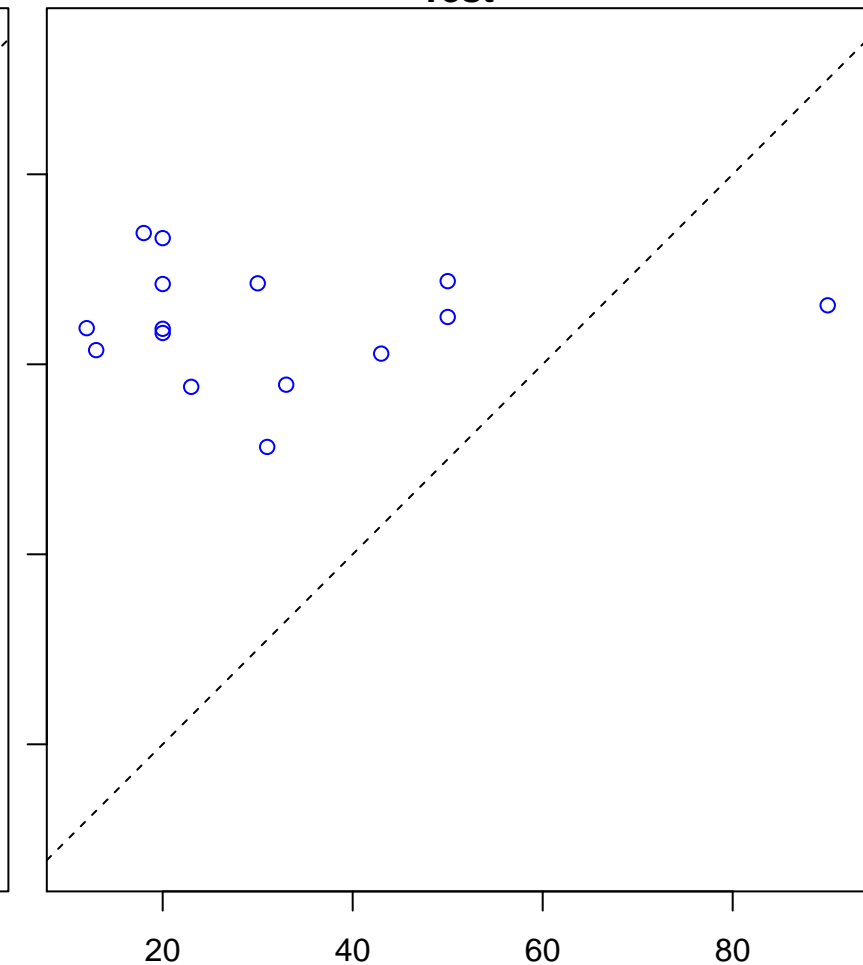


cellular response to unfolded protein (Score: 5.404174)

Control

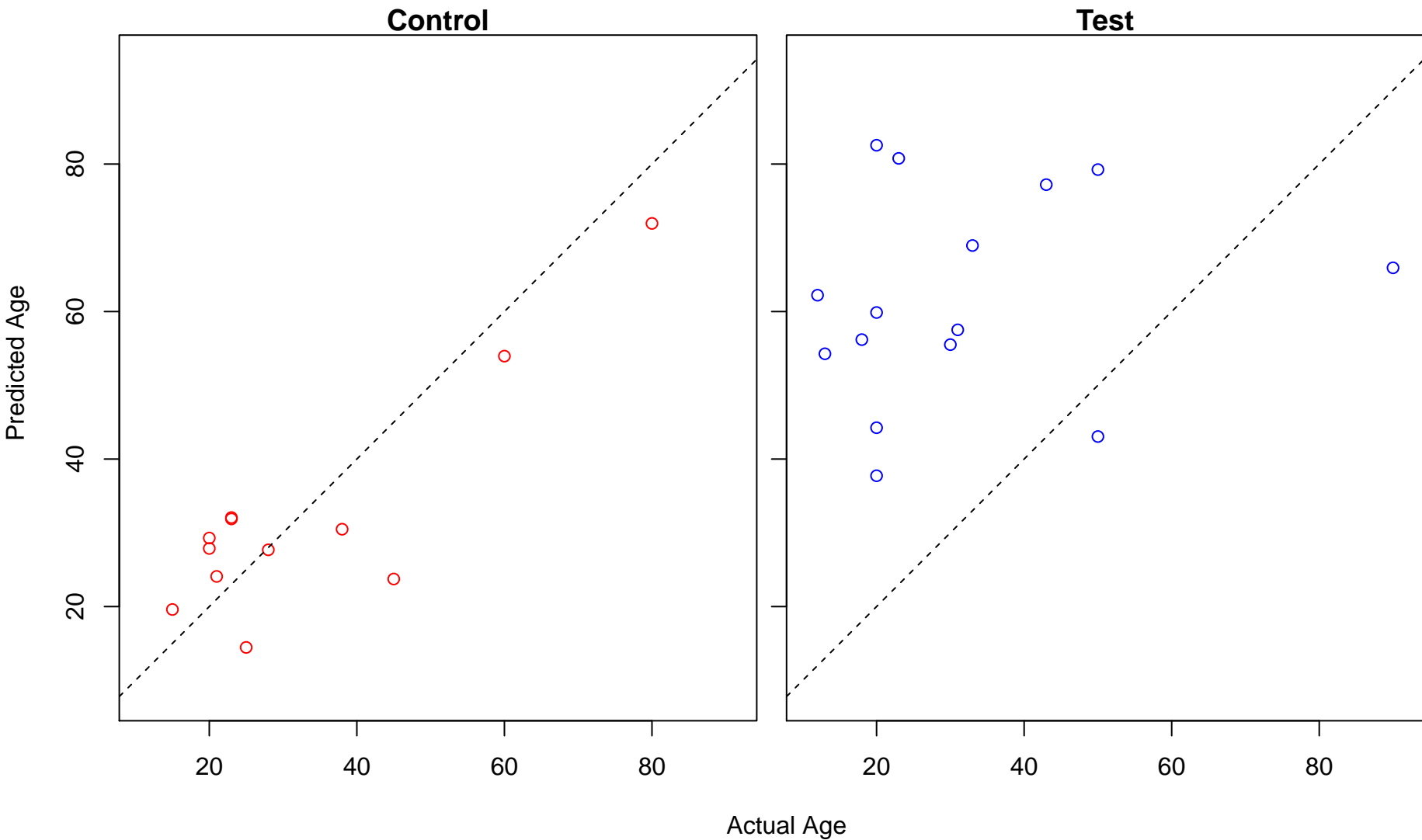


Test

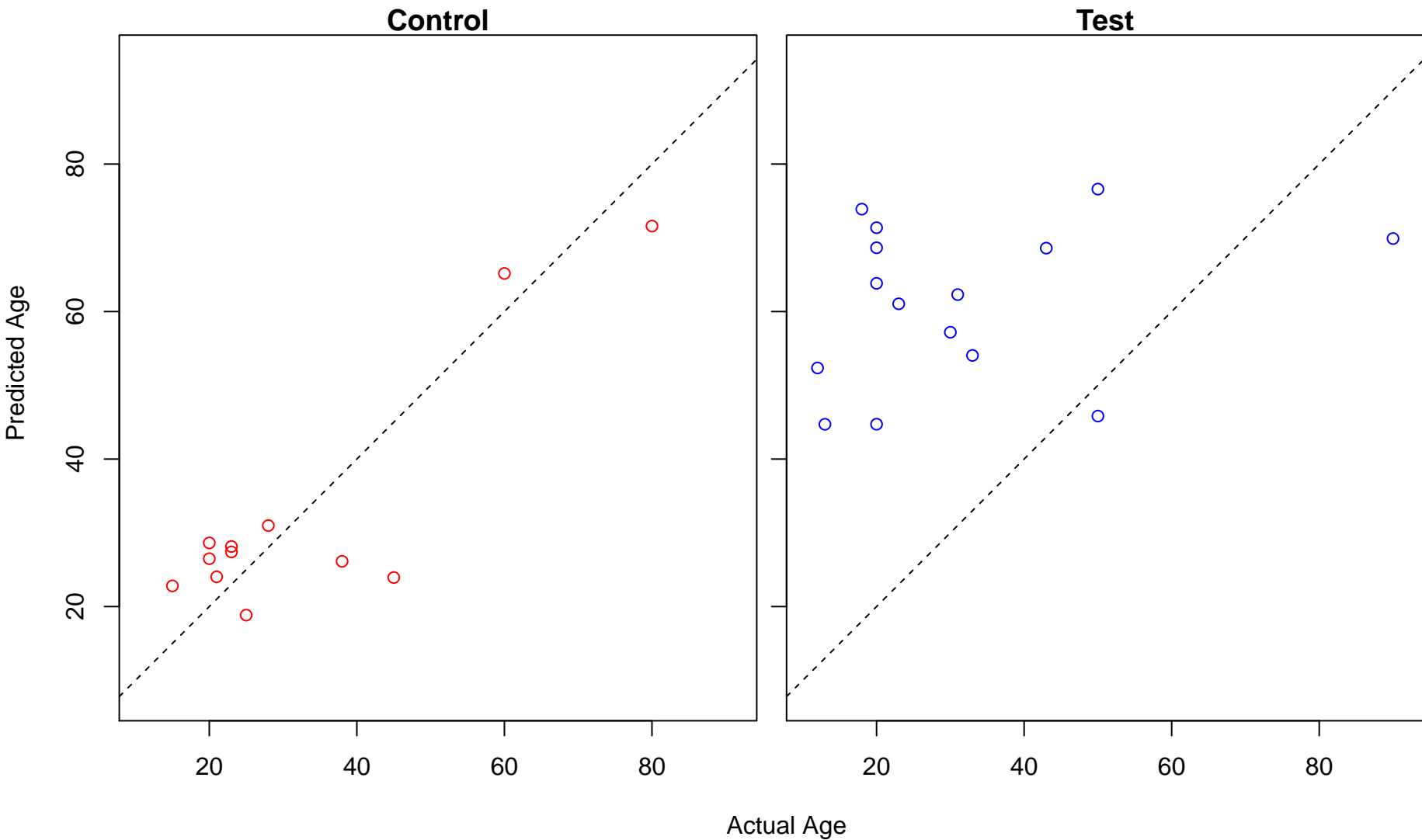


Actual Age

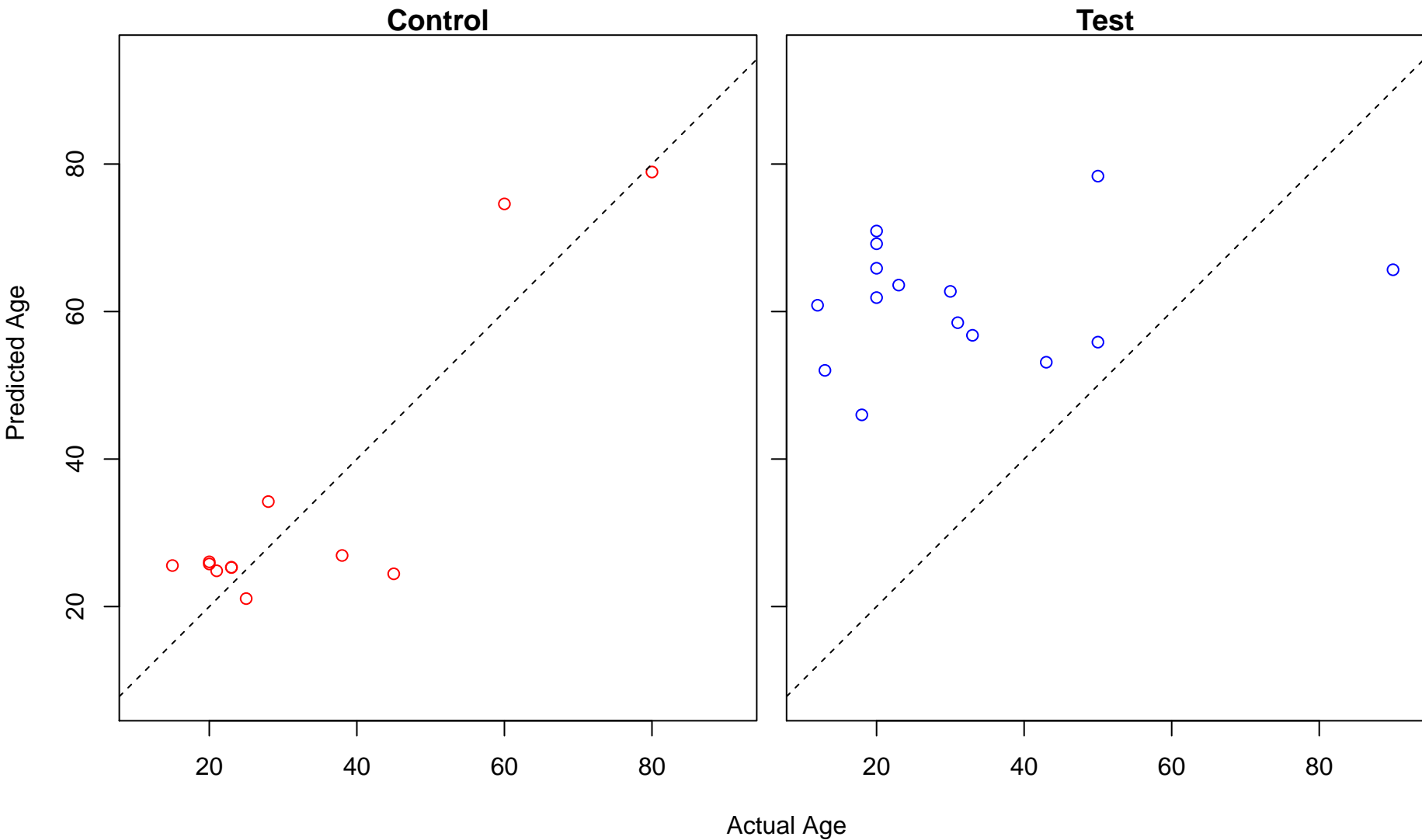
regulation of hematopoietic stem cell proliferation (Score: 5.403804)



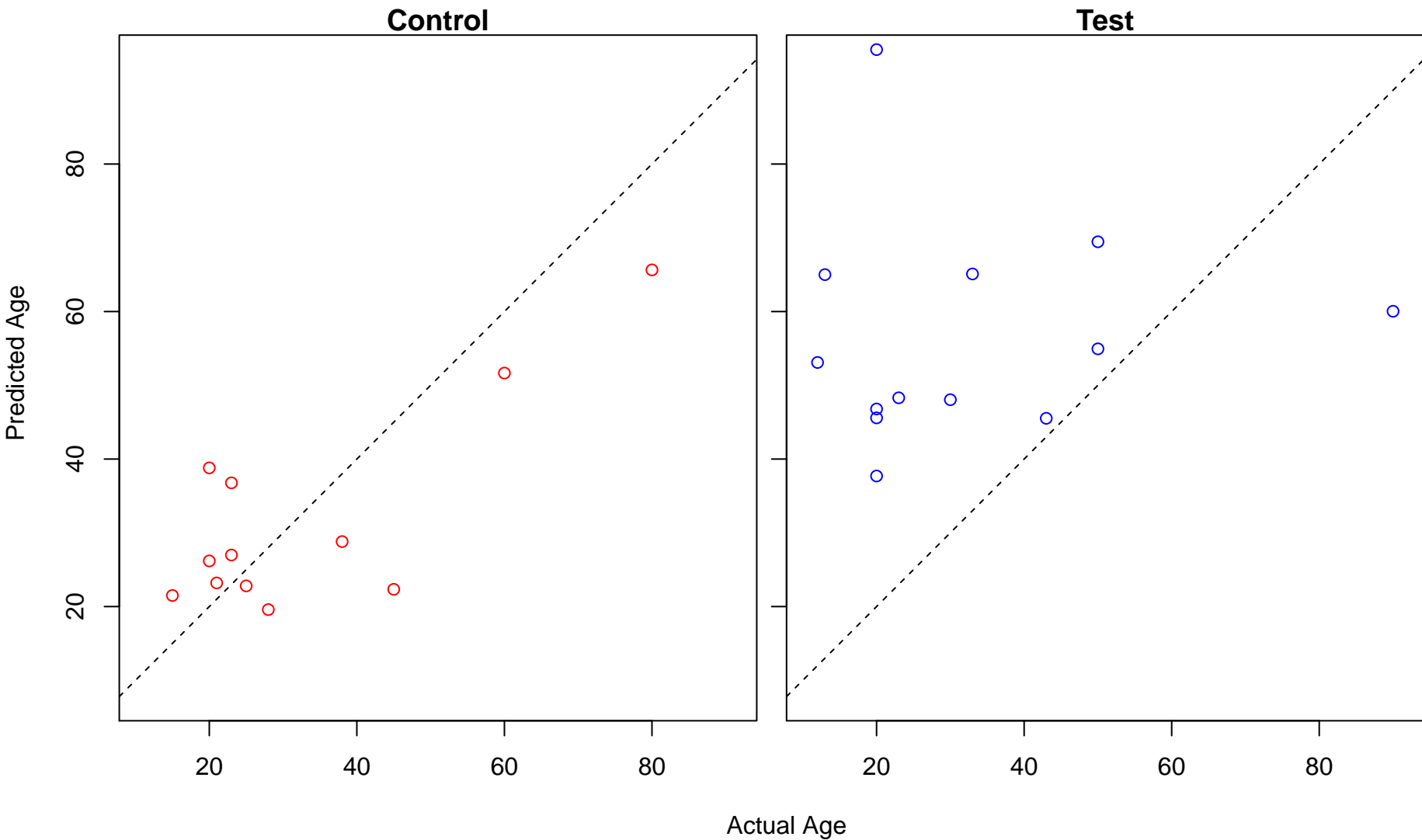
positive regulation of wound healing (Score: 5.403685)



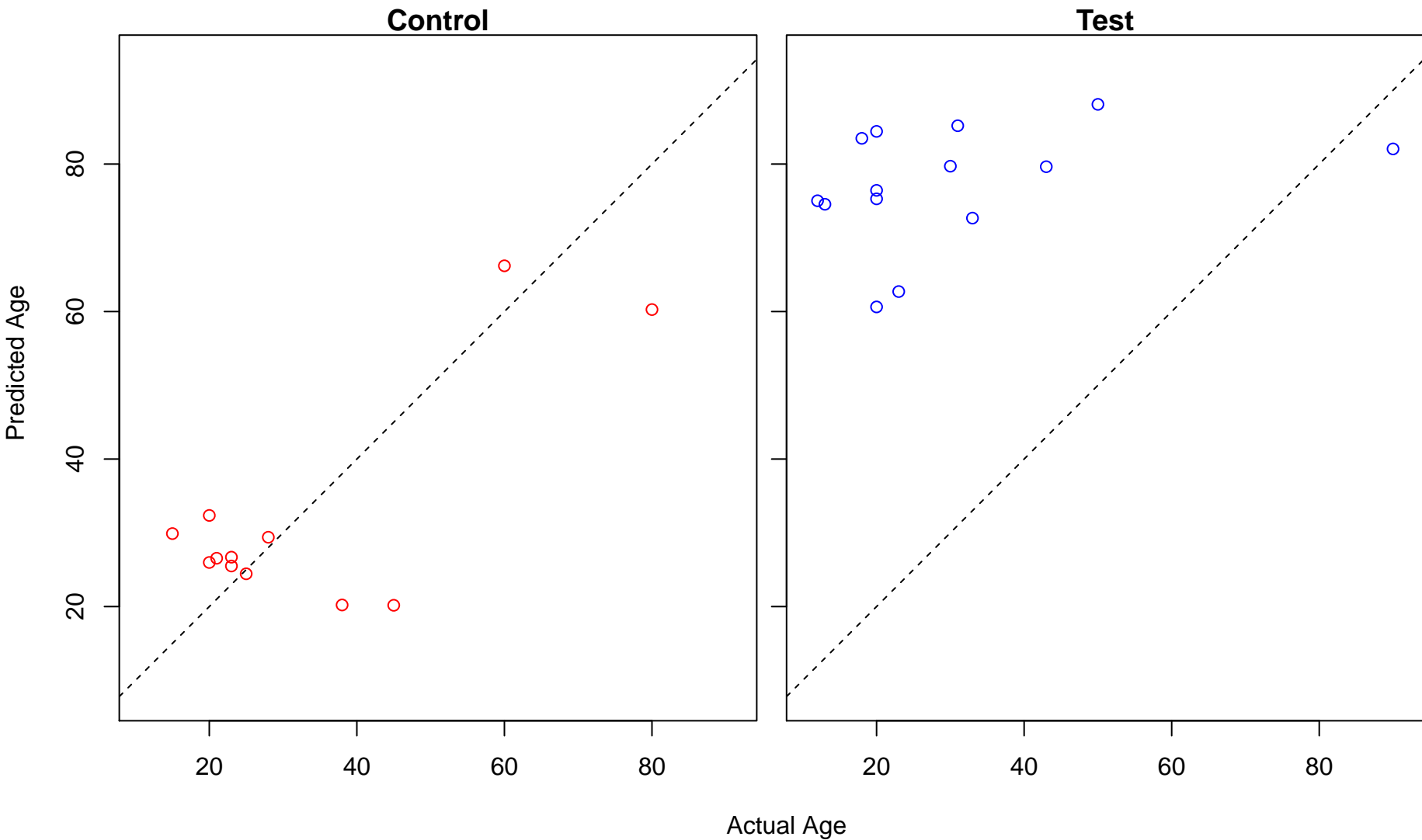
regulation of DNA recombination (Score: 5.402497)



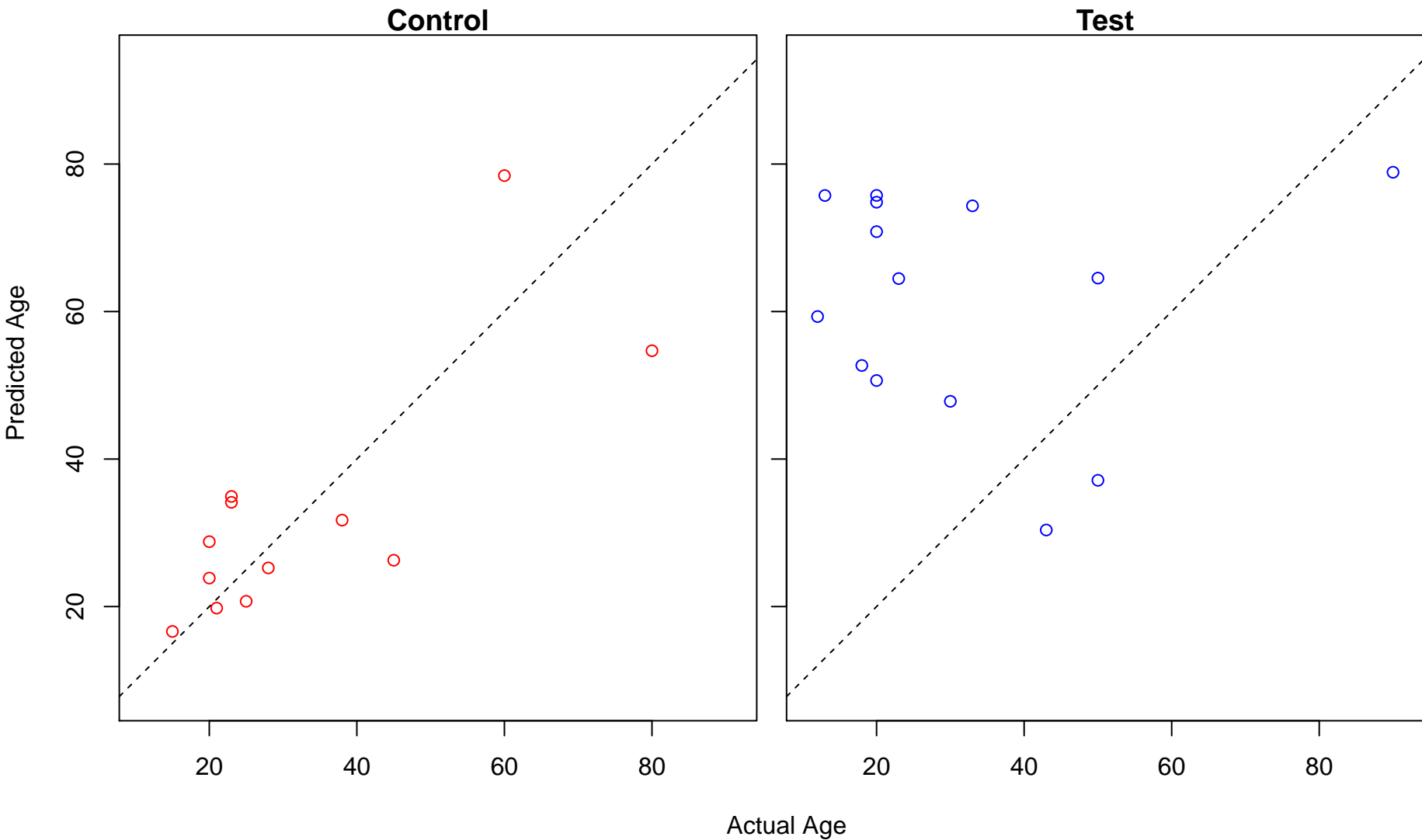
response to pain (Score: 5.401325)



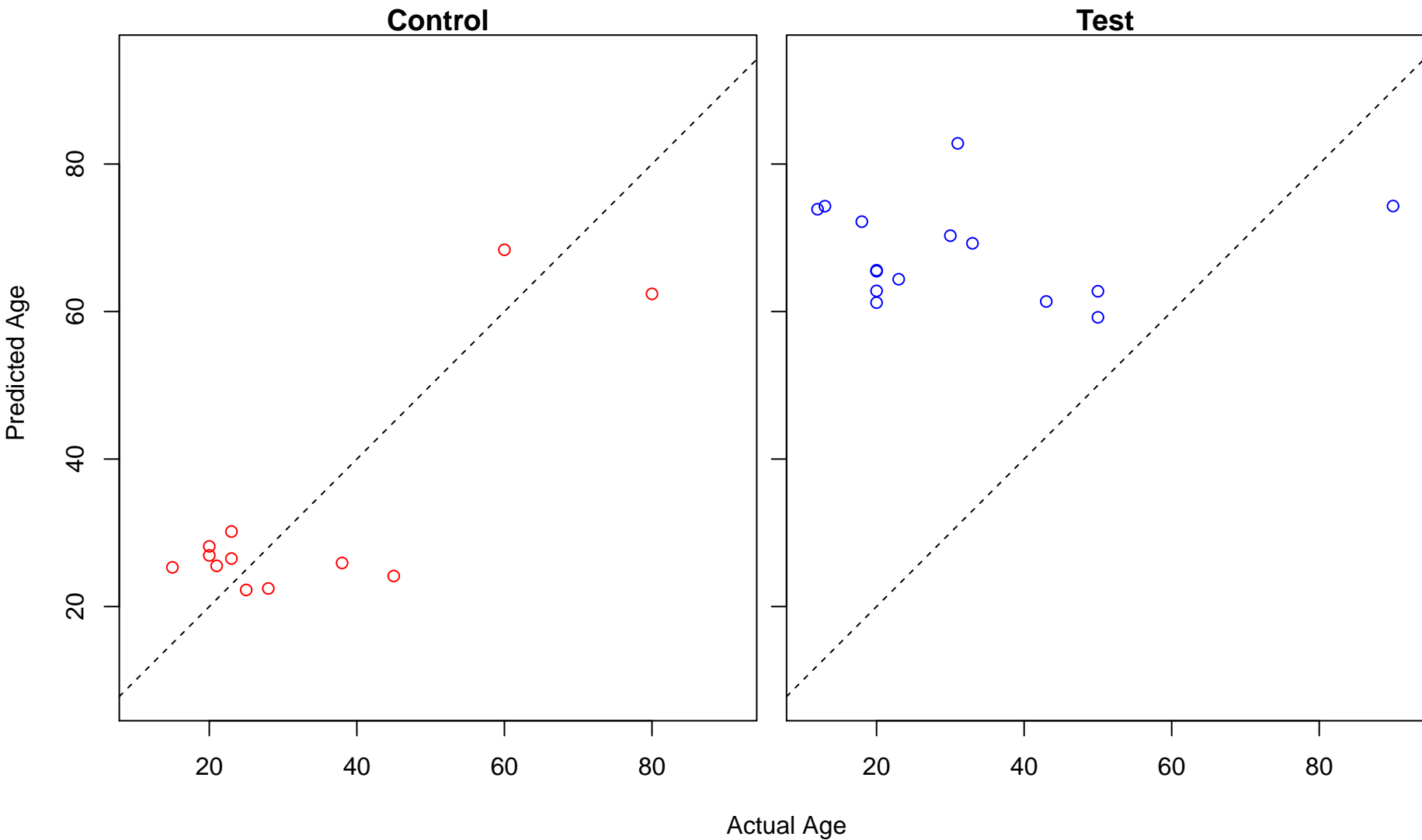
sodium ion homeostasis (Score: 5.400721)



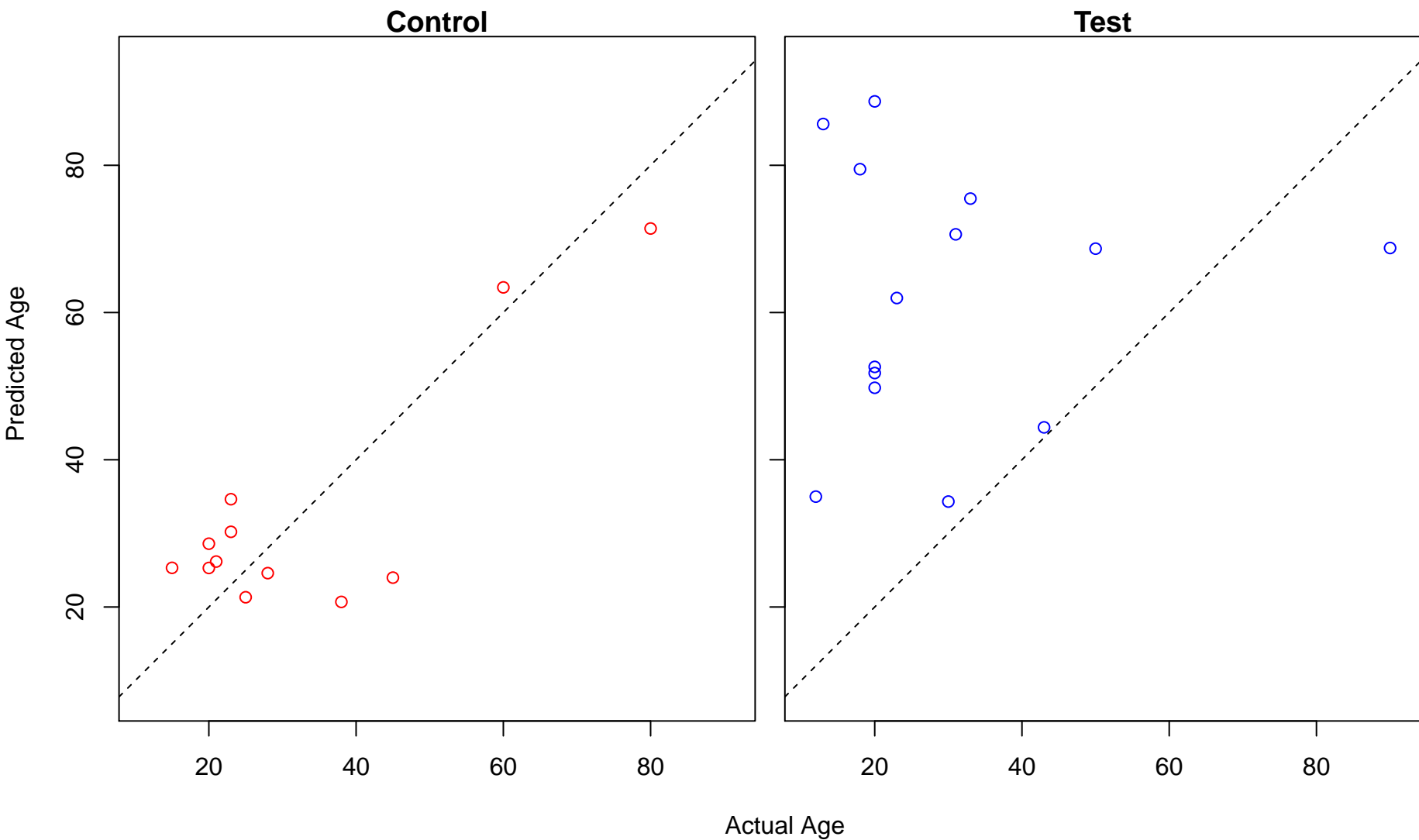
dendritic cell differentiation (Score: 5.400026)



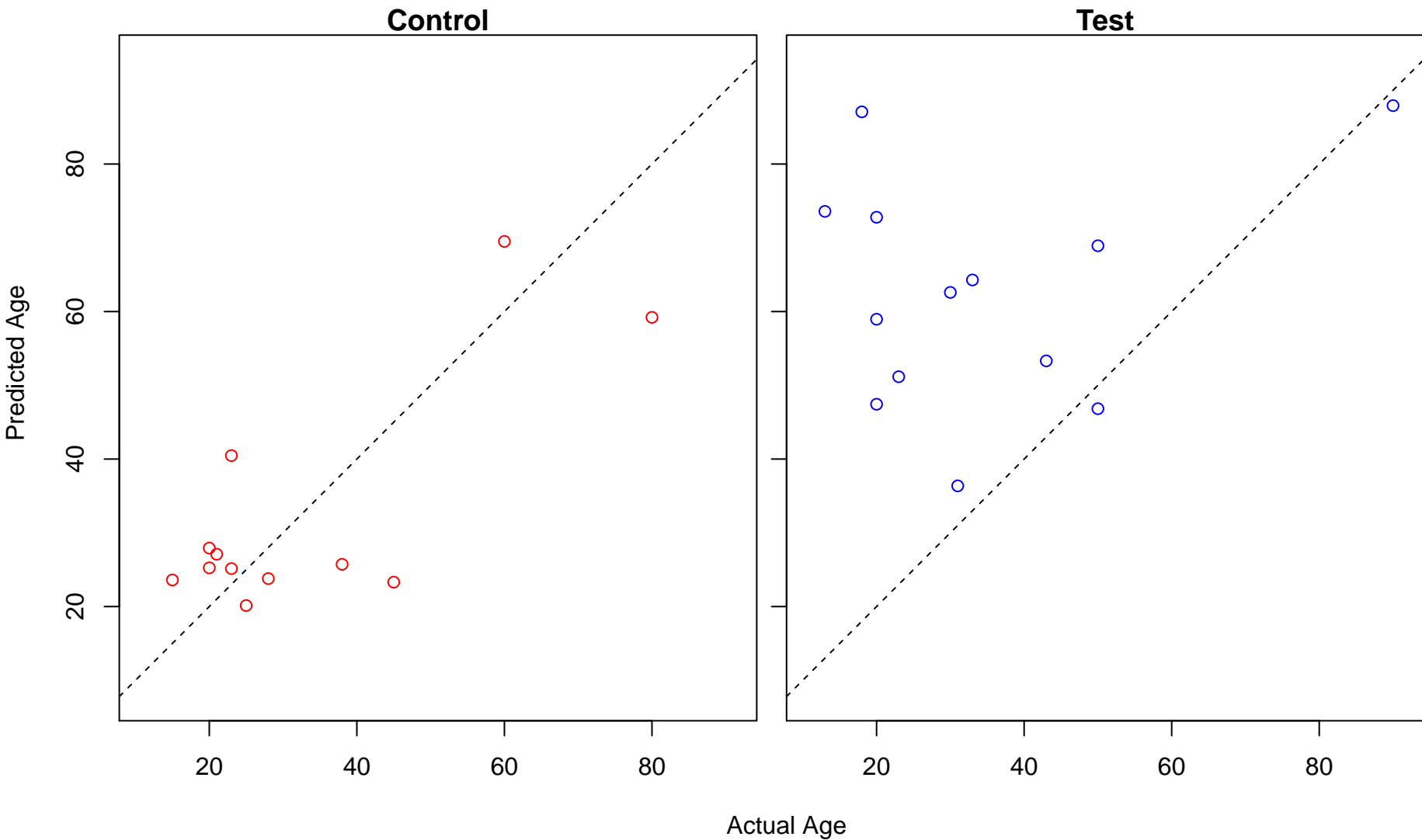
positive regulation of neuron apoptotic process (Score: 5.399149)



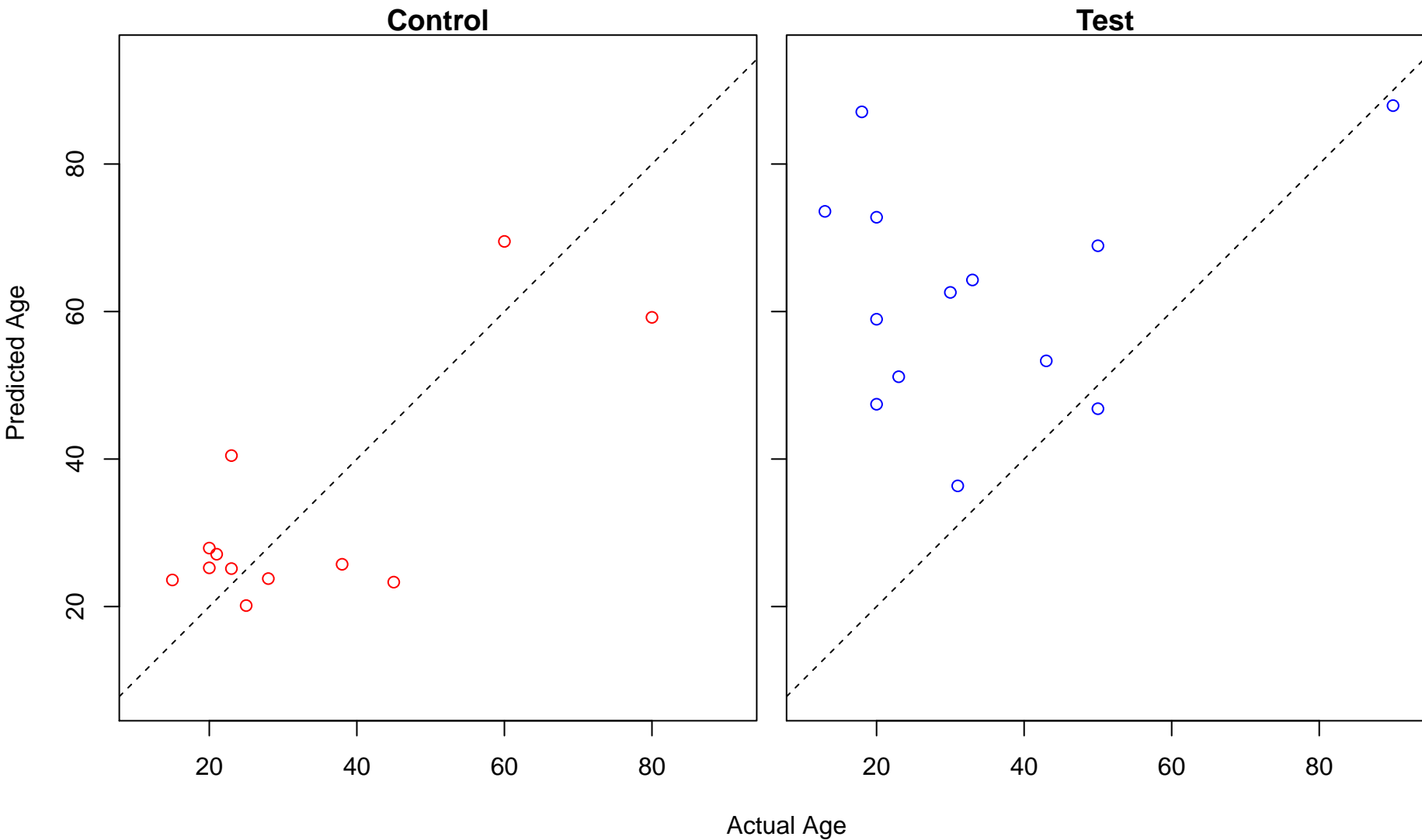
lipid homeostasis (Score: 5.398333)



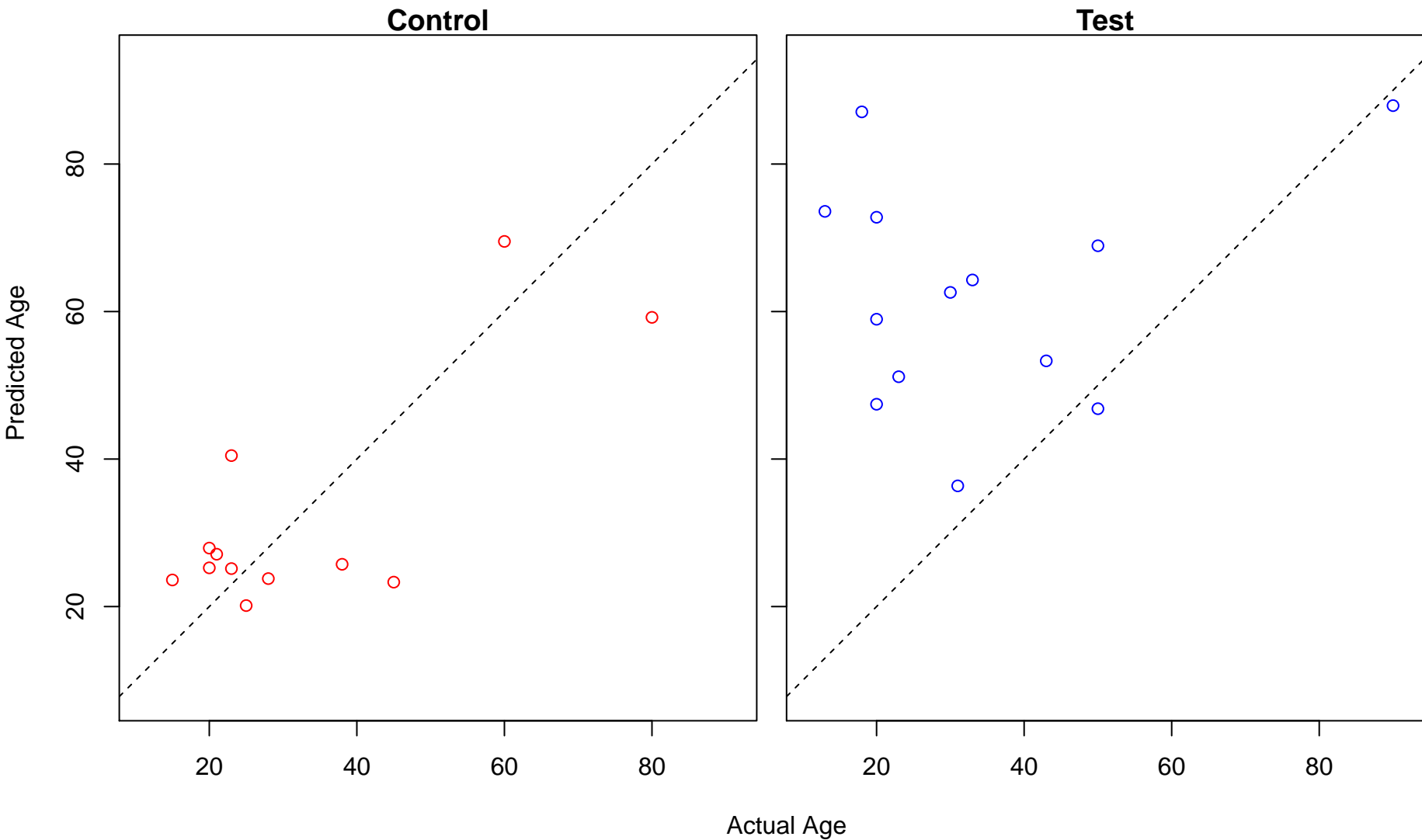
histidine metabolic process (Score: 5.397974)



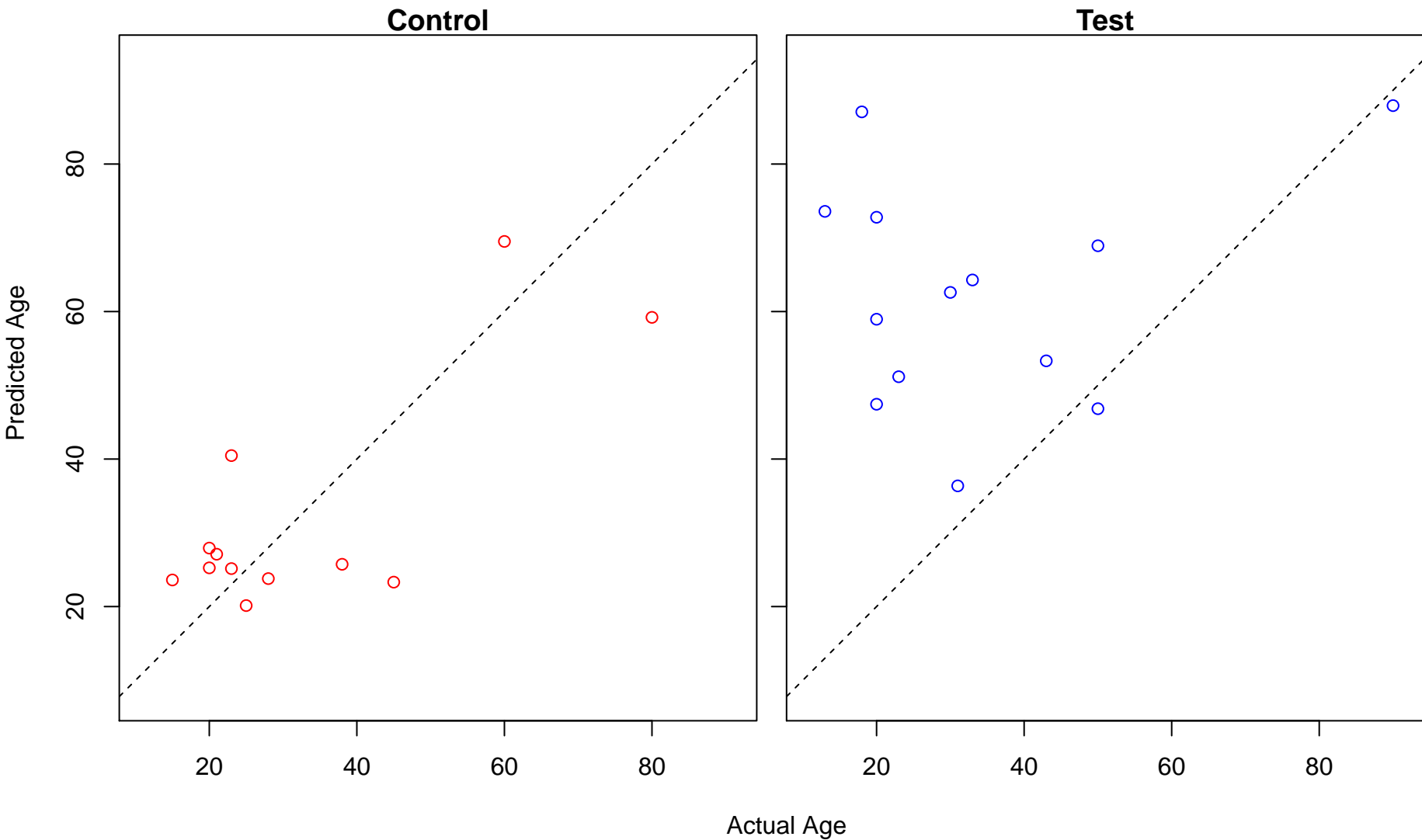
histidine catabolic process (Score: 5.397974)



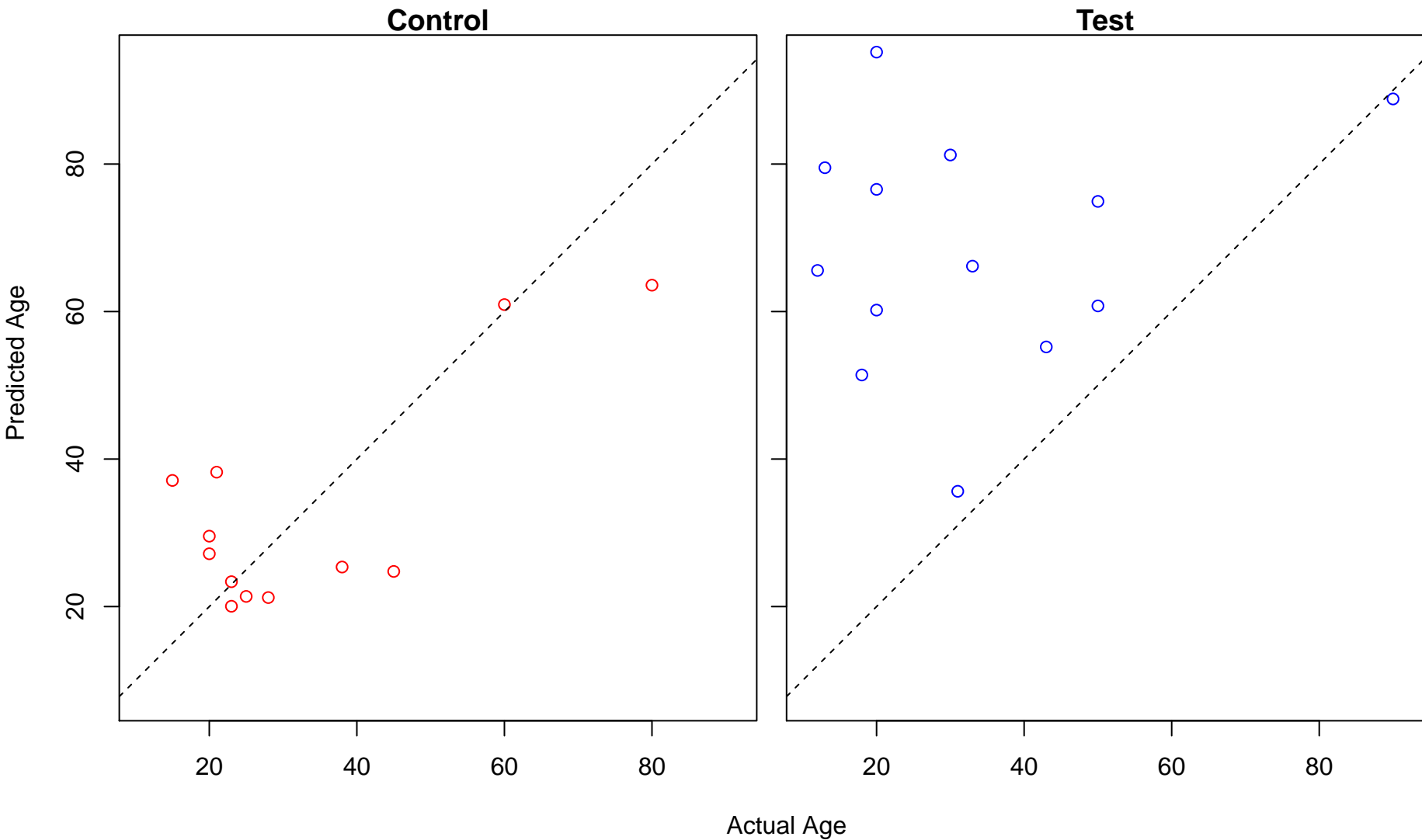
imidazole-containing compound catabolic process (Score: 5.397974)



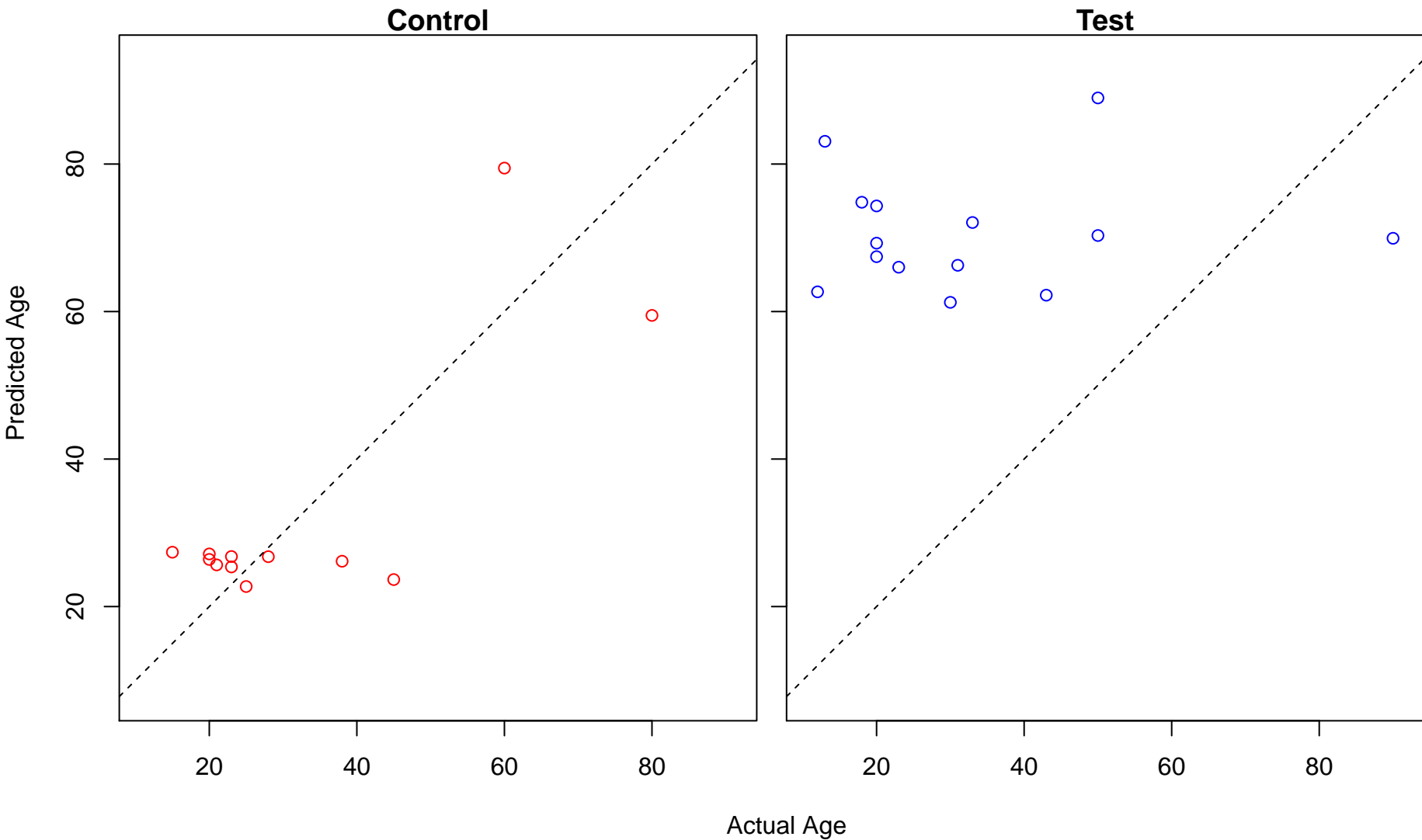
imidazole-containing compound metabolic process (Score: 5.397836)



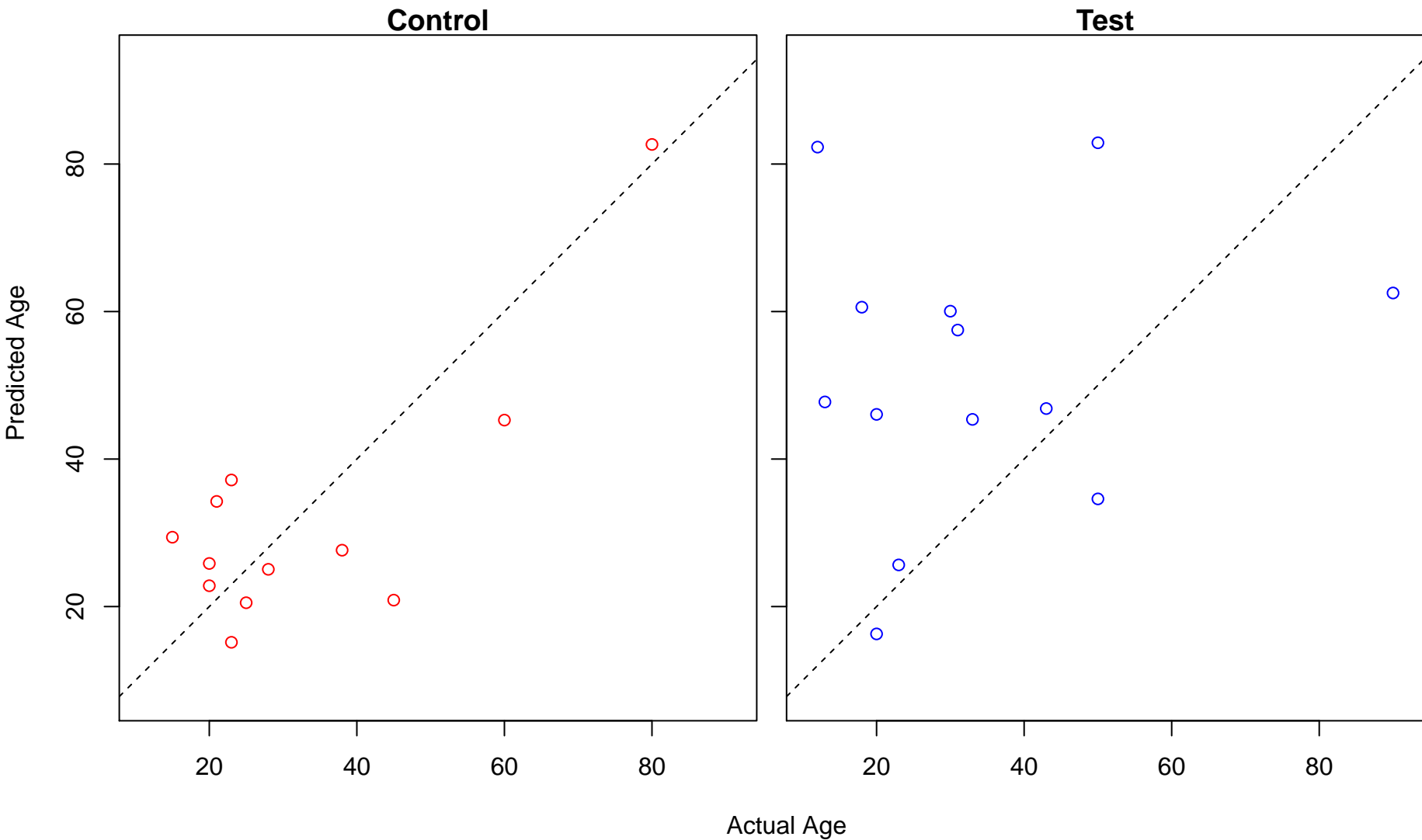
lens development in camera-type eye (Score: 5.395645)



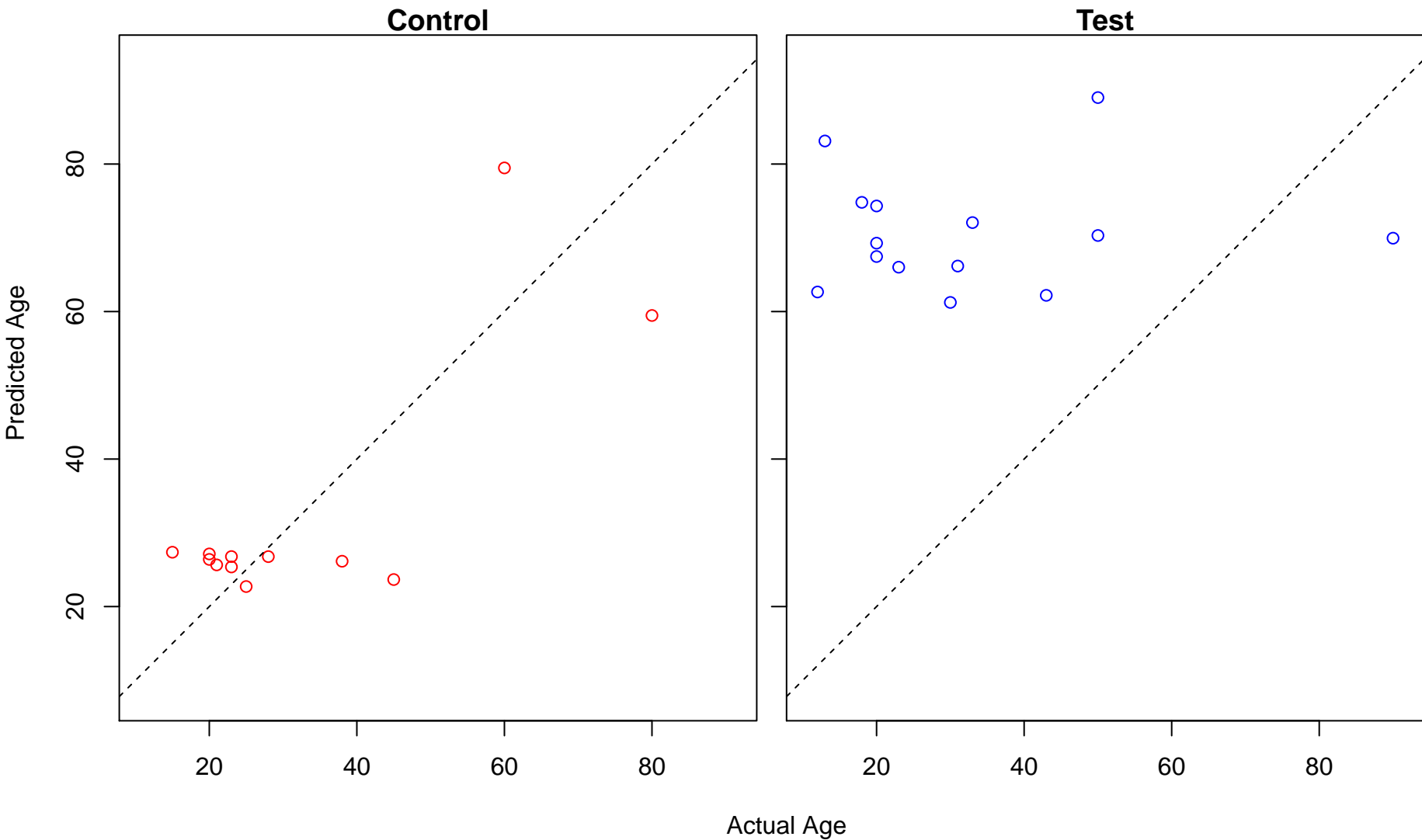
signal transduction by protein phosphorylation (Score: 5.394623)



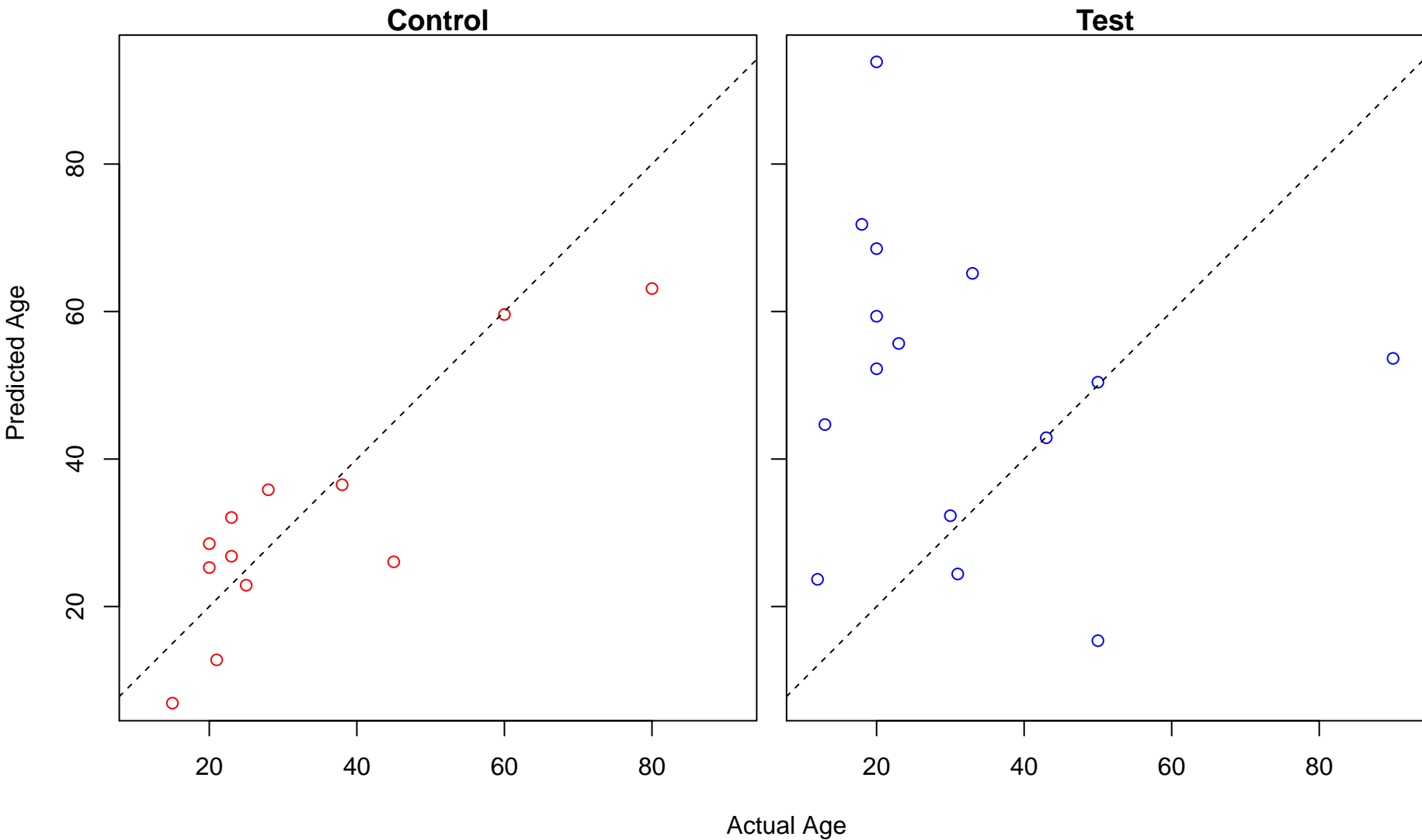
cellular response to metal ion (Score: 5.394549)



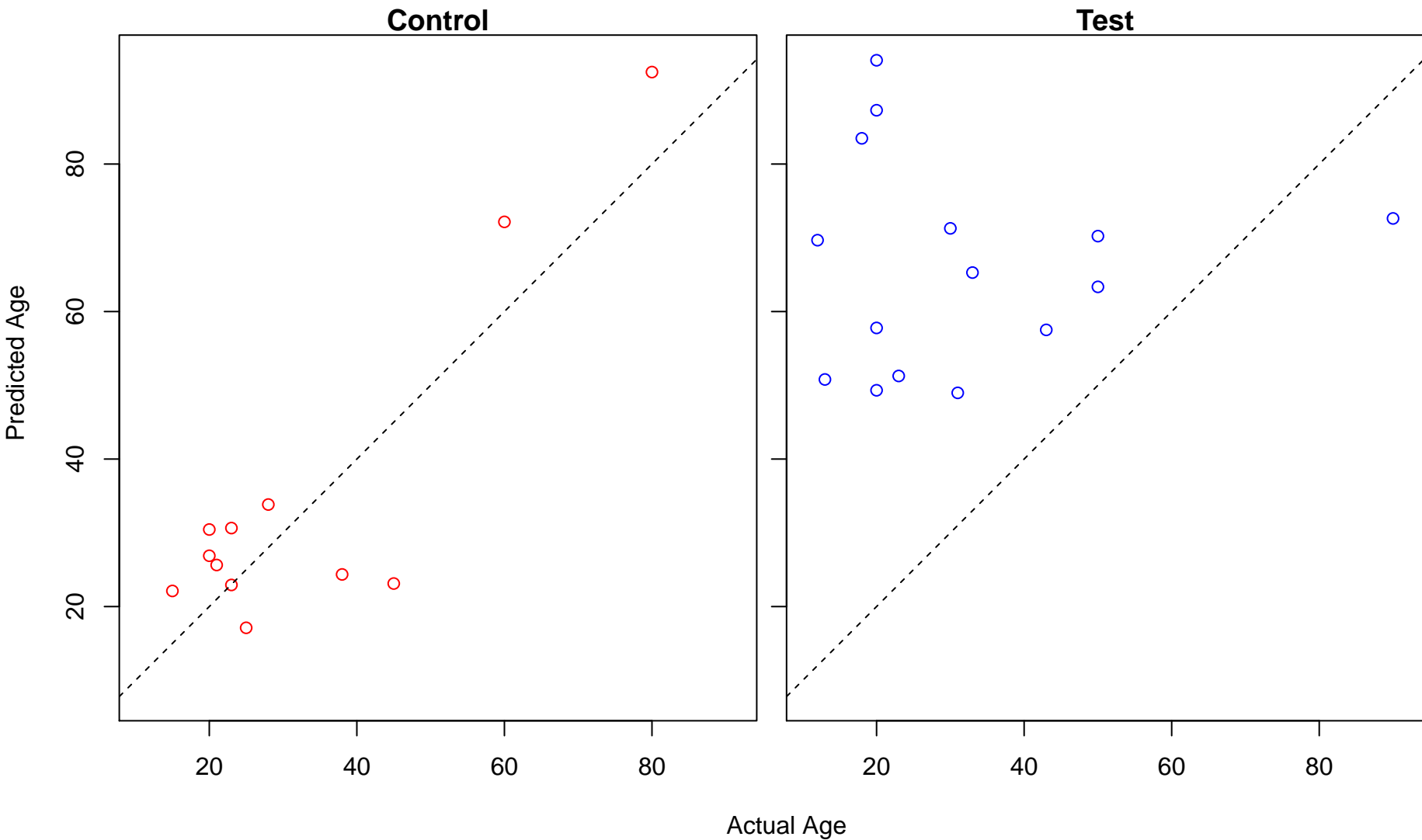
MAPK cascade (Score: 5.392934)



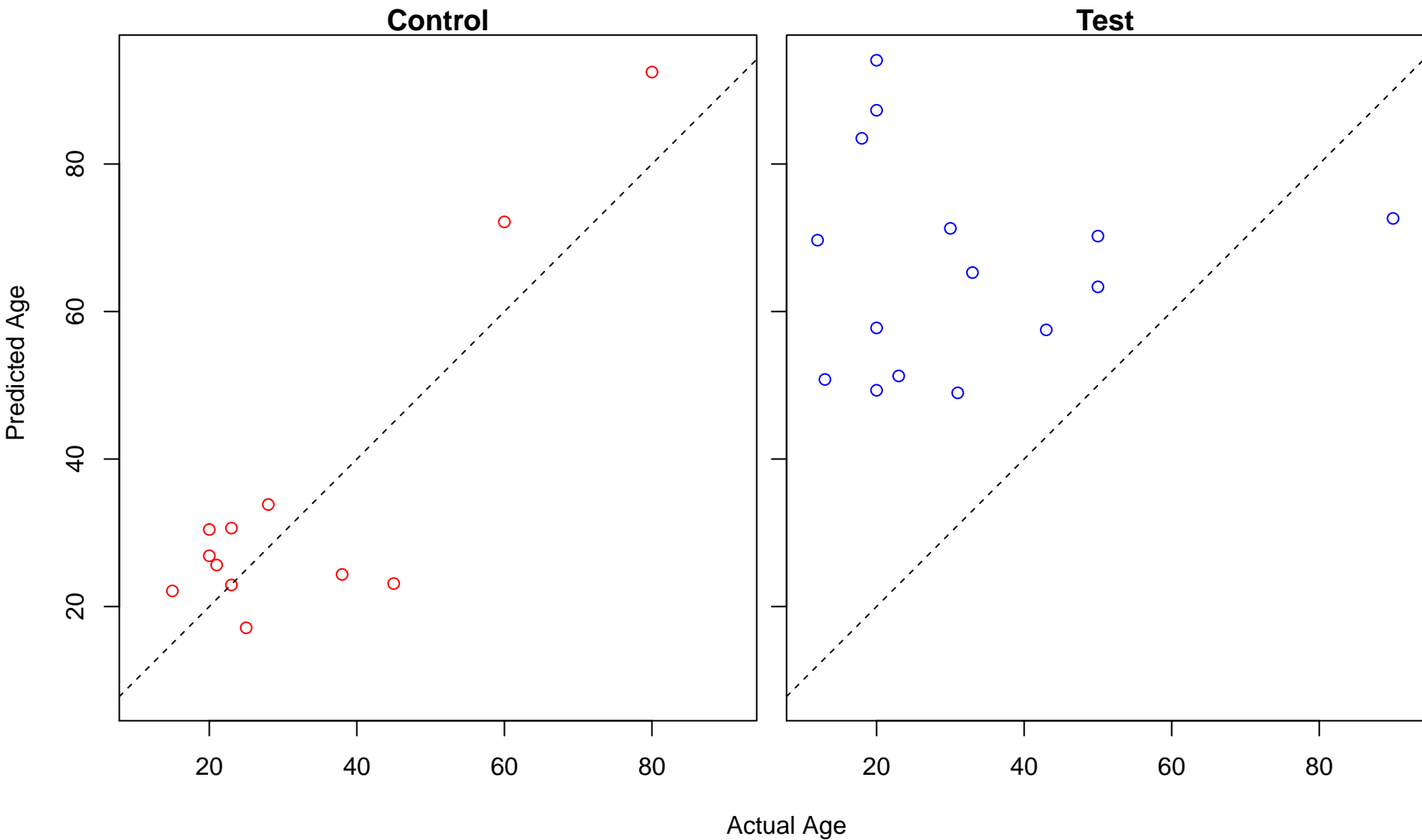
centriole-centriole cohesion (Score: 5.390988)



establishment of melanosome localization (Score: 5.389861)

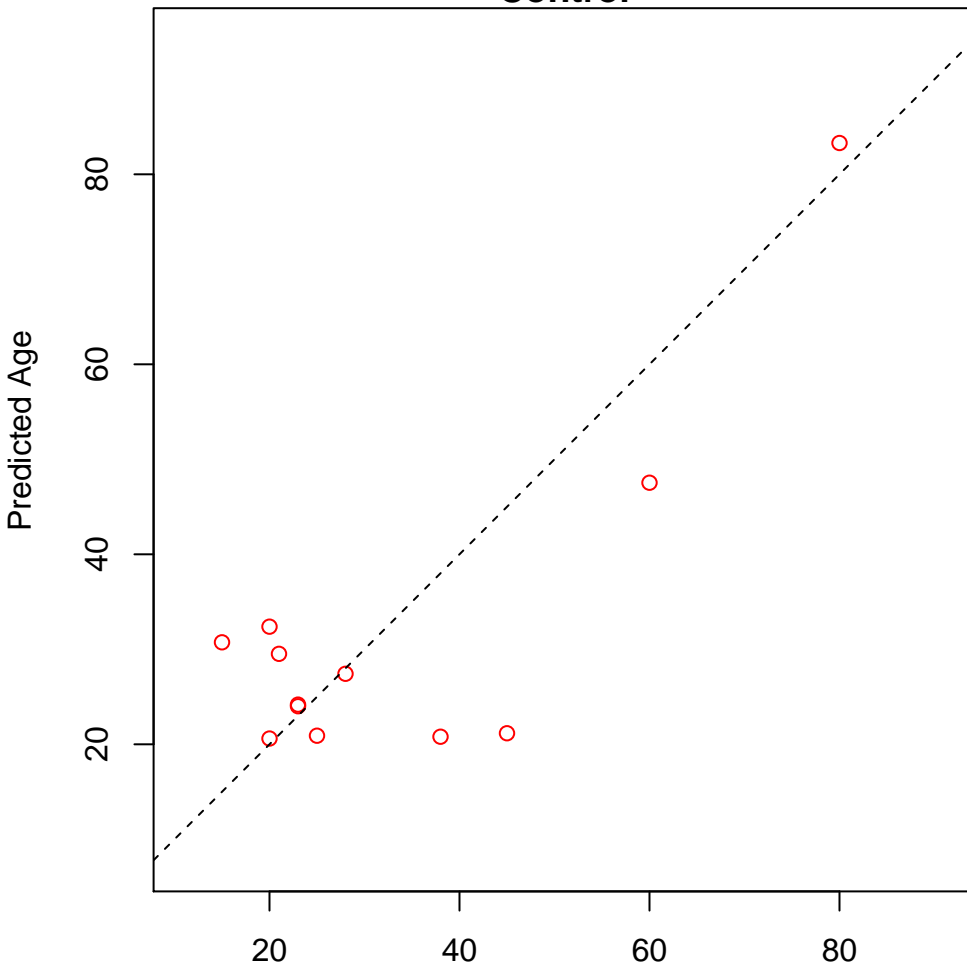


establishment of pigment granule localization (Score: 5.389861)

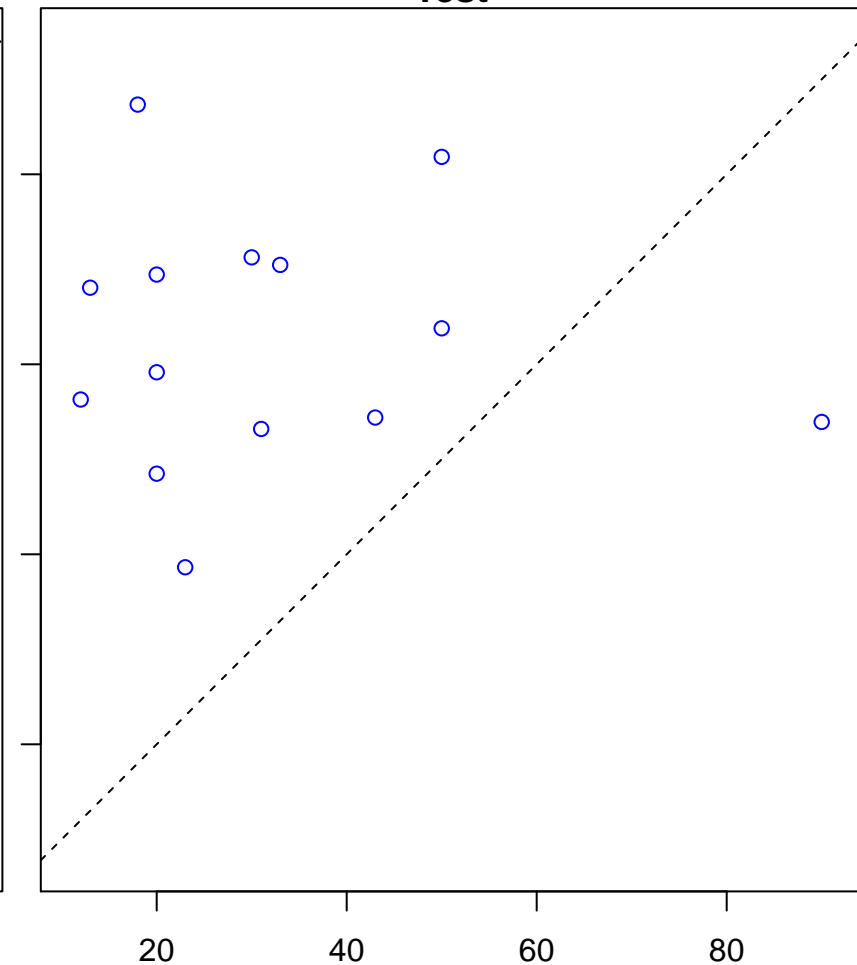


post-translational protein modification (Score: 5.387070)

Control

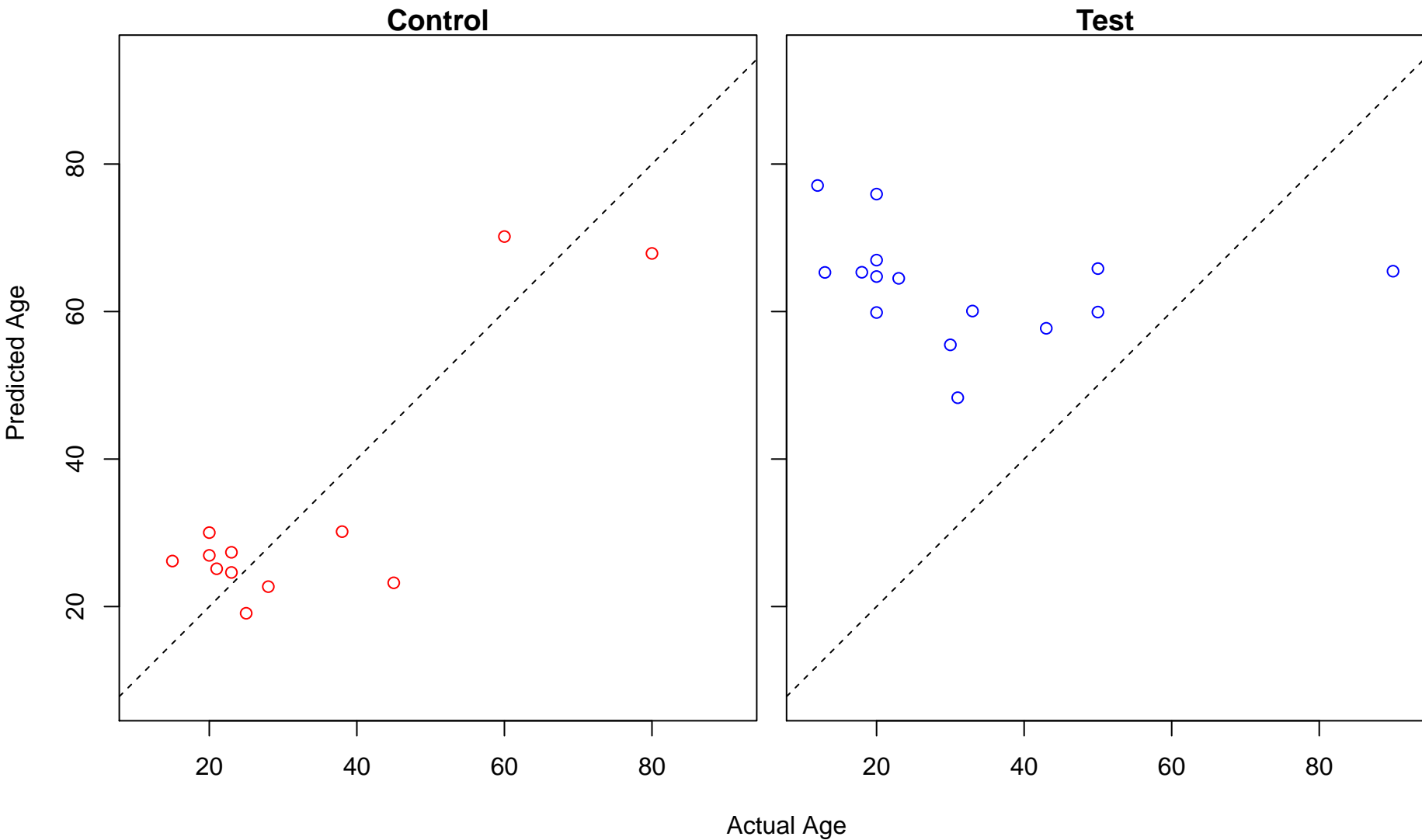


Test

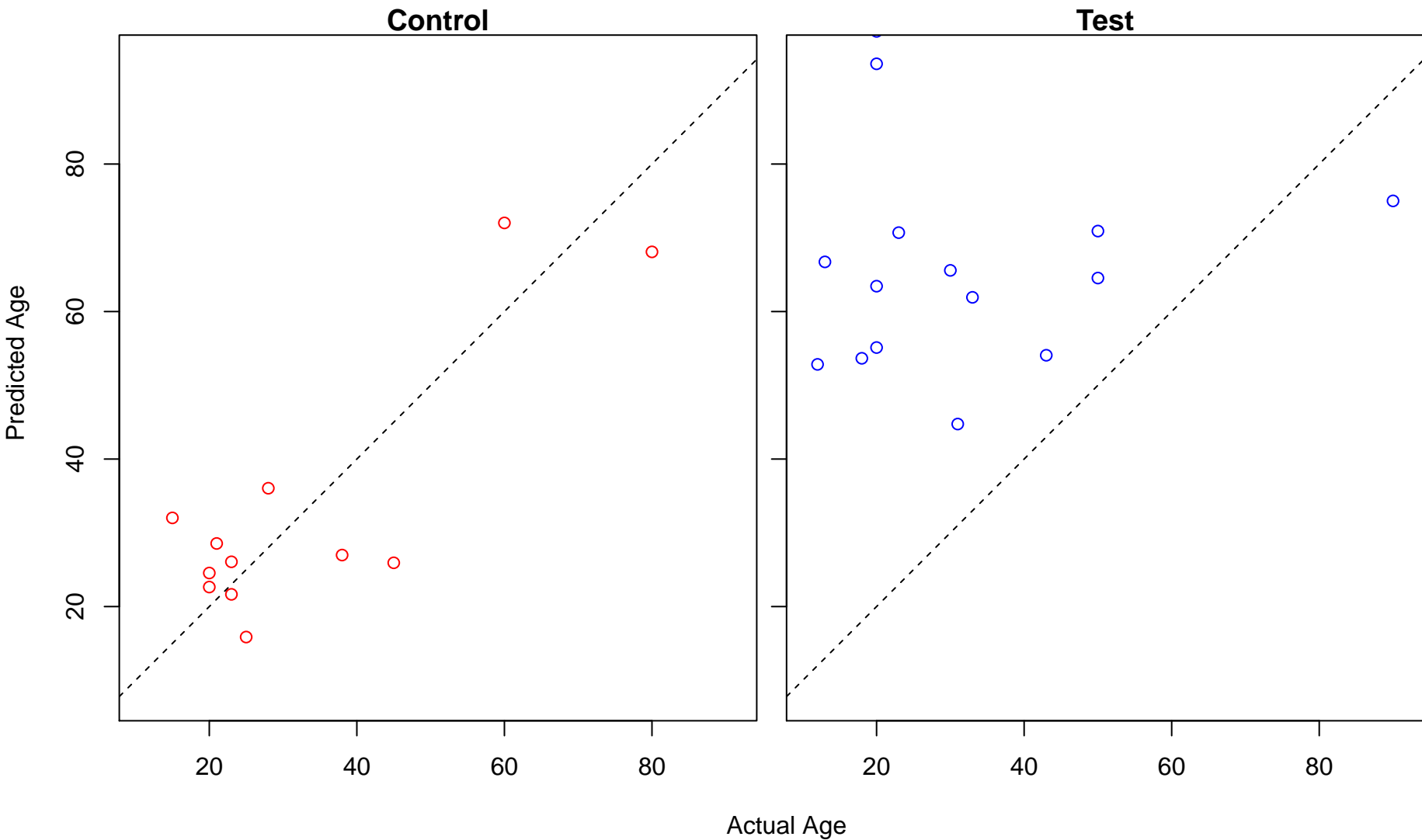


Actual Age

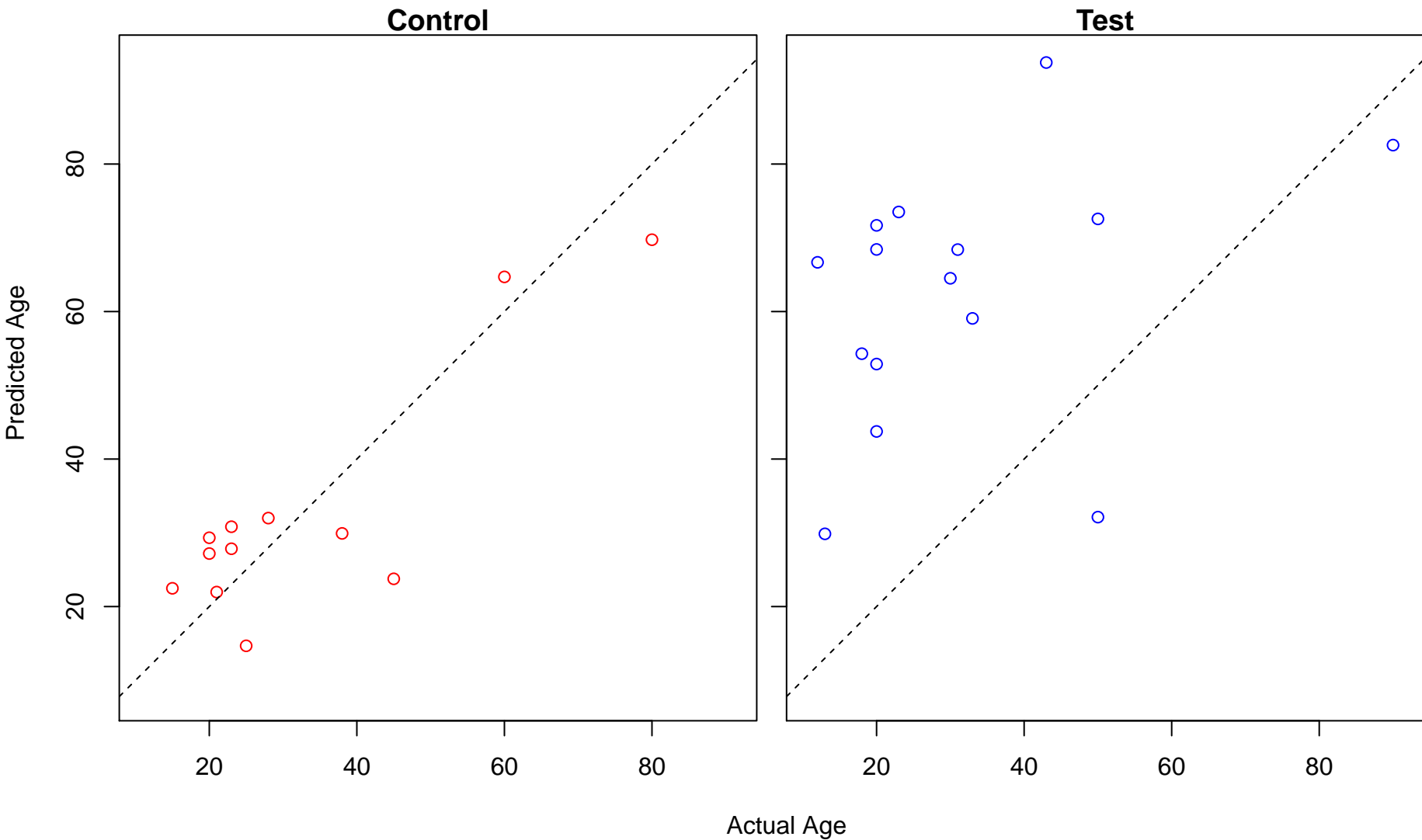
regulation of translational elongation (Score: 5.384843)



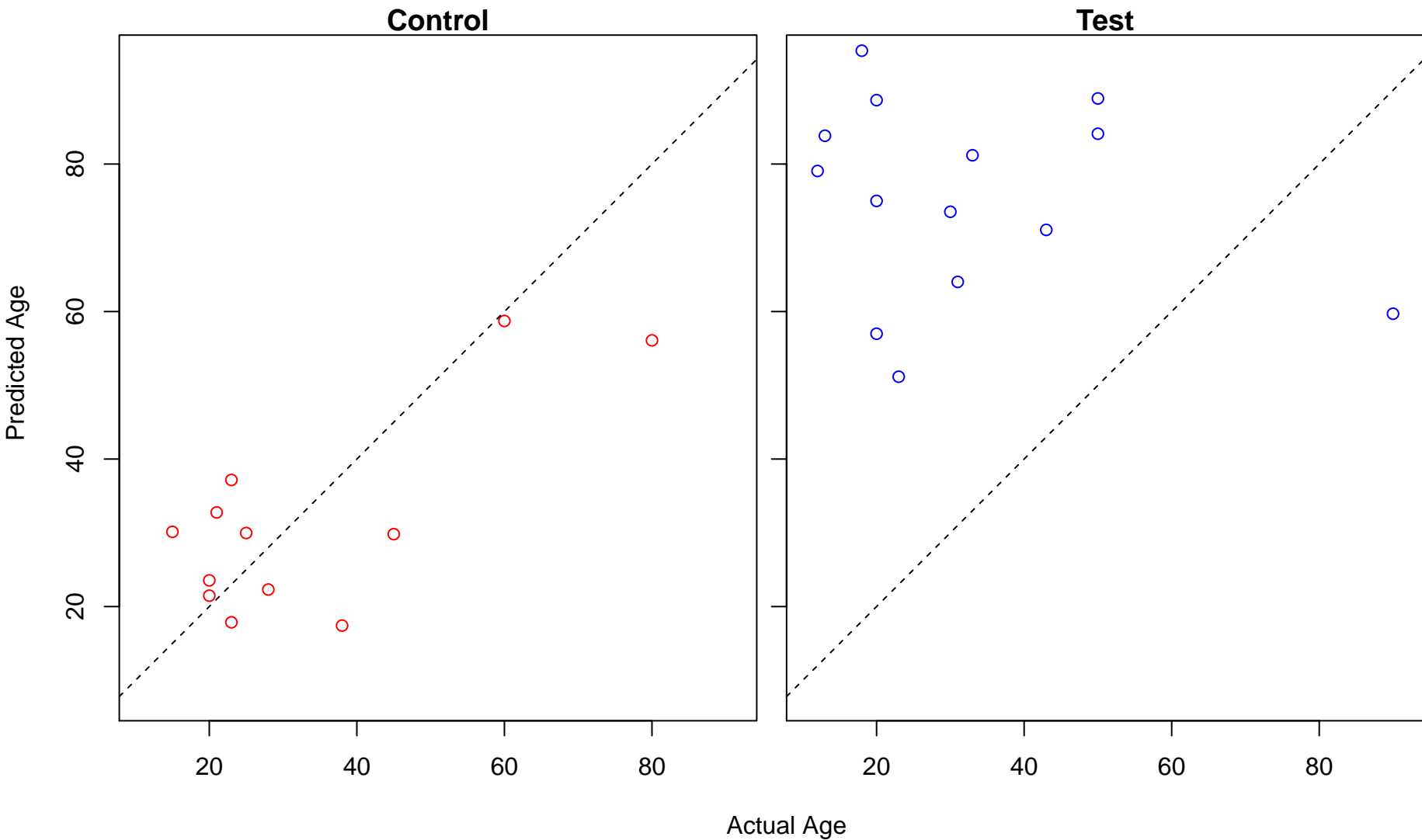
response to UV (Score: 5.384151)



nonmotile primary cilium assembly (Score: 5.380355)

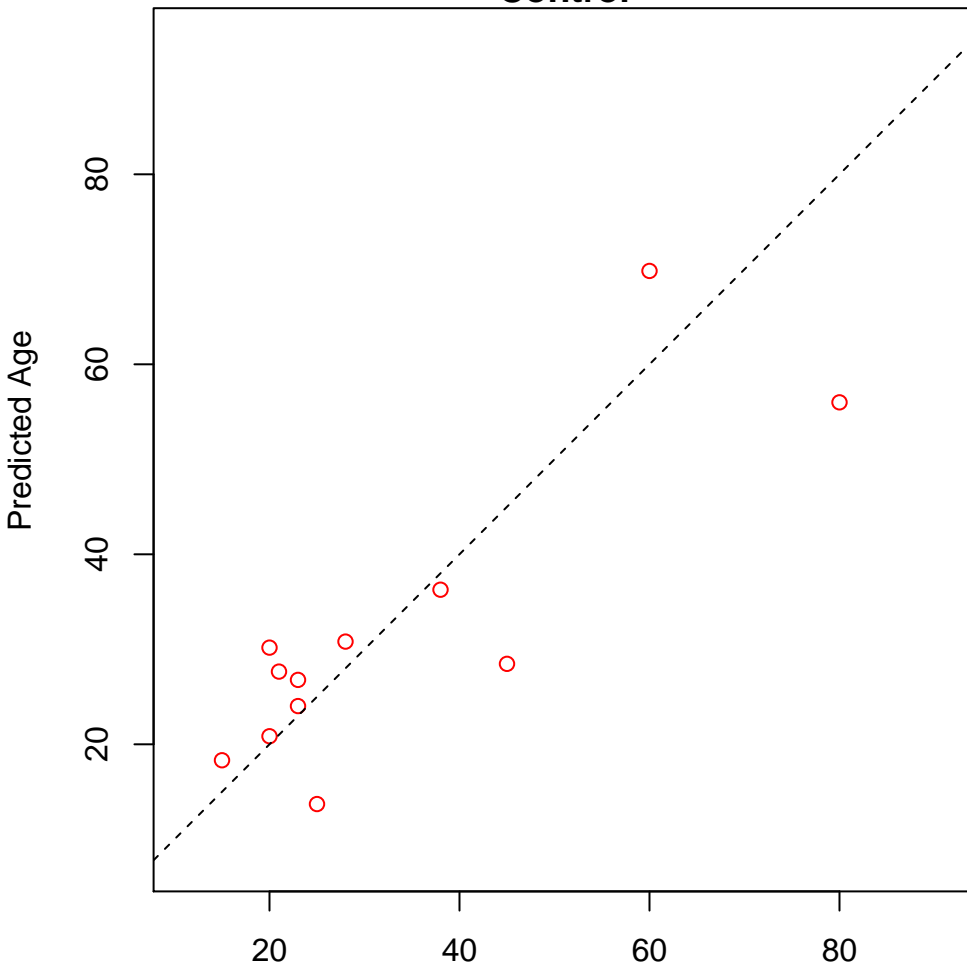


GABAergic neuron differentiation (Score: 5.380044)

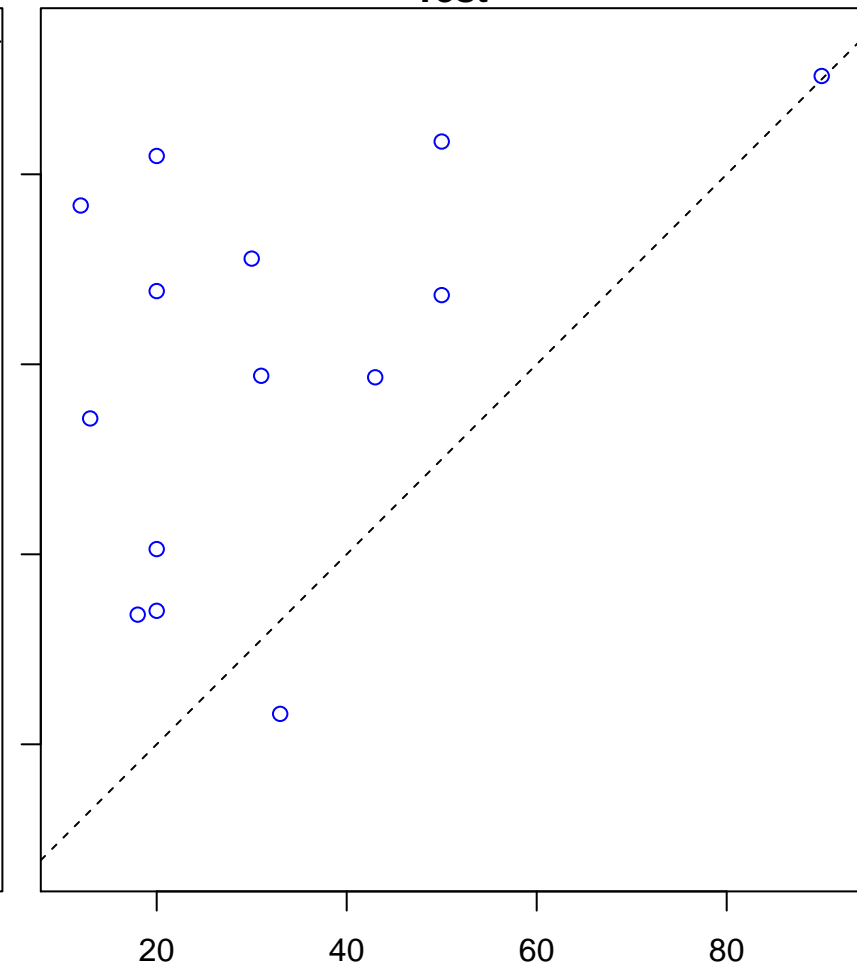


retina morphogenesis in camera-type eye (Score: 5.379683)

Control

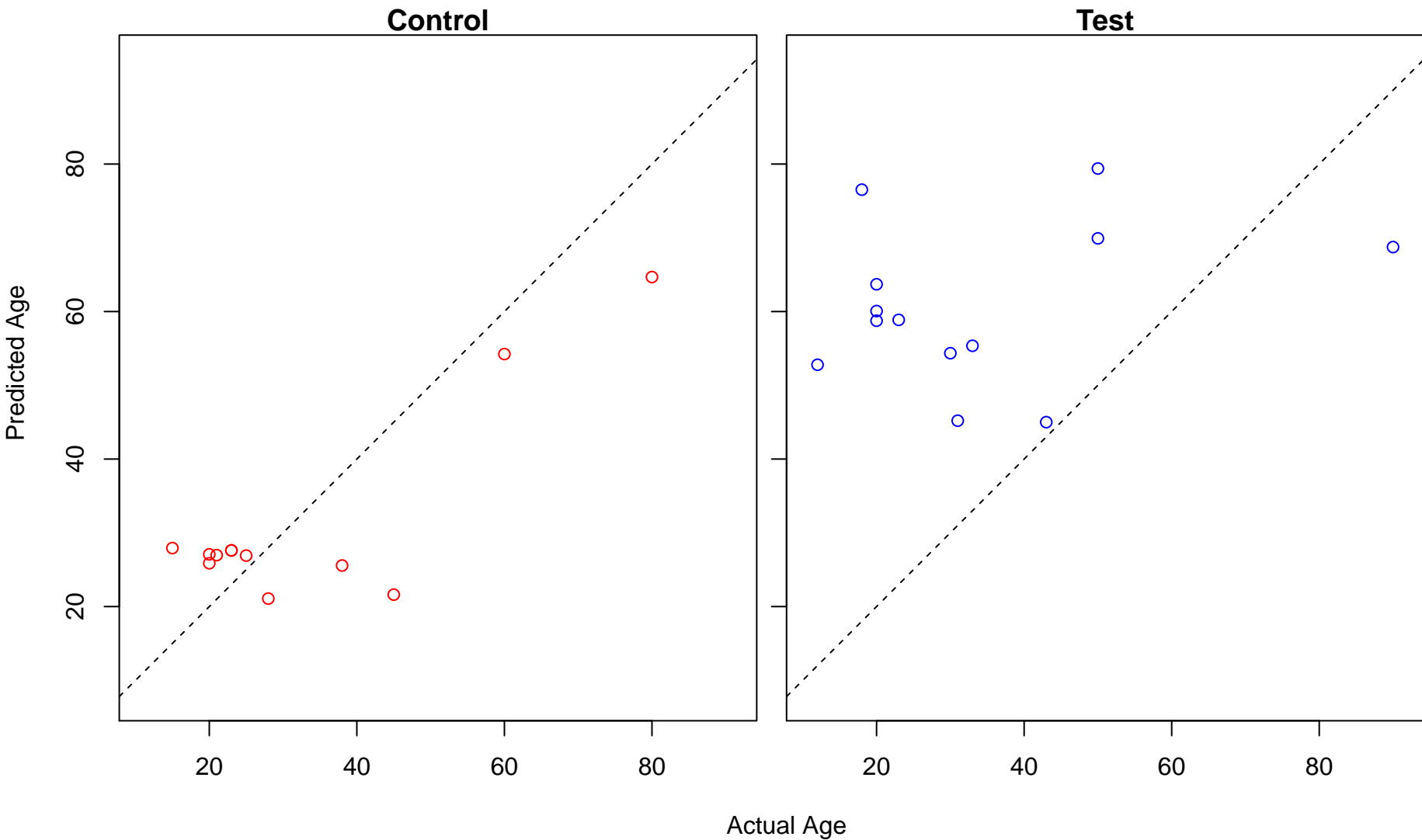


Test

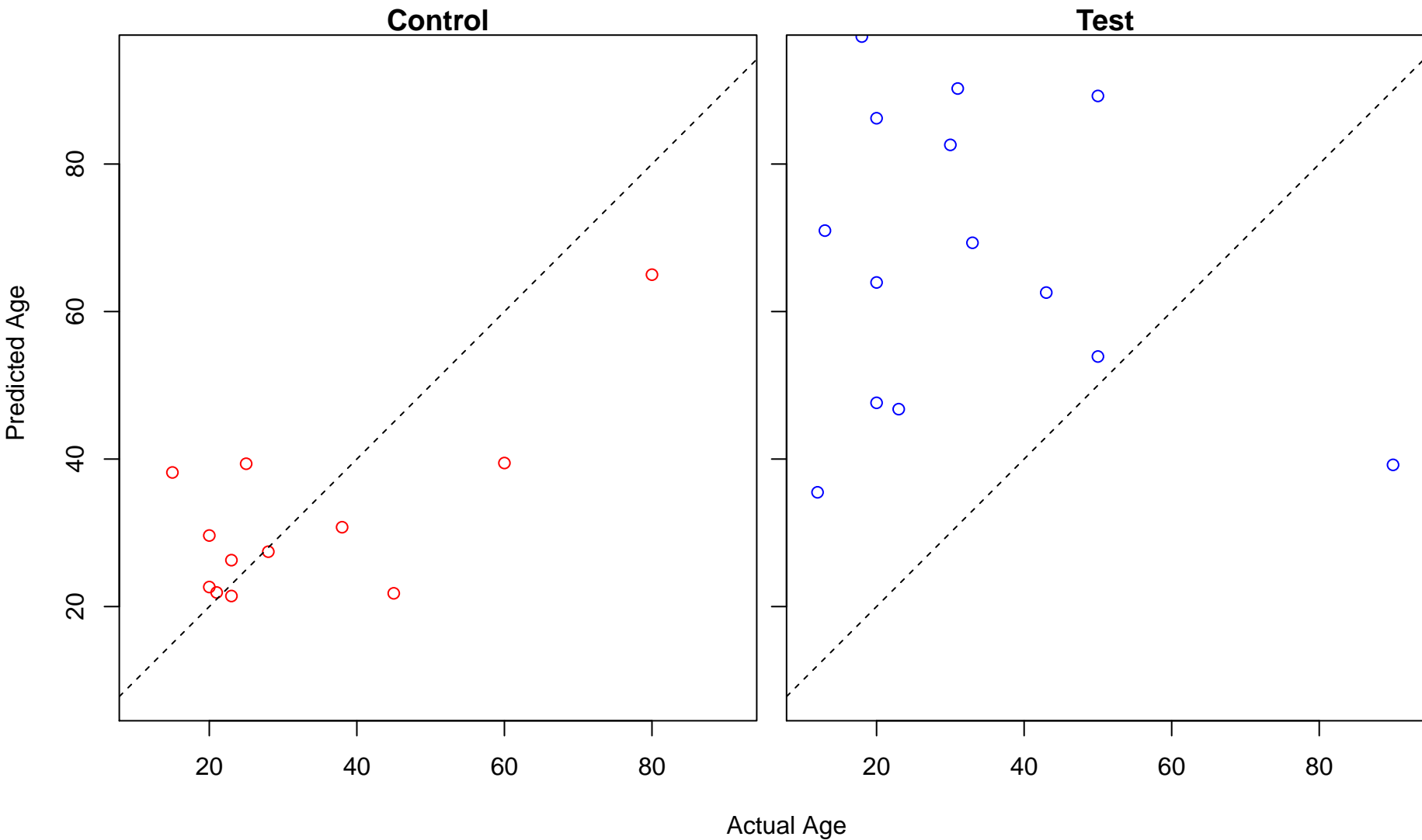


Actual Age

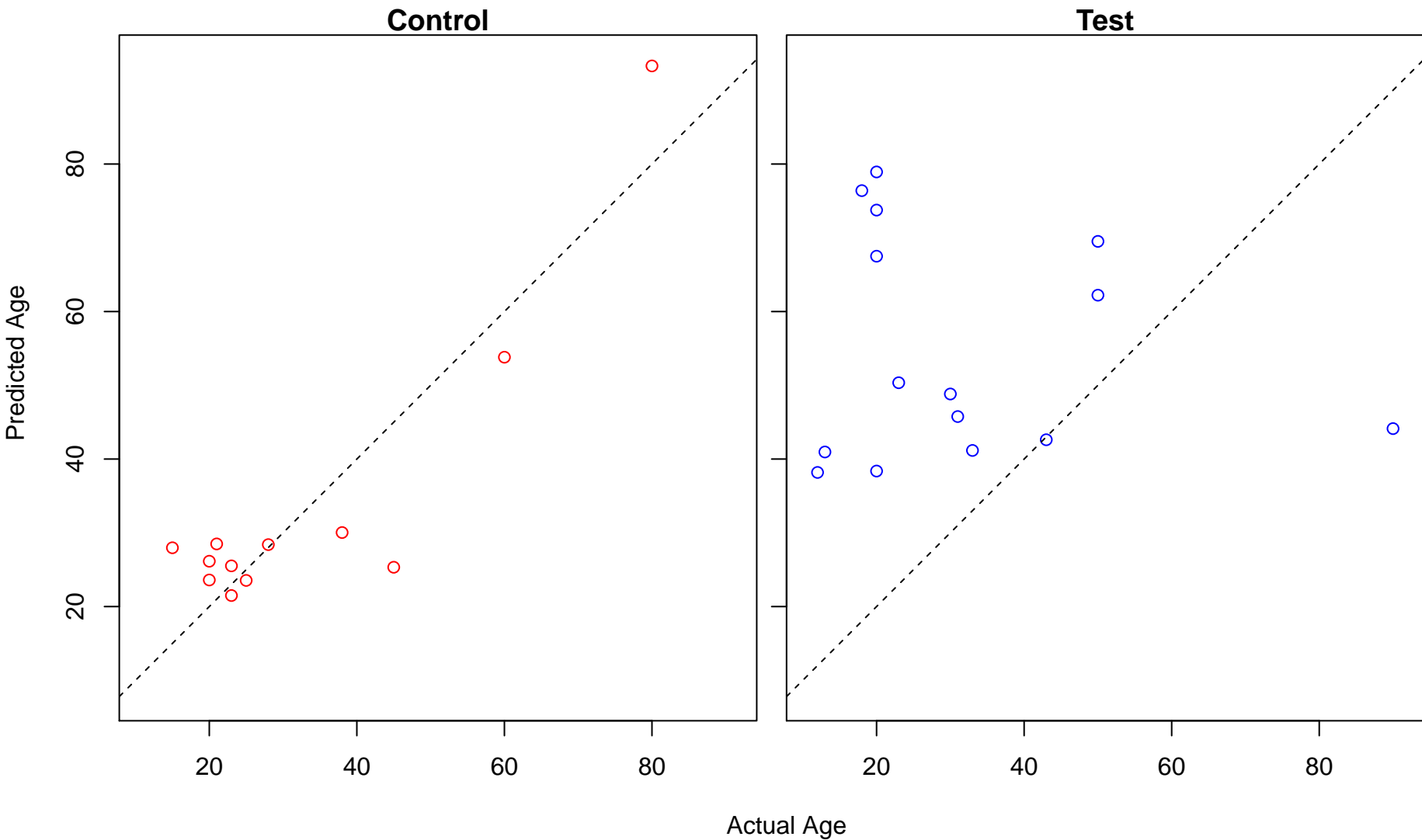
negative regulation of cellular amide metabolic process (Score: 5.378012)



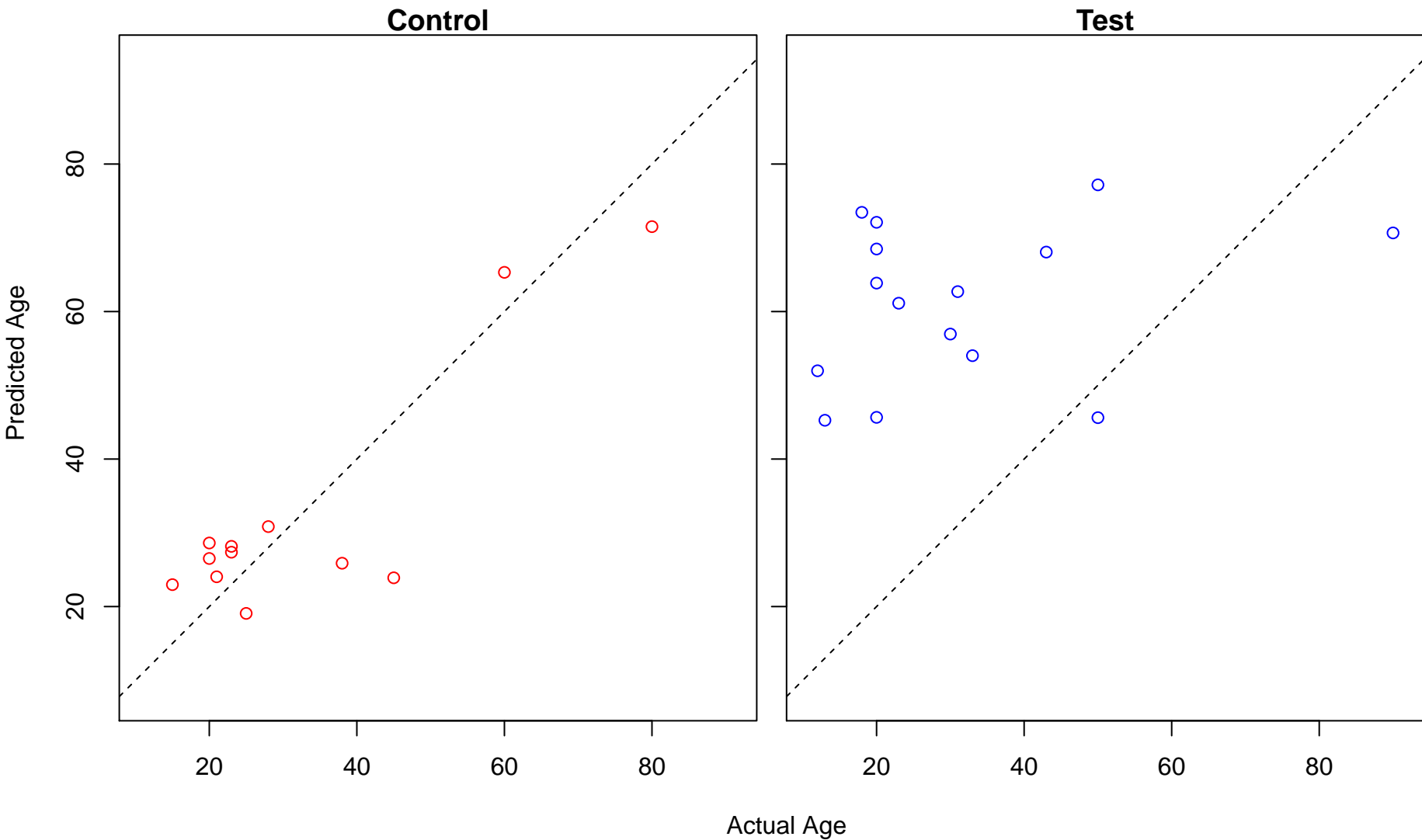
negative regulation of fertilization (Score: 5.377723)



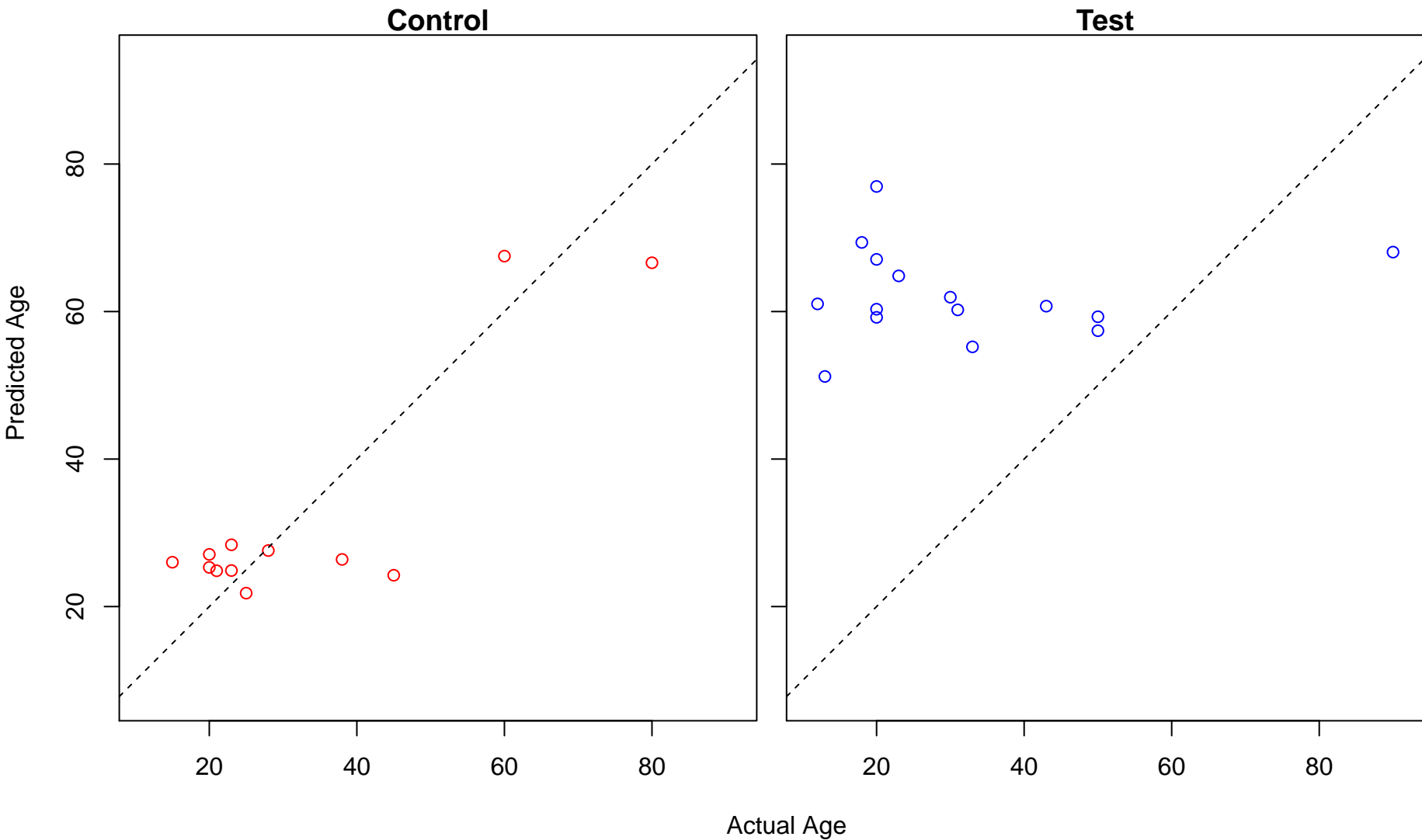
neurological system process (Score: 5.377122)



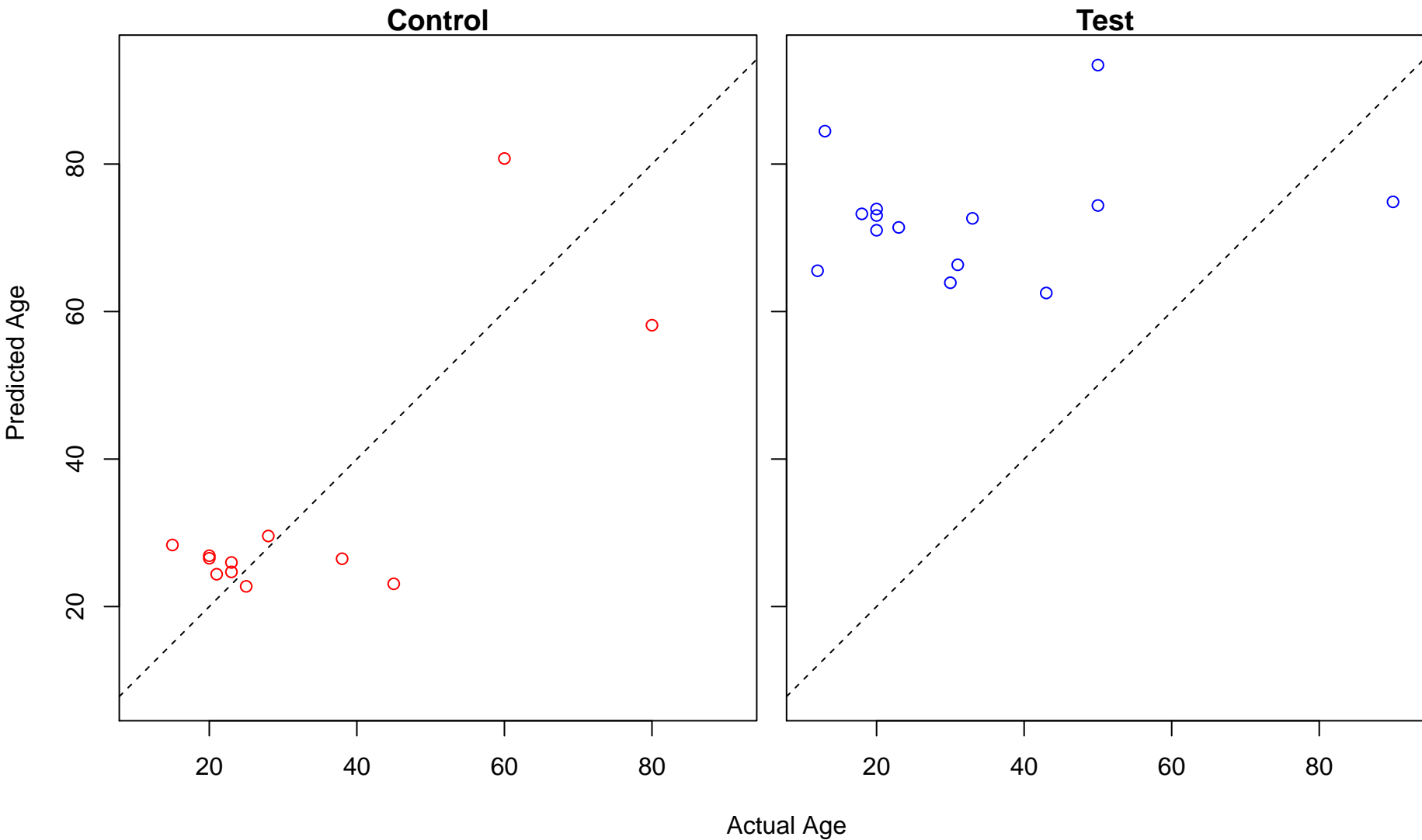
positive regulation of alpha-beta T cell differentiation (Score: 5.373217)



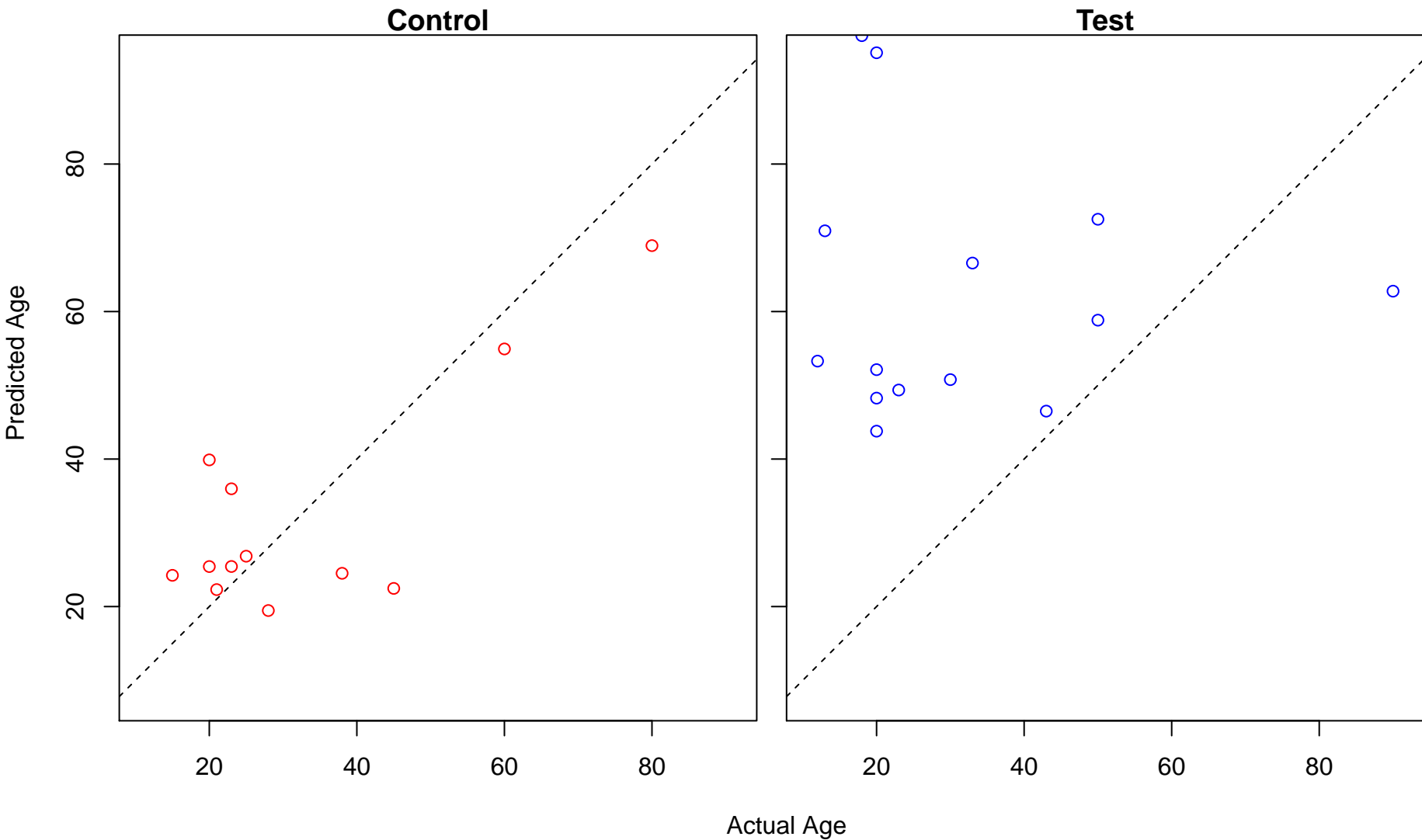
glycerolipid metabolic process (Score: 5.370691)



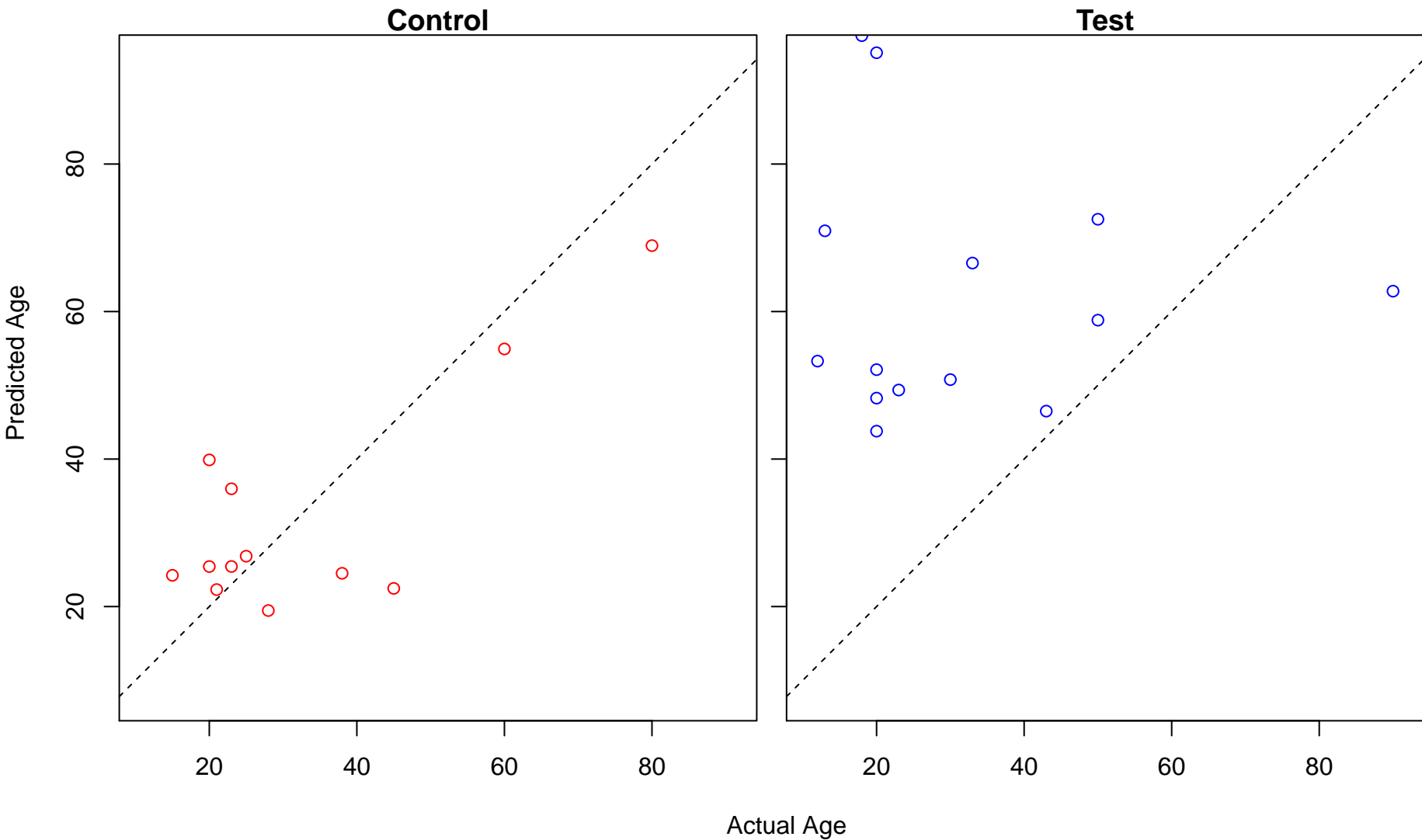
macromitophagy (Score: 5.369779)



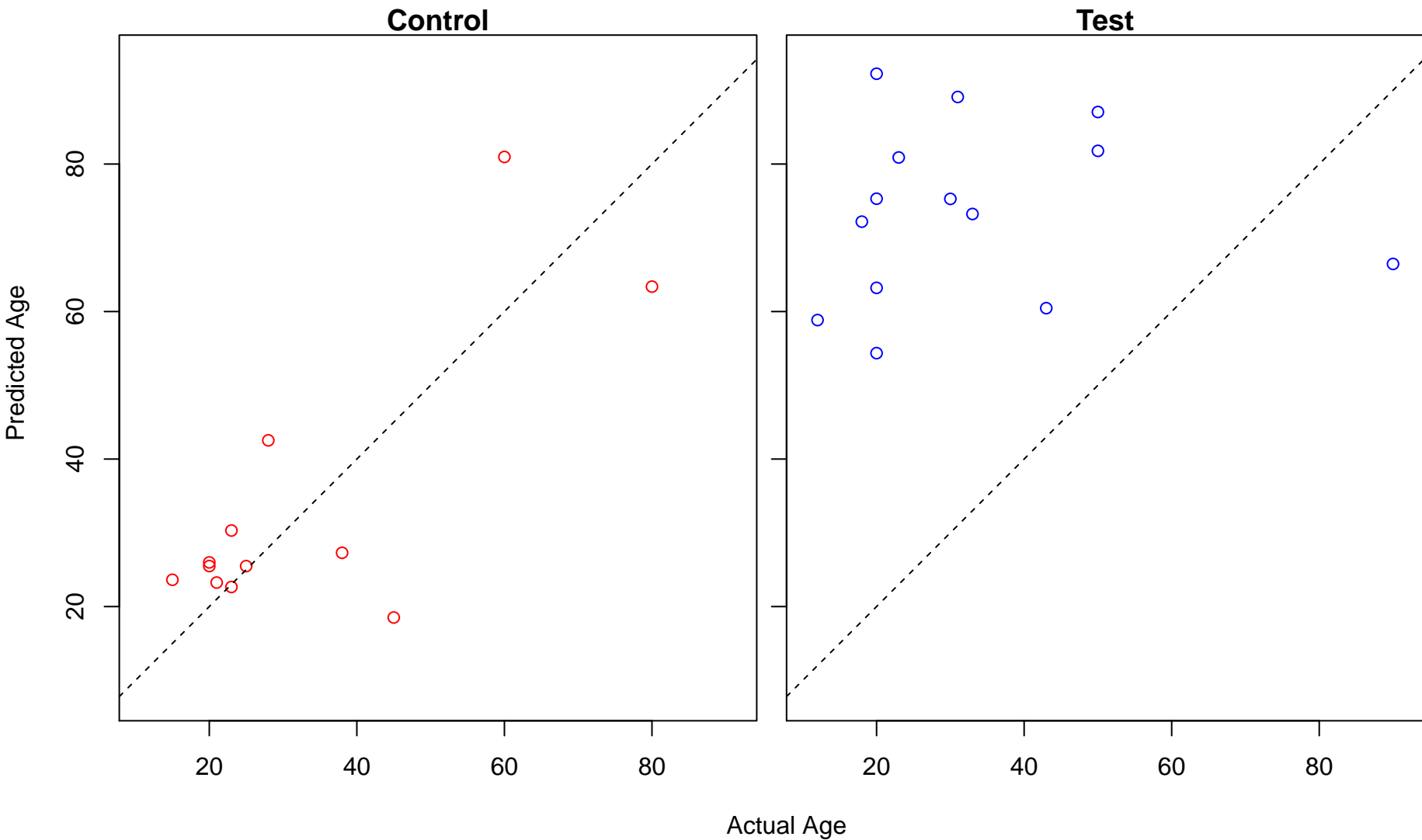
catechol-containing compound biosynthetic process (Score: 5.368802)



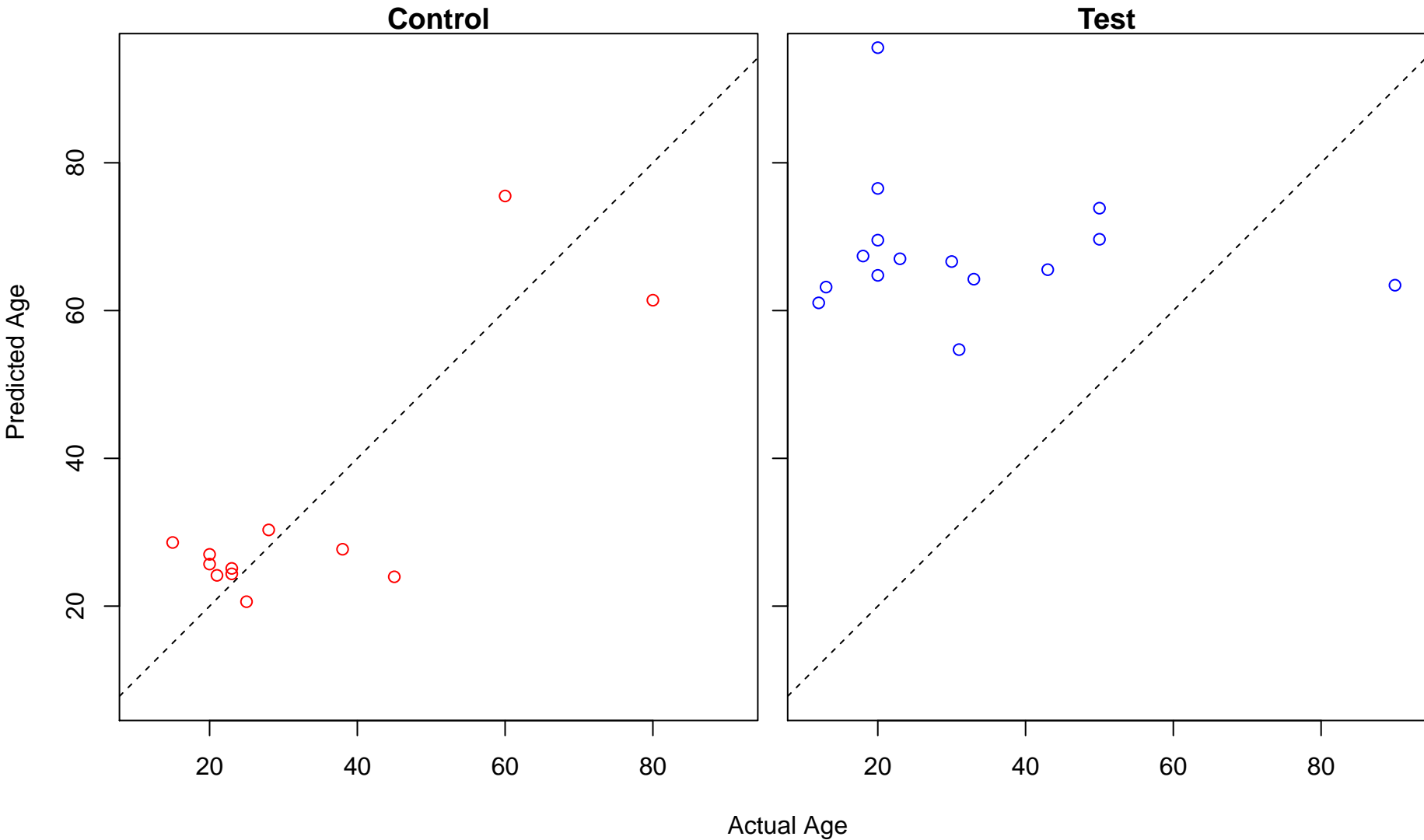
catecholamine biosynthetic process (Score: 5.368802)



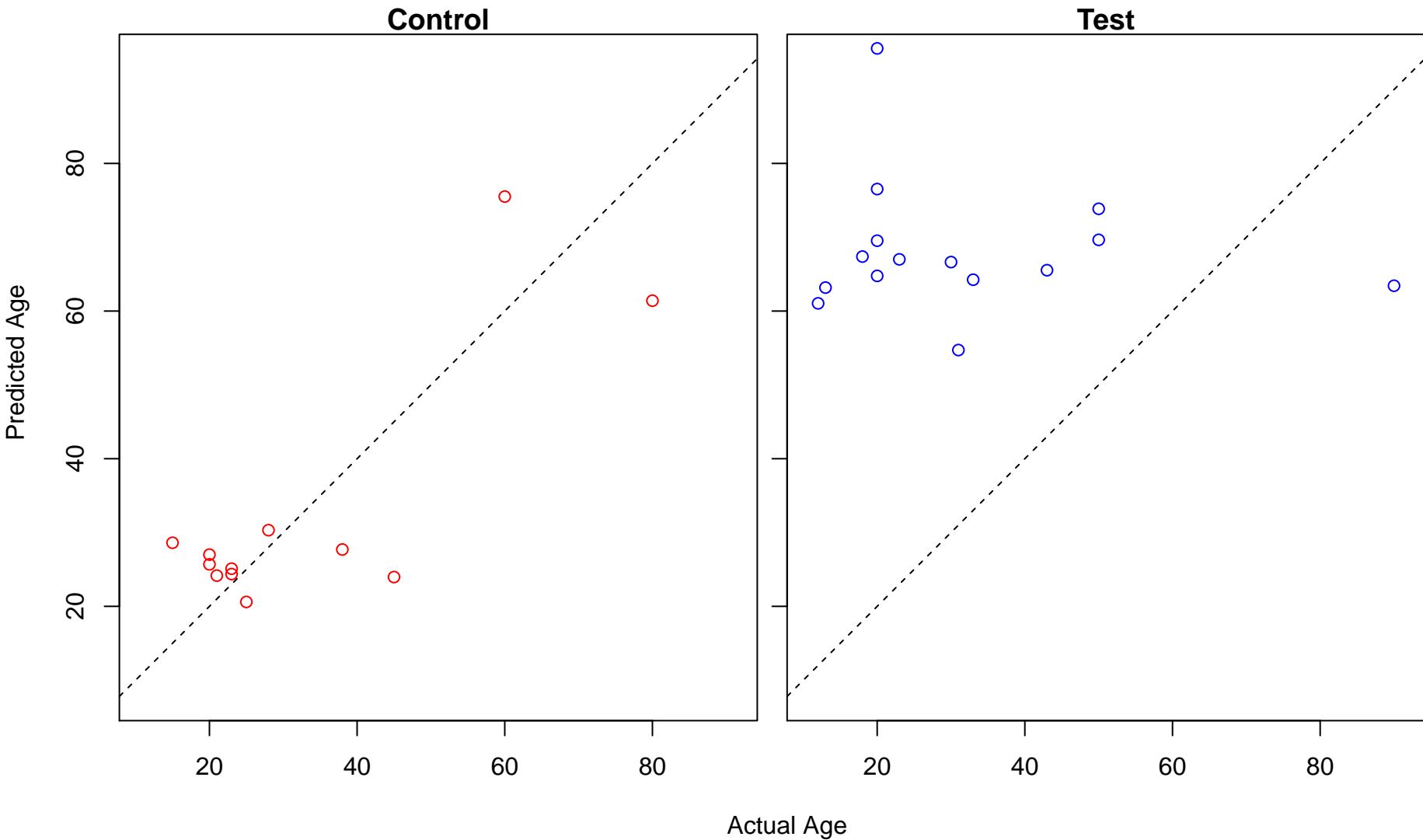
positive regulation of leukocyte chemotaxis (Score: 5.366347)



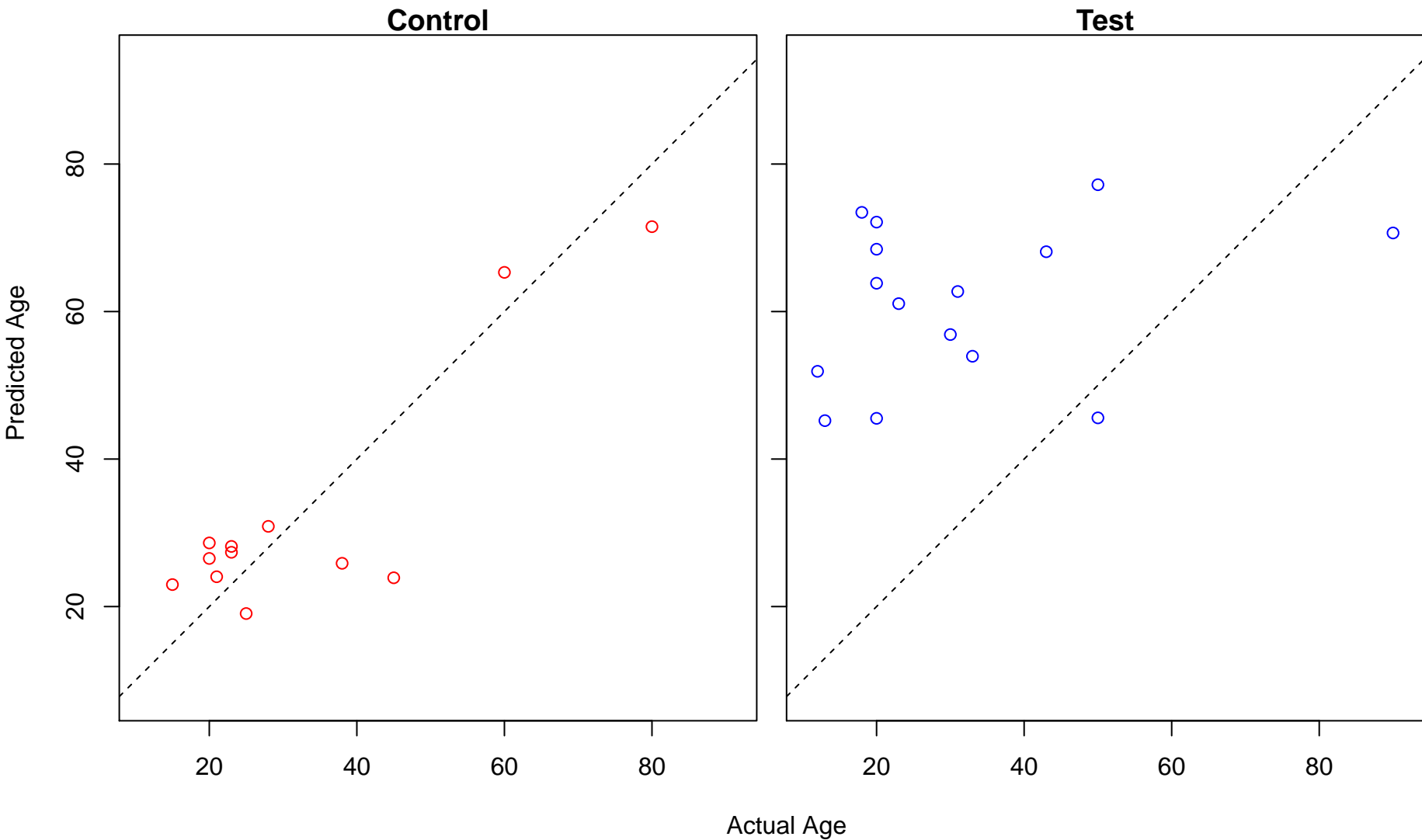
regulation of cardiac muscle cell contraction (Score: 5.364622)



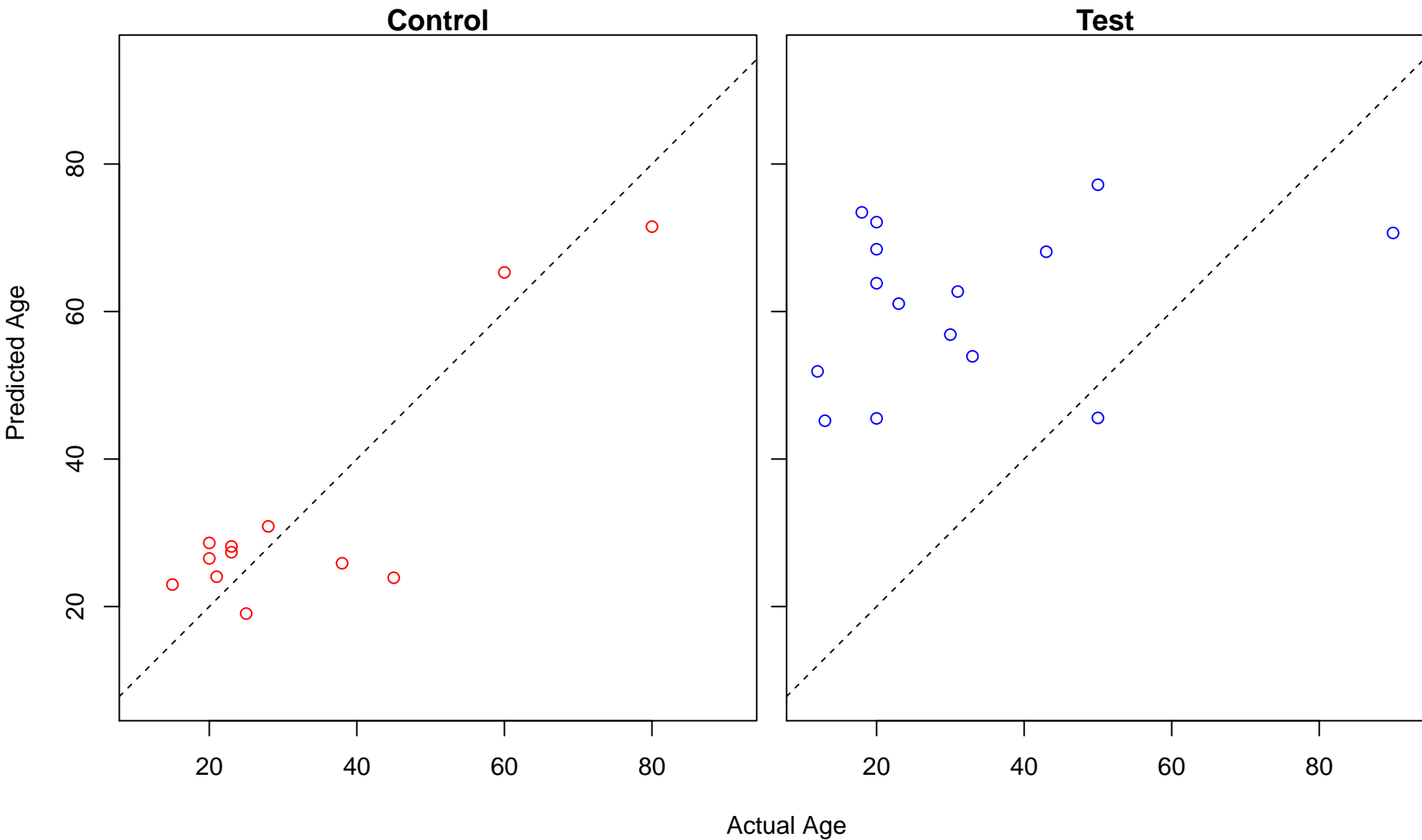
regulation of actin filament-based movement (Score: 5.363960)



positive regulation of CD4-positive, alpha-beta T cell differentiation (Score: 5.363432)

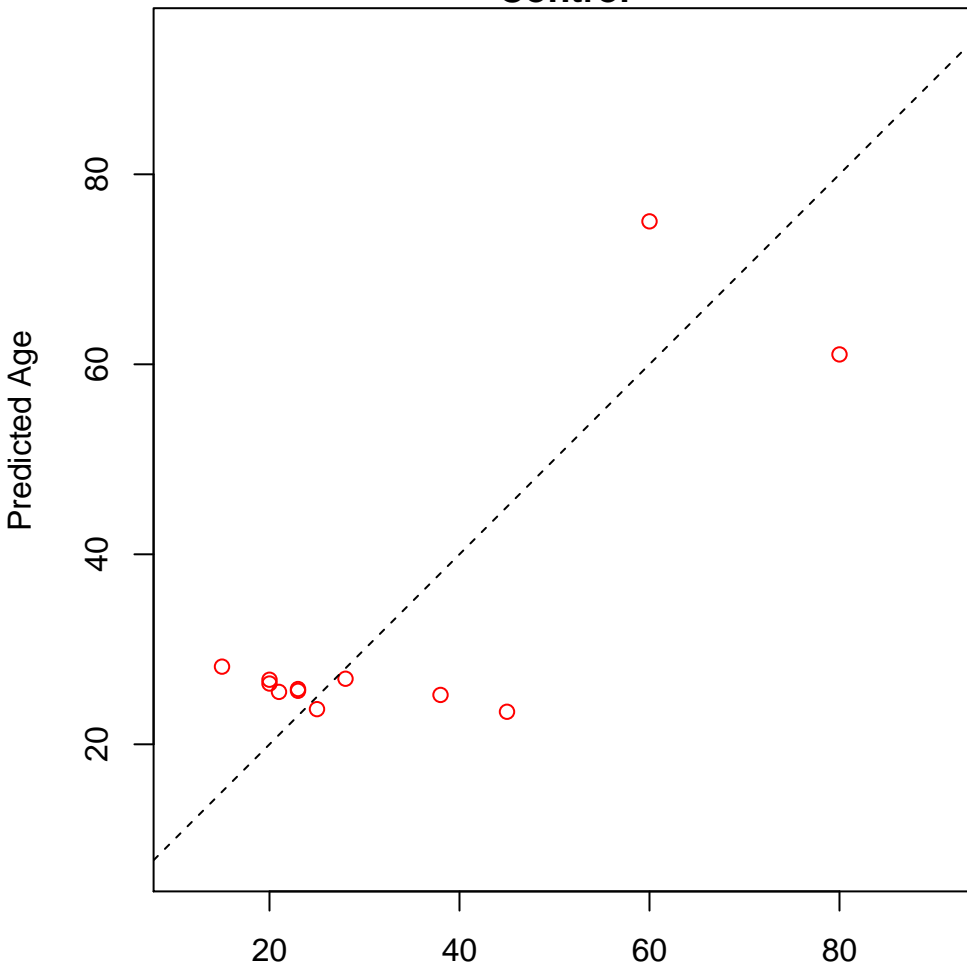


positive regulation of T-helper cell differentiation (Score: 5.363071)

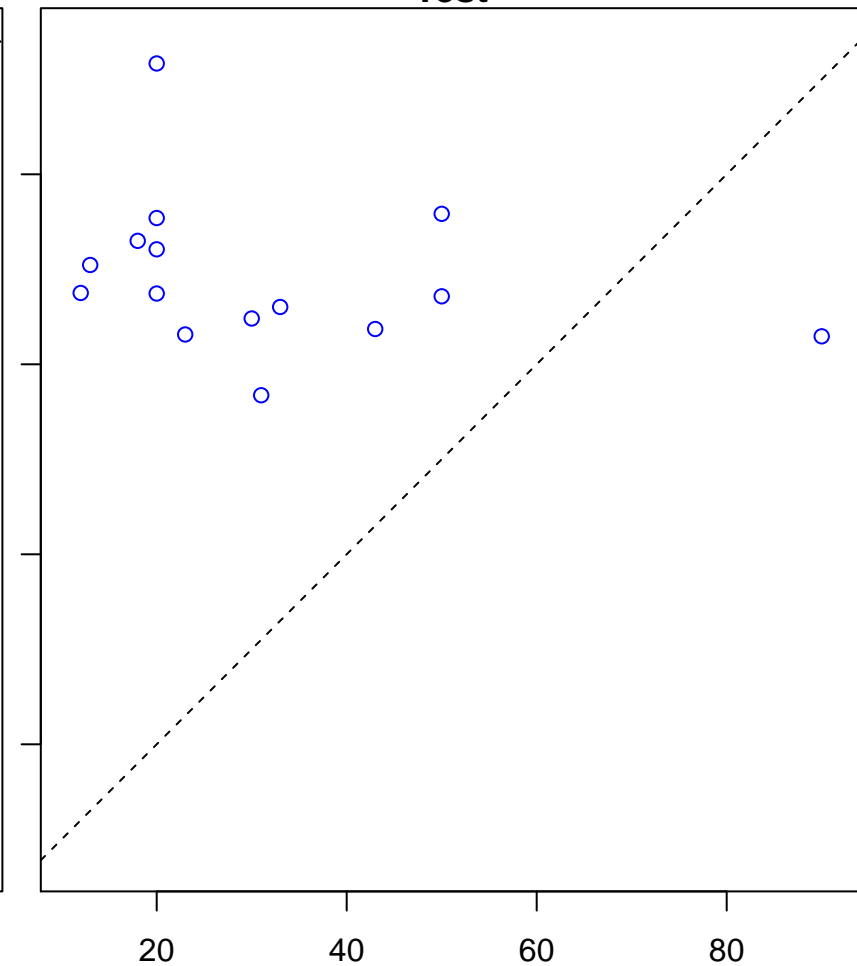


regulation of neuron apoptotic process (Score: 5.362048)

Control



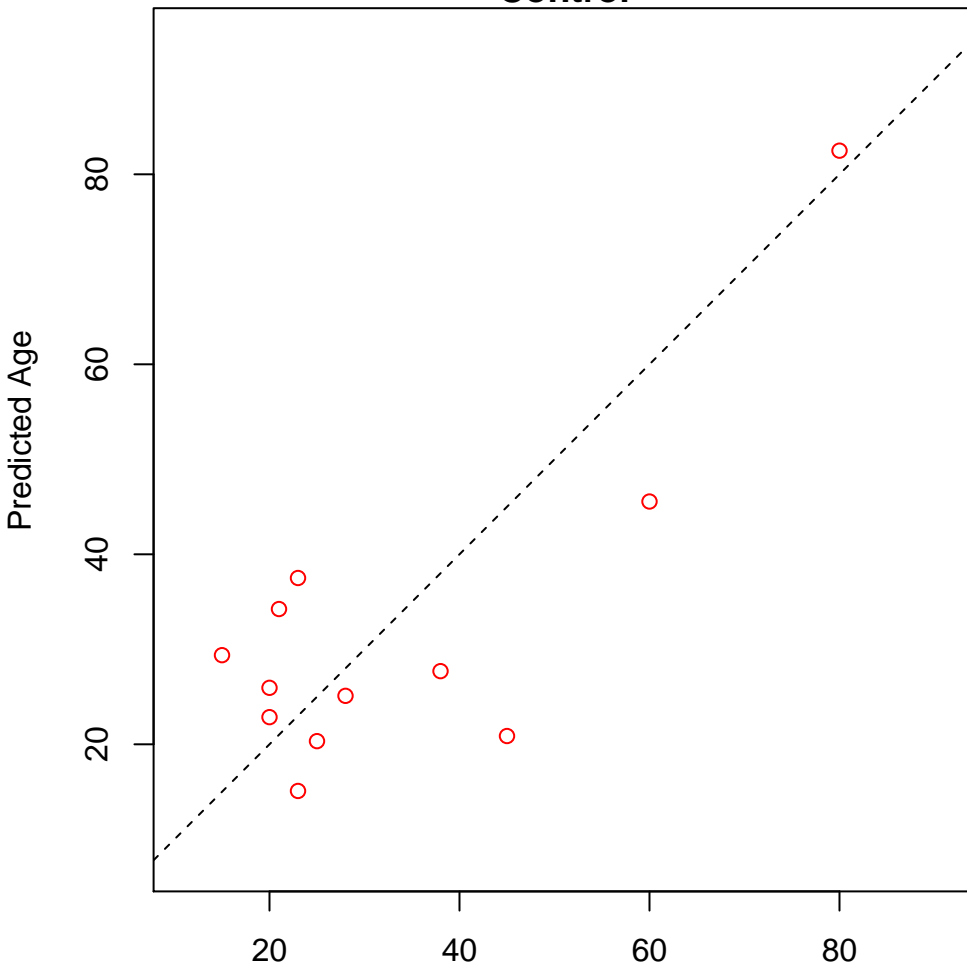
Test



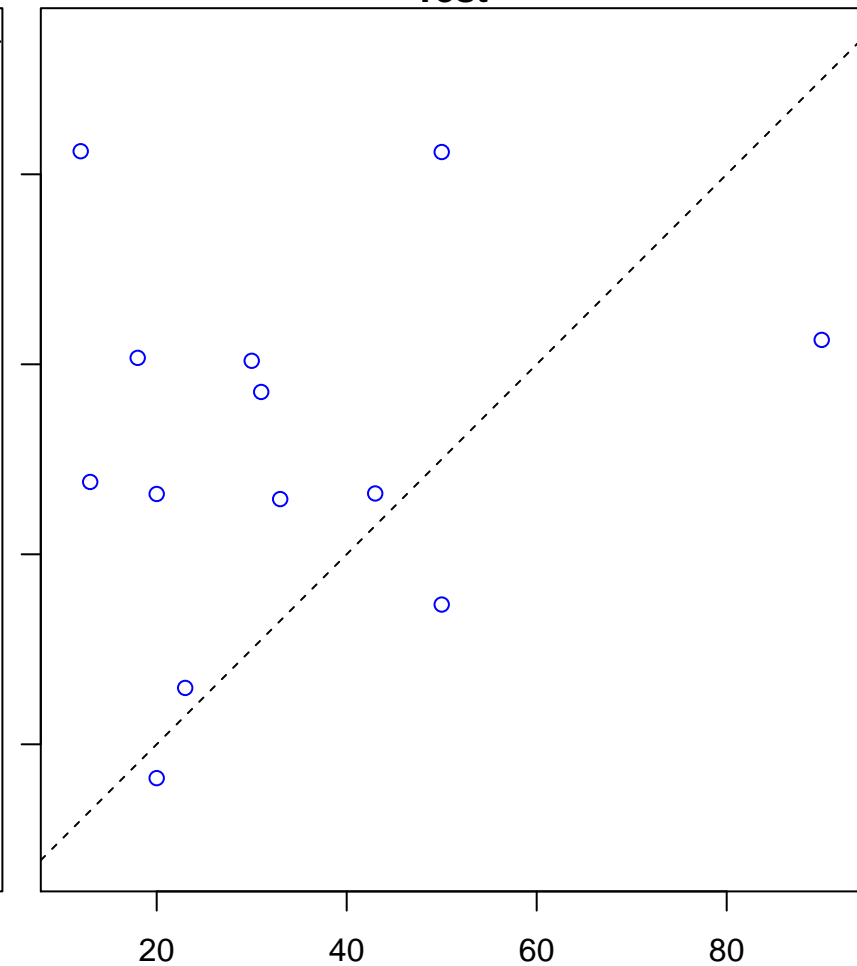
Actual Age

cellular response to inorganic substance (Score: 5.361907)

Control

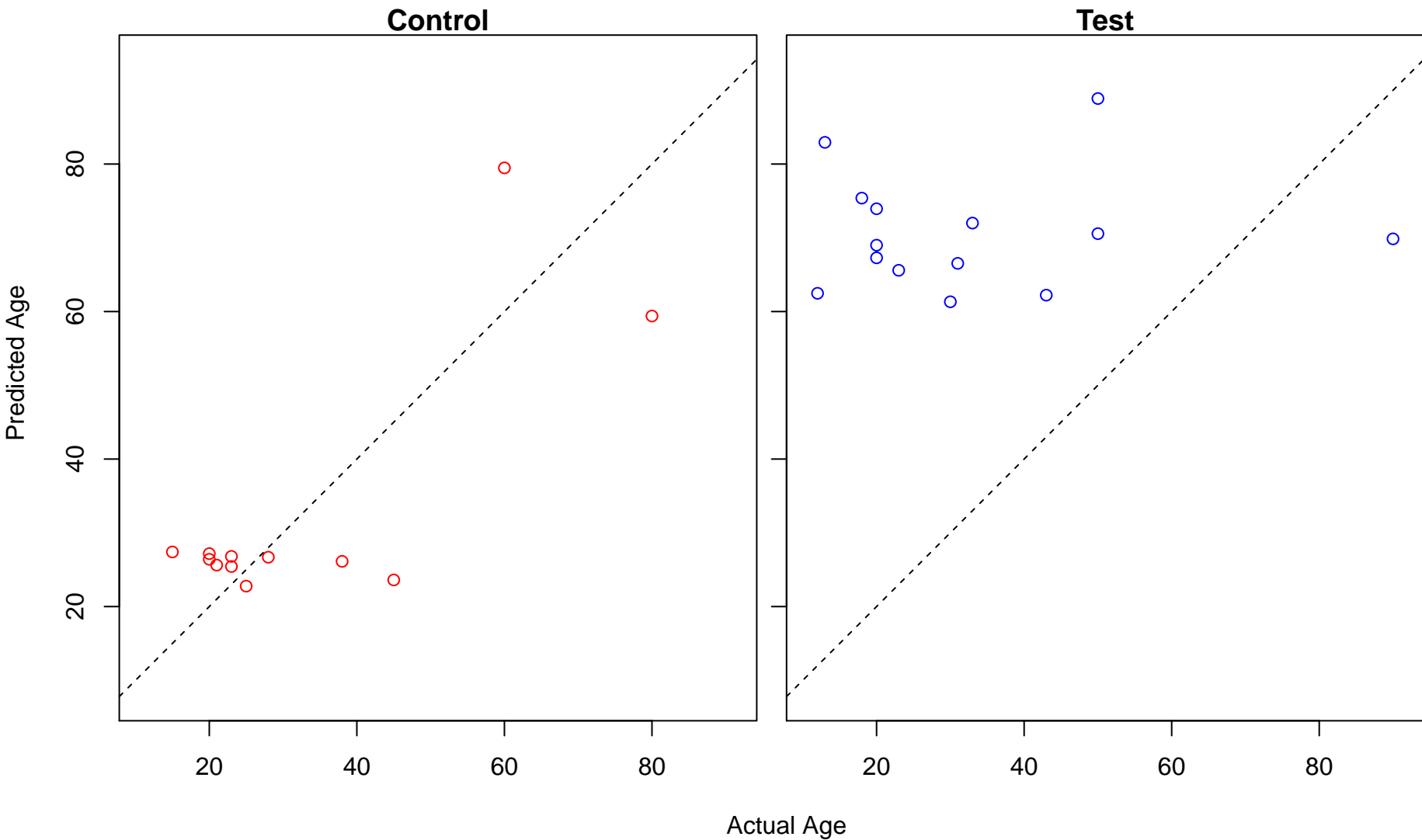


Test

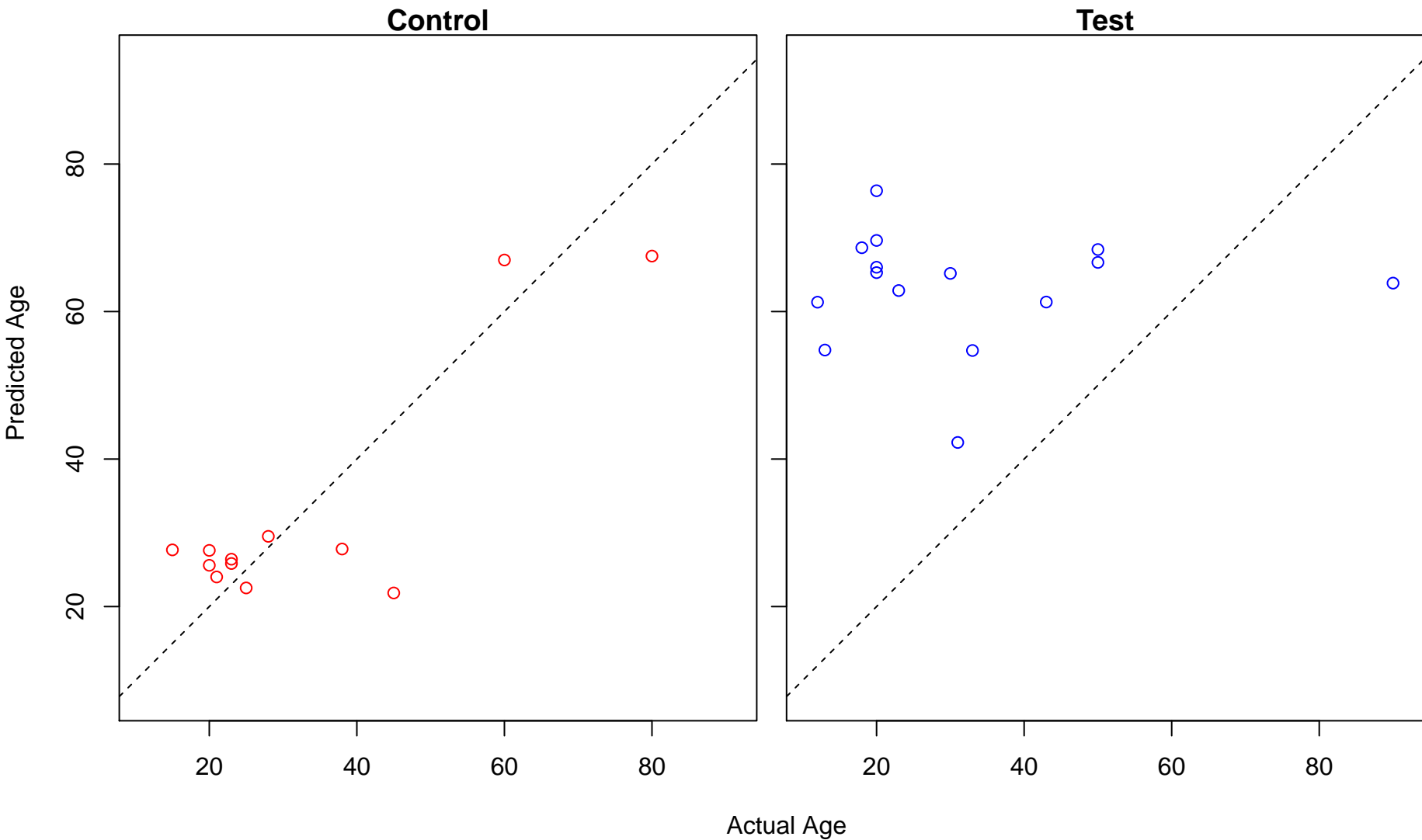


Actual Age

Fc-epsilon receptor signaling pathway (Score: 5.359995)

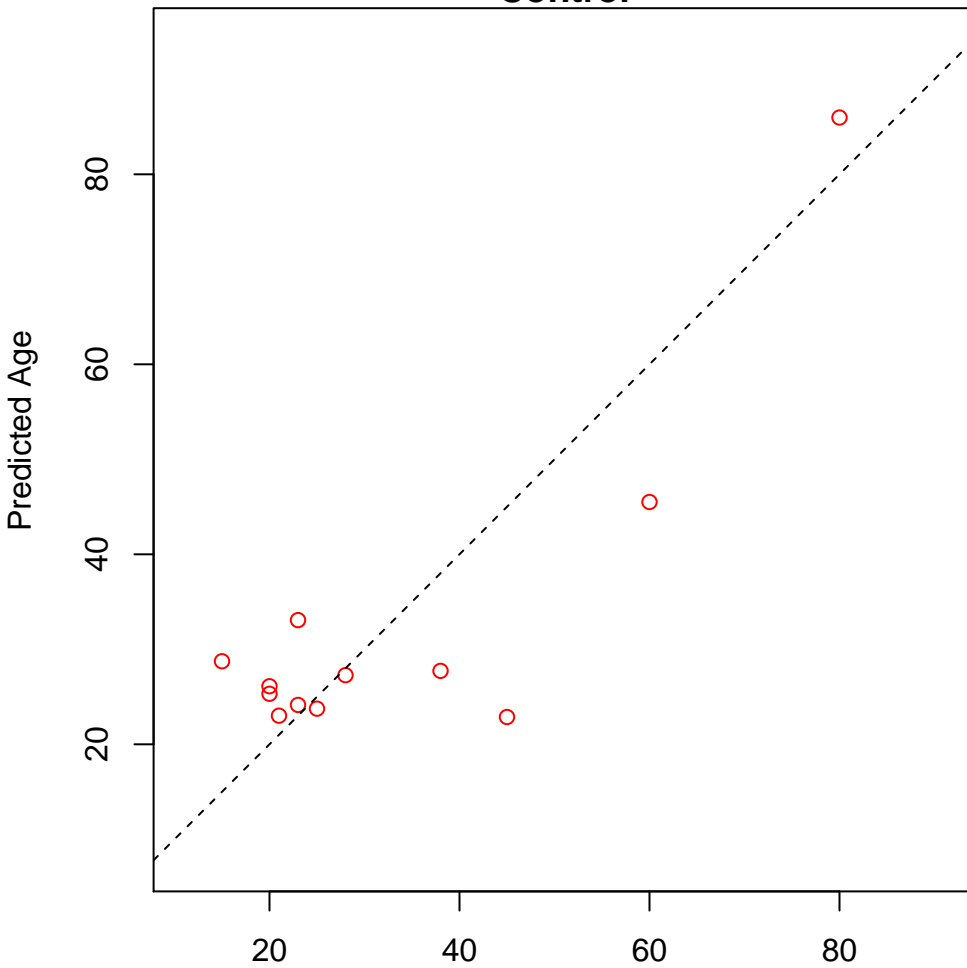


ossification (Score: 5.358880)

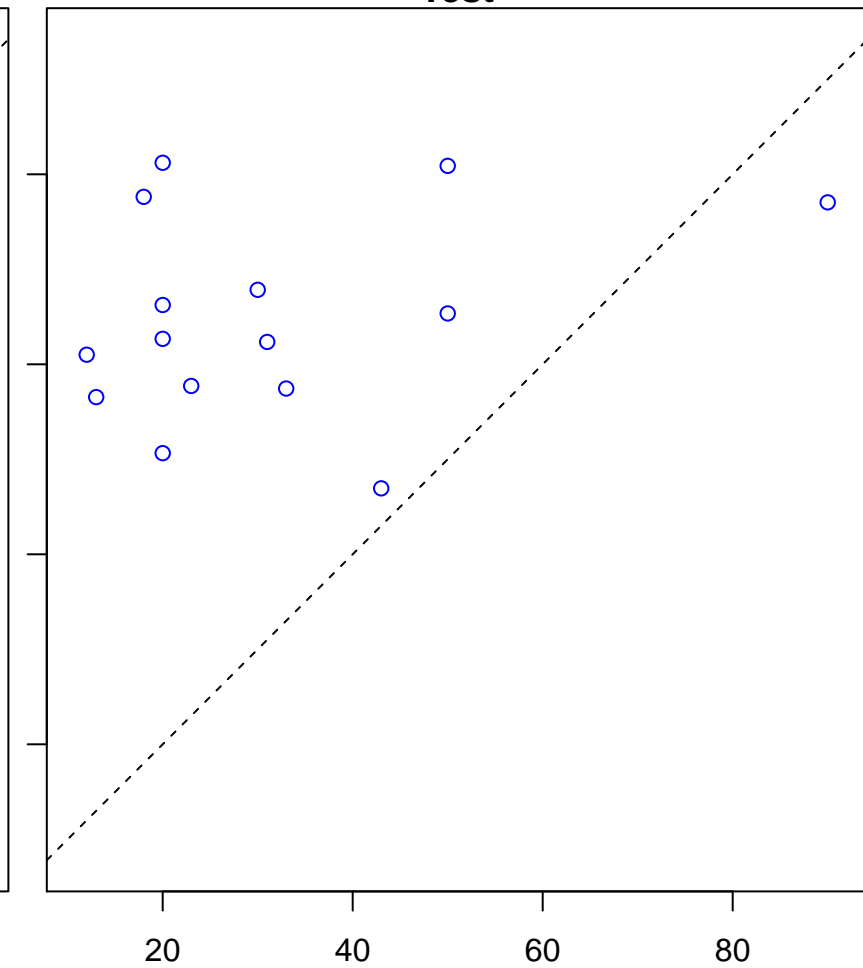


regulation of chromosome organization (Score: 5.356907)

Control

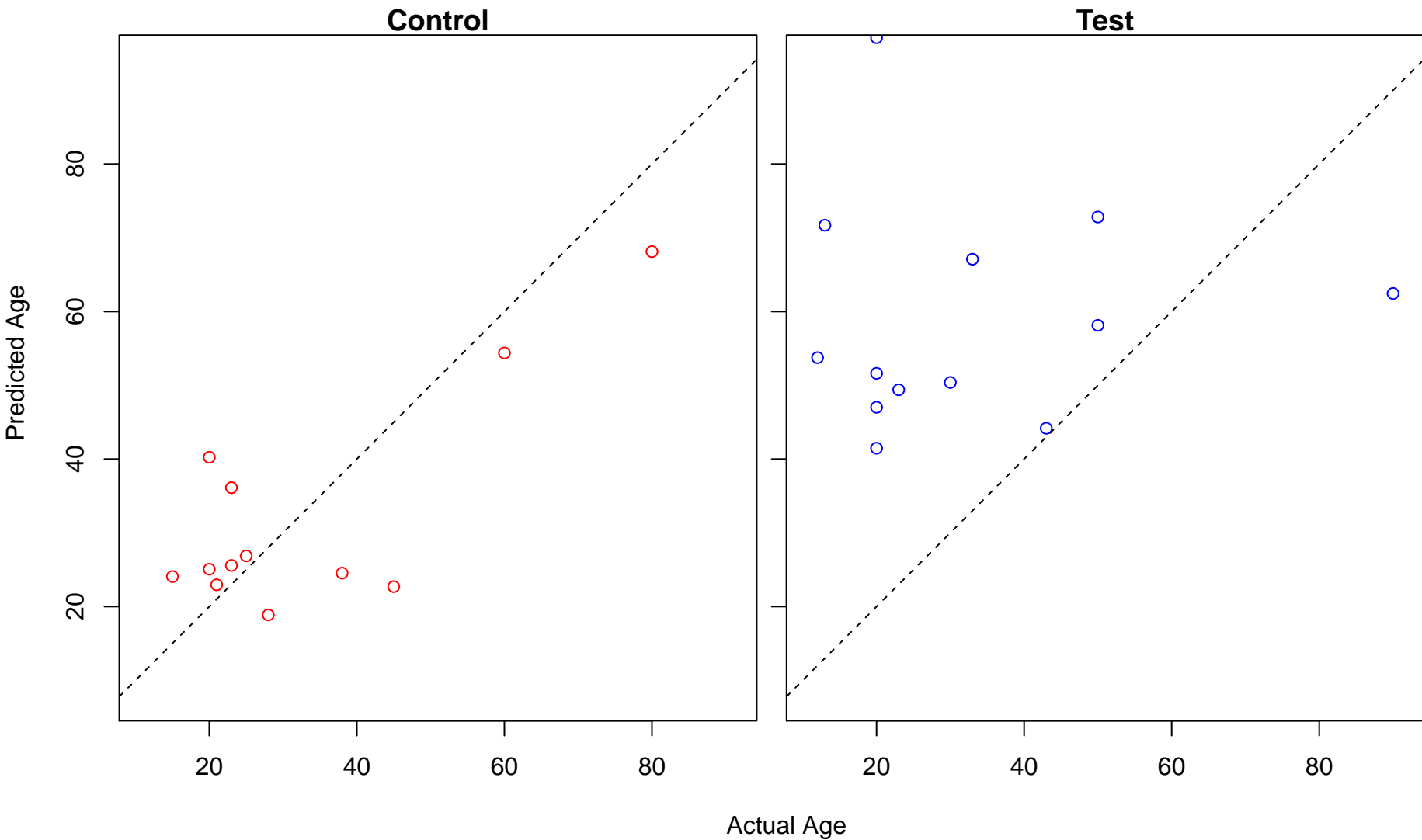


Test

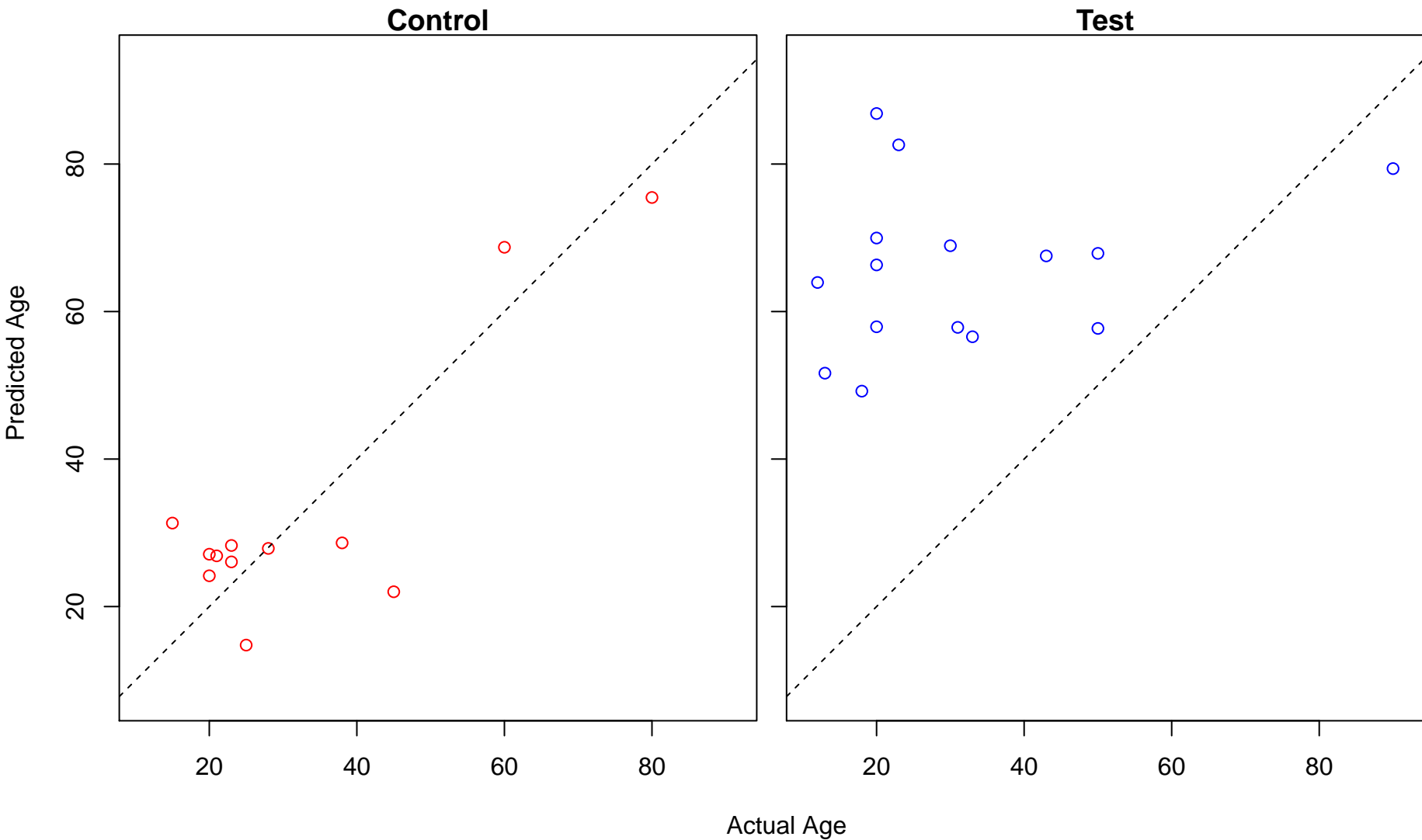


Actual Age

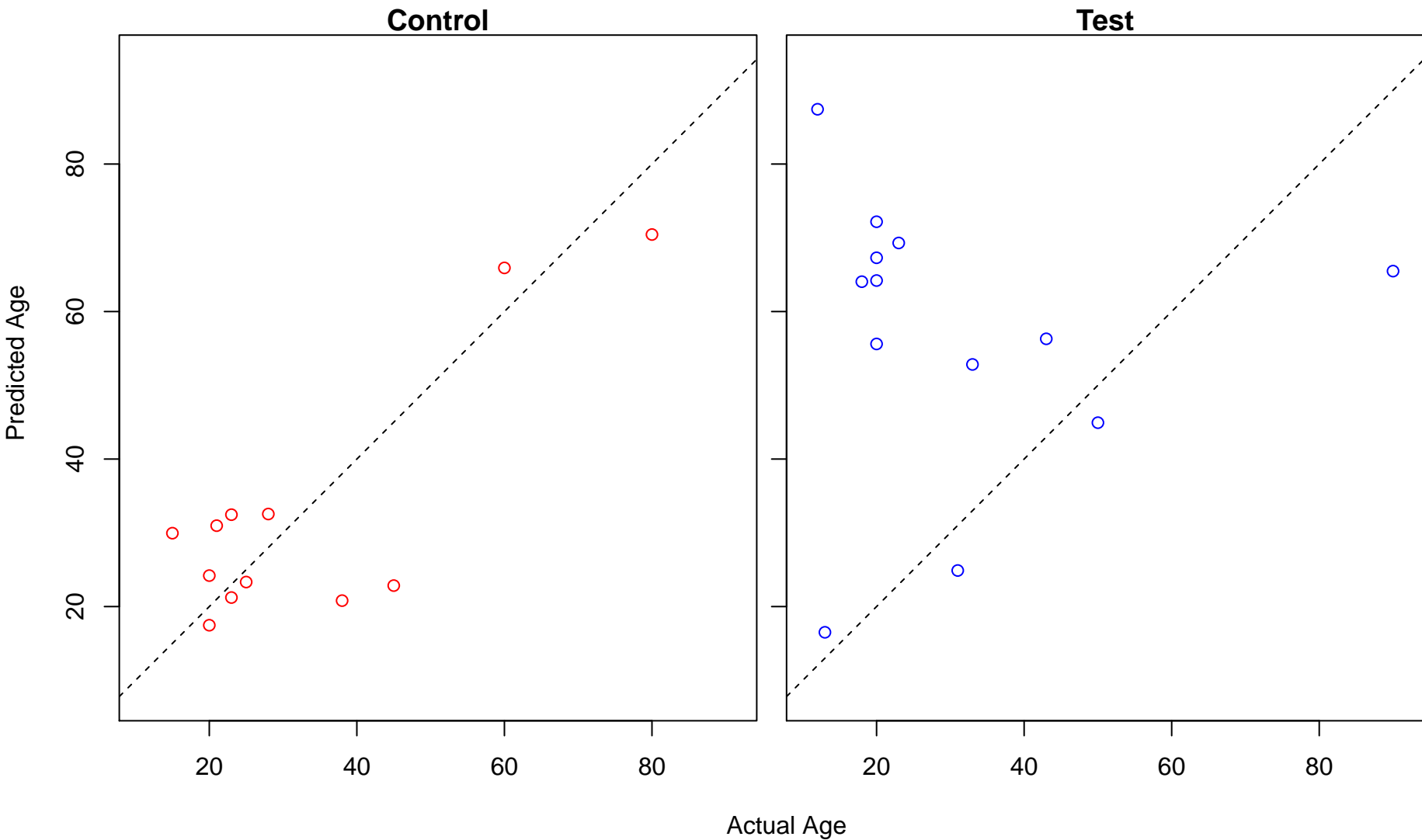
dopamine biosynthetic process (Score: 5.354311)



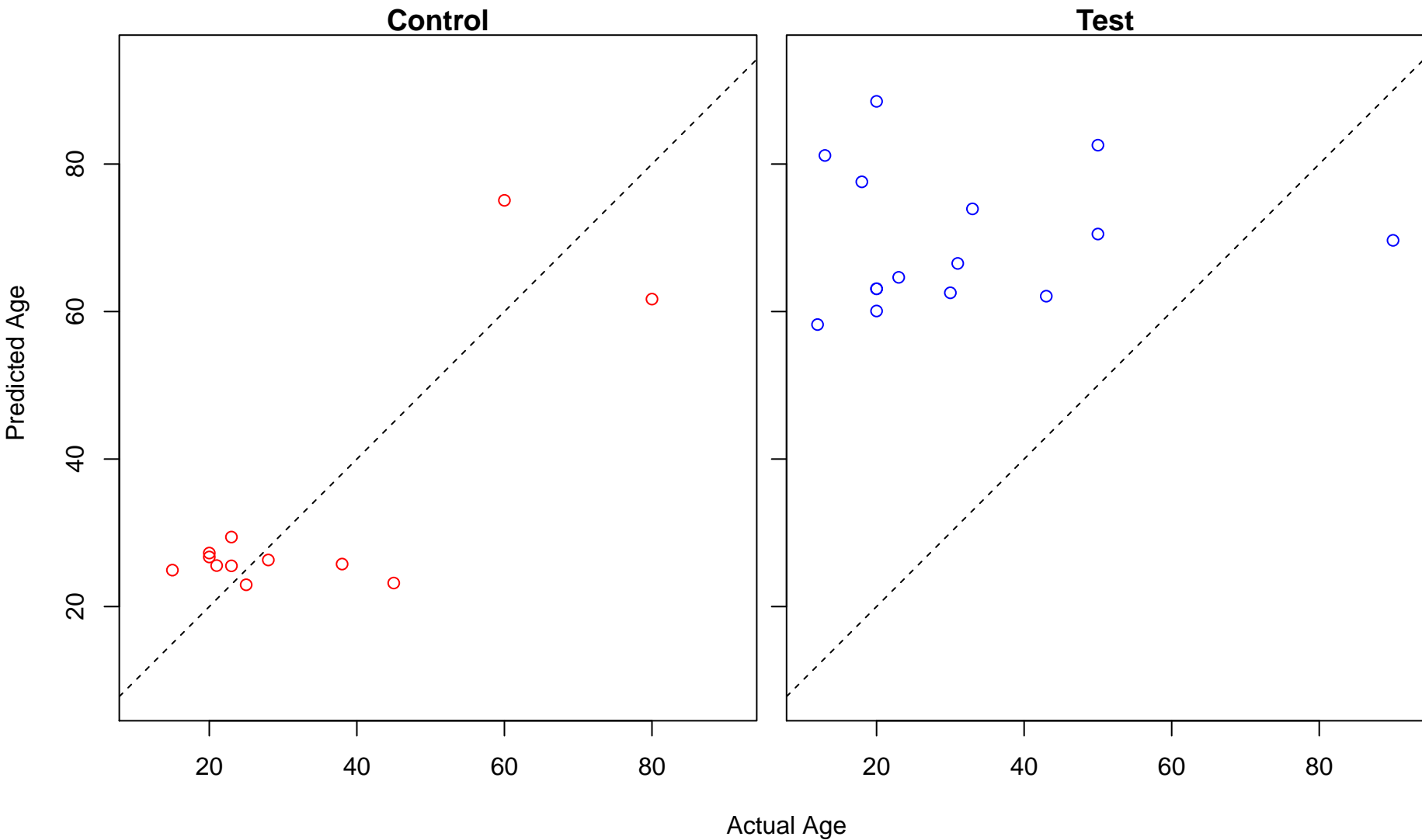
histone phosphorylation (Score: 5.352399)



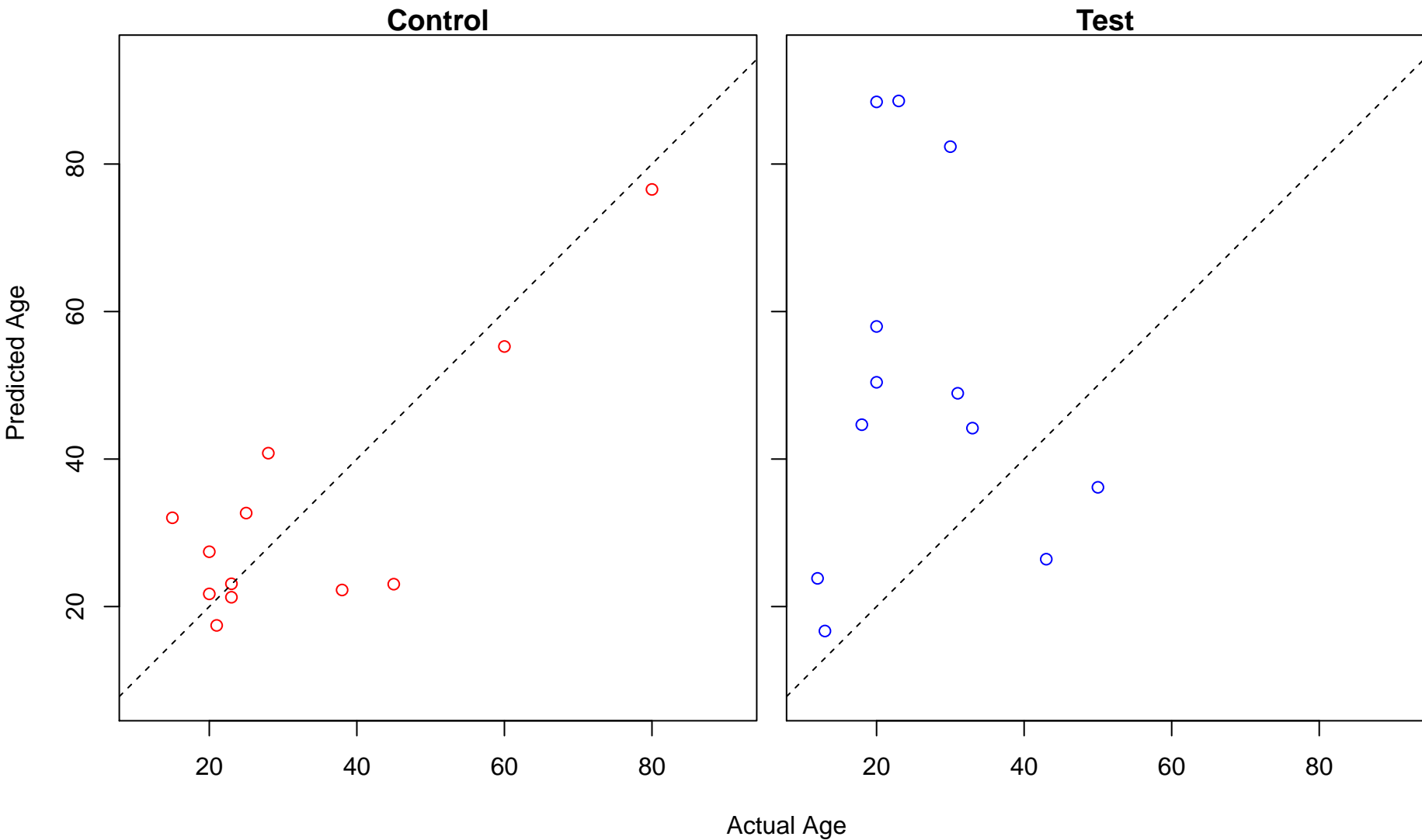
membrane budding (Score: 5.348208)



regulation of T cell proliferation (Score: 5.348035)

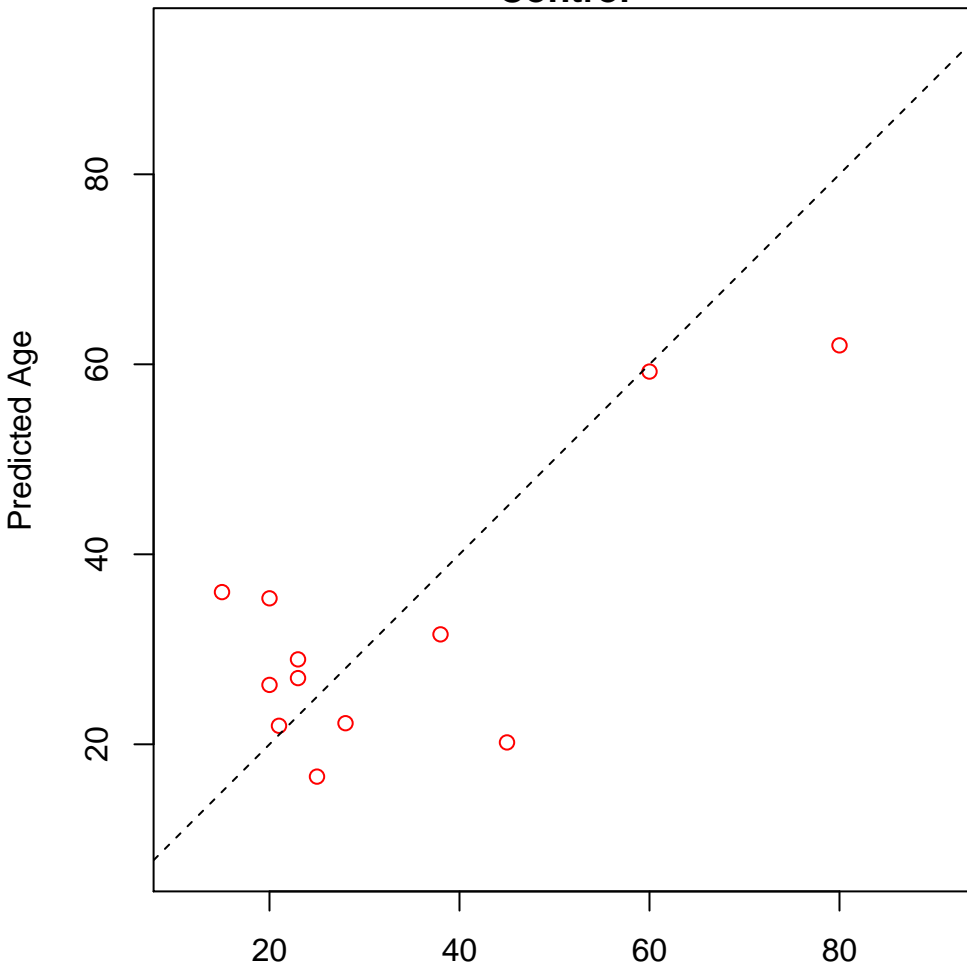


columnar/cuboidal epithelial cell differentiation (Score: 5.346745)

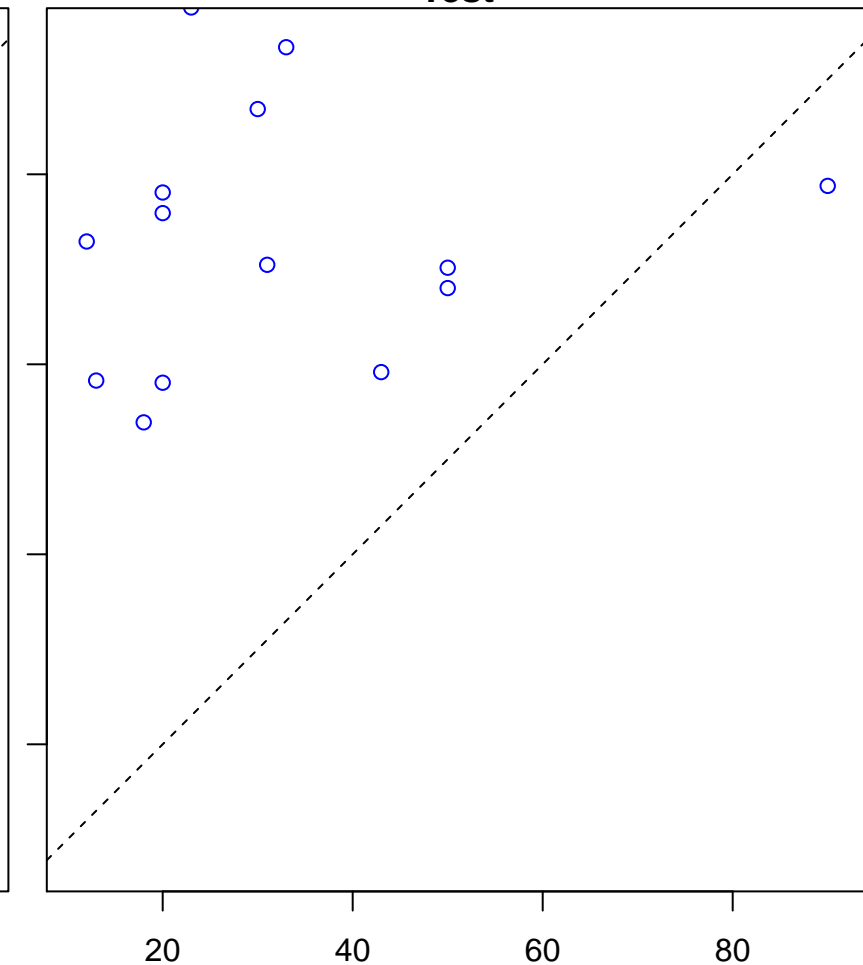


cellular phosphate ion homeostasis (Score: 5.343830)

Control

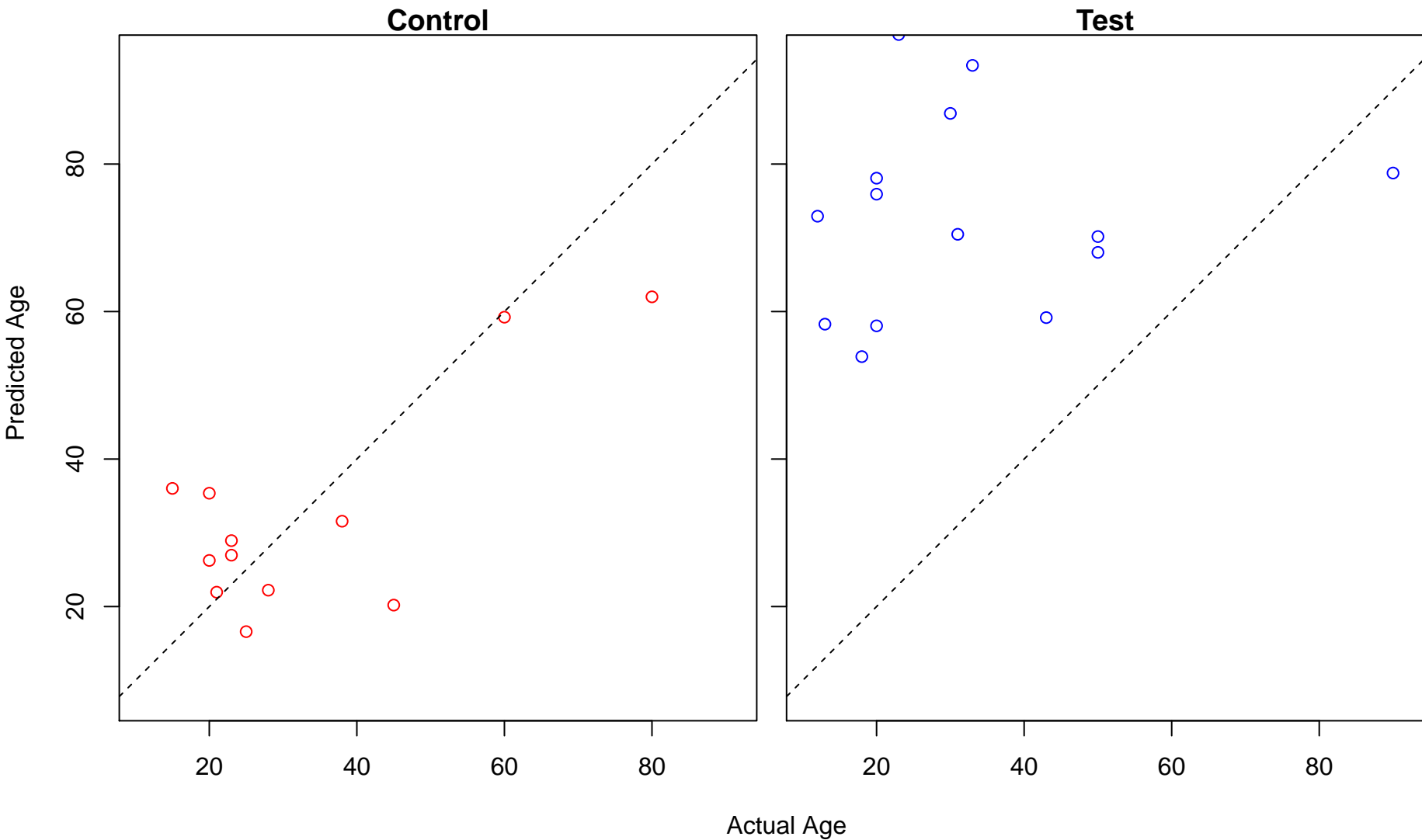


Test

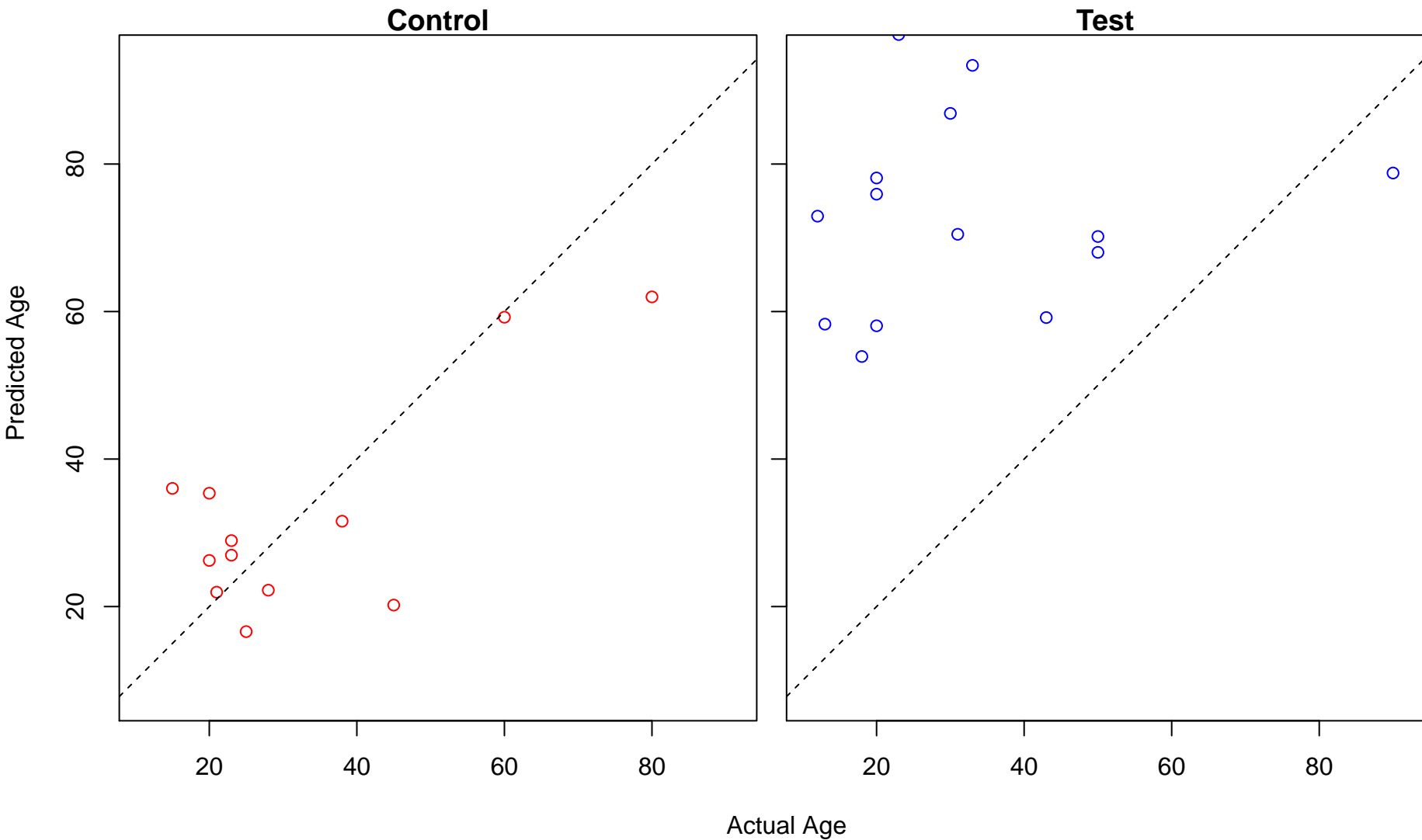


Actual Age

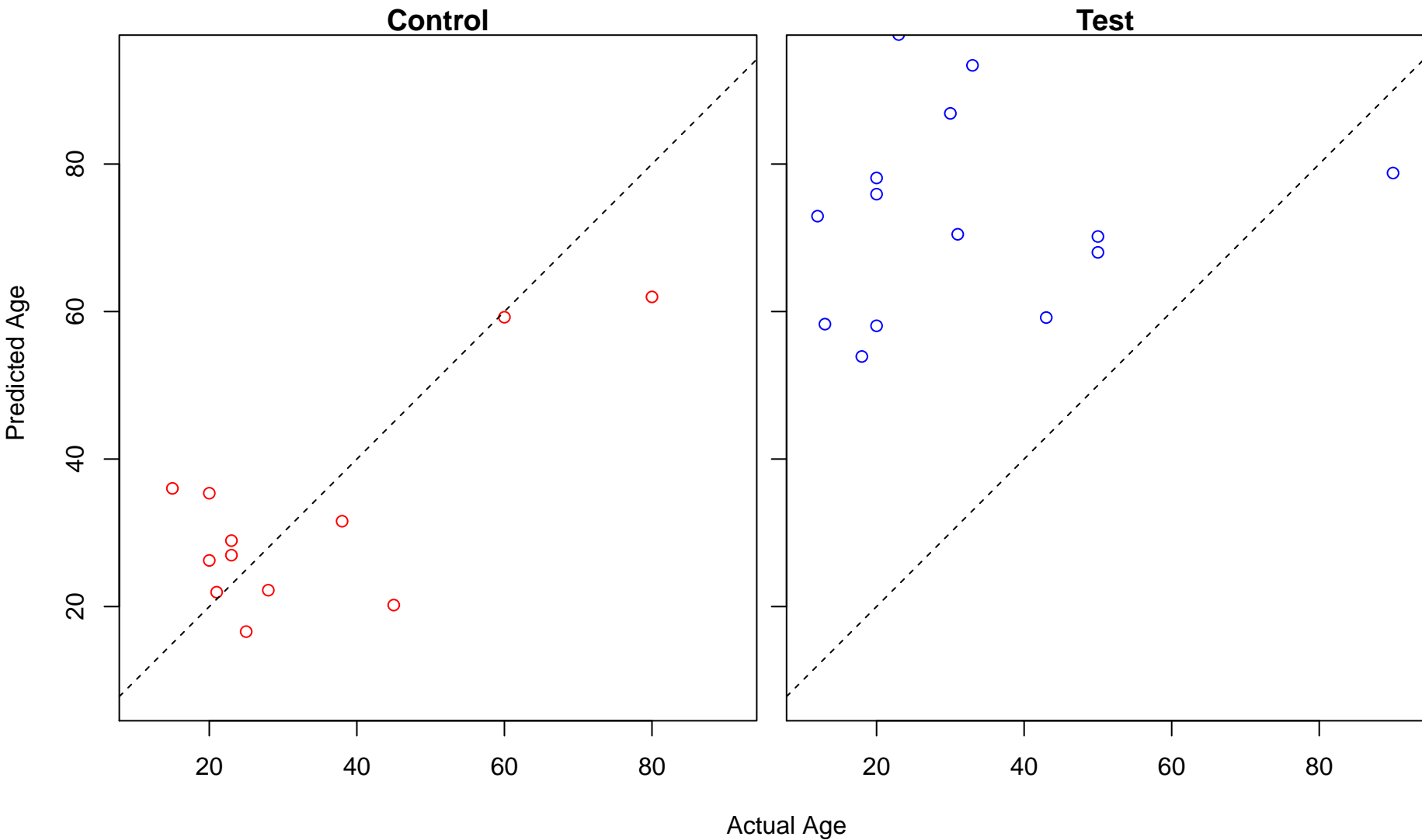
cellular trivalent inorganic anion homeostasis (Score: 5.343830)



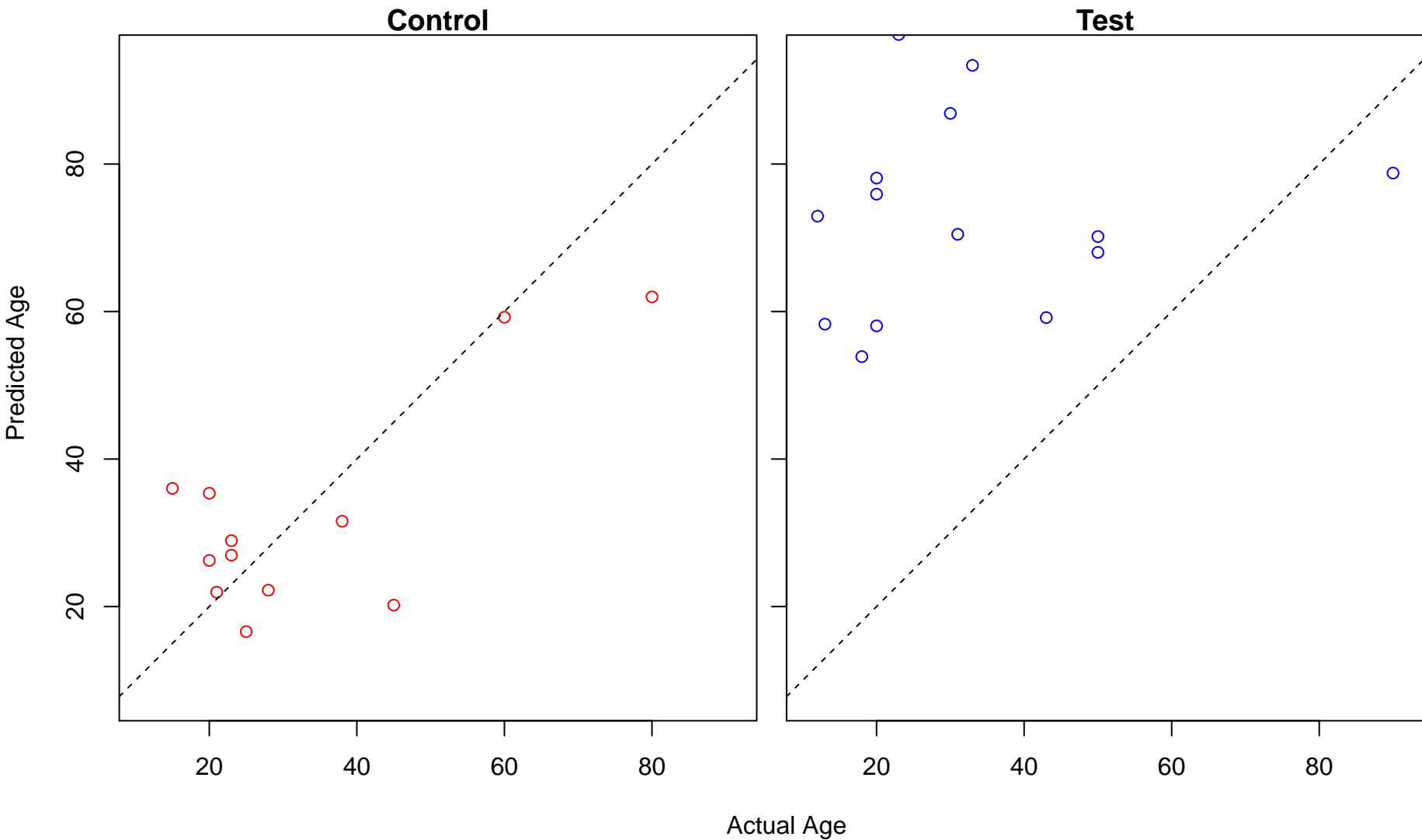
cellular anion homeostasis (Score: 5.343637)



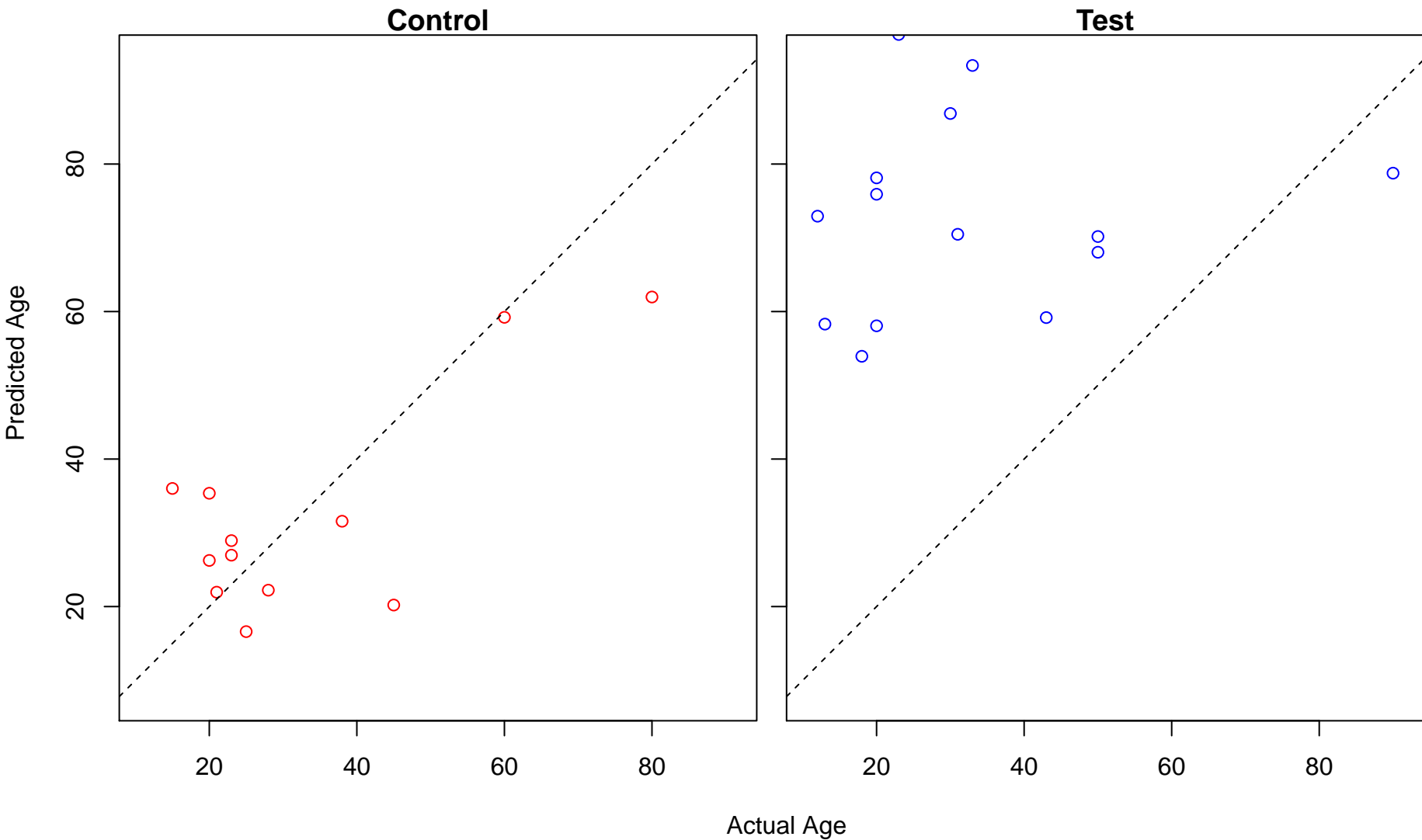
cellular monovalent inorganic anion homeostasis (Score: 5.343637)



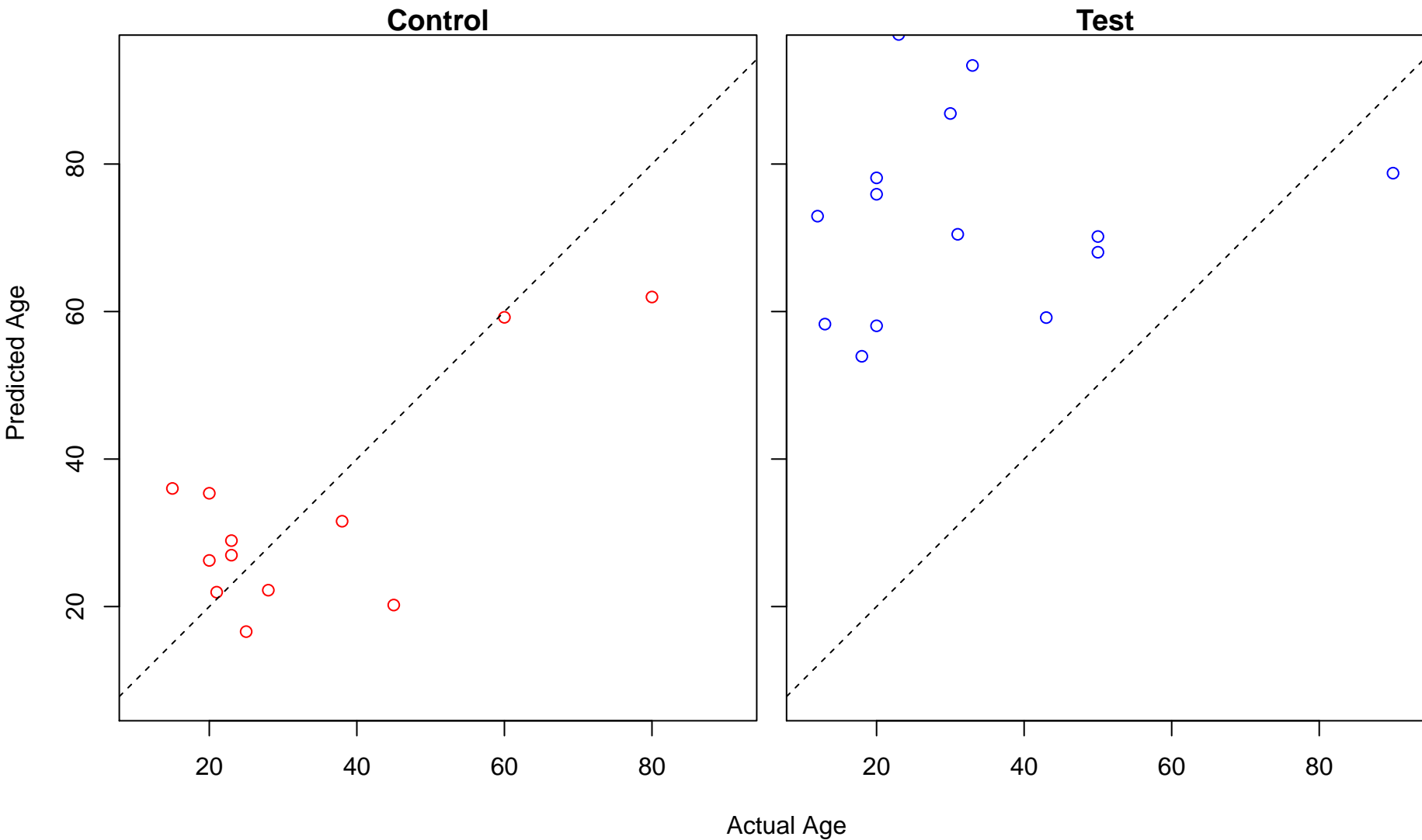
cellular divalent inorganic anion homeostasis (Score: 5.343202)



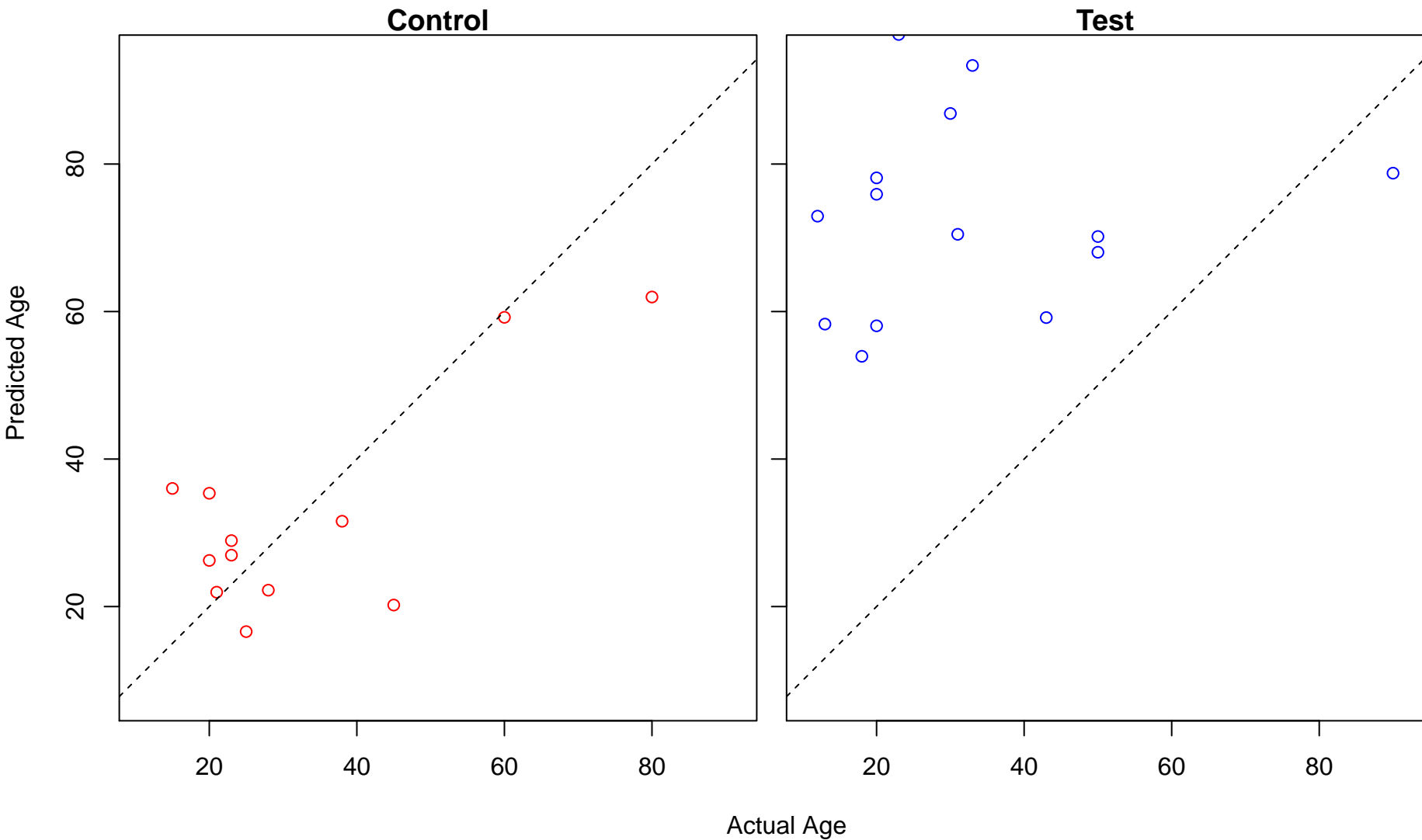
divalent inorganic anion homeostasis (Score: 5.343200)



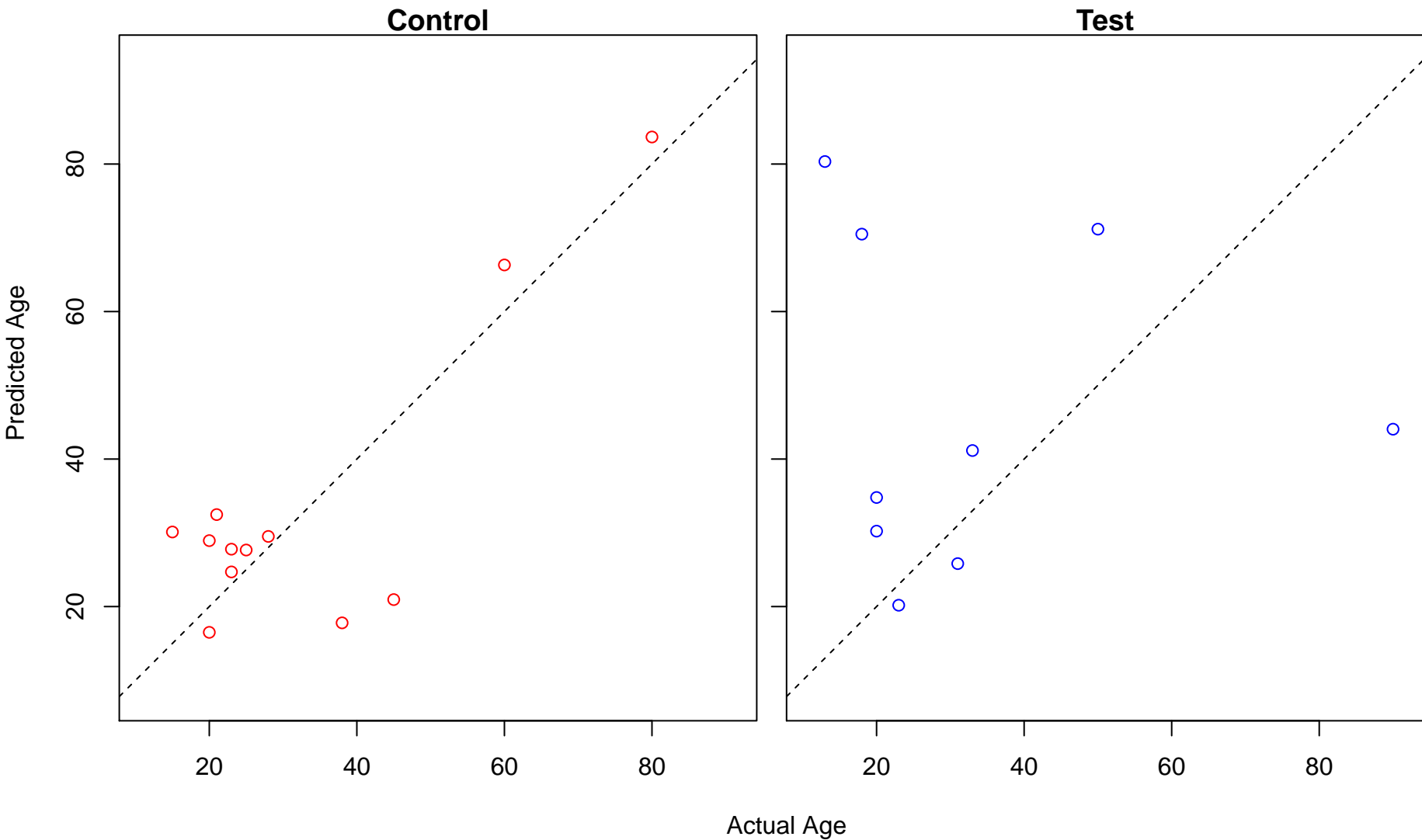
phosphate ion homeostasis (Score: 5.343191)



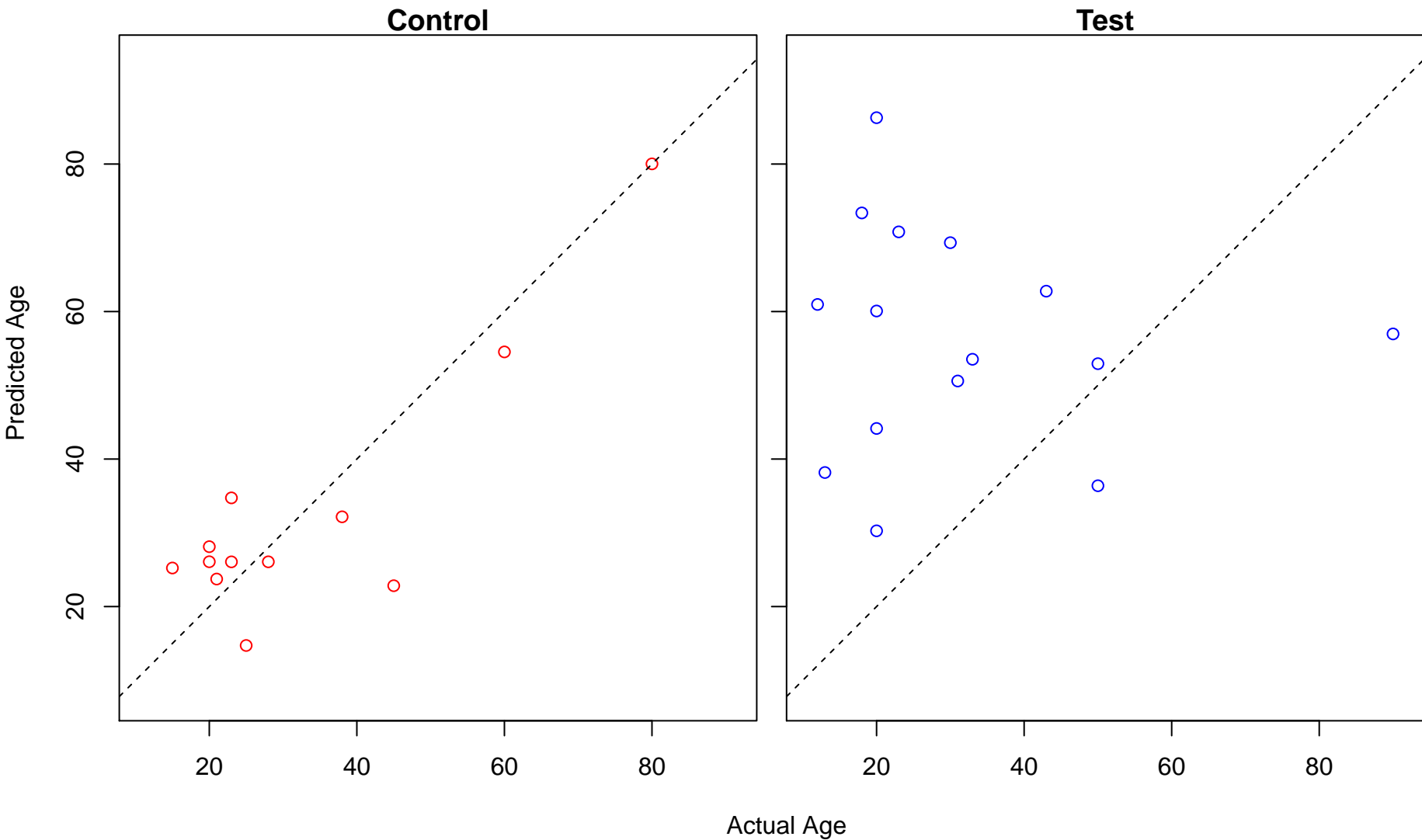
trivalent inorganic anion homeostasis (Score: 5.343191)



response to estrogen (Score: 5.341715)

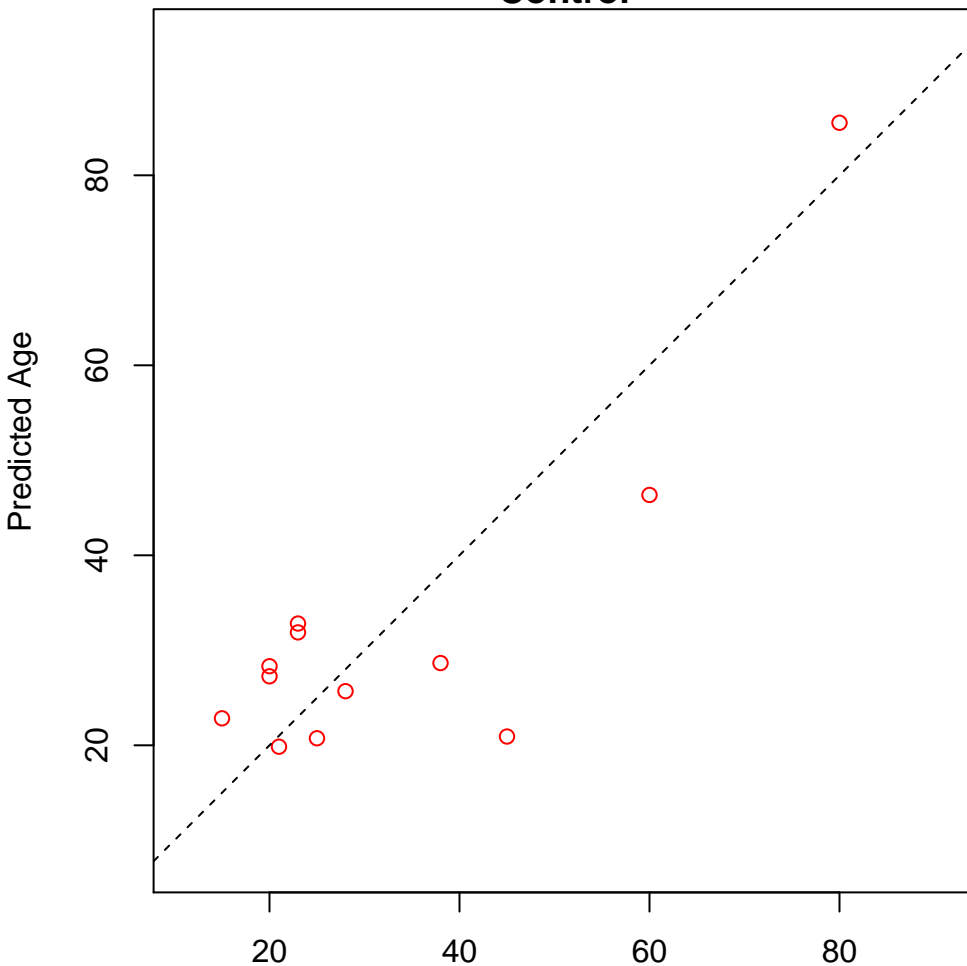


negative regulation of peptidyl-serine phosphorylation (Score: 5.337983)

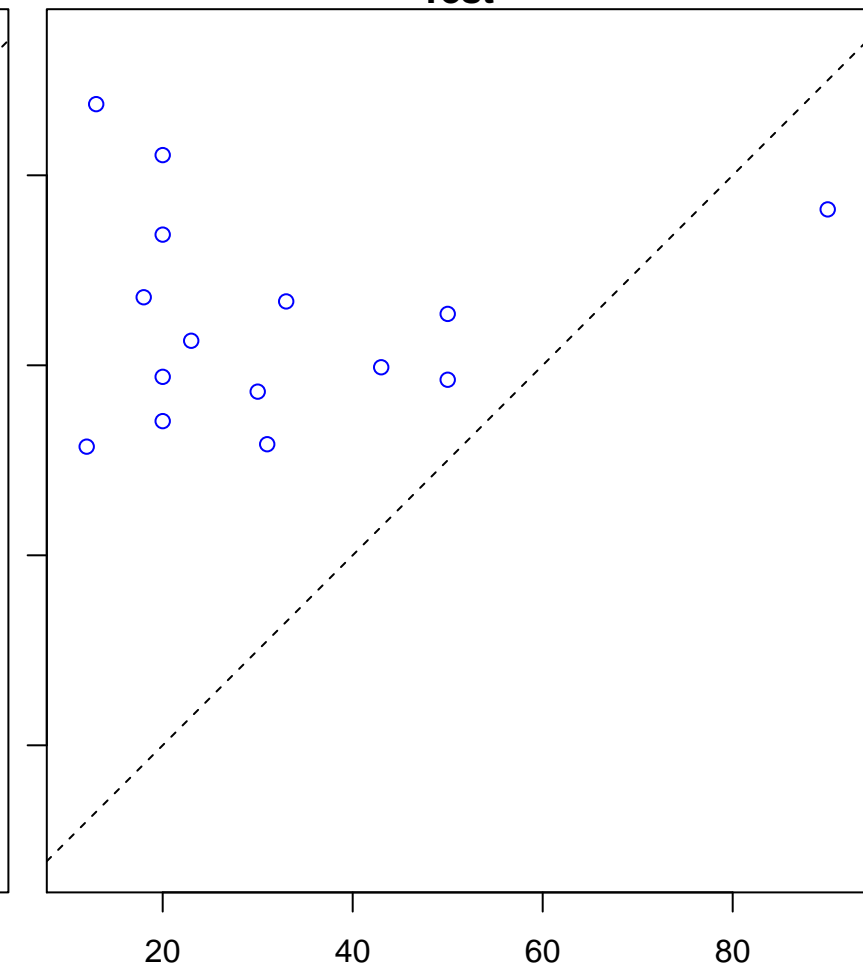


regulation of histone H3-K4 methylation (Score: 5.335829)

Control

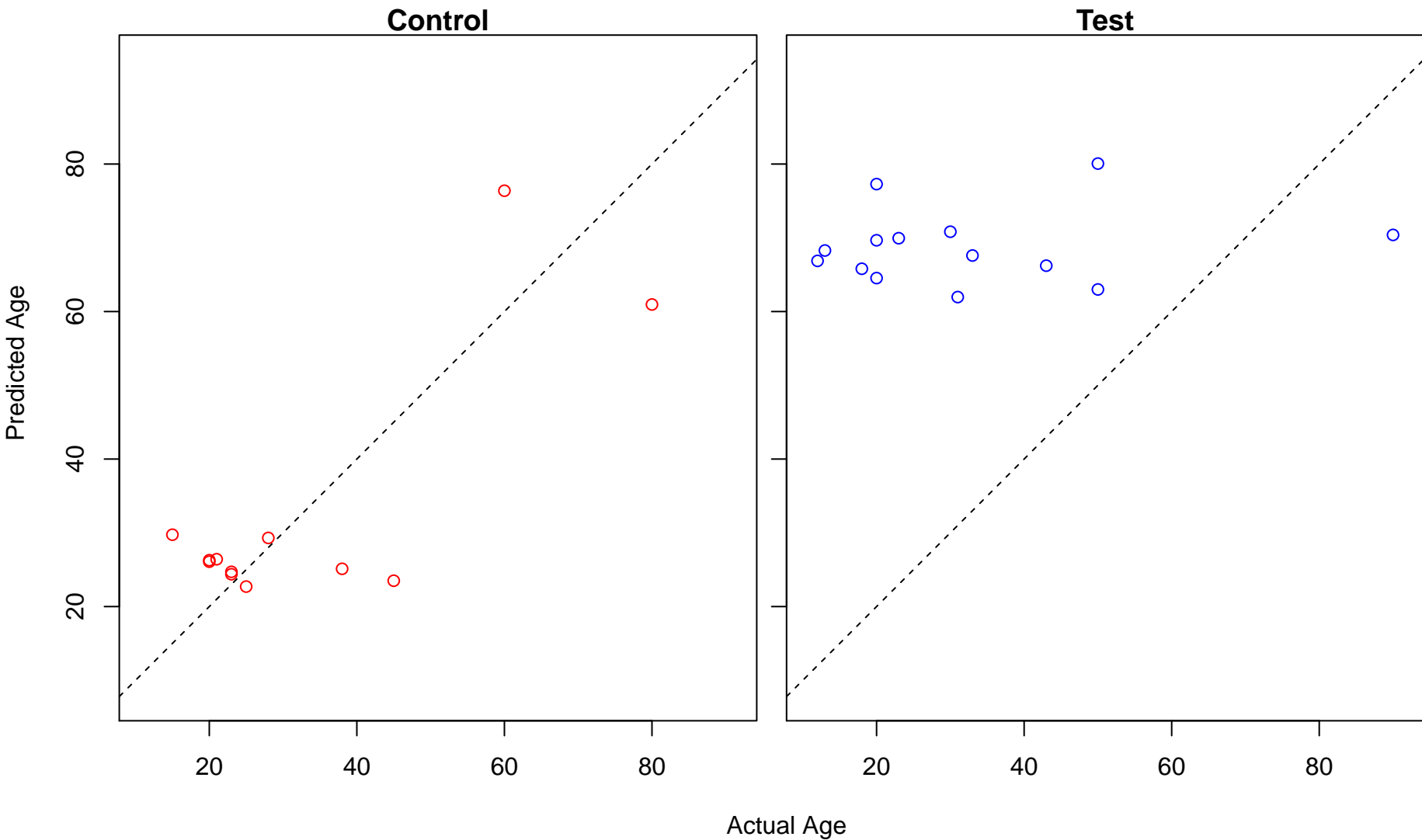


Test

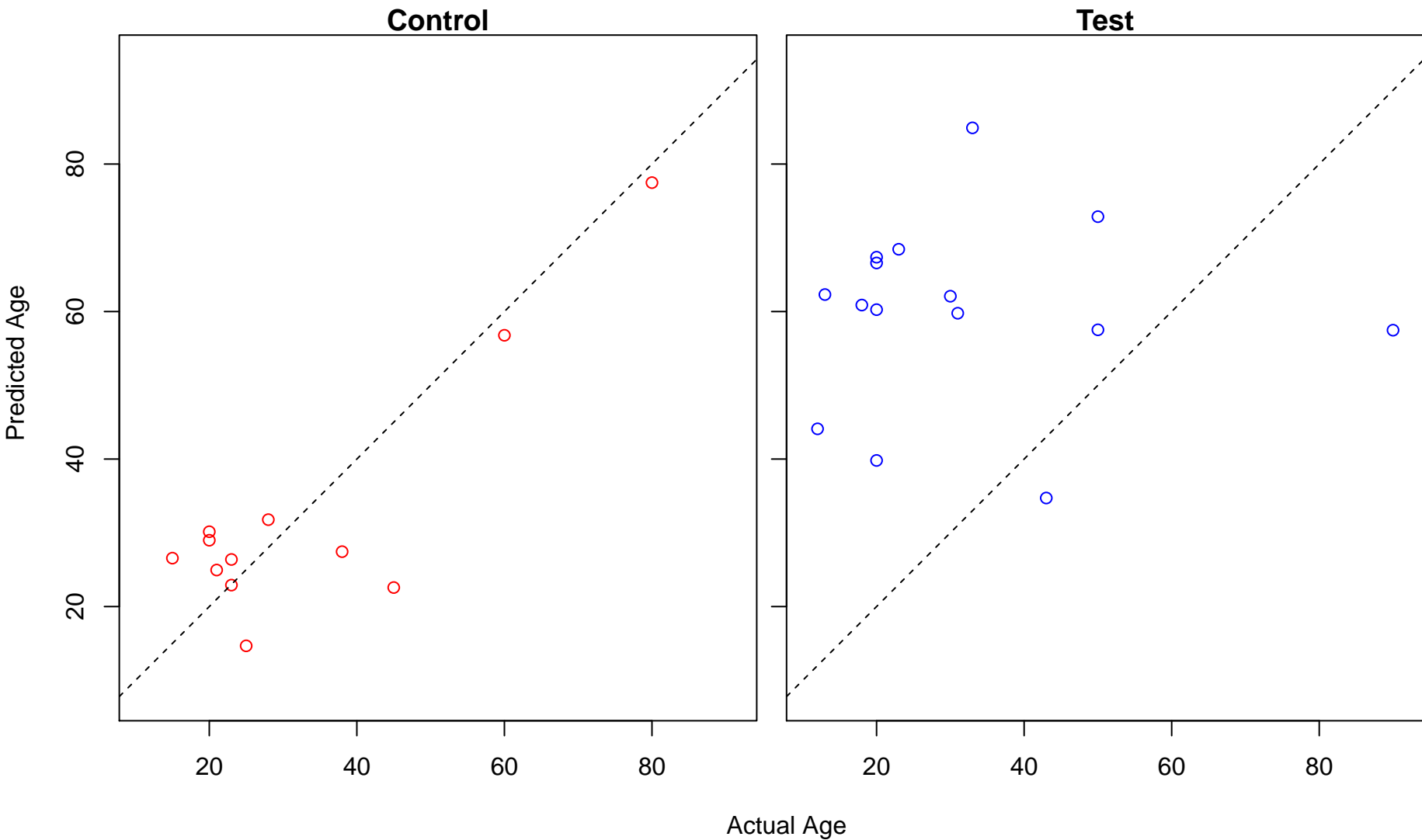


Actual Age

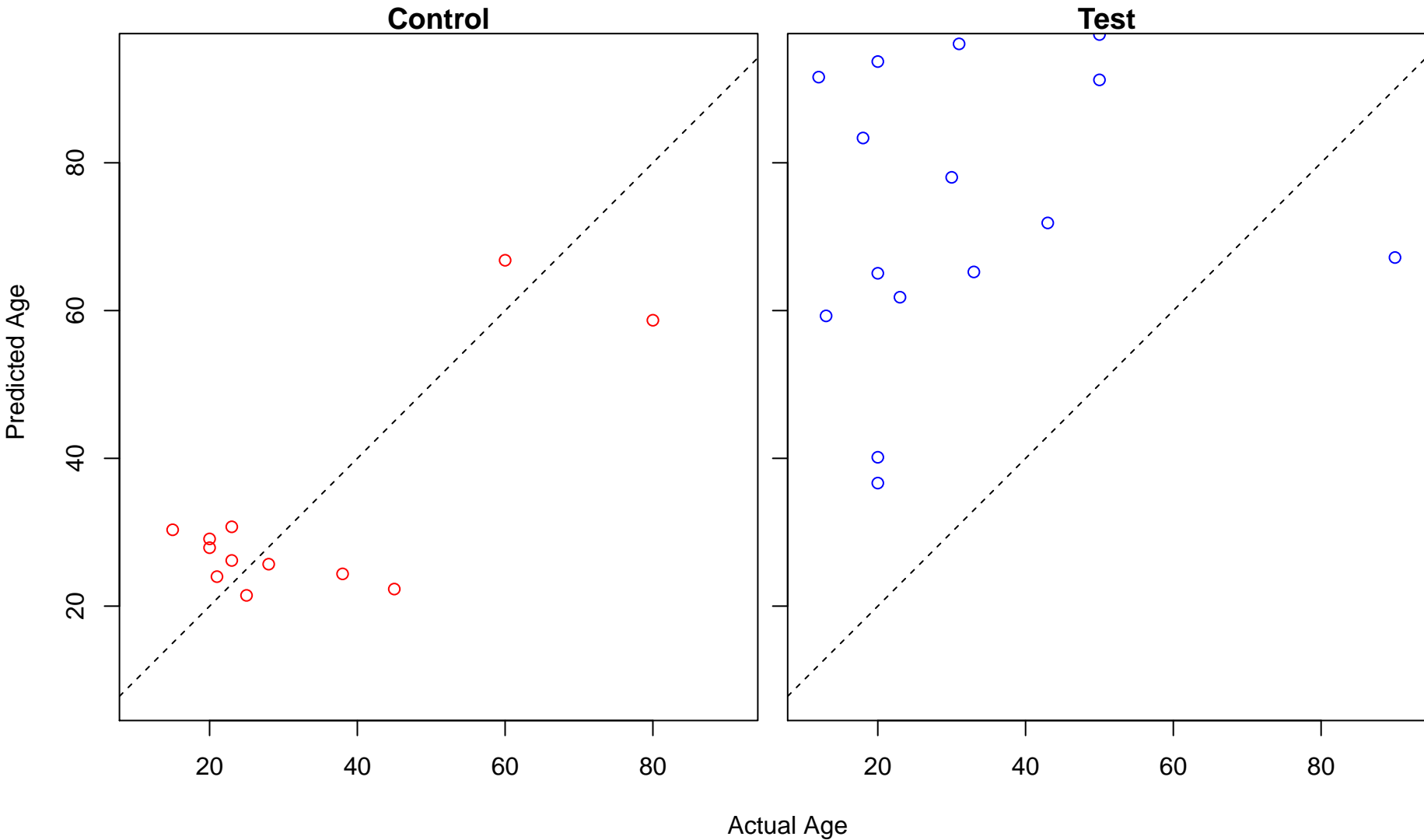
positive regulation of reproductive process (Score: 5.335460)



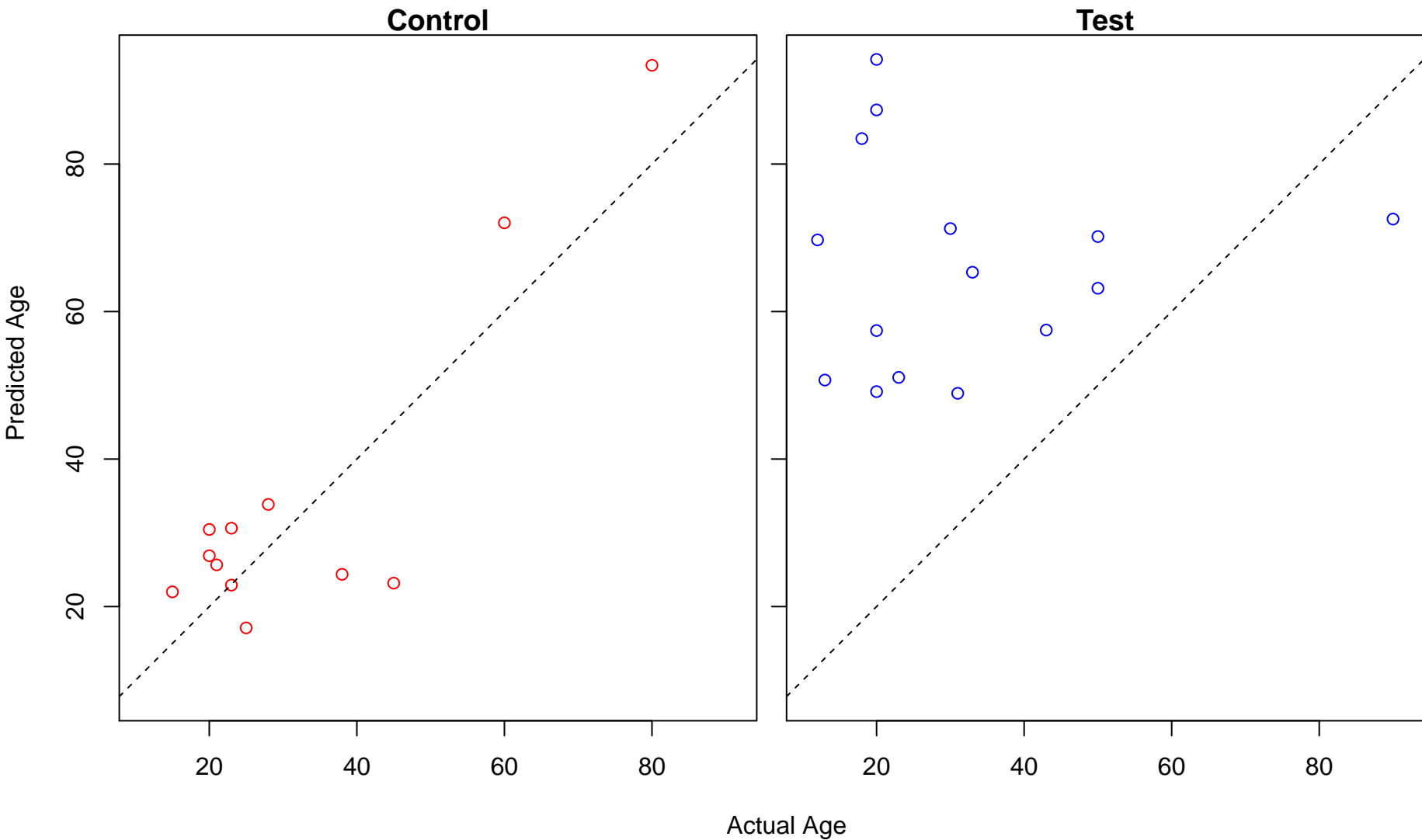
receptor recycling (Score: 5.331703)



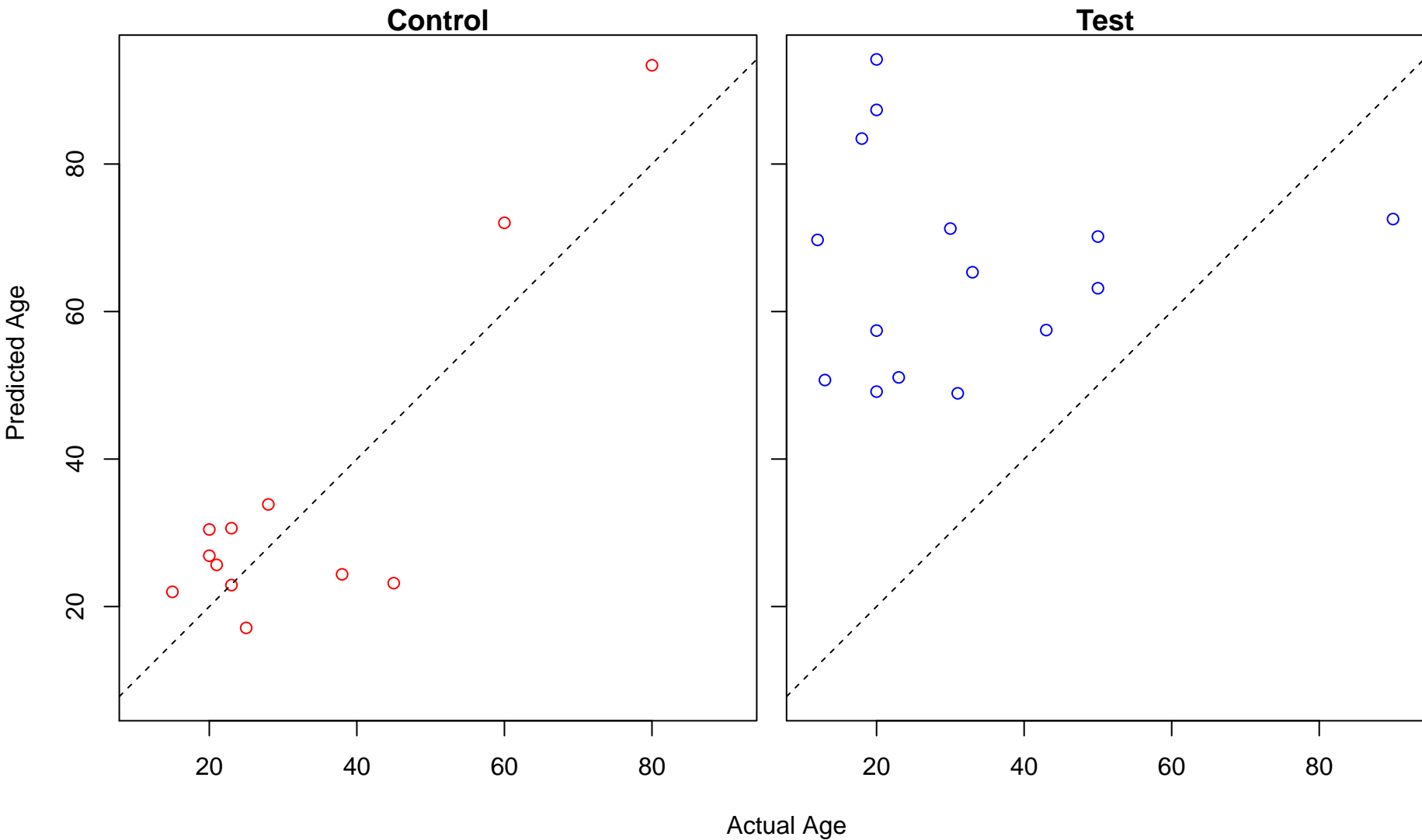
sensory perception of temperature stimulus (Score: 5.331253)



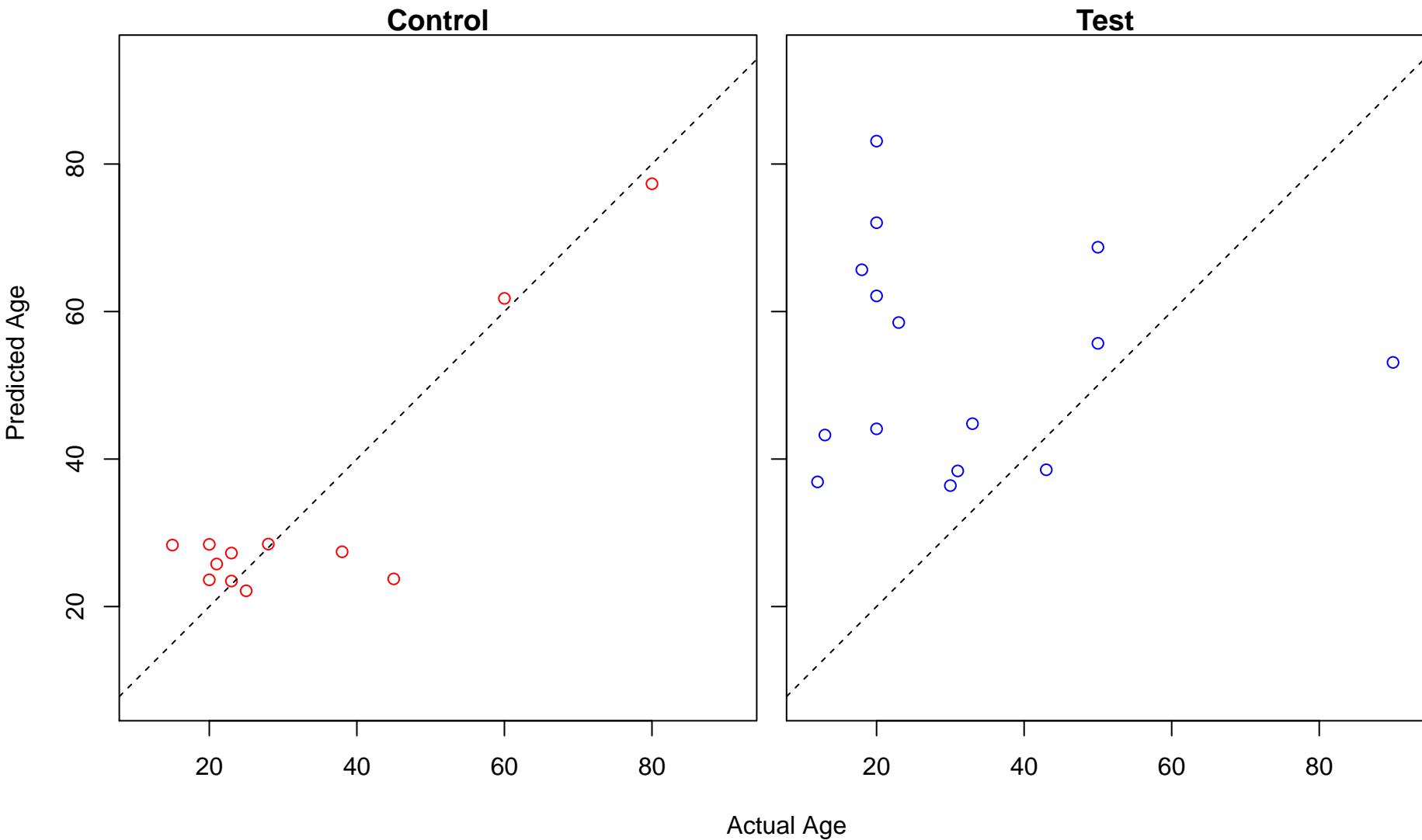
melanosome transport (Score: 5.327441)



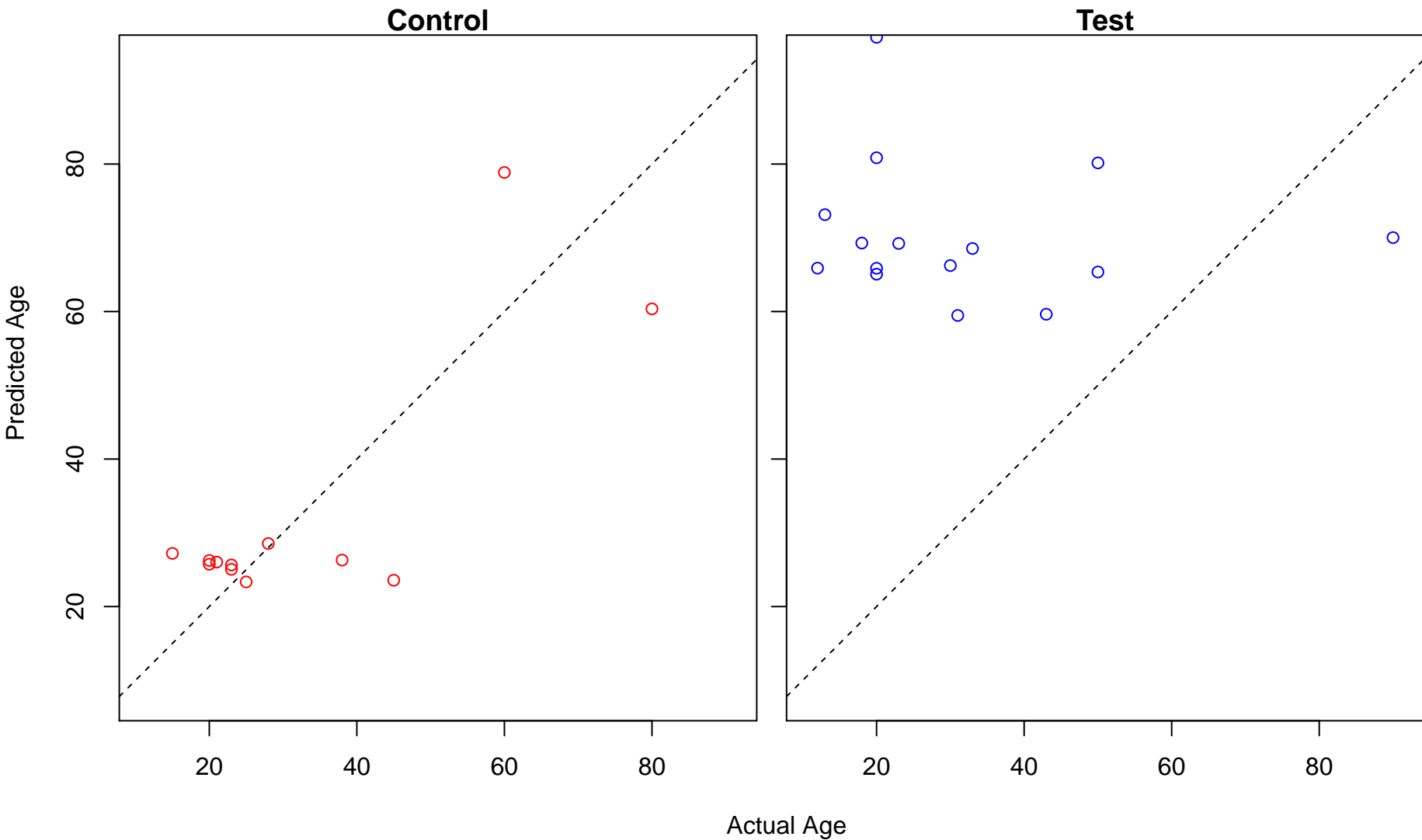
pigment granule transport (Score: 5.327441)



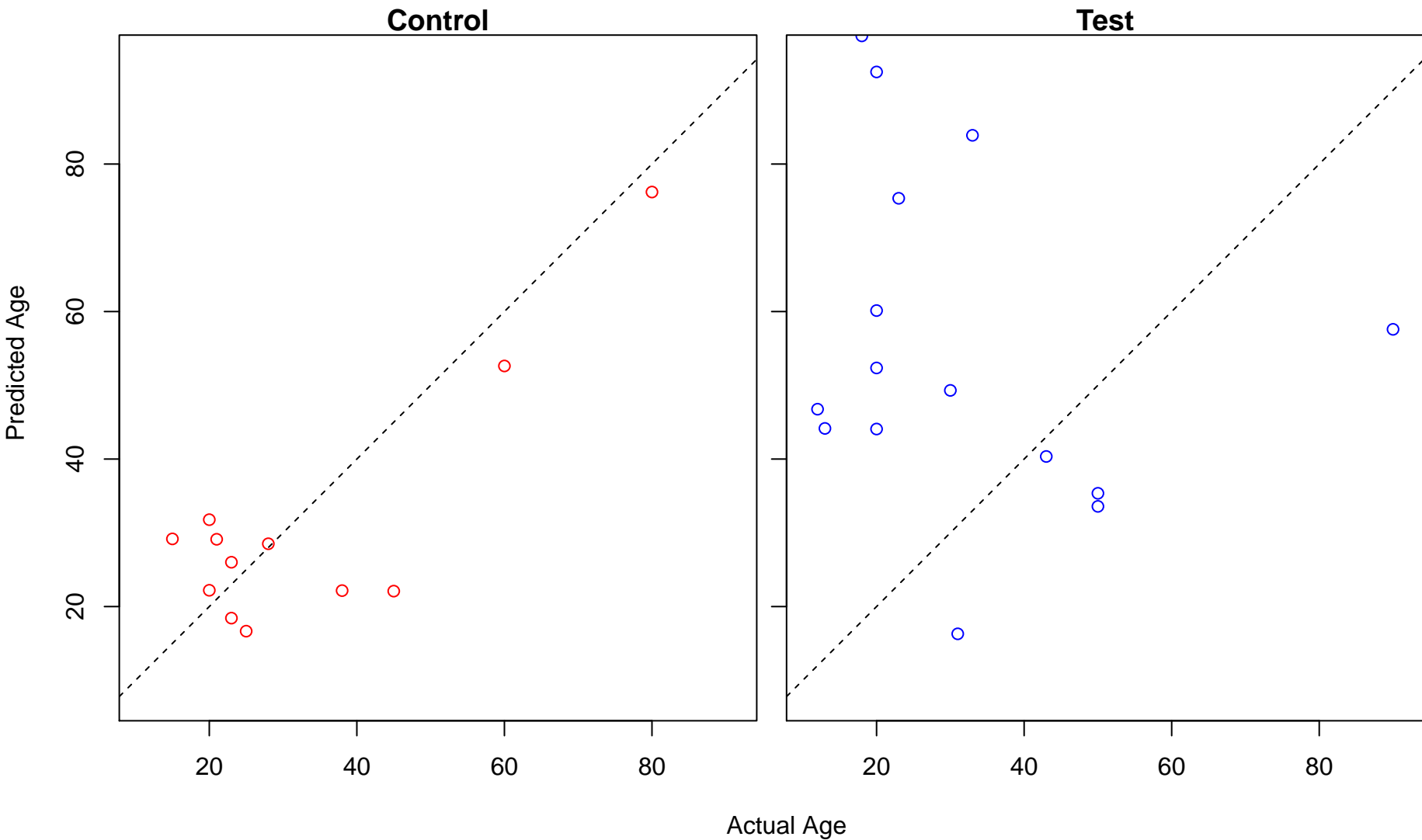
ERBB signaling pathway (Score: 5.327074)



positive regulation of epithelial cell migration (Score: 5.325299)

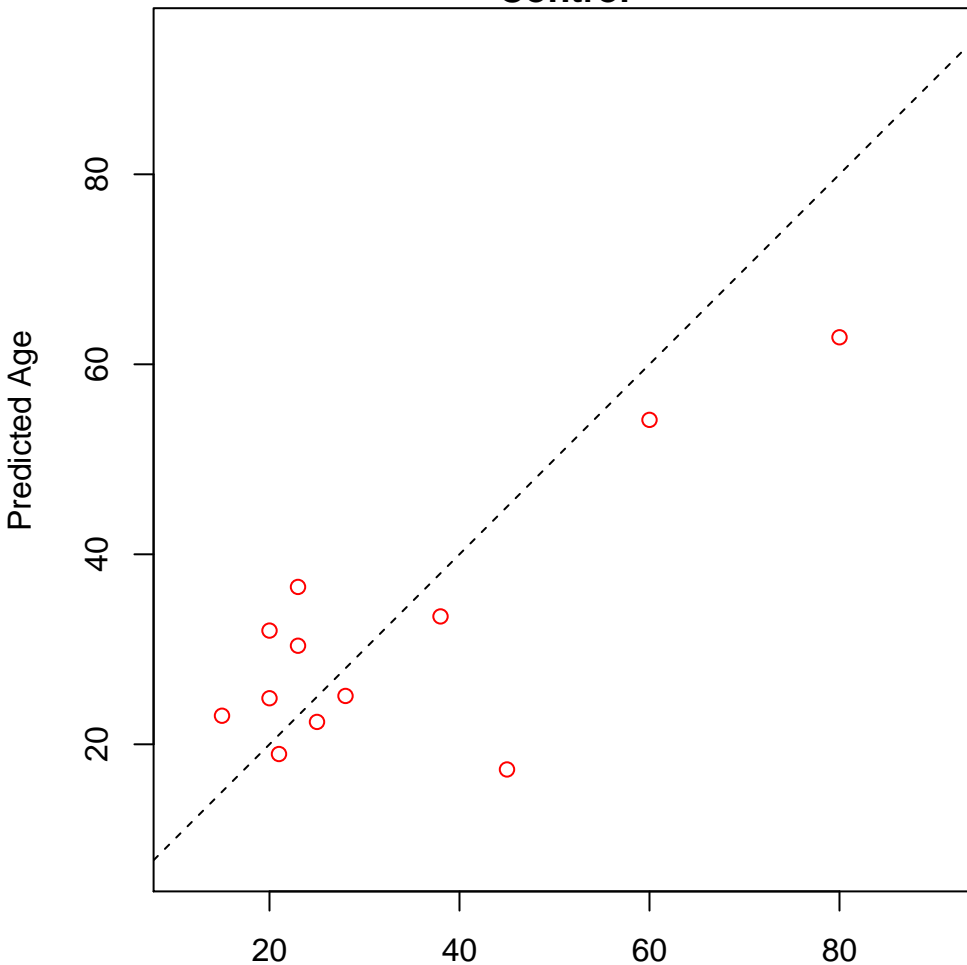


RNA localization (Score: 5.324613)

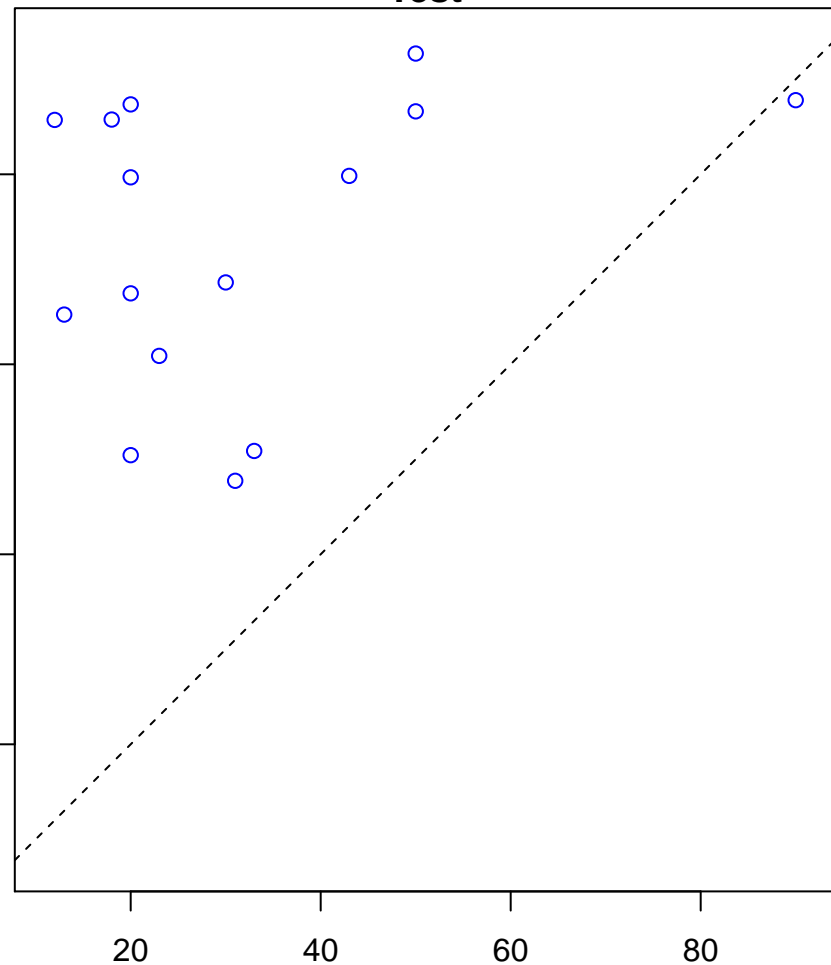


glandular epithelial cell differentiation (Score: 5.323251)

Control

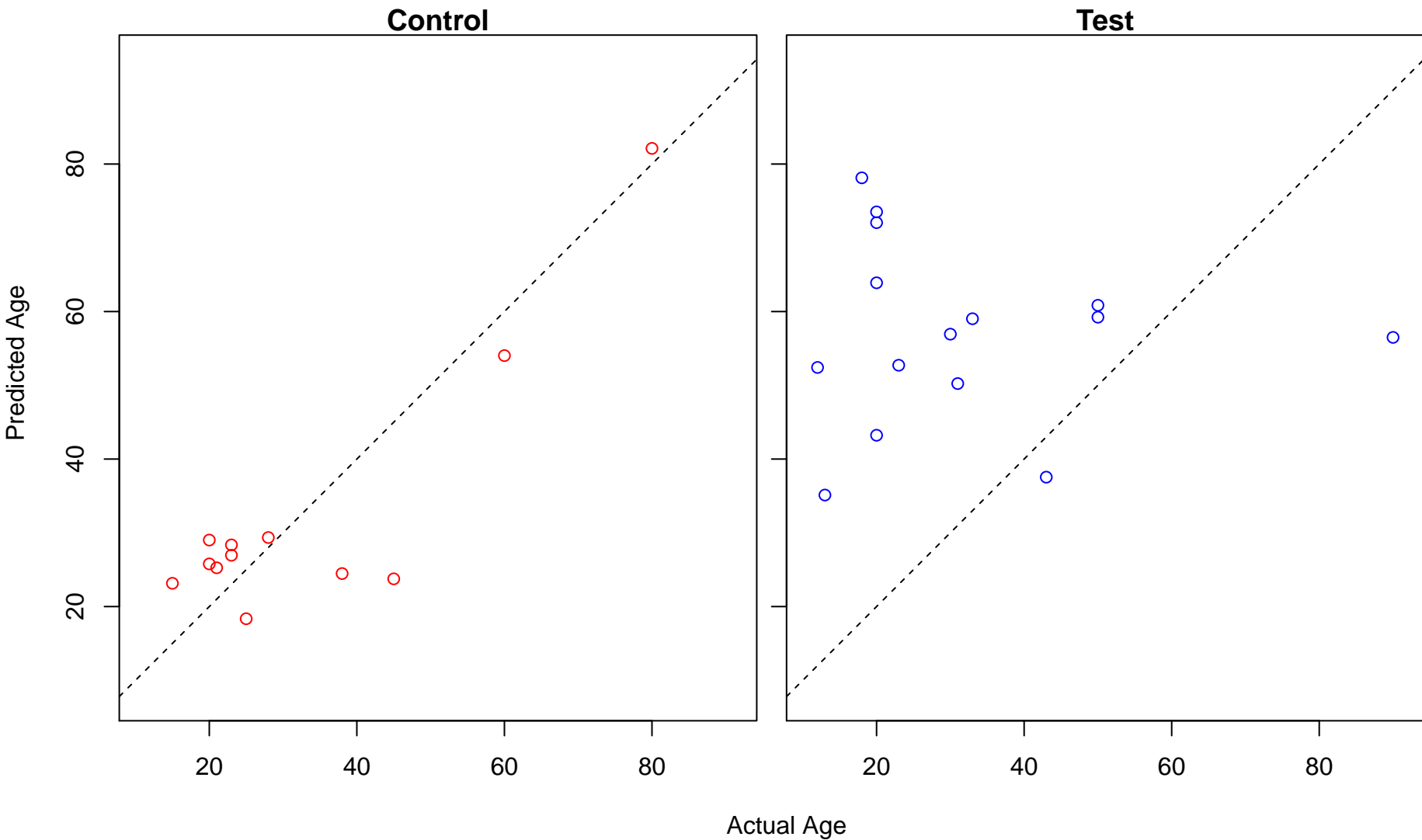


Test



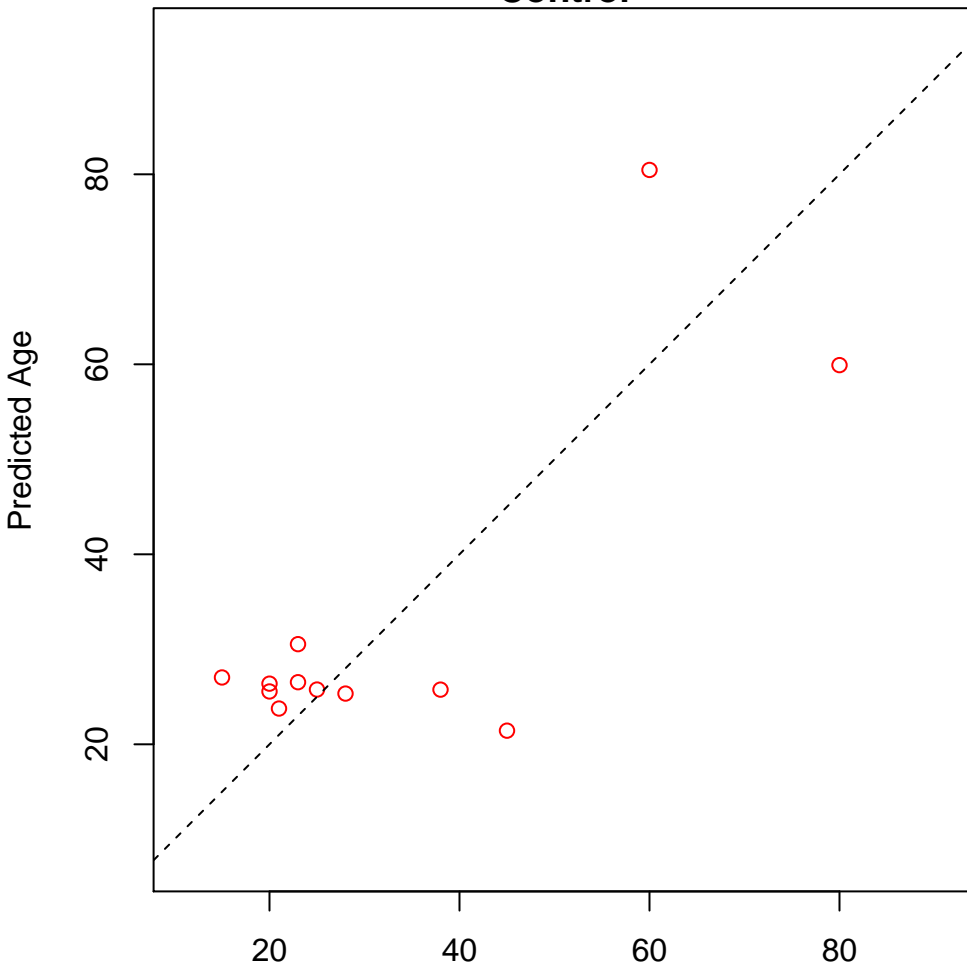
Actual Age

regulation of DNA replication (Score: 5.322457)

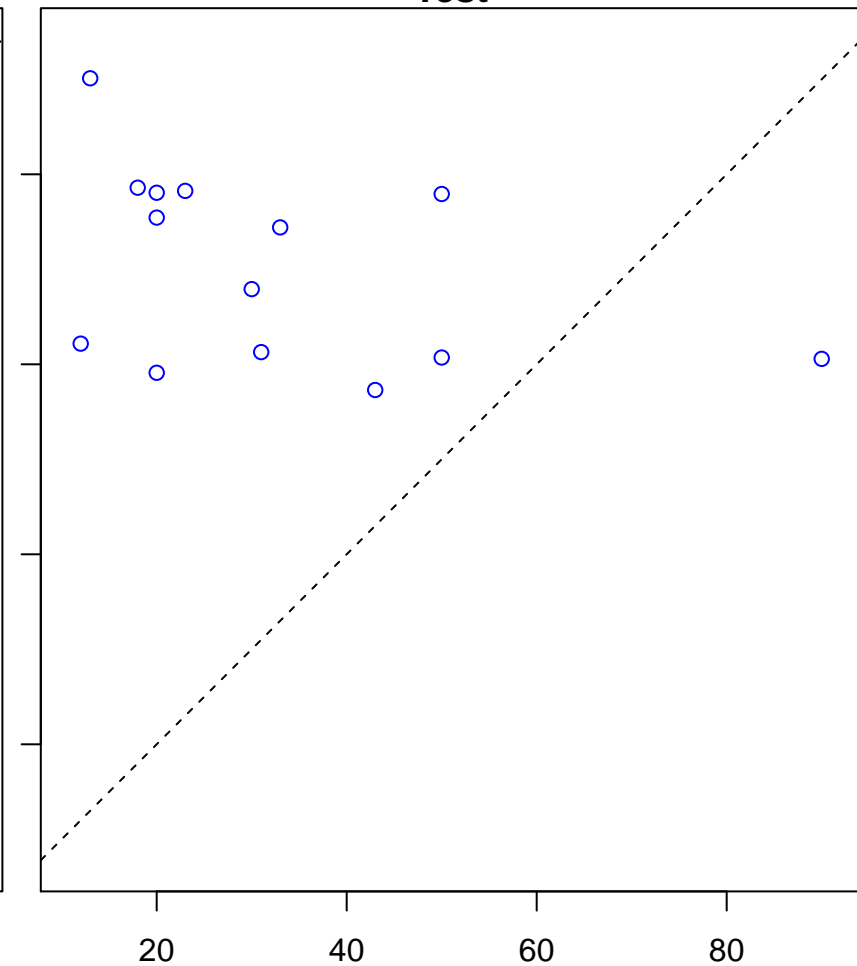


kidney mesenchyme development (Score: 5.321012)

Control

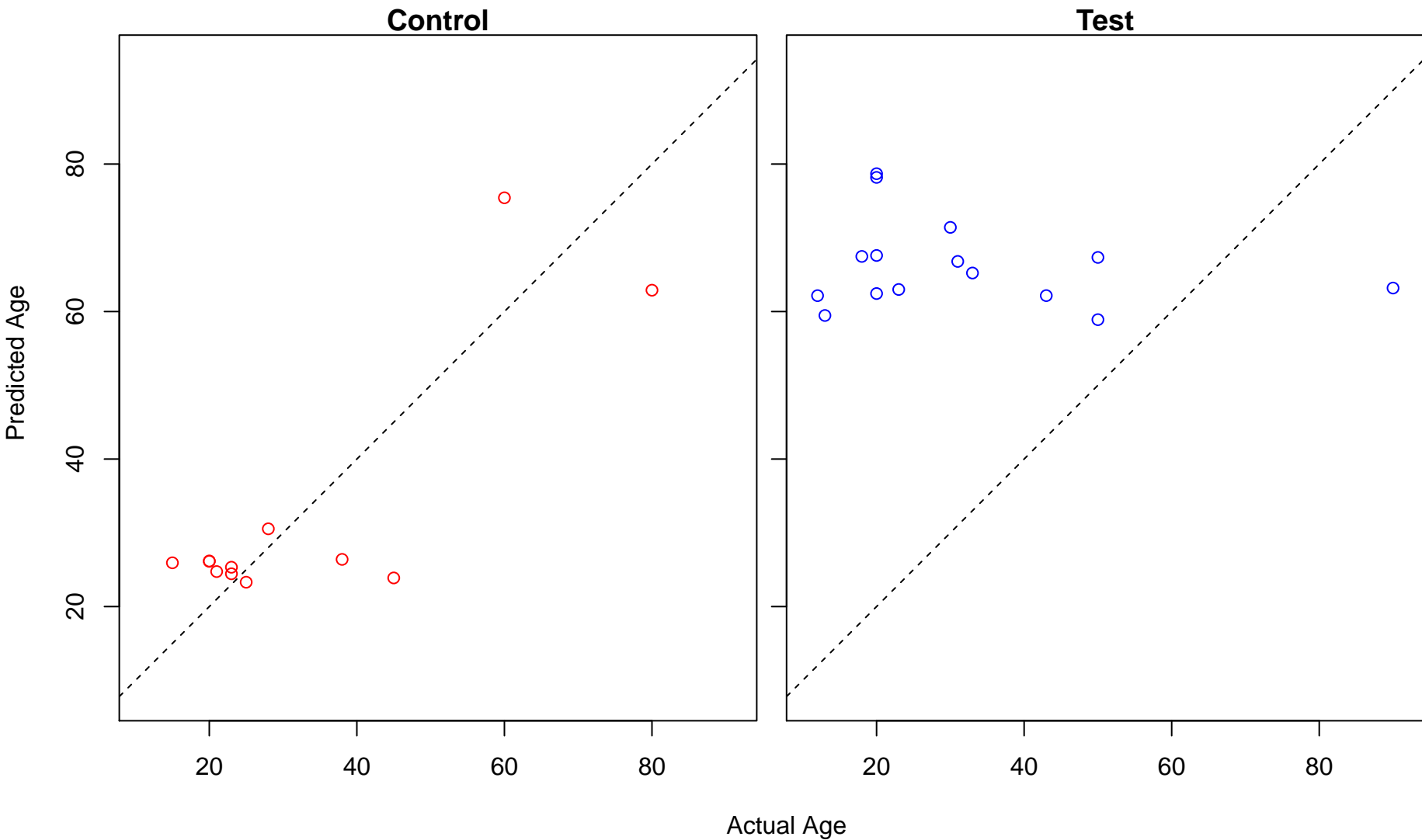


Test

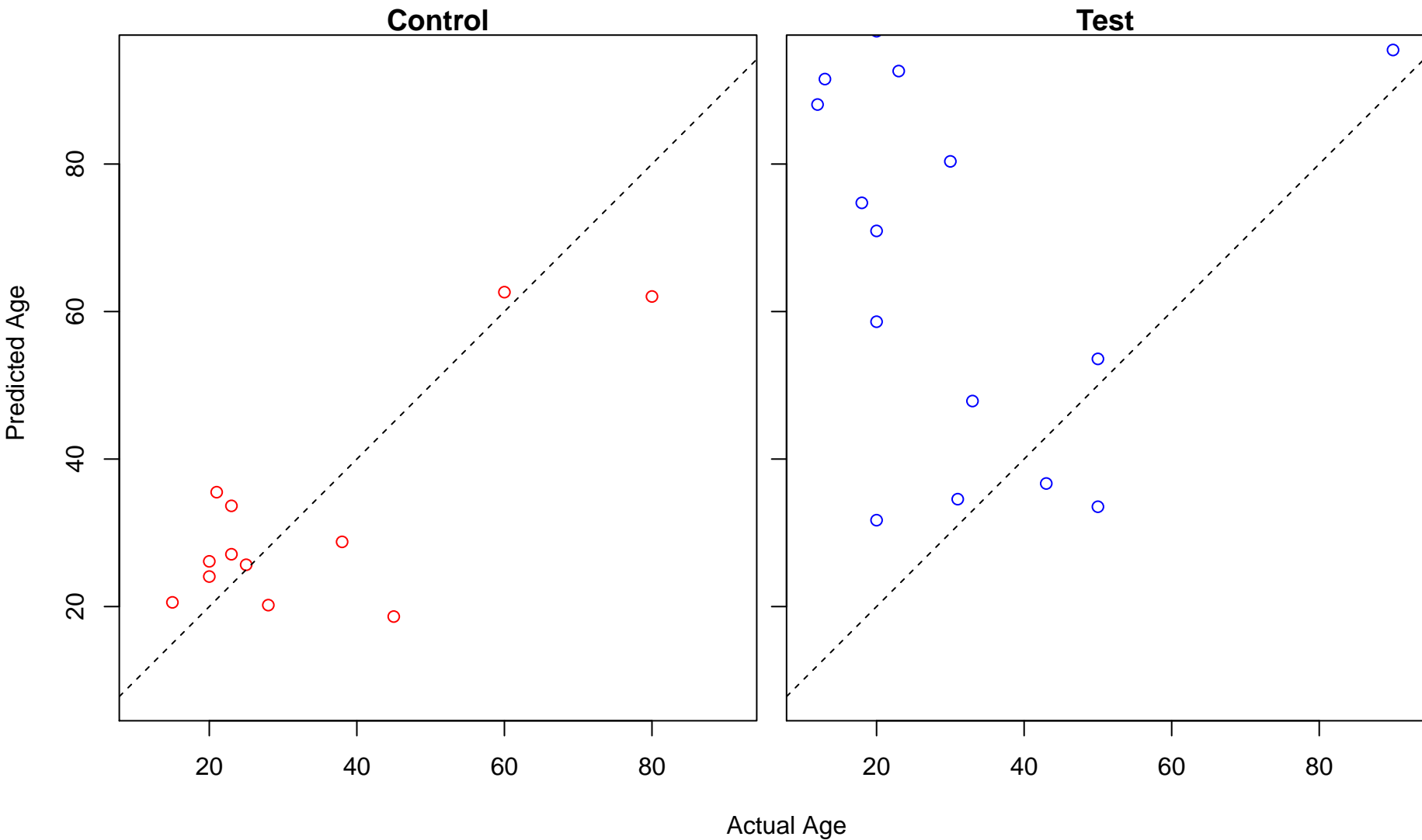


Actual Age

cellular response to amino acid starvation (Score: 5.320379)

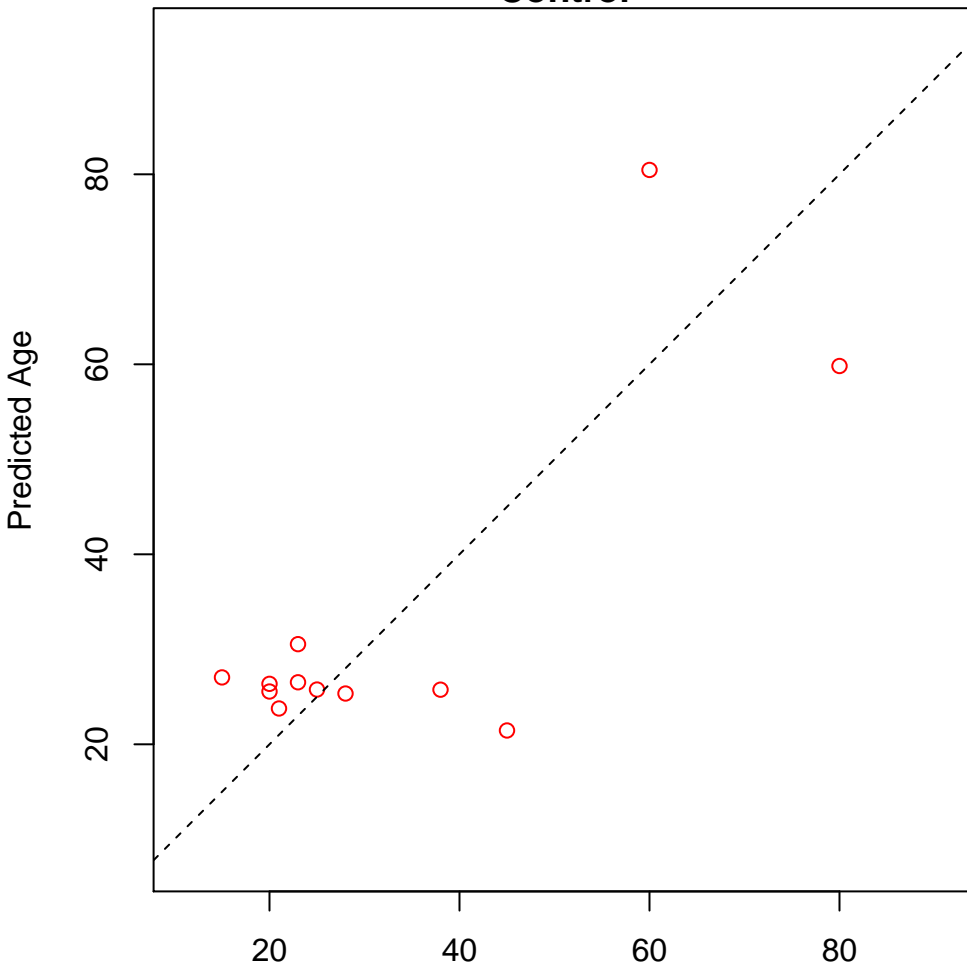


regulation of chemokine secretion (Score: 5.319977)

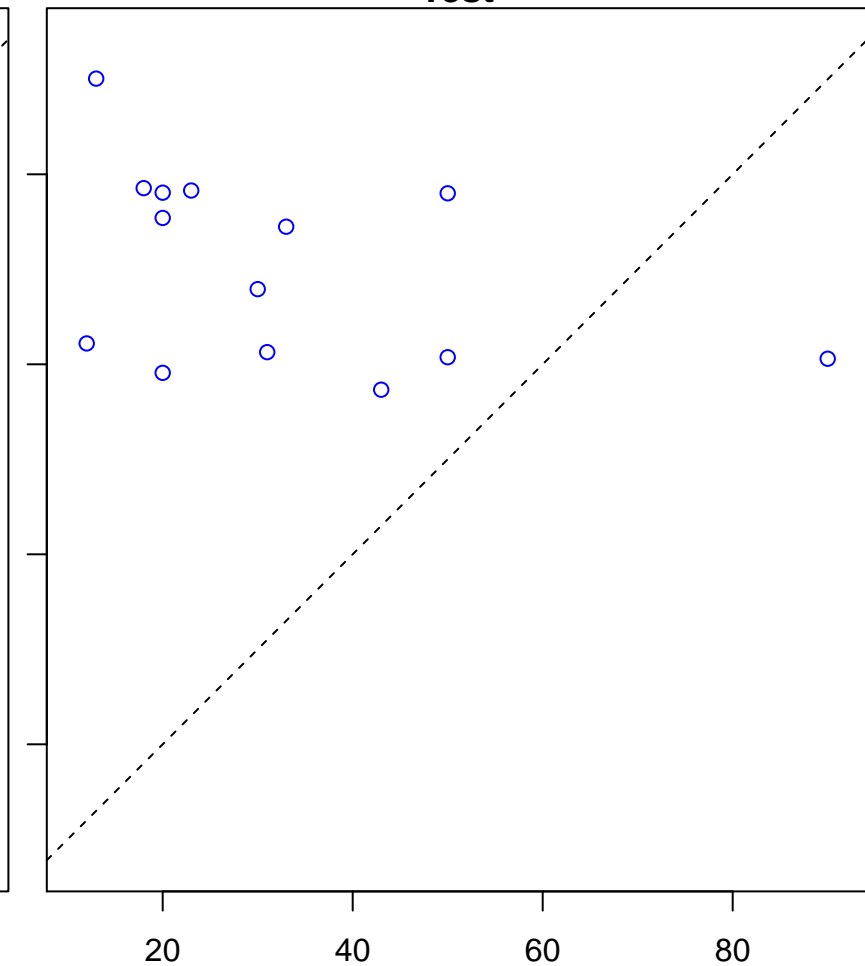


metanephric mesenchyme development (Score: 5.315160)

Control

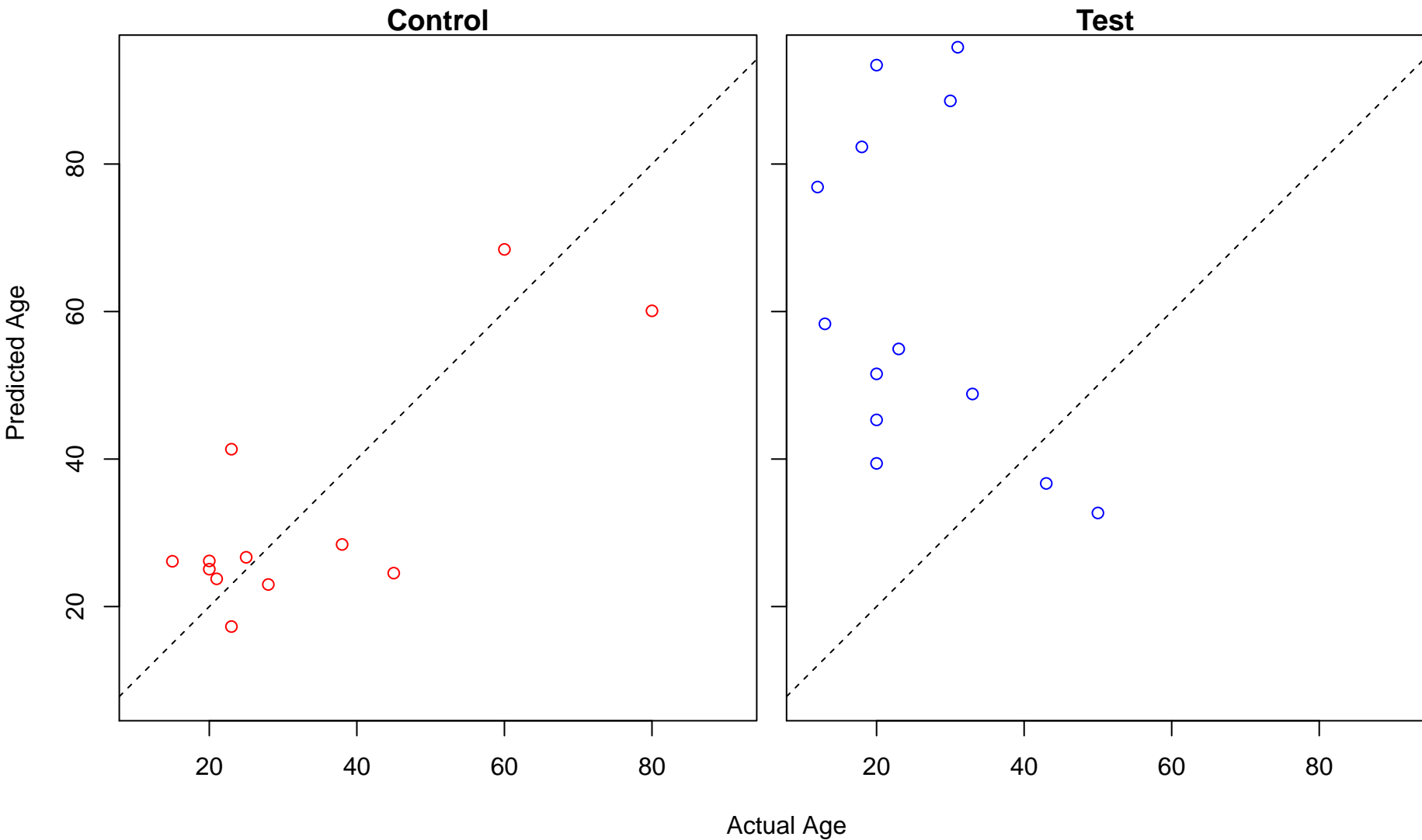


Test



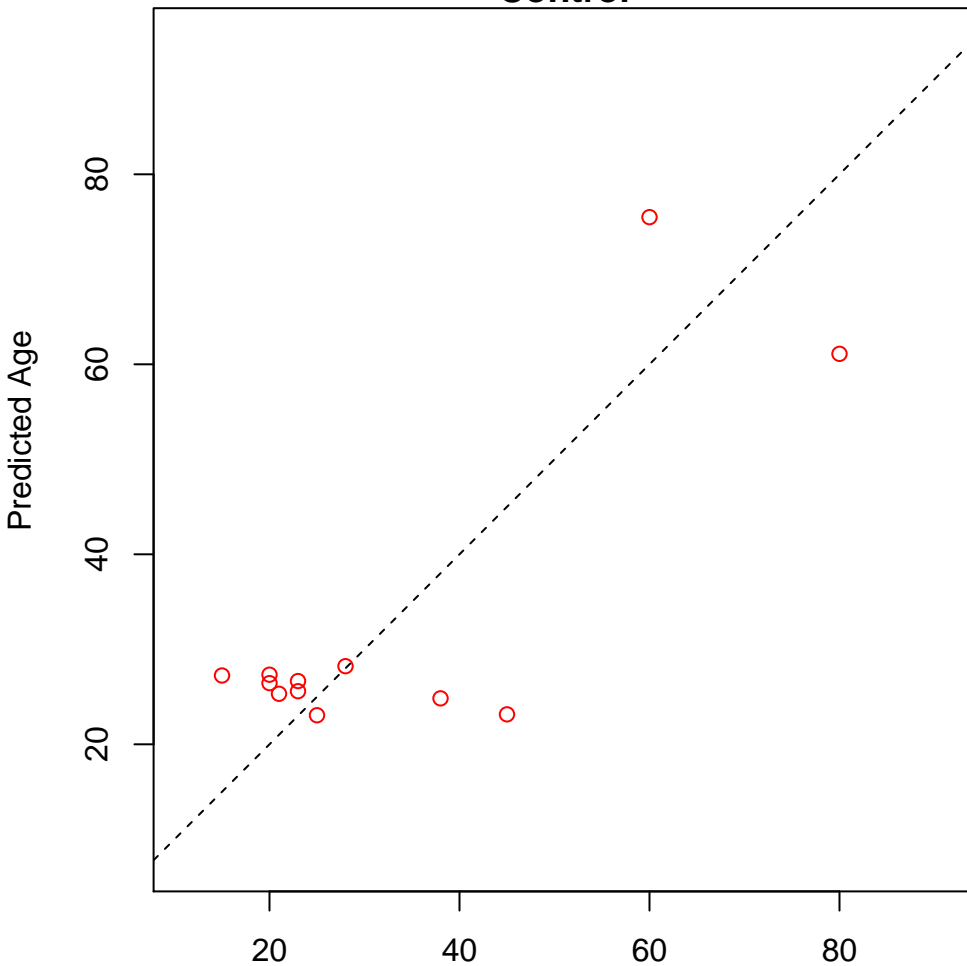
Actual Age

inactivation of MAPK activity (Score: 5.314985)

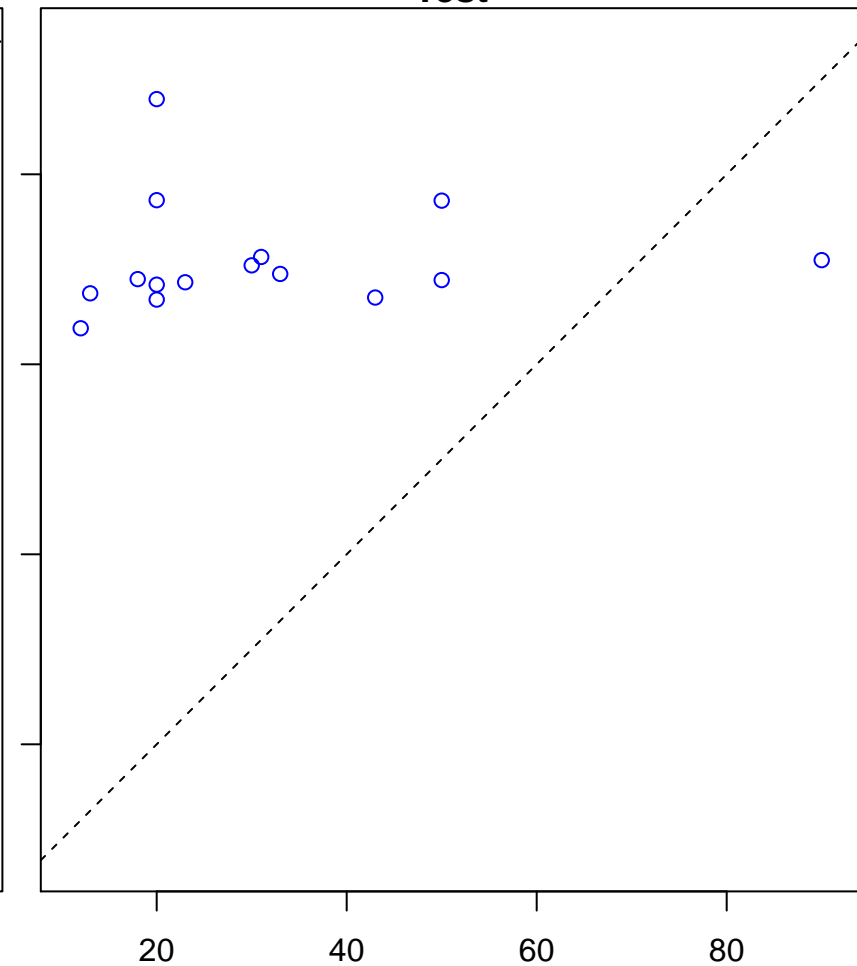


extrinsic apoptotic signaling pathway (Score: 5.314457)

Control

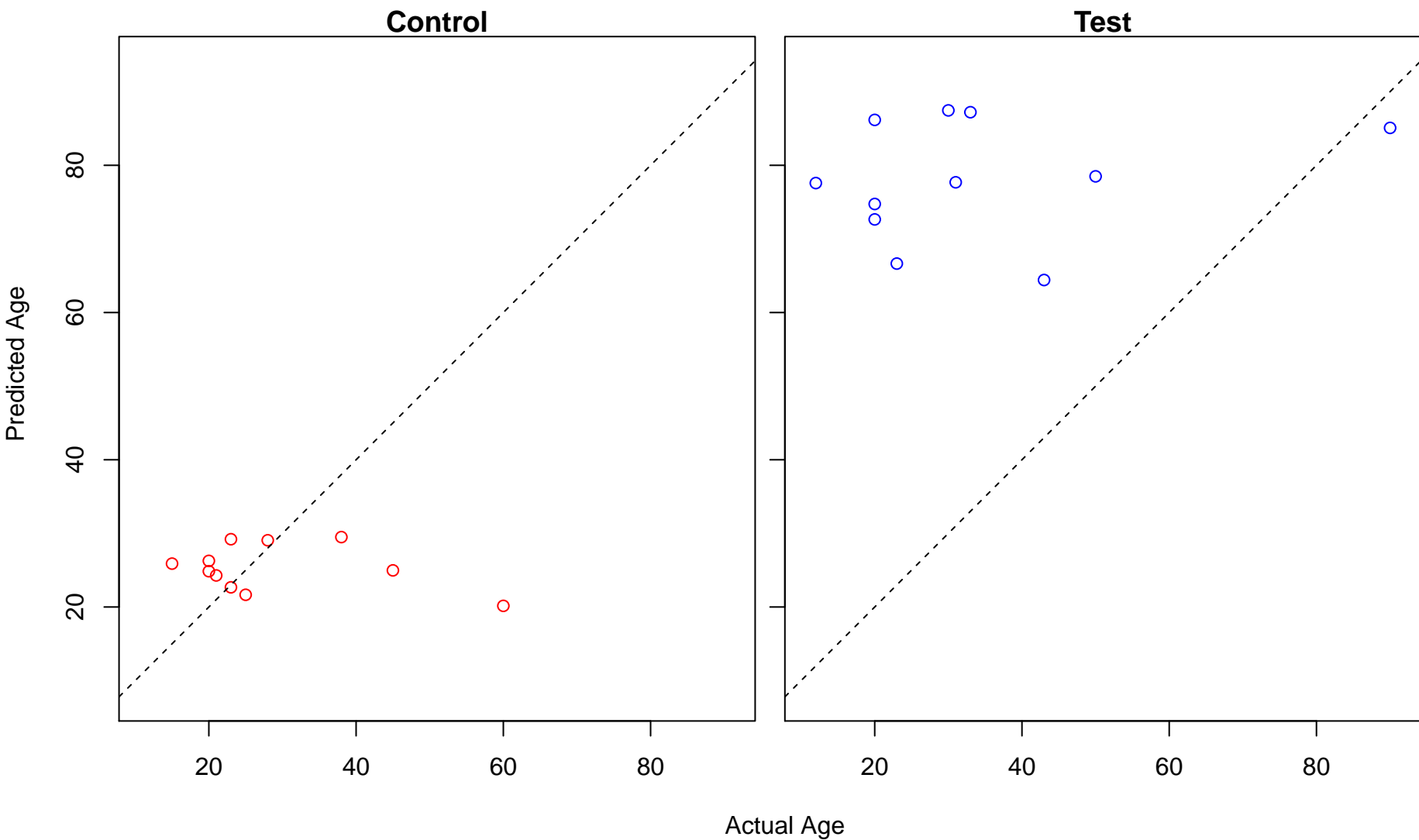


Test

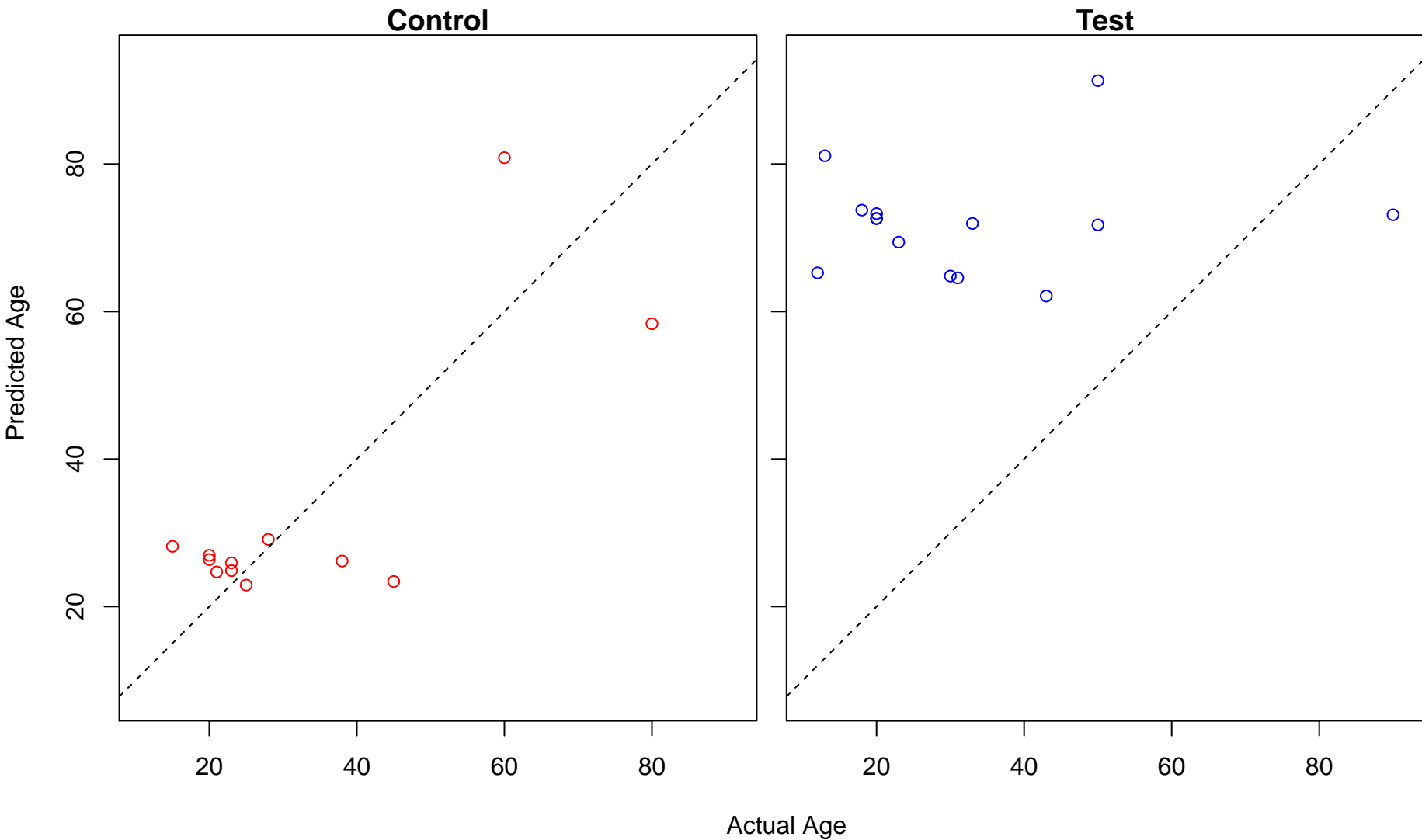


Actual Age

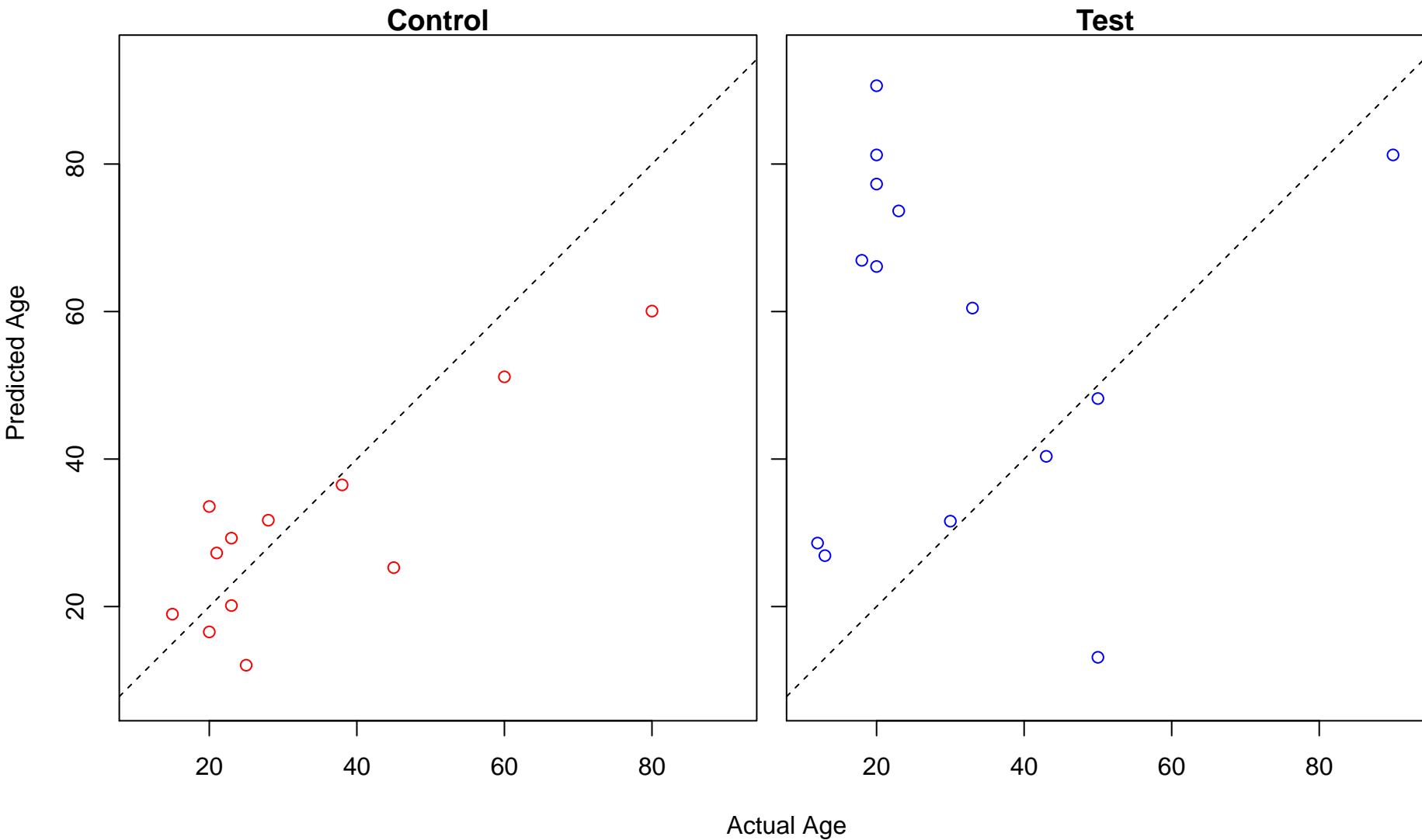
amyloid precursor protein catabolic process (Score: 5.313836)



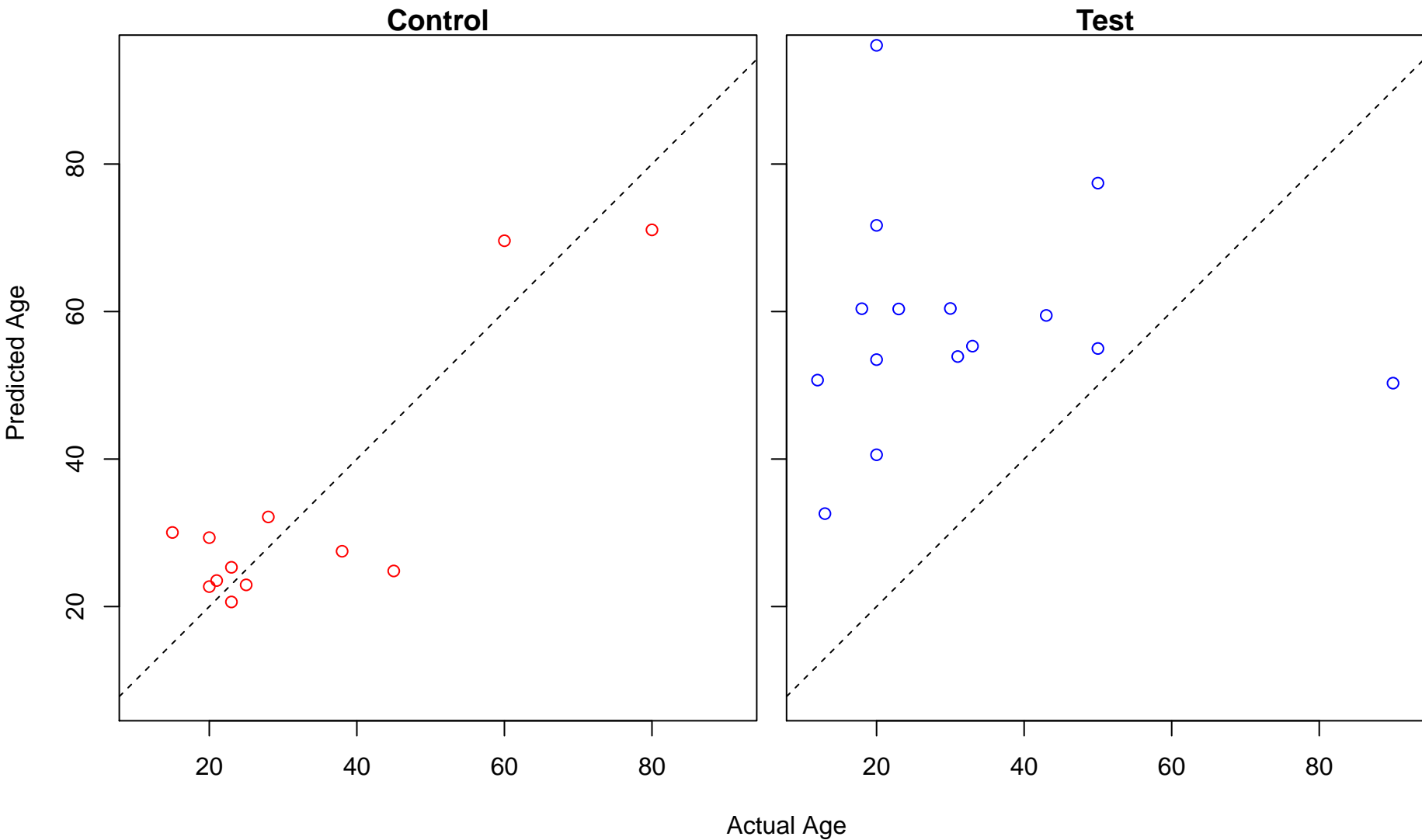
macroautophagy (Score: 5.310905)



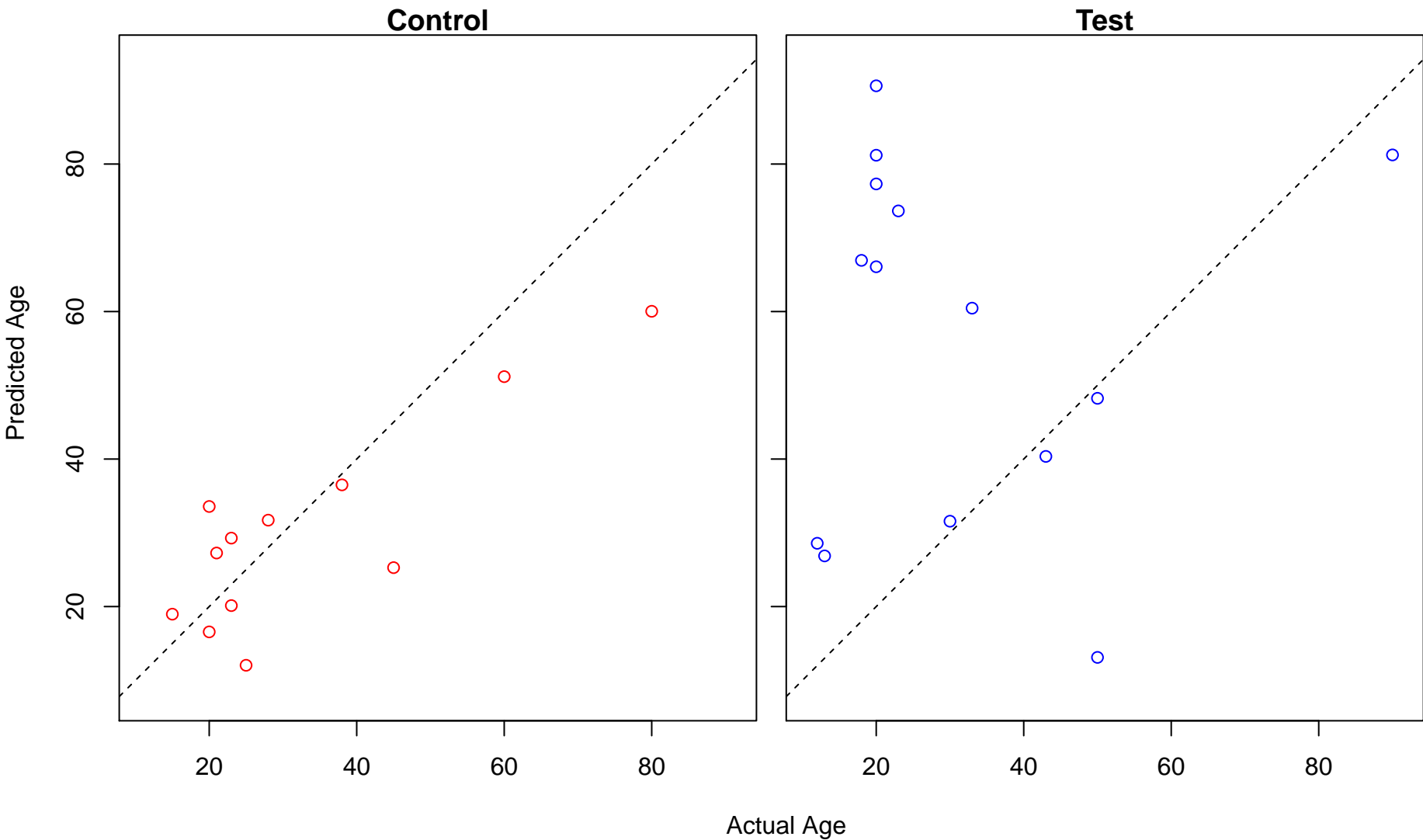
epithelial cilium movement (Score: 5.310849)



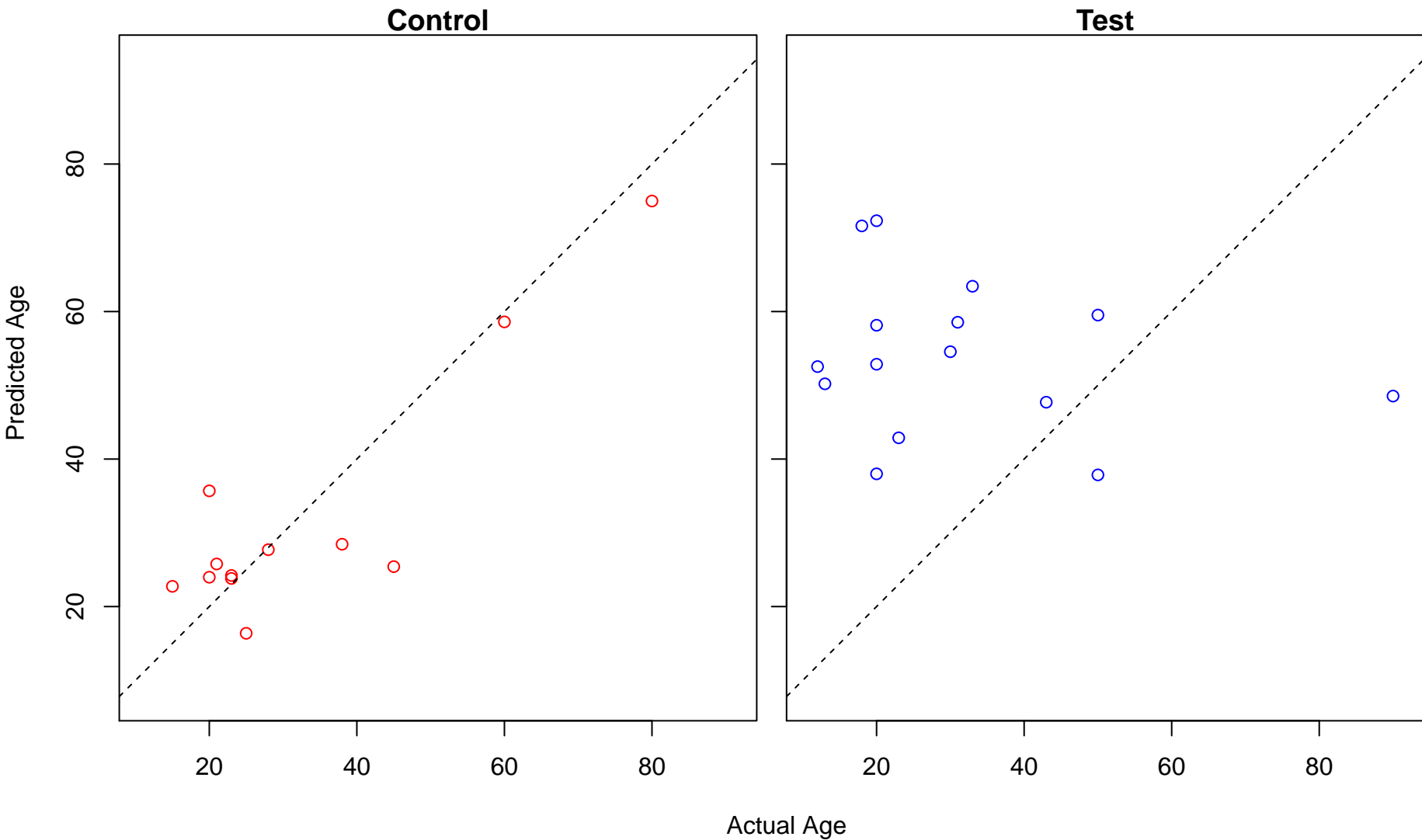
segment specification (Score: 5.306925)



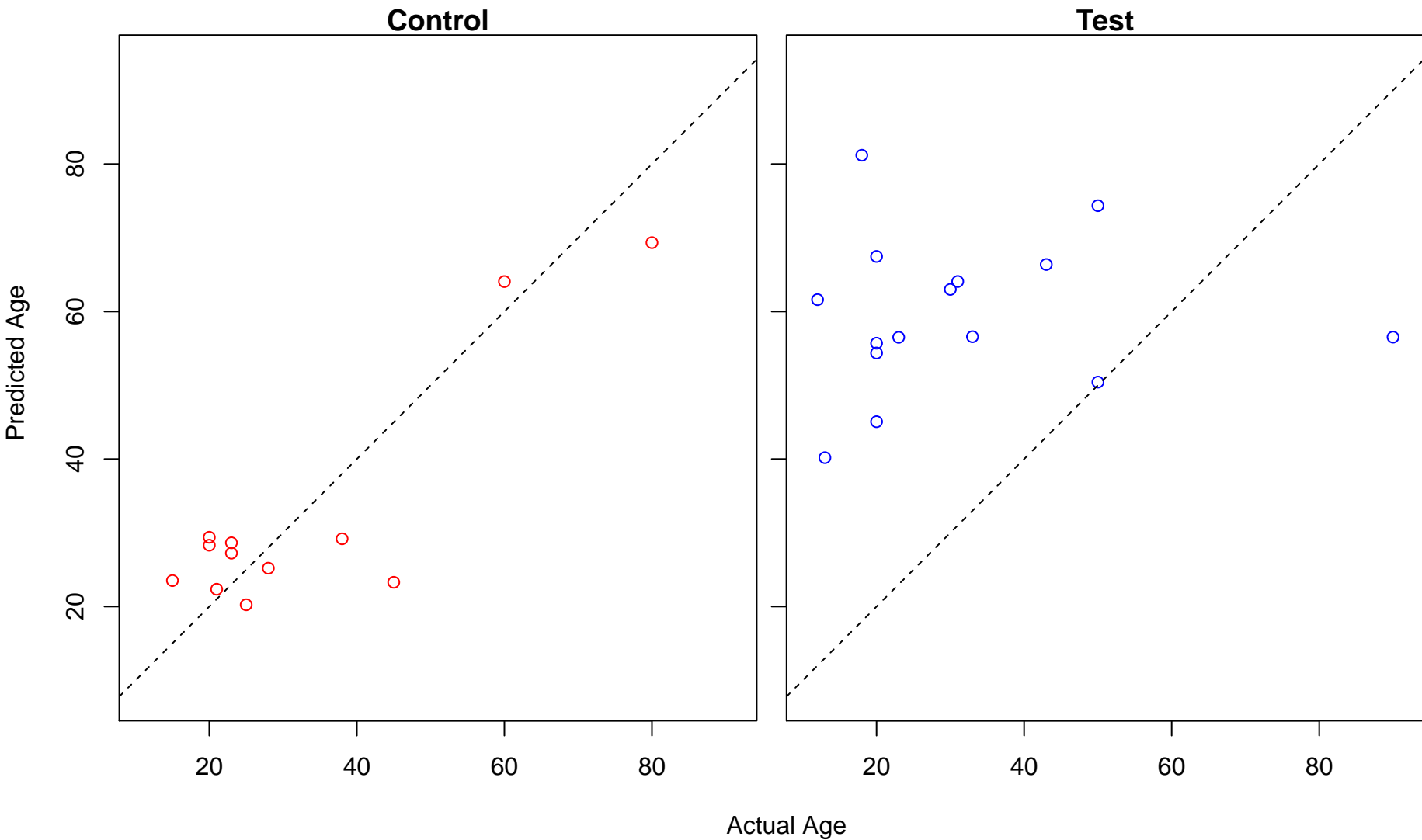
epithelial cilium movement involved in determination of left/right asymmetry (Score: 5.305252)



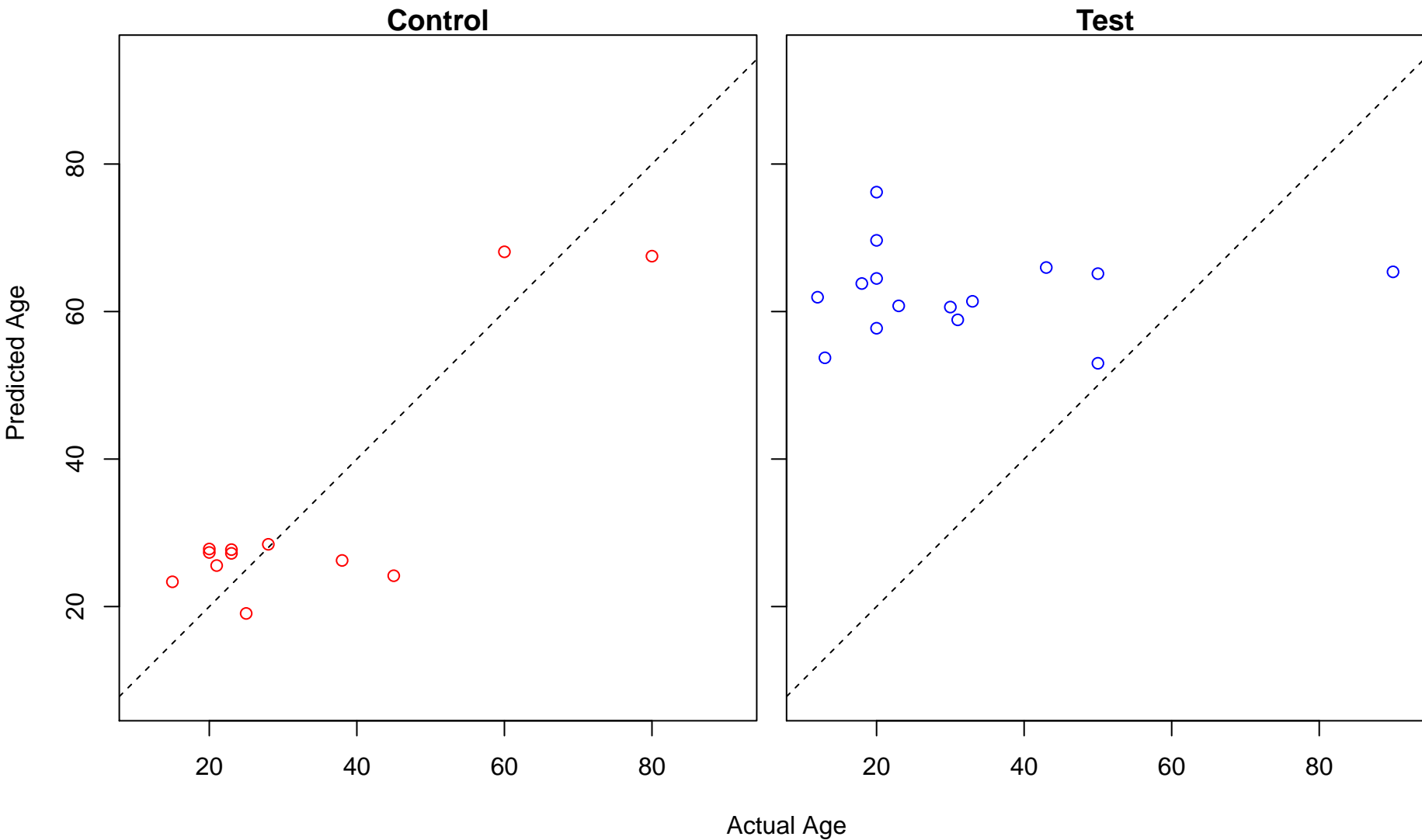
positive regulation of protein sumoylation (Score: 5.304942)



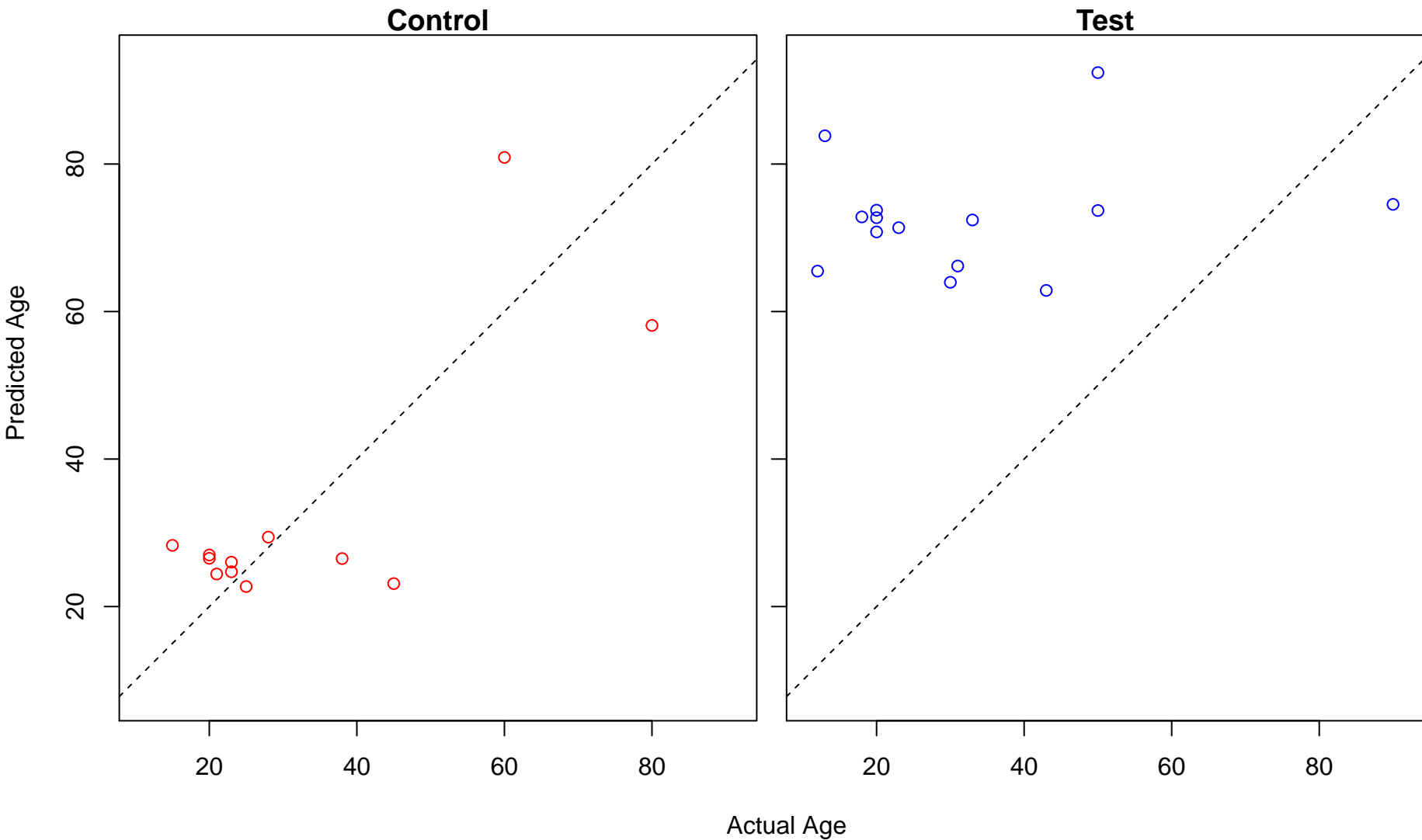
coenzyme transport (Score: 5.304364)



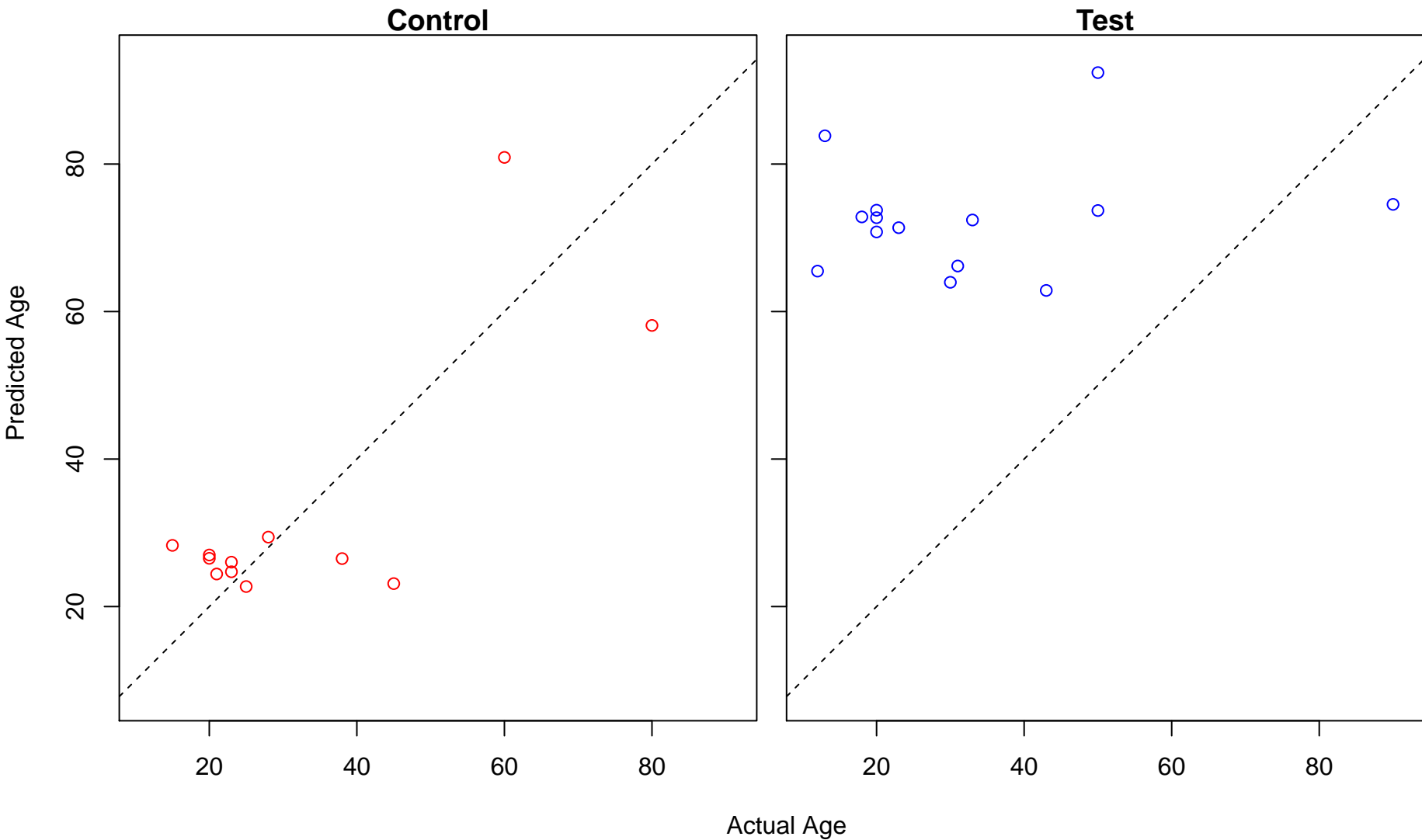
histone H3-K4 methylation (Score: 5.303359)



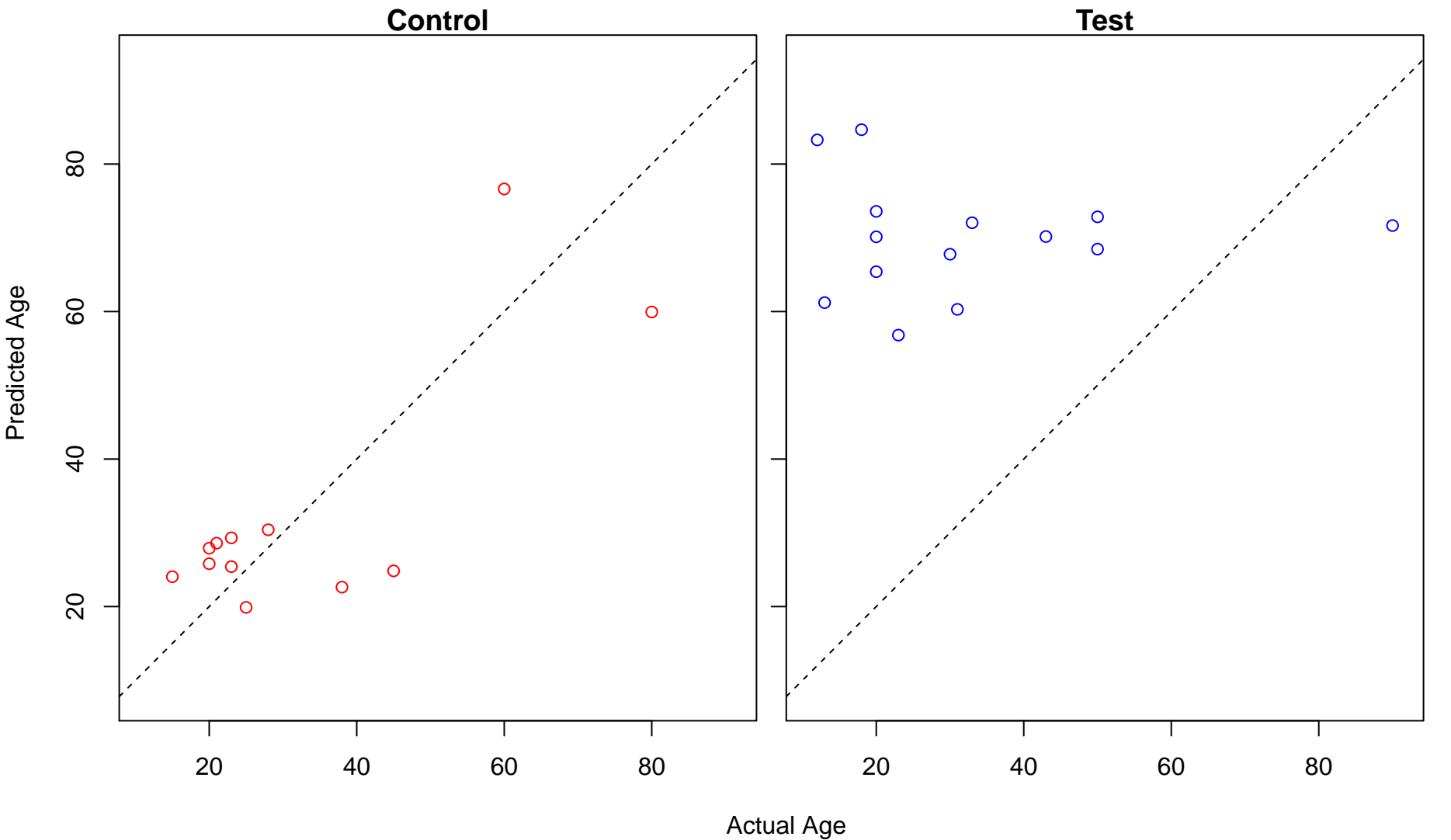
mitophagy (Score: 5.303035)



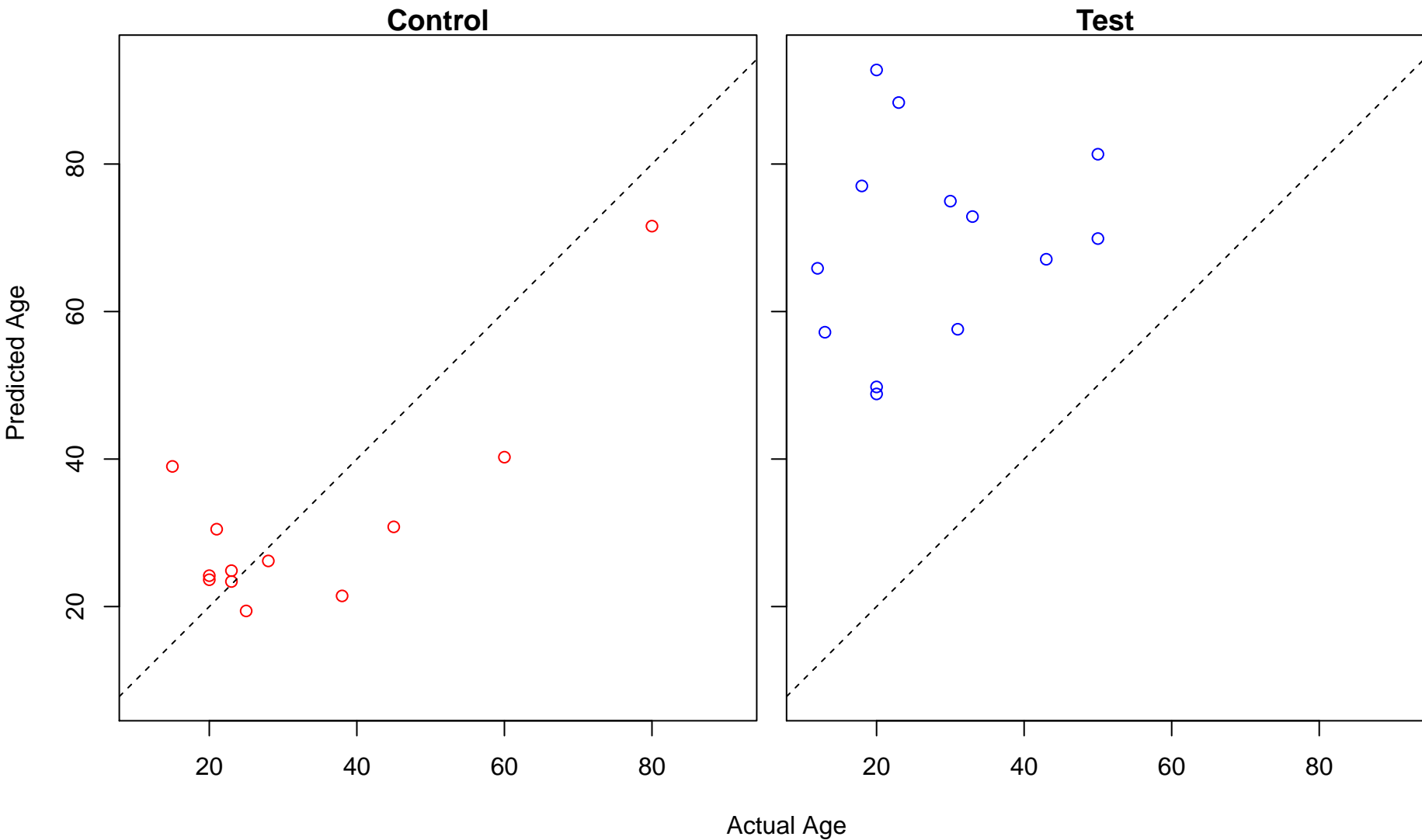
mitochondrion disassembly (Score: 5.303035)



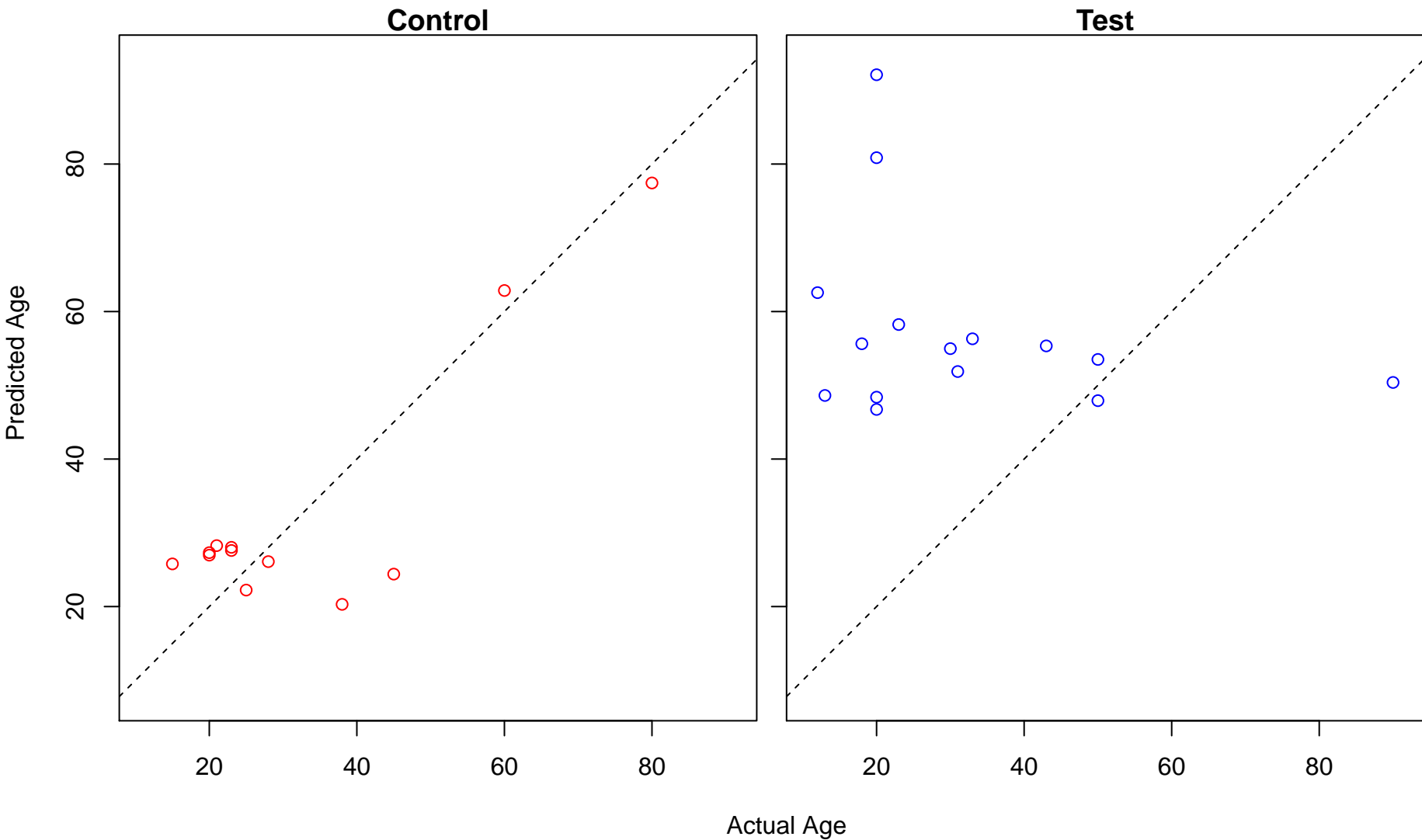
tion of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell



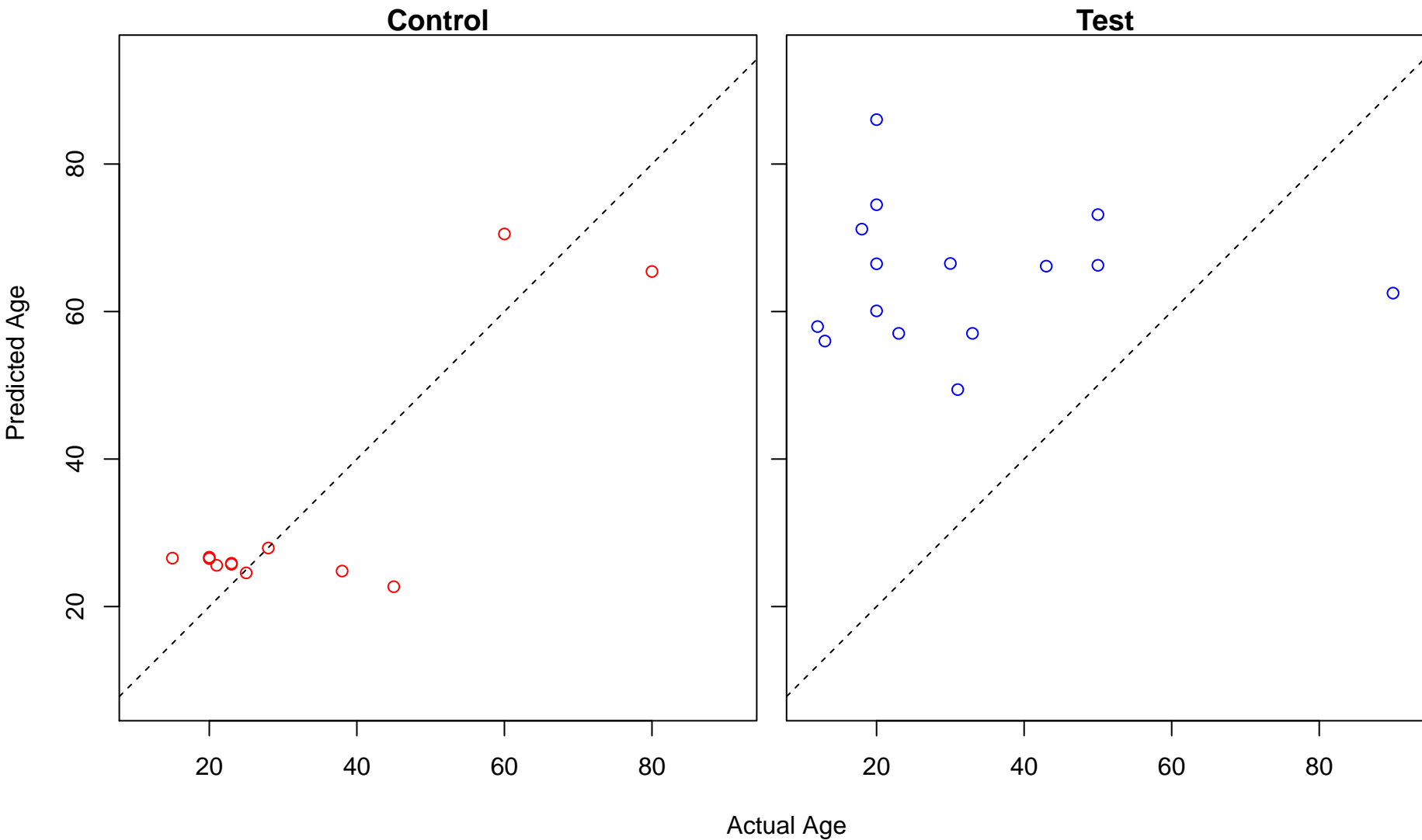
ketone body biosynthetic process (Score: 5.302965)



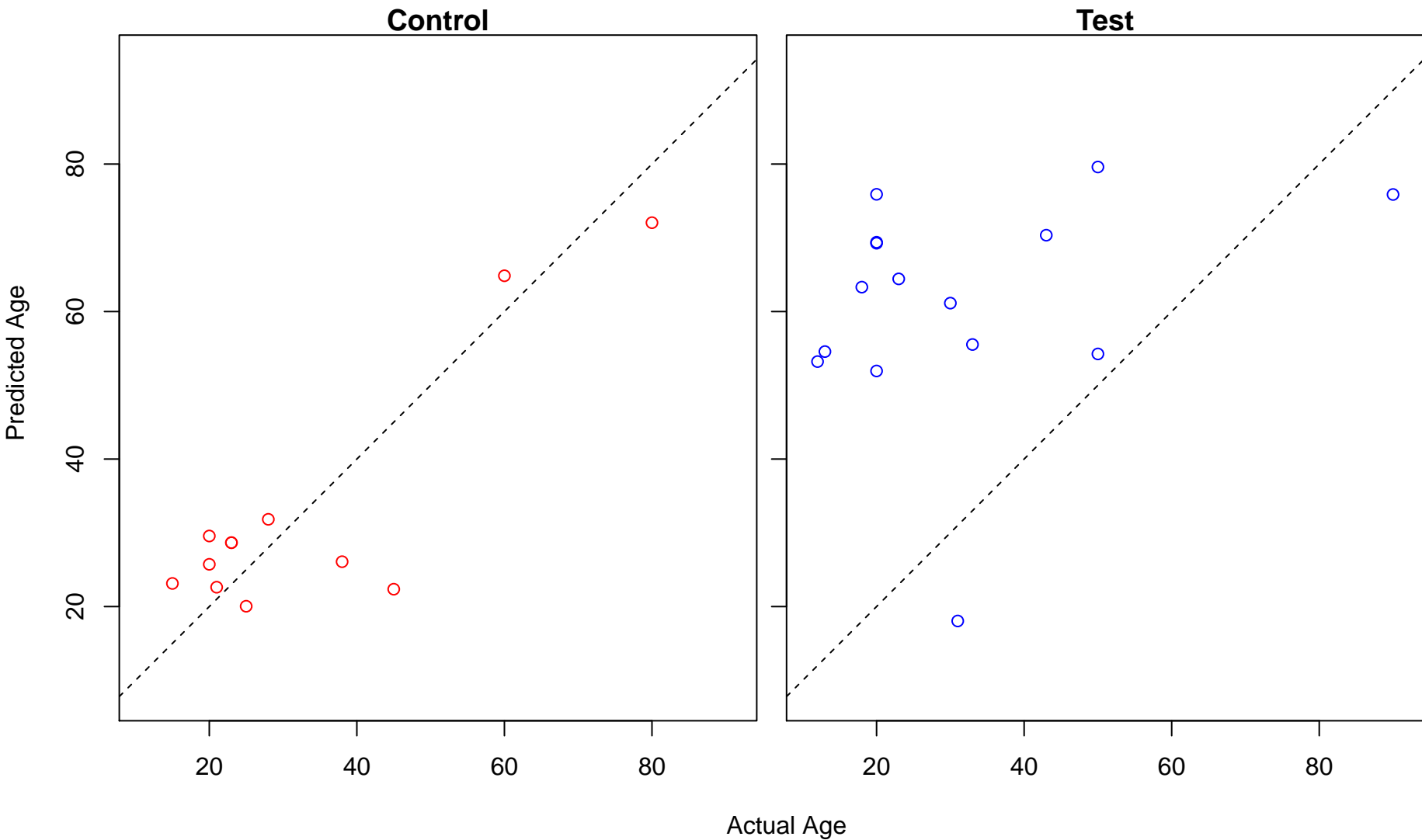
telomere maintenance via telomere lengthening (Score: 5.300605)



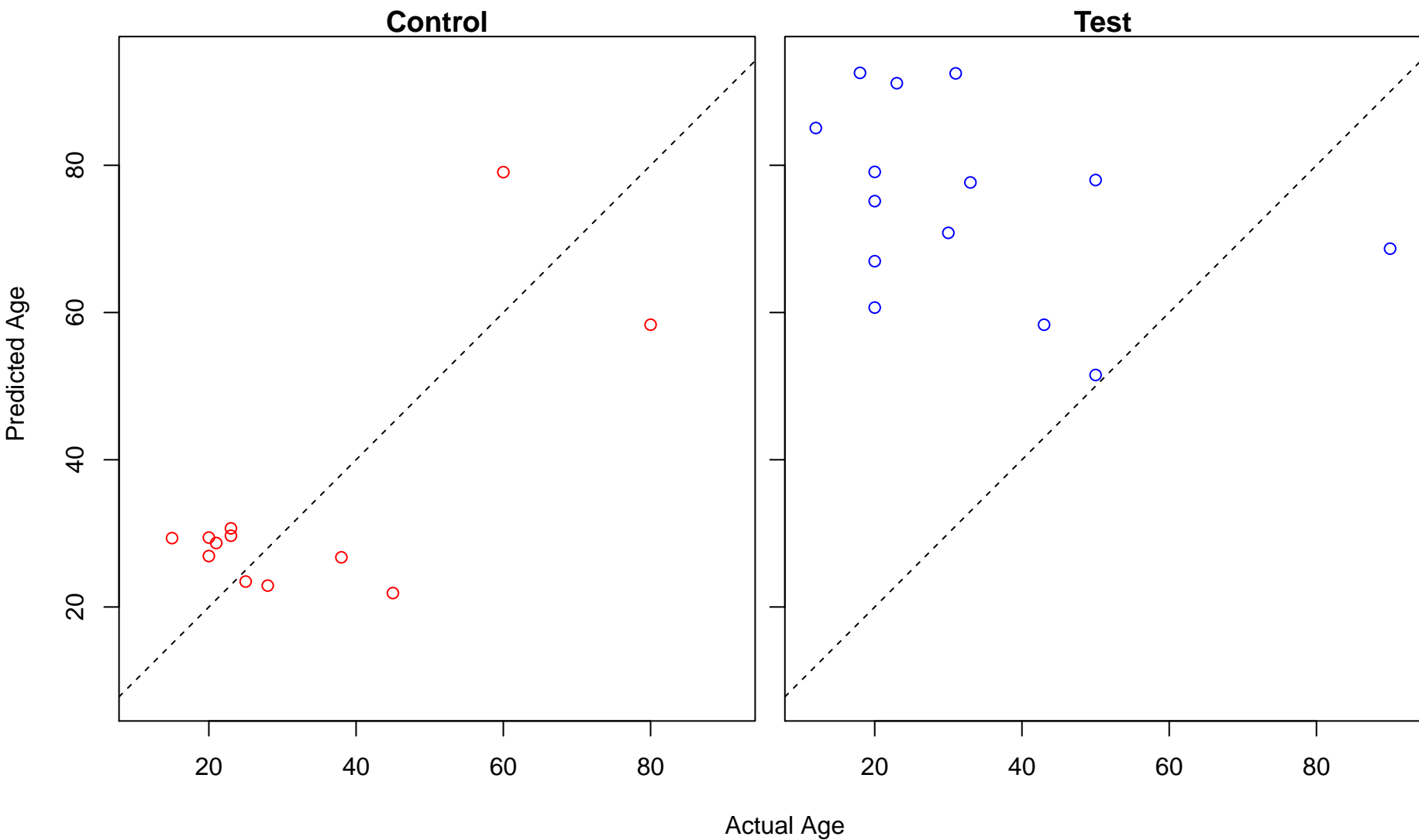
cardiolipin acyl-chain remodeling (Score: 5.298039)



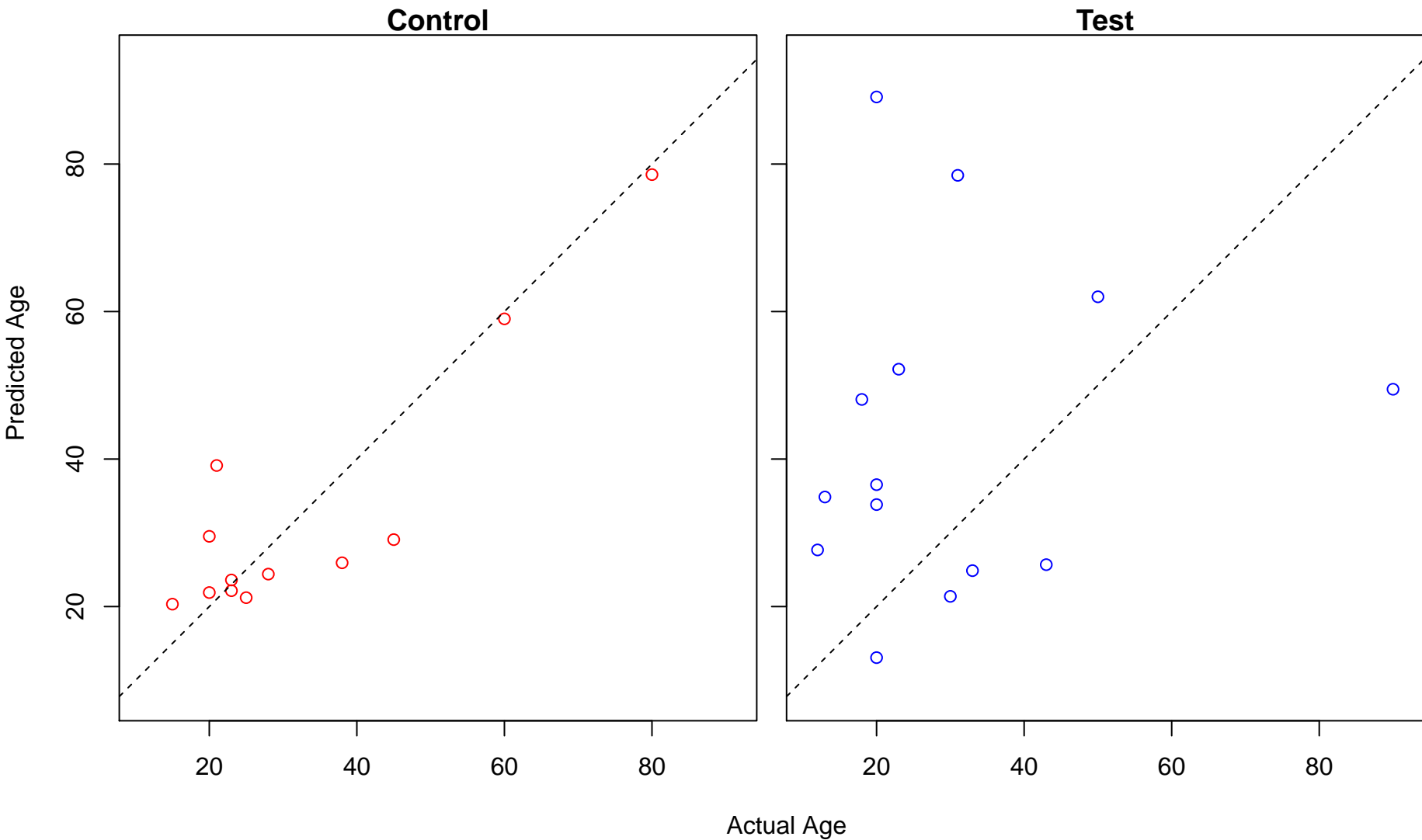
positive regulation of response to wounding (Score: 5.295392)



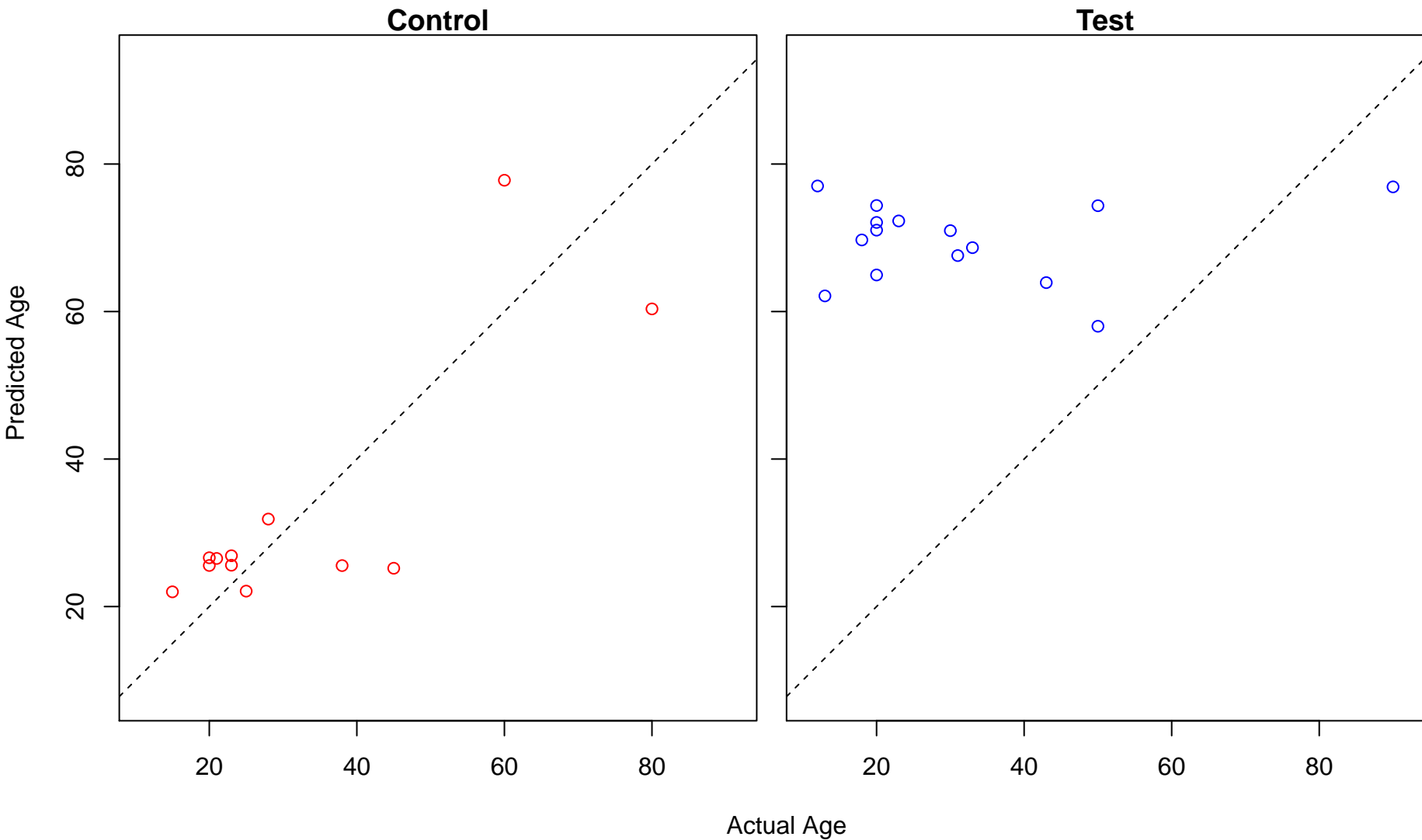
positive regulation of p38MAPK cascade (Score: 5.294712)



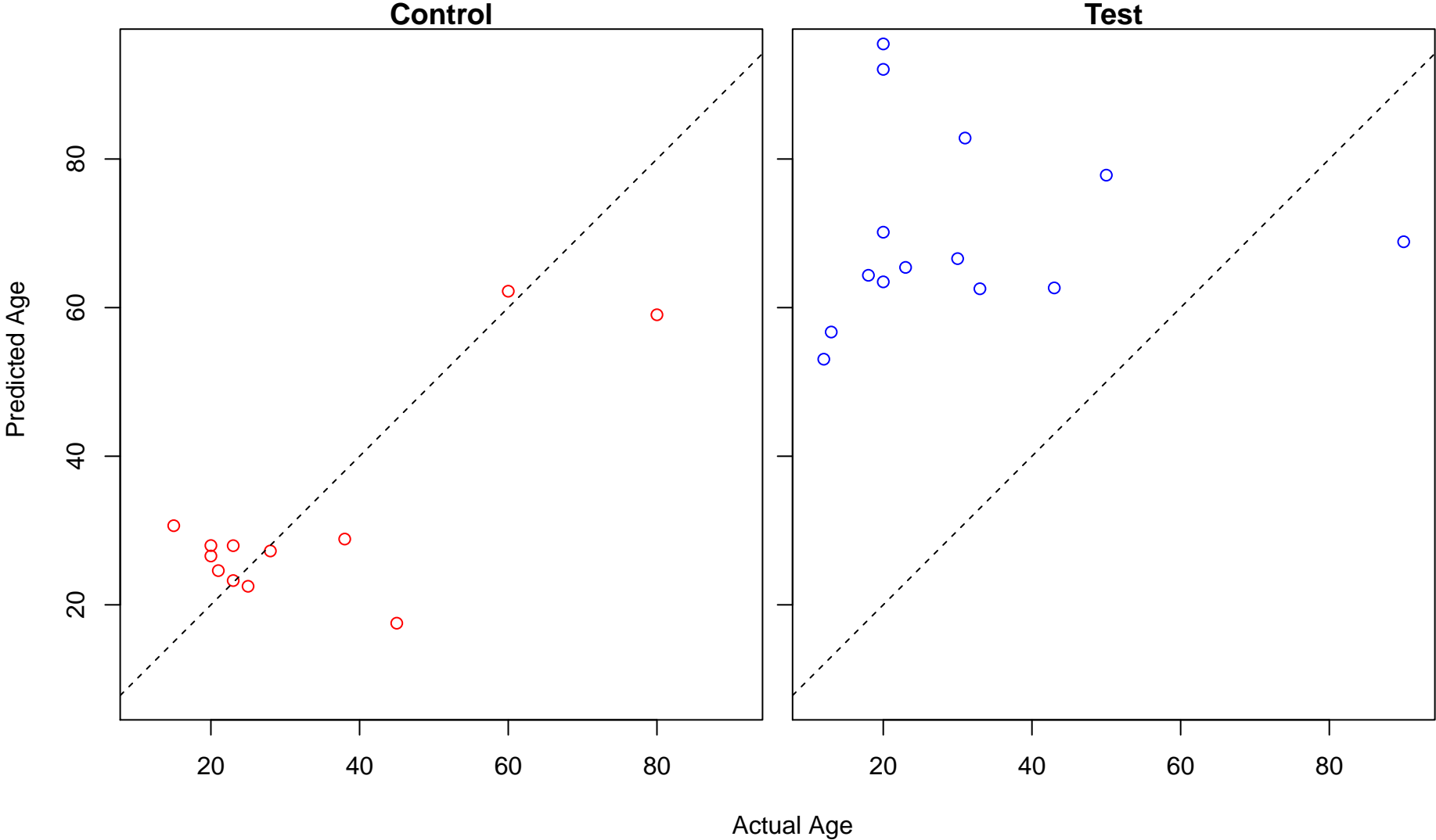
regulation of epithelial cell differentiation (Score: 5.294131)



positive regulation of cellular senescence (Score: 5.287923)

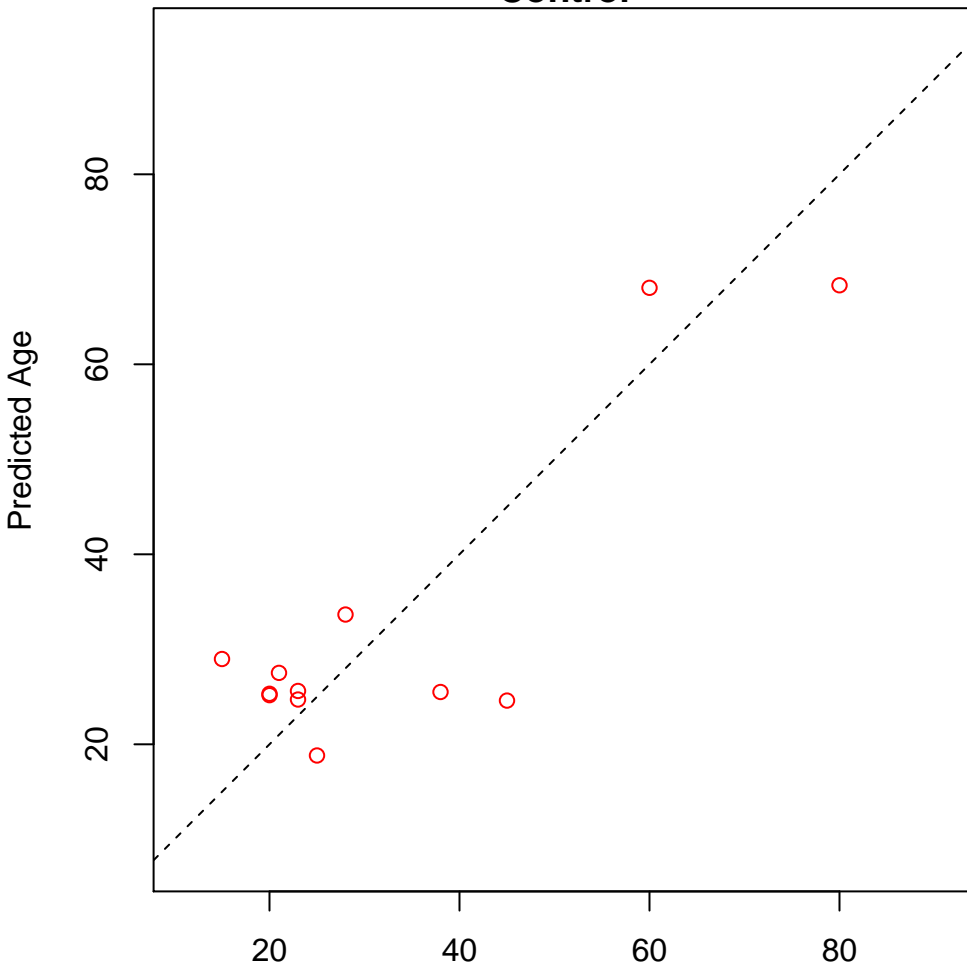


regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter (Score: 5.2)

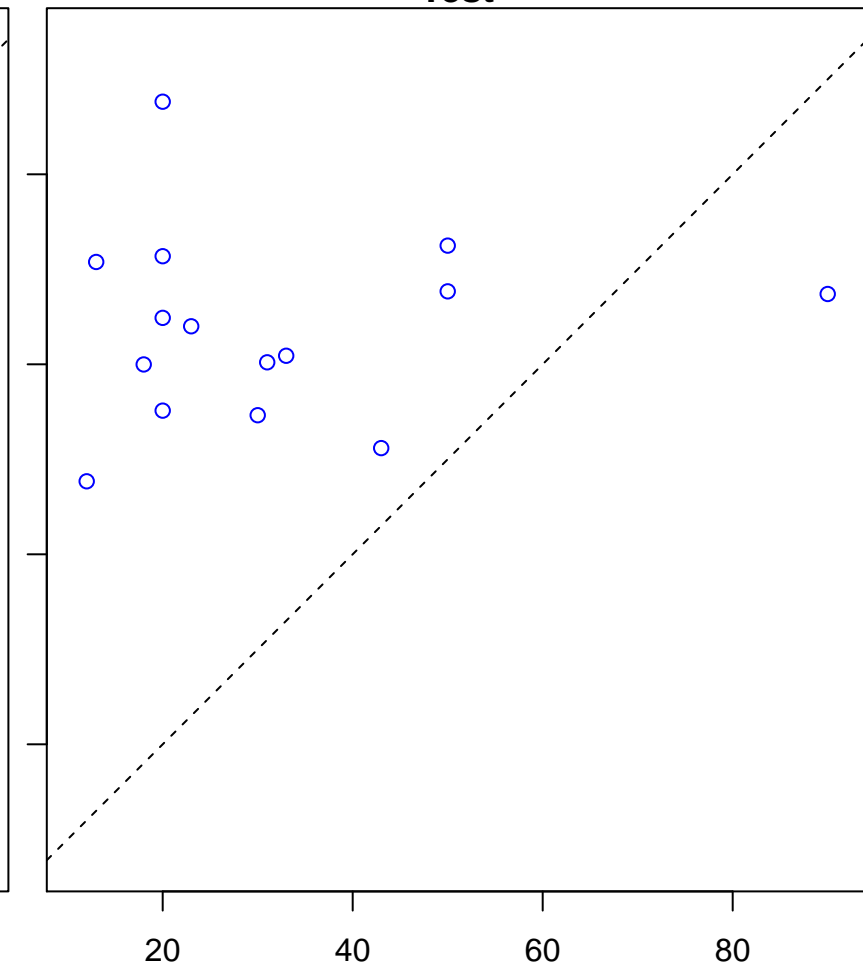


cellular response to light stimulus (Score: 5.284626)

Control

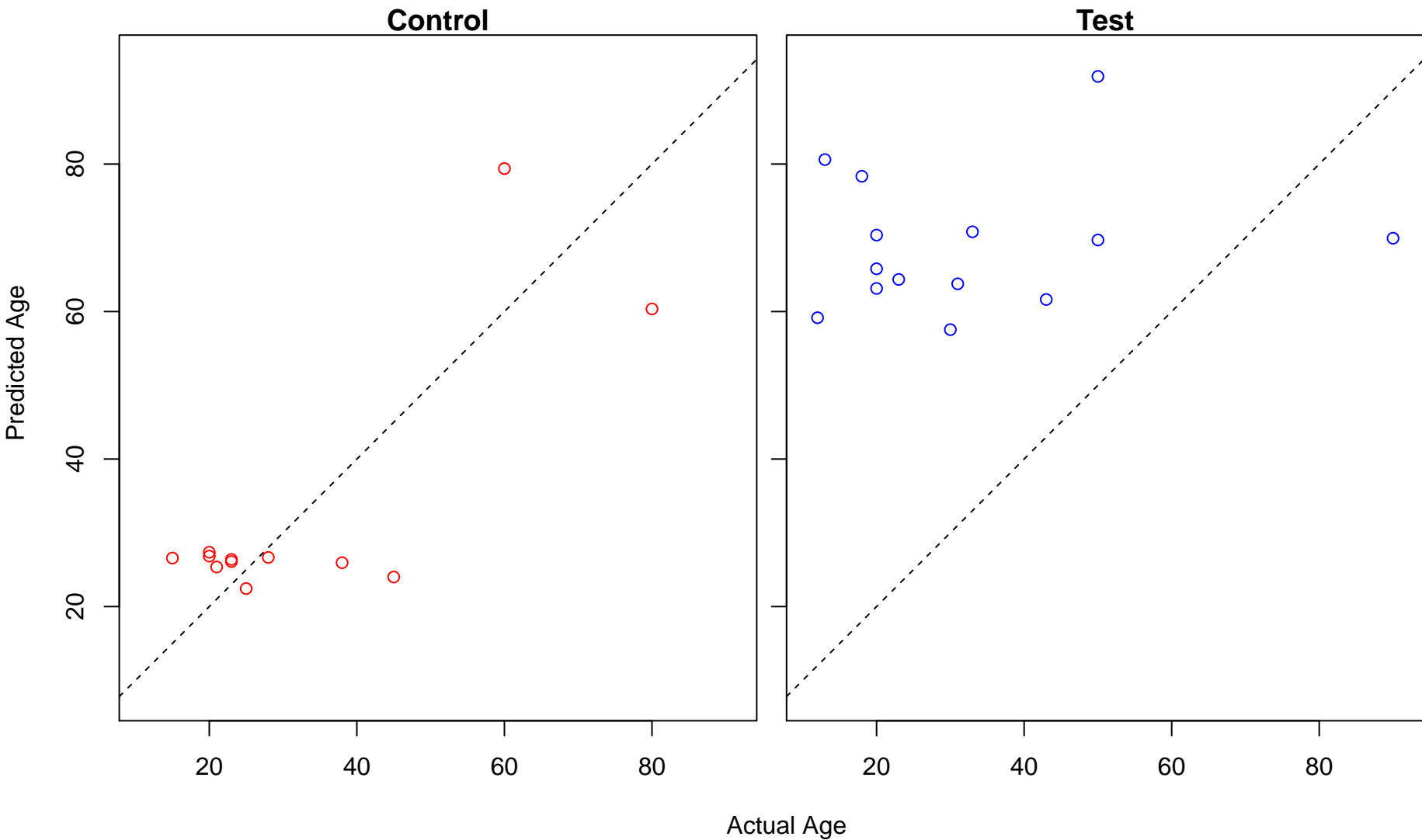


Test

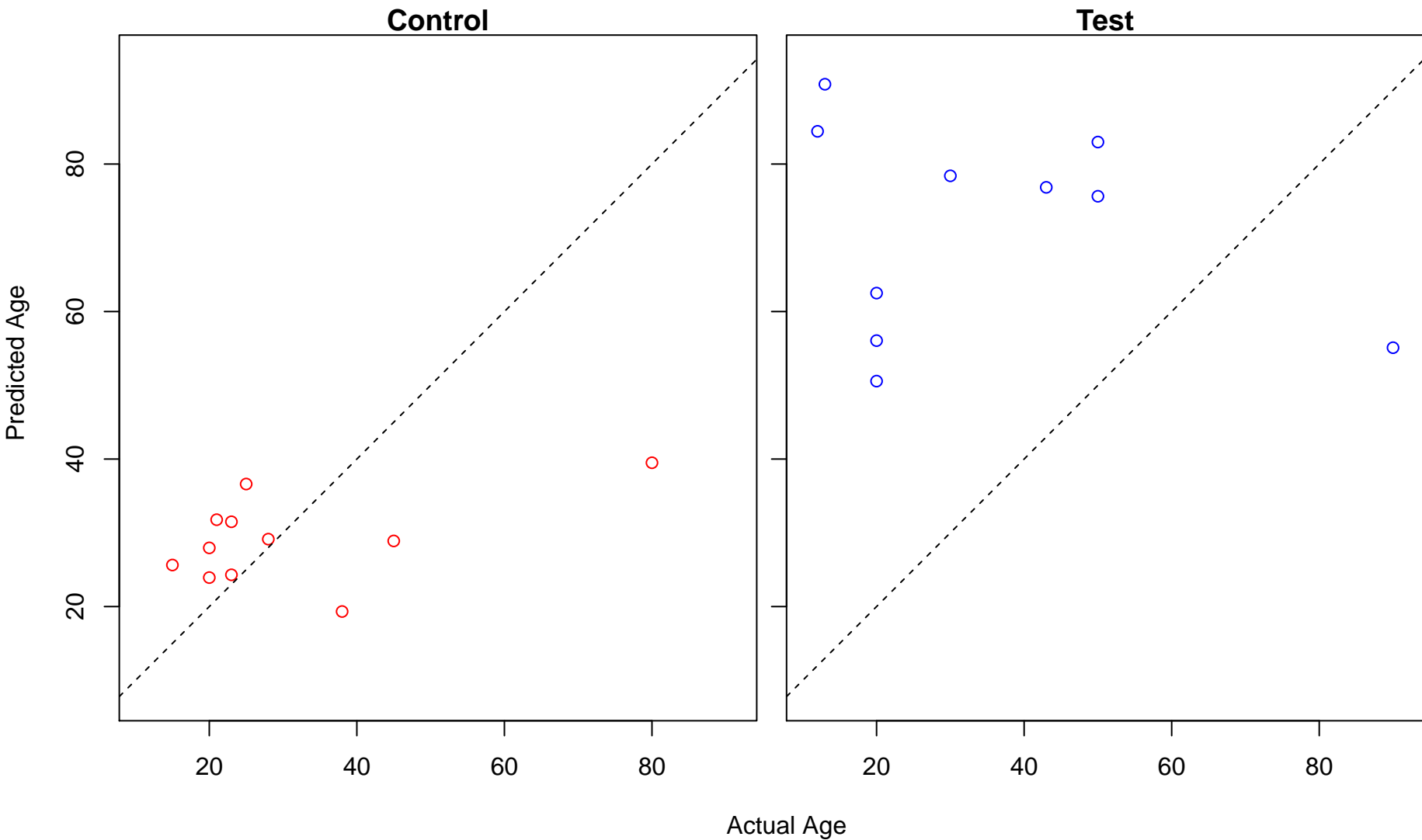


Actual Age

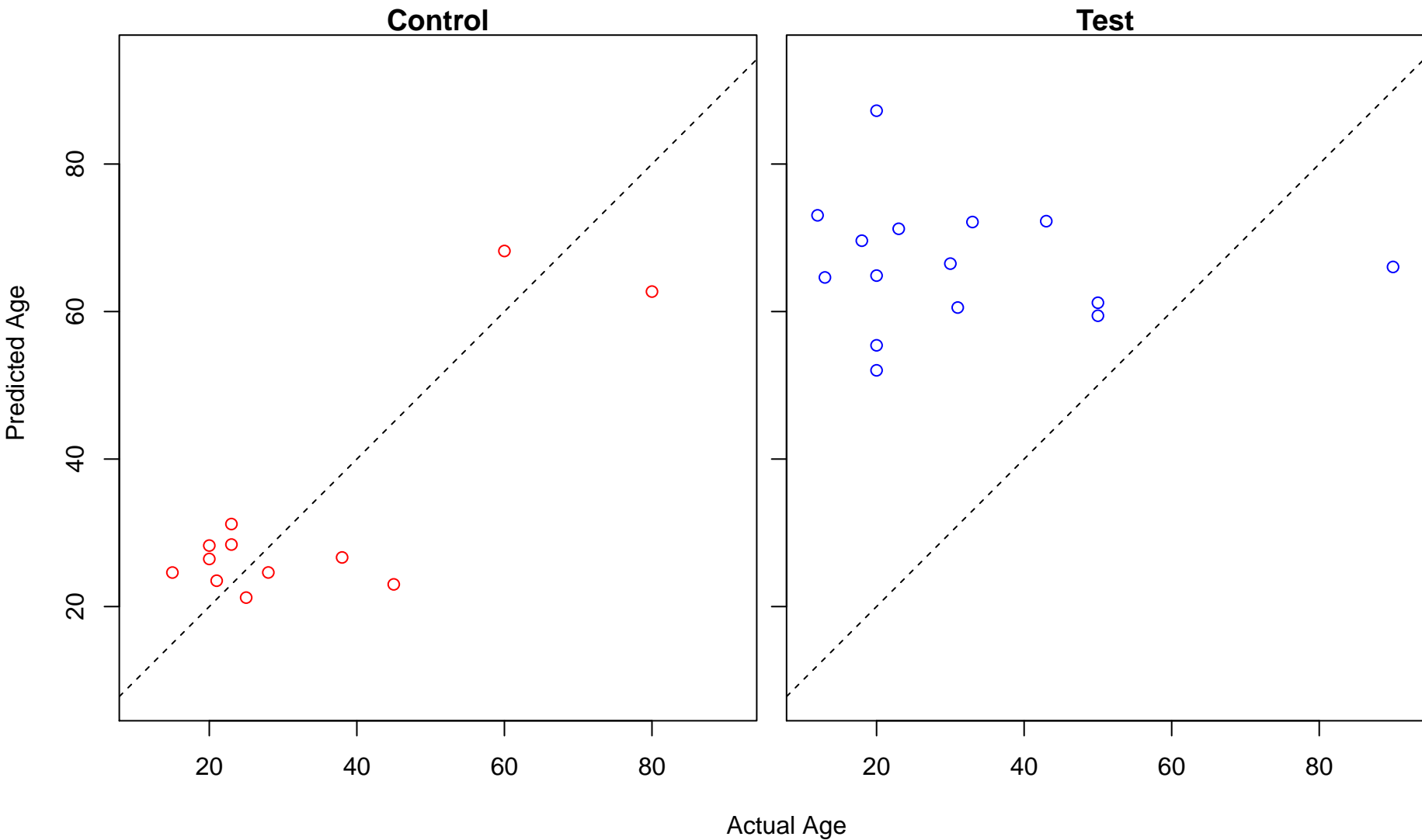
positive regulation of MAP kinase activity (Score: 5.282462)



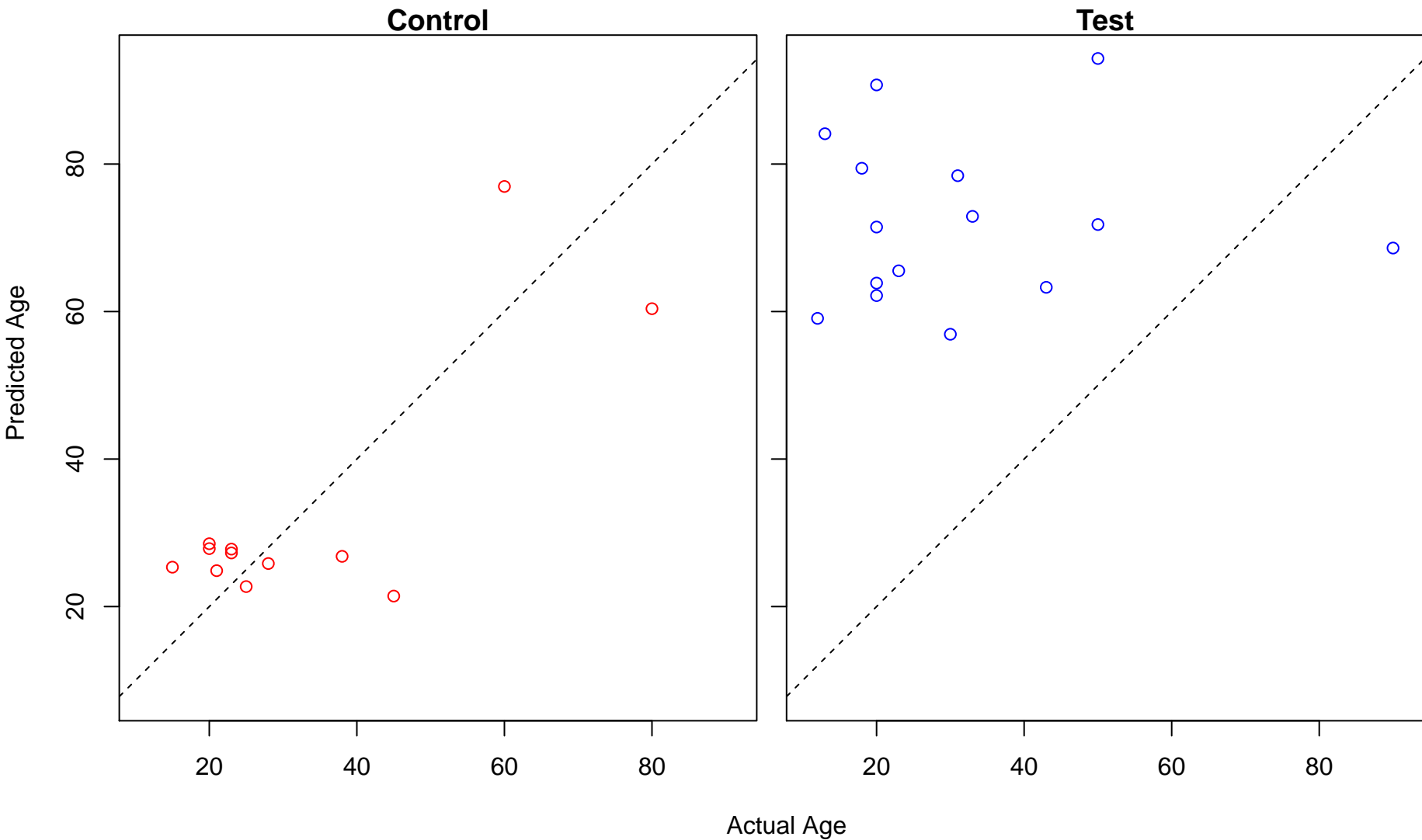
fibrinolysis (Score: 5.280559)



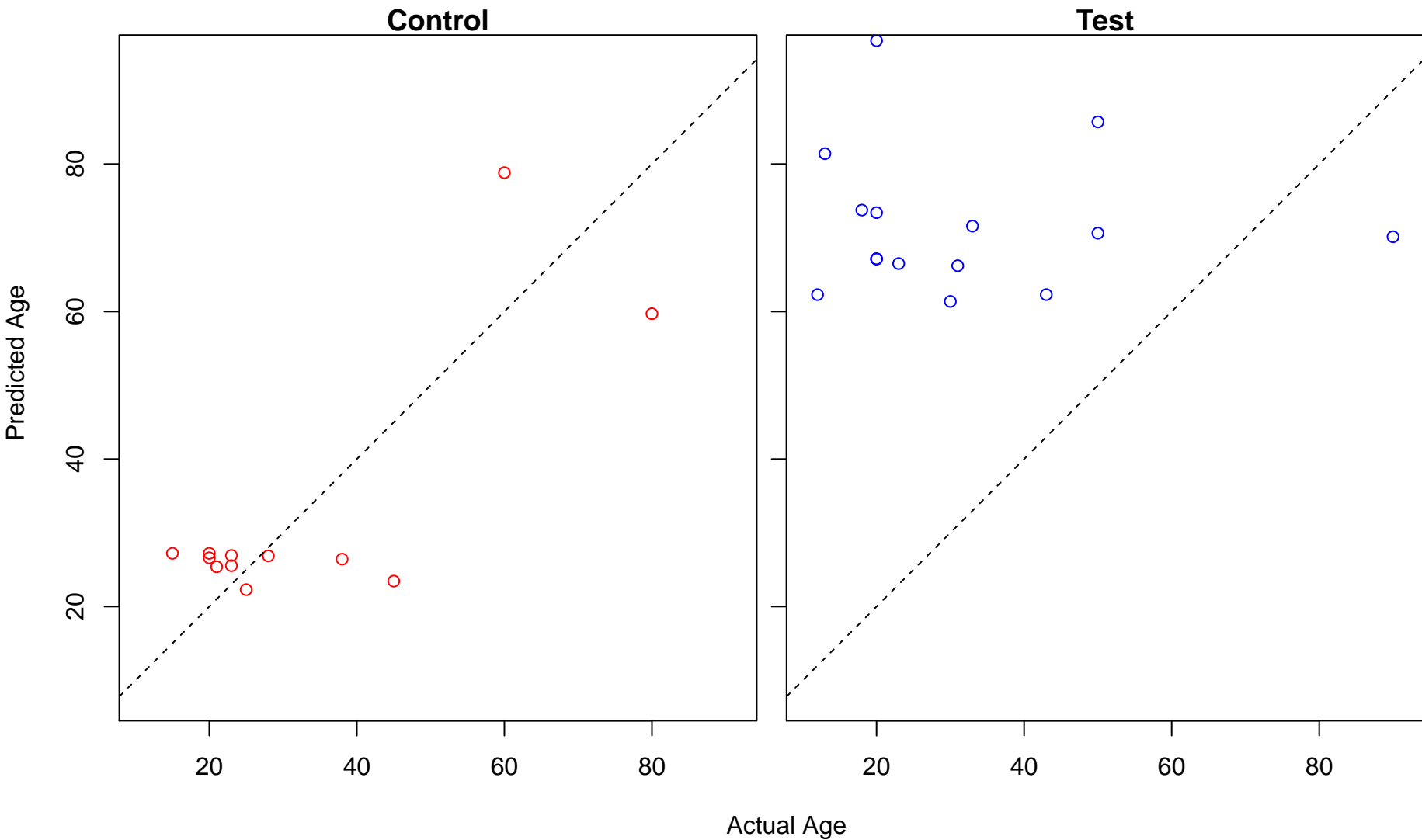
positive regulation of stem cell proliferation (Score: 5.279273)



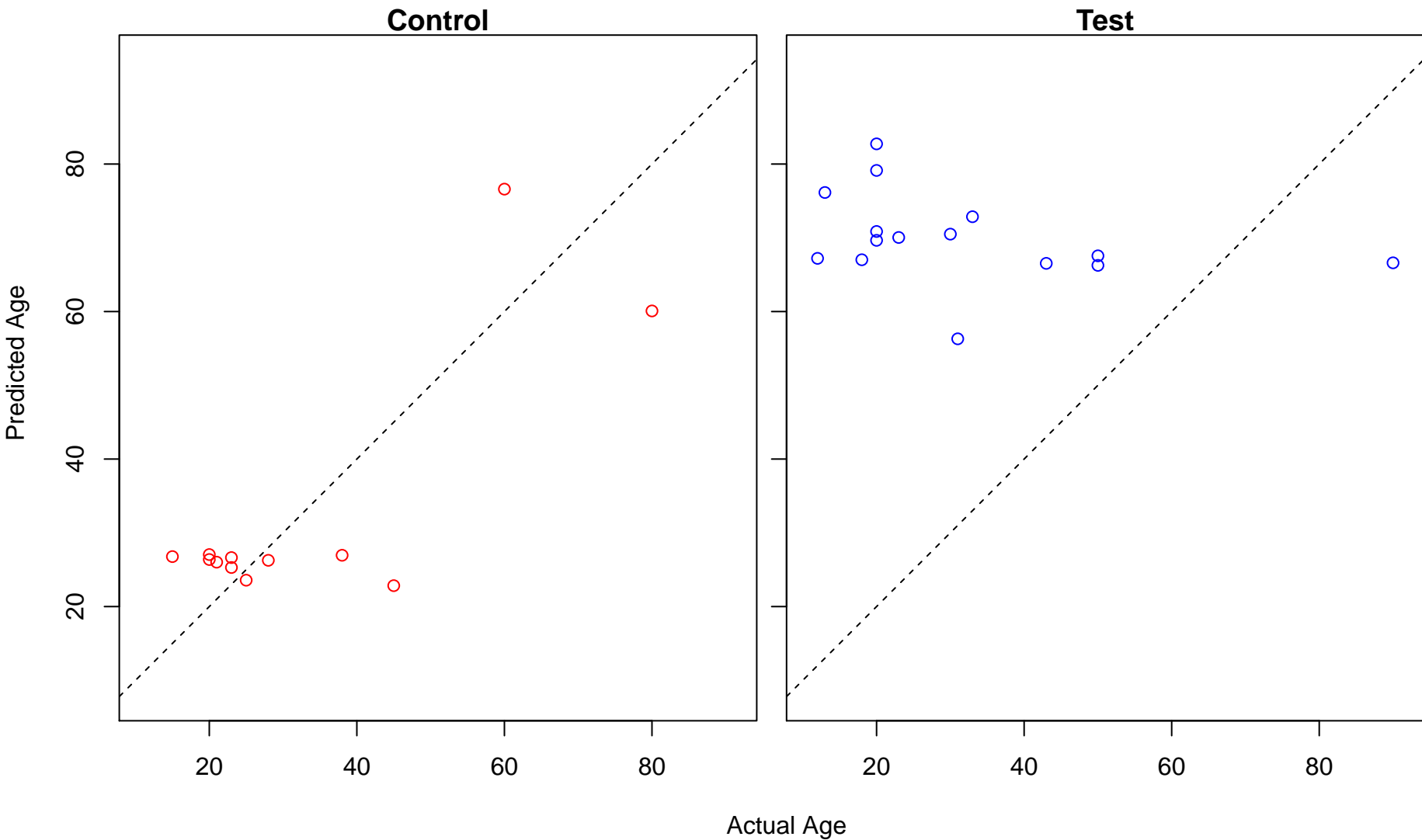
regulation of receptor-mediated endocytosis (Score: 5.274562)



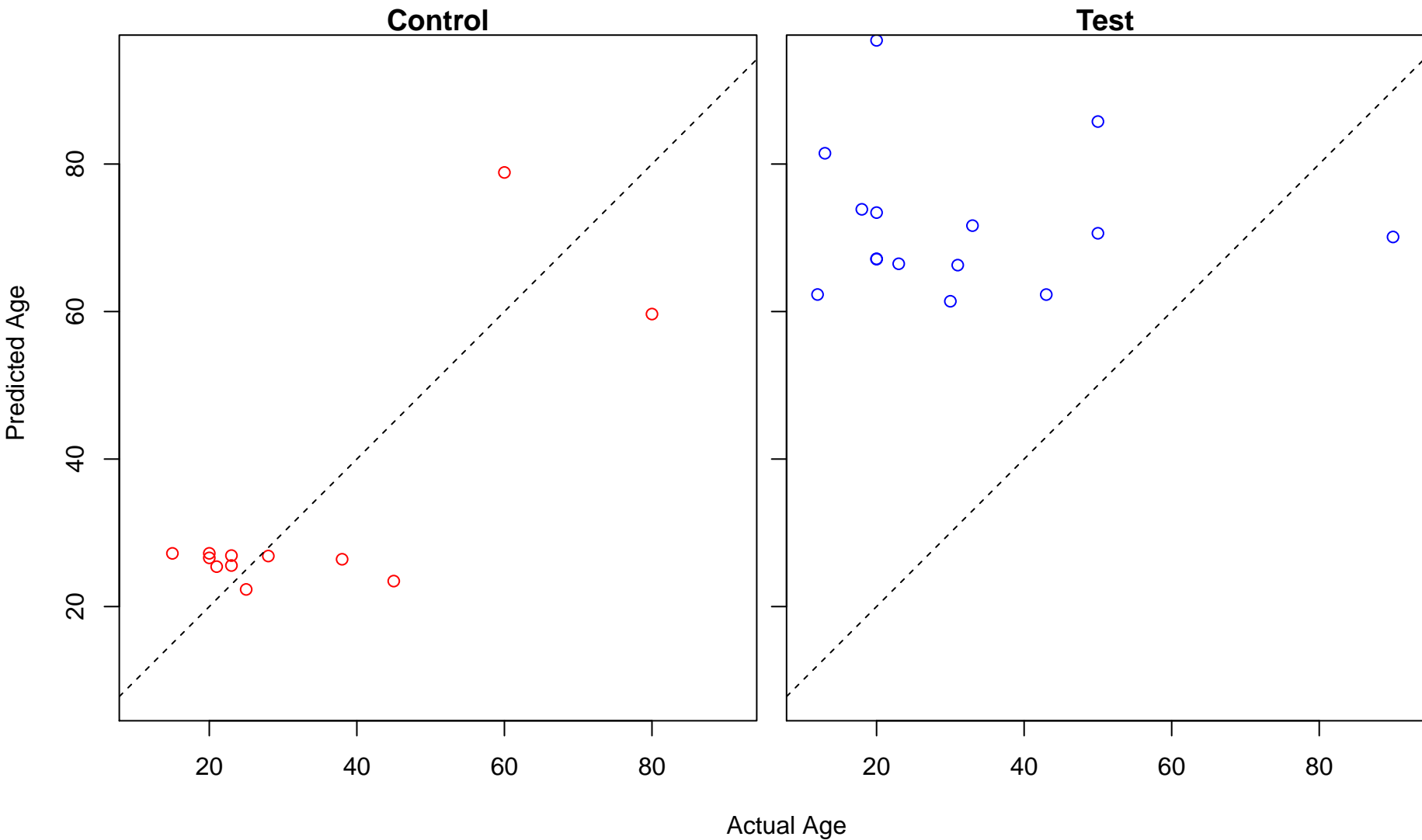
fibroblast growth factor receptor signaling pathway (Score: 5.273773)



hormone-mediated signaling pathway (Score: 5.272304)

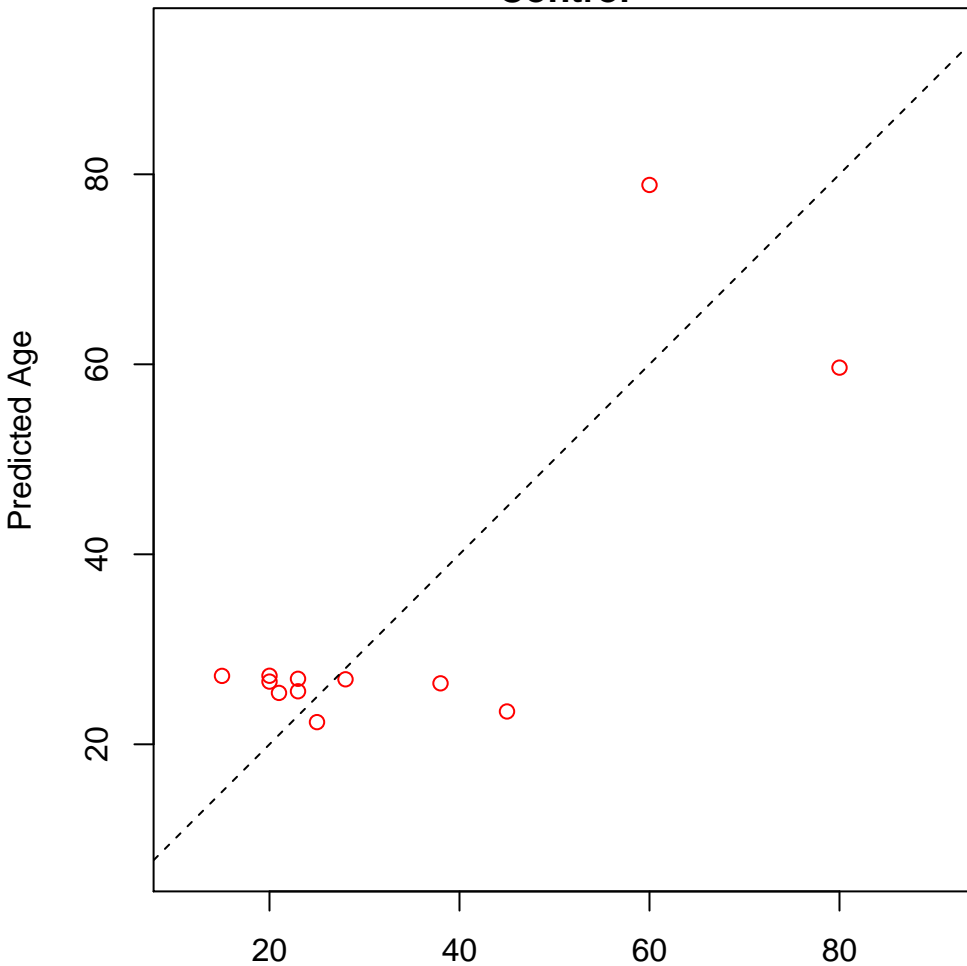


cellular response to fibroblast growth factor stimulus (Score: 5.271713)

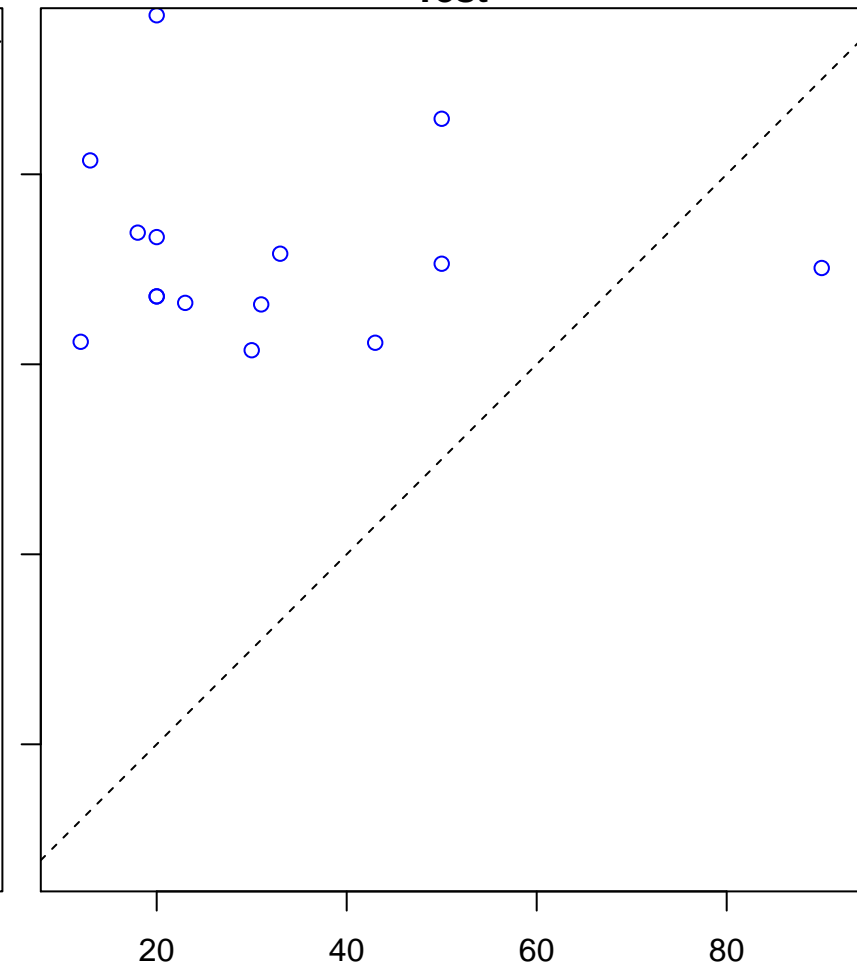


response to fibroblast growth factor (Score: 5.271631)

Control



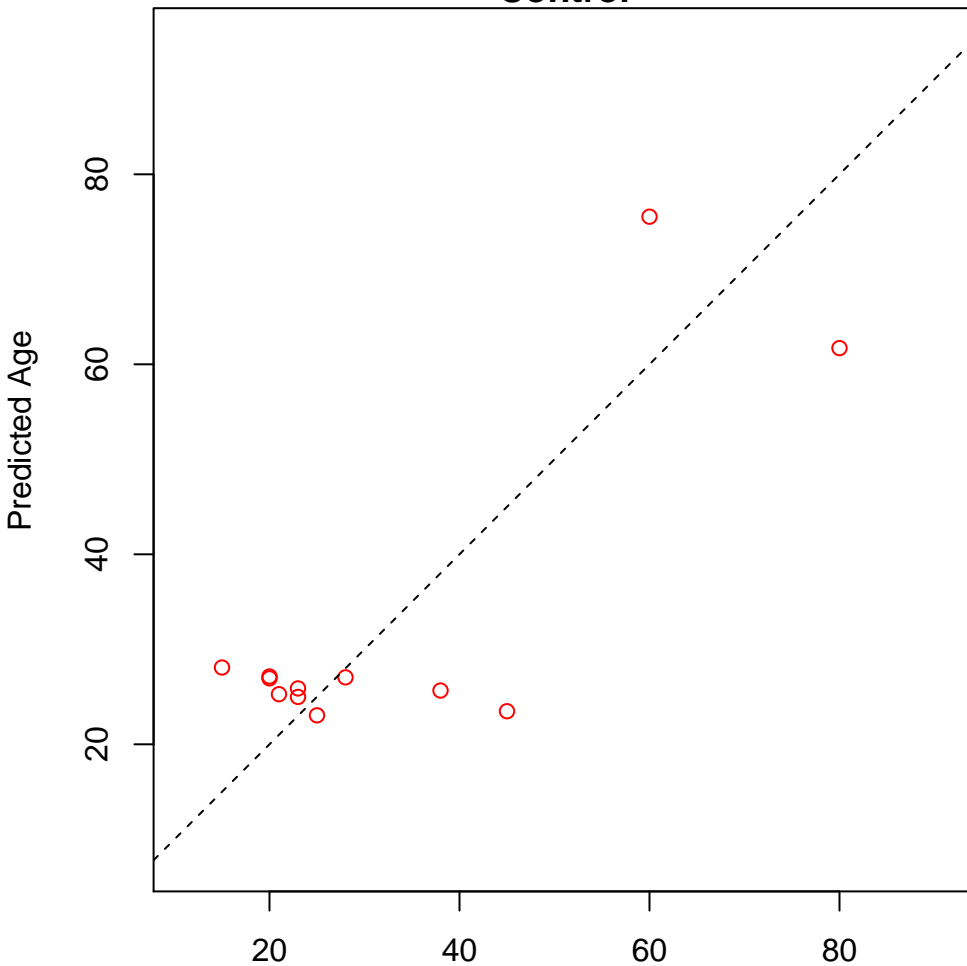
Test



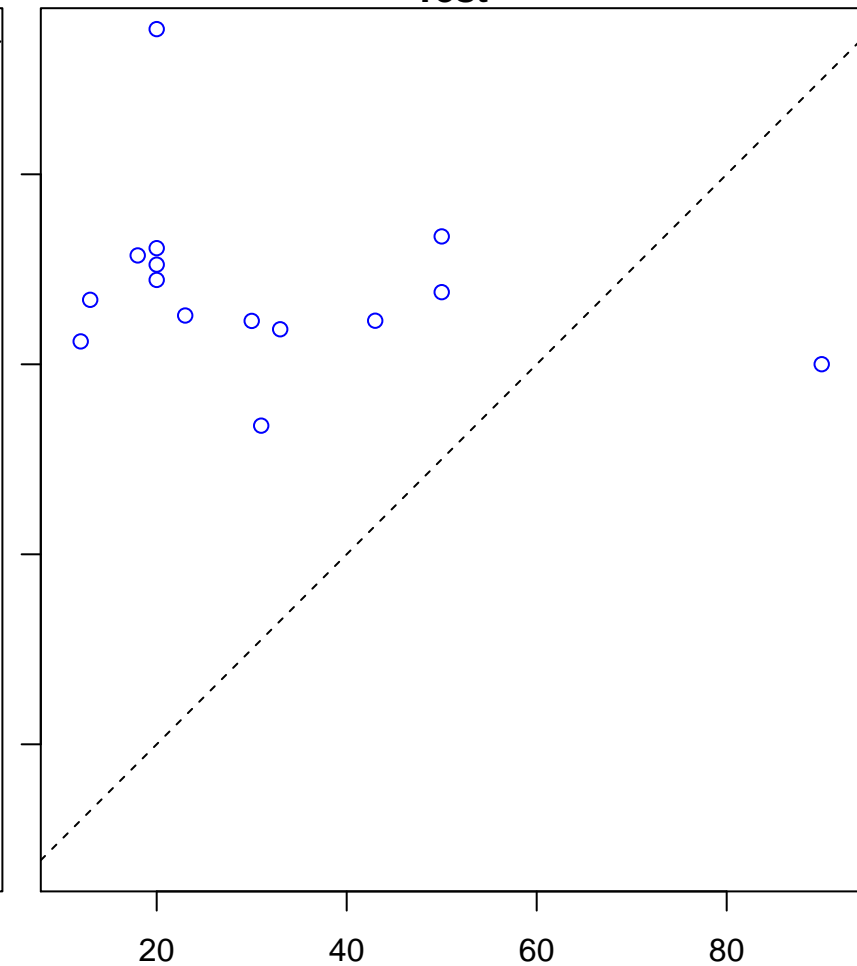
Actual Age

intermediate filament-based process (Score: 5.271056)

Control

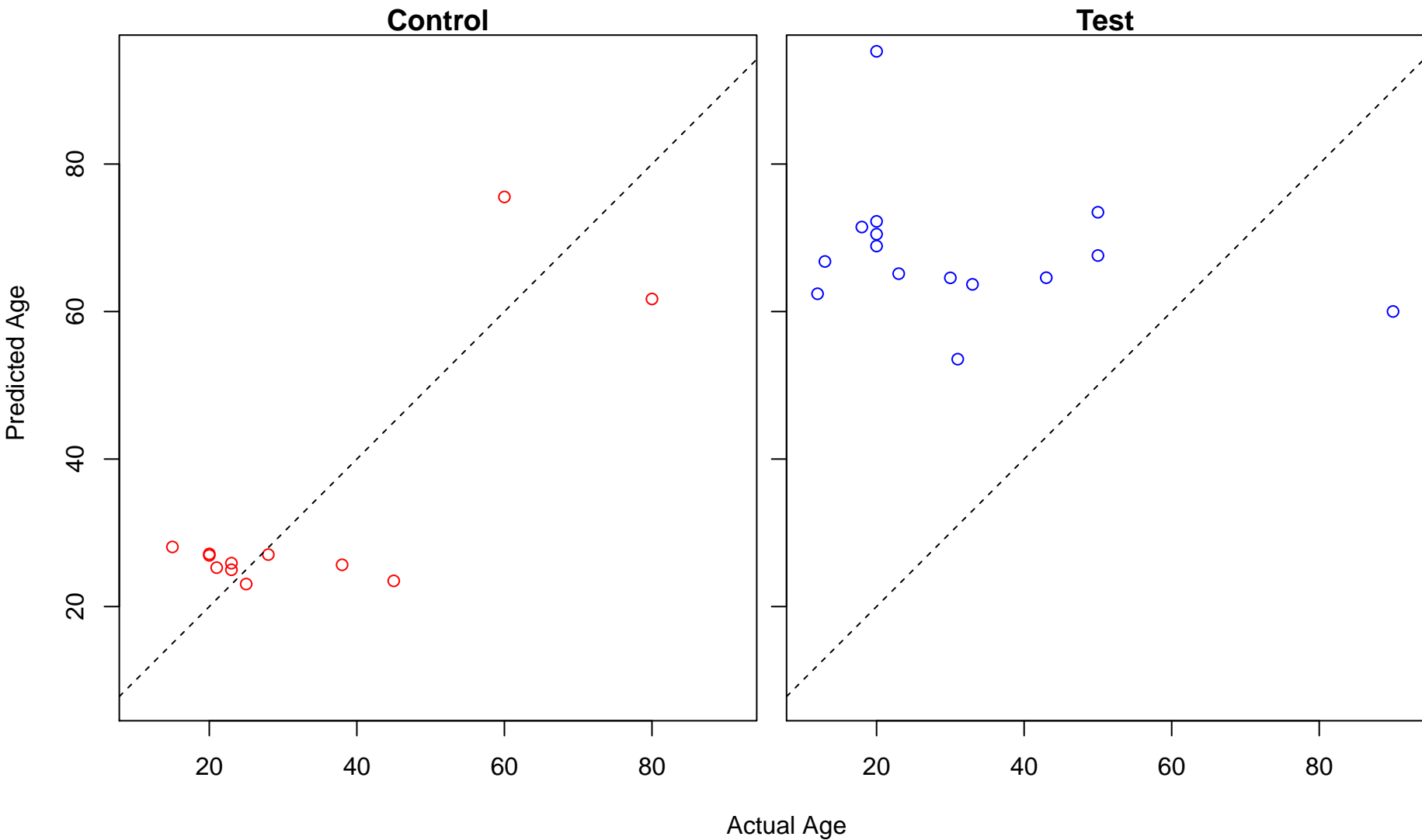


Test

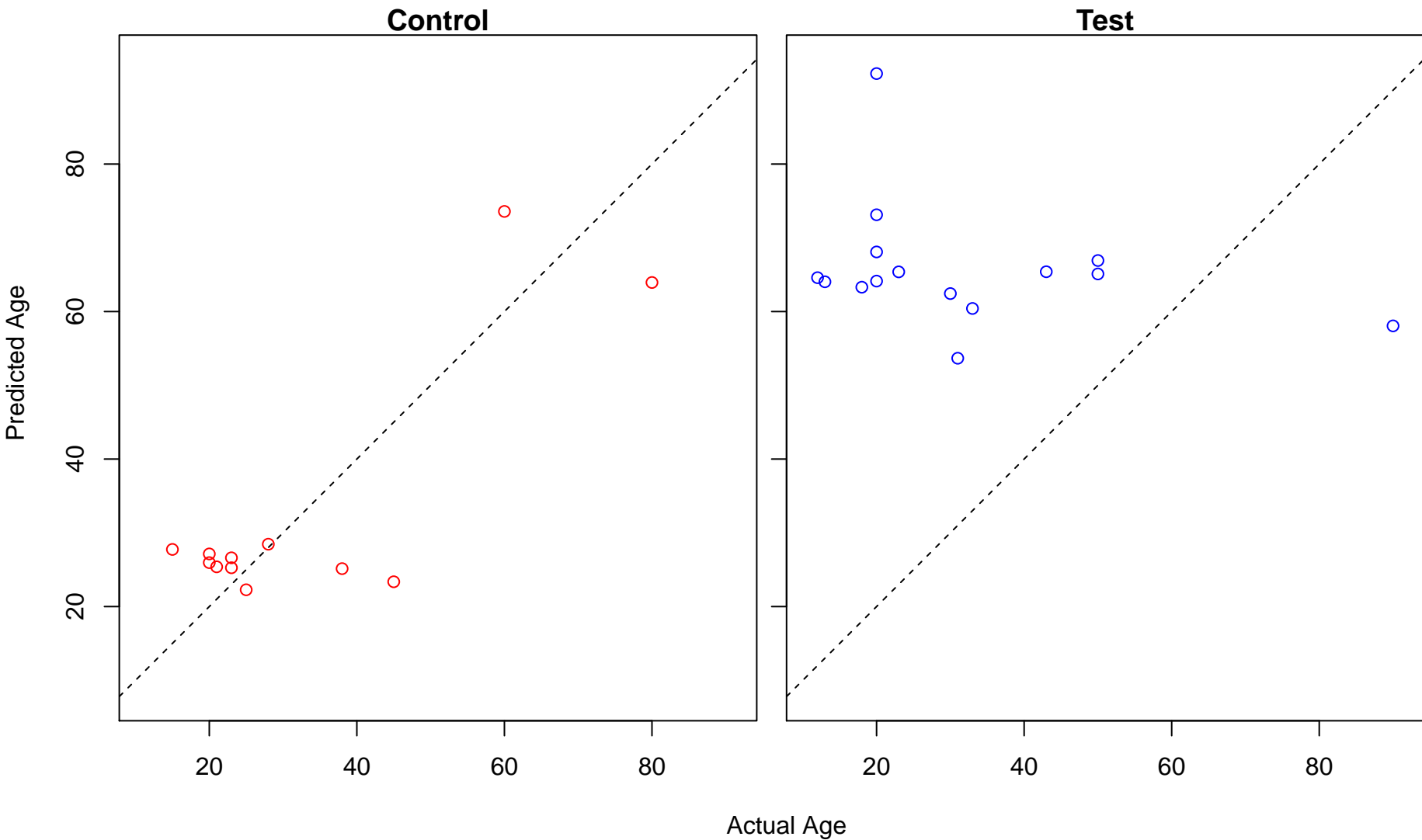


Actual Age

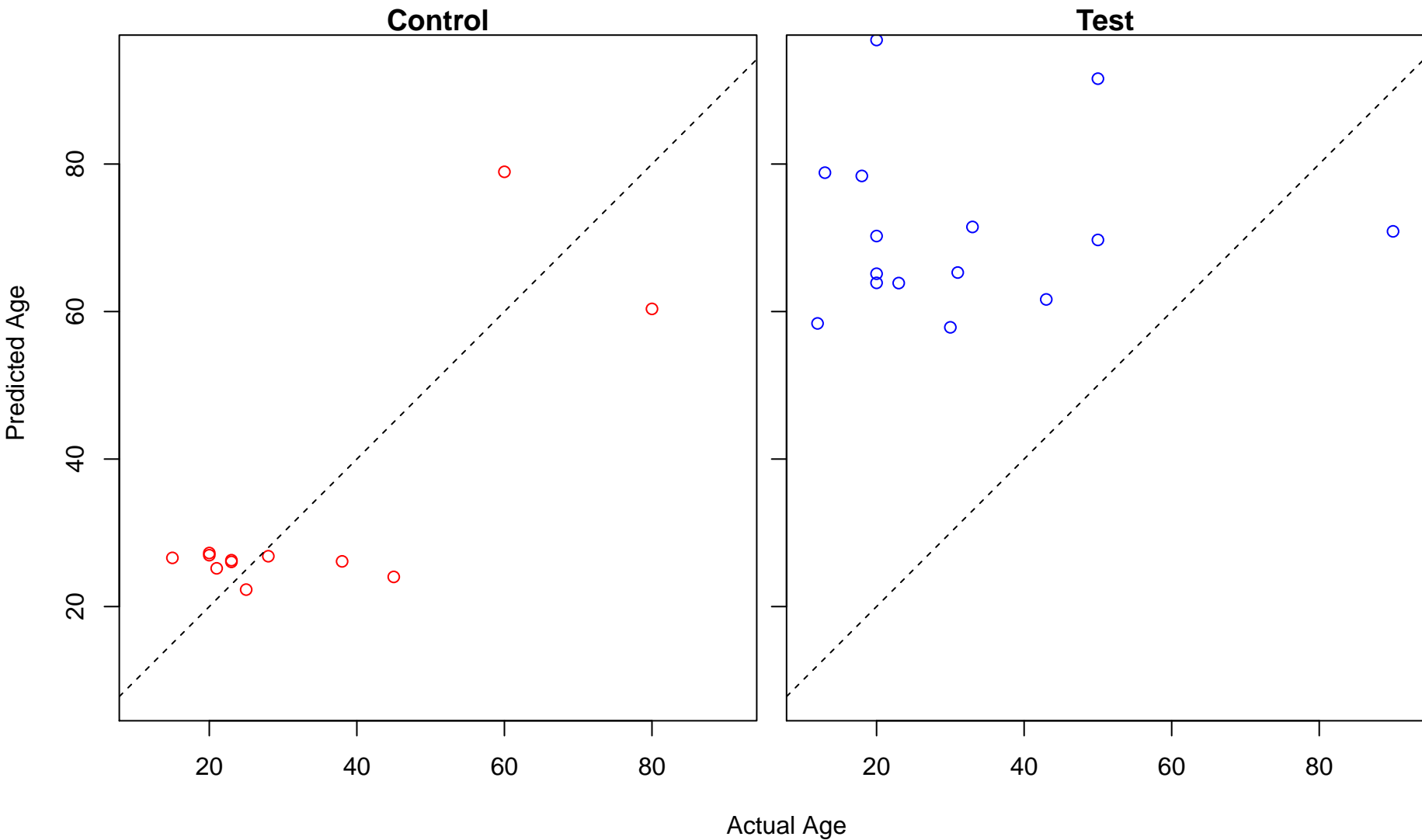
intermediate filament cytoskeleton organization (Score: 5.271056)



transmission of nerve impulse (Score: 5.270501)

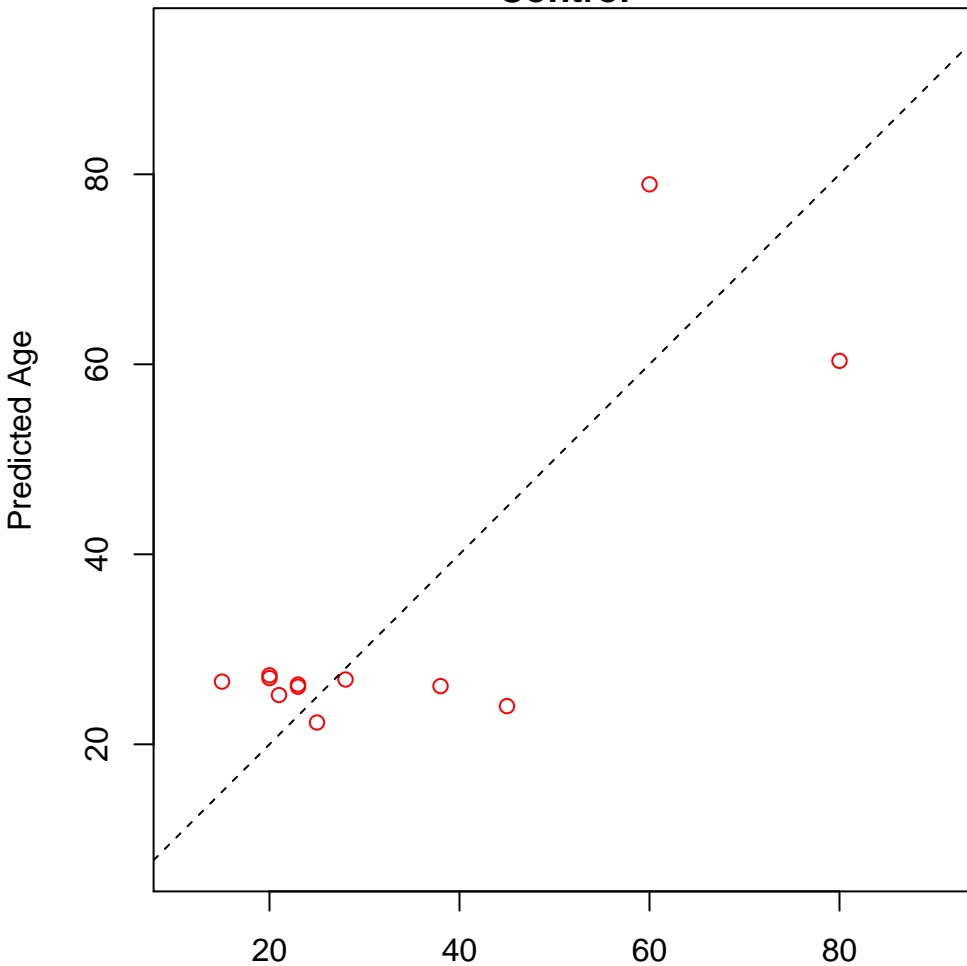


response to hypoxia (Score: 5.270465)

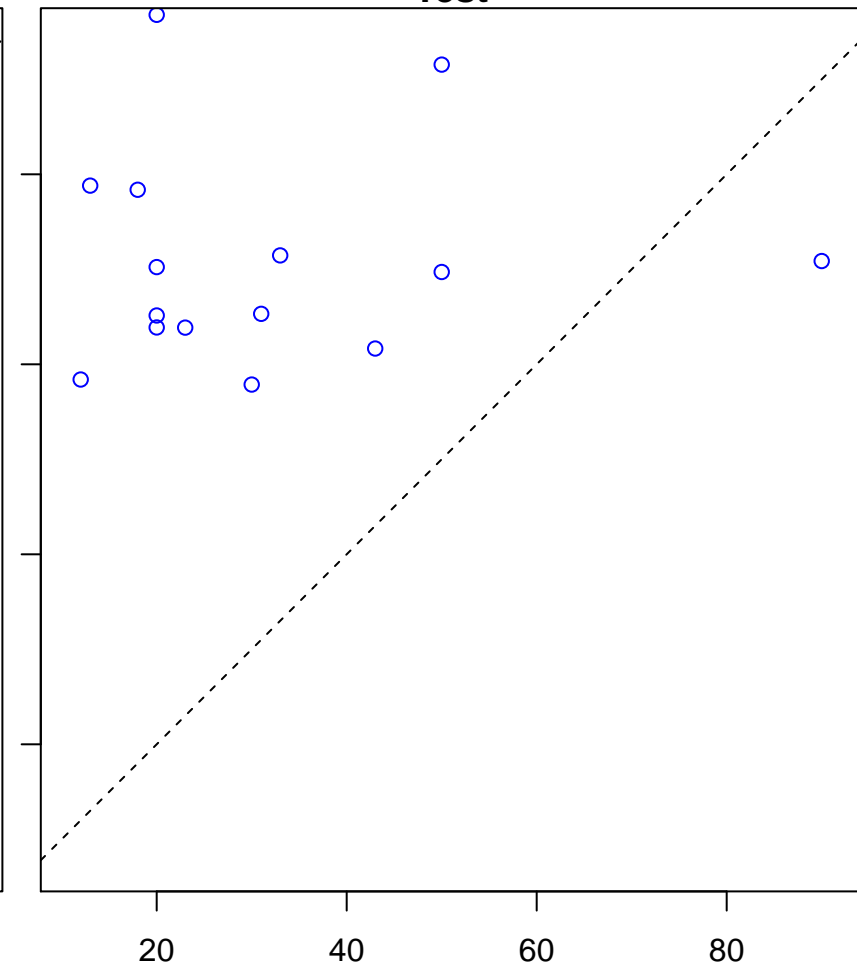


response to decreased oxygen levels (Score: 5.268950)

Control

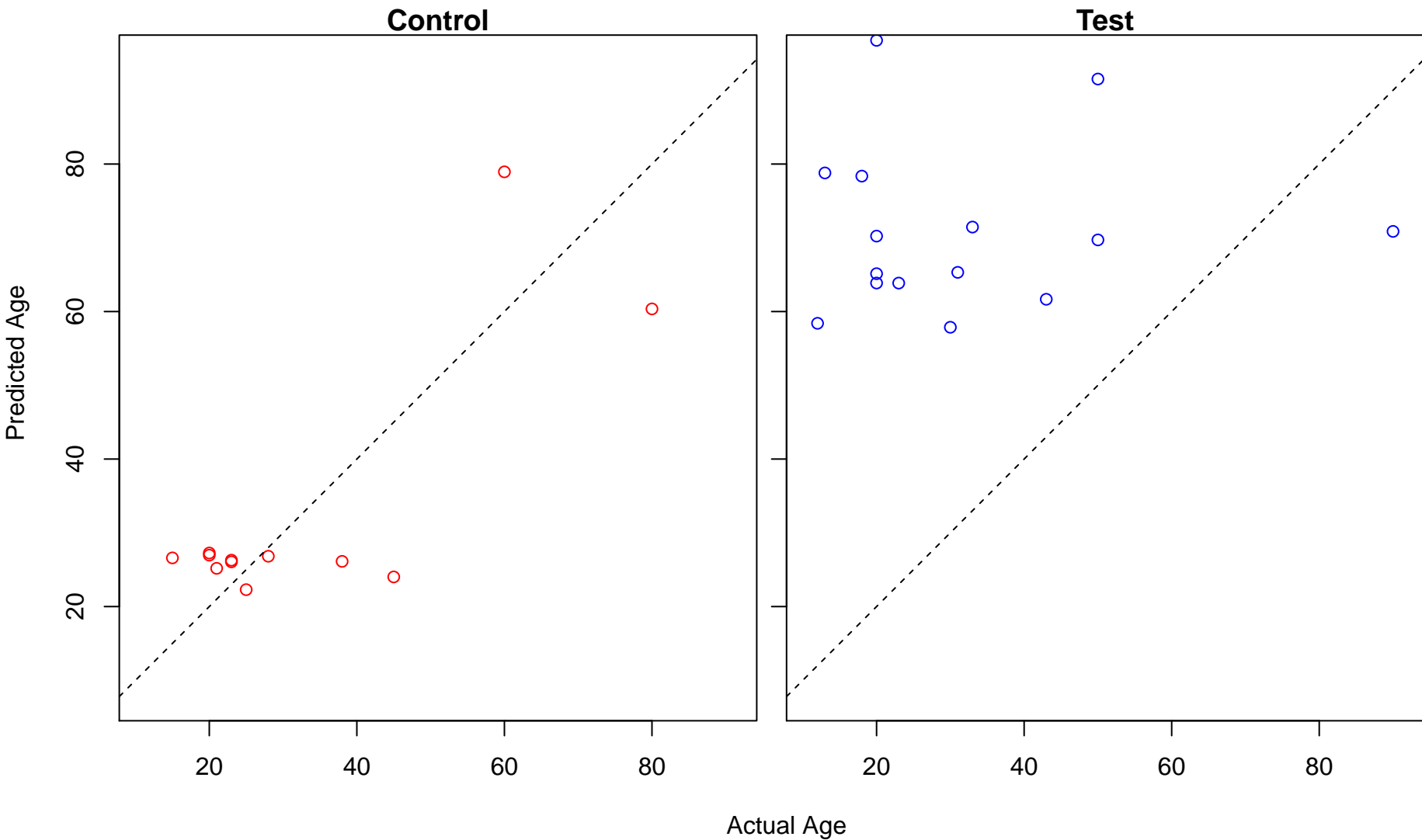


Test

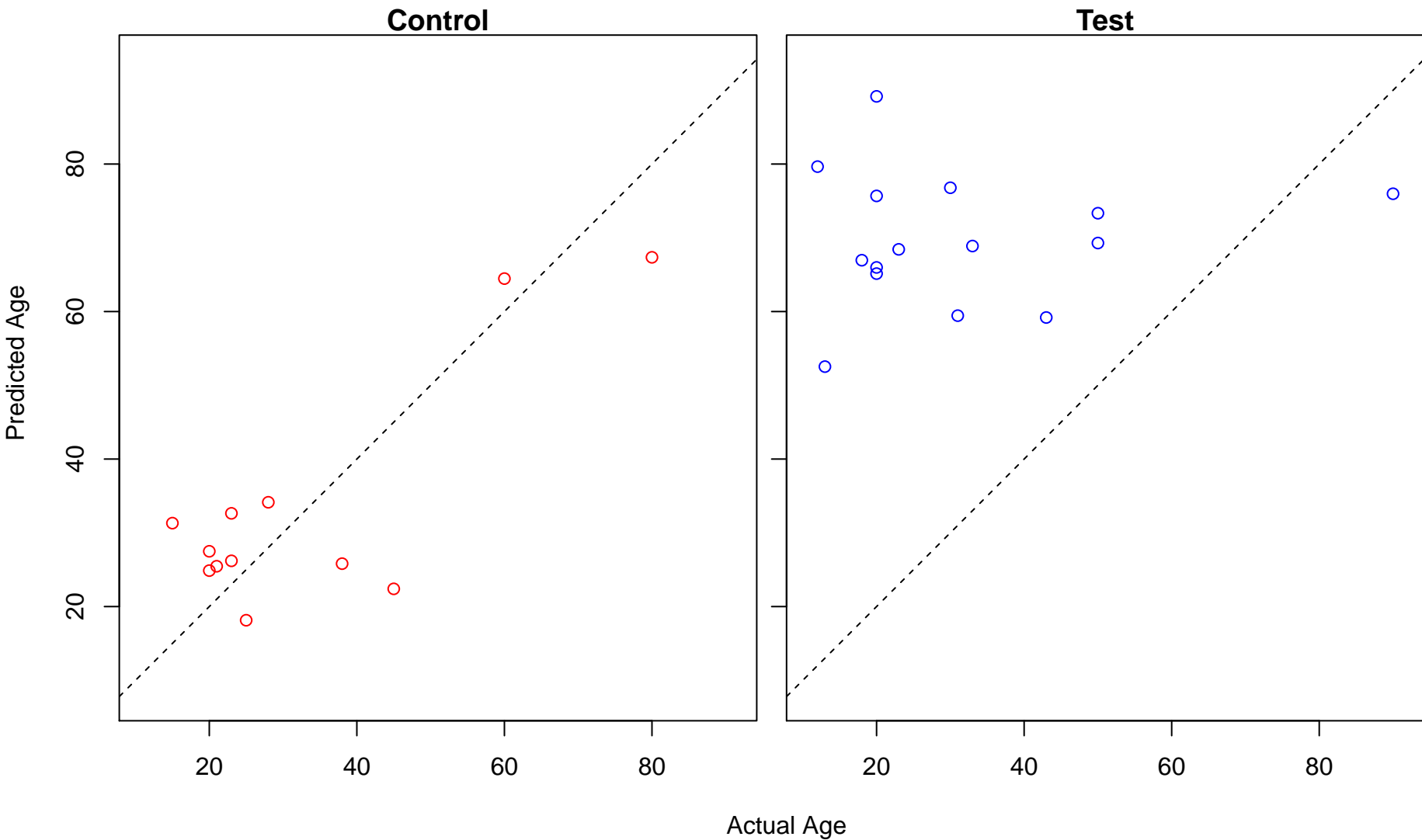


Actual Age

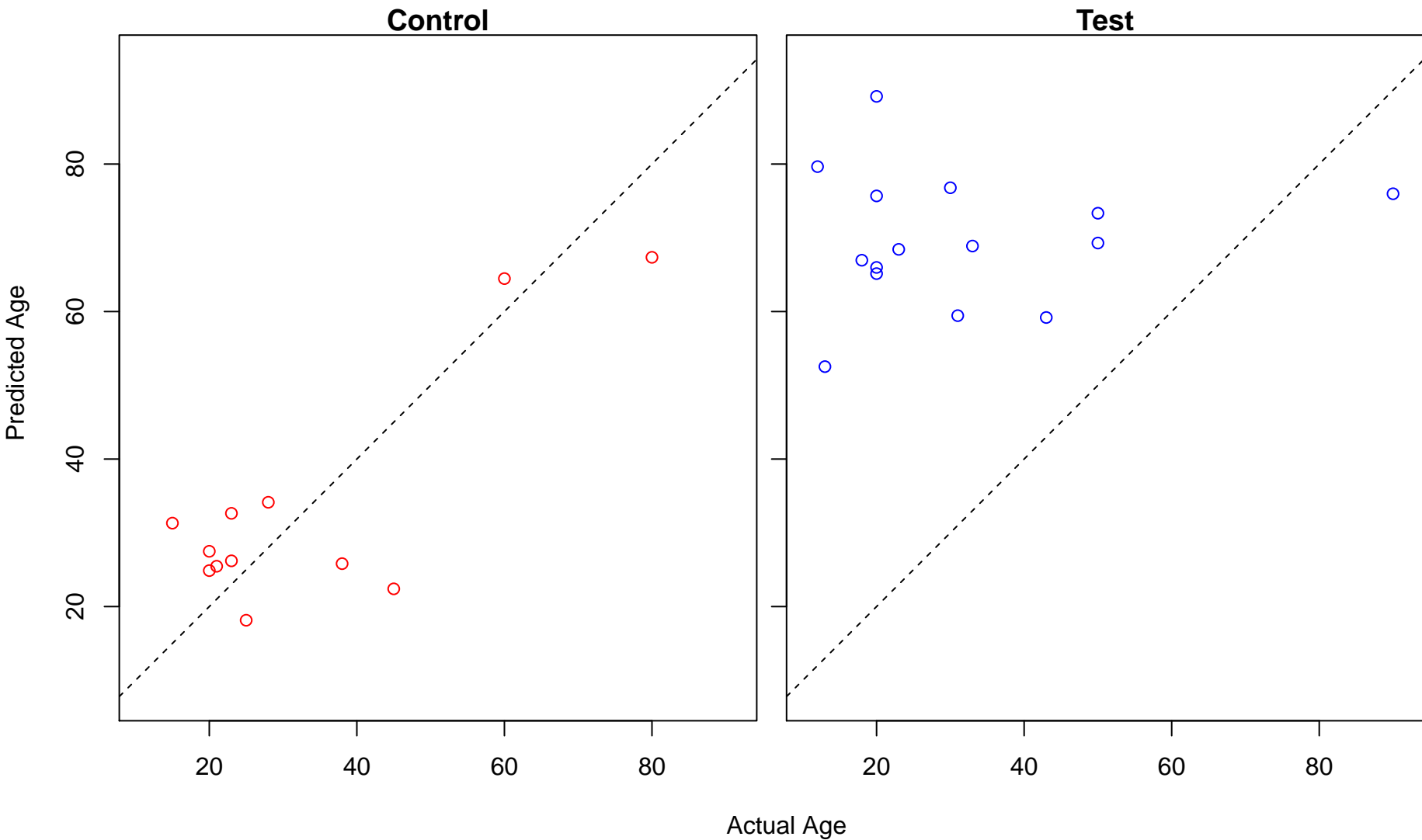
response to oxygen levels (Score: 5.267100)



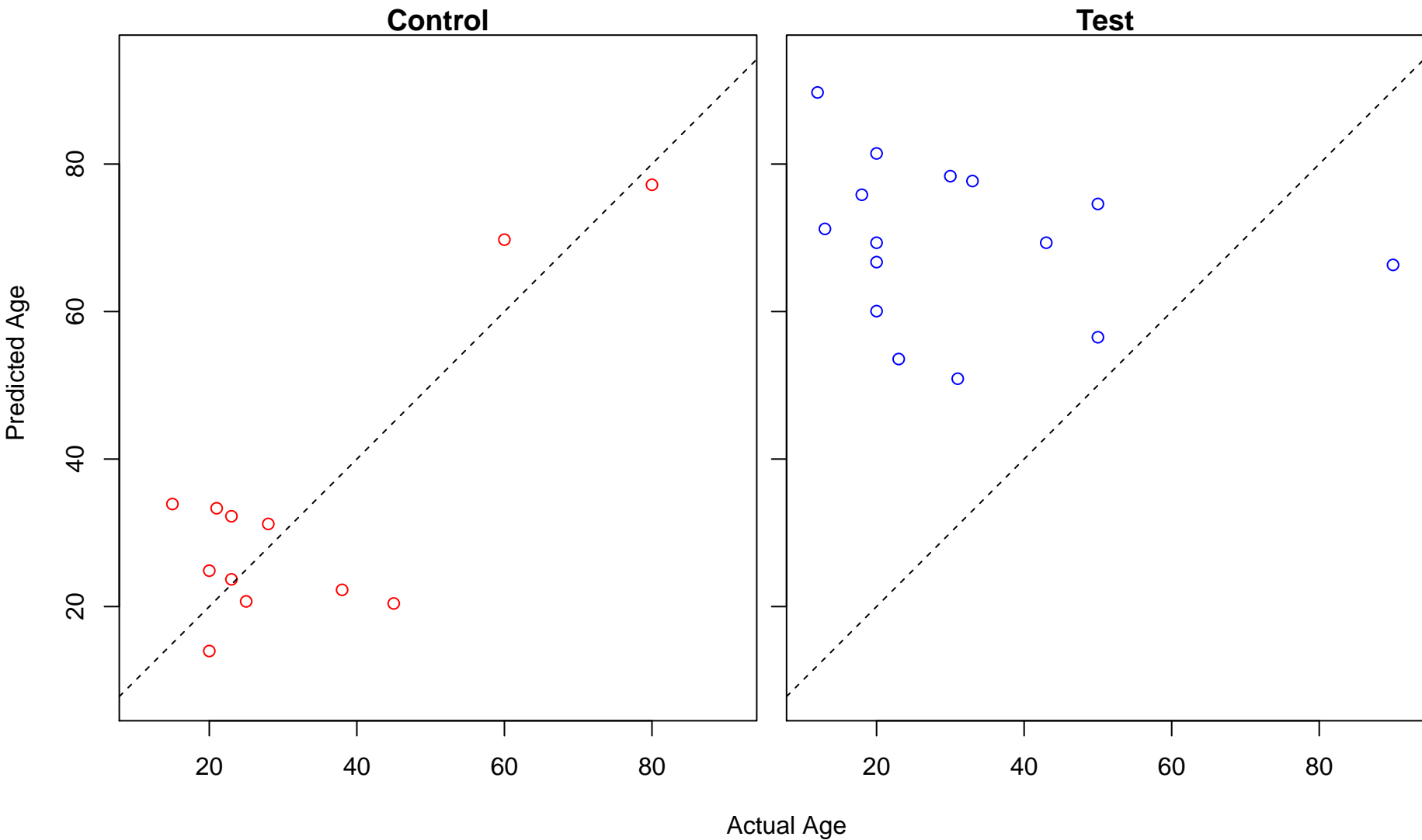
positive regulation of B cell mediated immunity (Score: 5.266841)



positive regulation of immunoglobulin mediated immune response (Score: 5.266841)

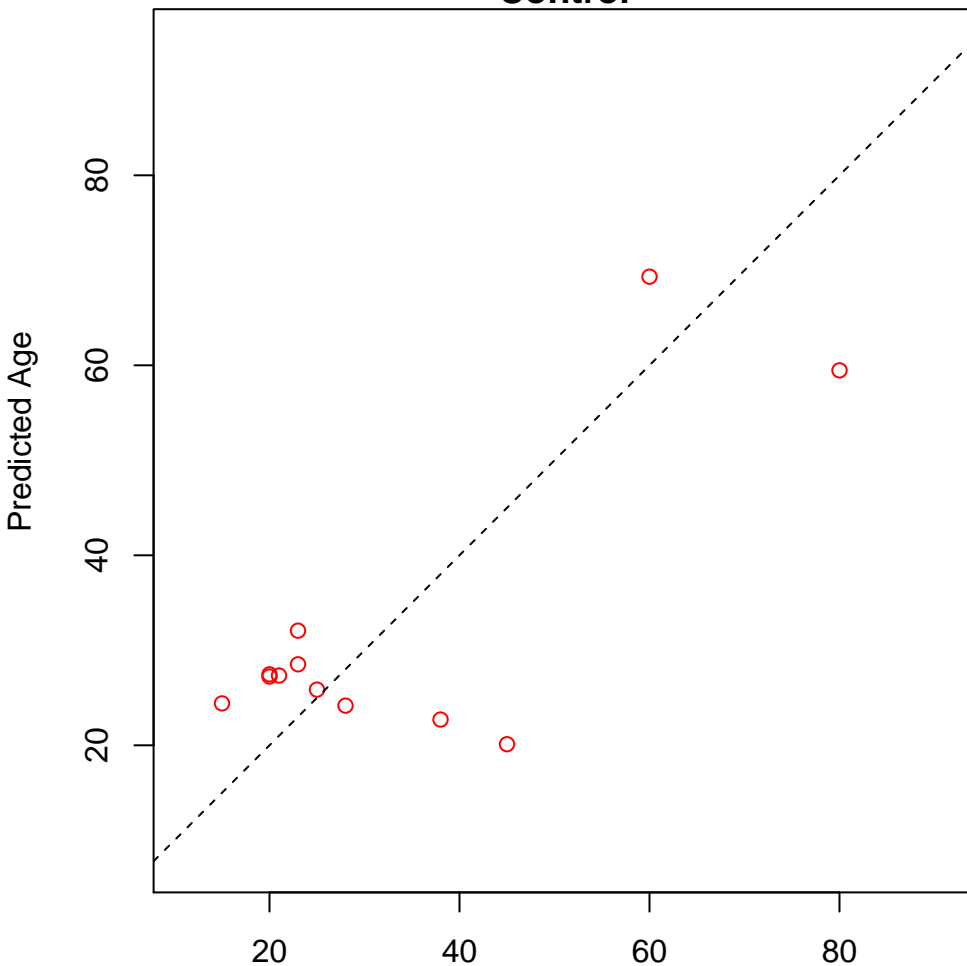


negative regulation of epidermal growth factor-activated receptor activity (Score: 5.266817)

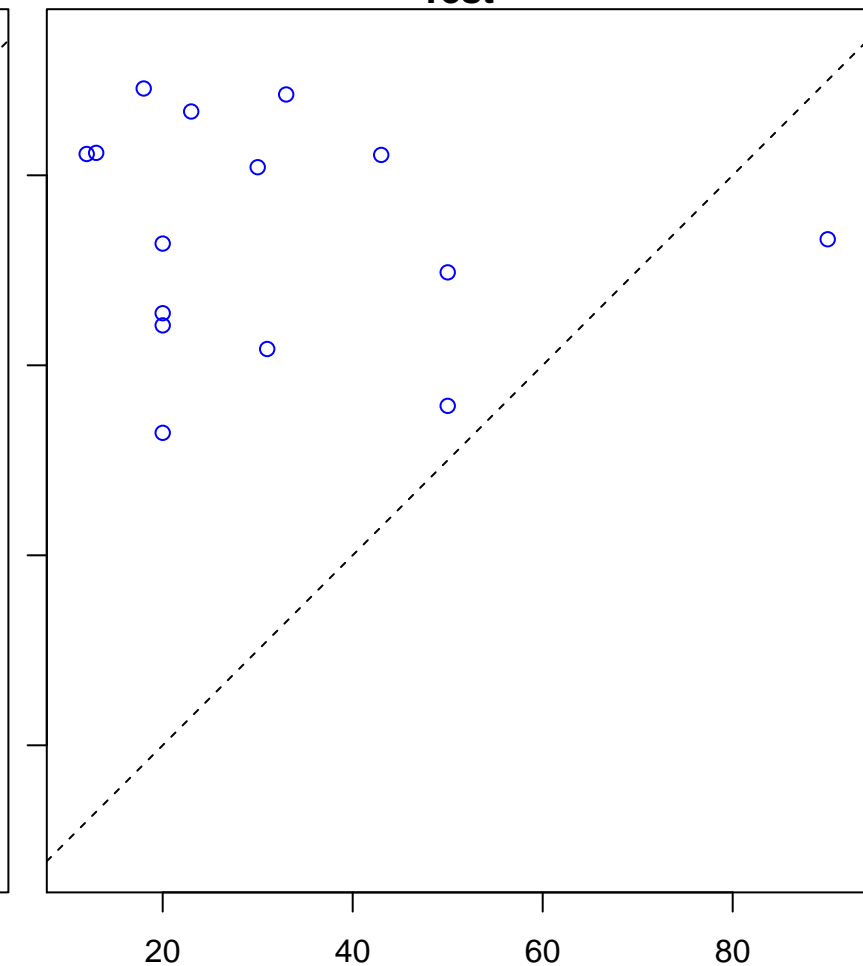


deoxyribonucleotide metabolic process (Score: 5.266580)

Control

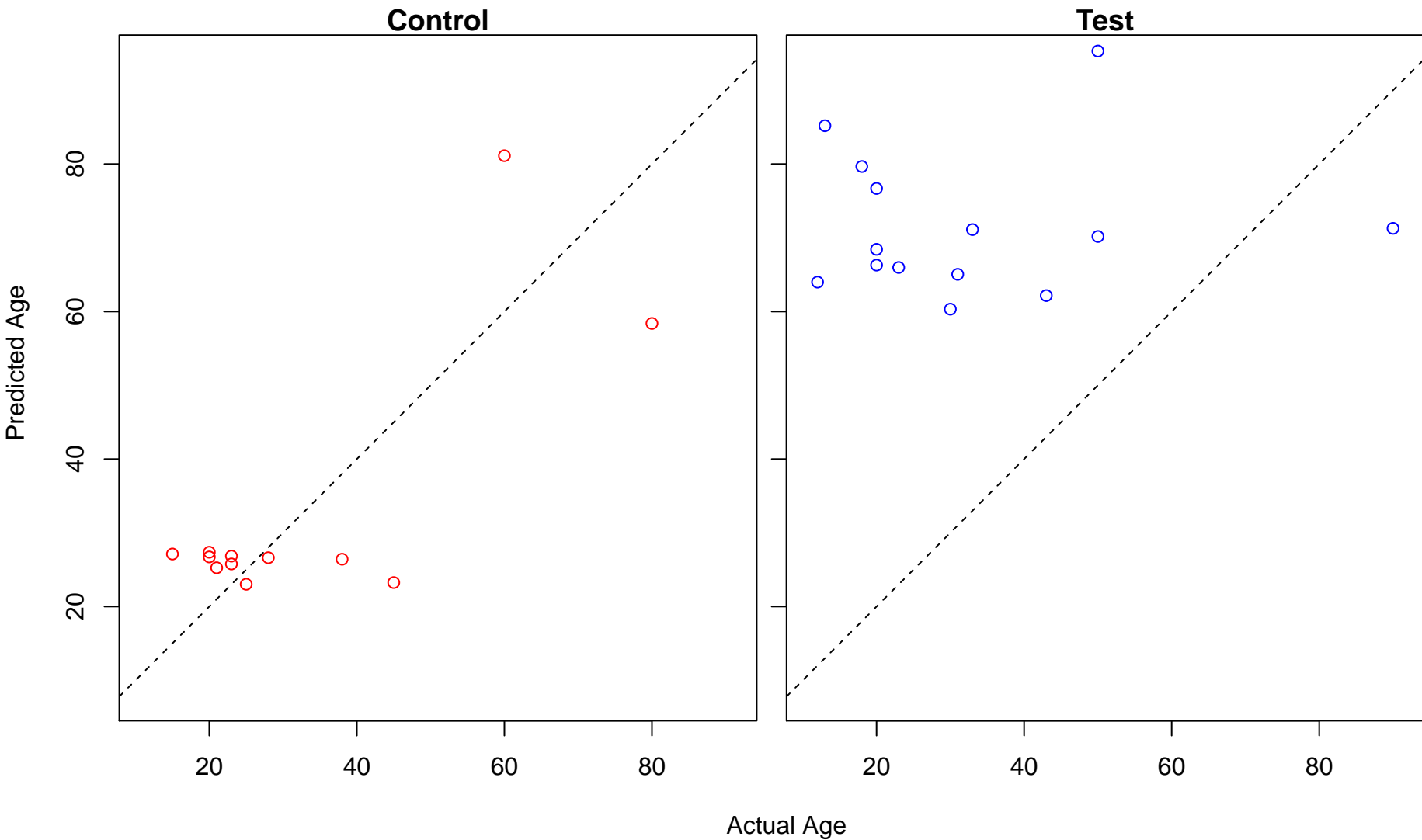


Test

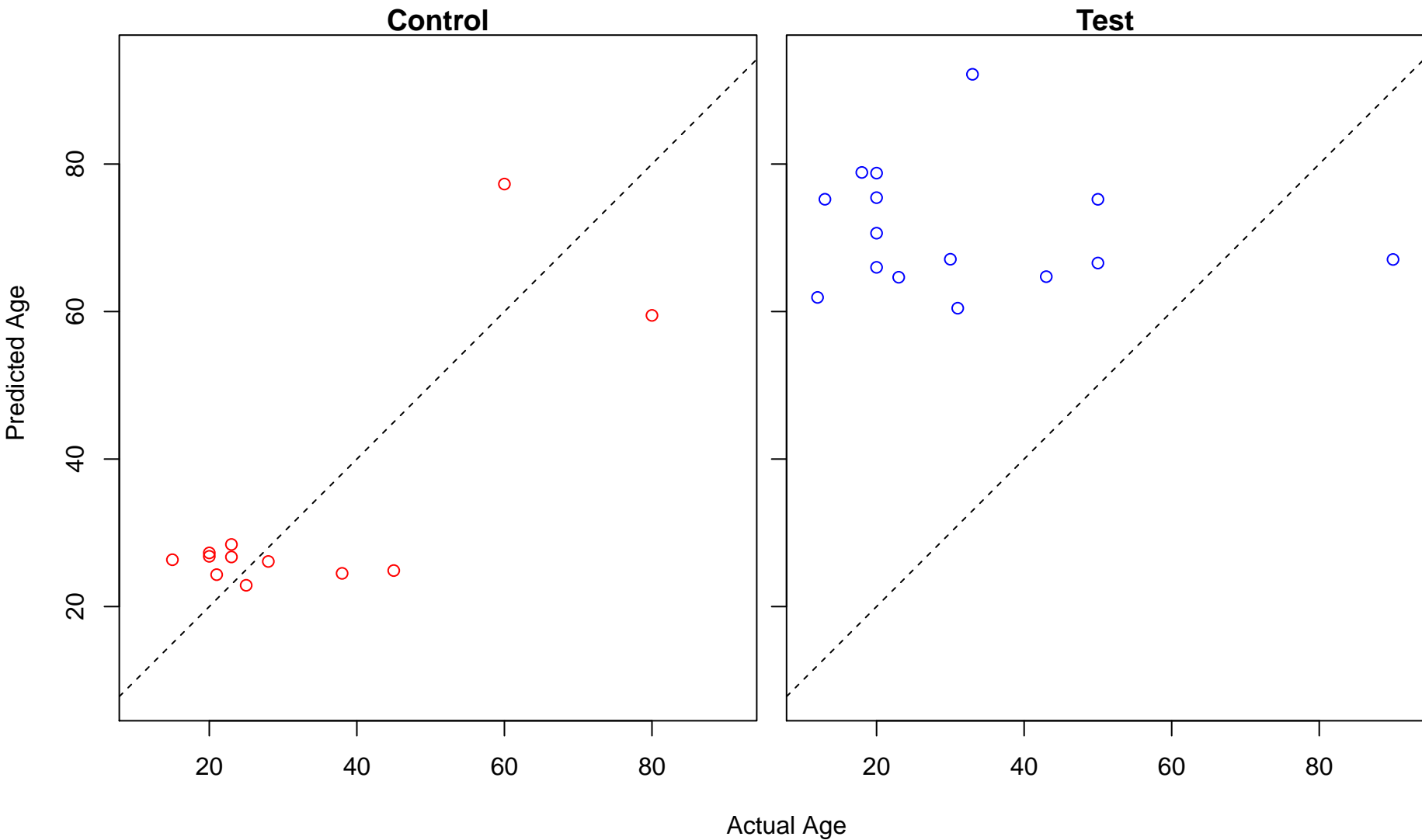


Actual Age

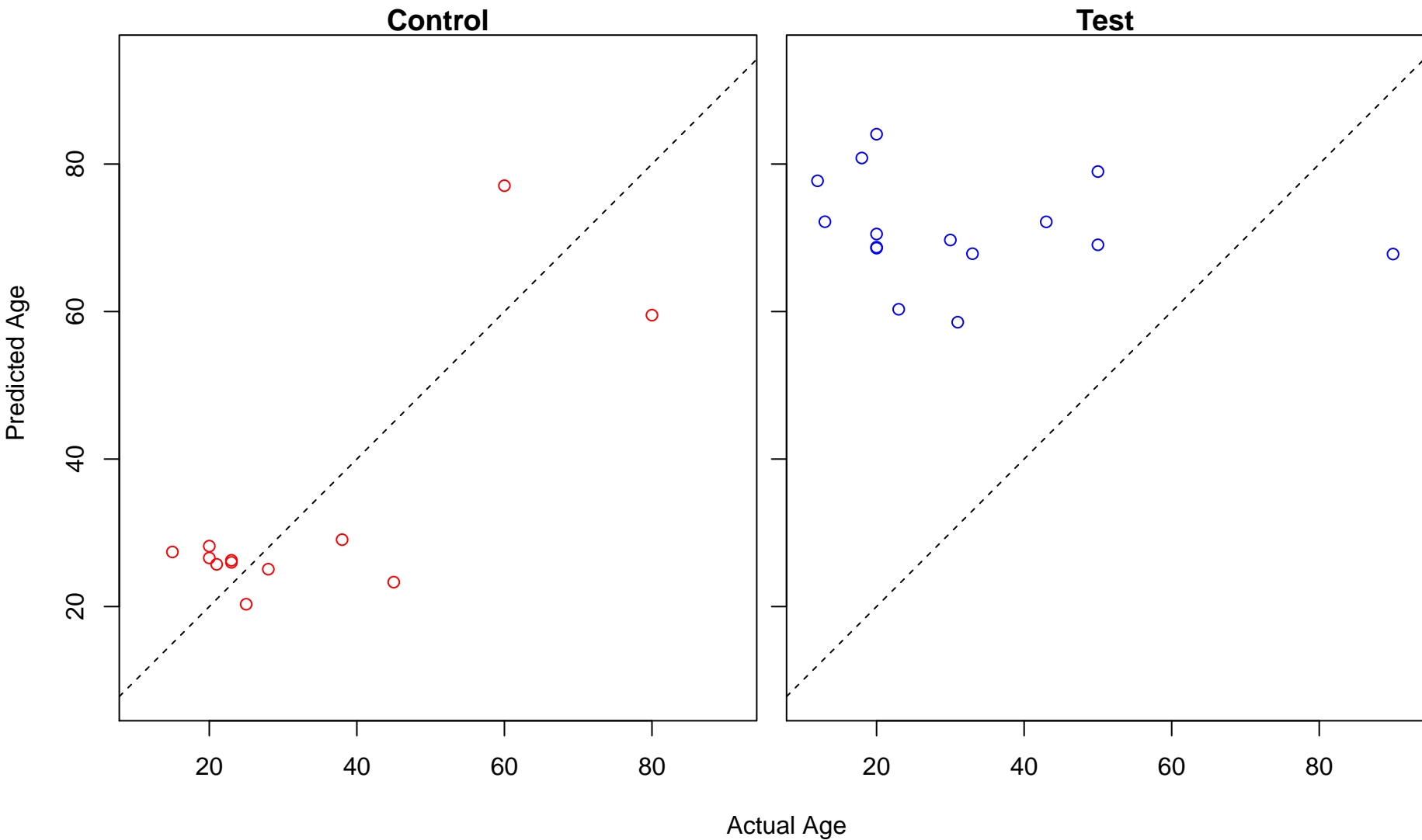
DNA recombination (Score: 5.265364)



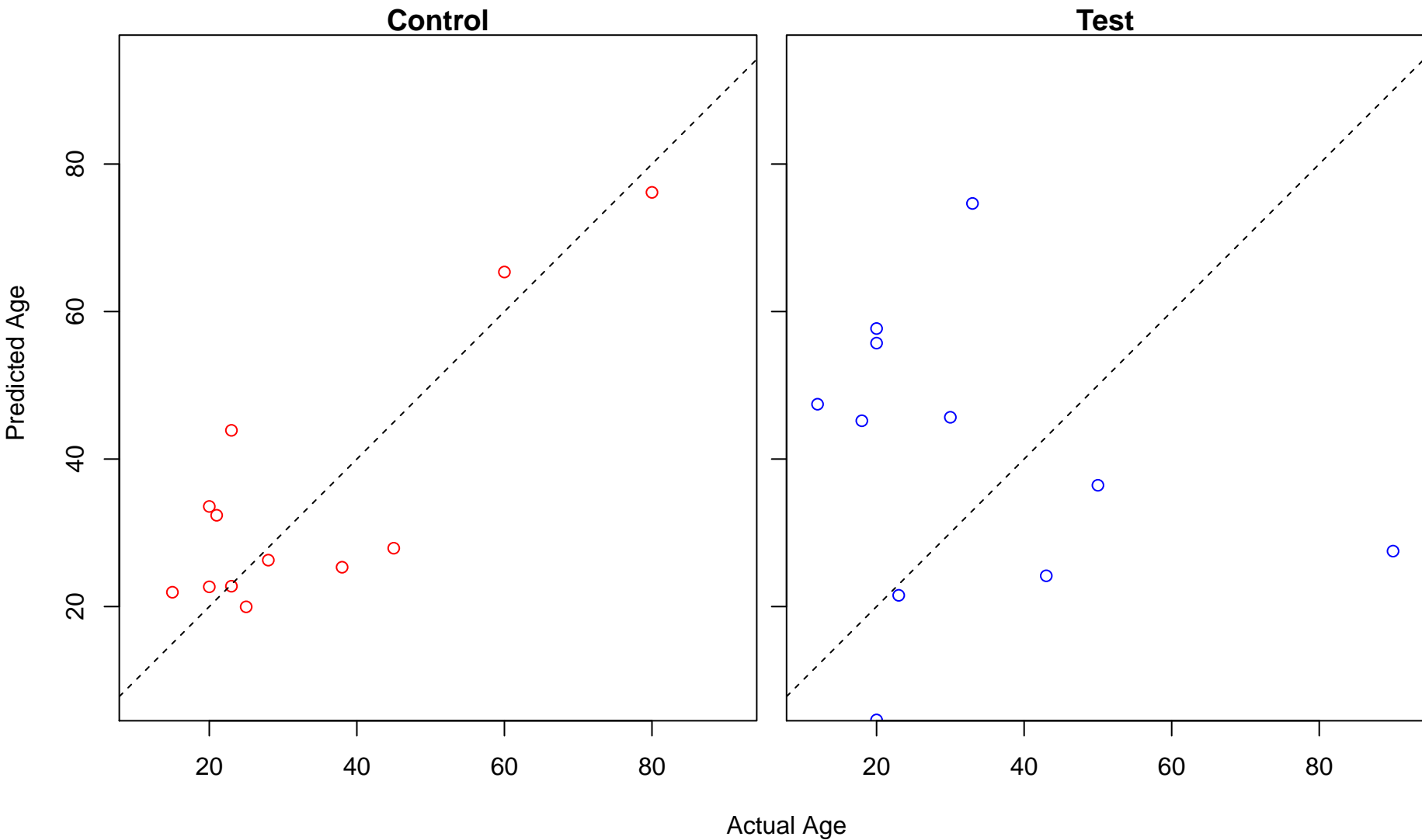
negative regulation of leukocyte apoptotic process (Score: 5.264697)



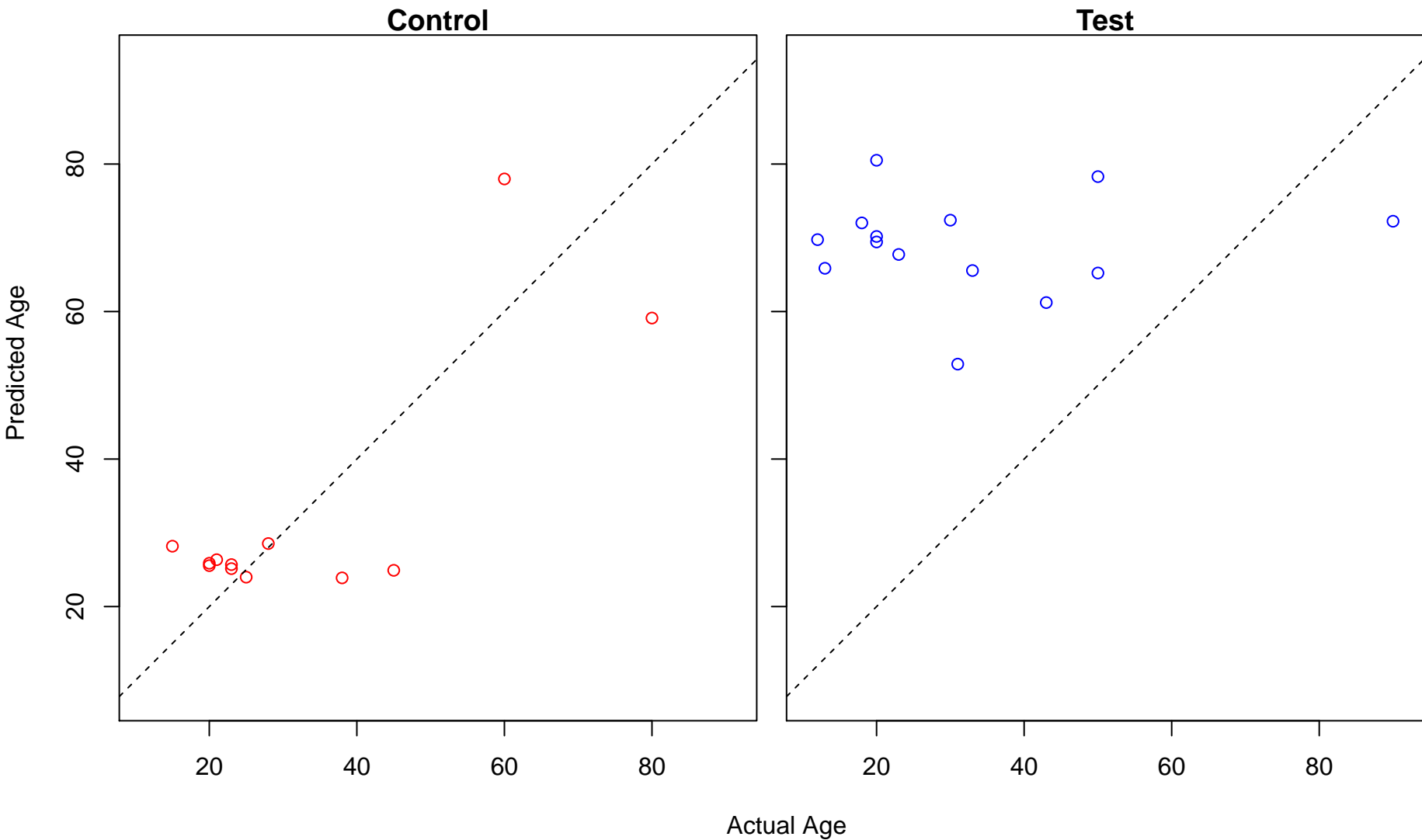
glutamine family amino acid metabolic process (Score: 5.263905)



response to drug (Score: 5.259440)

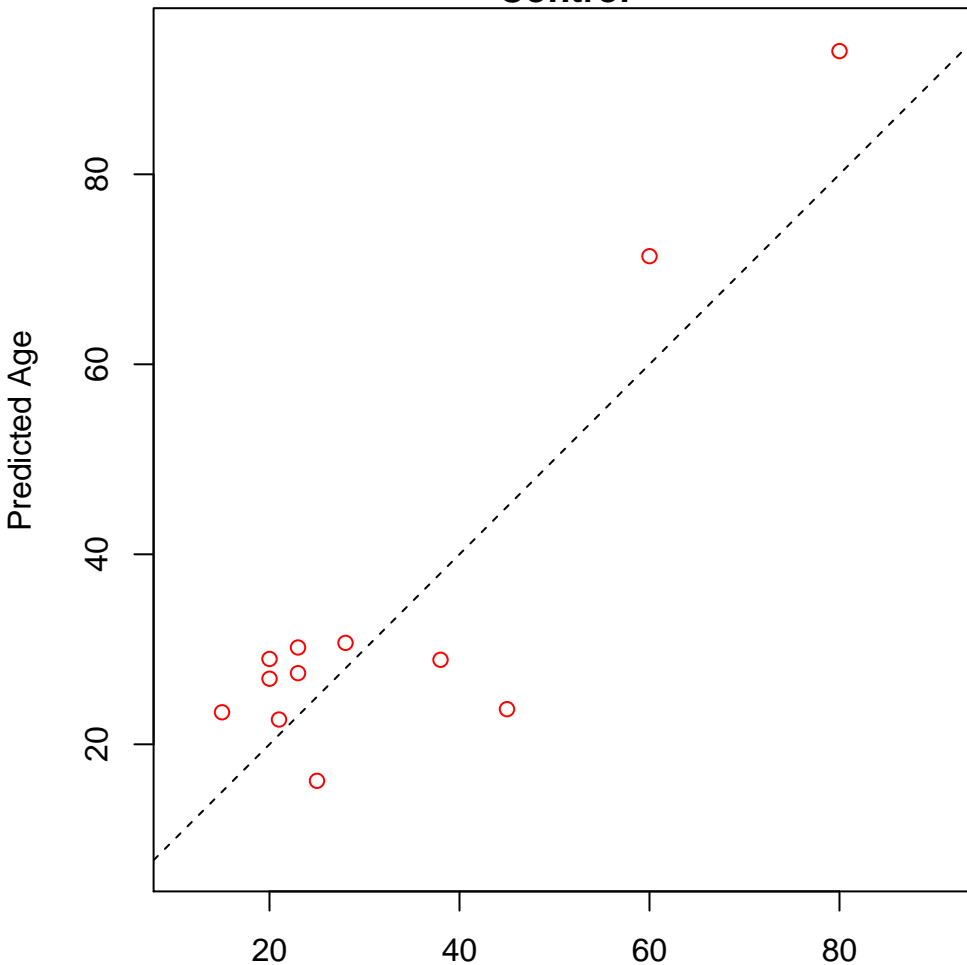


transcription elongation from RNA polymerase II promoter (Score: 5.259170)

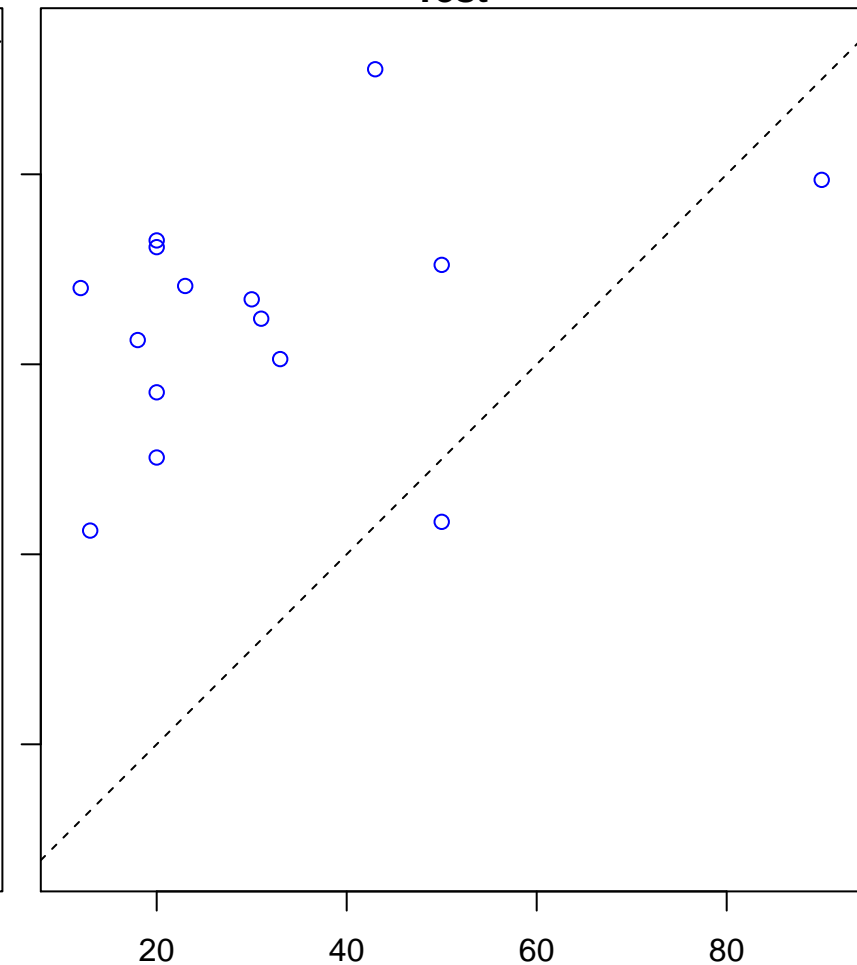


protein localization to cytoskeleton (Score: 5.258617)

Control

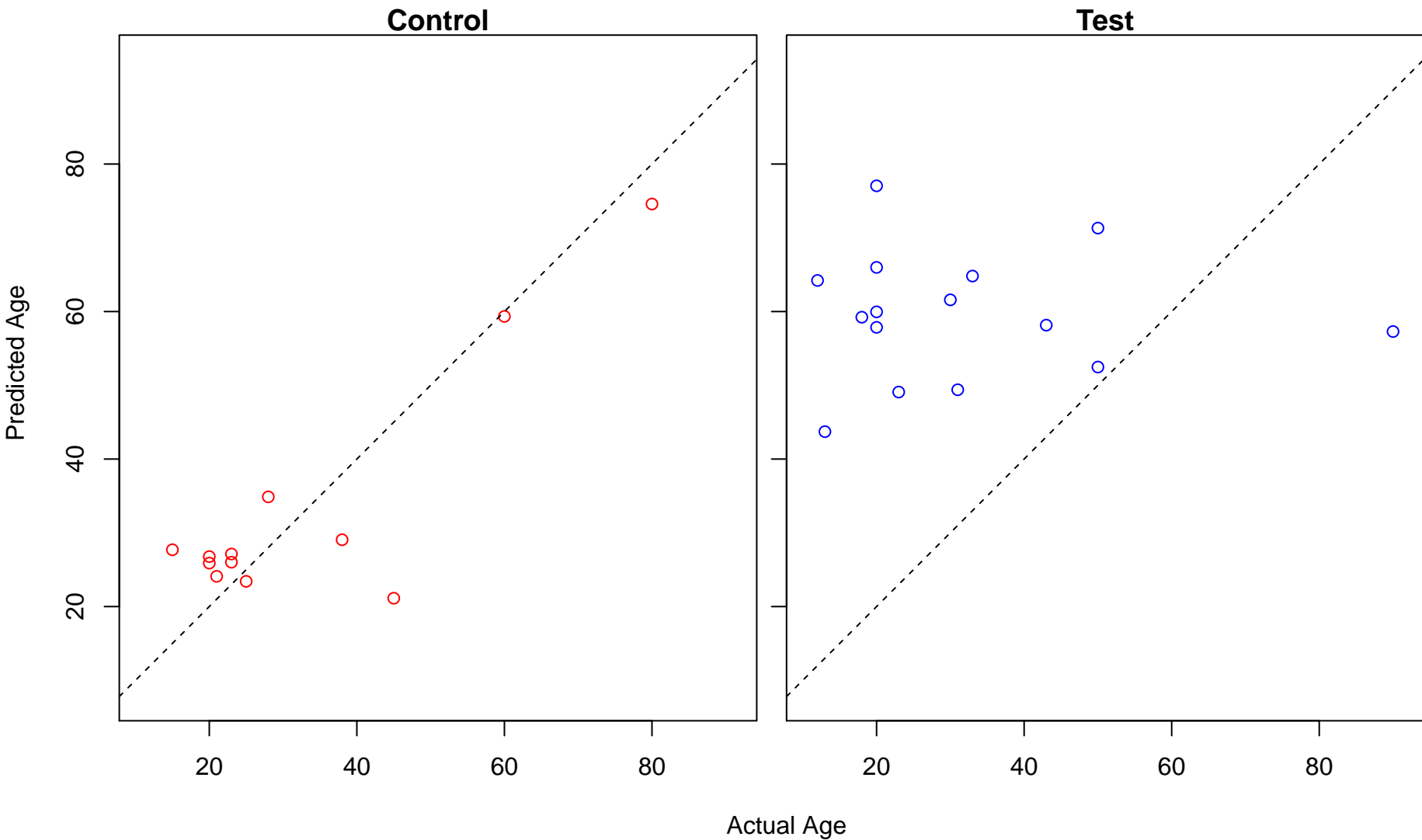


Test

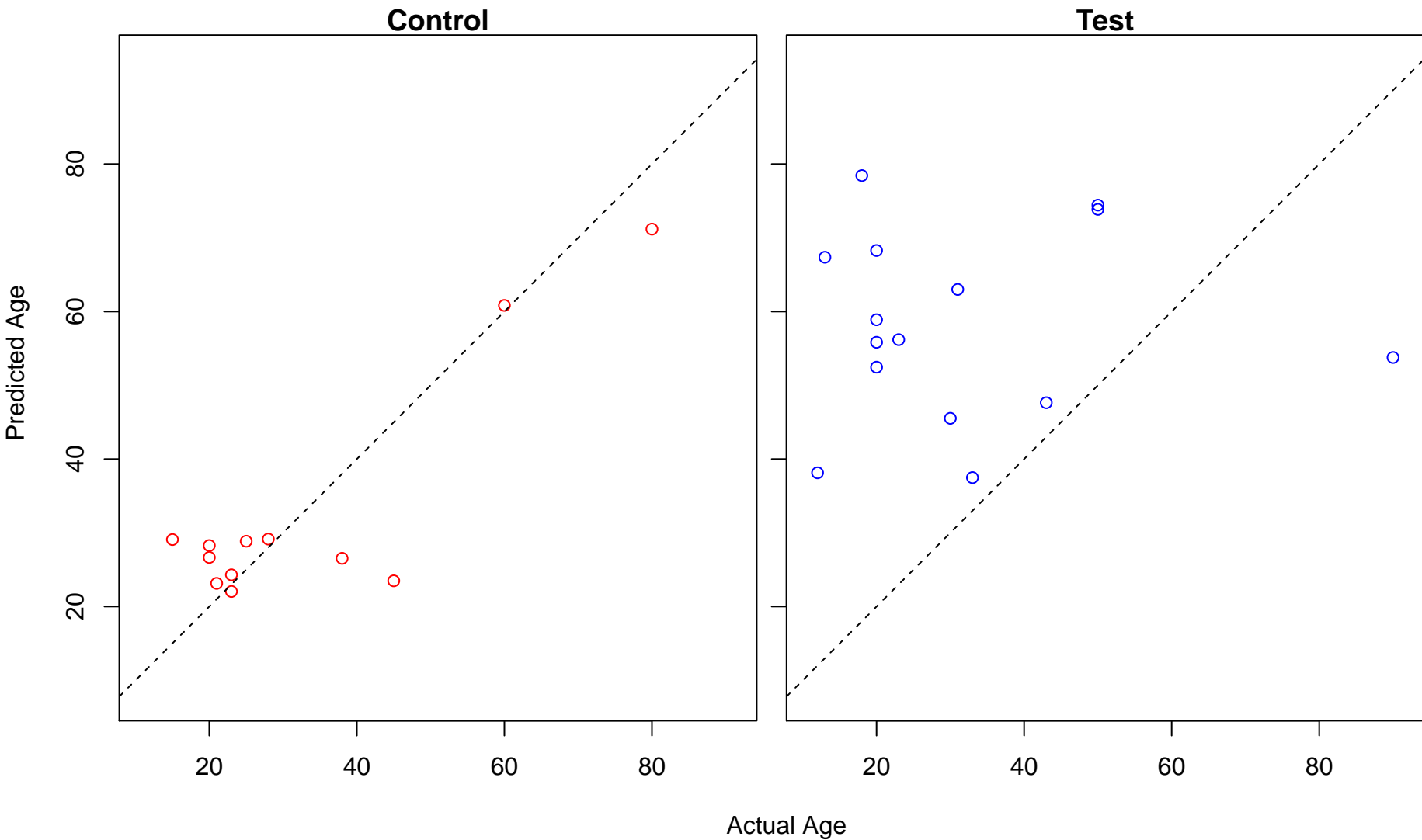


Actual Age

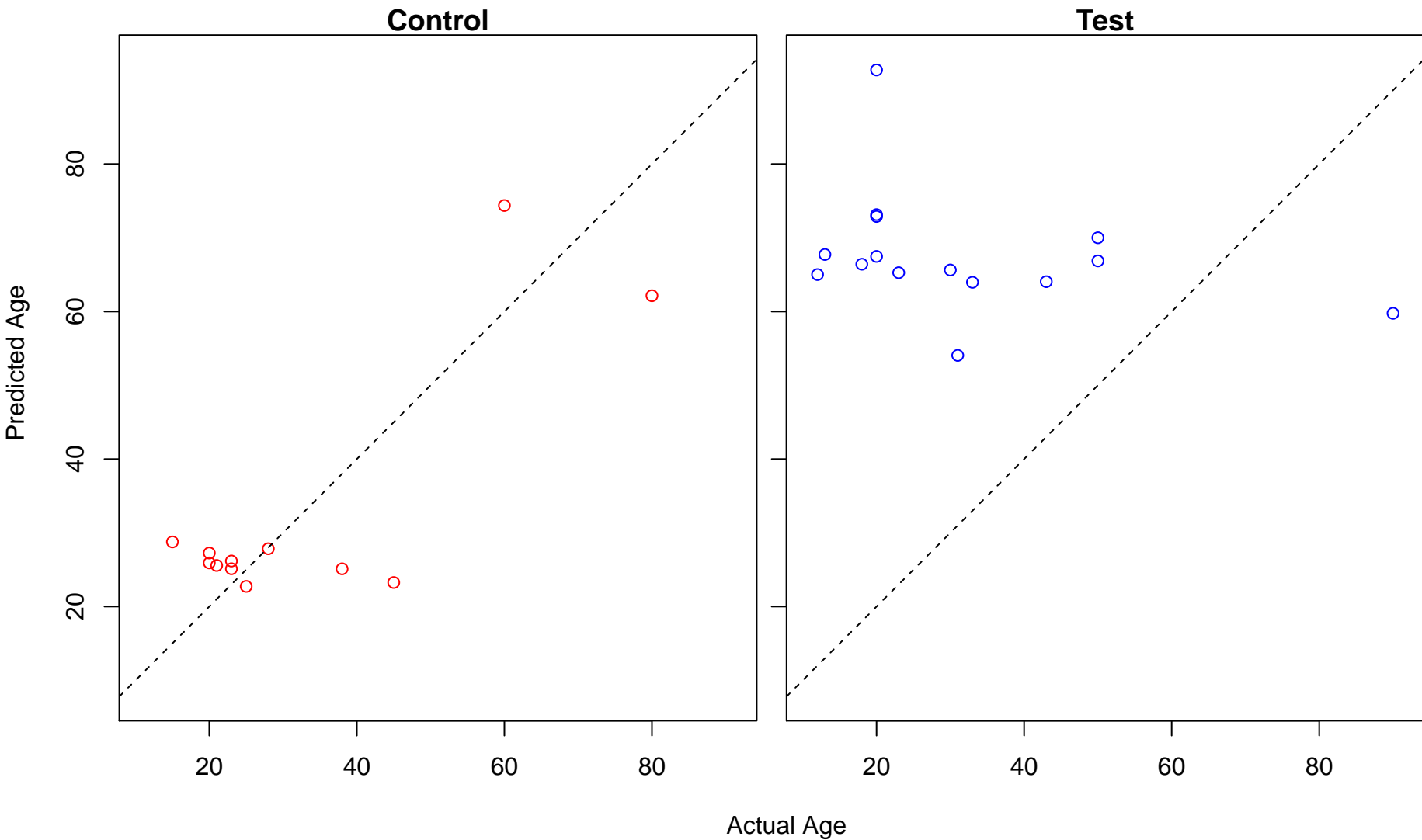
actin-mediated cell contraction (Score: 5.248583)



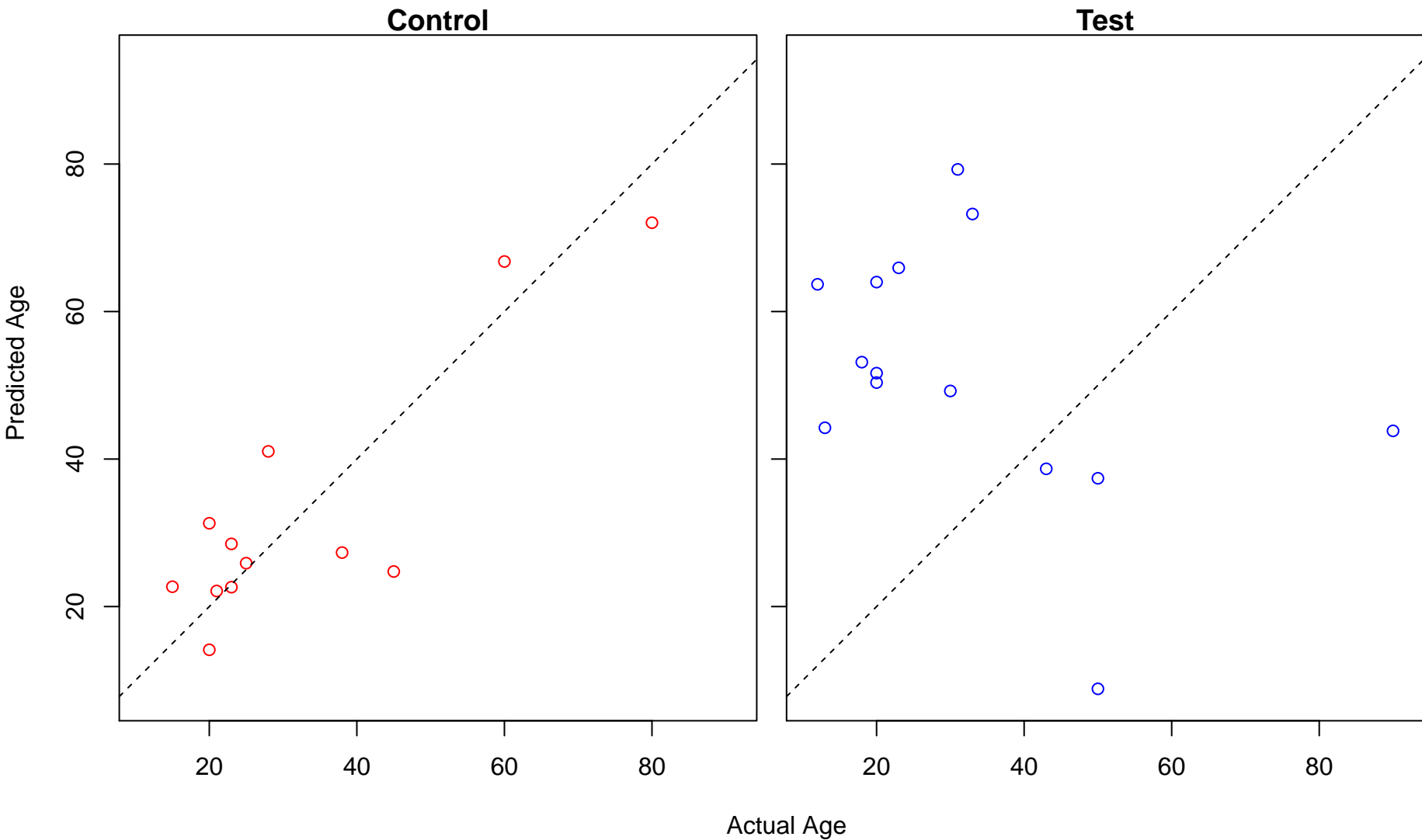
glucose catabolic process (Score: 5.248167)



behavior (Score: 5.246196)

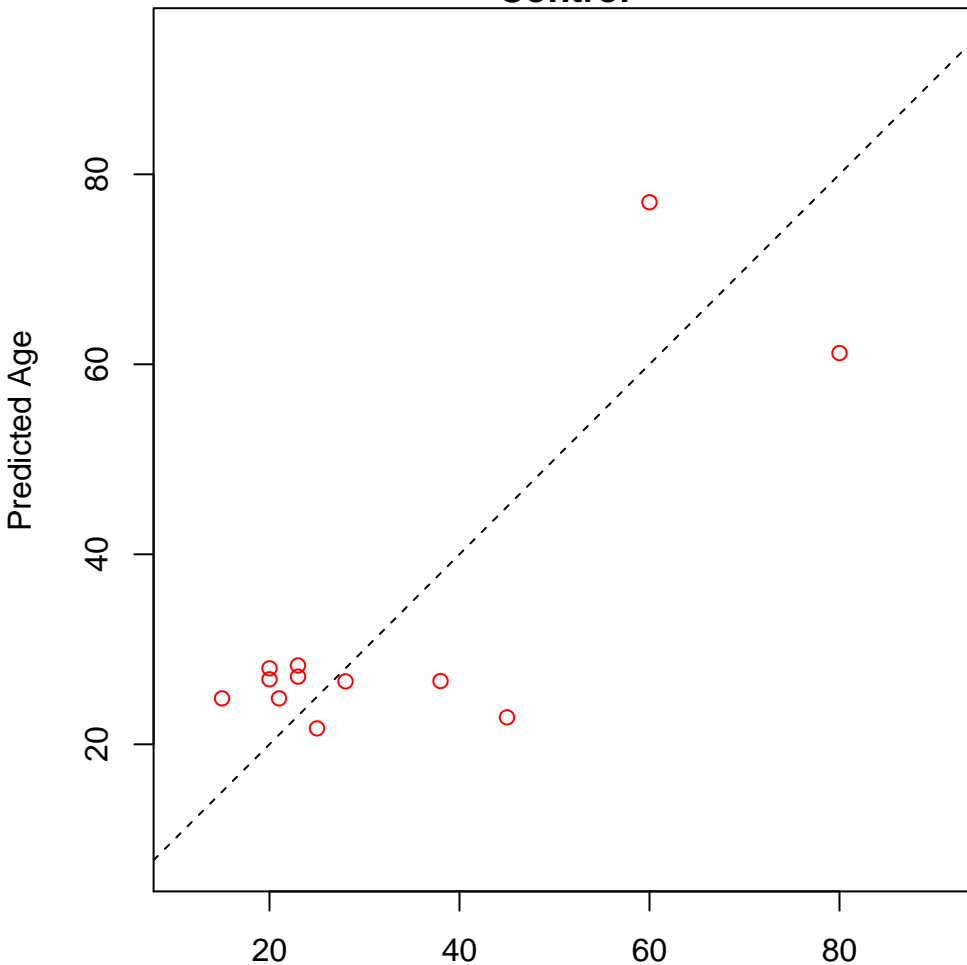


positive regulation of cyclin–dependent protein kinase activity (Score: 5.243996)

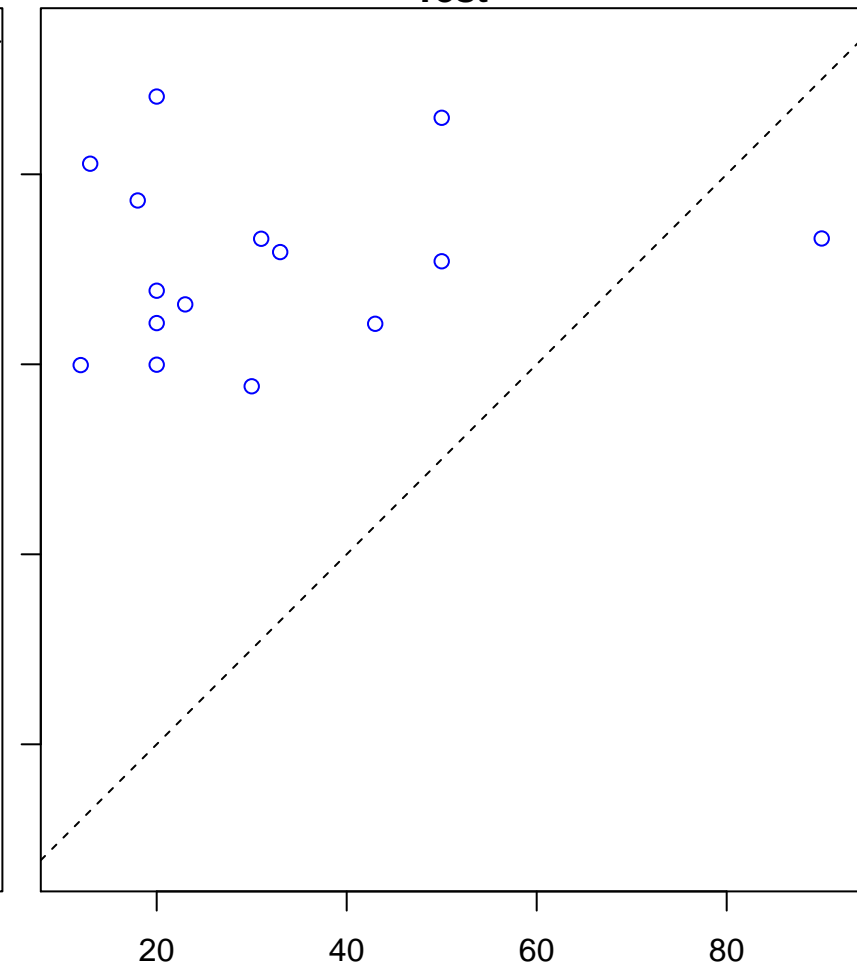


response to molecule of bacterial origin (Score: 5.243743)

Control

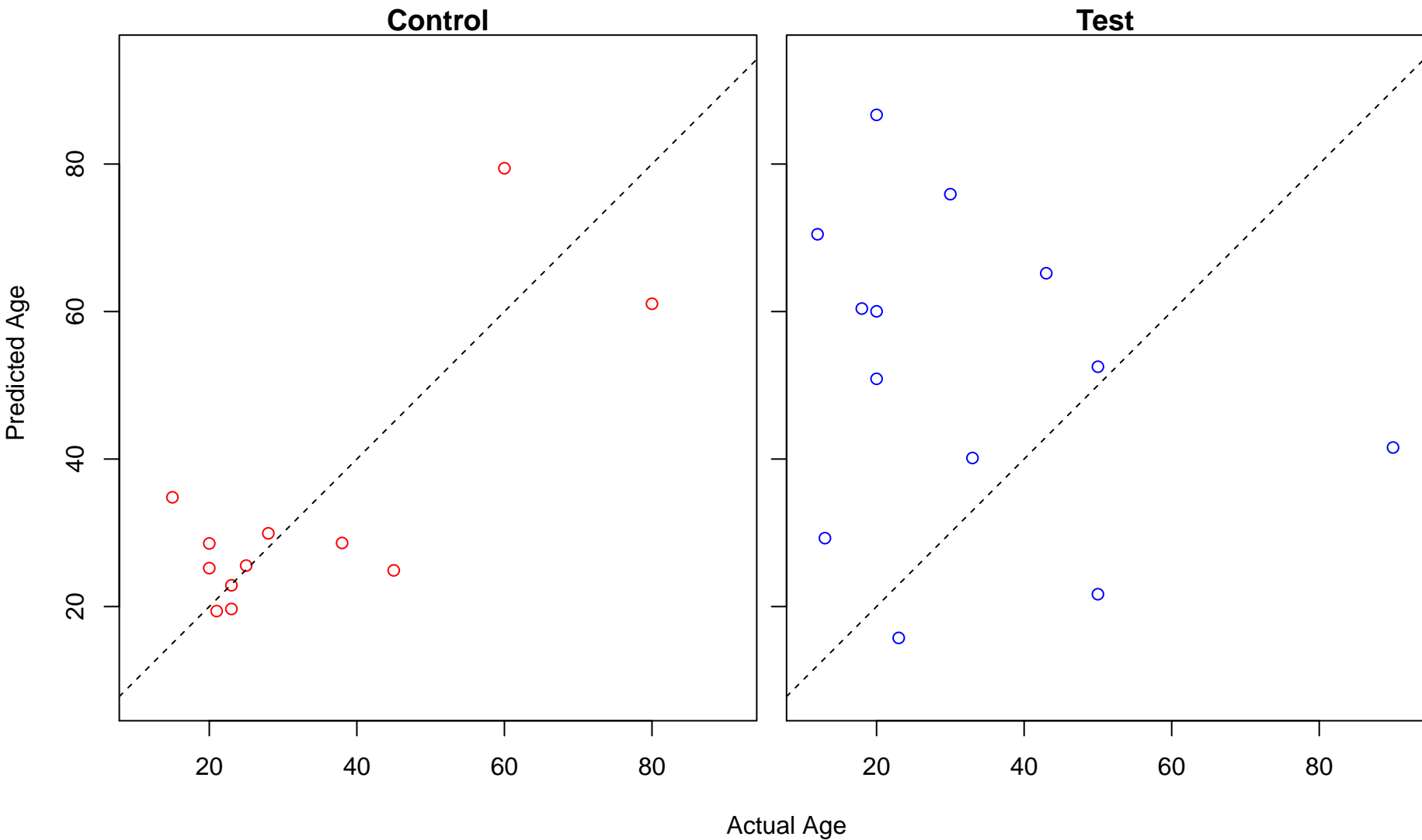


Test

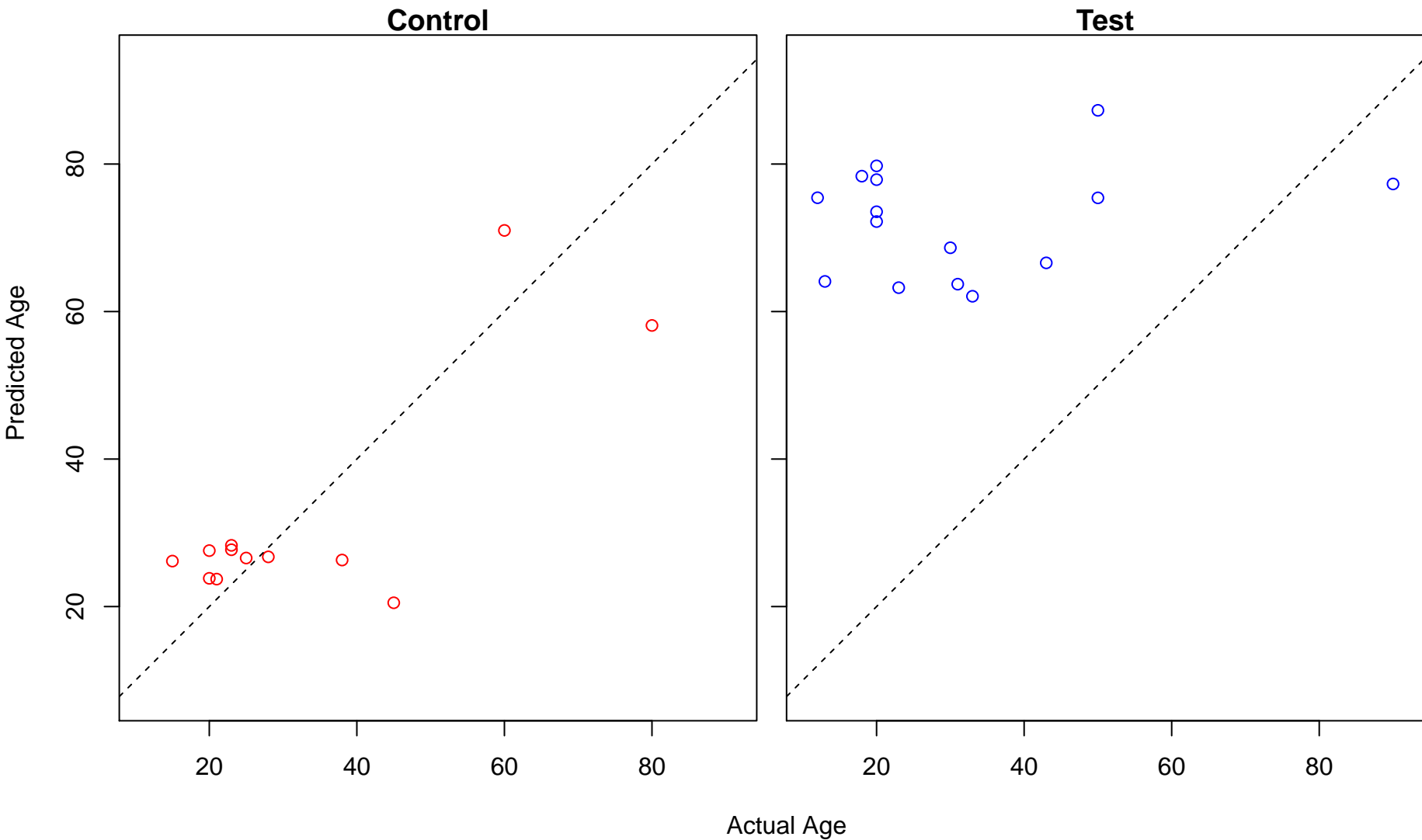


Actual Age

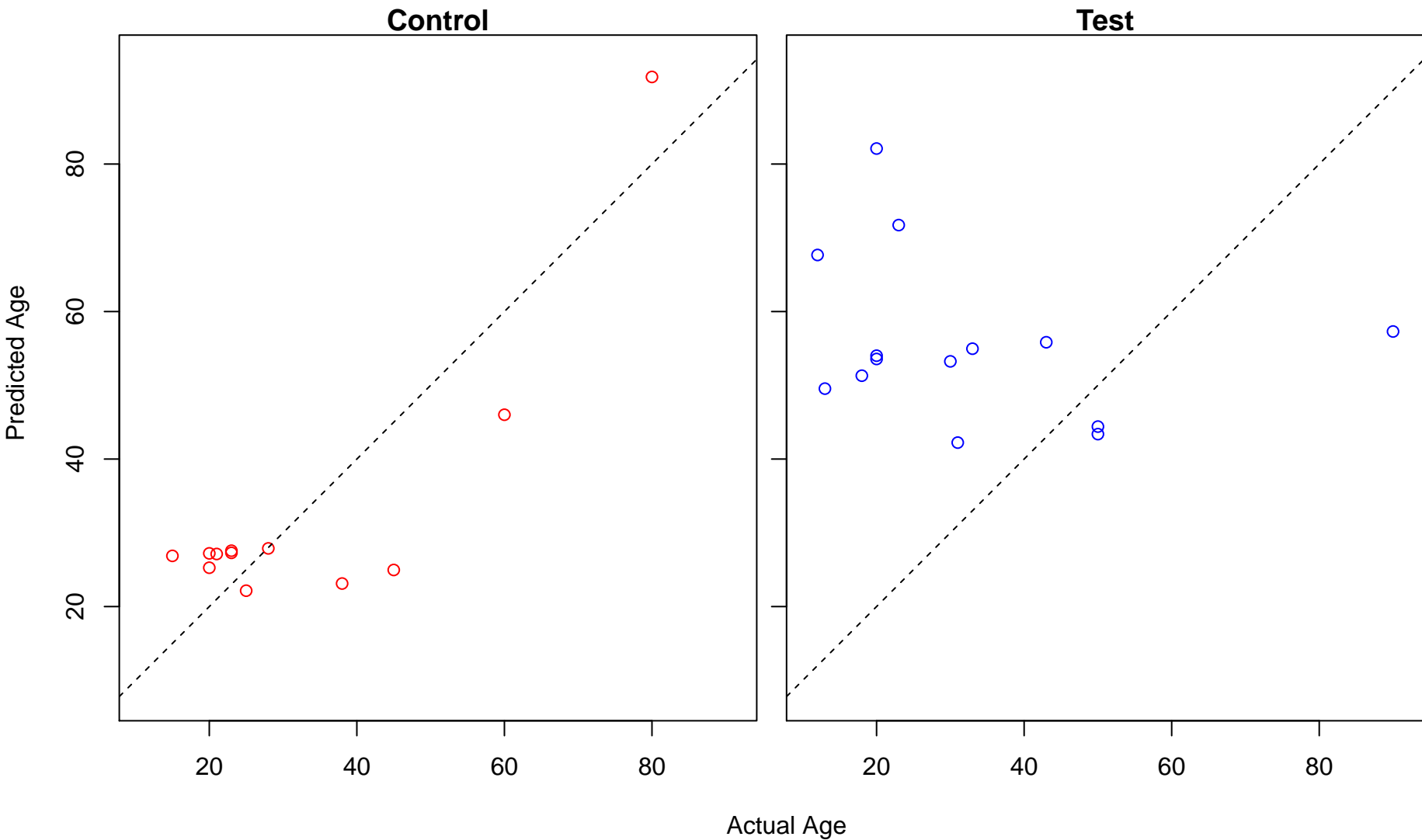
positive regulation of interleukin-6 production (Score: 5.241165)



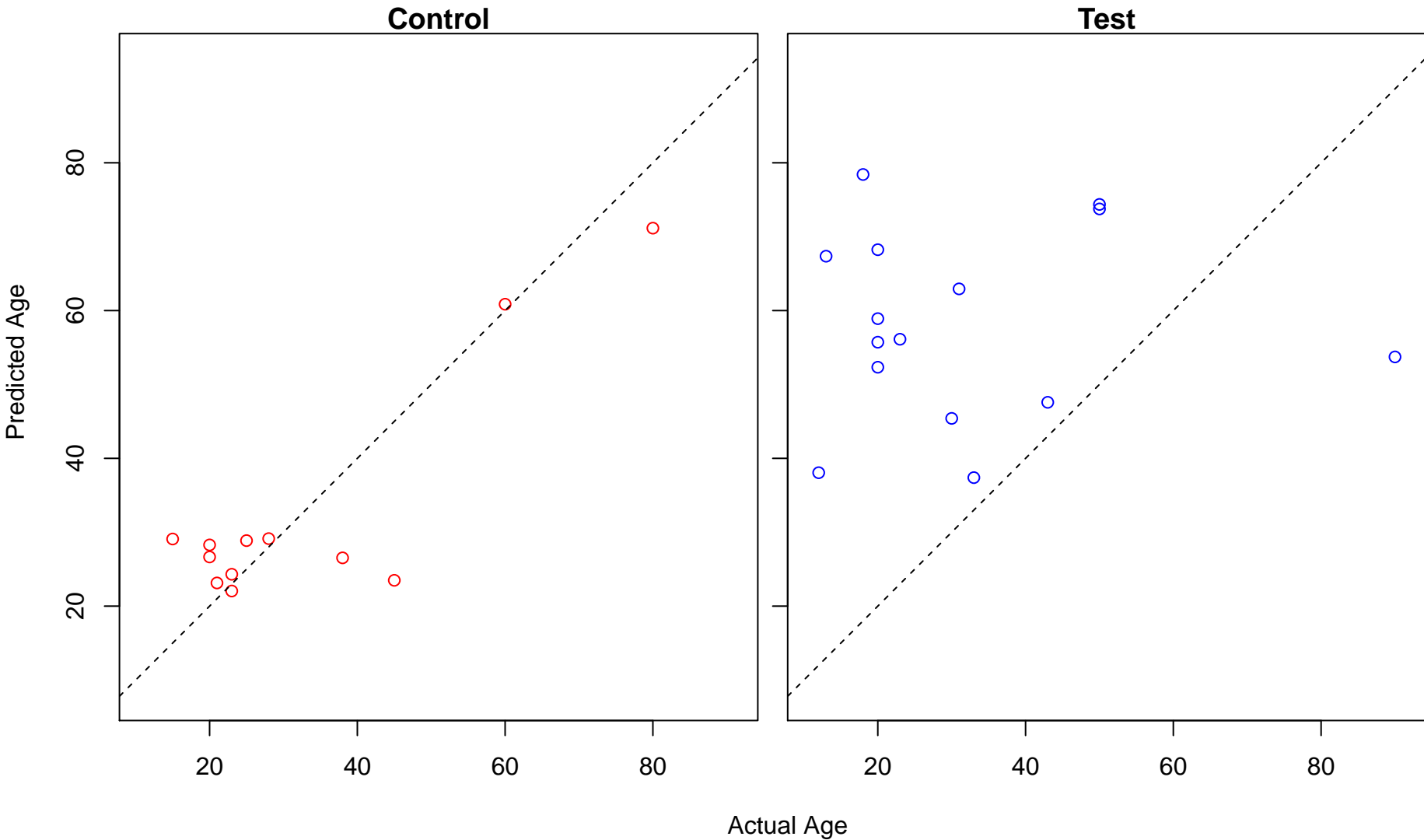
odontogenesis (Score: 5.239043)



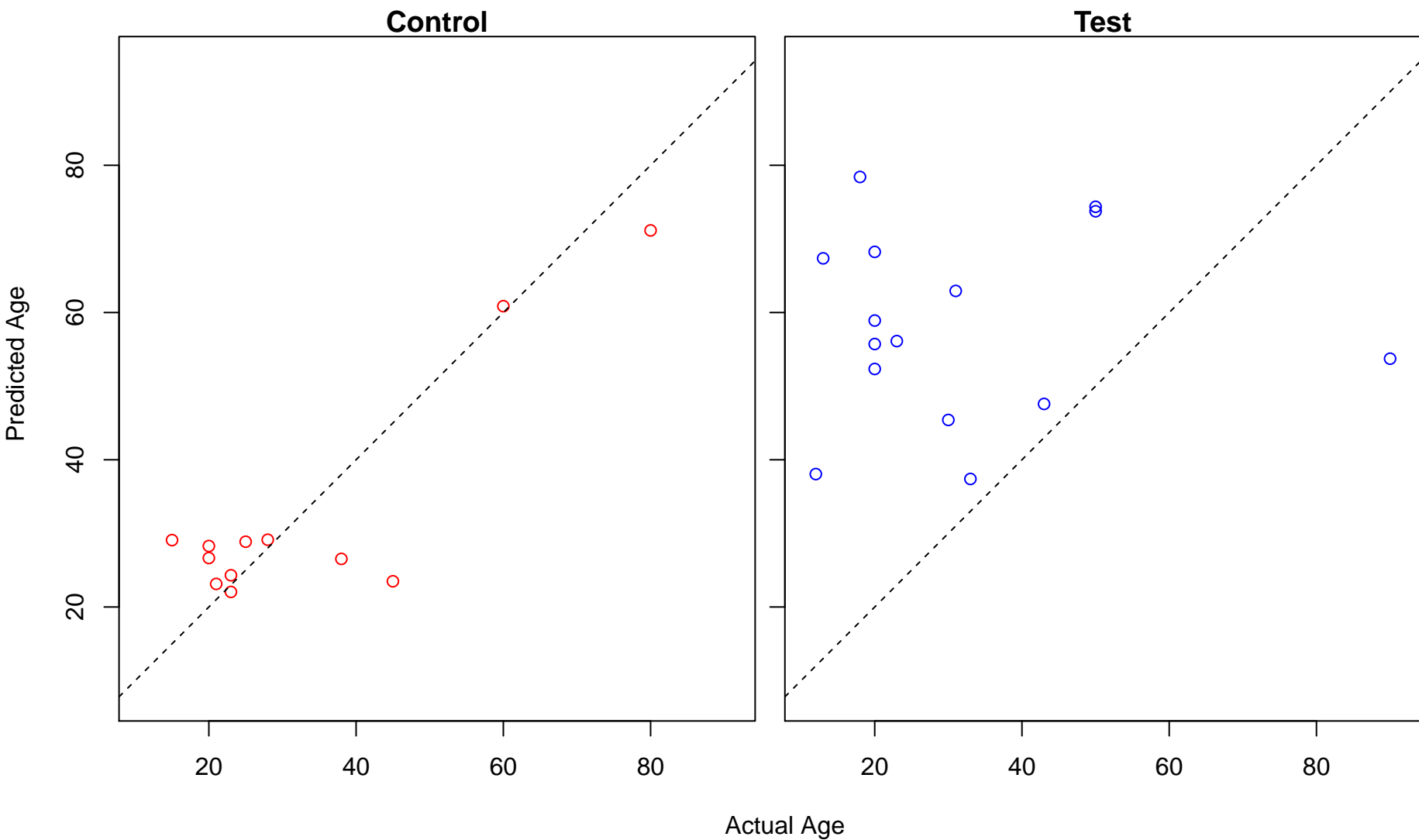
DNA strand elongation involved in DNA replication (Score: 5.235878)



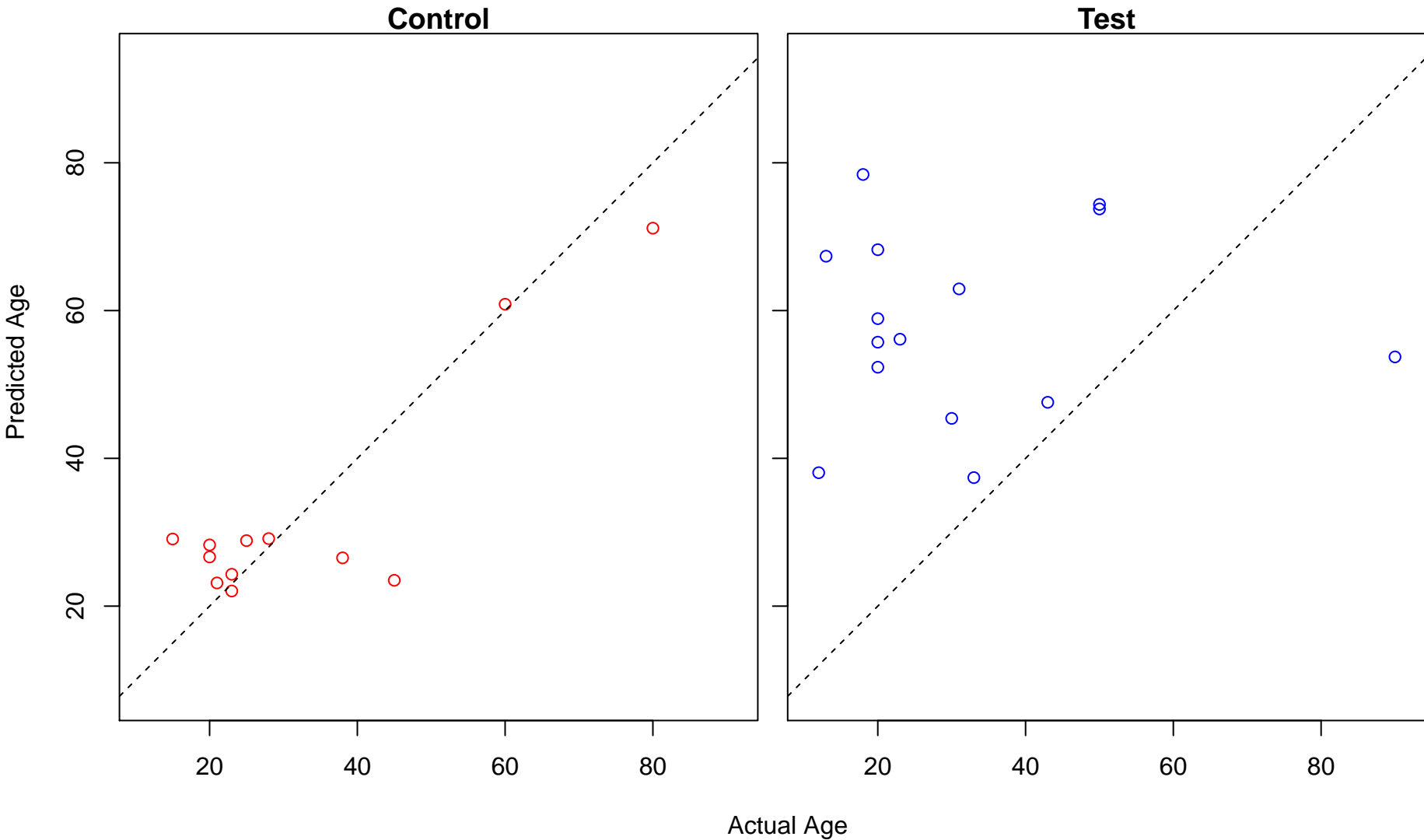
glycolytic process through fructose-6-phosphate (Score: 5.234130)



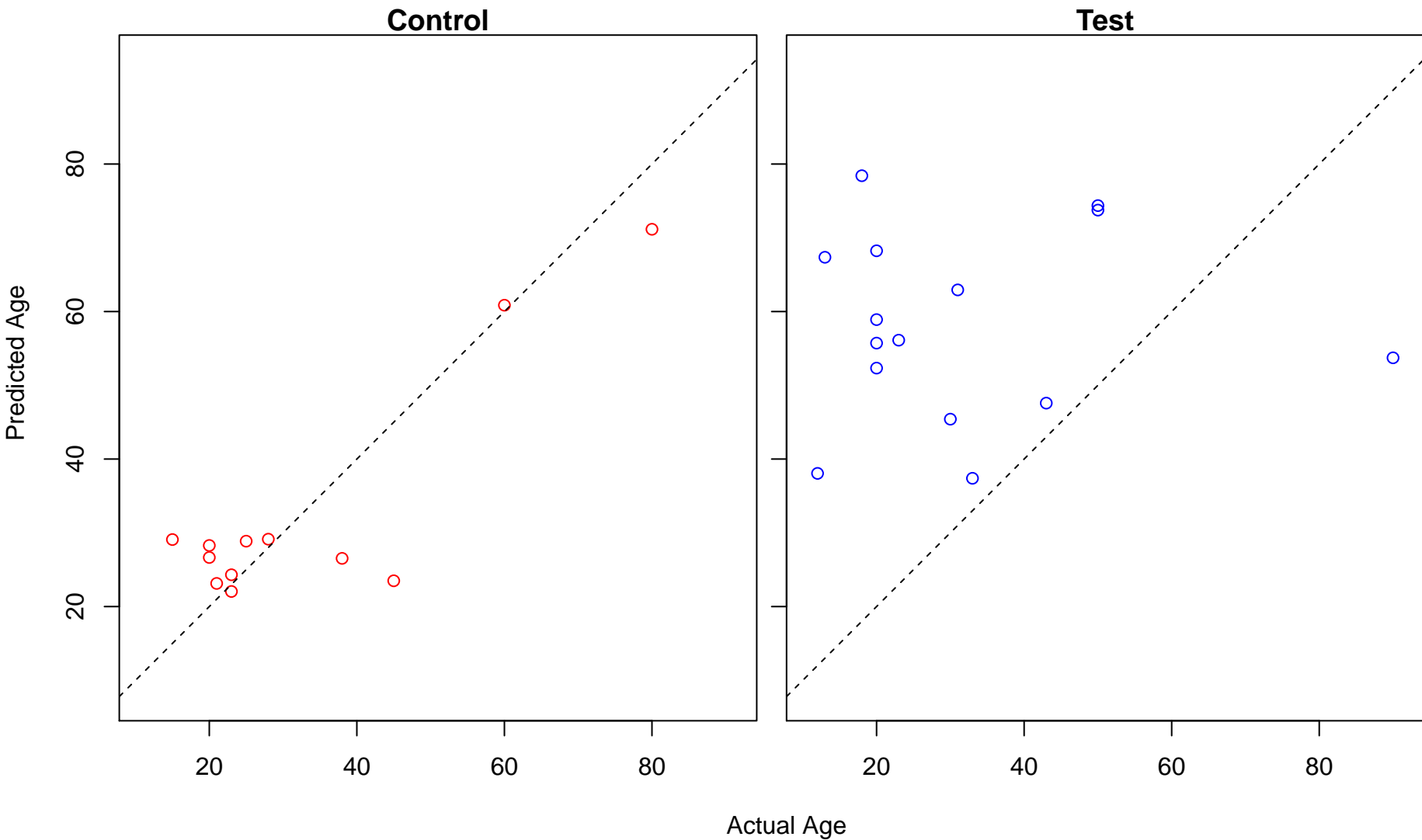
NADH regeneration (Score: 5.234130)



glycolytic process through glucose-6-phosphate (Score: 5.234130)

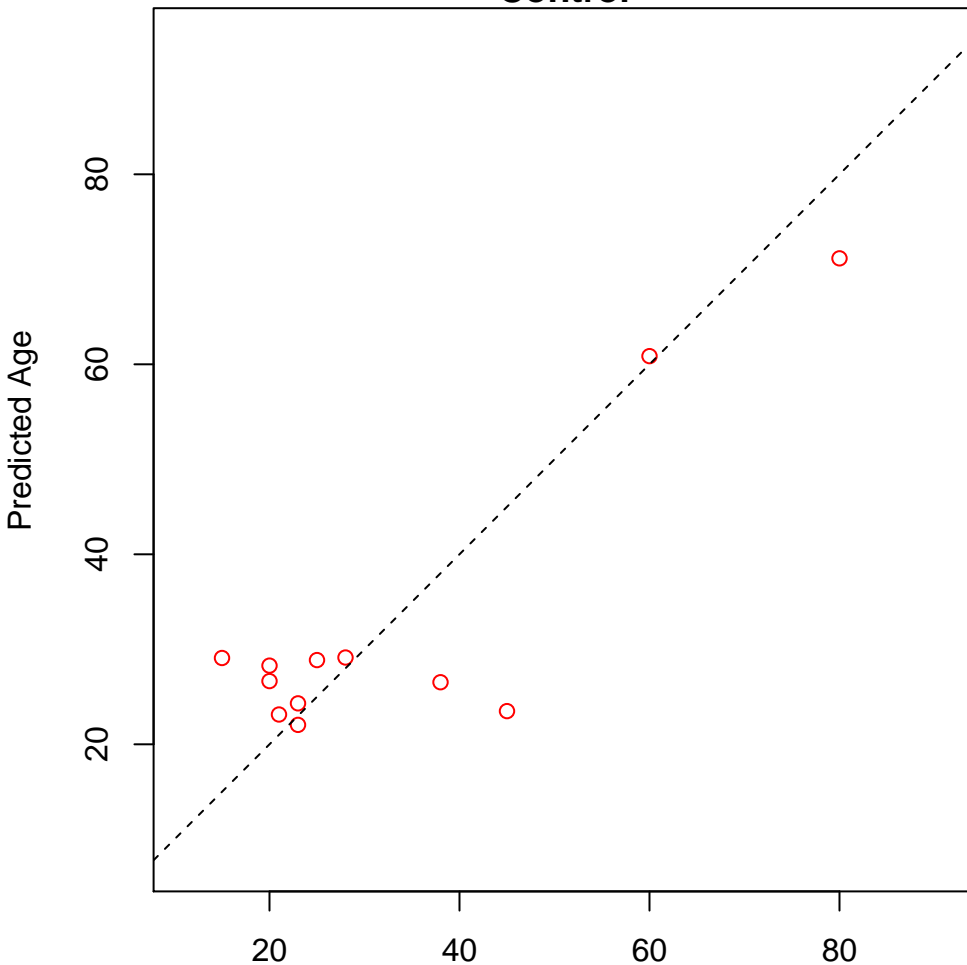


canonical glycolysis (Score: 5.234130)

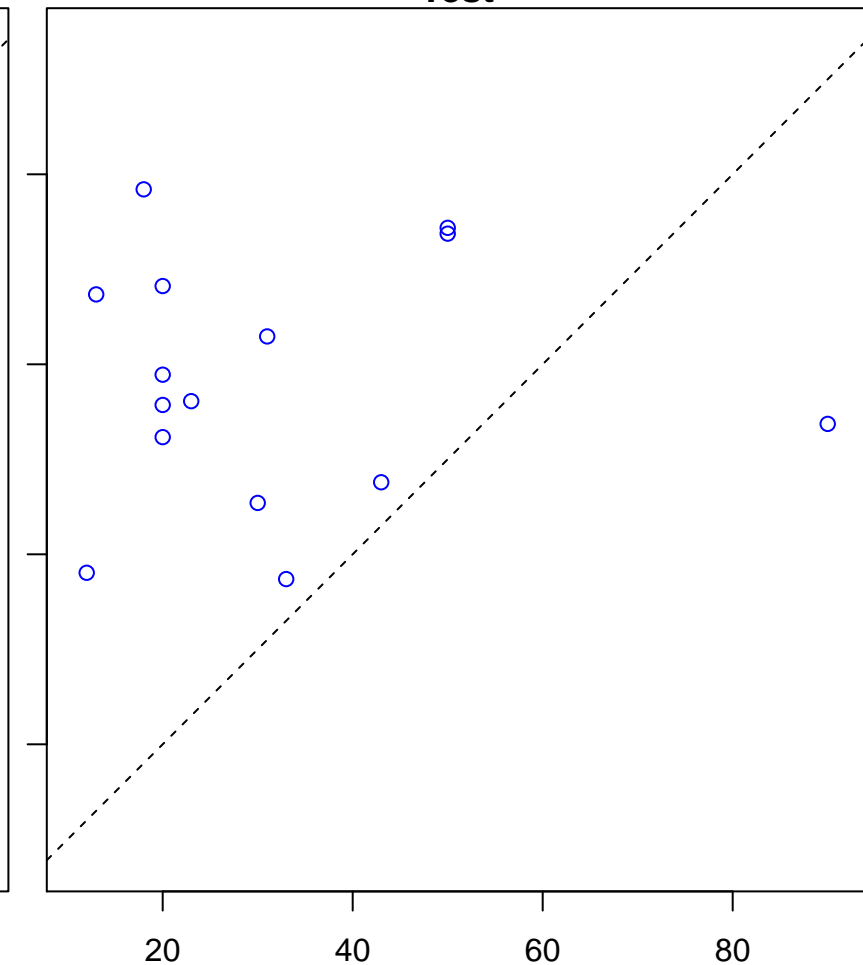


glucose catabolic process to pyruvate (Score: 5.234130)

Control

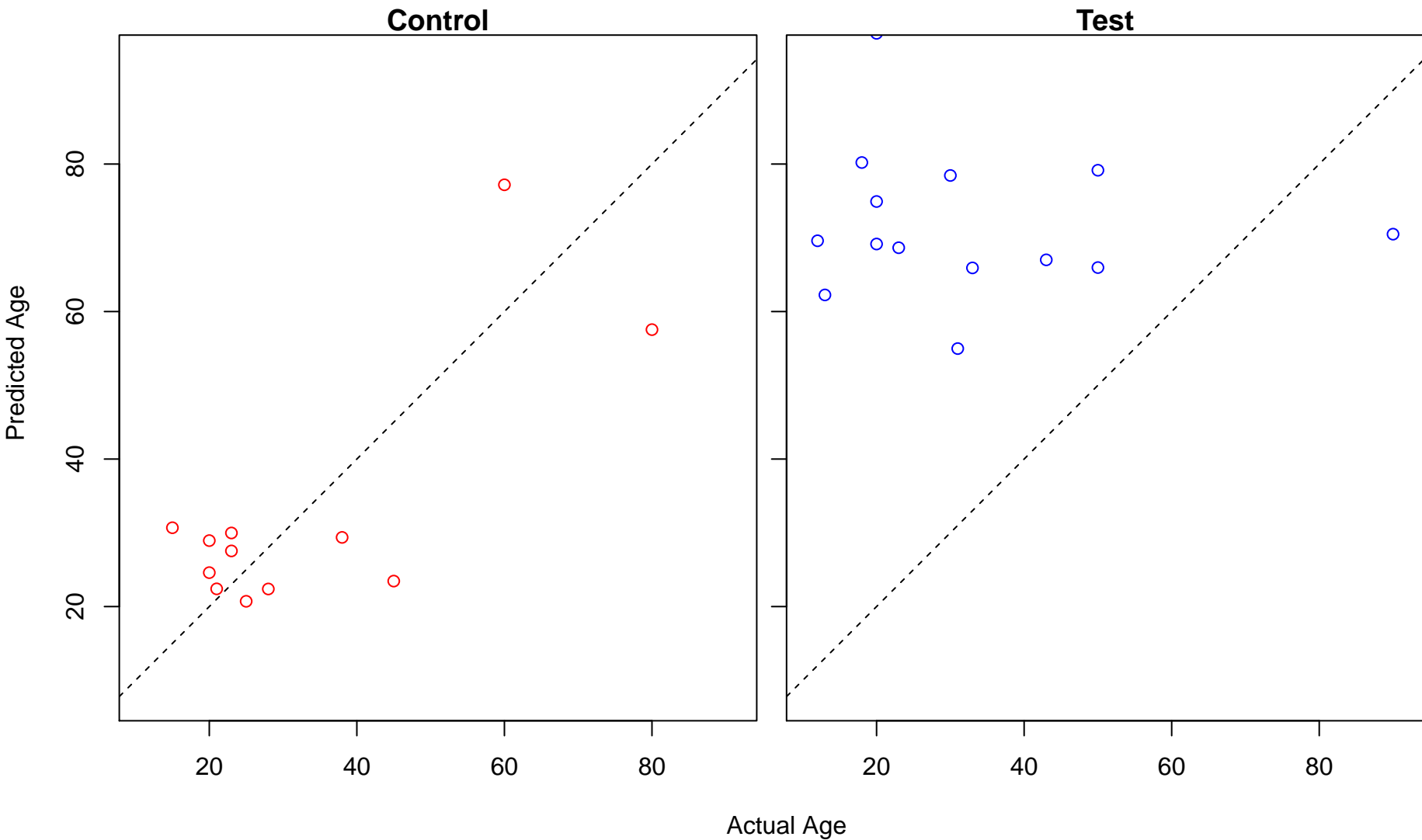


Test

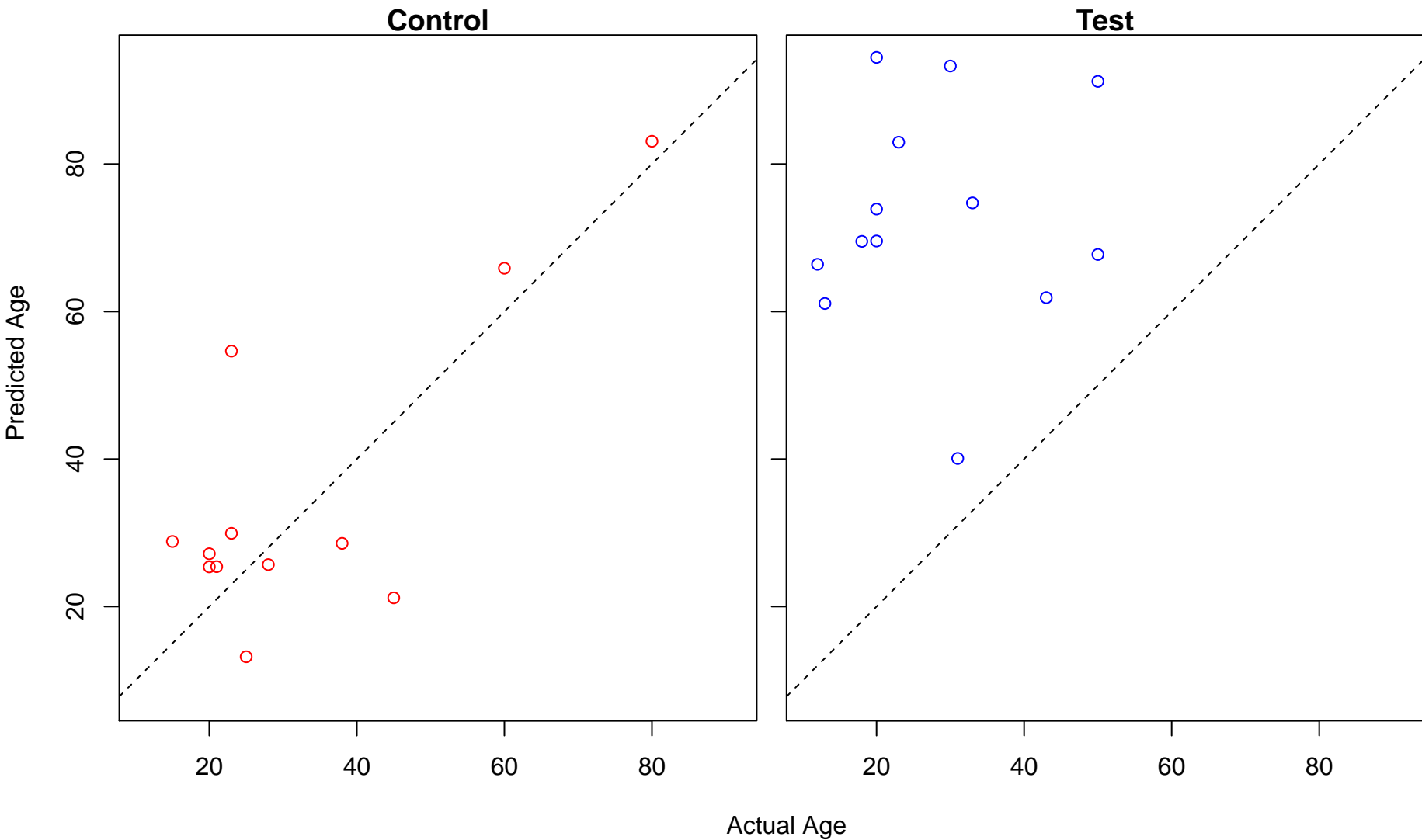


Actual Age

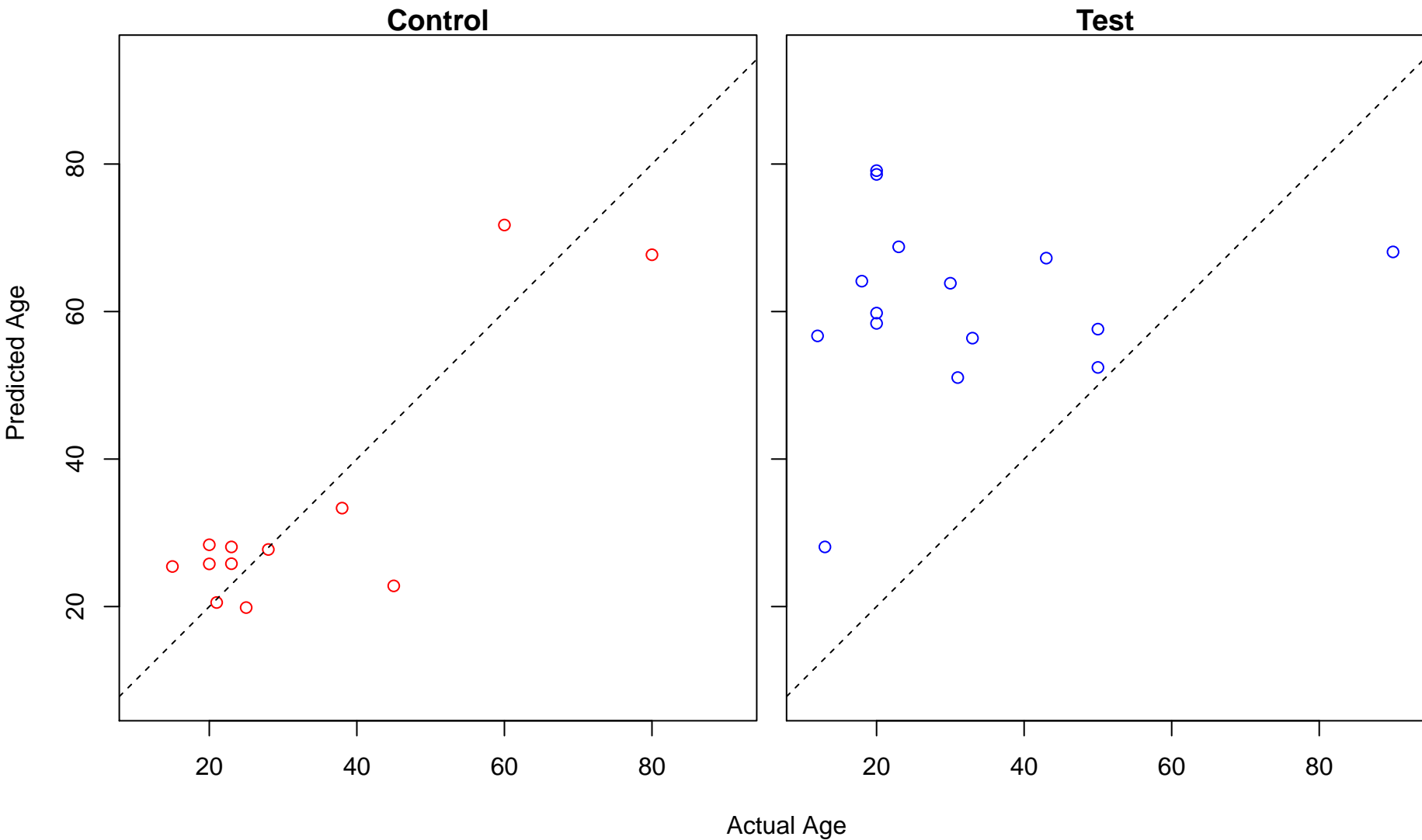
regulation of synaptic transmission, GABAergic (Score: 5.232014)



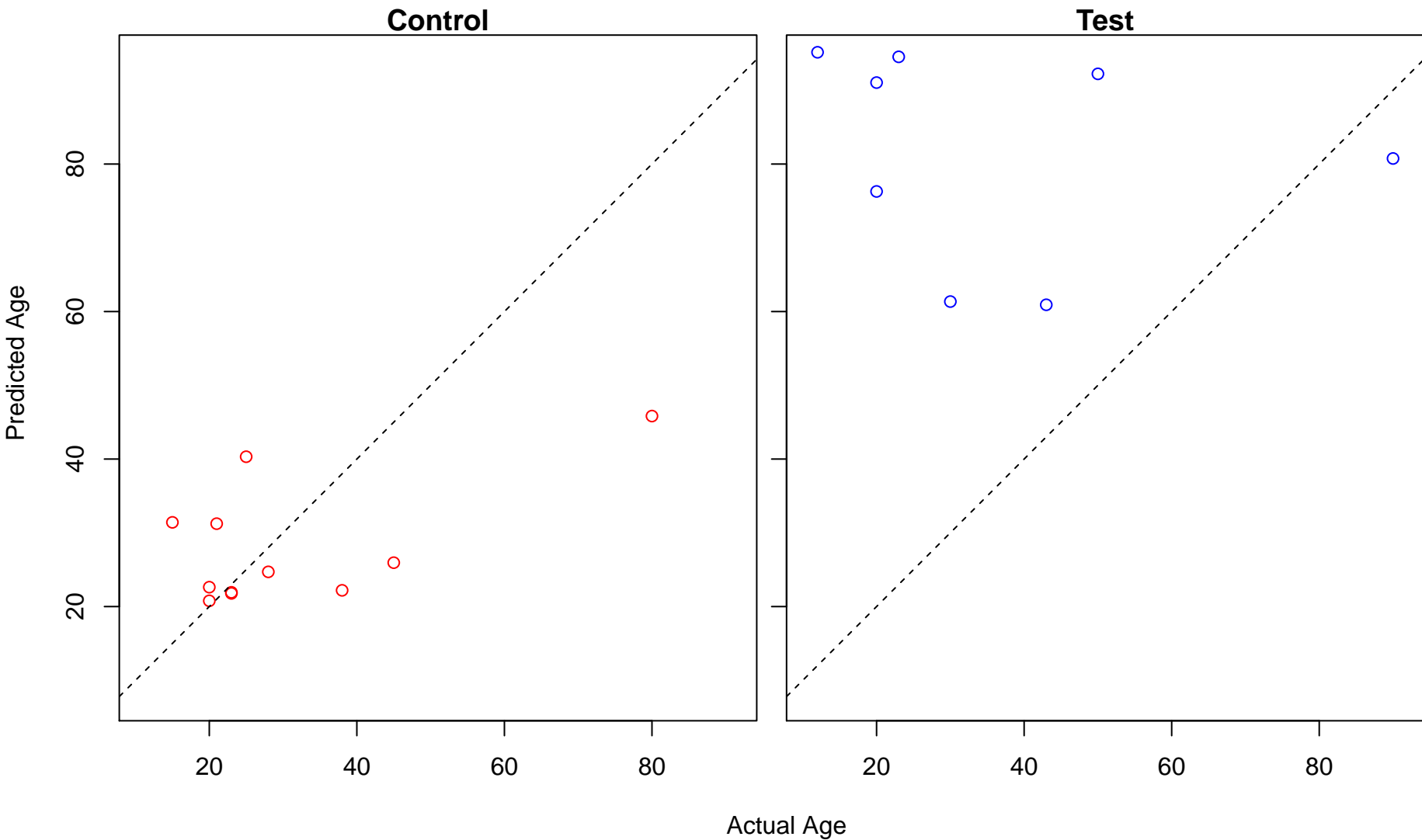
regulation of cellular extravasation (Score: 5.231094)



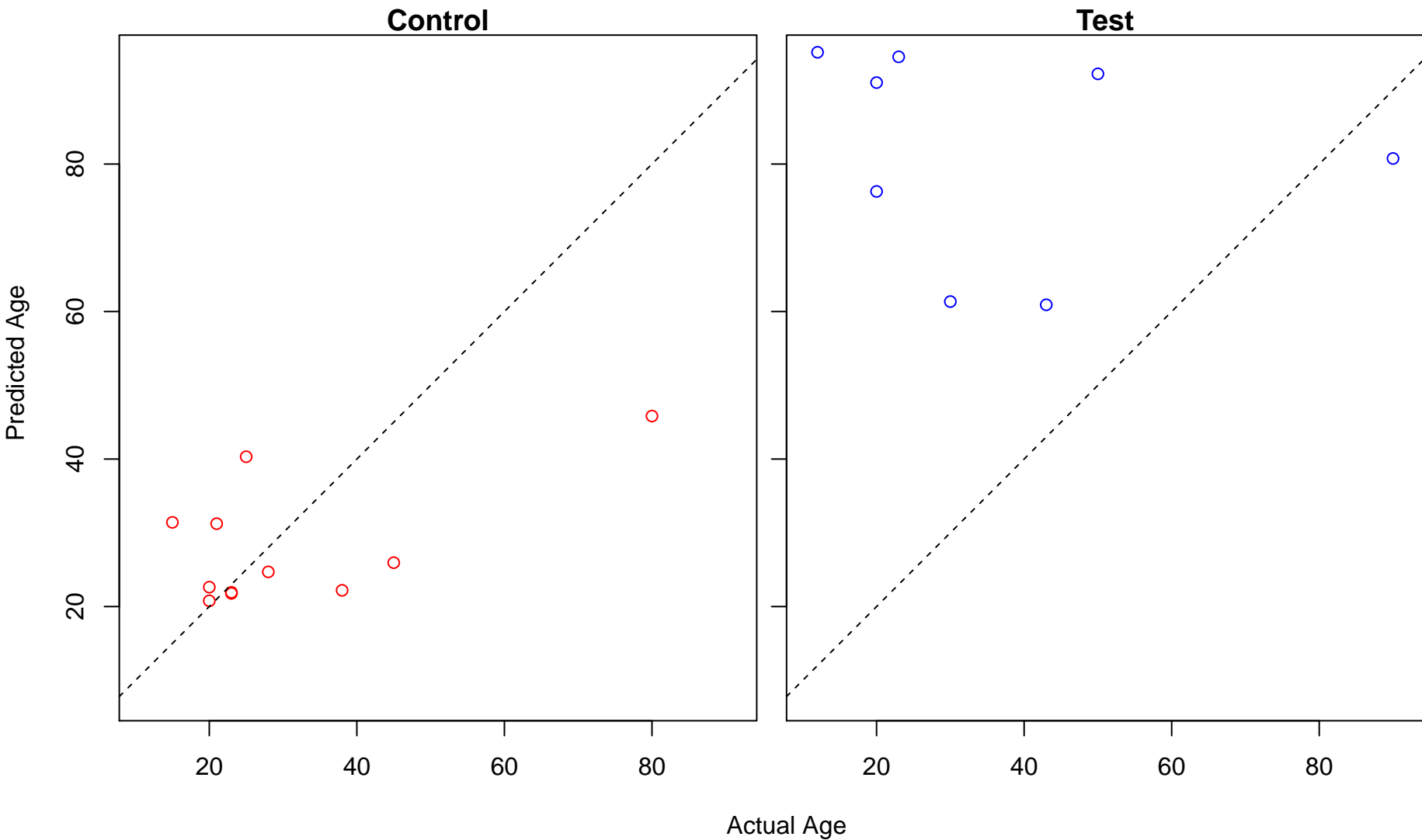
white fat cell differentiation (Score: 5.231050)



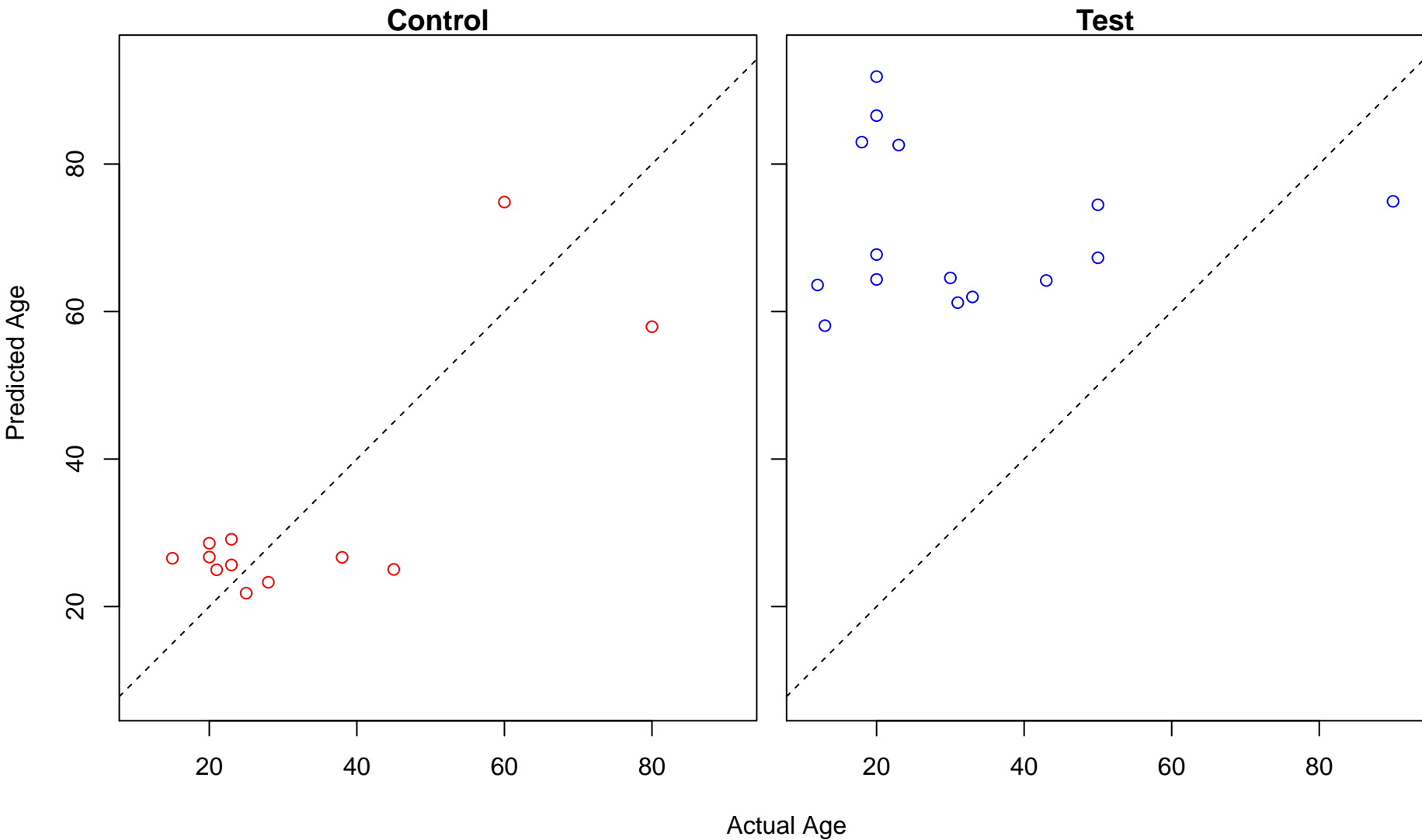
mitotic spindle elongation (Score: 5.228510)



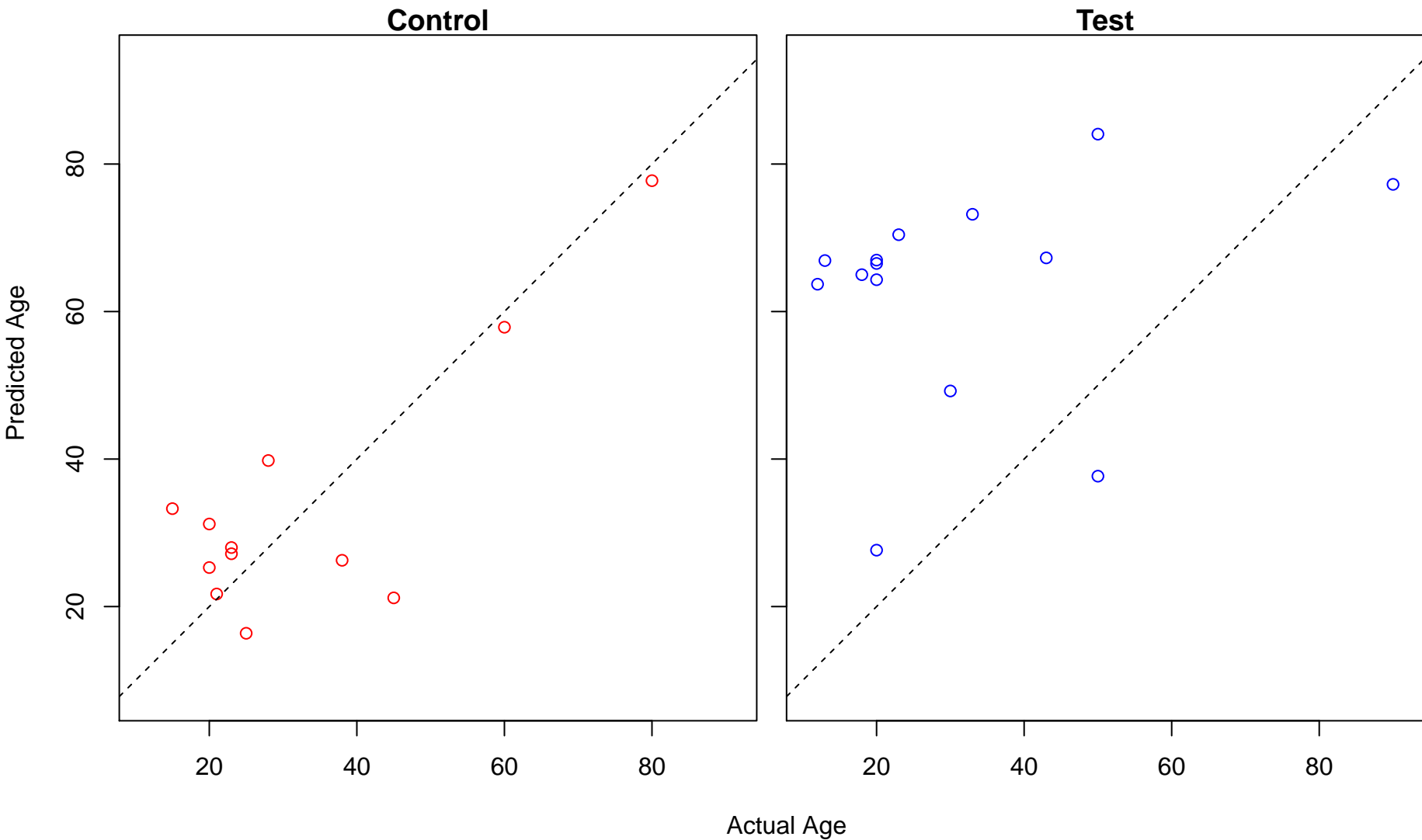
spindle elongation (Score: 5.228510)



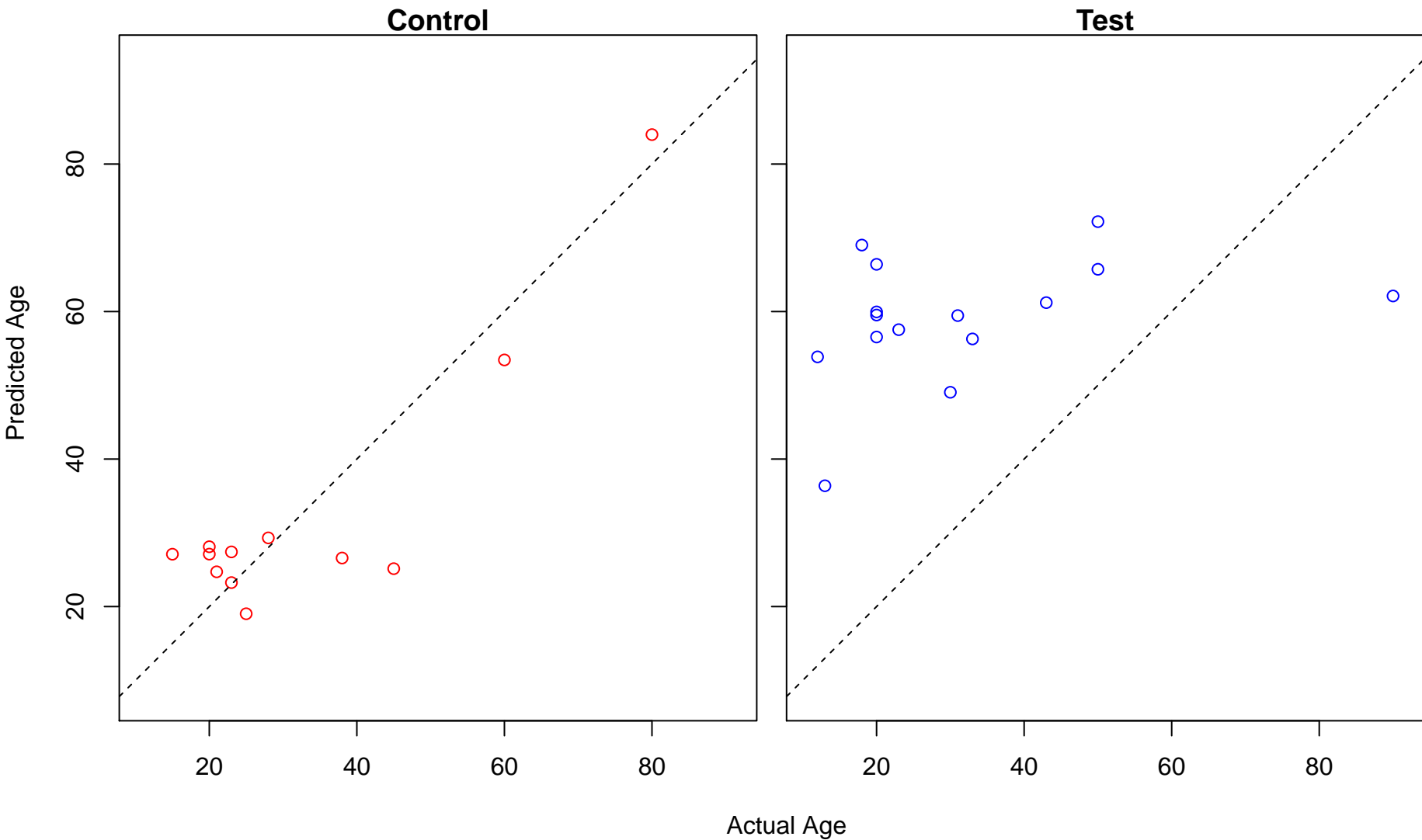
dopamine metabolic process (Score: 5.226971)



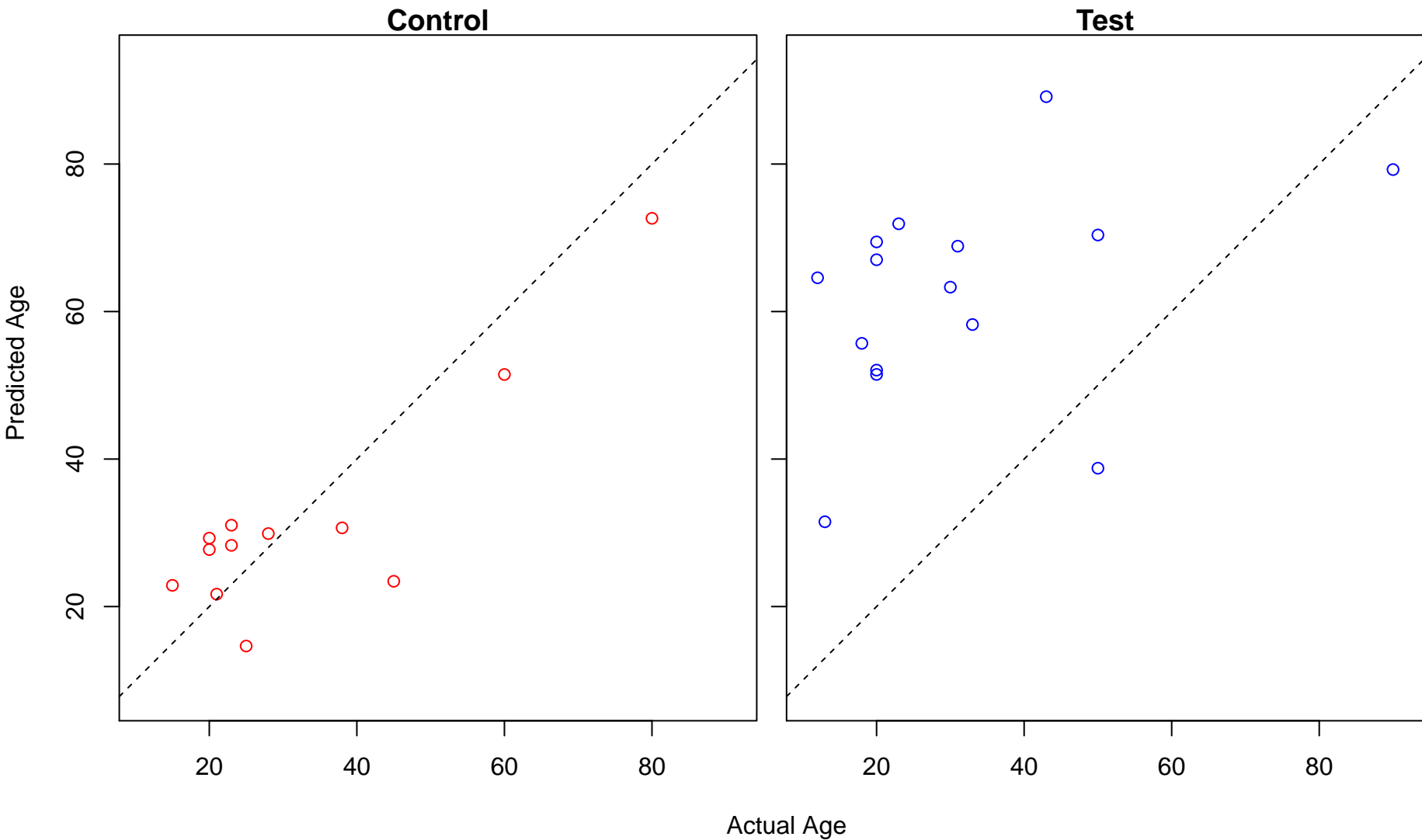
negative regulation of neuron projection development (Score: 5.226589)



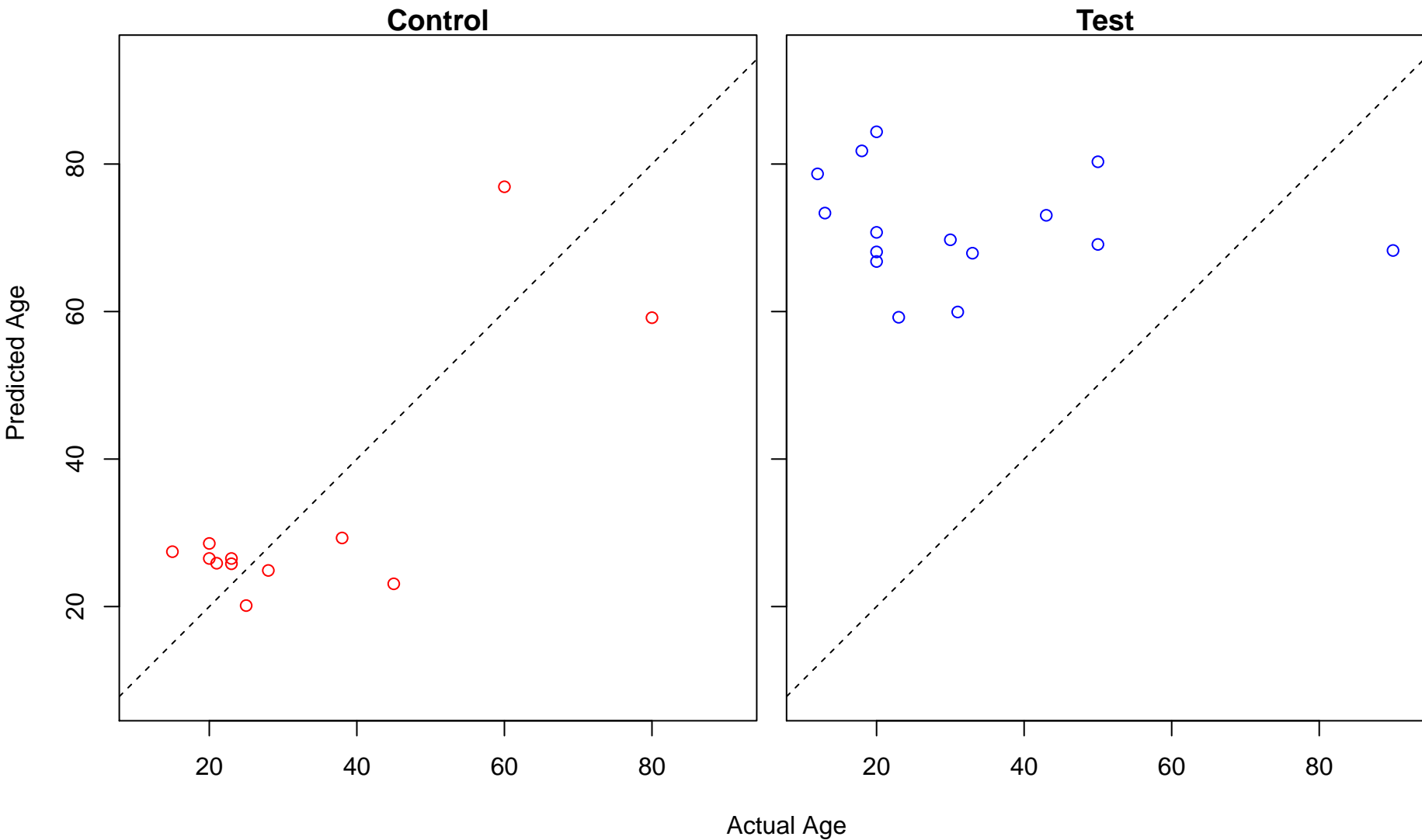
tRNA metabolic process (Score: 5.226477)



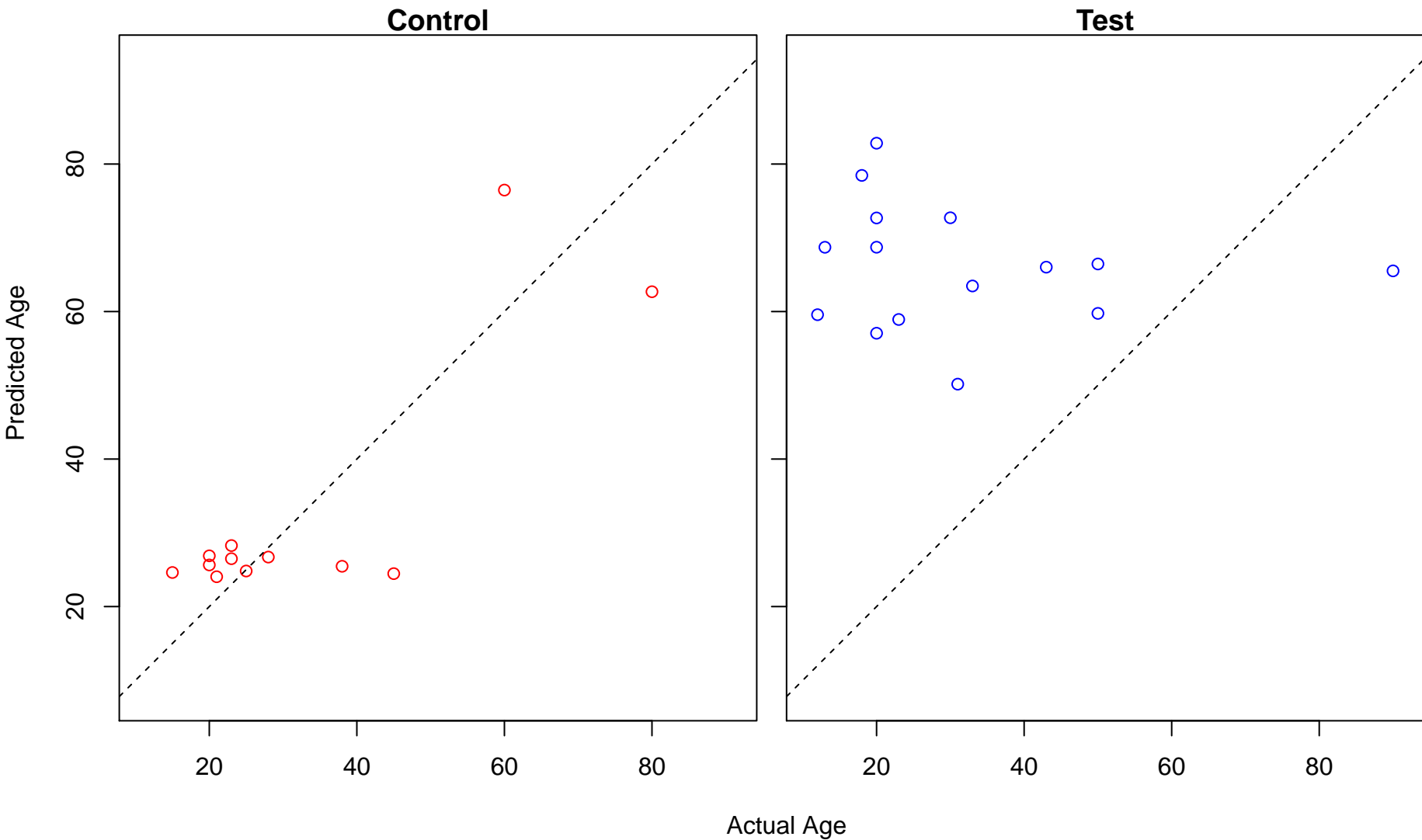
microtubule anchoring (Score: 5.226347)



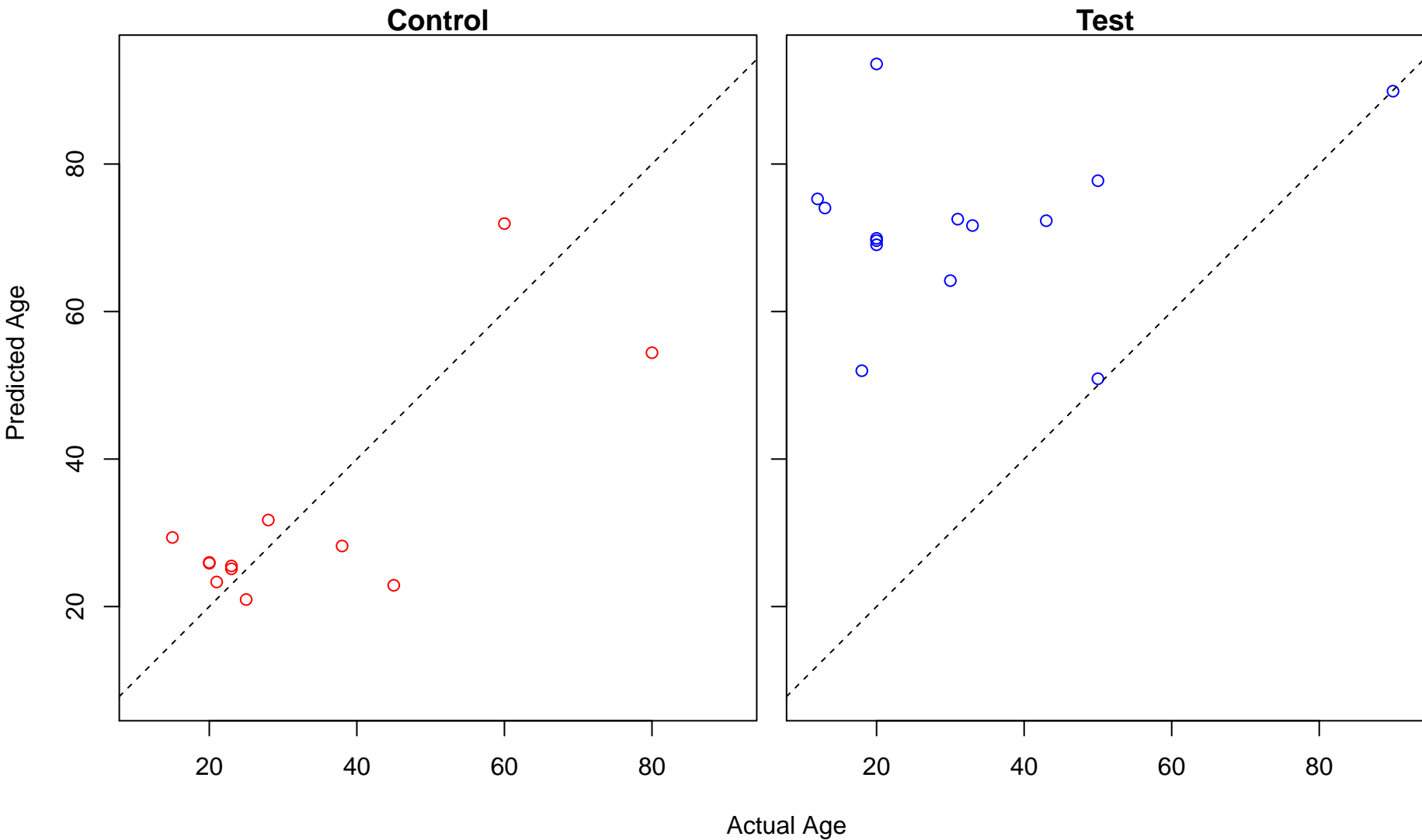
glutamate metabolic process (Score: 5.224303)



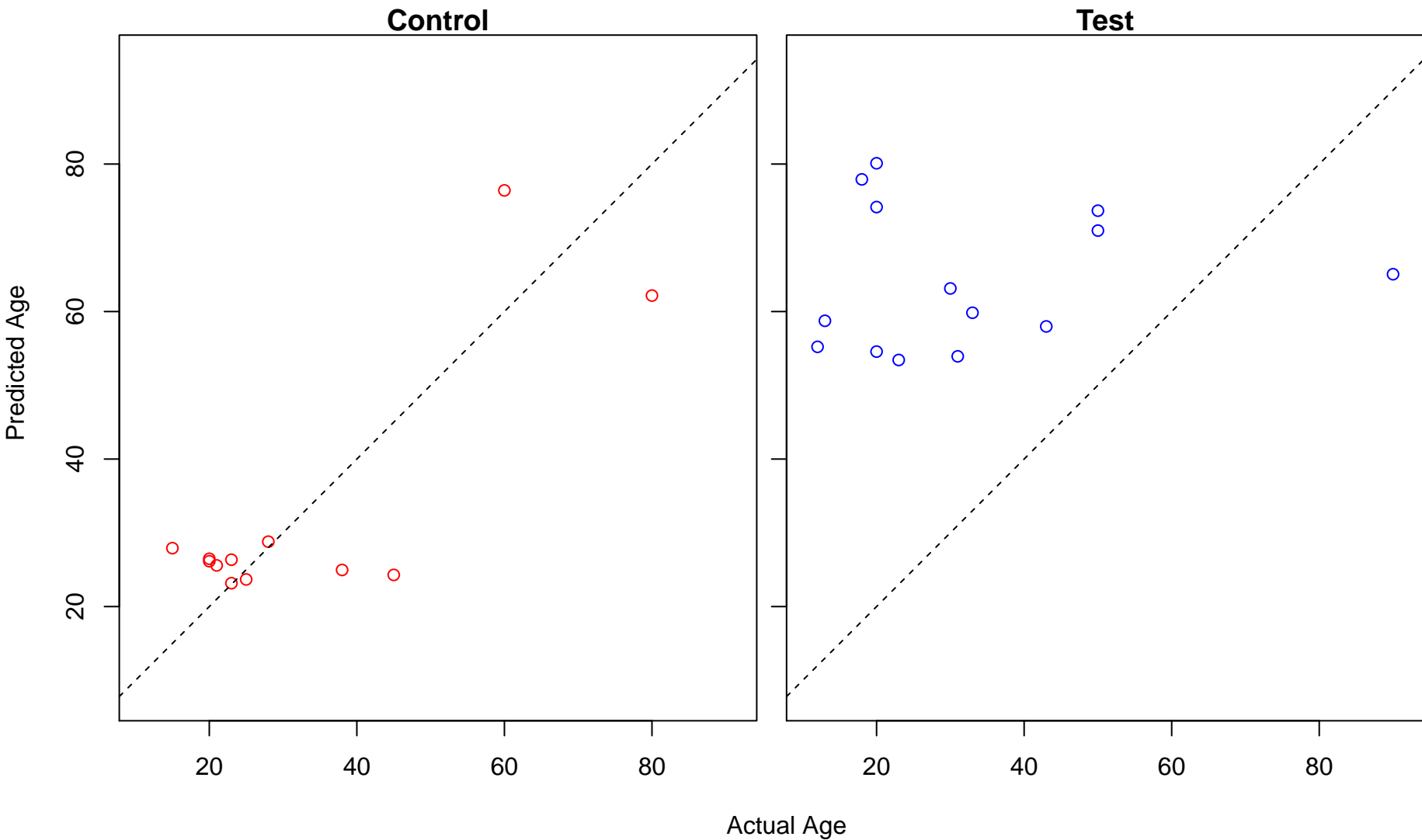
peptide hormone processing (Score: 5.223696)



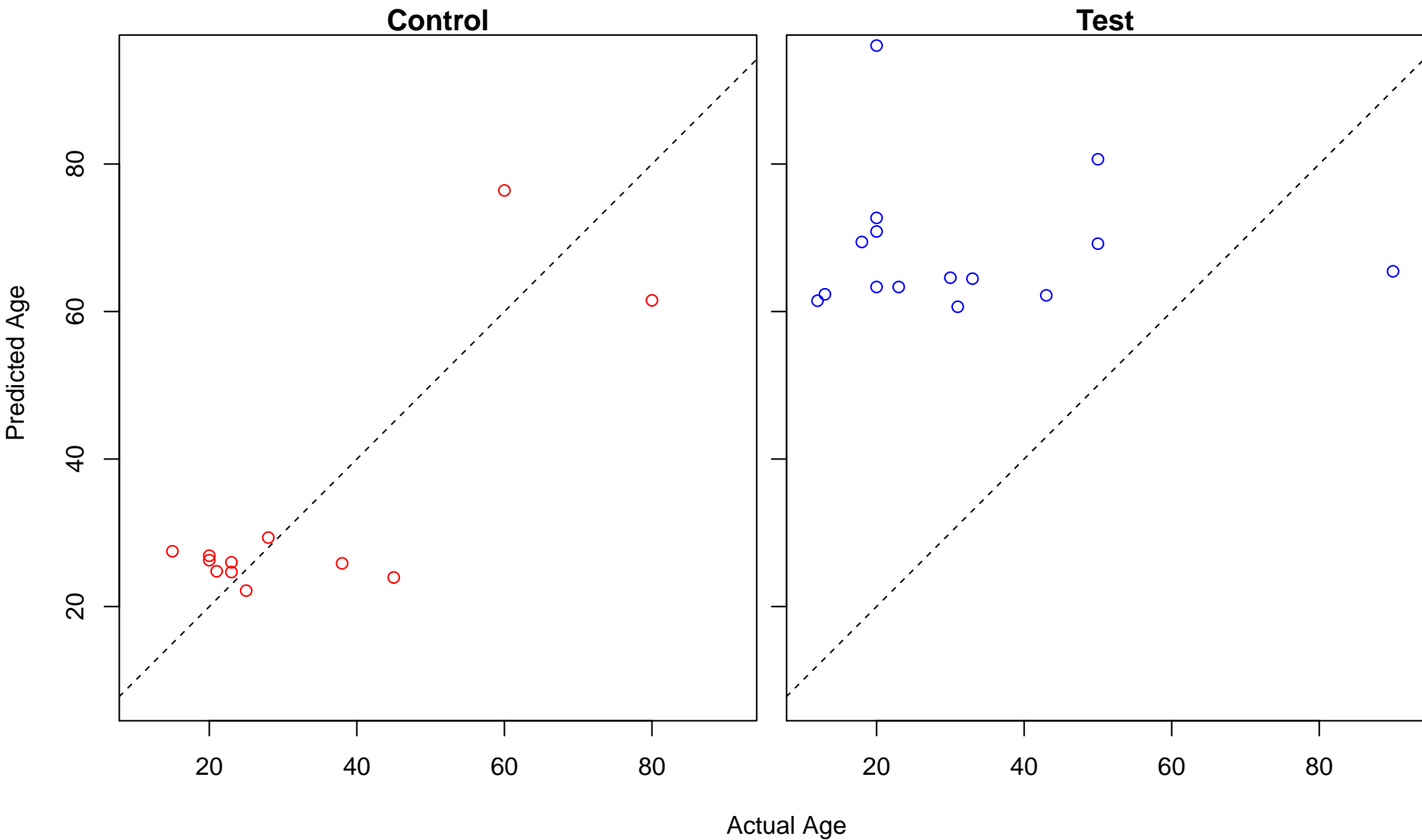
negative regulation of interleukin-6 secretion (Score: 5.223549)



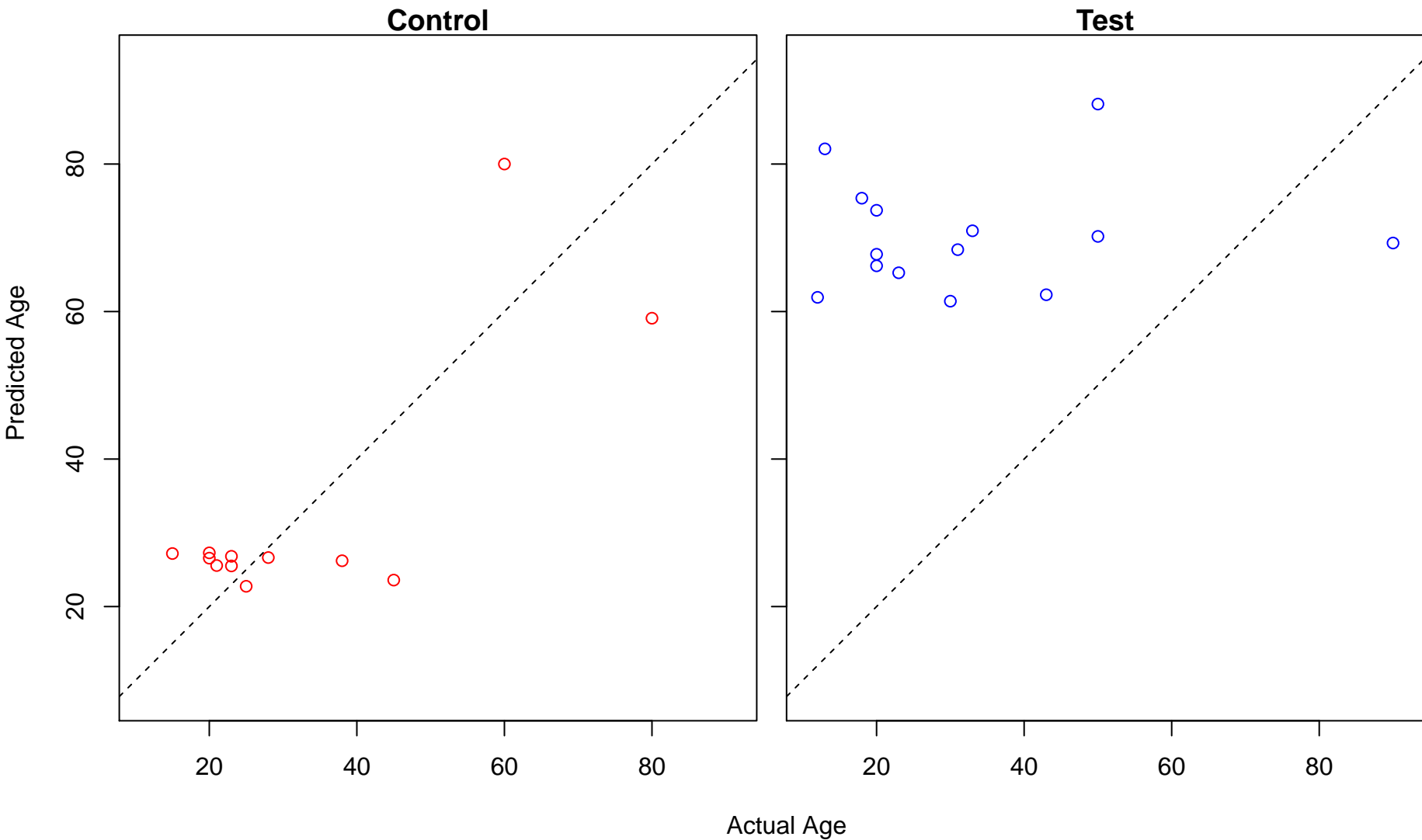
positive regulation of G2/M transition of mitotic cell cycle (Score: 5.222124)



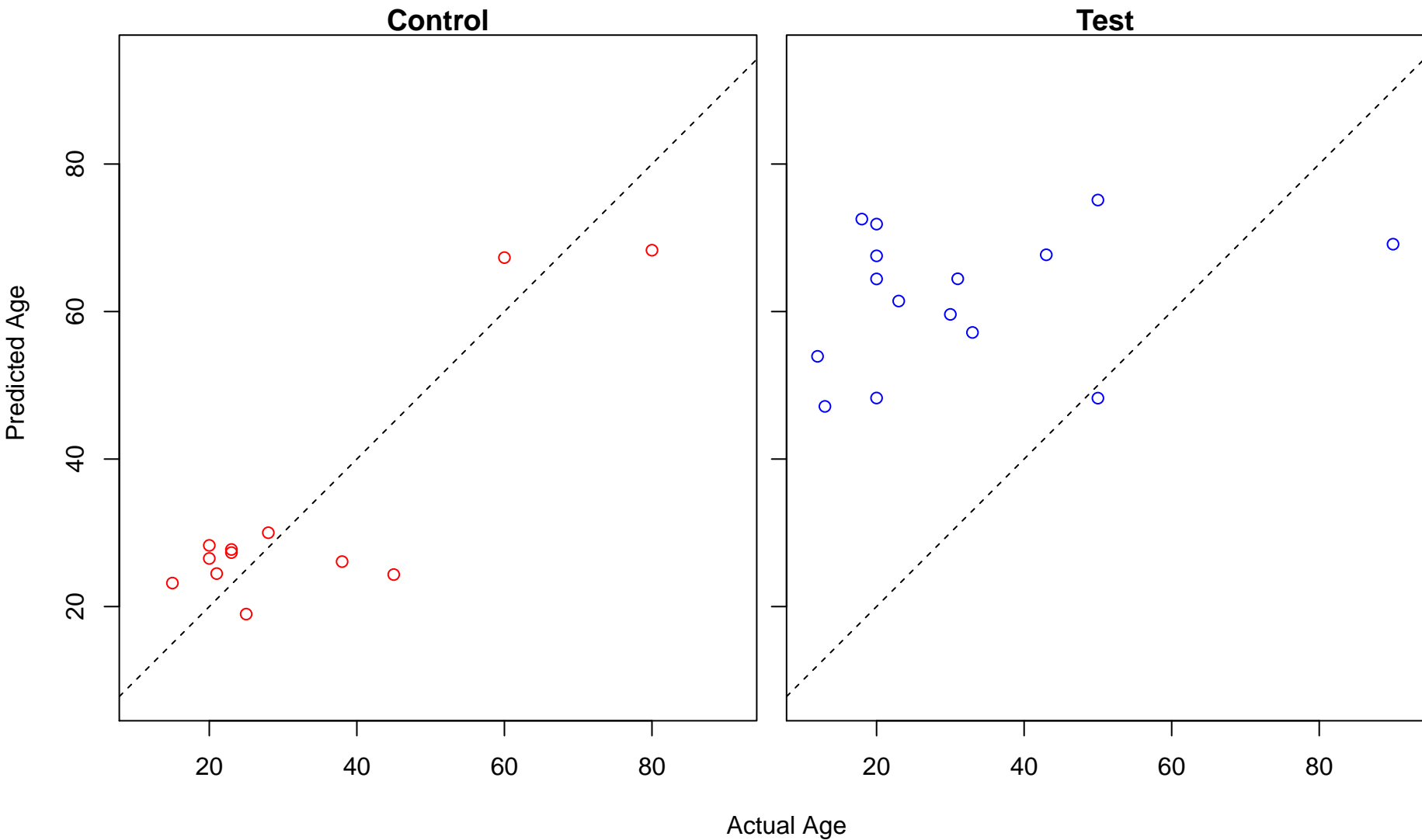
multicellular organismal reproductive process (Score: 5.220486)



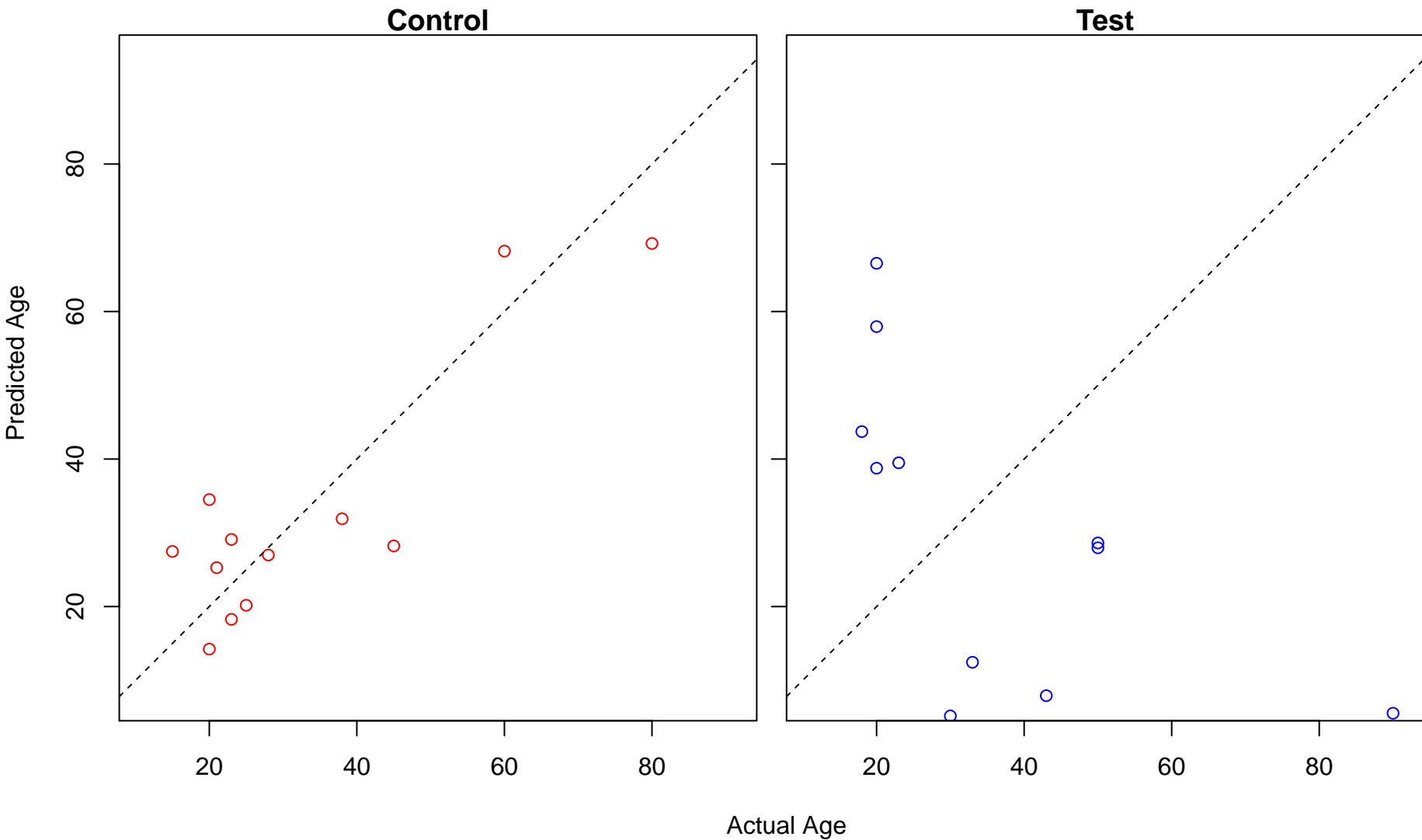
innate immune response-activating signal transduction (Score: 5.220240)



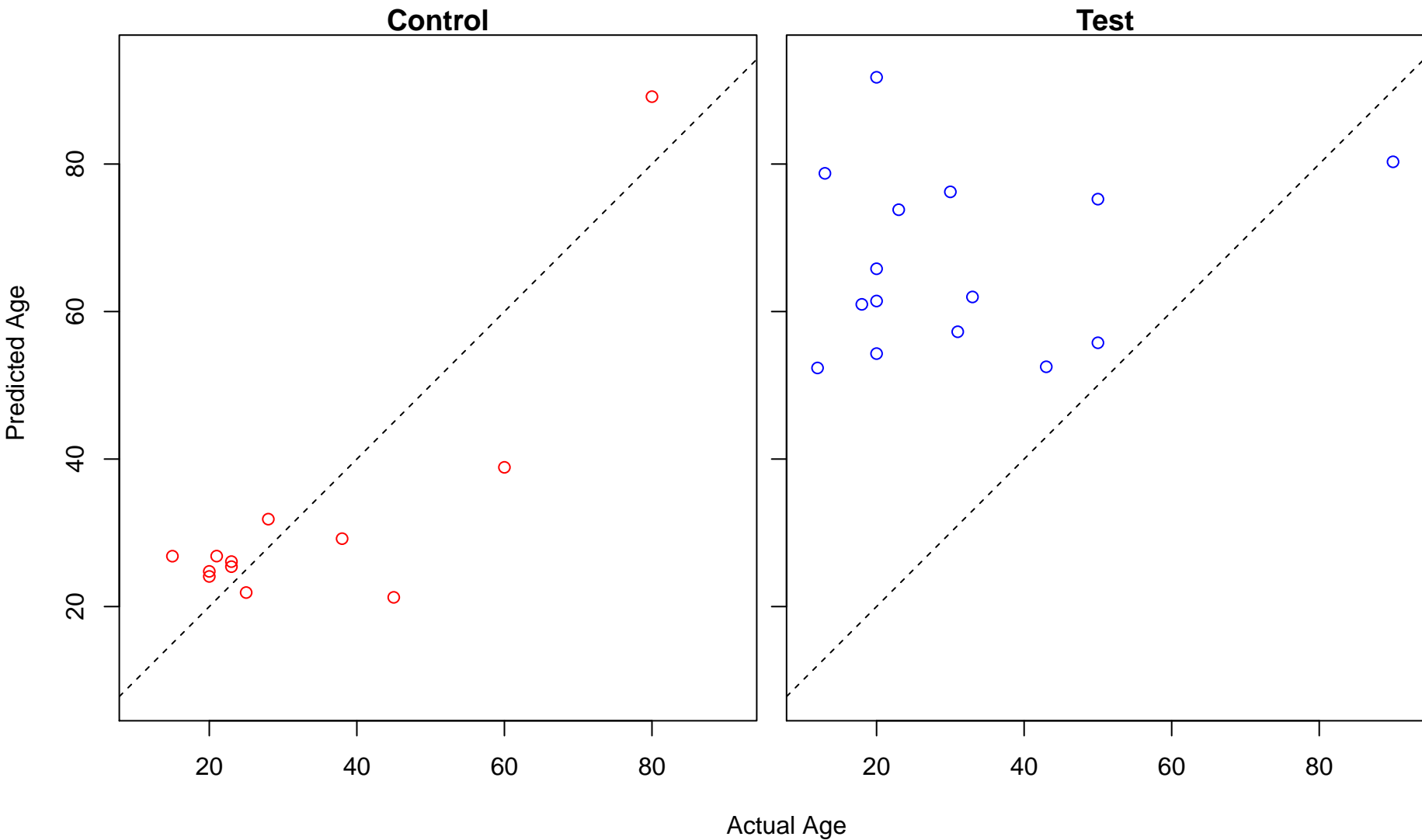
regulation of wound healing (Score: 5.219992)



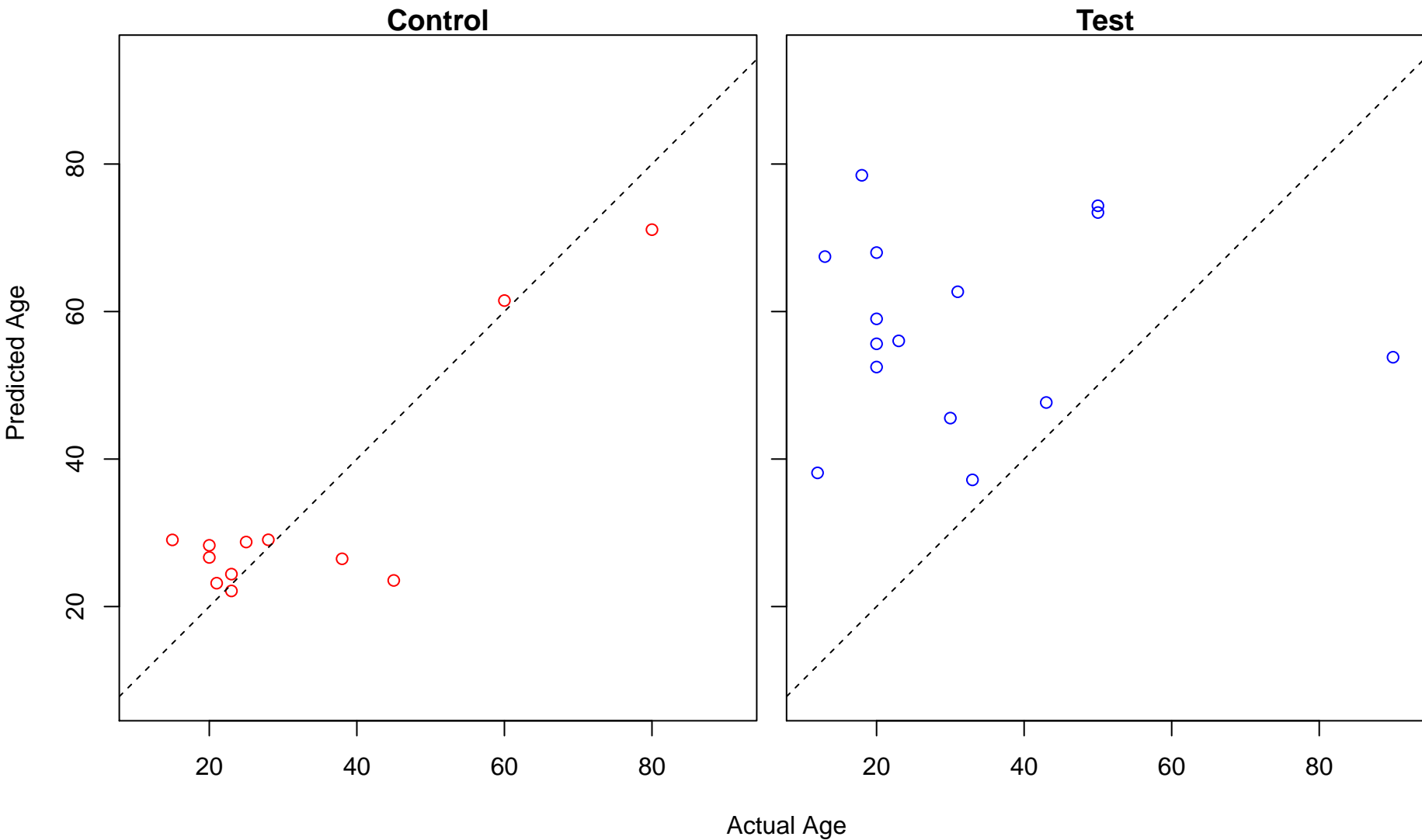
transcytosis (Score: 5.219607)



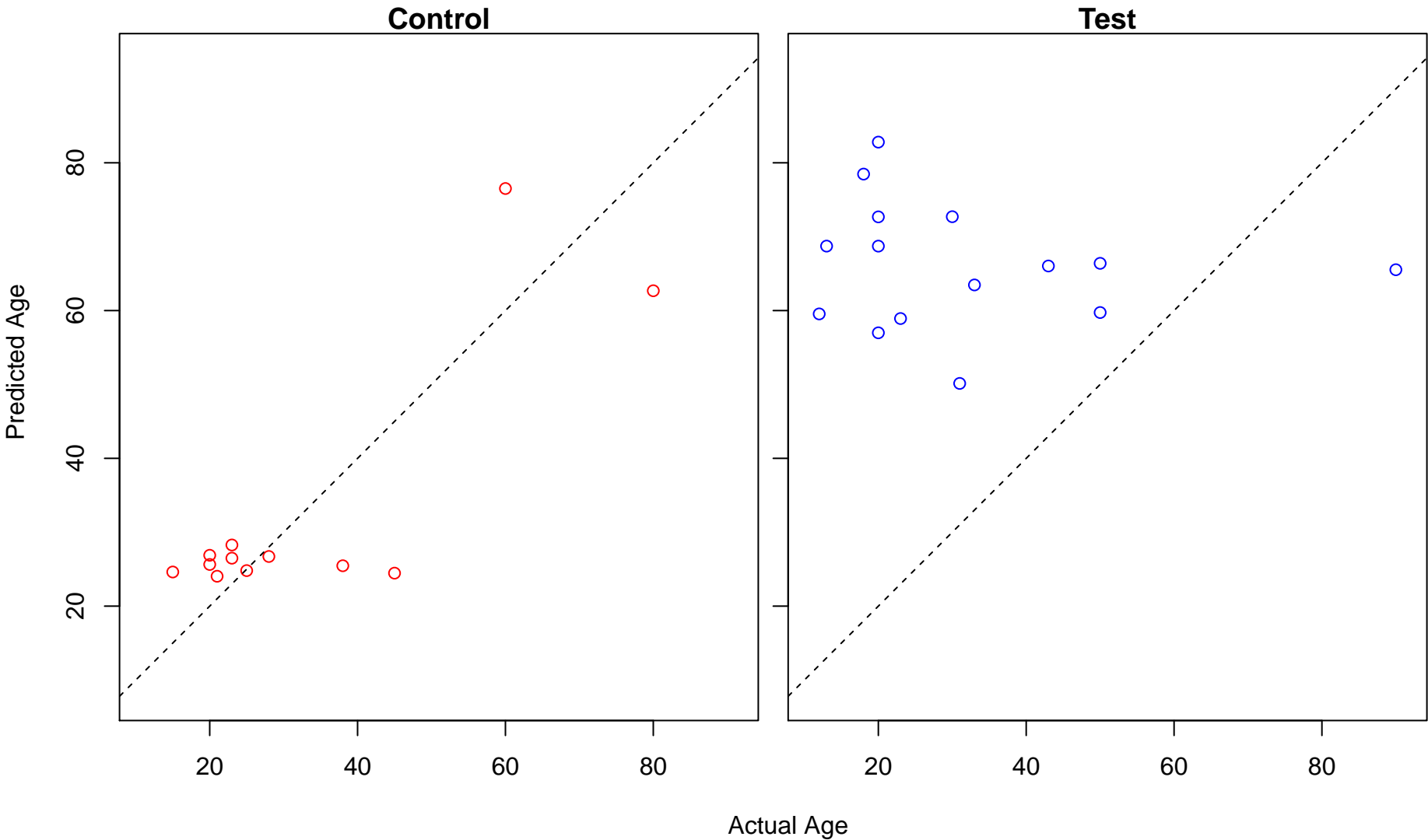
positive regulation of calcineurin–NFAT signaling cascade (Score: 5.217626)



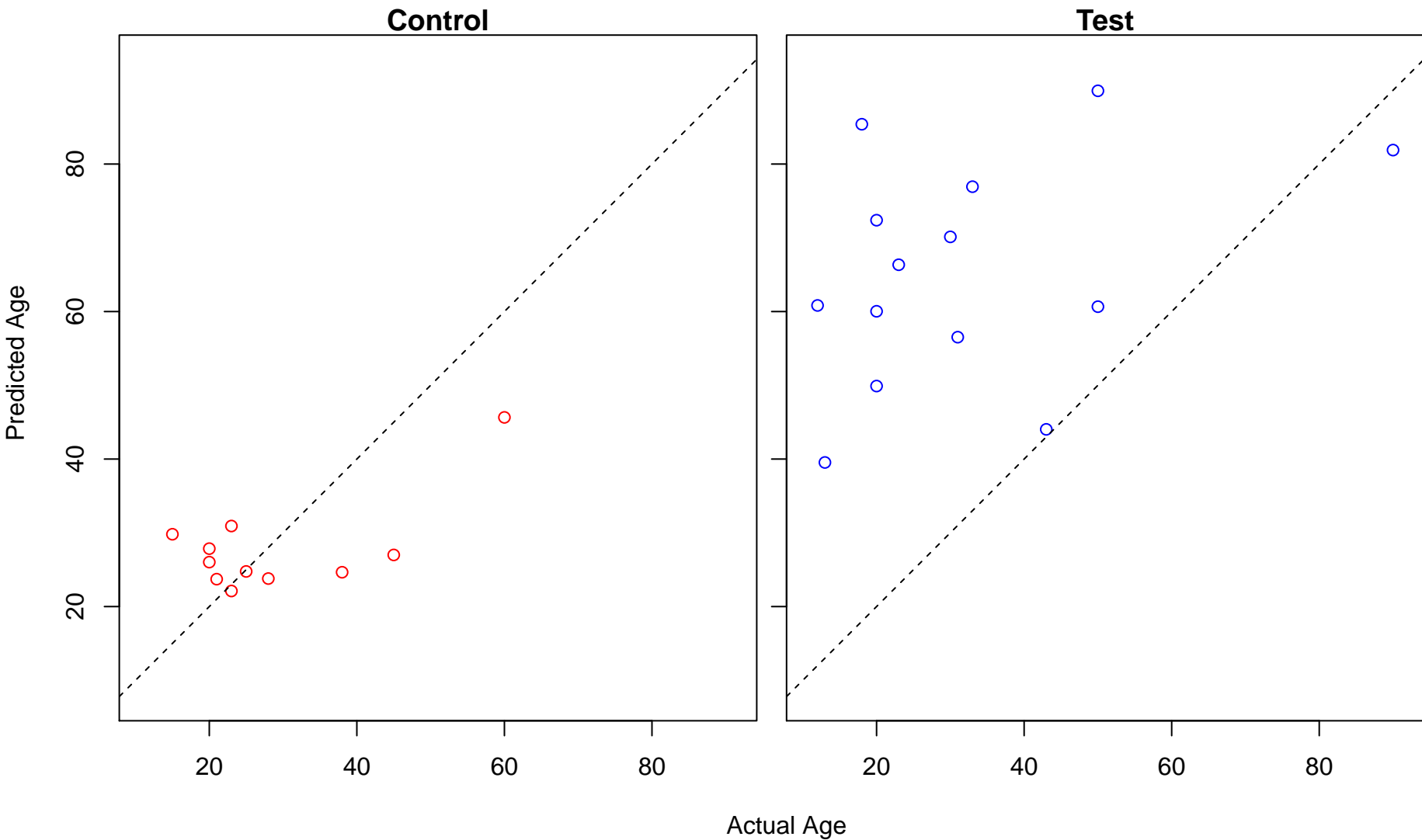
hexose catabolic process (Score: 5.217465)



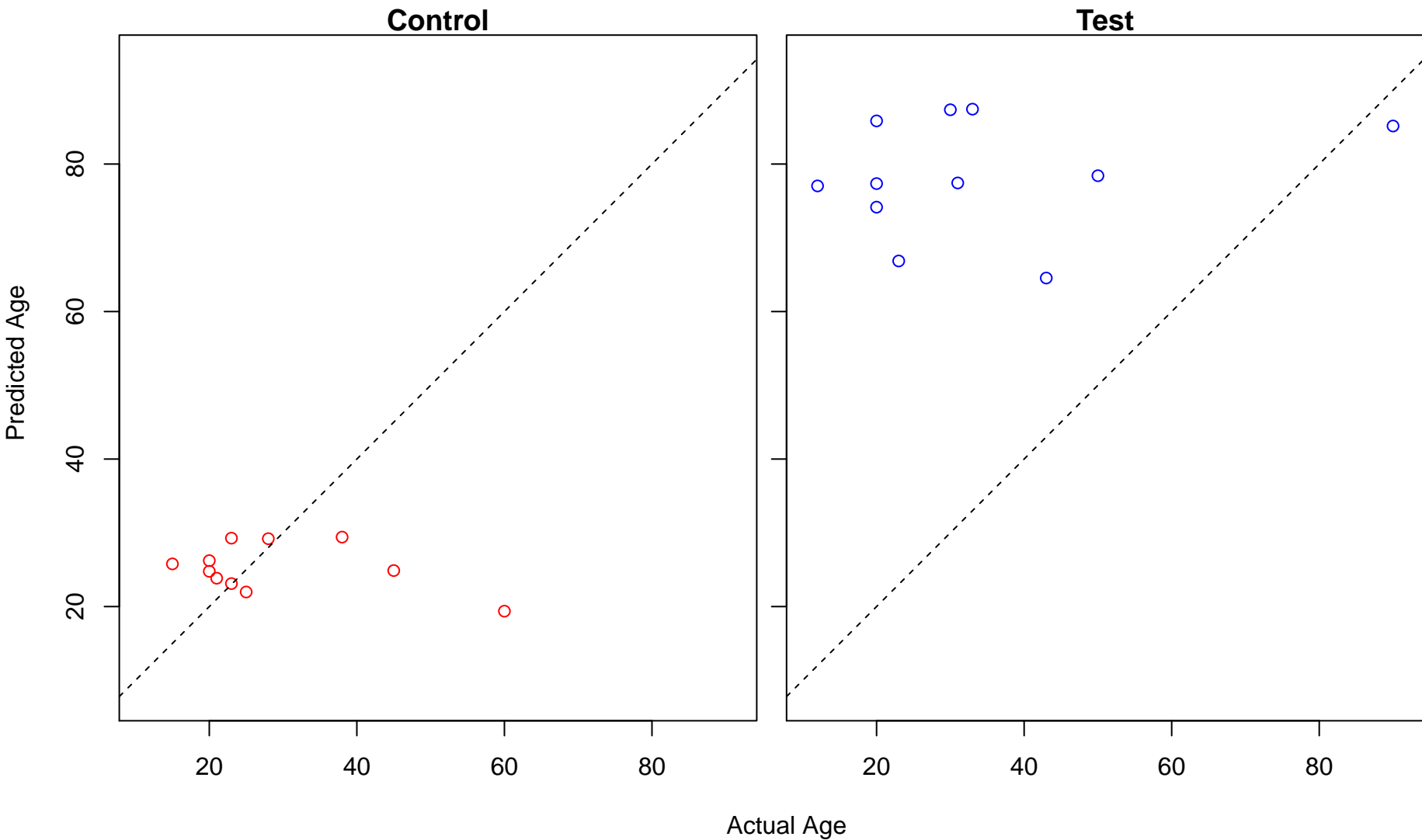
regulation of systemic arterial blood pressure by circulatory renin–angiotensin (Score: 5.216248)



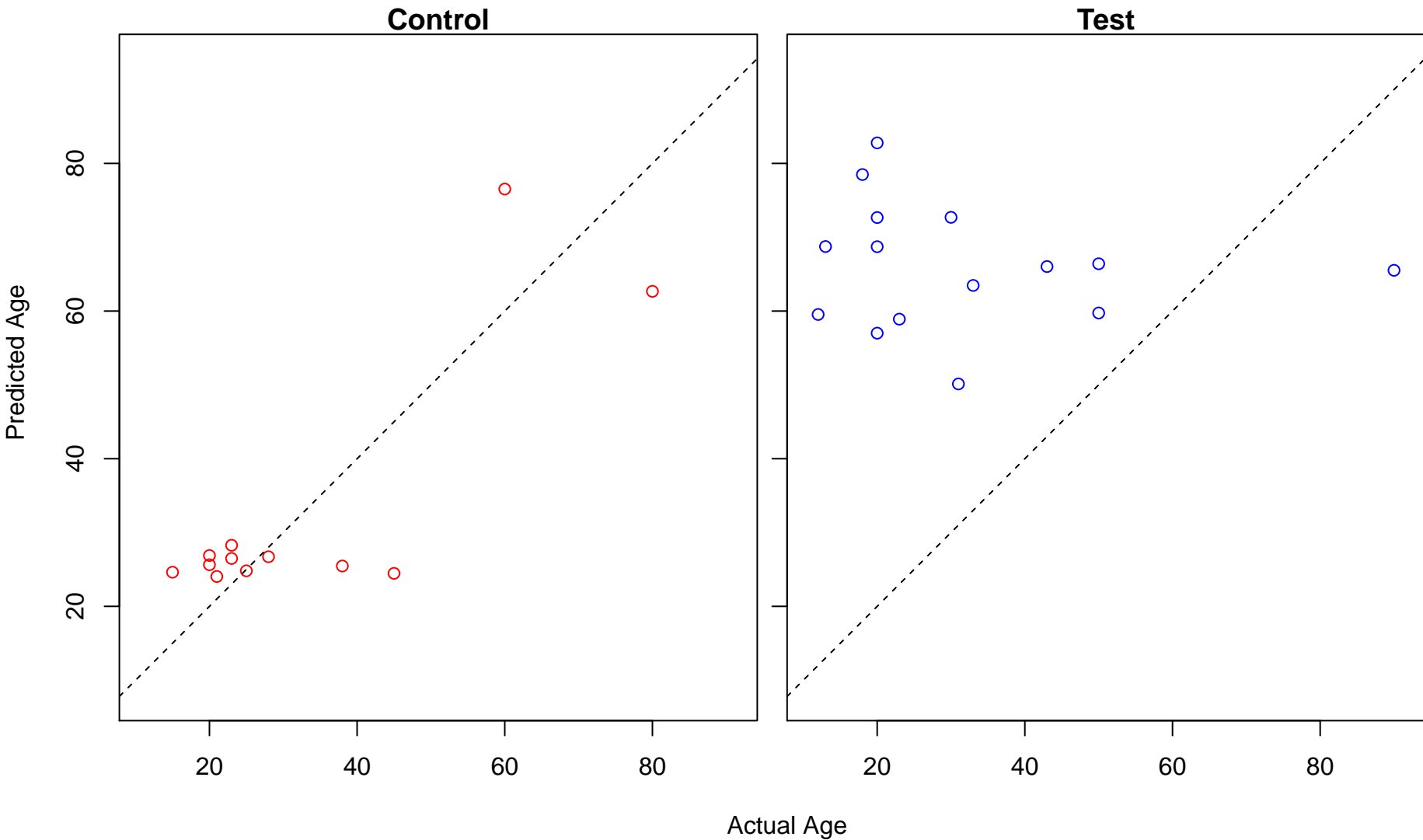
synaptic vesicle exocytosis (Score: 5.215808)



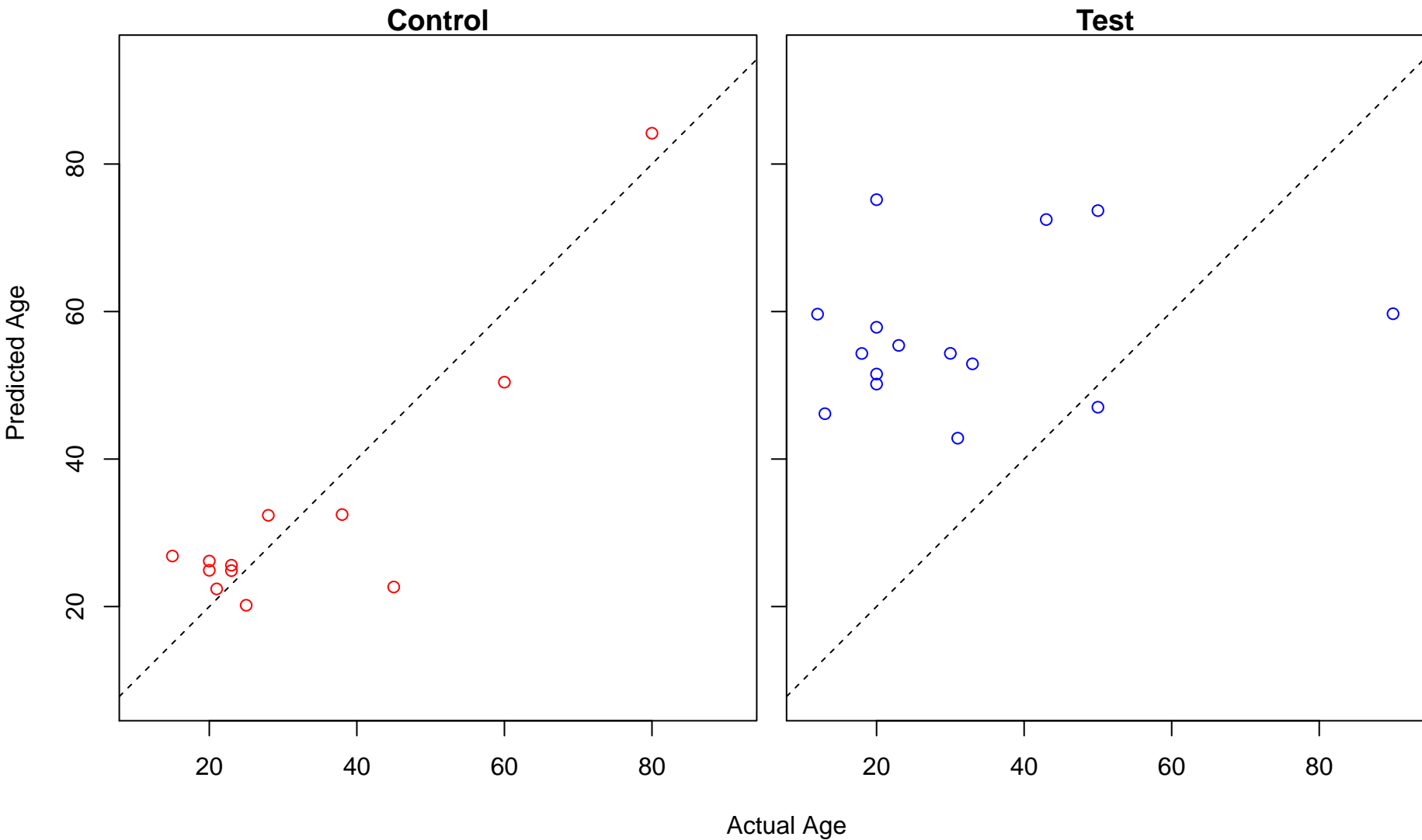
amyloid precursor protein metabolic process (Score: 5.215536)



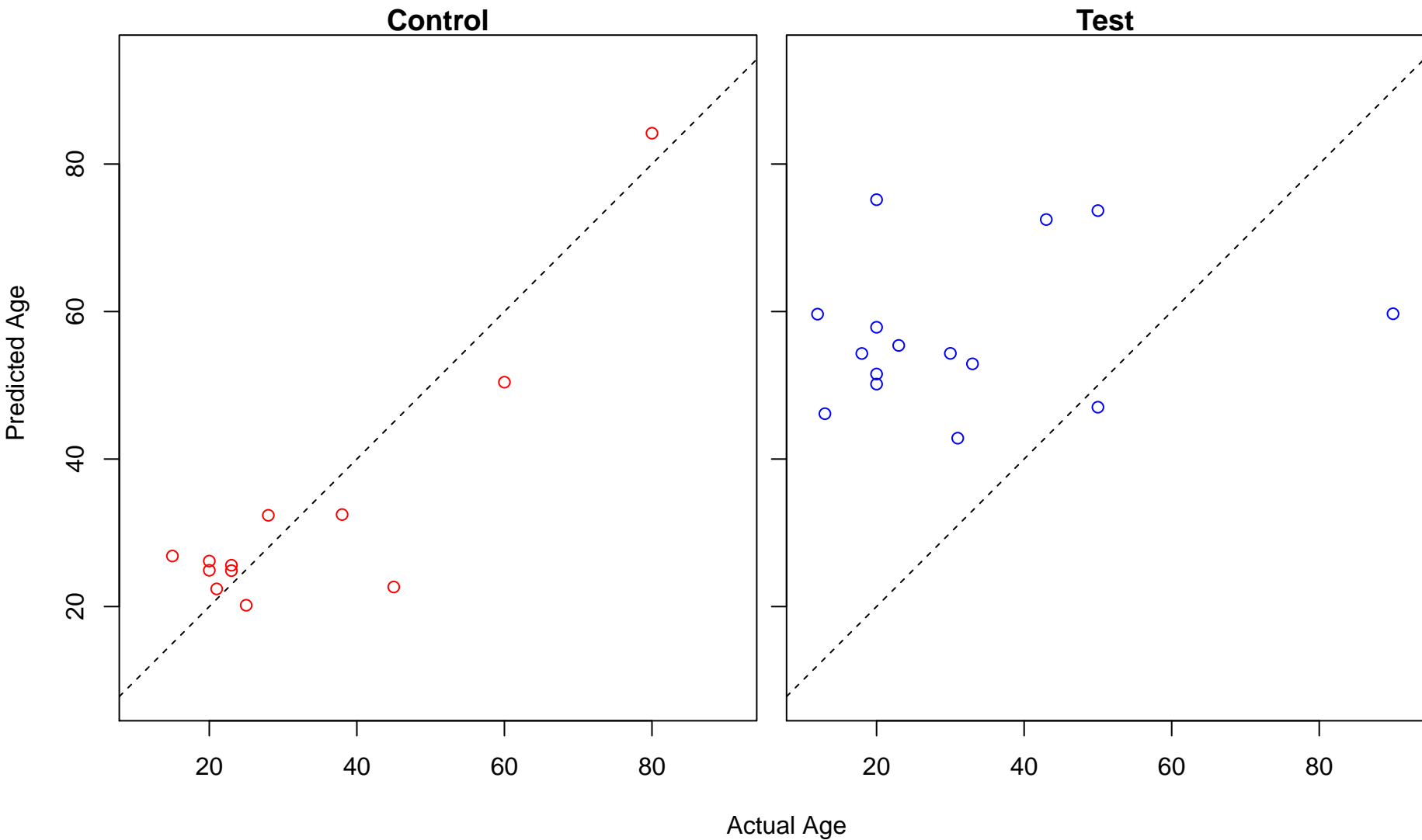
regulation of systemic arterial blood pressure by renin-angiotensin (Score: 5.214011)



regulation of tube size (Score: 5.212286)

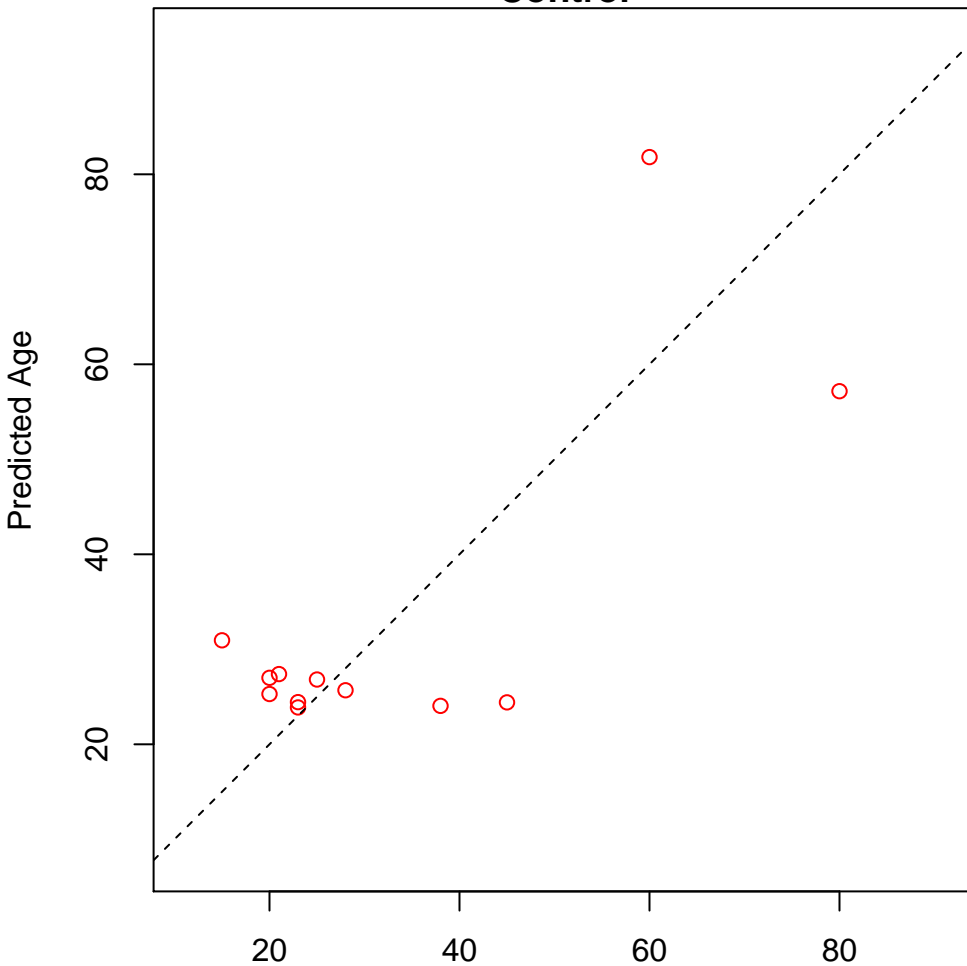


regulation of blood vessel size (Score: 5.212286)

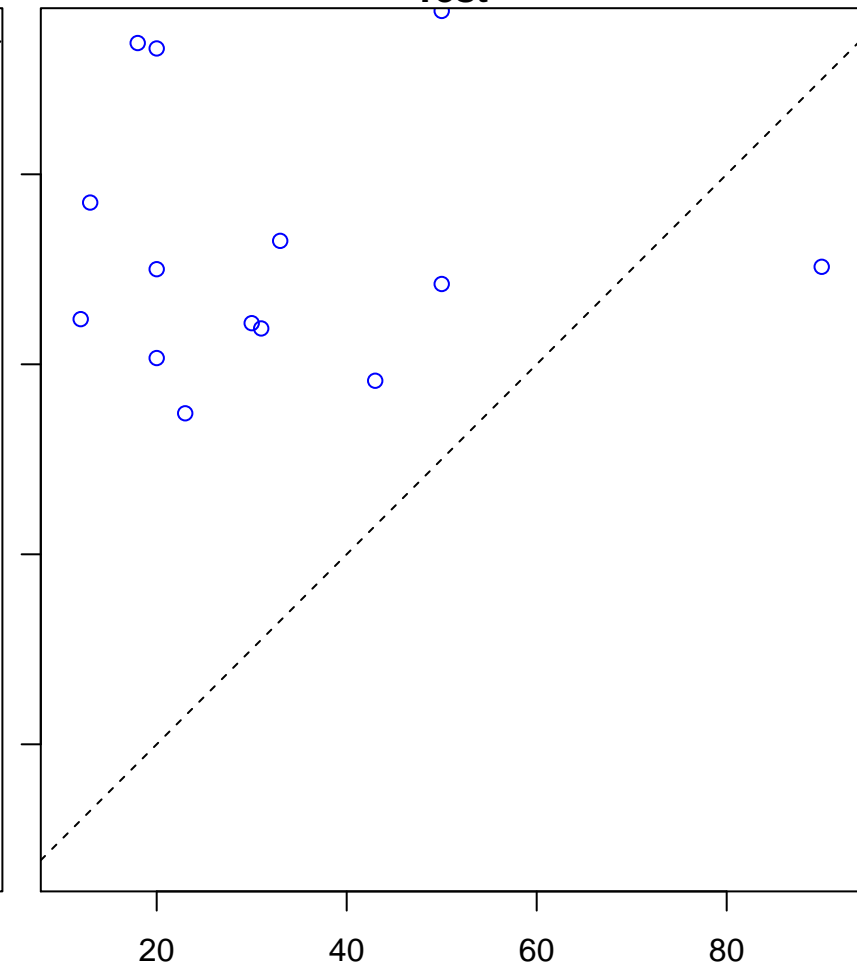


regulation of interleukin-23 production (Score: 5.212190)

Control

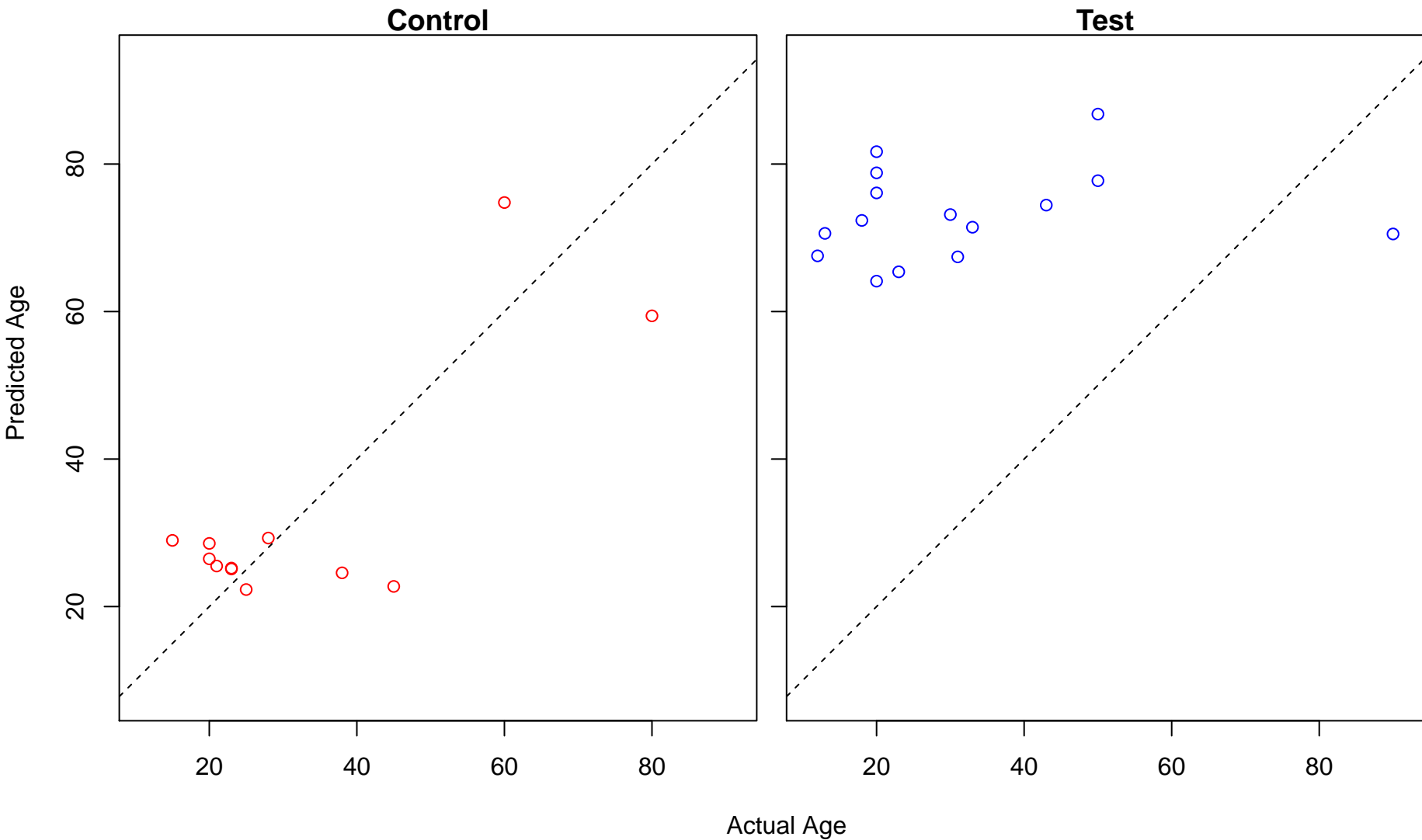


Test

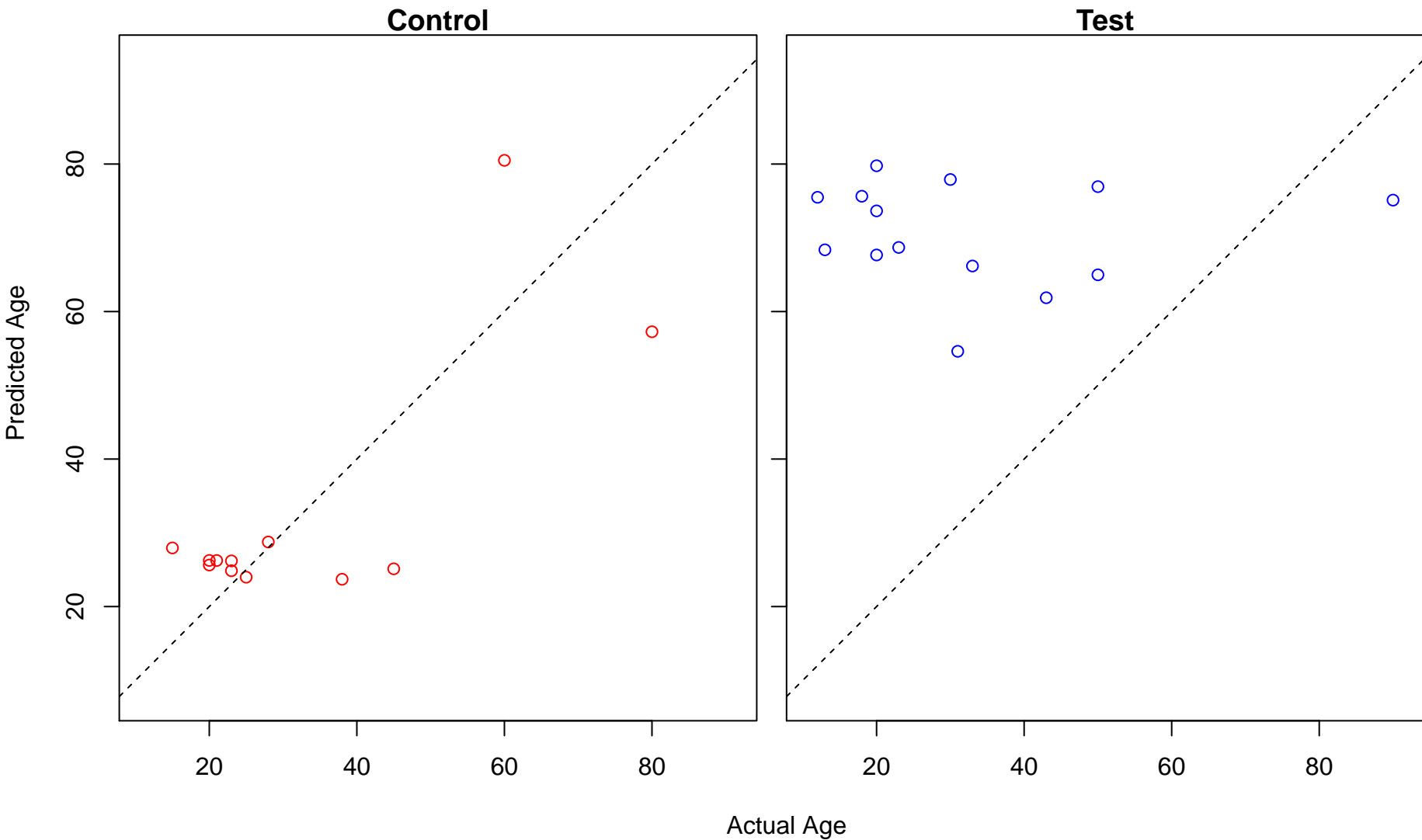


Actual Age

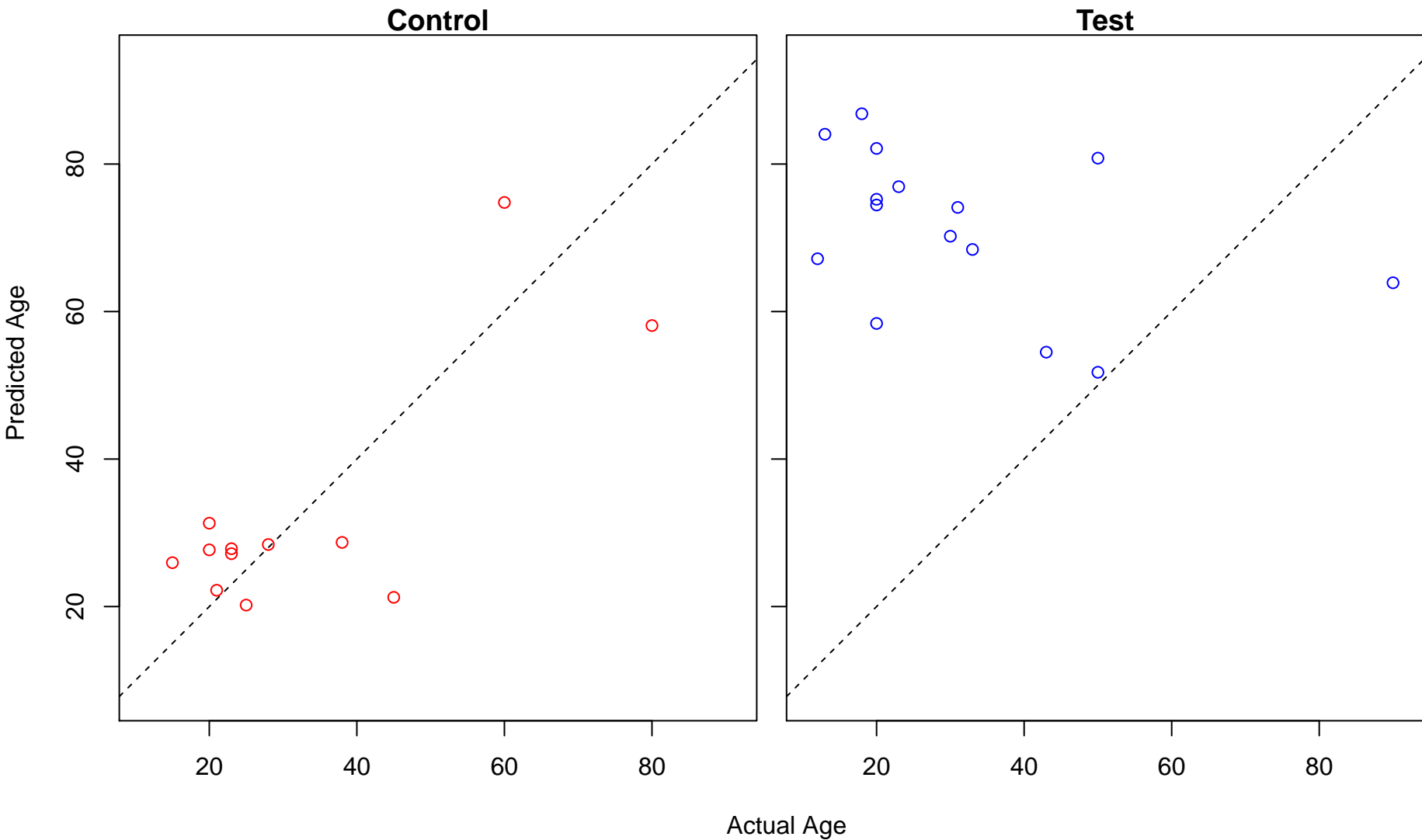
regulation of cardiac conduction (Score: 5.210391)



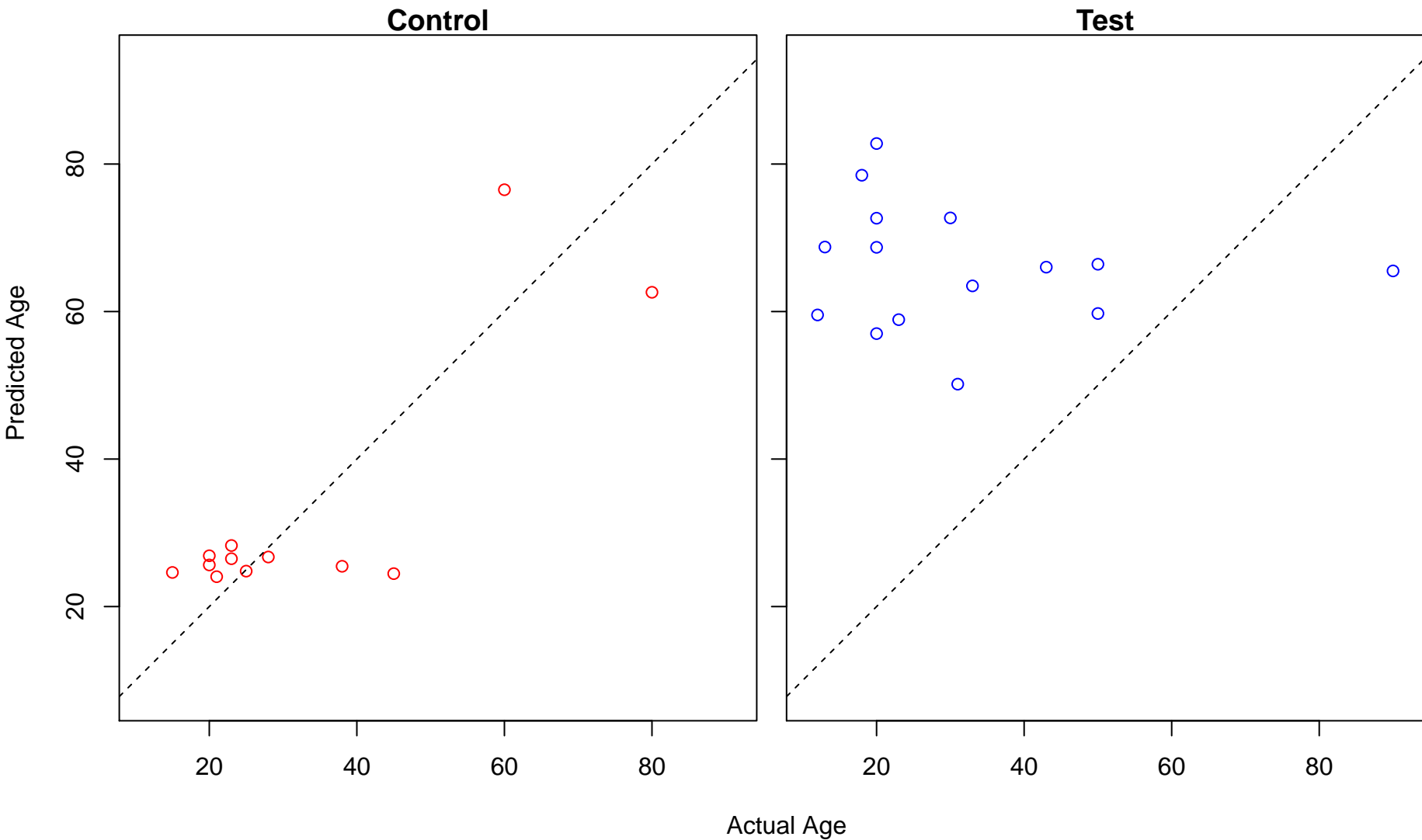
7-methylguanosine RNA capping (Score: 5.208776)



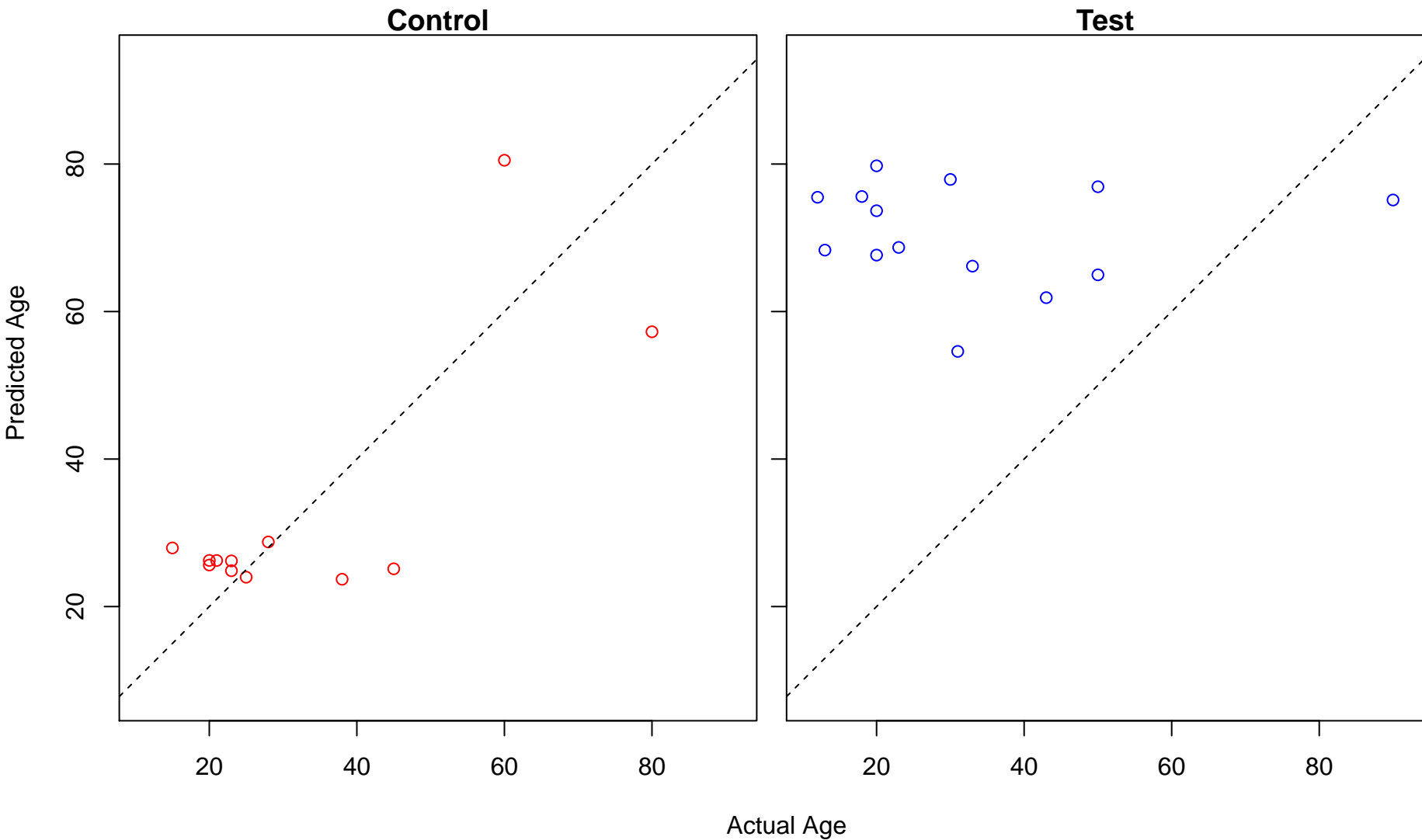
regulation of production of small RNA involved in gene silencing by RNA (Score: 5.208225)



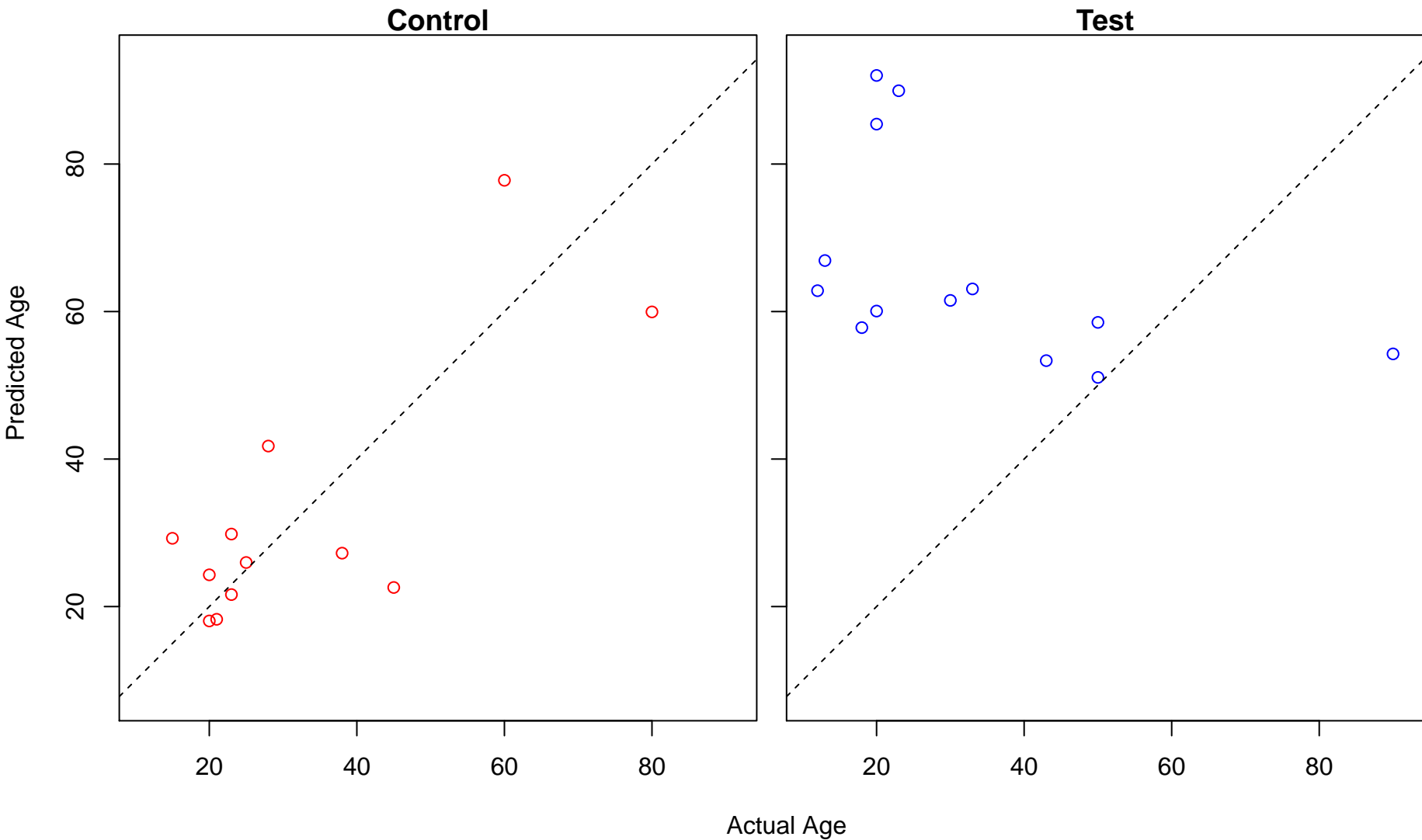
regulation of systemic arterial blood pressure by hormone (Score: 5.207136)



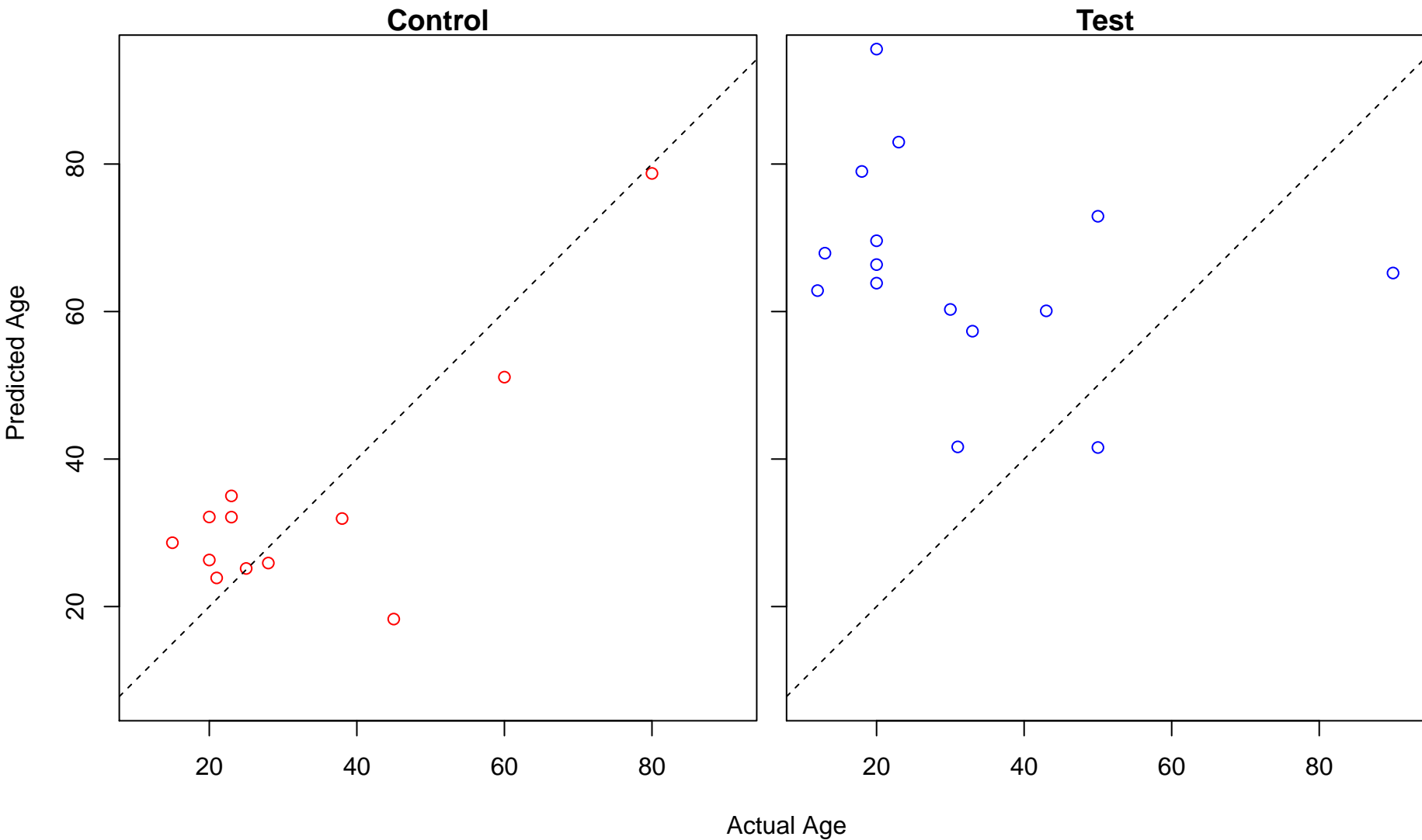
7-methylguanosine mRNA capping (Score: 5.206573)



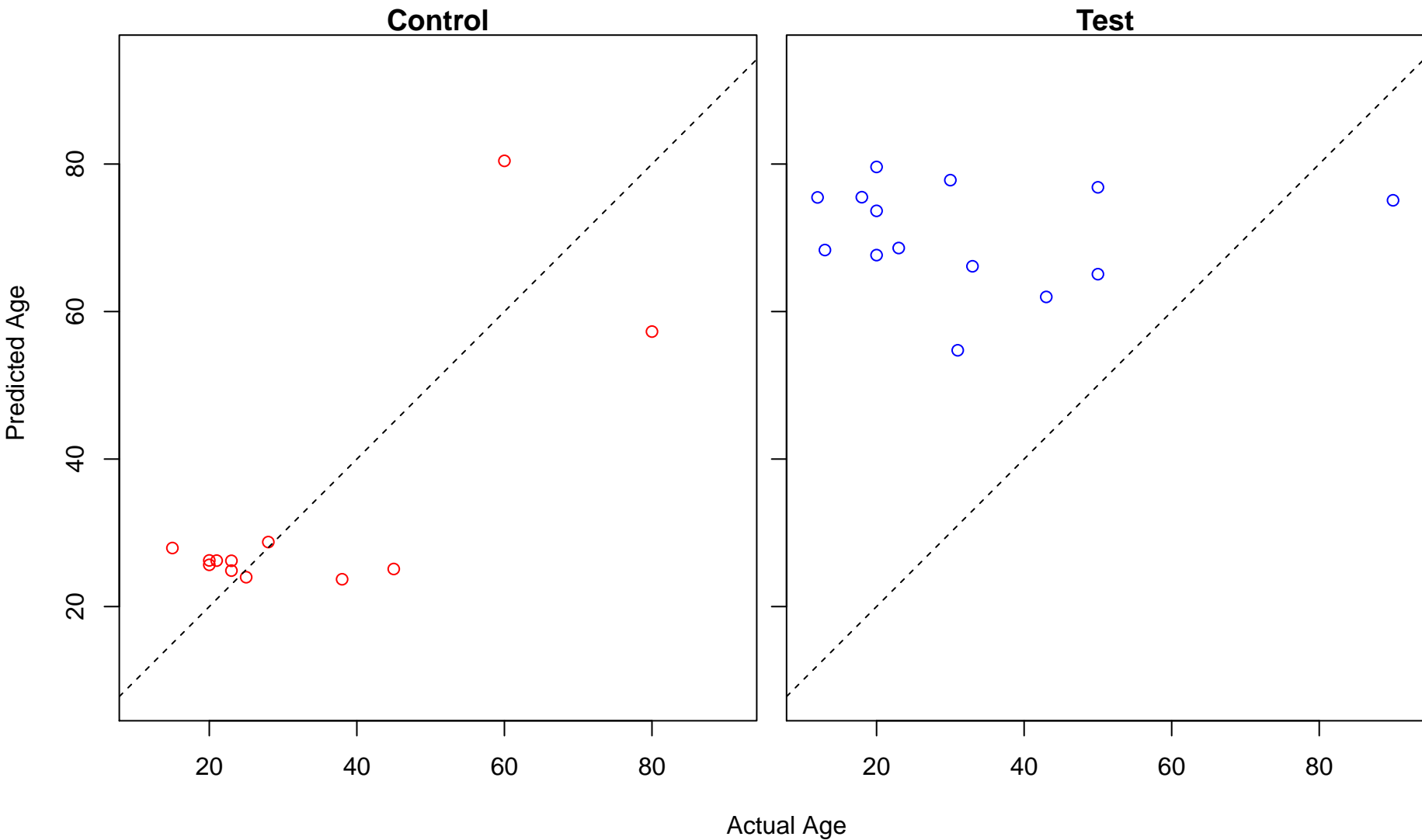
regulation of cartilage development (Score: 5.204545)



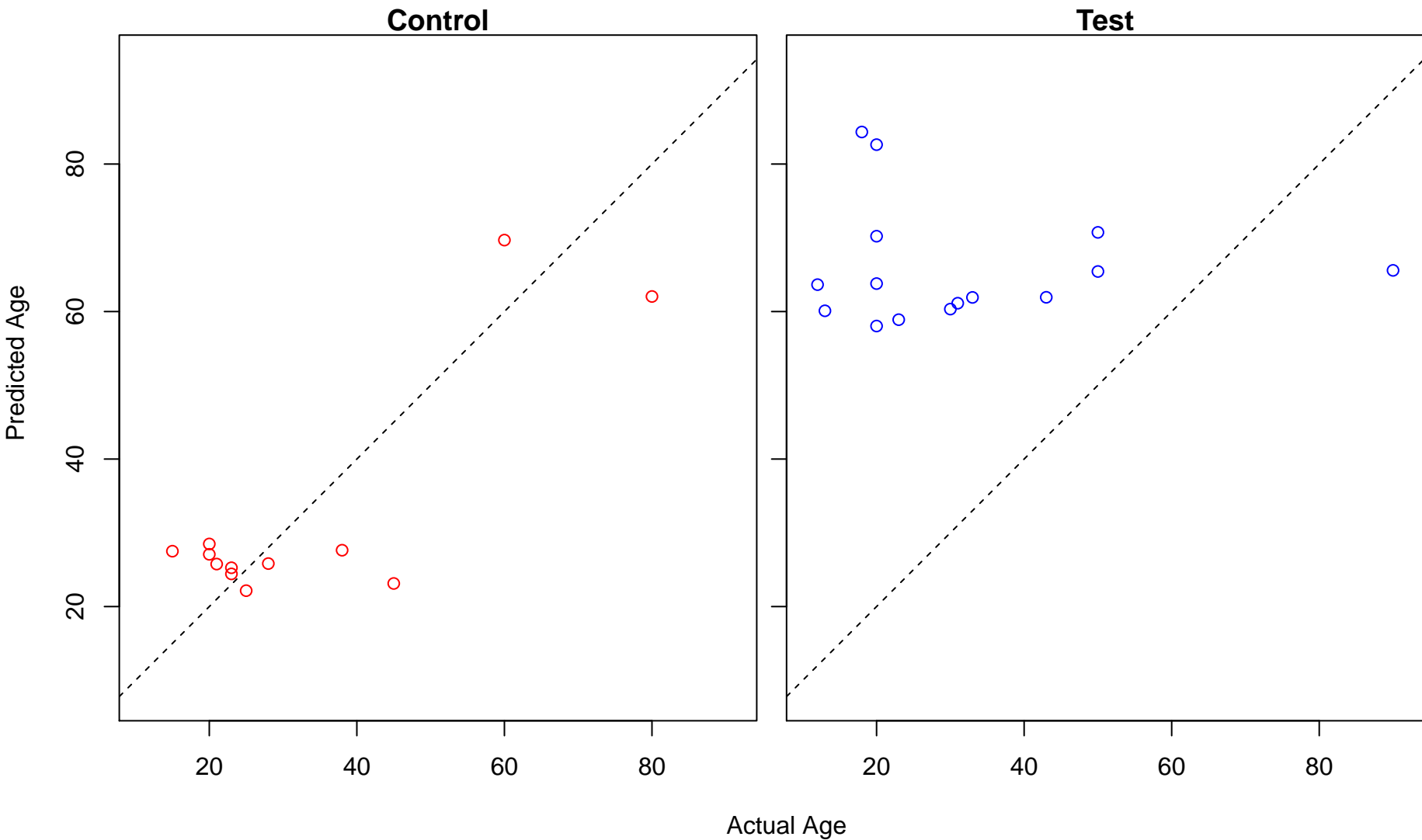
positive regulation of mesenchymal cell proliferation (Score: 5.203388)



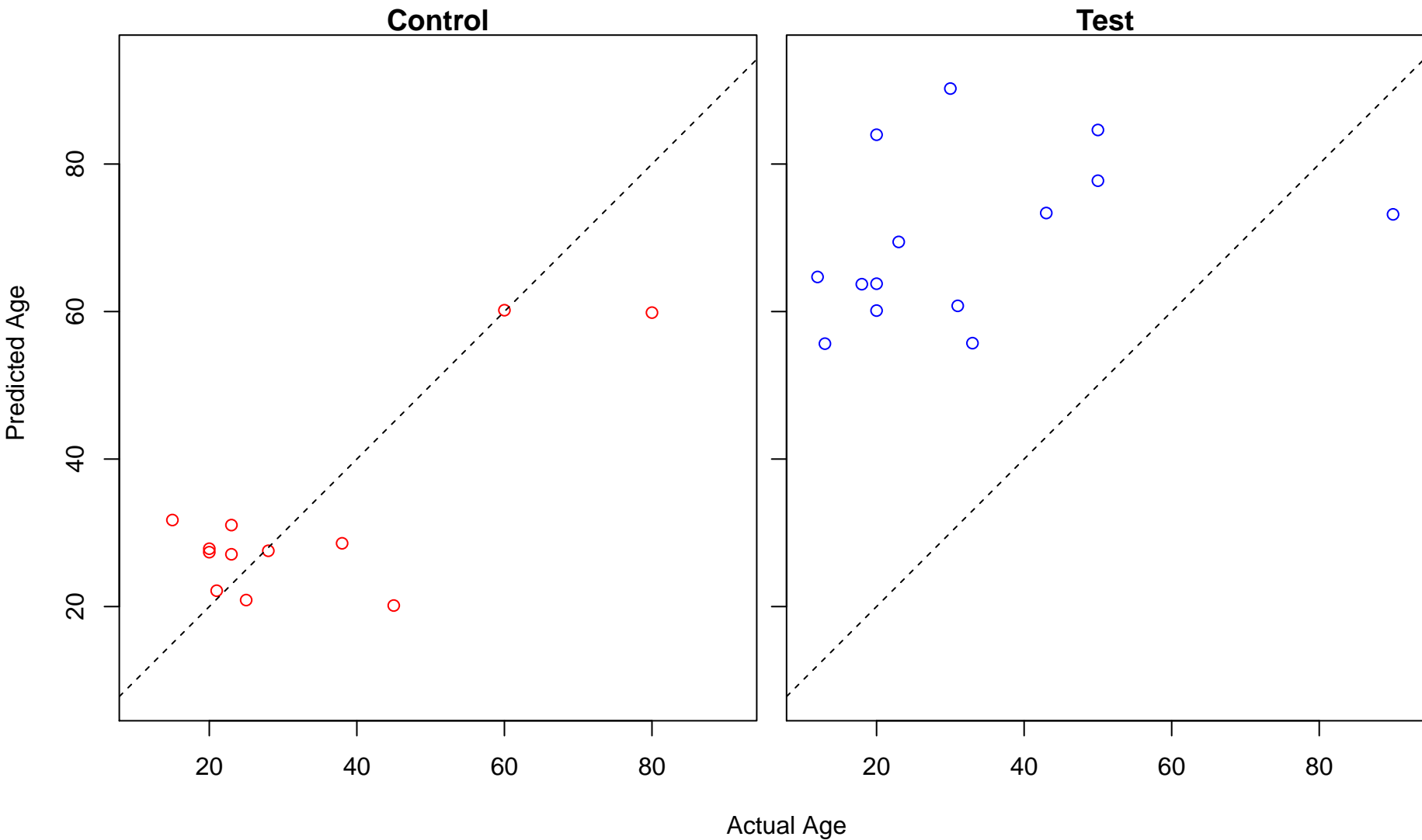
RNA capping (Score: 5.202768)



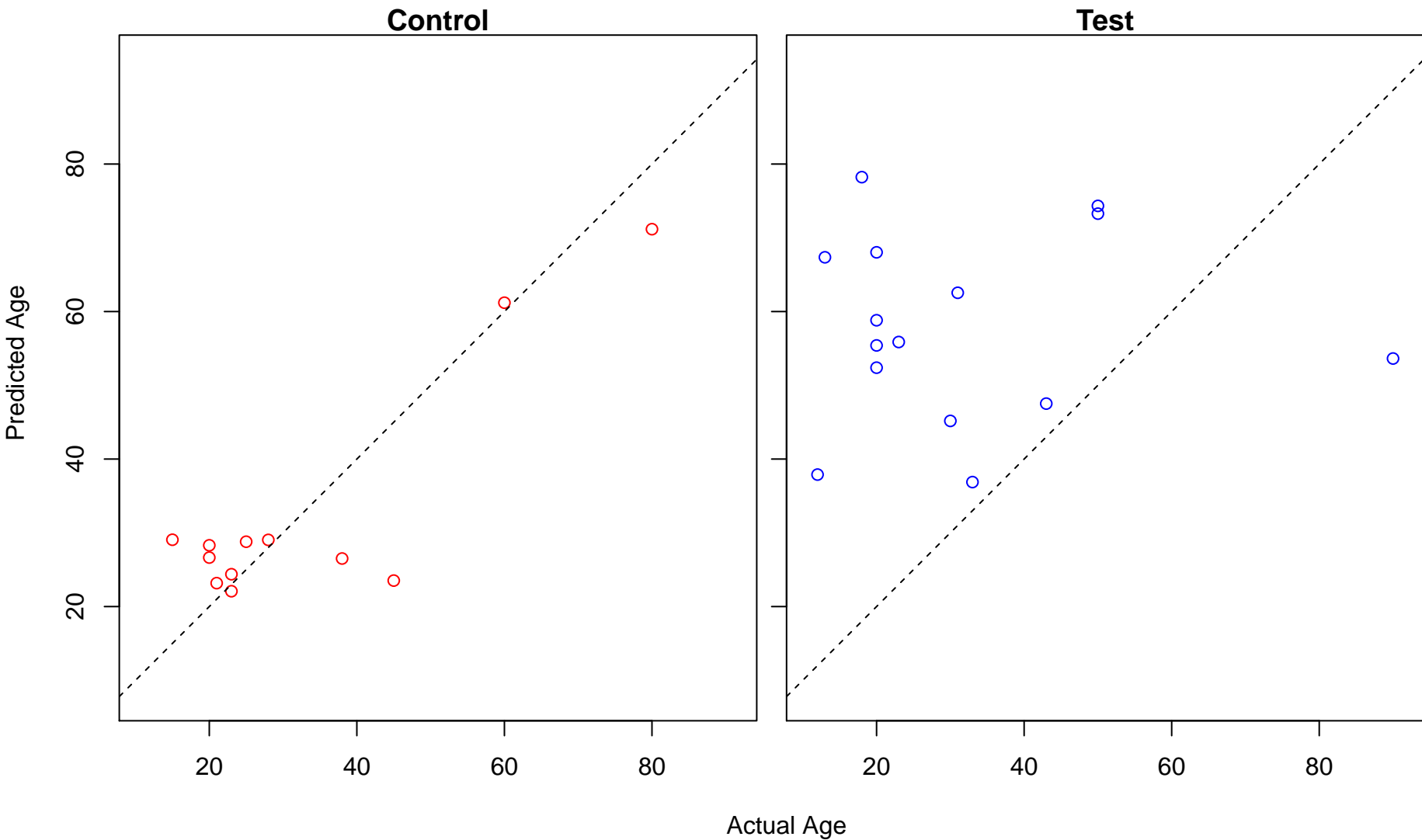
positive regulation of cell morphogenesis involved in differentiation (Score: 5.201808)



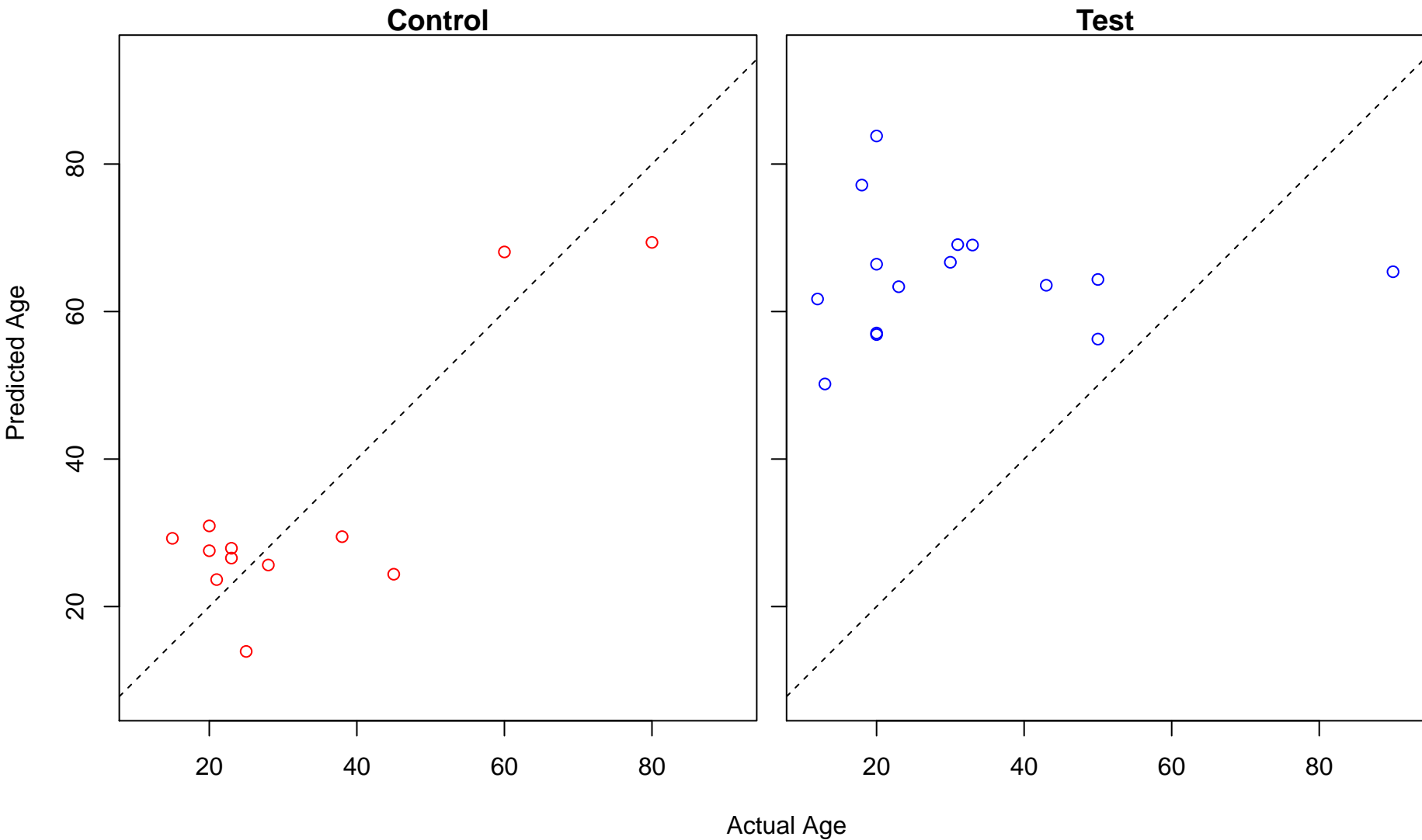
keratan sulfate catabolic process (Score: 5.199841)



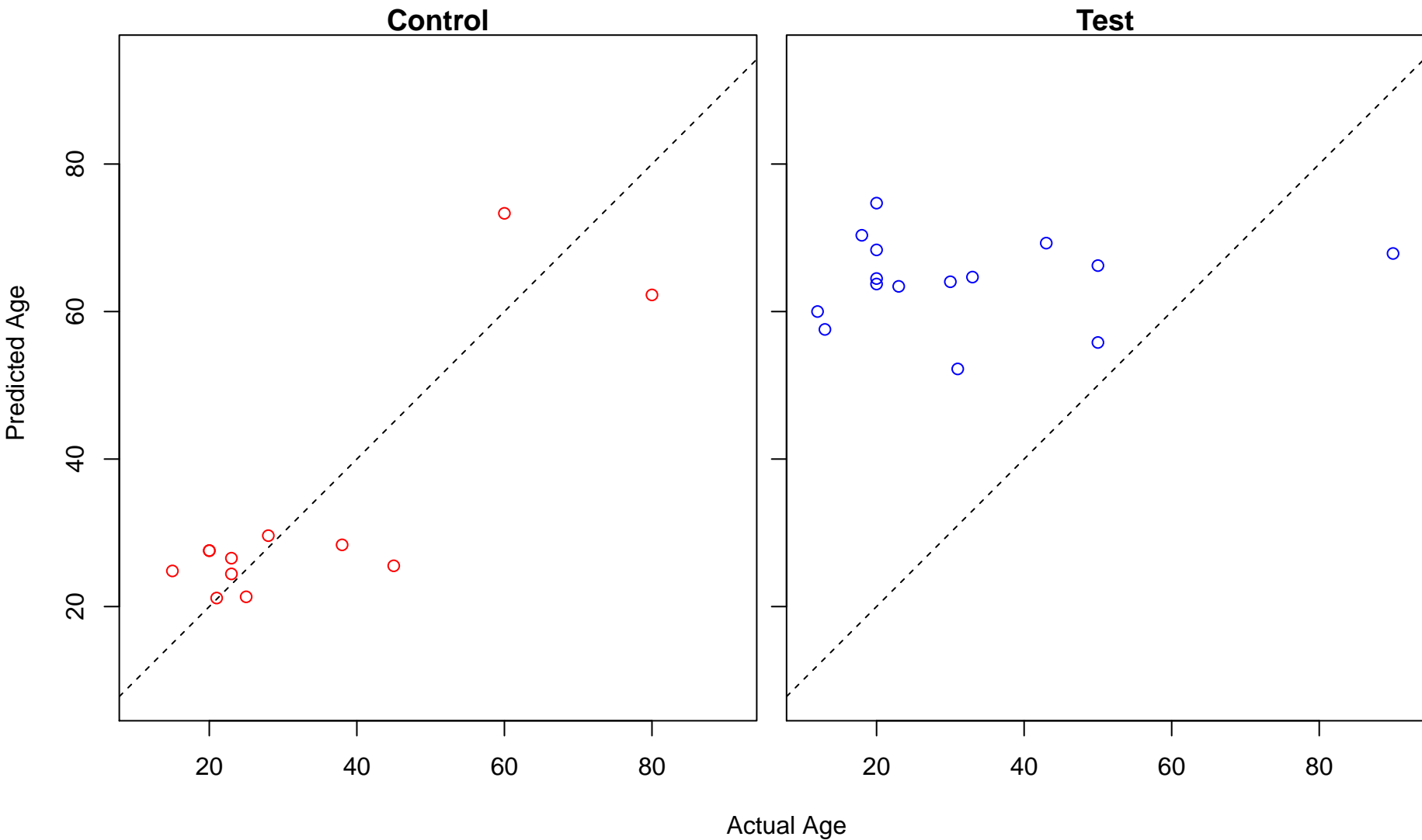
glycolytic process (Score: 5.199569)



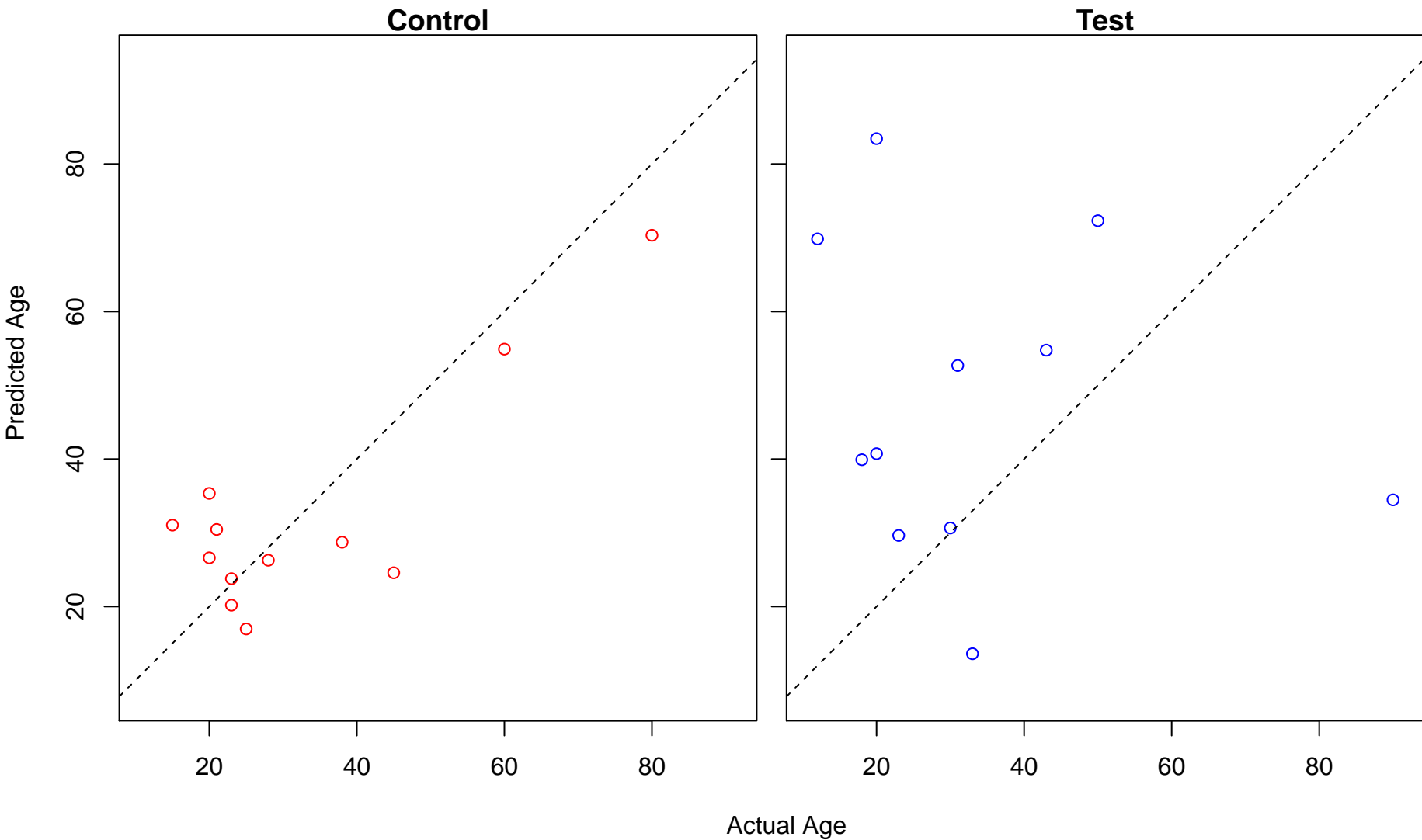
positive regulation of lipid metabolic process (Score: 5.199492)



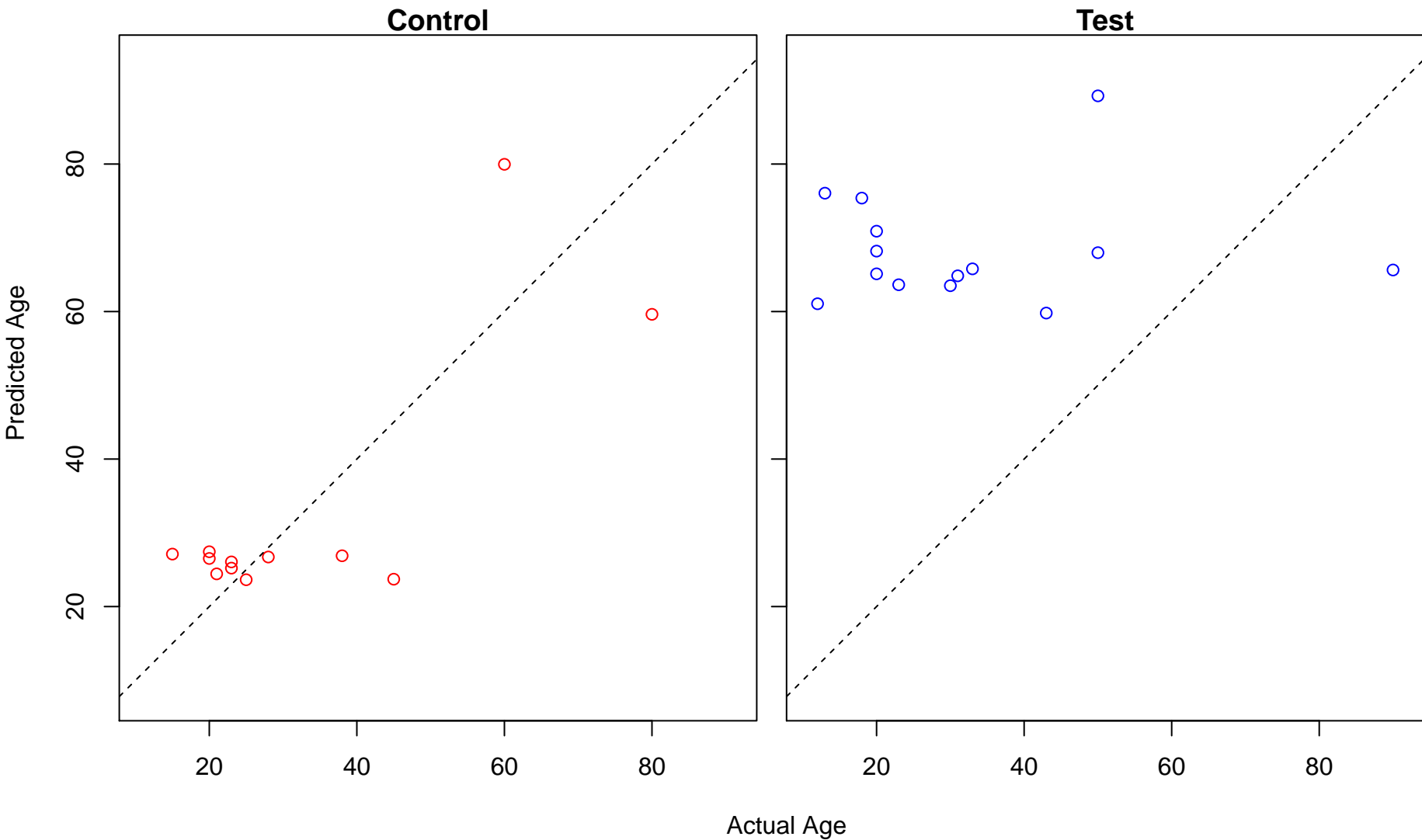
detection of mechanical stimulus (Score: 5.197766)



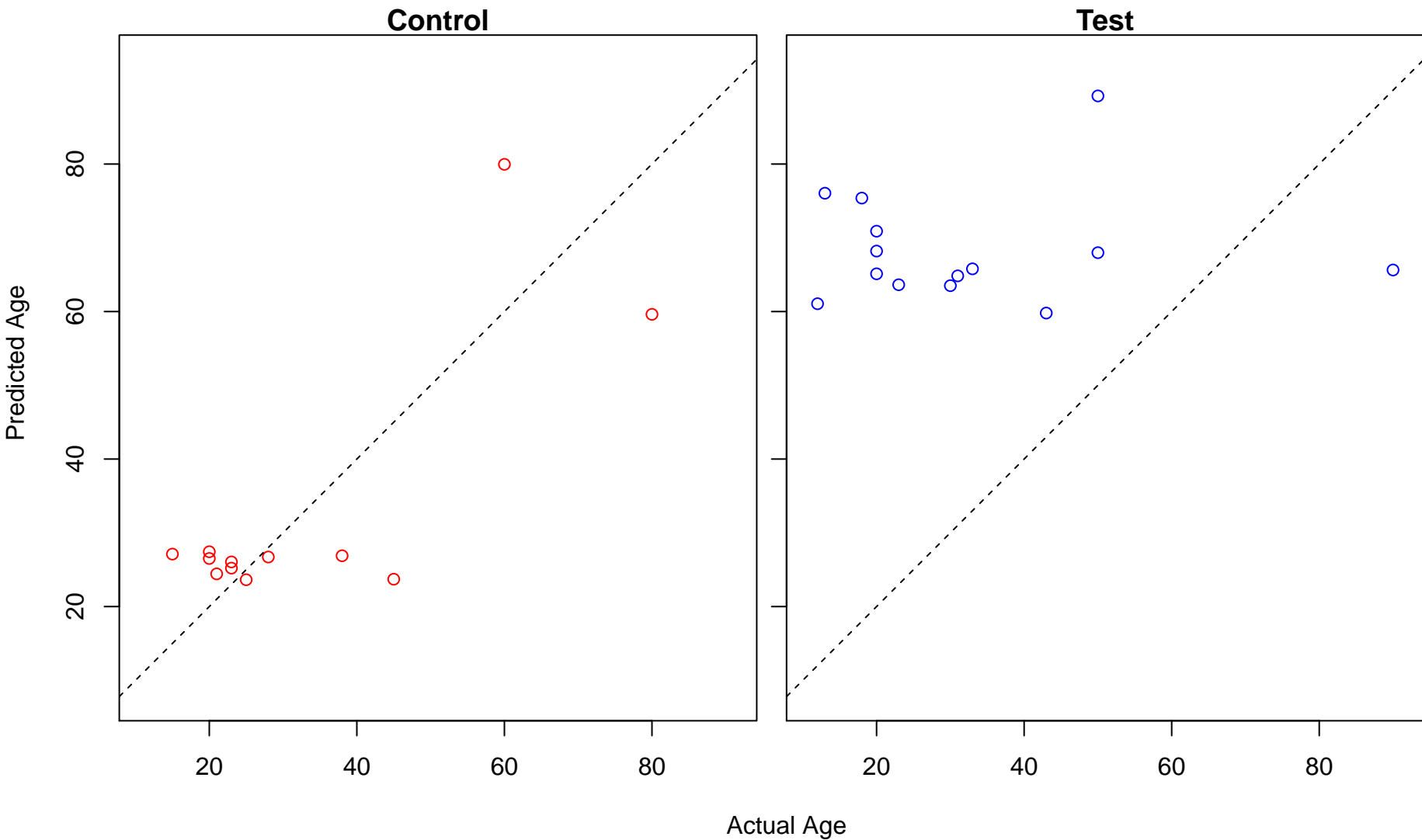
alcohol biosynthetic process (Score: 5.196530)



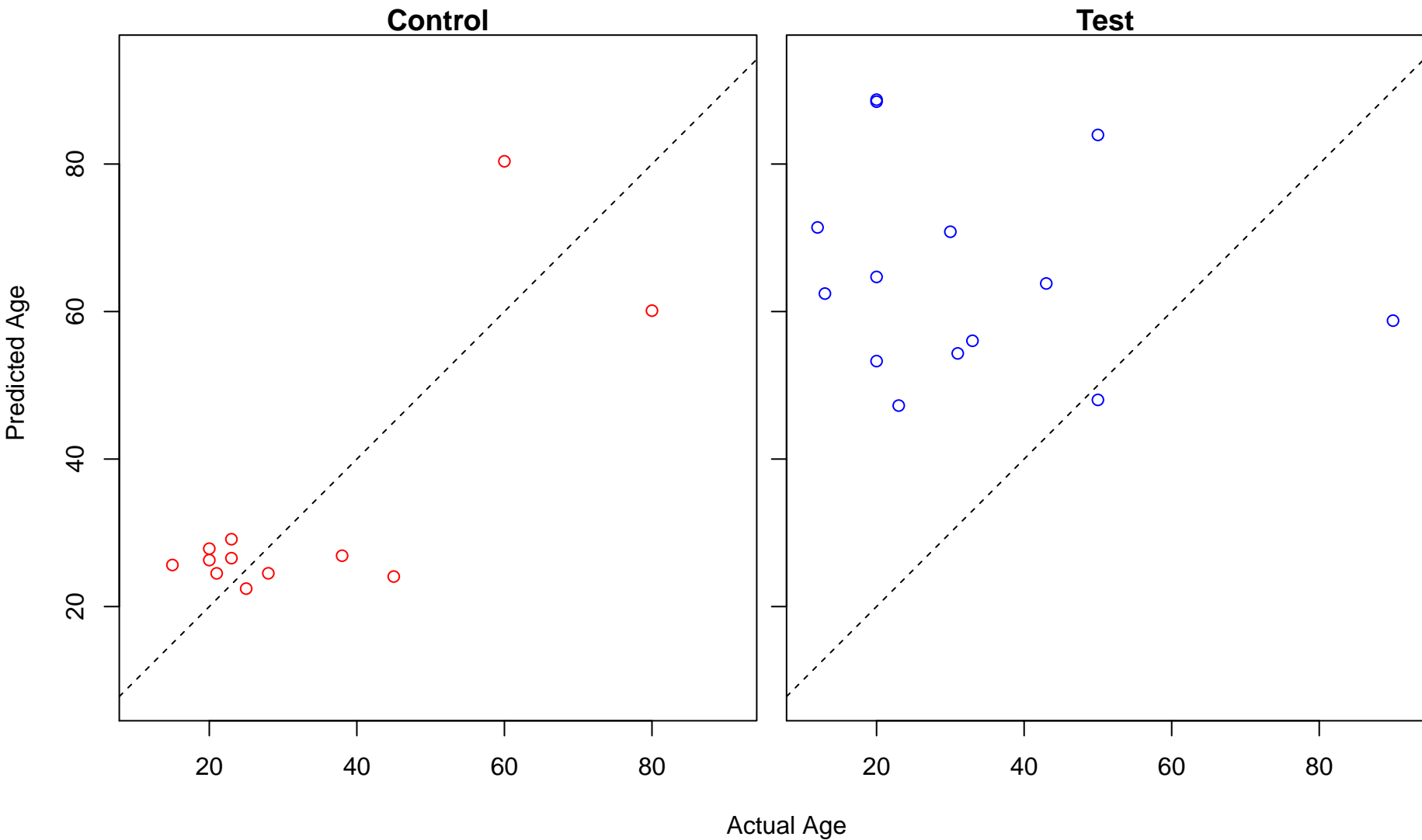
regulation of mRNA stability (Score: 5.195030)



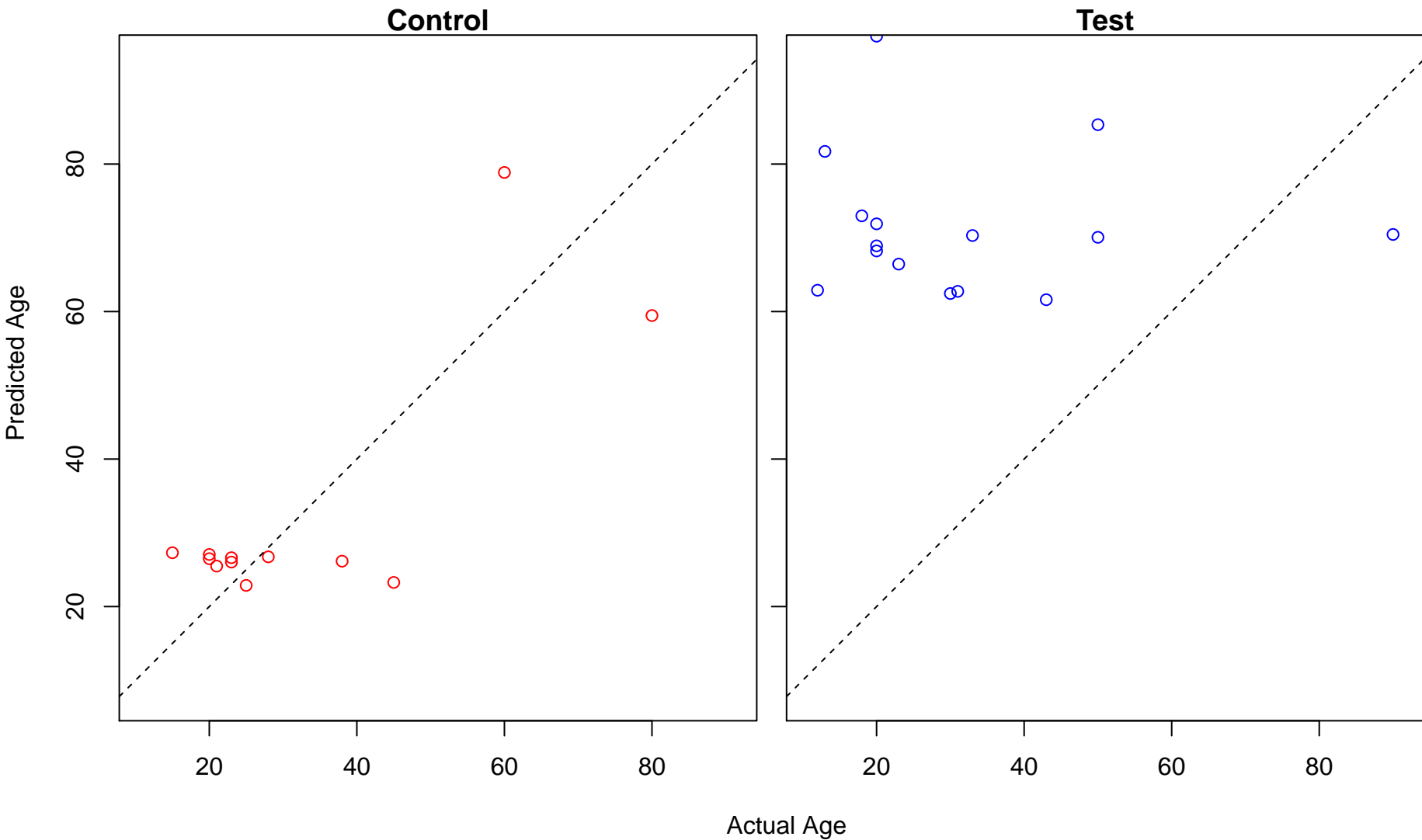
regulation of RNA stability (Score: 5.195024)



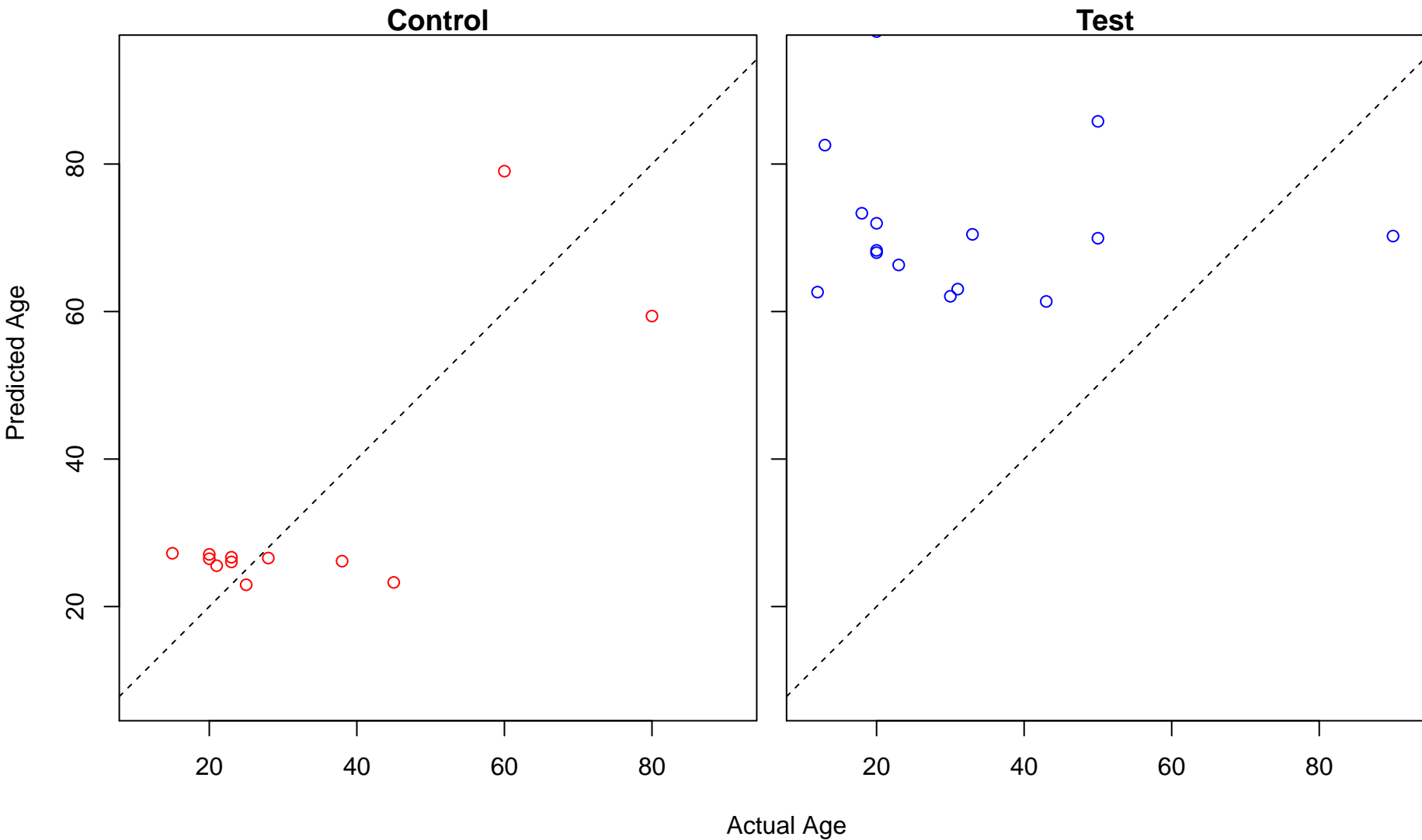
interleukin-8 production (Score: 5.194465)



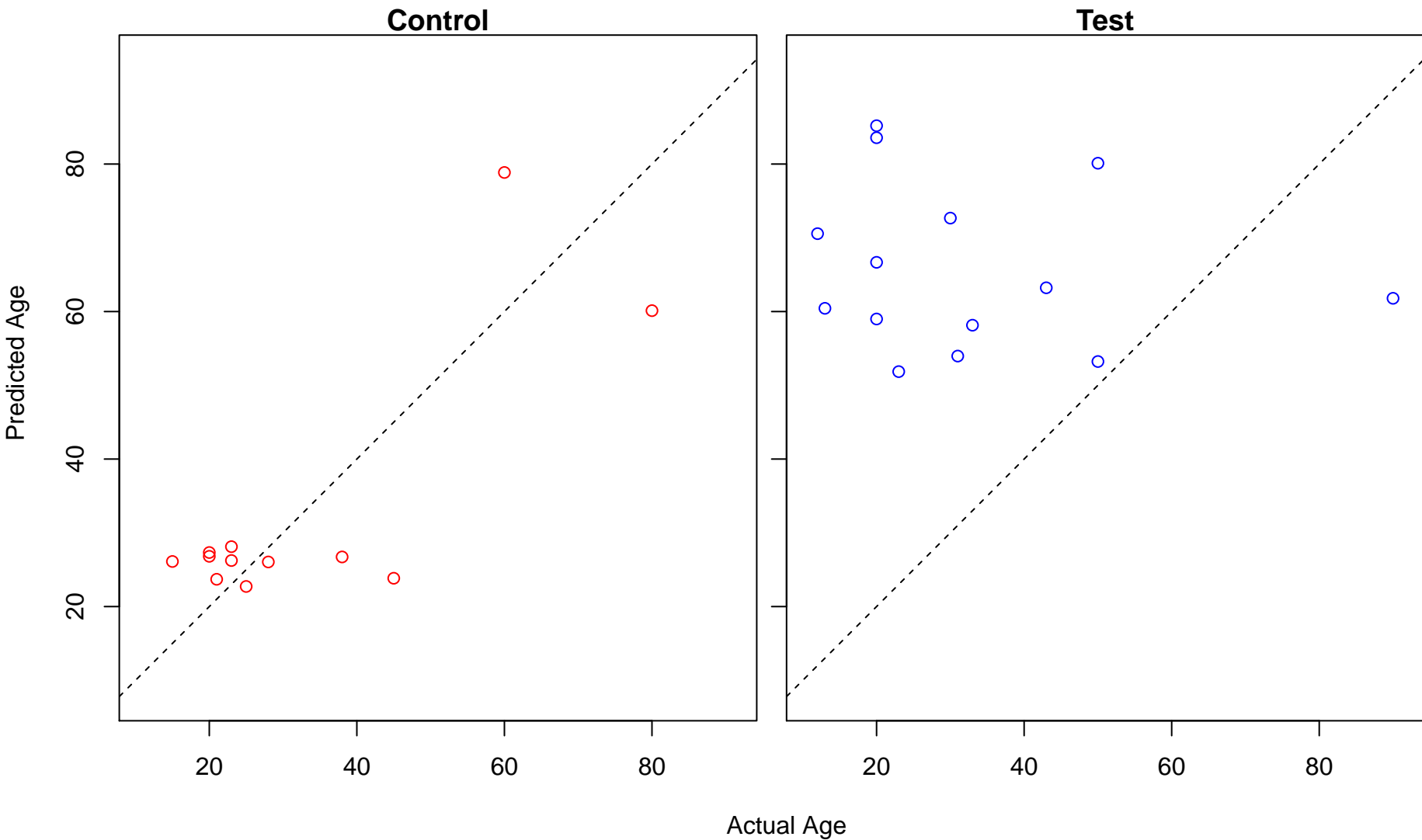
response to insulin (Score: 5.192269)



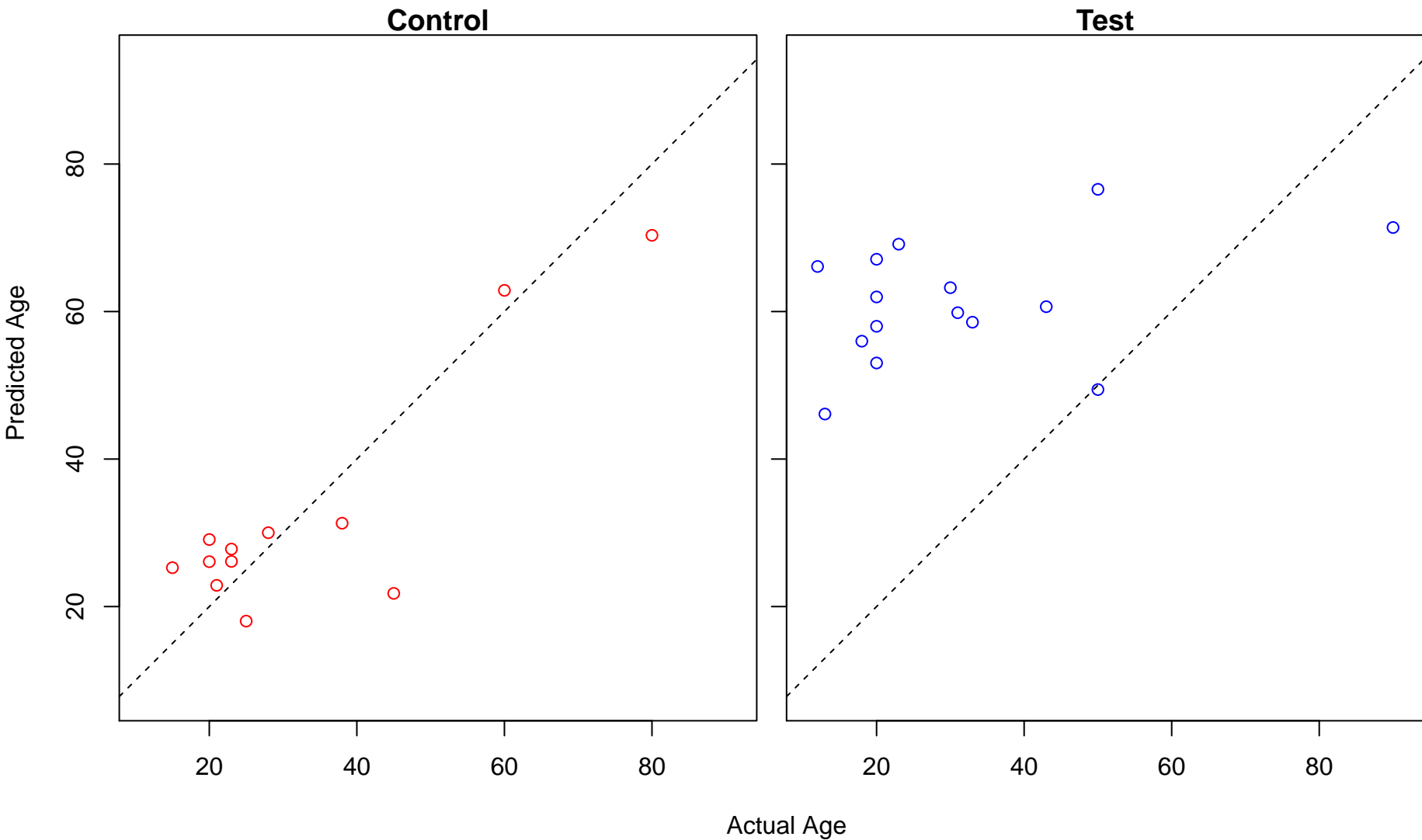
insulin receptor signaling pathway (Score: 5.190697)



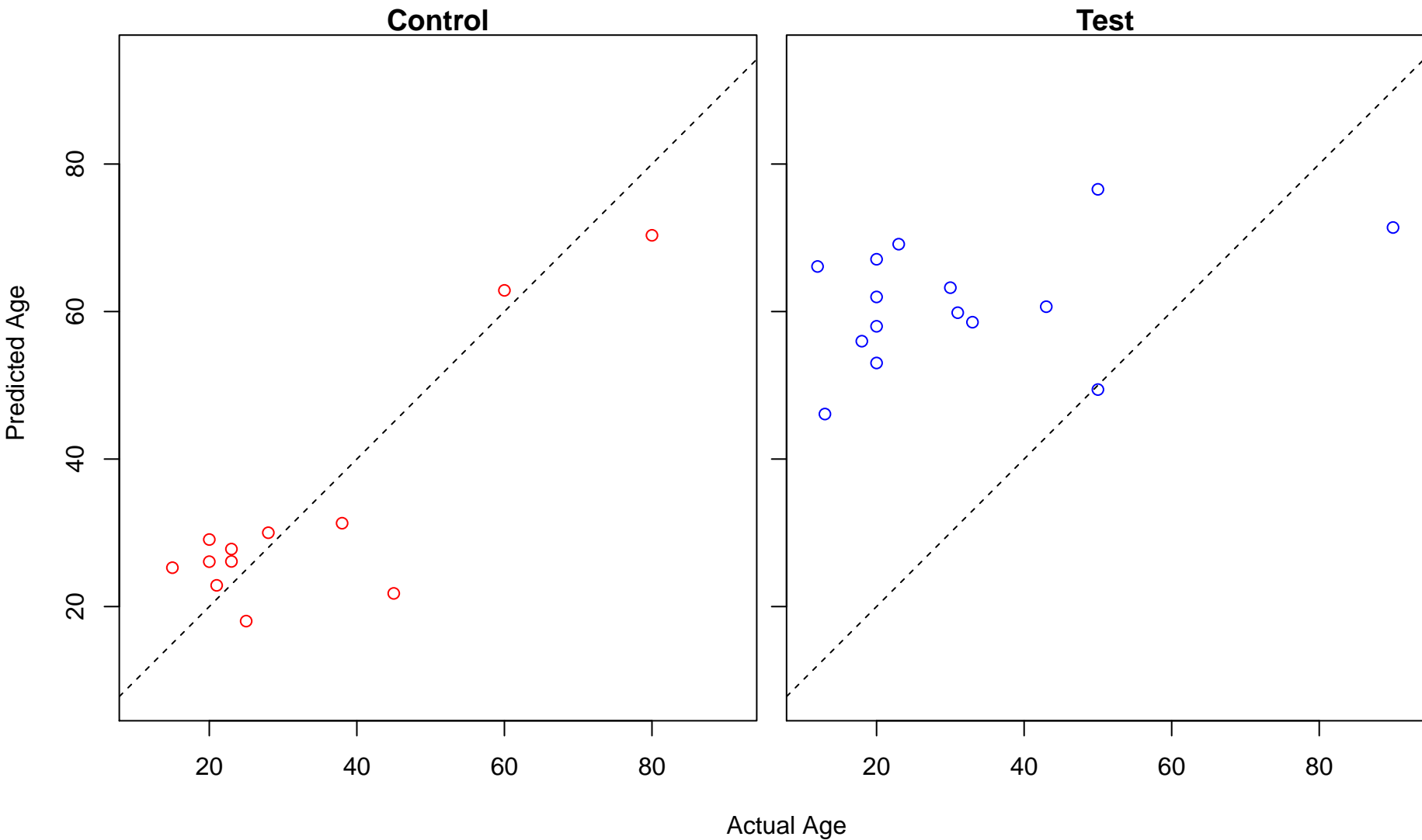
peptide transport (Score: 5.190166)



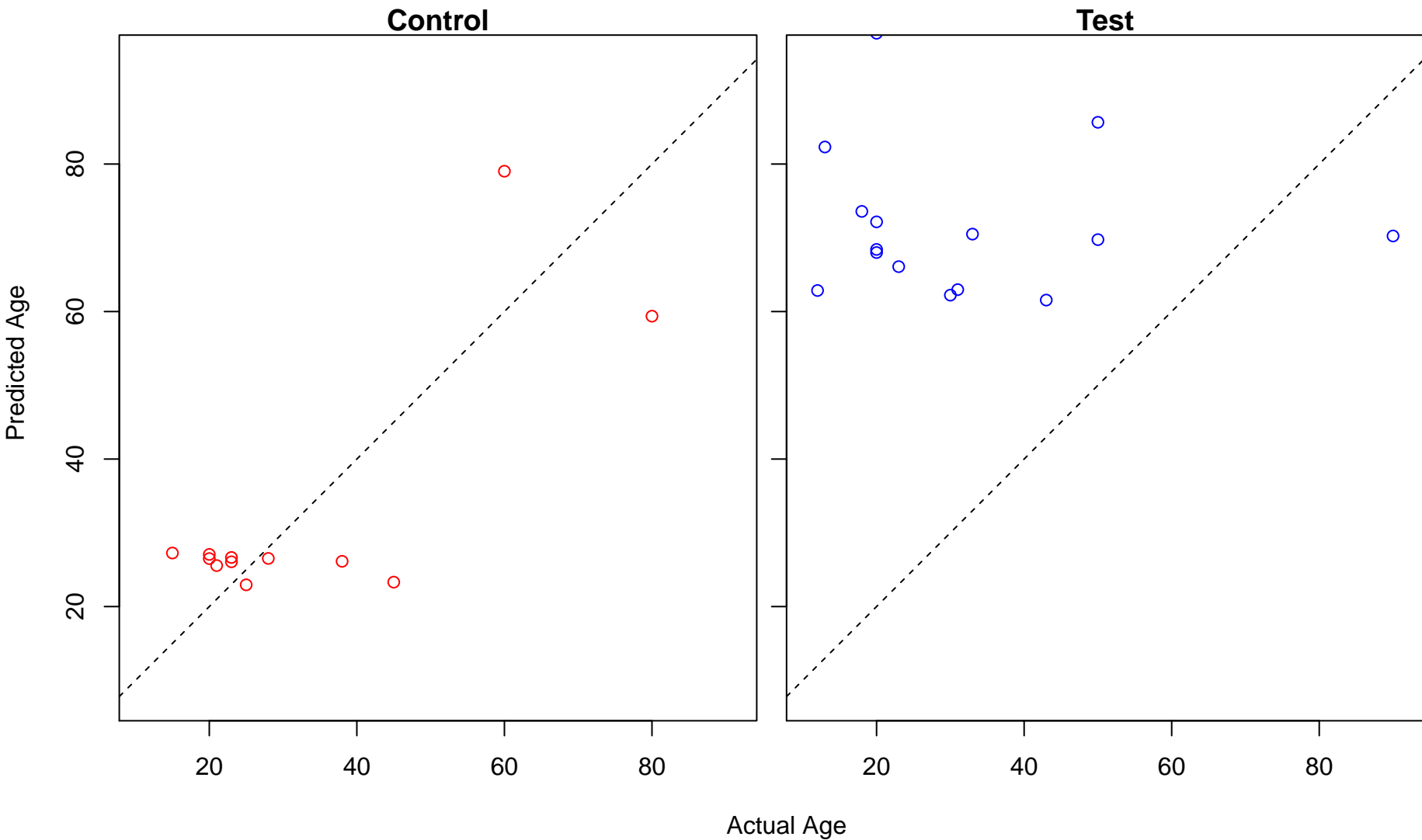
lysosome organization (Score: 5.190120)



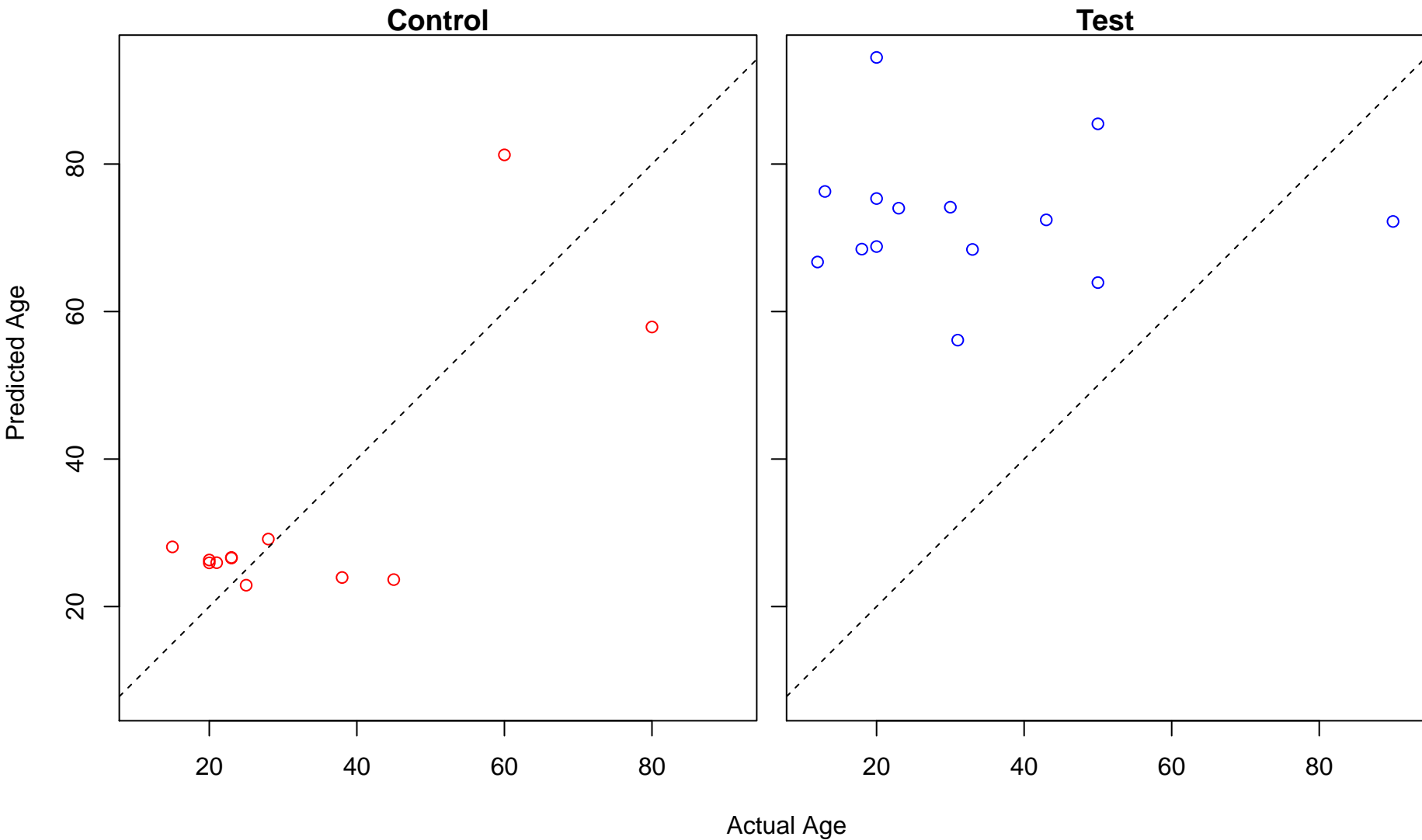
lytic vacuole organization (Score: 5.190120)



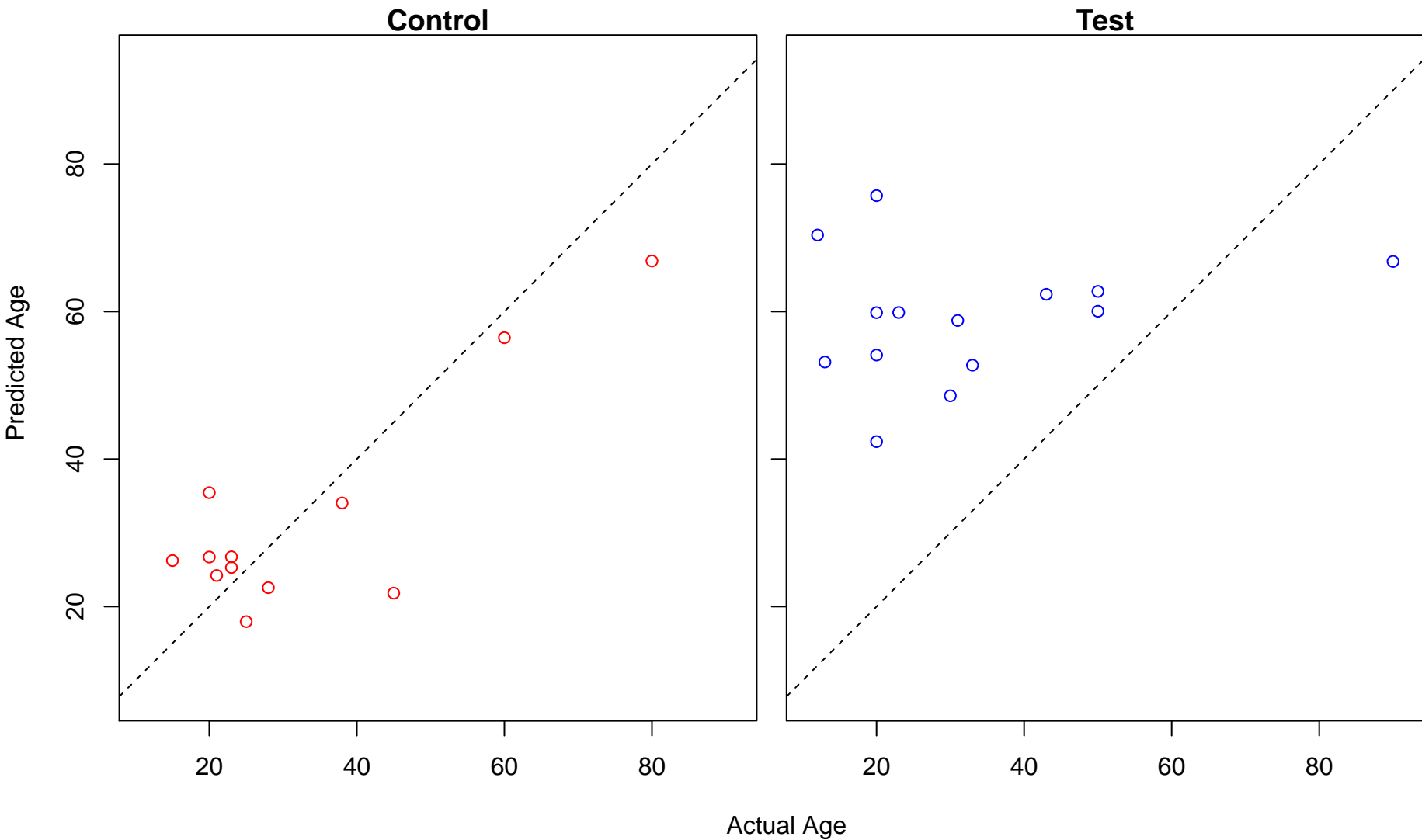
cellular response to insulin stimulus (Score: 5.186960)



heme biosynthetic process (Score: 5.186684)

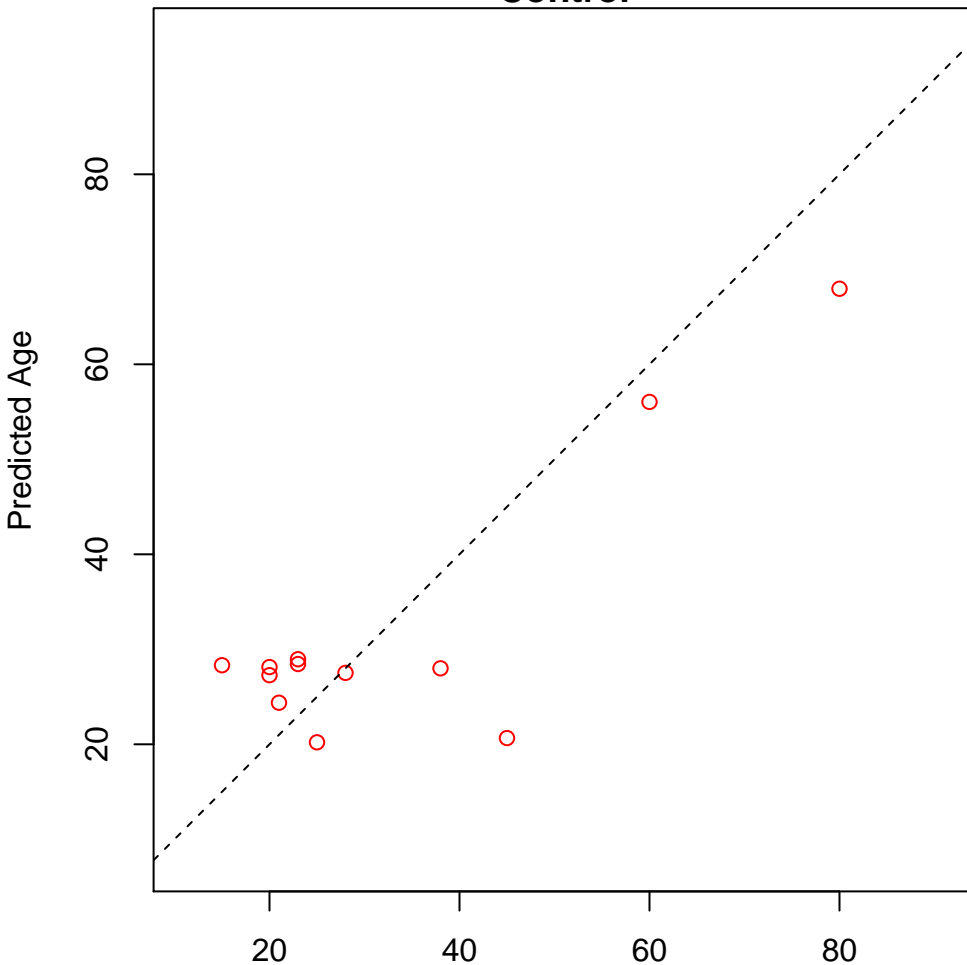


positive regulation of stem cell differentiation (Score: 5.185754)

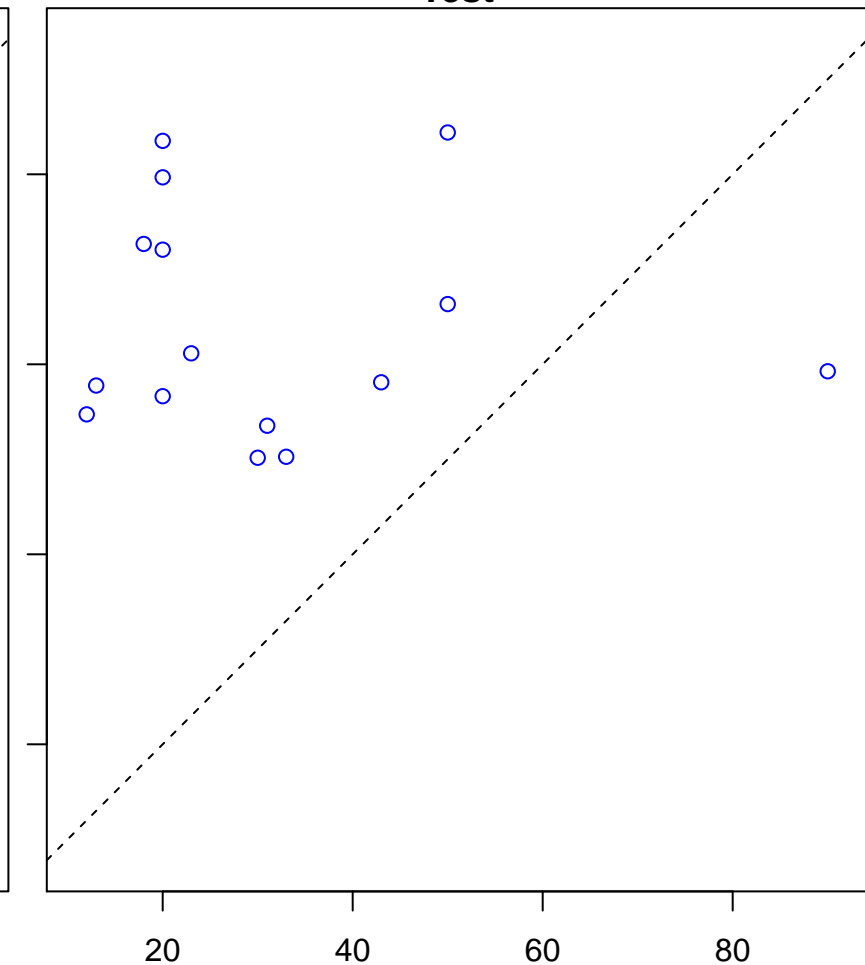


postsynaptic membrane organization (Score: 5.183328)

Control

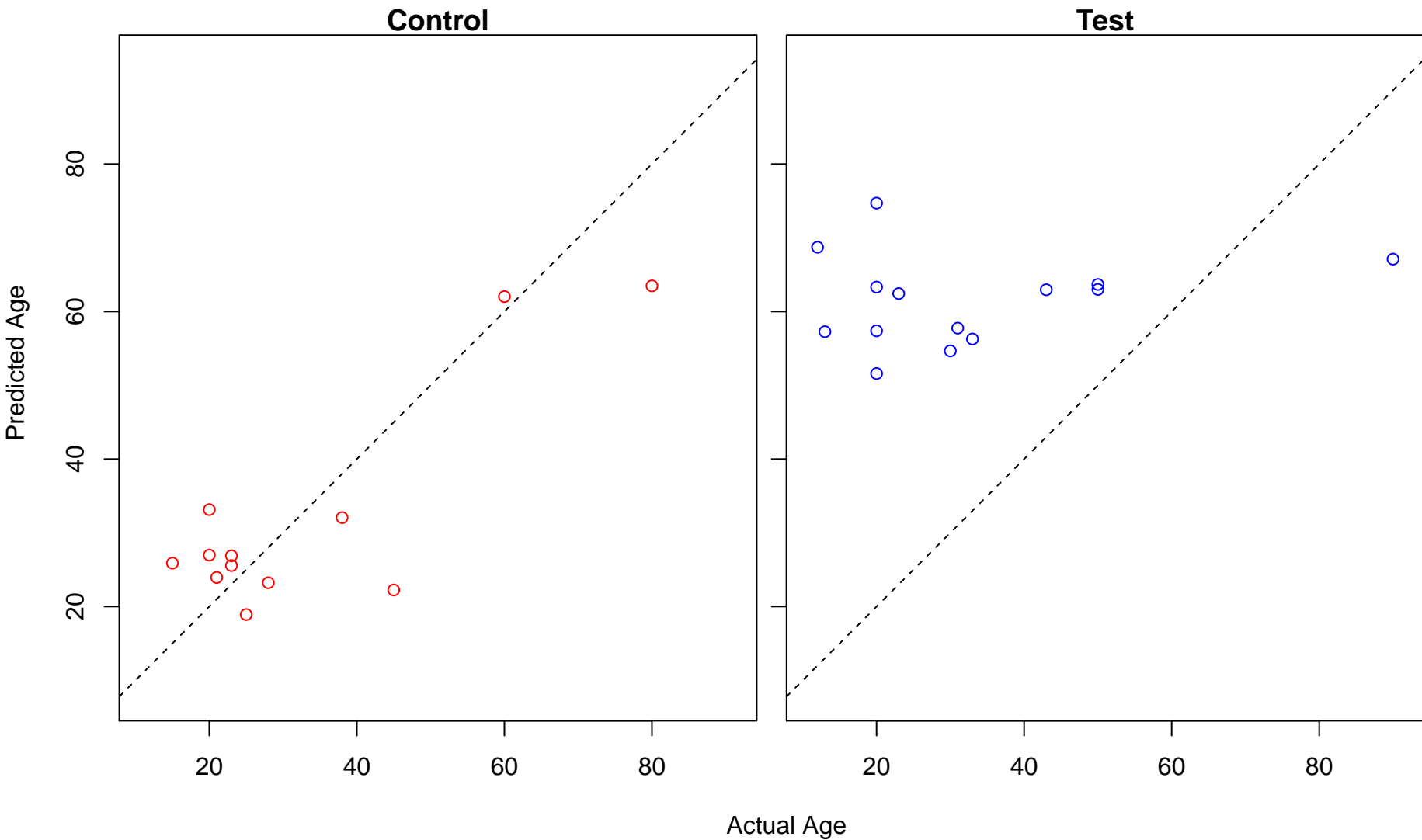


Test

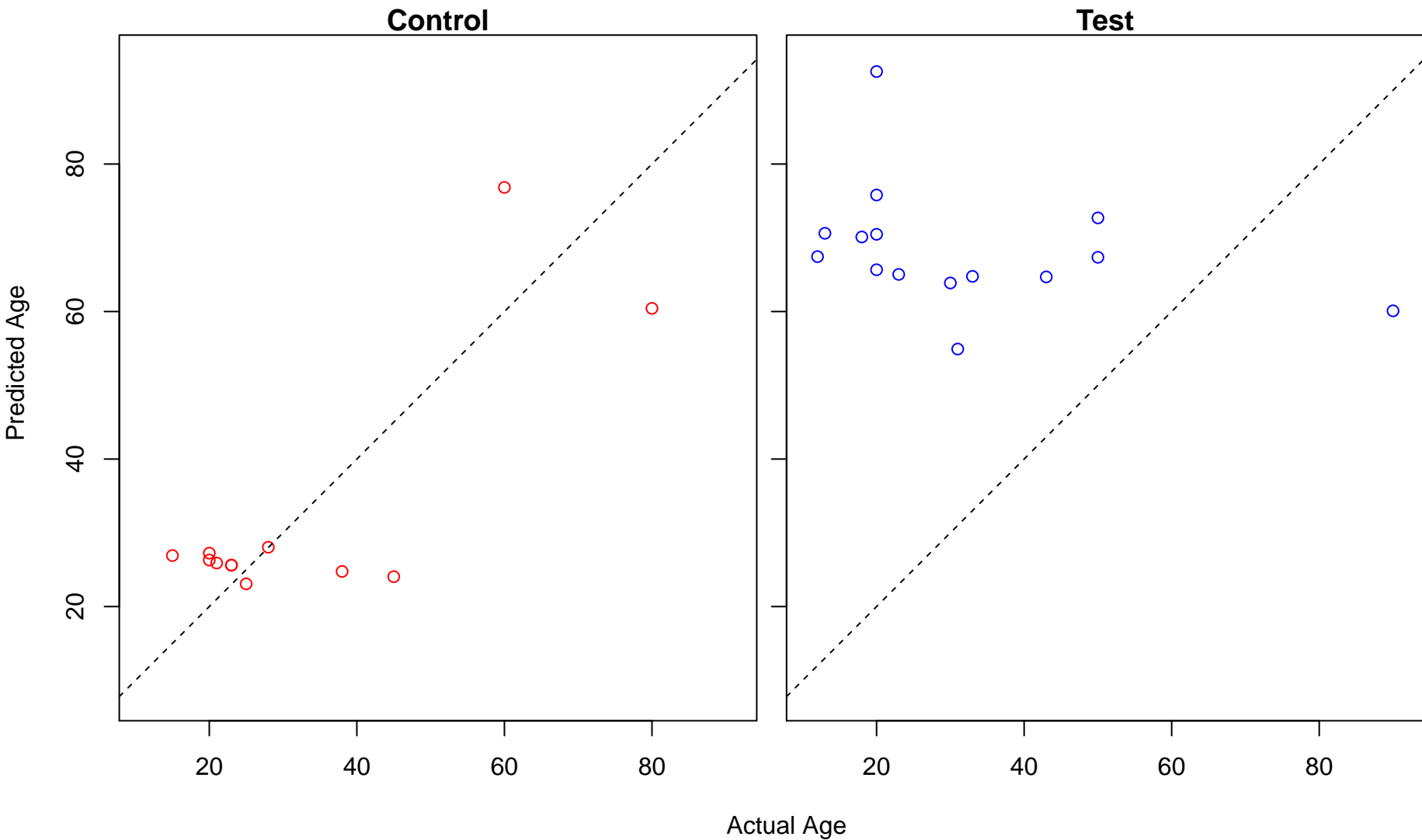


Actual Age

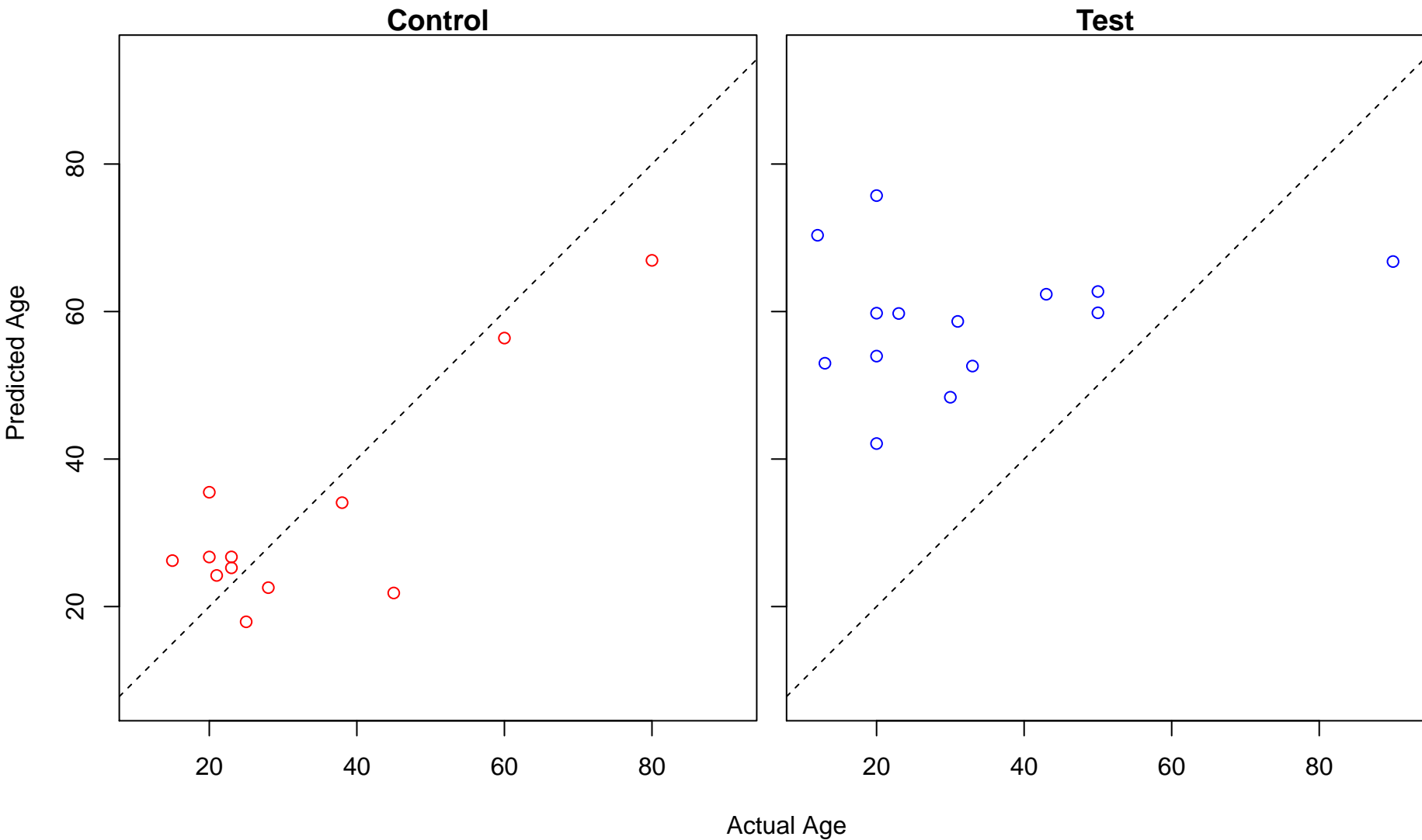
regulation of stem cell differentiation (Score: 5.182527)



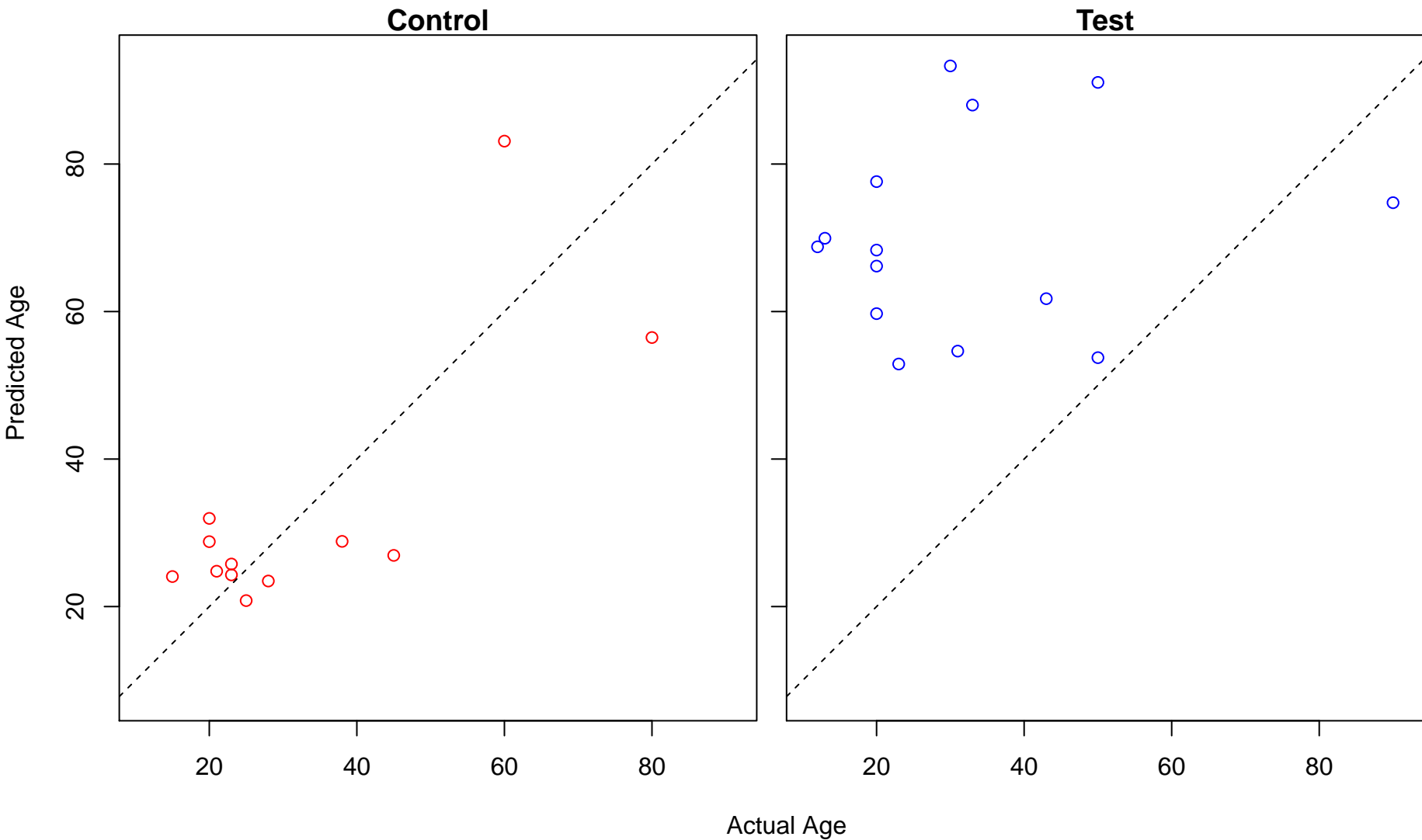
aging (Score: 5.182291)



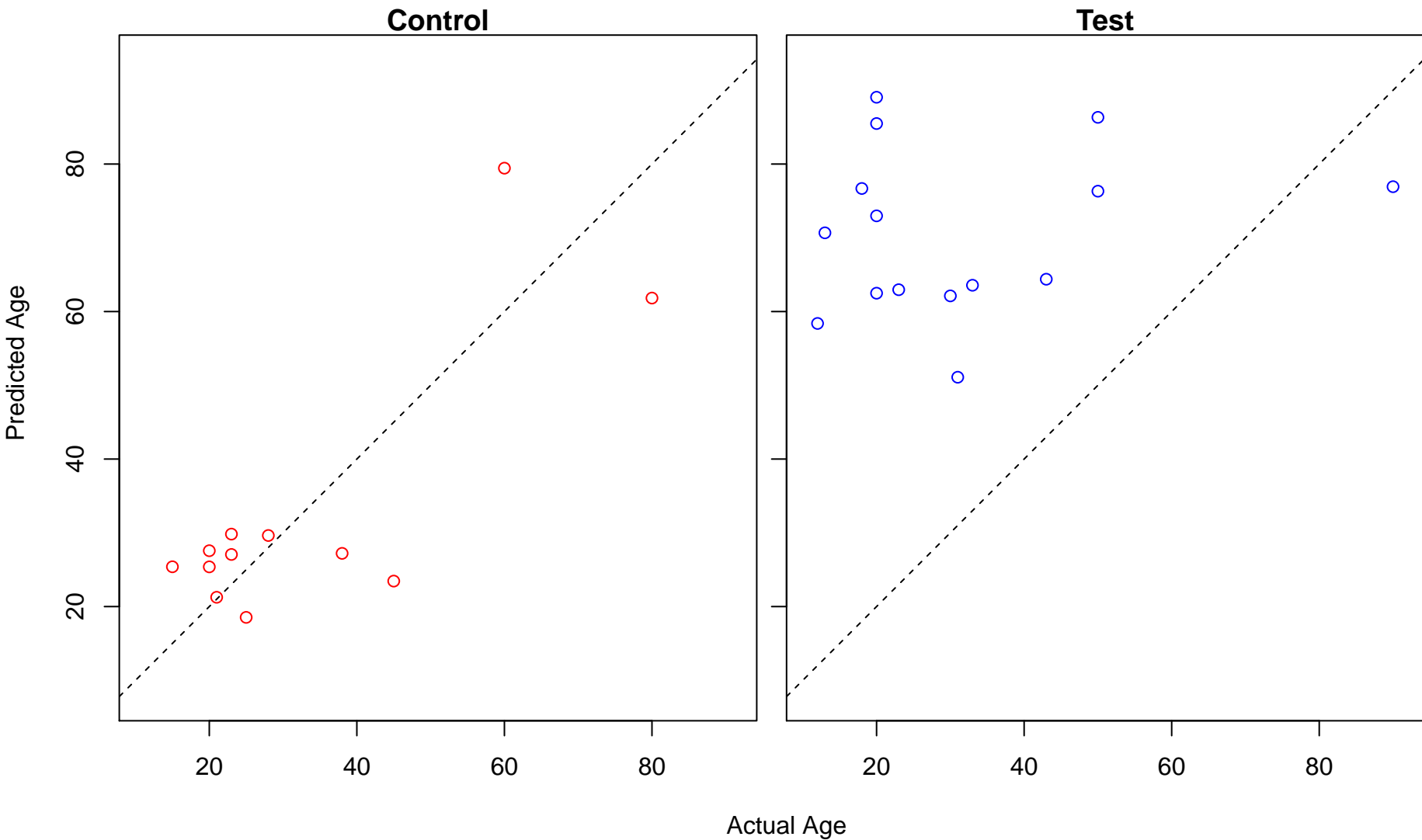
positive regulation of epithelial to mesenchymal transition (Score: 5.181870)



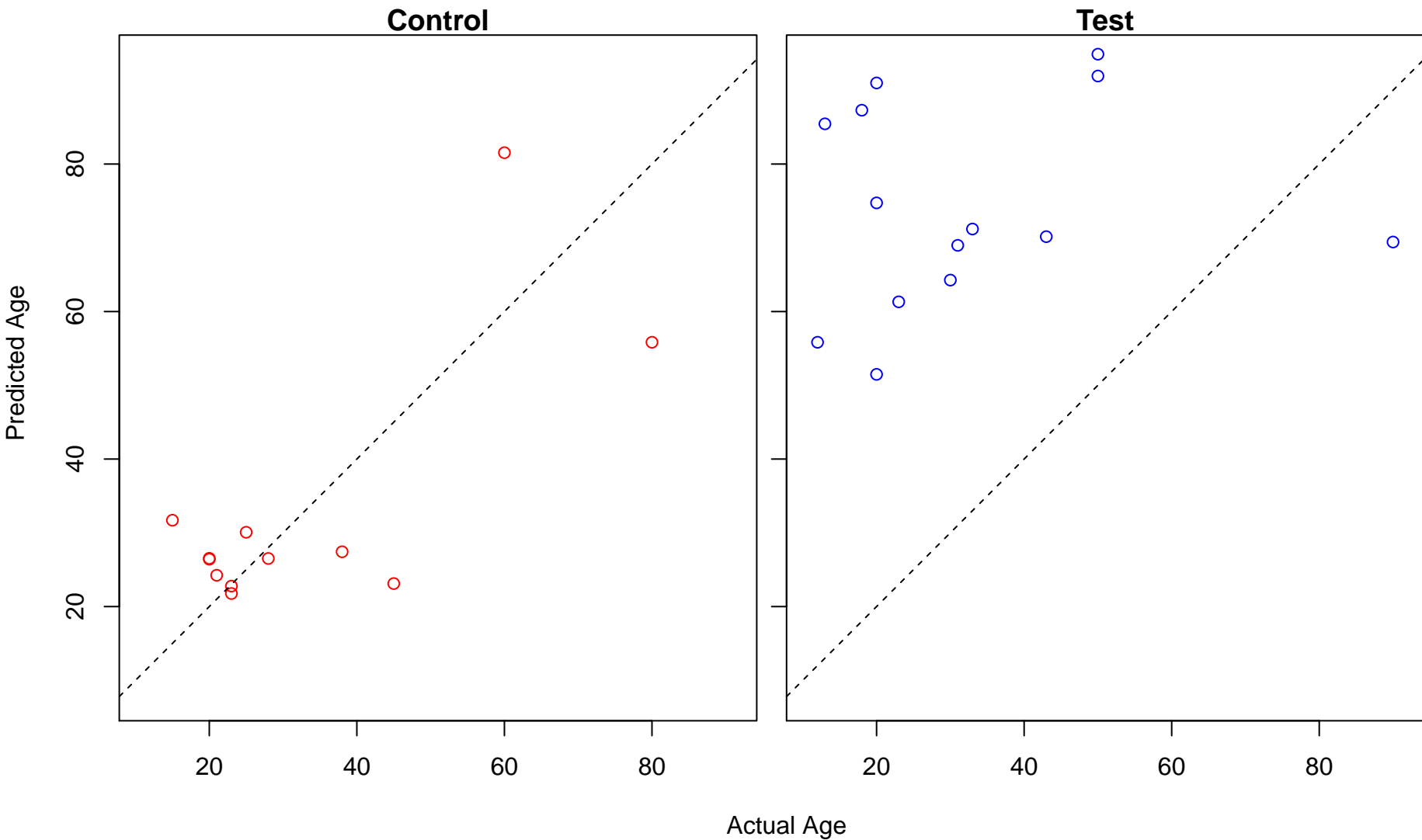
regulation of platelet-derived growth factor receptor signaling pathway (Score: 5.180431)



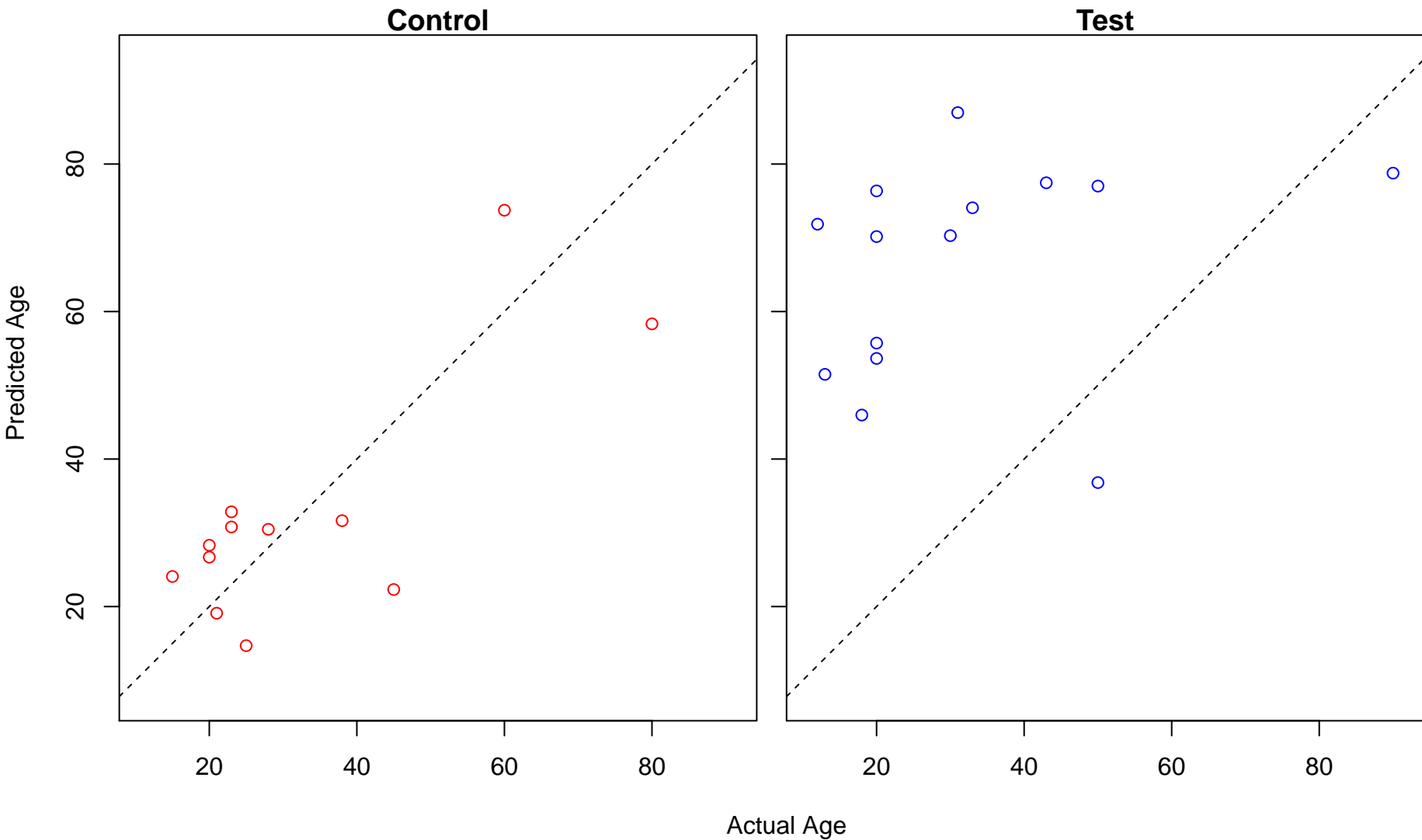
regulation of vascular endothelial growth factor signaling pathway (Score: 5.180046)



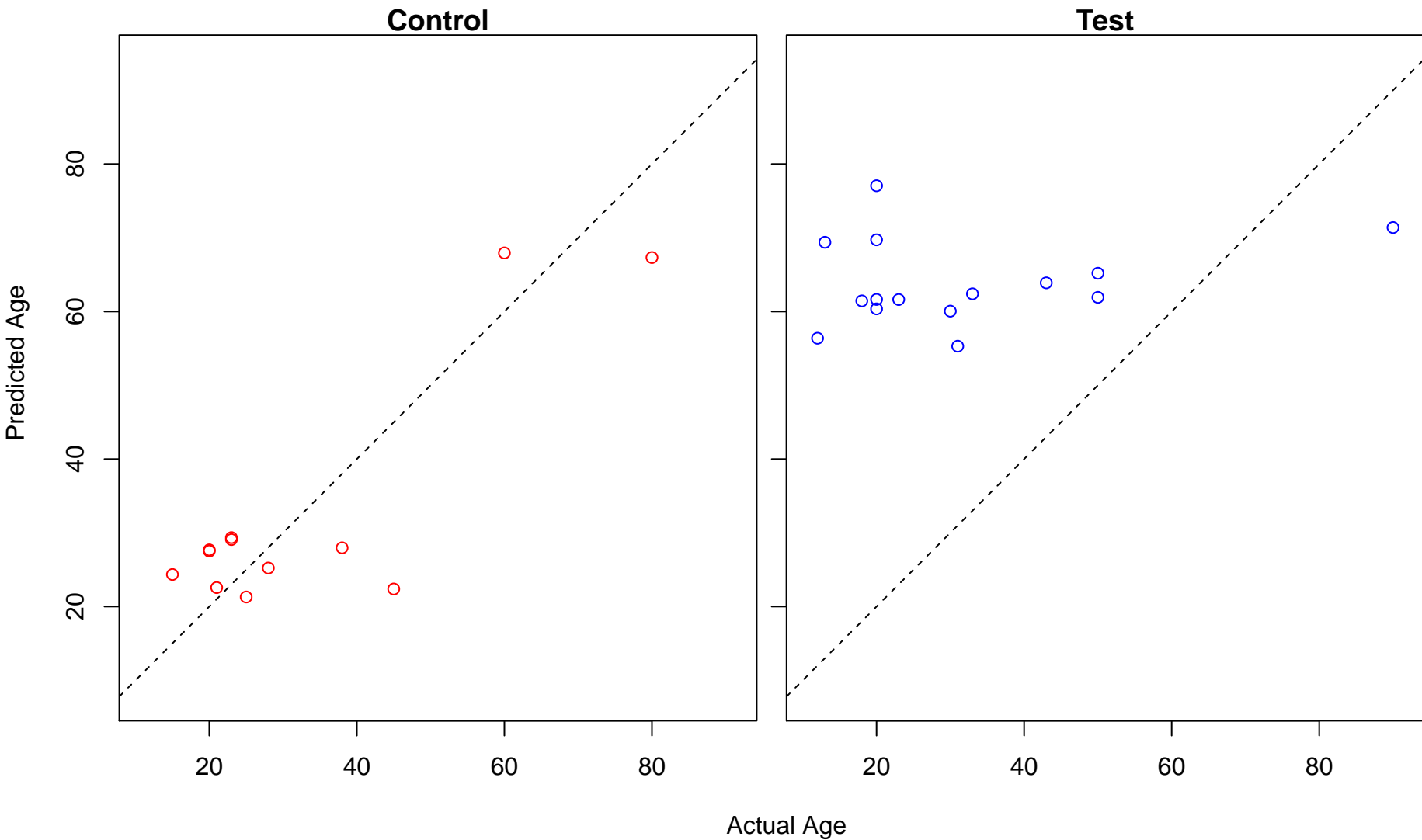
neuron apoptotic process (Score: 5.177508)



positive regulation of smoothened signaling pathway (Score: 5.177057)

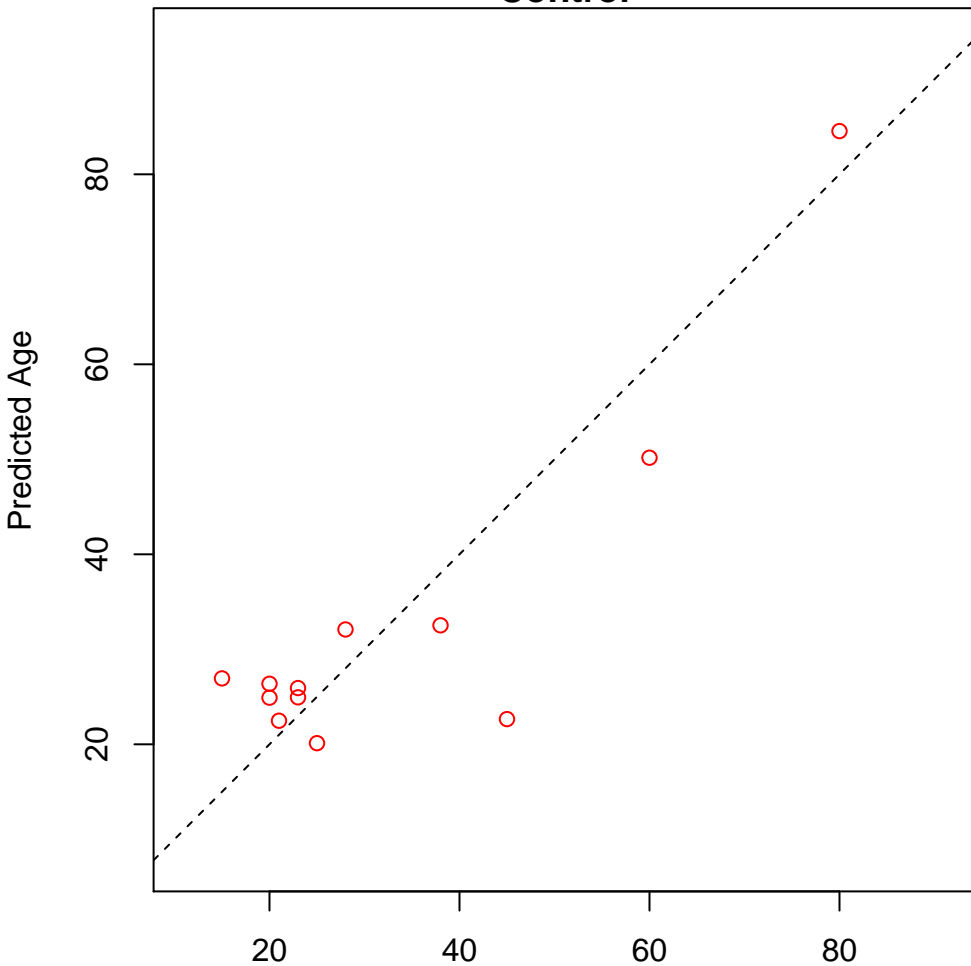


positive regulation of histone H3-K4 methylation (Score: 5.175637)

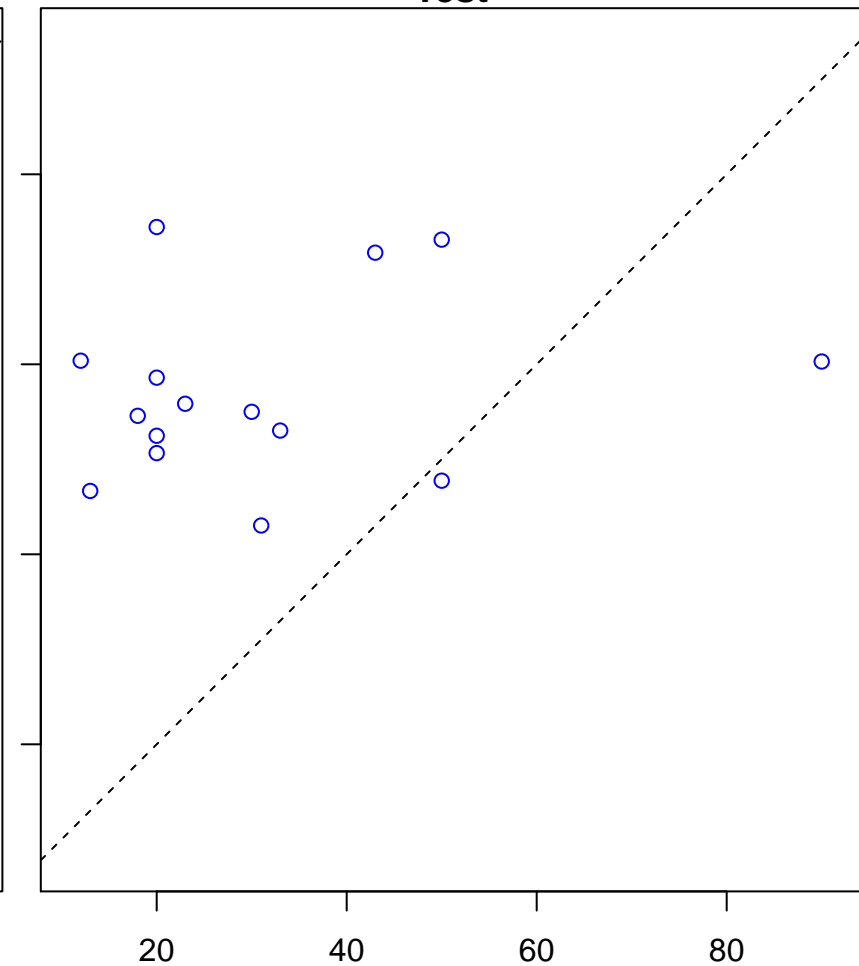


vascular process in circulatory system (Score: 5.175551)

Control

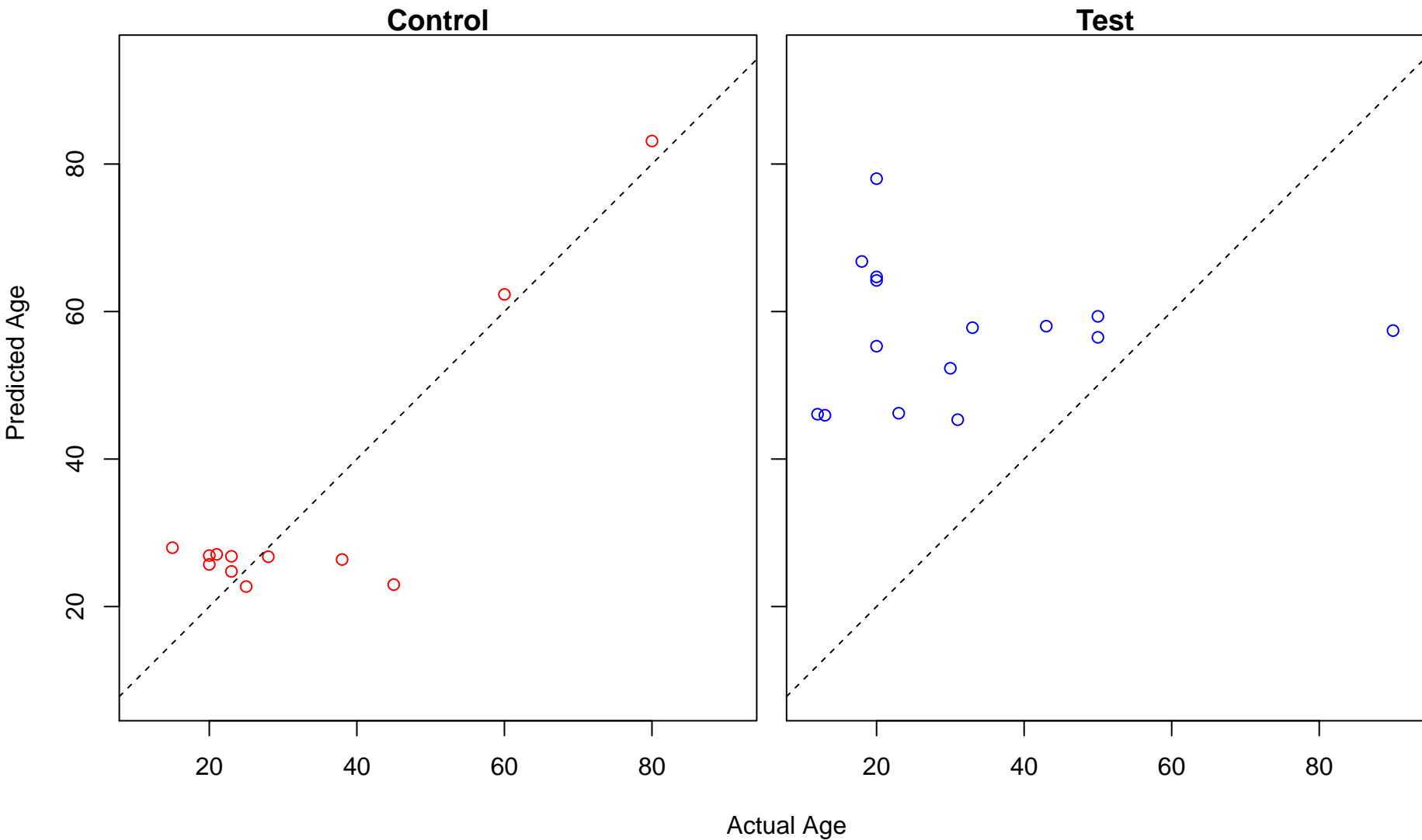


Test

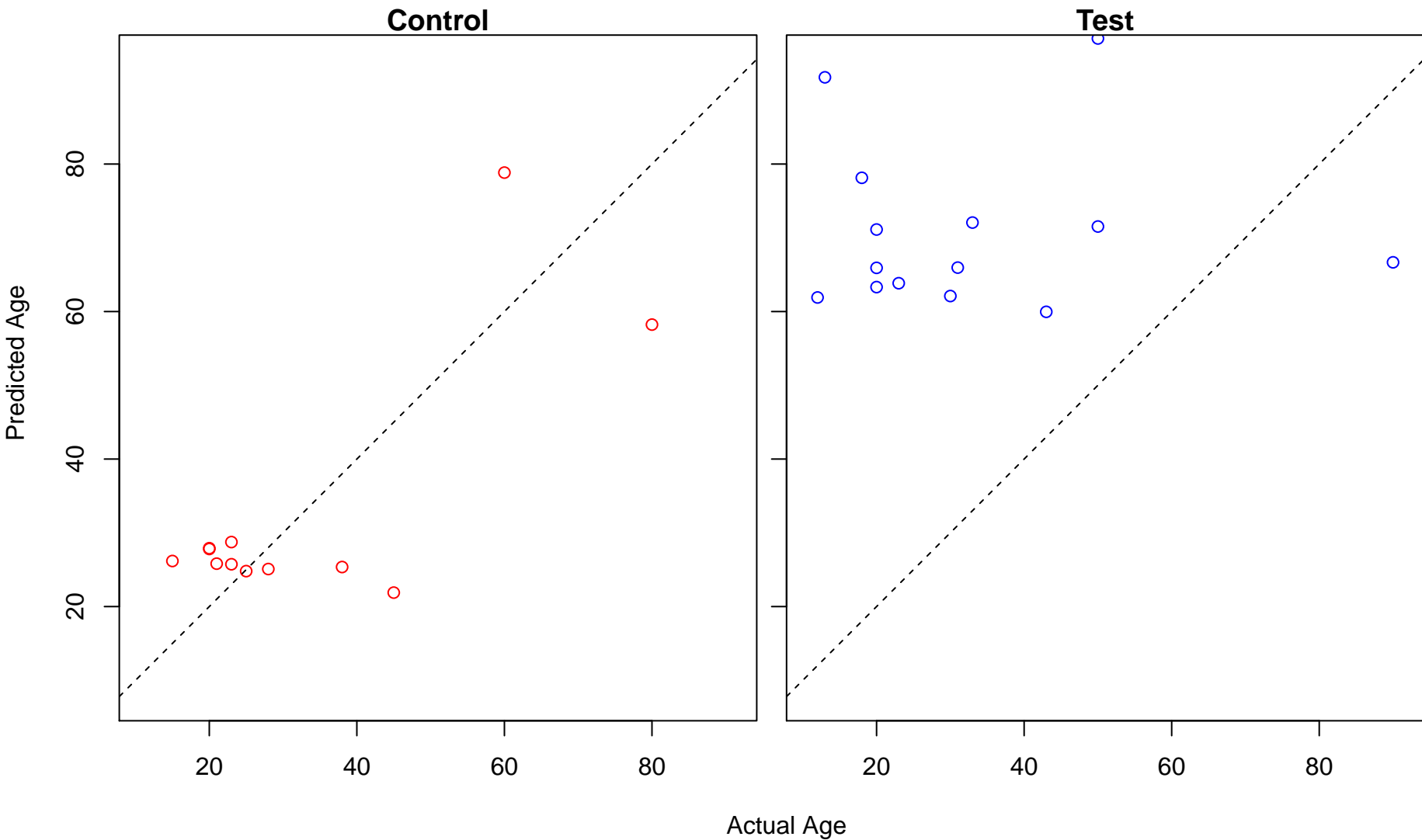


Actual Age

positive regulation of cell projection organization (Score: 5.173057)

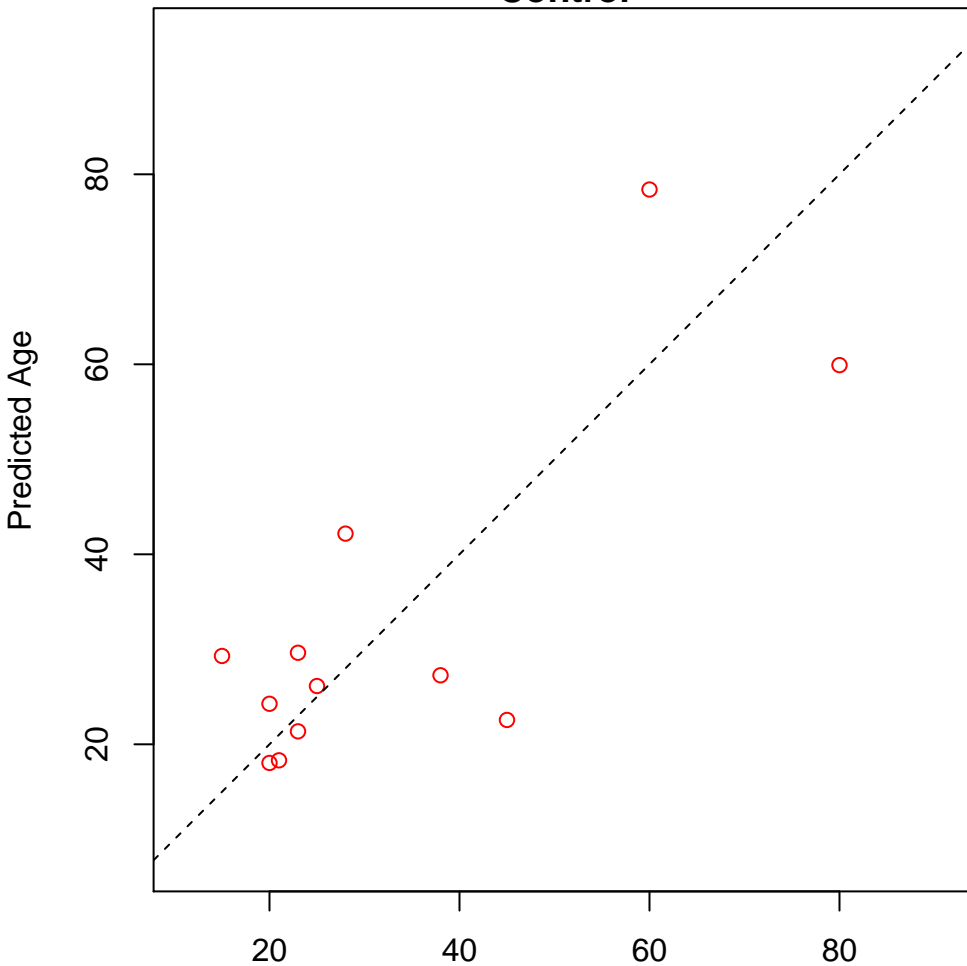


protein tetramerization (Score: 5.172933)

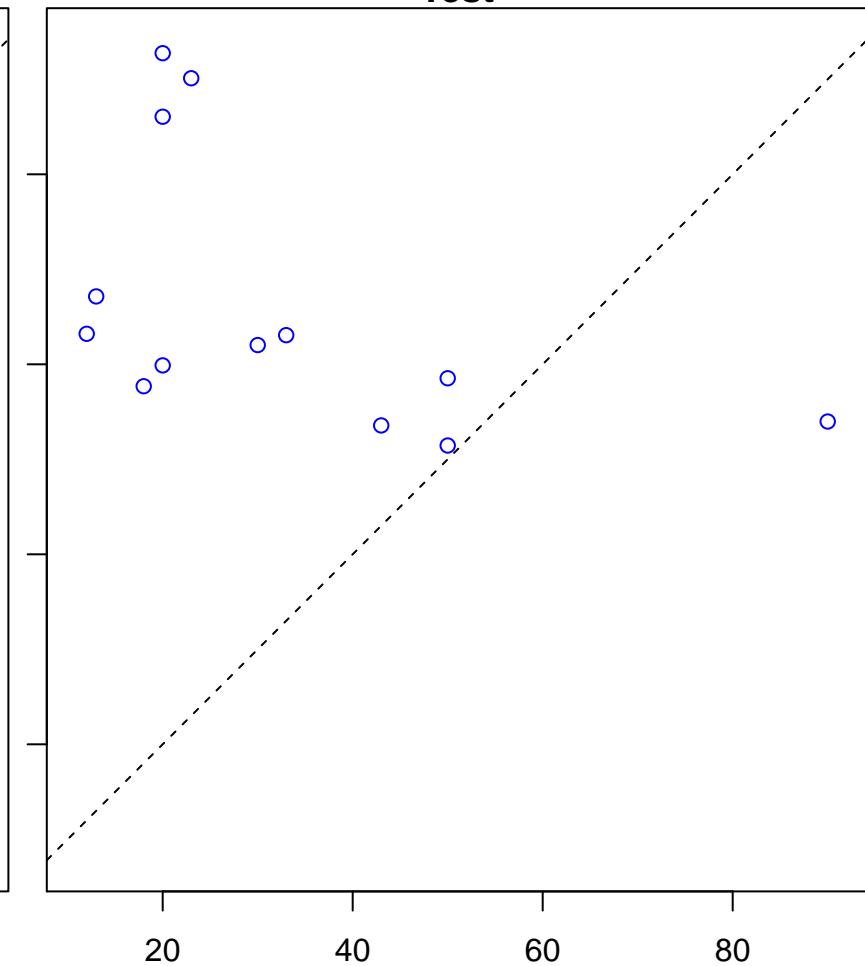


regulation of chondrocyte differentiation (Score: 5.172828)

Control

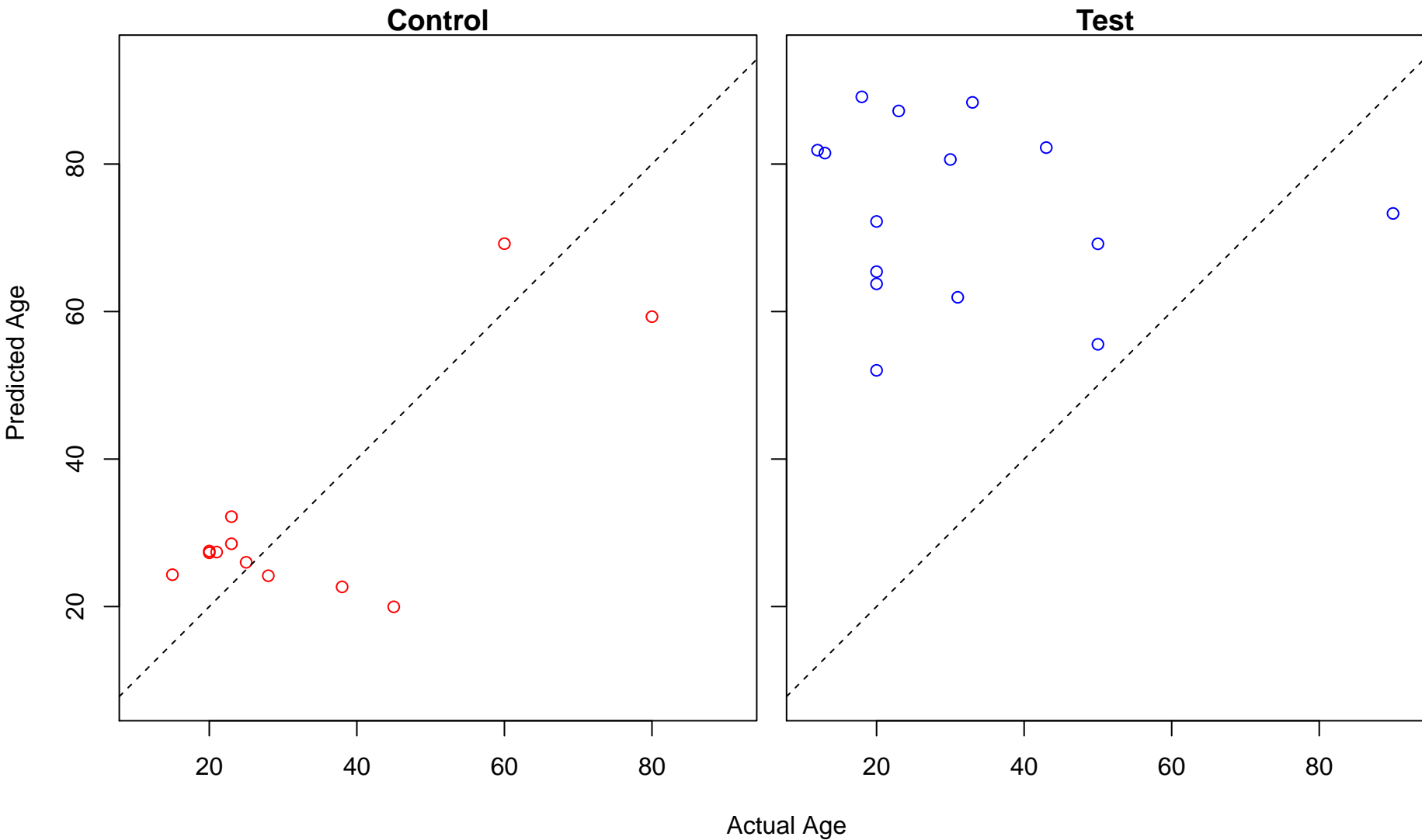


Test

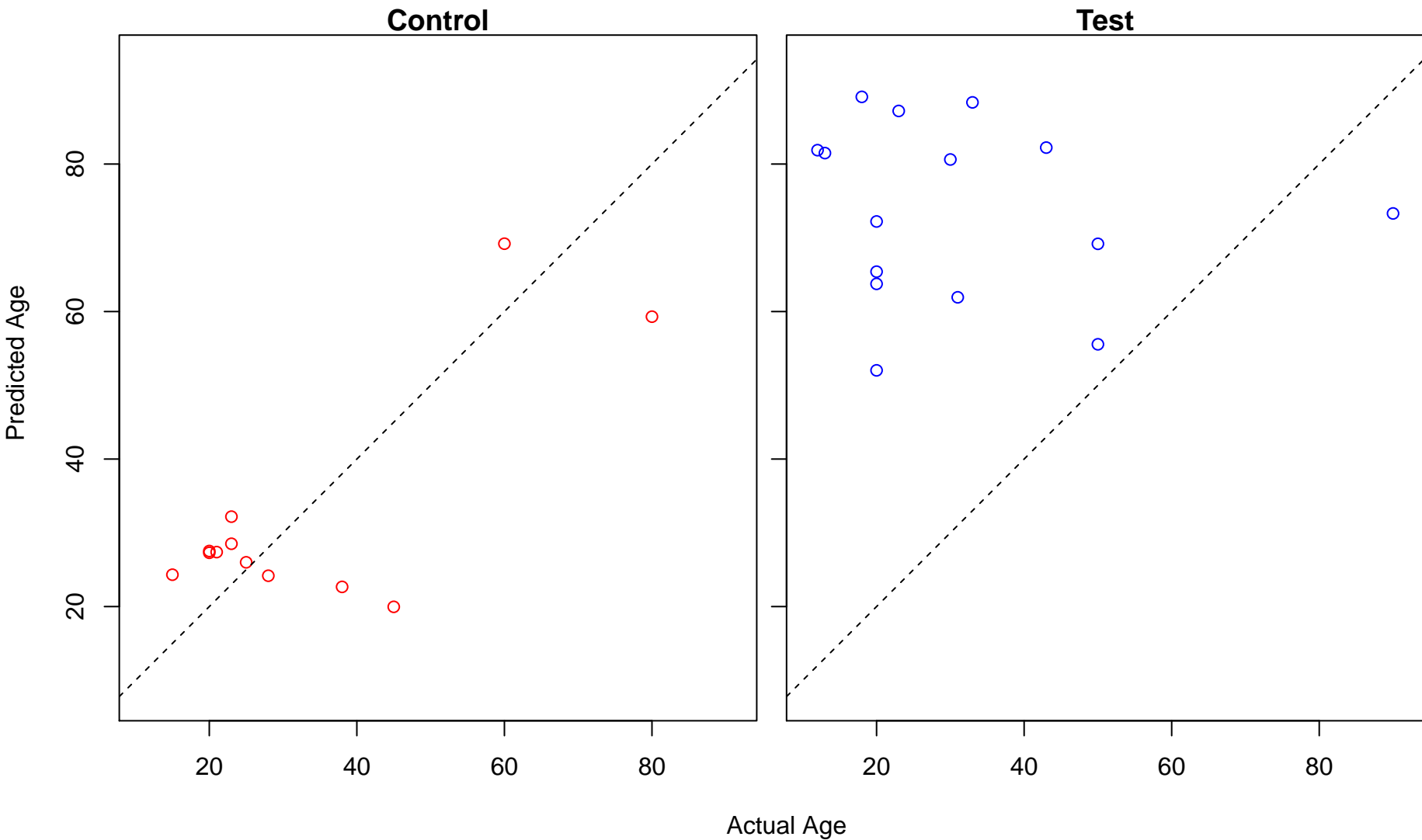


Actual Age

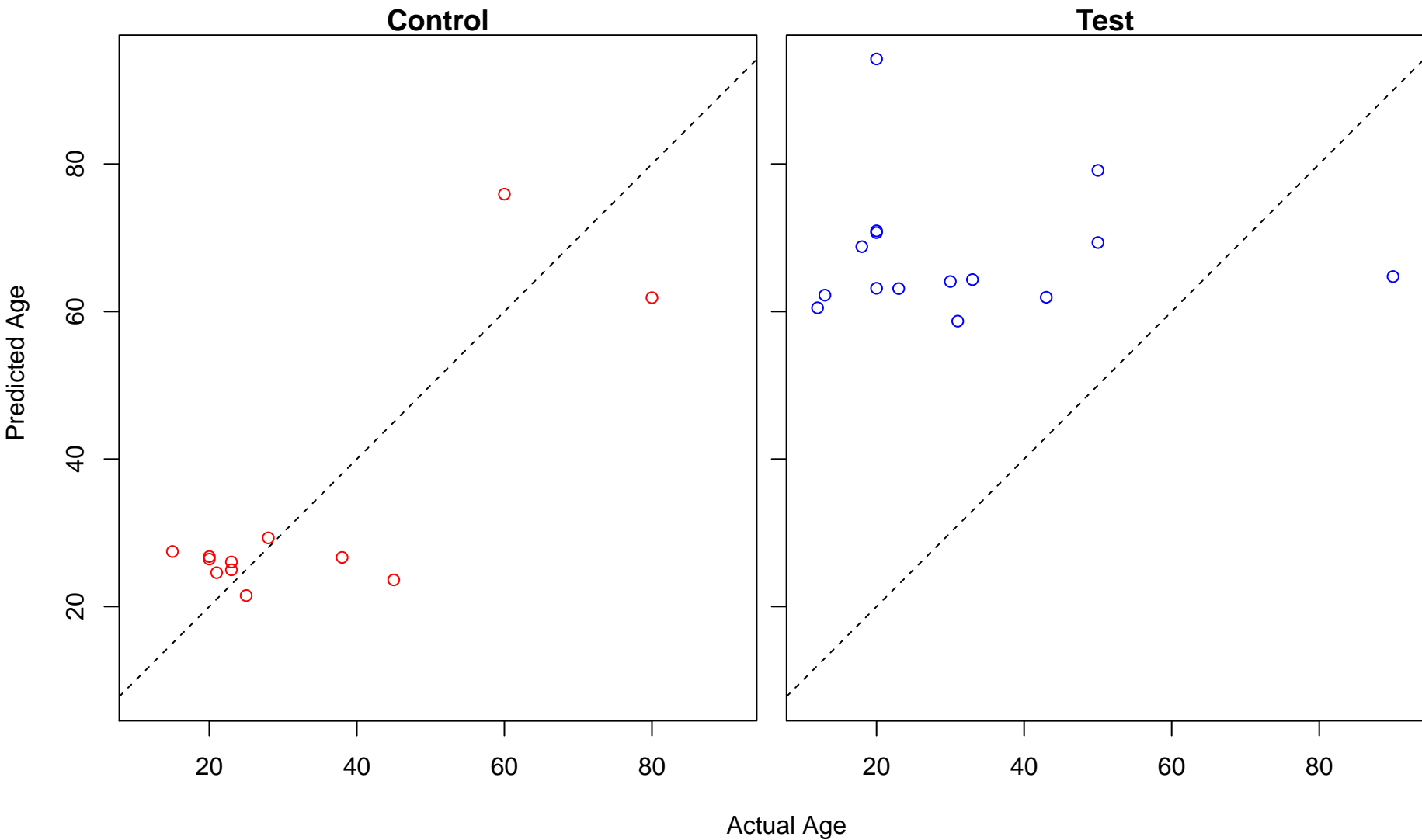
2'-deoxyribonucleotide metabolic process (Score: 5.172814)



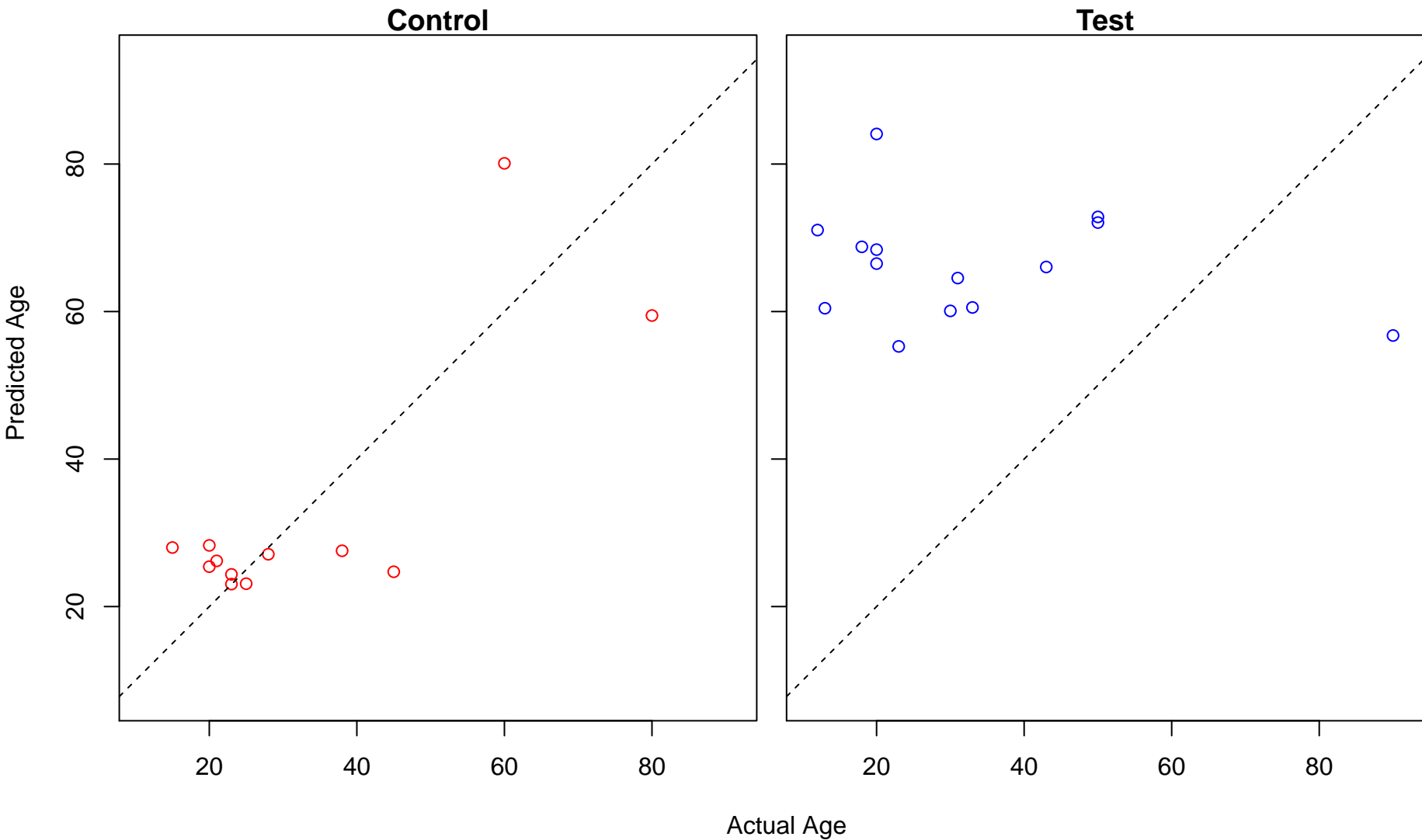
deoxyribose phosphate metabolic process (Score: 5.172814)



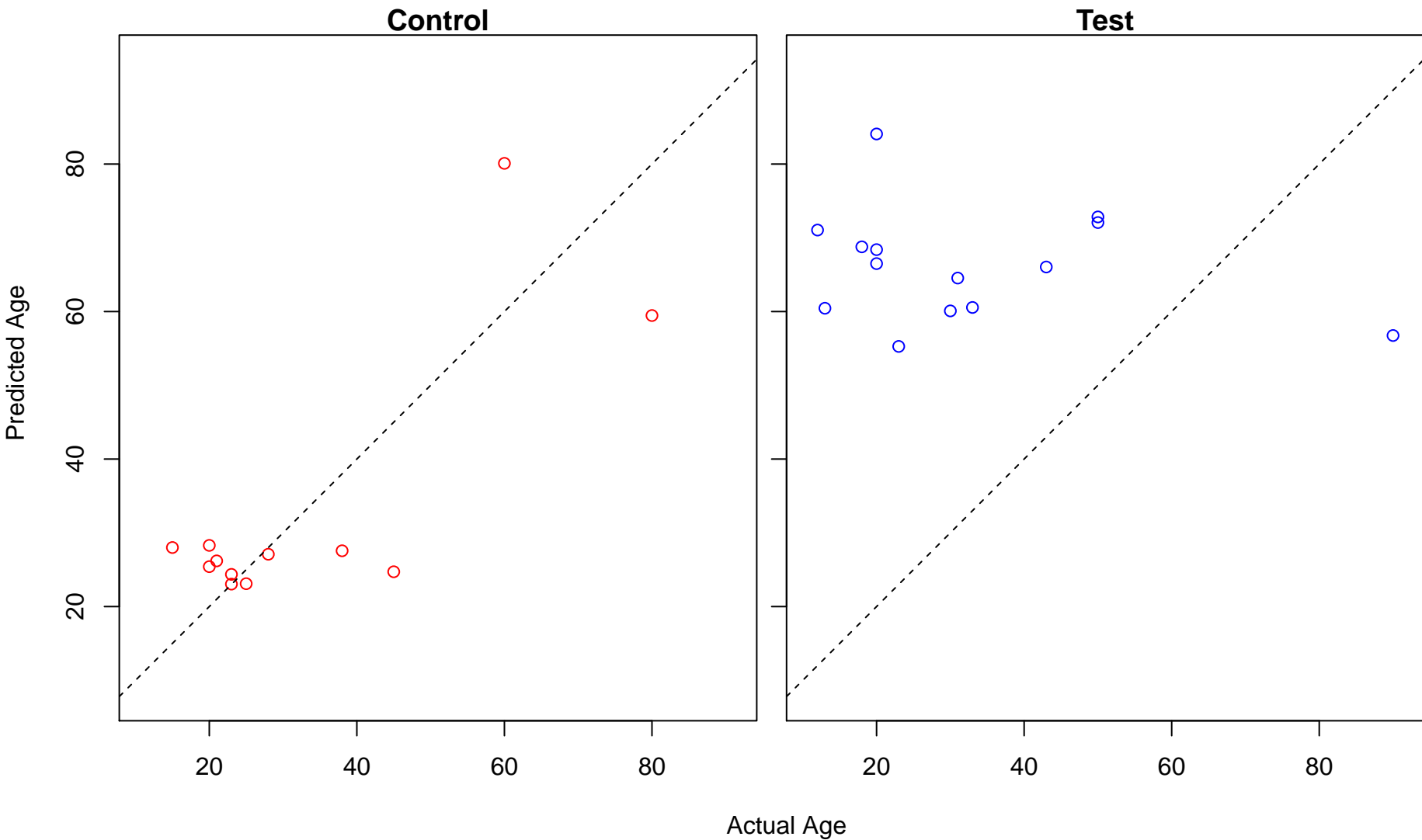
multicellular organism reproduction (Score: 5.168518)



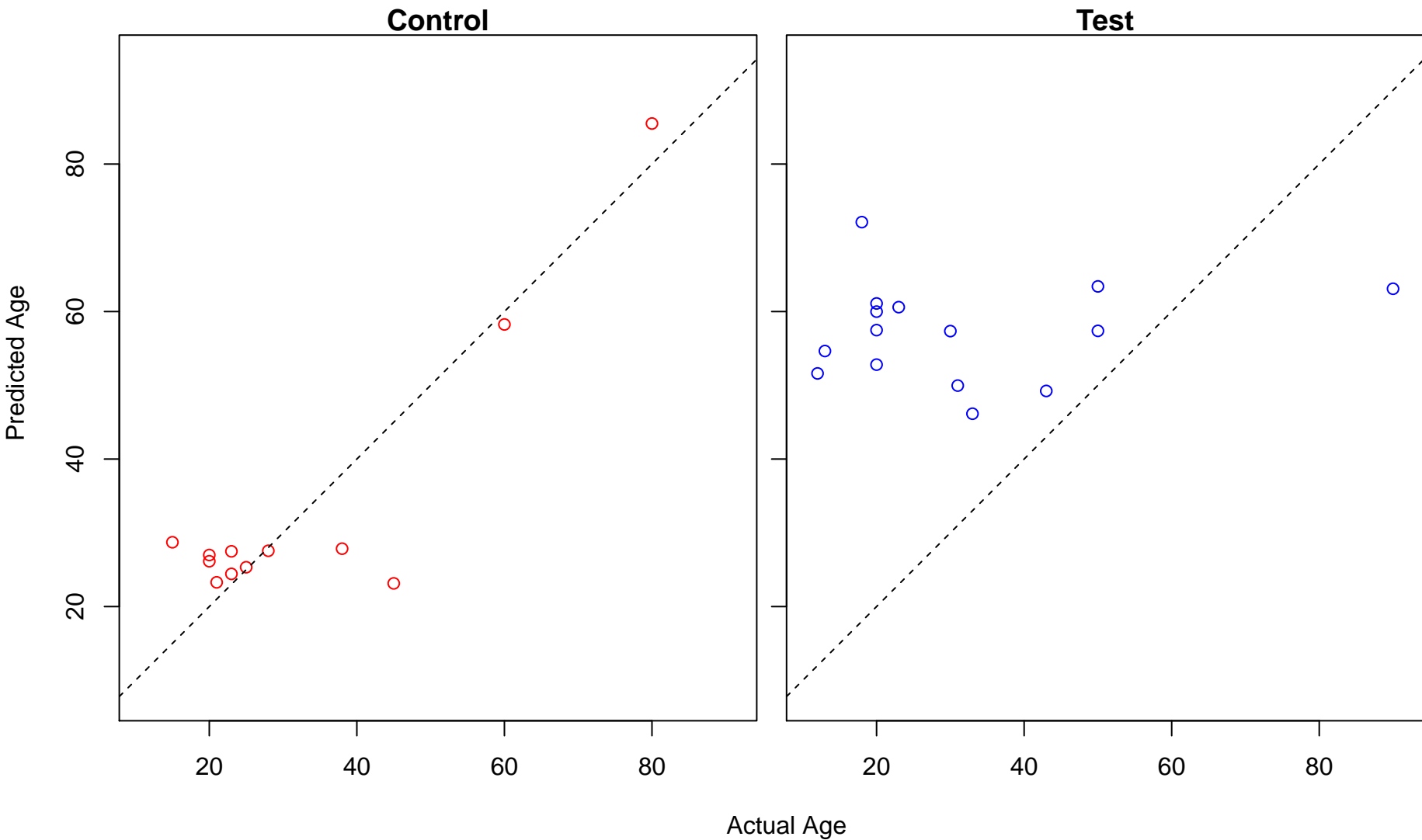
gonad development (Score: 5.167964)



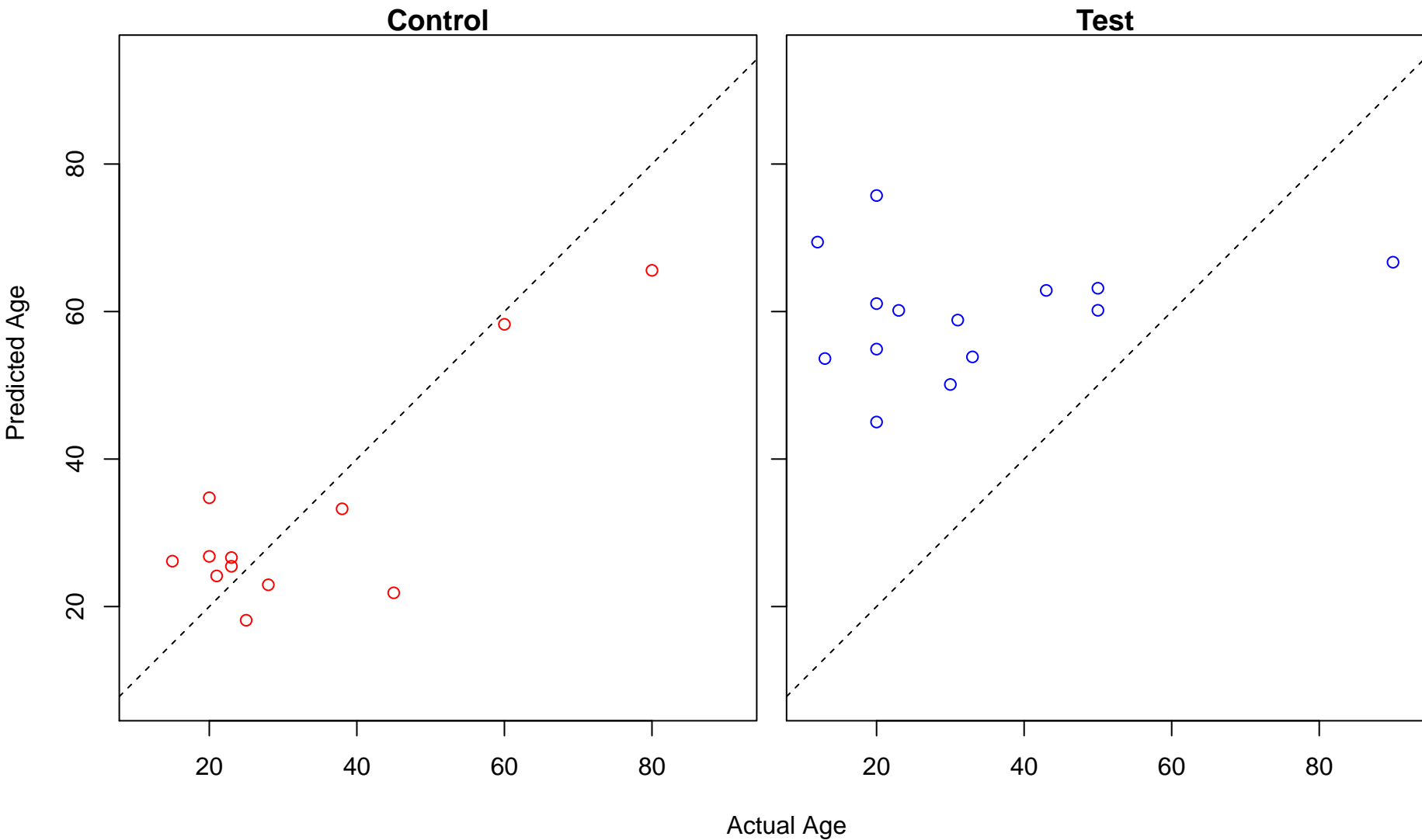
development of primary sexual characteristics (Score: 5.167955)



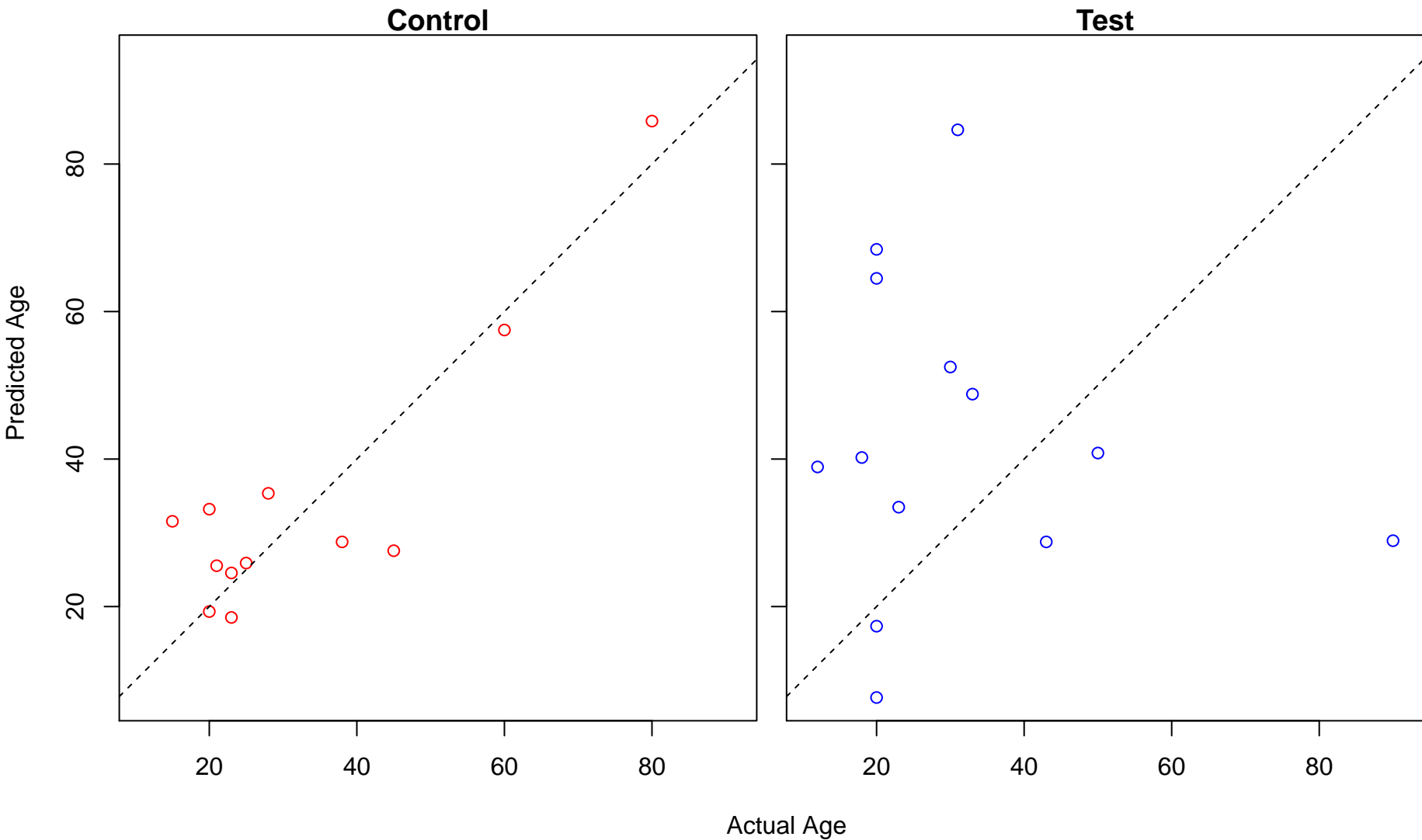
coenzyme metabolic process (Score: 5.167792)



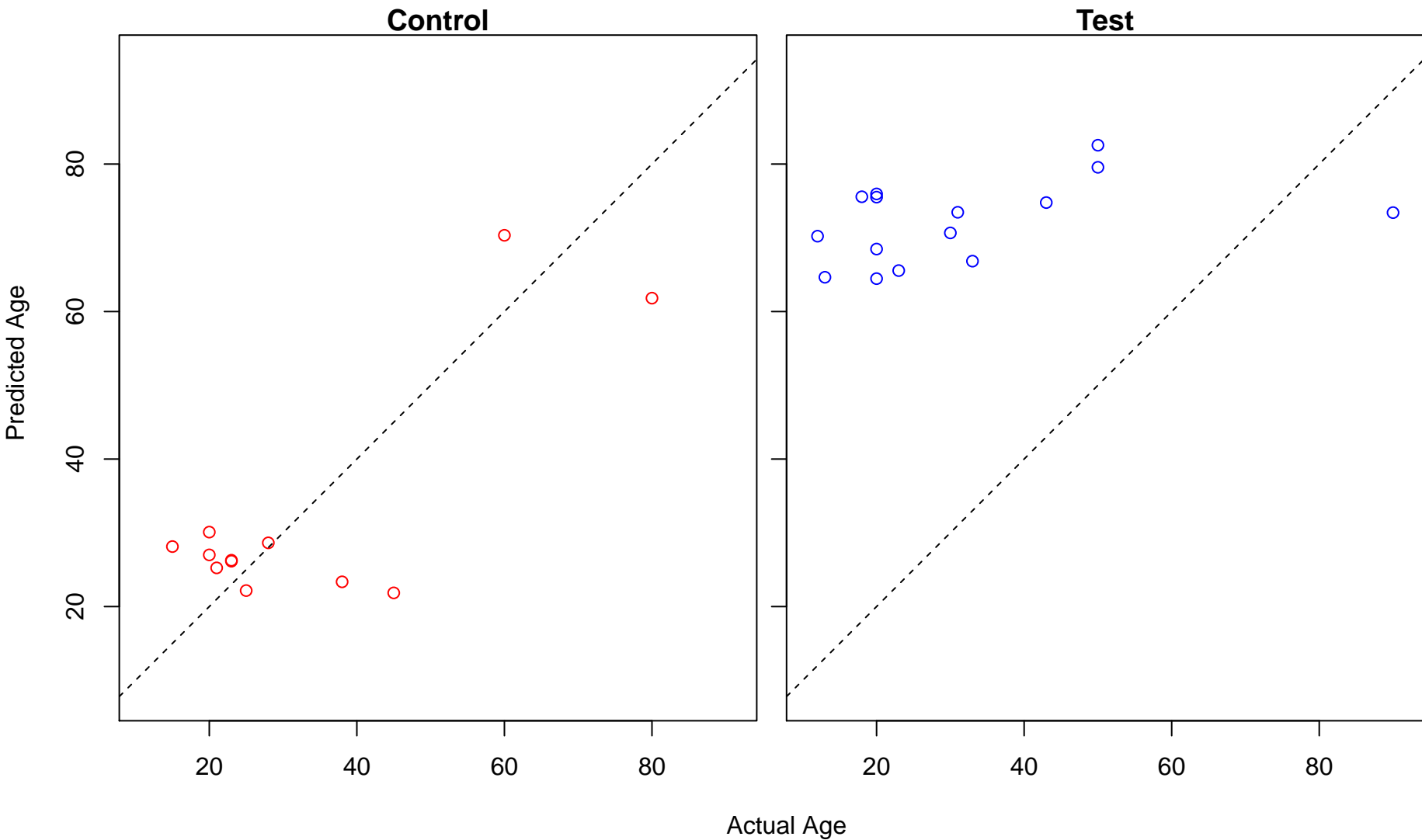
regulation of epithelial to mesenchymal transition (Score: 5.165909)



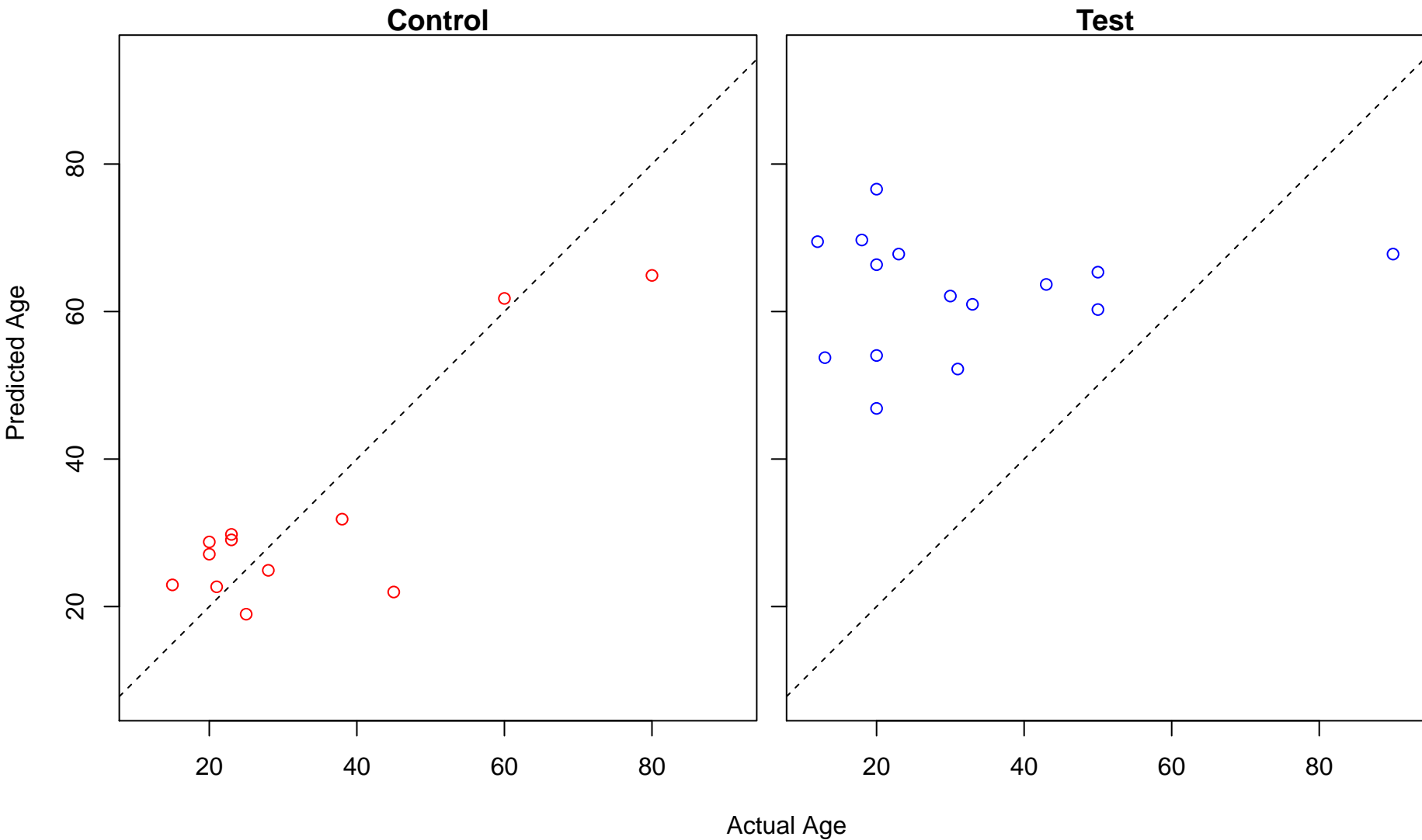
negative regulation of cellular component organization (Score: 5.164804)



second-messenger-mediated signaling (Score: 5.163684)

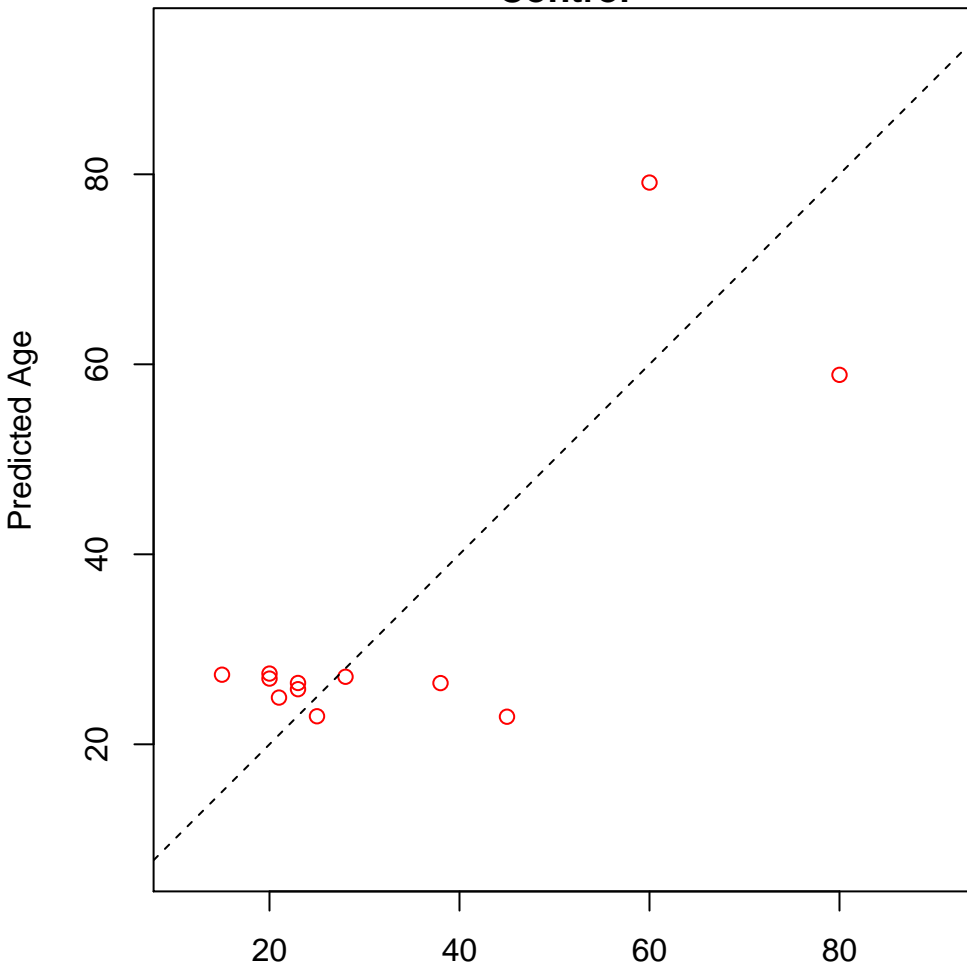


forebrain neuron differentiation (Score: 5.162915)

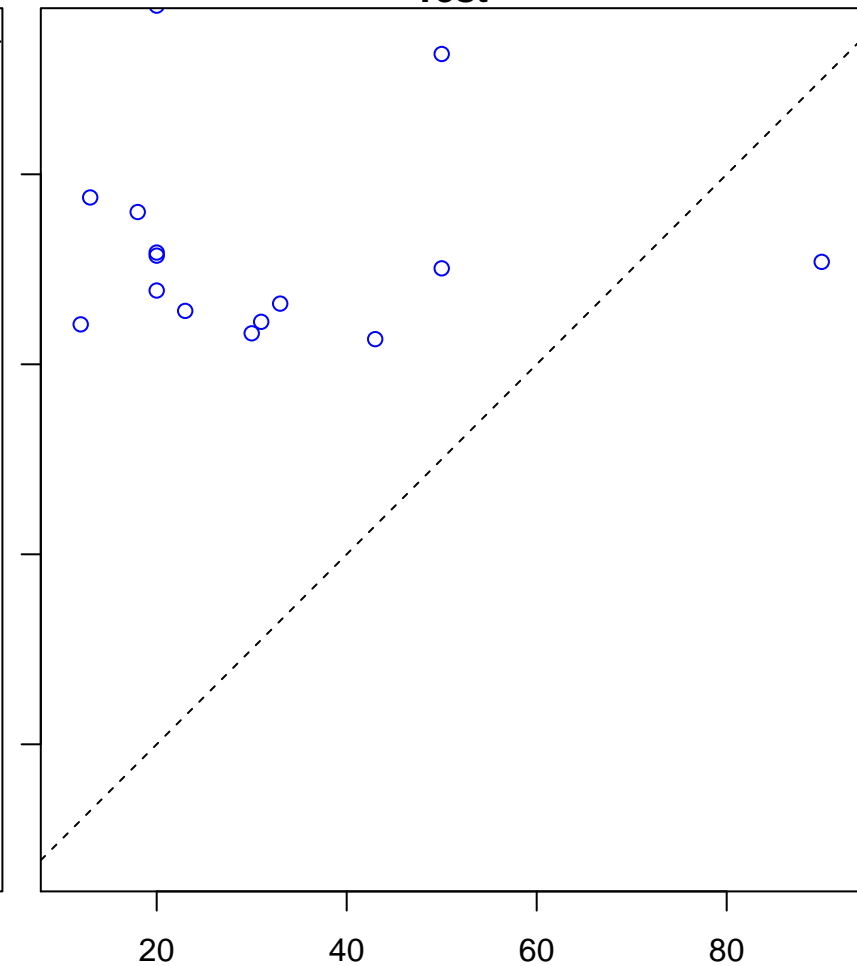


regulation of protein catabolic process (Score: 5.162877)

Control

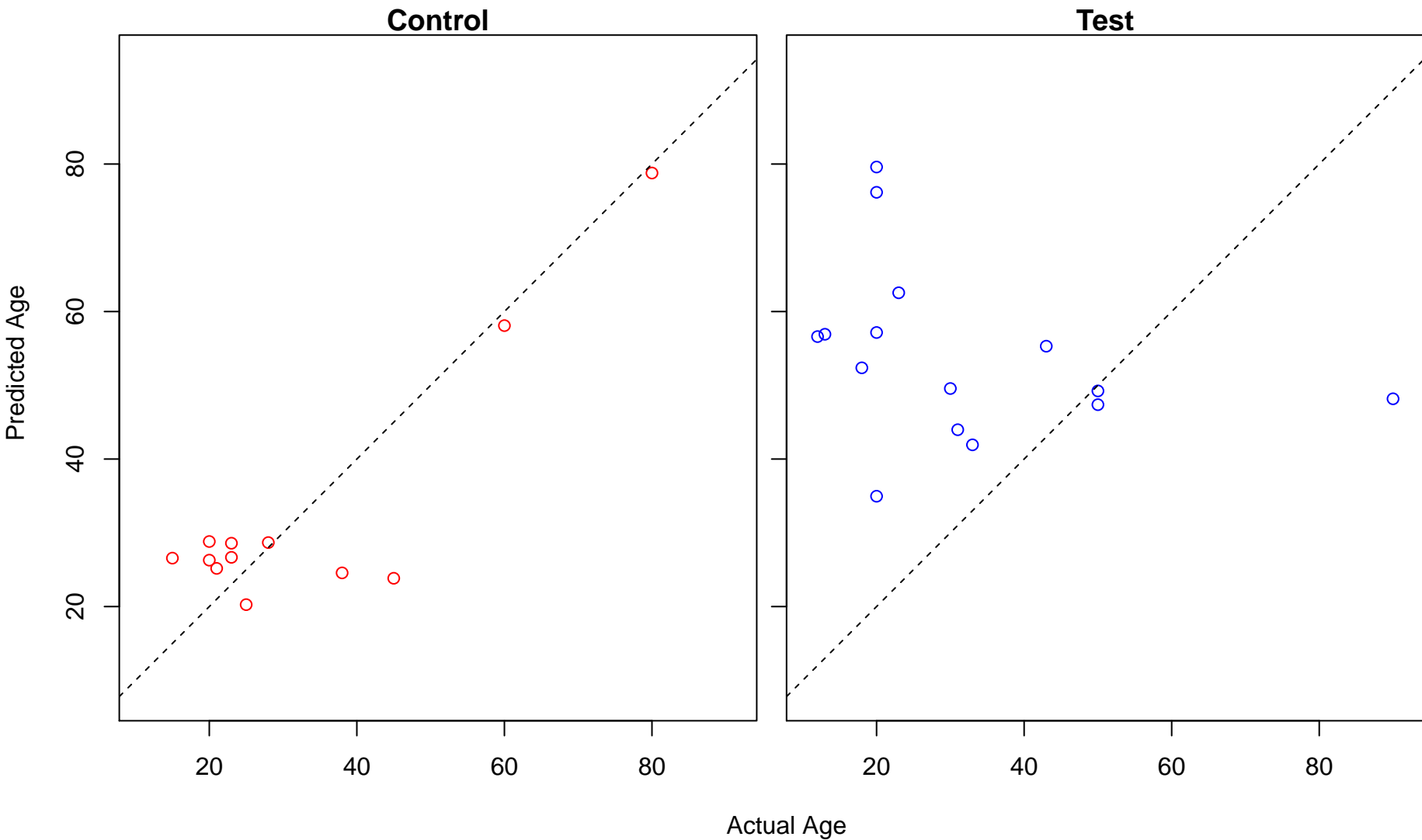


Test

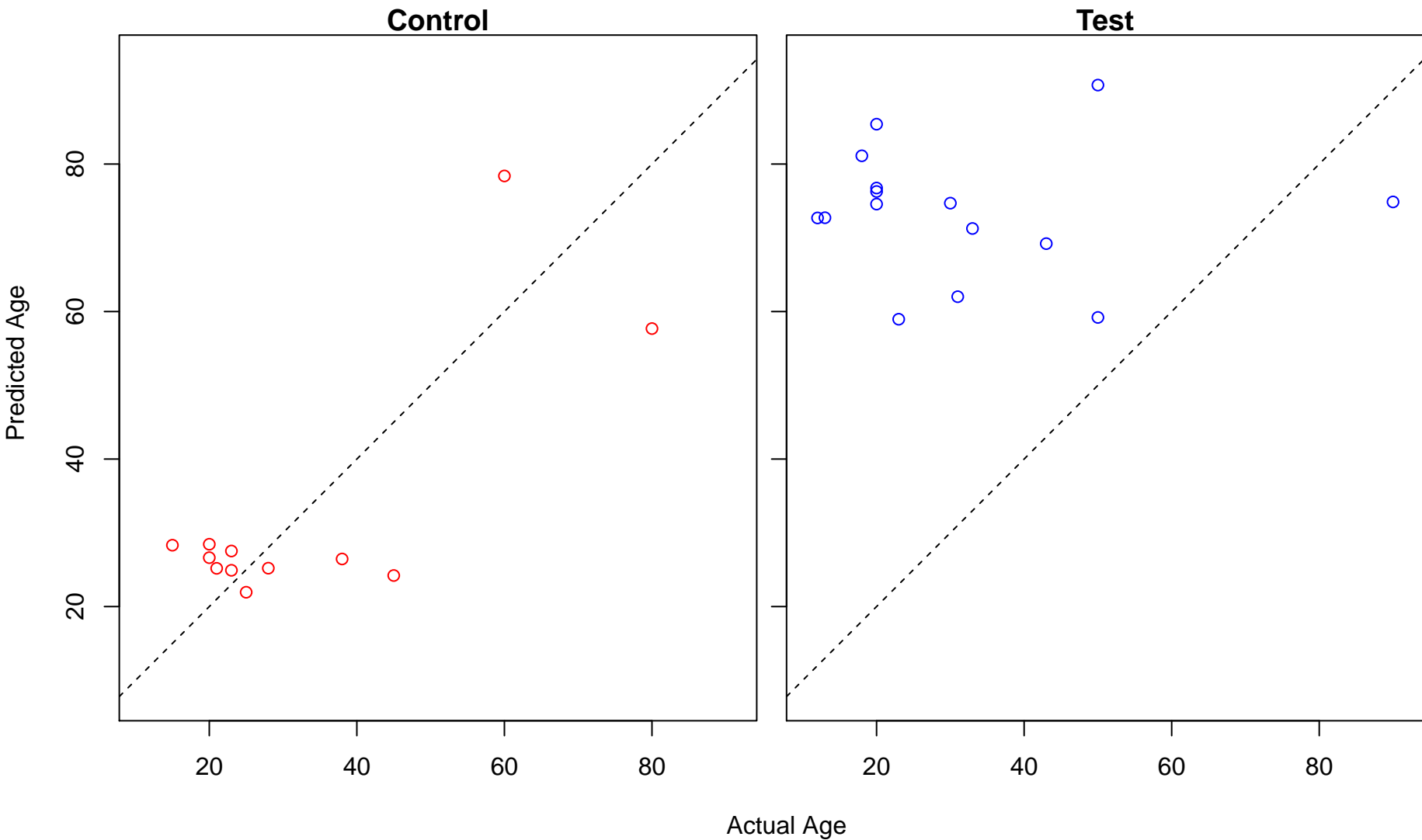


Actual Age

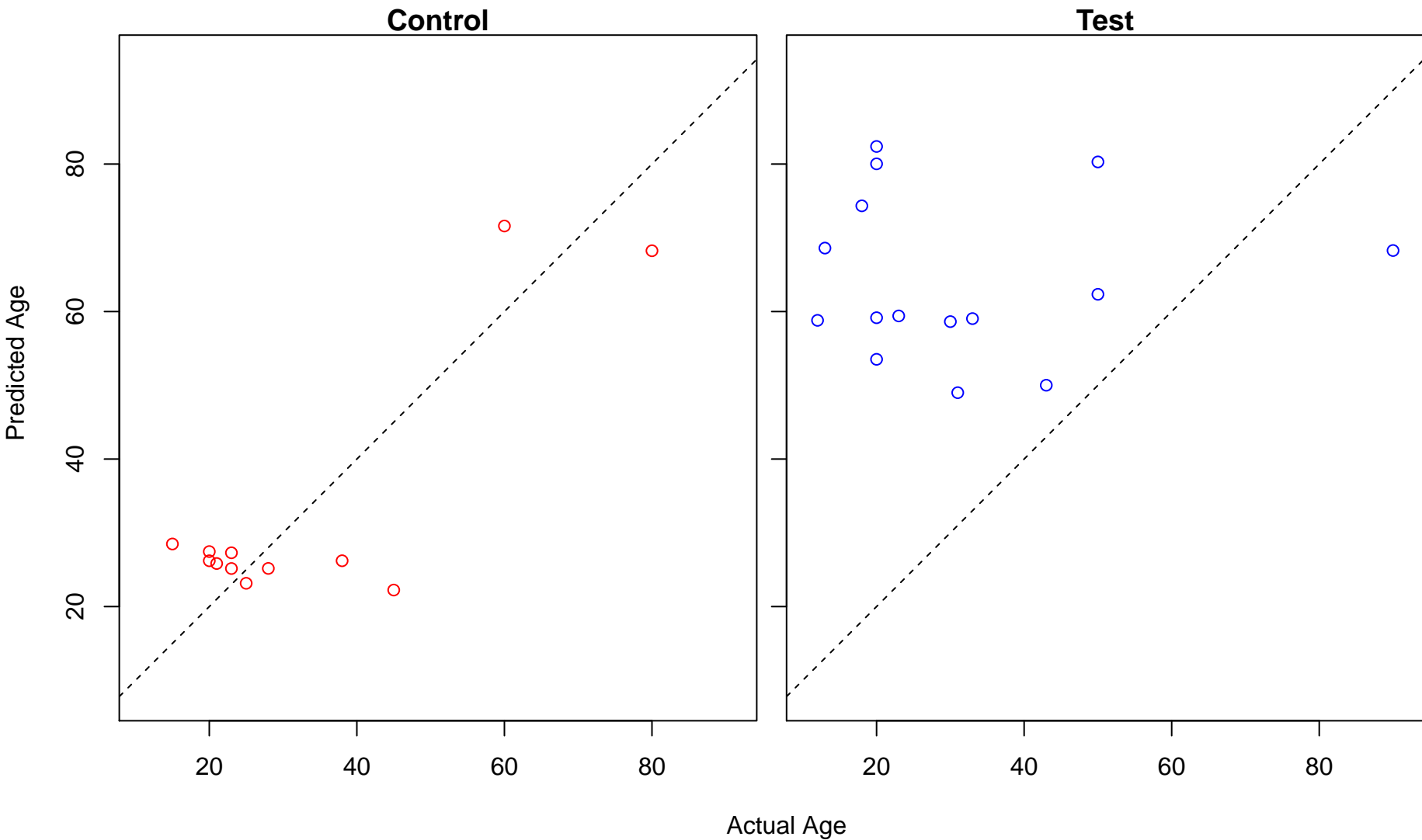
muscle cell cellular homeostasis (Score: 5.162631)



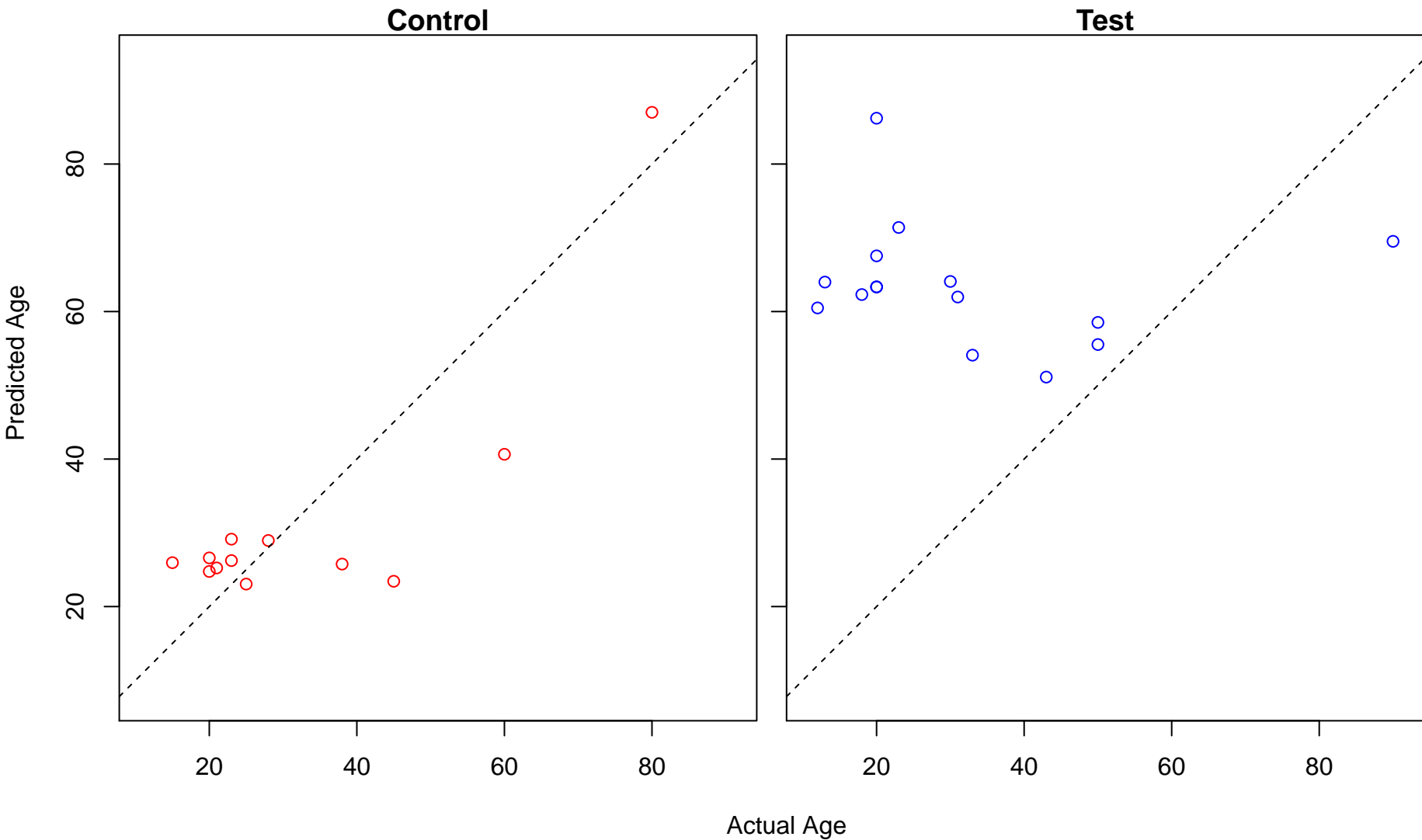
positive regulation of epithelial cell proliferation (Score: 5.160419)



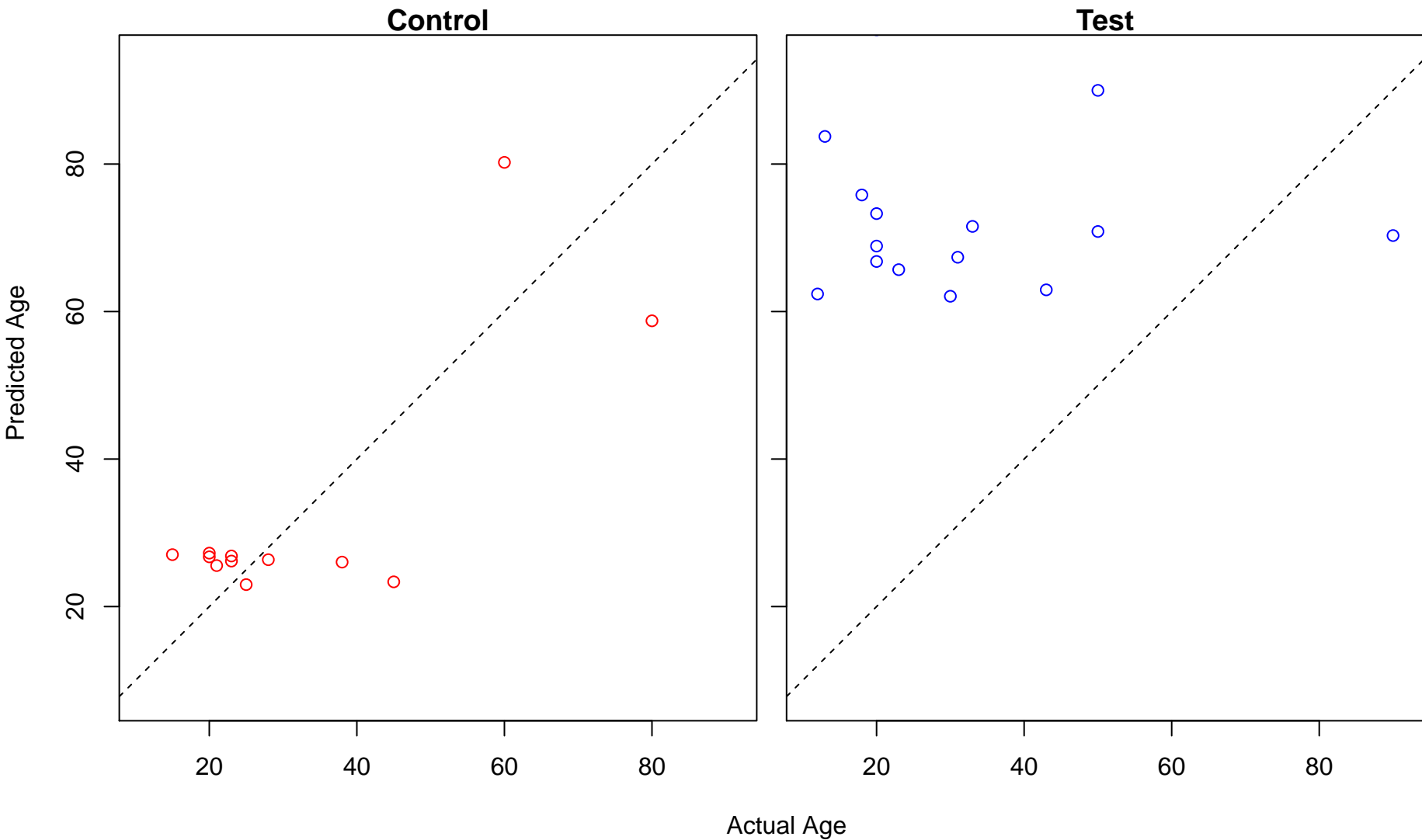
positive regulation of cellular protein catabolic process (Score: 5.160252)



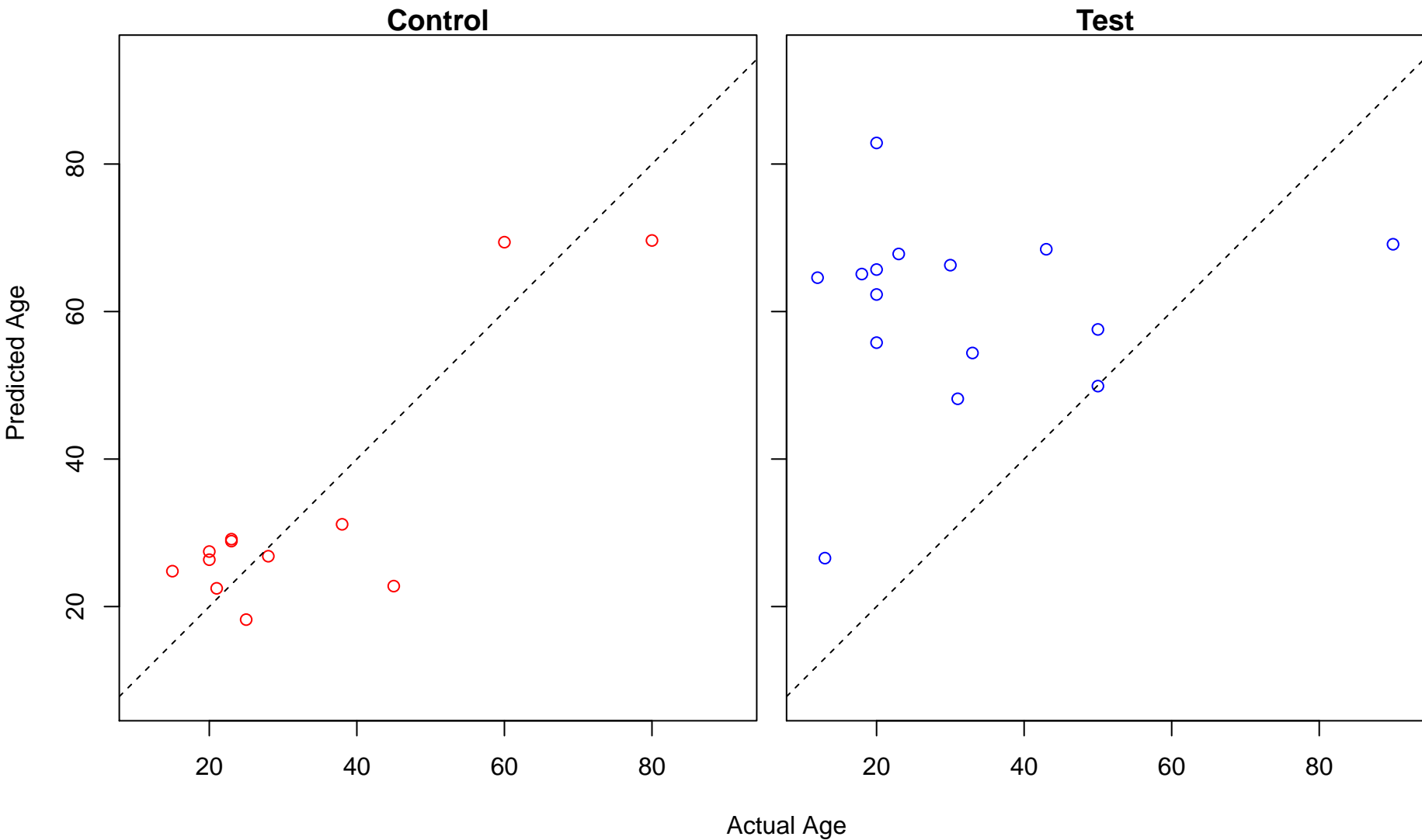
polyamine metabolic process (Score: 5.158970)



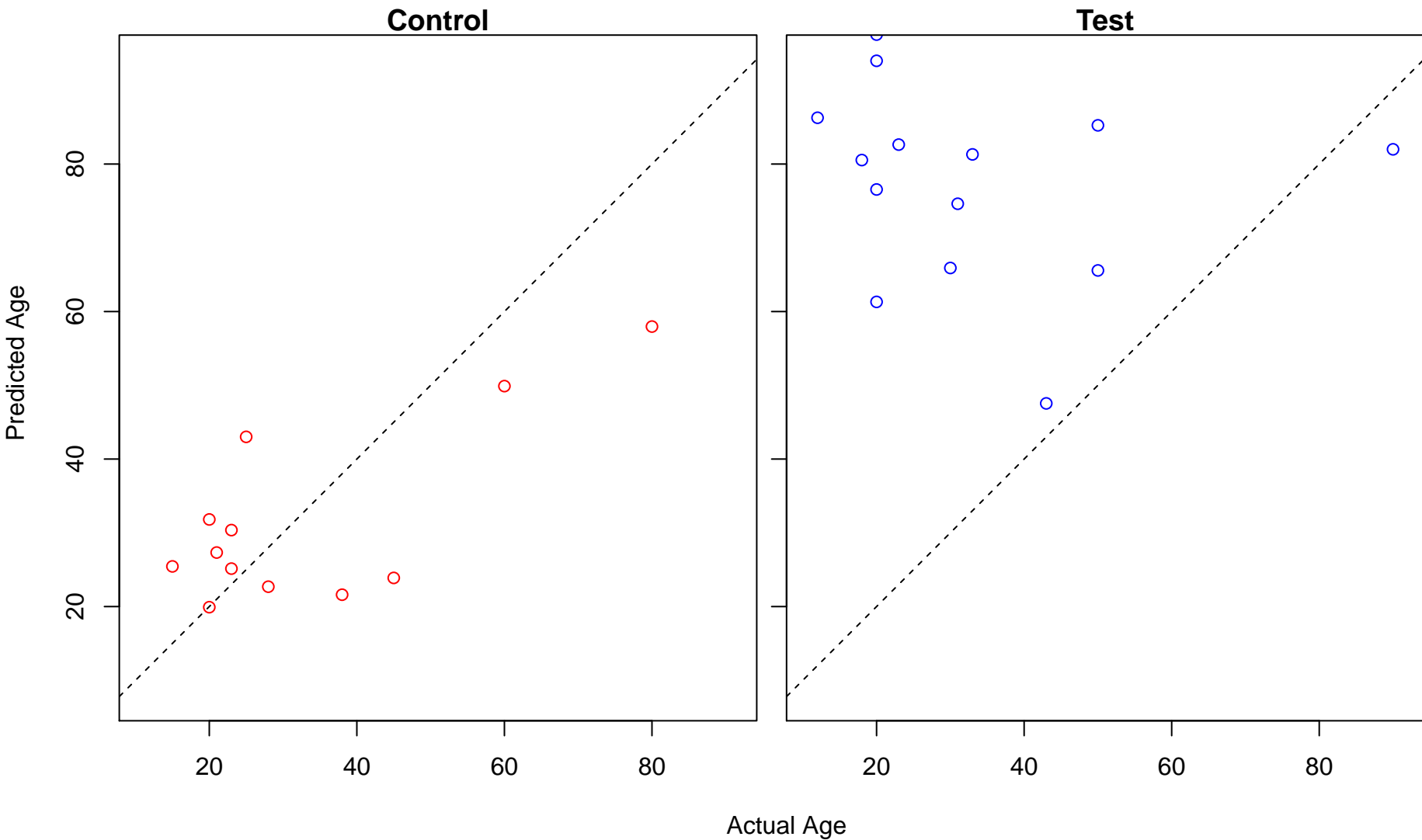
positive regulation of innate immune response (Score: 5.158378)



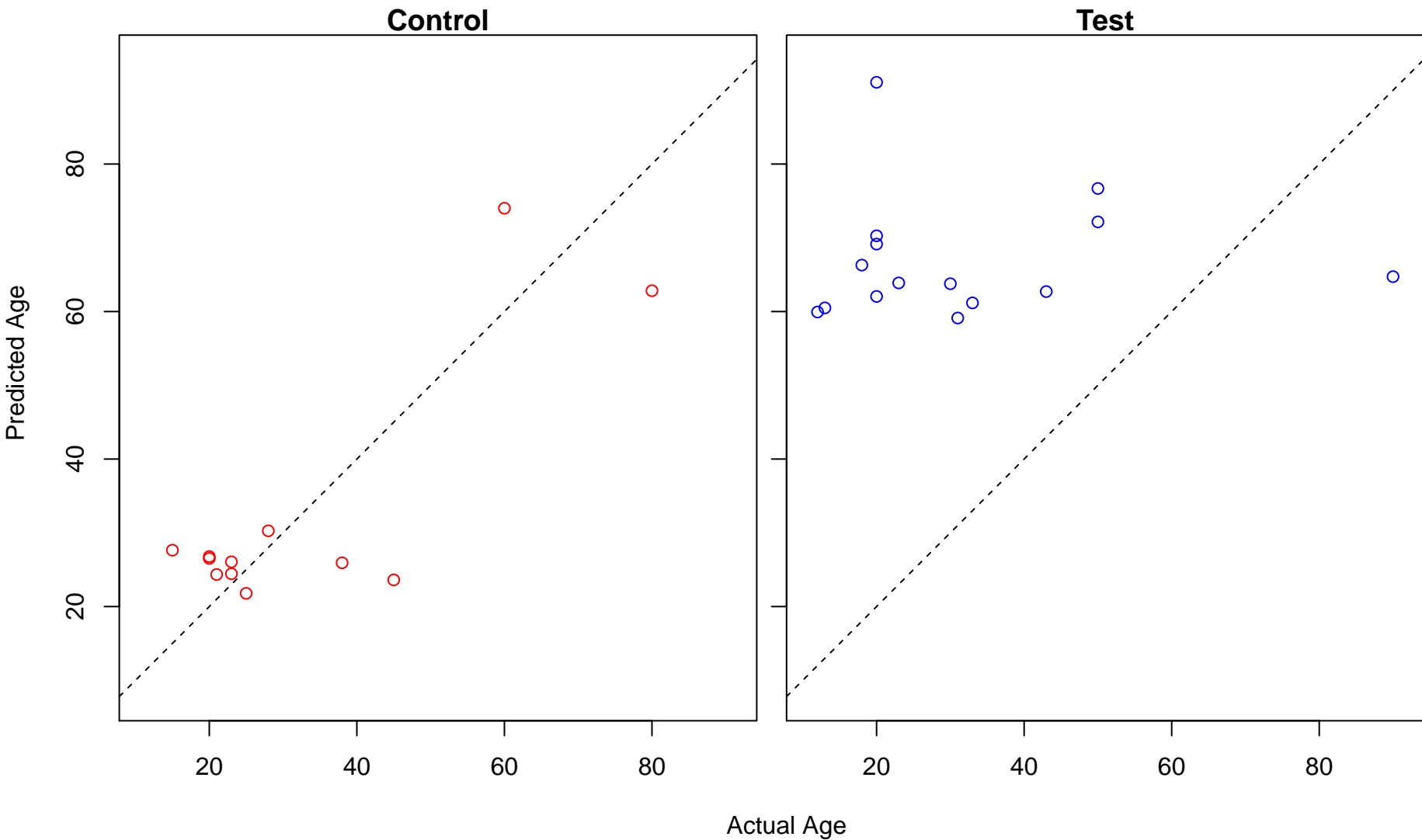
viral genome replication (Score: 5.157528)



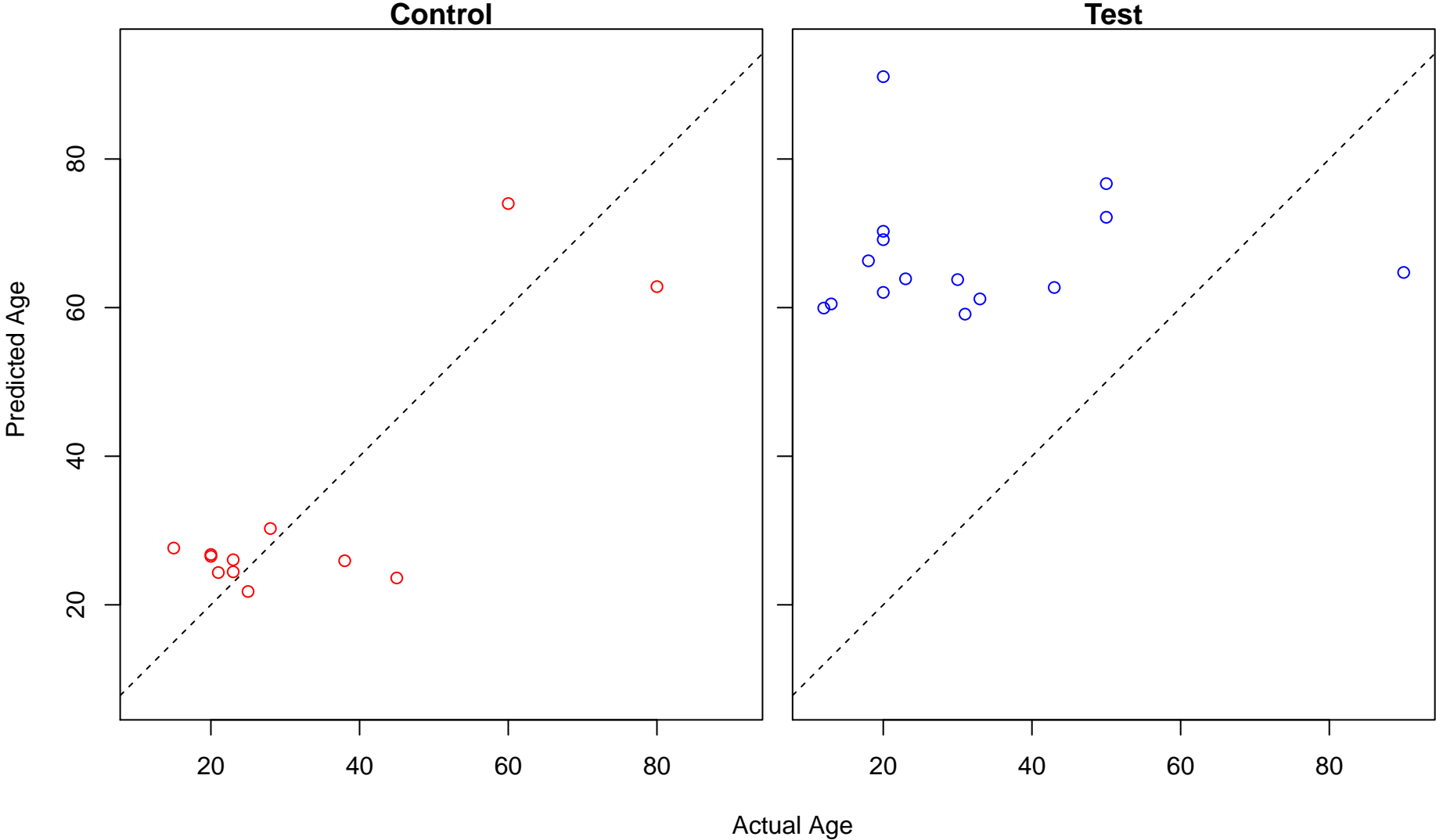
melanocyte differentiation (Score: 5.157052)



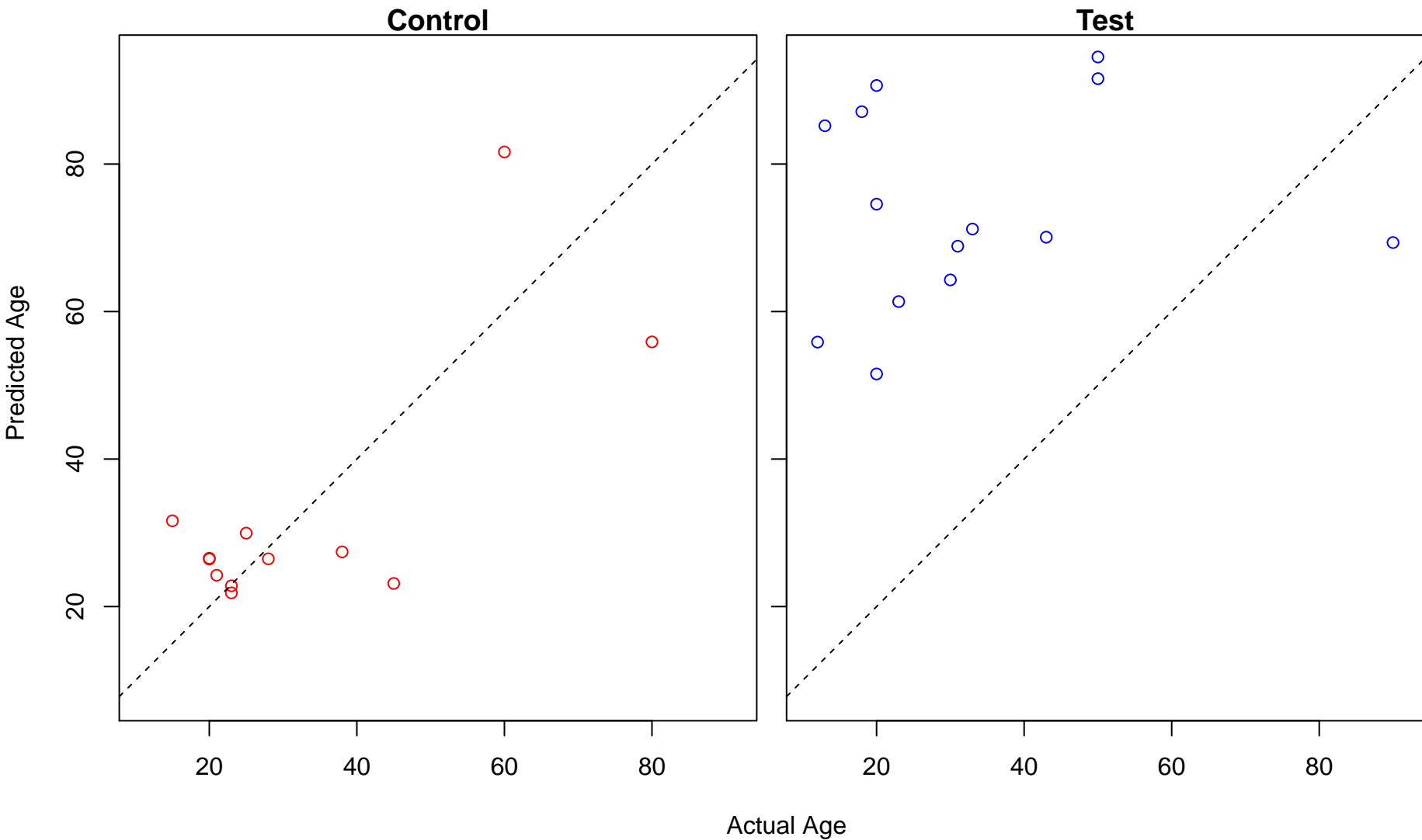
male gamete generation (Score: 5.155843)



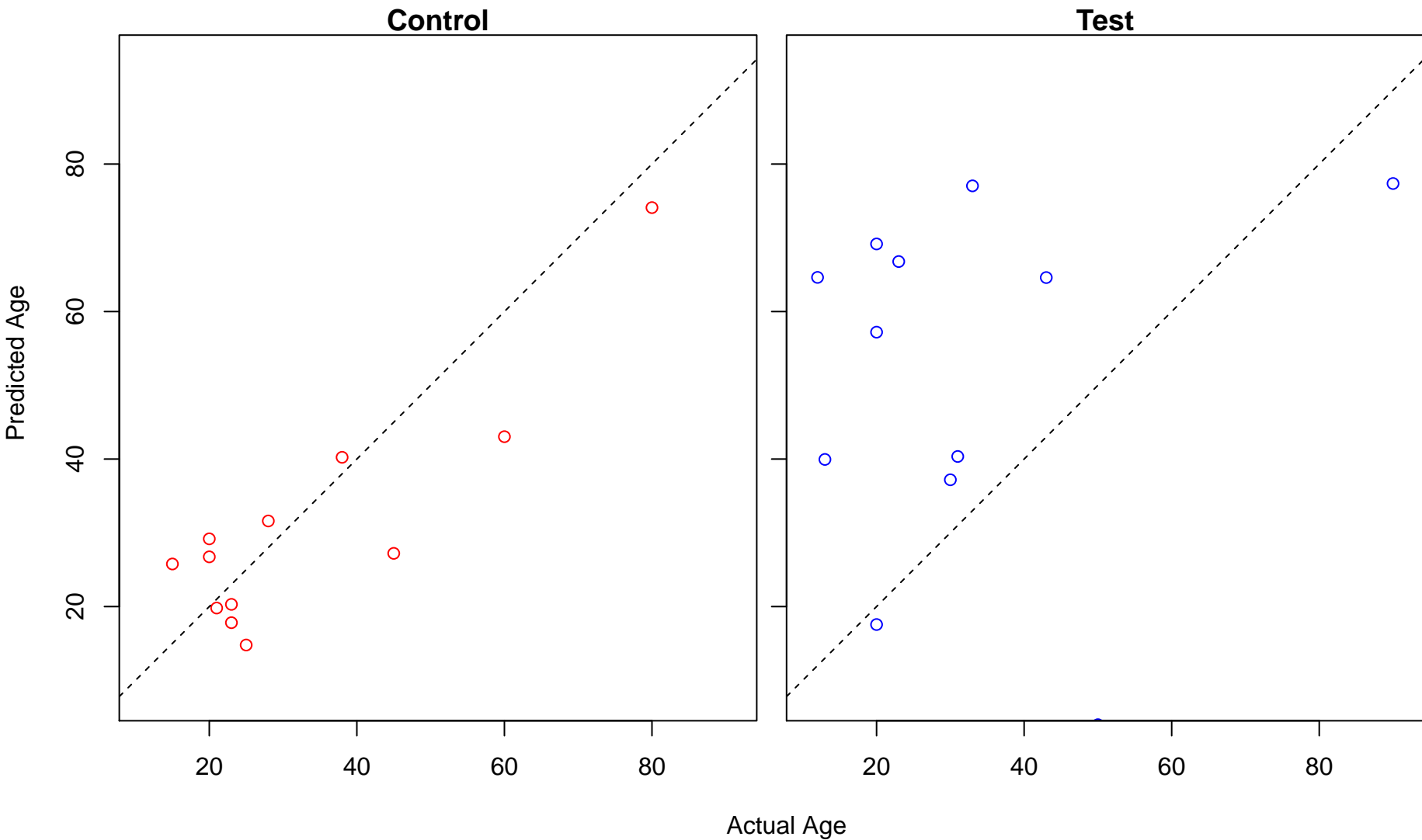
spermatogenesis (Score: 5.155687)



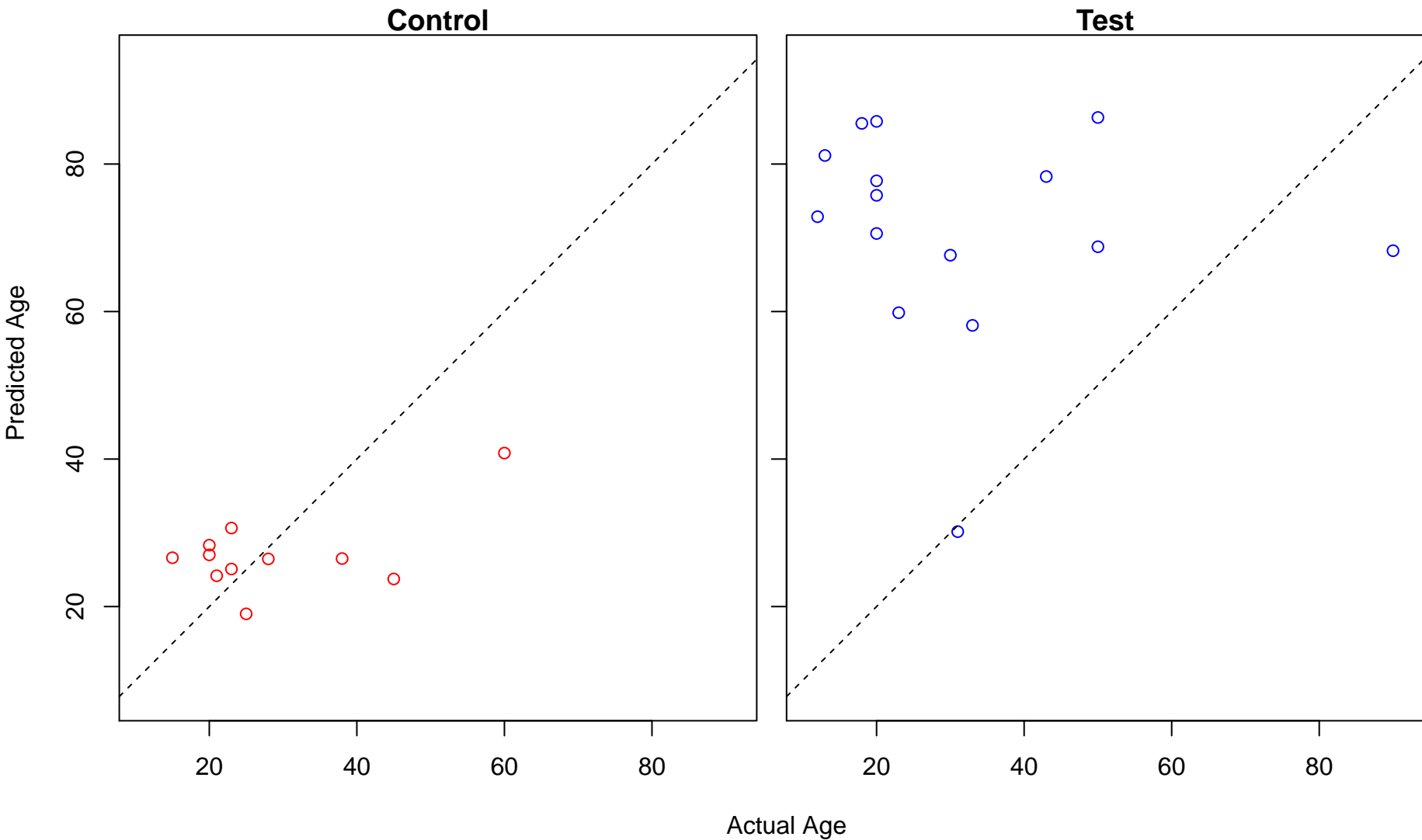
neuron death (Score: 5.155422)



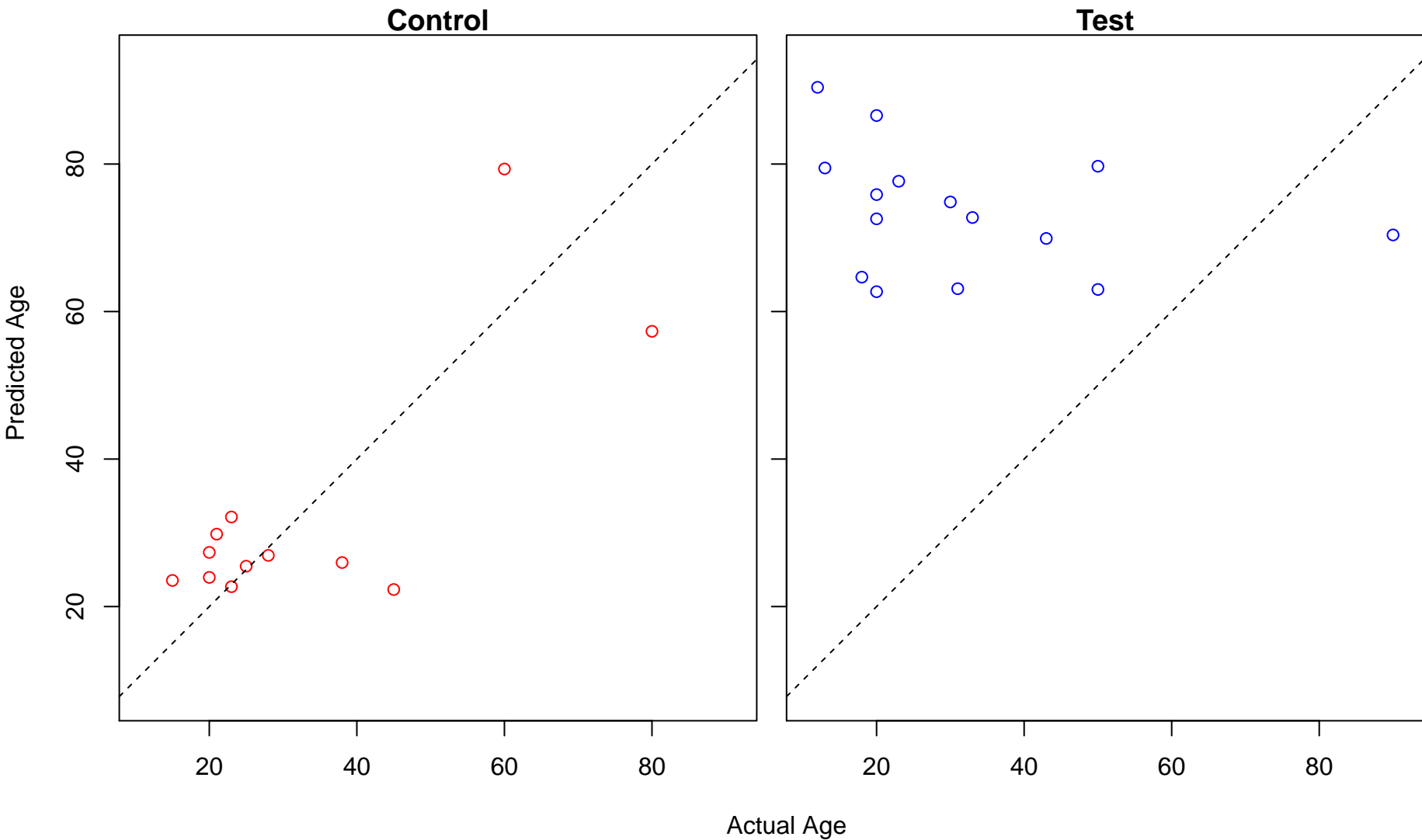
nephron tubule development (Score: 5.155289)



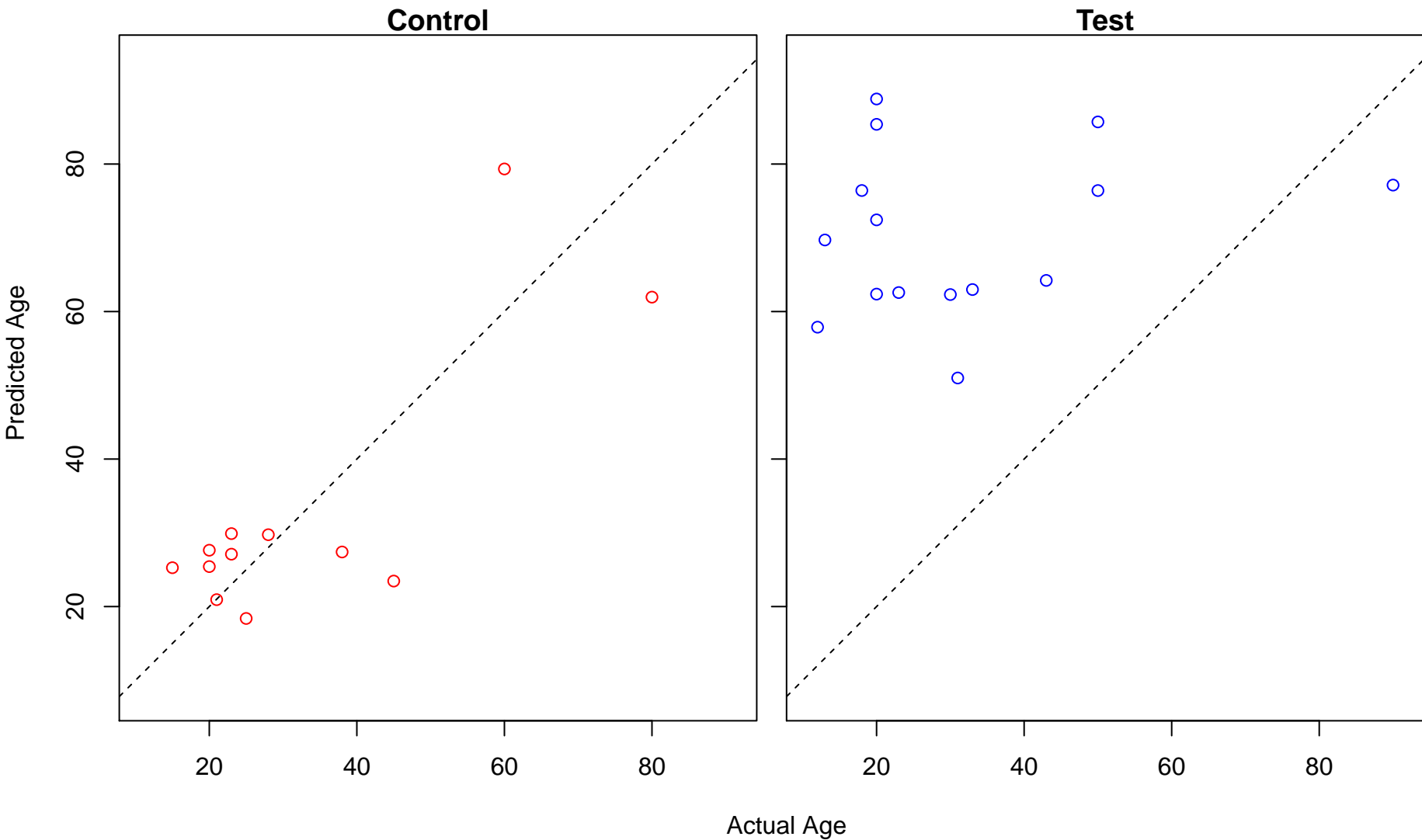
regulation of macrophage derived foam cell differentiation (Score: 5.154823)



neuron fate commitment (Score: 5.154064)

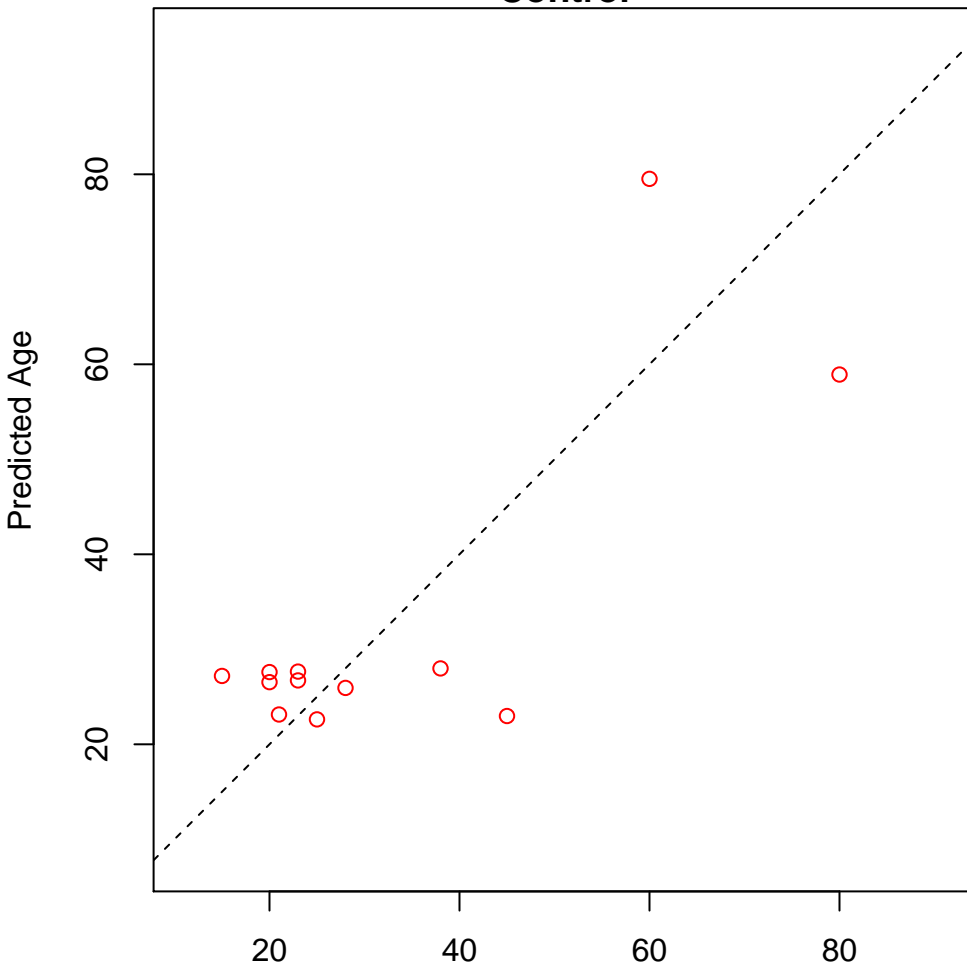


regulation of cellular response to vascular endothelial growth factor stimulus (Score: 5.153945)

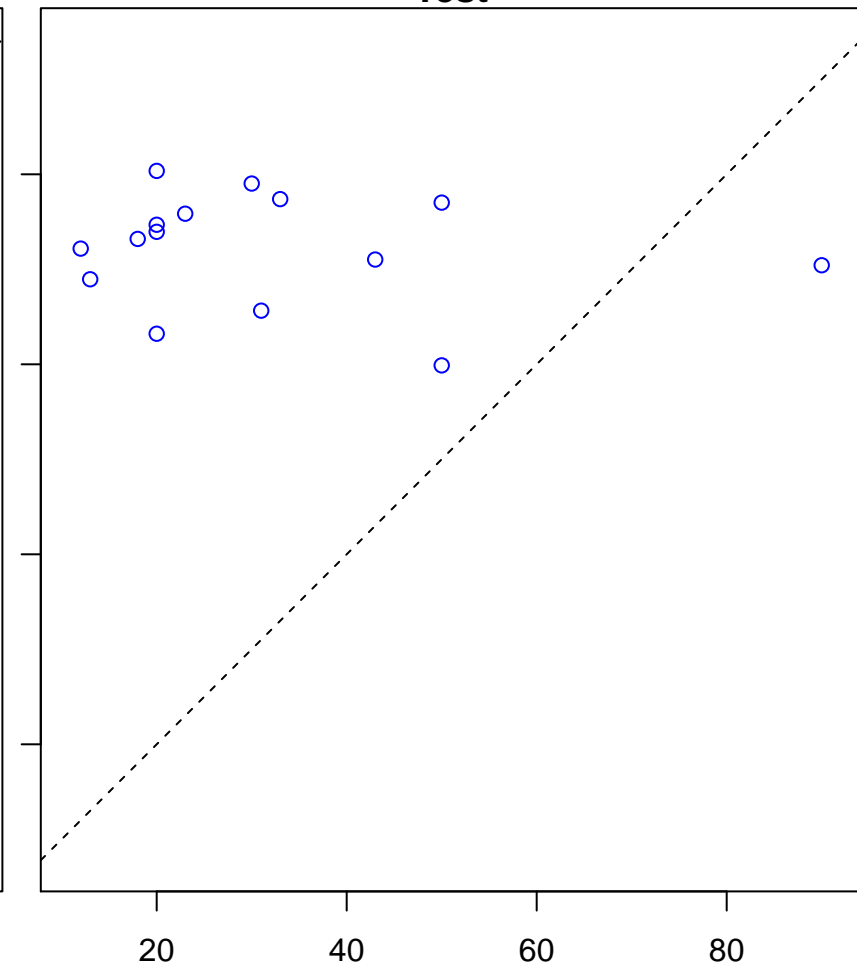


glomerular epithelial cell development (Score: 5.152138)

Control



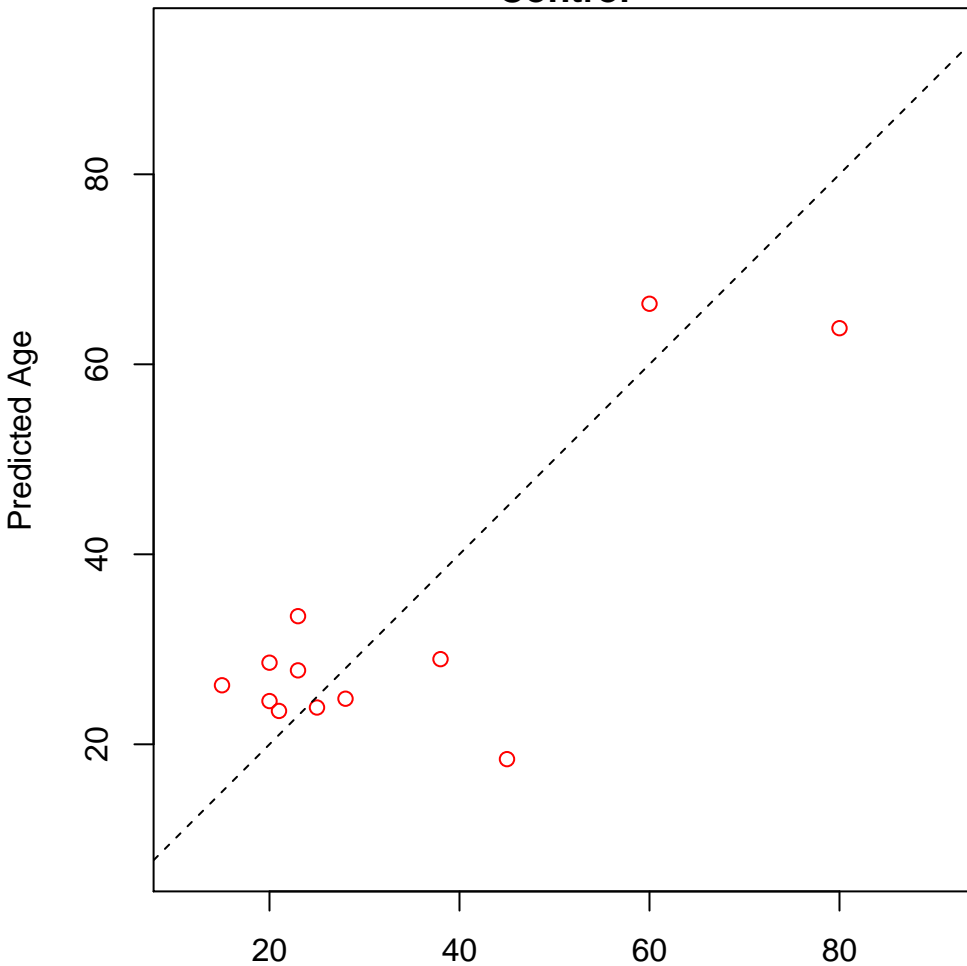
Test



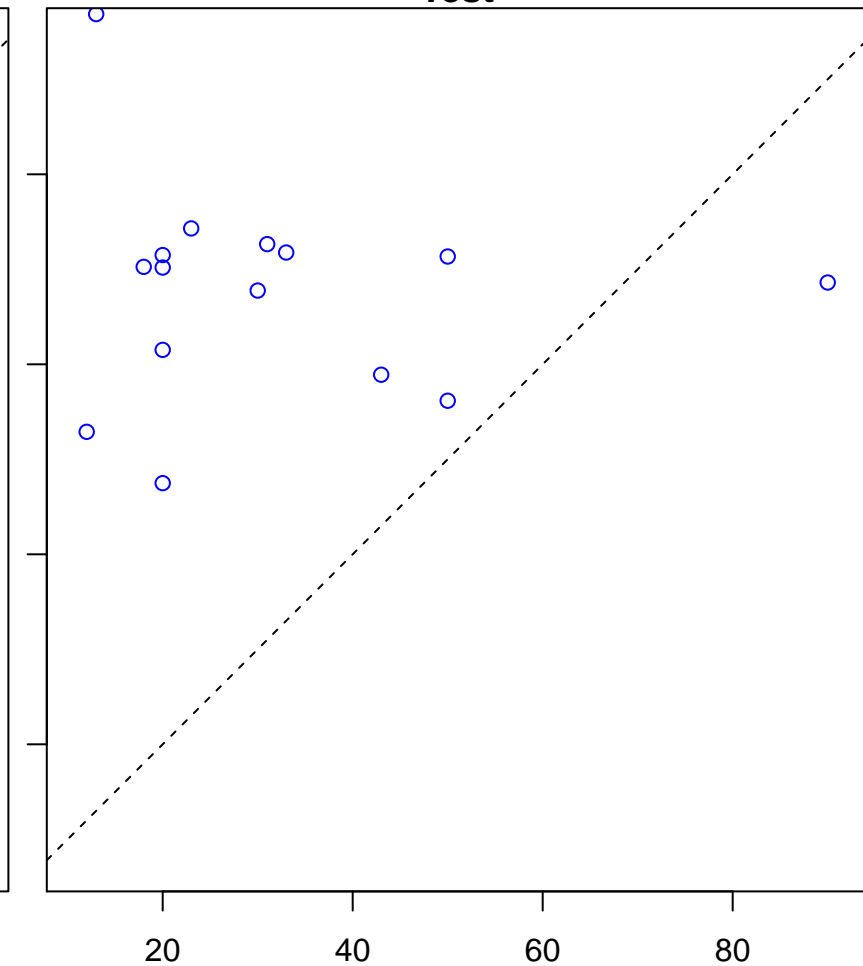
Actual Age

regulation of T cell cytokine production (Score: 5.151740)

Control

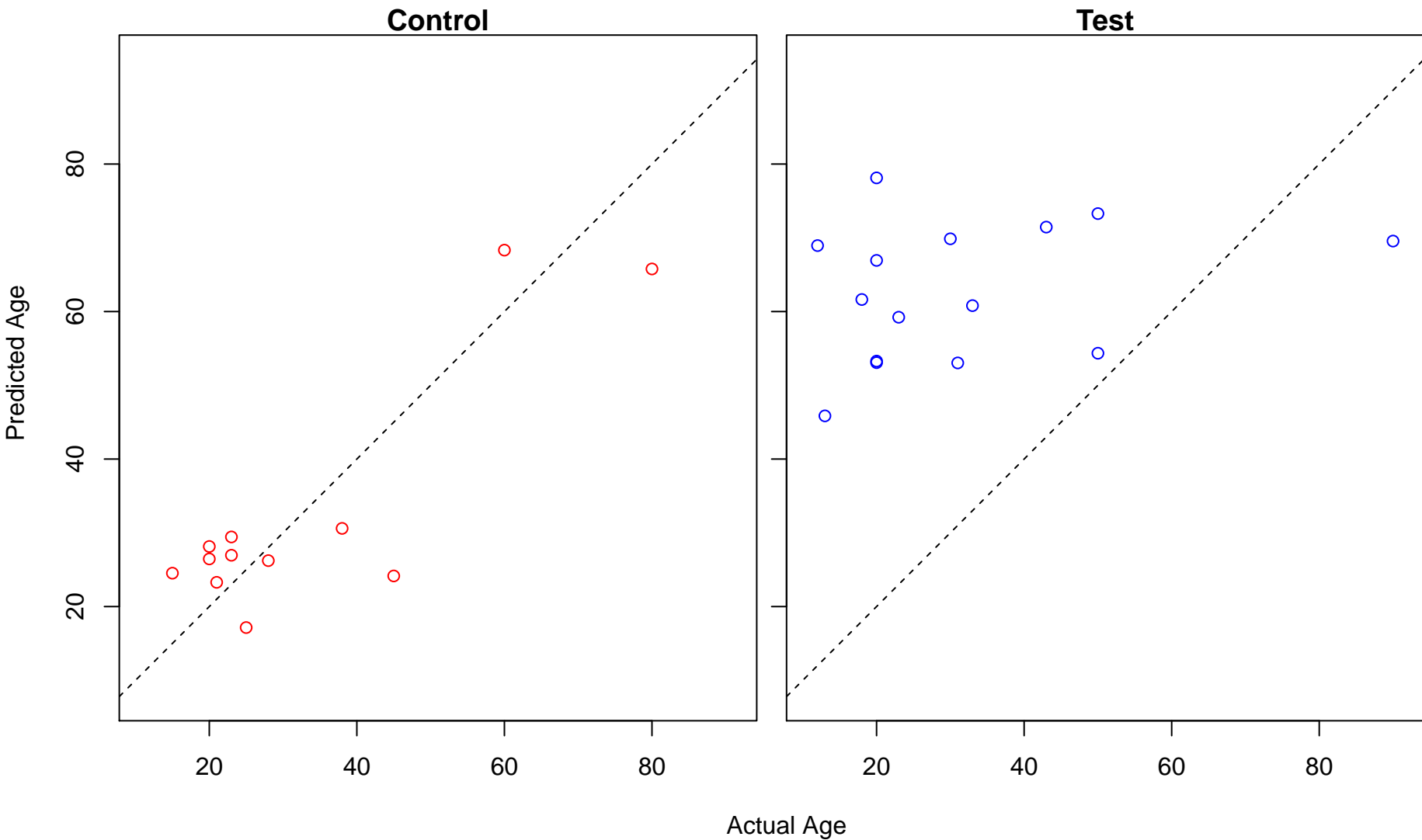


Test

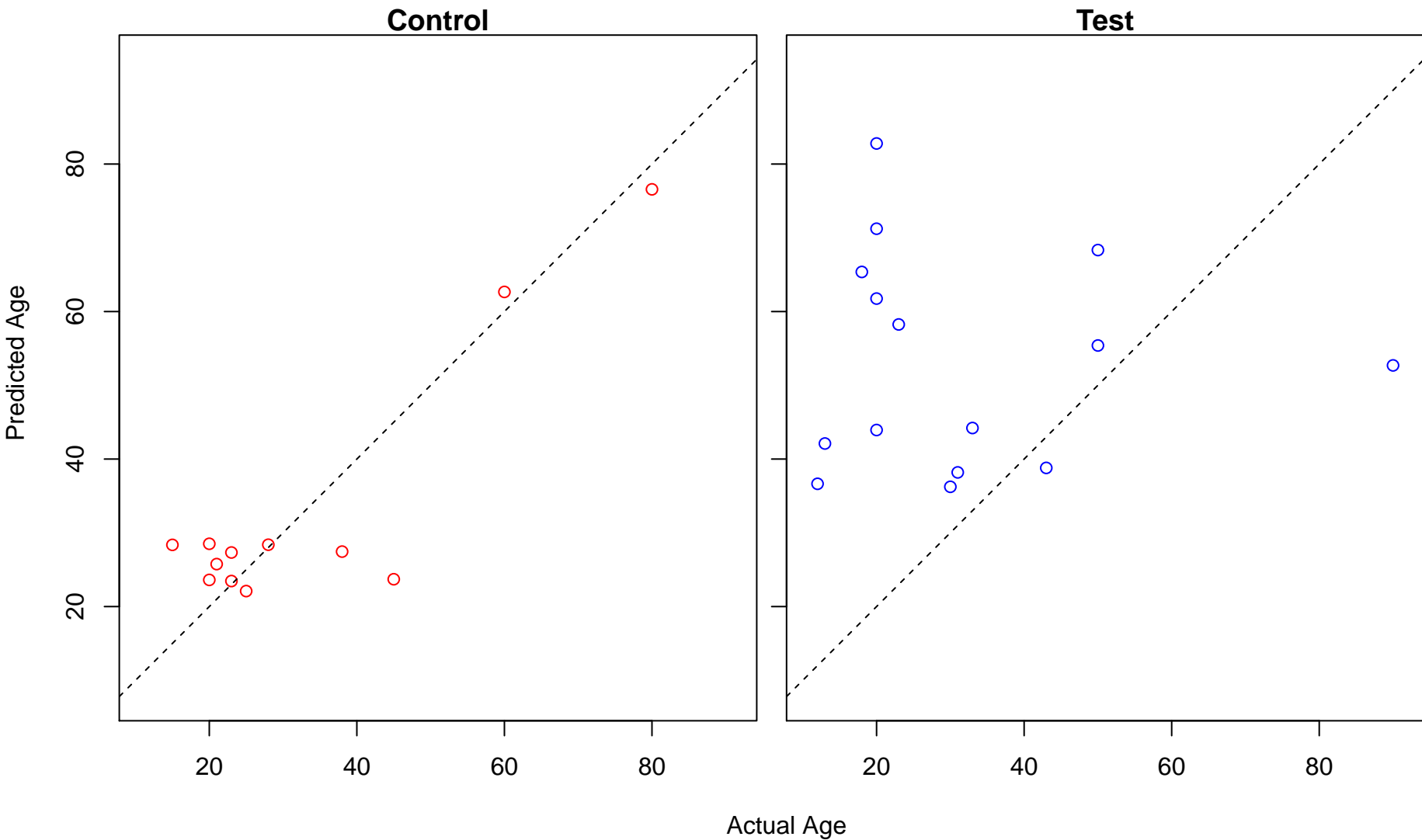


Actual Age

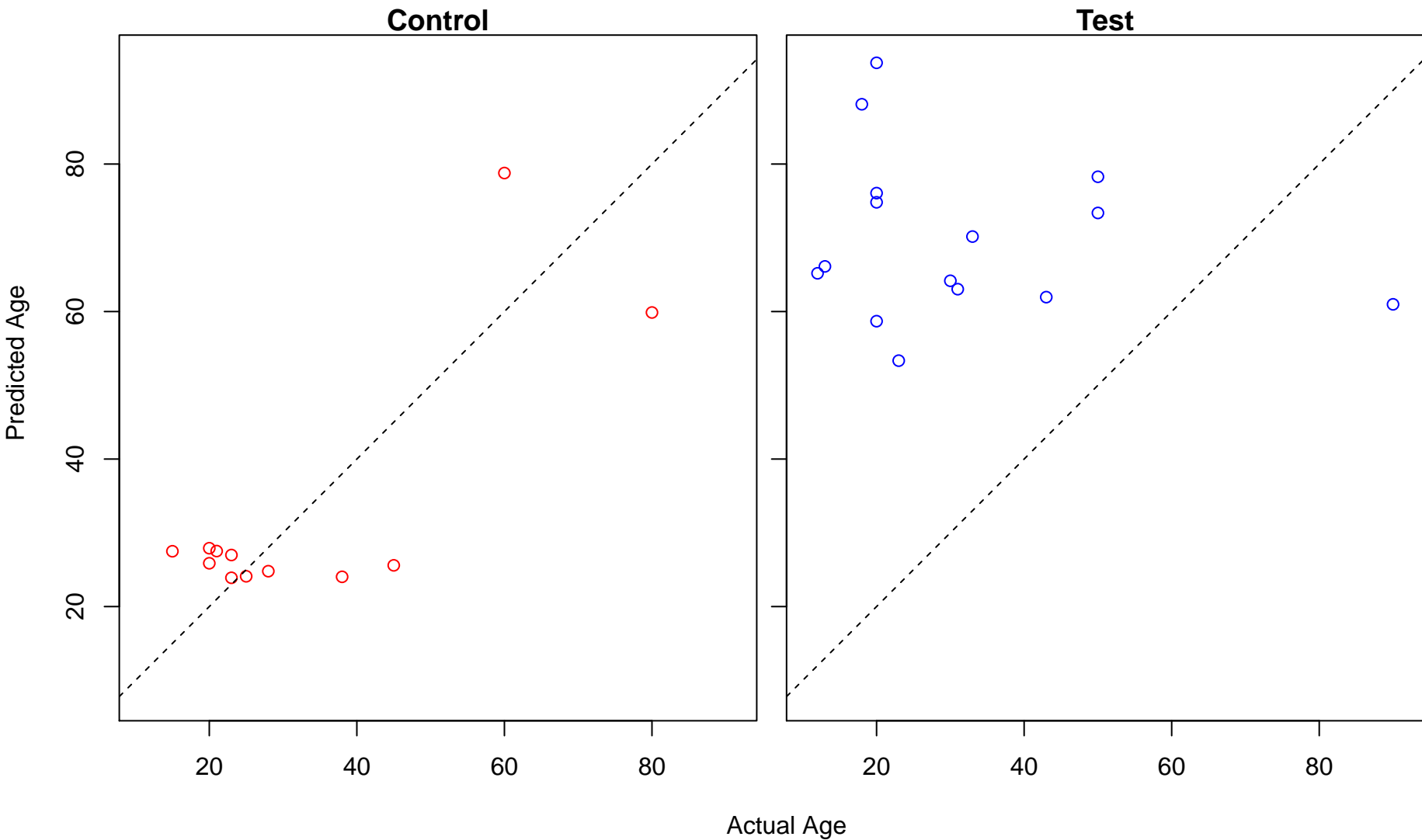
zinc II ion transport (Score: 5.151009)



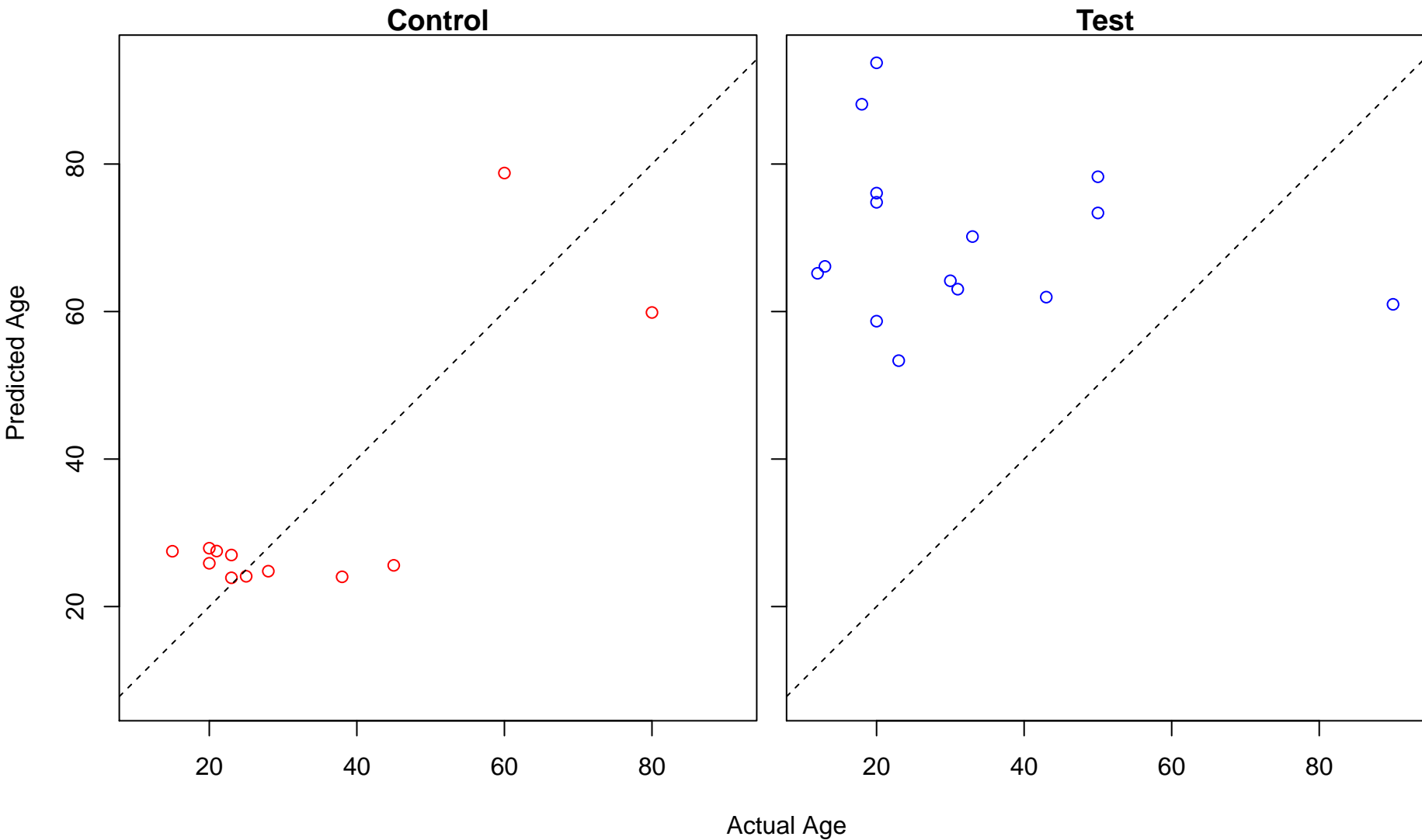
epidermal growth factor receptor signaling pathway (Score: 5.149366)



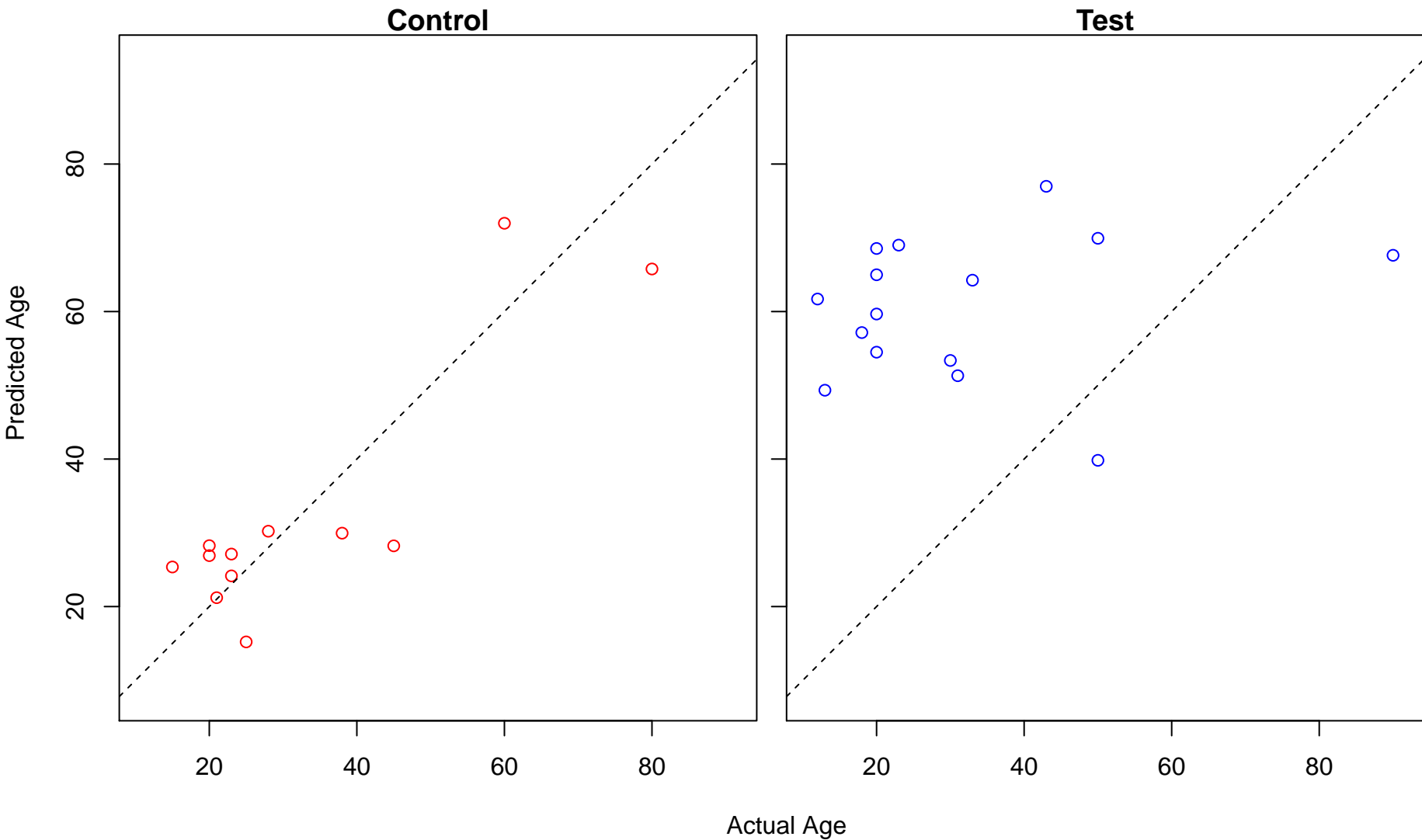
regulation of focal adhesion assembly (Score: 5.148314)



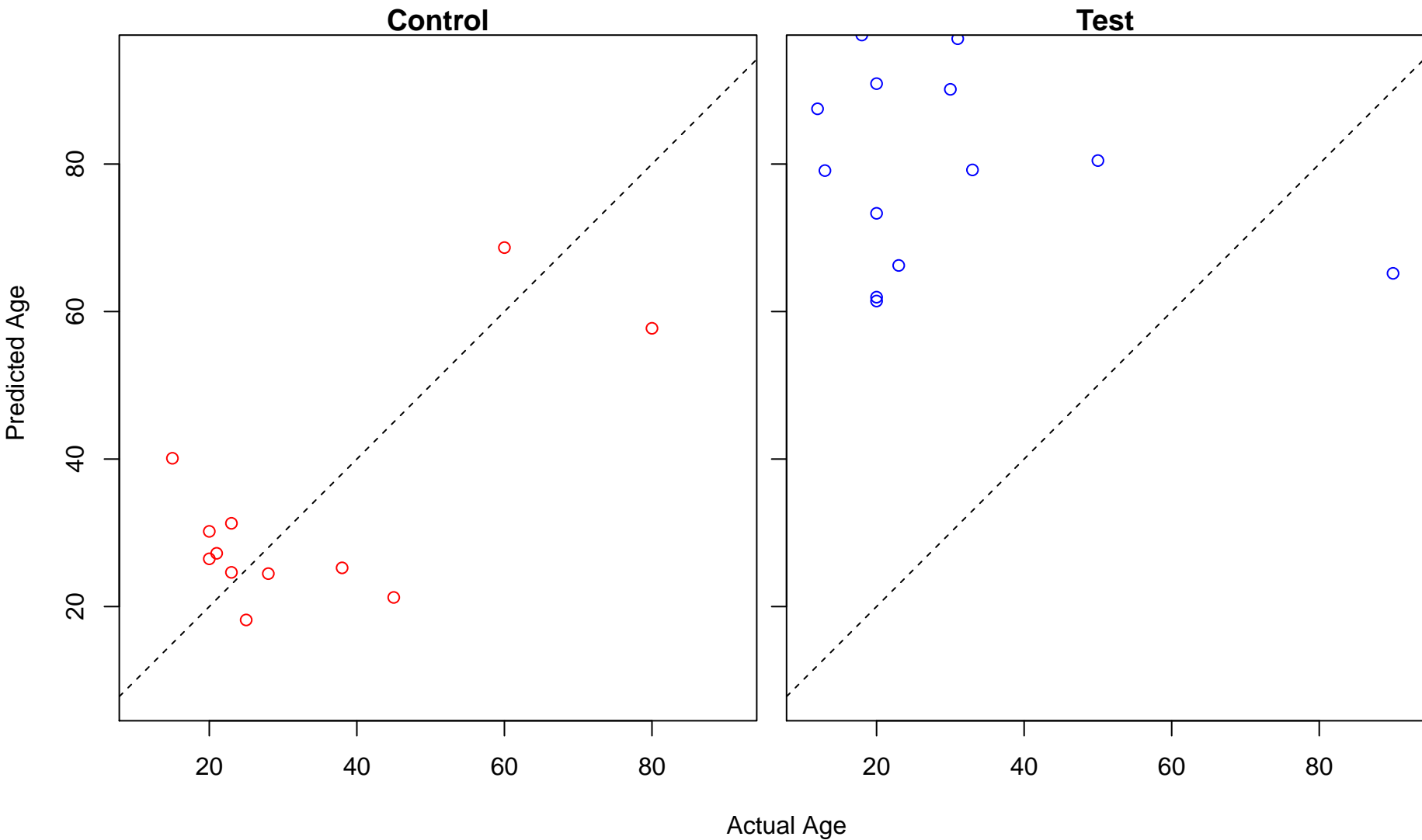
regulation of cell-substrate junction assembly (Score: 5.148314)



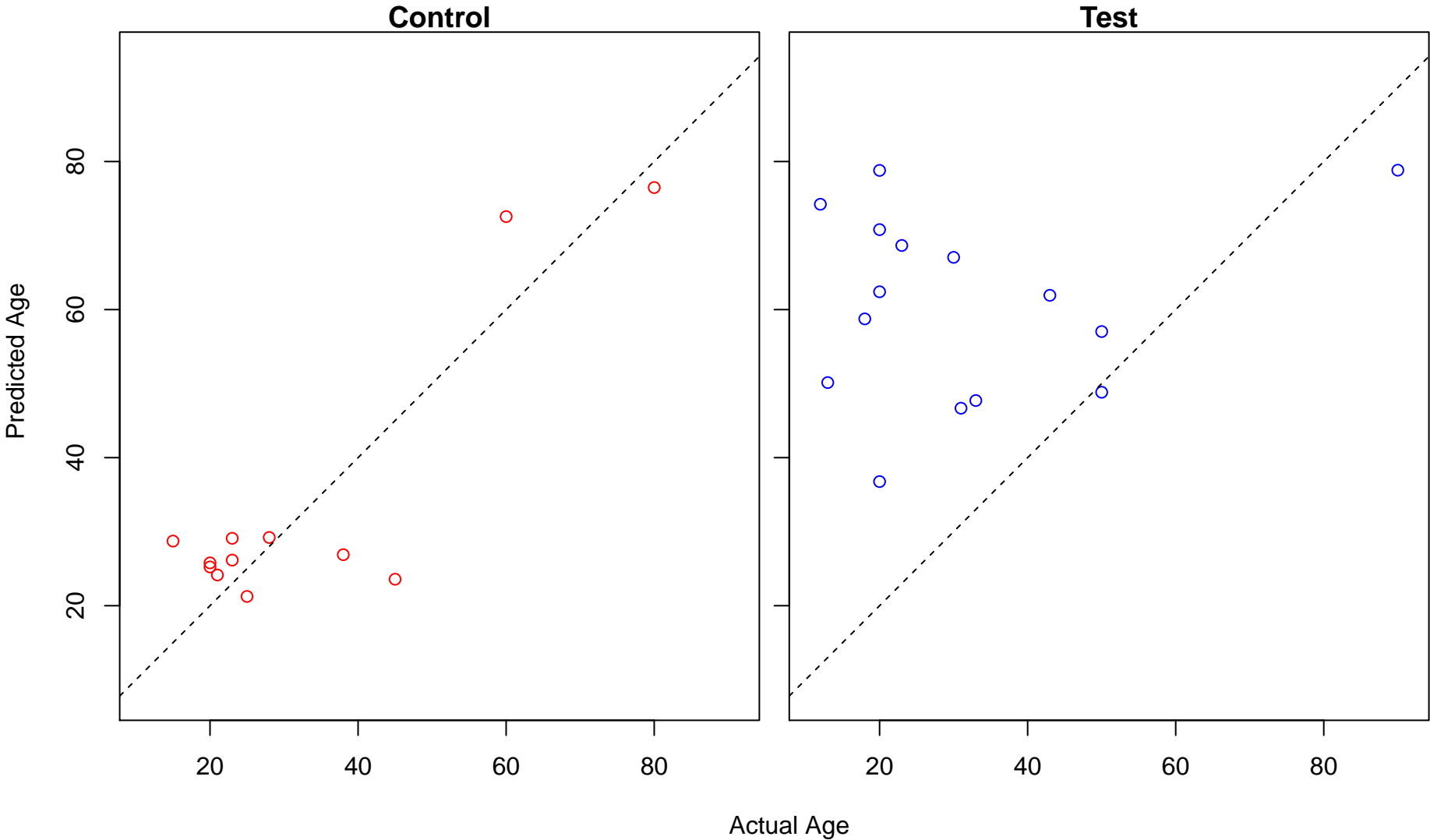
distal tubule development (Score: 5.147751)



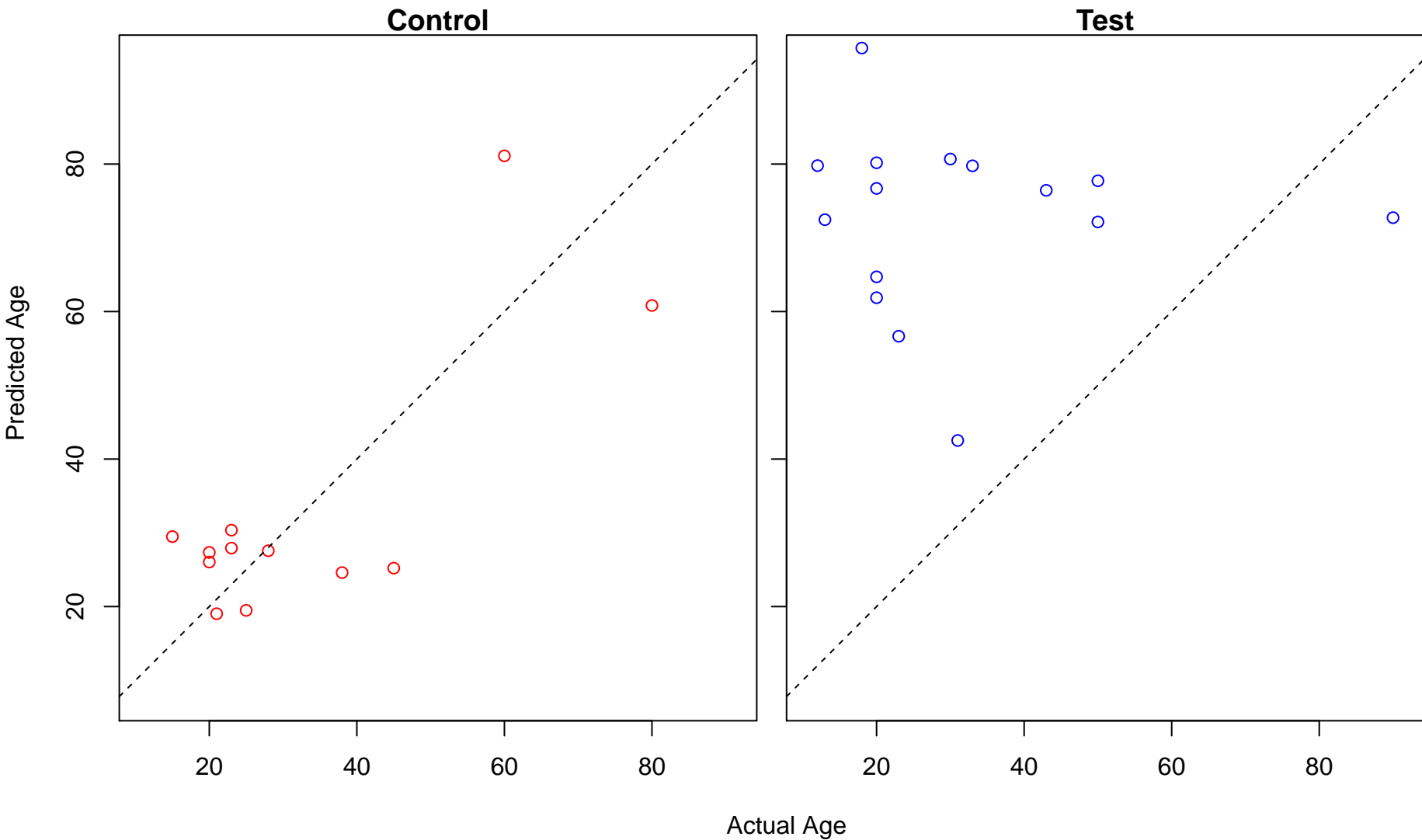
sphingoid metabolic process (Score: 5.146702)



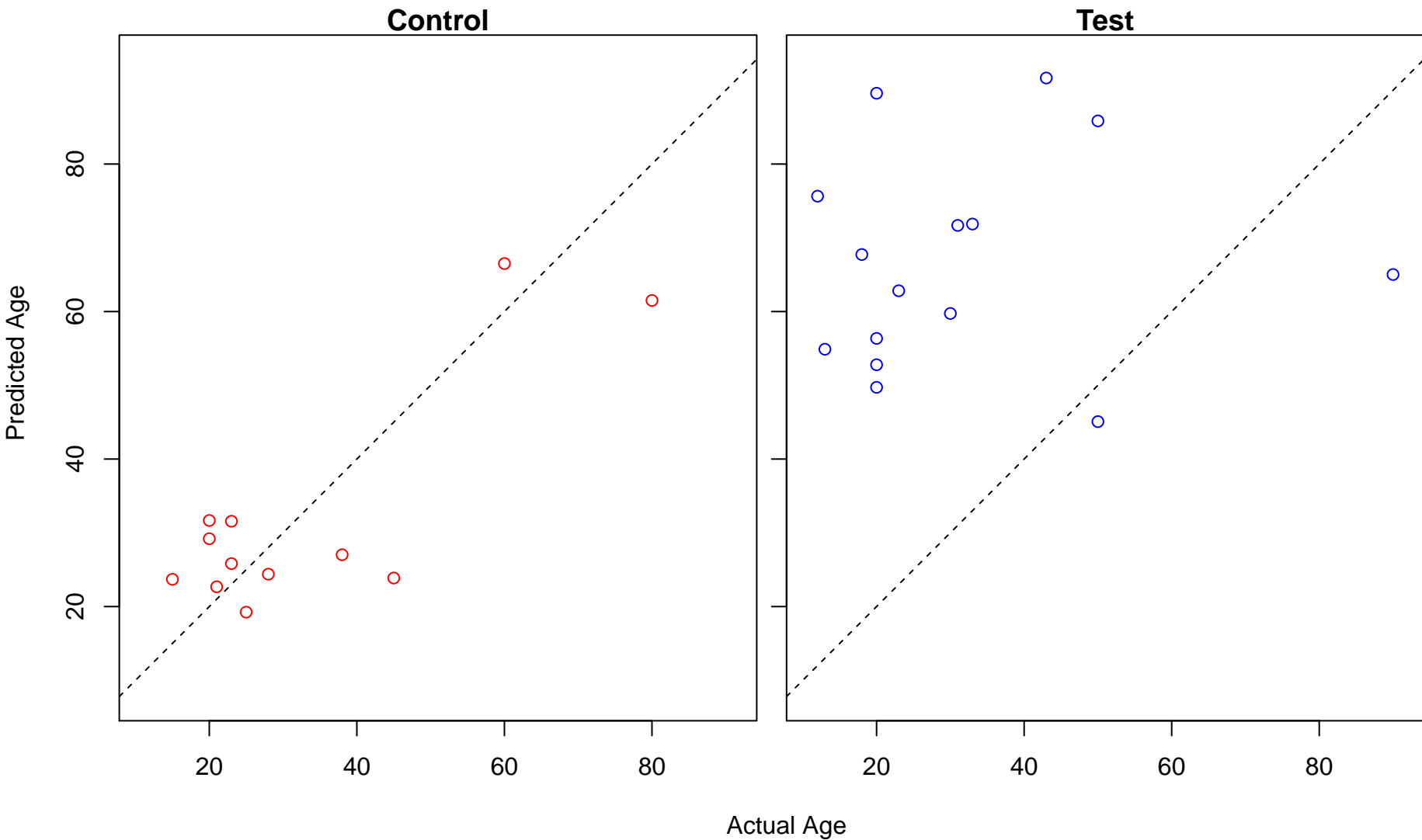
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (Score: 5.144)



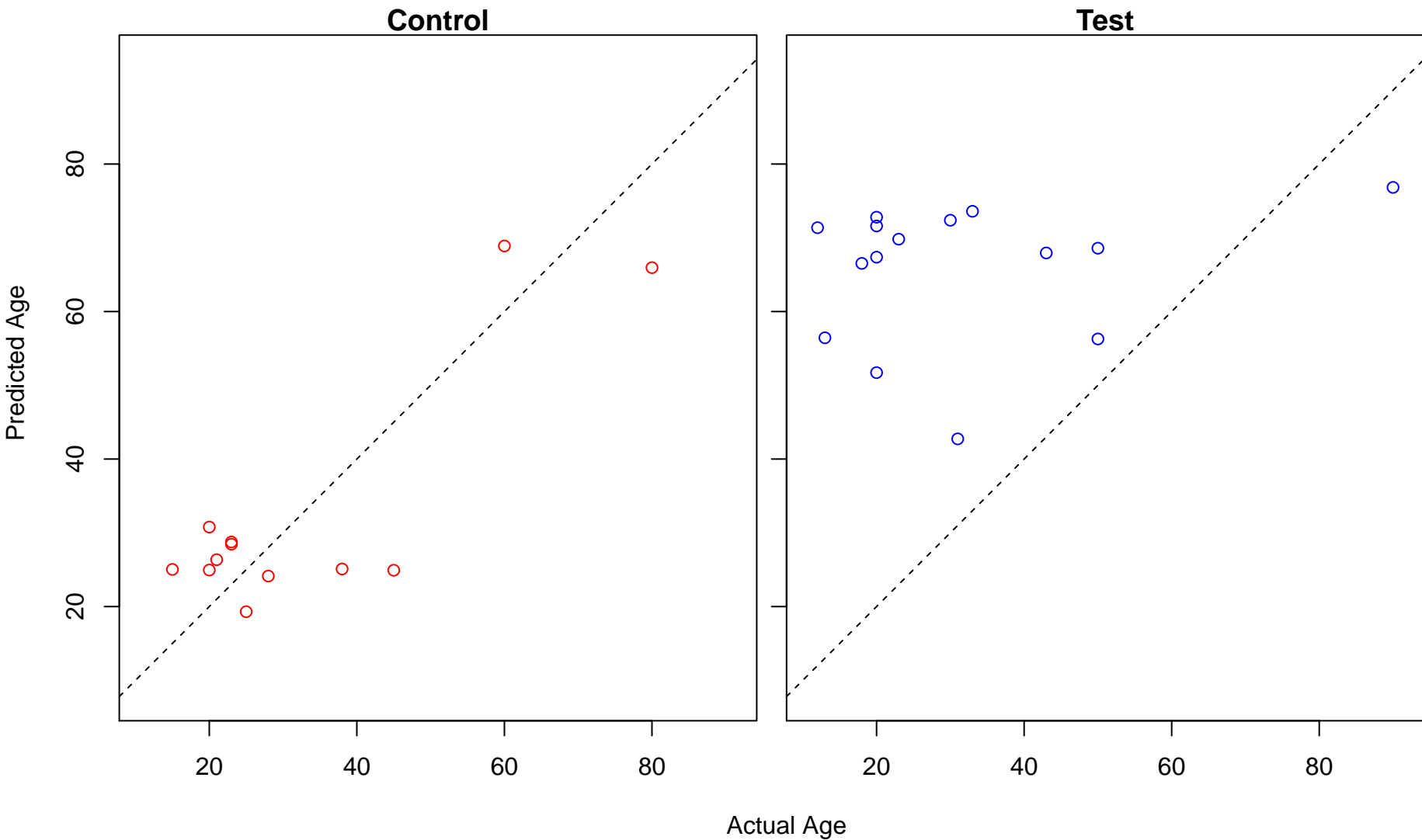
calcium ion transport into cytosol (Score: 5.142955)



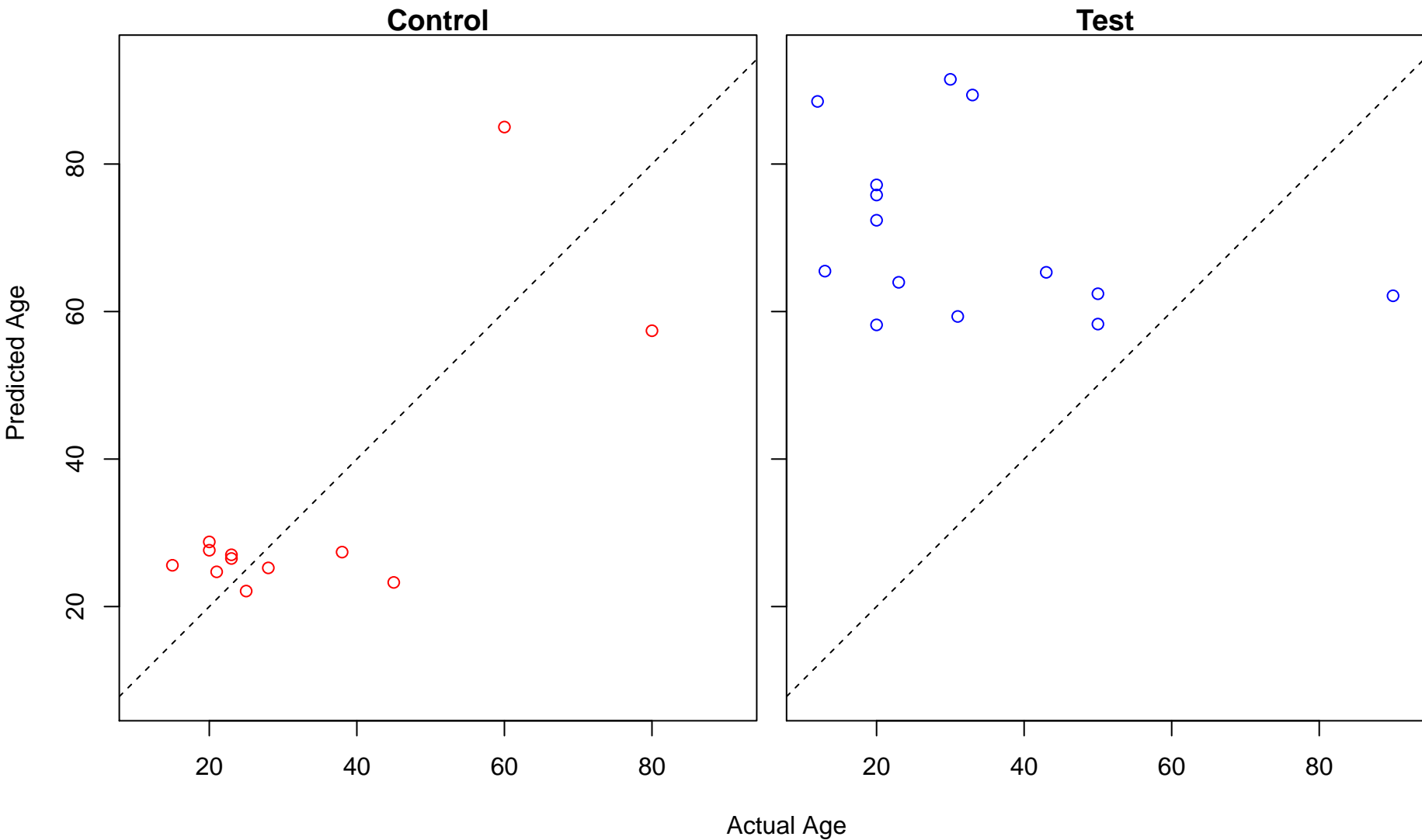
aromatic amino acid transport (Score: 5.142045)



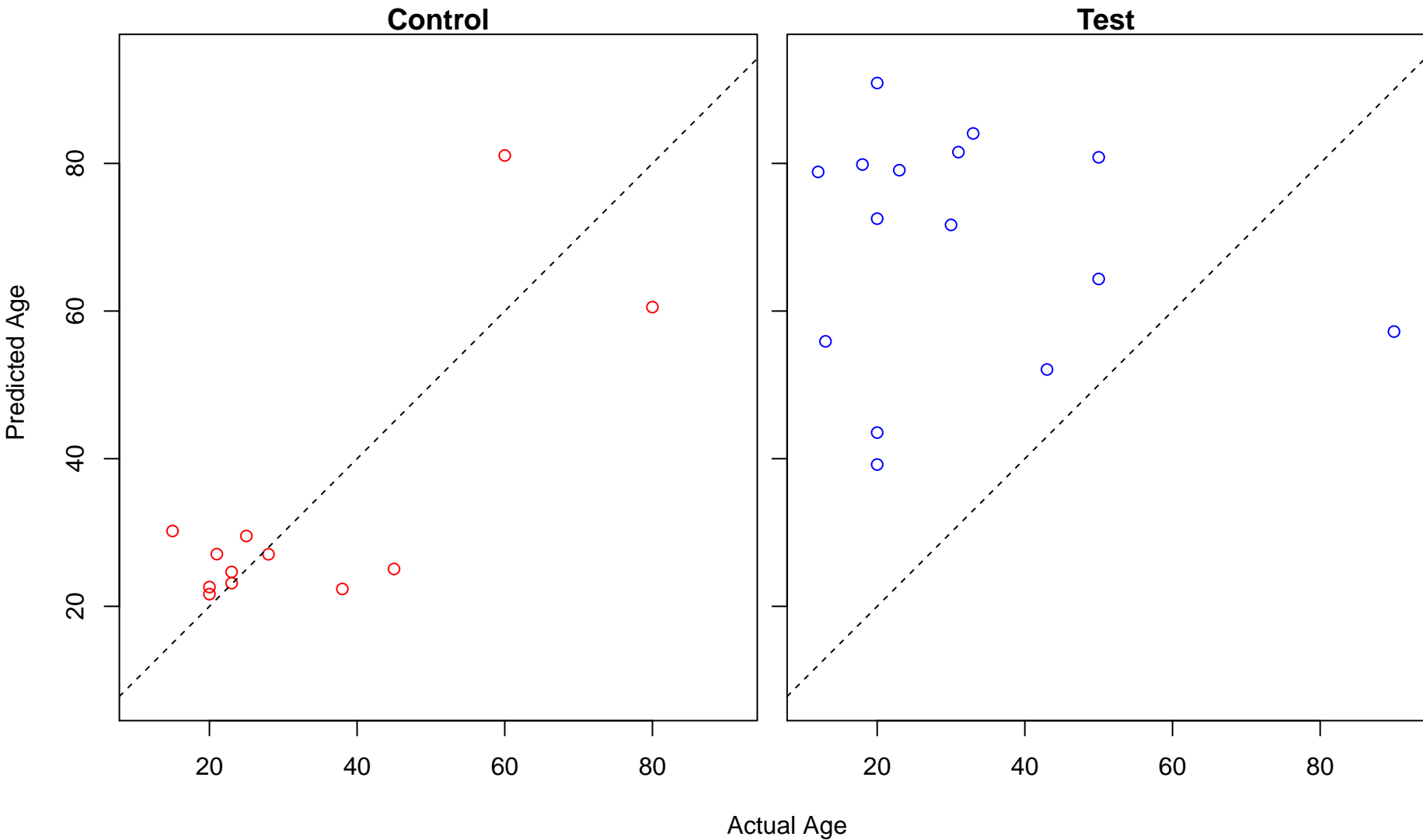
transepithelial transport (Score: 5.142033)



insulin secretion (Score: 5.140839)

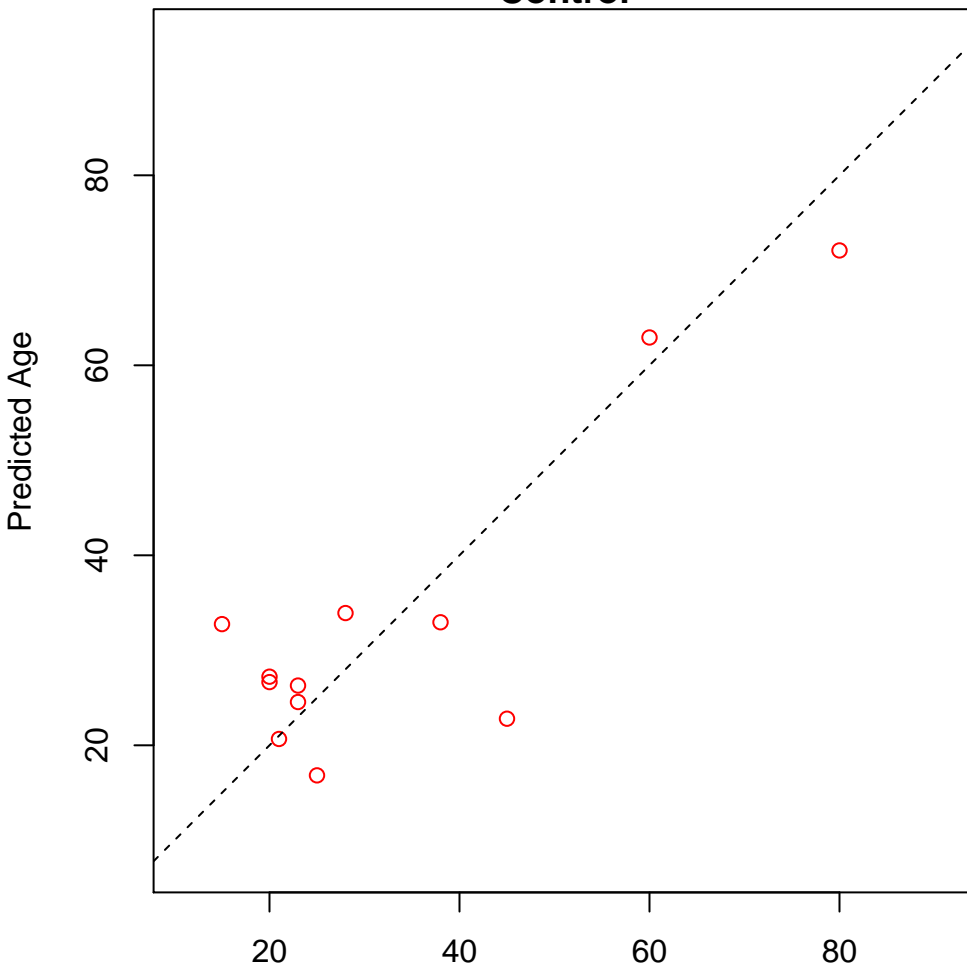


glomerular visceral epithelial cell development (Score: 5.140695)

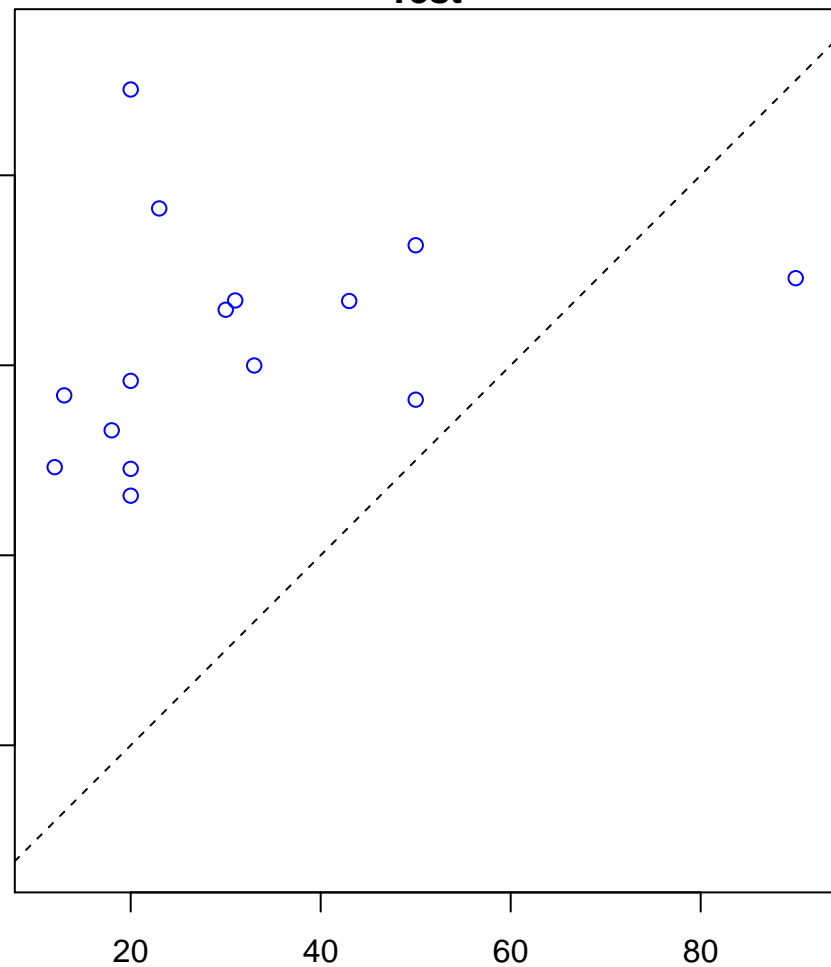


3'-UTR-mediated mRNA destabilization (Score: 5.140471)

Control



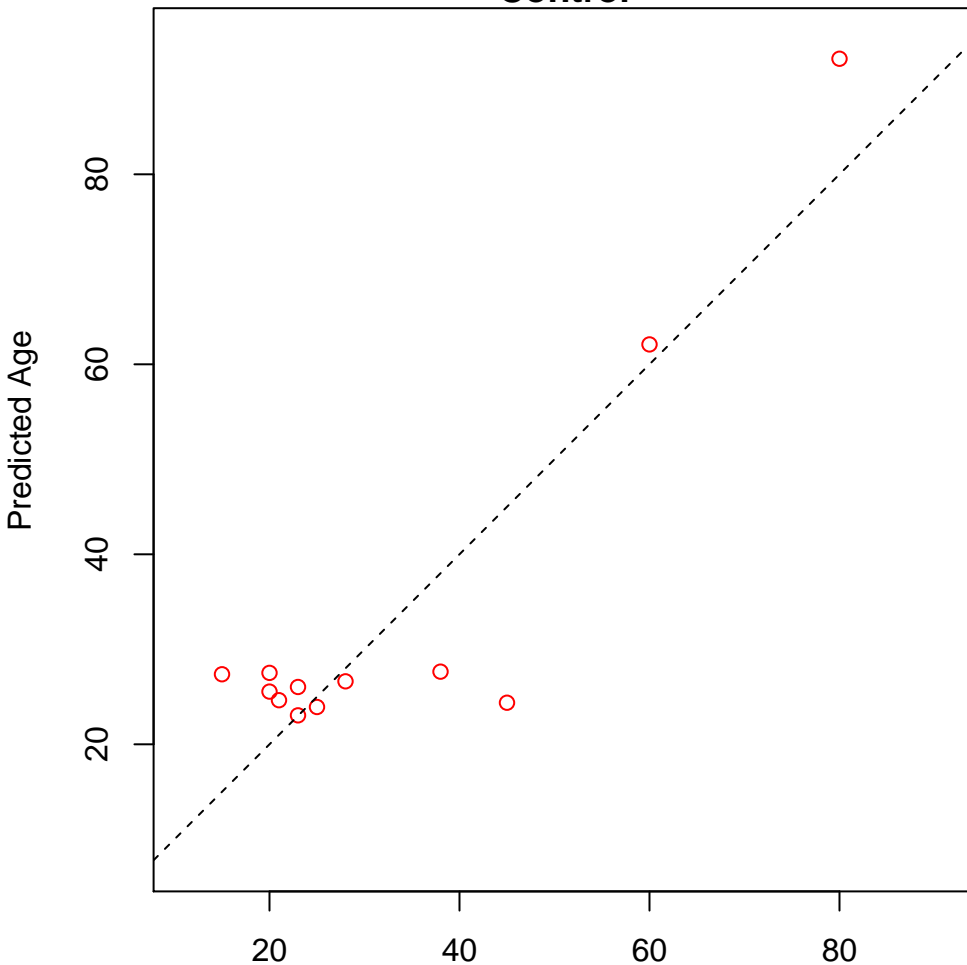
Test



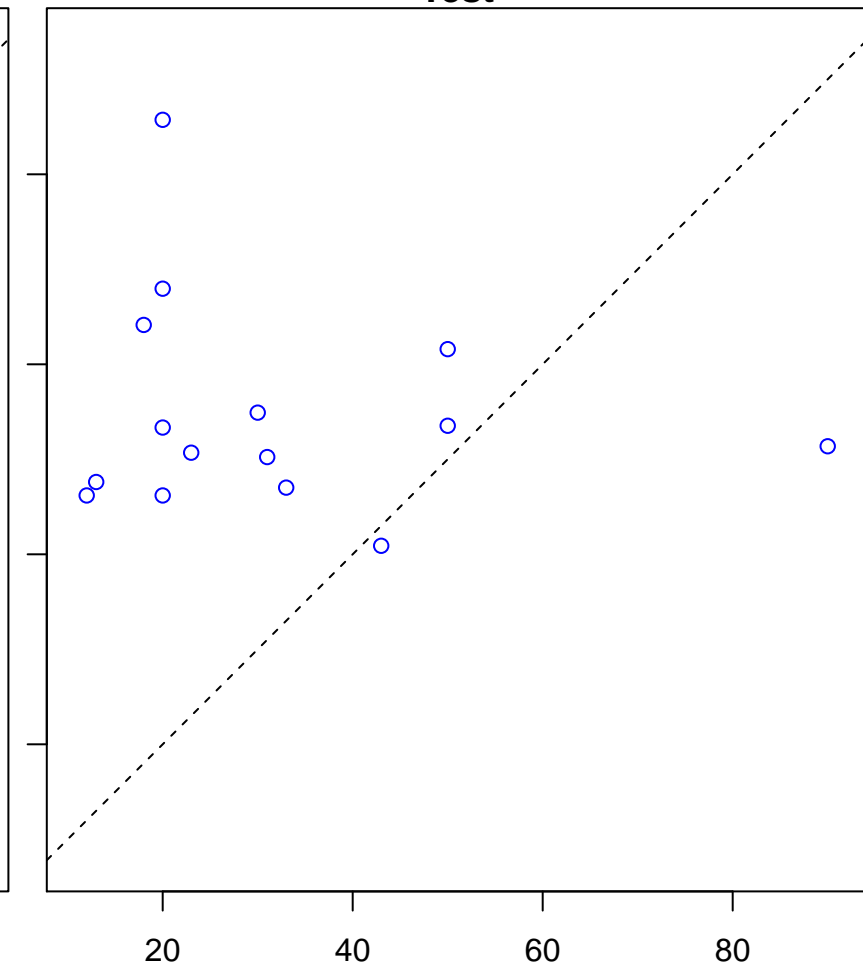
Actual Age

regulation of protein complex assembly (Score: 5.139827)

Control

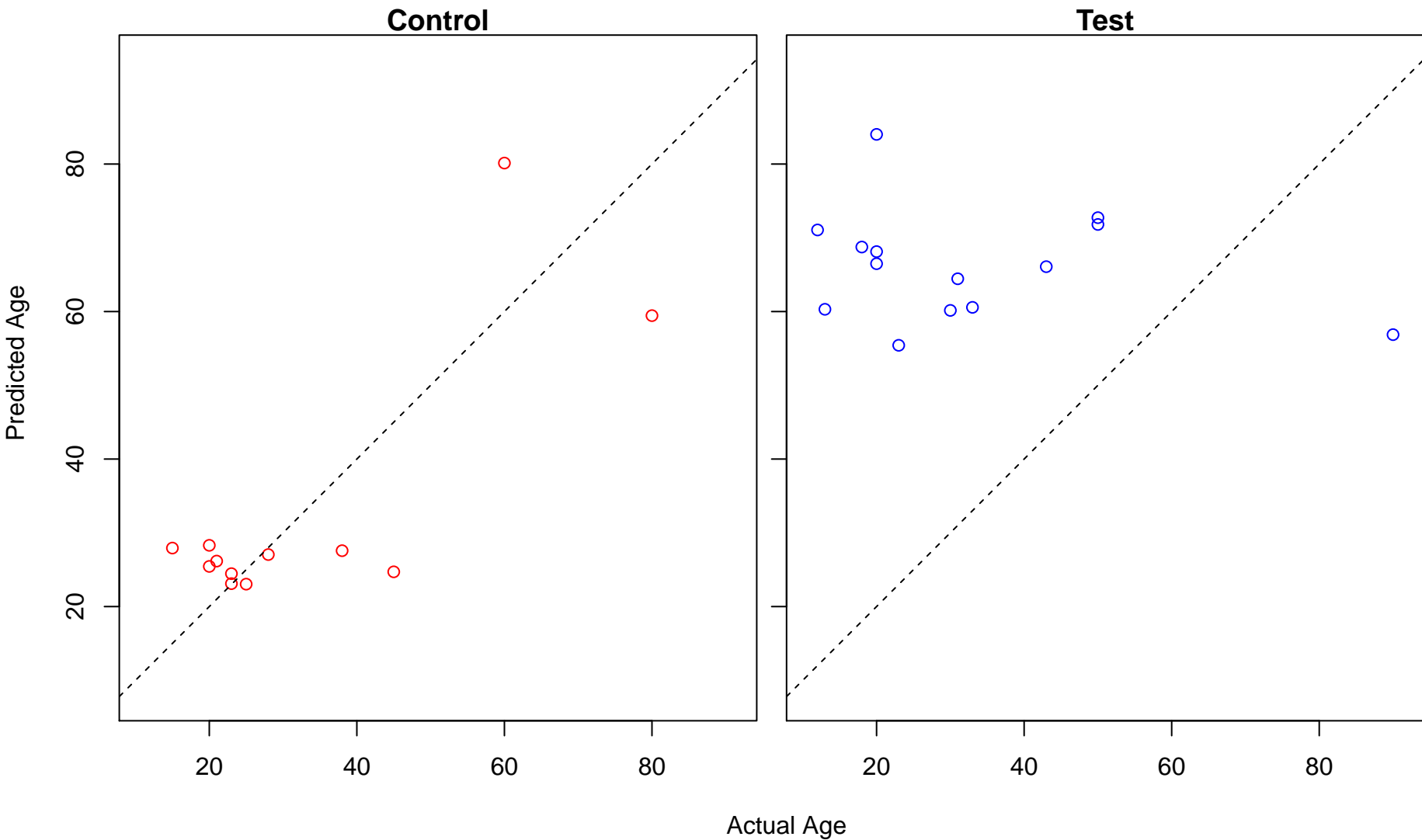


Test

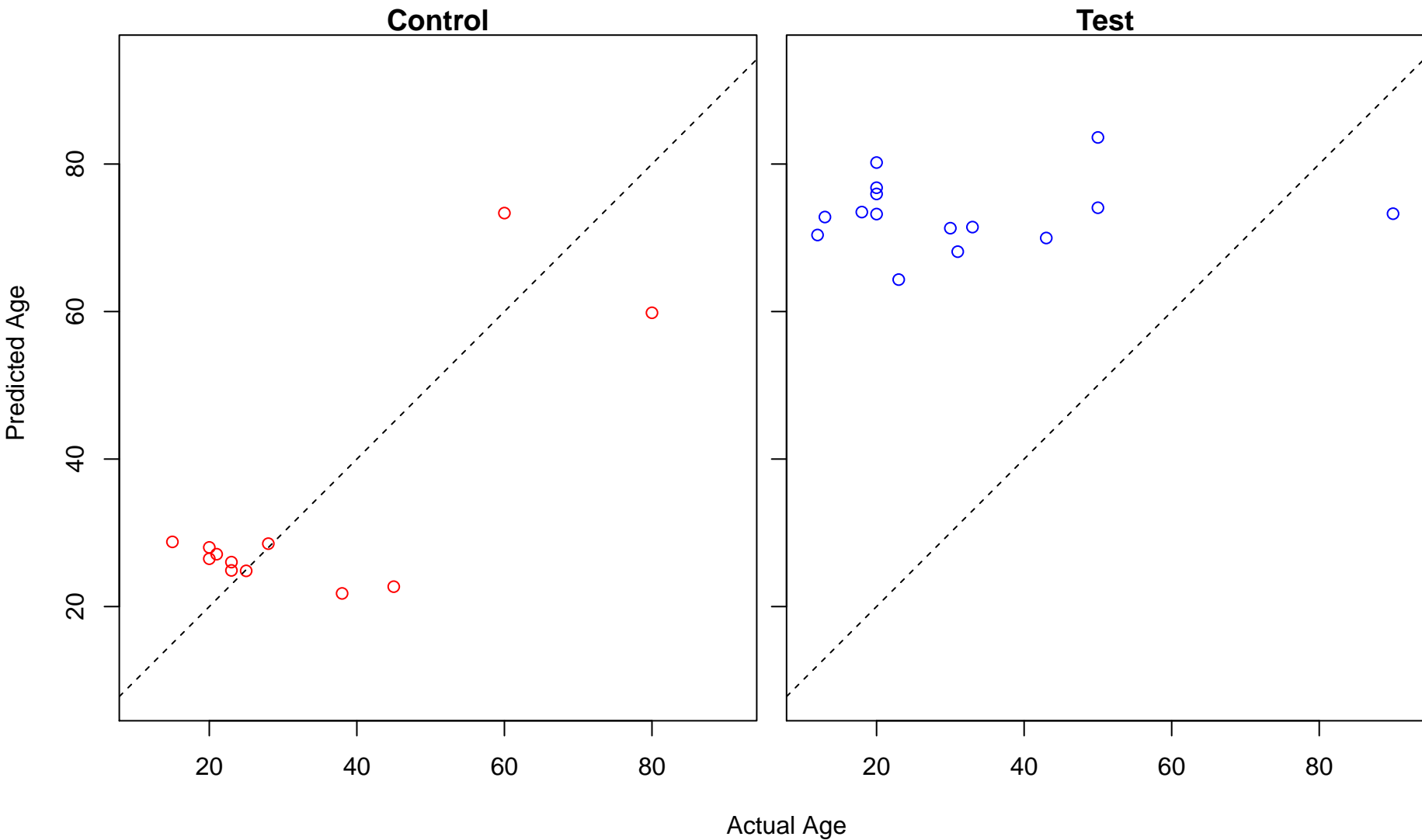


Actual Age

sex differentiation (Score: 5.139119)

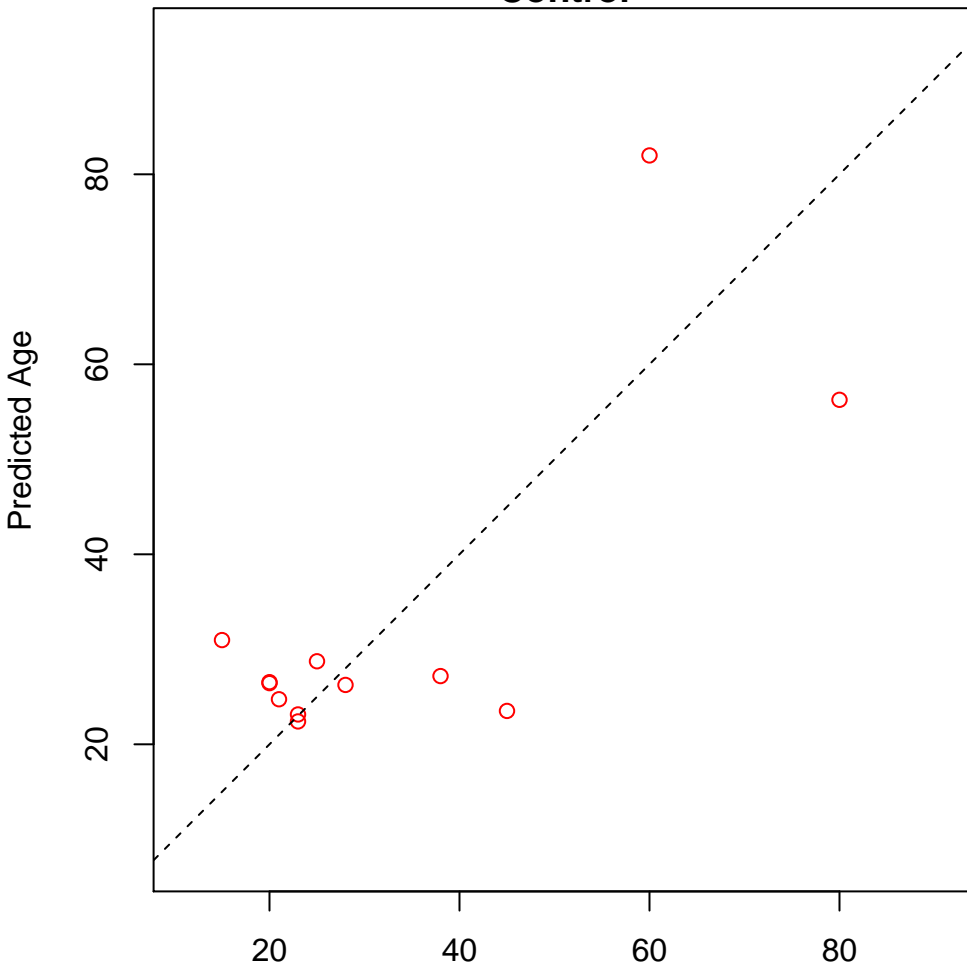


regulation of defense response to virus by host (Score: 5.138954)

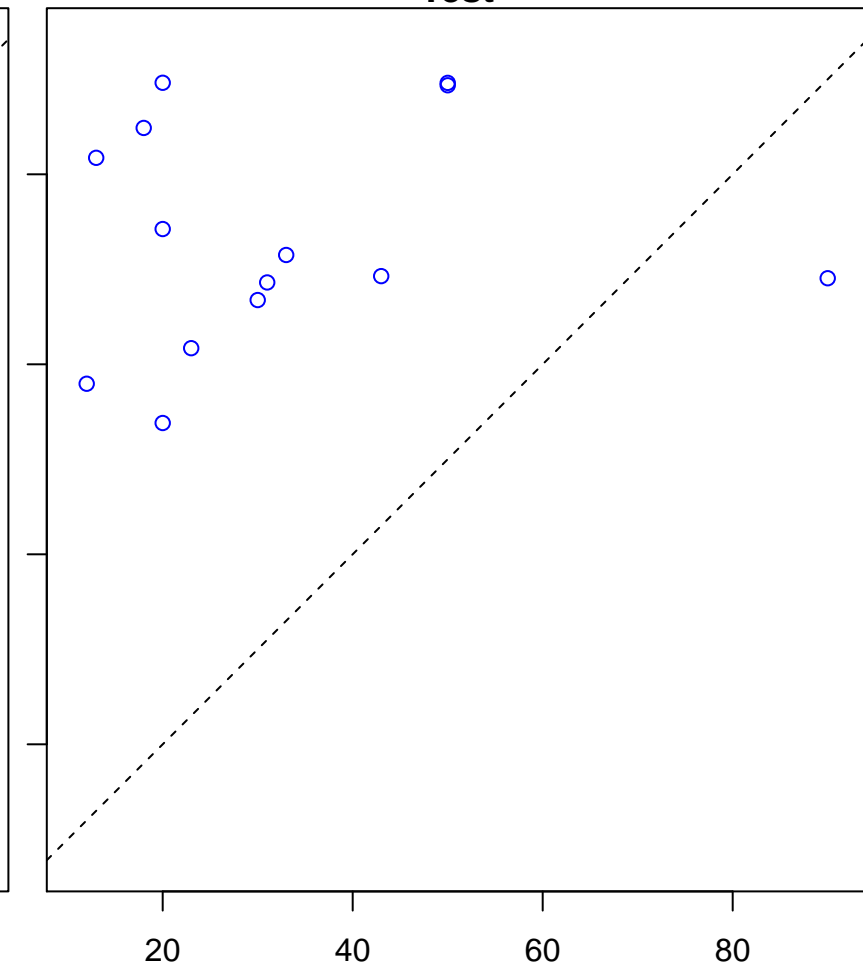


cell-type specific apoptotic process (Score: 5.138919)

Control



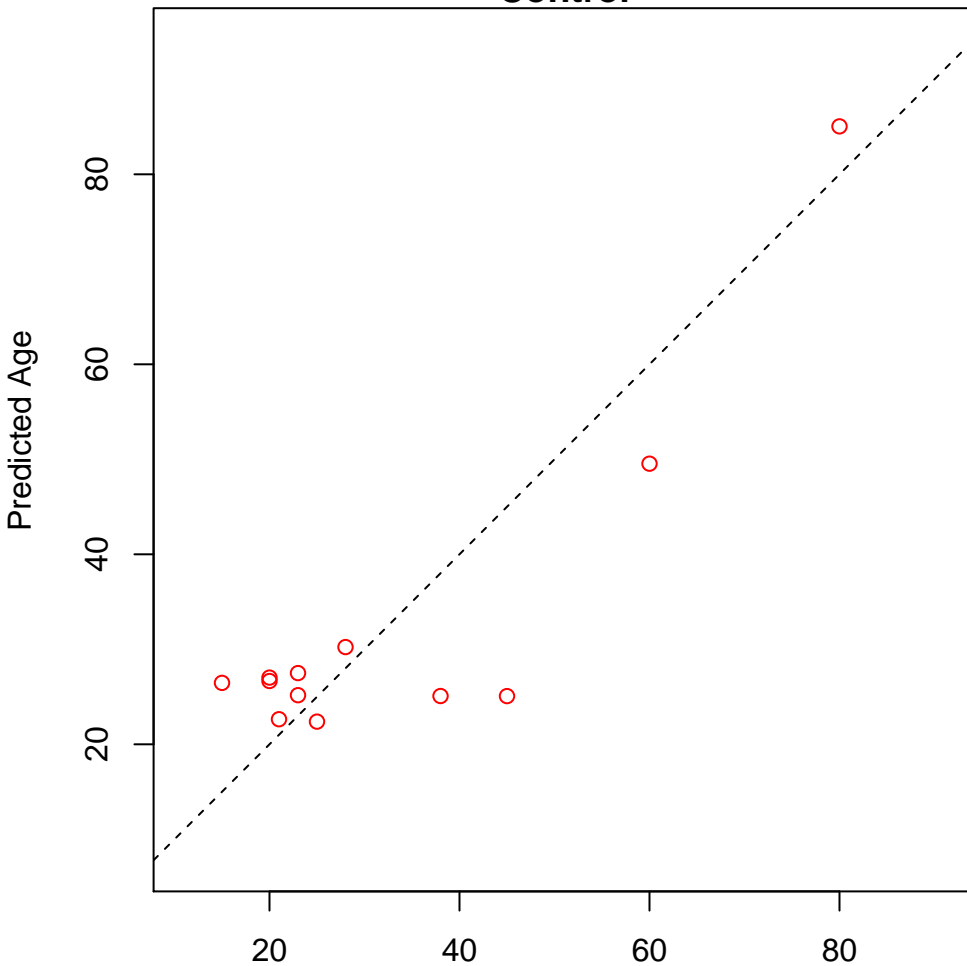
Test



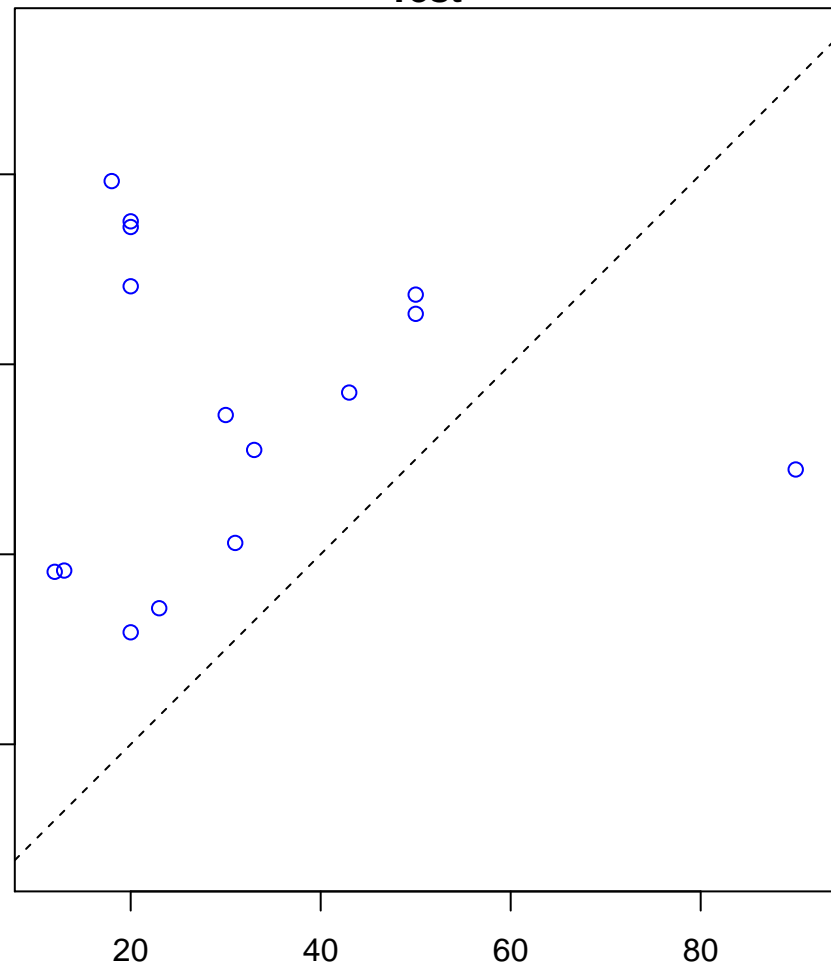
Actual Age

regulation of sulfur metabolic process (Score: 5.137590)

Control

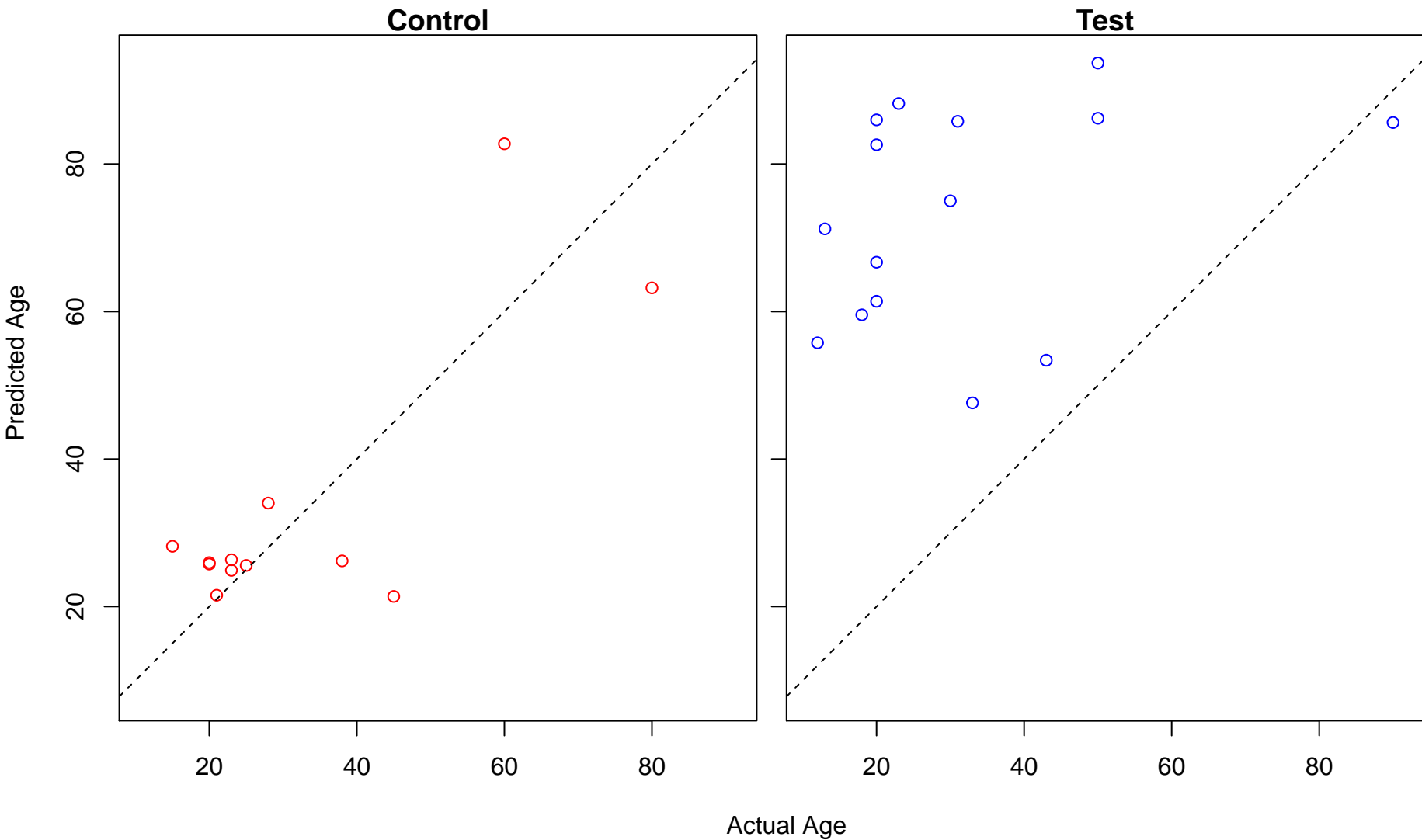


Test

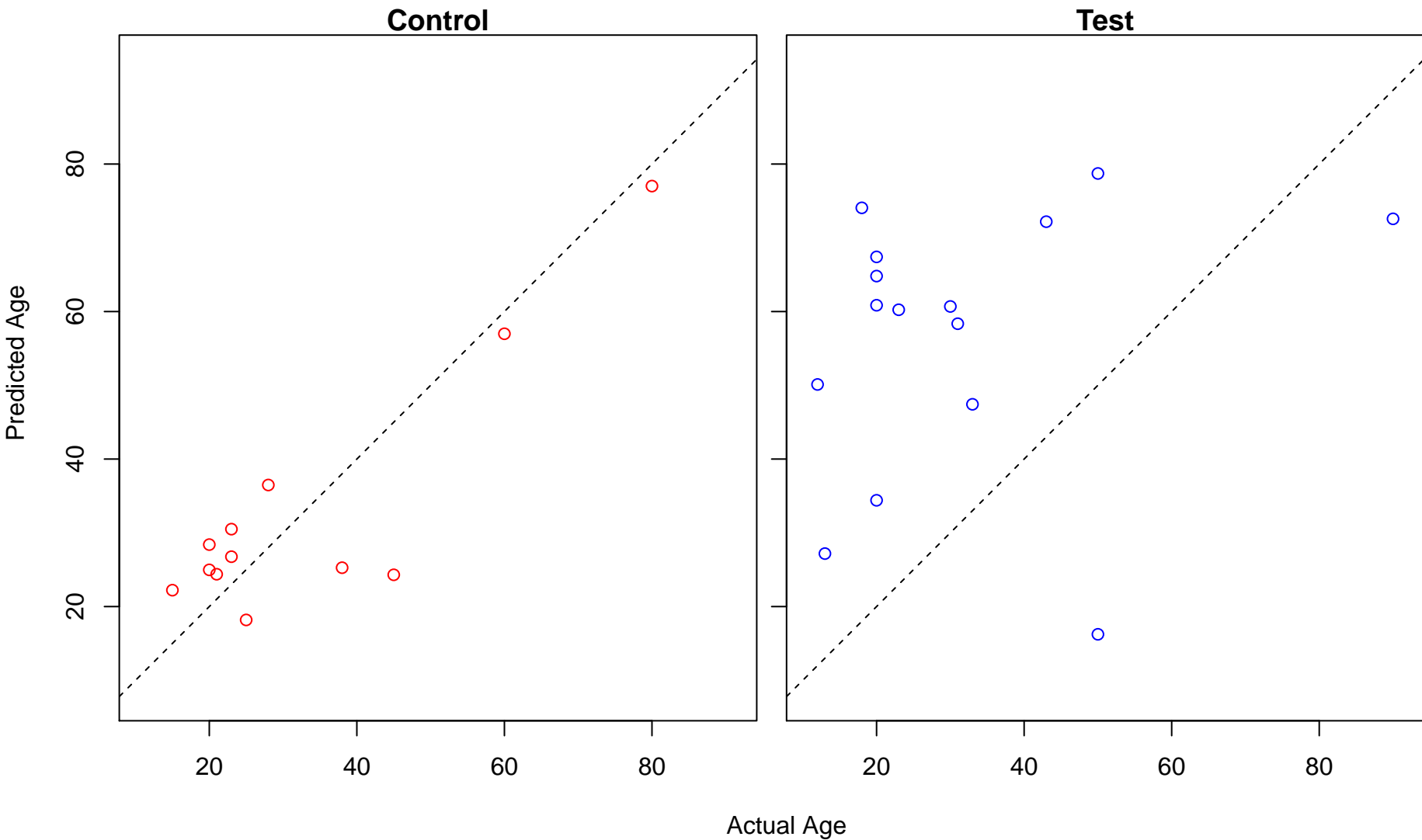


Actual Age

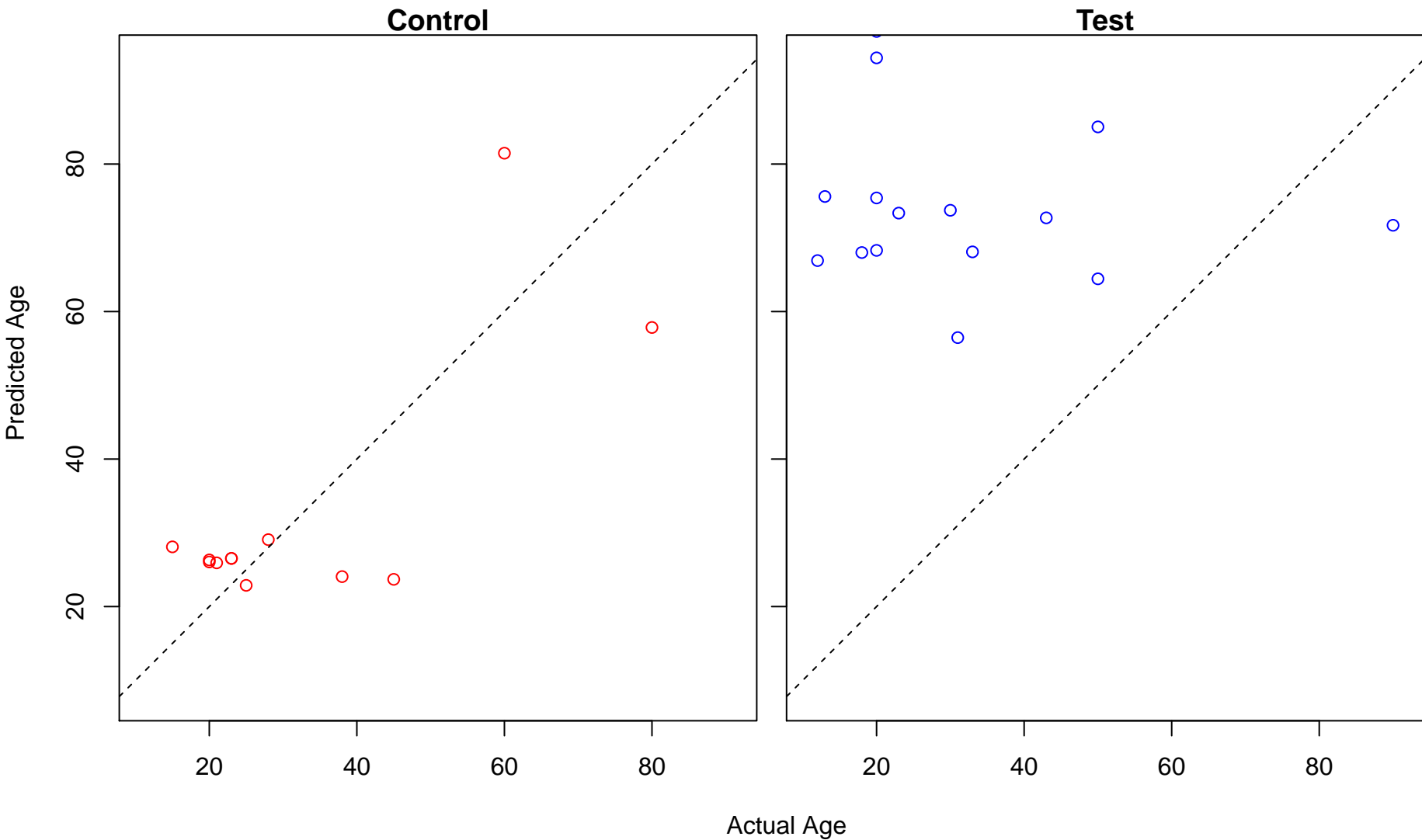
regulation of entry of bacterium into host cell (Score: 5.136387)



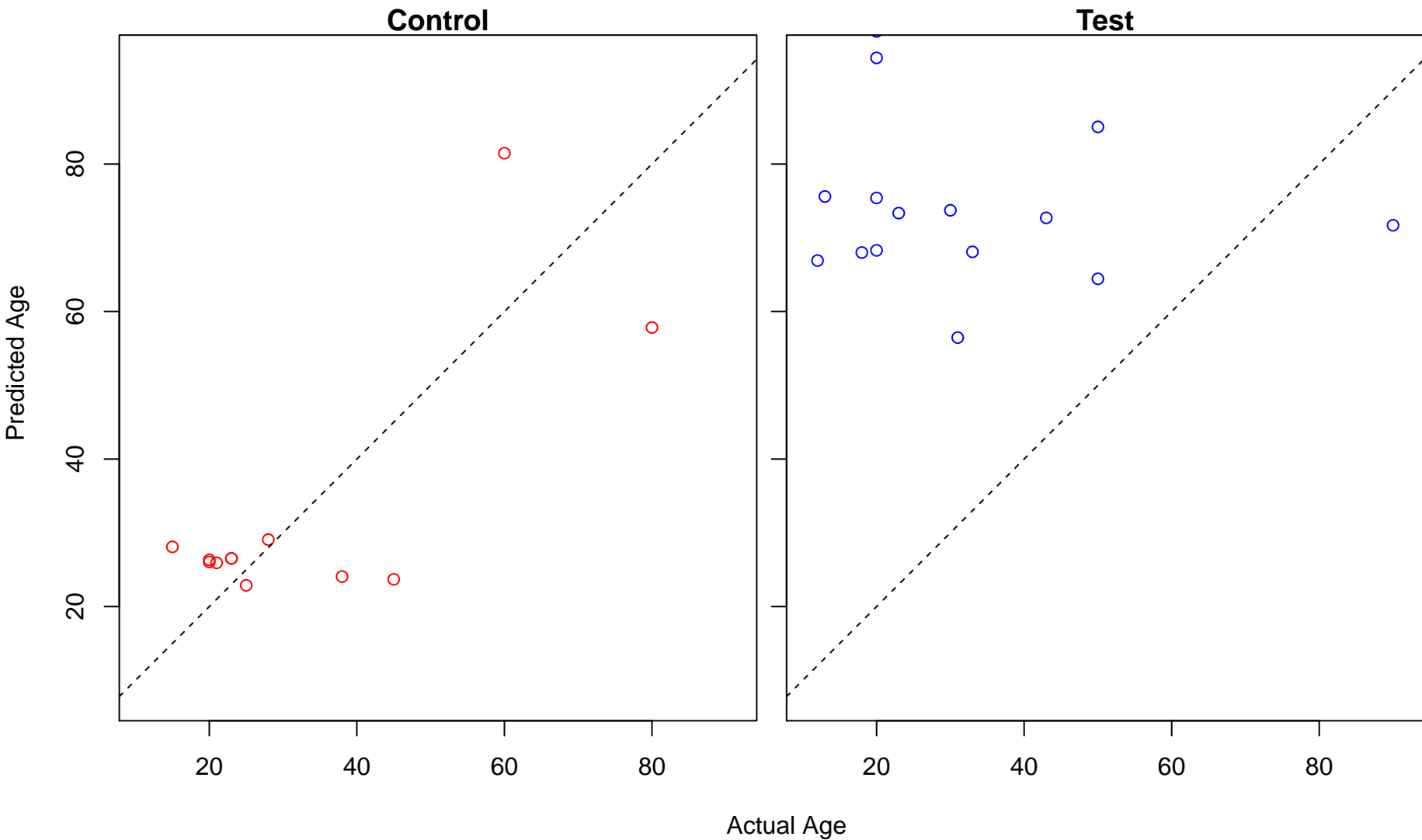
positive regulation of vesicle fusion (Score: 5.136352)



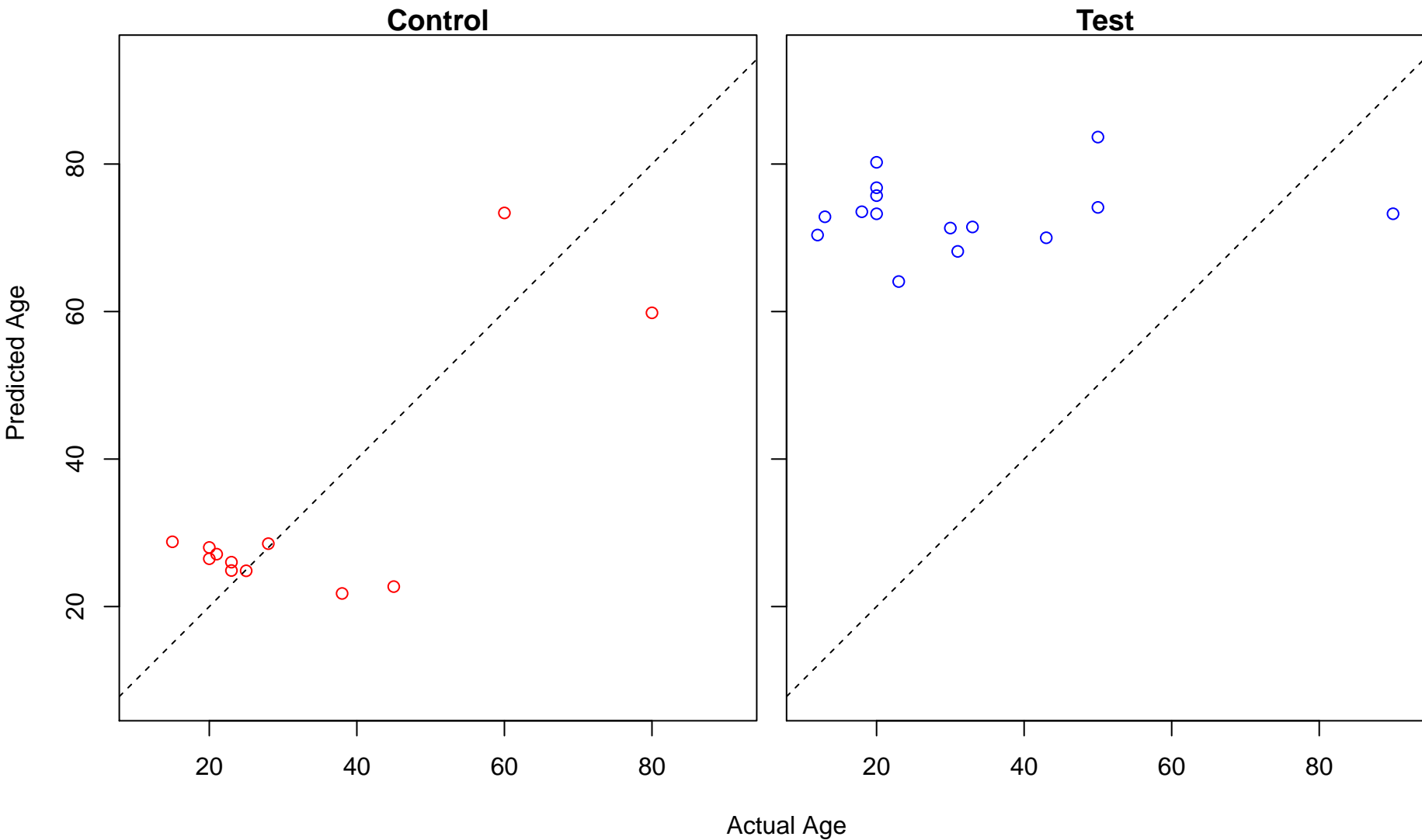
porphyrin-containing compound biosynthetic process (Score: 5.134953)



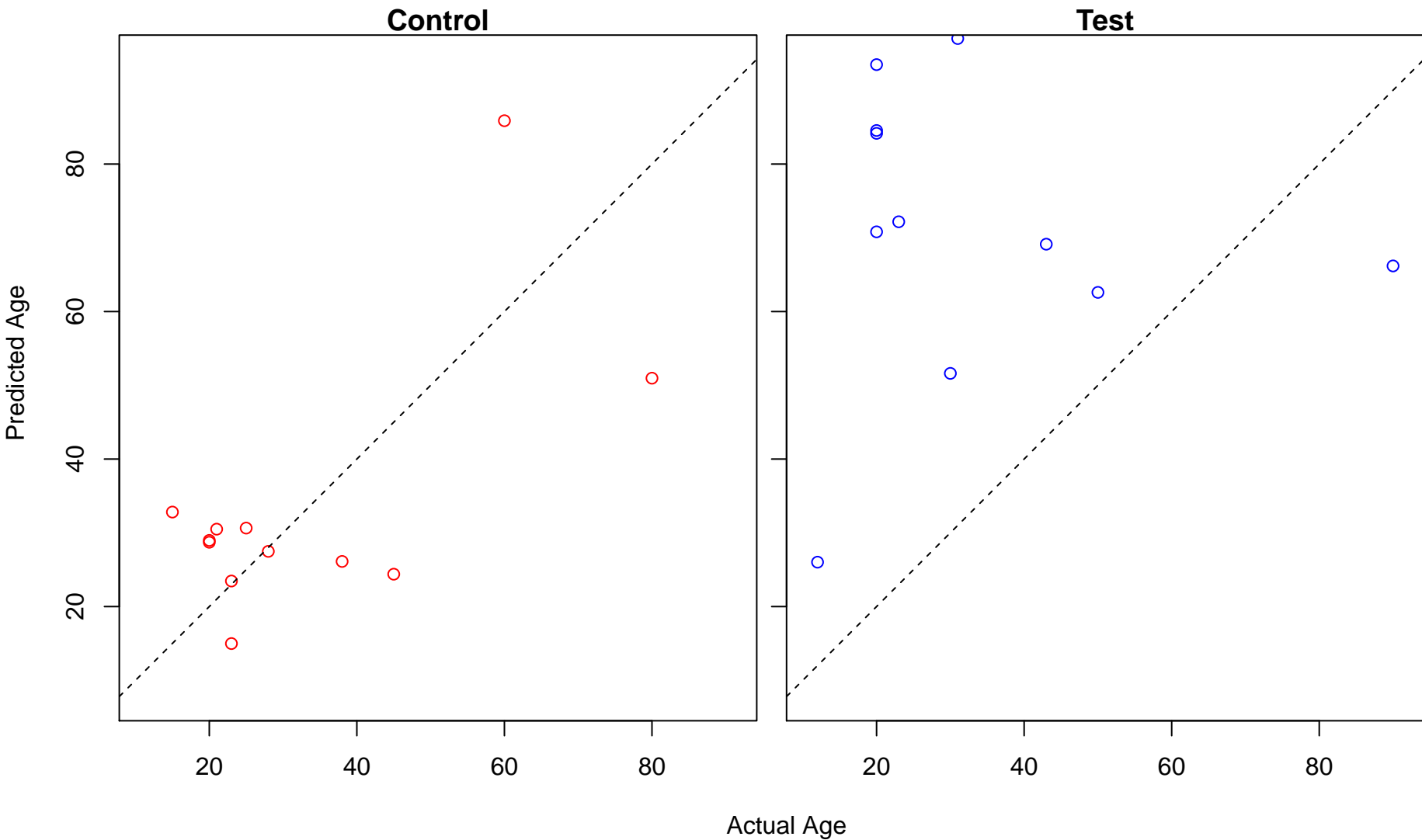
tetrapyrrole biosynthetic process (Score: 5.134953)



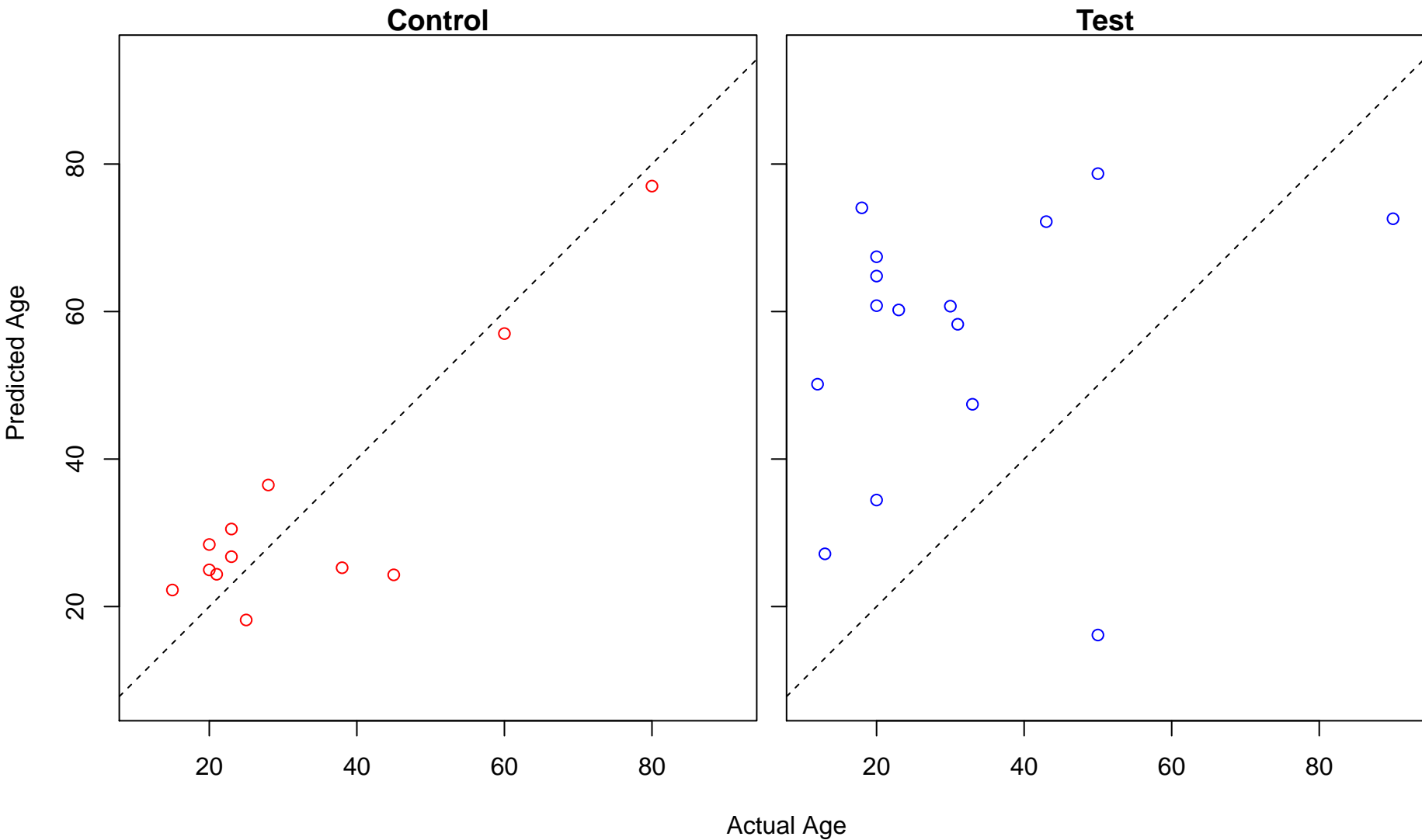
positive regulation of defense response to virus by host (Score: 5.134936)



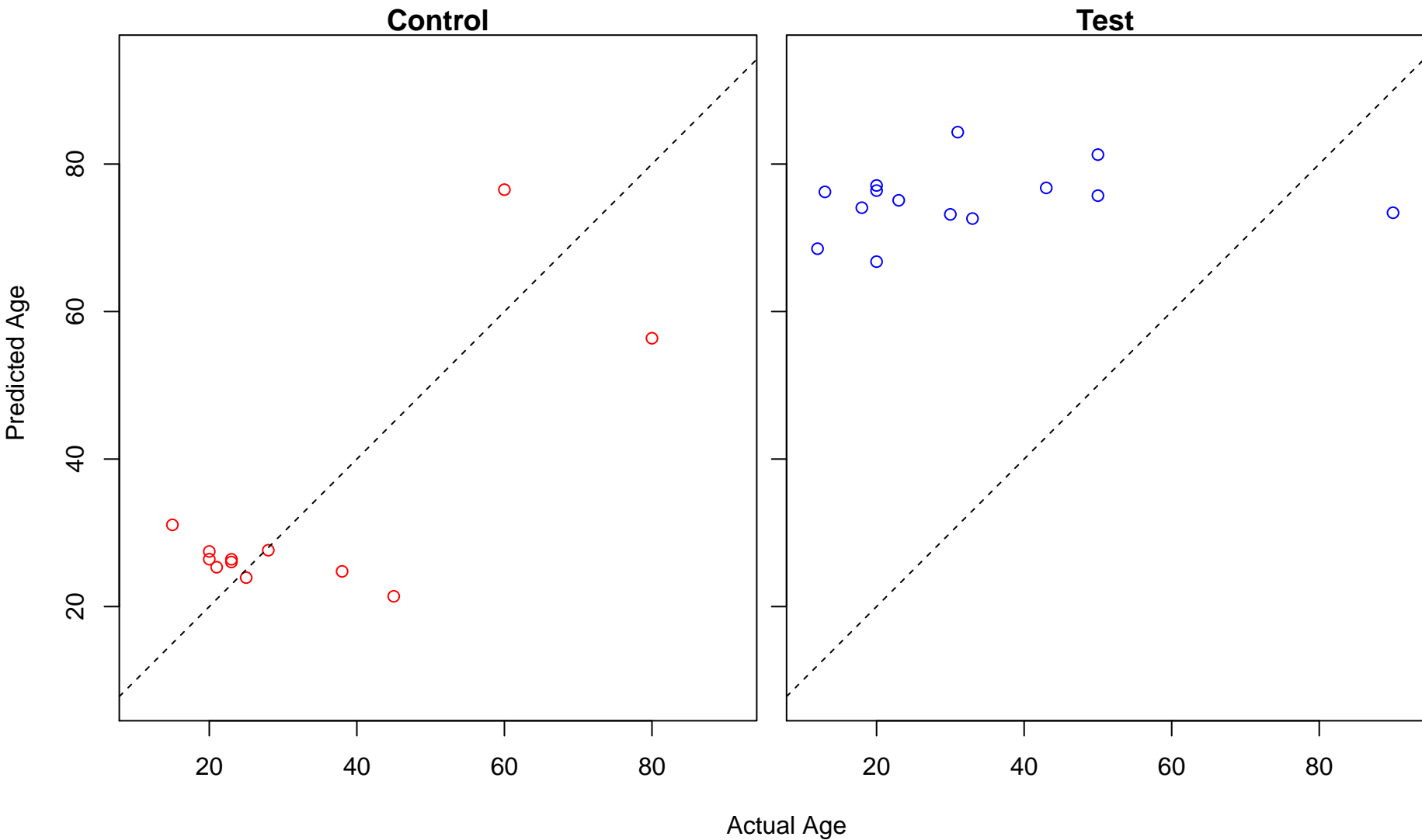
high-density lipoprotein particle assembly (Score: 5.132335)



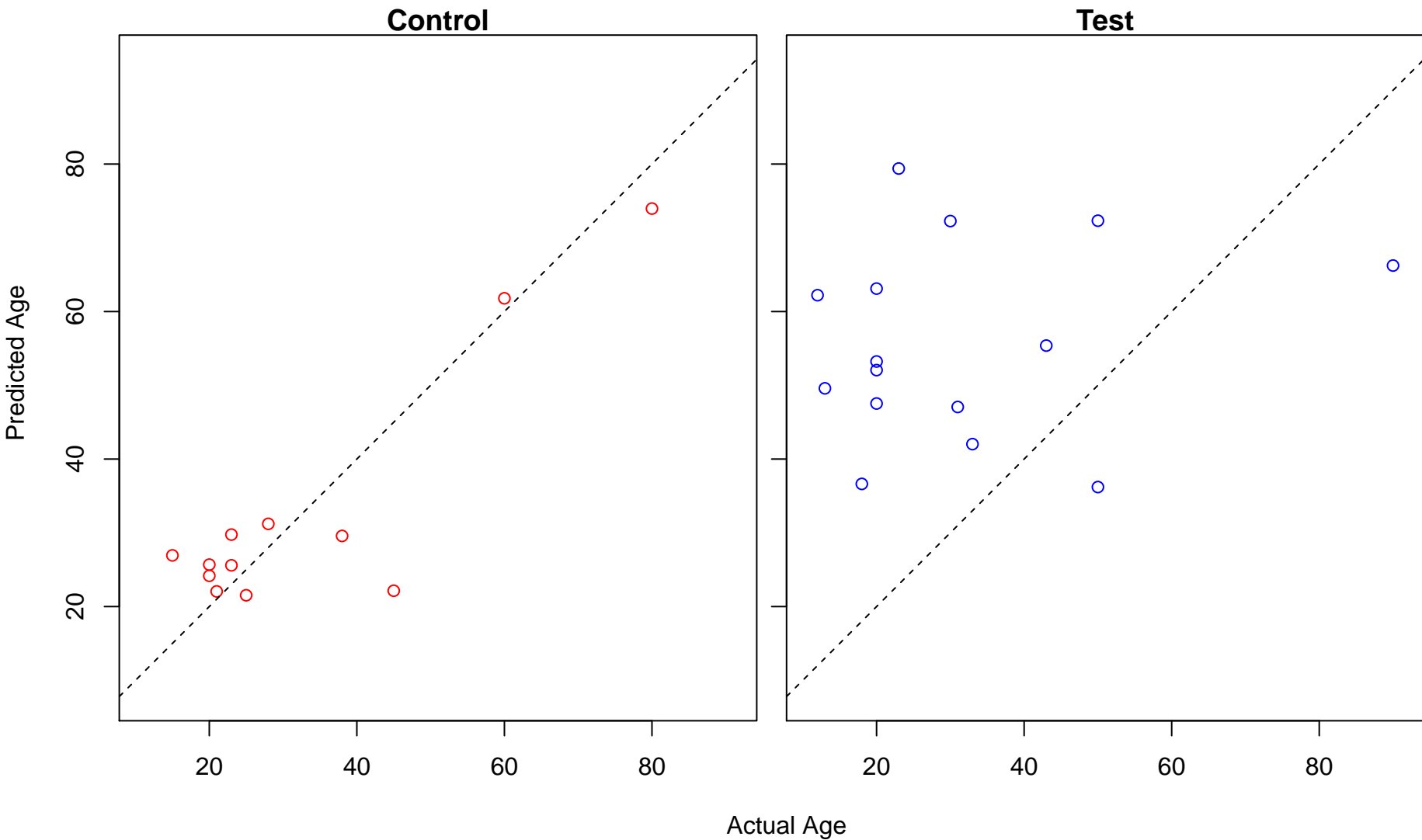
regulation of vesicle fusion (Score: 5.131891)



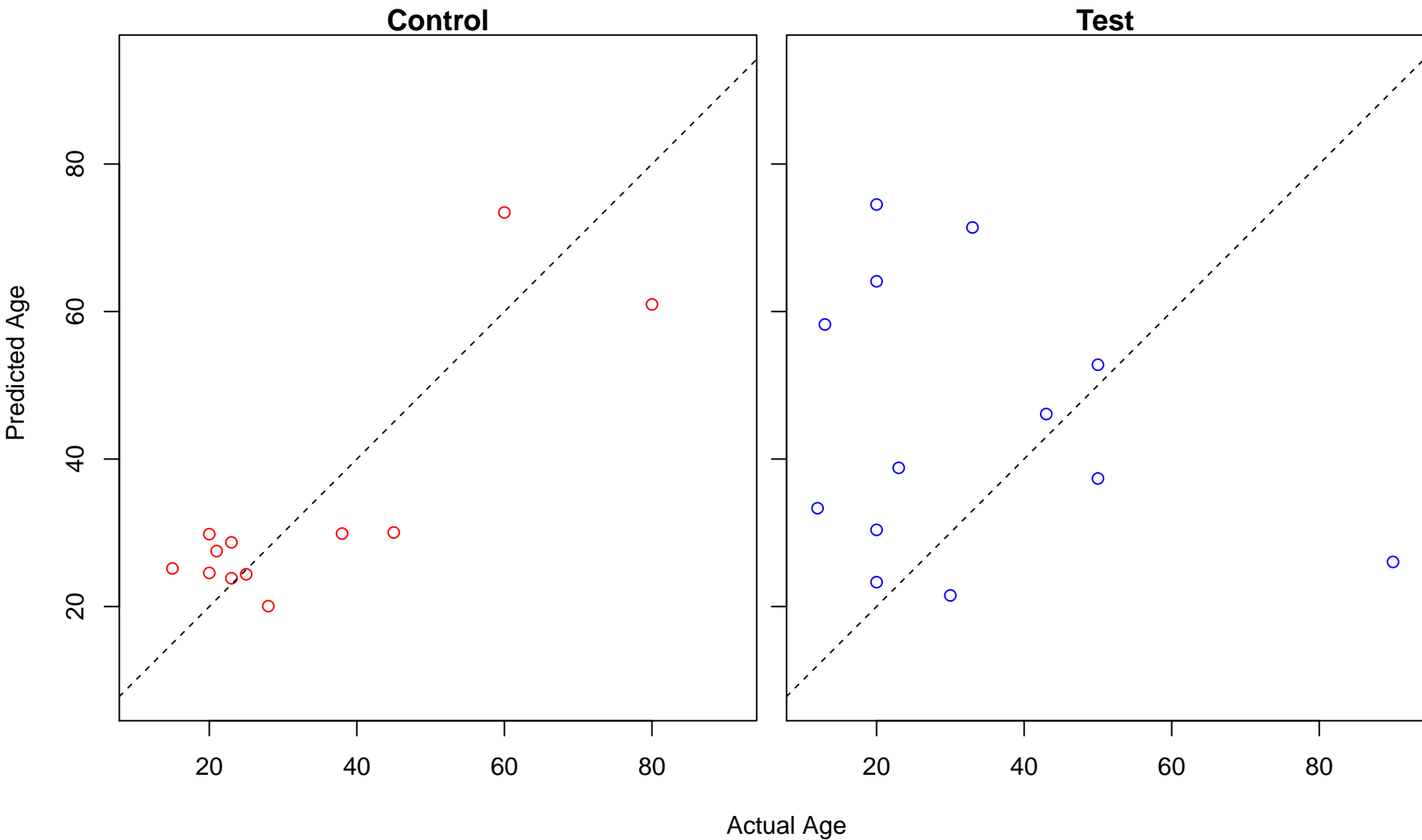
negative regulation of reactive oxygen species metabolic process (Score: 5.130845)



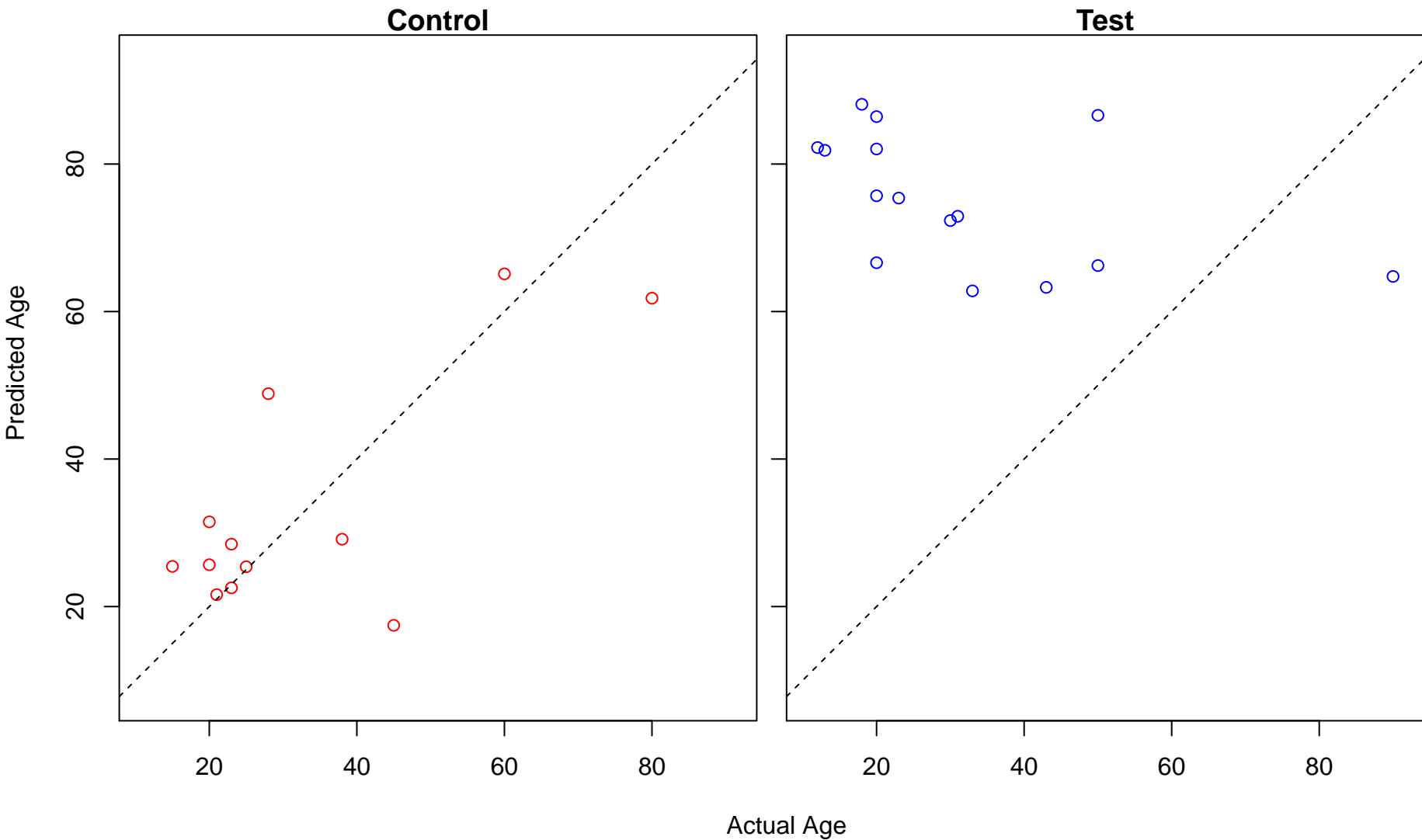
eye pigmentation (Score: 5.129338)



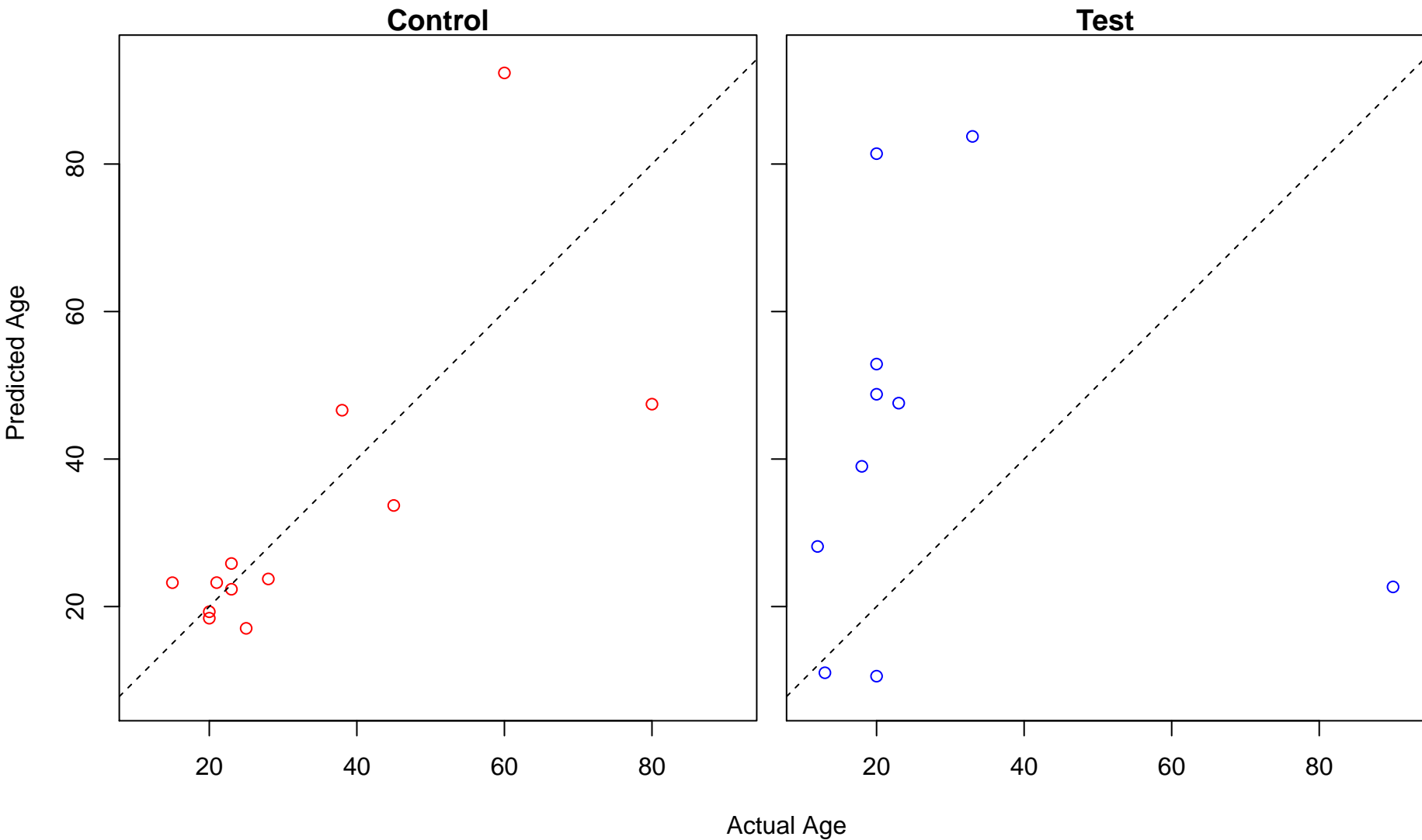
sulfate transmembrane transport (Score: 5.122720)



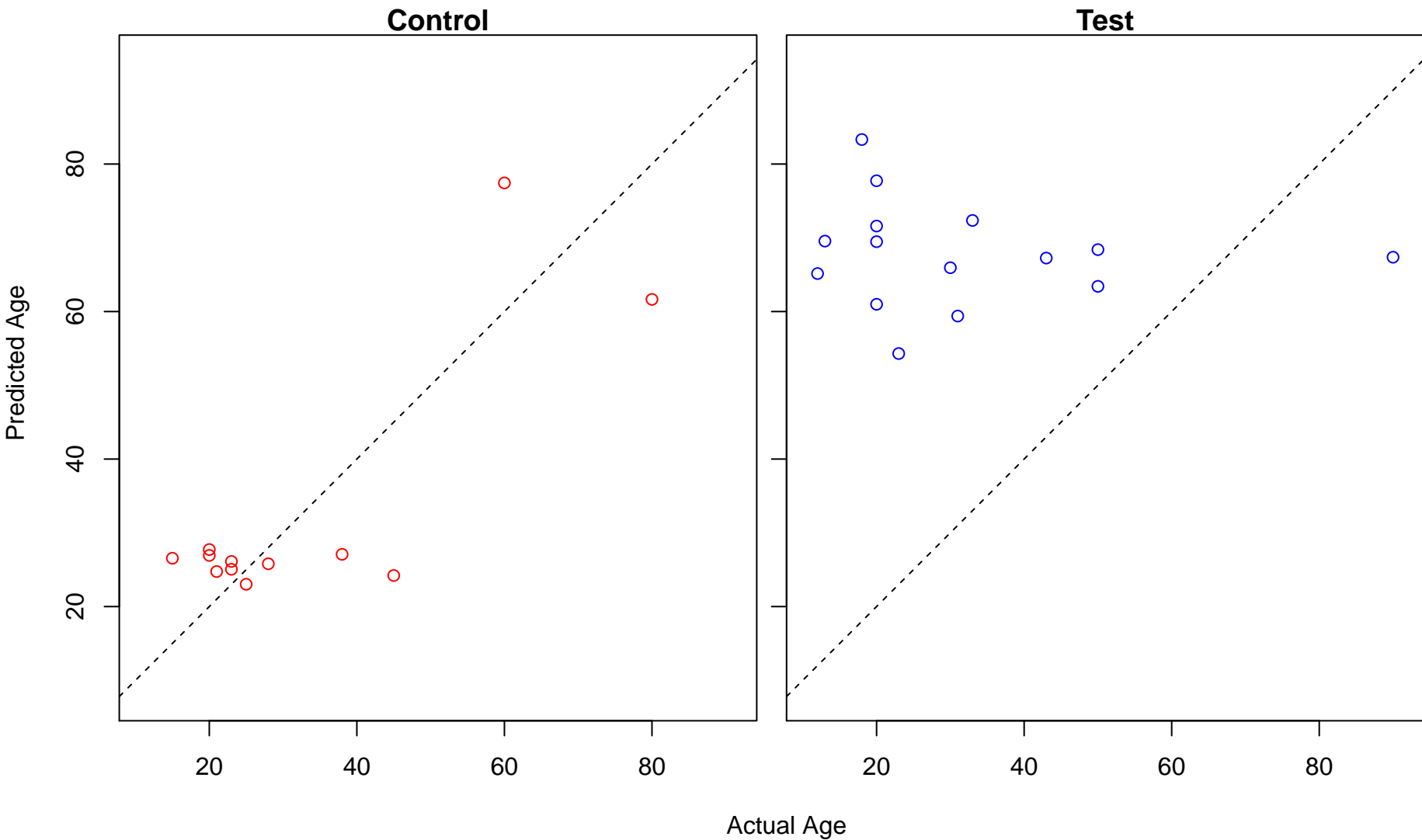
regulation of macrophage cytokine production (Score: 5.119159)



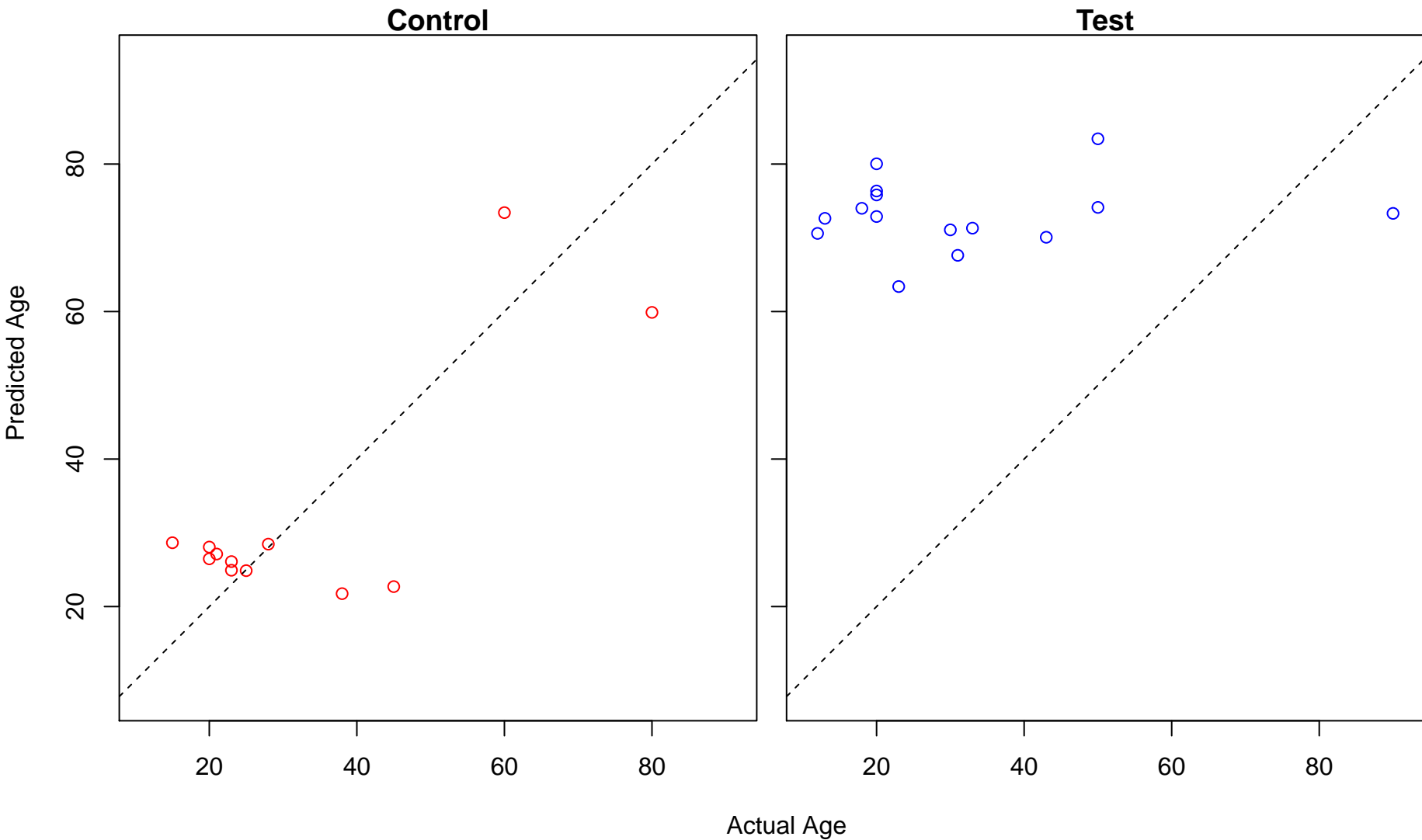
positive regulation of cartilage development (Score: 5.118504)



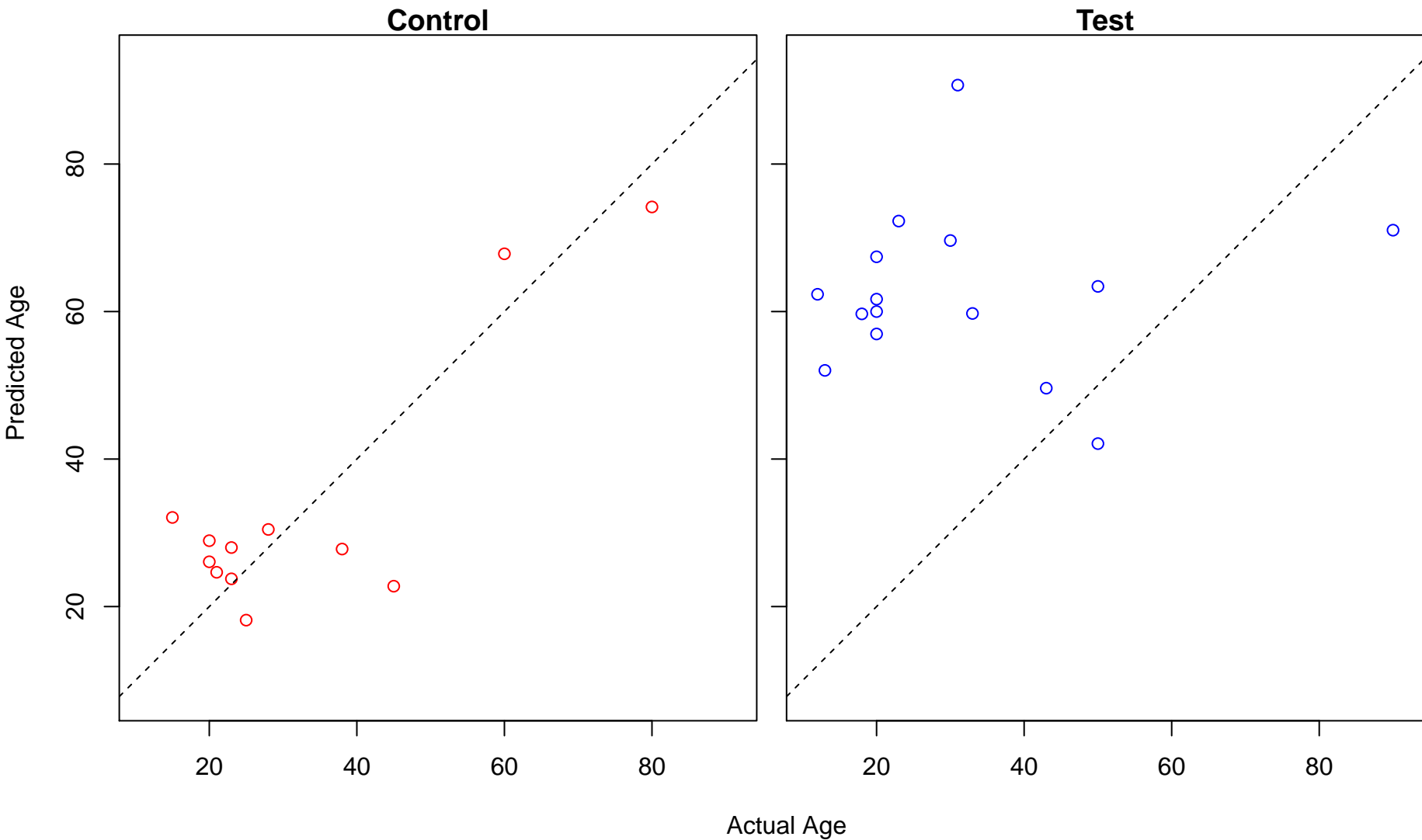
dendrite development (Score: 5.118223)



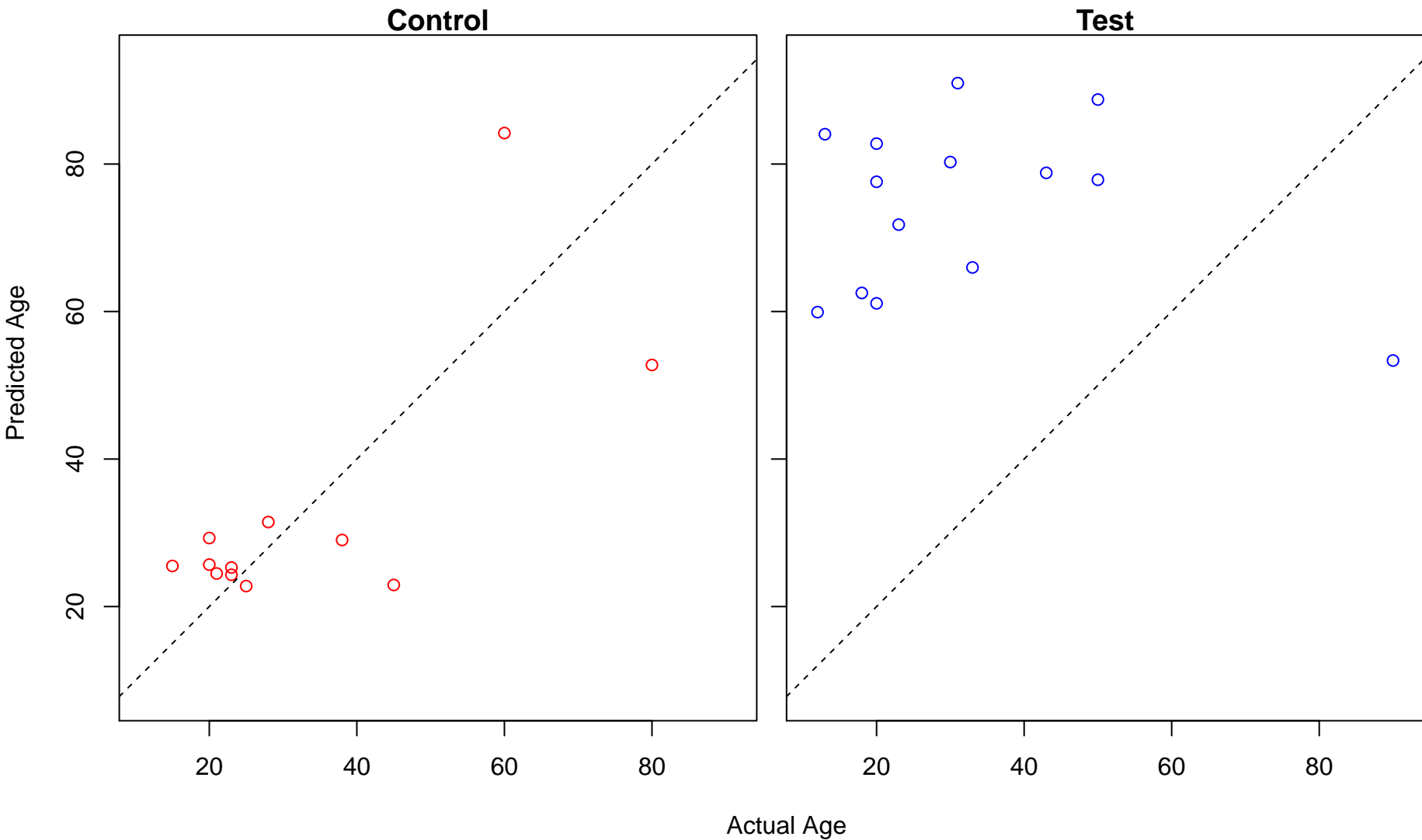
xenophagy (Score: 5.117497)



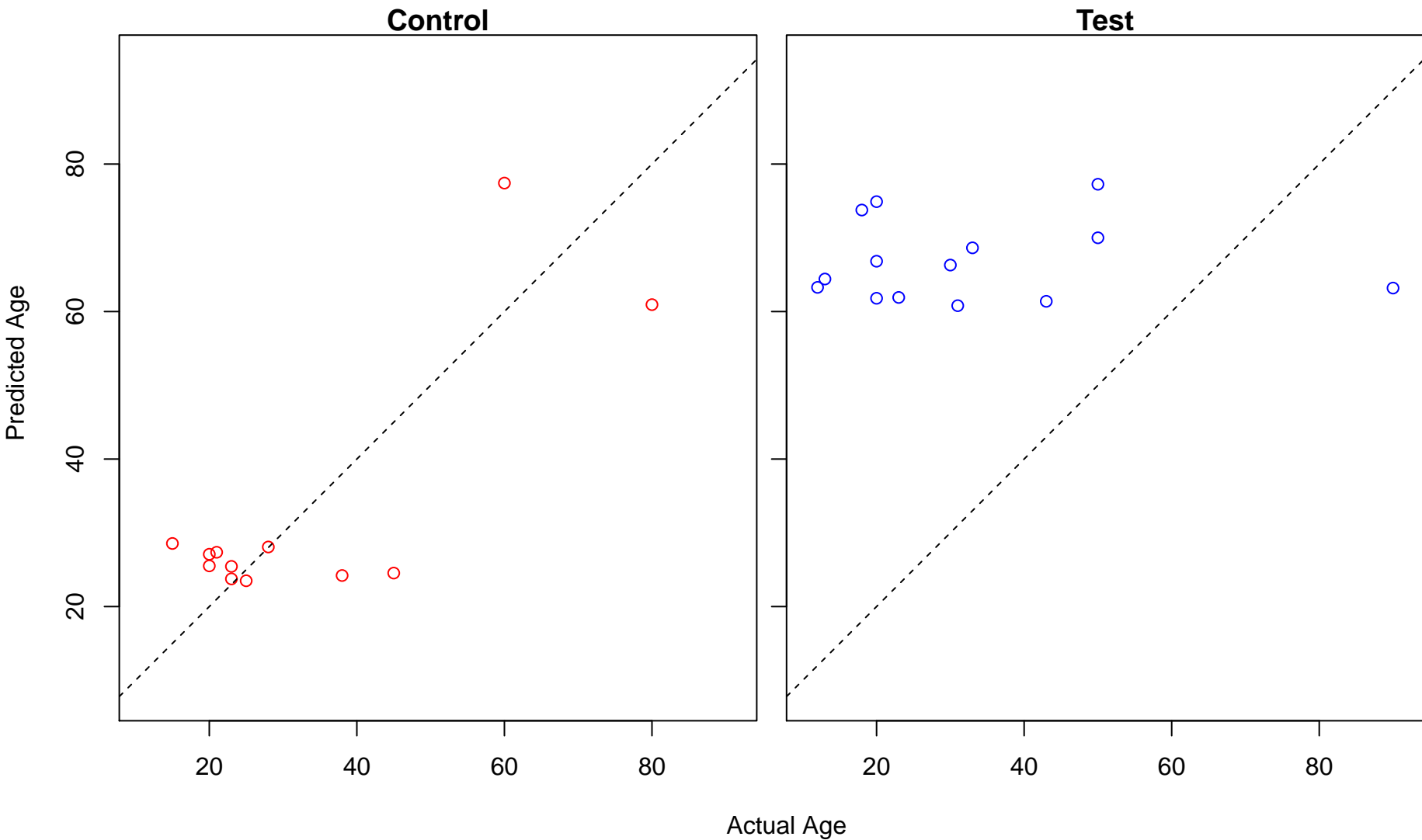
negative regulation of release of cytochrome c from mitochondria (Score: 5.116489)



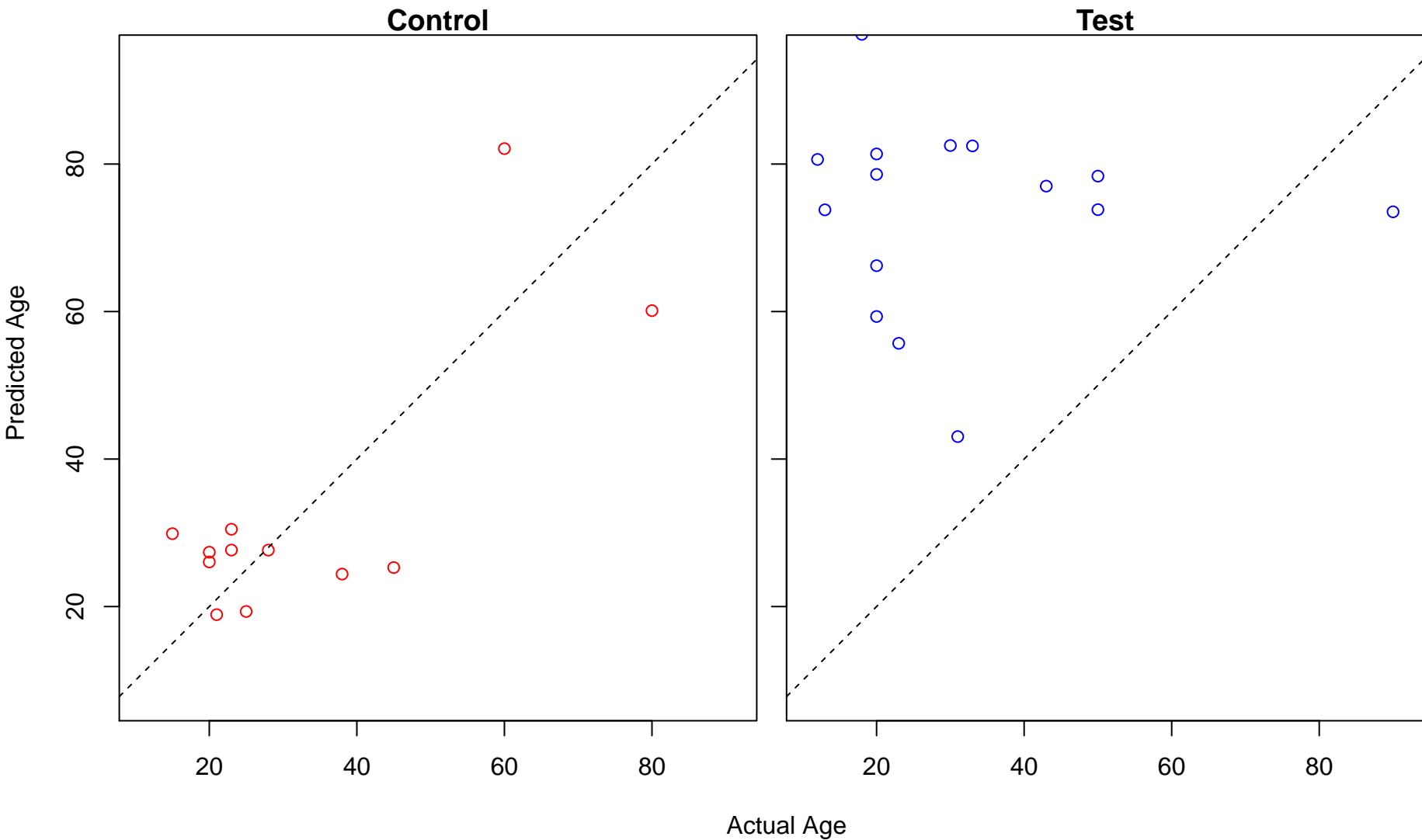
positive regulation of response to cytokine stimulus (Score: 5.116014)



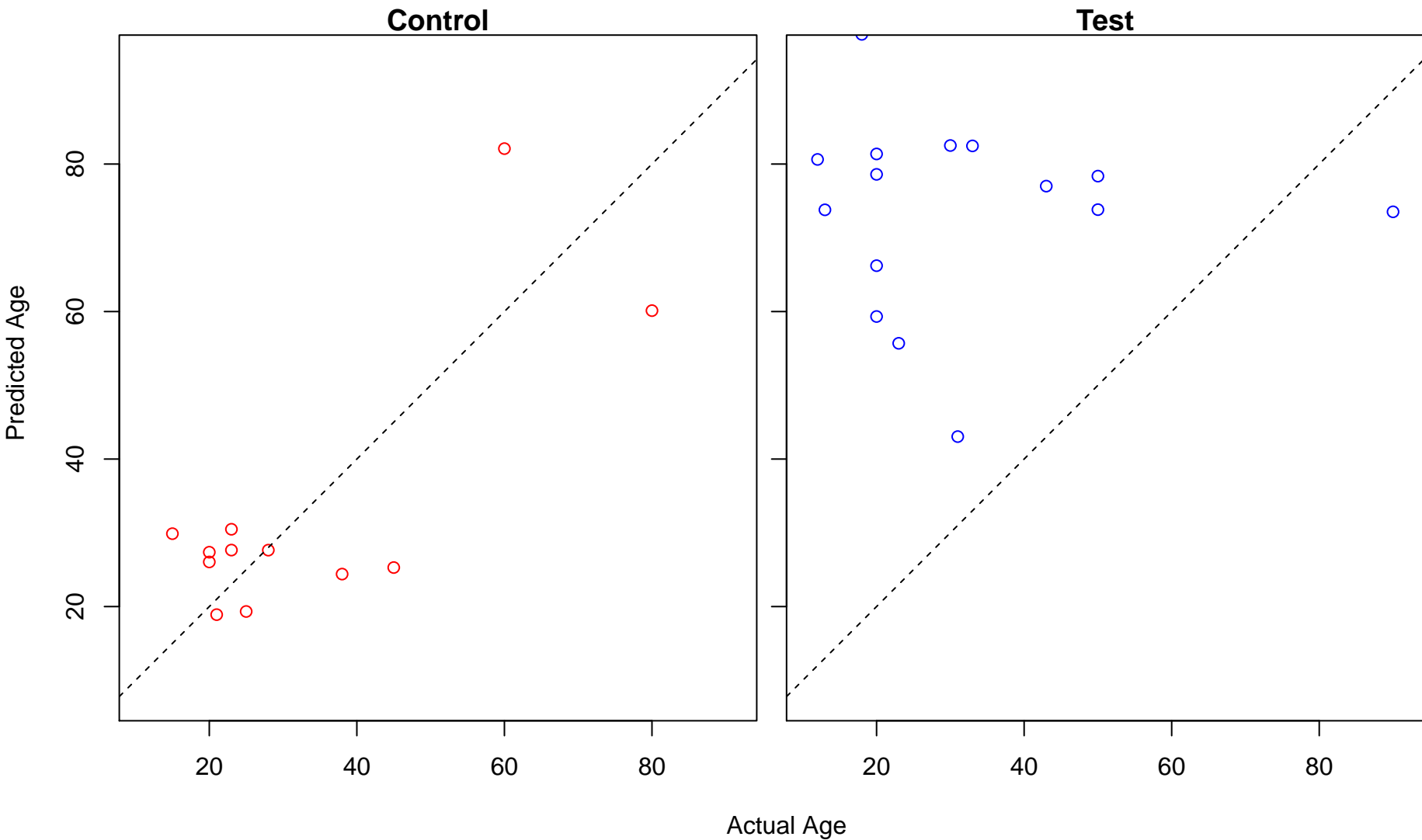
positive regulation of cell-matrix adhesion (Score: 5.115569)



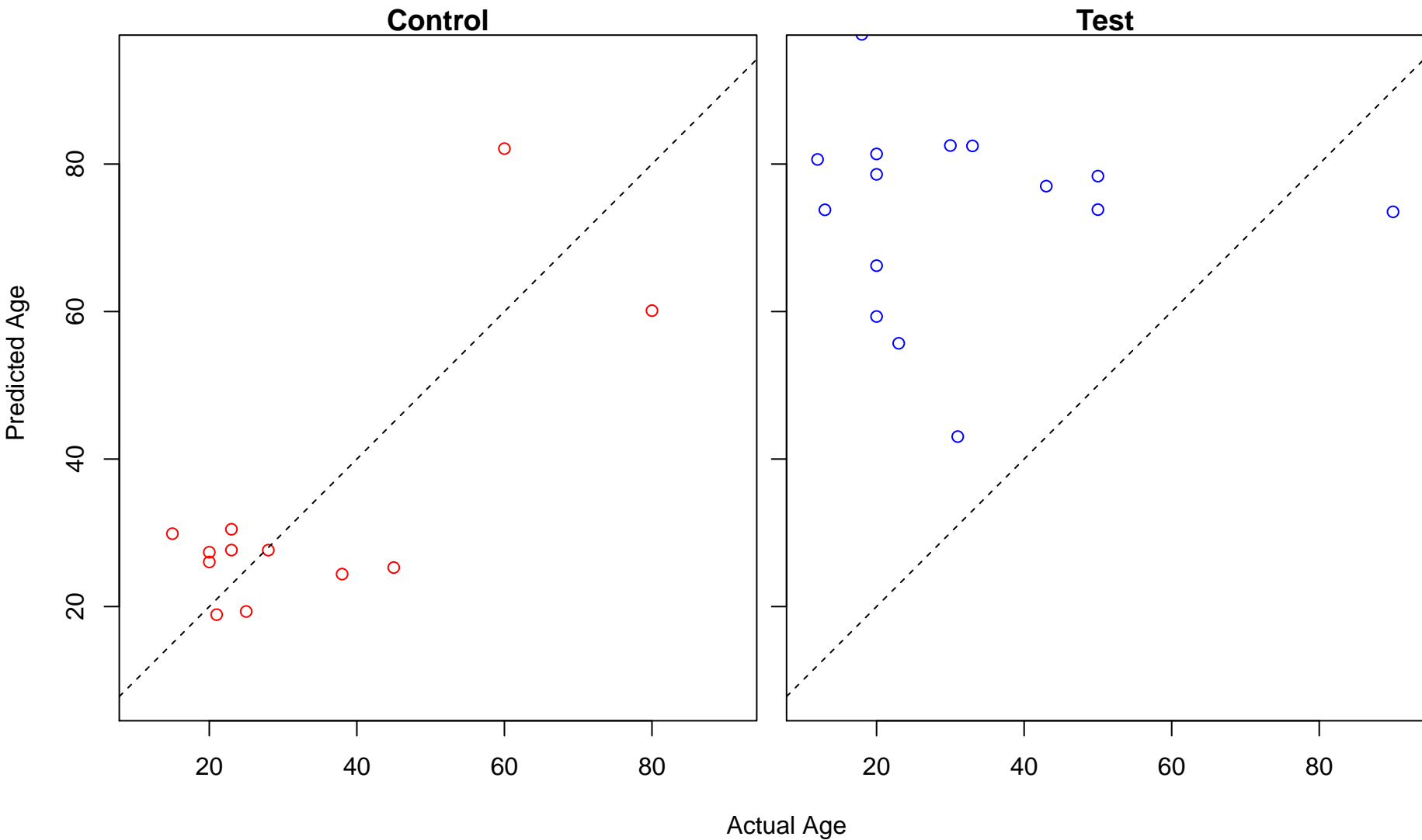
release of sequestered calcium ion into cytosol (Score: 5.114197)



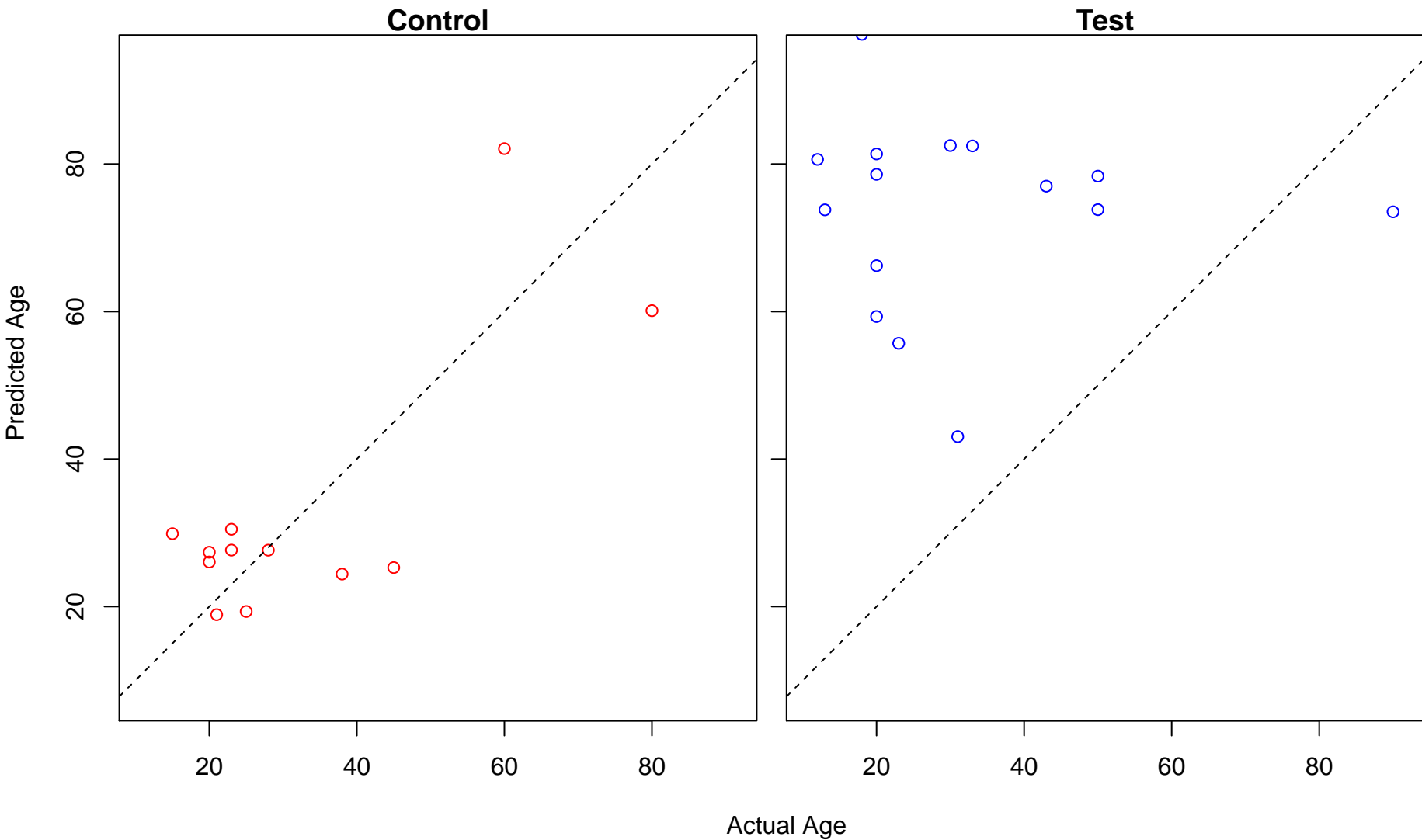
negative regulation of sequestering of calcium ion (Score: 5.114197)



calcium ion transmembrane import into cytosol (Score: 5.114197)

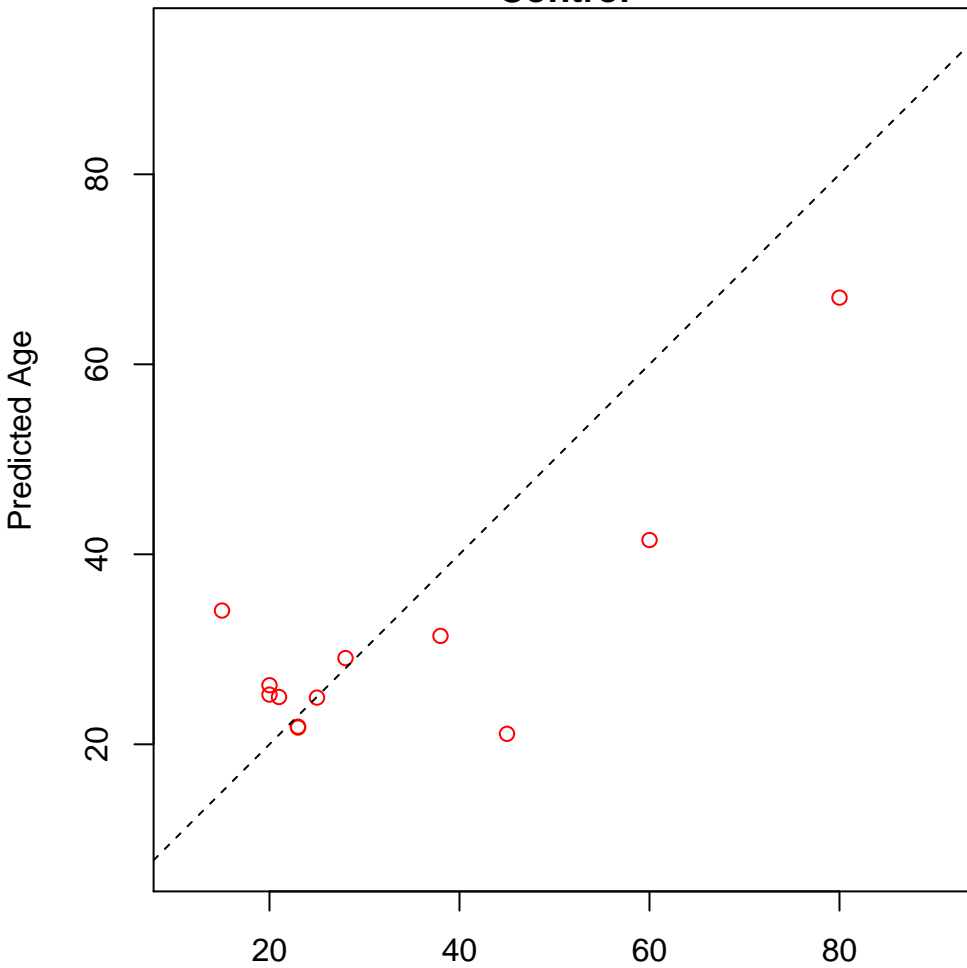


calcium ion import into cytosol (Score: 5.114197)

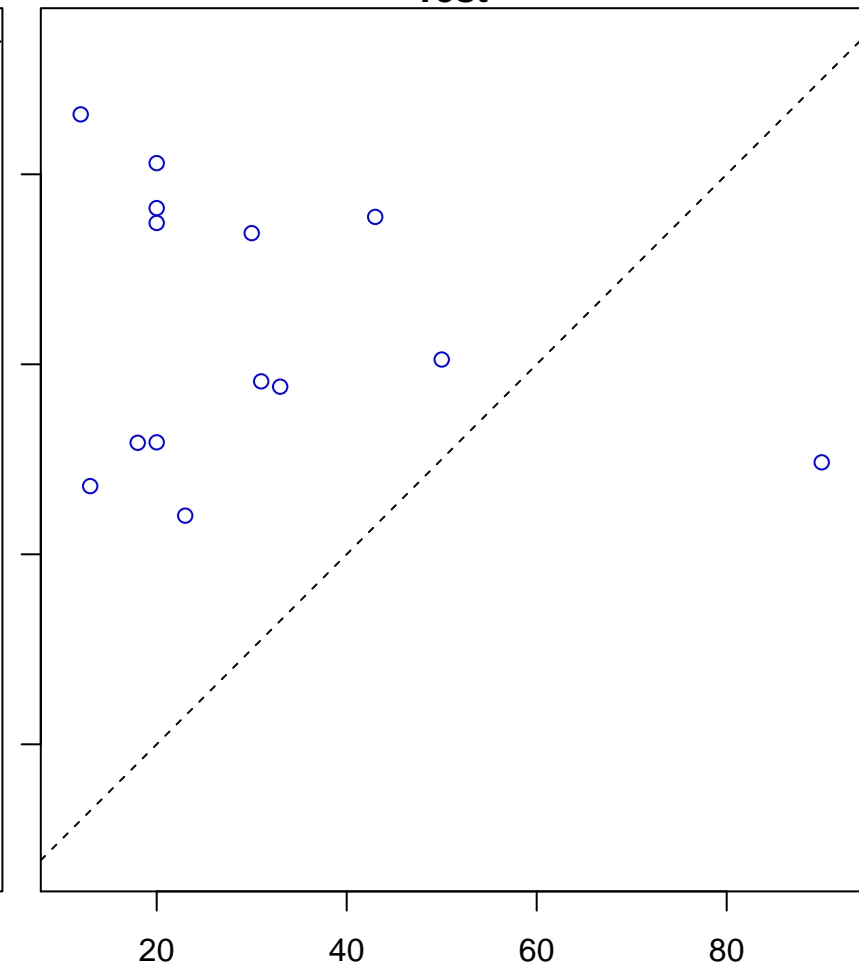


glucose 6-phosphate metabolic process (Score: 5.113201)

Control

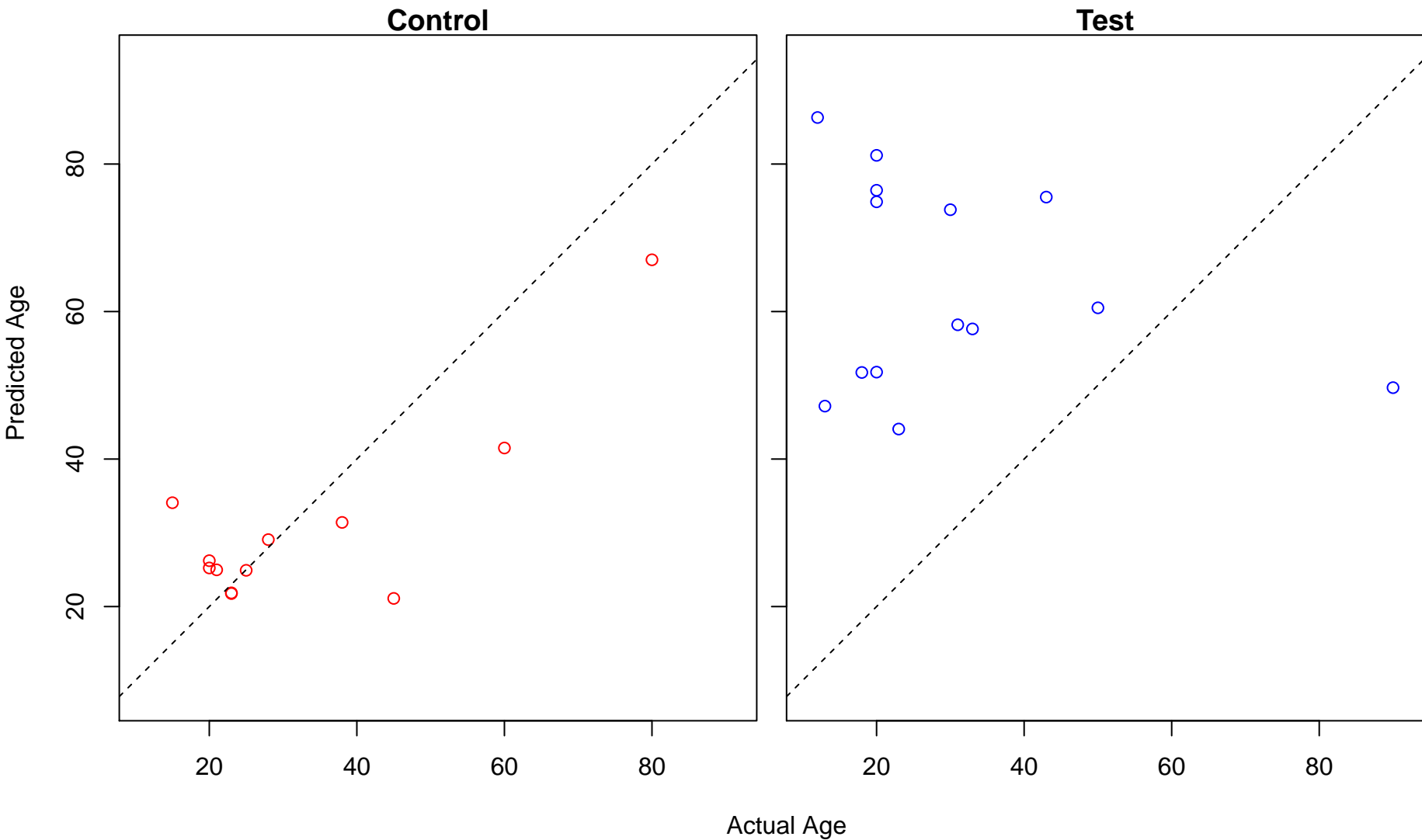


Test



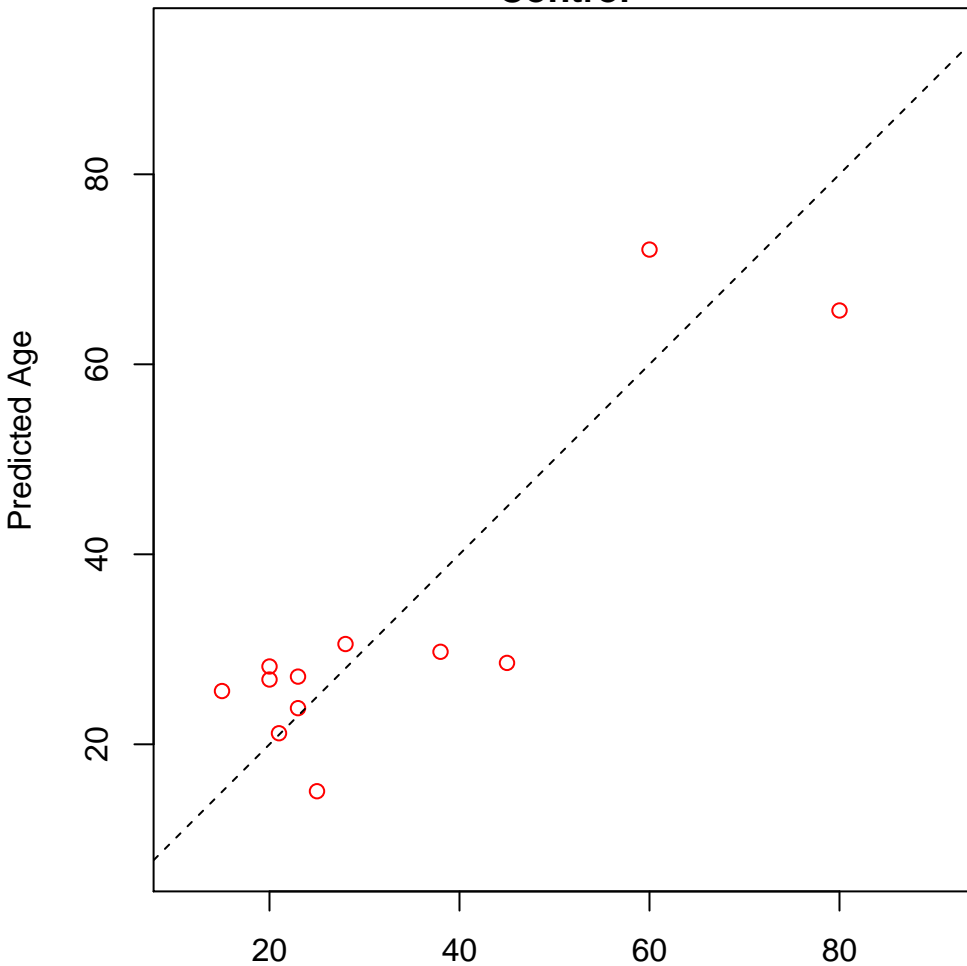
Actual Age

pentose-phosphate shunt (Score: 5.113157)

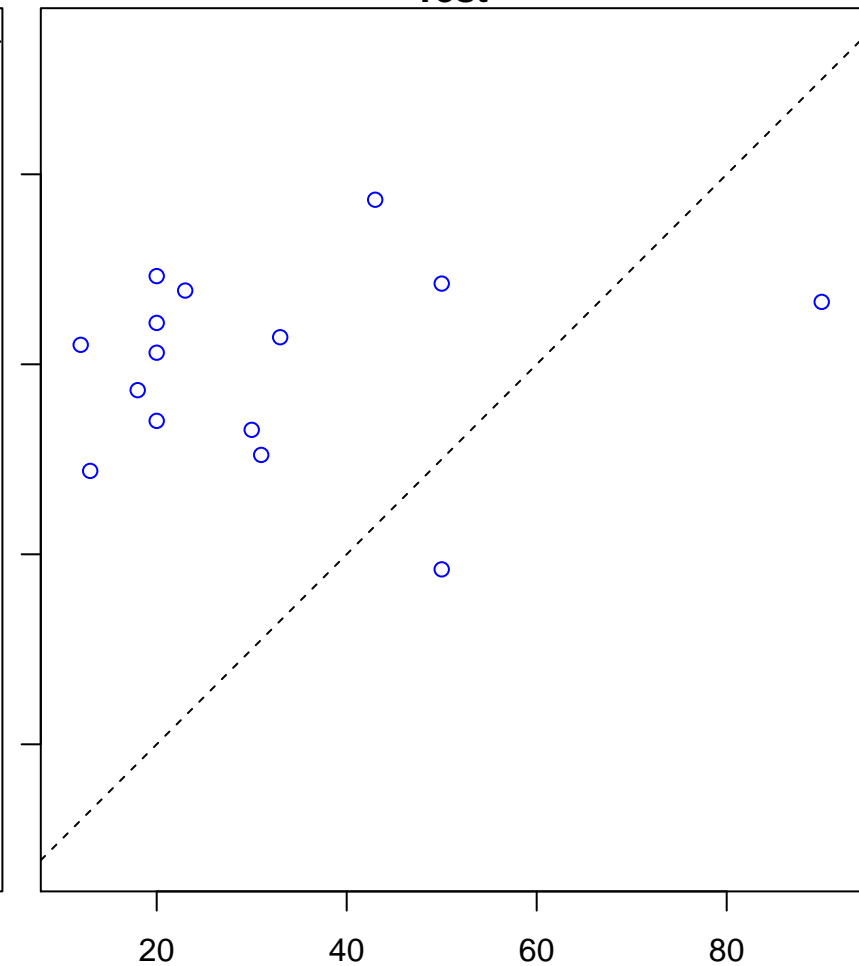


metanephric distal tubule development (Score: 5.111781)

Control

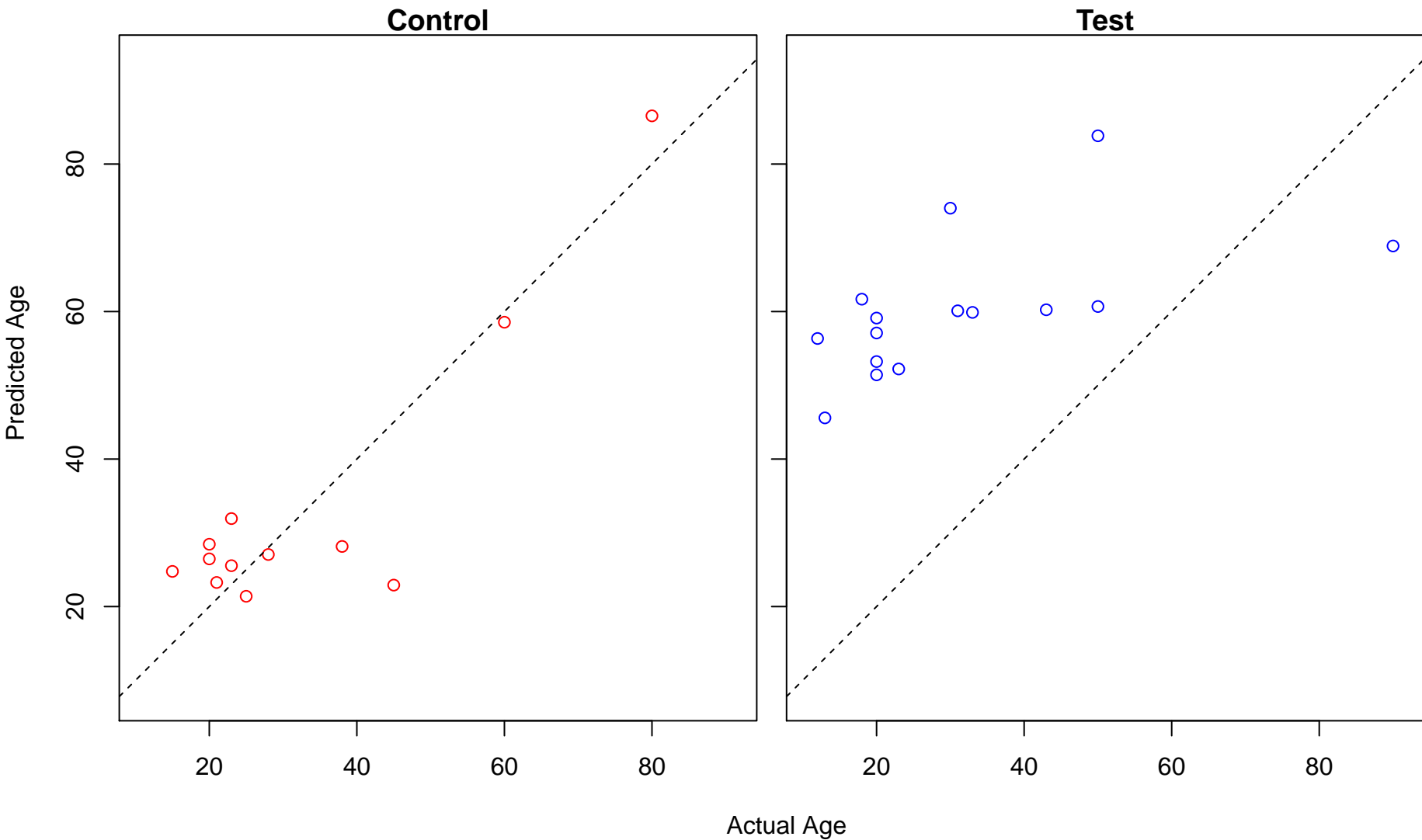


Test

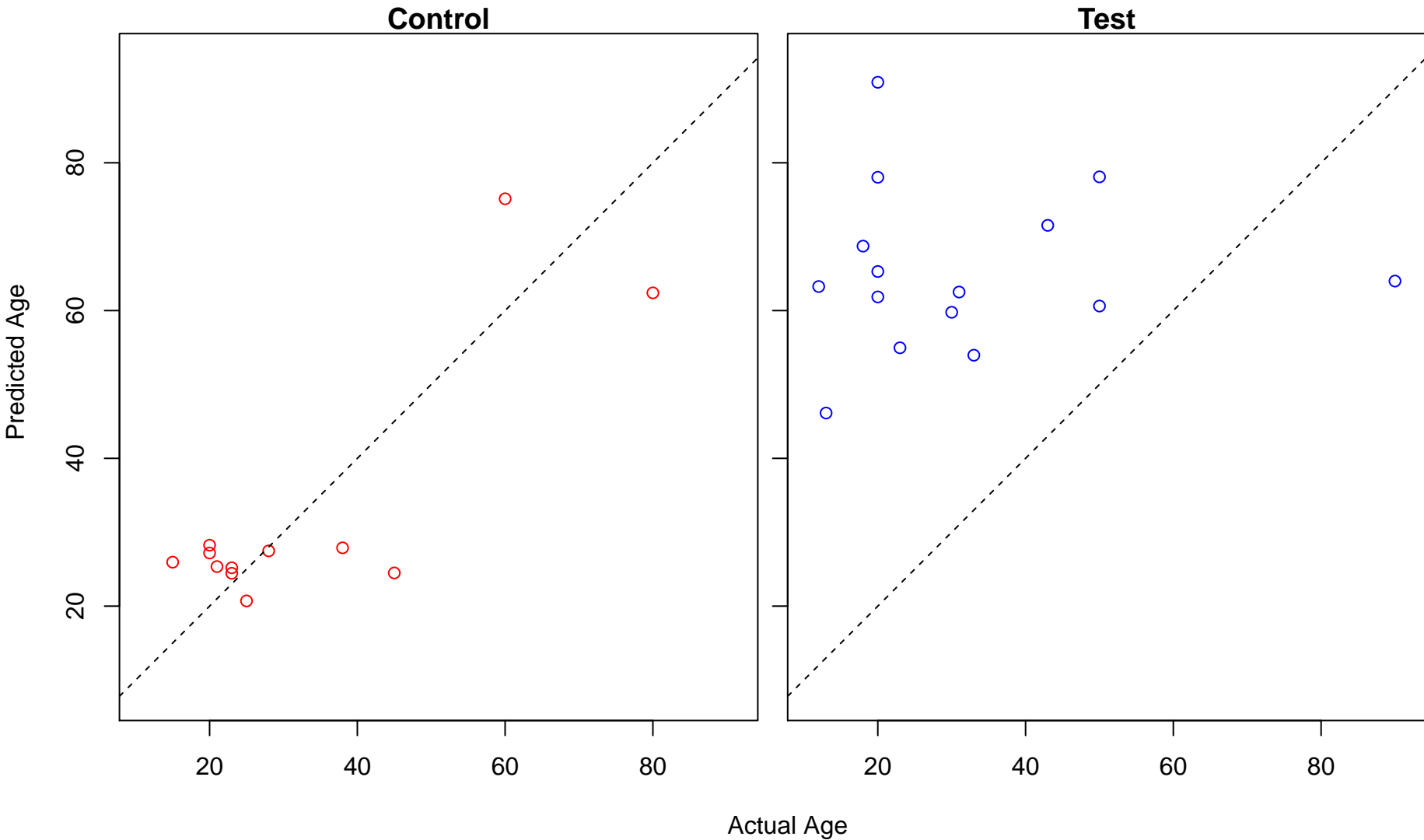


Actual Age

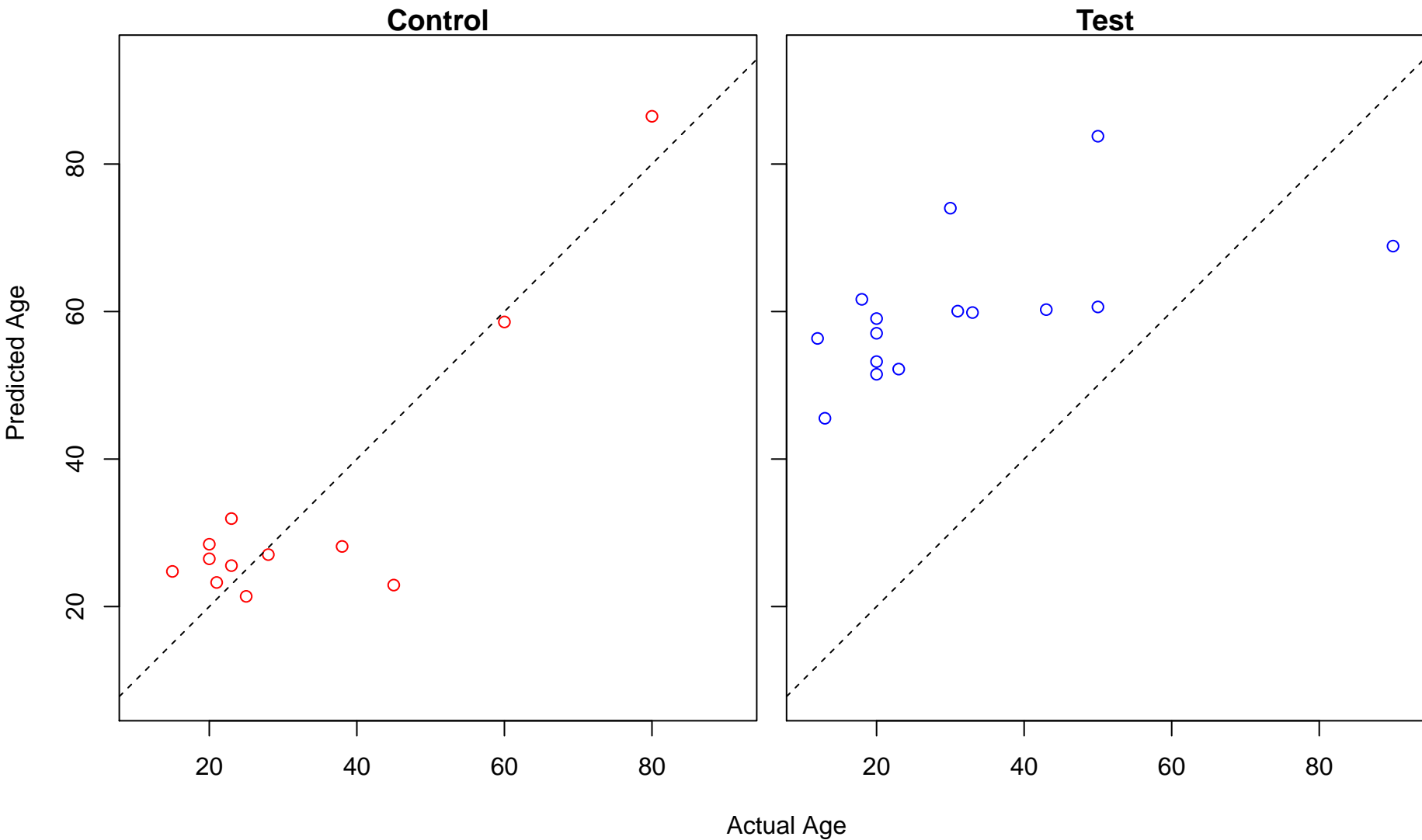
mesoderm formation (Score: 5.109148)



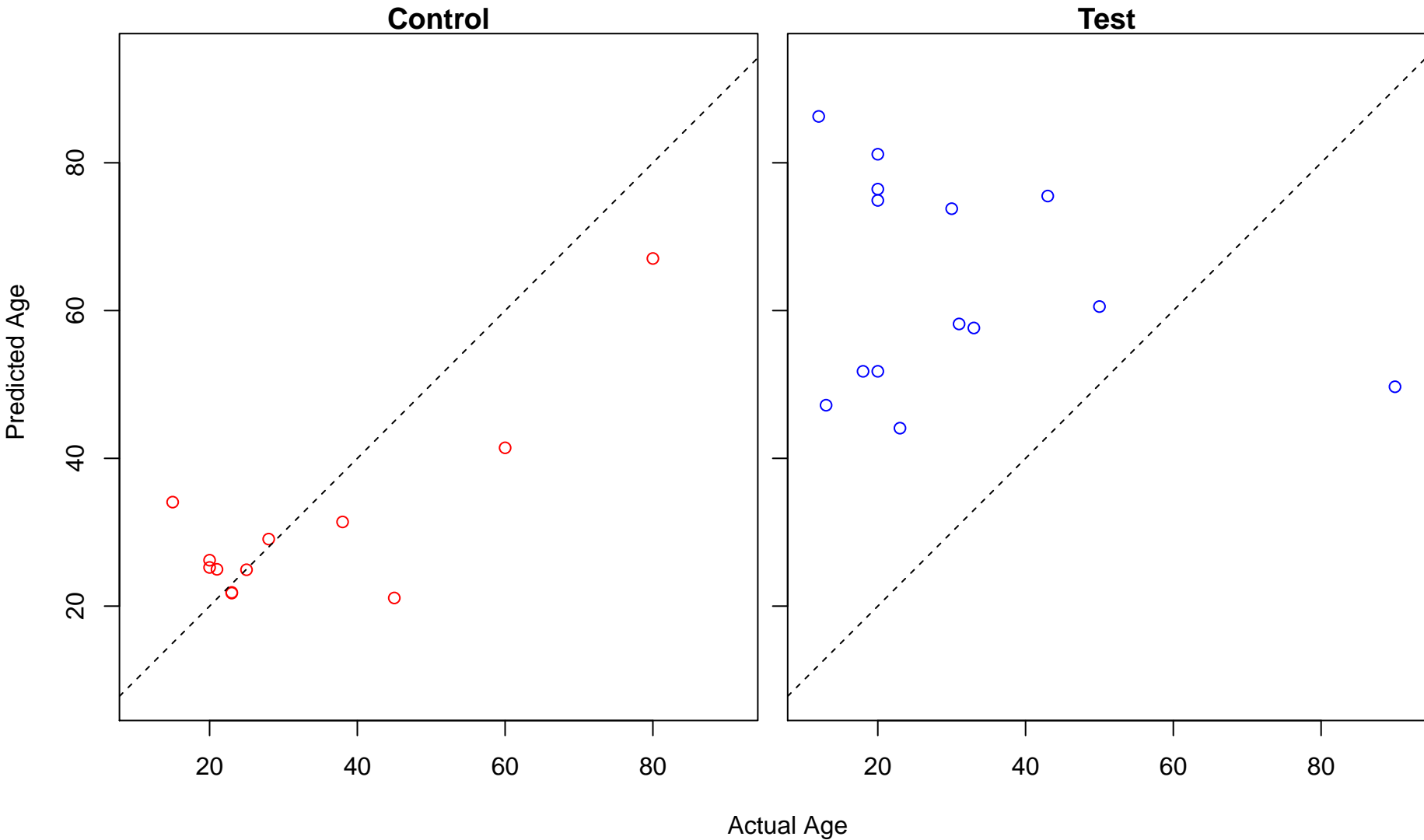
cellular response to steroid hormone stimulus (Score: 5.108606)



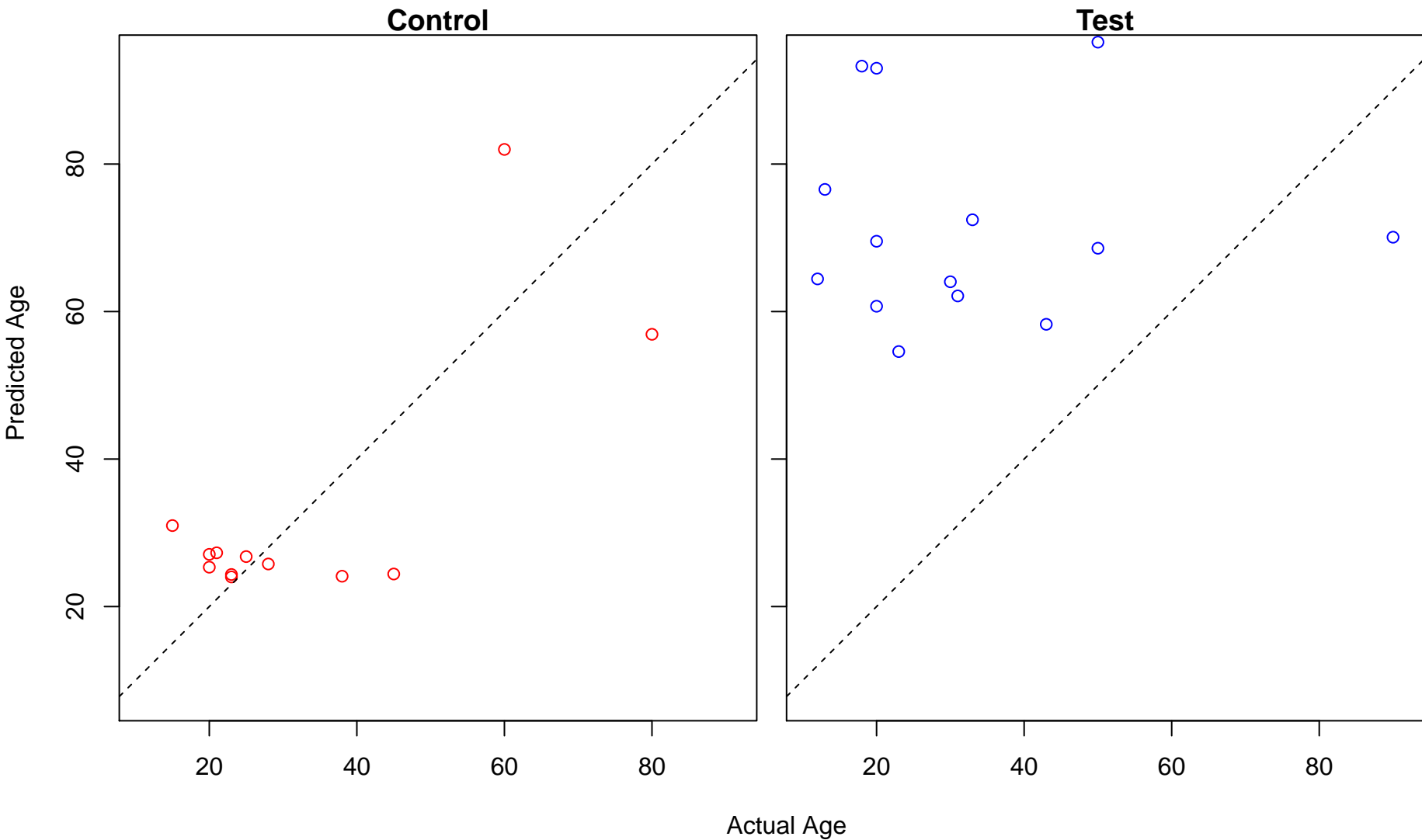
mesoderm morphogenesis (Score: 5.108402)



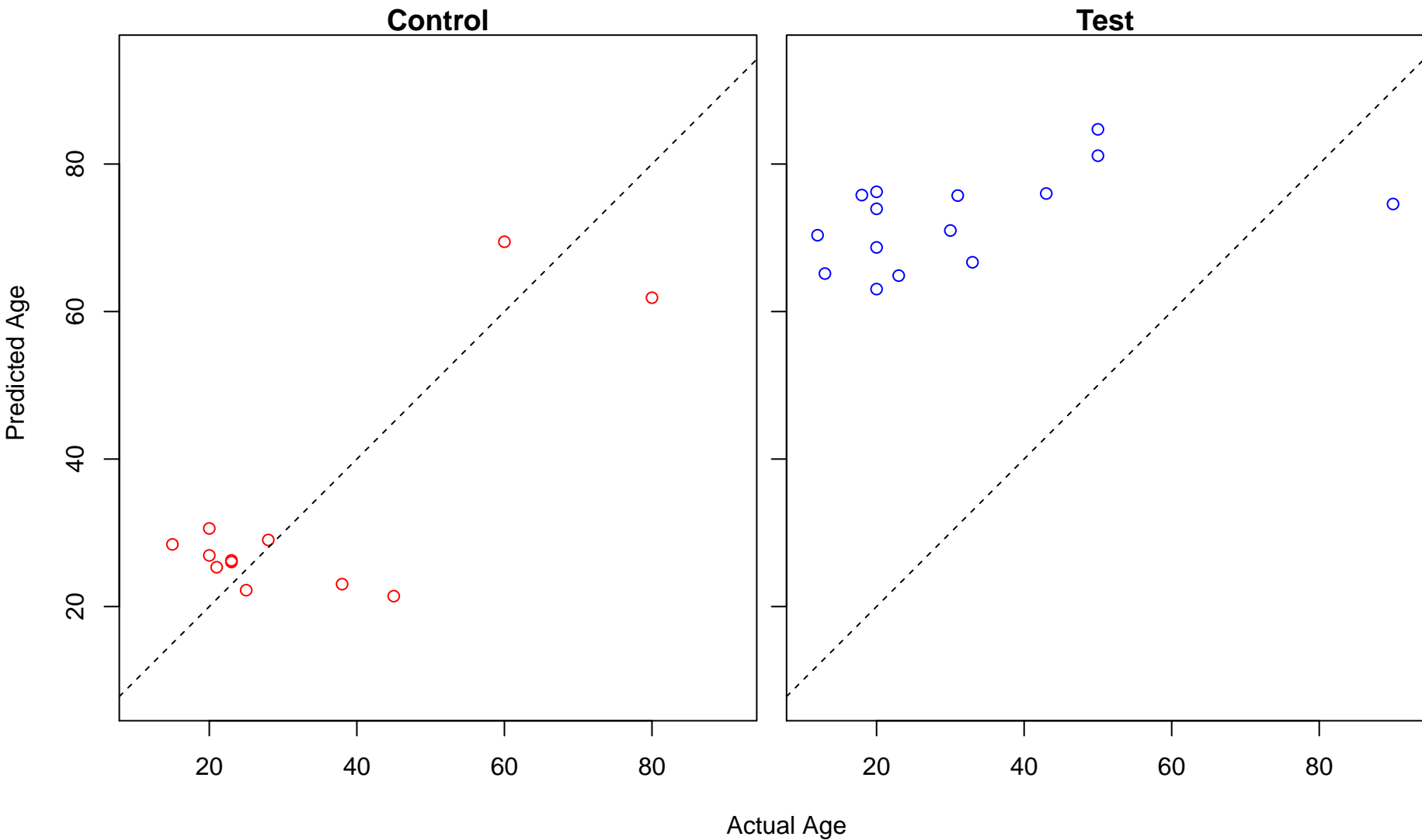
glyceraldehyde-3-phosphate metabolic process (Score: 5.106146)



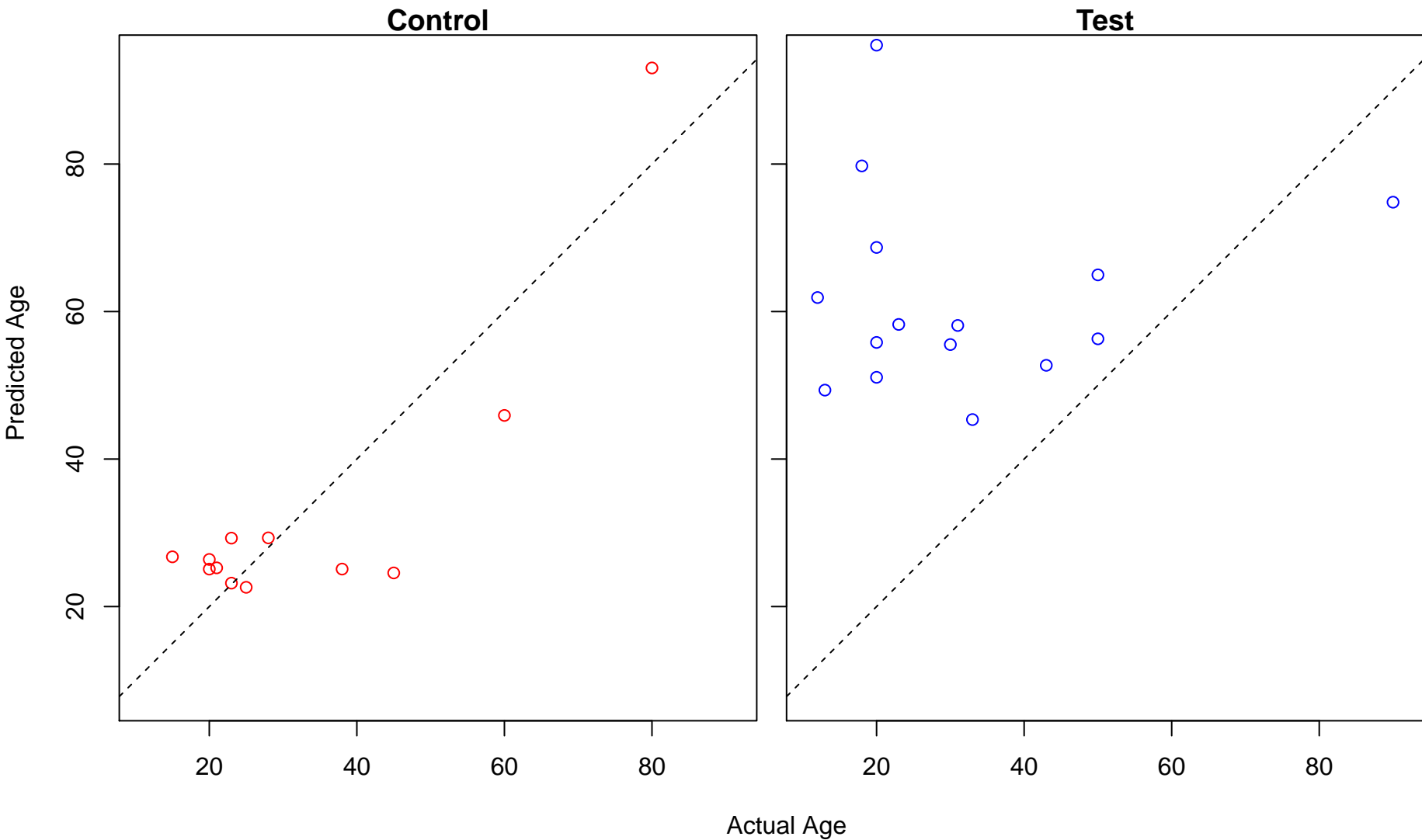
regulation of hydrogen peroxide metabolic process (Score: 5.105660)



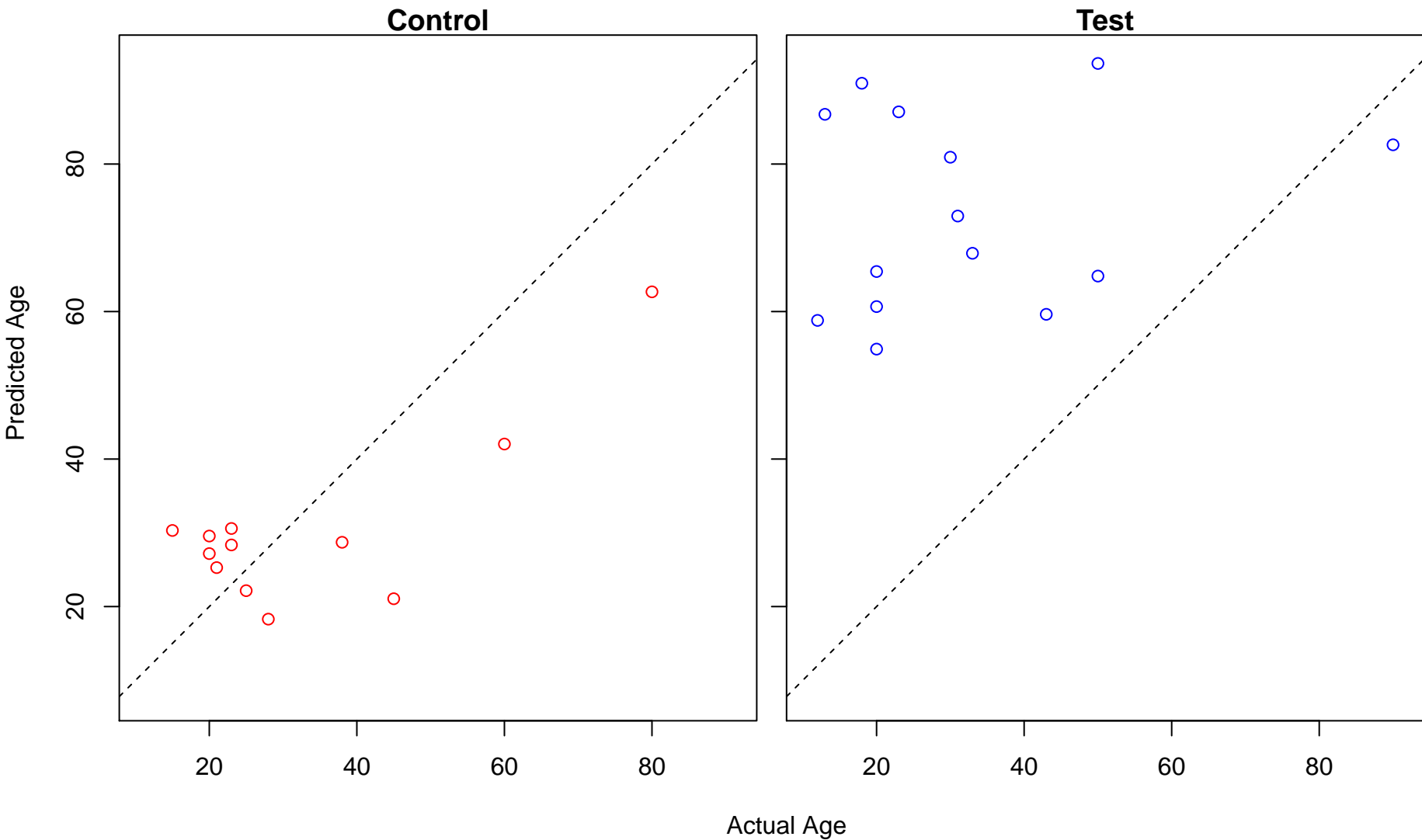
calcium-mediated signaling (Score: 5.105467)



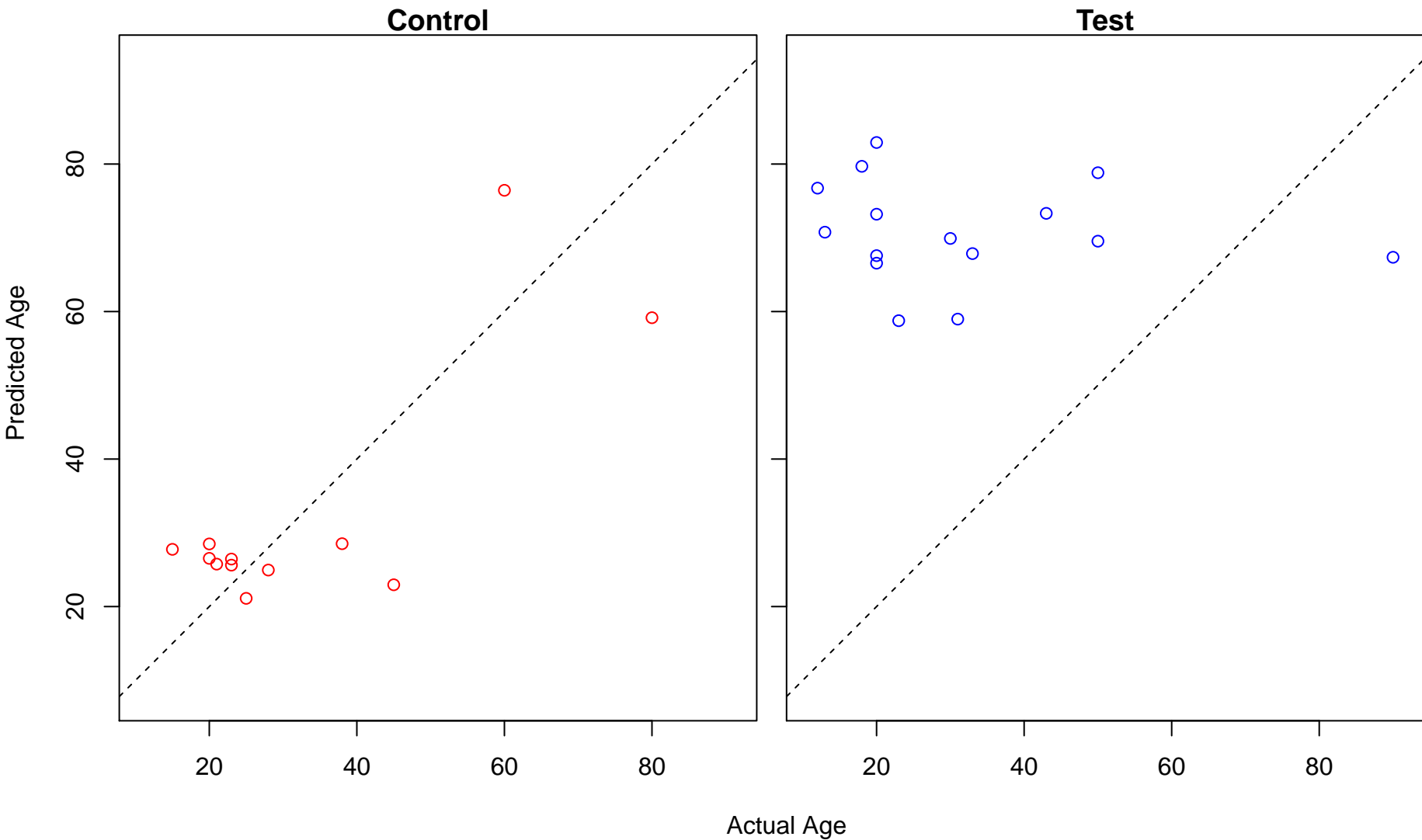
circadian rhythm (Score: 5.104190)



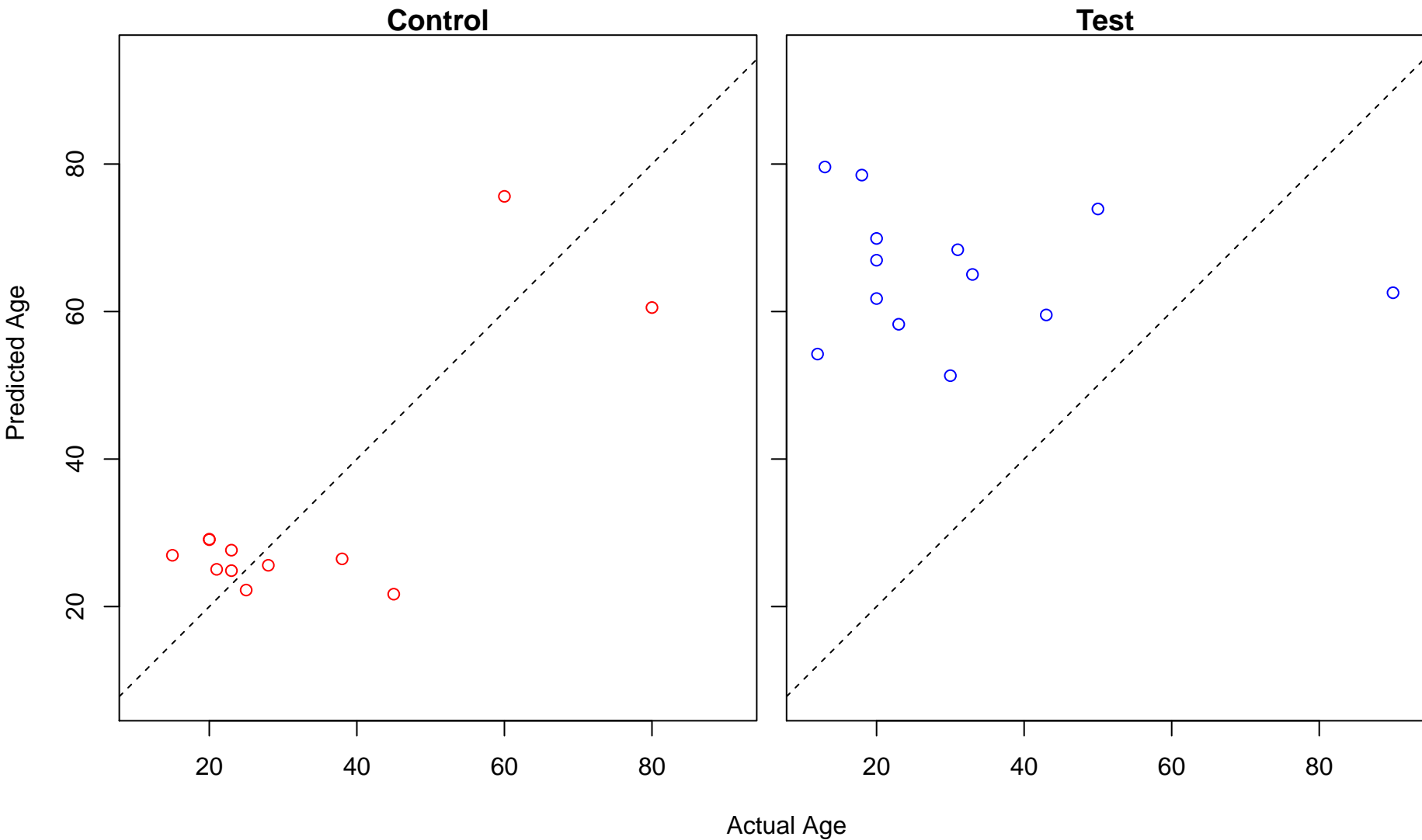
cell differentiation in spinal cord (Score: 5.103424)



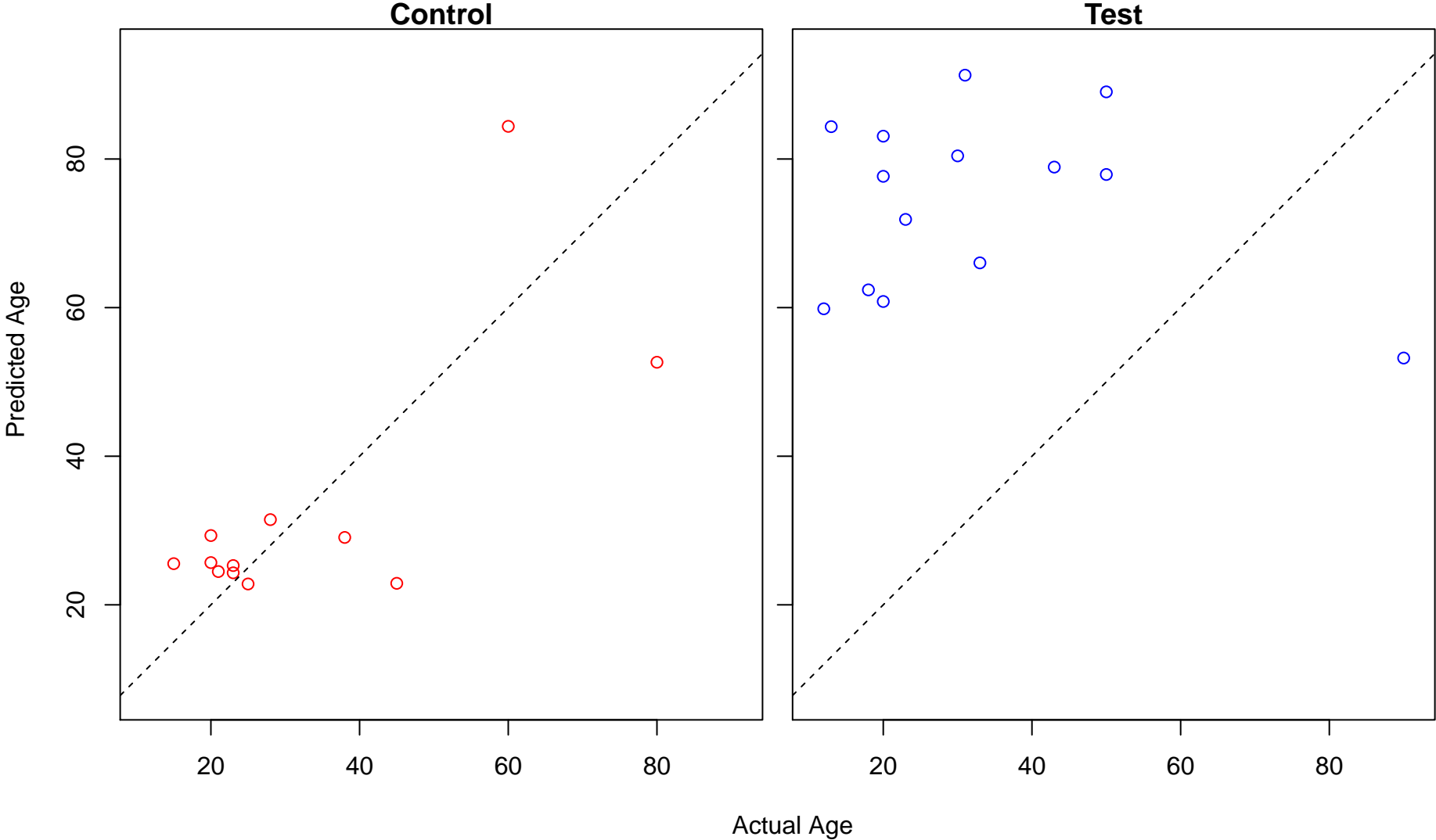
dicarboxylic acid metabolic process (Score: 5.103280)



protein heterotetramerization (Score: 5.102995)

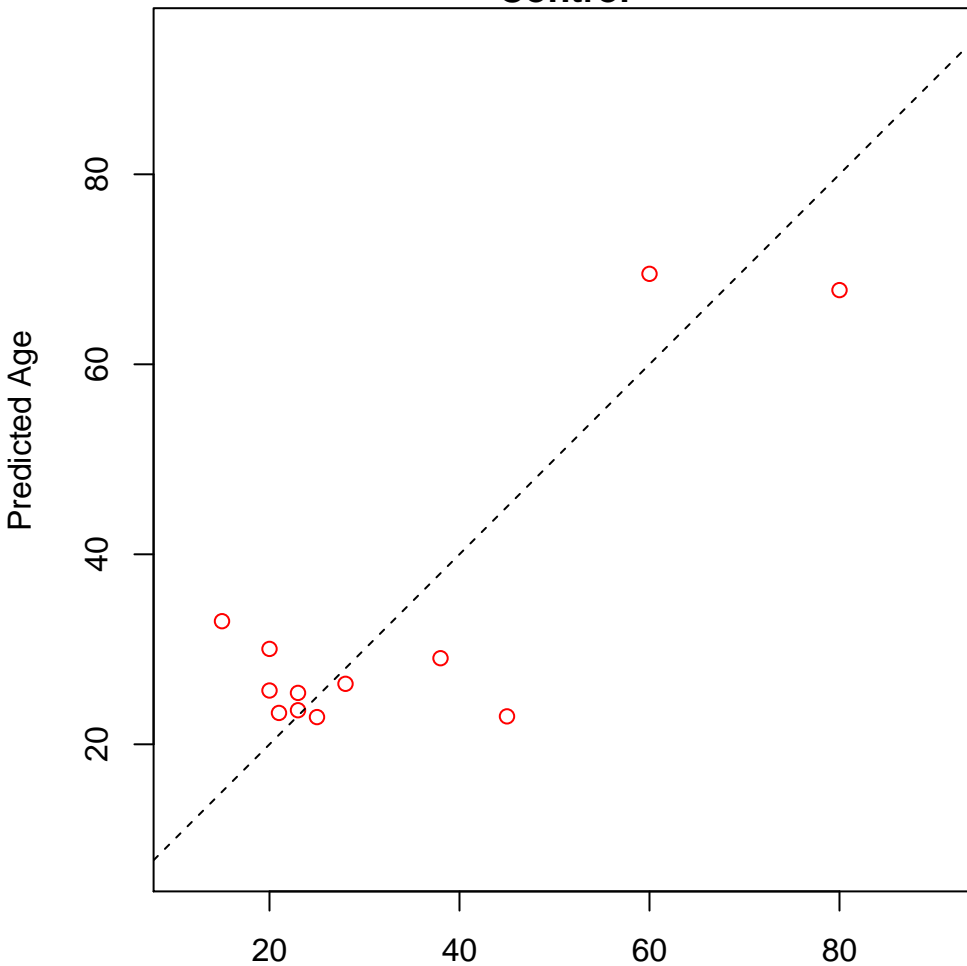


positive regulation of cytokine-mediated signaling pathway (Score: 5.102443)

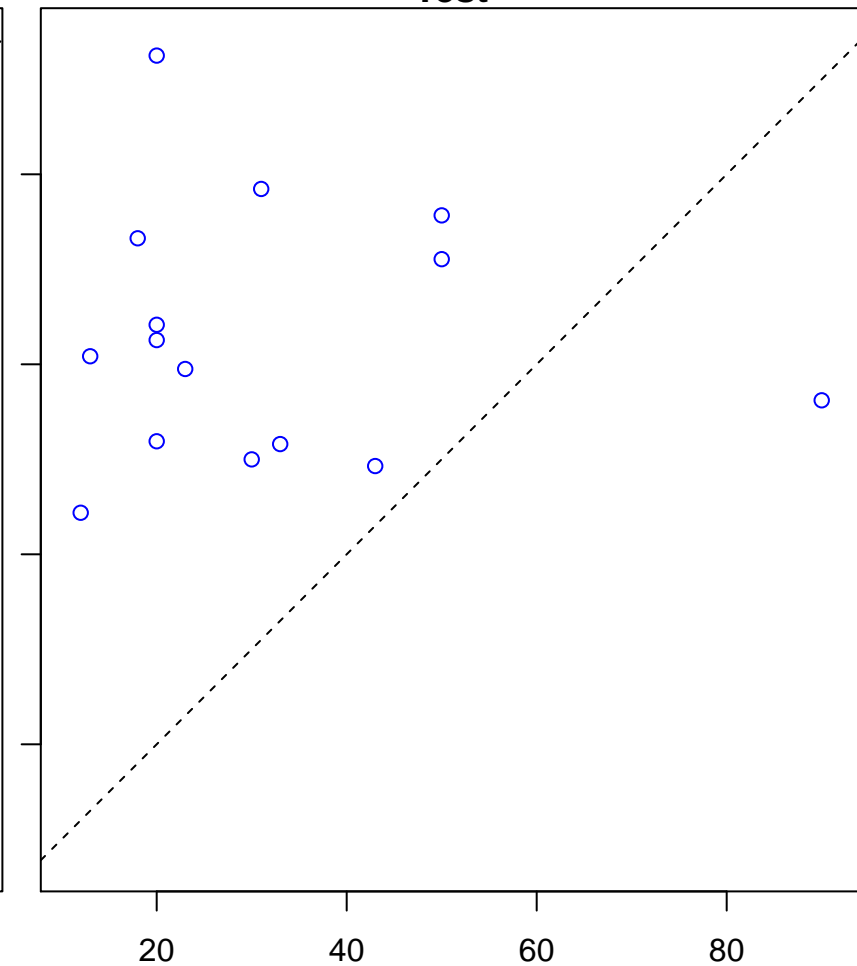


multicellular organismal homeostasis (Score: 5.100029)

Control

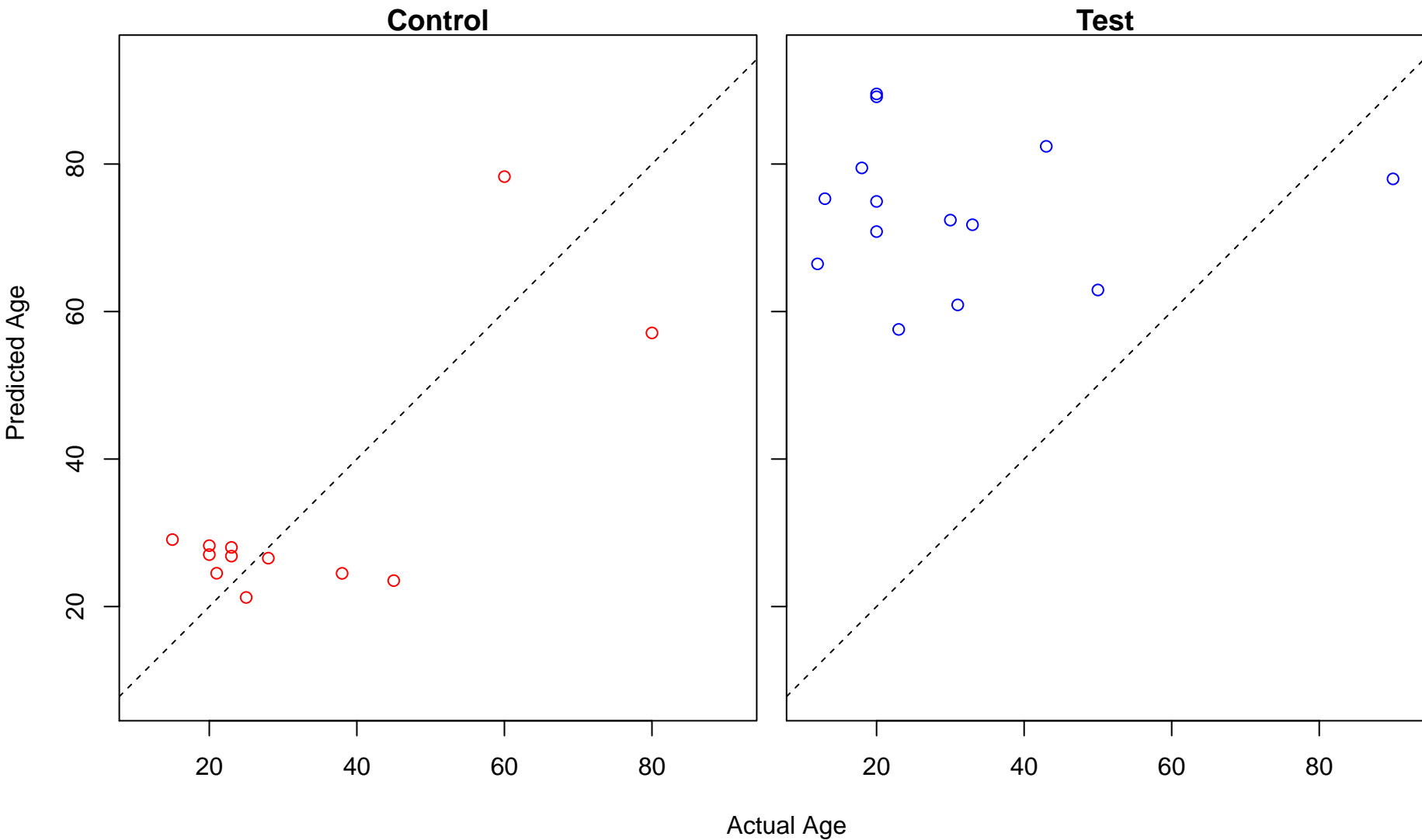


Test

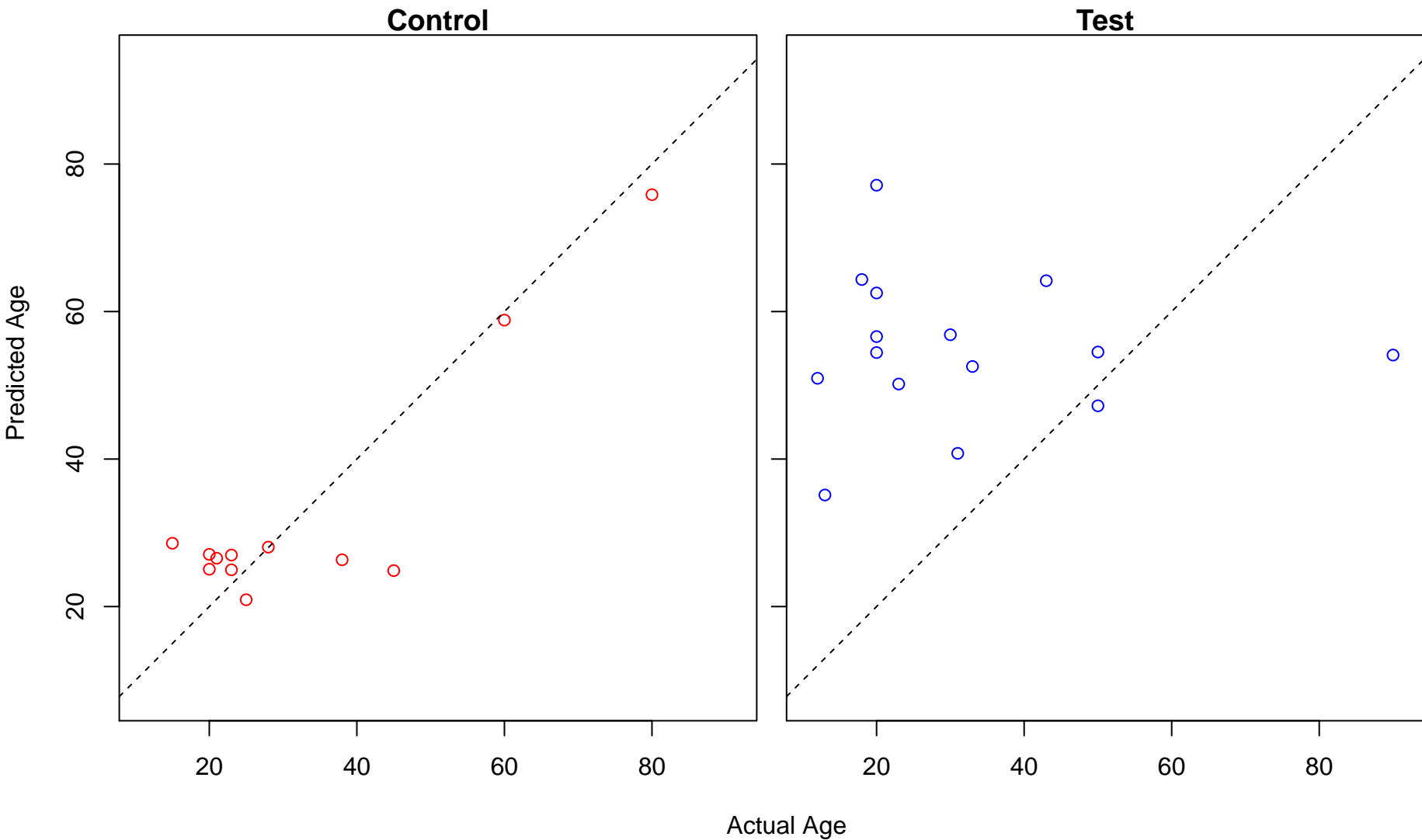


Actual Age

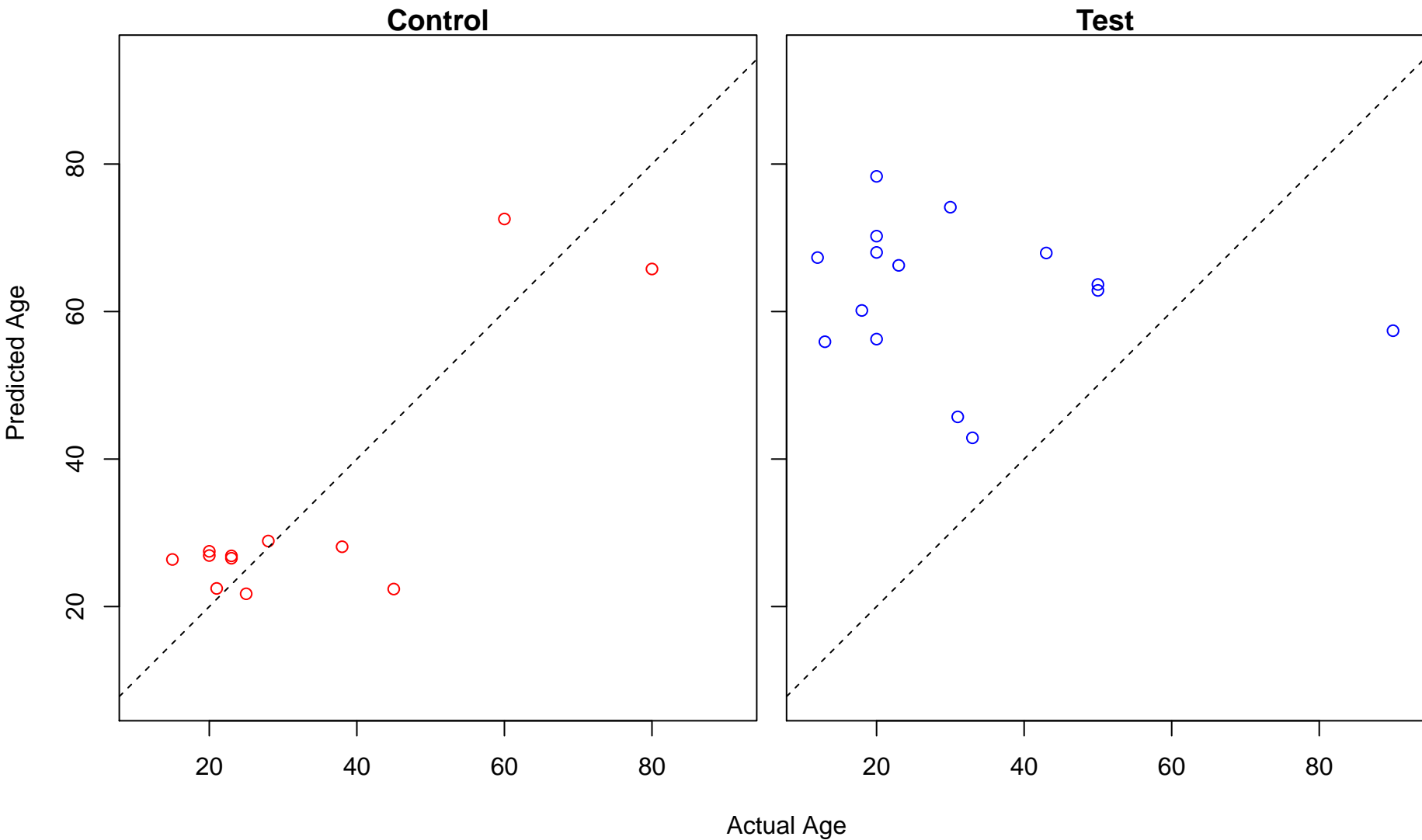
bicellular tight junction assembly (Score: 5.097460)



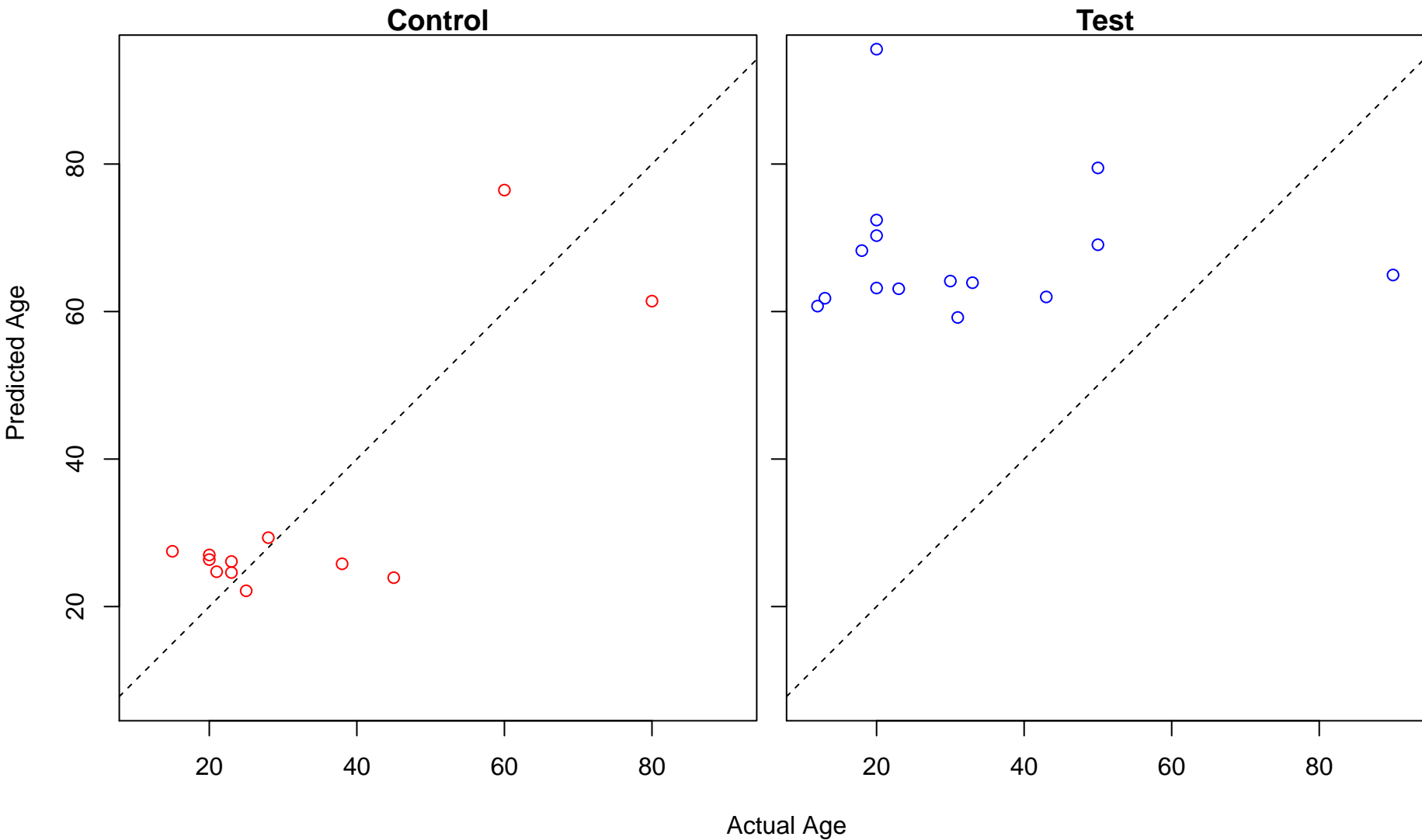
establishment of localization by movement along microtubule (Score: 5.096140)



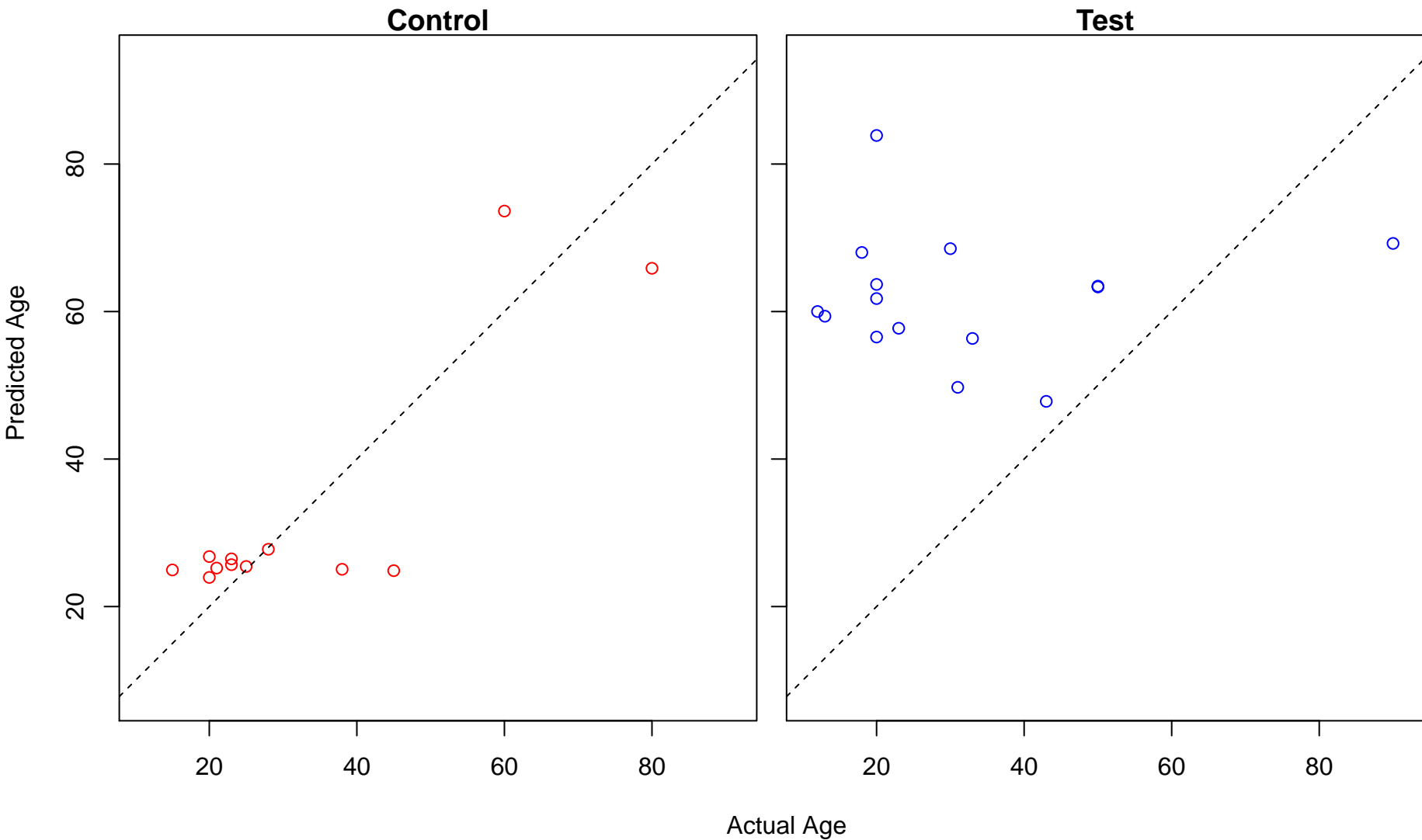
lipoxin metabolic process (Score: 5.091384)



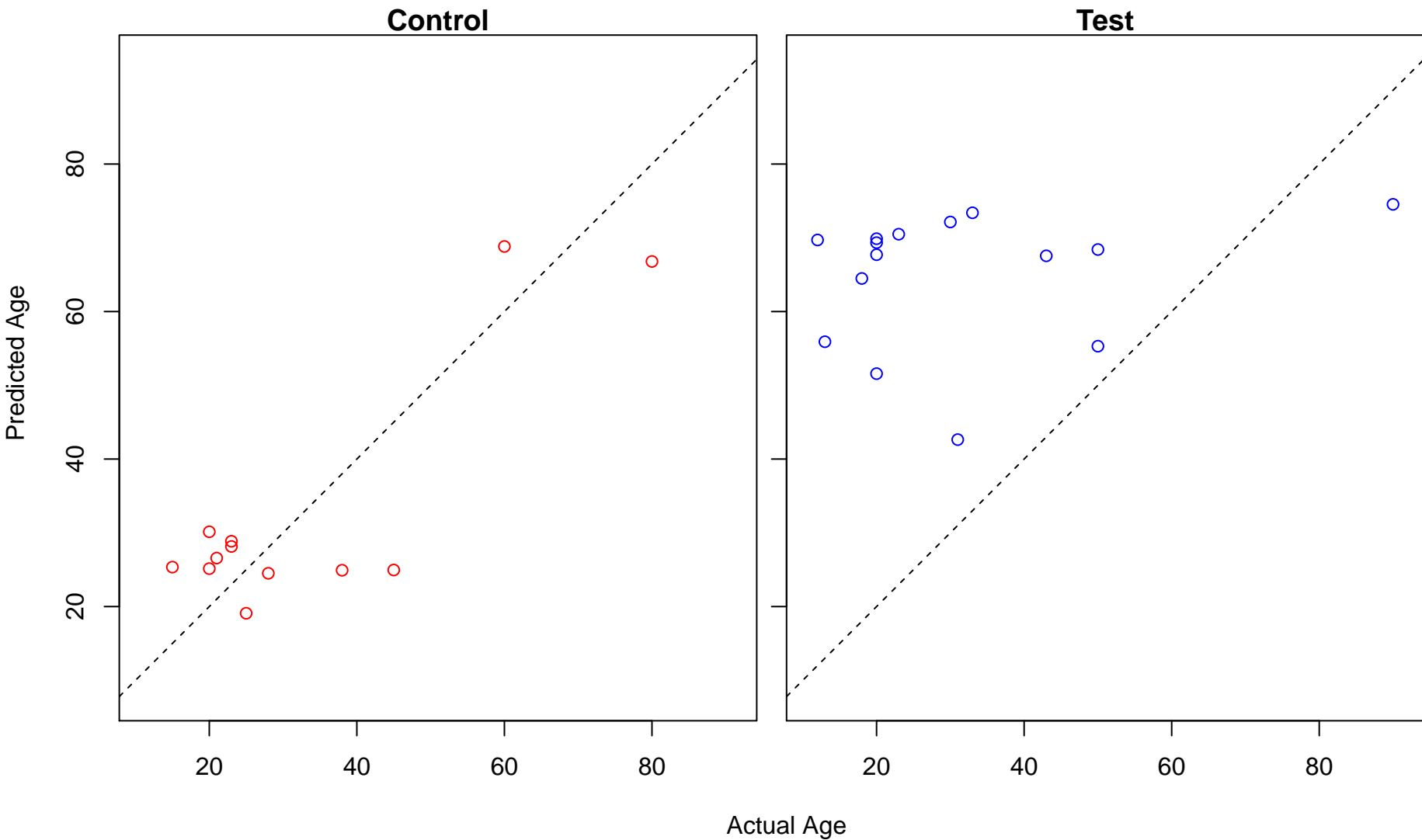
gamete generation (Score: 5.089517)



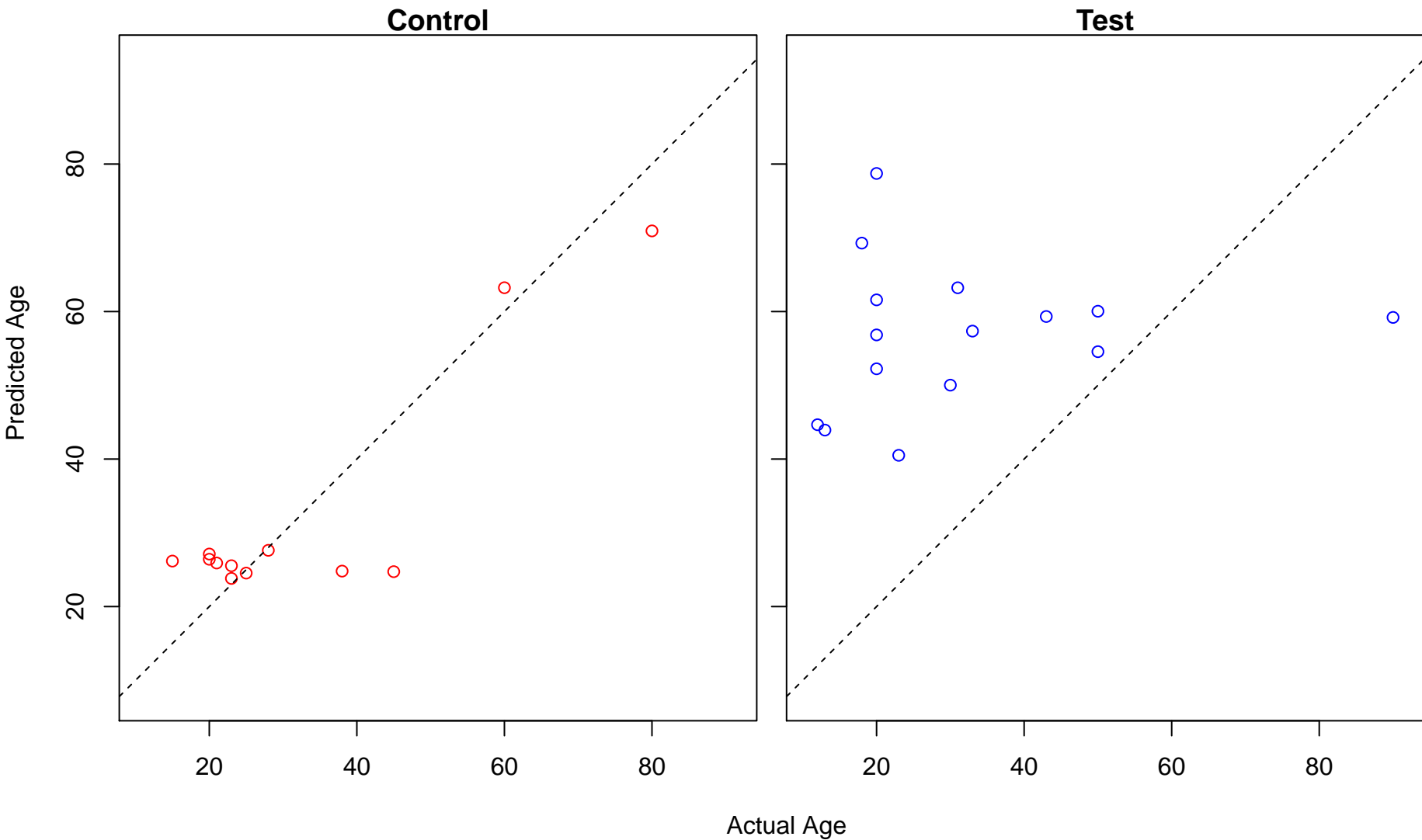
regulation of receptor recycling (Score: 5.086240)



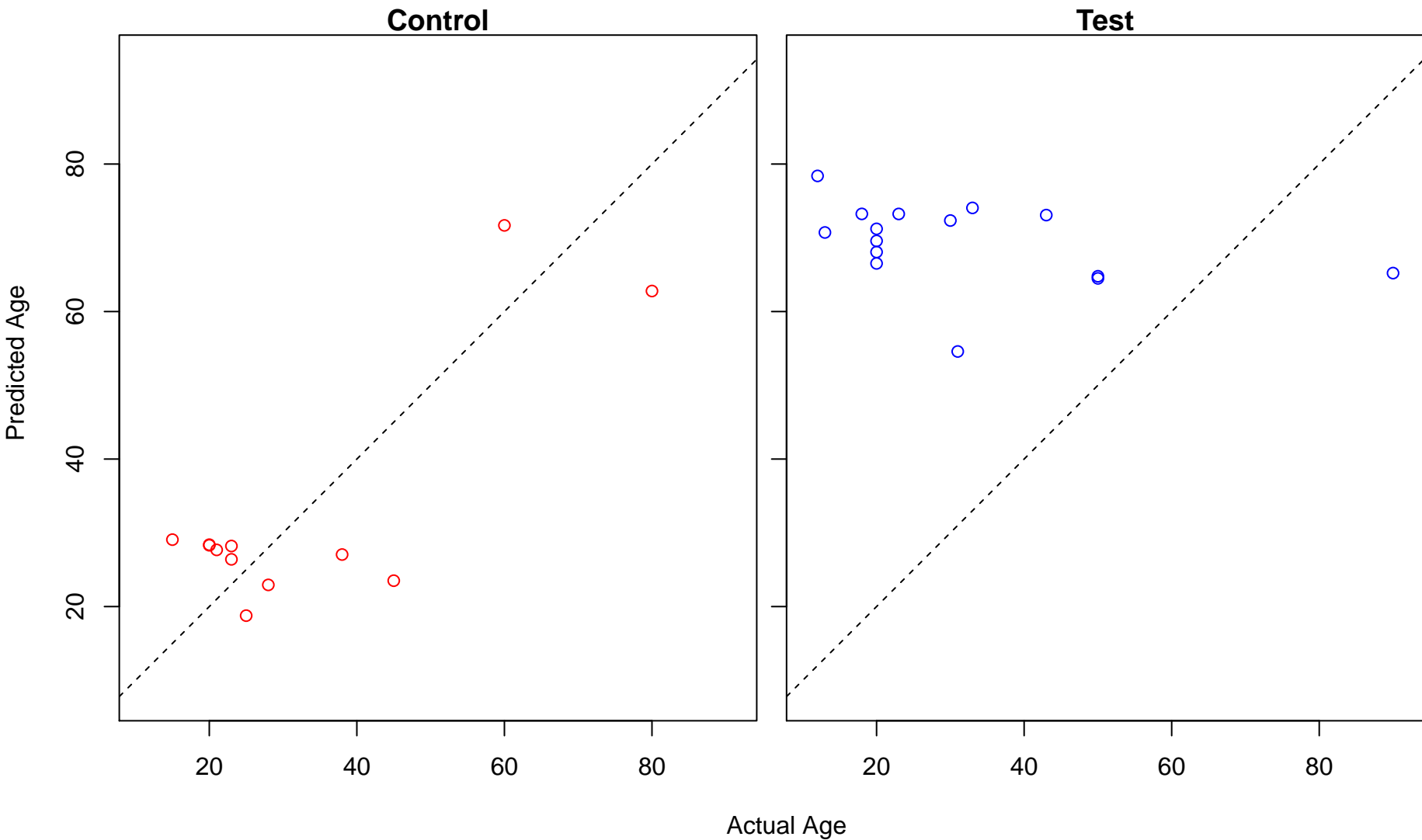
AV node cell to bundle of His cell communication (Score: 5.084198)



regulation of filopodium assembly (Score: 5.082293)

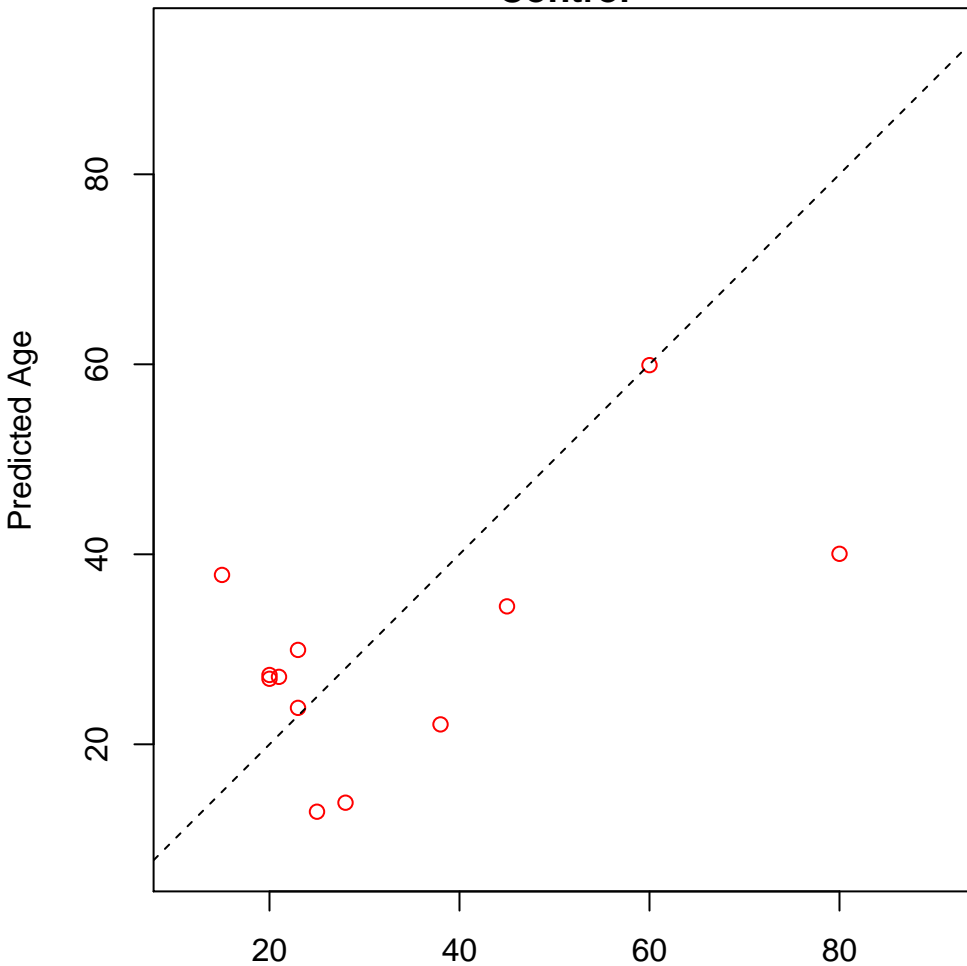


folic acid-containing compound metabolic process (Score: 5.080103)

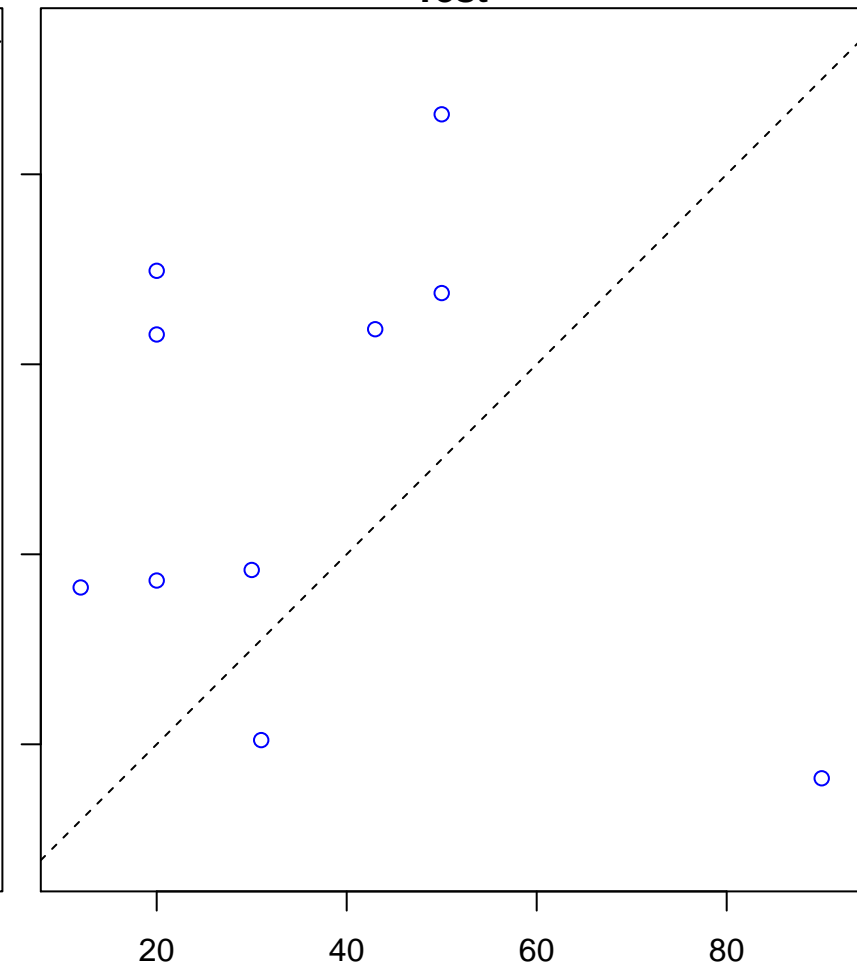


regulation of renal sodium excretion (Score: 5.079832)

Control

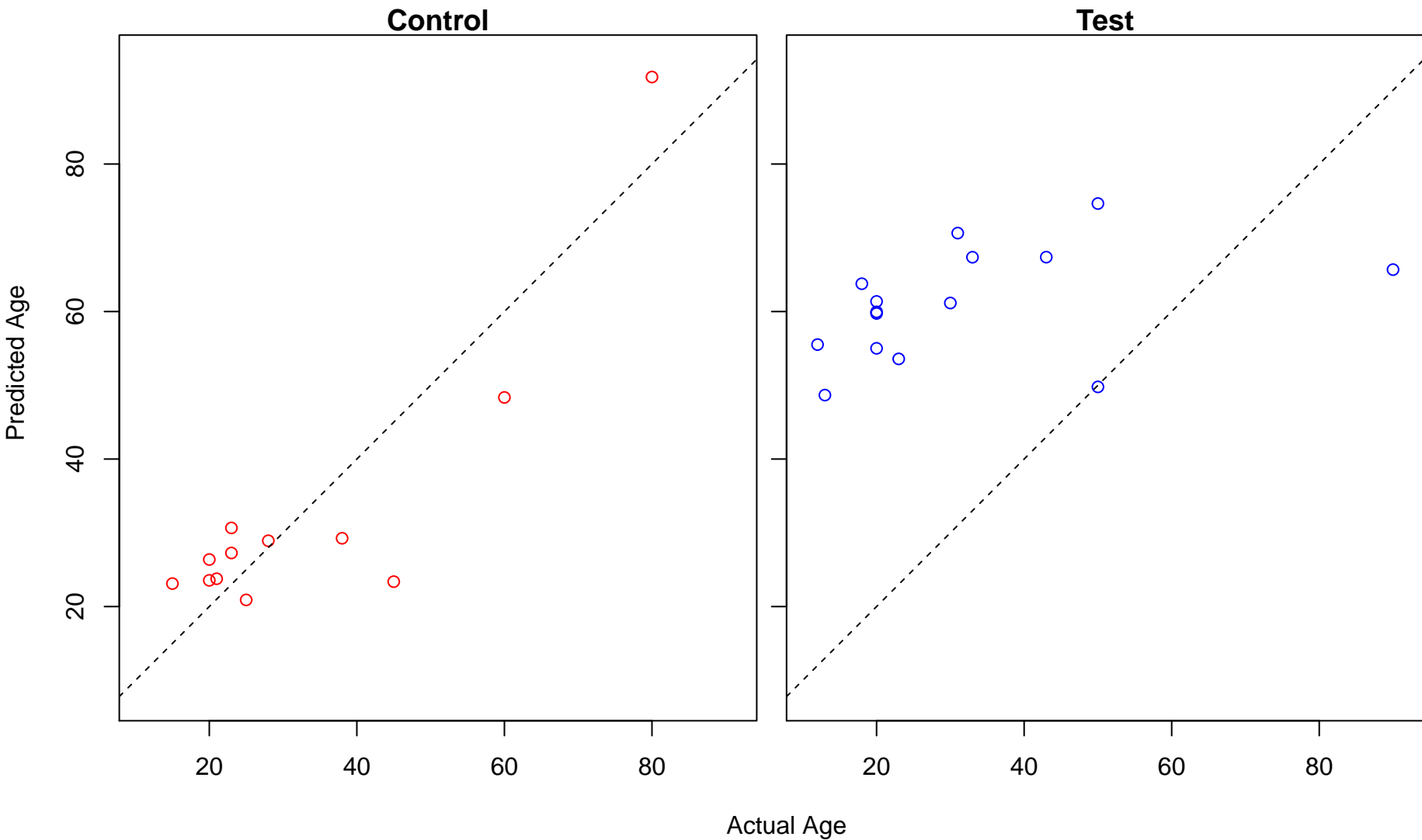


Test

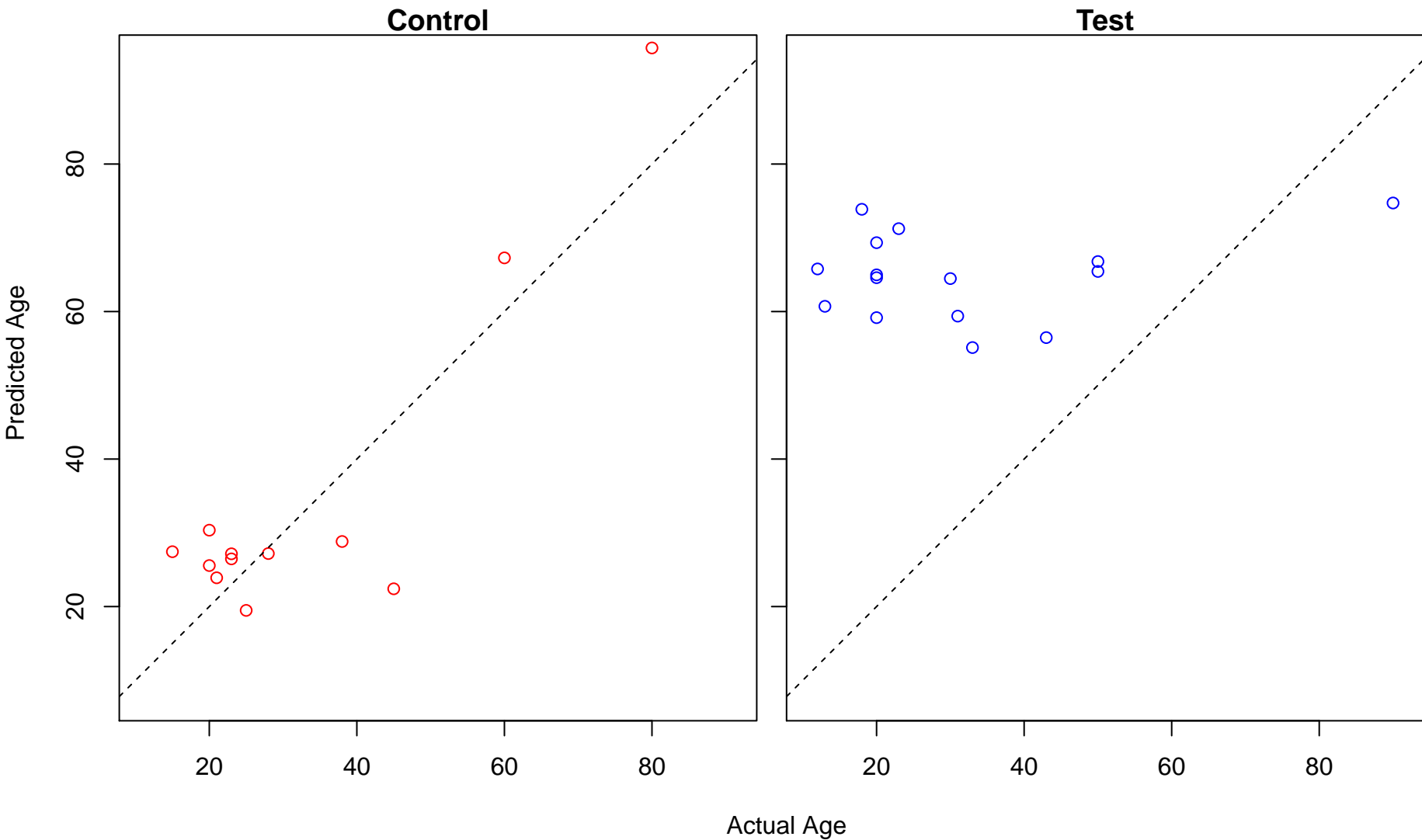


Actual Age

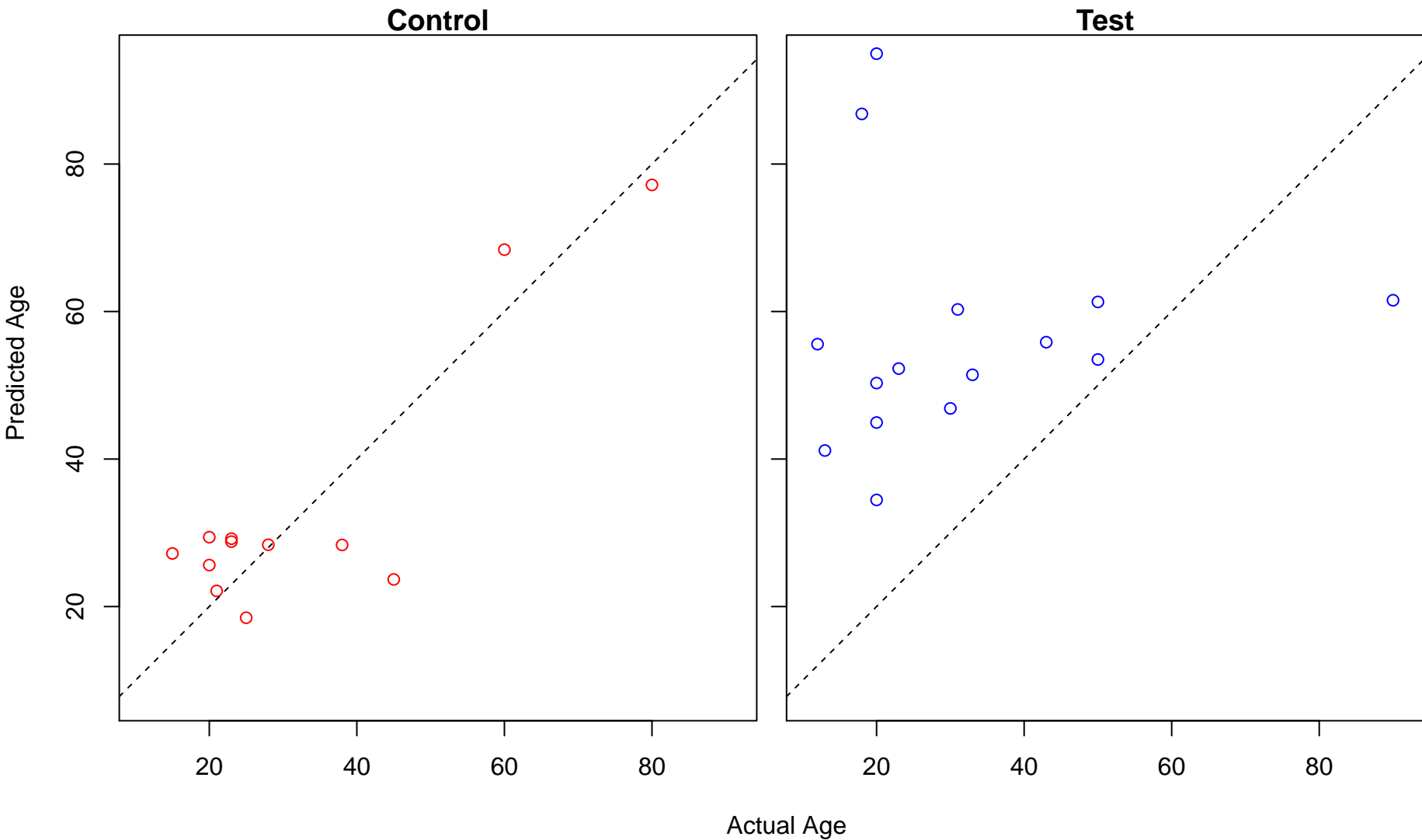
purine-containing compound salvage (Score: 5.078584)



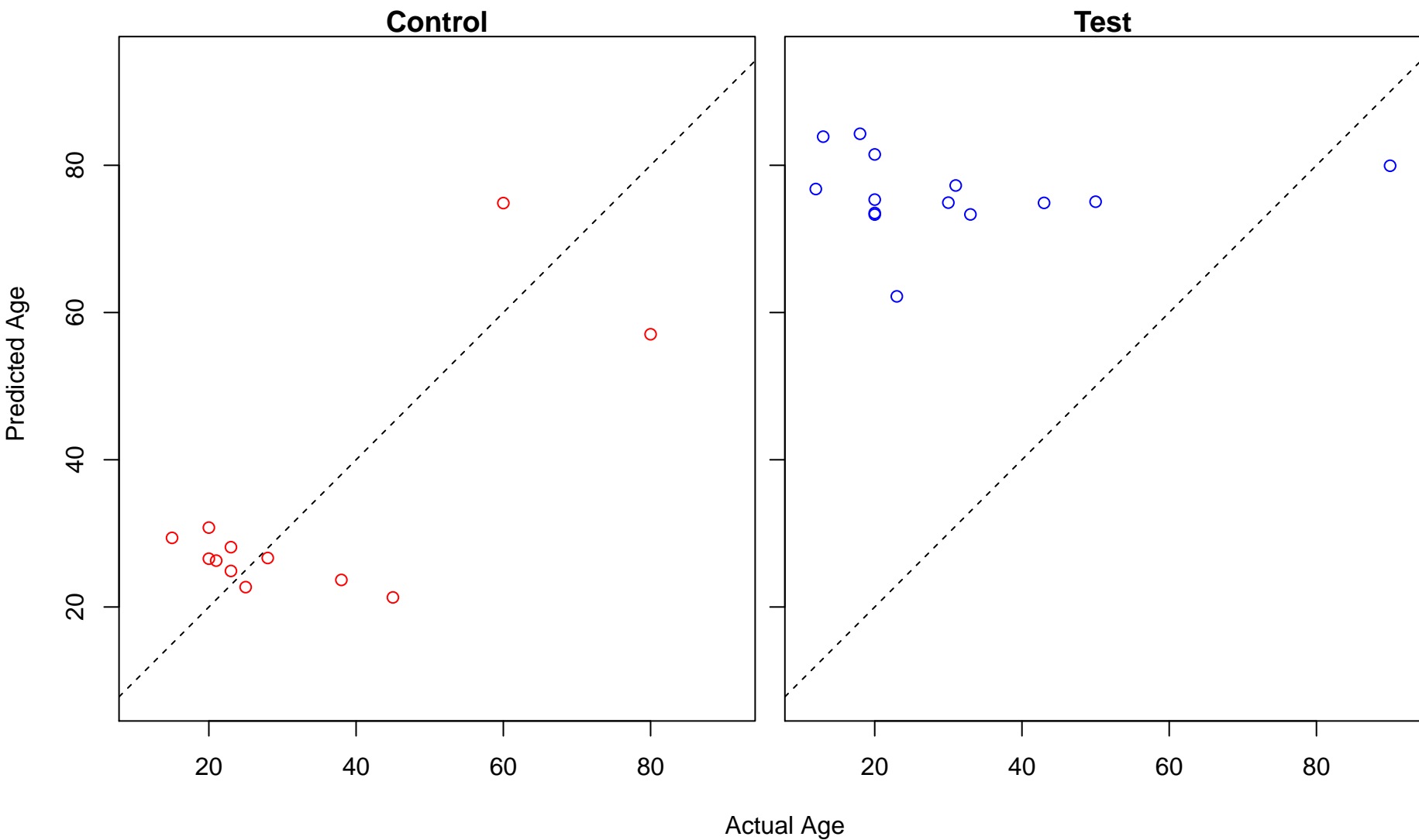
negative regulation of protein phosphorylation (Score: 5.076414)



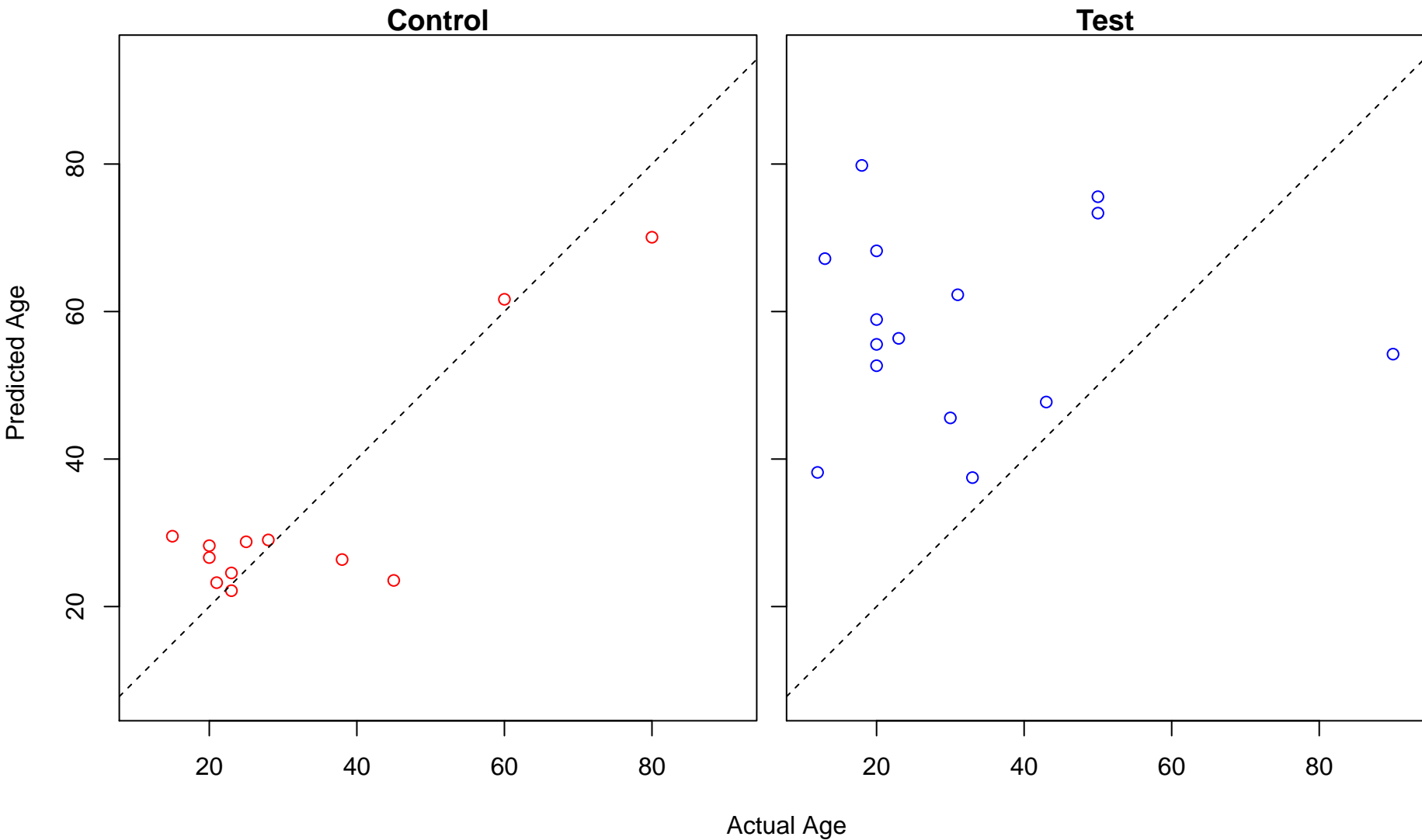
early endosome to late endosome transport (Score: 5.076314)



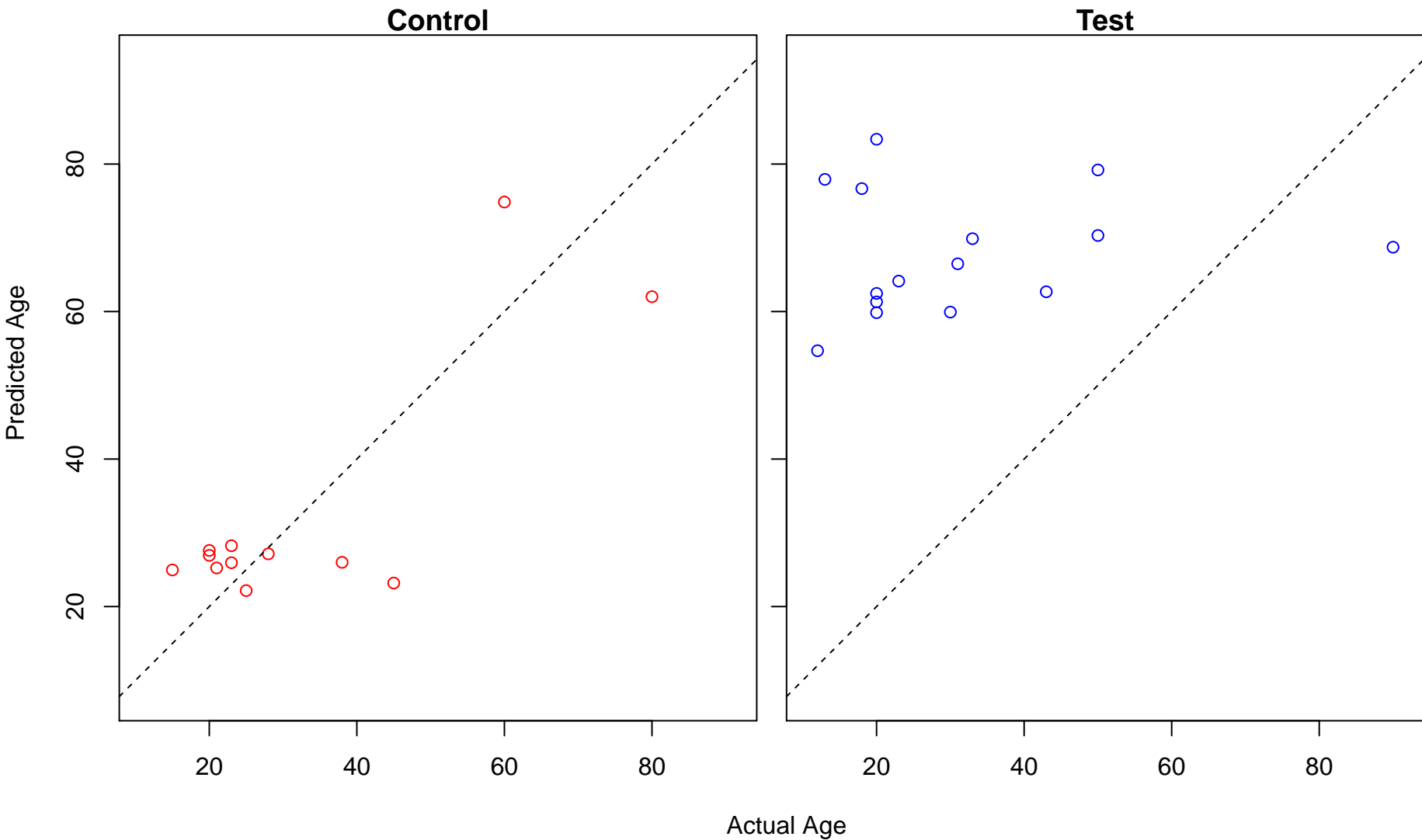
import into cell (Score: 5.075983)



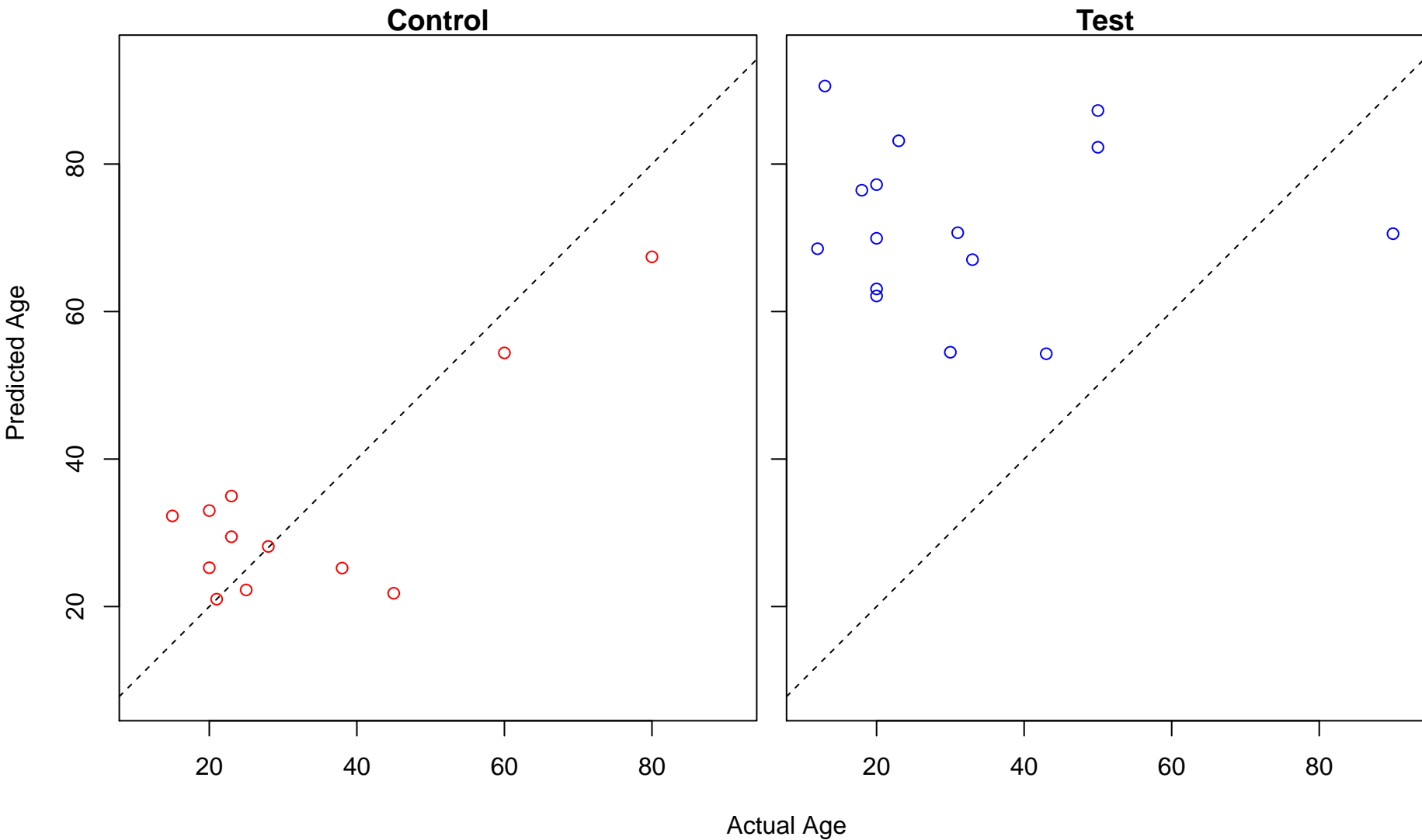
monosaccharide catabolic process (Score: 5.074998)



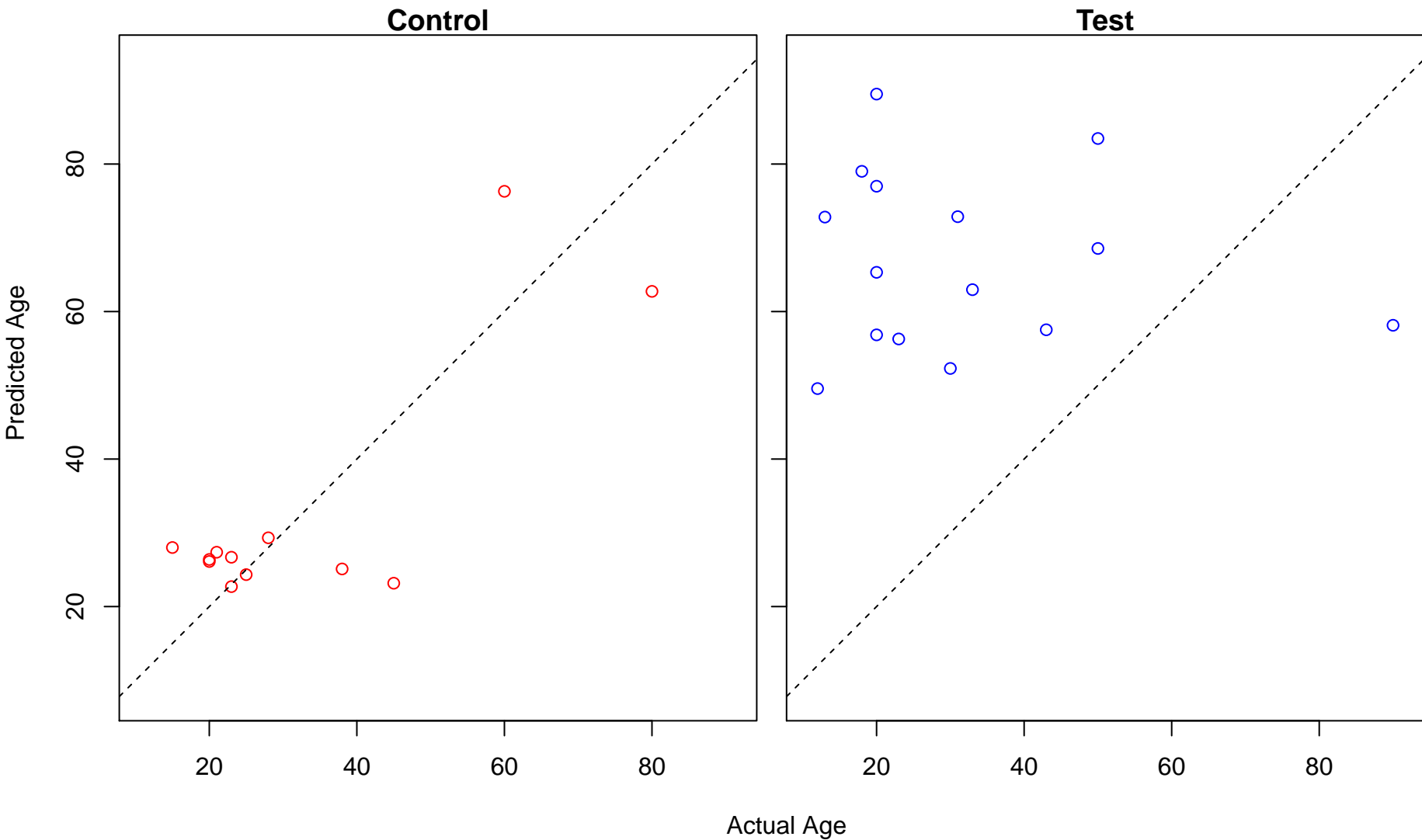
positive regulation of leukocyte proliferation (Score: 5.074486)



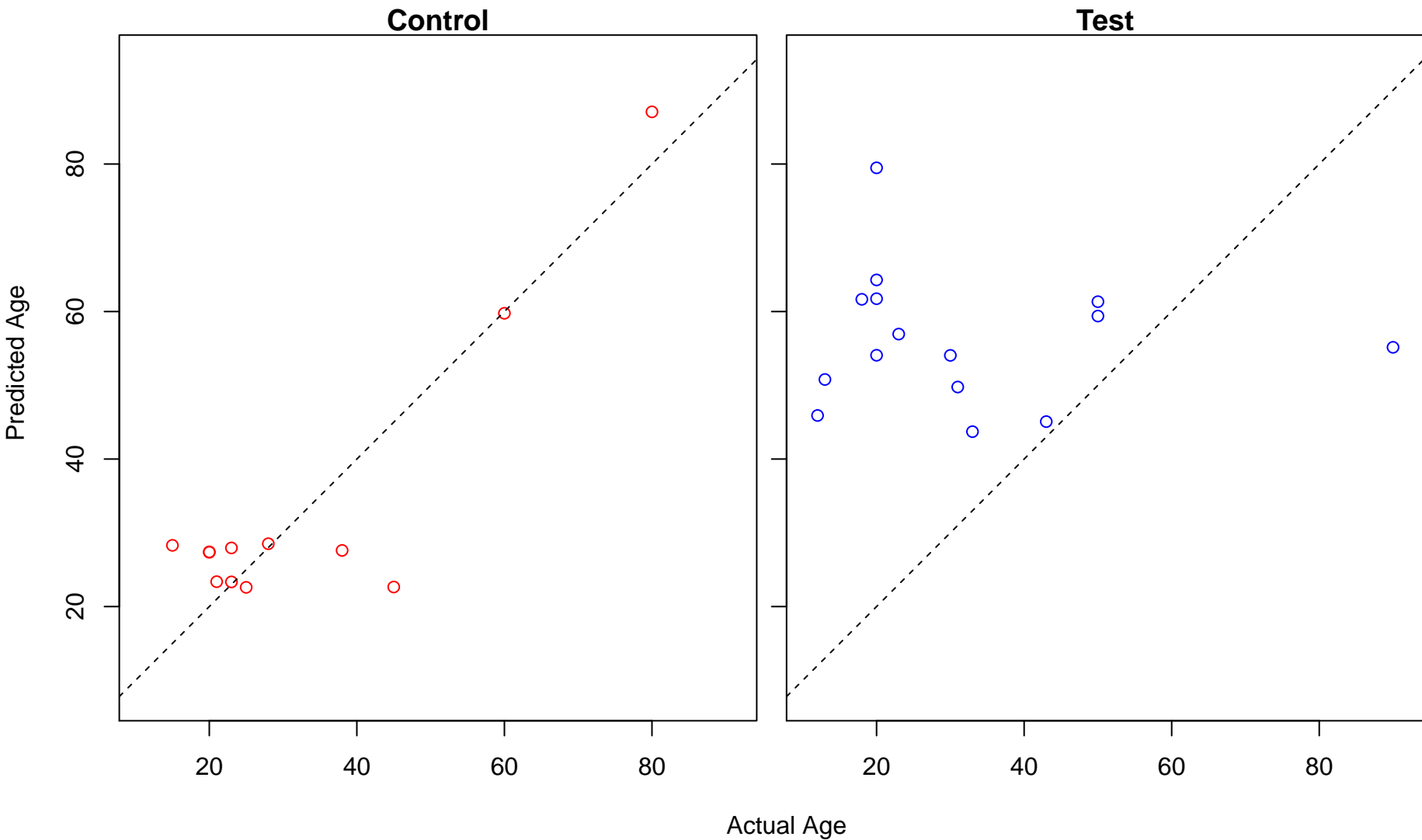
positive regulation of fatty acid beta-oxidation (Score: 5.073896)



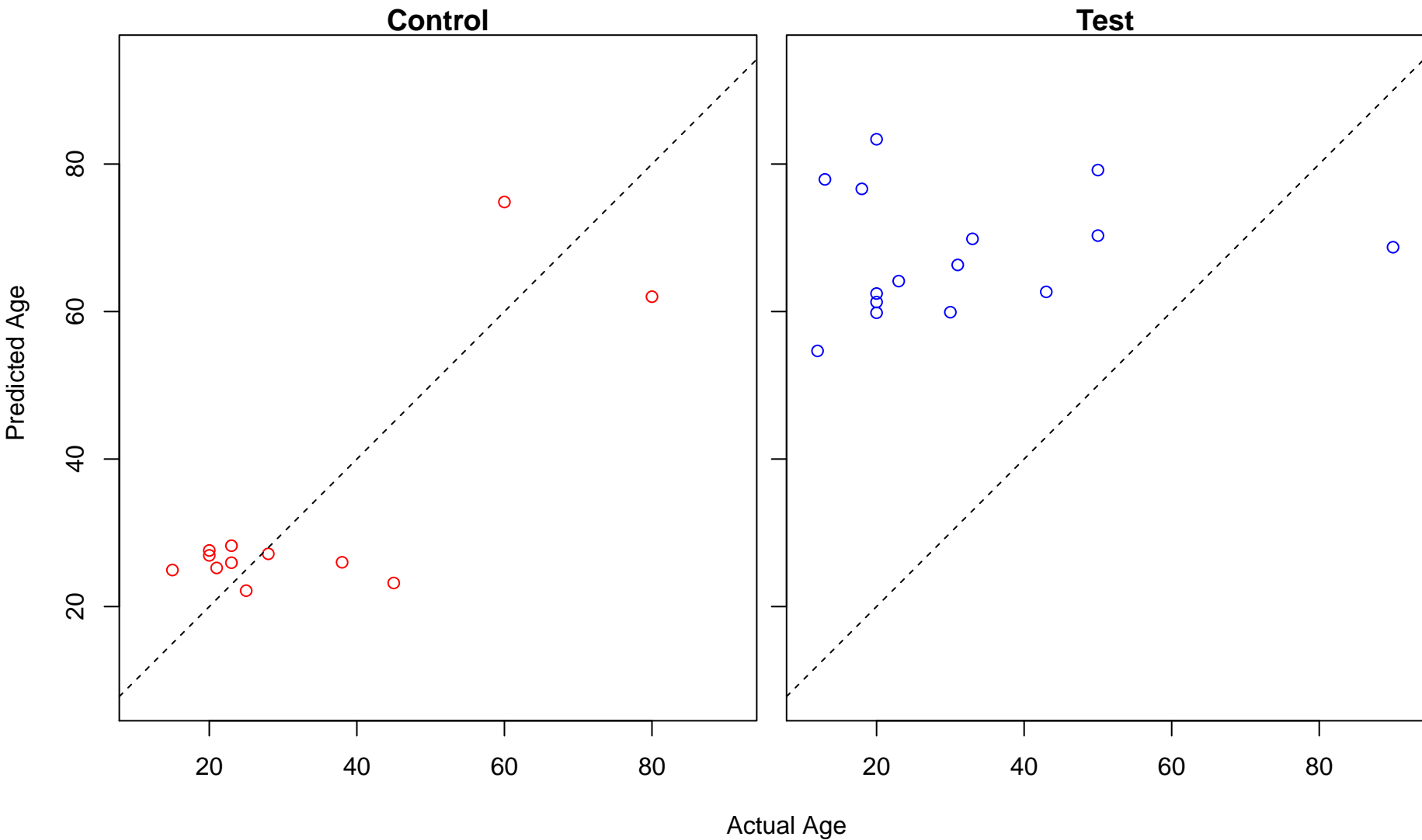
midbrain development (Score: 5.073809)



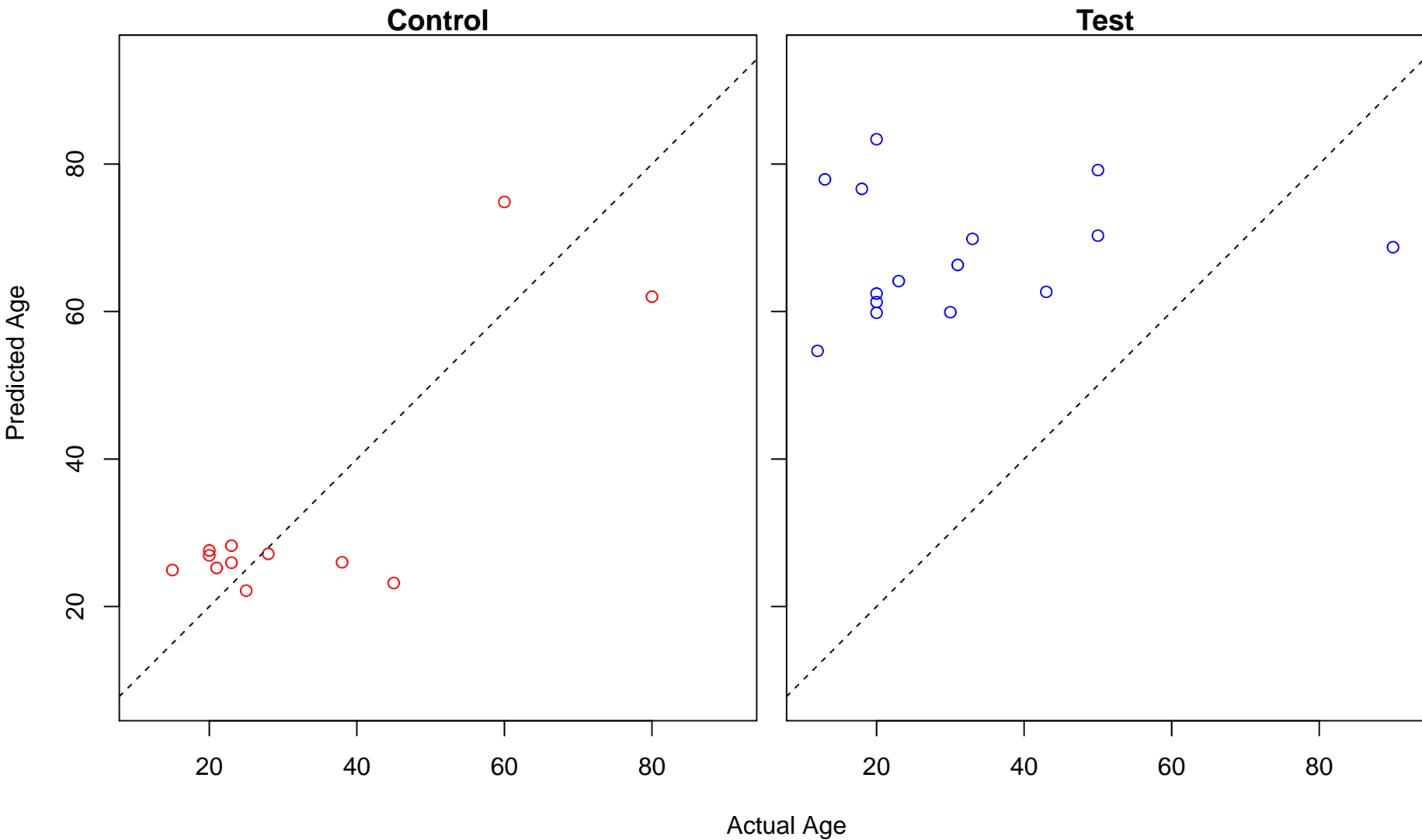
secretion by cell (Score: 5.071964)



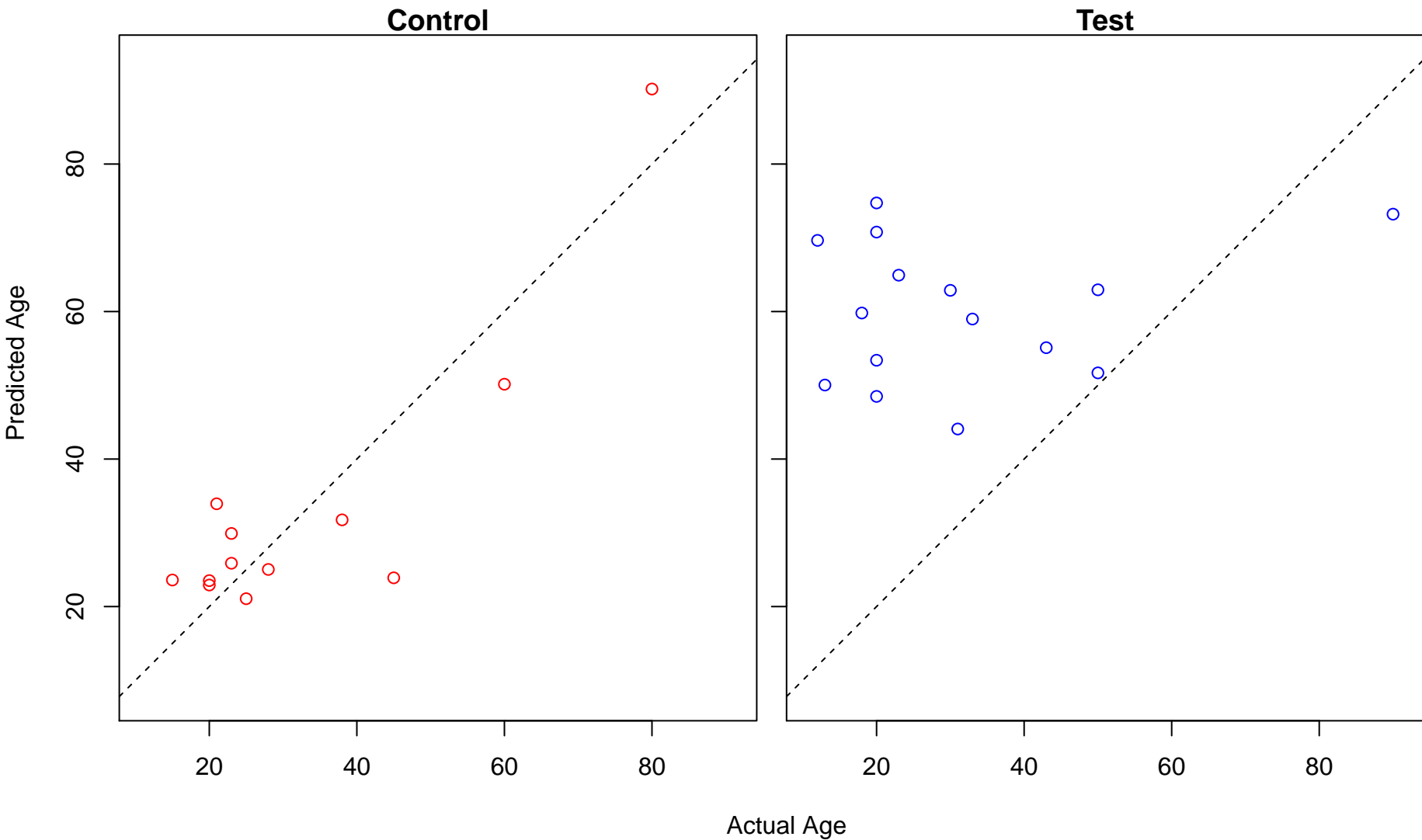
positive regulation of mononuclear cell proliferation (Score: 5.070805)



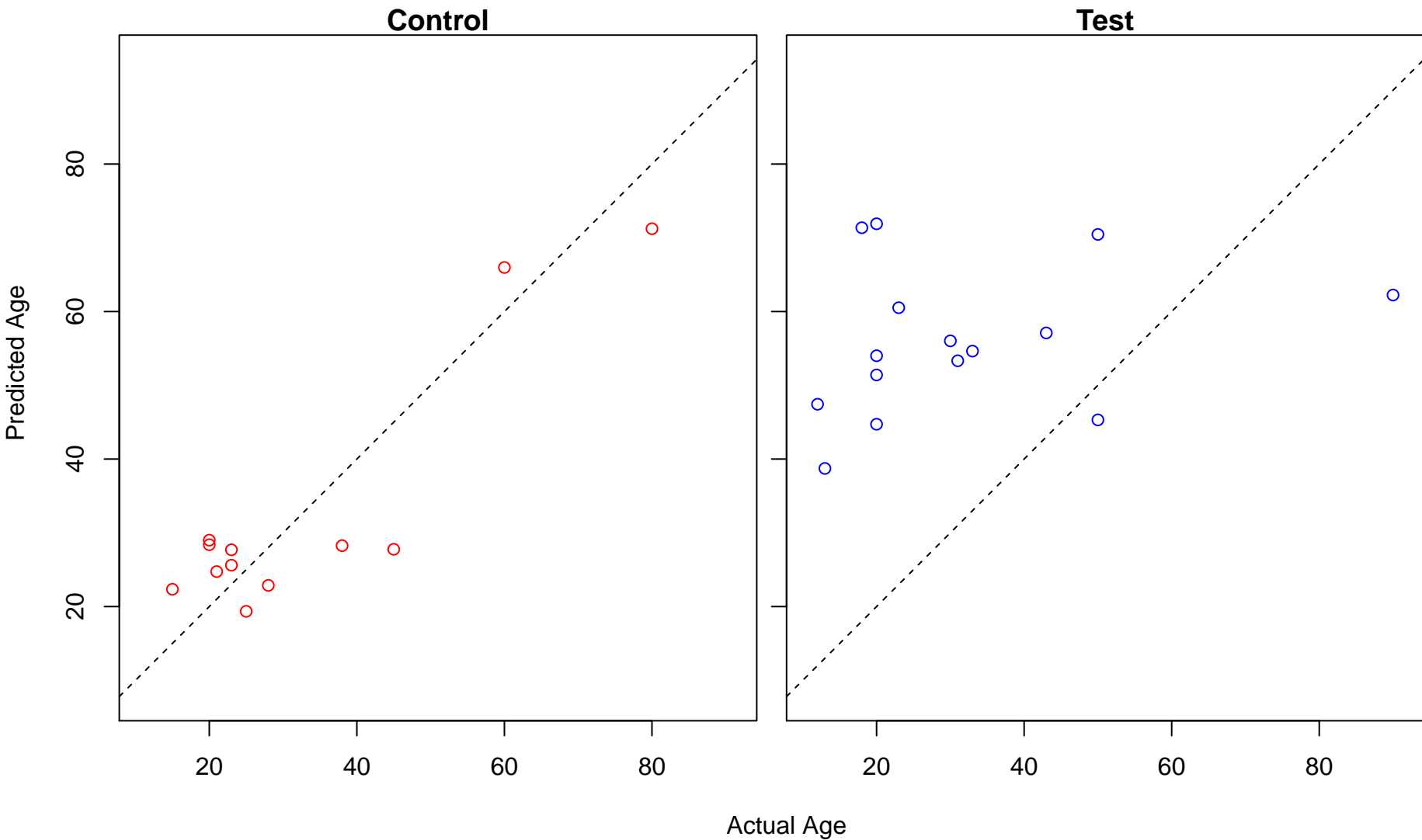
positive regulation of lymphocyte proliferation (Score: 5.070788)



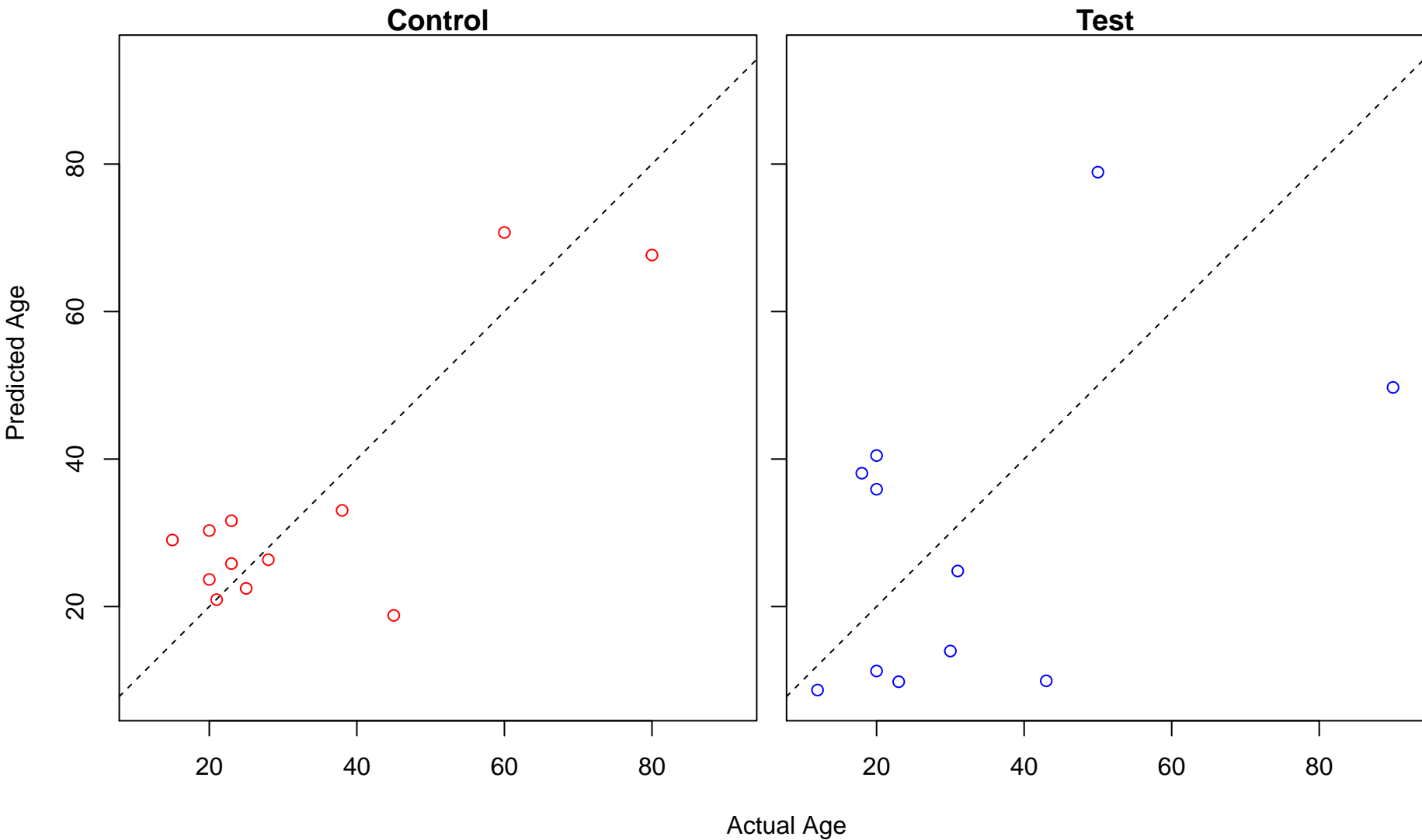
negative regulation of small GTPase mediated signal transduction (Score: 5.068677)



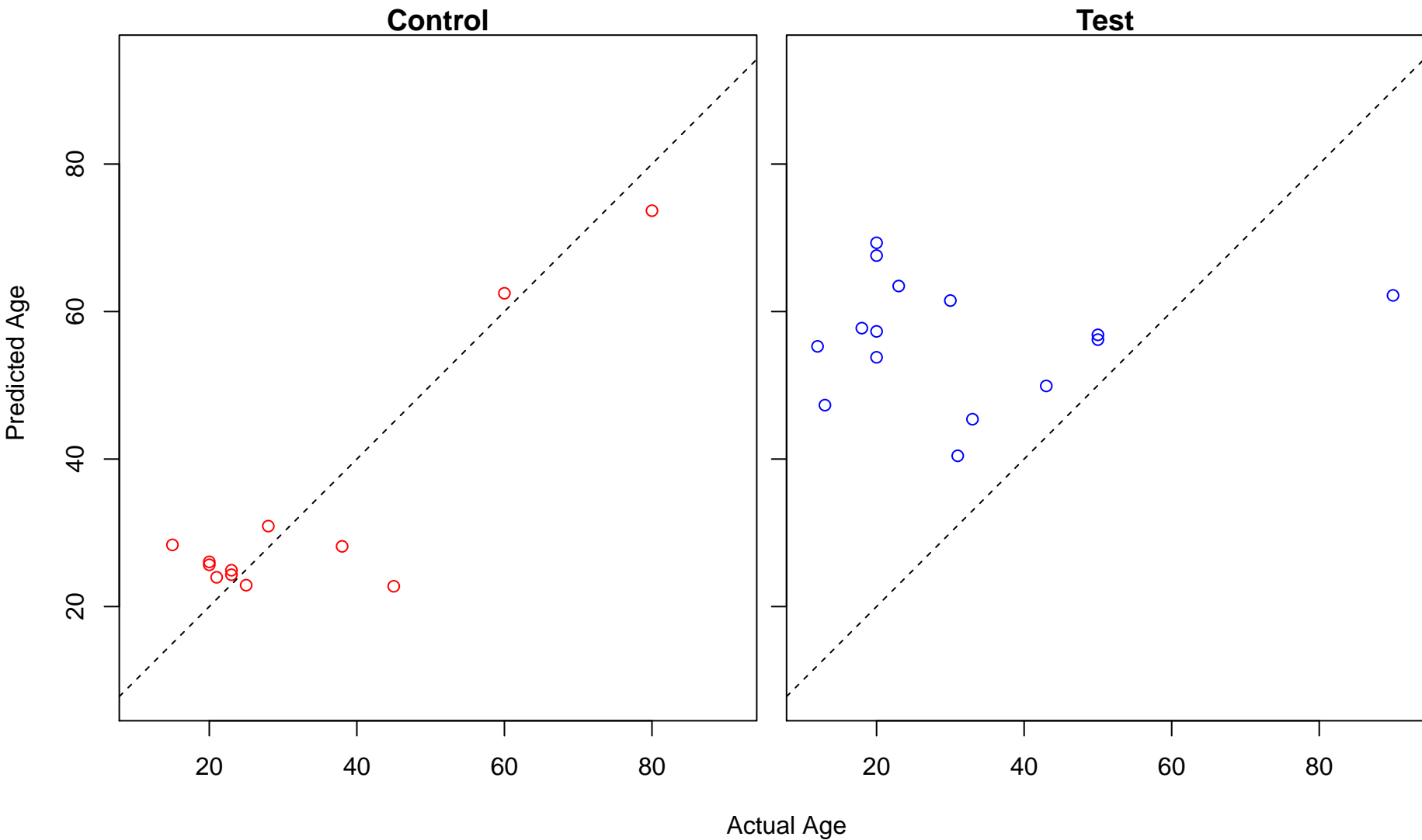
cardiac myofibril assembly (Score: 5.068419)



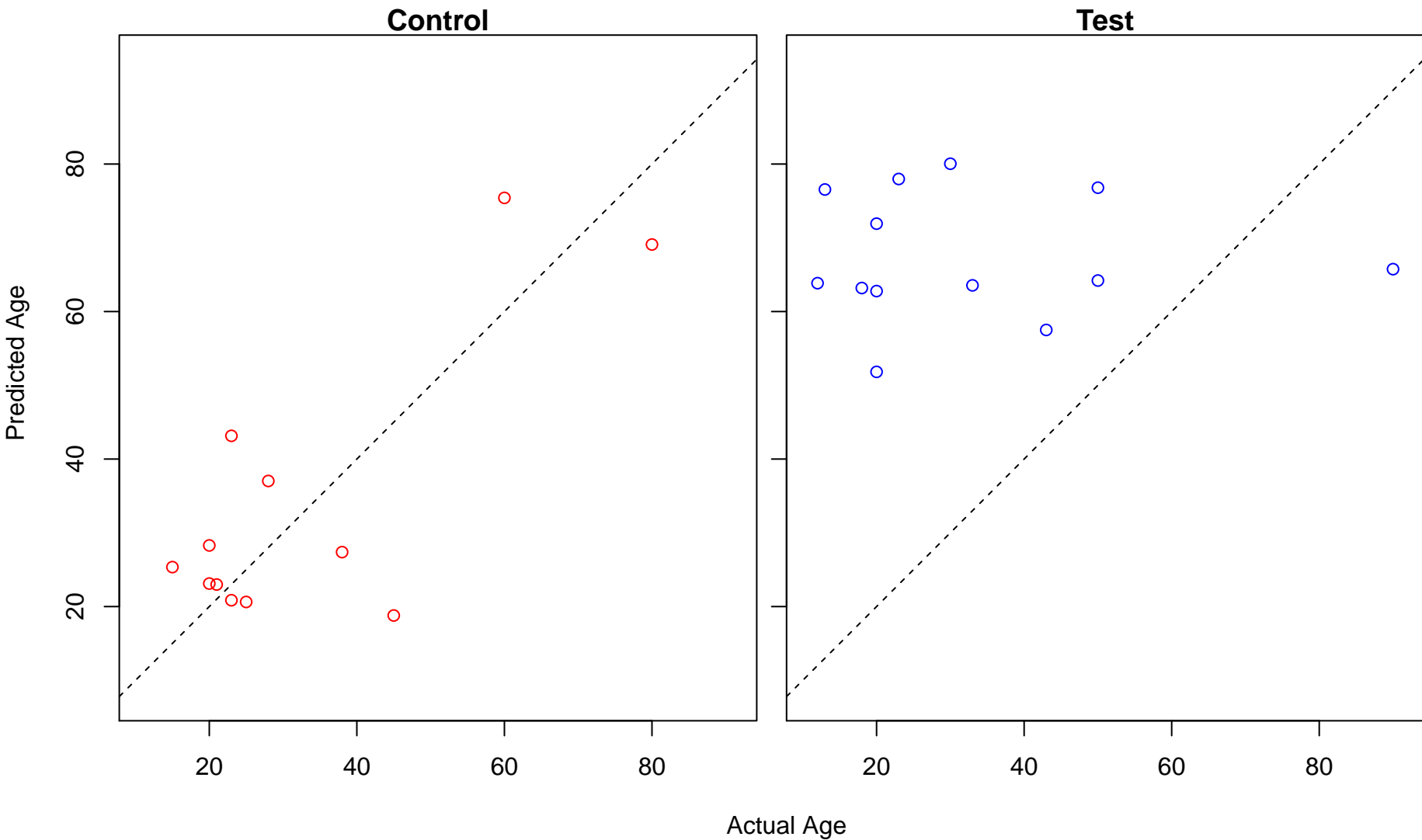
maintenance of organ identity (Score: 5.067637)



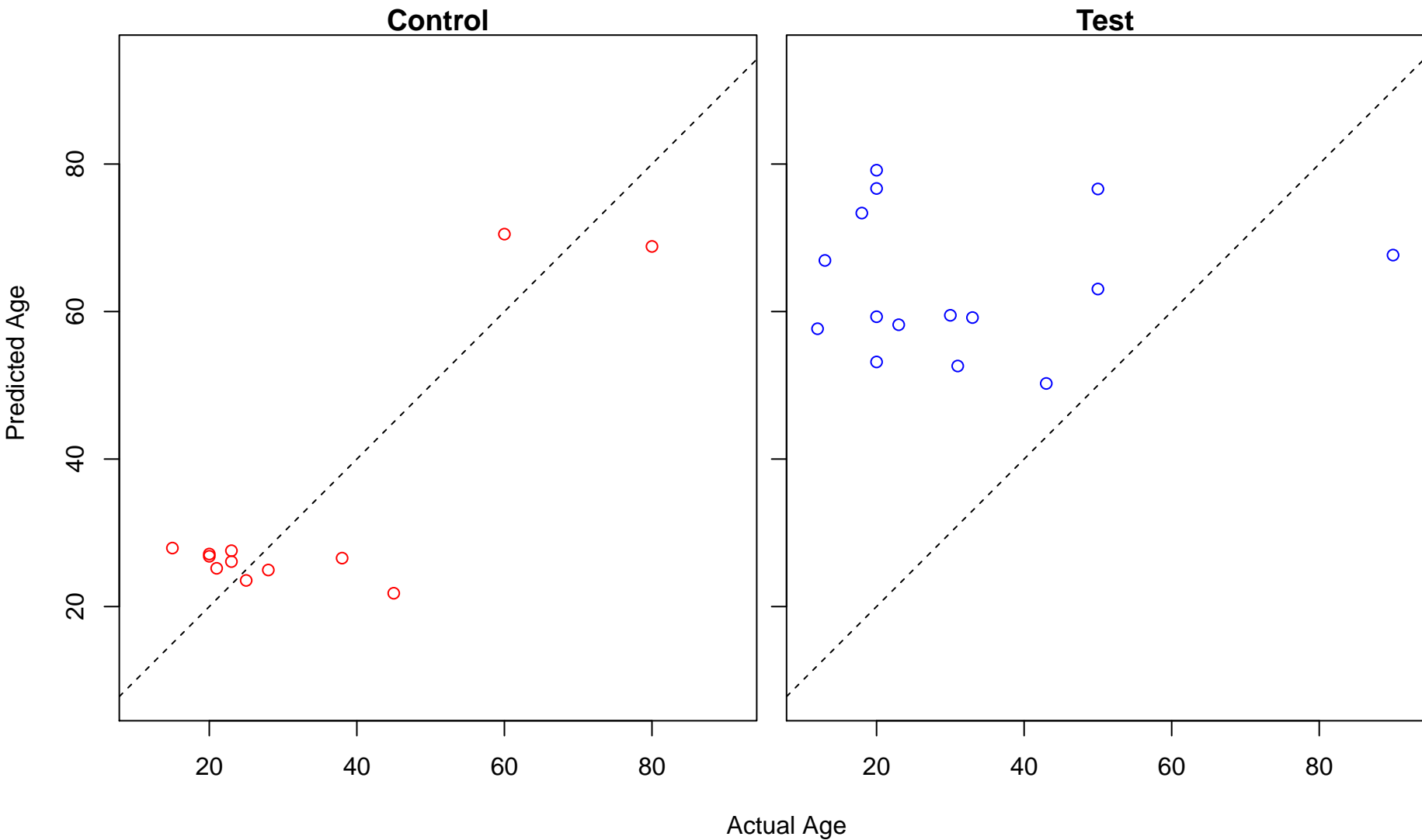
microtubule polymerization or depolymerization (Score: 5.067069)



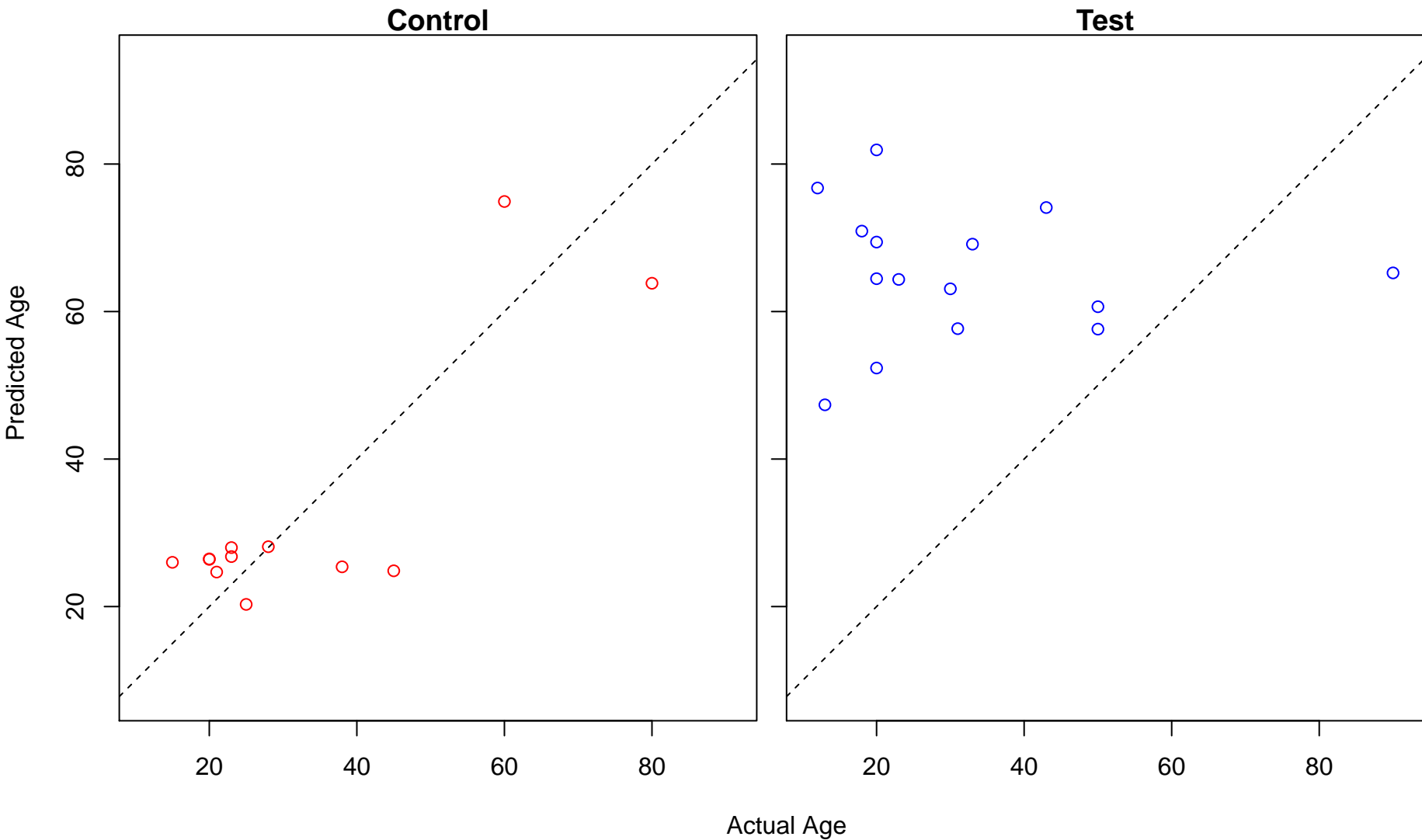
adaptive immune response (Score: 5.064067)



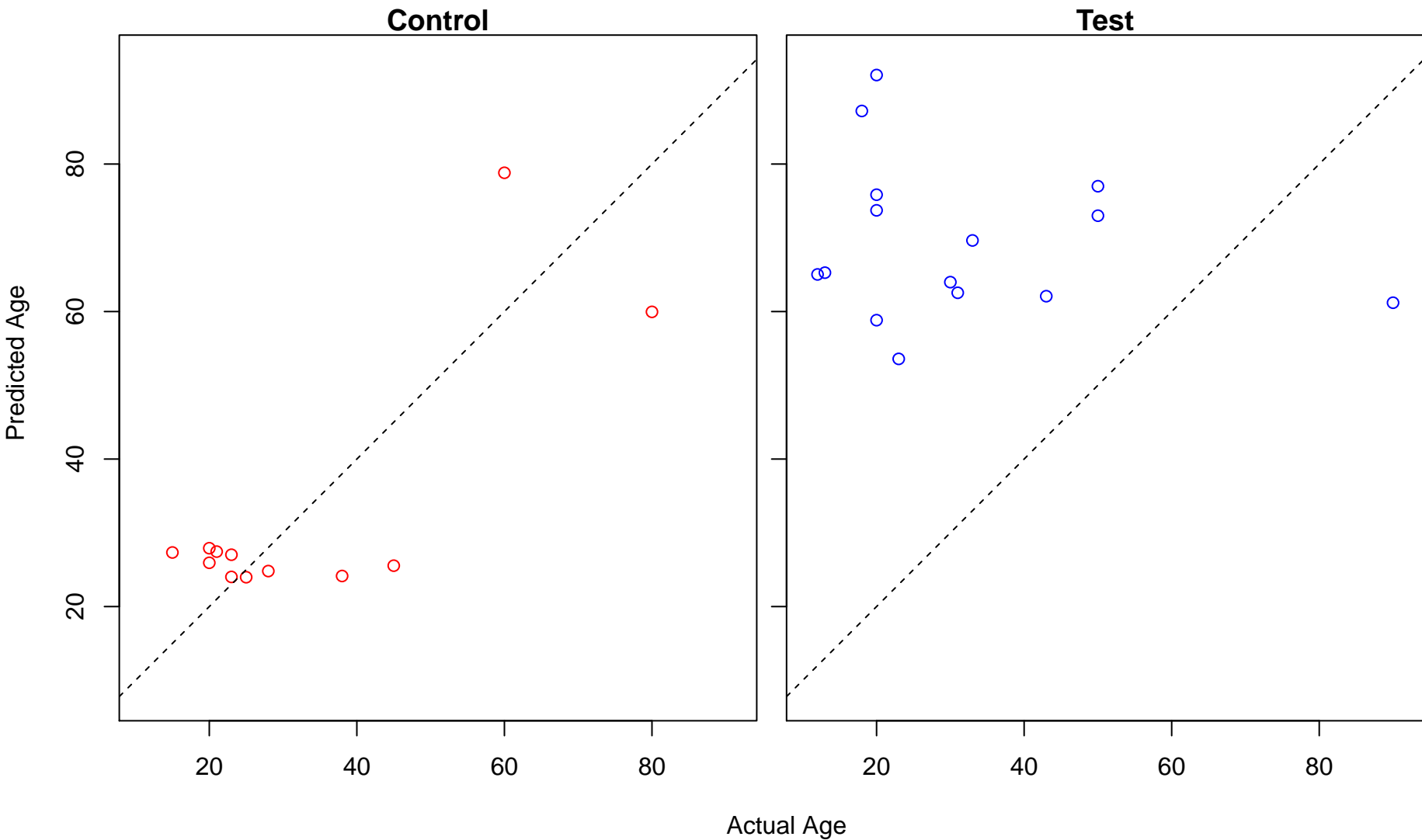
positive regulation of cellular catabolic process (Score: 5.063937)



regulation of cell-cell adhesion mediated by cadherin (Score: 5.063591)

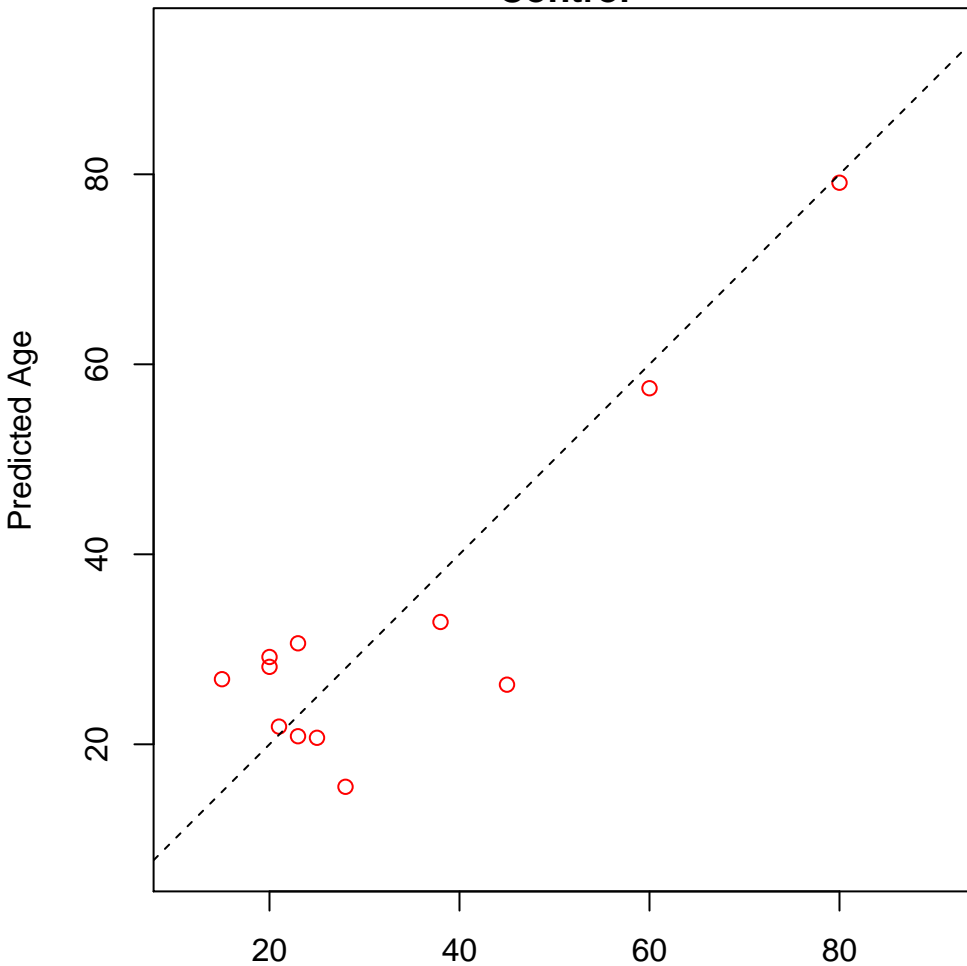


regulation of adherens junction organization (Score: 5.062865)

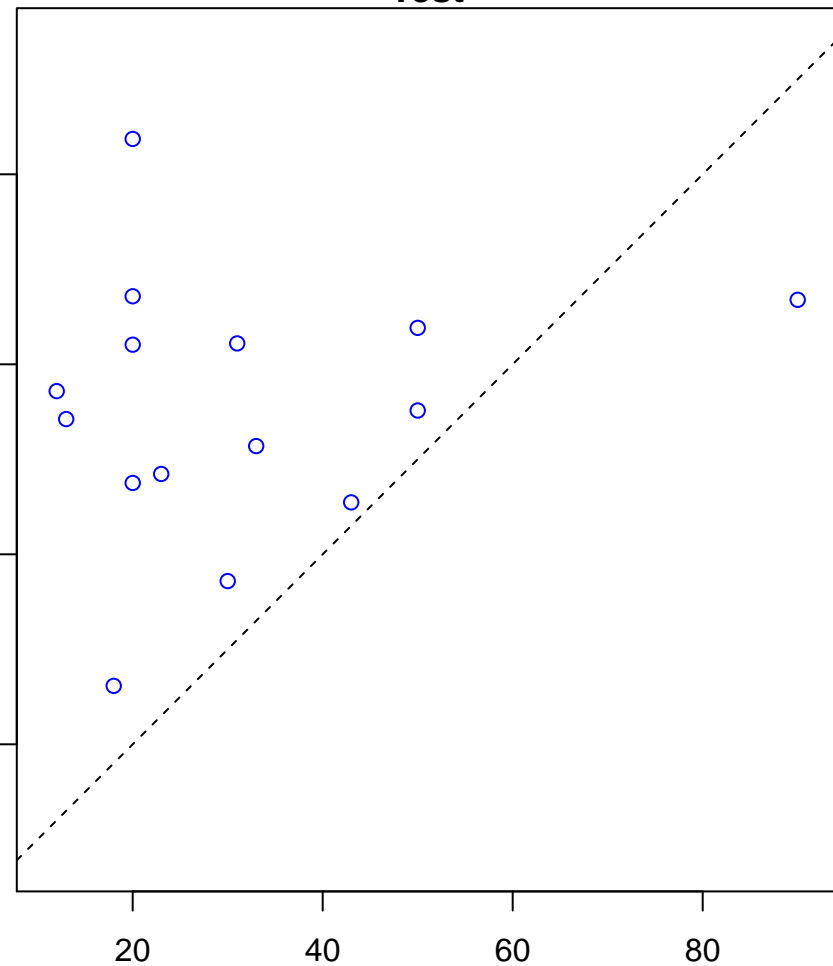


ammonium transmembrane transport (Score: 5.060648)

Control

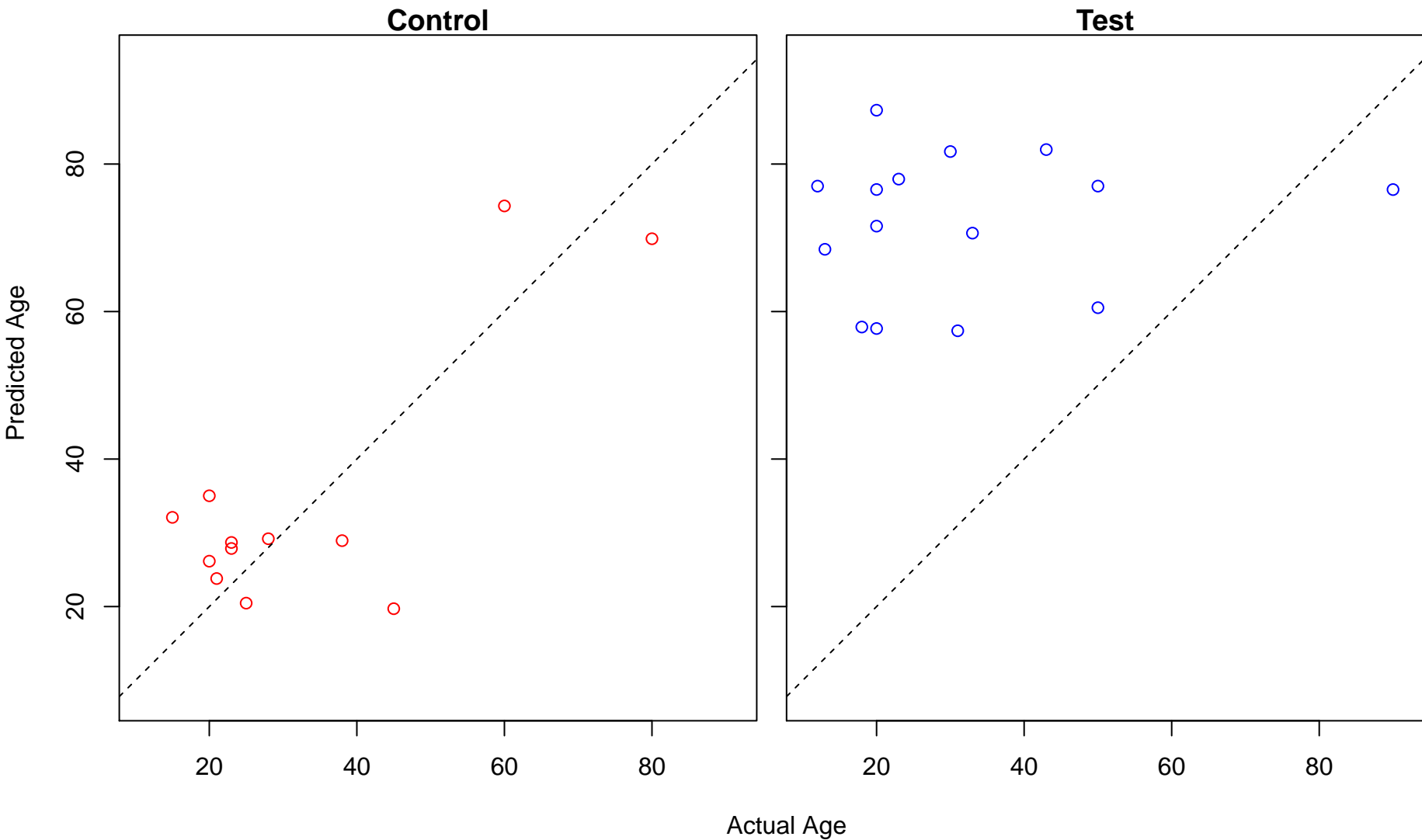


Test



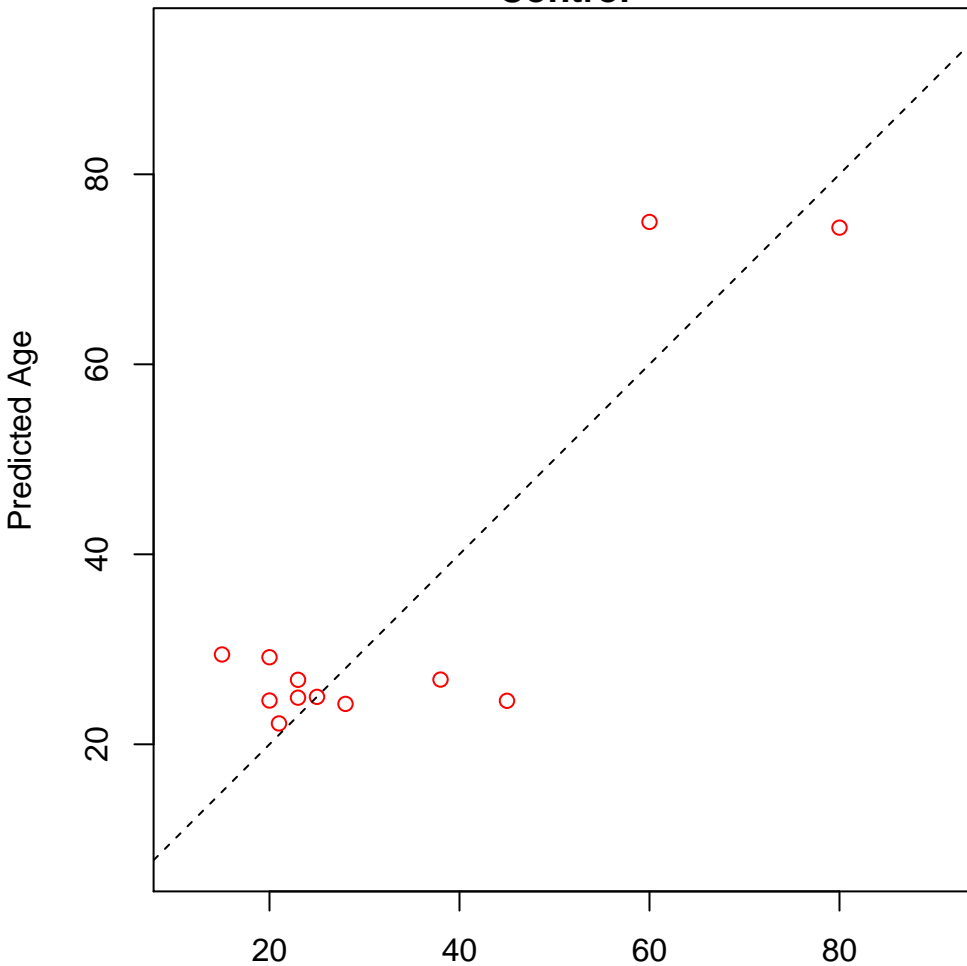
Actual Age

regulation of fatty acid oxidation (Score: 5.059295)

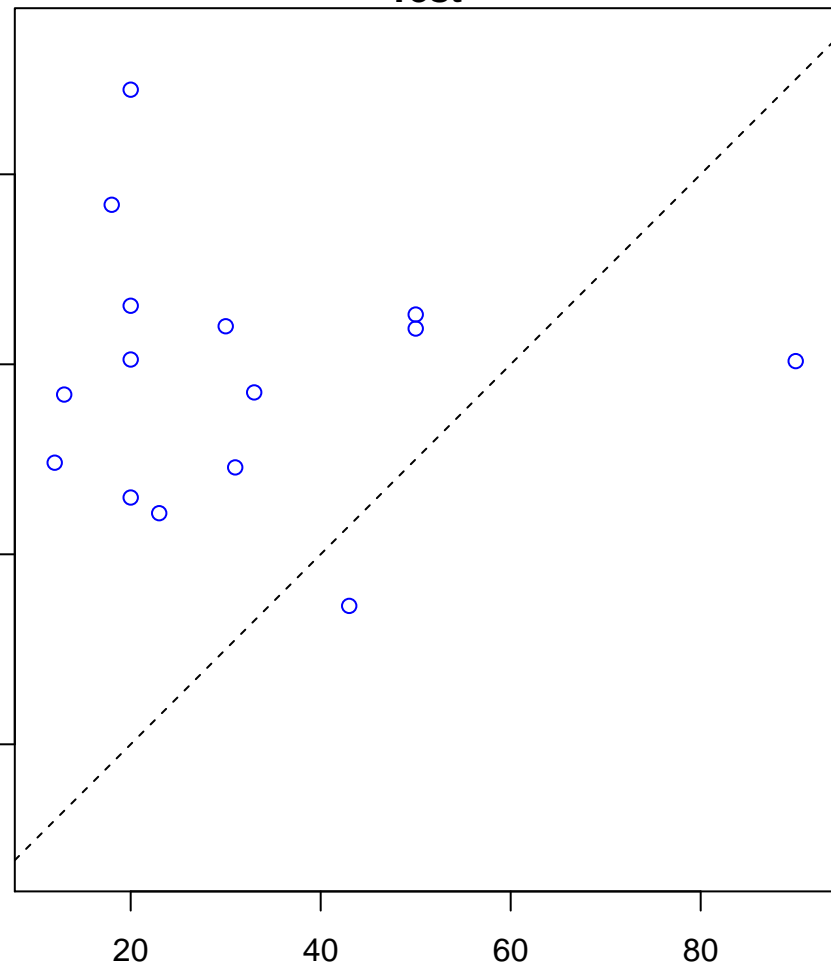


nucleotide-sugar metabolic process (Score: 5.056460)

Control

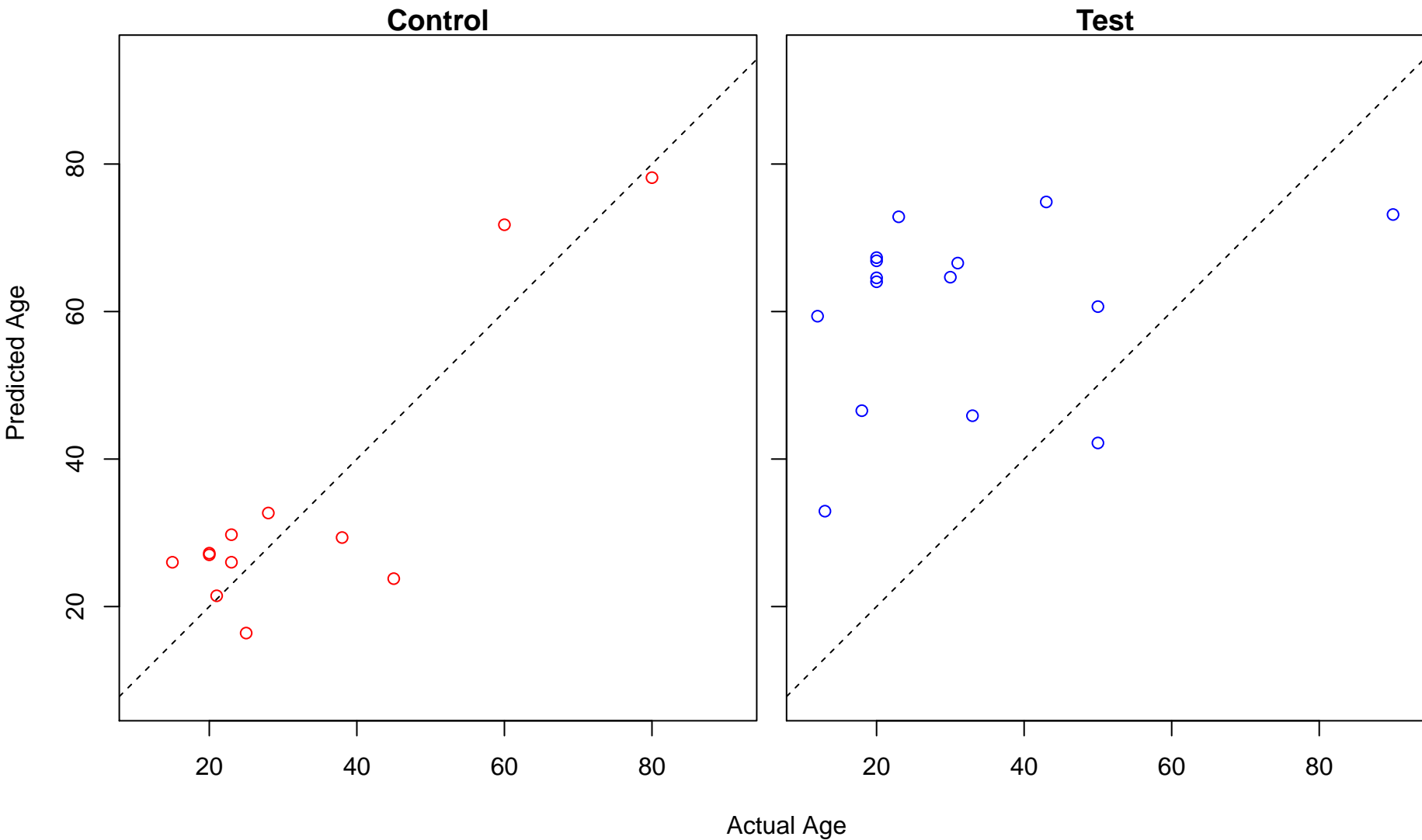


Test



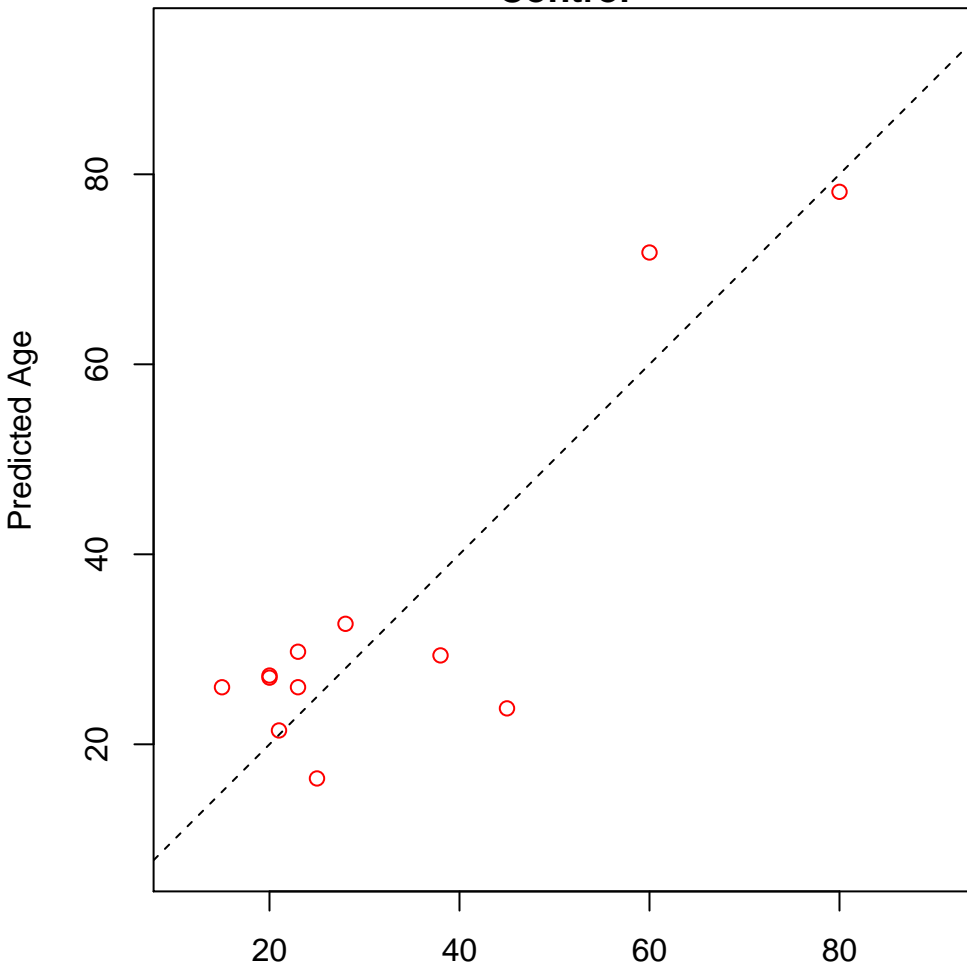
Actual Age

intraciliary transport (Score: 5.054822)

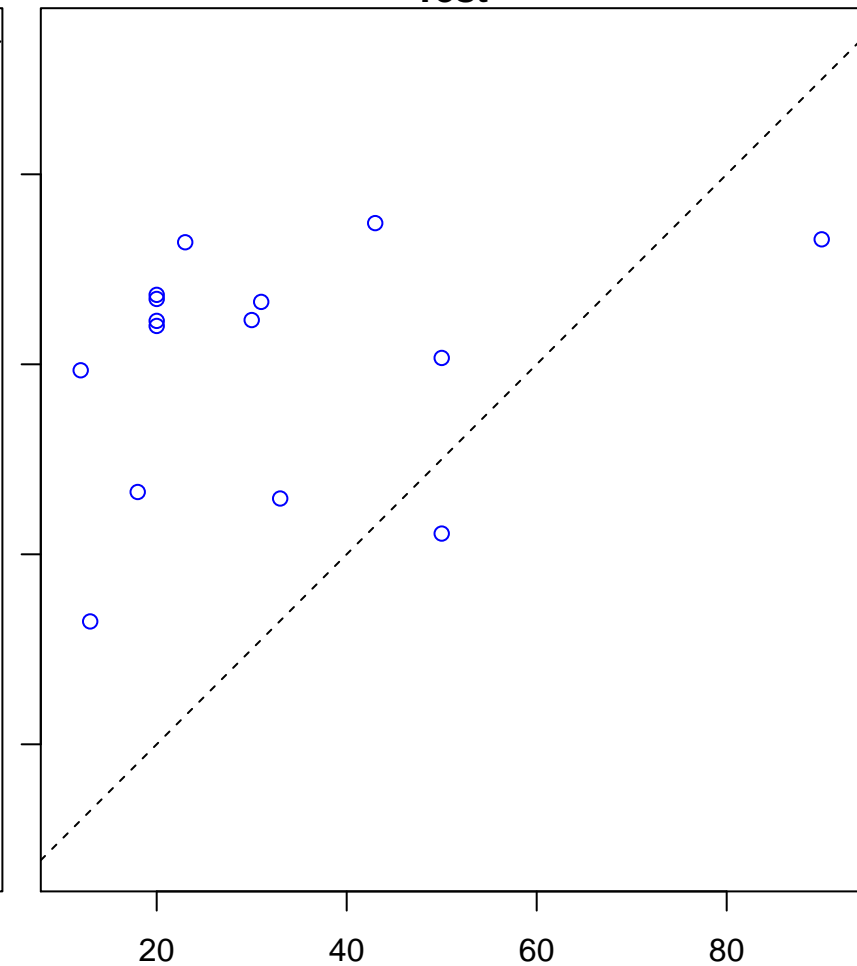


protein transport along microtubule (Score: 5.054822)

Control

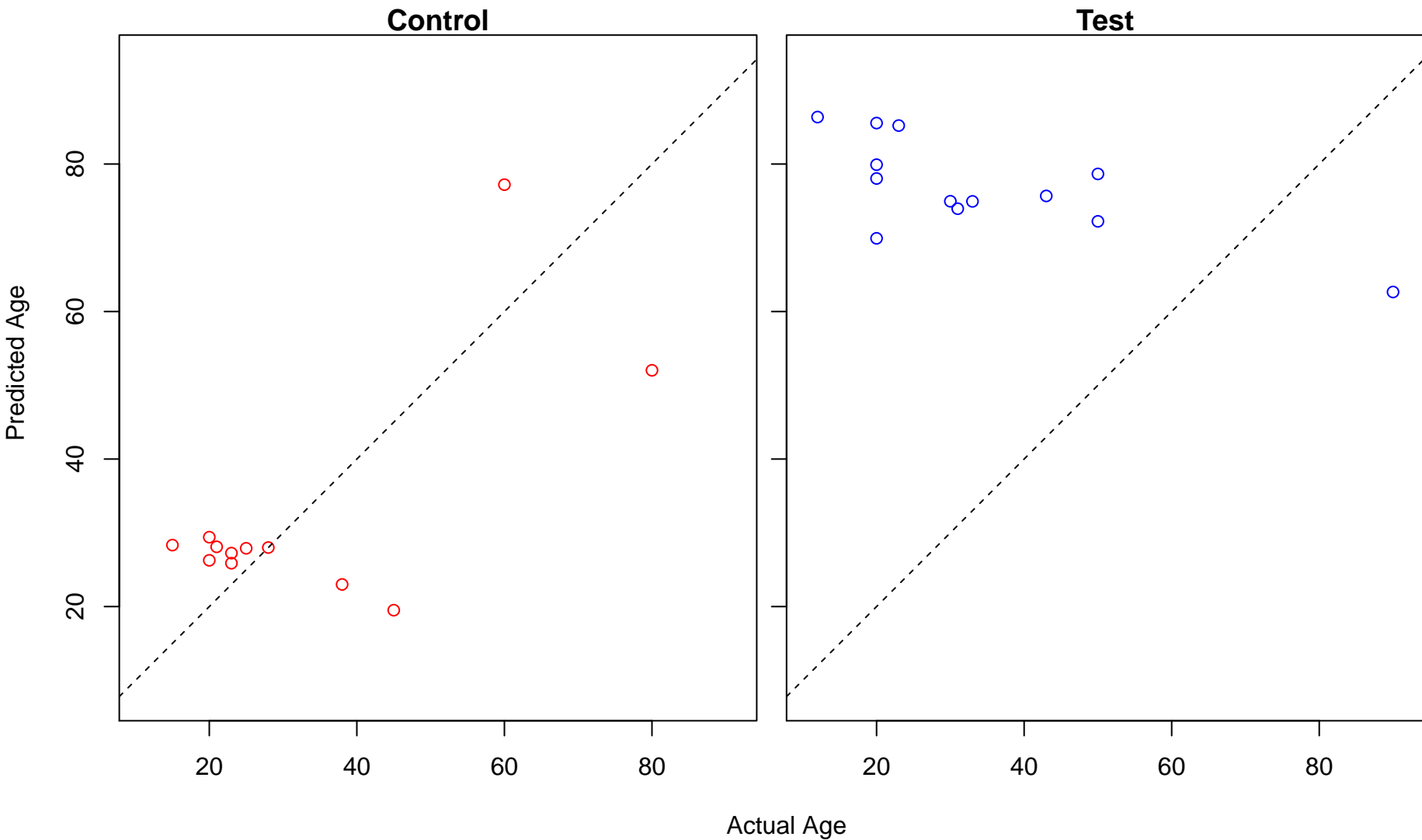


Test

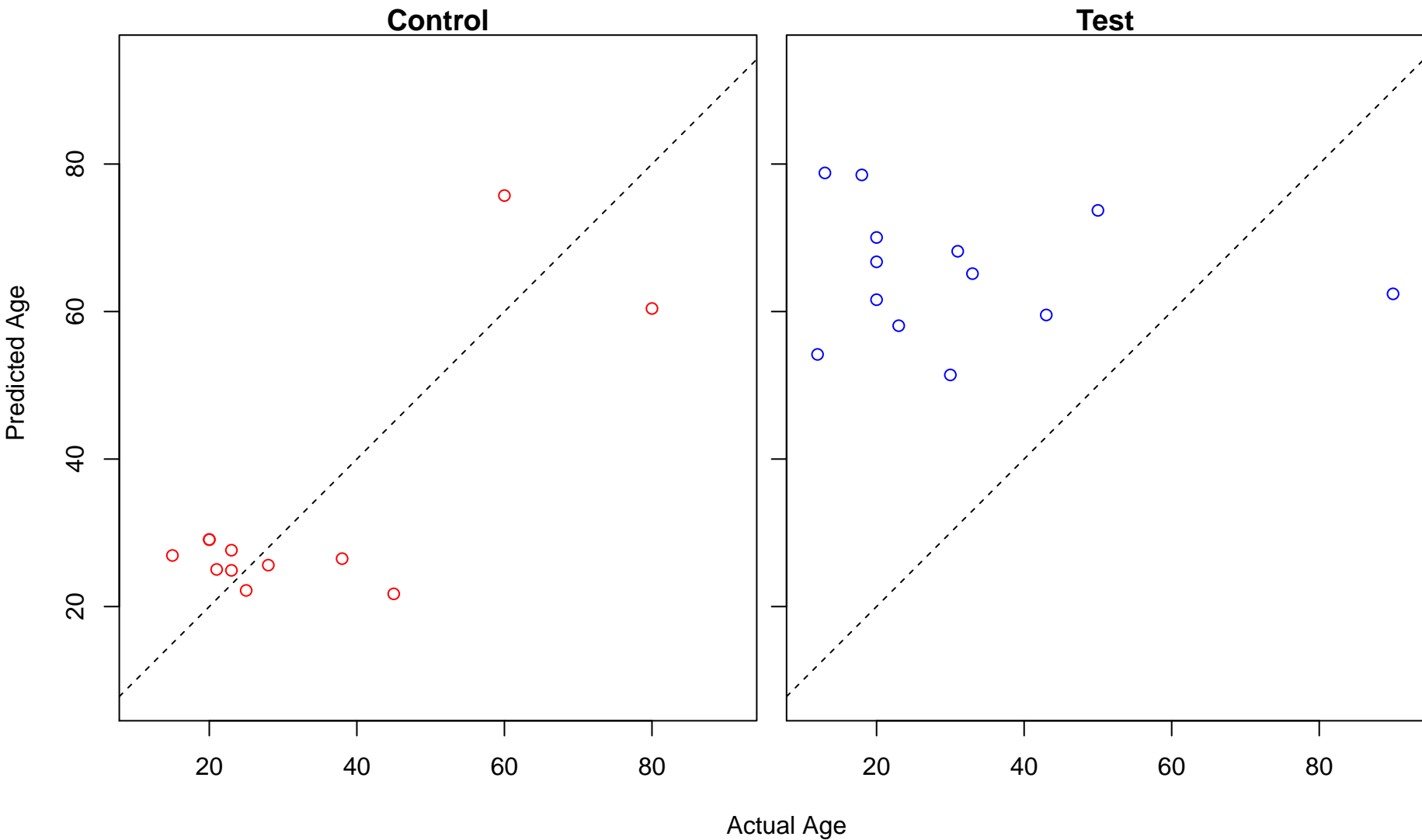


Actual Age

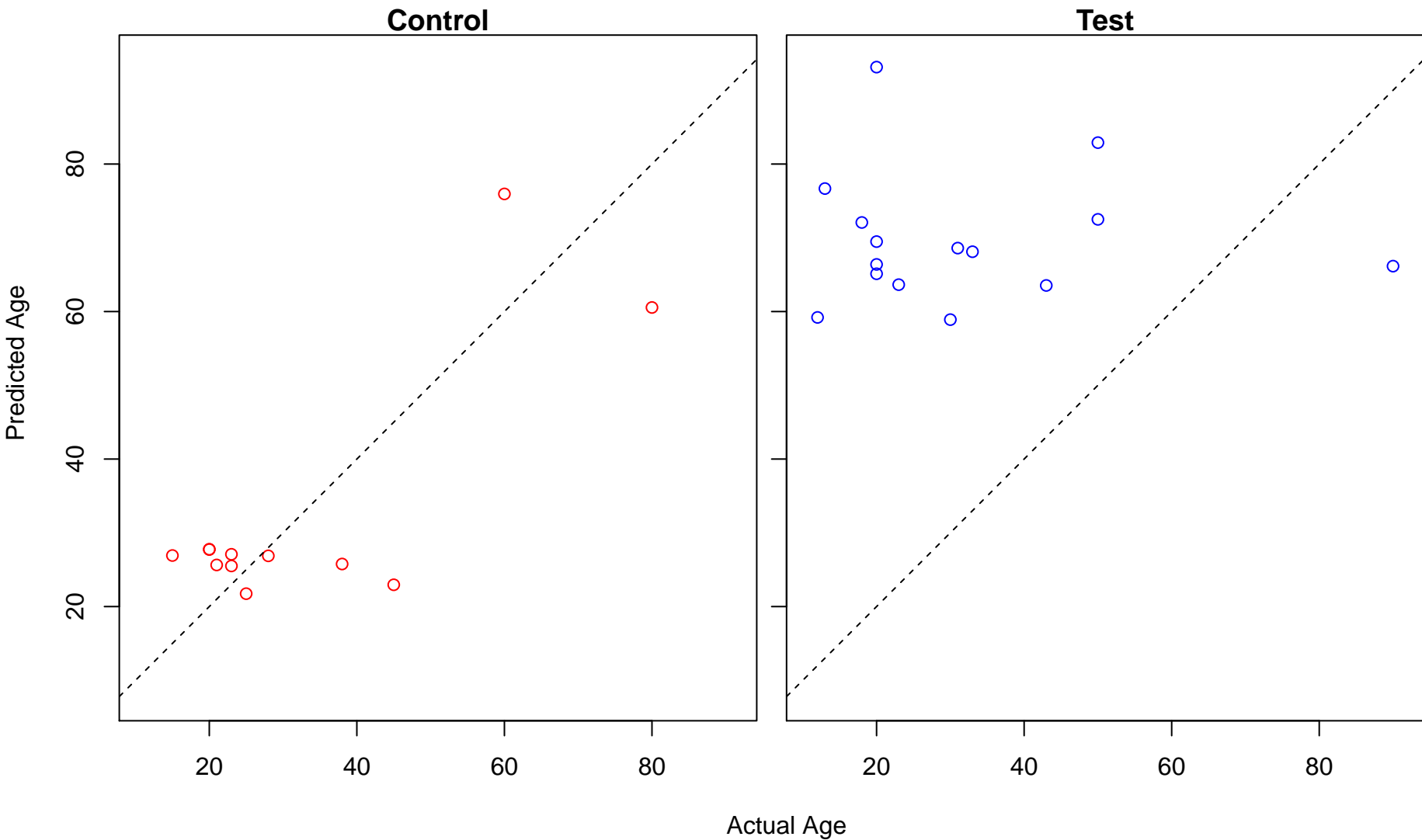
regulation of meiotic nuclear division (Score: 5.054806)



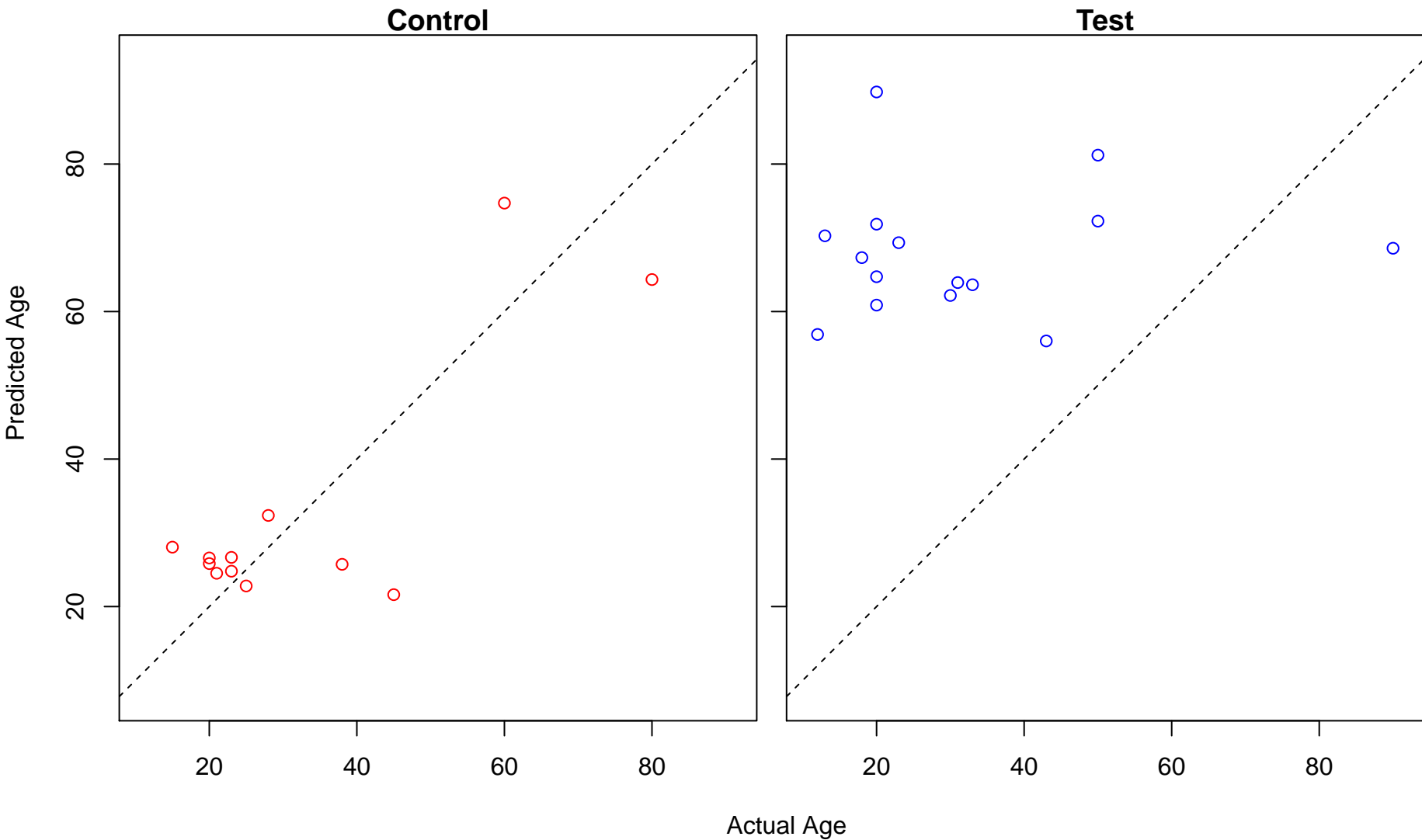
membrane raft assembly (Score: 5.054545)



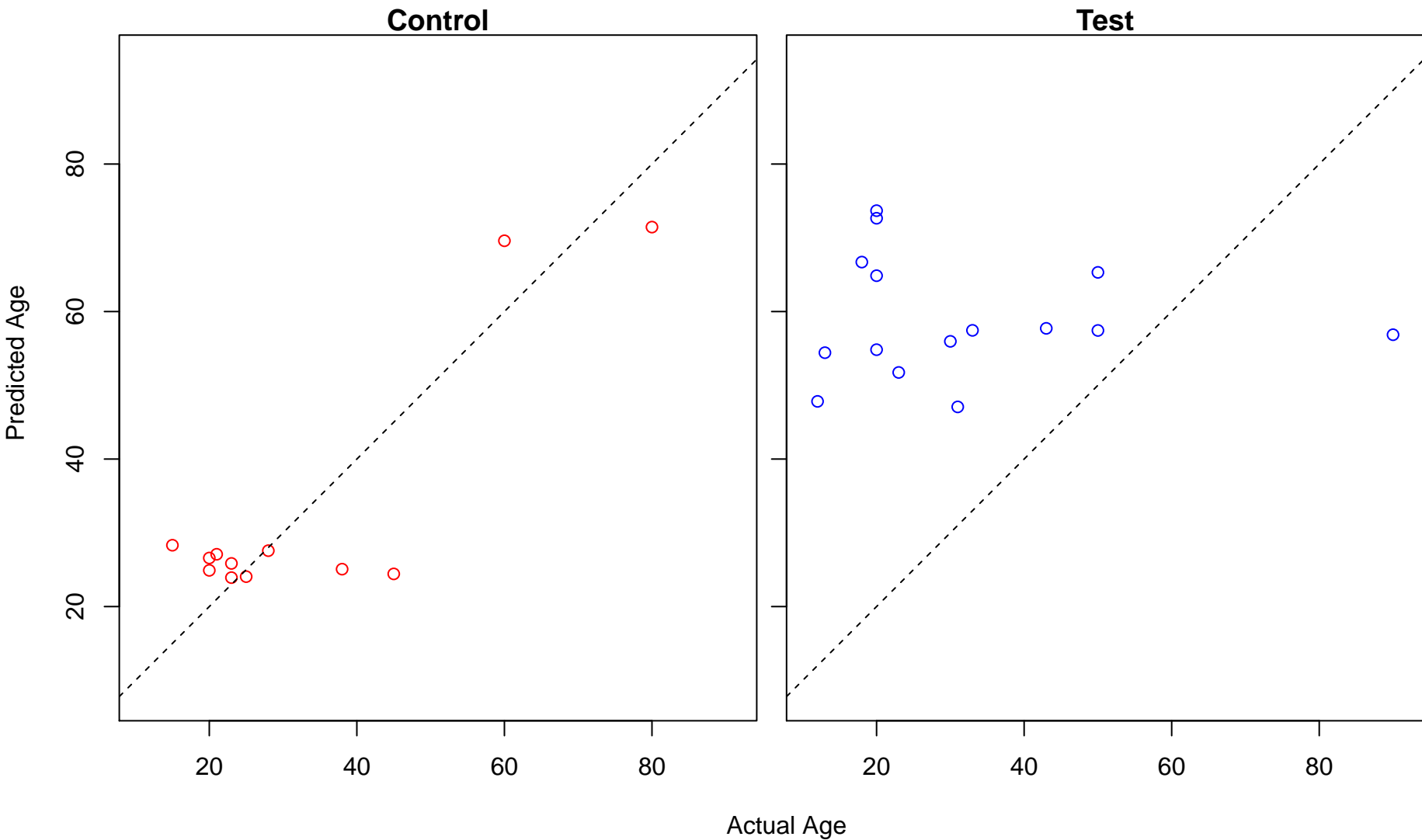
muscle system process (Score: 5.054480)



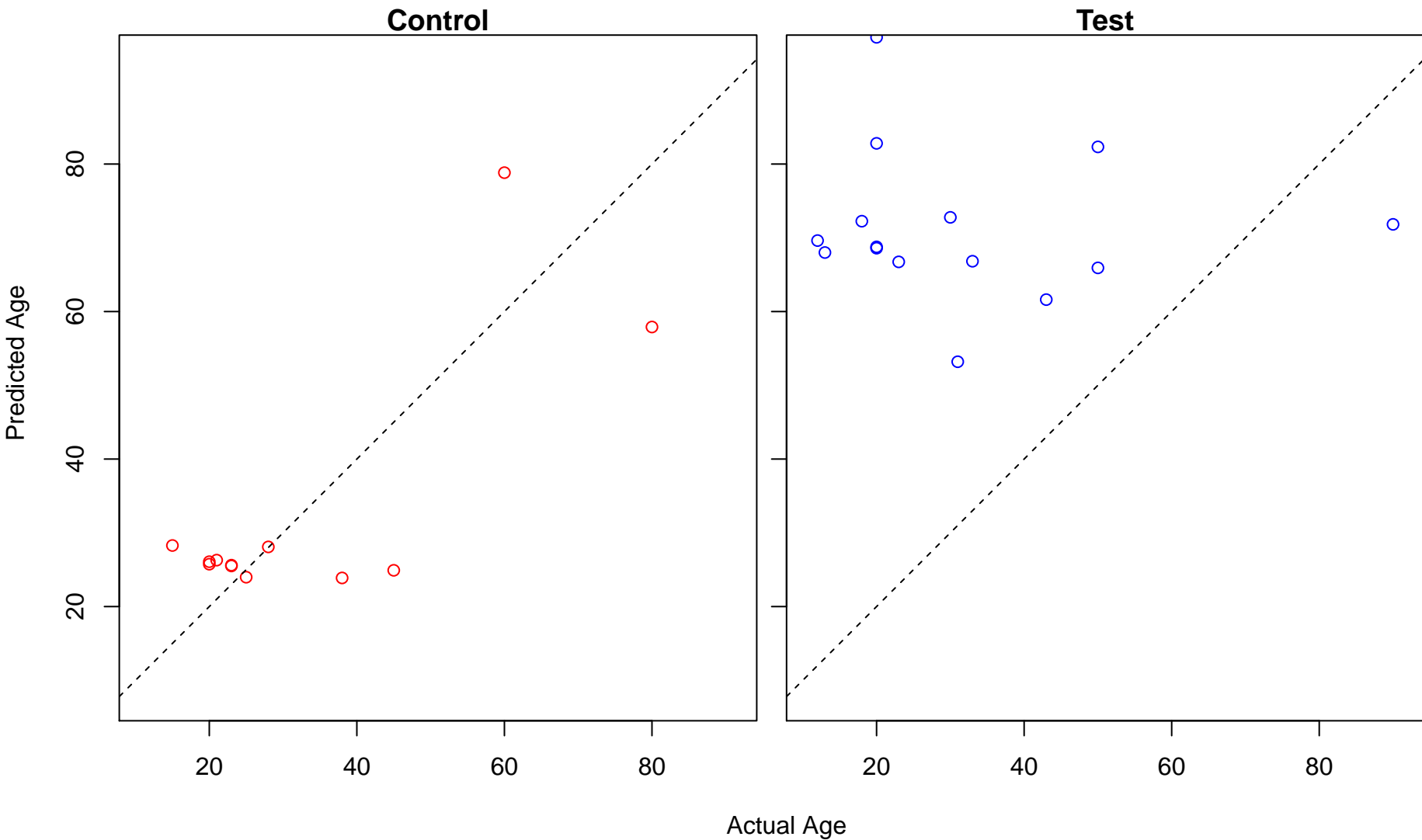
positive regulation of MAPK cascade (Score: 5.054343)



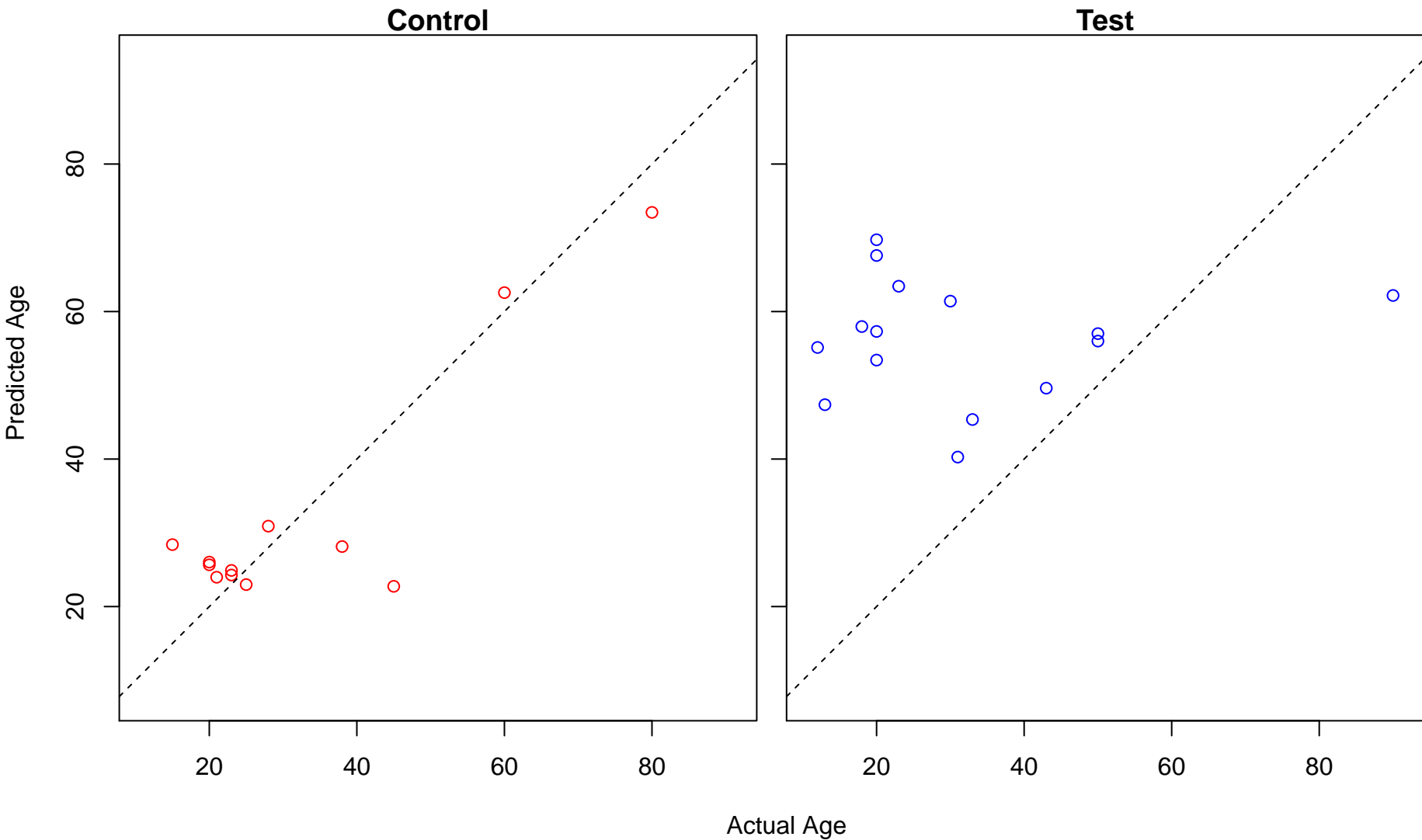
regulation of microtubule cytoskeleton organization (Score: 5.052284)



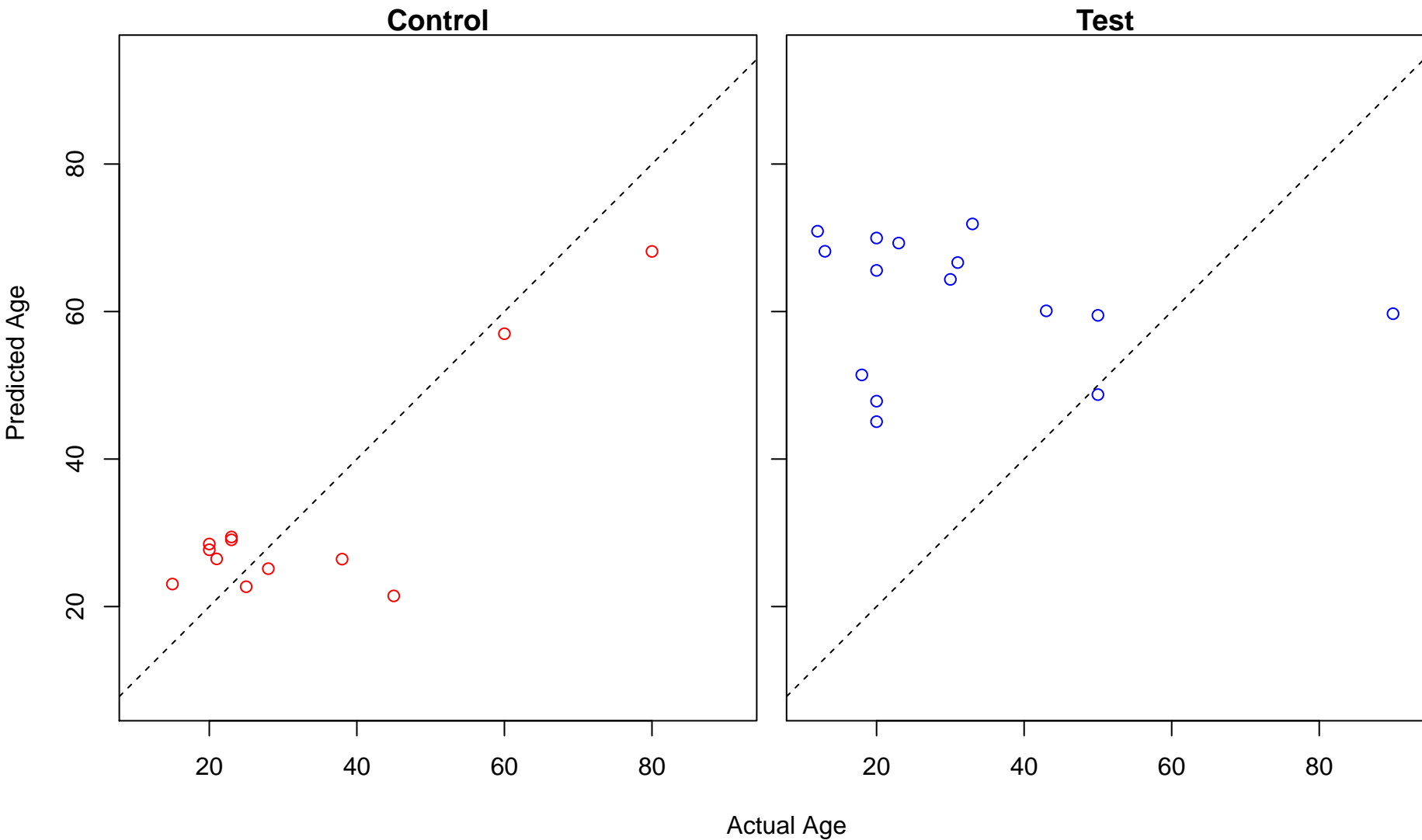
positive regulation of viral transcription (Score: 5.049607)



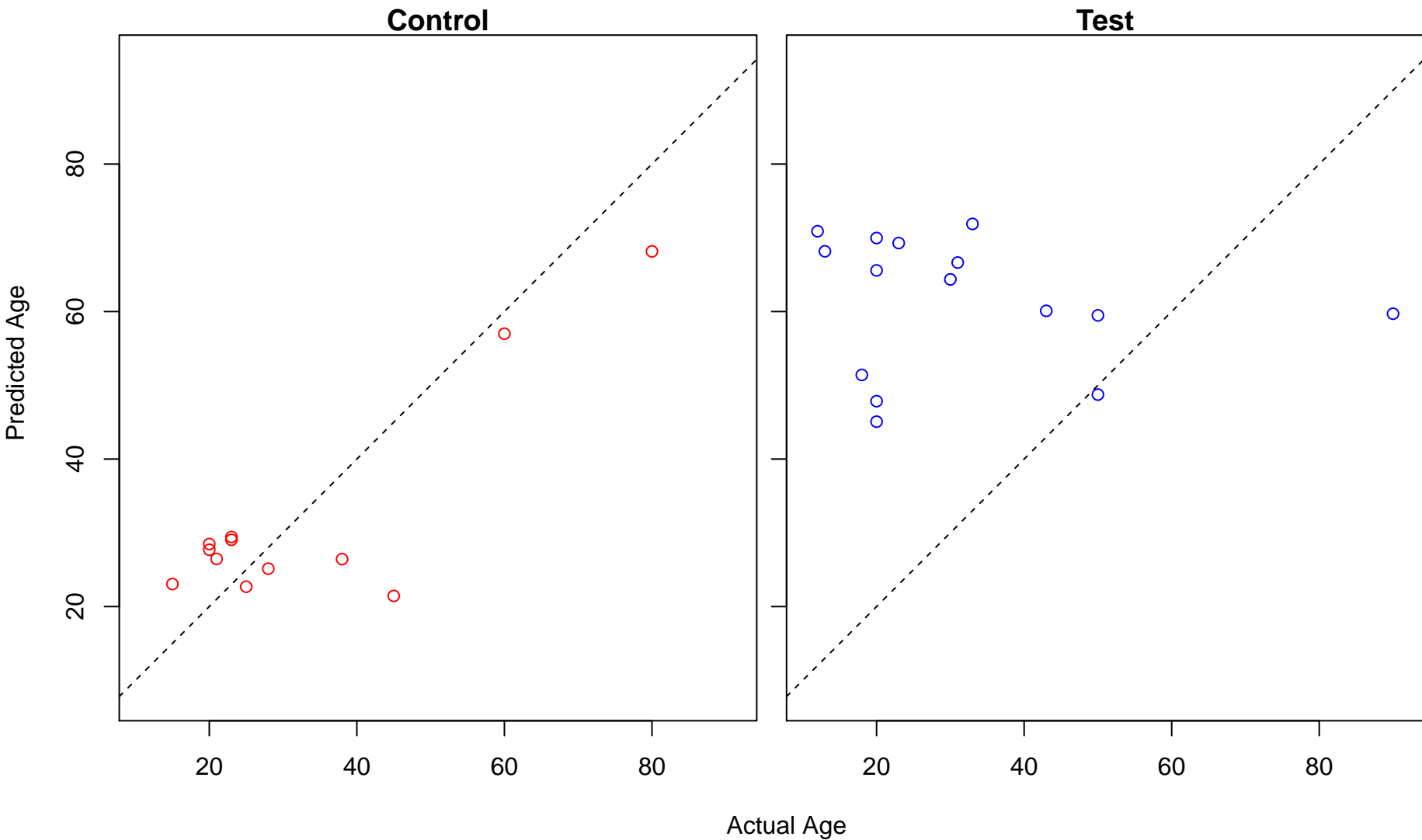
microtubule polymerization (Score: 5.046989)



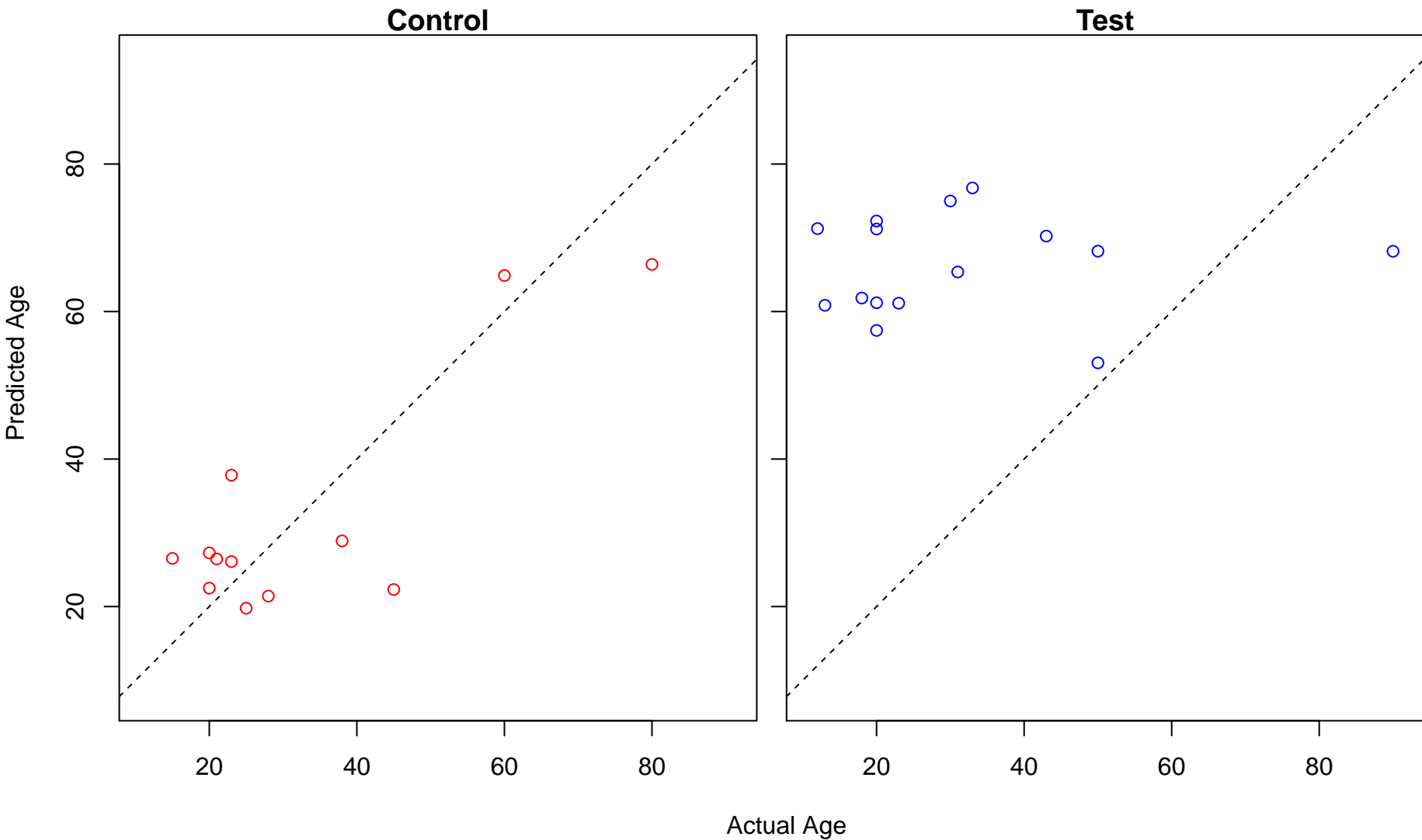
response to macrophage colony-stimulating factor (Score: 5.046520)



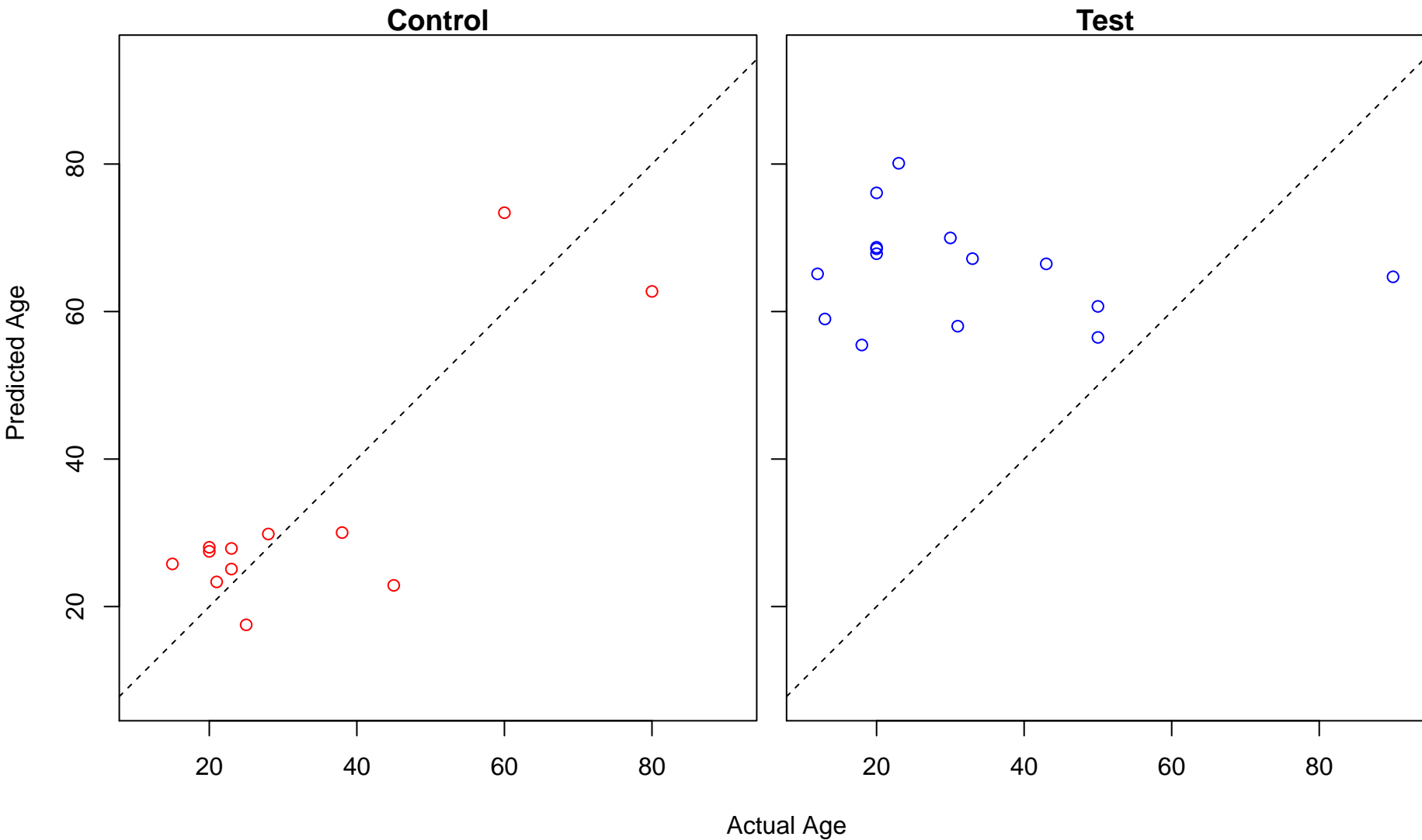
cellular response to macrophage colony-stimulating factor stimulus (Score: 5.046520)



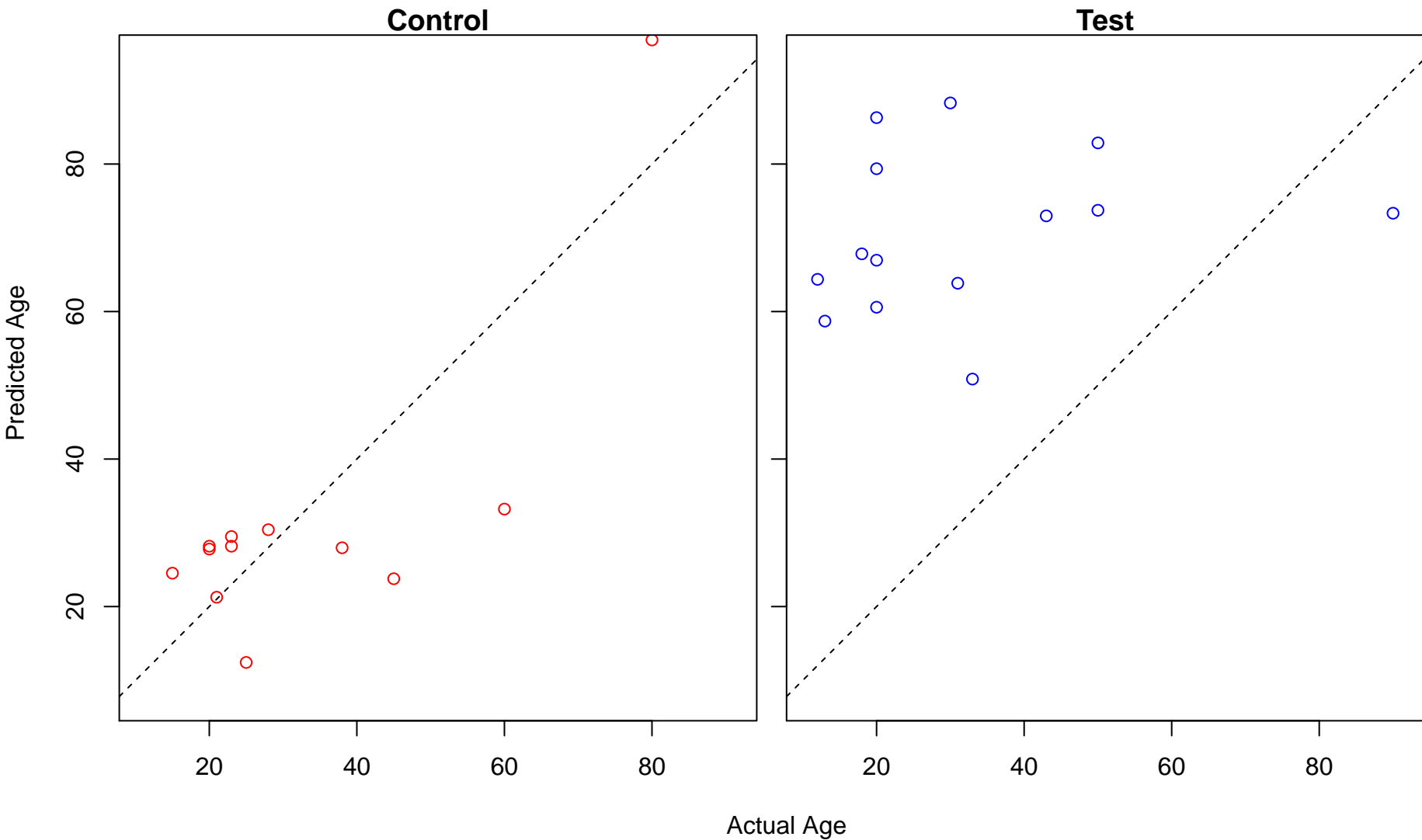
steroid catabolic process (Score: 5.046499)



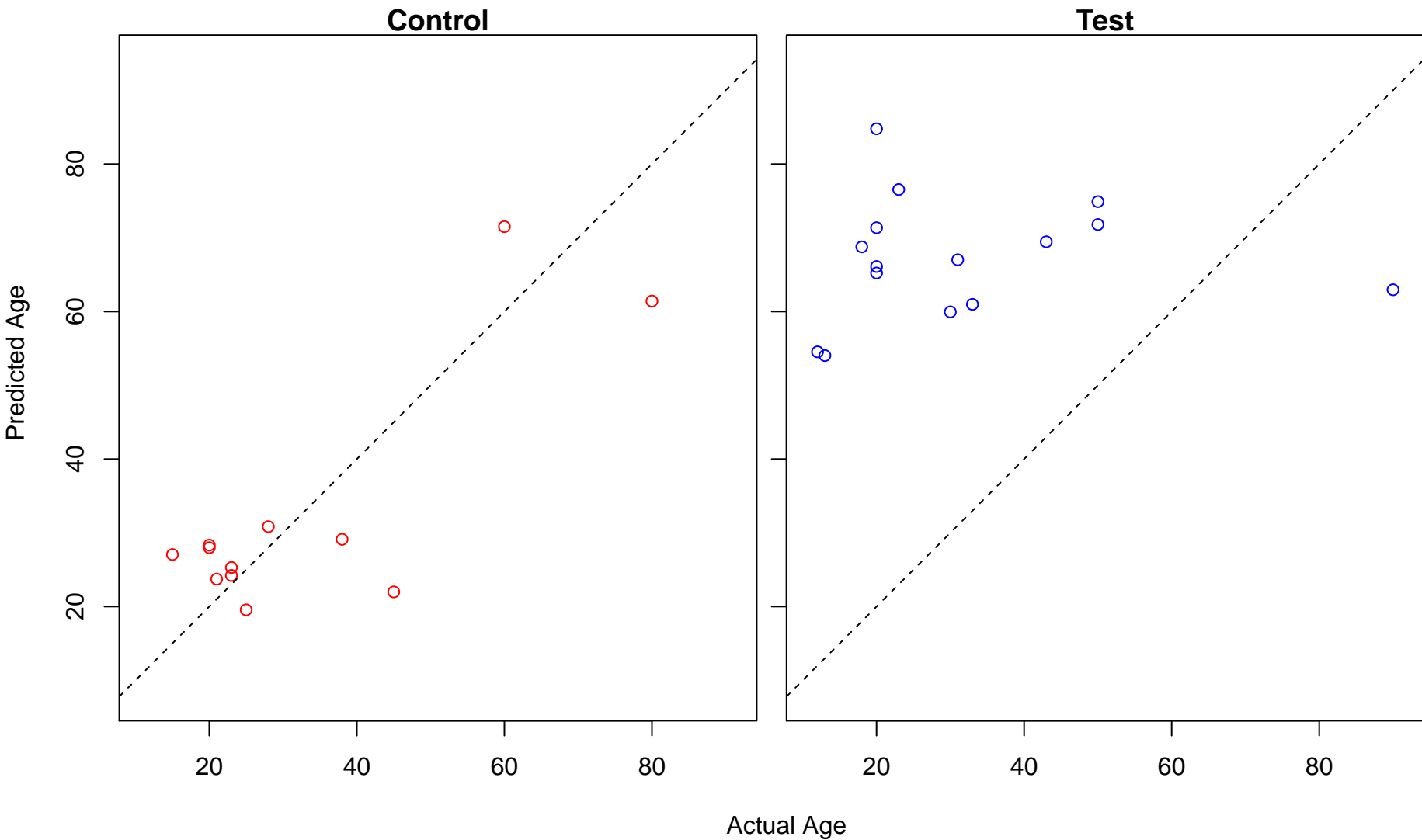
protein polyglutamylation (Score: 5.044710)



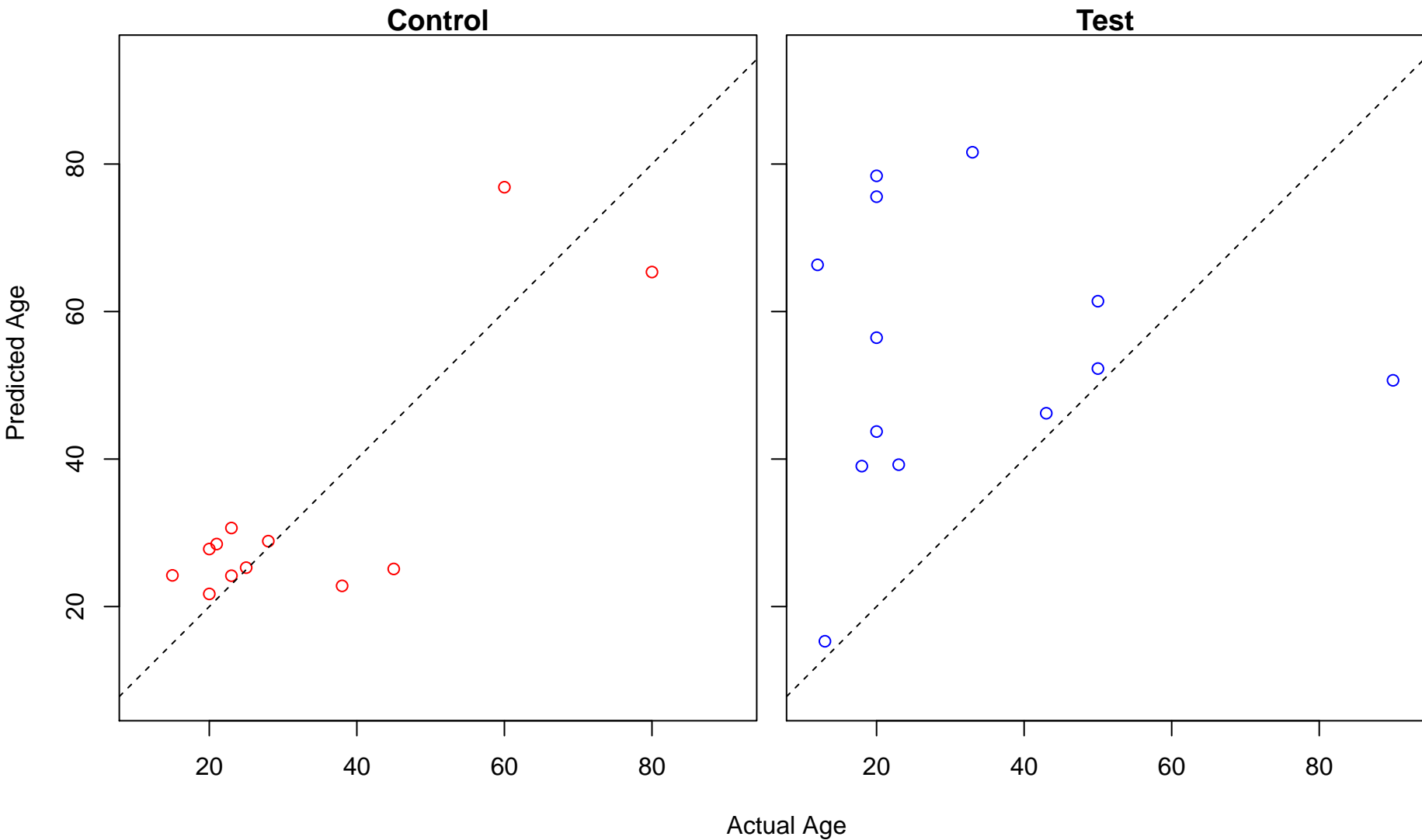
rRNA catabolic process (Score: 5.044033)



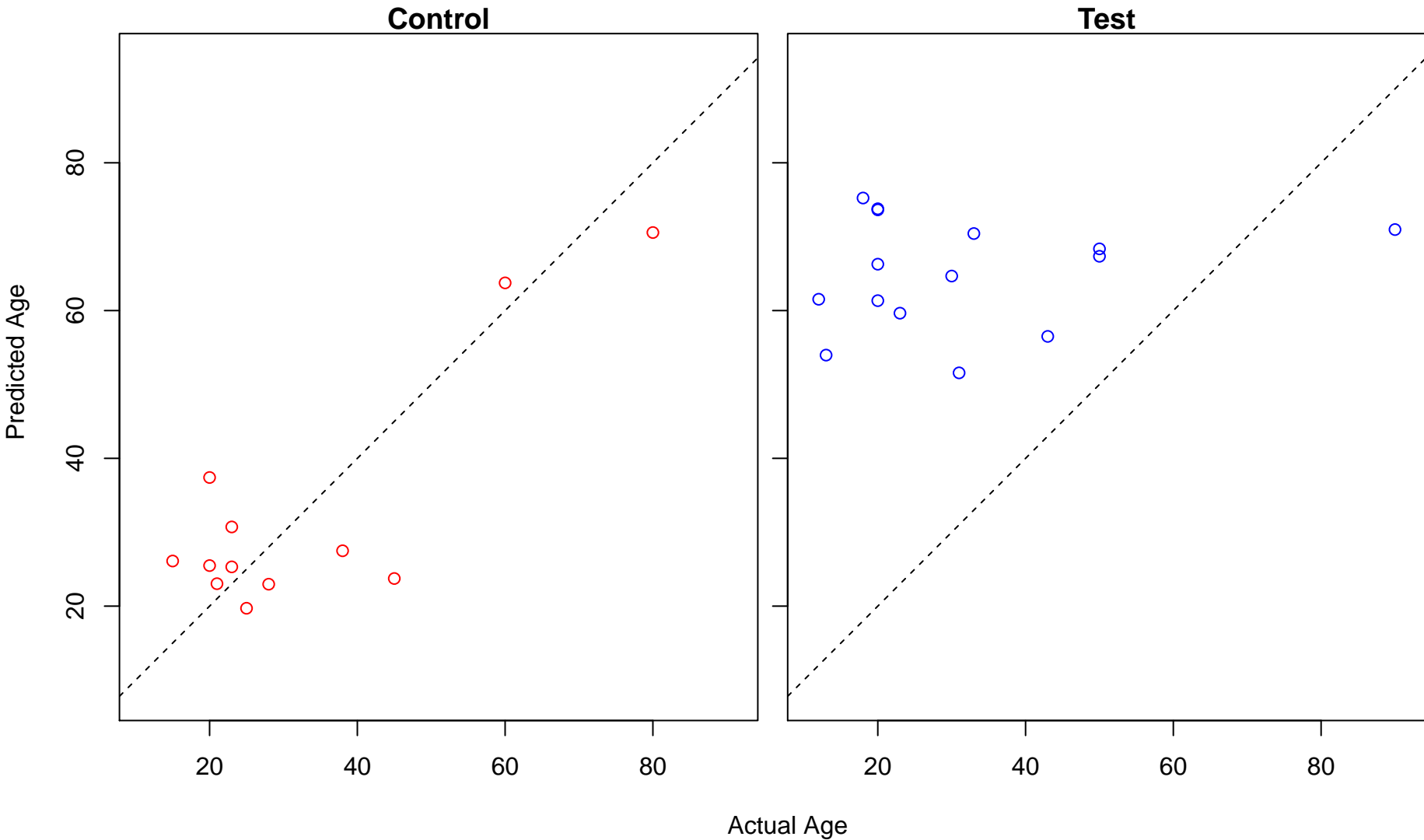
cytosolic calcium ion transport (Score: 5.043862)



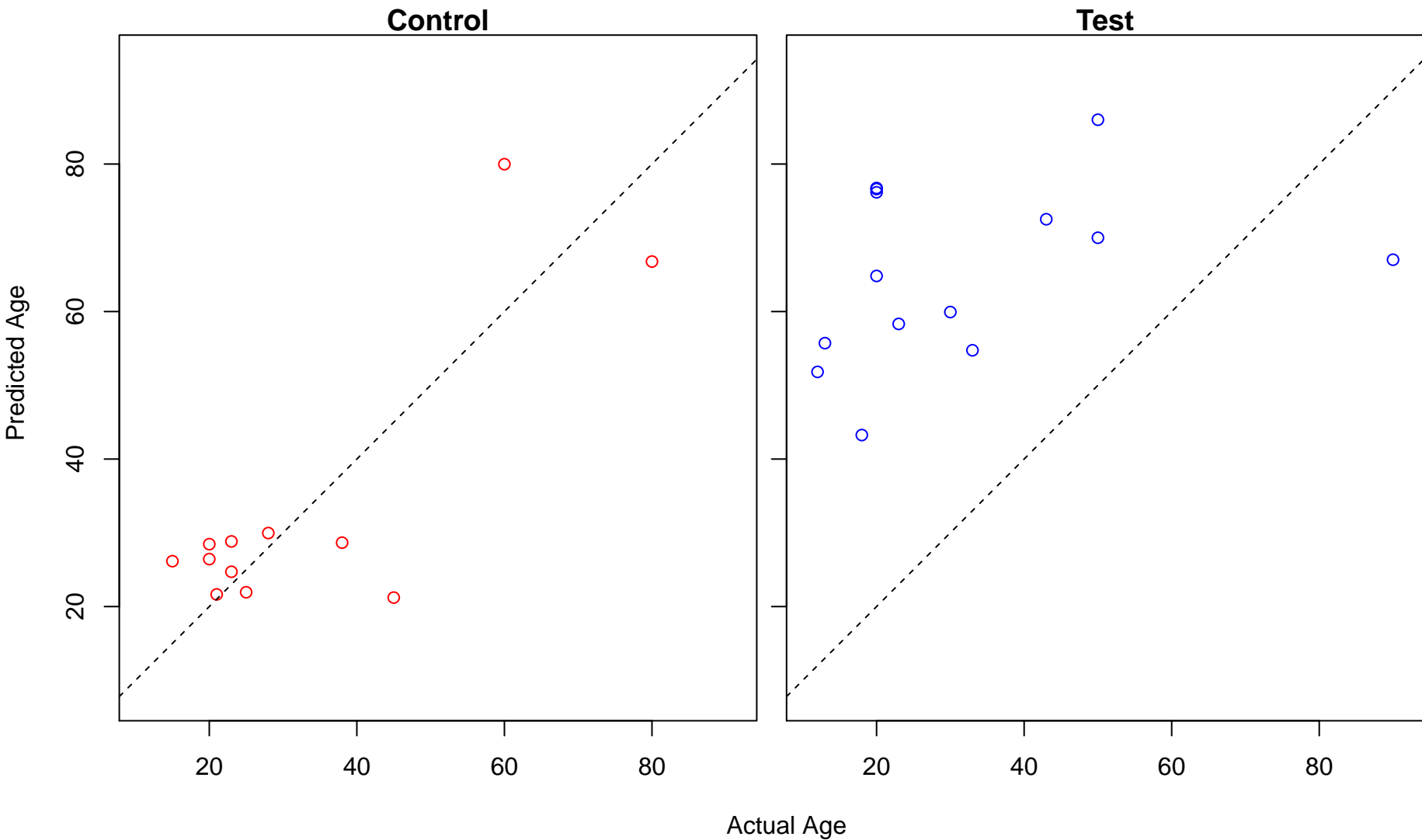
purinergic receptor signaling pathway (Score: 5.042919)



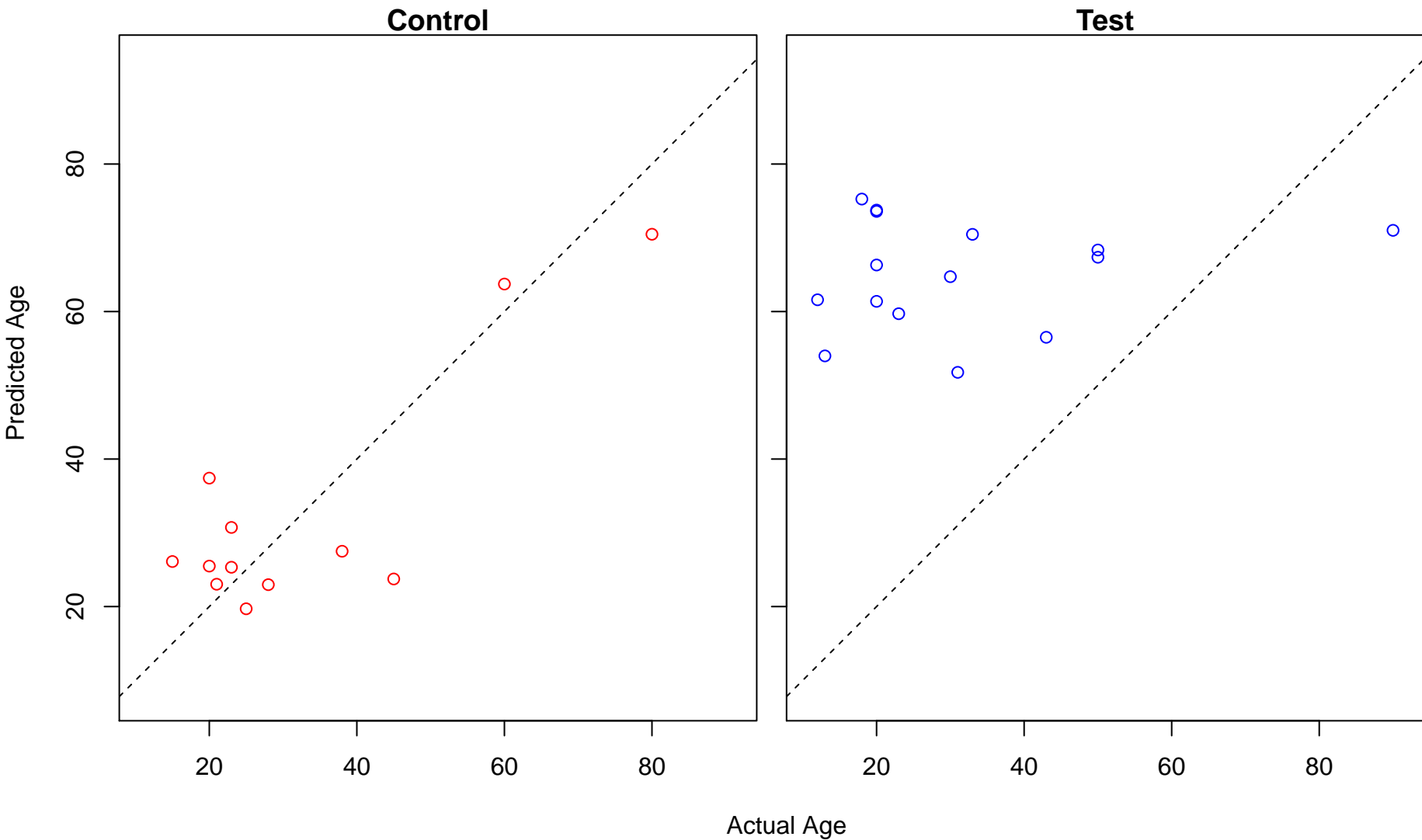
regulation of polysaccharide biosynthetic process (Score: 5.041881)



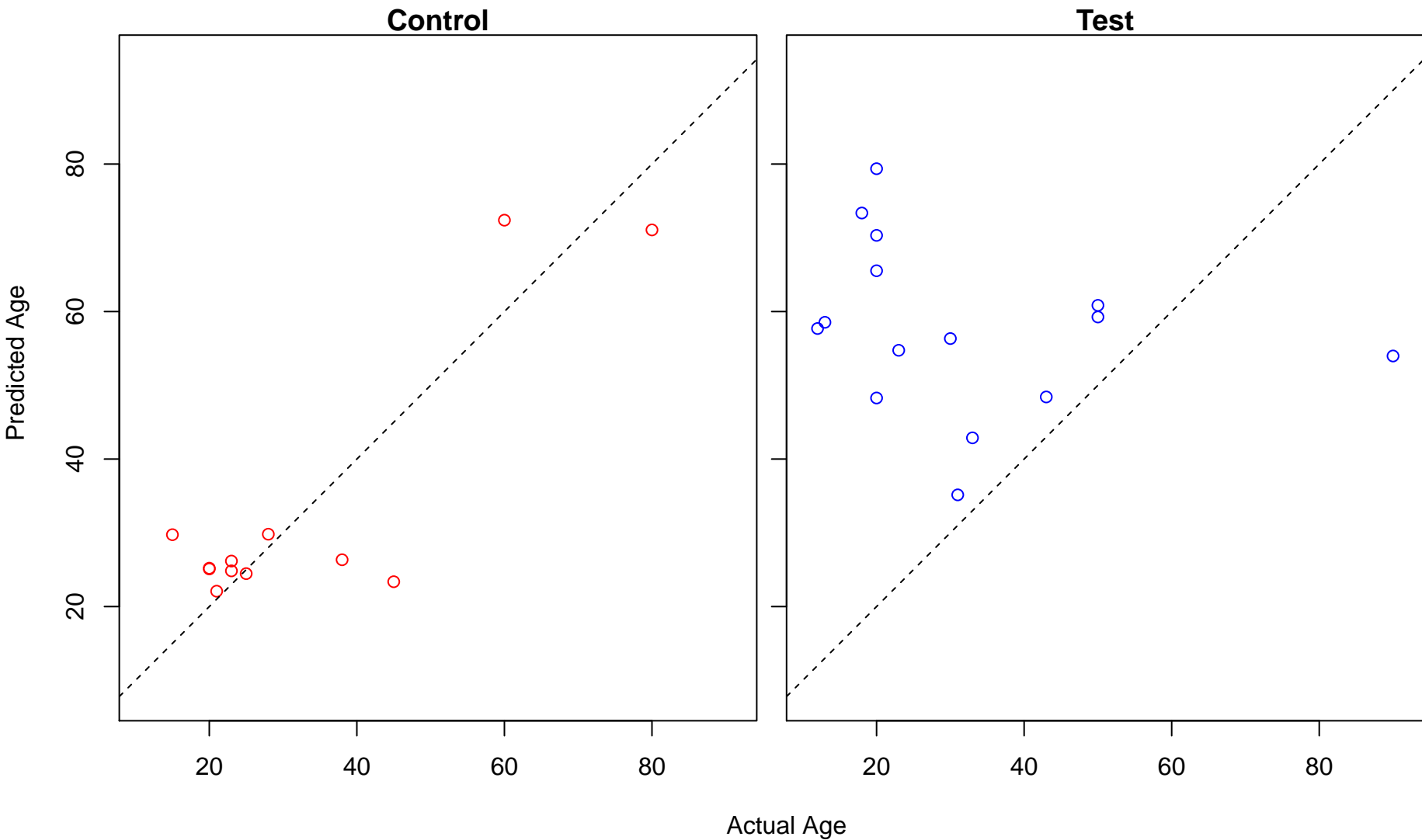
activation of cysteine-type endopeptidase activity (Score: 5.040549)



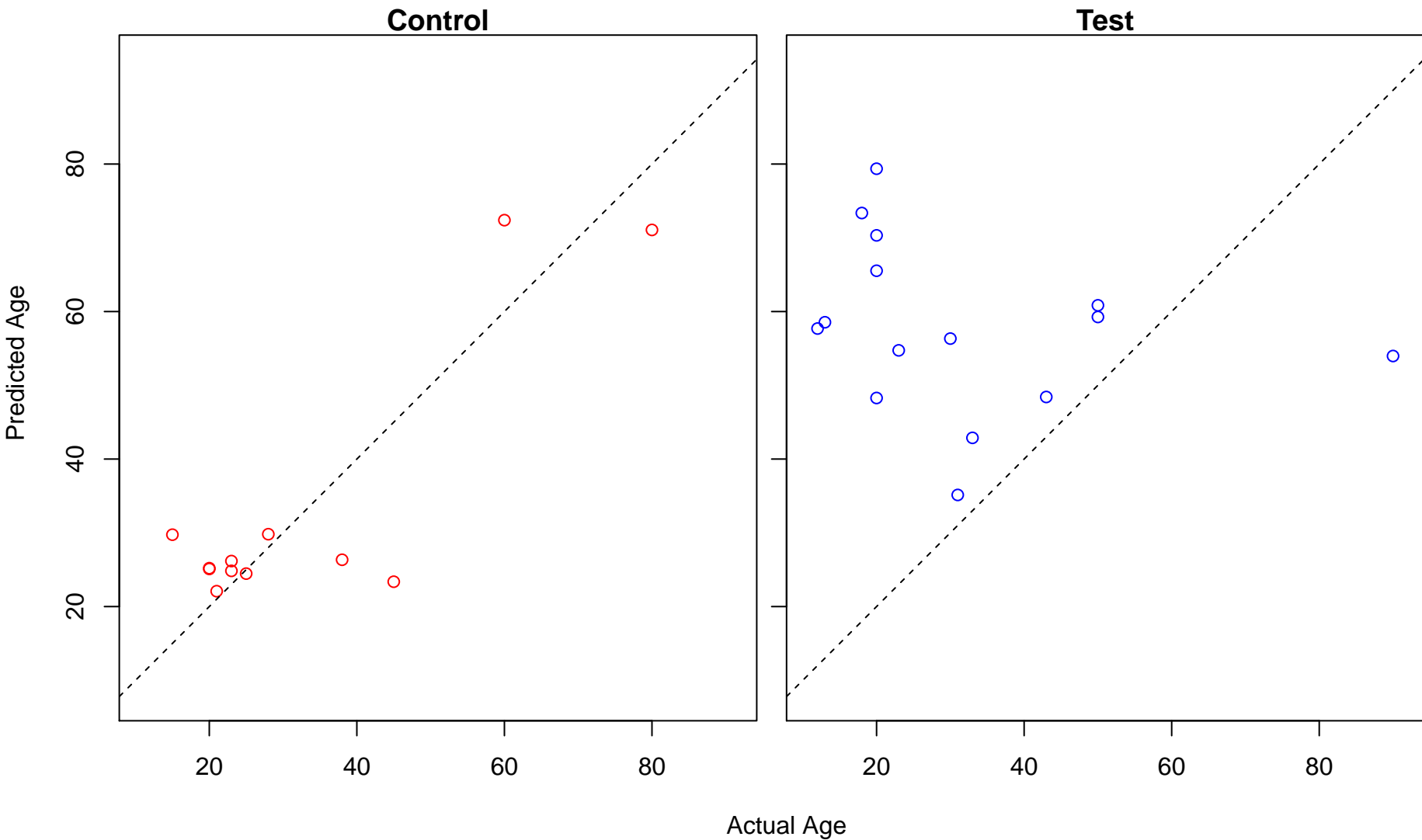
regulation of polysaccharide metabolic process (Score: 5.039763)



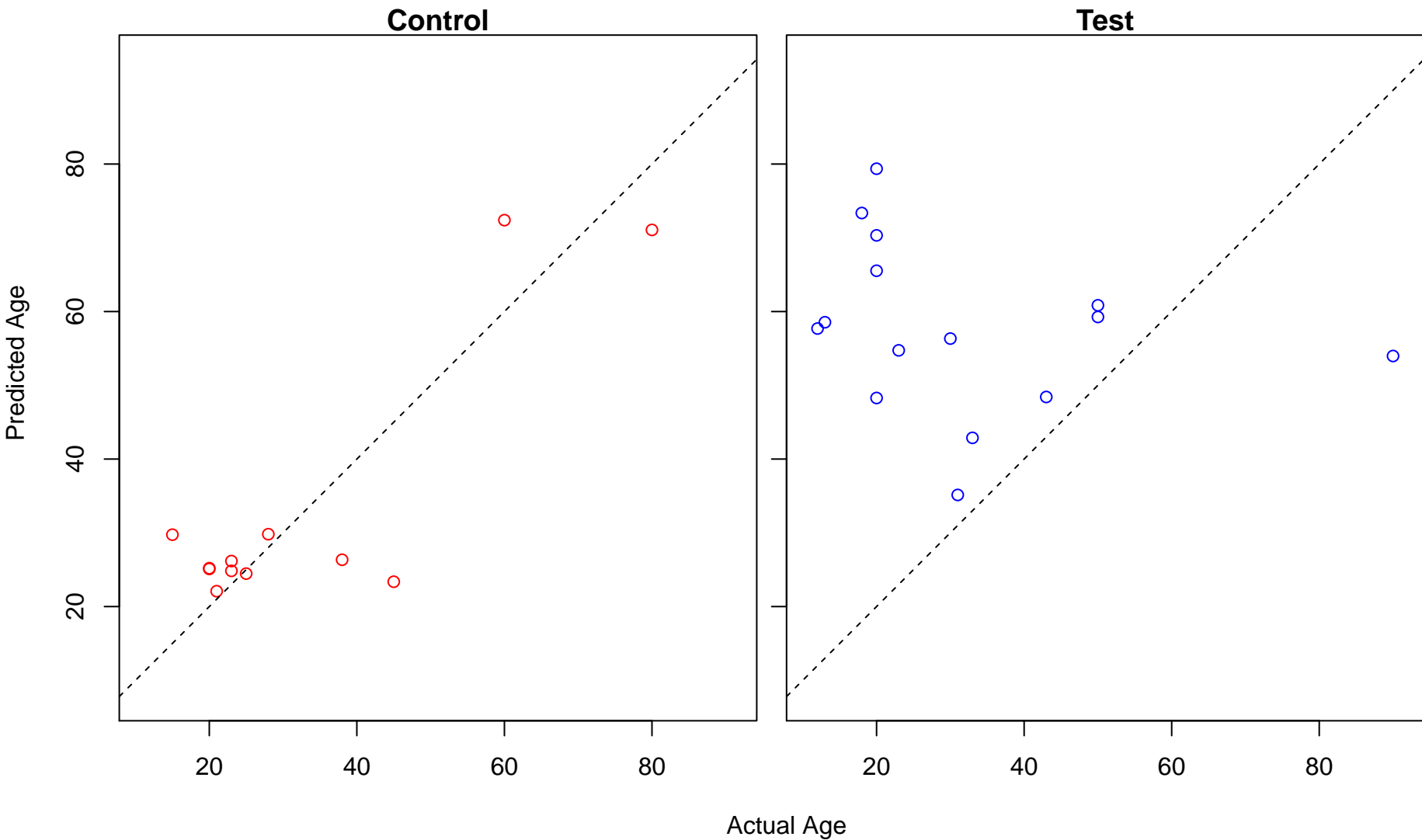
spindle assembly checkpoint (Score: 5.038913)



mitotic spindle assembly checkpoint (Score: 5.038389)

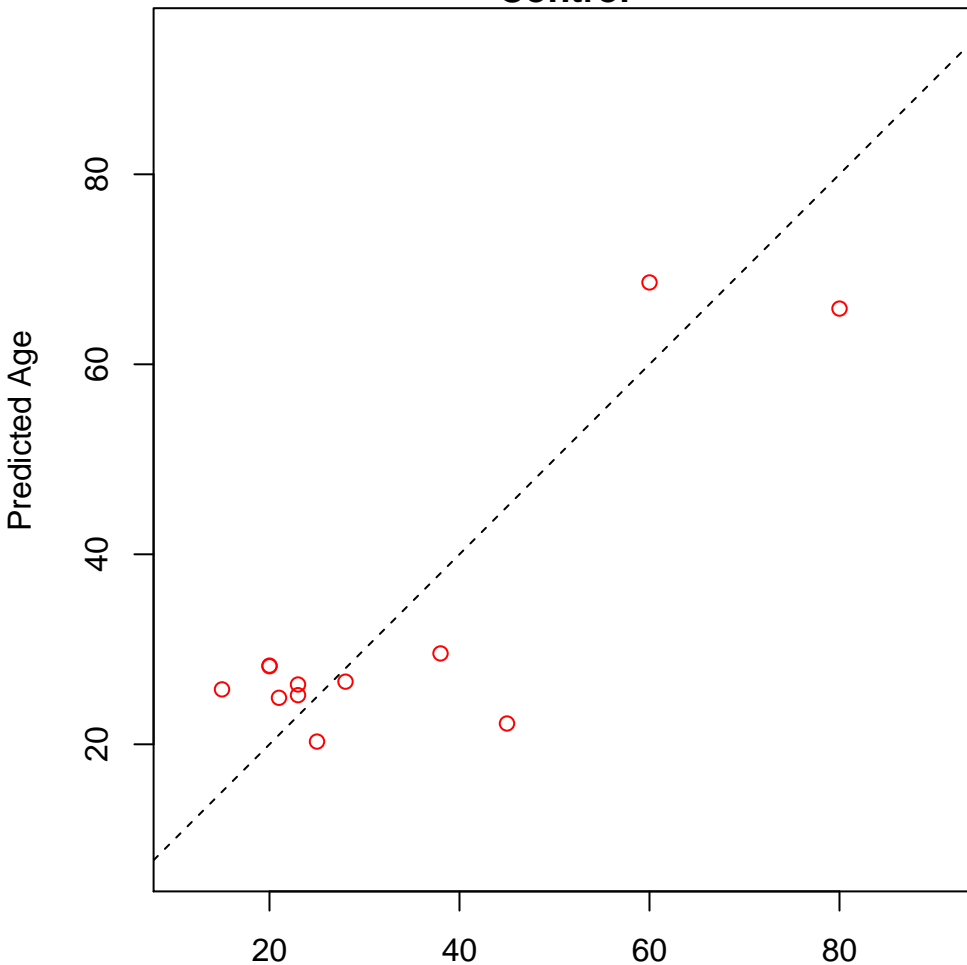


negative regulation of ubiquitin protein ligase activity (Score: 5.038389)

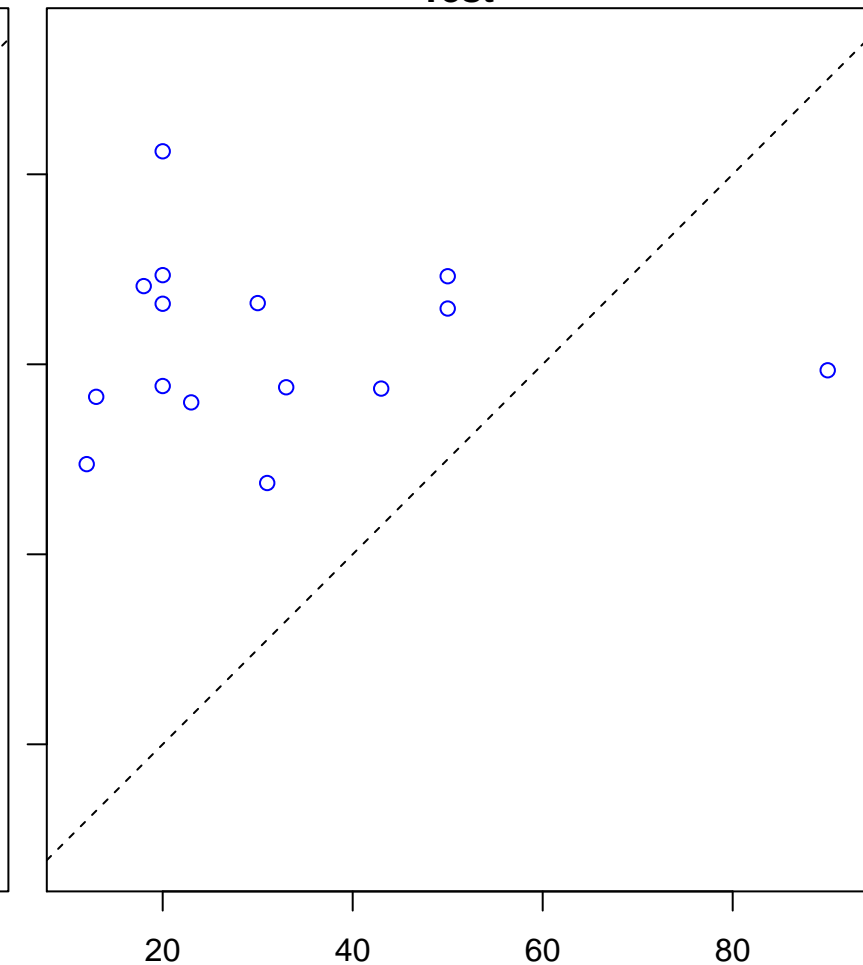


mammary gland epithelium development (Score: 5.038065)

Control

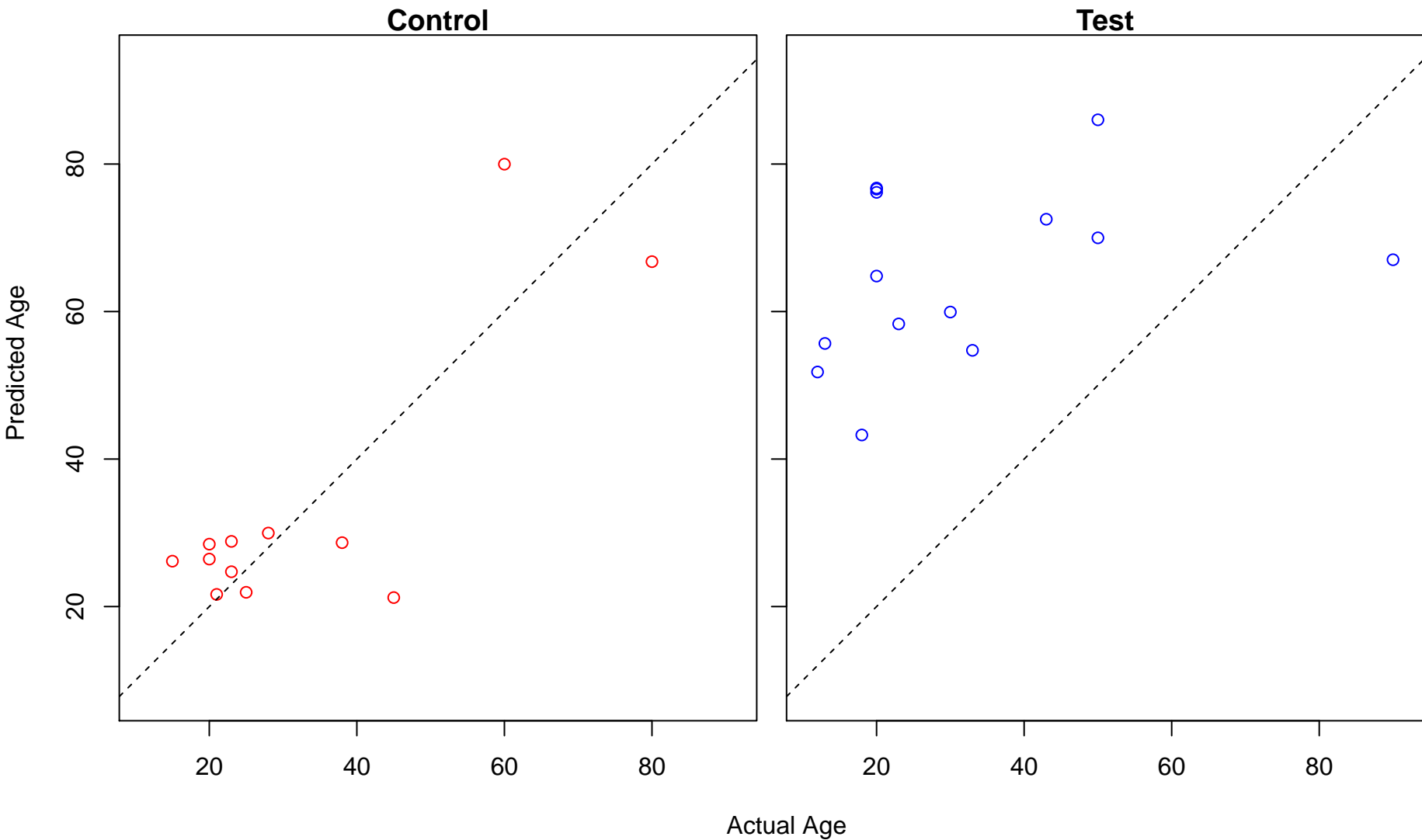


Test

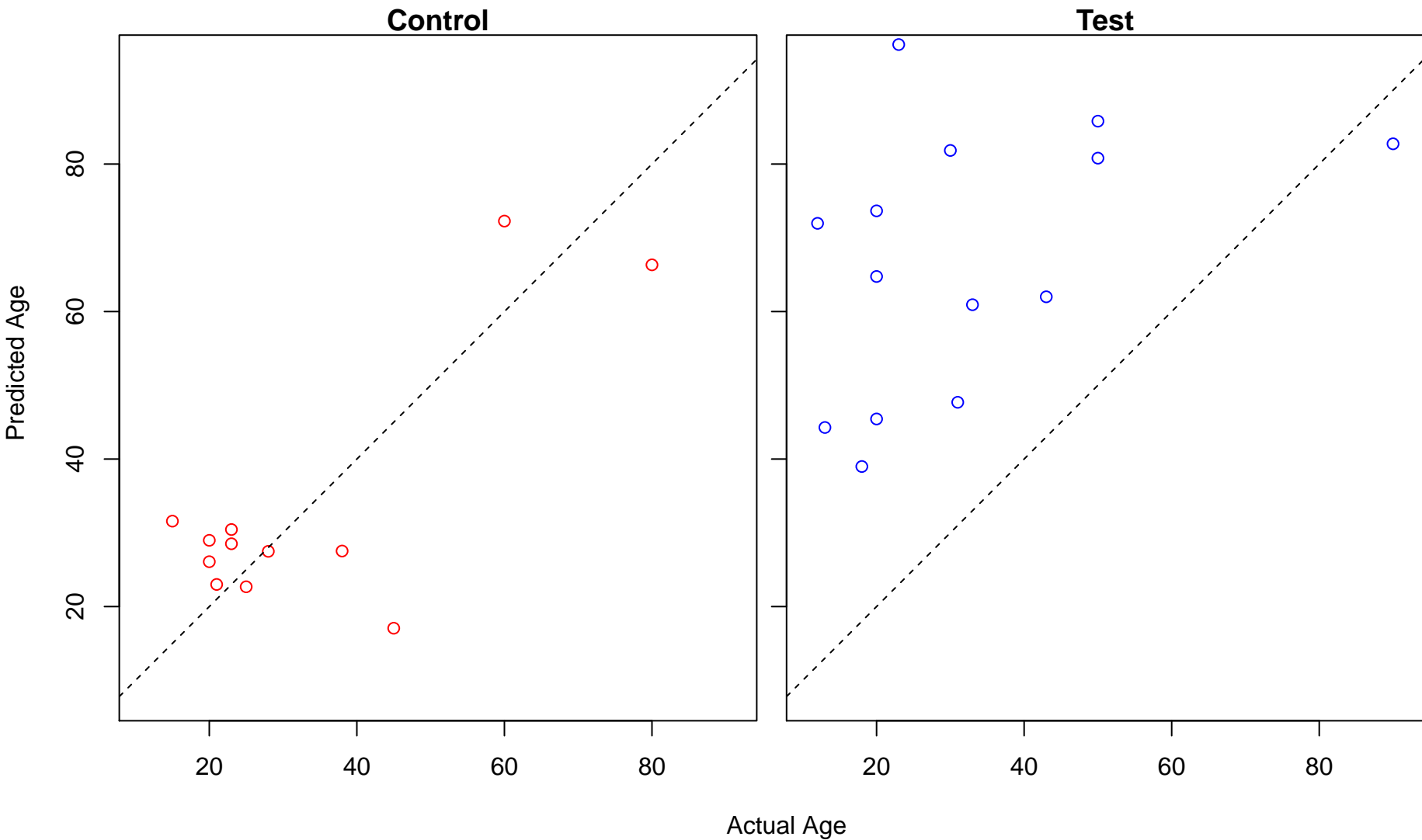


Actual Age

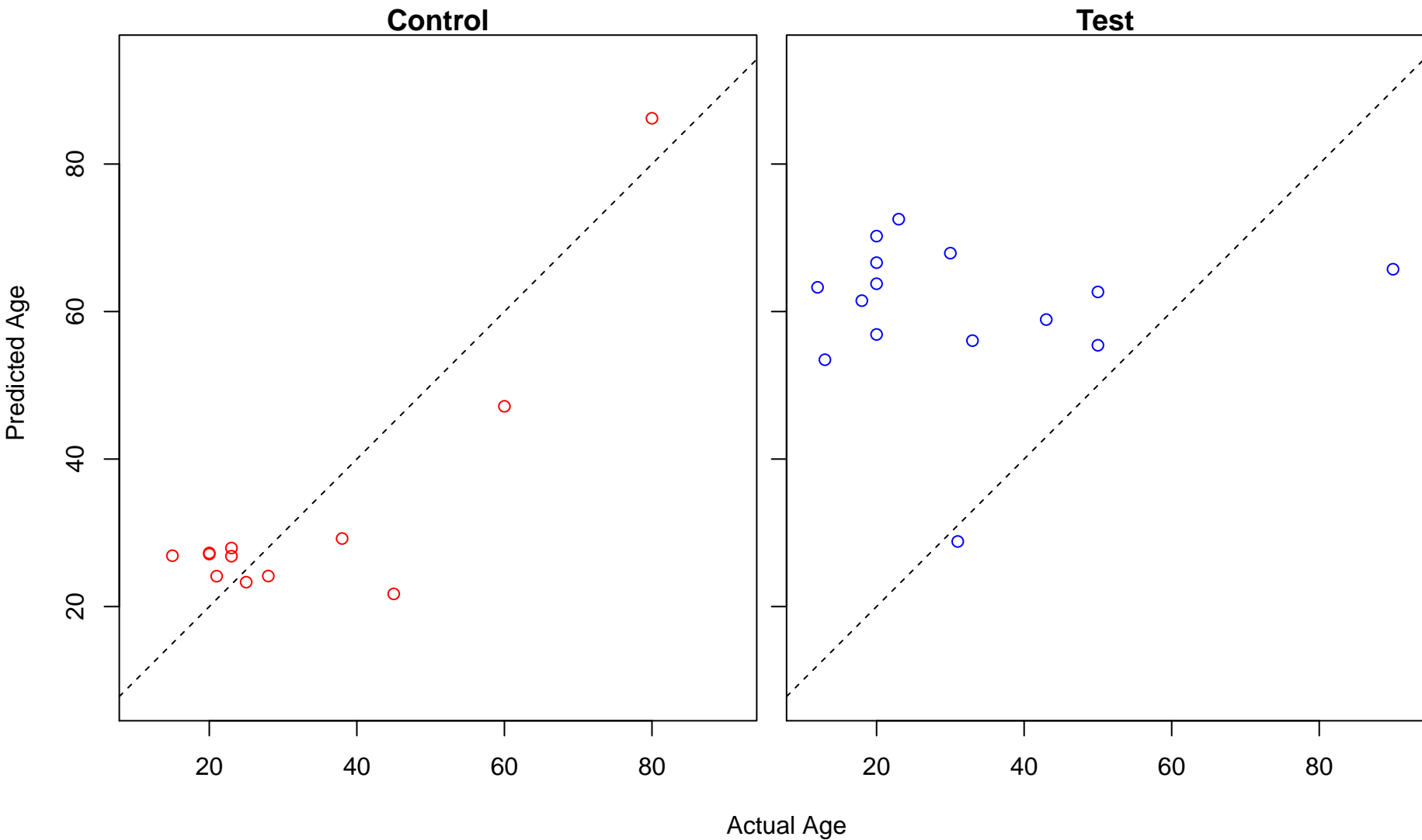
zymogen activation (Score: 5.036564)



ceramide catabolic process (Score: 5.035874)

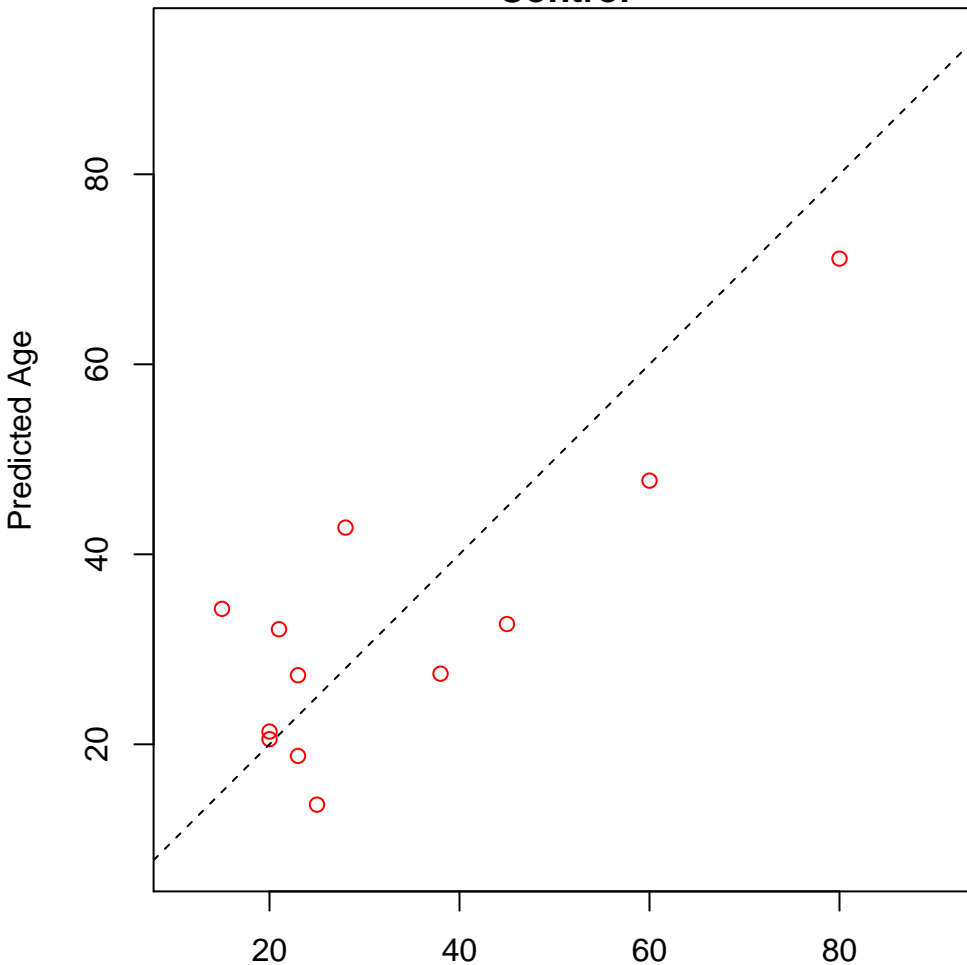


cardiac muscle cell action potential (Score: 5.034459)

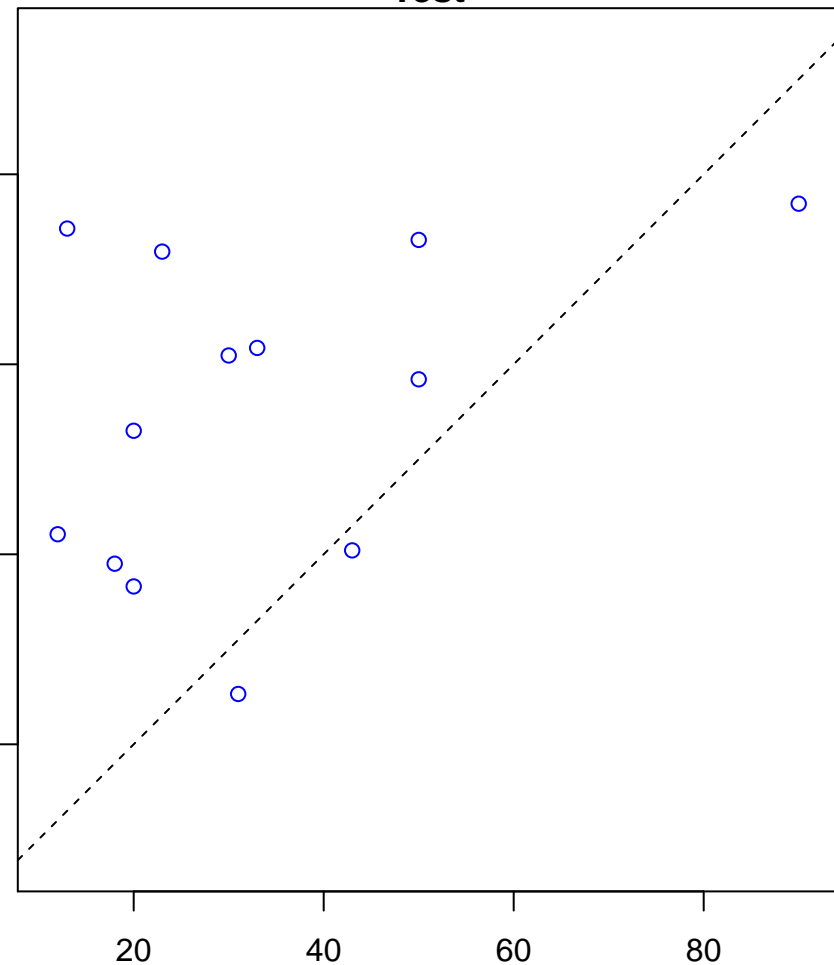


cellular response to toxic substance (Score: 5.033092)

Control

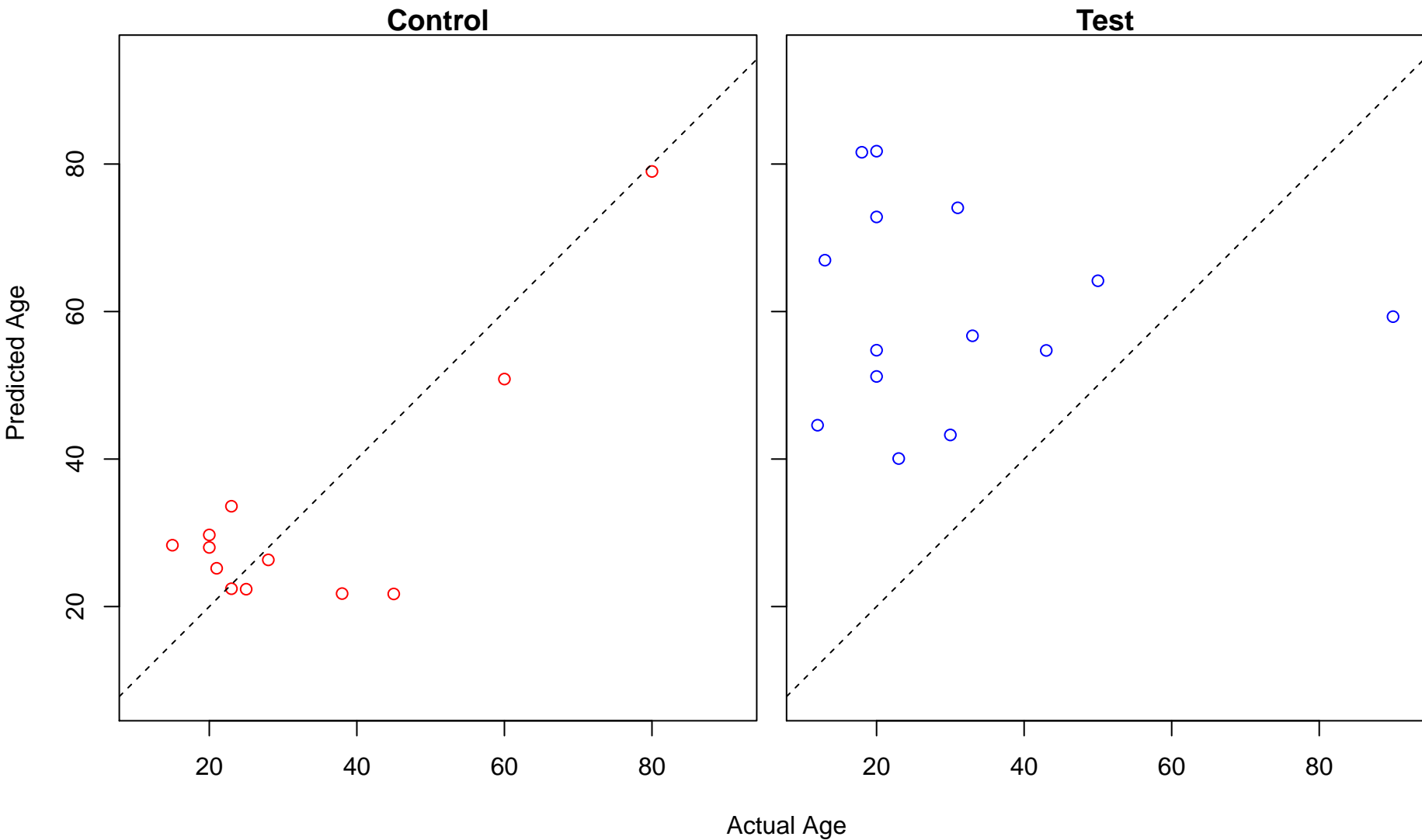


Test

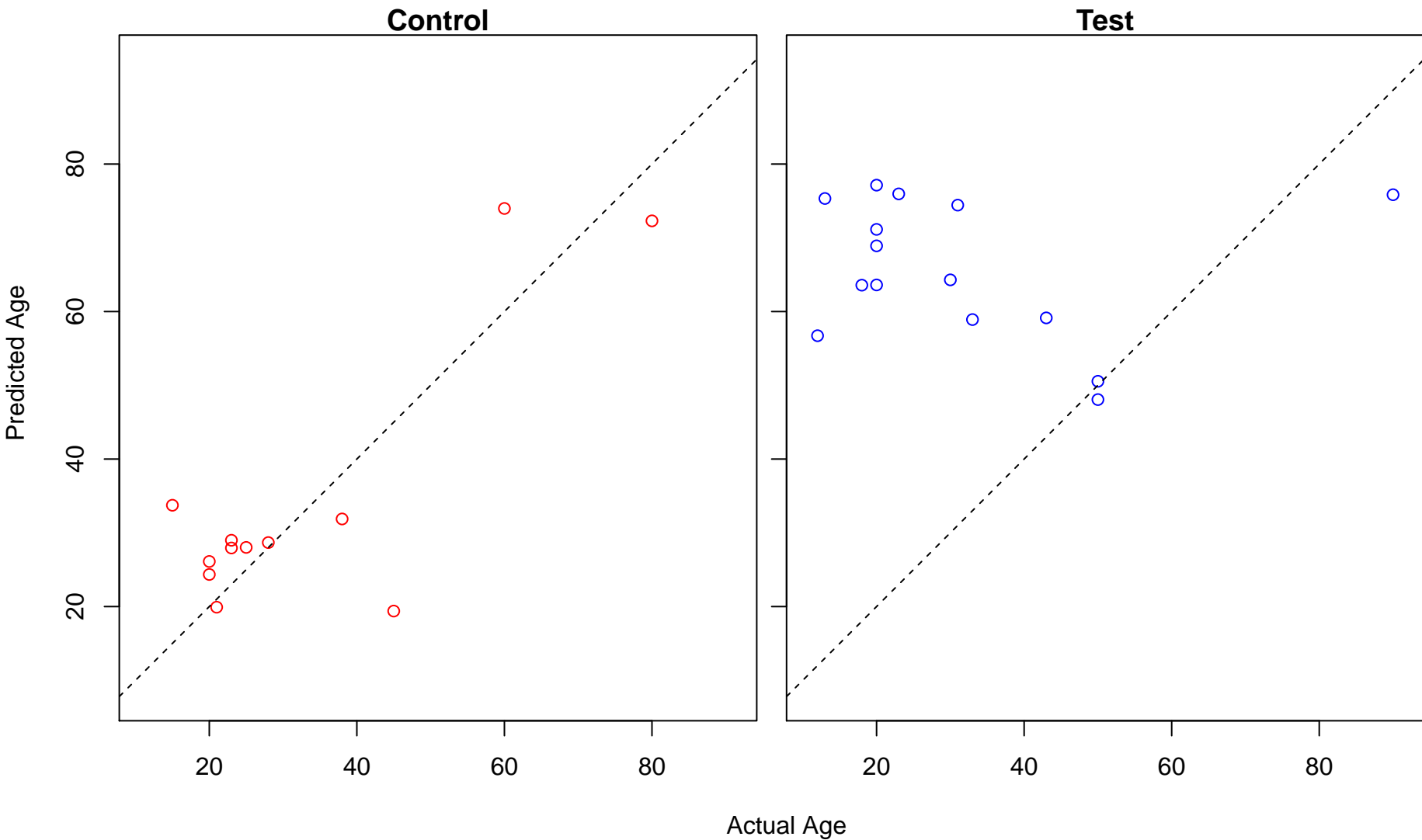


Actual Age

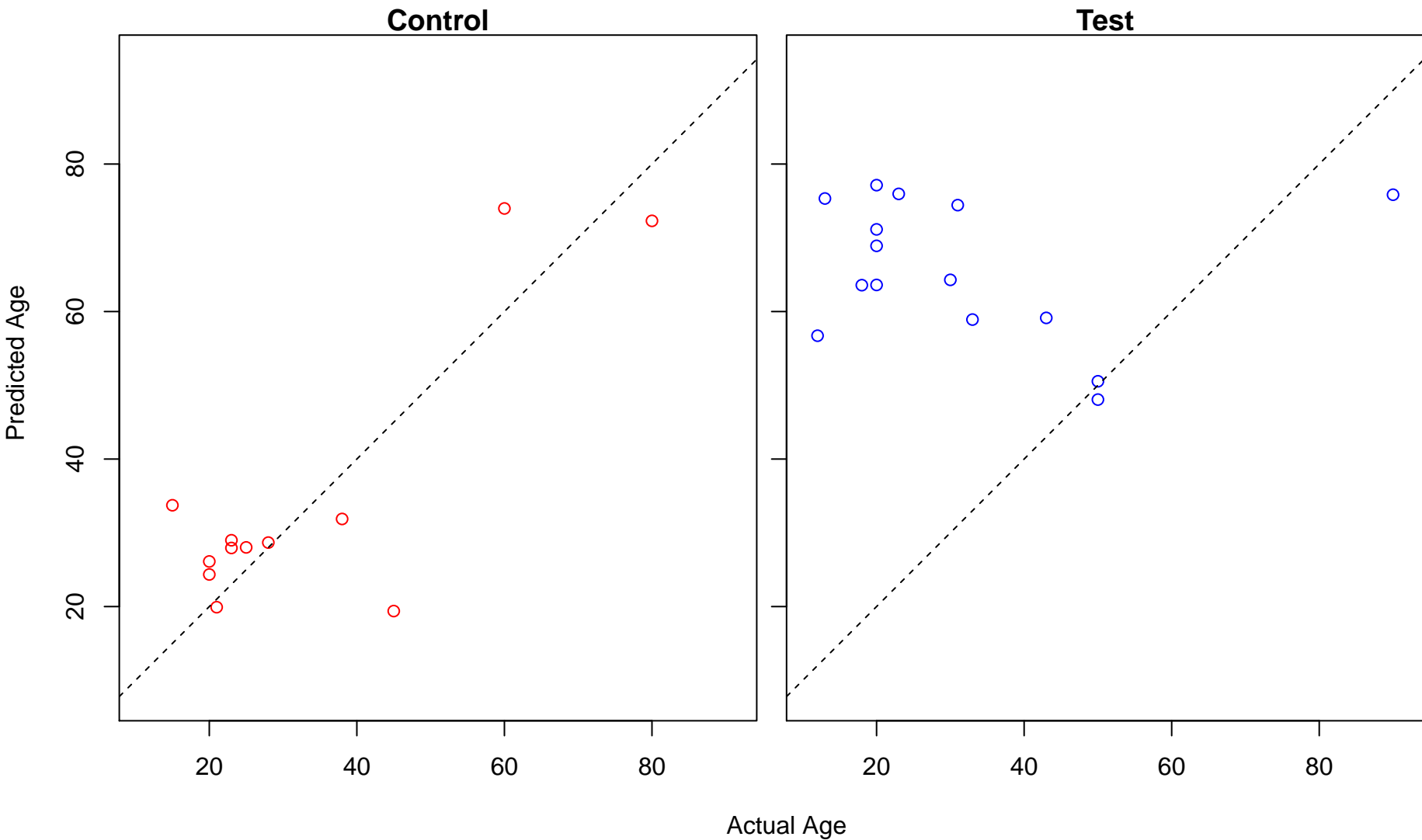
positive regulation of natural killer cell mediated cytotoxicity (Score: 5.032692)



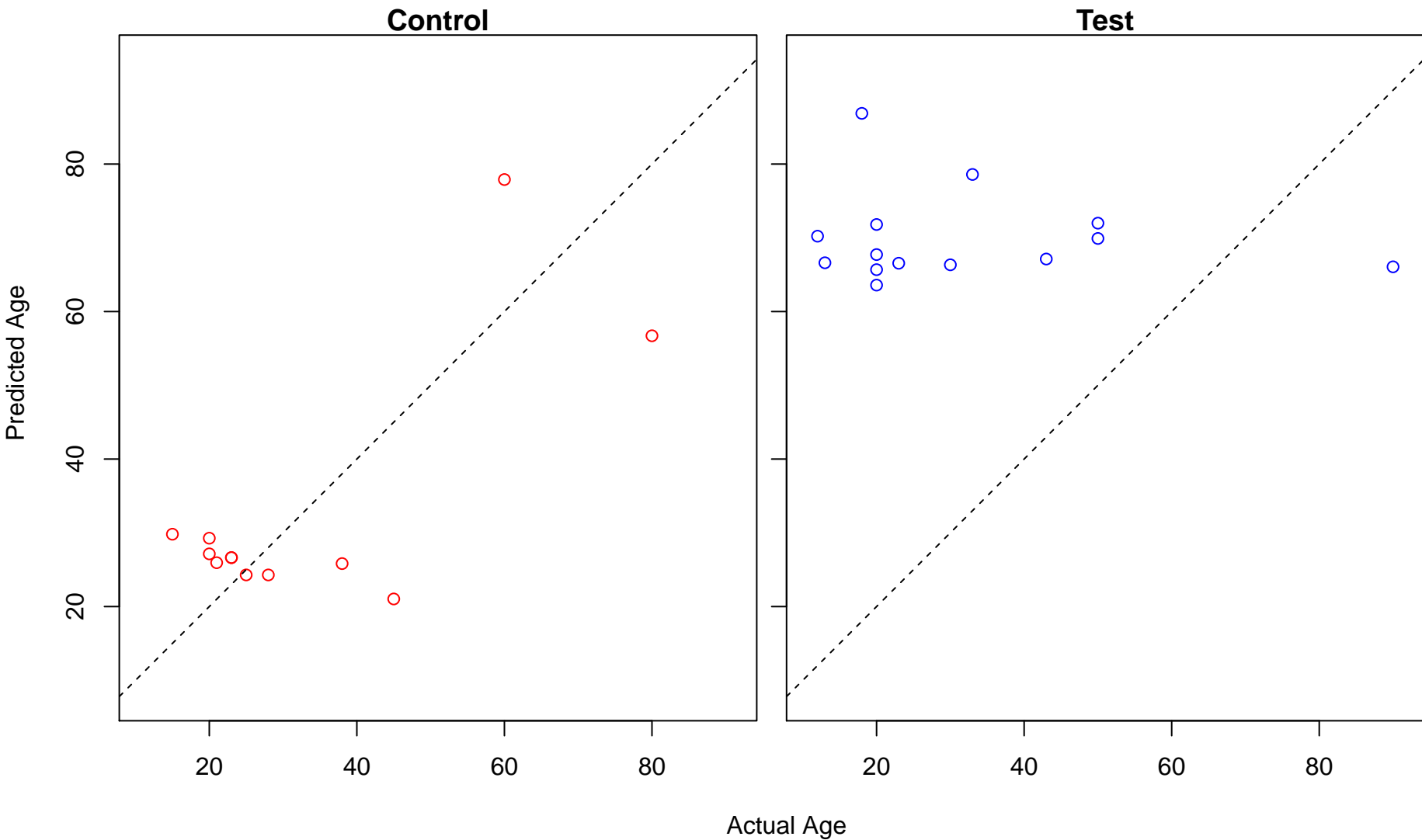
lipoprotein transport (Score: 5.031298)



lipoprotein localization (Score: 5.031298)

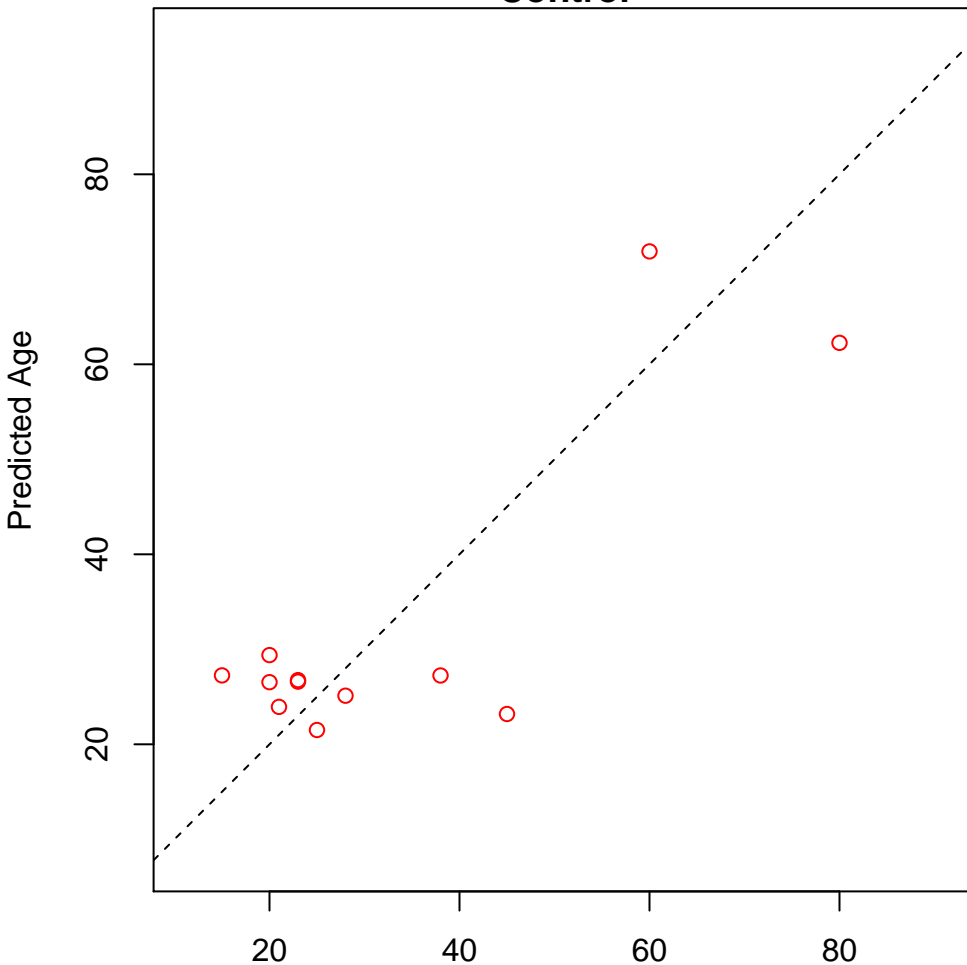


regulation of dendritic cell apoptotic process (Score: 5.030562)

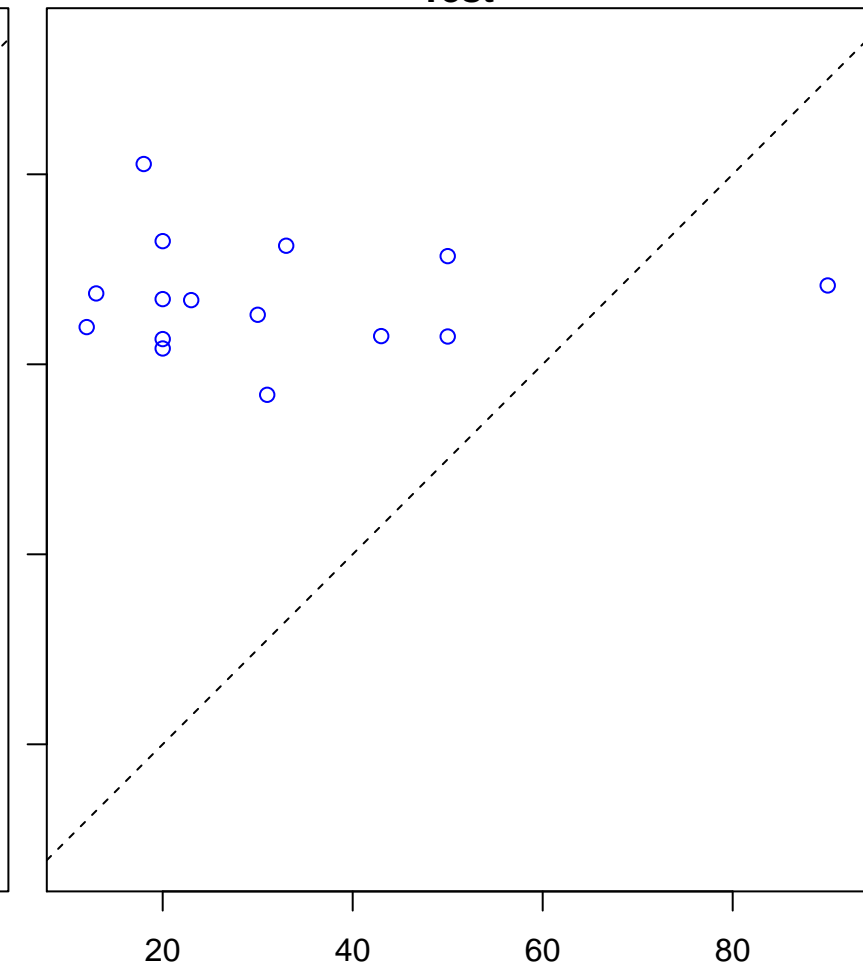


hematopoietic stem cell proliferation (Score: 5.029233)

Control



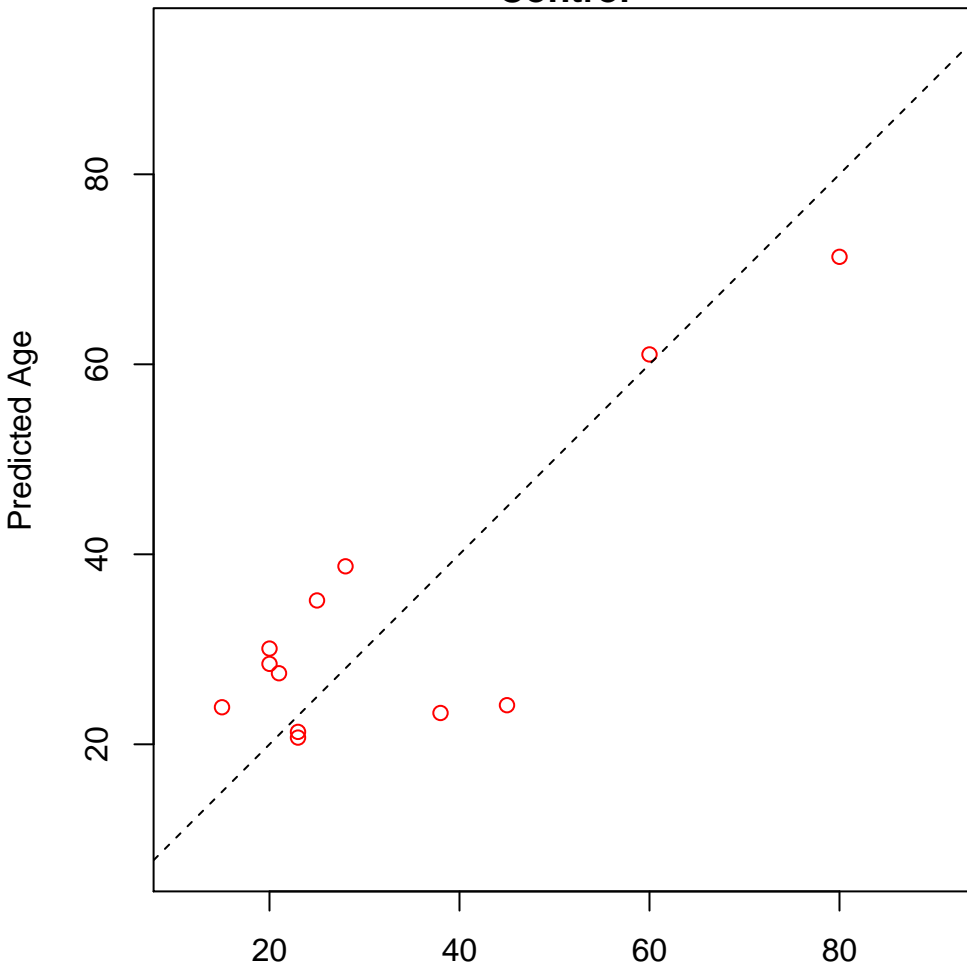
Test



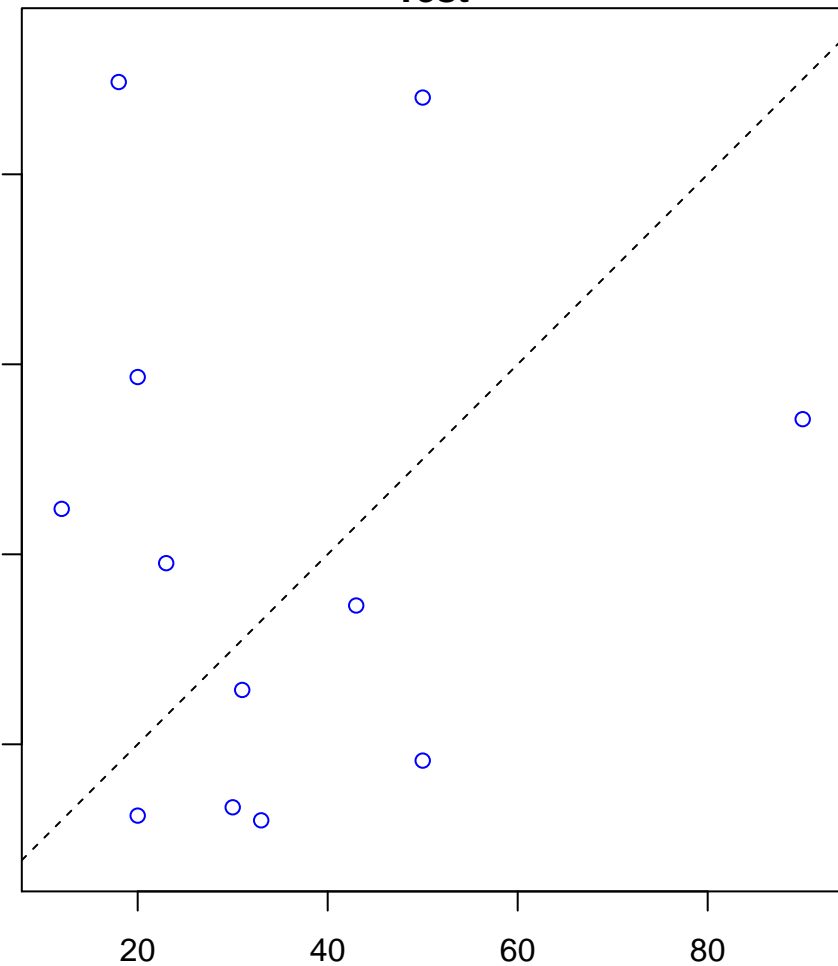
Actual Age

hydrogen peroxide metabolic process (Score: 5.028371)

Control

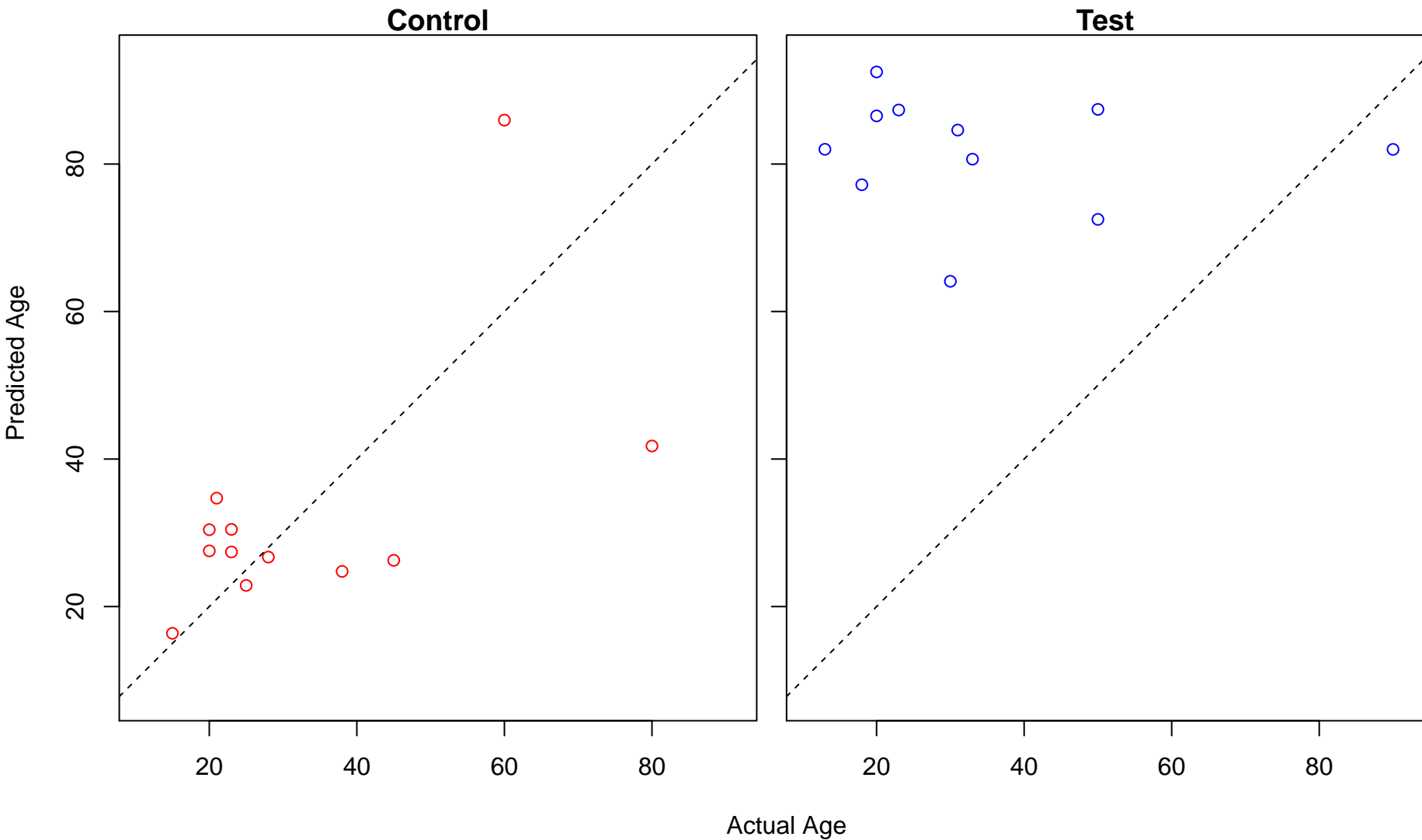


Test

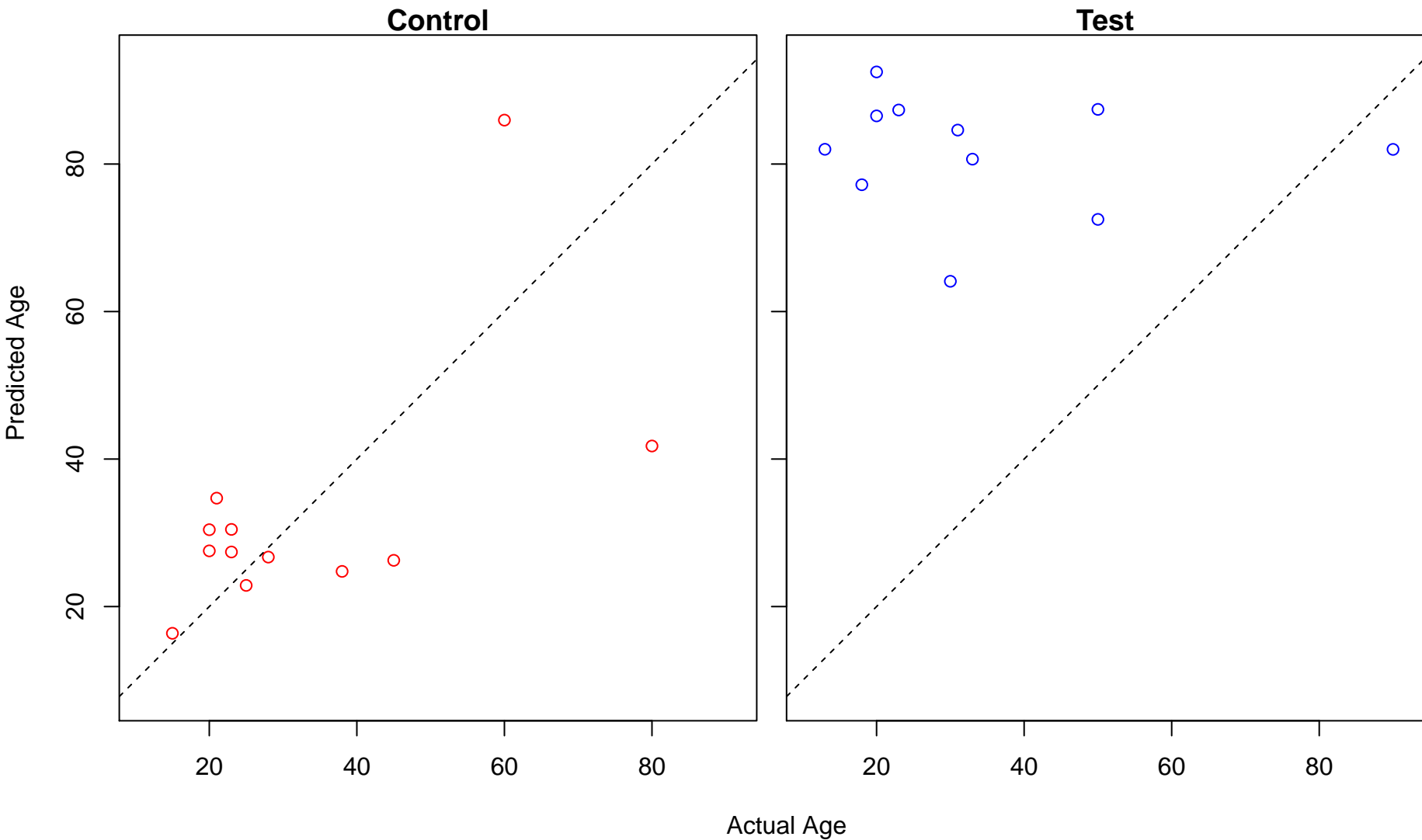


Actual Age

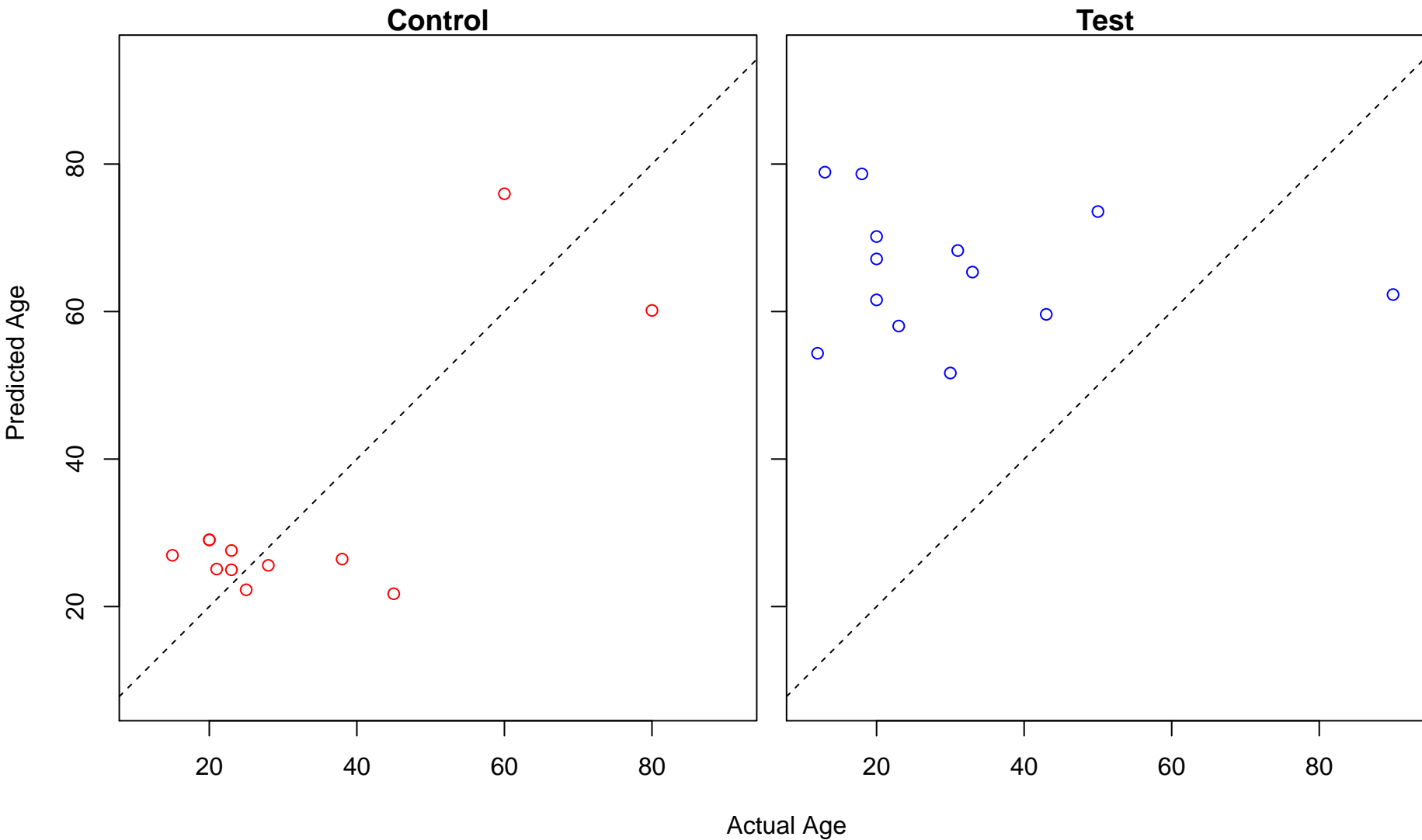
detection of light stimulus involved in visual perception (Score: 5.026182)



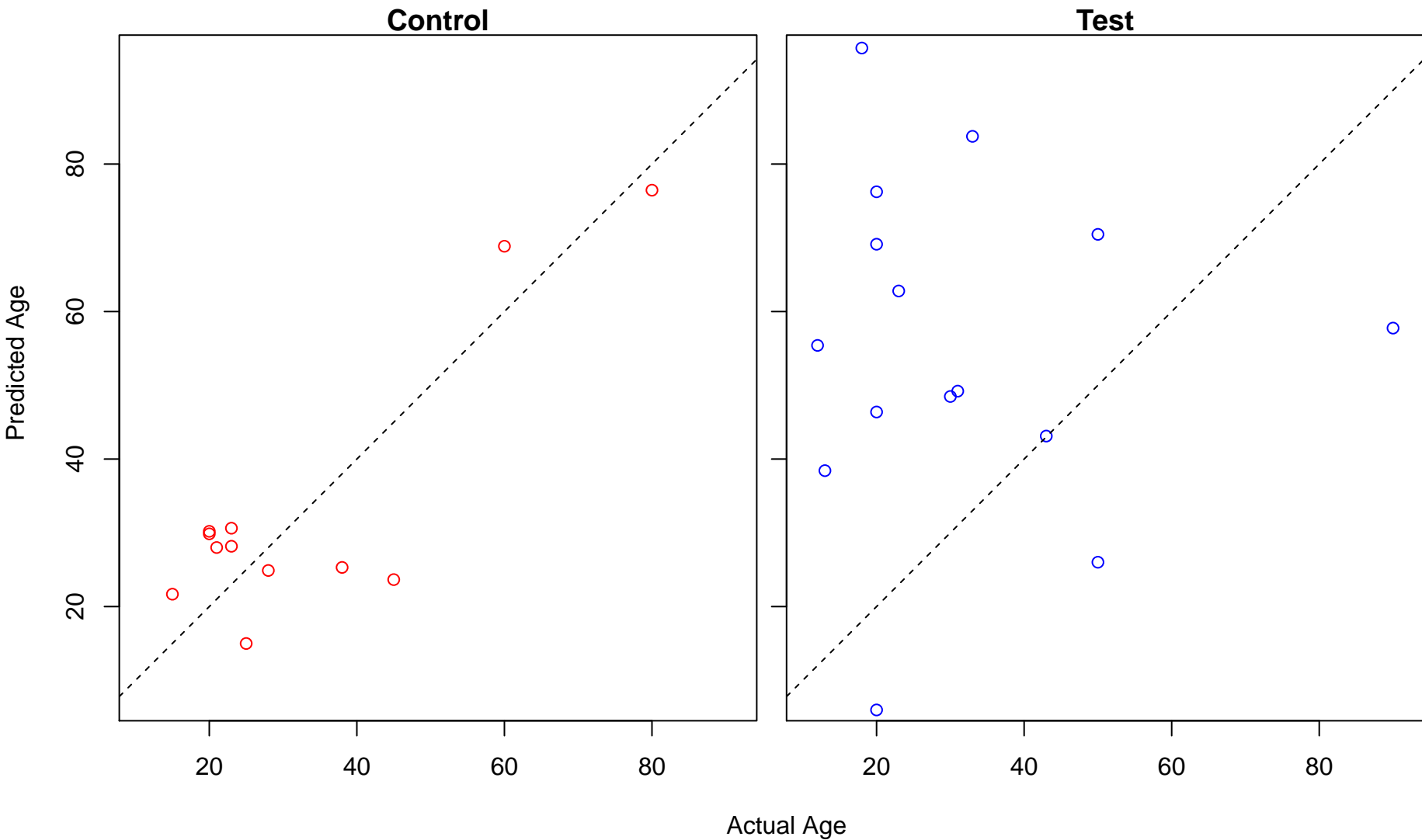
detection of light stimulus involved in sensory perception (Score: 5.026182)



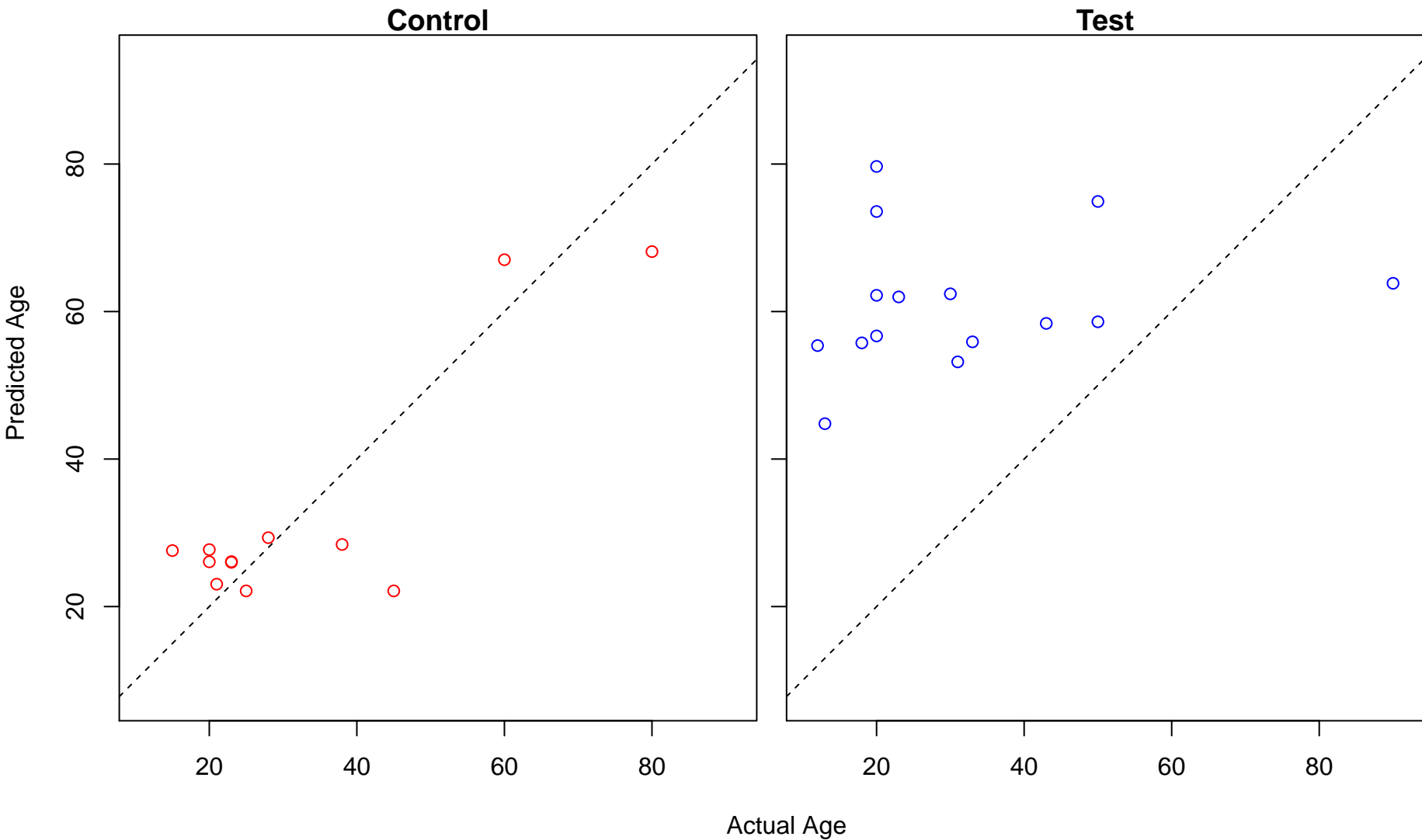
membrane raft organization (Score: 5.025244)



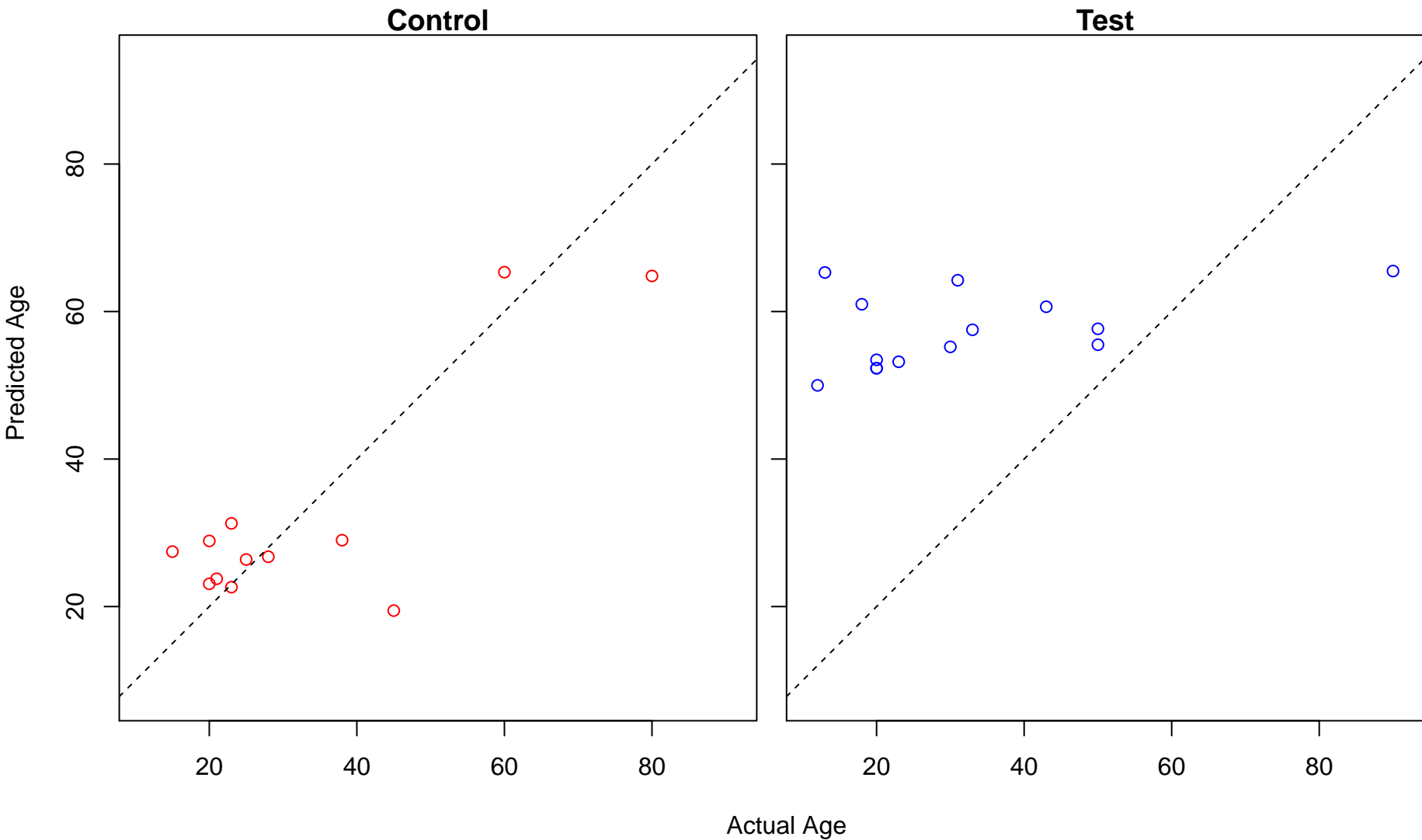
telomere maintenance (Score: 5.023645)



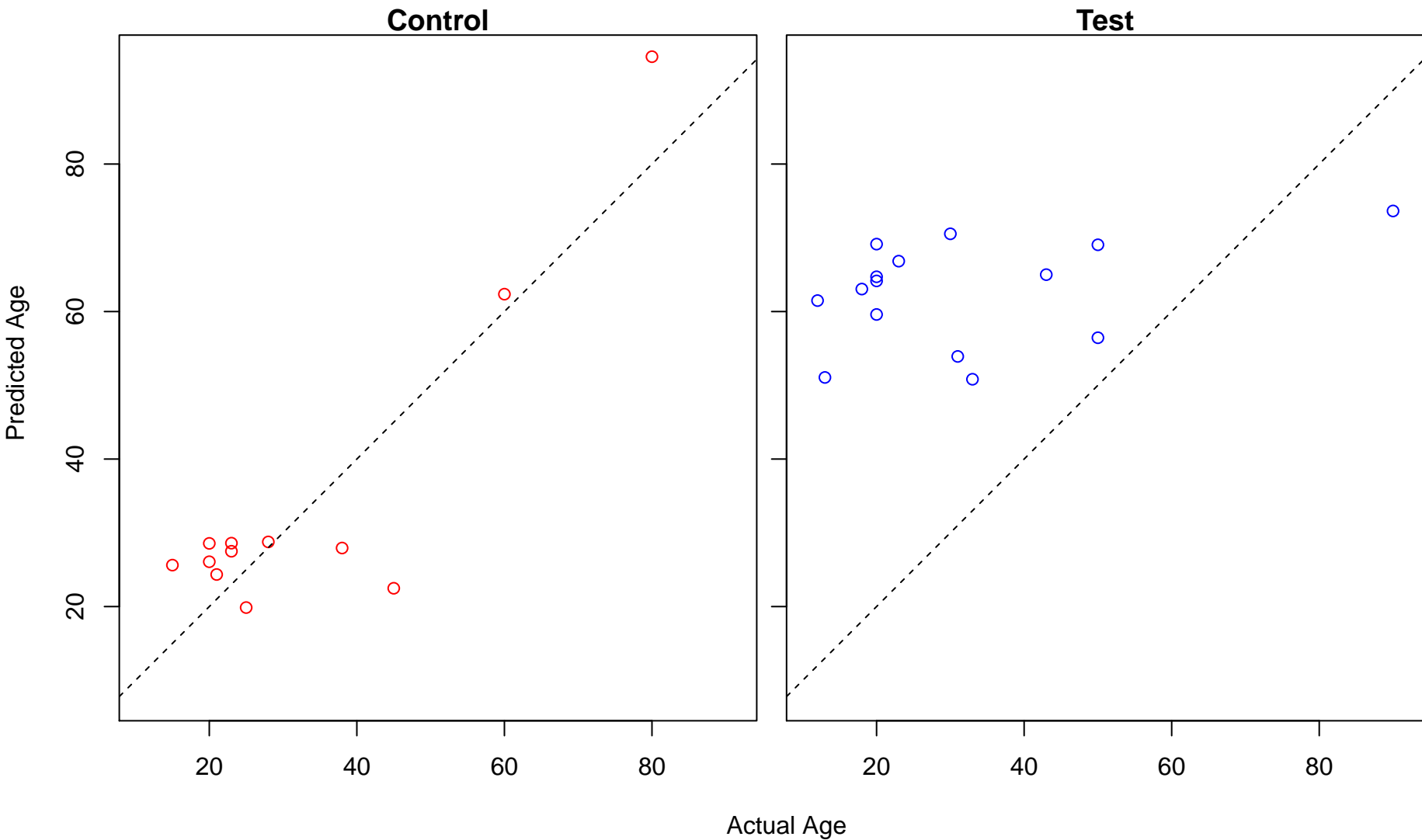
regulation of pH (Score: 5.022789)



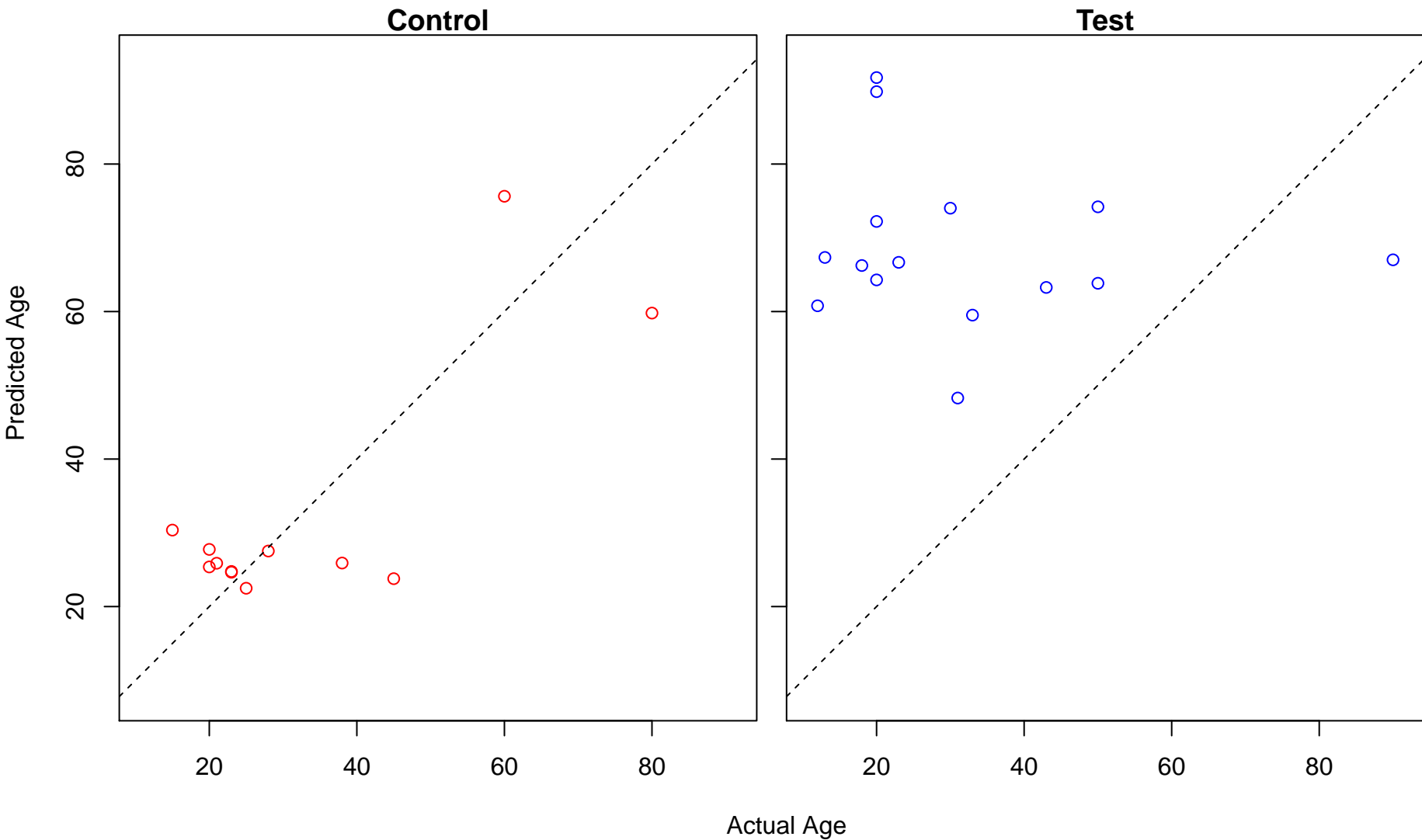
negative regulation of antigen processing and presentation (Score: 5.022599)



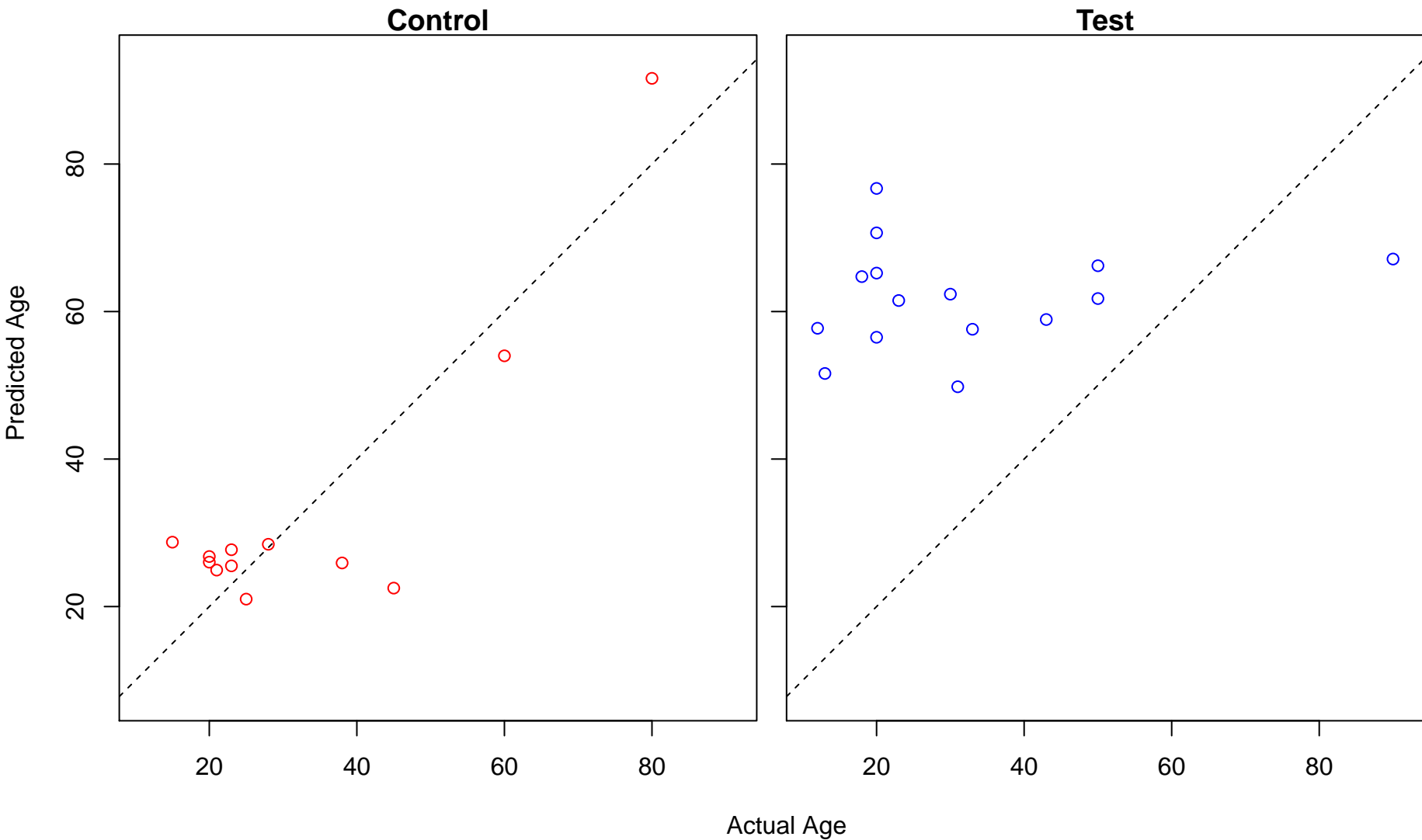
peroxisome organization (Score: 5.021364)



negative regulation of mRNA polyadenylation (Score: 5.018829)

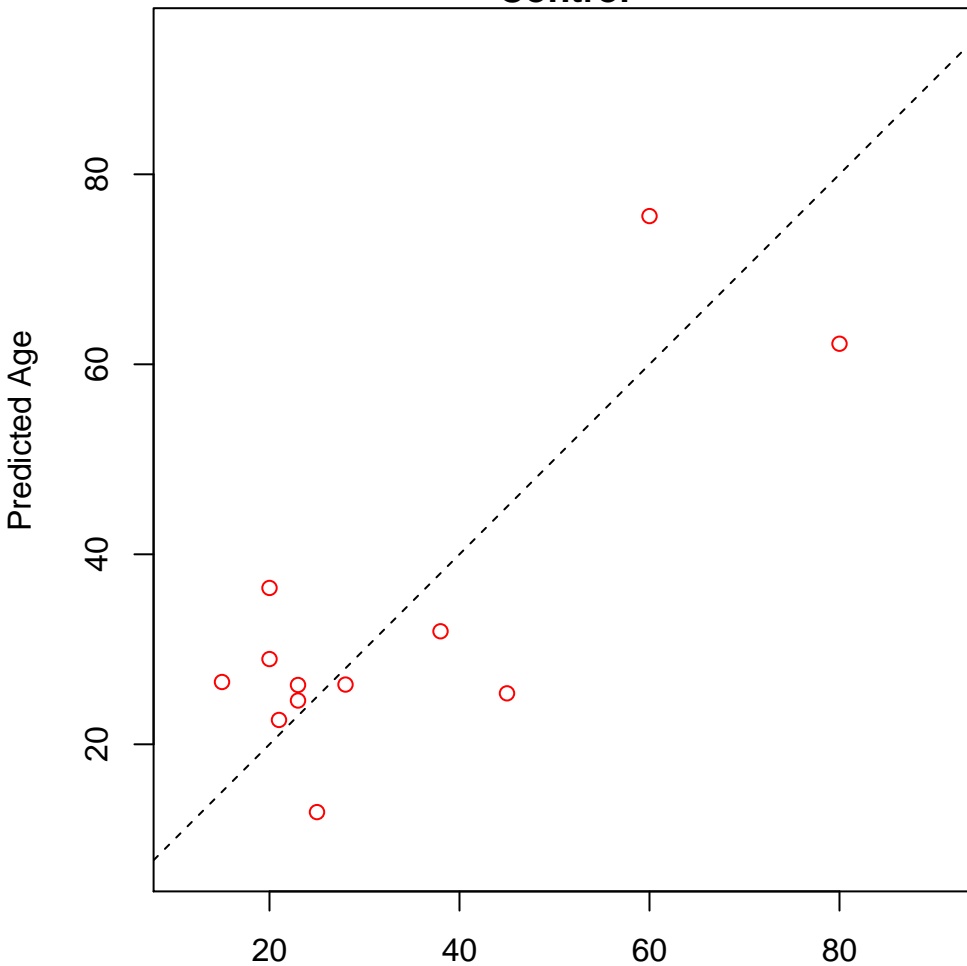


organelle localization (Score: 5.015327)

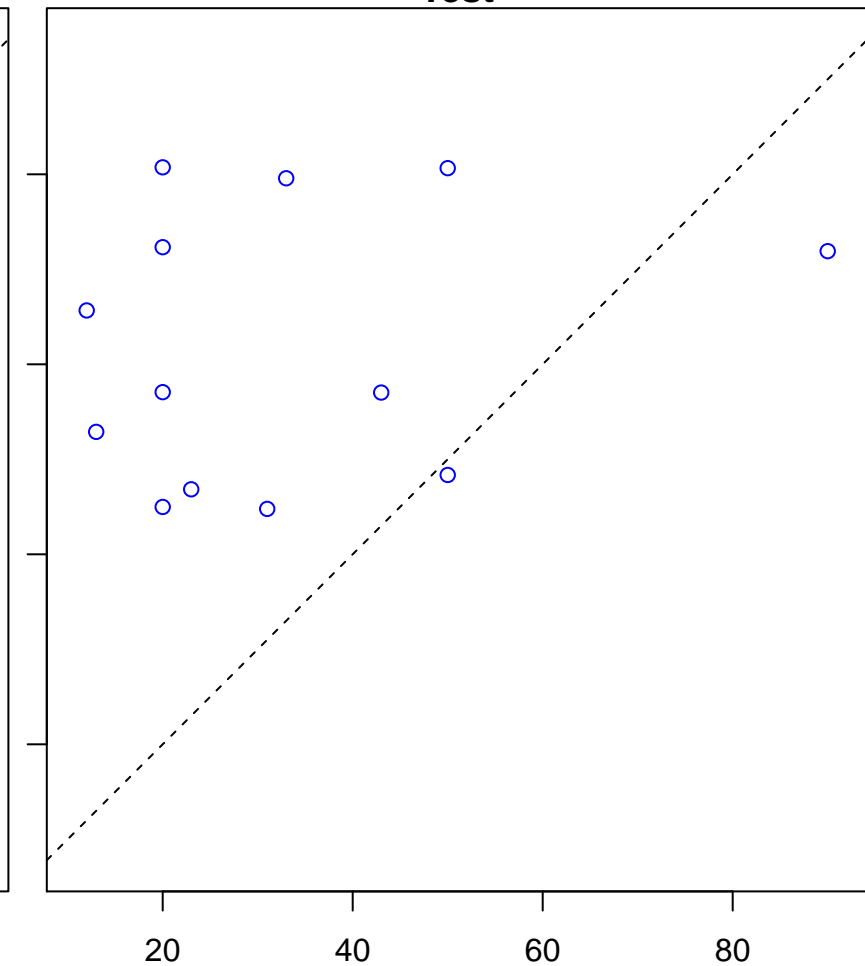


blood coagulation, fibrin clot formation (Score: 5.015177)

Control



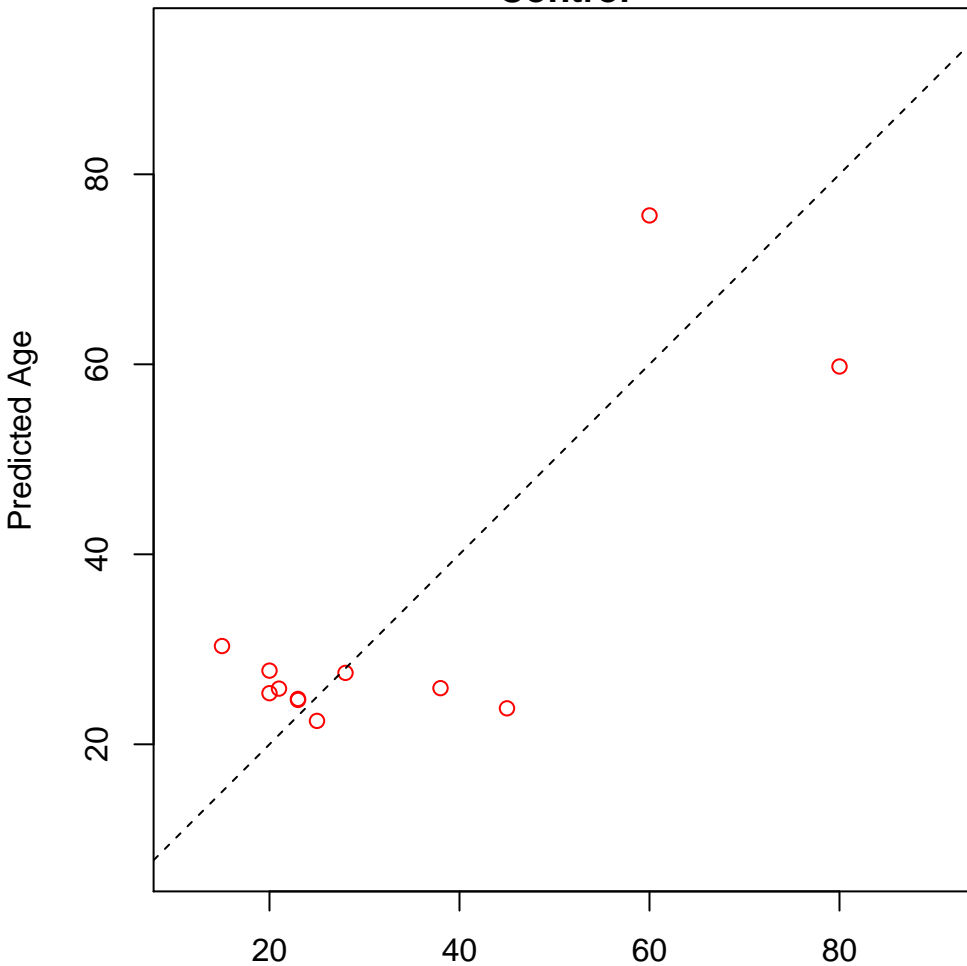
Test



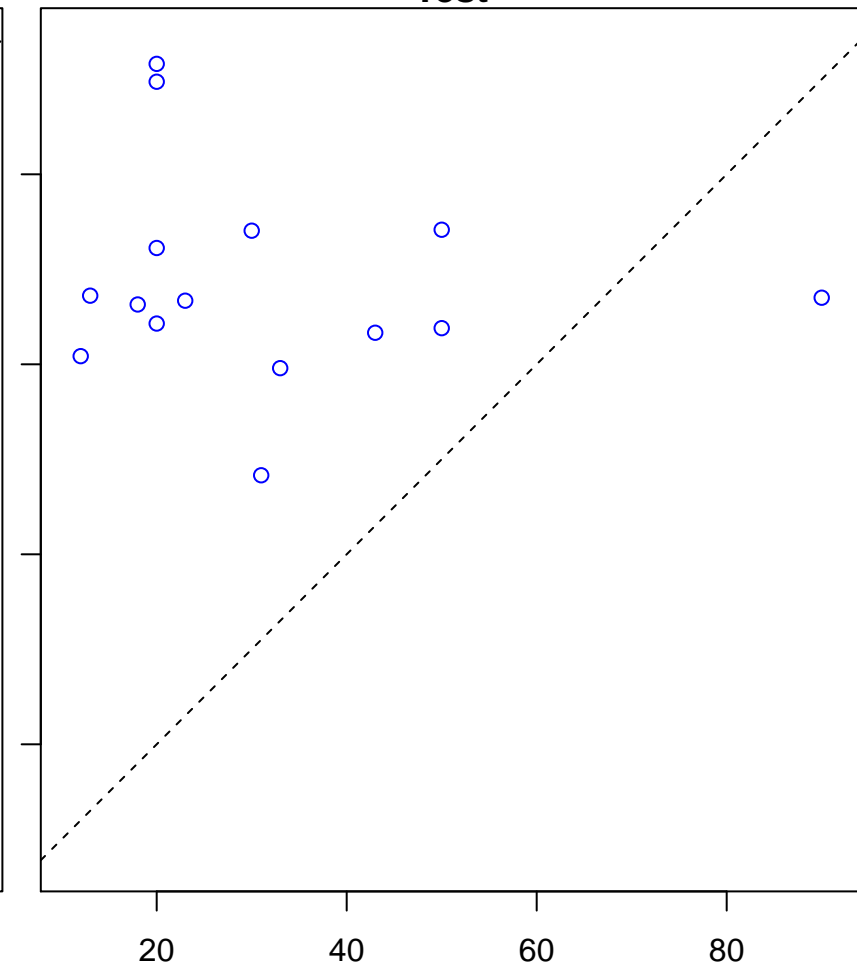
Actual Age

regulation of mRNA polyadenylation (Score: 5.013657)

Control

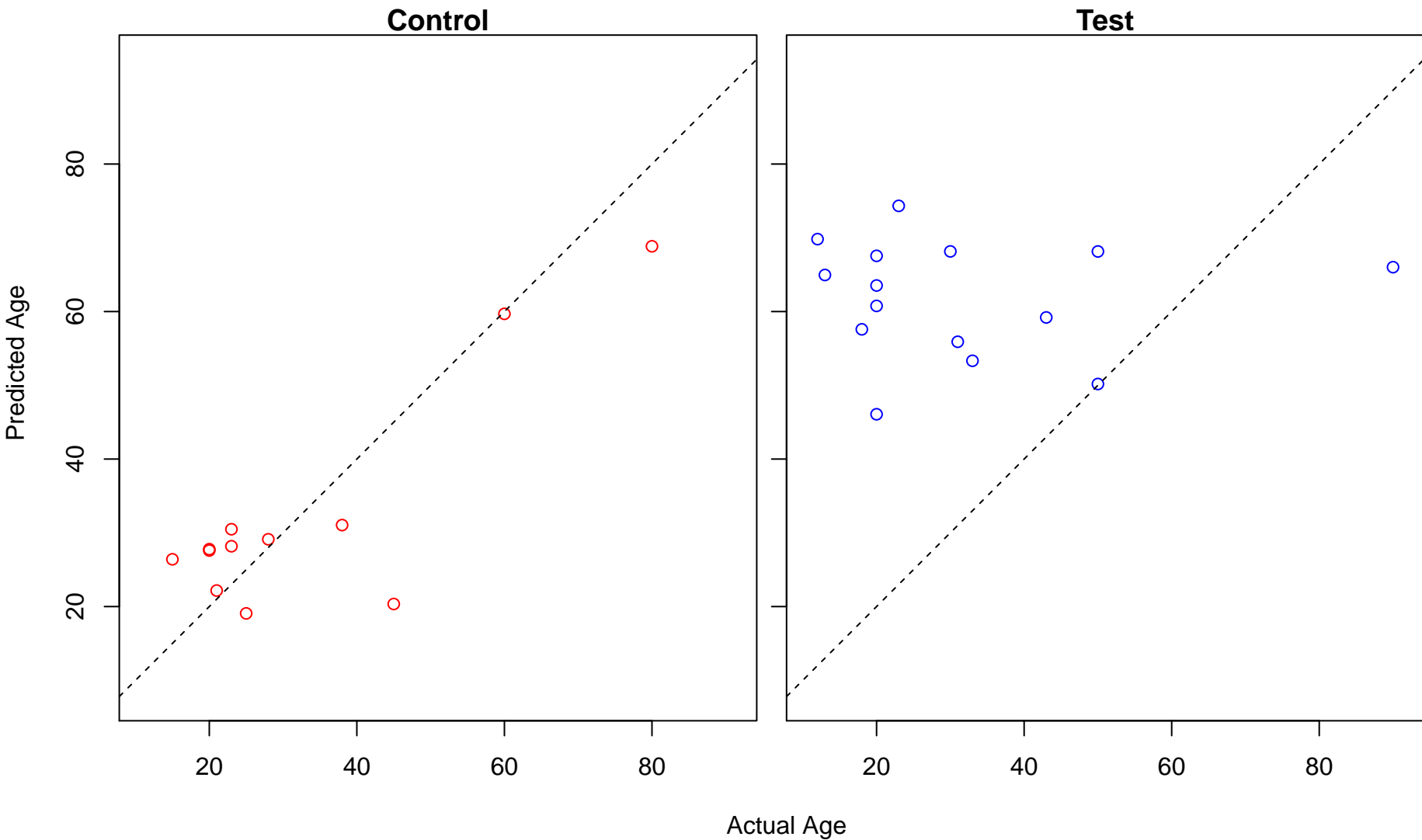


Test

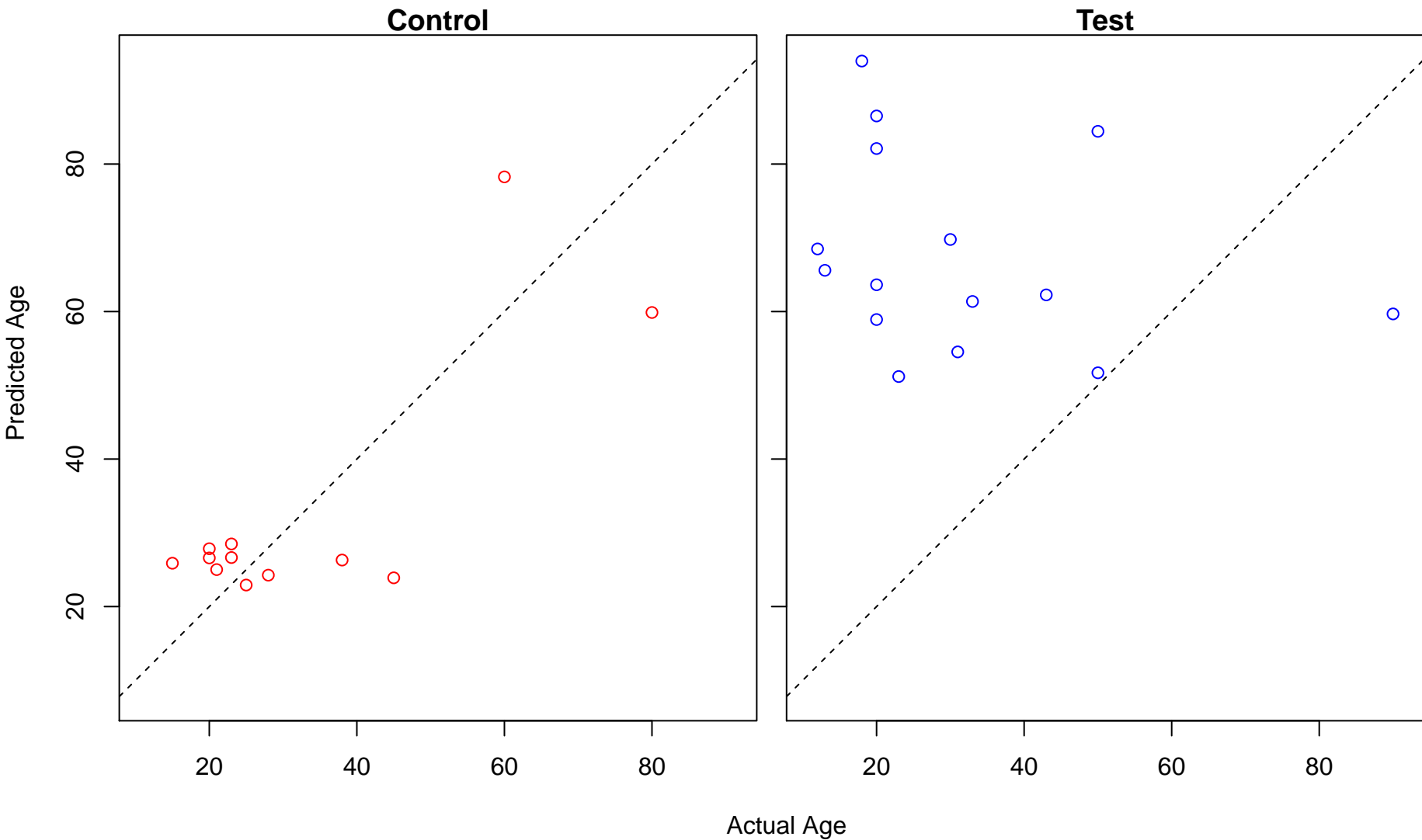


Actual Age

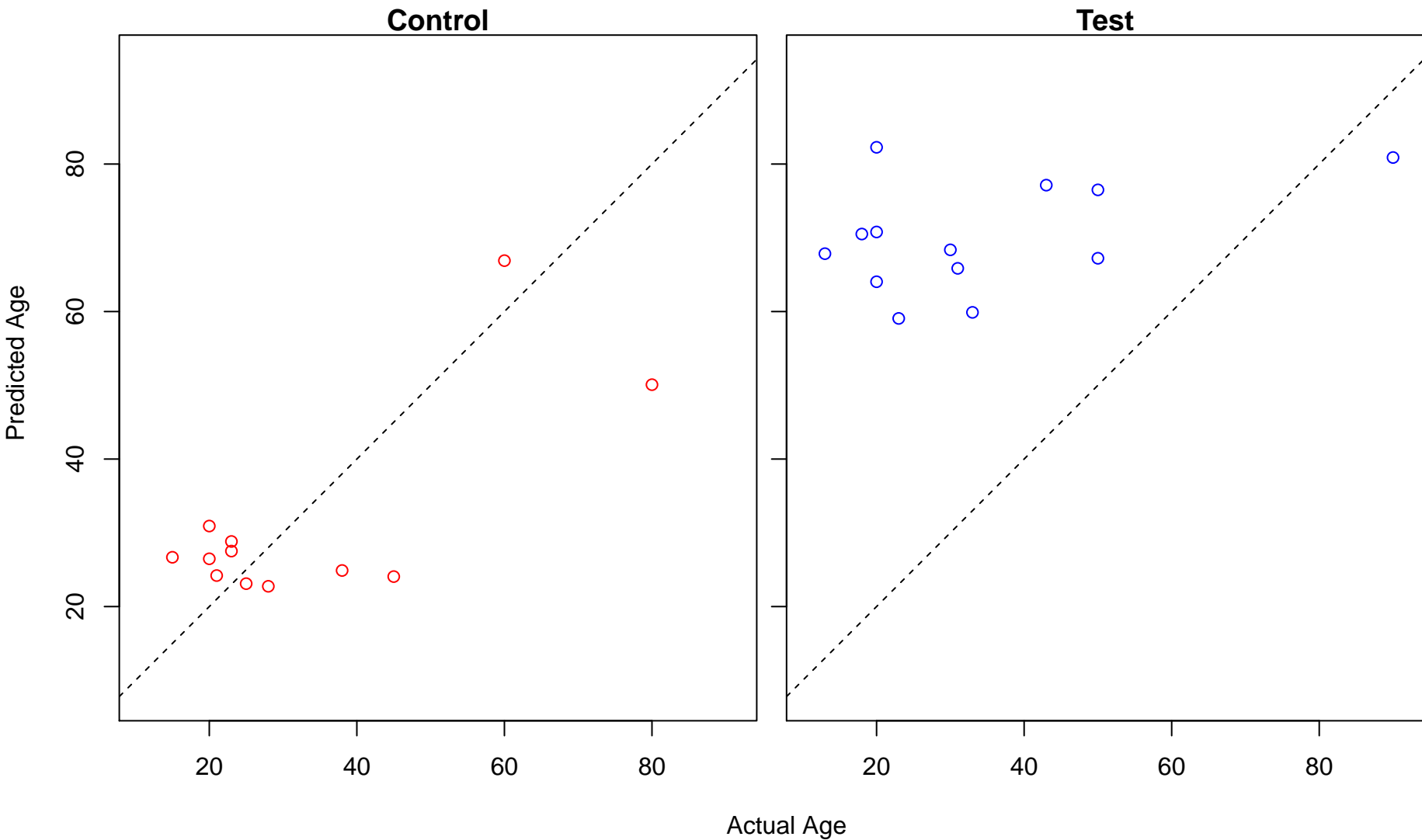
regulation of gene silencing (Score: 5.013235)



positive regulation of glycoprotein metabolic process (Score: 5.013182)

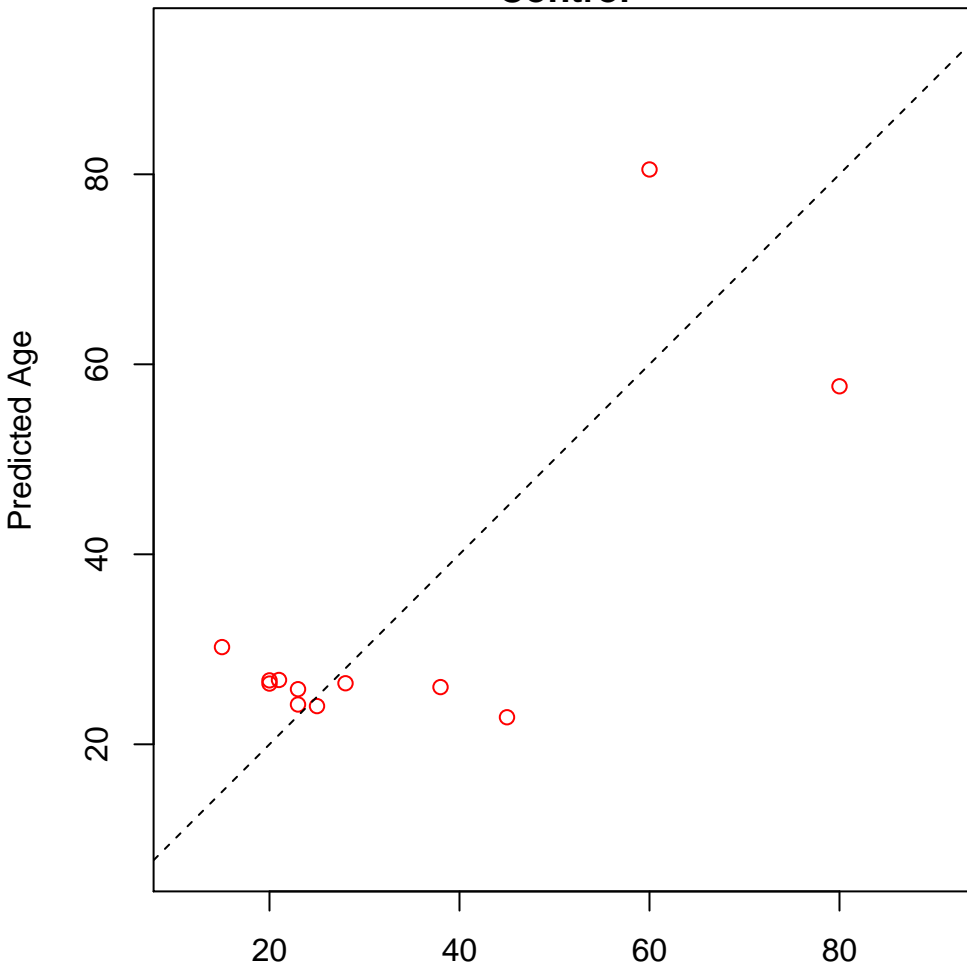


multicellular organismal iron ion homeostasis (Score: 5.011384)

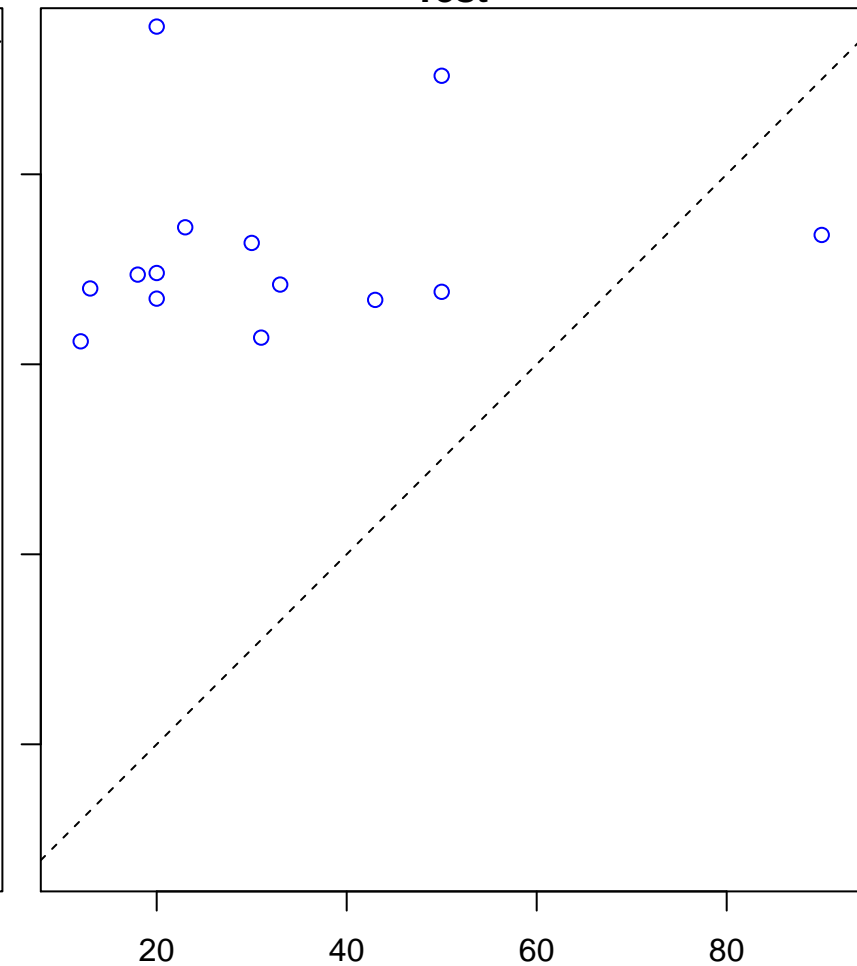


protein localization to chromosome (Score: 5.01157)

Control

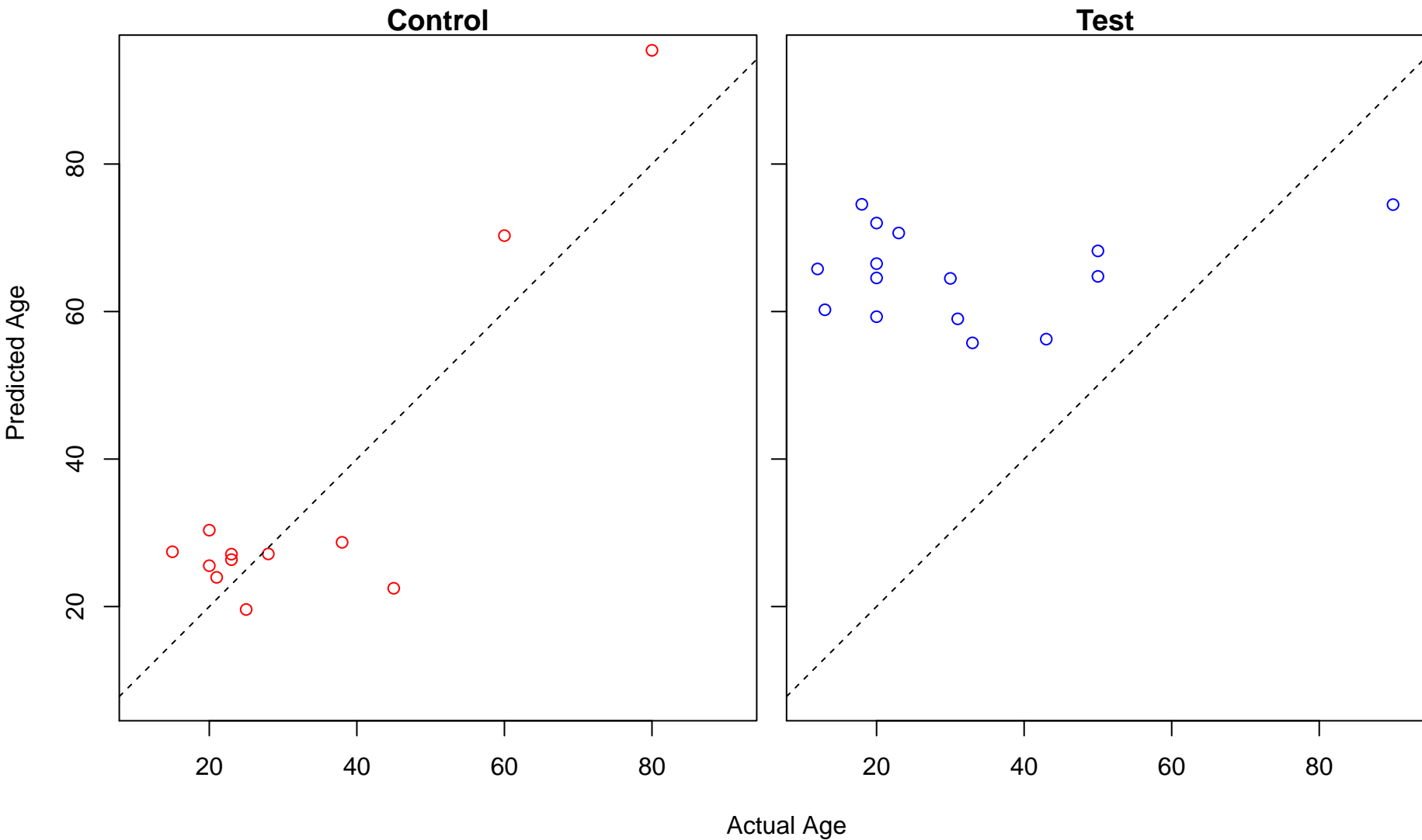


Test

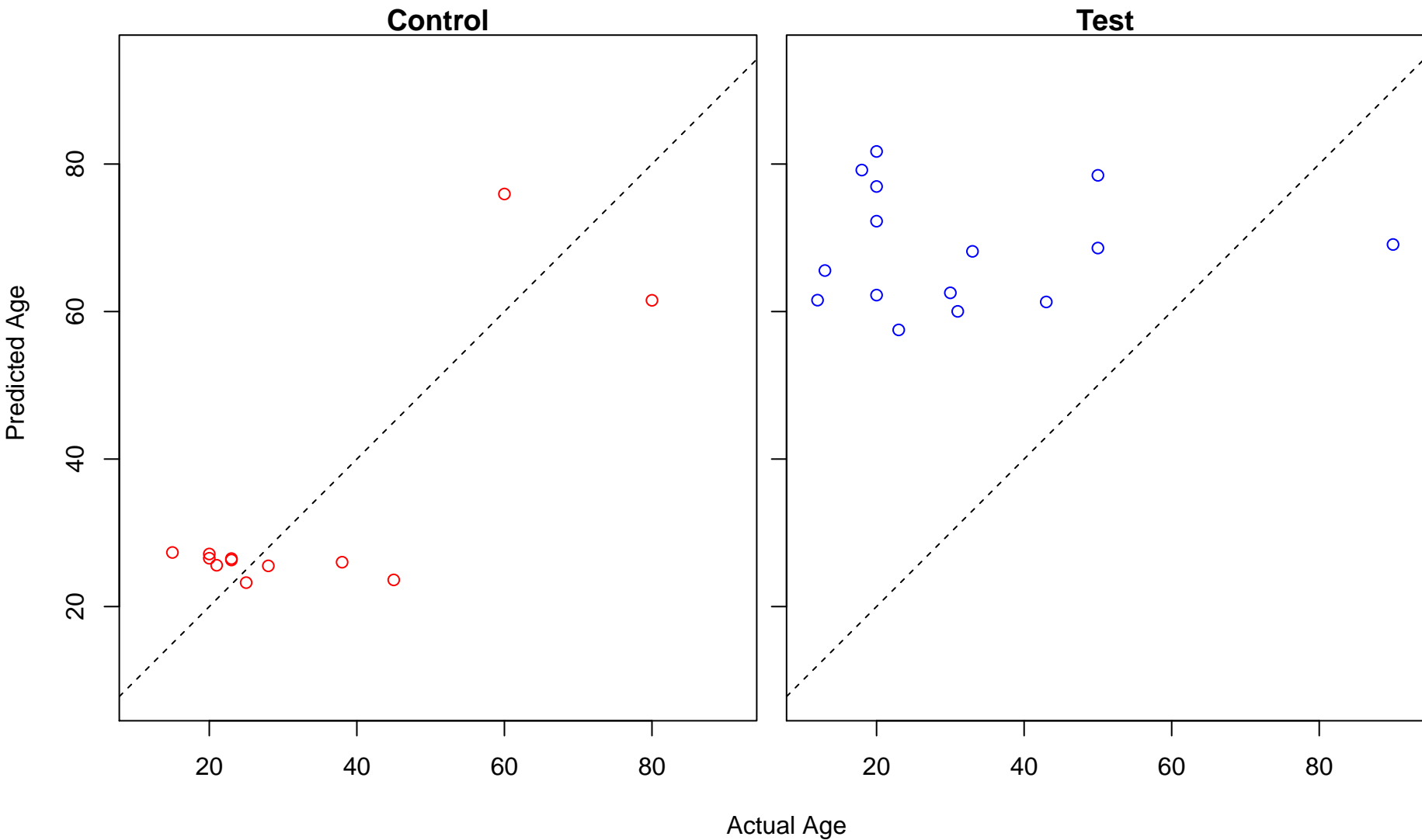


Actual Age

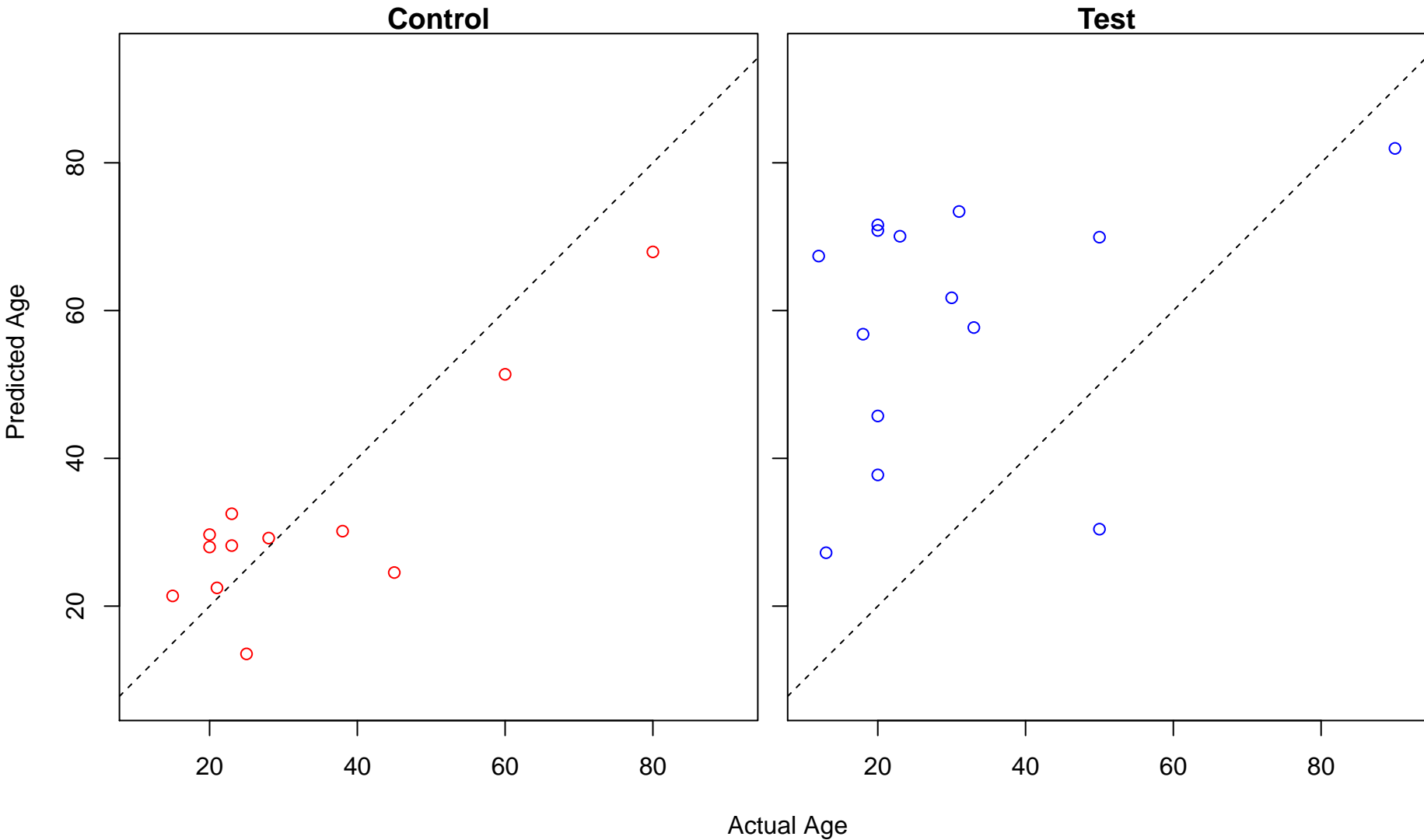
negative regulation of phosphorylation (Score: 5.010760)



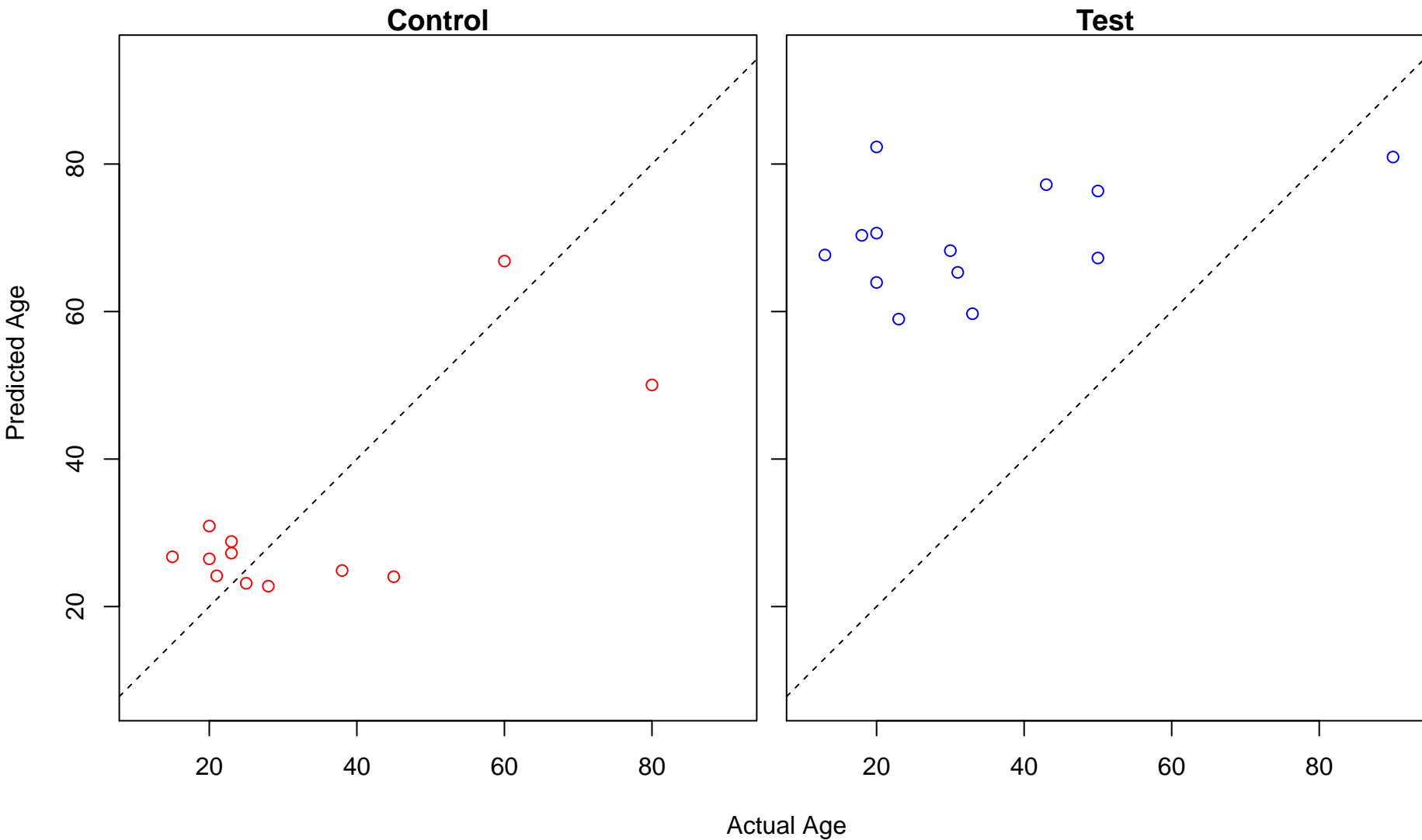
regulation of Ras protein signal transduction (Score: 5.010286)



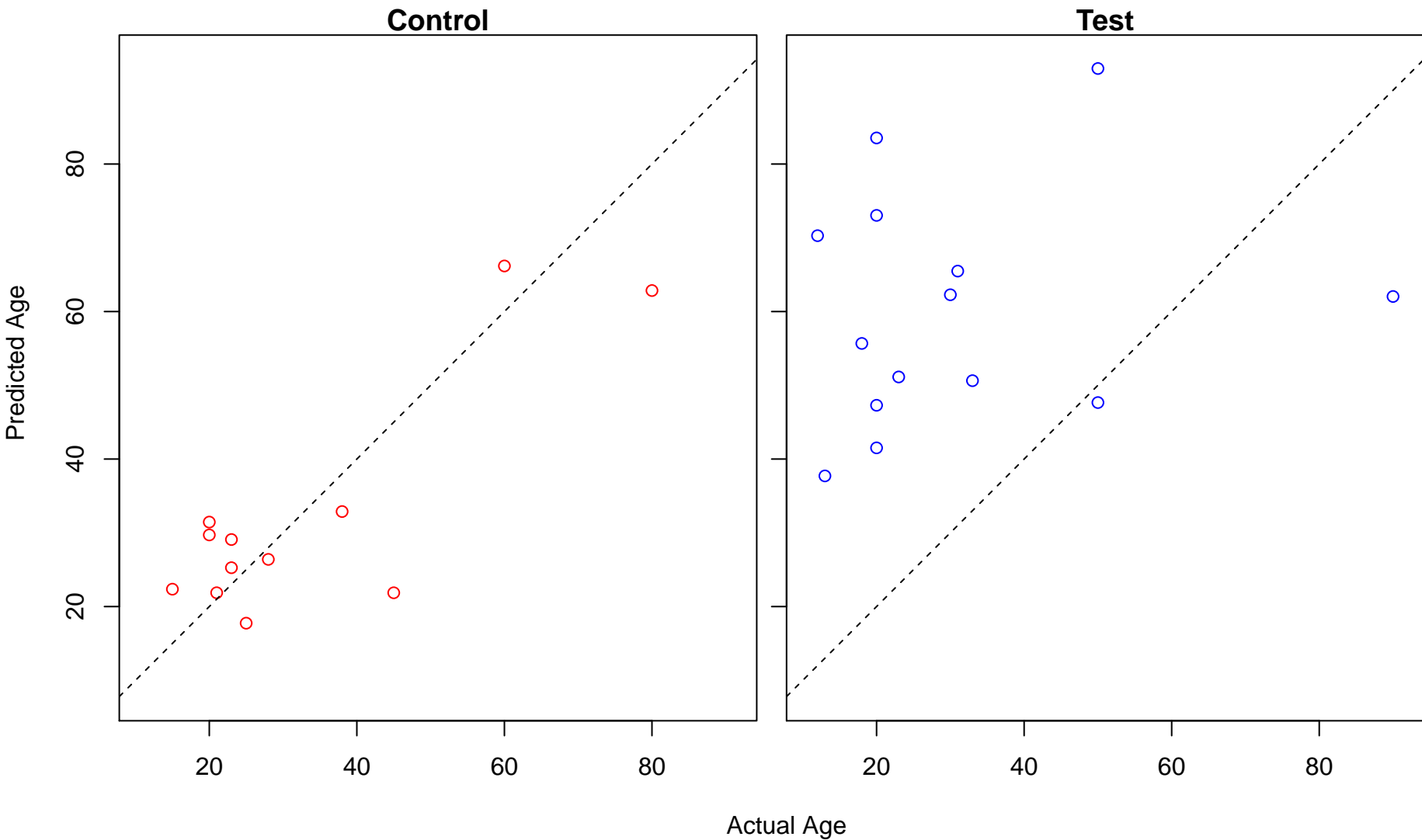
intraciliary transport involved in cilium morphogenesis (Score: 5.008880)



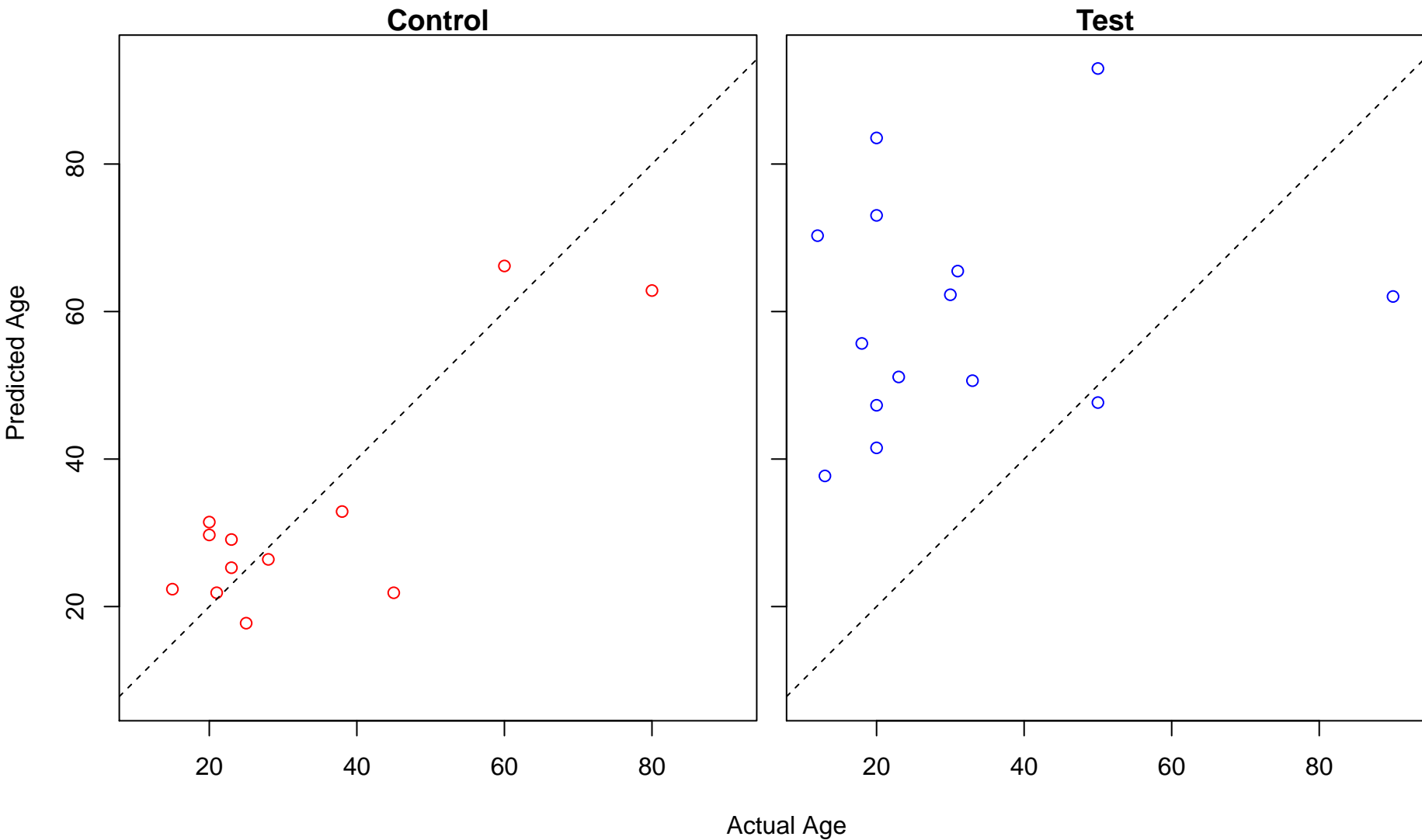
iron ion transmembrane transport (Score: 5.008425)



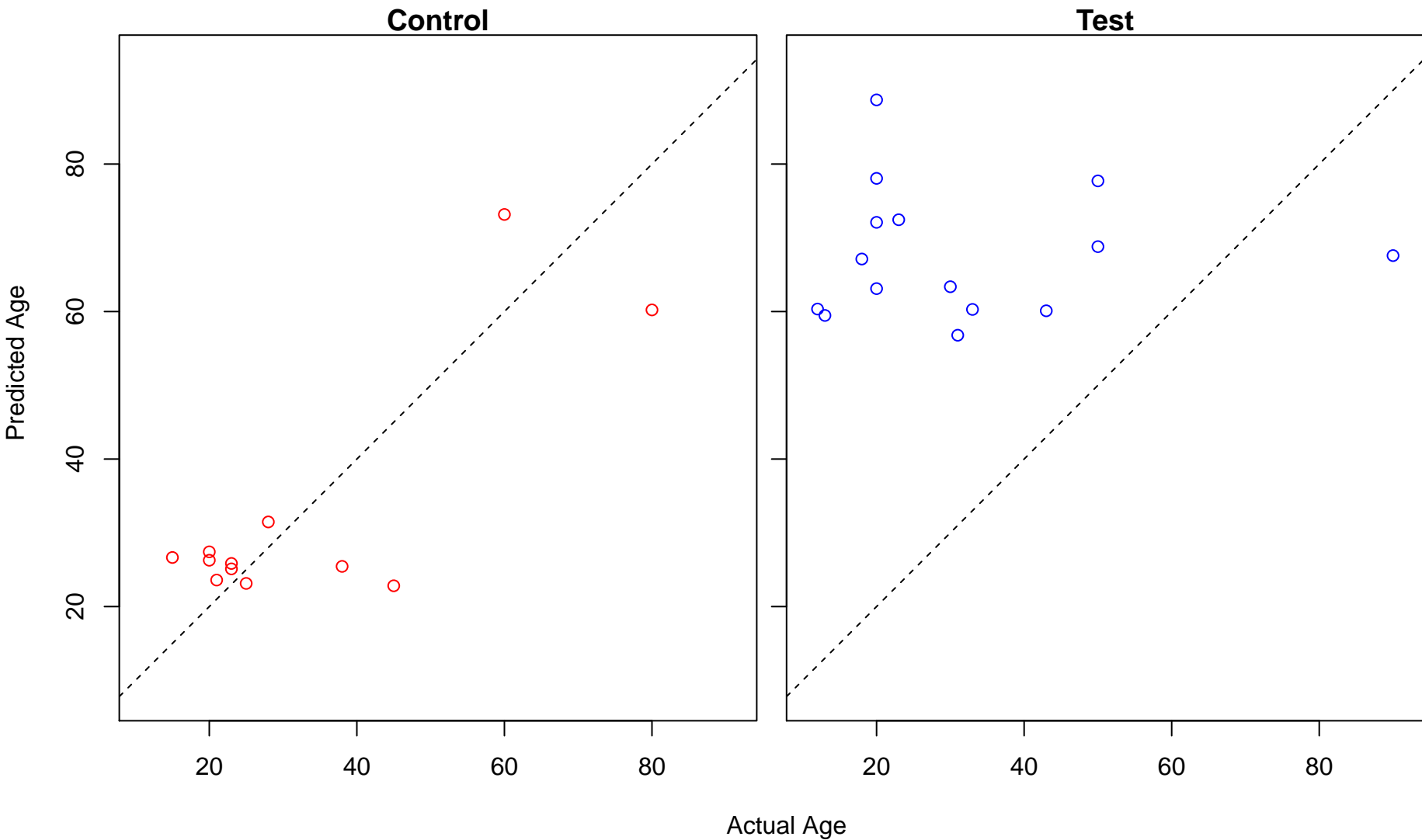
activation of store-operated calcium channel activity (Score: 5.007787)



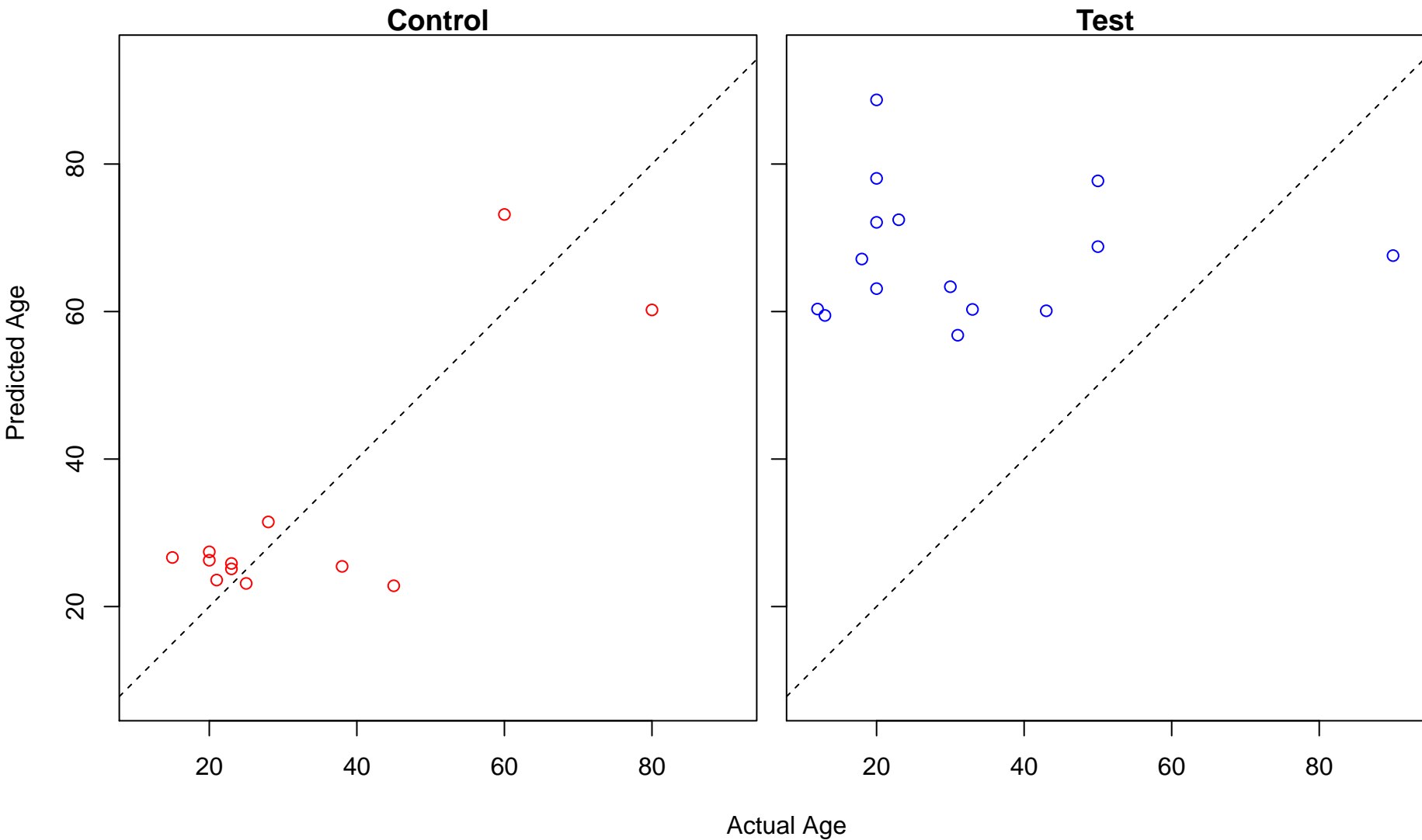
positive regulation of store-operated calcium channel activity (Score: 5.007787)



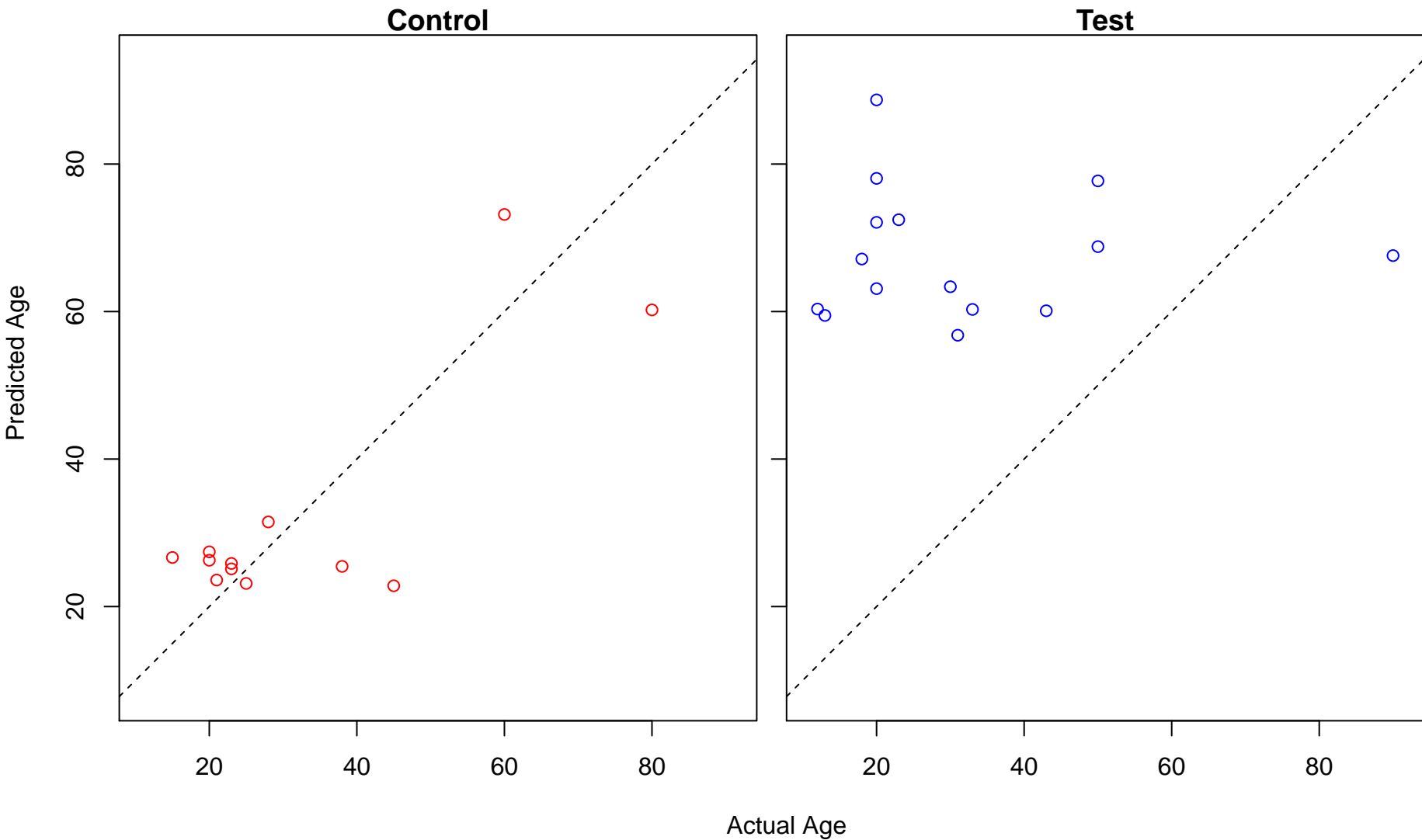
ubiquinone metabolic process (Score: 5.007470)



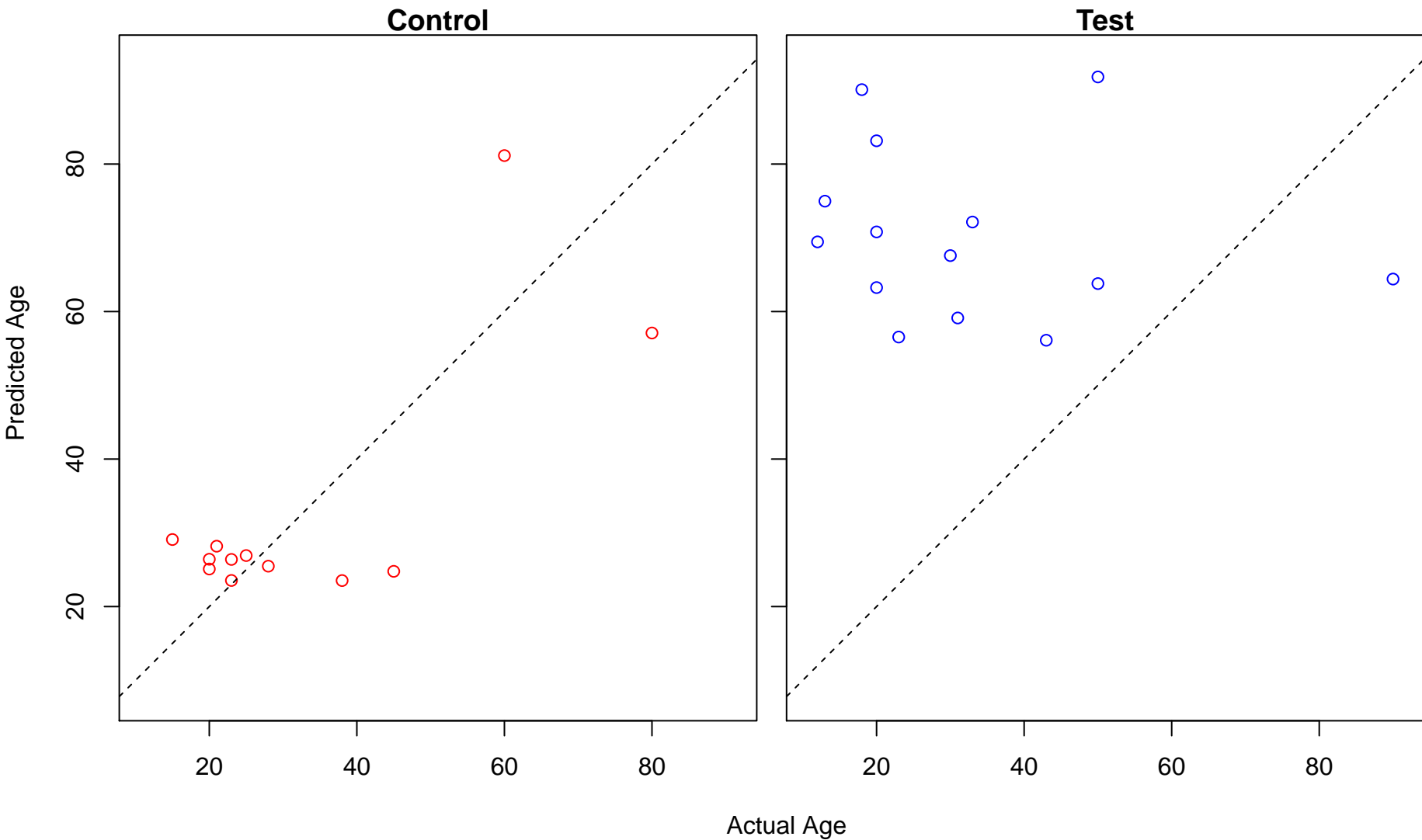
ubiquinone biosynthetic process (Score: 5.007470)



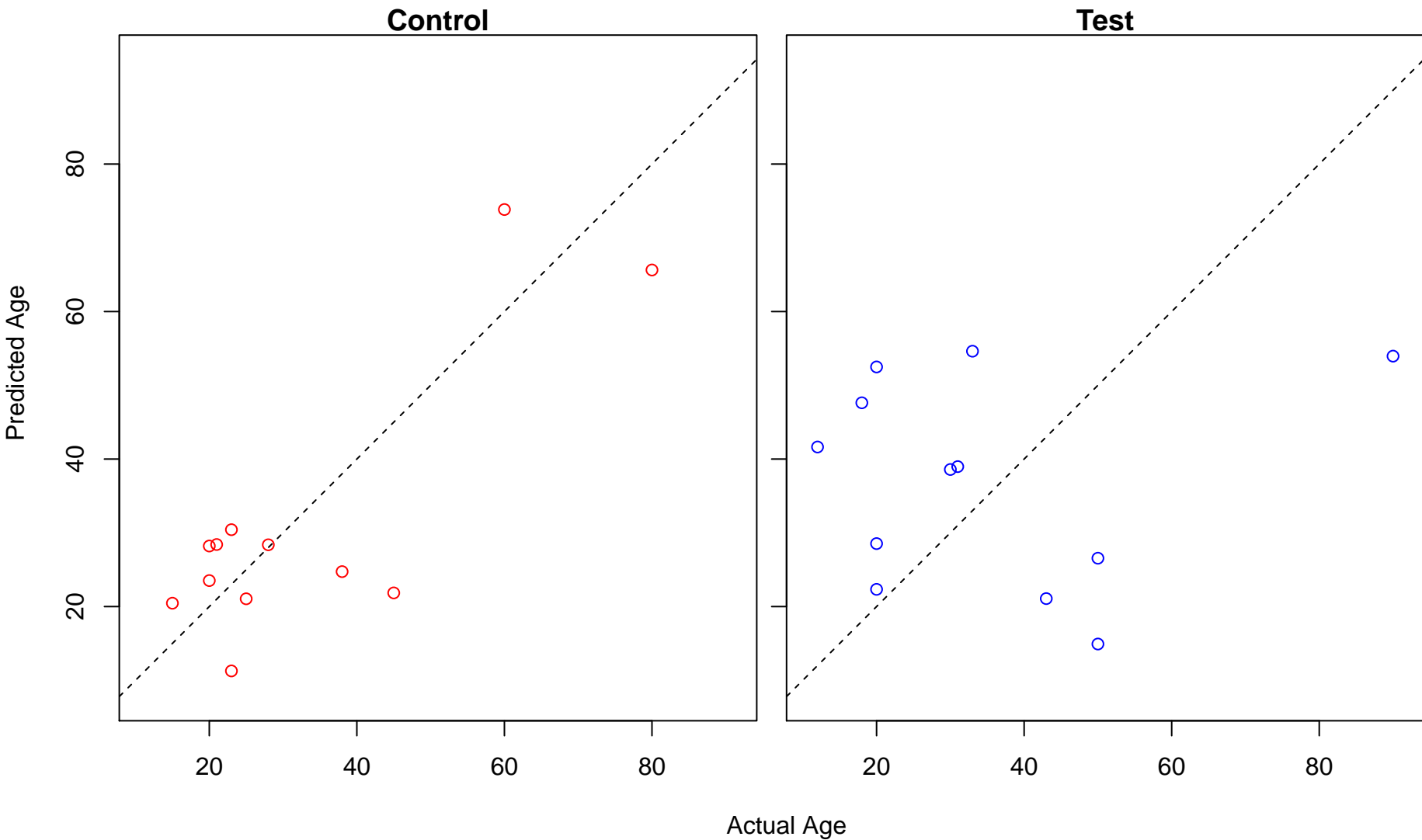
quinone biosynthetic process (Score: 5.007470)



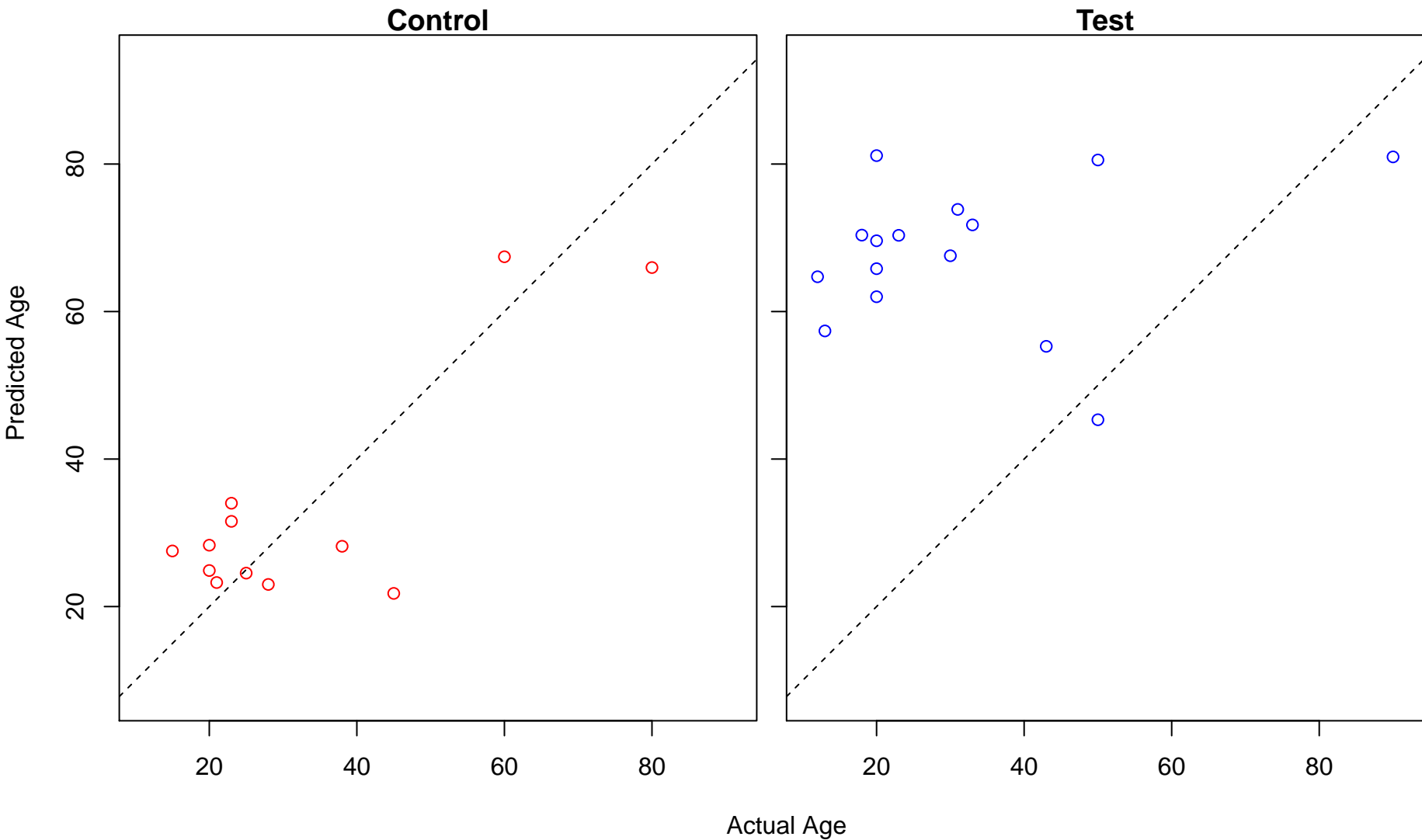
positive regulation of lamellipodium organization (Score: 5.006288)



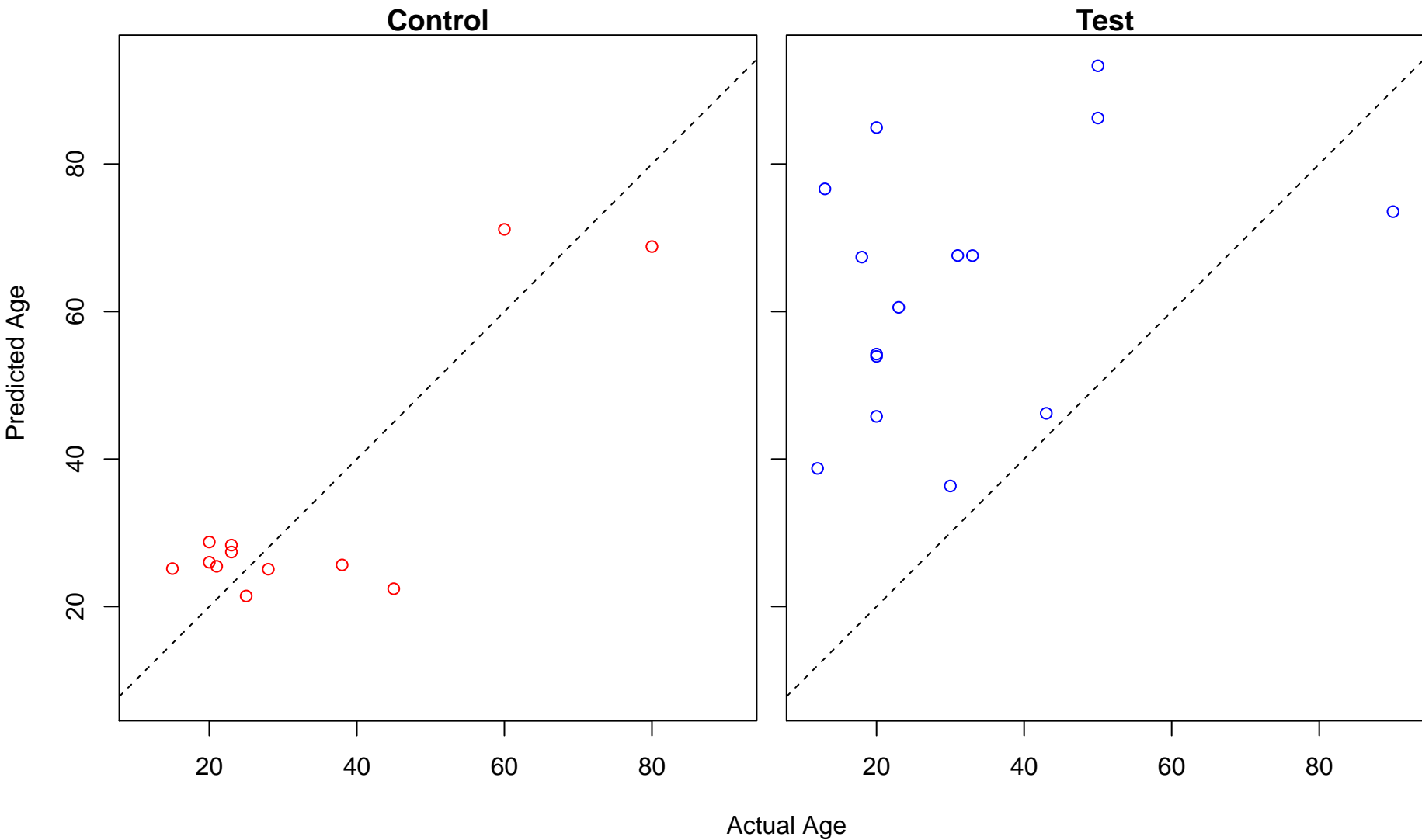
regulation of thymocyte apoptotic process (Score: 5.005649)



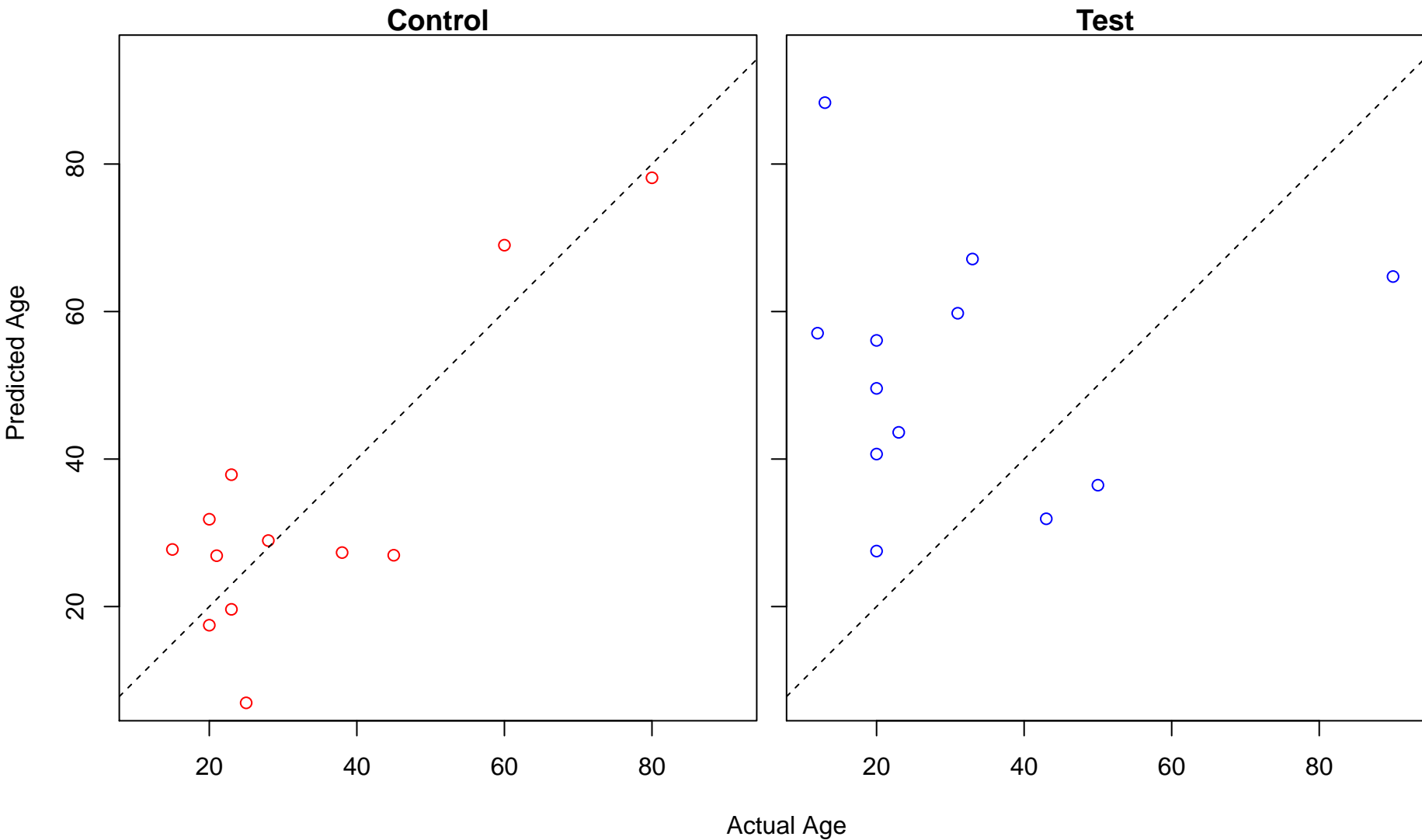
pathway-restricted SMAD protein phosphorylation (Score: 5.005182)



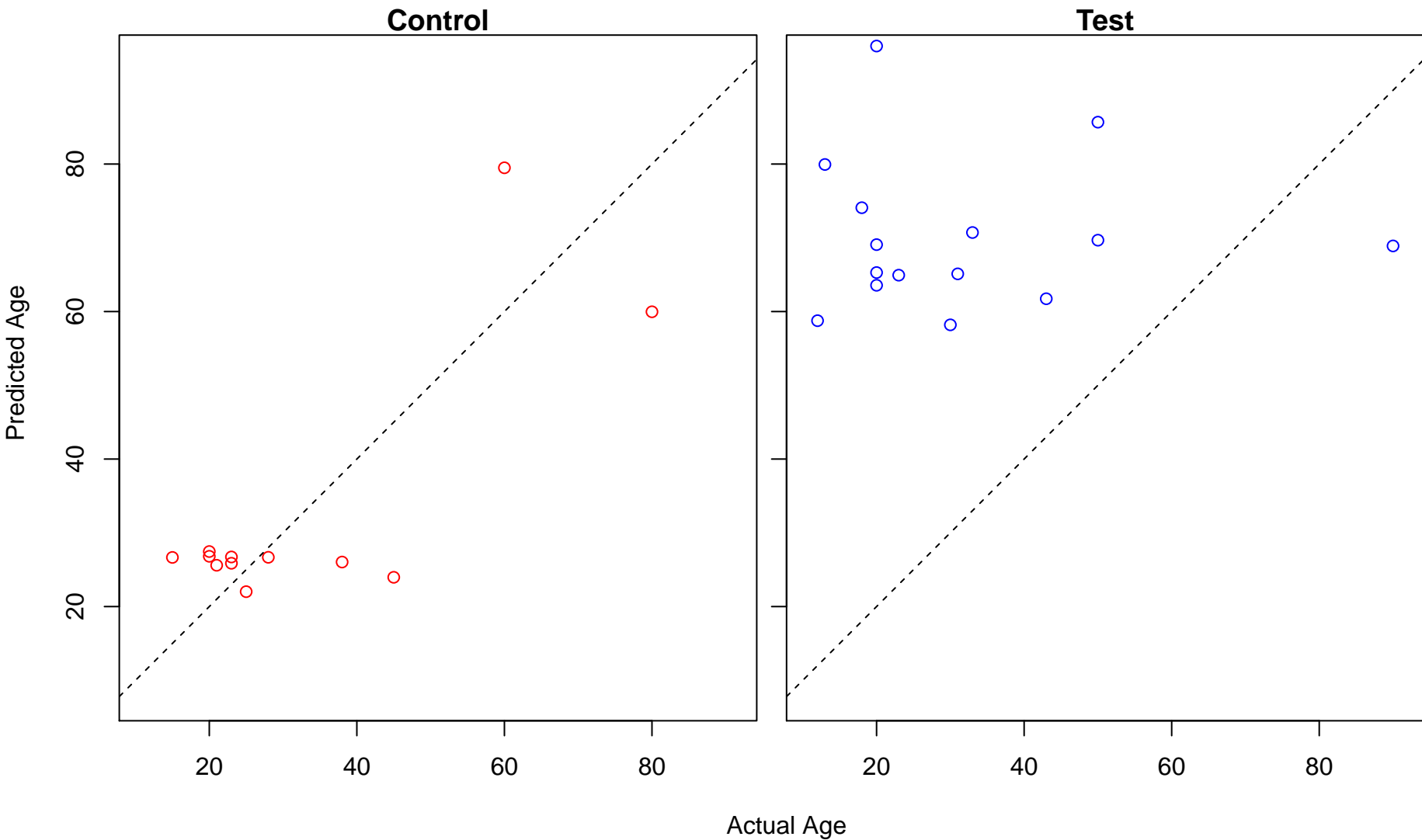
positive regulation of protein tyrosine kinase activity (Score: 5.004308)



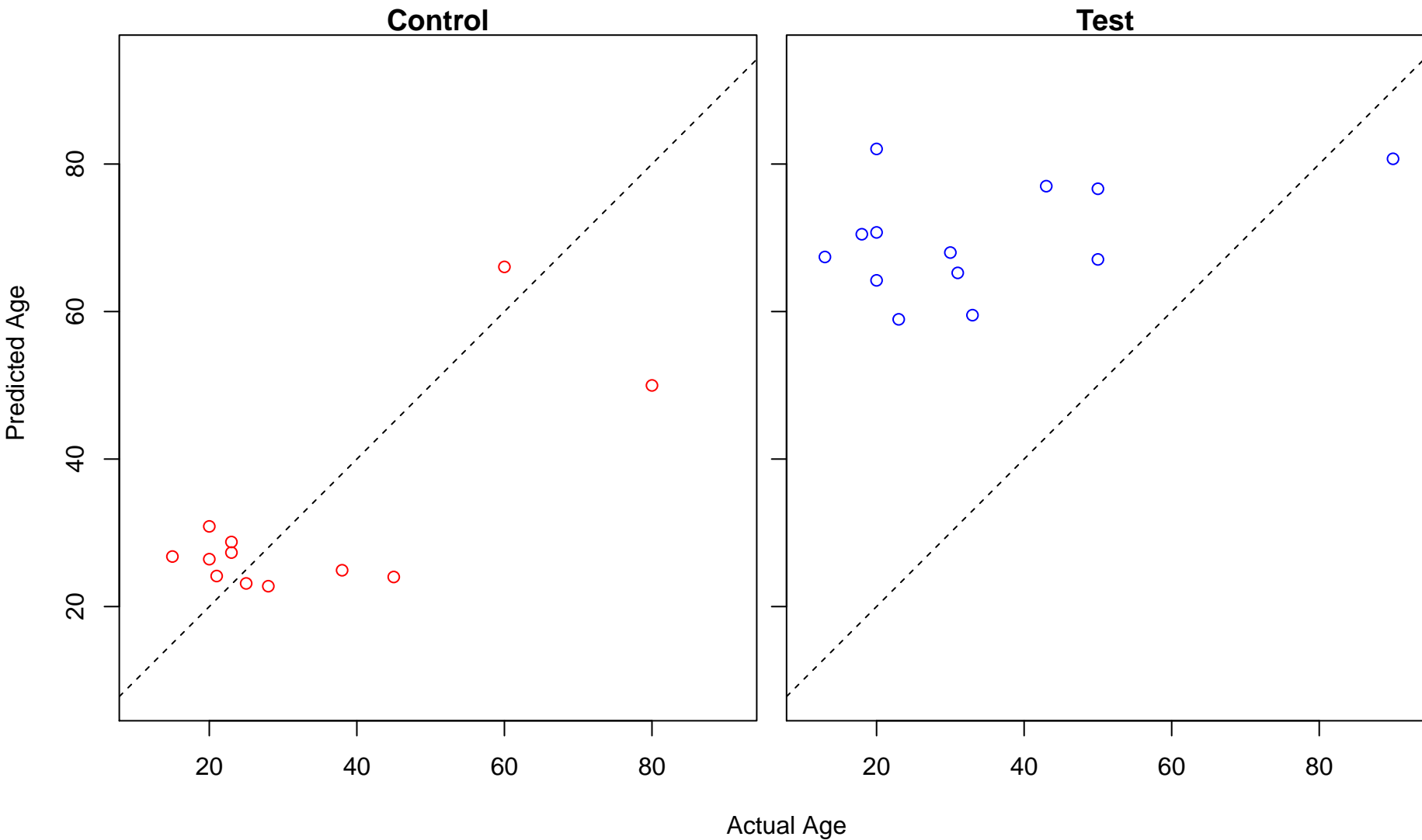
regulation of glomerular mesangial cell proliferation (Score: 5.000331)



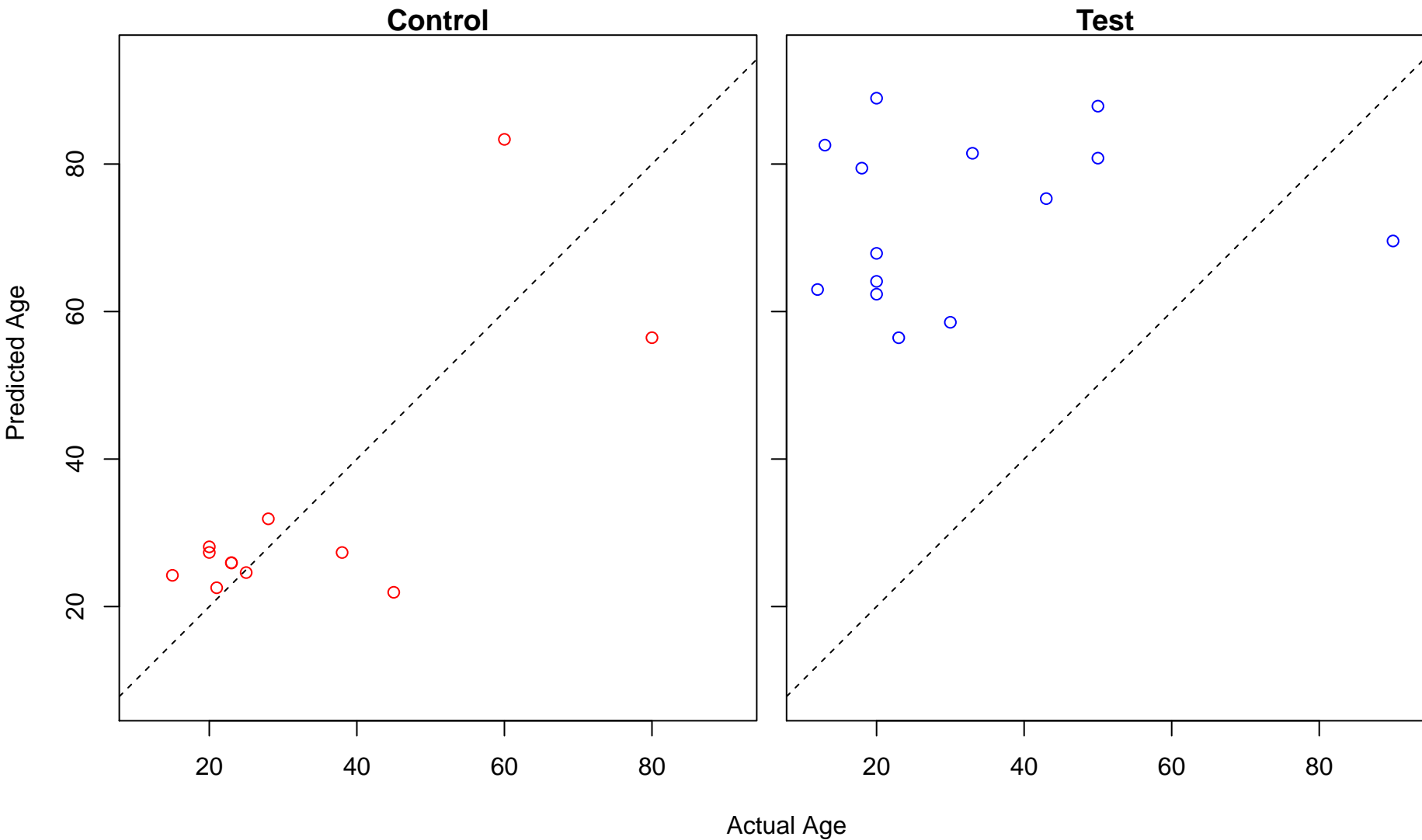
positive regulation of protein serine/threonine kinase activity (Score: 4.998324)



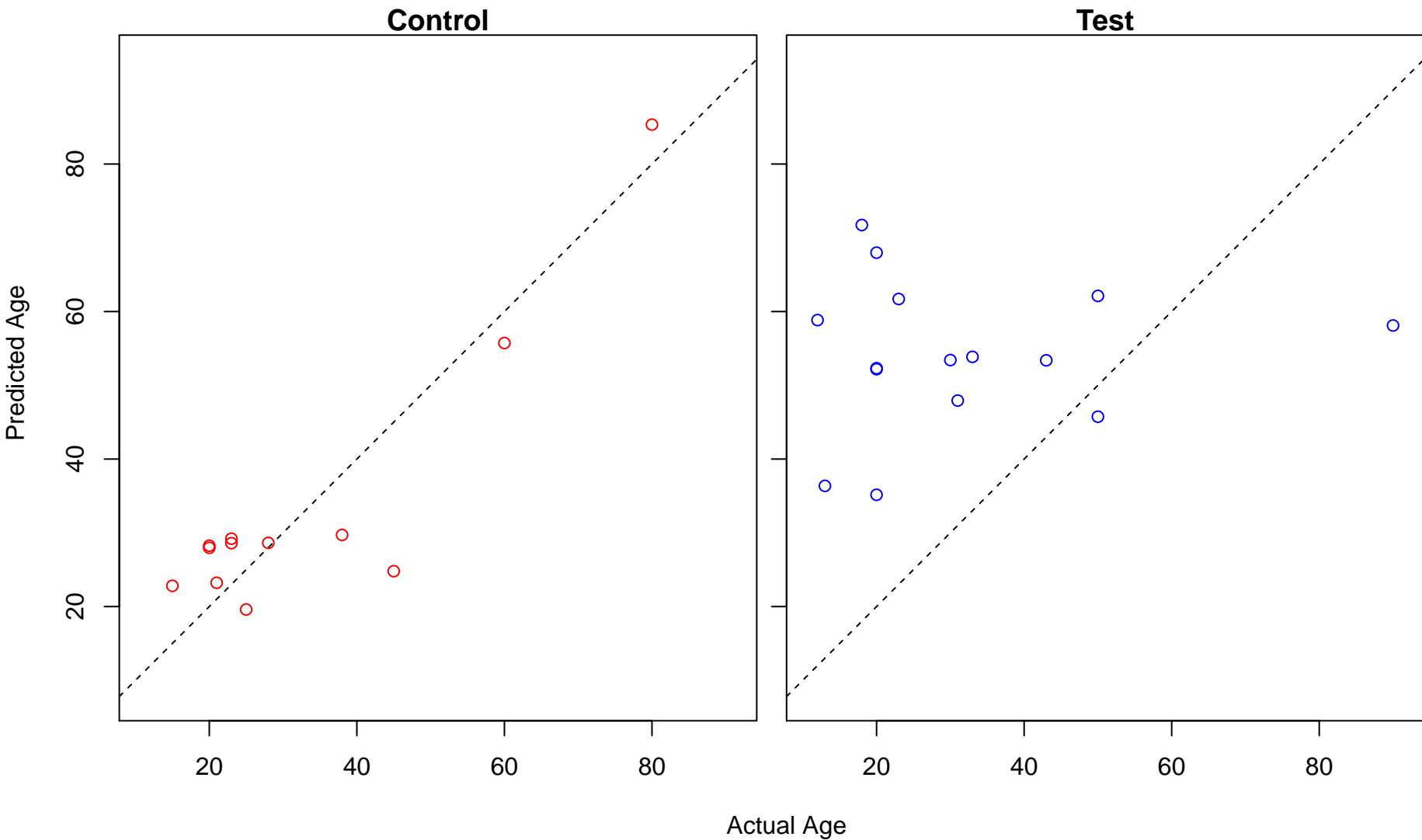
ferrous iron transport (Score: 4.997394)



cell-cell junction assembly (Score: 4.993786)

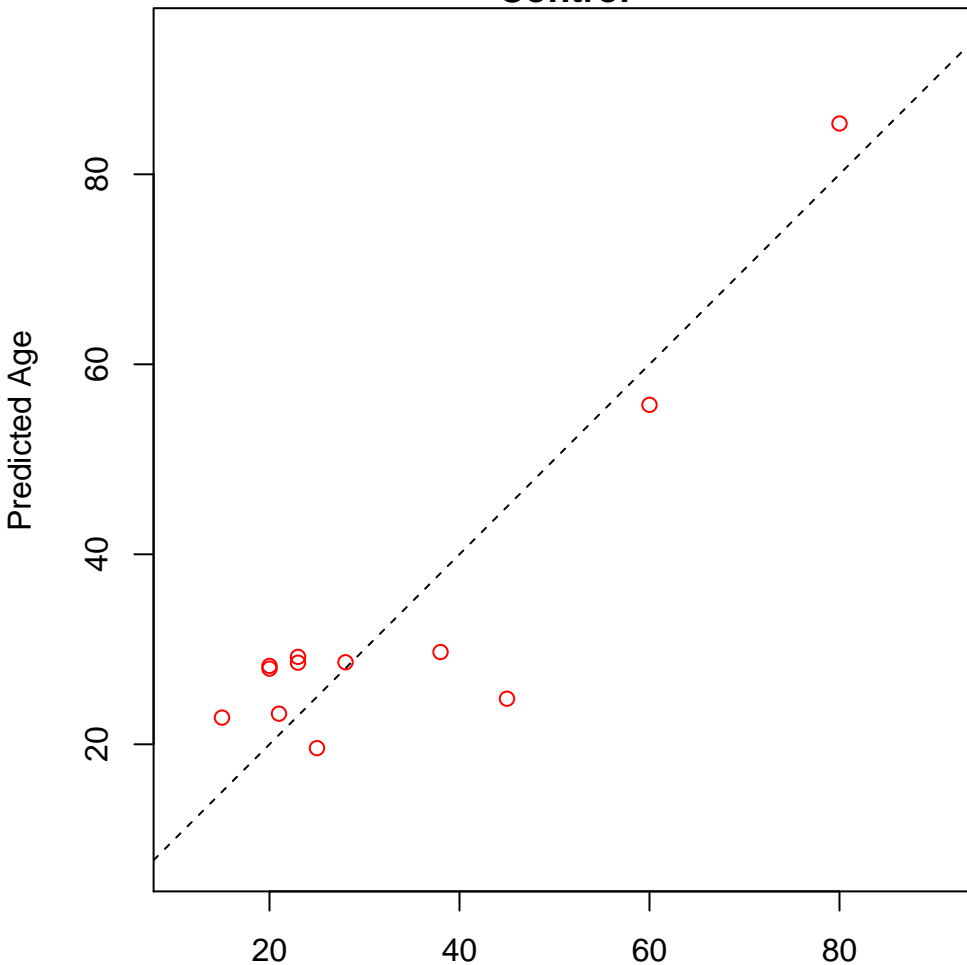


dolichyl diphosphate biosynthetic process (Score: 4.992220)

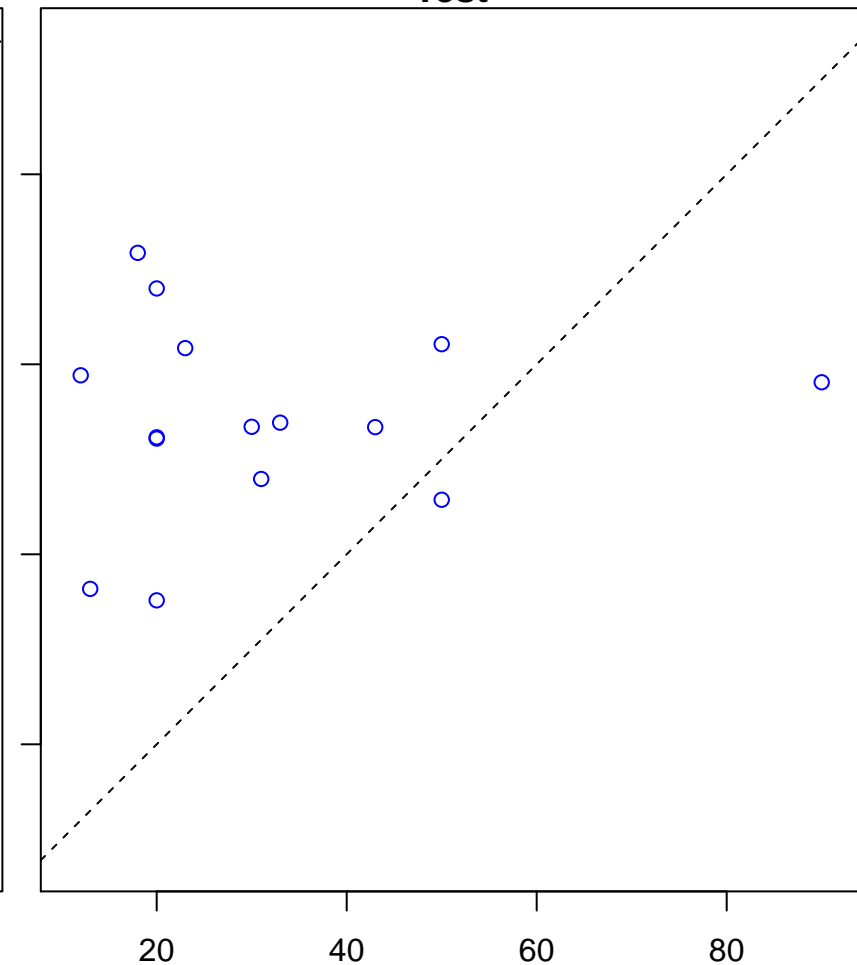


dolichyl diphosphate metabolic process (Score: 4.992220)

Control

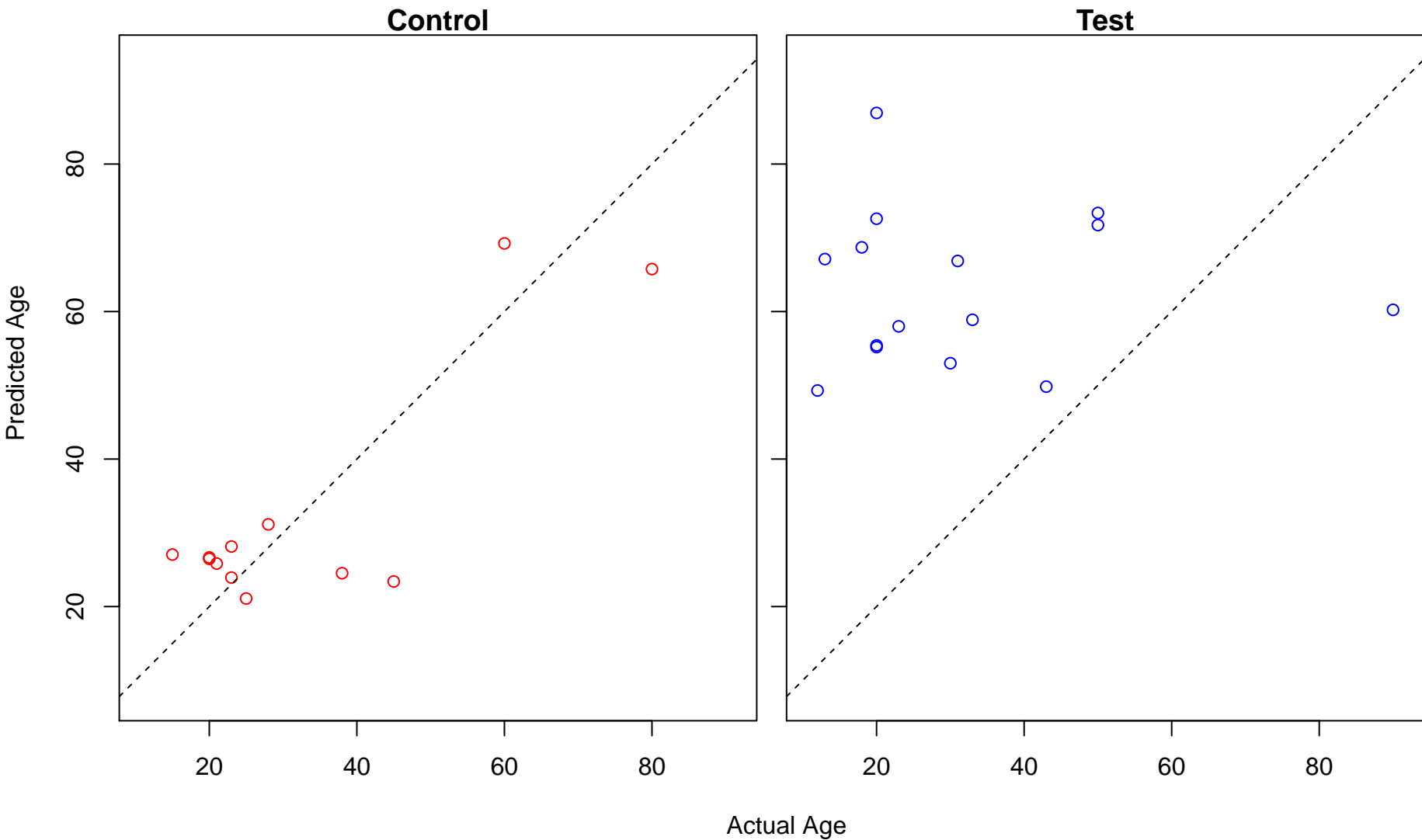


Test

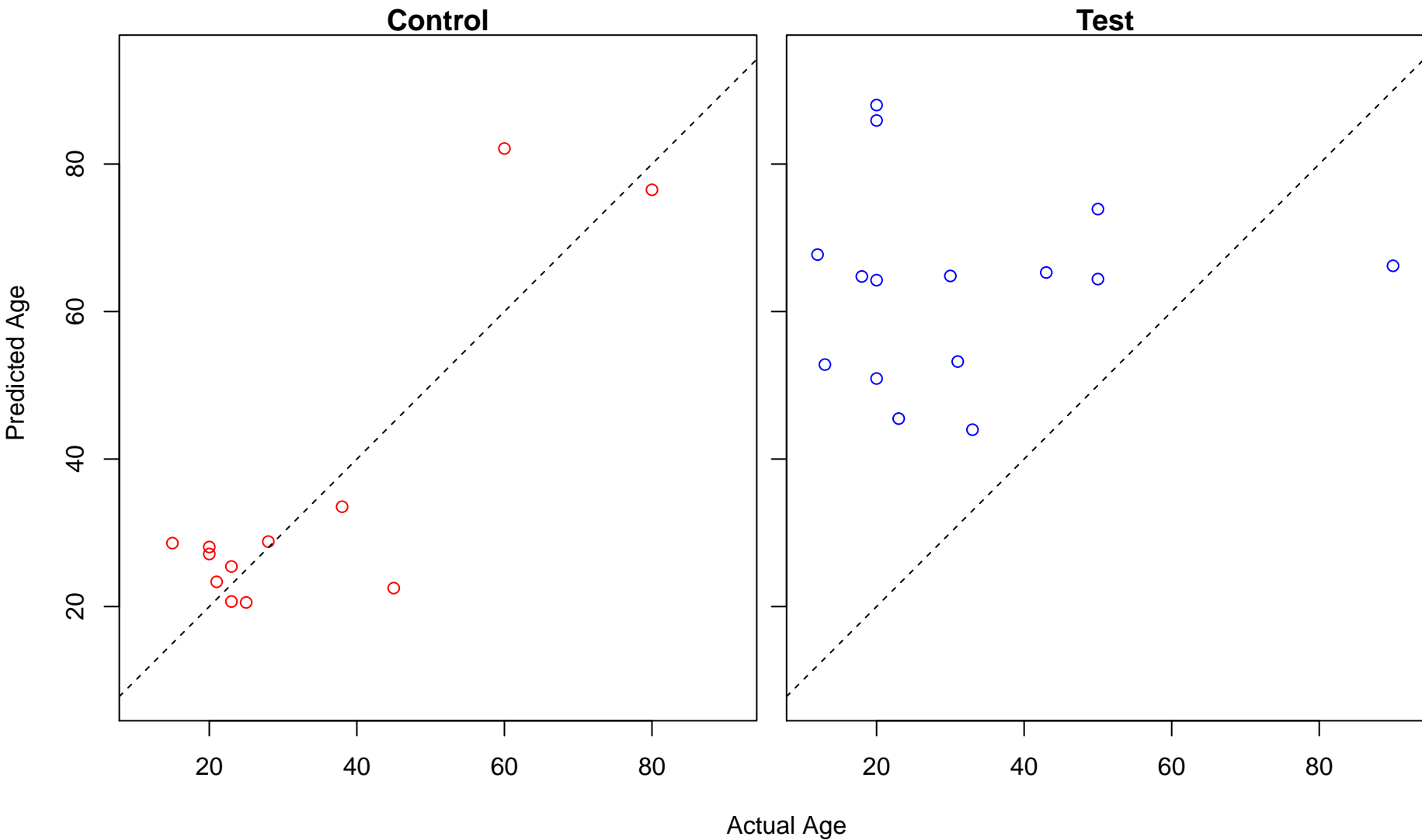


Actual Age

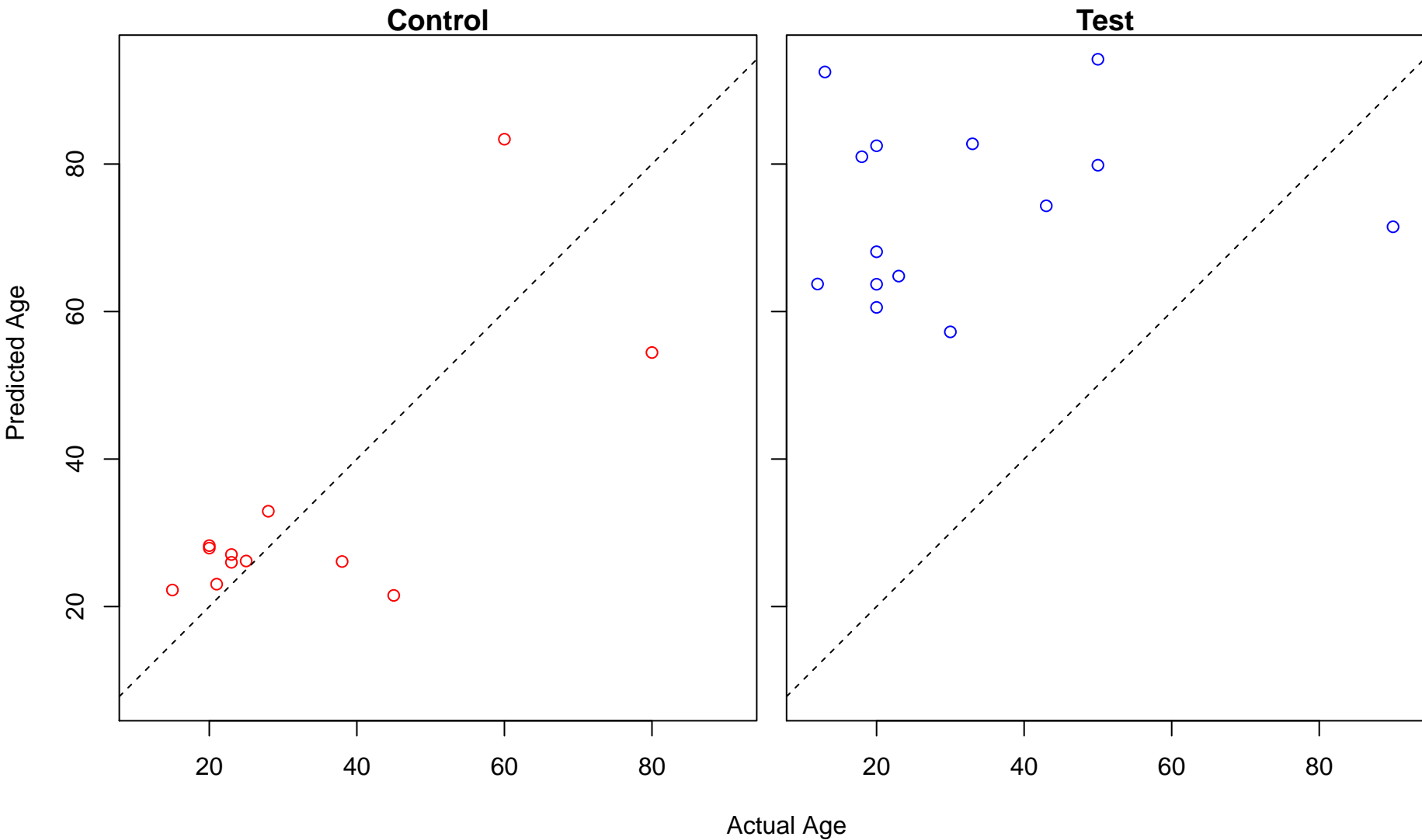
negative regulation of homeostatic process (Score: 4.989421)



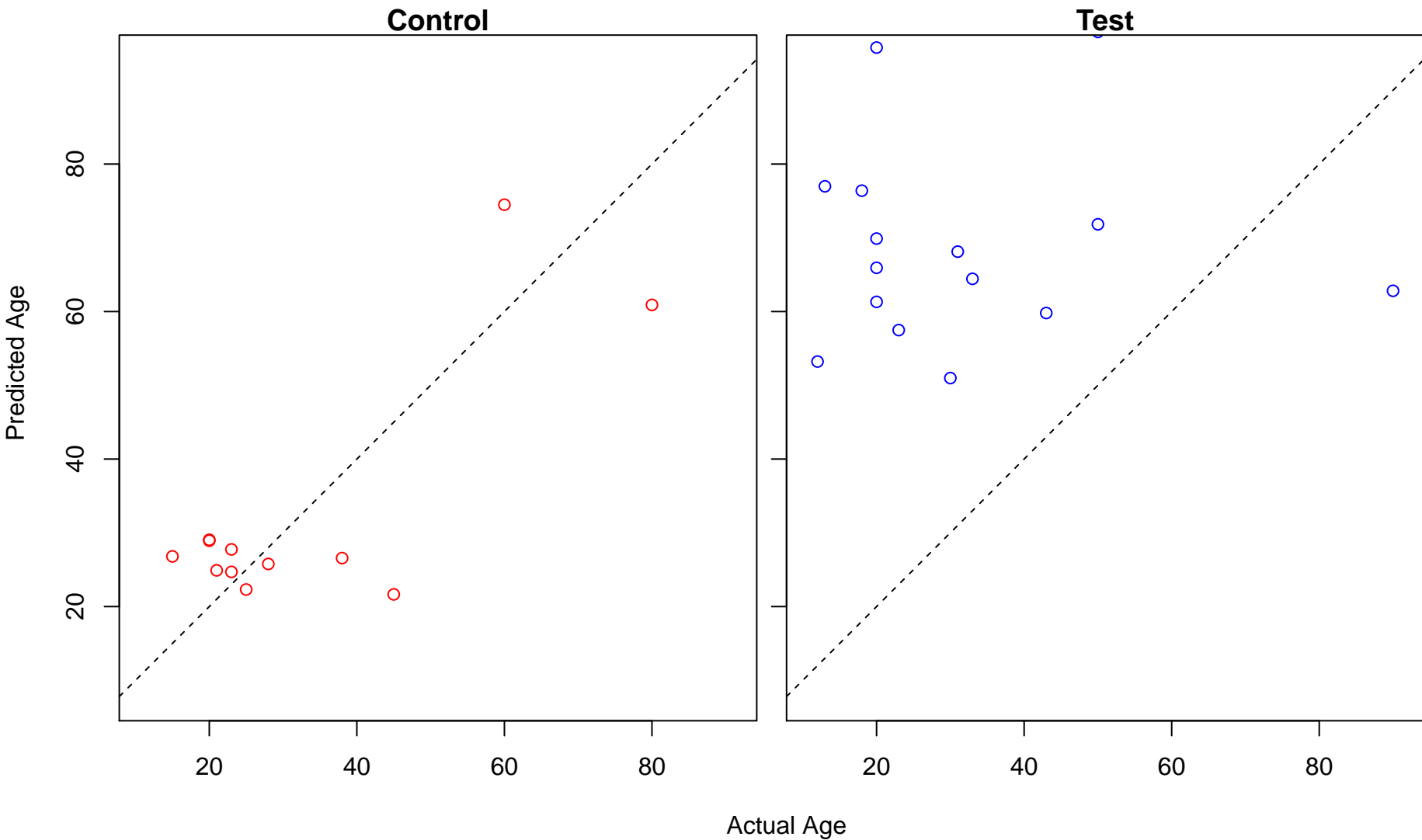
cellular response to calcium ion (Score: 4.988231)



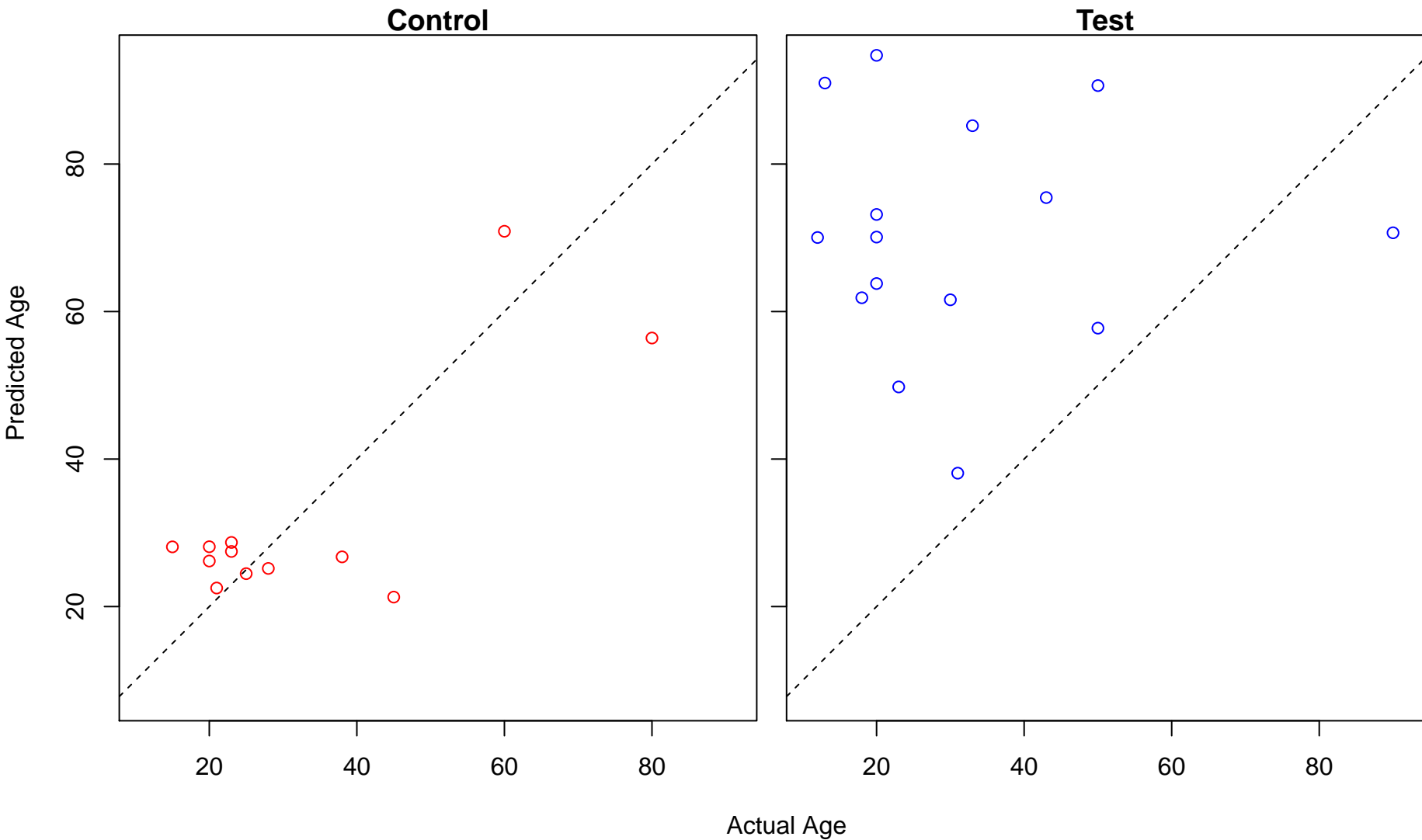
regulation of behavior (Score: 4.987557)



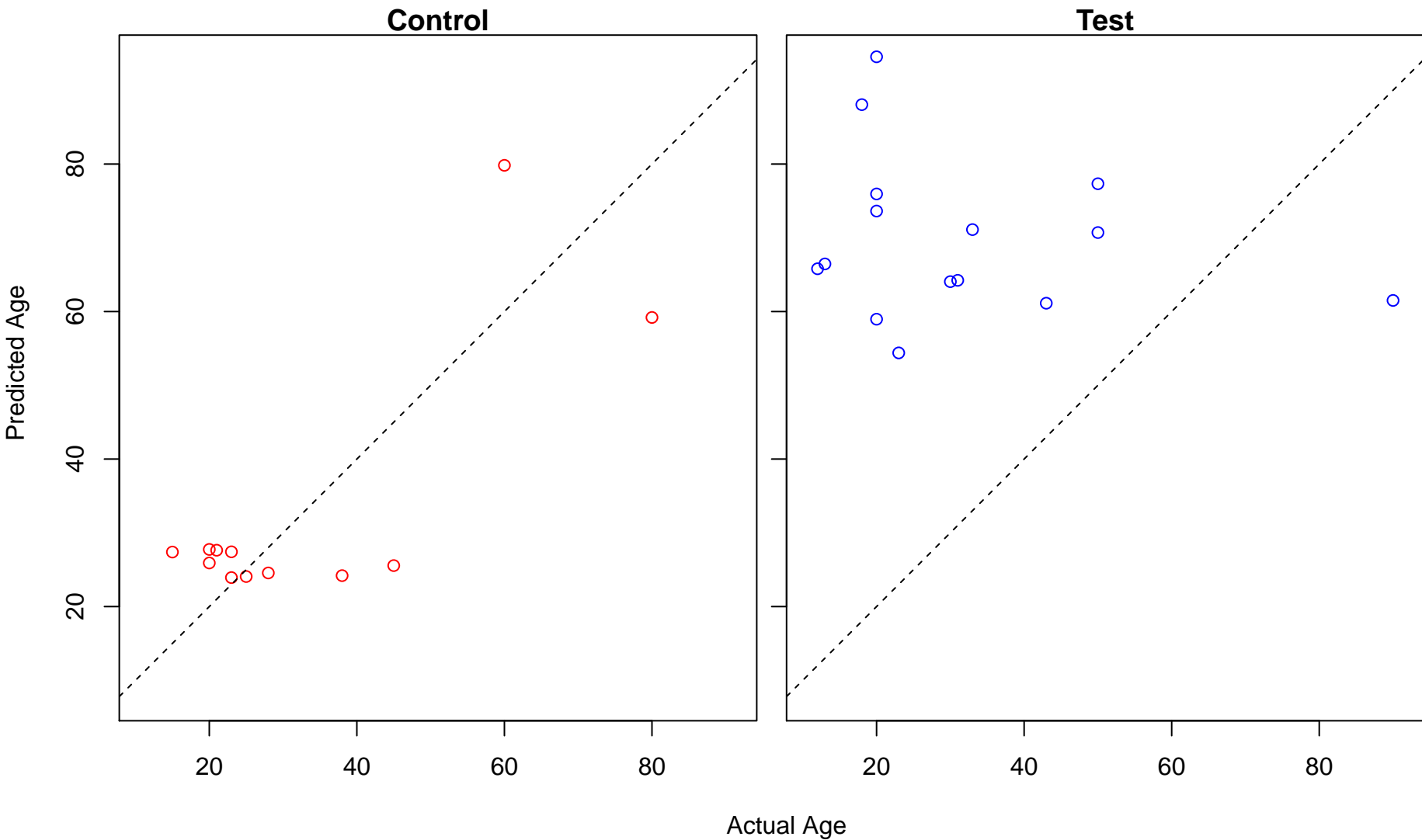
myeloid leukocyte differentiation (Score: 4.985867)



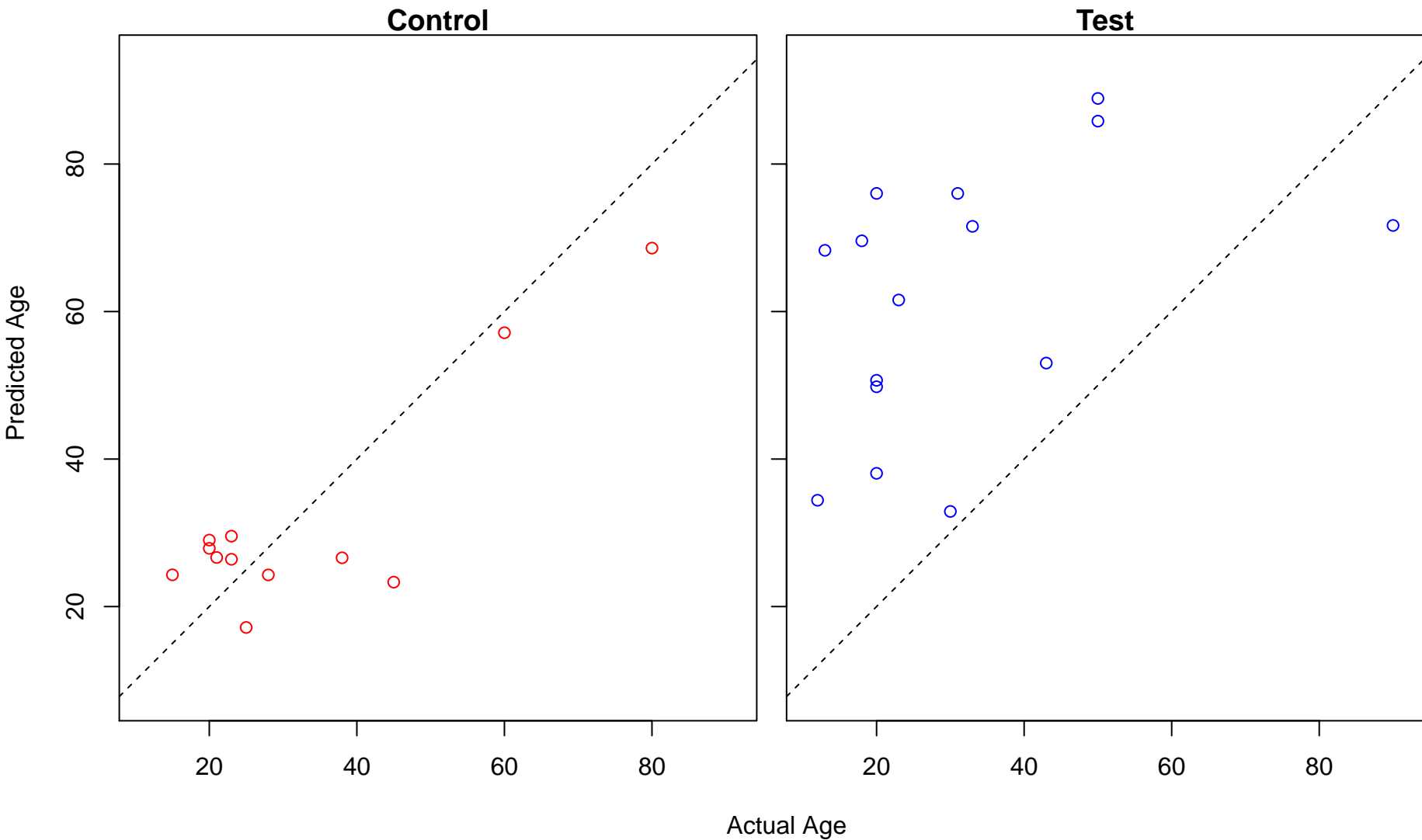
antifungal humoral response (Score: 4.985030)



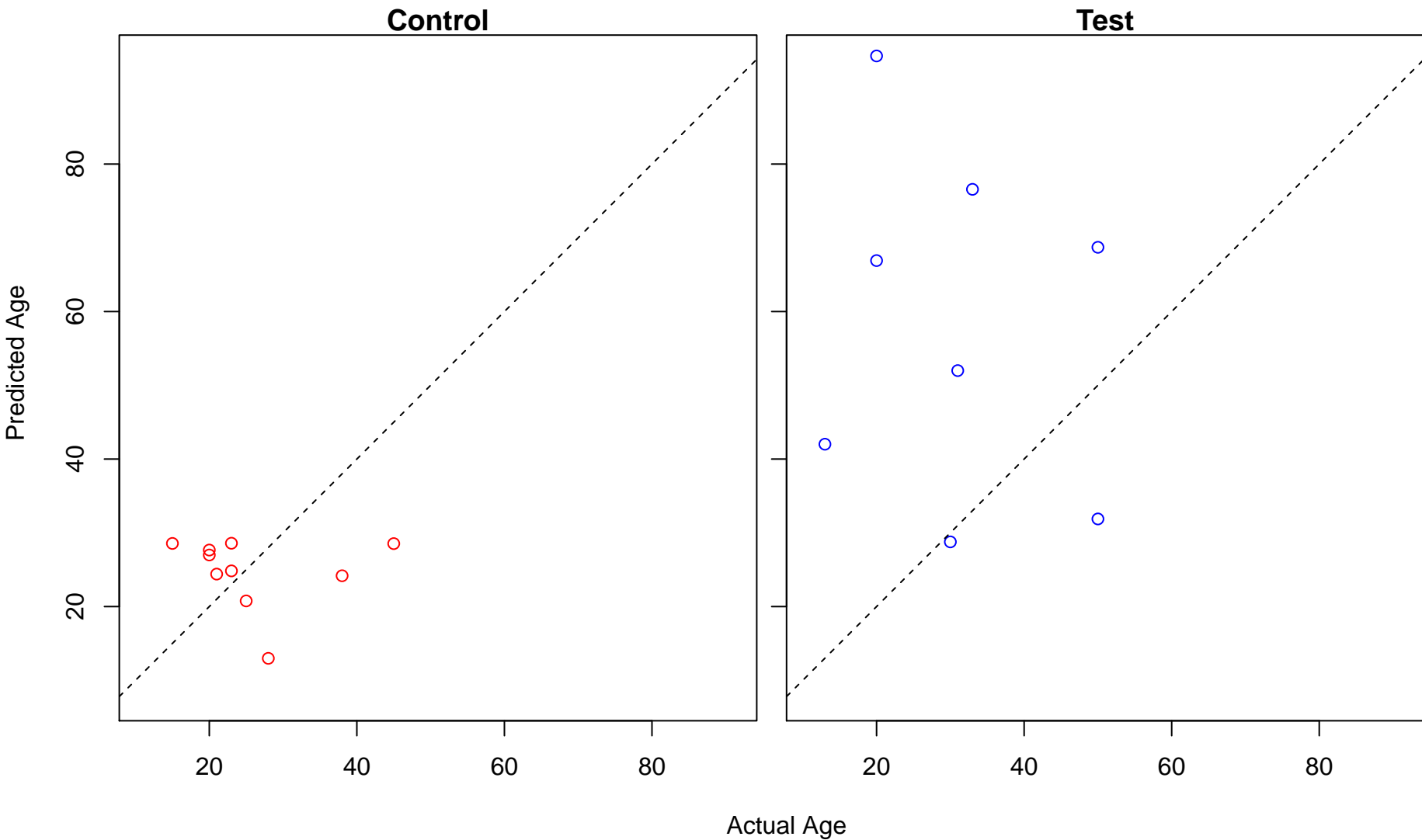
regulation of cell junction assembly (Score: 4.983535)



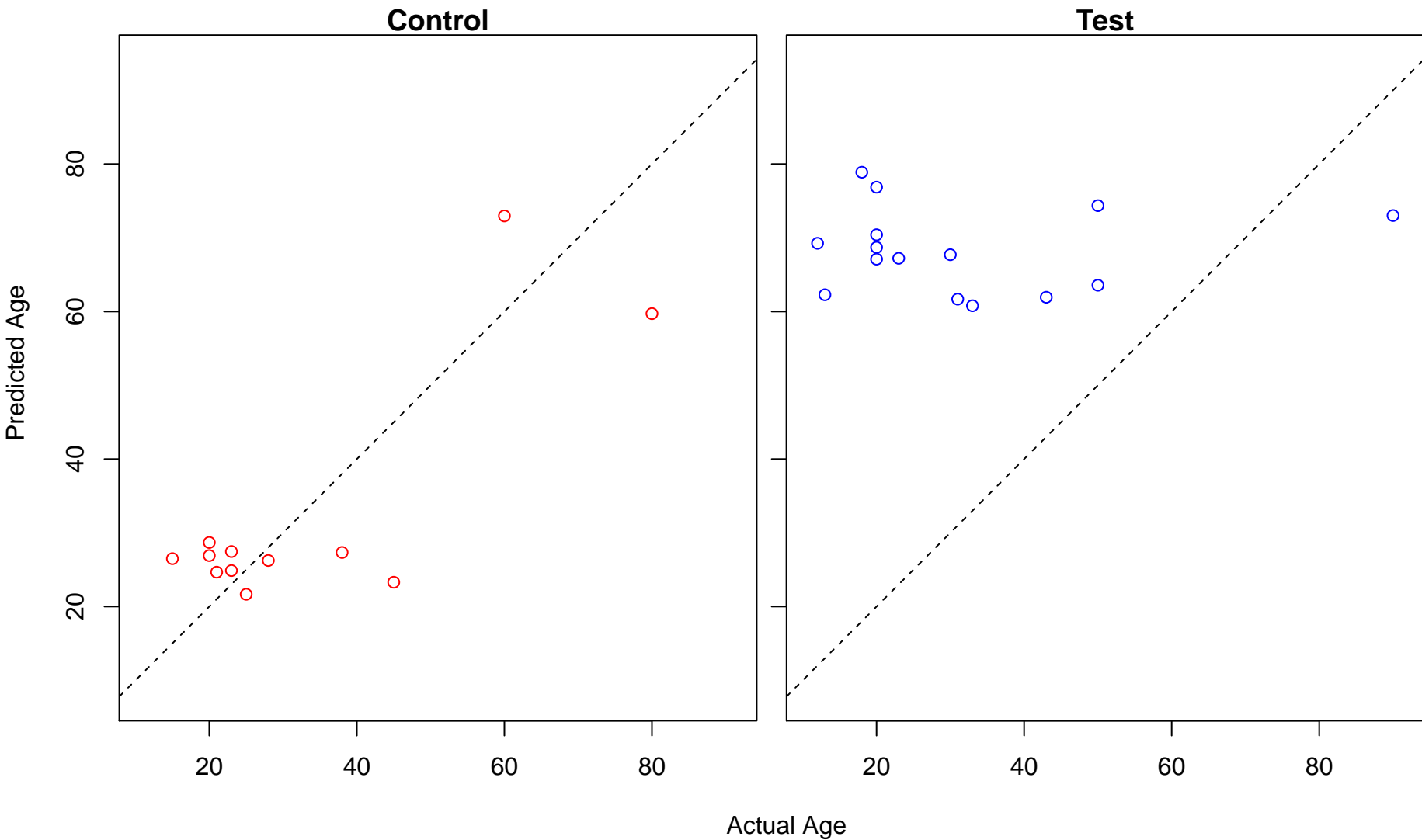
regulation of protein tyrosine kinase activity (Score: 4.982988)



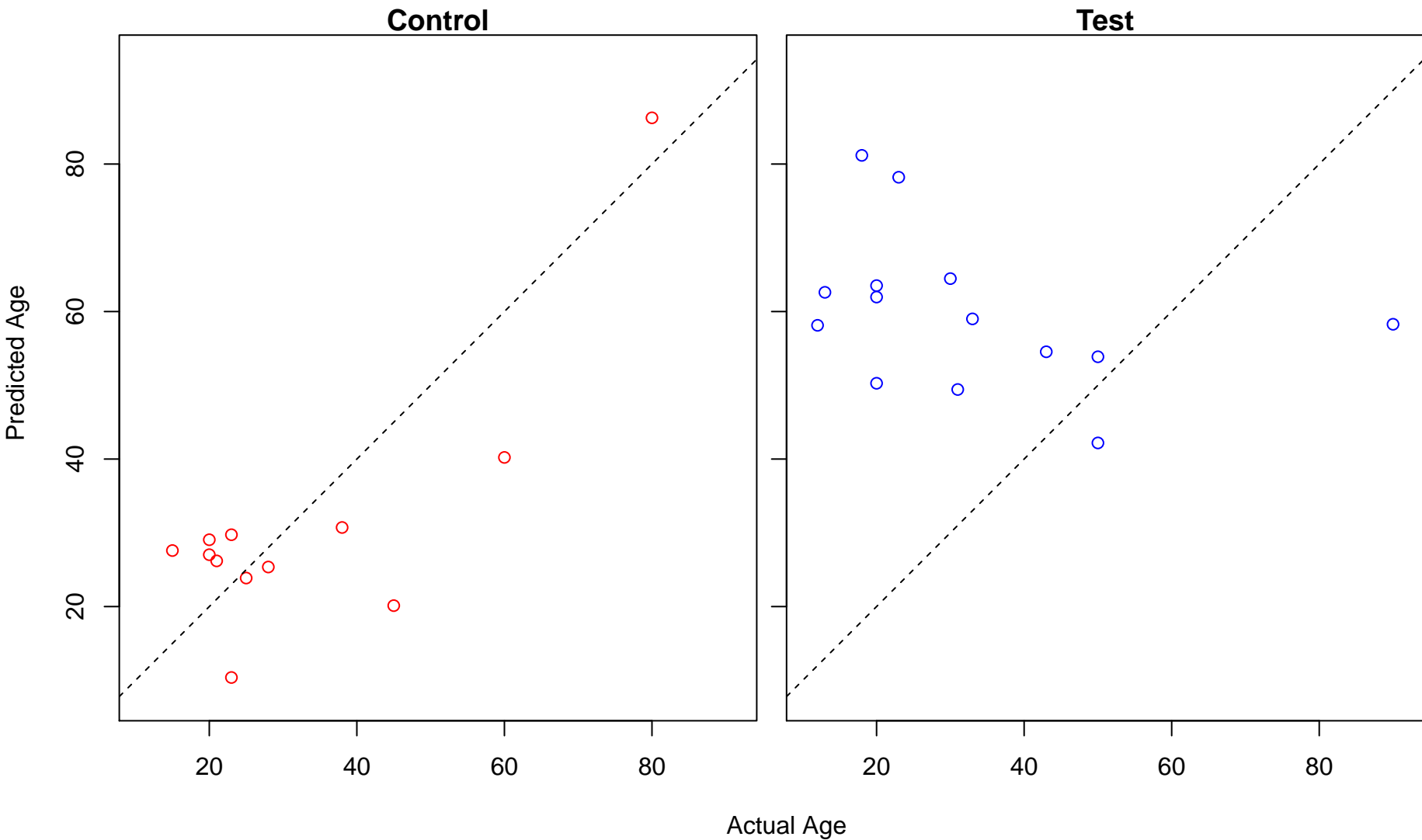
detection of chemical stimulus involved in sensory perception of smell (Score: 4.981883)



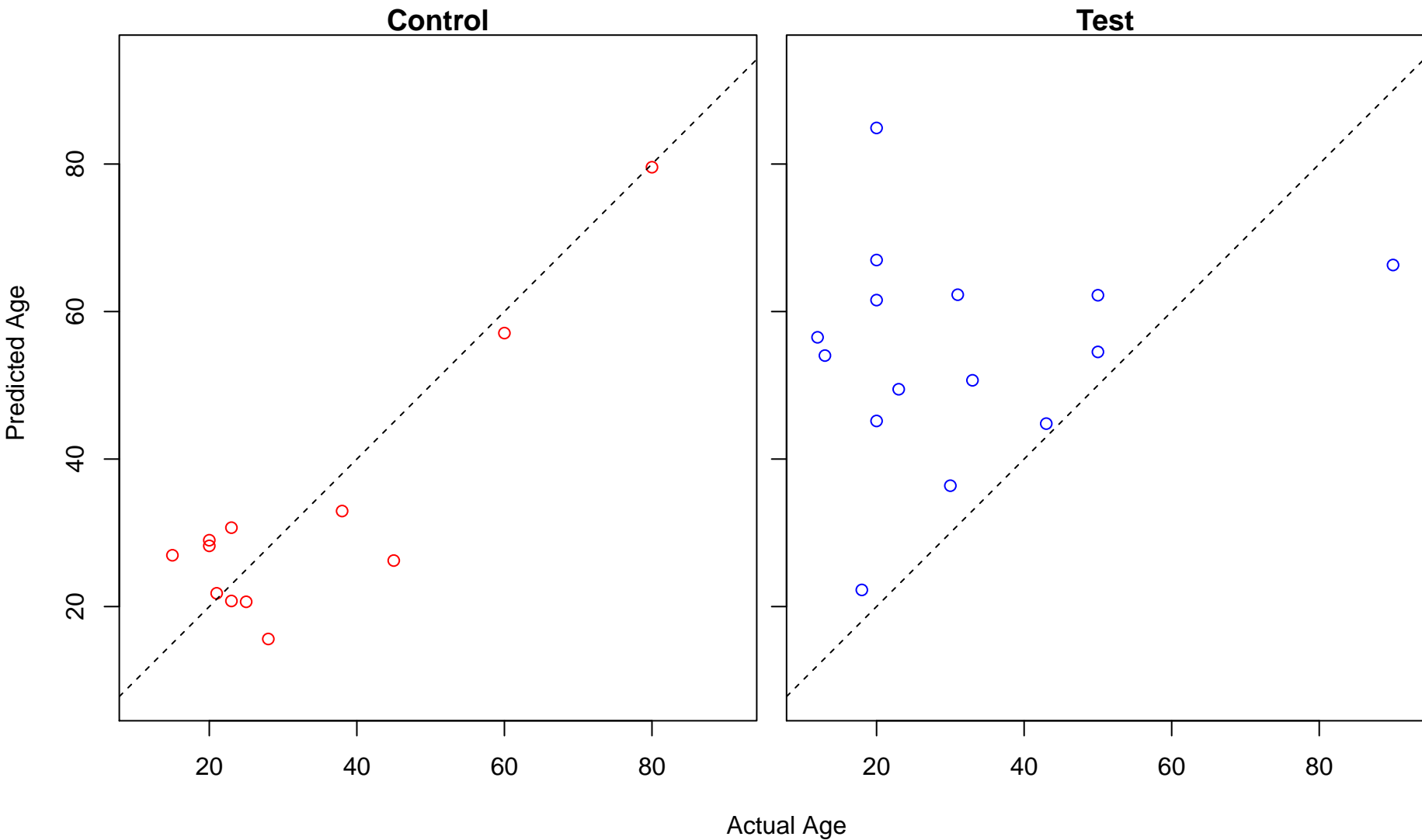
negative regulation of protein kinase activity (Score: 4.981344)



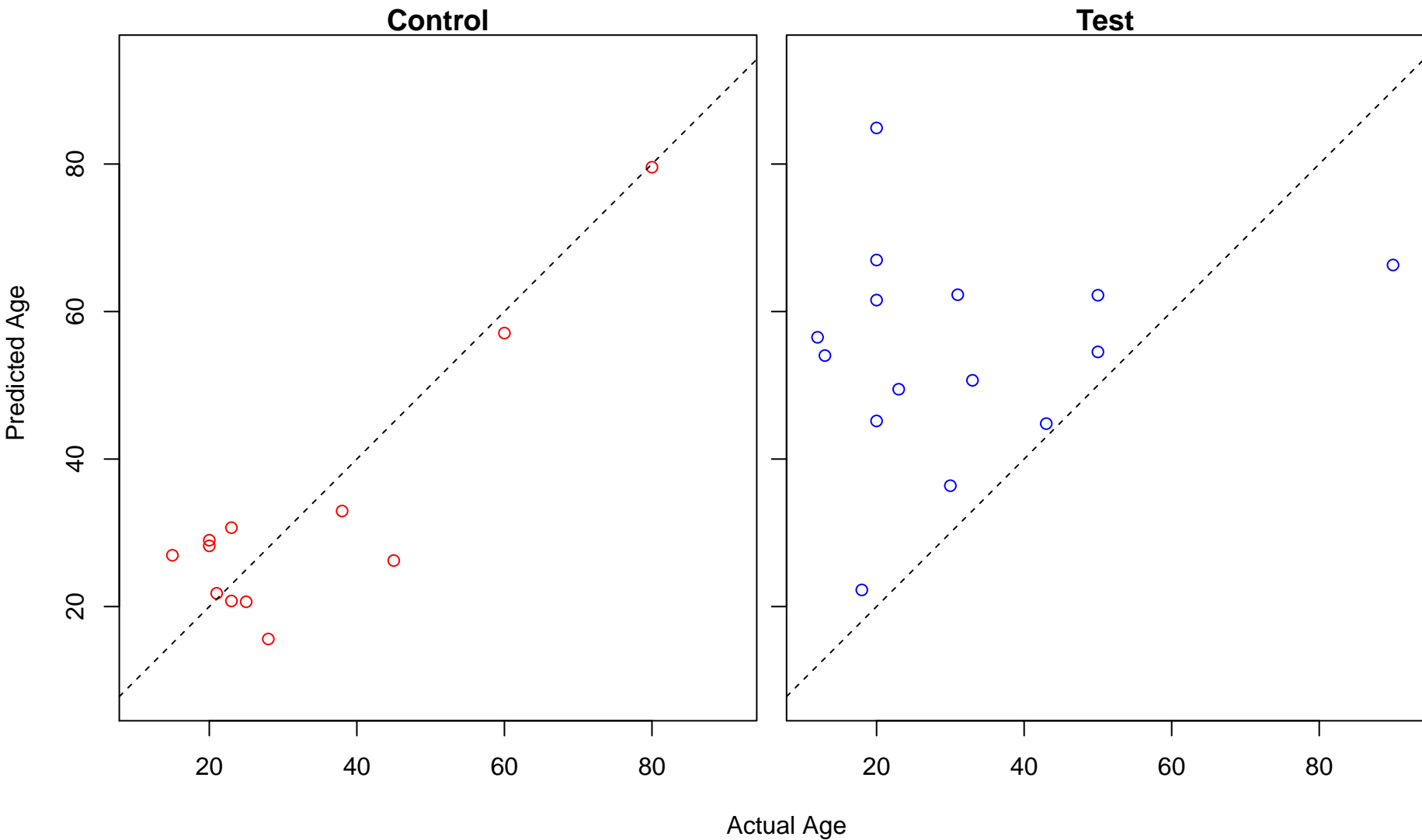
negative regulation of kidney development (Score: 4.981176)



amino-acid betaine transport (Score: 4.979882)

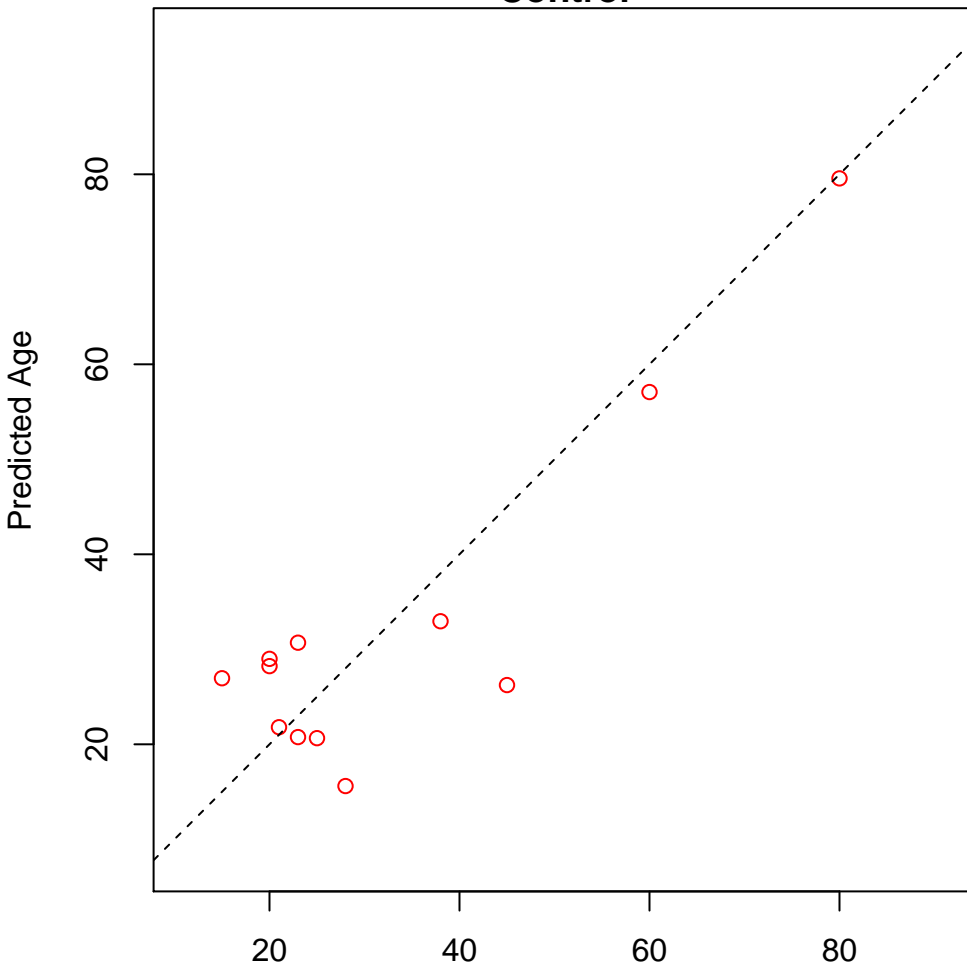


carnitine transport (Score: 4.979882)

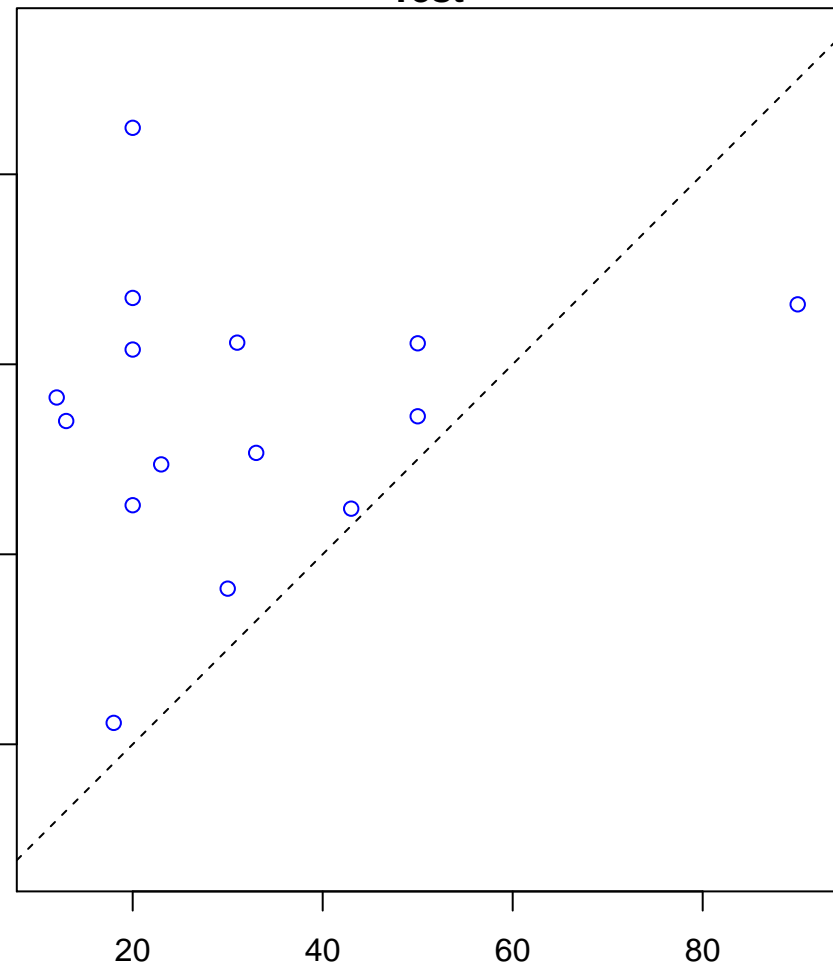


carnitine transmembrane transport (Score: 4.979872)

Control

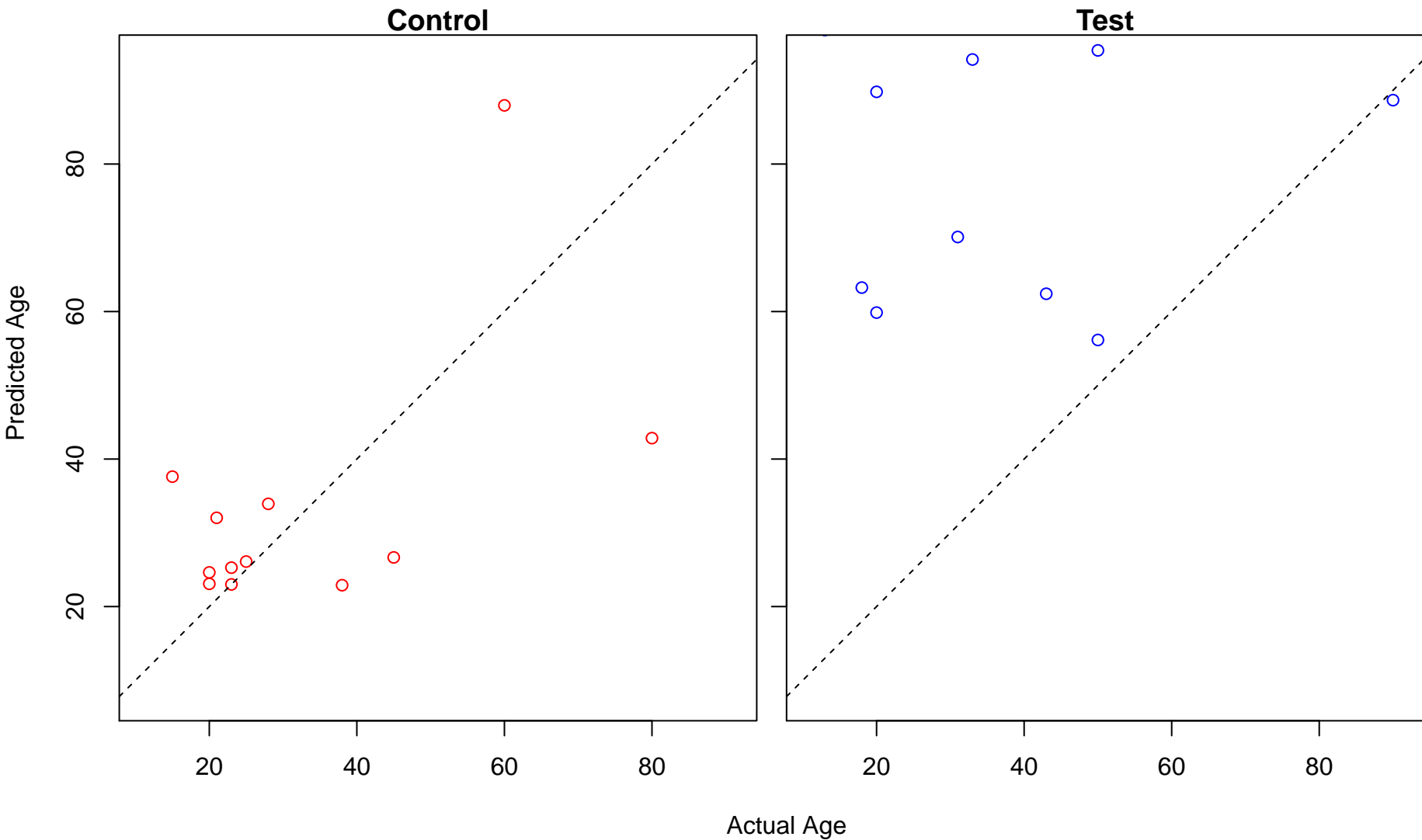


Test



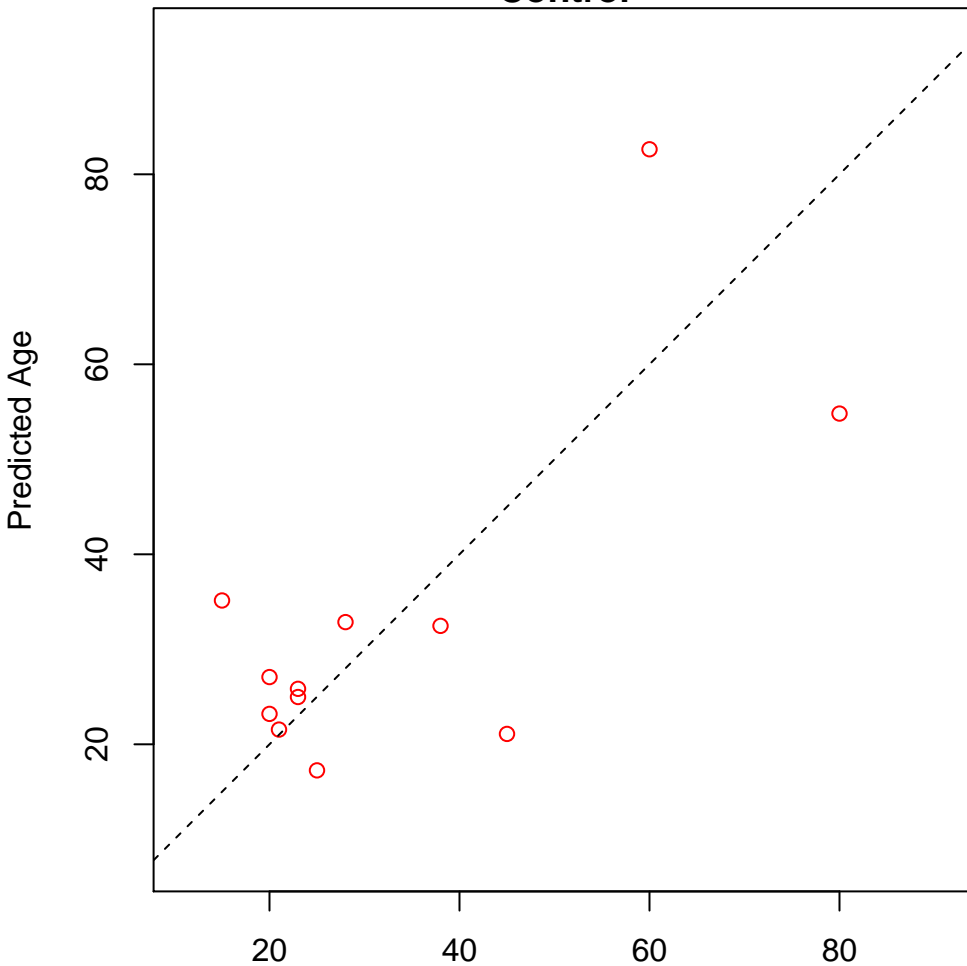
Actual Age

regulation of hexokinase activity (Score: 4.976696)

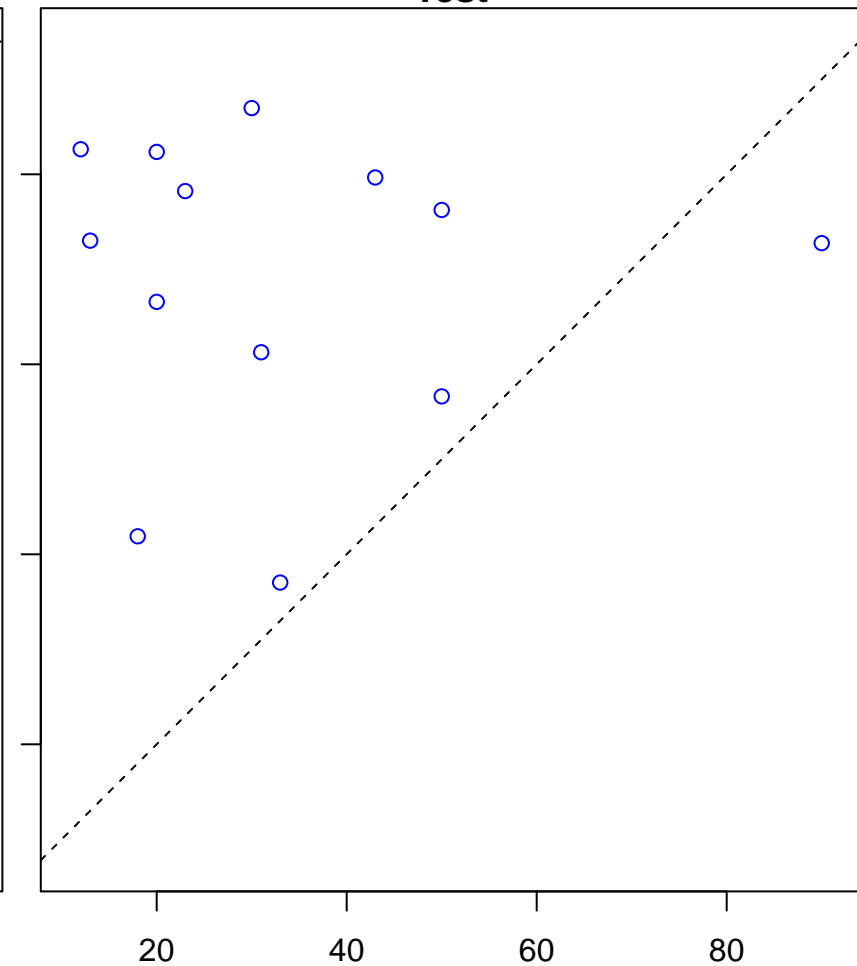


blood coagulation, intrinsic pathway (Score: 4.973218)

Control

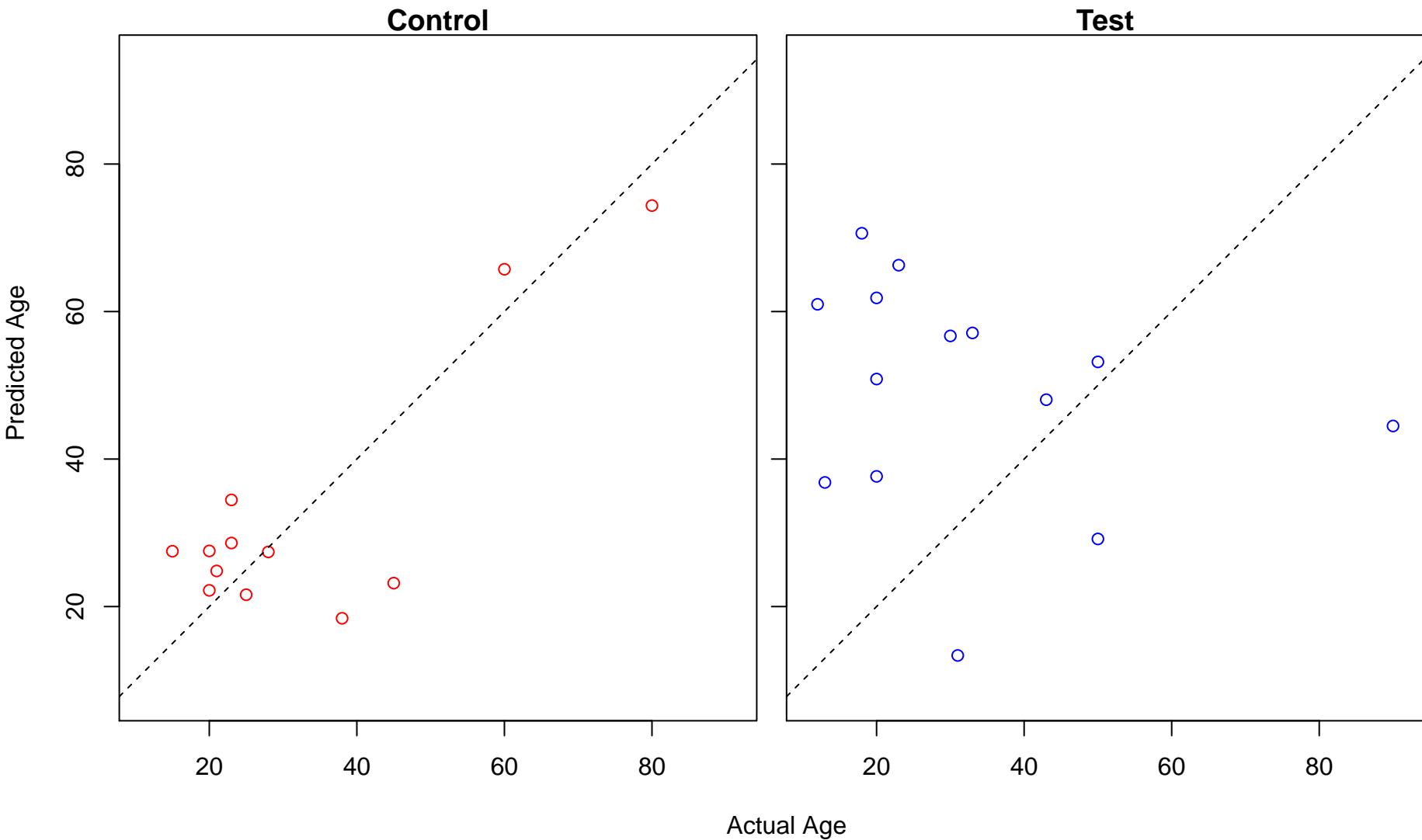


Test

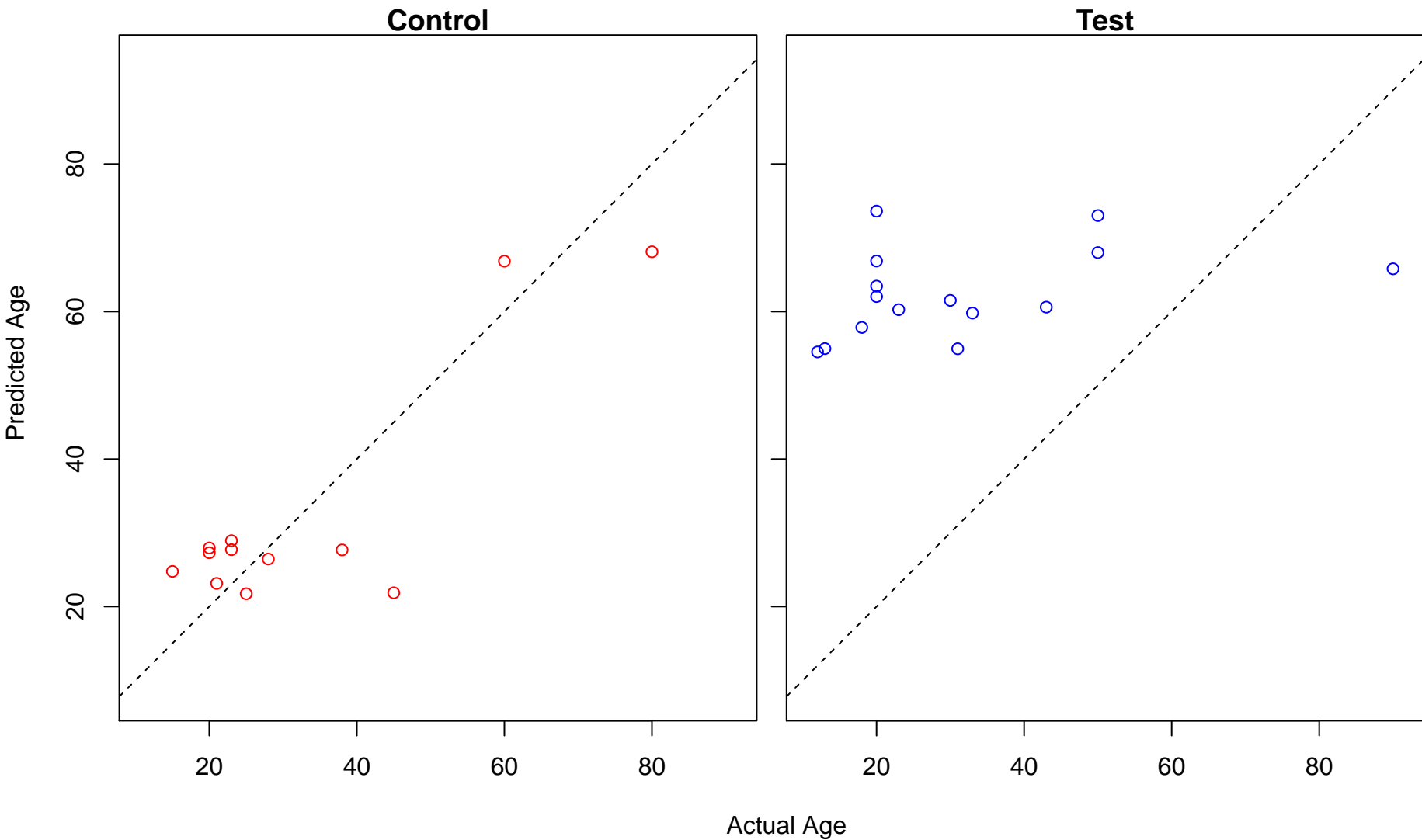


Actual Age

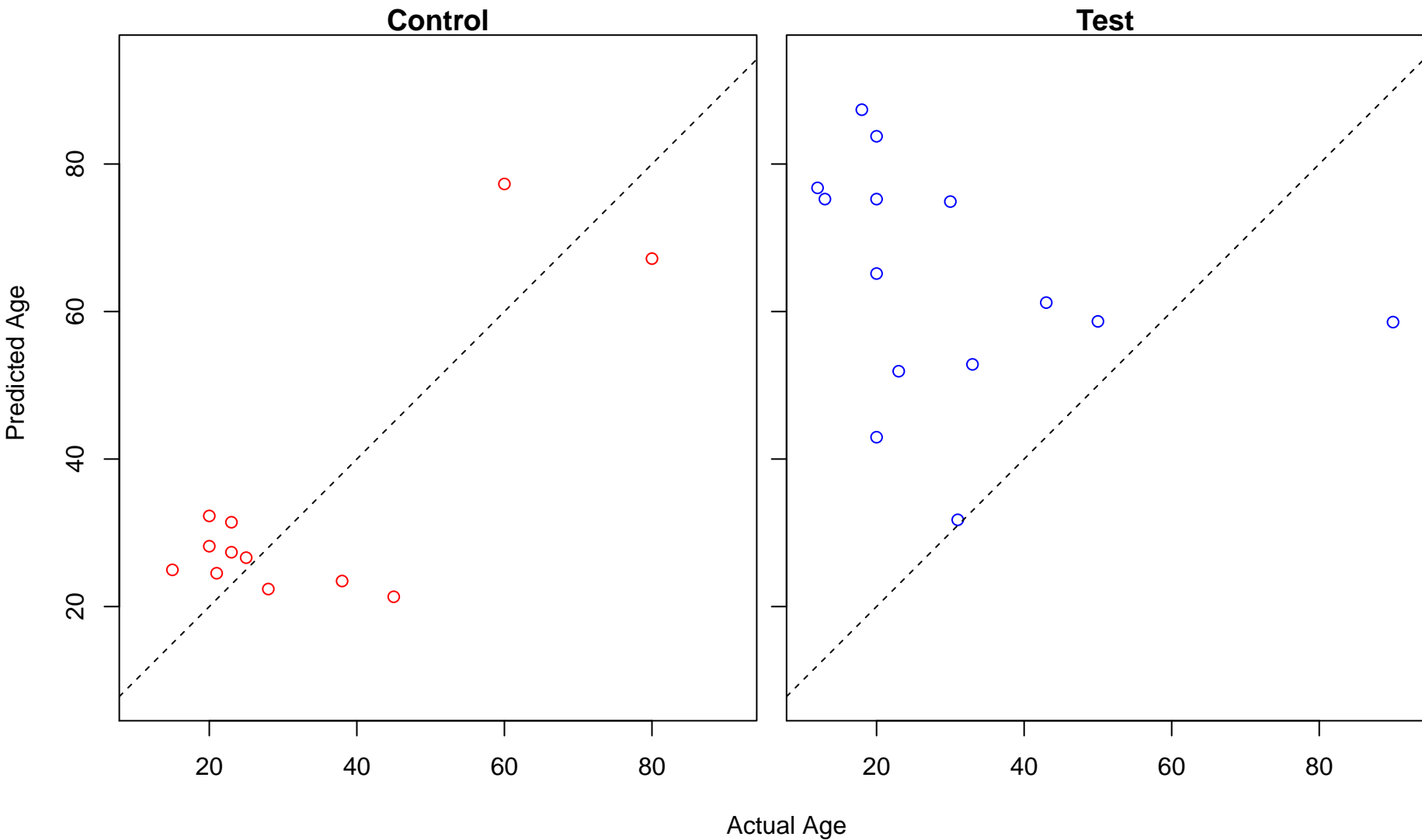
alpha-amino acid catabolic process (Score: 4.971482)



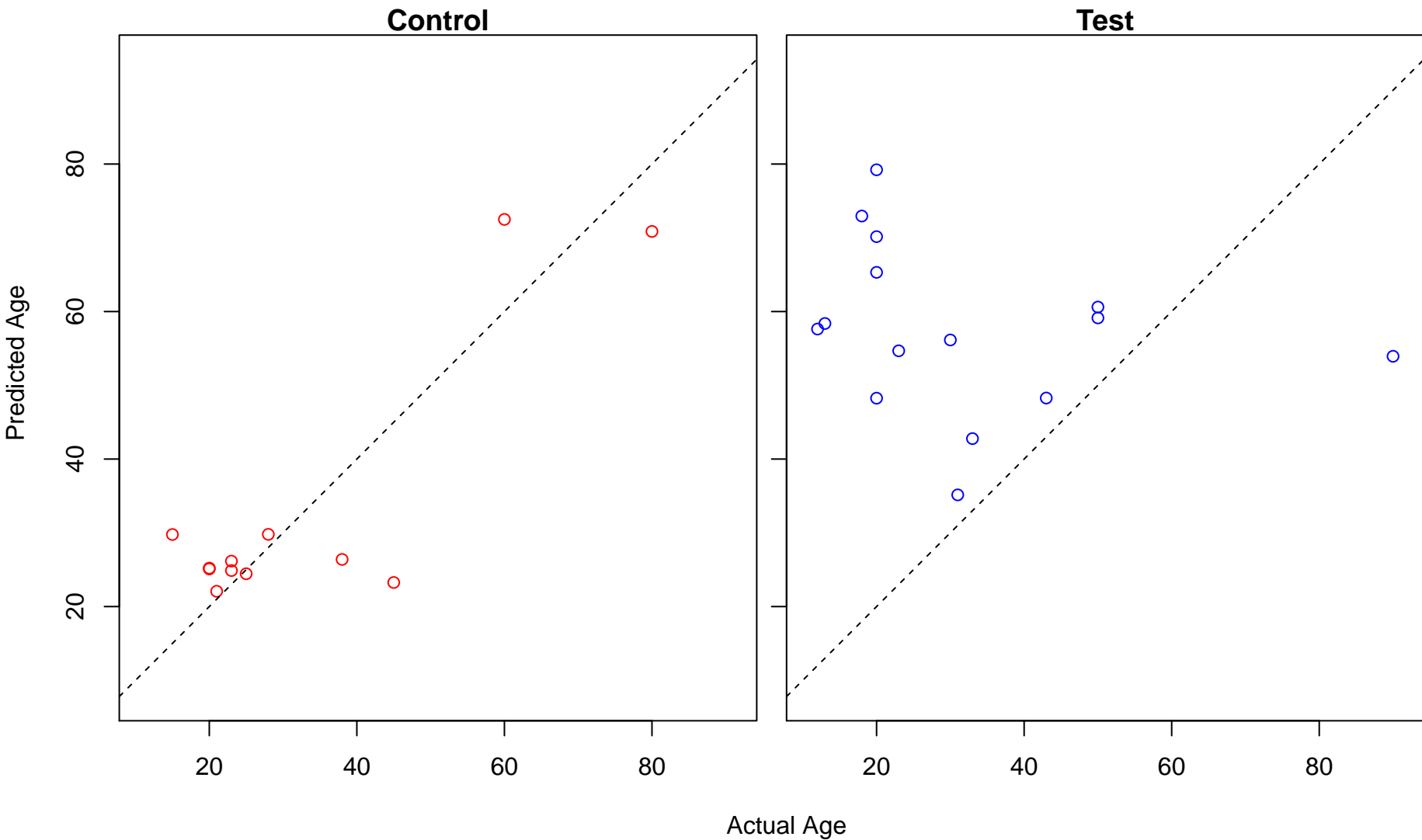
positive regulation of myeloid leukocyte differentiation (Score: 4.969563)



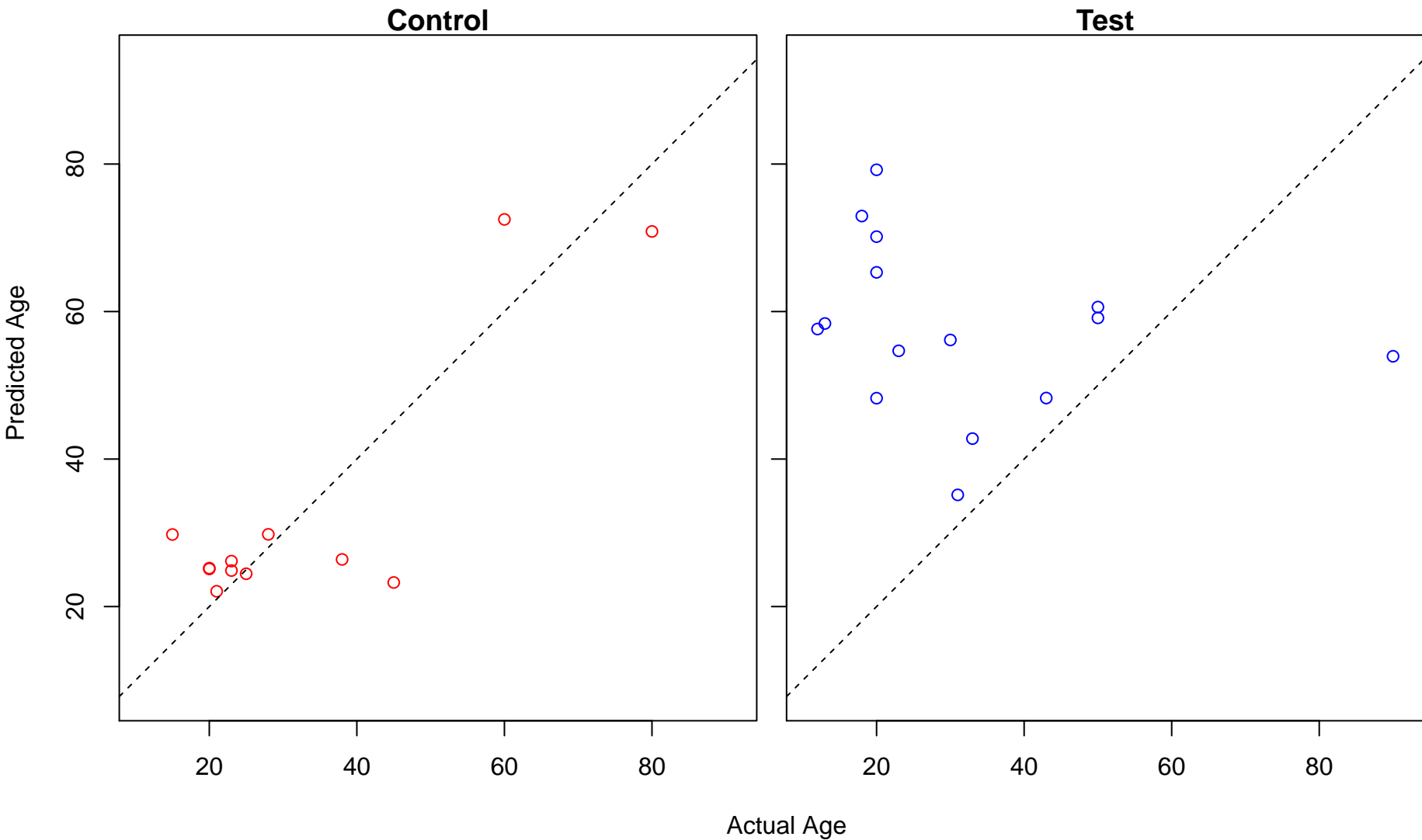
positive regulation of cellular amino acid metabolic process (Score: 4.969047)



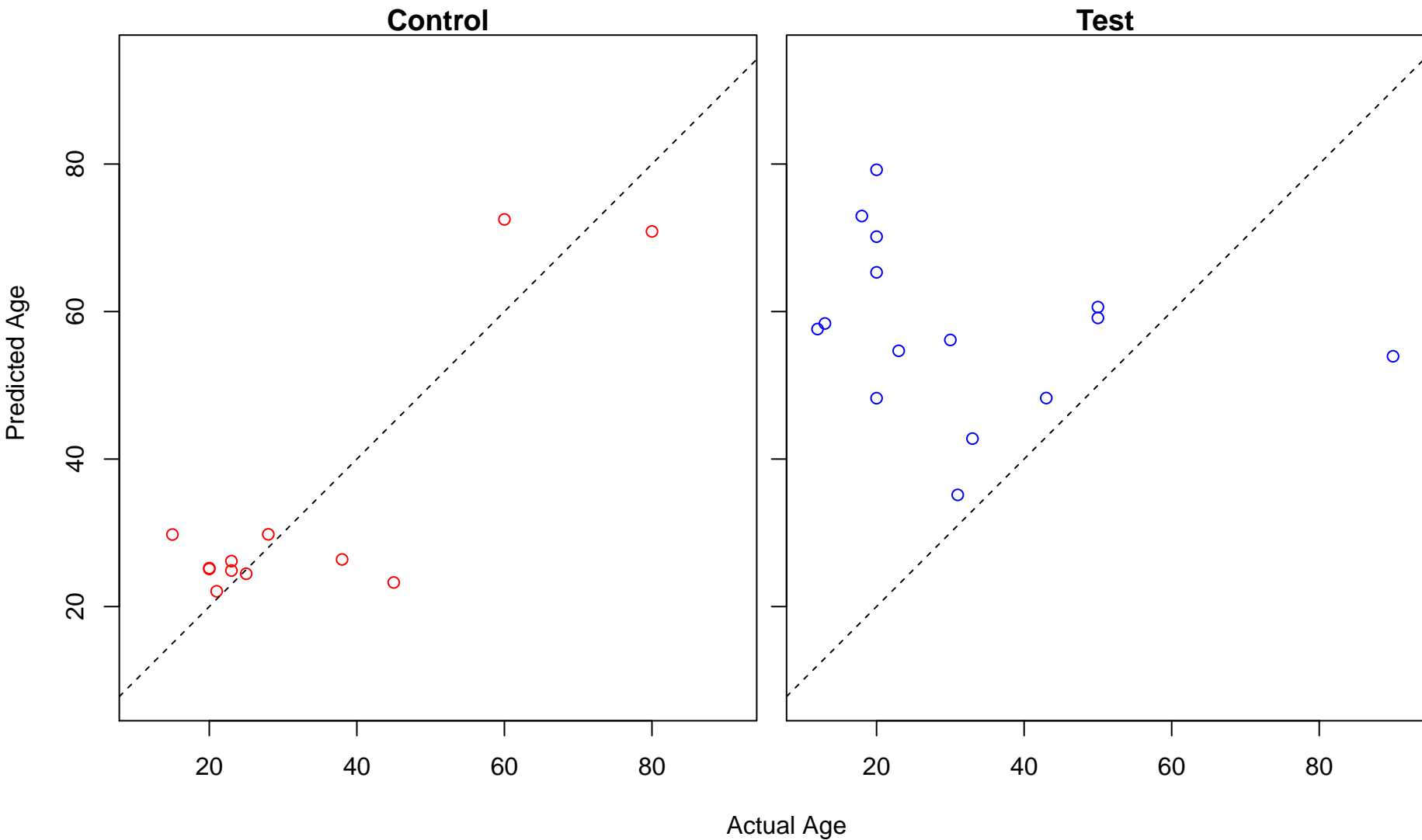
negative regulation of mitotic metaphase/anaphase transition (Score: 4.968857)



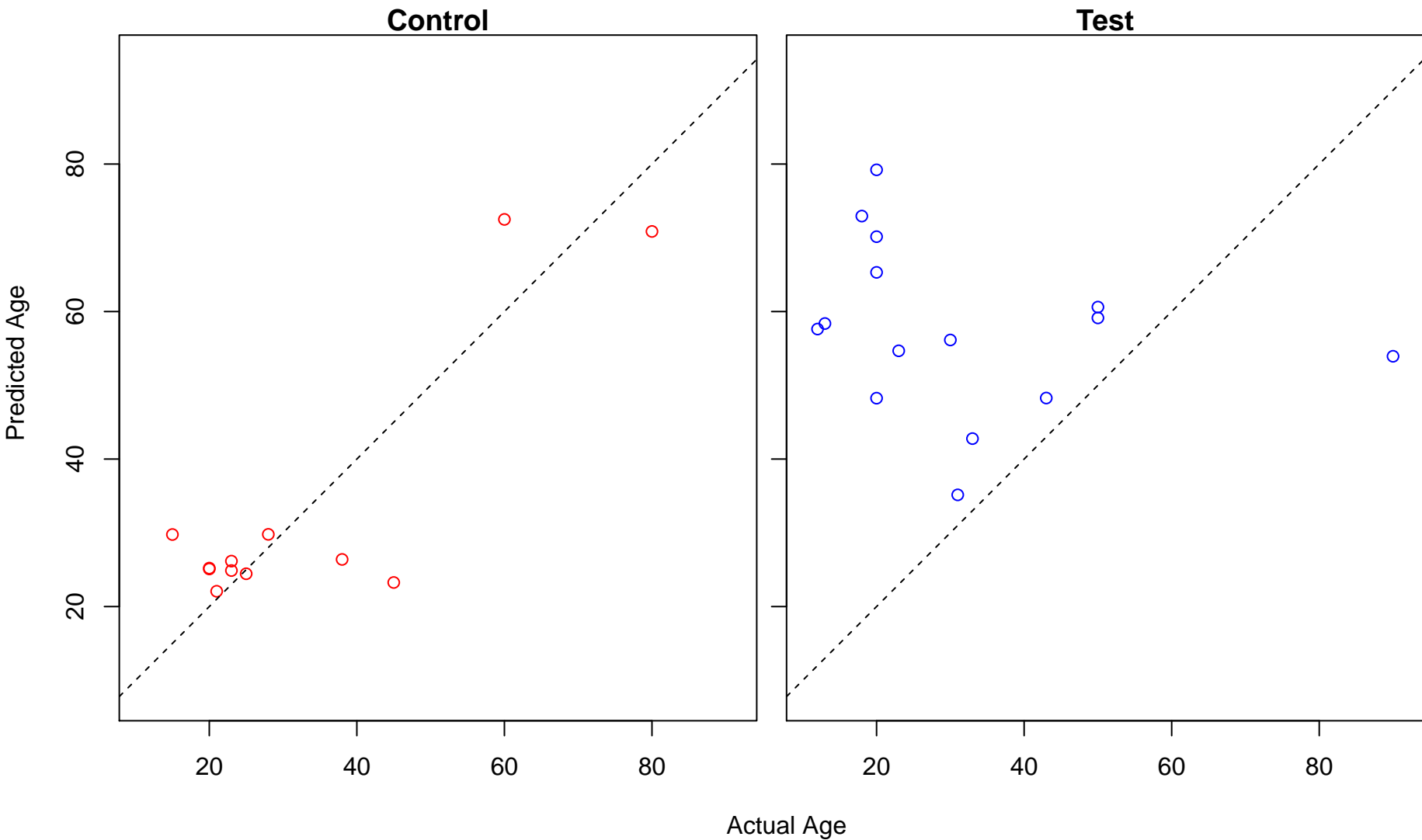
mitotic spindle checkpoint (Score: 4.968857)



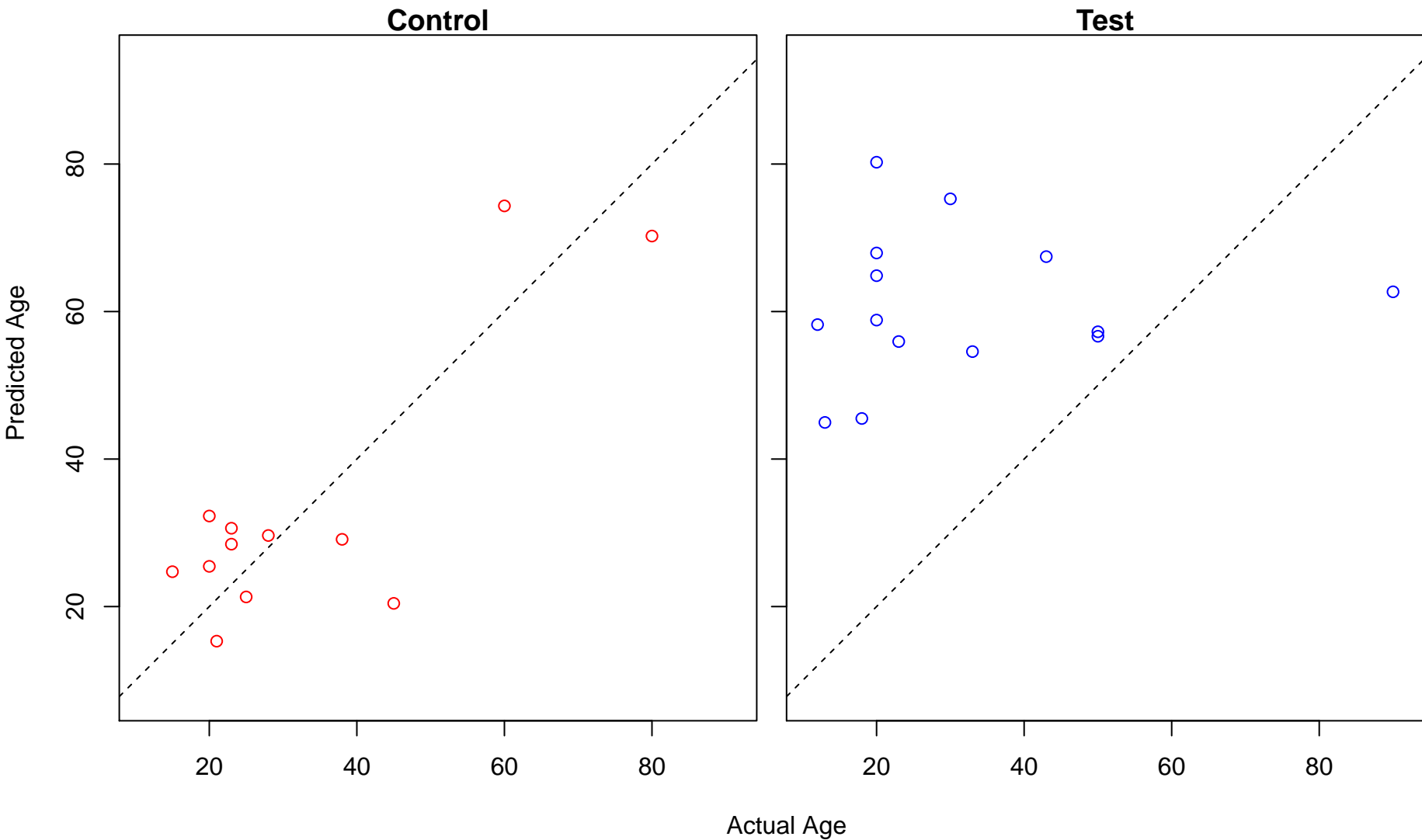
negative regulation of mitotic sister chromatid separation (Score: 4.968857)



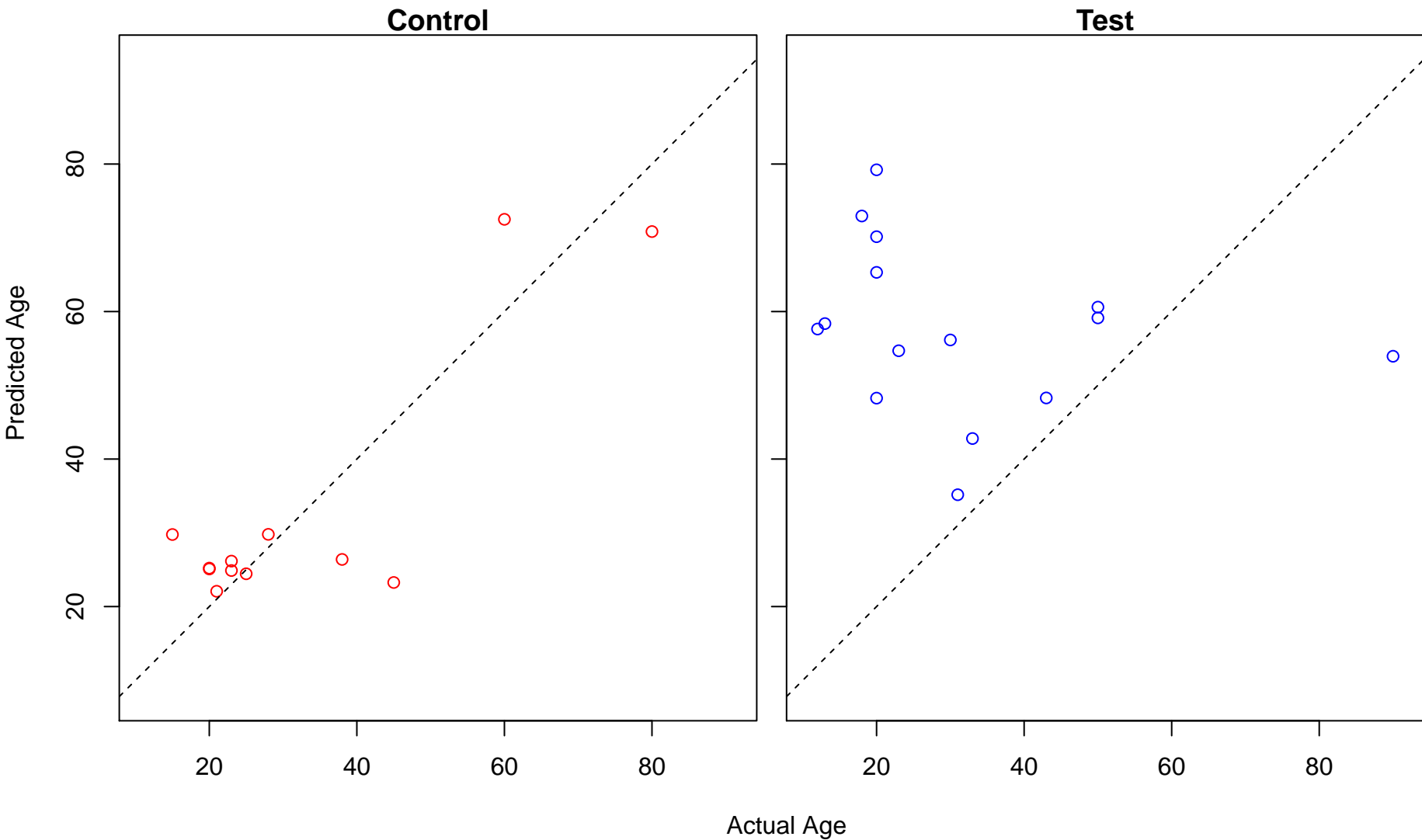
negative regulation of metaphase/anaphase transition of cell cycle (Score: 4.968279)



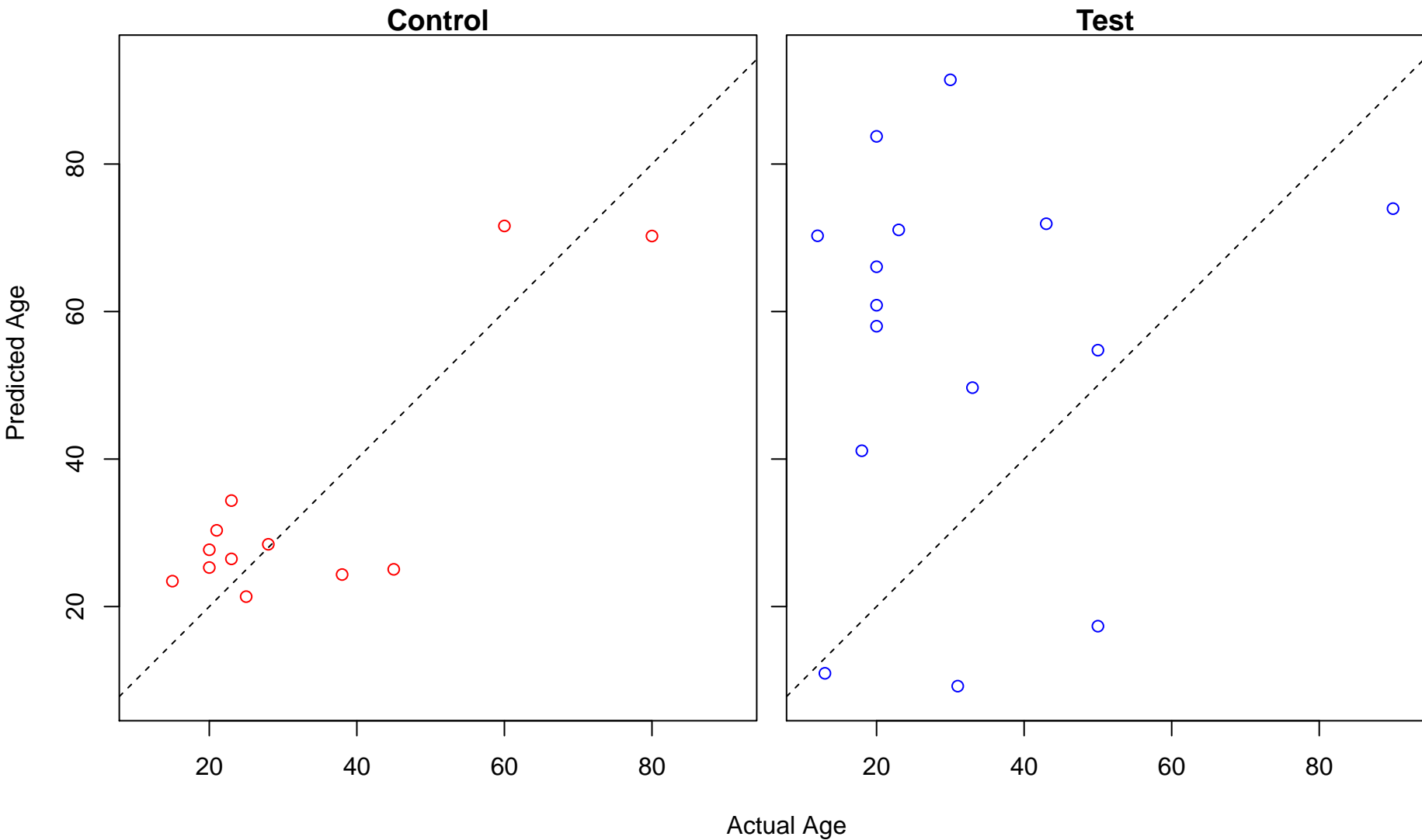
cytokine production (Score: 4.96623)



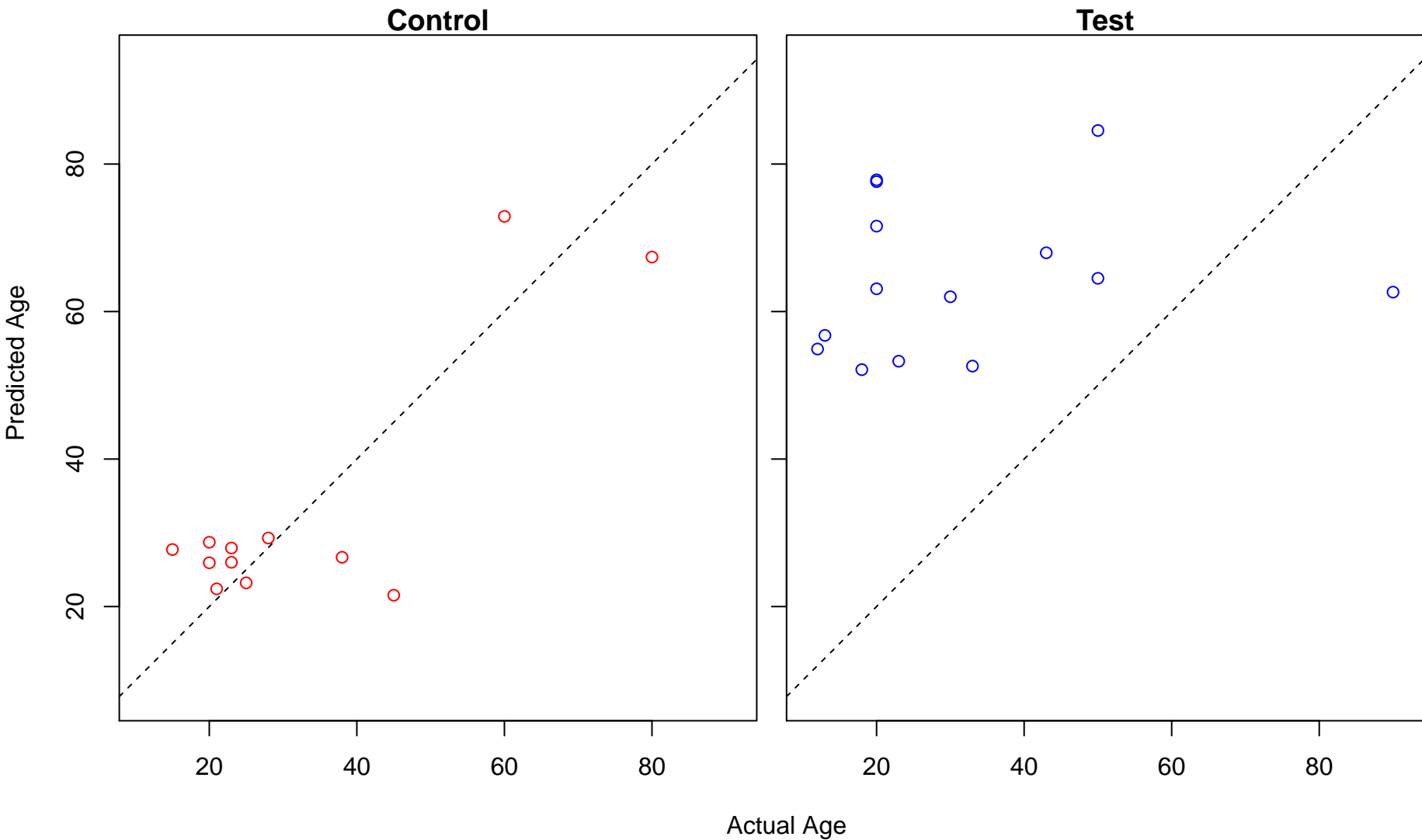
spindle checkpoint (Score: 4.966344)



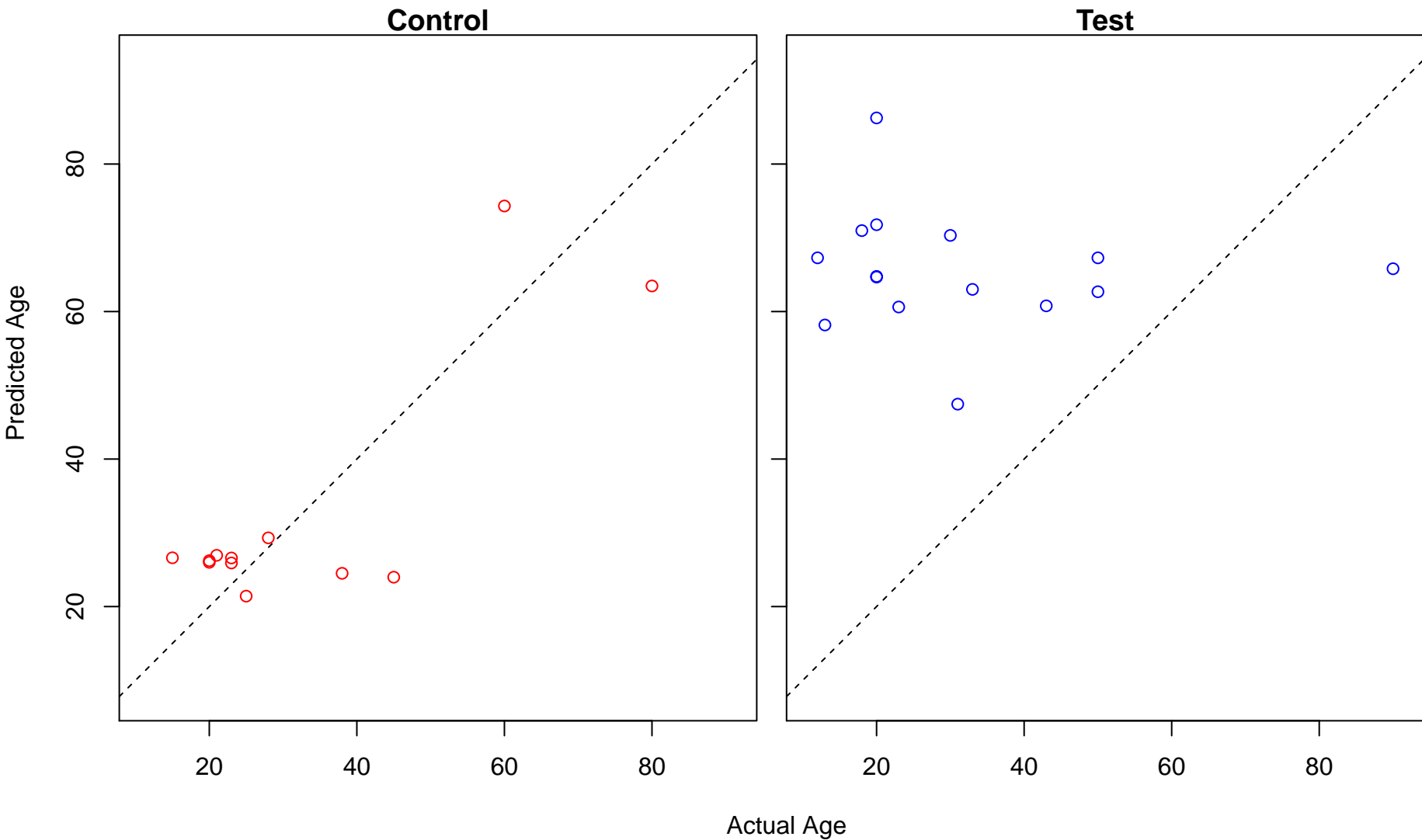
mitochondrion localization (Score: 4.966087)



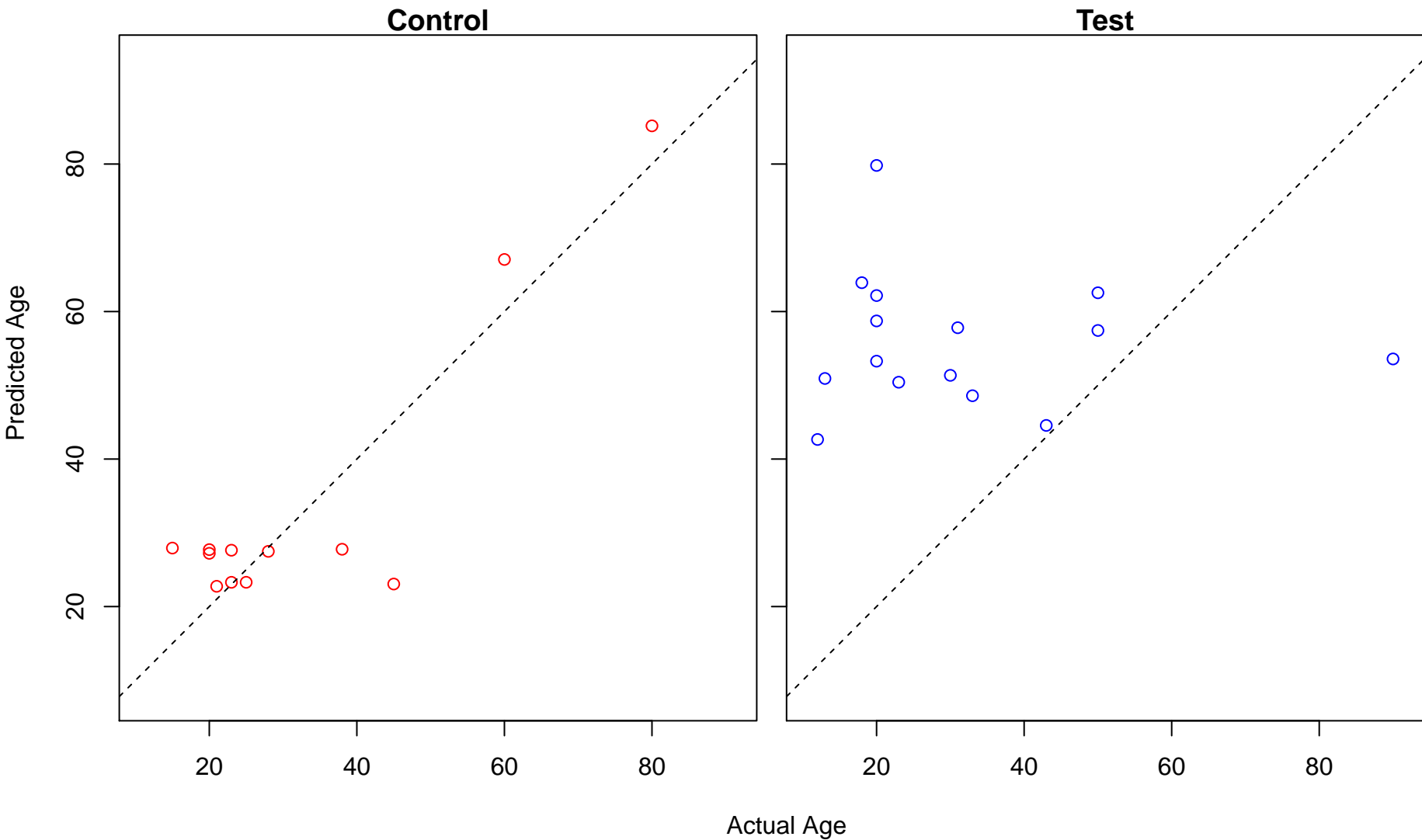
regulation of cysteine-type endopeptidase activity (Score: 4.963015)



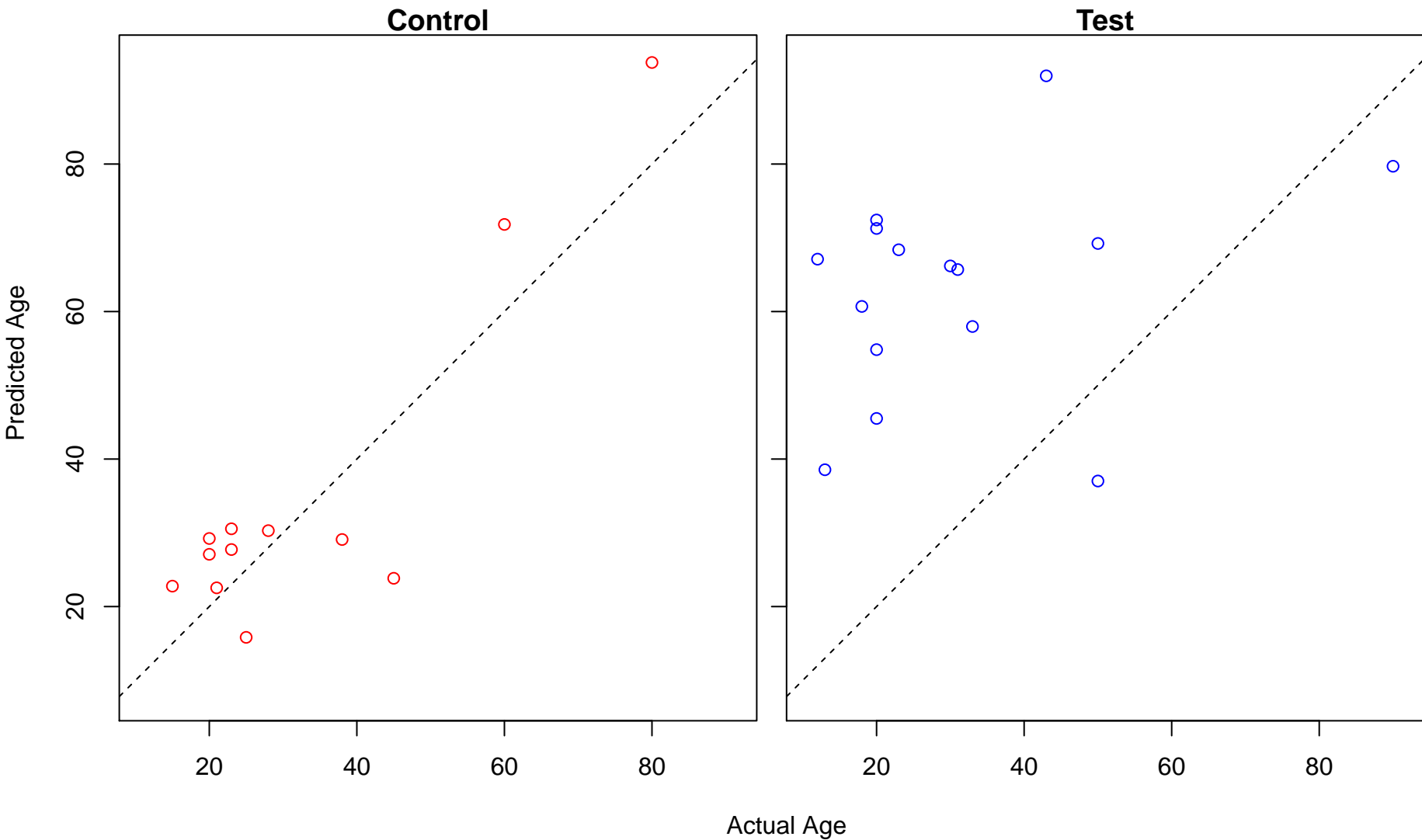
positive regulation of cyclin-dependent protein serine/threonine kinase activity (Score: 4.960601)



secretion (Score: 4.959412)

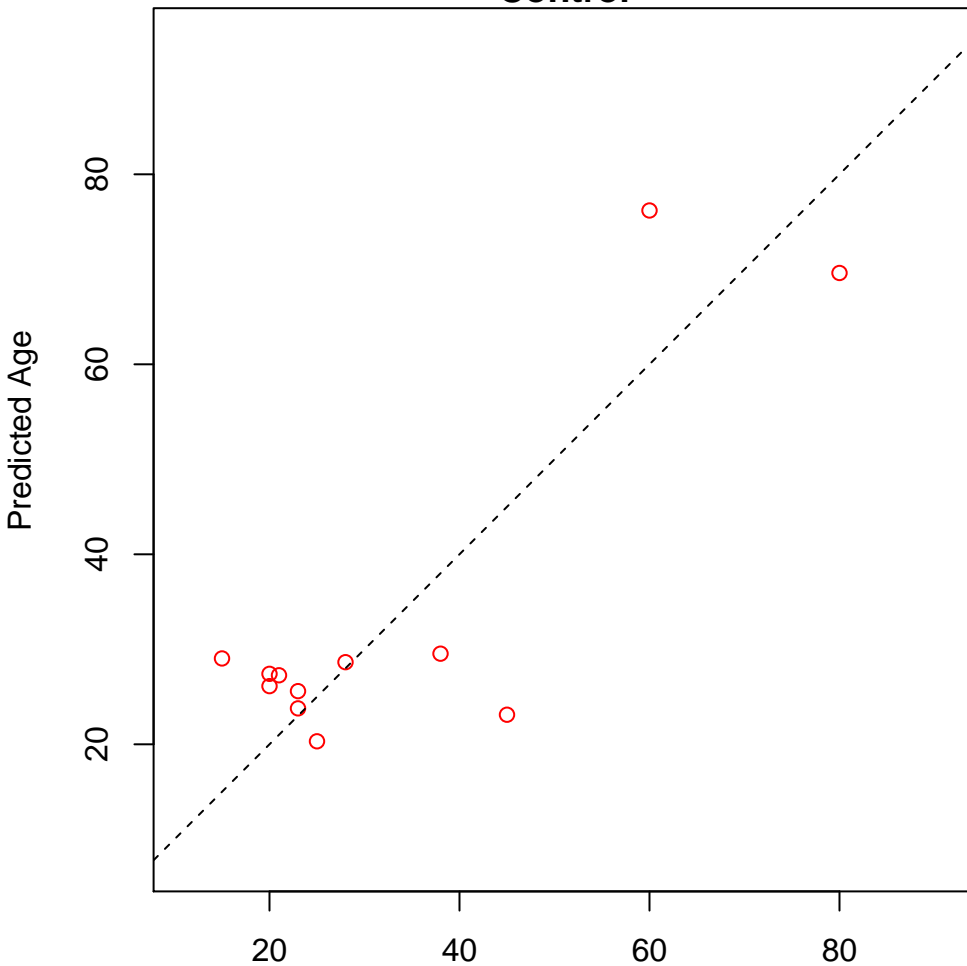


protein localization to microtubule cytoskeleton (Score: 4.958853)

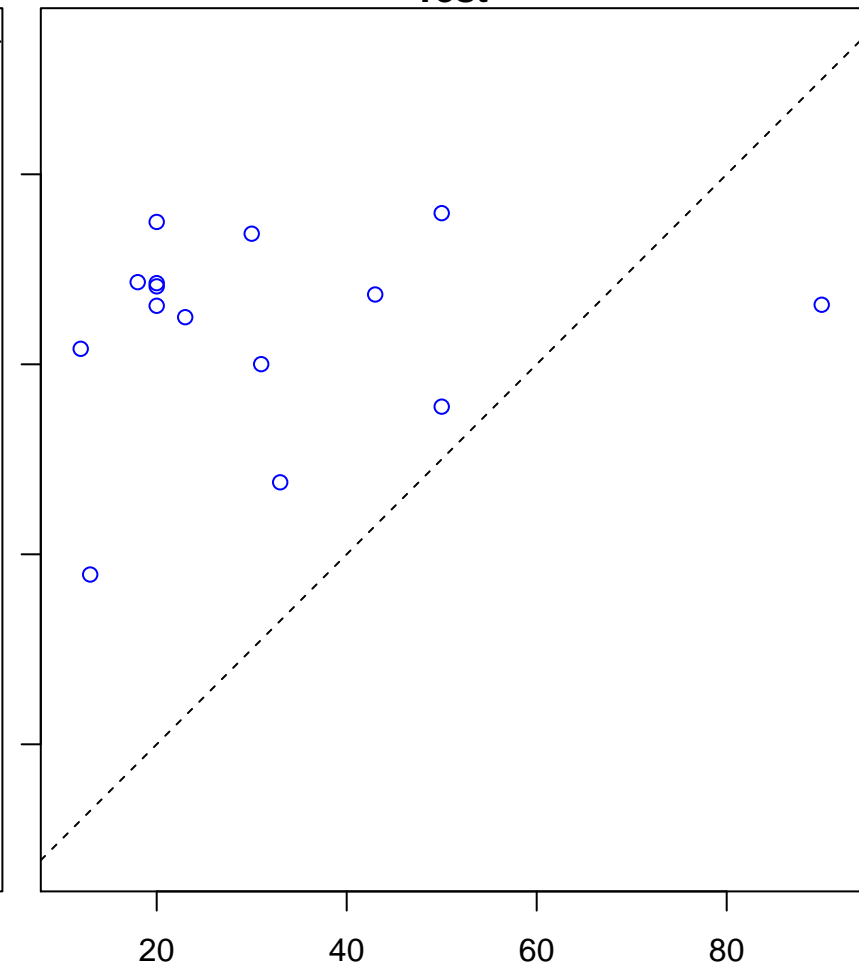


extracellular structure organization (Score: 4.957758)

Control

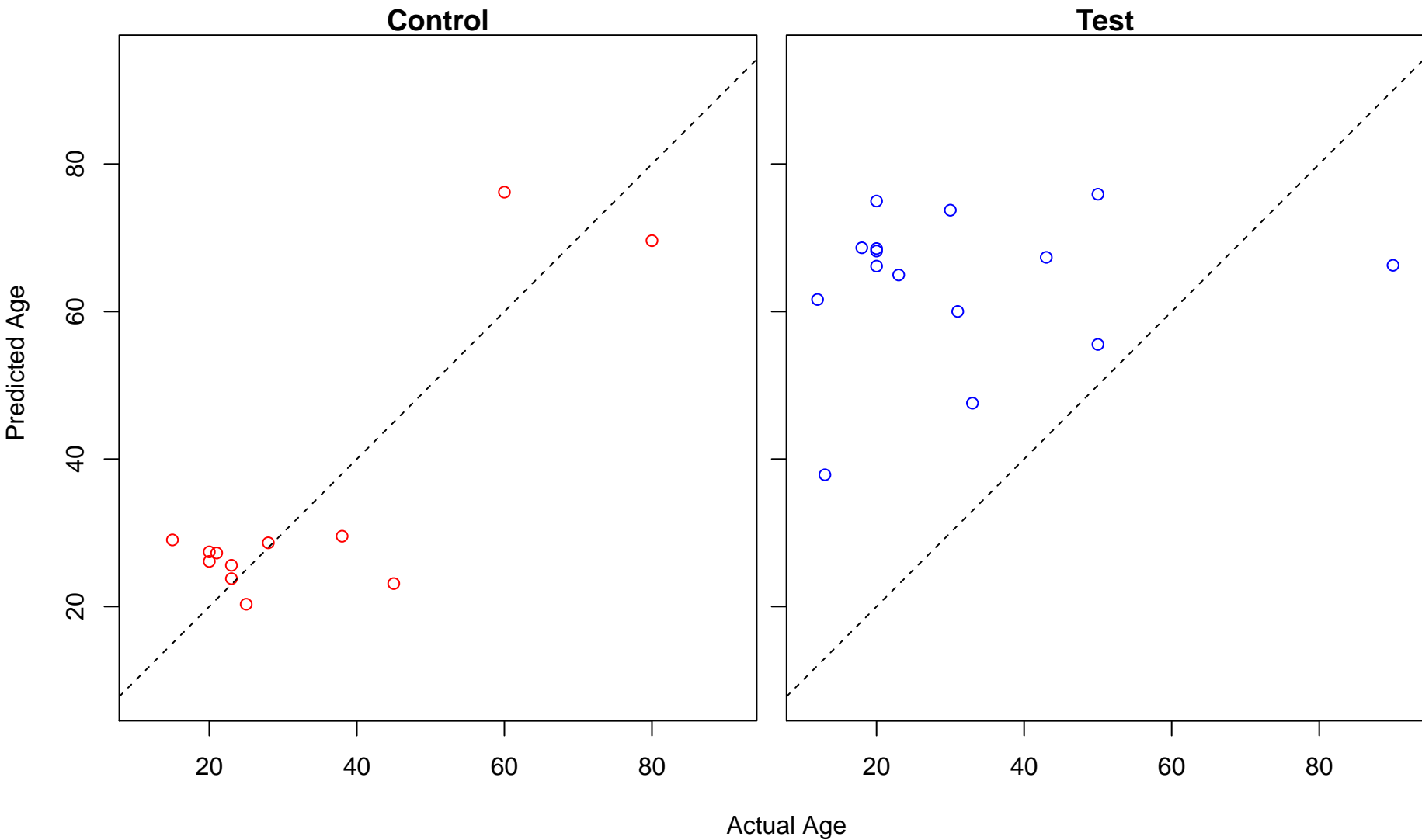


Test

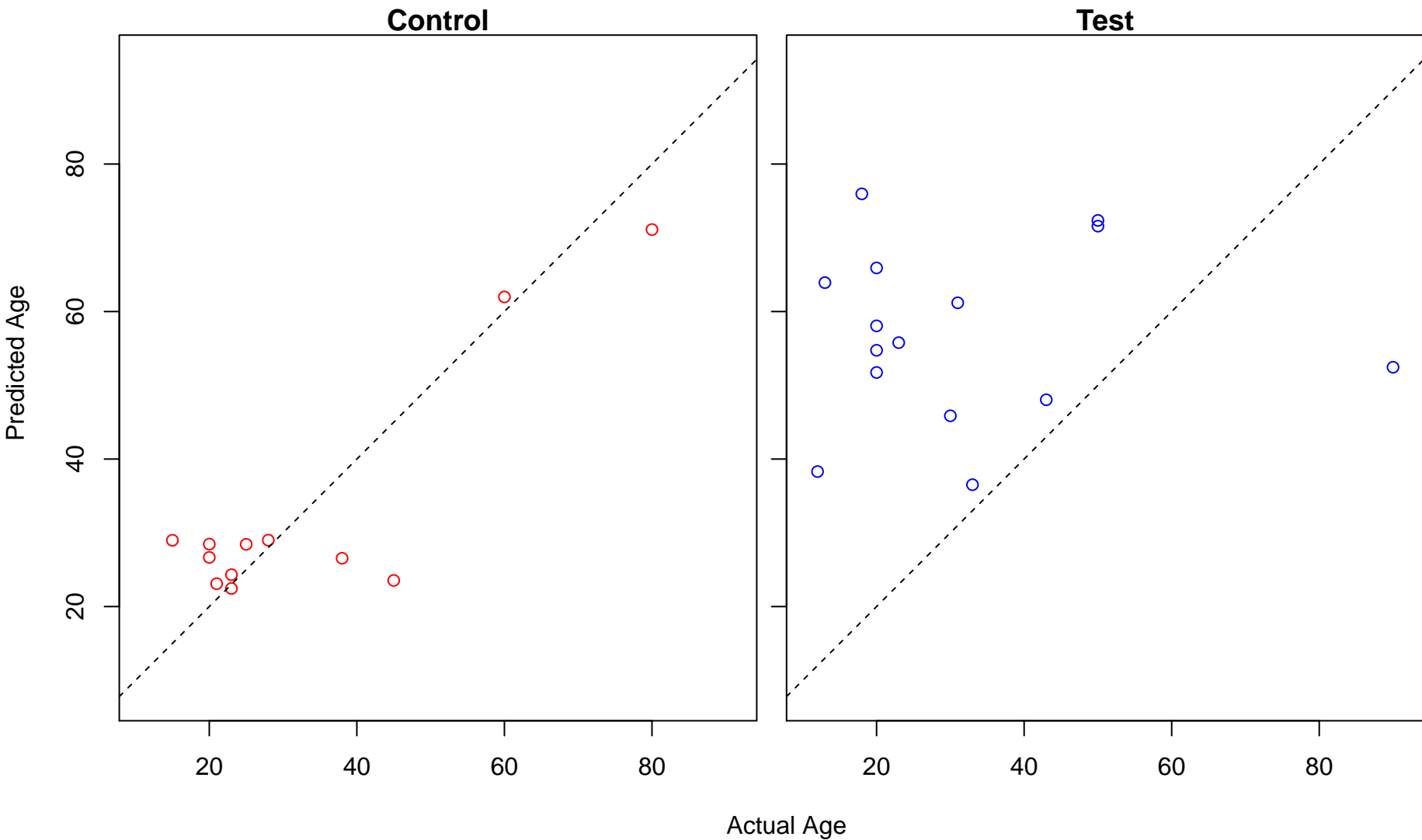


Actual Age

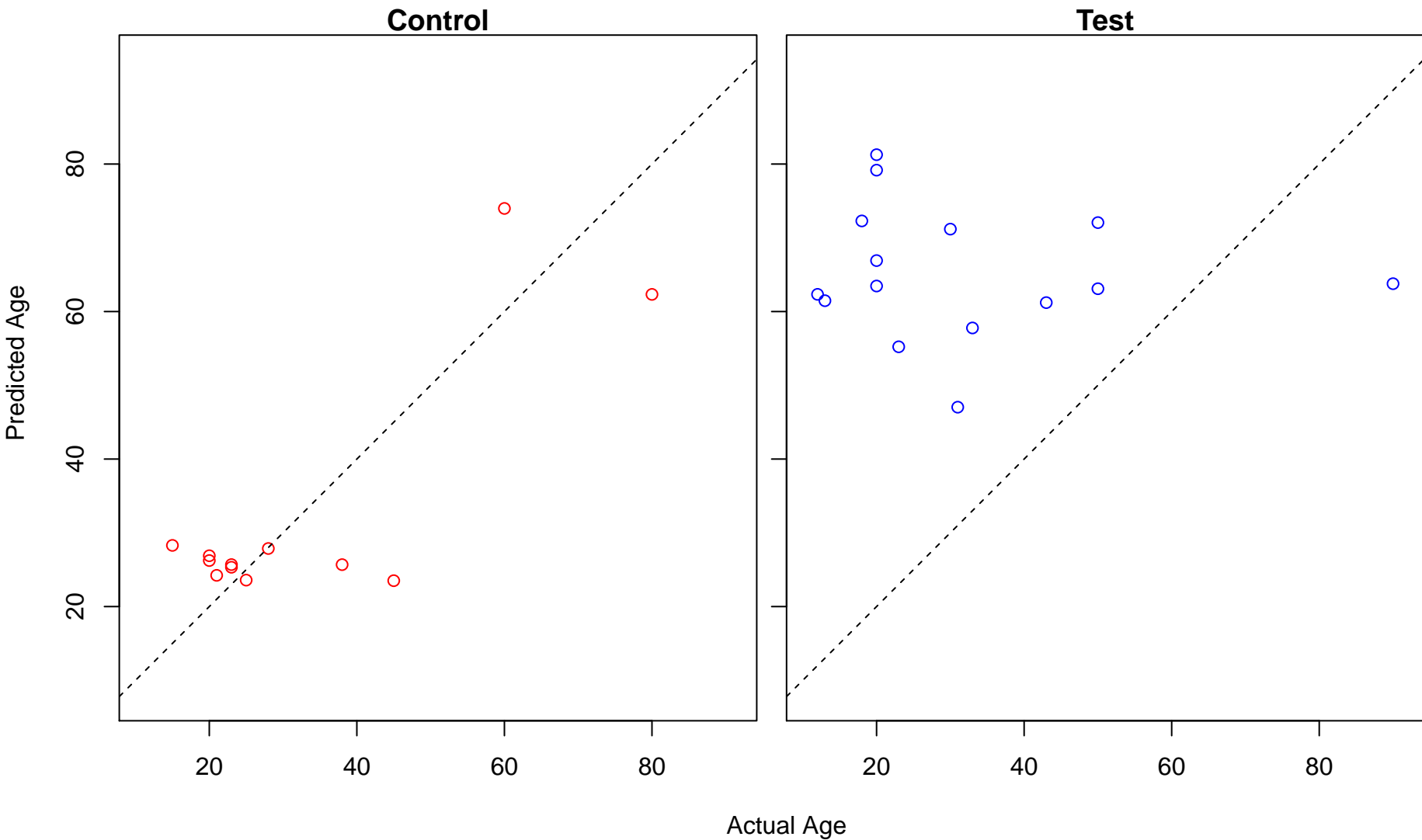
extracellular matrix organization (Score: 4.957757)



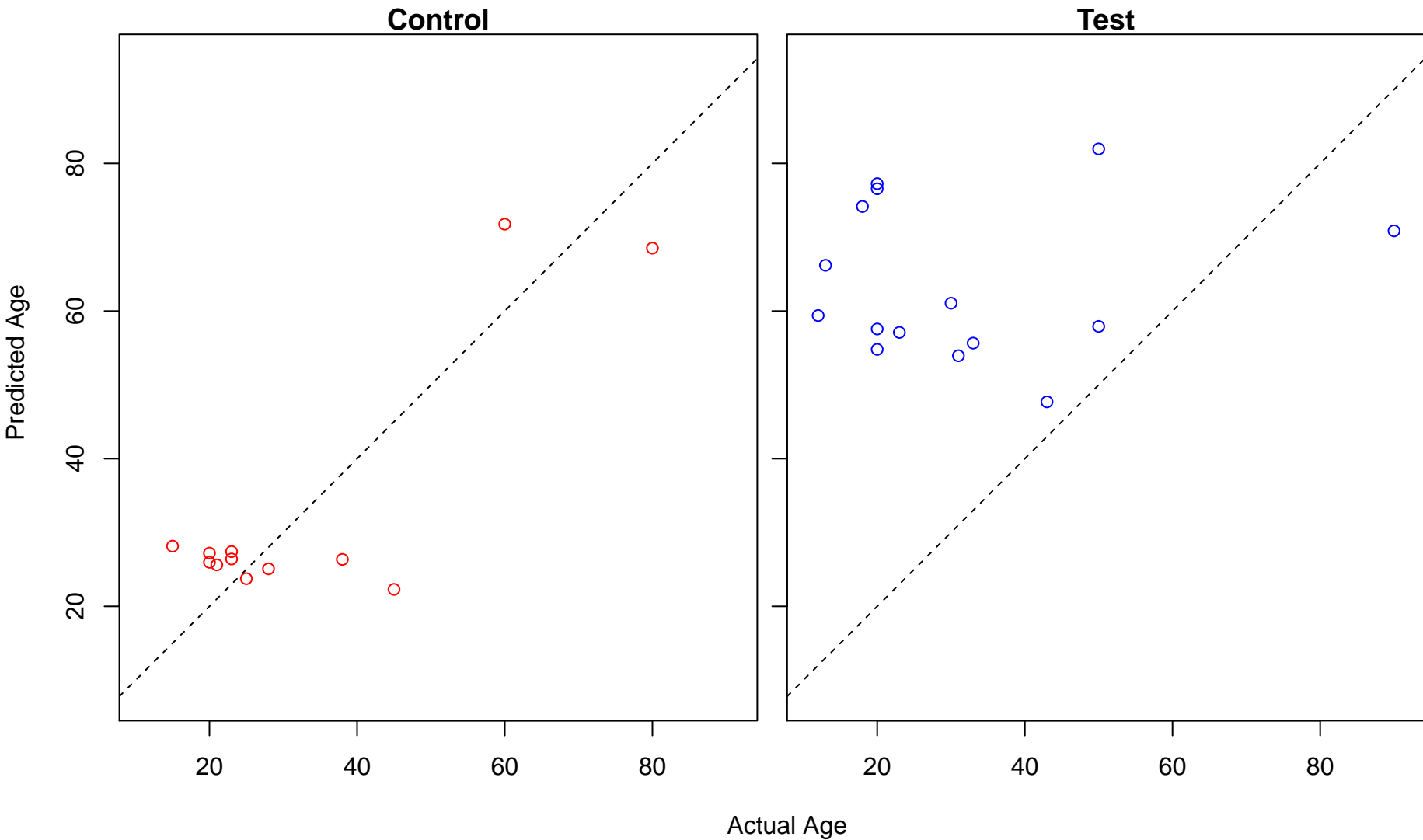
NADH metabolic process (Score: 4.955997)



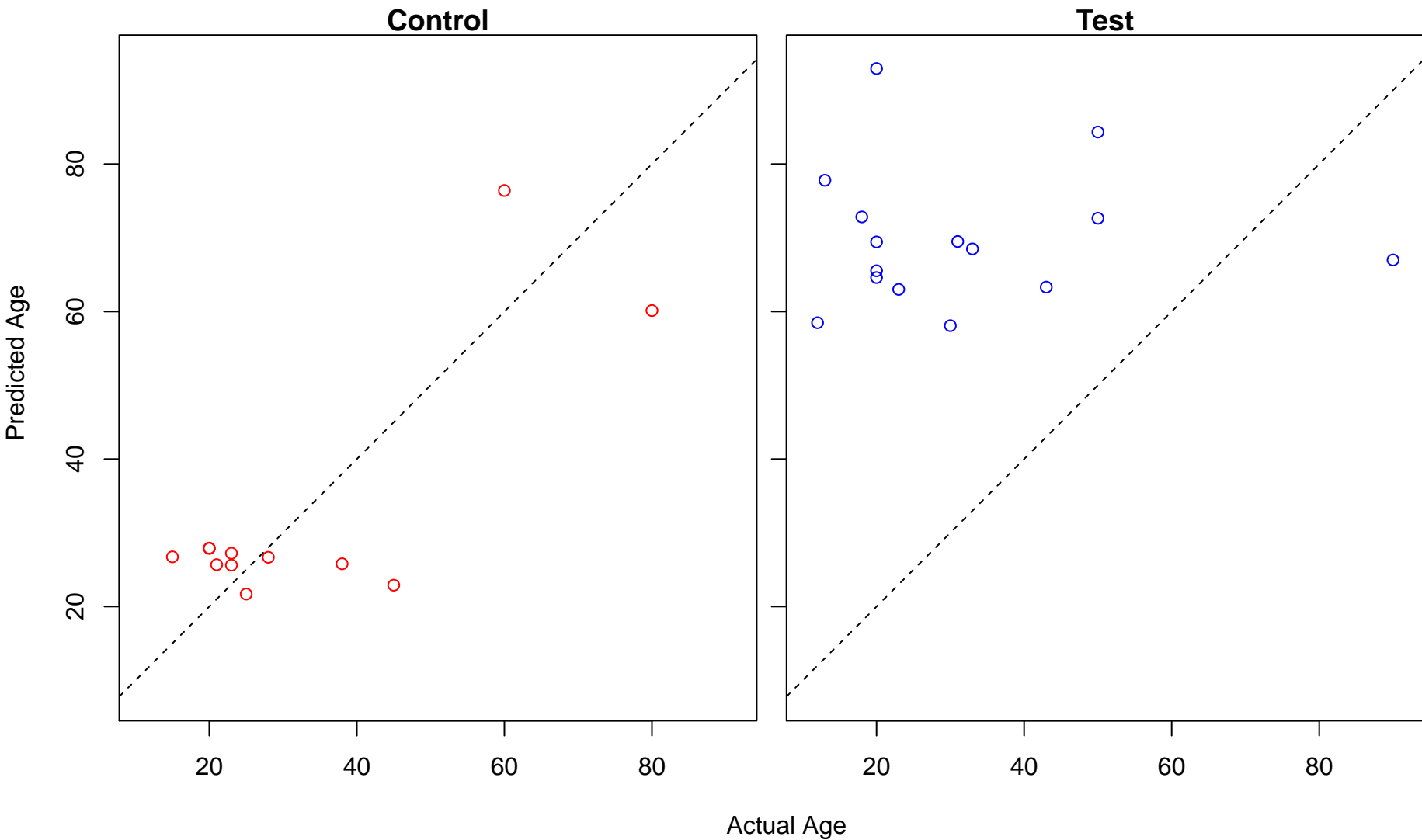
citrate metabolic process (Score: 4.955397)



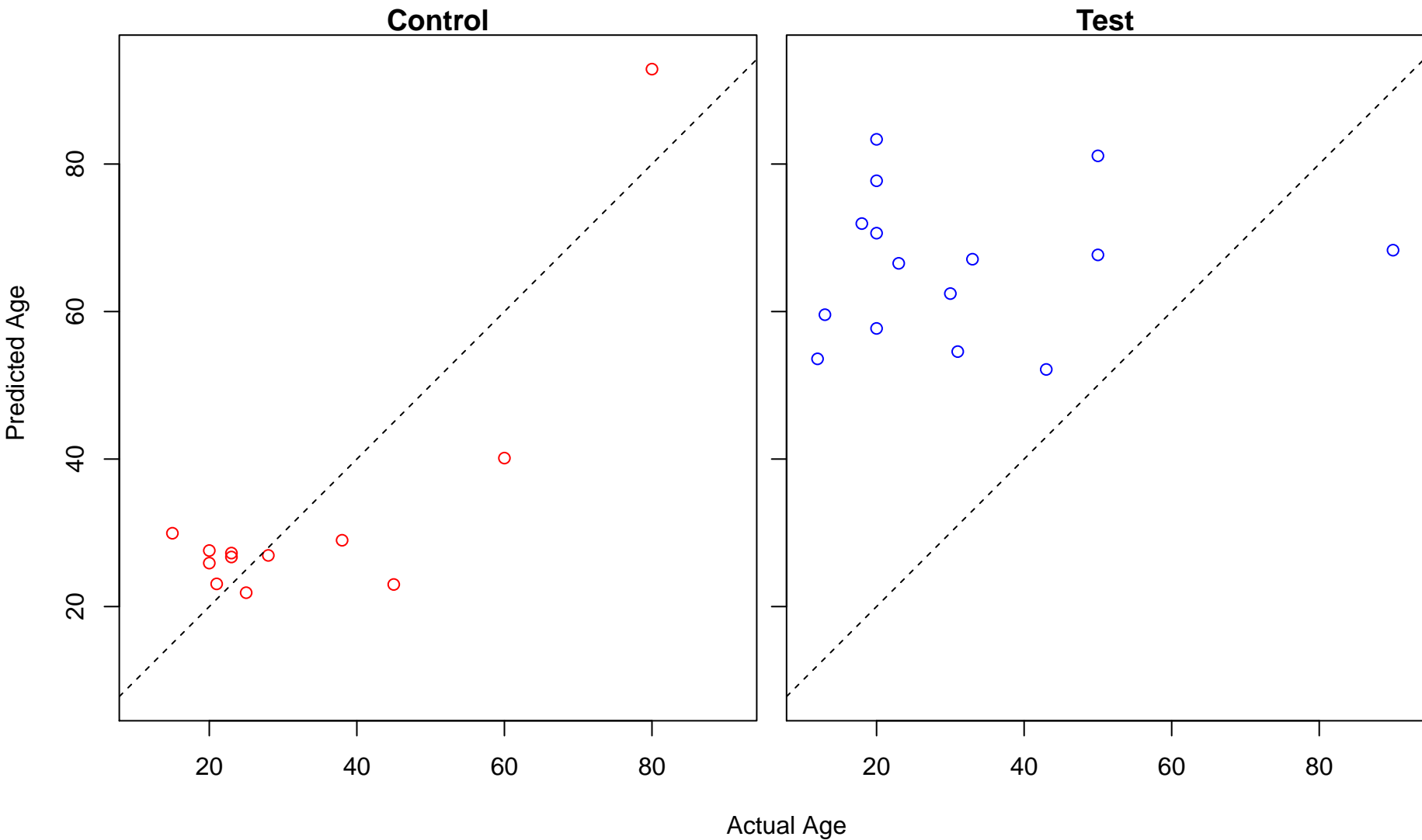
regulation of proteolysis involved in cellular protein catabolic process (Score: 4.955046)



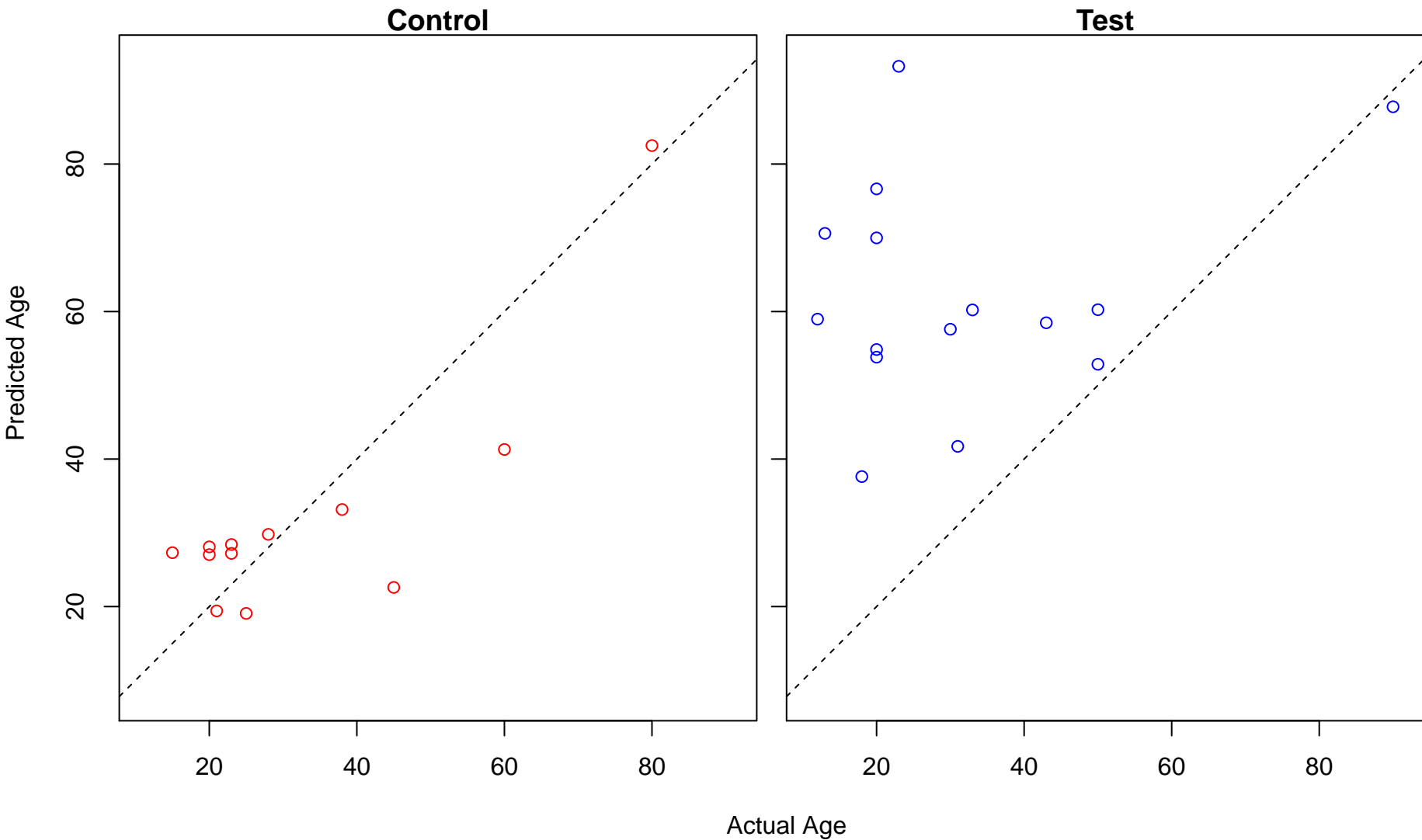
muscle contraction (Score: 4.954618)



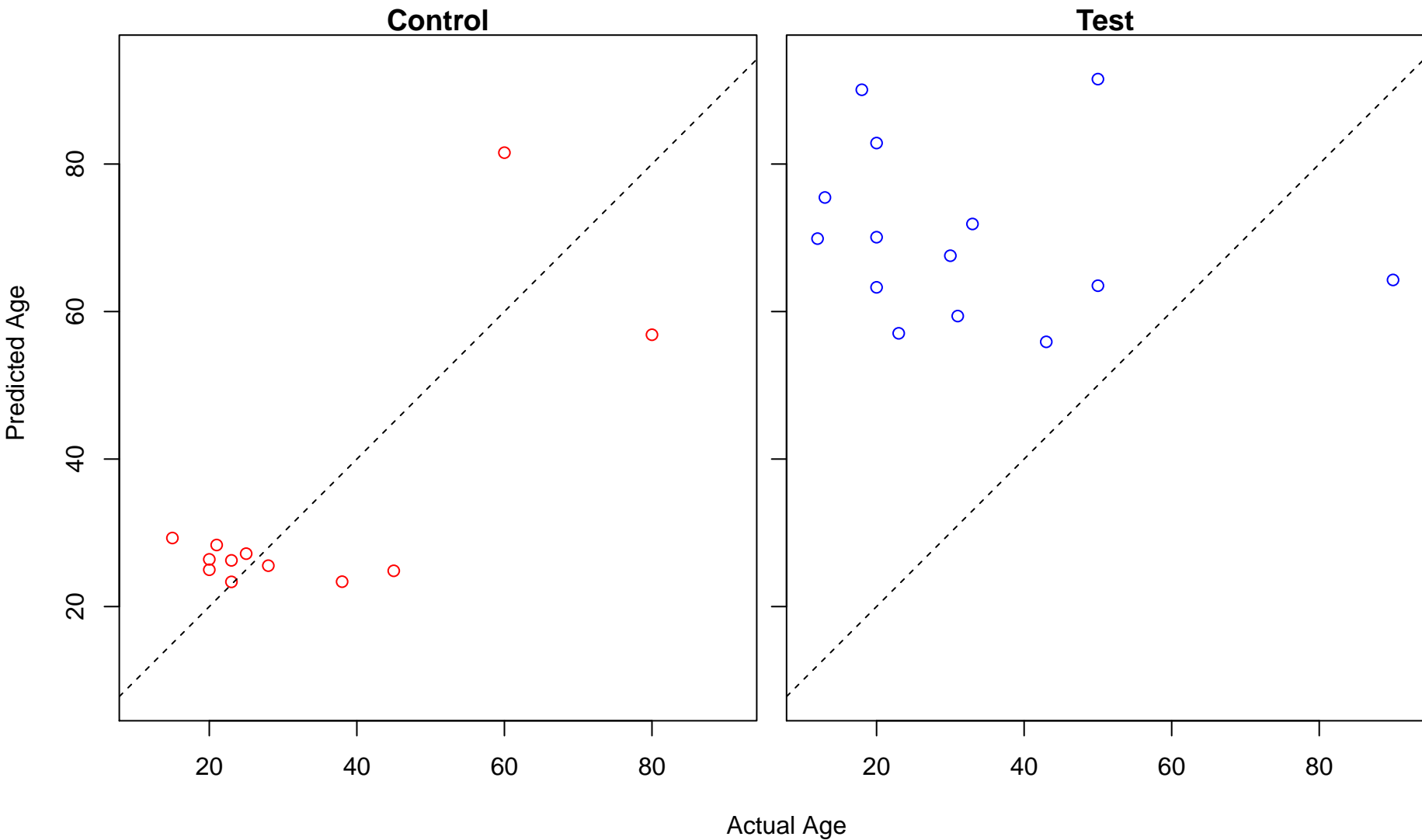
positive regulation of chromosome organization (Score: 4.954507)



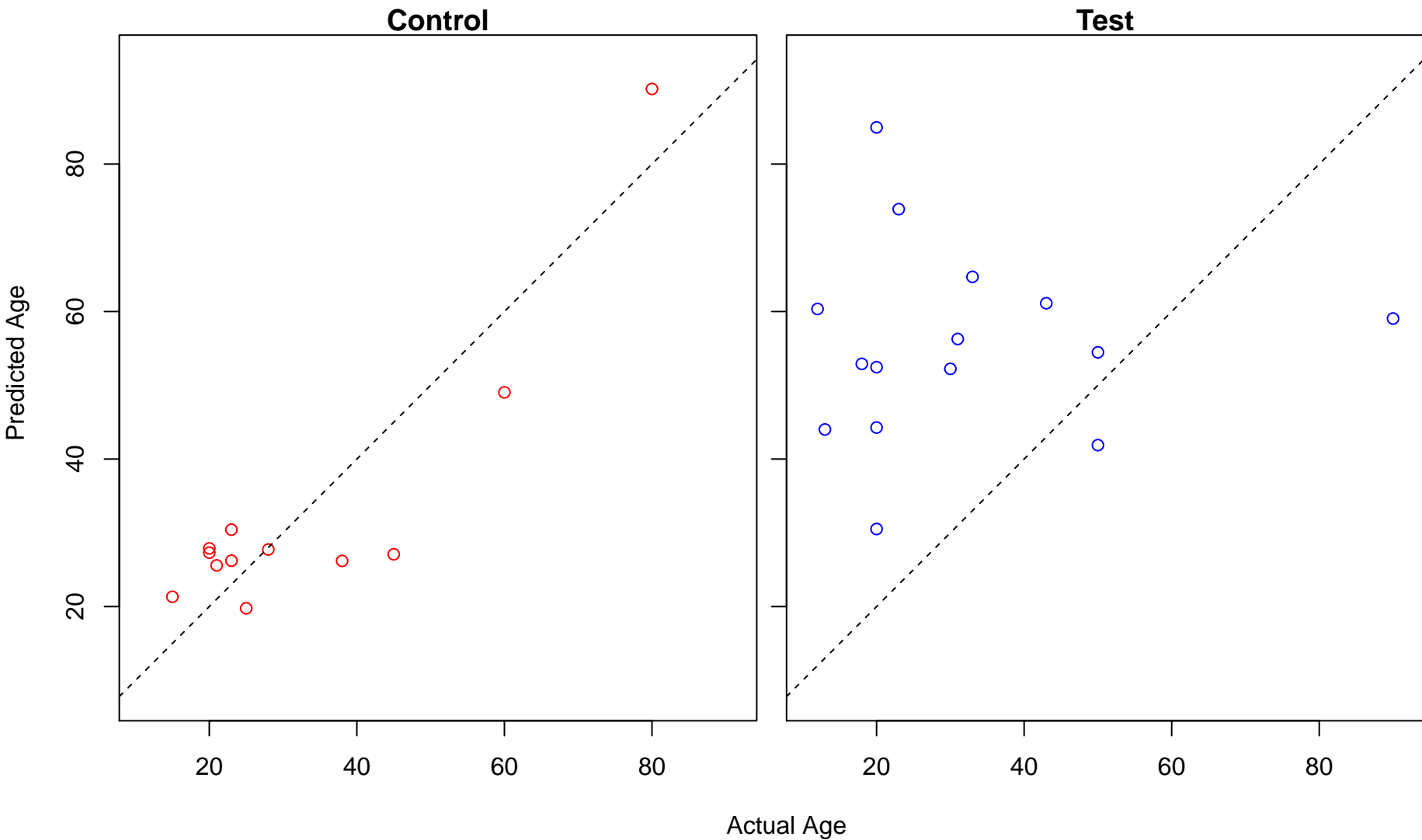
astrocyte development (Score: 4.952239)



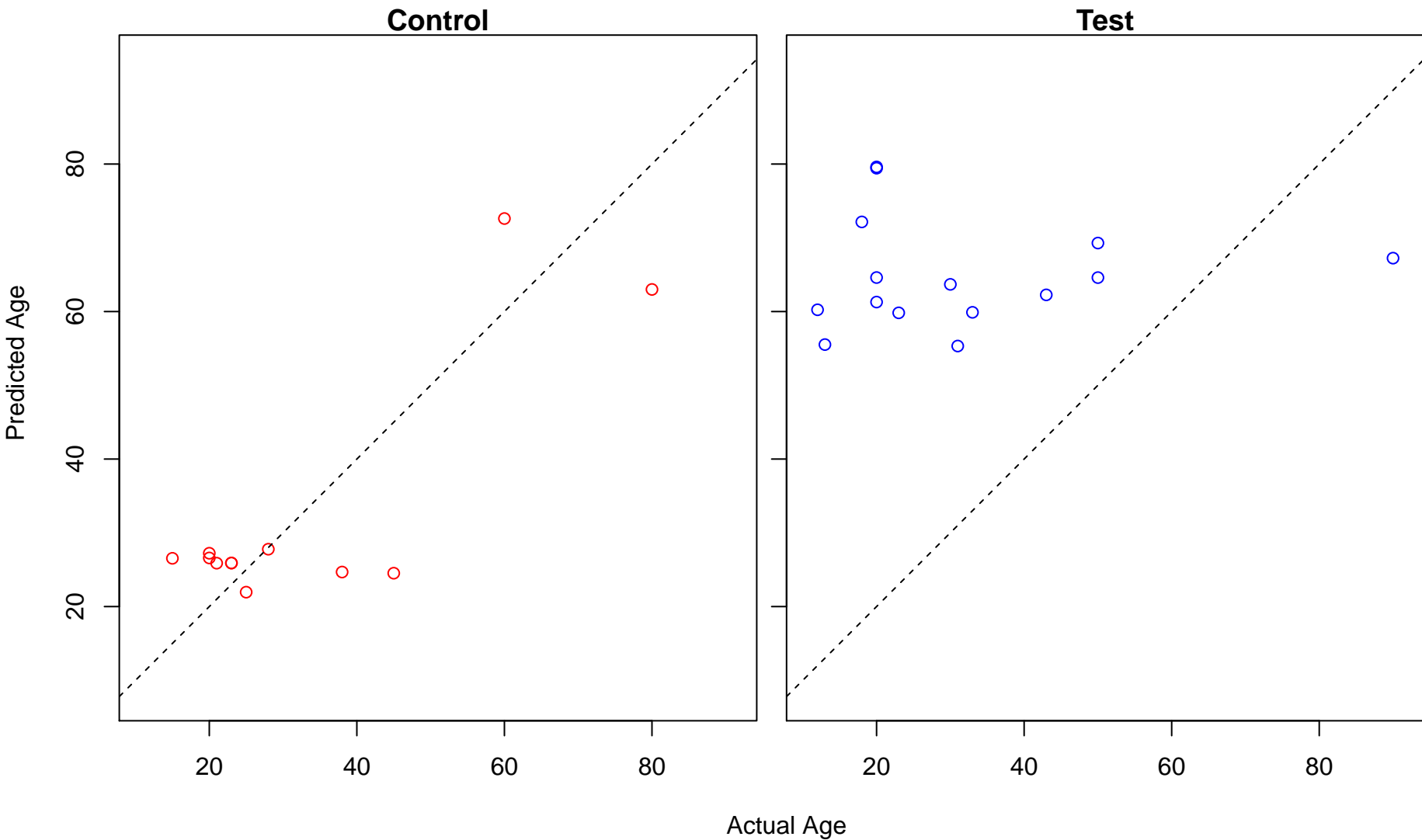
positive regulation of lamellipodium assembly (Score: 4.947818)



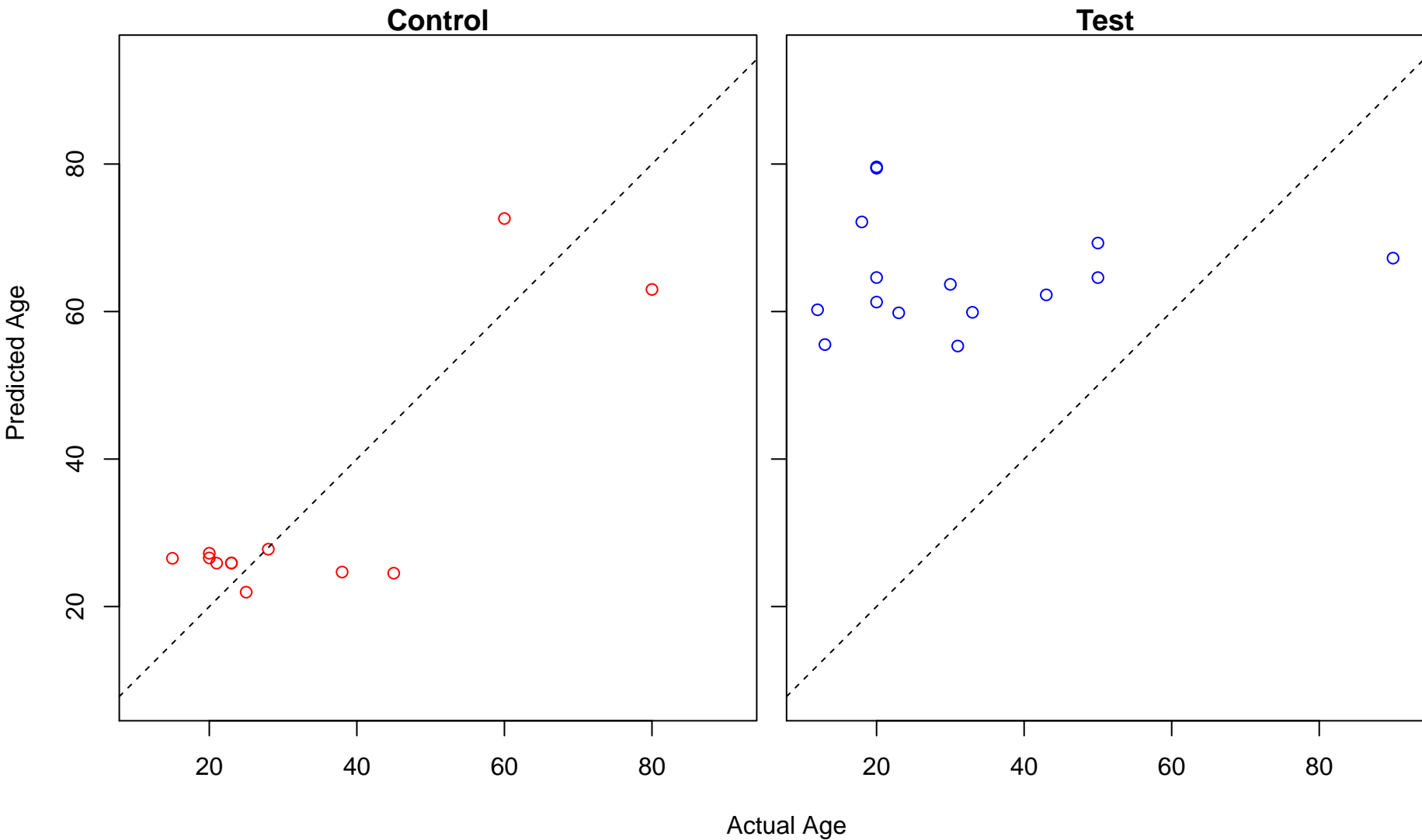
mitochondrial fragmentation involved in apoptotic process (Score: 4.946423)



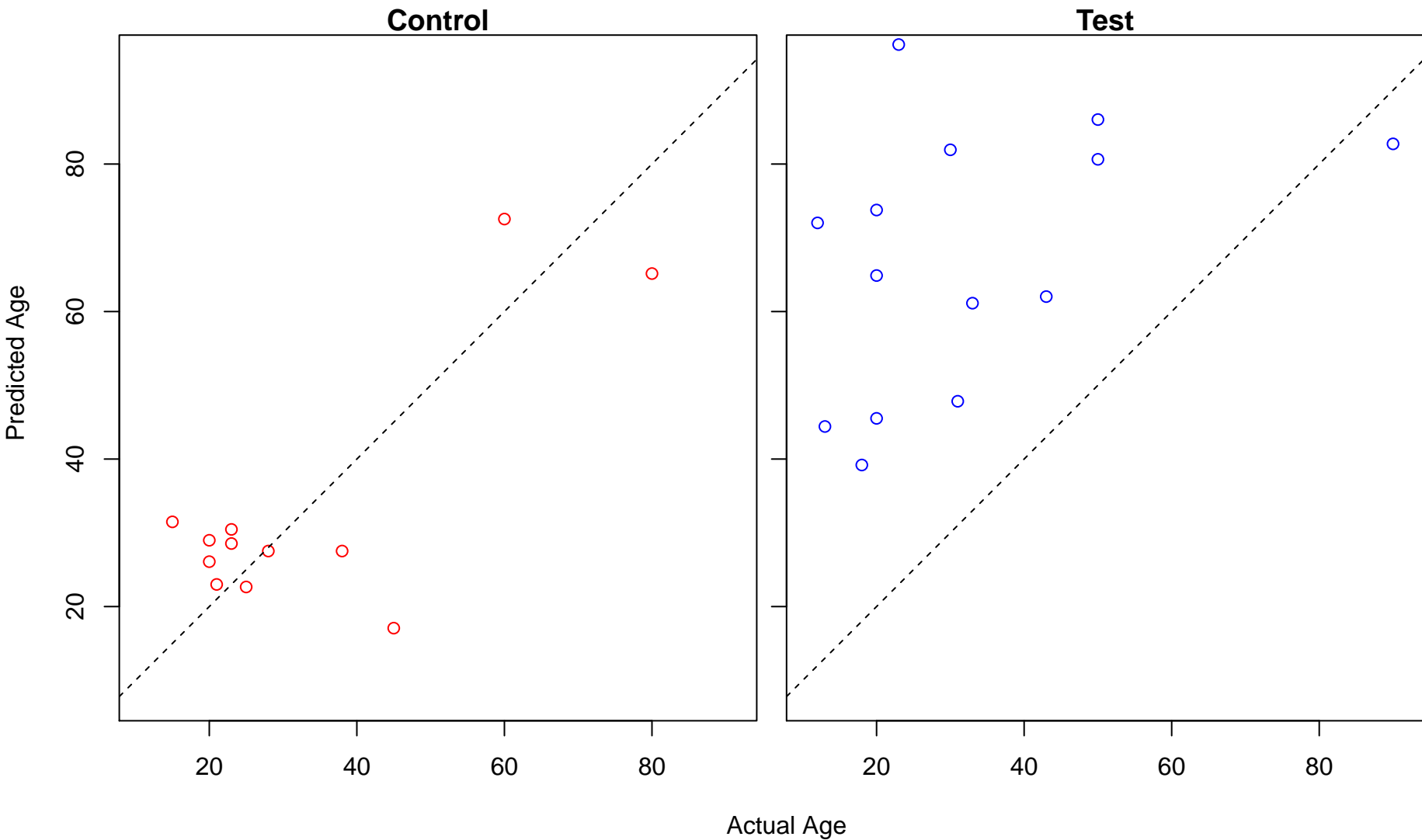
chromosome localization (Score: 4.945079)



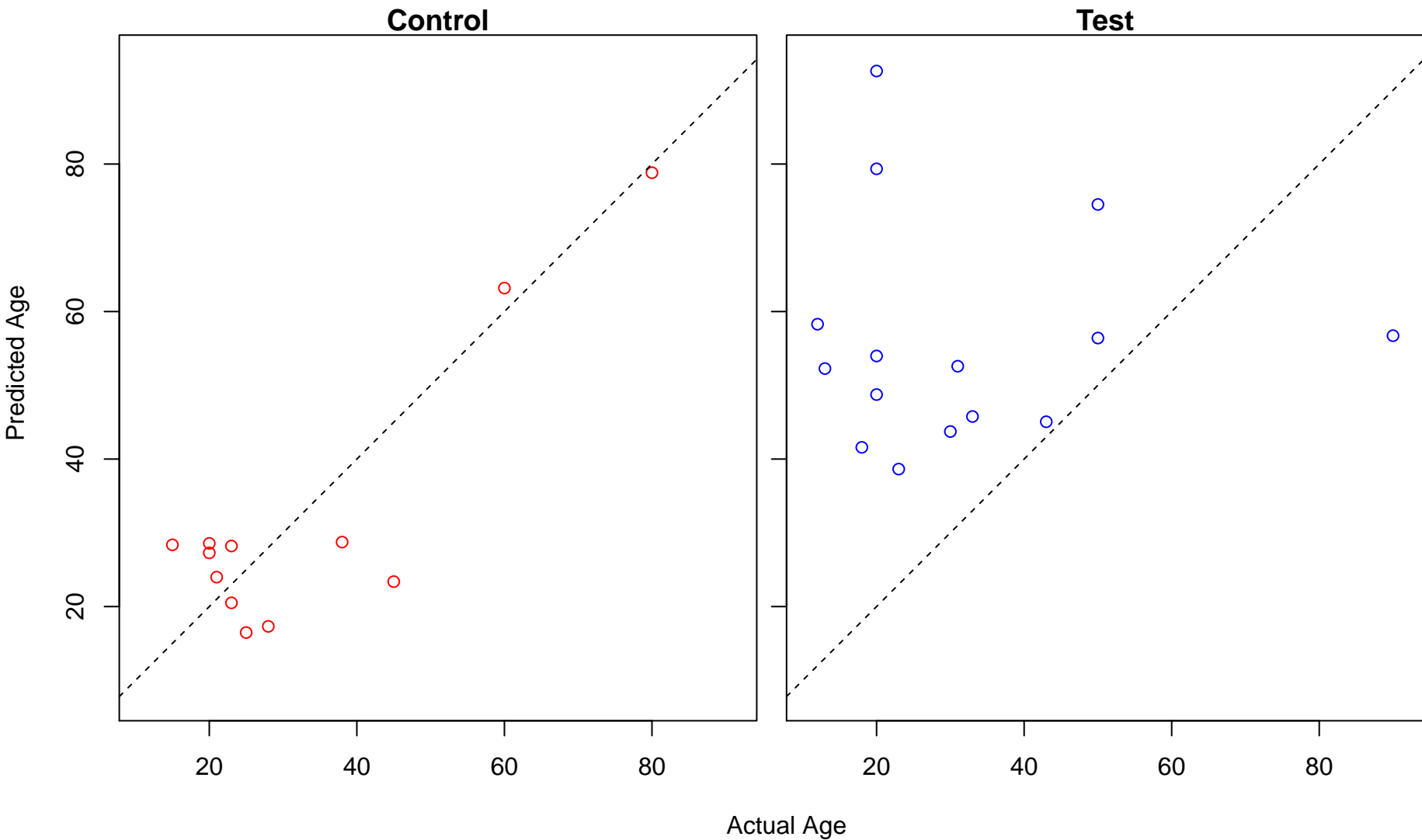
establishment of chromosome localization (Score: 4.945079)



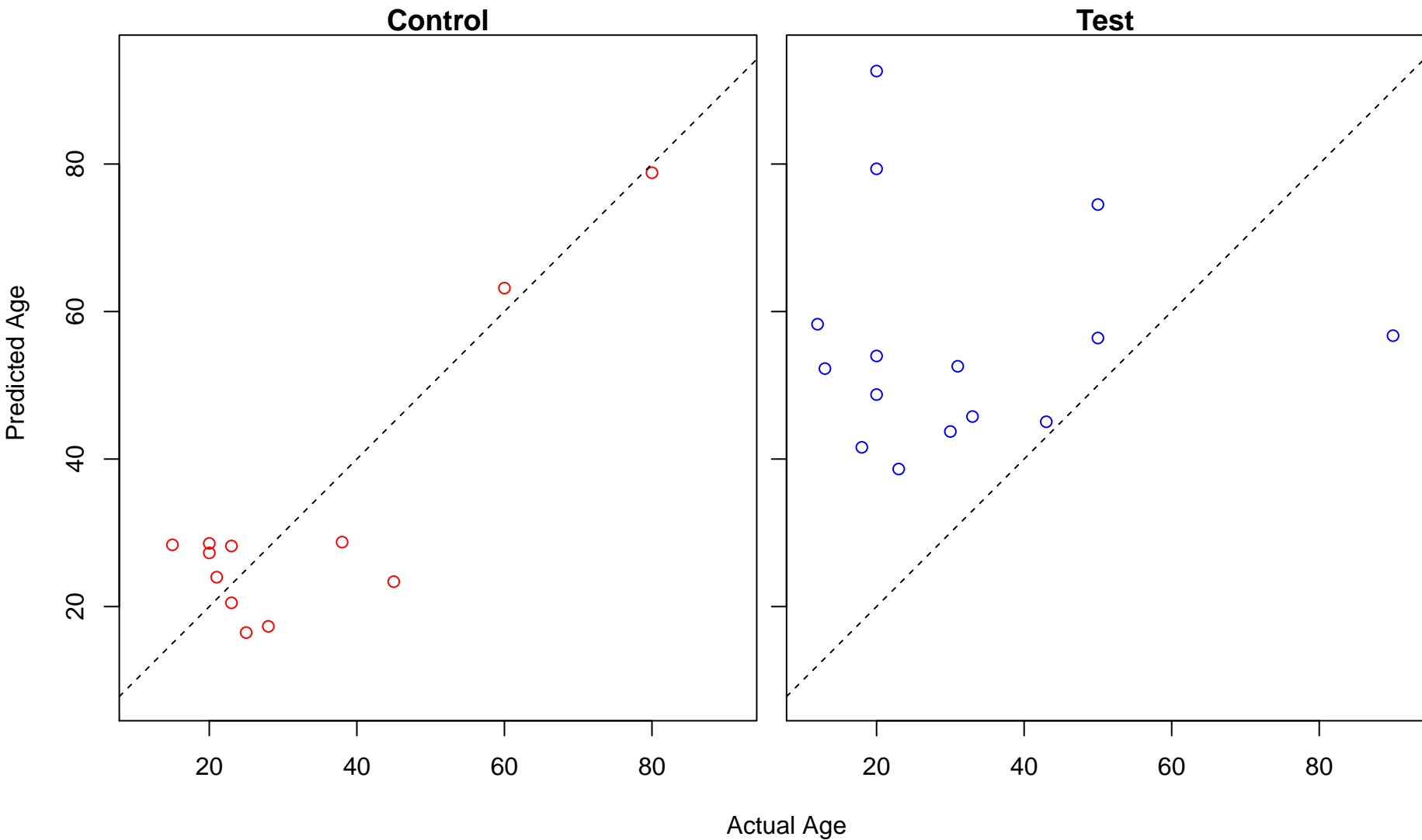
glycosphingolipid catabolic process (Score: 4.941565)



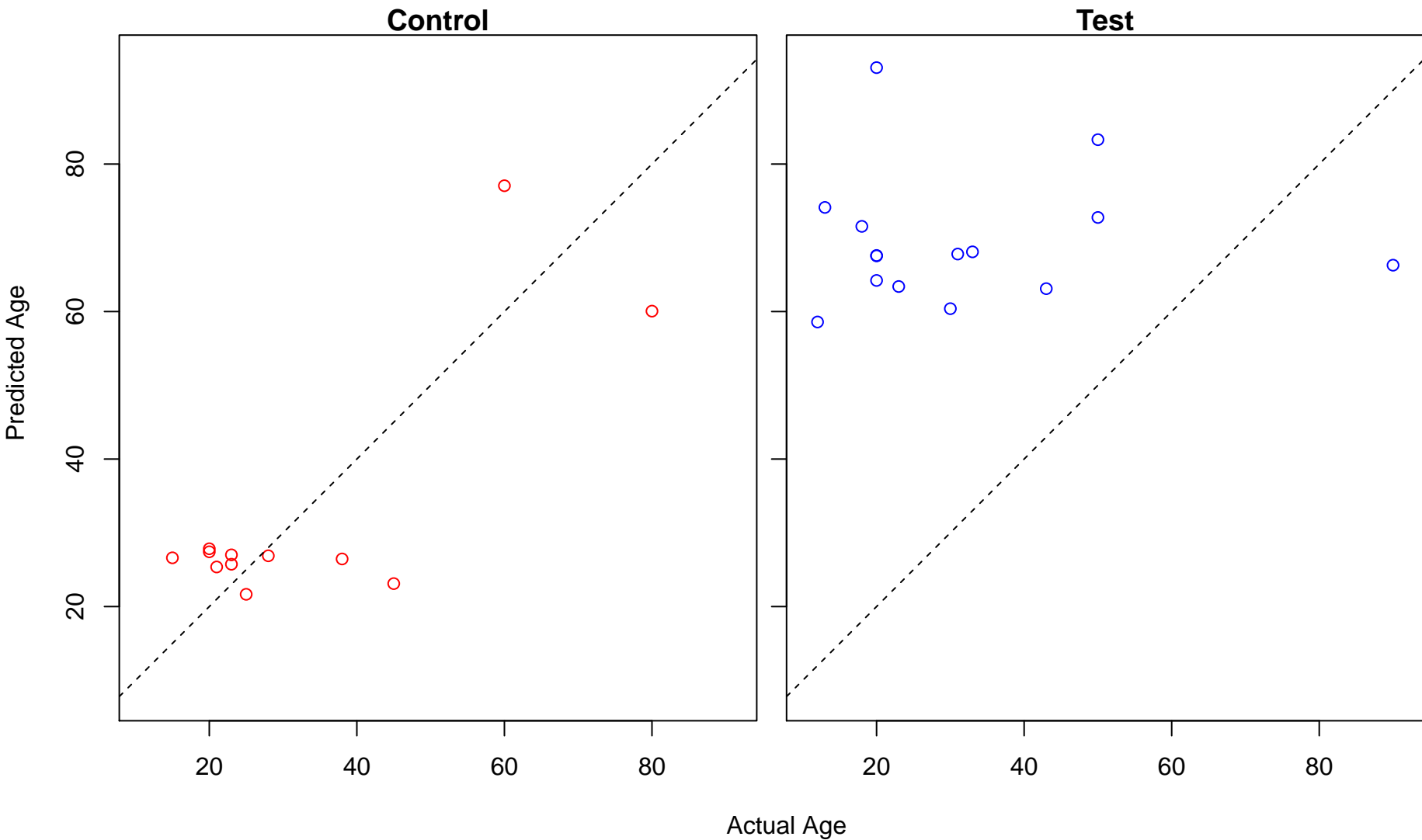
single fertilization (Score: 4.940325)



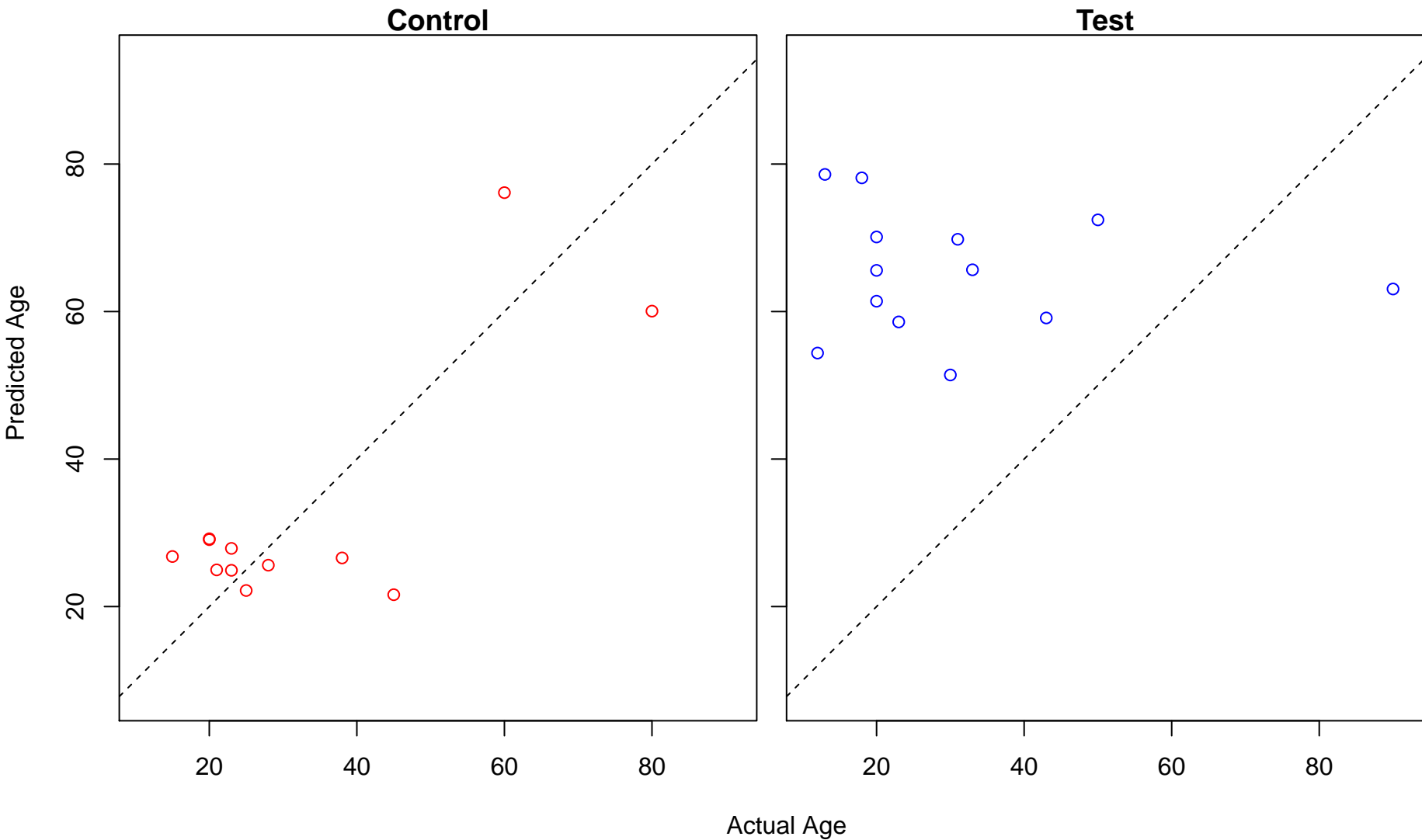
fertilization (Score: 4.939685)



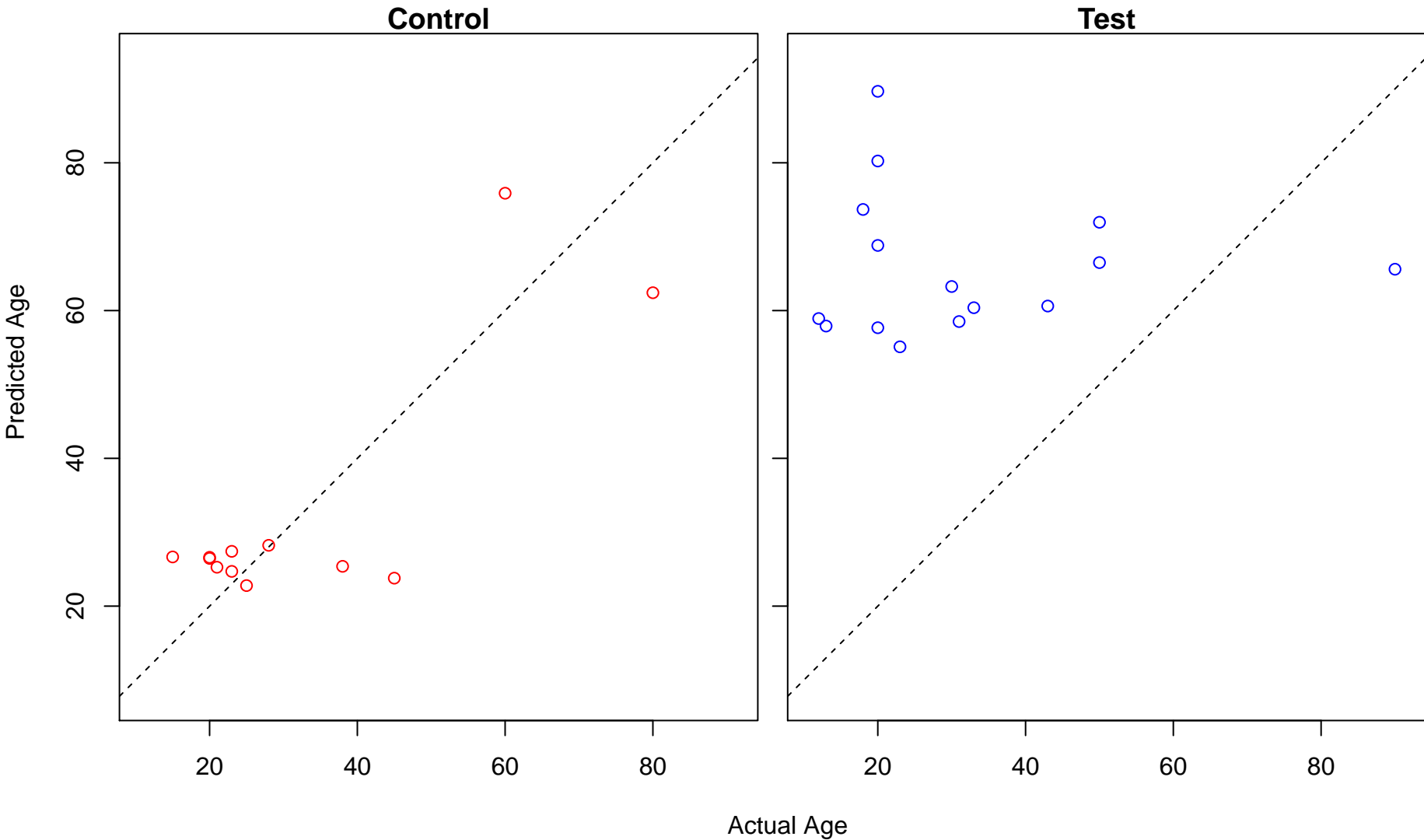
negative regulation of transport (Score: 4.938237)



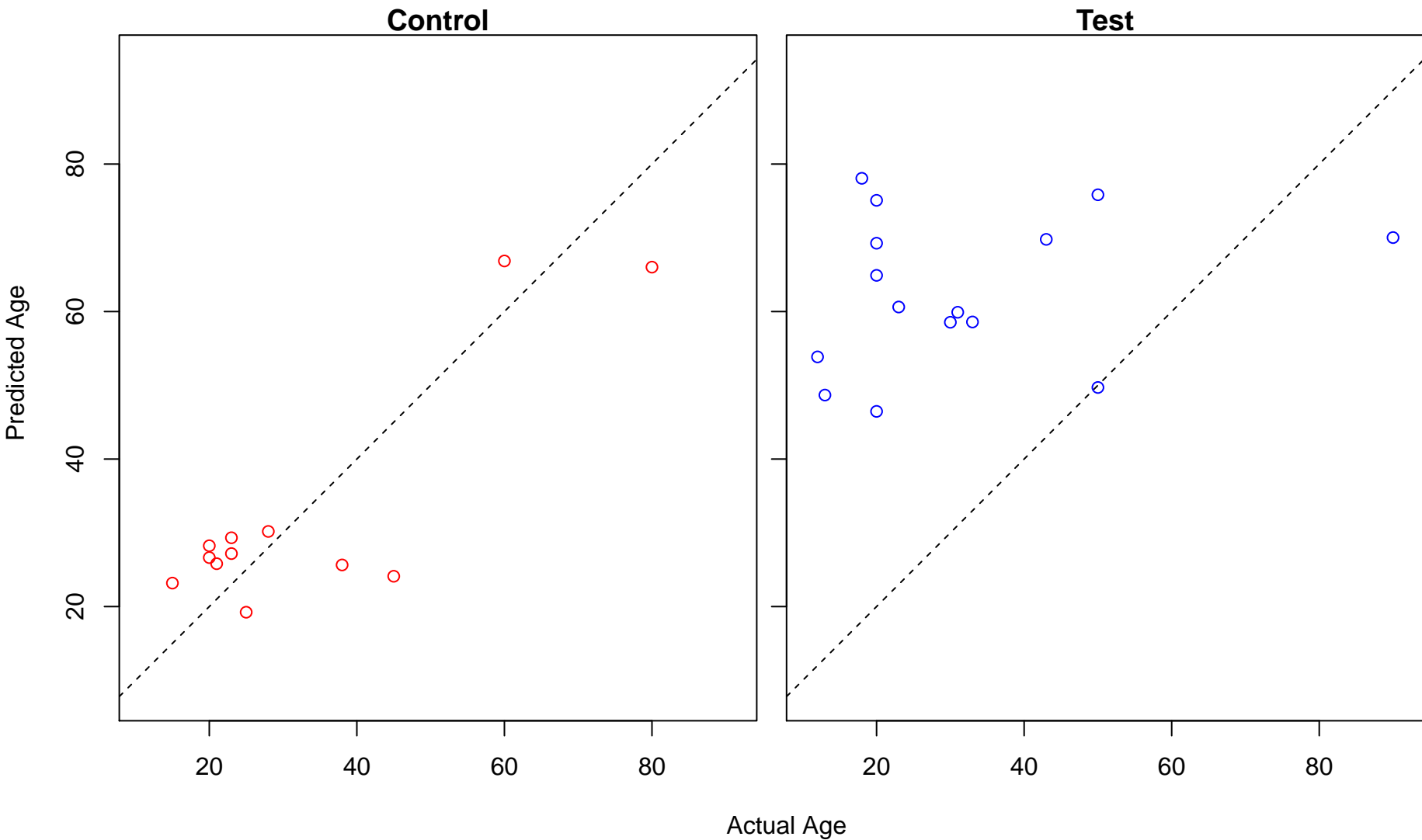
negative regulation of receptor internalization (Score: 4.935068)



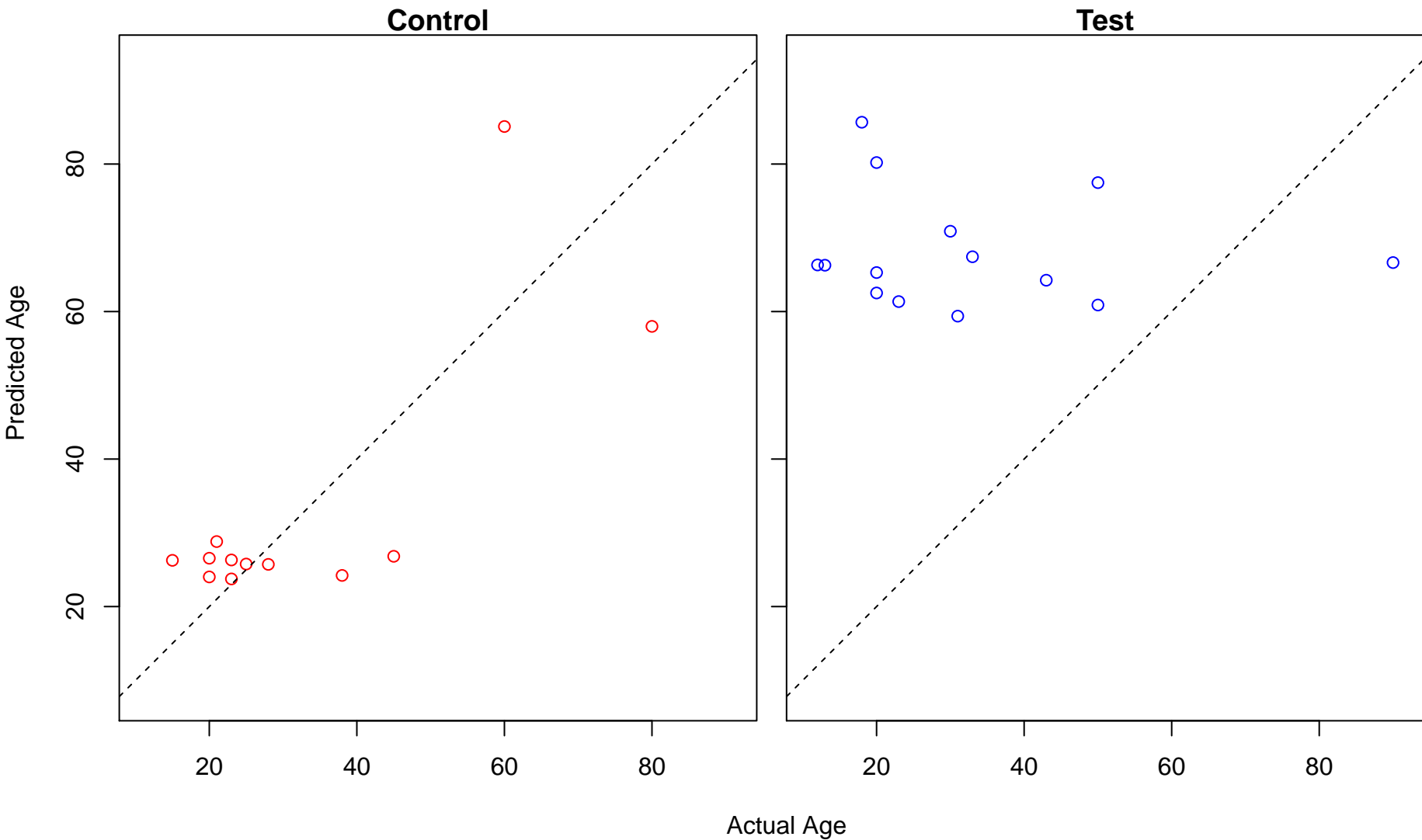
regulation of G2/M transition of mitotic cell cycle (Score: 4.934962)



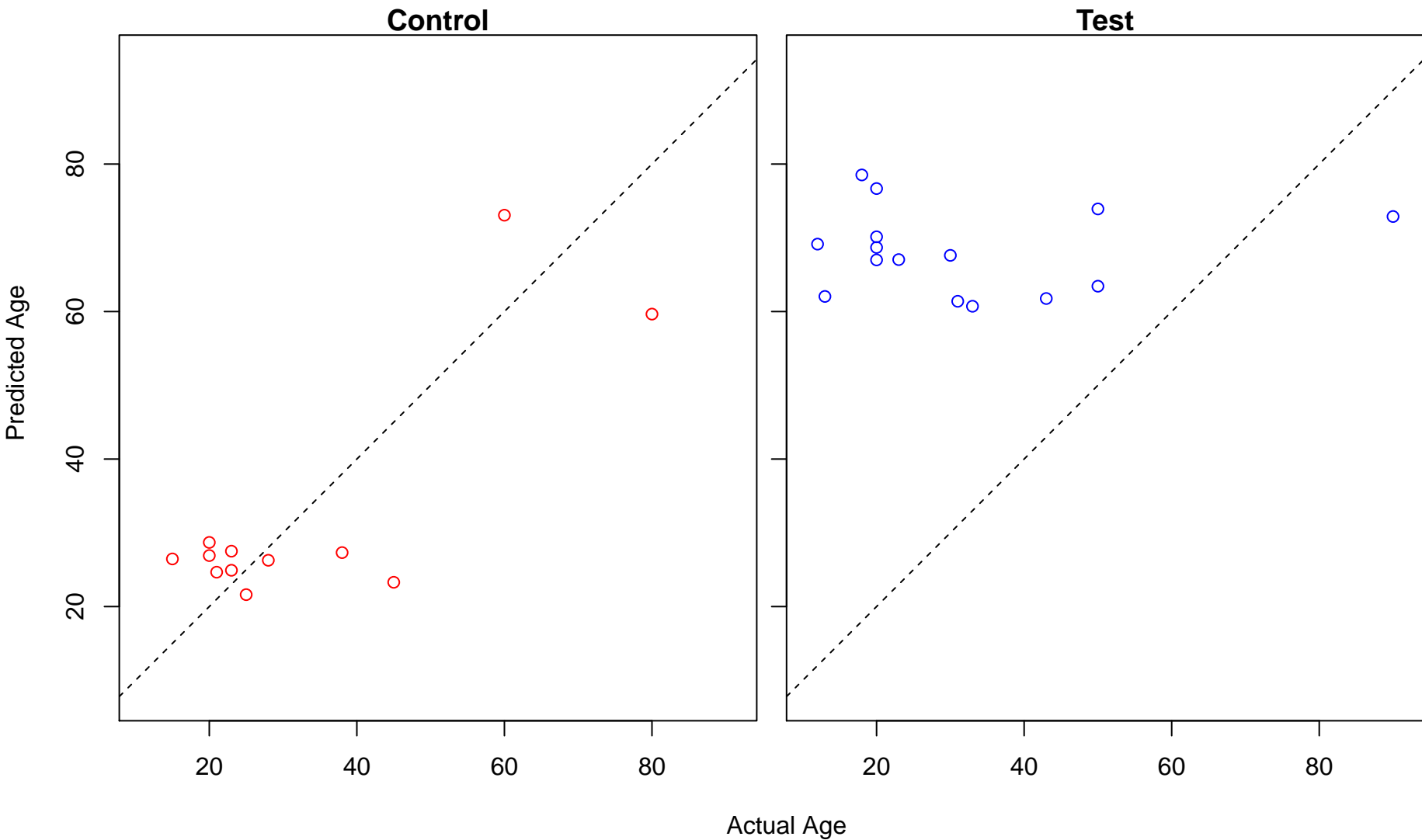
peptide cross-linking (Score: 4.931994)



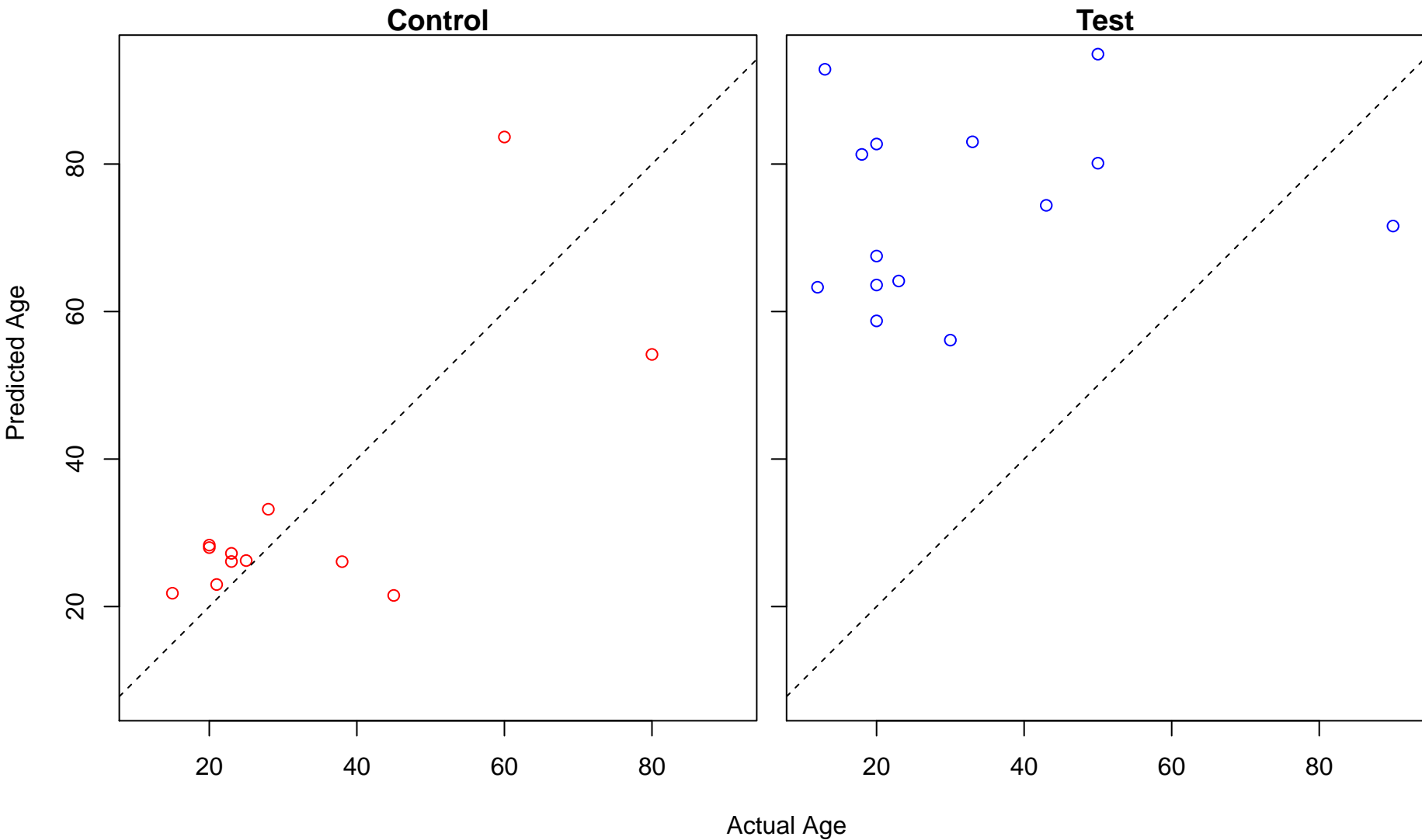
protein to membrane docking (Score: 4.931920)



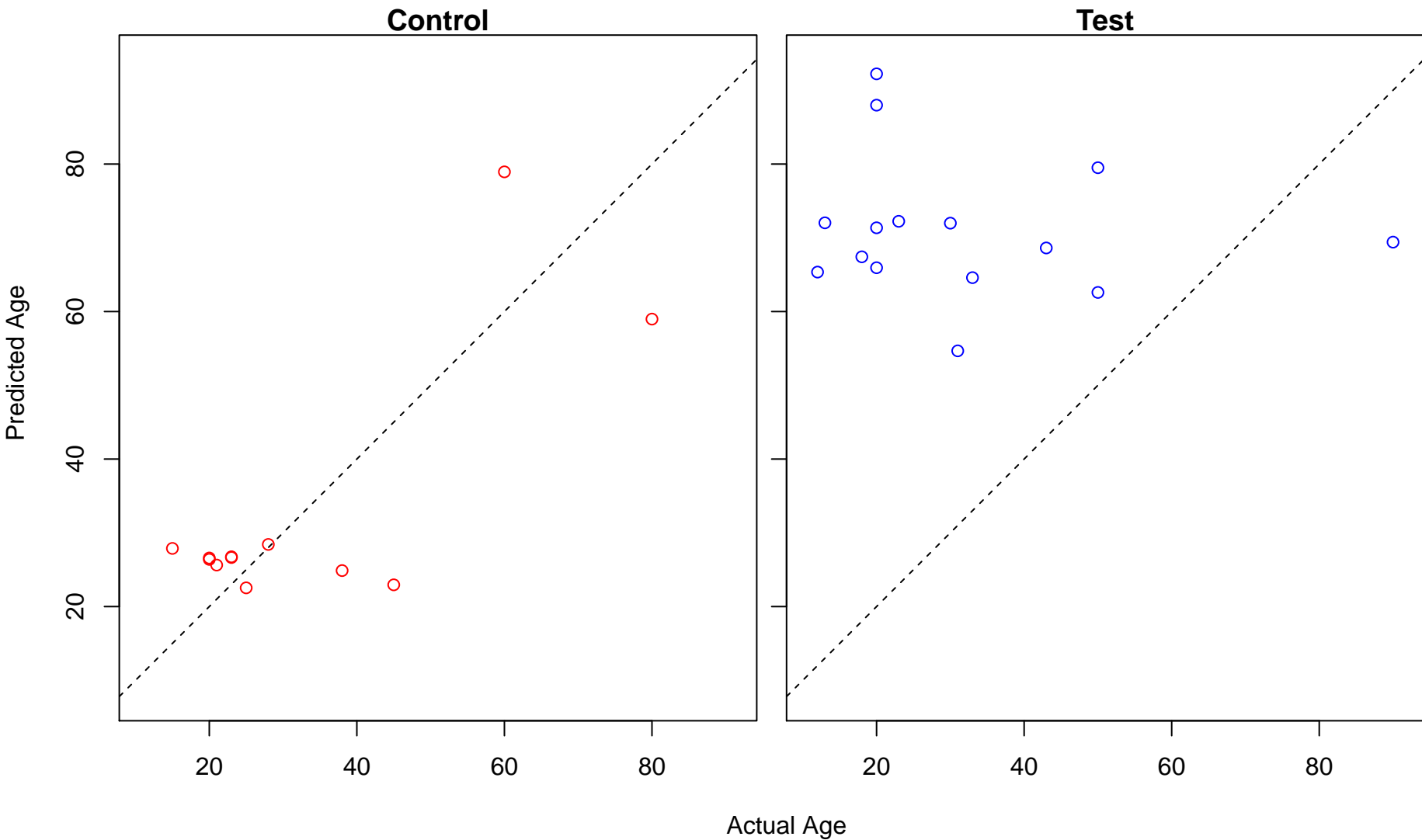
negative regulation of kinase activity (Score: 4.930833)



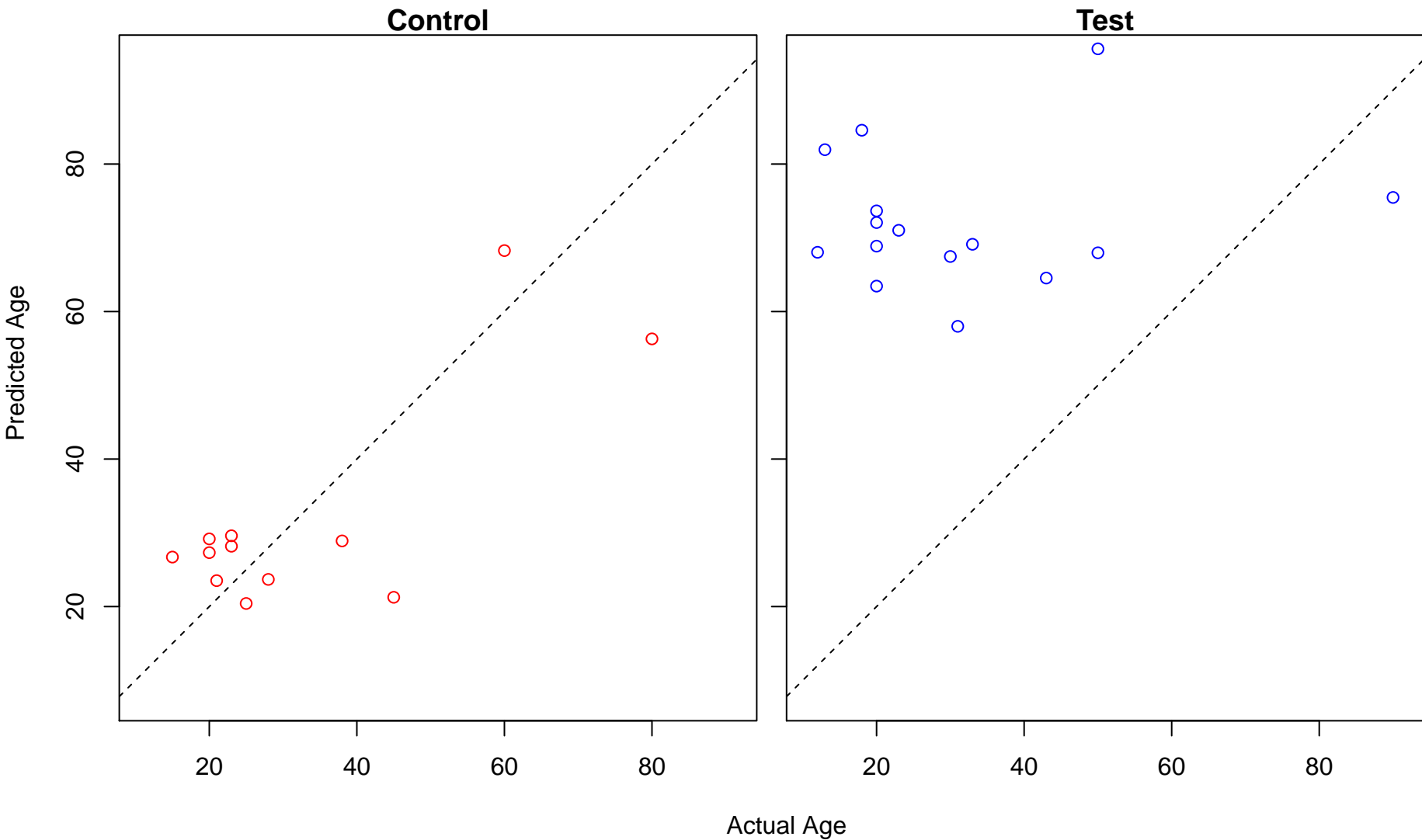
regulation of chemotaxis (Score: 4.925303)



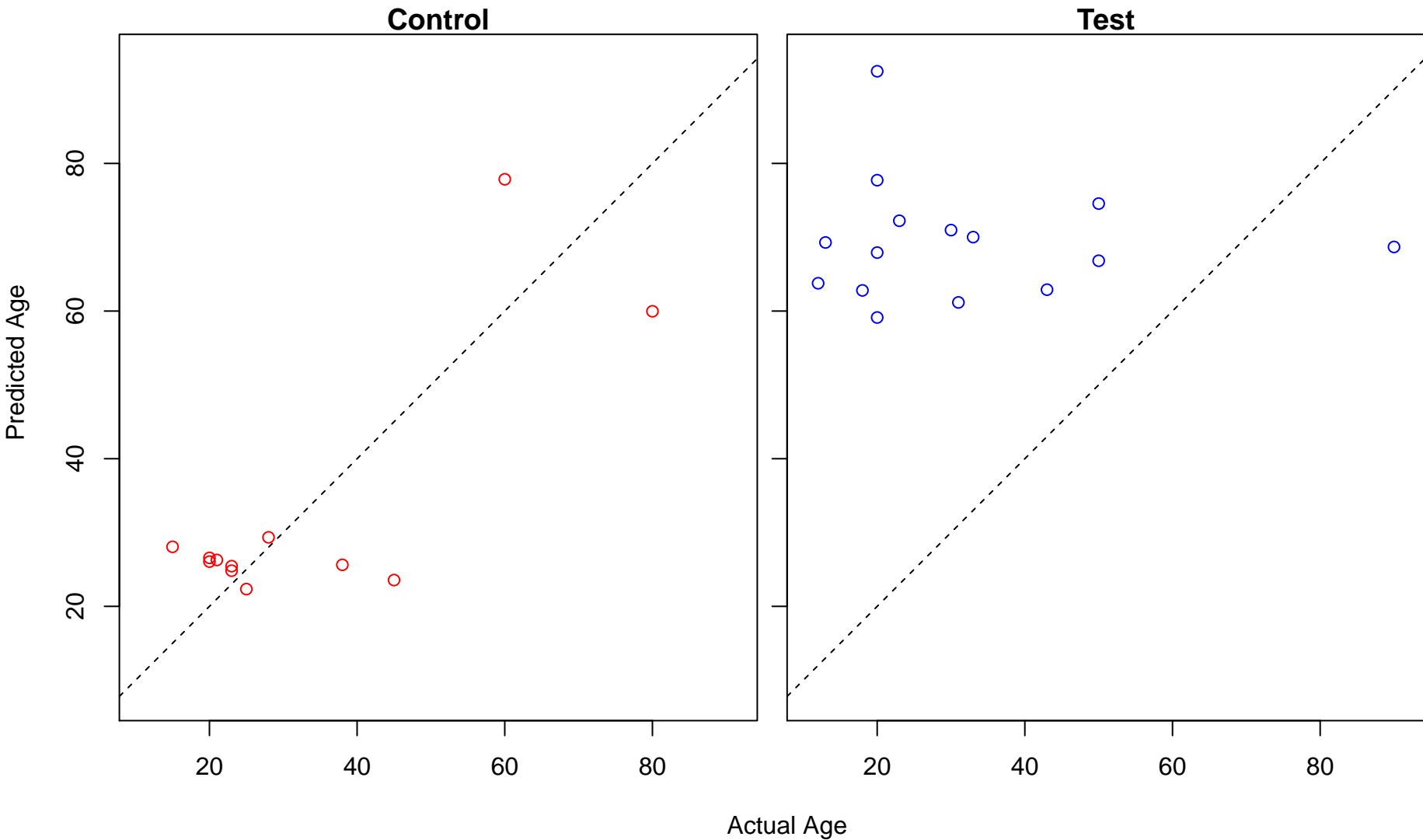
pigment biosynthetic process (Score: 4.925233)



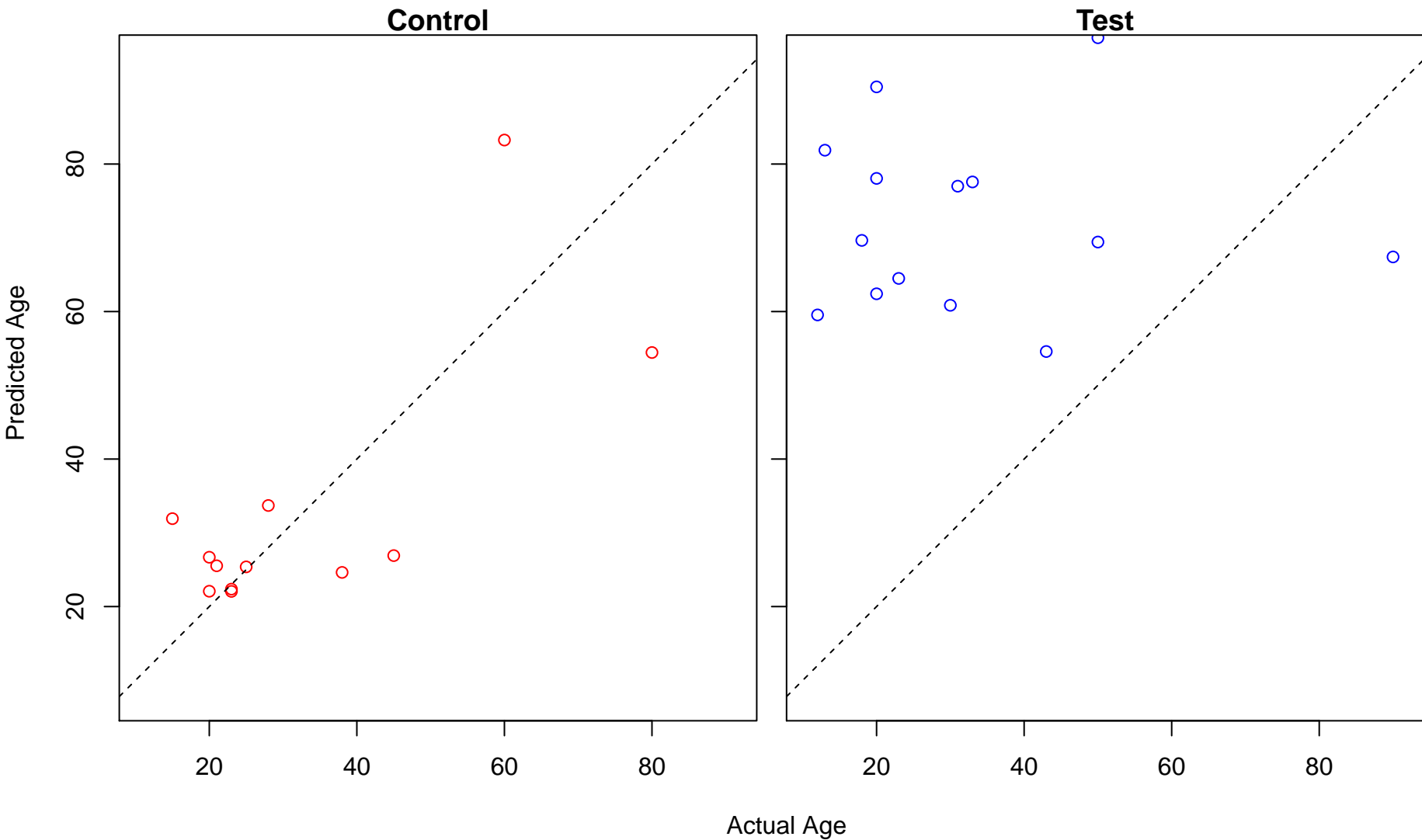
autonomic nervous system development (Score: 4.924726)



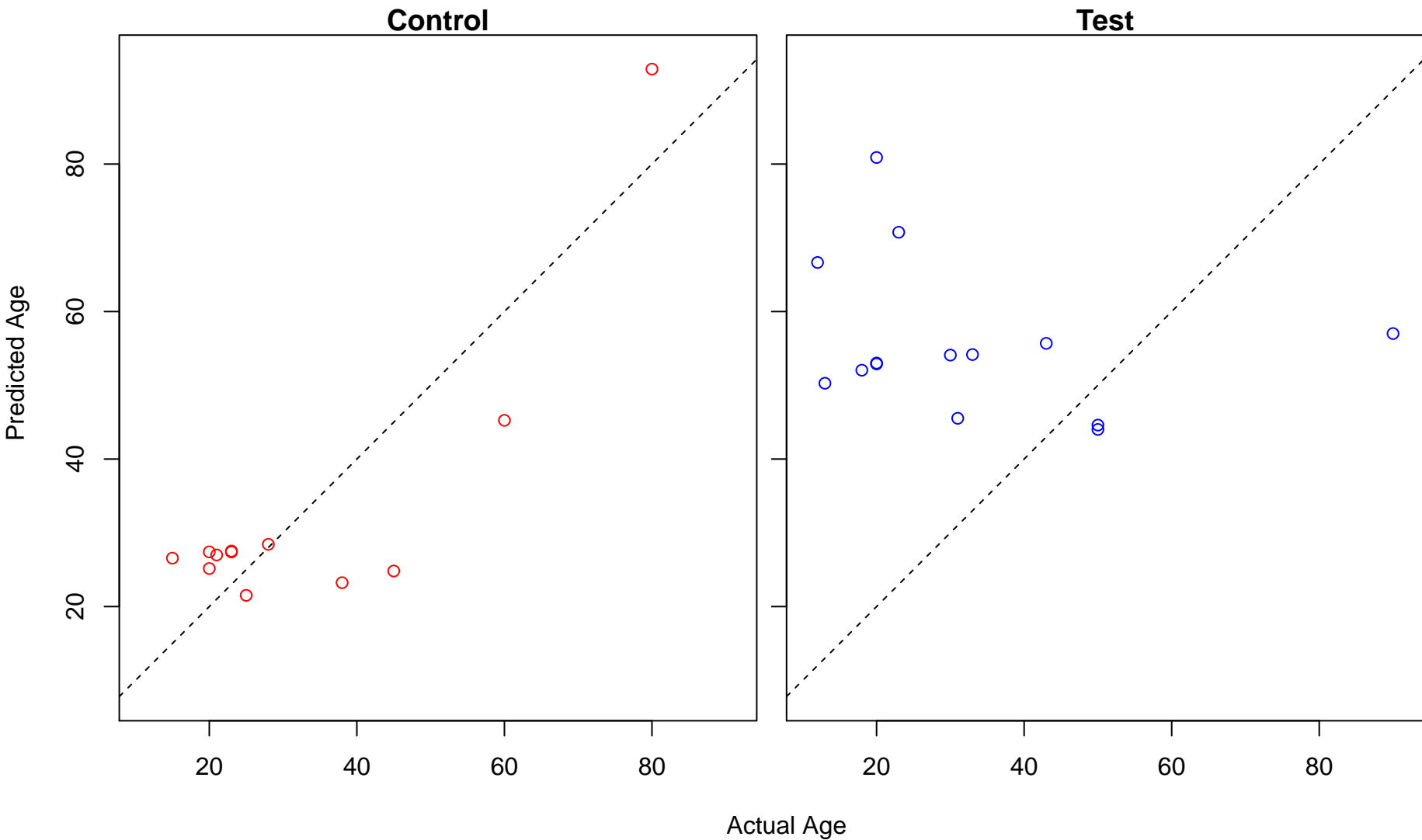
positive regulation of endothelial cell migration (Score: 4.923100)



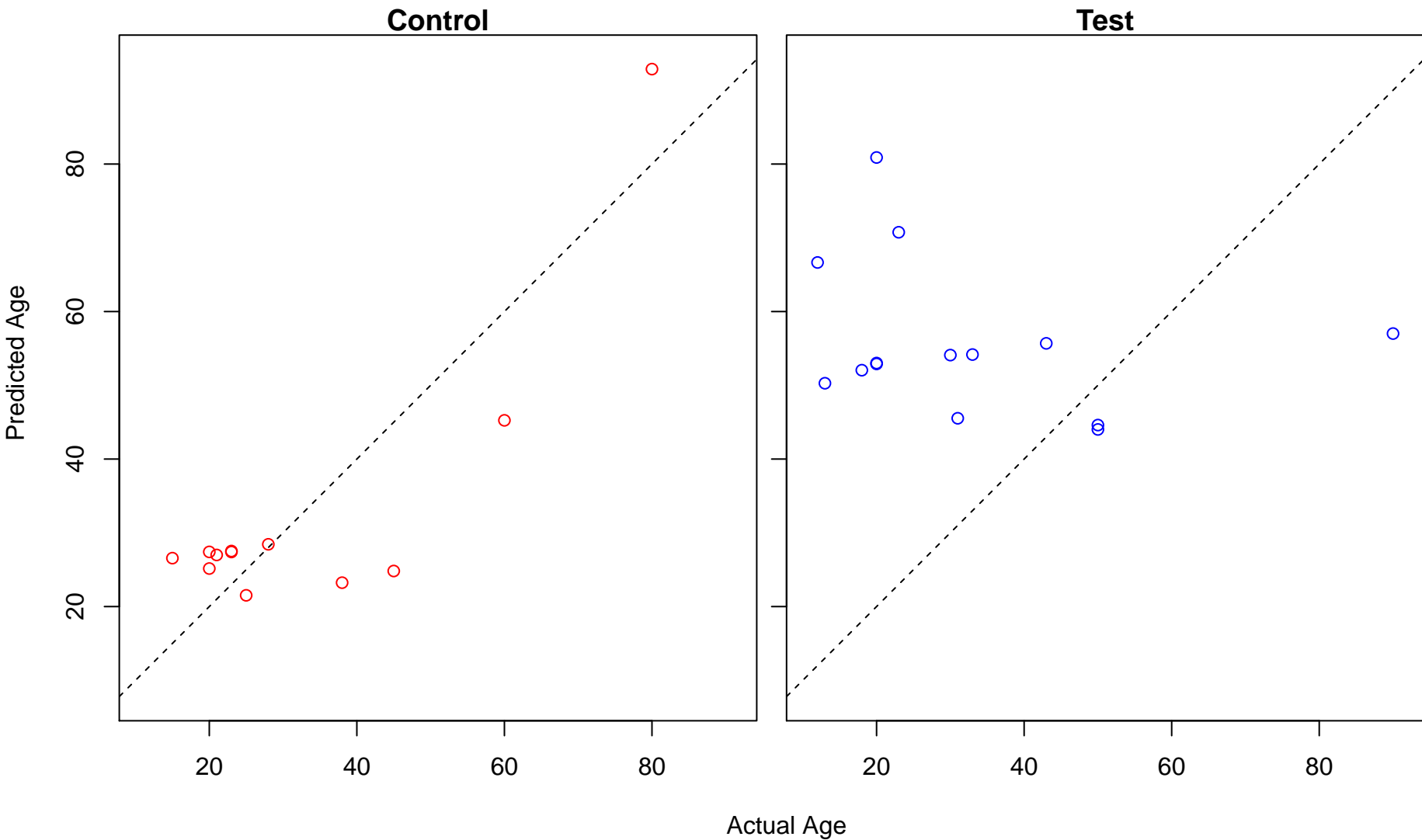
epithelial cell morphogenesis (Score: 4.919679)



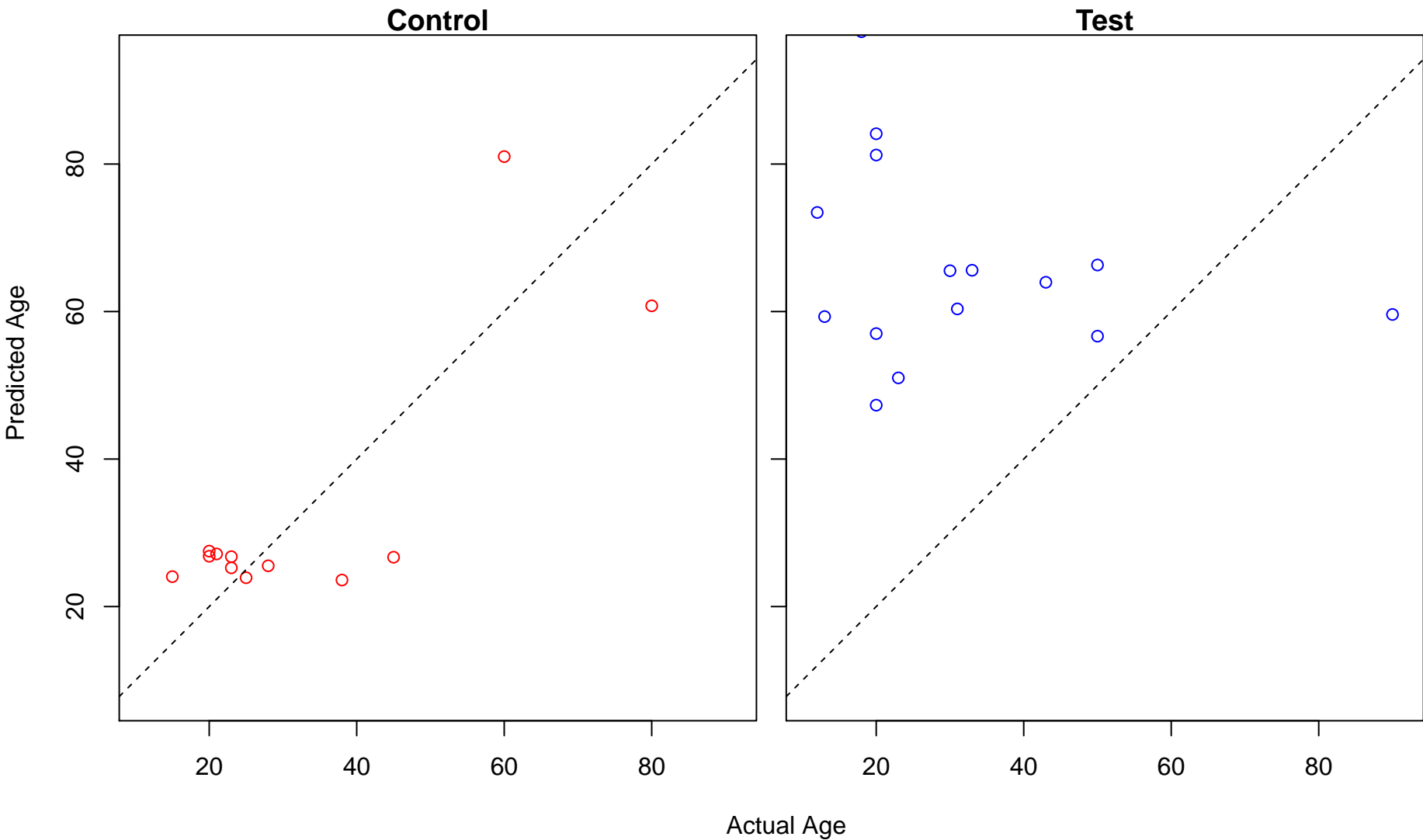
nuclear DNA replication (Score: 4.919591)



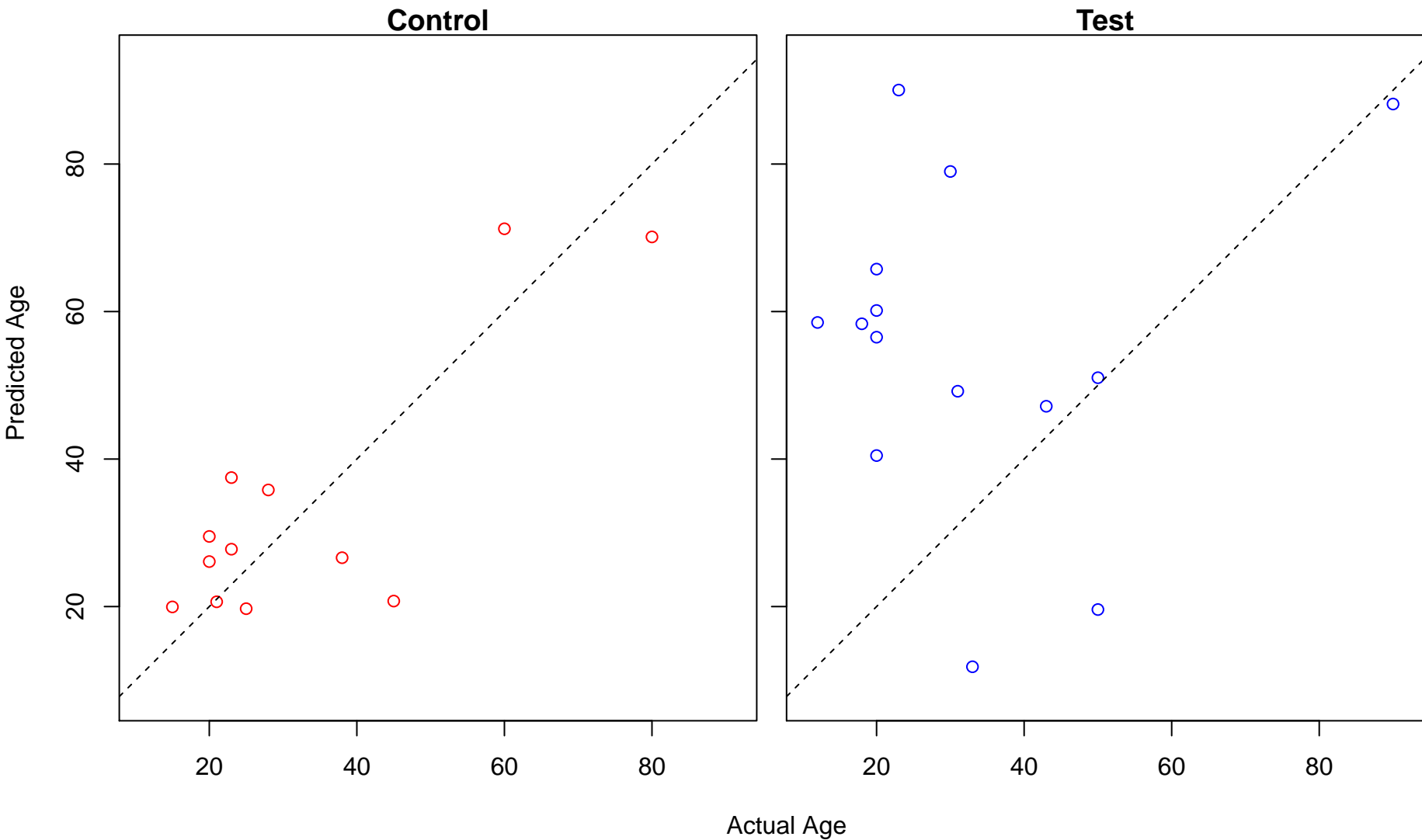
cell cycle DNA replication (Score: 4.919591)



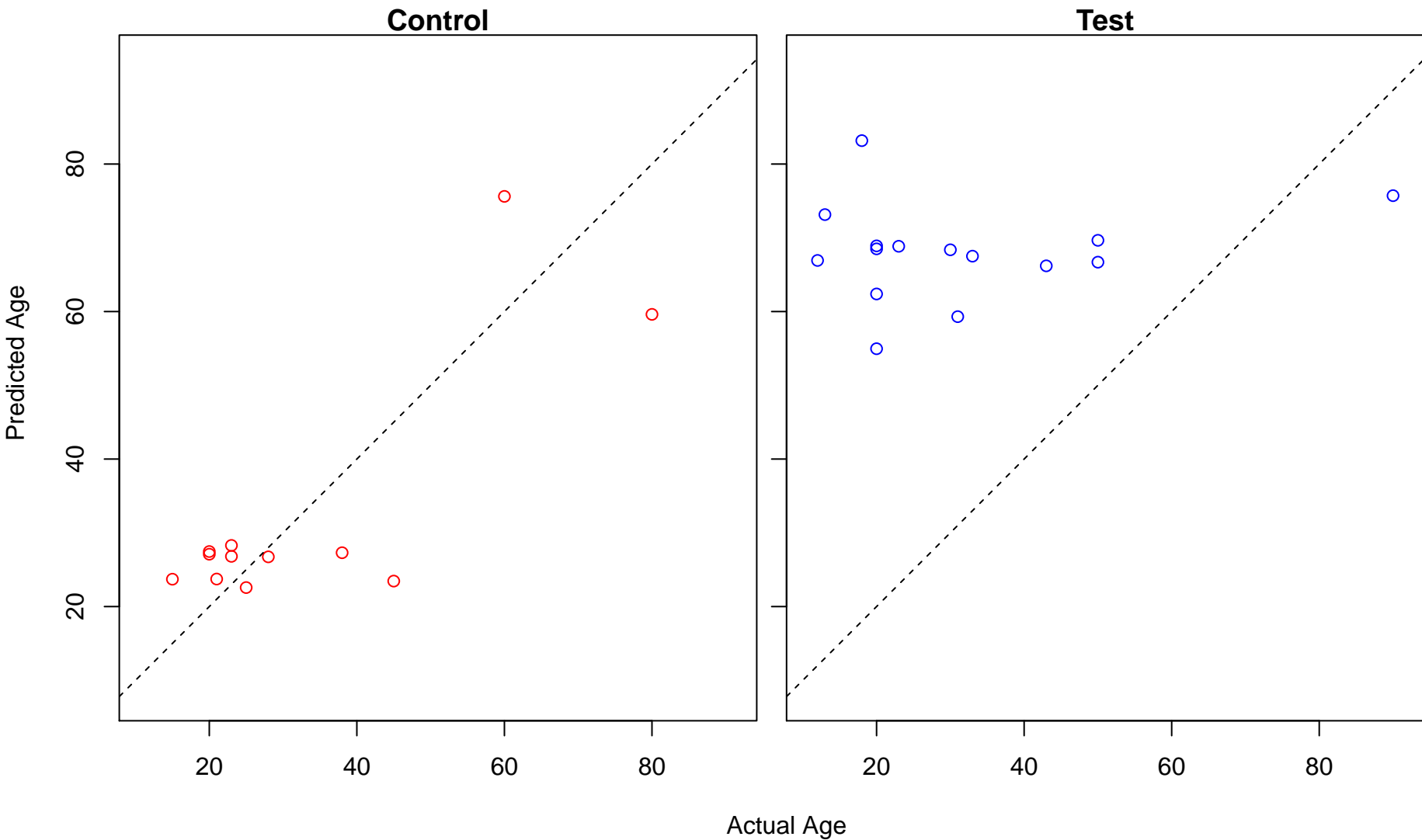
activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c (Score: 4



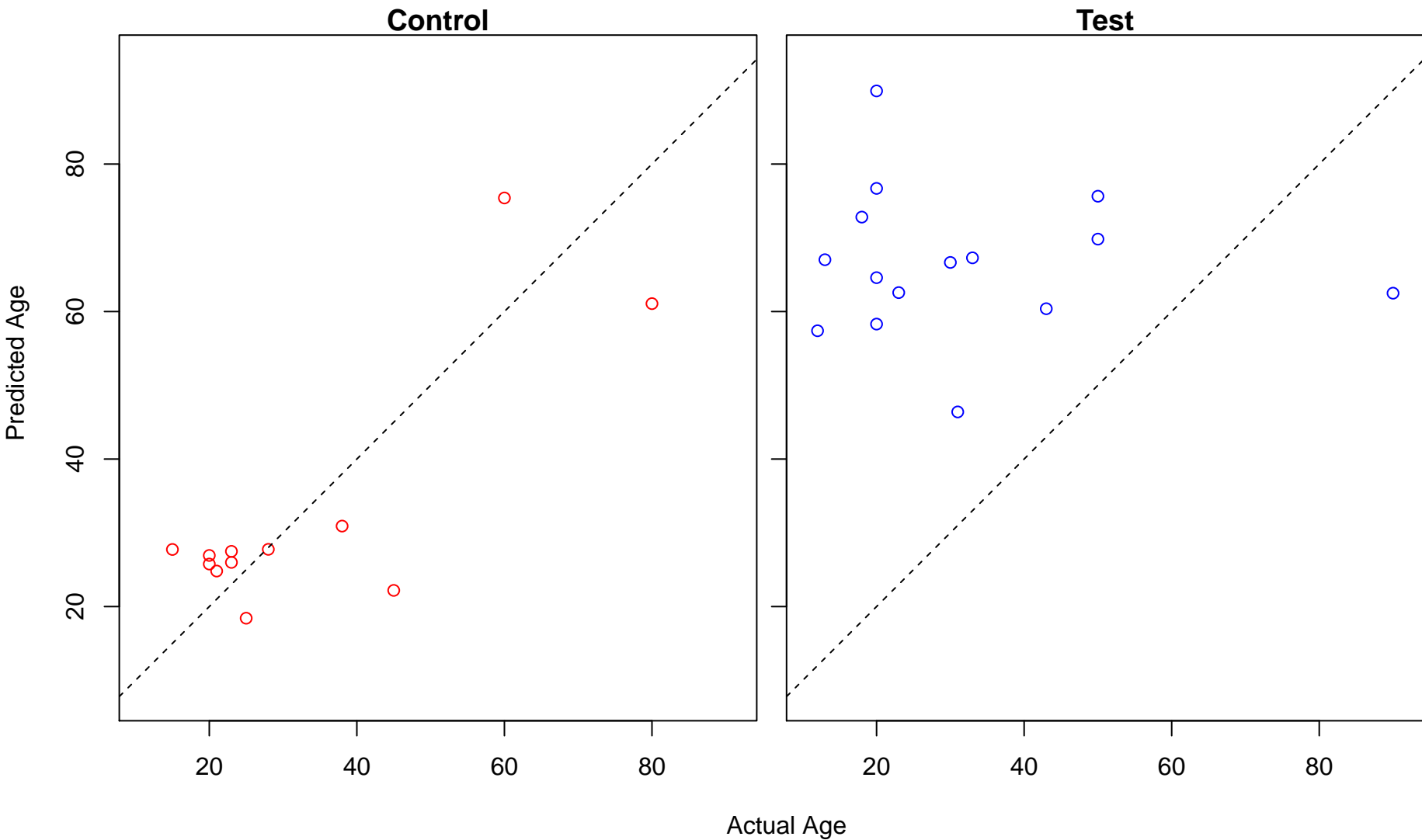
regulation of neuronal synaptic plasticity (Score: 4.916044)



positive regulation of double-strand break repair (Score: 4.916006)

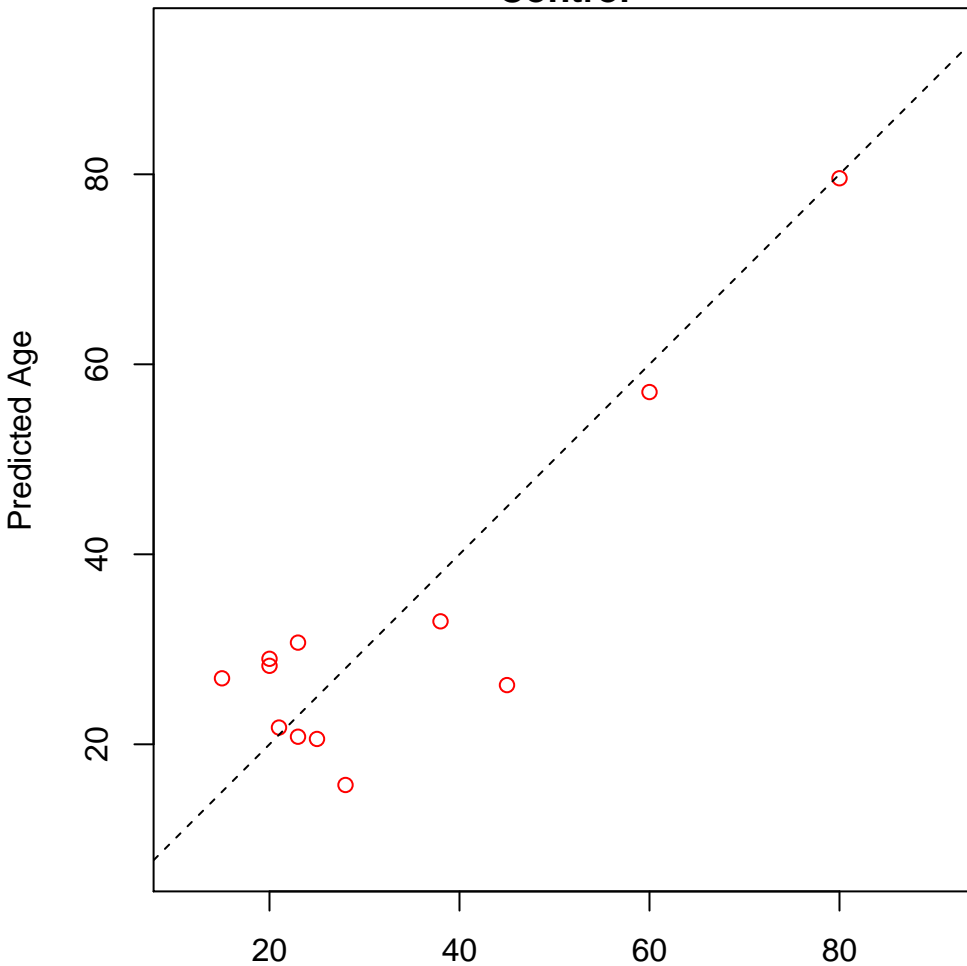


single-organism membrane fusion (Score: 4.915592)

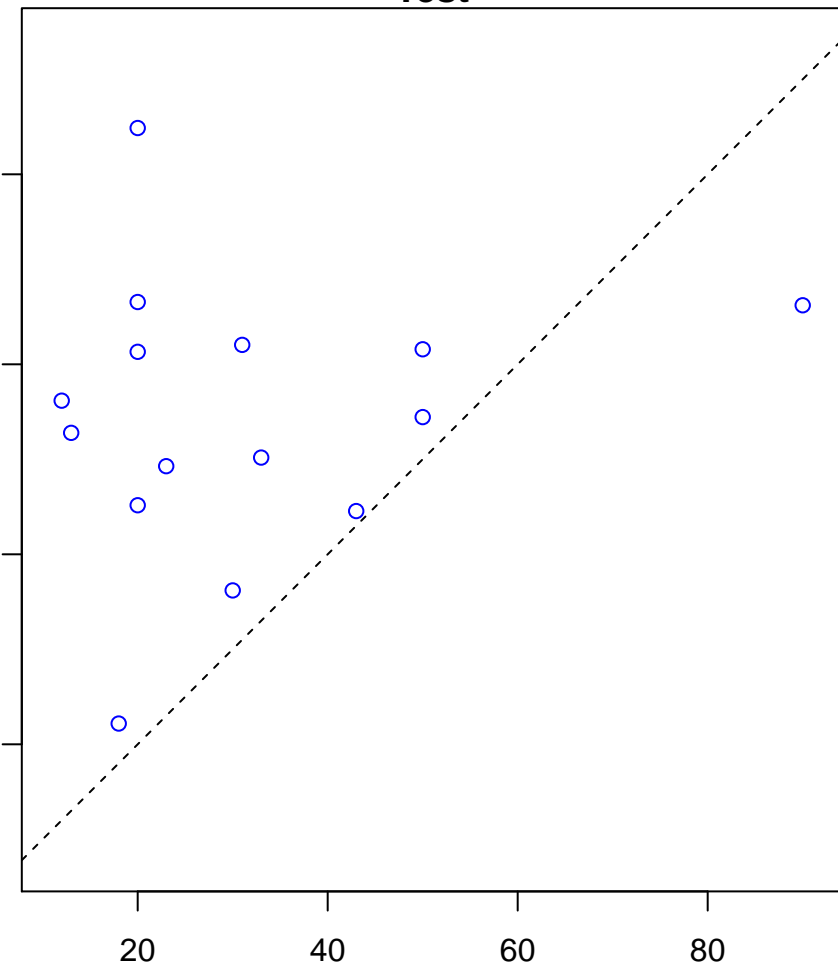


quaternary ammonium group transport (Score: 4.915562)

Control



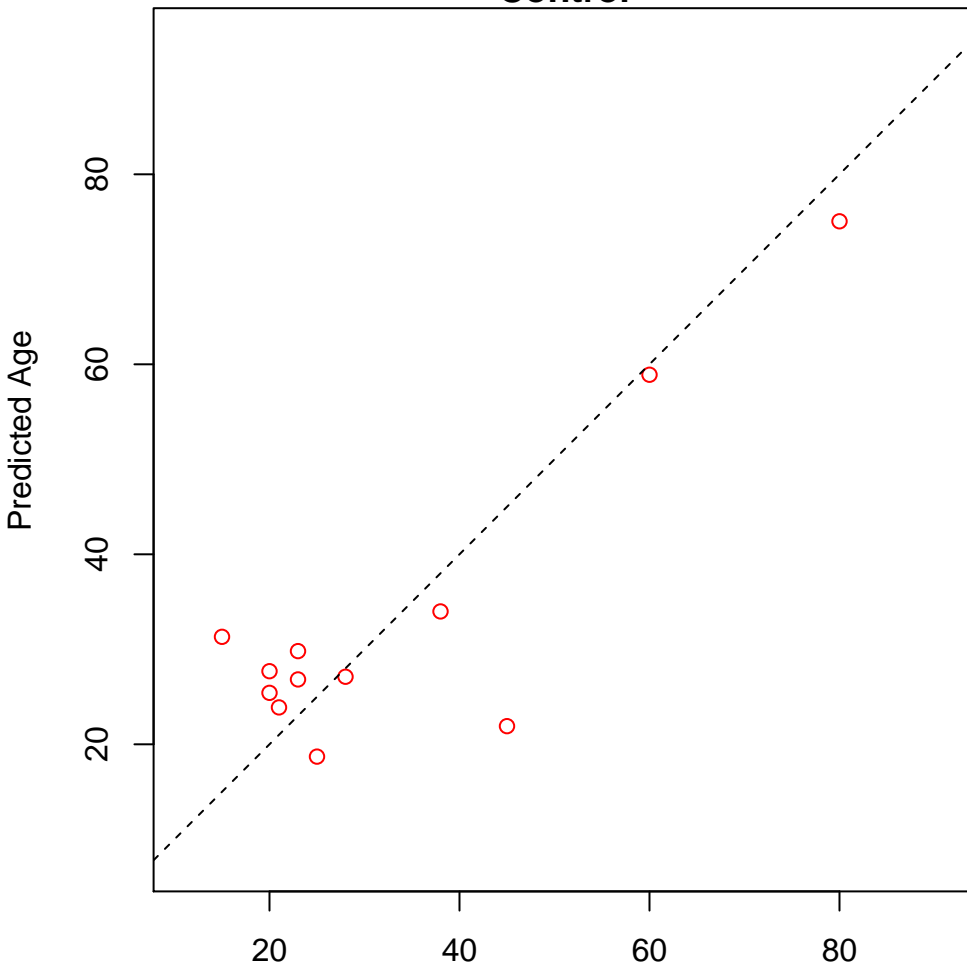
Test



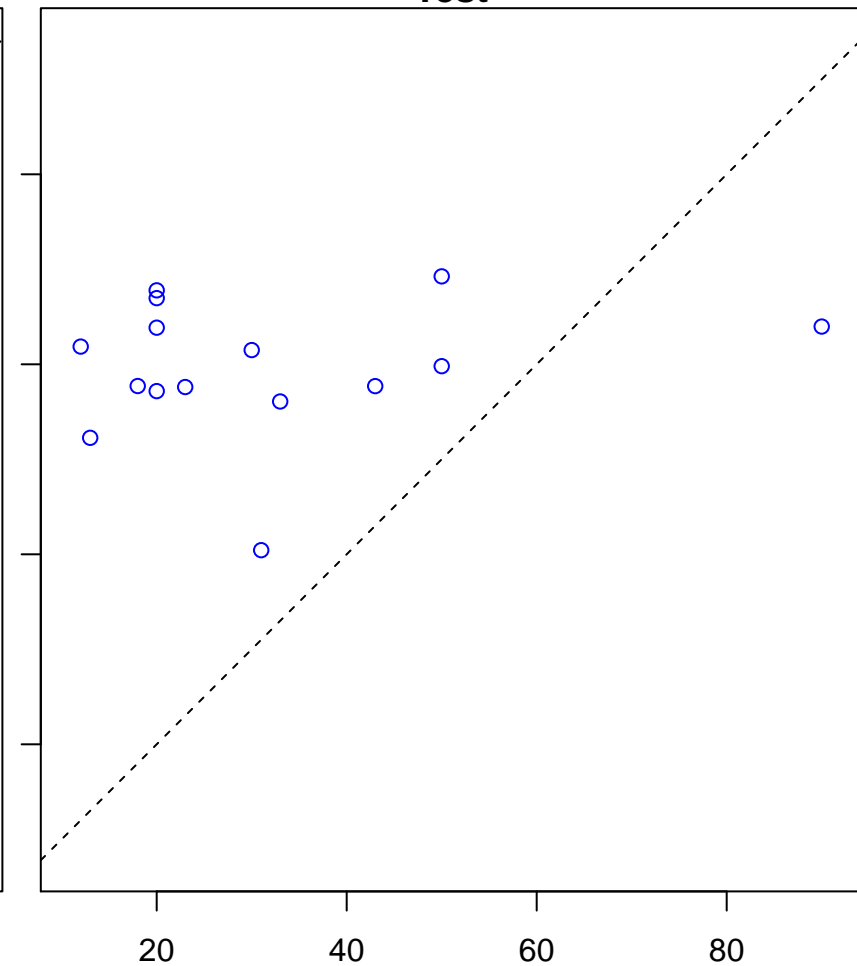
Actual Age

blood vessel endothelial cell migration (Score: 4.915091)

Control



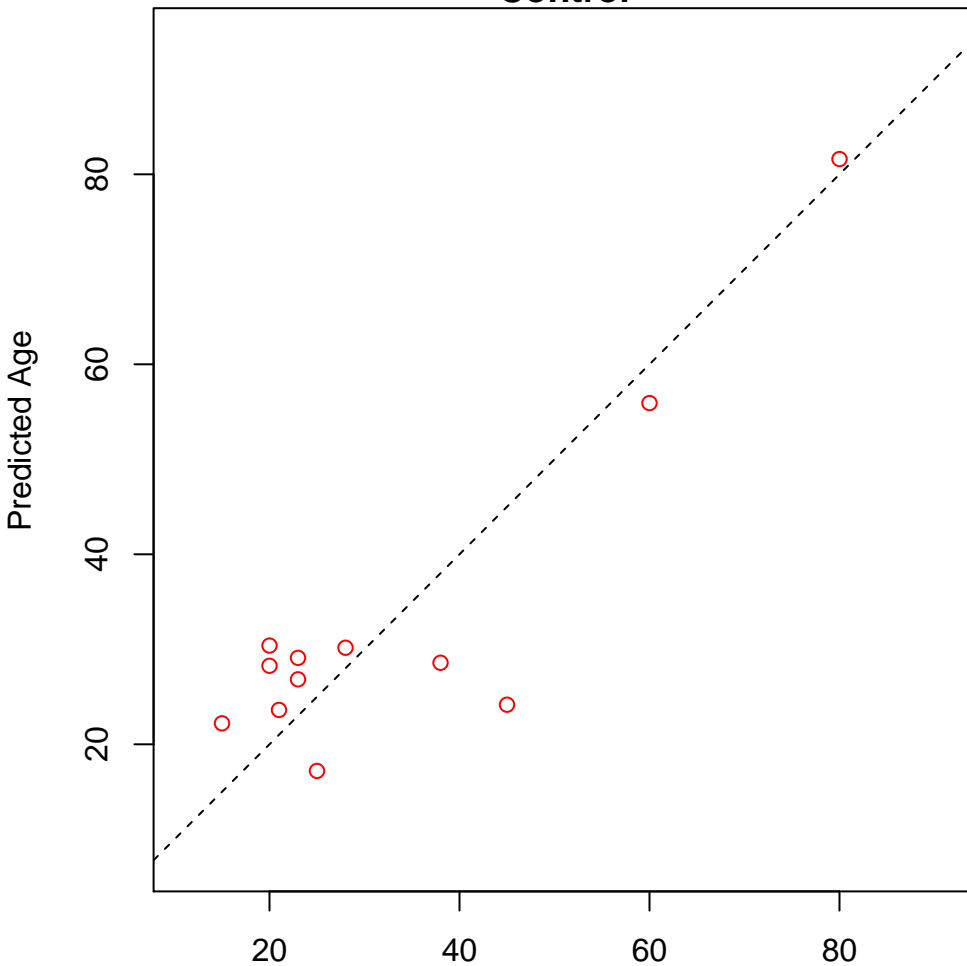
Test



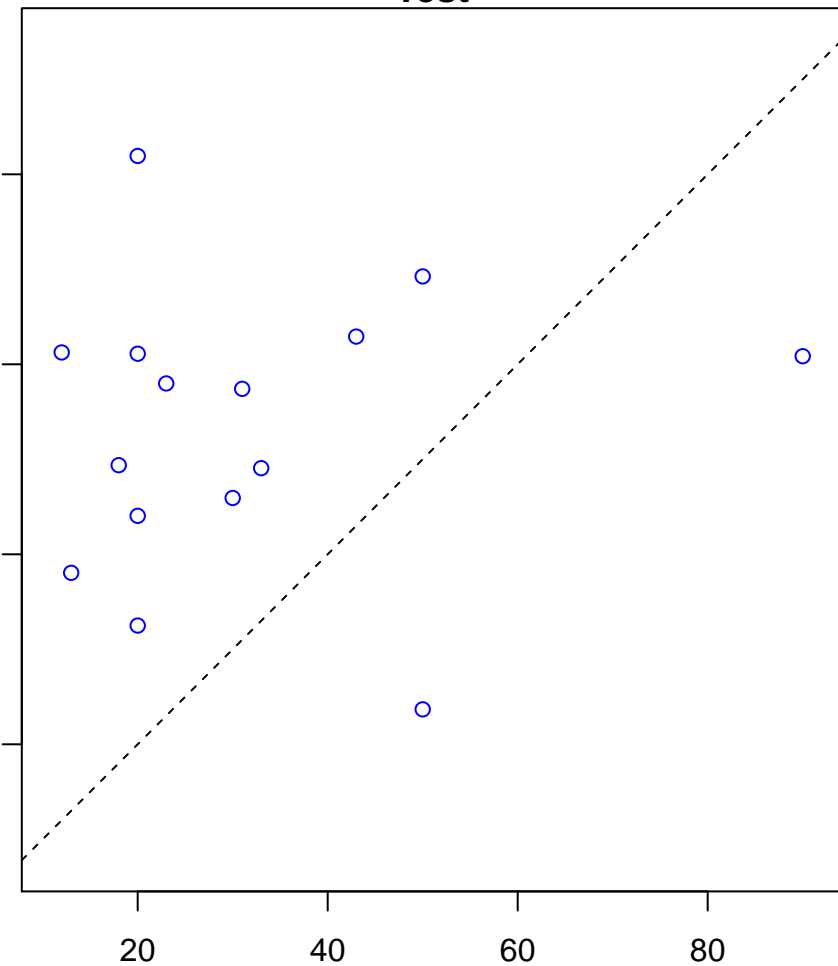
Actual Age

endoplasmic reticulum organization (Score: 4.914044)

Control

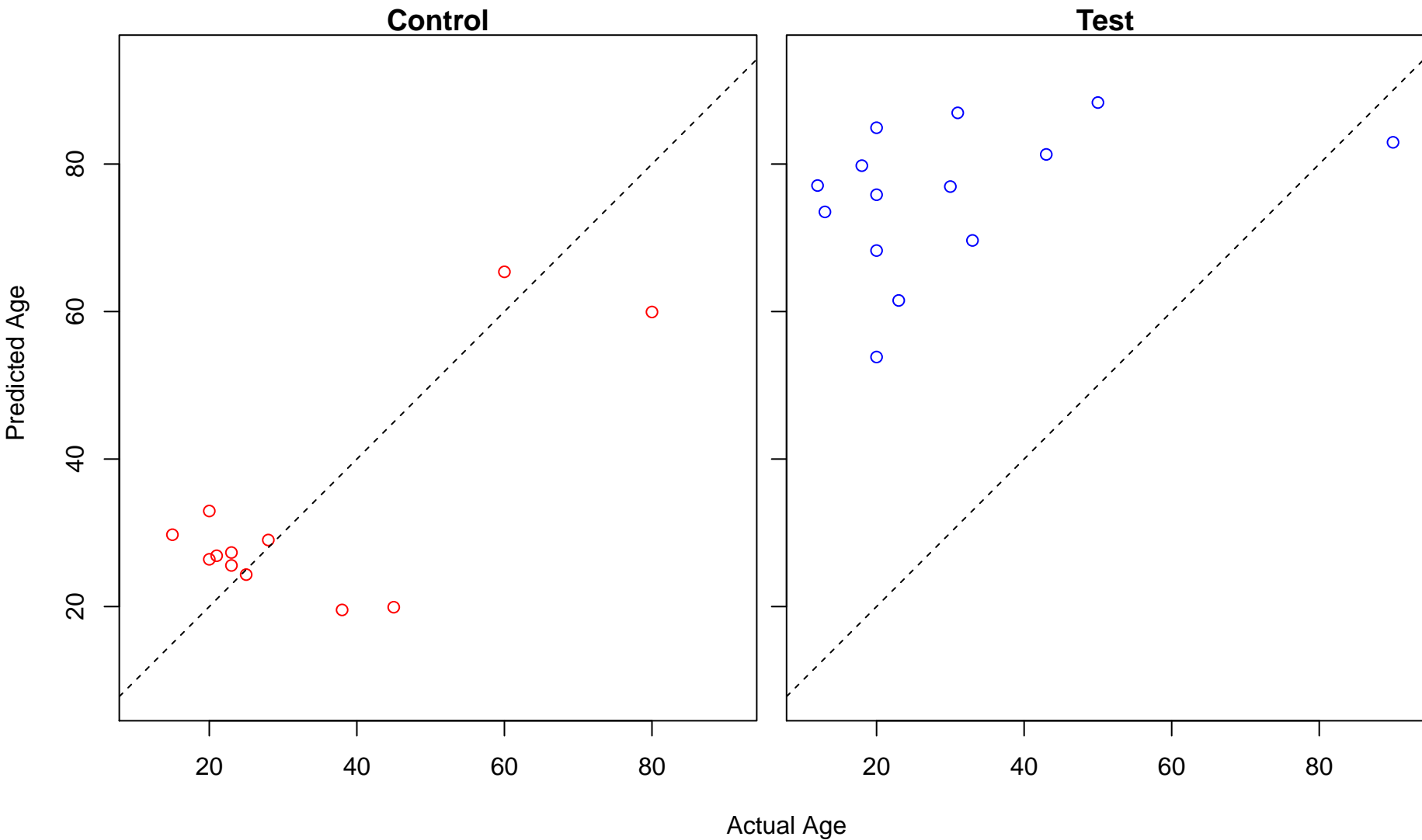


Test

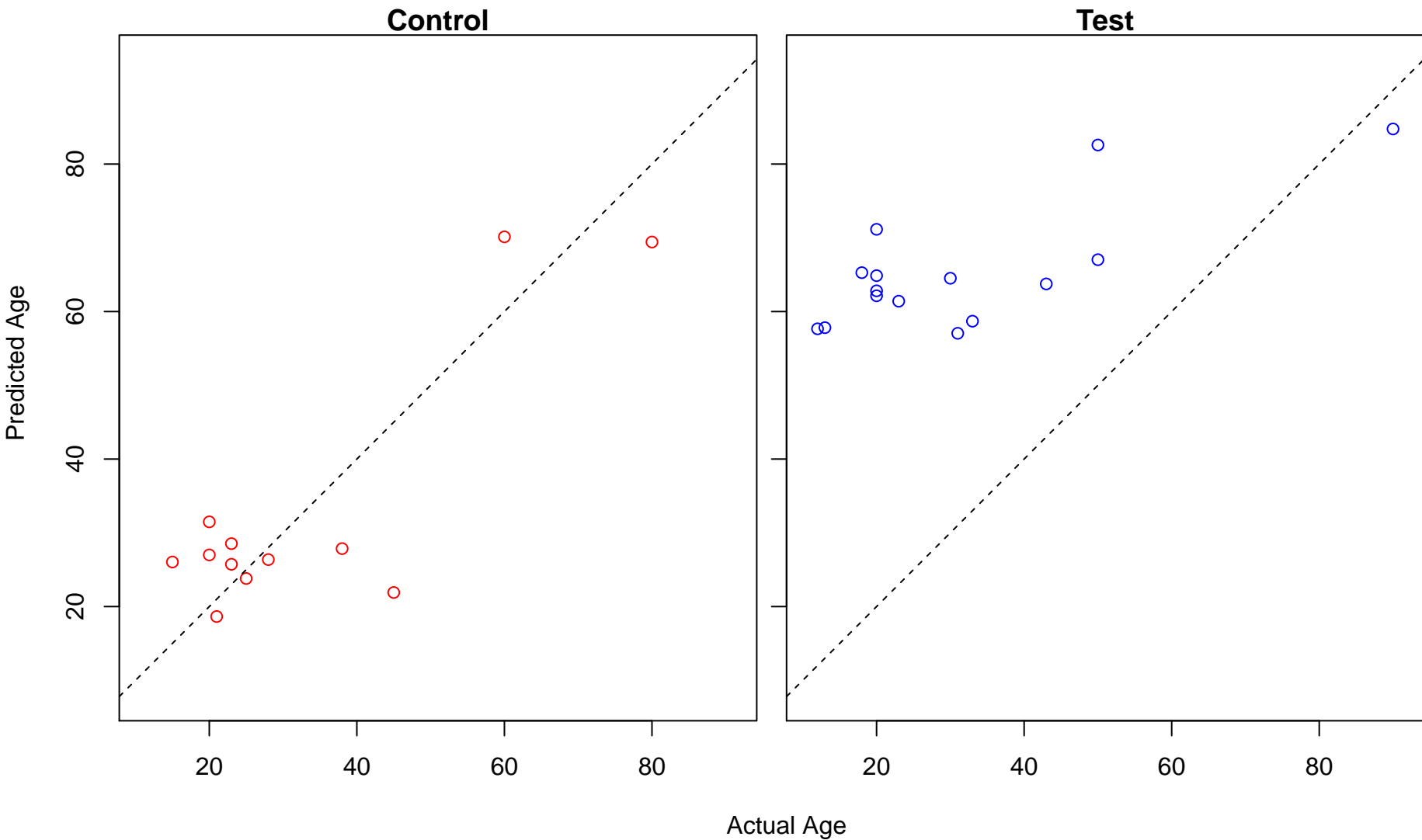


Actual Age

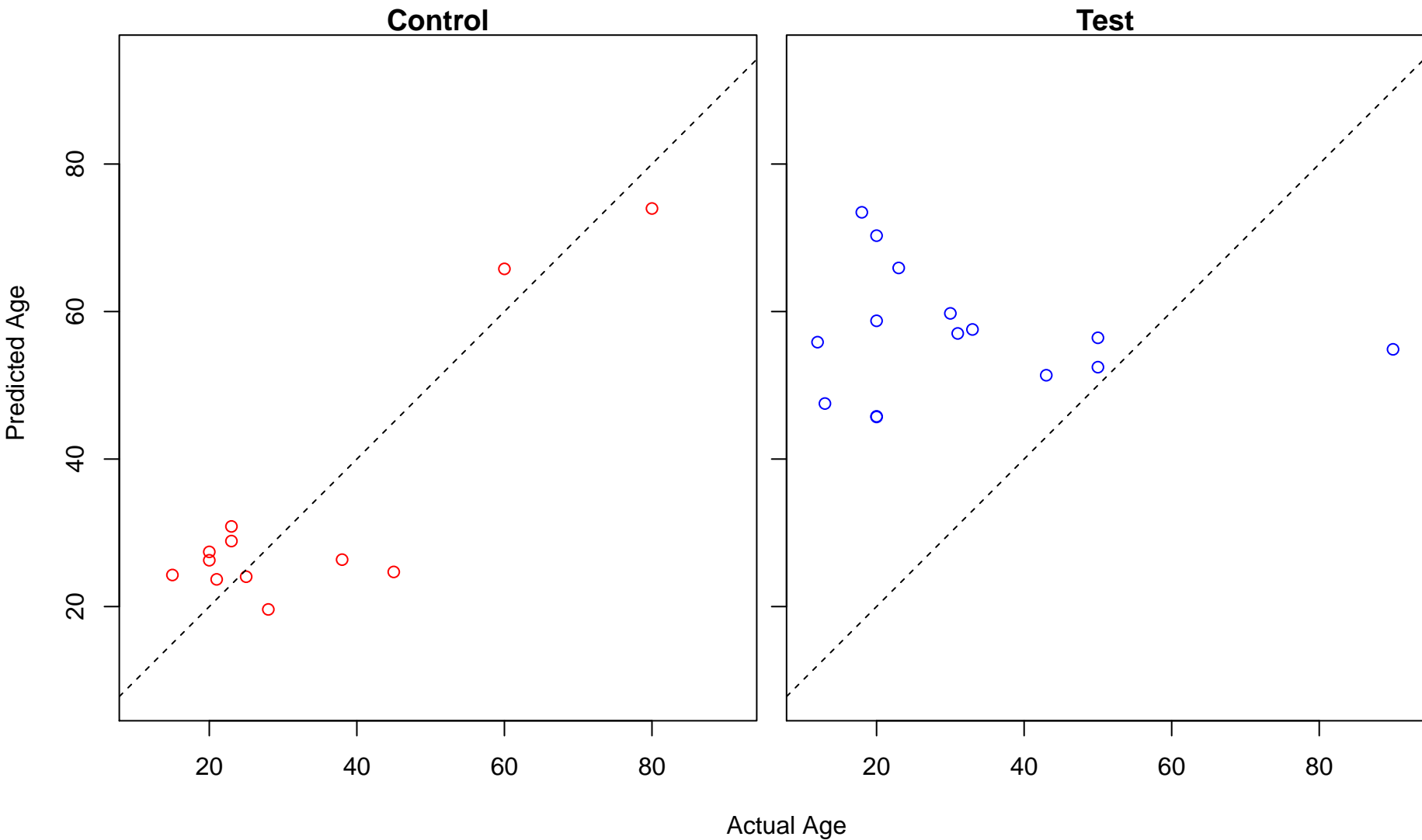
cell communication by electrical coupling involved in cardiac conduction (Score: 4.914042)



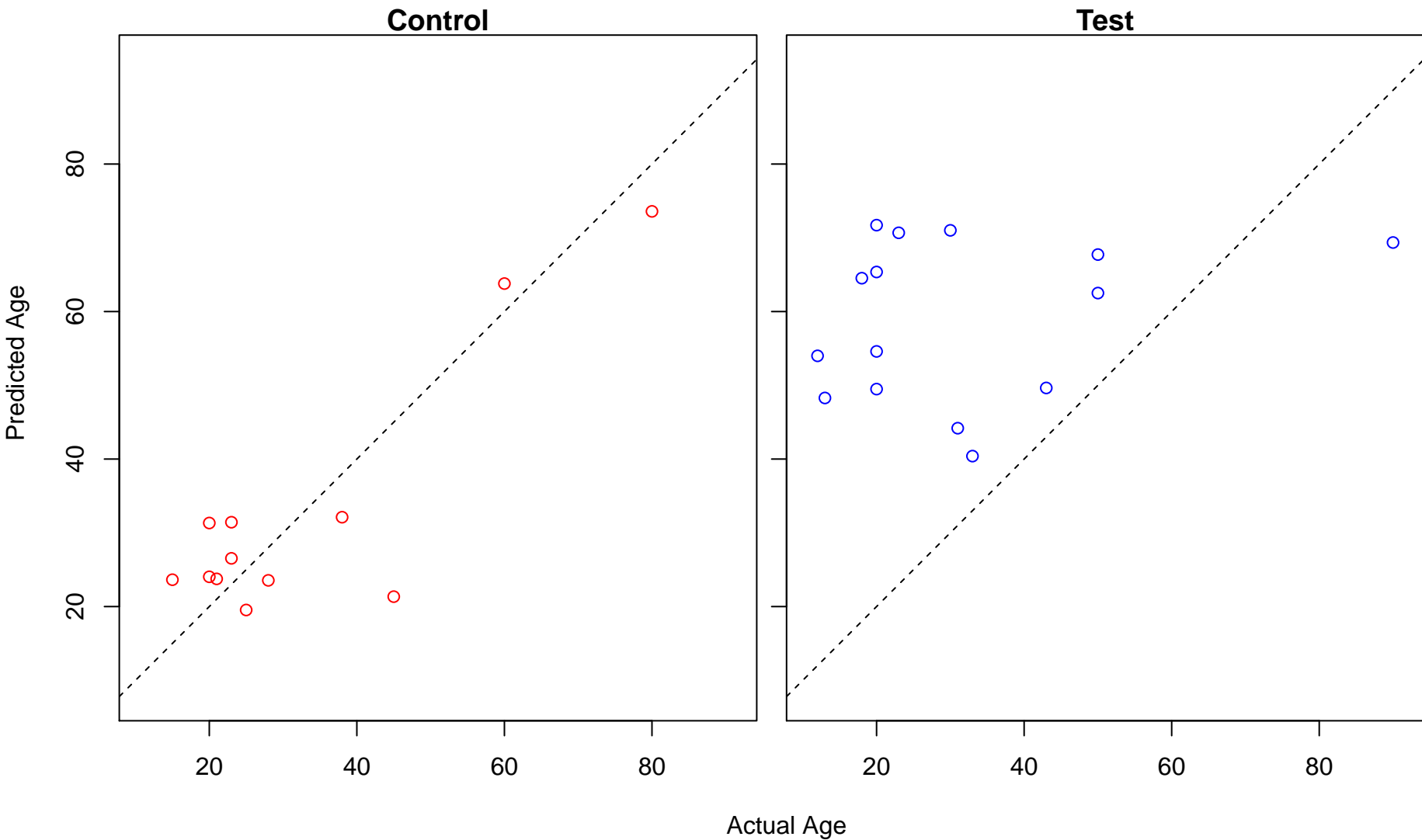
biotin metabolic process (Score: 4.913150)



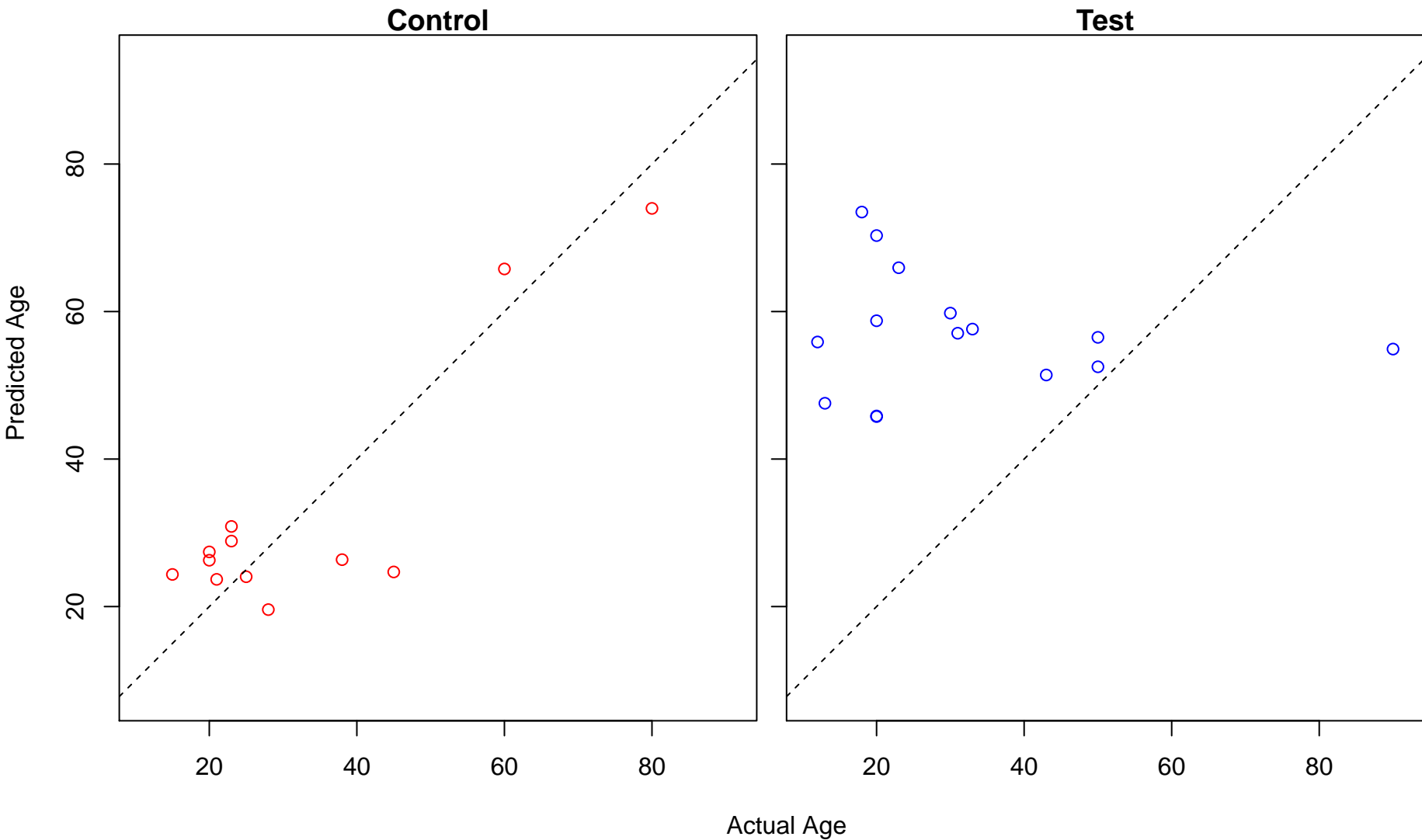
fatty acid elongation (Score: 4.913114)



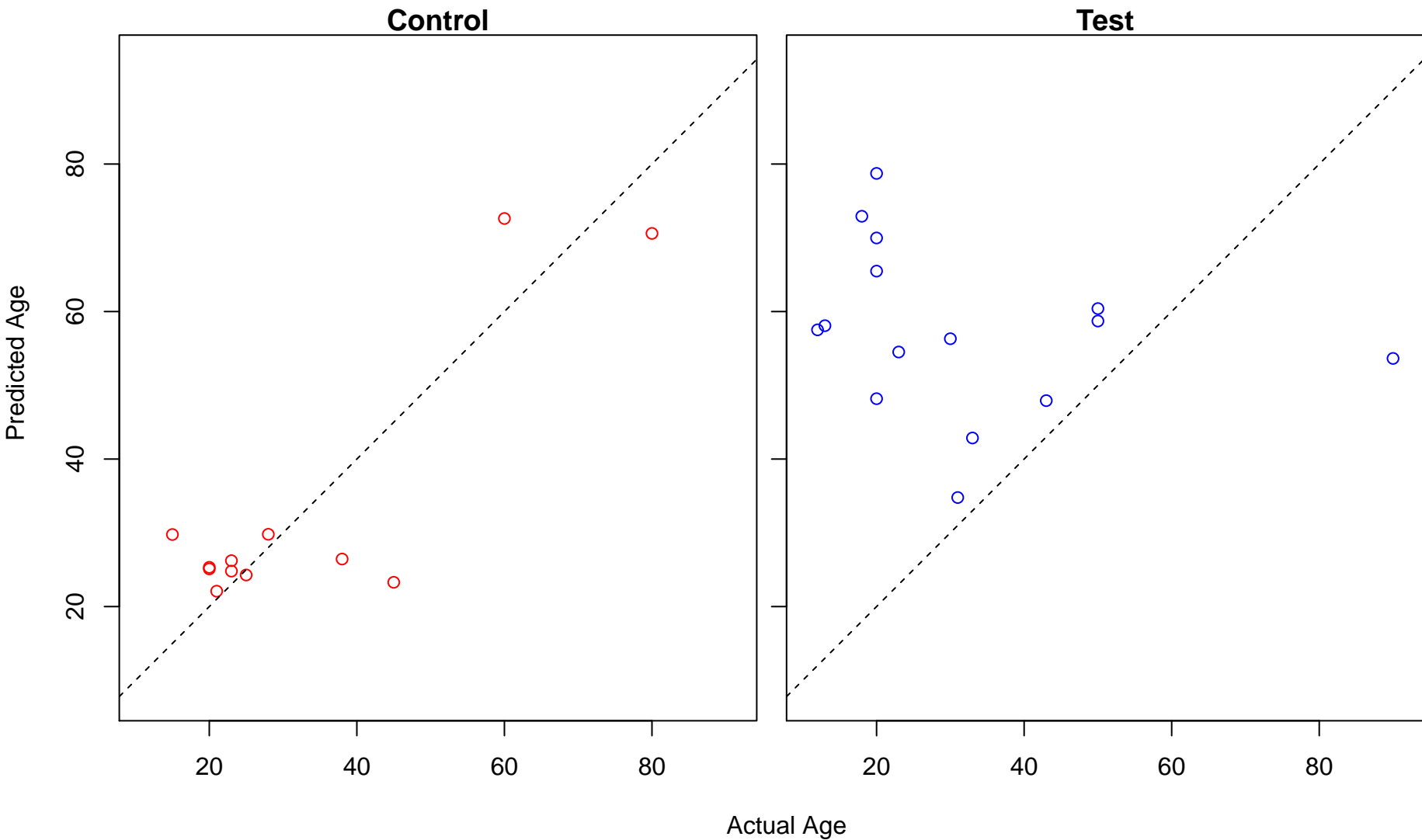
S-adenosylmethionine metabolic process (Score: 4.913027)



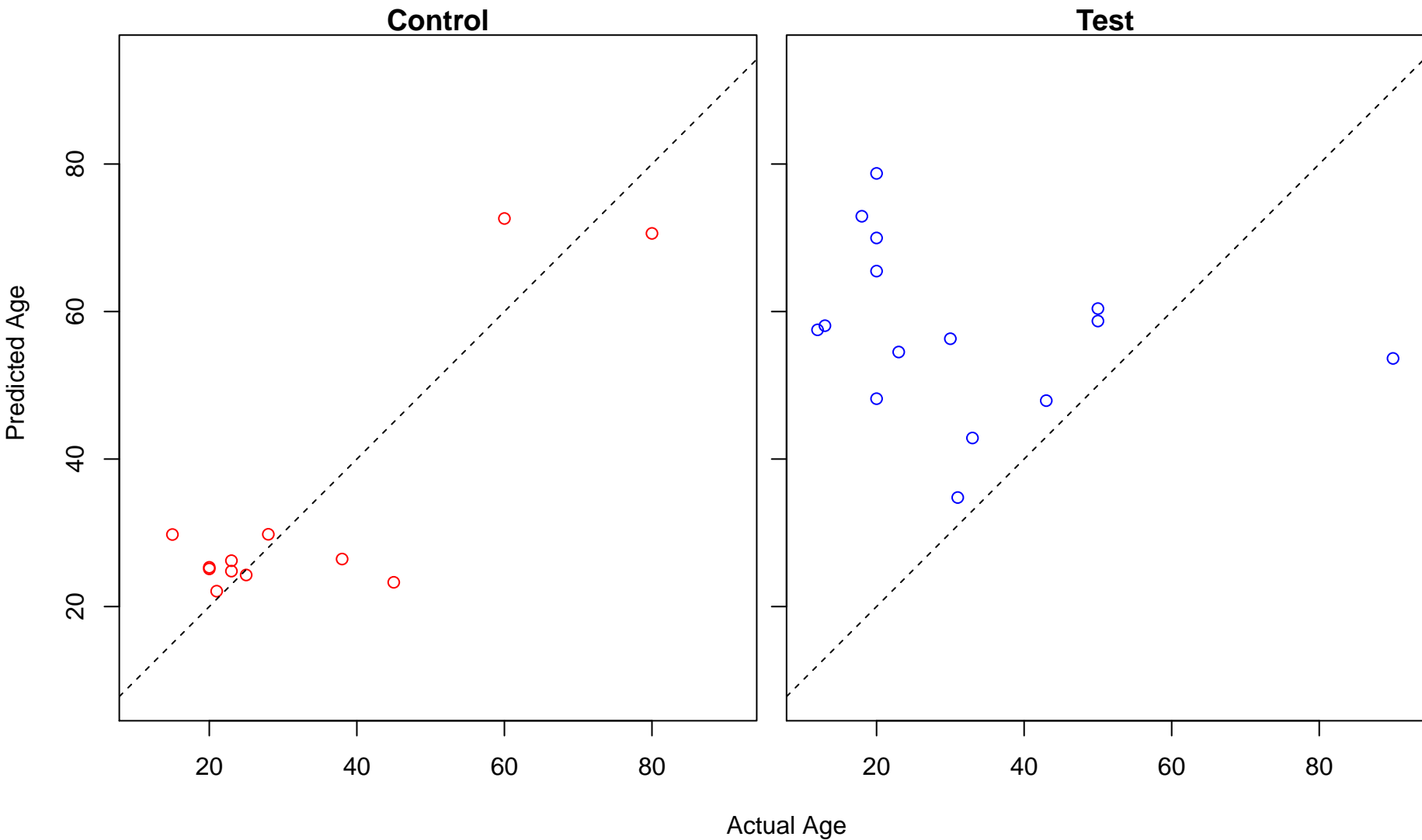
very long-chain fatty acid biosynthetic process (Score: 4.912041)



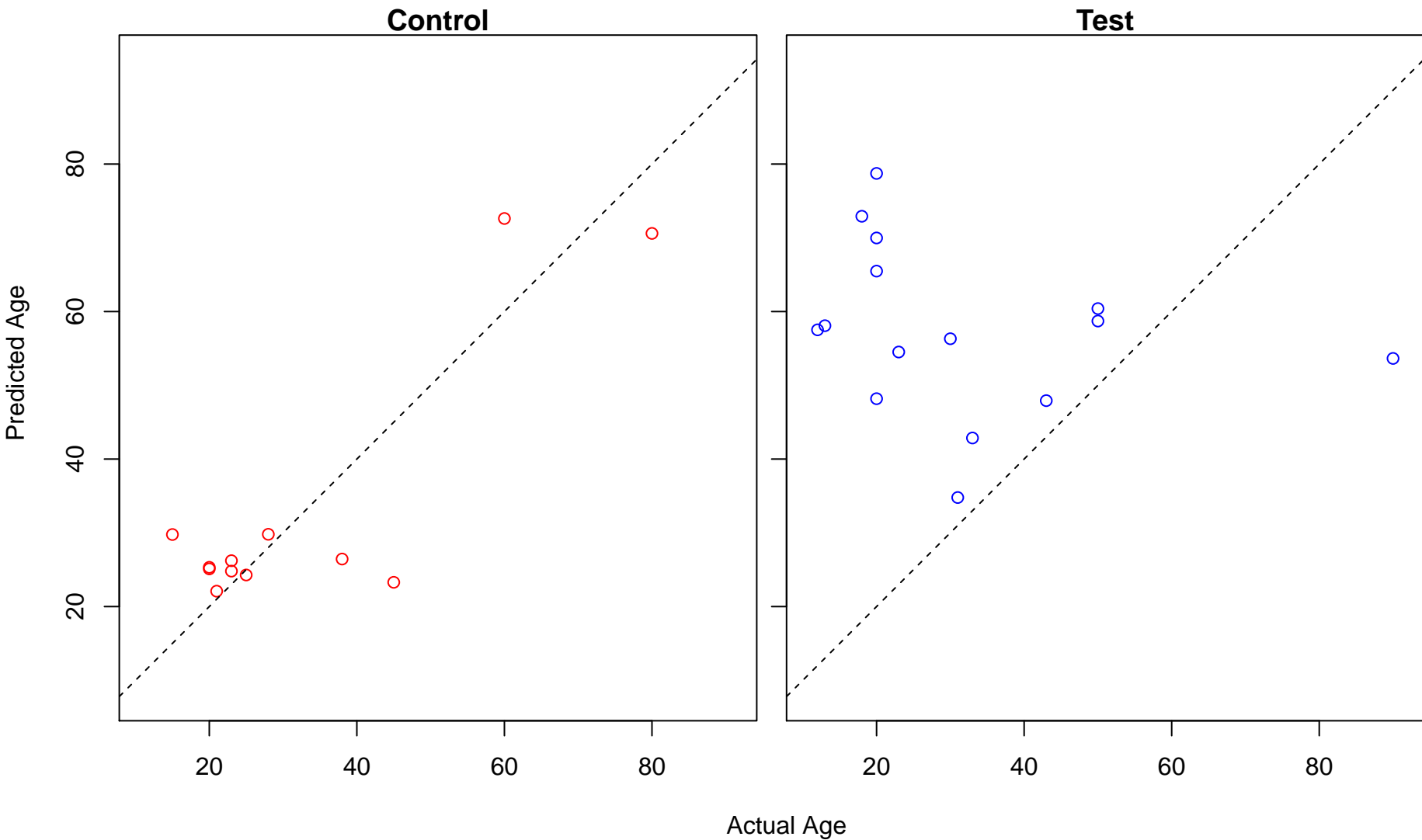
negative regulation of sister chromatid segregation (Score: 4.911906)



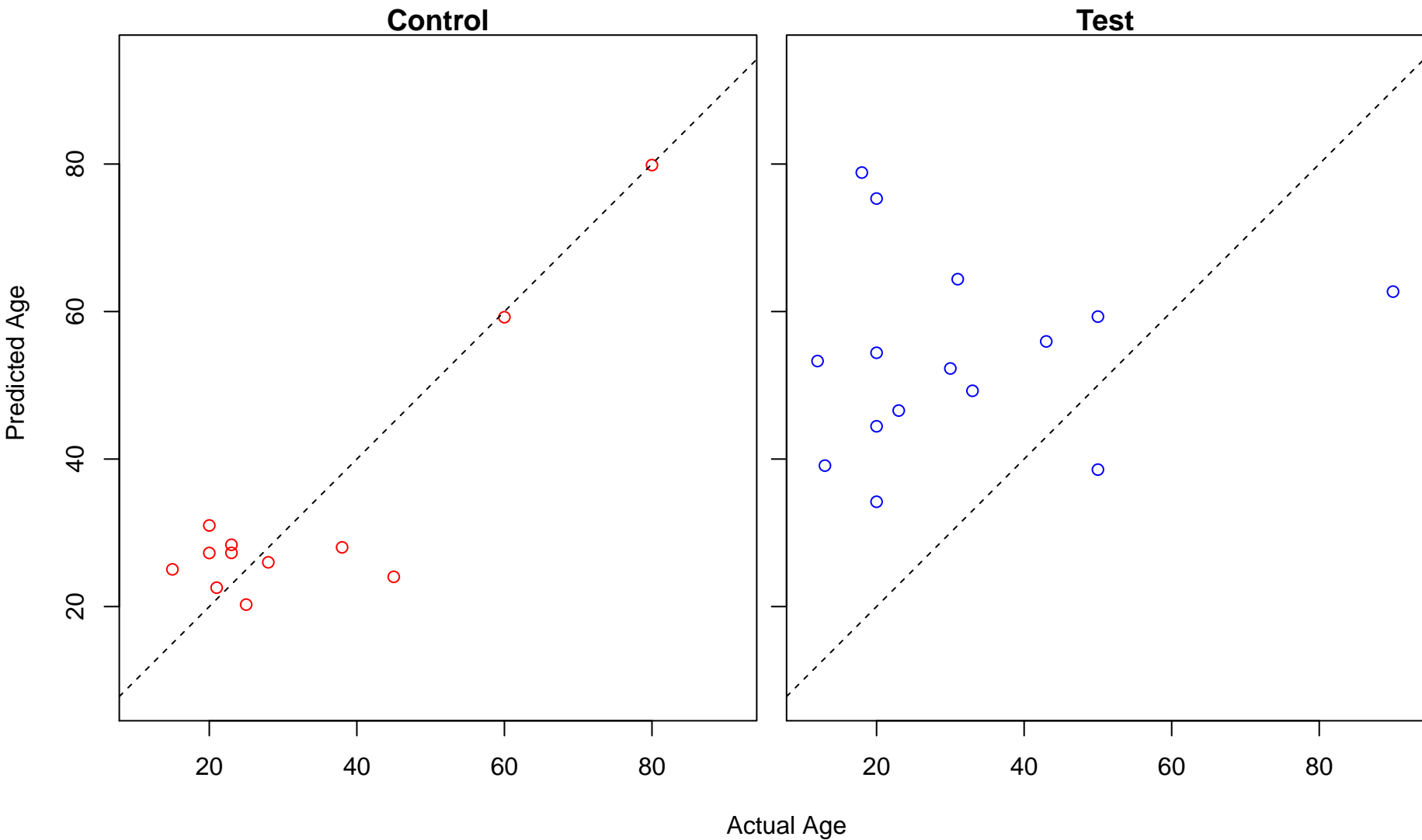
negative regulation of mitotic sister chromatid segregation (Score: 4.911906)



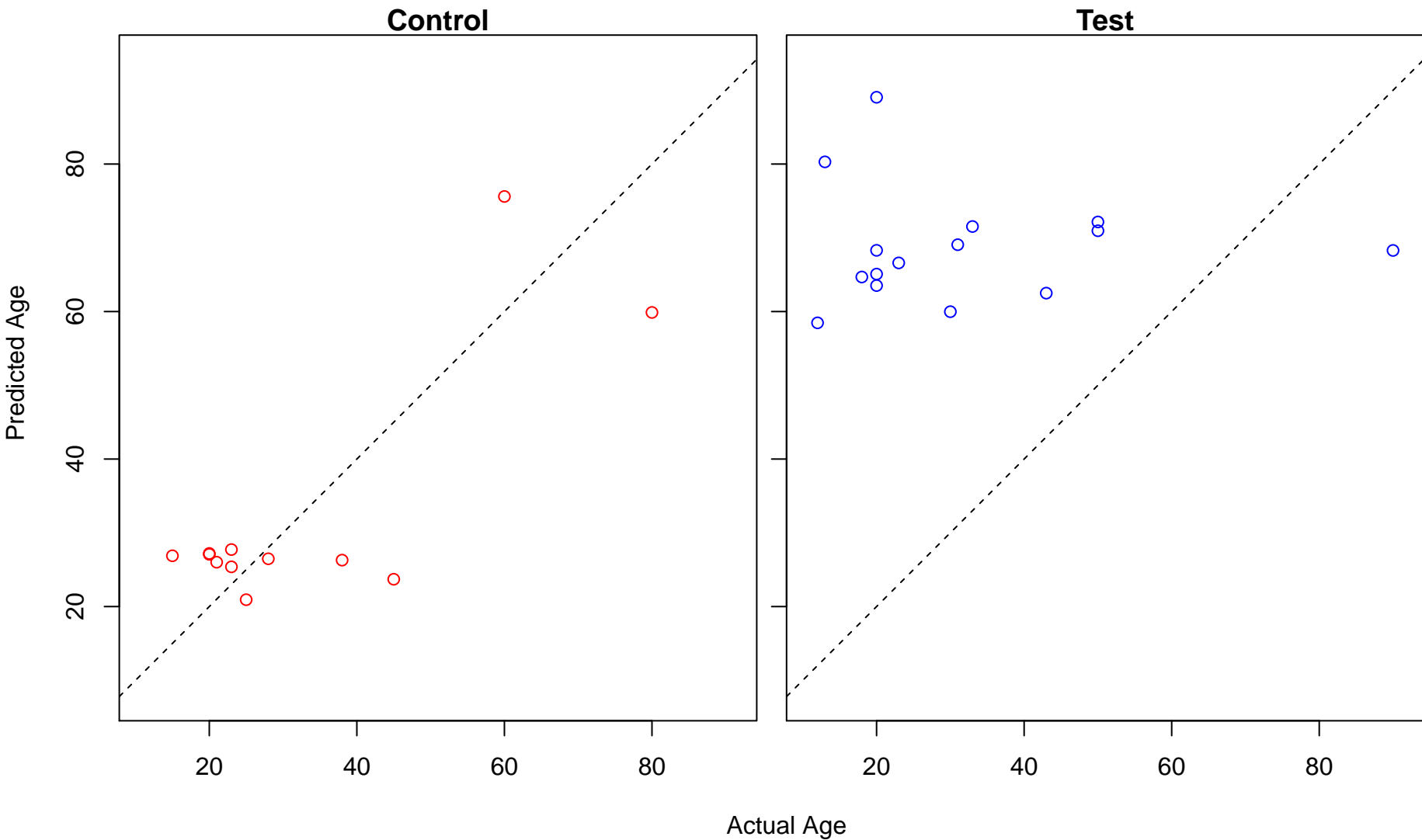
negative regulation of chromosome segregation (Score: 4.911906)



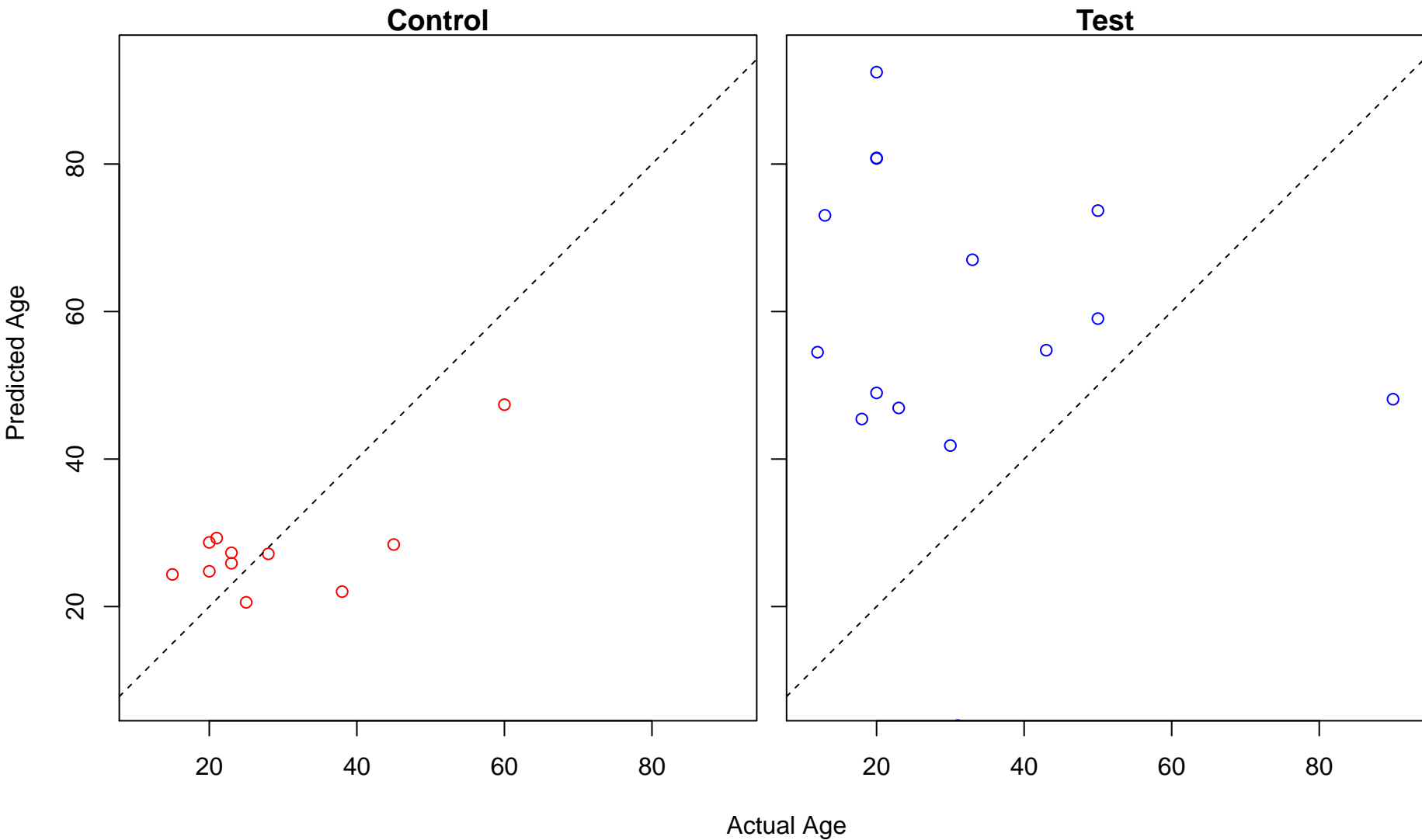
regulation of protein exit from endoplasmic reticulum (Score: 4.911511)



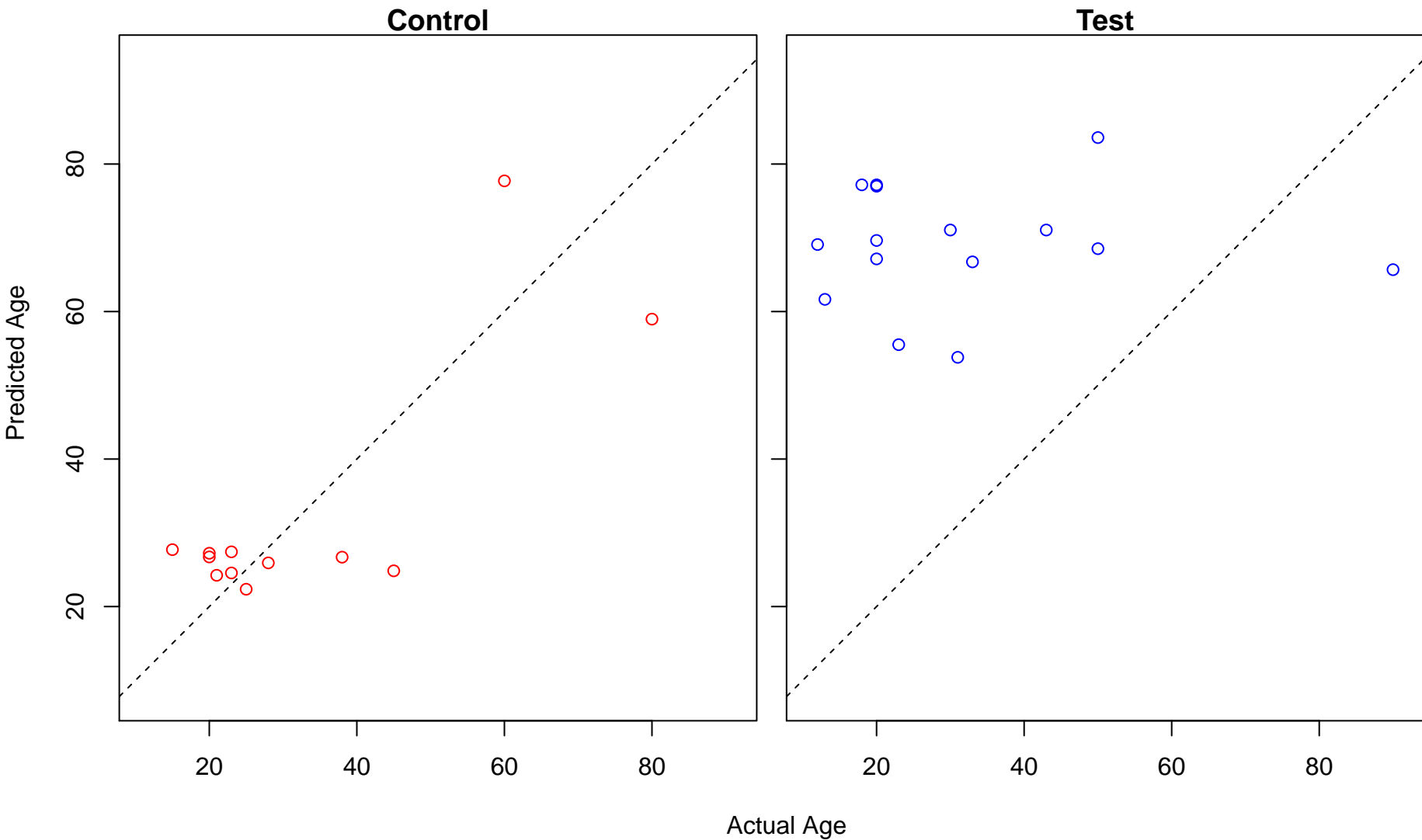
regulation of G-protein coupled receptor protein signaling pathway (Score: 4.910587)



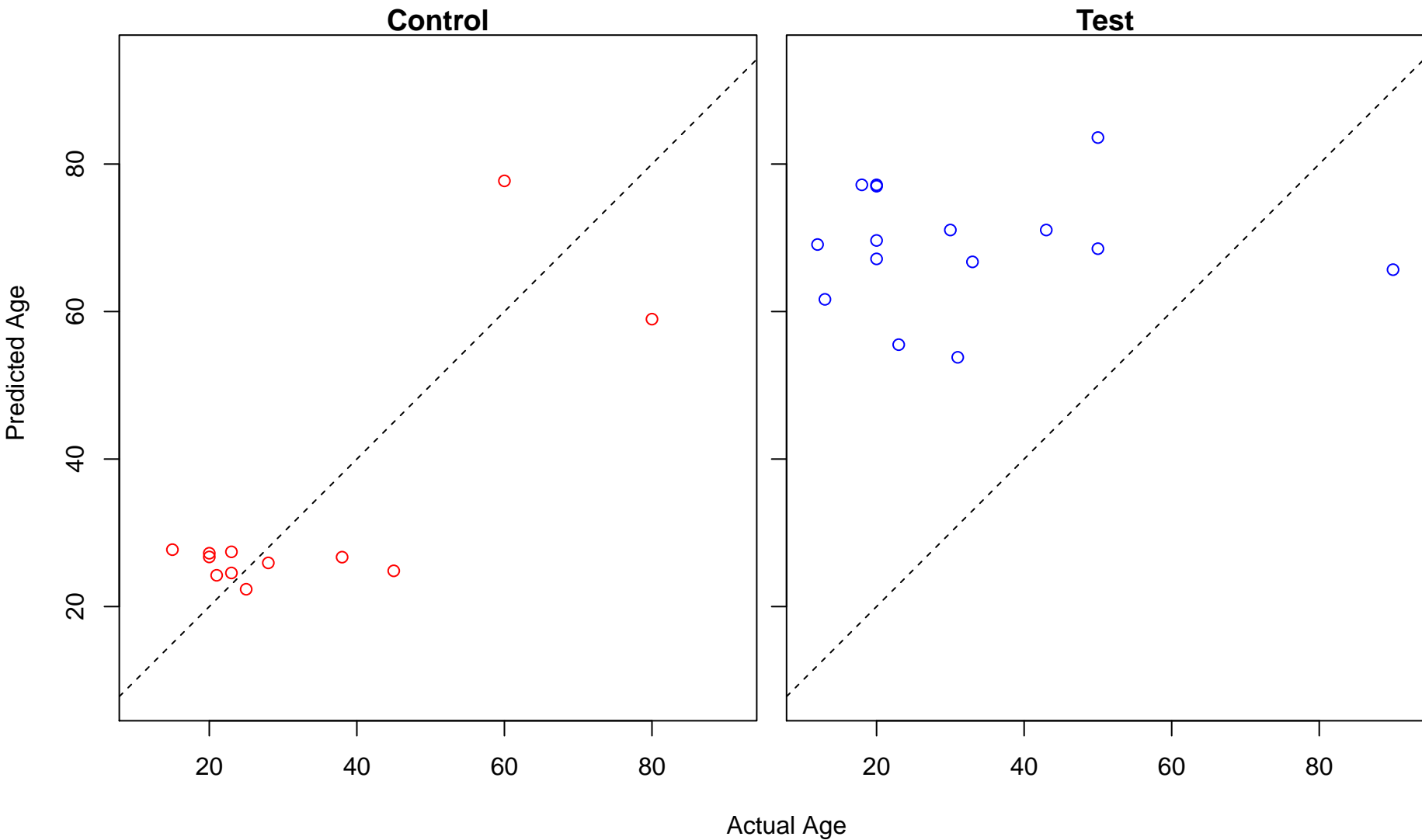
regulation of myeloid cell apoptotic process (Score: 4.909989)



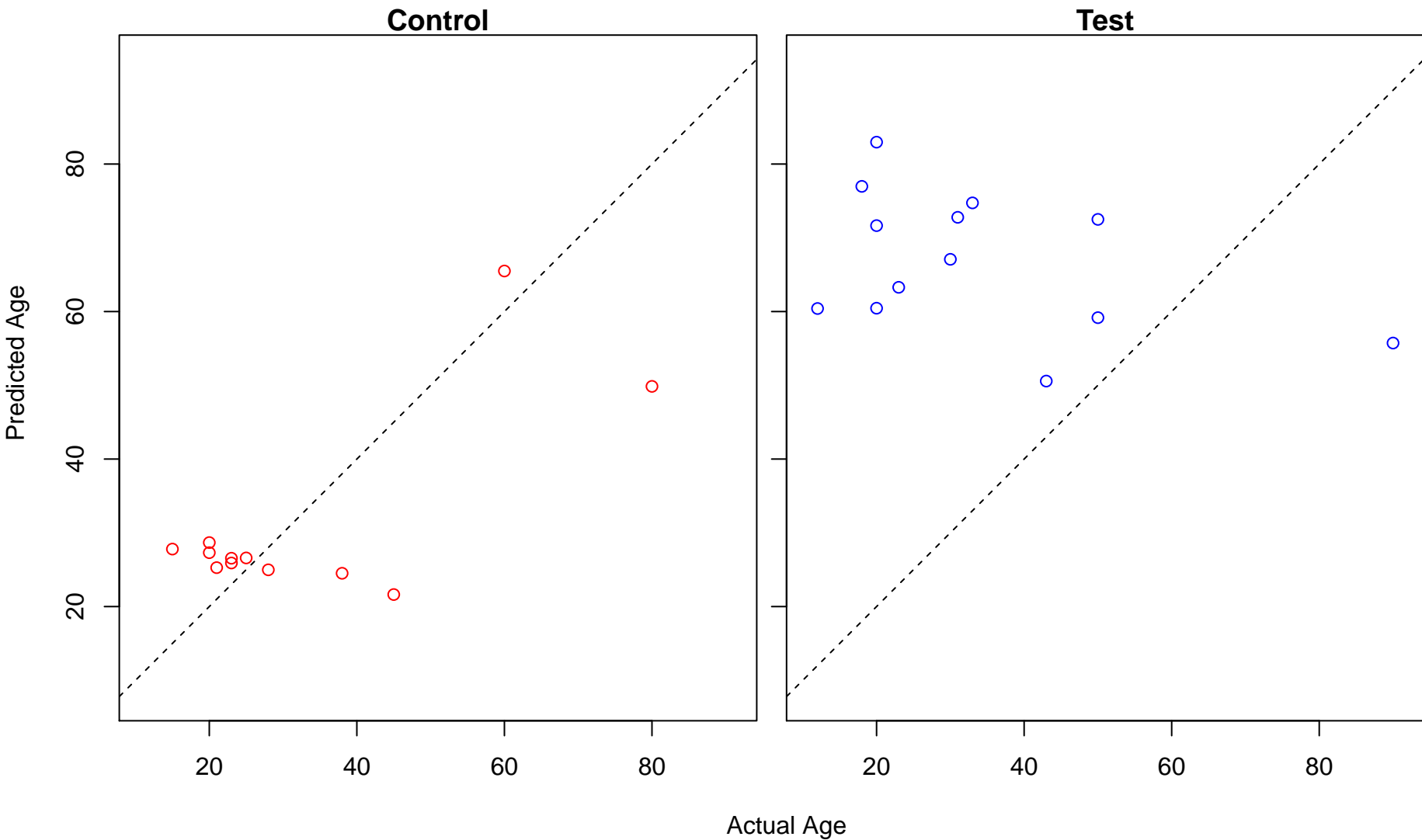
dolichol-linked oligosaccharide biosynthetic process (Score: 4.909781)



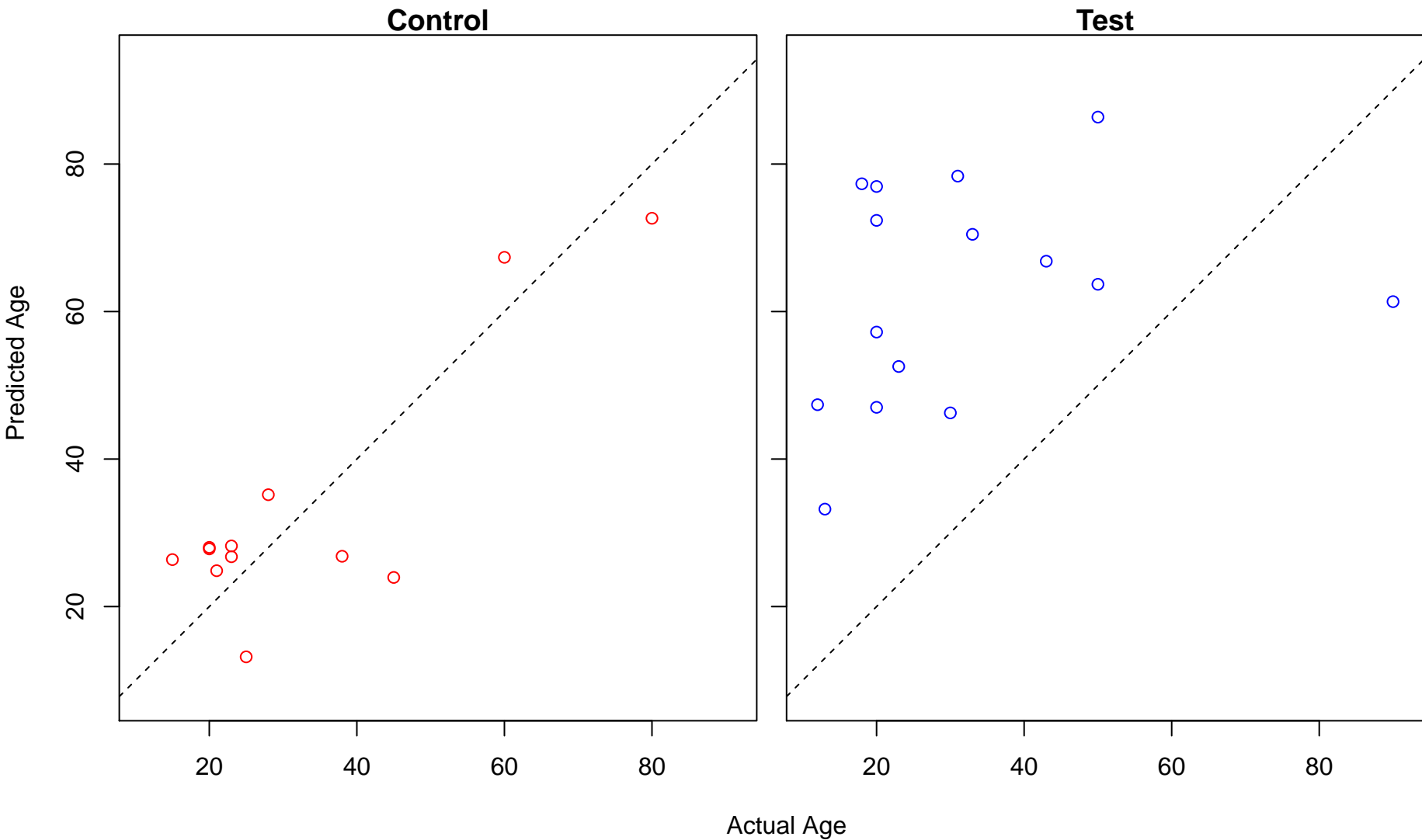
oligosaccharide–lipid intermediate biosynthetic process (Score: 4.909781)



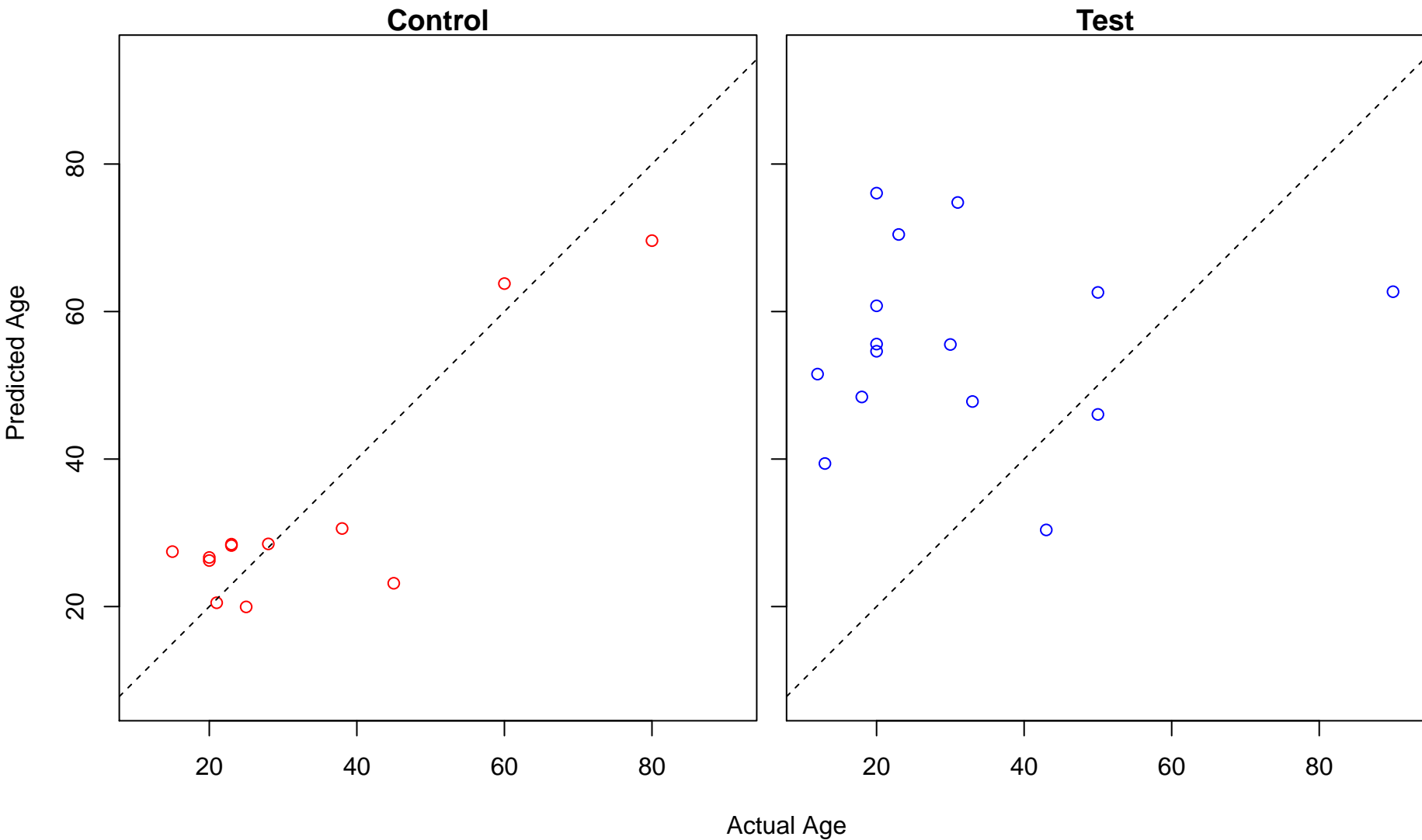
regulation of cardioblast differentiation (Score: 4.909084)



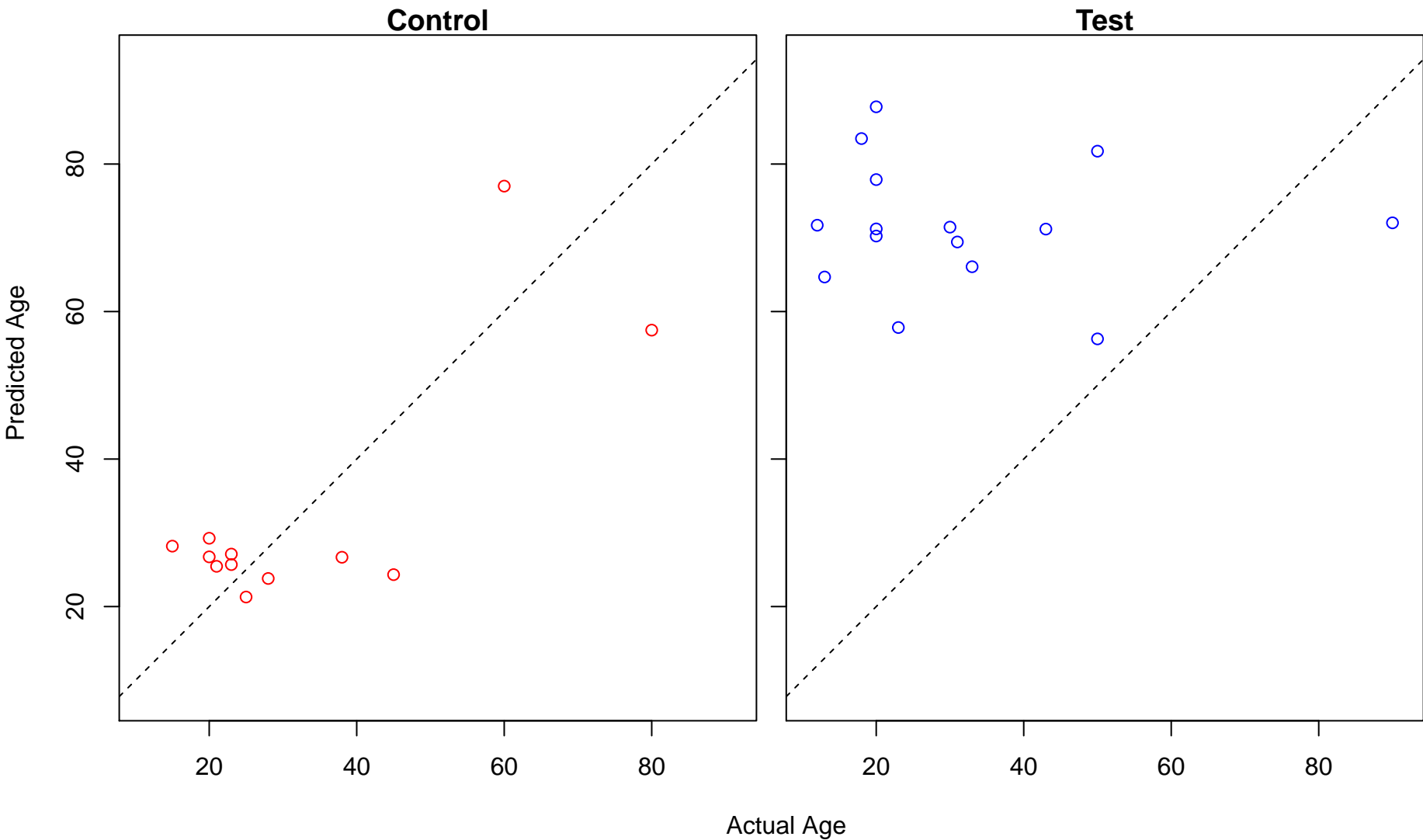
monocyte chemotaxis (Score: 4.908731)



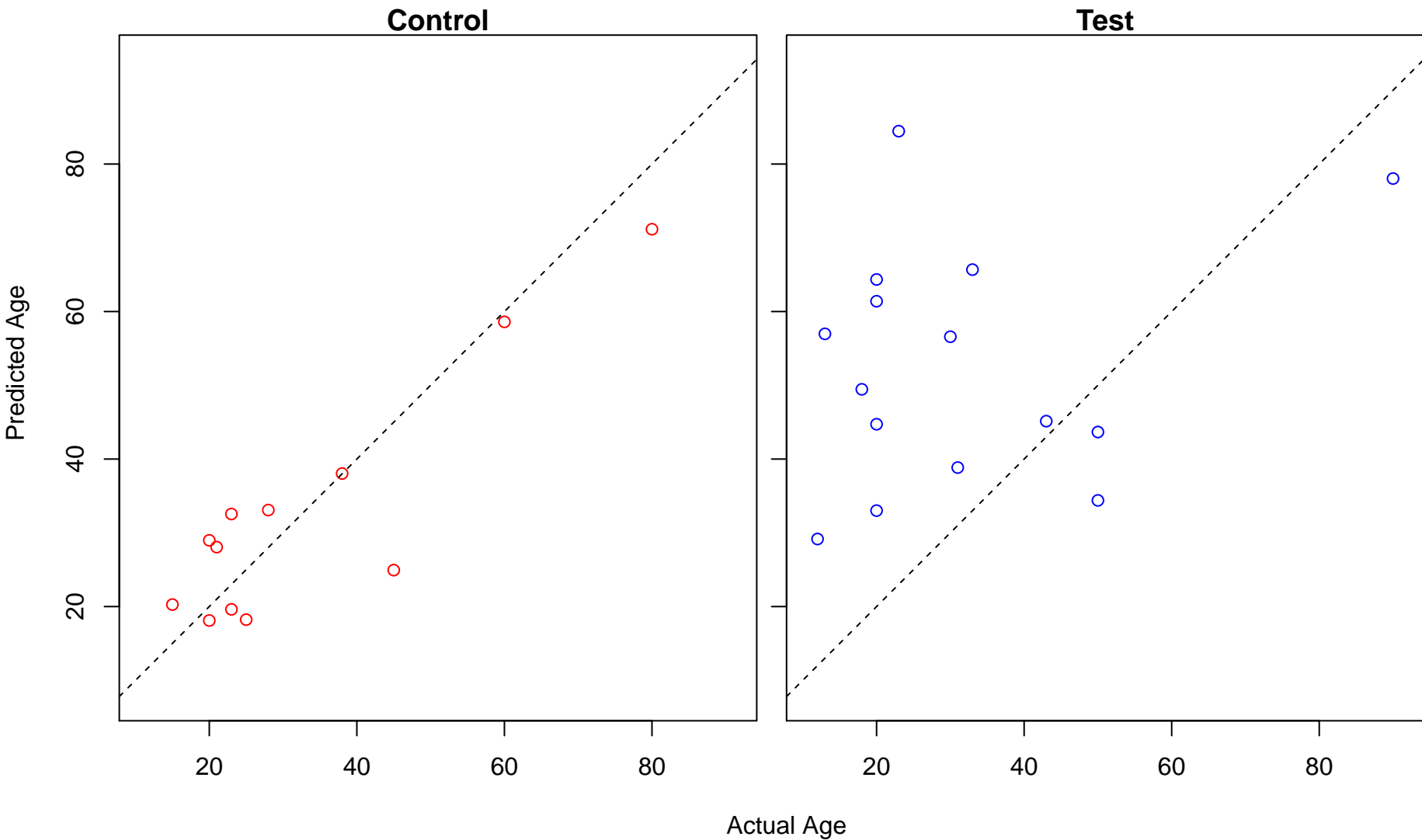
posttranscriptional gene silencing (Score: 4.907345)



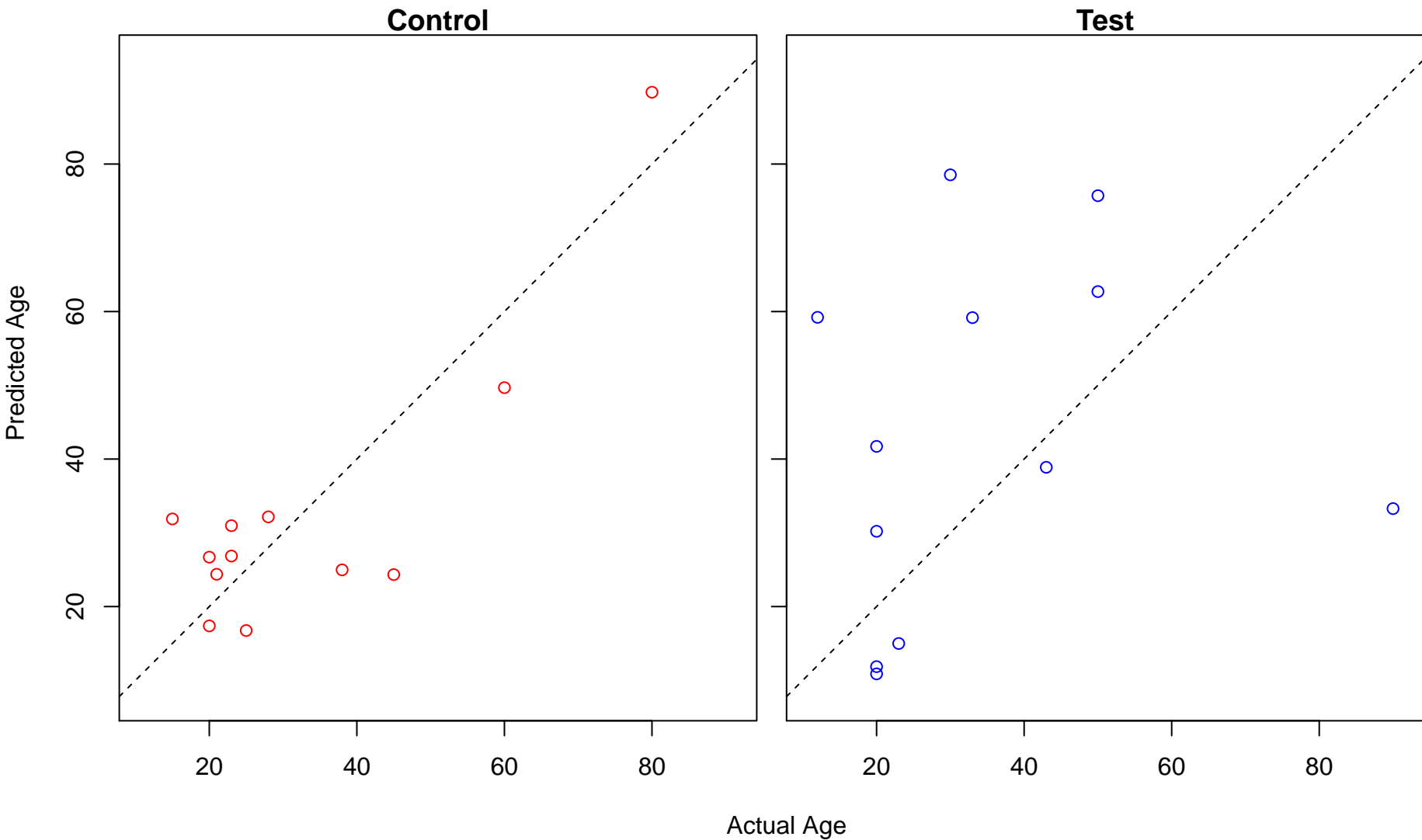
positive regulation of ER-associated ubiquitin-dependent protein catabolic process (Score: 4.90617)



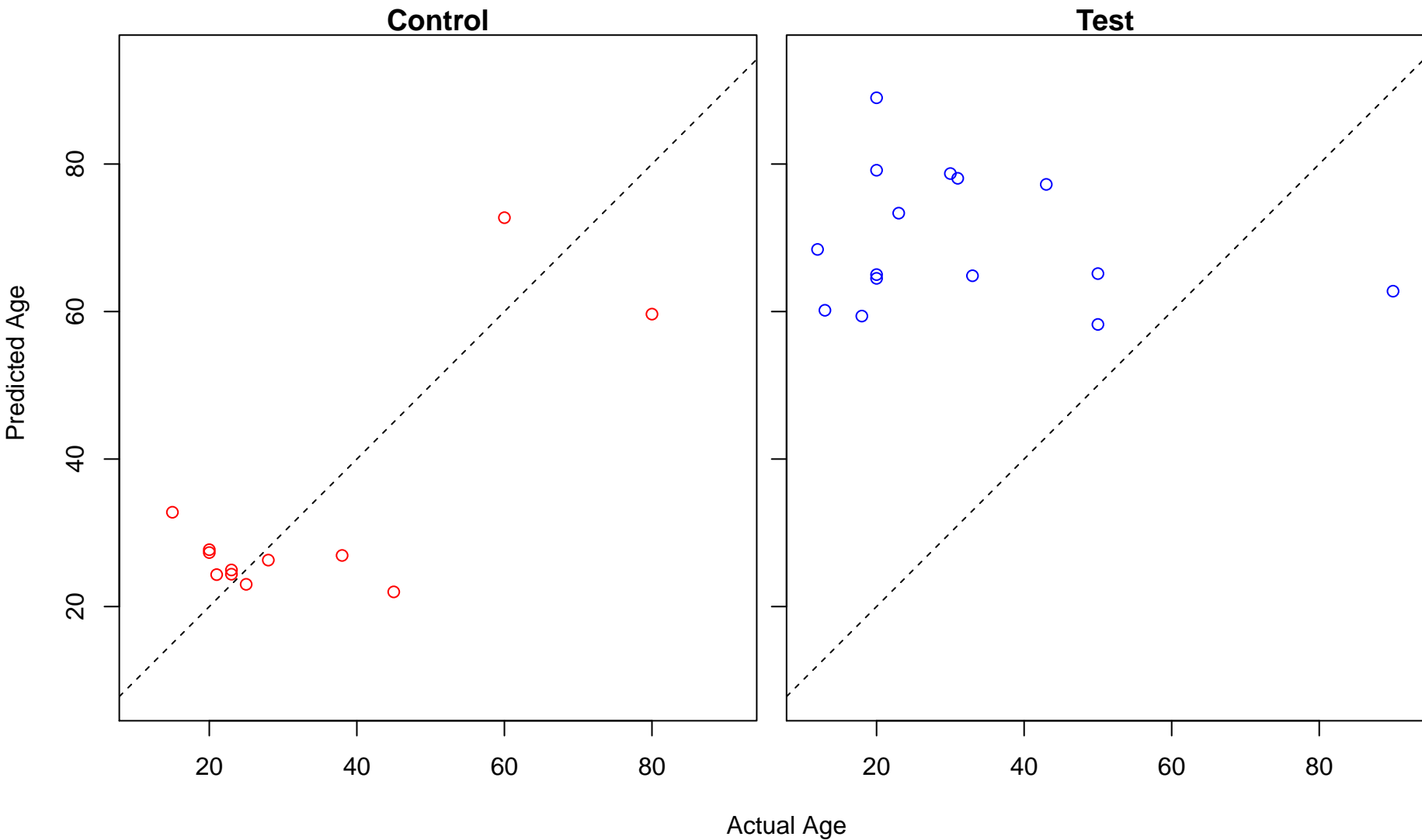
forebrain neuron development (Score: 4.904100)



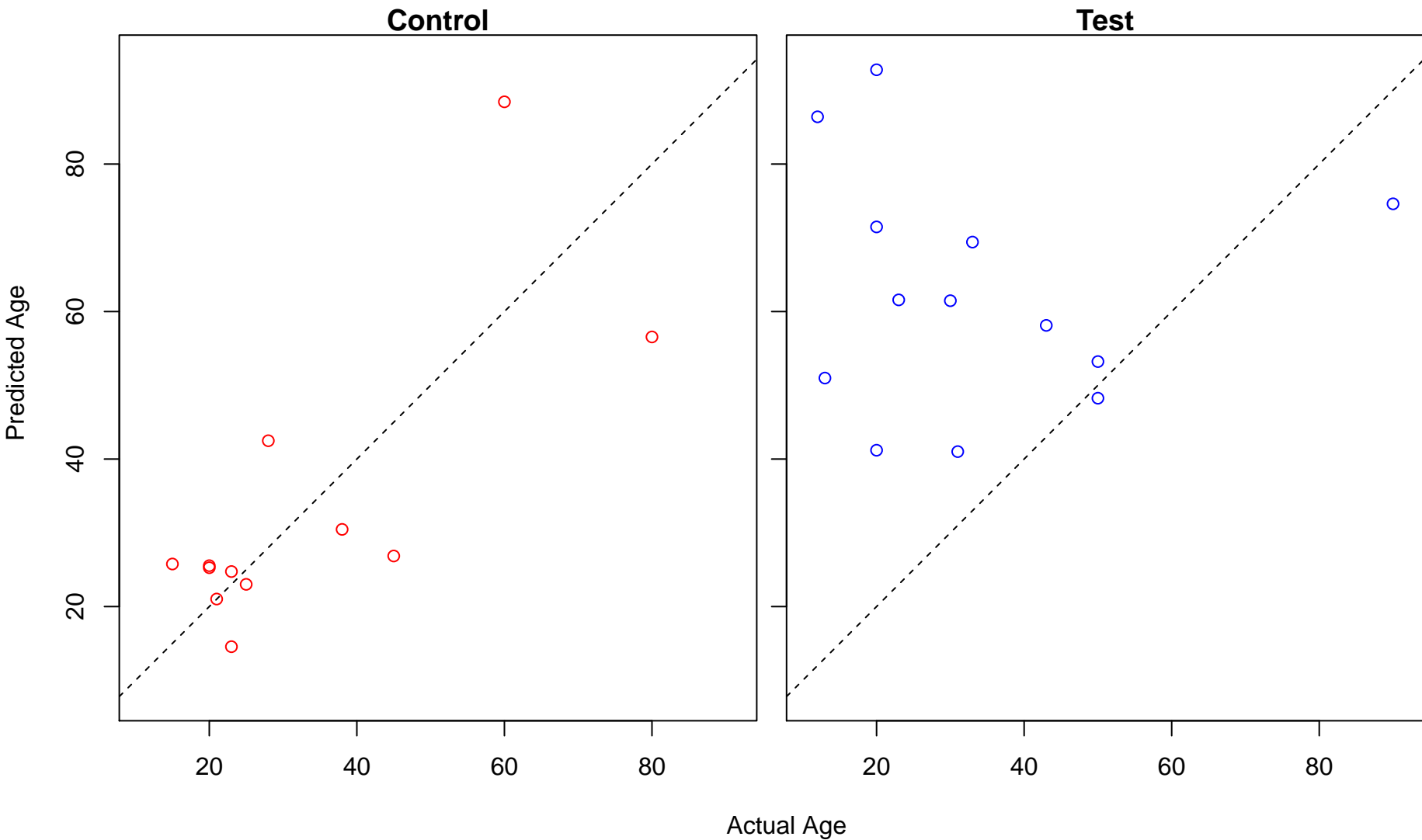
membrane fusion (Score: 4.903591)



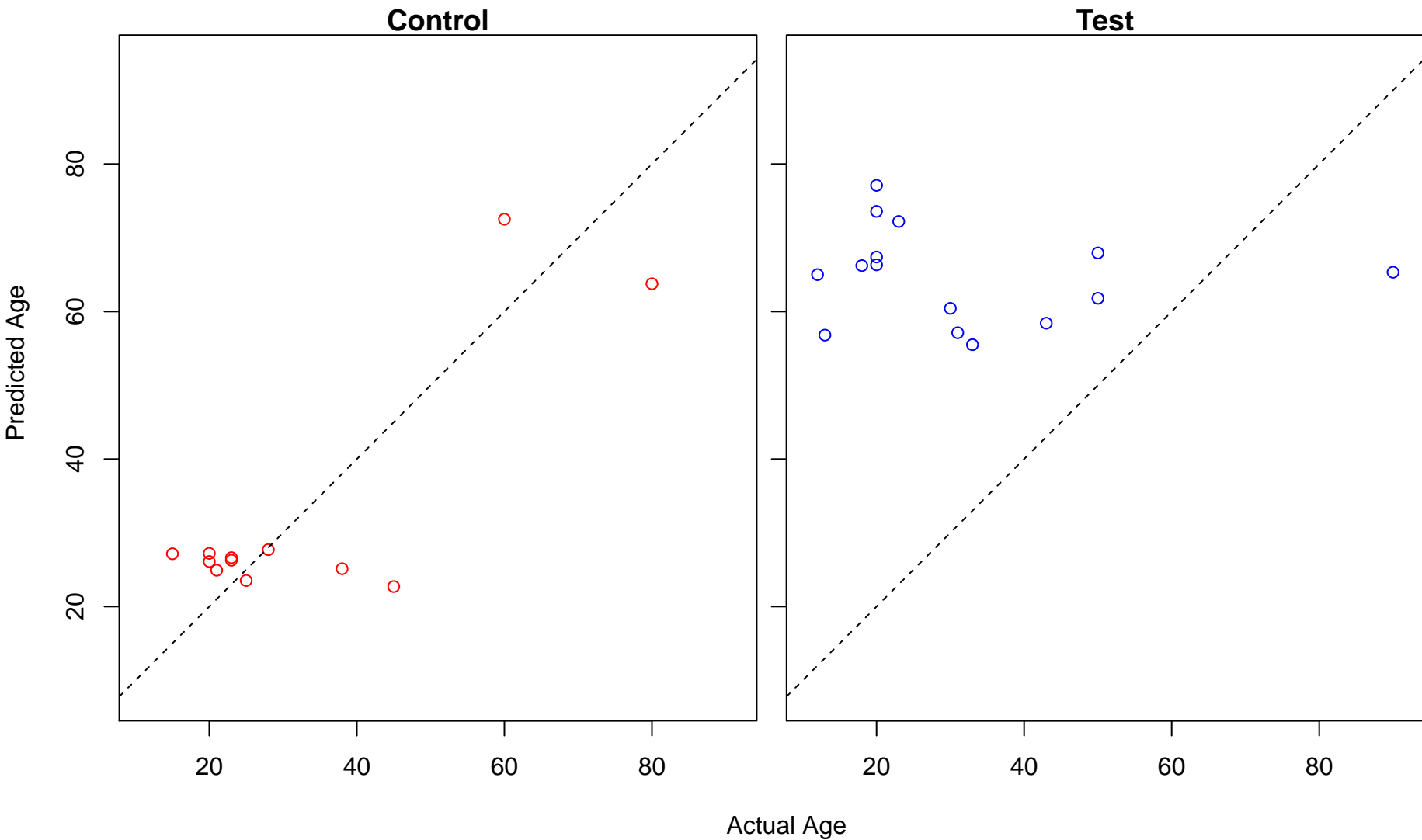
energy homeostasis (Score: 4.900936)



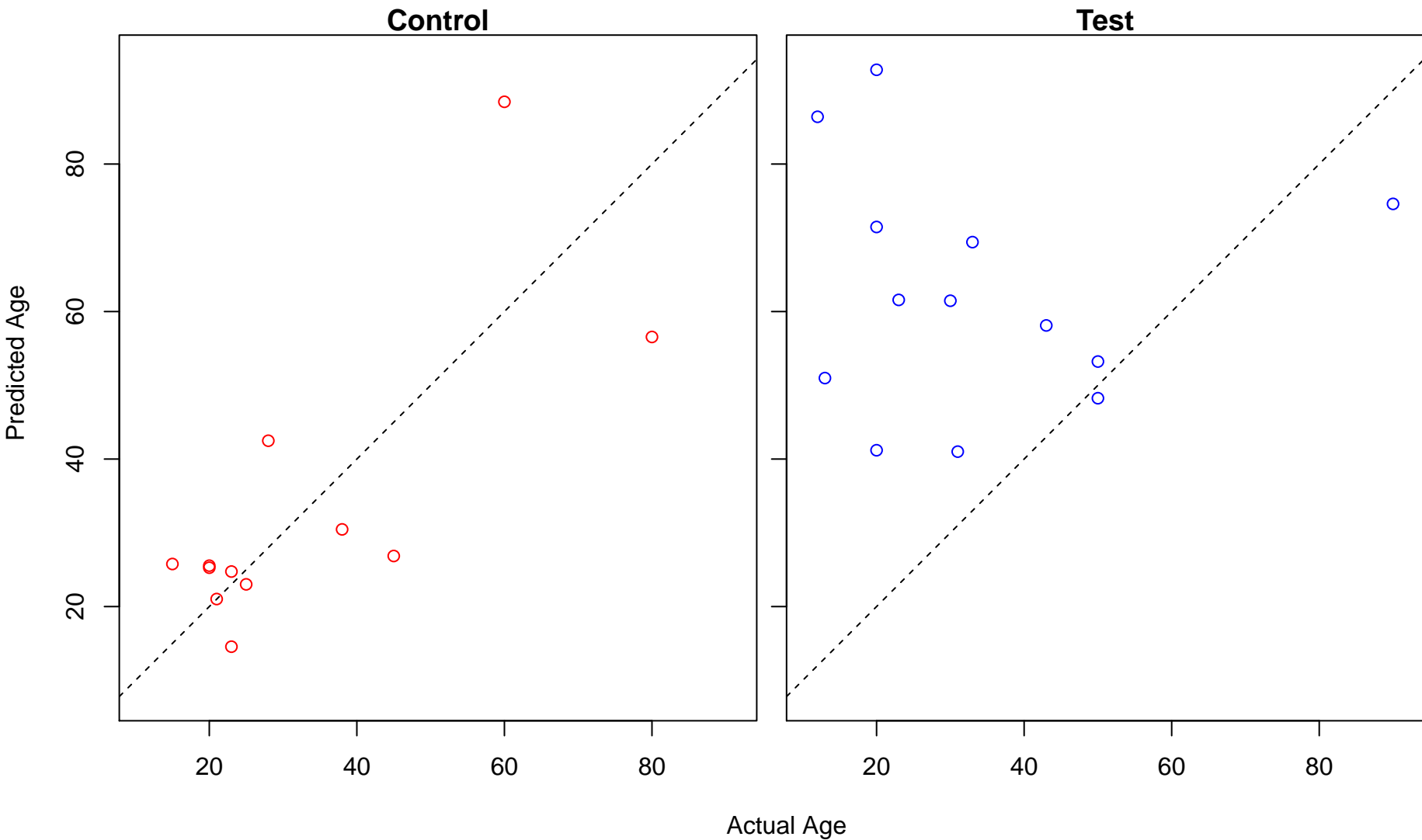
pyrimidine-containing compound biosynthetic process (Score: 4.900161)



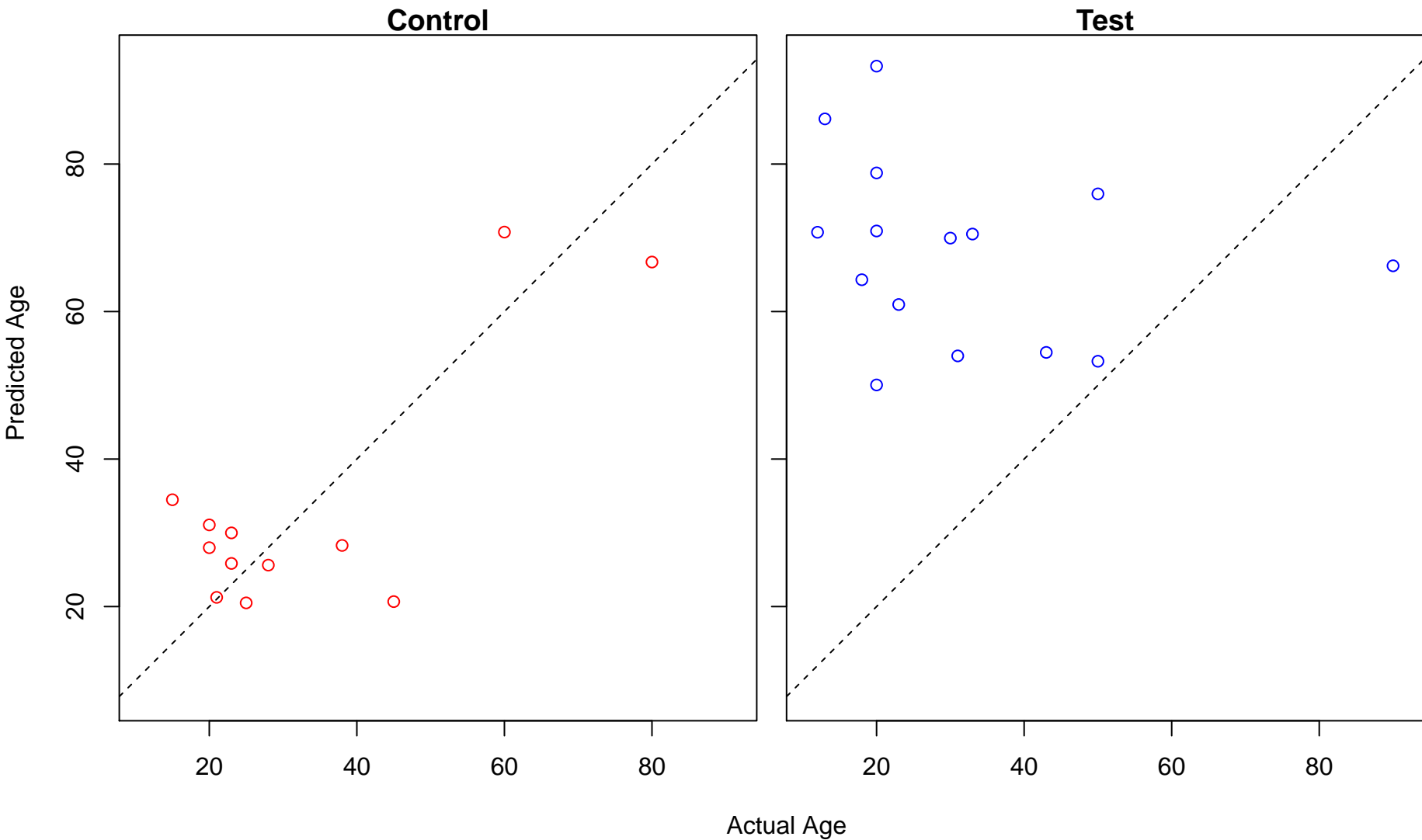
RNA modification (Score: 4.899951)



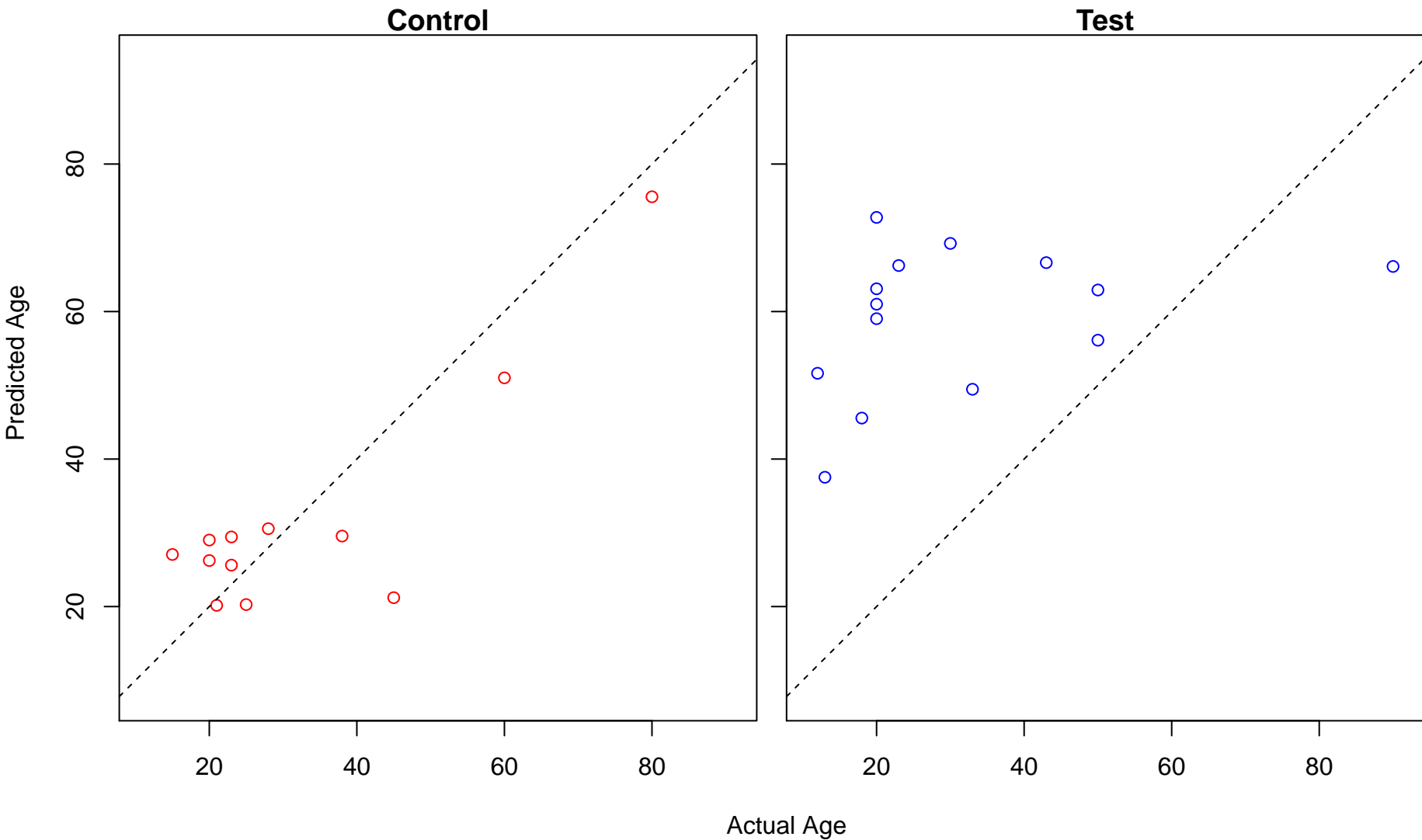
pyrimidine nucleoside biosynthetic process (Score: 4.899599)



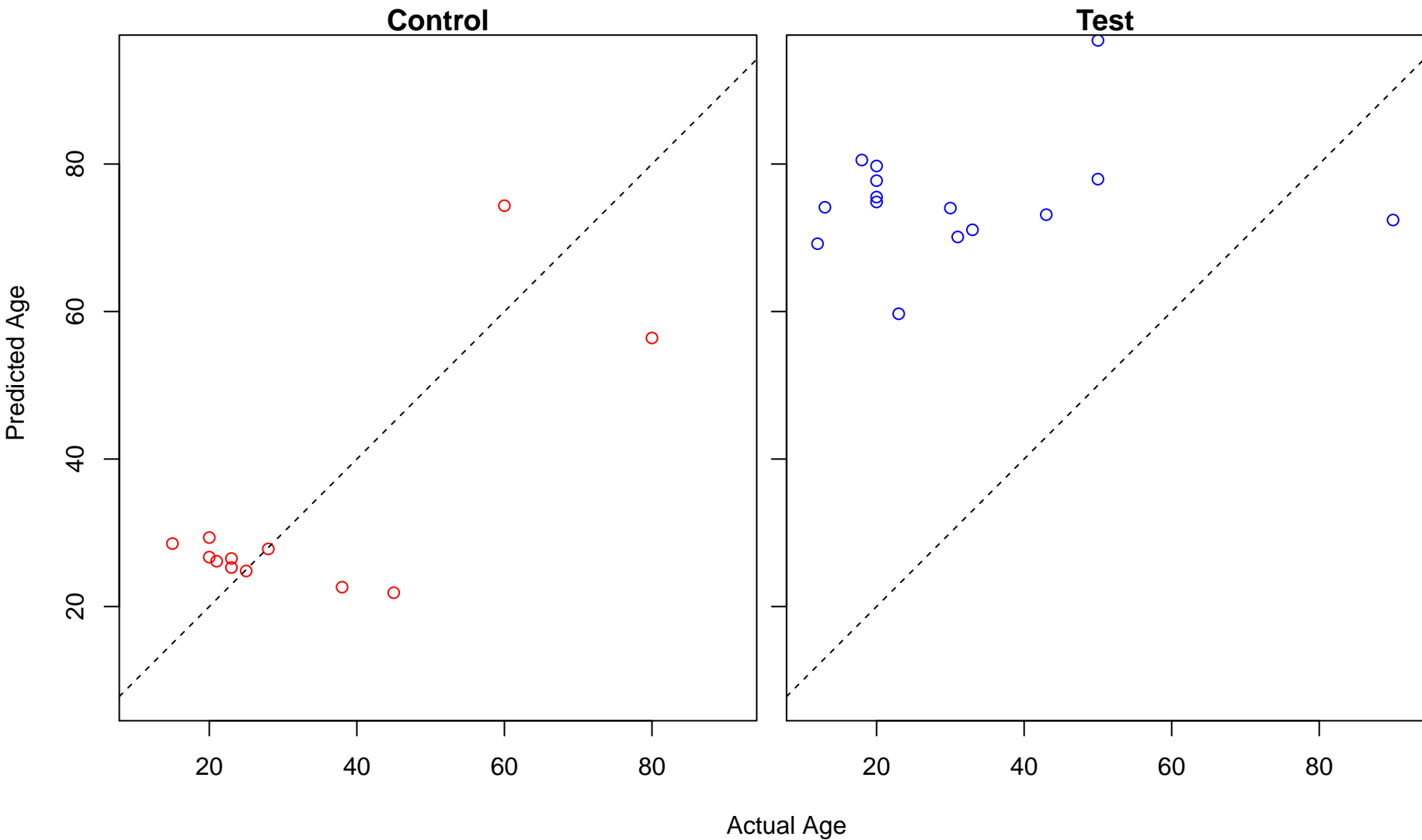
thyroid gland development (Score: 4.895632)



maintenance of location (Score: 4.895562)

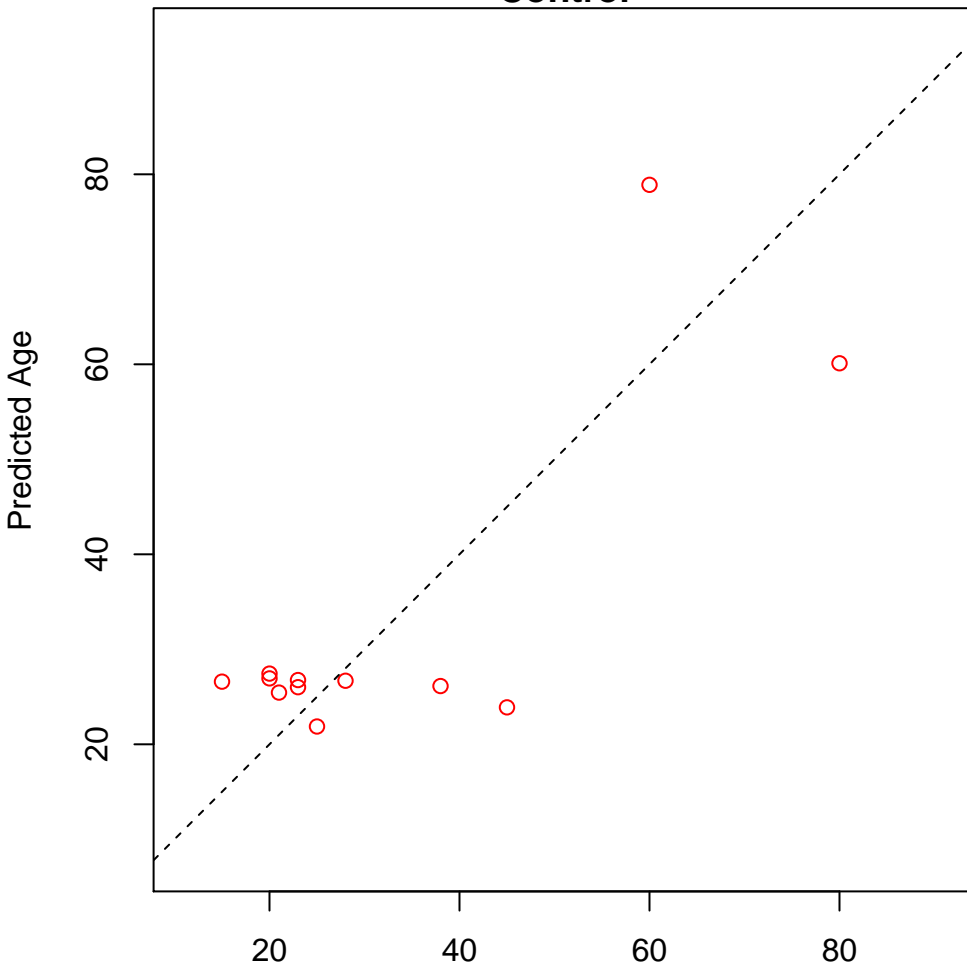


monovalent inorganic cation homeostasis (Score: 4.895140)

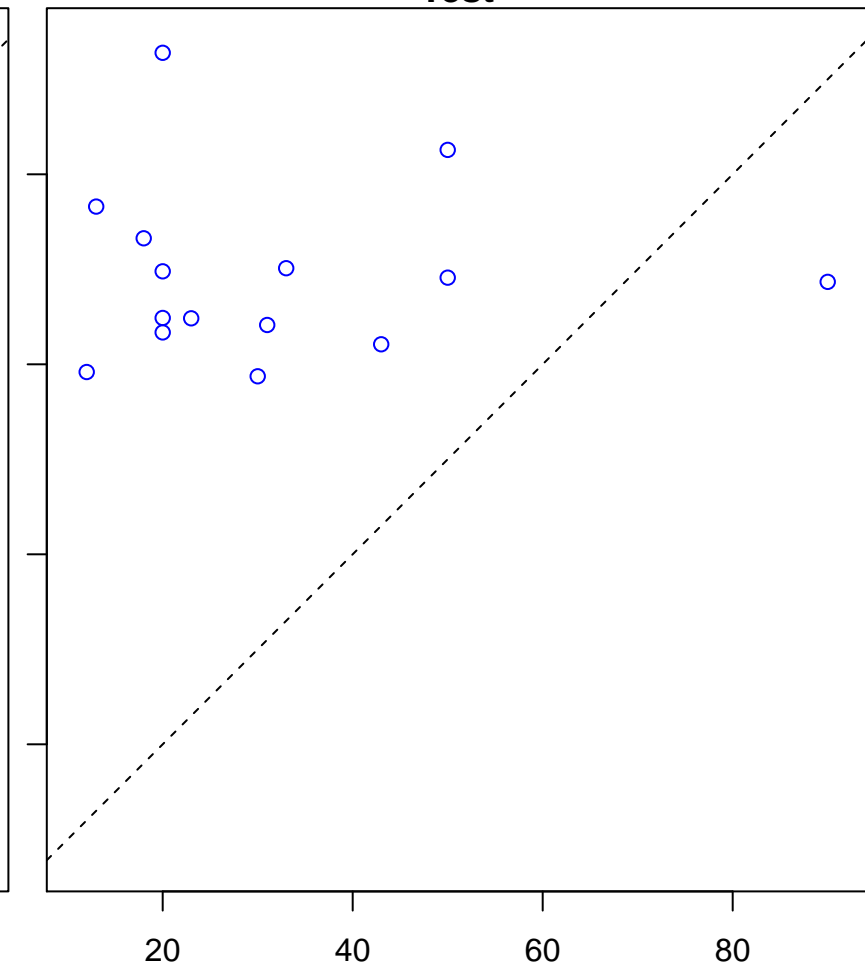


activation of protein kinase activity (Score: 4.892044)

Control

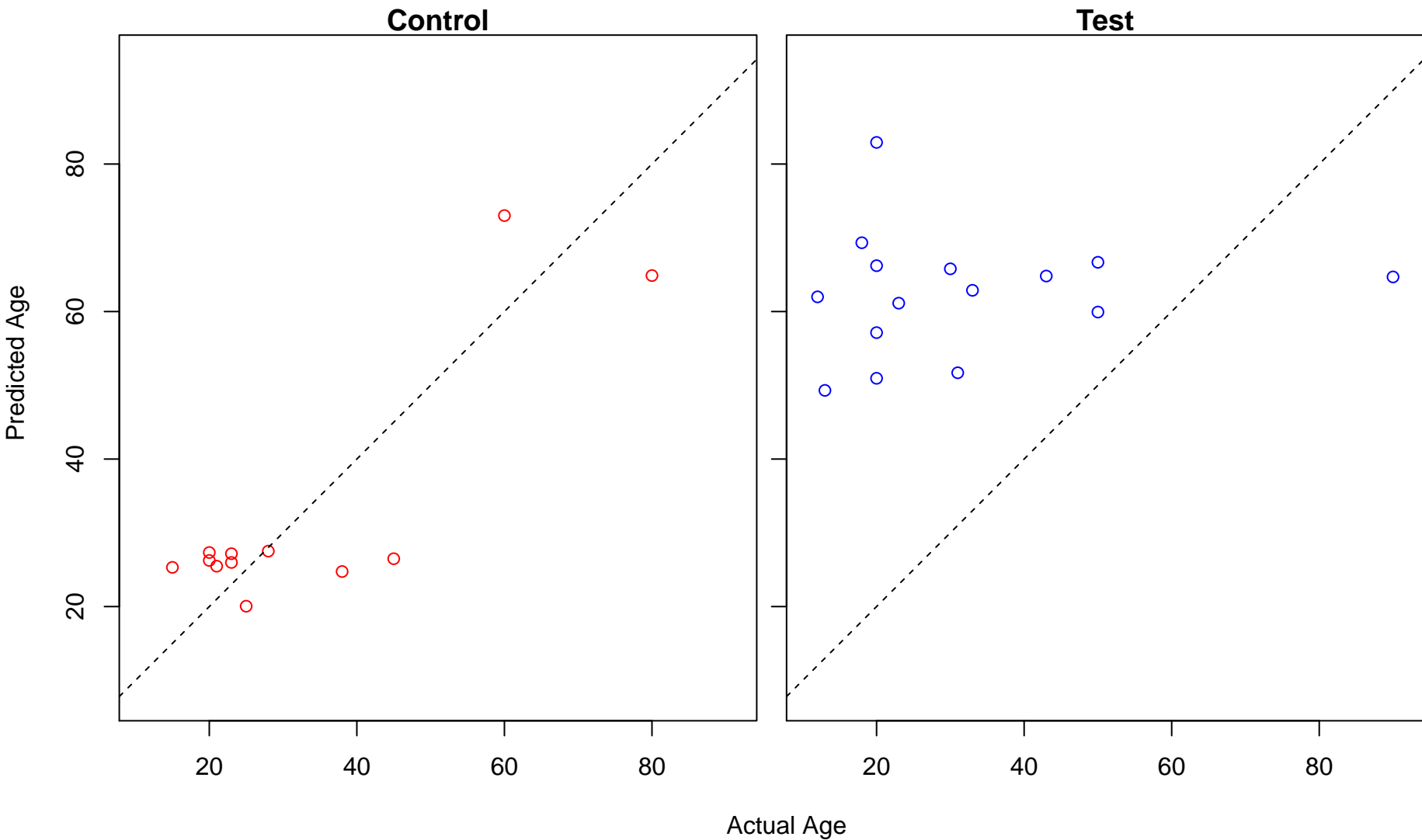


Test



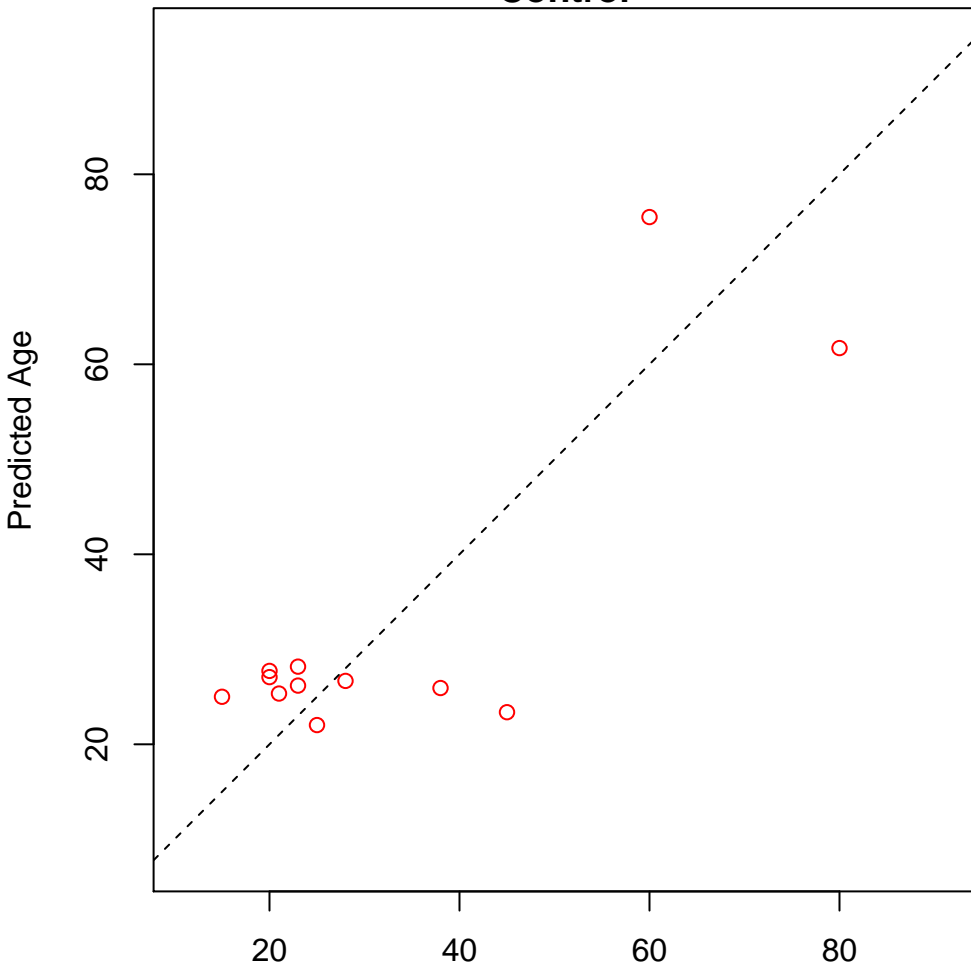
Actual Age

posttranslational protein targeting to membrane (Score: 4.891747)

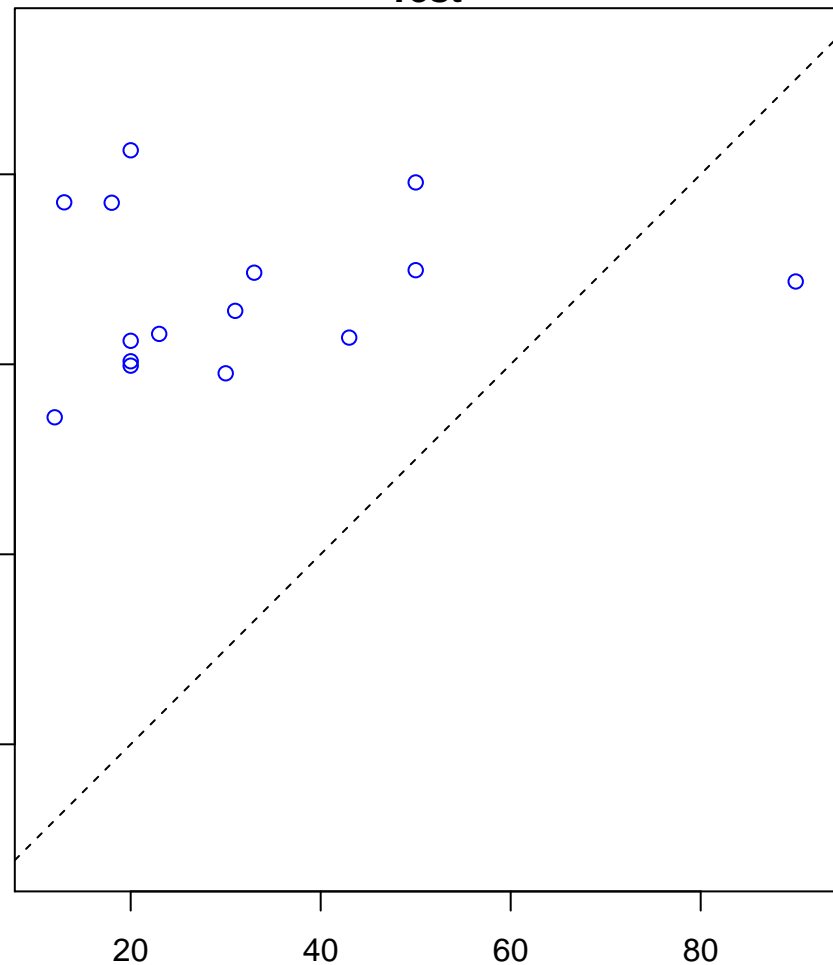


positive regulation of T cell proliferation (Score: 4.890472)

Control

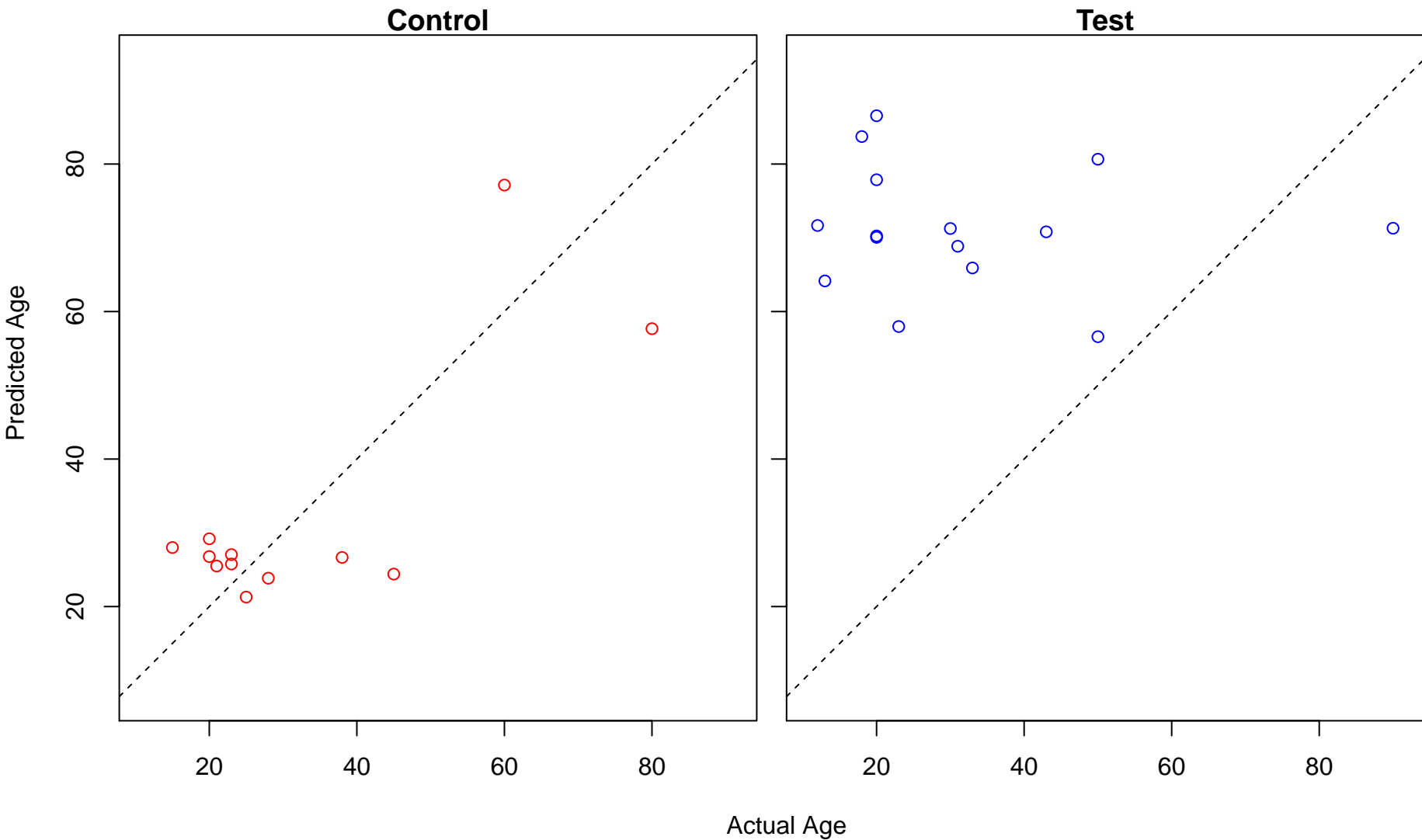


Test

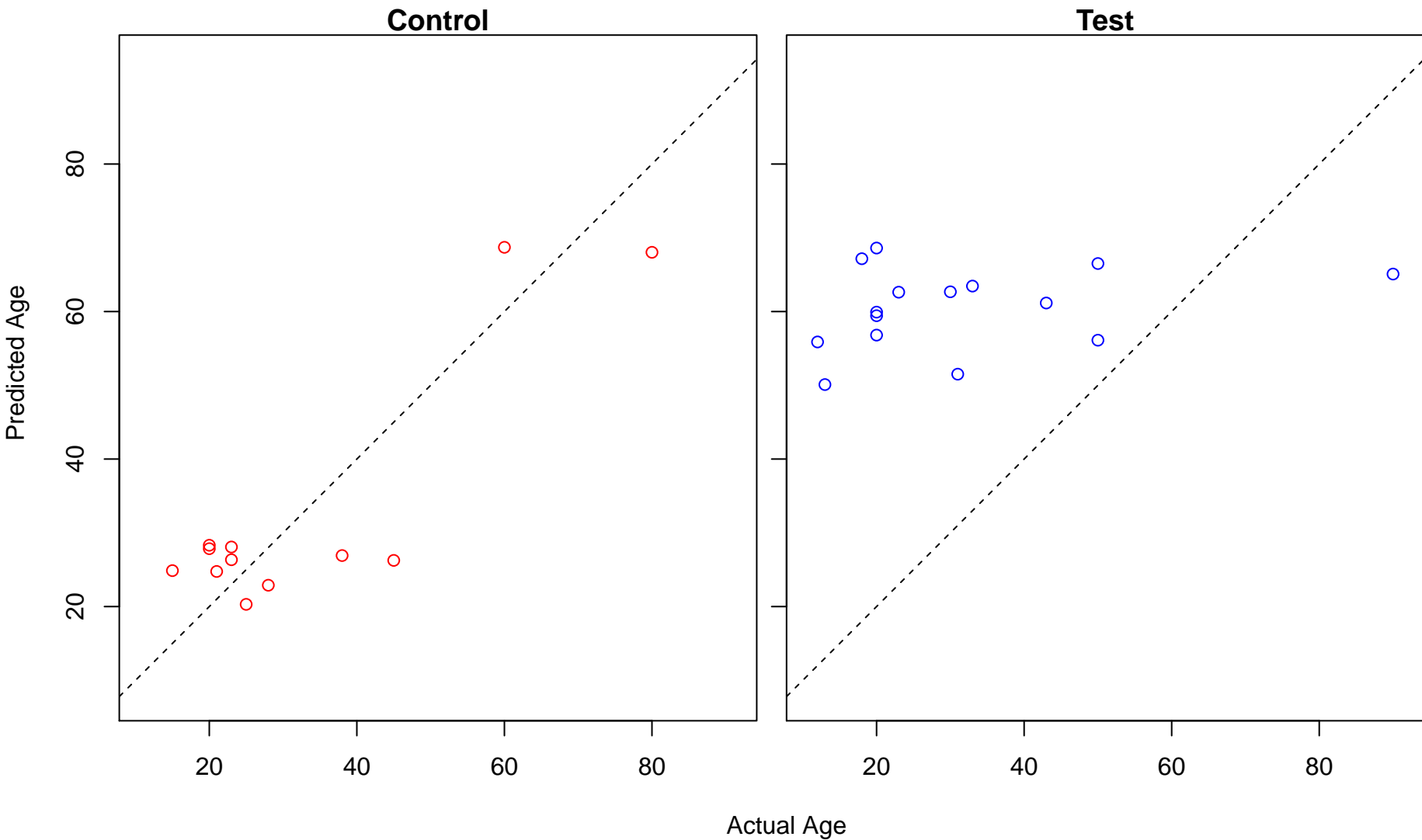


Actual Age

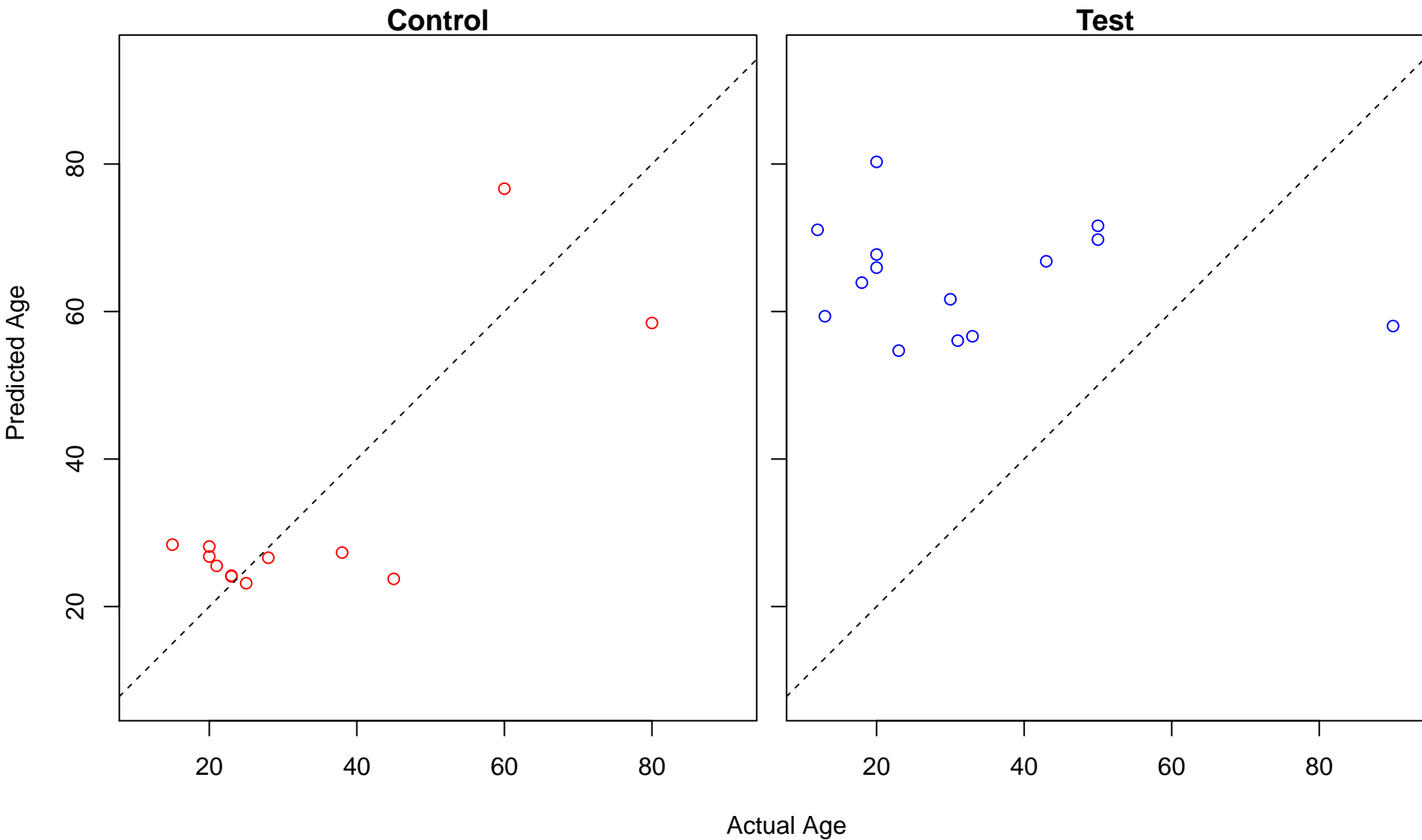
regulation of ER-associated ubiquitin-dependent protein catabolic process (Score: 4.888490)



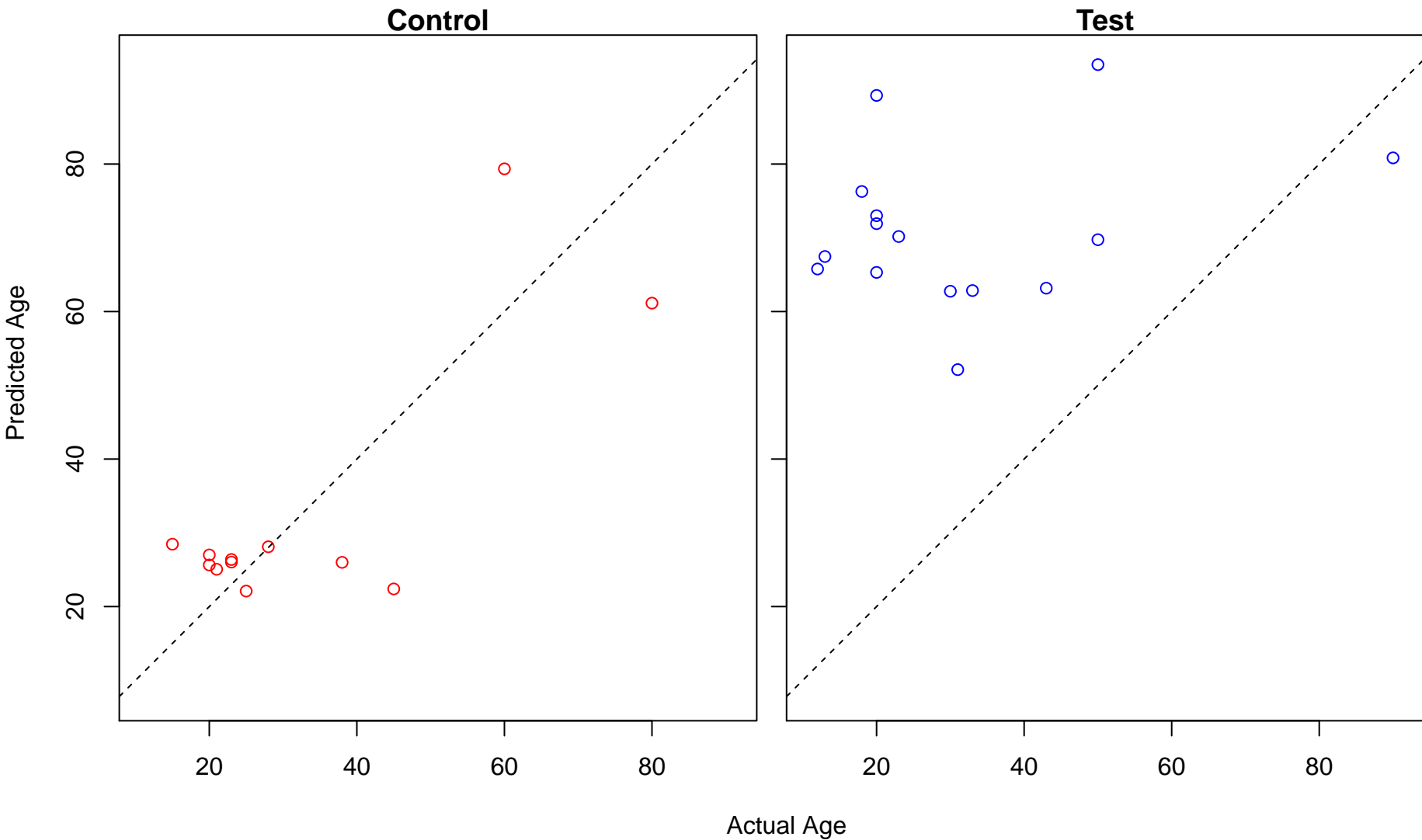
cardiac muscle cell development (Score: 4.888351)



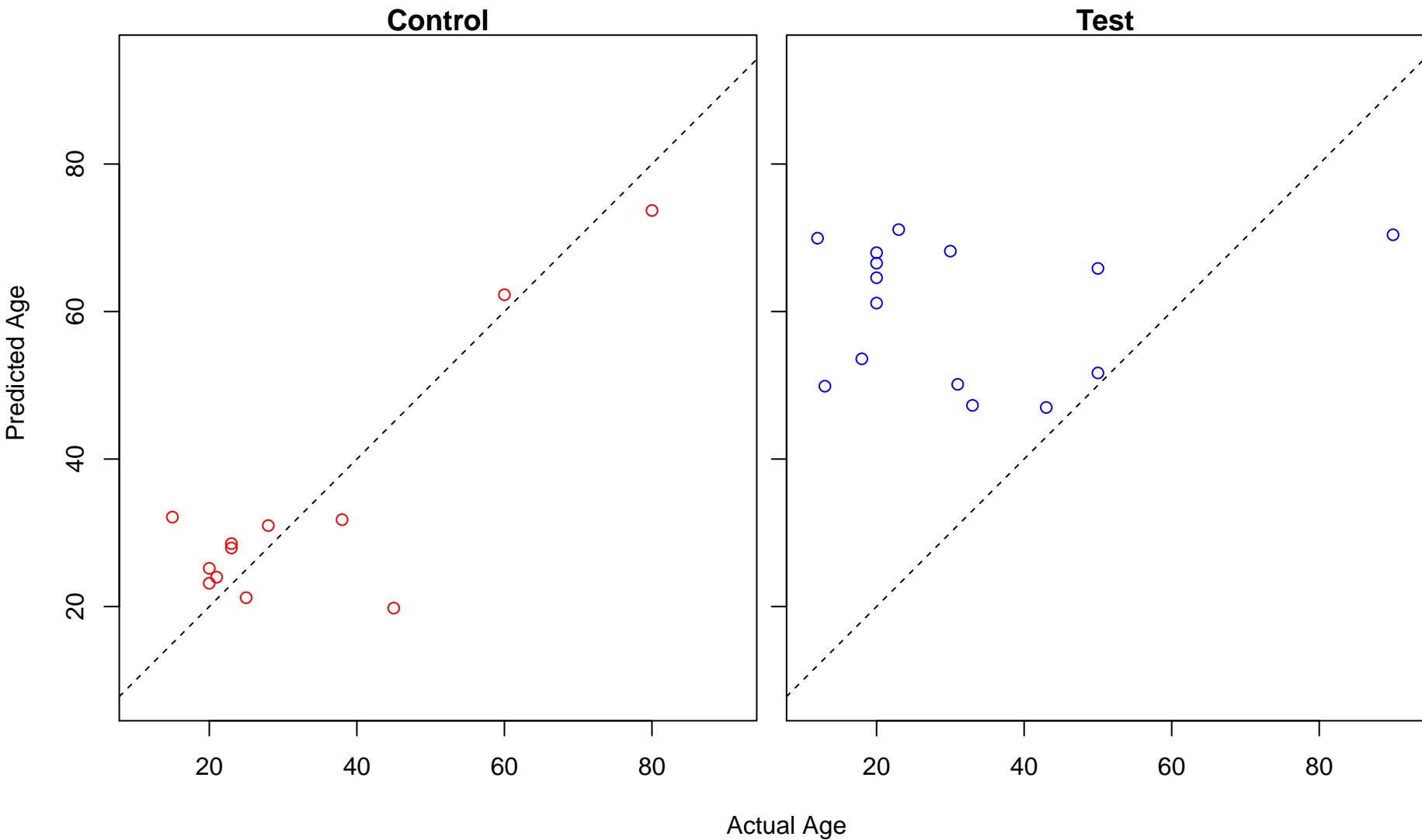
regulation of lipid biosynthetic process (Score: 4.883318)



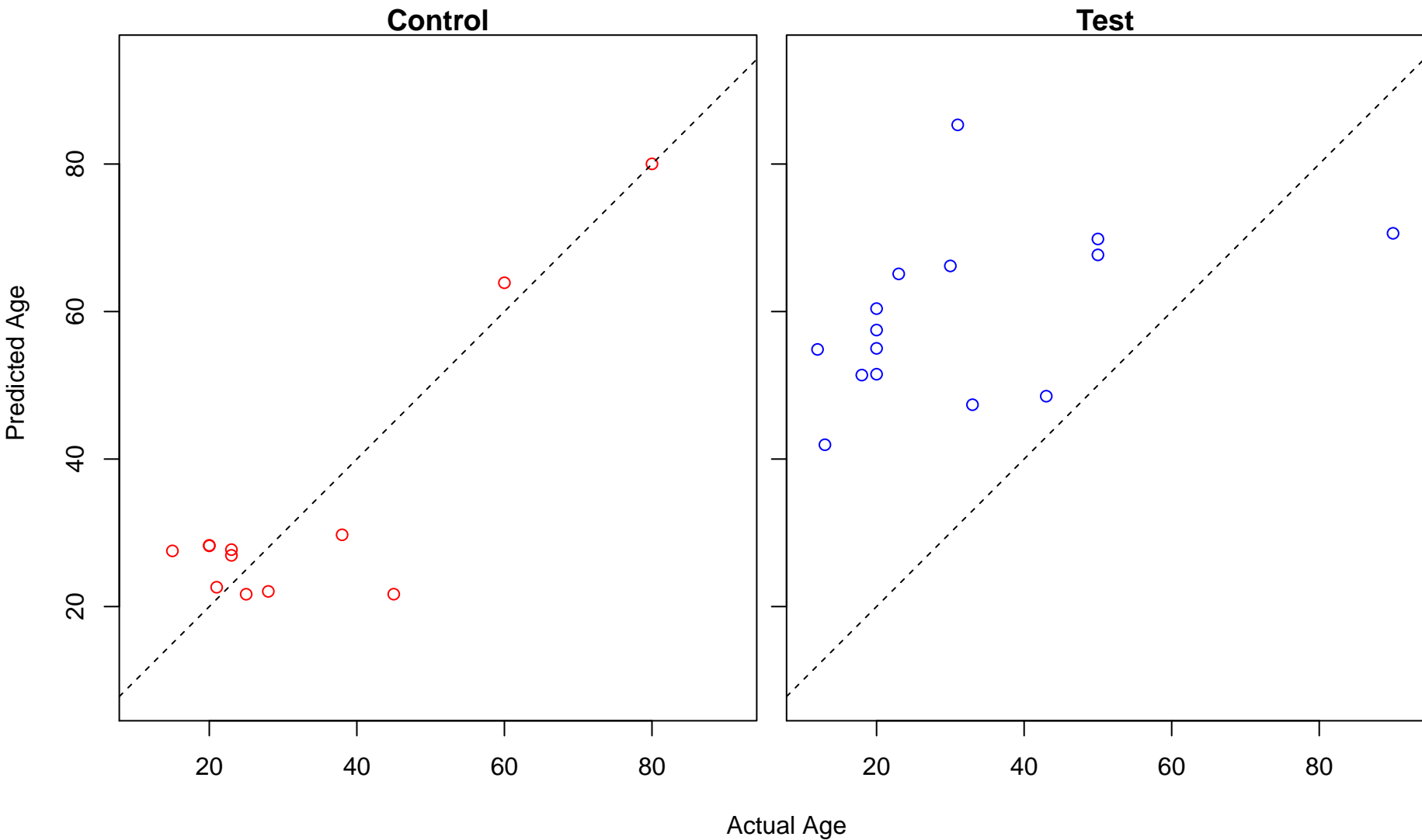
negative regulation of ERBB signaling pathway (Score: 4.882727)



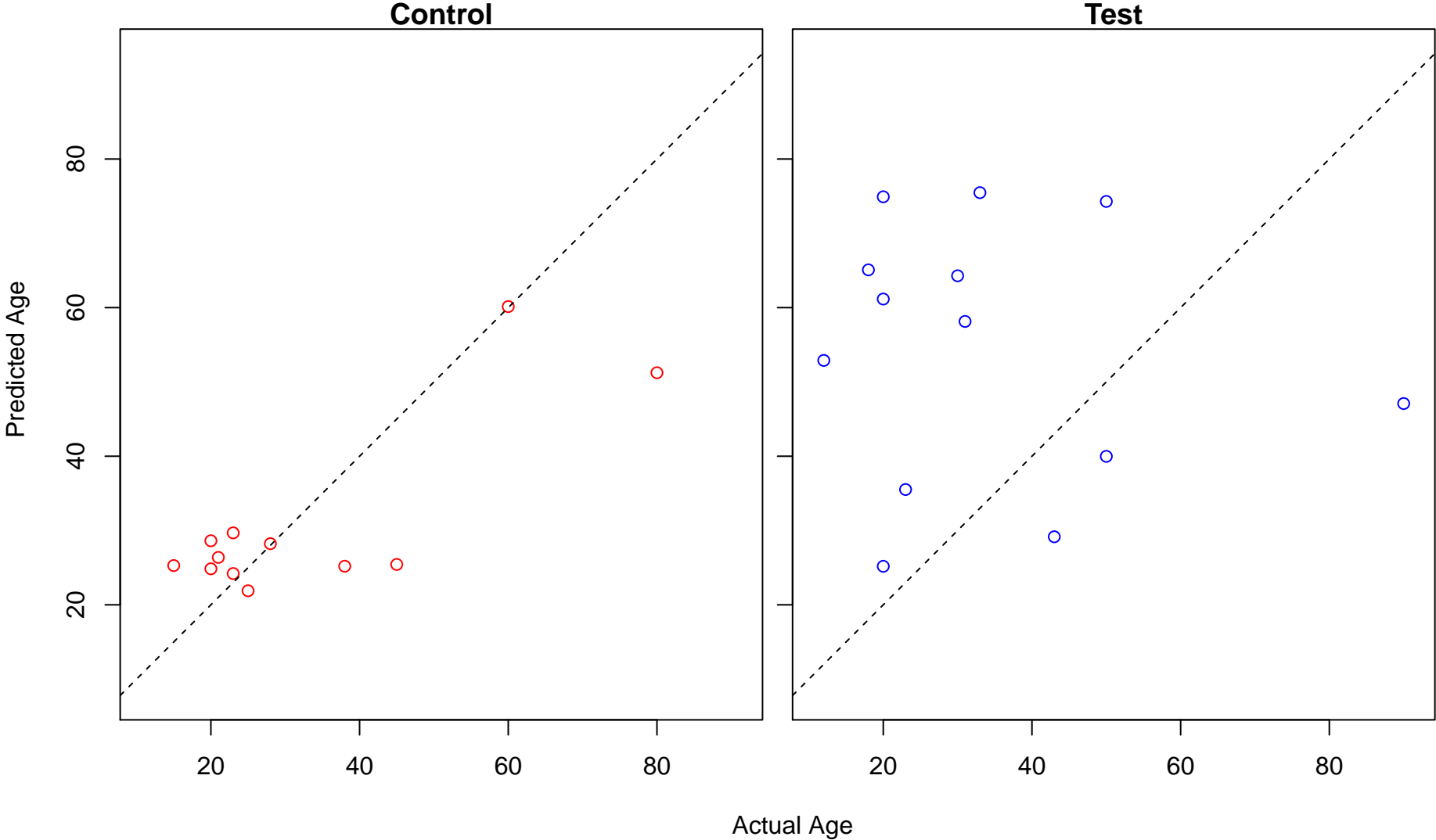
positive regulation of axonogenesis (Score: 4.882704)



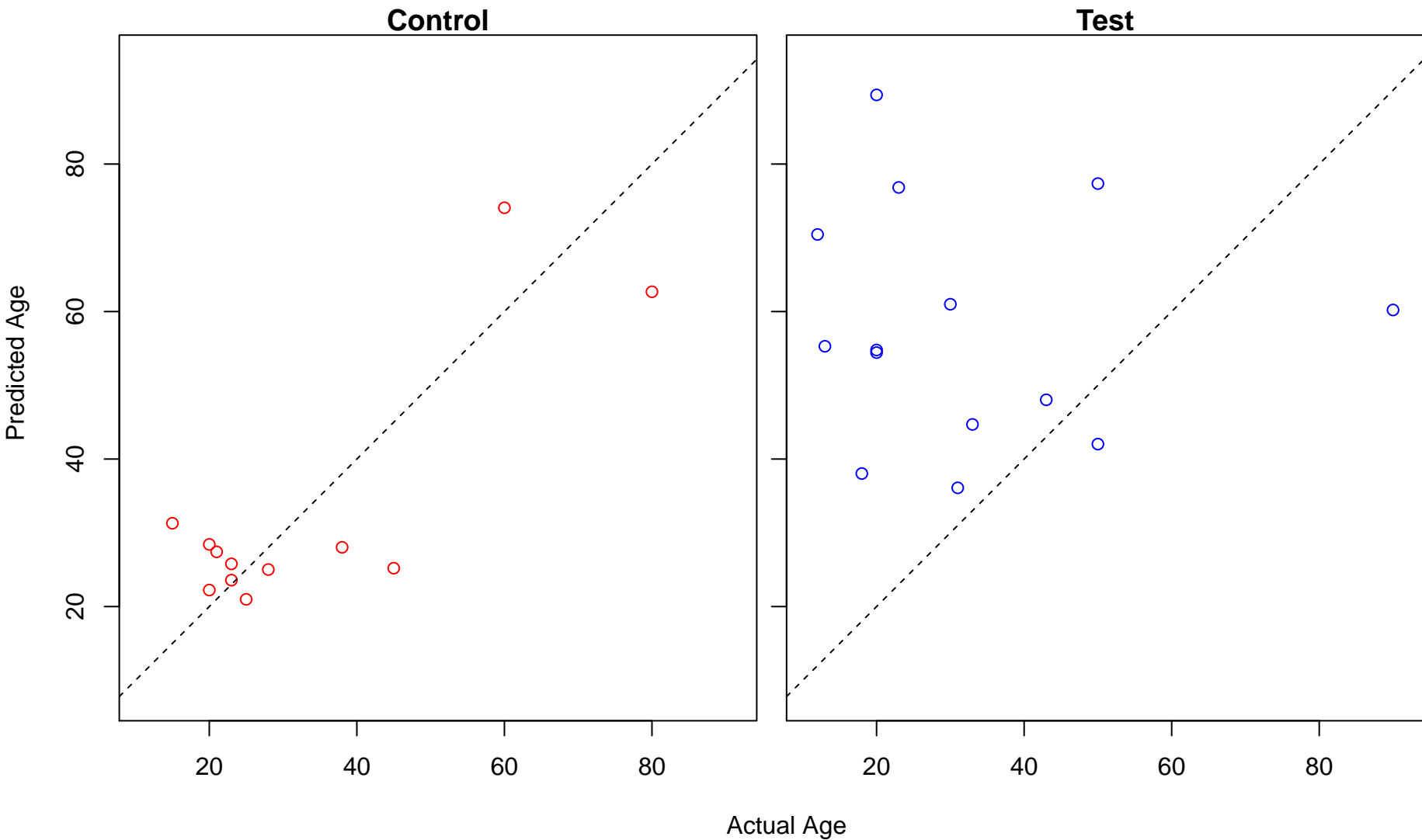
cellular response to virus (Score: 4.881933)



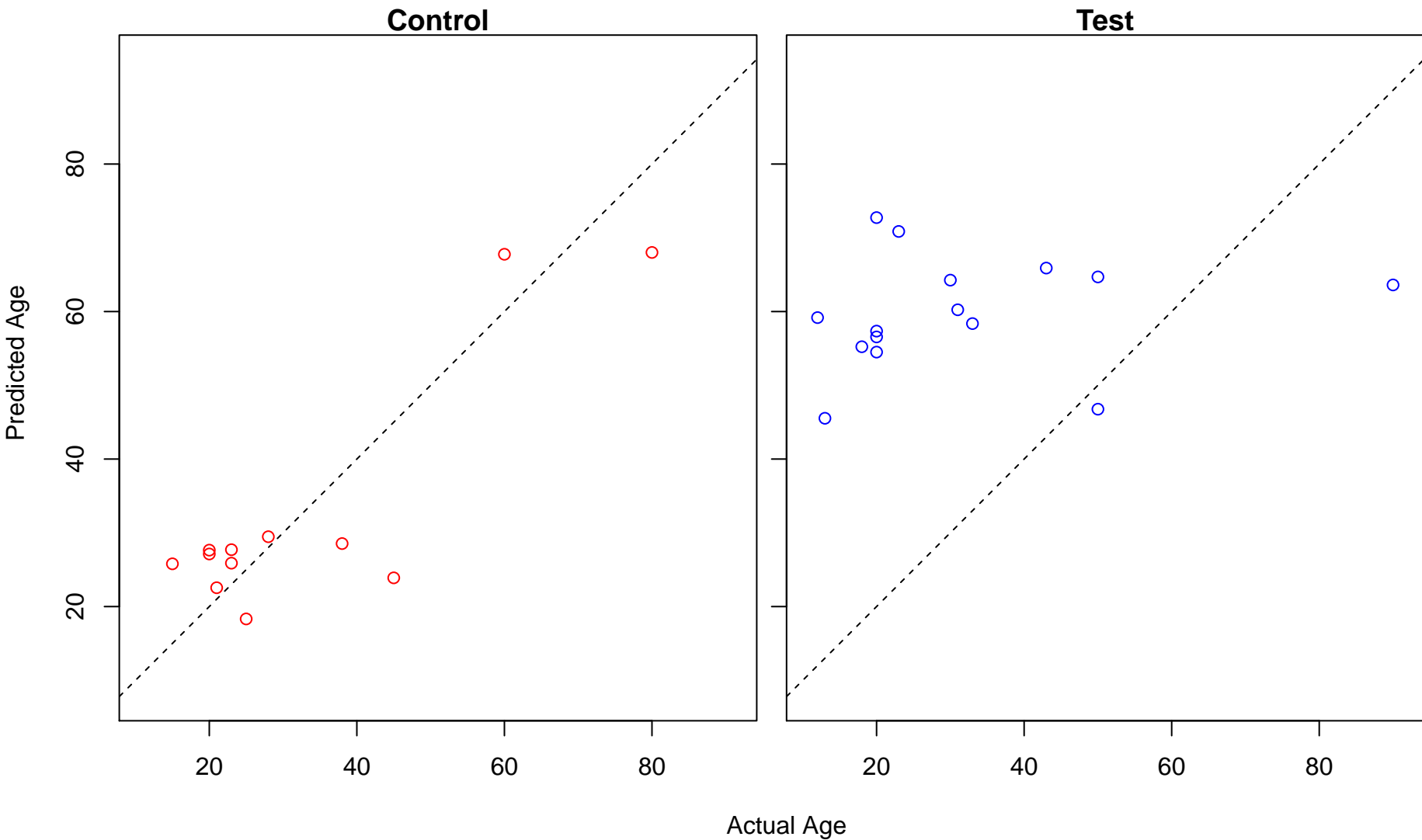
regulation of atrial cardiac muscle cell membrane depolarization (Score: 4.879736)



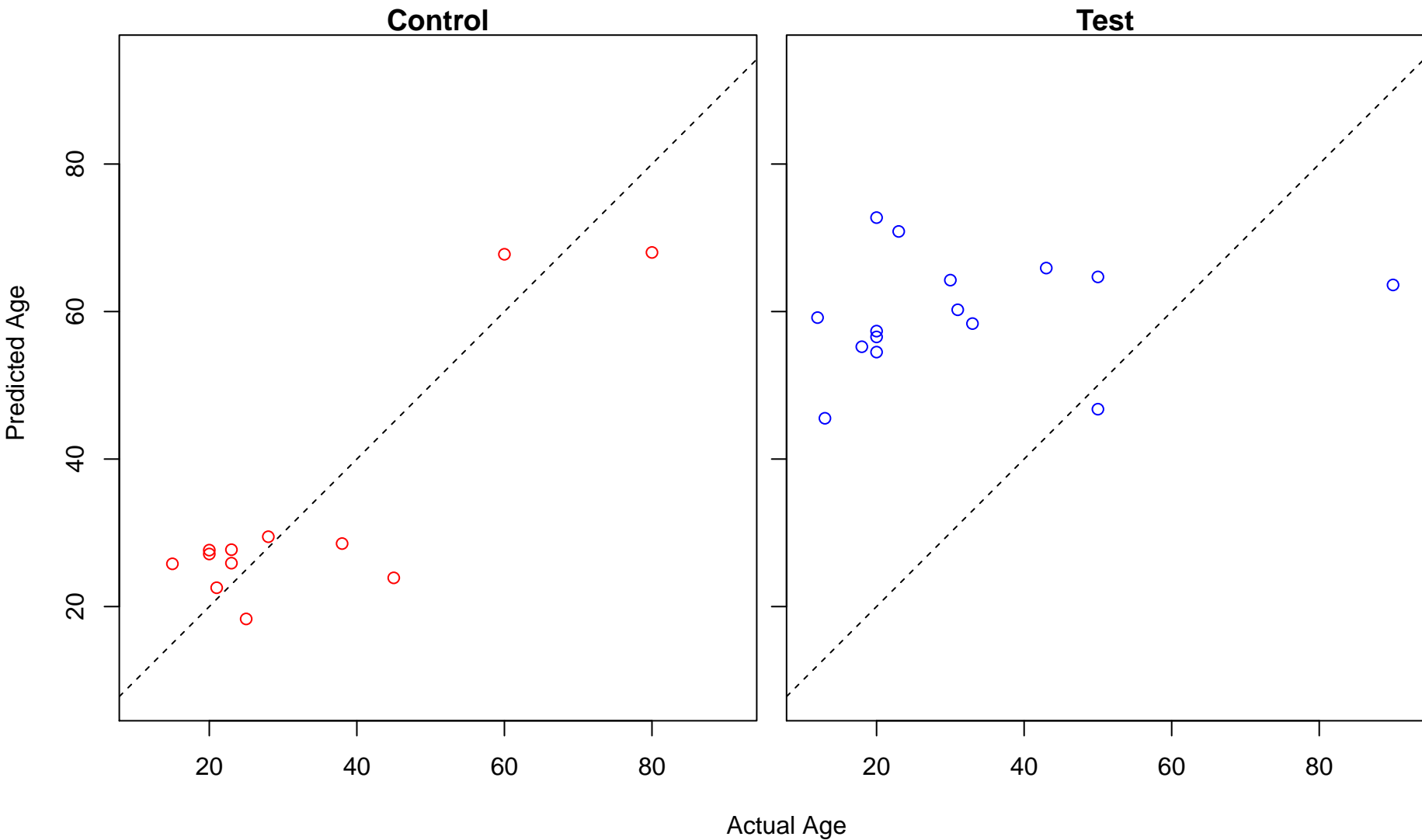
cell-cell recognition (Score: 4.879184)



plus-end-directed vesicle transport along microtubule (Score: 4.877351)

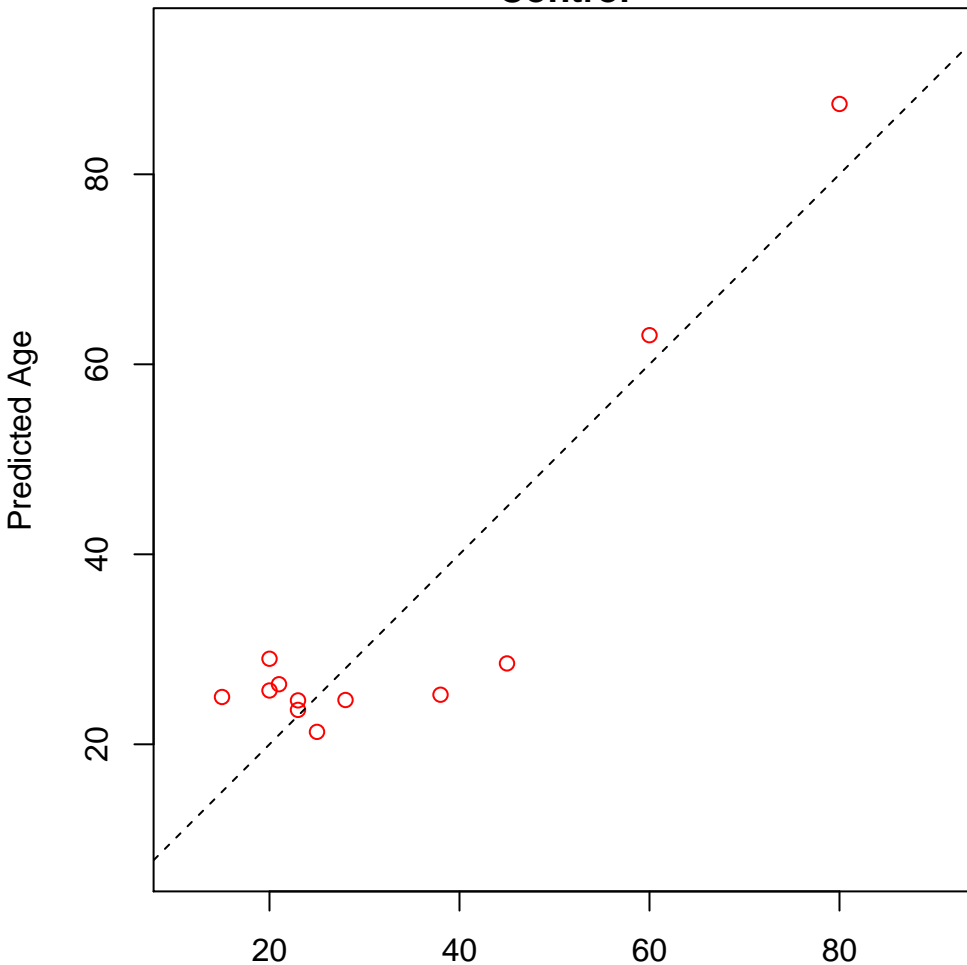


plus-end-directed organelle transport along microtubule (Score: 4.877351)

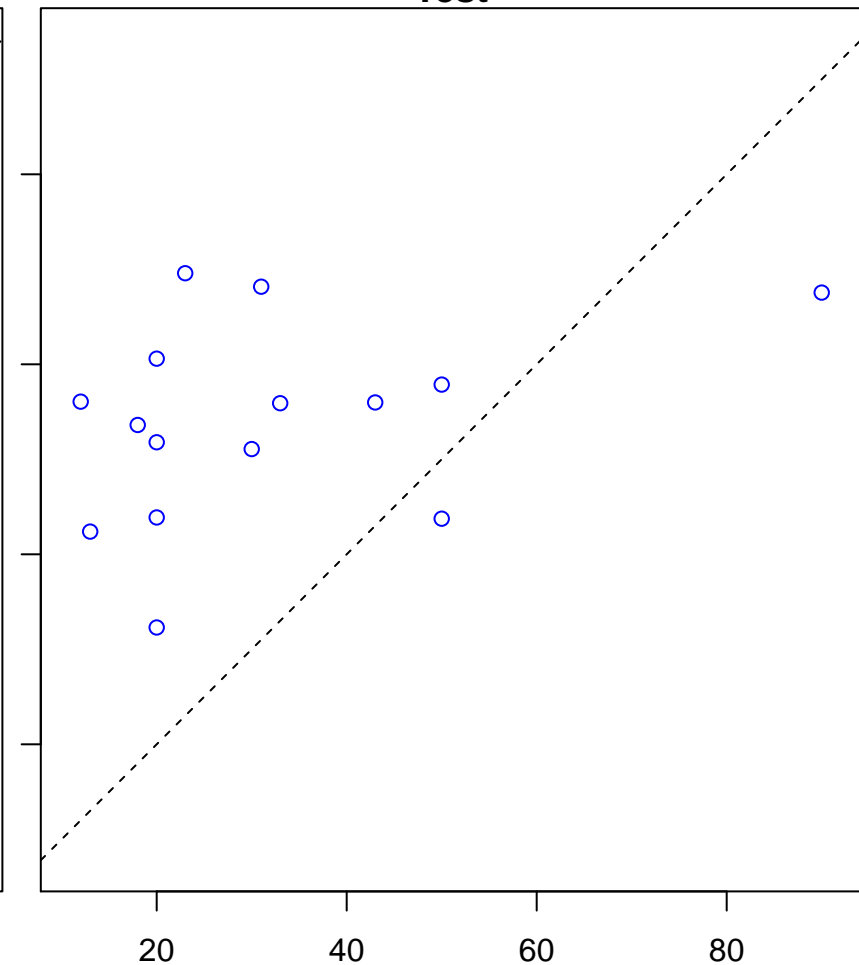


intermediate filament bundle assembly (Score: 4.877297)

Control

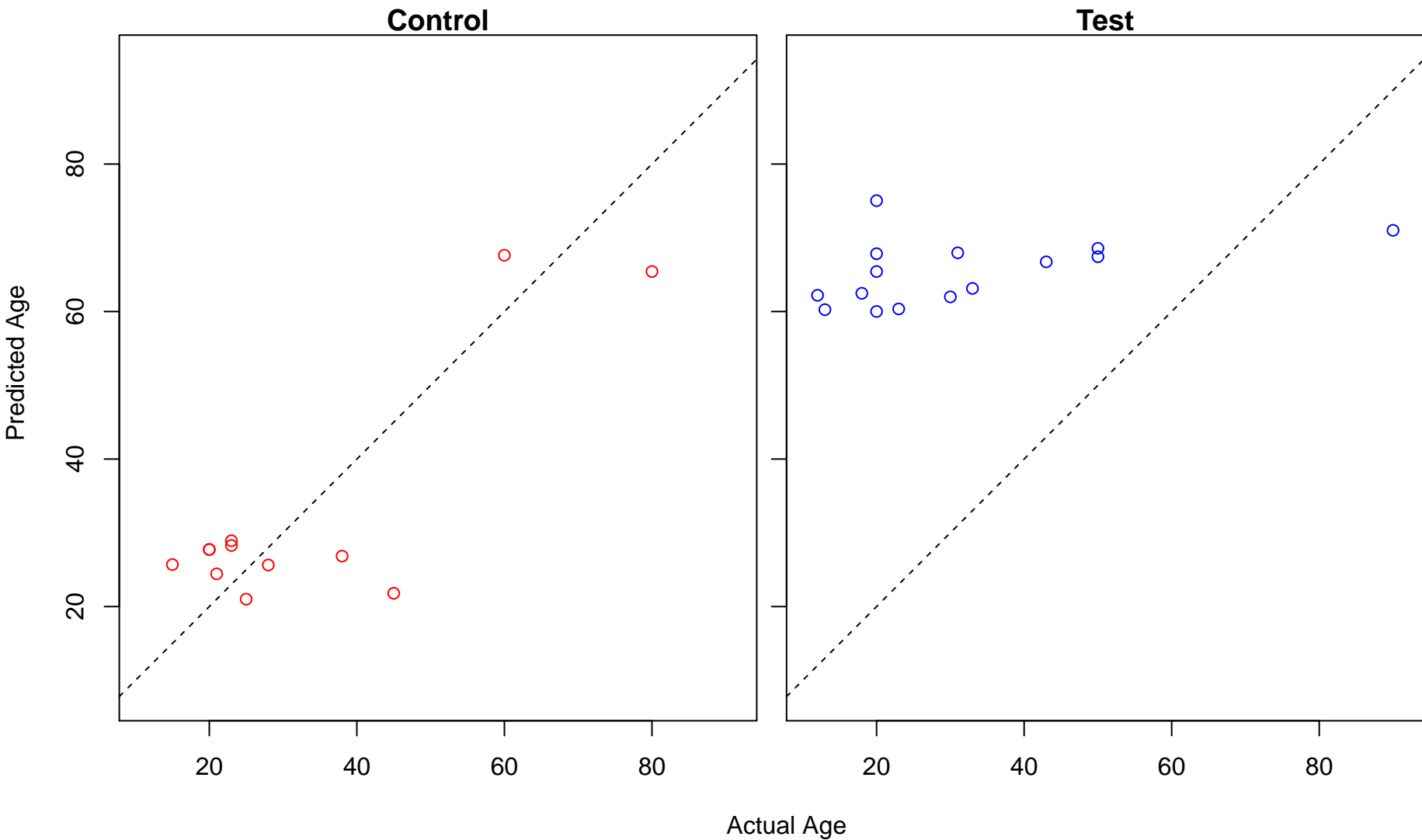


Test

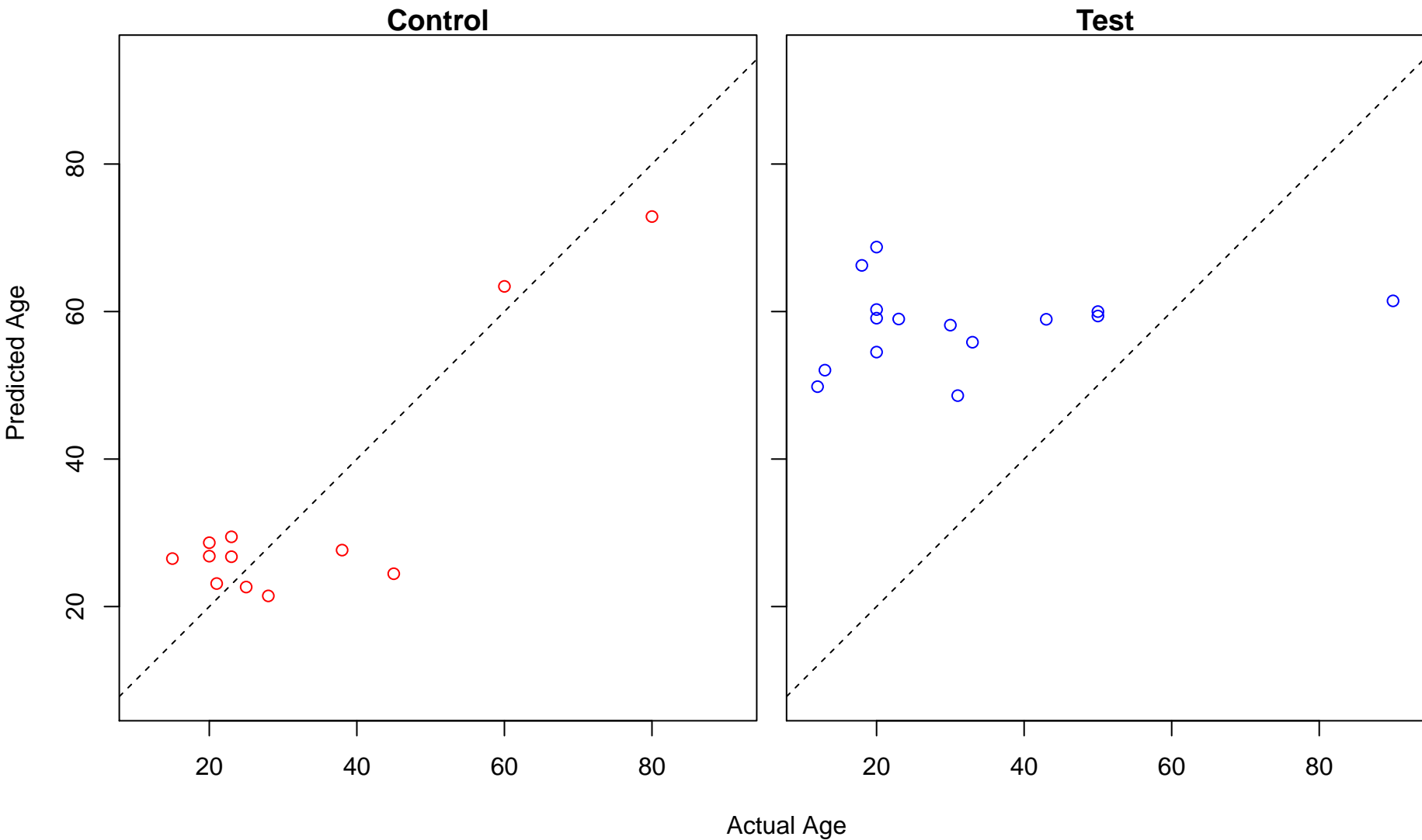


Actual Age

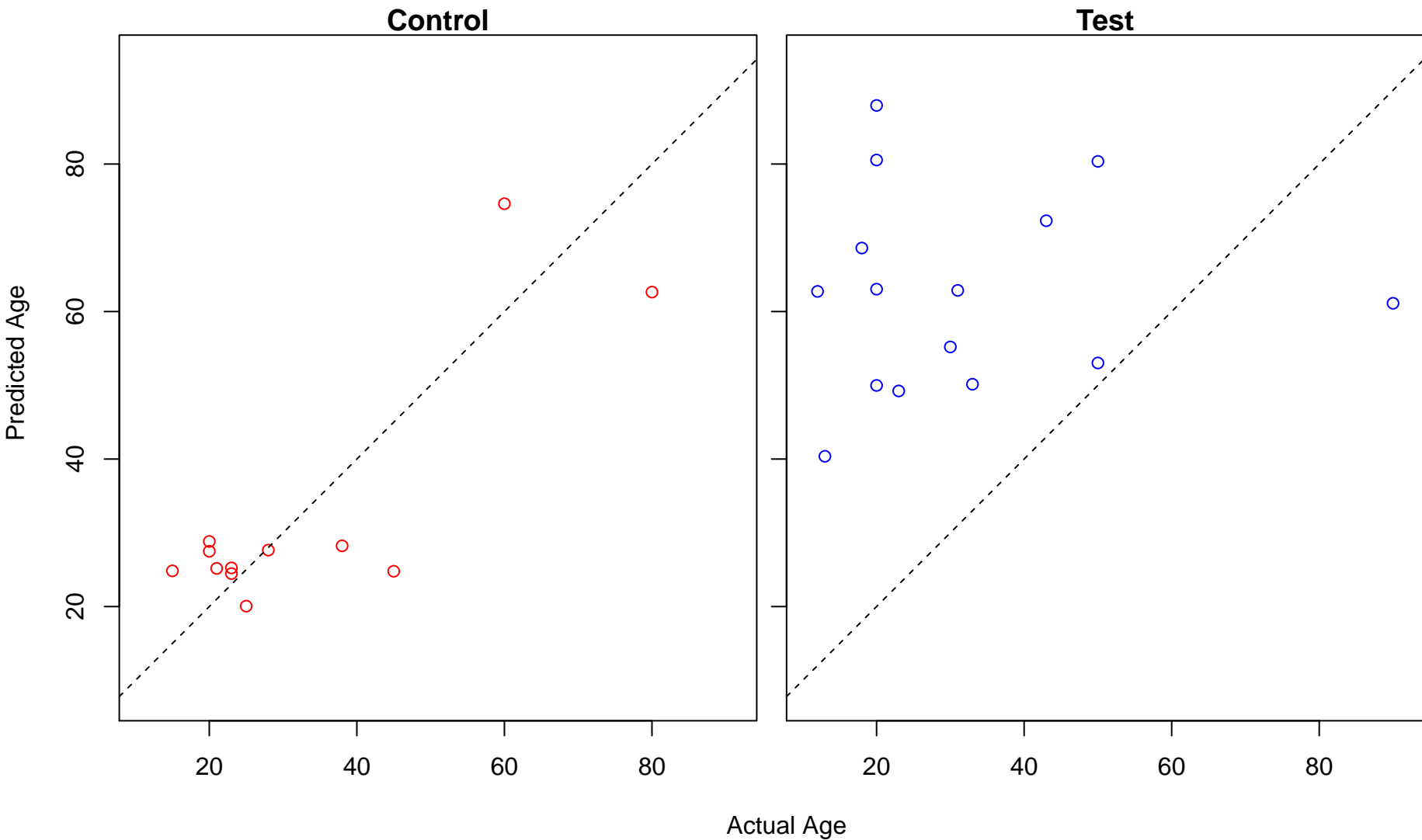
cellular response to retinoic acid (Score: 4.876621)



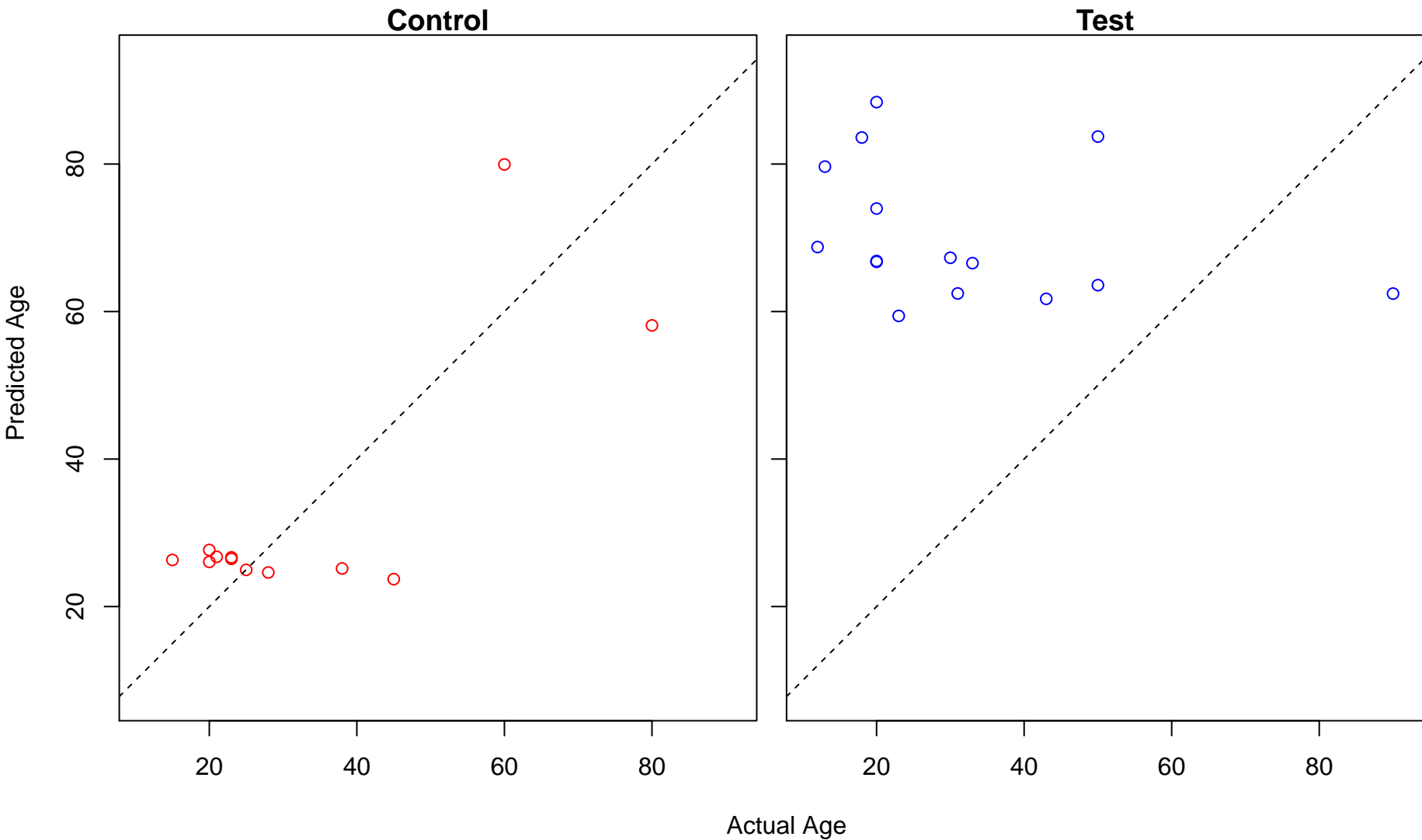
regulation of synapse assembly (Score: 4.876098)



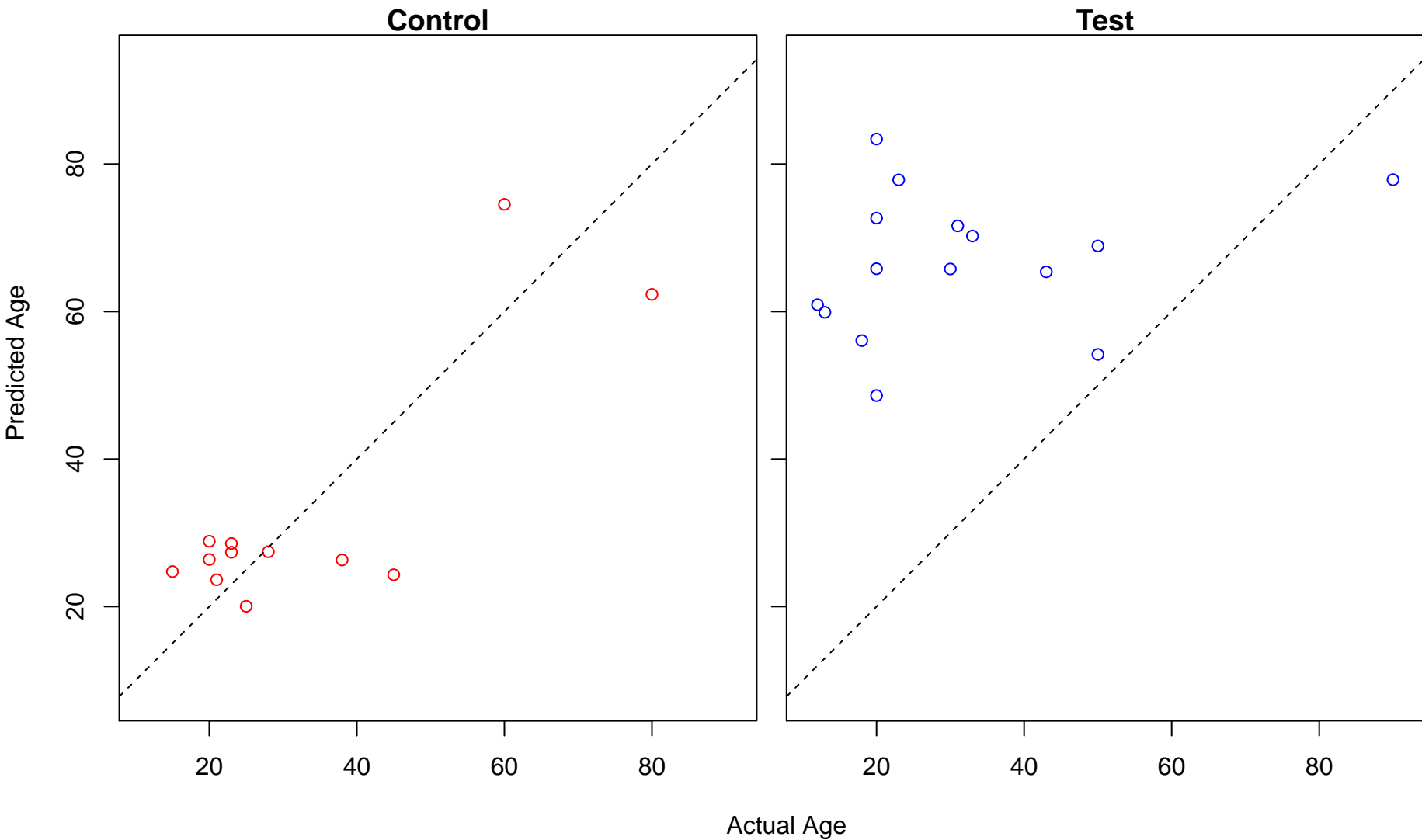
cellular response to corticosteroid stimulus (Score: 4.876028)



positive regulation of protein polymerization (Score: 4.871954)

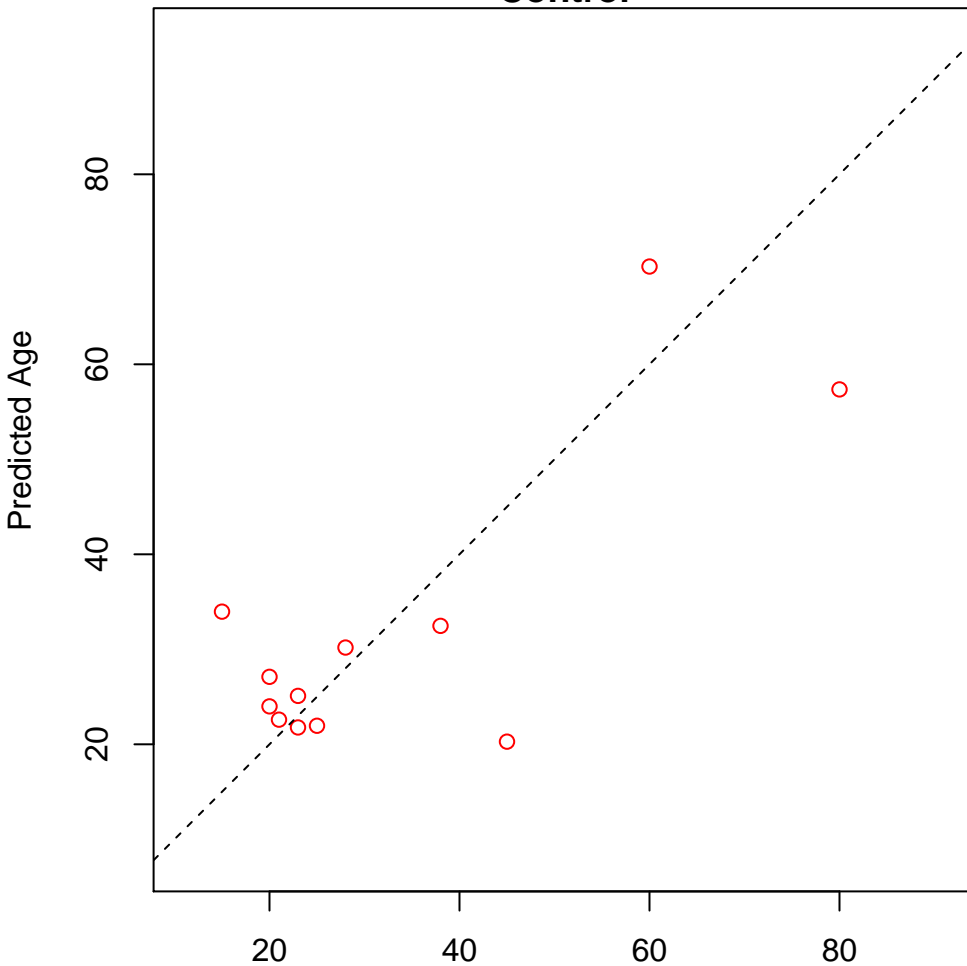


snRNA transcription from RNA polymerase III promoter (Score: 4.871821)

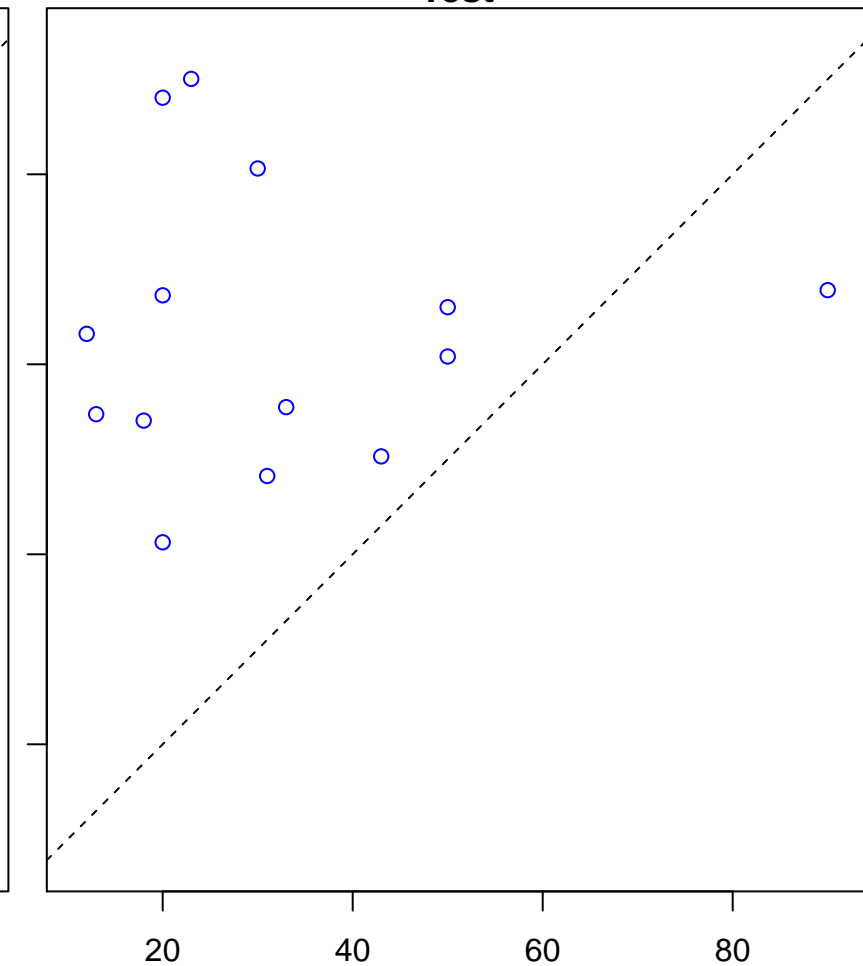


peptidyl-arginine omega-N-methylation (Score: 4.870515)

Control

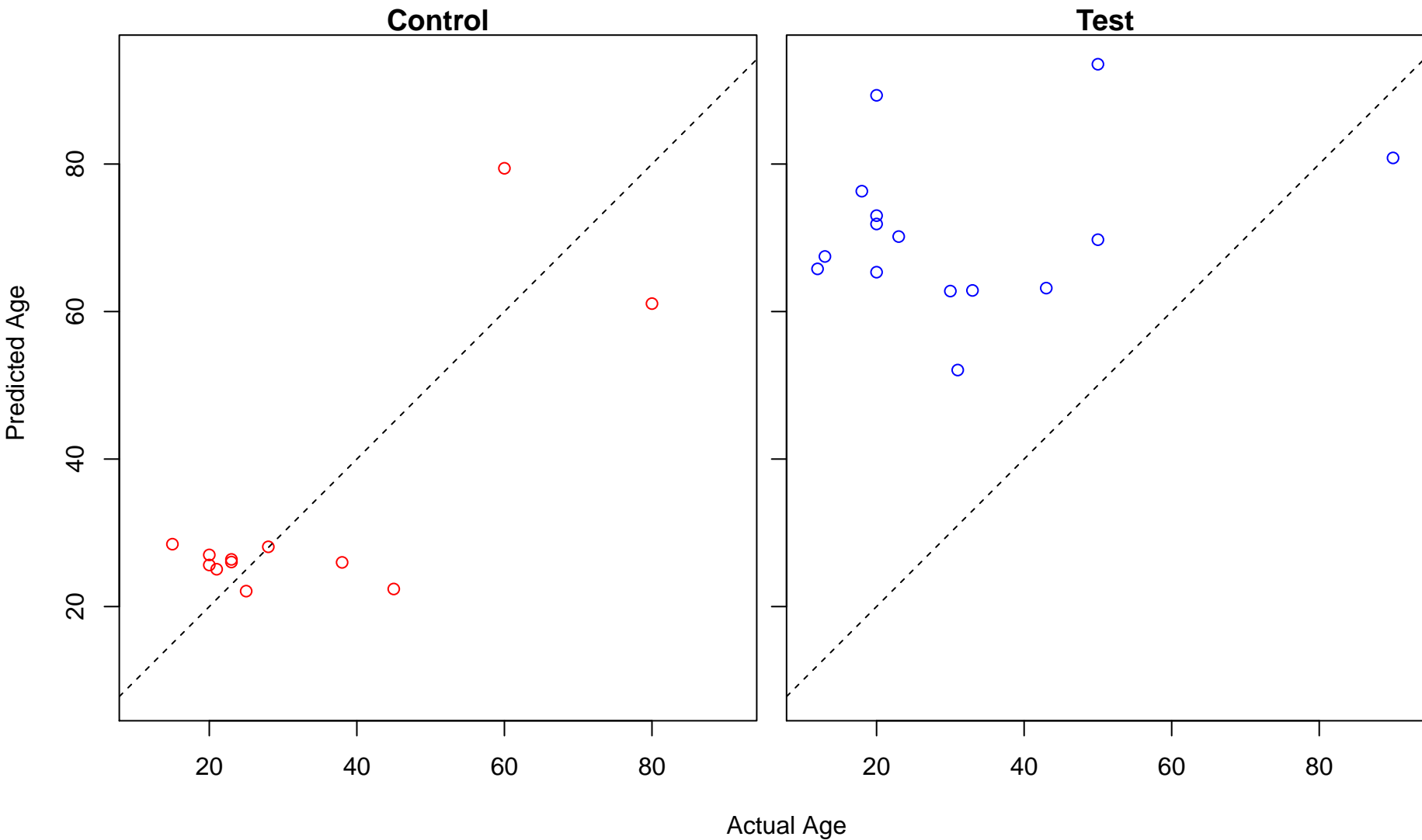


Test

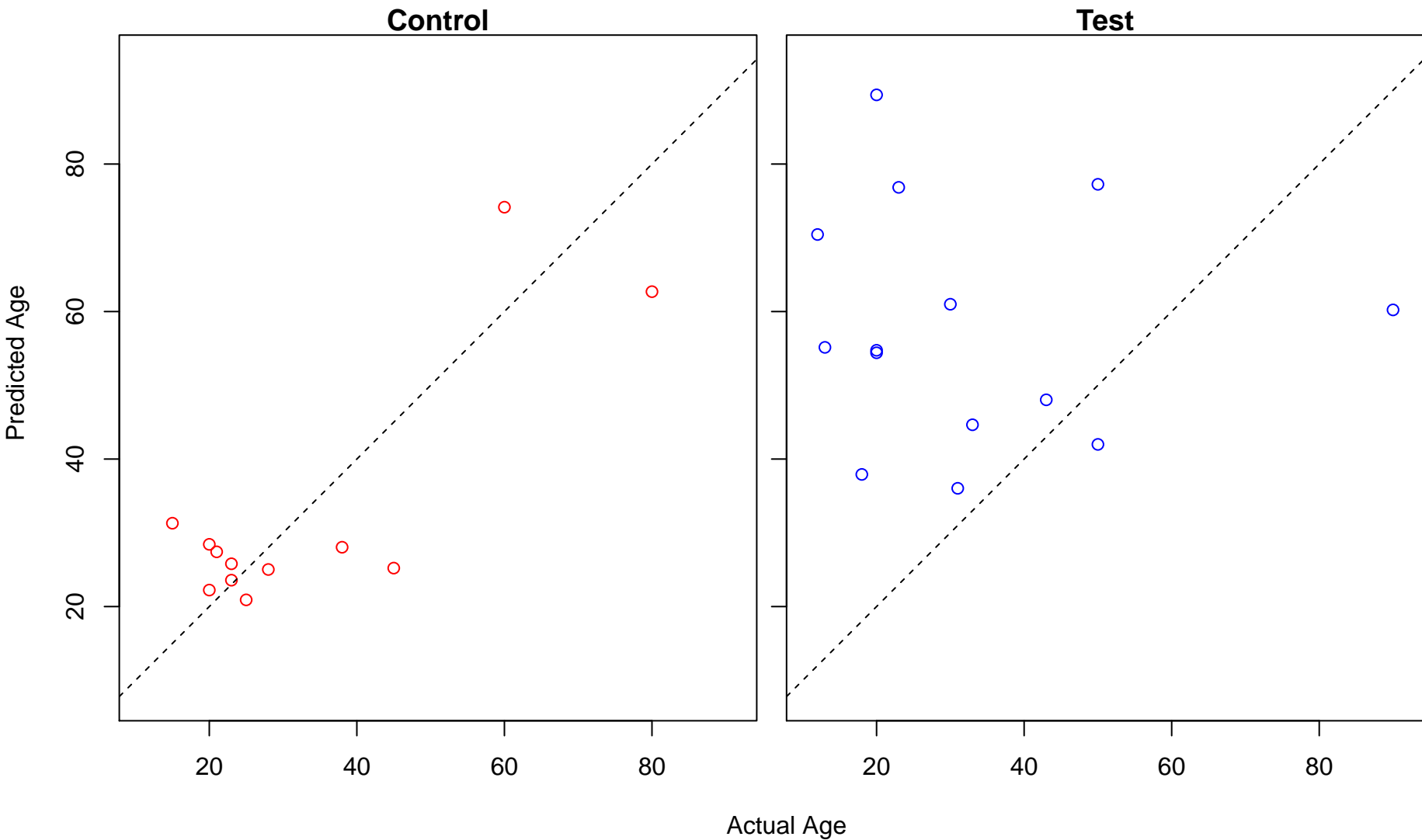


Actual Age

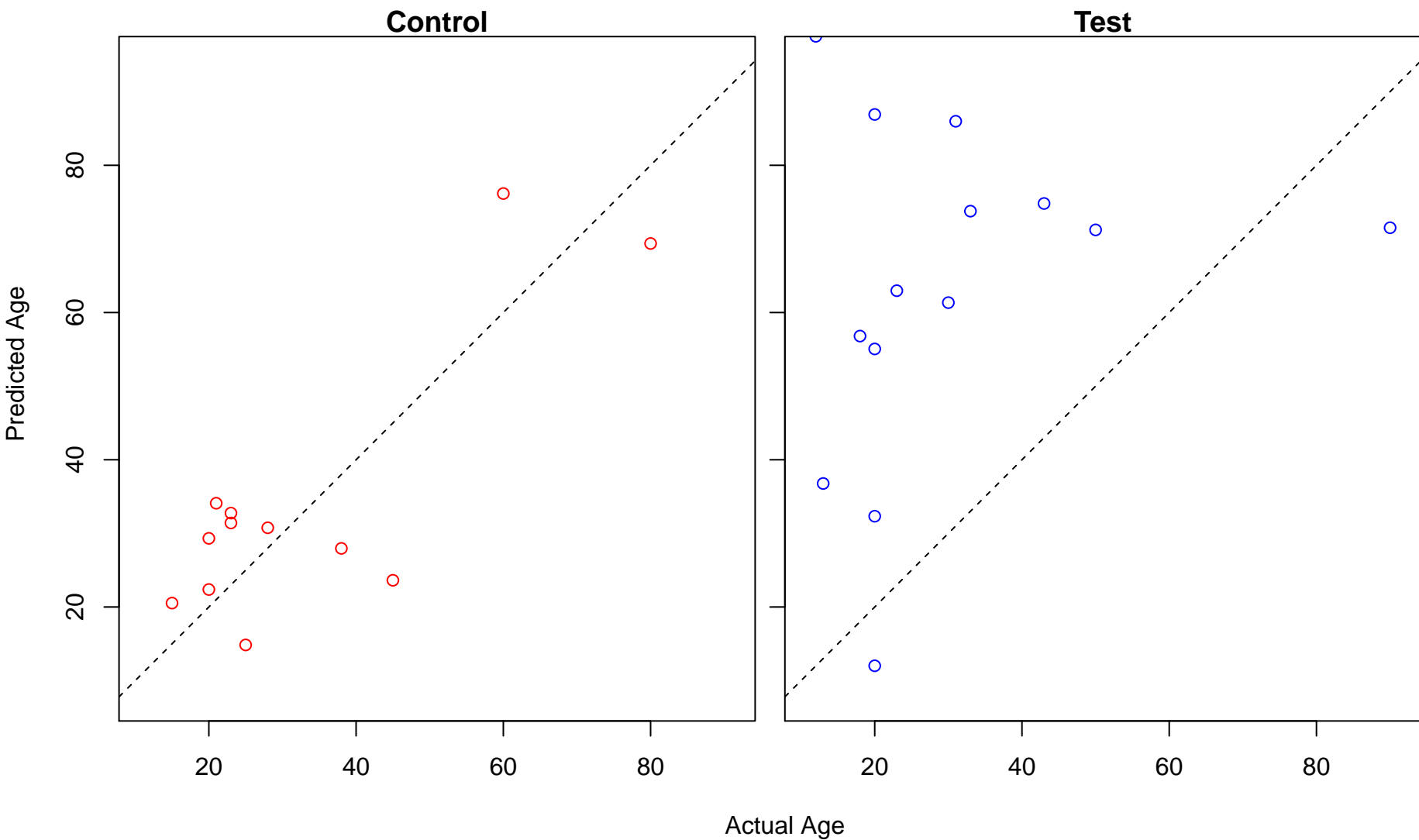
negative regulation of epidermal growth factor receptor signaling pathway (Score: 4.869874)



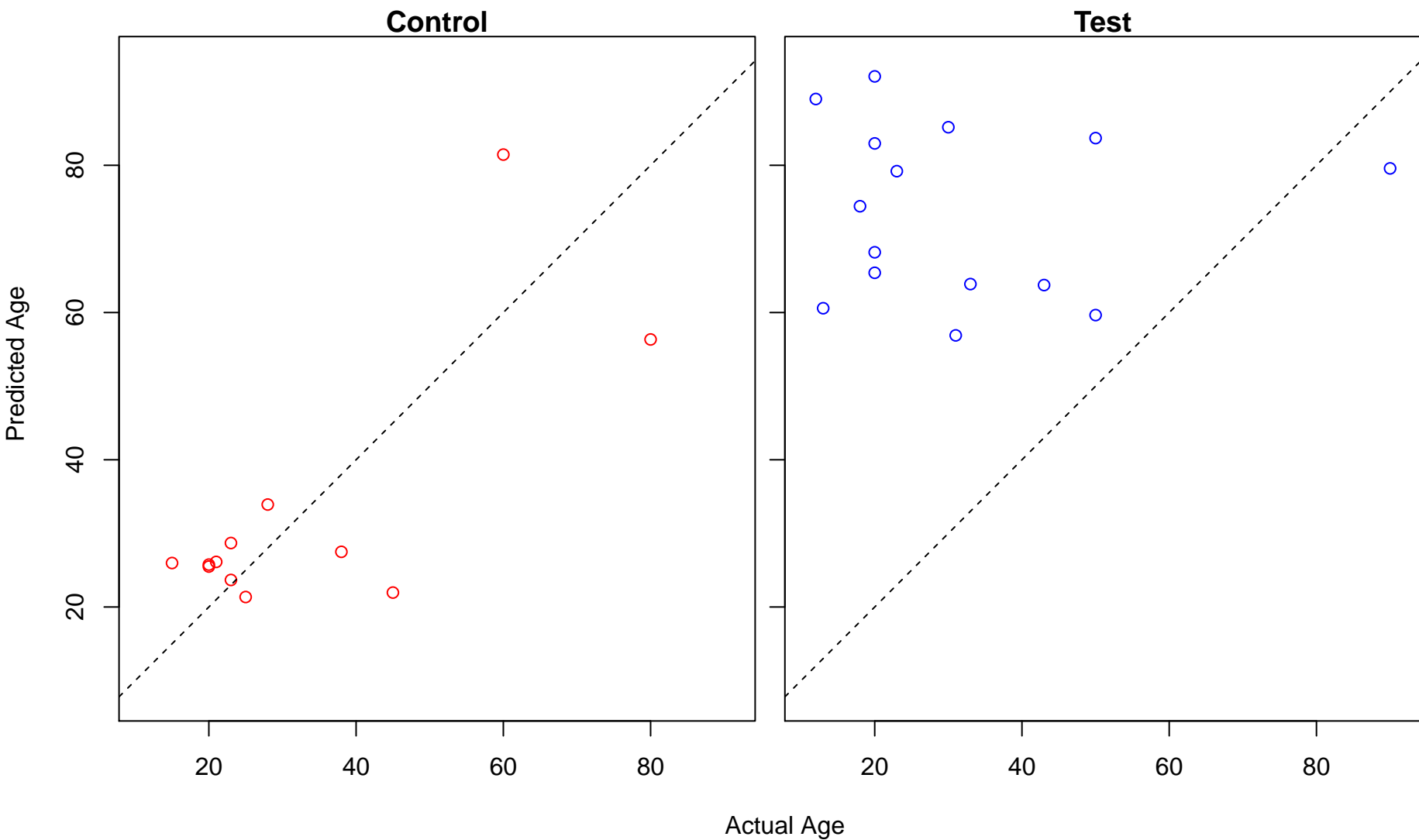
sperm-egg recognition (Score: 4.868247)



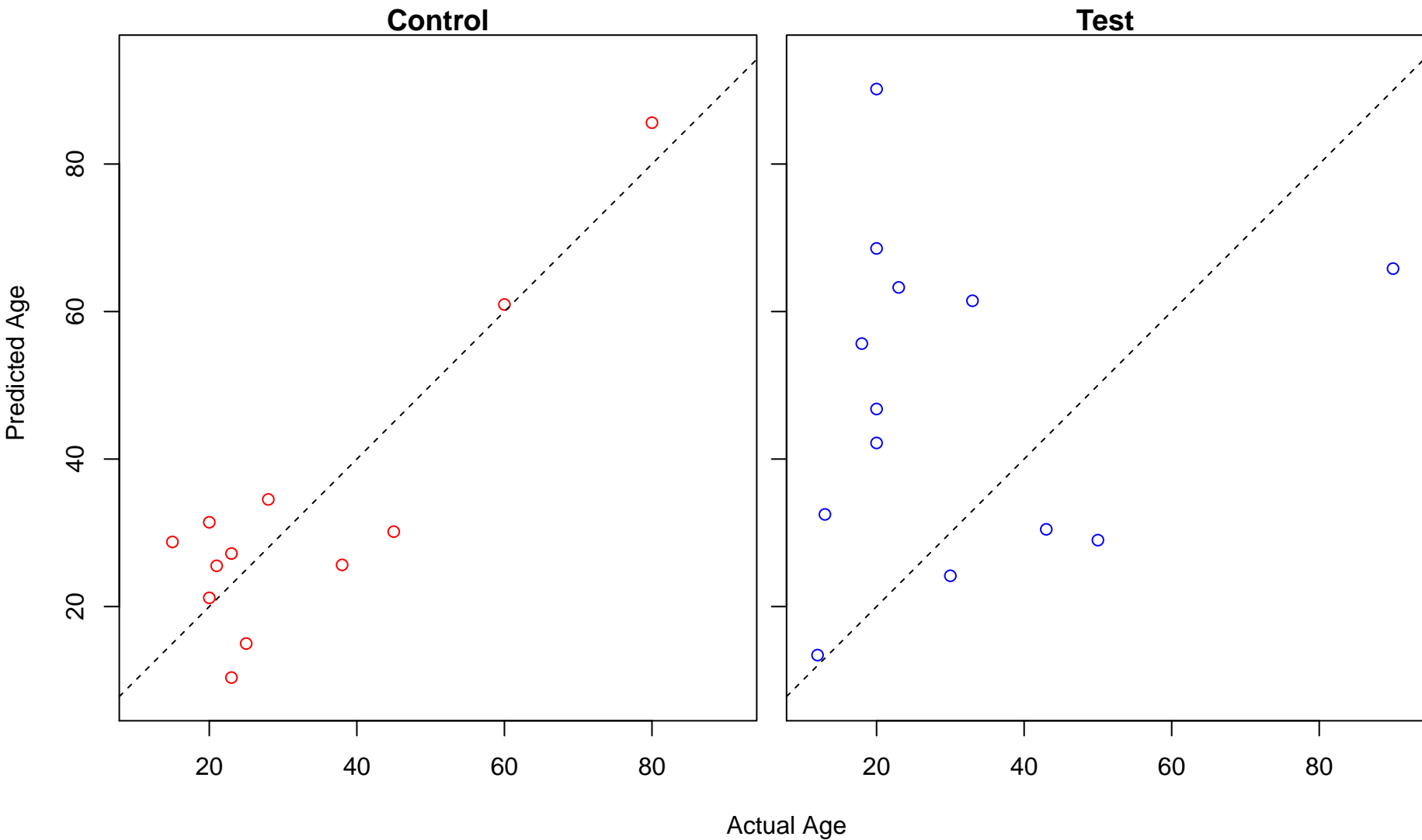
positive regulation of mast cell activation (Score: 4.867372)



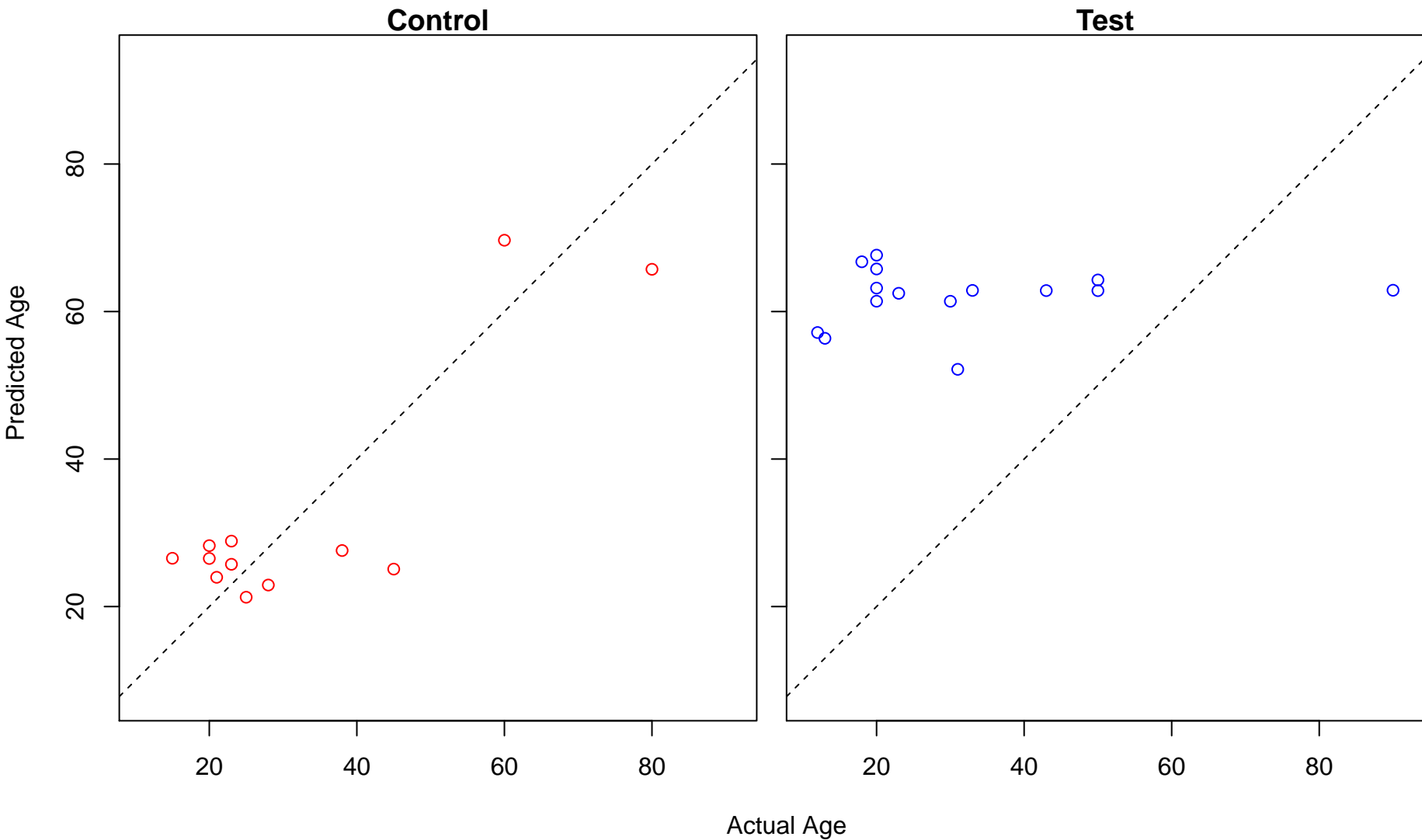
spleen development (Score: 4.866895)



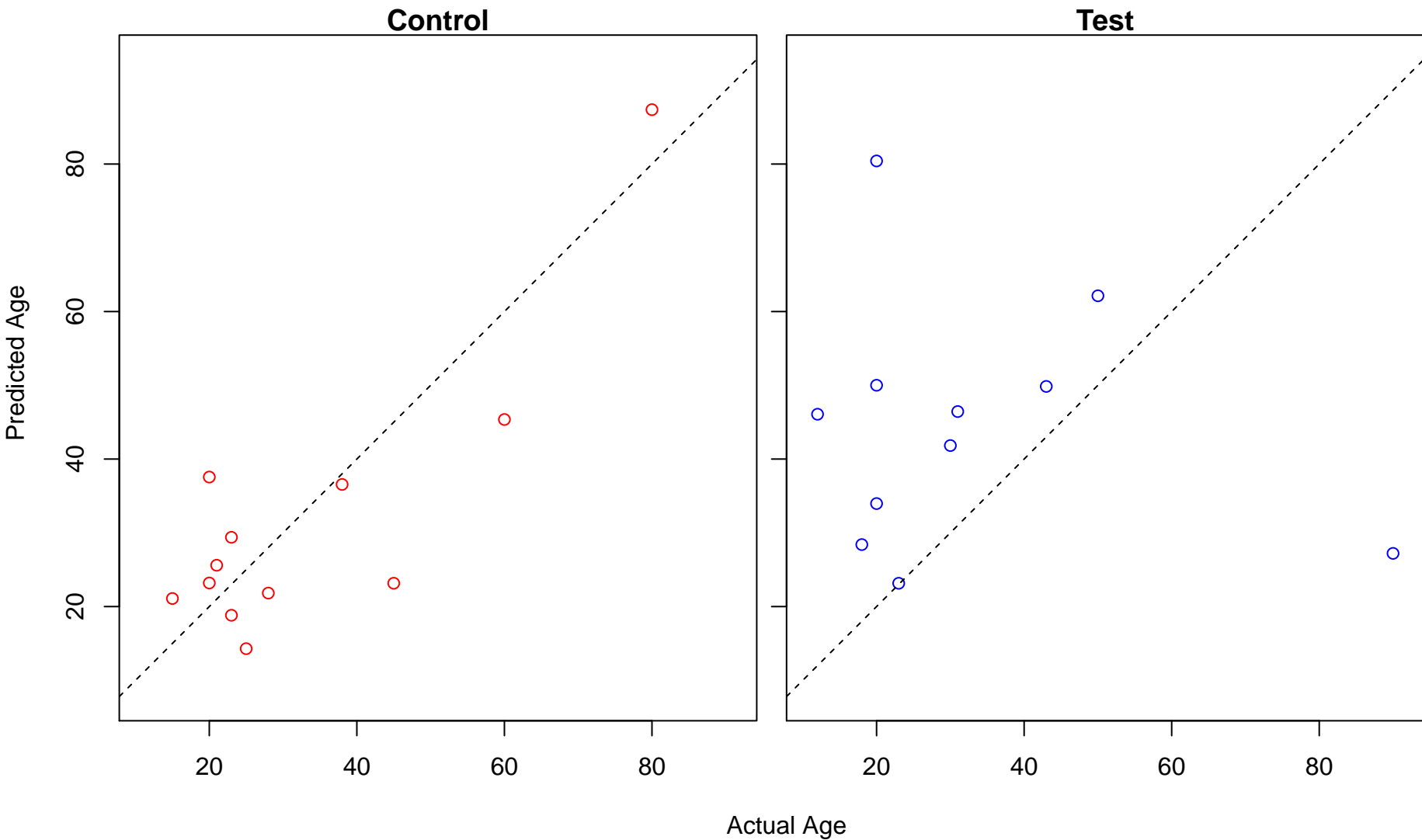
cyclic-nucleotide-mediated signaling (Score: 4.866335)



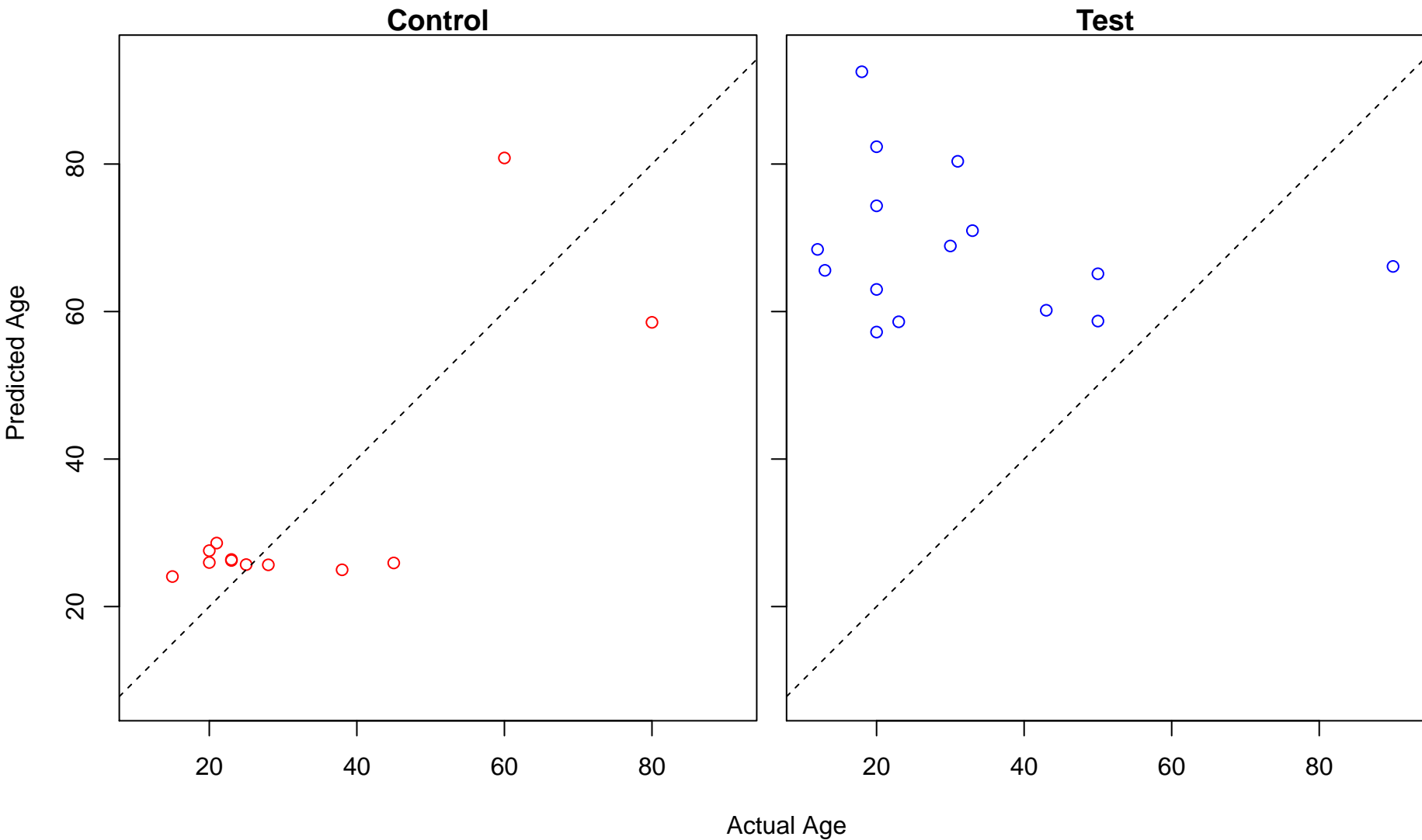
organ growth (Score: 4.865412)



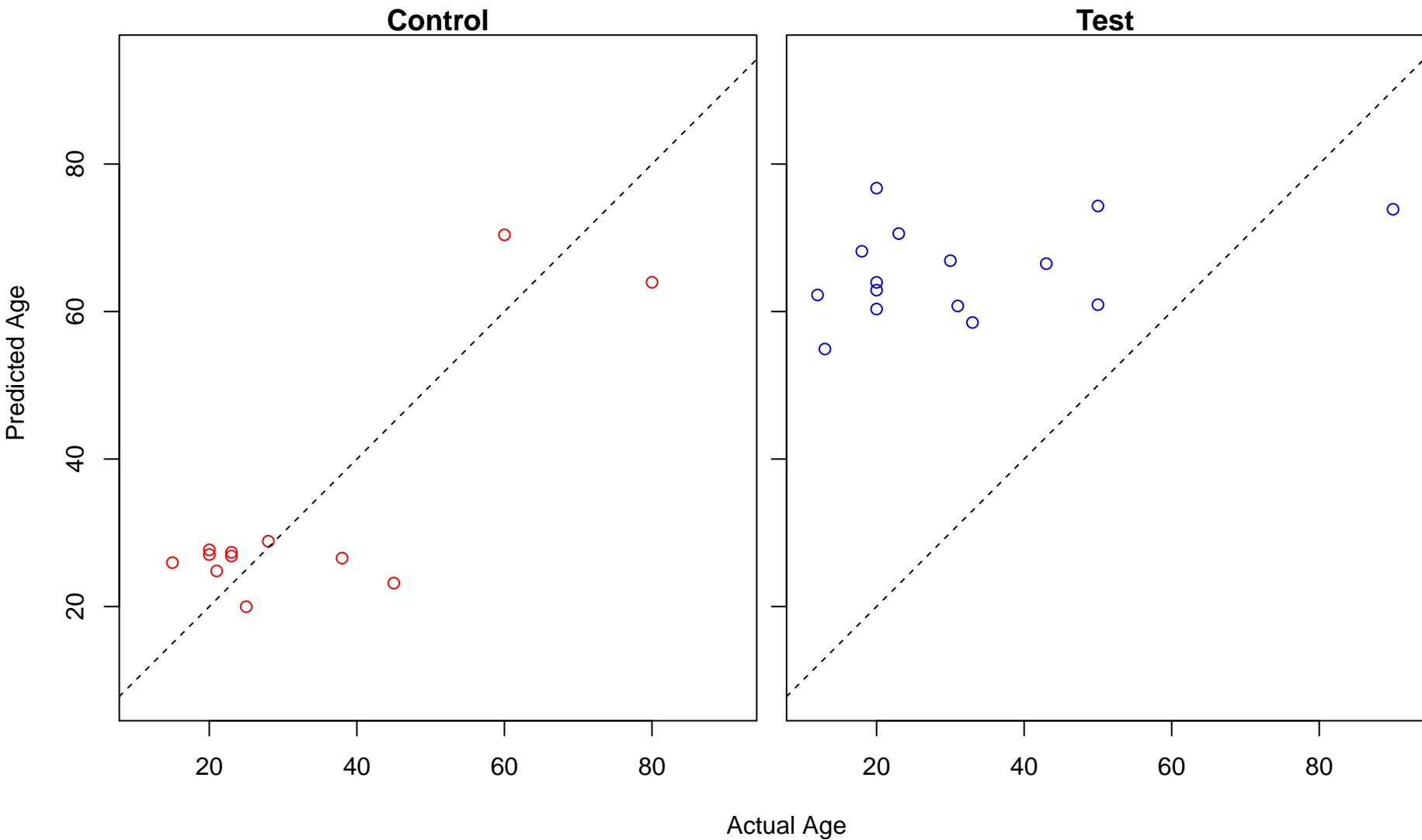
multicellular organismal macromolecule metabolic process (Score: 4.859992)



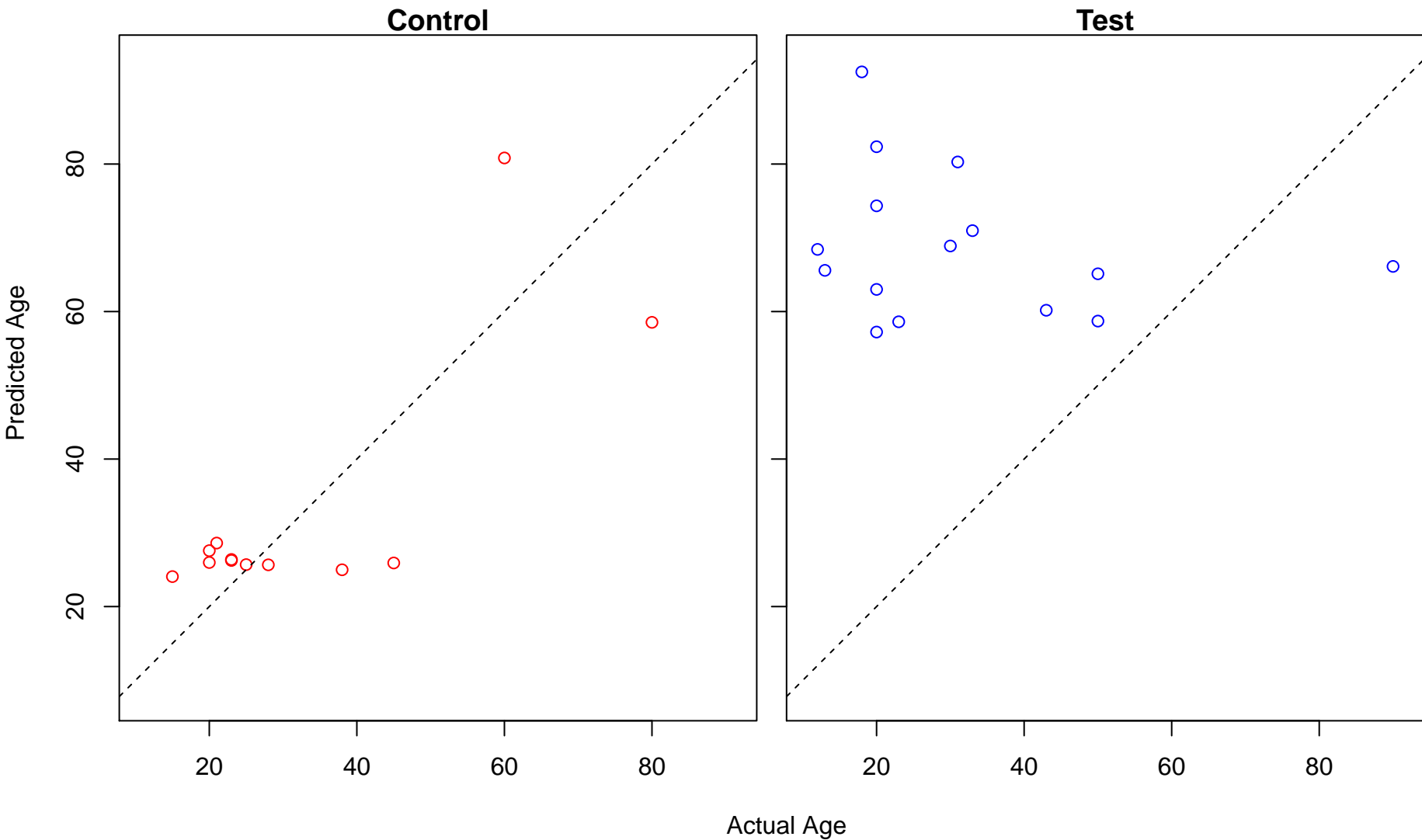
negative regulation of purine nucleotide metabolic process (Score: 4.858775)



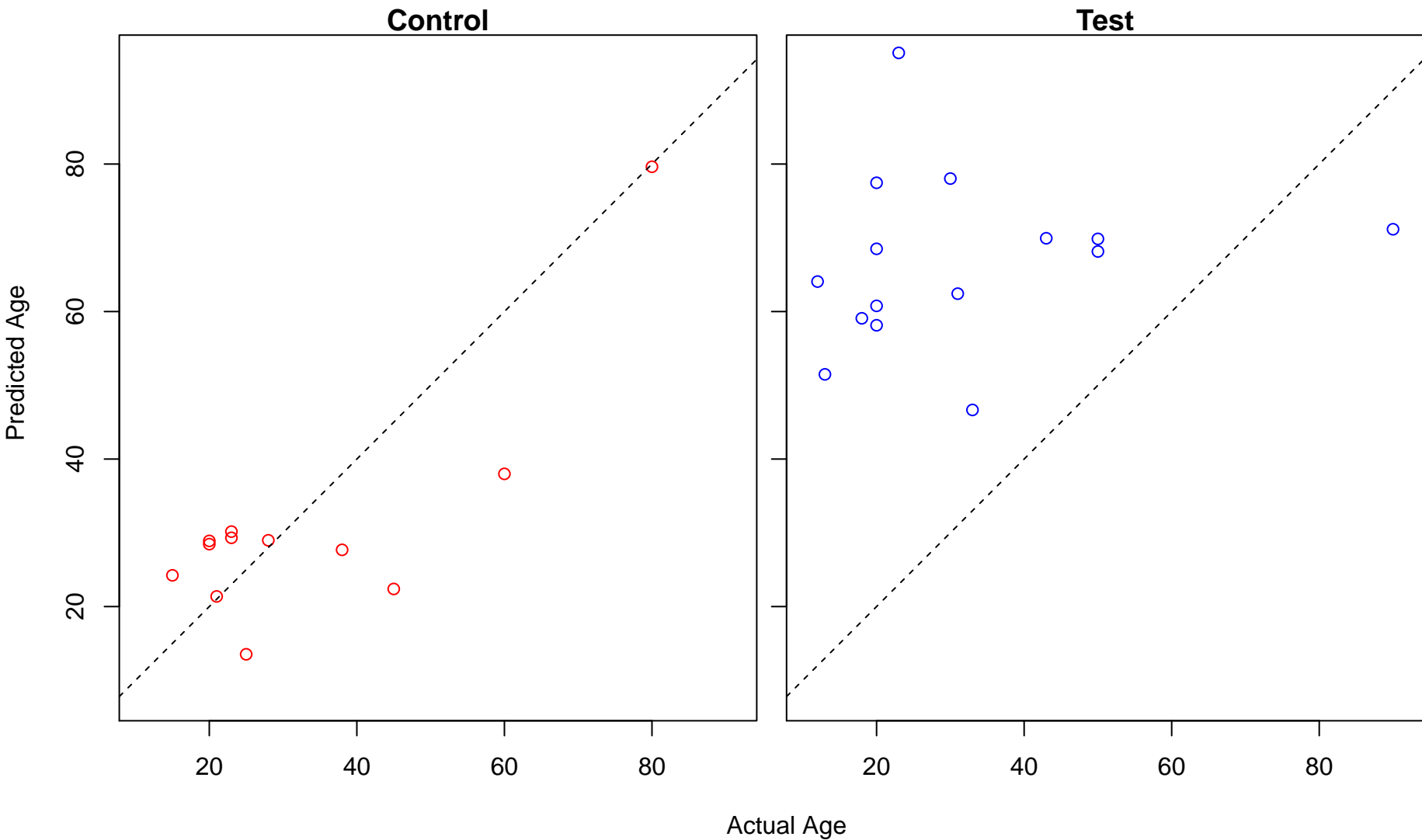
negative regulation of secretion by cell (Score: 4.858172)



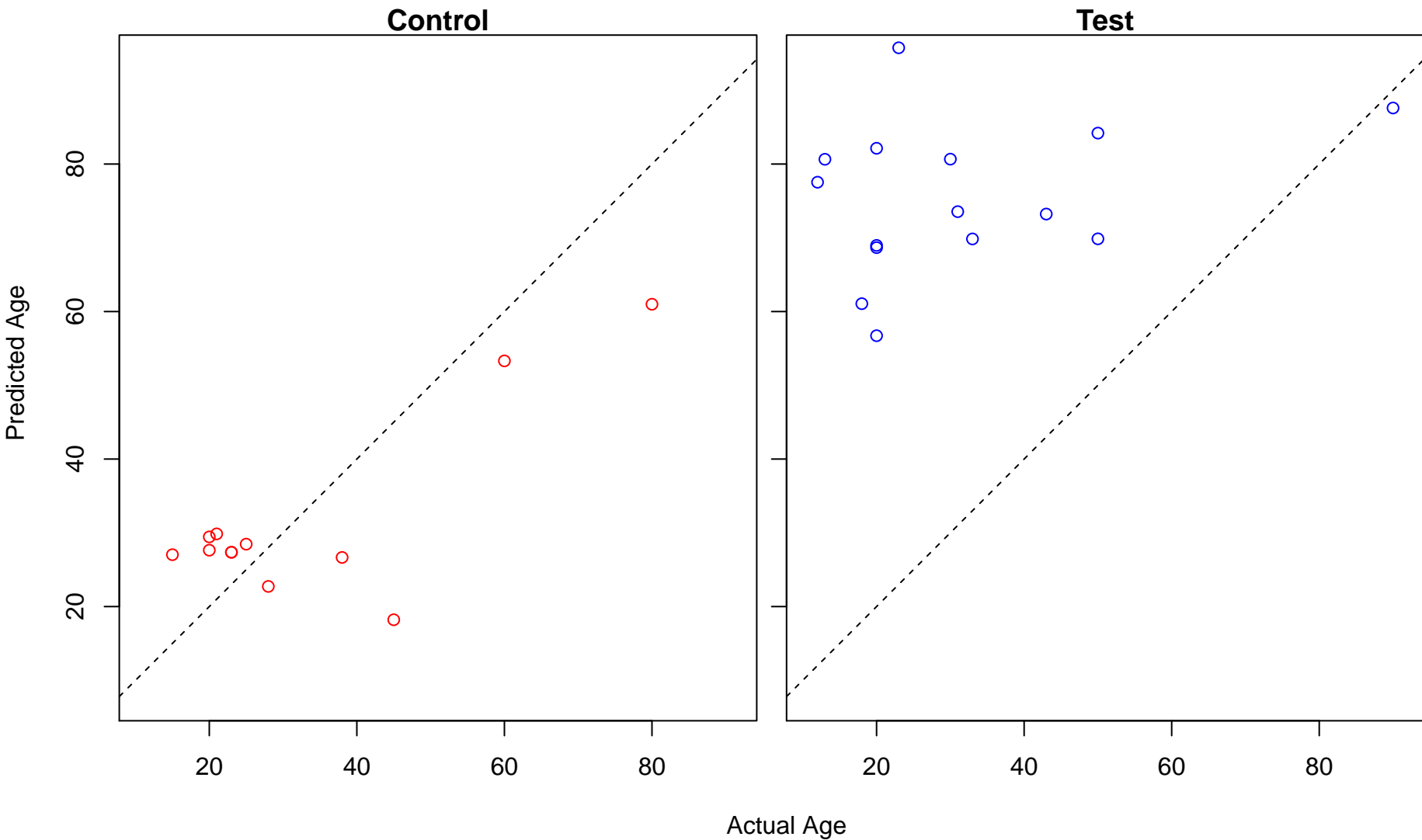
negative regulation of nucleotide metabolic process (Score: 4.857478)



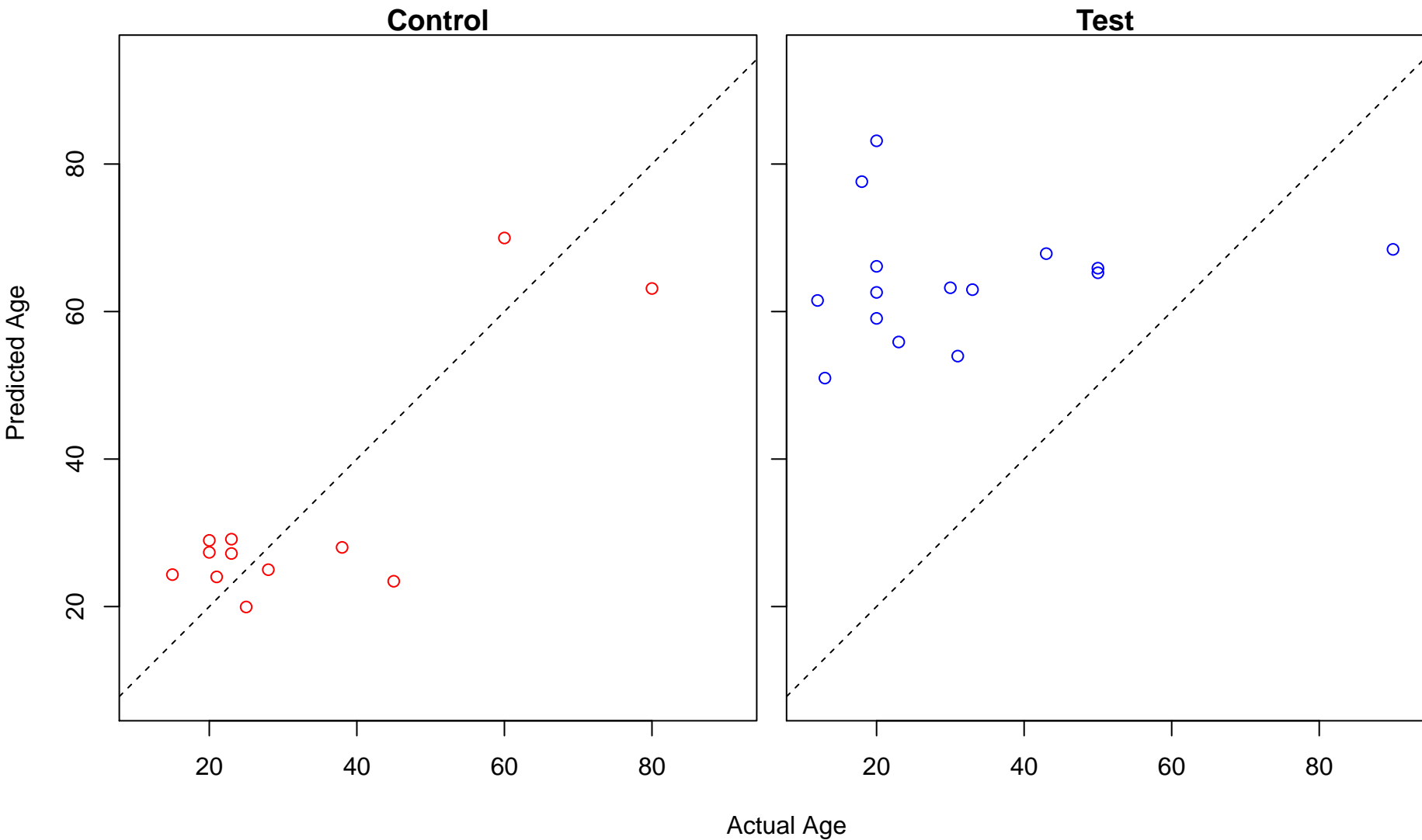
ncRNA catabolic process (Score: 4.853831)



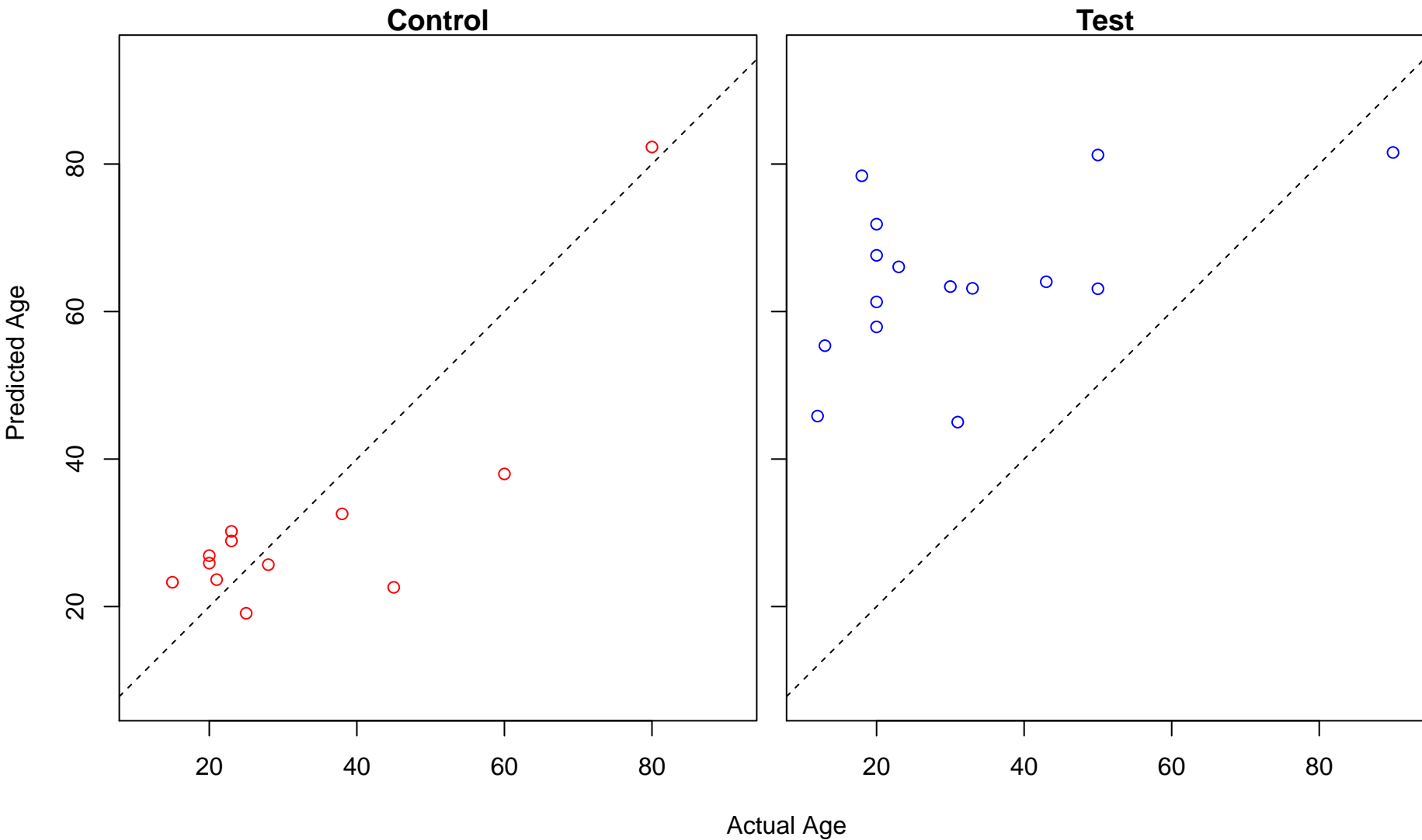
positive regulation of catecholamine secretion (Score: 4.853778)



amino acid transport (Score: 4.853270)

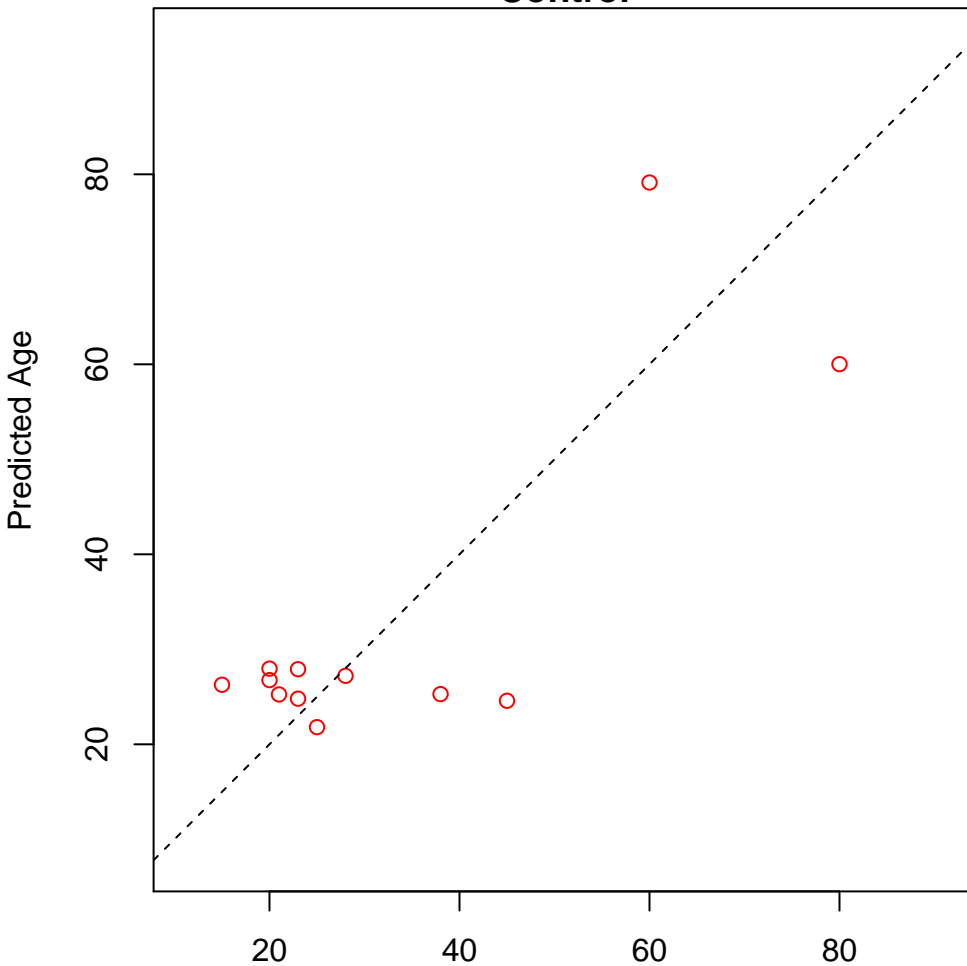


regulation of ventricular cardiac muscle cell action potential (Score: 4.852847)

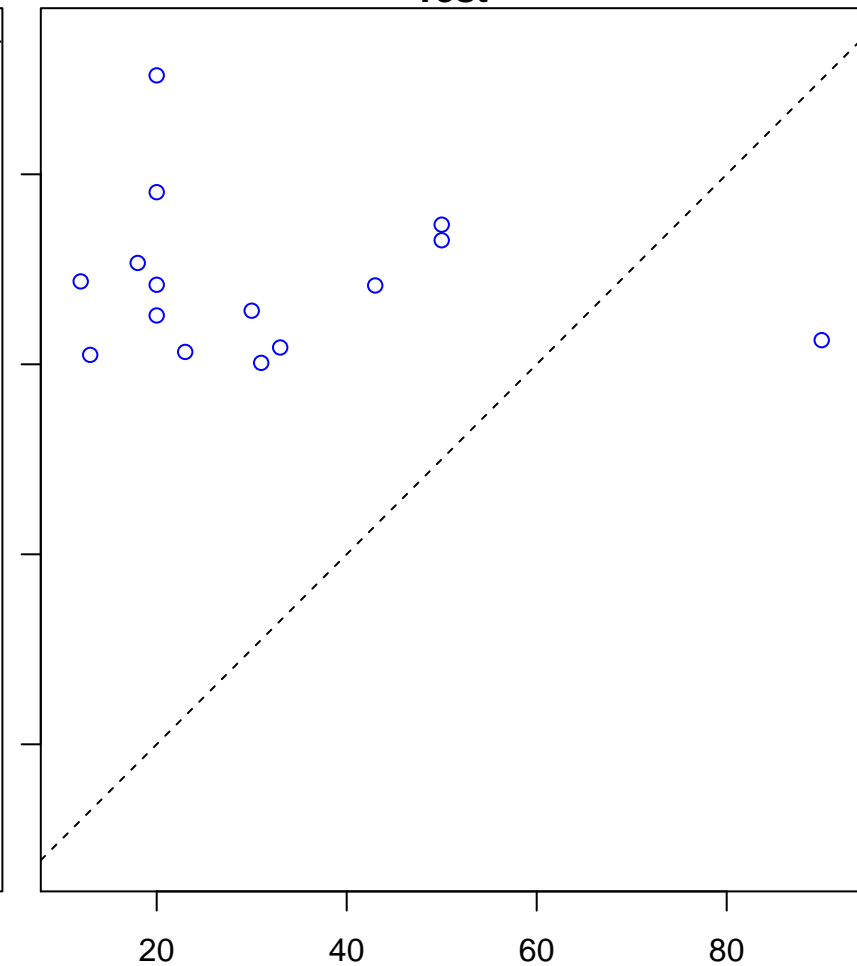


actin polymerization or depolymerization (Score: 4.852448)

Control

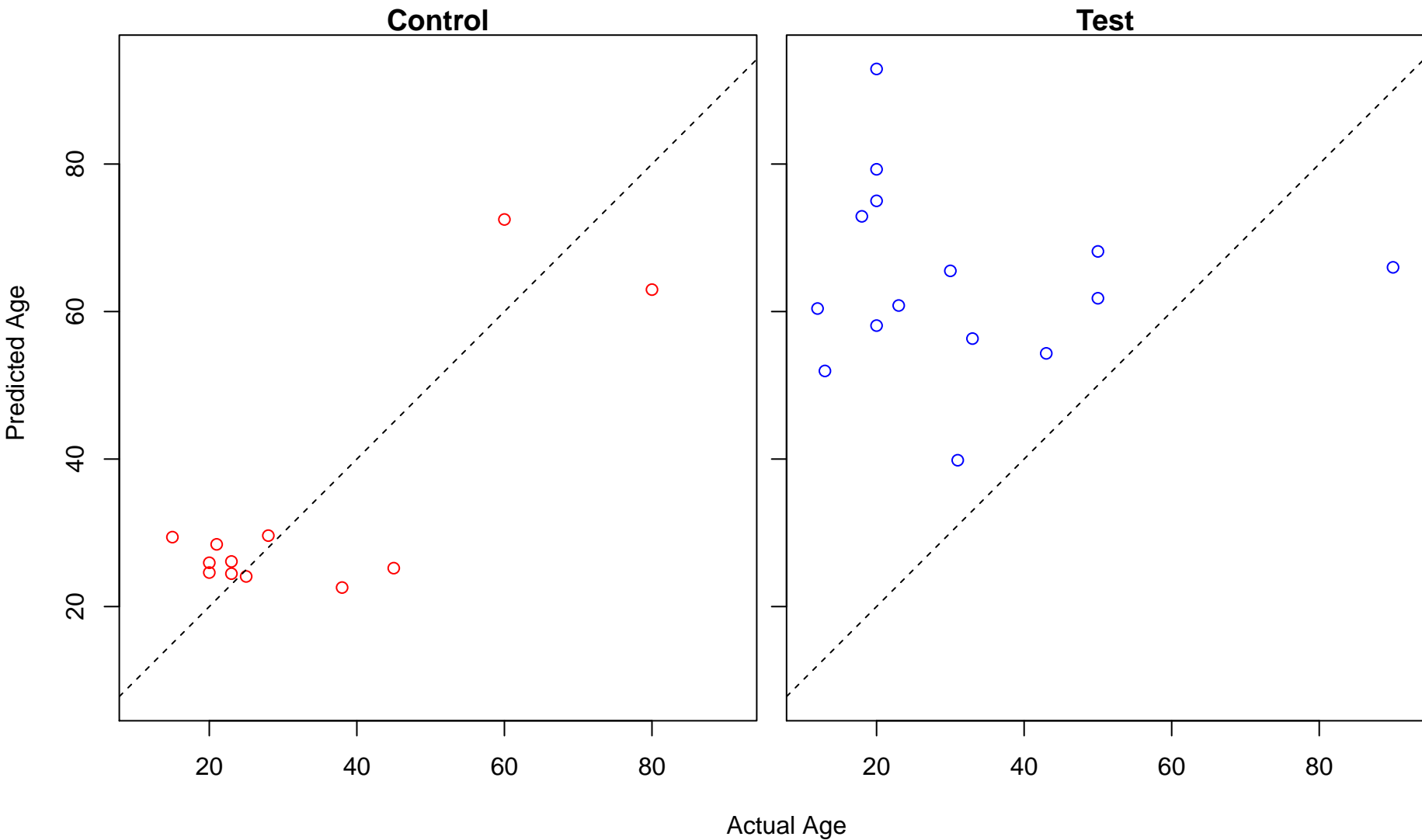


Test

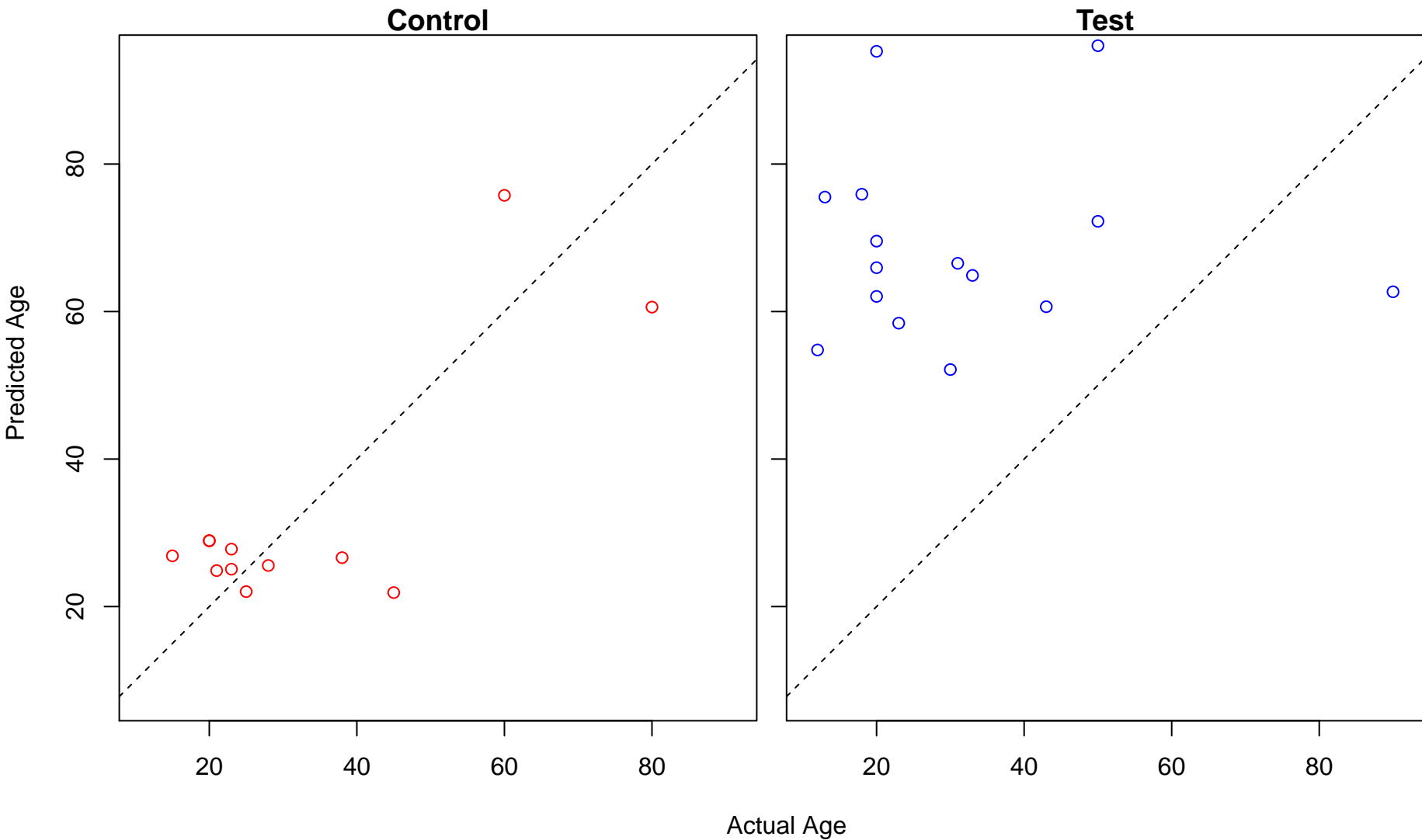


Actual Age

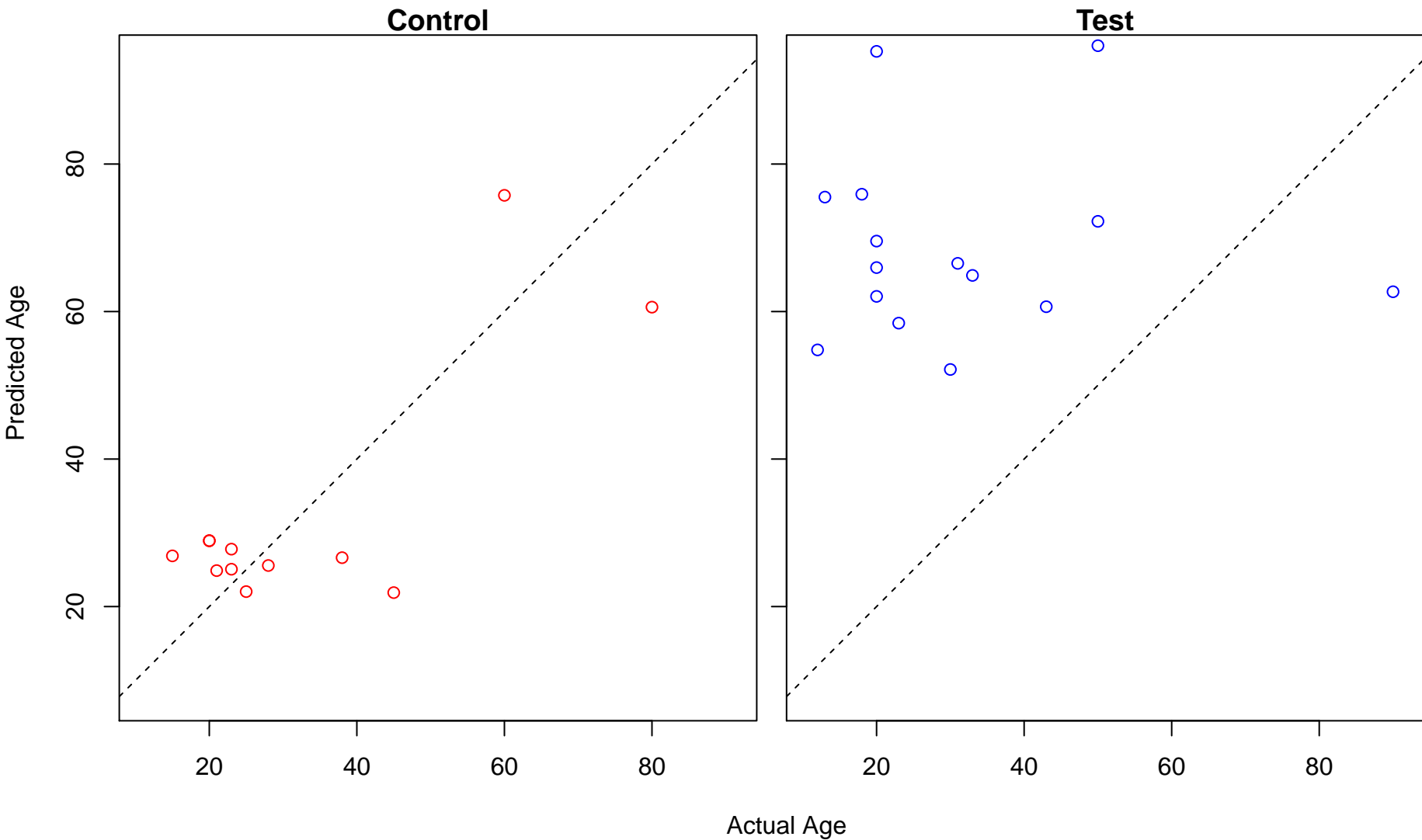
mitochondrial respiratory chain complex assembly (Score: 4.852371)



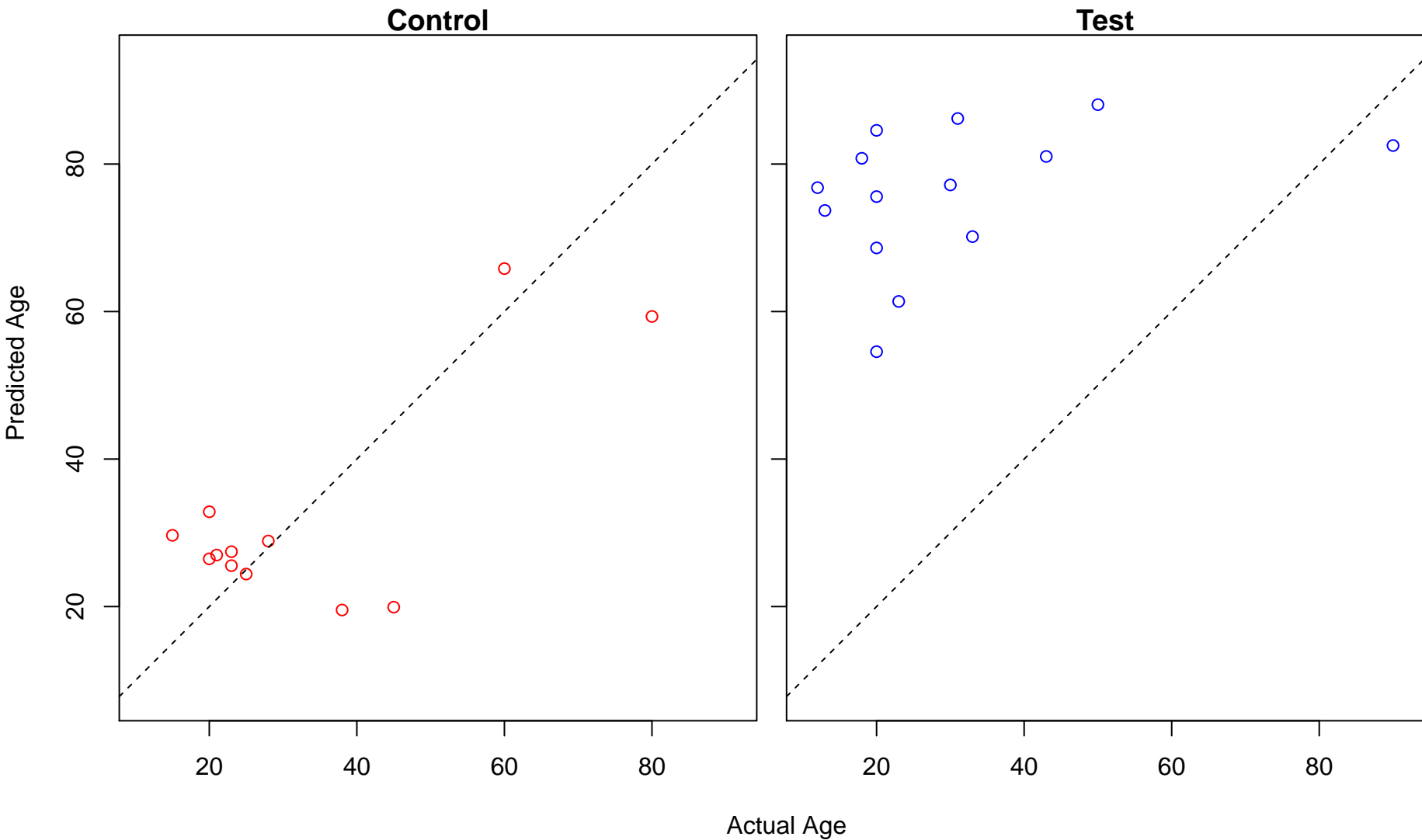
membrane assembly (Score: 4.849227)



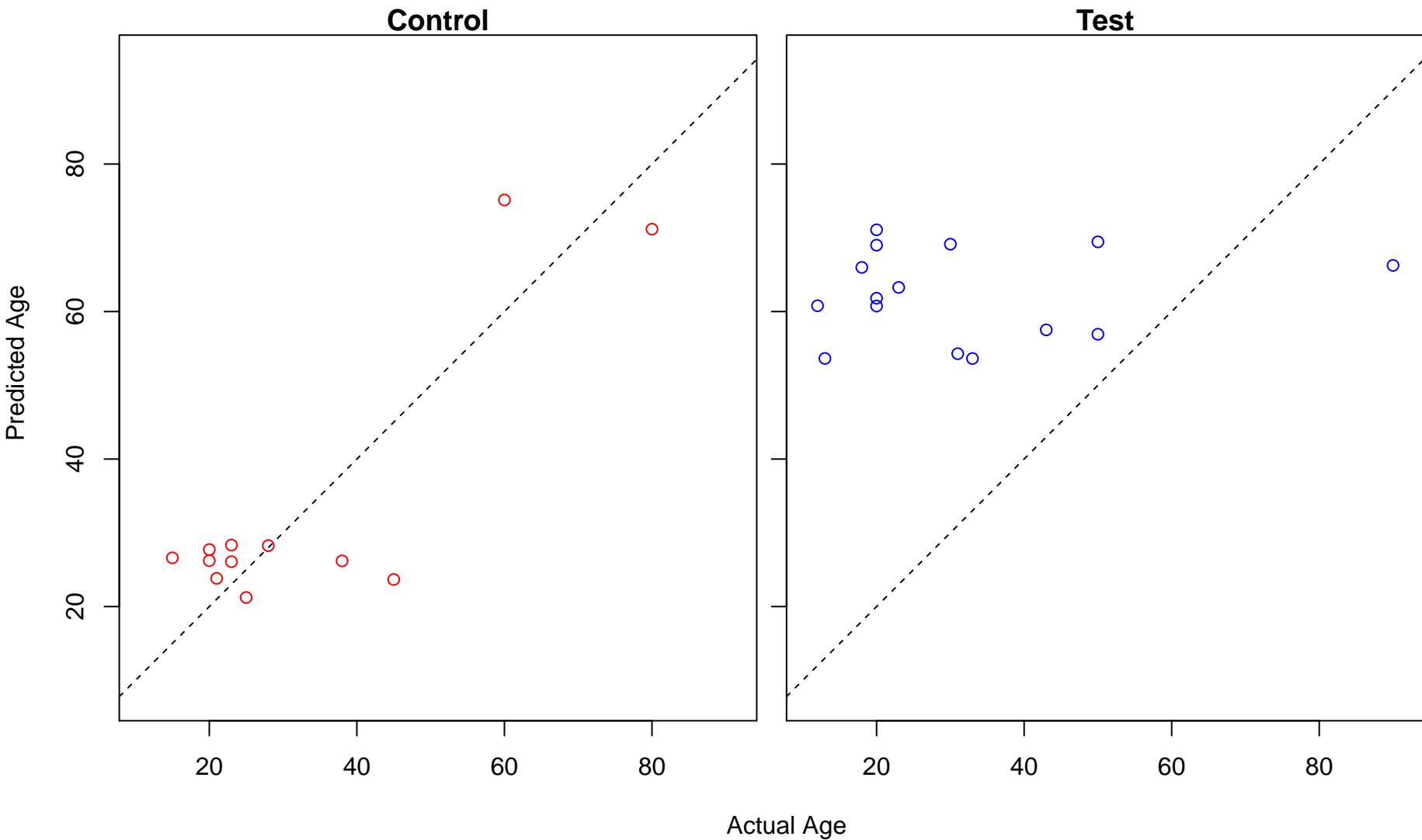
membrane biogenesis (Score: 4.848943)



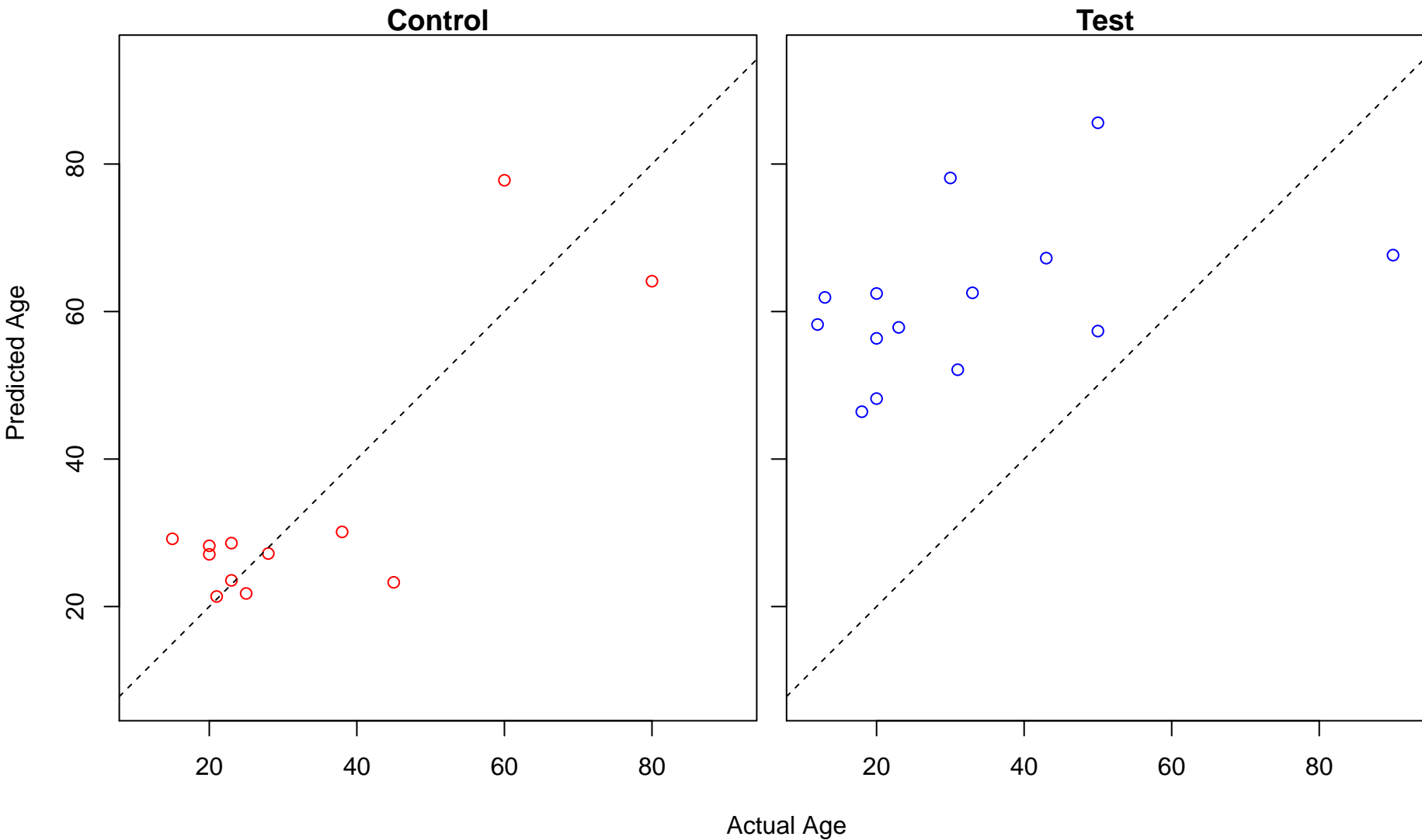
cellular sodium ion homeostasis (Score: 4.848523)



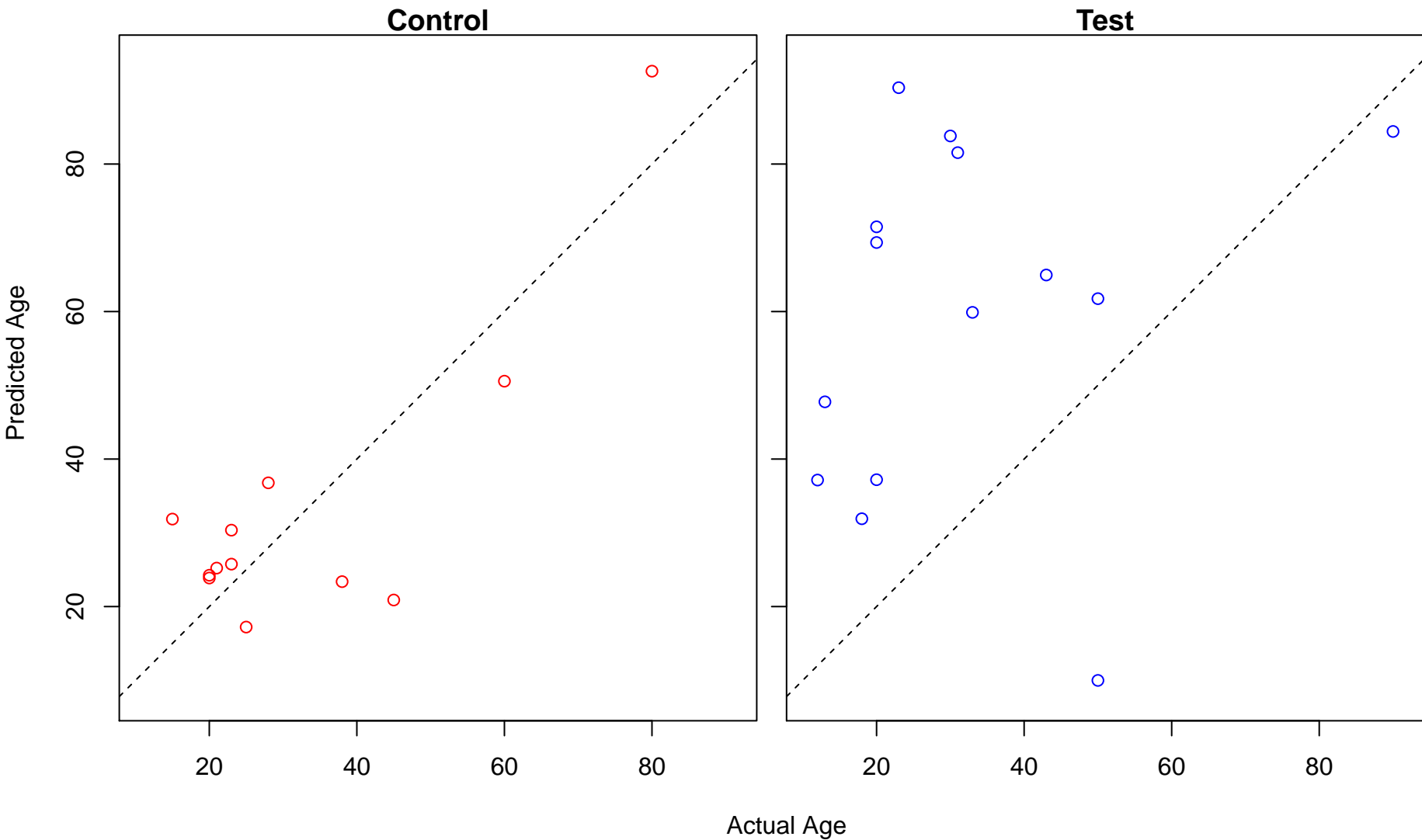
response to unfolded protein (Score: 4.845521)



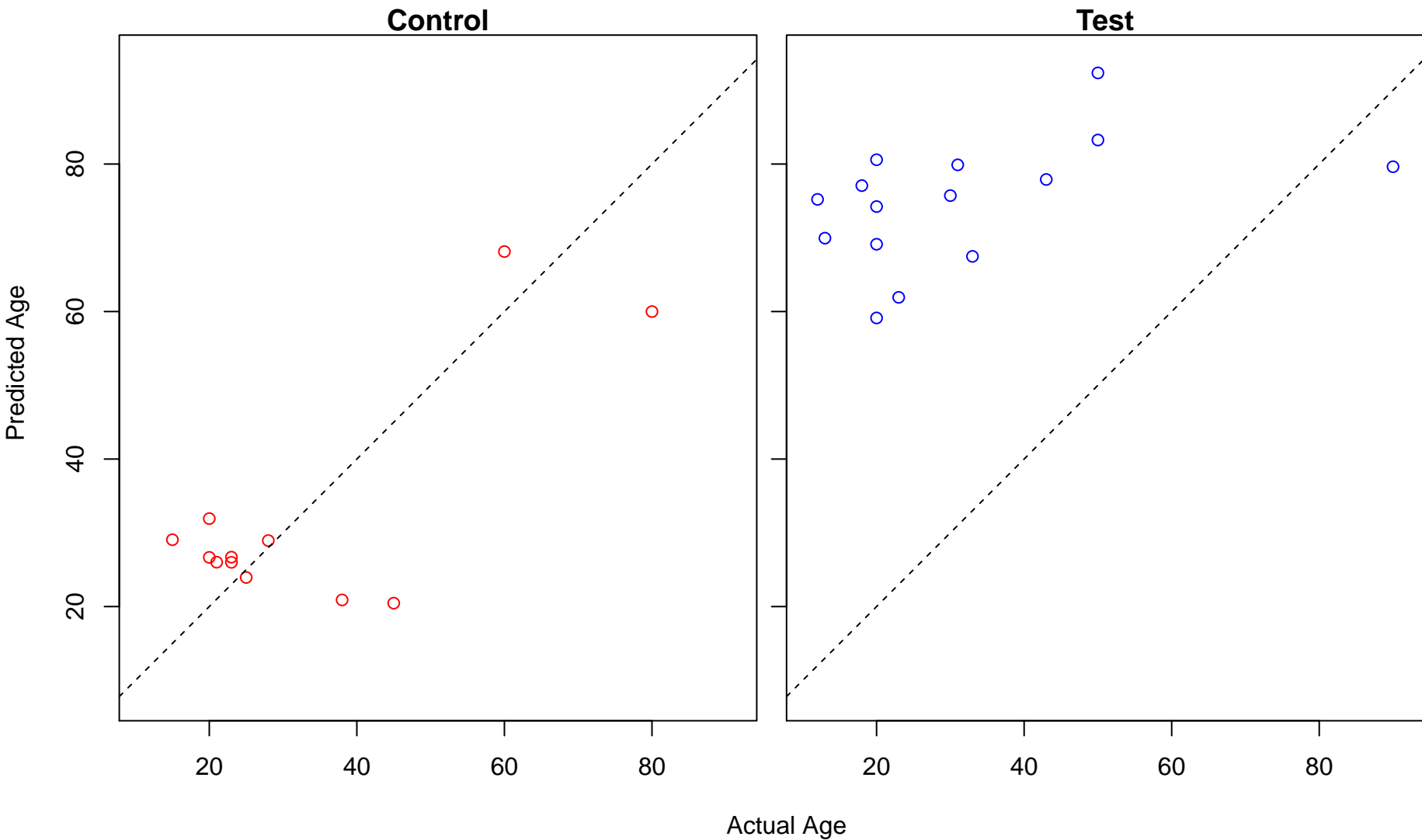
proline metabolic process (Score: 4.845137)



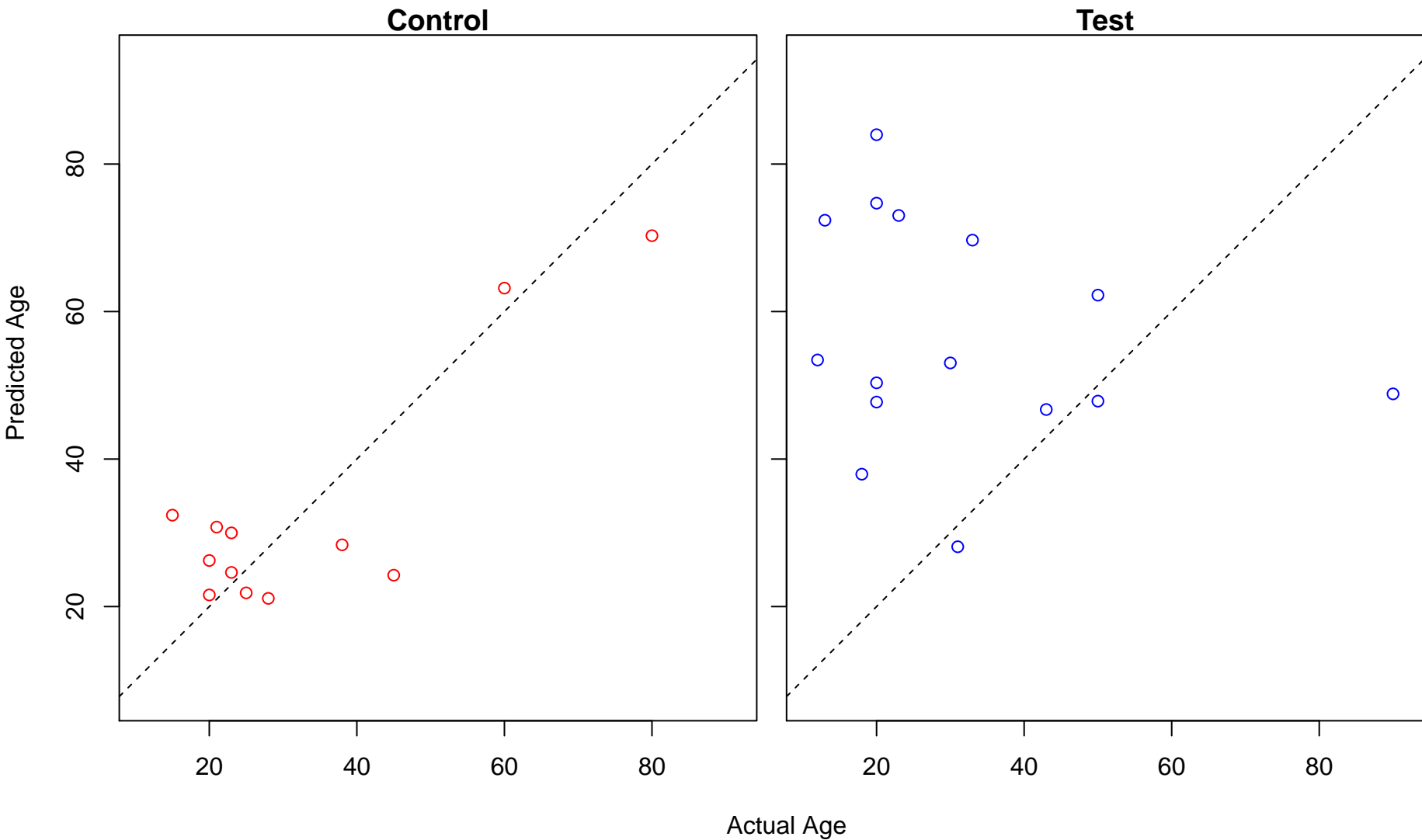
positive regulation of macrophage activation (Score: 4.844487)



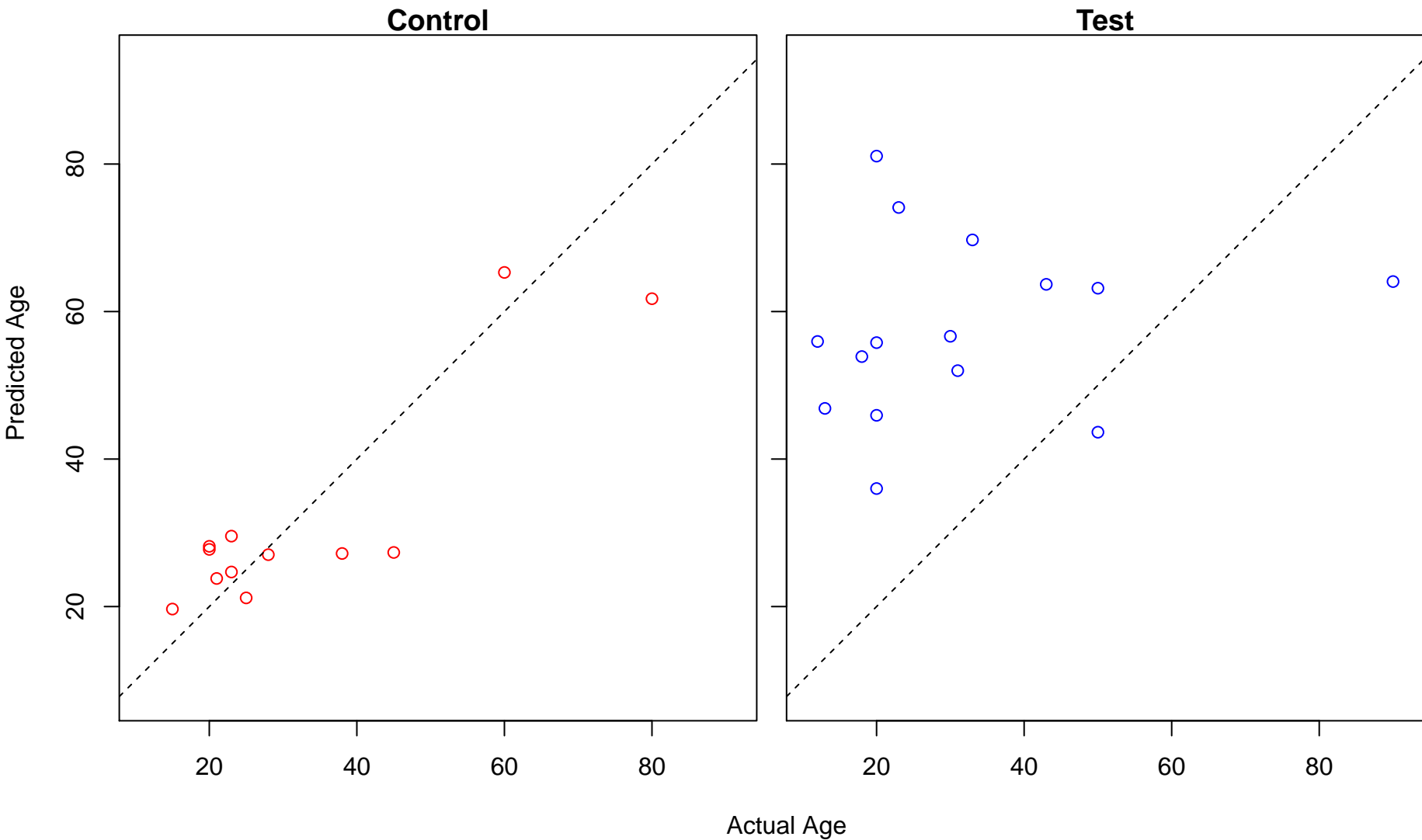
cardiac muscle contraction (Score: 4.844144)



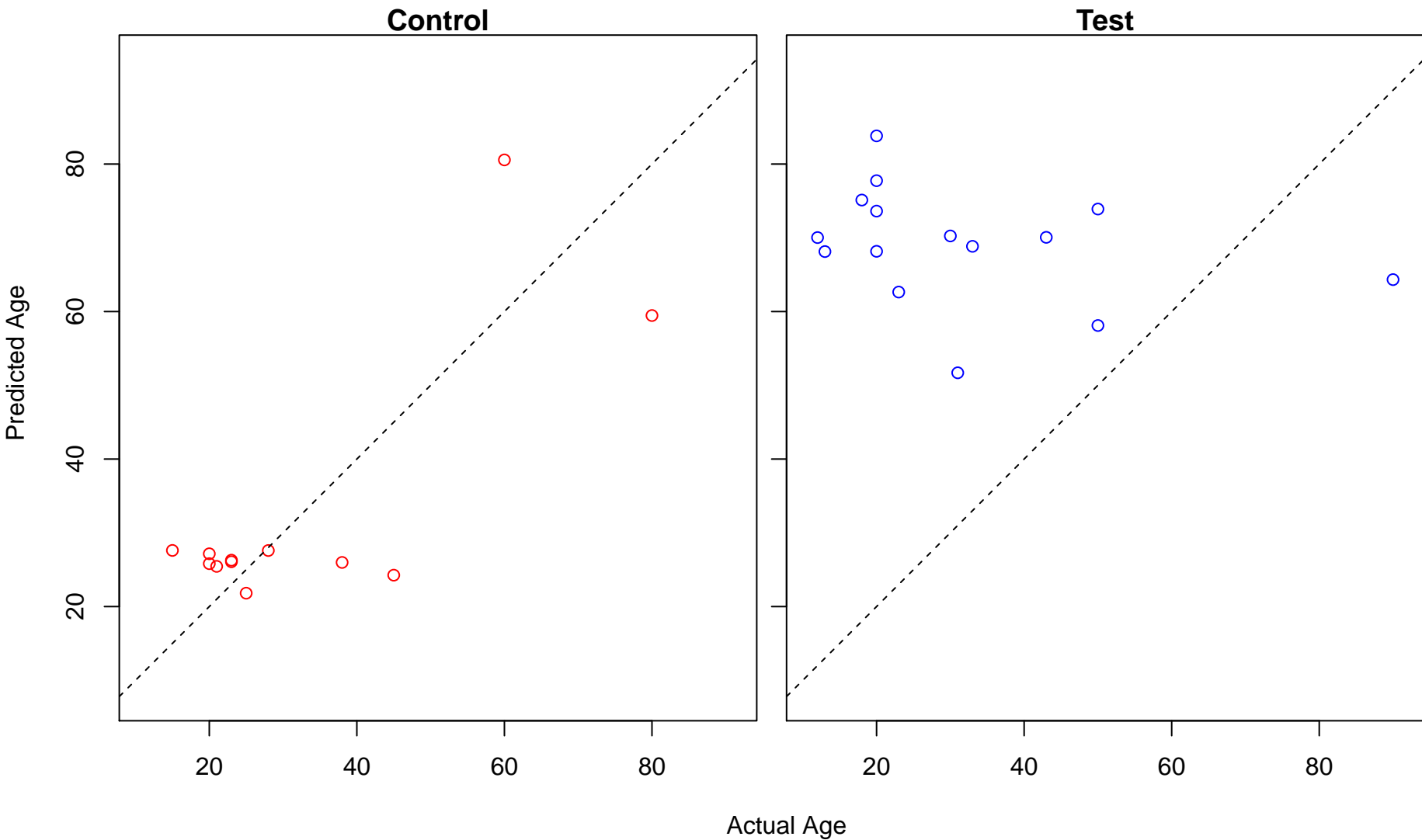
glucocorticoid metabolic process (Score: 4.843940)



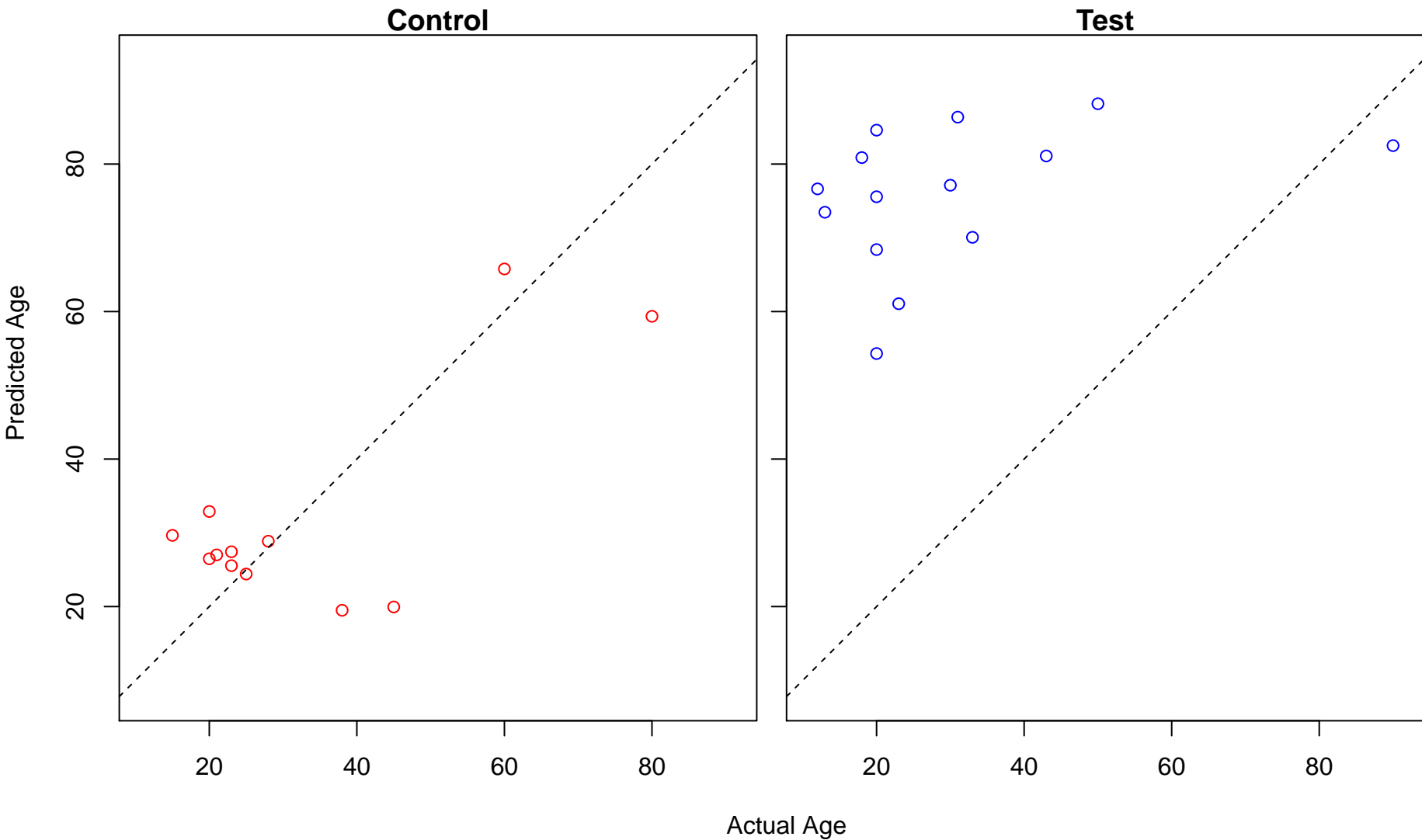
regulation of tyrosine phosphorylation of Stat5 protein (Score: 4.842194)



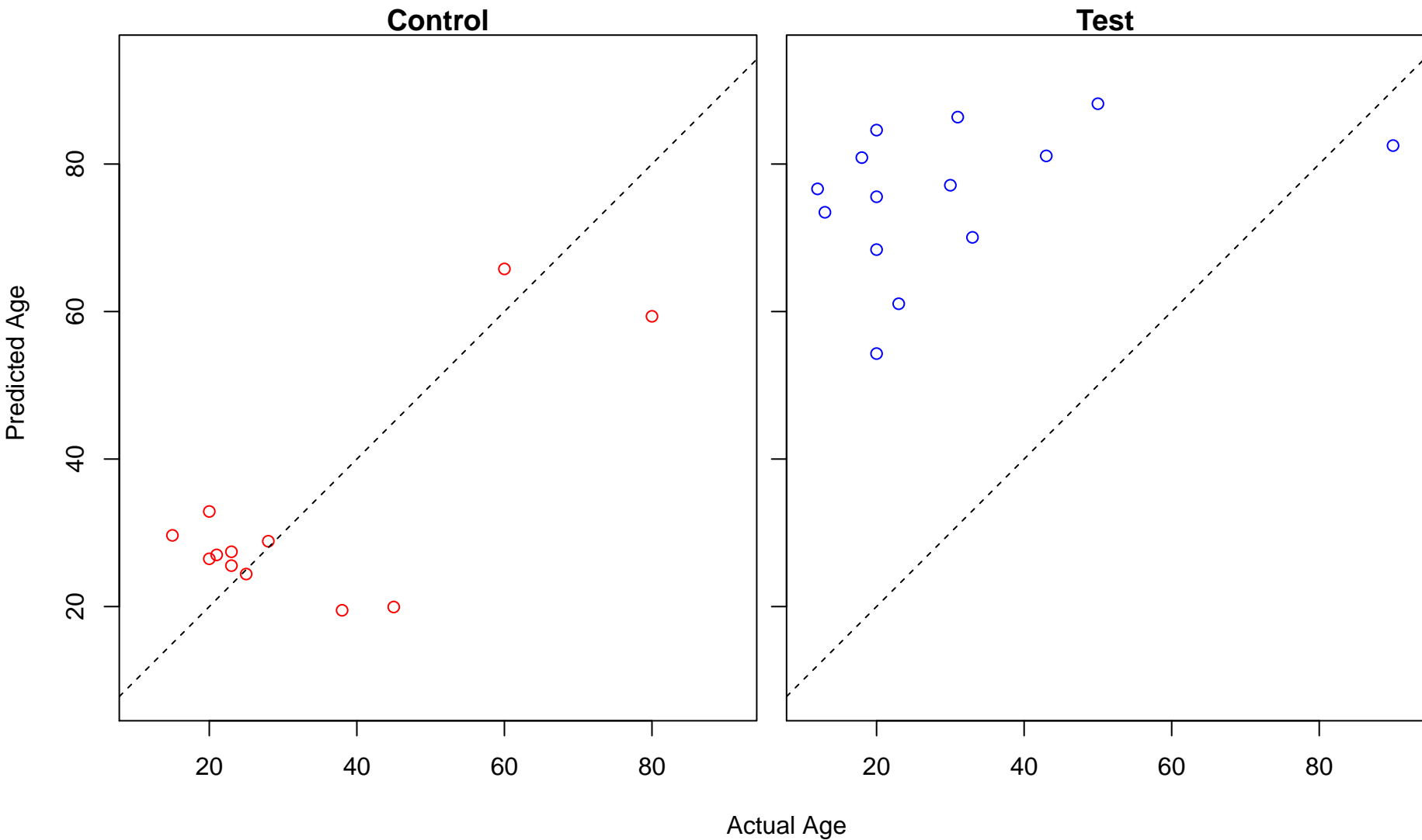
positive regulation of transcription elongation from RNA polymerase II promoter (Score: 4.842016)



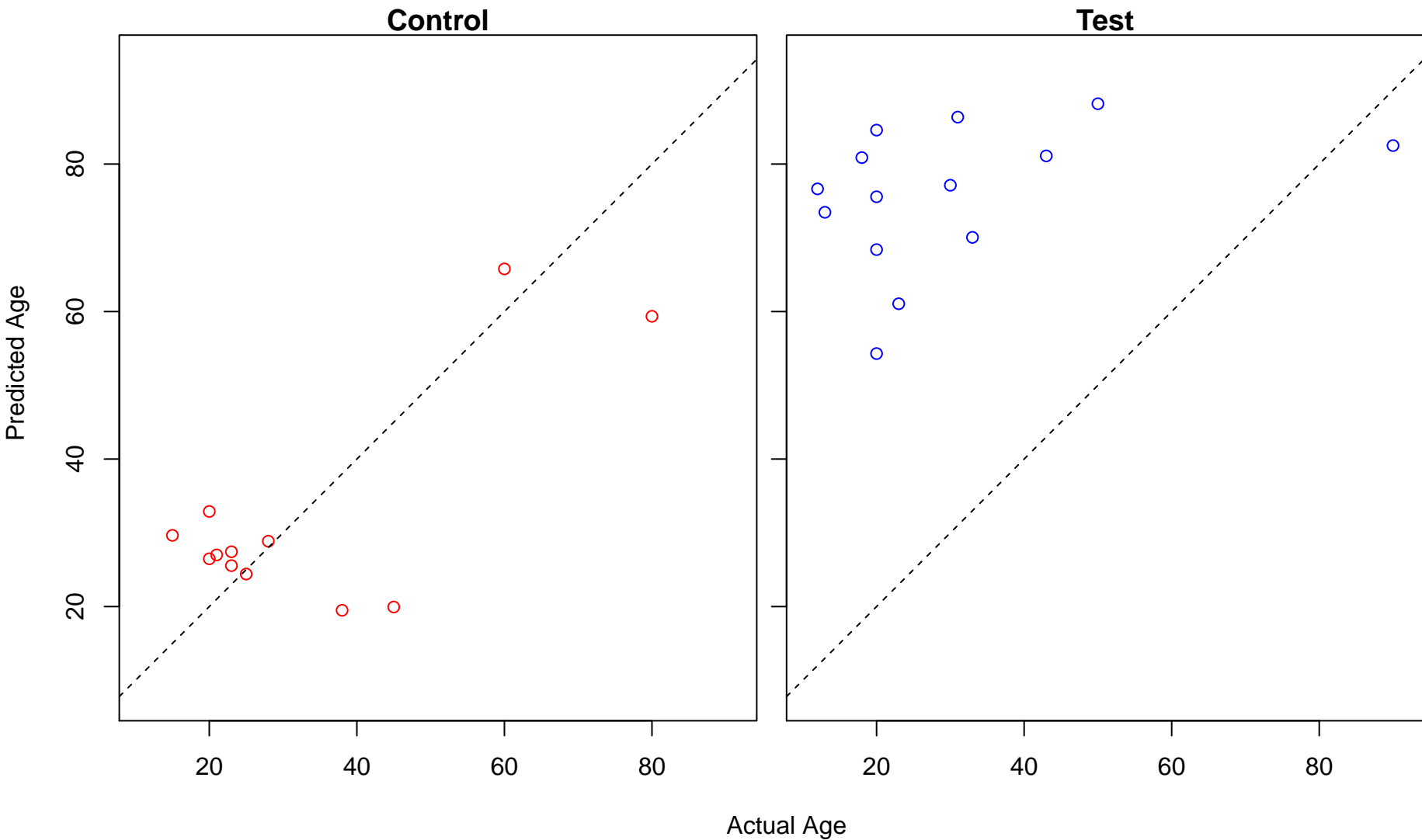
sodium ion export (Score: 4.841626)



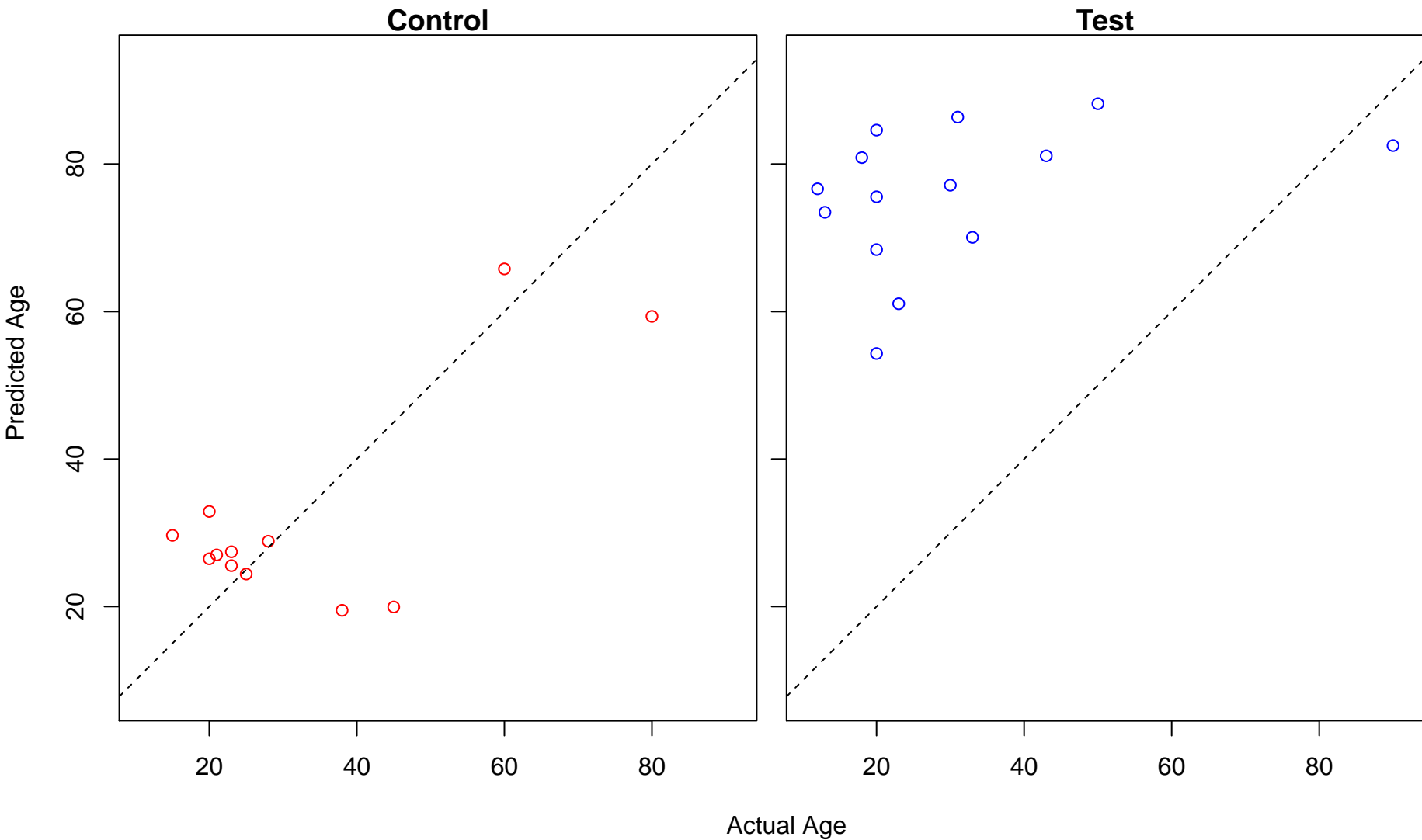
ATP hydrolysis coupled transmembrane transport (Score: 4.841067)



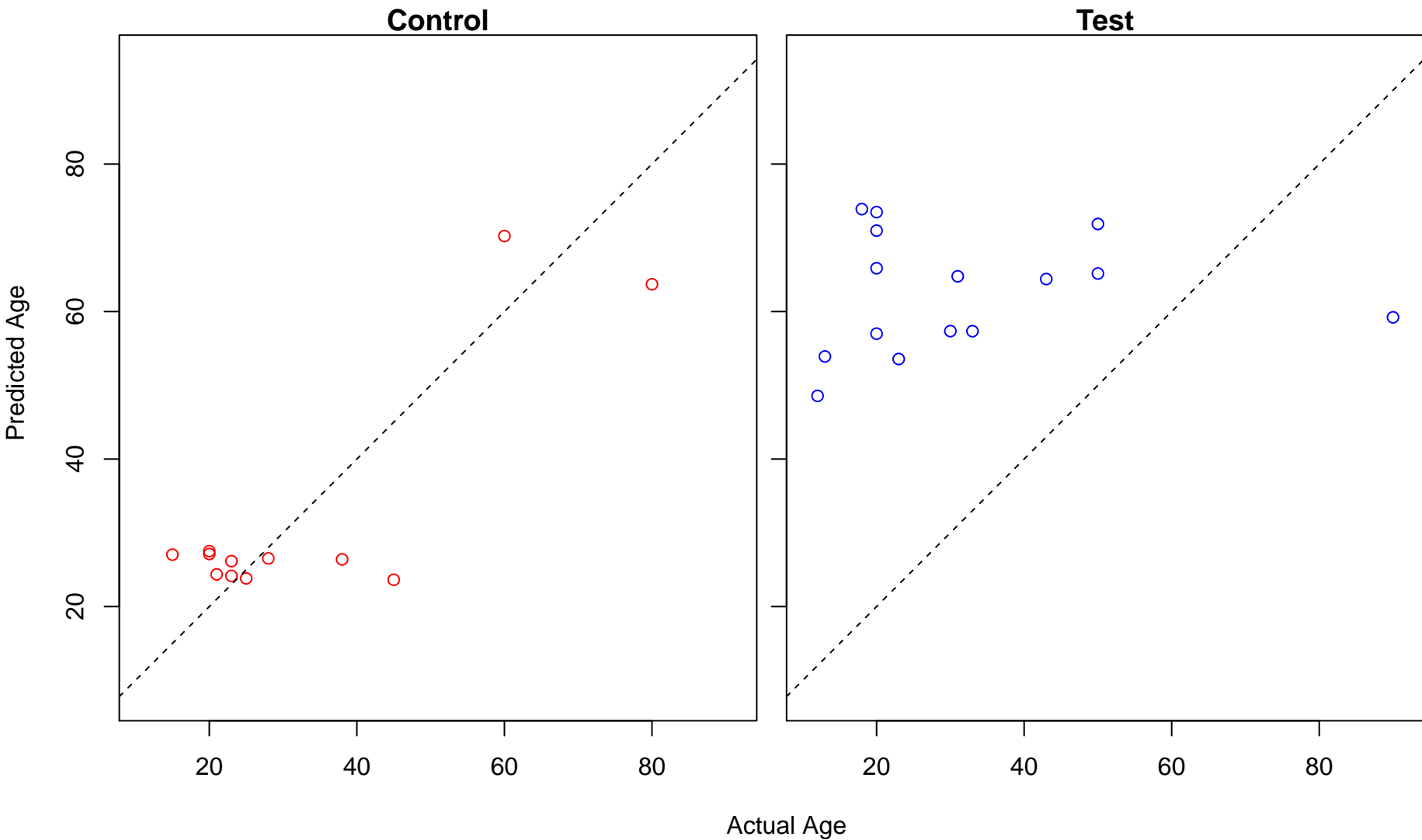
sodium ion export from cell (Score: 4.841062)



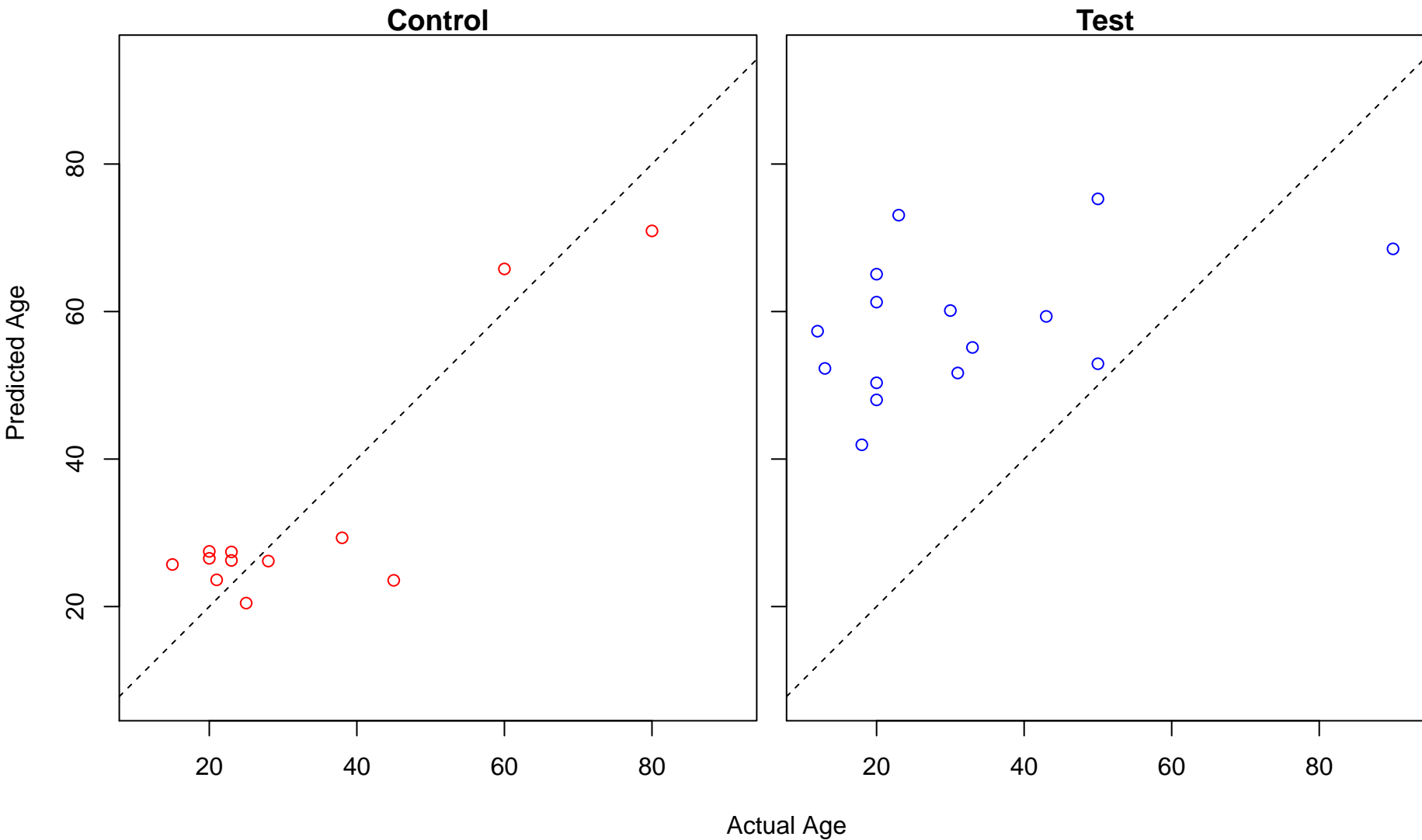
establishment or maintenance of transmembrane electrochemical gradient (Score: 4.840640)



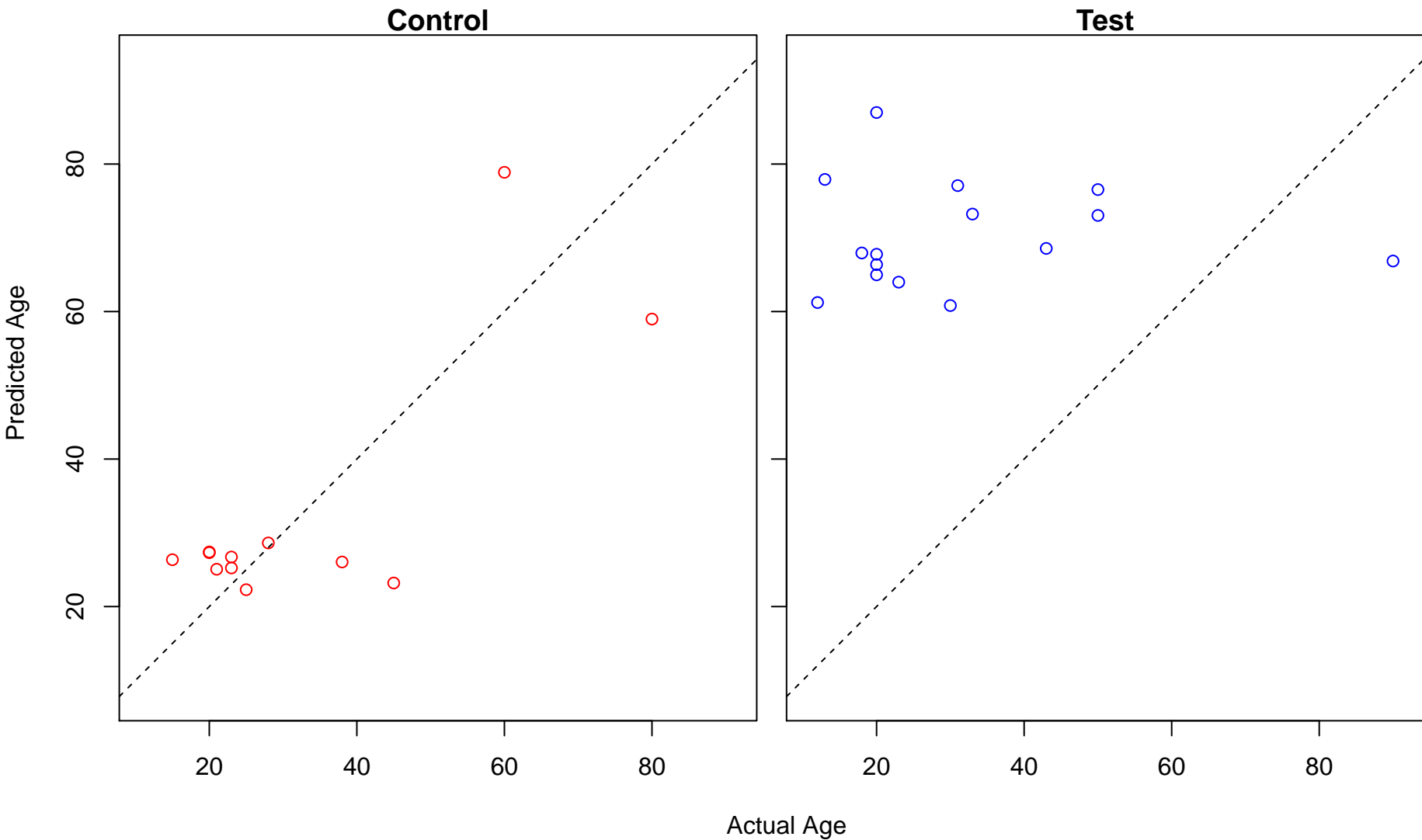
positive regulation of muscle cell differentiation (Score: 4.839291)



DNA synthesis involved in DNA repair (Score: 4.839124)

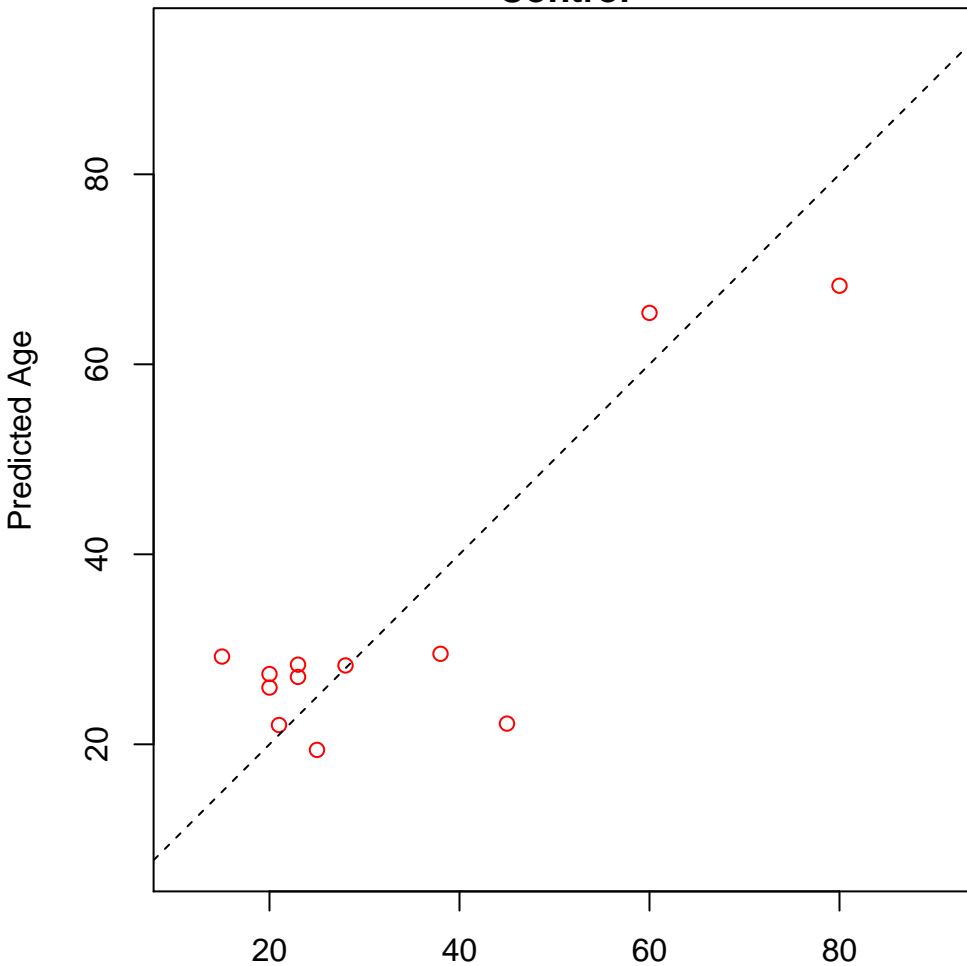


regulation of system process (Score: 4.837970)

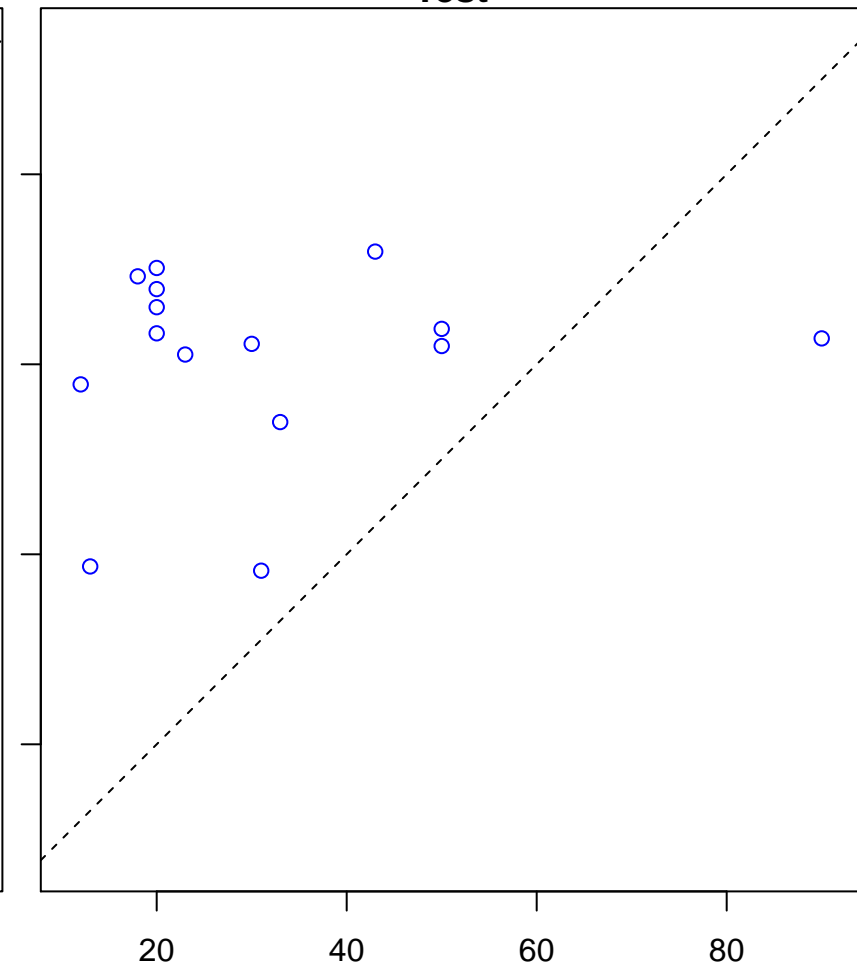


monocarboxylic acid catabolic process (Score: 4.837578)

Control

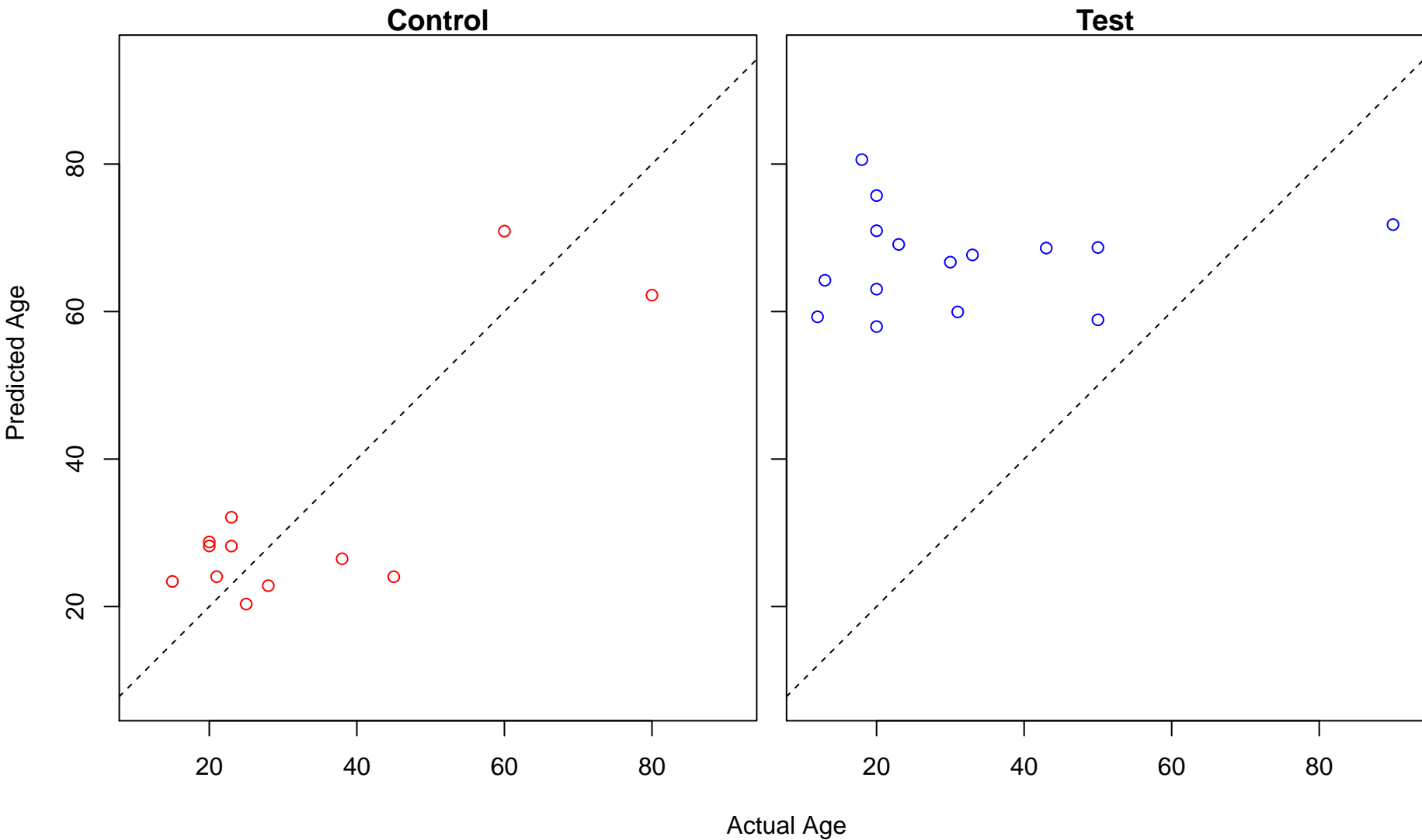


Test

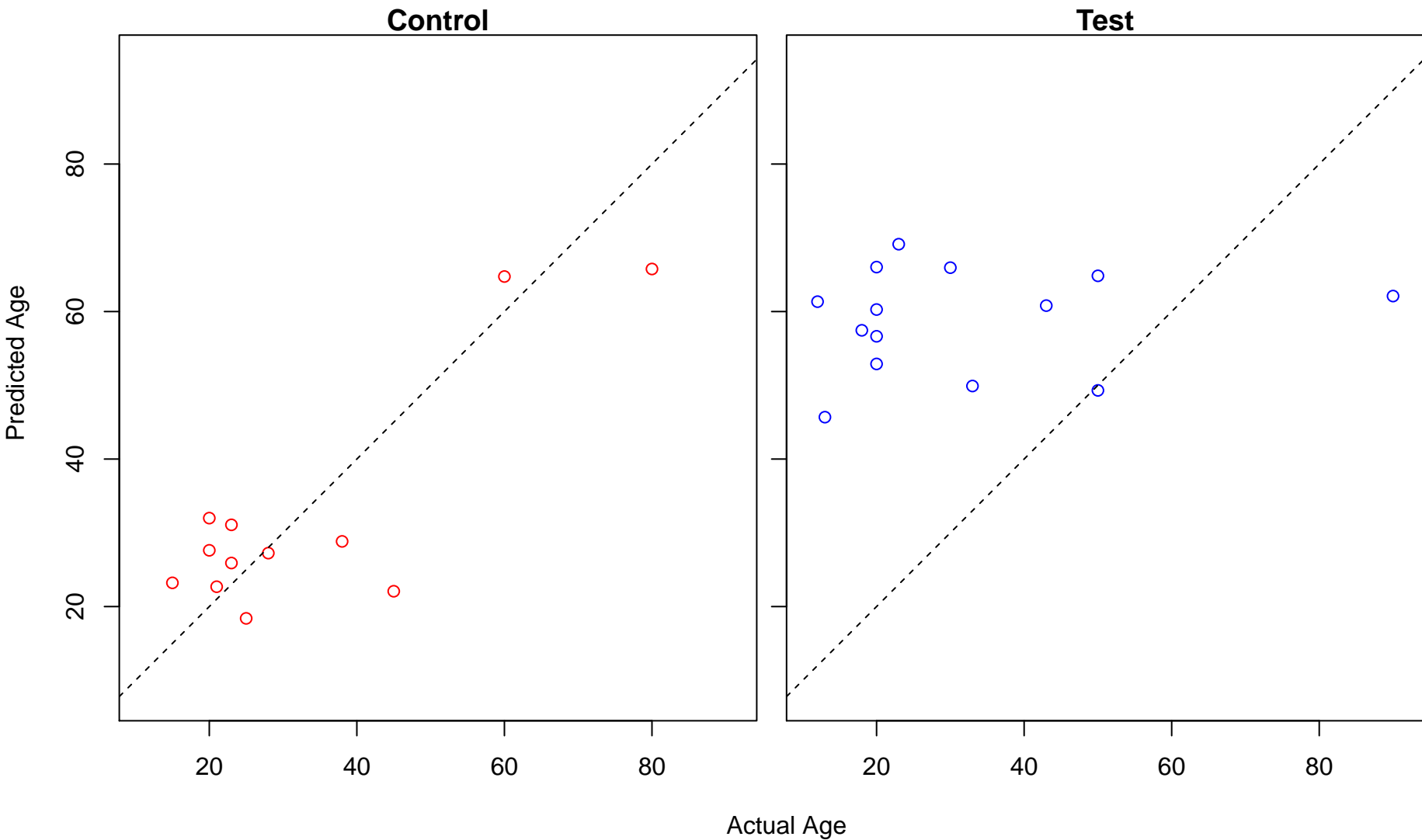


Actual Age

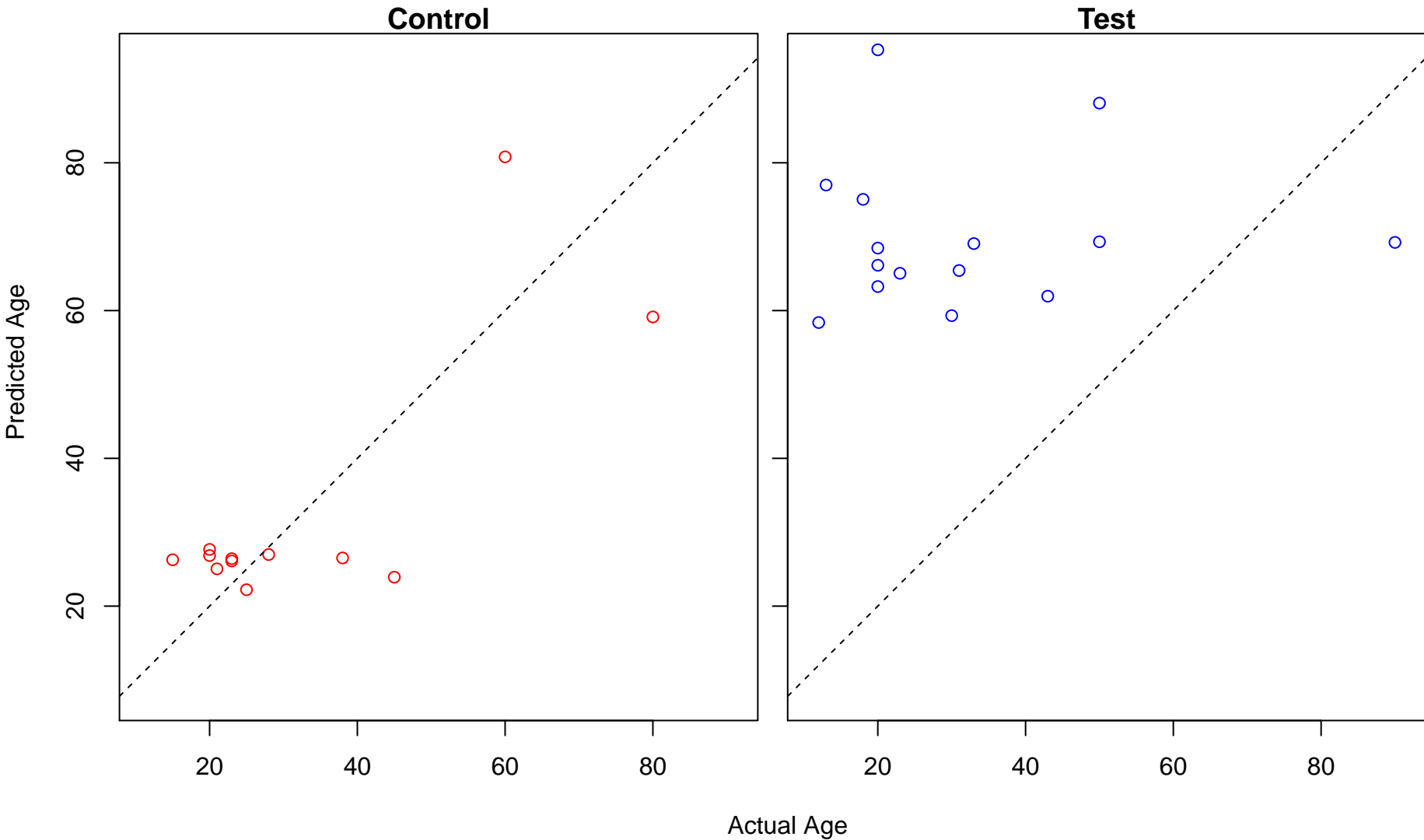
protein localization to chromosome, centromeric region (Score: 4.837014)



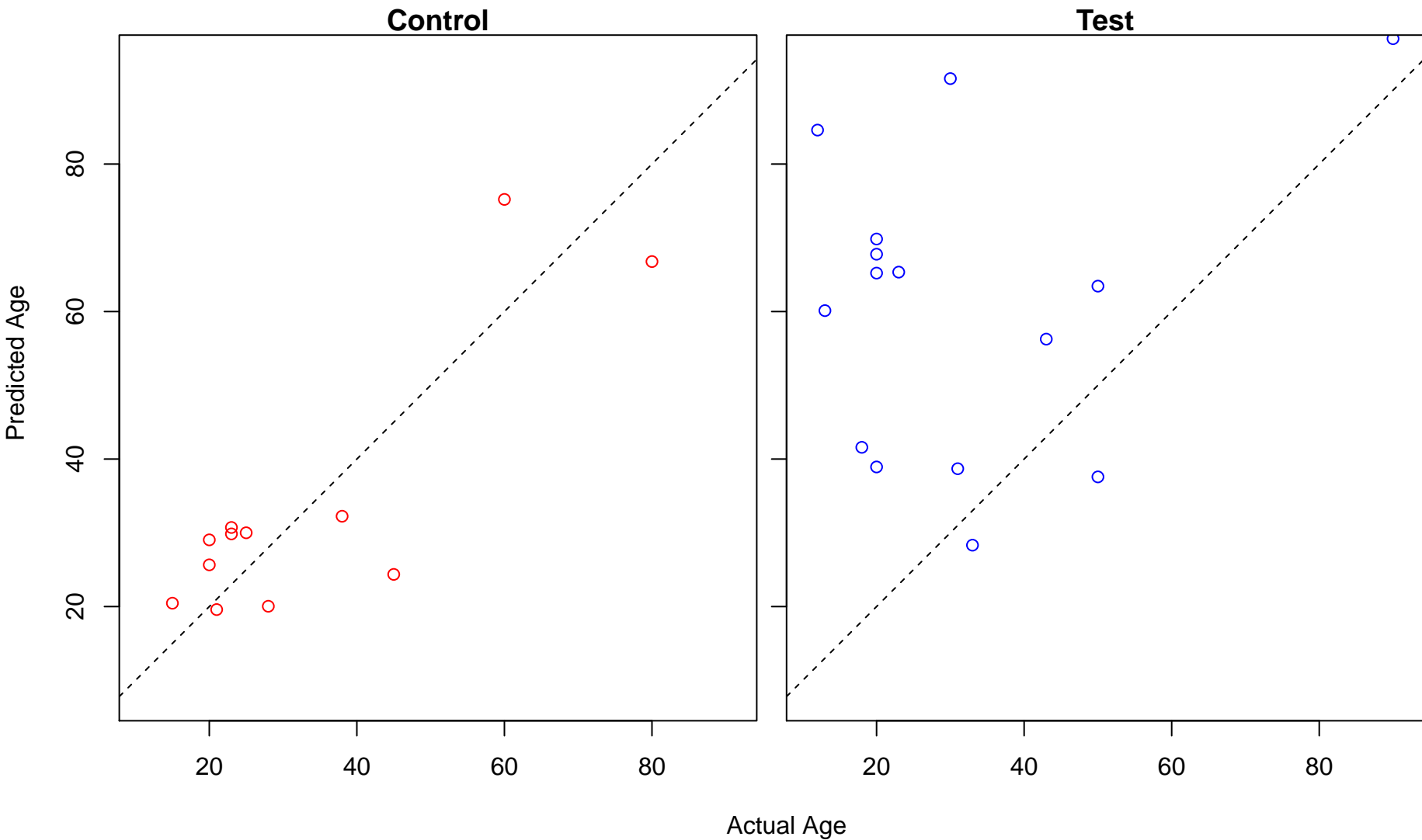
glycerol metabolic process (Score: 4.834837)



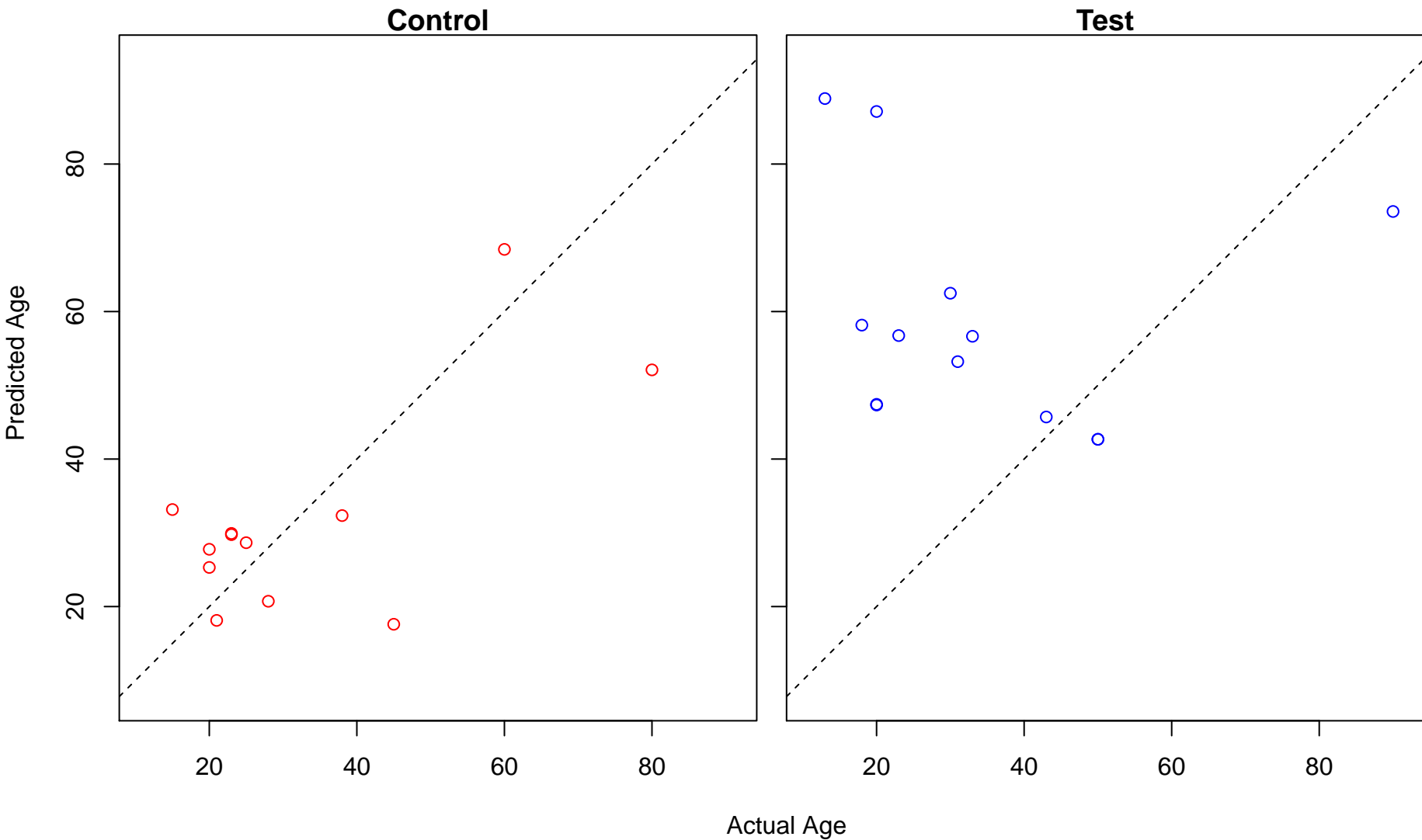
regulation of response to cytokine stimulus (Score: 4.831243)



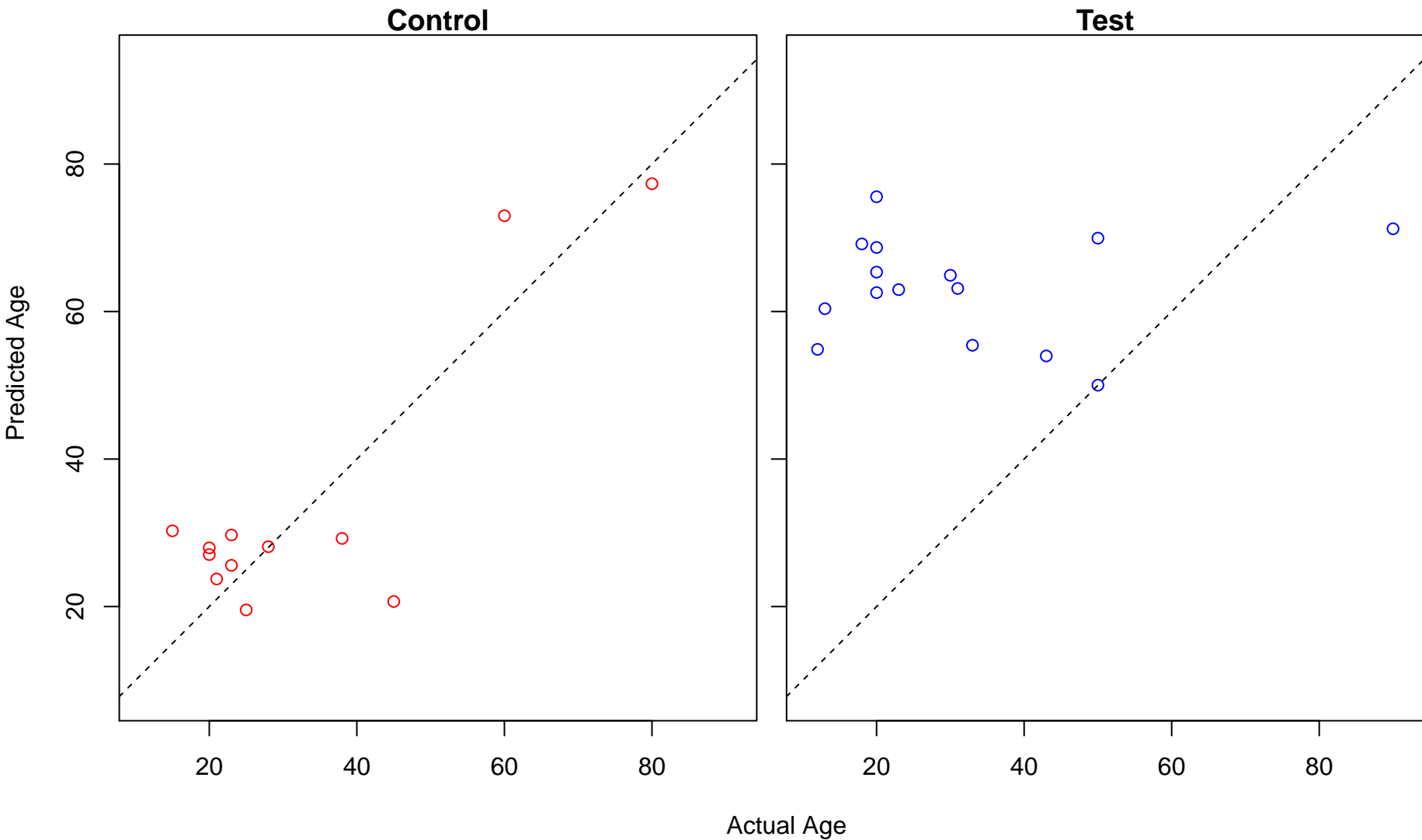
detection of mechanical stimulus involved in sensory perception (Score: 4.831018)



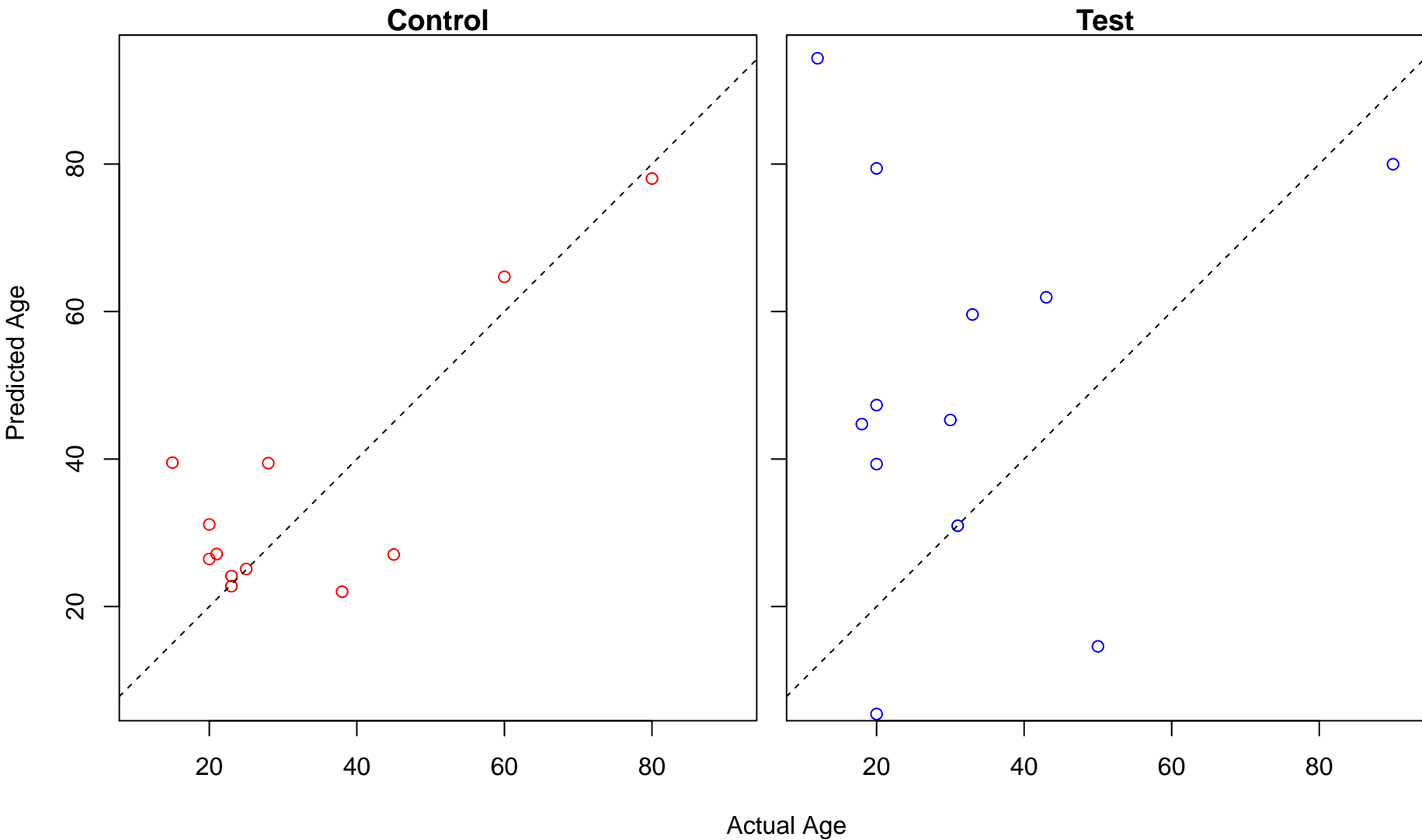
negative regulation of osteoclast differentiation (Score: 4.830288)



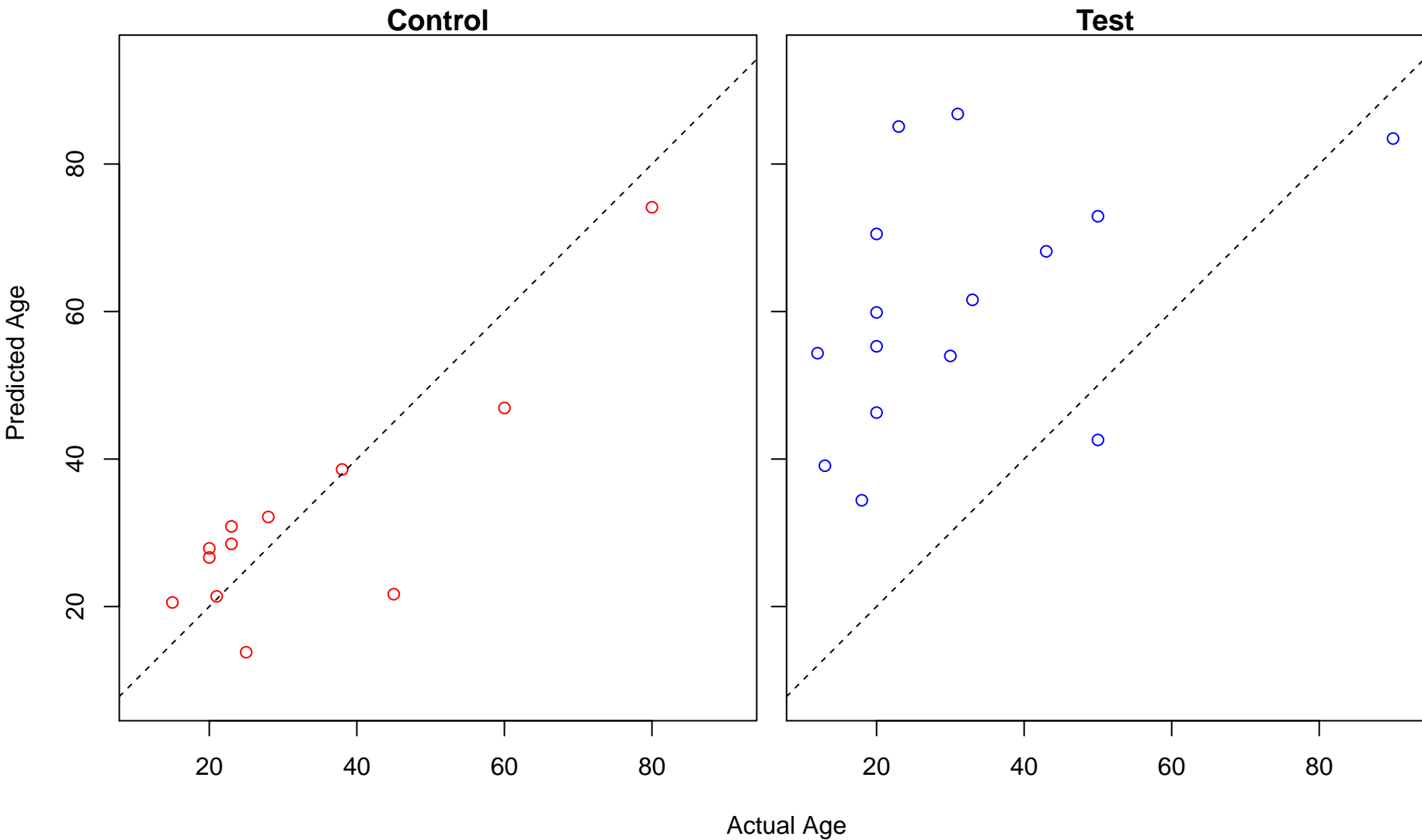
positive regulation of nucleocytoplasmic transport (Score: 4.830025)



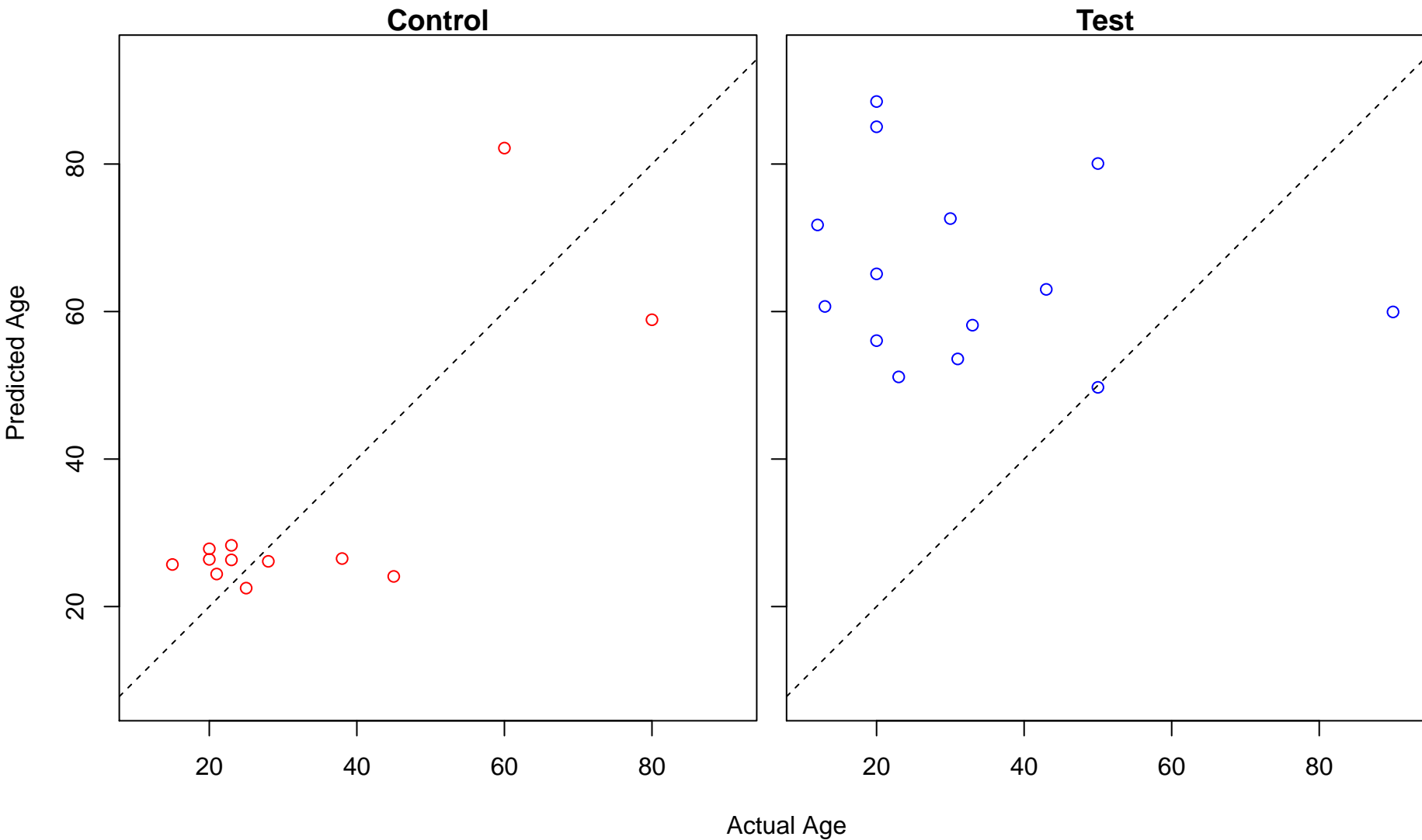
tetrahydrofolate metabolic process (Score: 4.829930)



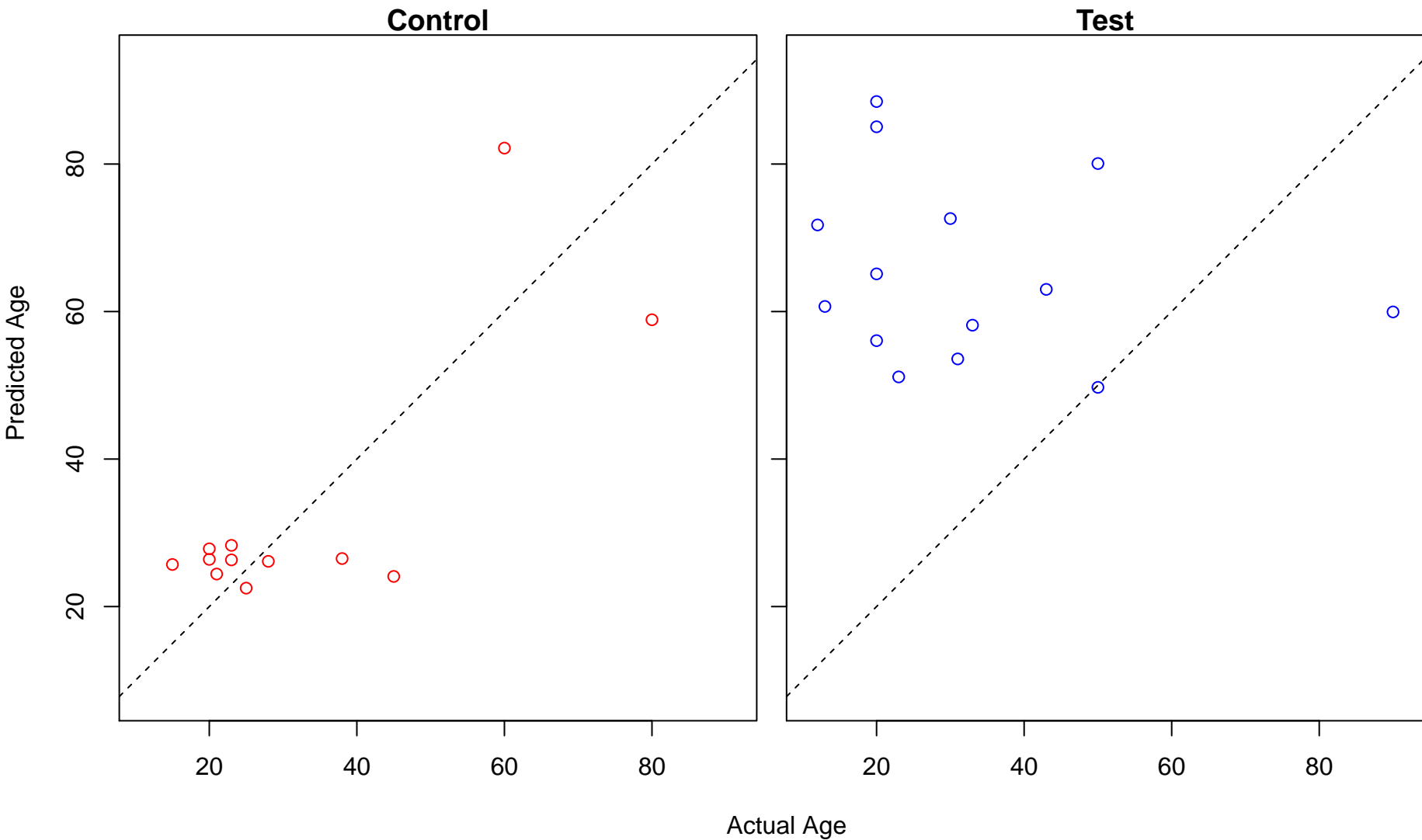
cilium movement (Score: 4.828696)



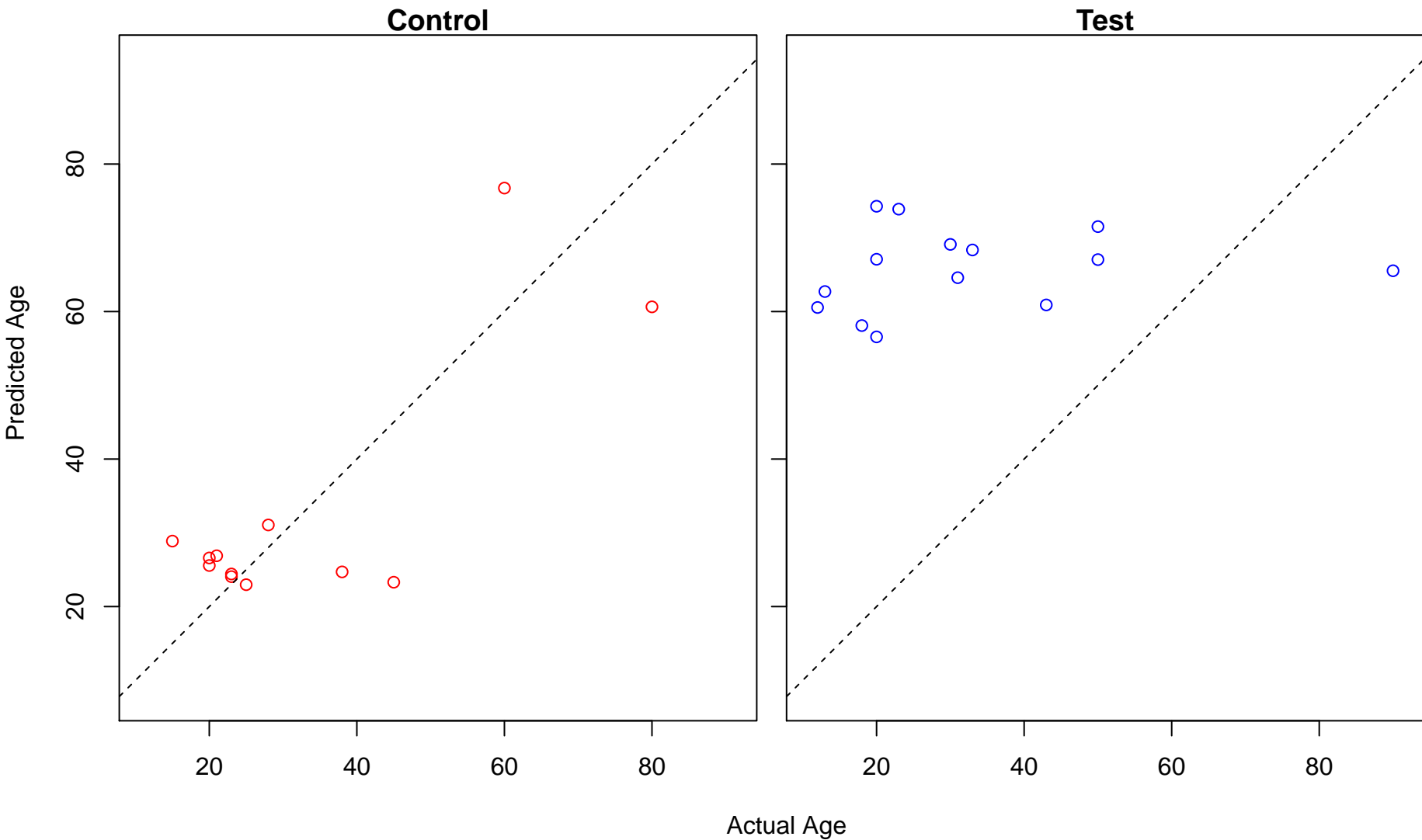
peptide secretion (Score: 4.828368)



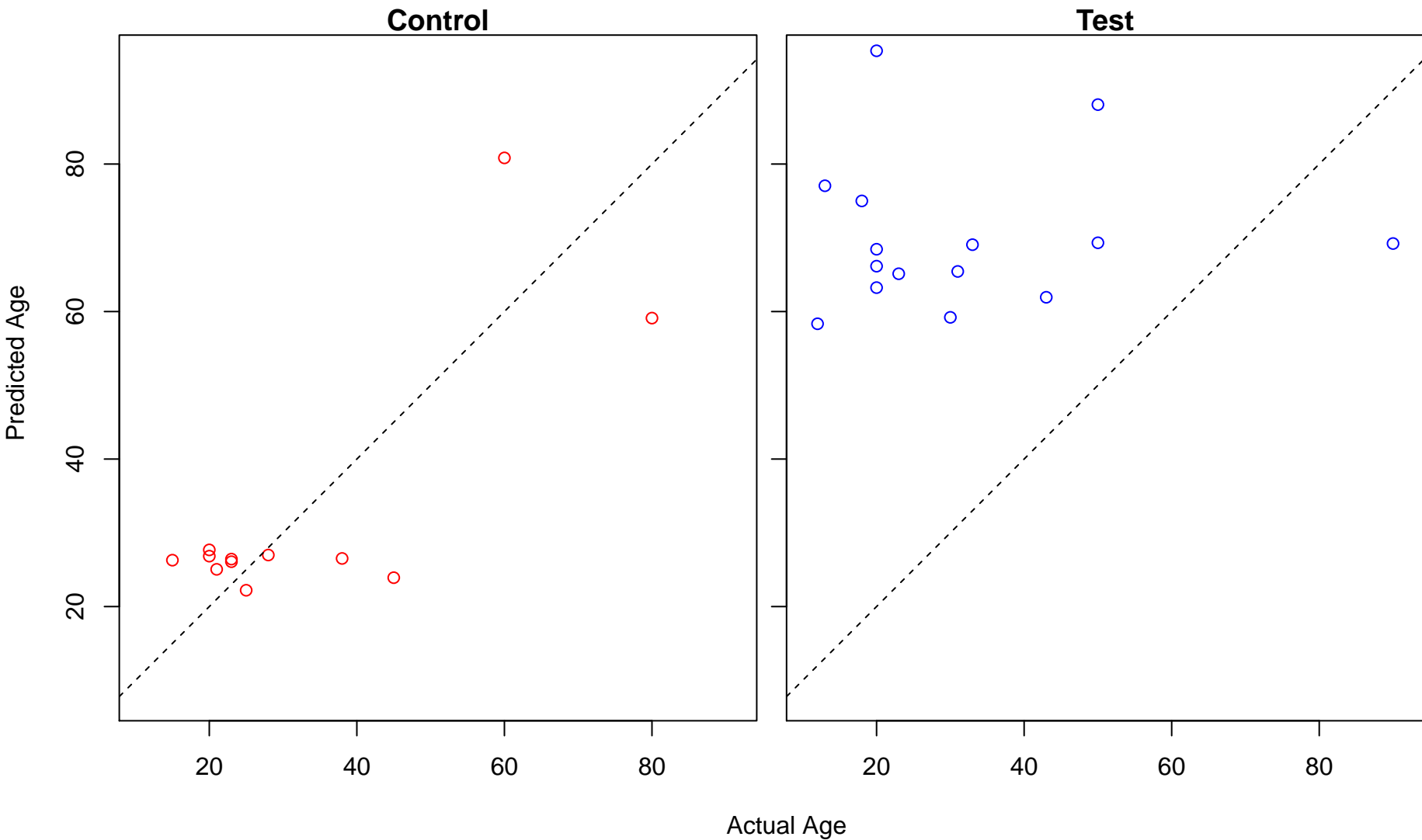
peptide hormone secretion (Score: 4.828368)



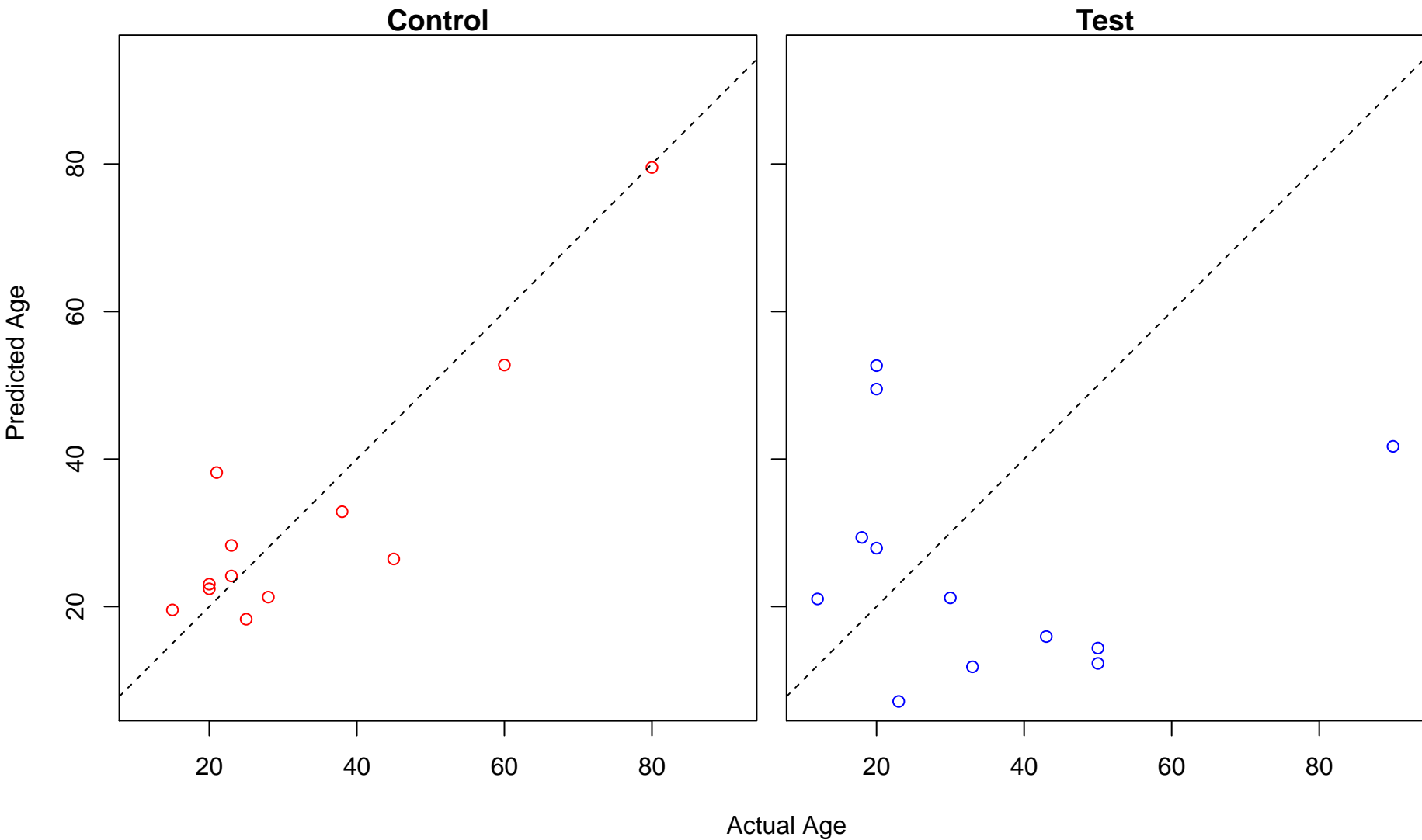
regulation of metalloenzyme activity (Score: 4.827126)



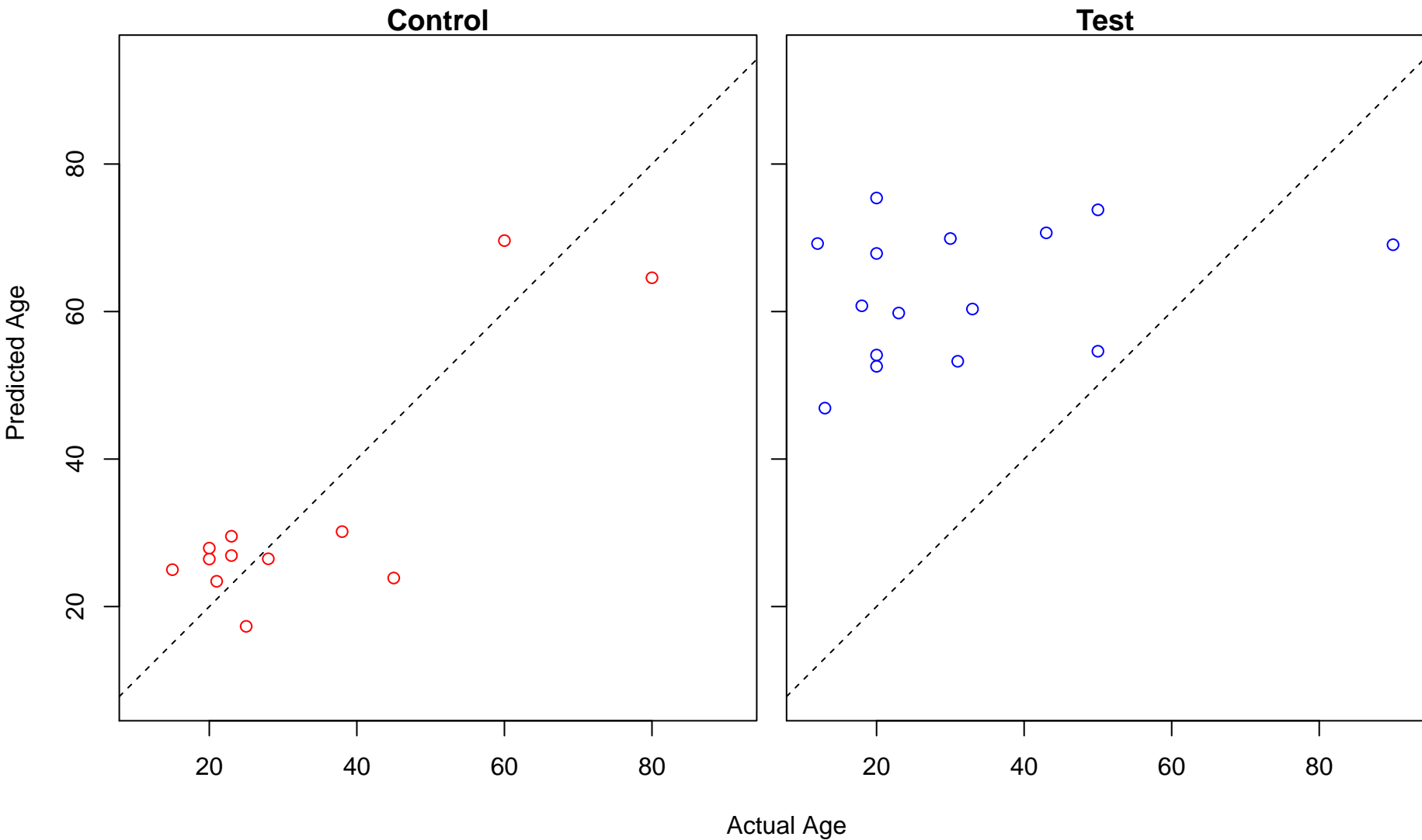
regulation of cytokine-mediated signaling pathway (Score: 4.826182)



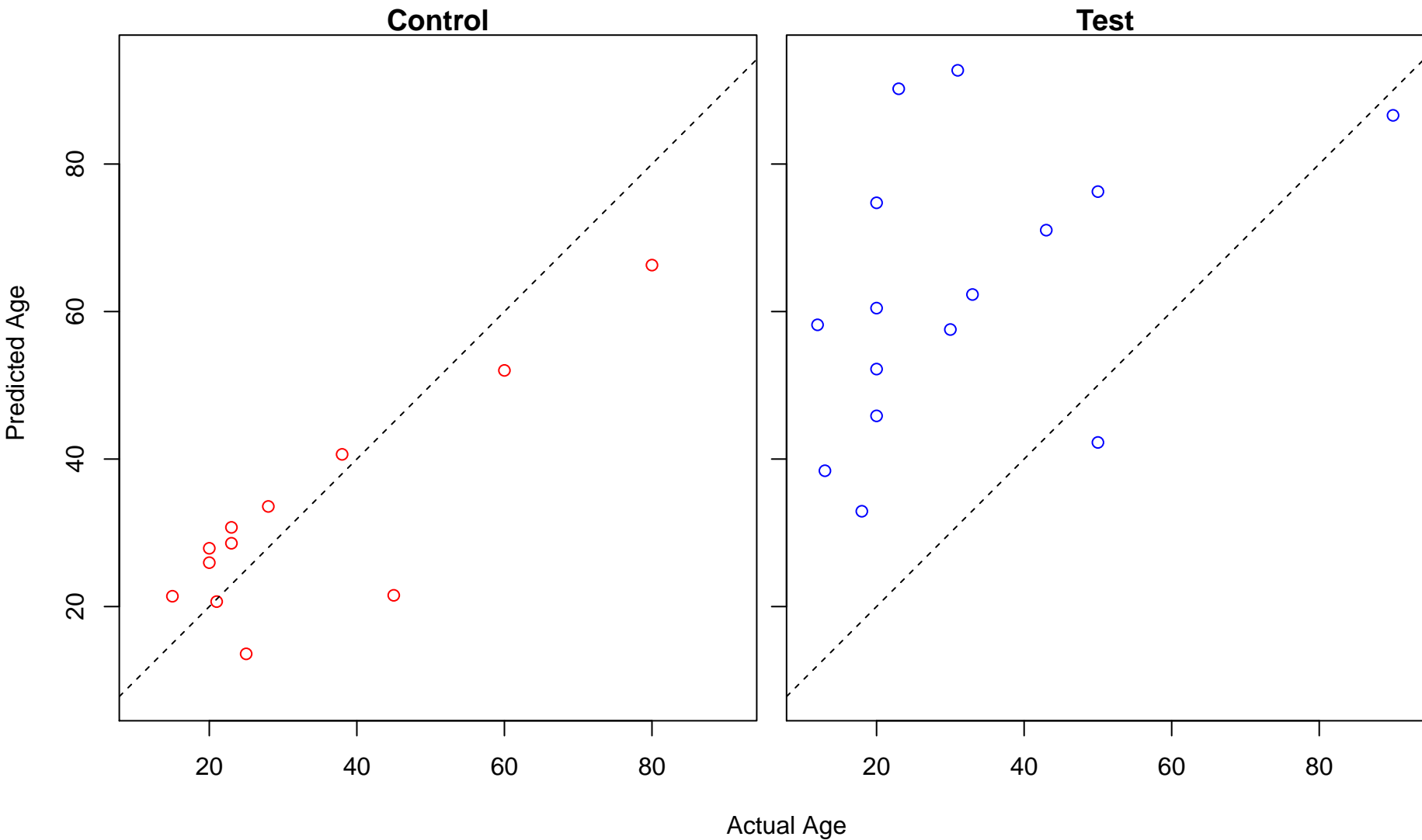
mRNA modification (Score: 4.82228)



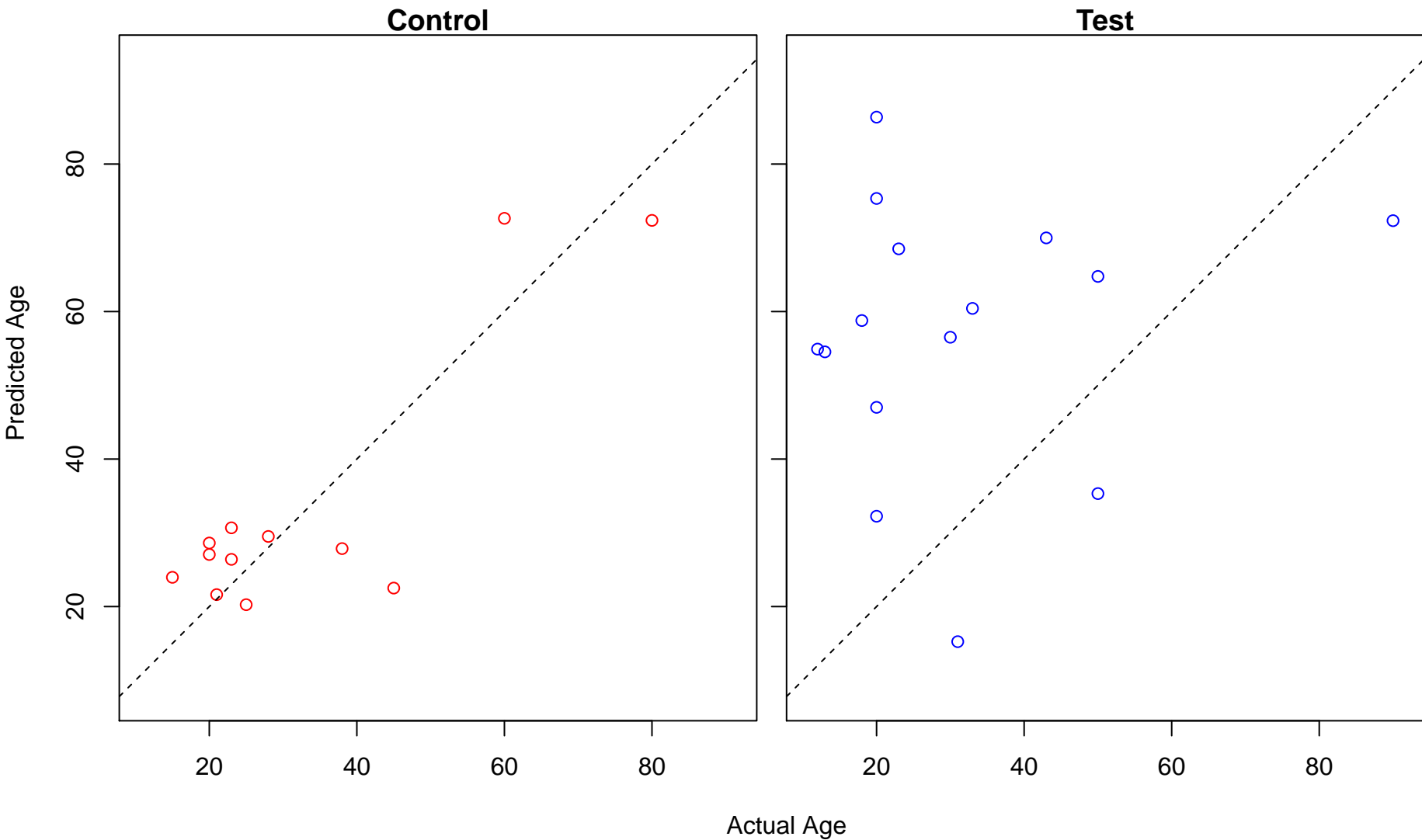
zinc II ion transmembrane transport (Score: 4.821770)



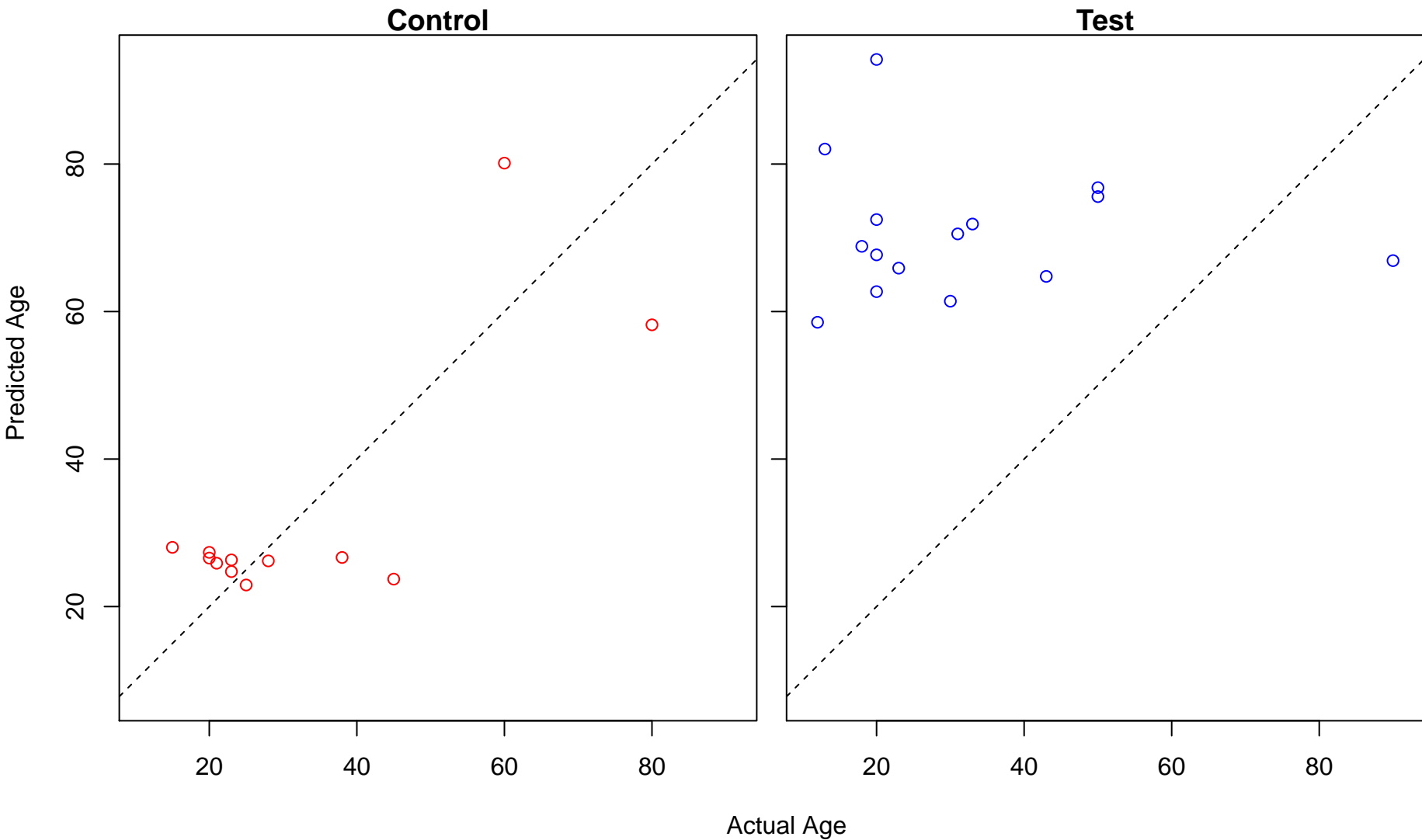
outer dynein arm assembly (Score: 4.820148)



positive regulation of interferon-gamma biosynthetic process (Score: 4.819809)

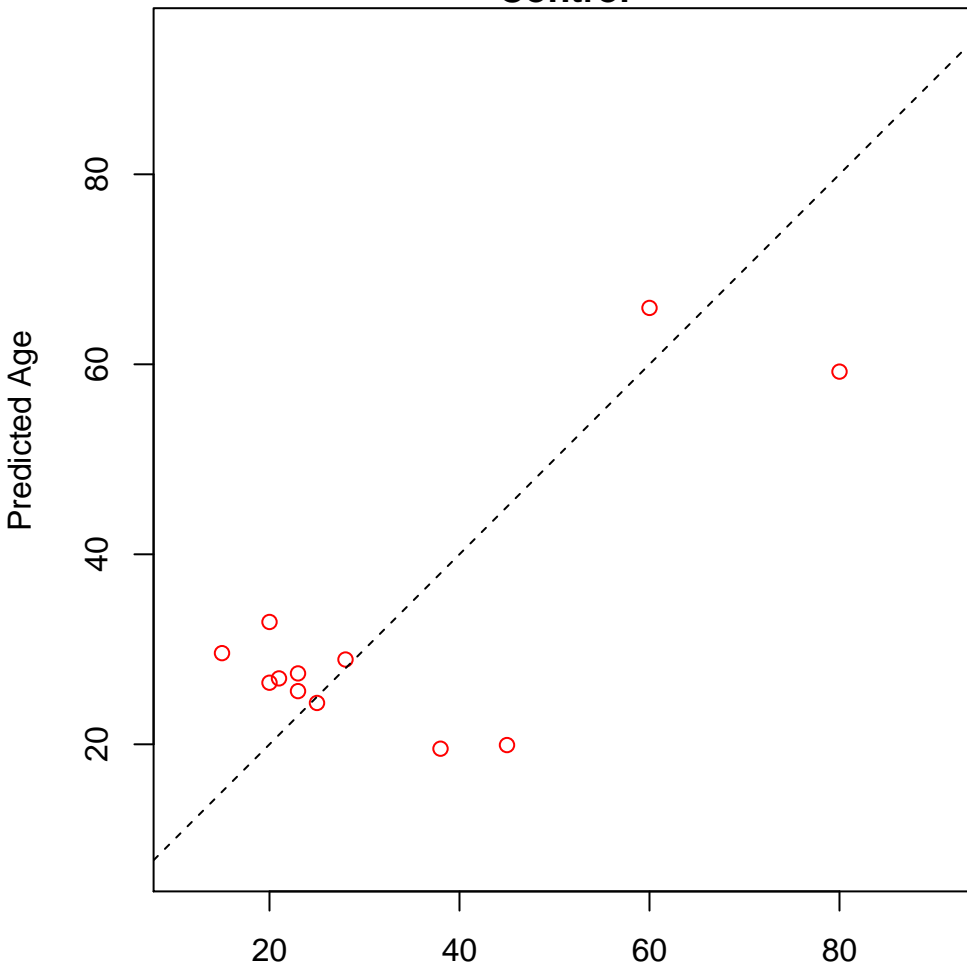


carbohydrate catabolic process (Score: 4.819705)

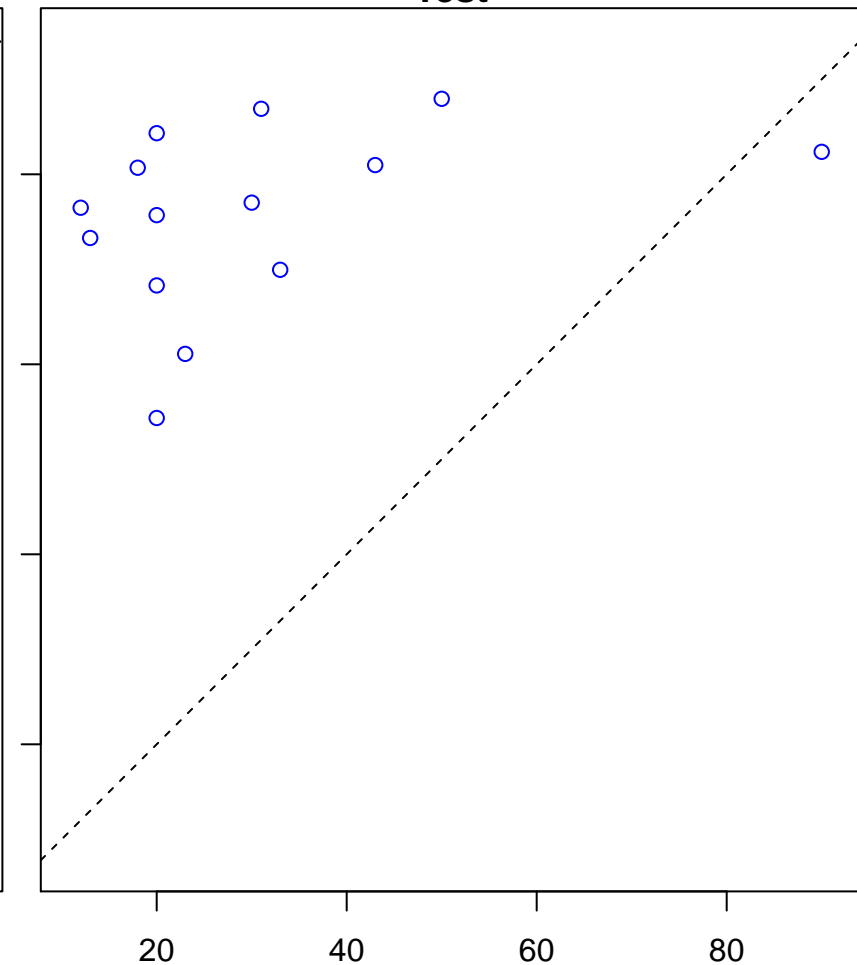


cellular potassium ion homeostasis (Score: 4.819481)

Control

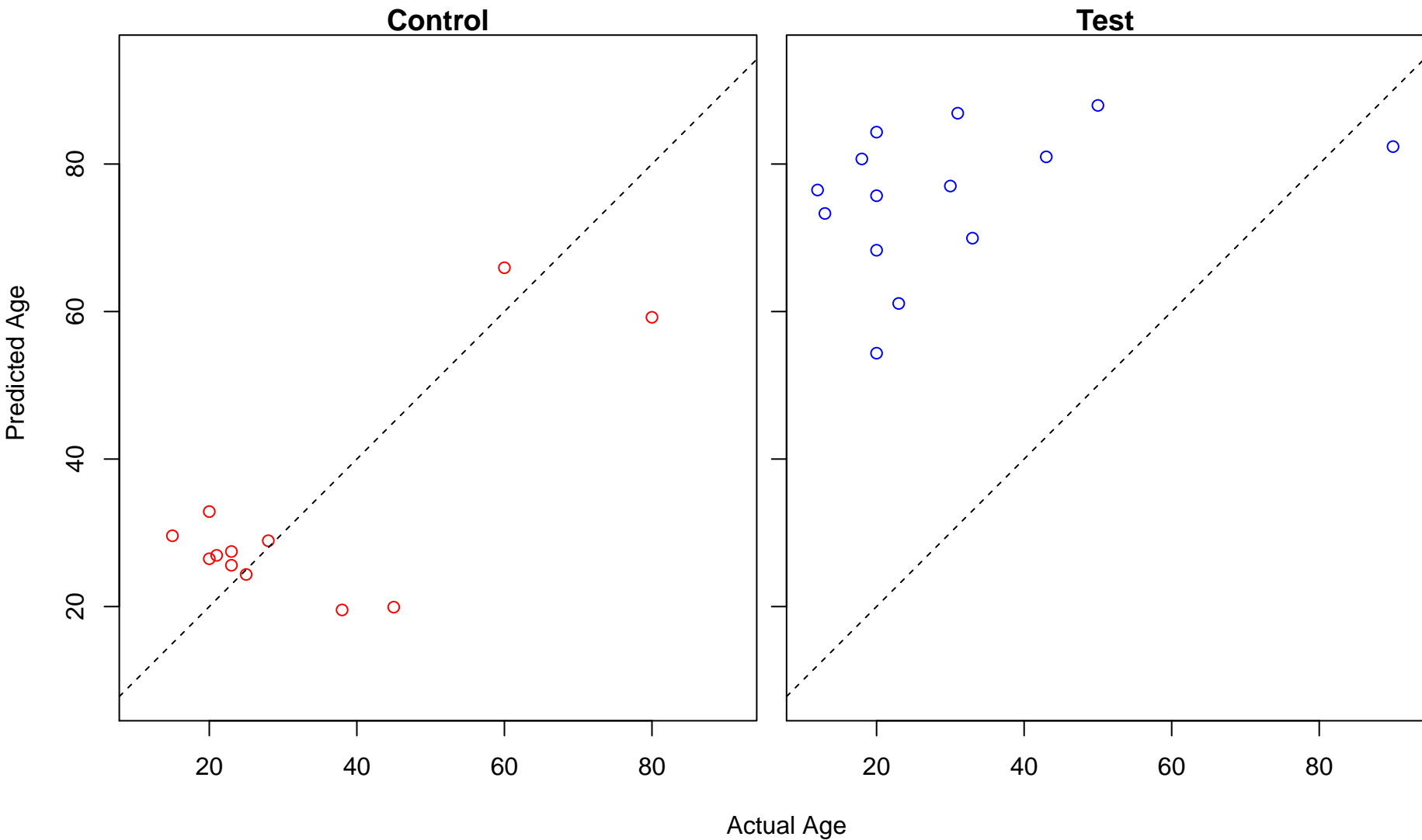


Test



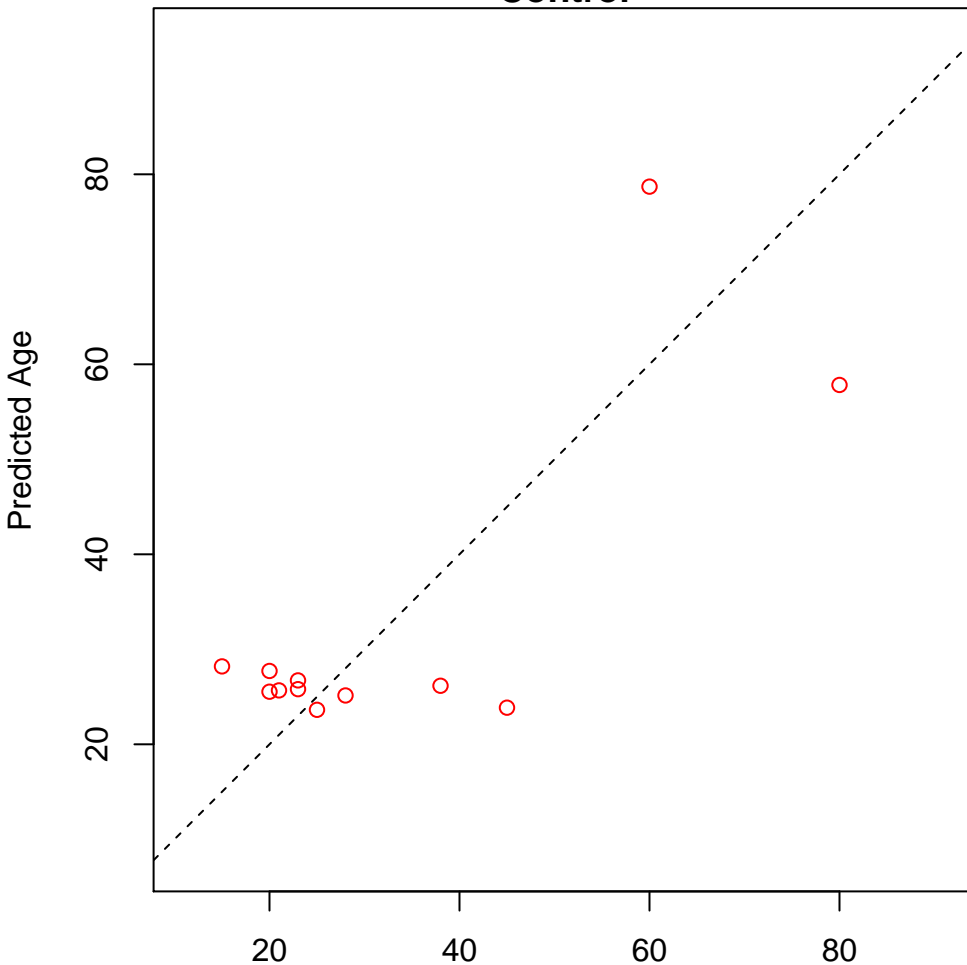
Actual Age

potassium ion homeostasis (Score: 4.818895)

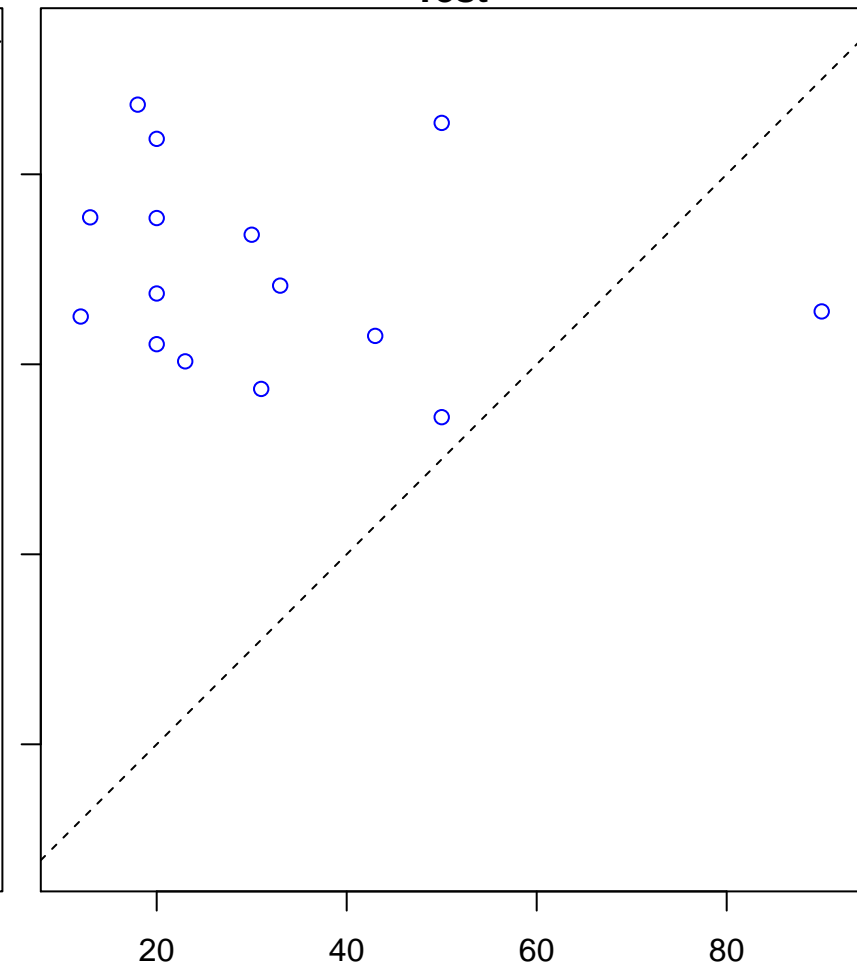


establishment of epithelial cell polarity (Score: 4.817612)

Control

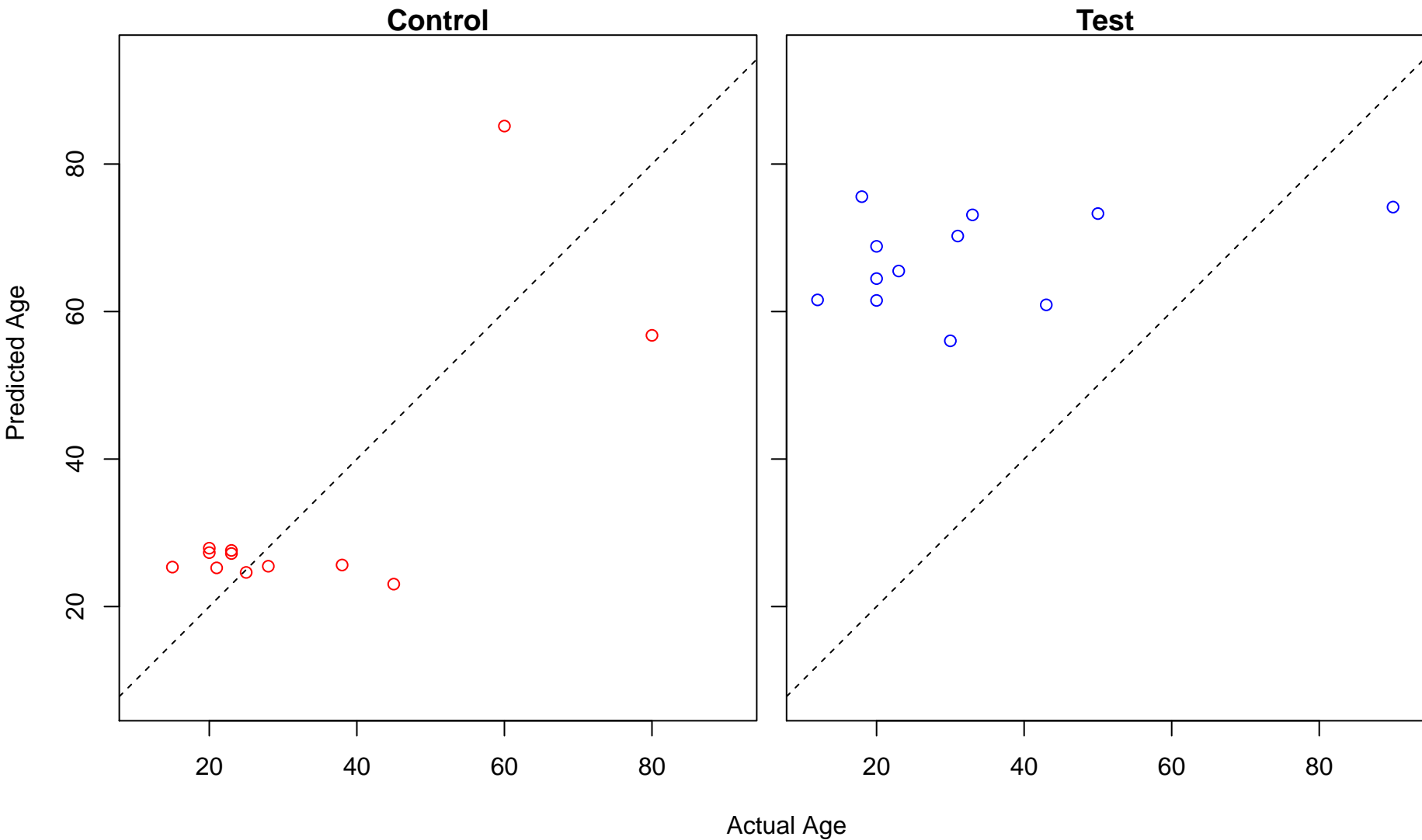


Test



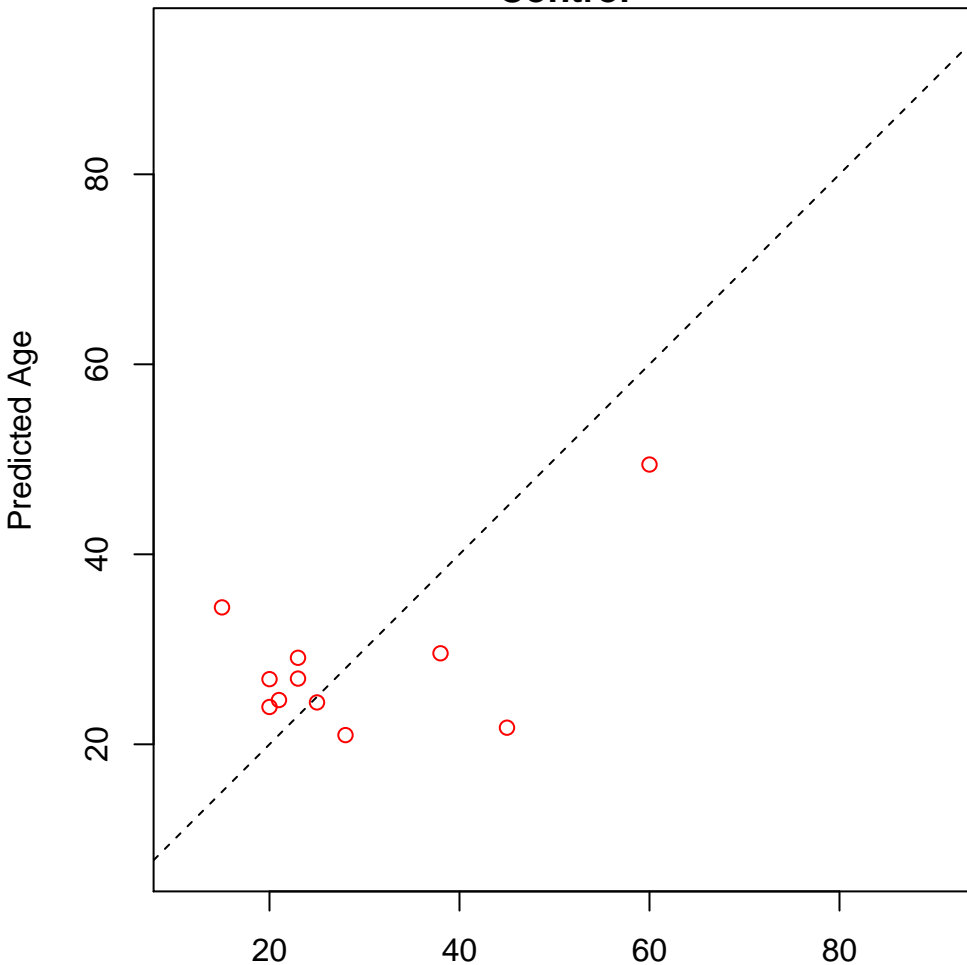
Actual Age

cellular response to epidermal growth factor stimulus (Score: 4.815878)

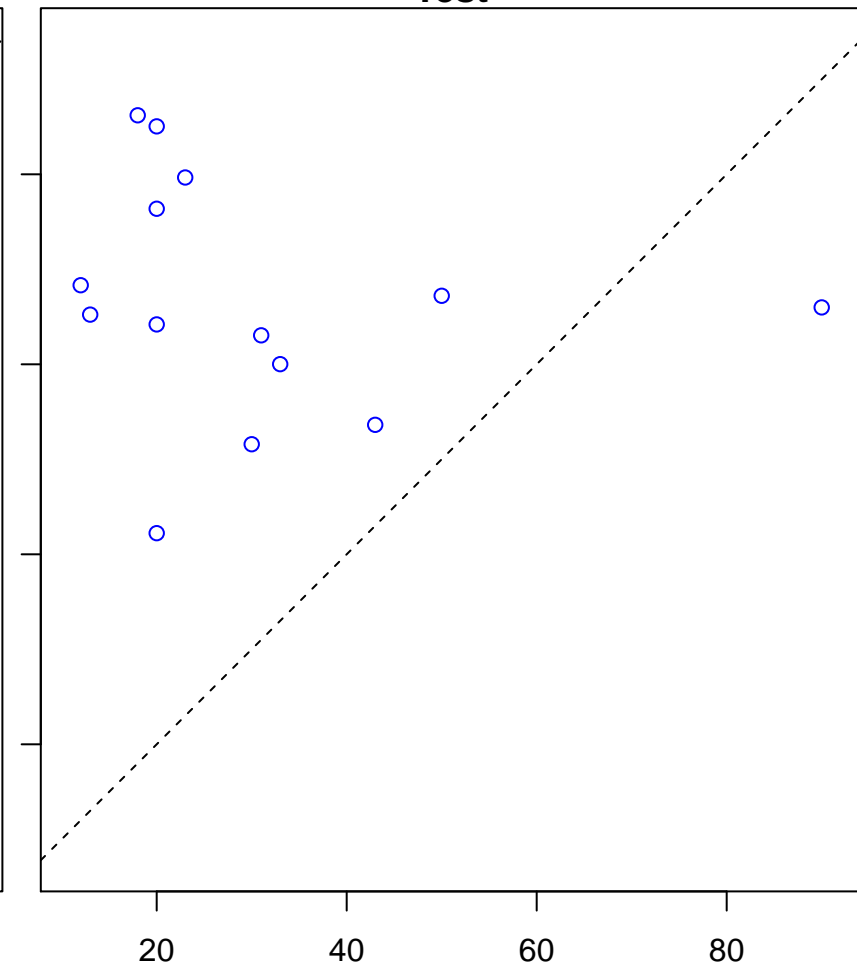


cardiac right ventricle morphogenesis (Score: 4.813707)

Control

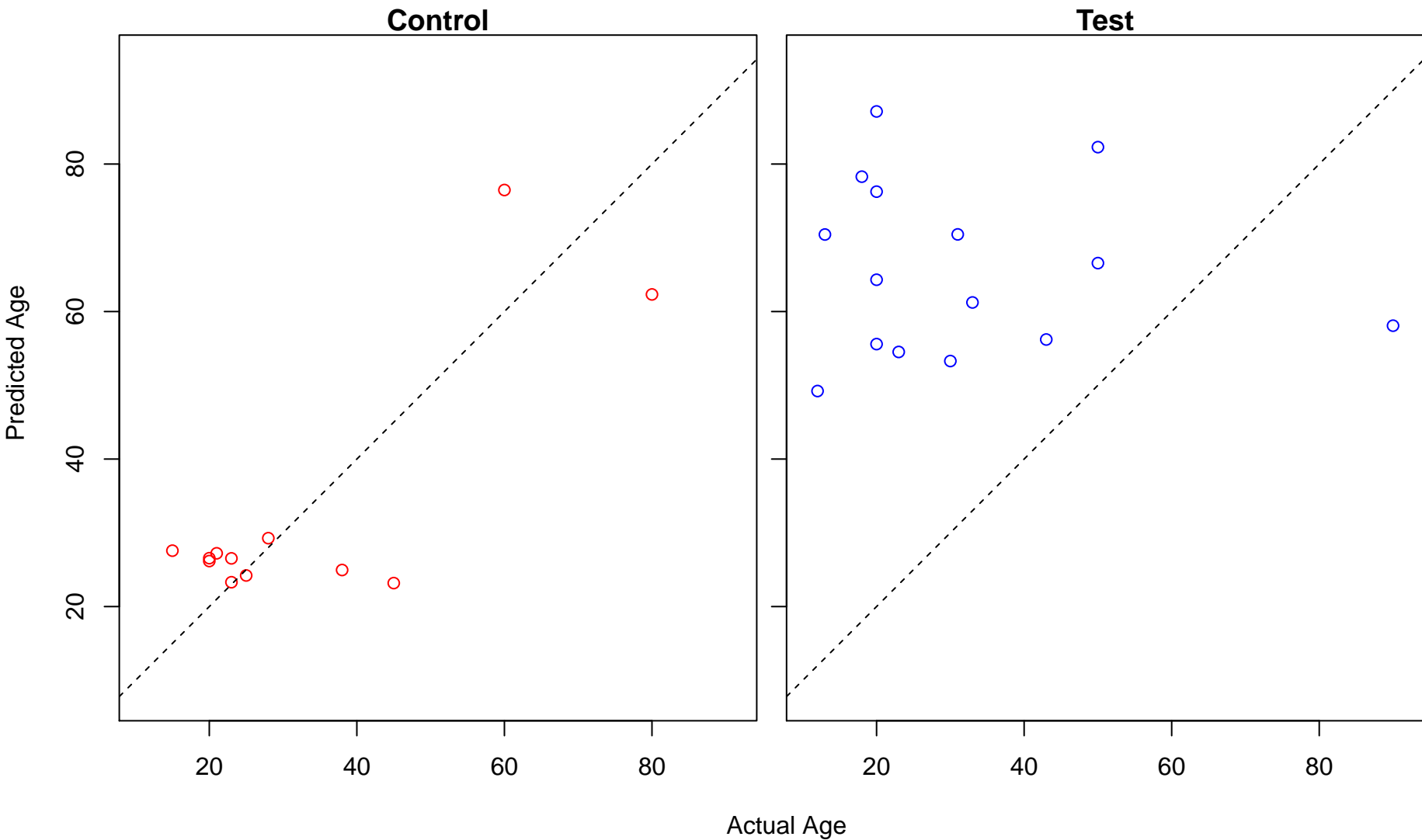


Test

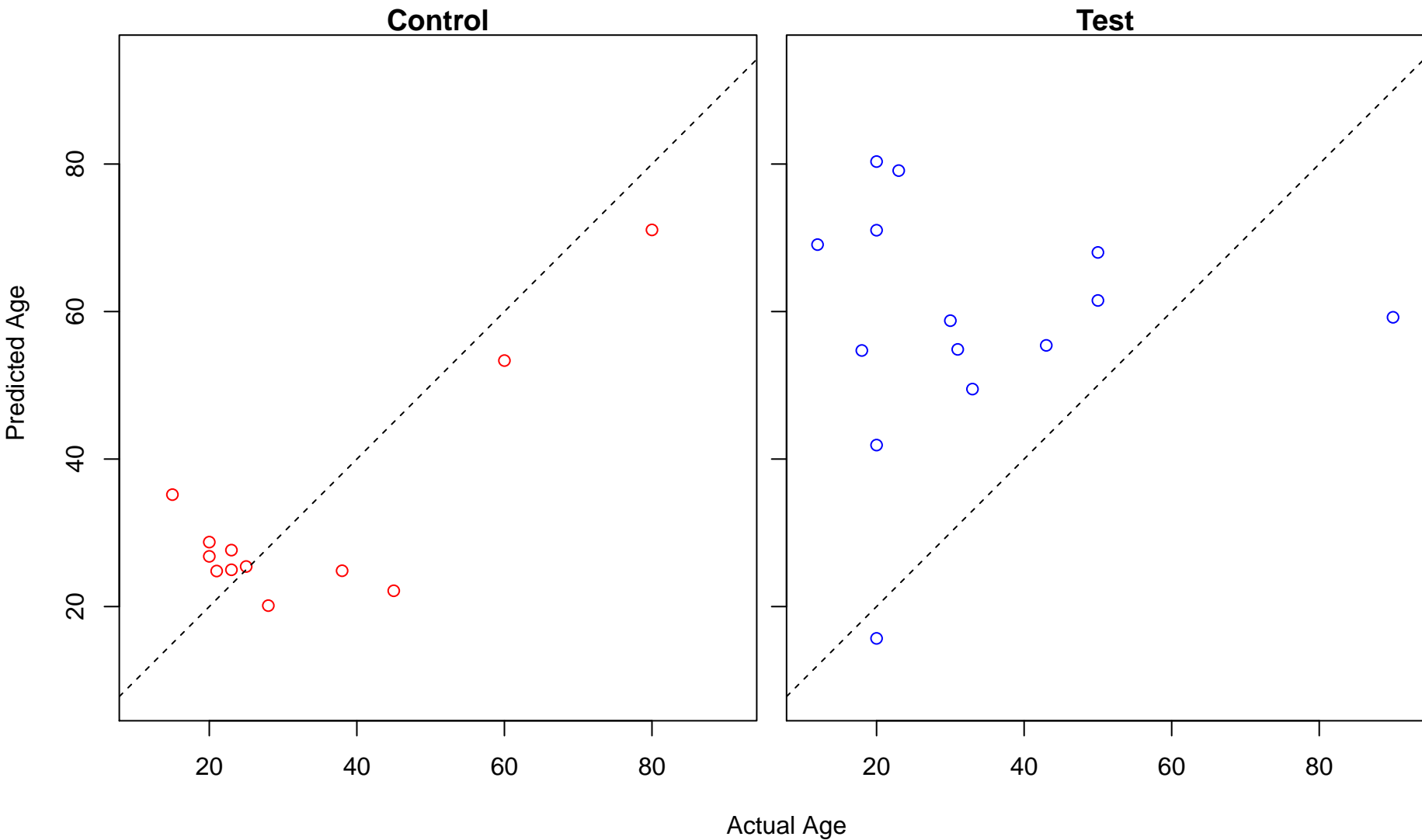


Actual Age

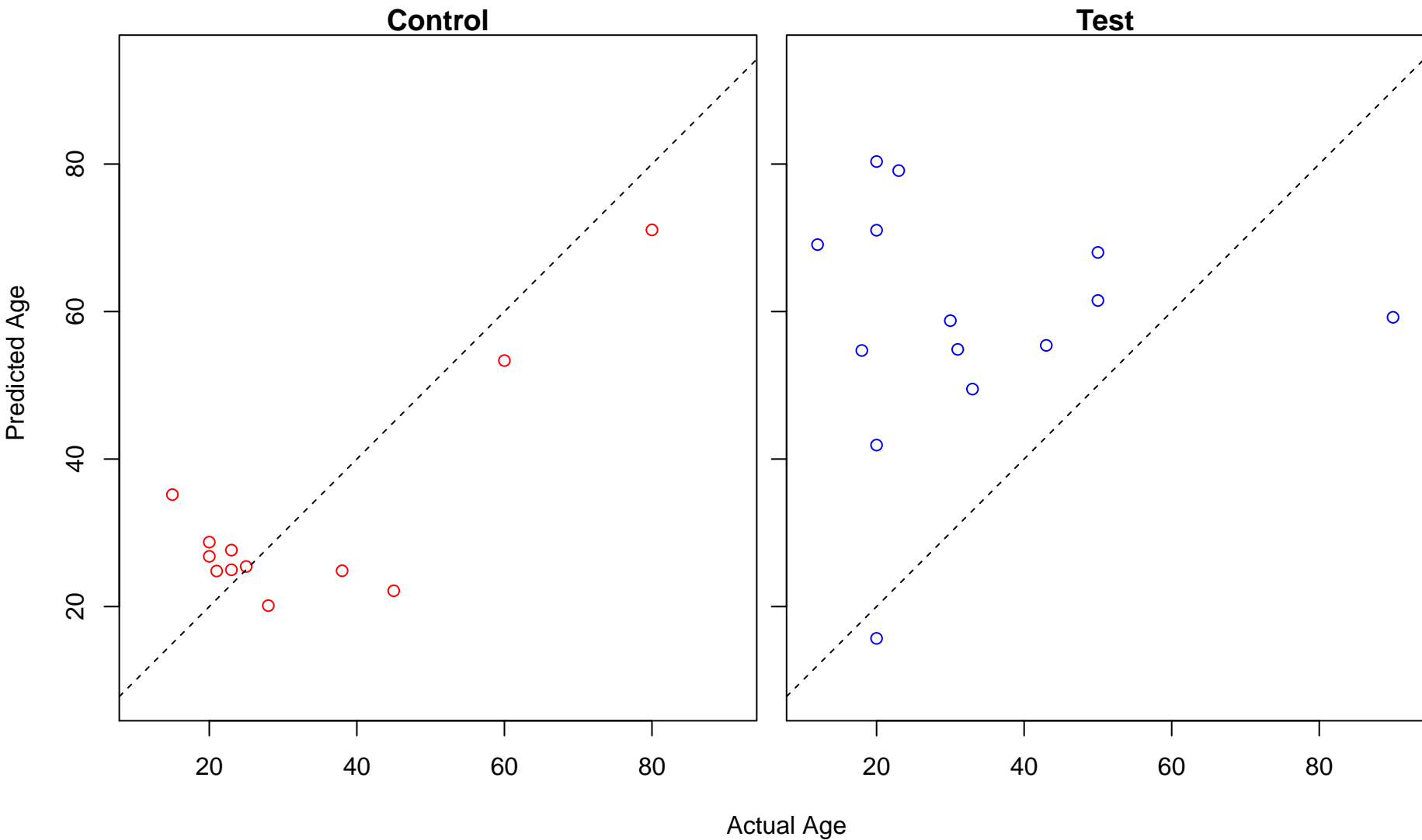
substantia nigra development (Score: 4.811473)



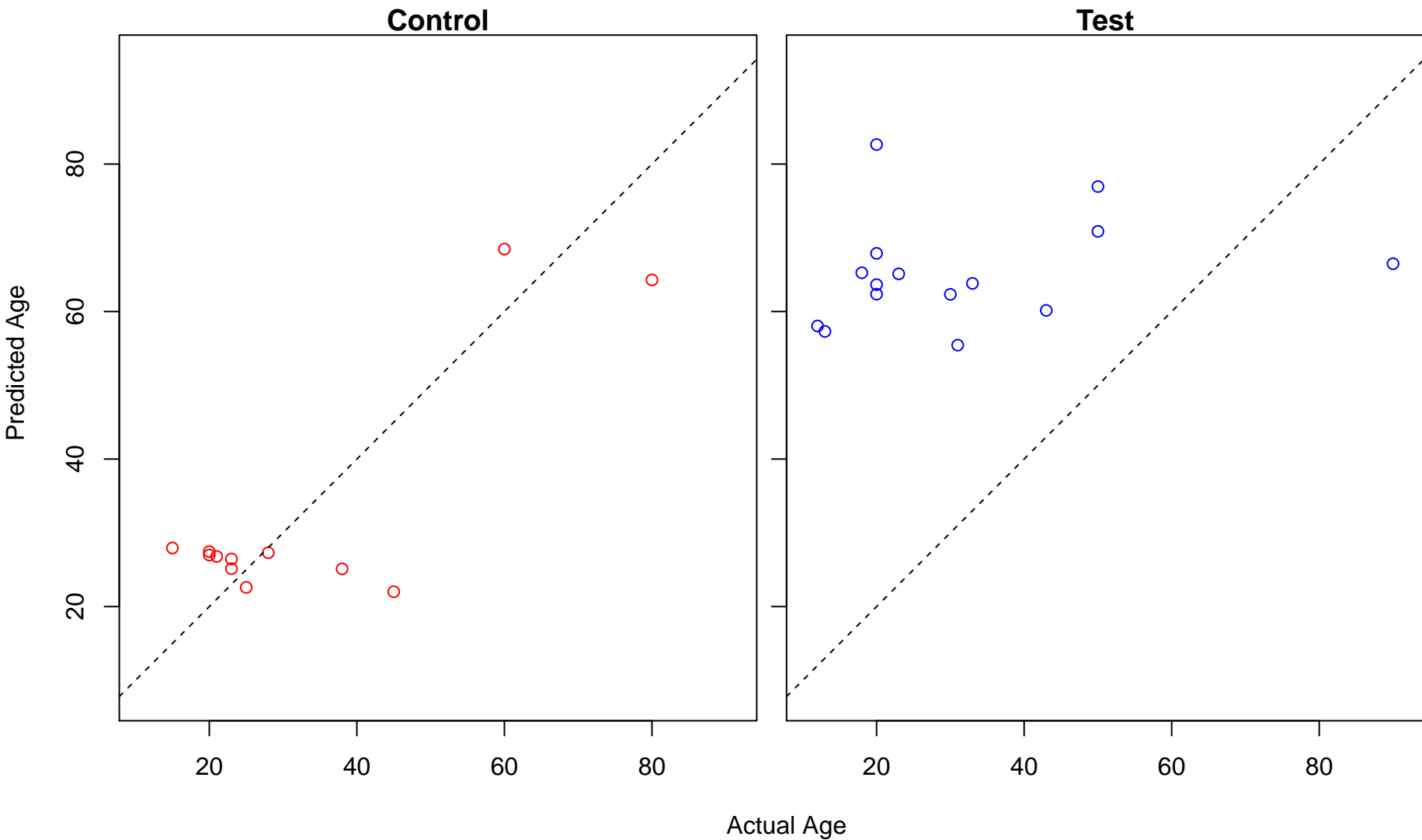
cellular response to nitric oxide (Score: 4.810624)



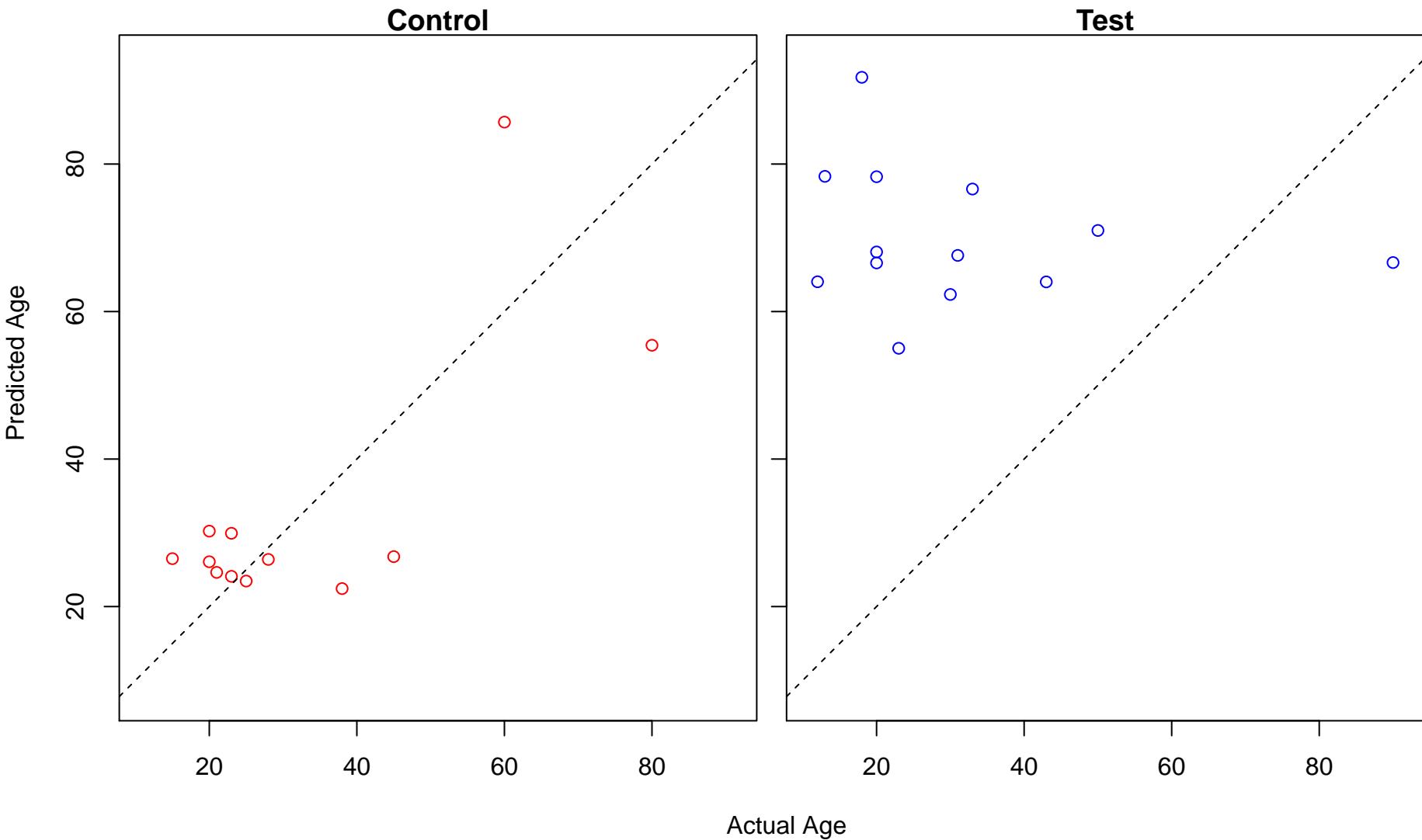
cellular response to reactive nitrogen species (Score: 4.810624)



regulation of calcium-mediated signaling (Score: 4.810305)

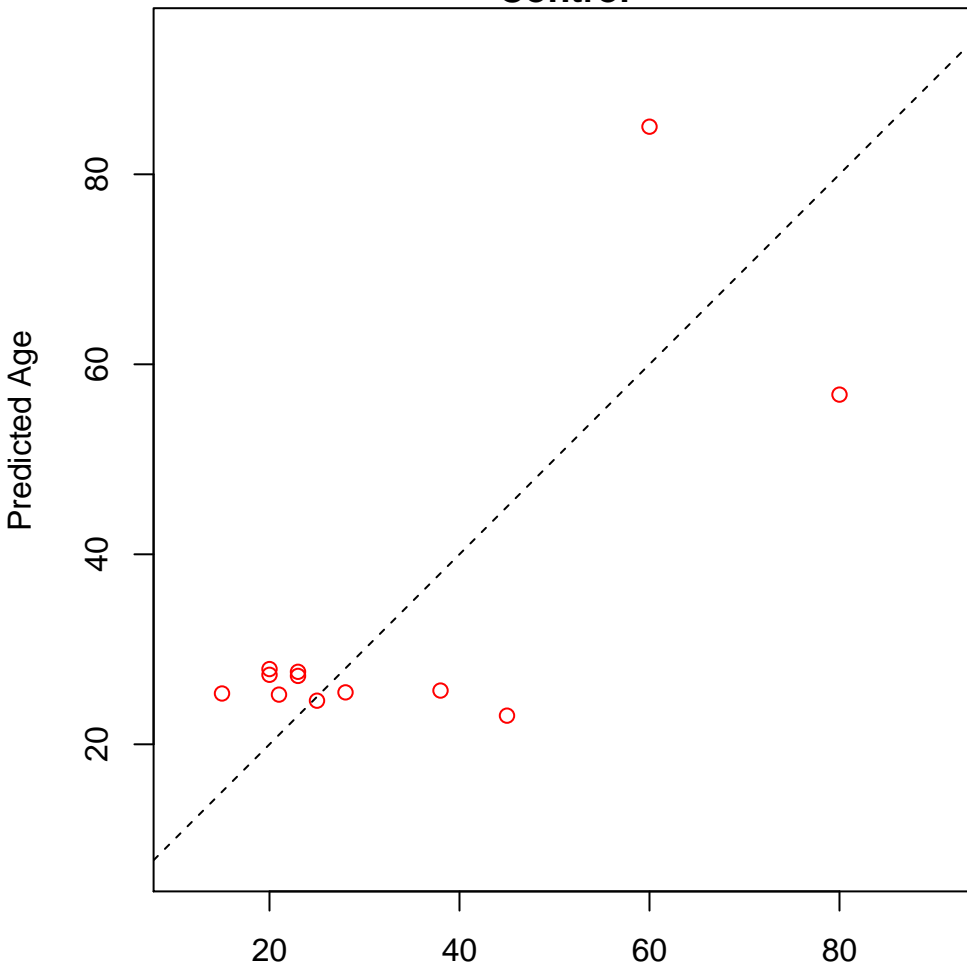


positive regulation of release of cytochrome c from mitochondria (Score: 4.809185)

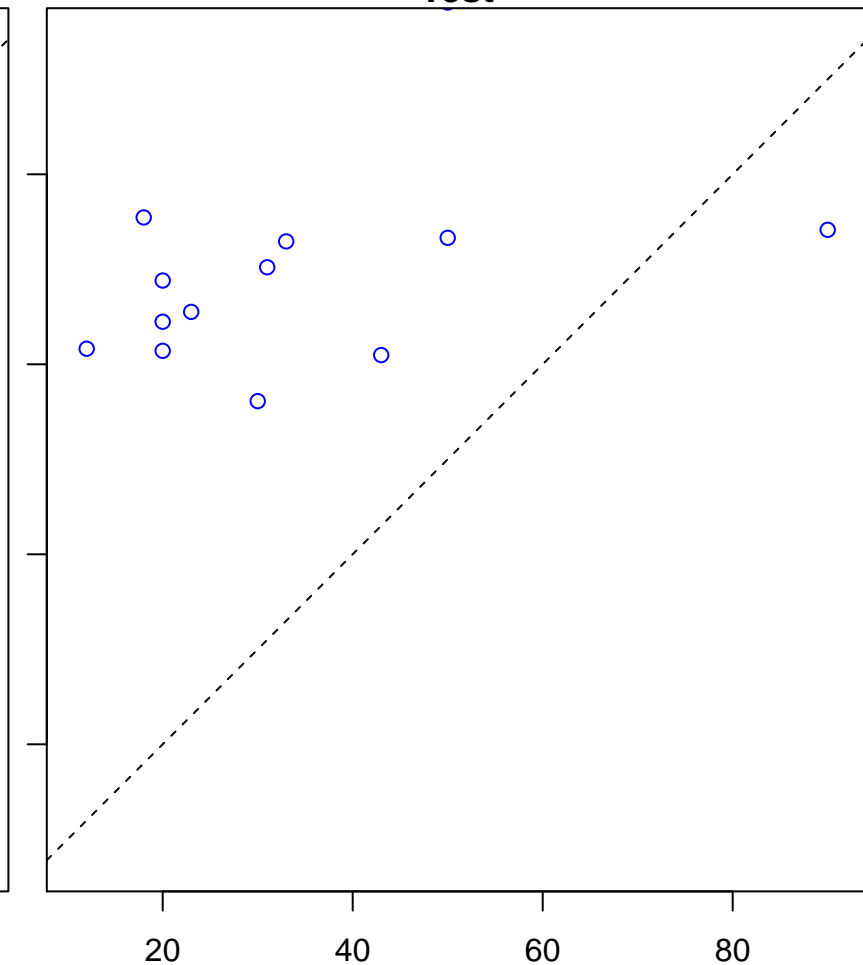


response to epidermal growth factor (Score: 4.808095)

Control

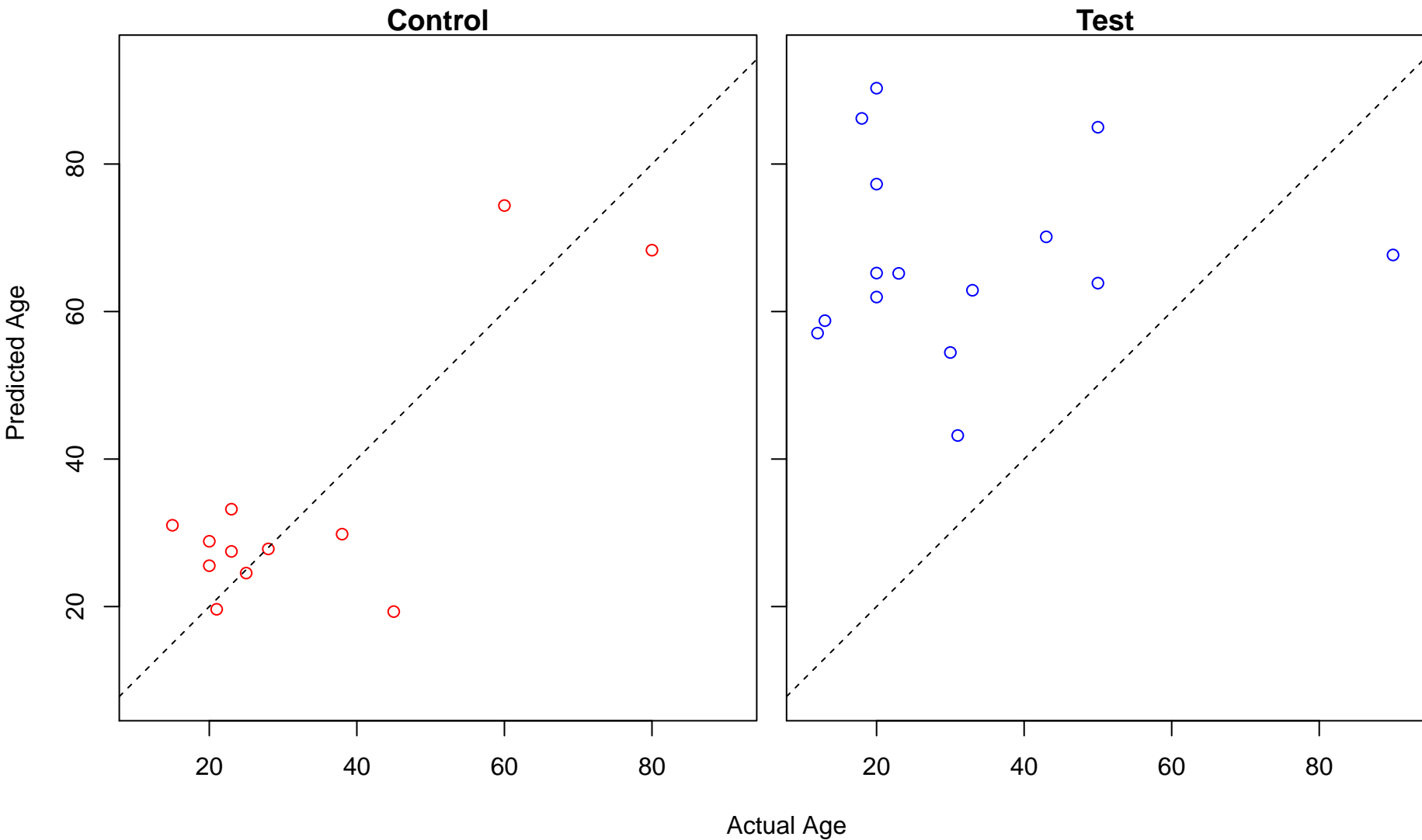


Test

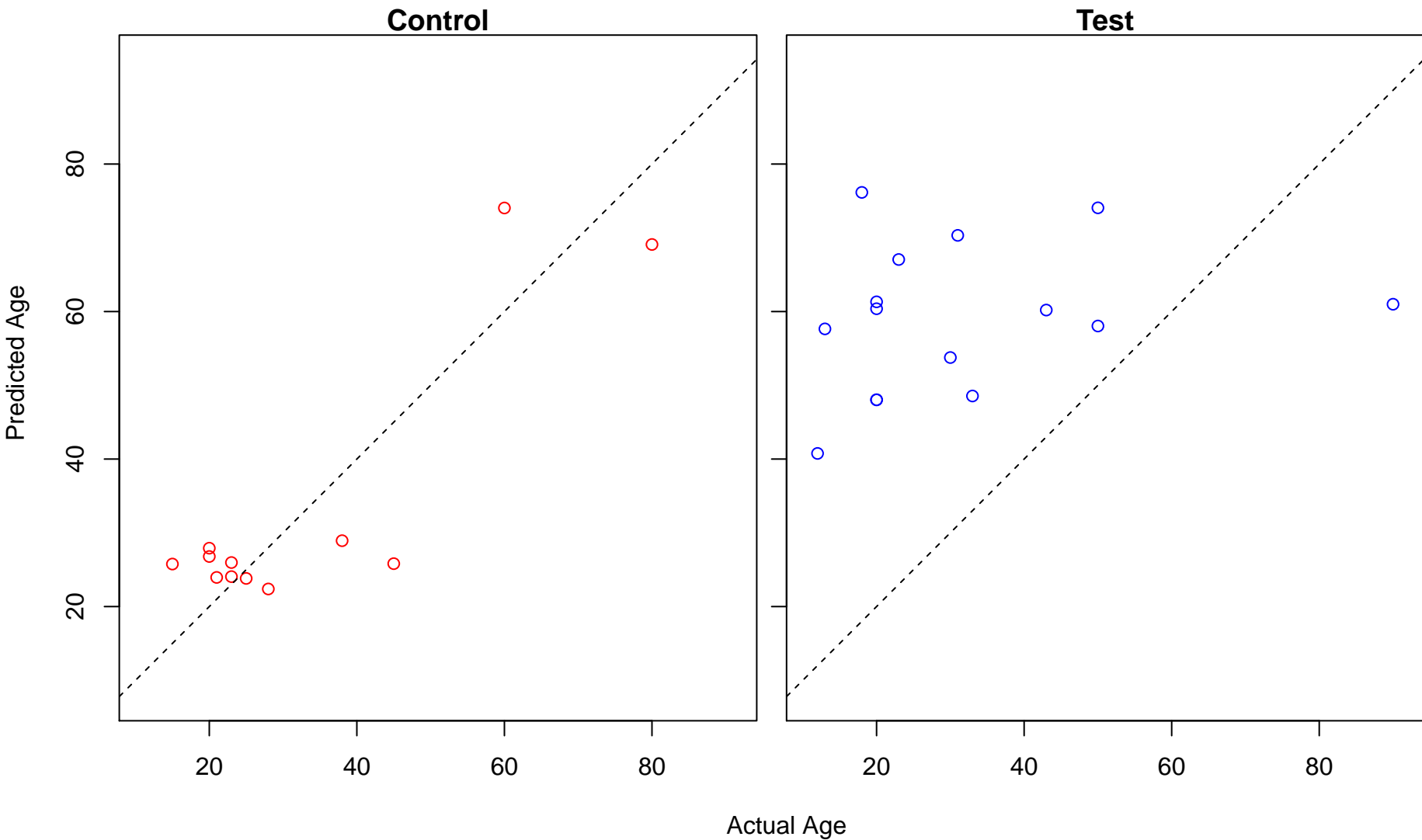


Actual Age

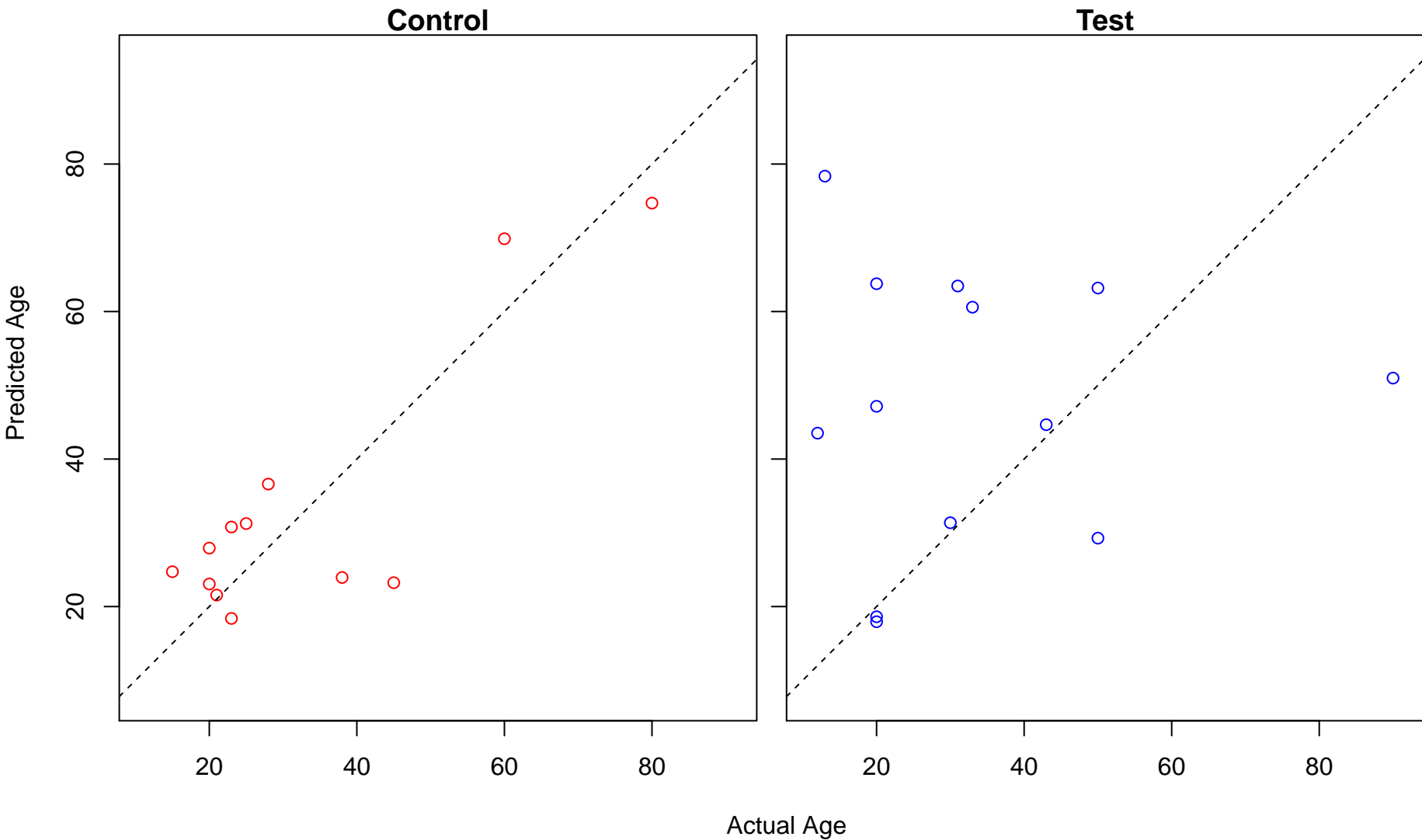
regulation of T cell migration (Score: 4.807338)



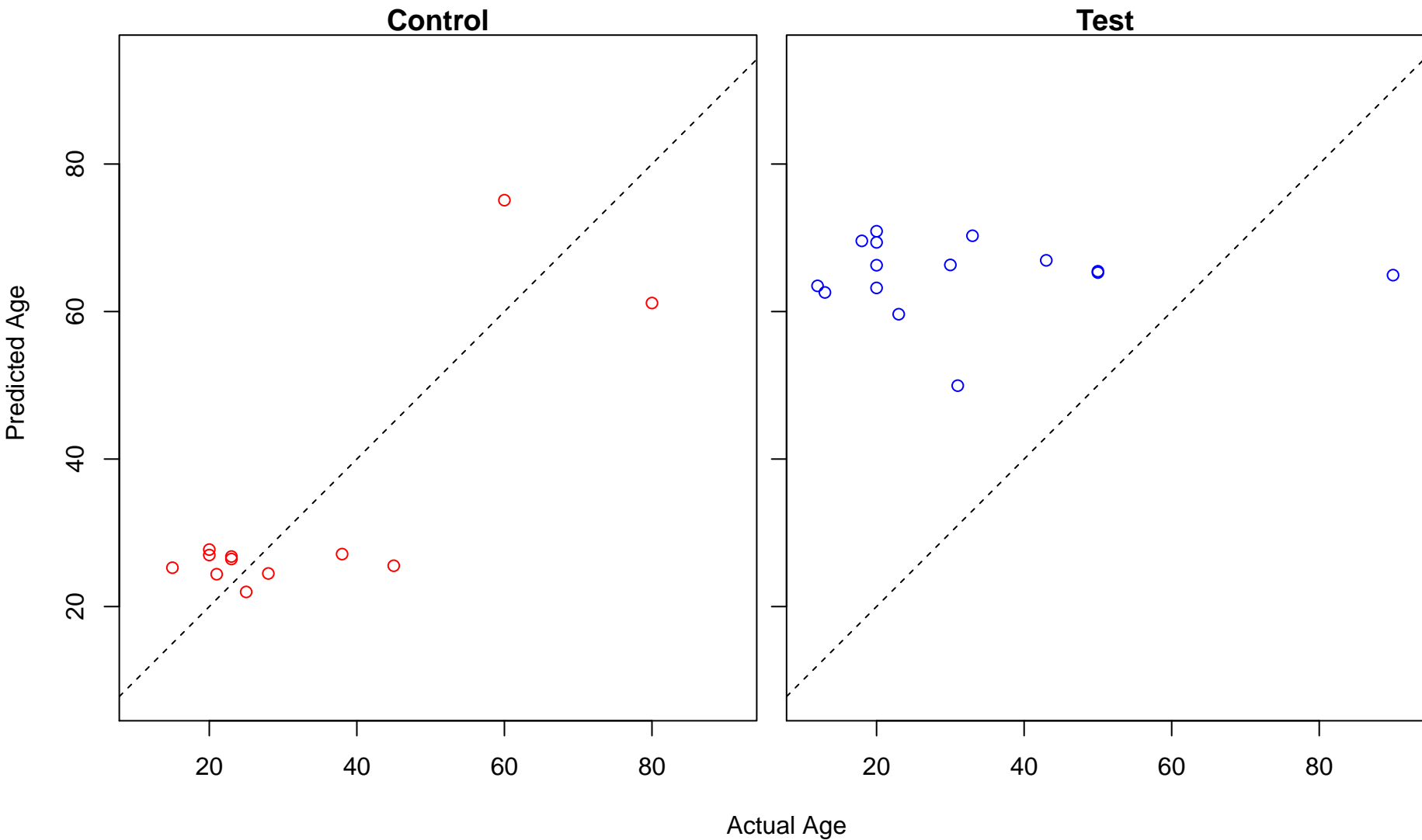
gap junction assembly (Score: 4.805658)



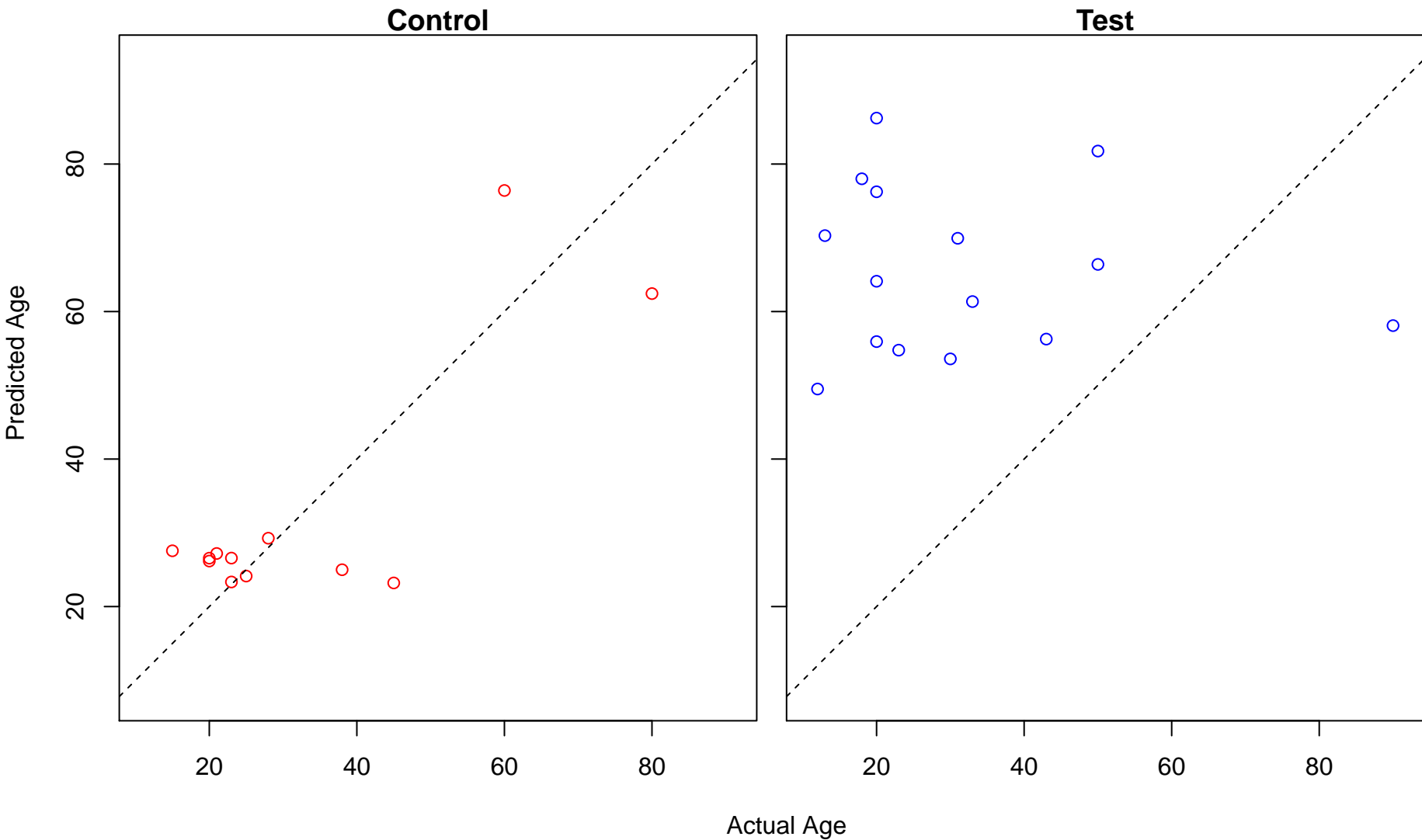
protein ADP-ribosylation (Score: 4.805494)



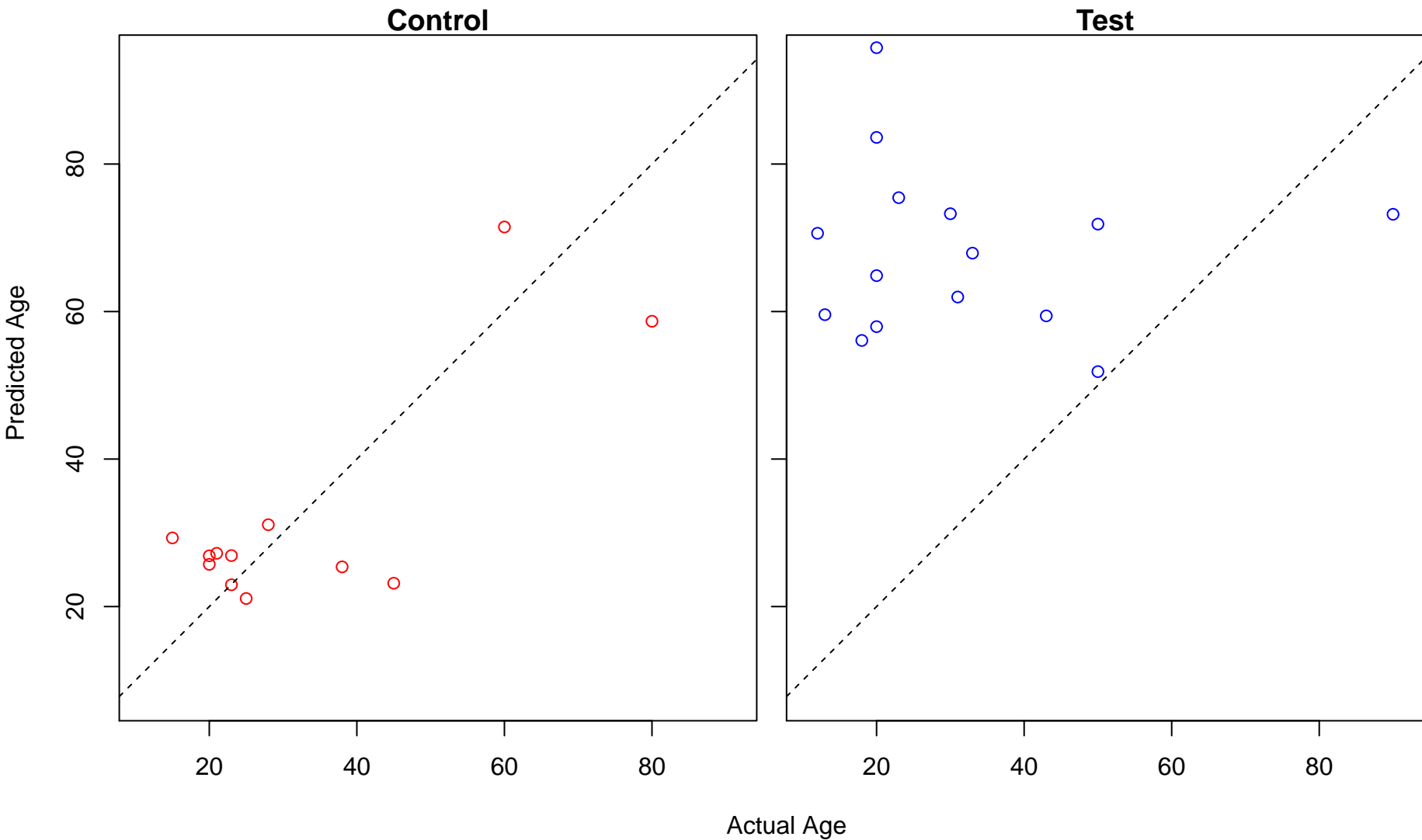
cardiac muscle tissue development (Score: 4.805380)



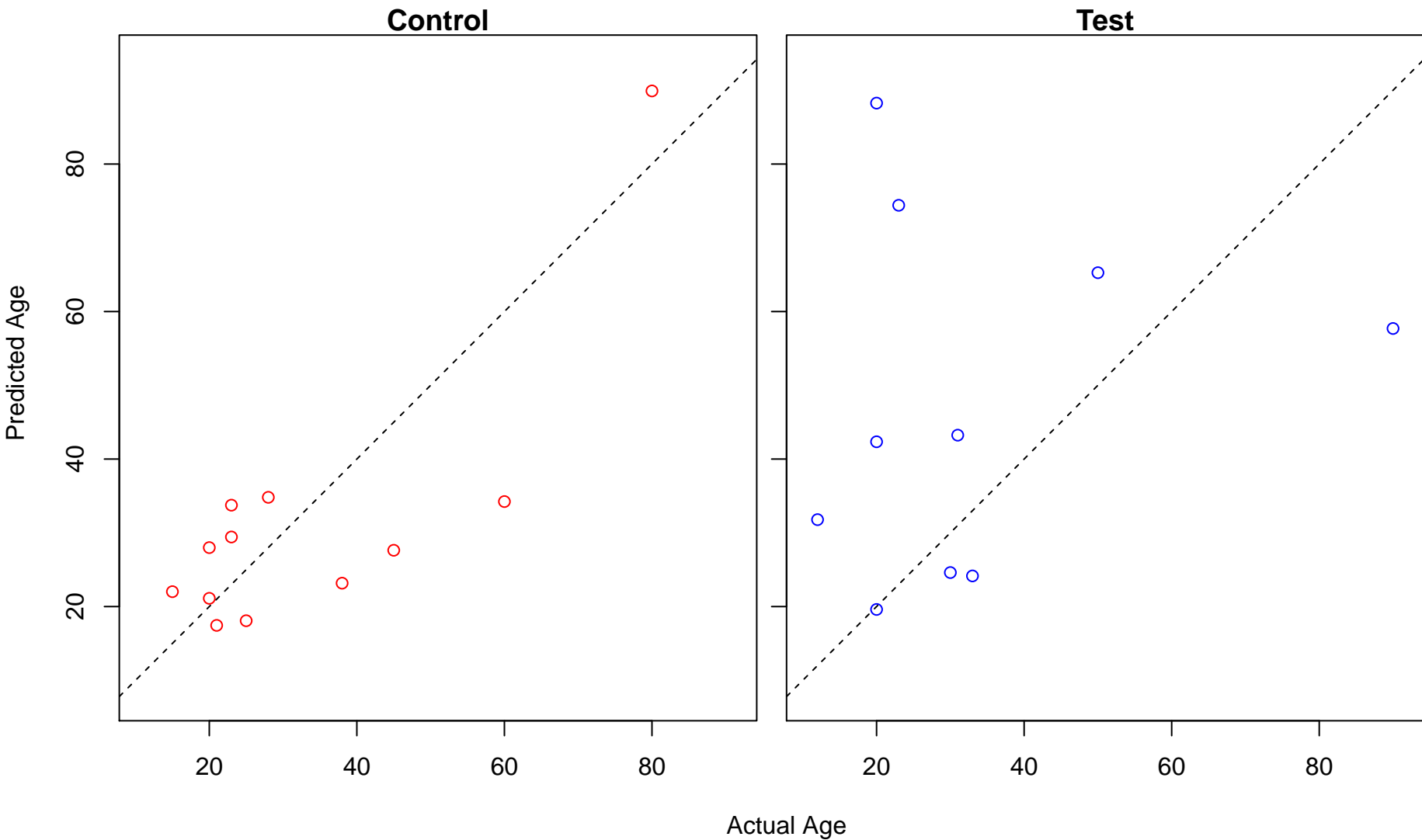
neural nucleus development (Score: 4.803835)



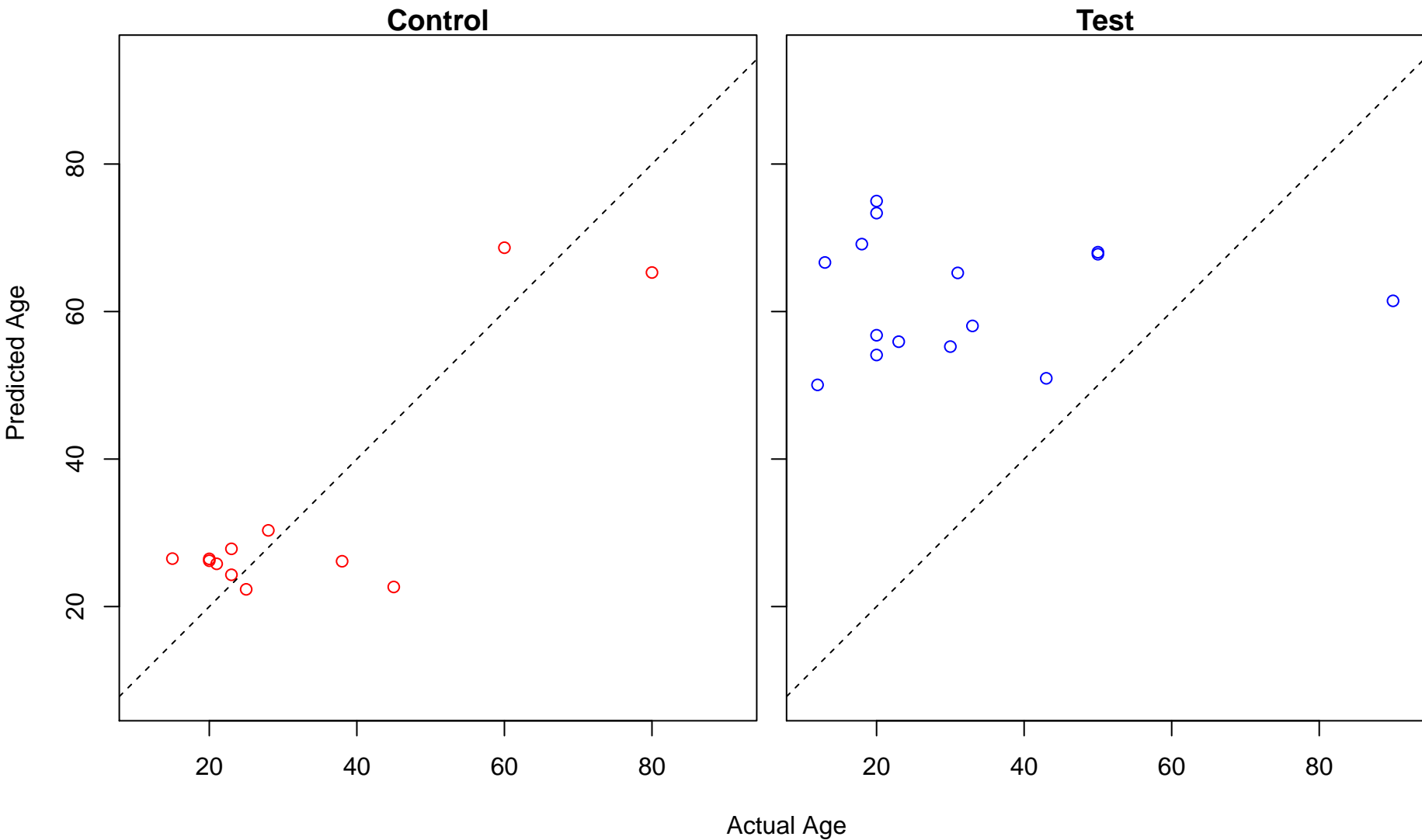
T cell homeostasis (Score: 4.802007)



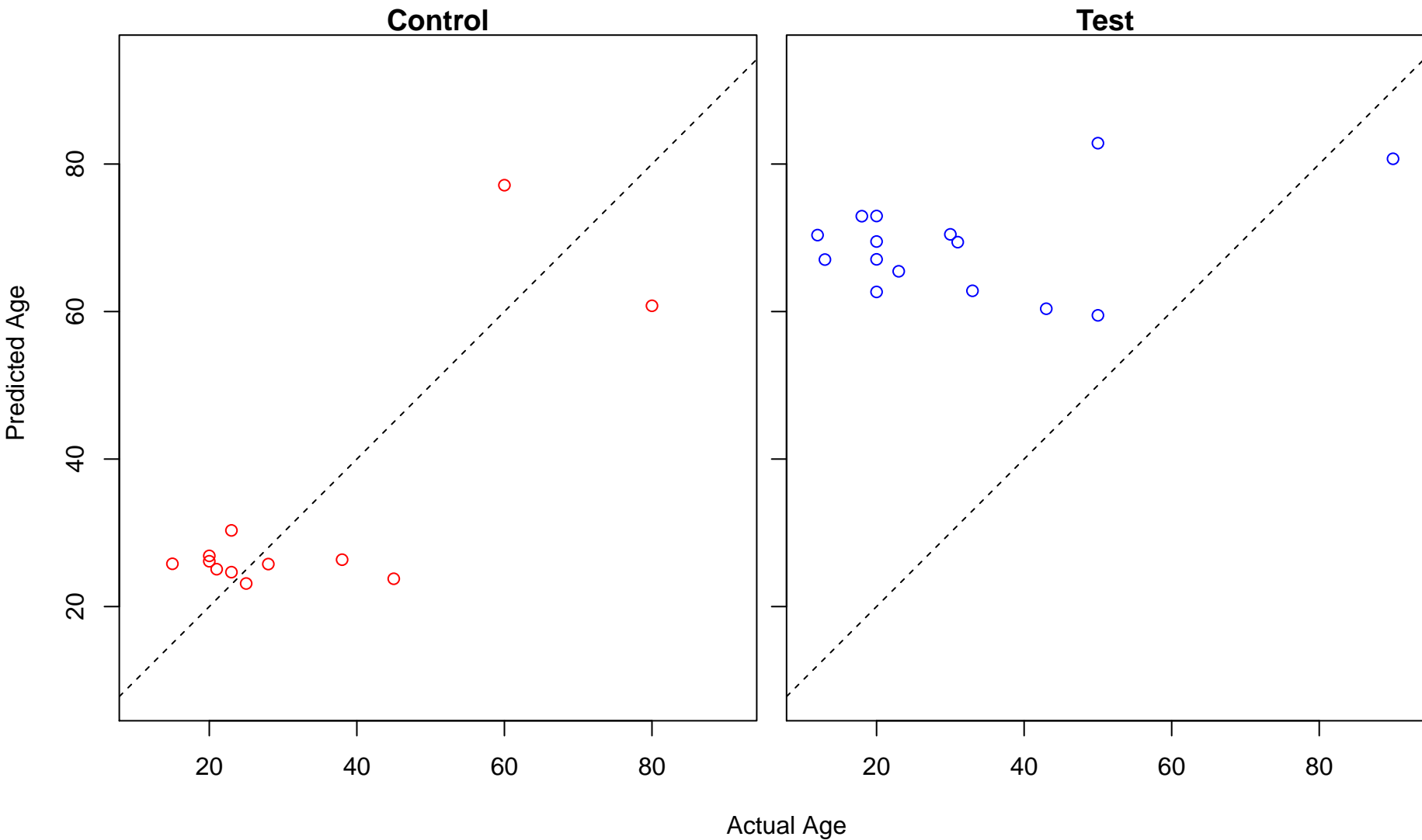
regulation of axon extension (Score: 4.801714)



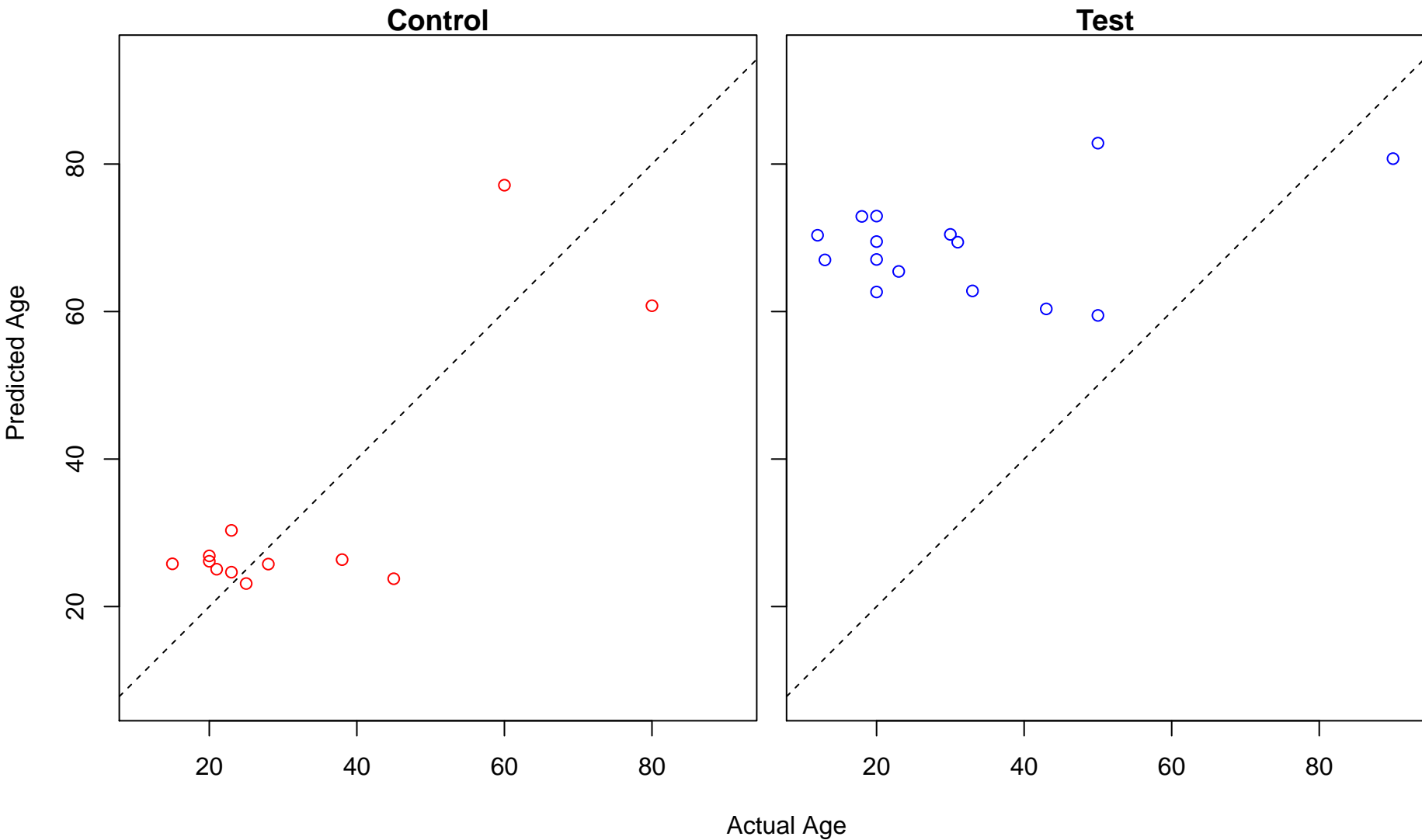
regulation of phosphatase activity (Score: 4.801526)



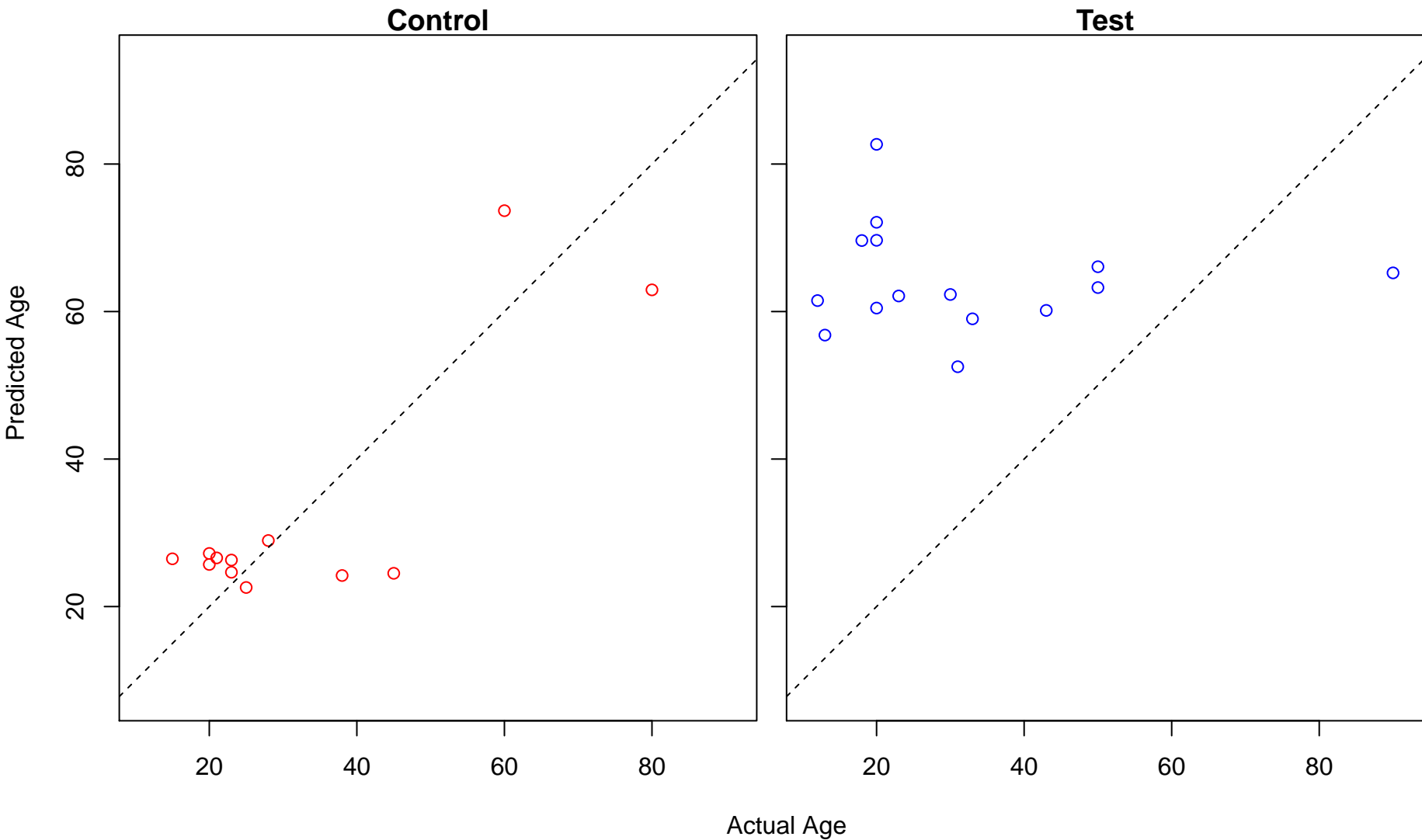
regulation of nuclear division (Score: 4.799135)



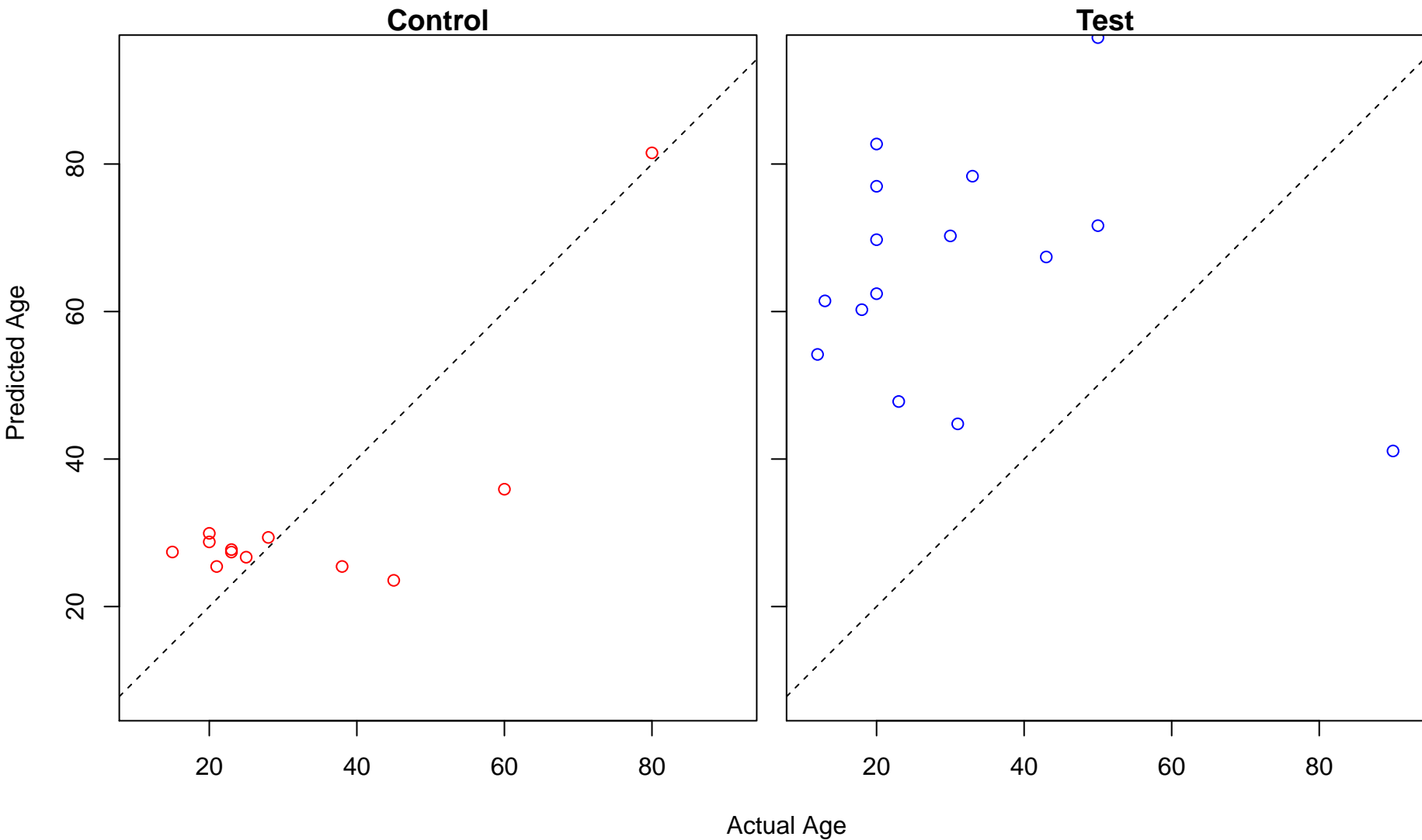
regulation of mitotic nuclear division (Score: 4.798051)



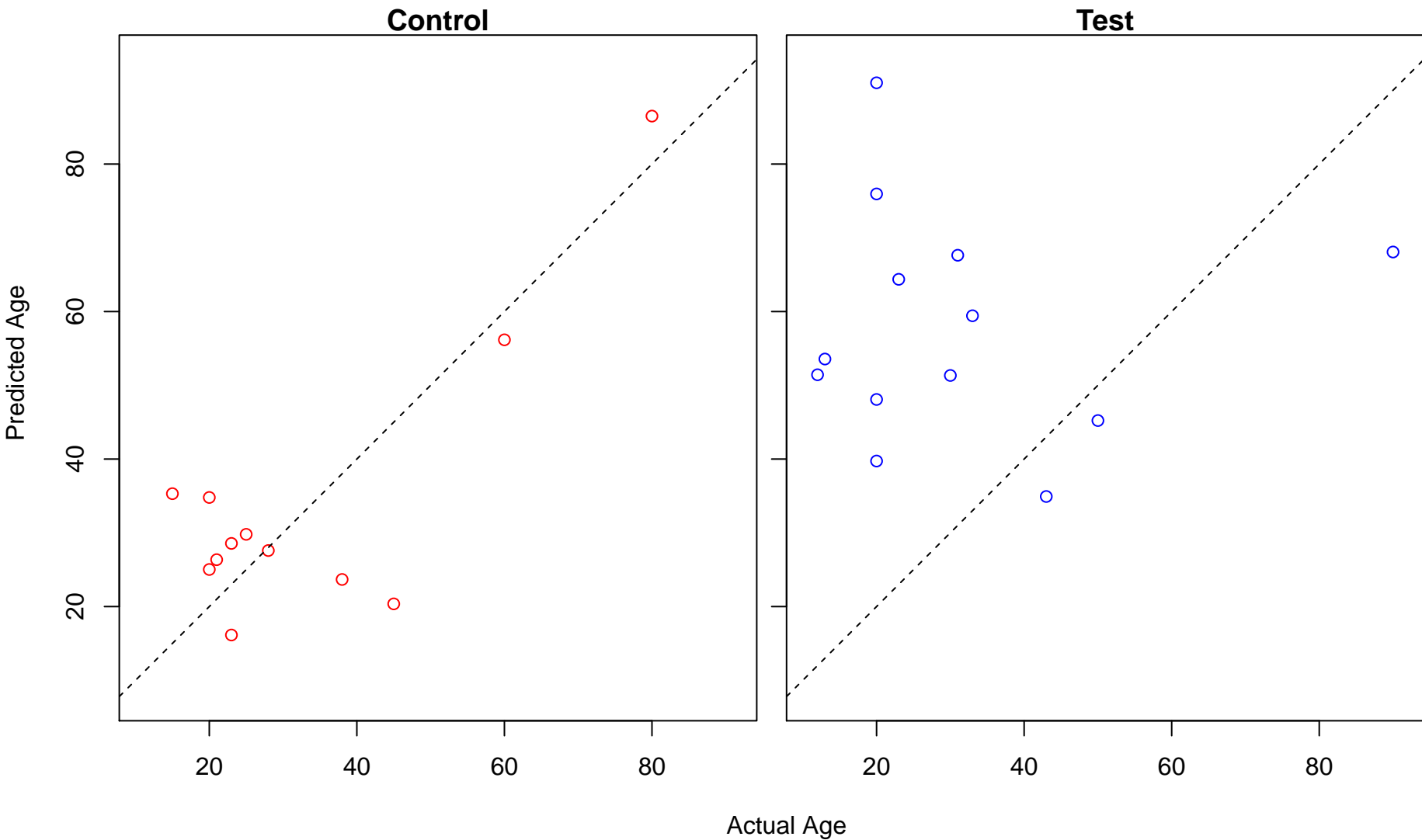
mitochondrial translation (Score: 4.797413)



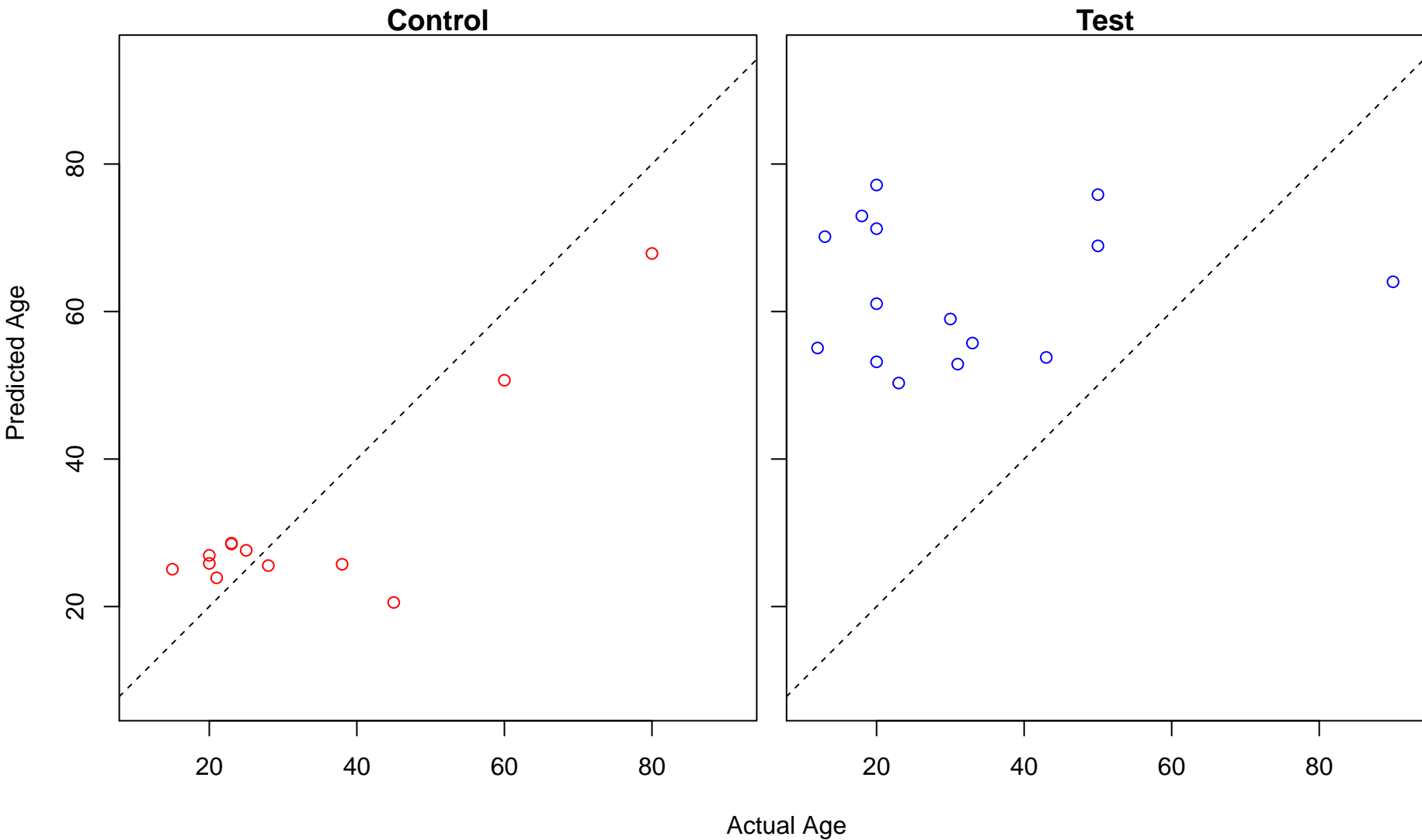
positive regulation of synapse assembly (Score: 4.795104)



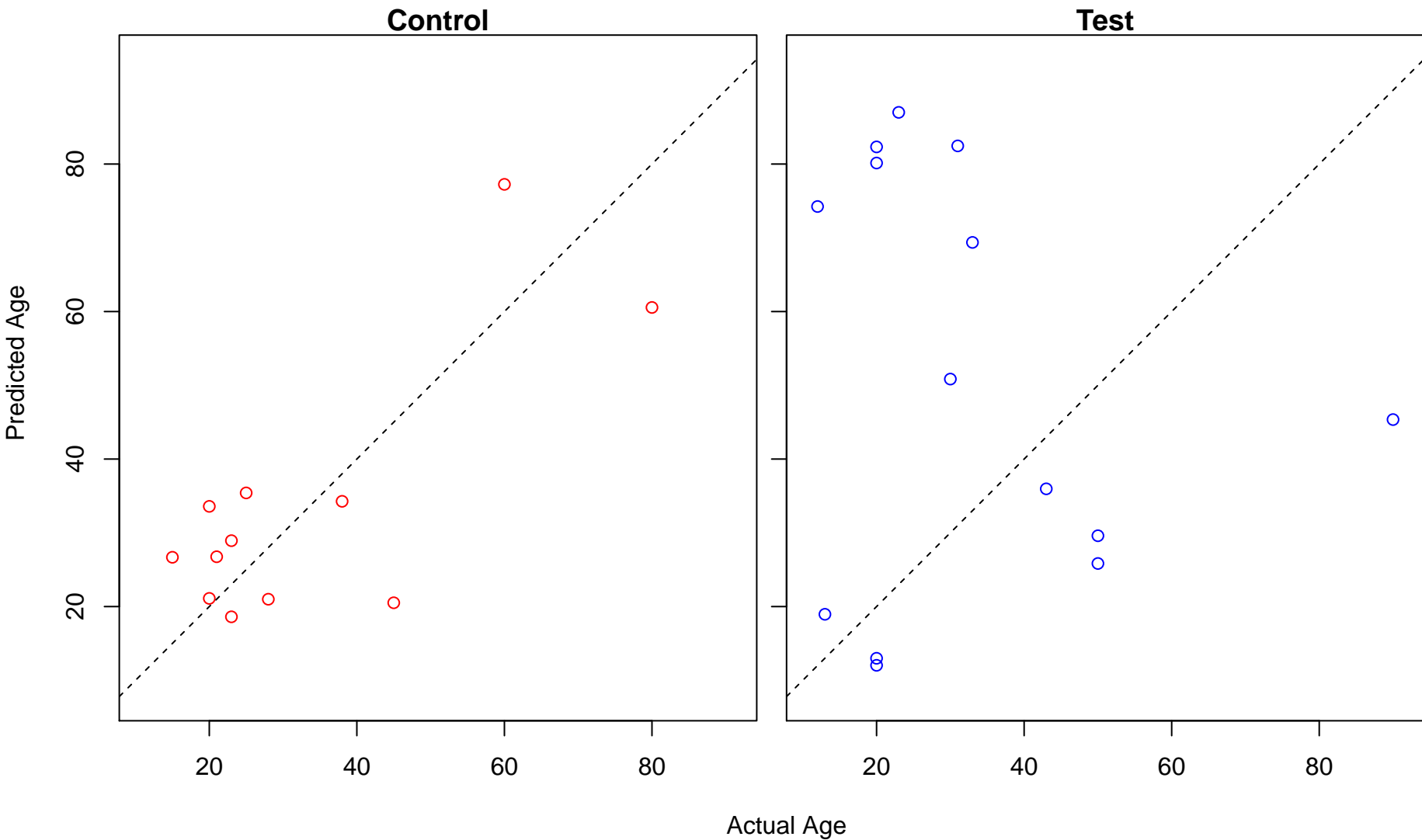
regulation of mRNA metabolic process (Score: 4.792693)



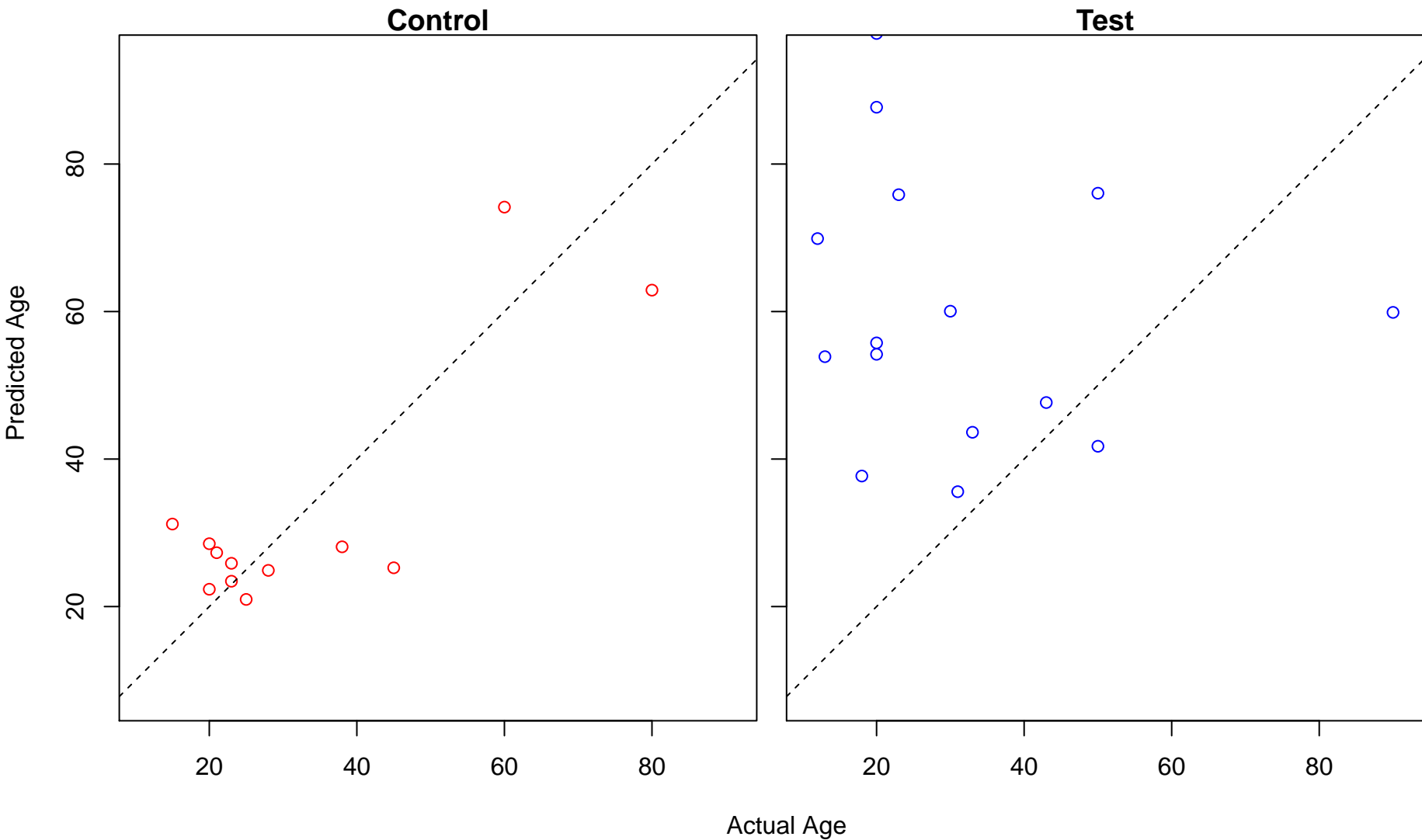
positive regulation of cellular amide metabolic process (Score: 4.791411)



polyamine transport (Score: 4.787415)

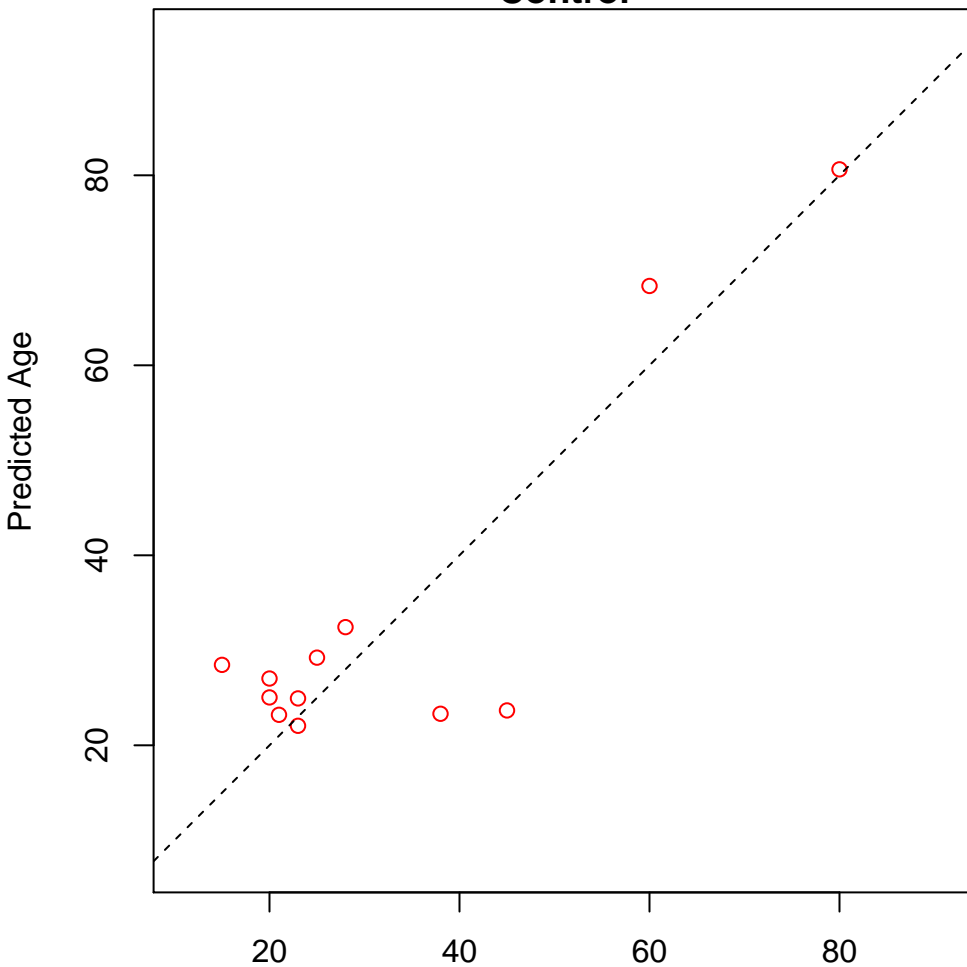


sperm capacitation (Score: 4.787381)

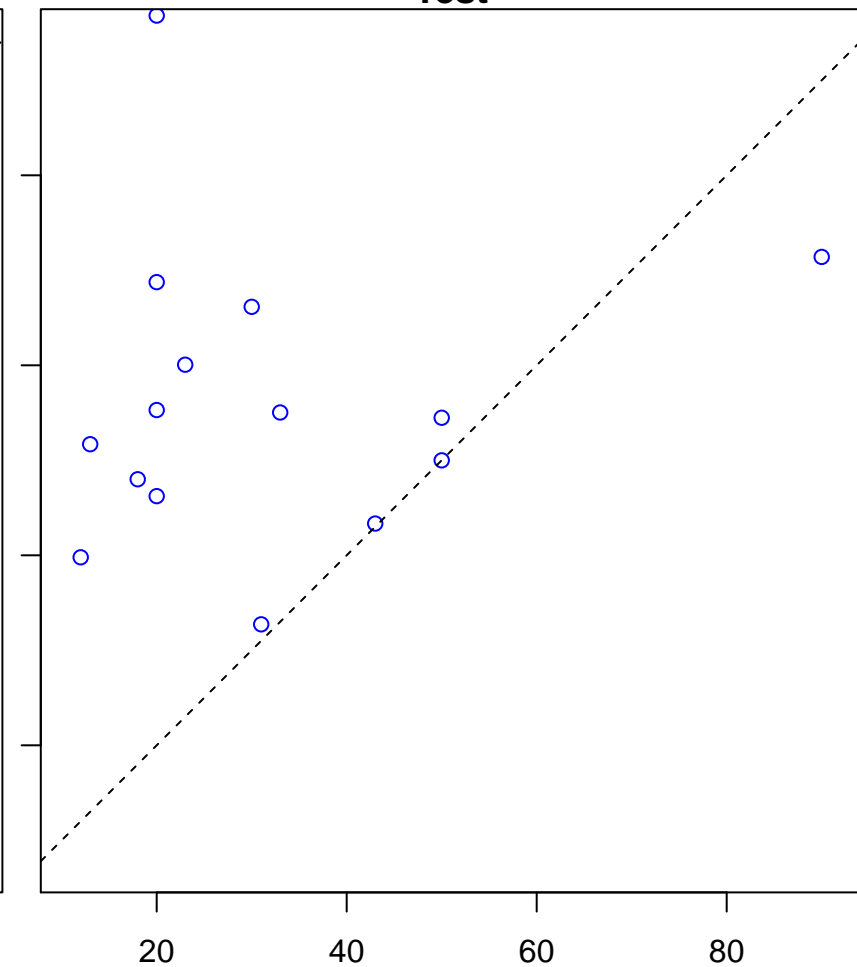


positive regulation of receptor recycling (Score: 4.786806)

Control

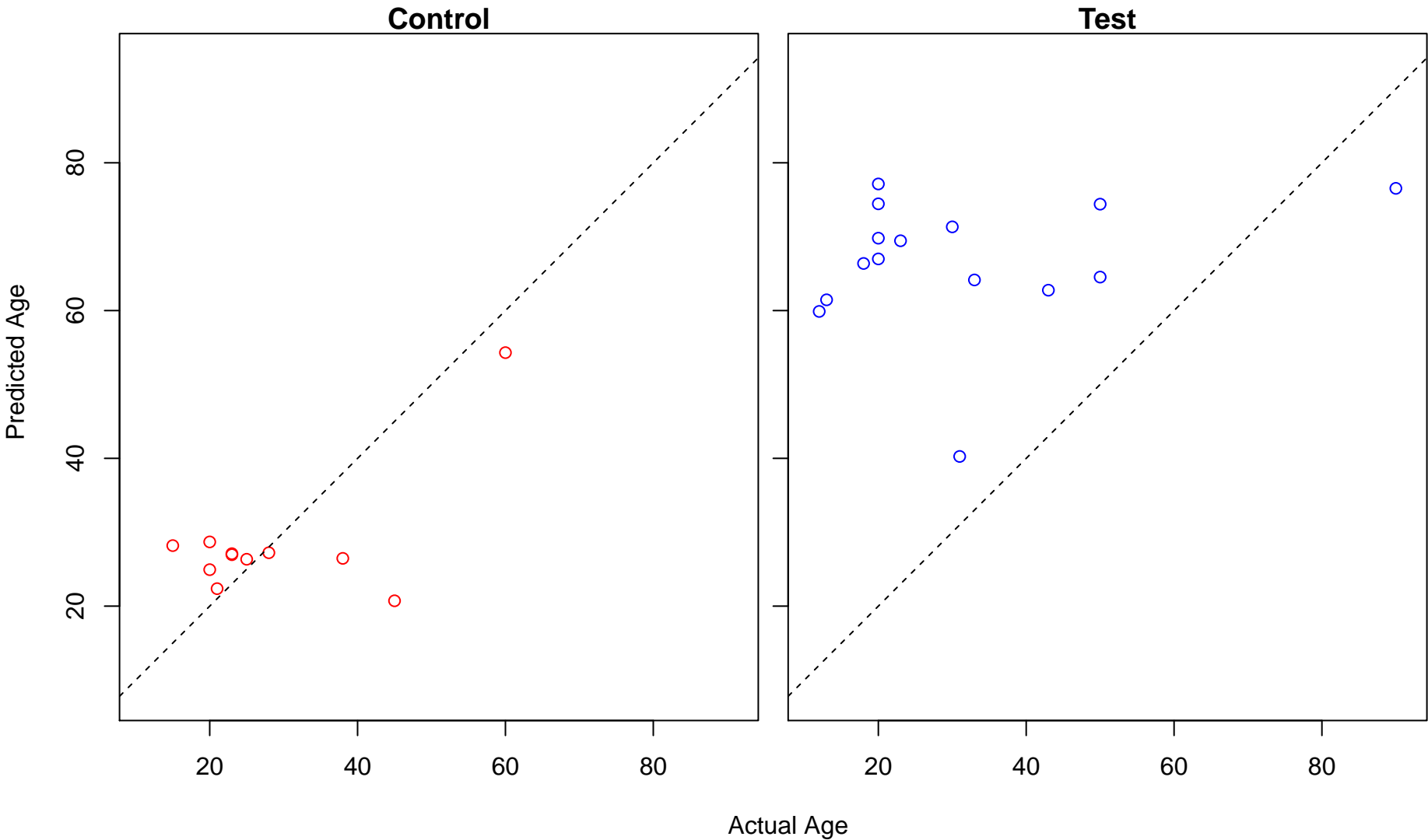


Test



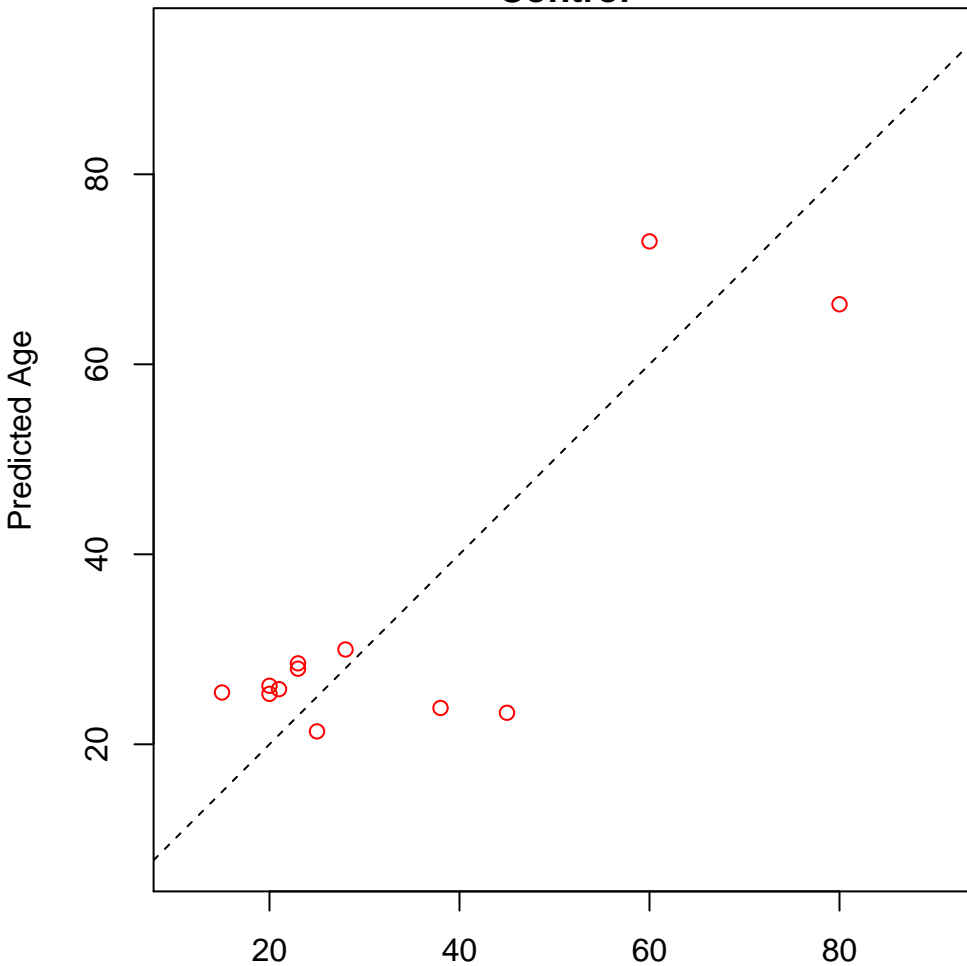
Actual Age

ventricular cardiac muscle cell action potential (Score: 4.786054)

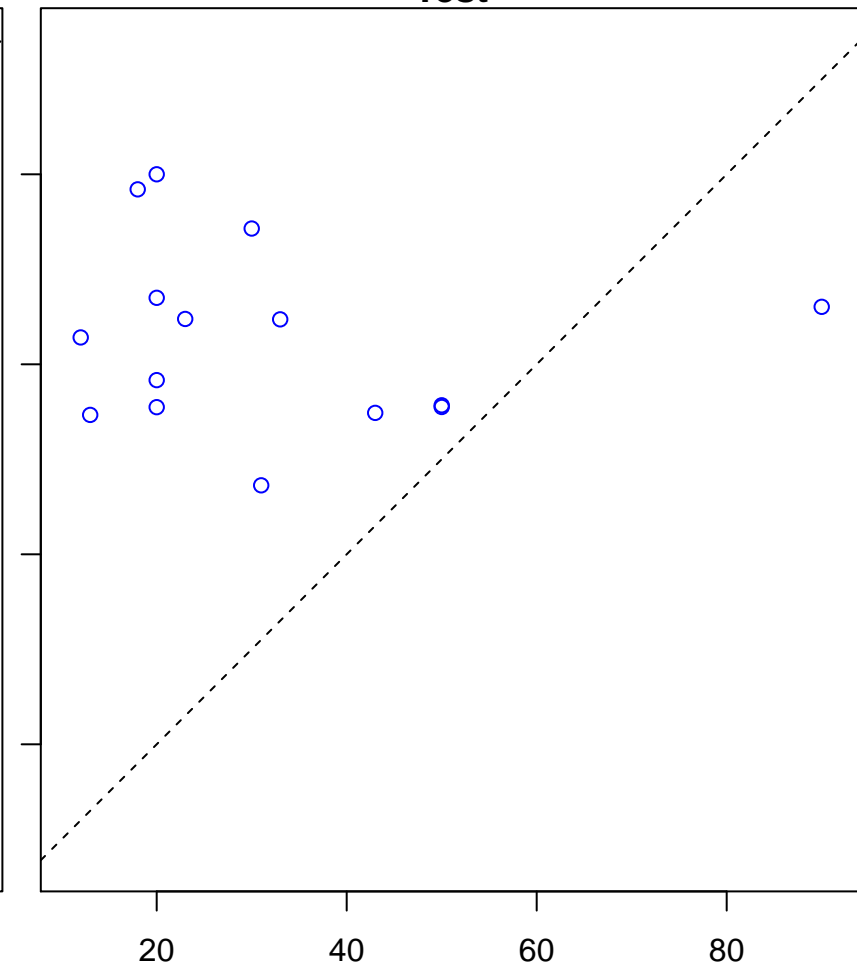


retrograde transport, endosome to Golgi (Score: 4.785966)

Control

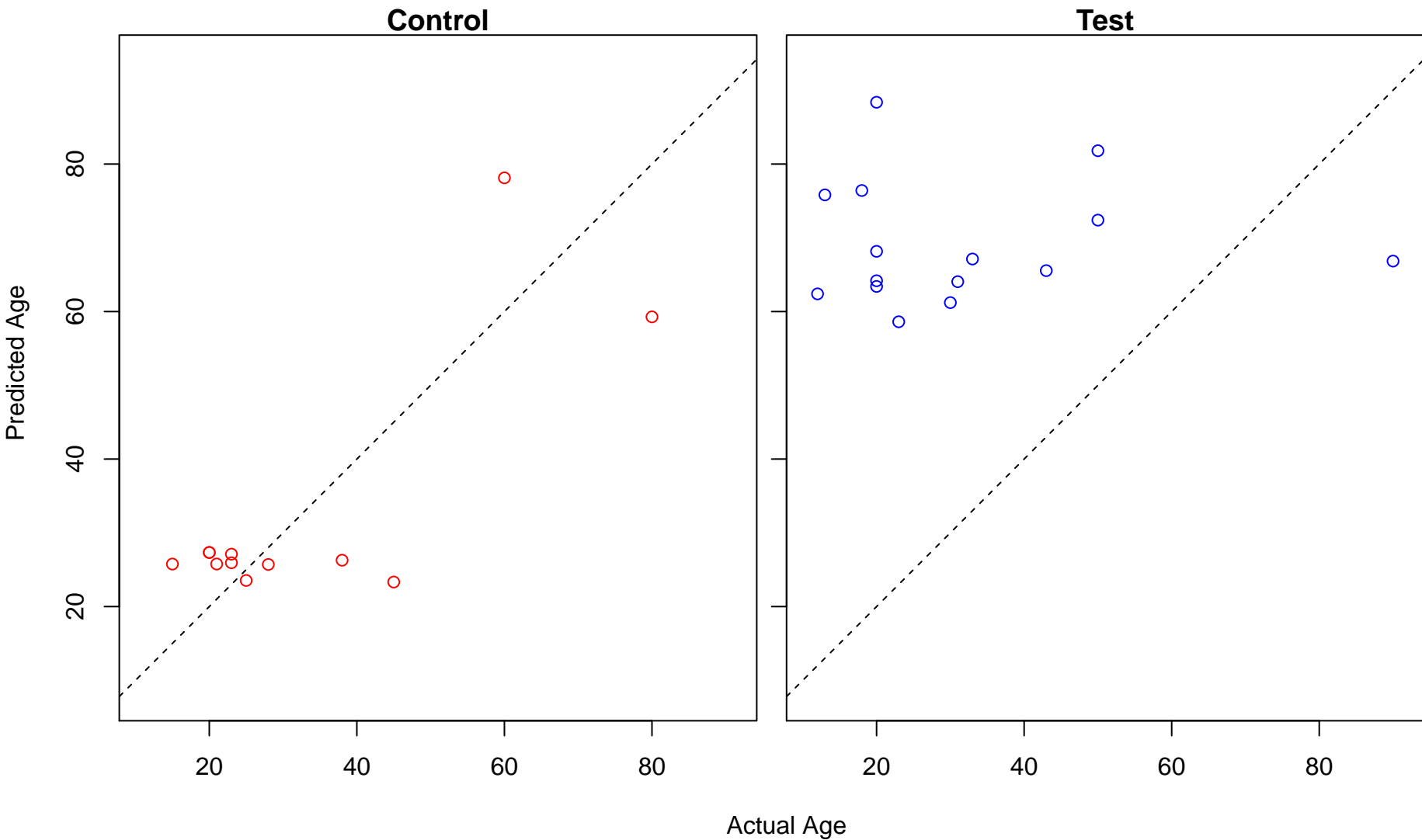


Test

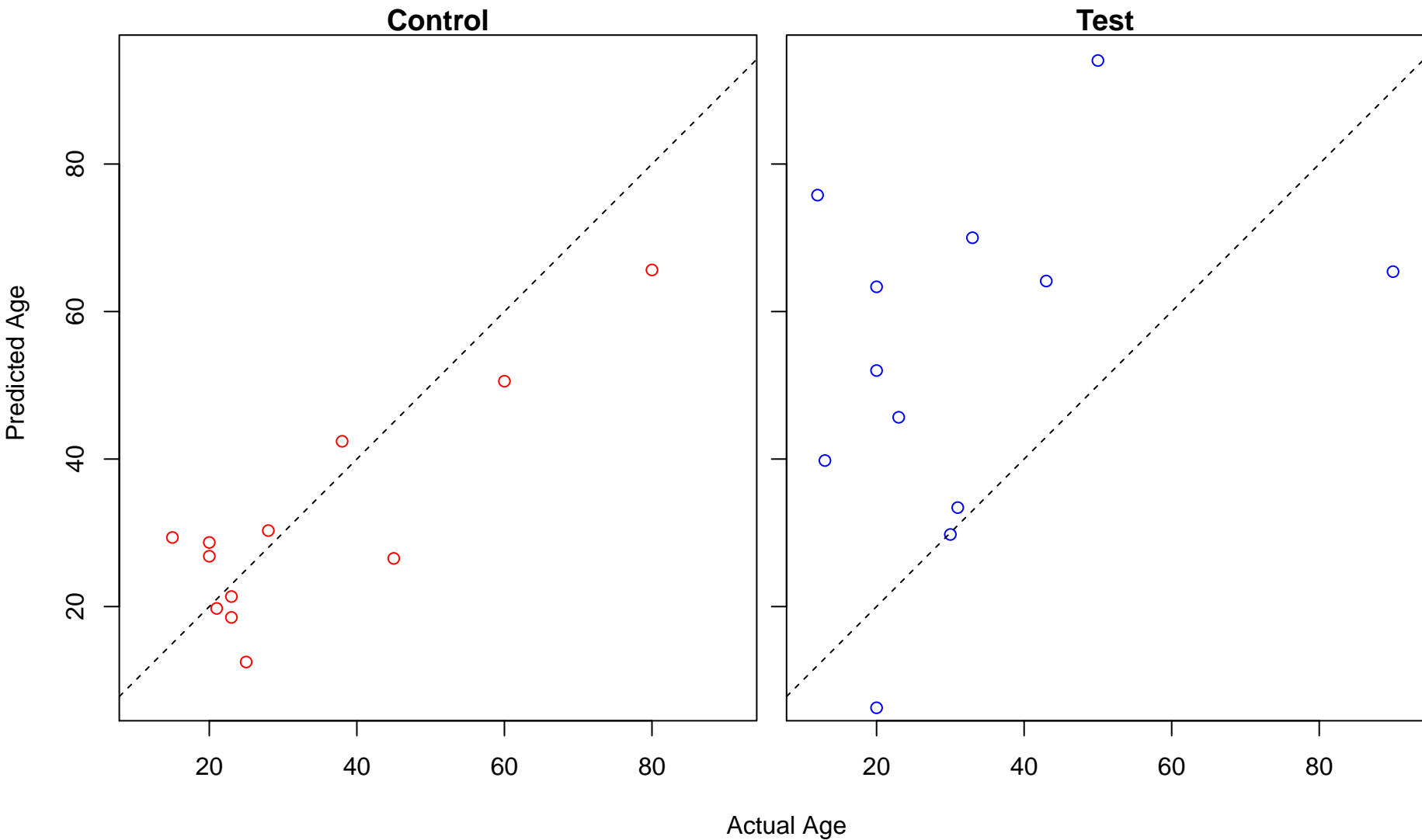


Actual Age

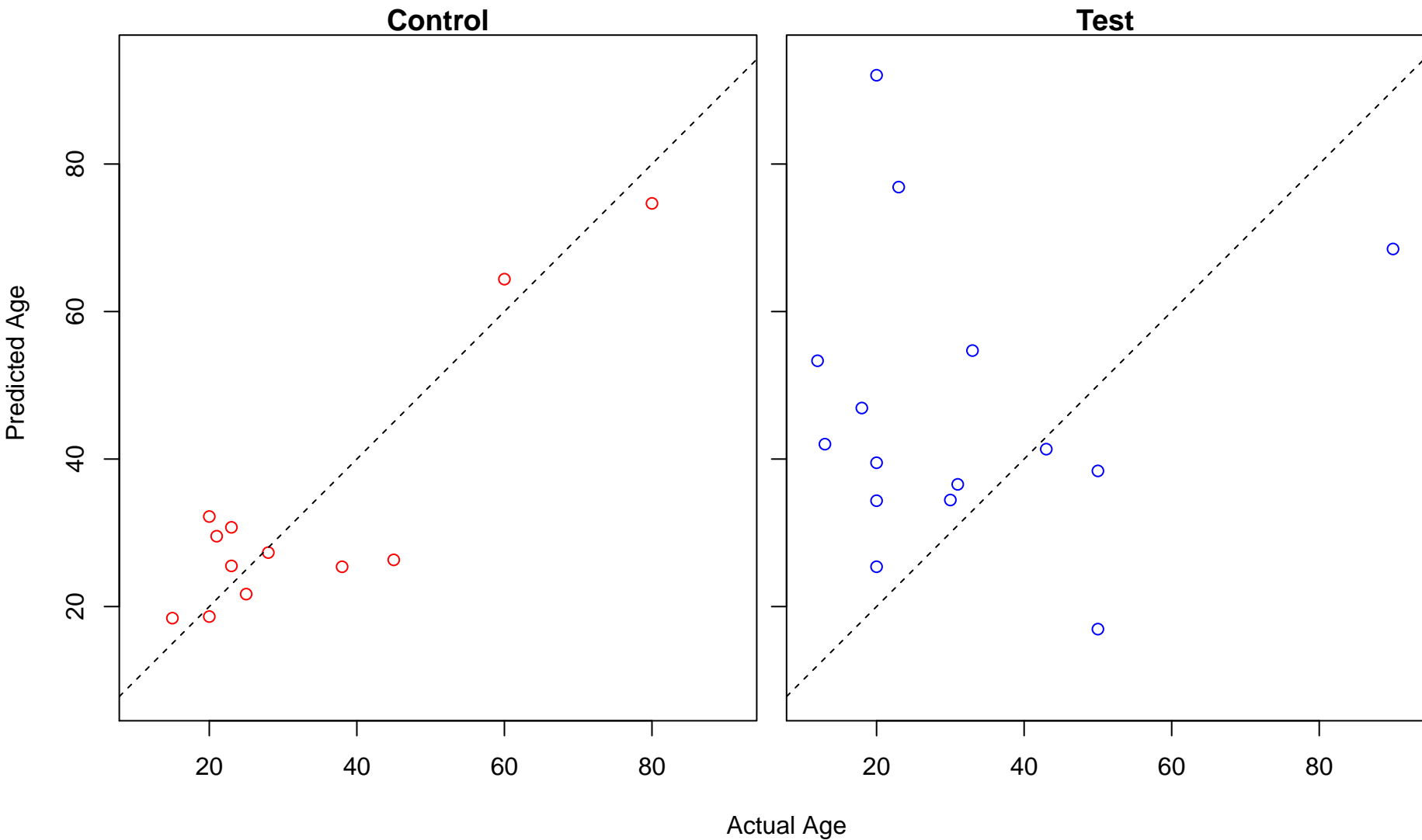
positive regulation of cell proliferation (Score: 4.785704)



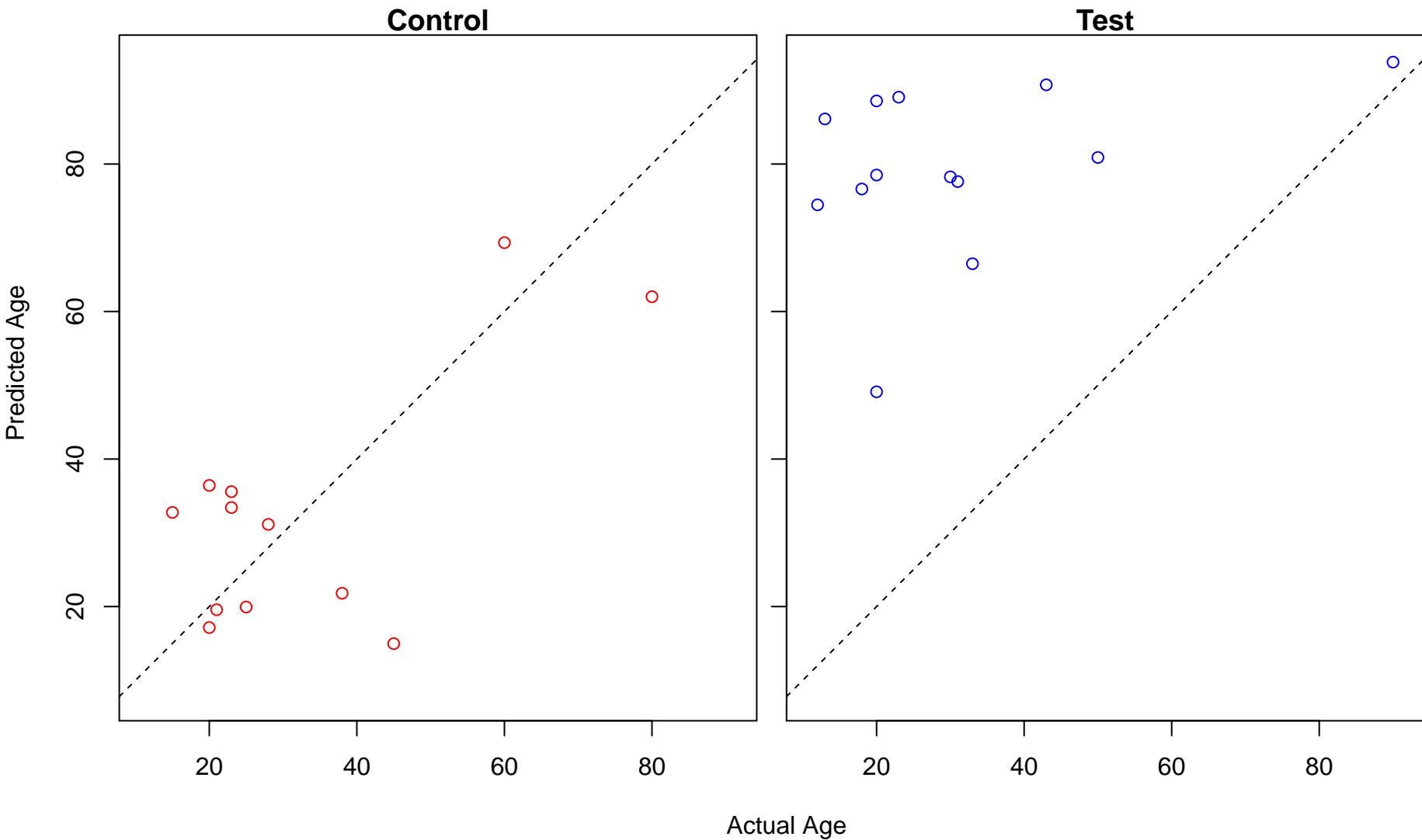
renal tubule morphogenesis (Score: 4.784187)



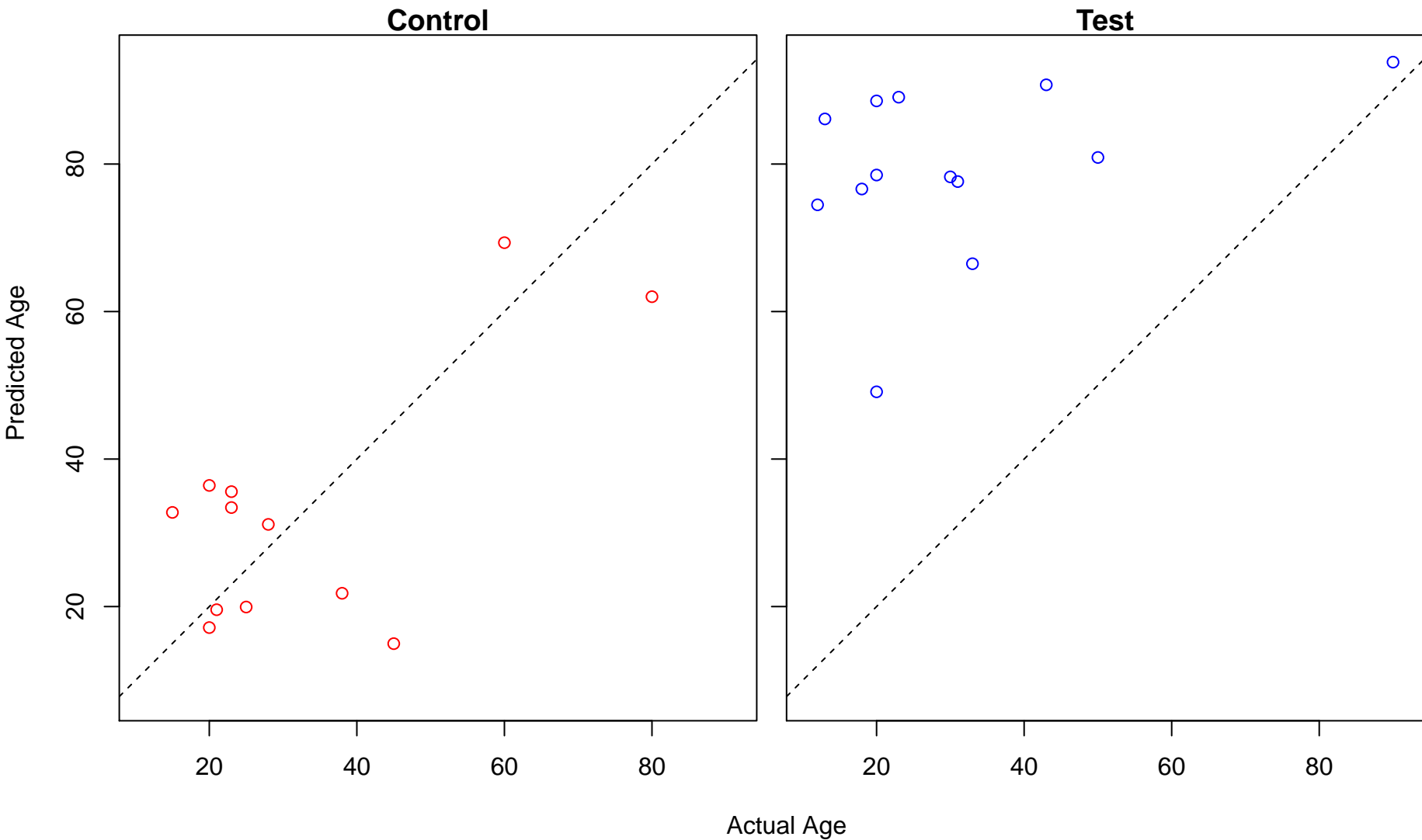
tRNA methylation (Score: 4.780494)



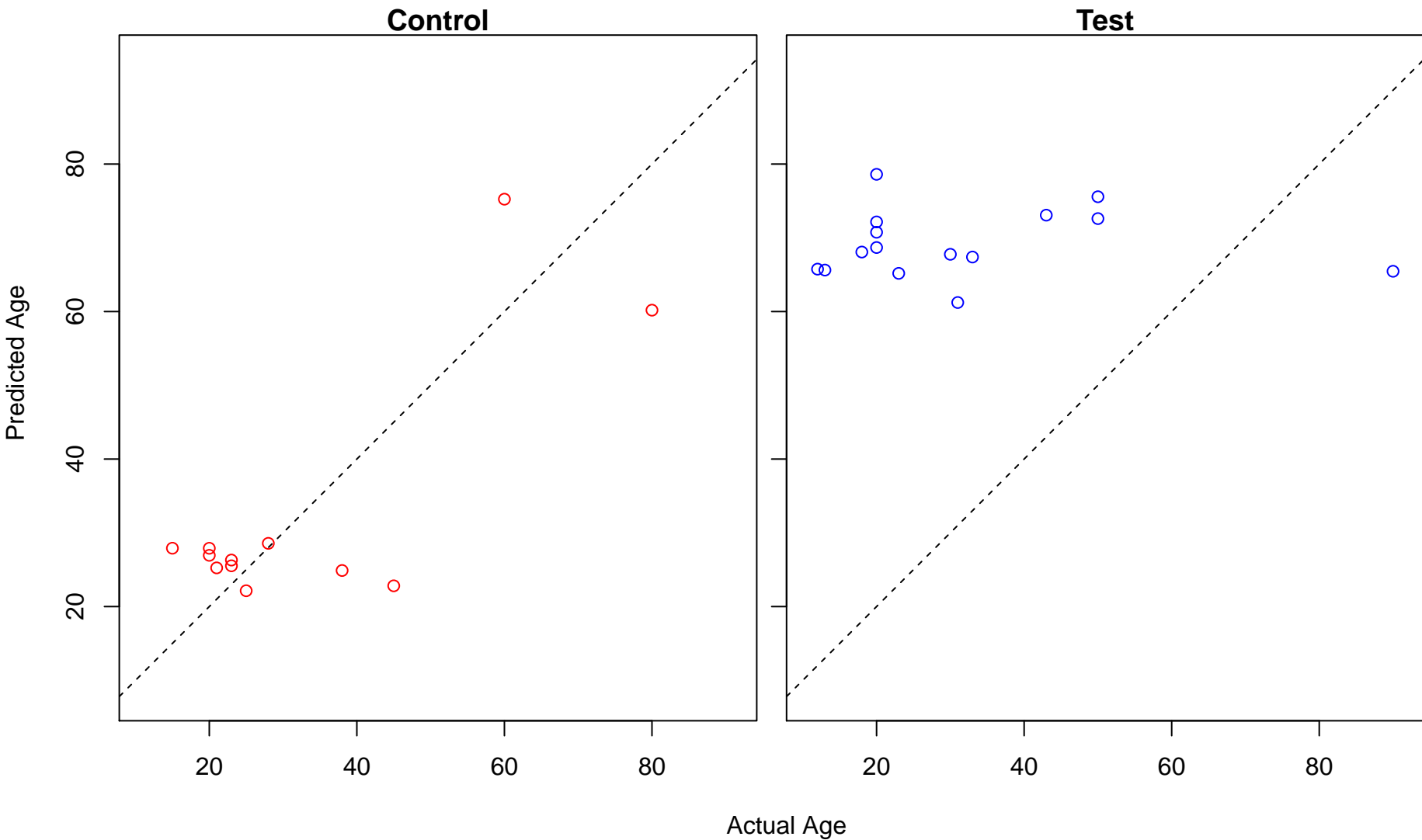
nuclear RNA surveillance (Score: 4.778990)



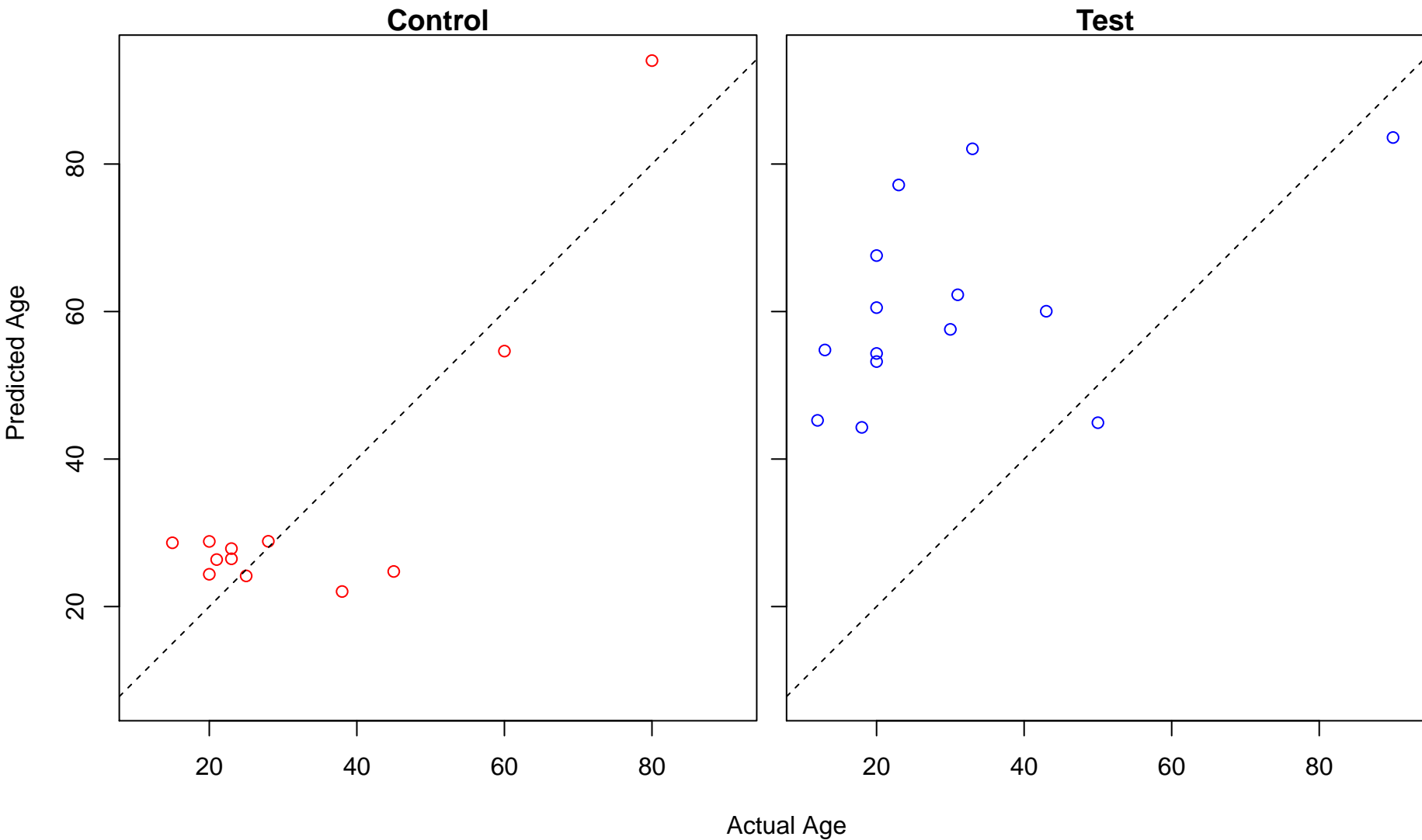
nuclear mRNA surveillance (Score: 4.778990)



multicellular organismal signaling (Score: 4.777561)

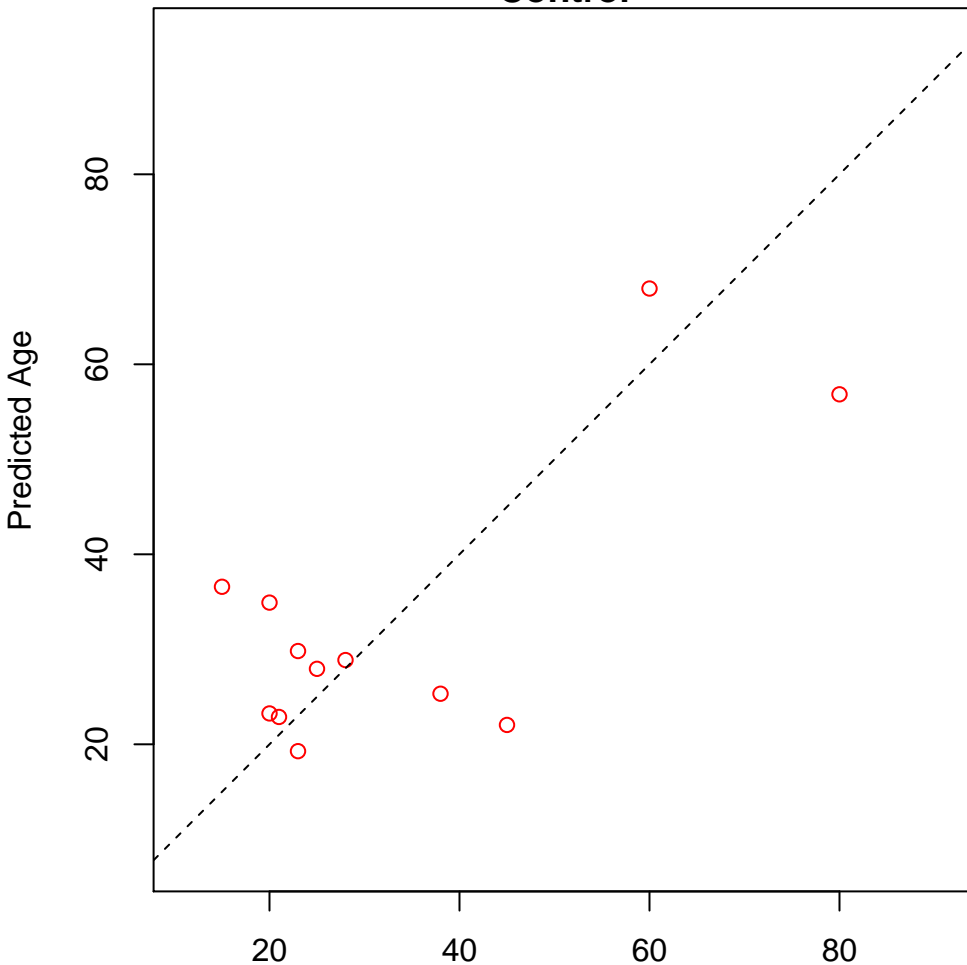


regulation of Rho protein signal transduction (Score: 4.776198)

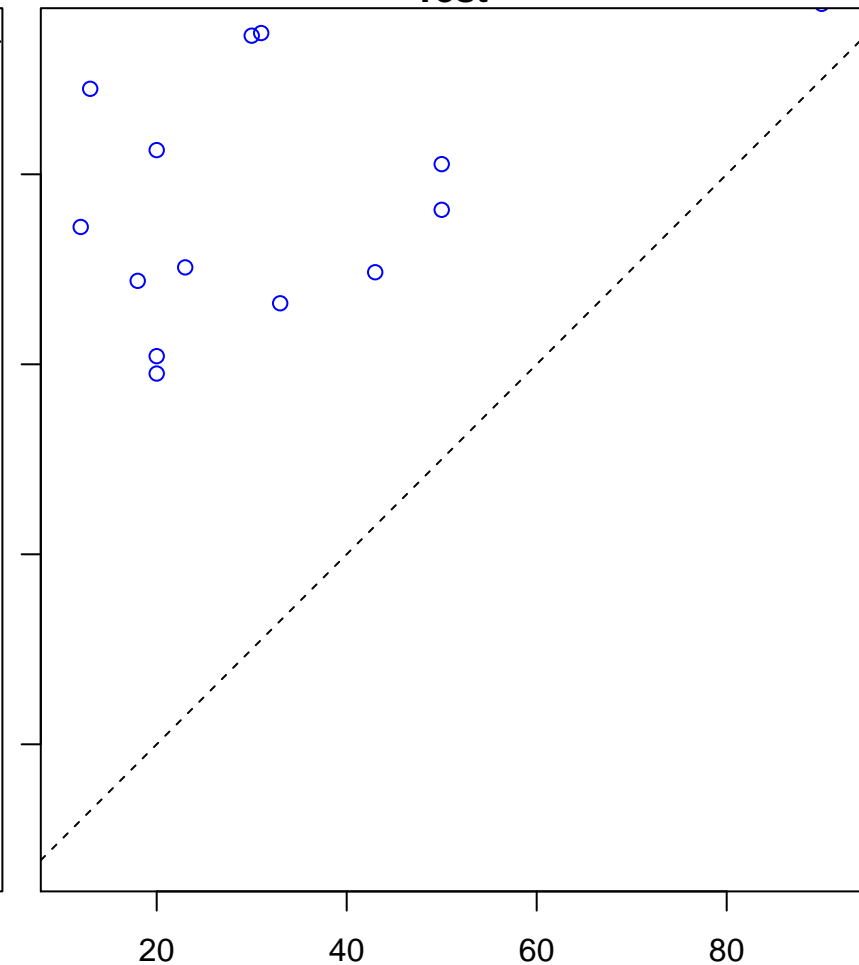


coronary vasculature morphogenesis (Score: 4.775721)

Control

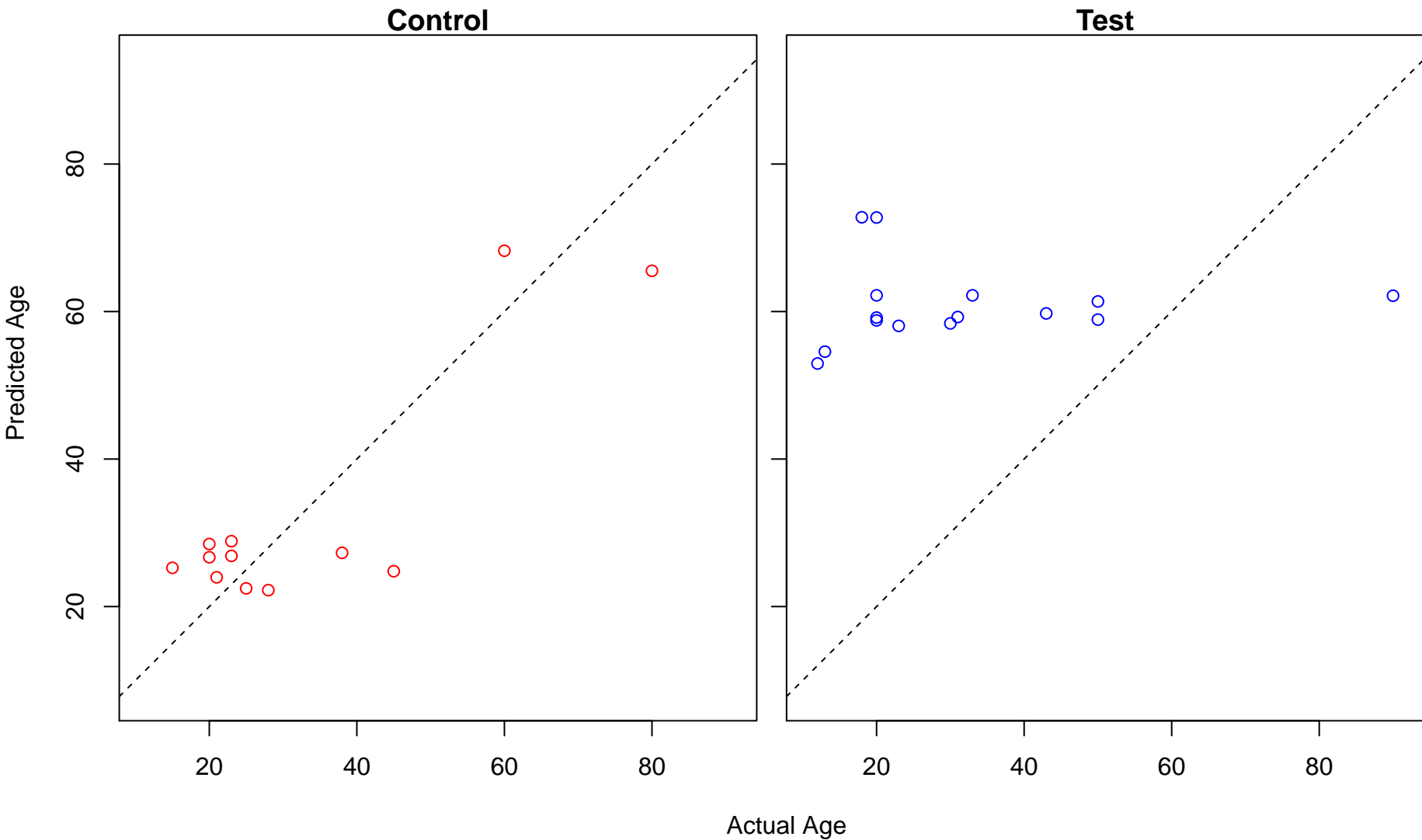


Test

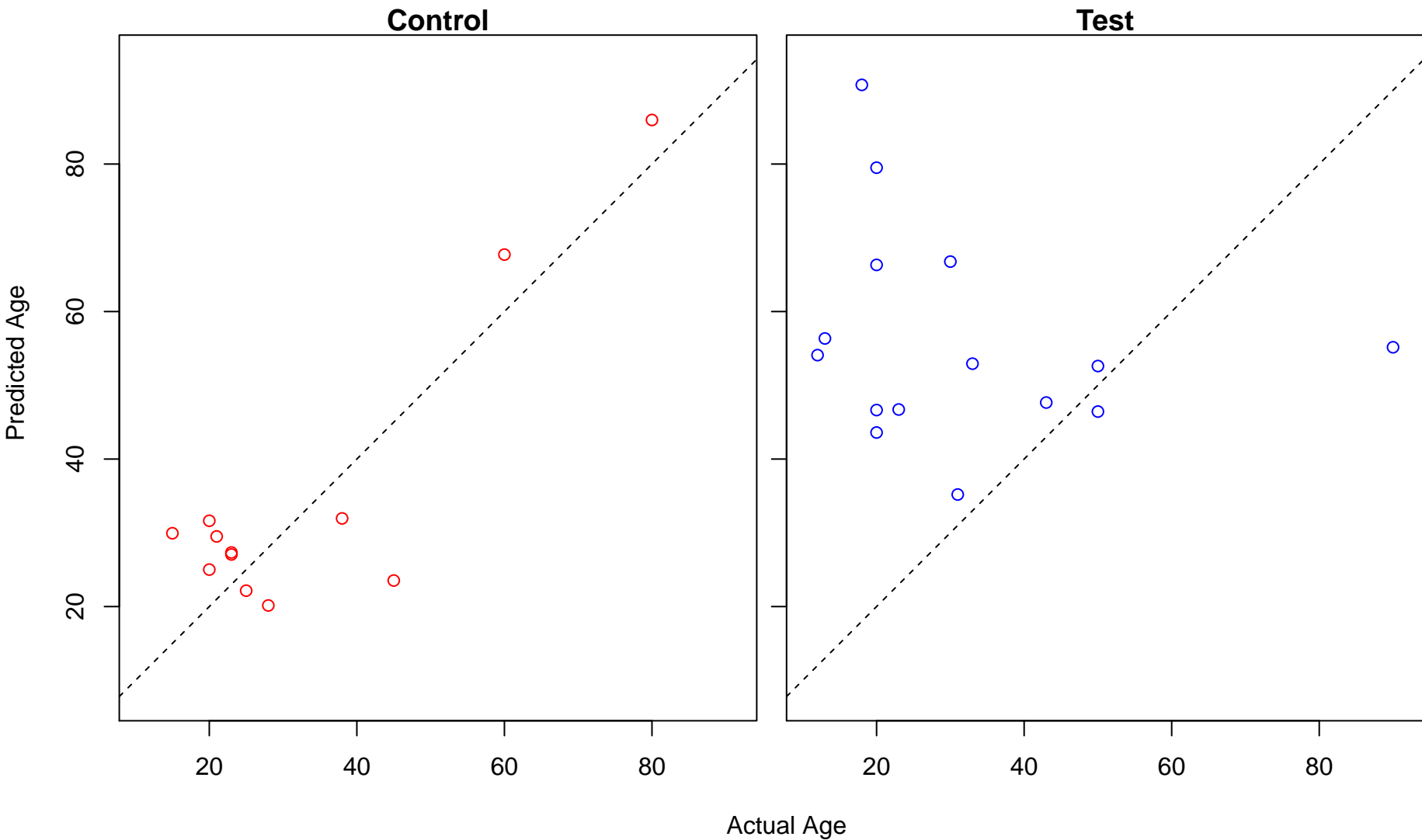


Actual Age

regulation of synapse organization (Score: 4.775480)

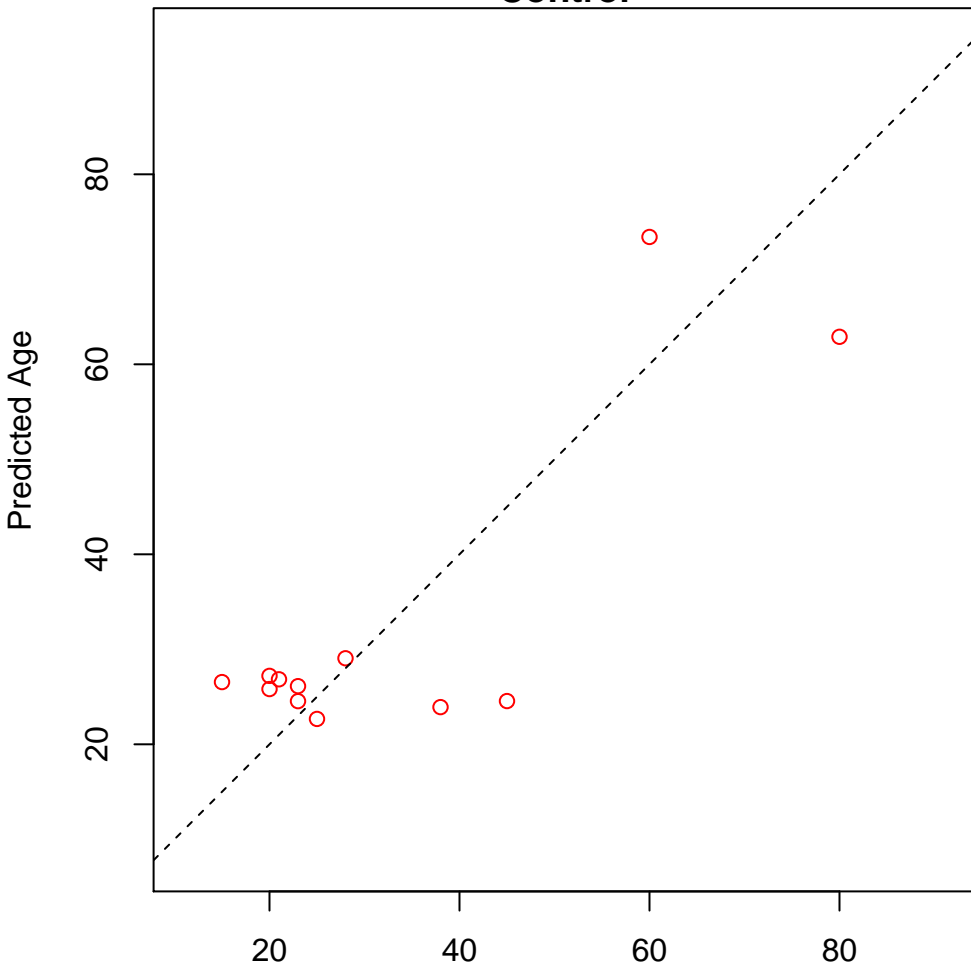


positive regulation of cellular response to insulin stimulus (Score: 4.774205)

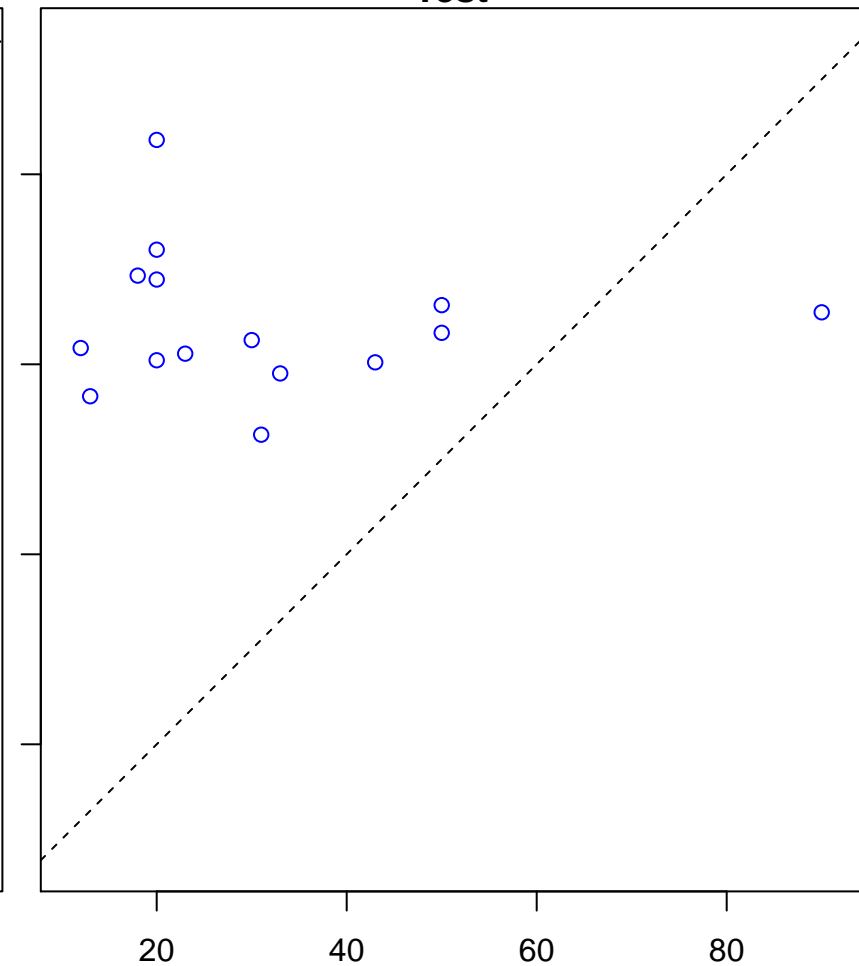


mitochondrial translational elongation (Score: 4.771215)

Control

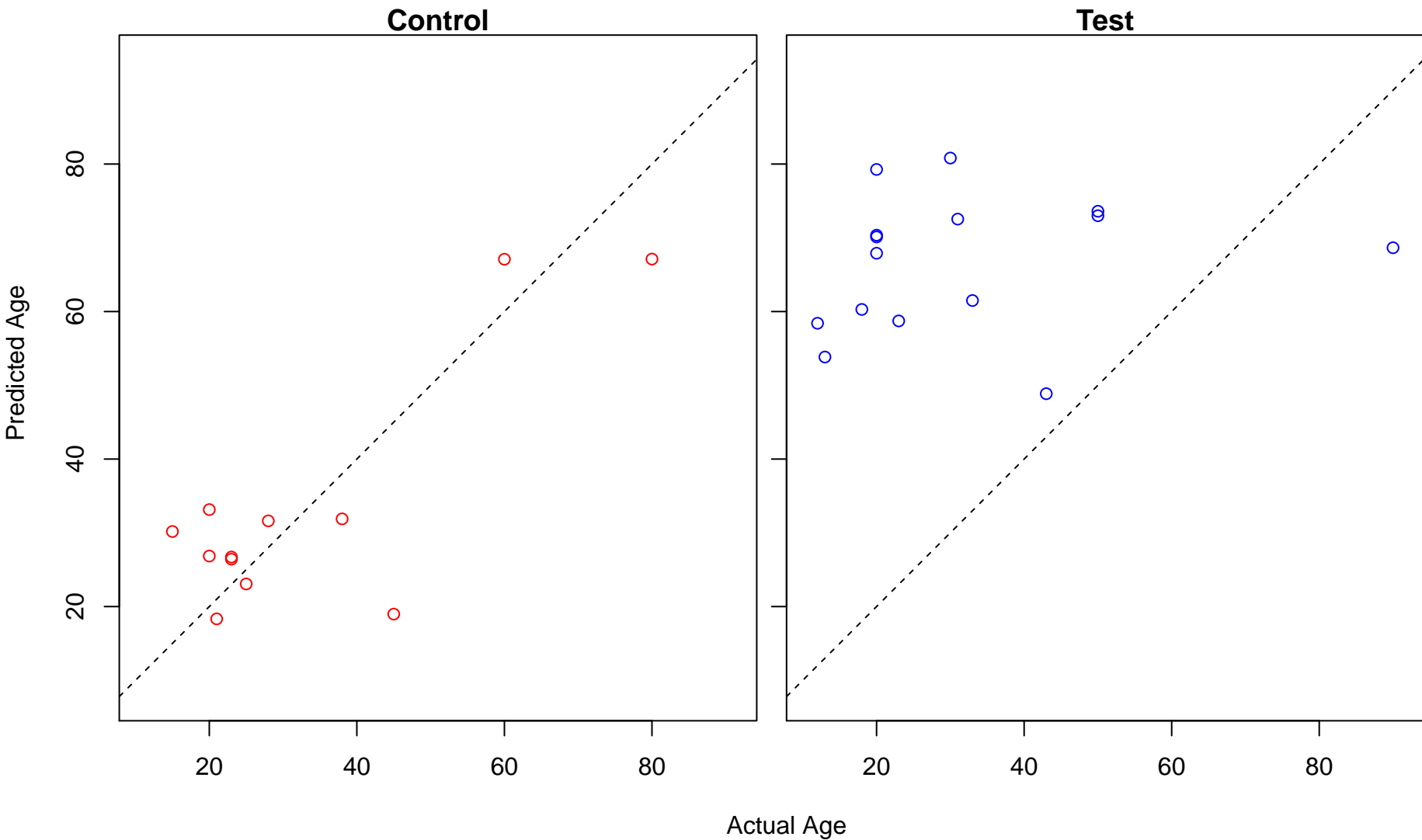


Test

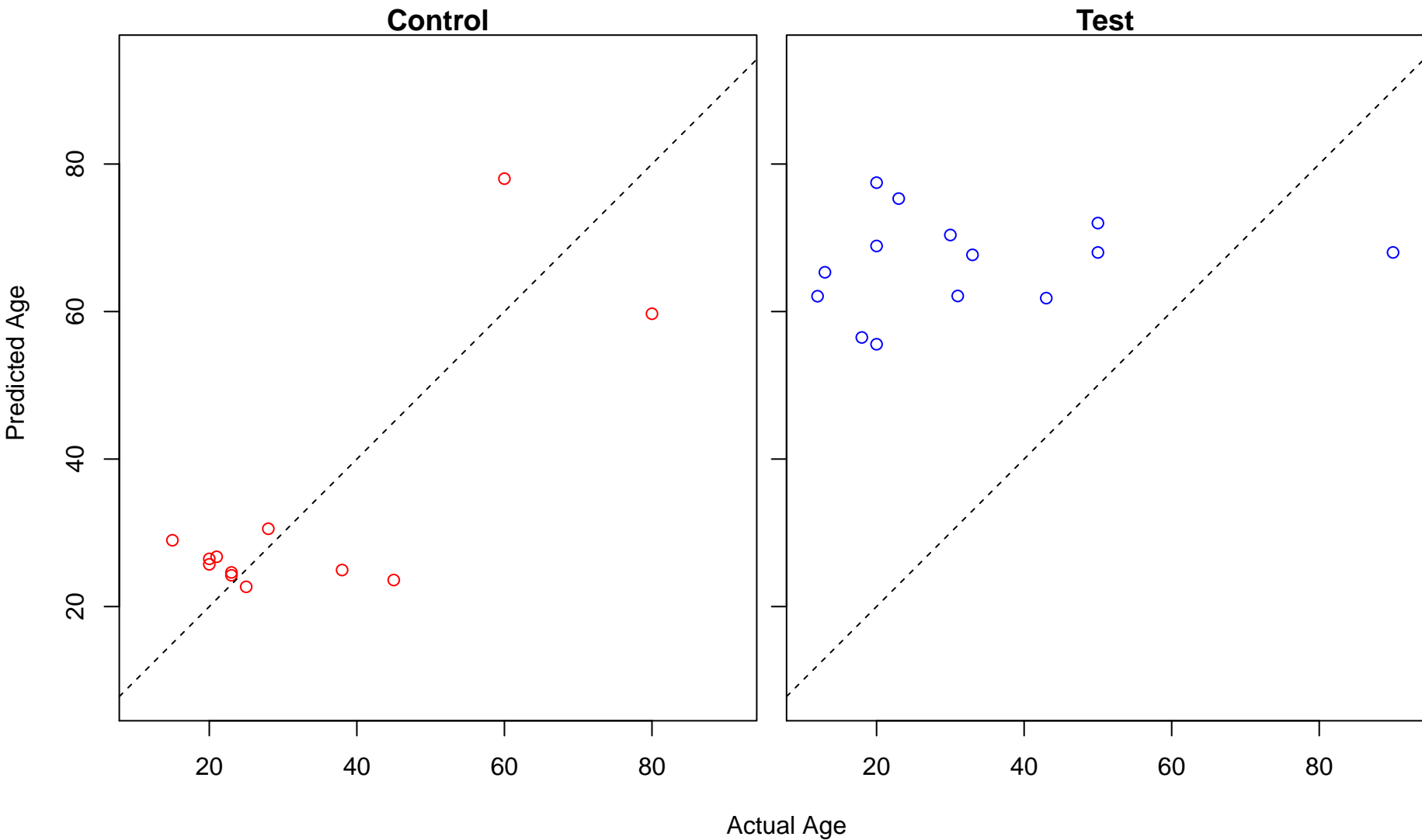


Actual Age

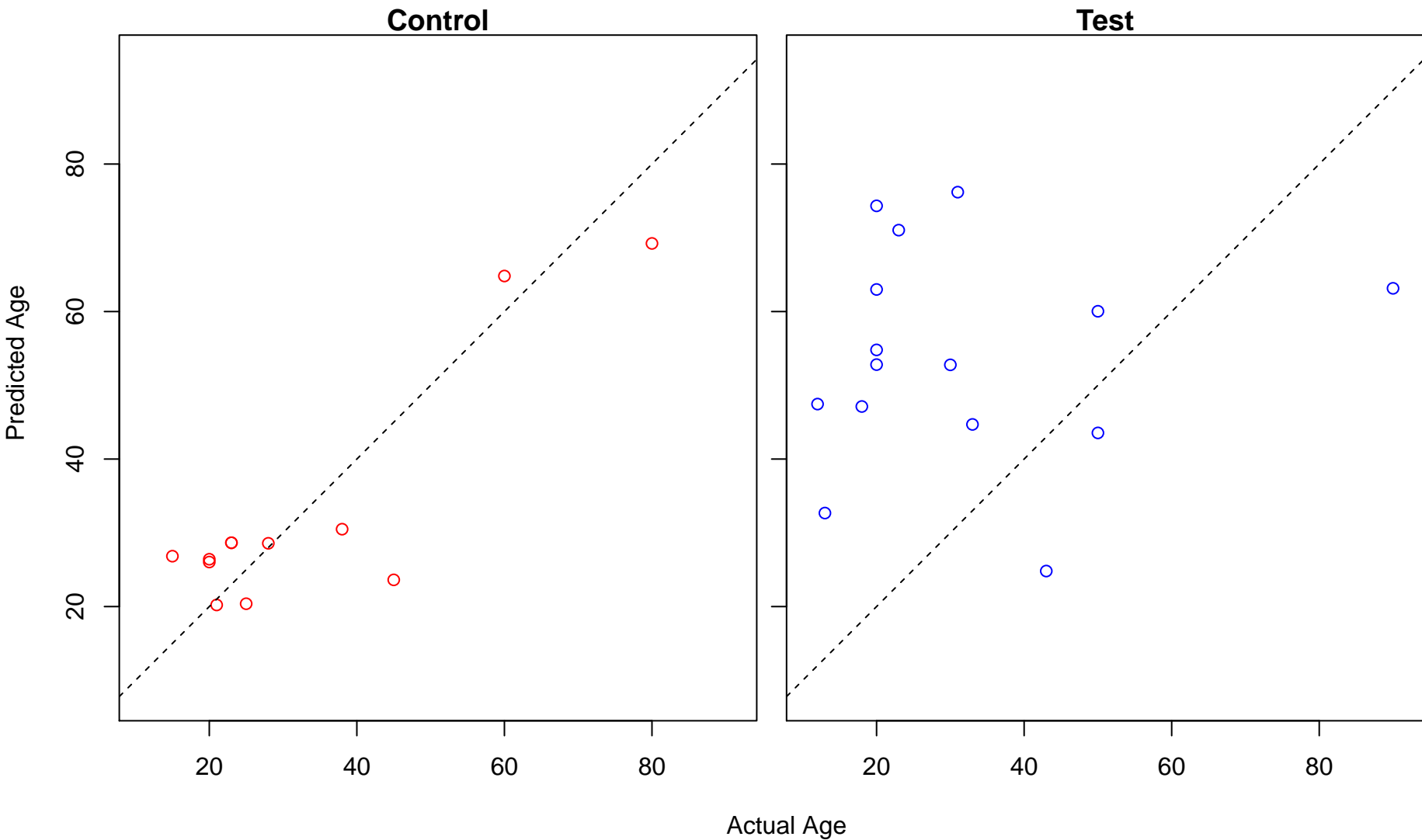
negative regulation of gene silencing (Score: 4.771159)



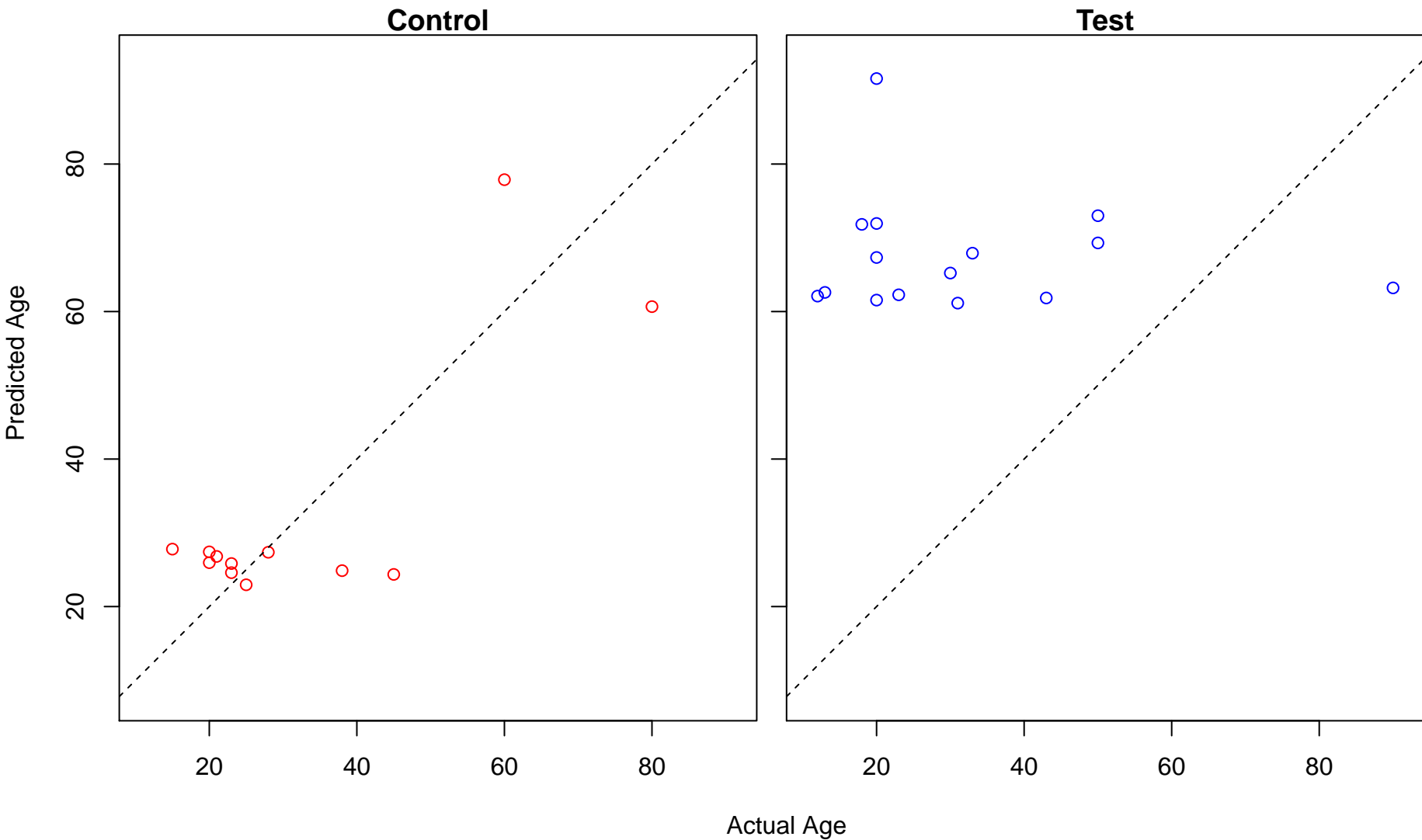
positive regulation of blood vessel endothelial cell migration (Score: 4.769557)



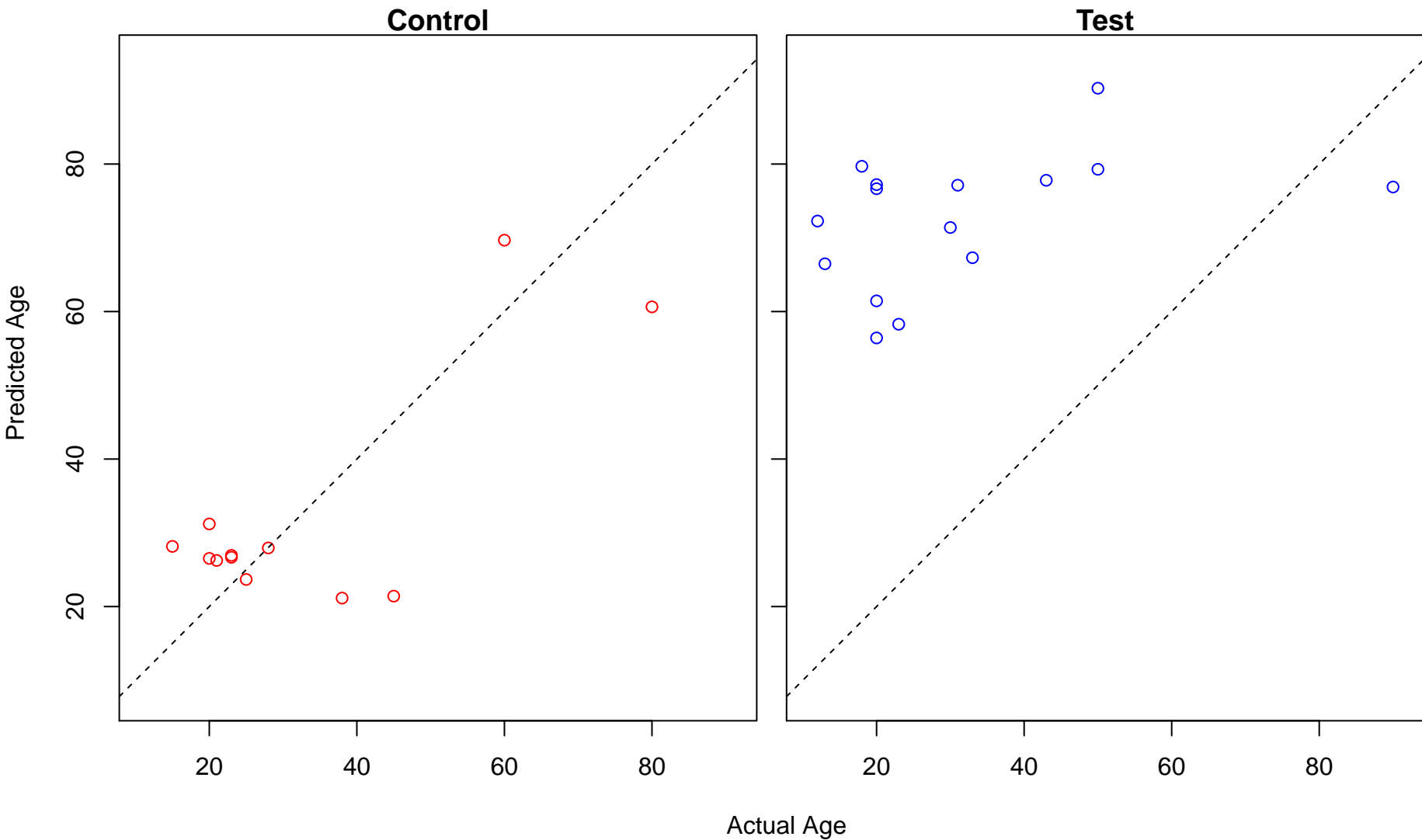
posttranscriptional gene silencing by RNA (Score: 4.769245)



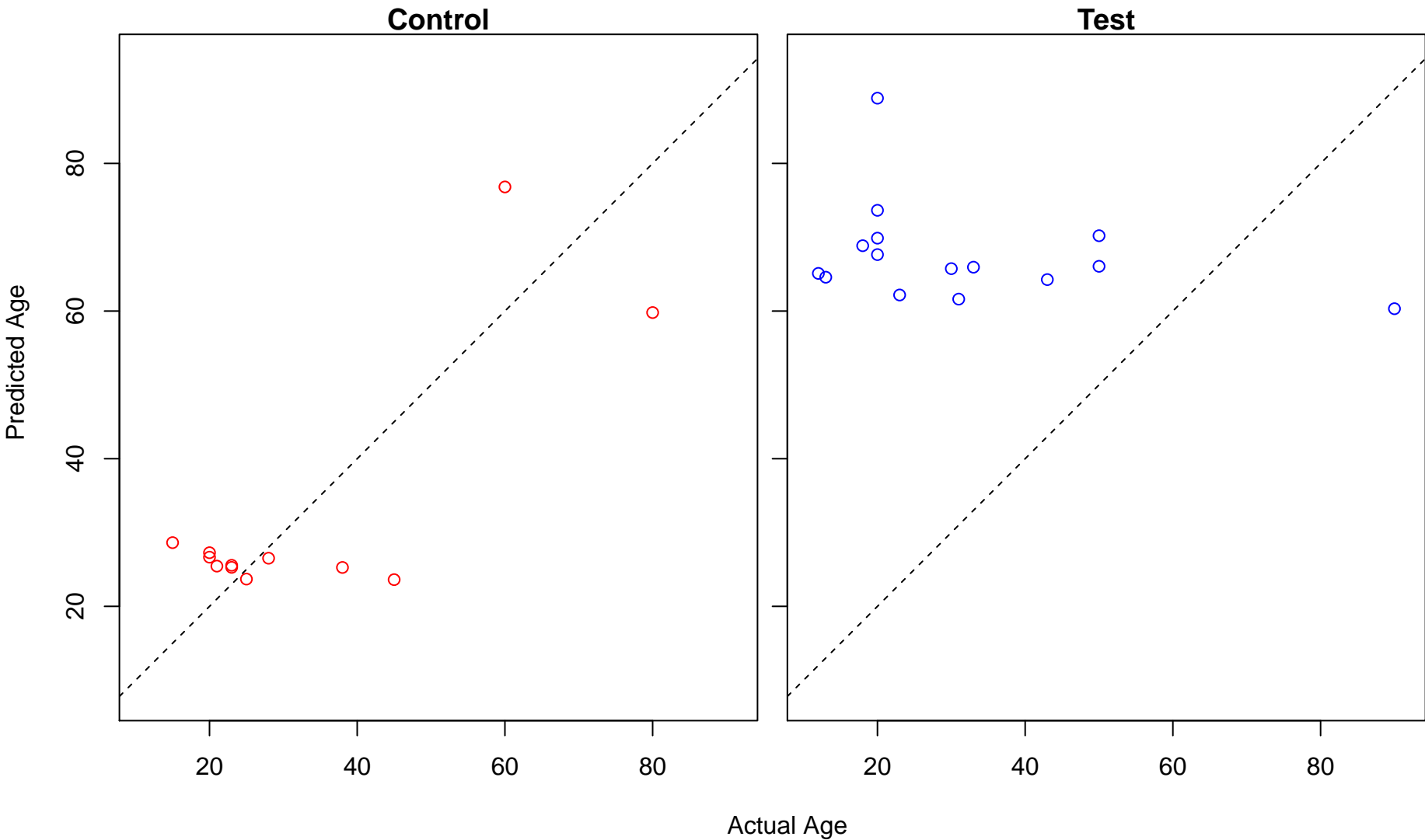
regulation of cell-matrix adhesion (Score: 4.768950)



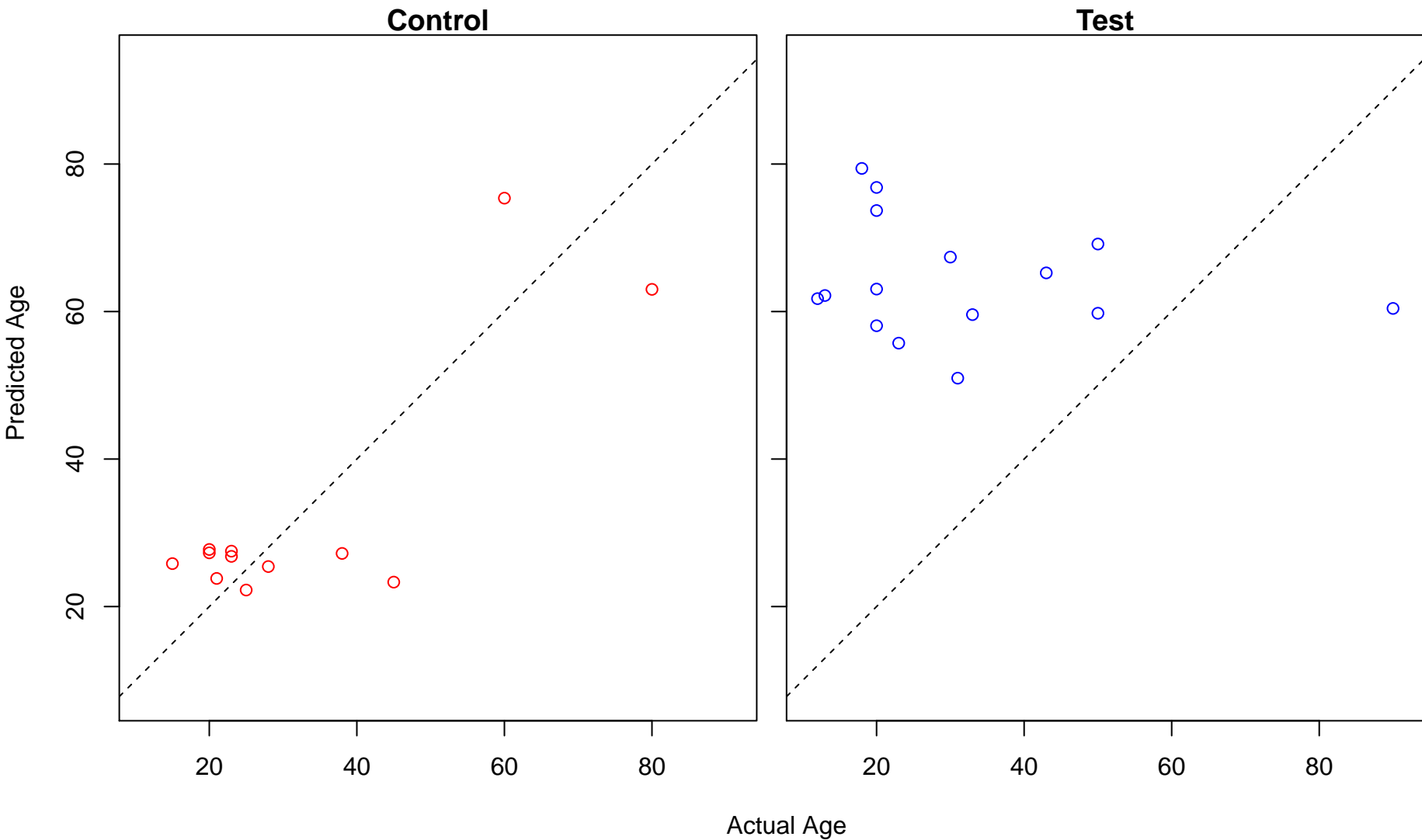
positive regulation of sodium ion transport (Score: 4.766726)



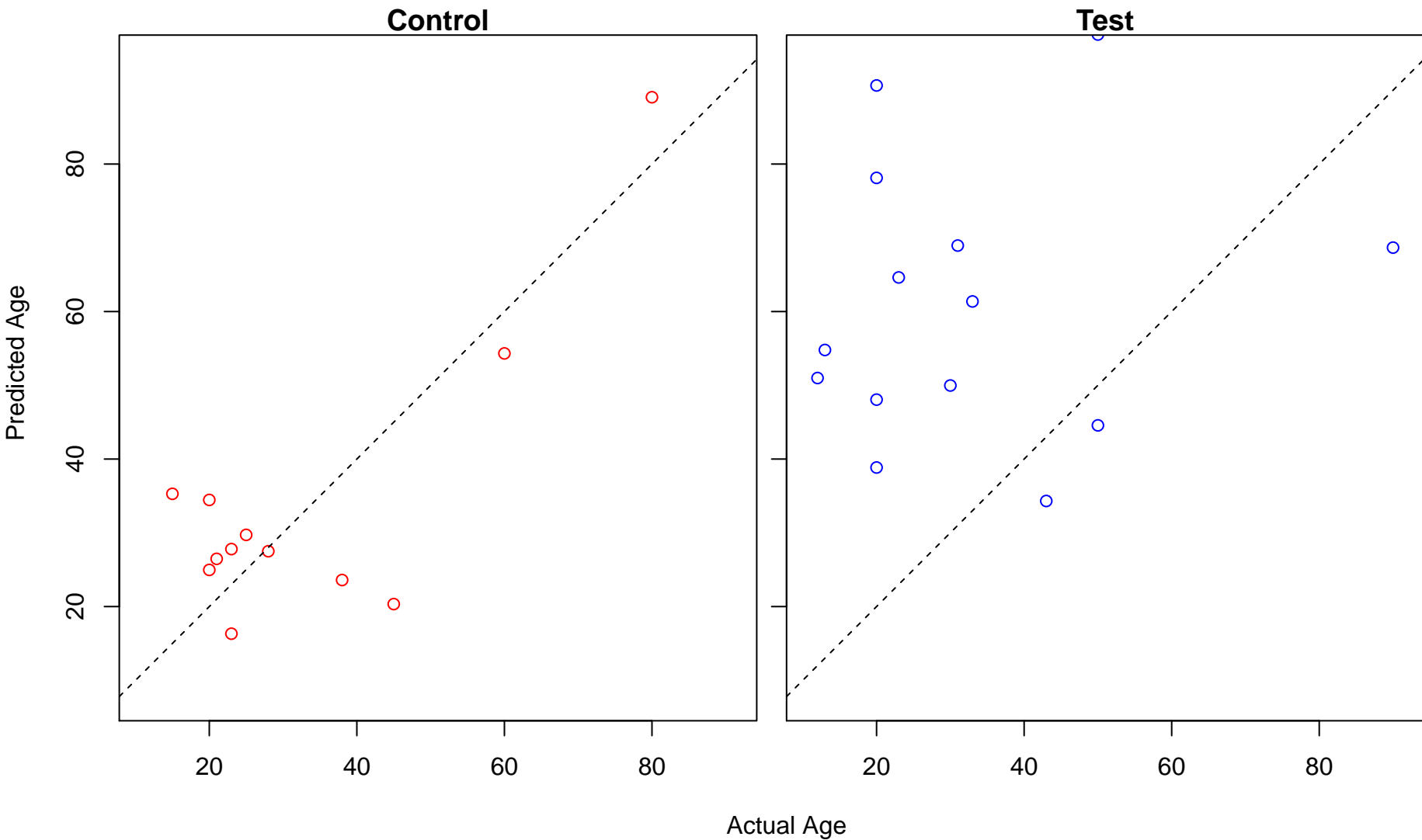
regulation of oxidative stress-induced intrinsic apoptotic signaling pathway (Score: 4.766432)



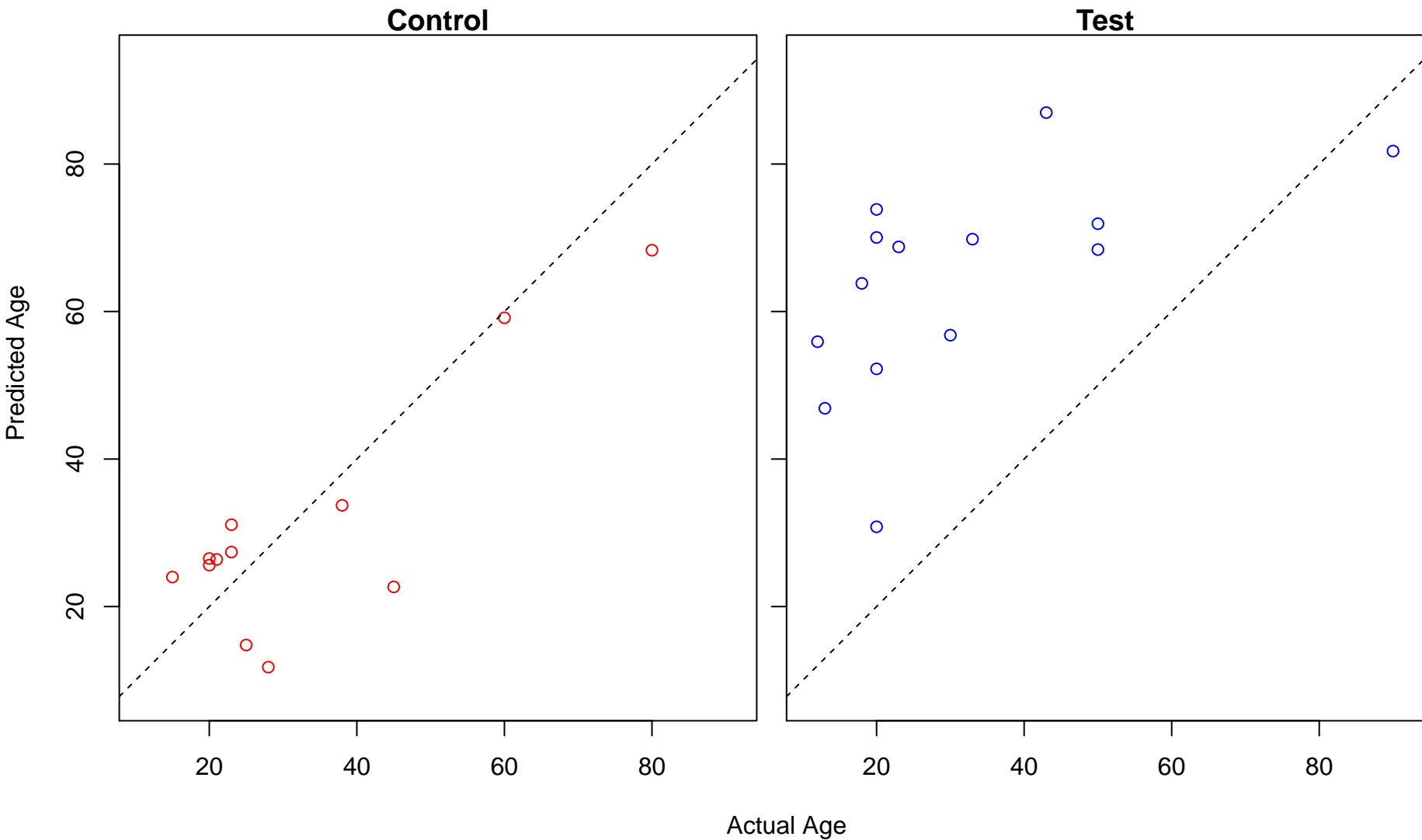
cargo loading into vesicle (Score: 4.765402)



regulation of mRNA processing (Score: 4.764620)

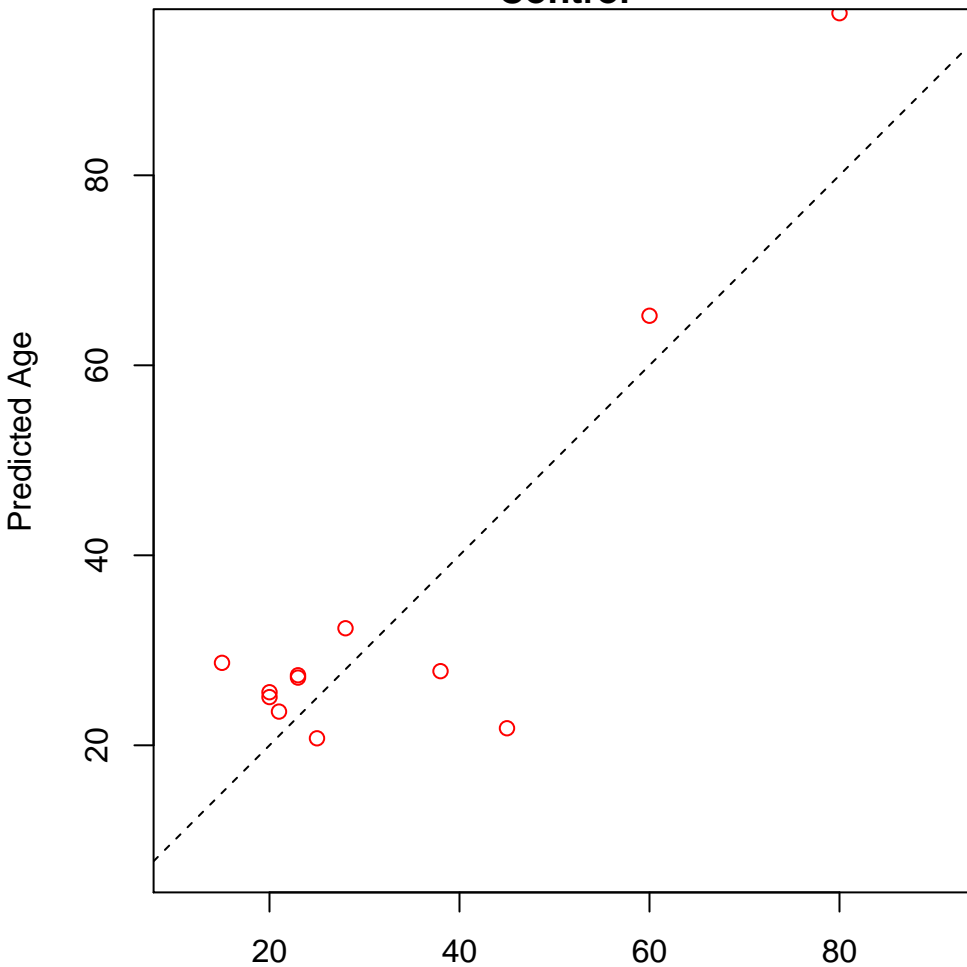


regulation of heart rate by cardiac conduction (Score: 4.761674)

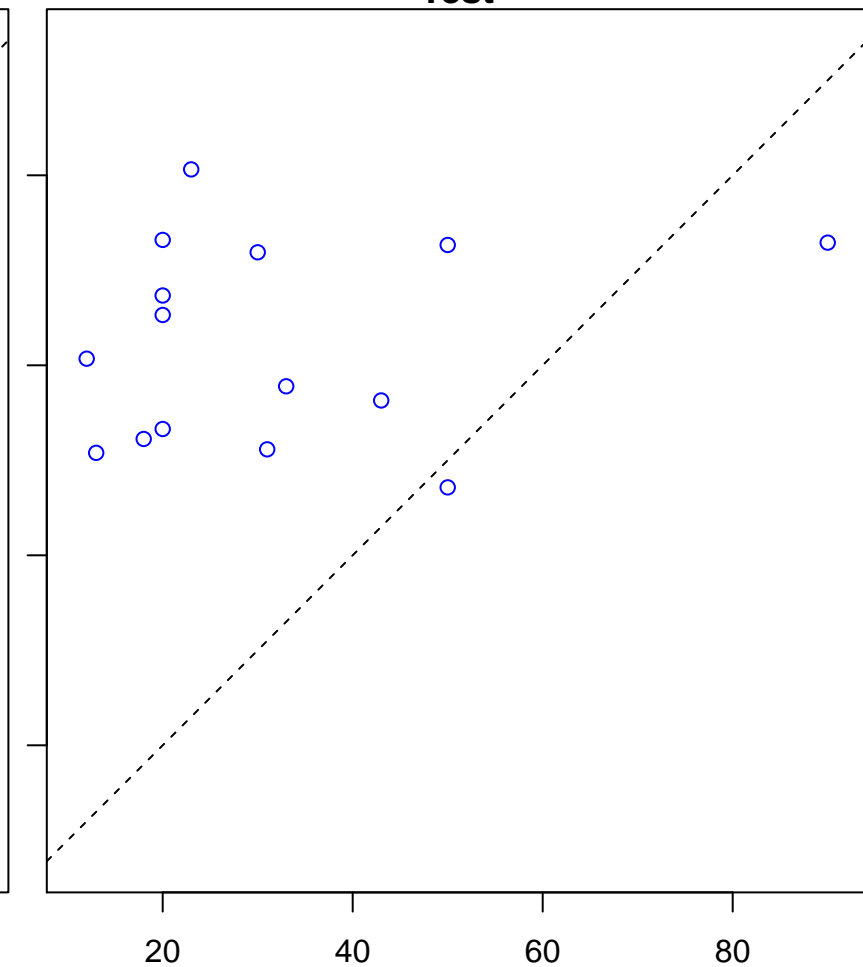


glycerophospholipid metabolic process (Score: 4.760846)

Control

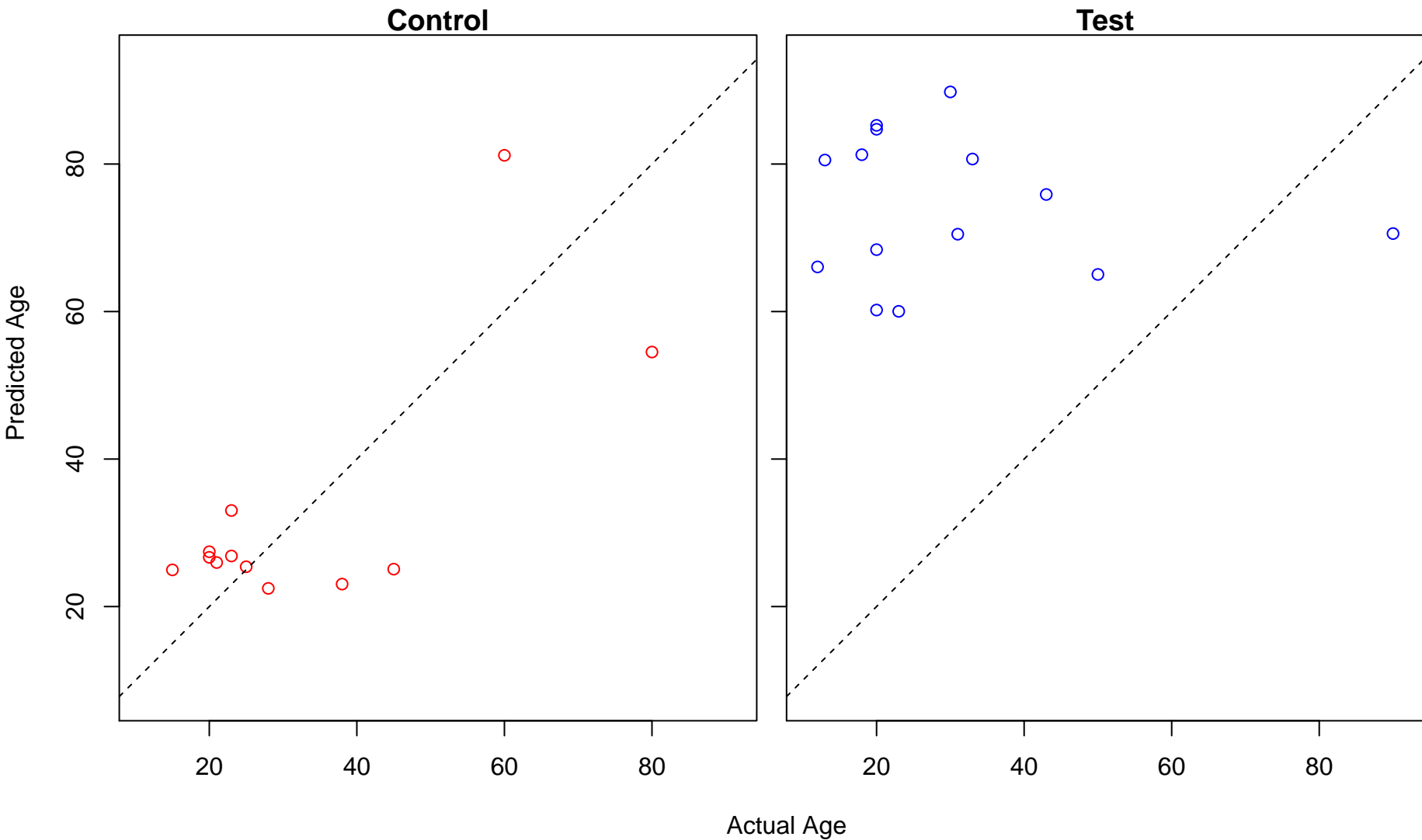


Test

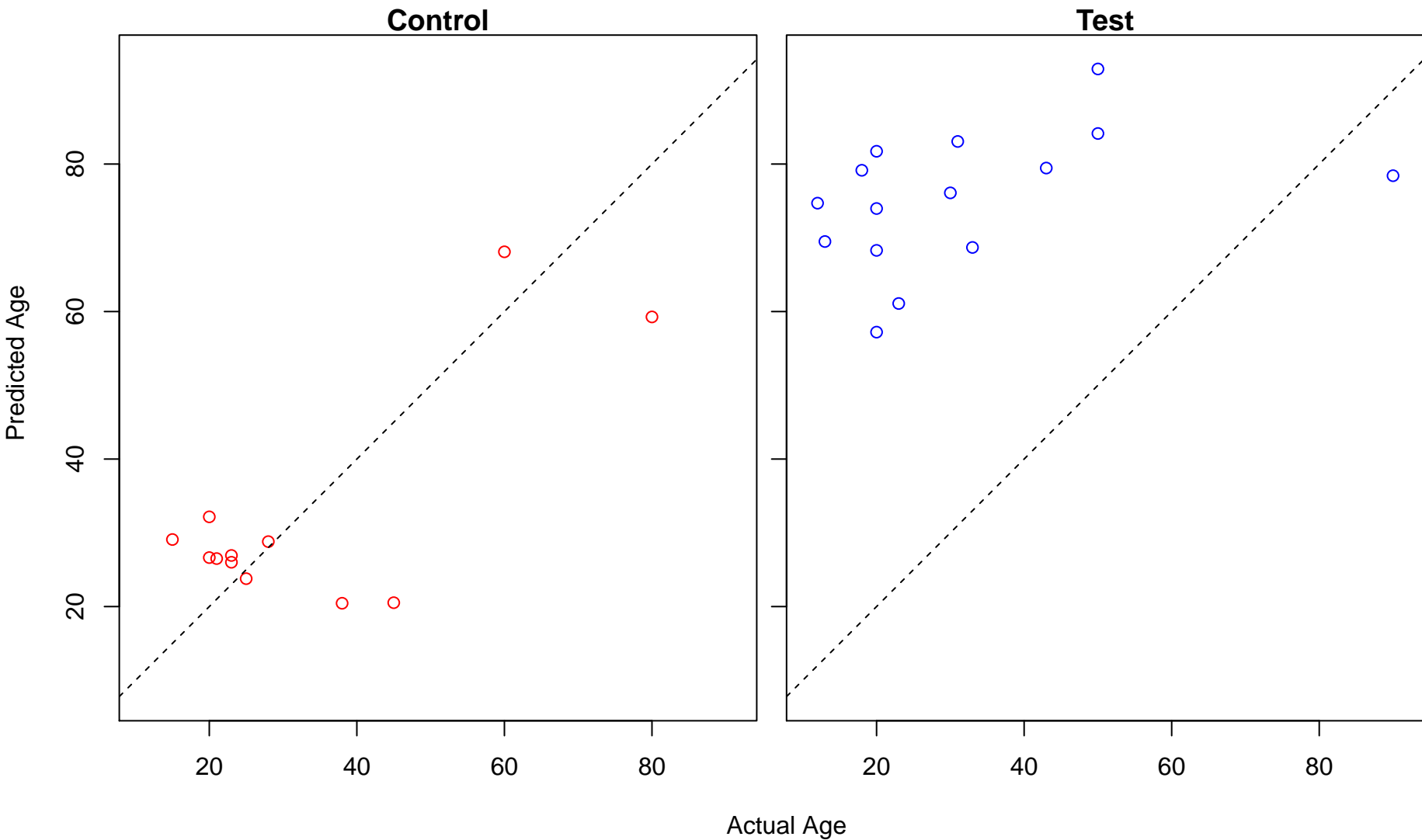


Actual Age

cellular response to arsenic-containing substance (Score: 4.758860)

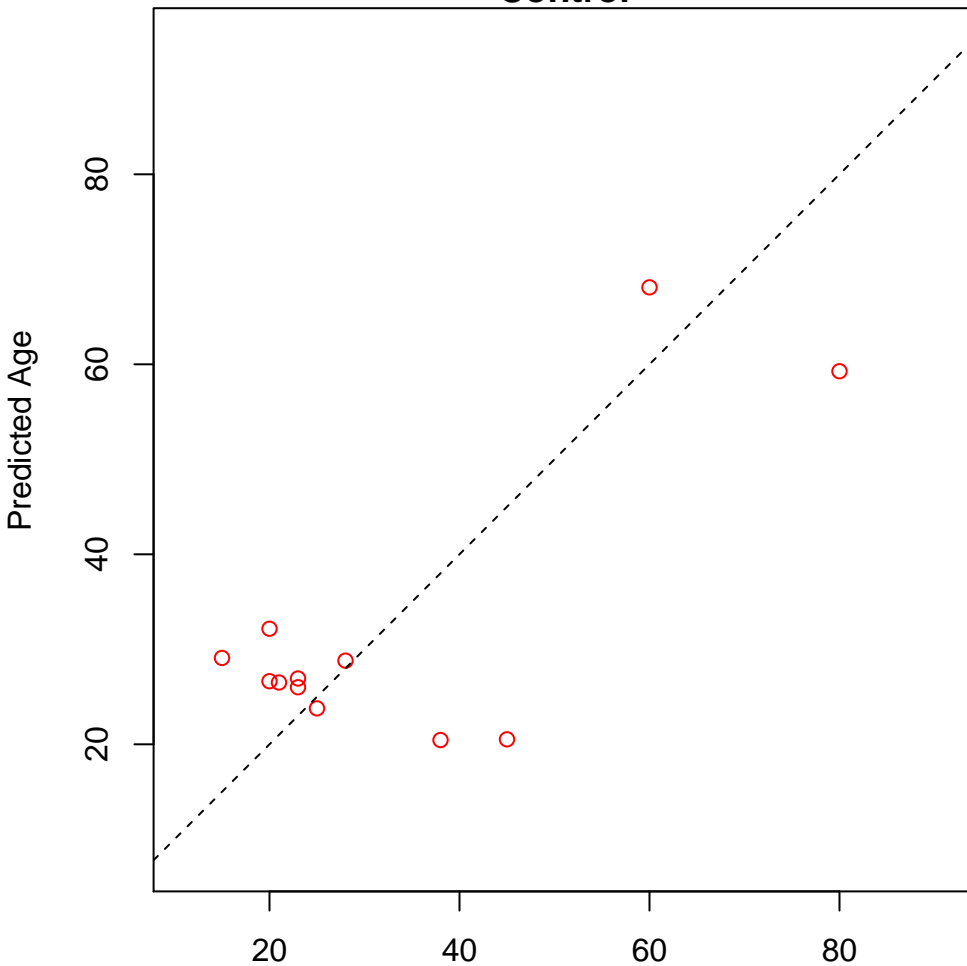


cellular potassium ion transport (Score: 4.756584)

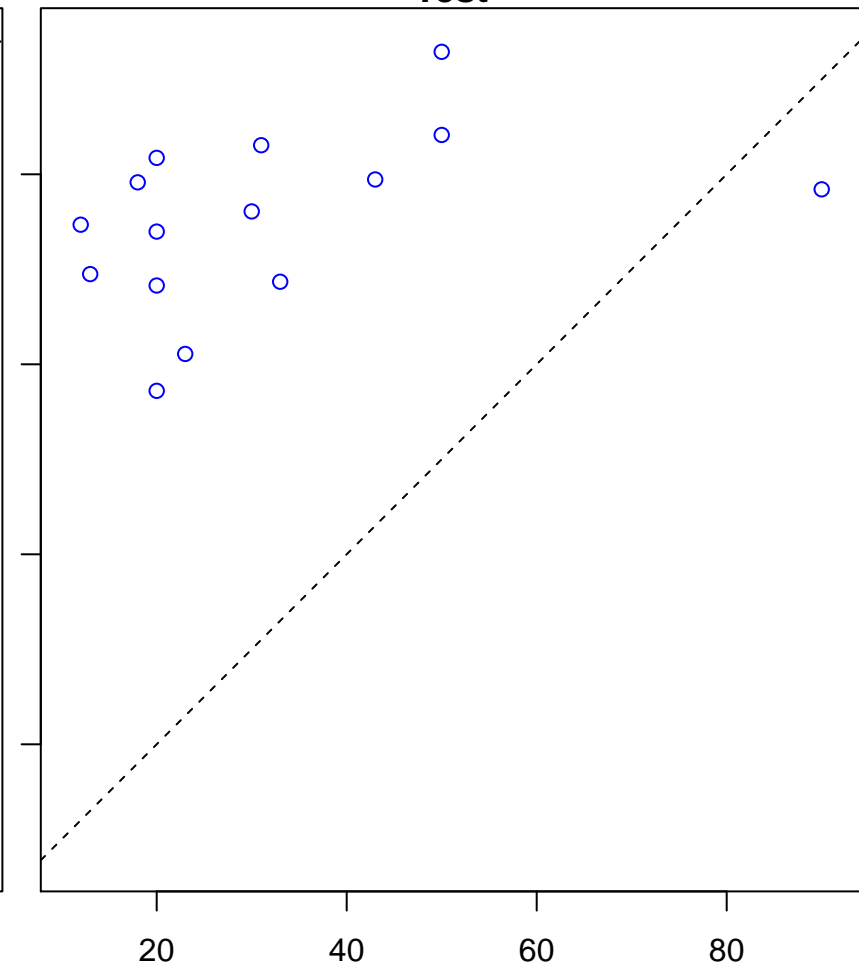


potassium ion transmembrane transport (Score: 4.756584)

Control

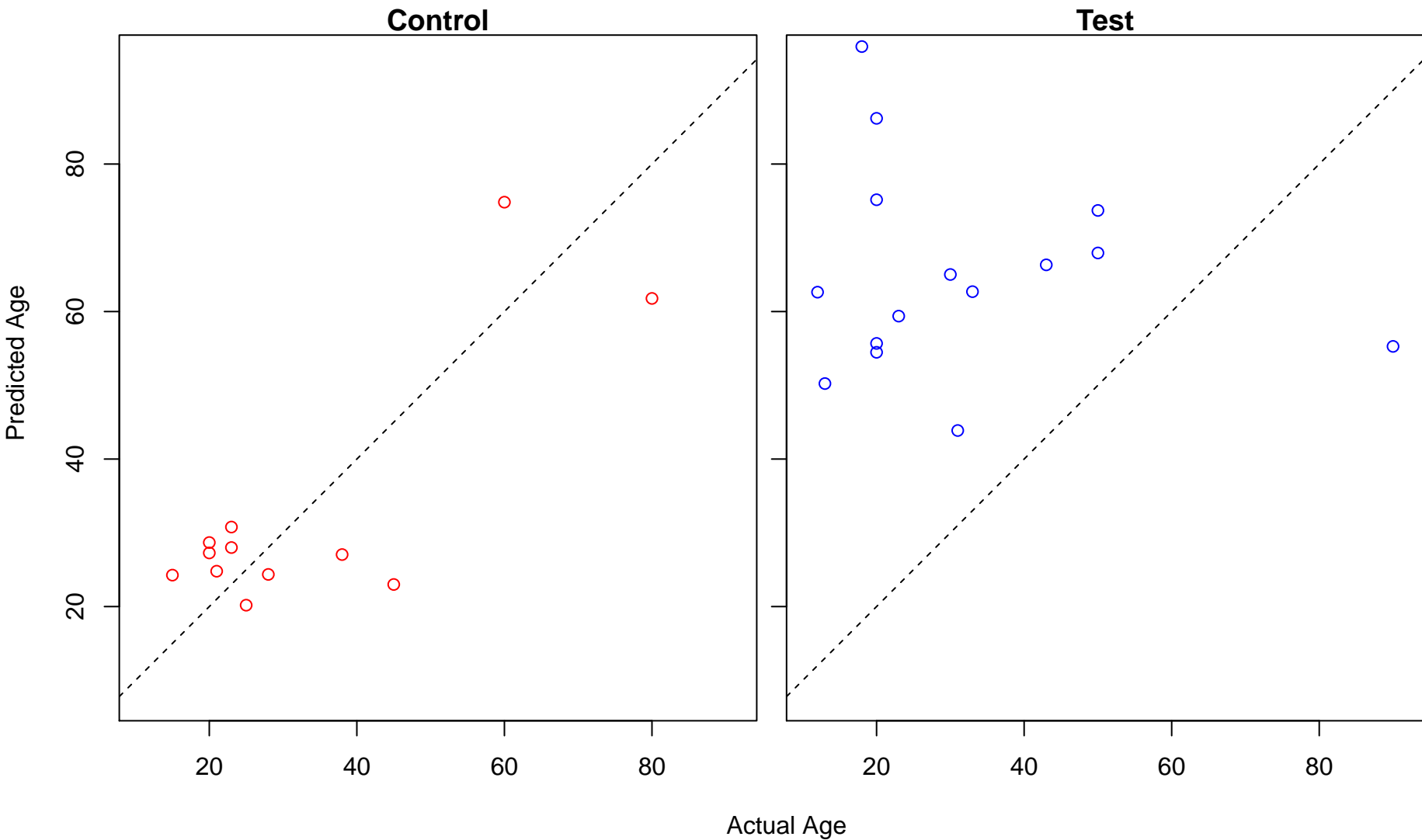


Test

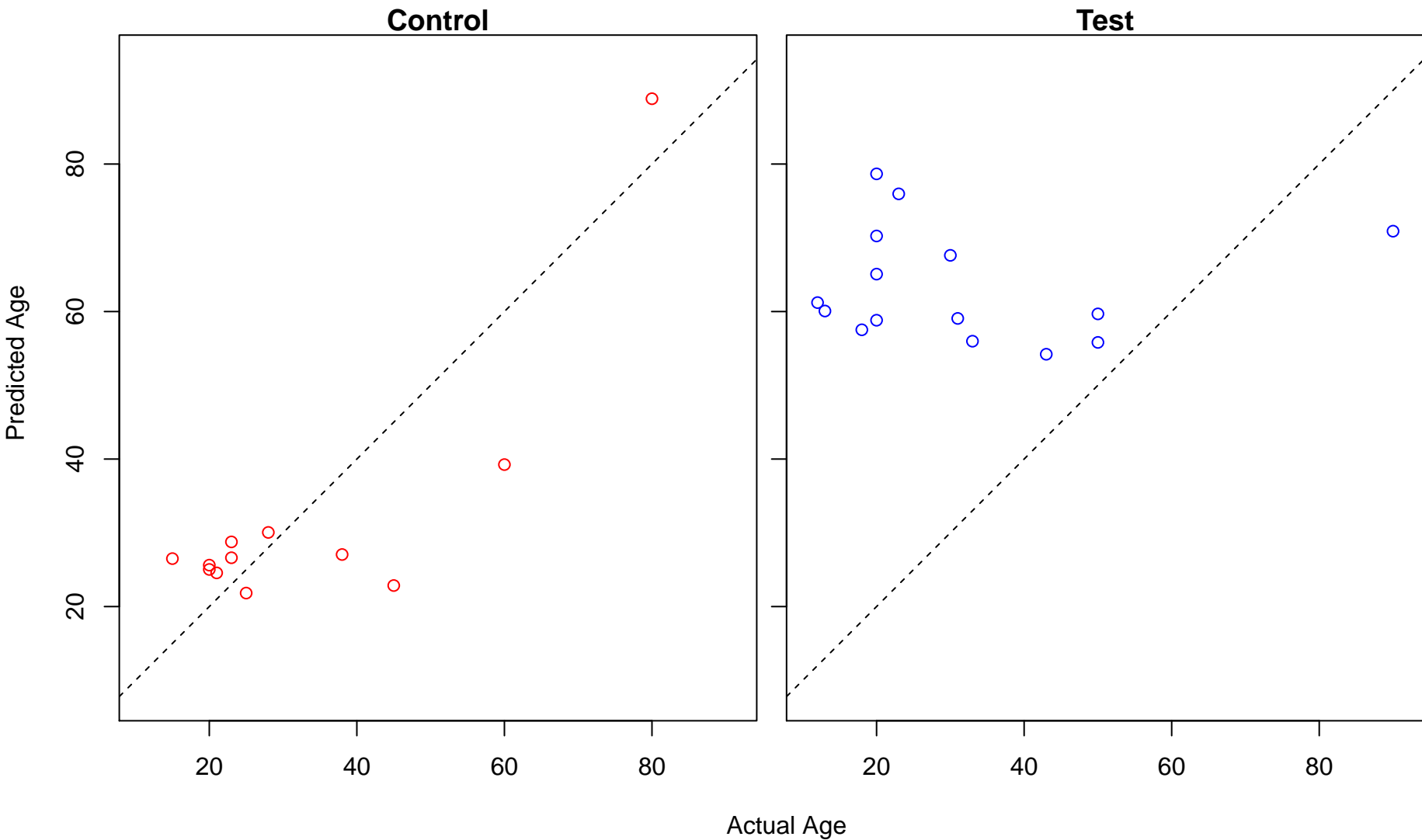


Actual Age

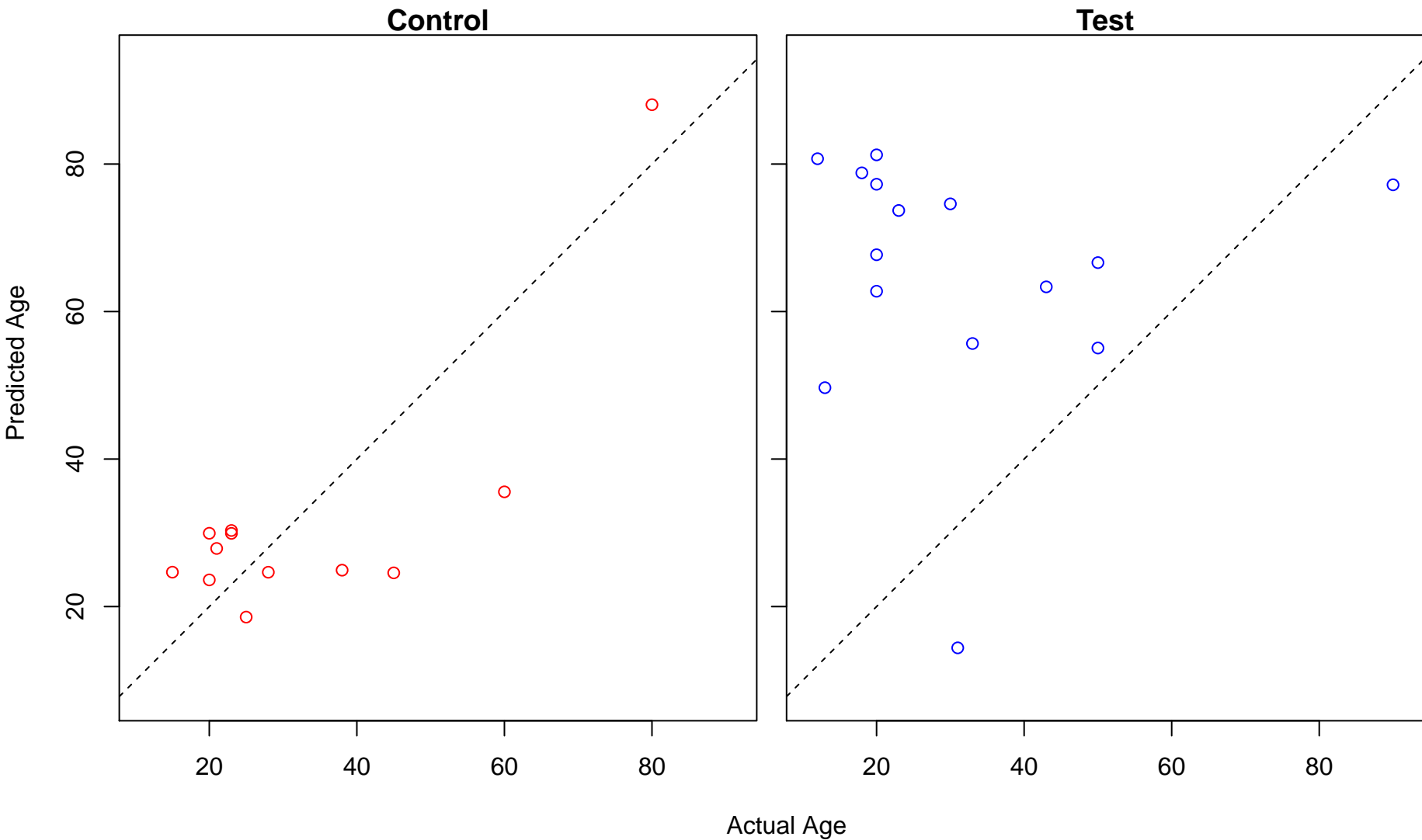
purinergic nucleotide receptor signaling pathway (Score: 4.755725)



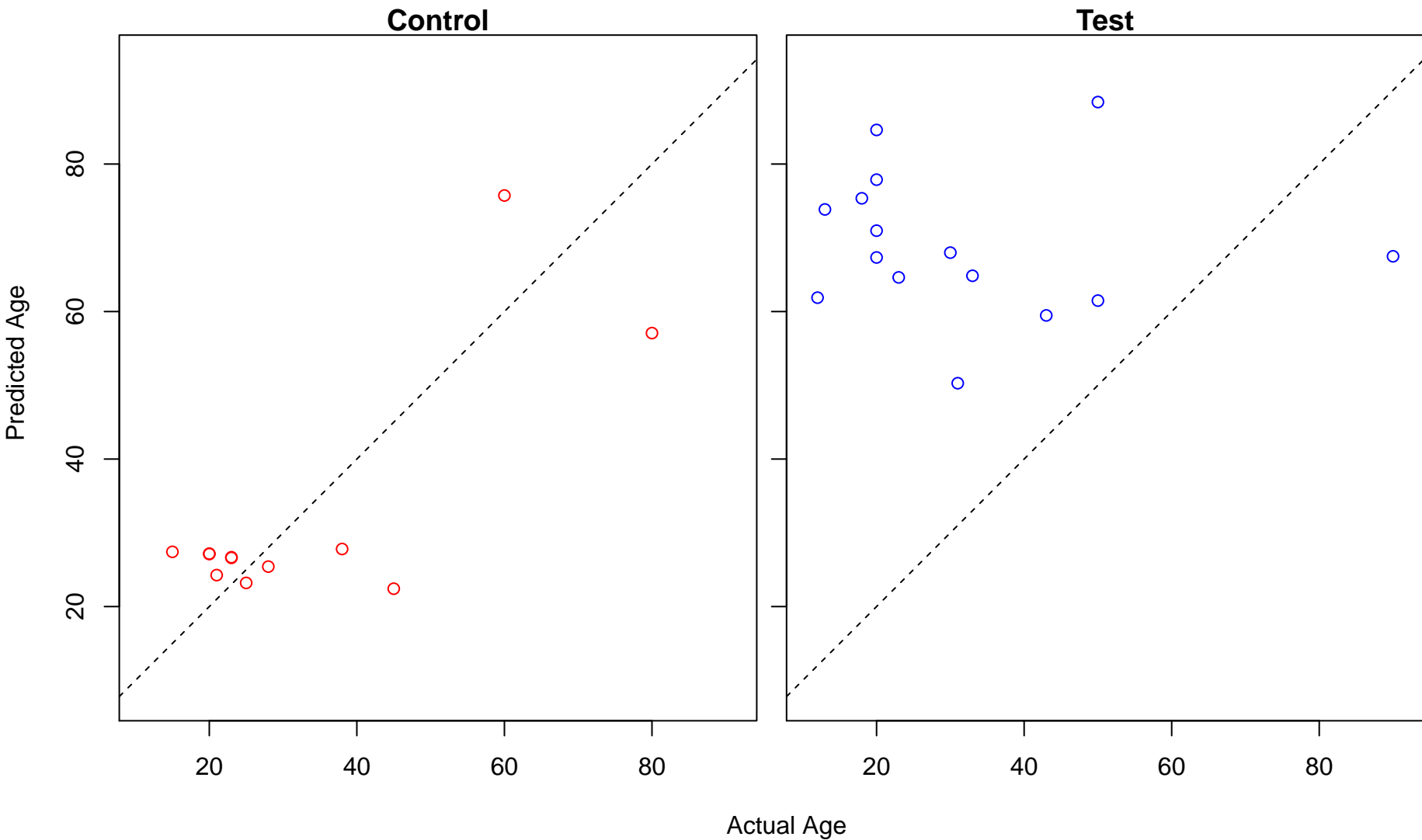
amine metabolic process (Score: 4.75565)



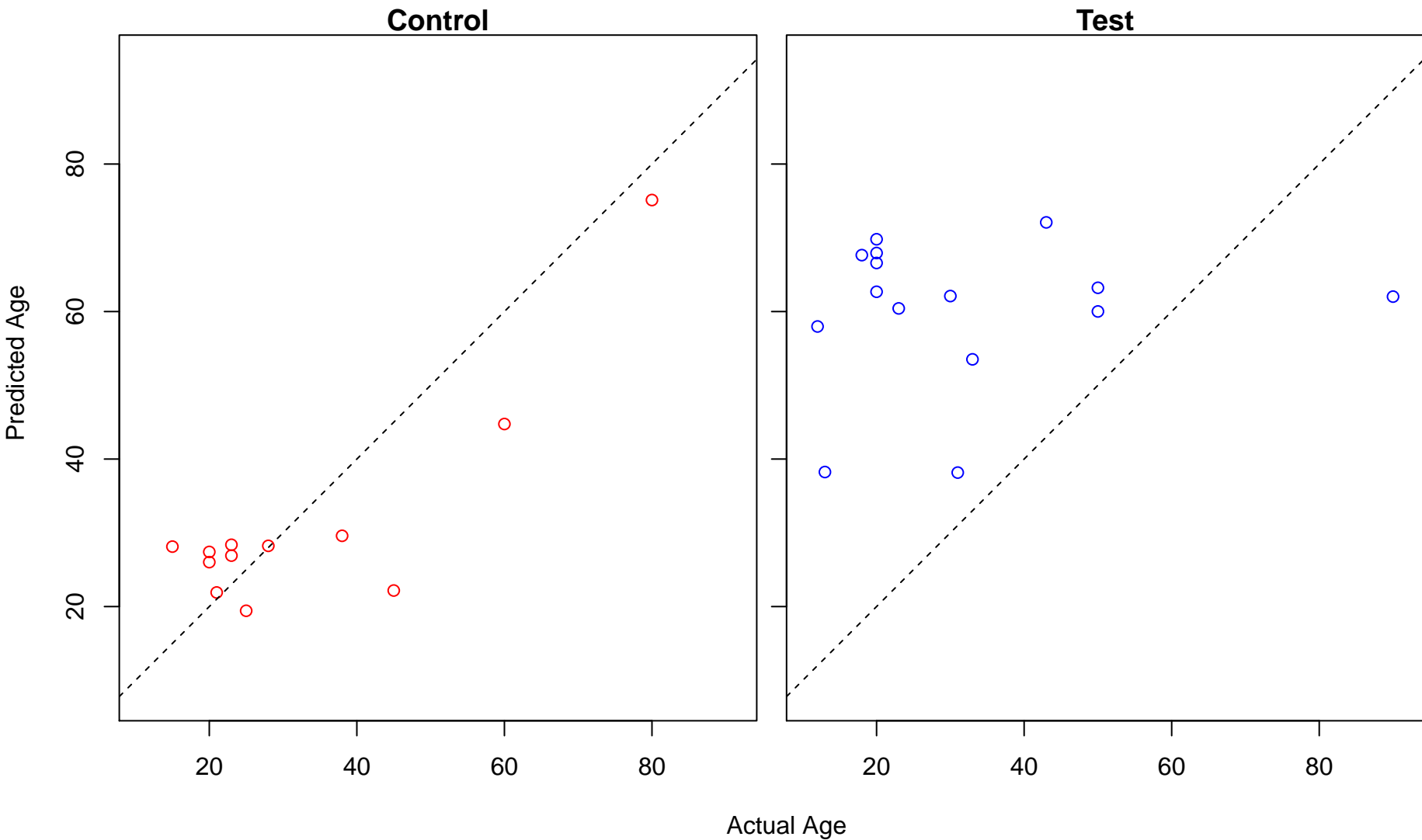
epithelial structure maintenance (Score: 4.754459)



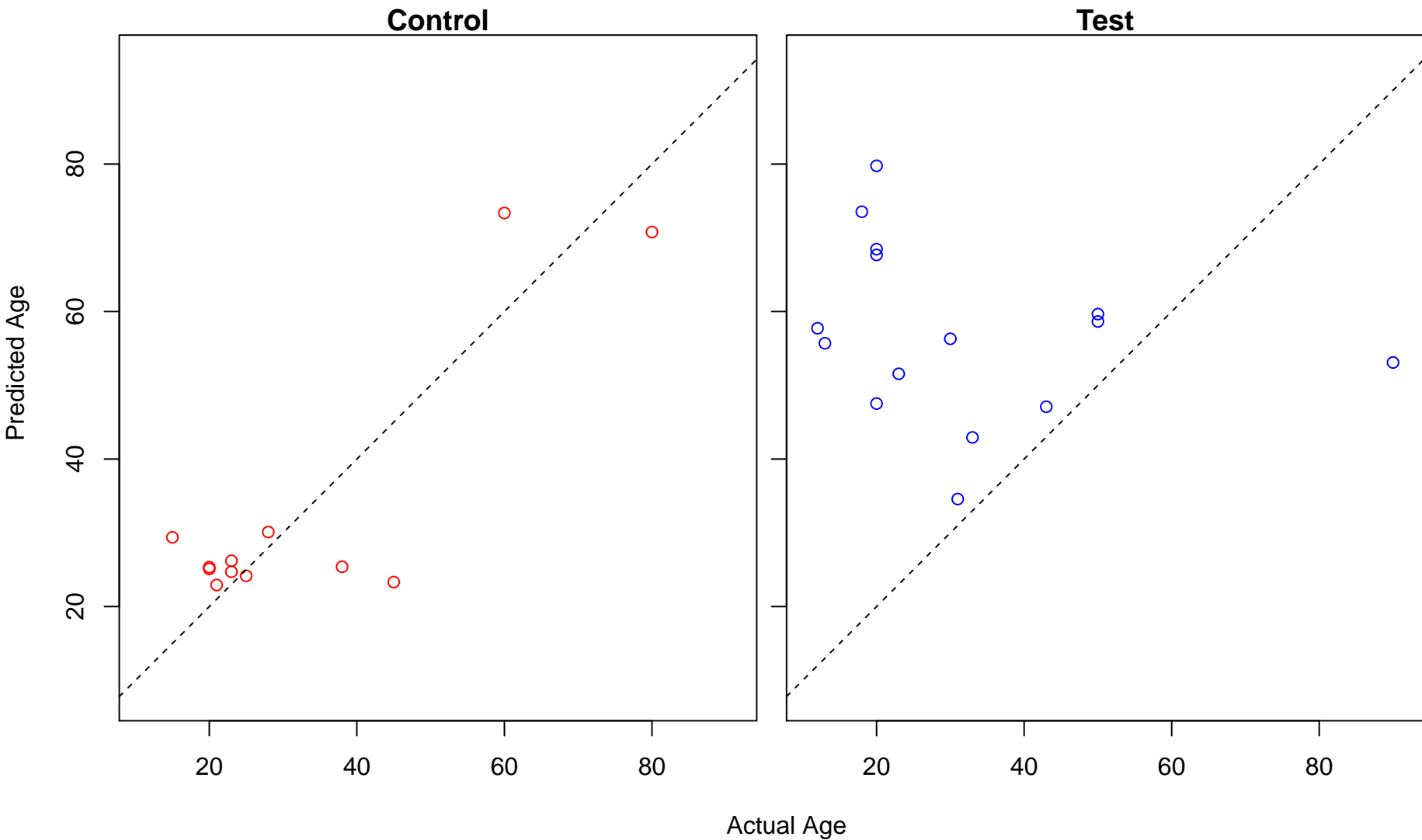
embryonic skeletal system morphogenesis (Score: 4.752824)



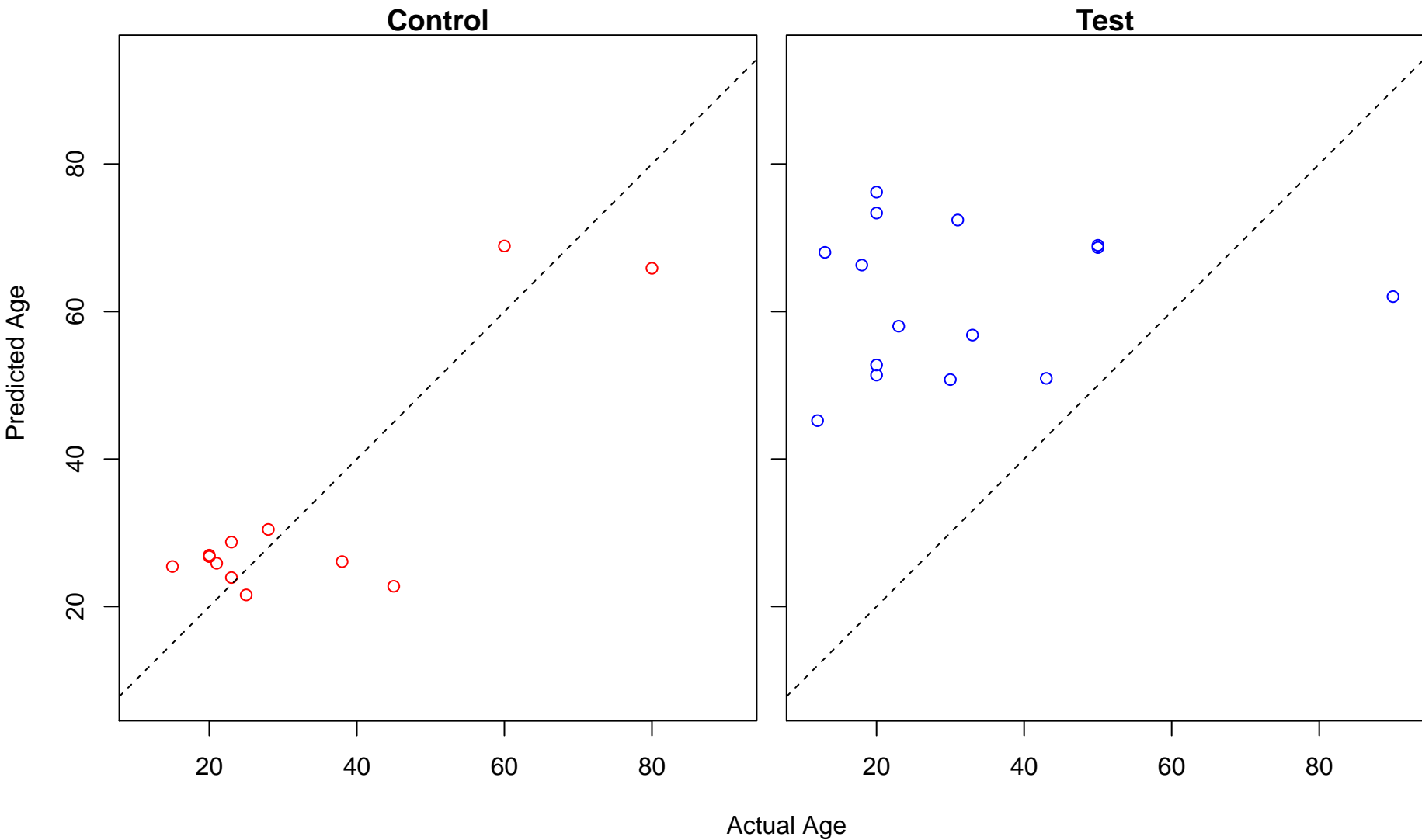
fatty acid catabolic process (Score: 4.752777)



negative regulation of mitotic nuclear division (Score: 4.752131)

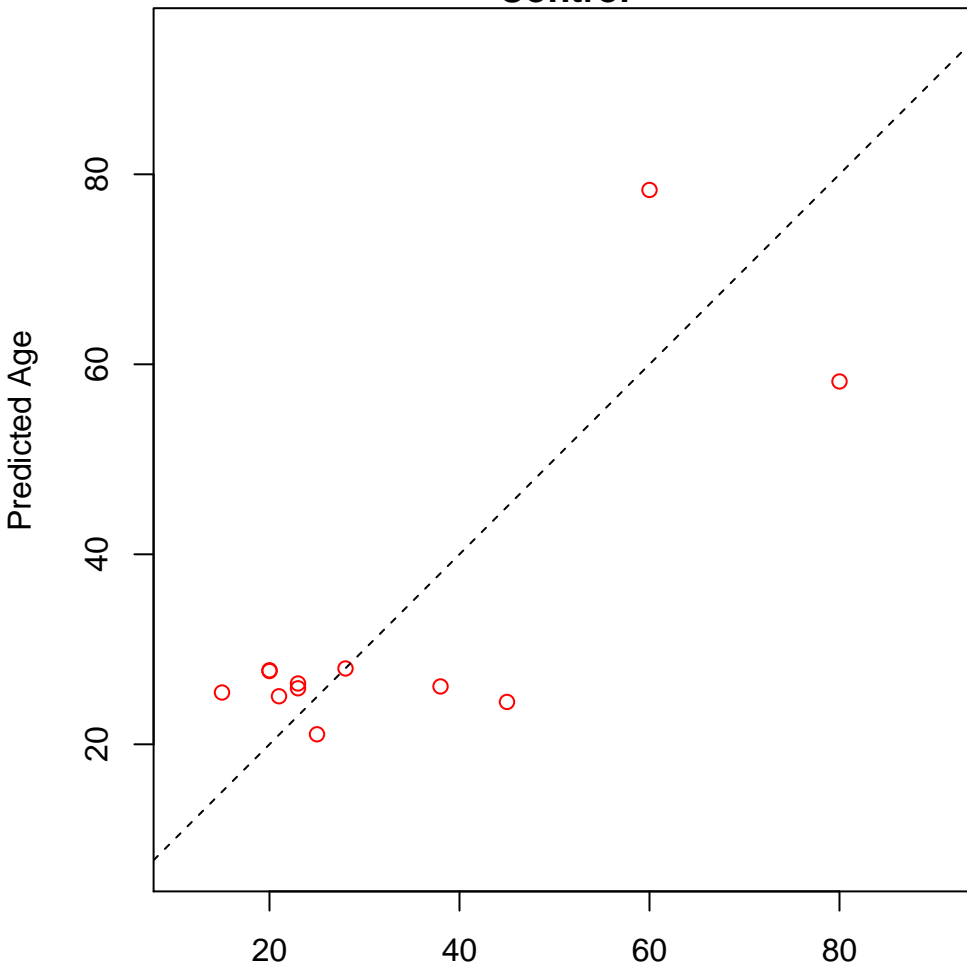


positive regulation of phosphatase activity (Score: 4.749484)

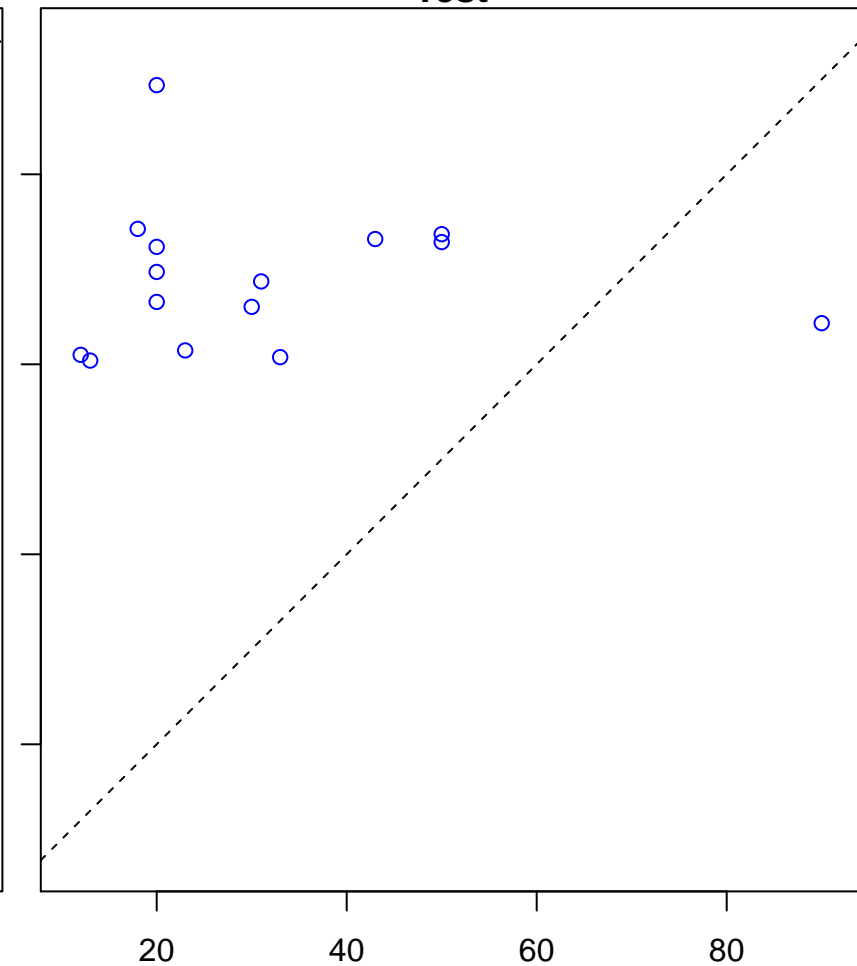


regulation of interleukin-8 production (Score: 4.749235)

Control

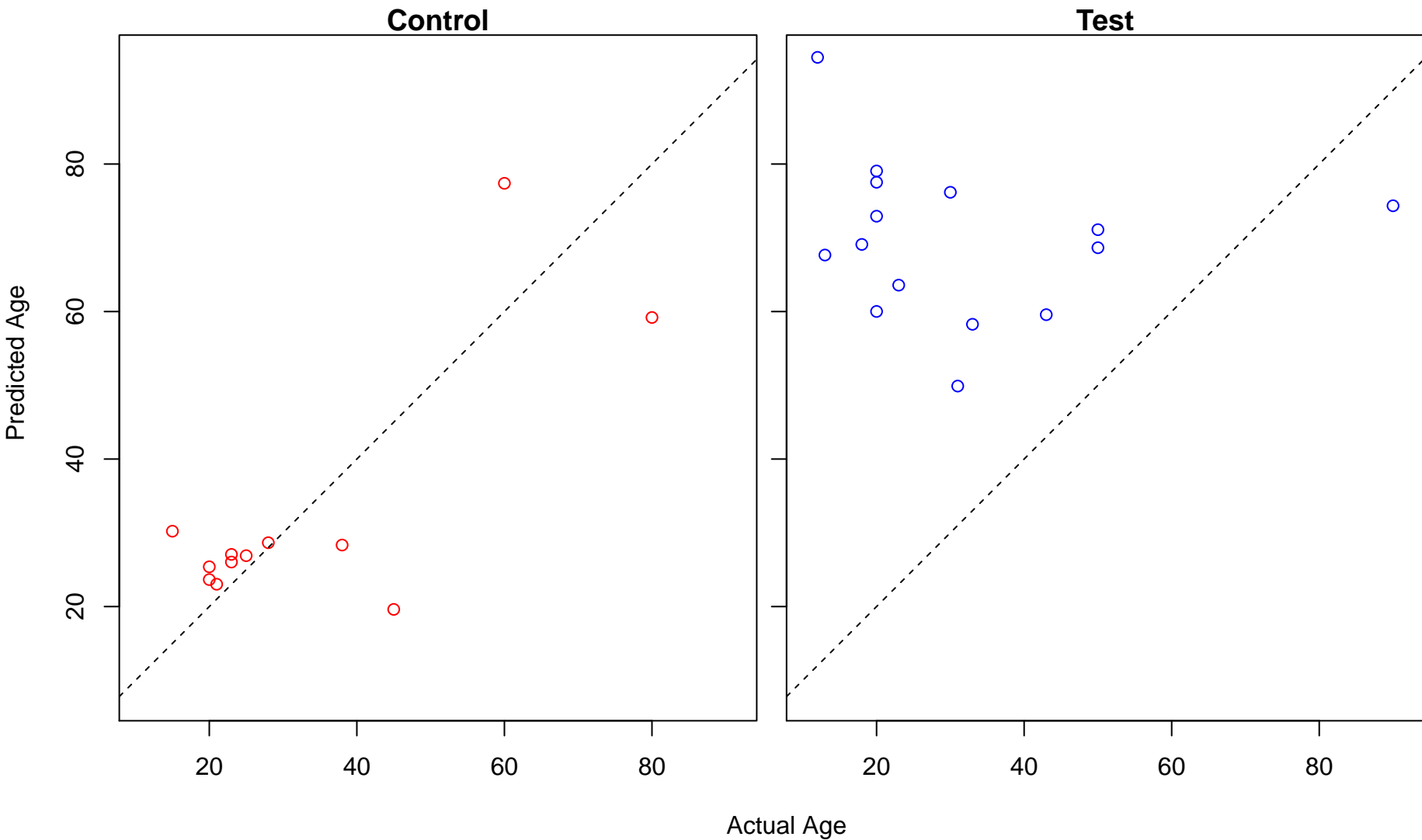


Test

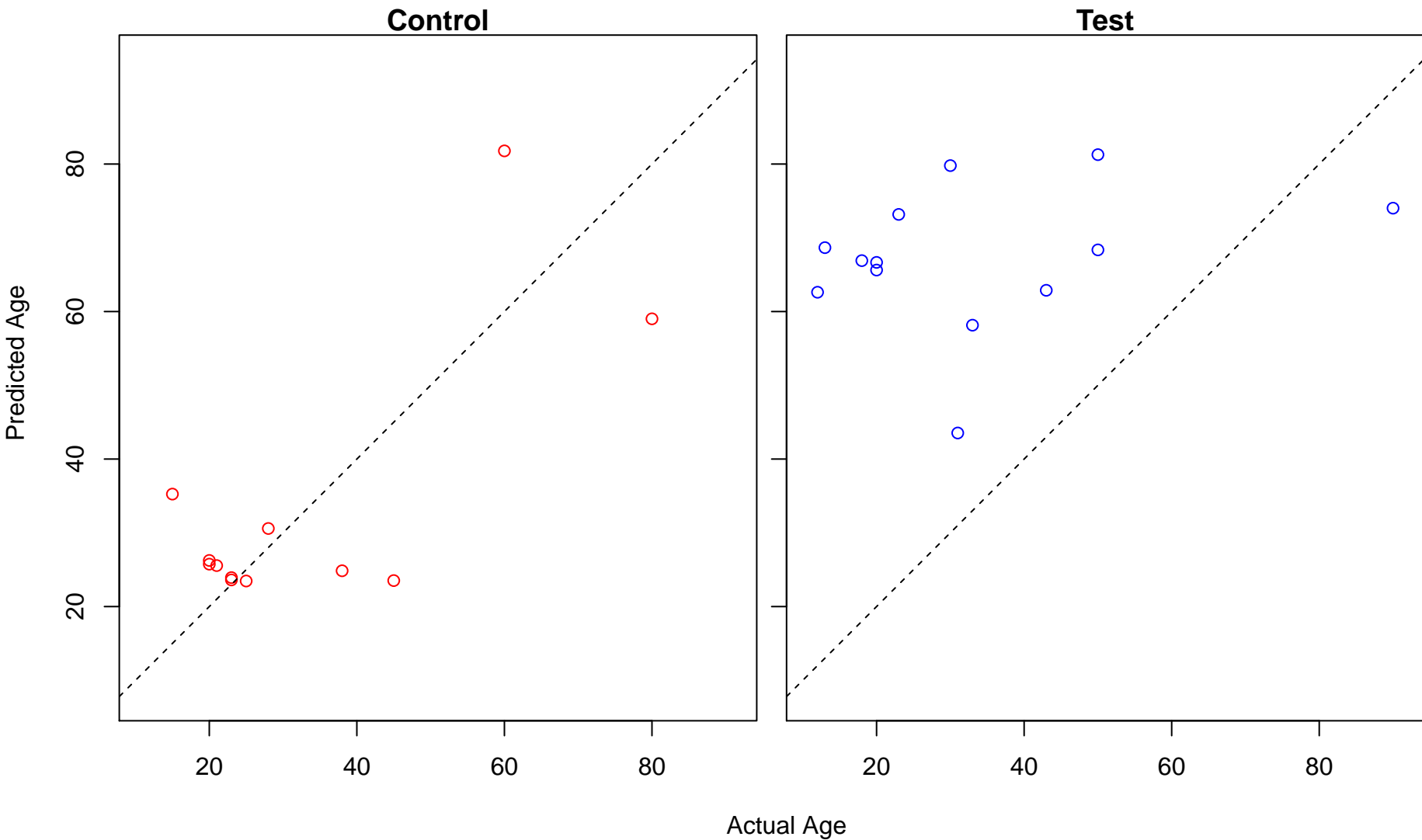


Actual Age

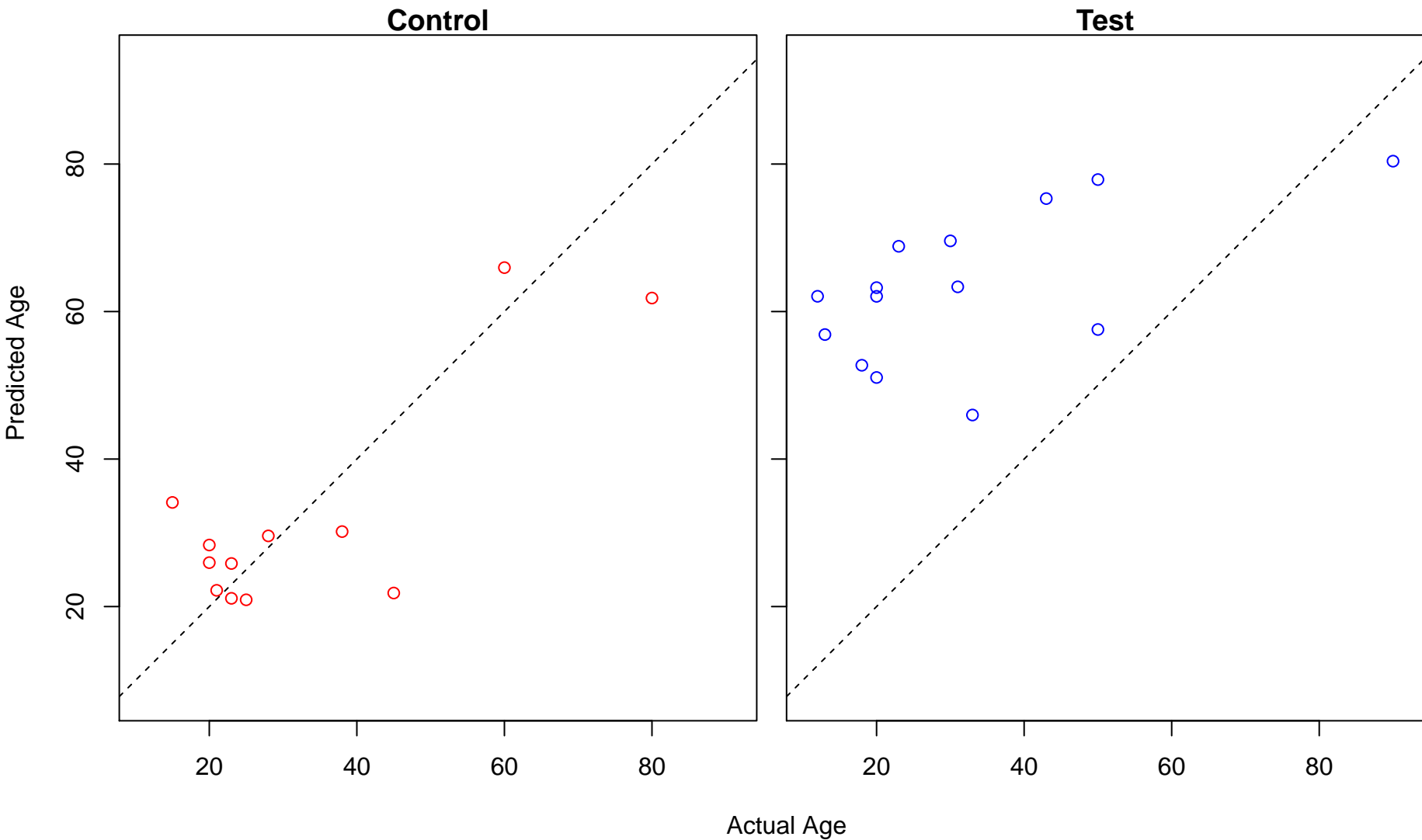
regulation of osteoblast proliferation (Score: 4.748503)



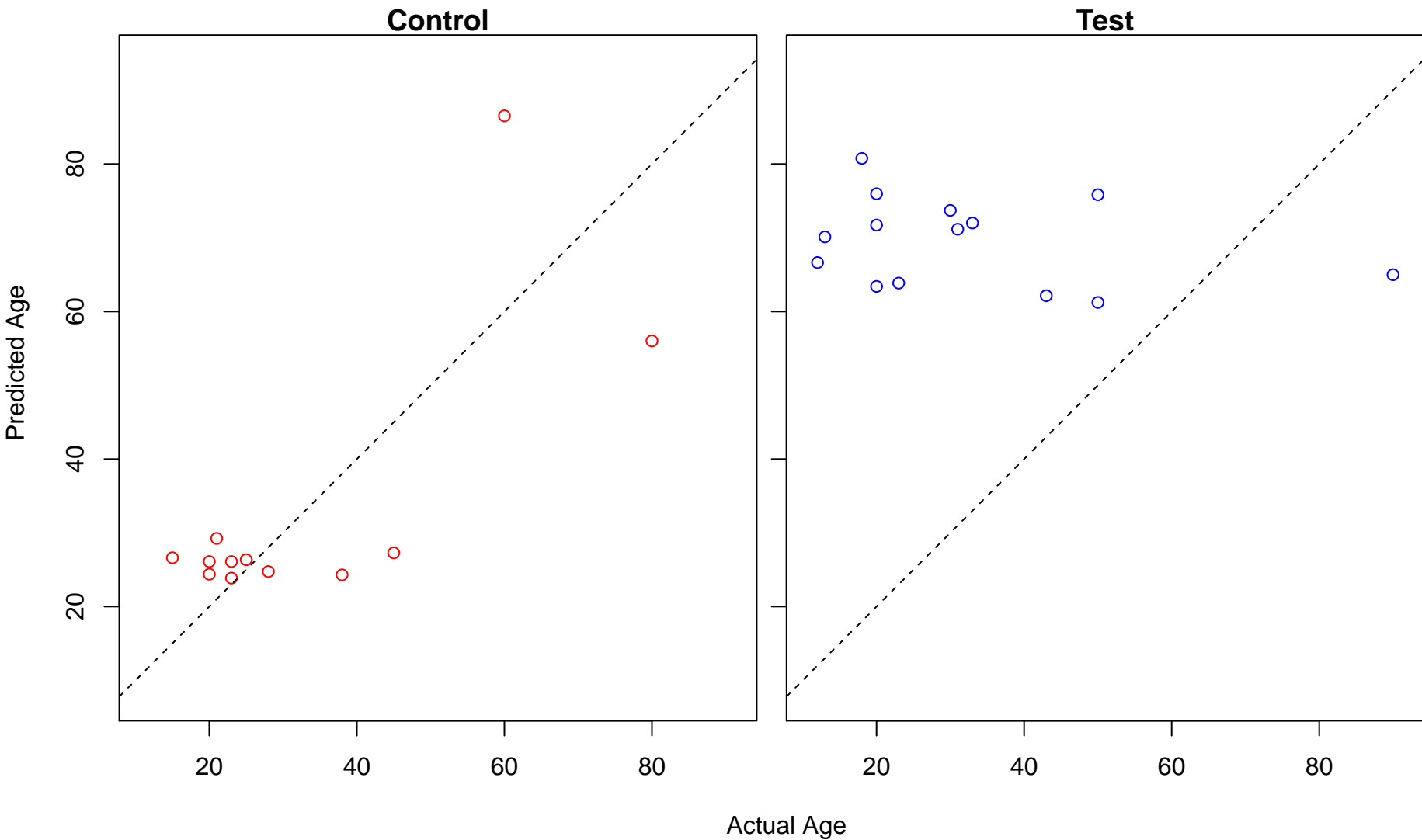
negative regulation of mRNA 3'-end processing (Score: 4.747450)



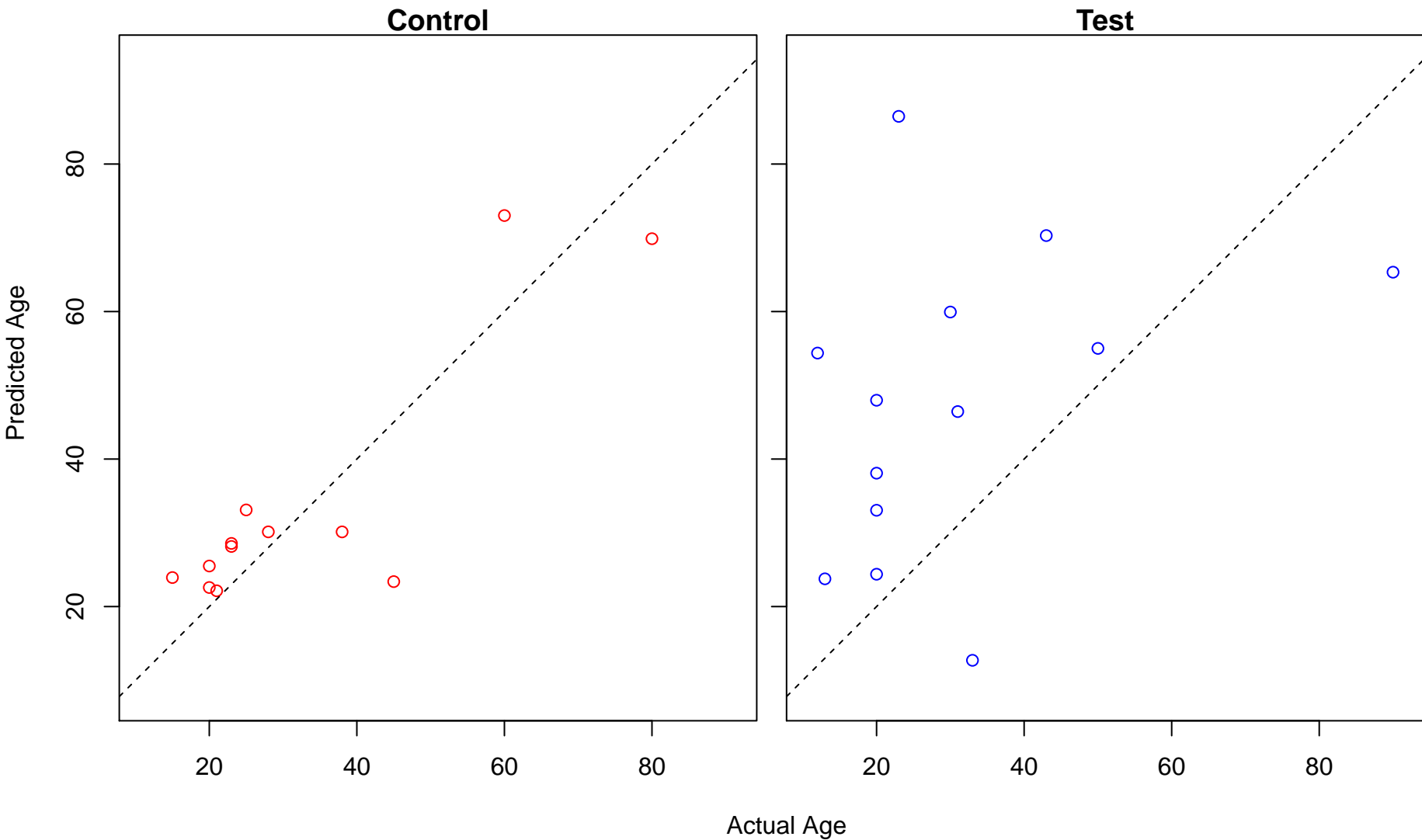
protein autoprocessing (Score: 4.745391)



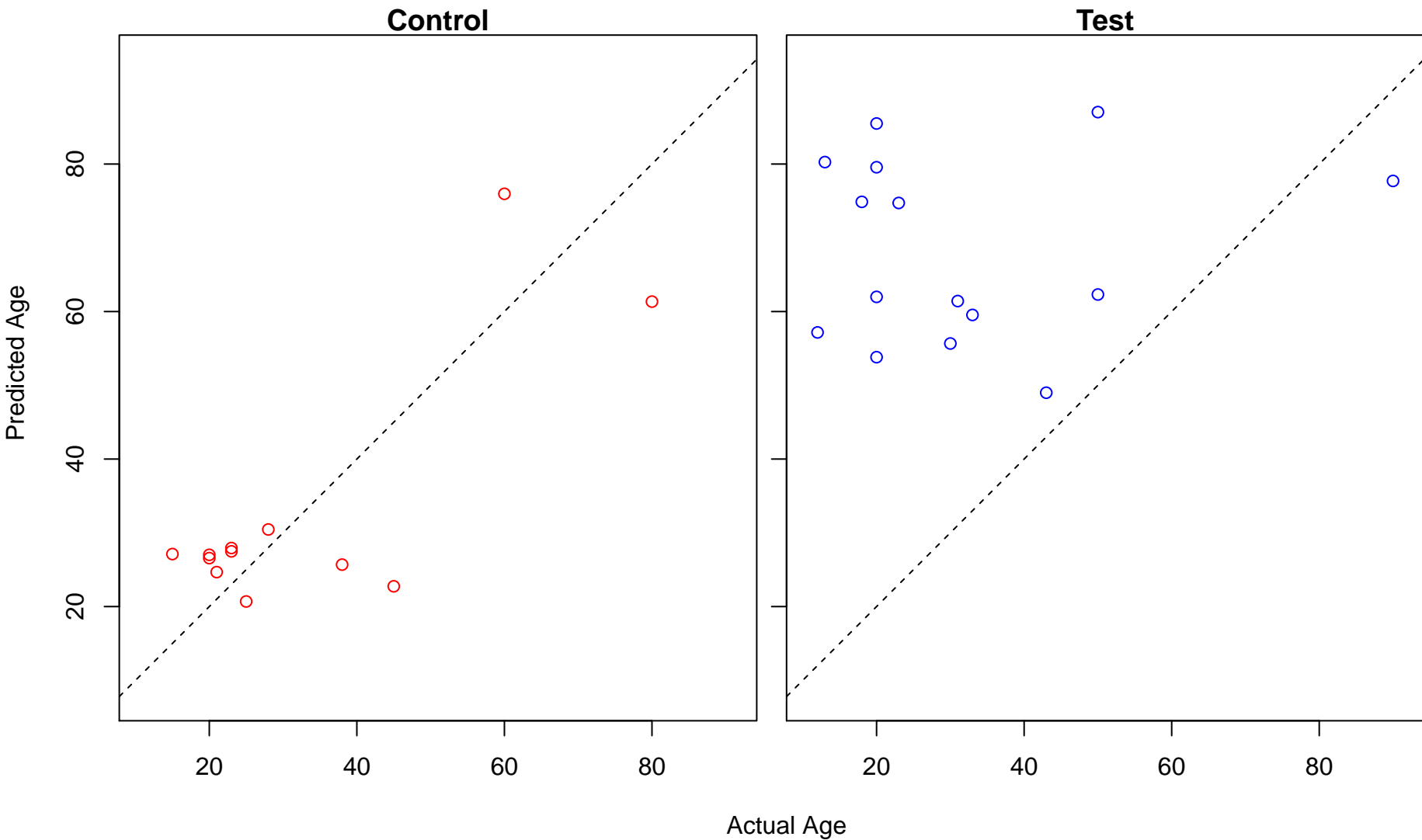
negative regulation of viral entry into host cell (Score: 4.745238)



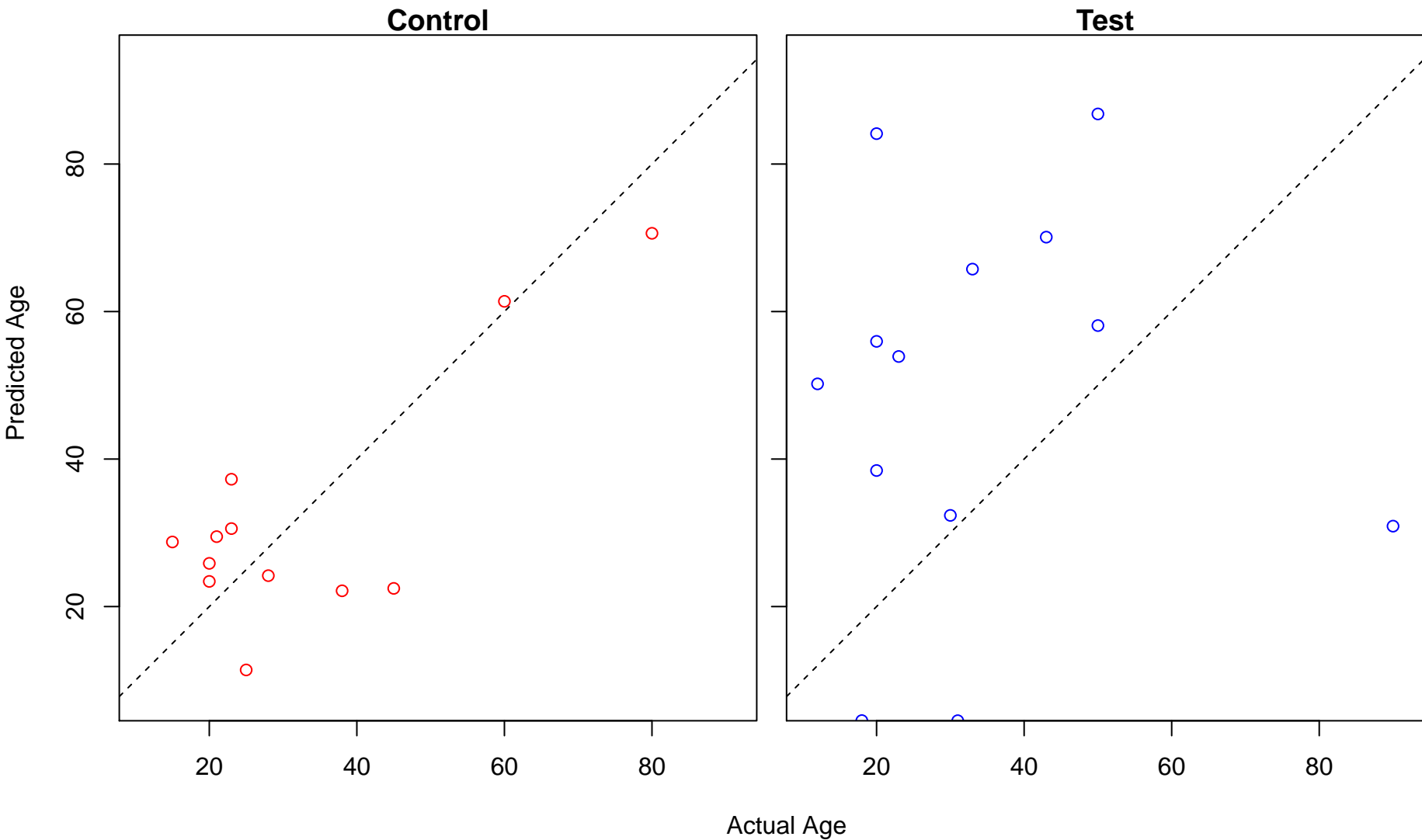
positive regulation of toll-like receptor 3 signaling pathway (Score: 4.743973)



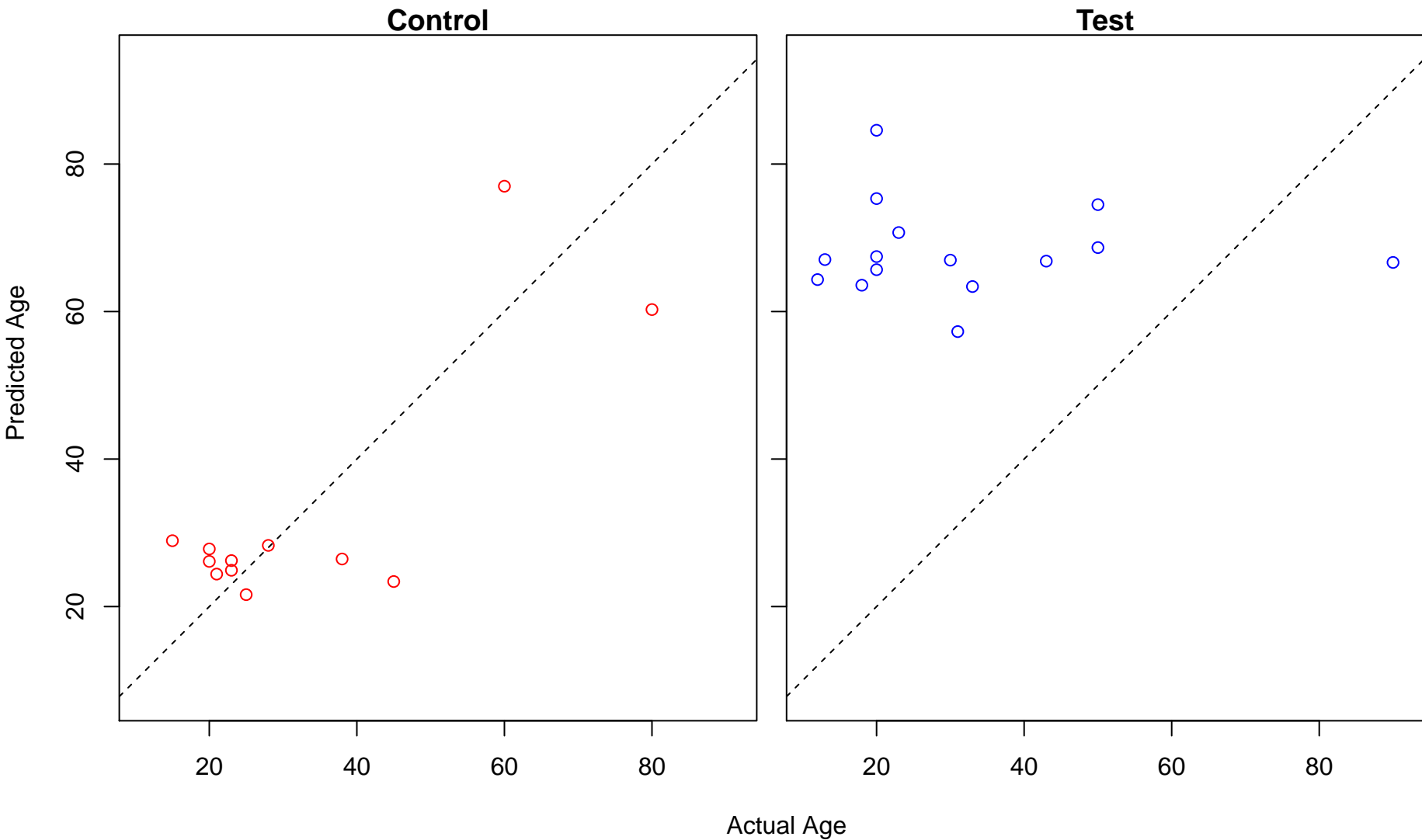
monosaccharide metabolic process (Score: 4.742297)



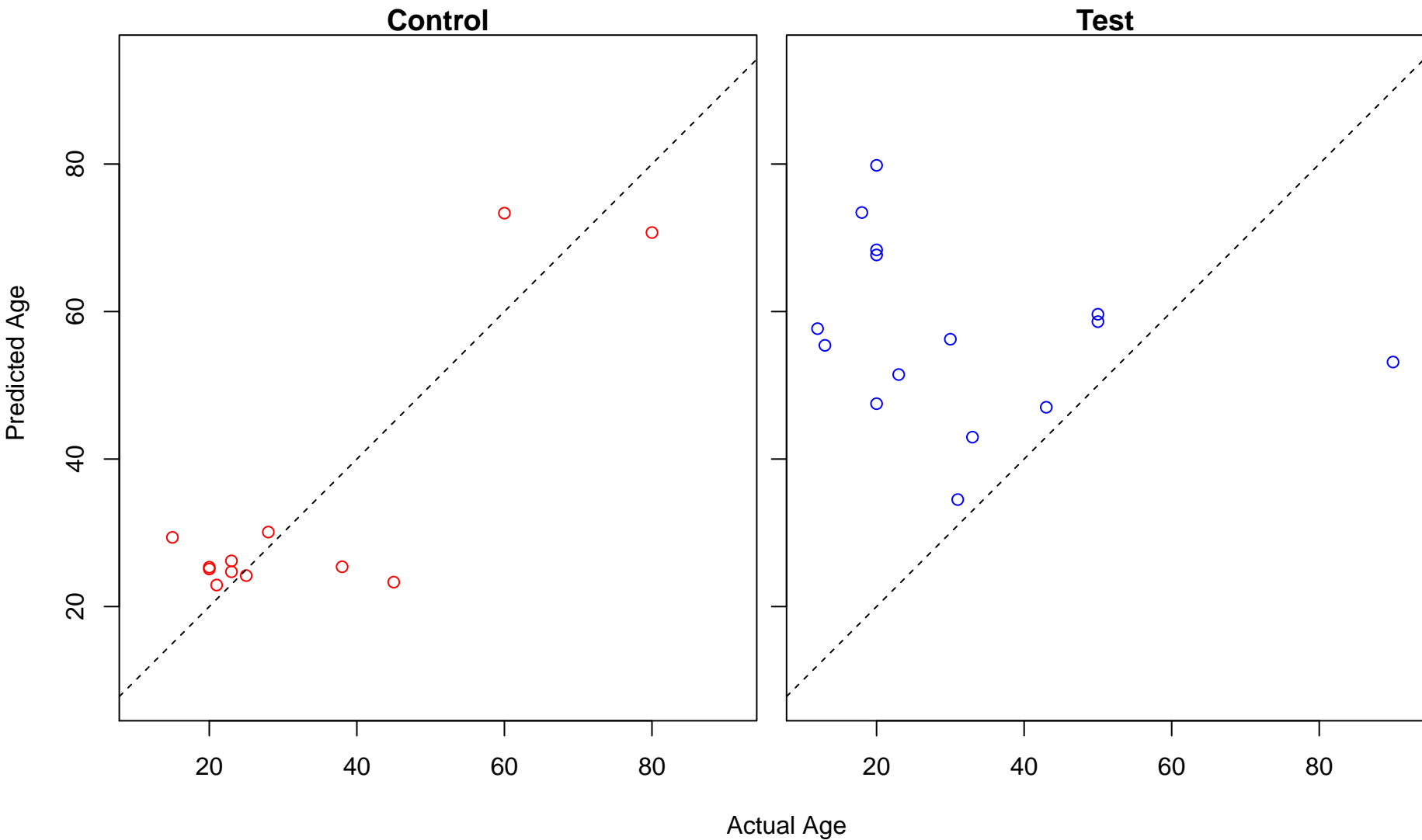
regulation of cell maturation (Score: 4.741087)



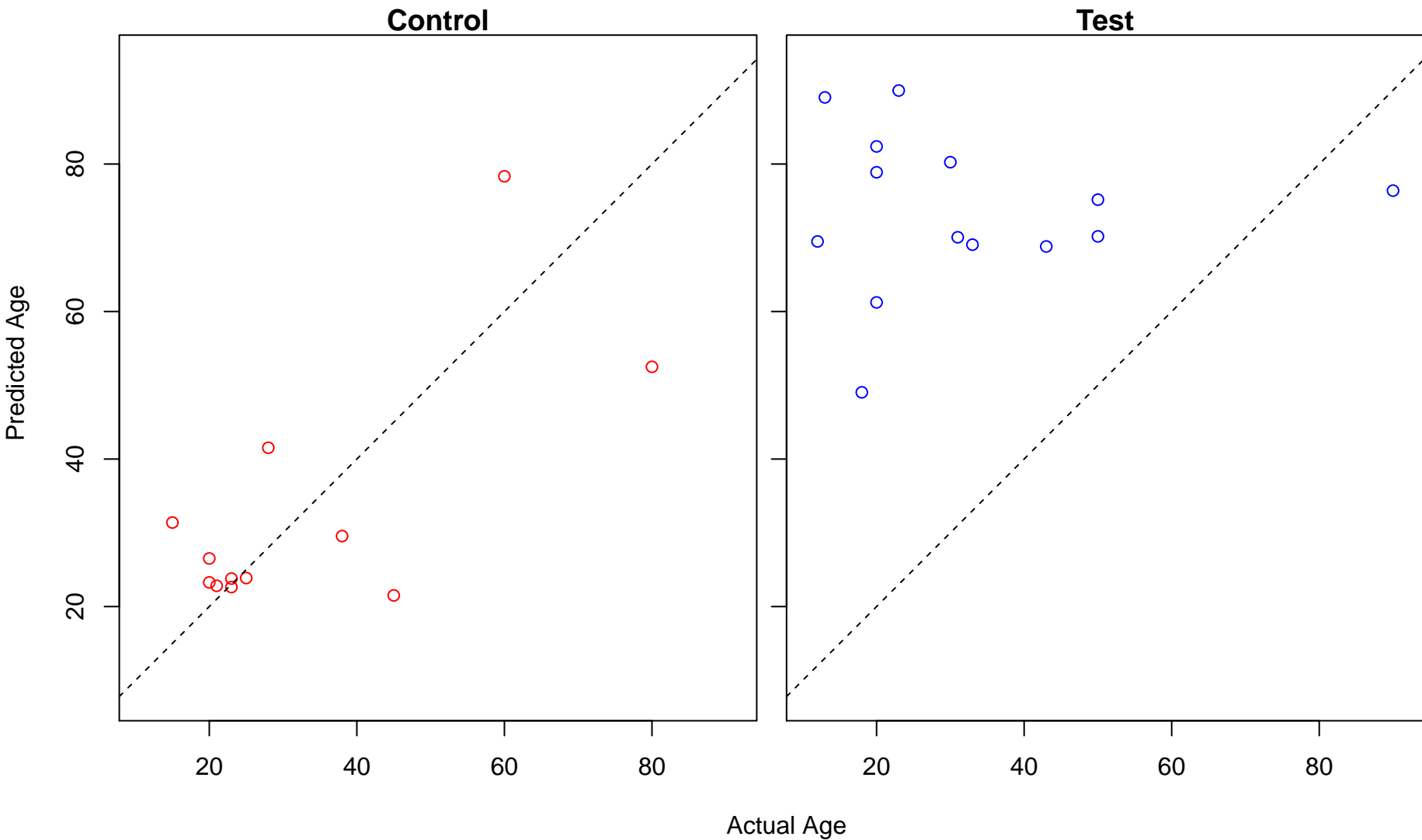
epithelial cell development (Score: 4.738372)



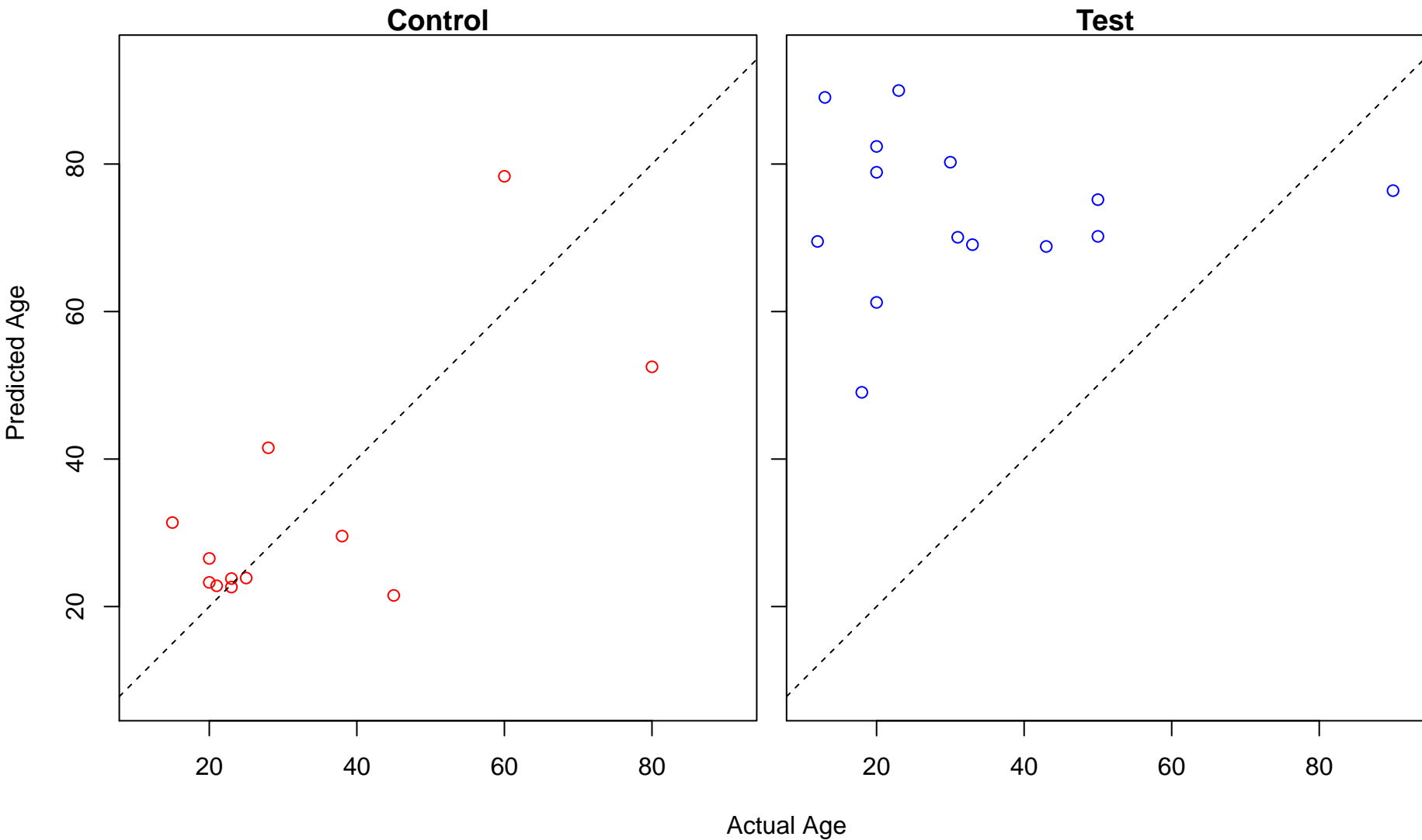
negative regulation of nuclear division (Score: 4.738355)



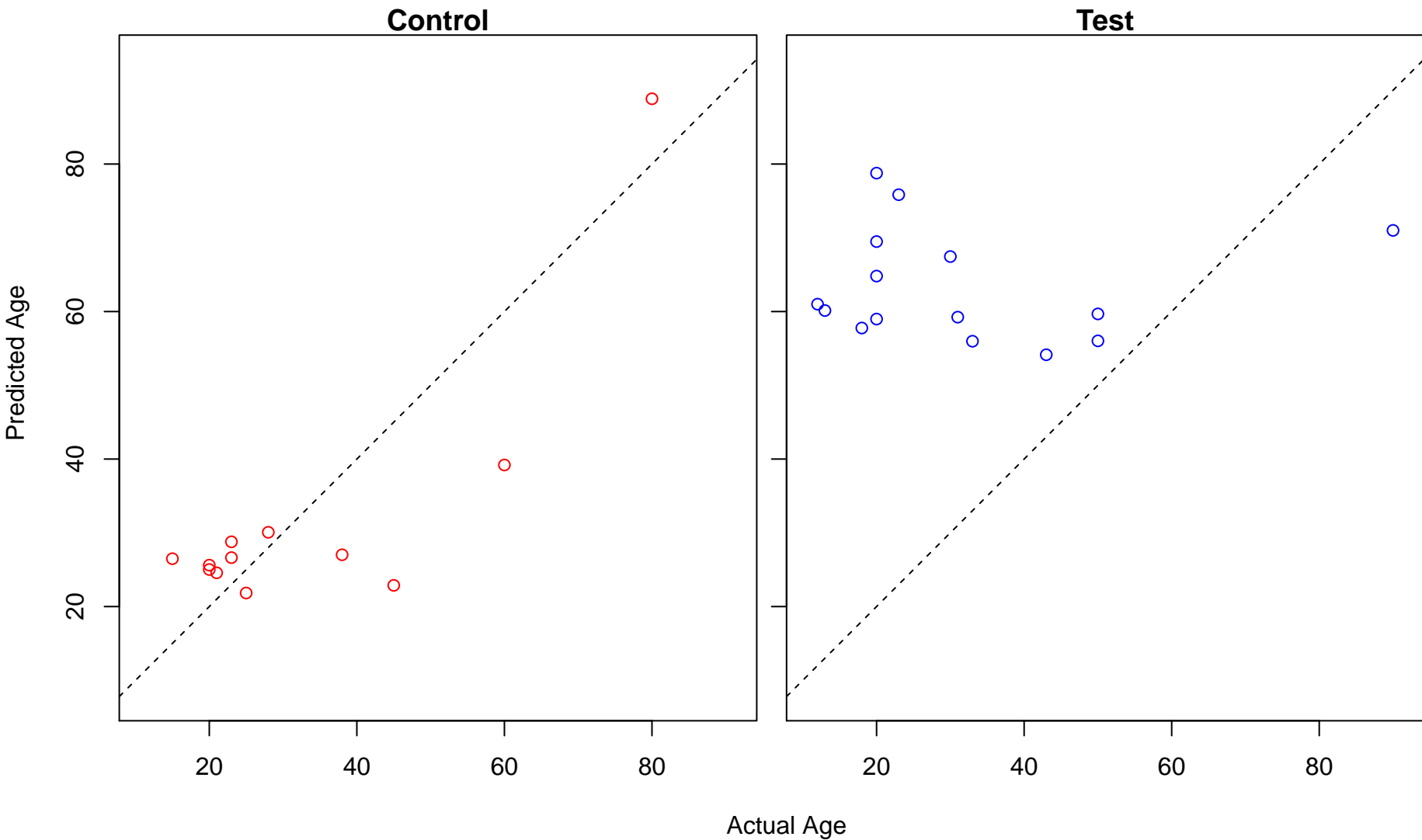
negative regulation of cardiac muscle tissue growth (Score: 4.737090)



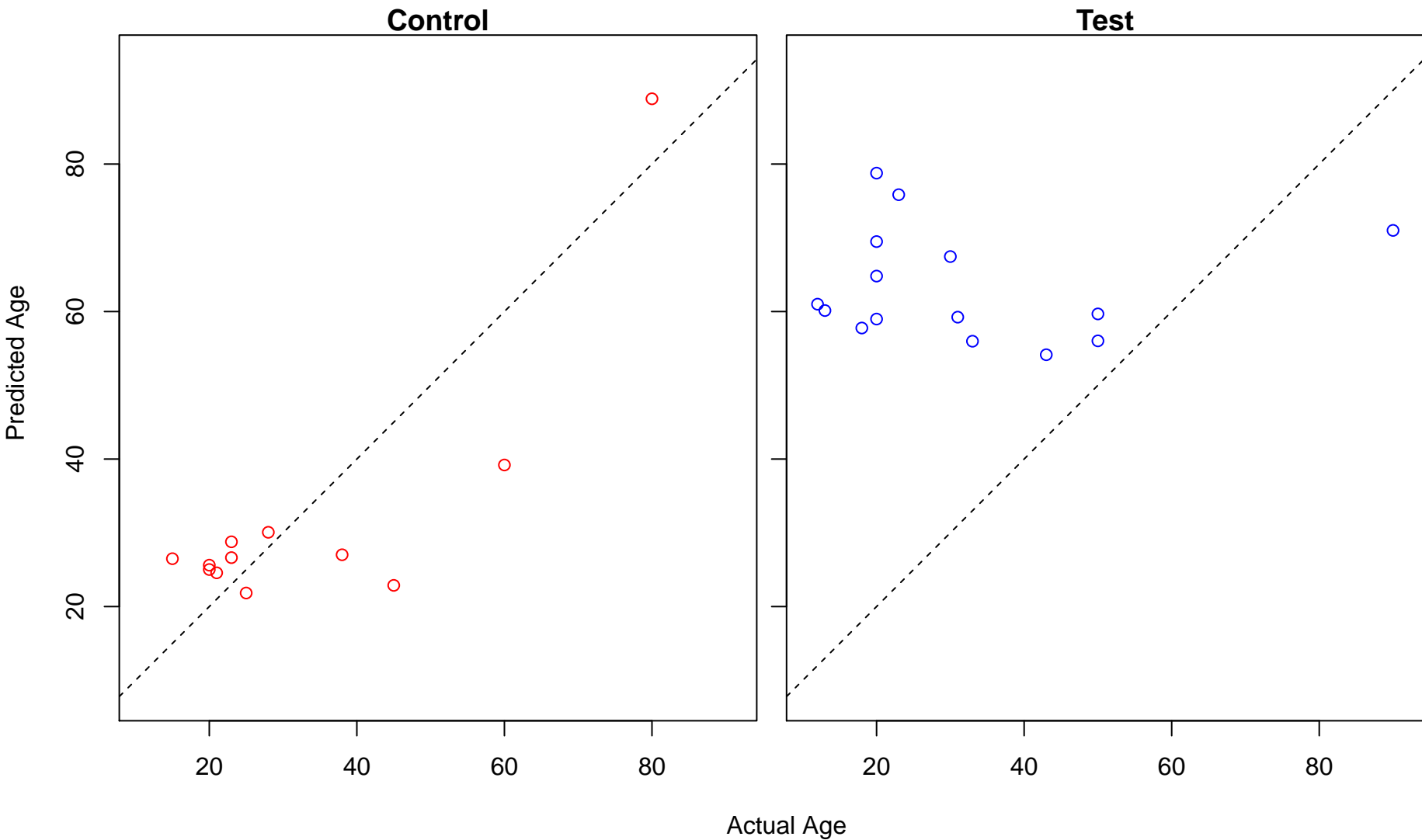
negative regulation of heart growth (Score: 4.737090)



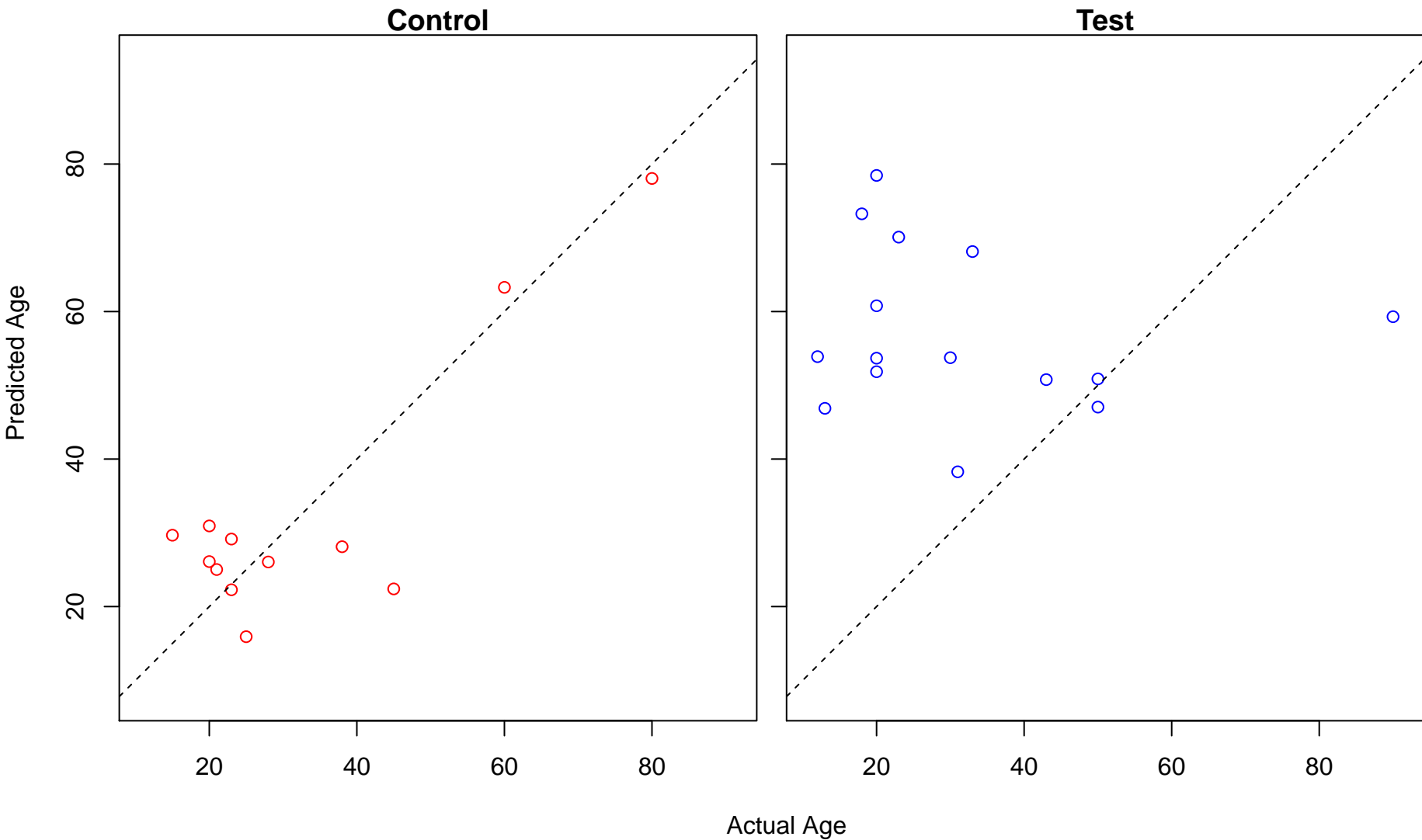
cellular biogenic amine metabolic process (Score: 4.735863)



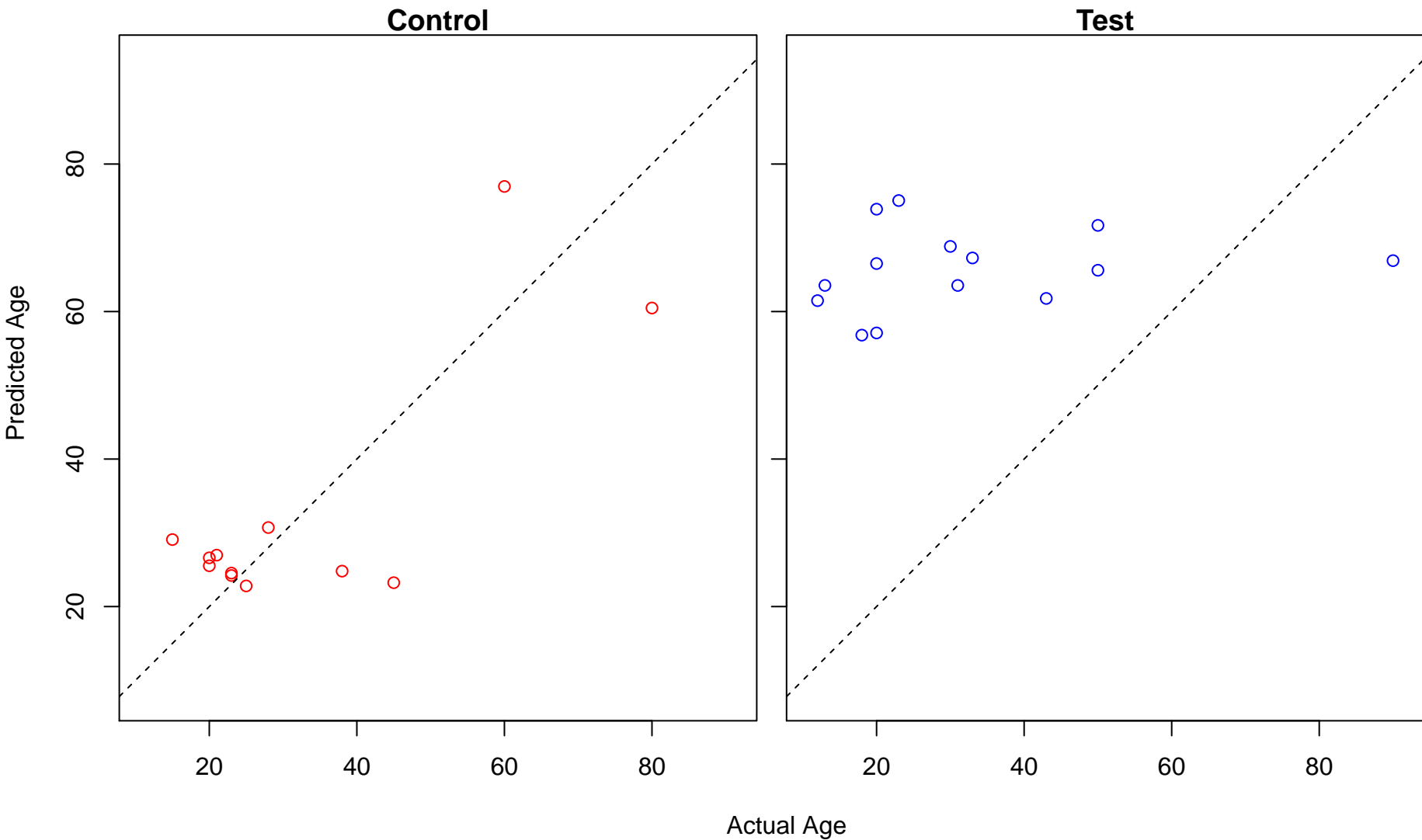
cellular amine metabolic process (Score: 4.735863)



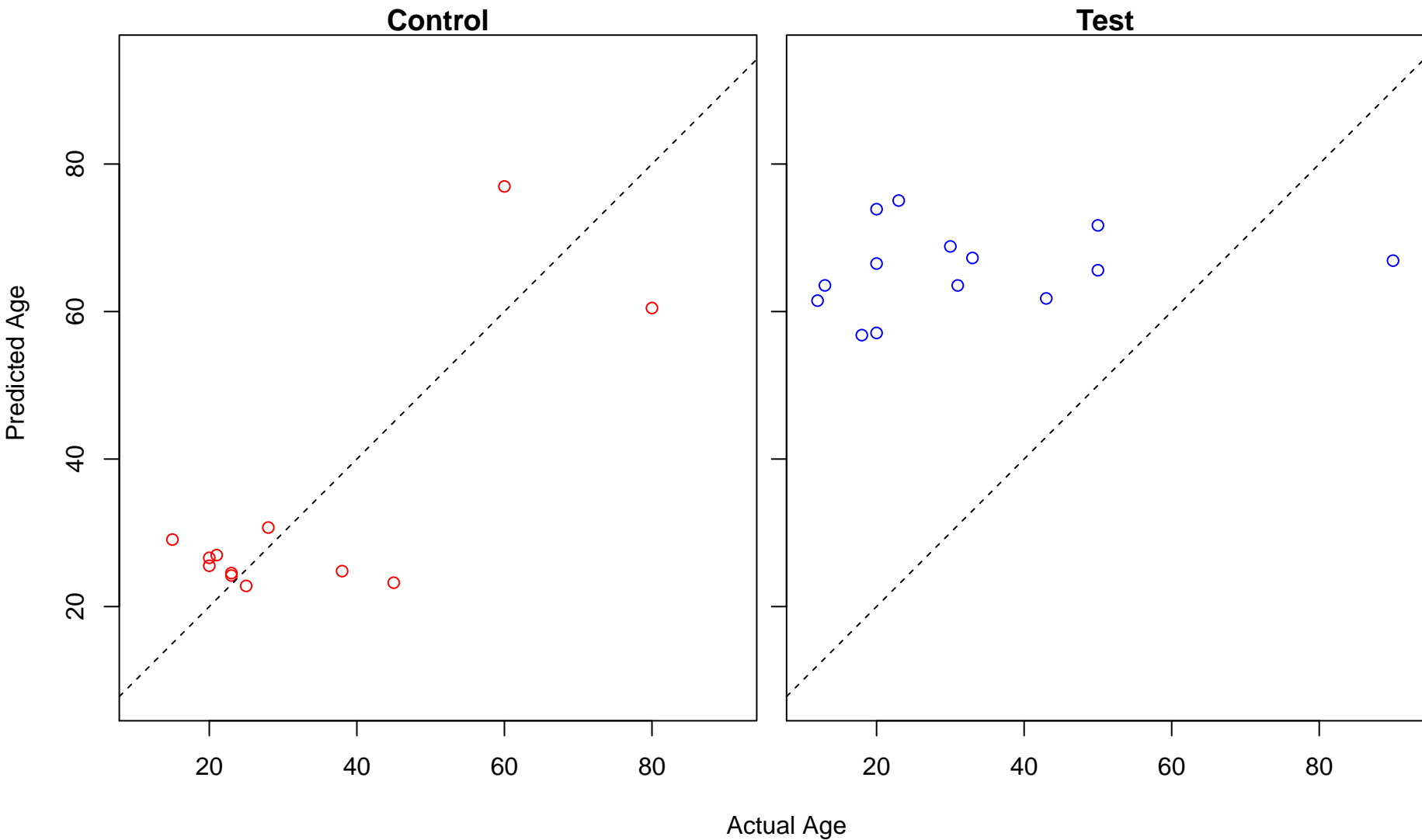
regulation of mRNA splicing, via spliceosome (Score: 4.735678)



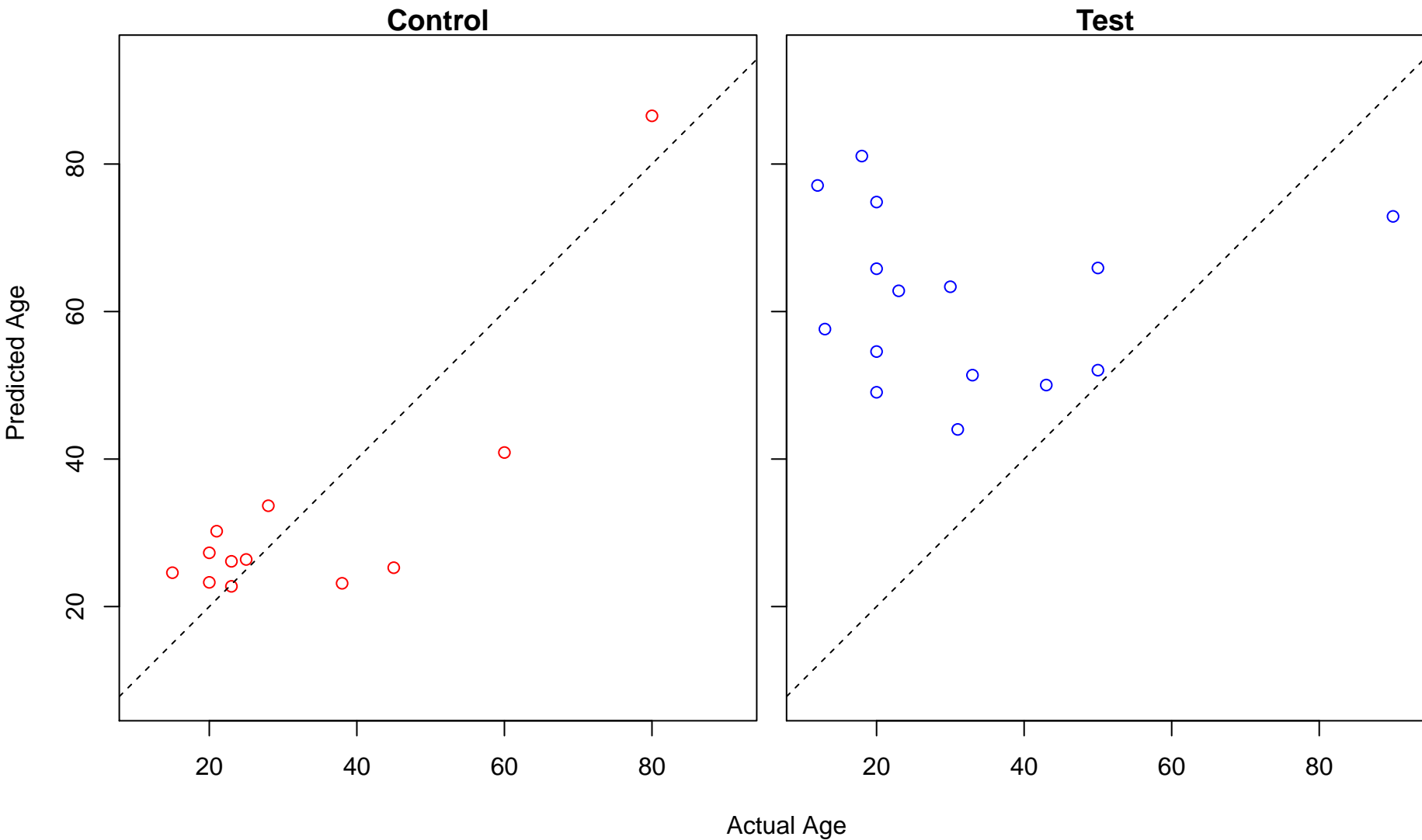
platelet formation (Score: 4.735538)



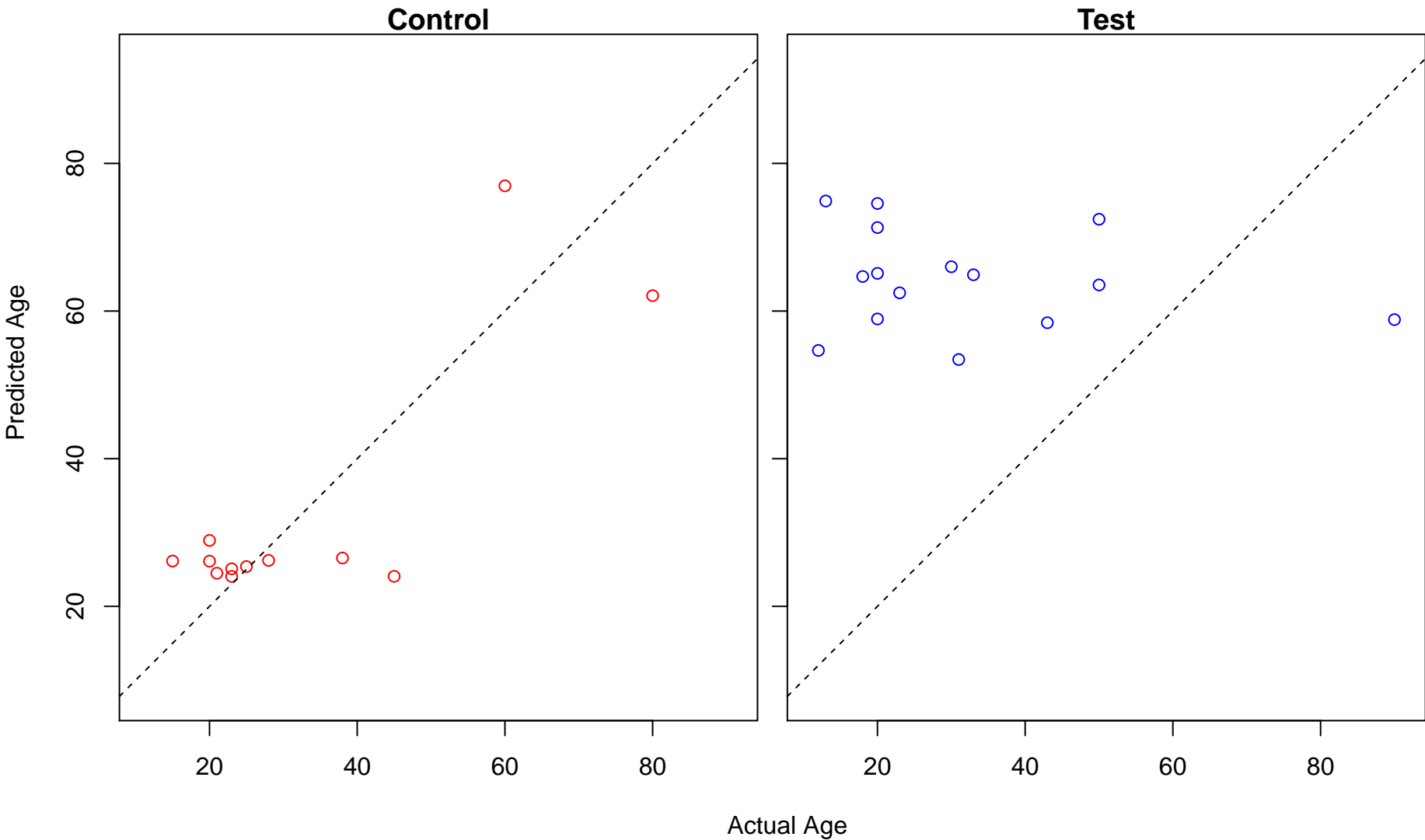
platelet morphogenesis (Score: 4.735538)



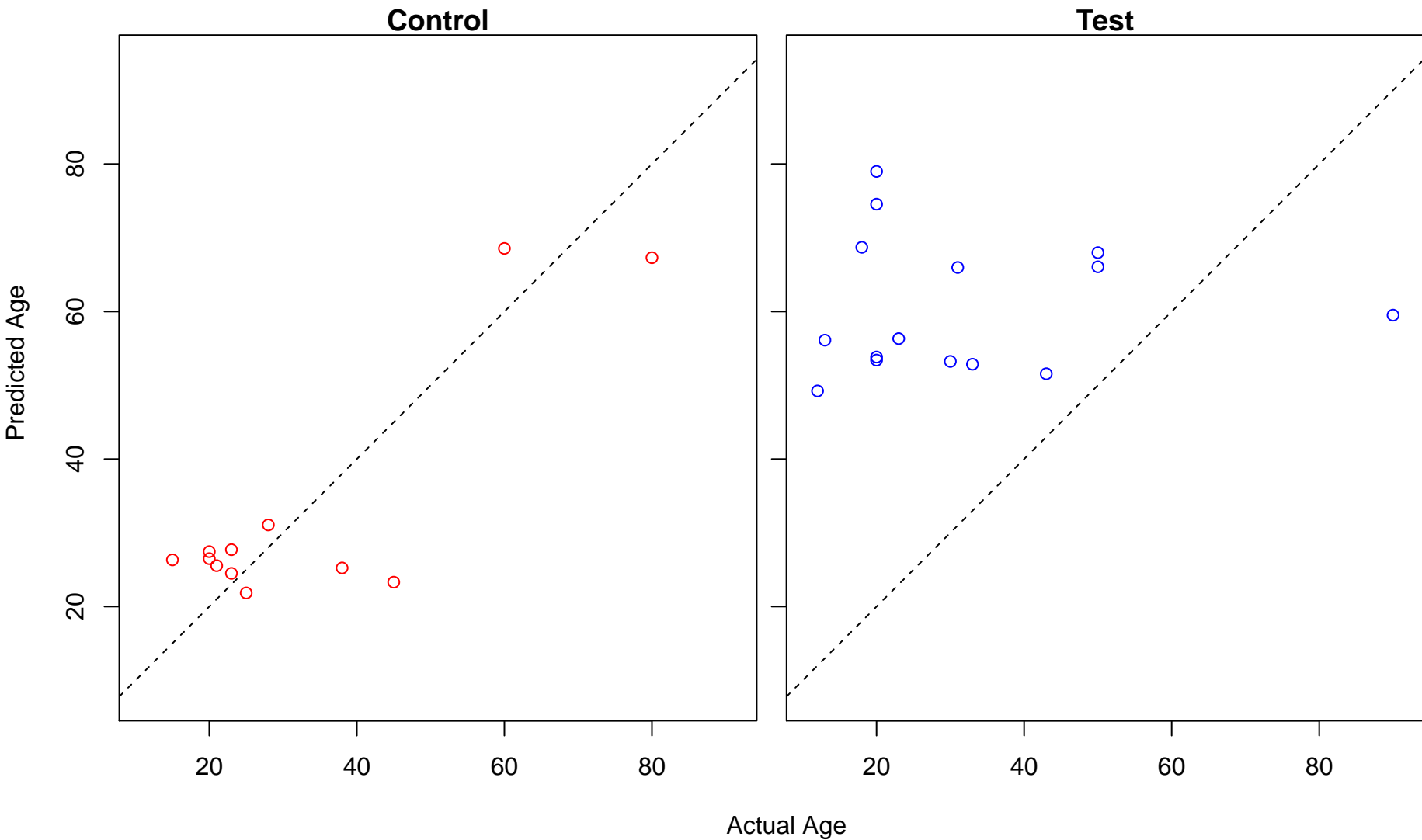
pinocytosis (Score: 4.734726)



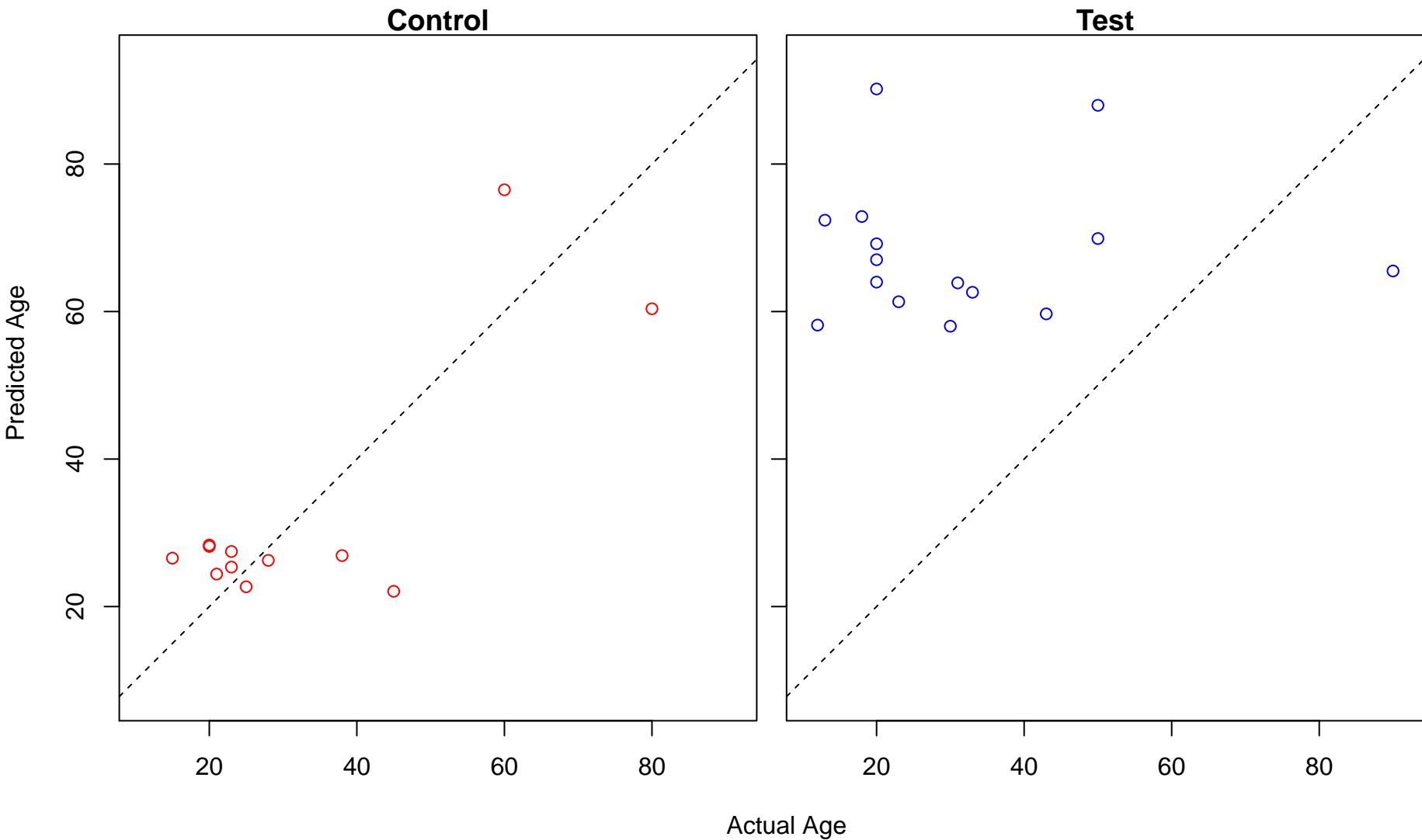
activation of signaling protein activity involved in unfolded protein response (Score: 4.734216)



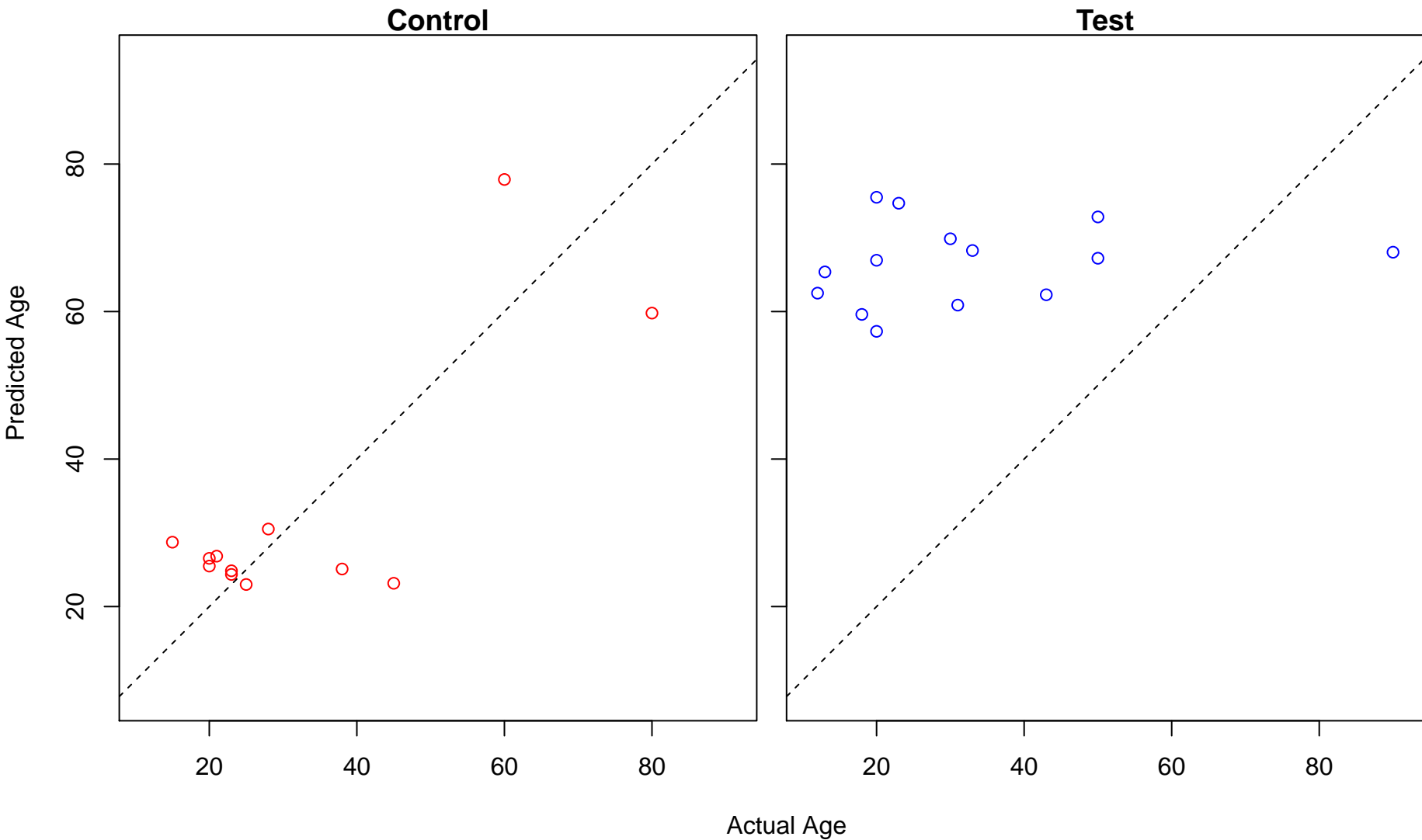
negative regulation of transmembrane transport (Score: 4.732756)



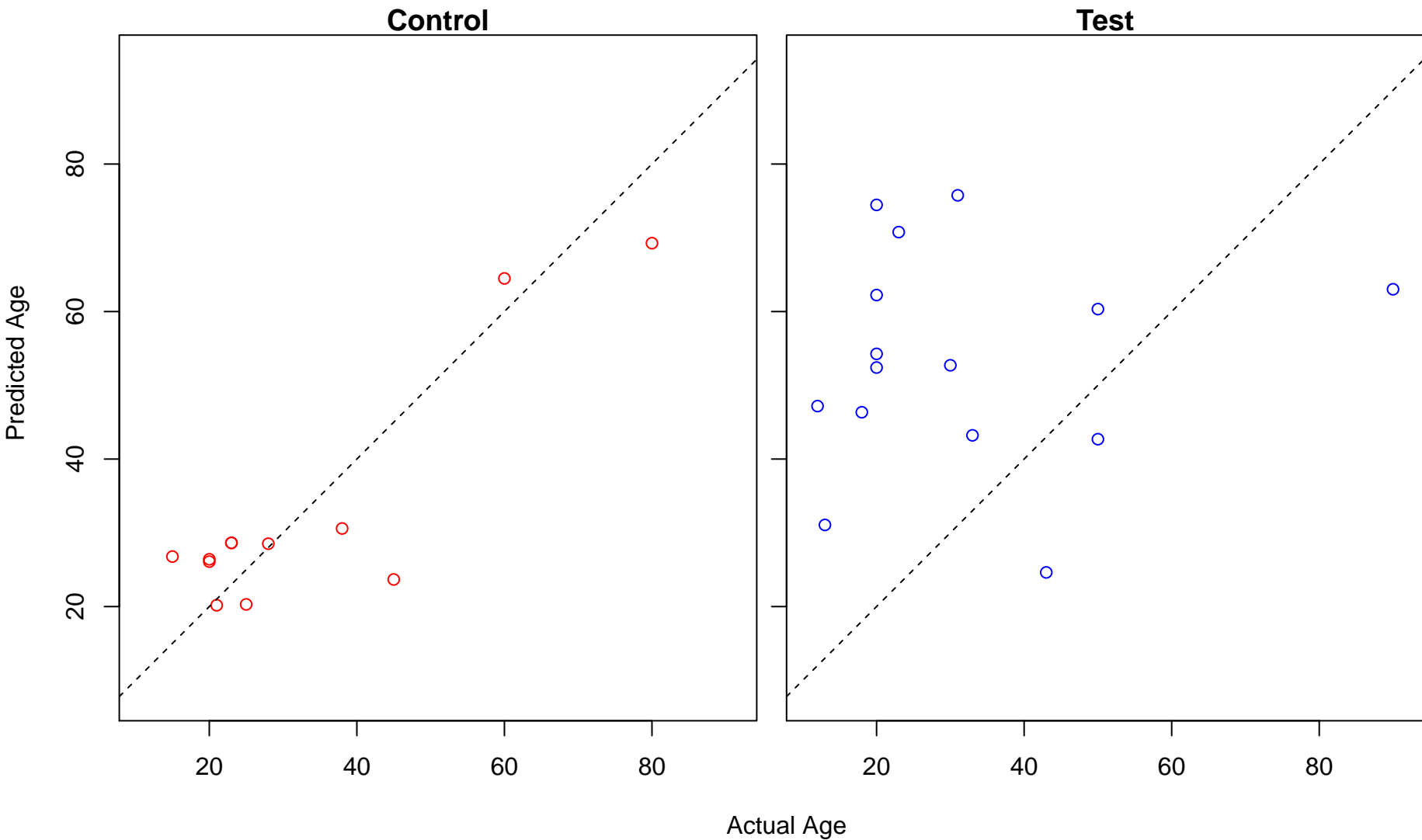
negative regulation of cellular catabolic process (Score: 4.729009)



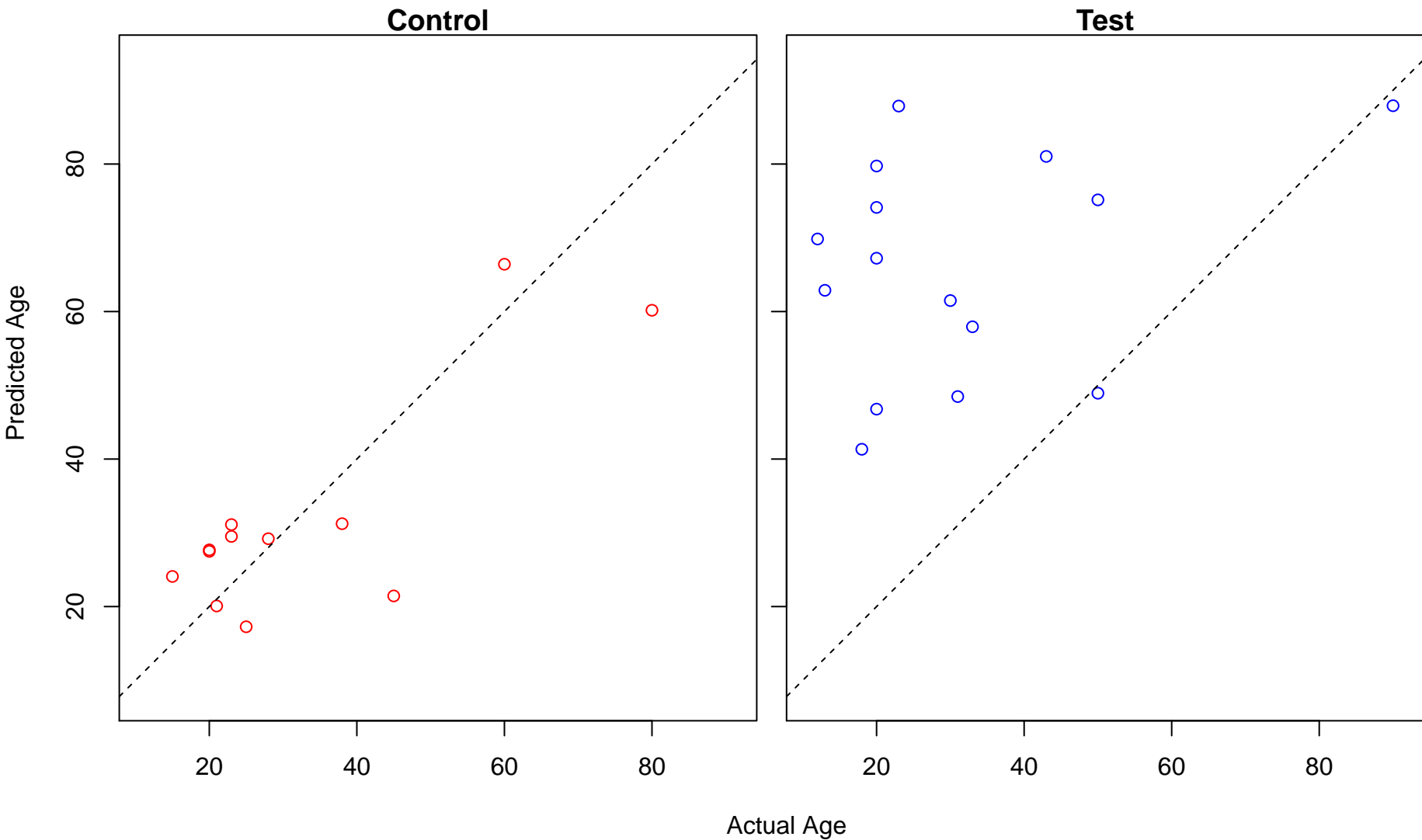
positive regulation of protein targeting to membrane (Score: 4.728546)



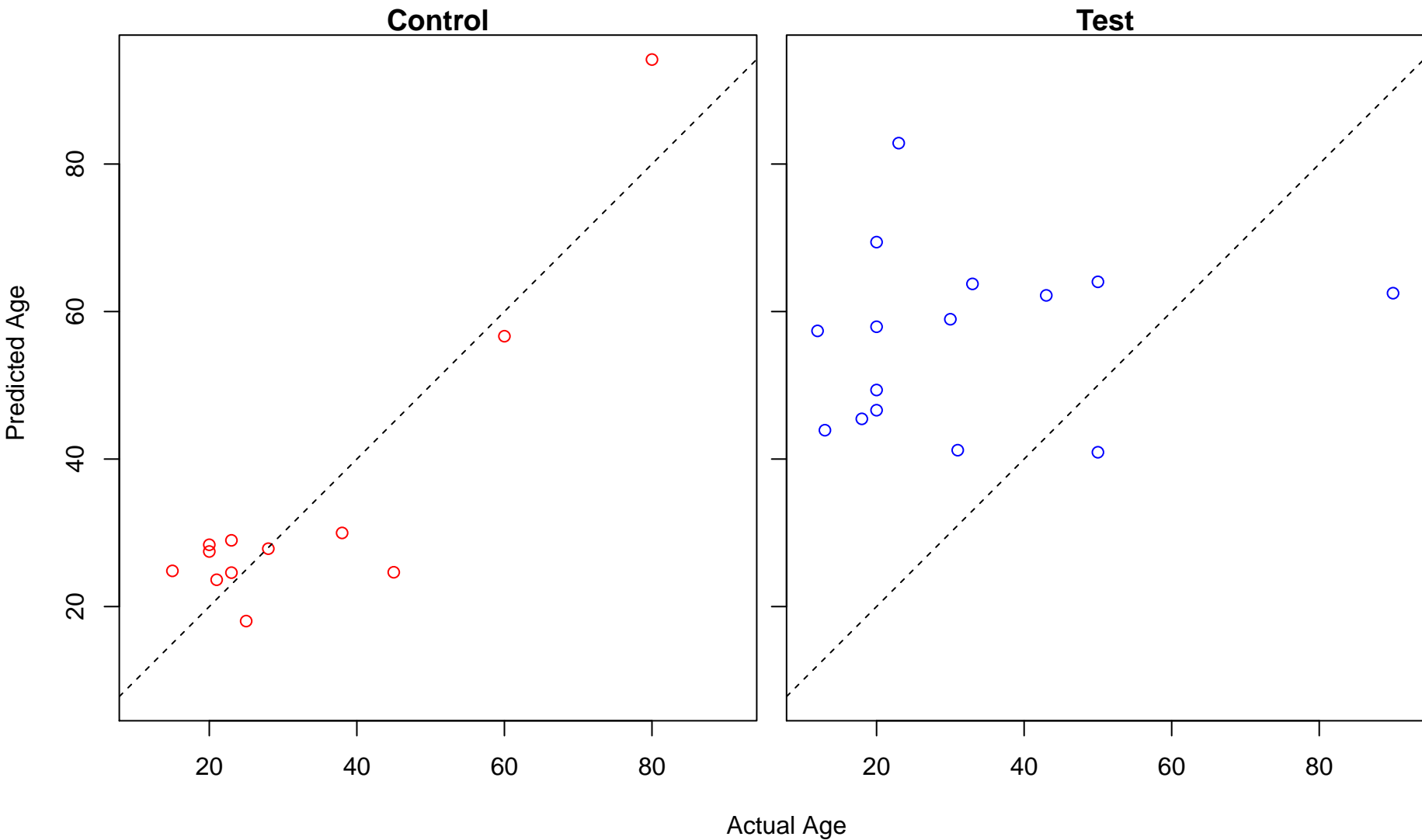
gene silencing by miRNA (Score: 4.728096)



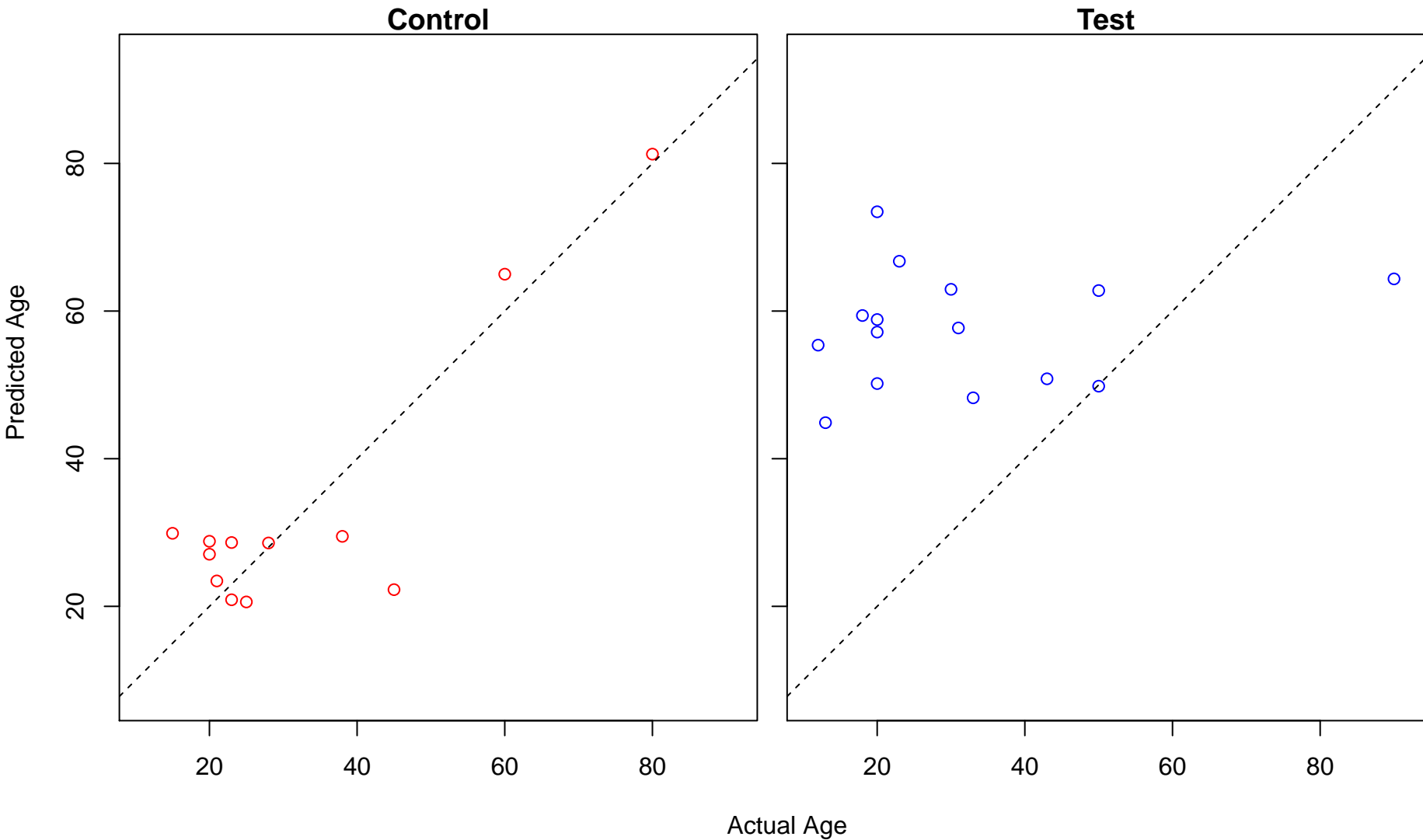
regulation of somitogenesis (Score: 4.727641)



positive regulation of lipid kinase activity (Score: 4.726023)

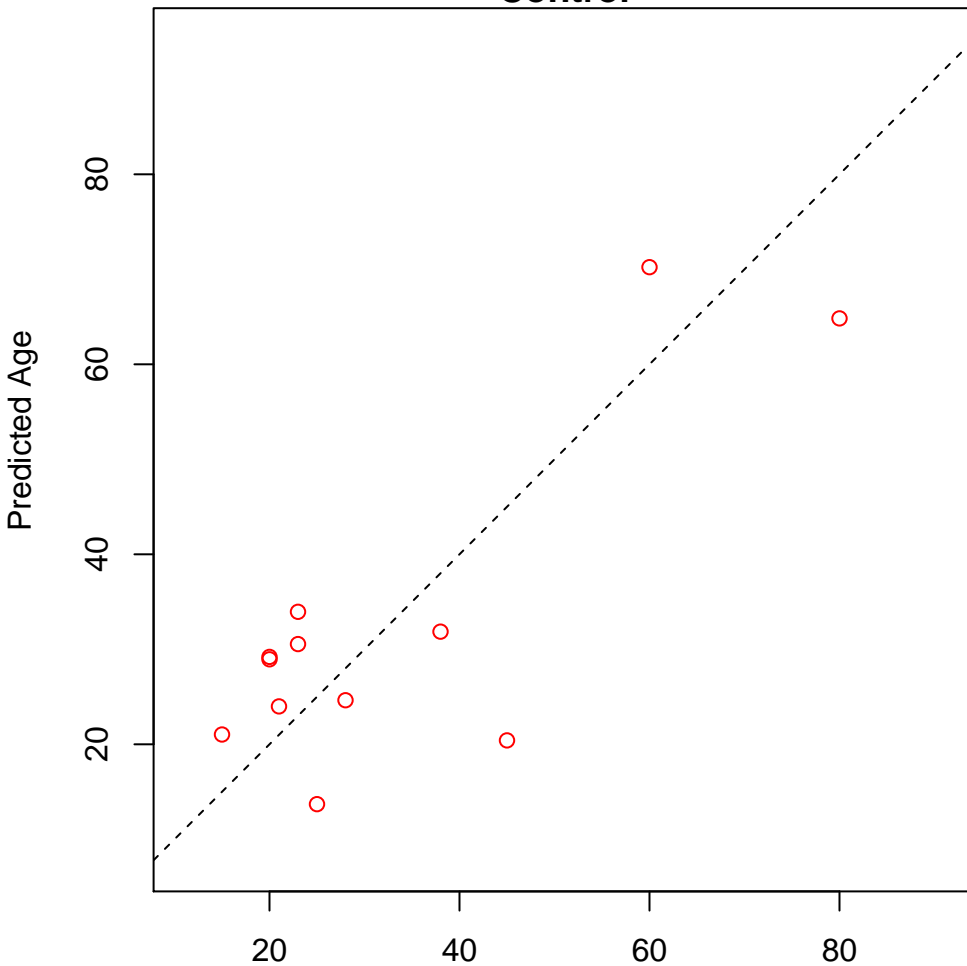


positive regulation of dendrite development (Score: 4.724799)

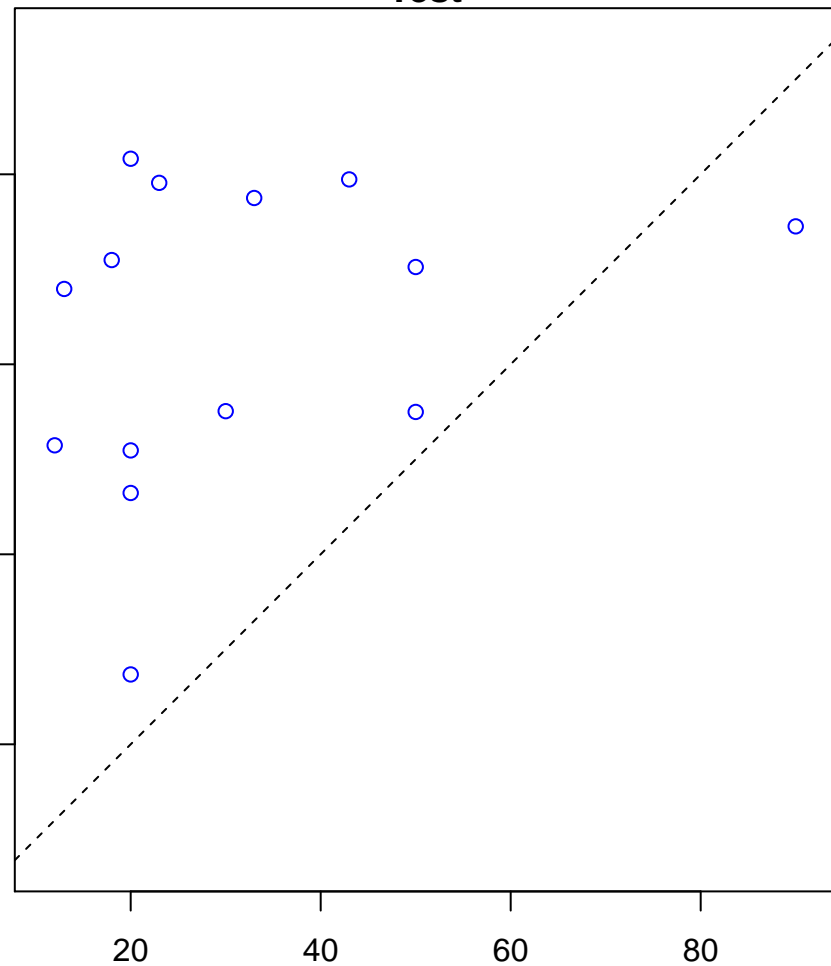


regulation of membrane depolarization (Score: 4.722444)

Control

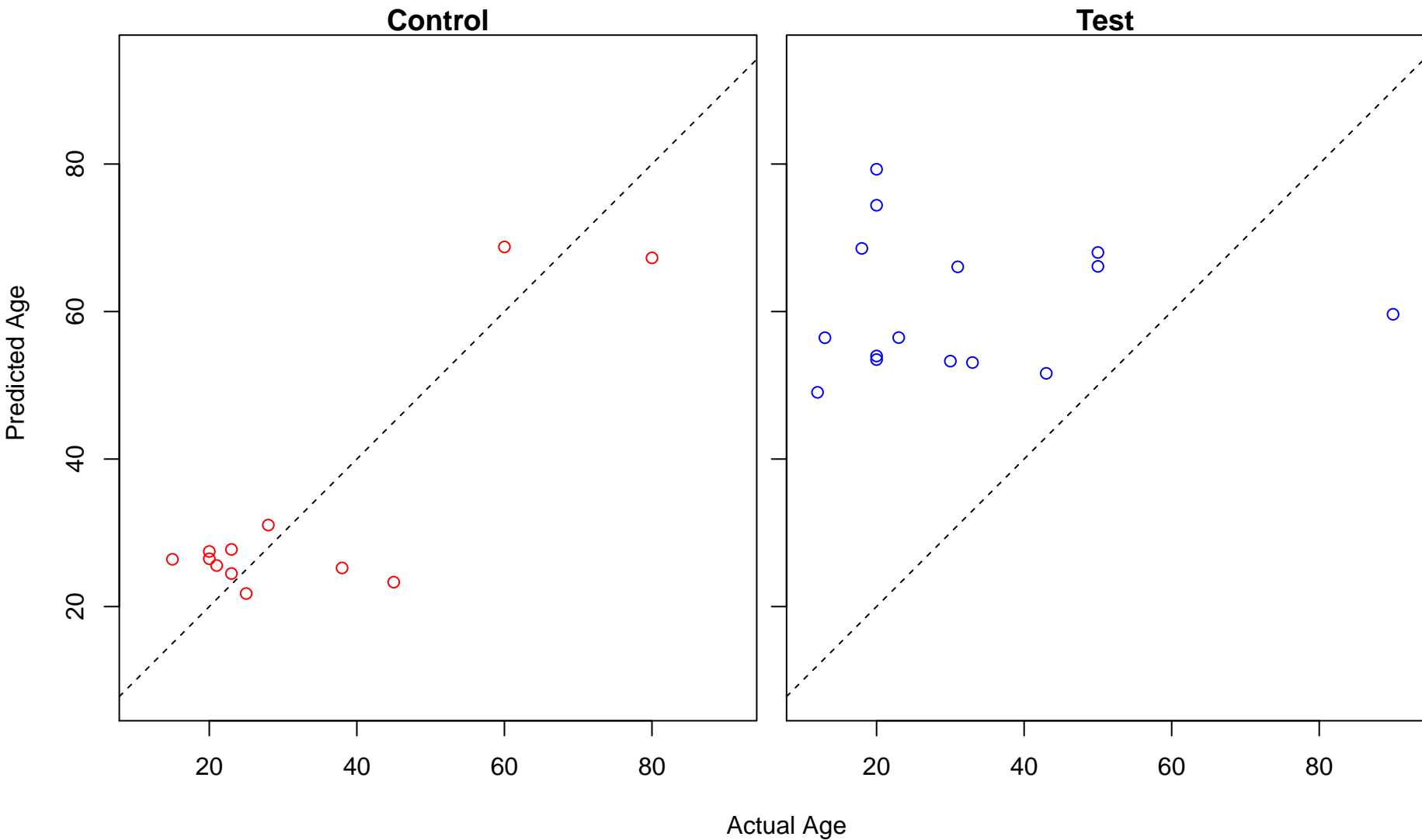


Test

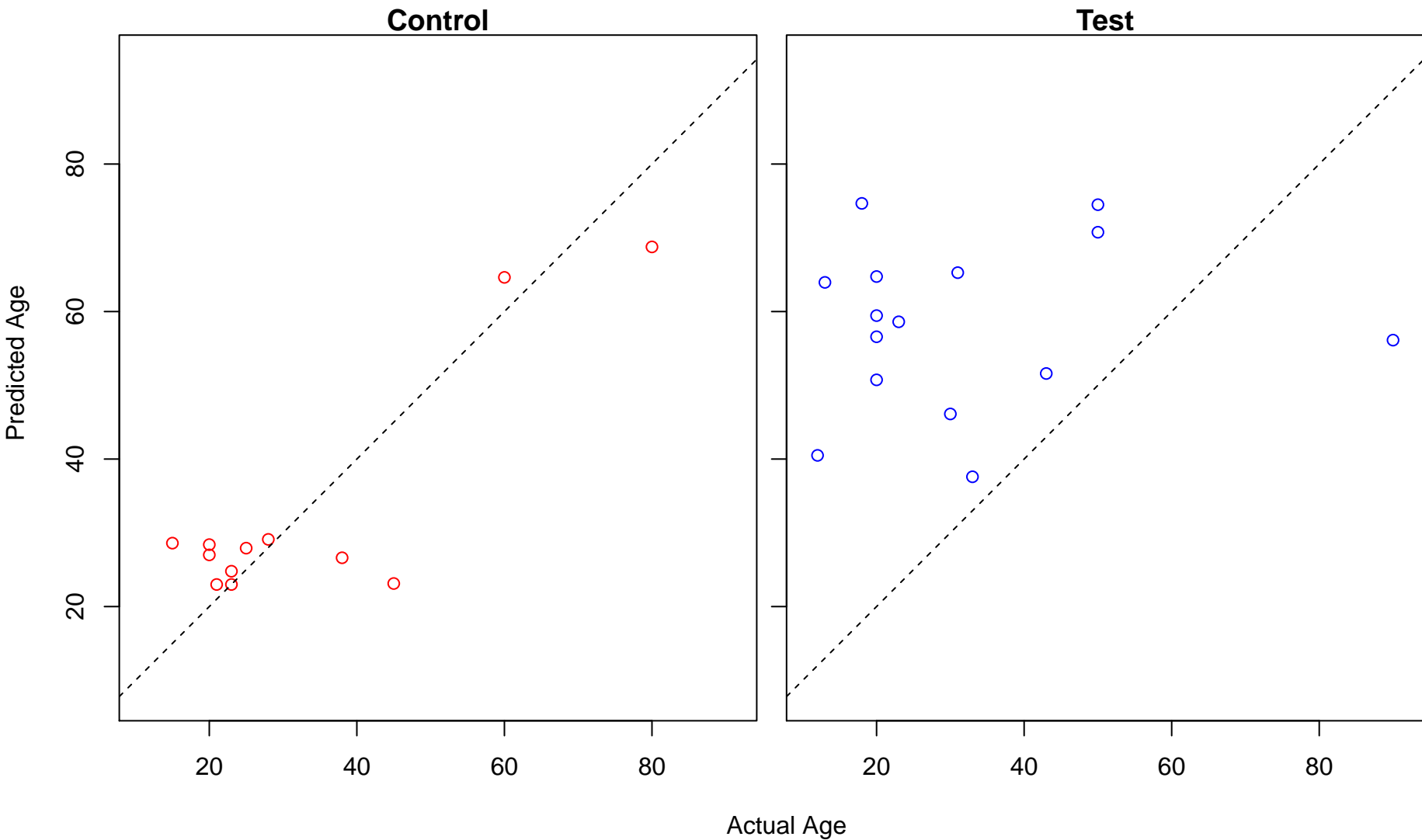


Actual Age

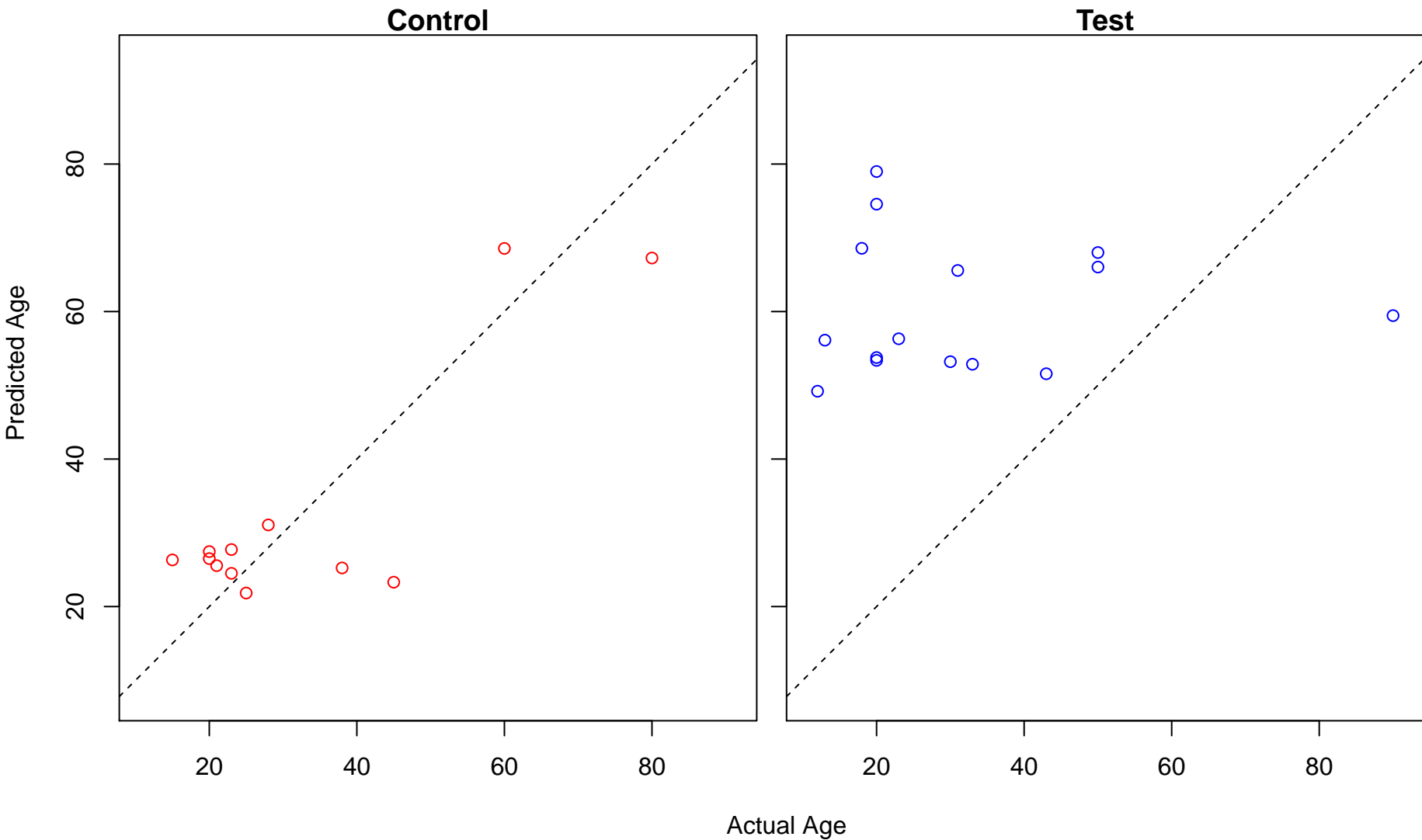
negative regulation of ion transport (Score: 4.720990)



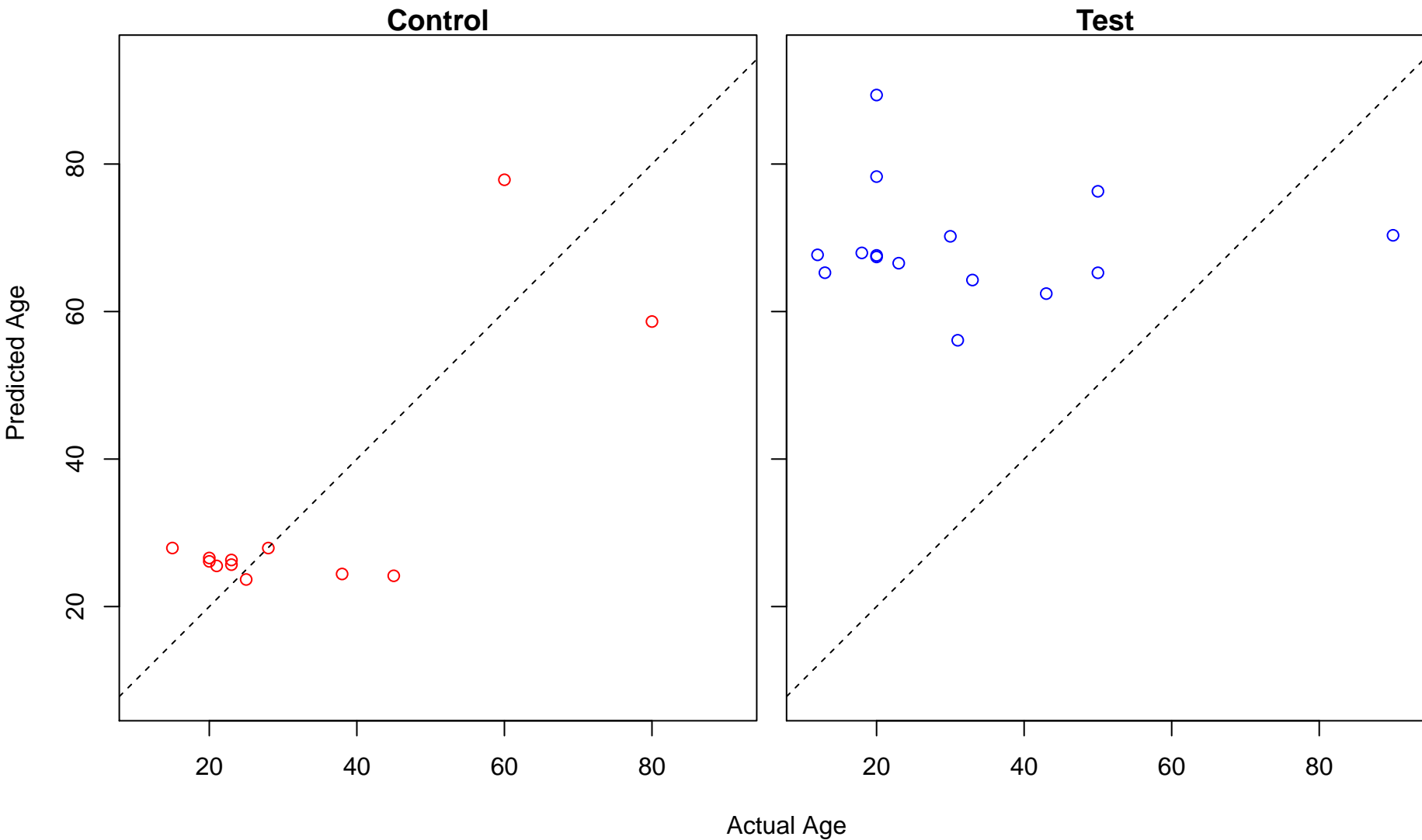
ATP generation from ADP (Score: 4.718625)



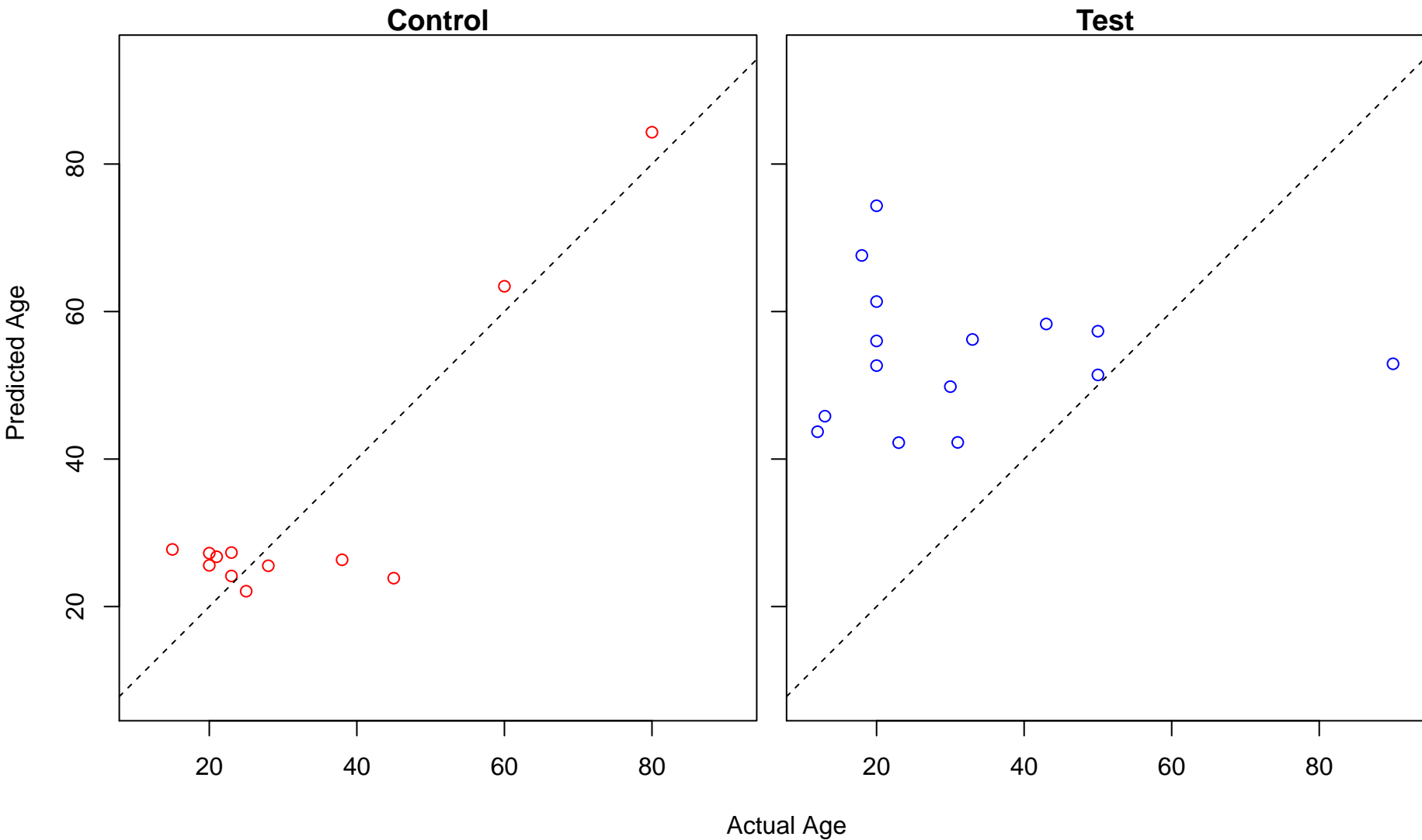
negative regulation of ion transmembrane transport (Score: 4.717663)



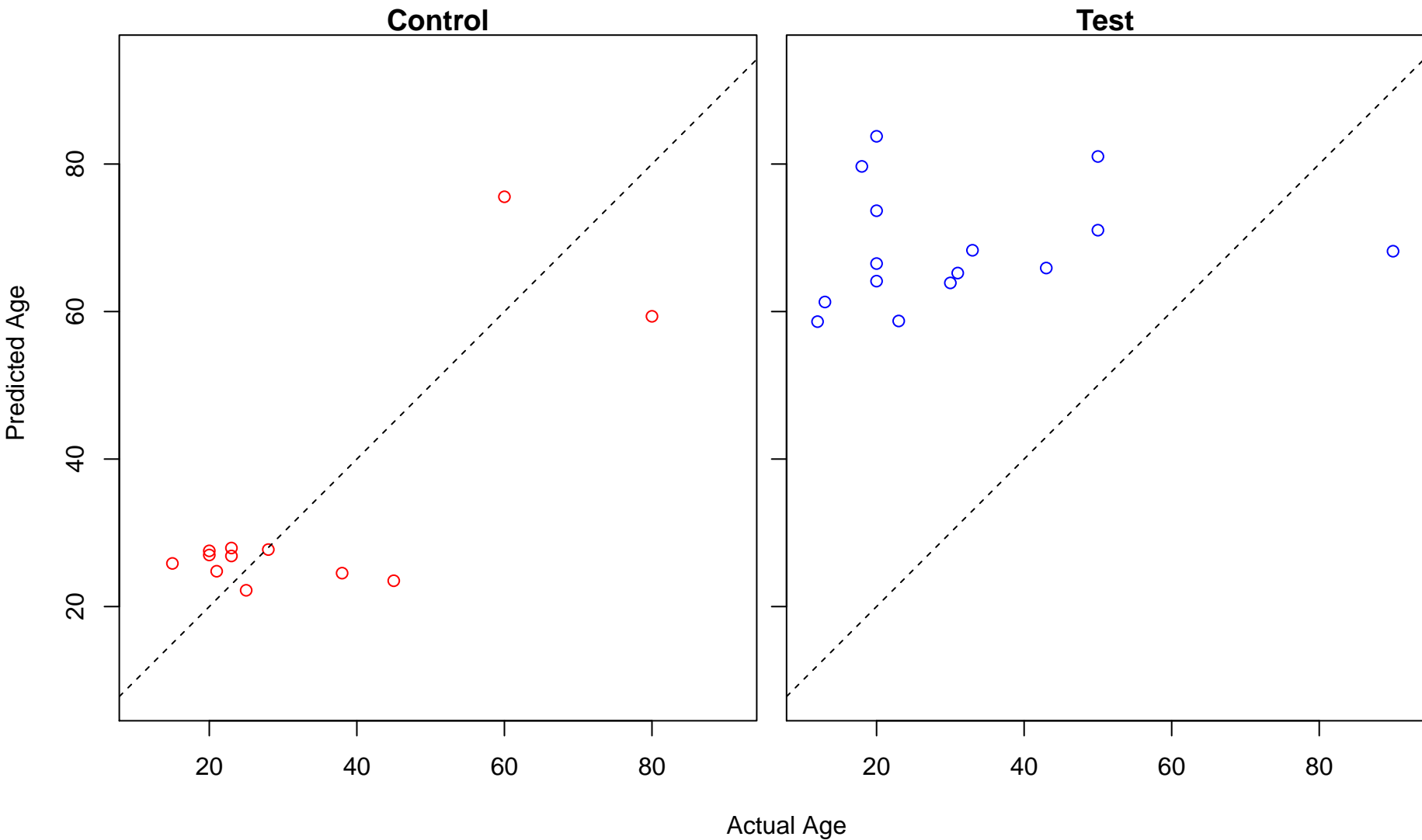
regulation of viral transcription (Score: 4.715756)



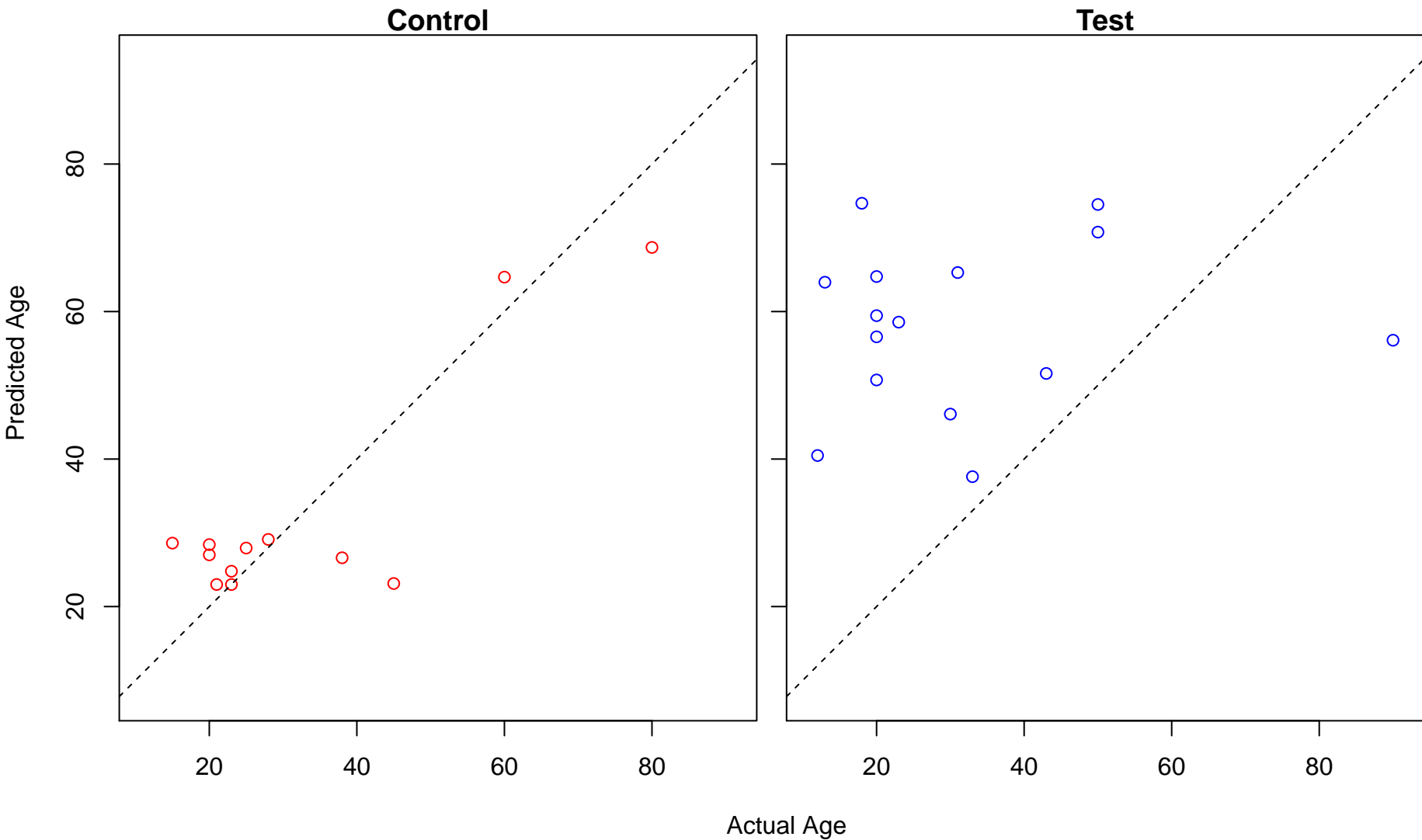
Golgi organization (Score: 4.712563)



regulation of exocytosis (Score: 4.711104)

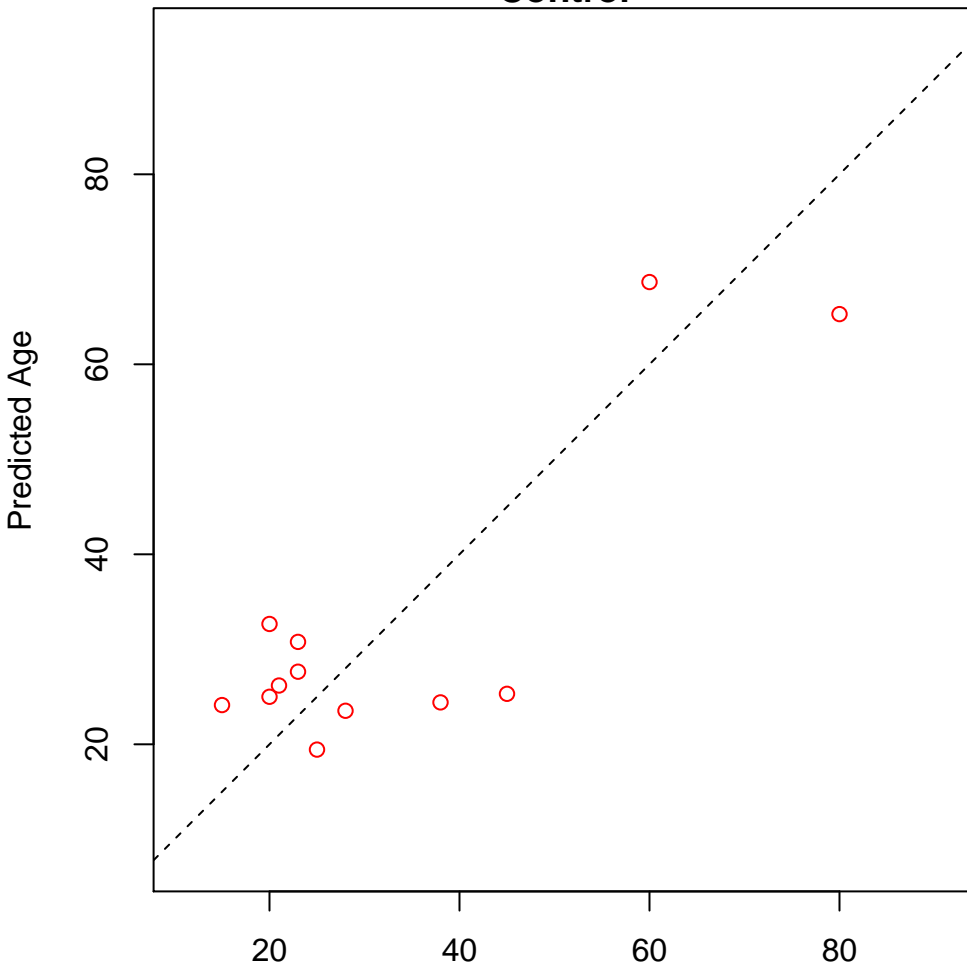


ADP metabolic process (Score: 4.709305)

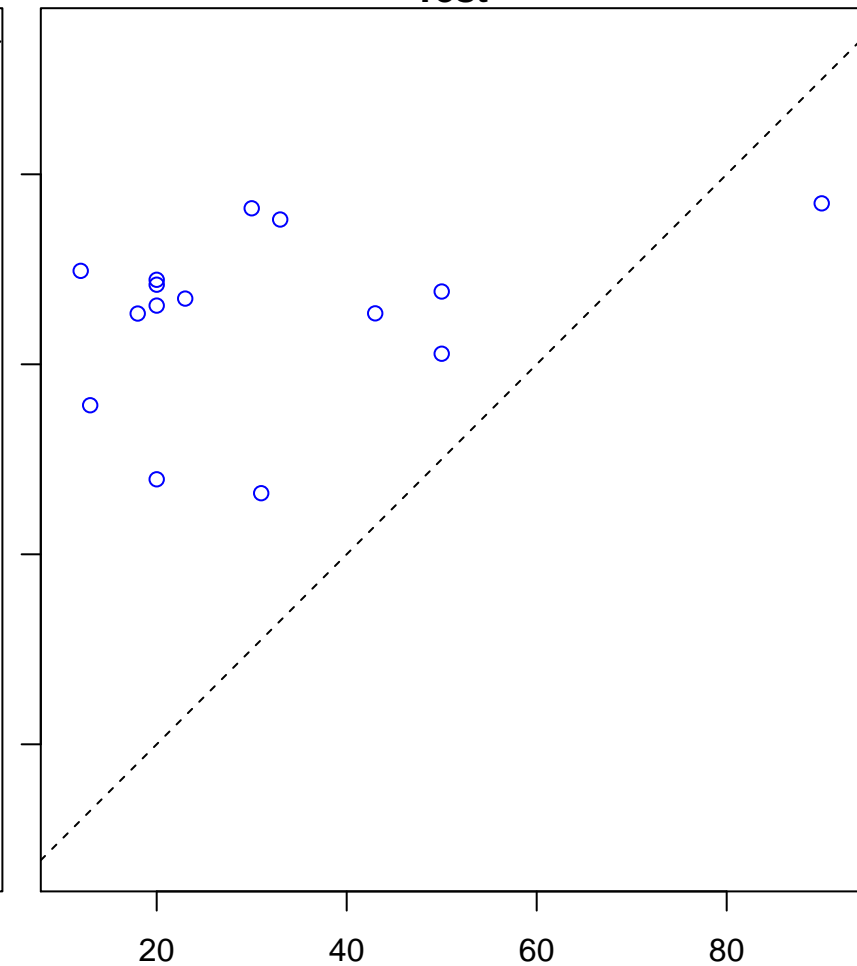


cardiac muscle fiber development (Score: 4.704994)

Control

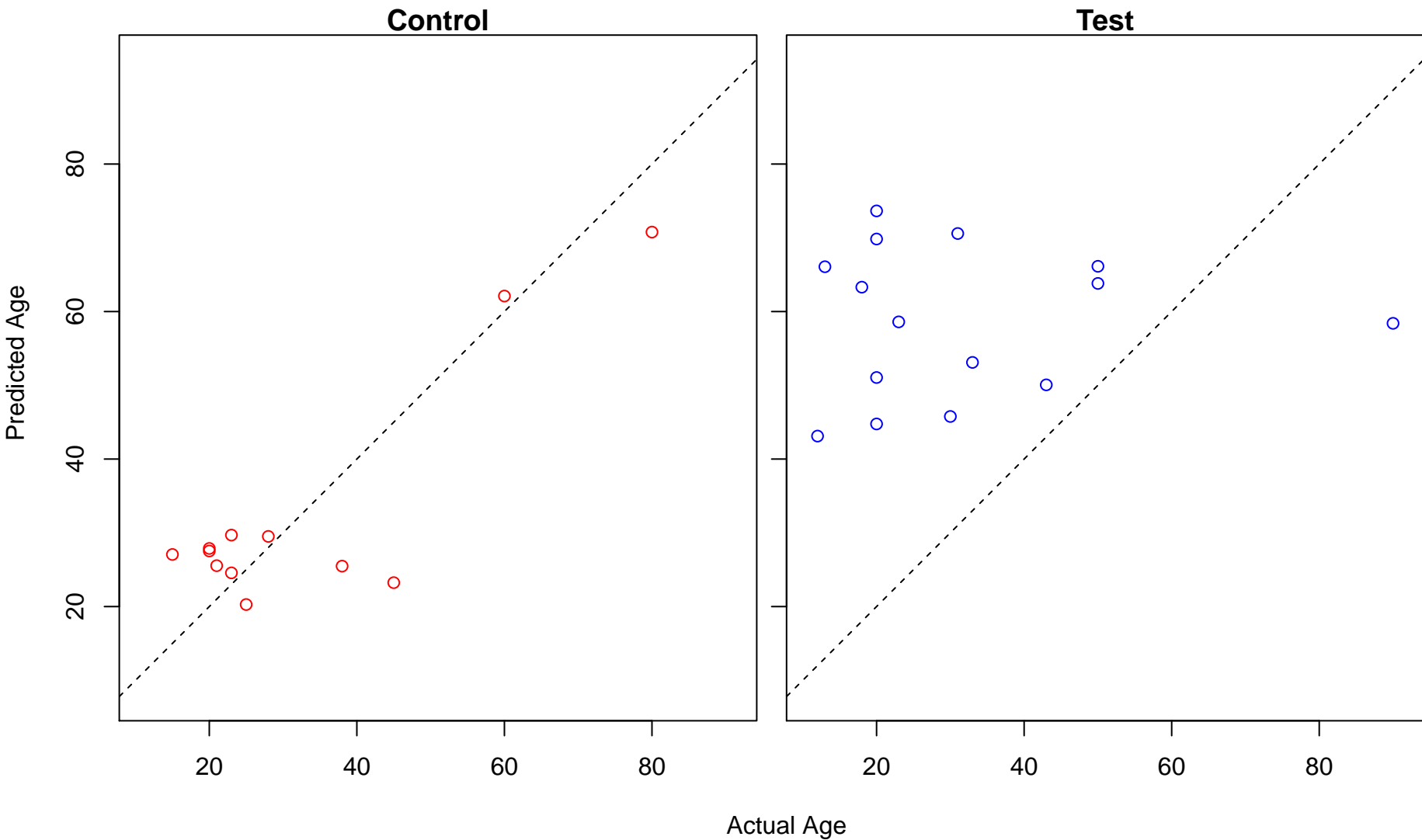


Test

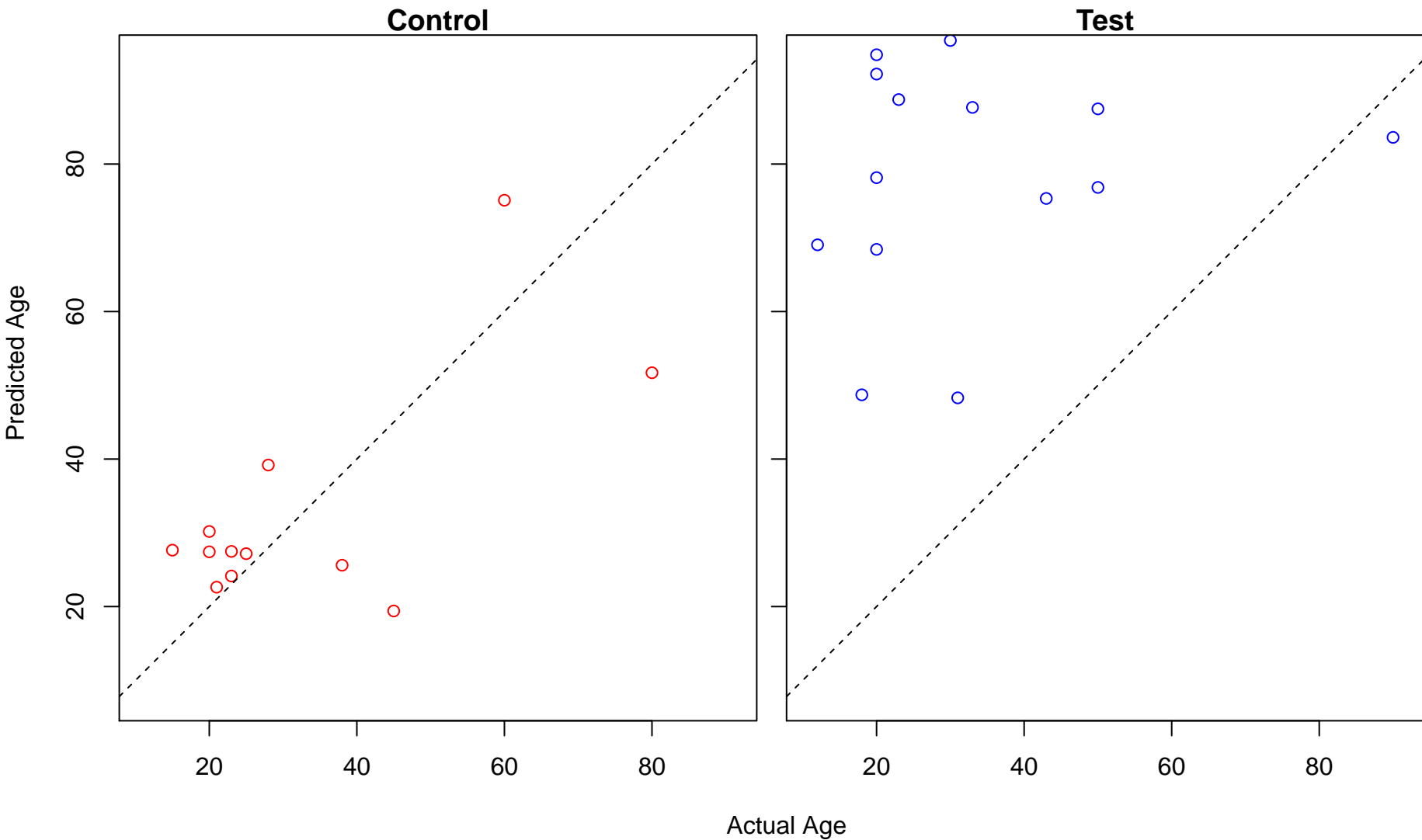


Actual Age

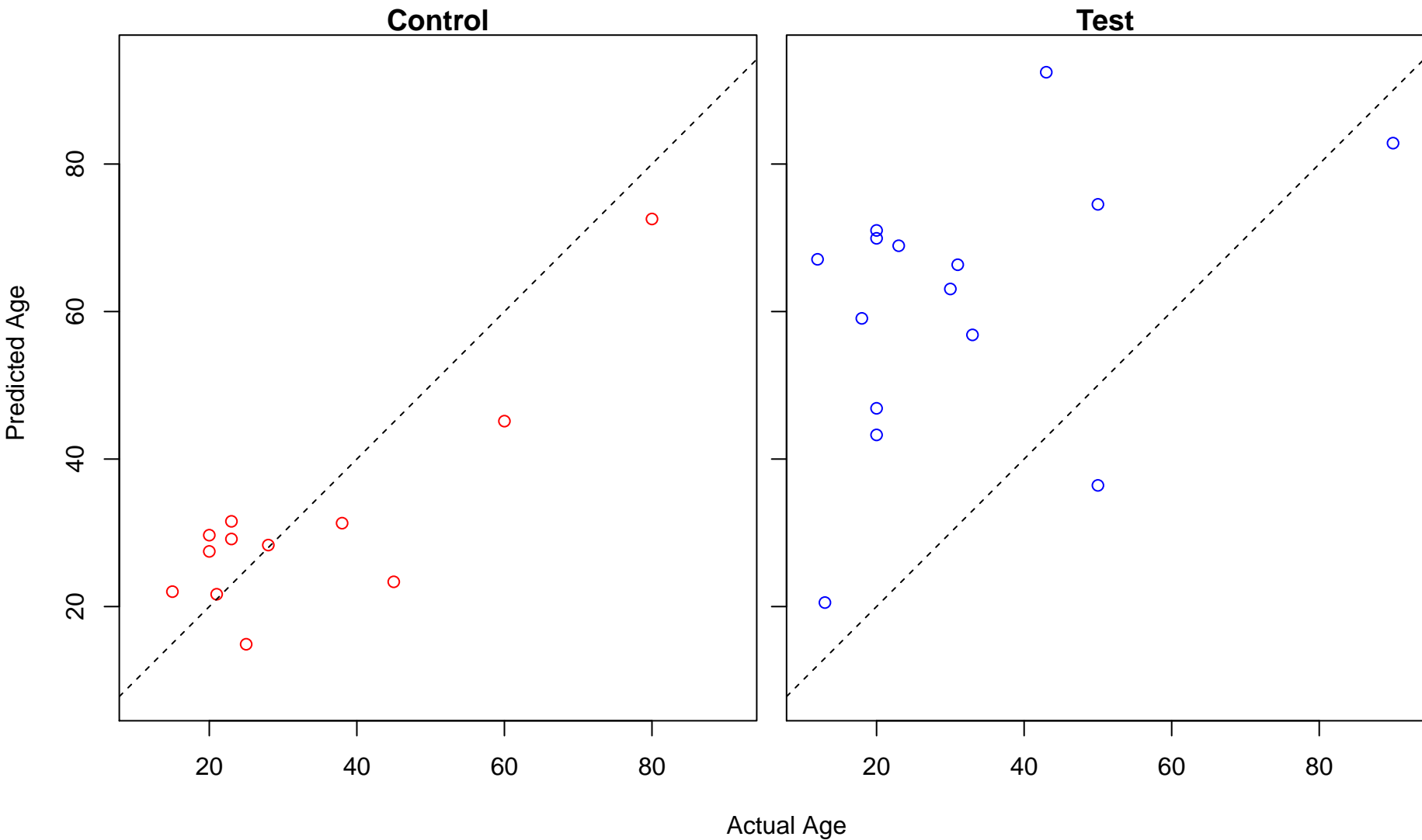
single-organism carbohydrate catabolic process (Score: 4.704268)



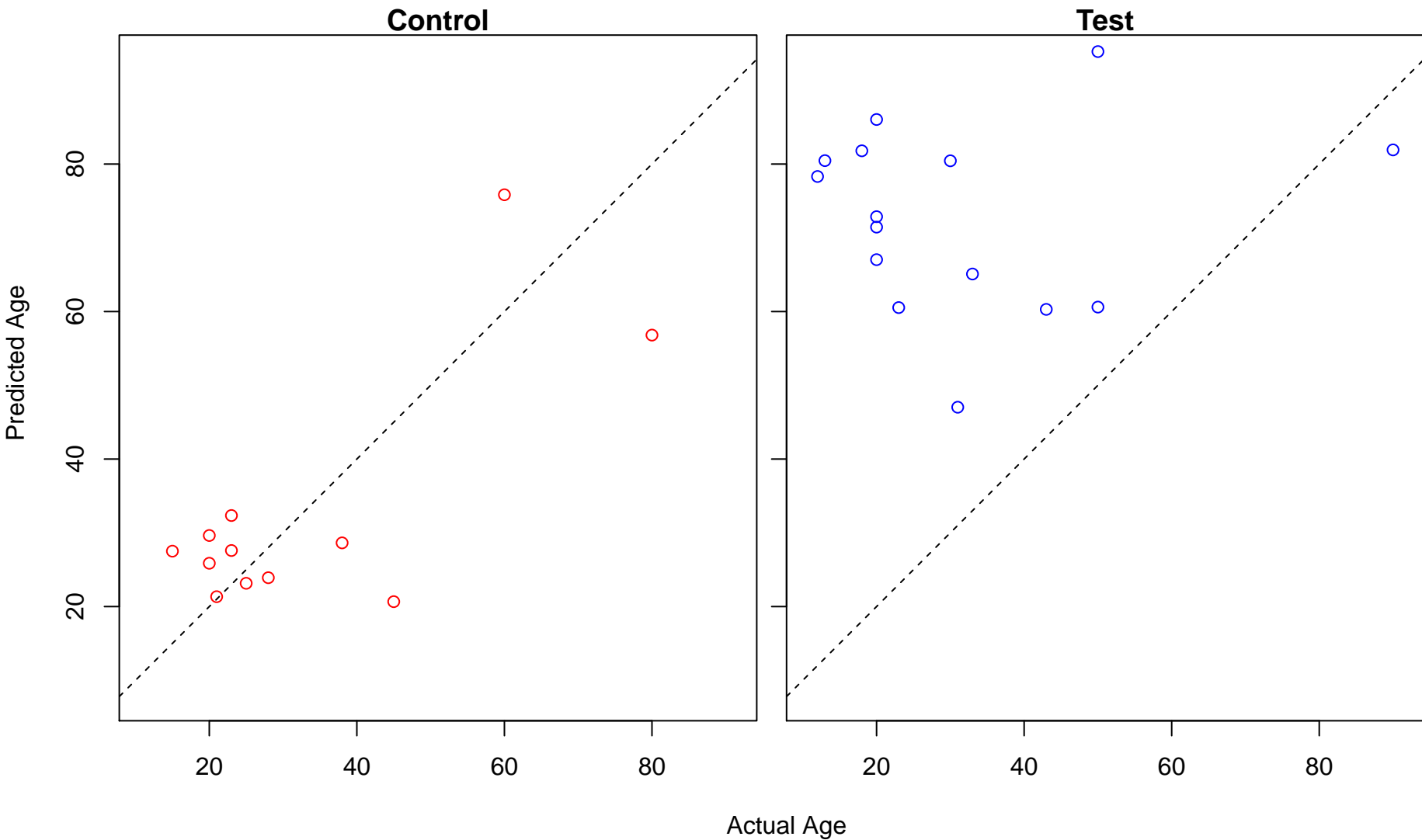
regulation of catecholamine secretion (Score: 4.703440)



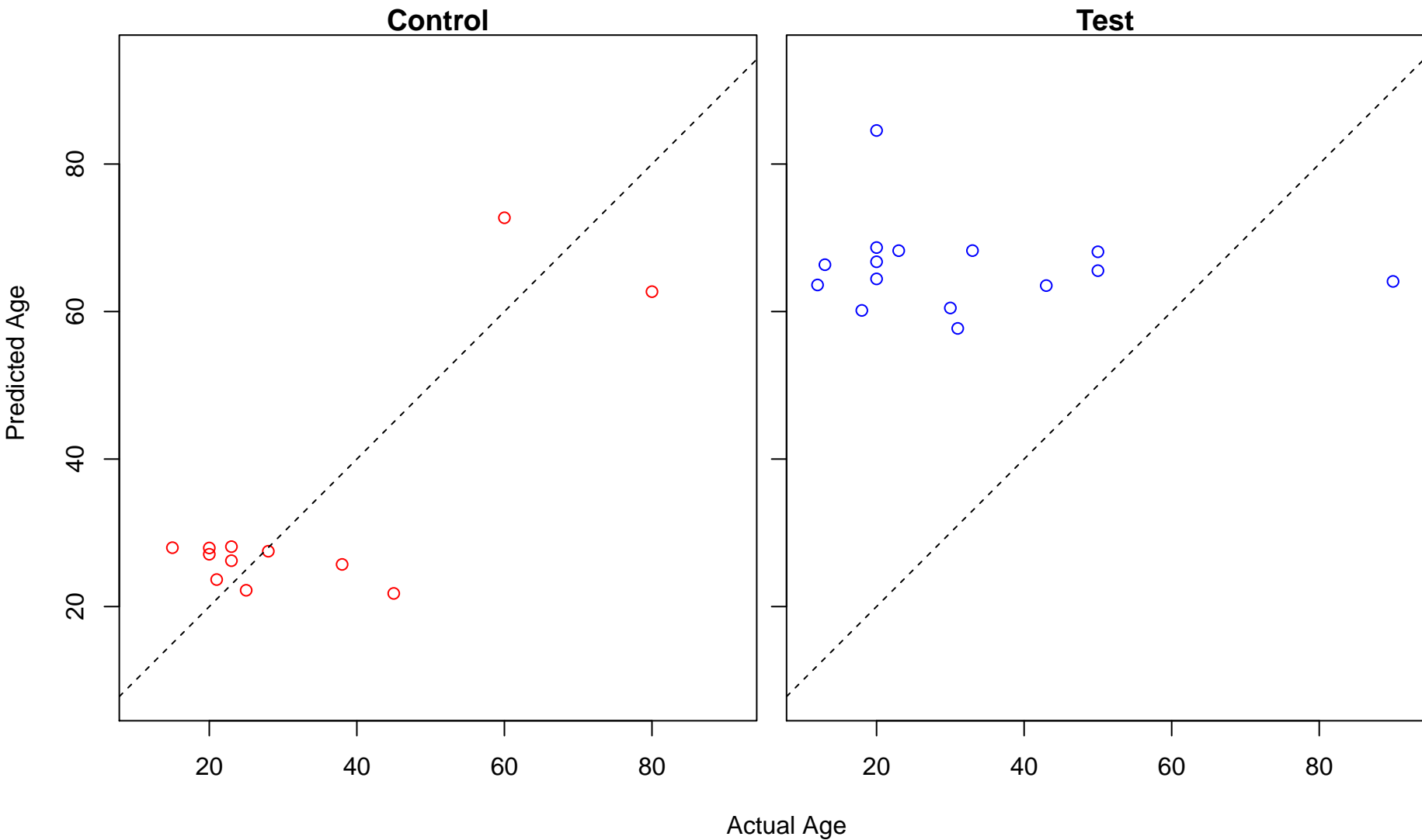
cell proliferation in forebrain (Score: 4.702176)



cardiac septum morphogenesis (Score: 4.701187)

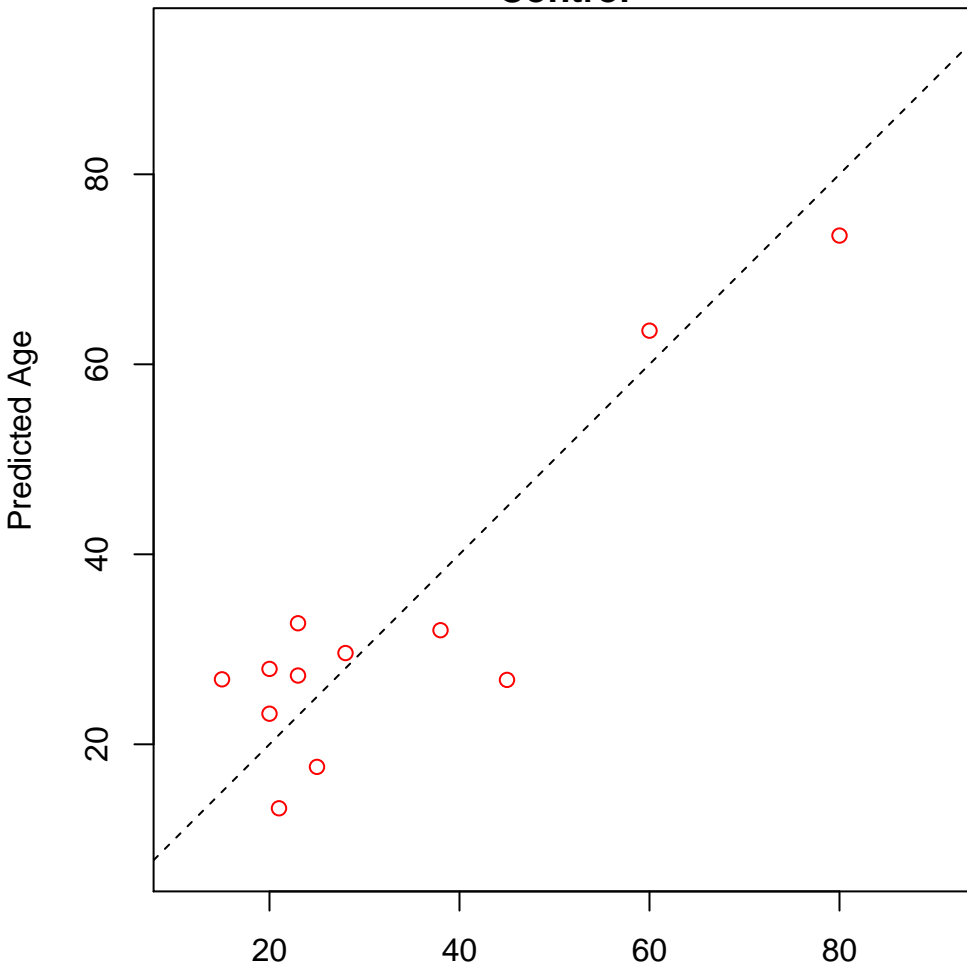


sensory organ morphogenesis (Score: 4.701051)

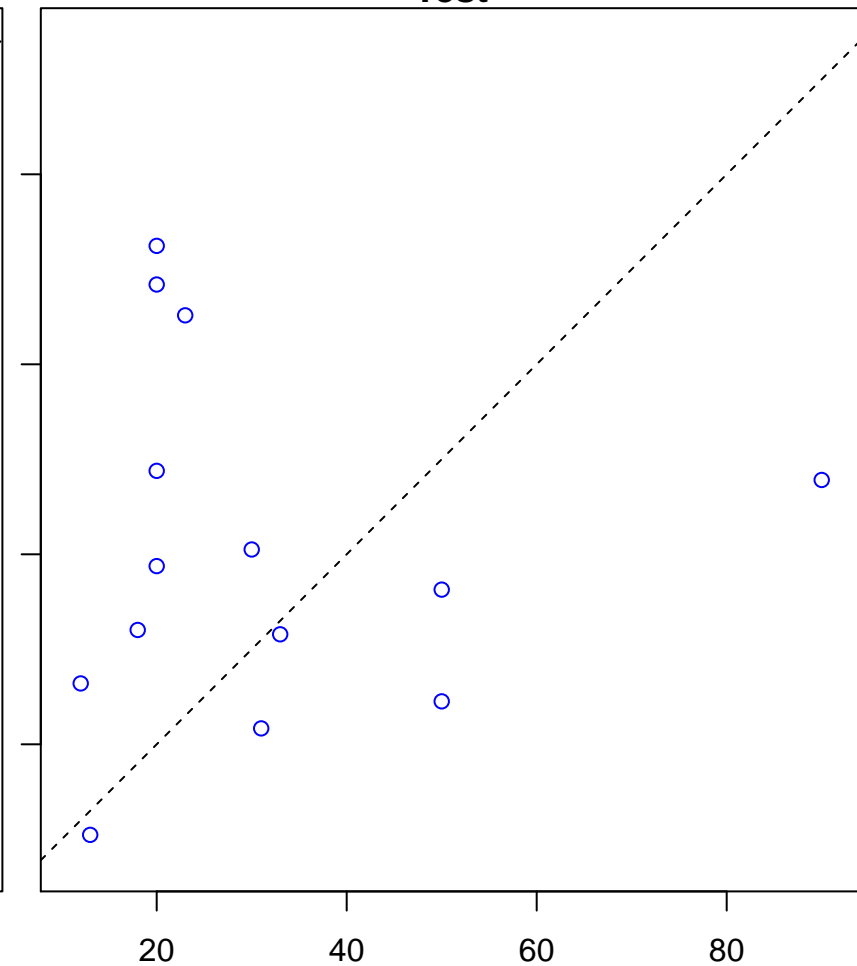


RNA phosphodiester bond hydrolysis (Score: 4.699970)

Control

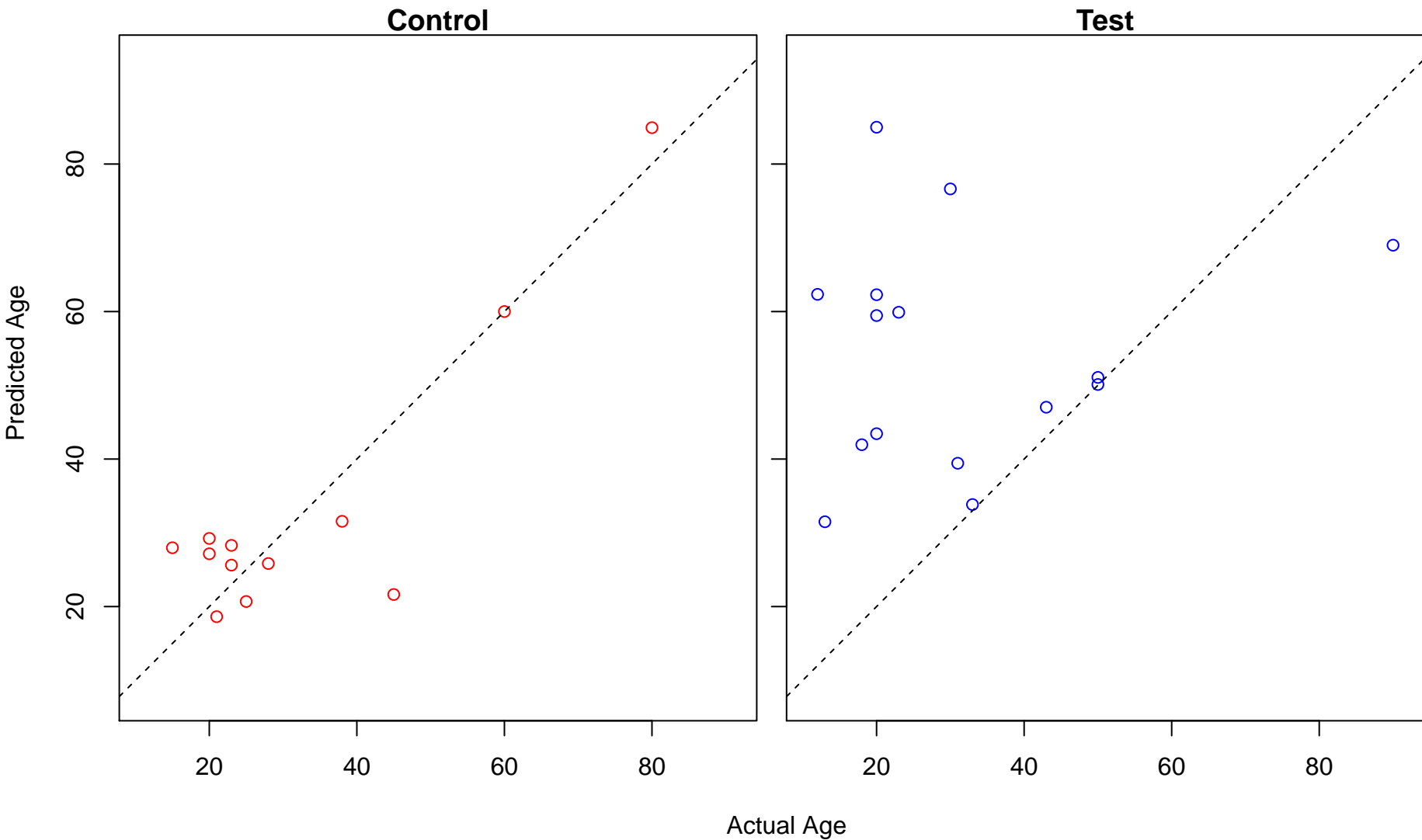


Test

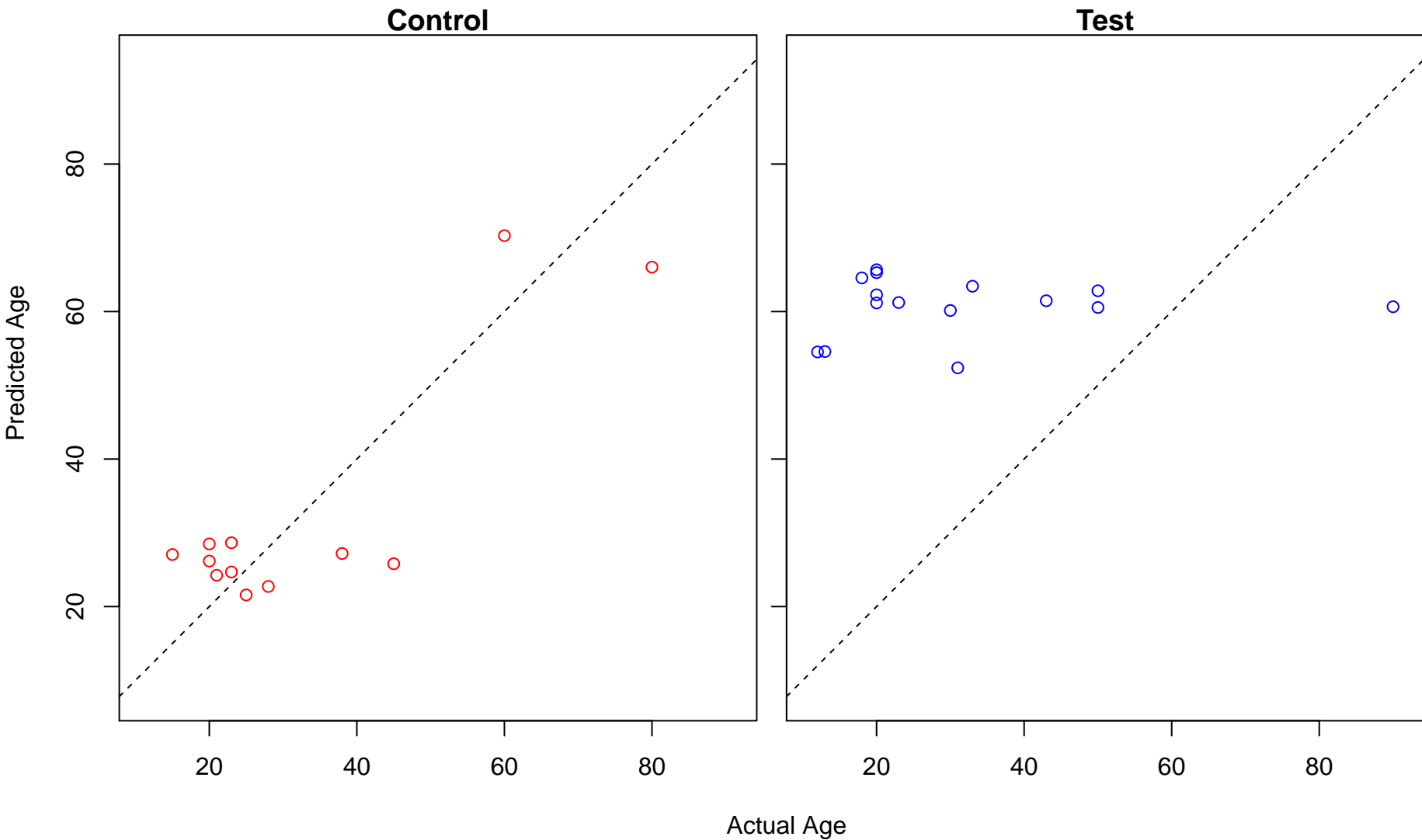


Actual Age

negative regulation by host of viral genome replication (Score: 4.699096)

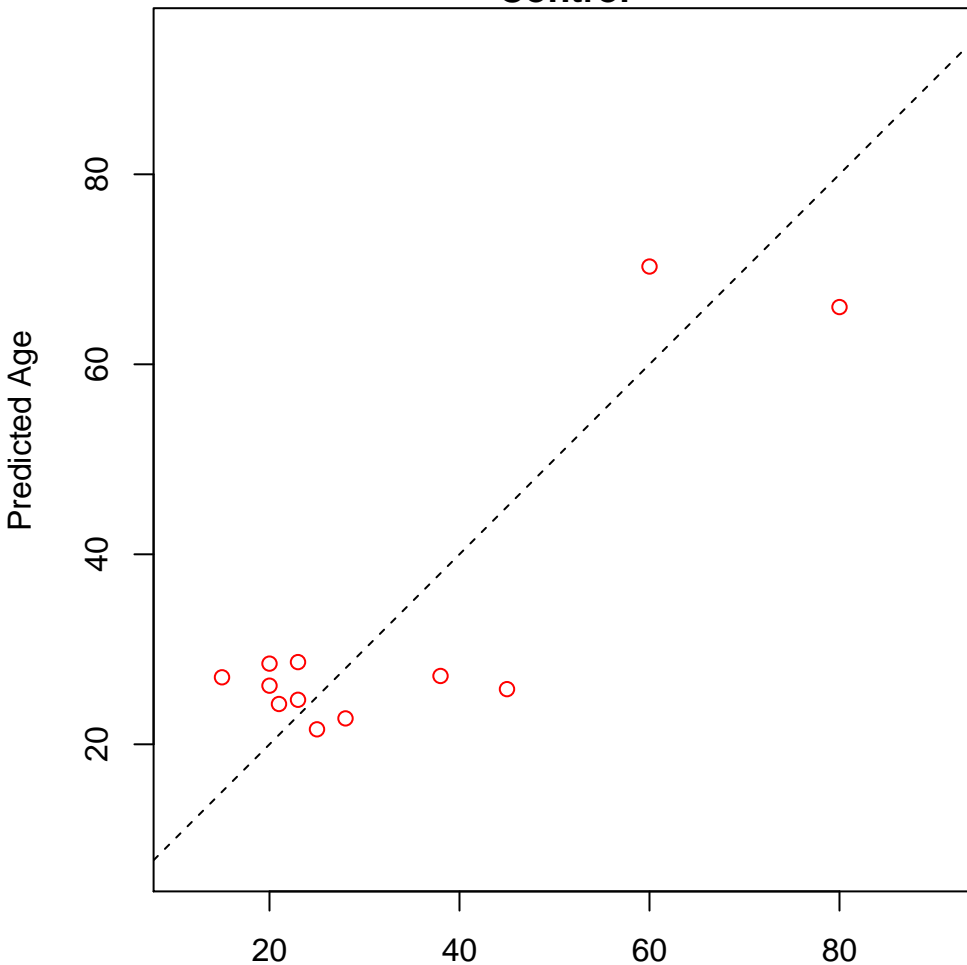


physiological muscle hypertrophy (Score: 4.698608)

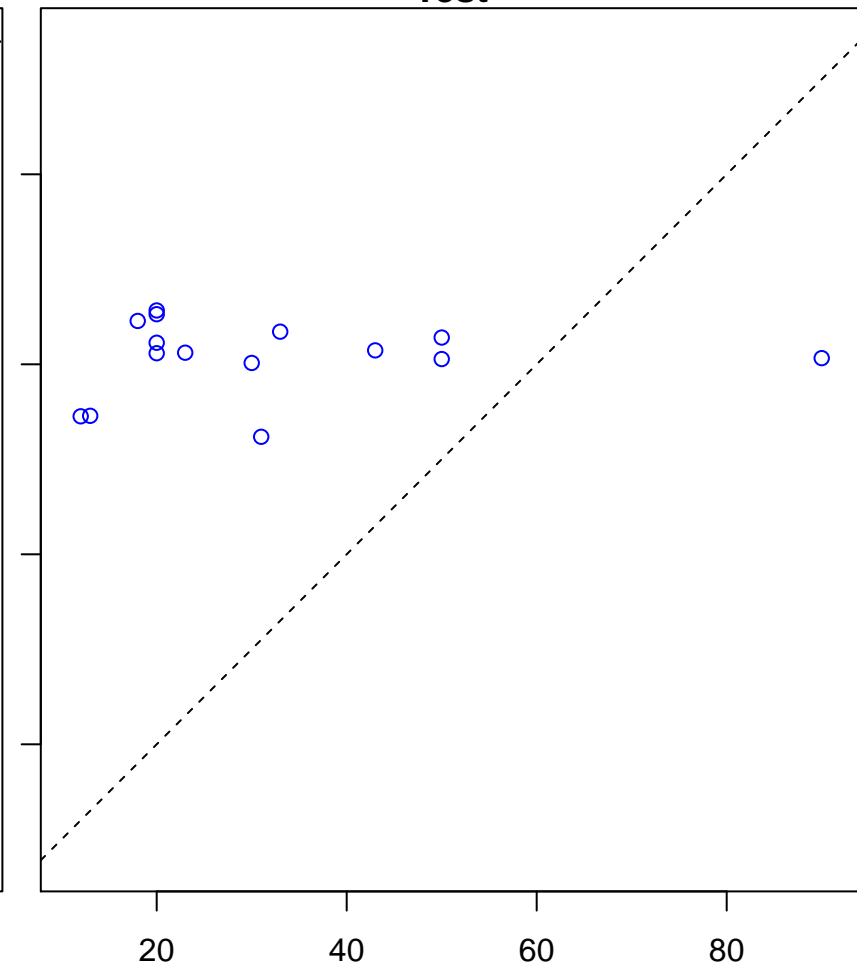


physiological cardiac muscle hypertrophy (Score: 4.698608)

Control

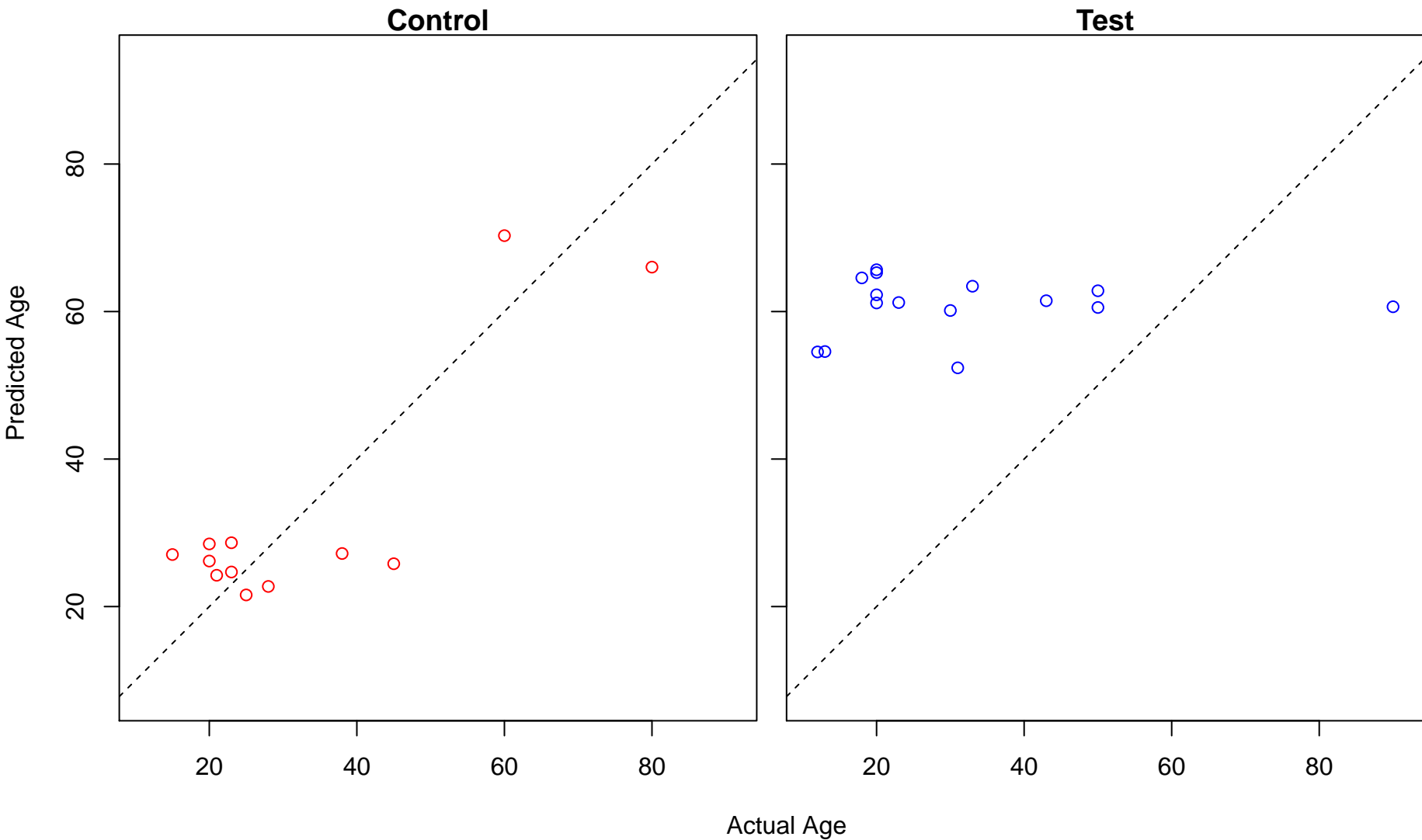


Test

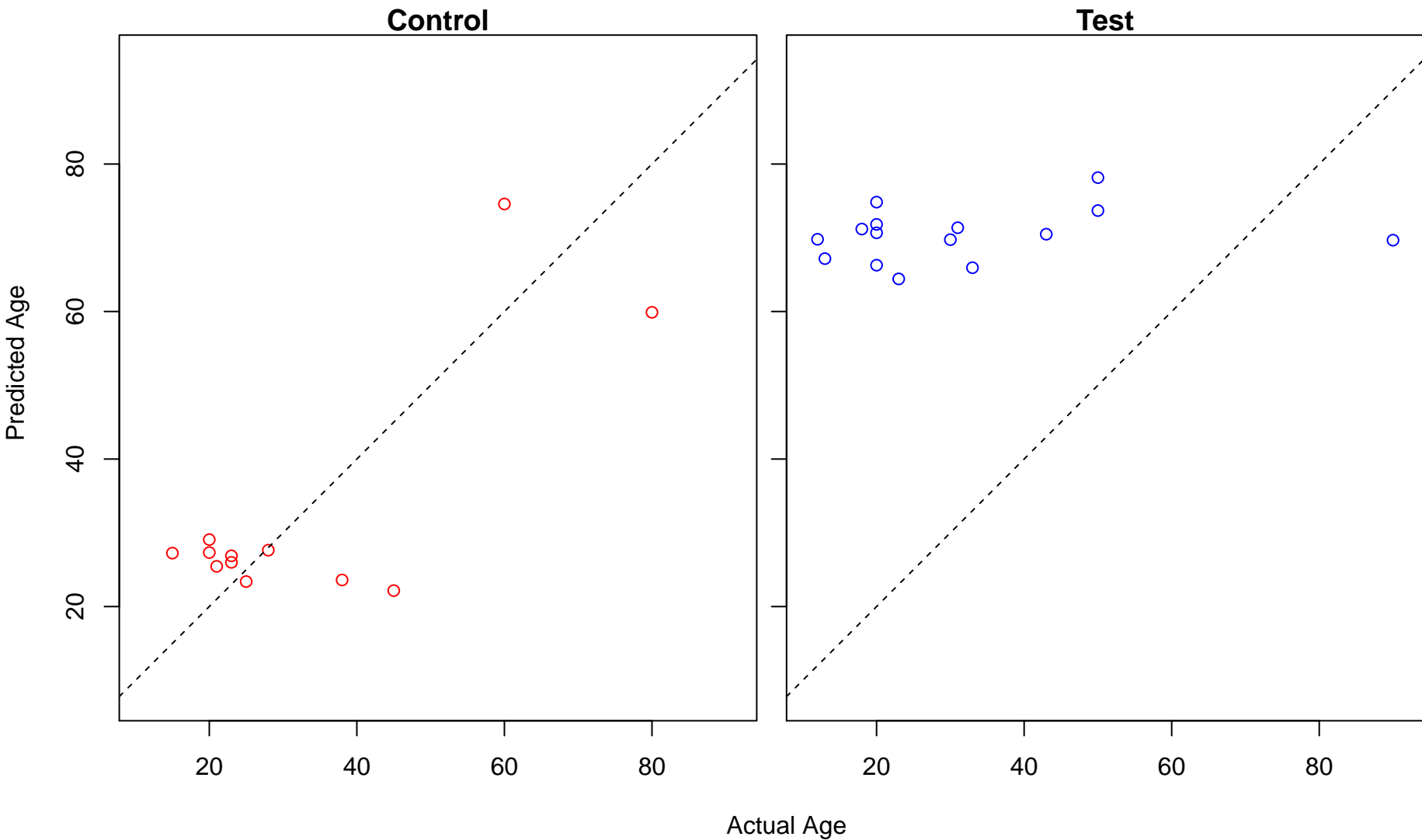


Actual Age

cell growth involved in cardiac muscle cell development (Score: 4.698608)

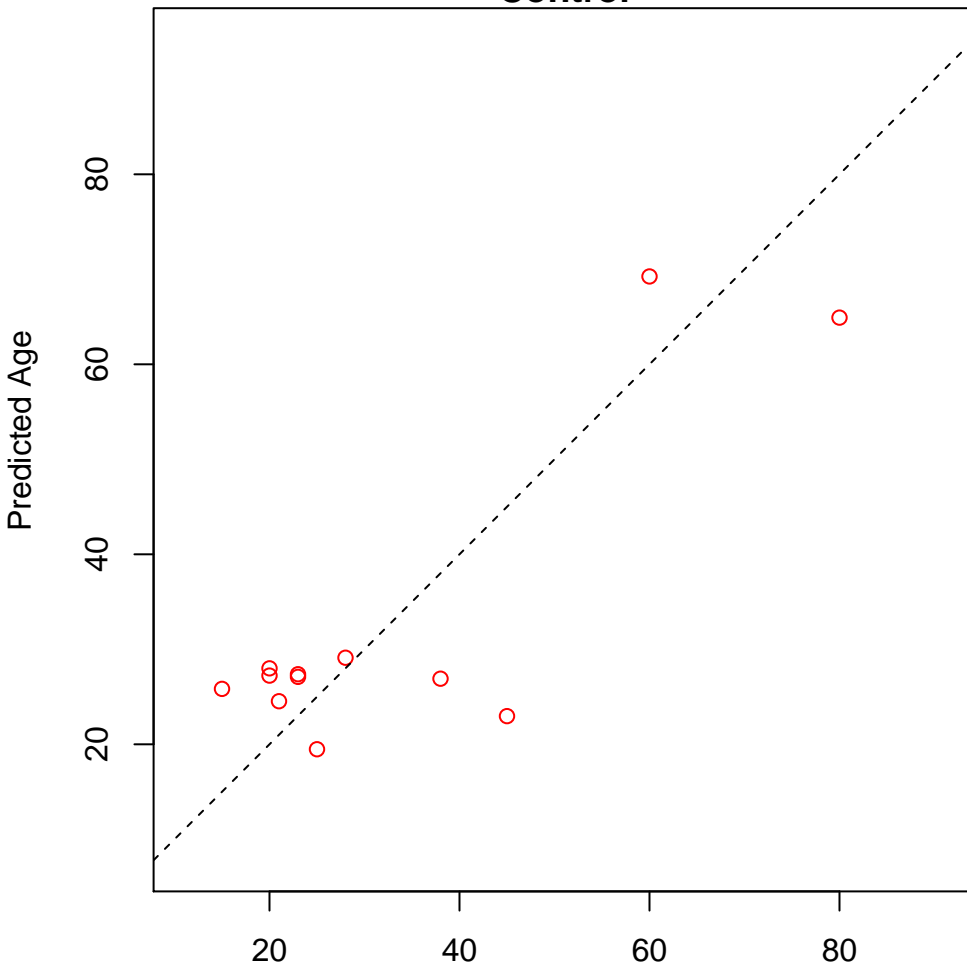


regulation of ATPase activity (Score: 4.698164)

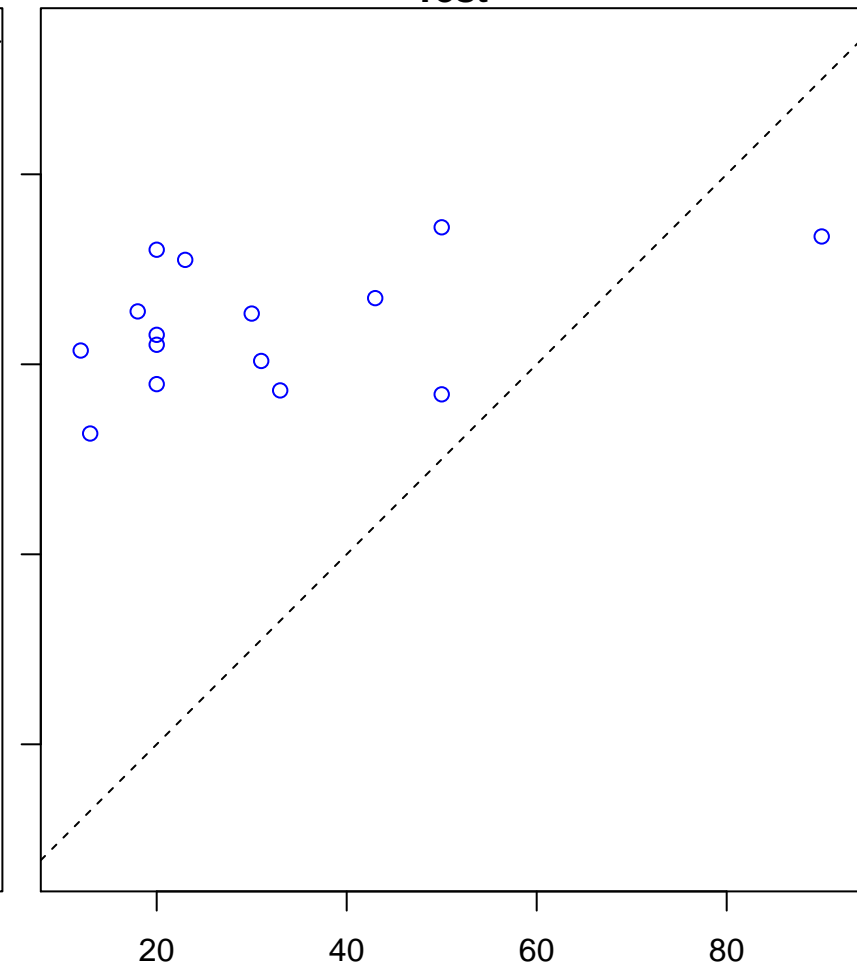


negative regulation of protein secretion (Score: 4.697446)

Control

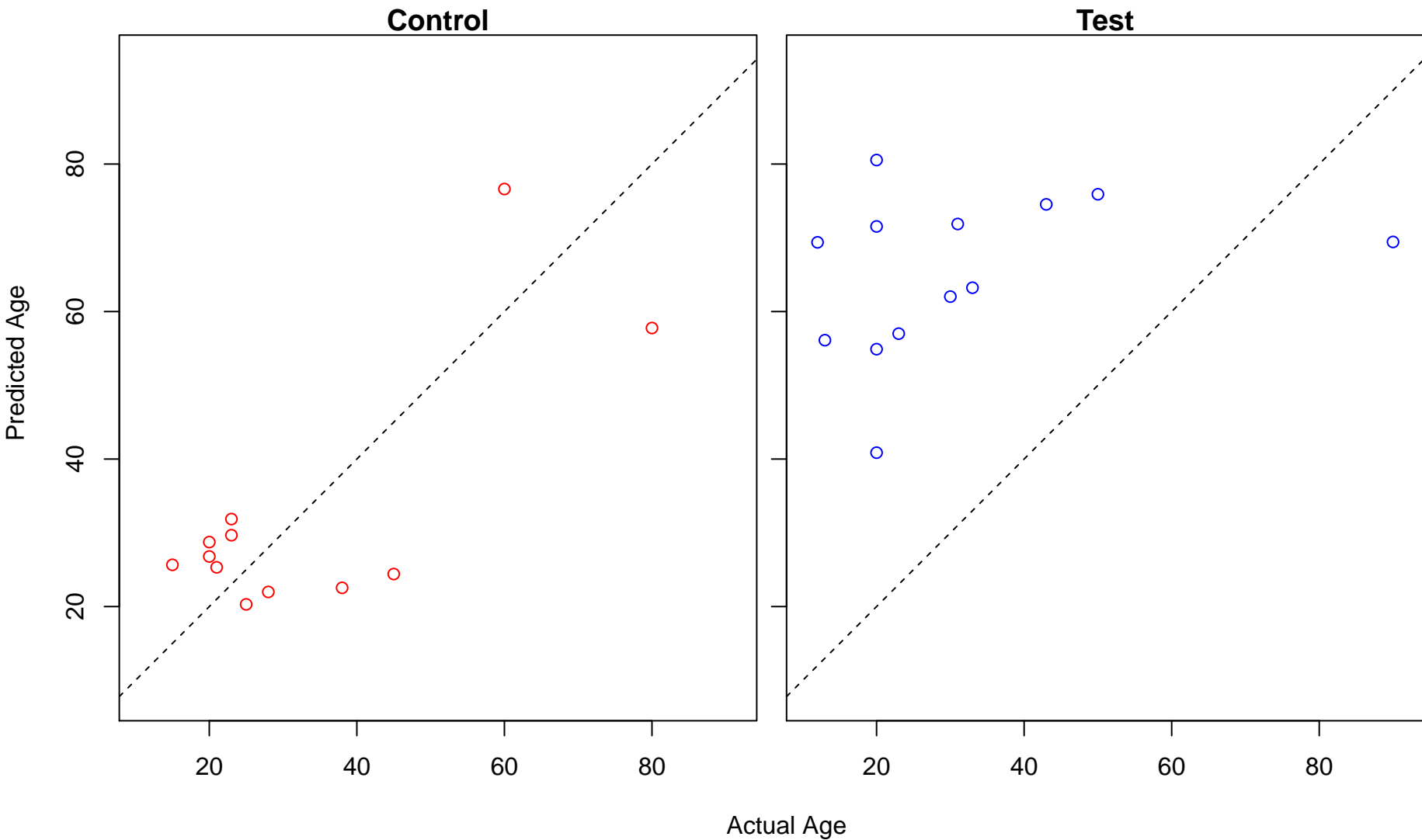


Test

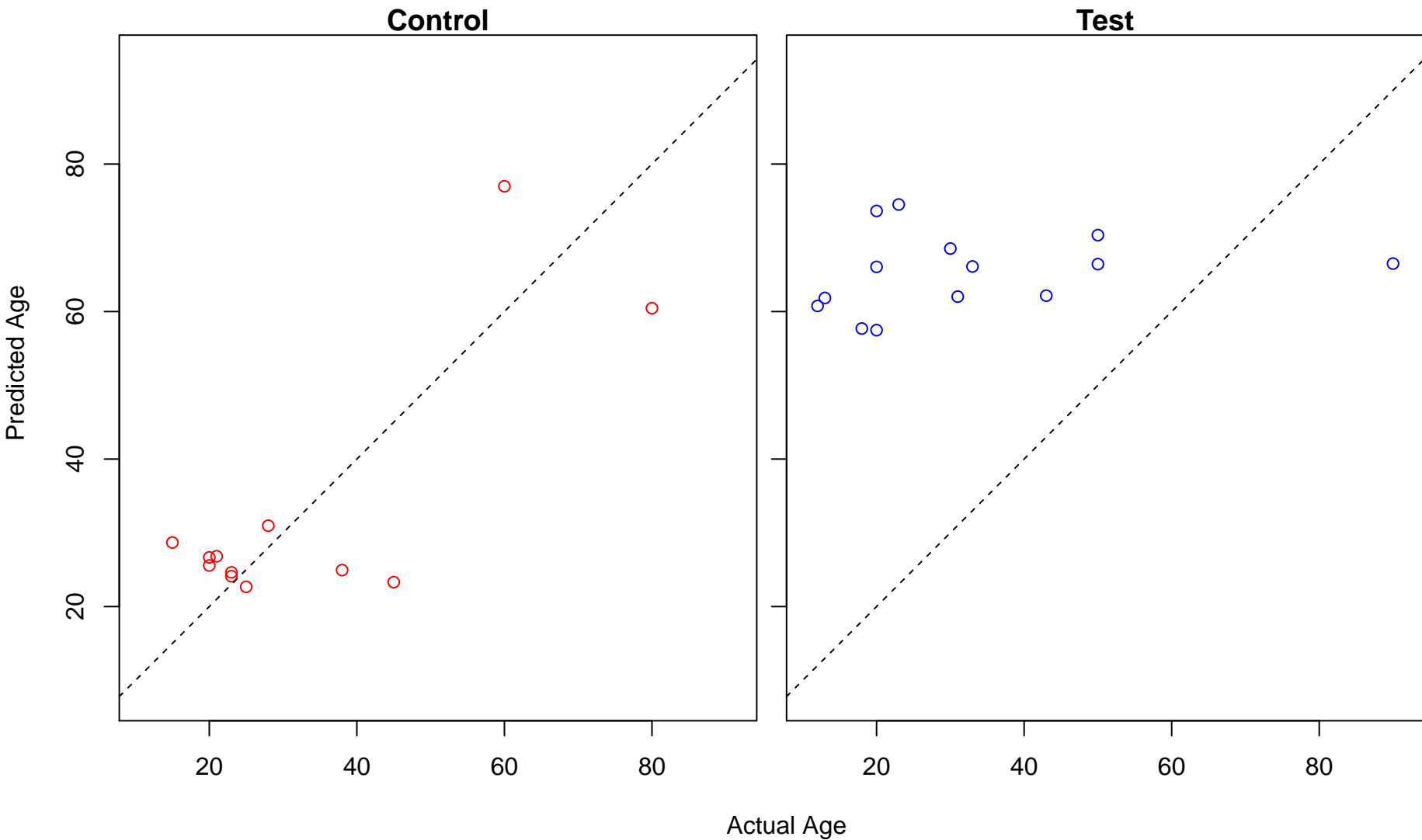


Actual Age

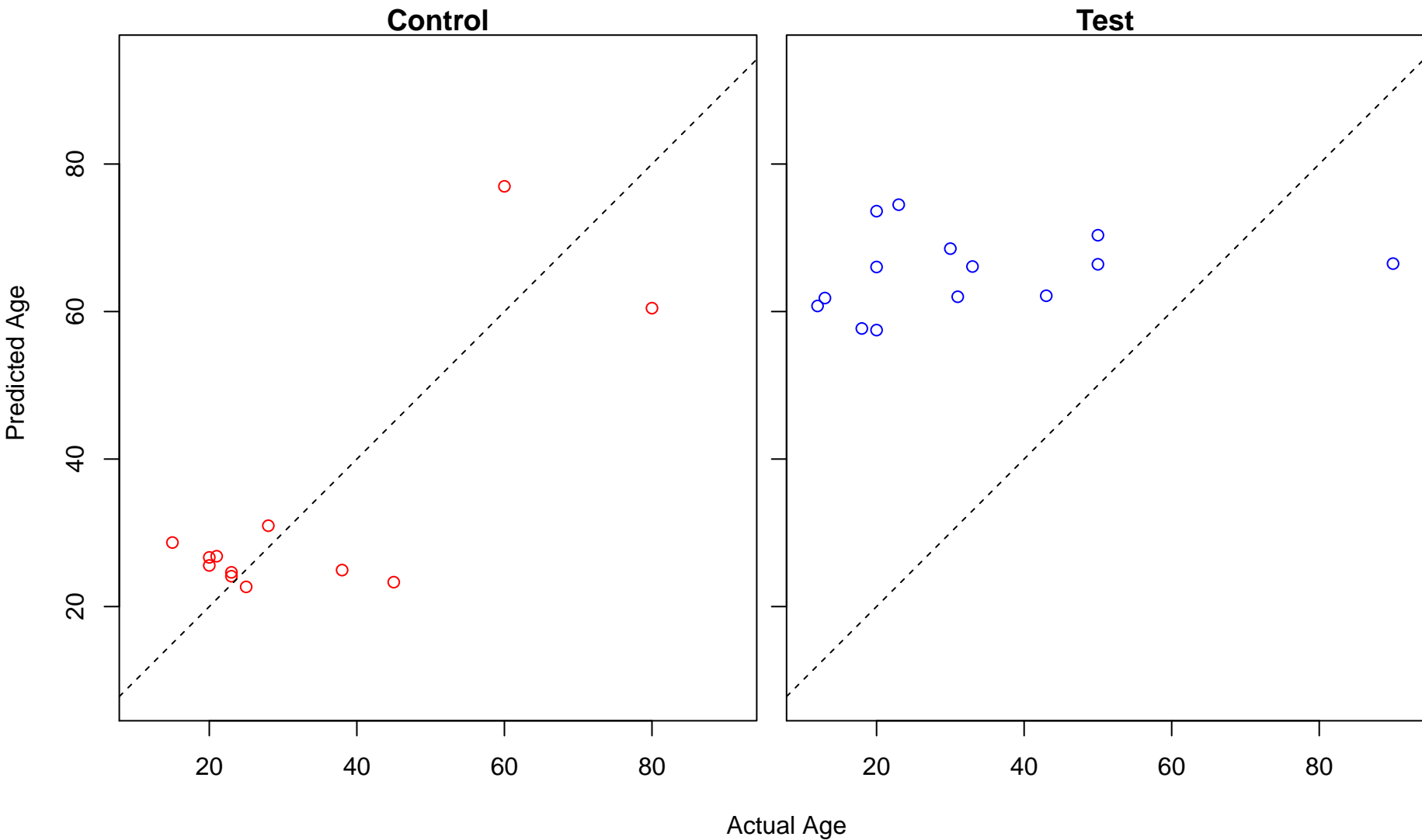
immature B cell differentiation (Score: 4.696769)



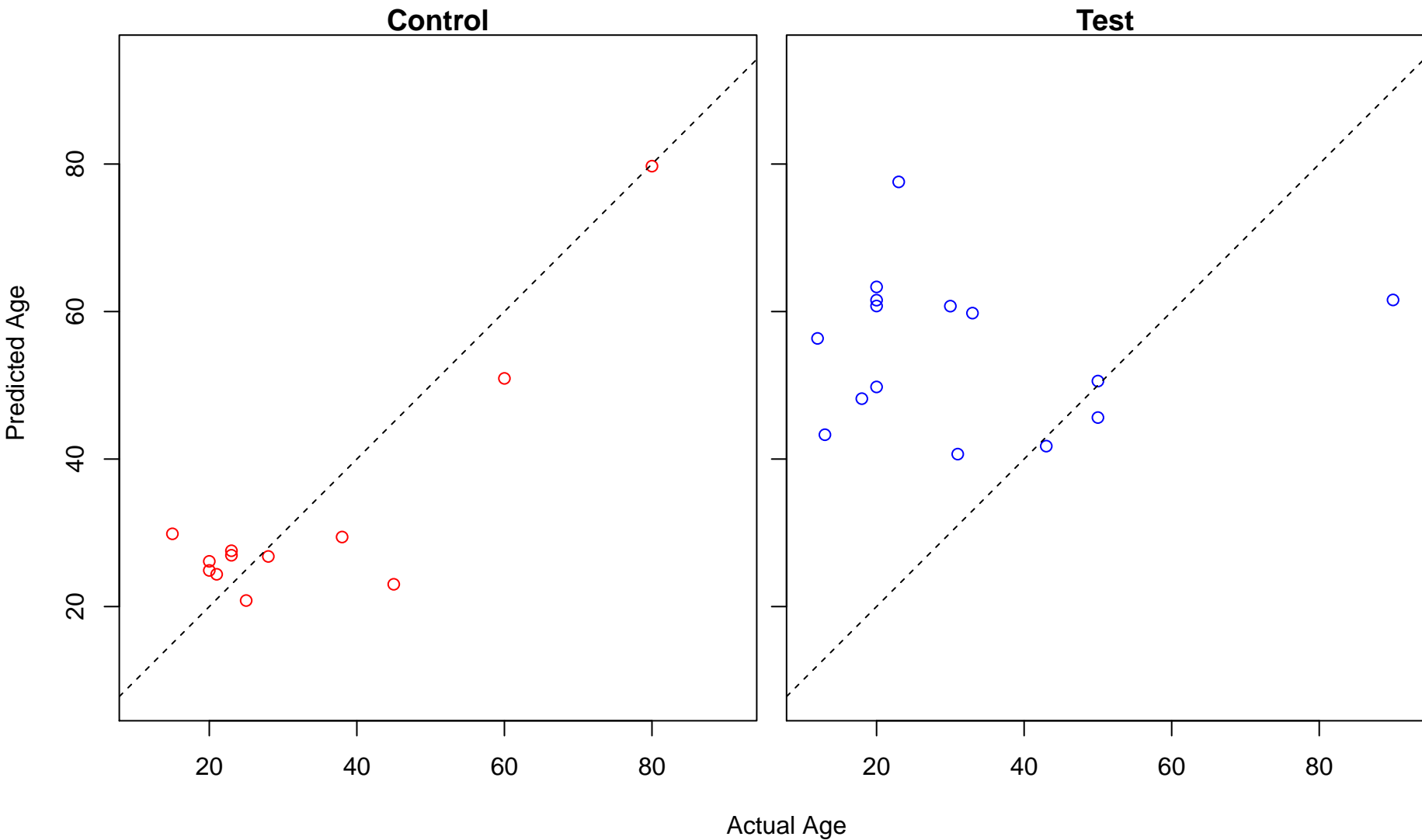
regulation of microtubule depolymerization (Score: 4.696633)



negative regulation of microtubule depolymerization (Score: 4.695622)

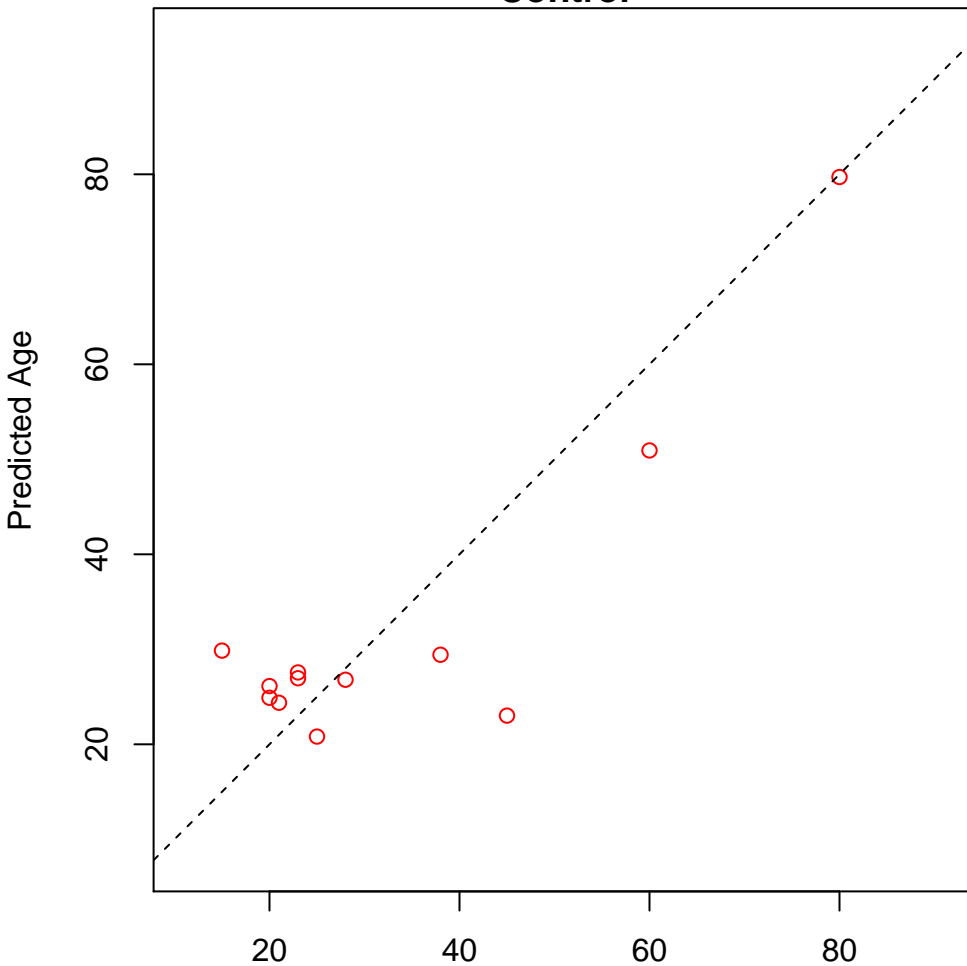


cholesterol biosynthetic process (Score: 4.692201)

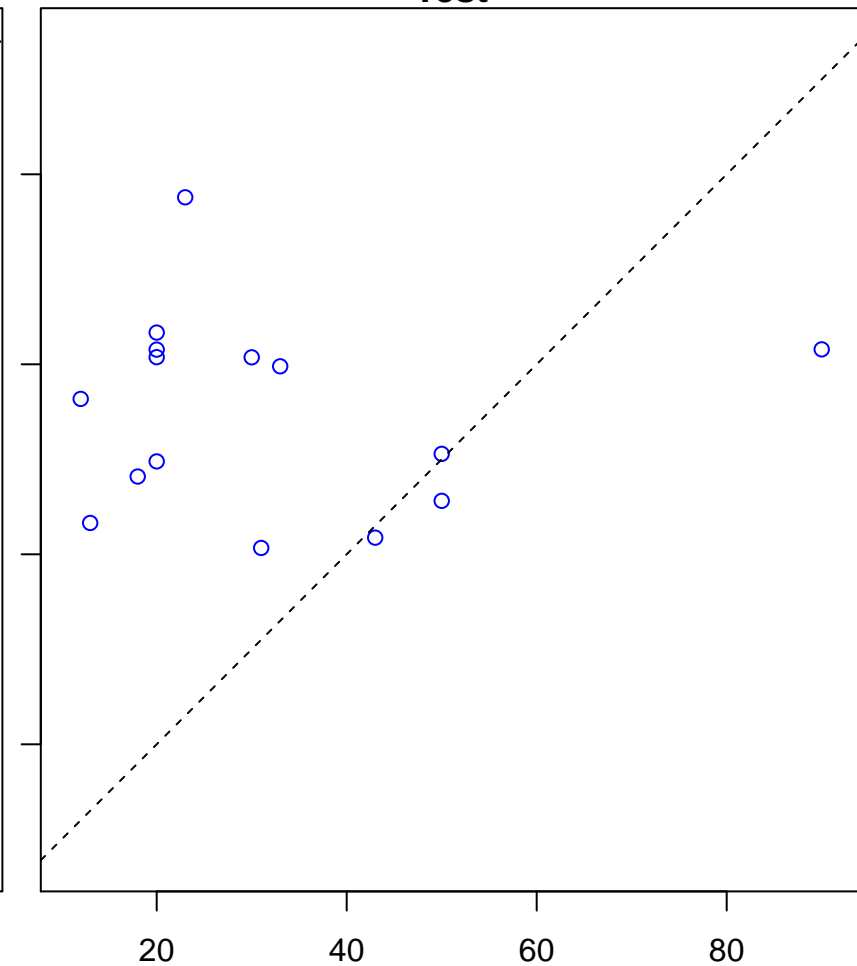


secondary alcohol biosynthetic process (Score: 4.692201)

Control

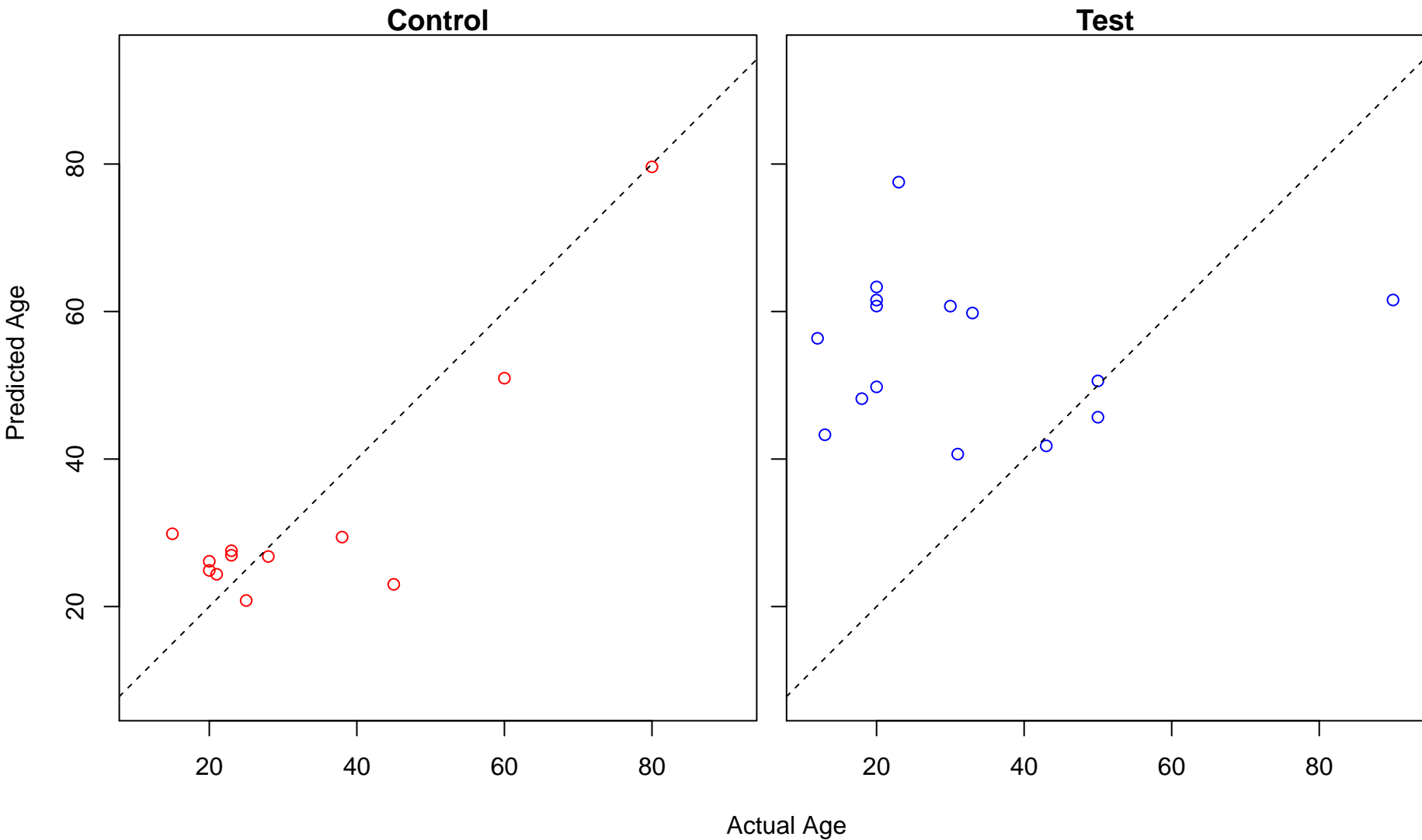


Test

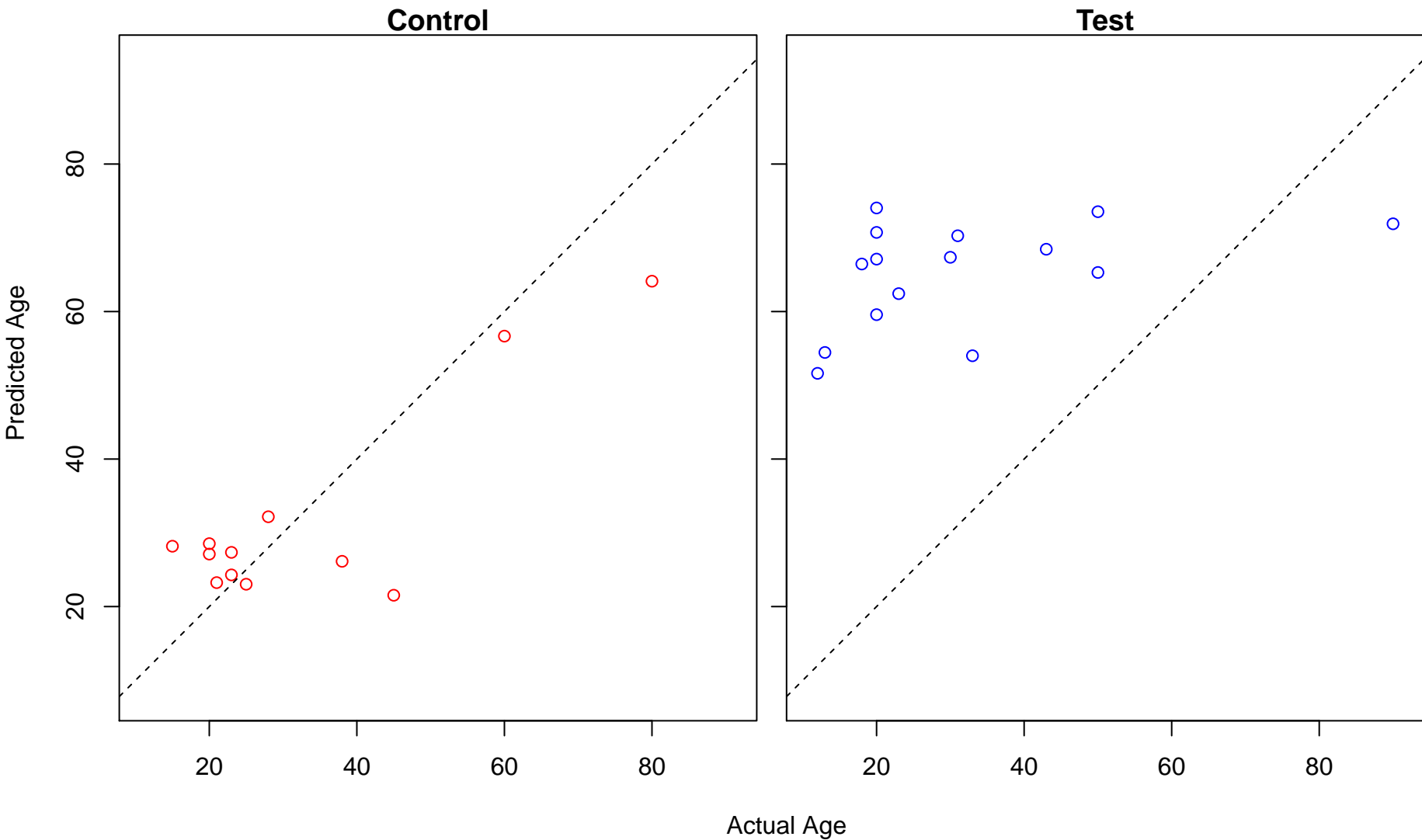


Actual Age

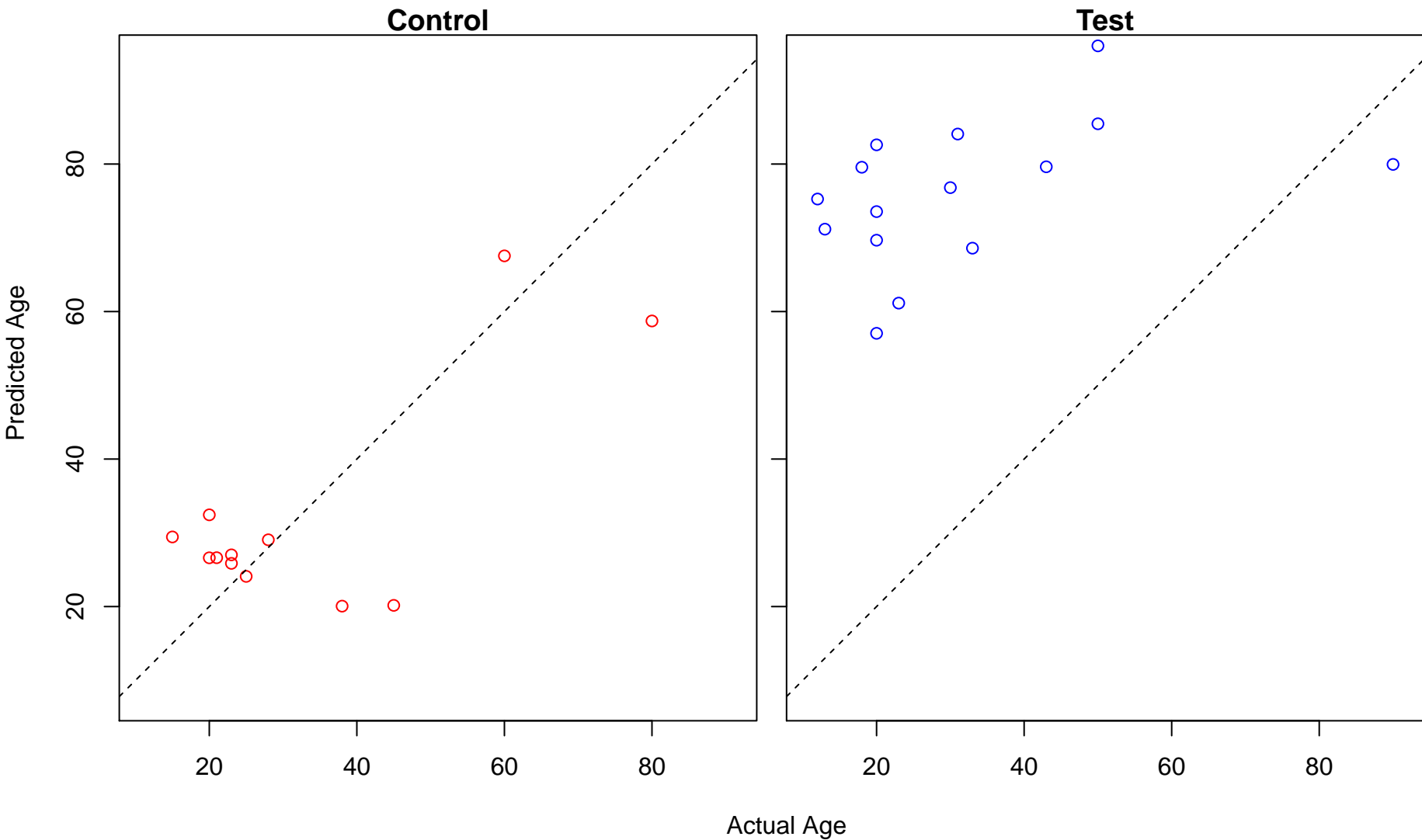
sterol biosynthetic process (Score: 4.69218)



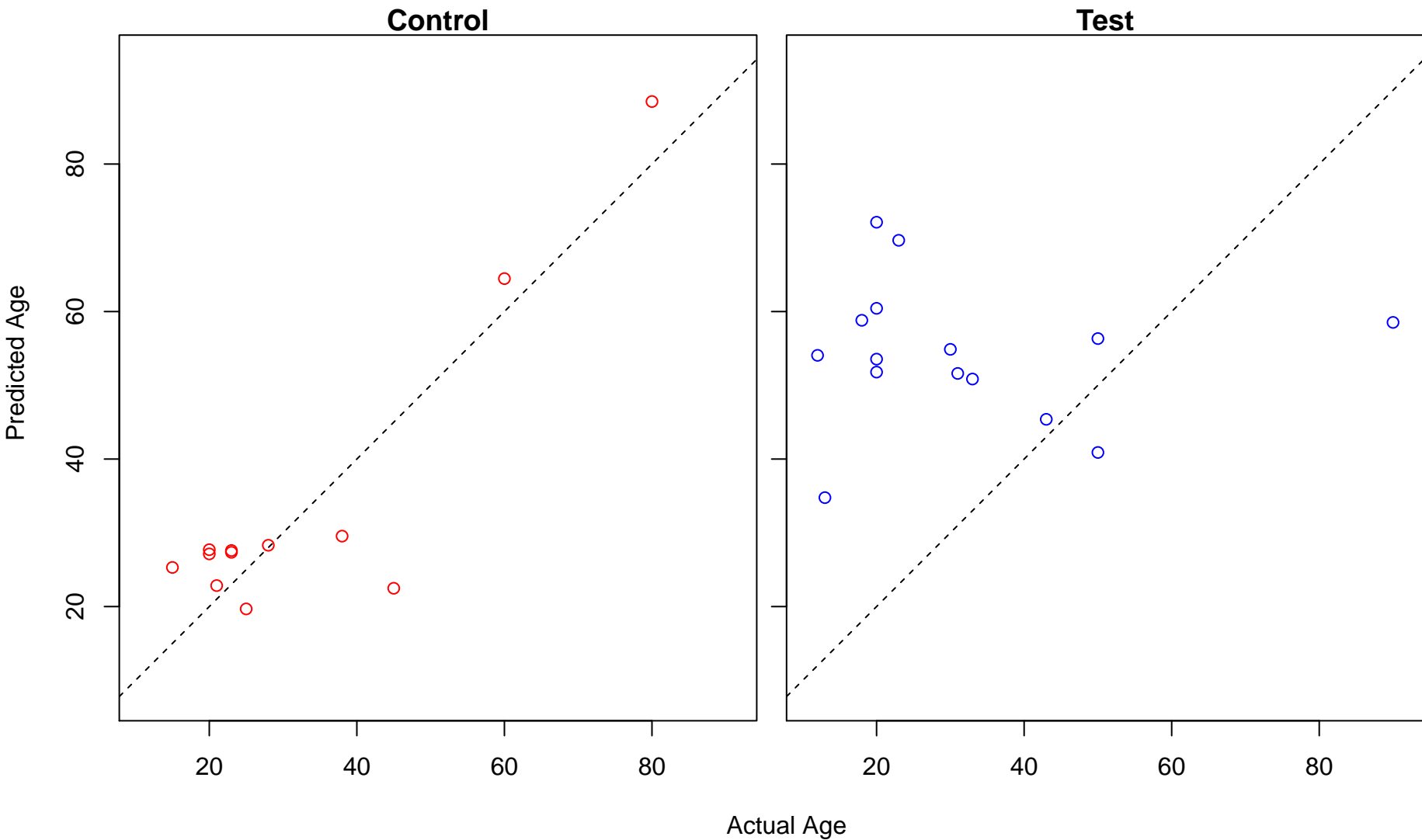
extracellular matrix disassembly (Score: 4.692039)



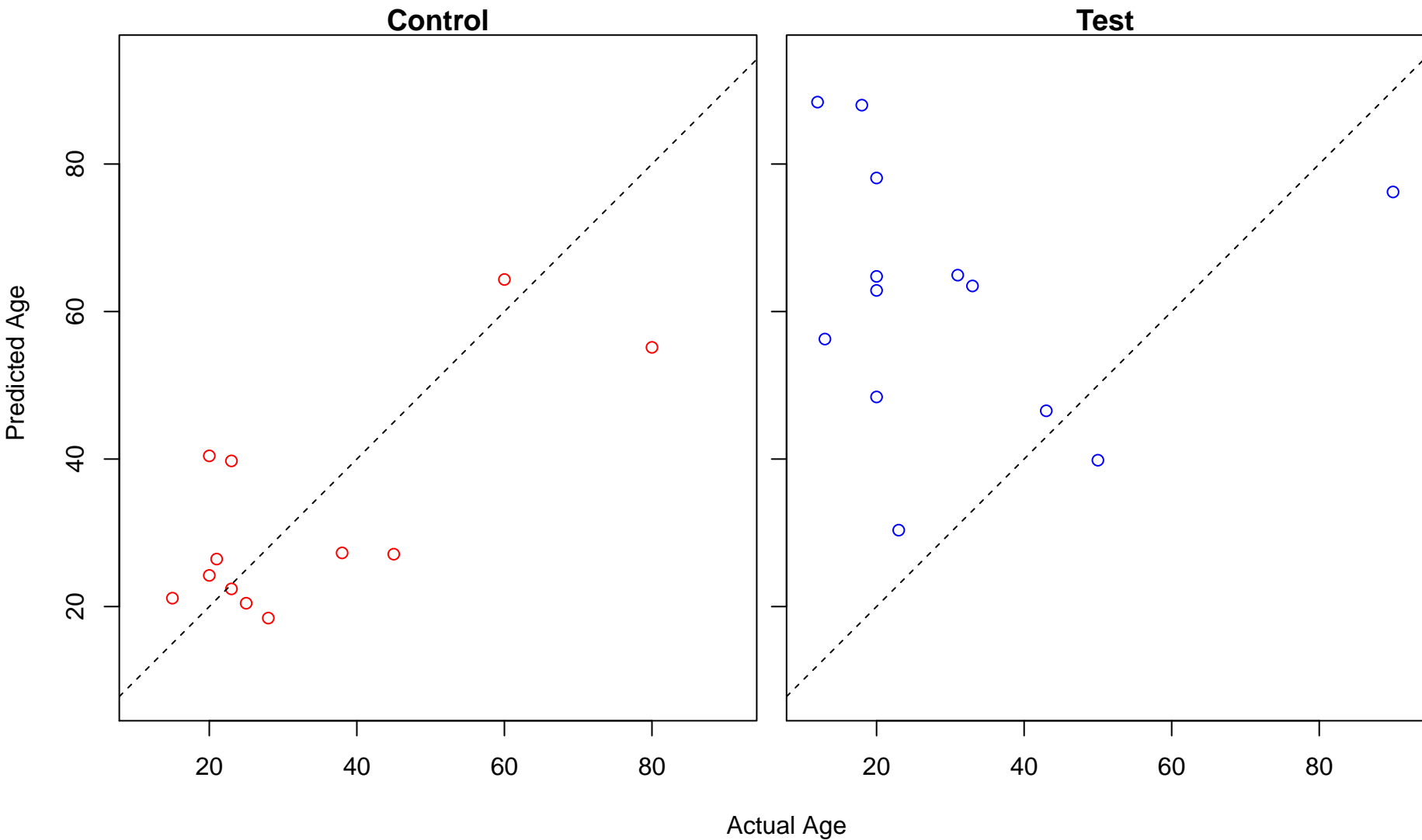
membrane repolarization (Score: 4.690930)



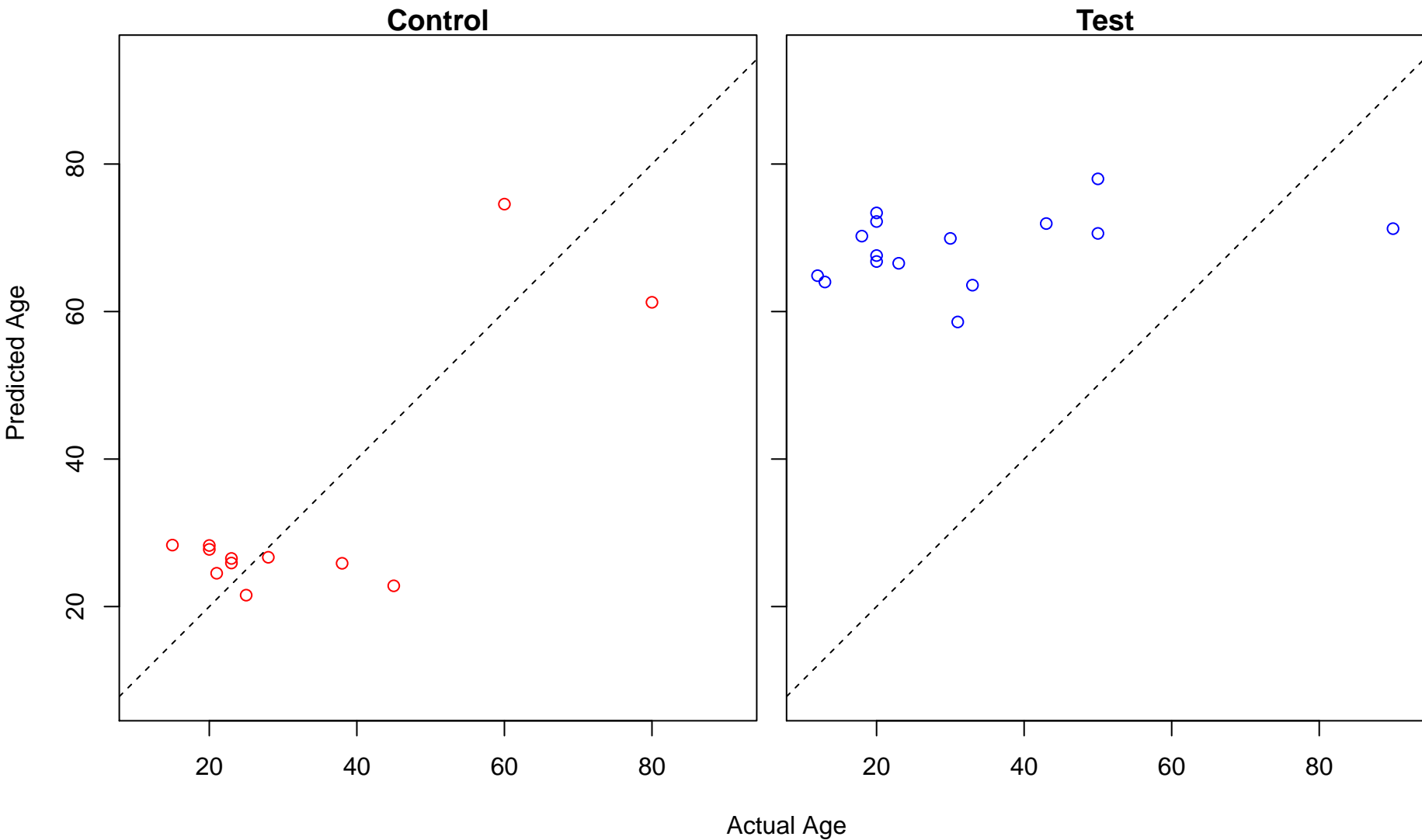
protein K48-linked ubiquitination (Score: 4.687469)



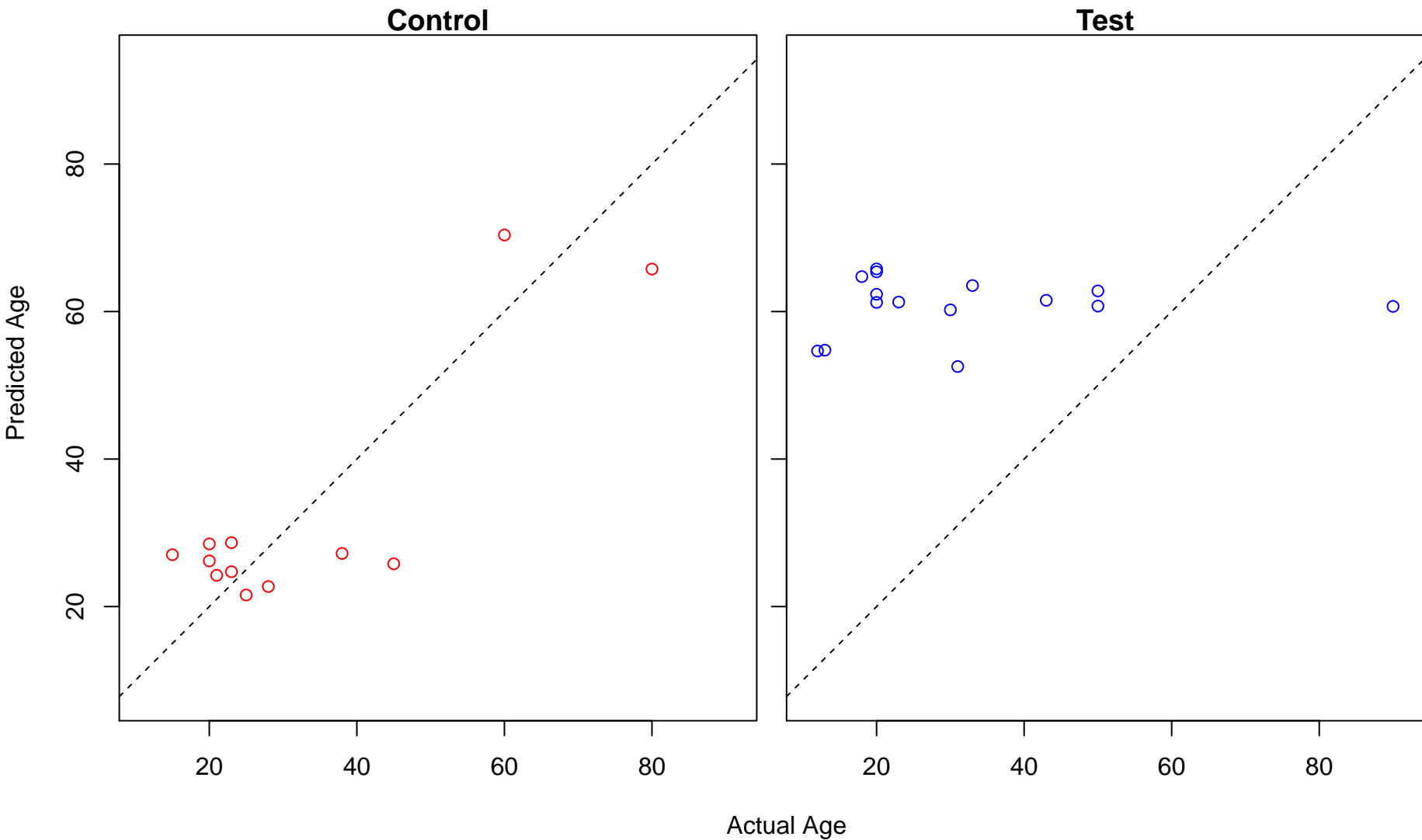
parturition (Score: 4.68662)



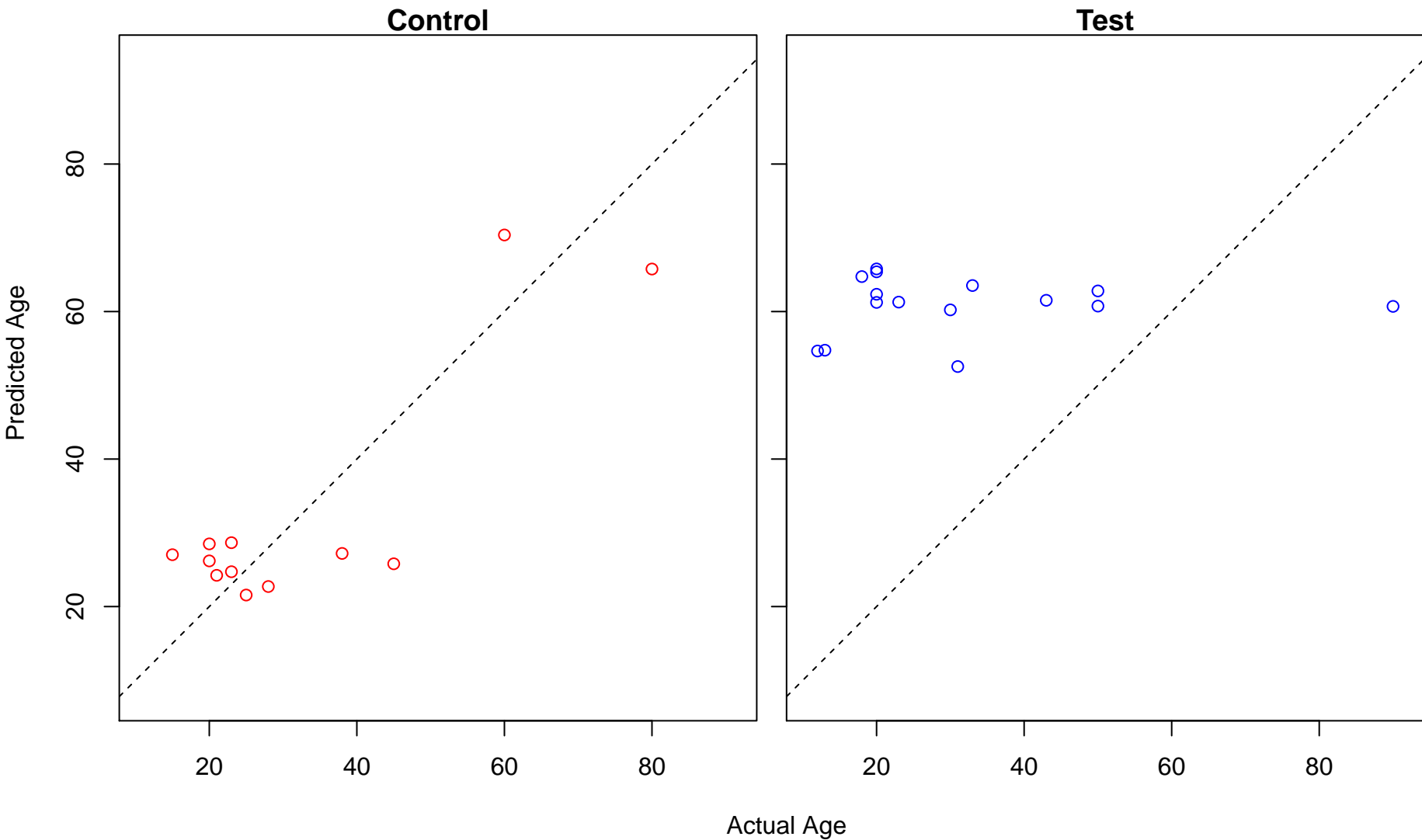
establishment of protein localization to plasma membrane (Score: 4.685640)



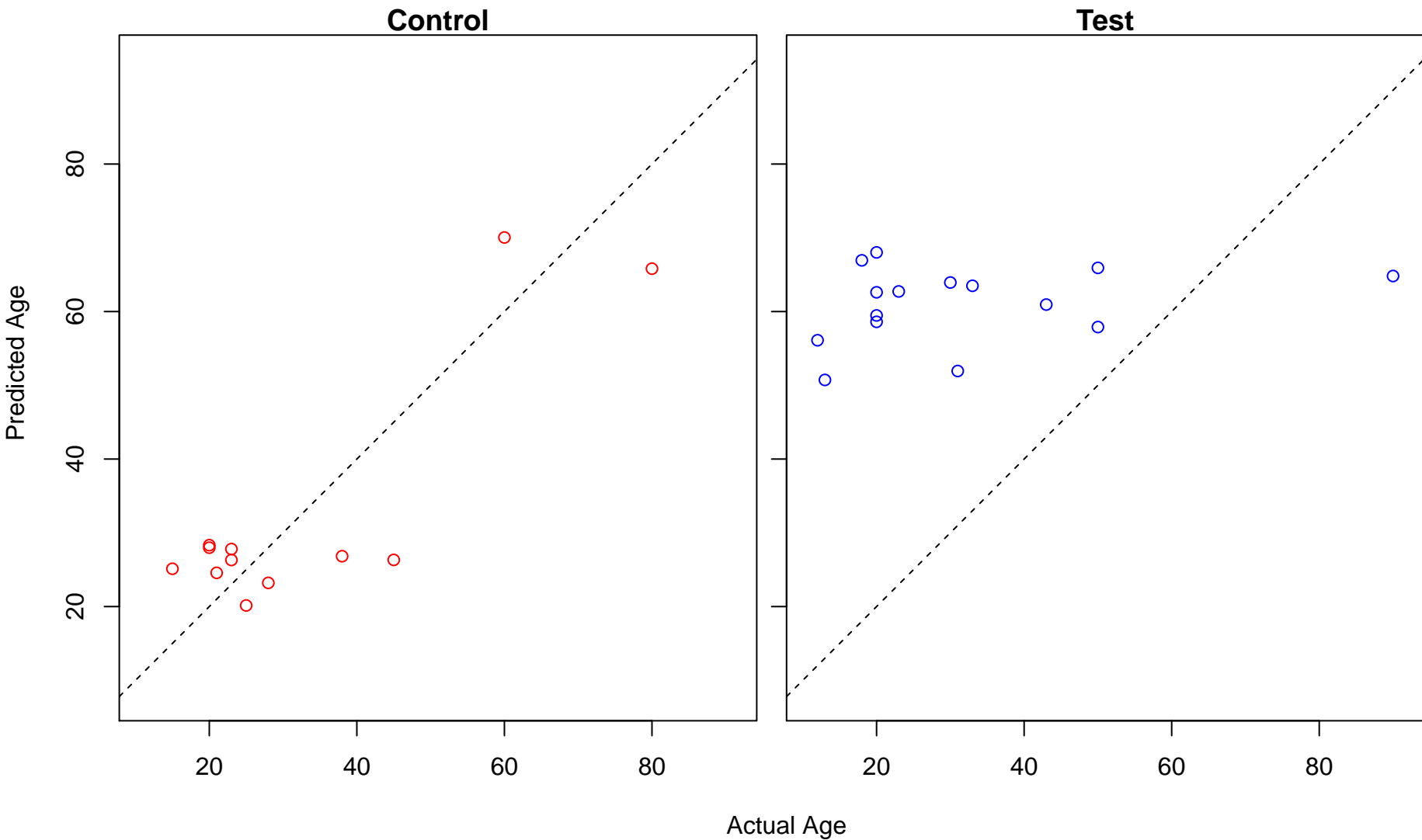
striated muscle hypertrophy (Score: 4.685171)



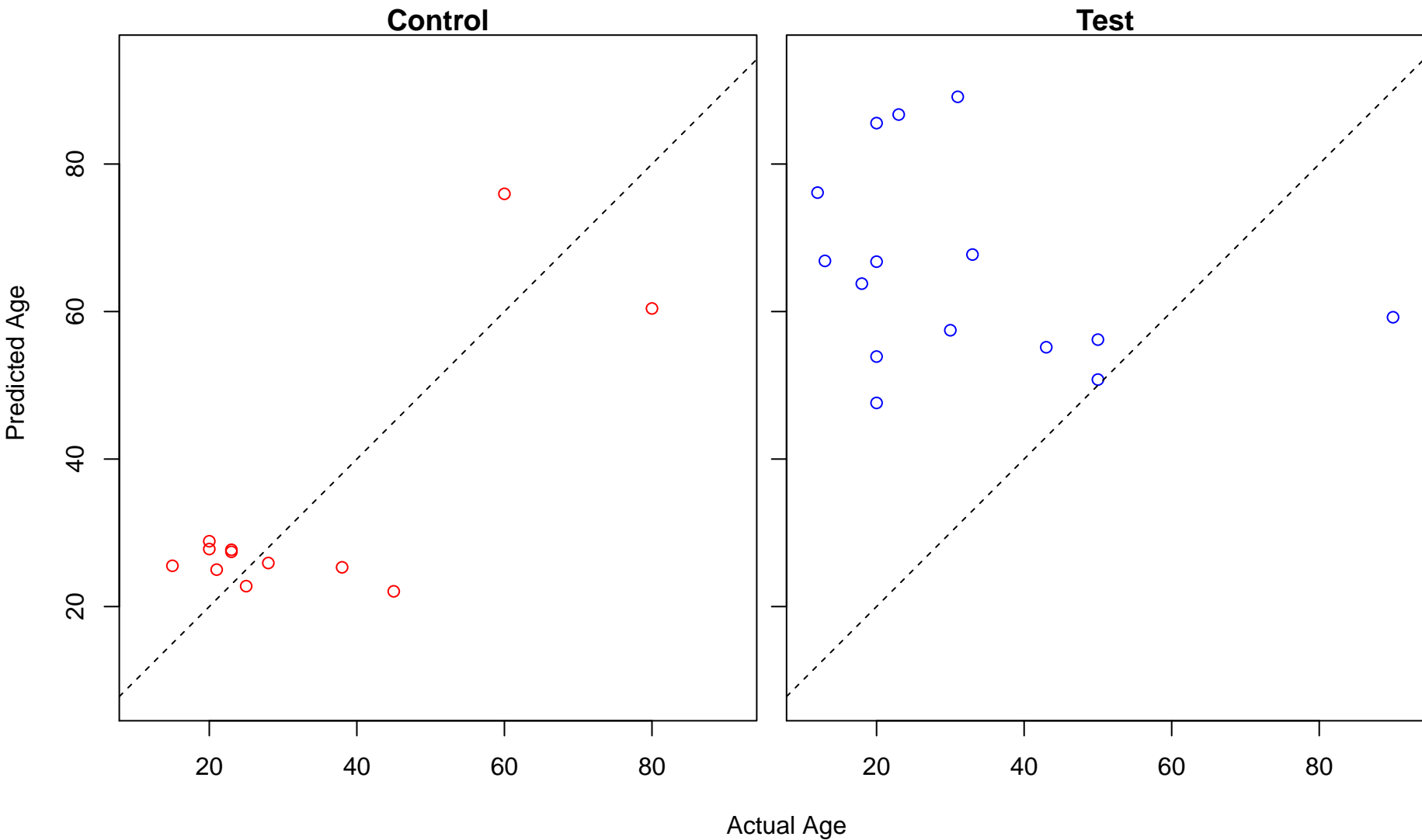
cardiac muscle hypertrophy (Score: 4.684869)



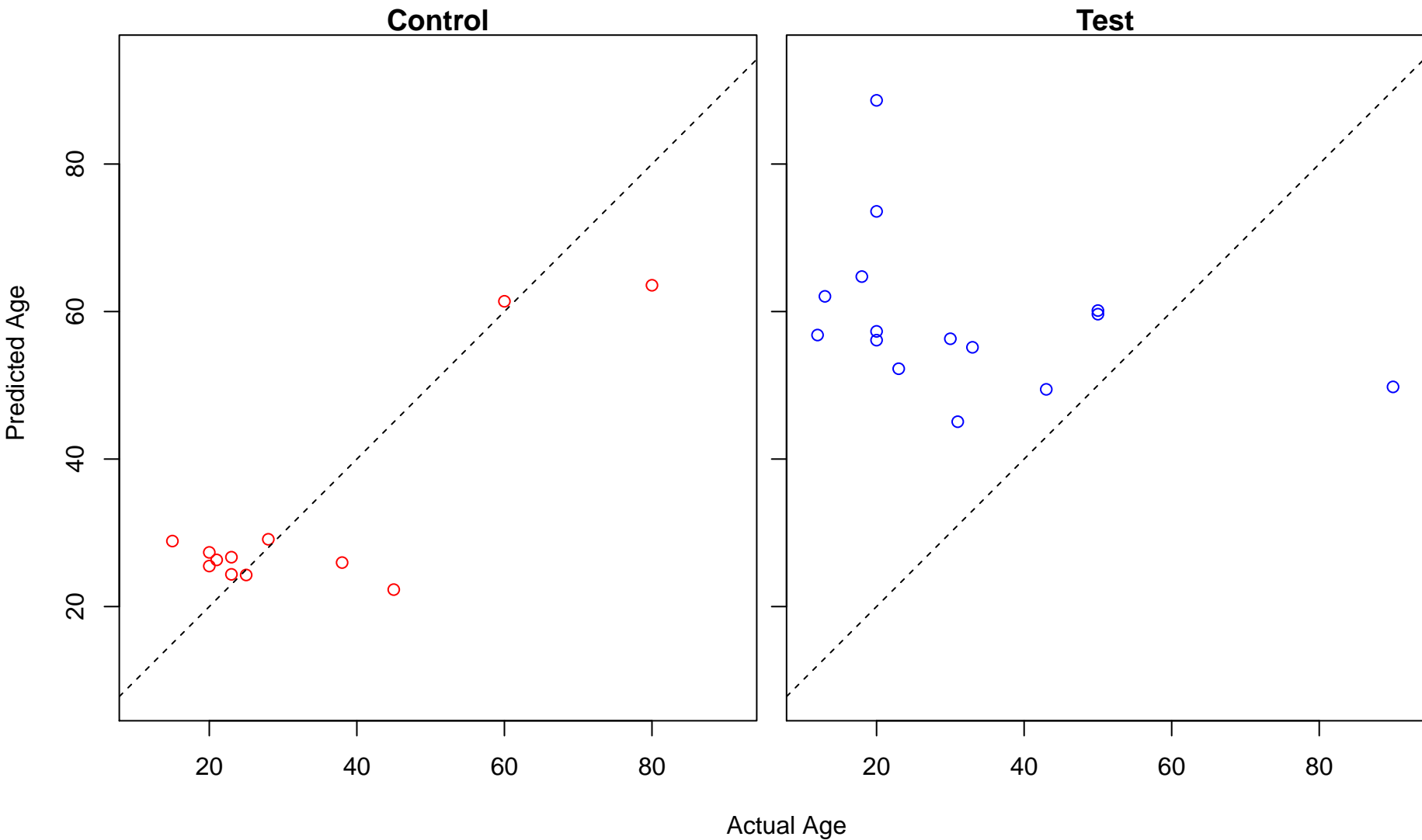
cardiac muscle cell differentiation (Score: 4.682667)



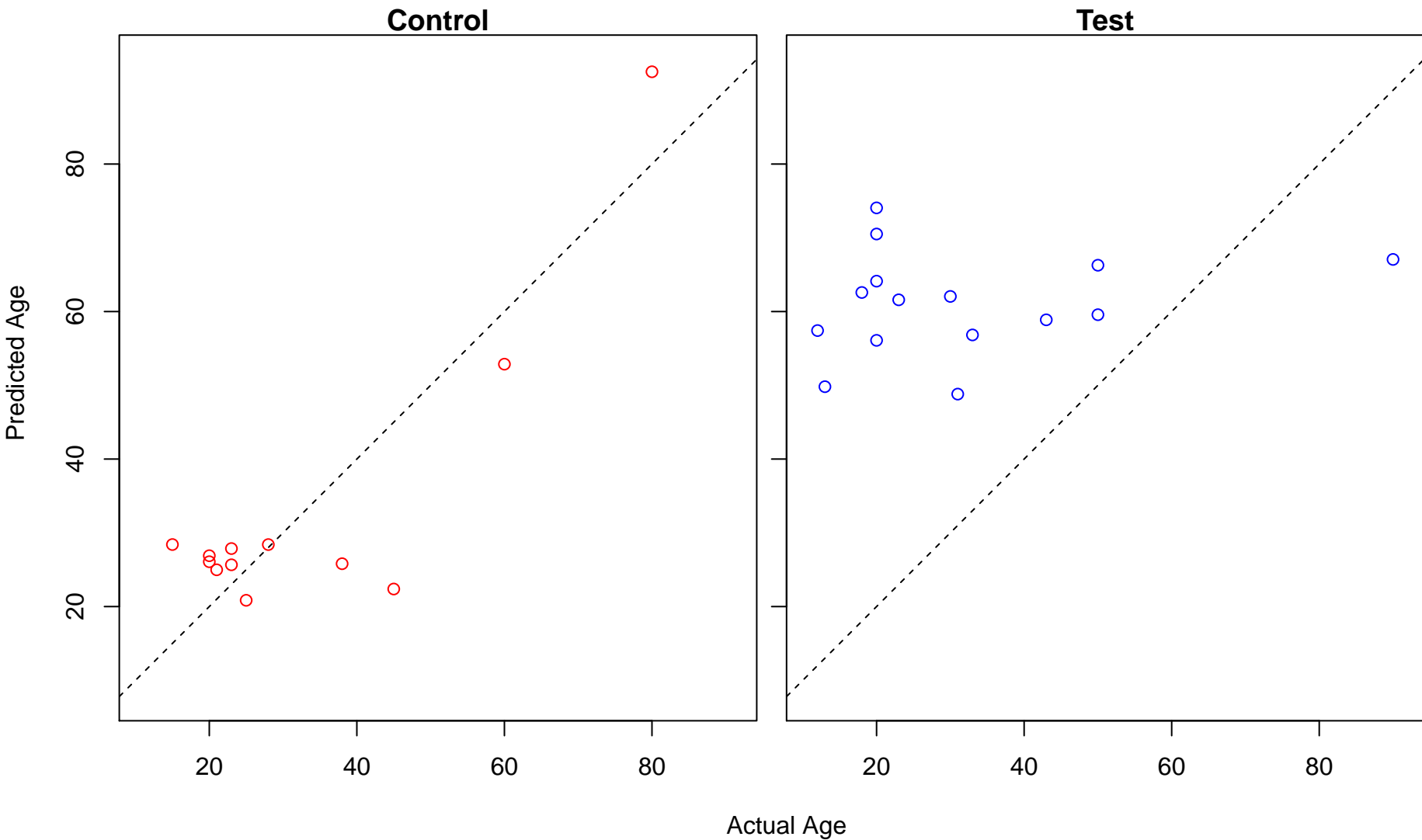
phospholipid scrambling (Score: 4.682378)



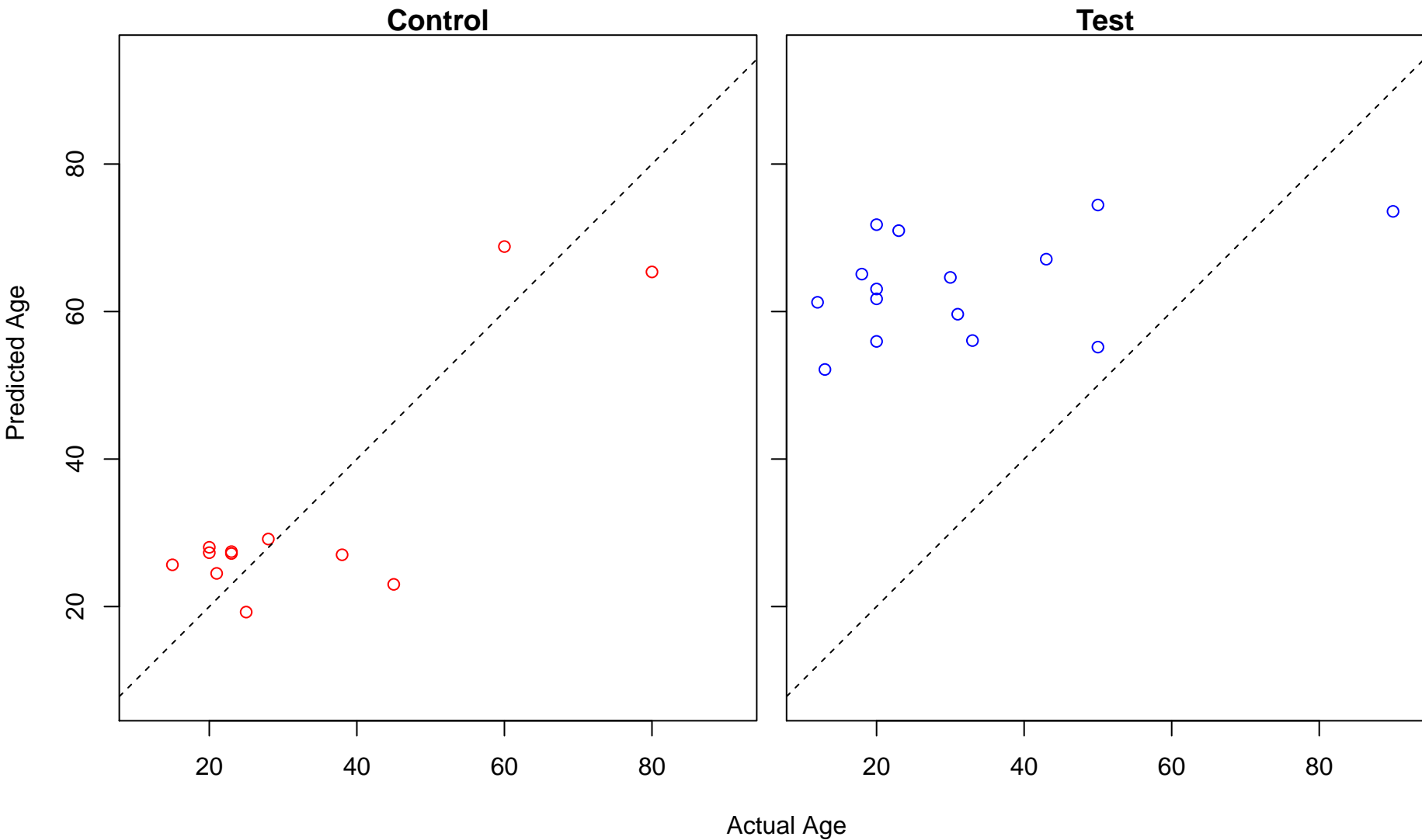
glial cell differentiation (Score: 4.682049)



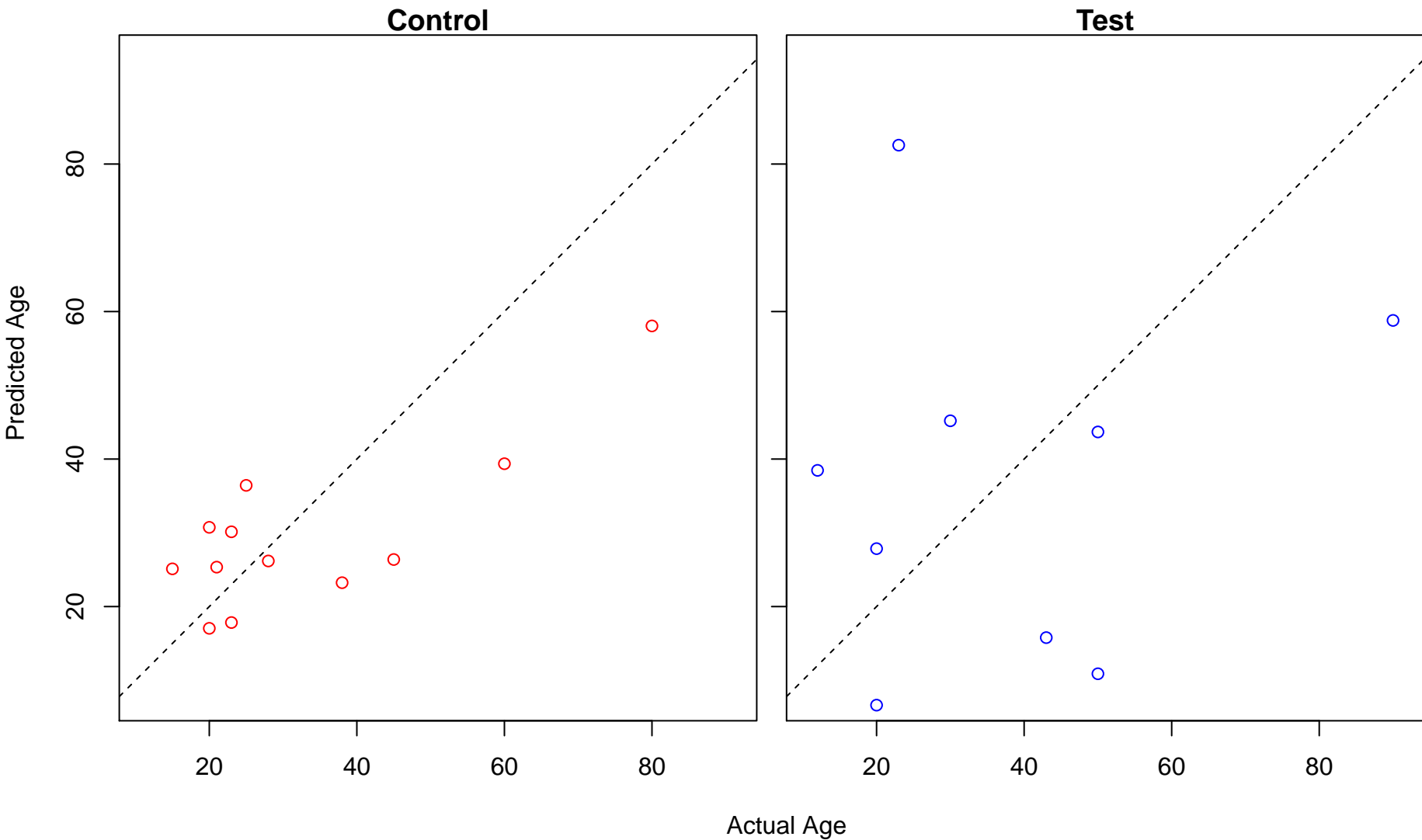
establishment of organelle localization (Score: 4.680947)



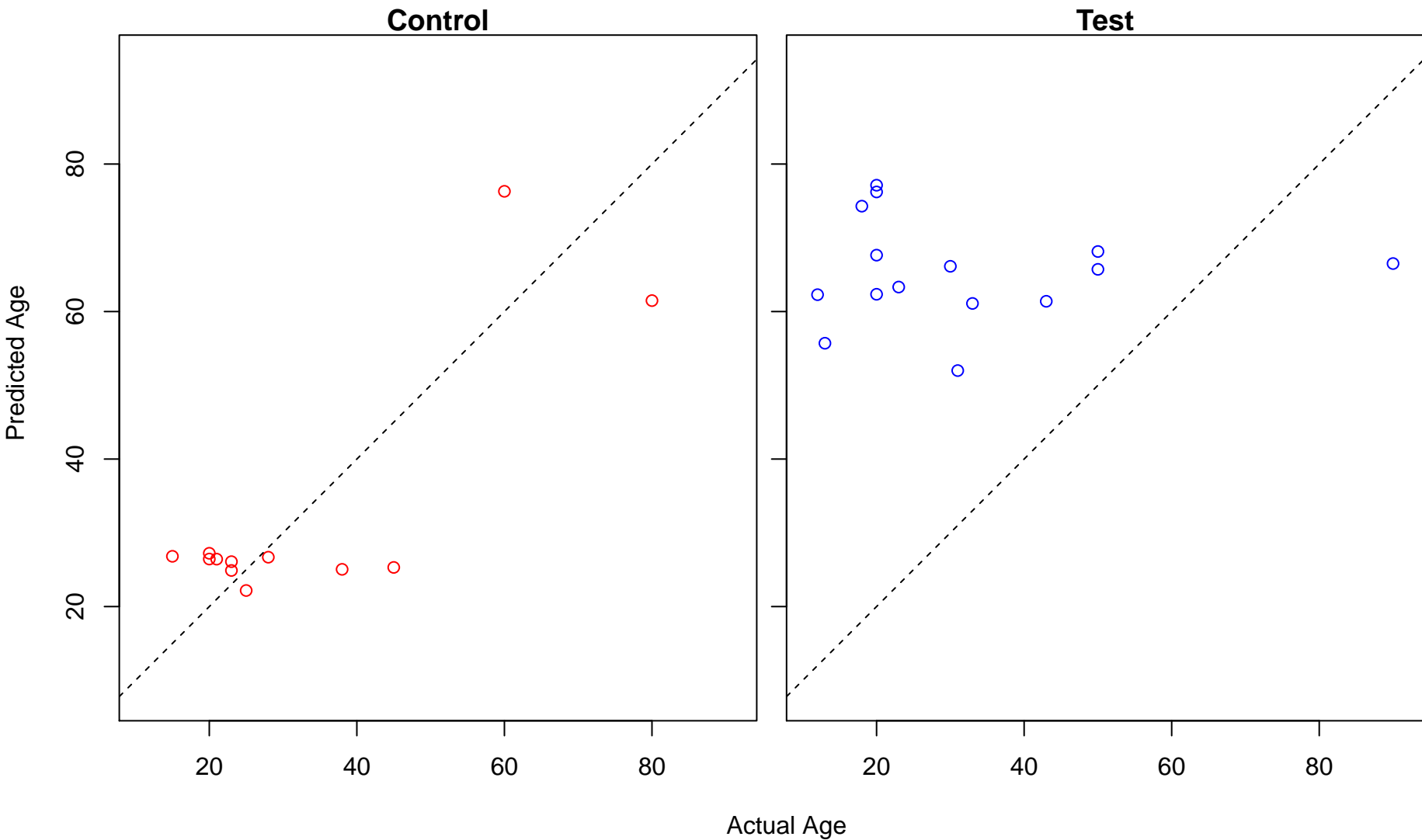
negative regulation of cytokine secretion (Score: 4.680810)



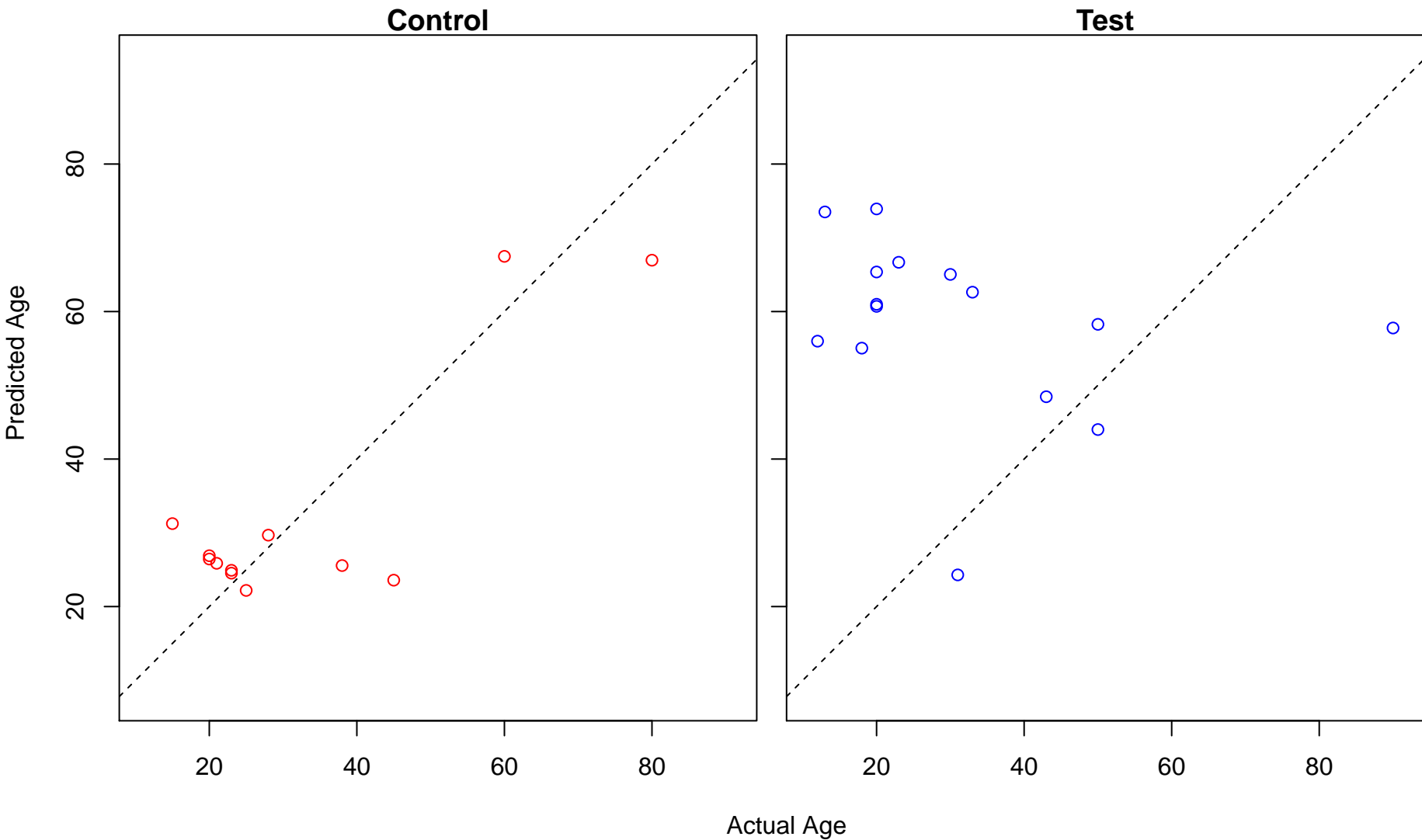
vitamin catabolic process (Score: 4.679023)



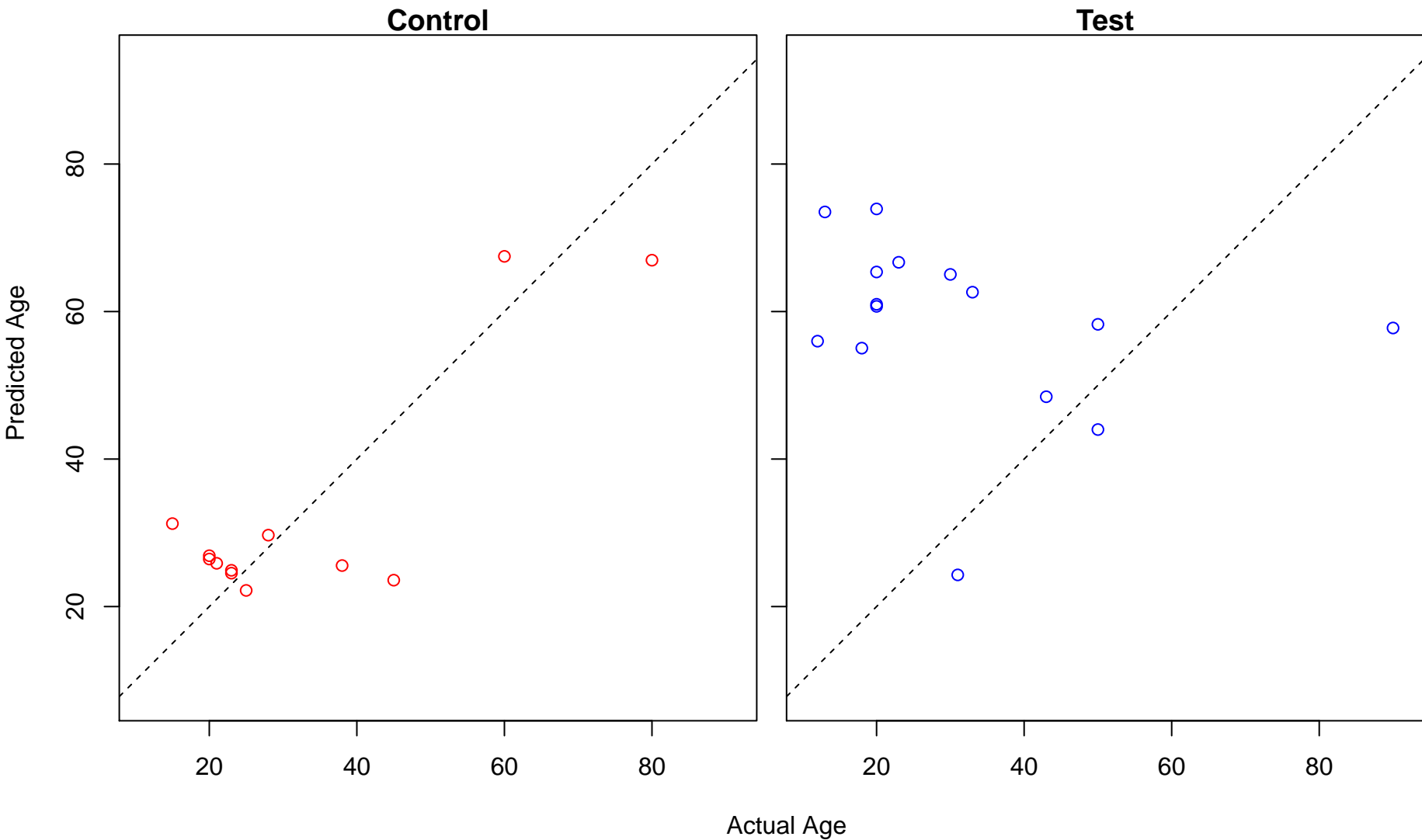
cell separation after cytokinesis (Score: 4.678037)



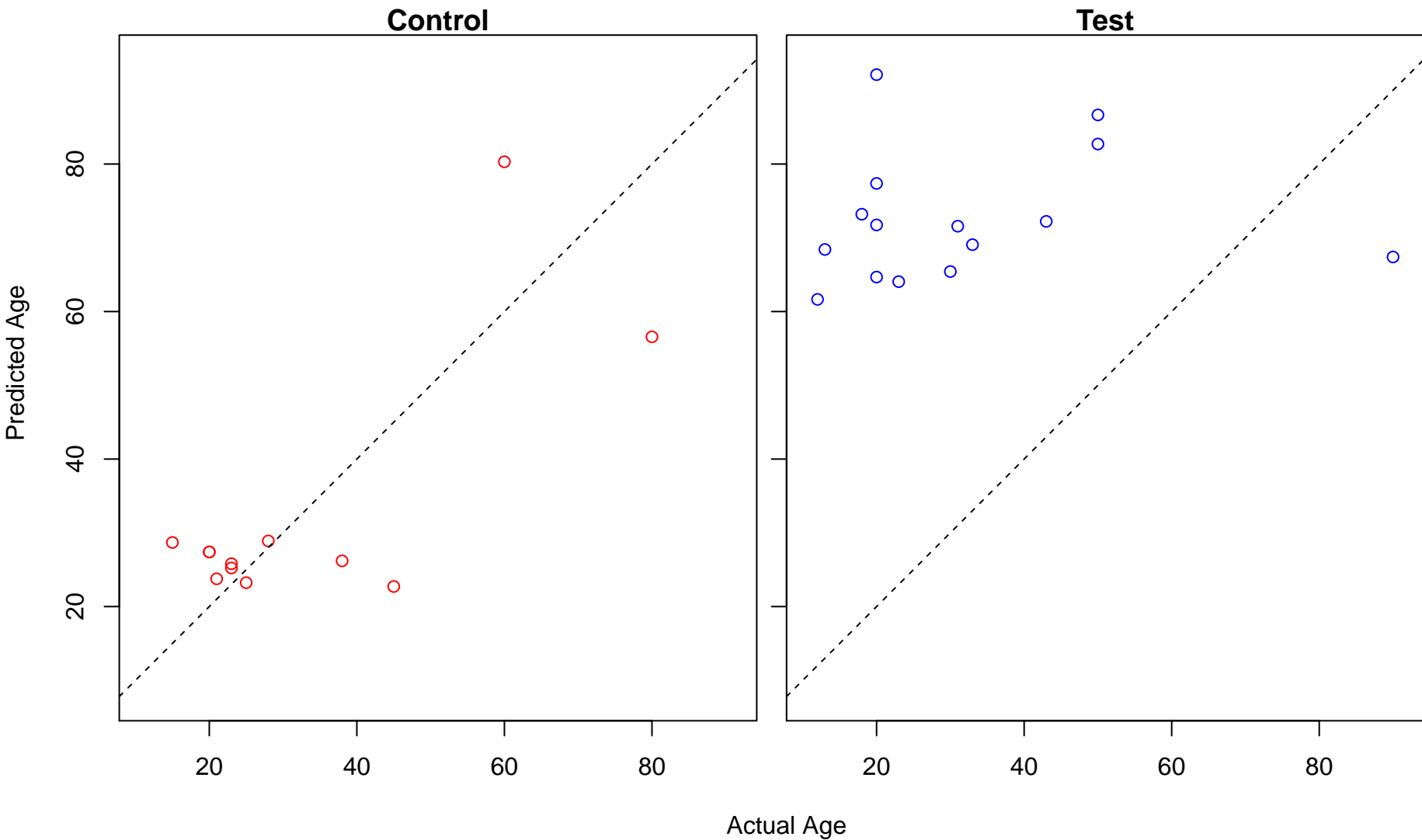
melanosome organization (Score: 4.677447)



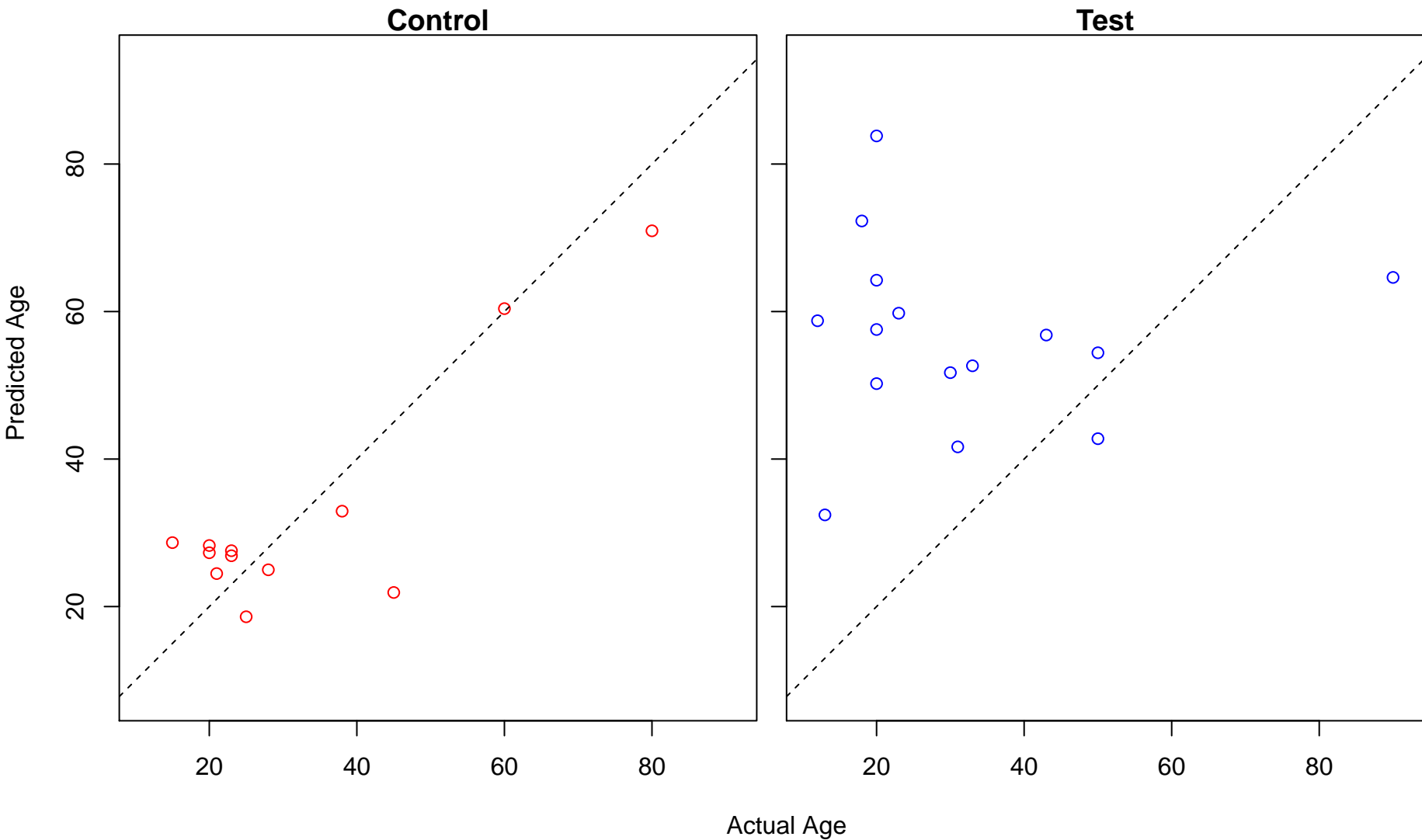
pigment granule organization (Score: 4.677447)



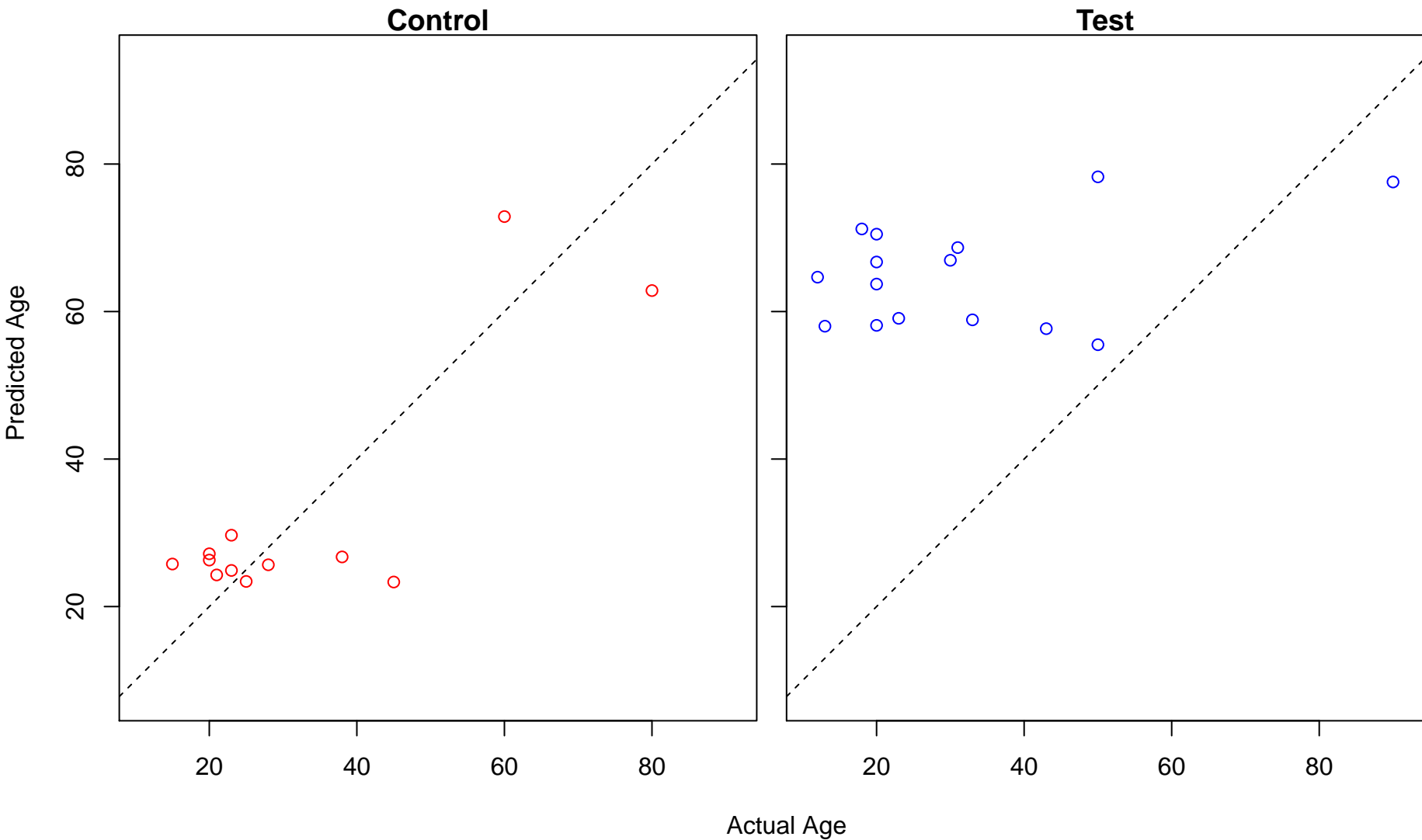
protein stabilization (Score: 4.676974)



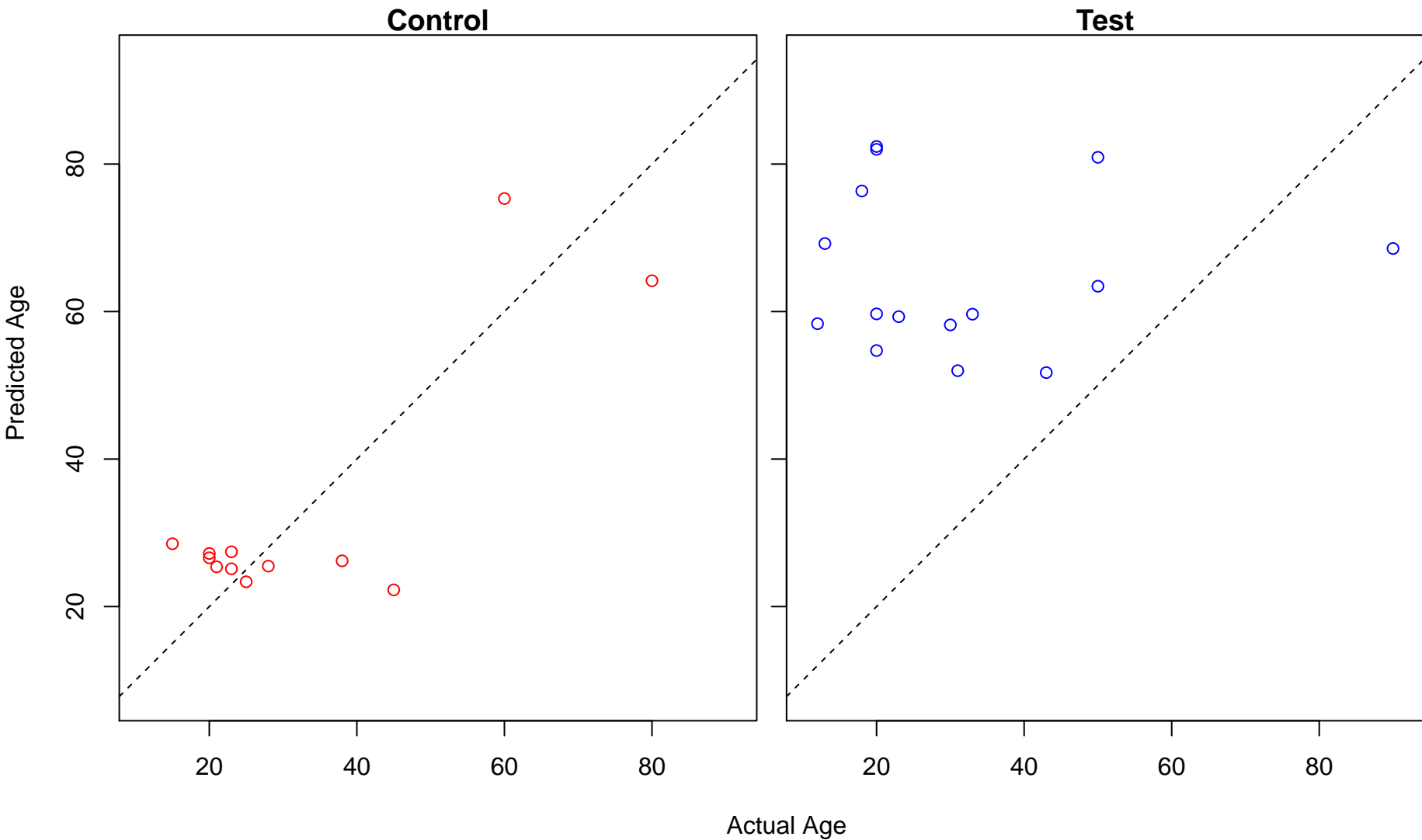
negative regulation of lymphocyte migration (Score: 4.676204)



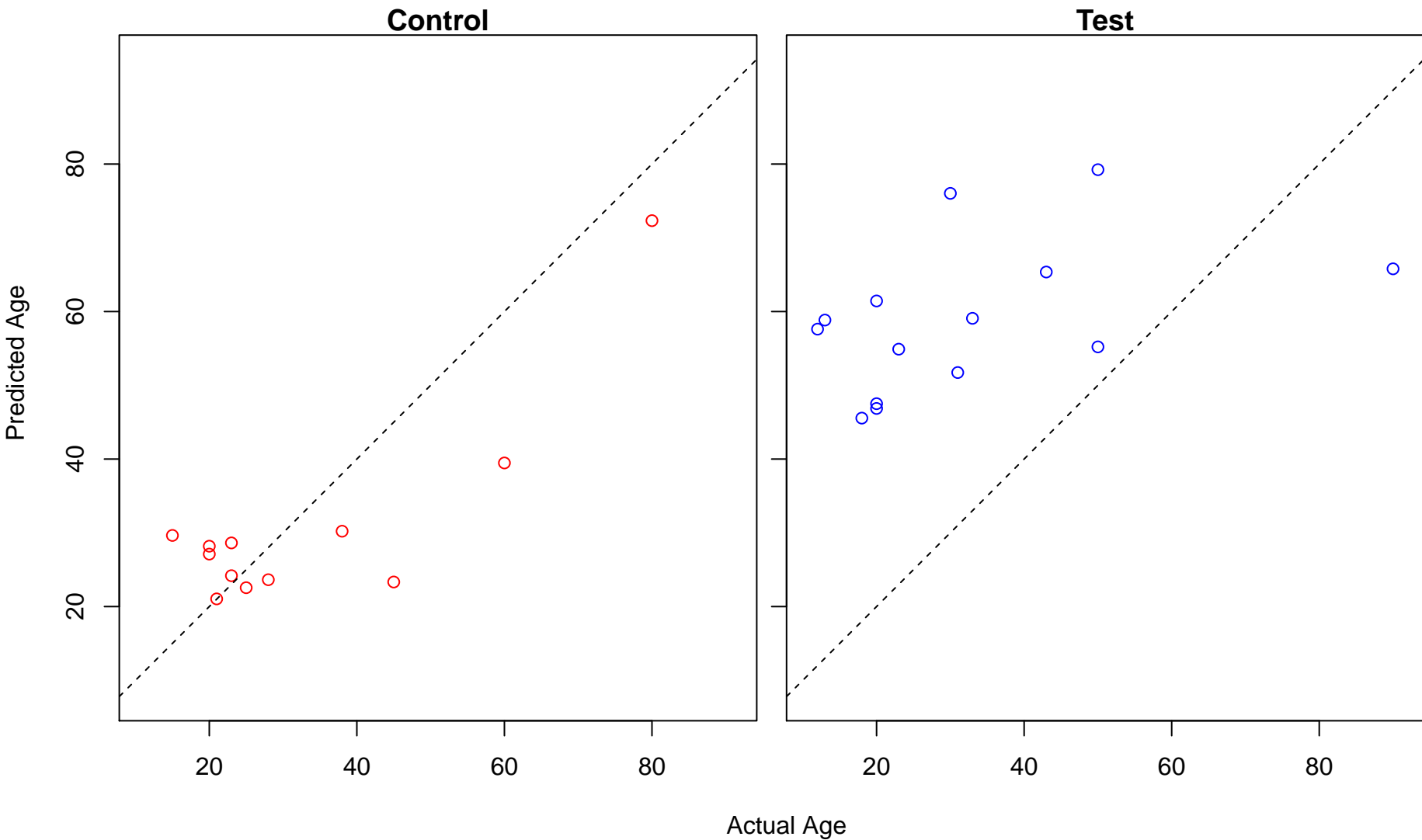
regulation of chromosome segregation (Score: 4.674470)



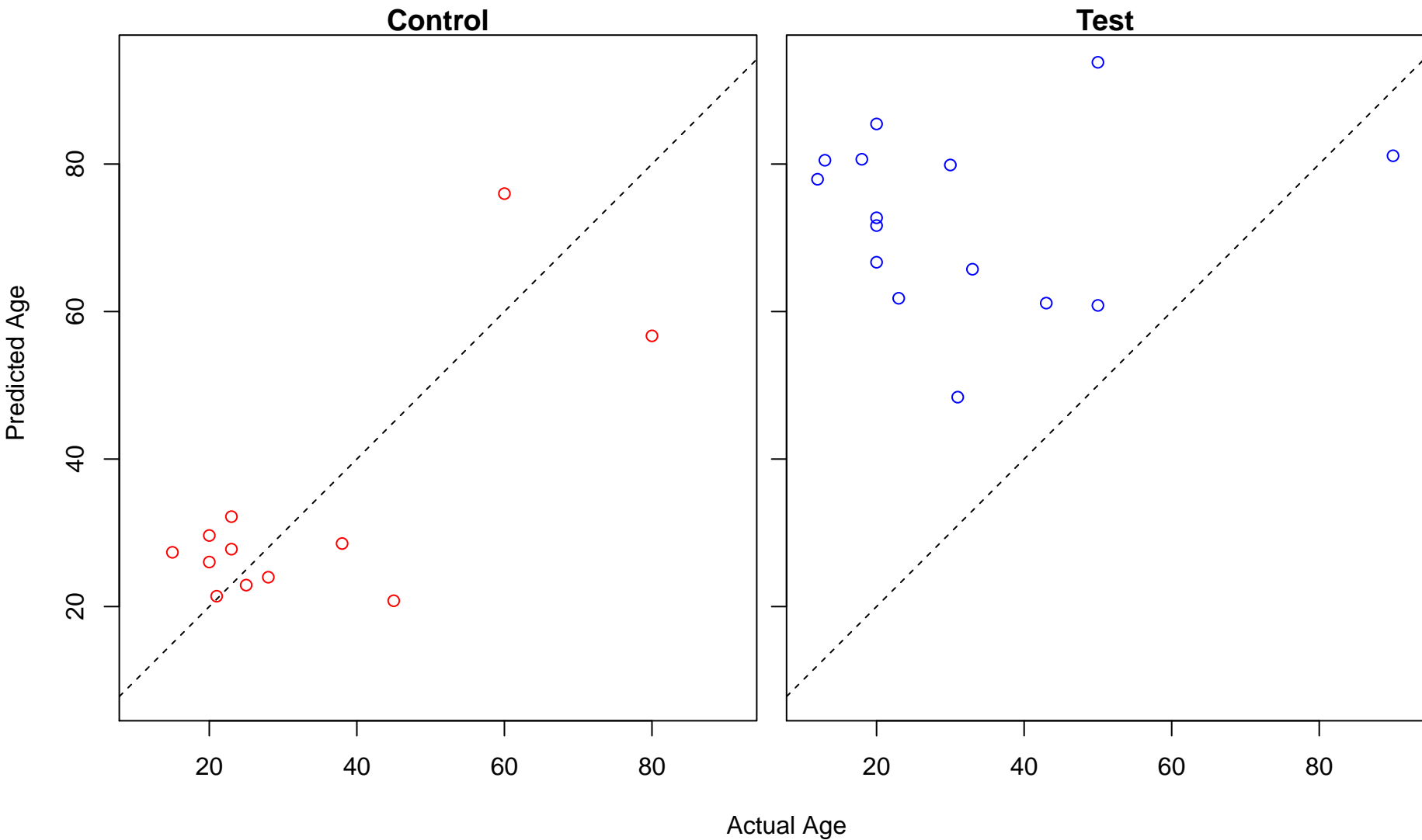
positive regulation of protein catabolic process (Score: 4.670760)



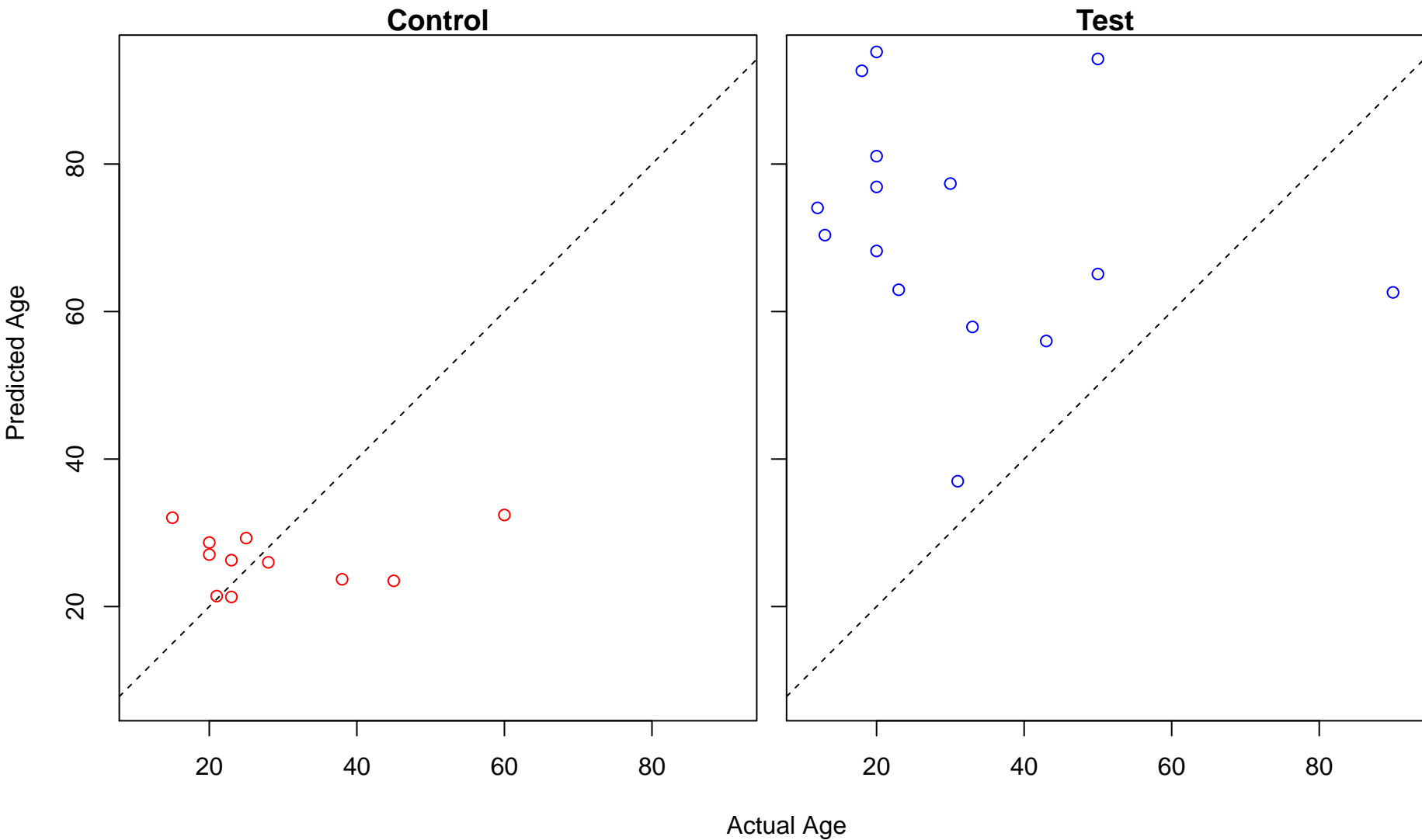
citrulline biosynthetic process (Score: 4.669491)



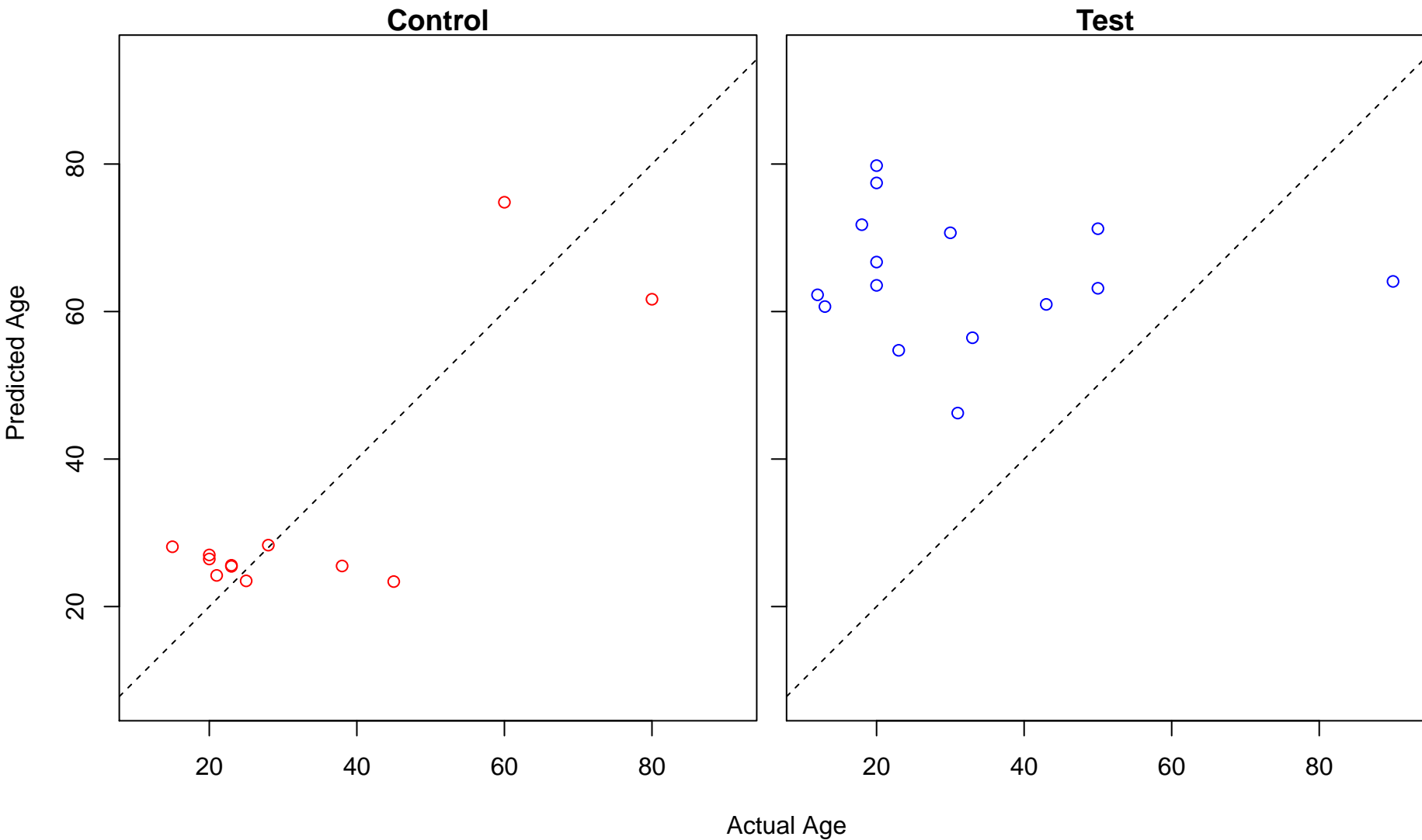
cardiac septum development (Score: 4.667345)



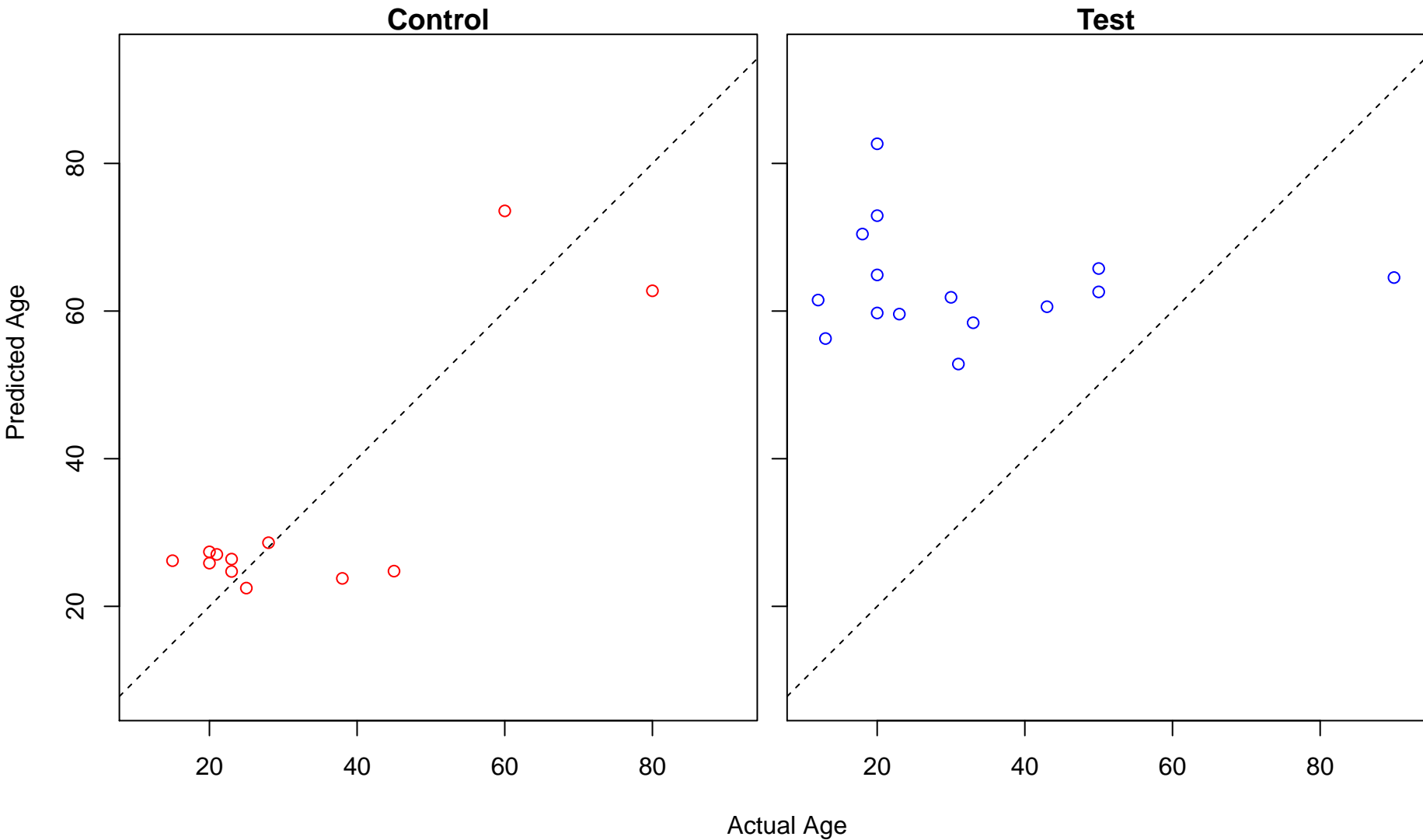
regulation of transcription regulatory region DNA binding (Score: 4.665636)



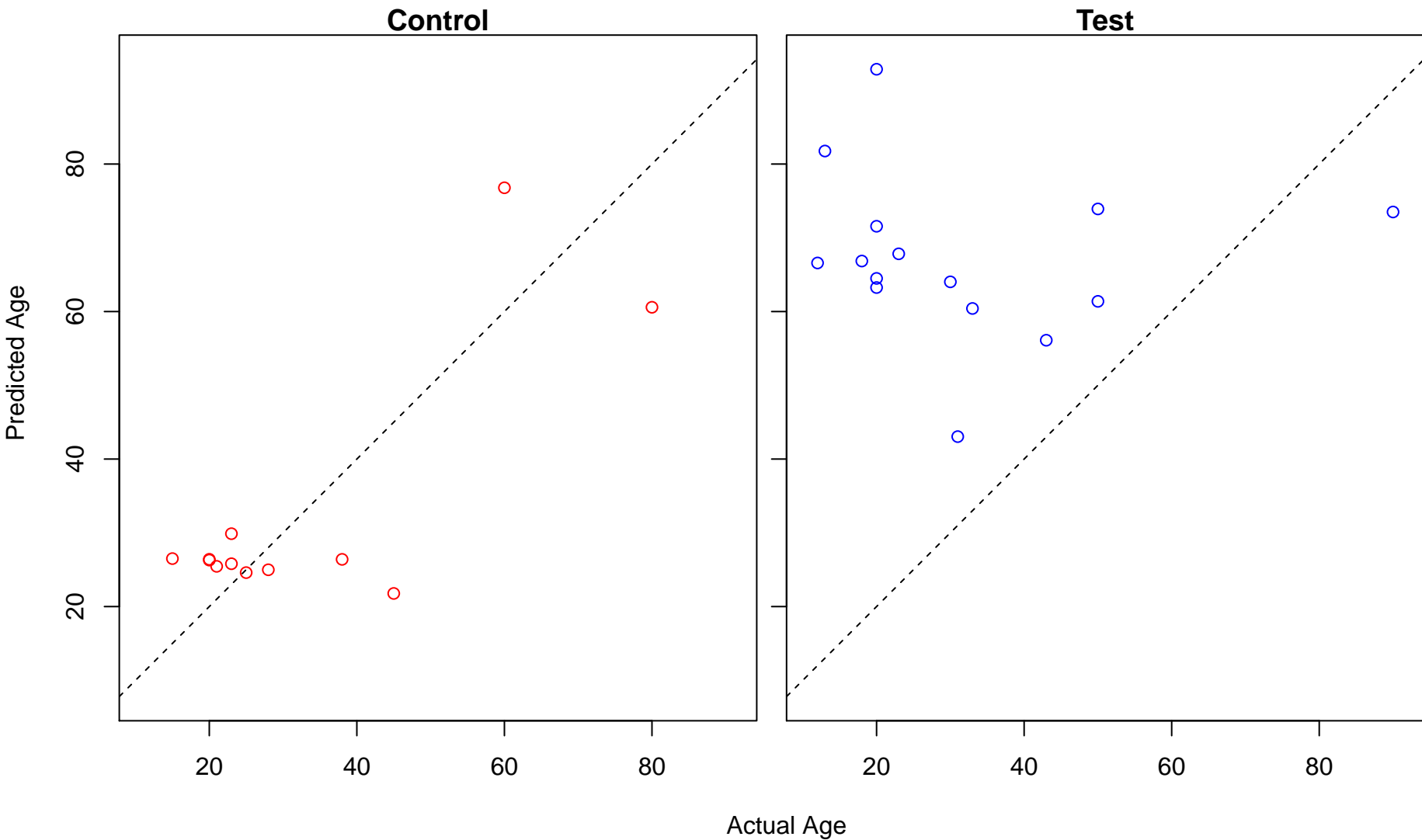
tricarboxylic acid cycle (Score: 4.663223)



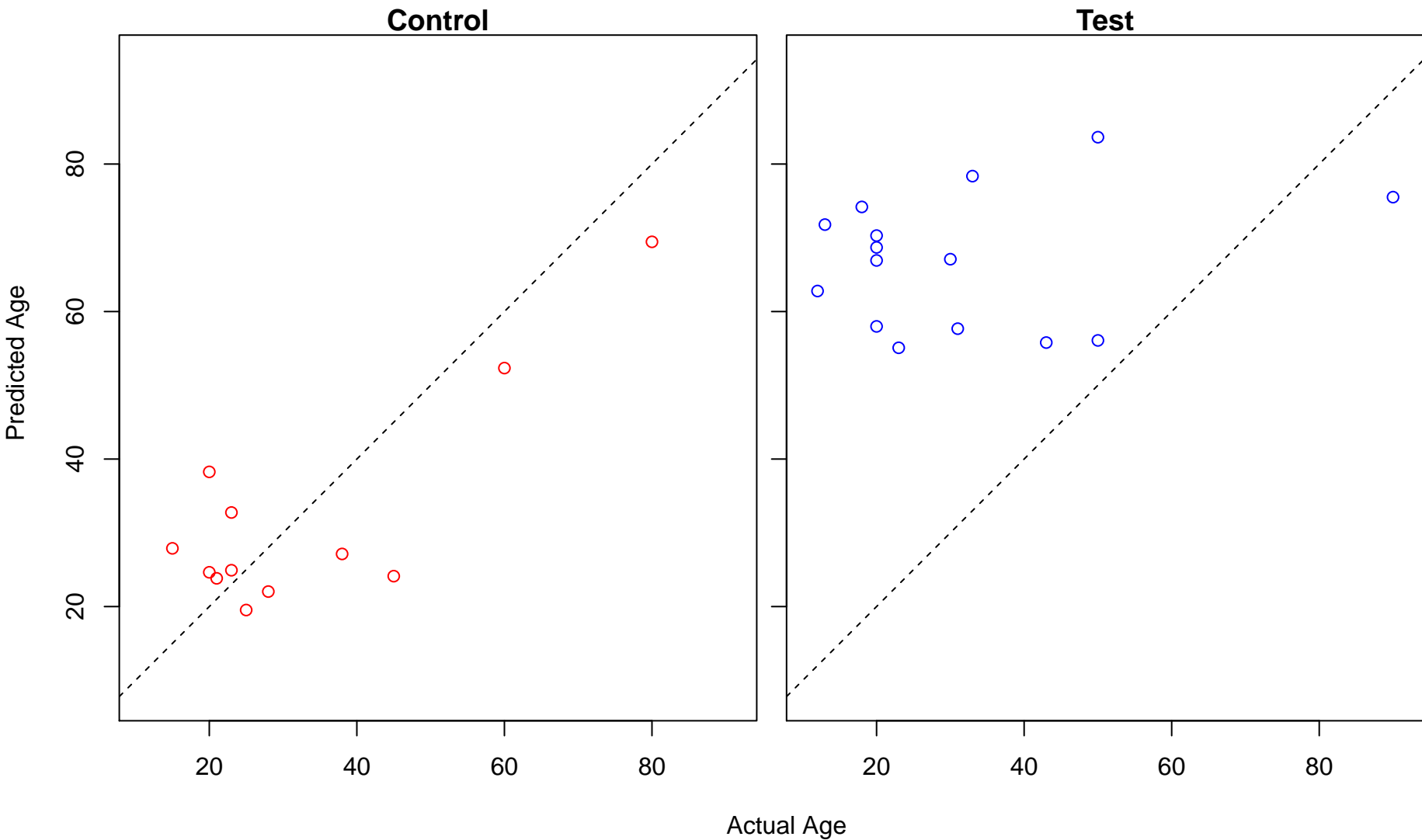
mitochondrial translational initiation (Score: 4.663005)



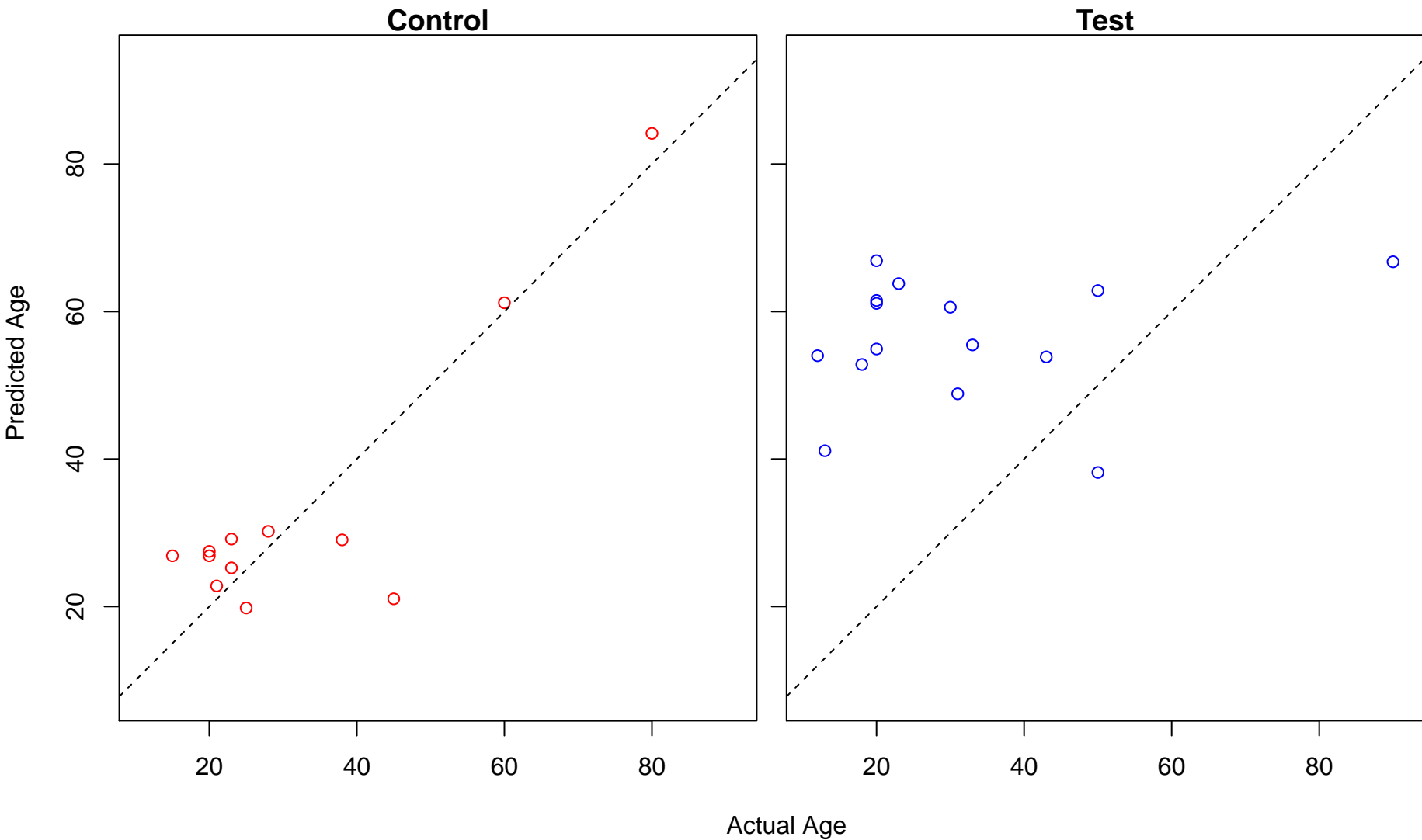
TOR signaling (Score: 4.662662)



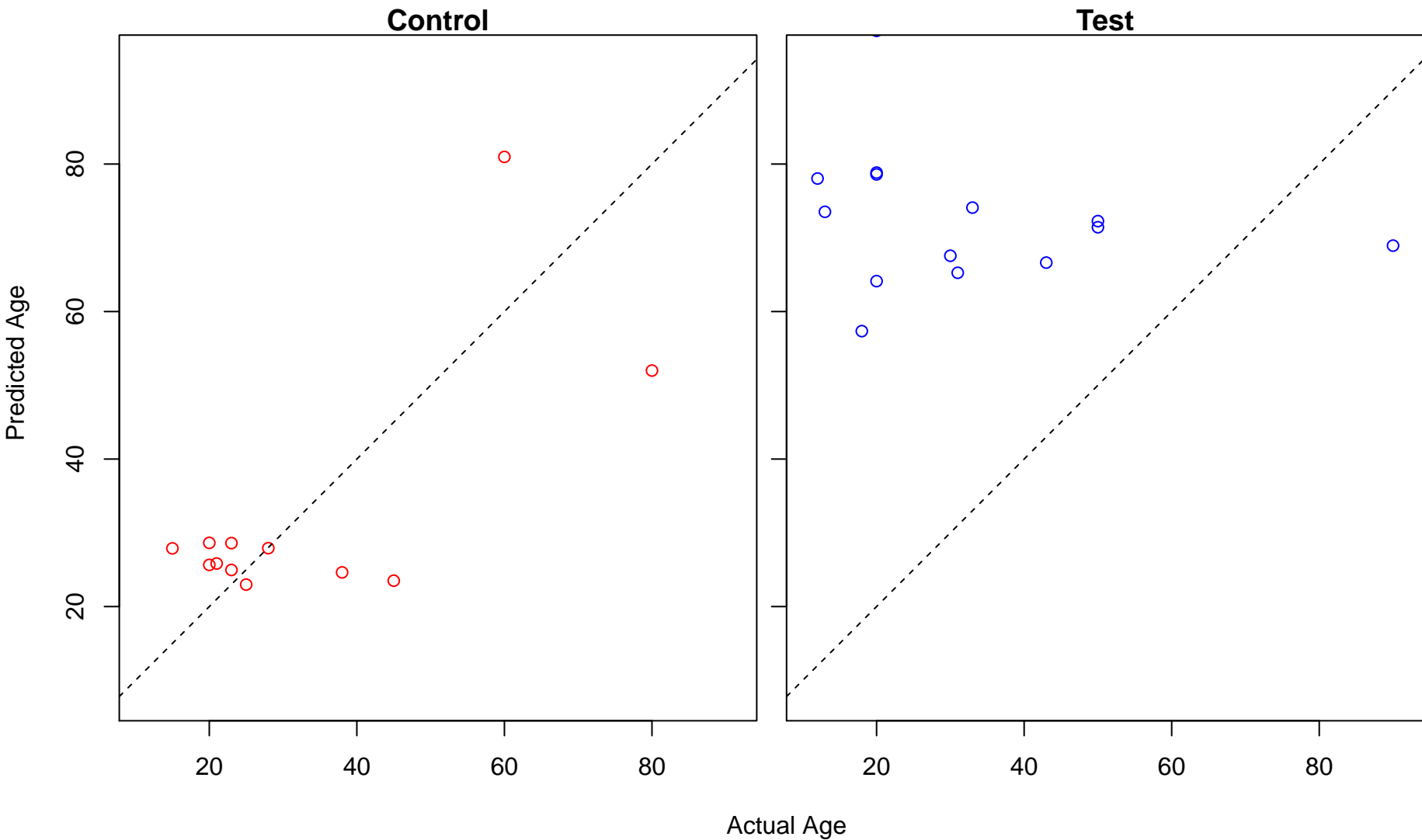
positive regulation of glycogen metabolic process (Score: 4.657695)



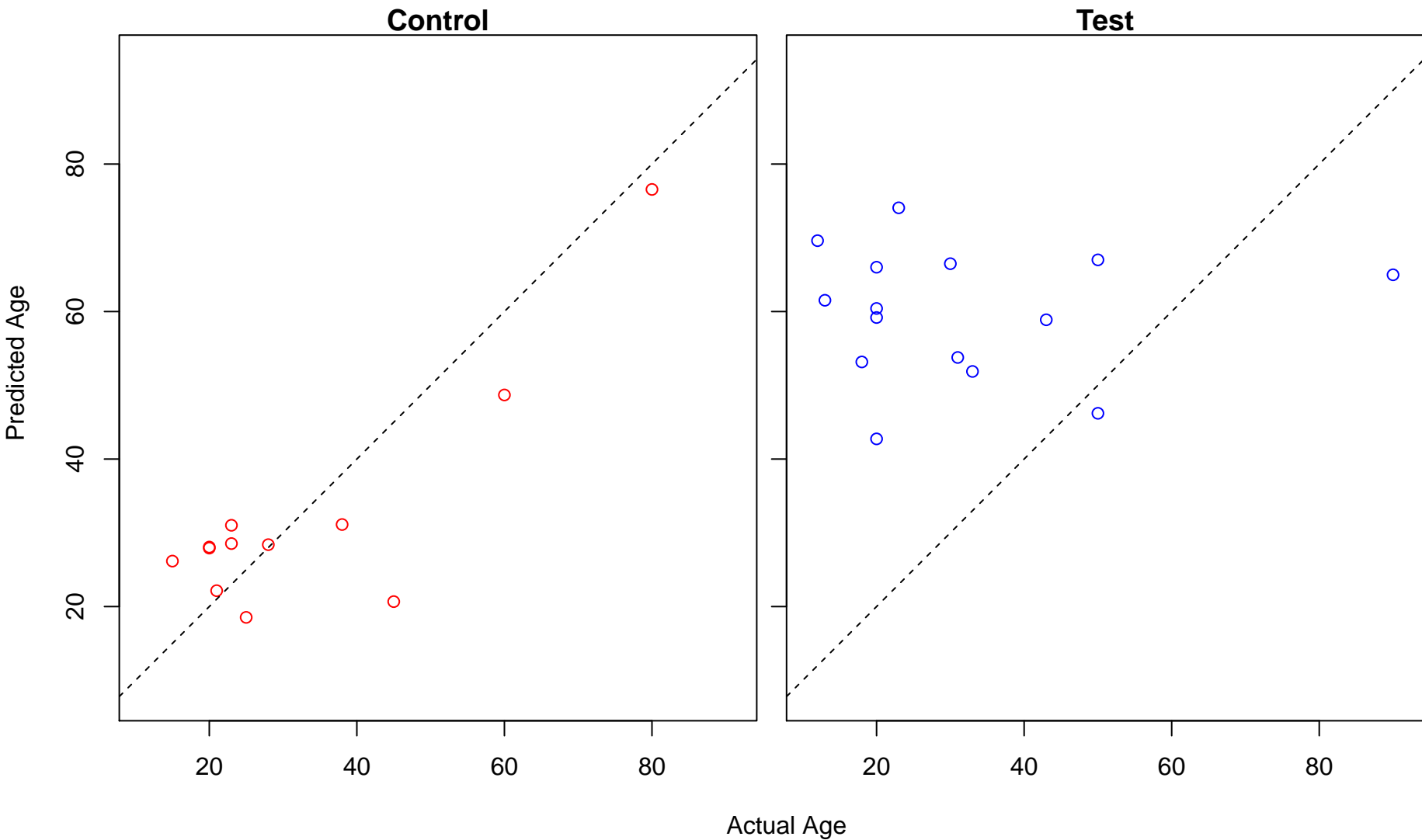
smoothened signaling pathway (Score: 4.657344)



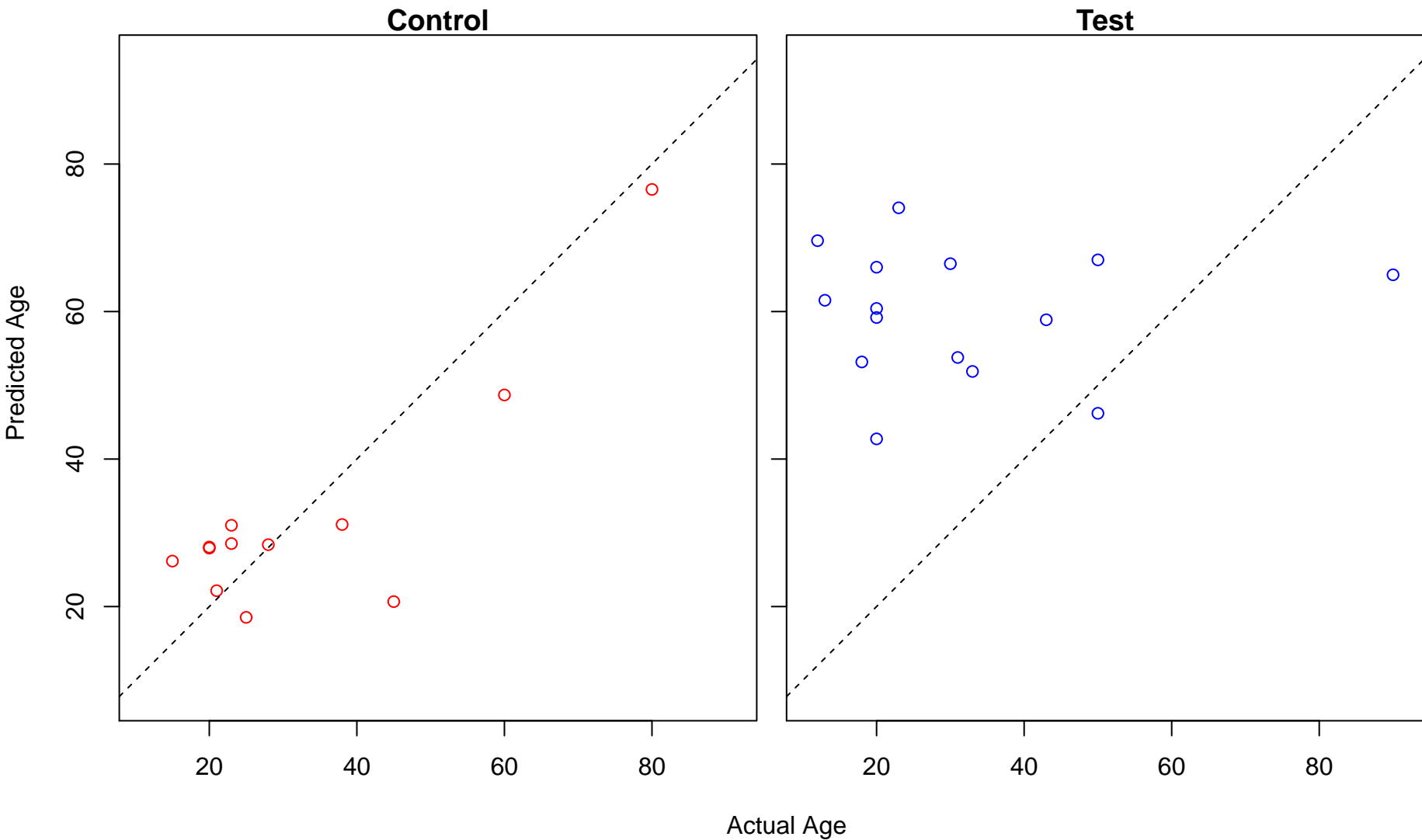
positive regulation of type 2 immune response (Score: 4.656697)



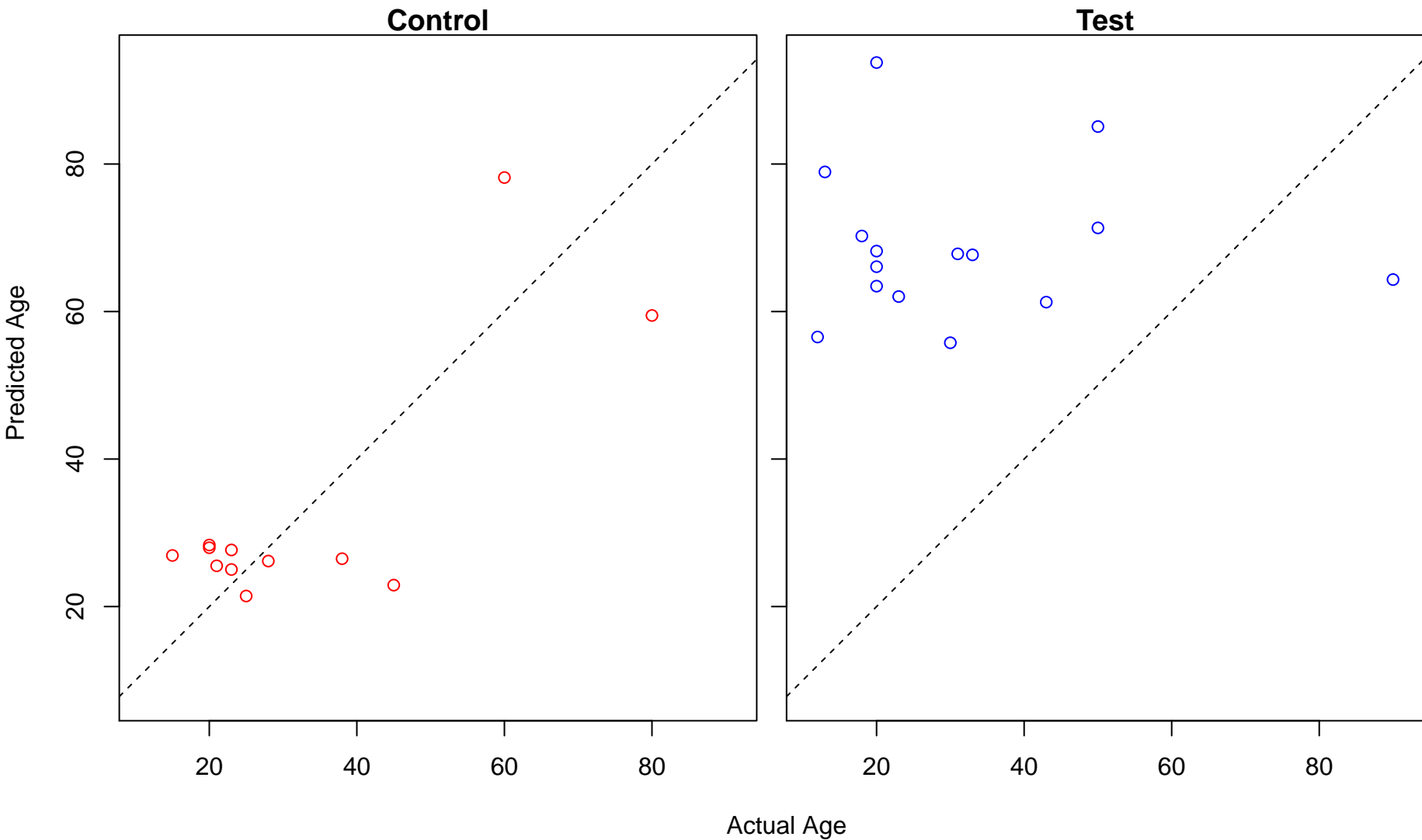
regulation of posttranscriptional gene silencing (Score: 4.656114)



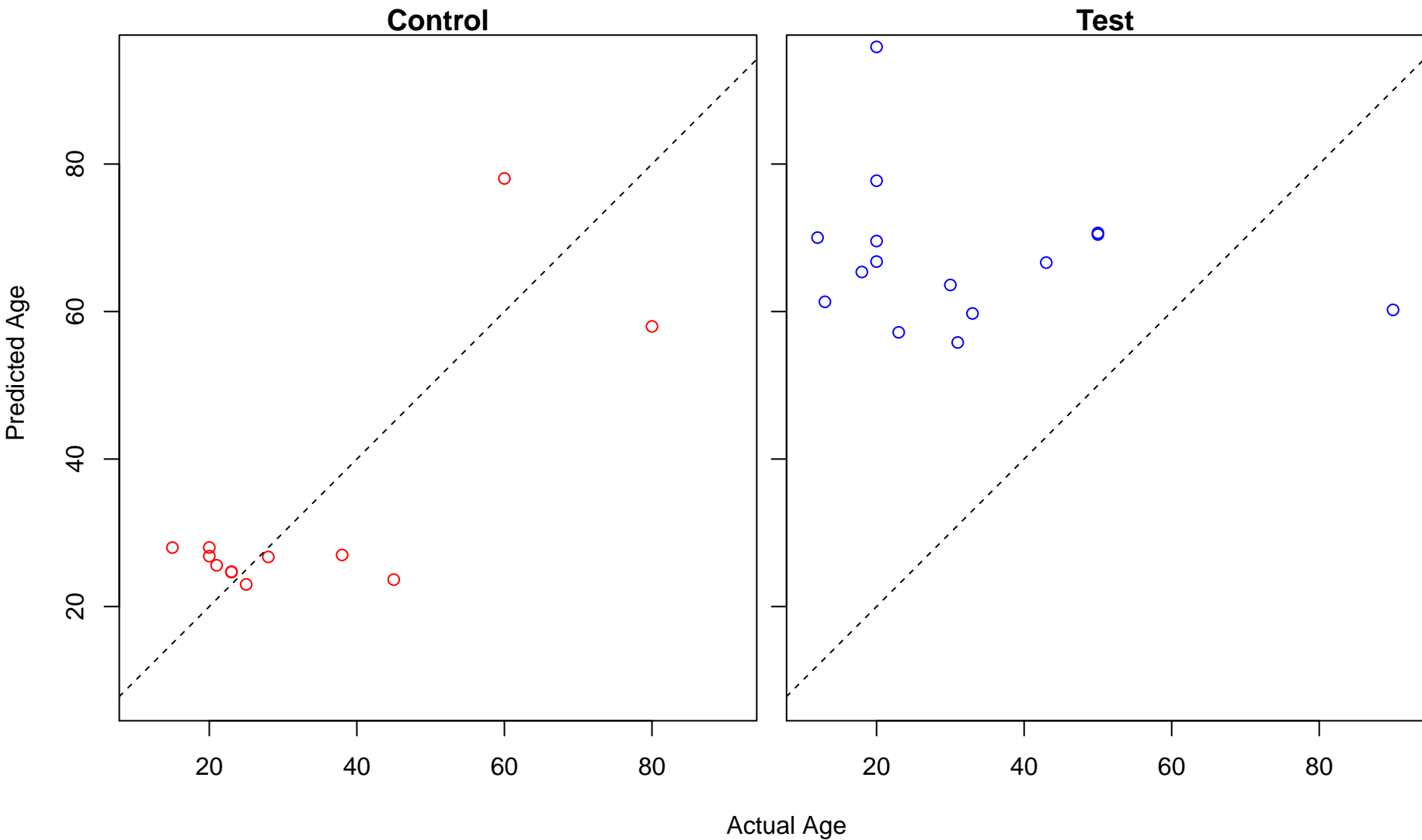
regulation of gene silencing by RNA (Score: 4.656114)



regulation of receptor activity (Score: 4.652924)

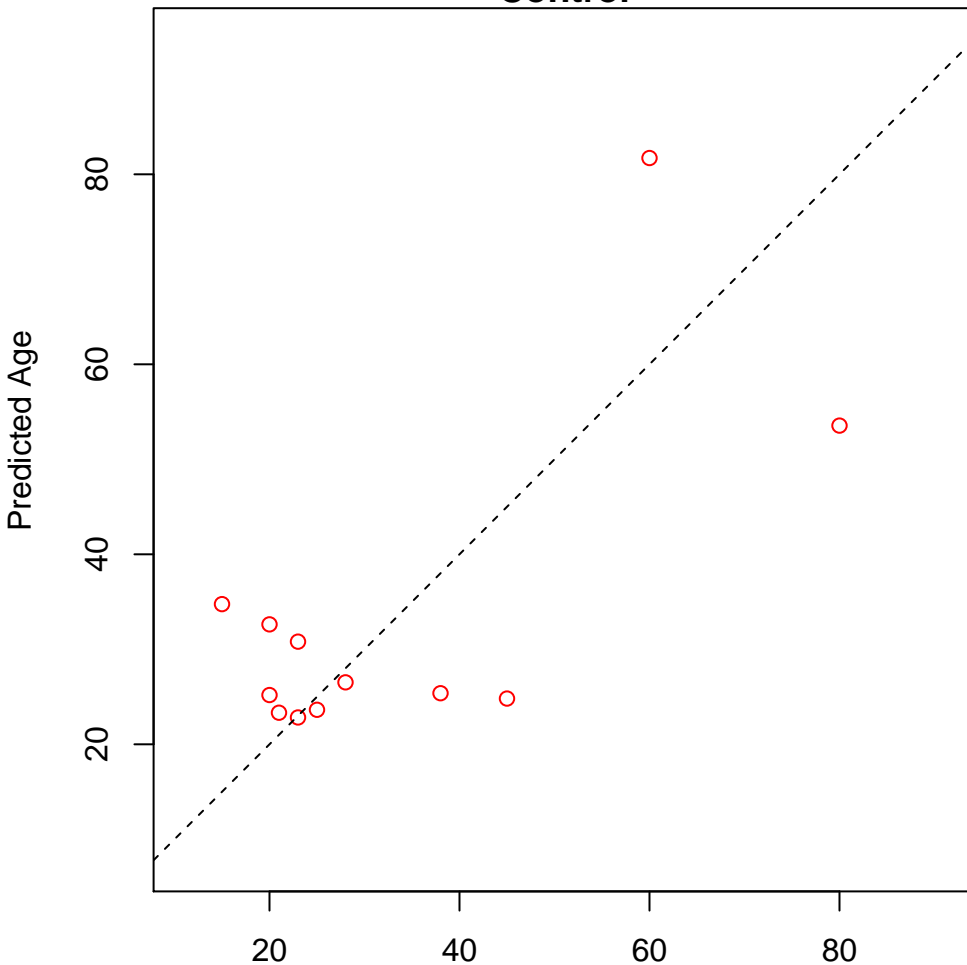


regulation of lipid metabolic process (Score: 4.650005)

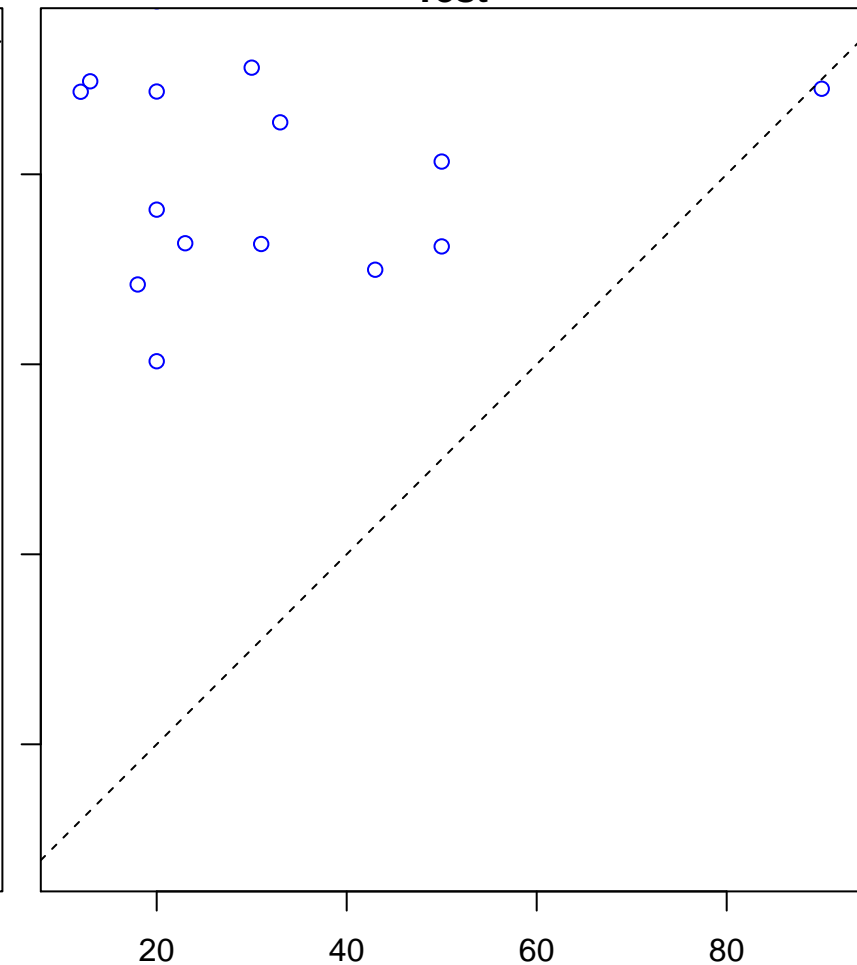


coronary vasculature development (Score: 4.649971)

Control

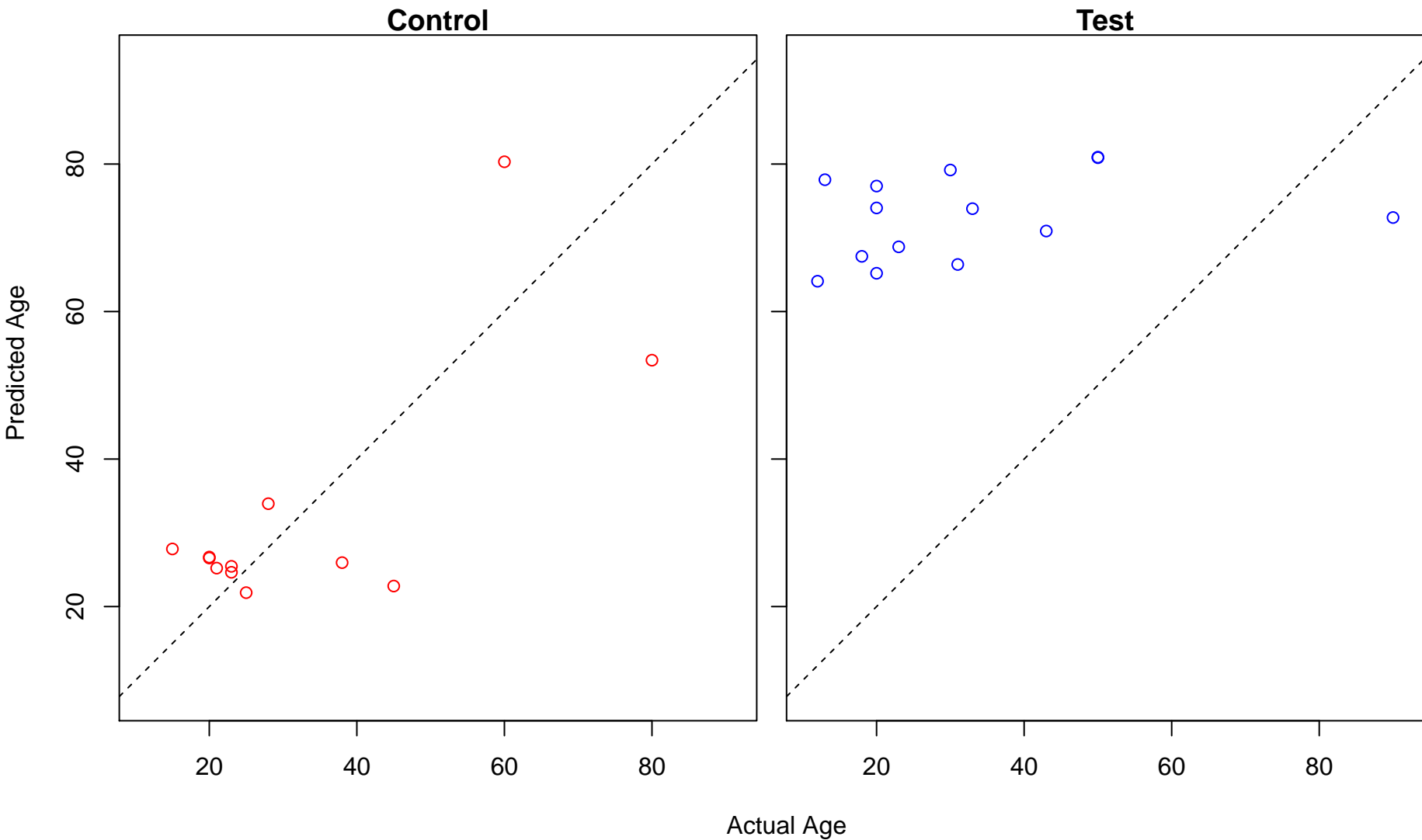


Test

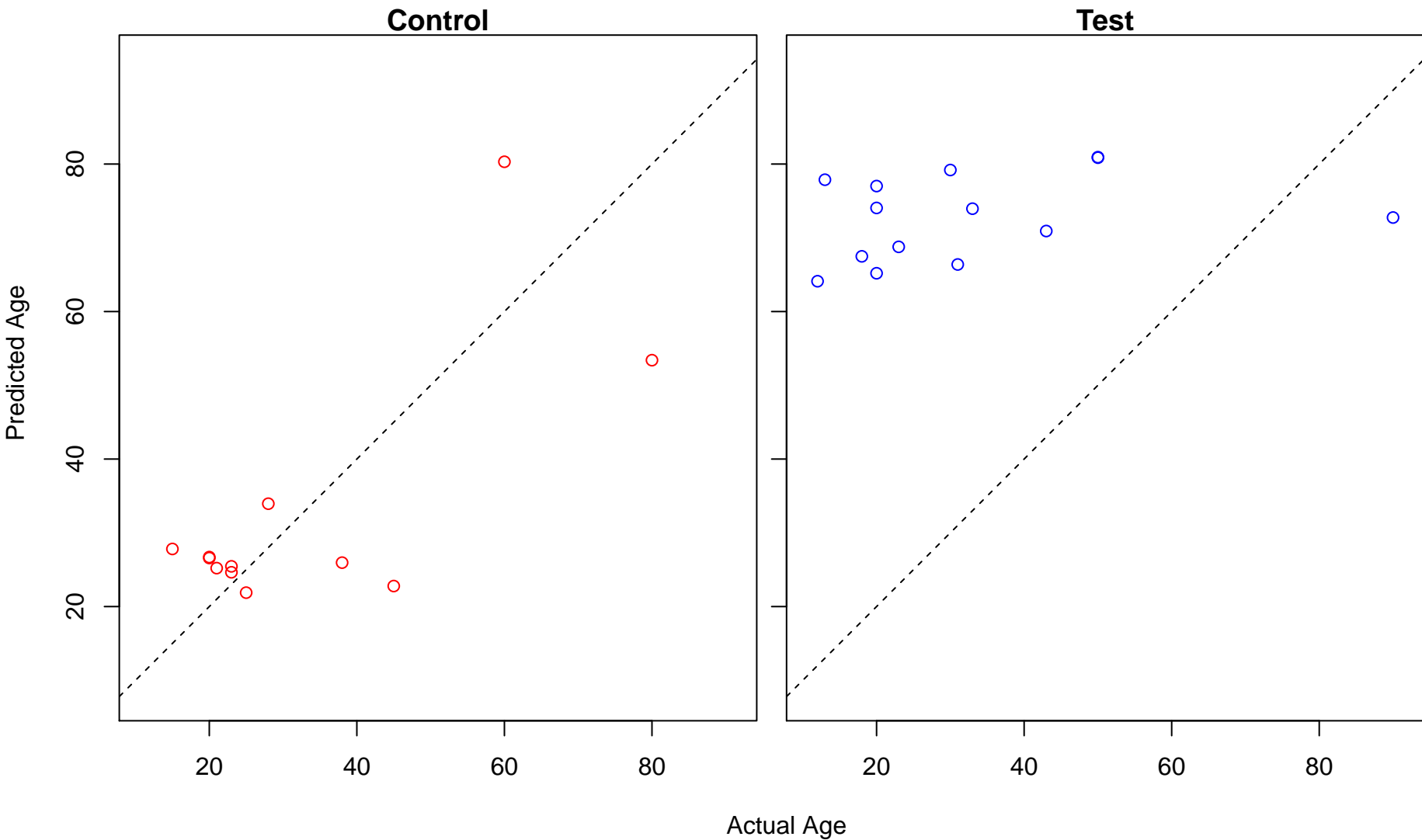


Actual Age

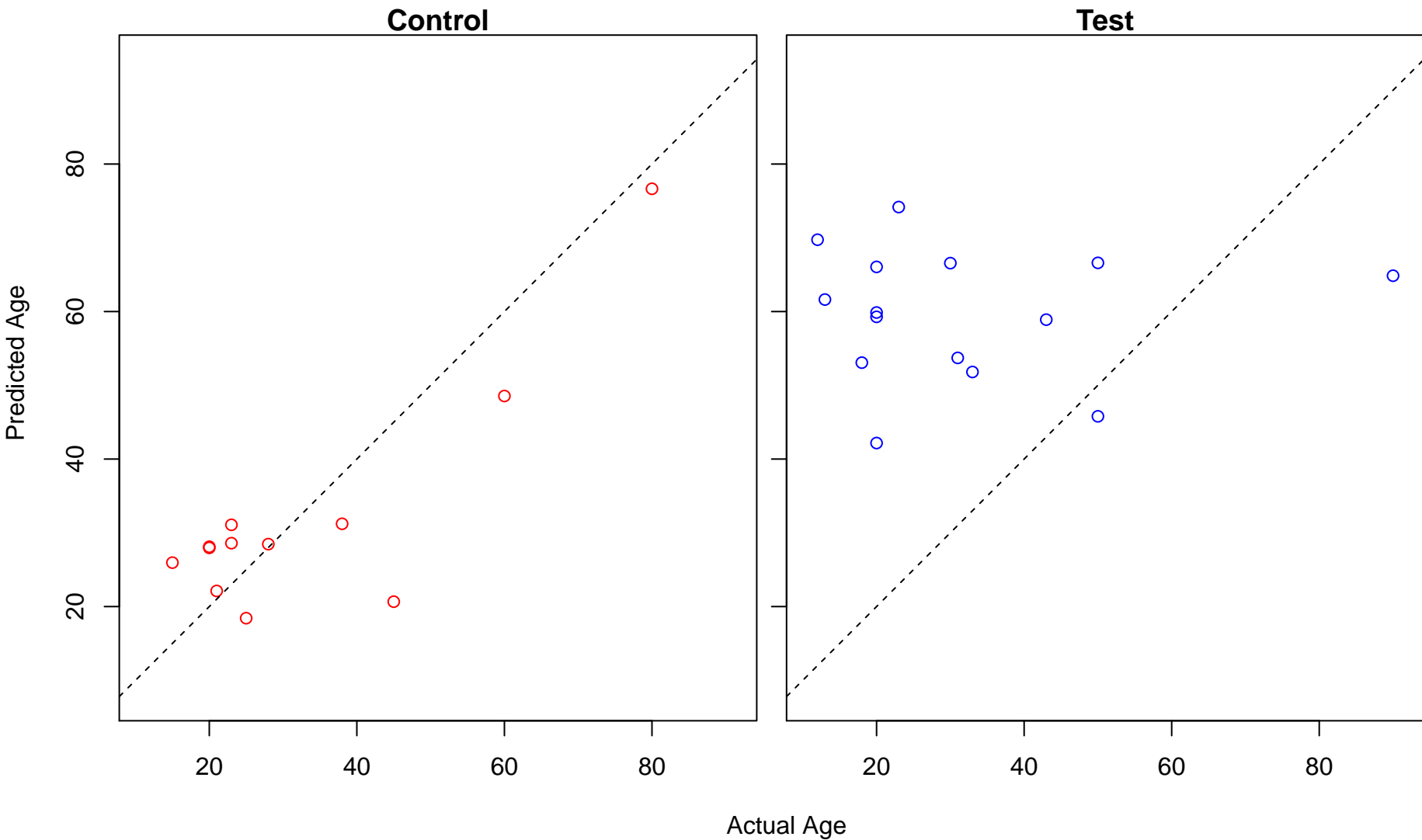
cerebellum development (Score: 4.648180)



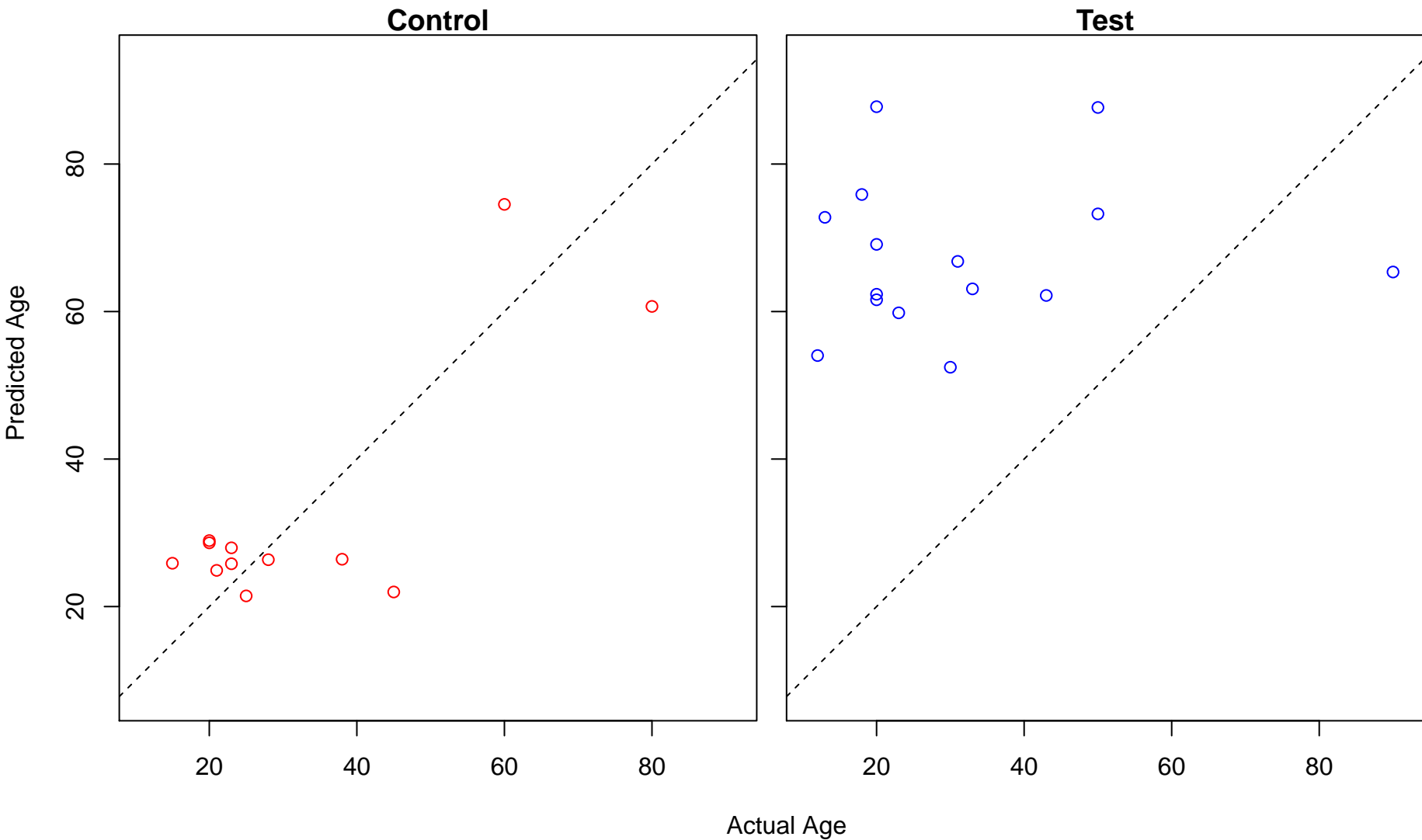
metencephalon development (Score: 4.648180)



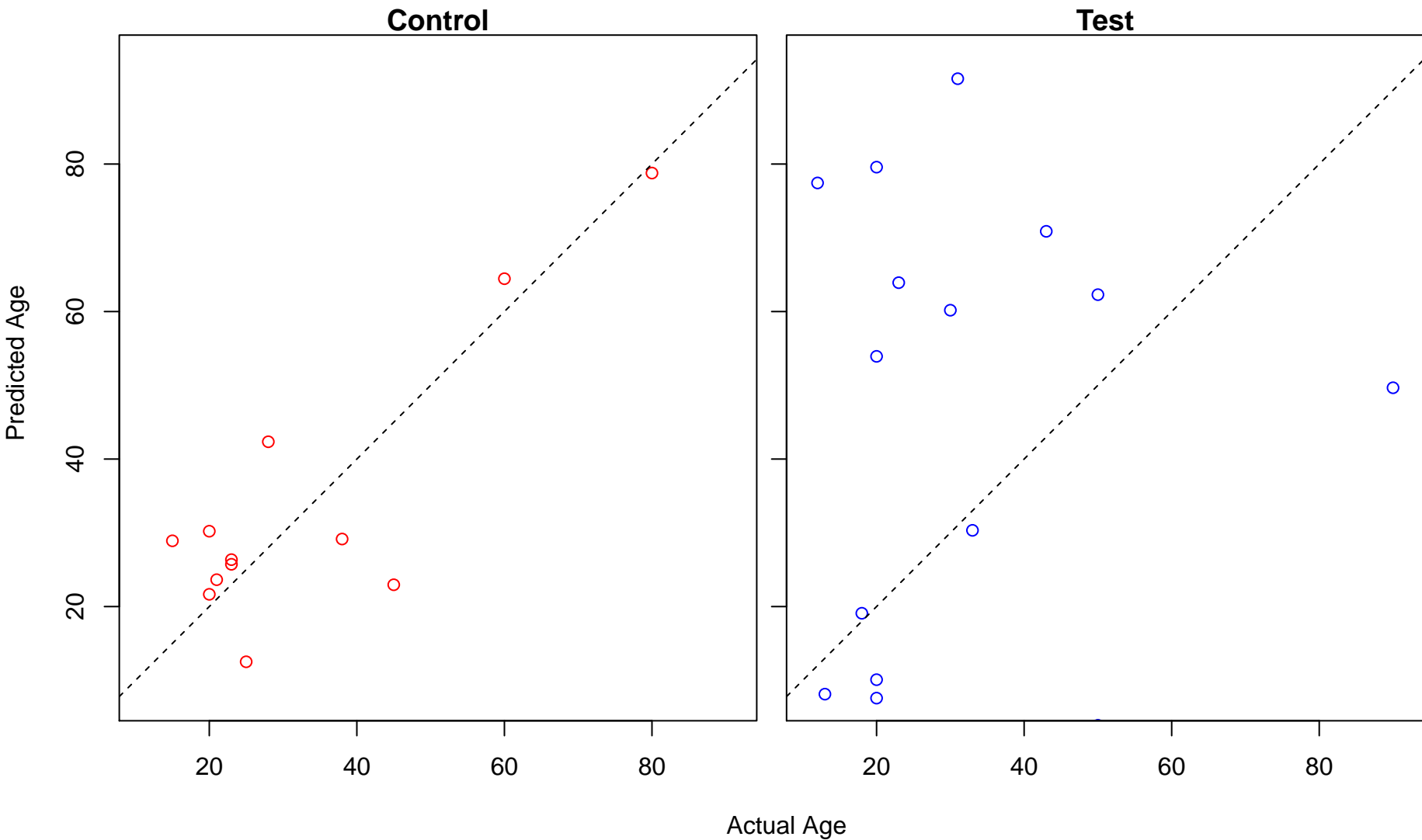
regulation of gene silencing by miRNA (Score: 4.647093)



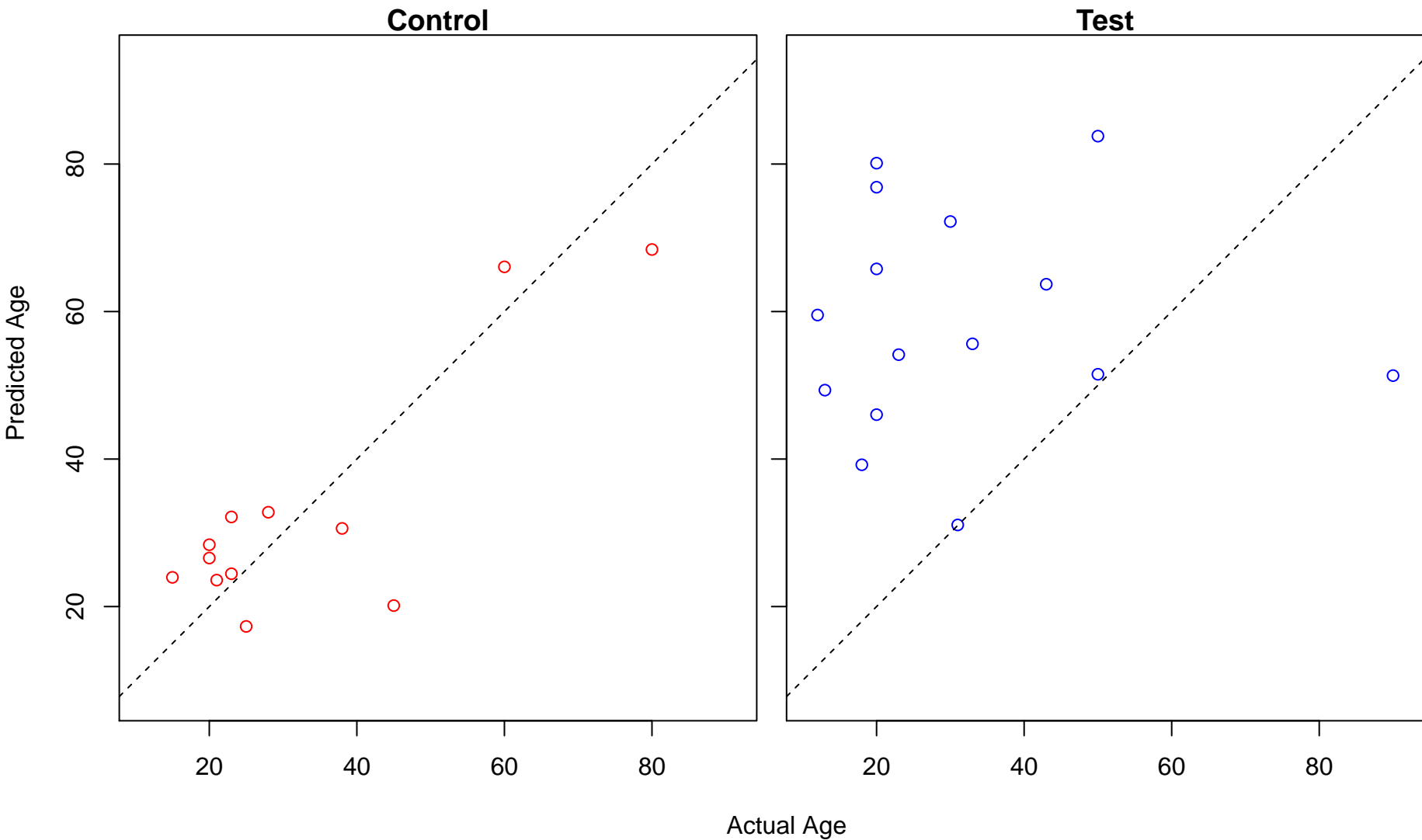
leukocyte differentiation (Score: 4.645432)



leukocyte tethering or rolling (Score: 4.645390)

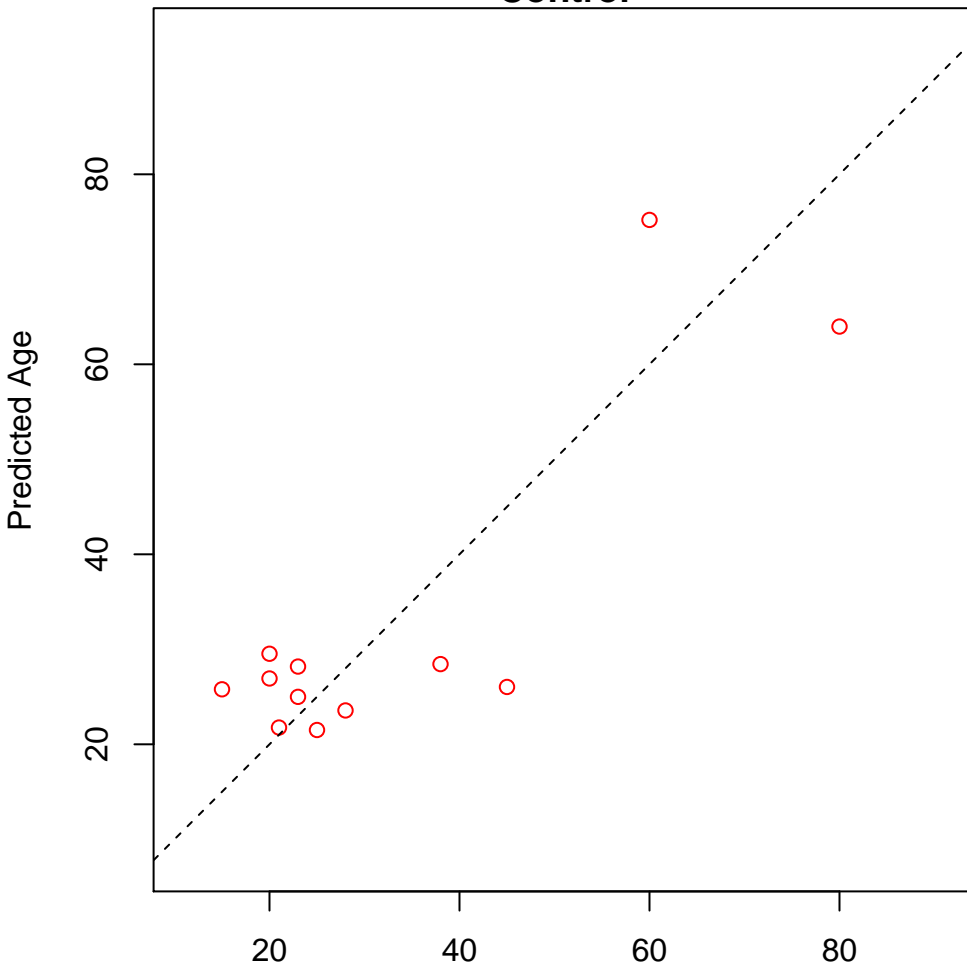


oligosaccharide catabolic process (Score: 4.645360)

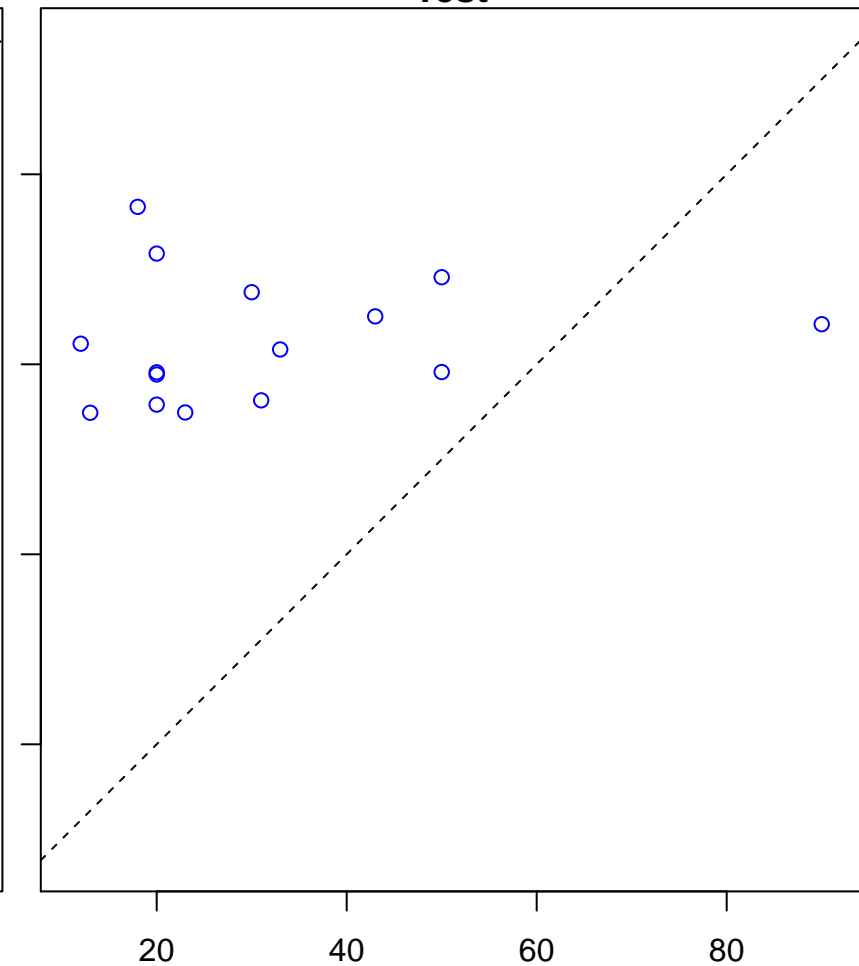


amino sugar biosynthetic process (Score: 4.644076)

Control

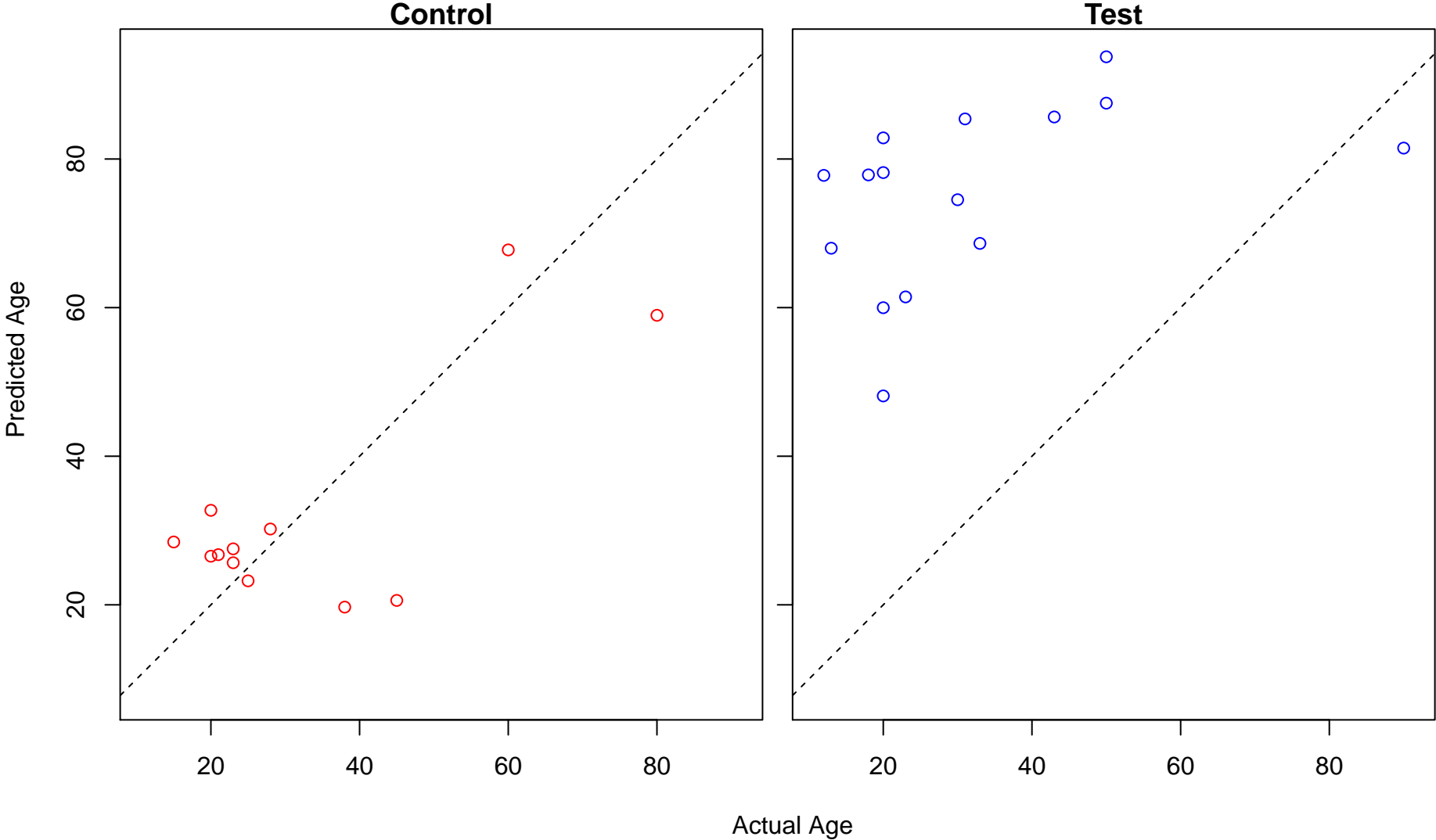


Test

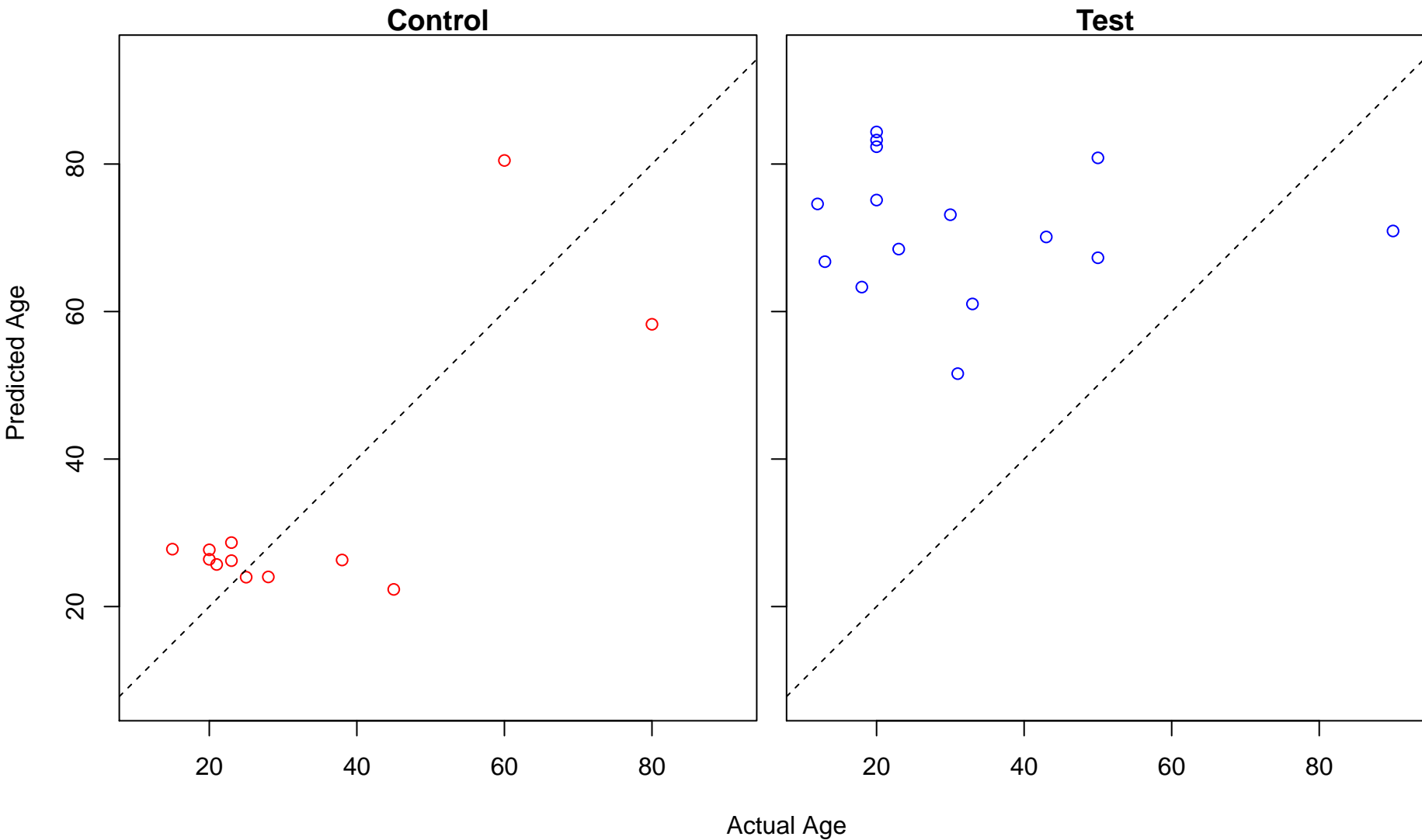


Actual Age

positive regulation of potassium ion transmembrane transporter activity (Score: 4.643912)

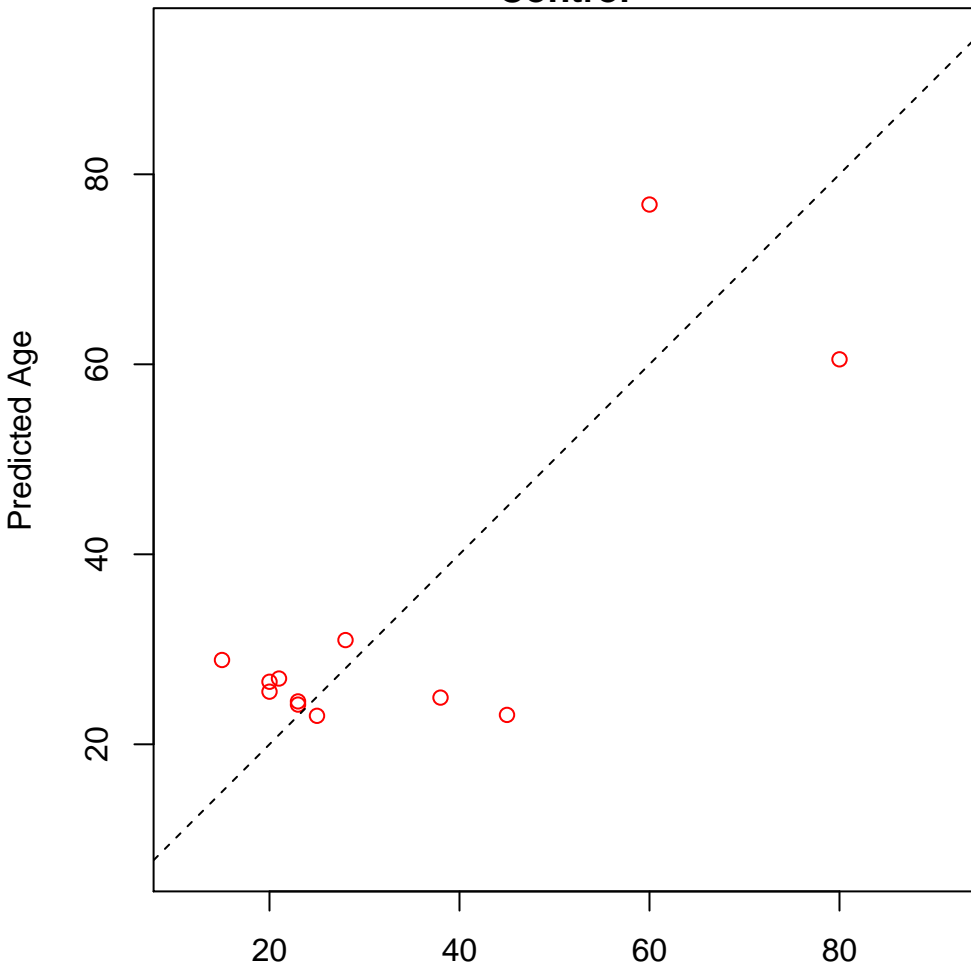


phospholipid catabolic process (Score: 4.643674)

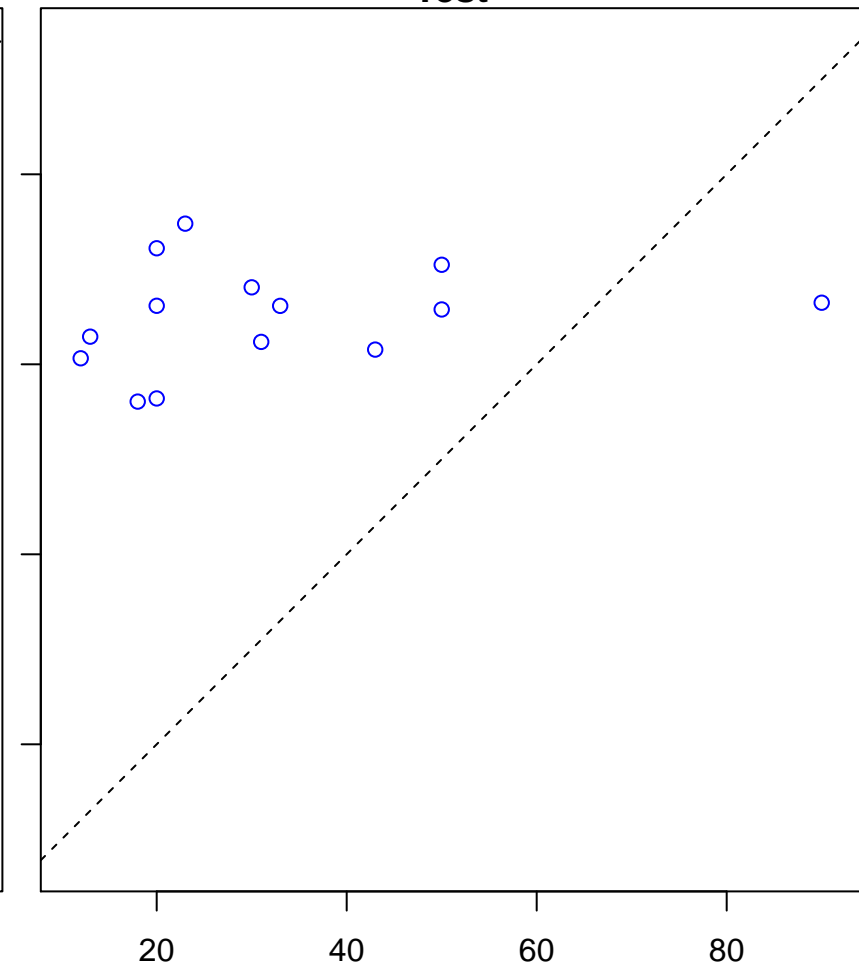


chemokine-mediated signaling pathway (Score: 4.642685)

Control

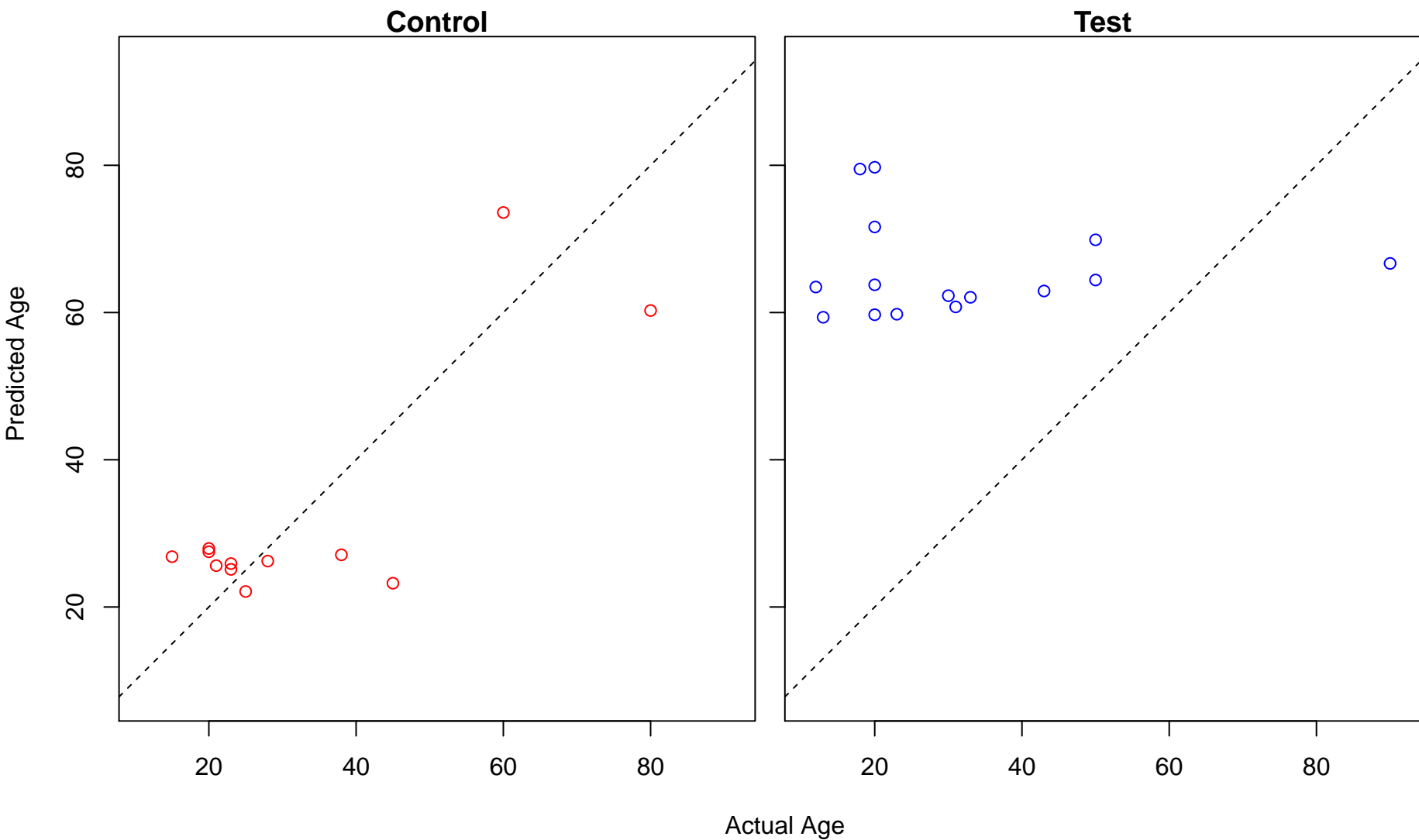


Test

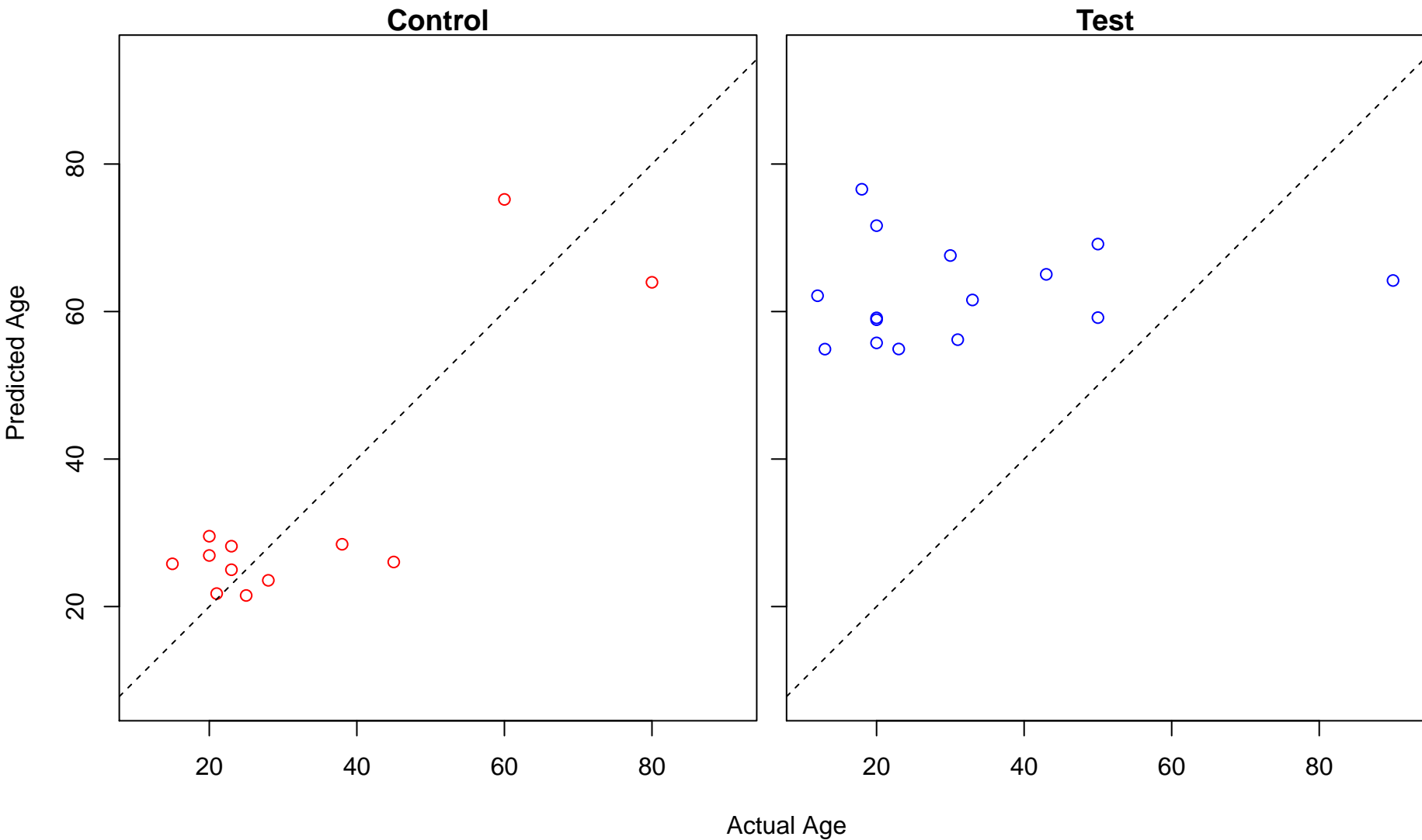


Actual Age

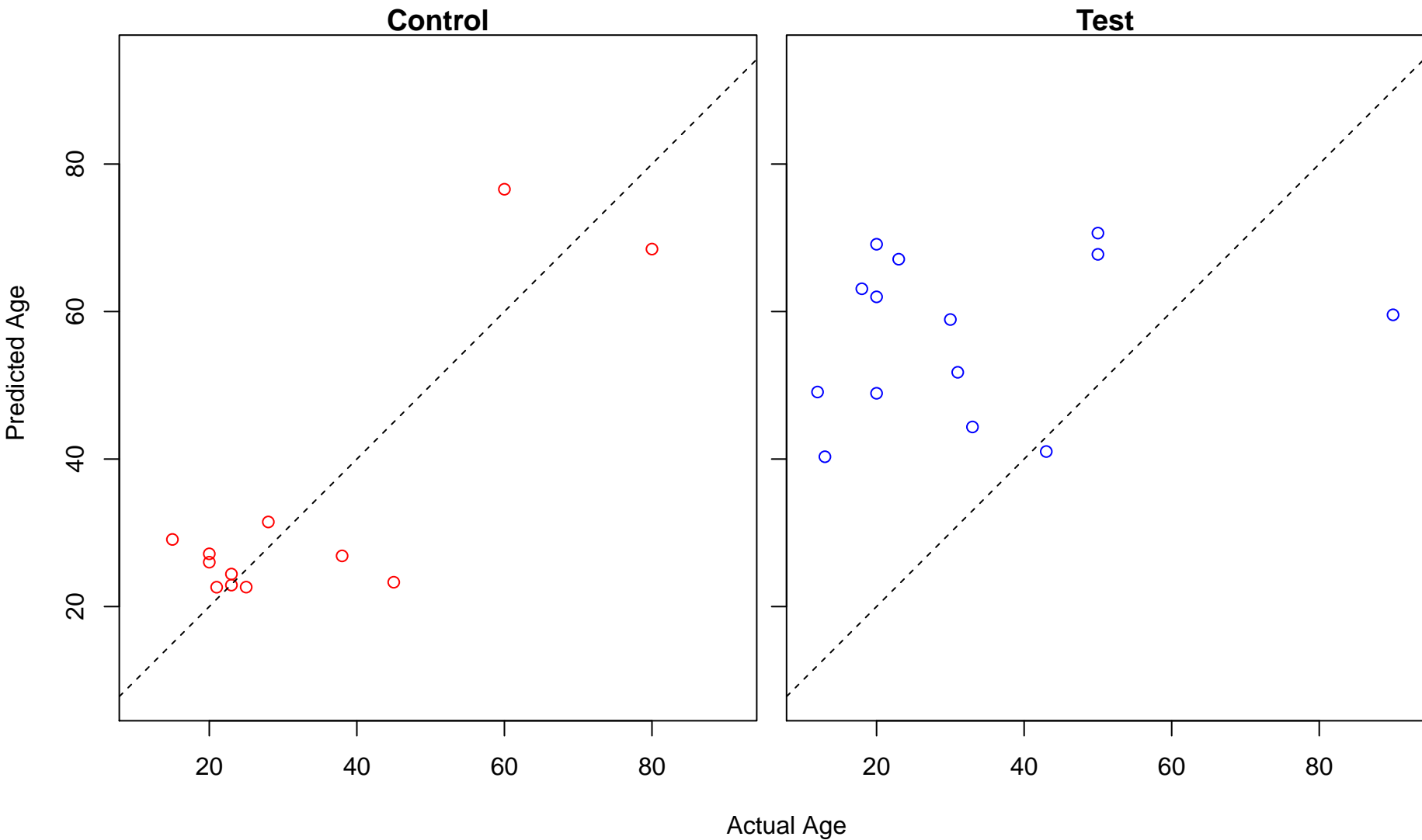
positive regulation of cell development (Score: 4.642408)



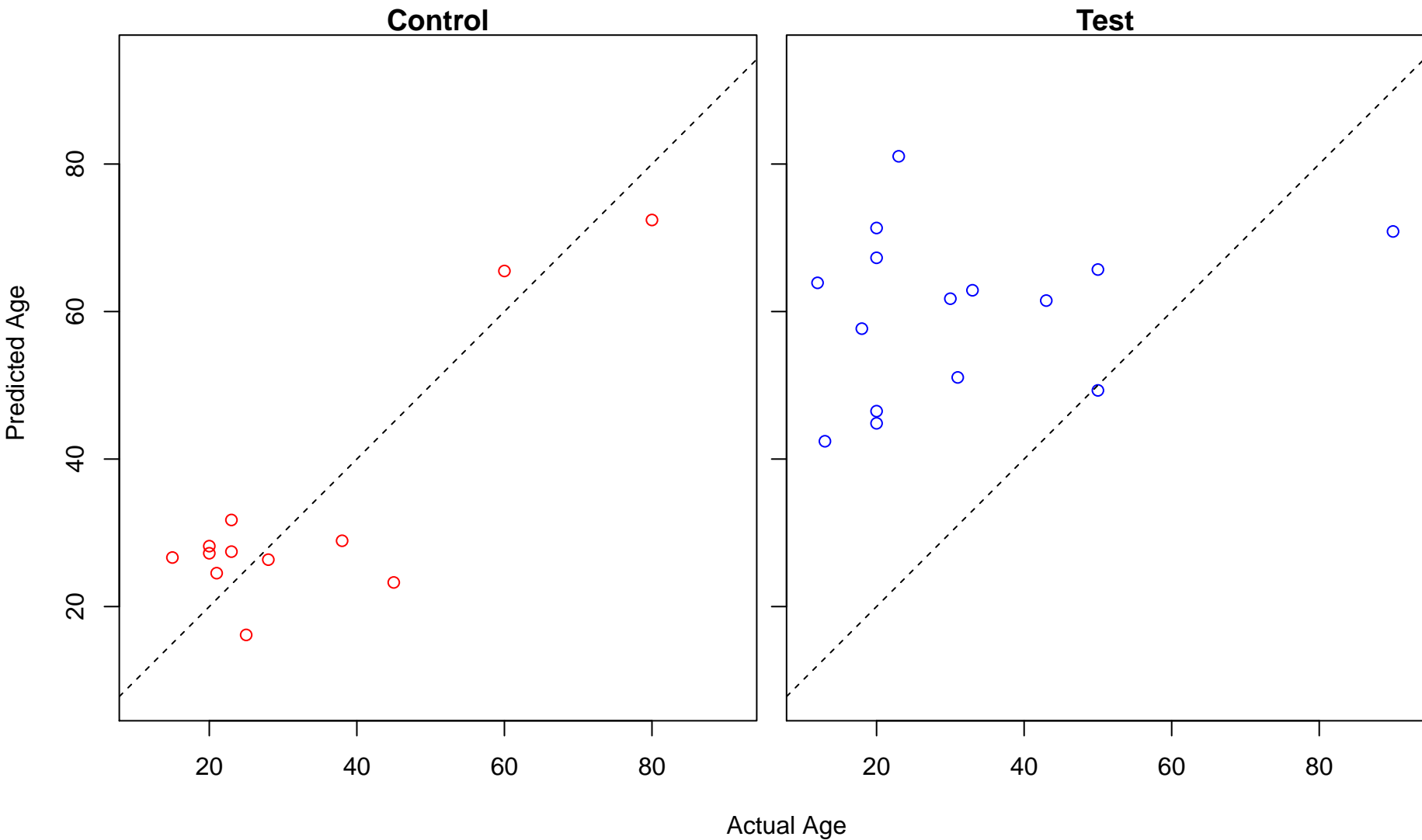
UDP-N-acetylglucosamine biosynthetic process (Score: 4.640960)



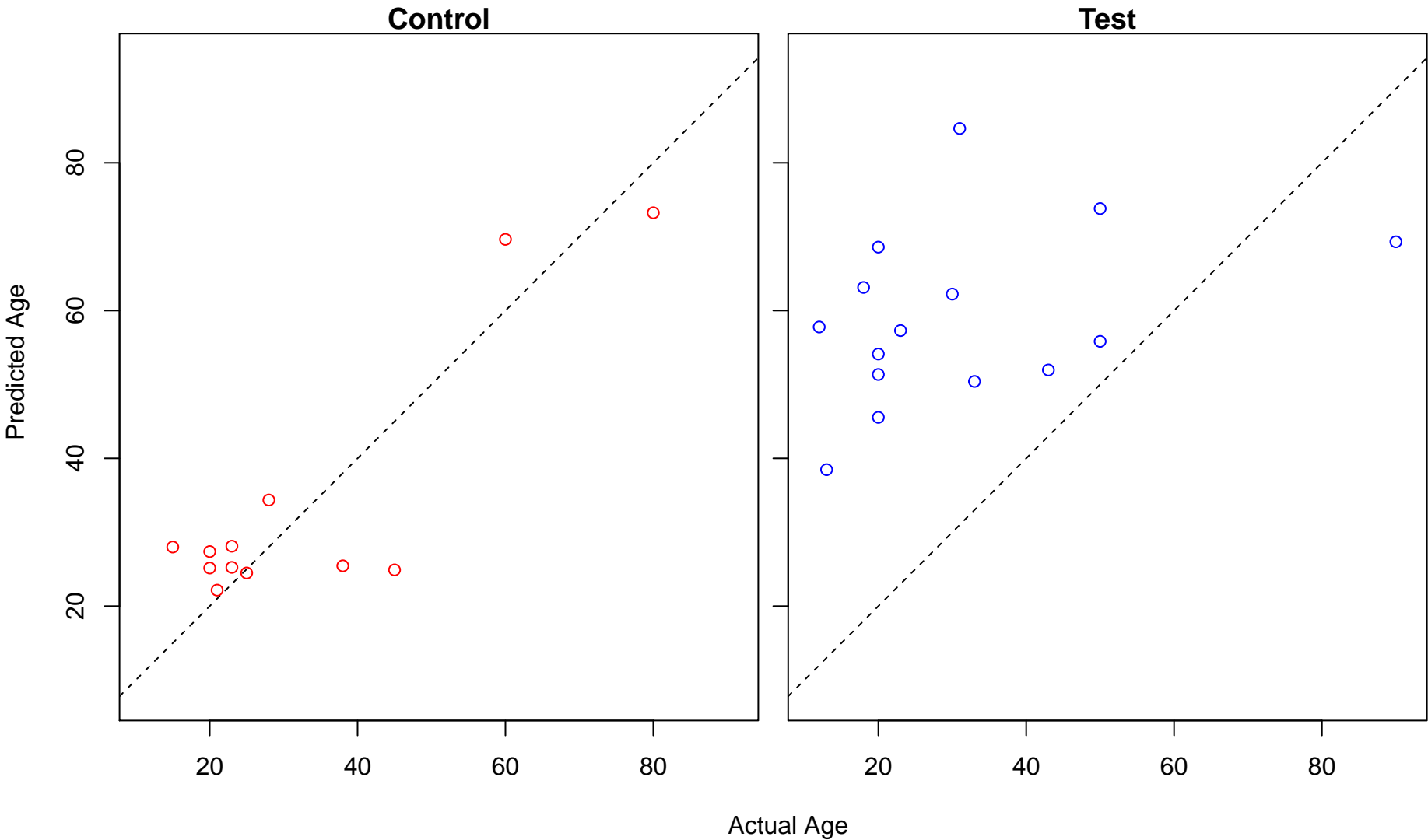
RNA splicing, via transesterification reactions (Score: 4.640435)



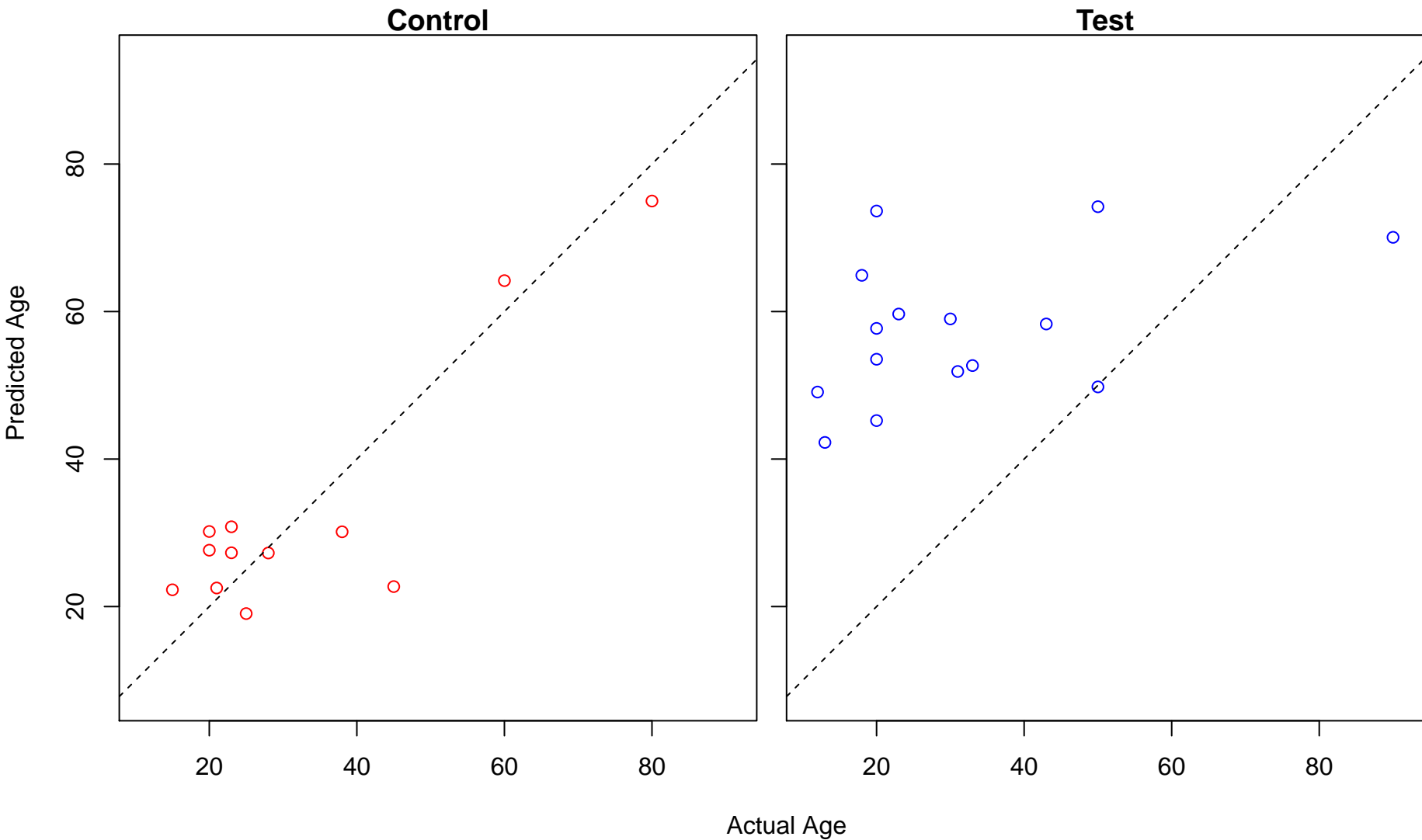
double-strand break repair via synthesis-dependent strand annealing (Score: 4.639547)



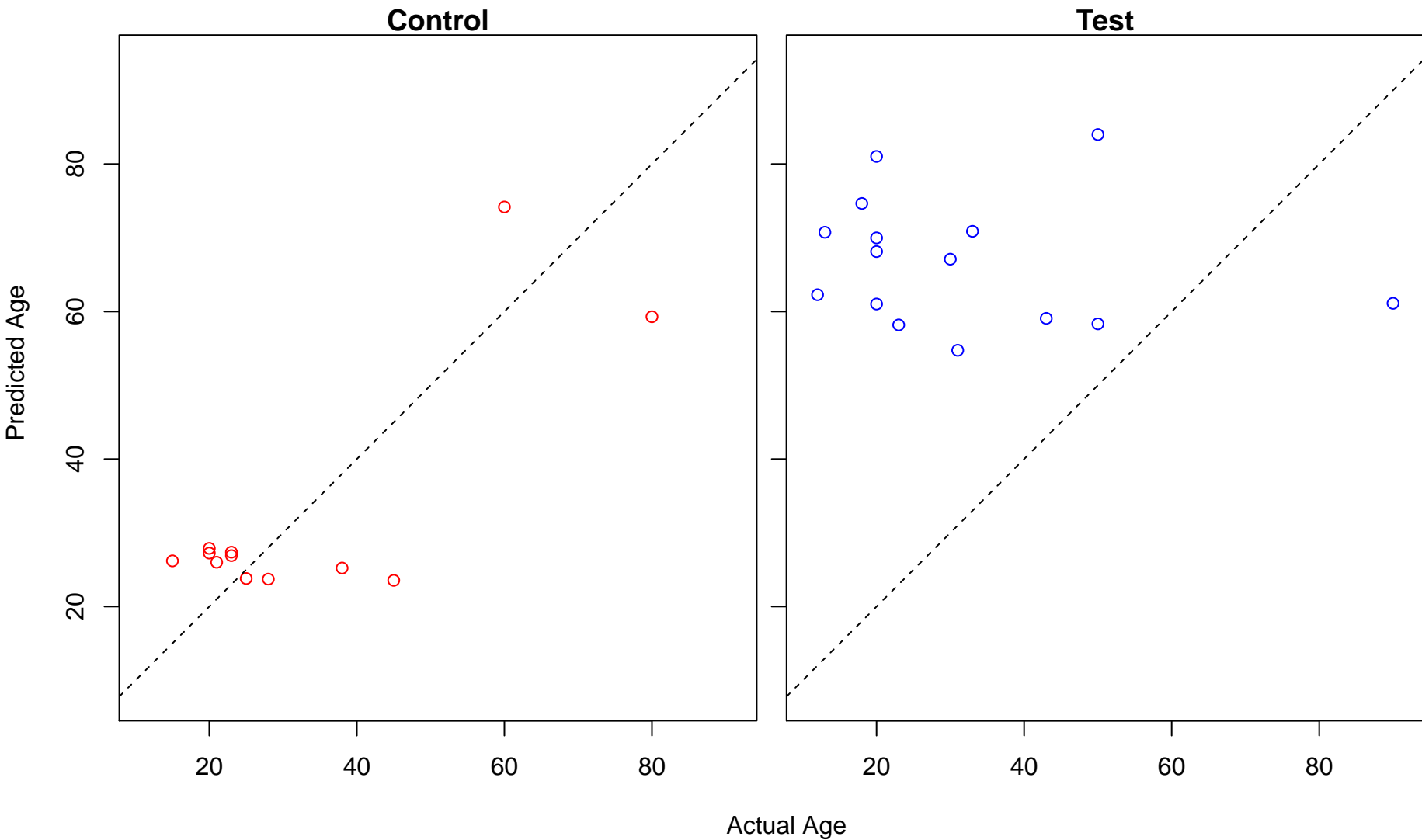
positive regulation of vacuole organization (Score: 4.639429)



oligosaccharide metabolic process (Score: 4.639246)

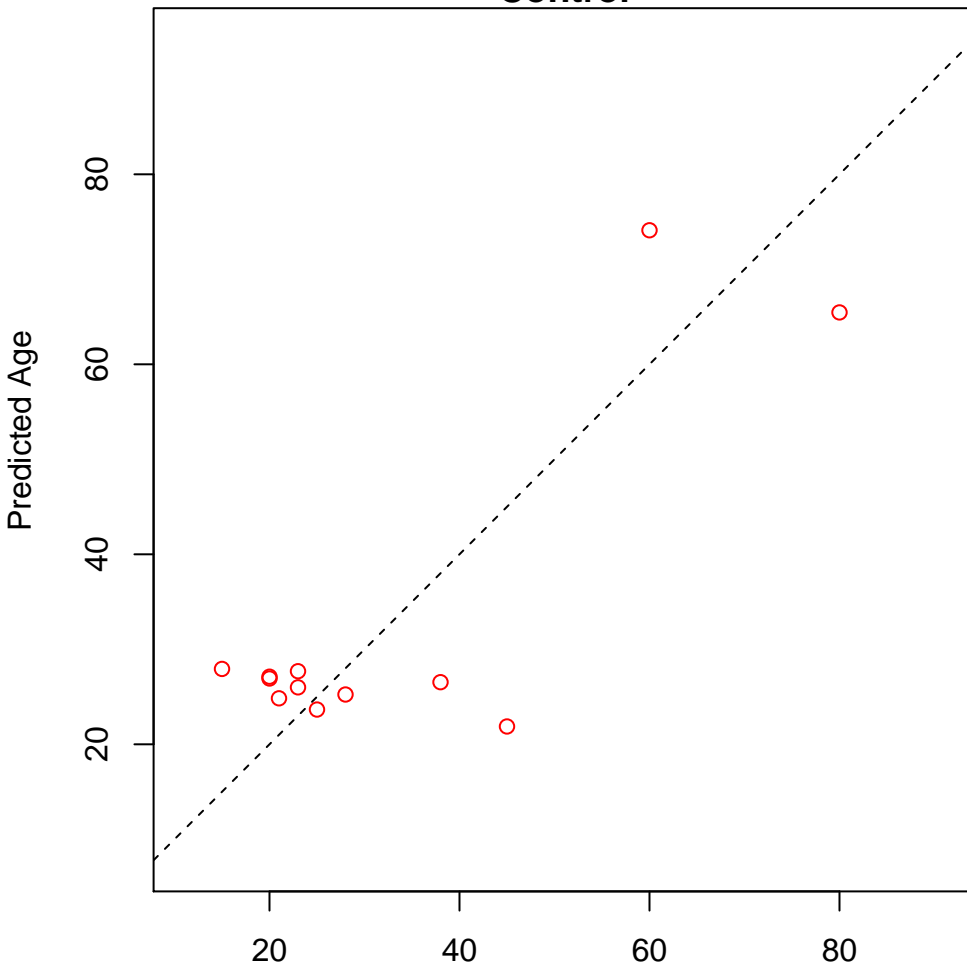


positive regulation of glycoprotein biosynthetic process (Score: 4.638967)

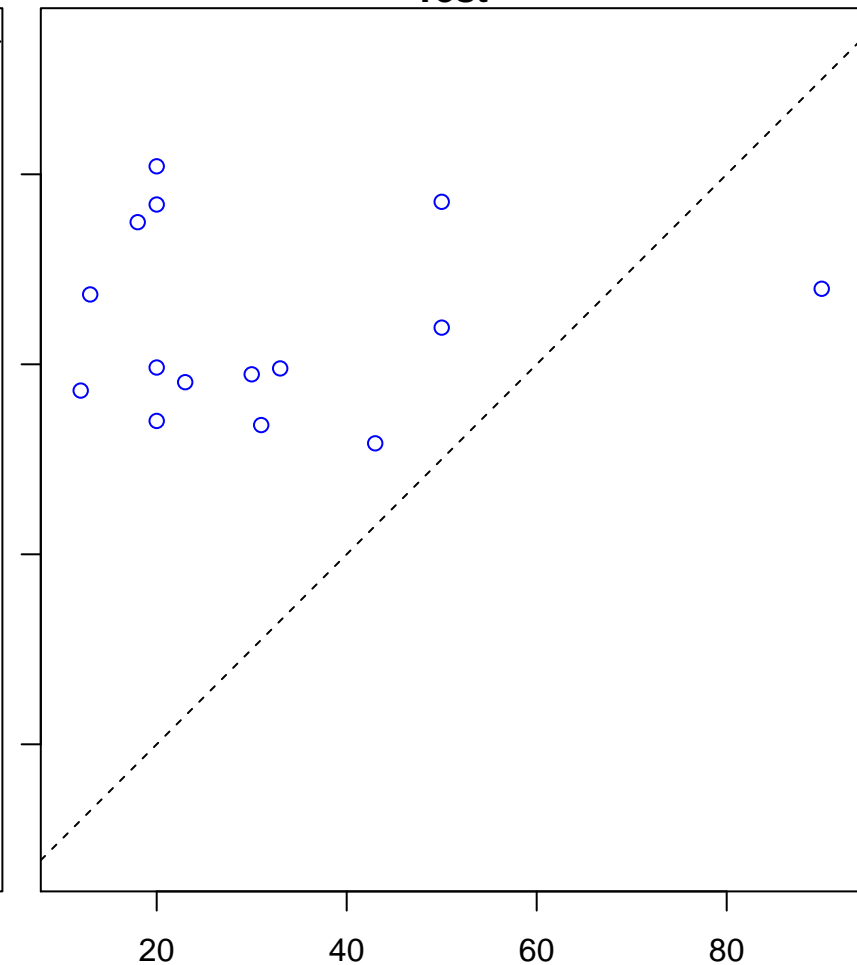


positive regulation of catabolic process (Score: 4.636366)

Control

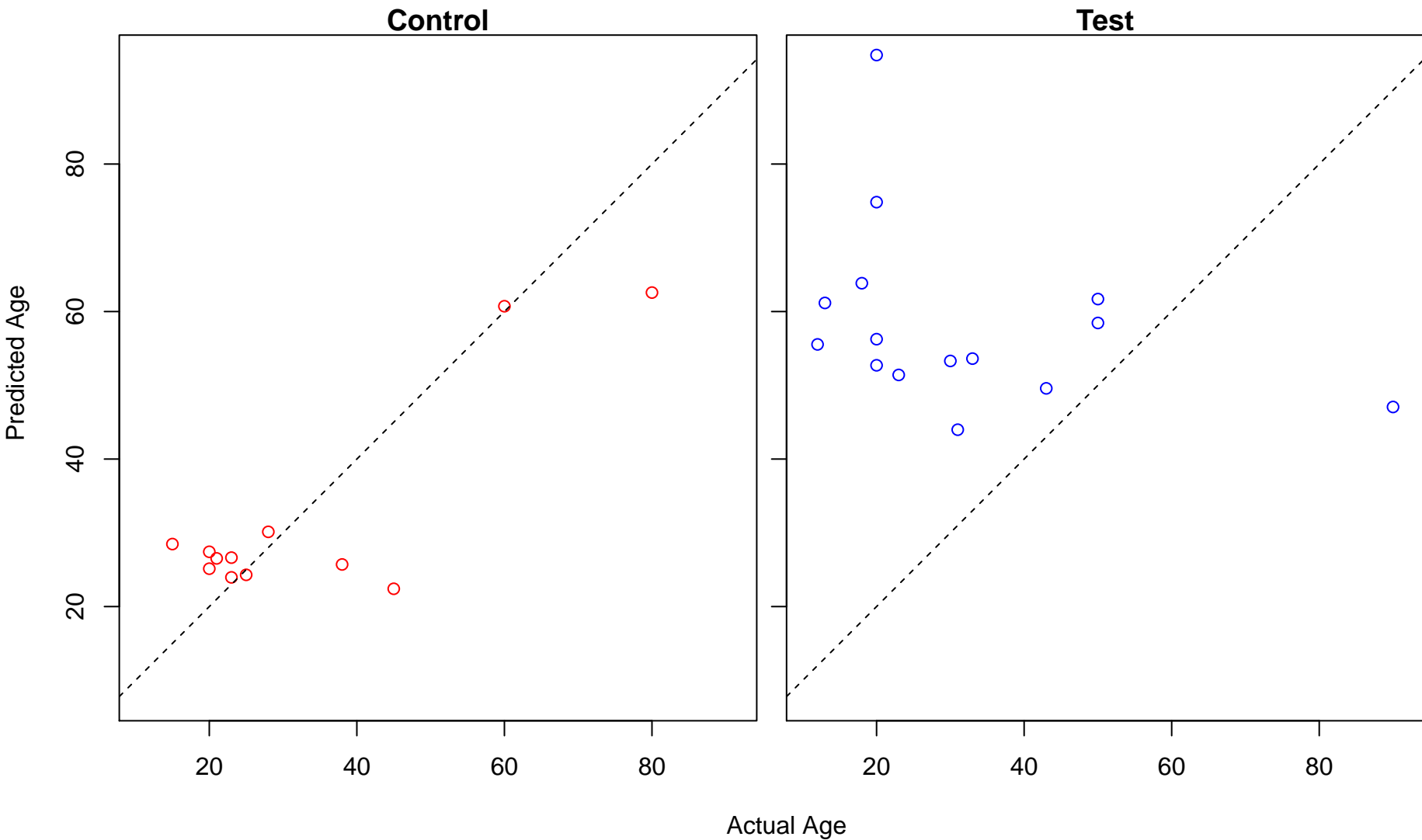


Test

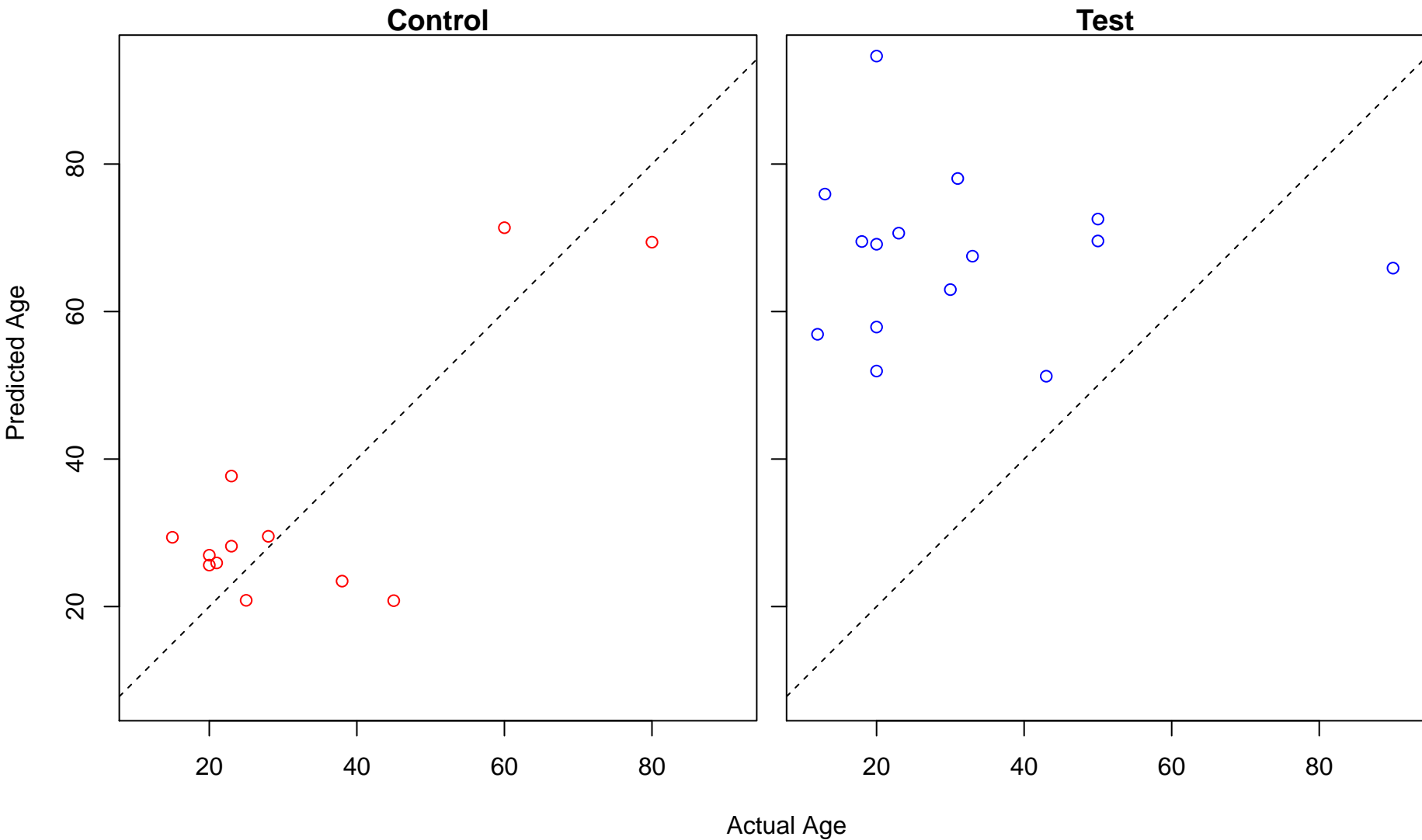


Actual Age

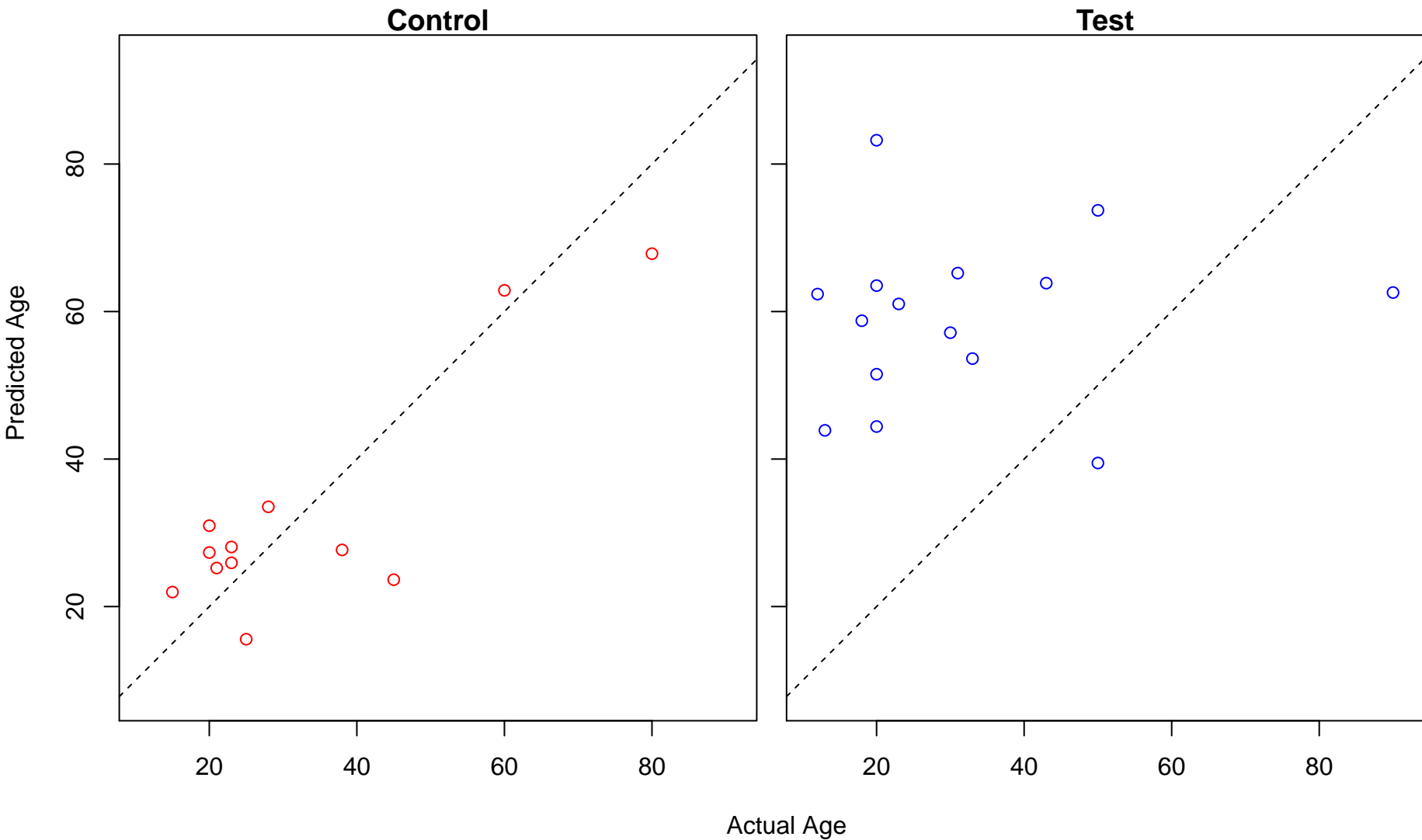
myelin maintenance (Score: 4.636307)



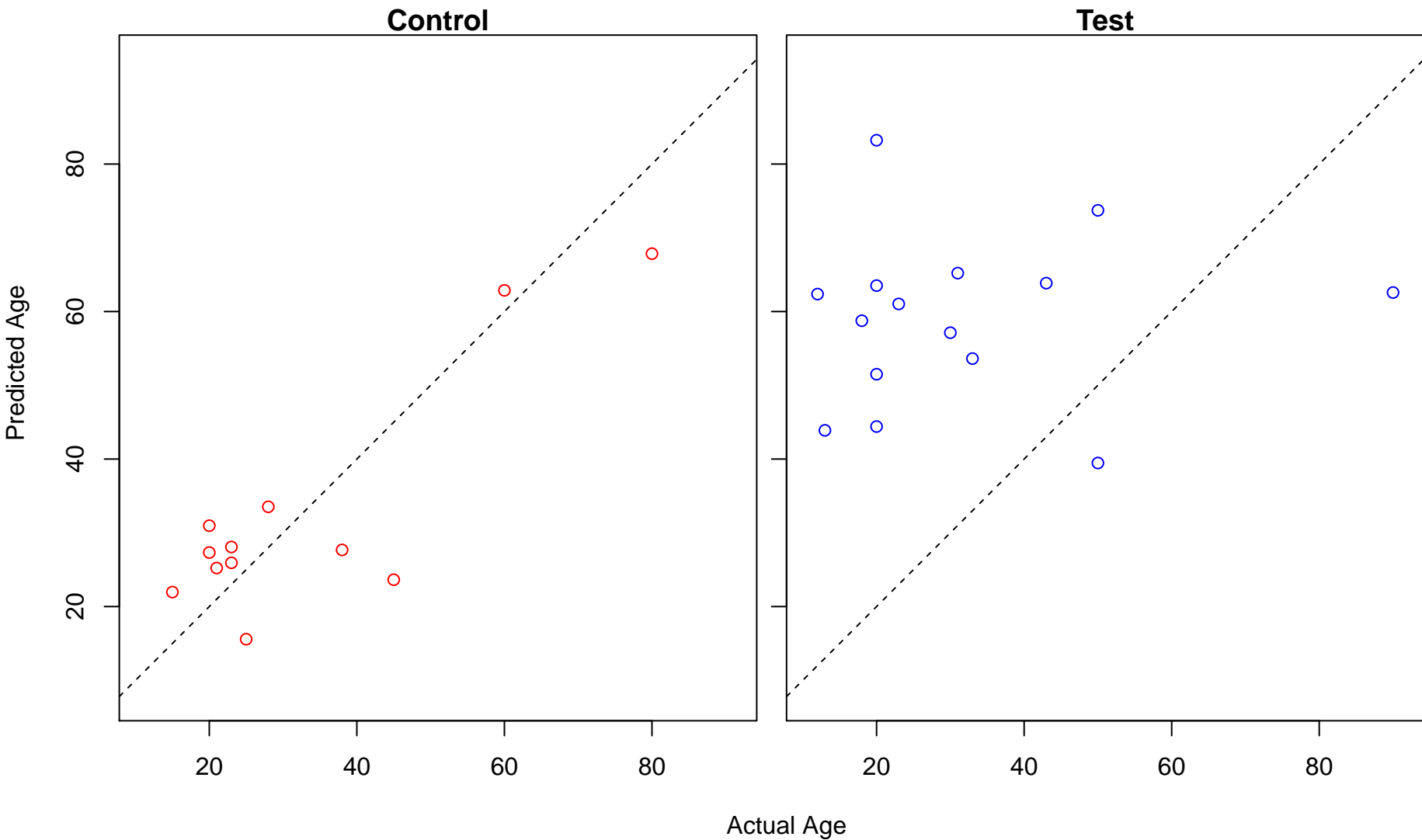
regulation of homeostatic process (Score: 4.635469)



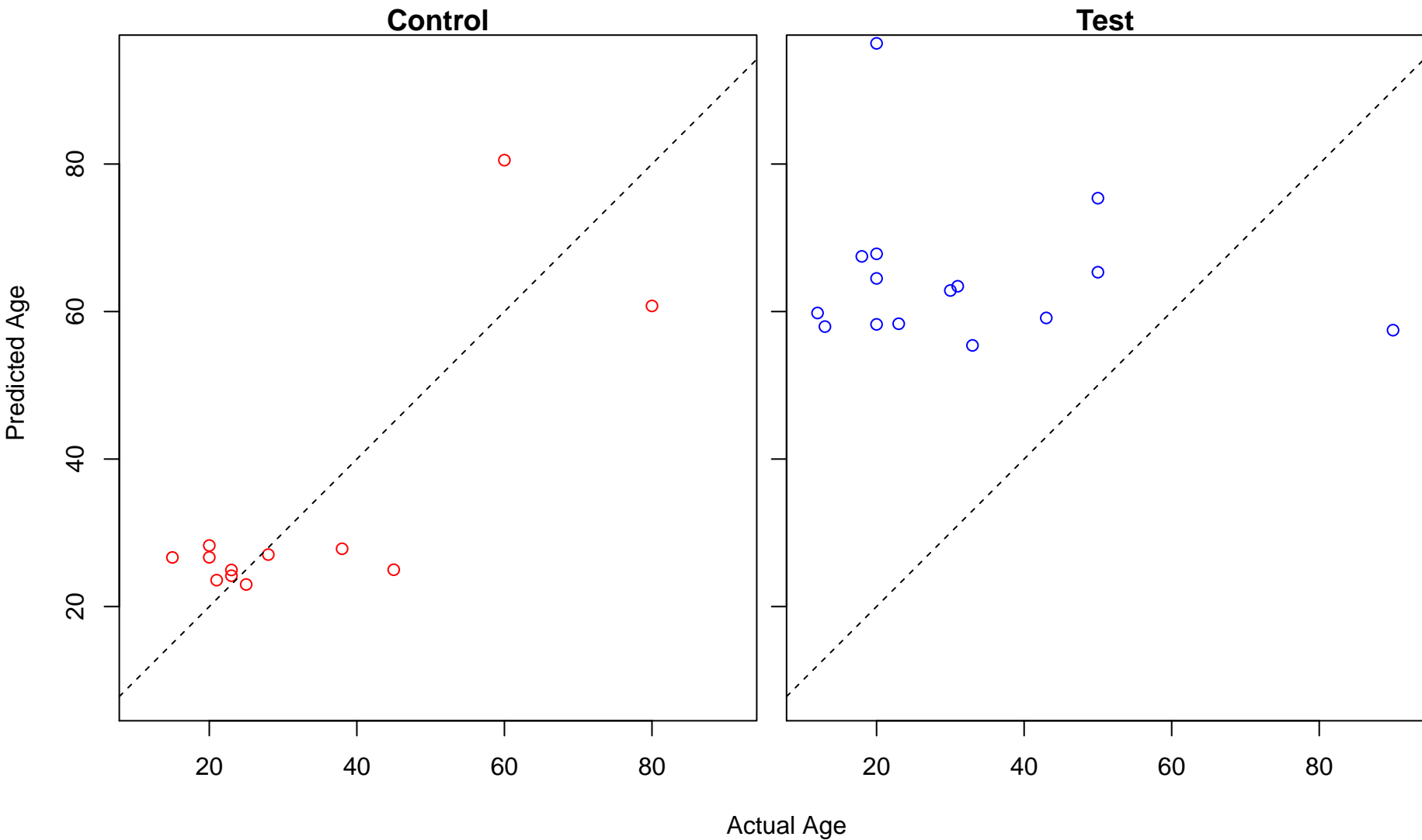
cerebral cortex radial glia guided migration (Score: 4.635023)



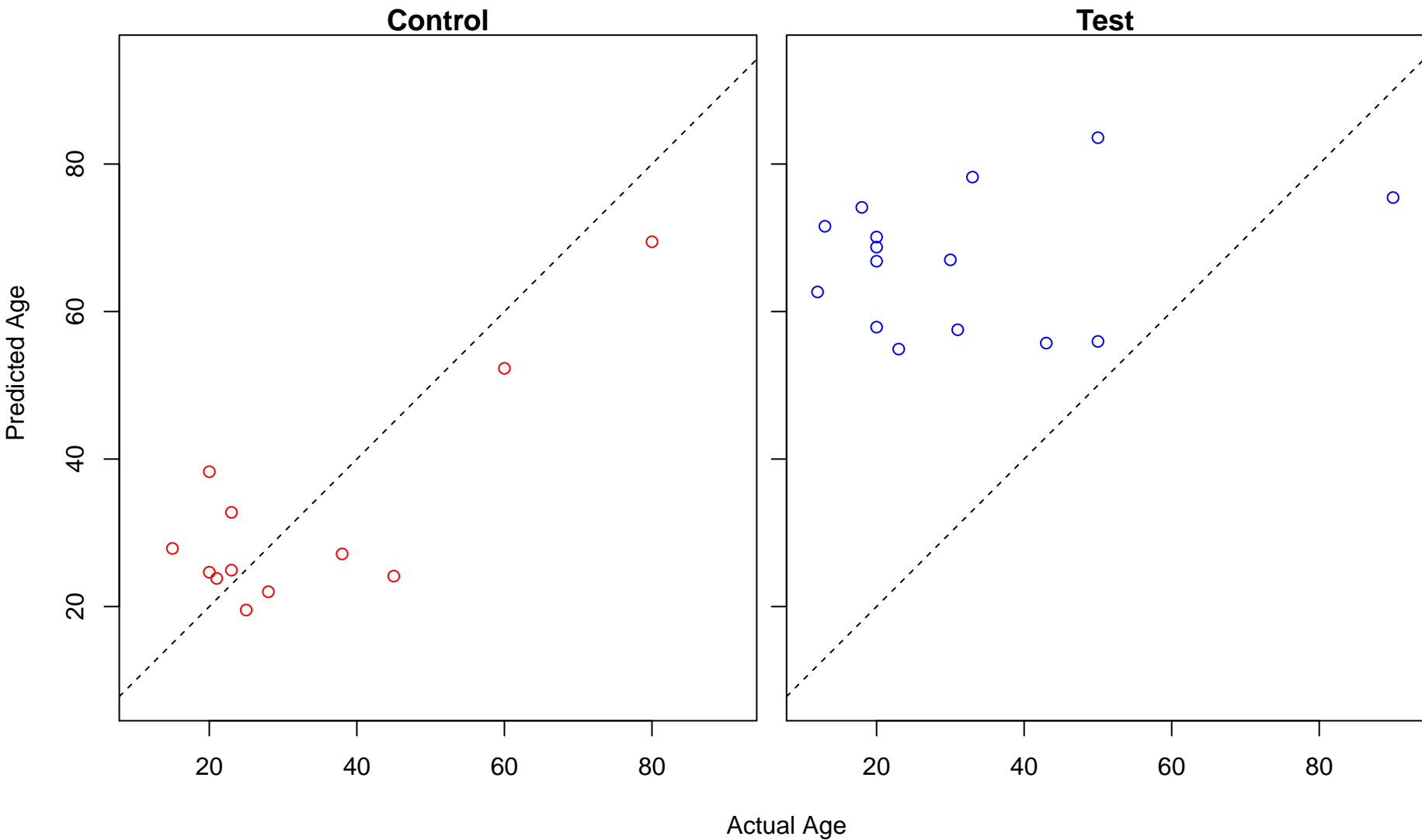
telencephalon glial cell migration (Score: 4.635023)



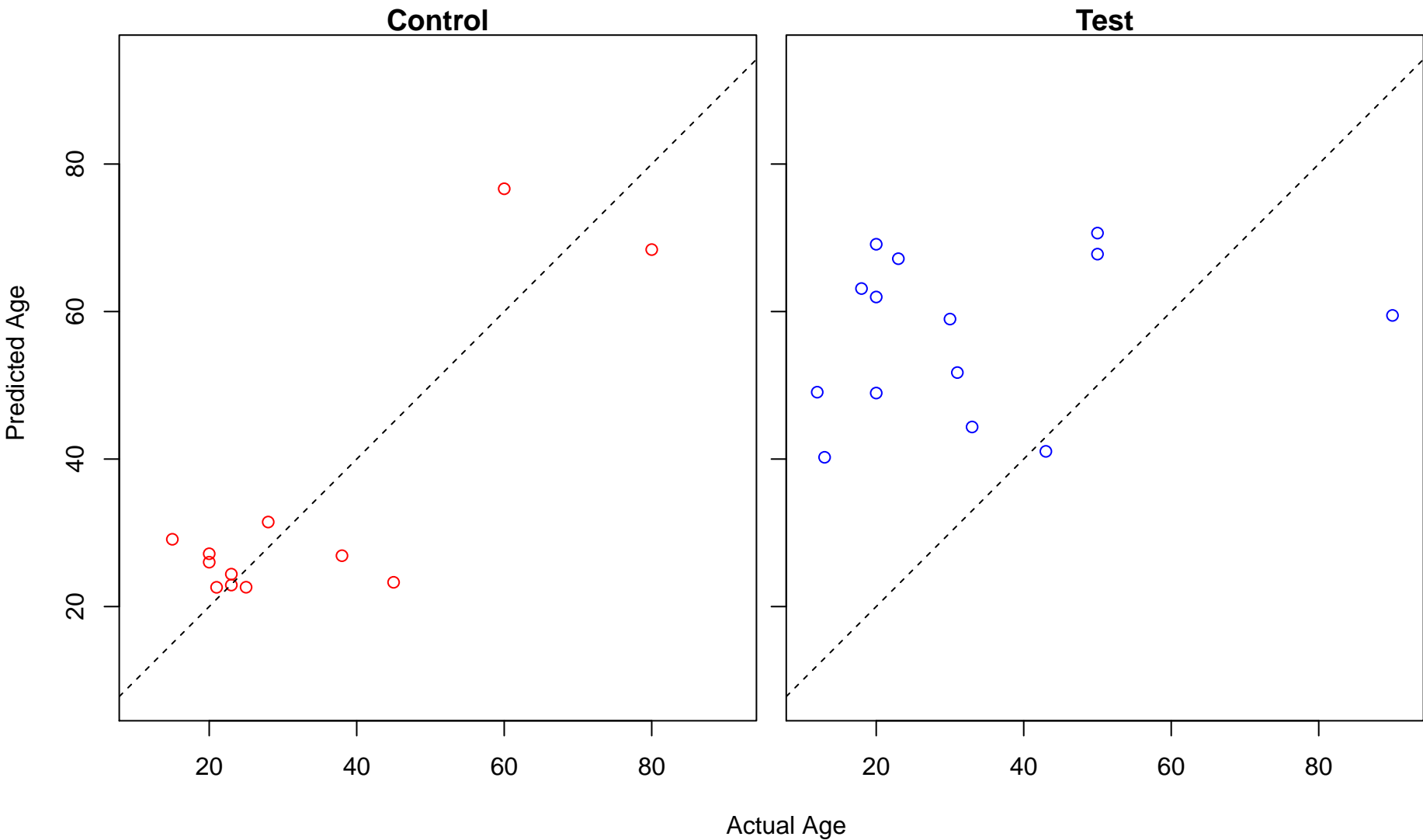
cellular response to nutrient levels (Score: 4.634702)



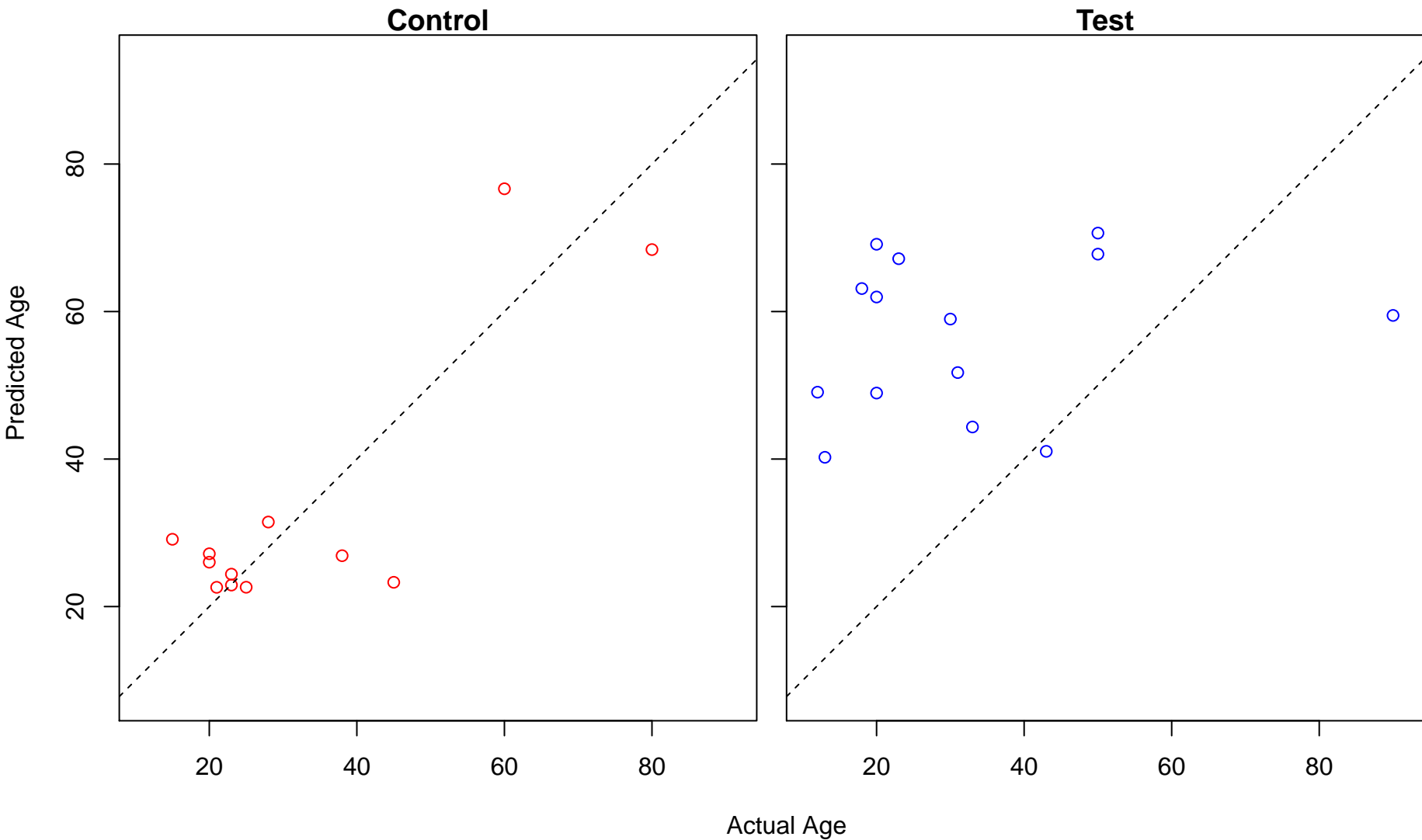
positive regulation of glycogen biosynthetic process (Score: 4.634171)



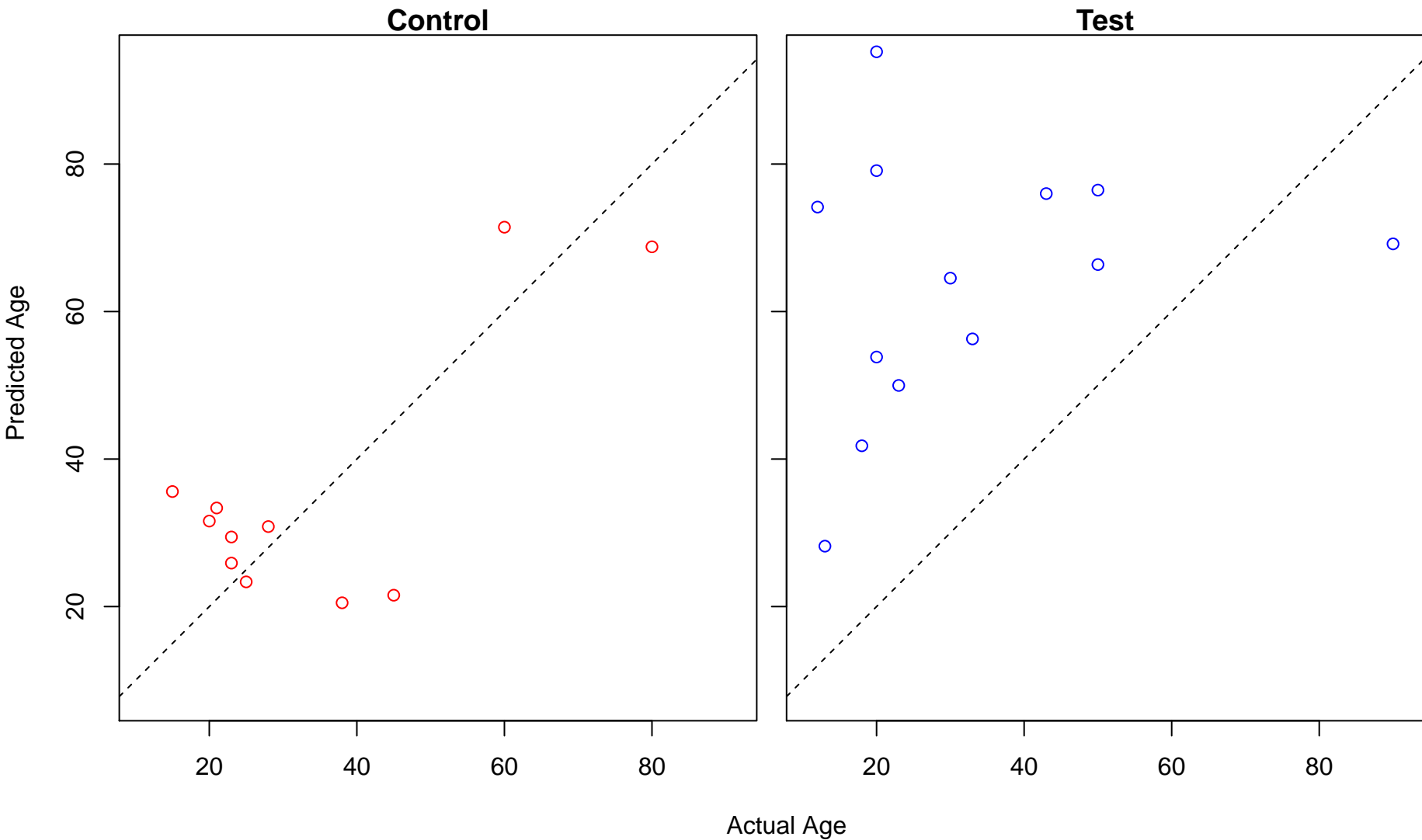
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (Score: 4.6331)



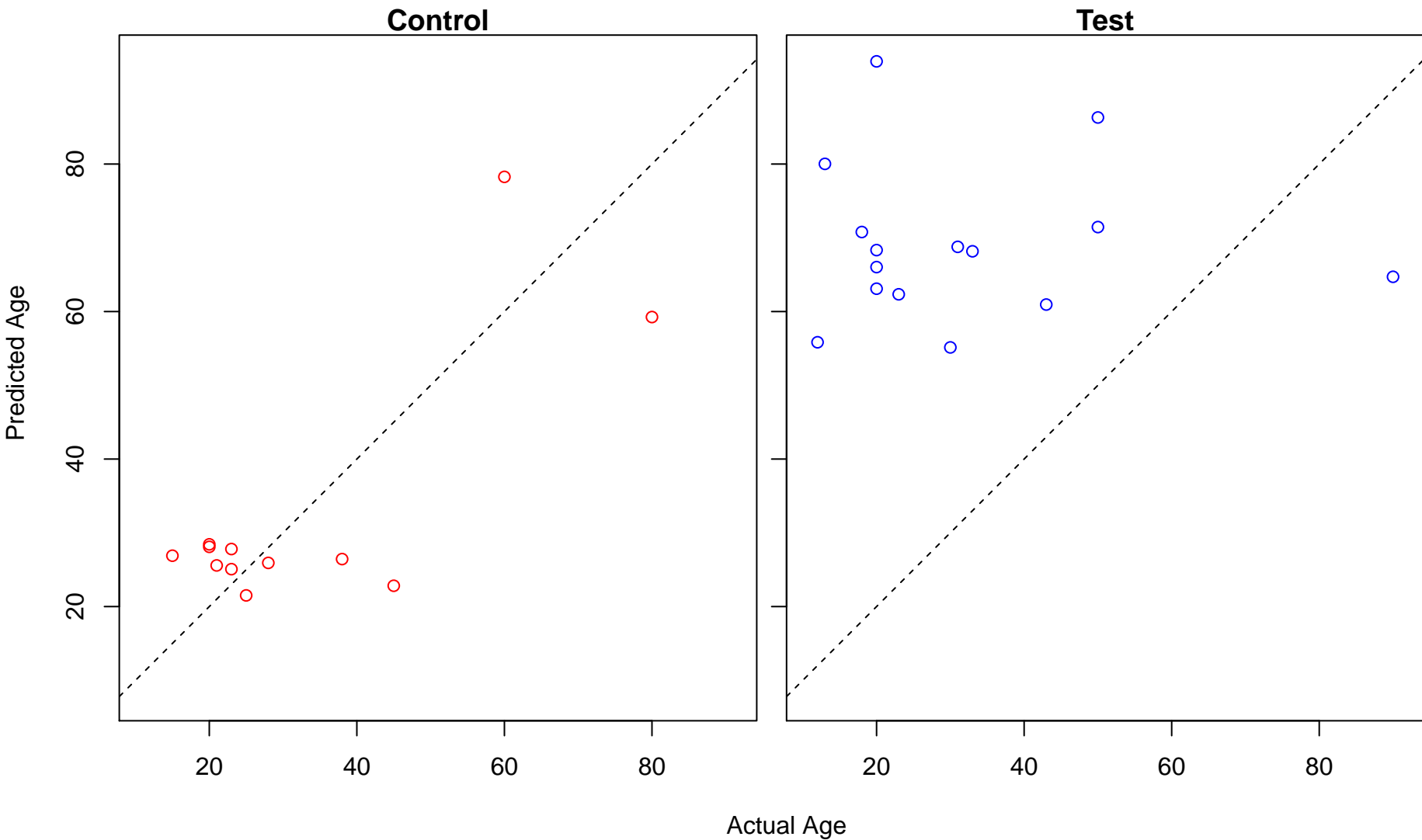
mRNA splicing, via spliceosome (Score: 4.633116)



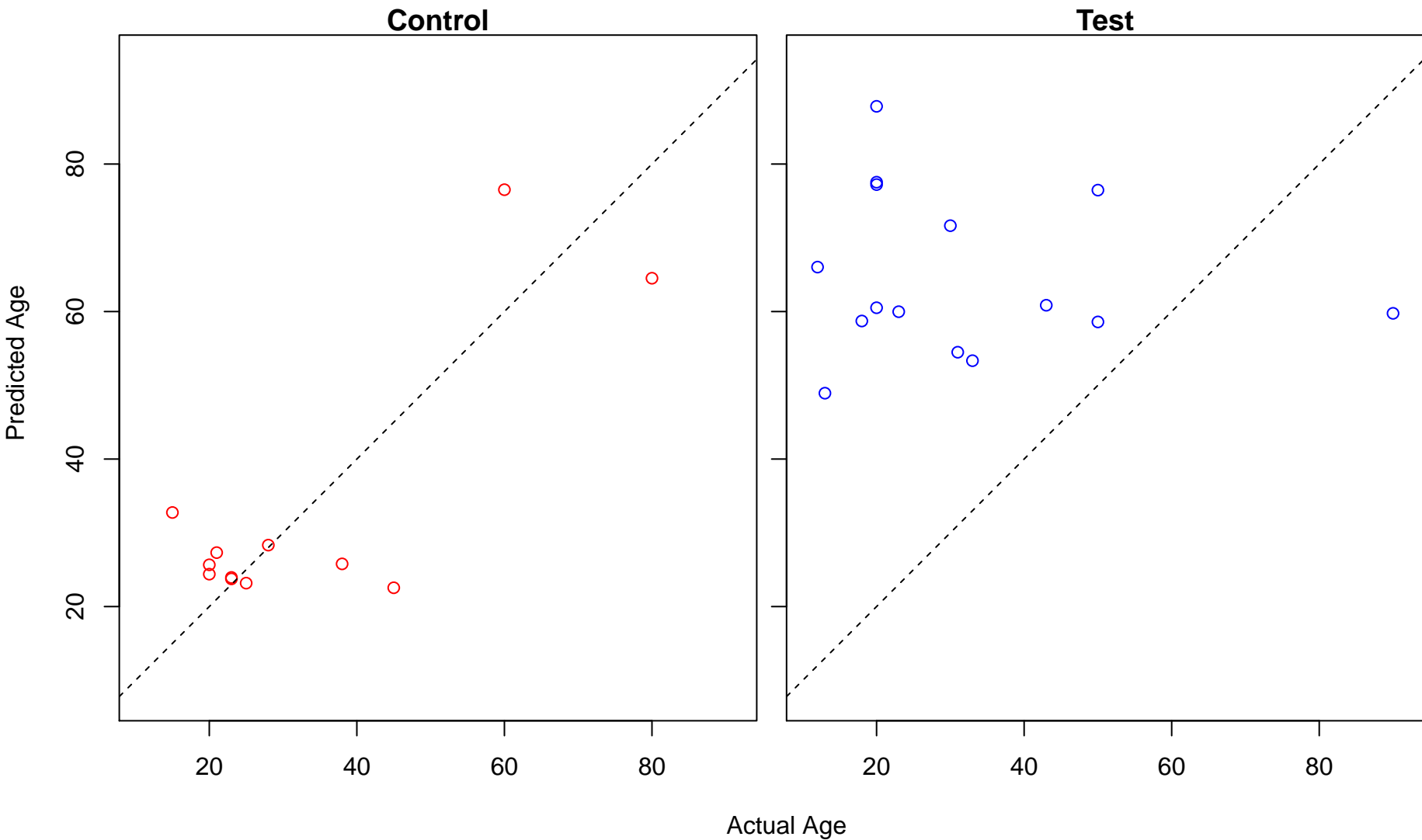
lymphocyte migration (Score: 4.632350)



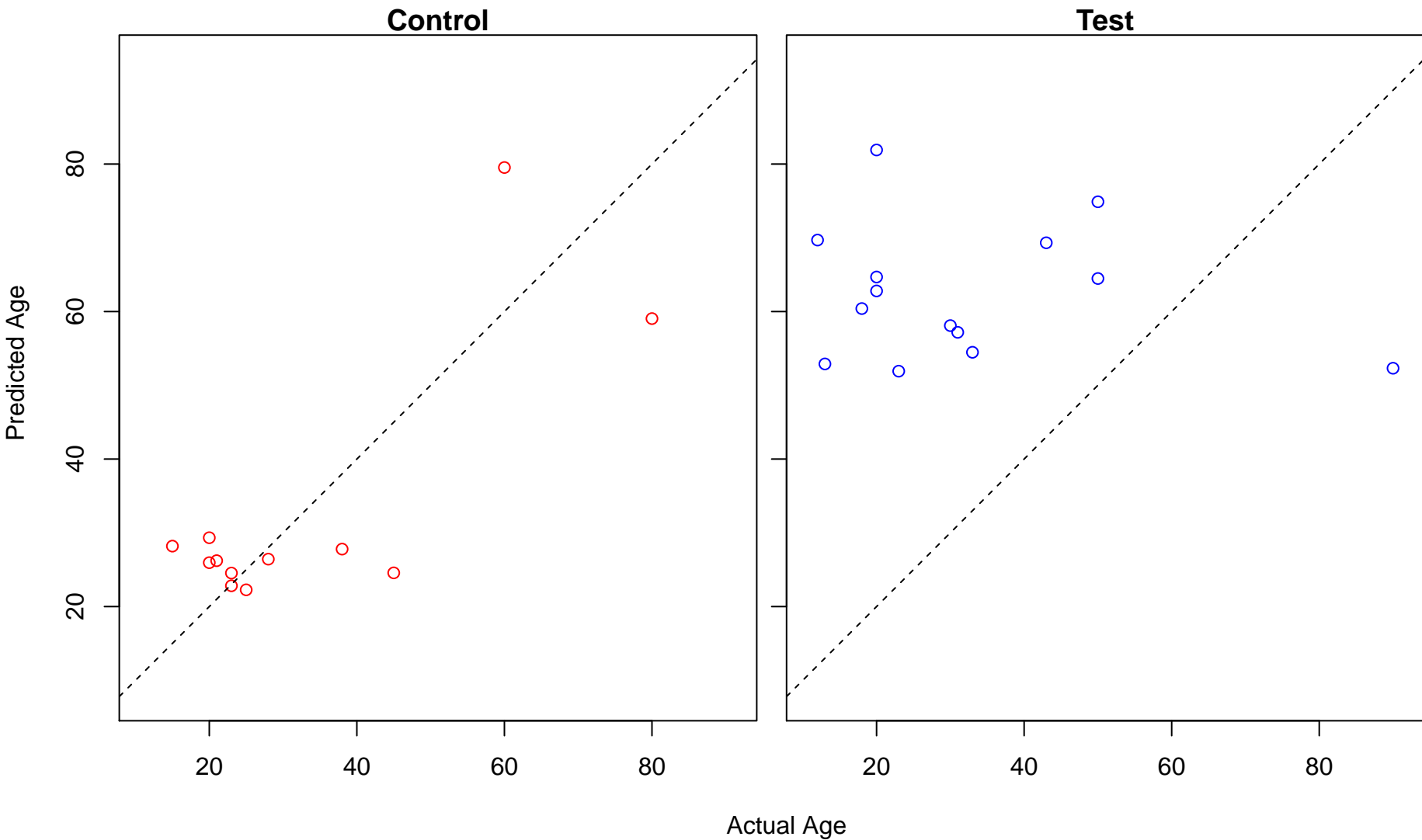
positive regulation of receptor activity (Score: 4.631306)



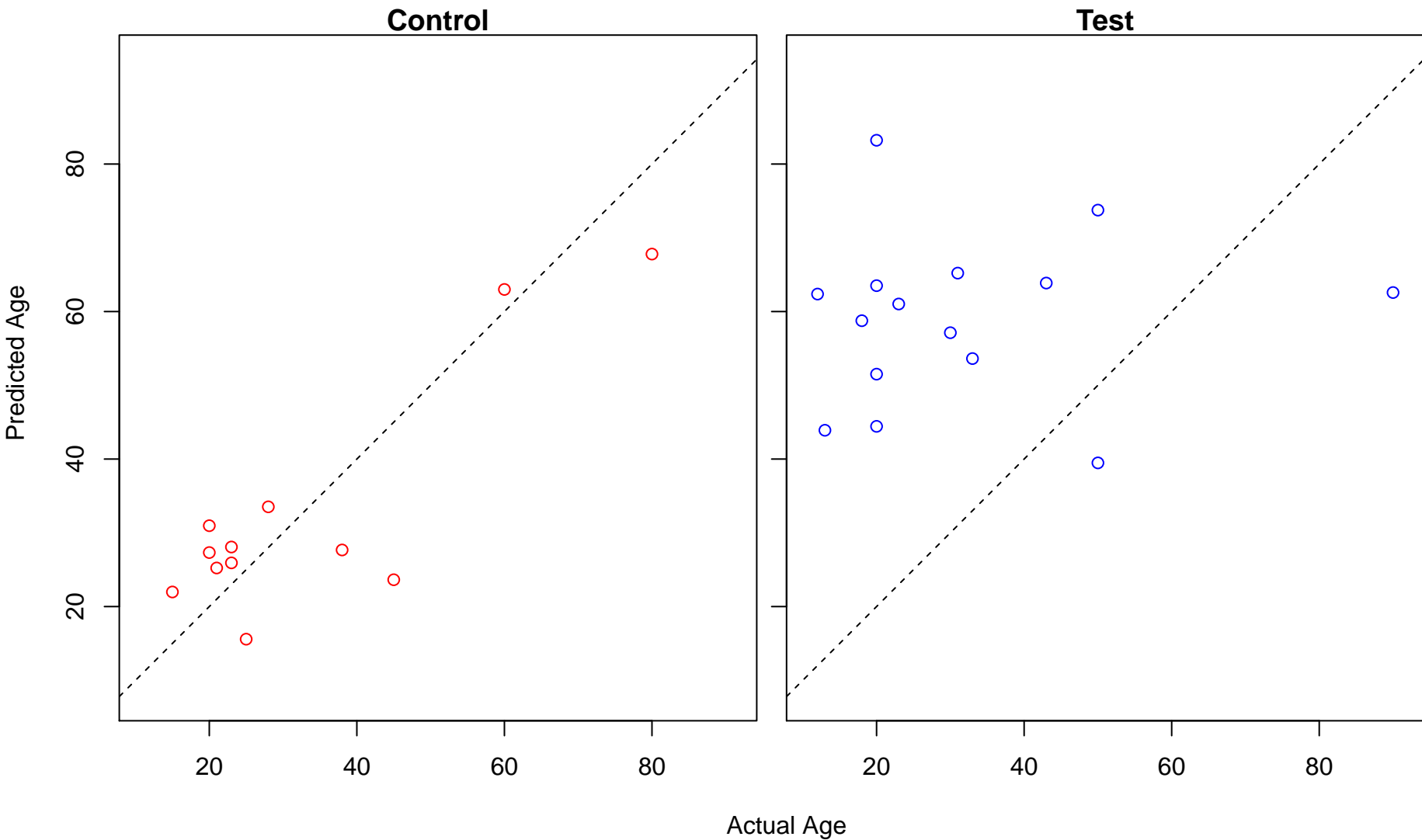
regulation of actin filament-based process (Score: 4.630395)



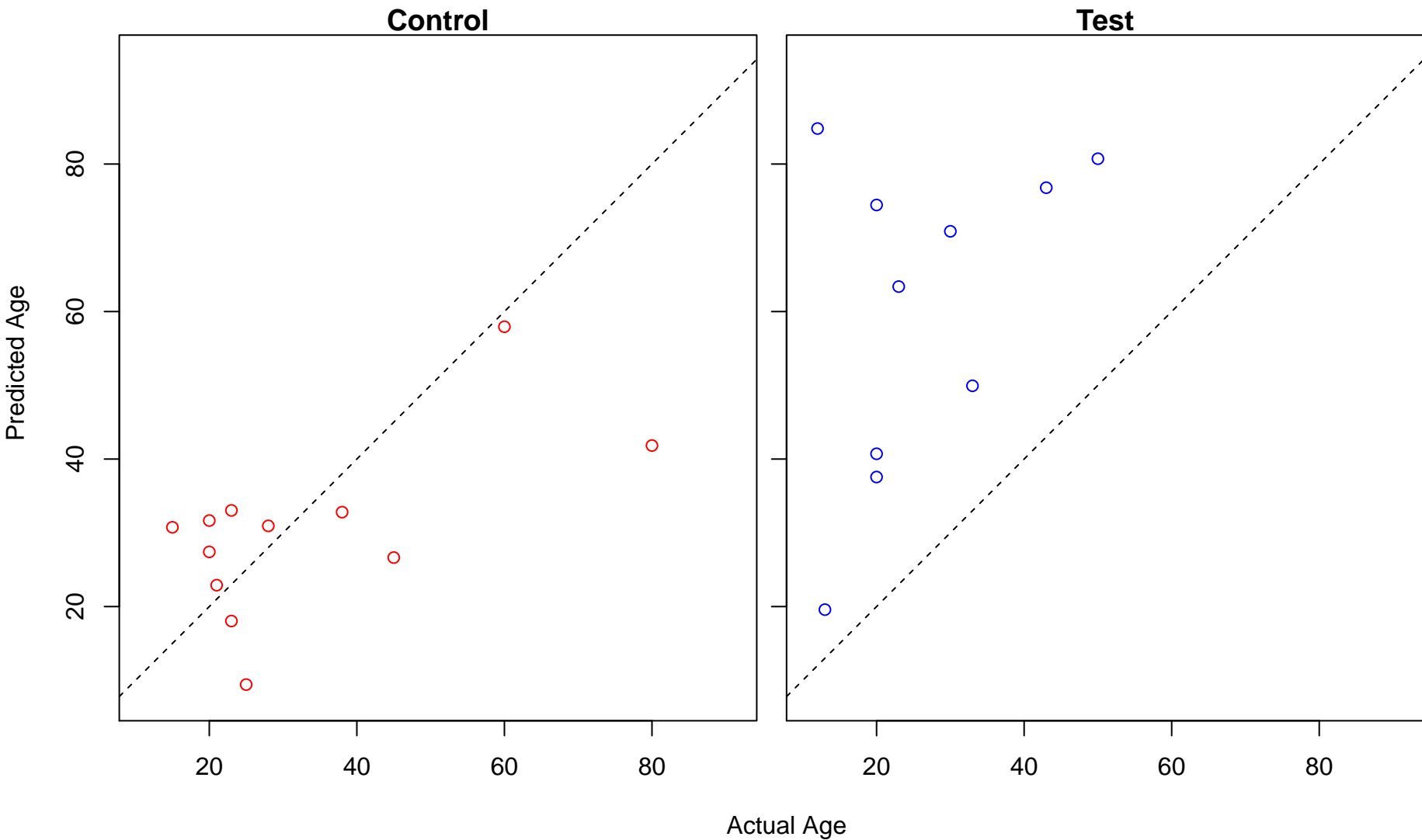
negative regulation of lipid biosynthetic process (Score: 4.628548)



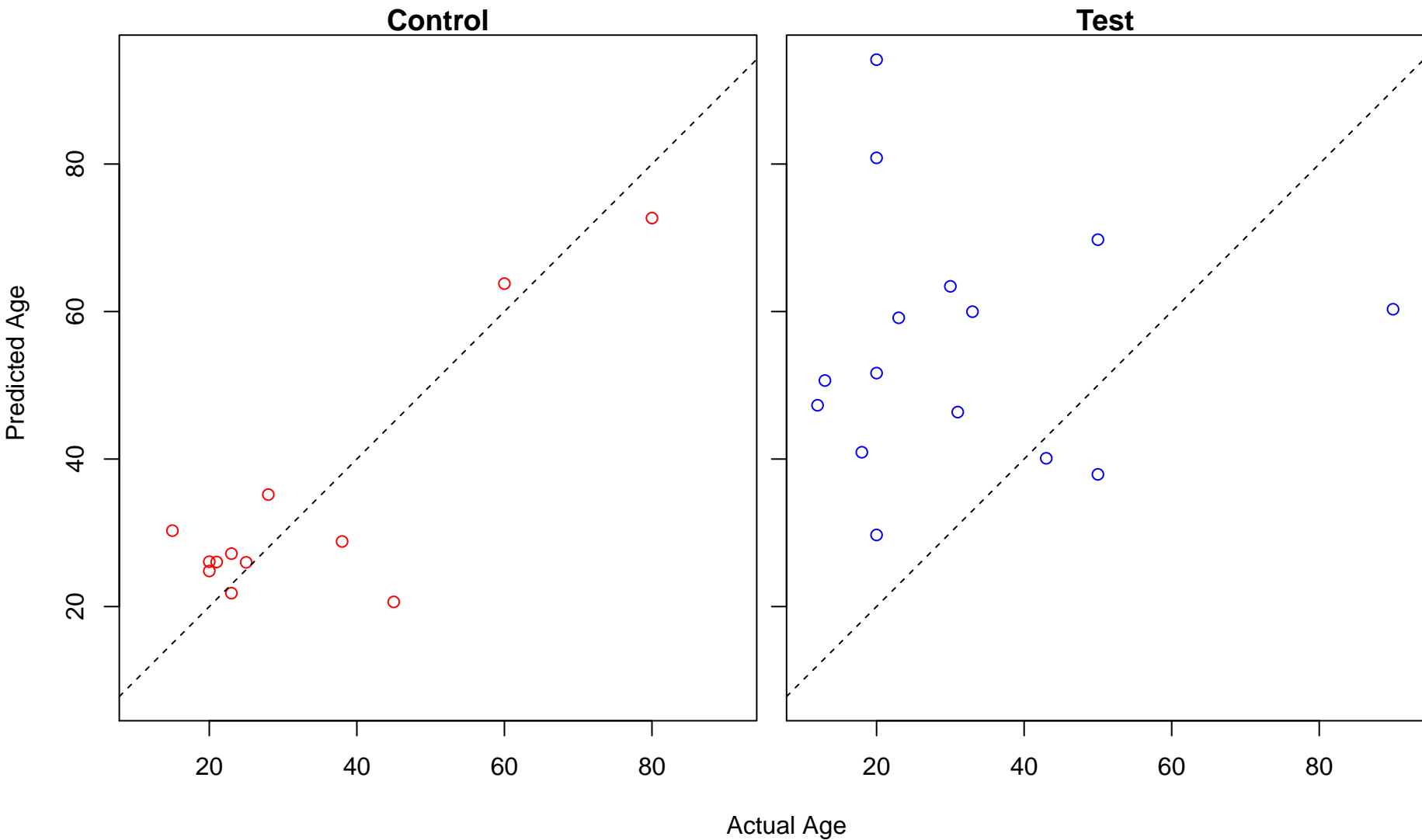
cerebral cortex radially oriented cell migration (Score: 4.626231)



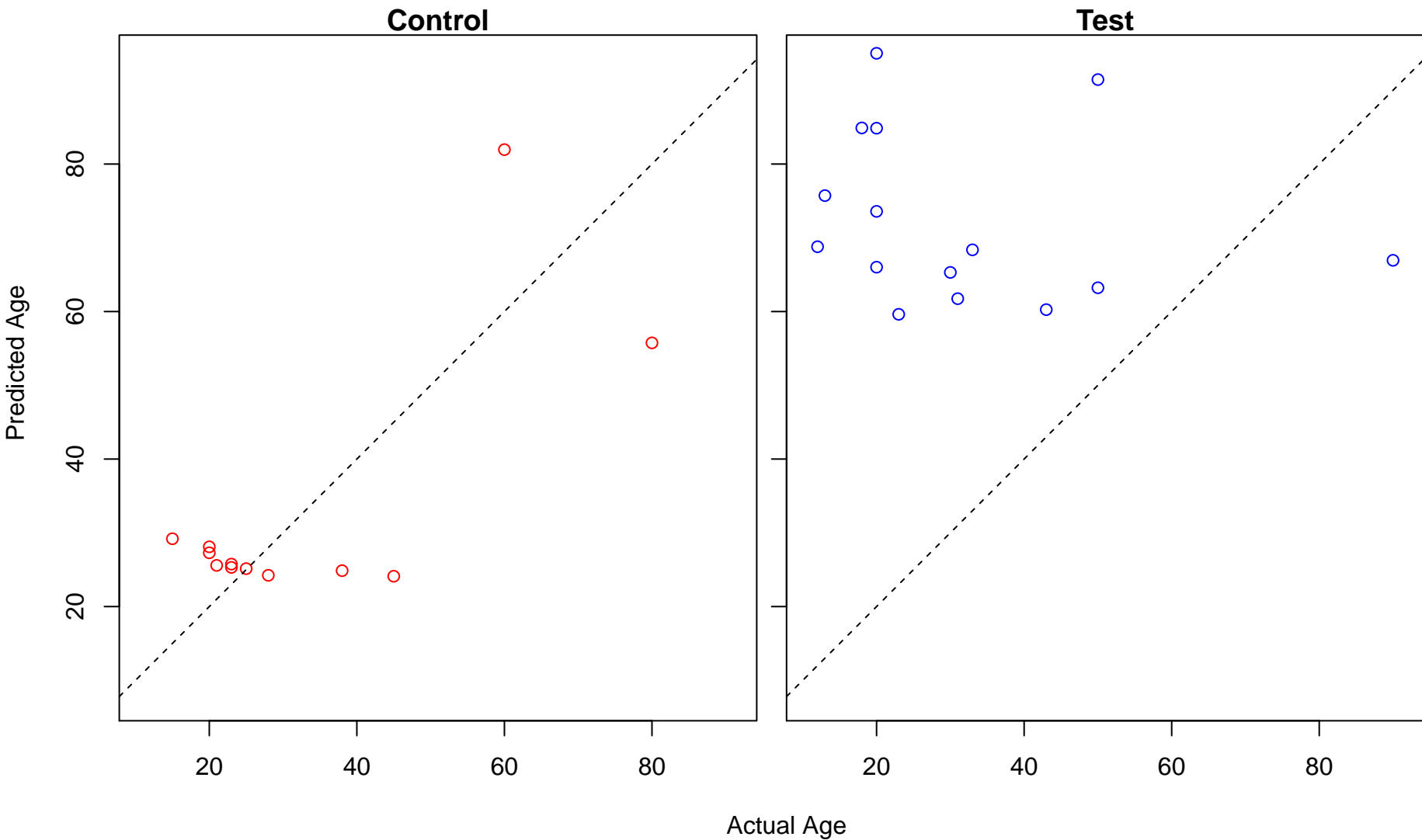
forebrain regionalization (Score: 4.625409)



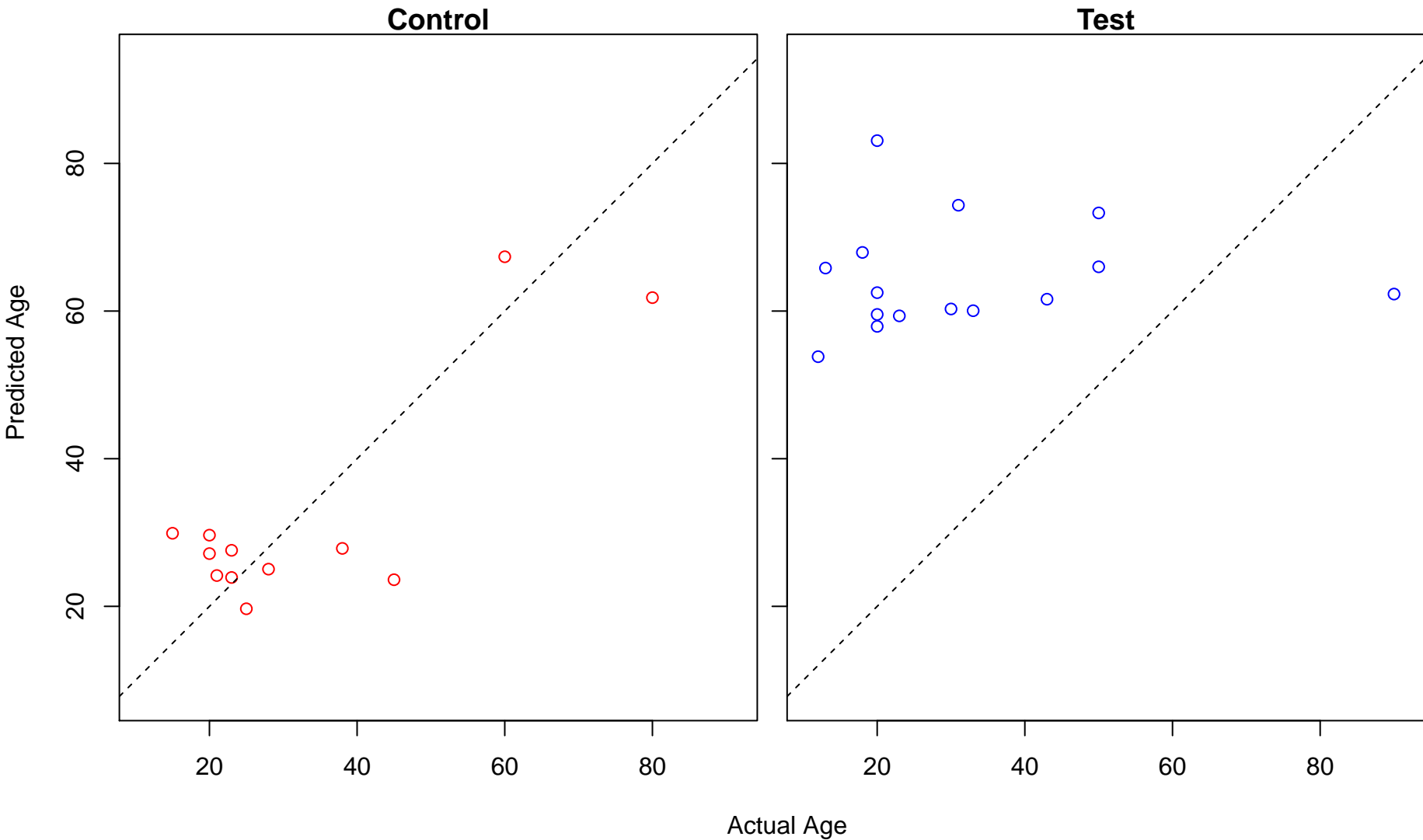
'de novo' protein folding (Score: 4.624261)



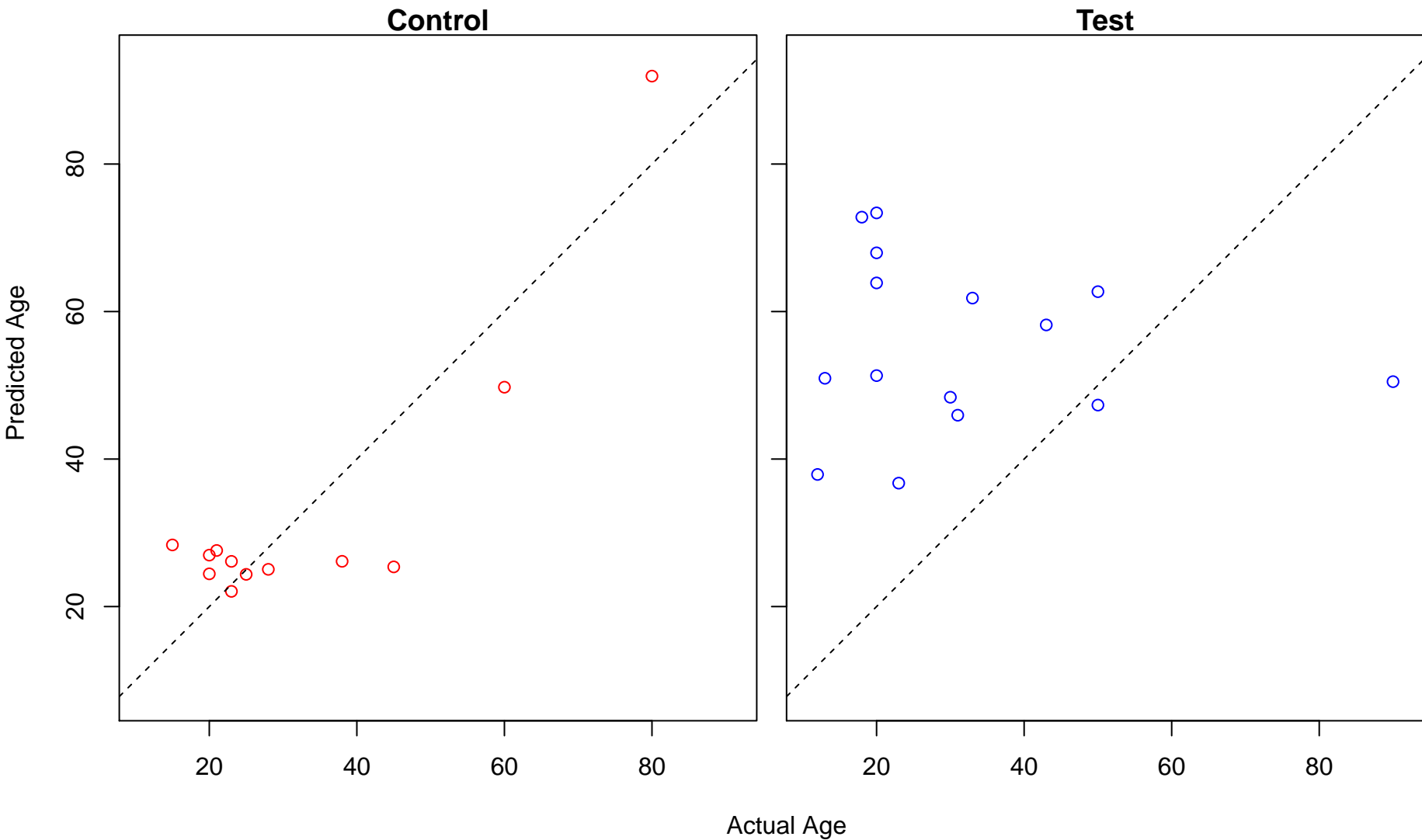
regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway (Score: 4.62305)



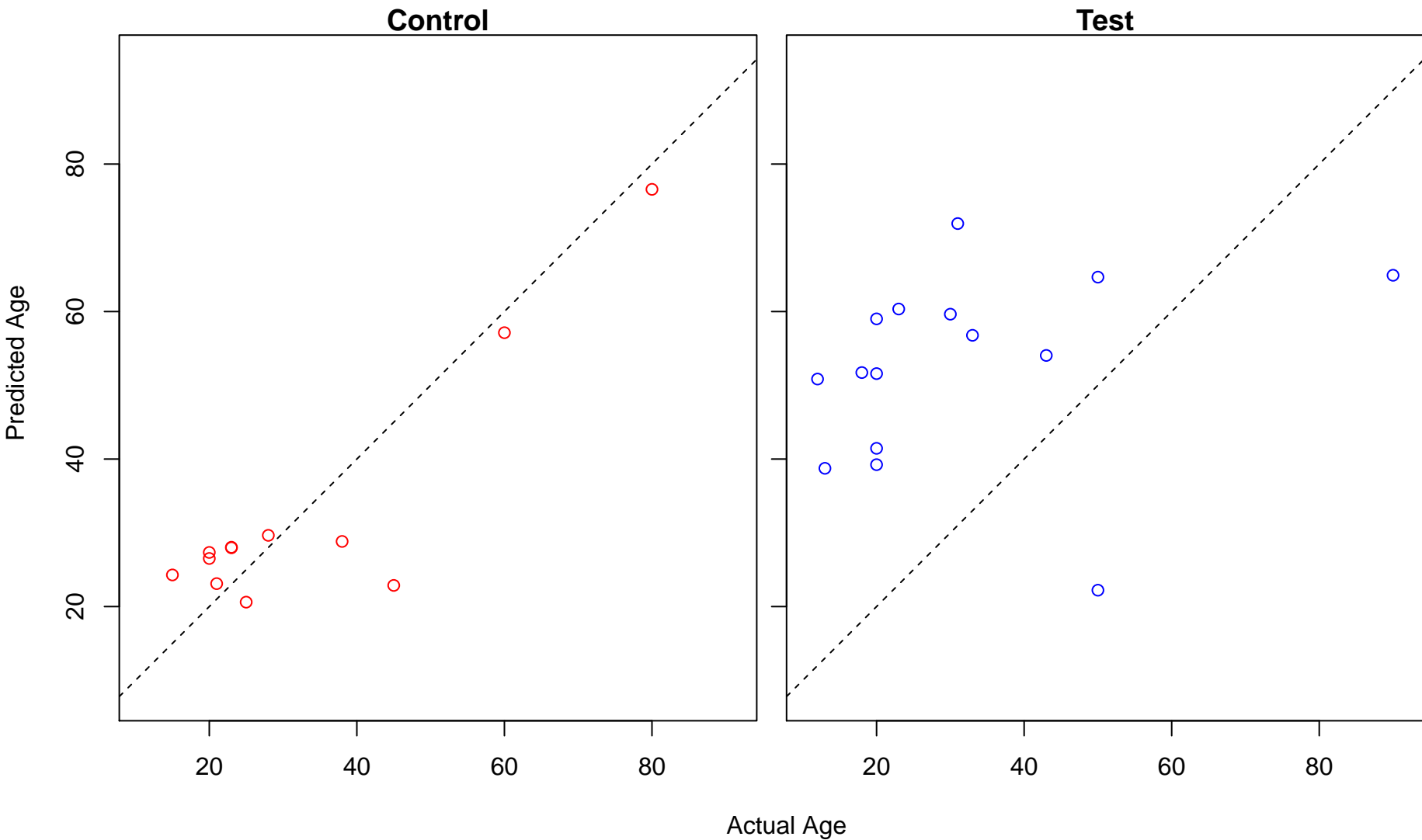
regulation of cation transmembrane transport (Score: 4.620864)



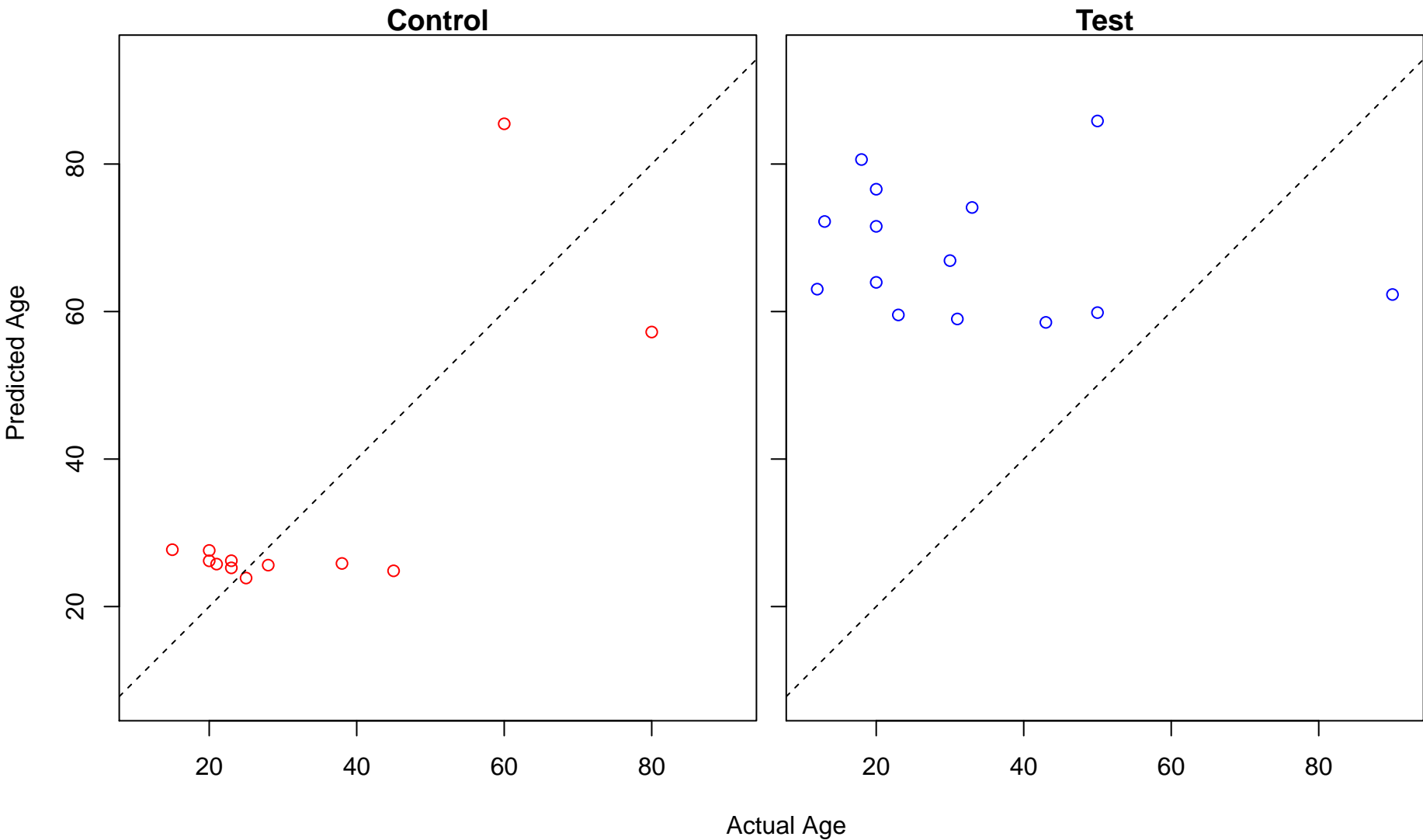
Golgi localization (Score: 4.619717)



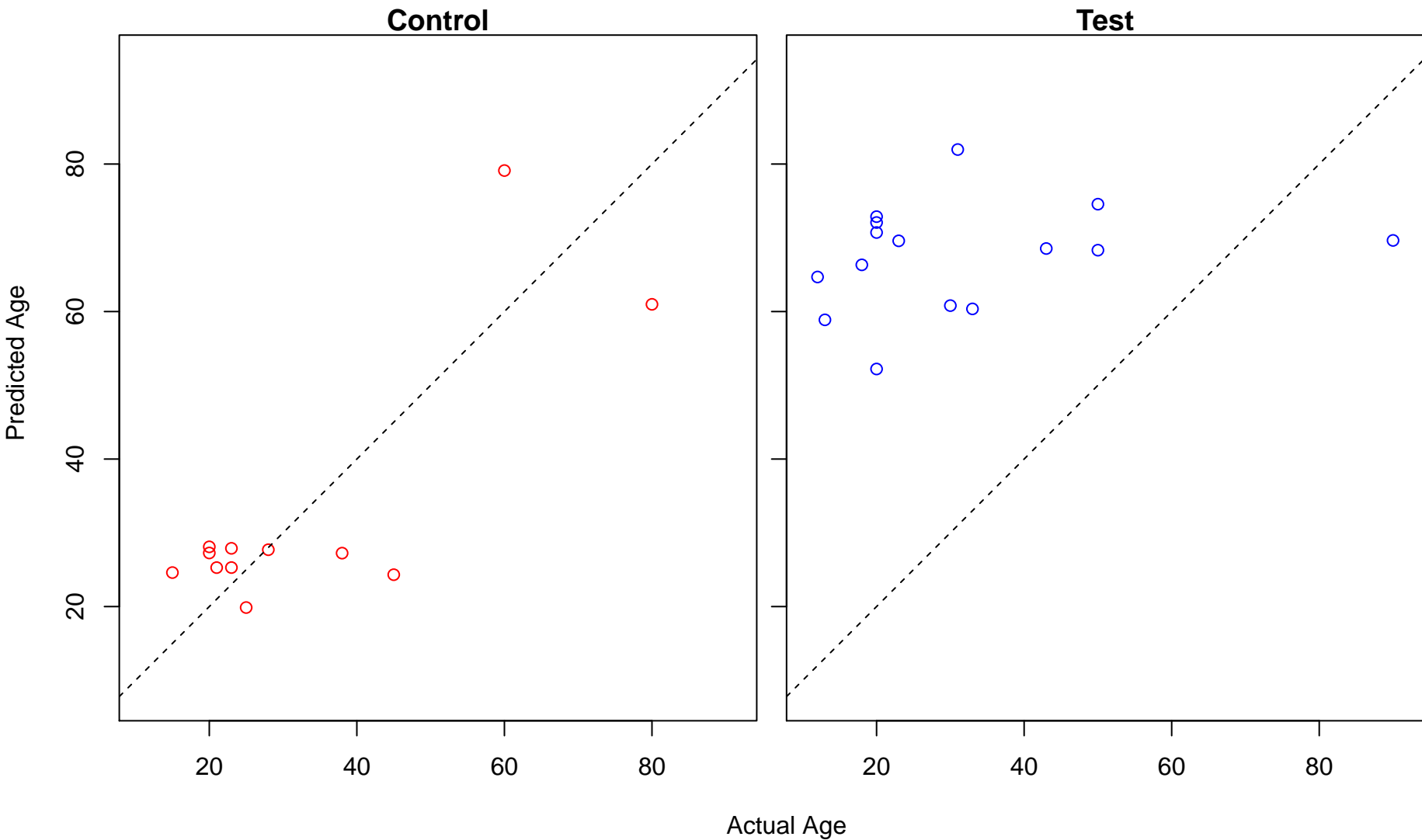
negative regulation of intracellular protein transport (Score: 4.616945)



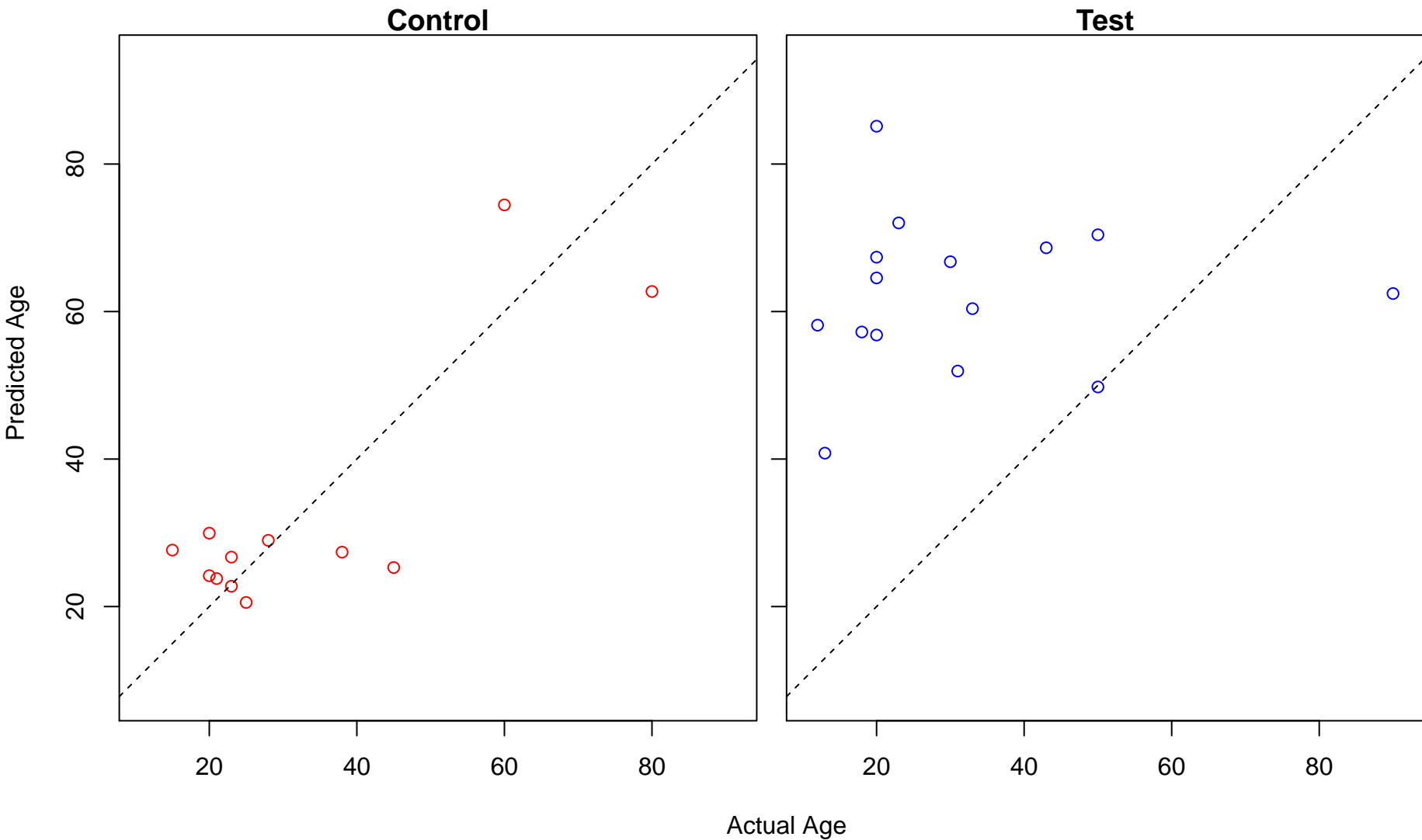
The regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (S



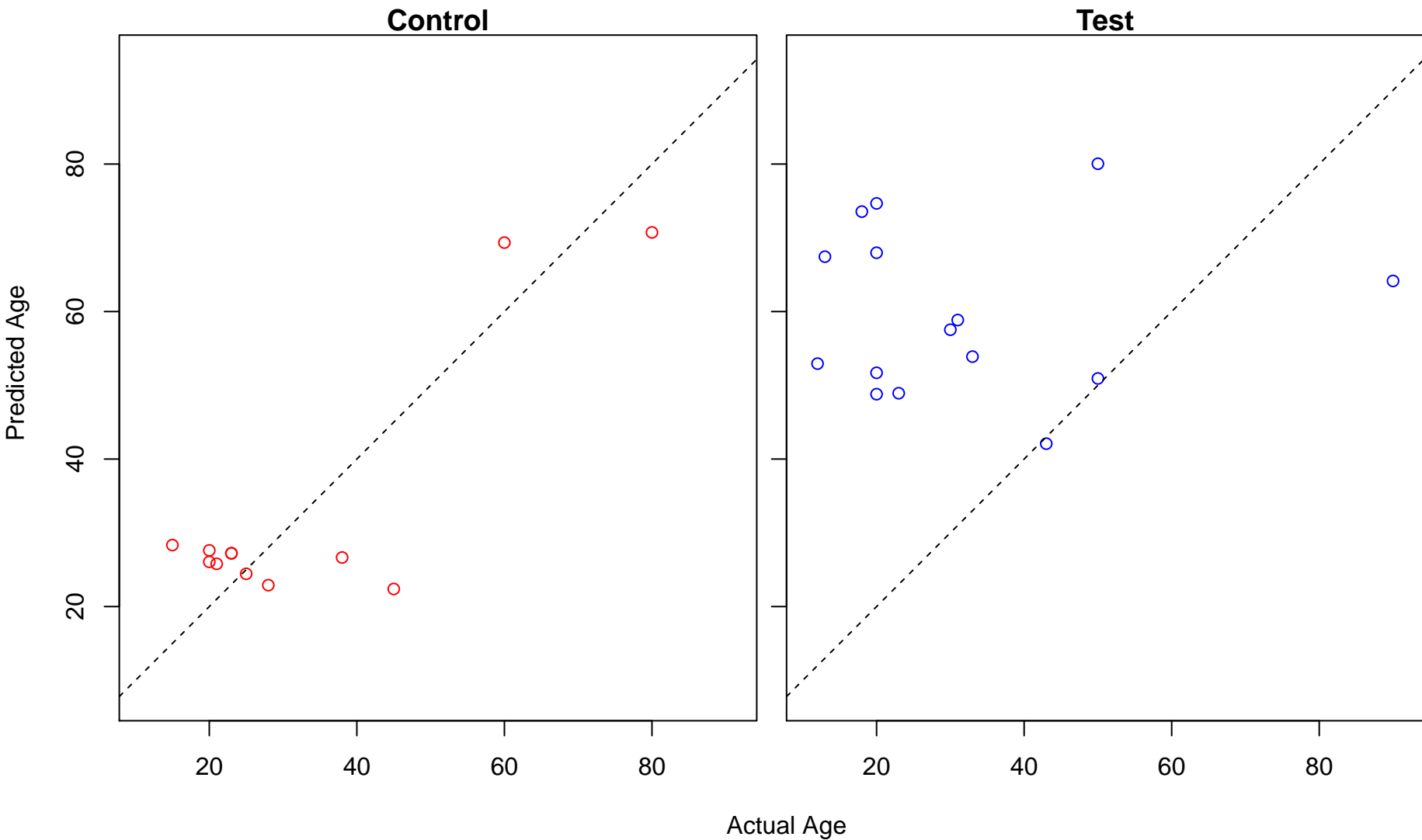
establishment of protein localization to mitochondrial membrane (Score: 4.615735)



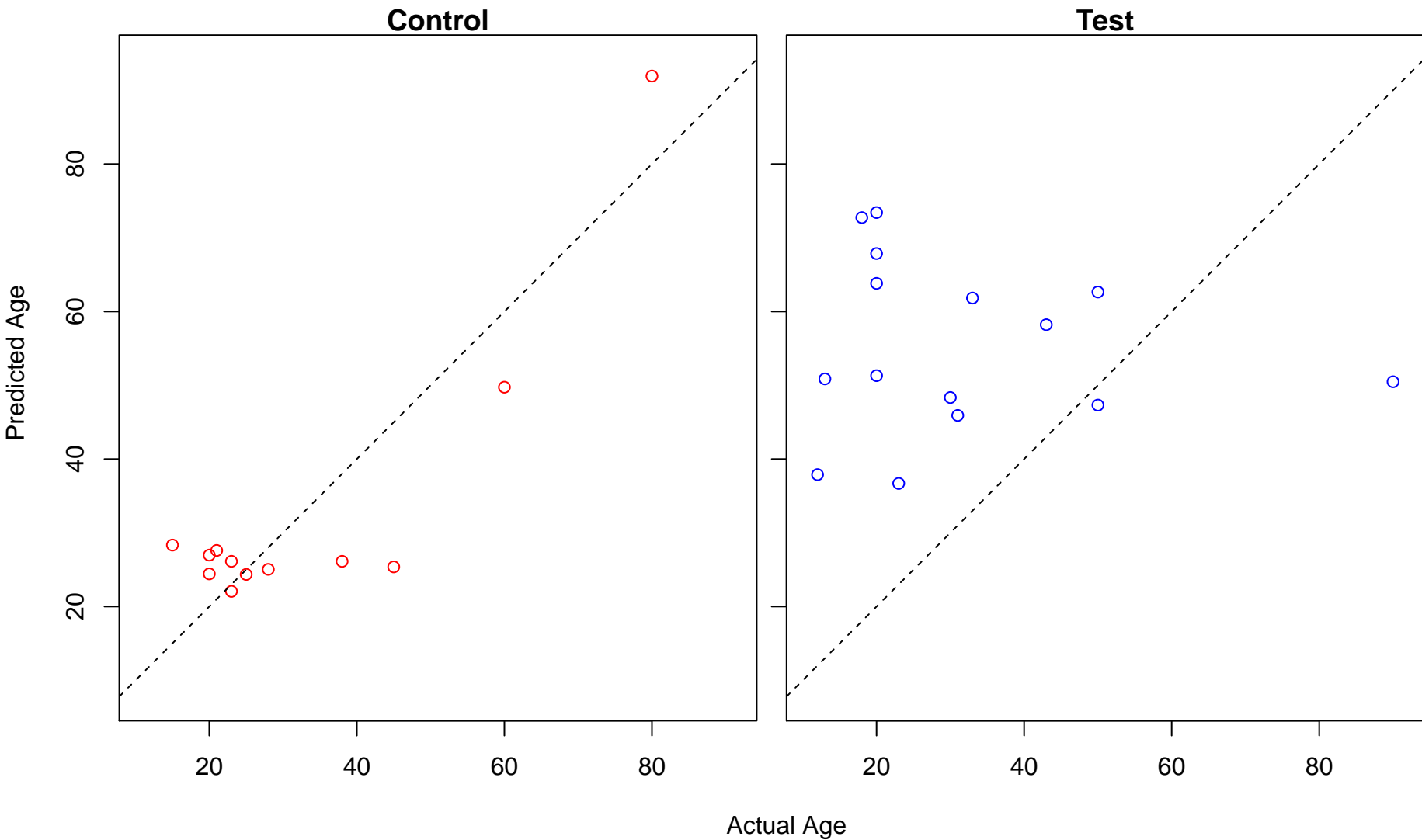
somitogenesis (Score: 4.614743)



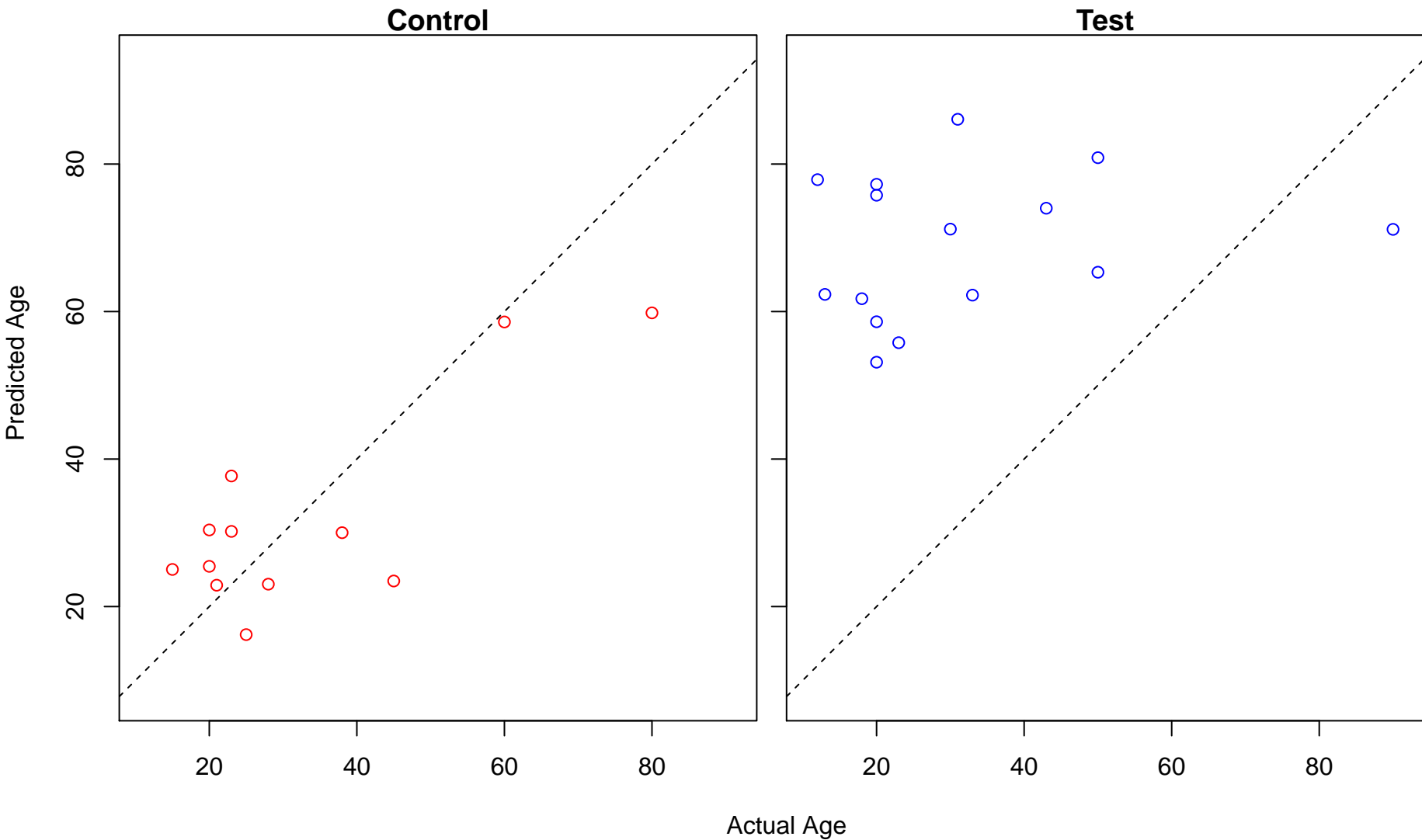
regulation of proteasomal protein catabolic process (Score: 4.614594)



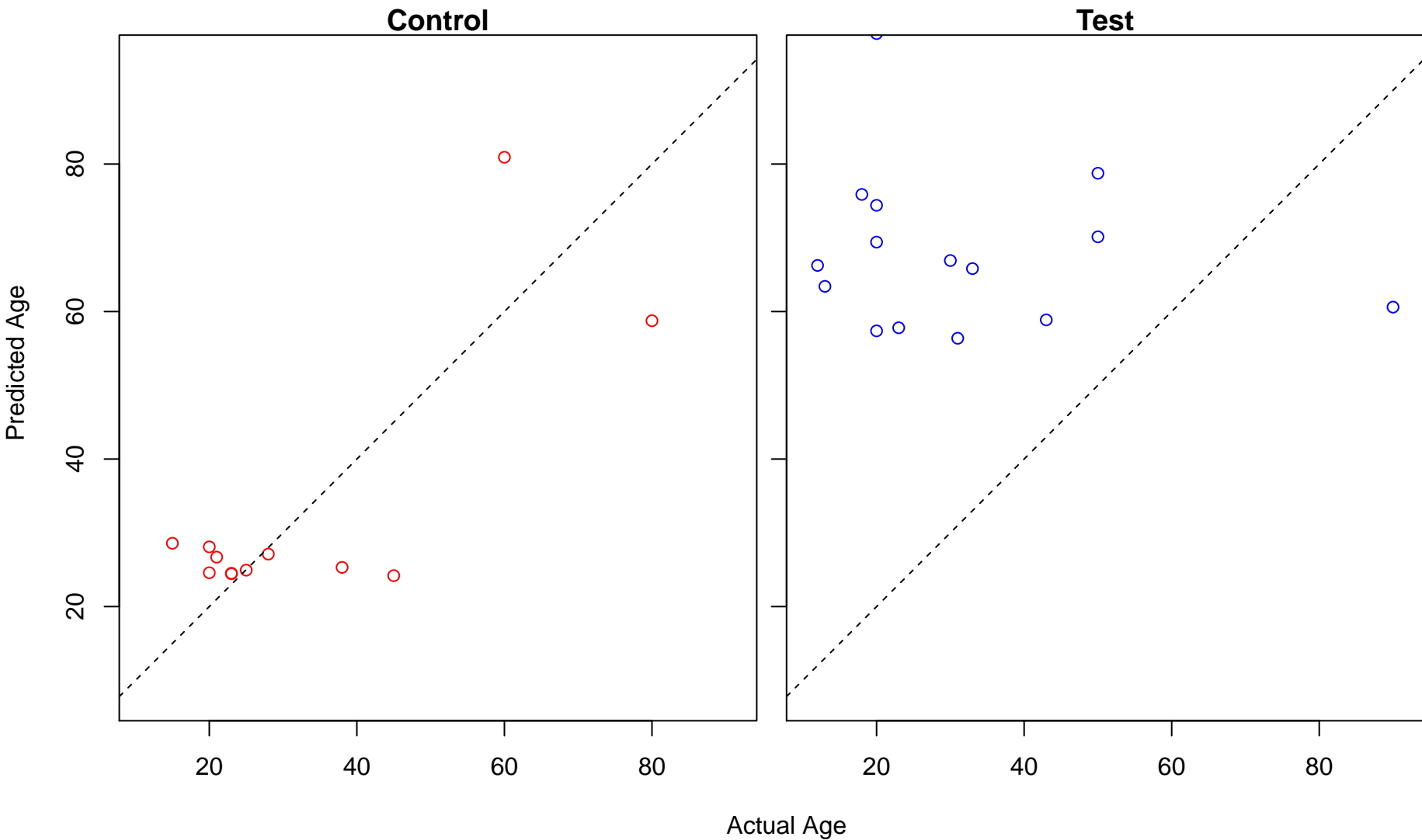
establishment of Golgi localization (Score: 4.613772)



iron ion import (Score: 4.612314)

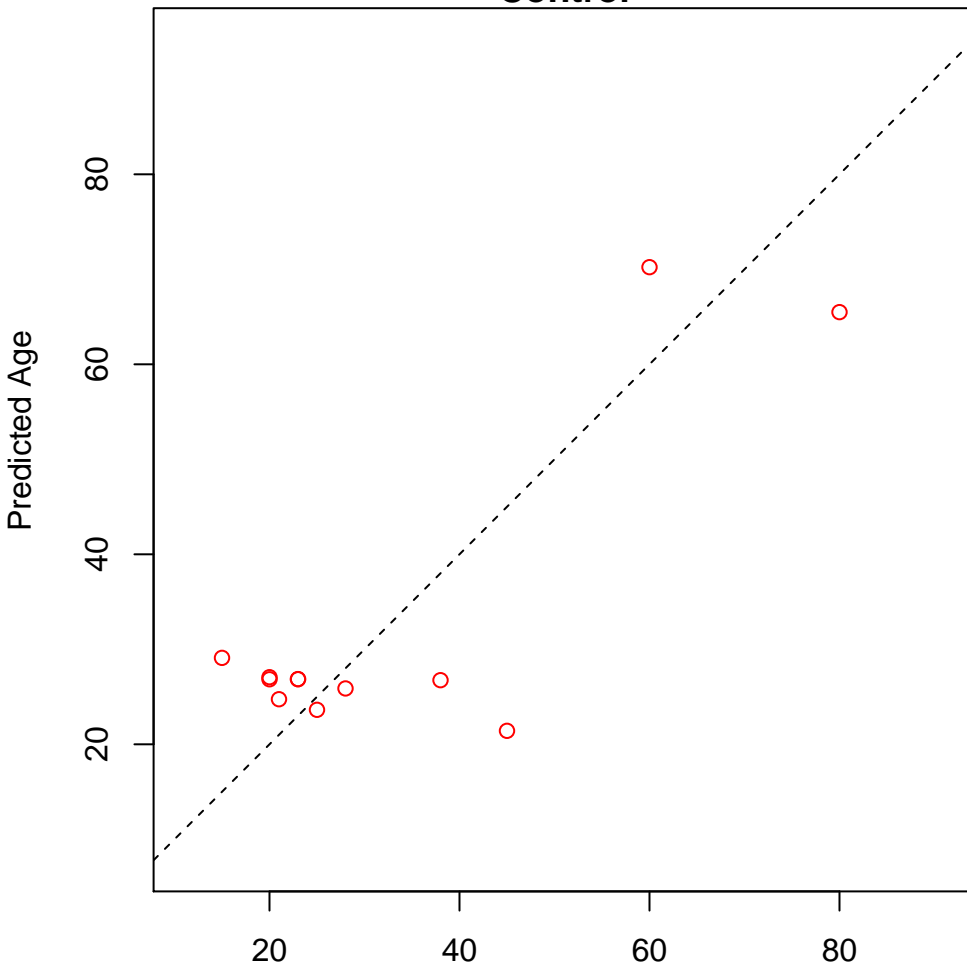


positive regulation of actin filament bundle assembly (Score: 4.611248)

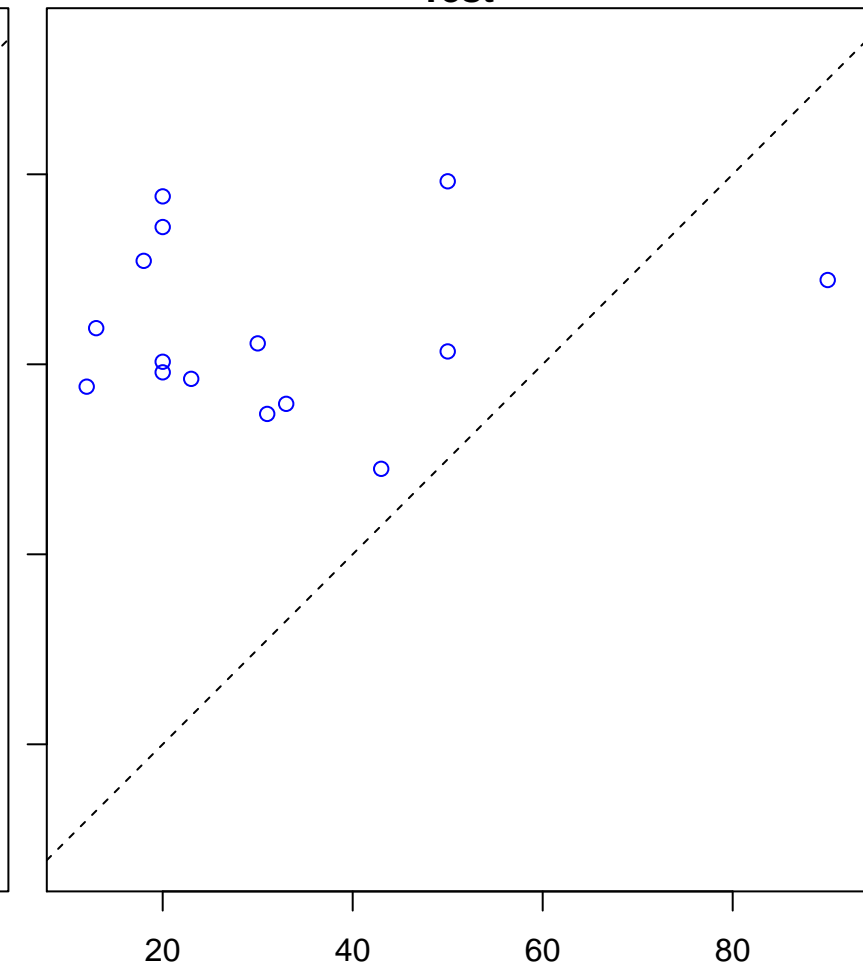


regulation of cellular catabolic process (Score: 4.61195)

Control

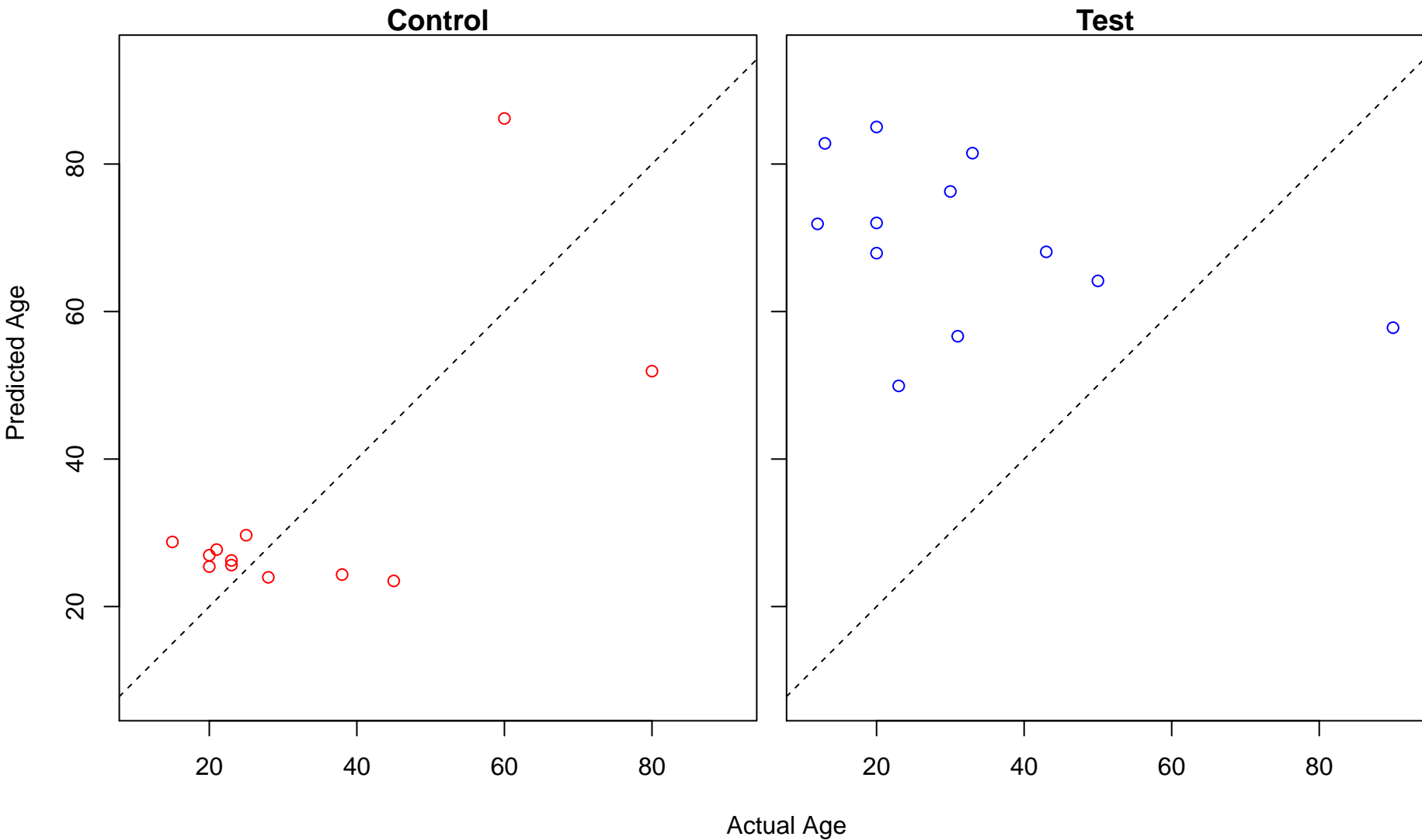


Test

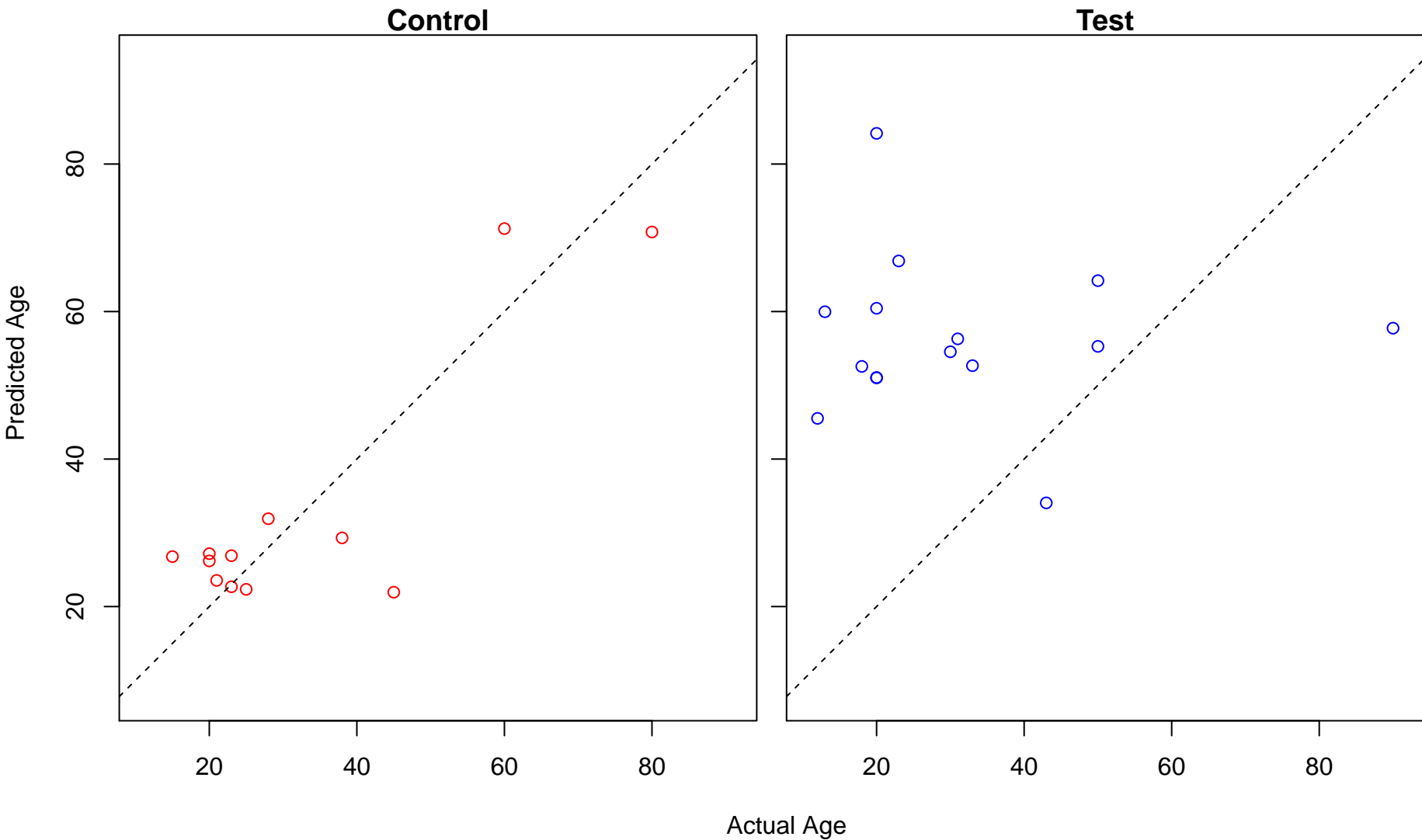


Actual Age

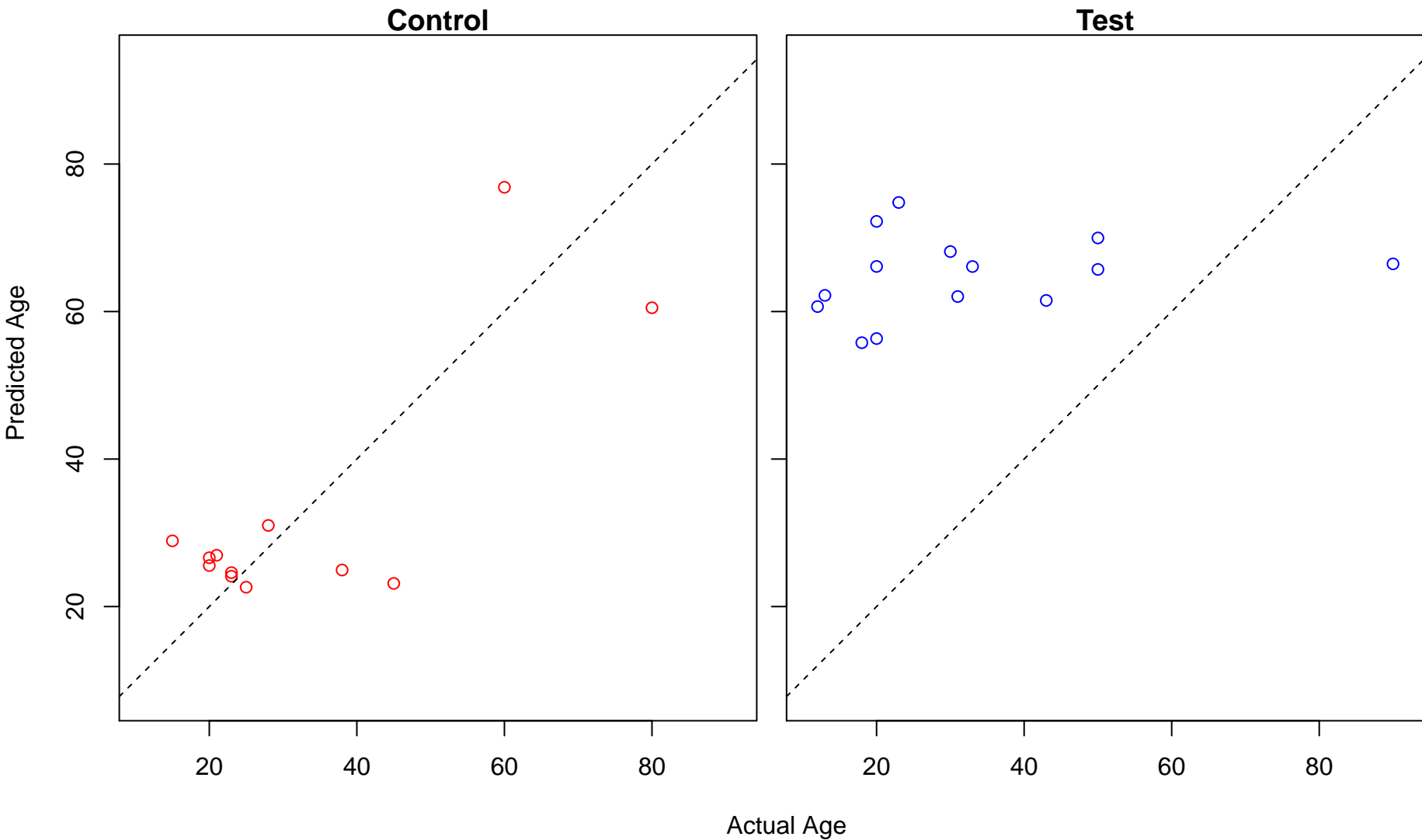
negative regulation of calcium-mediated signaling (Score: 4.610441)



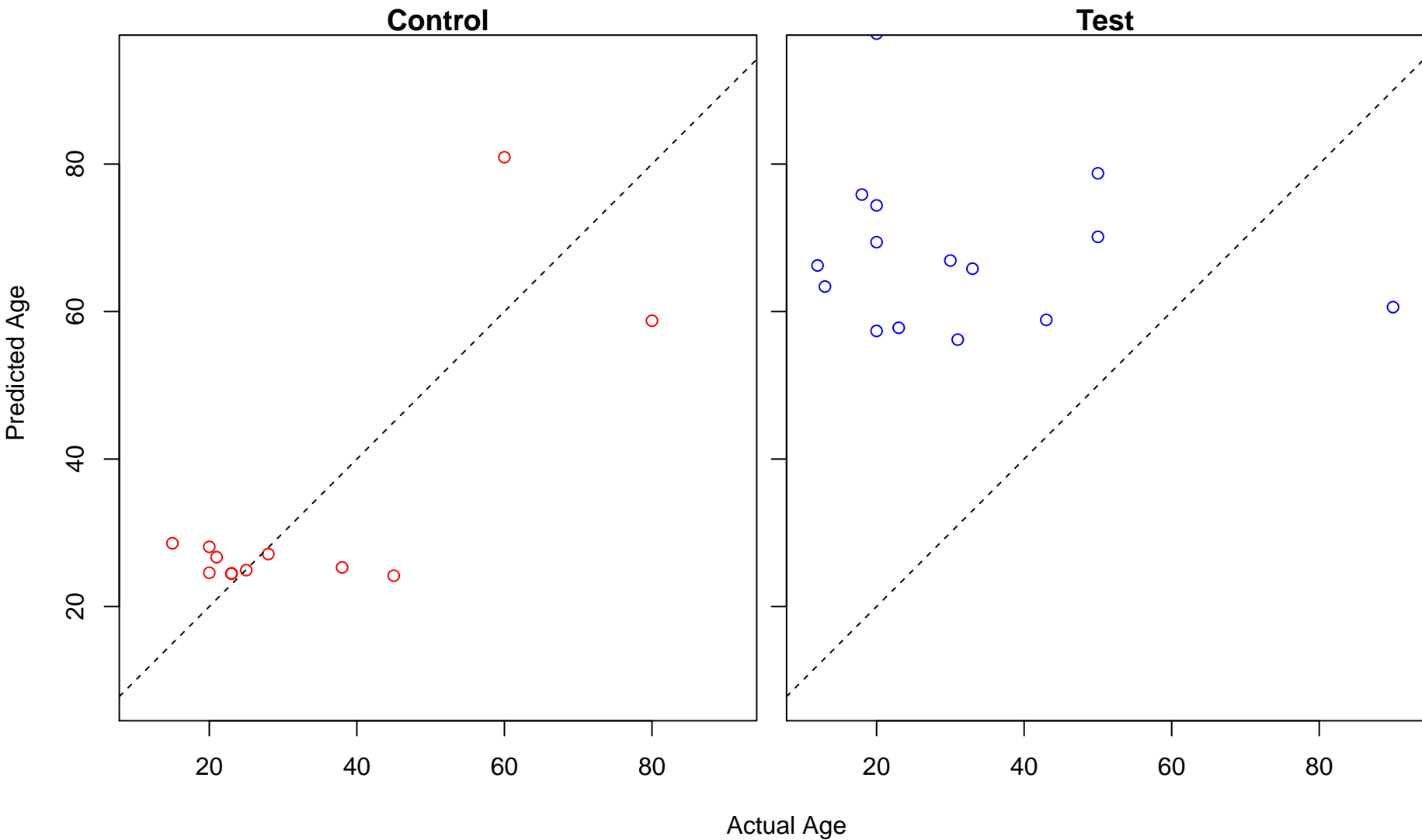
protein folding (Score: 4.609628)



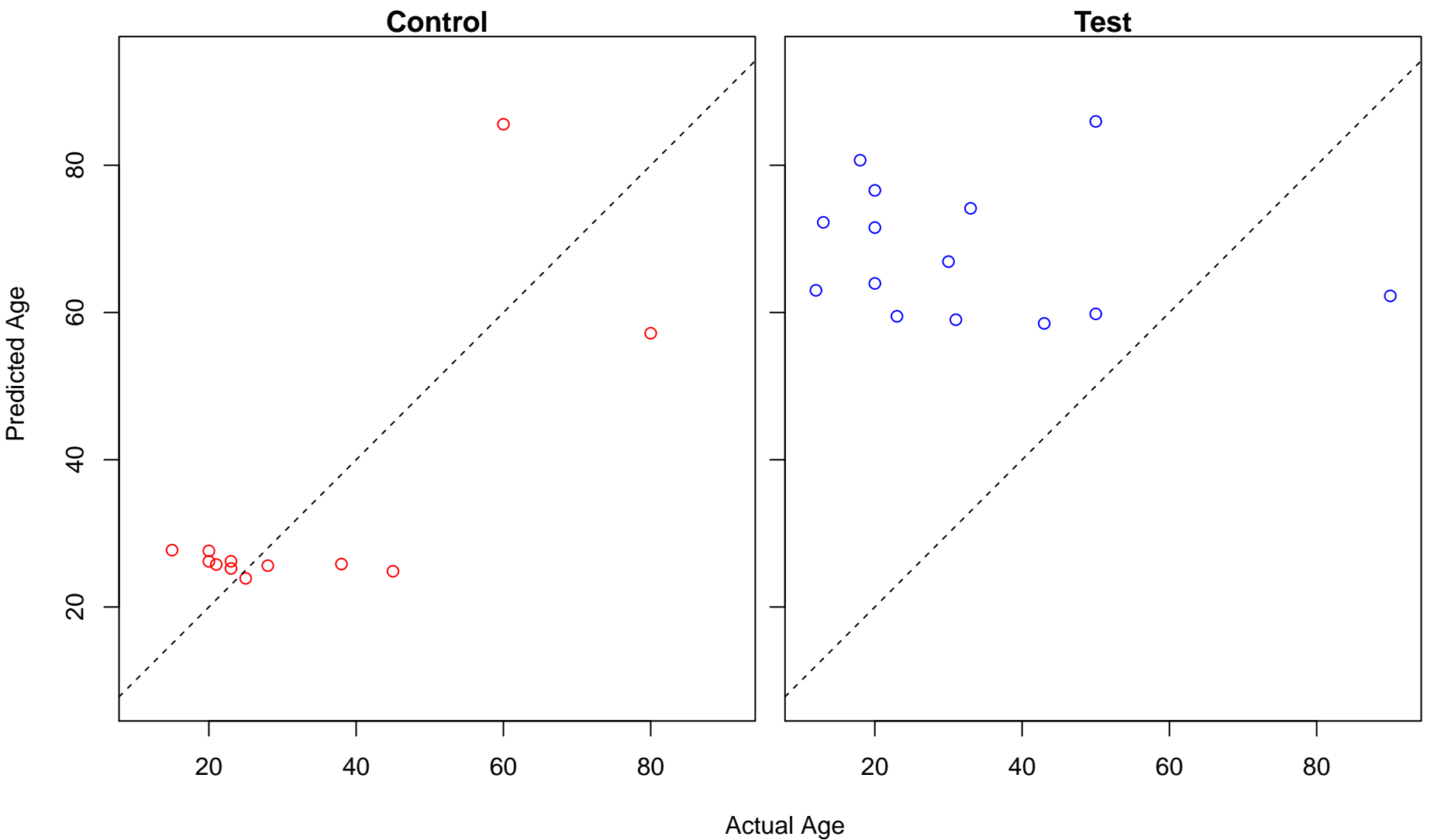
positive regulation of metalloenzyme activity (Score: 4.609236)



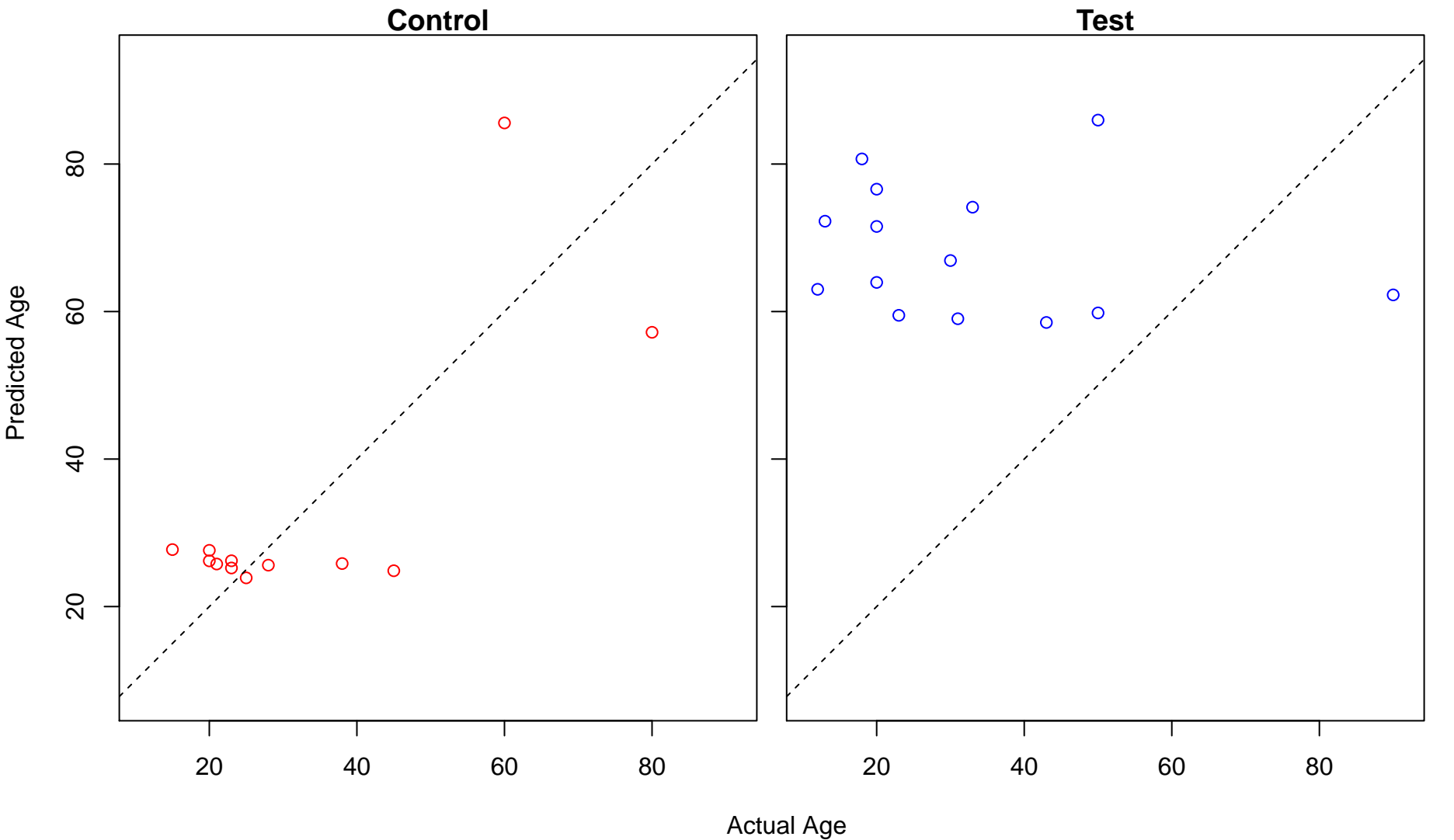
positive regulation of stress fiber assembly (Score: 4.608566)



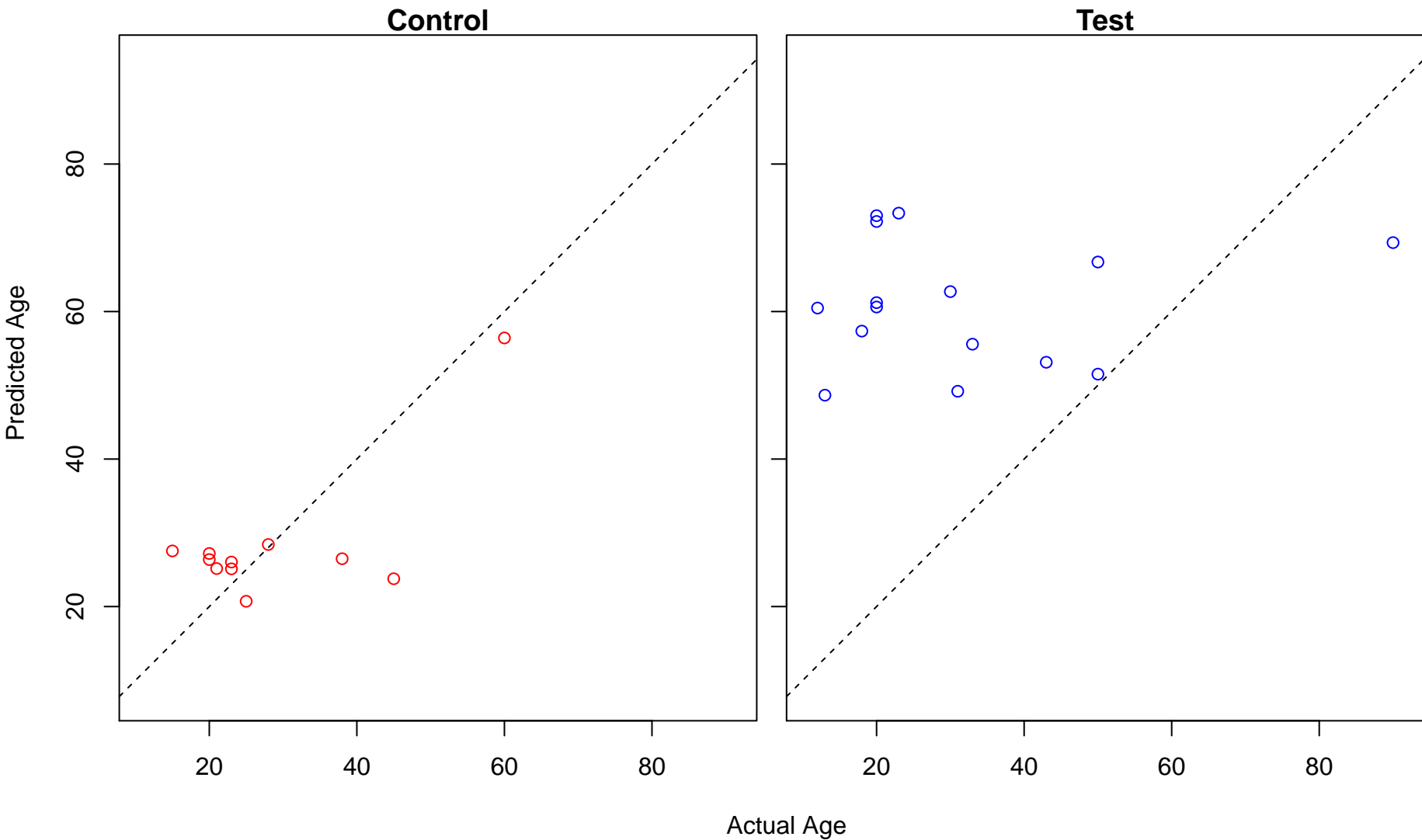
Regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (Score



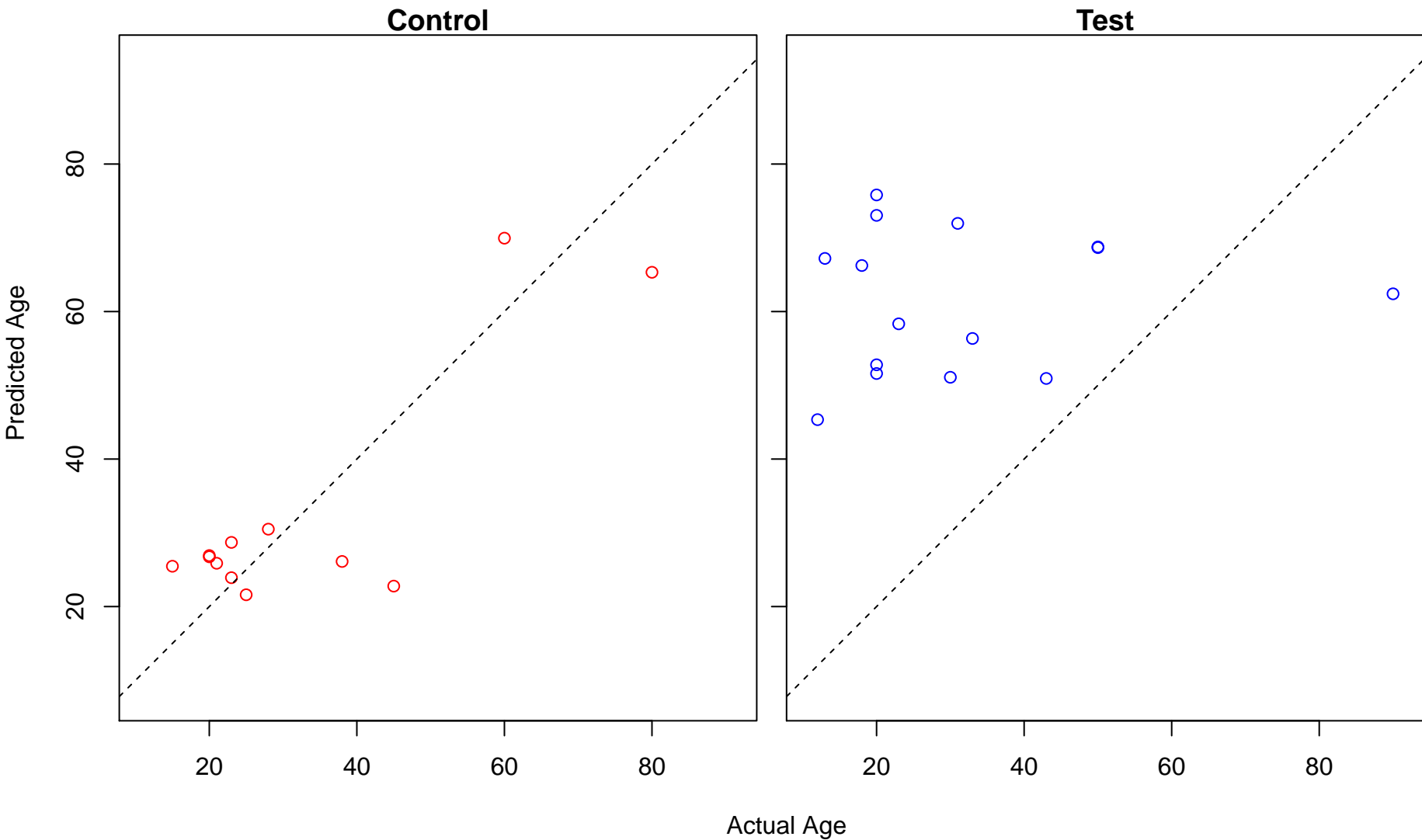
ve regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (S



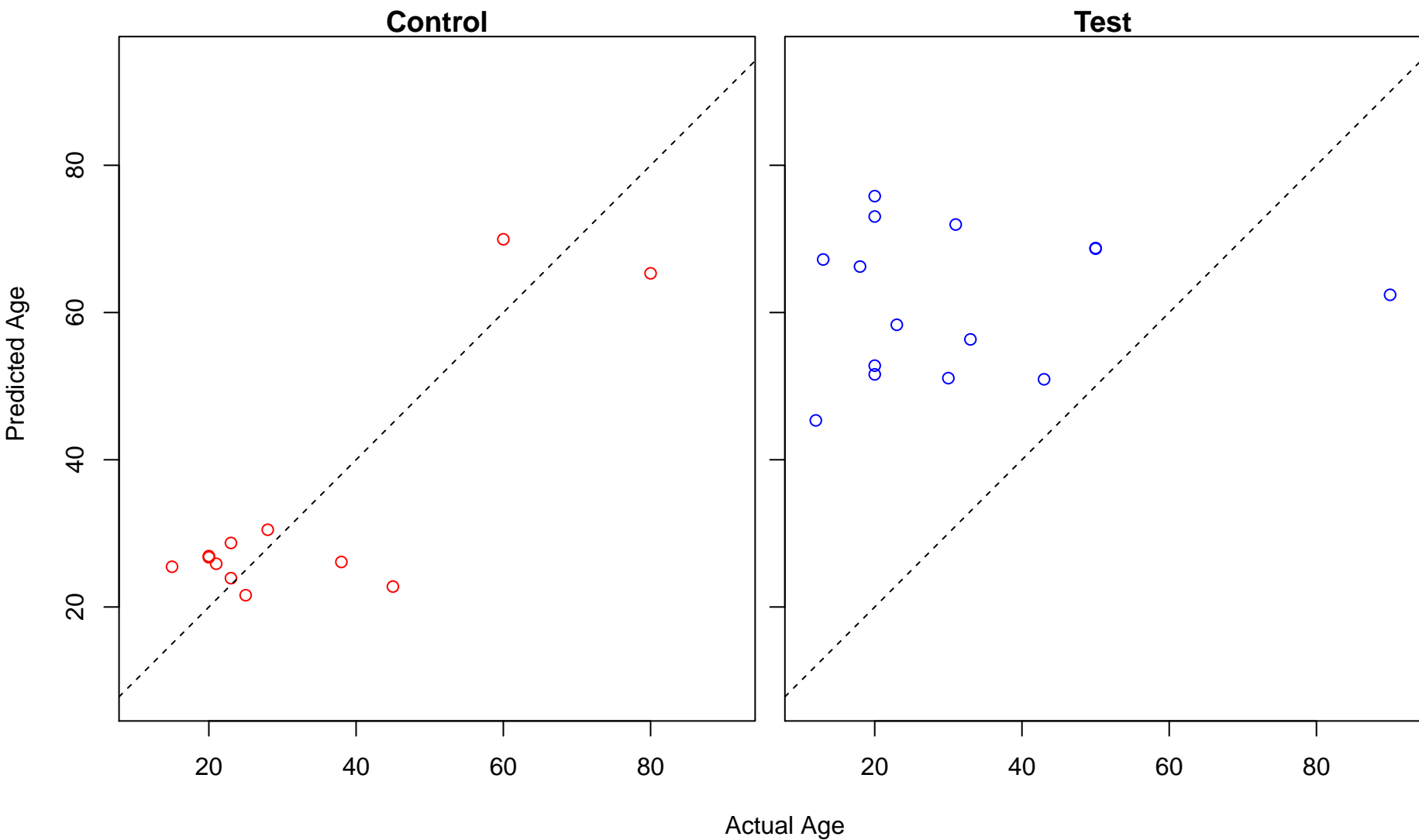
regulation of organelle assembly (Score: 4.606556)



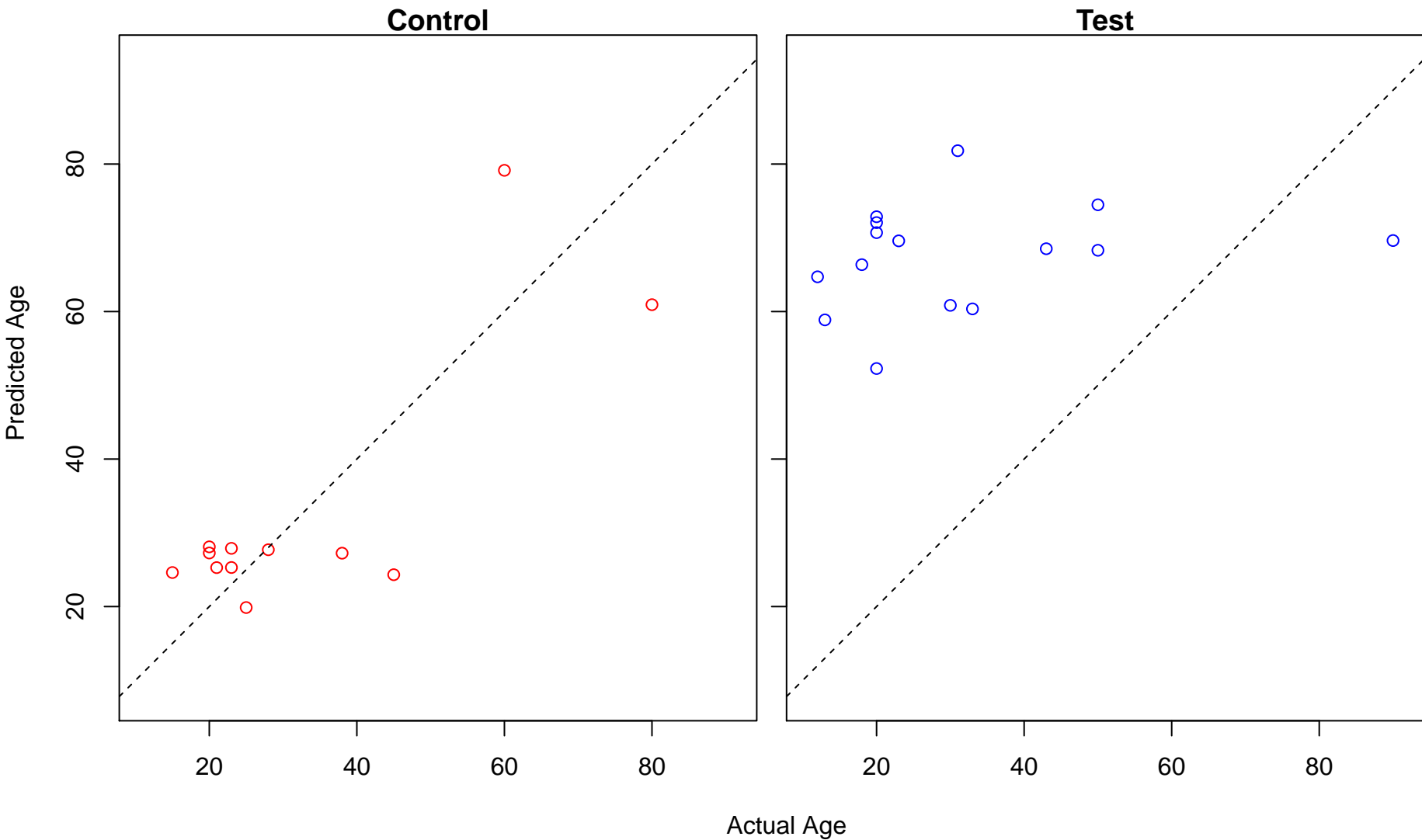
positive regulation of dephosphorylation (Score: 4.606496)



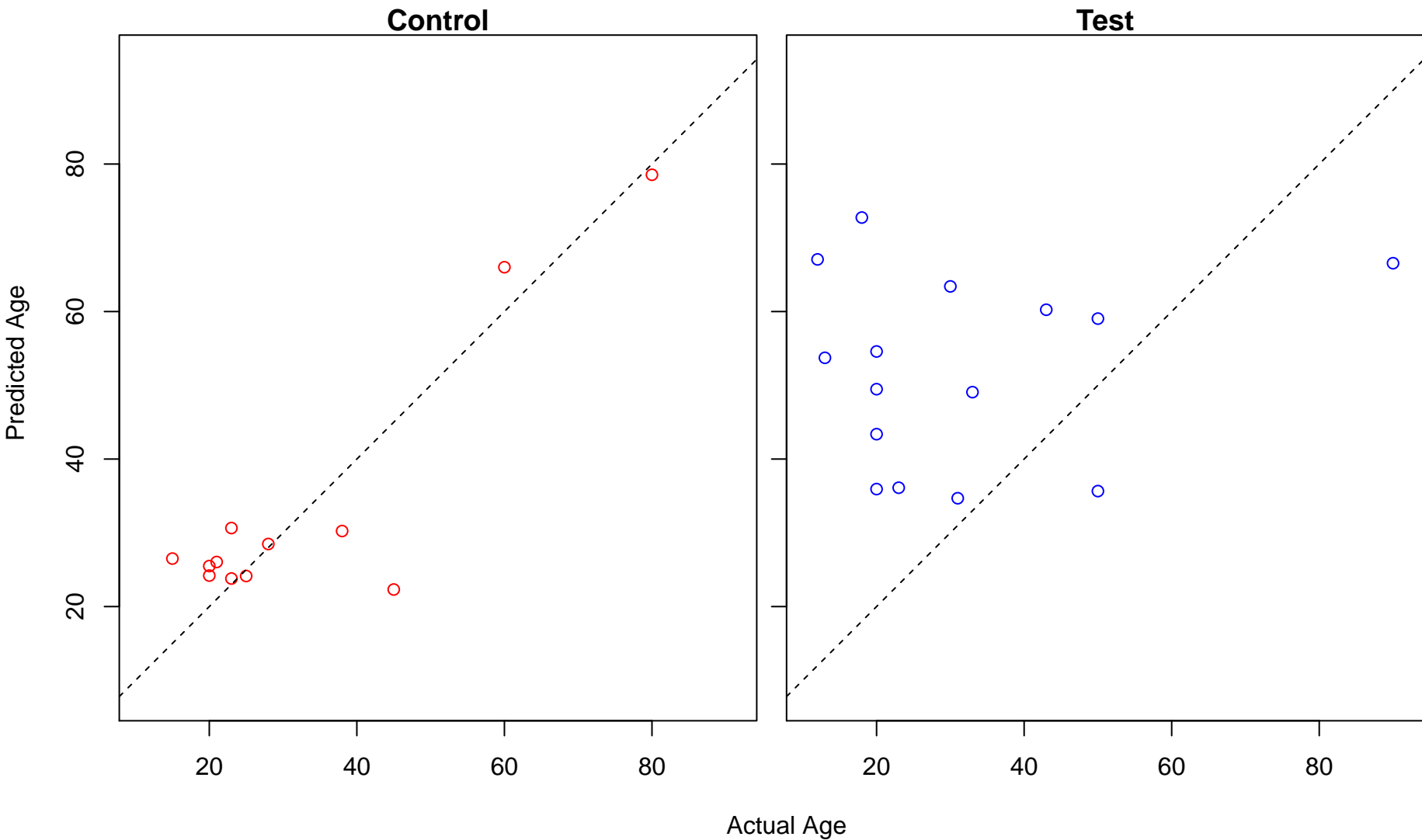
positive regulation of protein dephosphorylation (Score: 4.606496)



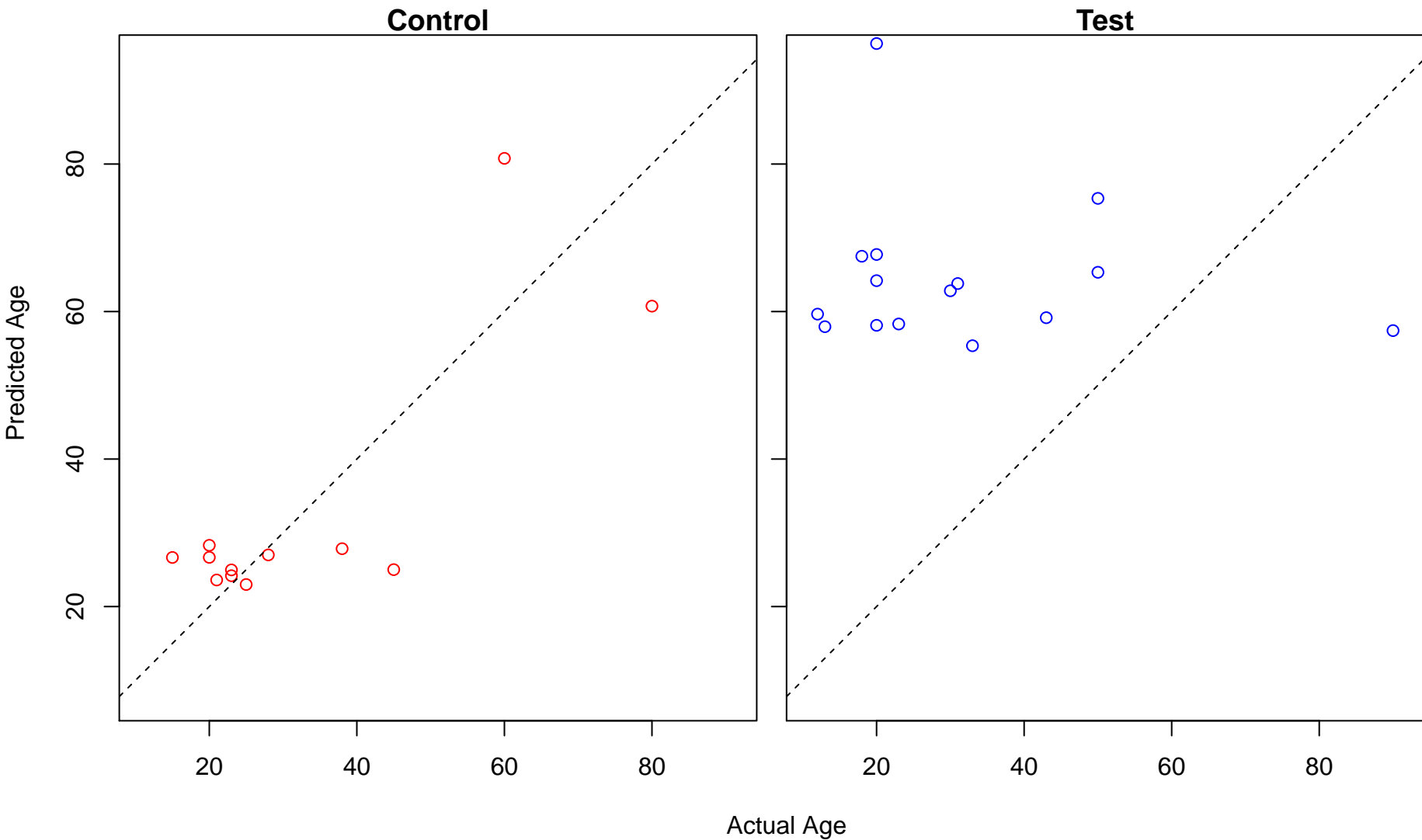
intracellular protein transmembrane import (Score: 4.605871)



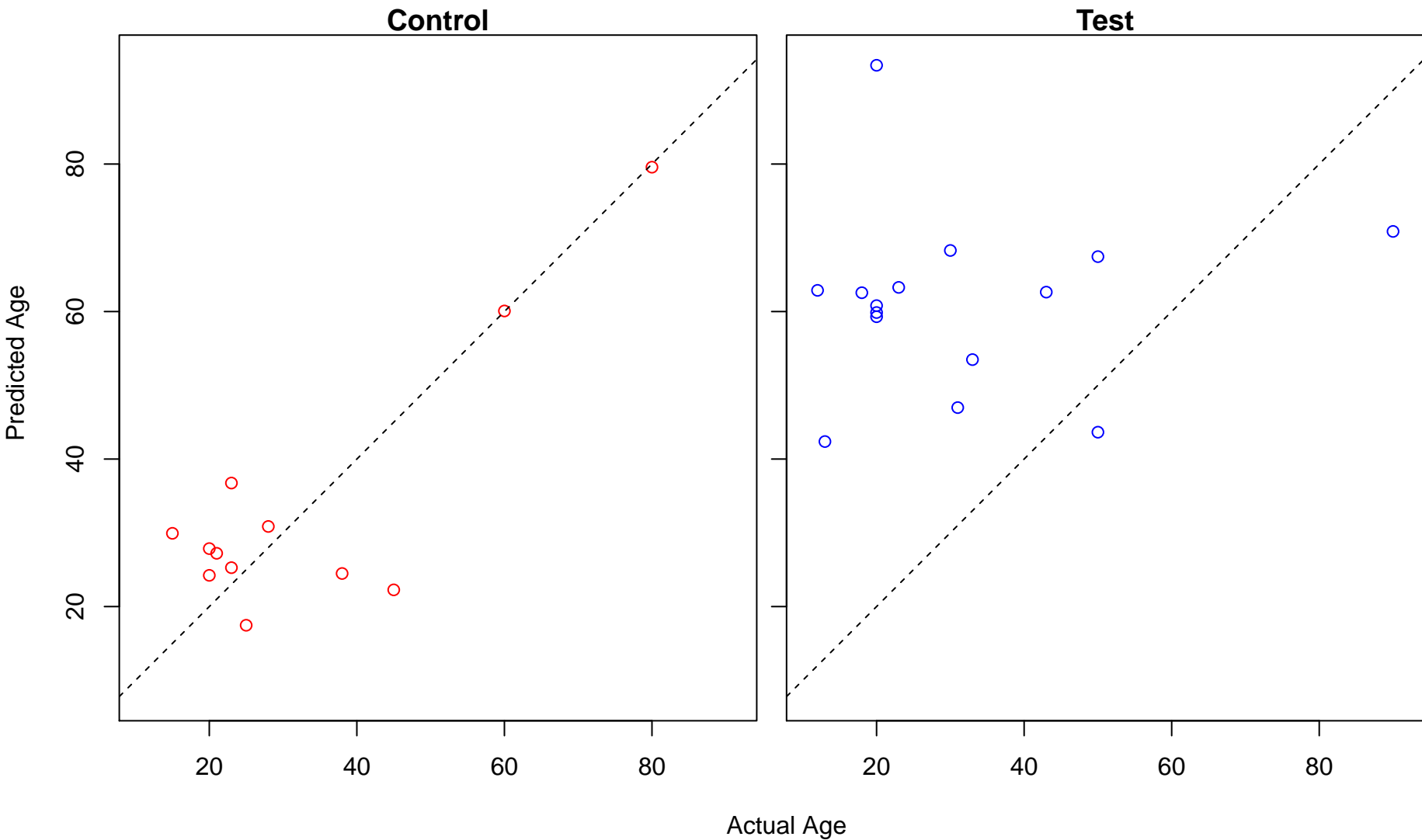
regulation of DNA-templated transcription, elongation (Score: 4.605271)



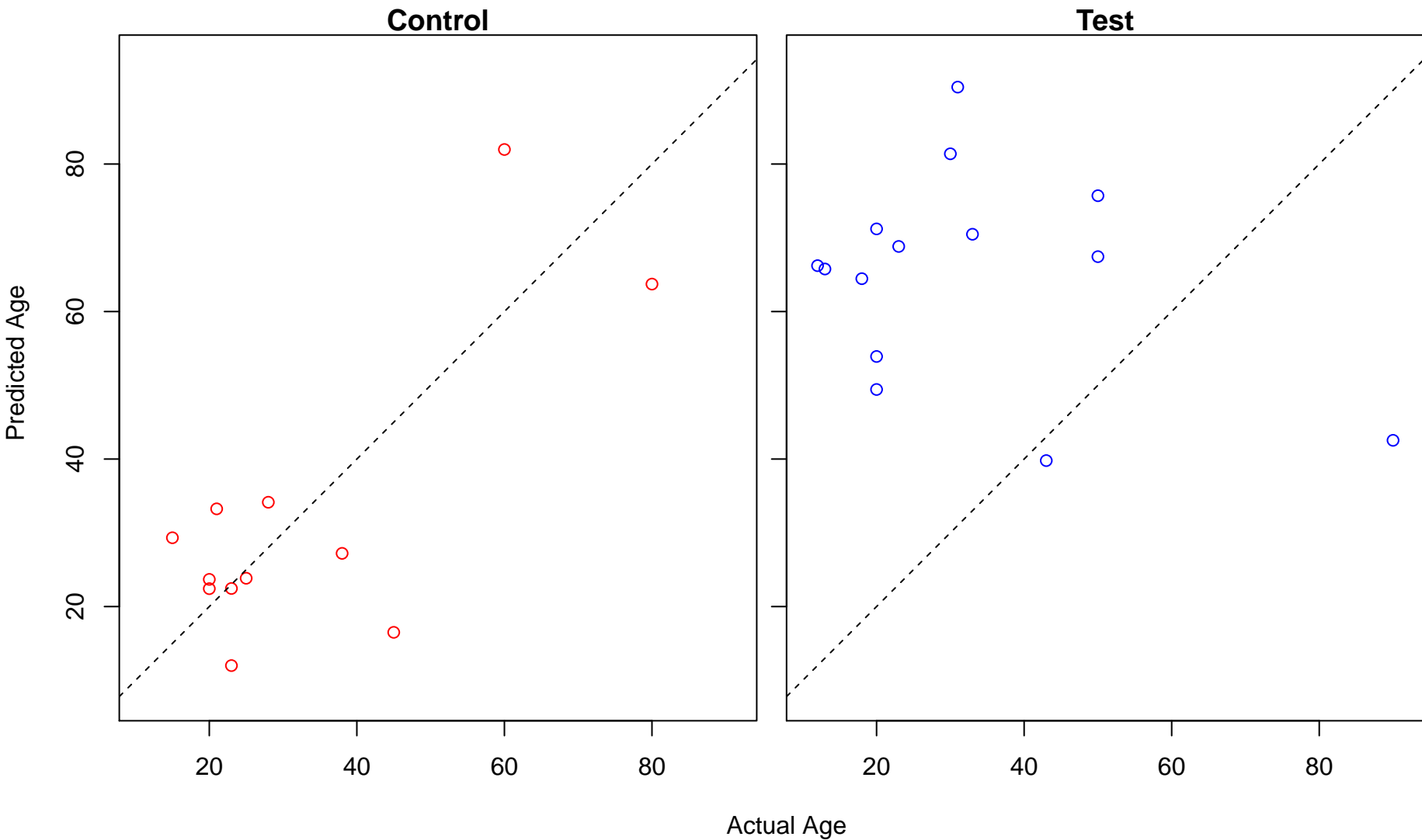
response to starvation (Score: 4.602339)



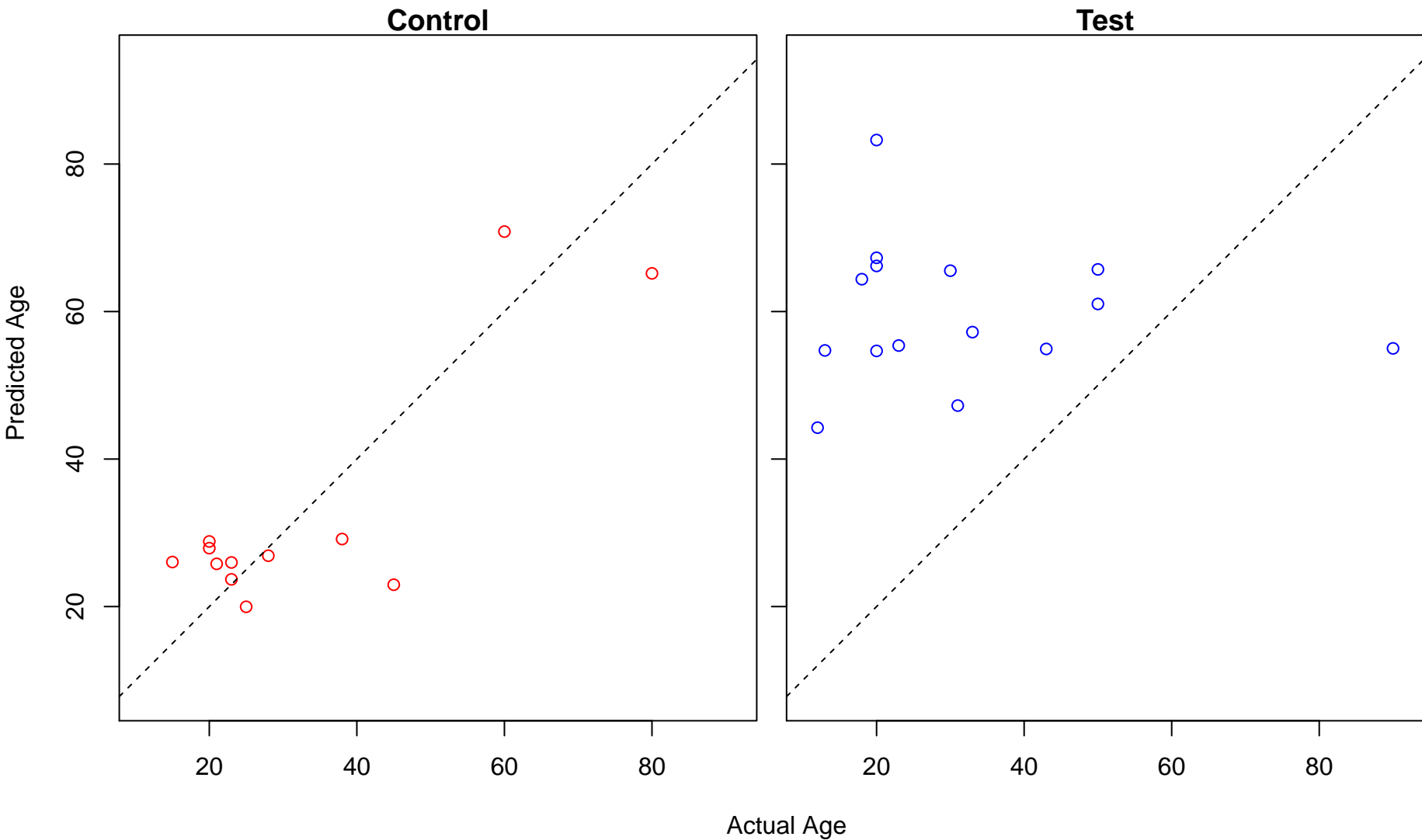
regulation of cytokine secretion (Score: 4.601883)



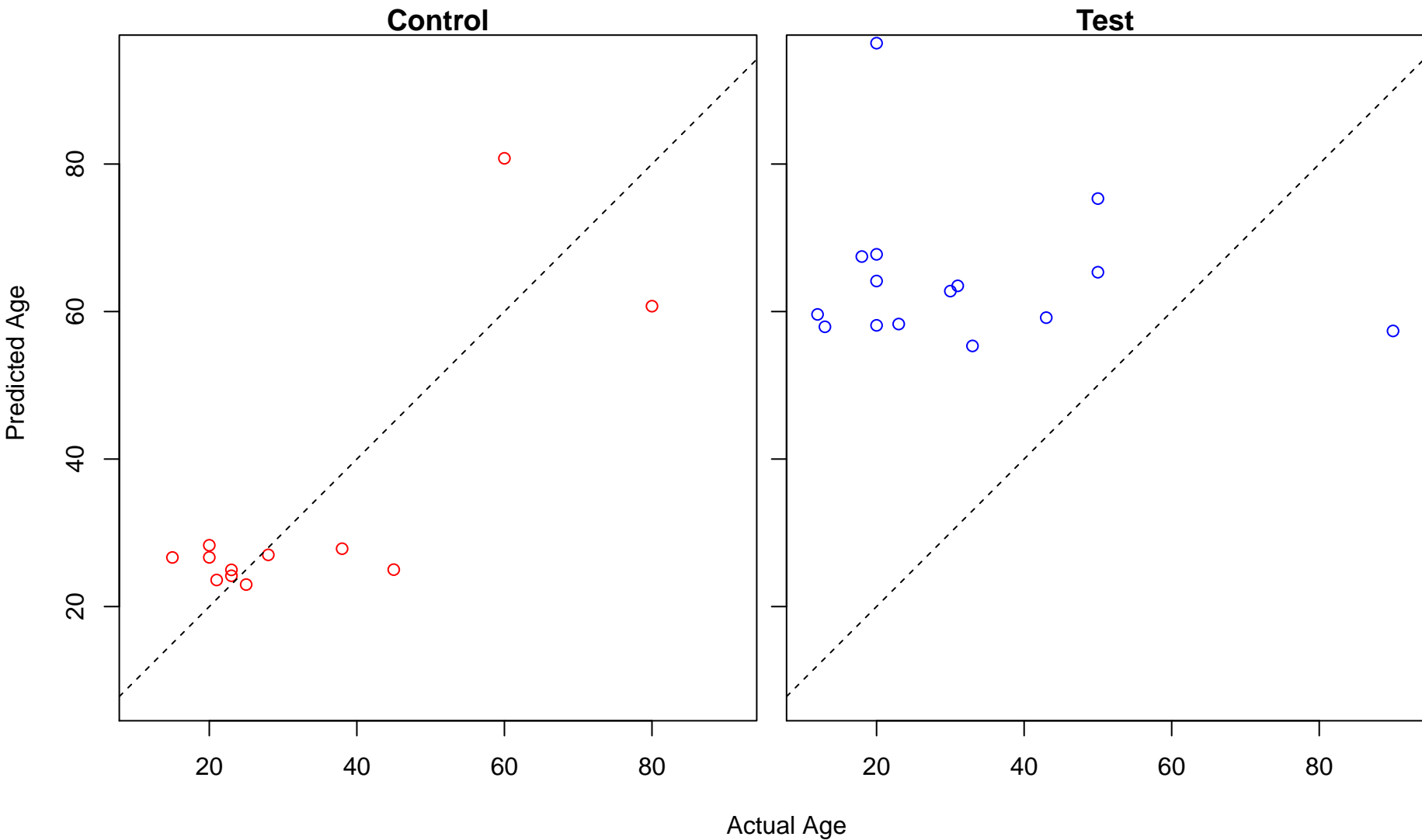
amyloid fibril formation (Score: 4.597693)



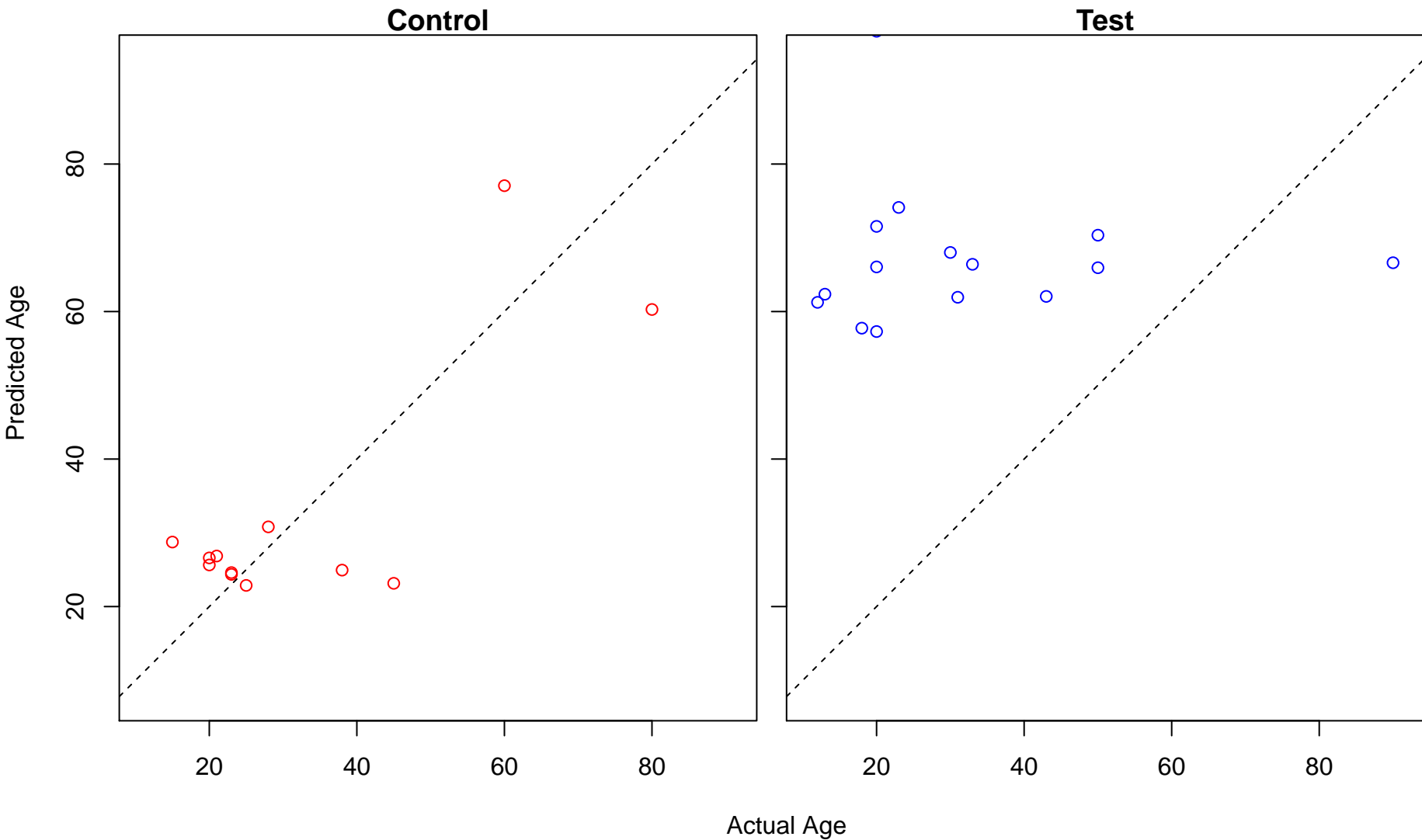
mammary gland epithelial cell differentiation (Score: 4.597381)



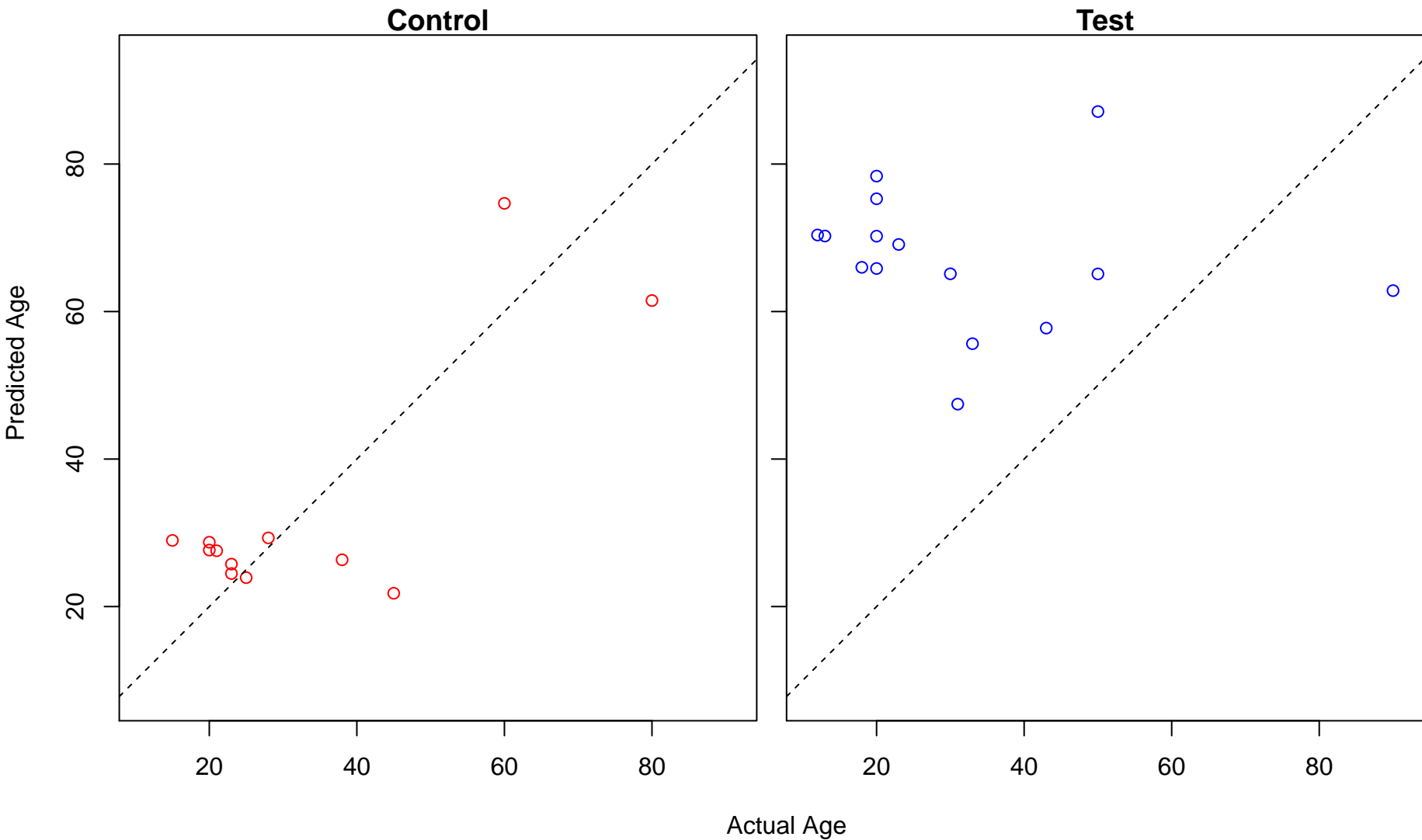
cellular response to starvation (Score: 4.596894)



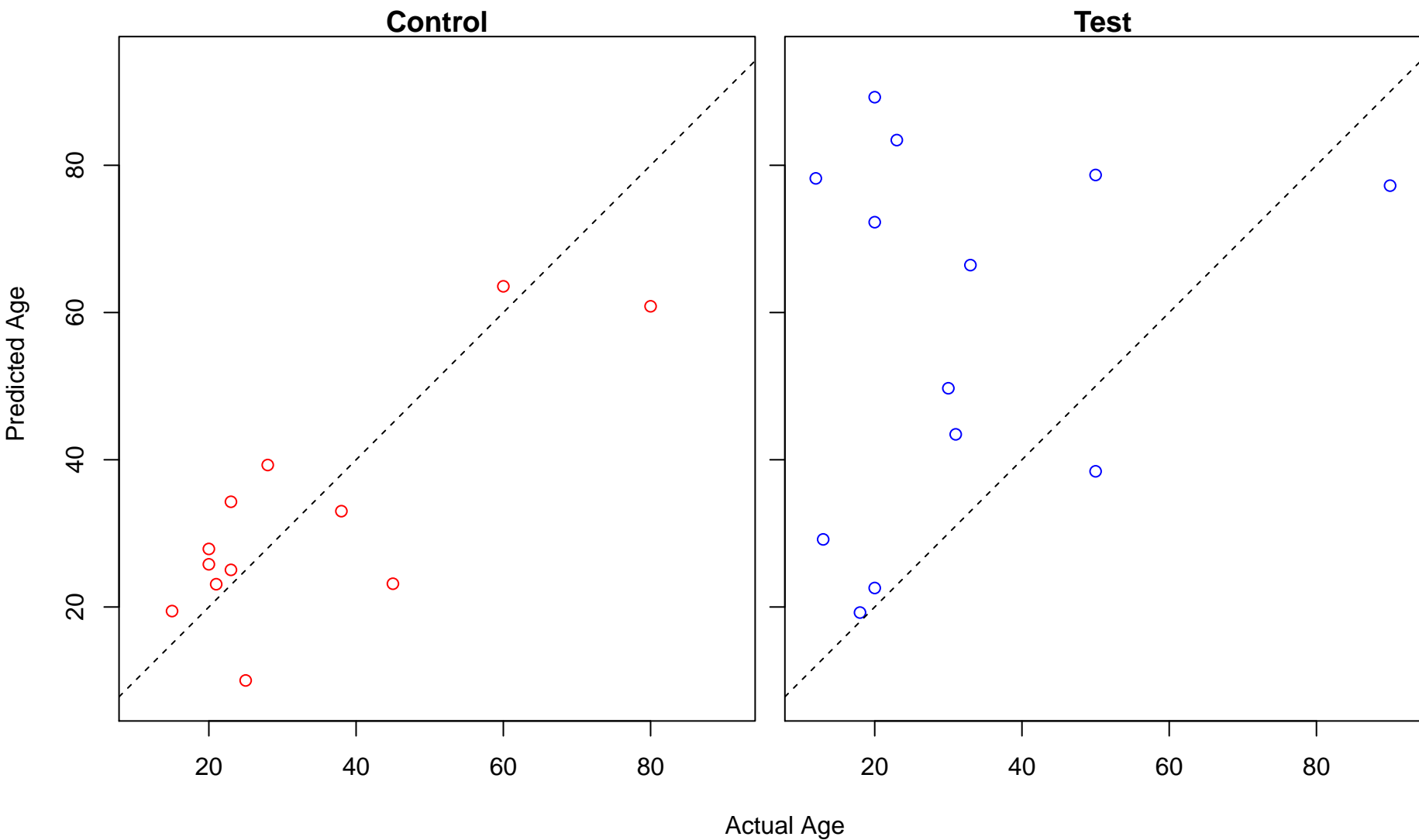
positive regulation of cell adhesion mediated by integrin (Score: 4.596045)



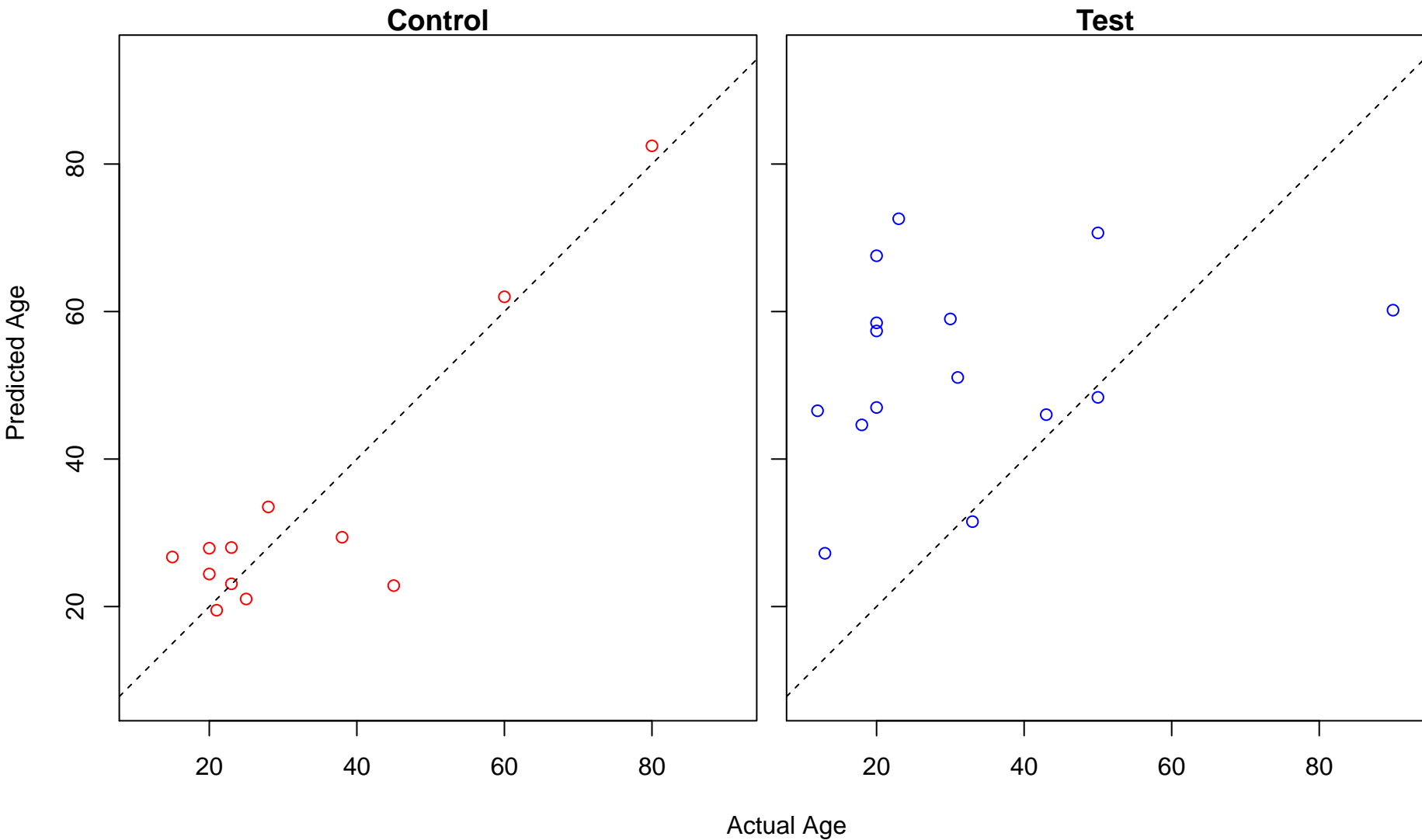
chaperone-mediated protein transport (Score: 4.592909)



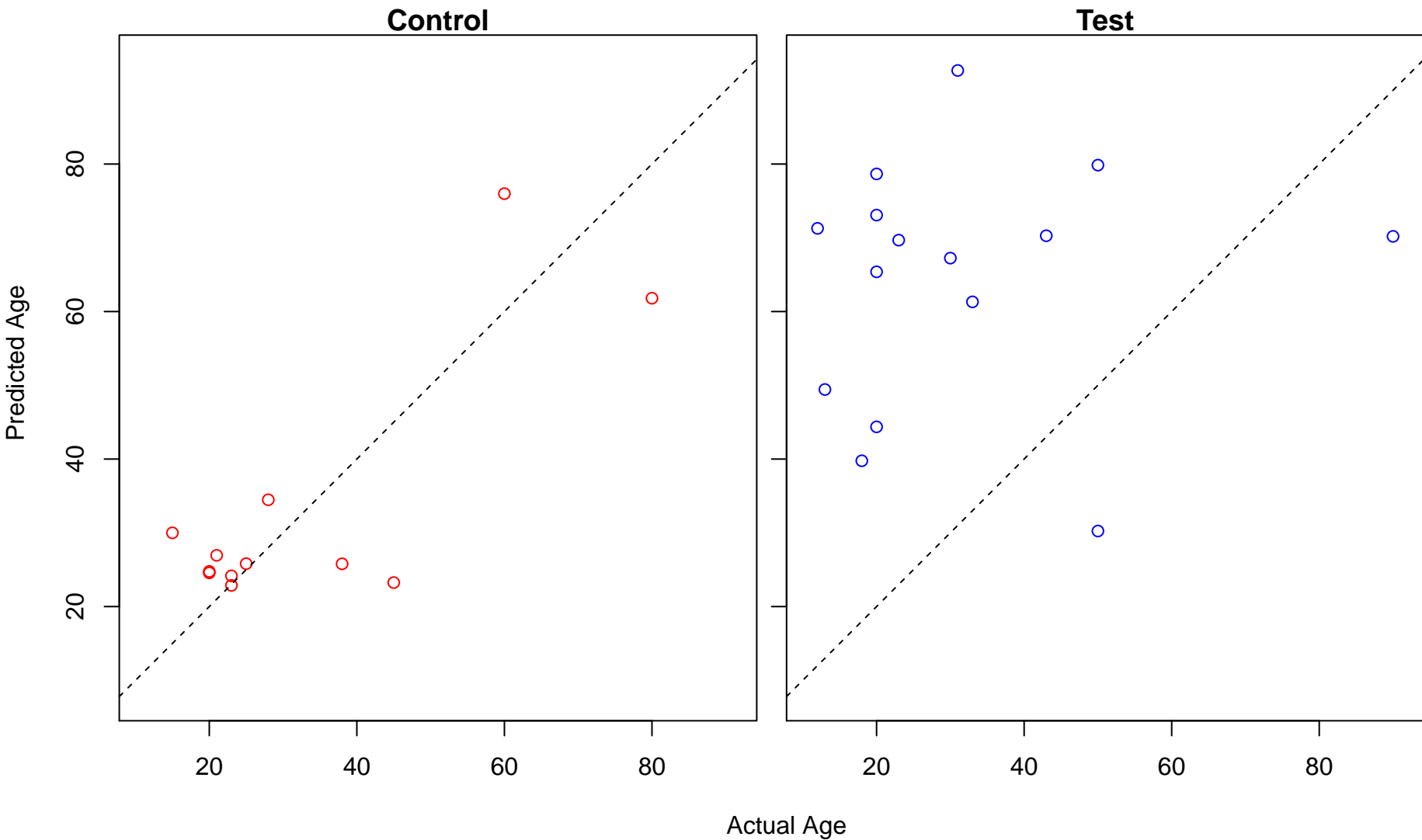
regulation of ventricular cardiac muscle cell membrane repolarization (Score: 4.592678)



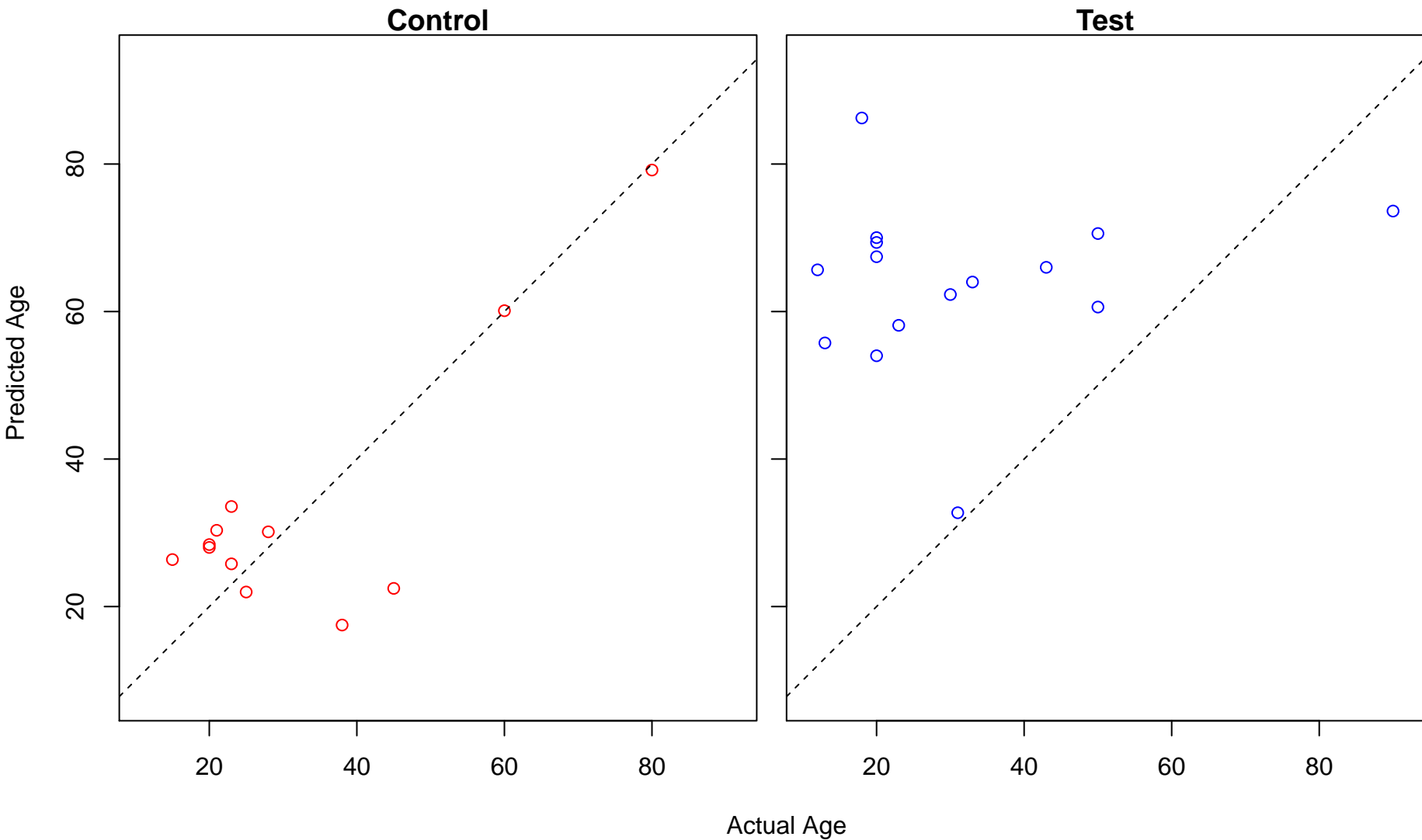
regulation of neurotransmitter levels (Score: 4.590469)



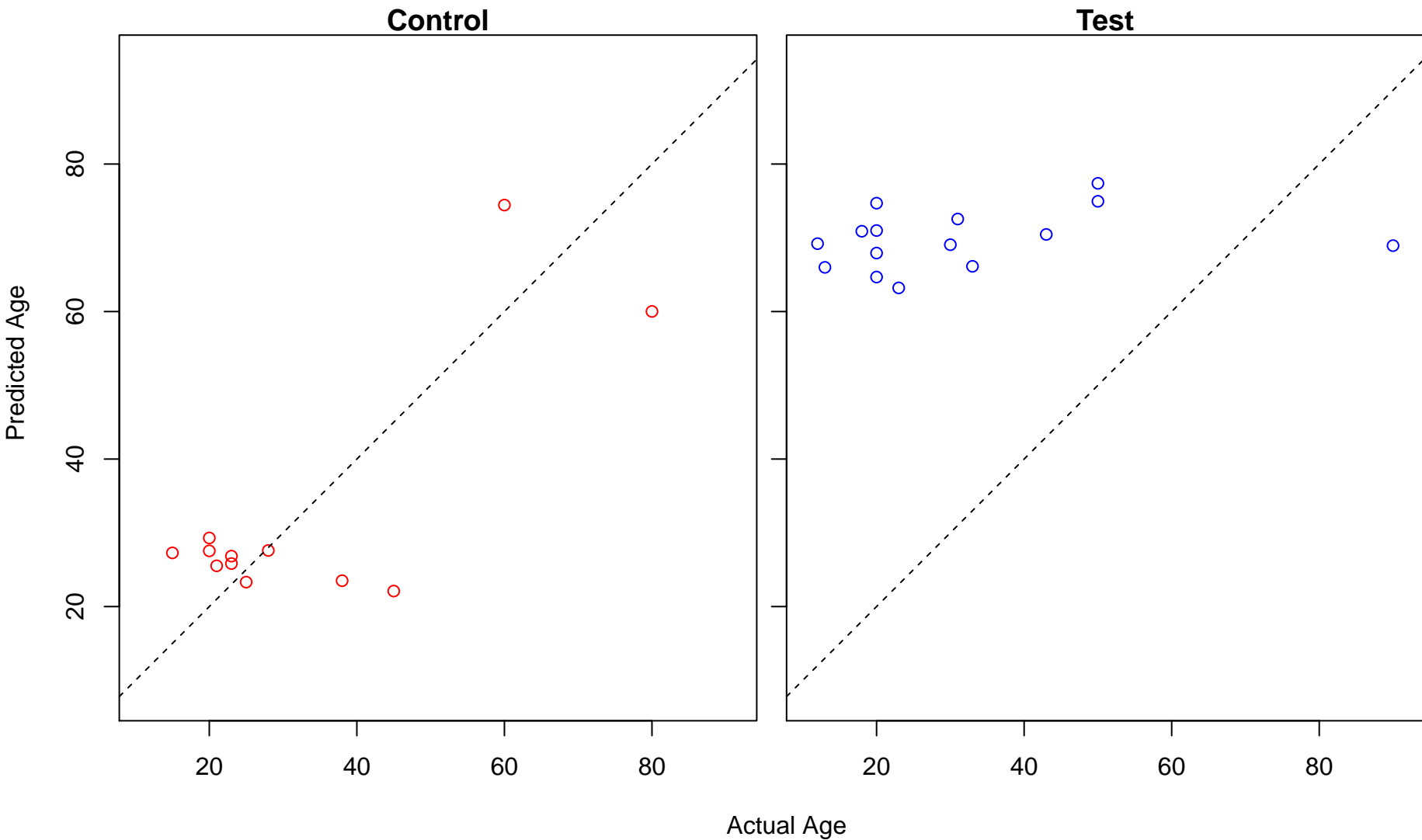
negative regulation of cell projection organization (Score: 4.590324)



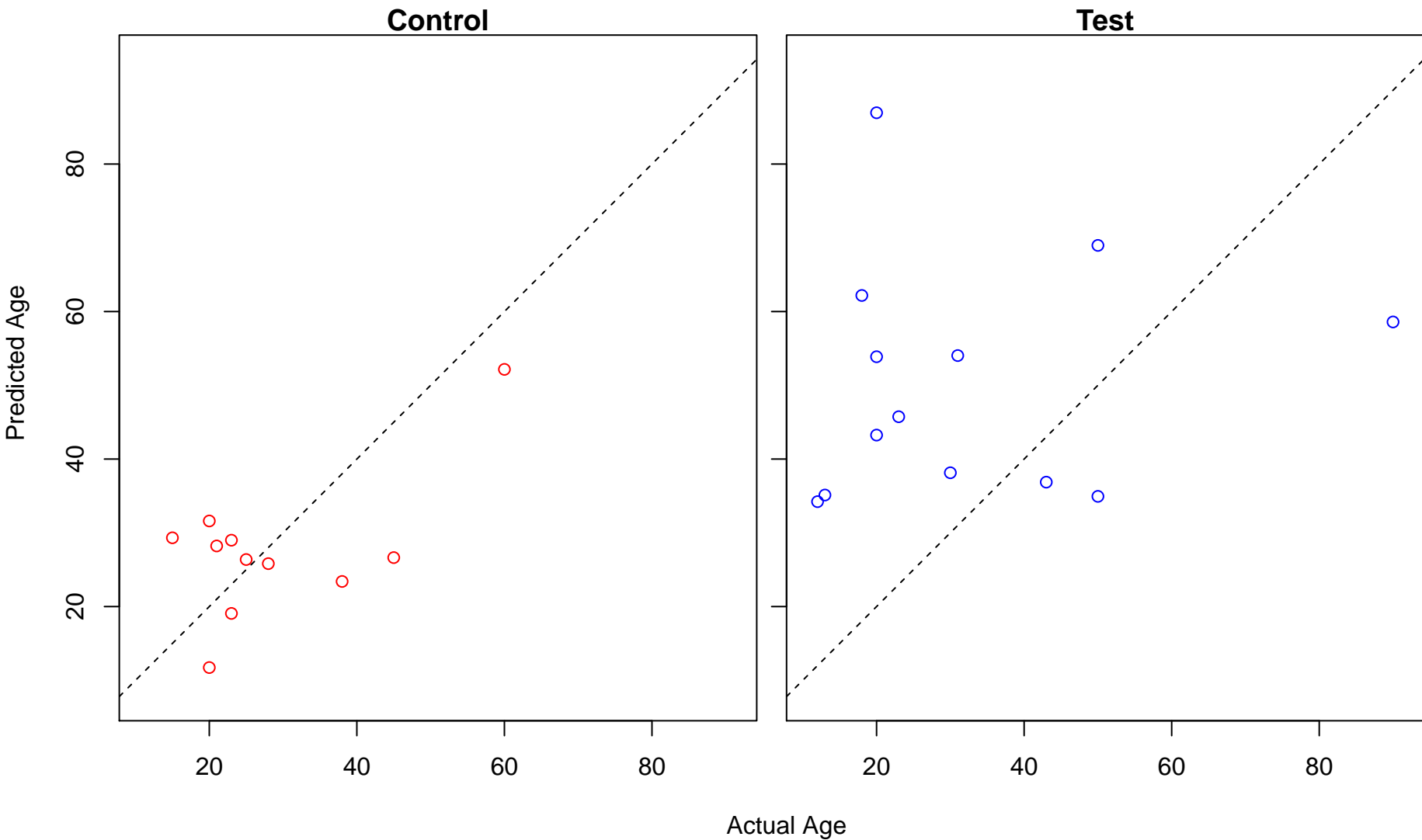
ncRNA transcription (Score: 4.589549)



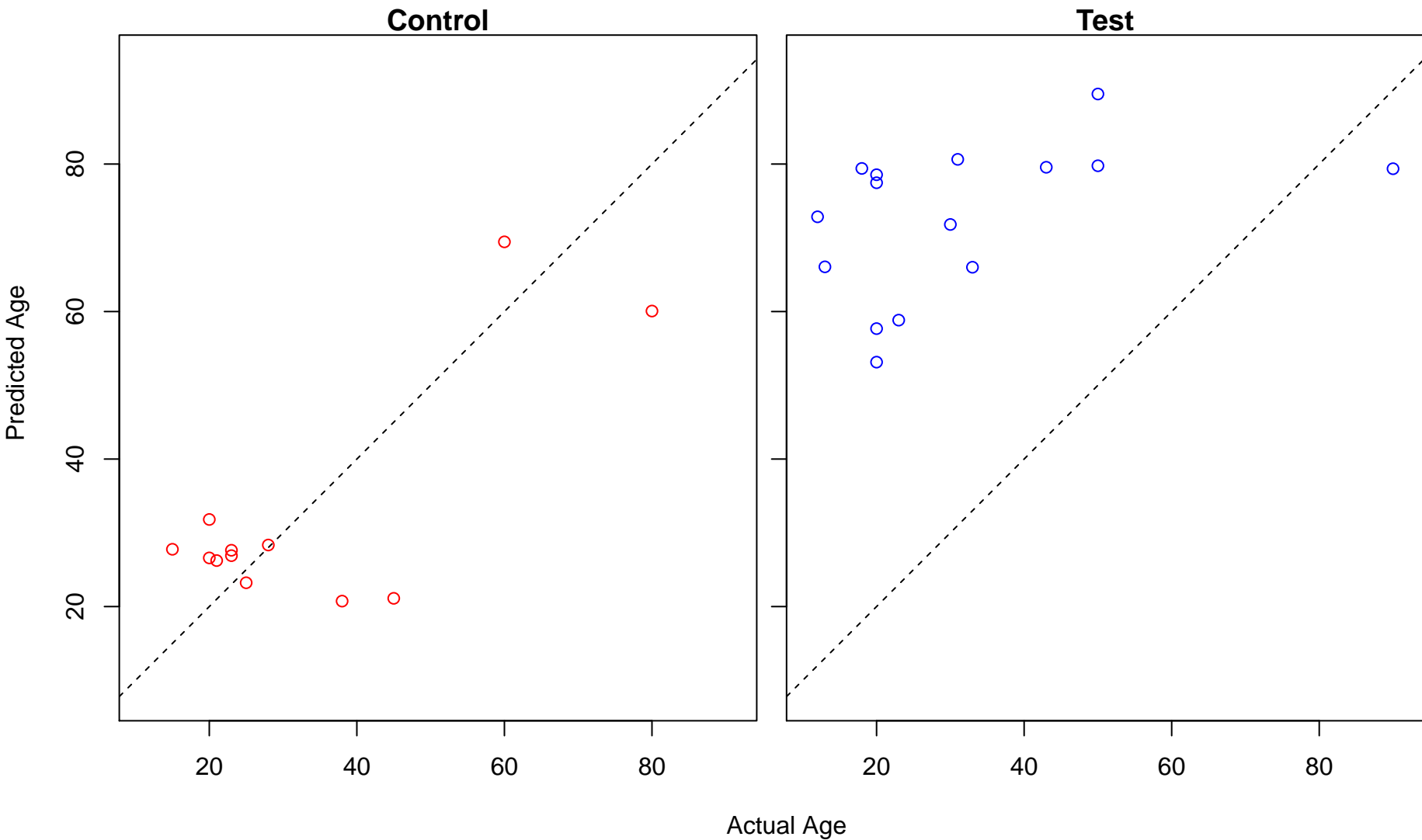
positive regulation of ATPase activity (Score: 4.588057)



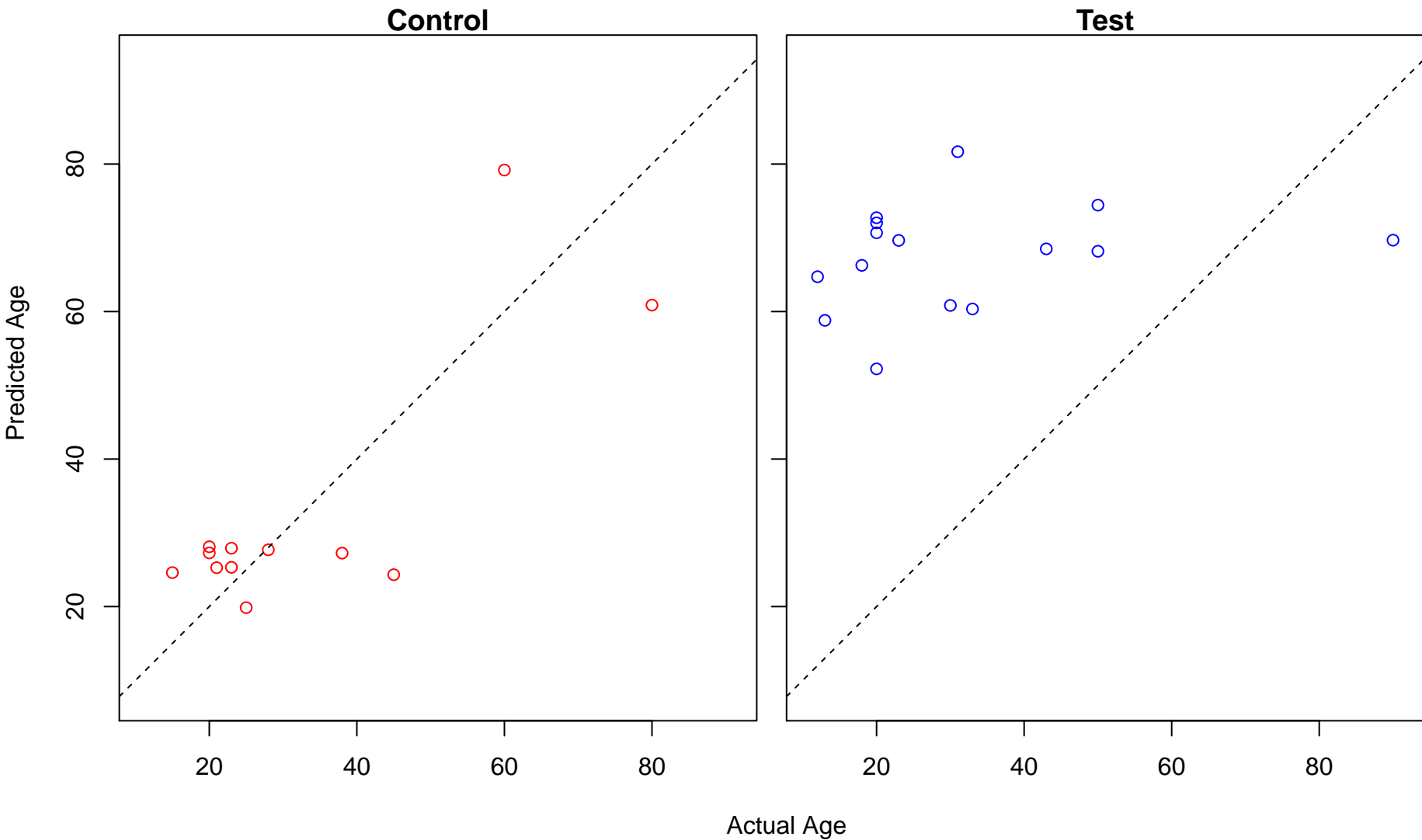
detection of chemical stimulus involved in sensory perception (Score: 4.588056)



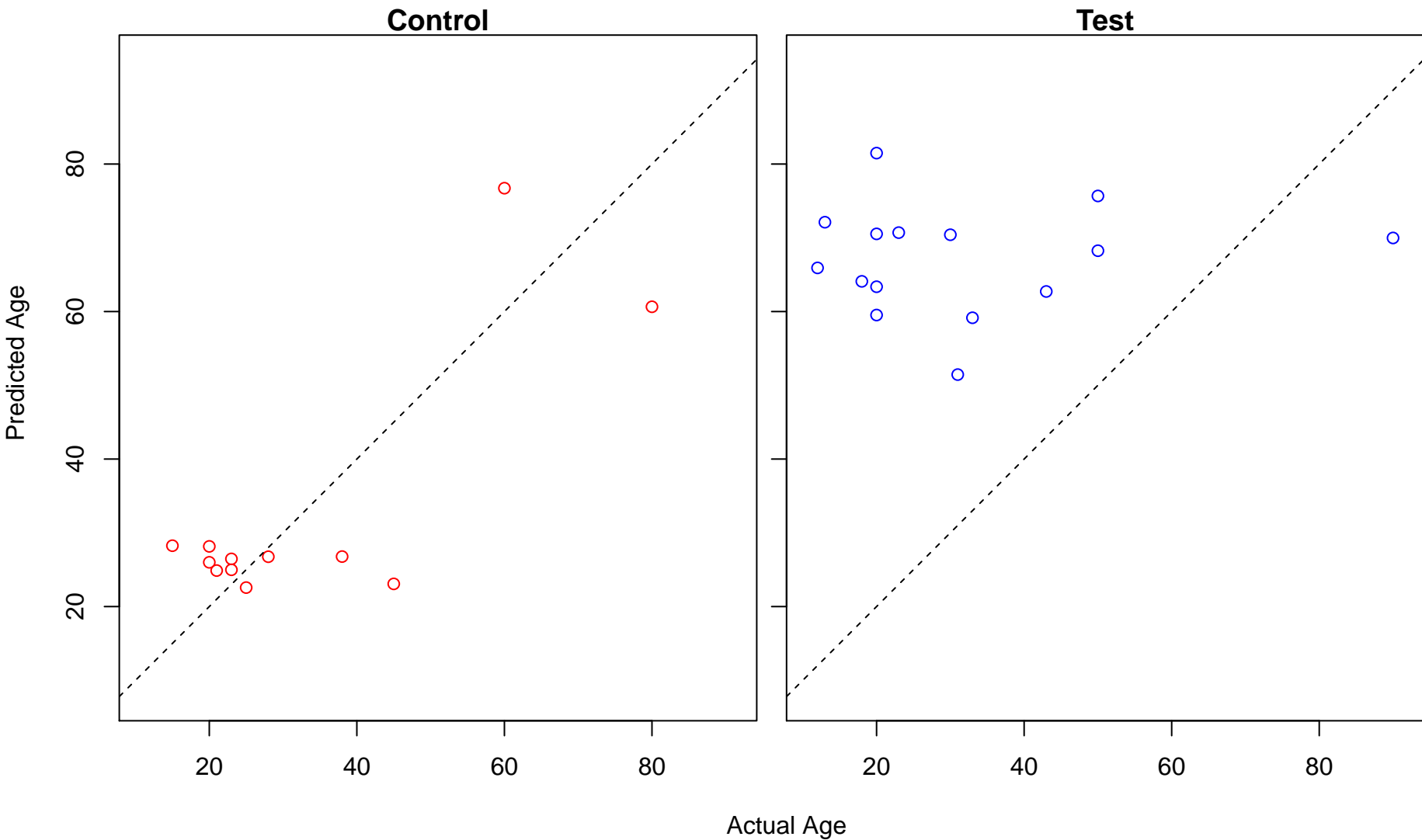
positive regulation of sodium ion transmembrane transporter activity (Score: 4.587738)



intracellular protein transmembrane transport (Score: 4.587017)

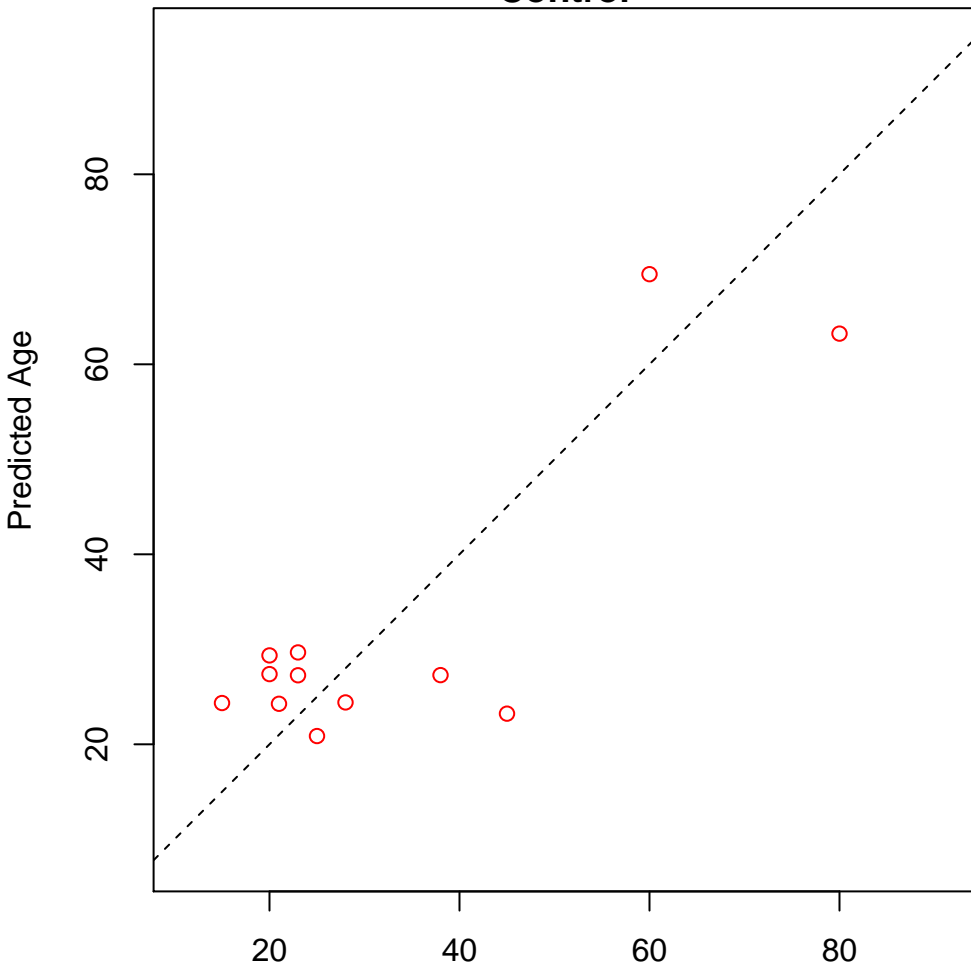


spindle organization (Score: 4.583696)

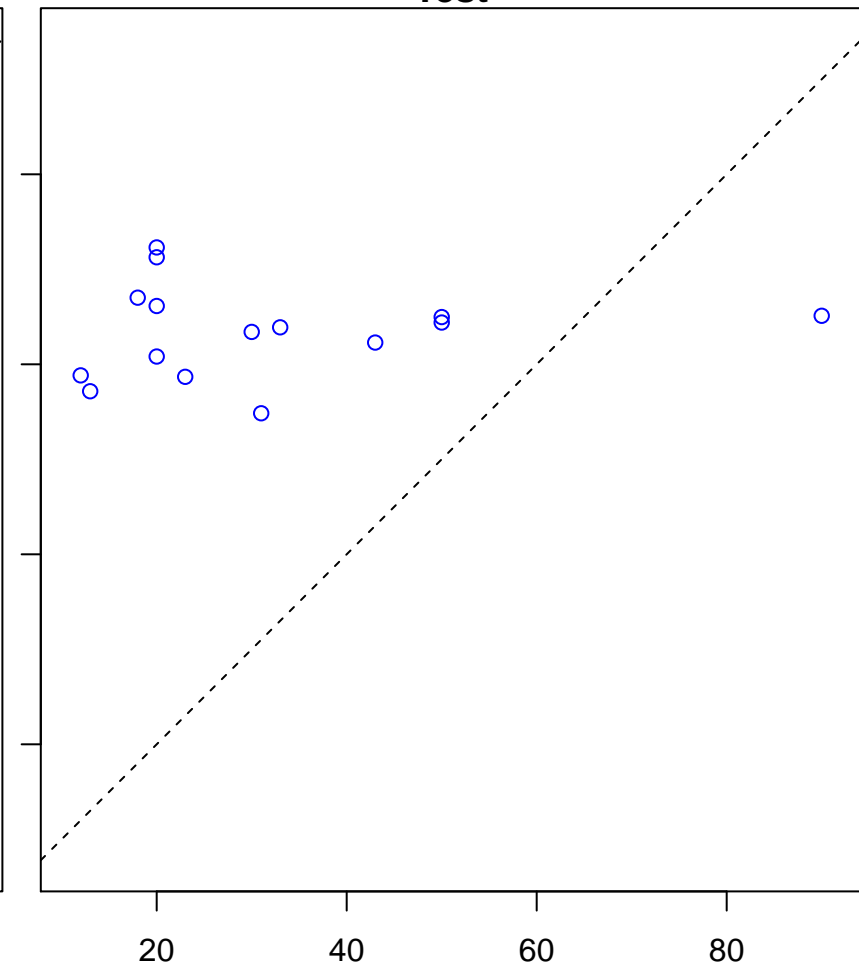


regulation of glucose metabolic process (Score: 4.583269)

Control

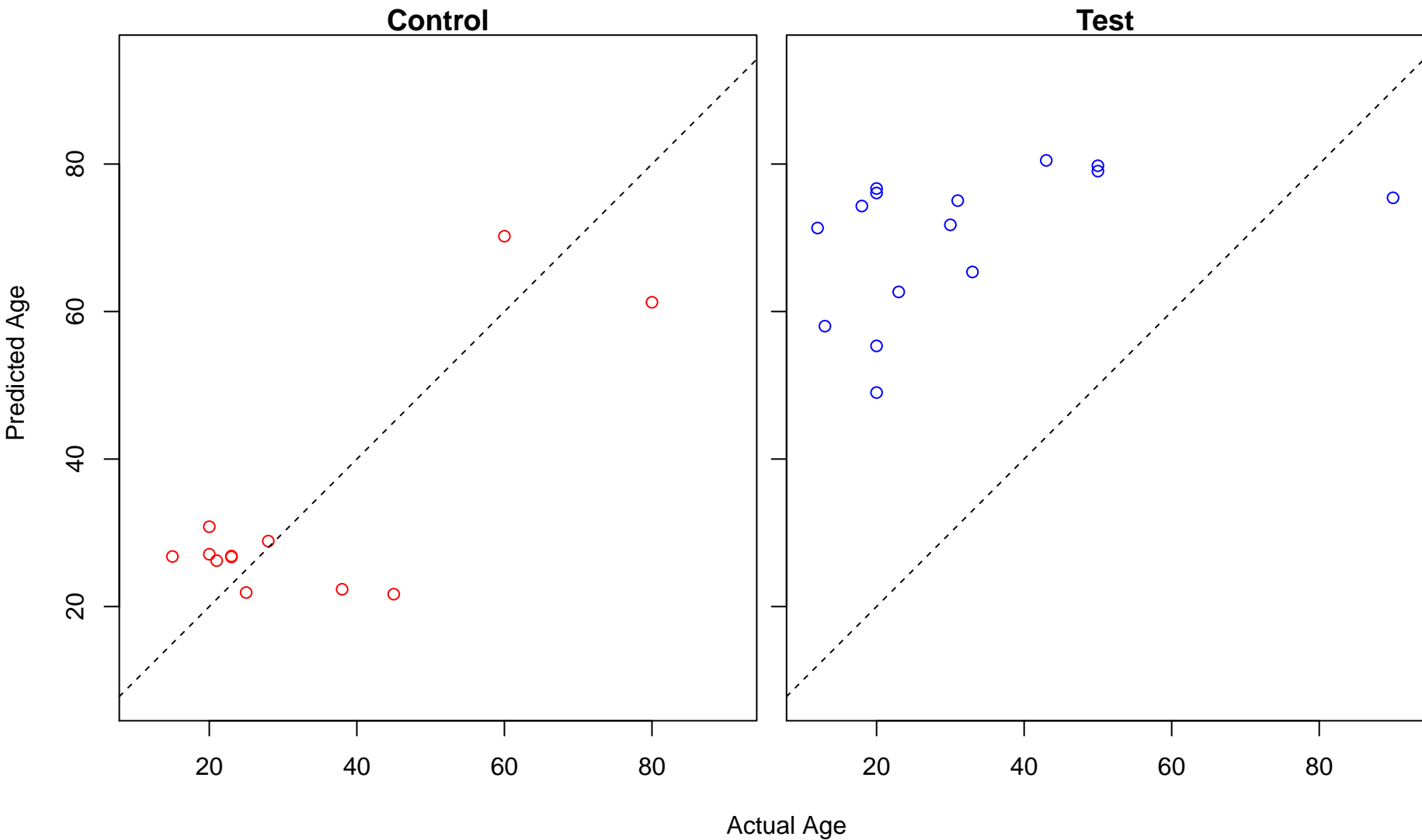


Test

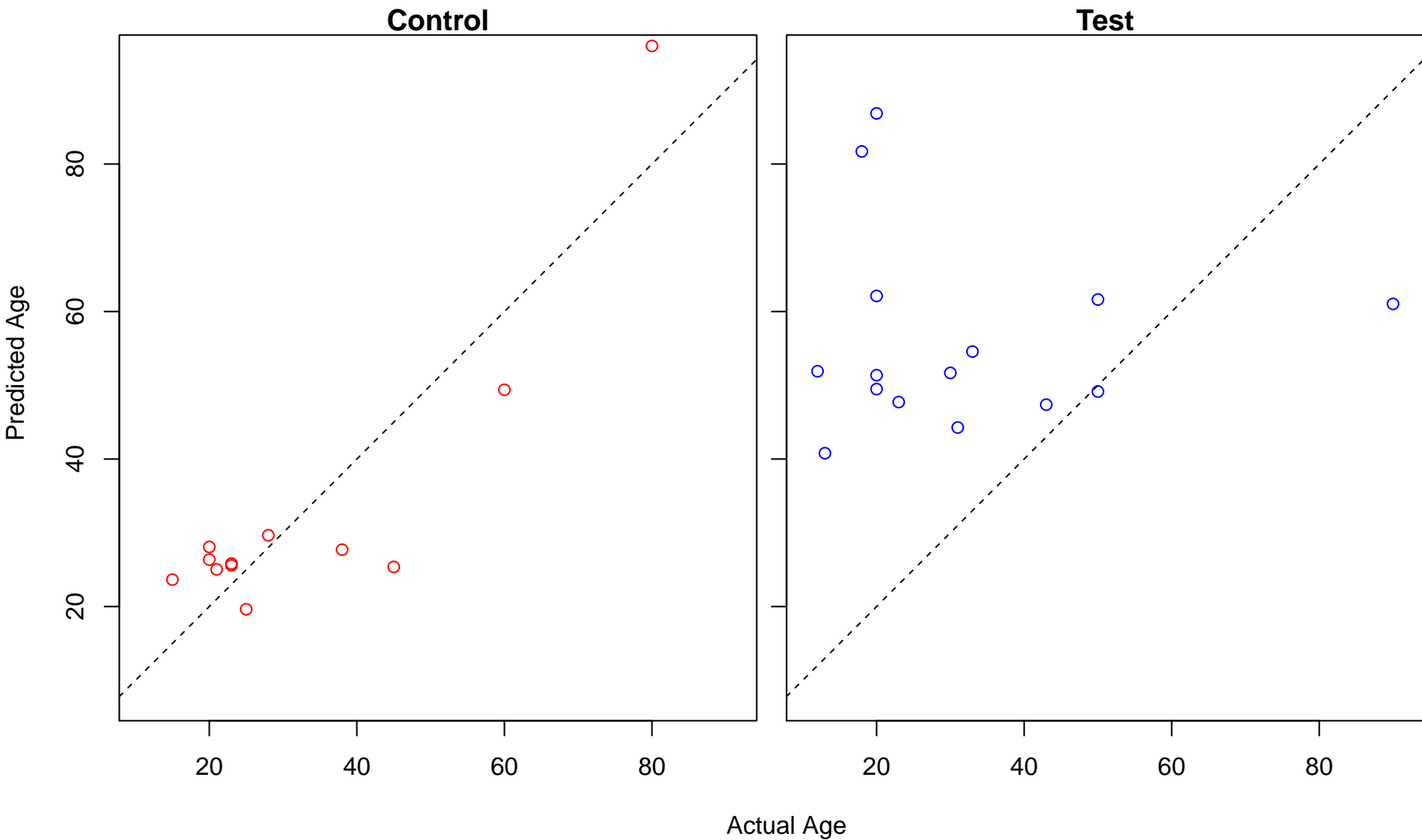


Actual Age

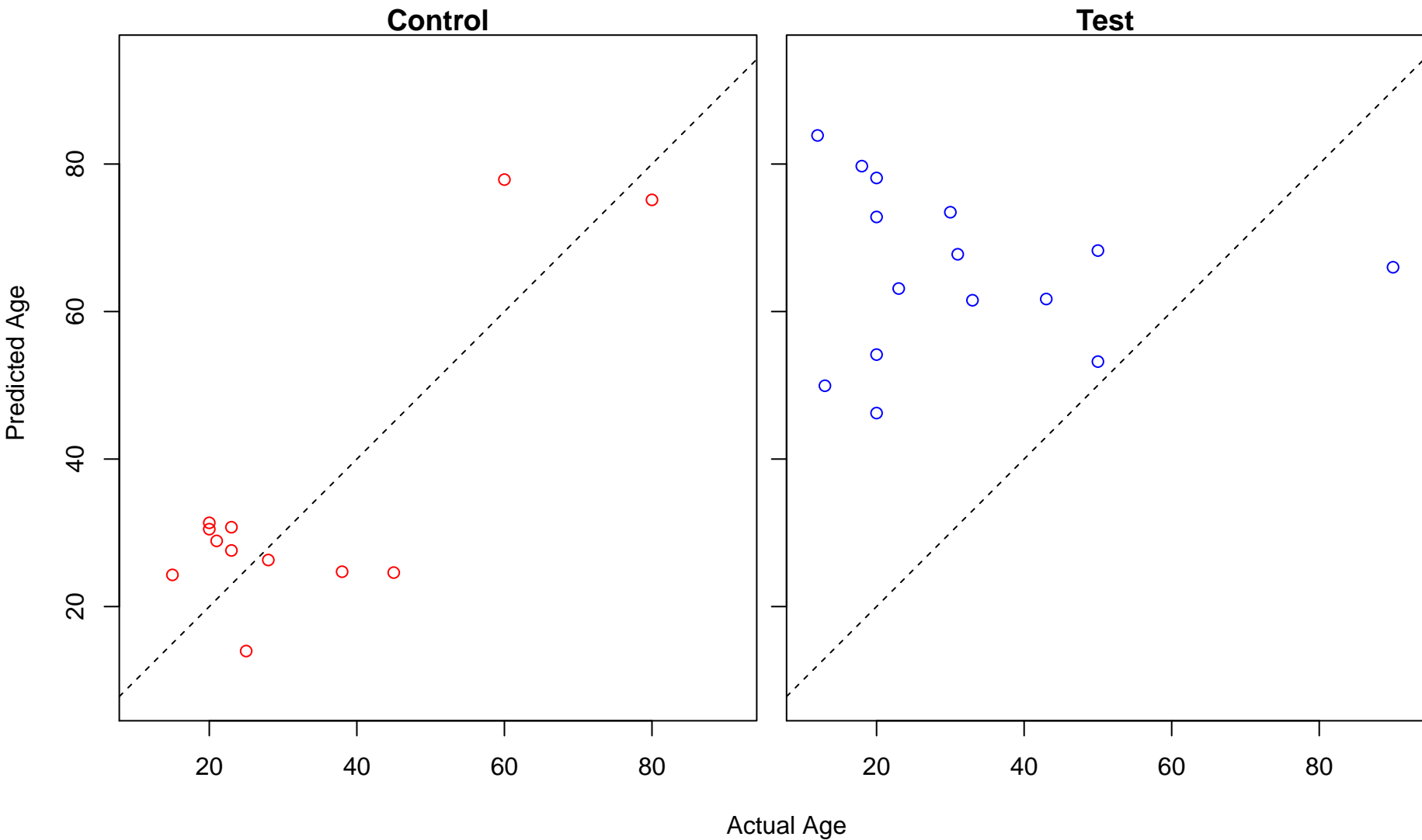
positive regulation of potassium ion transport (Score: 4.581920)



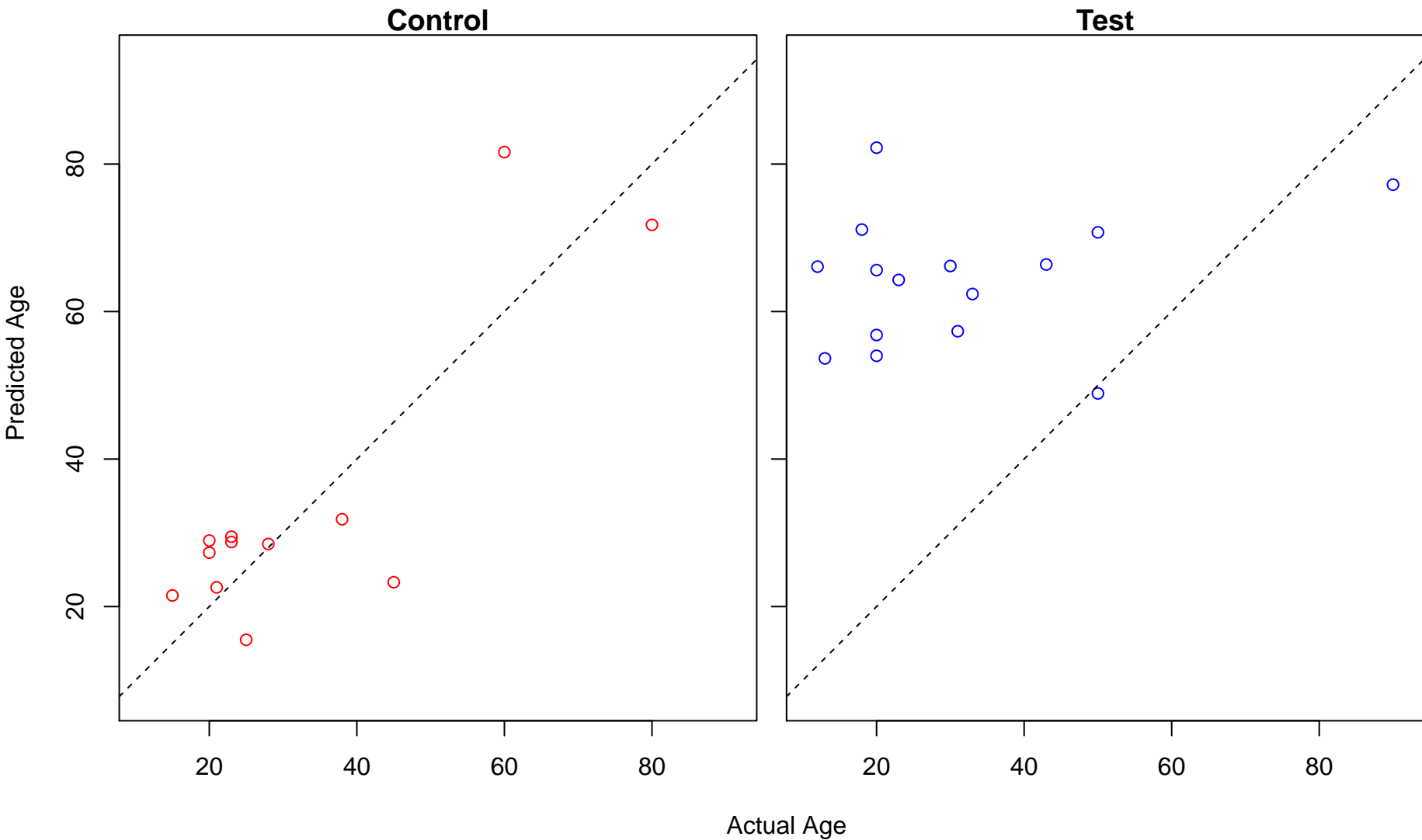
glycolipid biosynthetic process (Score: 4.578917)



negative regulation of interferon-beta production (Score: 4.578547)

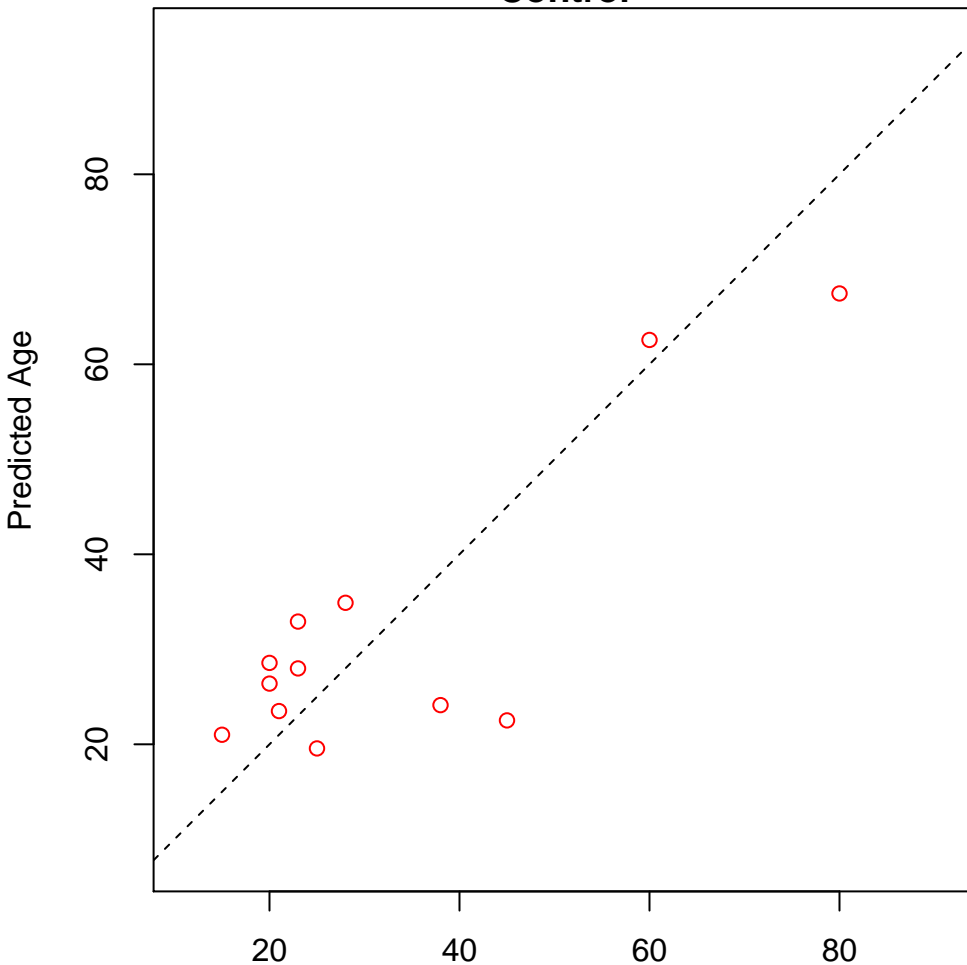


hippocampus development (Score: 4.577999)

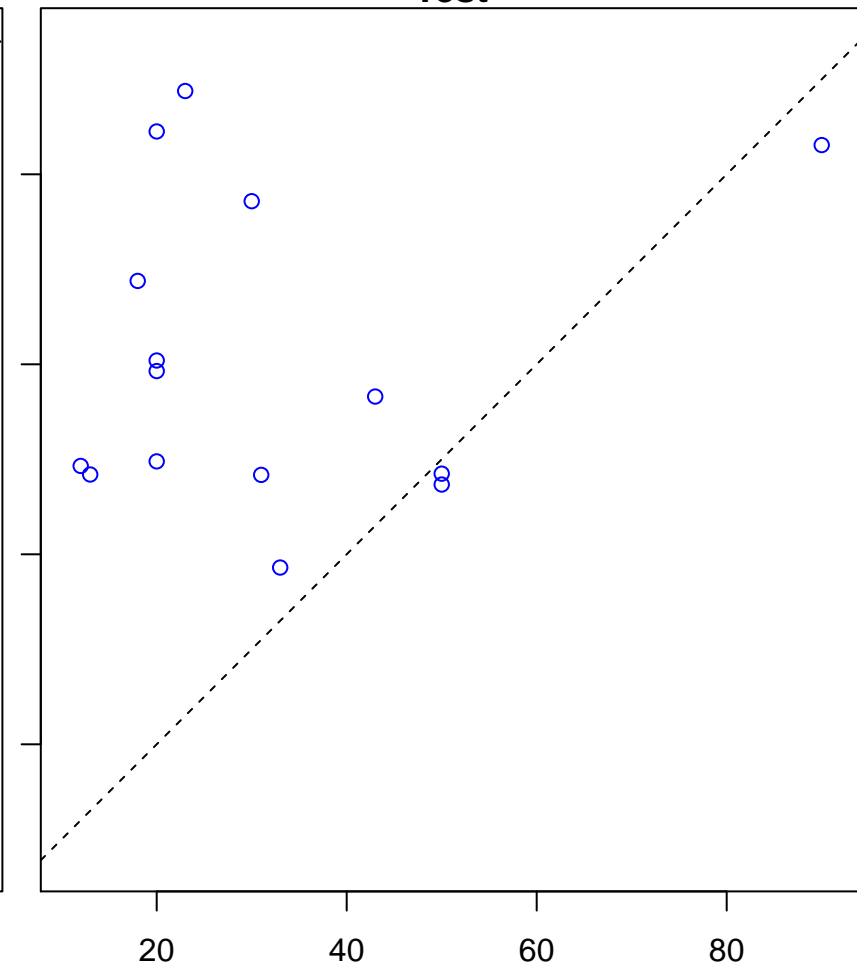


protein localization to kinetochore (Score: 4.577037)

Control

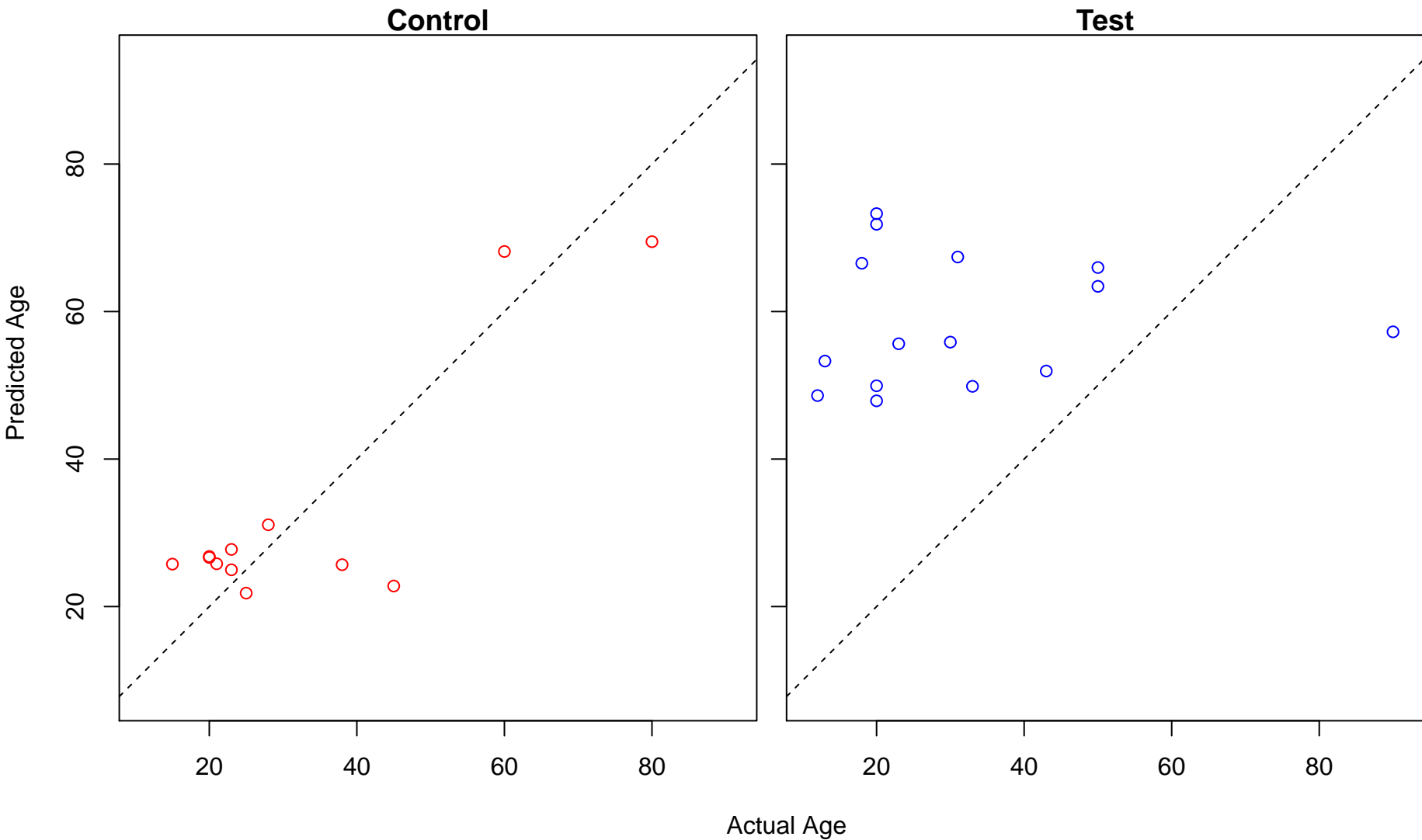


Test

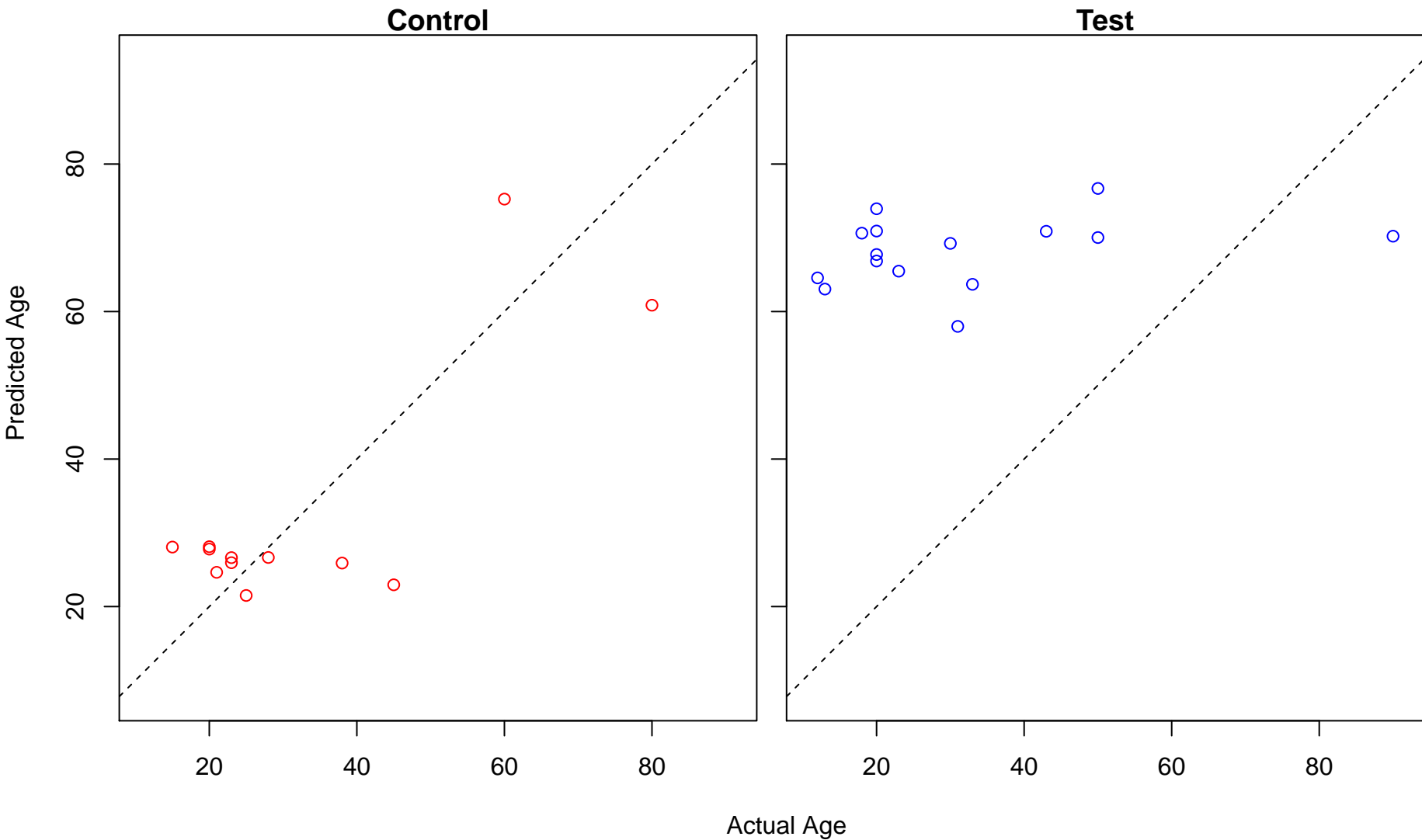


Actual Age

regulation of cation channel activity (Score: 4.576048)

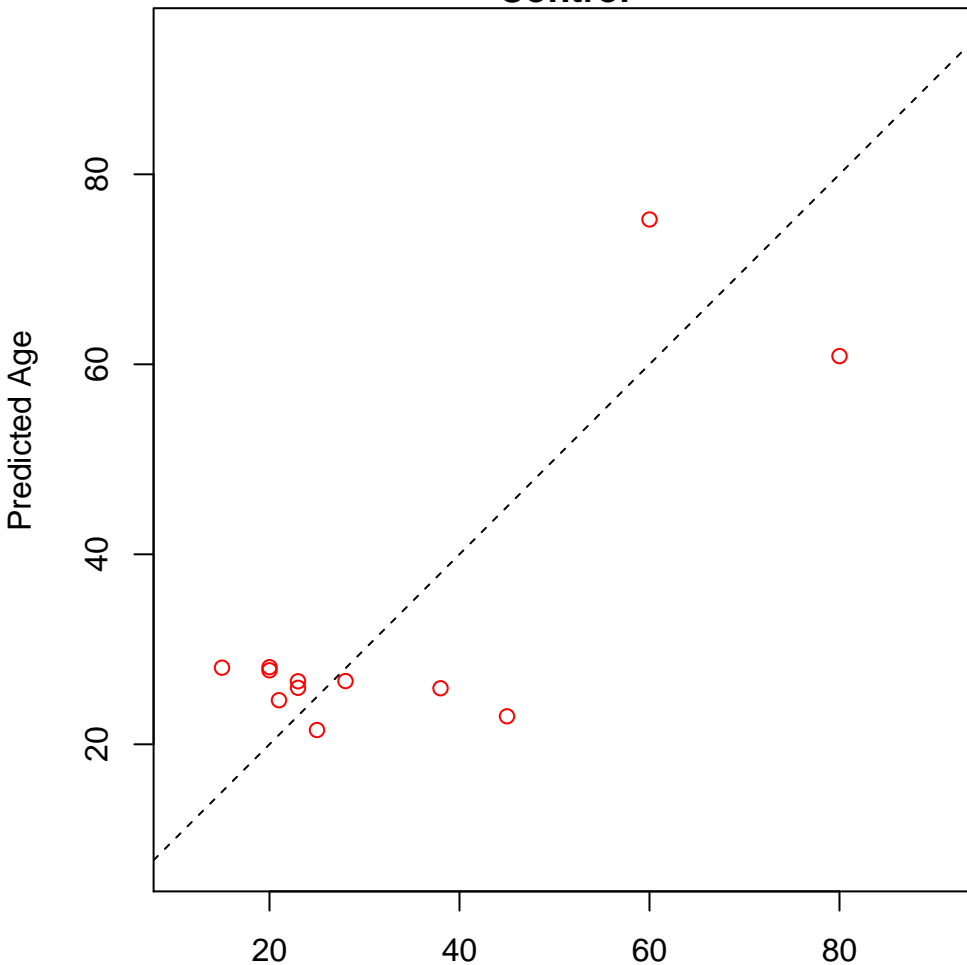


protein localization to plasma membrane (Score: 4.572523)

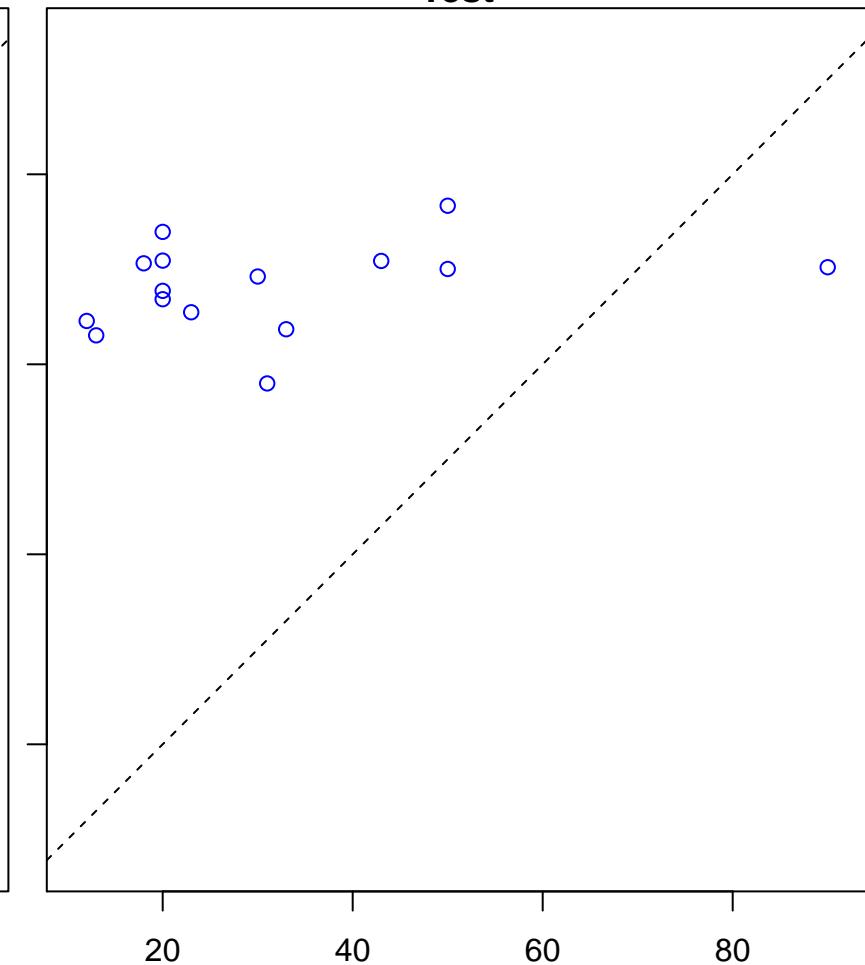


protein localization to cell periphery (Score: 4.572523)

Control

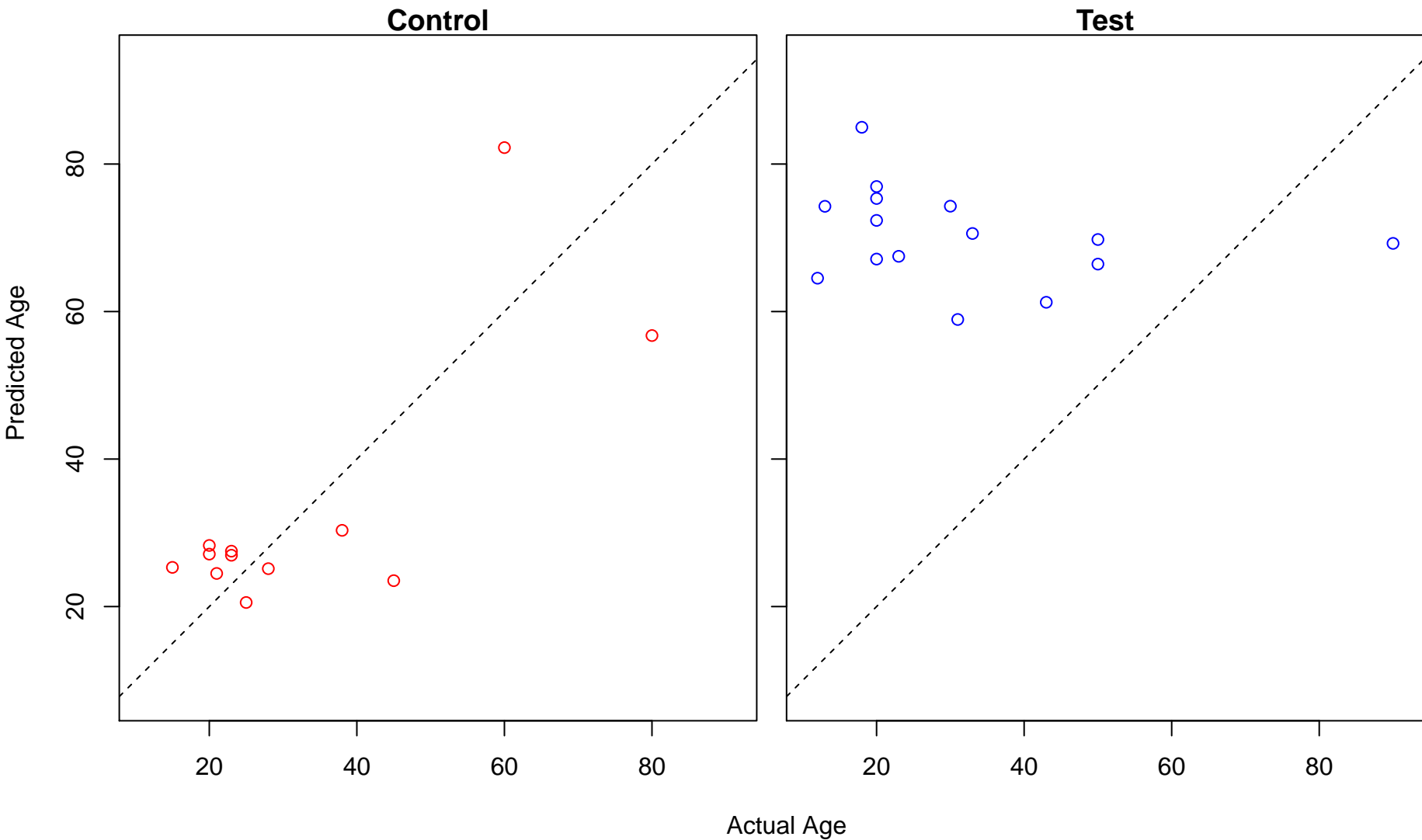


Test

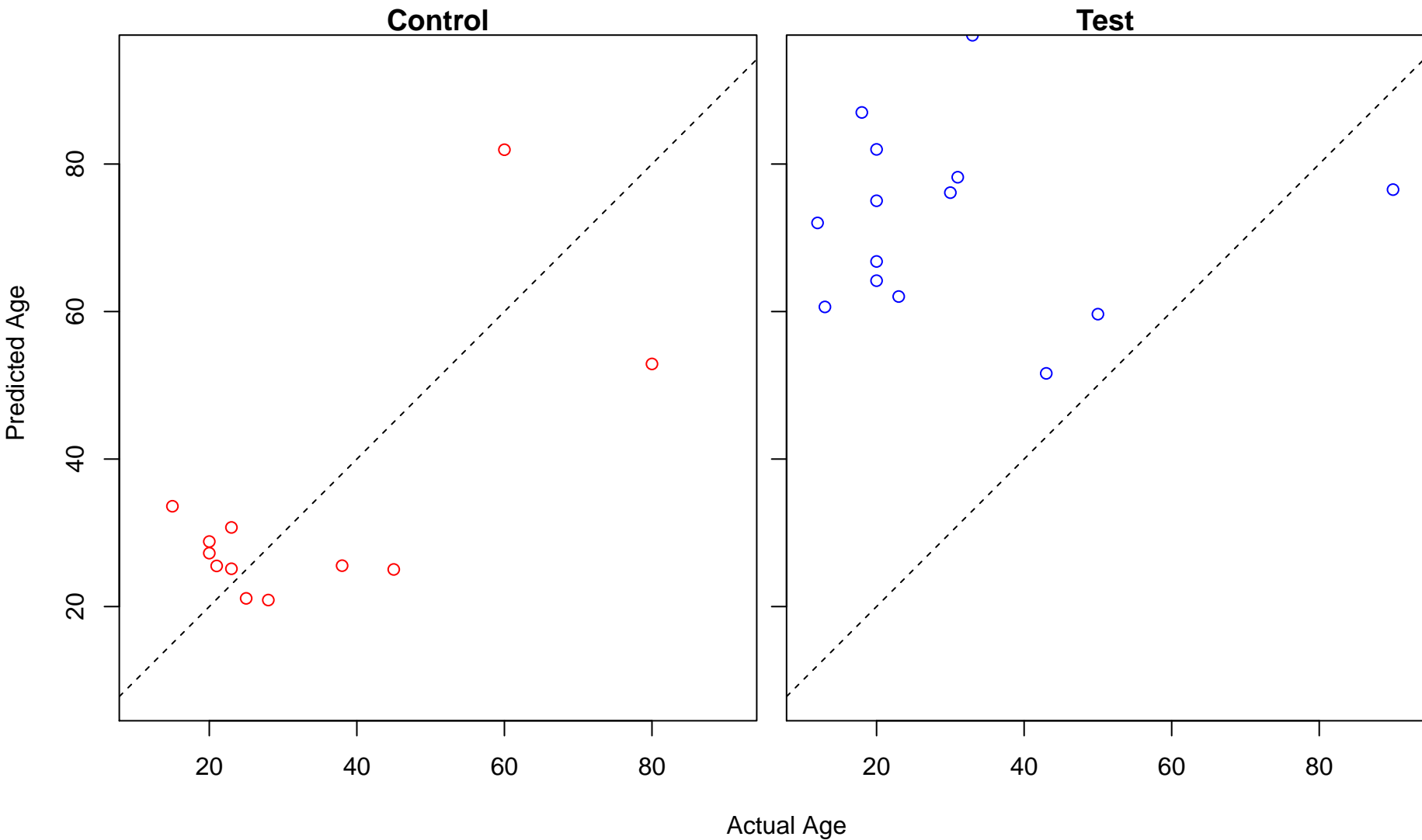


Actual Age

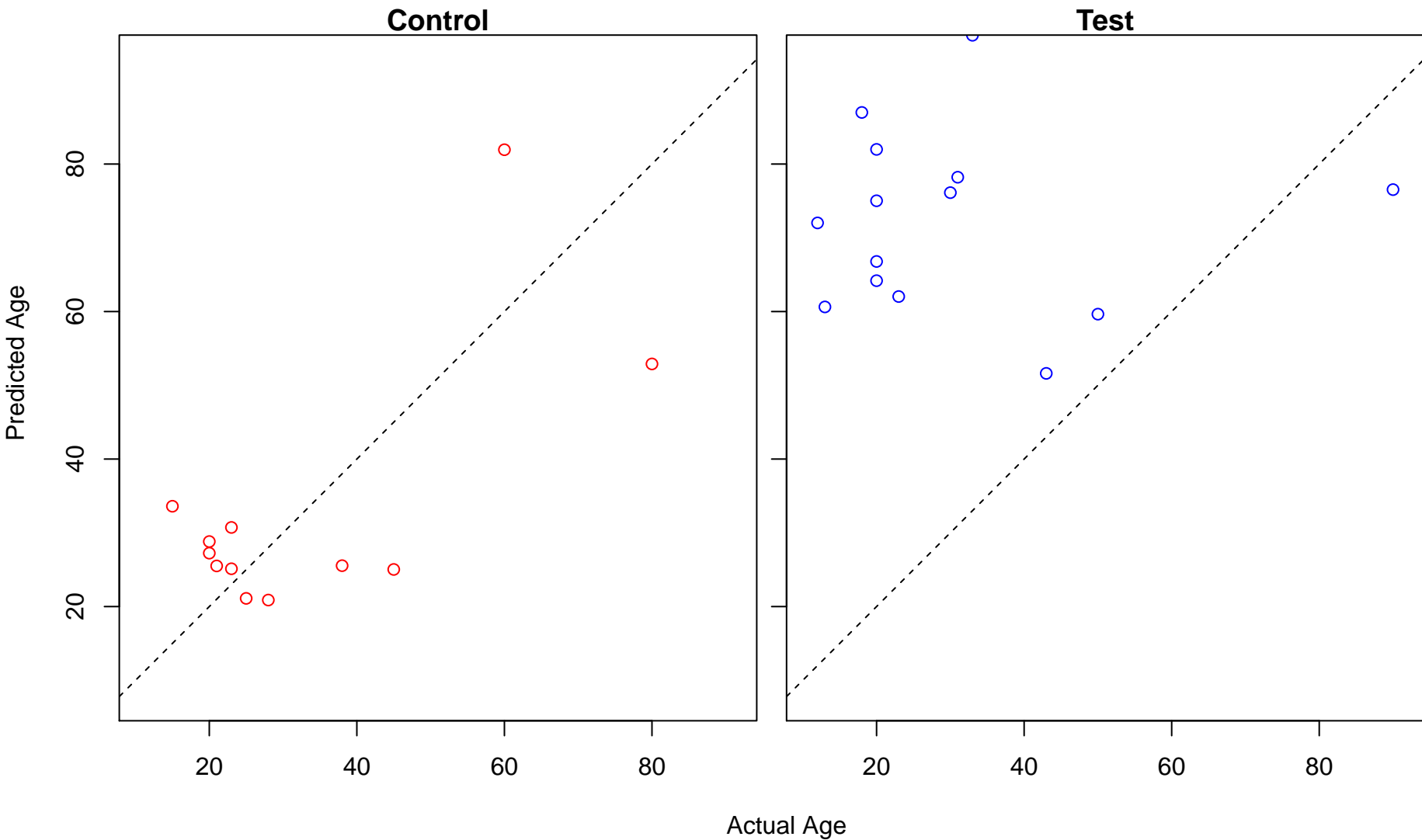
regulation of chromatin silencing (Score: 4.572168)



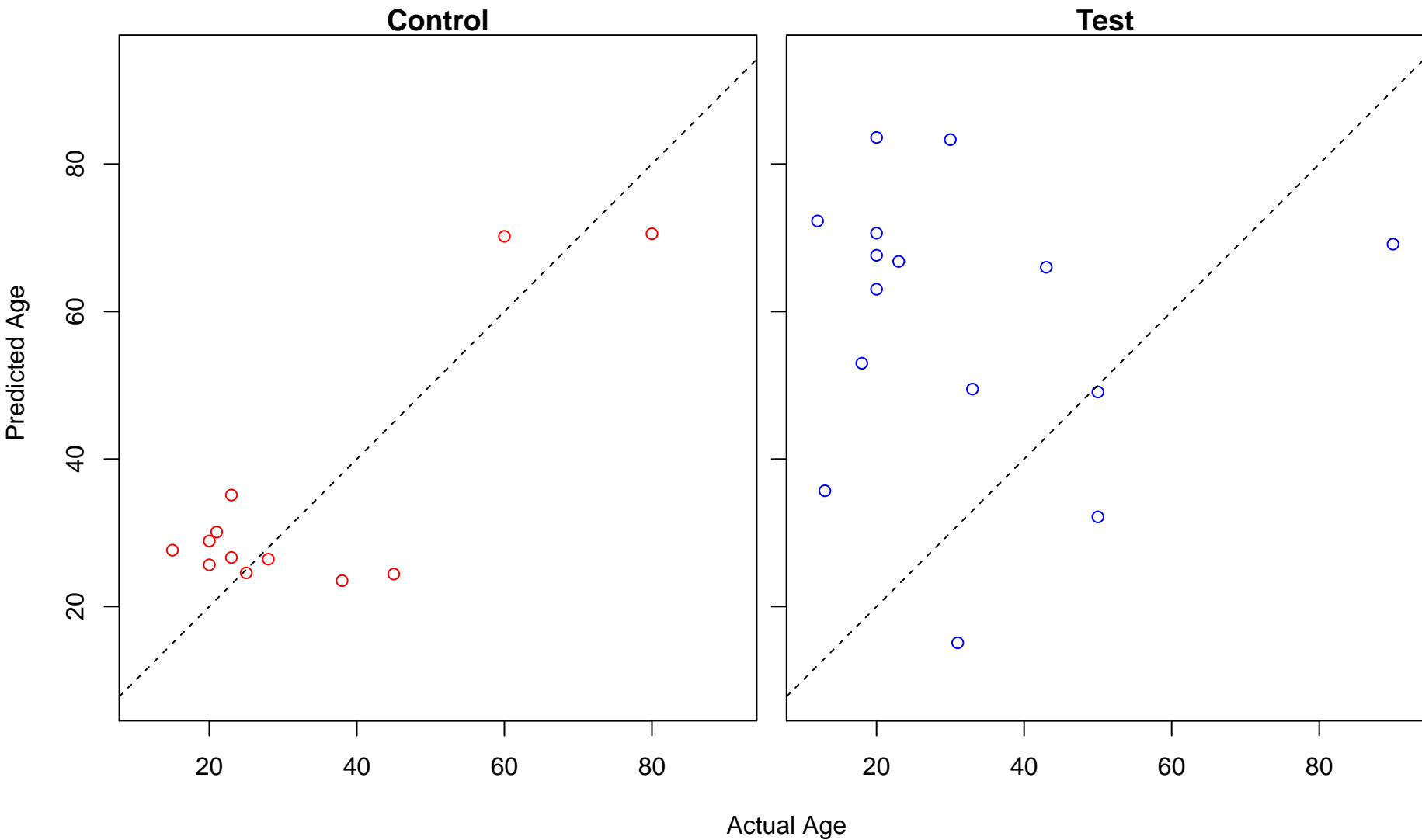
aortic valve development (Score: 4.571413)



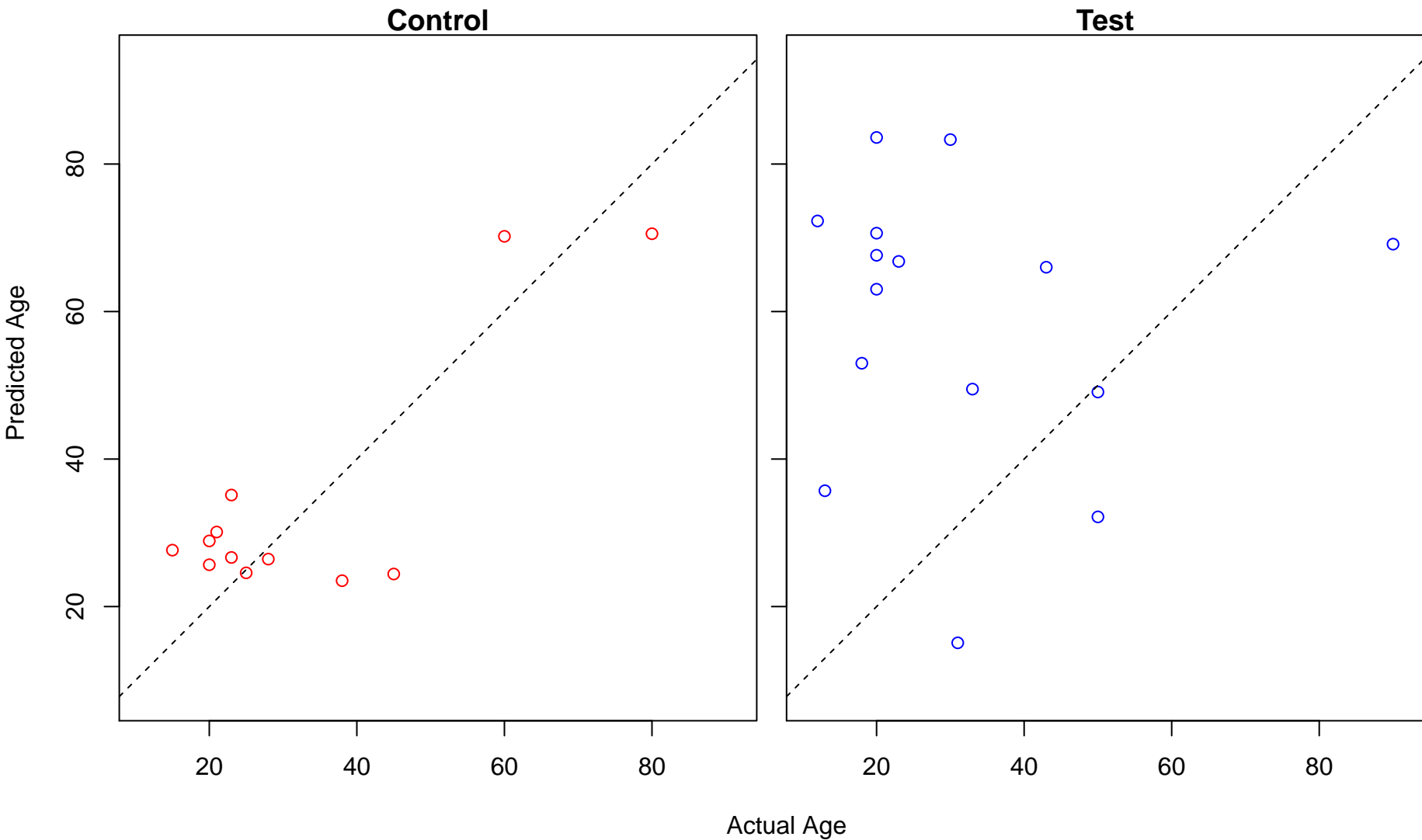
aortic valve morphogenesis (Score: 4.571413)



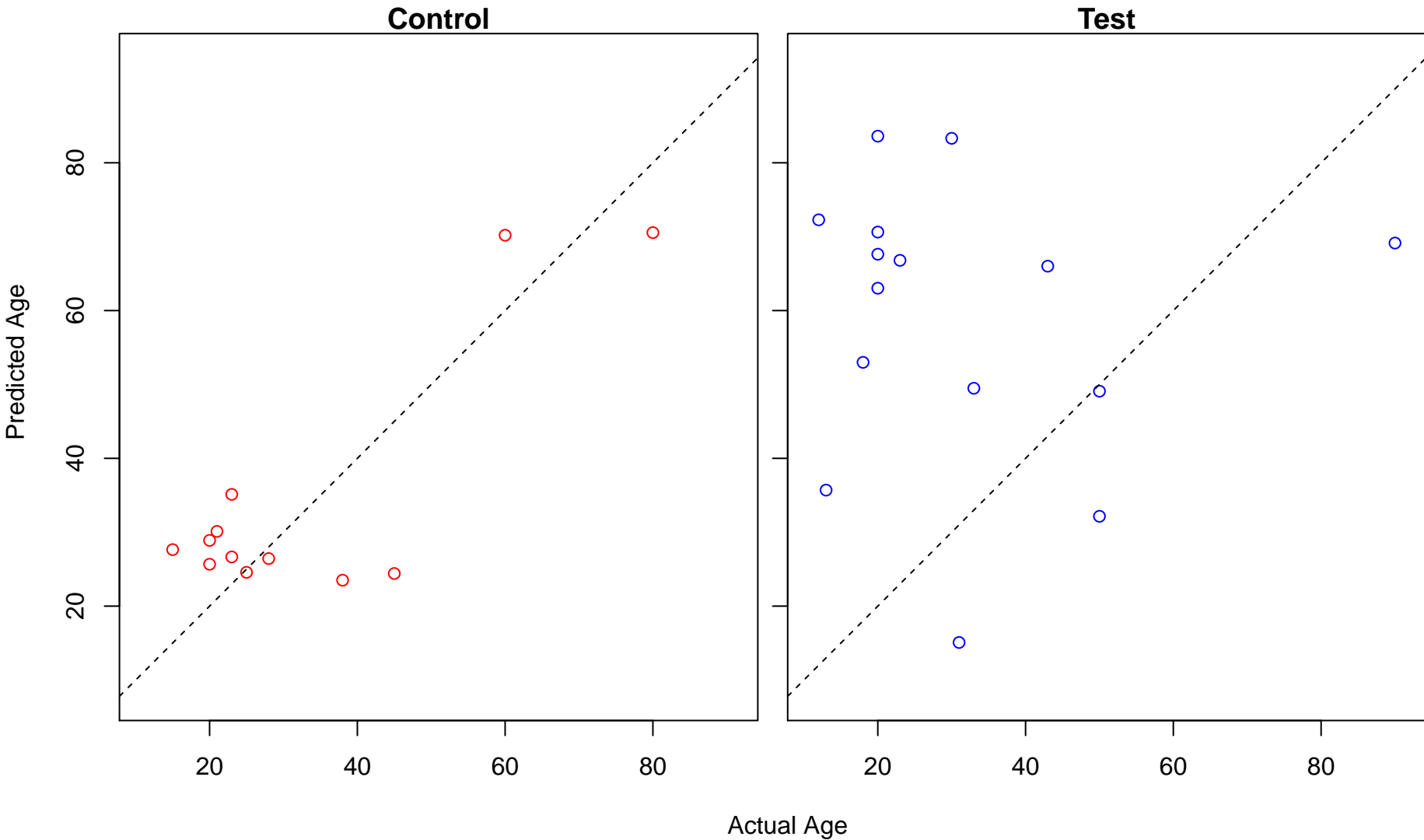
establishment of mitochondrion localization, microtubule-mediated (Score: 4.571135)



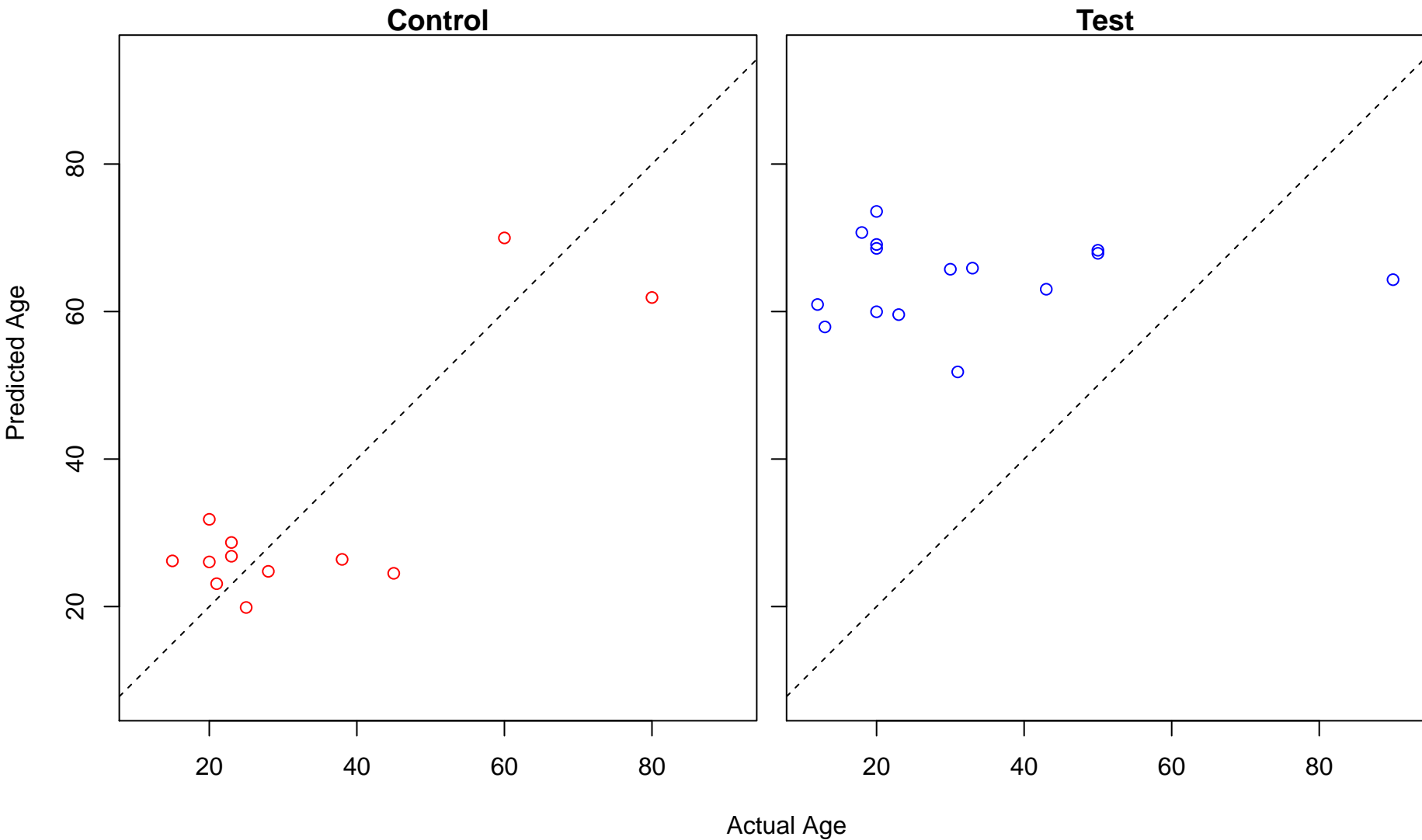
mitochondrion transport along microtubule (Score: 4.571135)



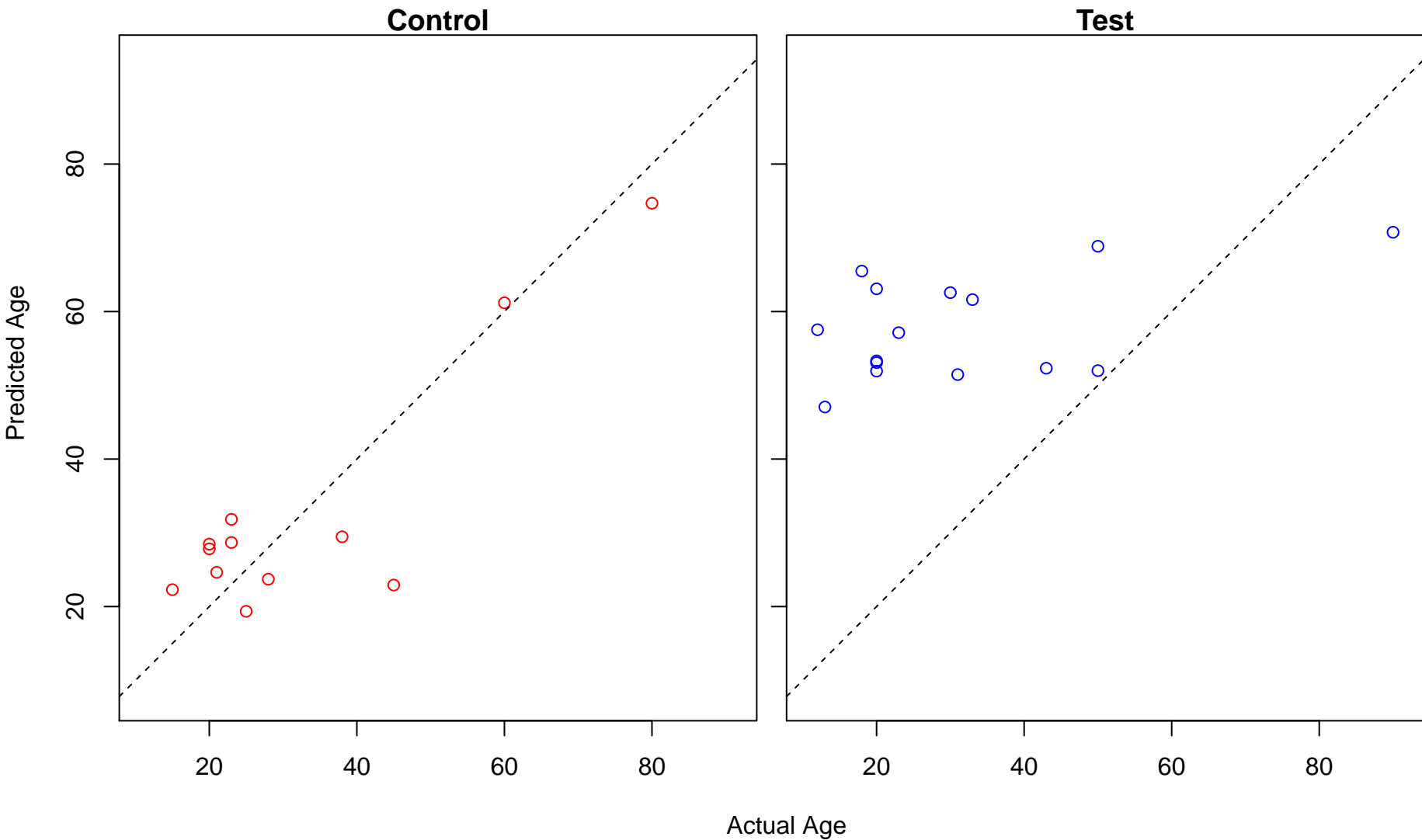
establishment of mitochondrion localization (Score: 4.571135)



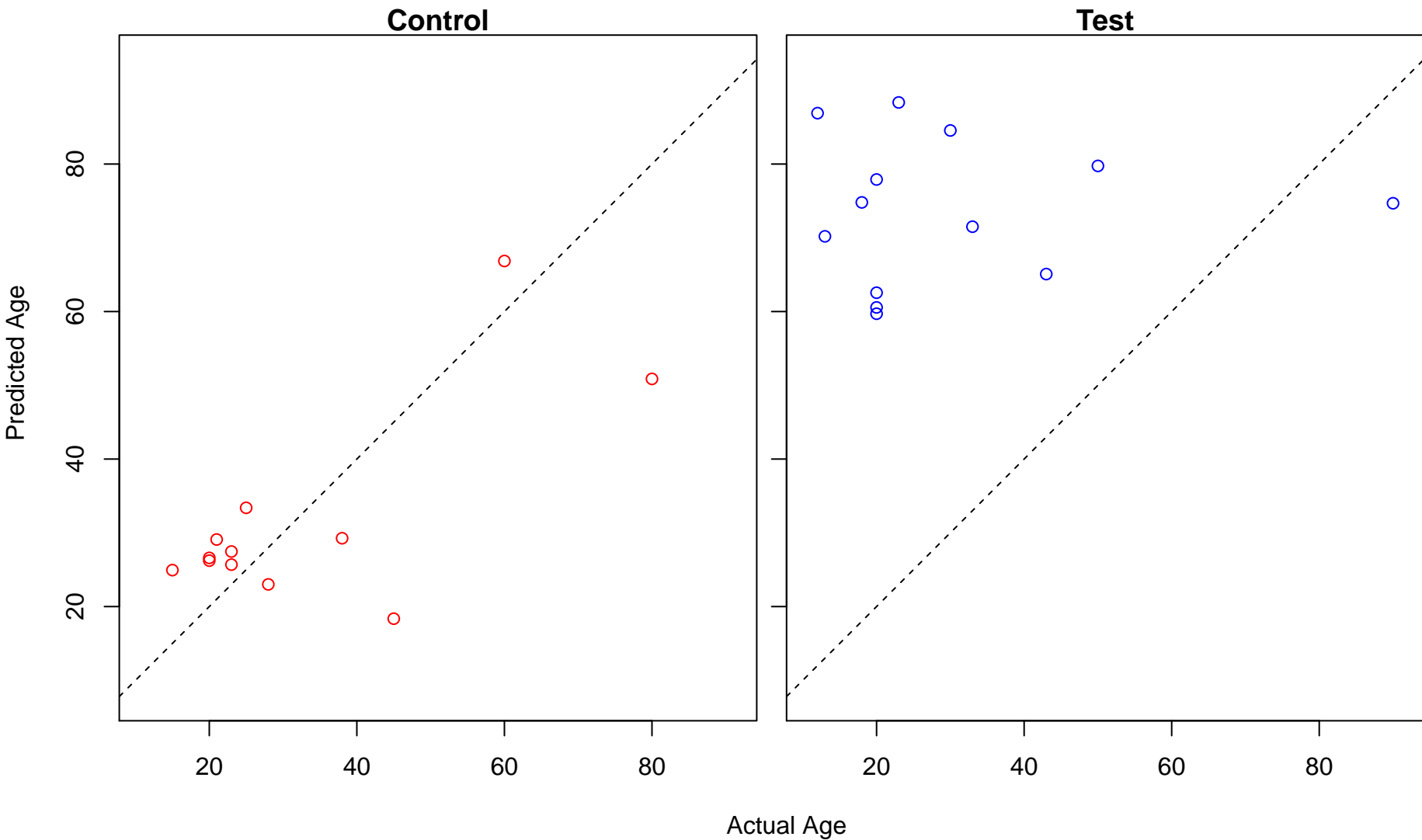
regulation of glycogen metabolic process (Score: 4.569754)



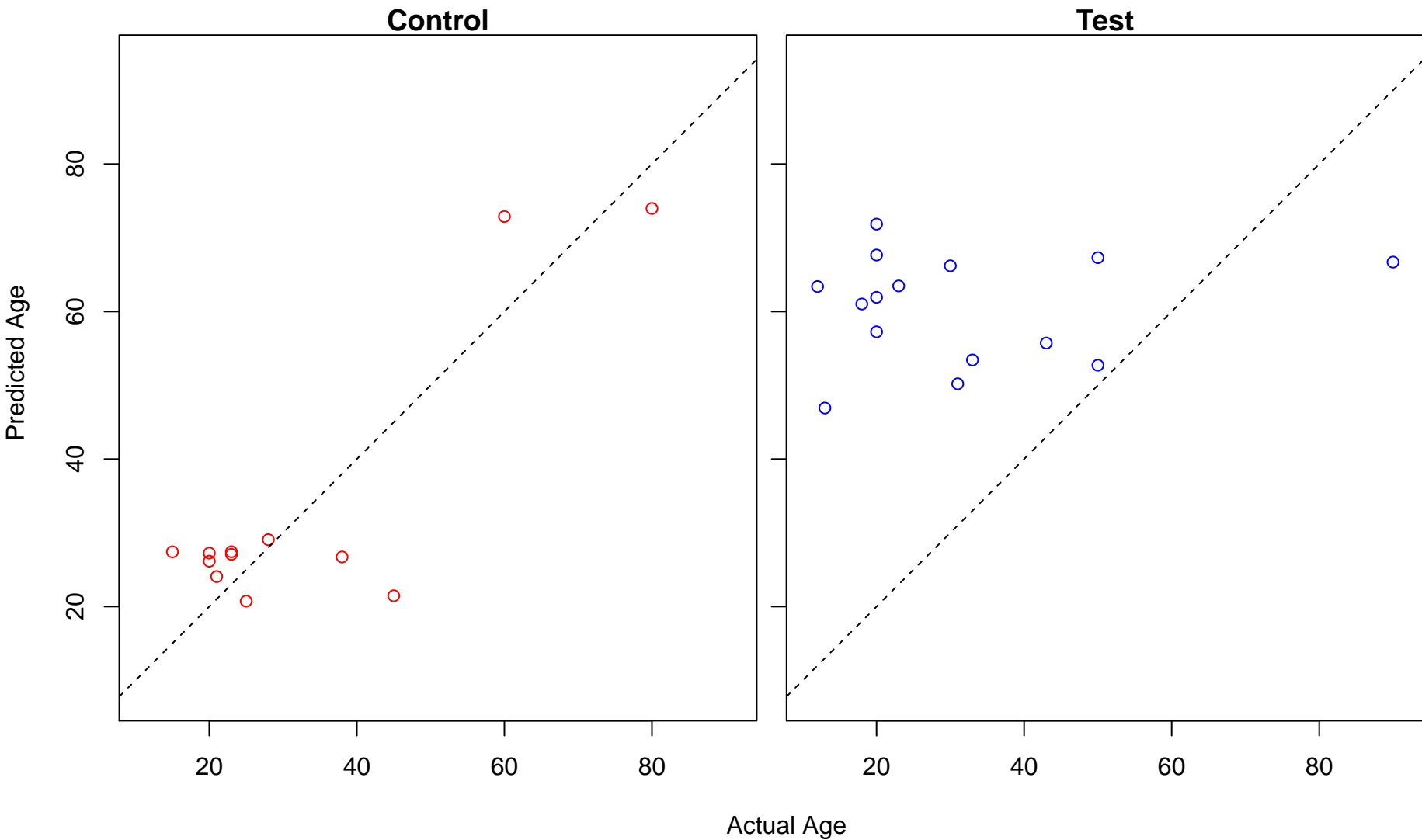
heterotypic cell-cell adhesion (Score: 4.569235)



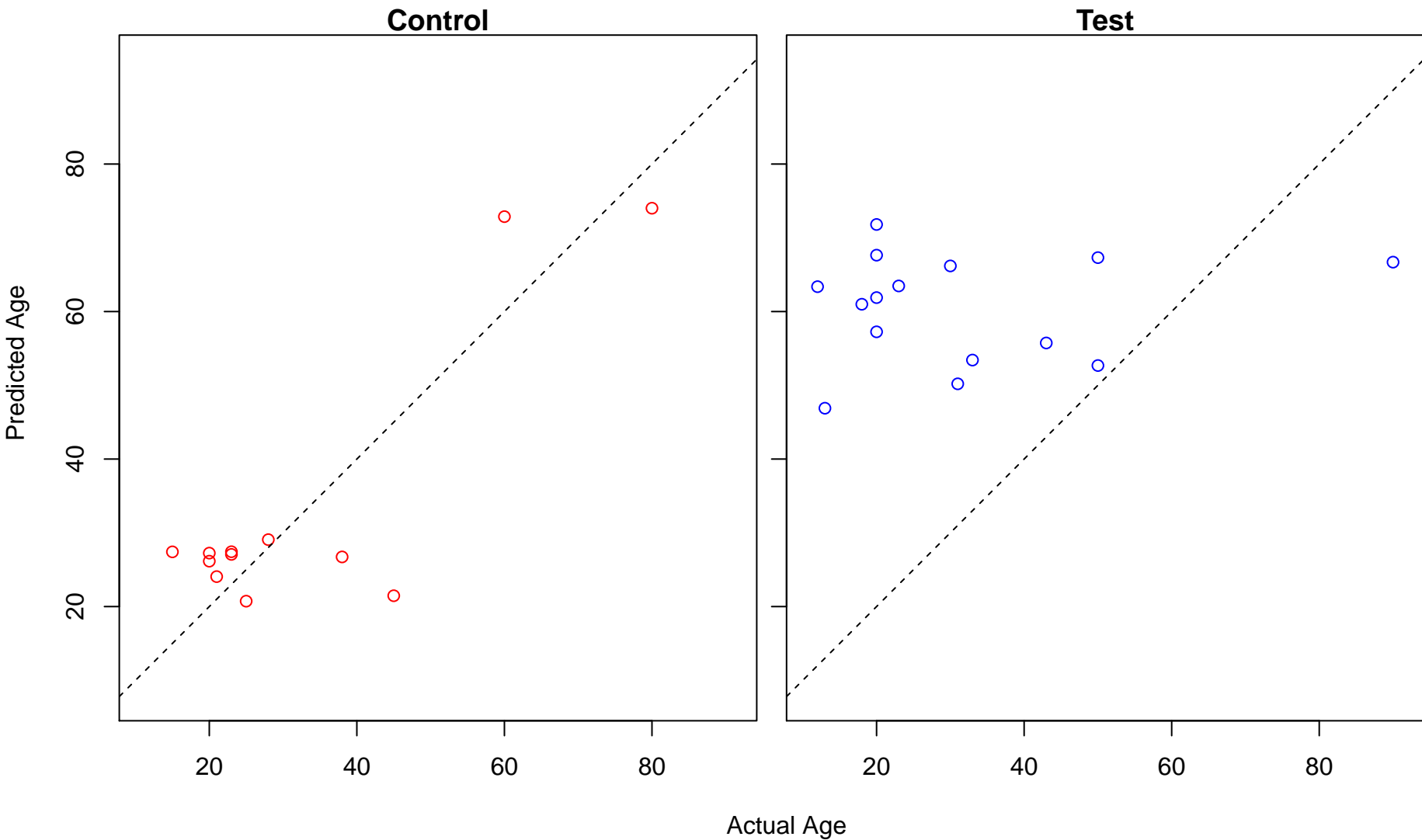
tachykinin receptor signaling pathway (Score: 4.567581)



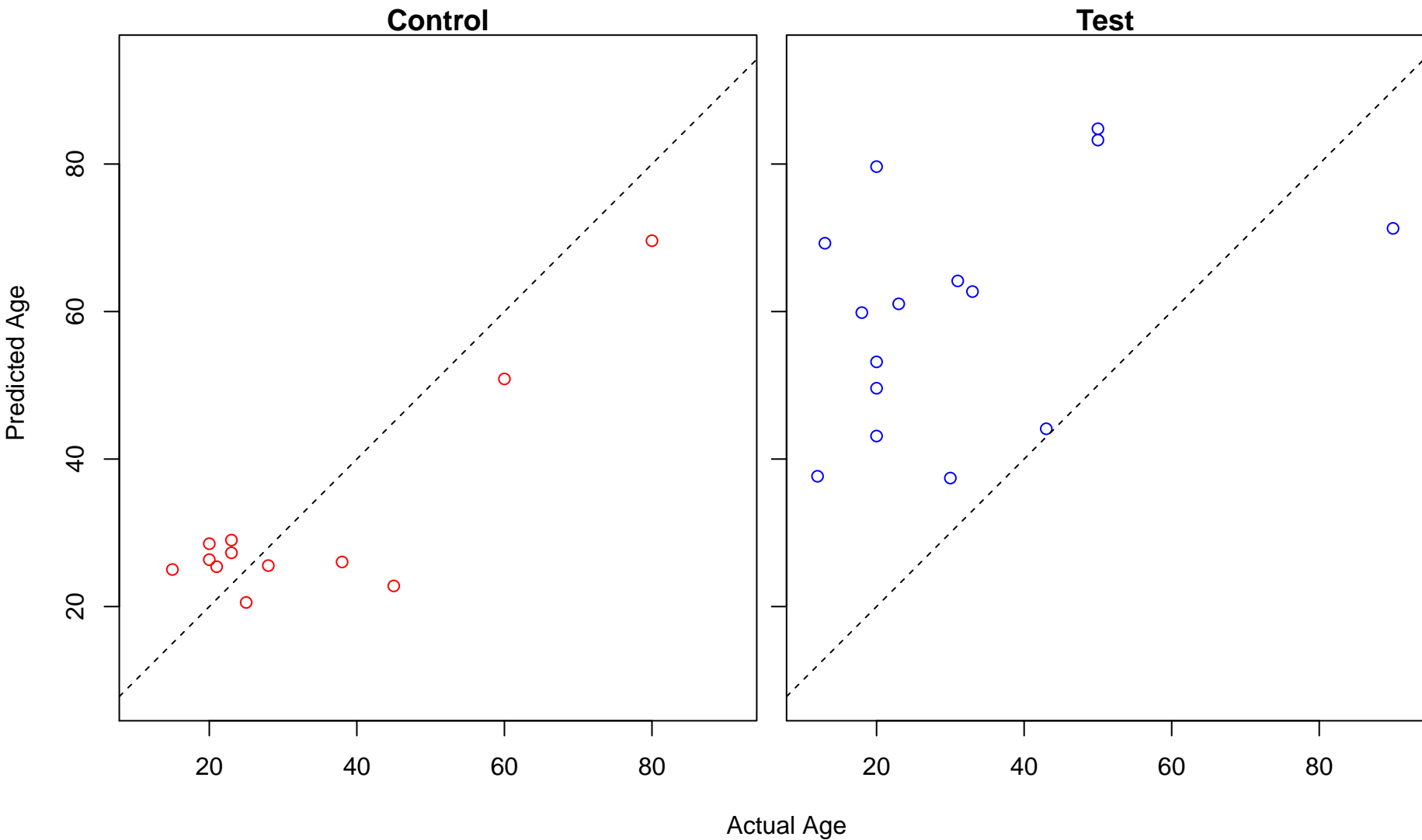
establishment of vesicle localization (Score: 4.566386)



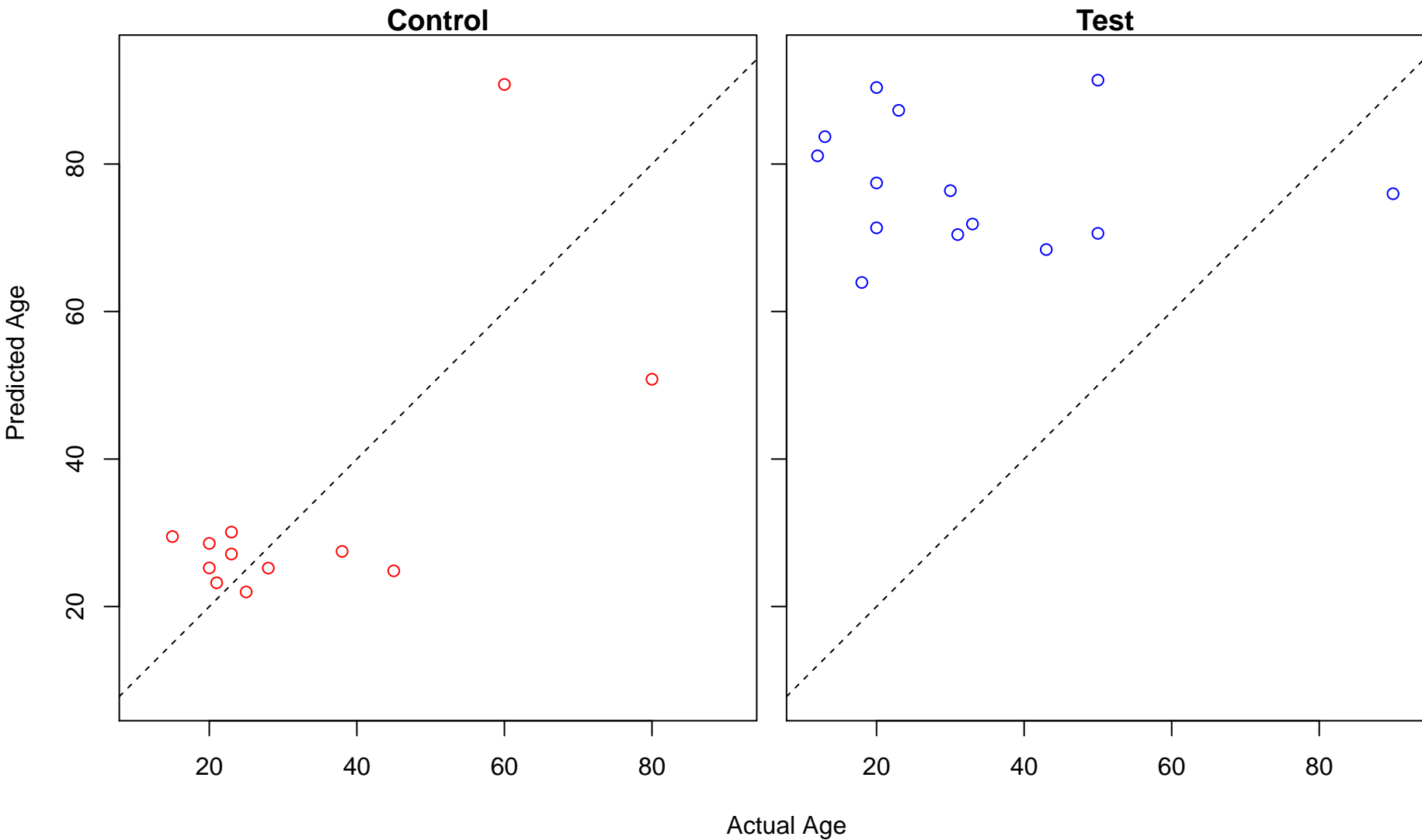
vesicle localization (Score: 4.566055)



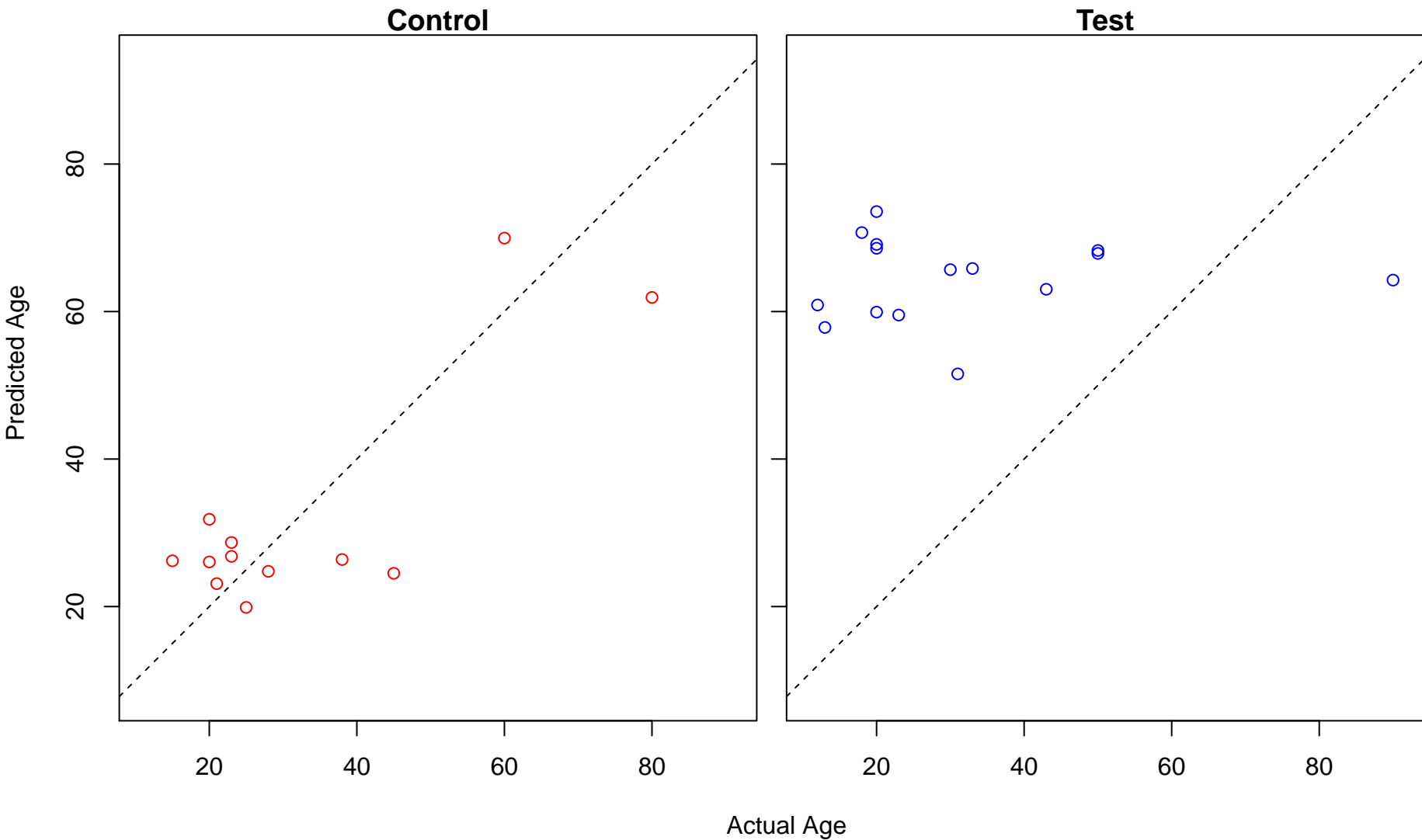
regulation of transforming growth factor beta production (Score: 4.564884)



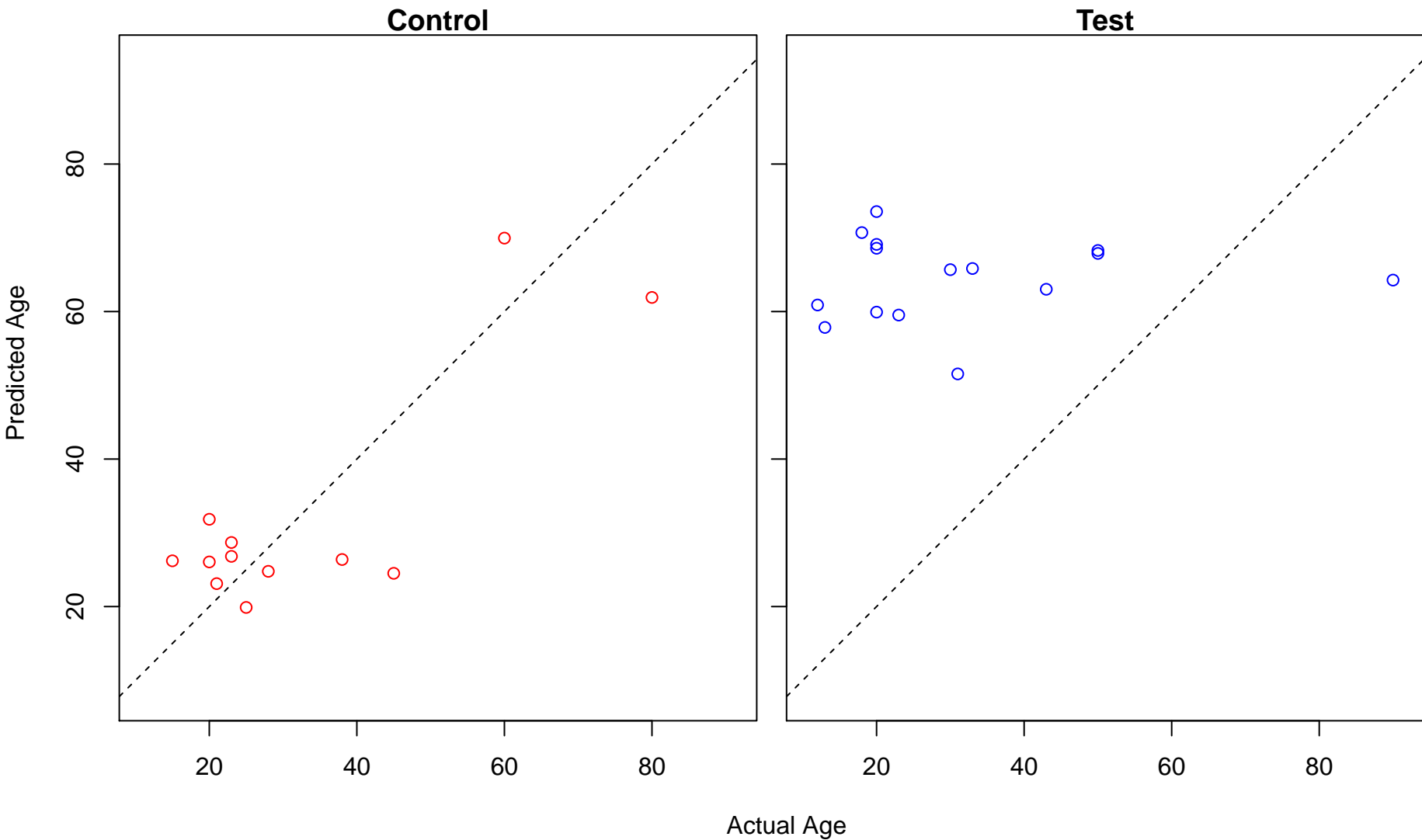
DNA methylation involved in gamete generation (Score: 4.564653)



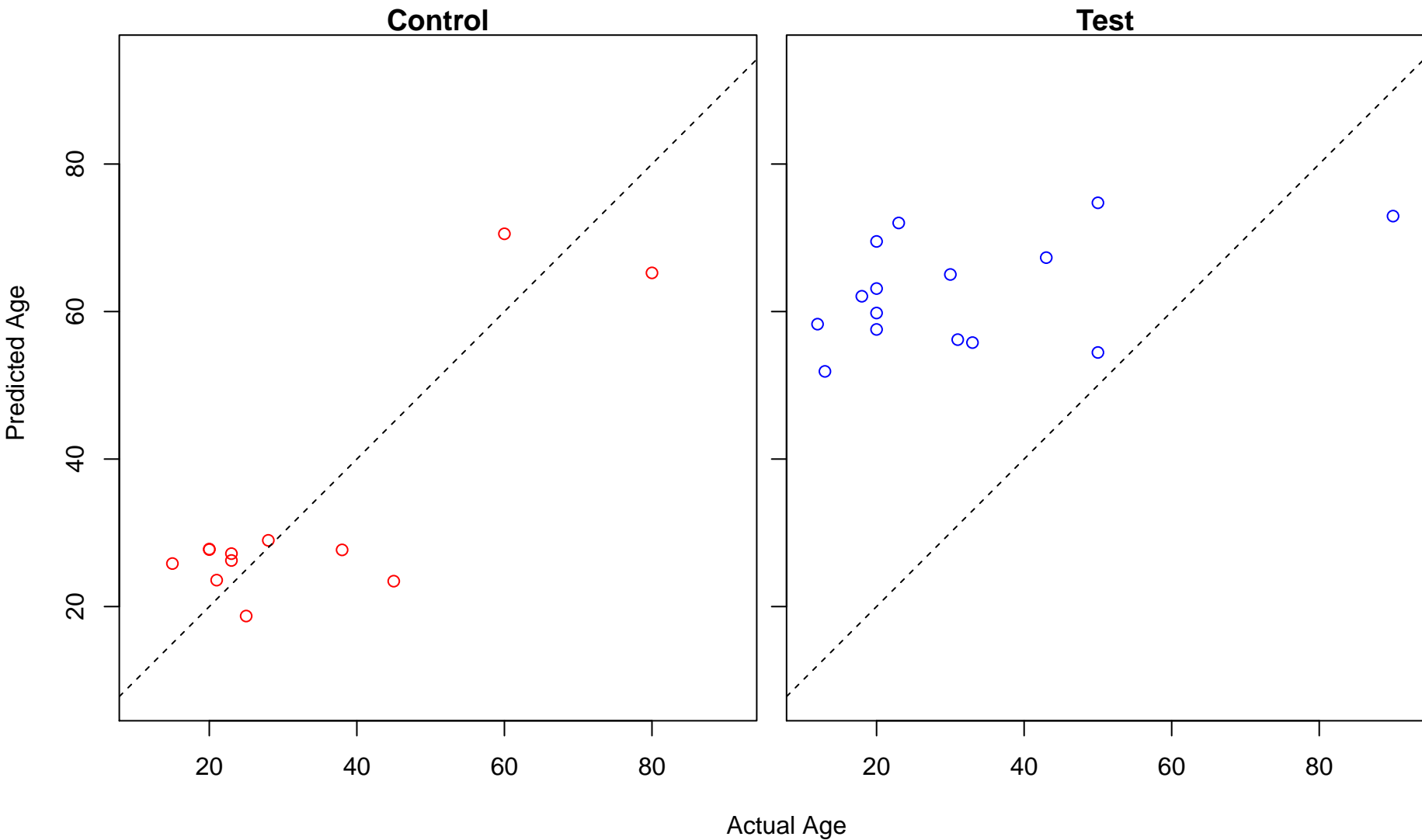
regulation of glycogen biosynthetic process (Score: 4.563483)



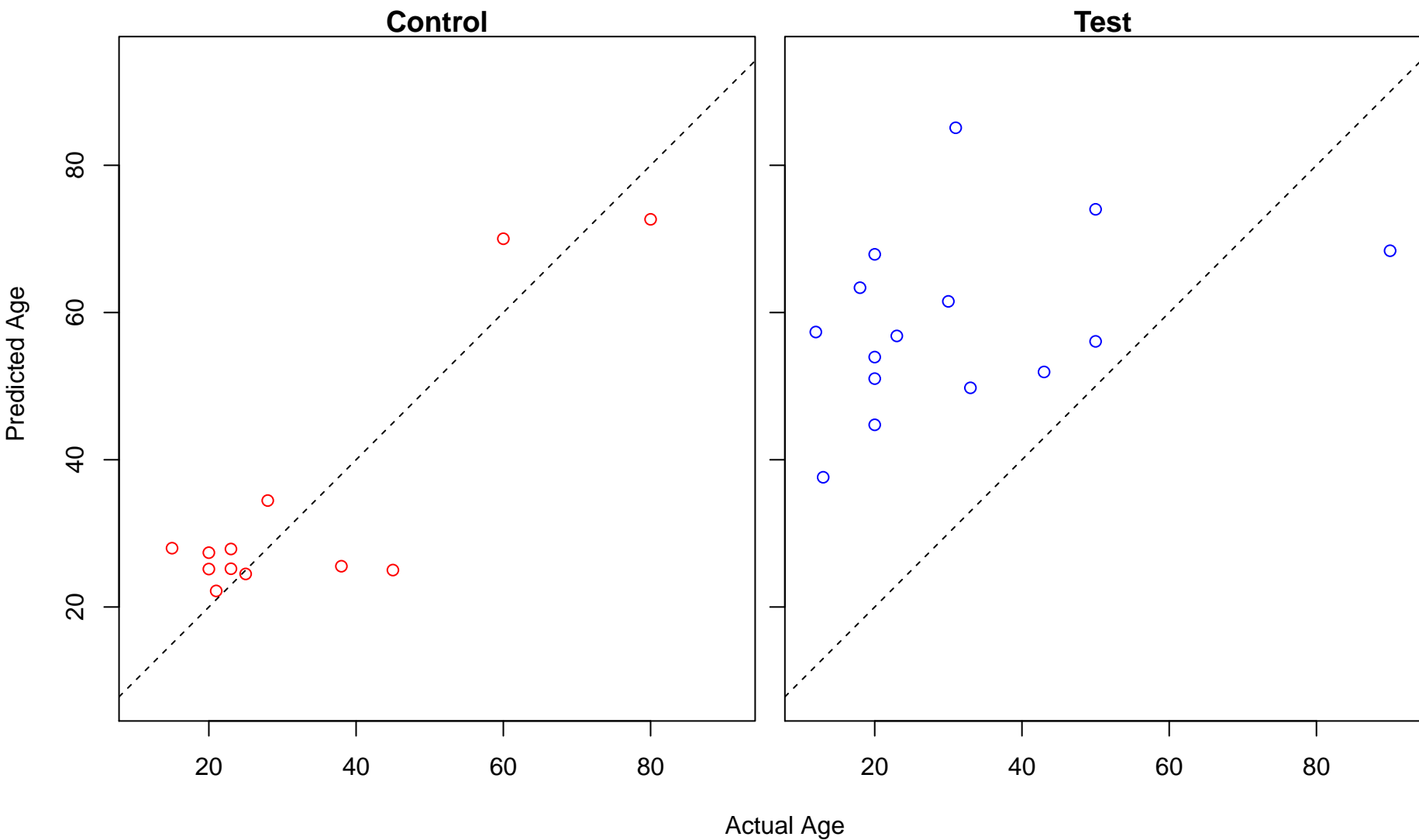
regulation of glucan biosynthetic process (Score: 4.563483)



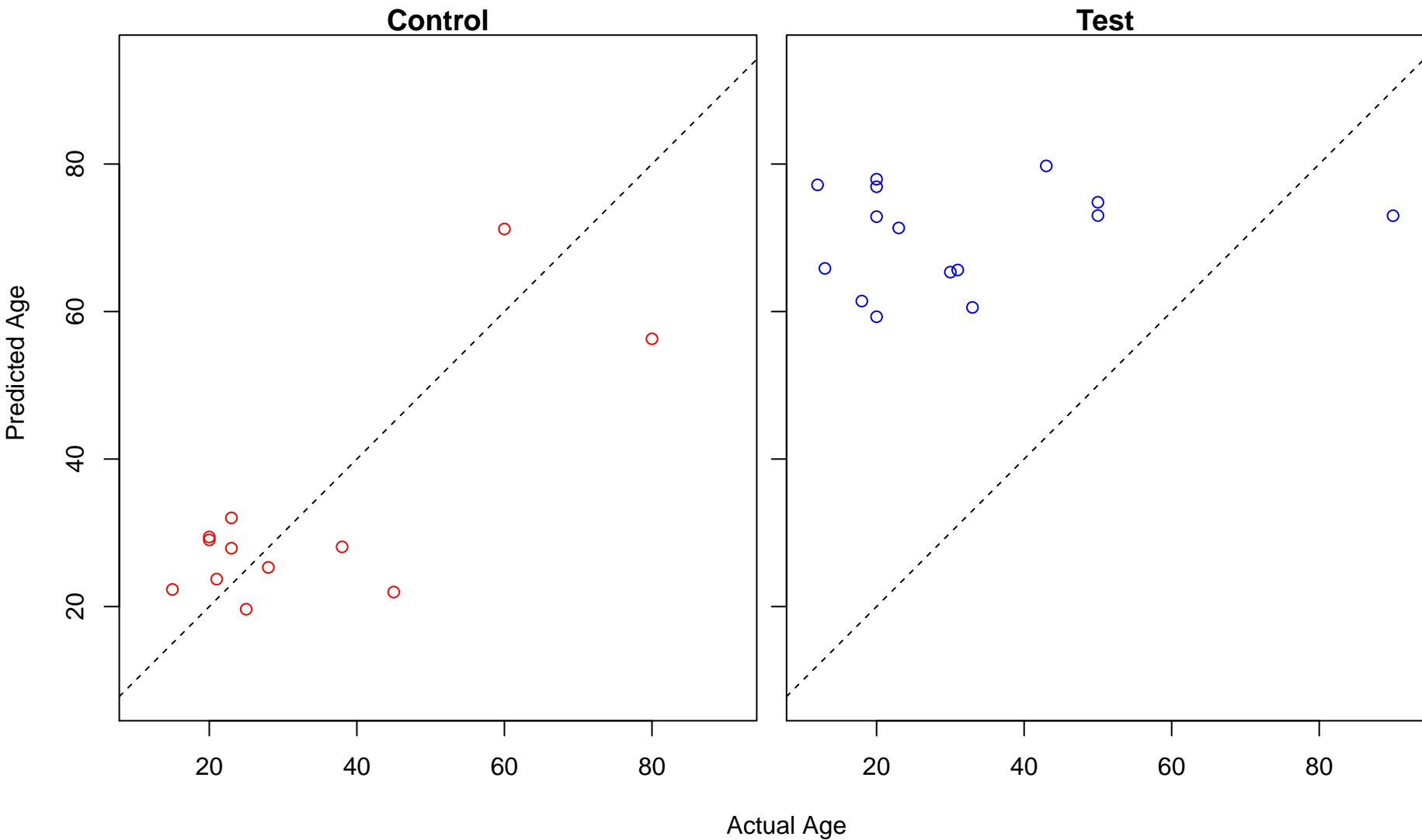
actin cytoskeleton reorganization (Score: 4.563074)



positive regulation of autophagosome assembly (Score: 4.560538)

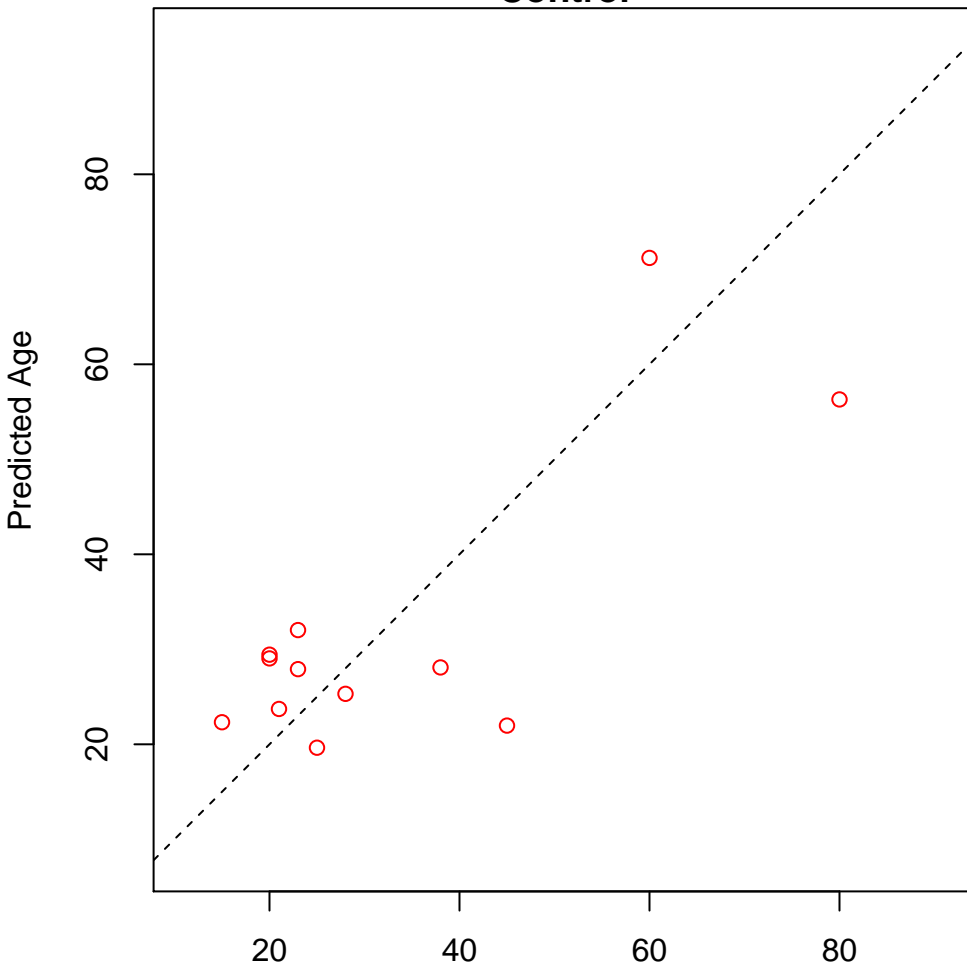


L-aspartate transport (Score: 4.560490)

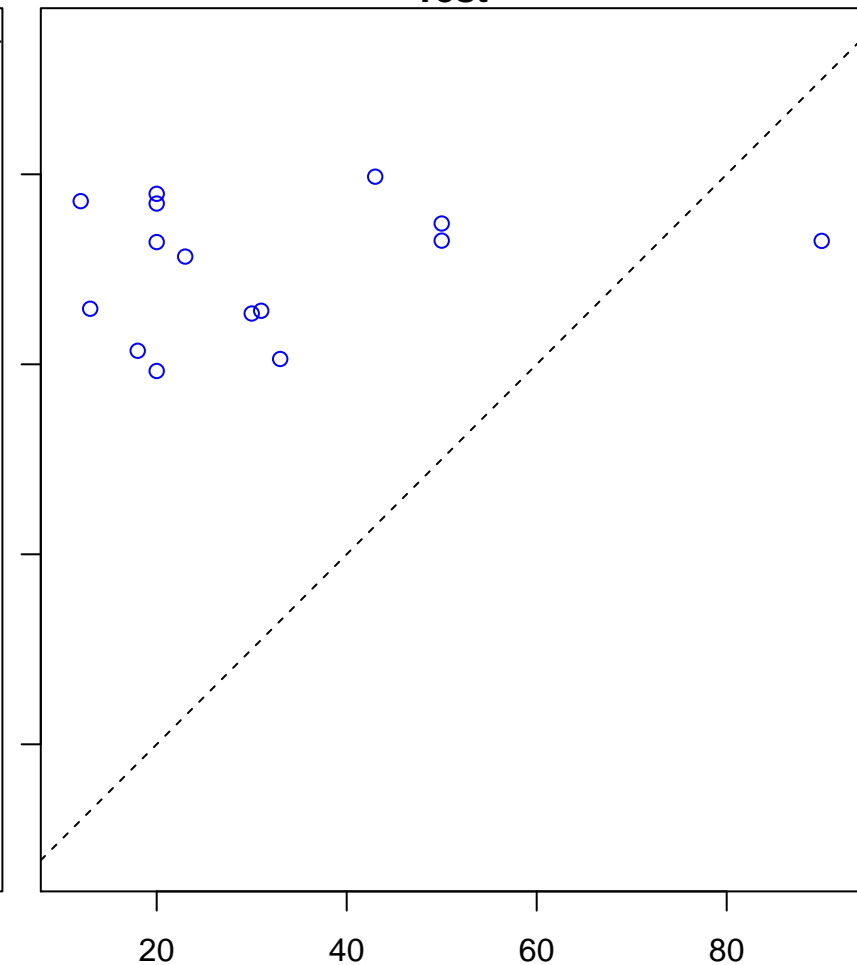


L-aspartate transmembrane transport (Score: 4.560490)

Control

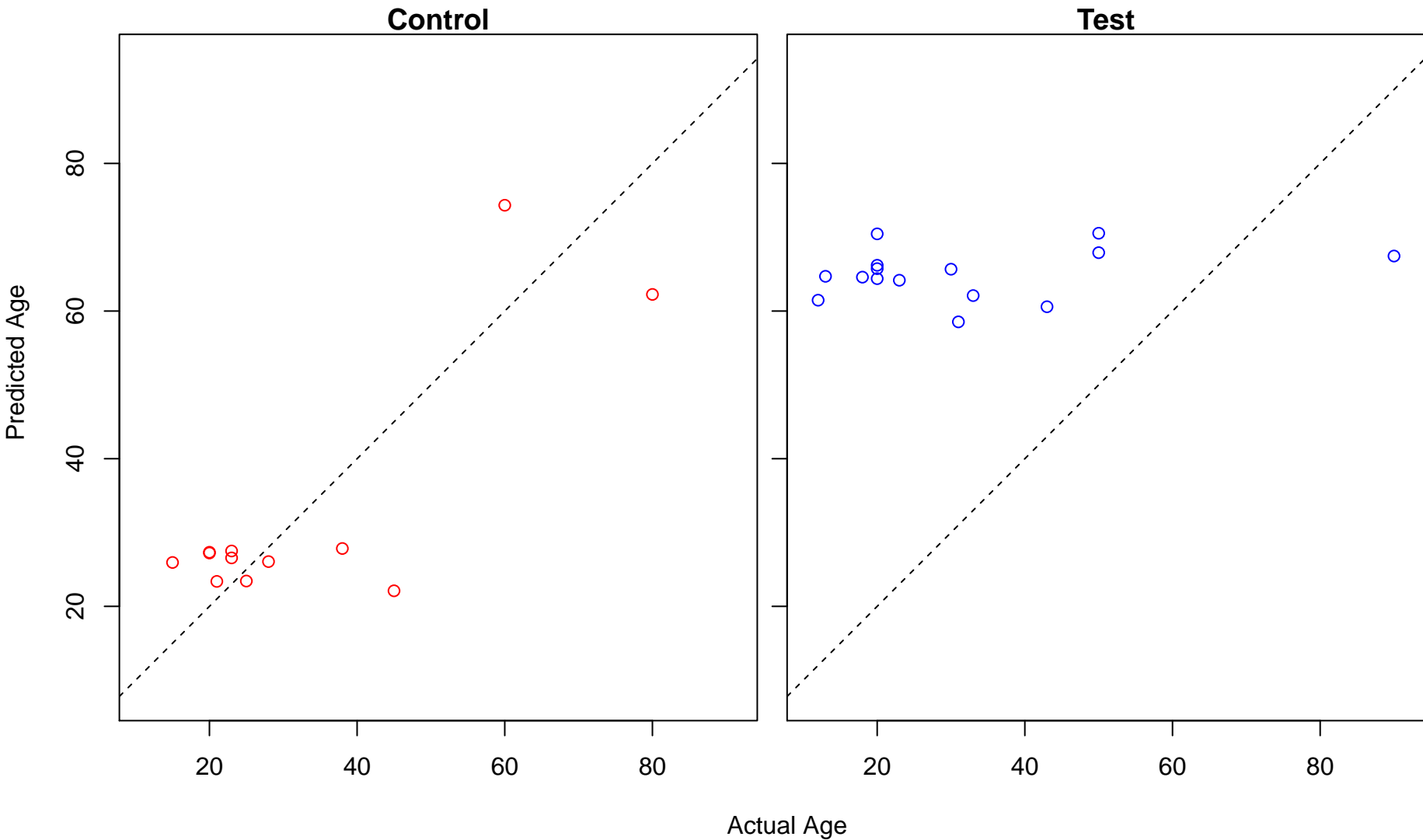


Test

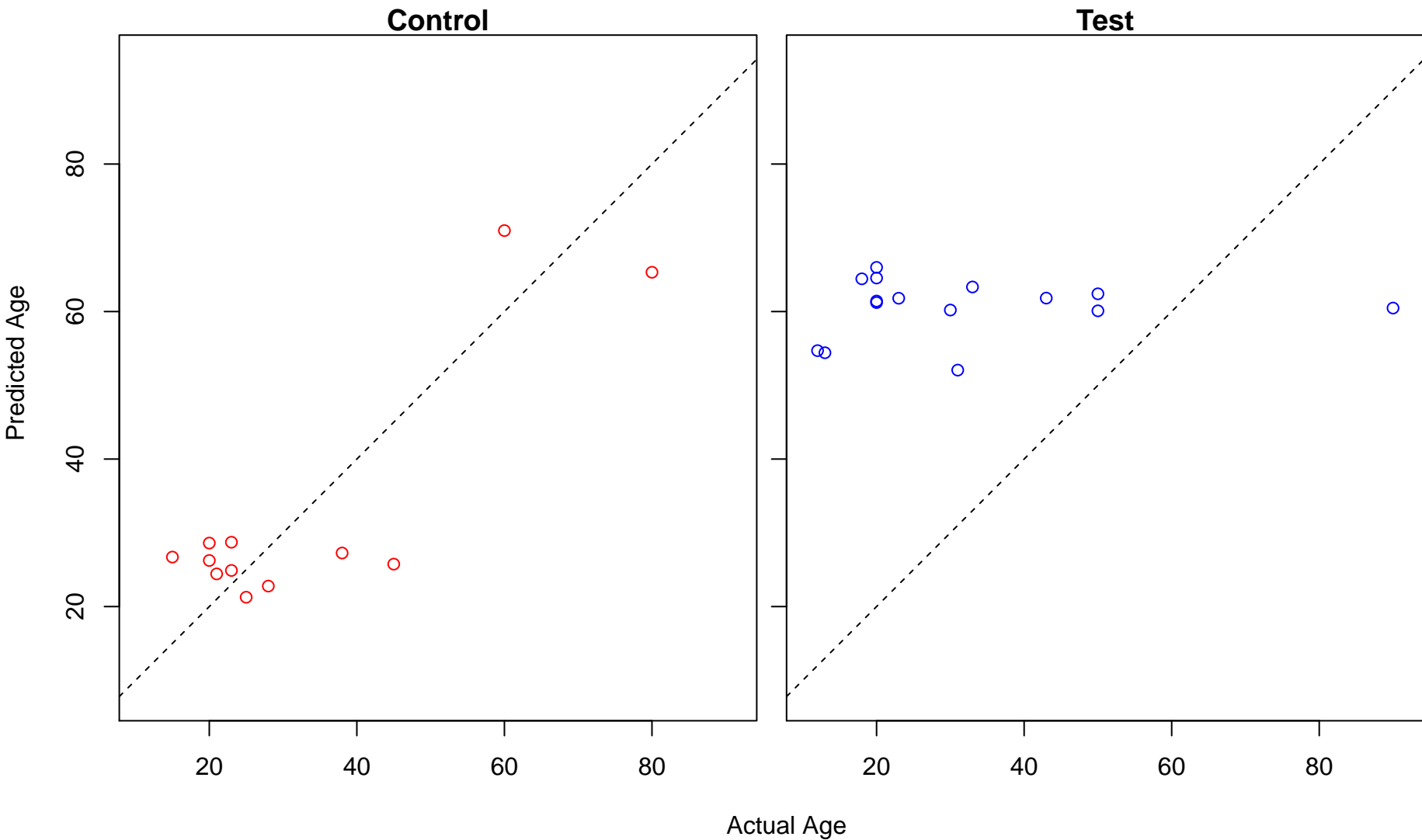


Actual Age

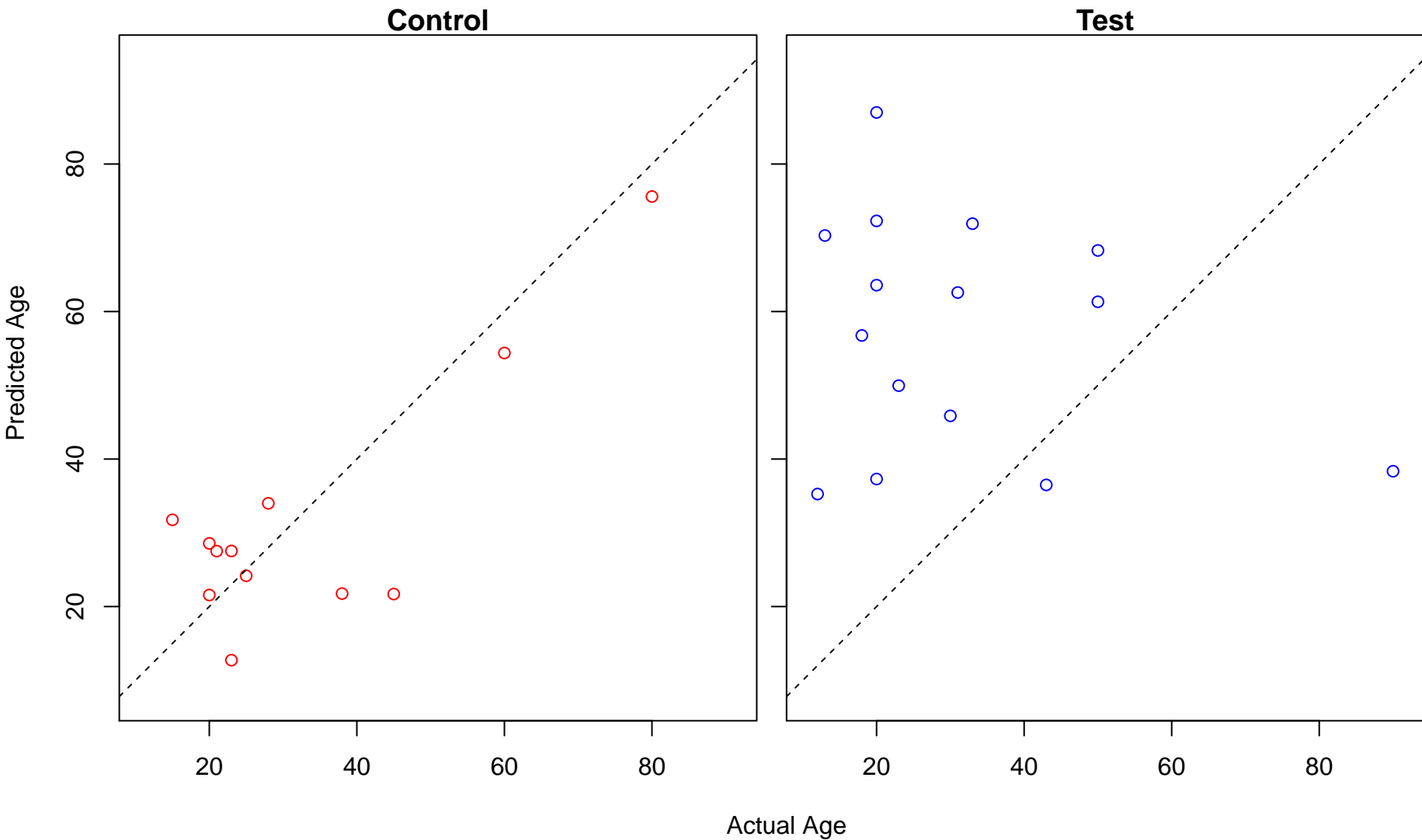
negative regulation of mRNA metabolic process (Score: 4.559516)



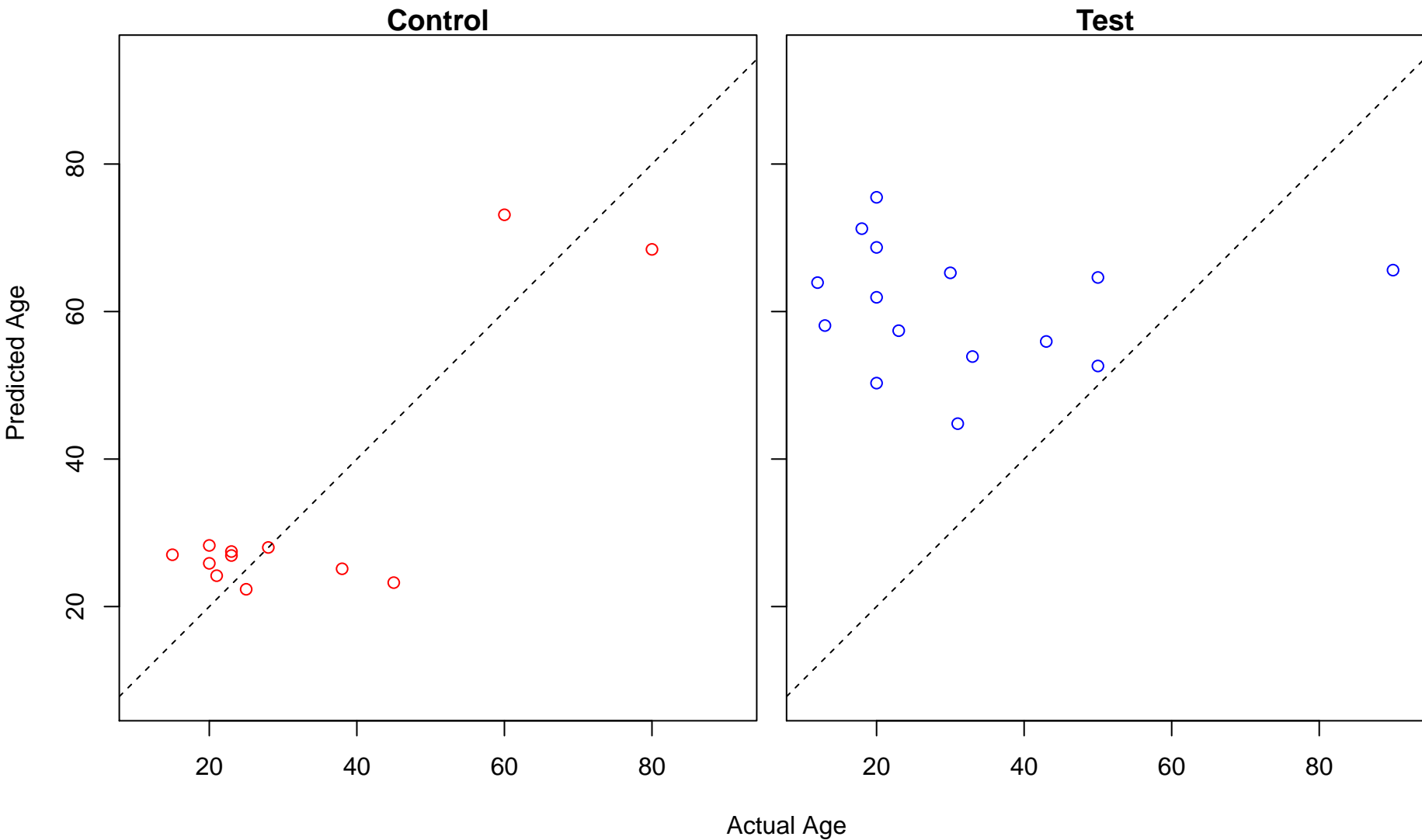
heart growth (Score: 4.557279)



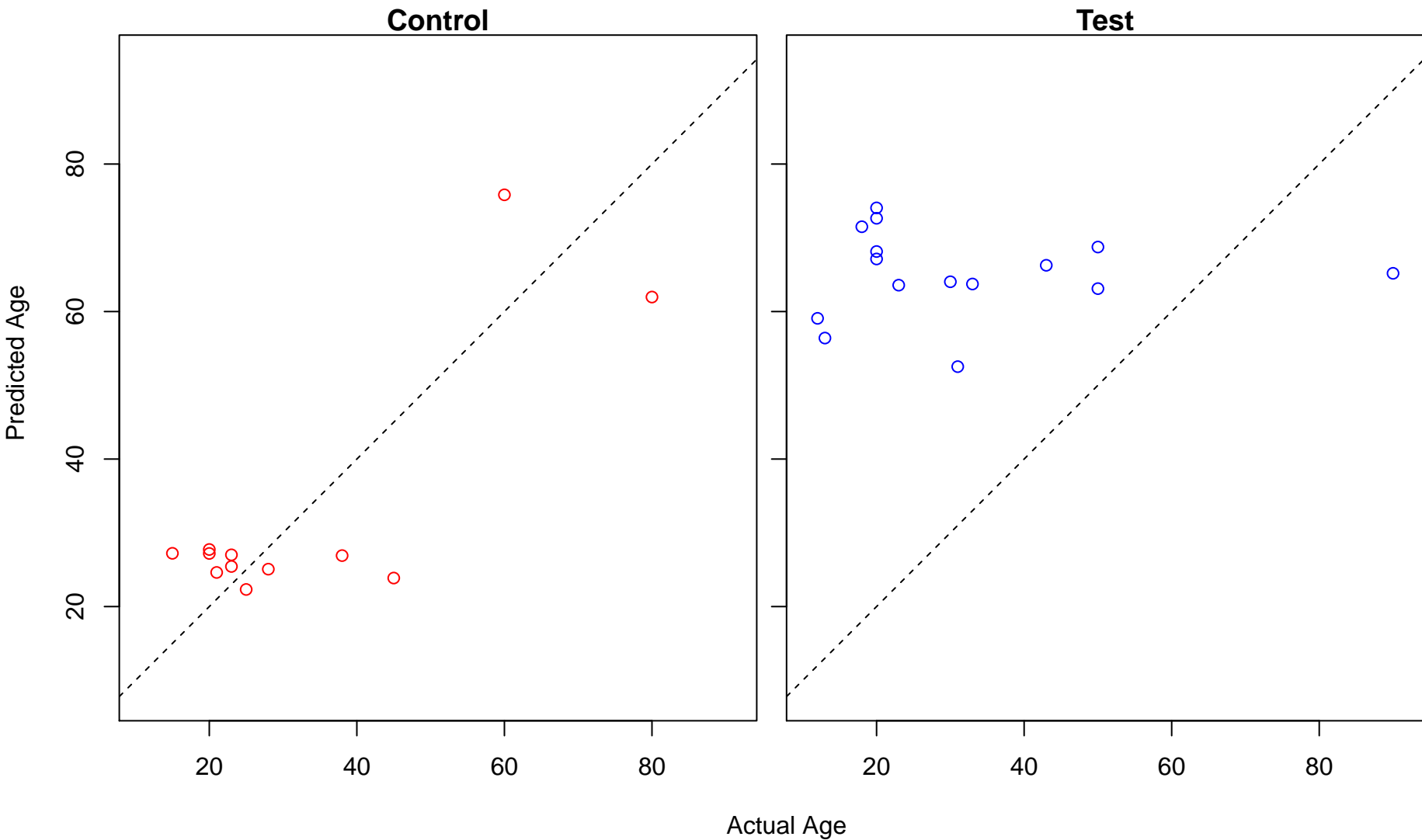
regulation of phospholipase C activity (Score: 4.557220)



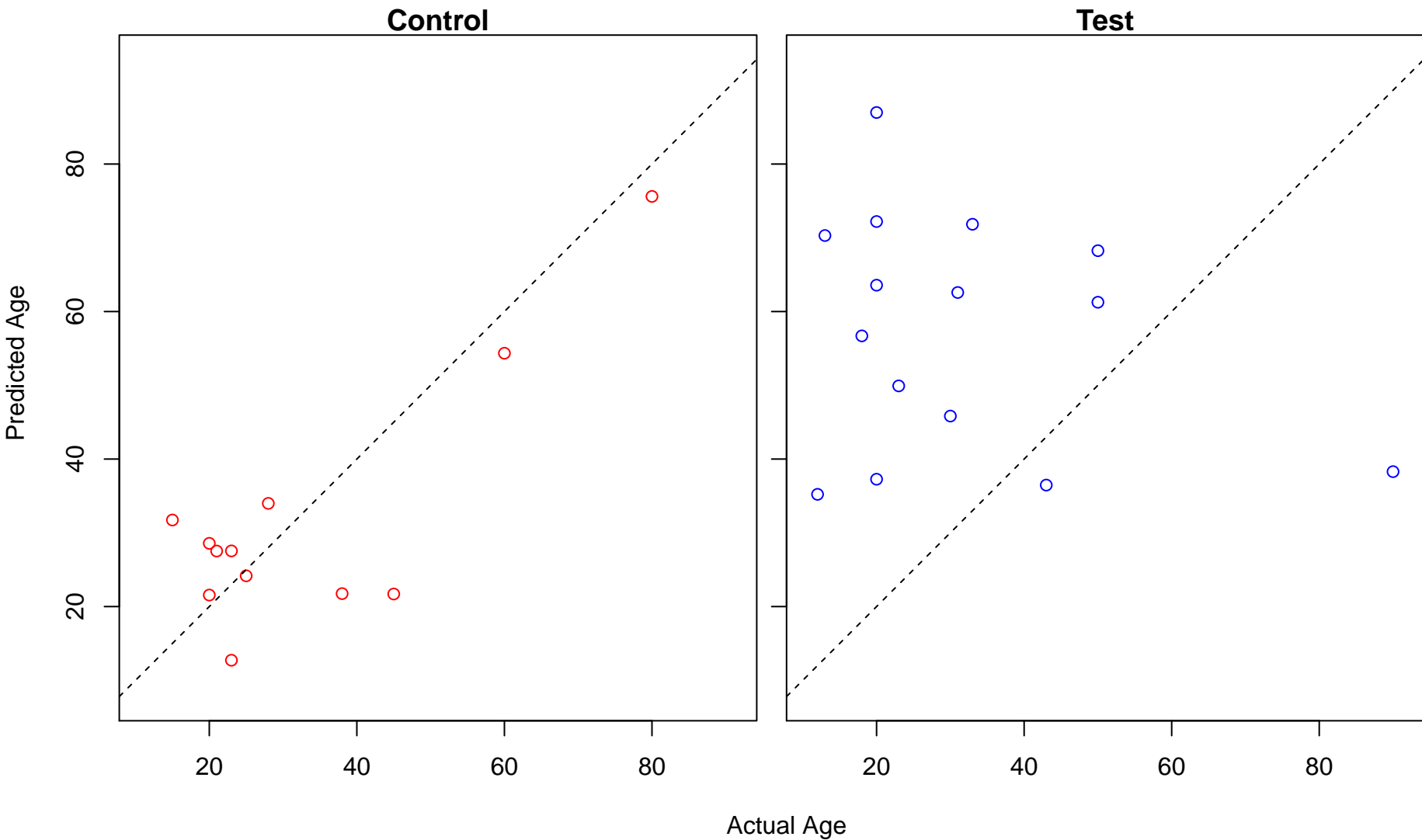
IRE1-mediated unfolded protein response (Score: 4.557018)



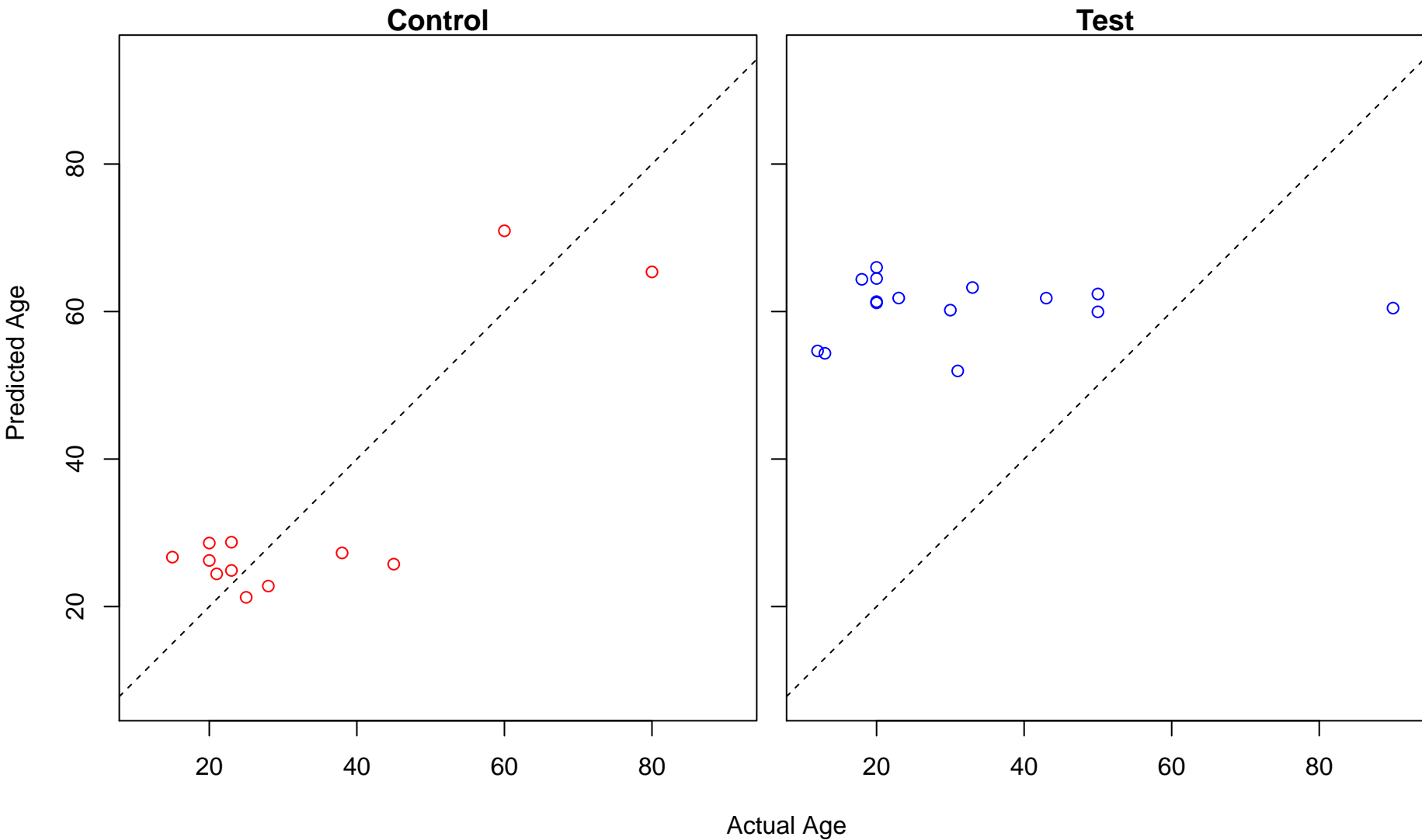
Golgi to plasma membrane transport (Score: 4.555436)



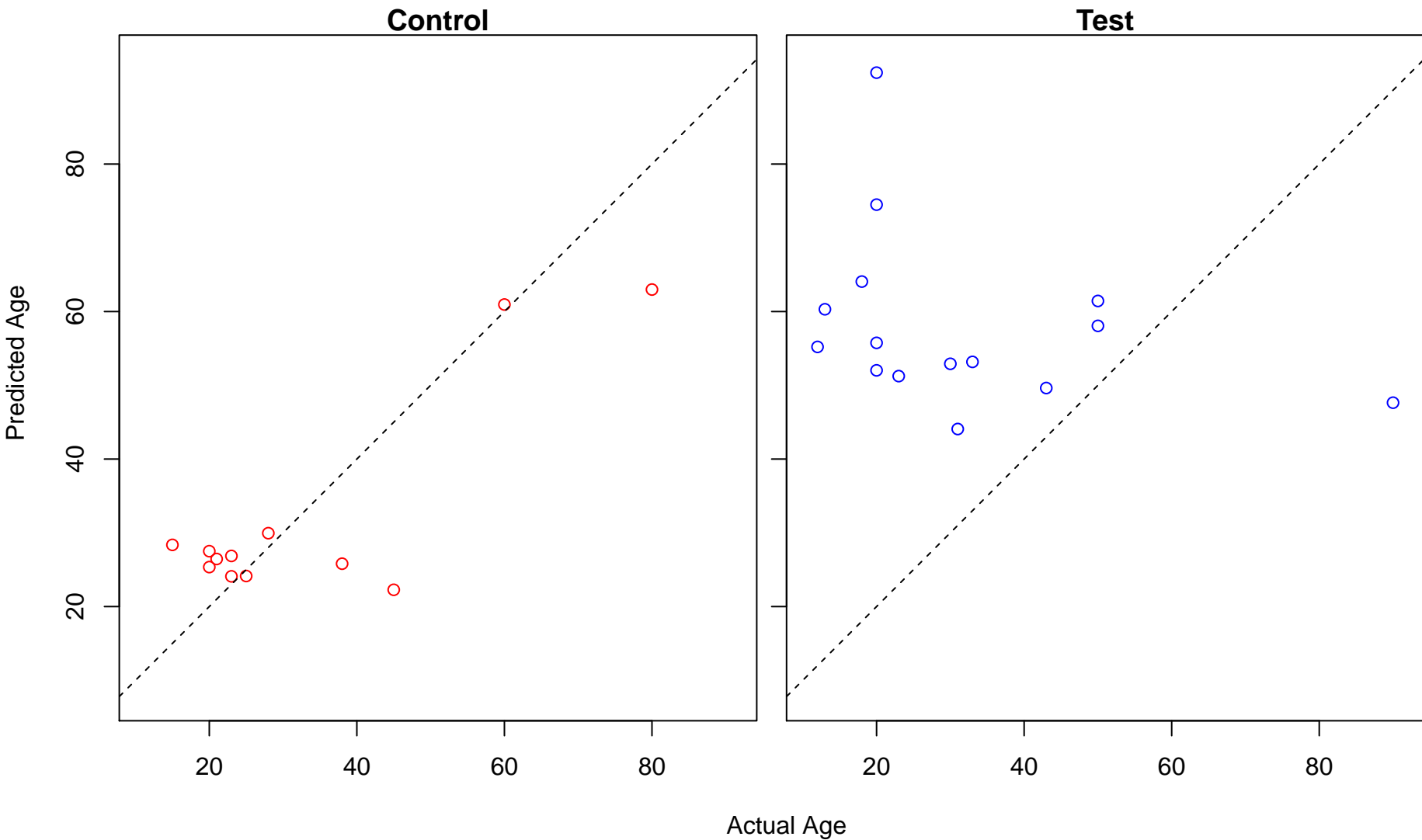
positive regulation of phospholipase C activity (Score: 4.554992)



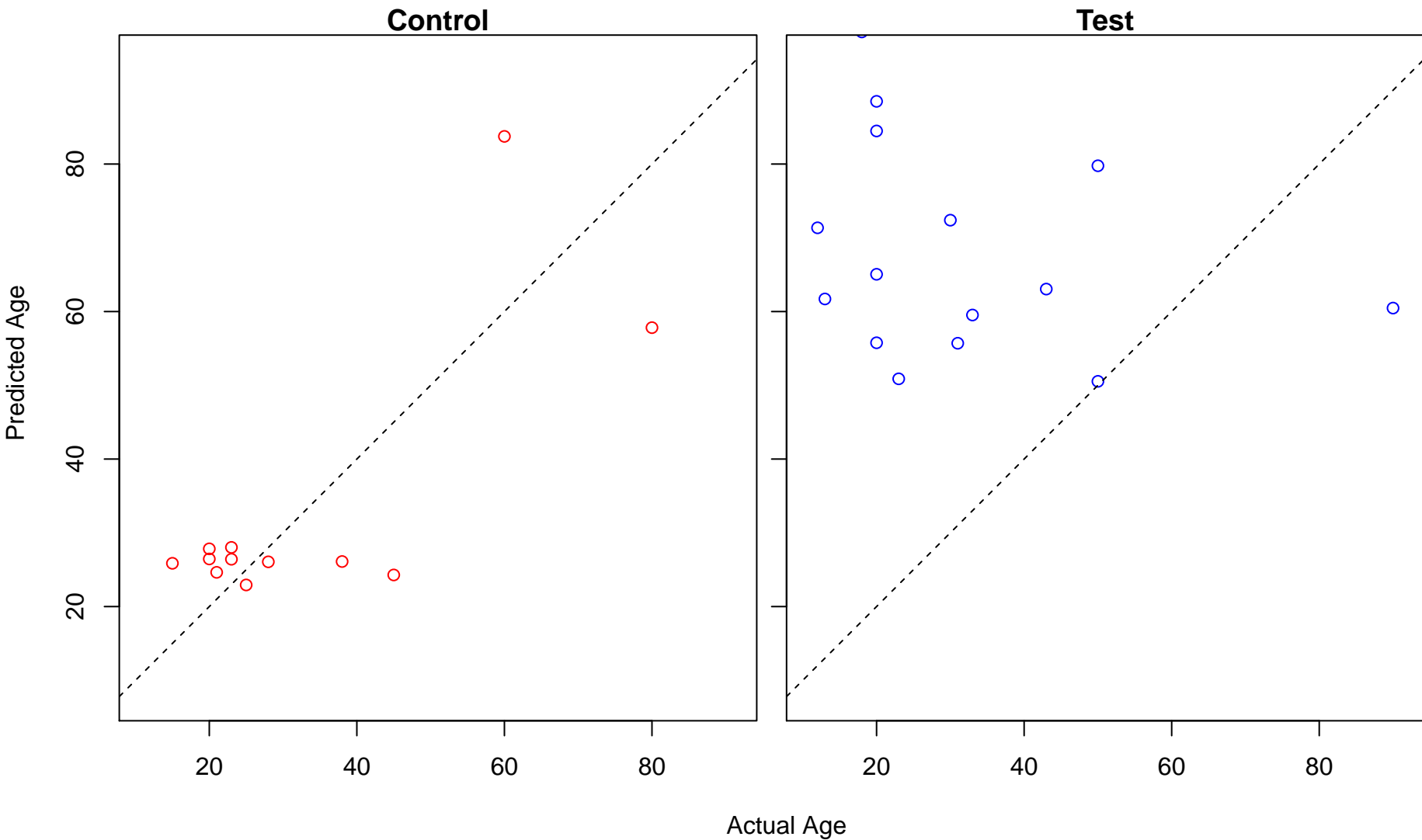
cardiac muscle tissue growth (Score: 4.554641)



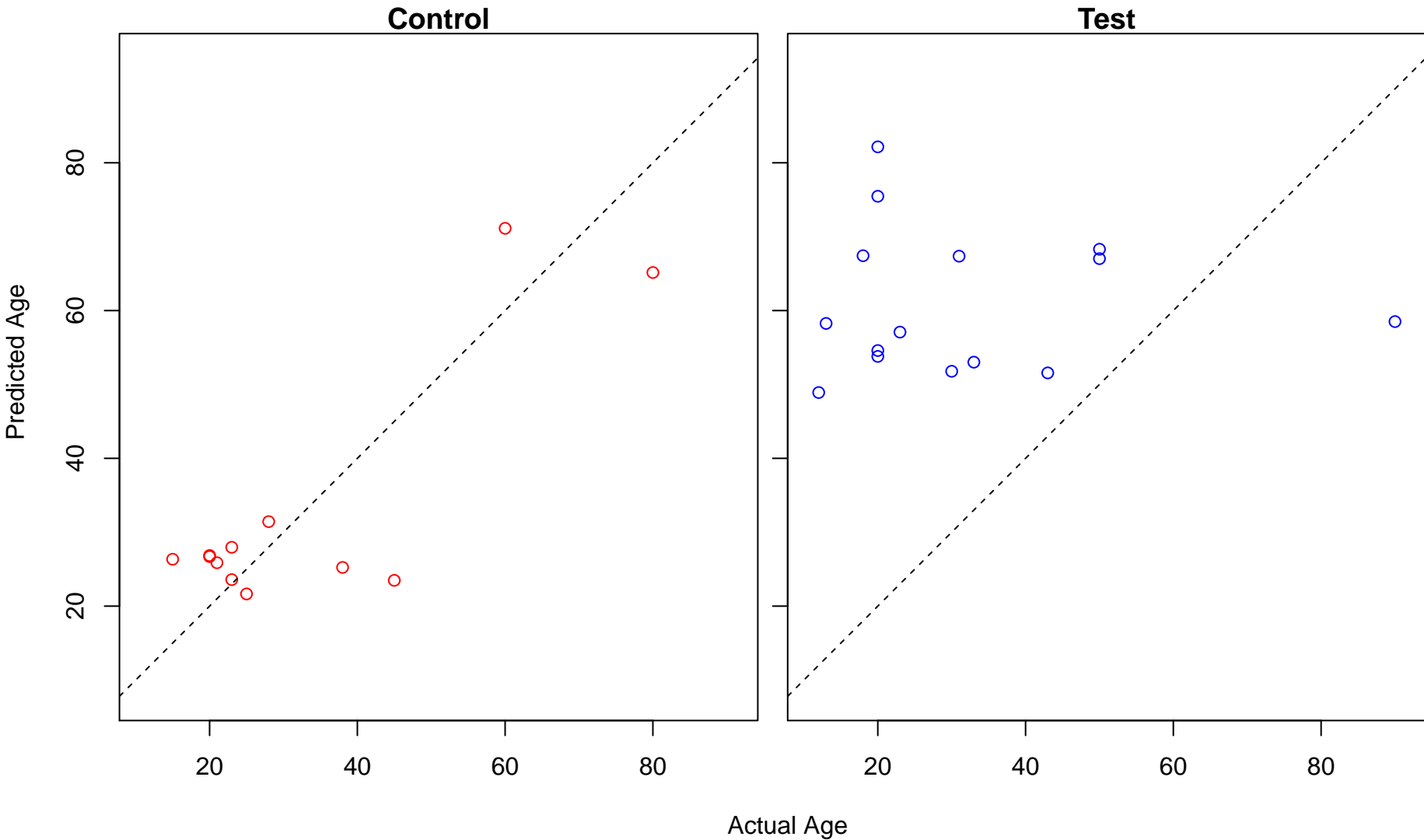
glial cell development (Score: 4.554176)



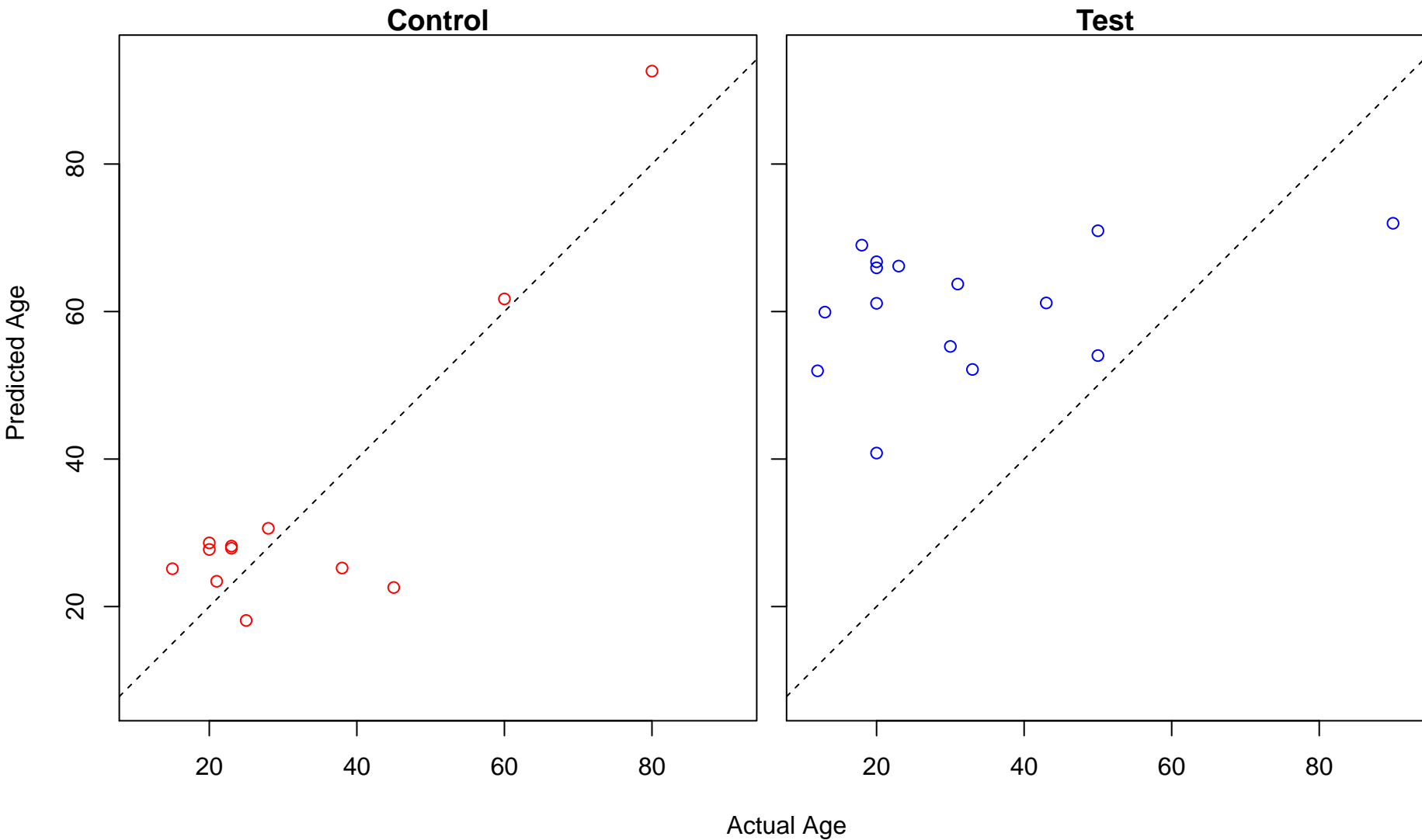
hormone transport (Score: 4.551071)



negative regulation of calcium ion transport (Score: 4.550834)

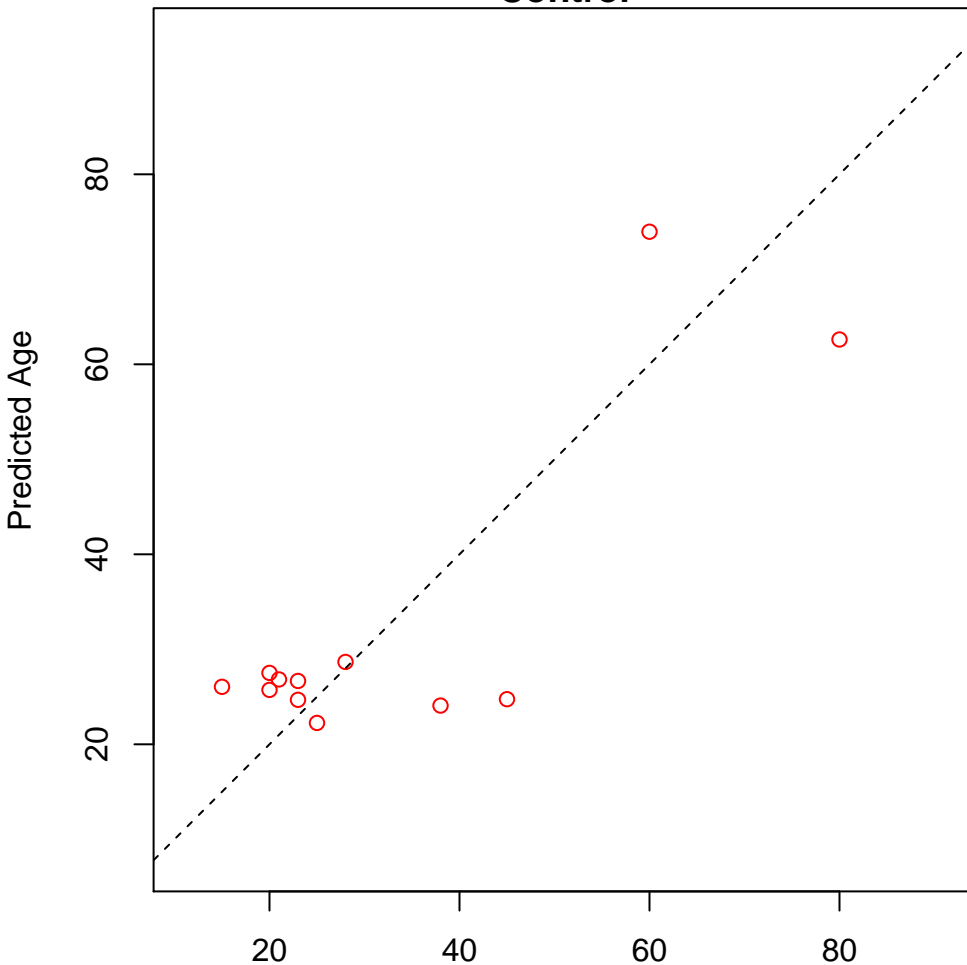


regulation of cell shape (Score: 4.550800)

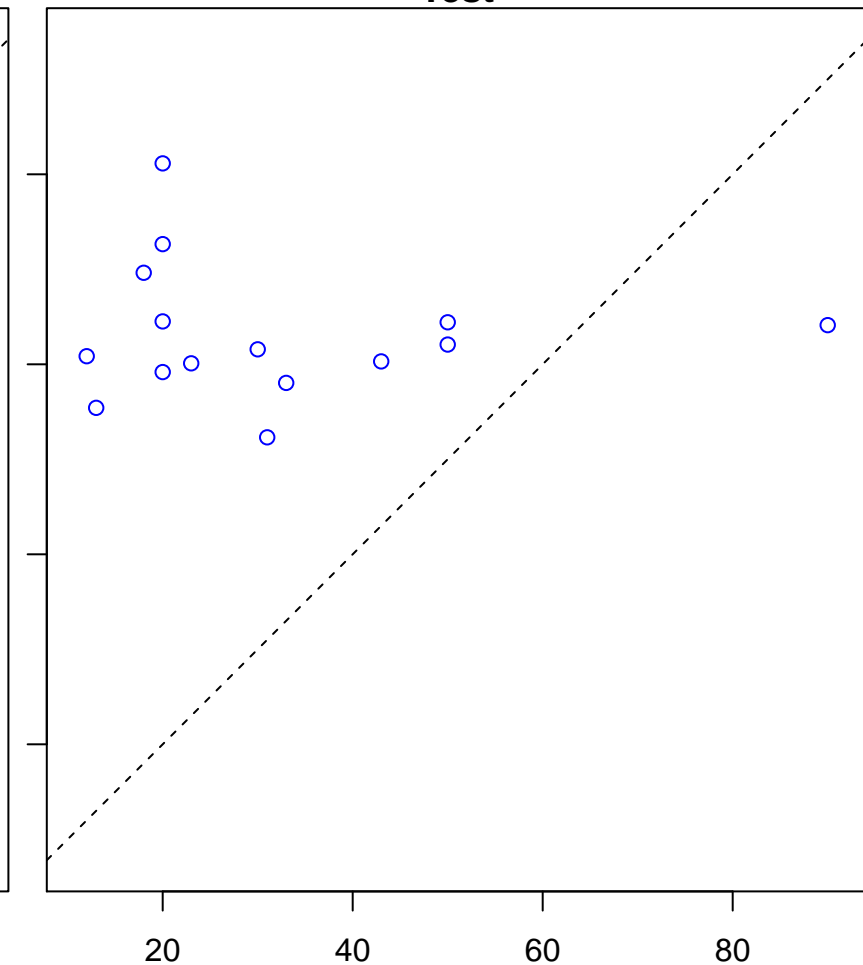


mitochondrial translational termination (Score: 4.549879)

Control

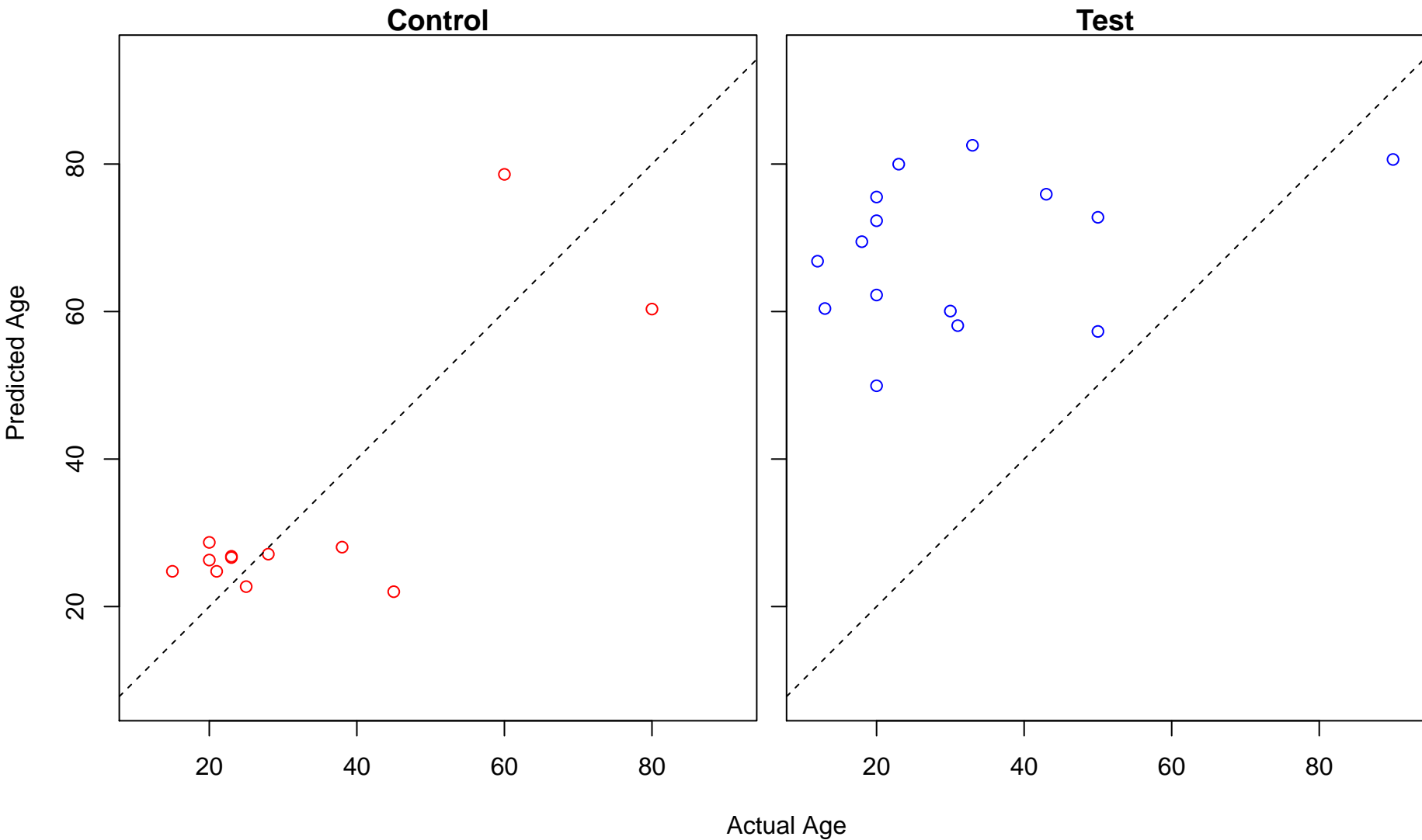


Test

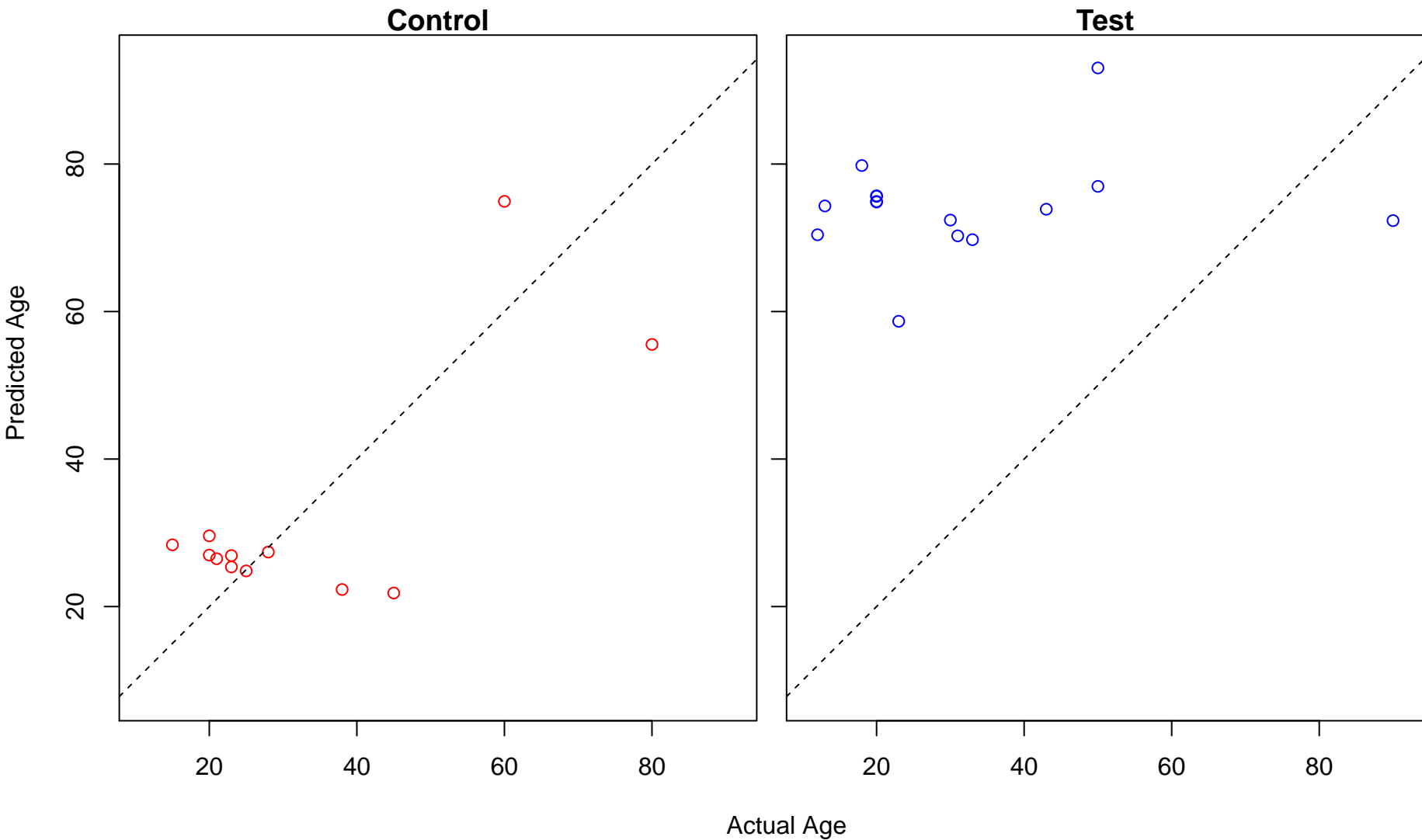


Actual Age

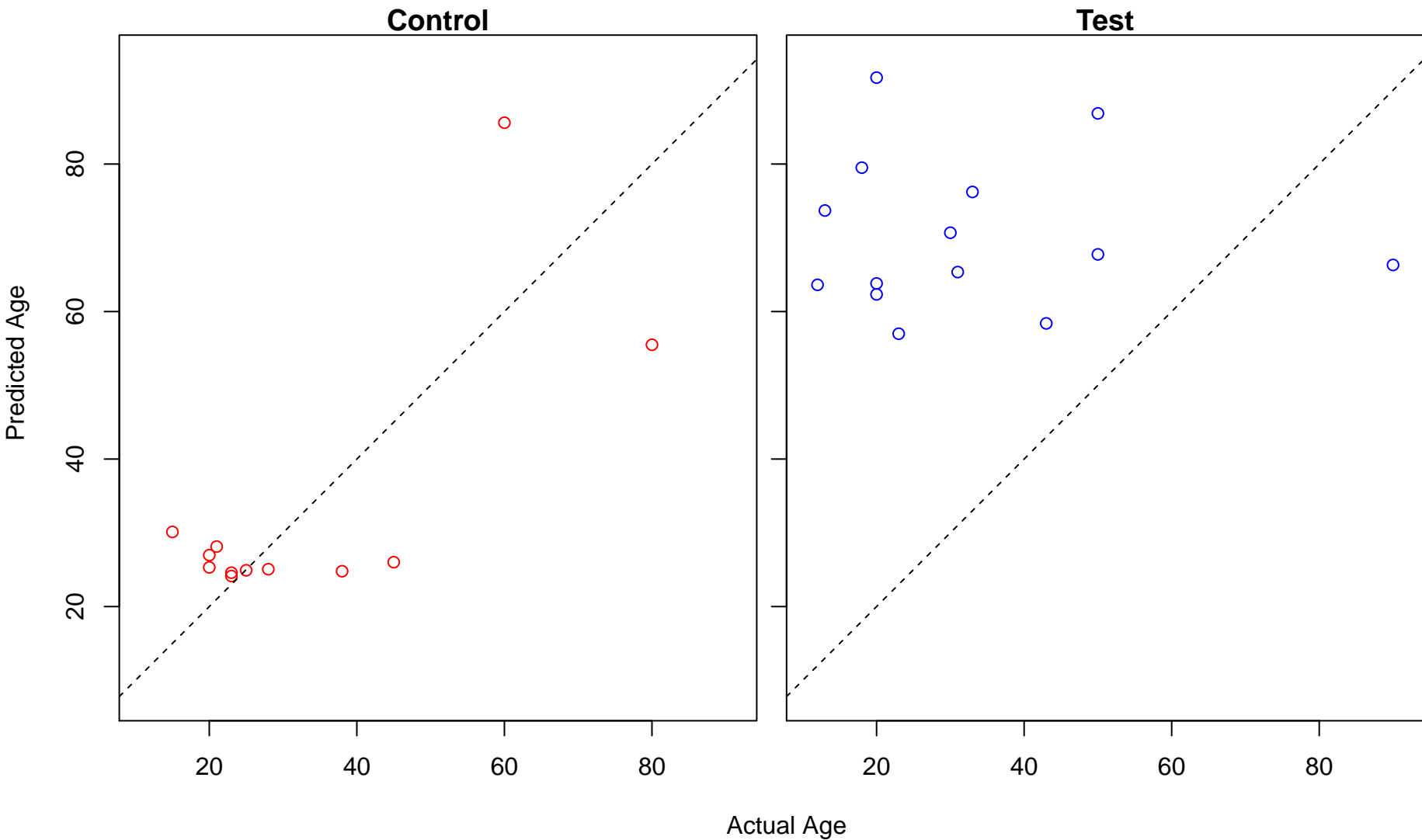
RNA (guanine-N7)-methylation (Score: 4.549143)



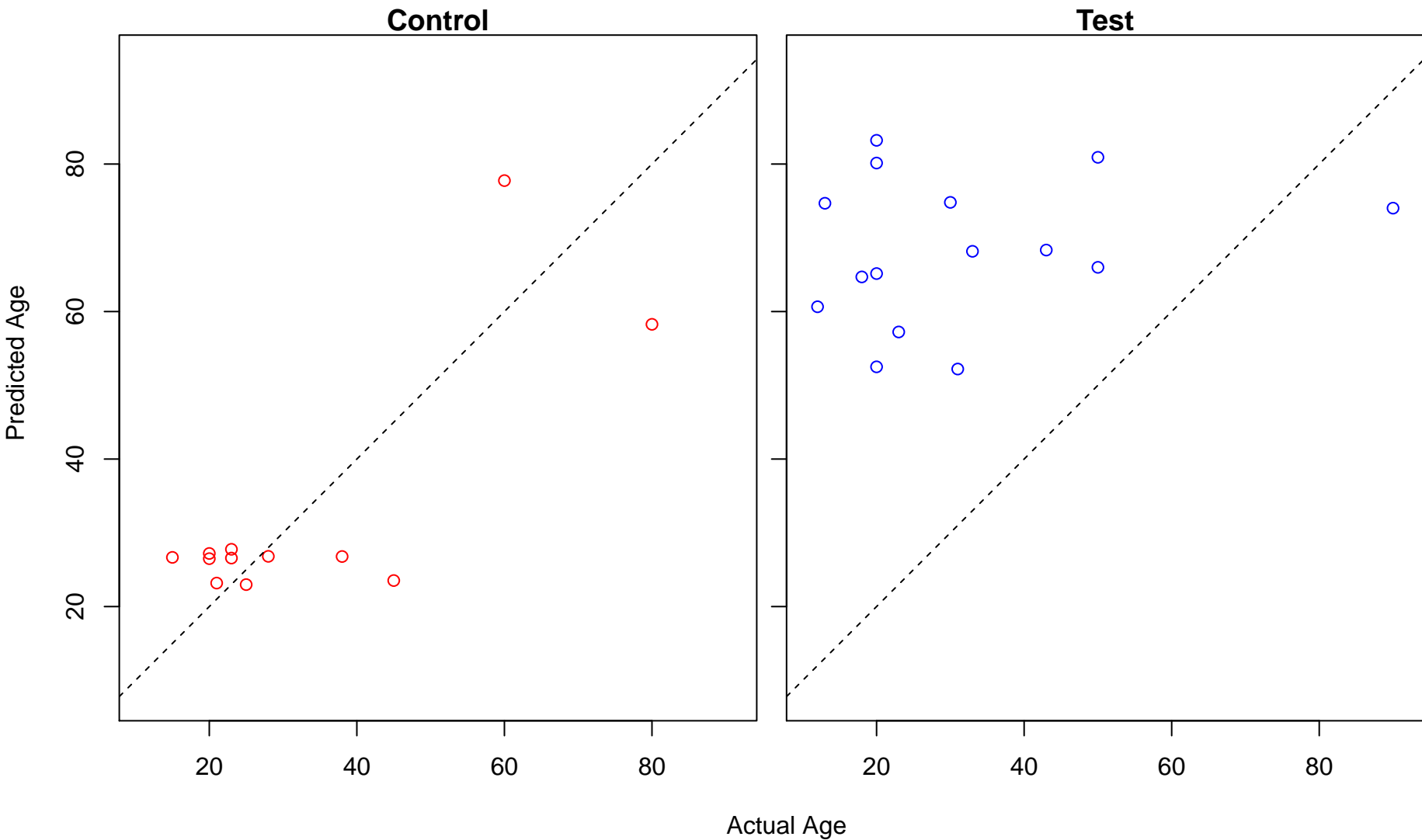
cellular monovalent inorganic cation homeostasis (Score: 4.548119)



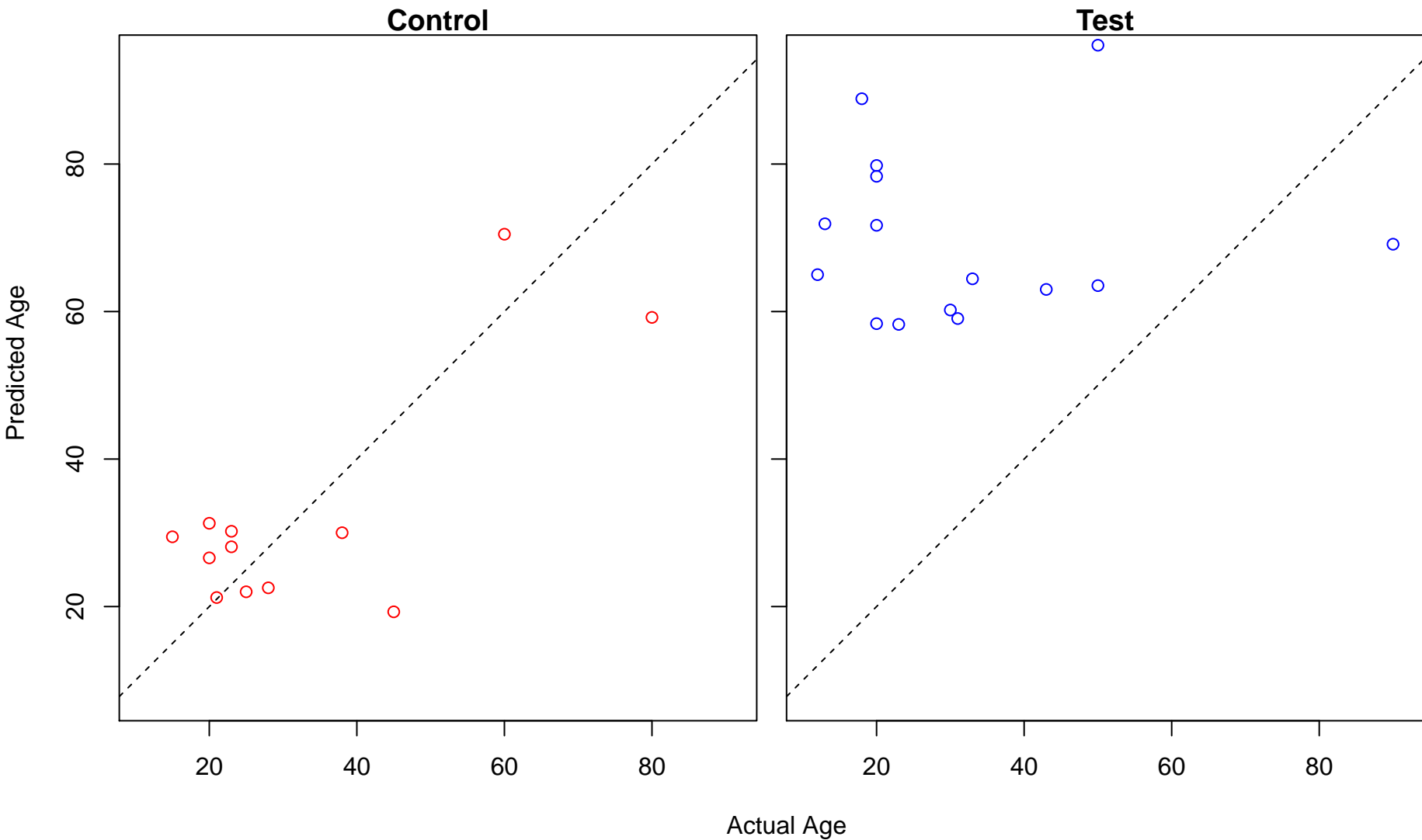
actin filament polymerization (Score: 4.546254)



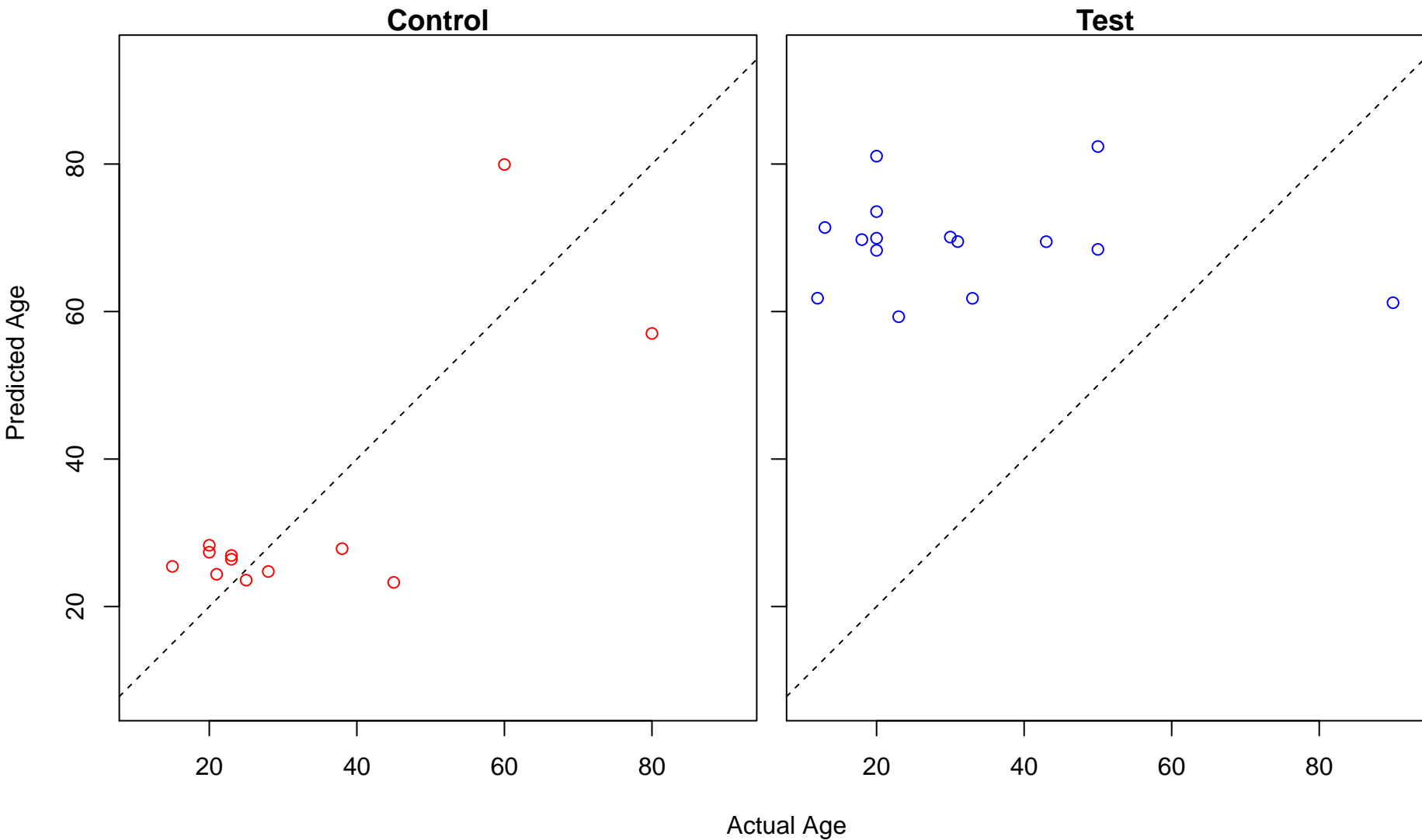
inorganic anion transport (Score: 4.543937)



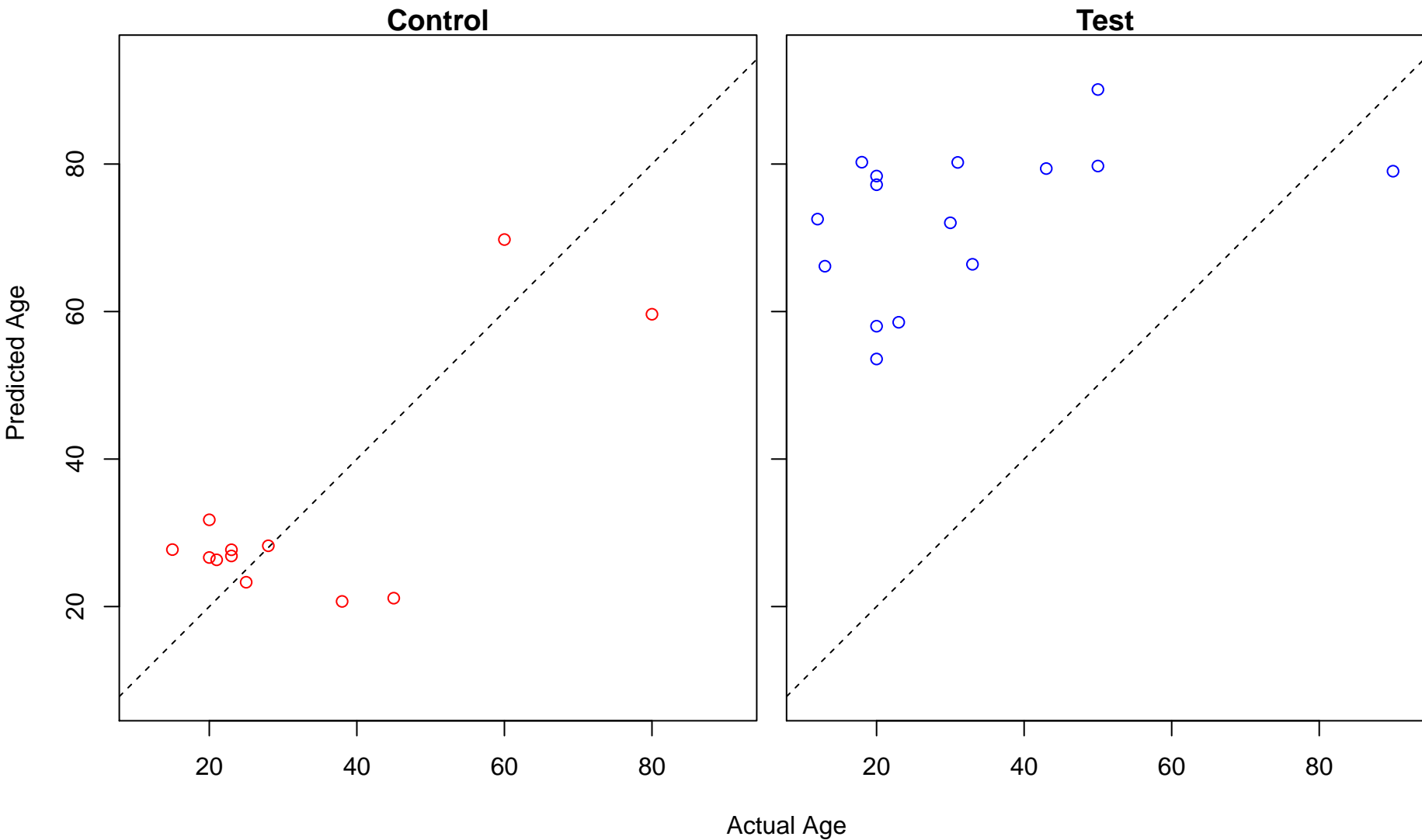
cardiac atrium morphogenesis (Score: 4.543359)



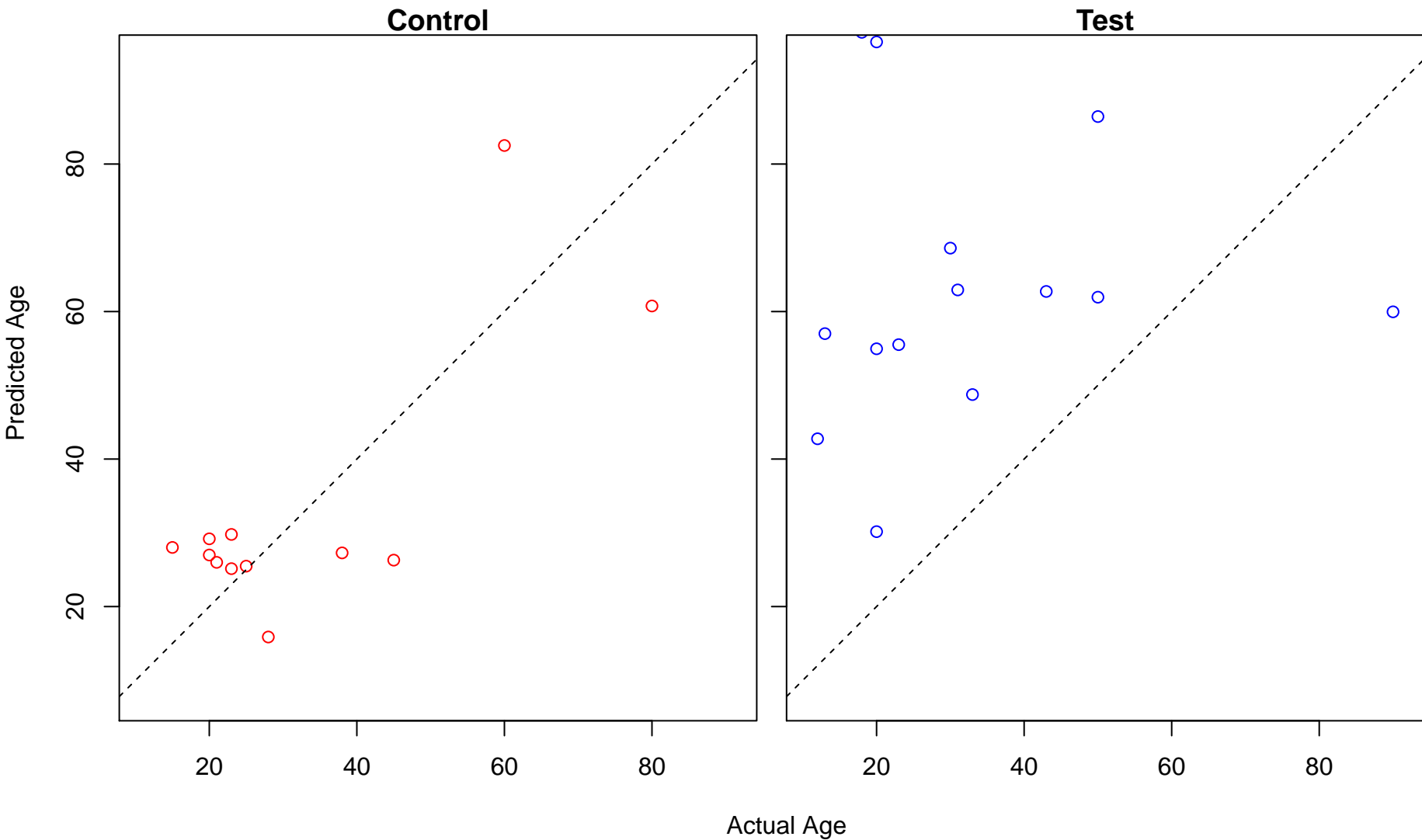
positive regulation of mRNA metabolic process (Score: 4.542412)



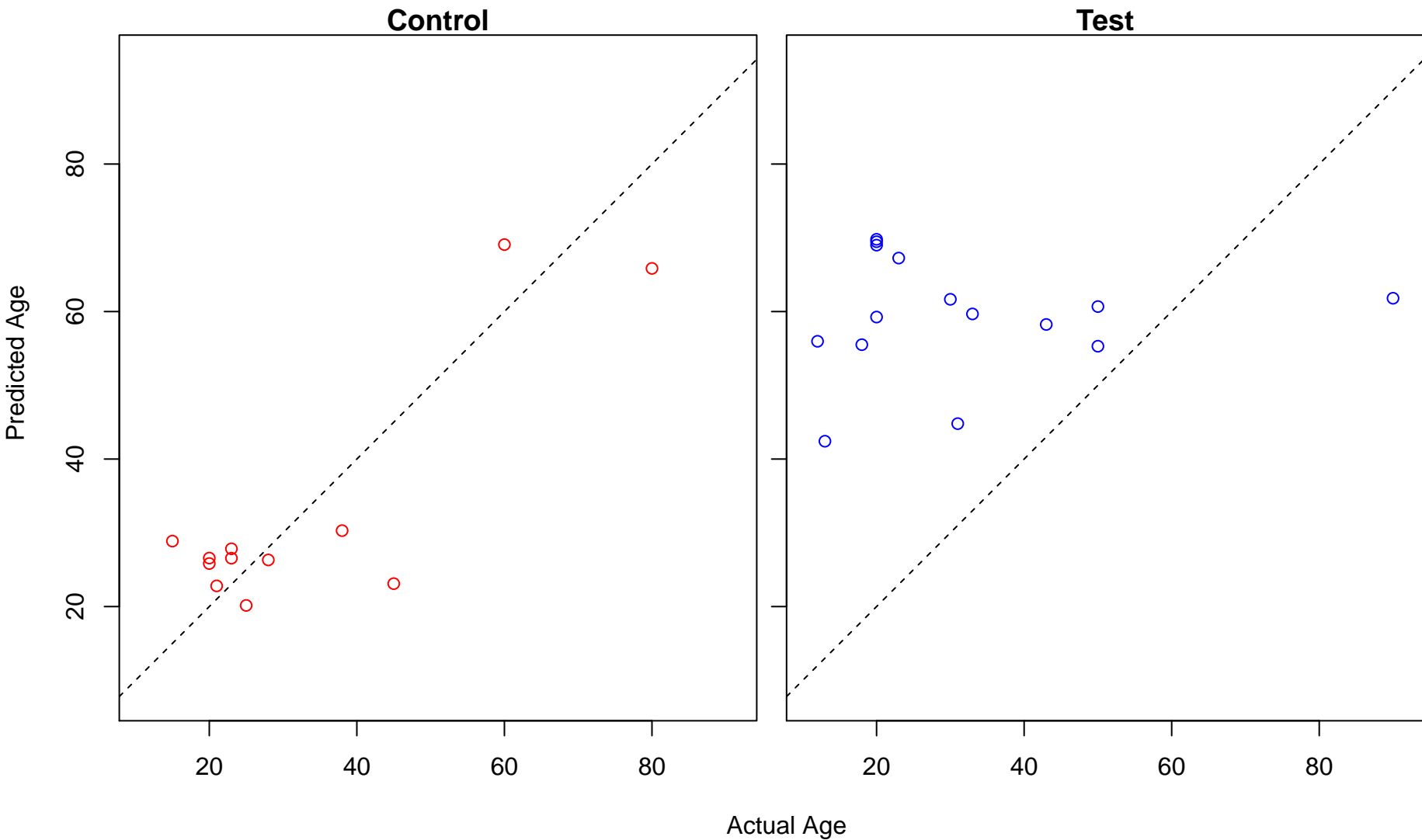
positive regulation of sodium ion transmembrane transport (Score: 4.542364)



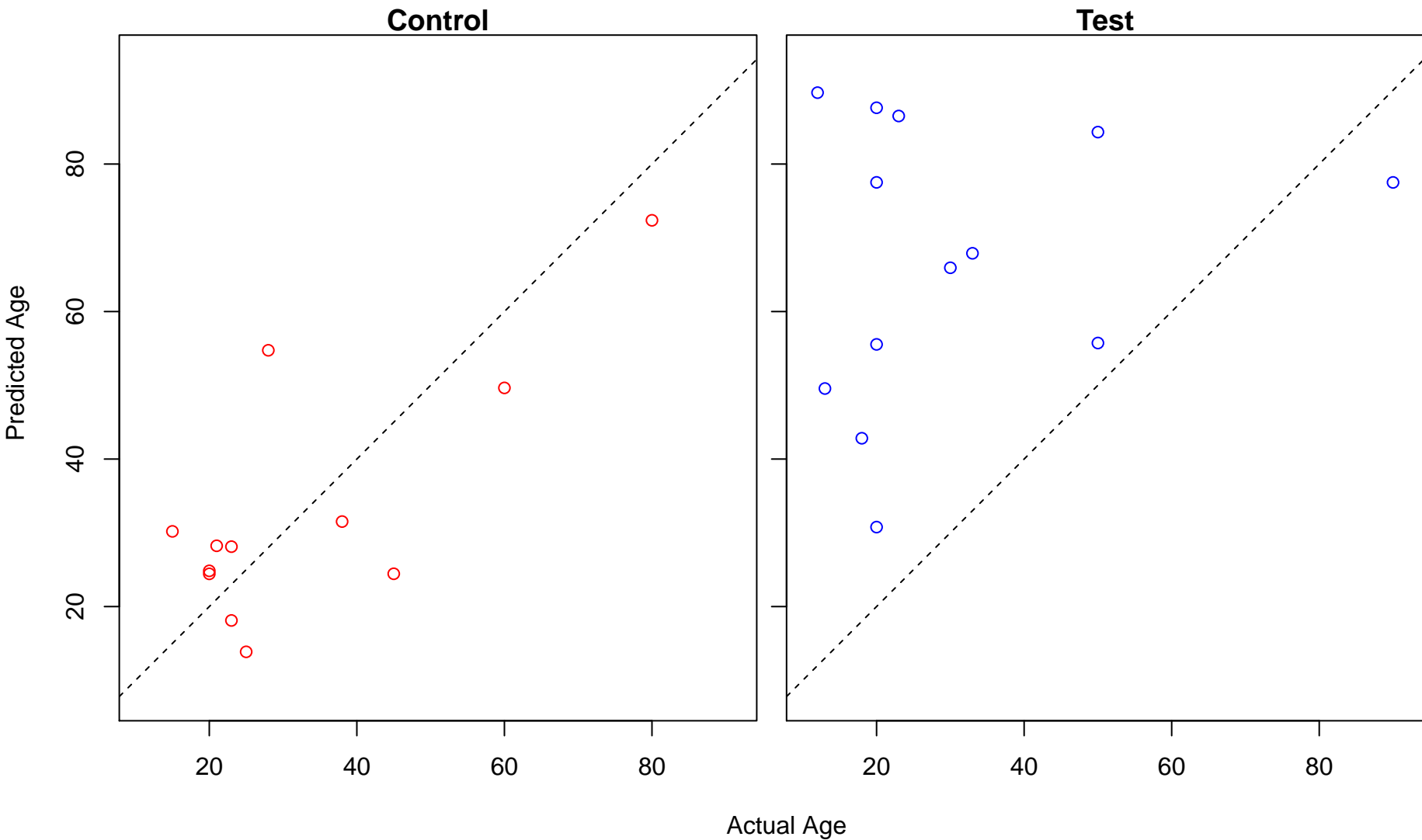
galactose metabolic process (Score: 4.541255)



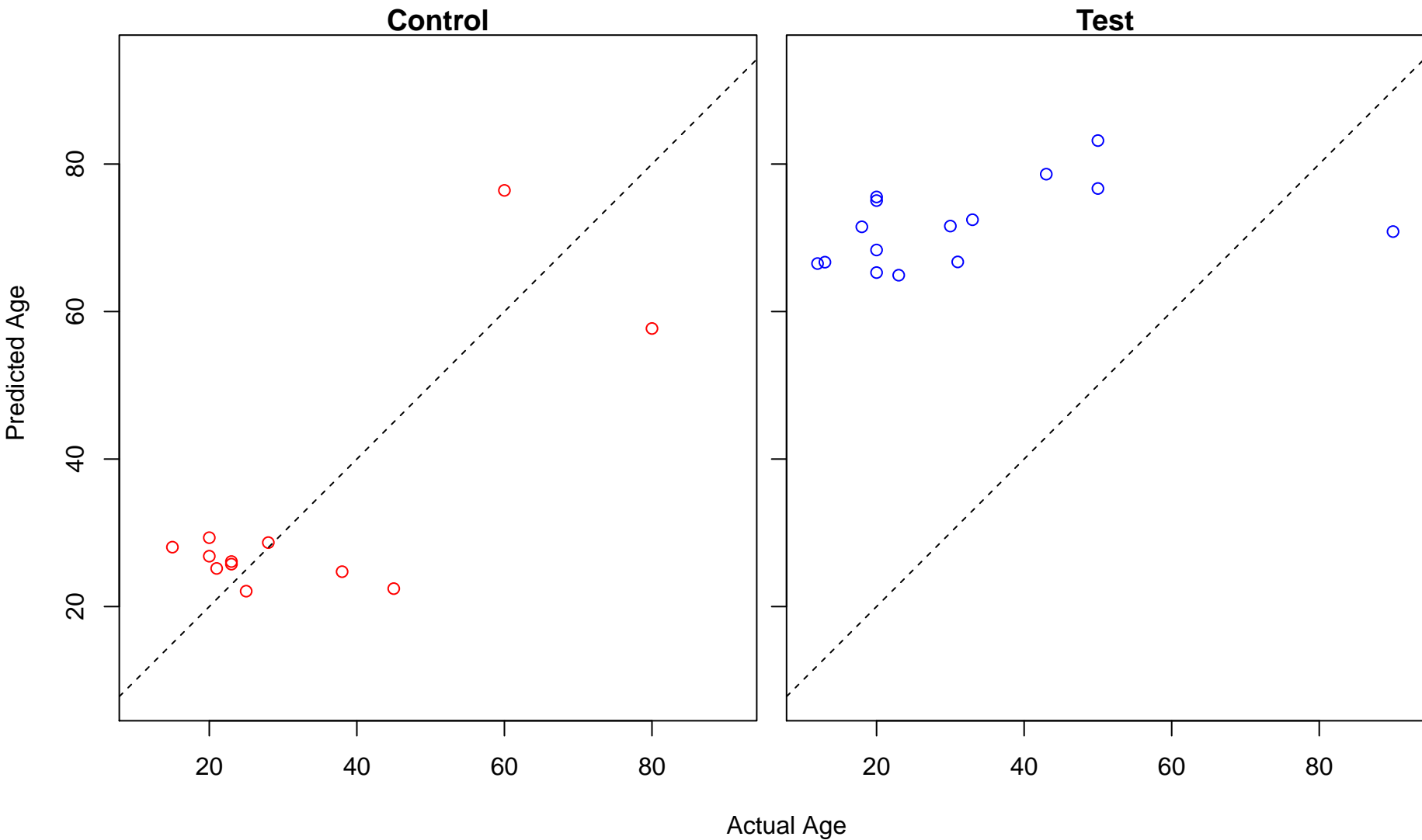
steroid biosynthetic process (Score: 4.538532)



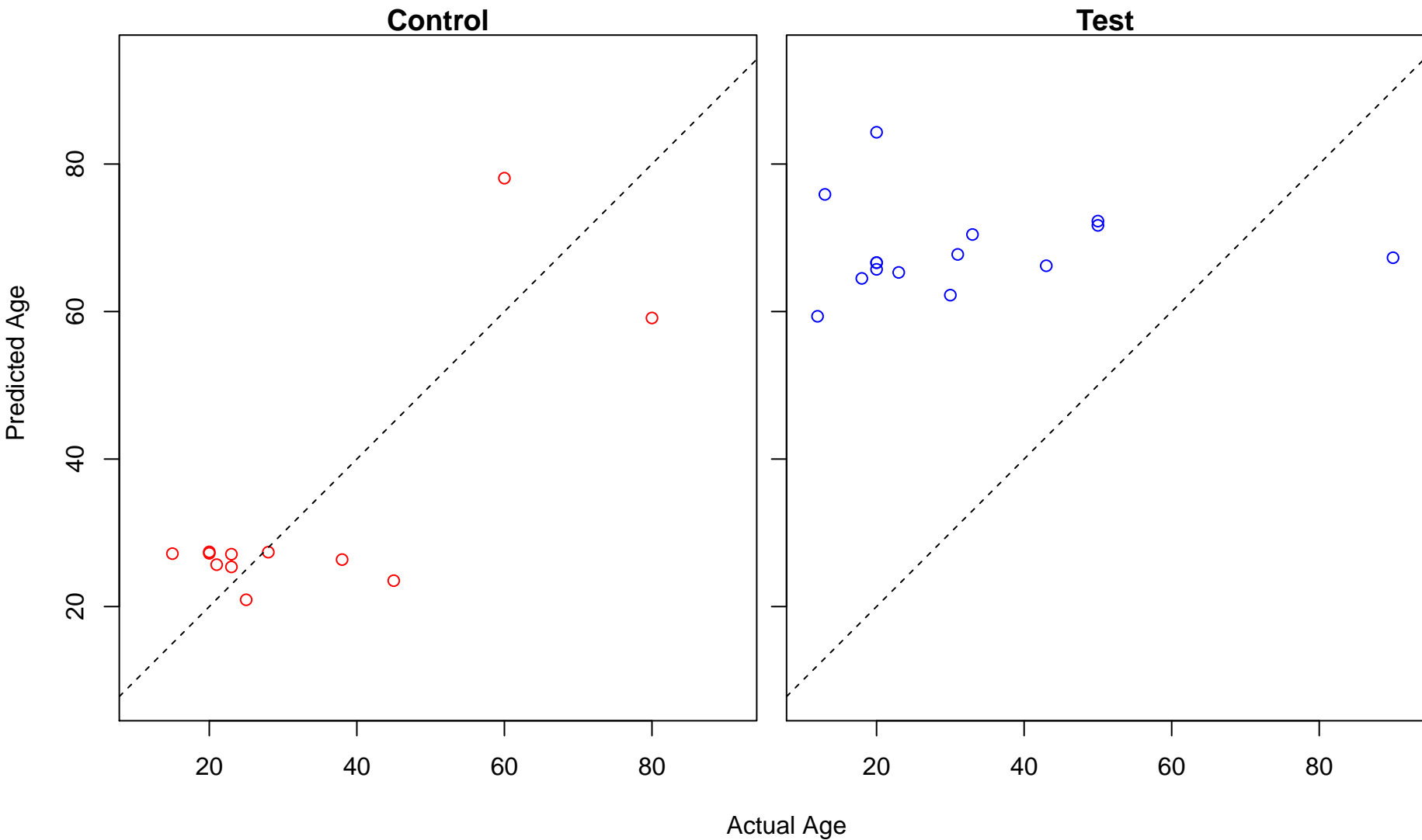
regulation of membrane repolarization (Score: 4.537733)



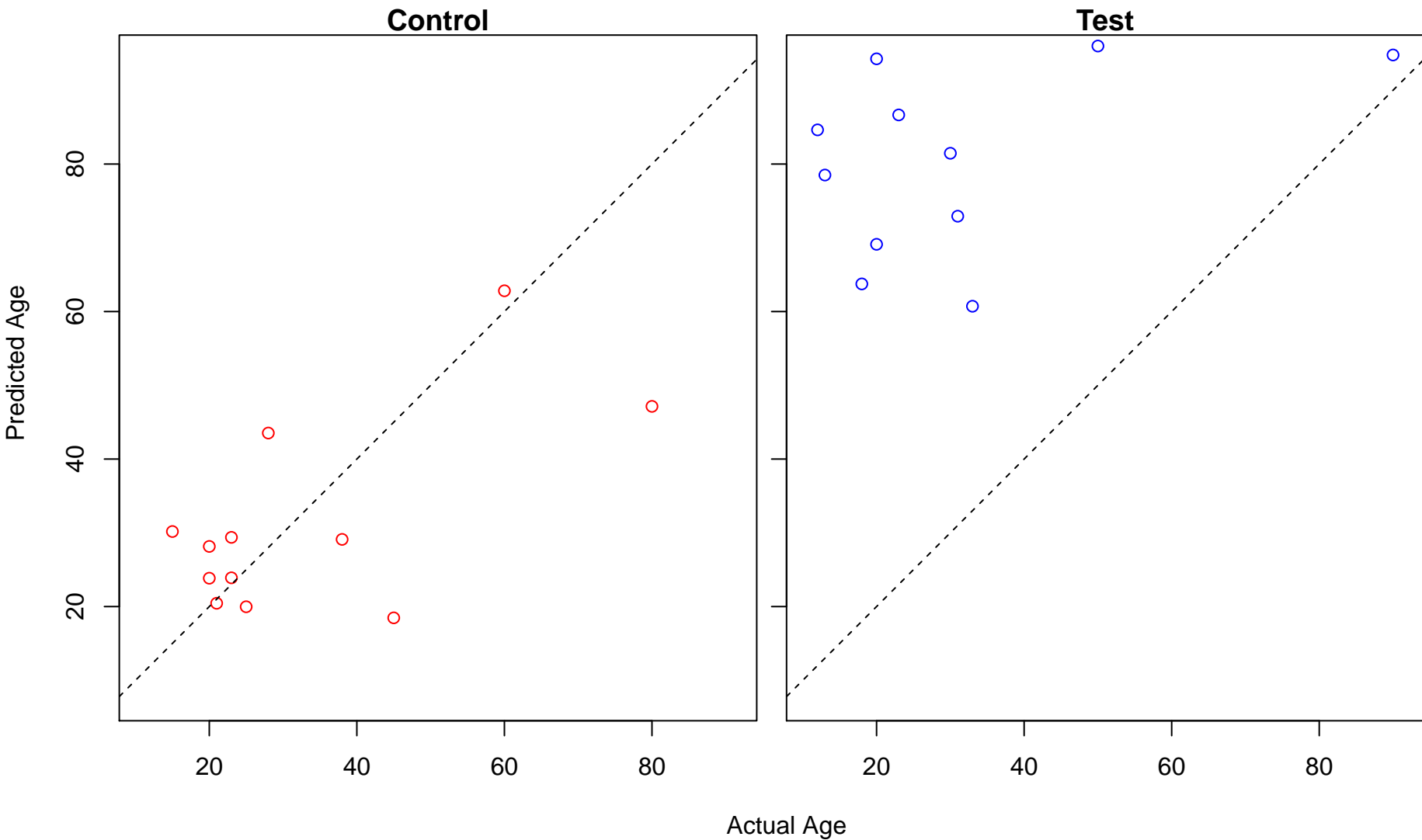
cardiac conduction (Score: 4.537207)



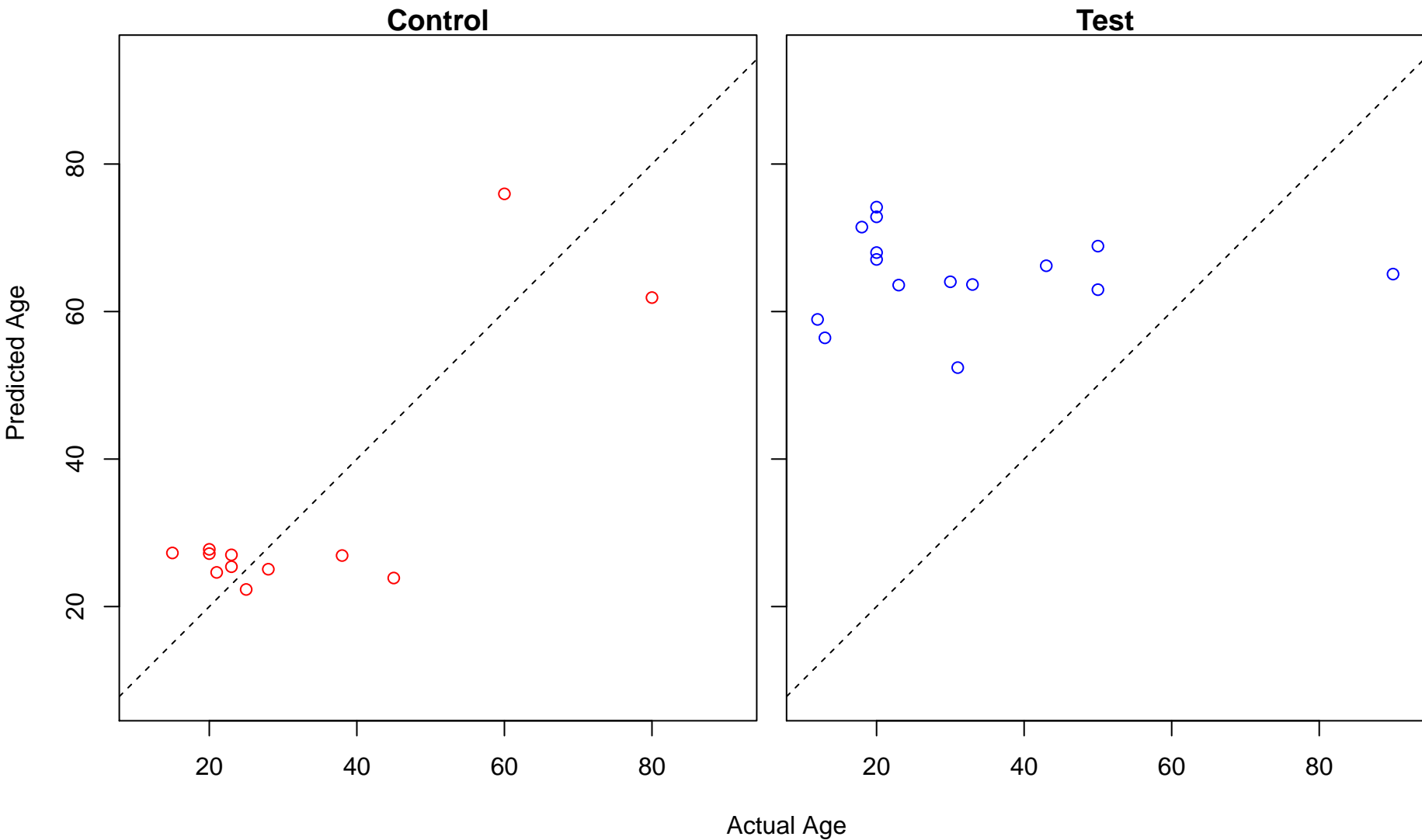
regulation of blood circulation (Score: 4.536566)



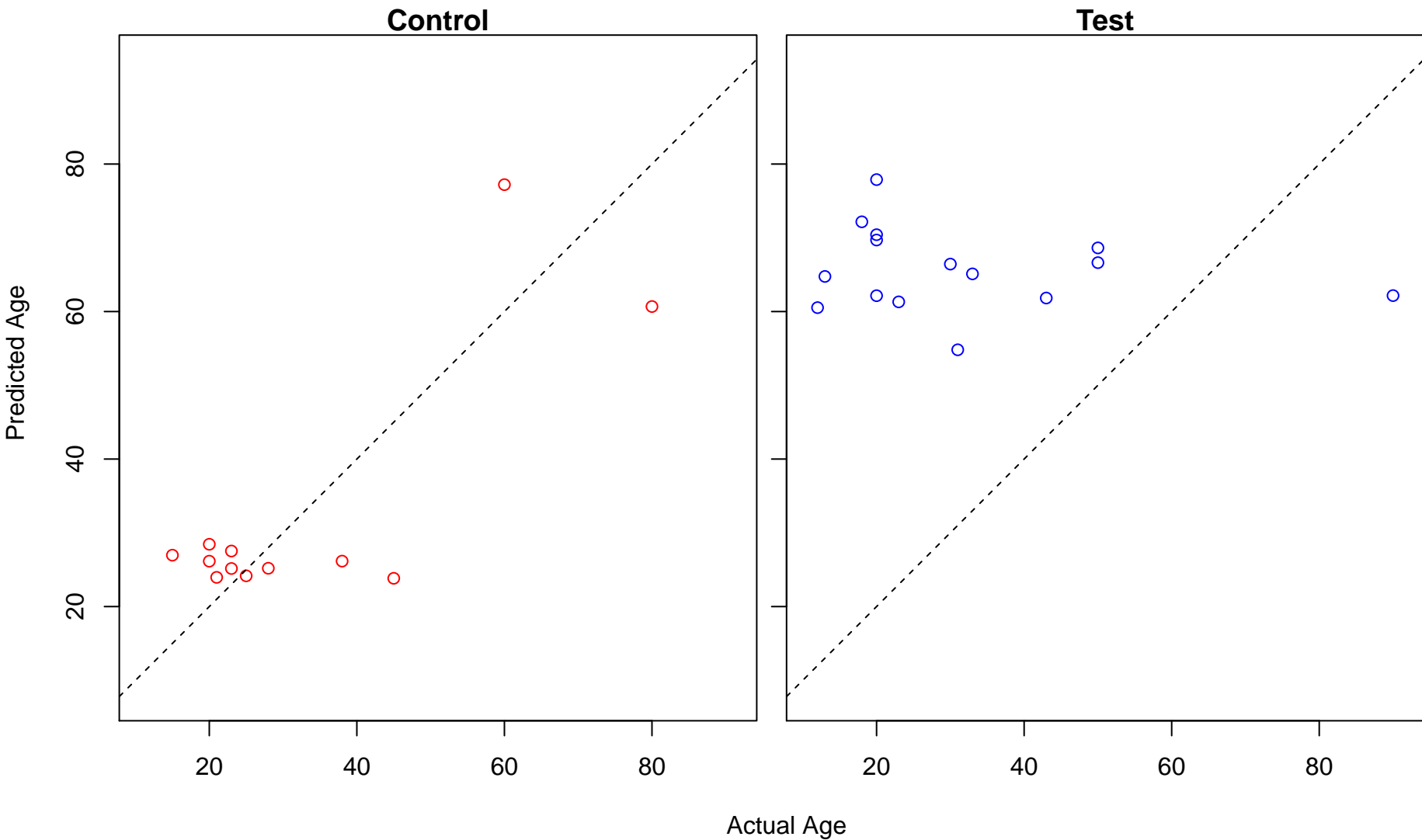
positive regulation of neuron death (Score: 4.535906)



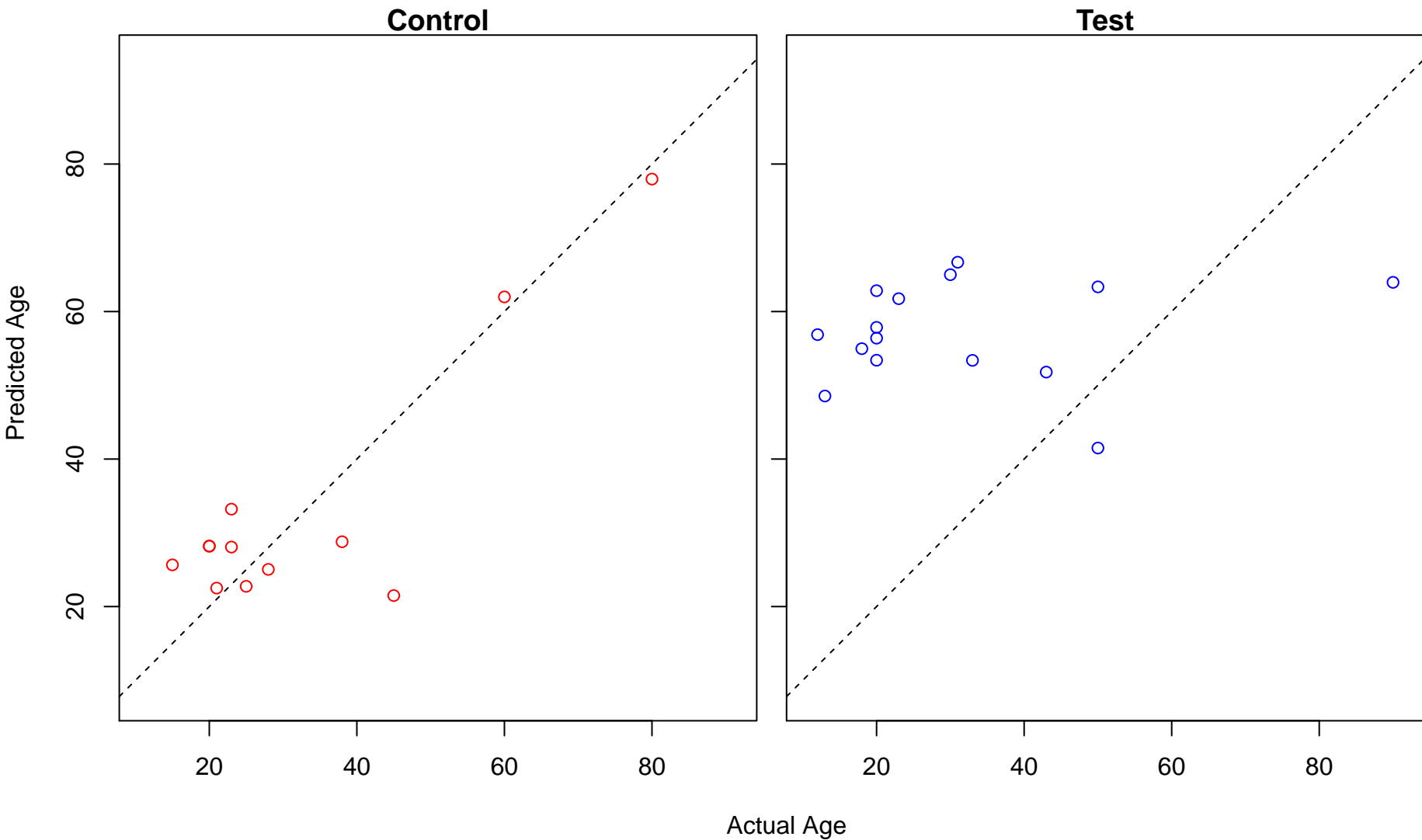
Golgi to plasma membrane protein transport (Score: 4.534998)



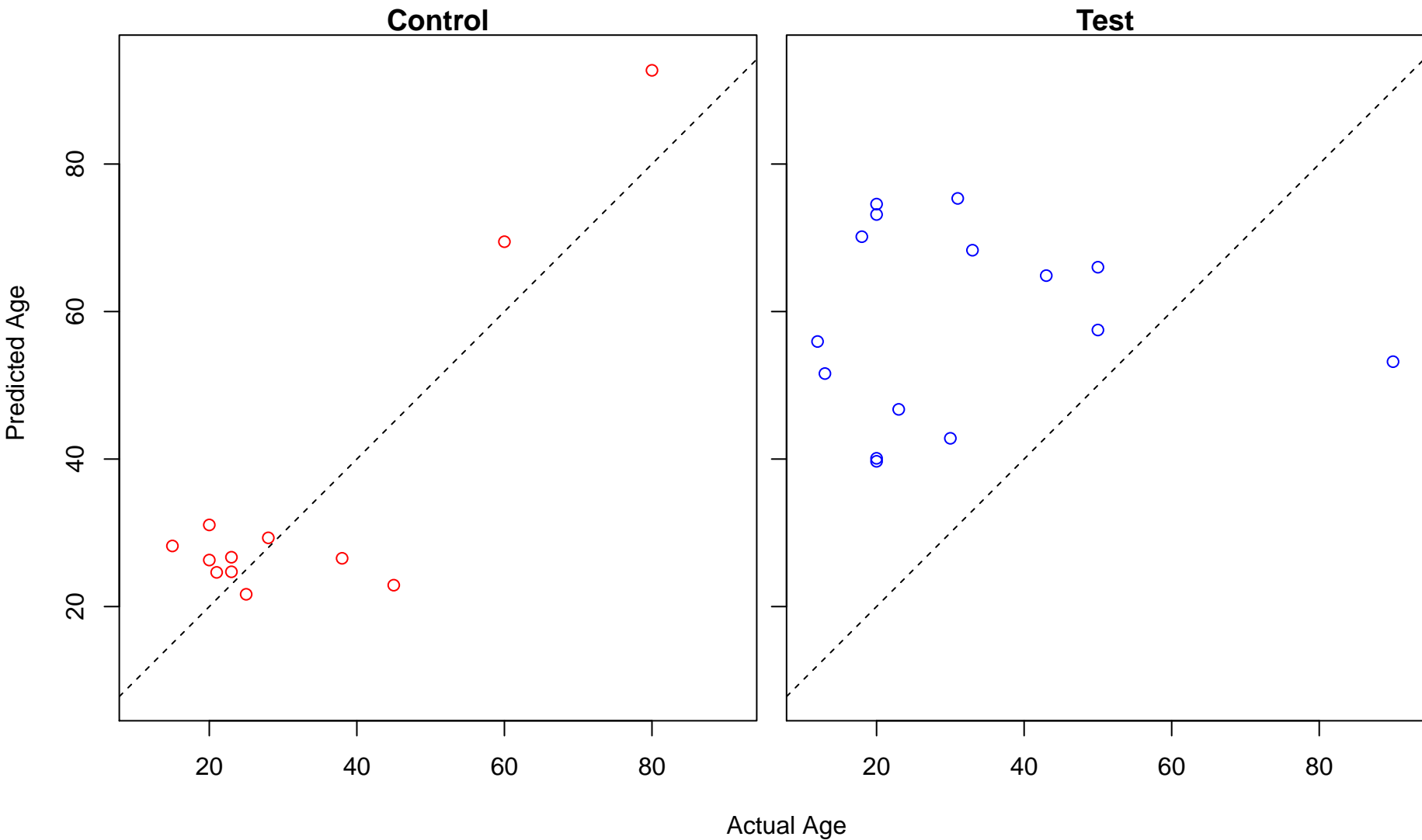
retrograde vesicle-mediated transport, Golgi to ER (Score: 4.532325)



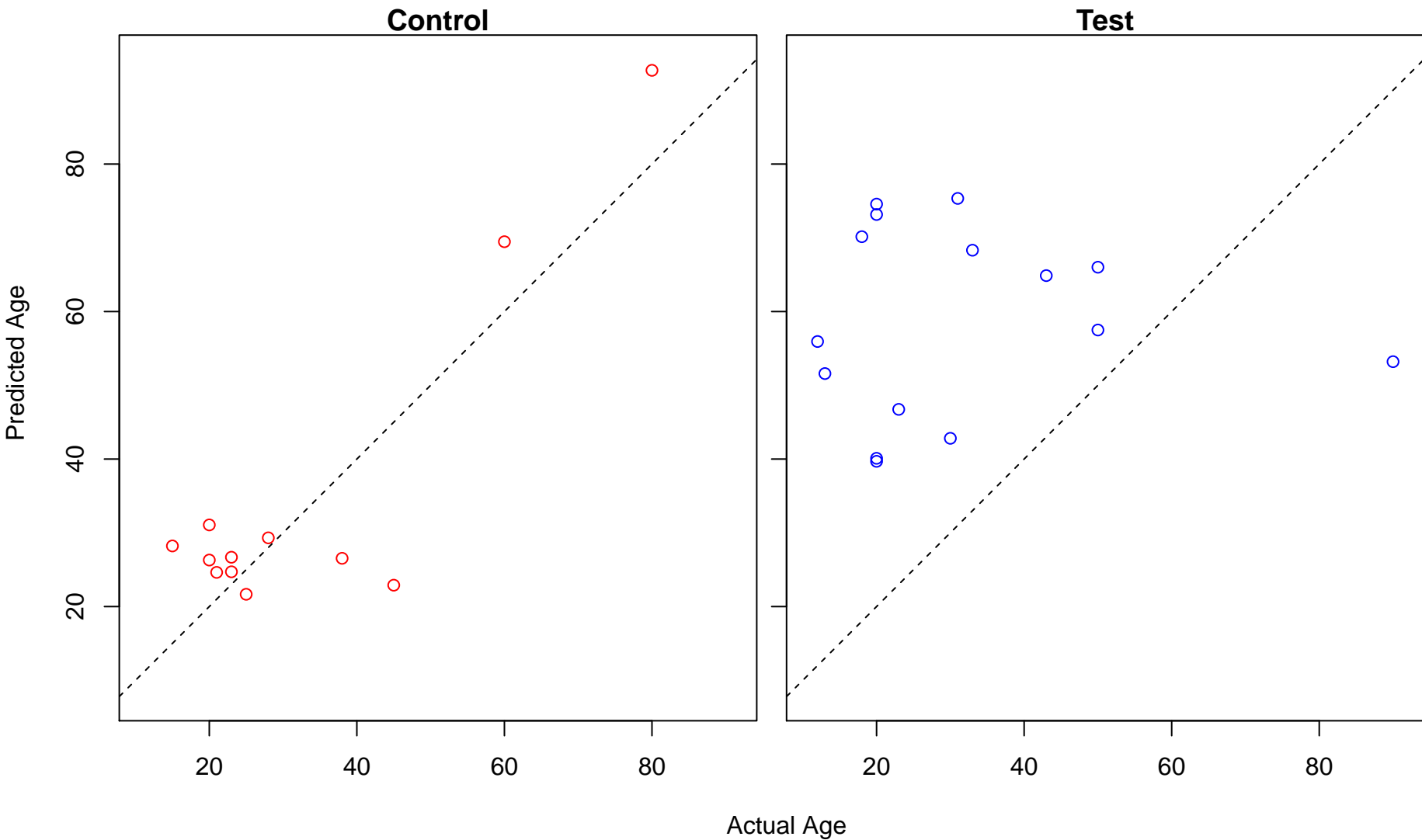
positive regulation of sprouting angiogenesis (Score: 4.532181)



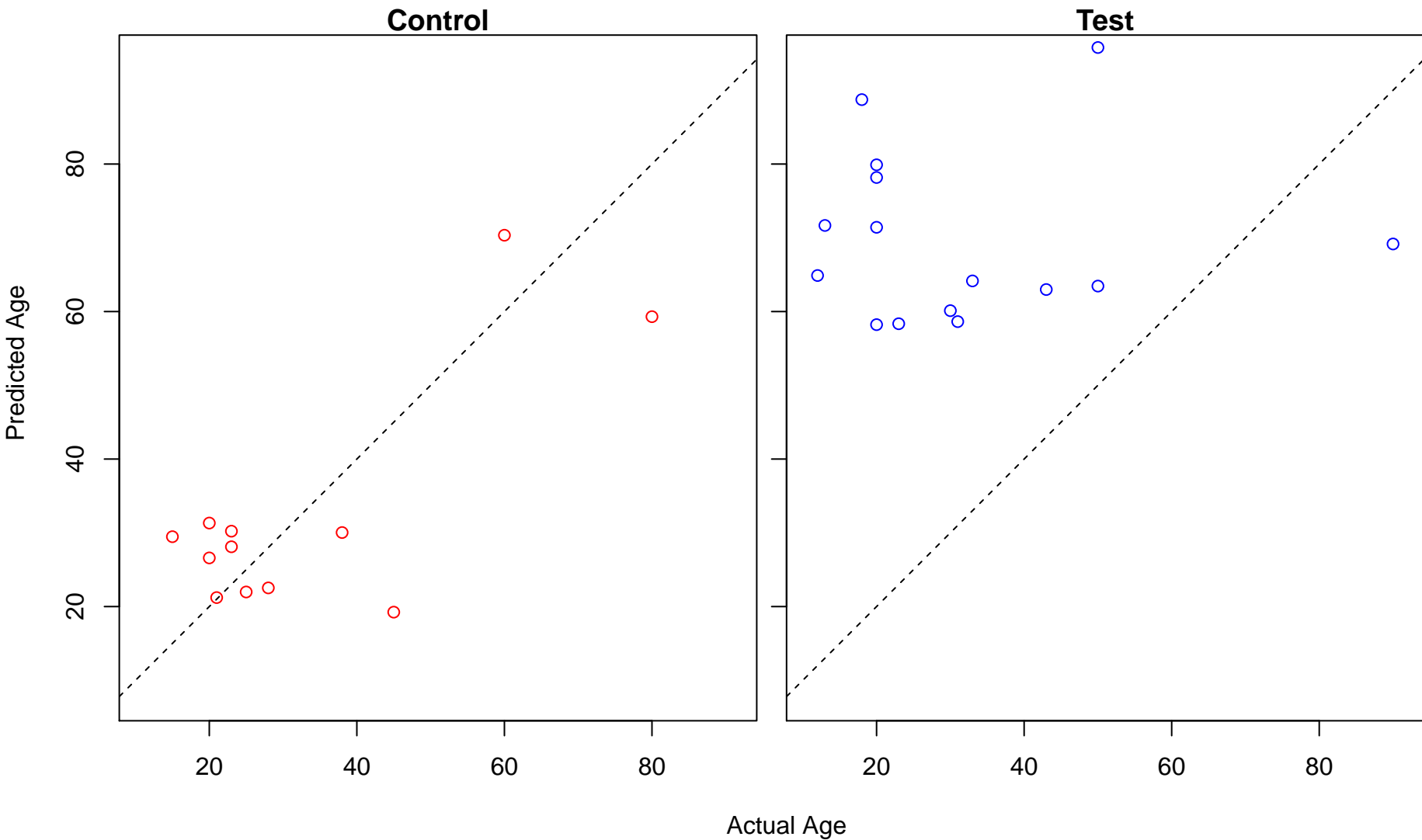
regulation of gene expression by genetic imprinting (Score: 4.531869)



genetic imprinting (Score: 4.531869)

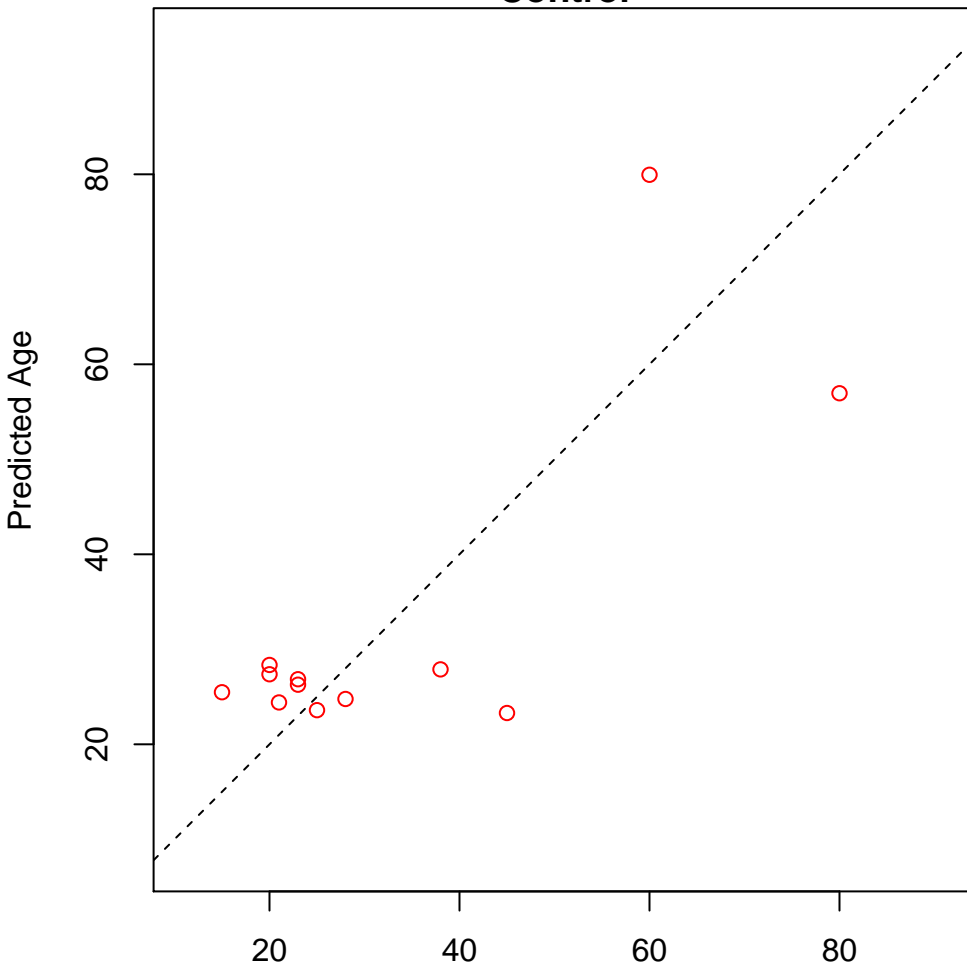


atrial septum morphogenesis (Score: 4.529819)

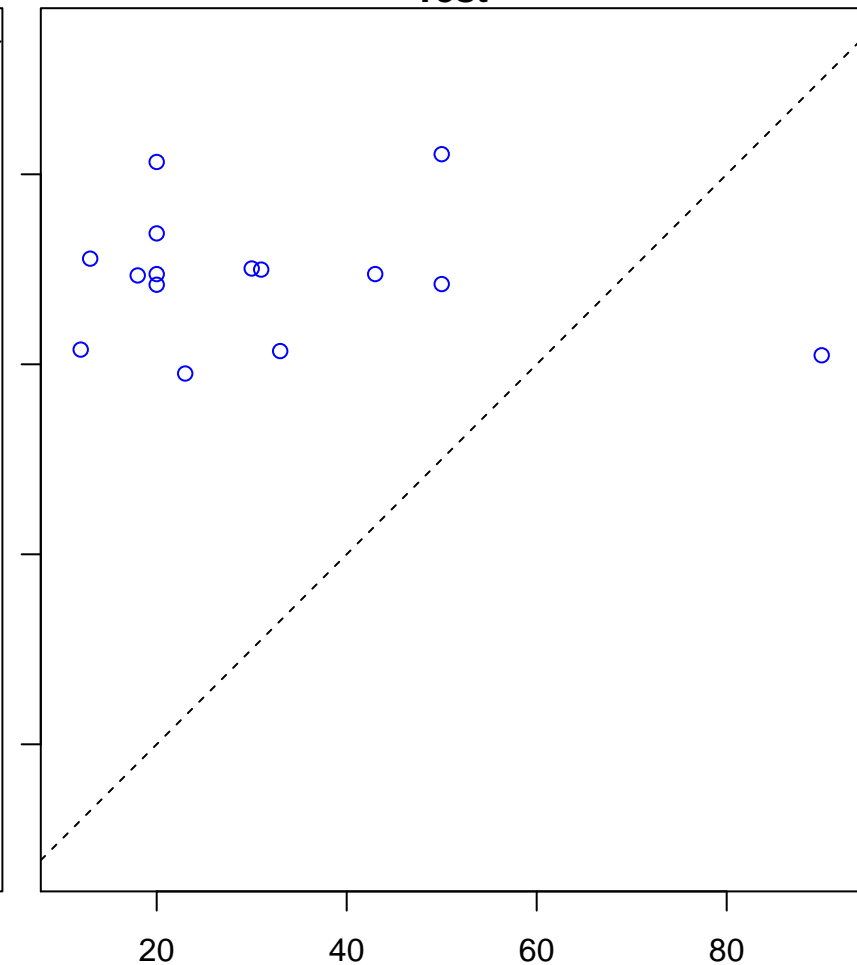


positive regulation of mRNA processing (Score: 4.526779)

Control



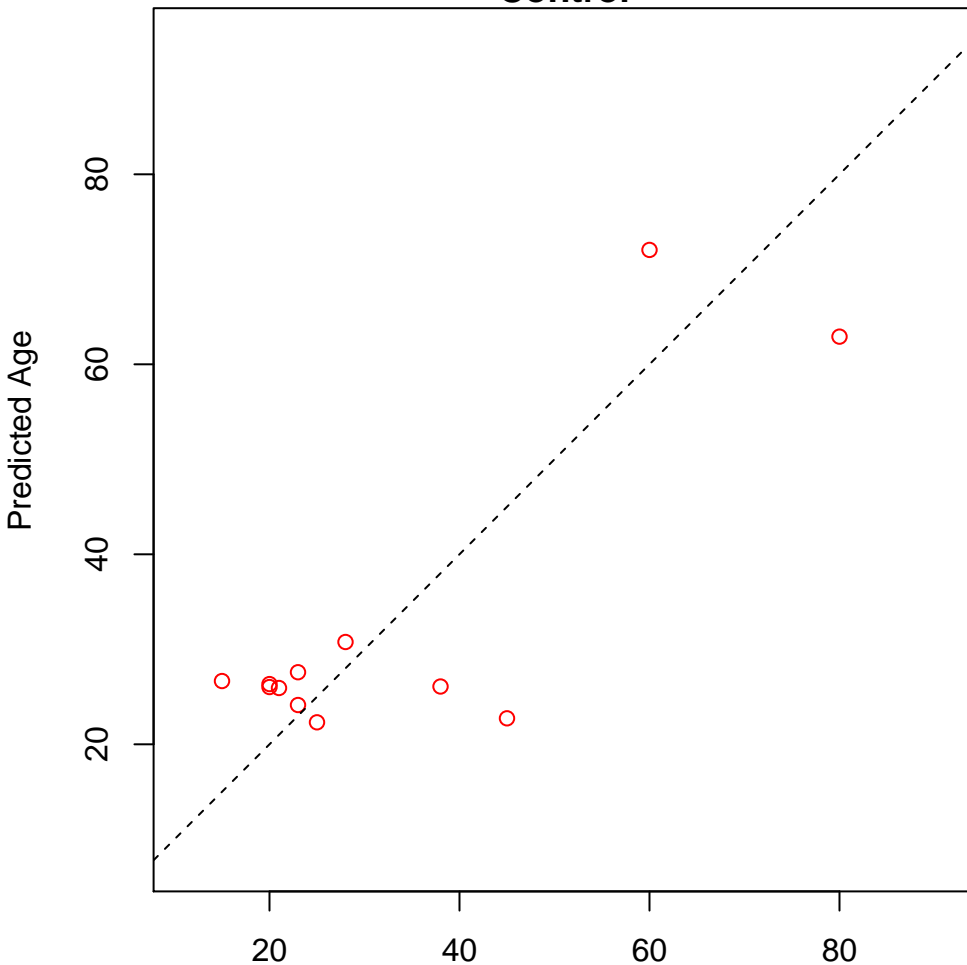
Test



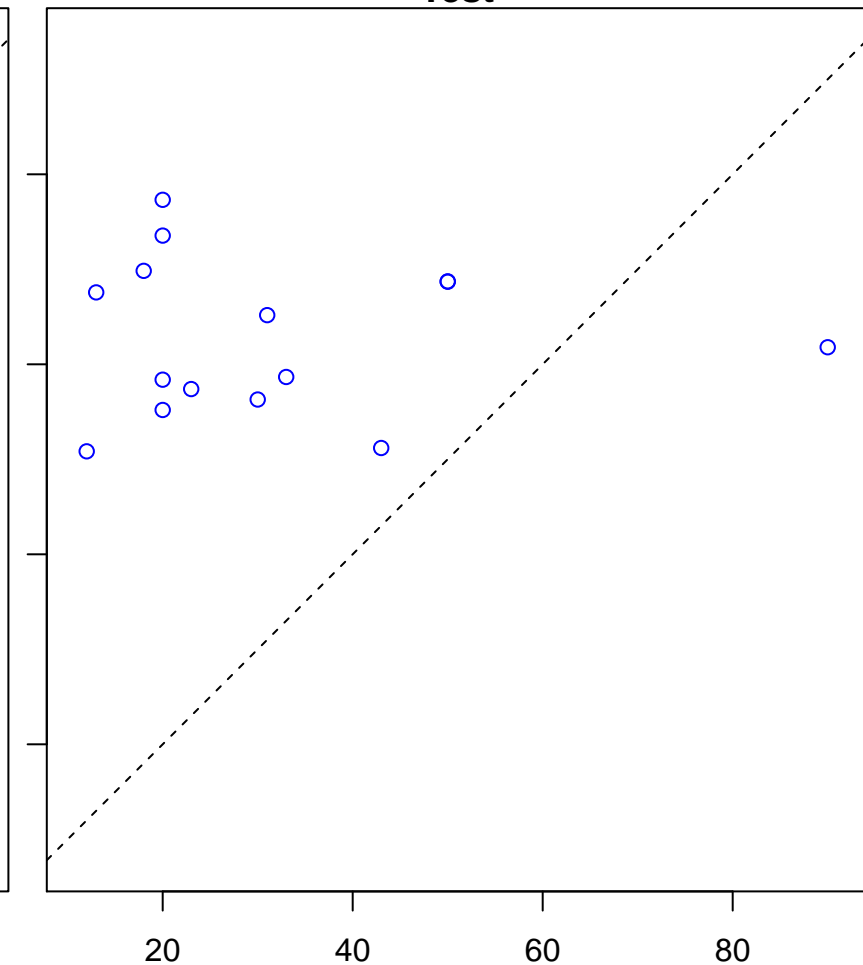
Actual Age

regulation of protein dephosphorylation (Score: 4.52699)

Control

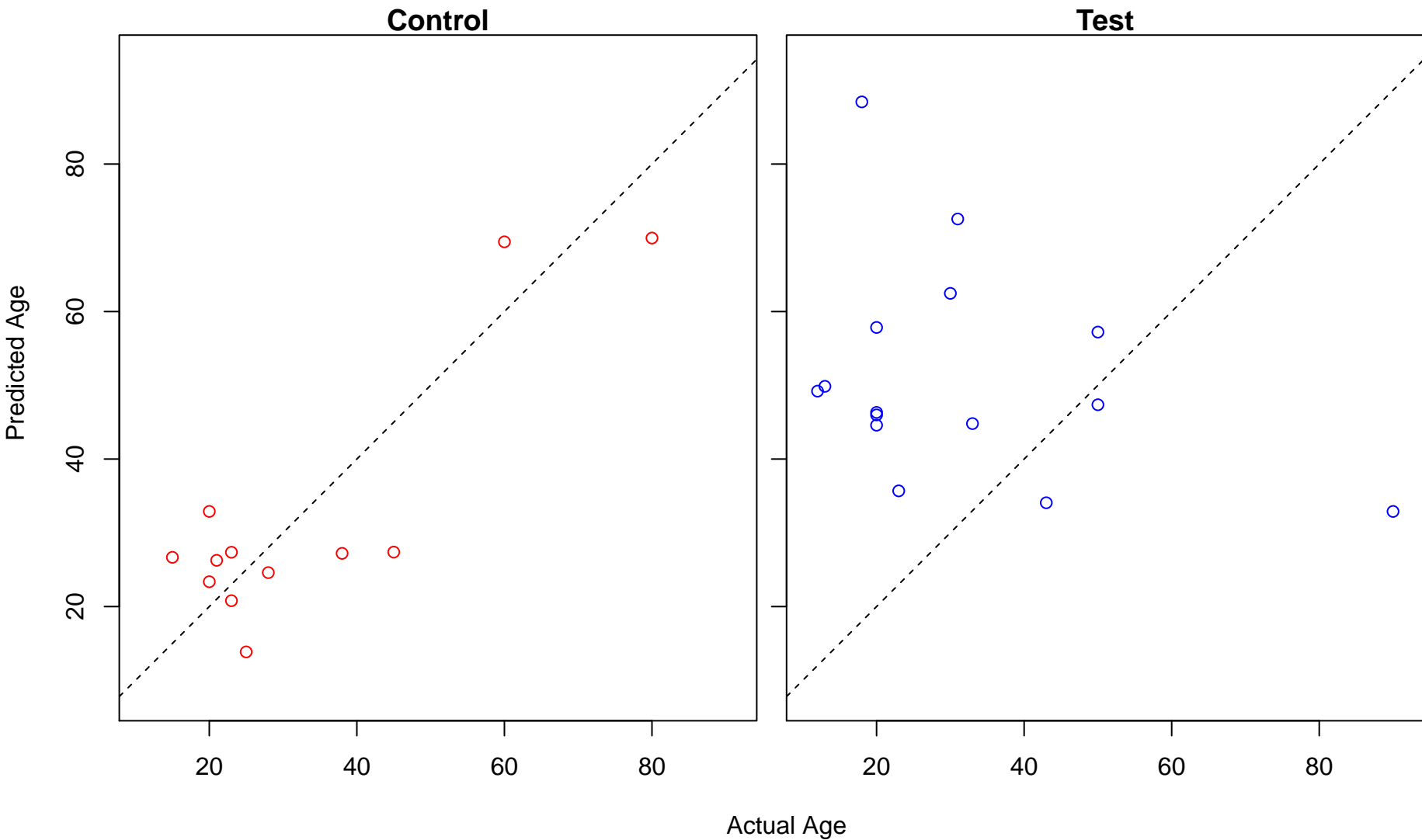


Test



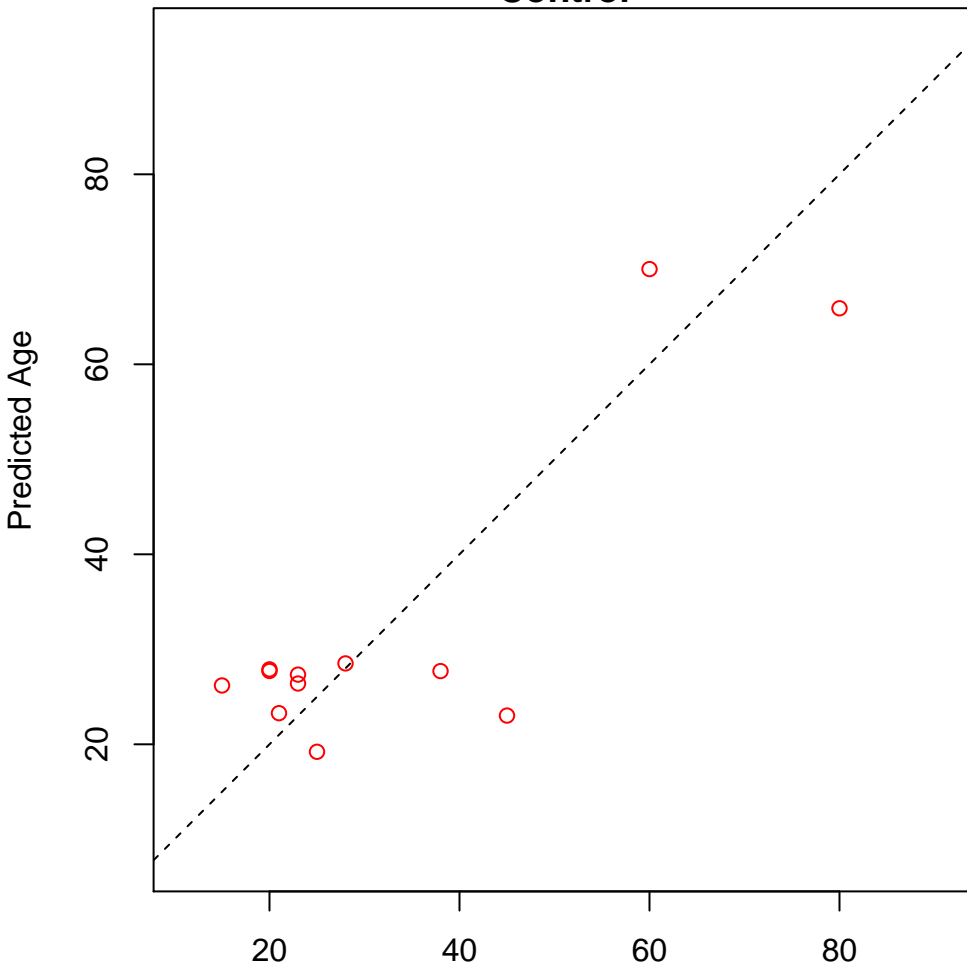
Actual Age

negative regulation of centriole replication (Score: 4.526557)

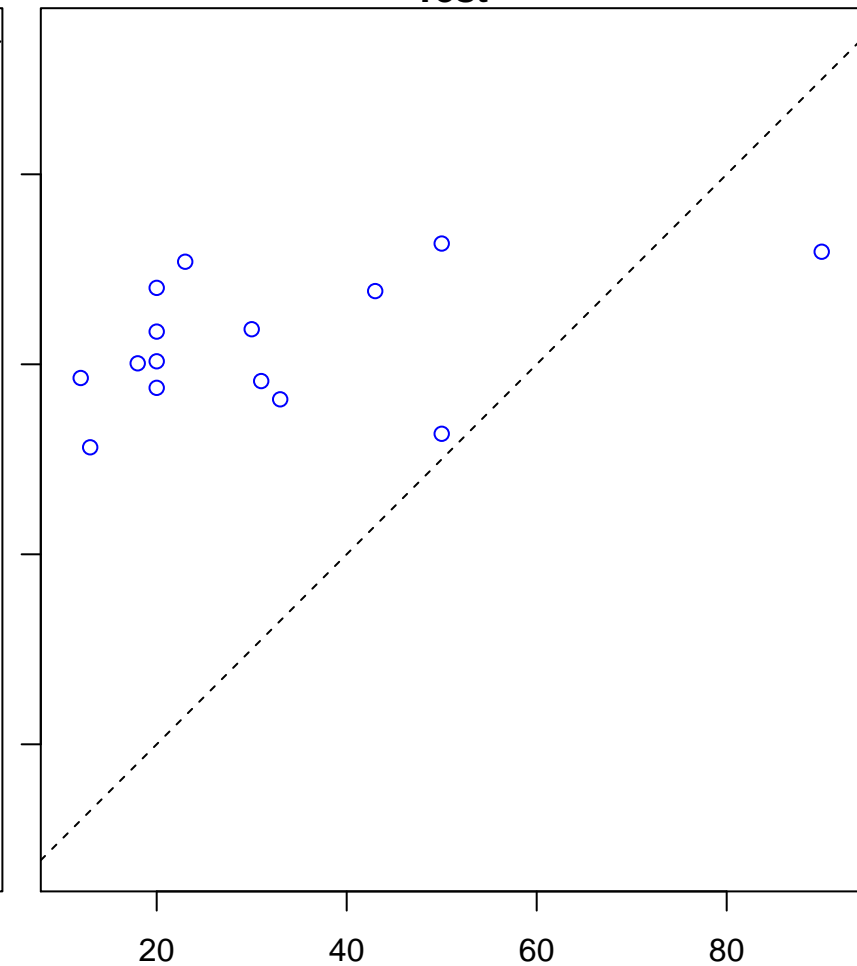


regulation of interleukin-2 production (Score: 4.525688)

Control

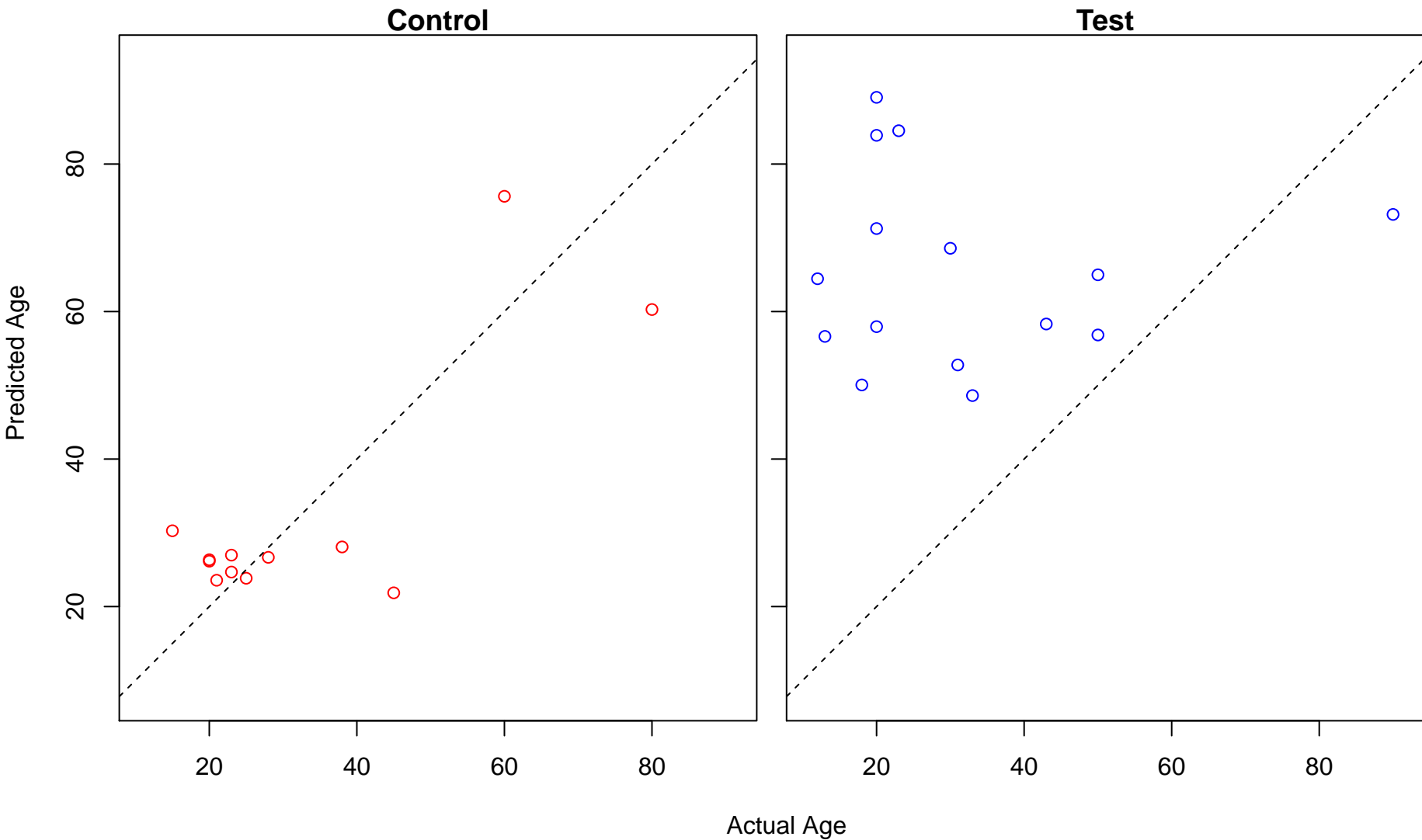


Test

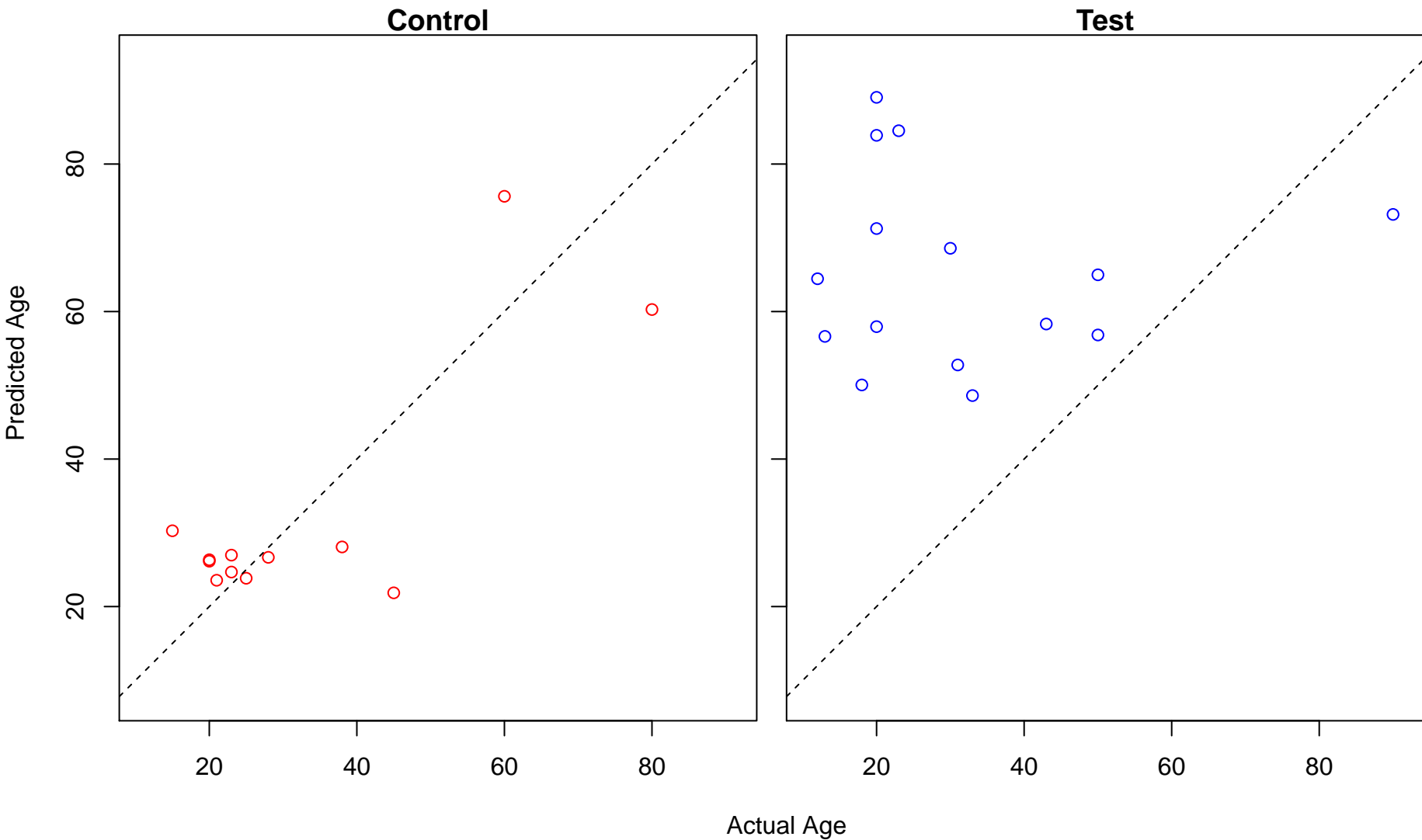


Actual Age

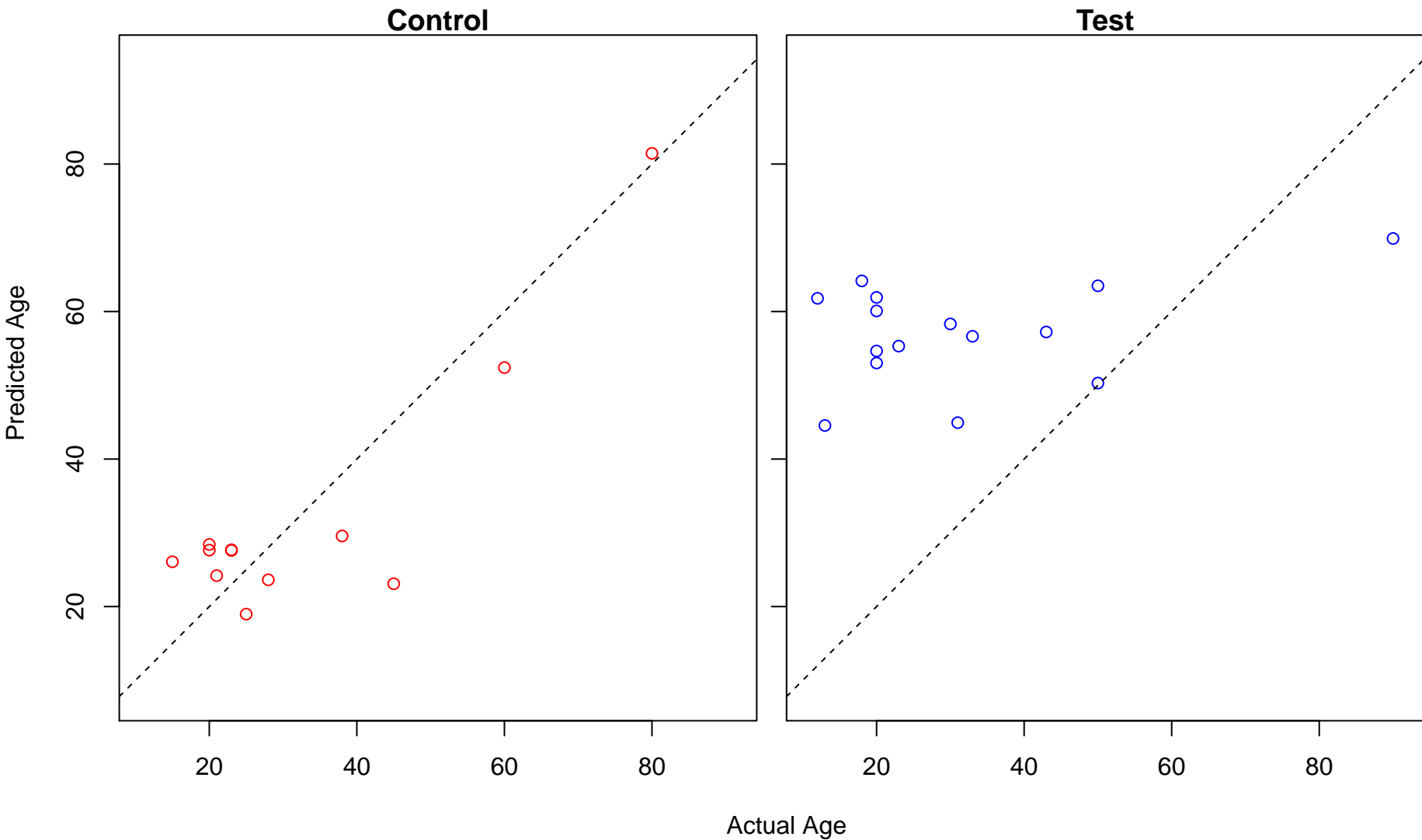
catecholamine metabolic process (Score: 4.525246)



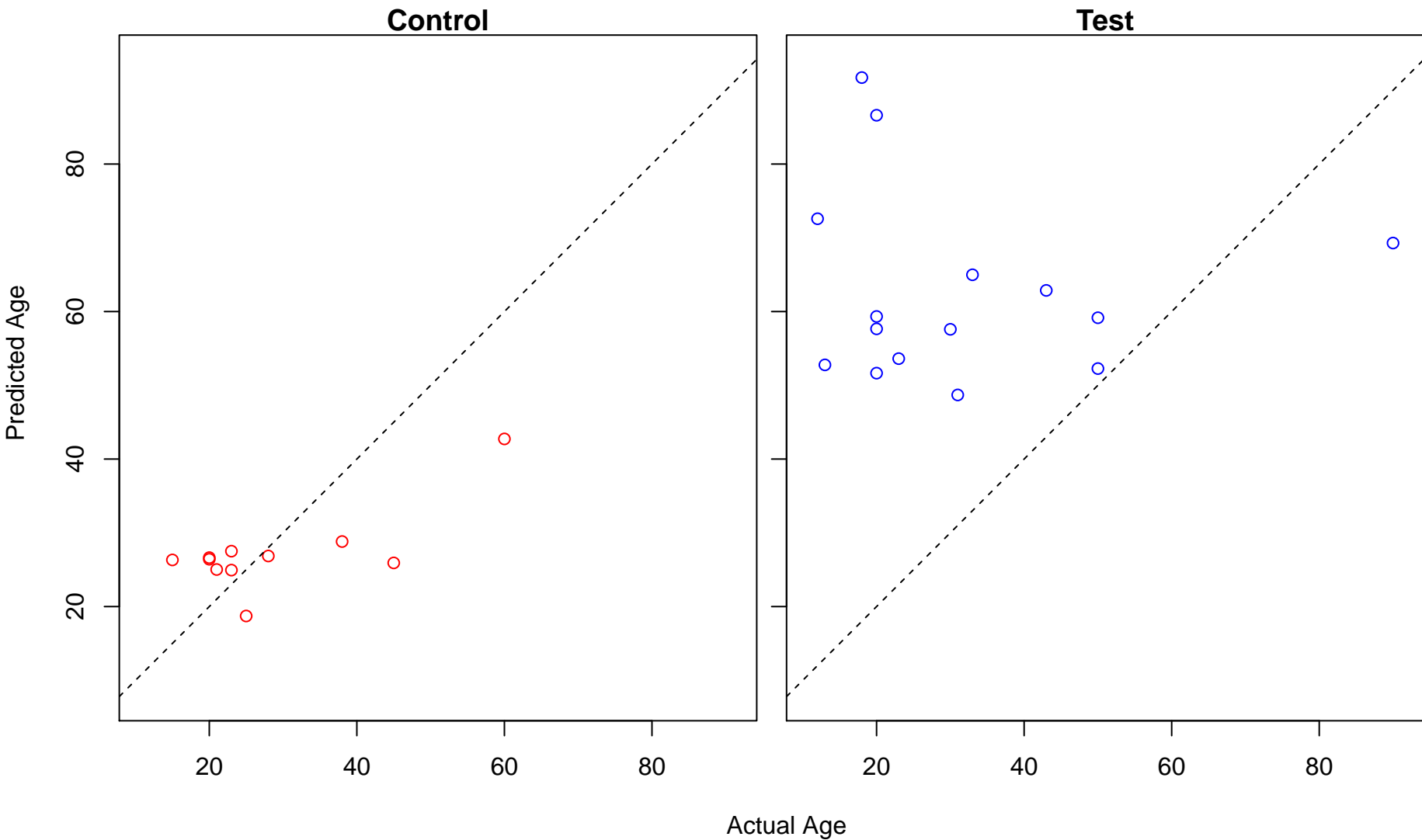
catechol-containing compound metabolic process (Score: 4.525246)



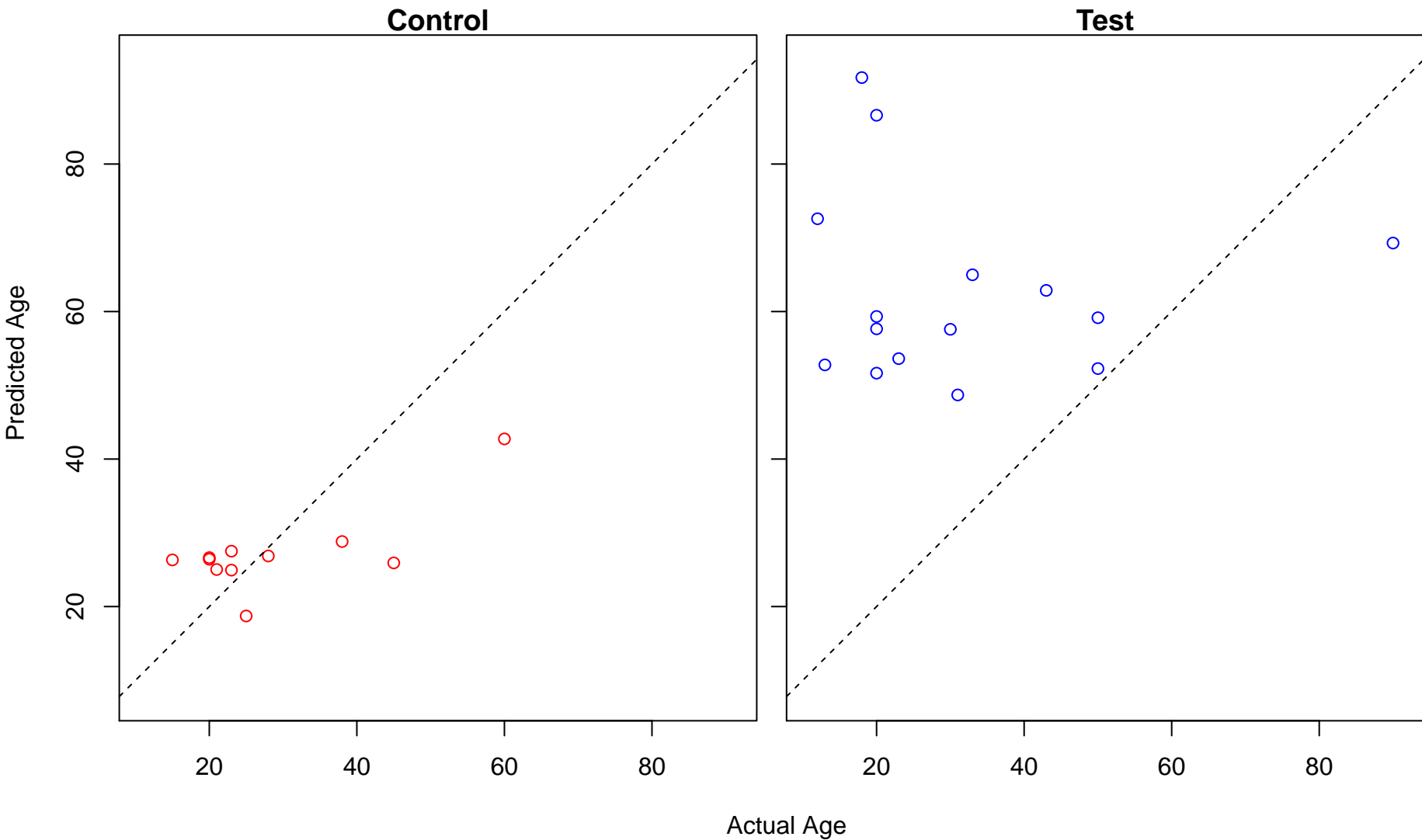
positive regulation of protein glycosylation (Score: 4.524413)



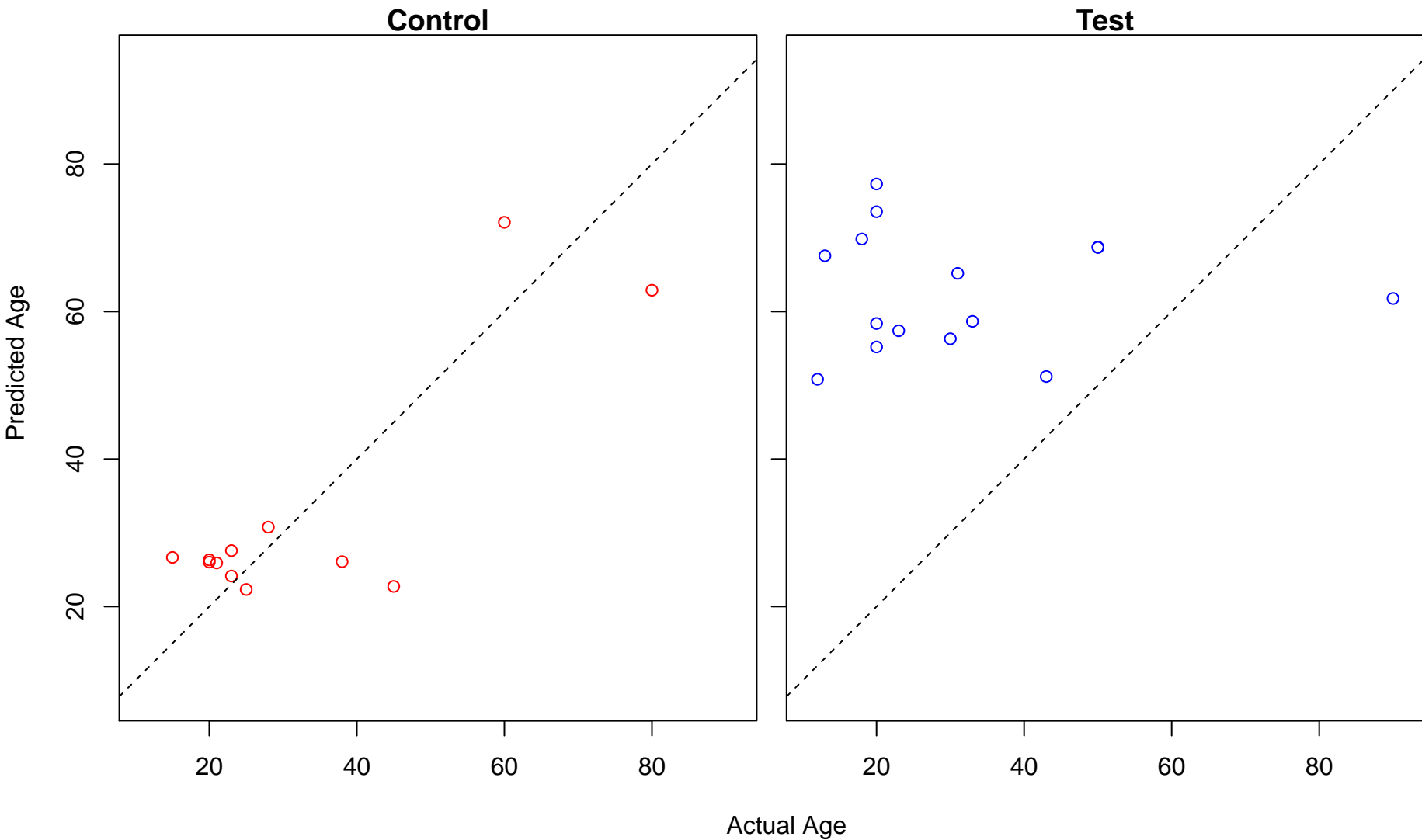
cytoplasmic translation (Score: 4.520425)



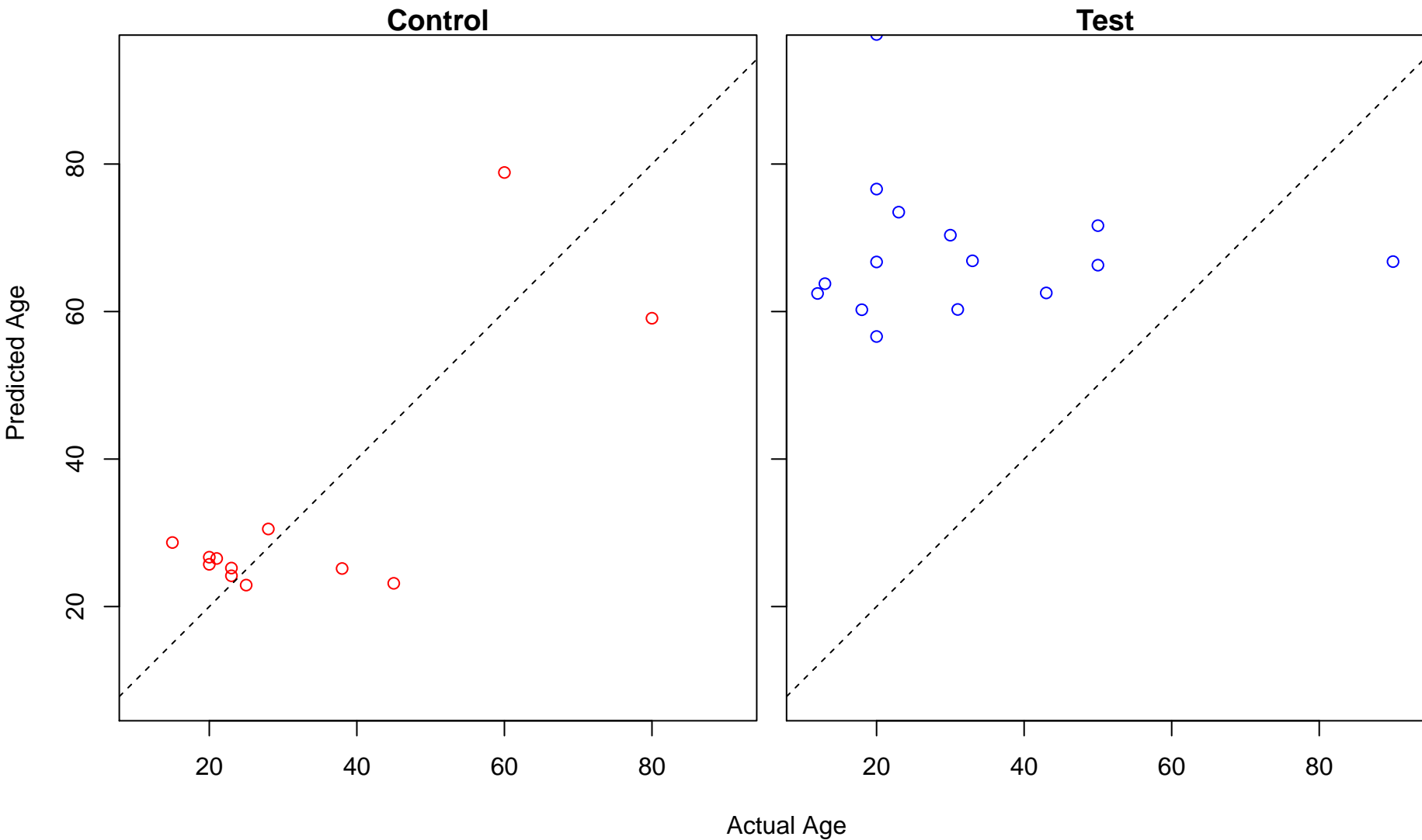
cytoplasmic translational initiation (Score: 4.520425)



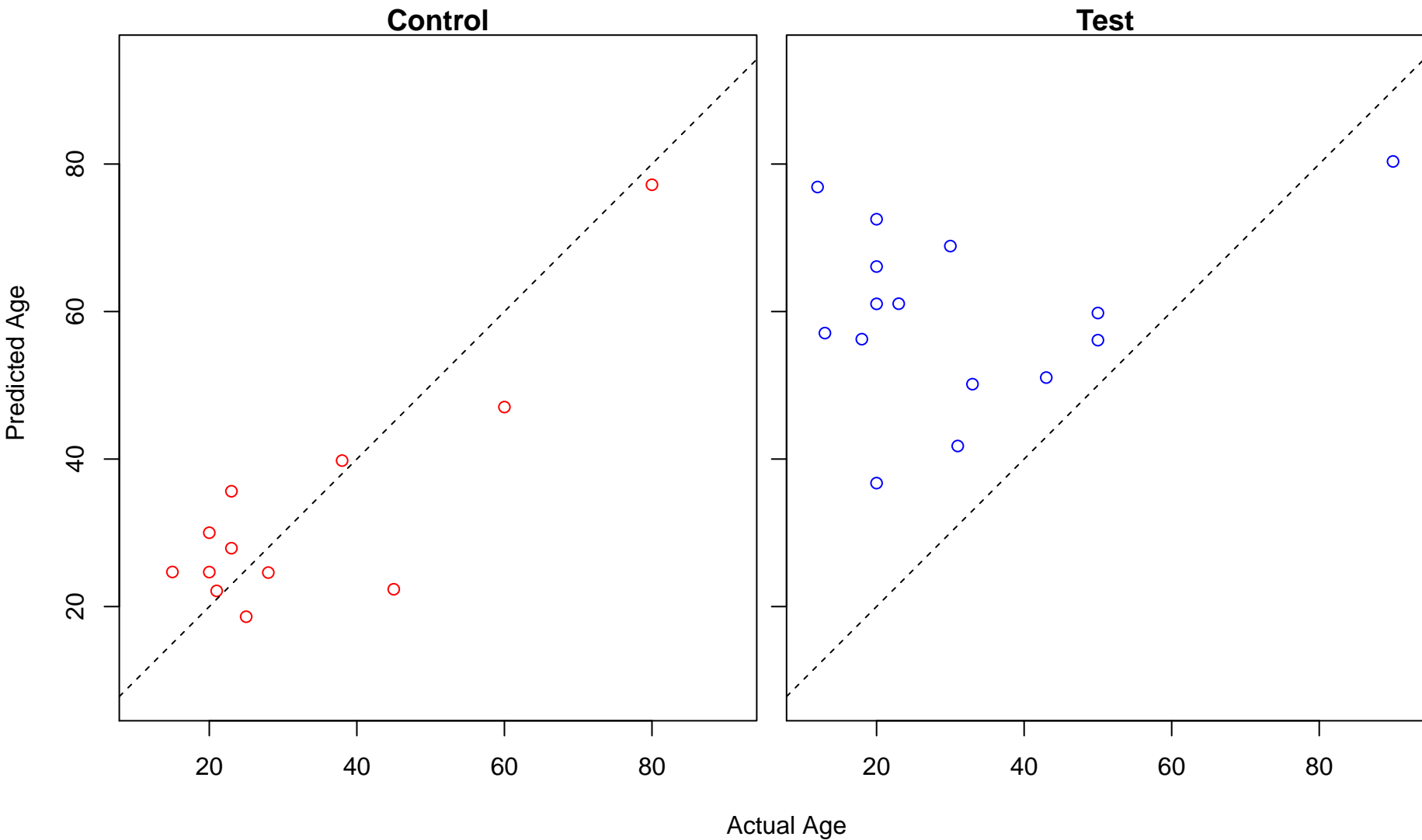
regulation of dephosphorylation (Score: 4.520189)



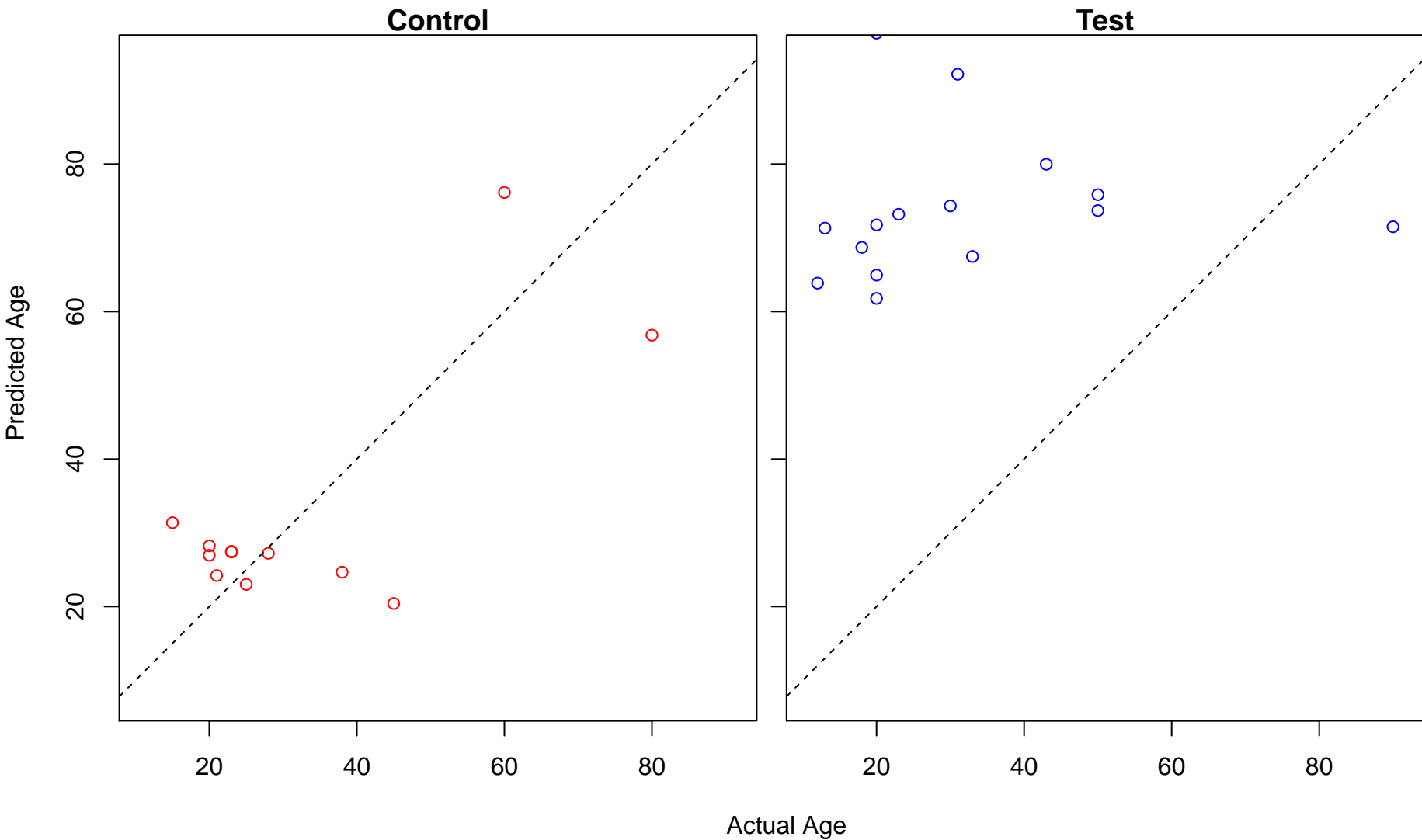
regulation of protein targeting to membrane (Score: 4.518539)



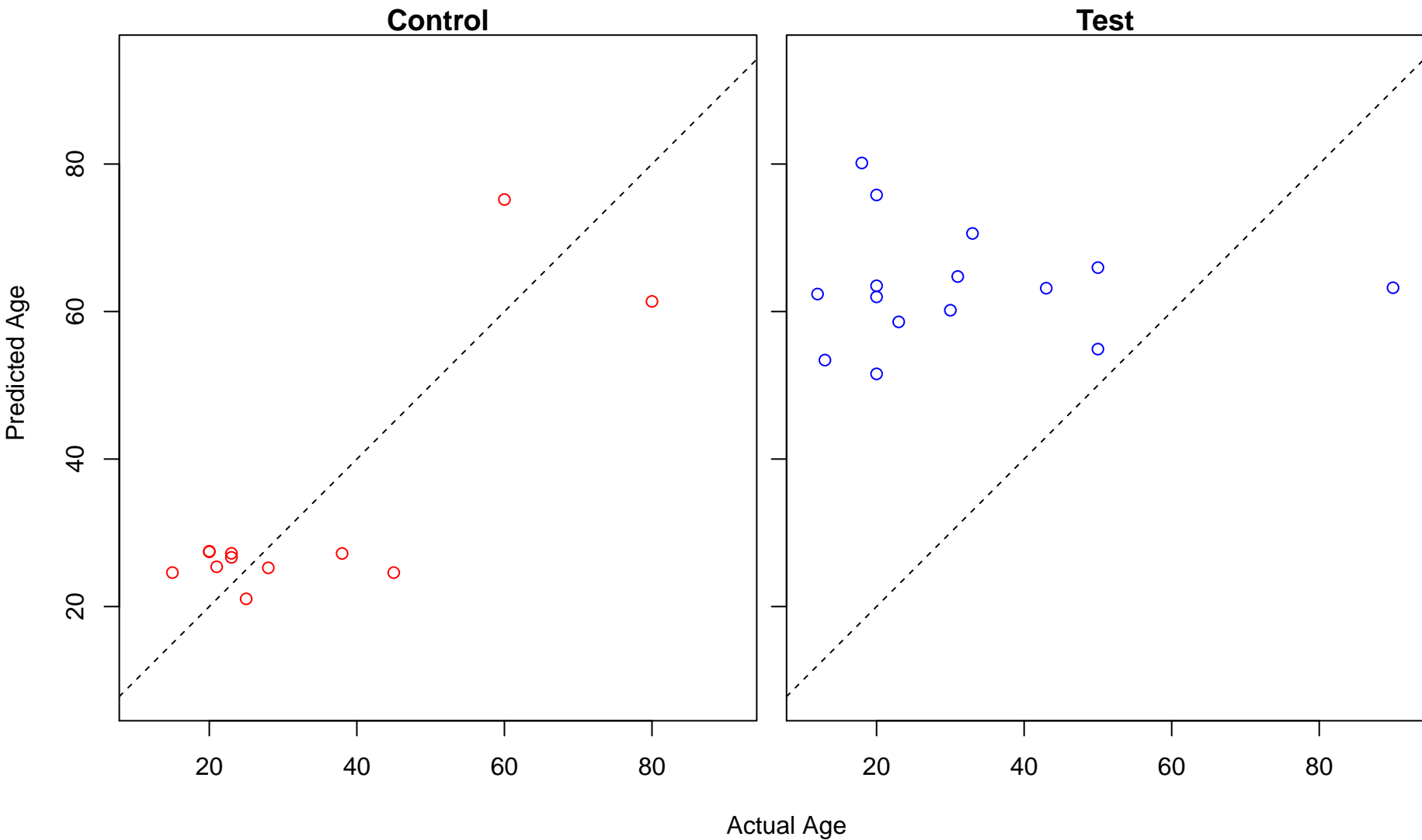
cell migration involved in sprouting angiogenesis (Score: 4.517576)



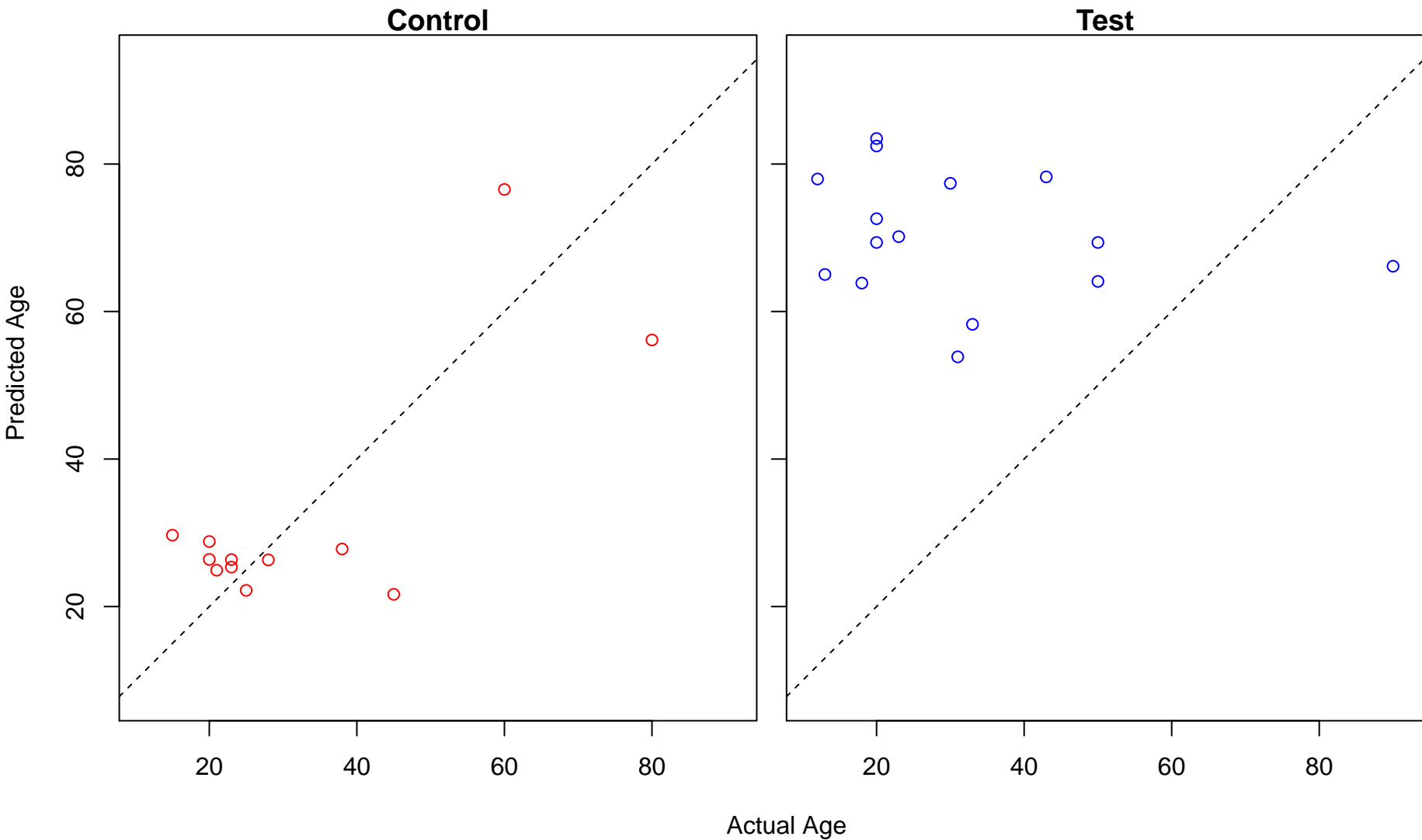
negative regulation of nitric-oxide synthase activity (Score: 4.516459)



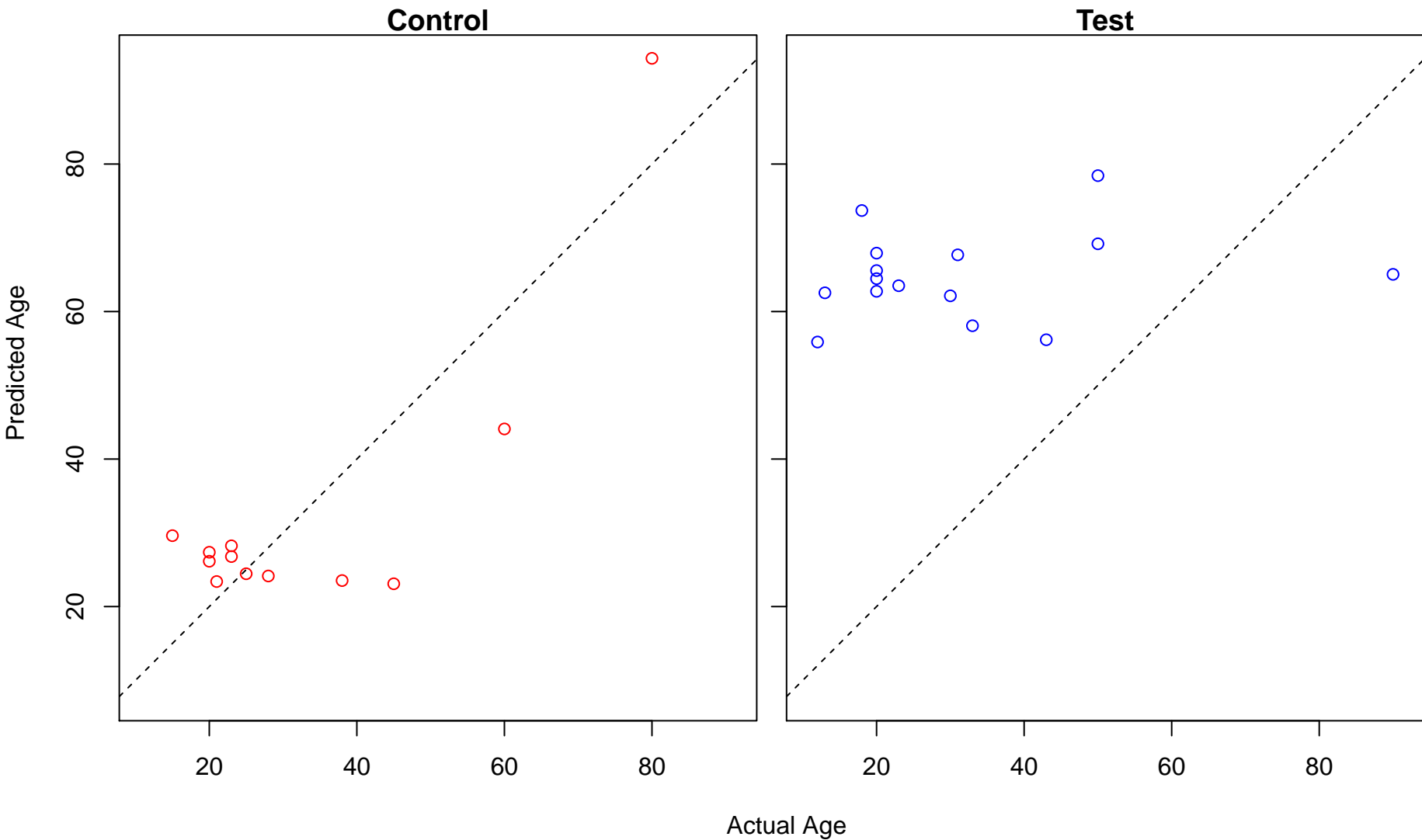
negative regulation of cyclin-dependent protein serine/threonine kinase activity (Score: 4.515794)



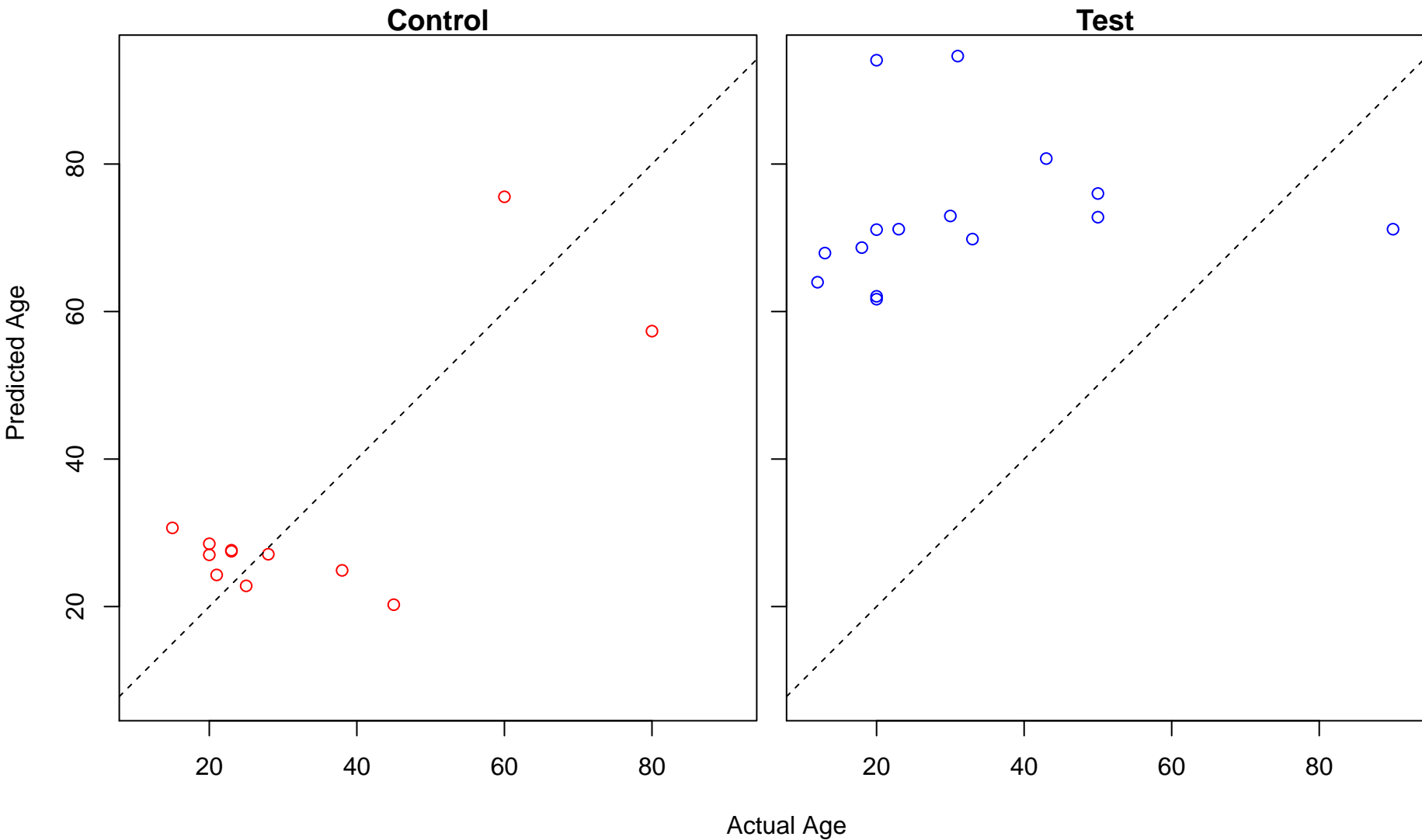
regulation of MDA-5 signaling pathway (Score: 4.514675)



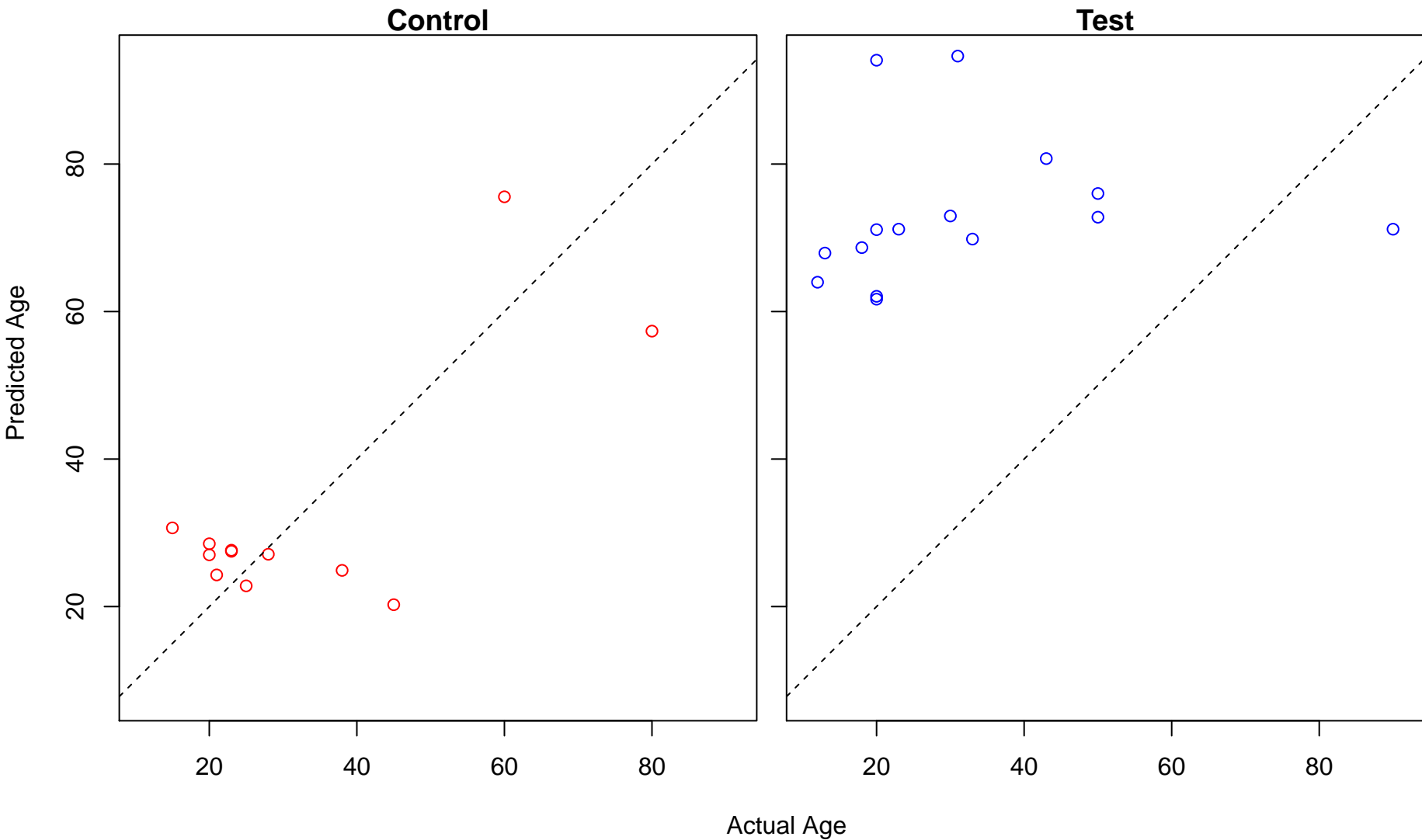
regulation of dendritic spine morphogenesis (Score: 4.512899)



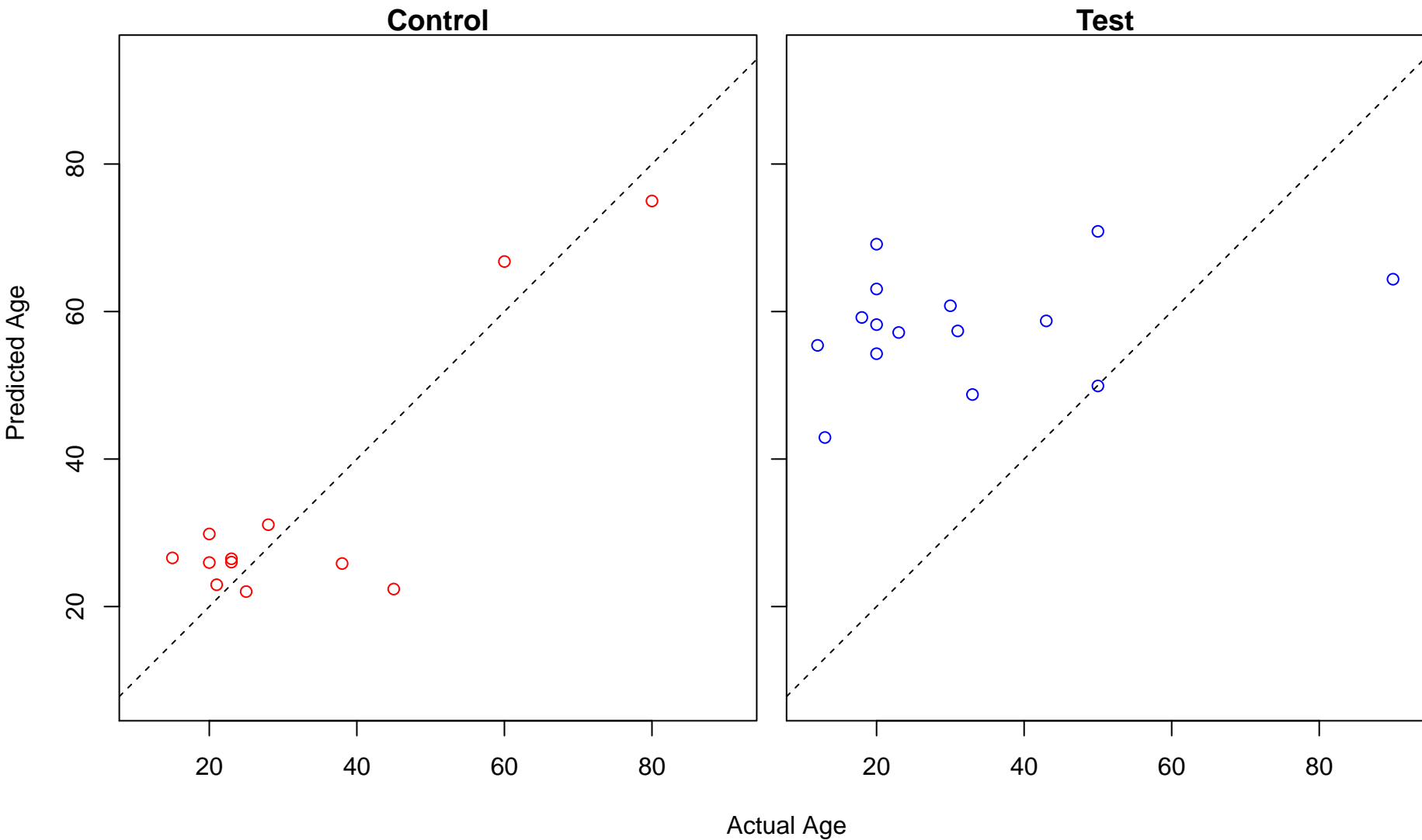
negative regulation of nitric oxide biosynthetic process (Score: 4.512706)



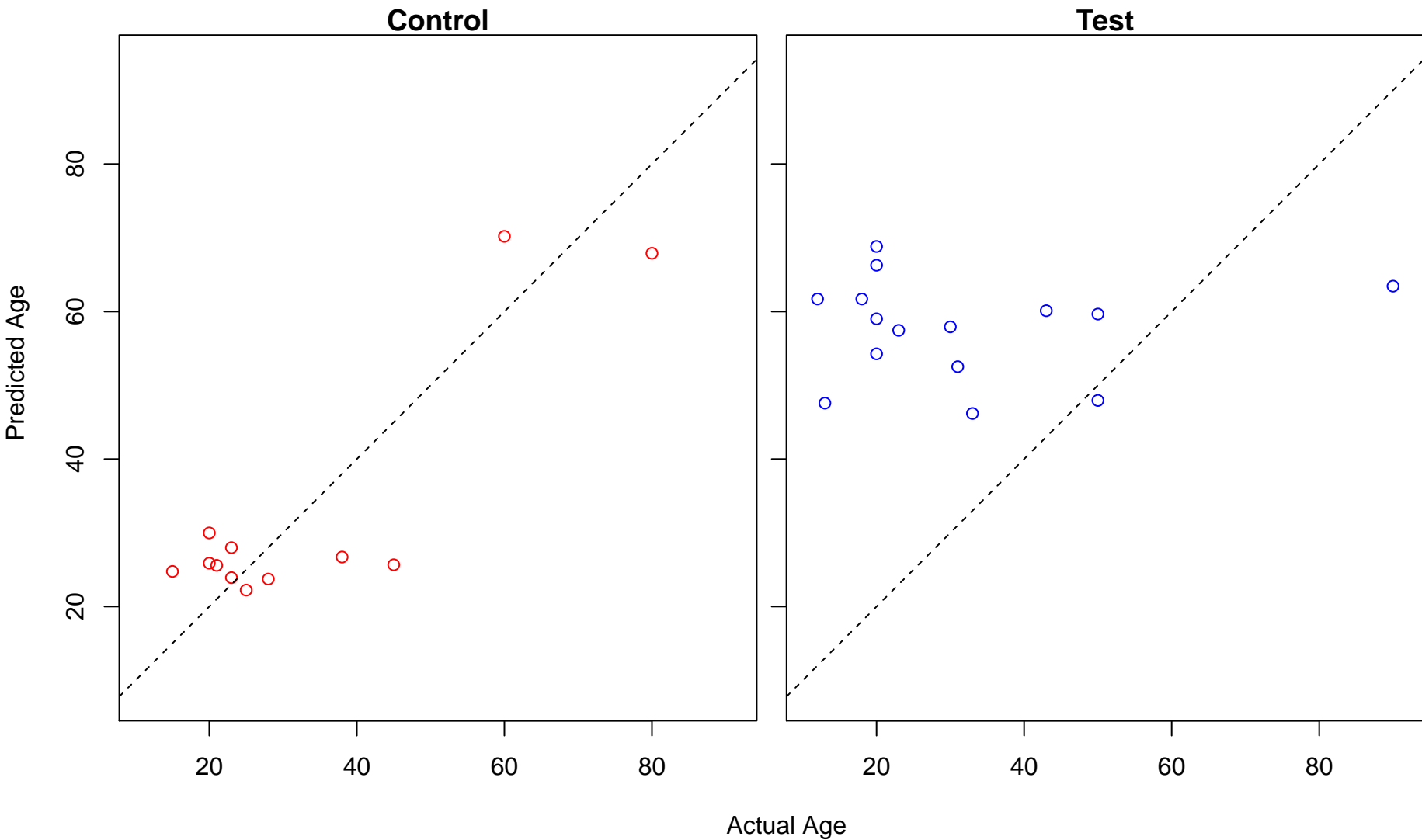
negative regulation of nitric oxide metabolic process (Score: 4.512706)



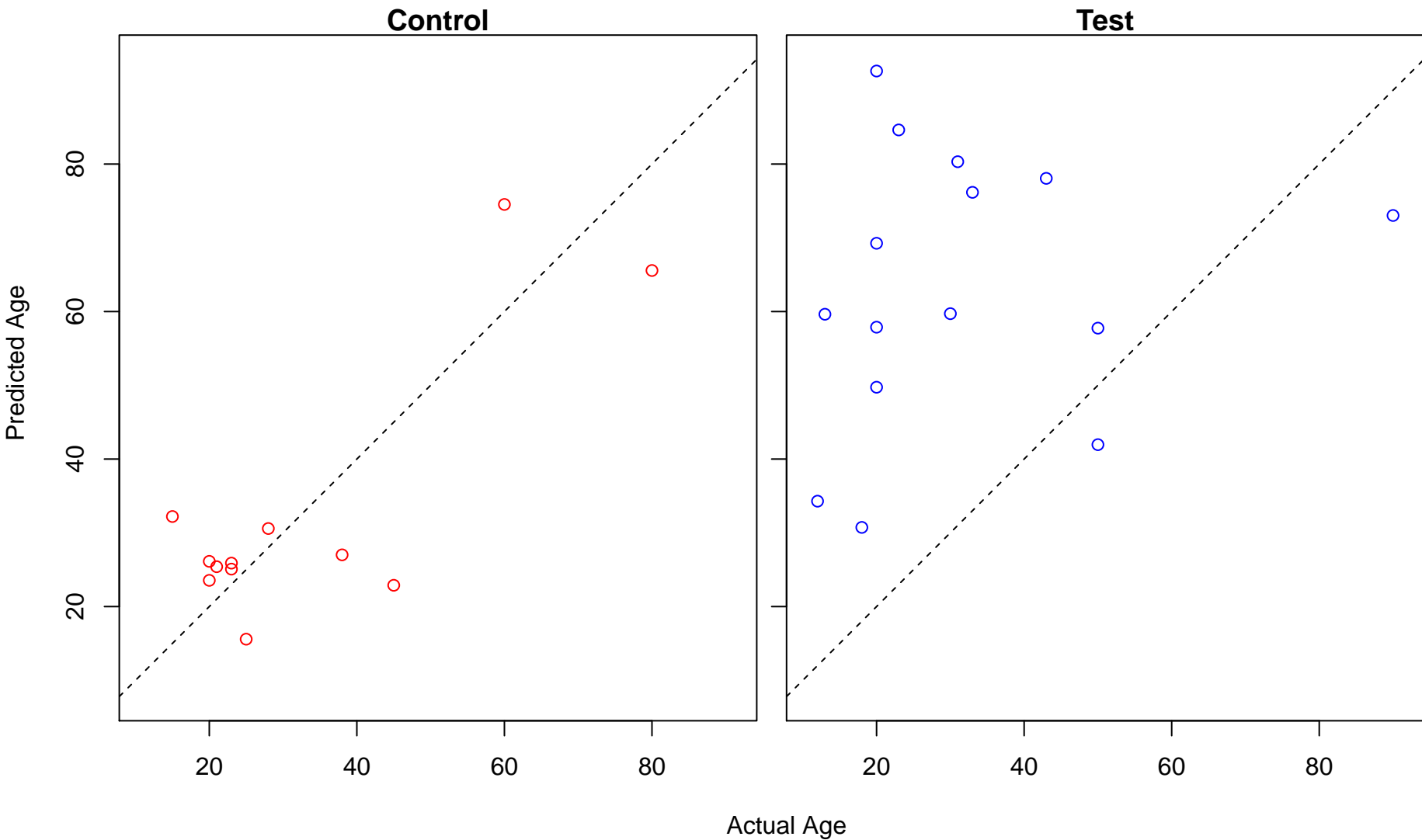
mitotic spindle assembly (Score: 4.511602)



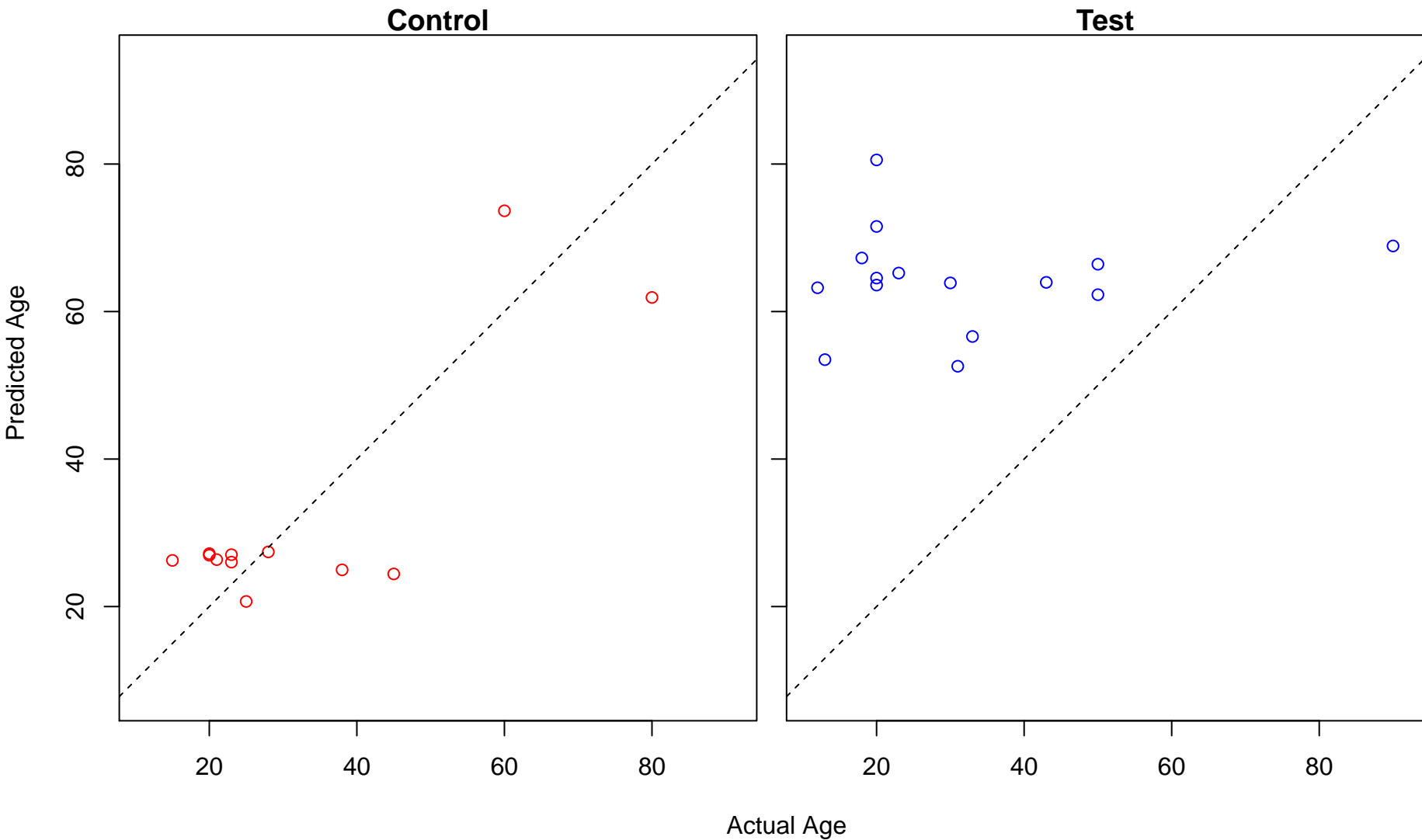
cellular component maintenance (Score: 4.506953)



non-canonical Wnt signaling pathway (Score: 4.504887)

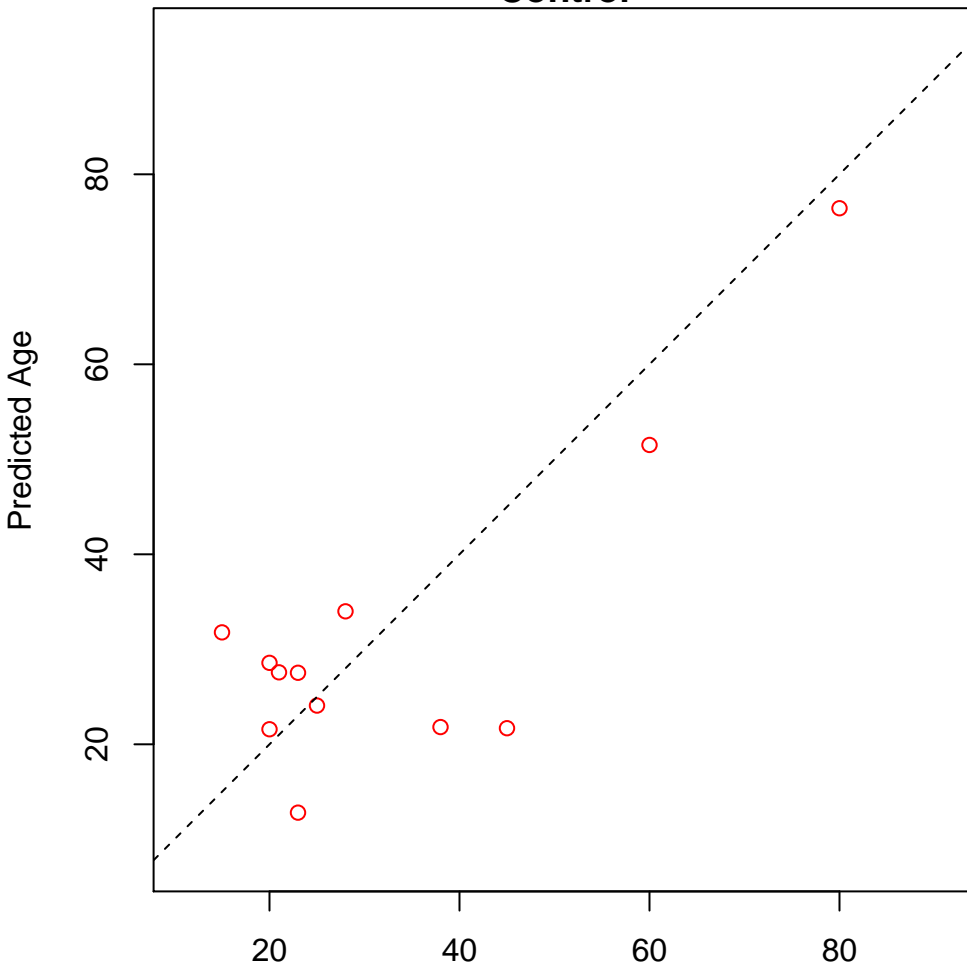


regulation of mitotic spindle assembly (Score: 4.503629)

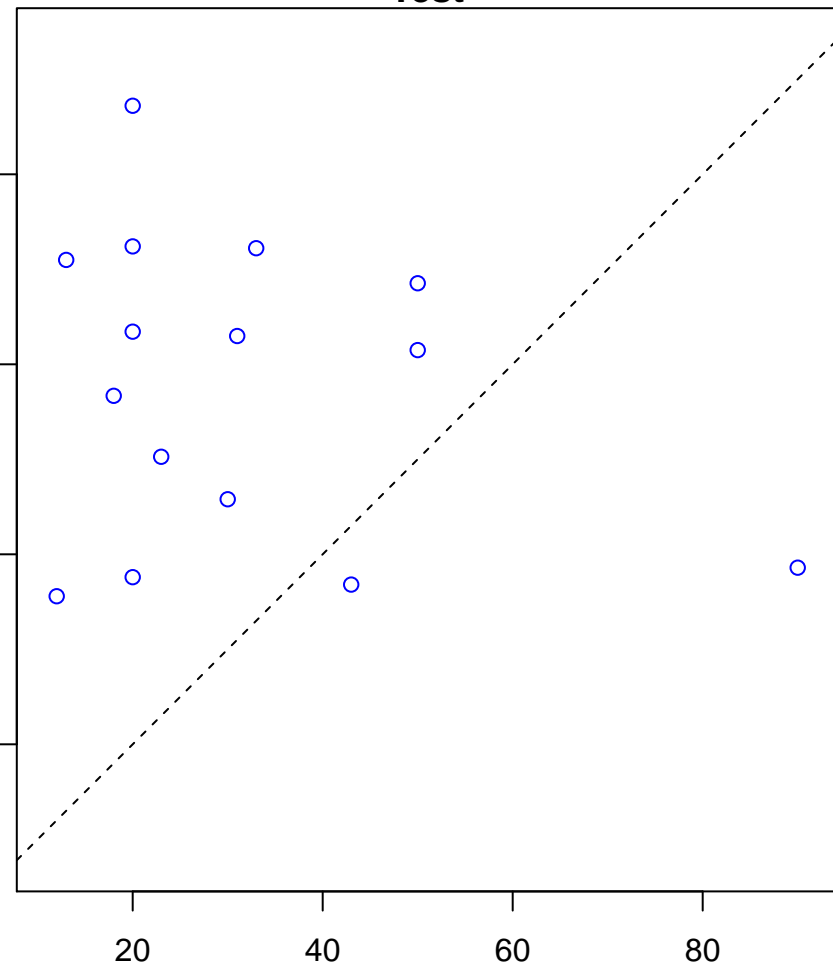


activation of phospholipase C activity (Score: 4.501896)

Control

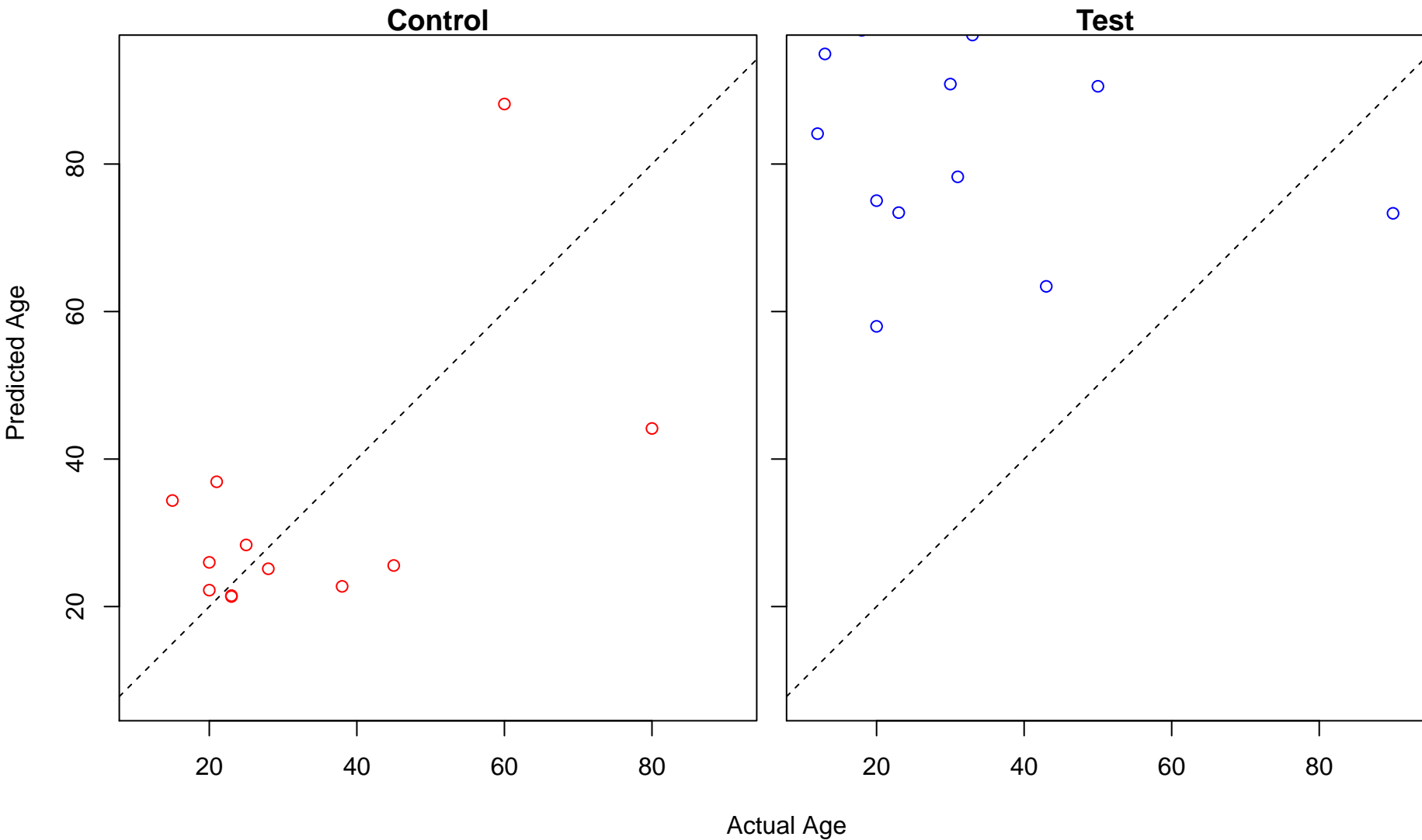


Test

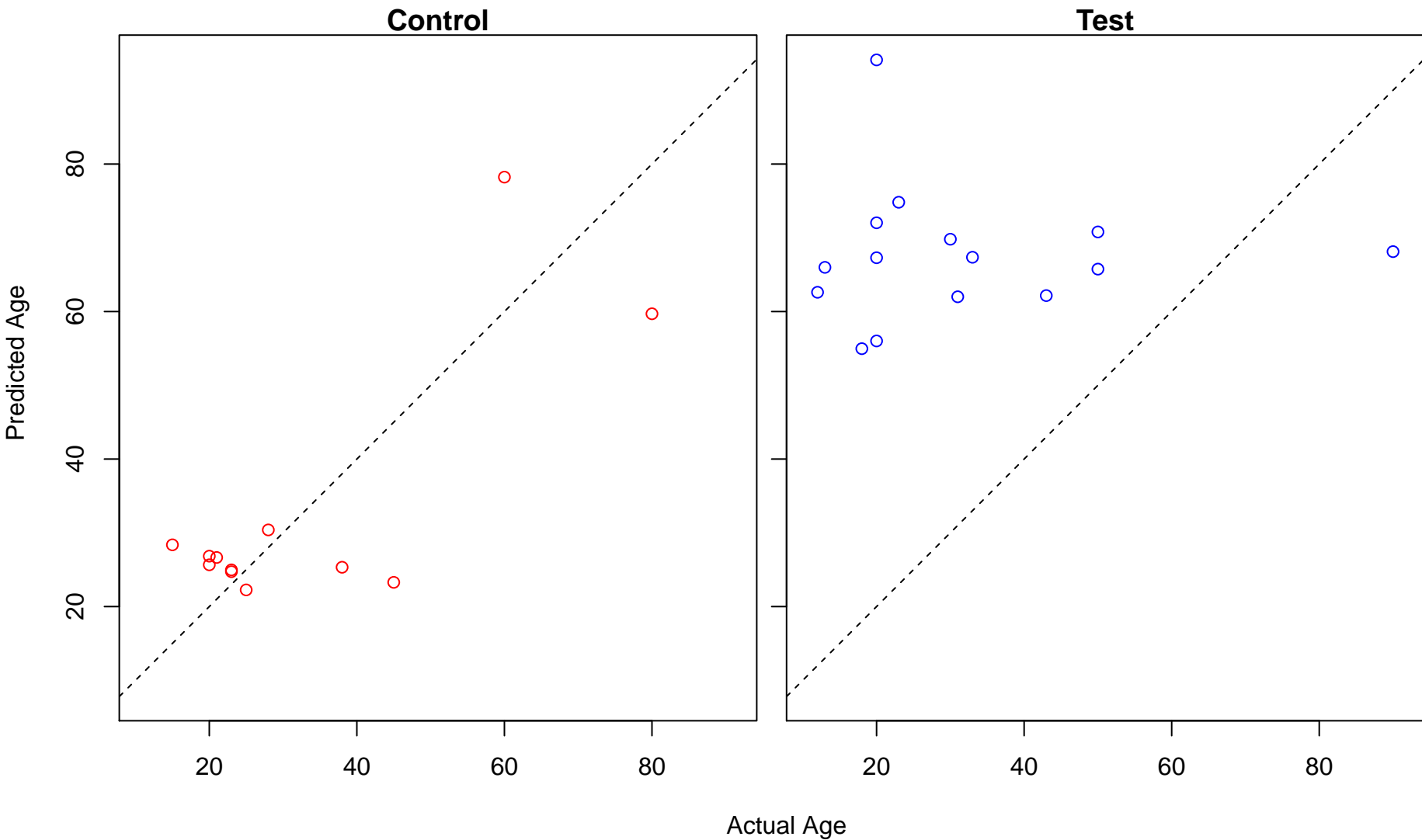


Actual Age

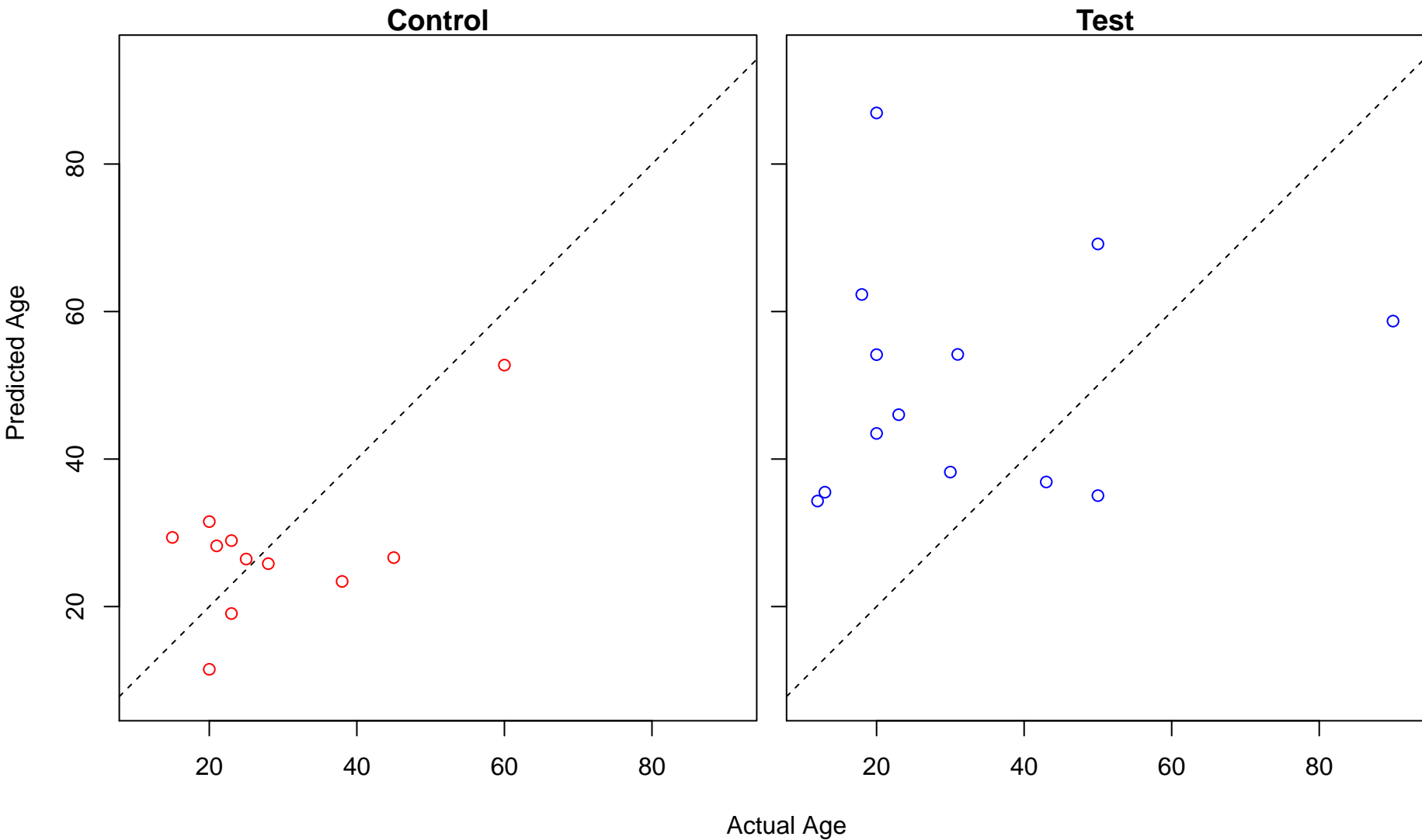
pyridine-containing compound biosynthetic process (Score: 4.501510)



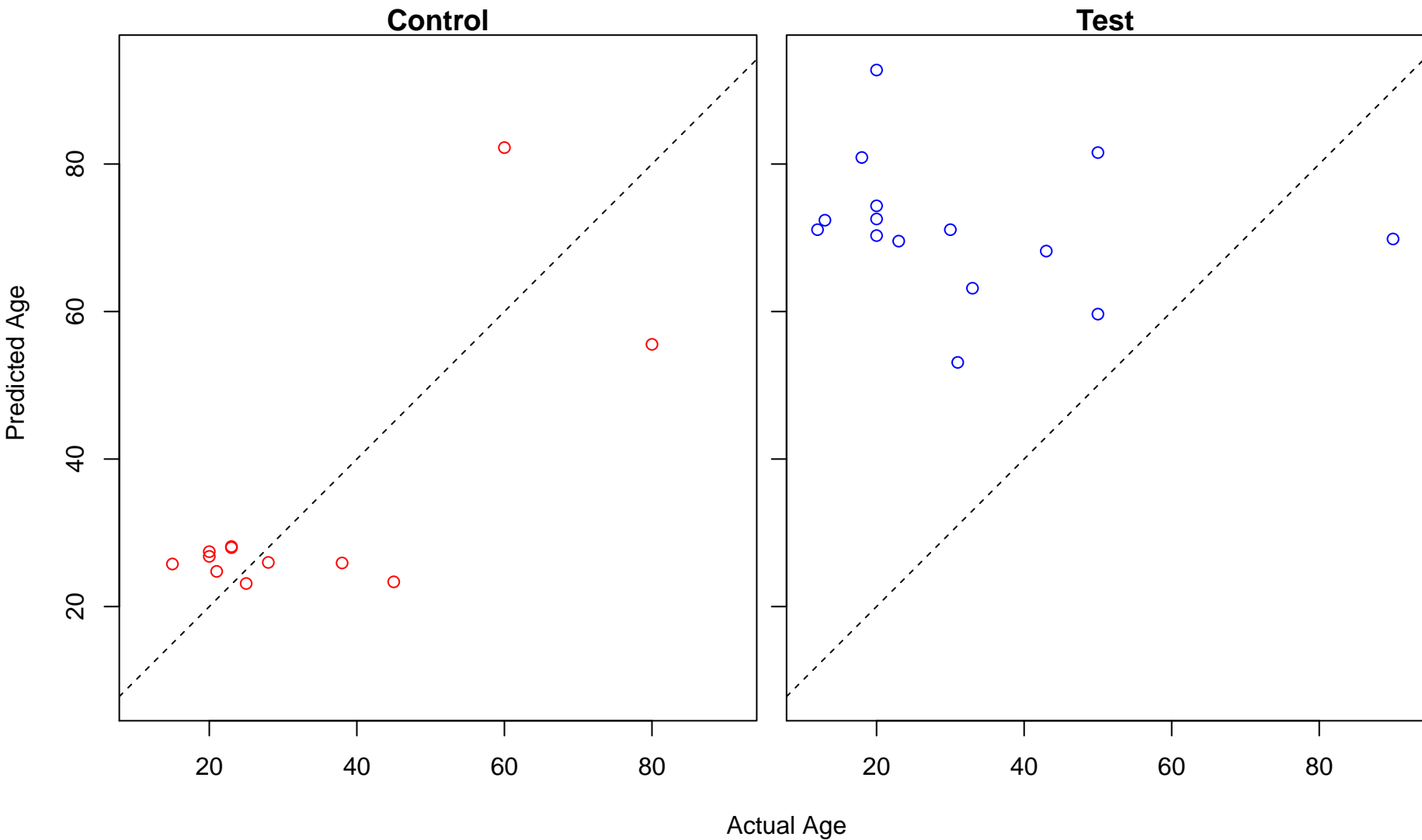
negative regulation of hematopoietic progenitor cell differentiation (Score: 4.501369)



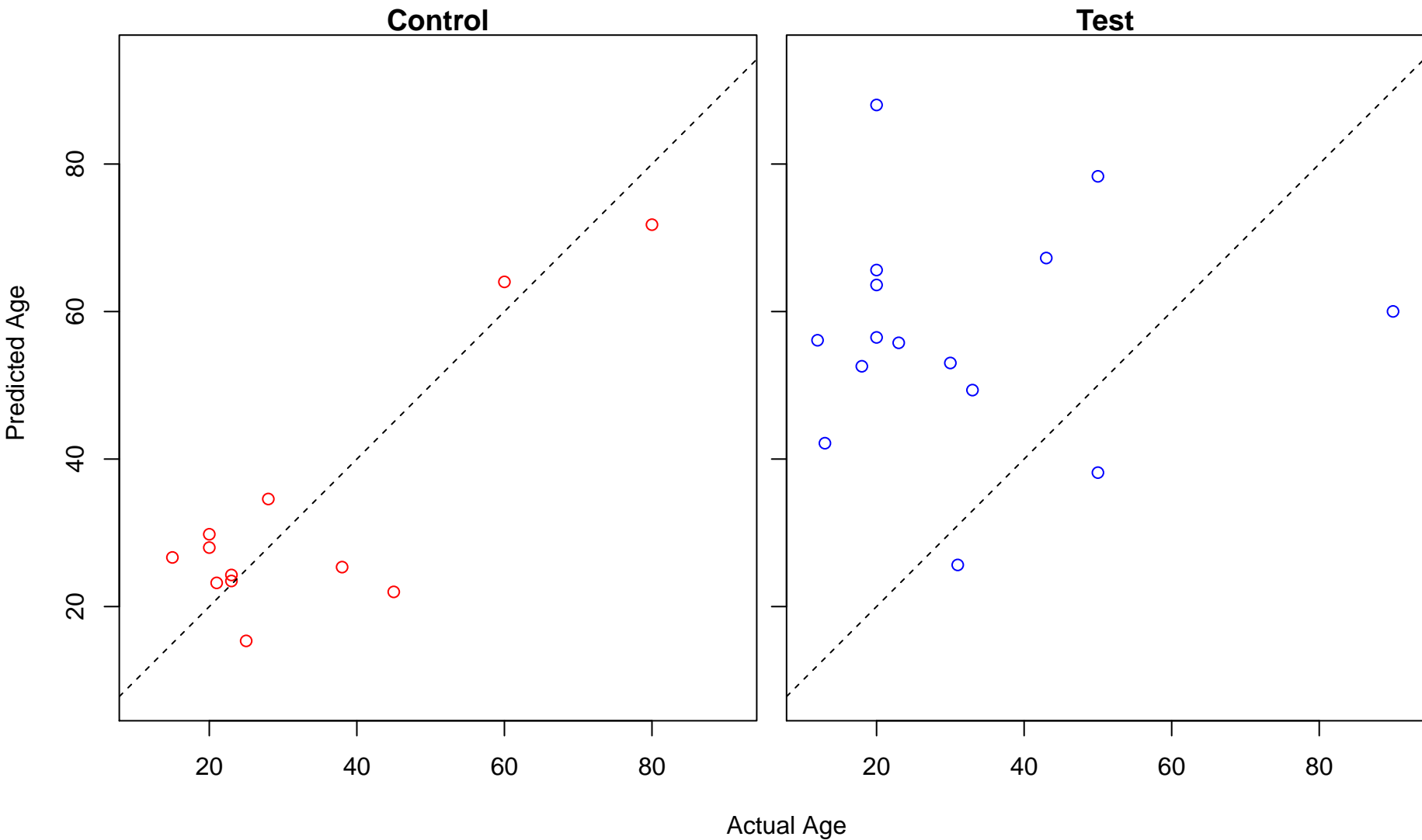
detection of chemical stimulus involved in sensory perception of taste (Score: 4.499847)



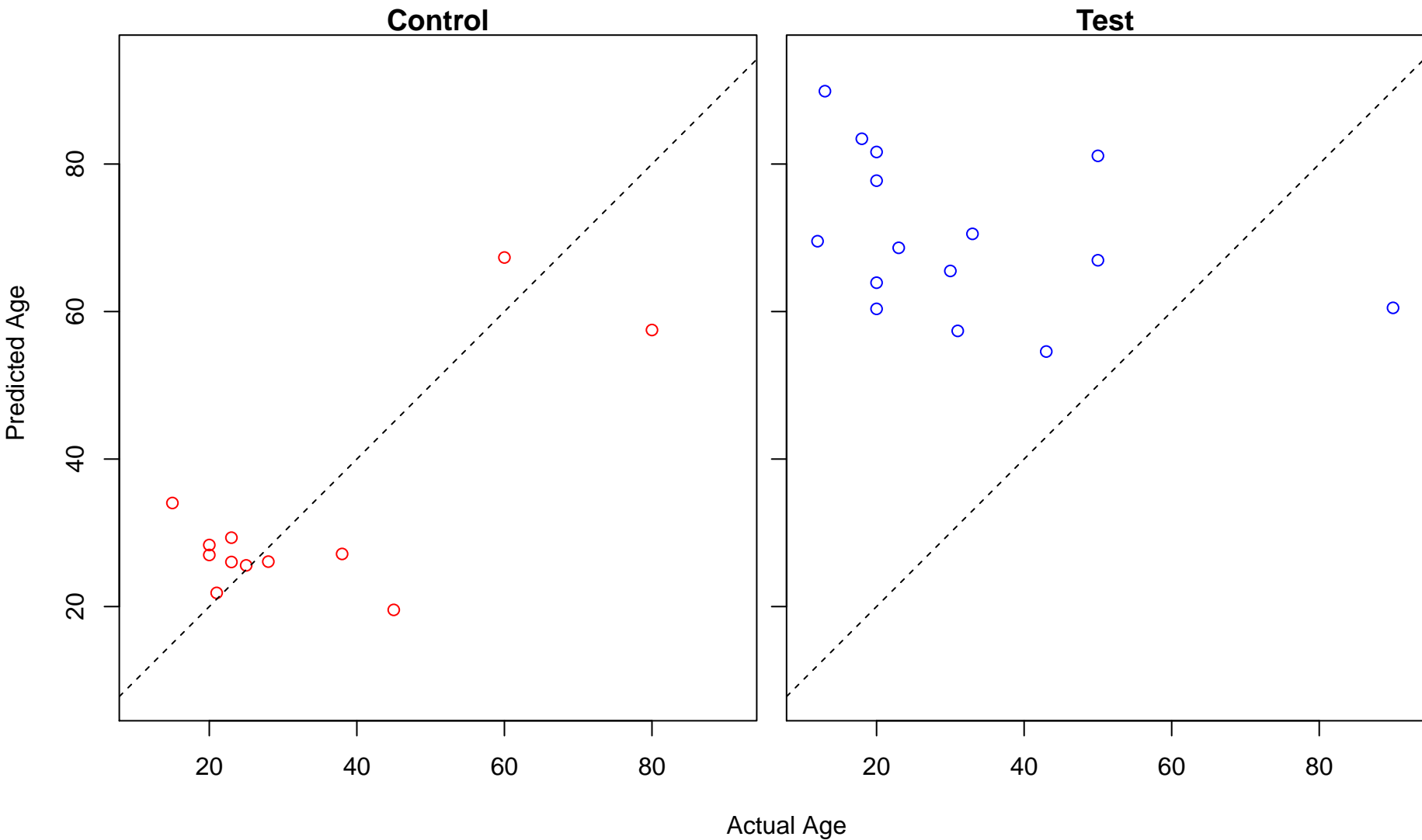
negative regulation of endothelial cell proliferation (Score: 4.492655)



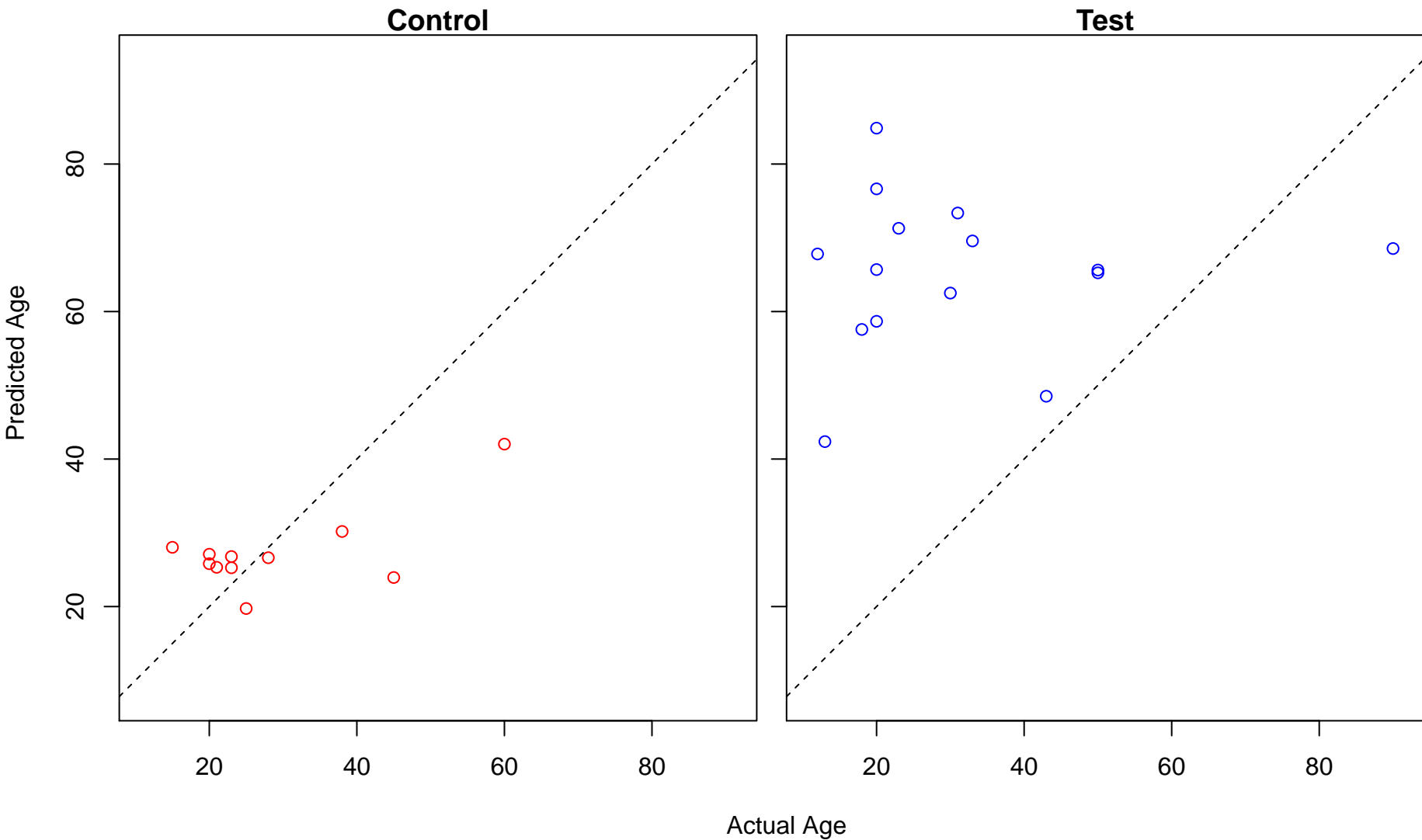
mature ribosome assembly (Score: 4.492382)



regulation of hippo signaling (Score: 4.491392)

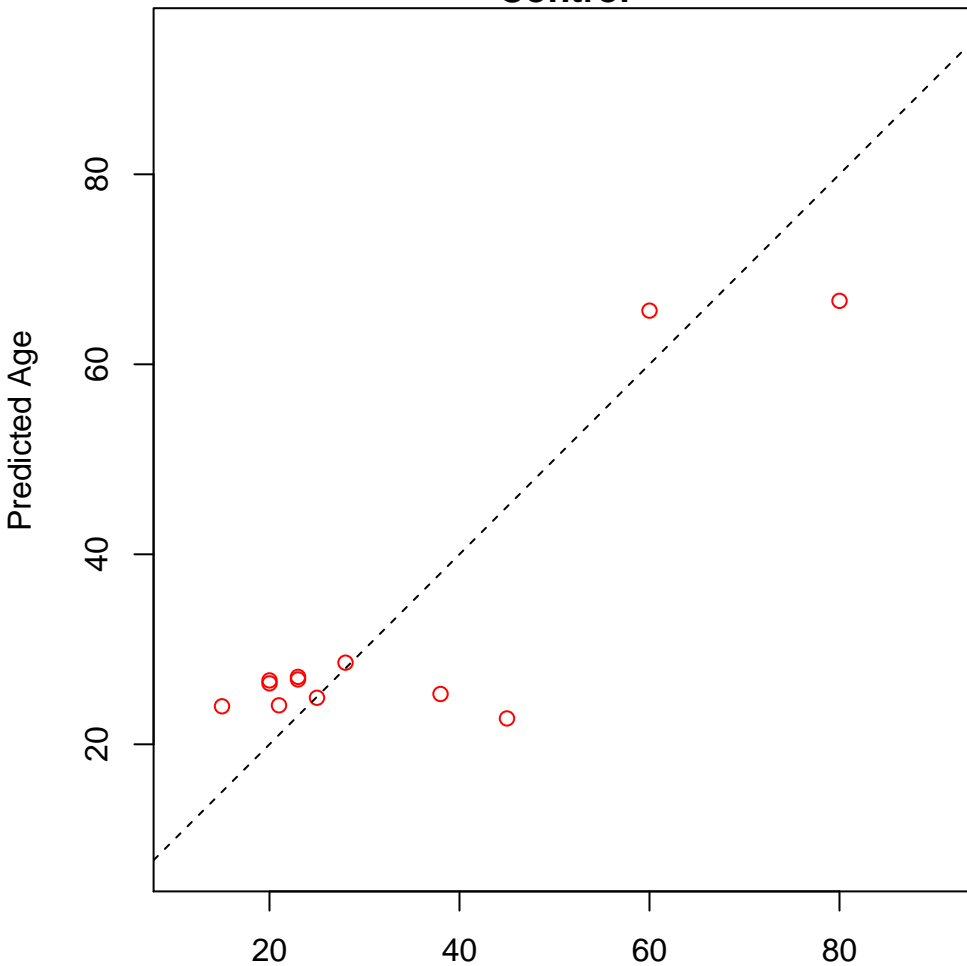


lateral ventricle development (Score: 4.489951)

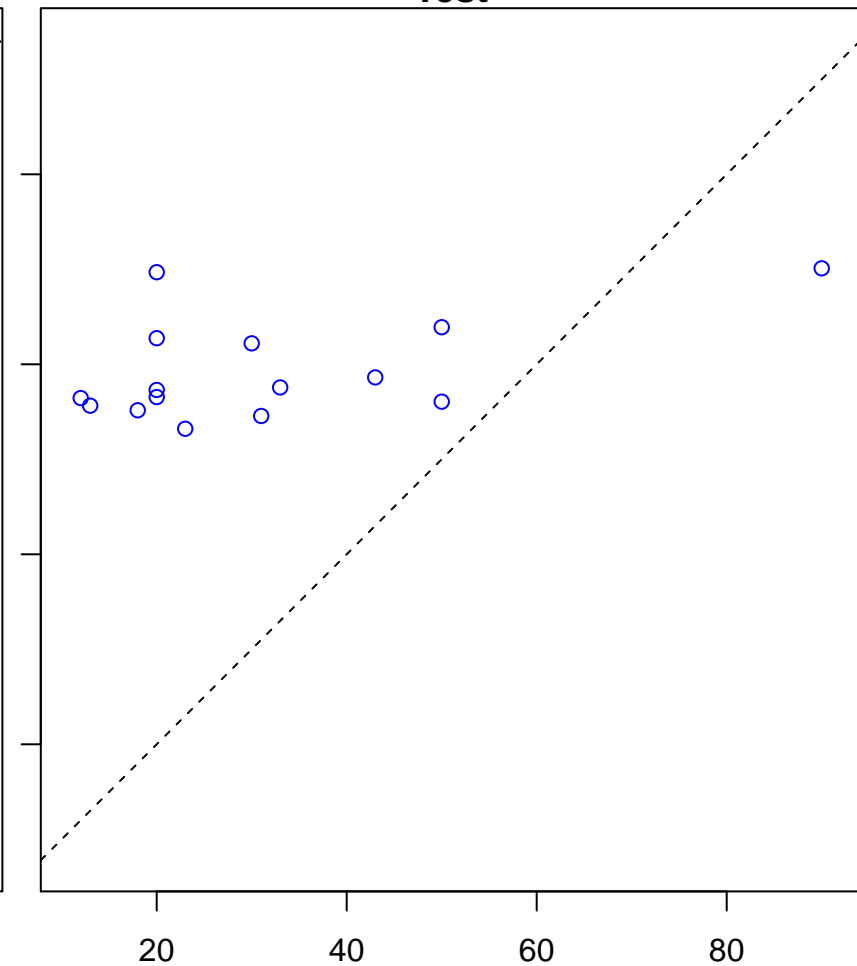


peptidyl-L-cysteine S-palmitoylation (Score: 4.487325)

Control

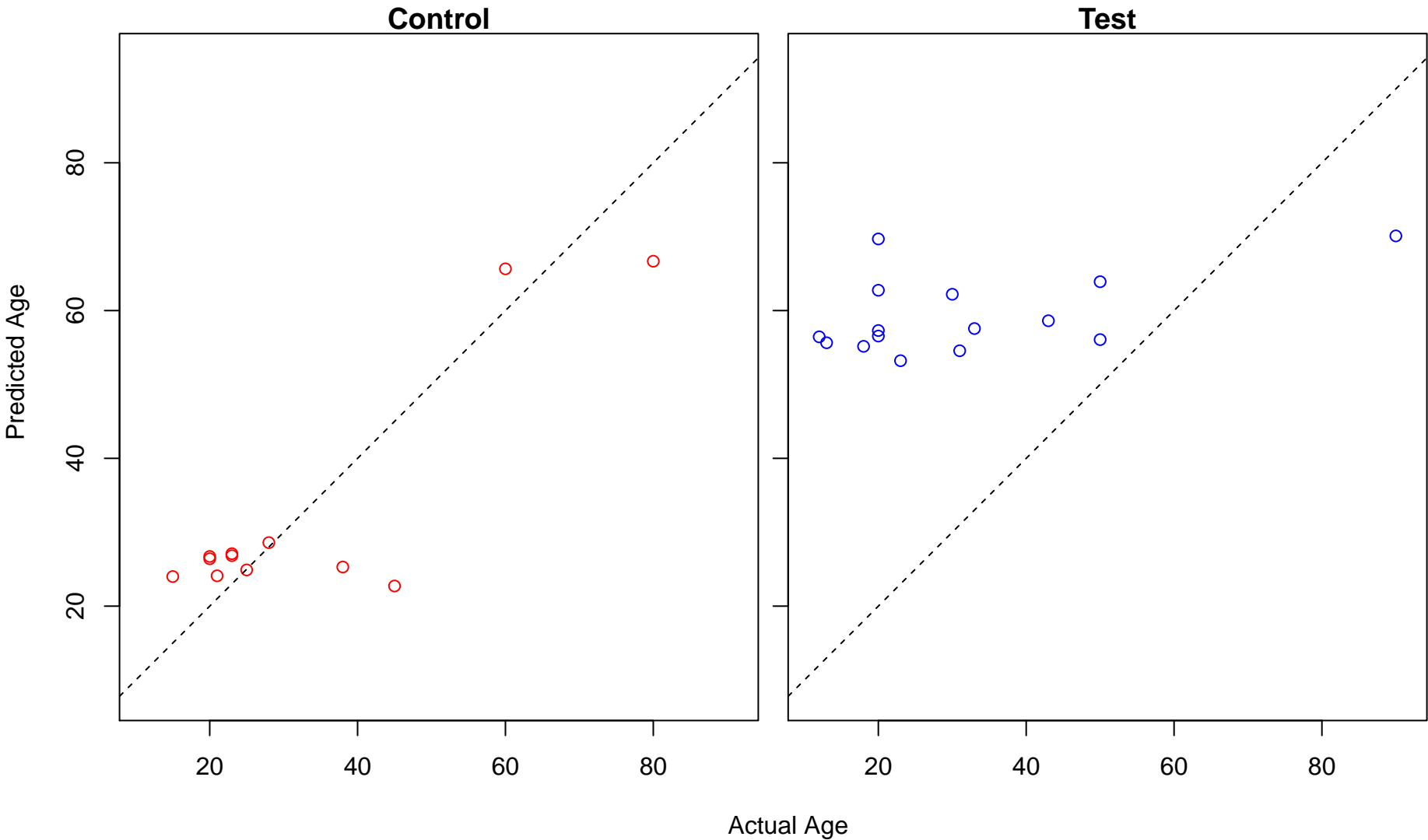


Test

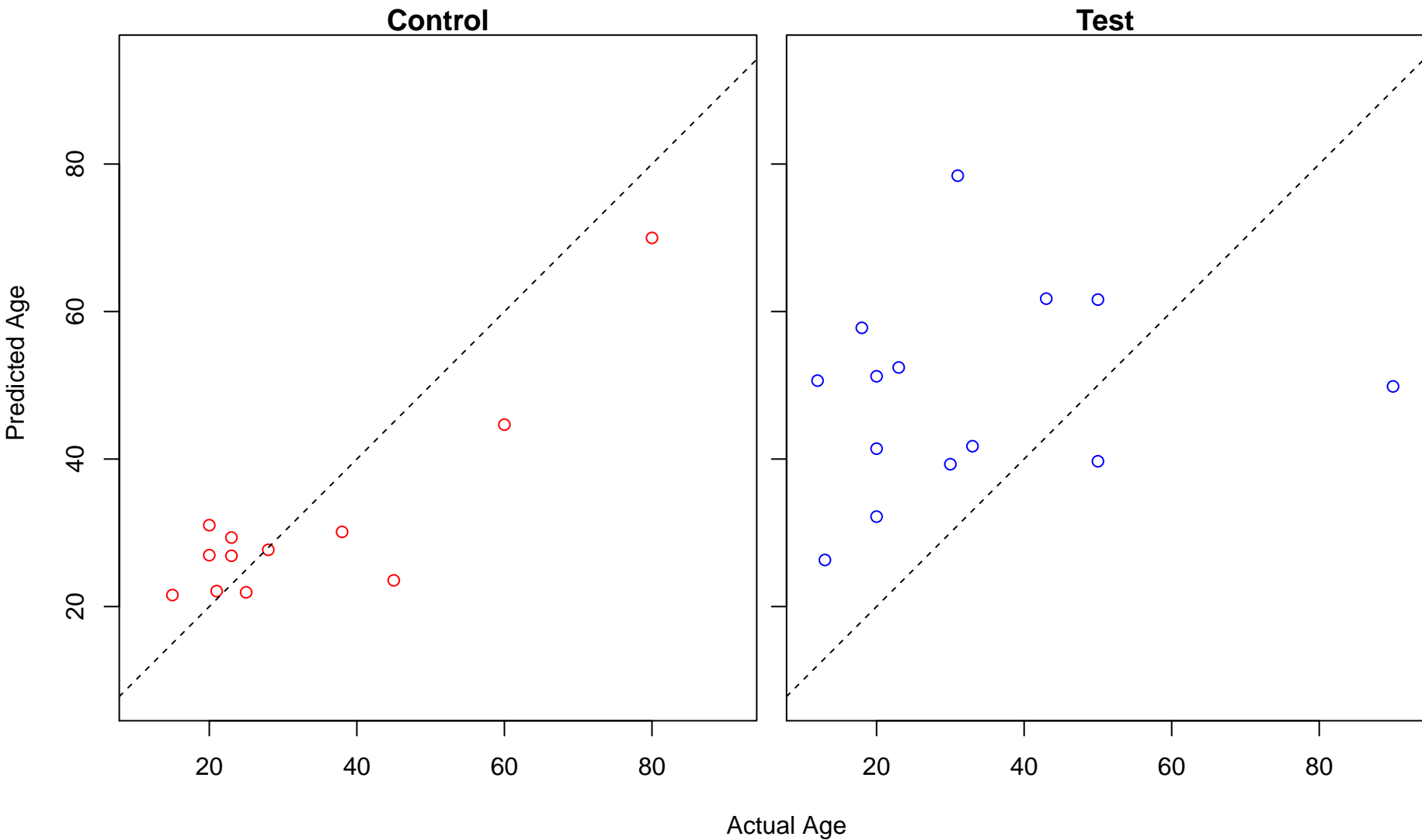


Actual Age

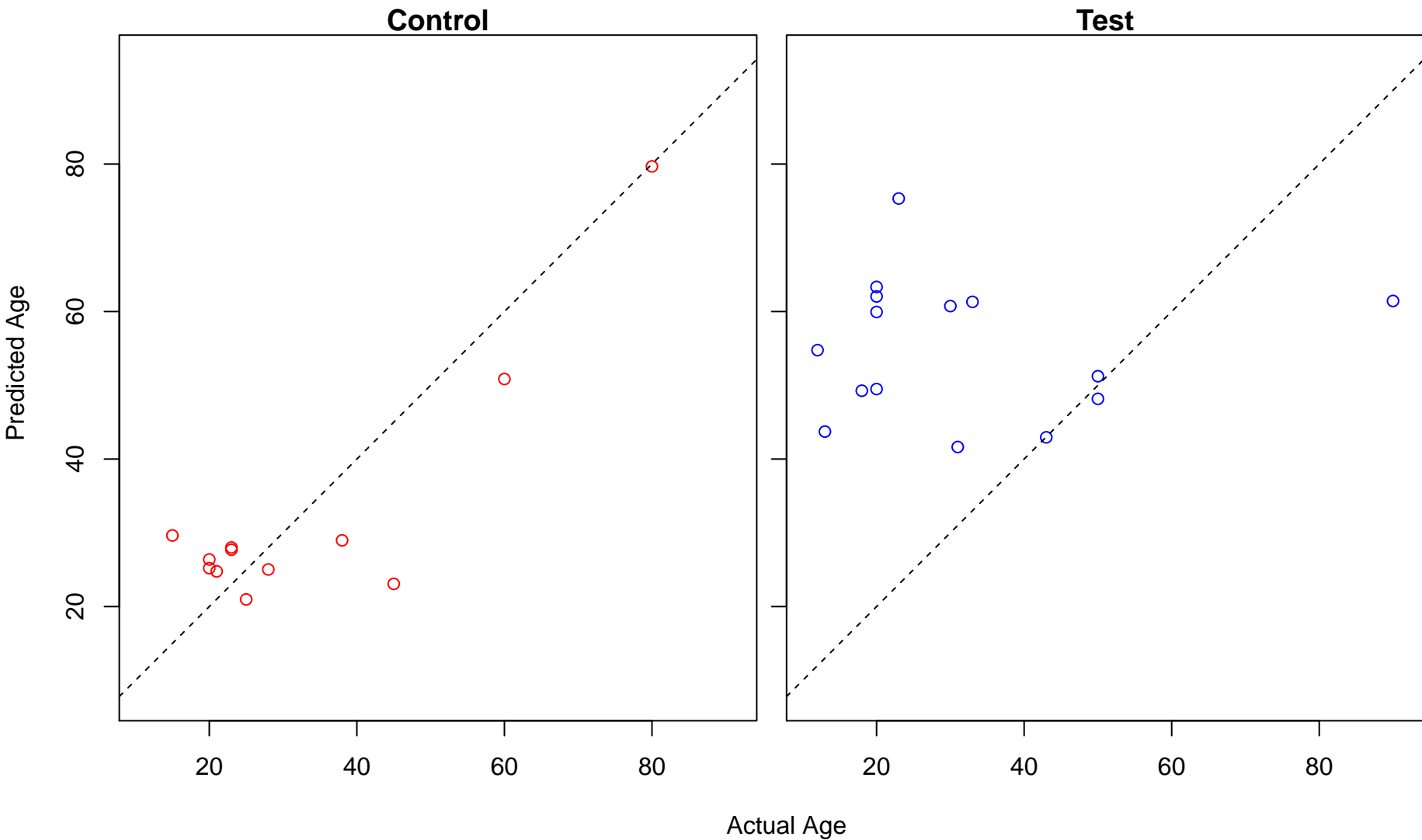
peptidyl-S-diacylglycerol-L-cysteine biosynthetic process from peptidyl-cysteine (Score: 4.48732)



regulation of vasoconstriction (Score: 4.487204)

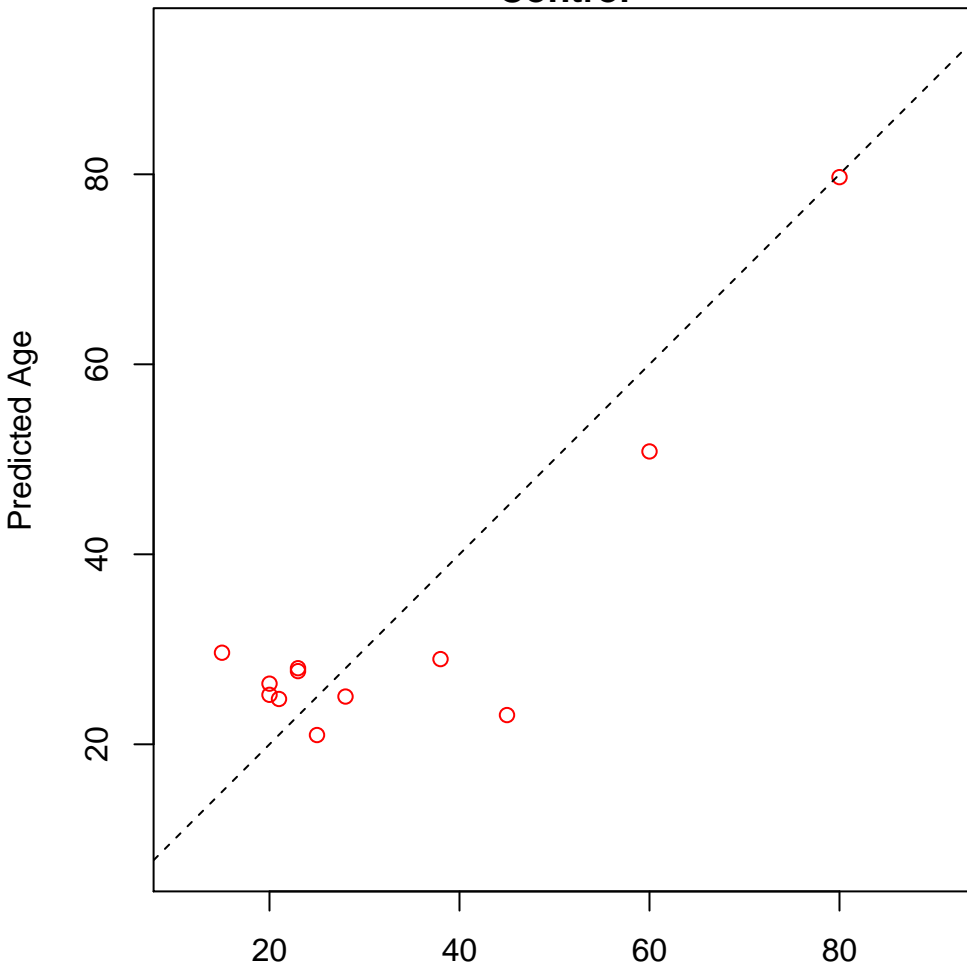


cholesterol metabolic process (Score: 4.485227)

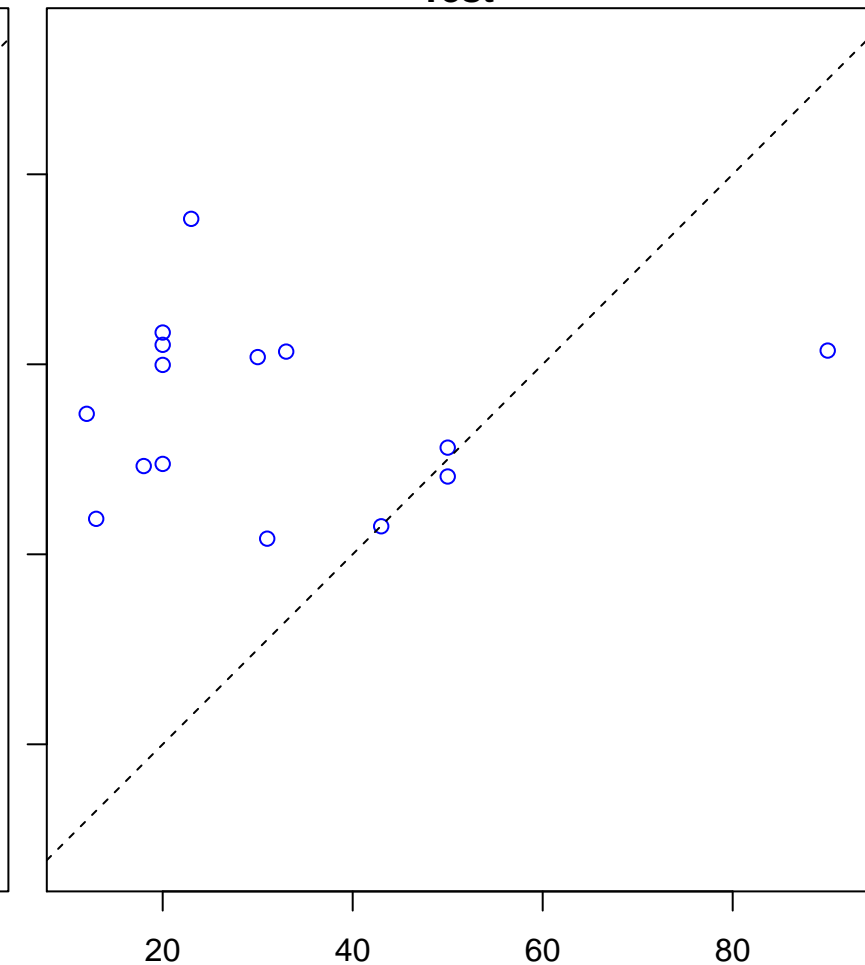


secondary alcohol metabolic process (Score: 4.484964)

Control

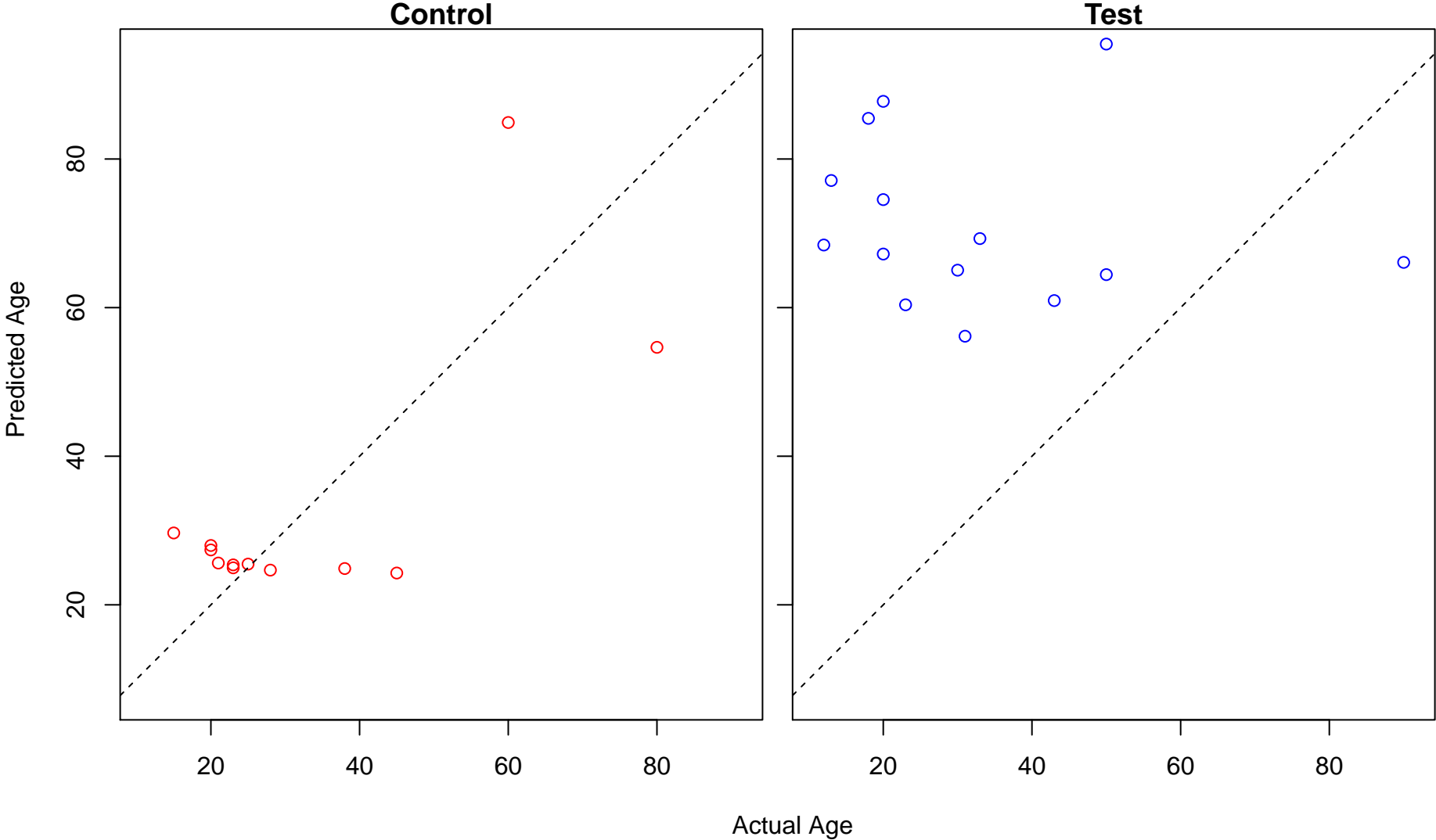


Test

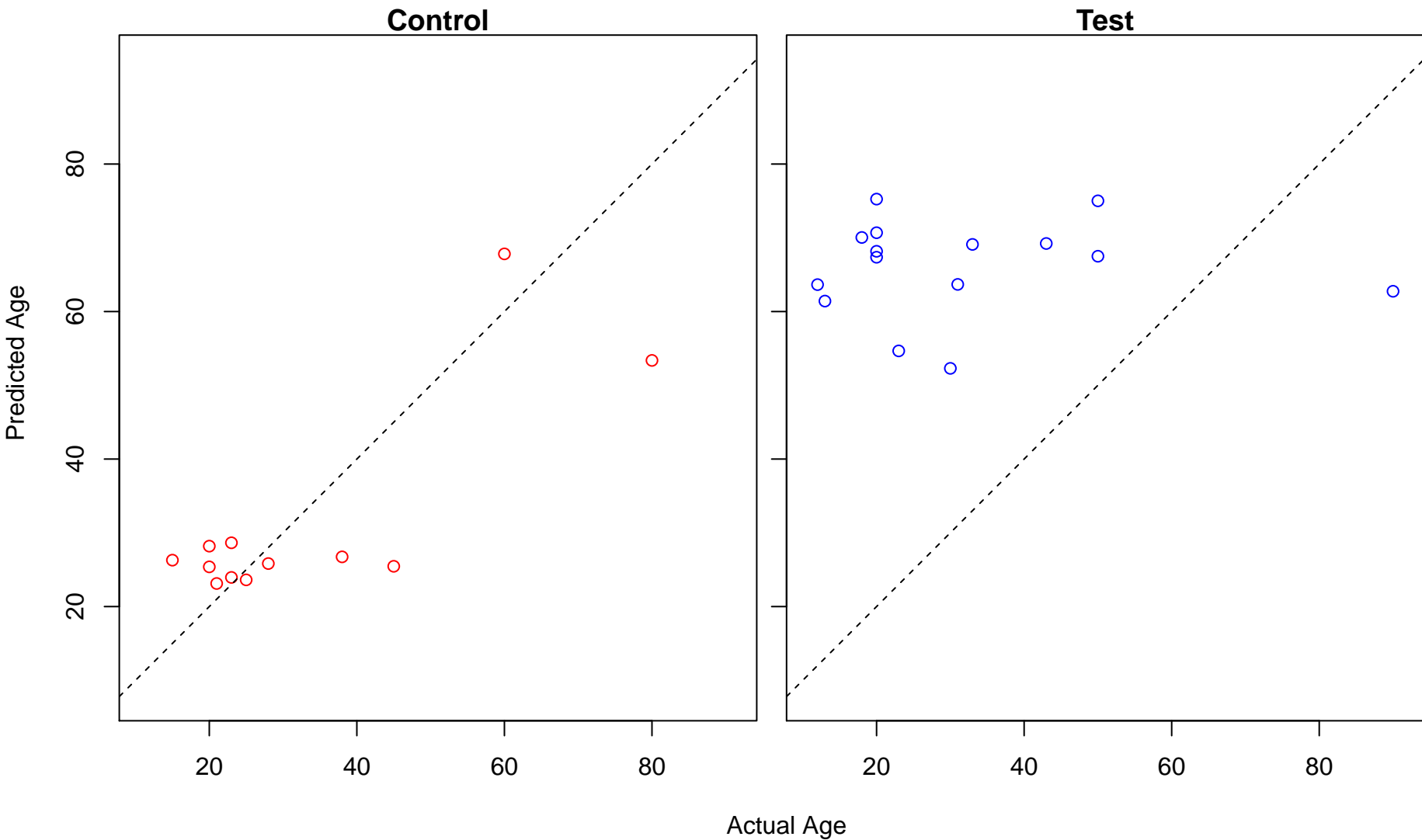


Actual Age

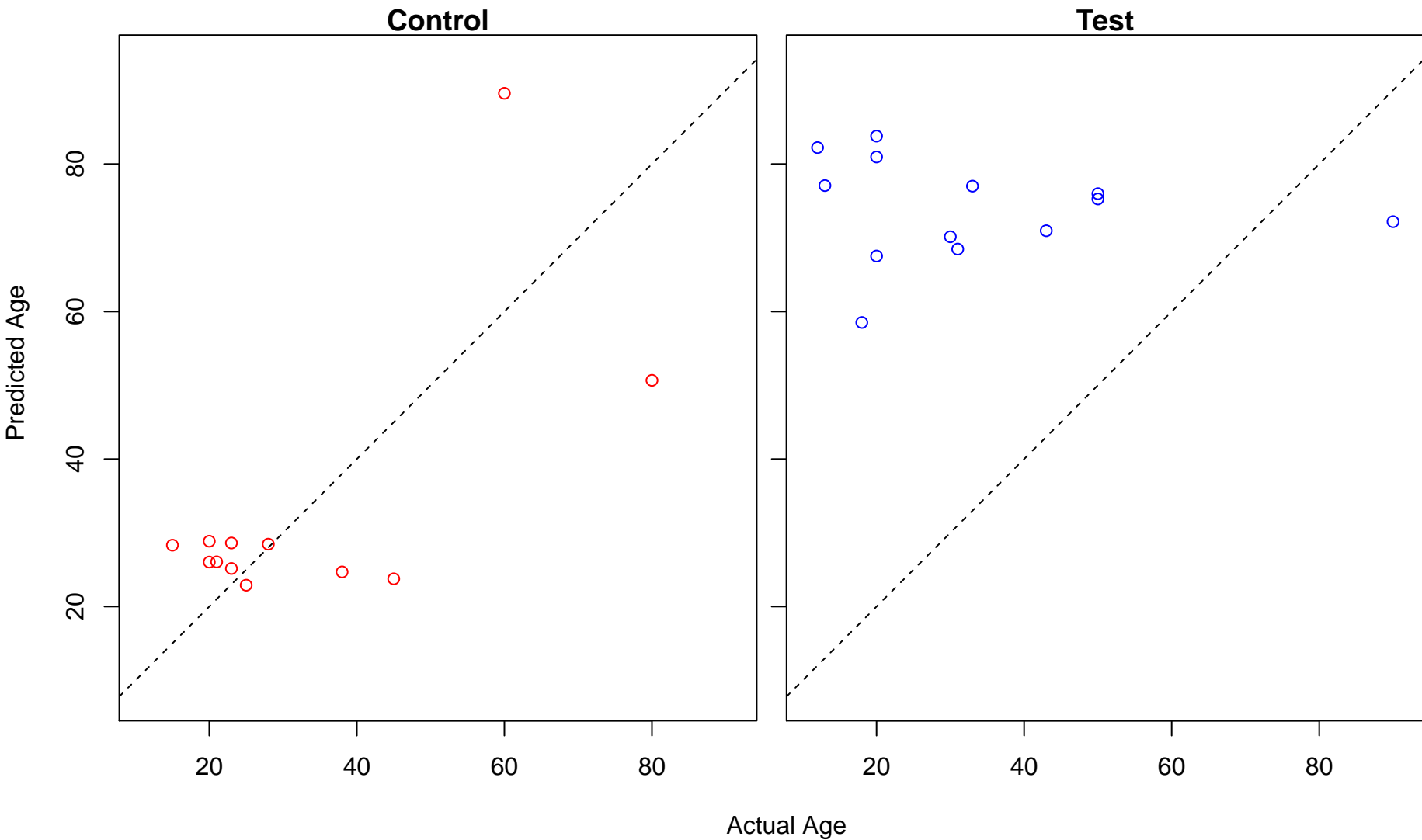
negative regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway (Score: 4.4)



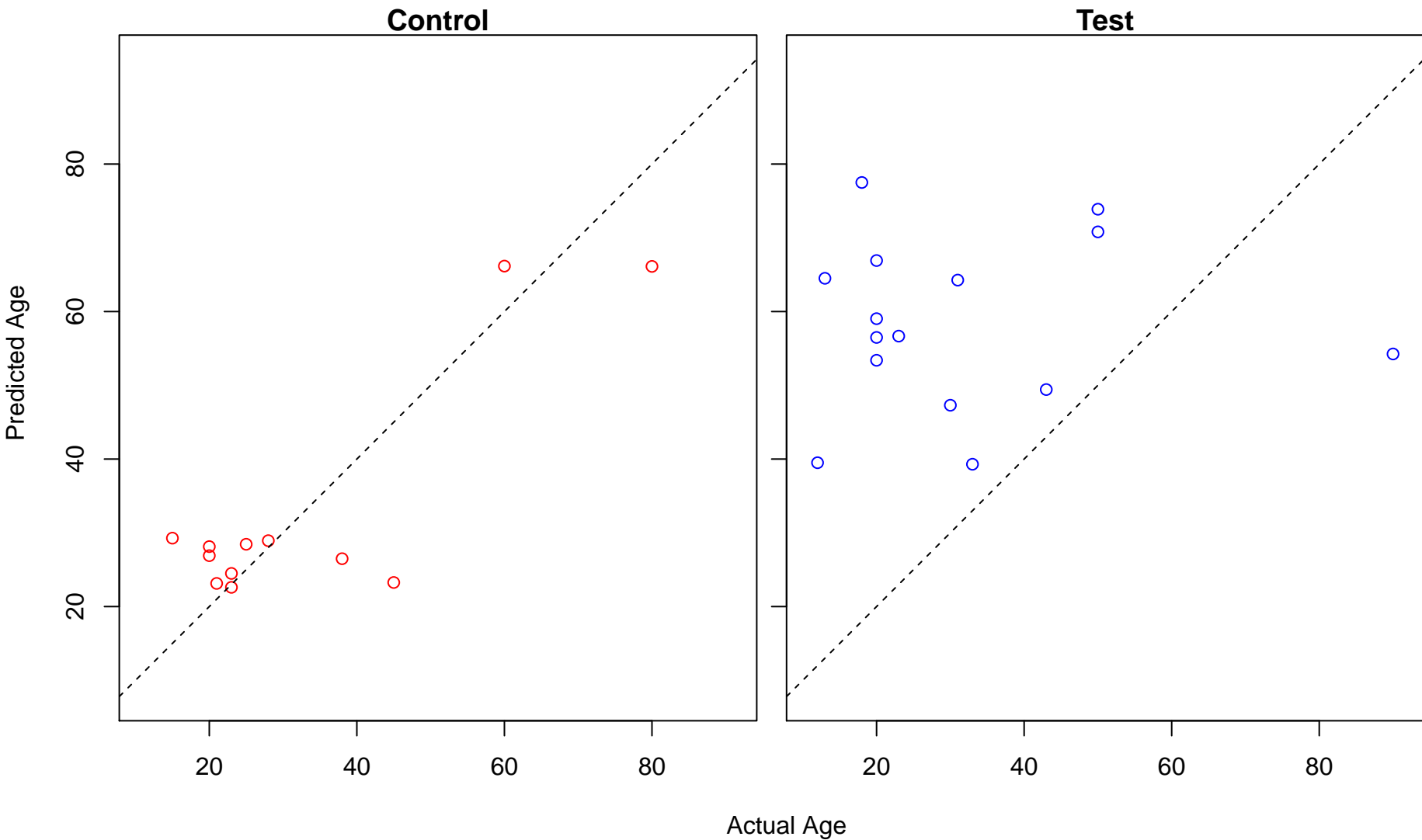
negative regulation of gastrulation (Score: 4.483065)



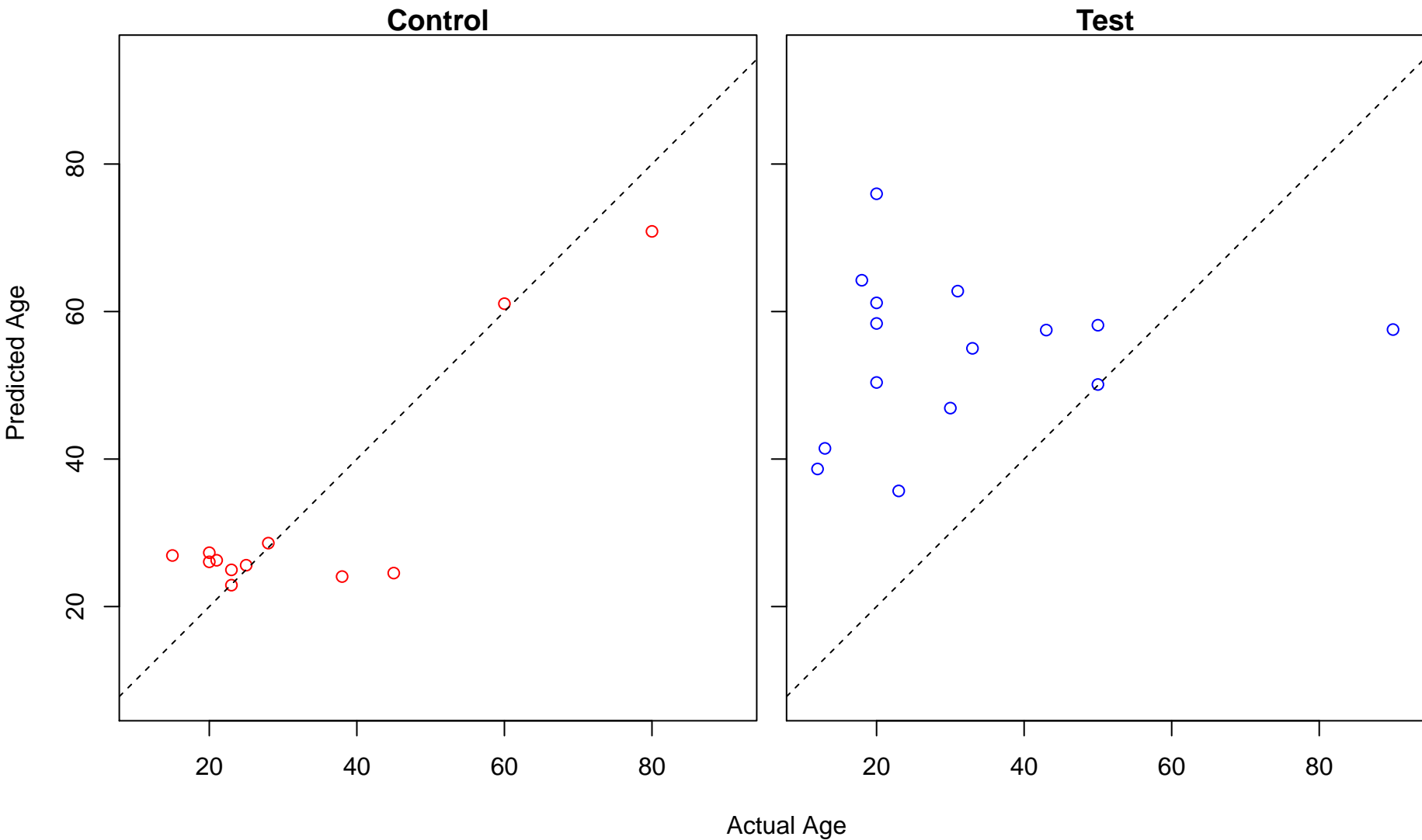
regulation of T-helper 2 cell cytokine production (Score: 4.477310)



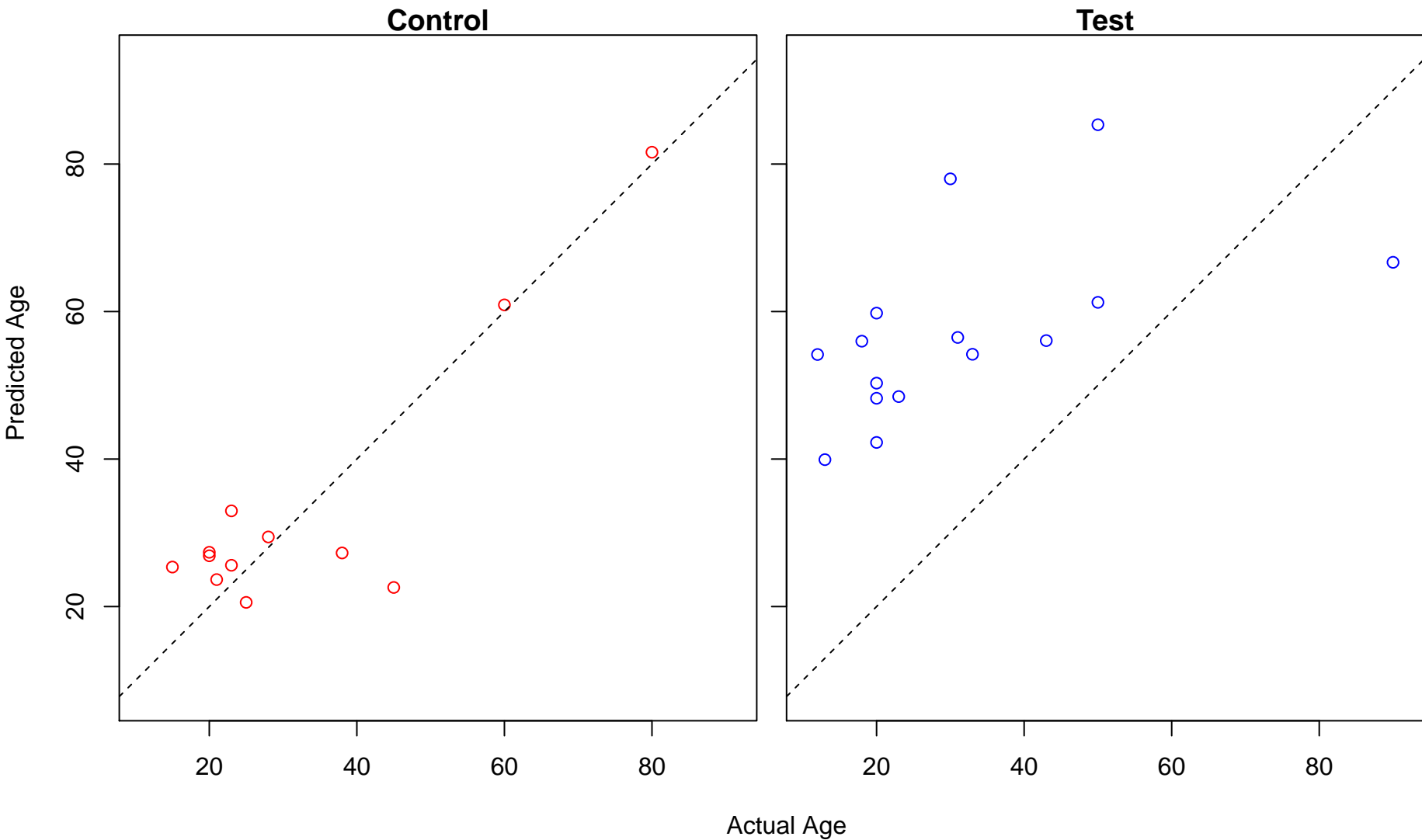
NAD metabolic process (Score: 4.475212)



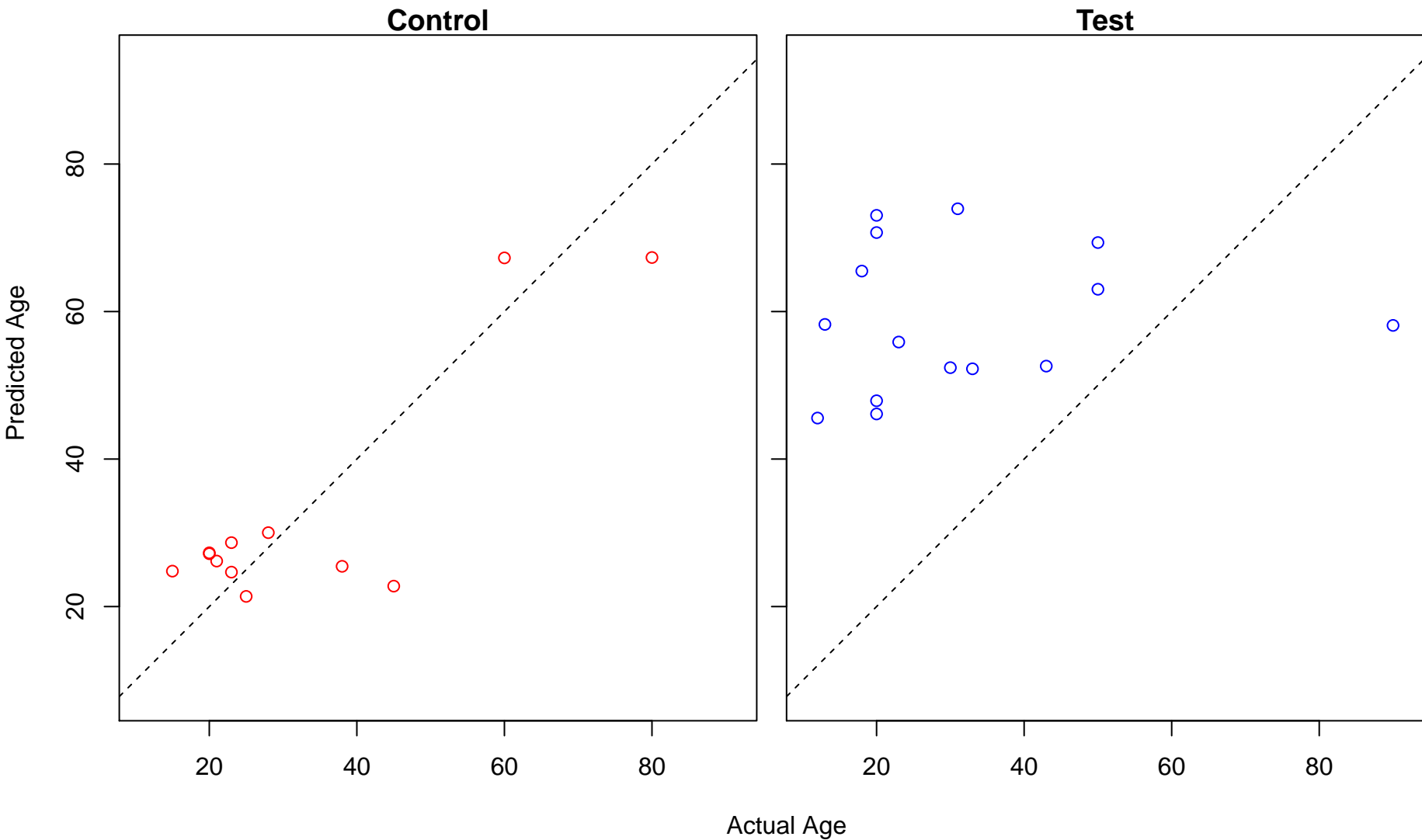
regulation of attachment of spindle microtubules to kinetochore (Score: 4.470833)



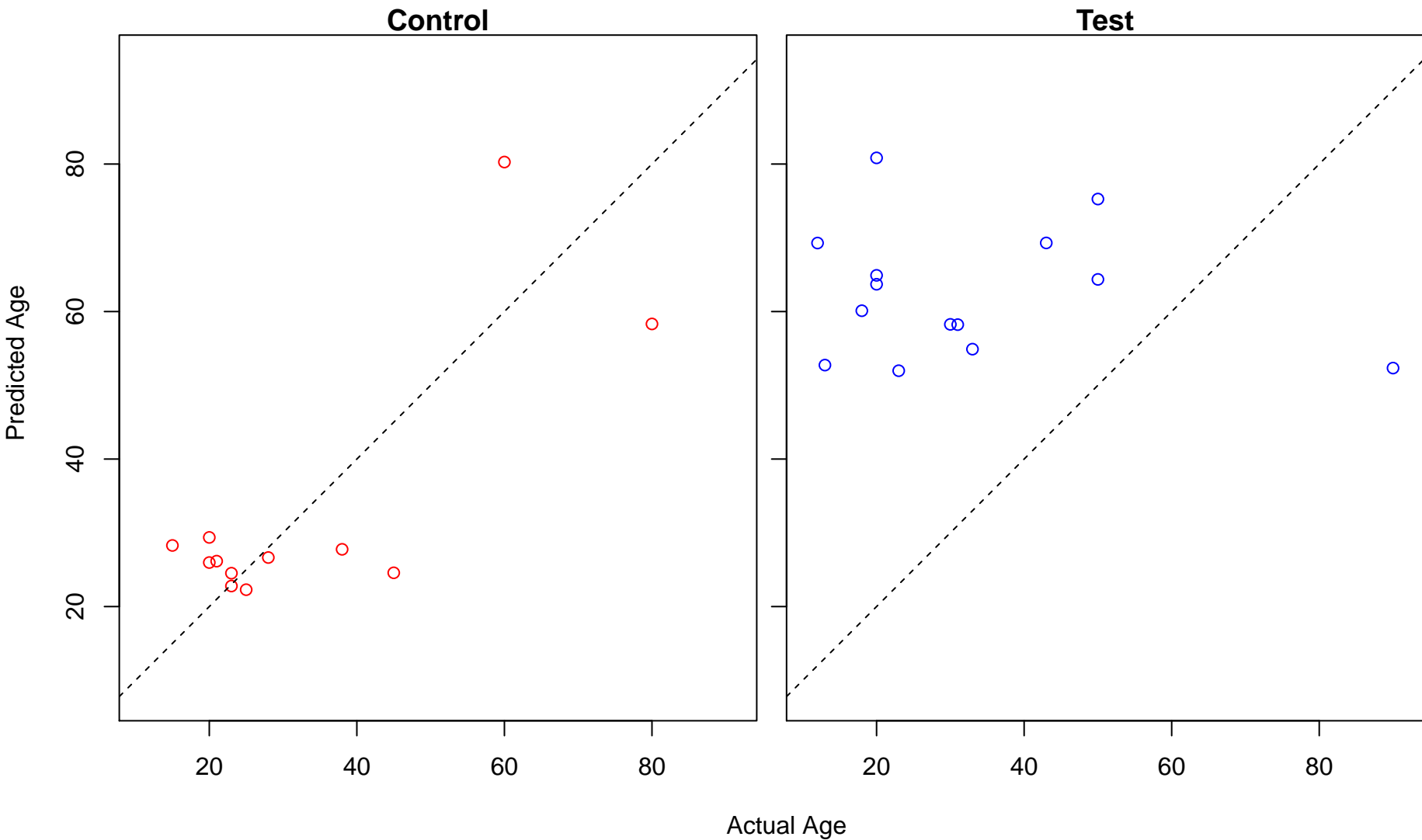
mesodermal cell differentiation (Score: 4.468384)



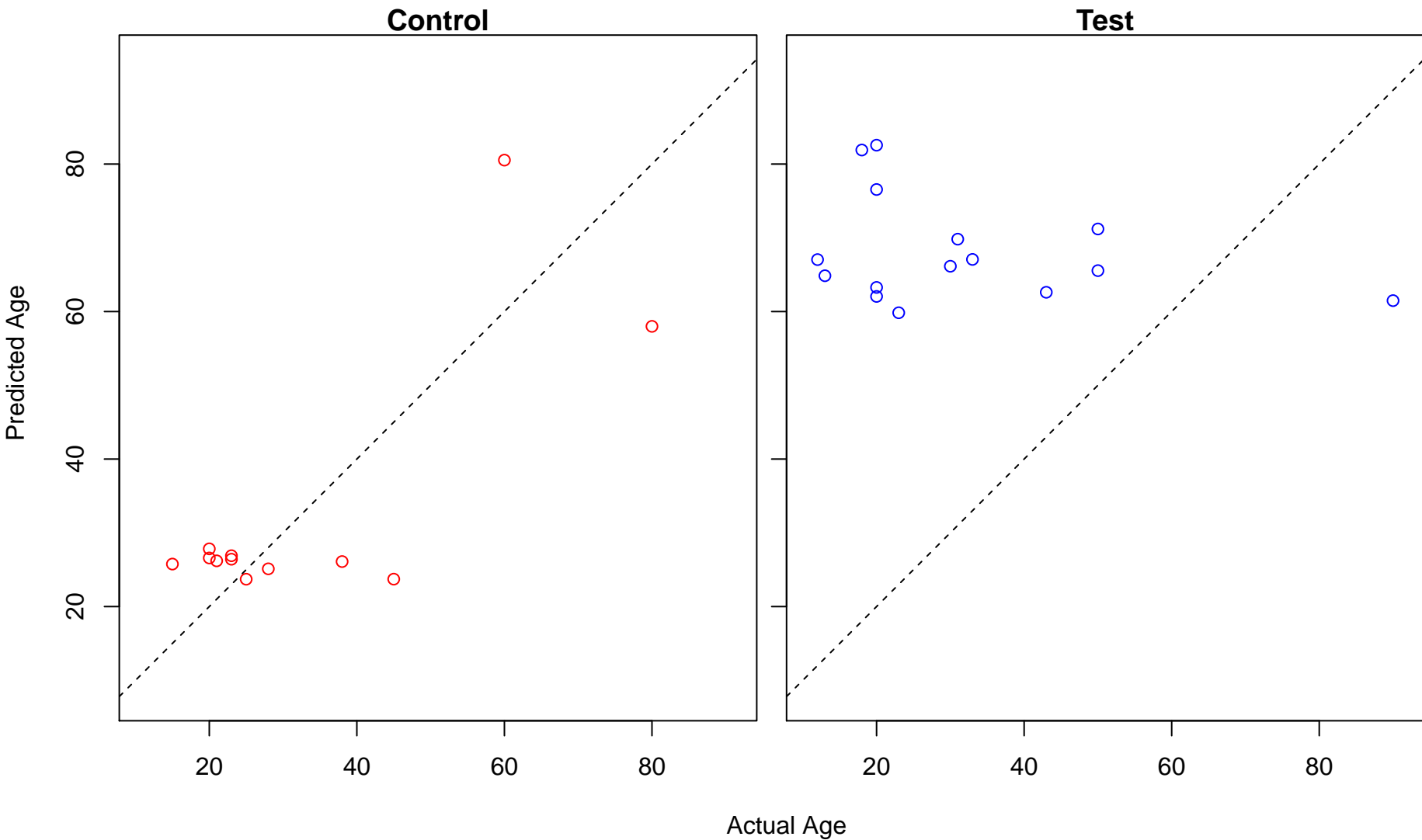
positive regulation of cation channel activity (Score: 4.468024)



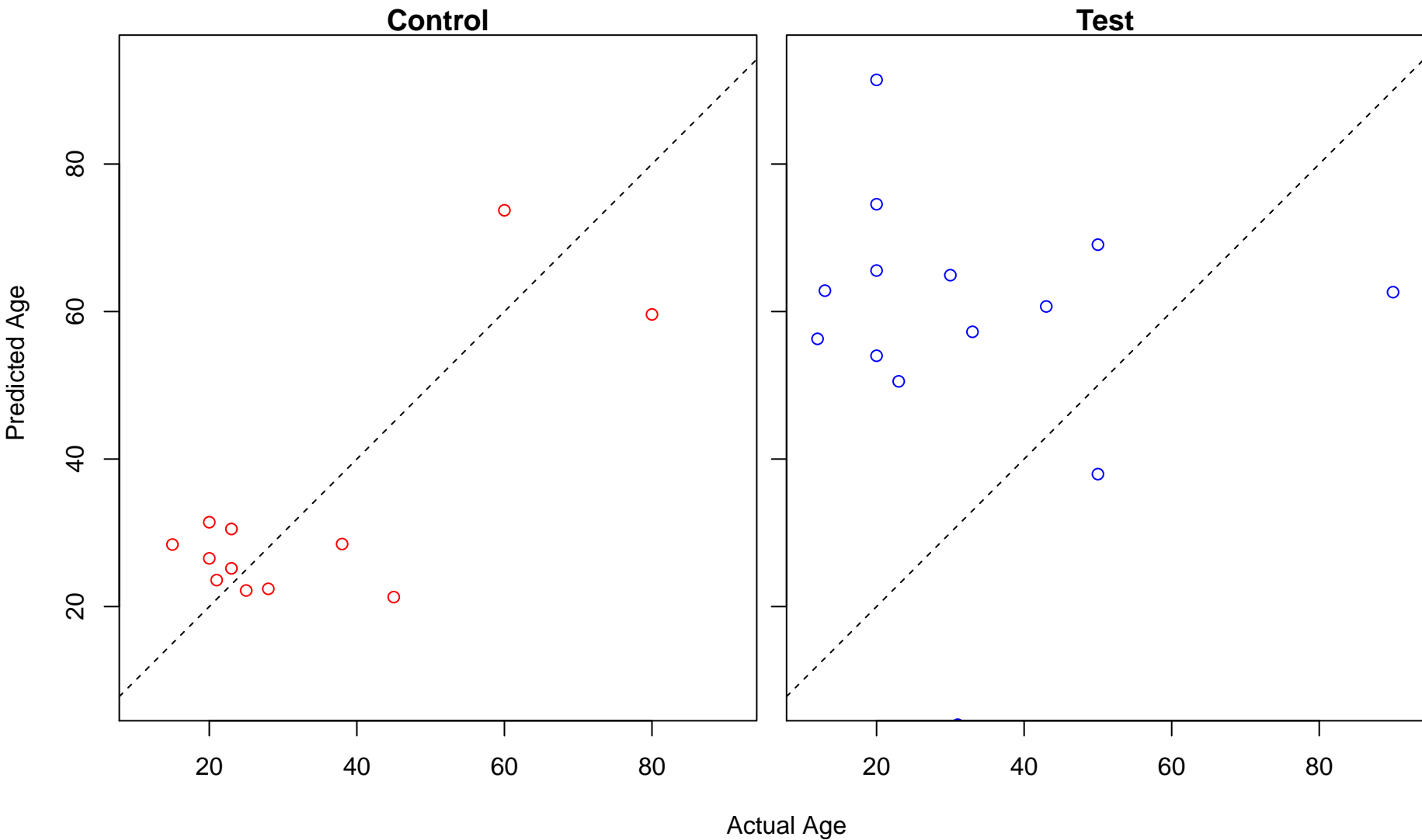
negative regulation of lipid metabolic process (Score: 4.468018)



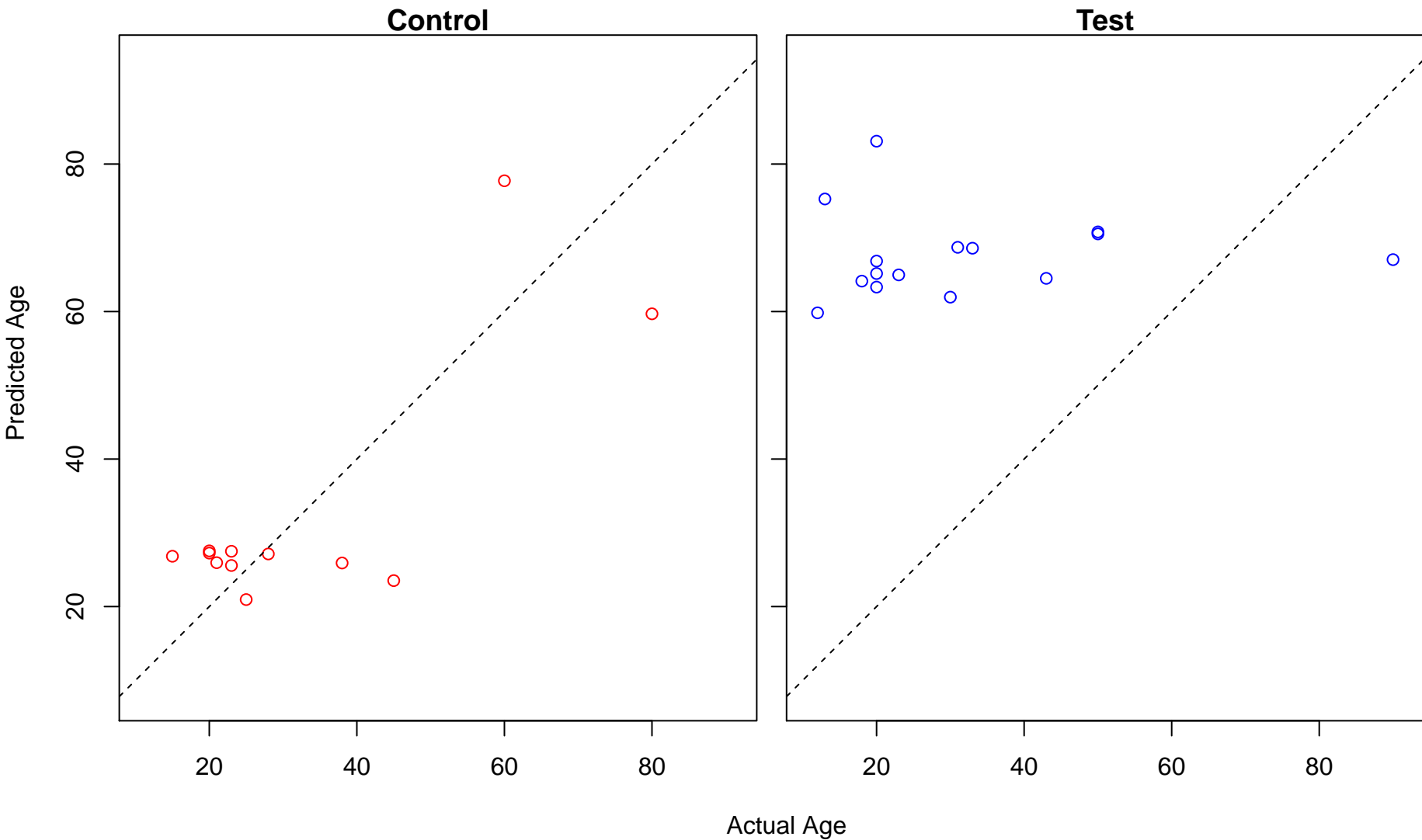
positive regulation of actin filament polymerization (Score: 4.465524)



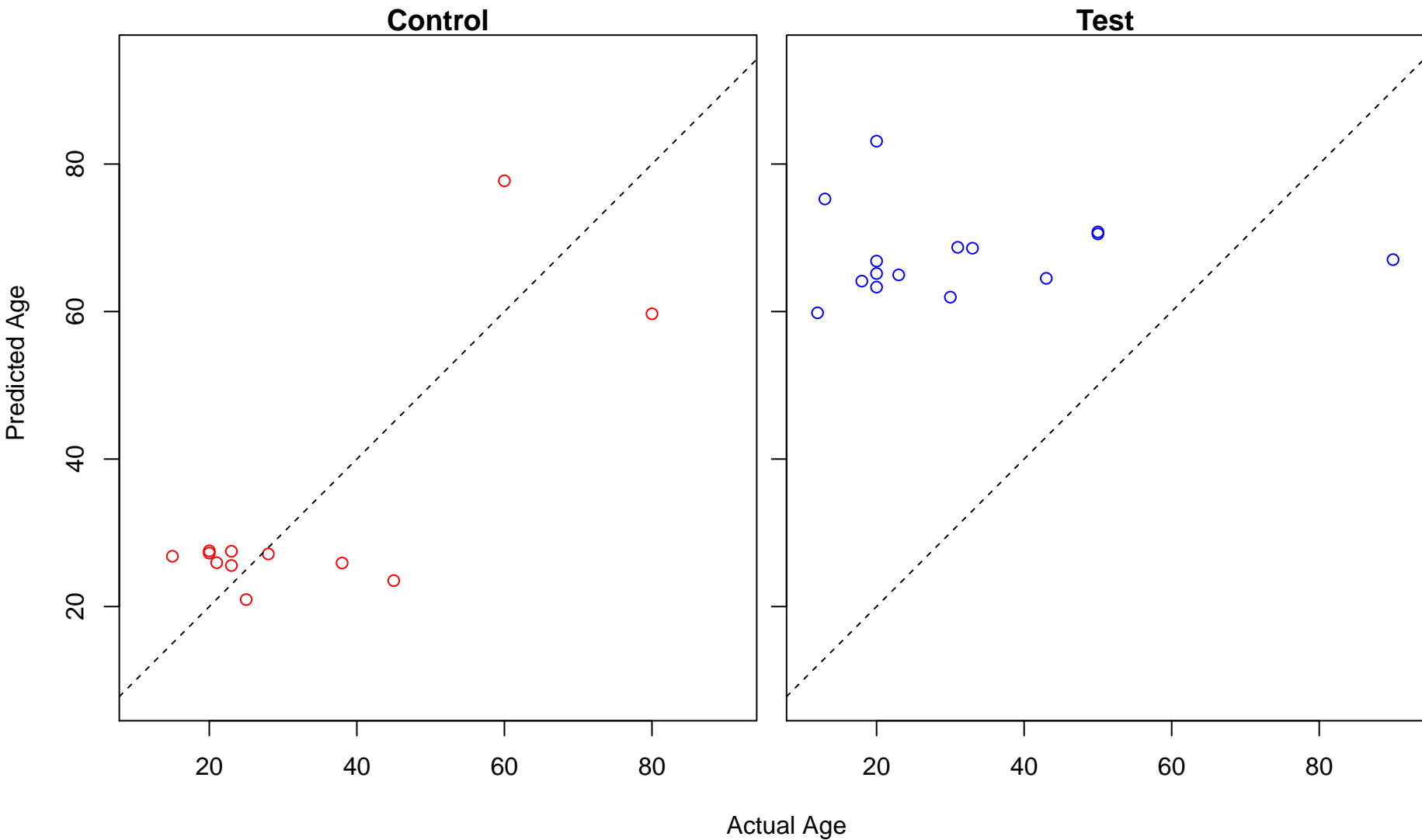
positive regulation of interleukin-8 biosynthetic process (Score: 4.464121)



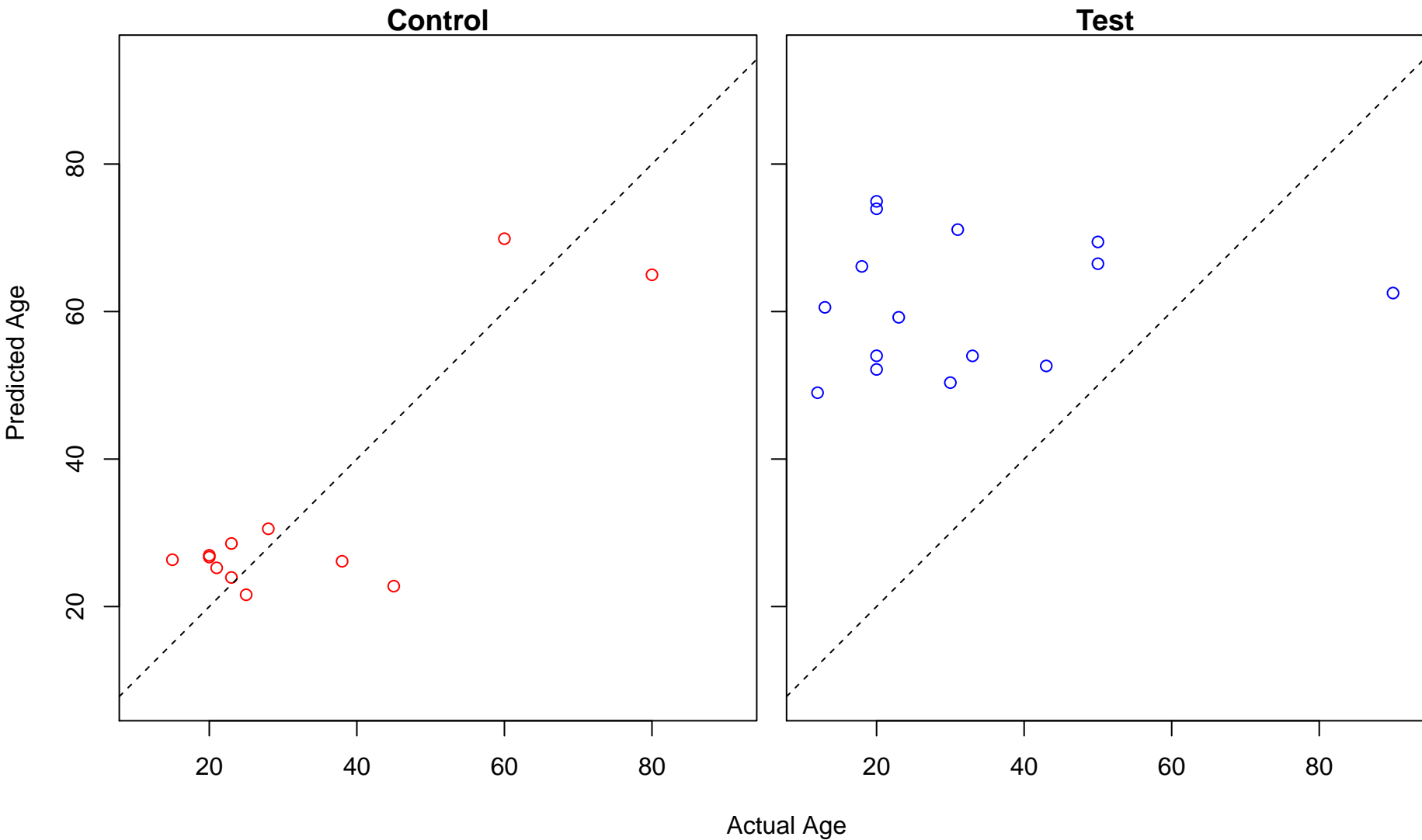
regulation of transmembrane transporter activity (Score: 4.459789)



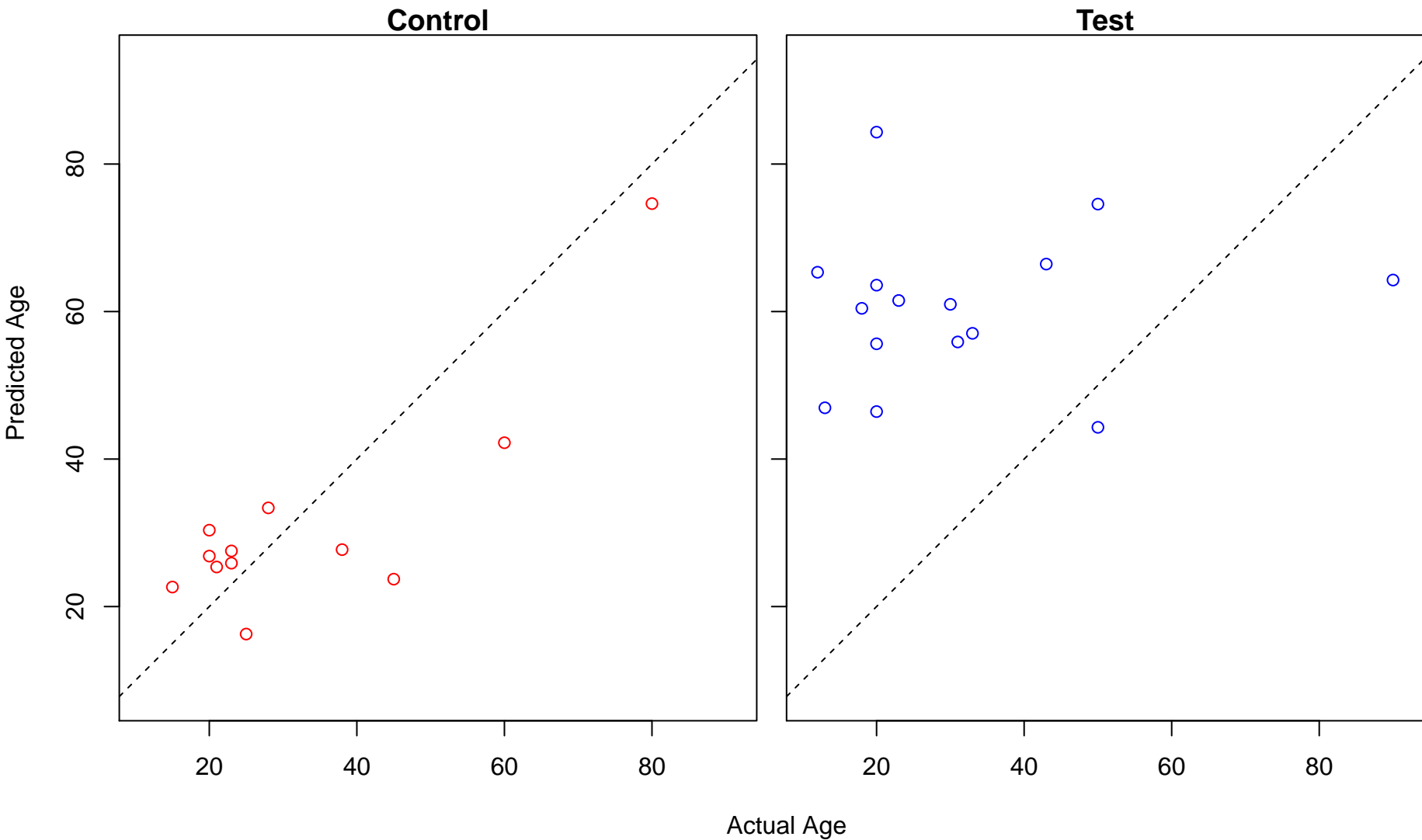
regulation of ion transmembrane transporter activity (Score: 4.459776)



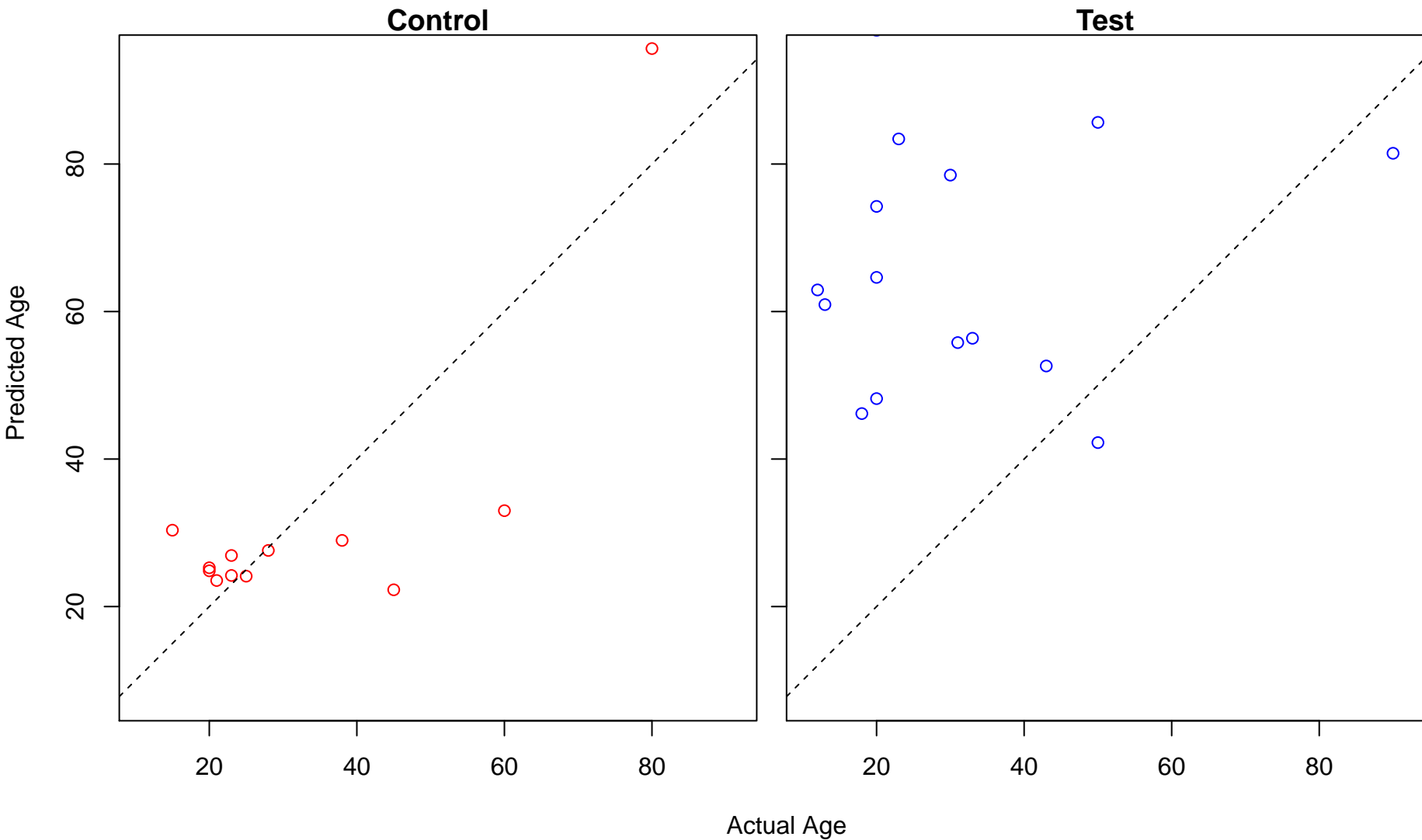
regulation of peptidyl–threonine phosphorylation (Score: 4.459288)



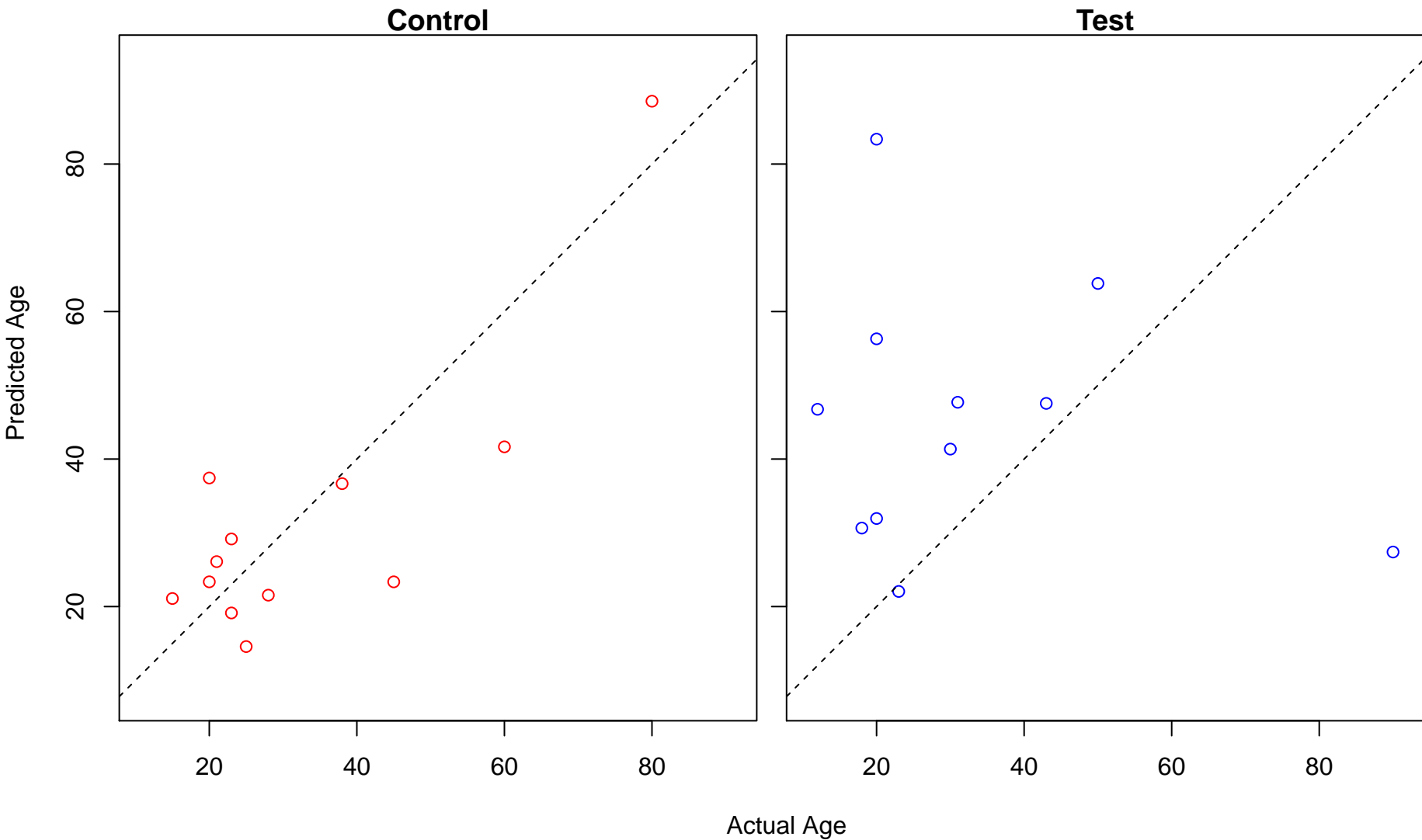
glial cell migration (Score: 4.458372)



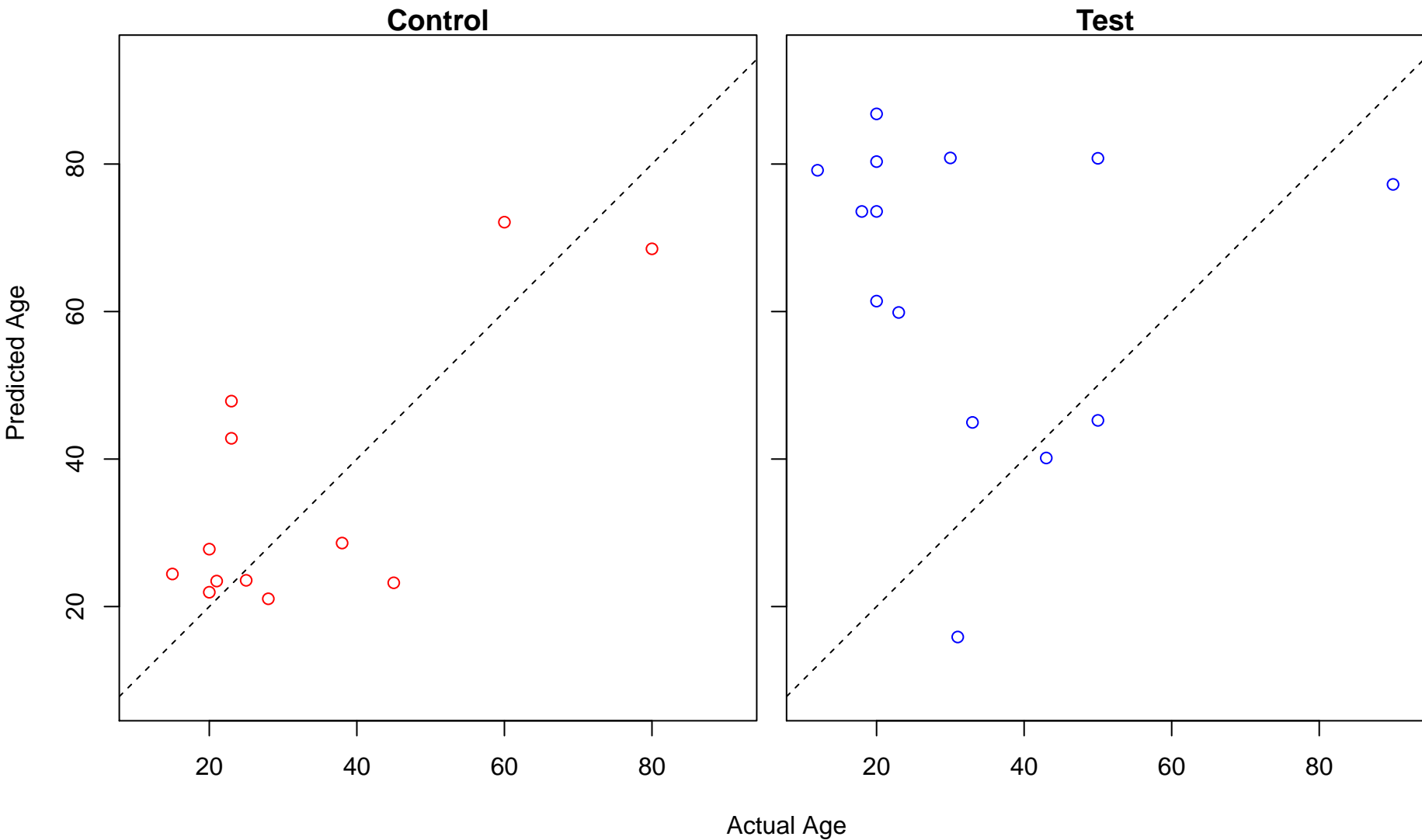
regulation of Arp2/3 complex-mediated actin nucleation (Score: 4.458176)



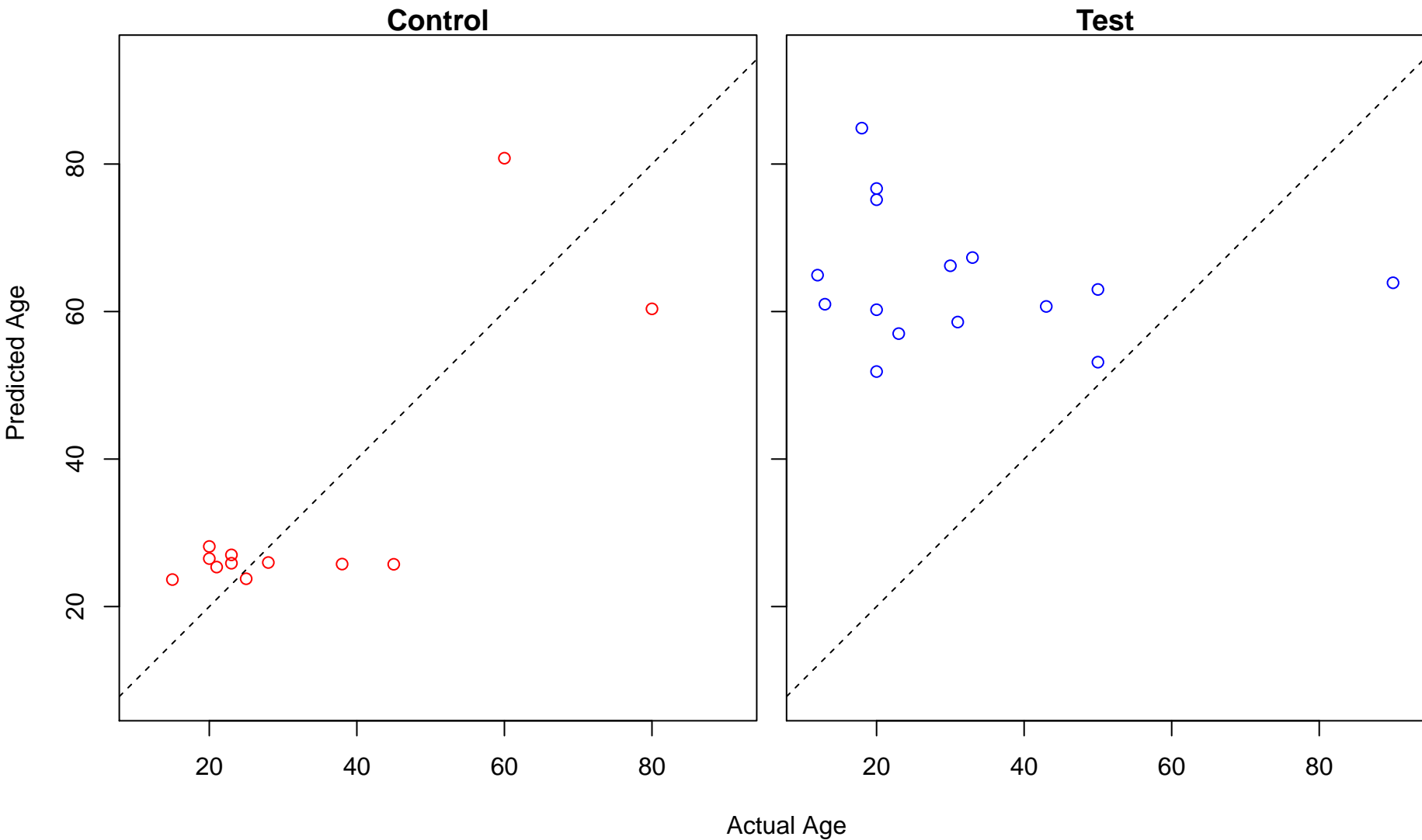
multicellular organismal metabolic process (Score: 4.455886)



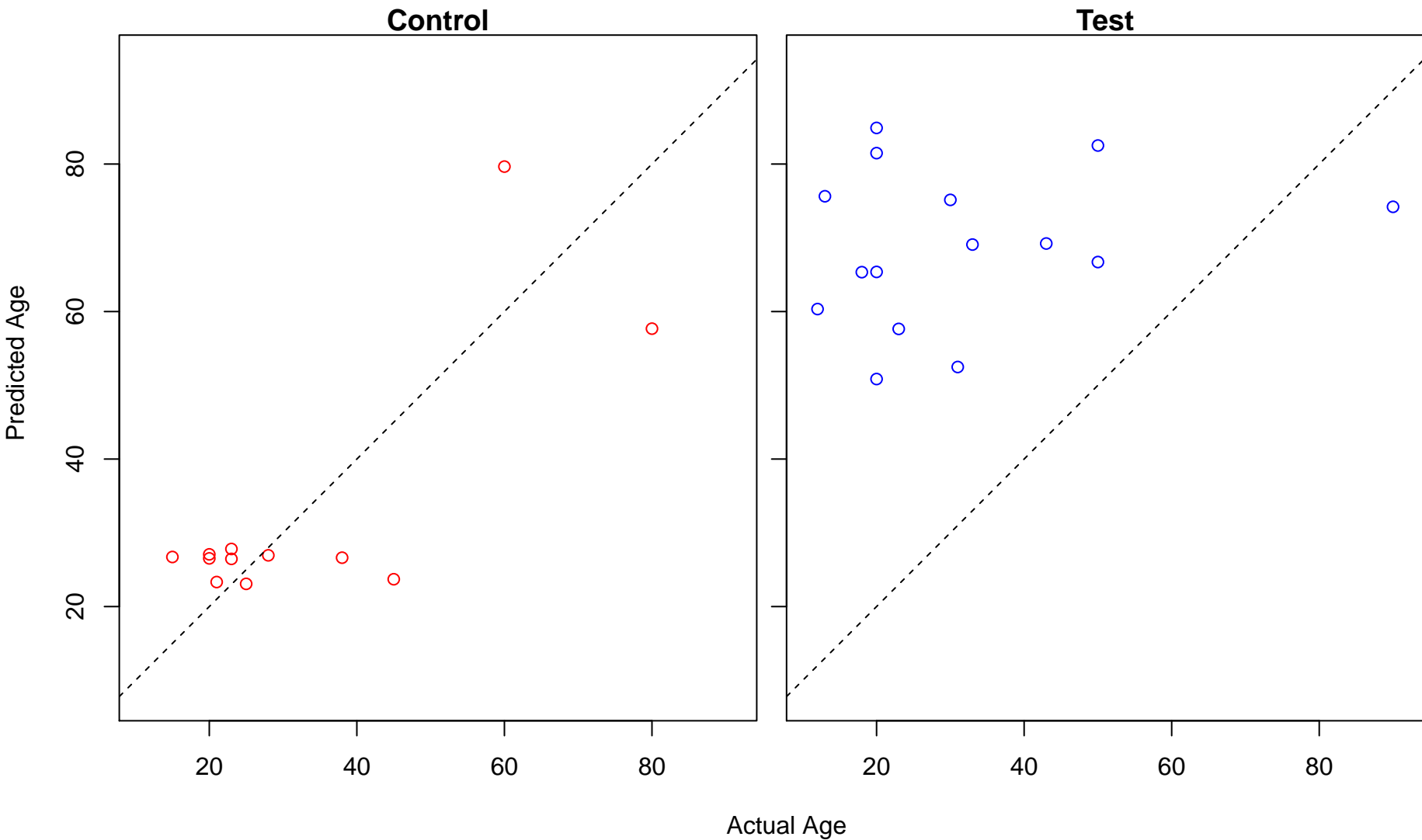
negative regulation of phospholipid metabolic process (Score: 4.455196)



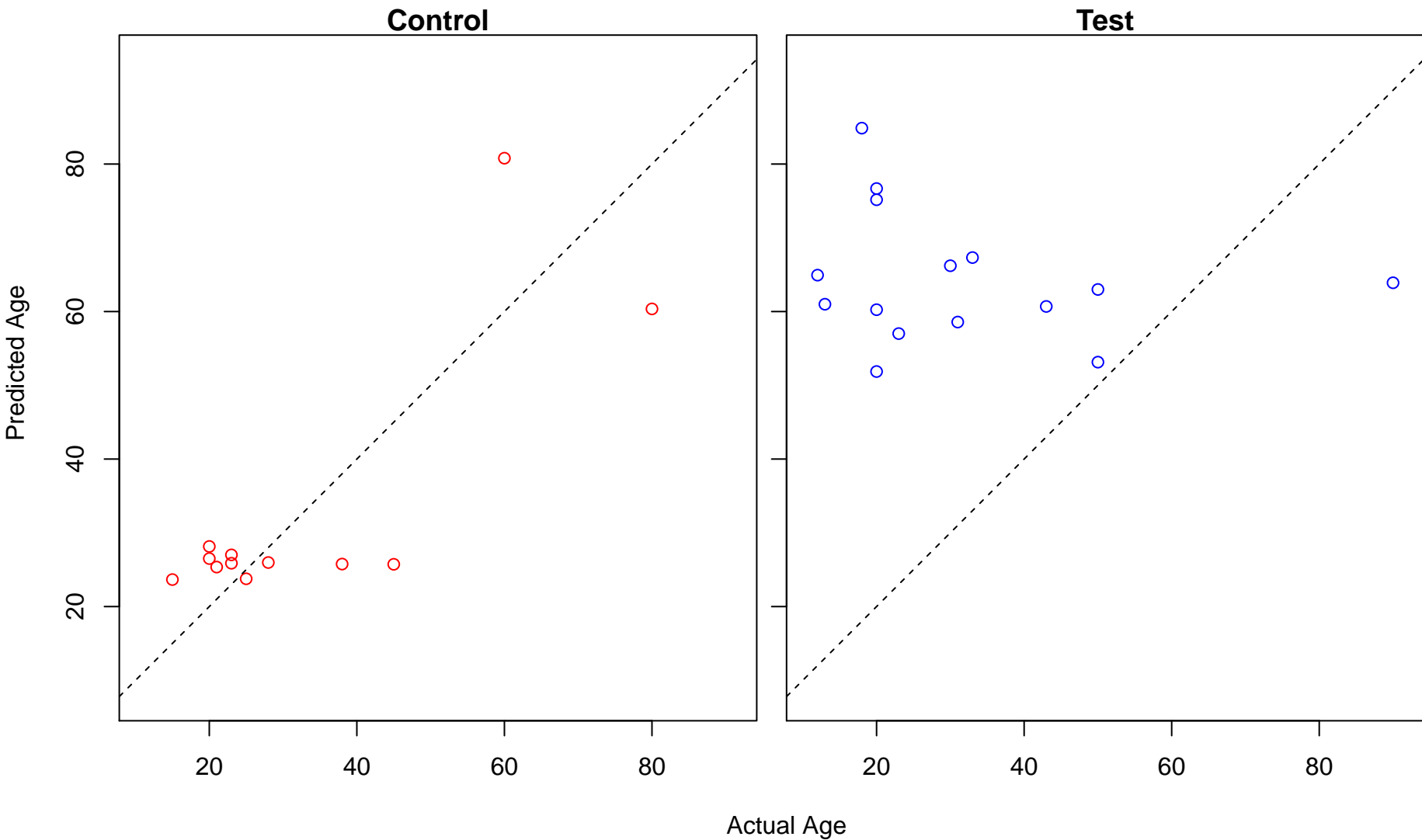
negative regulation of cAMP metabolic process (Score: 4.453695)



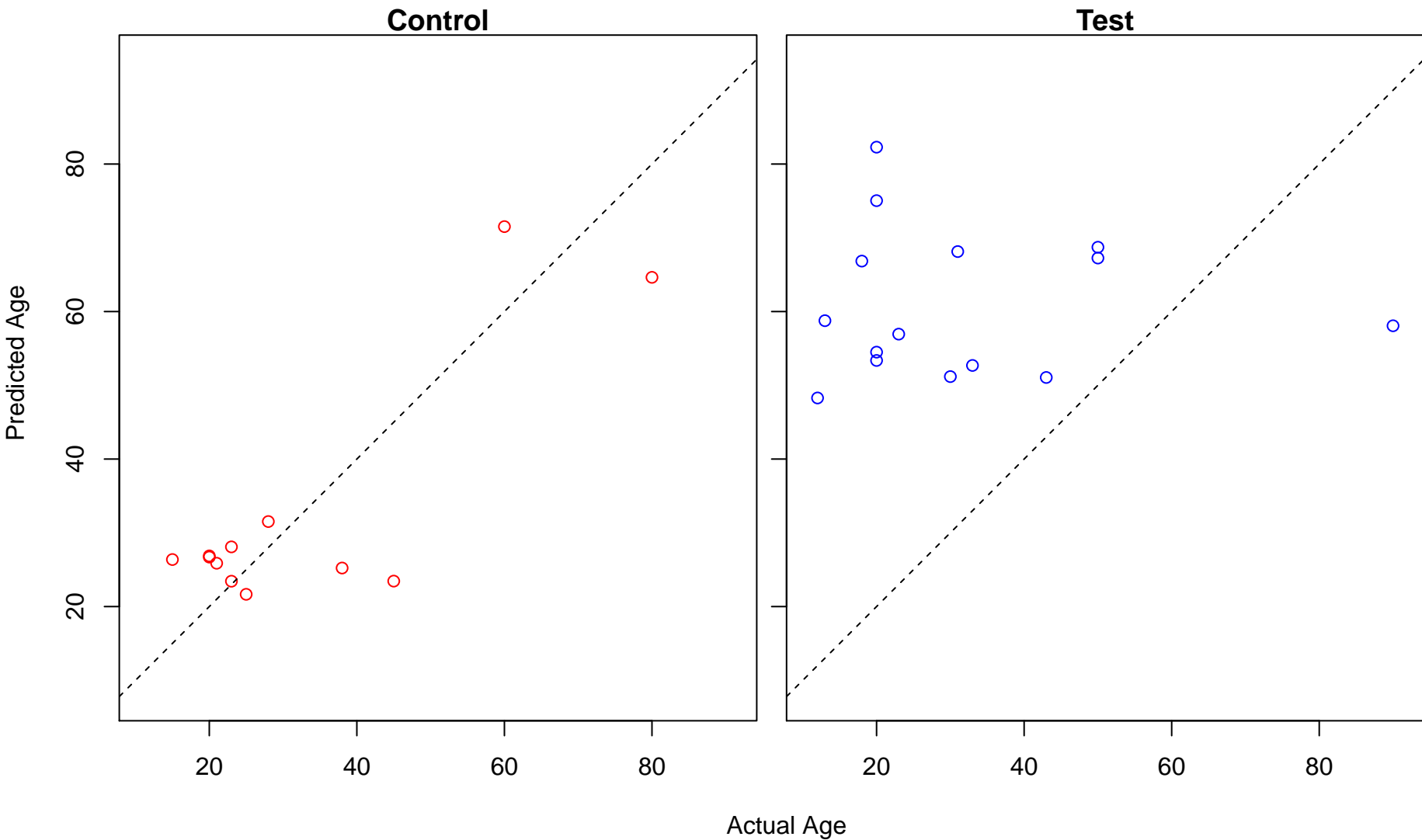
inorganic anion transmembrane transport (Score: 4.452852)



negative regulation of cyclic nucleotide metabolic process (Score: 4.452672)

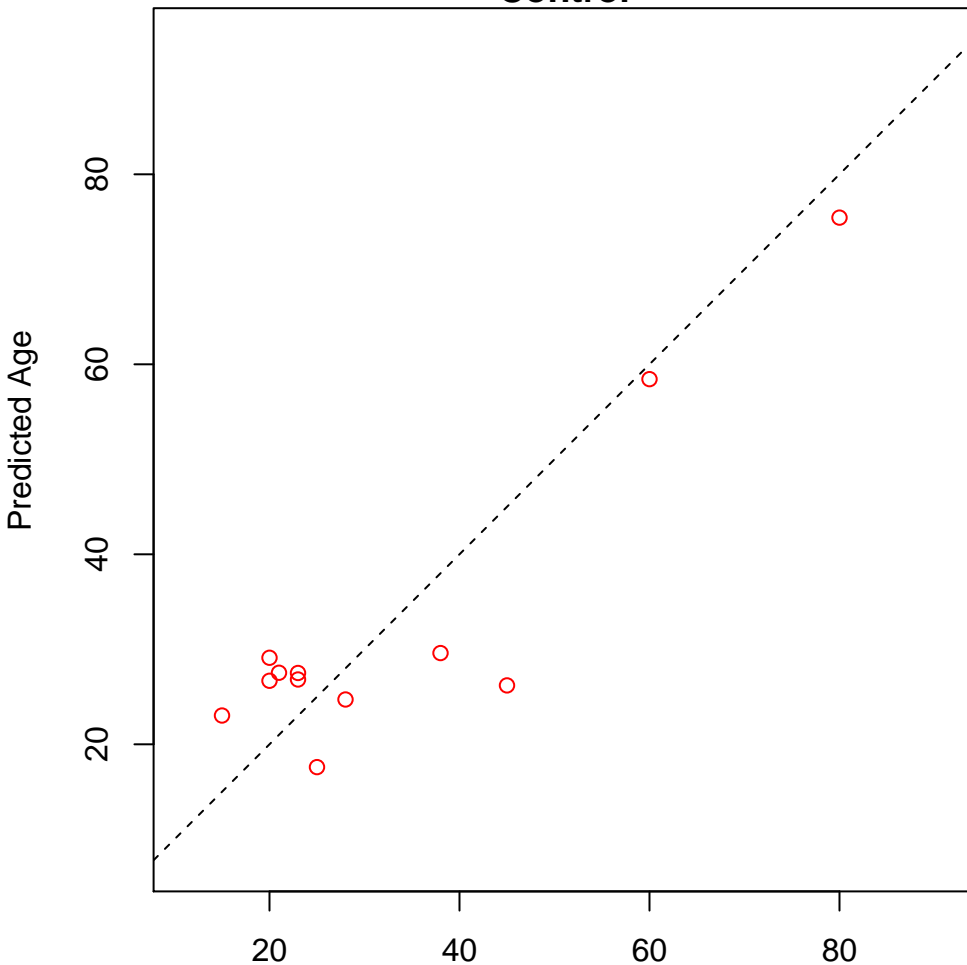


negative regulation of calcium ion import (Score: 4.451490)

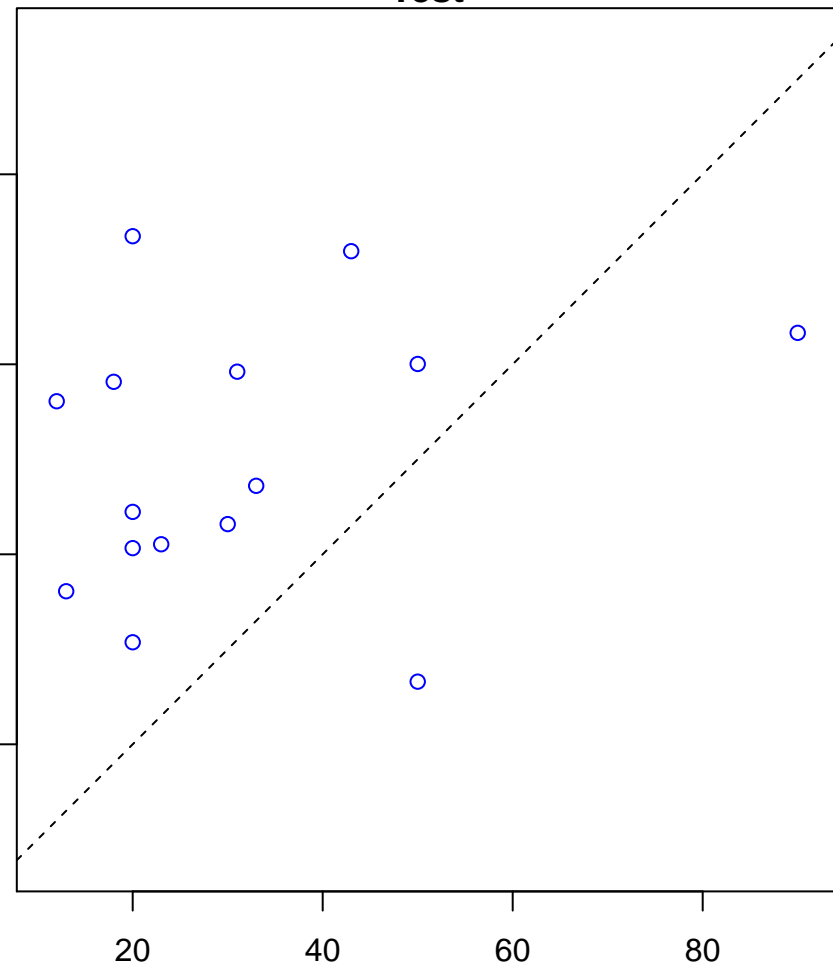


protein import into peroxisome matrix (Score: 4.450943)

Control

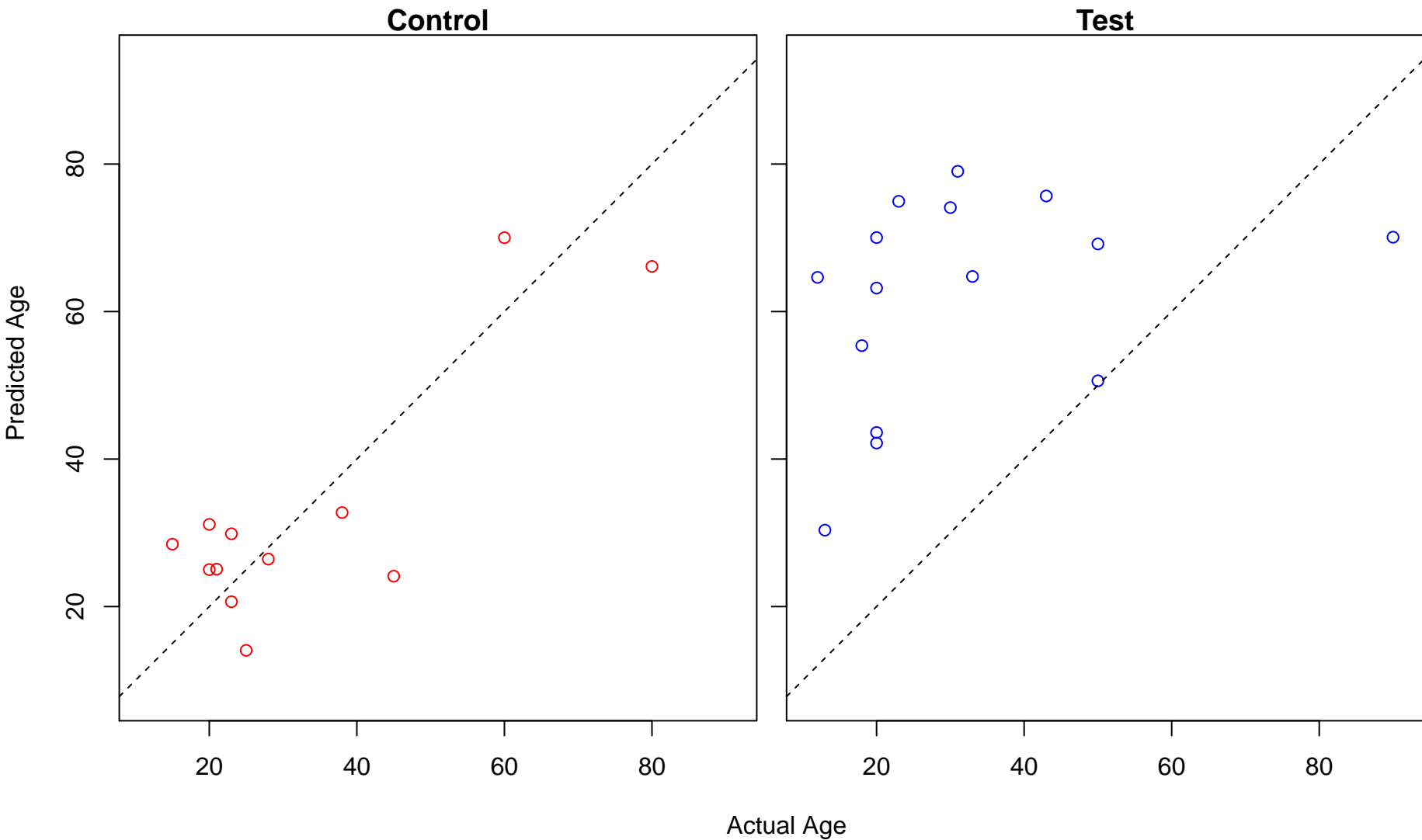


Test

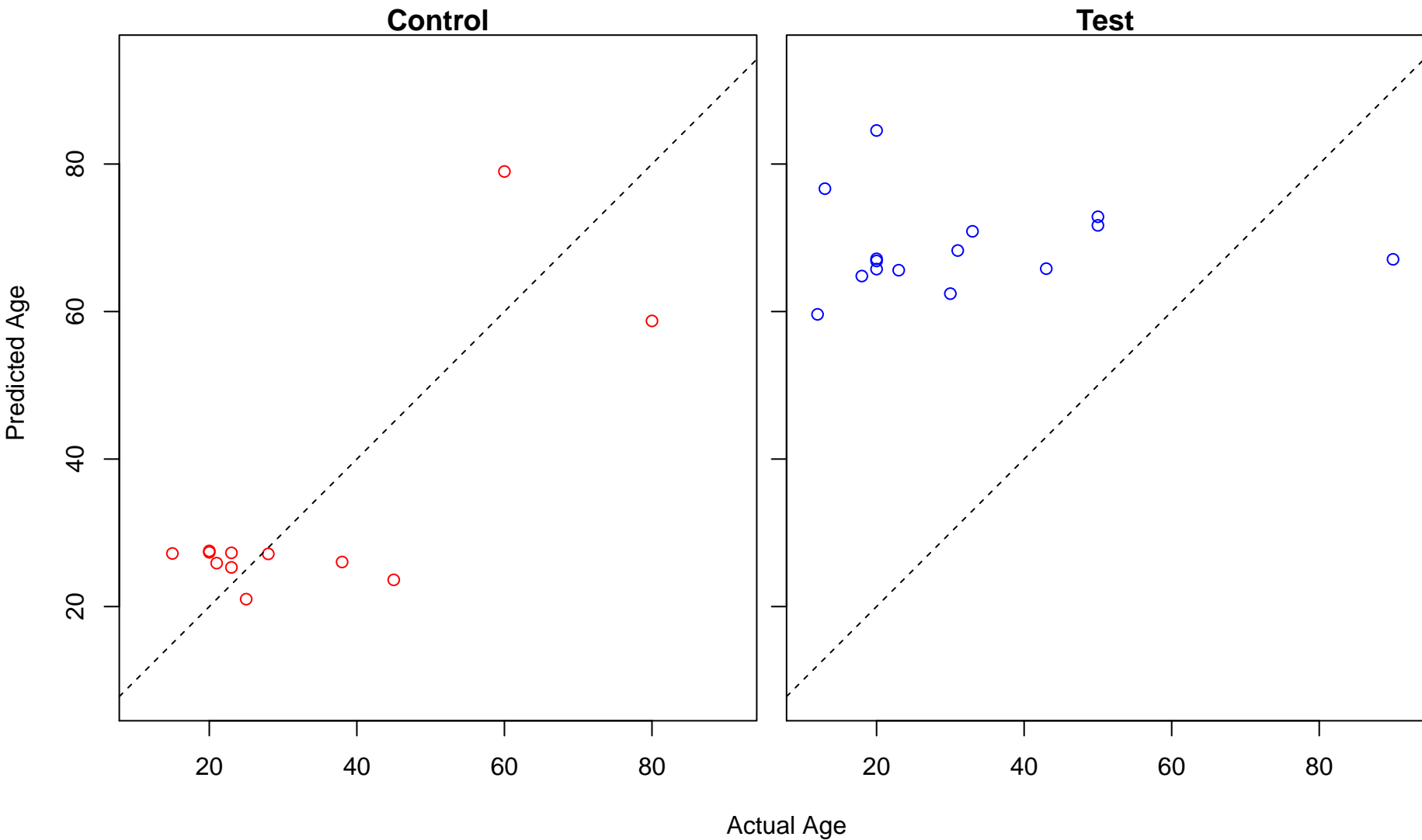


Actual Age

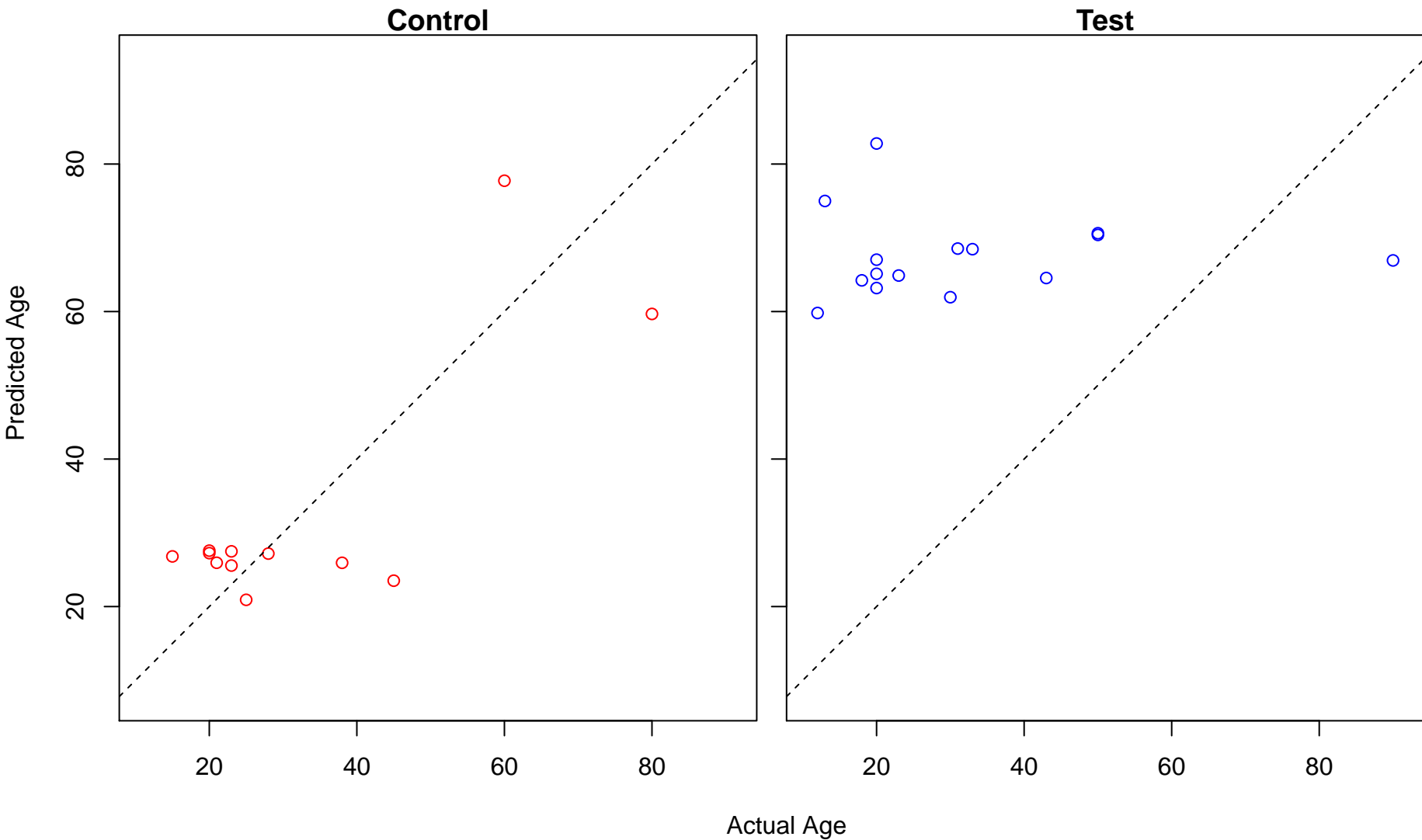
negative regulation of endoplasmic reticulum unfolded protein response (Score: 4.449530)



regulation of heart contraction (Score: 4.448653)

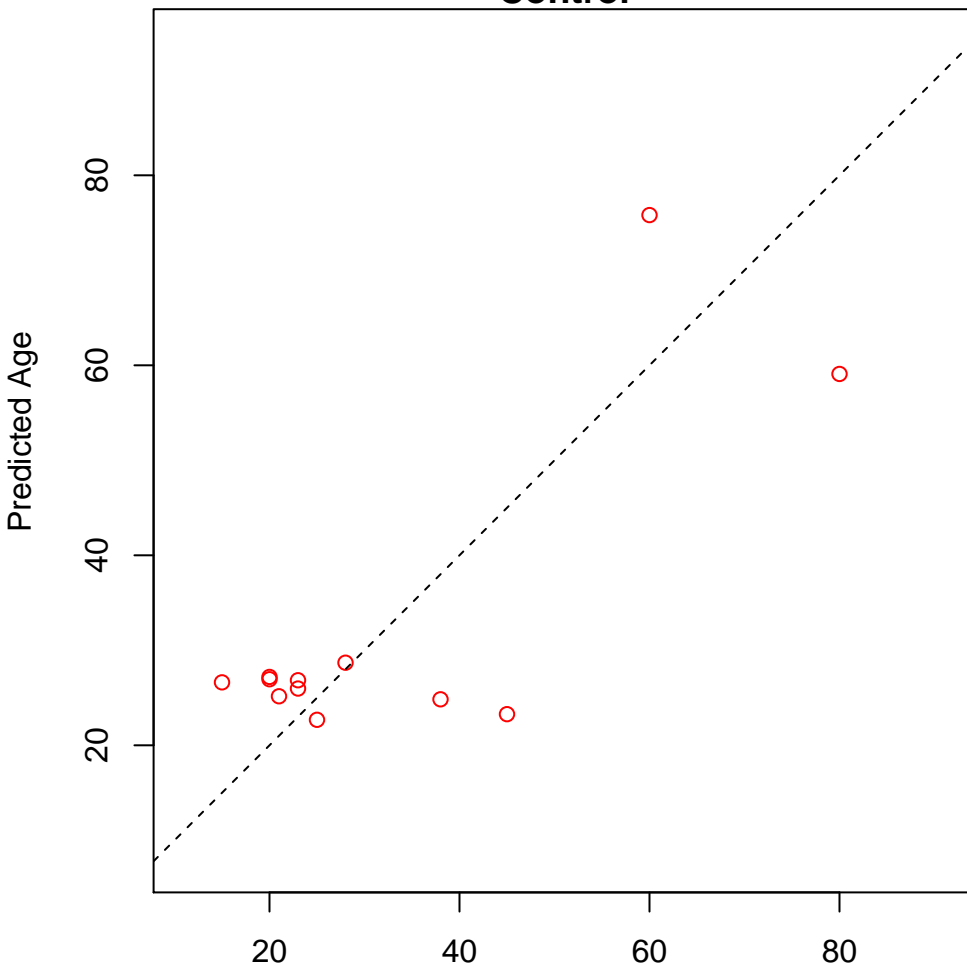


regulation of transporter activity (Score: 4.446393)

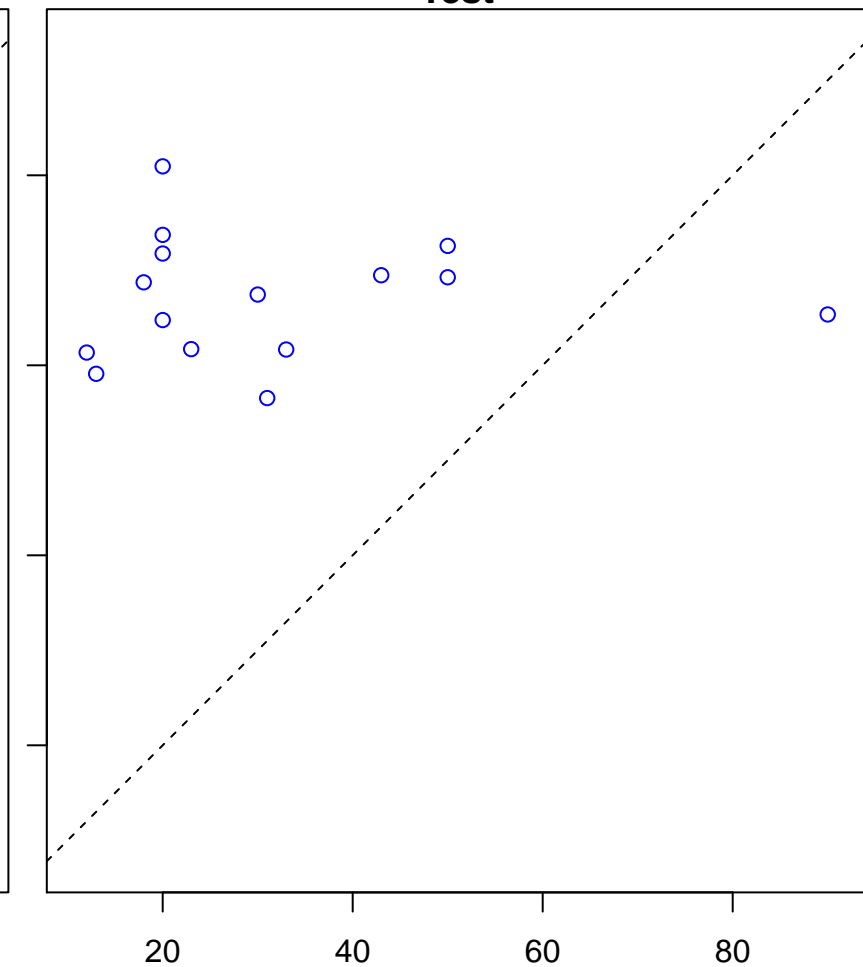


phosphatidylglycerol metabolic process (Score: 4.446273)

Control

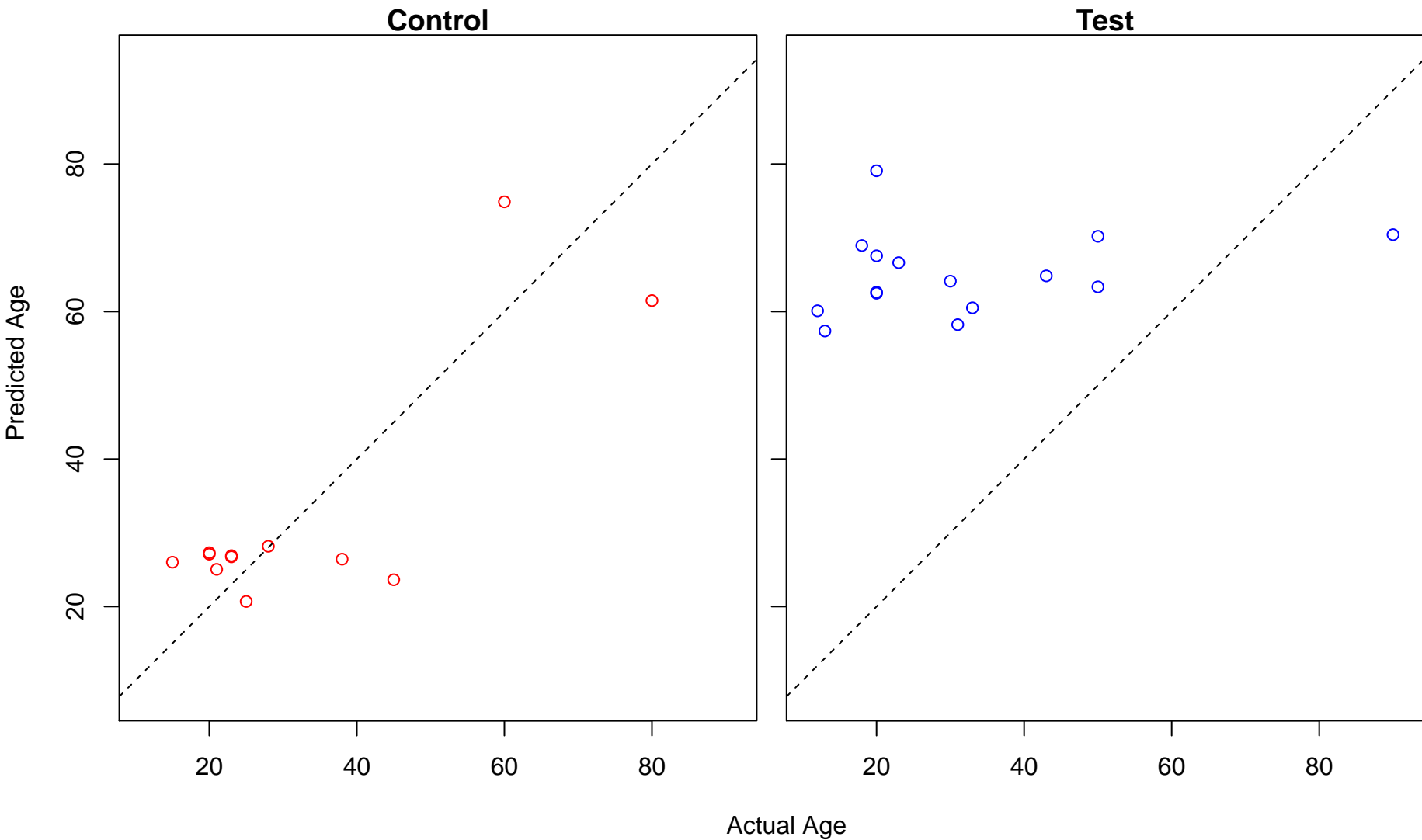


Test

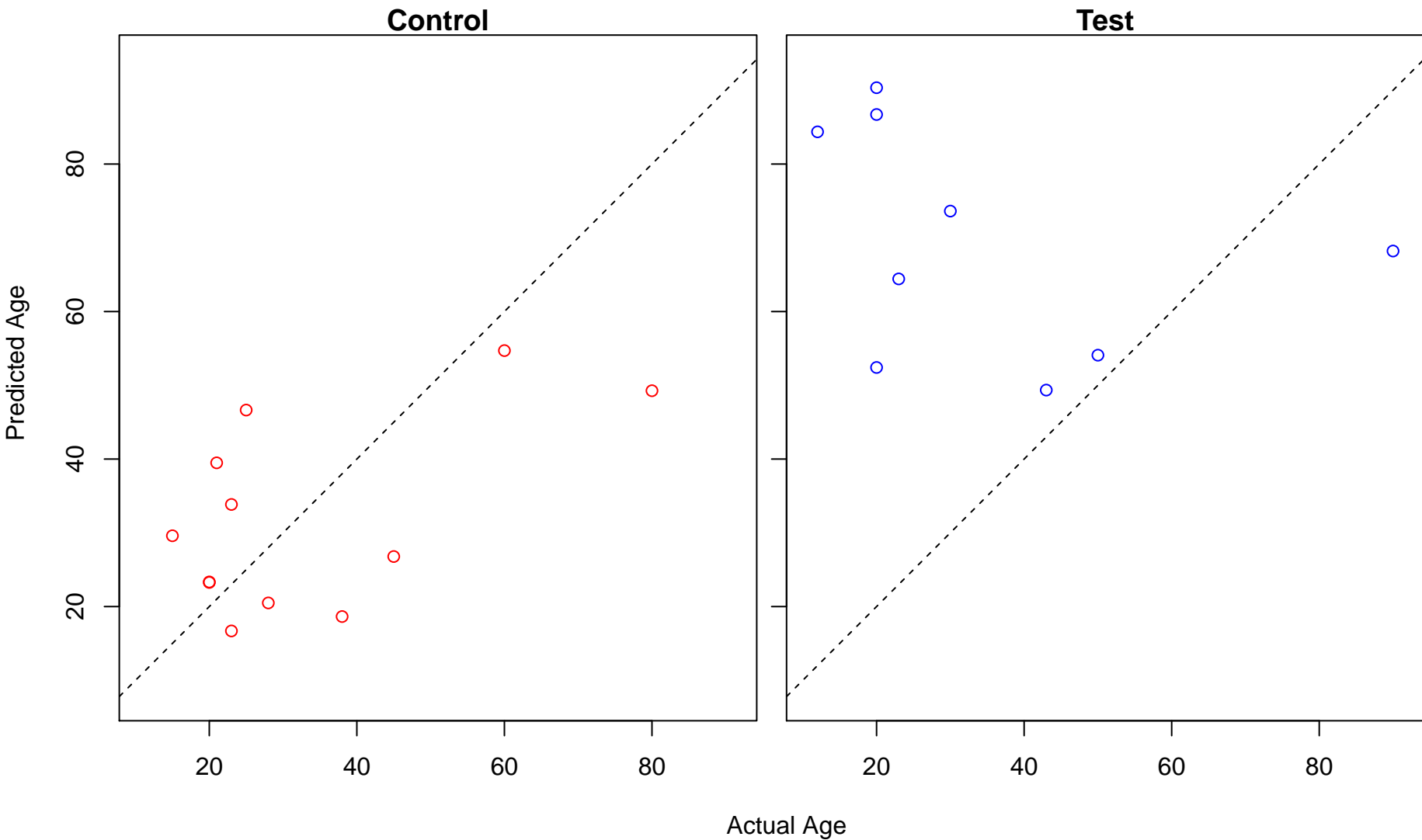


Actual Age

negative regulation of establishment of protein localization (Score: 4.446179)

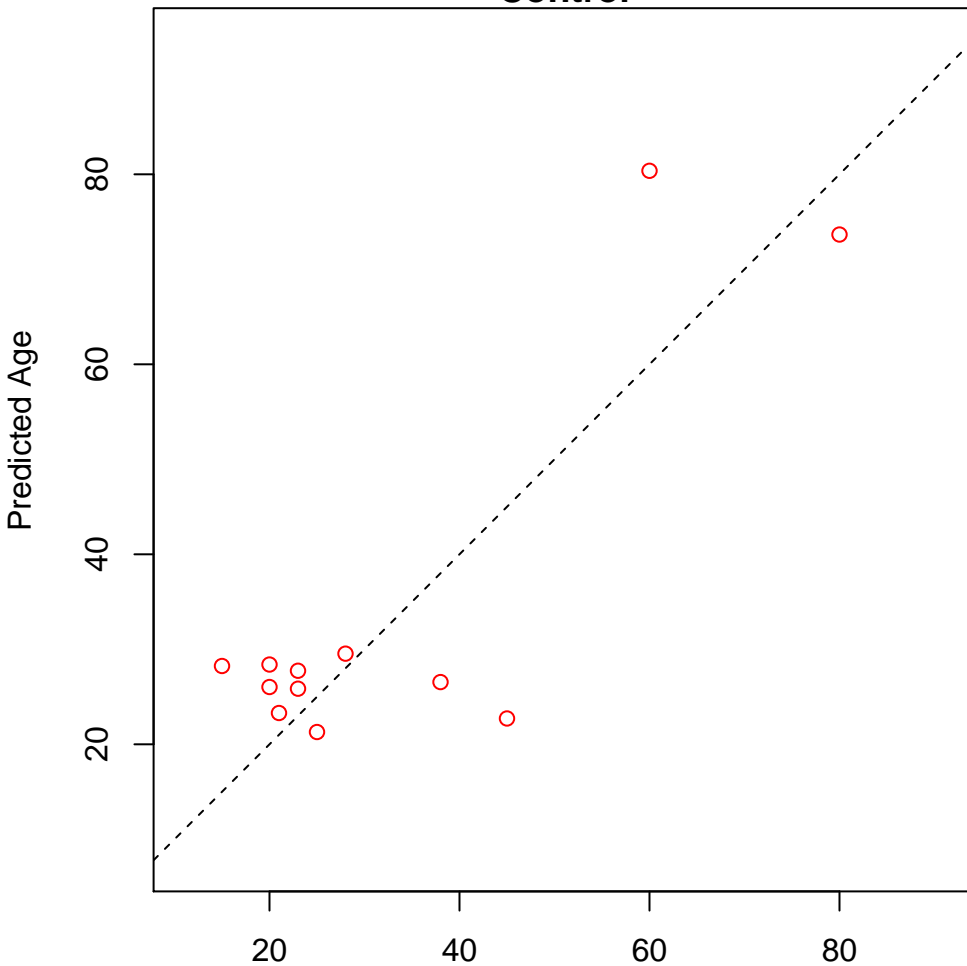


positive regulation of interleukin-23 production (Score: 4.445330)

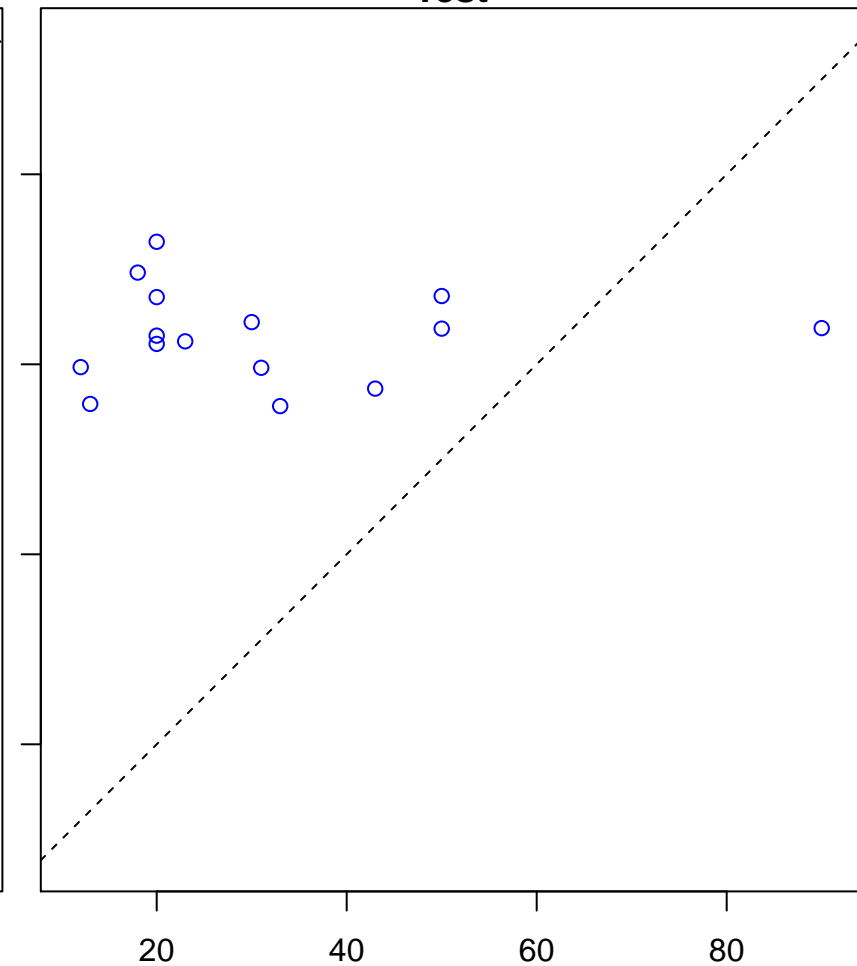


response to endoplasmic reticulum stress (Score: 4.444608)

Control

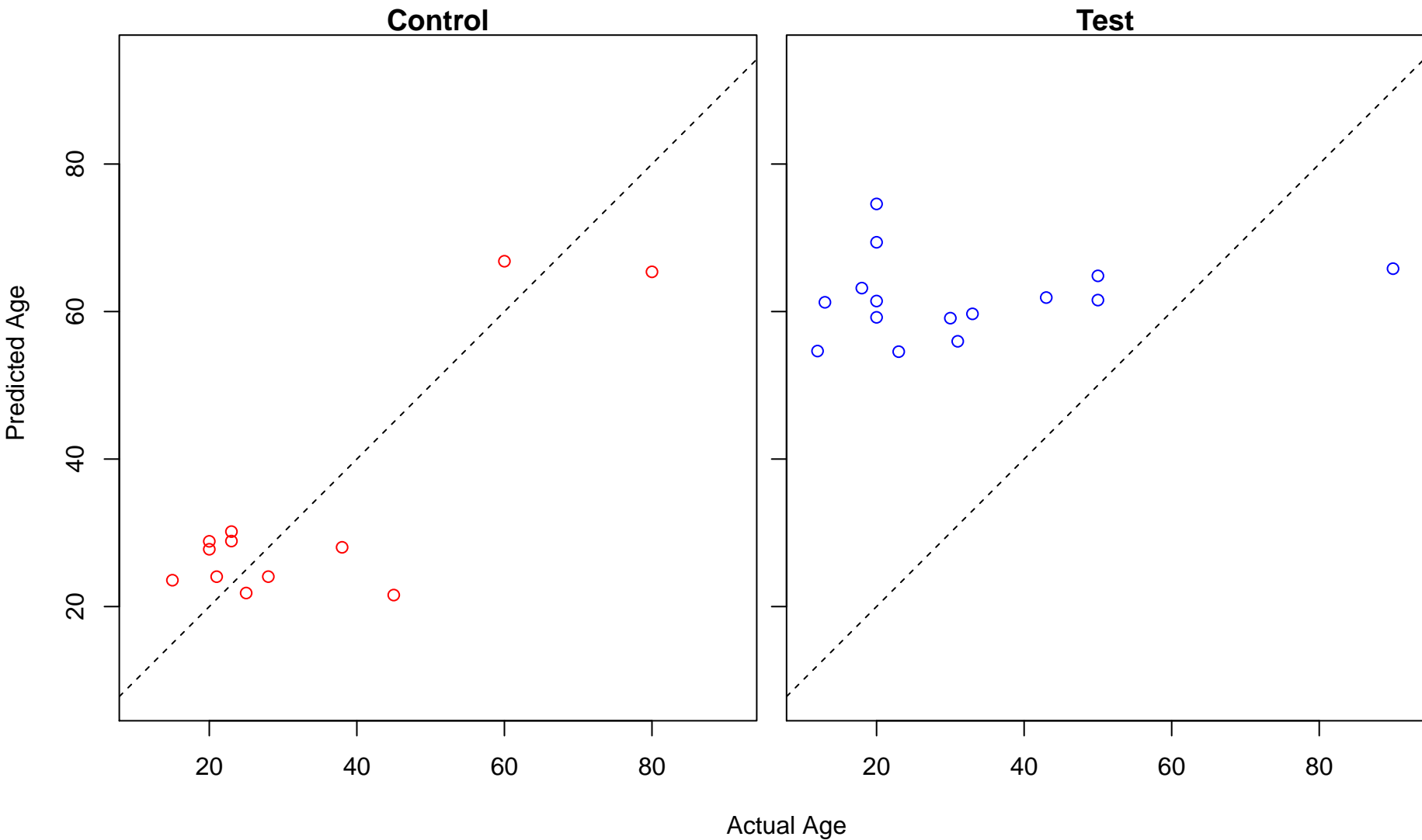


Test

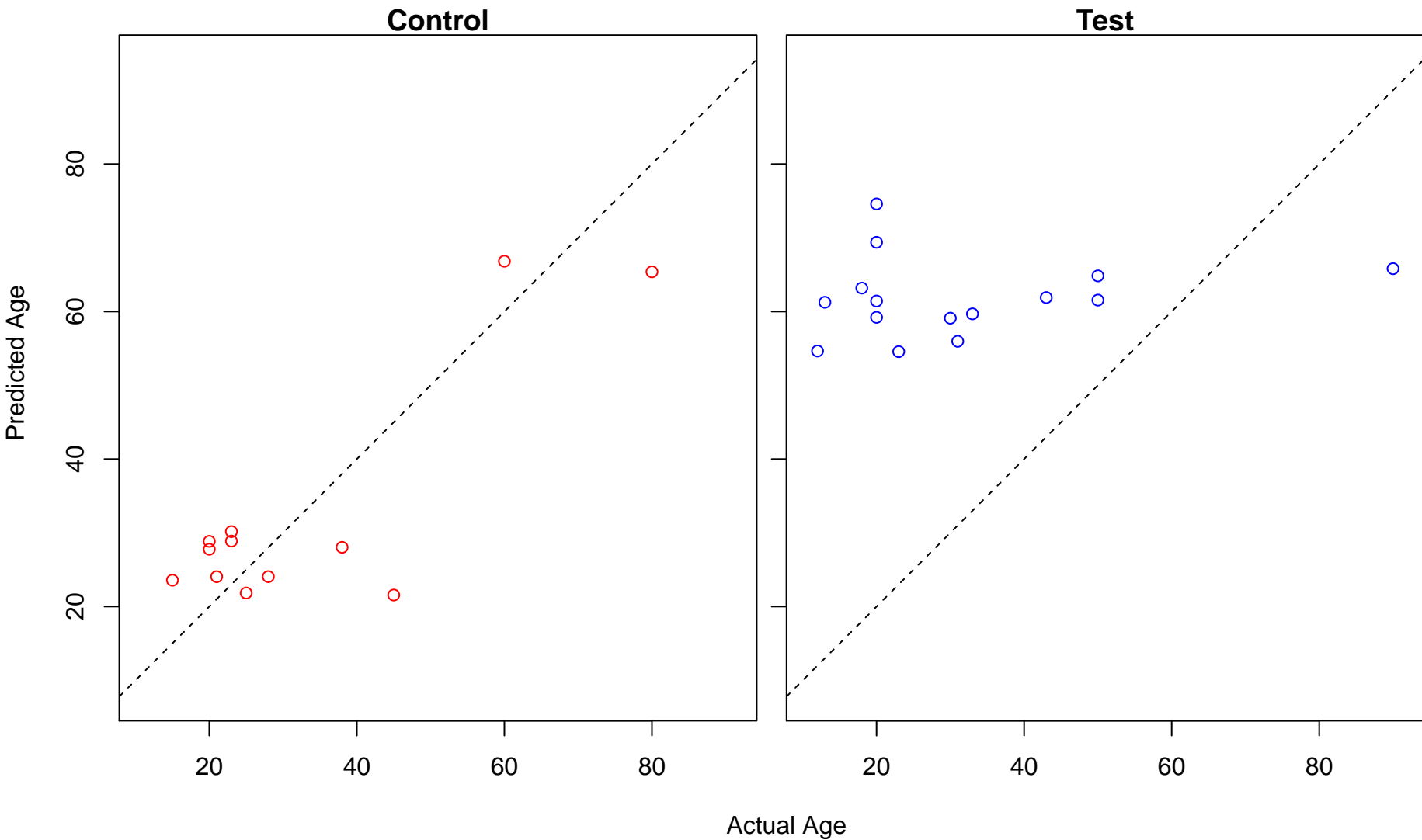


Actual Age

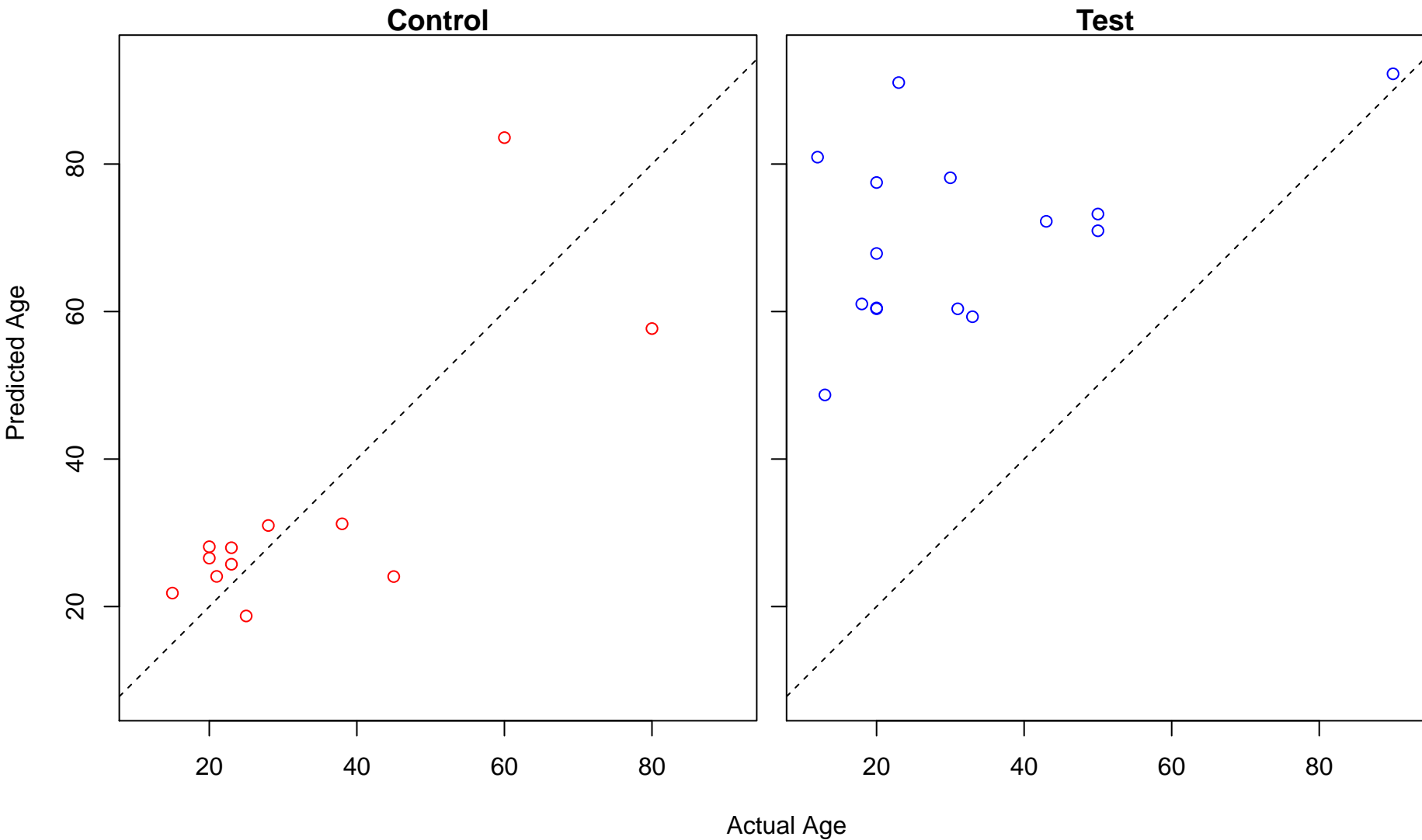
regulation of carbohydrate catabolic process (Score: 4.443683)



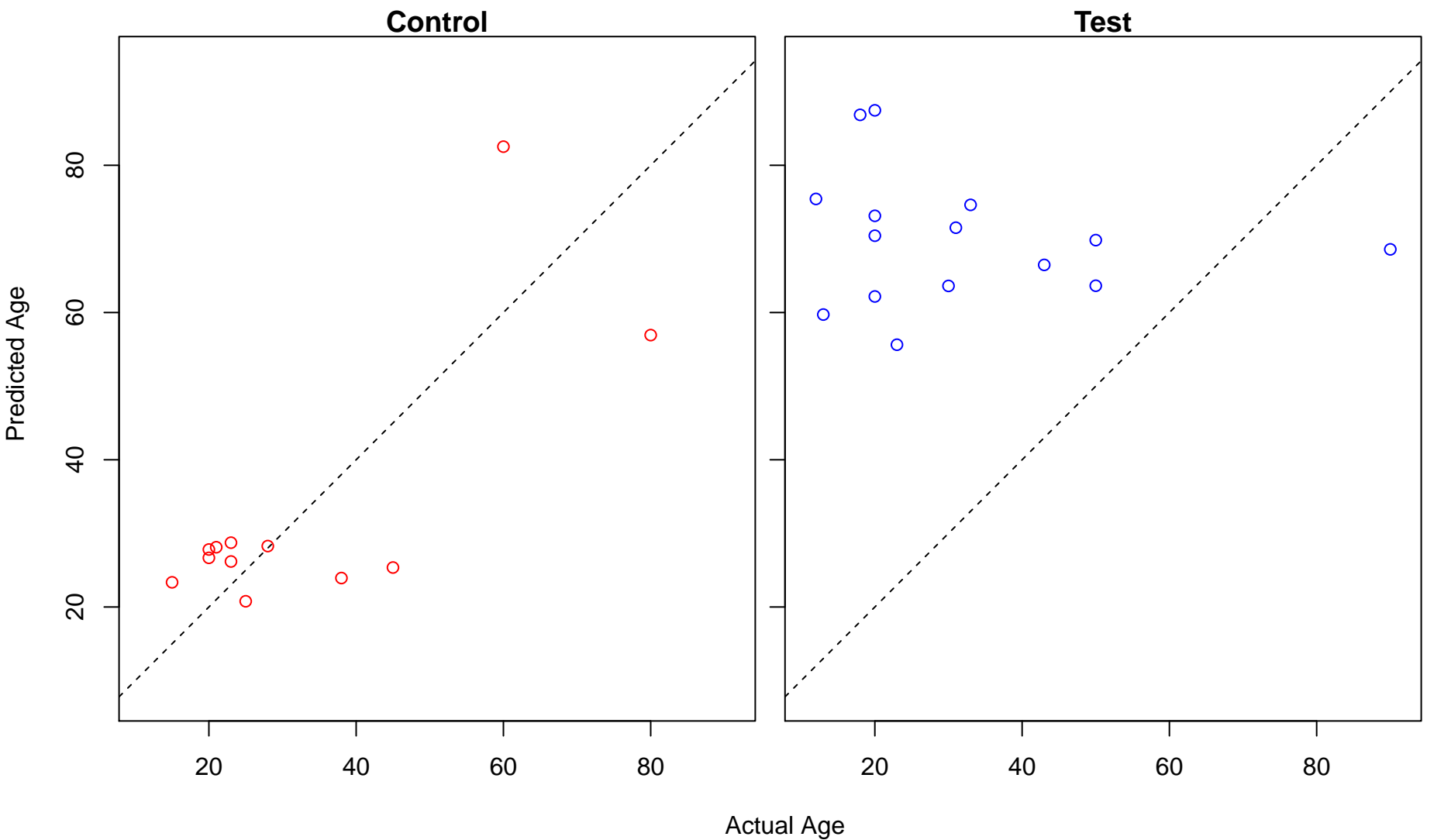
regulation of cellular carbohydrate catabolic process (Score: 4.443683)



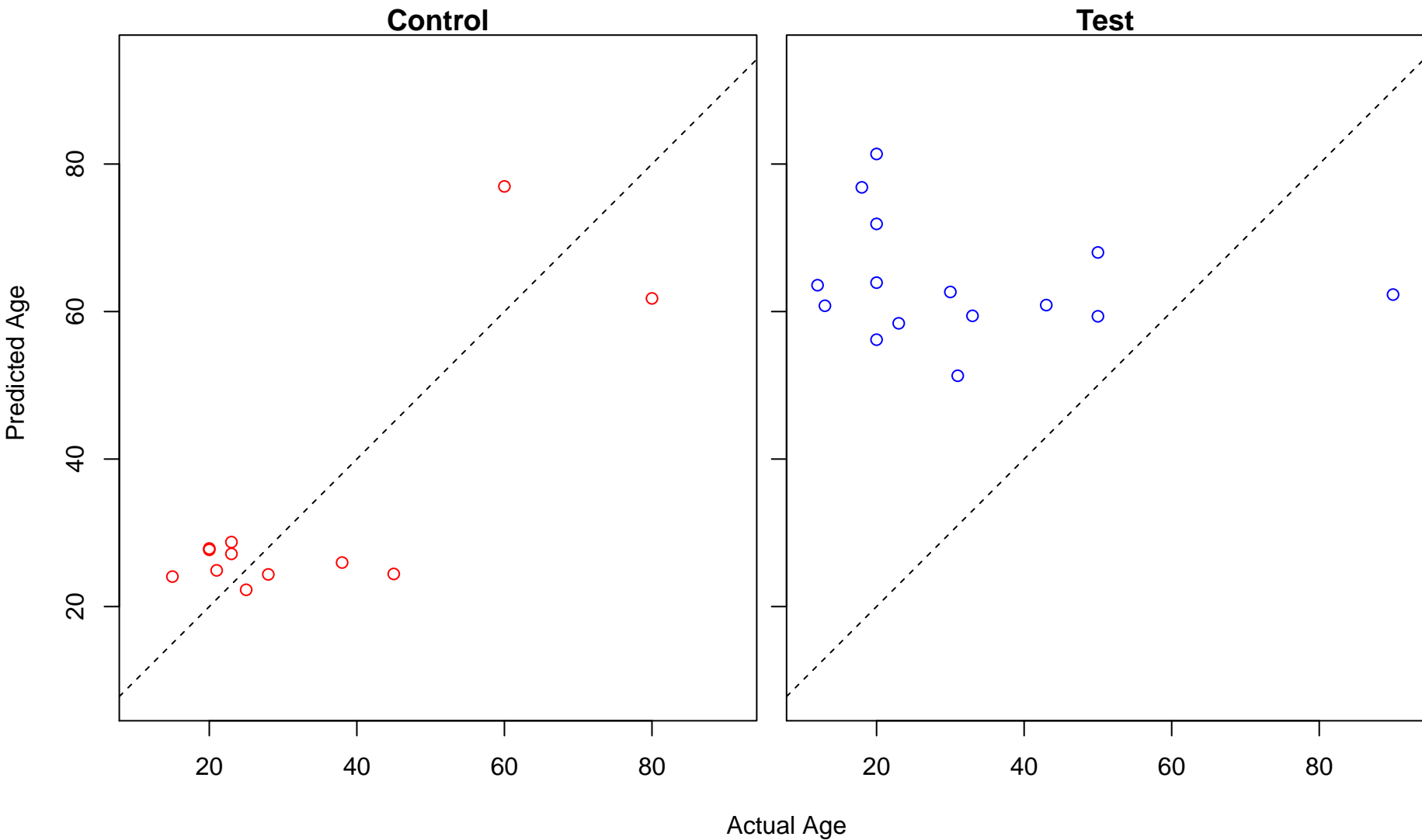
left/right axis specification (Score: 4.442459)



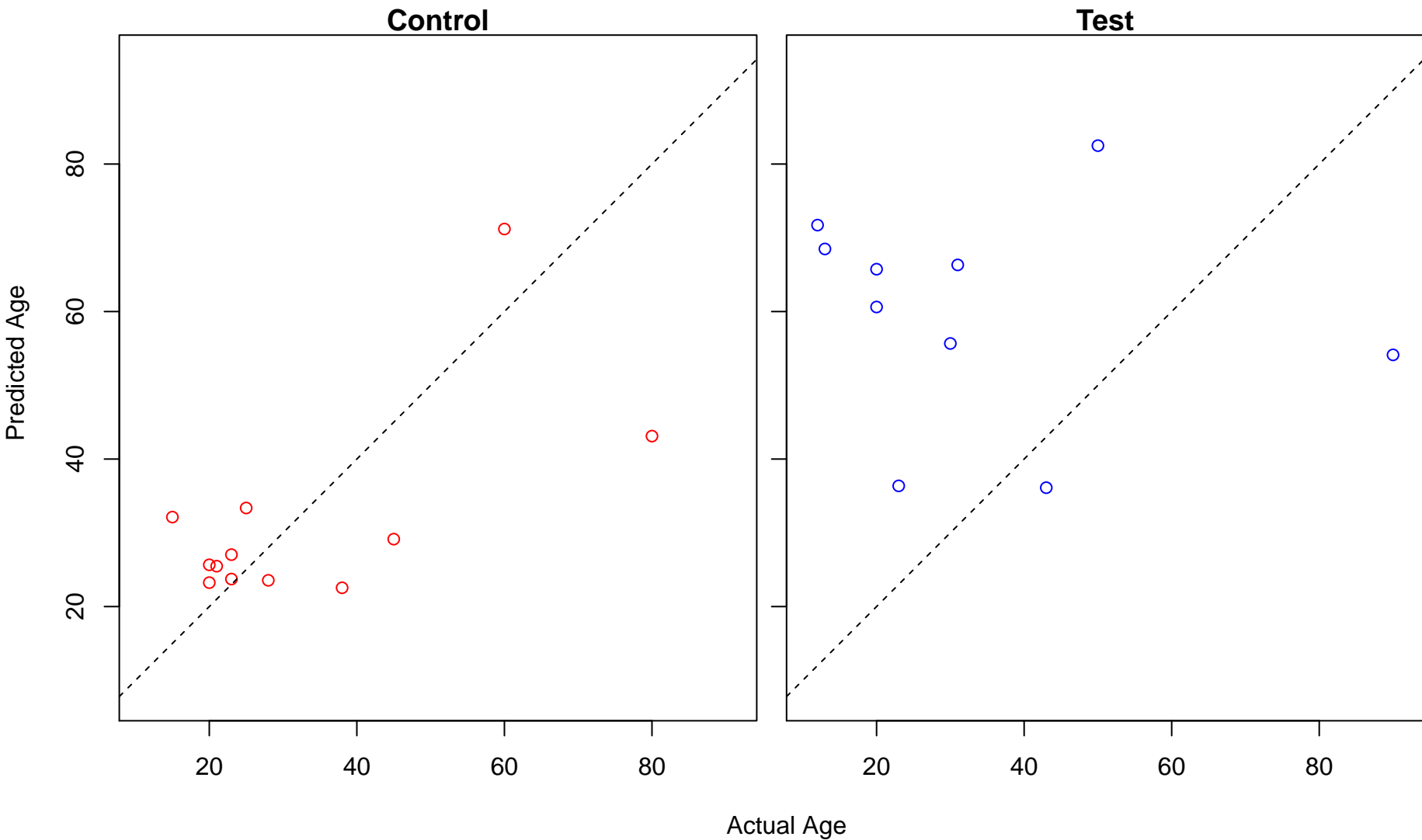
of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell cycle



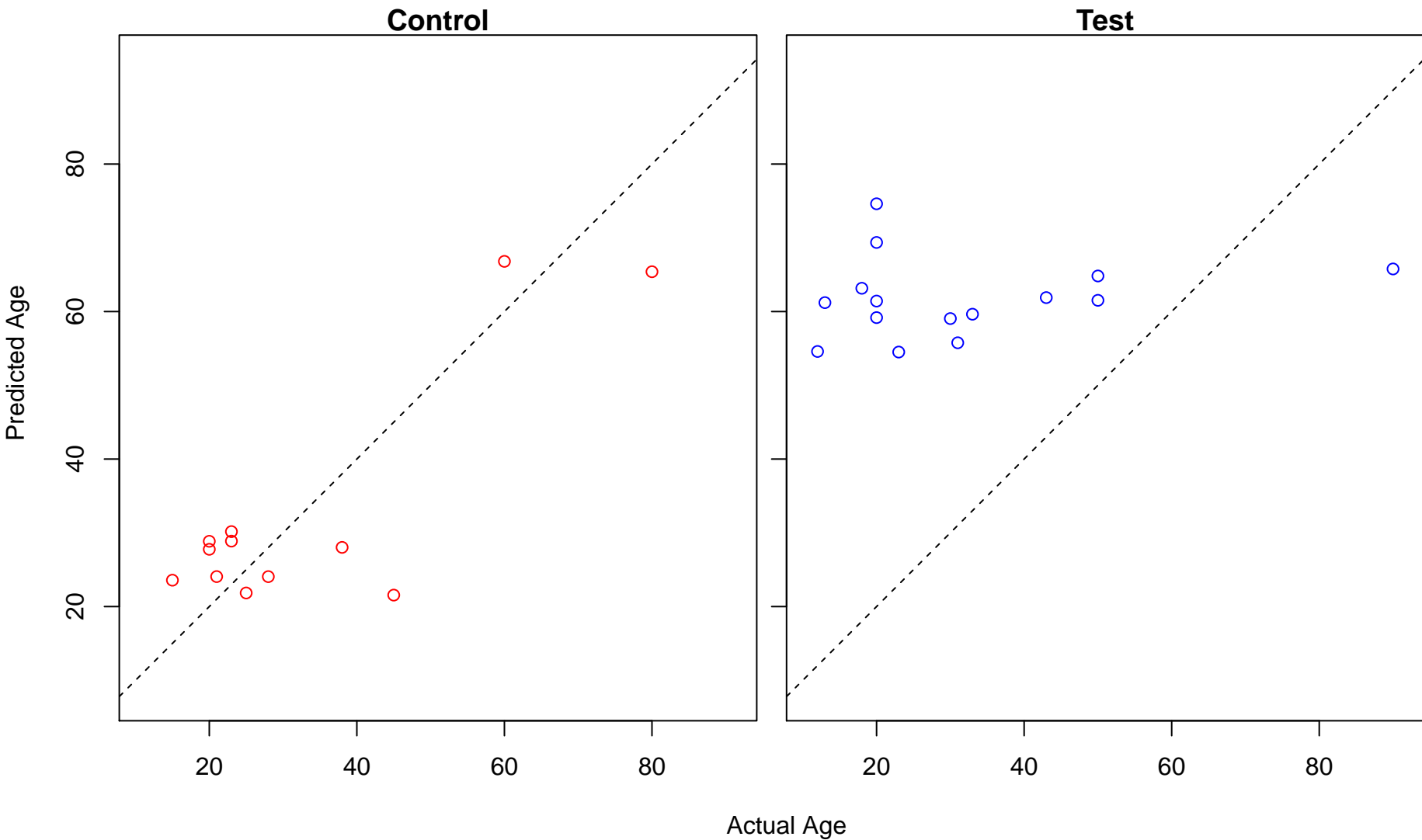
positive regulation of mRNA splicing, via spliceosome (Score: 4.439707)



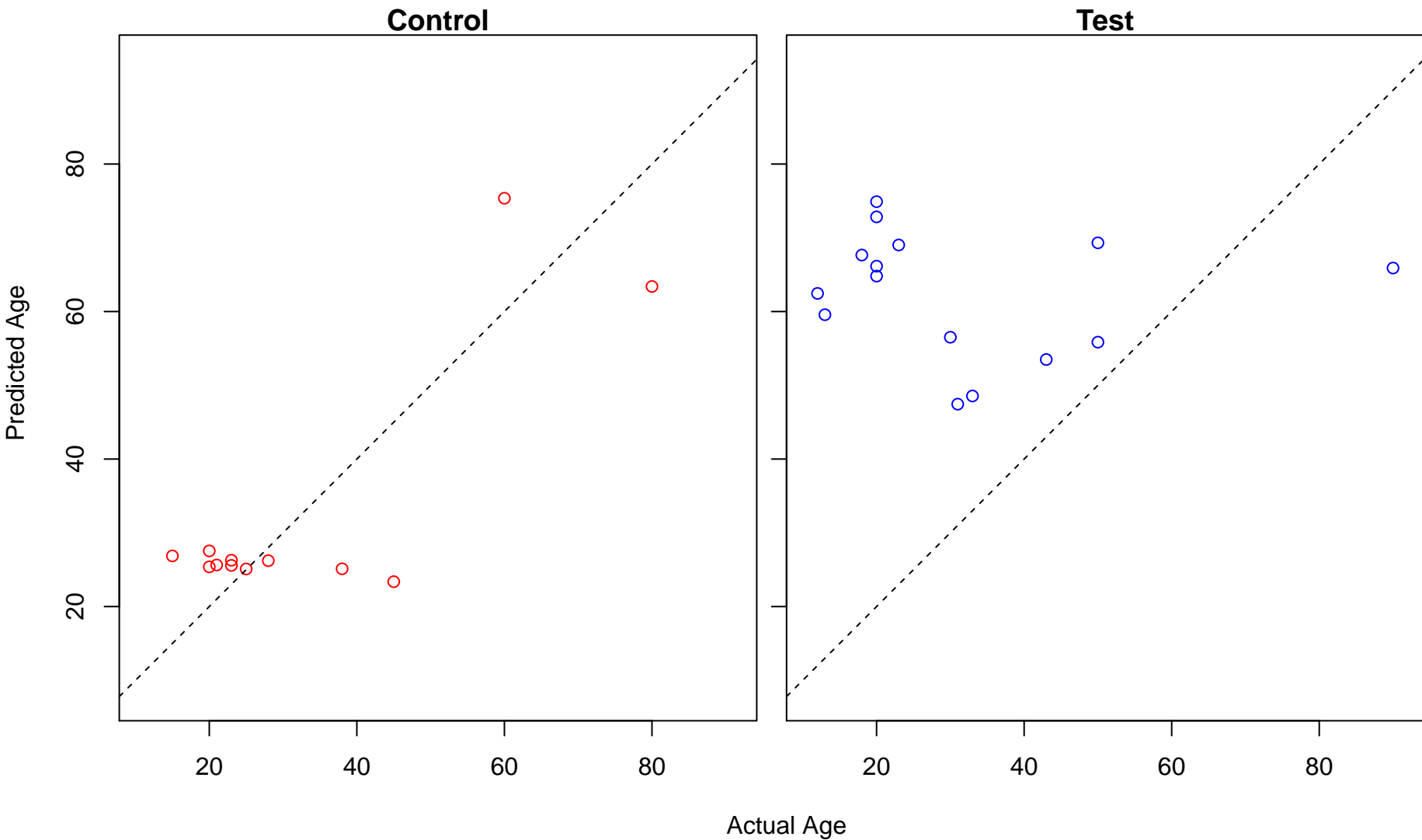
positive regulation of cell fate commitment (Score: 4.438912)



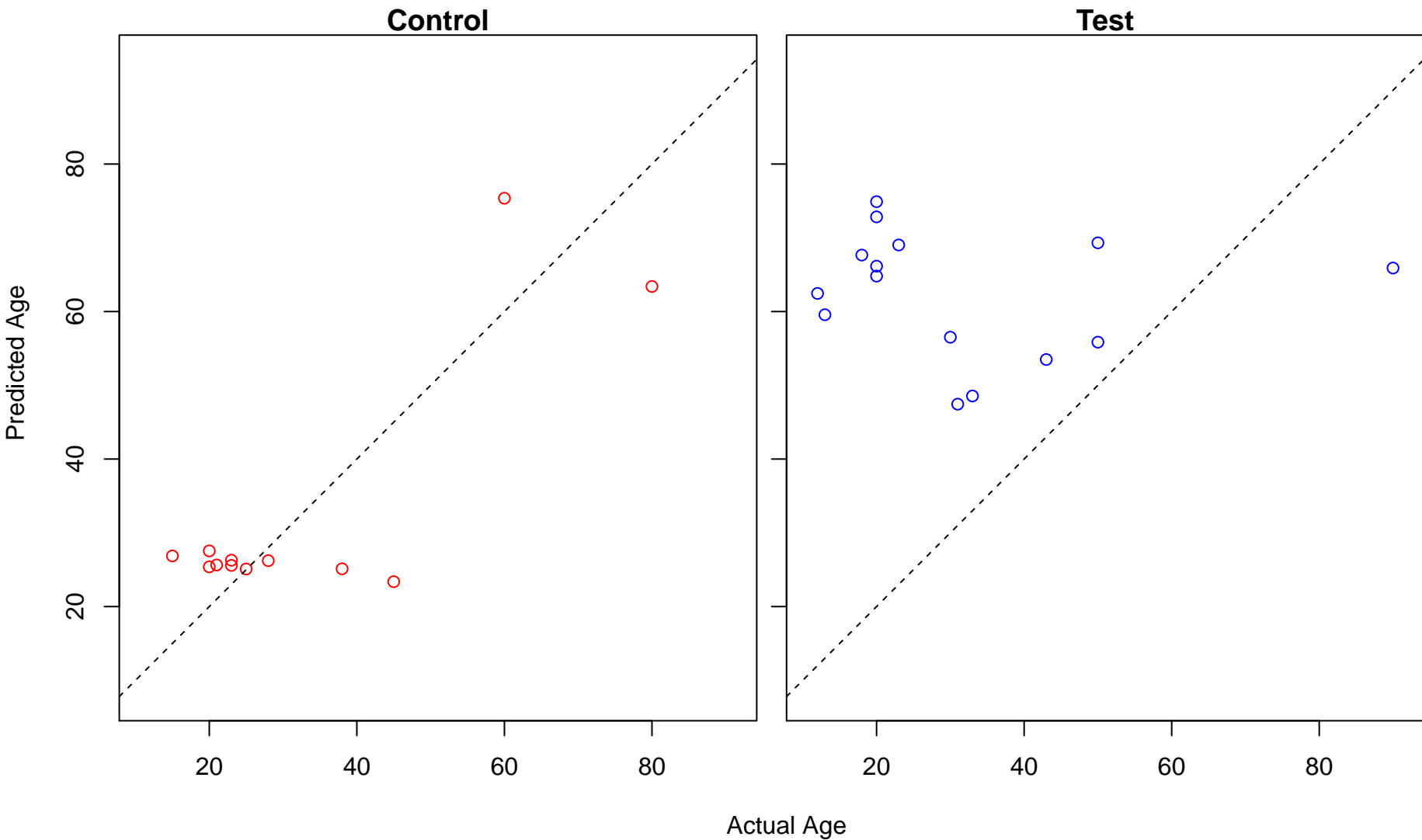
regulation of glycolytic process (Score: 4.438104)



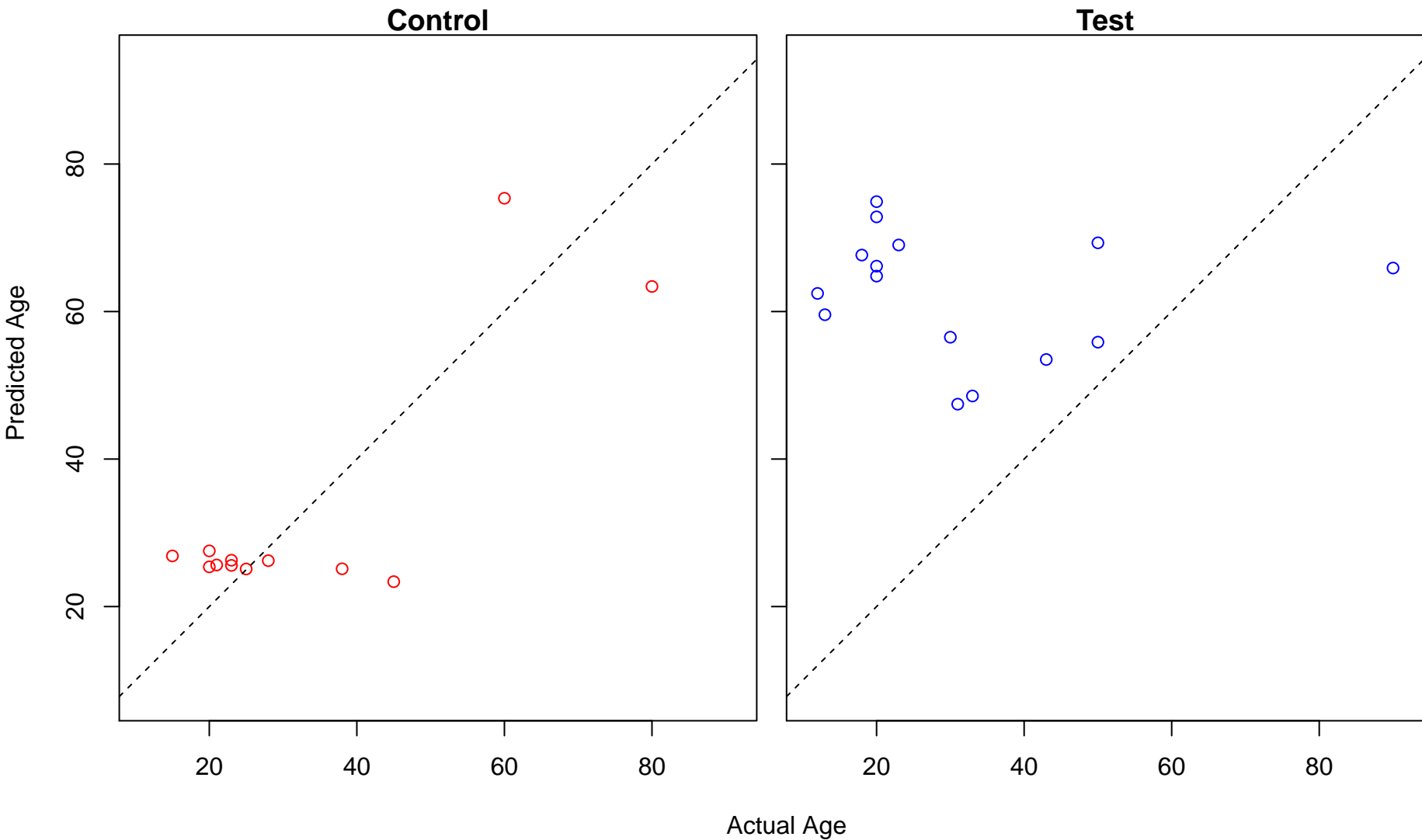
tRNA threonylcarbamoyladenosine metabolic process (Score: 4.435181)



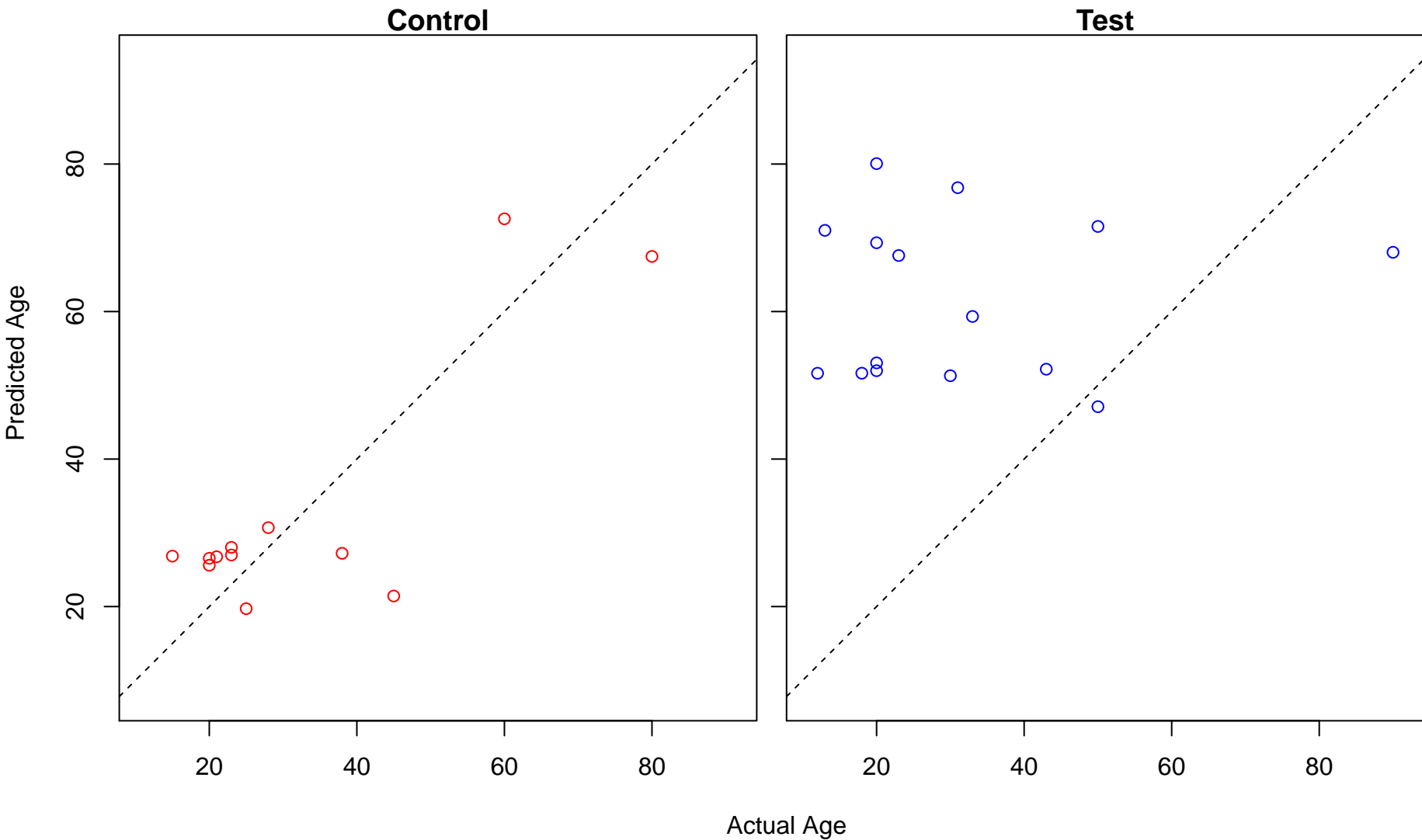
mitochondrial tRNA modification (Score: 4.435181)



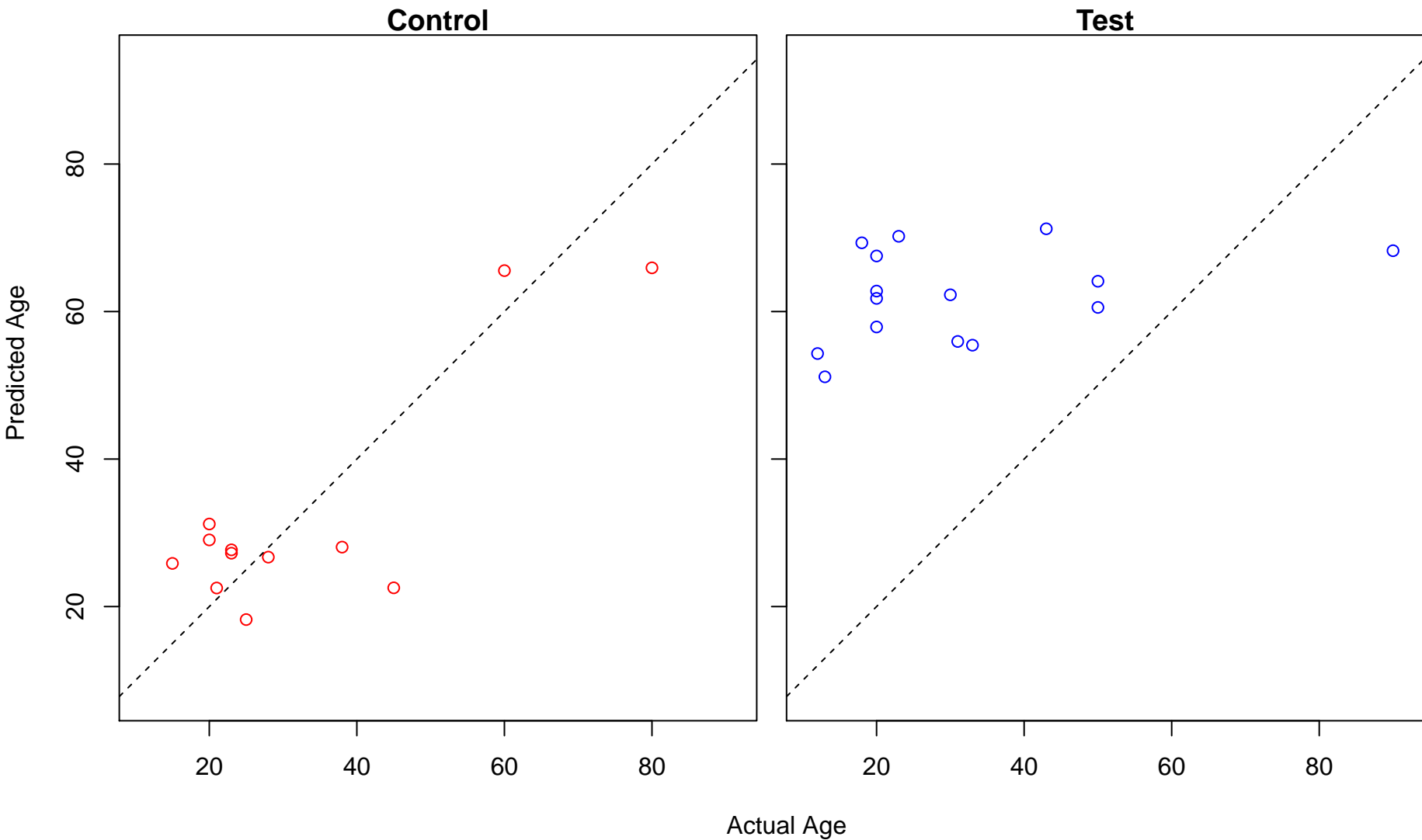
mitochondrial RNA modification (Score: 4.435181)



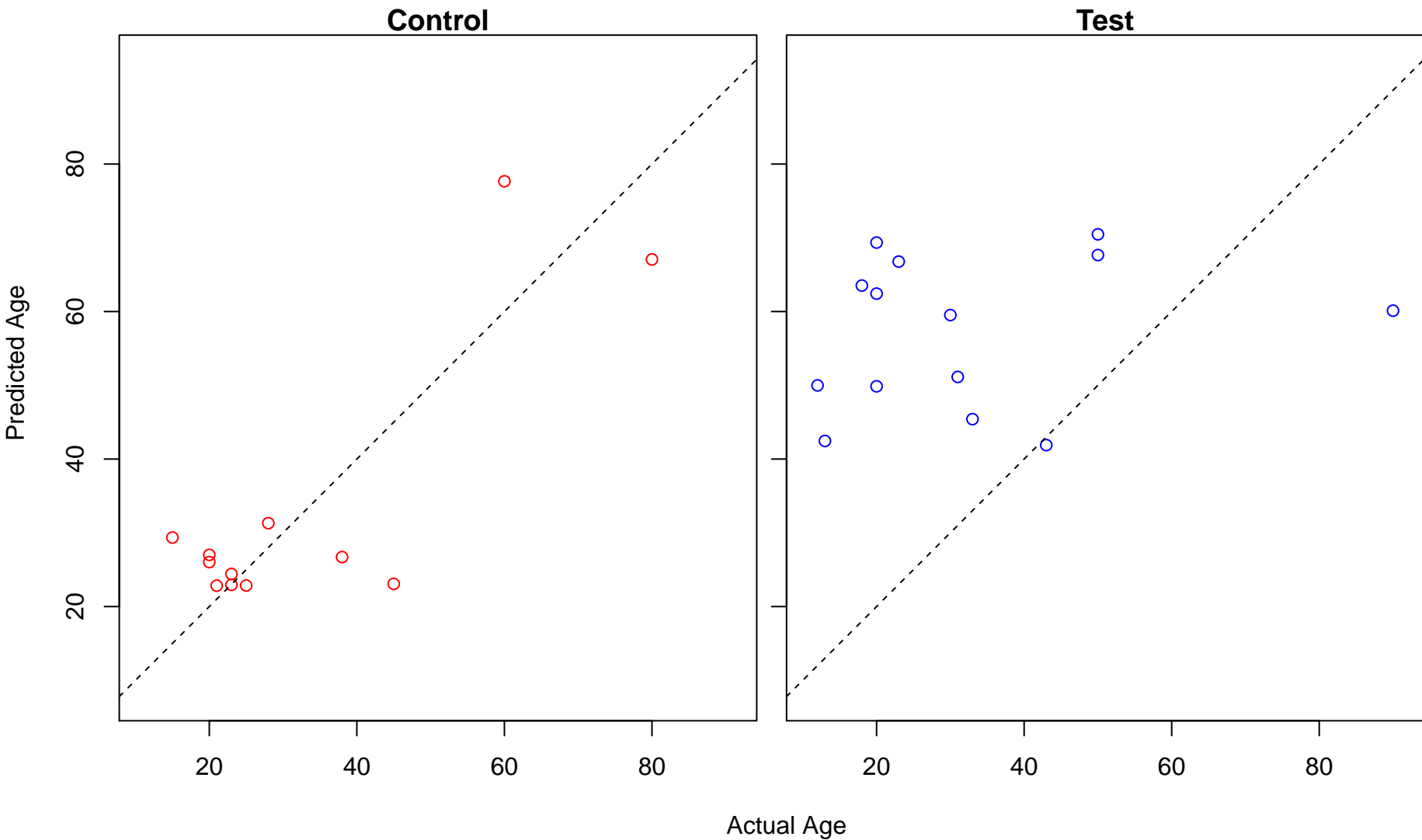
response to metal ion (Score: 4.432537)



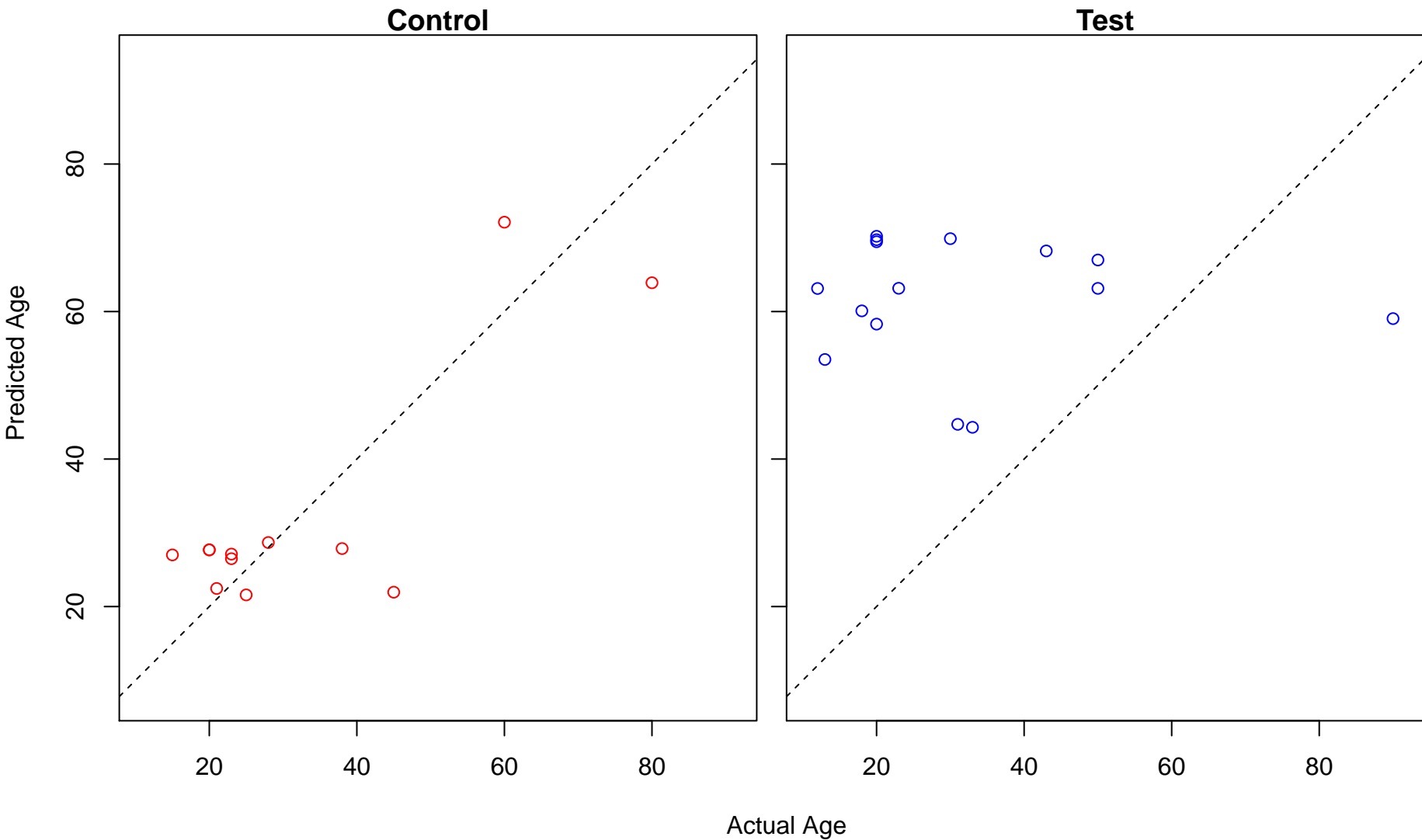
renal filtration (Score: 4.431981)



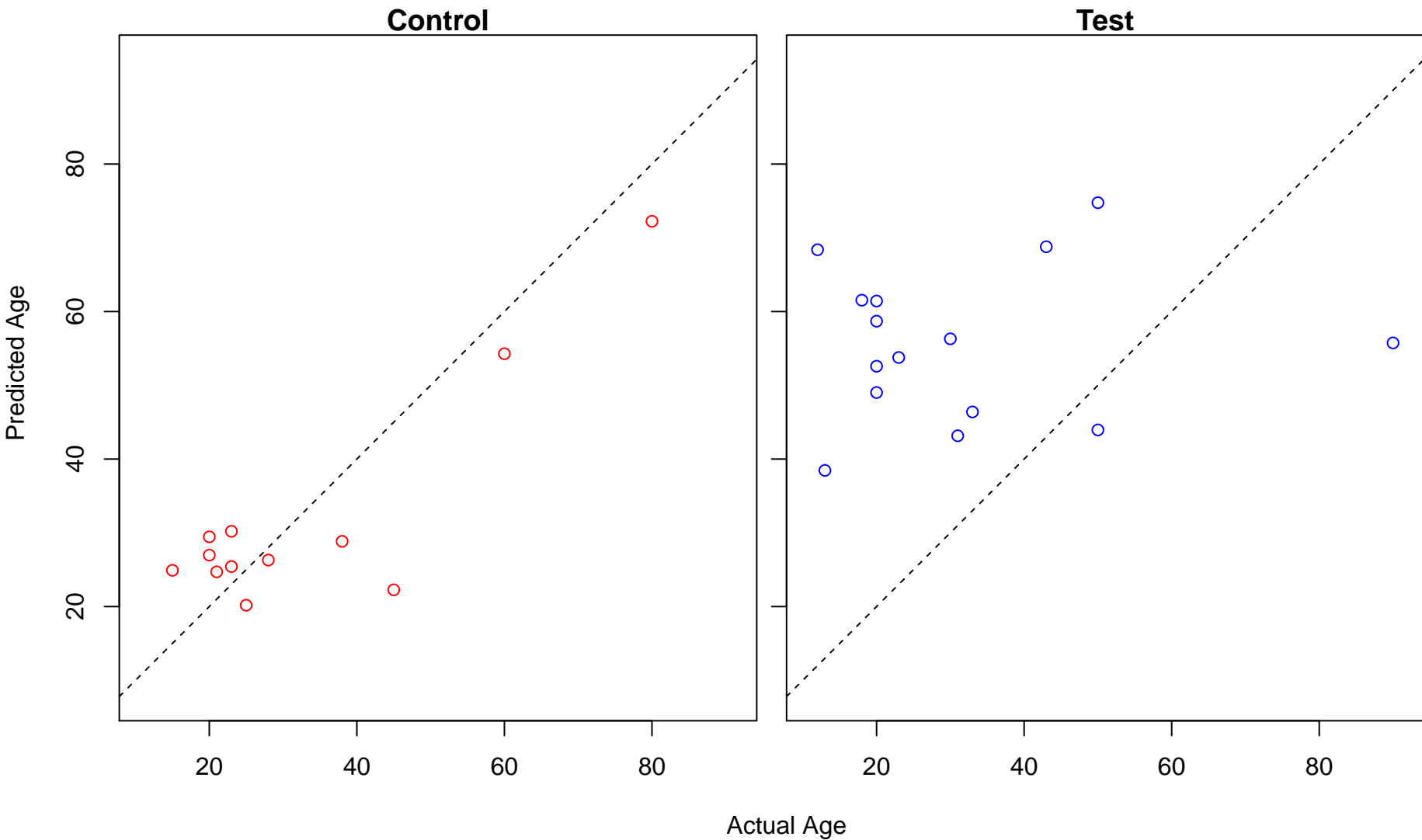
RNA splicing (Score: 4.430302)



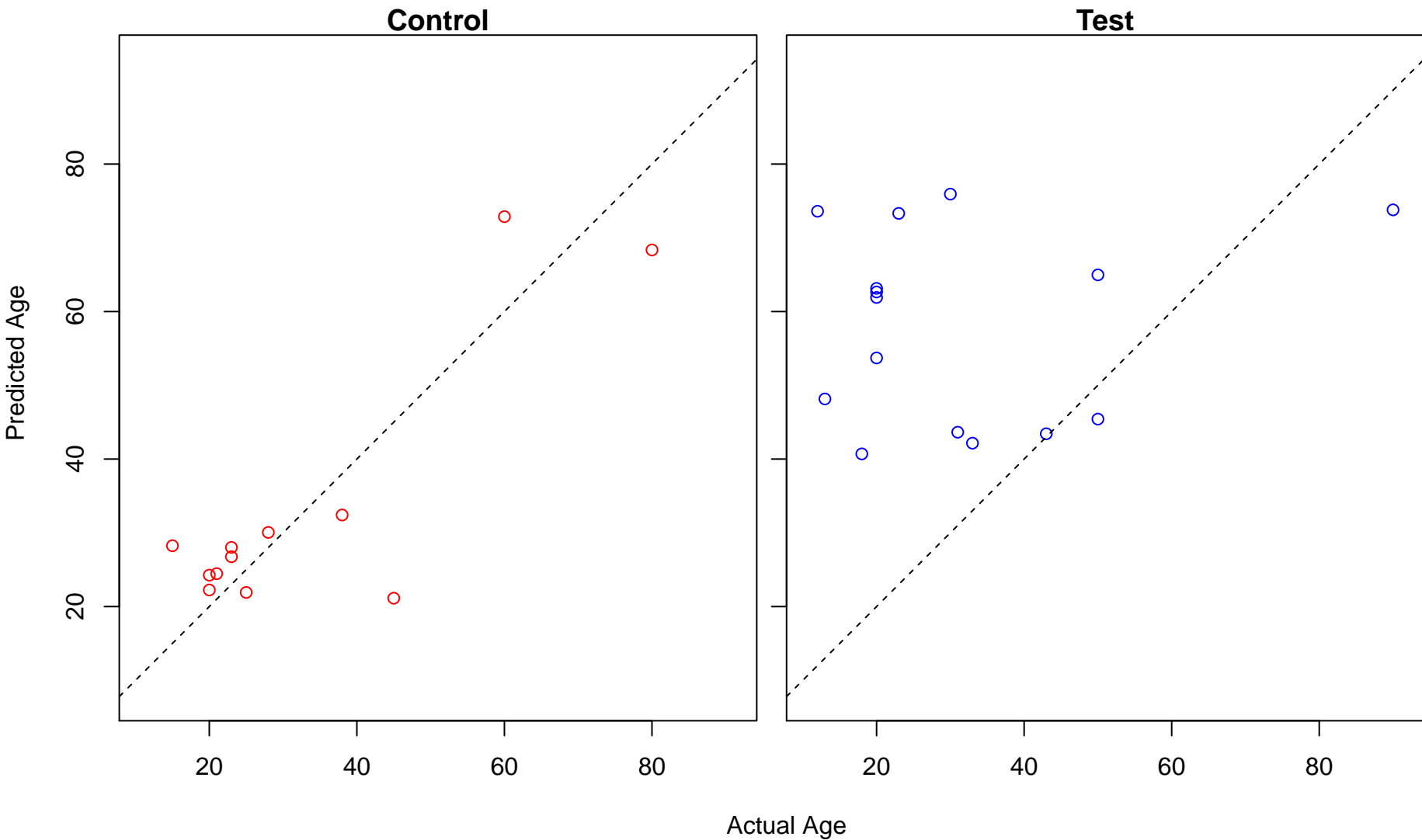
leukotriene metabolic process (Score: 4.430112)



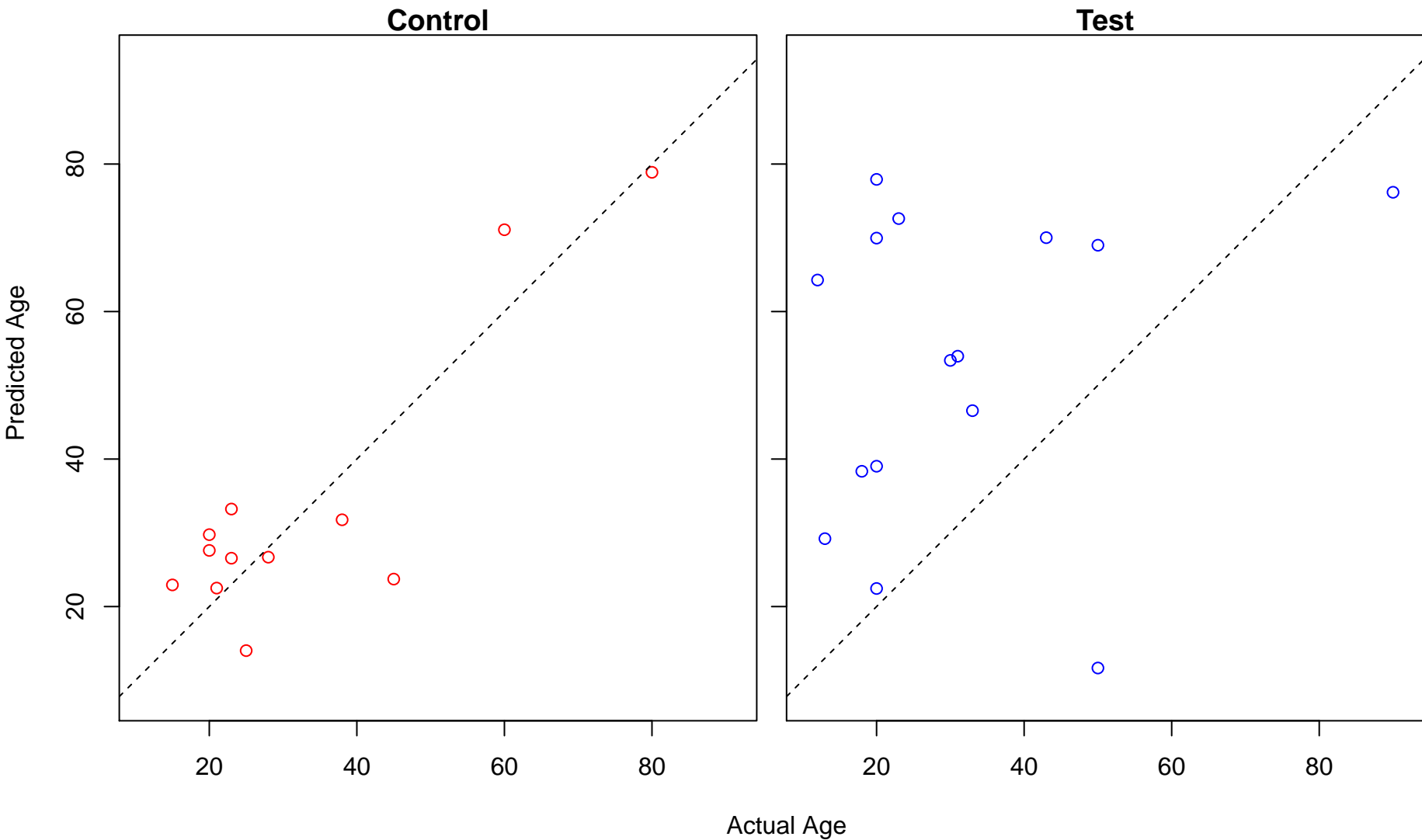
cell redox homeostasis (Score: 4.428293)



negative chemotaxis (Score: 4.426514)

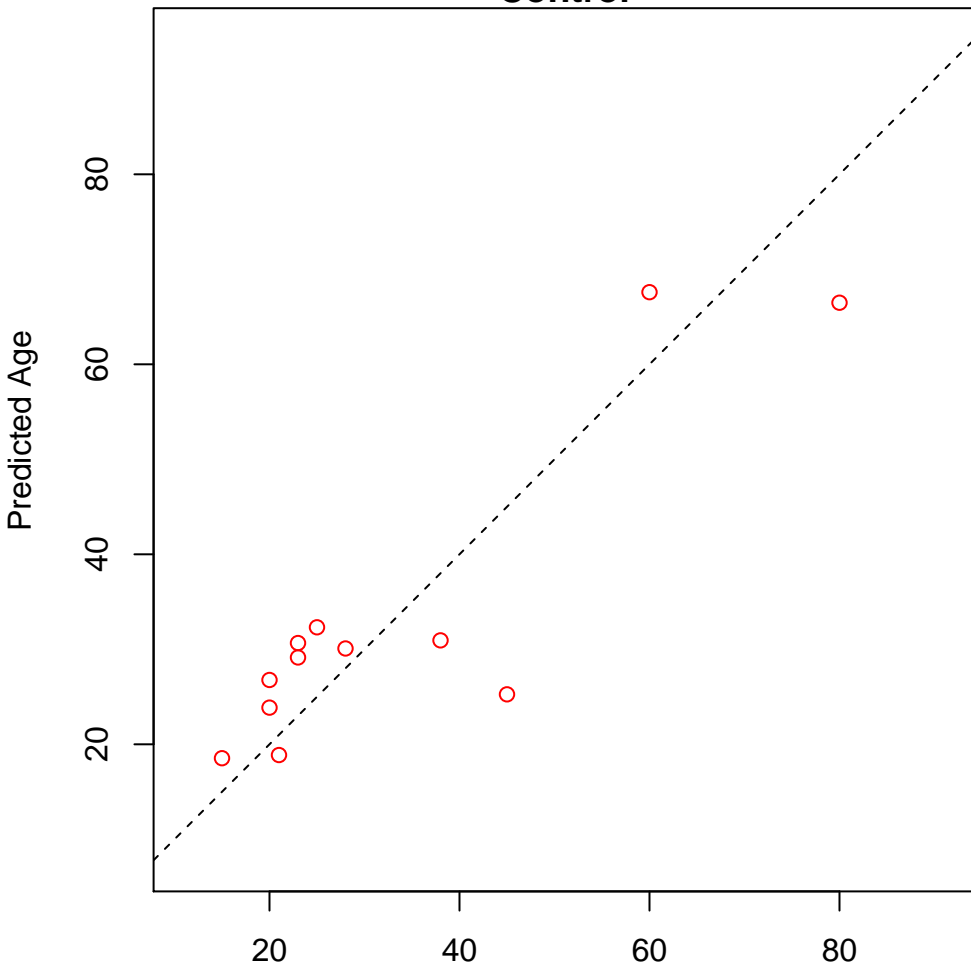


positive regulation of DNA-templated transcription, initiation (Score: 4.424188)

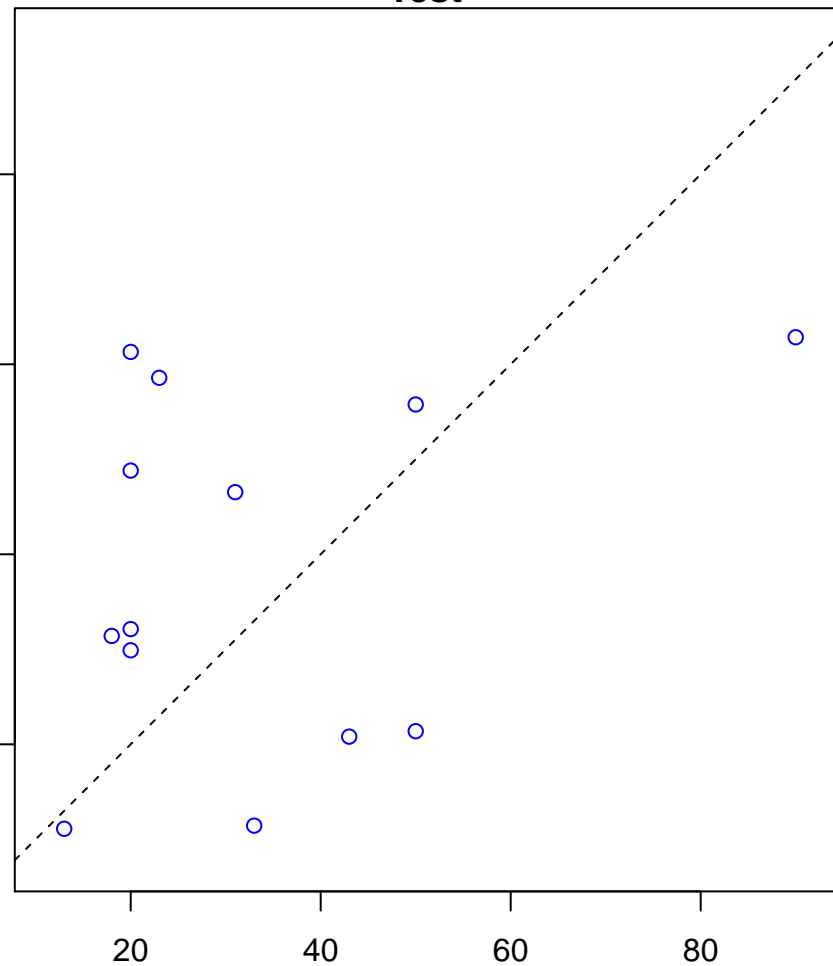


short-chain fatty acid metabolic process (Score: 4.423907)

Control



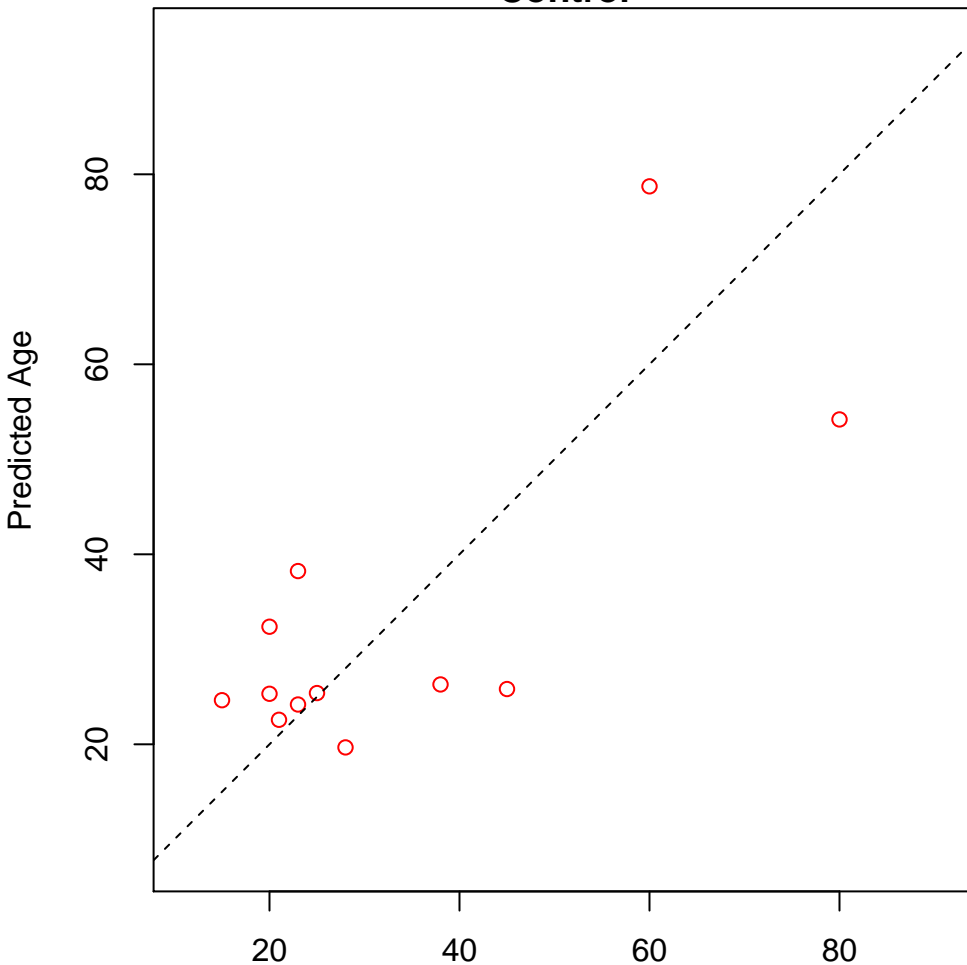
Test



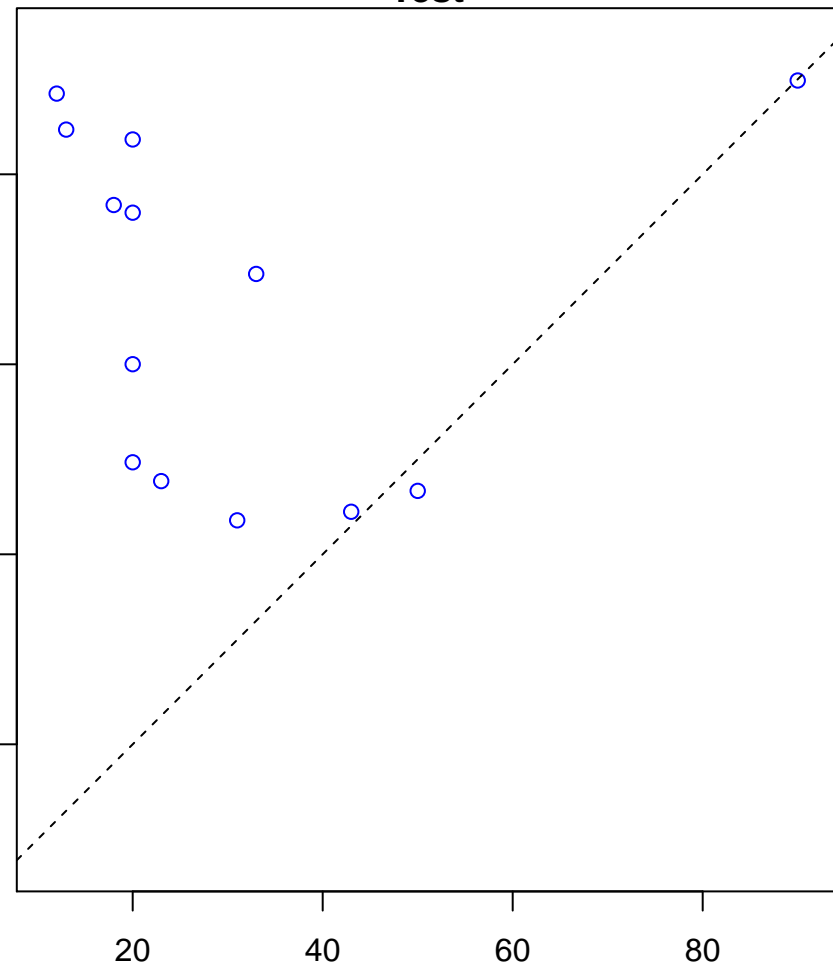
Actual Age

smooth muscle cell differentiation (Score: 4.422919)

Control

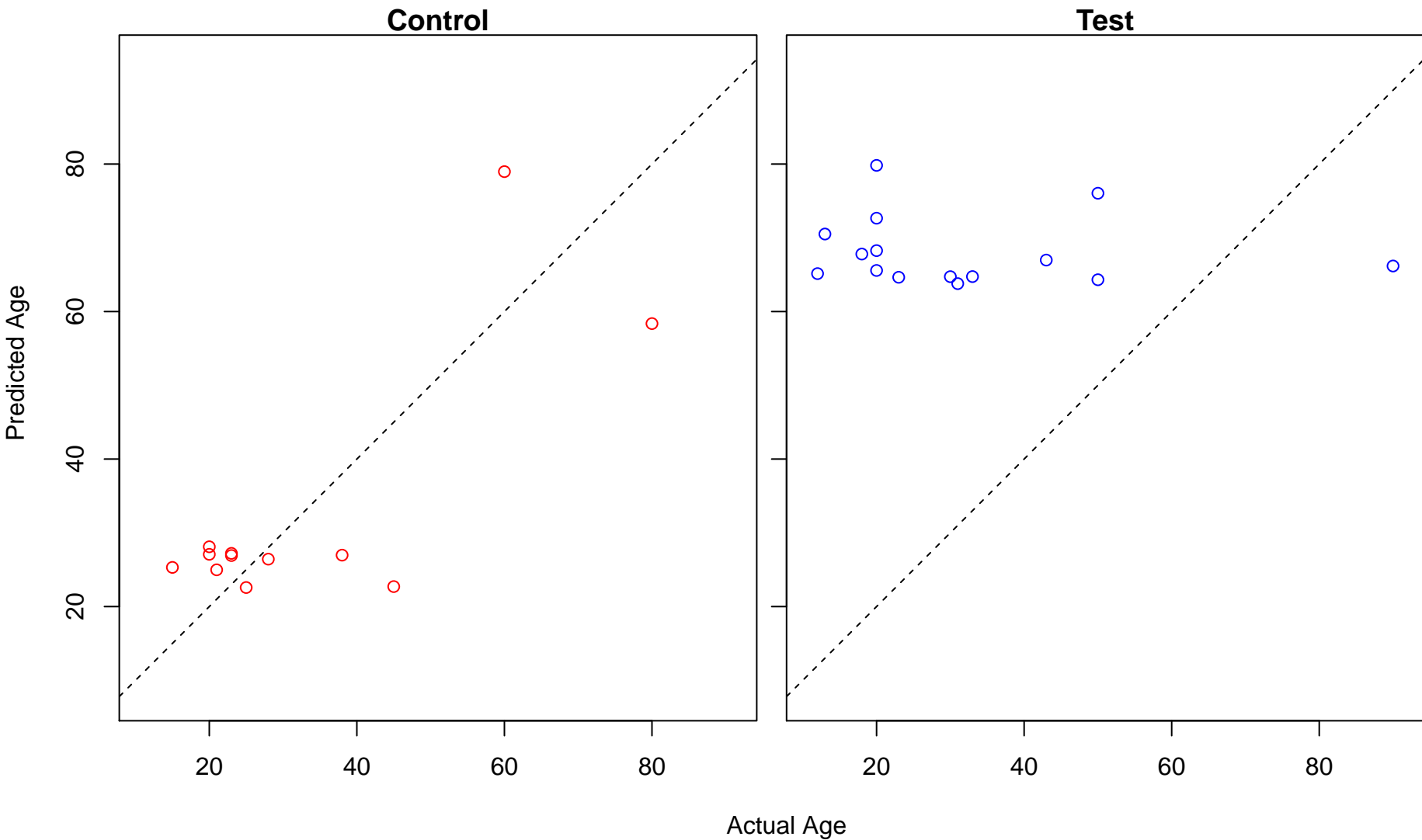


Test

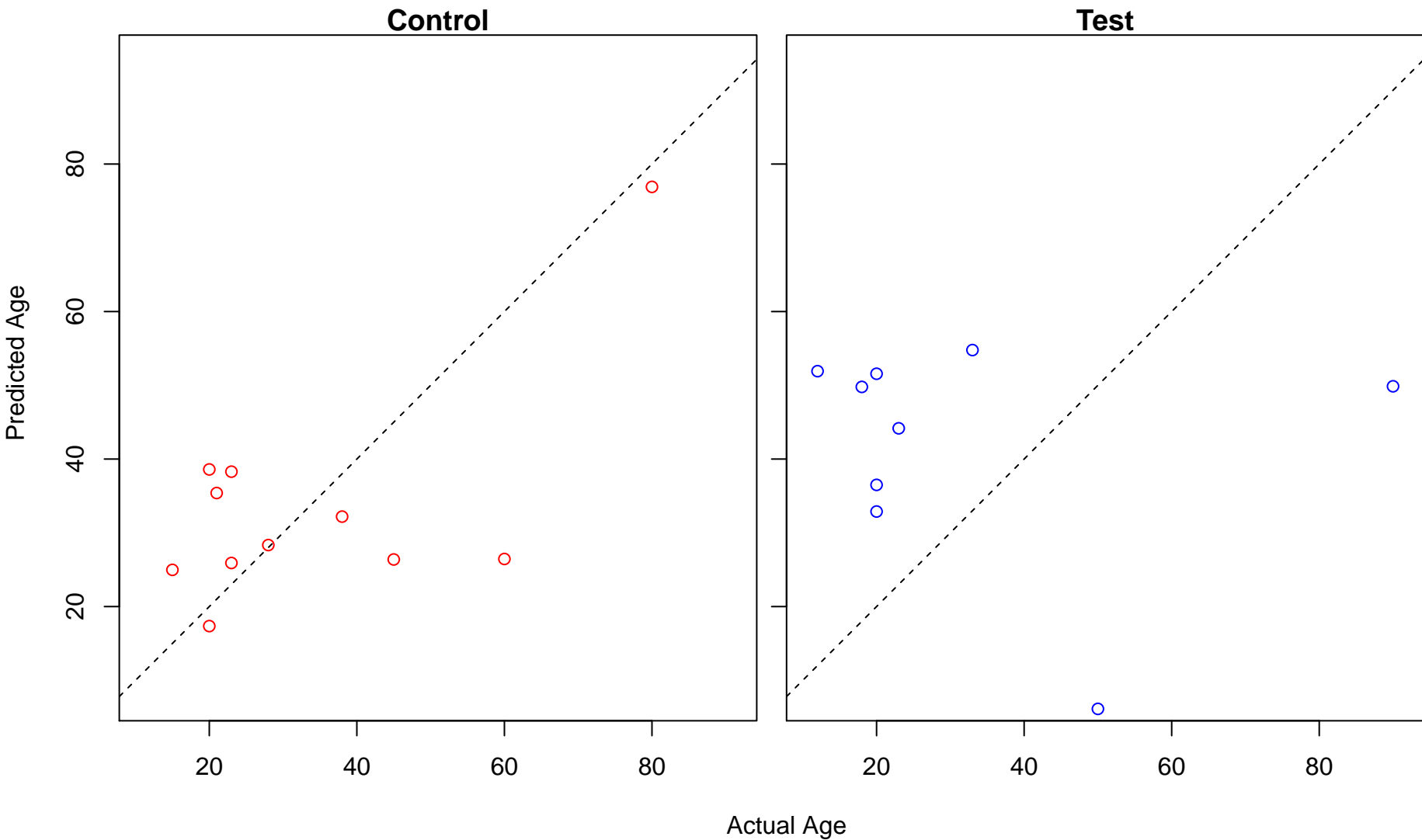


Actual Age

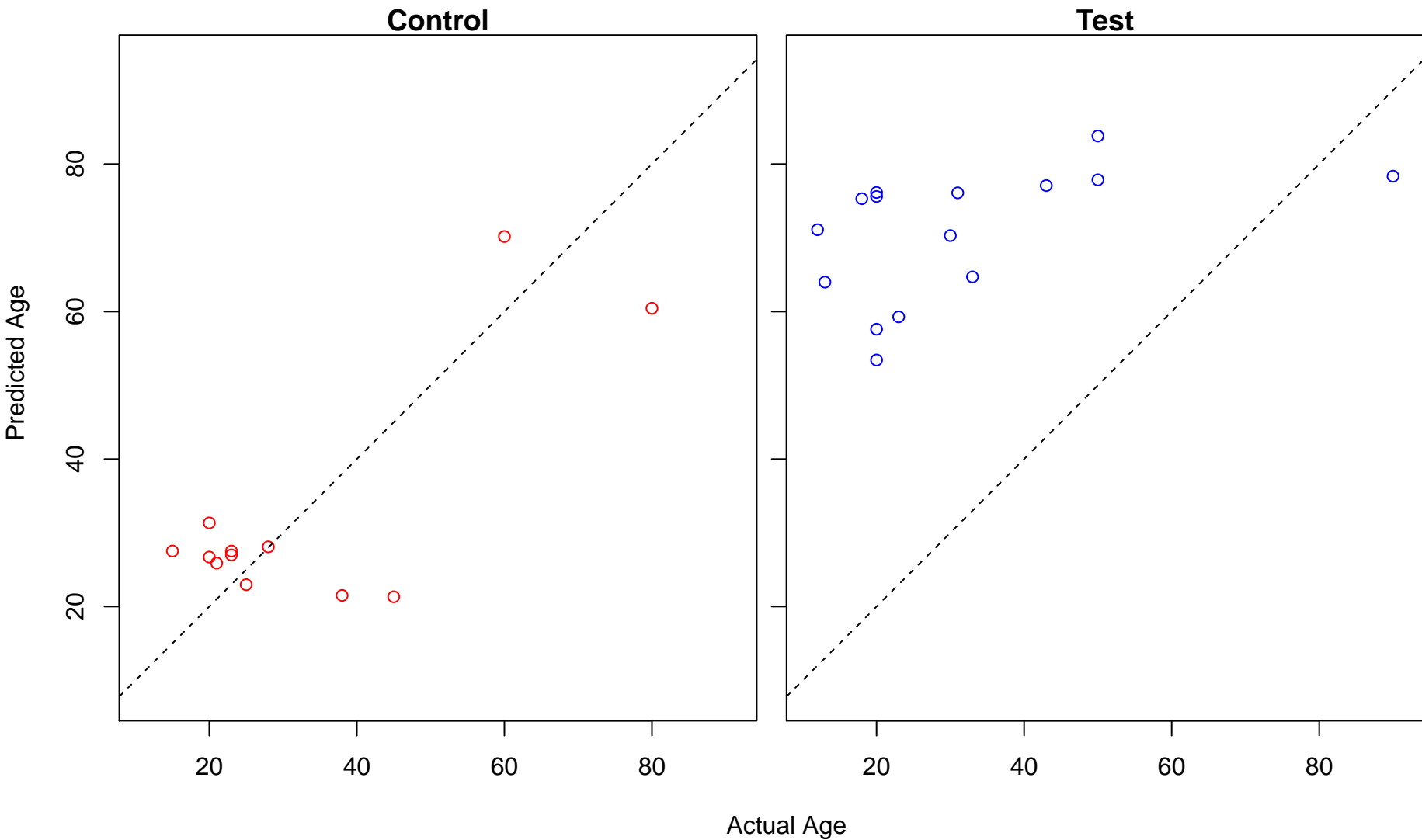
regulation of RNA splicing (Score: 4.417405)



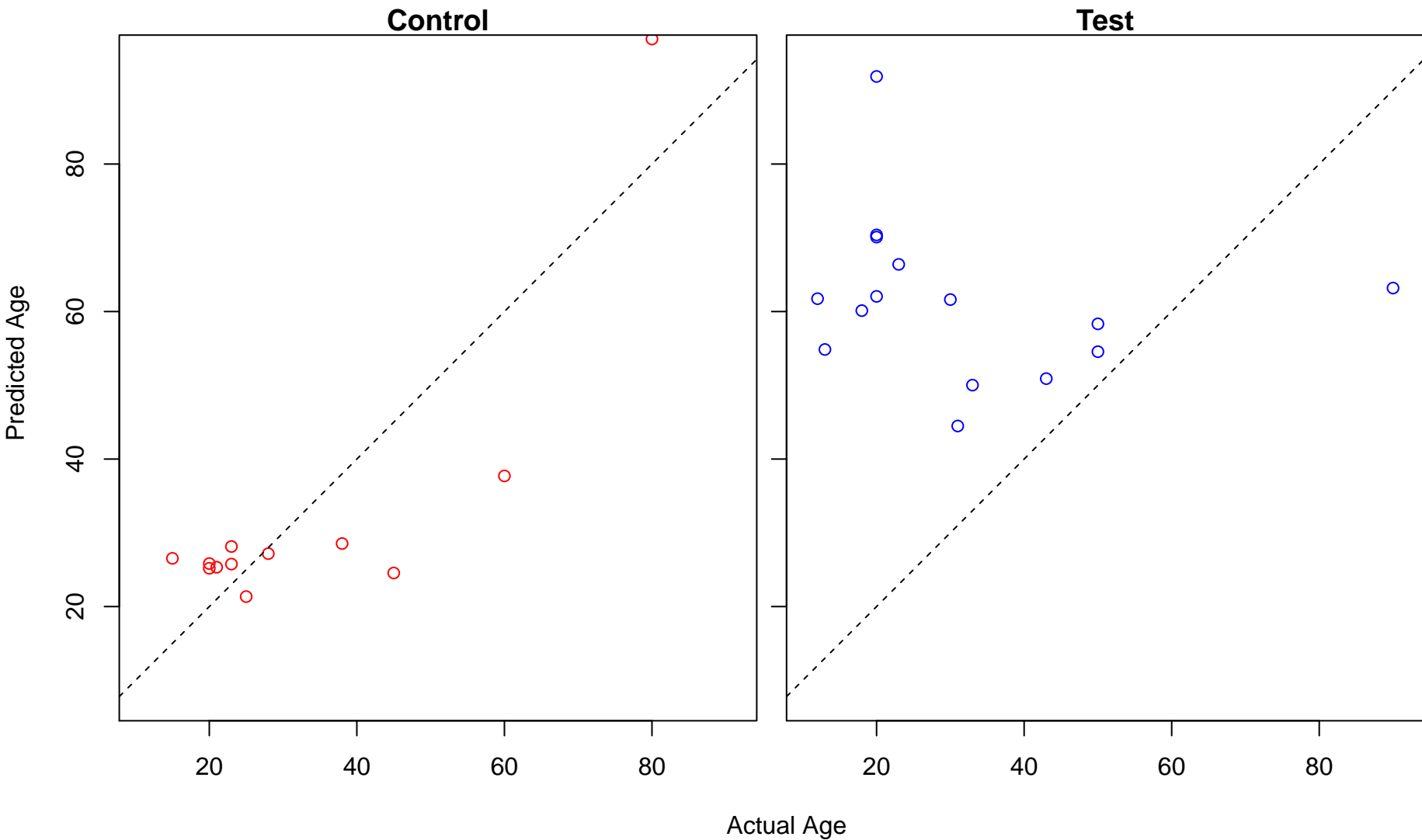
regulation of wound healing, spreading of epidermal cells (Score: 4.413318)



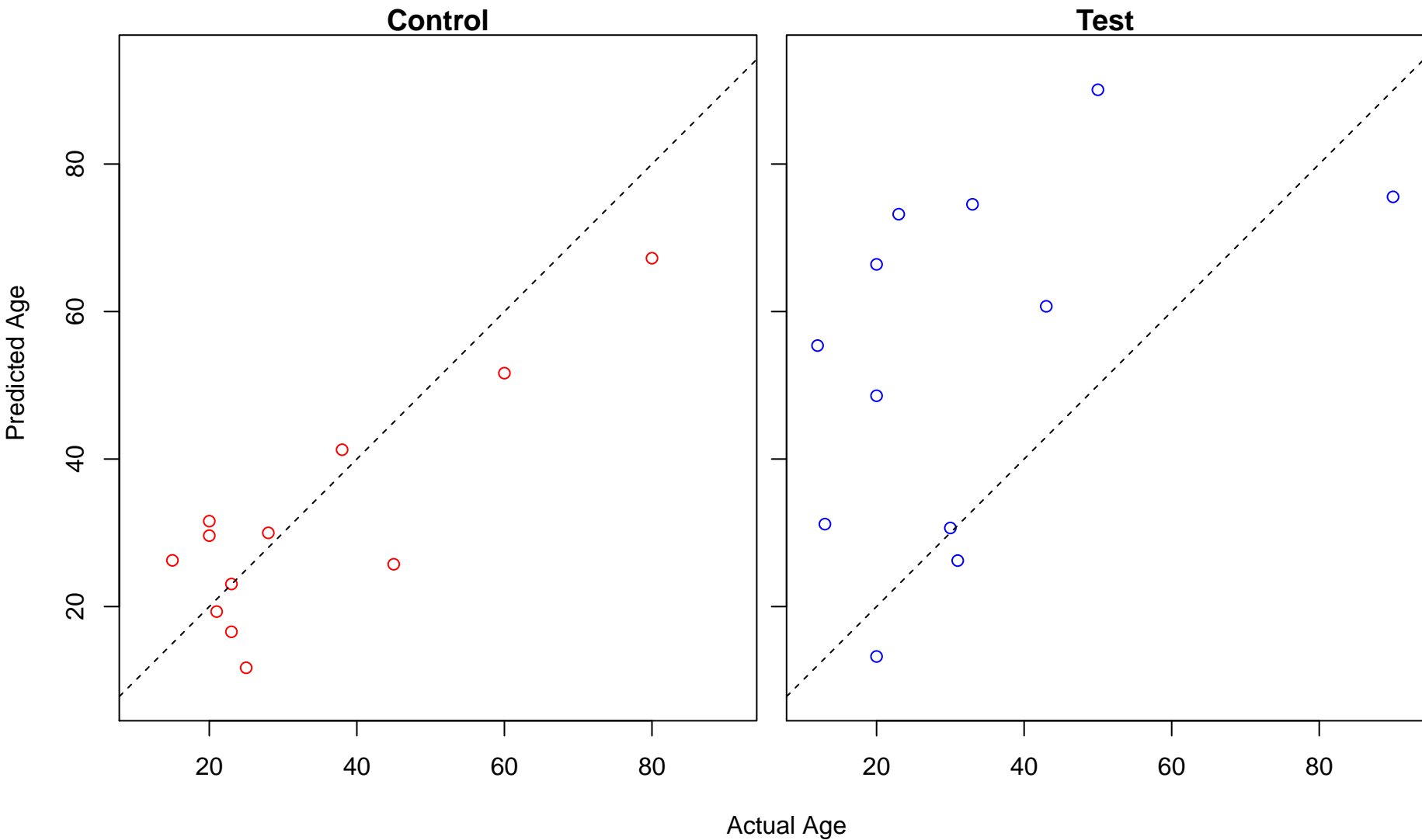
regulation of sodium ion transmembrane transporter activity (Score: 4.412512)



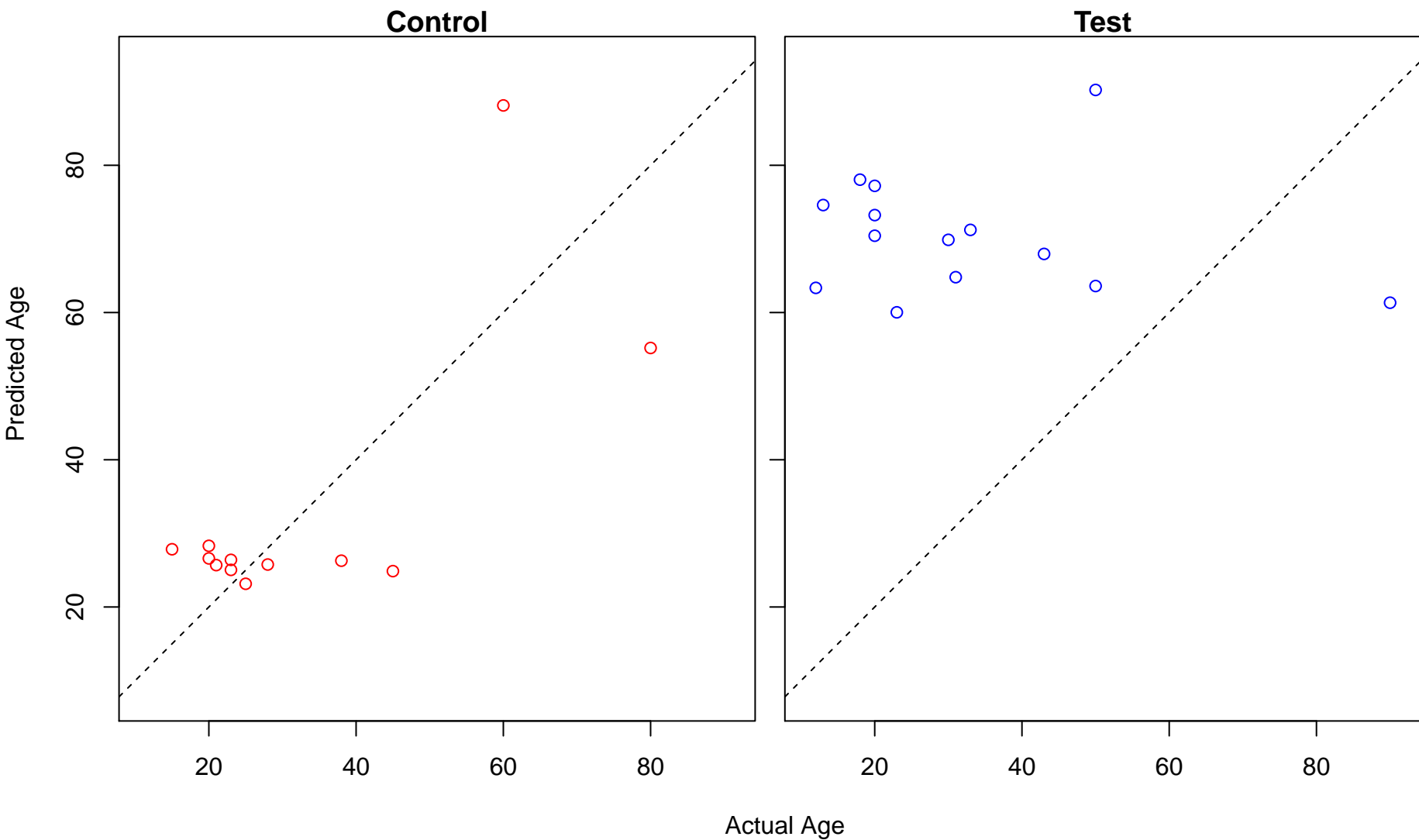
regulation of cellular ketone metabolic process (Score: 4.412143)



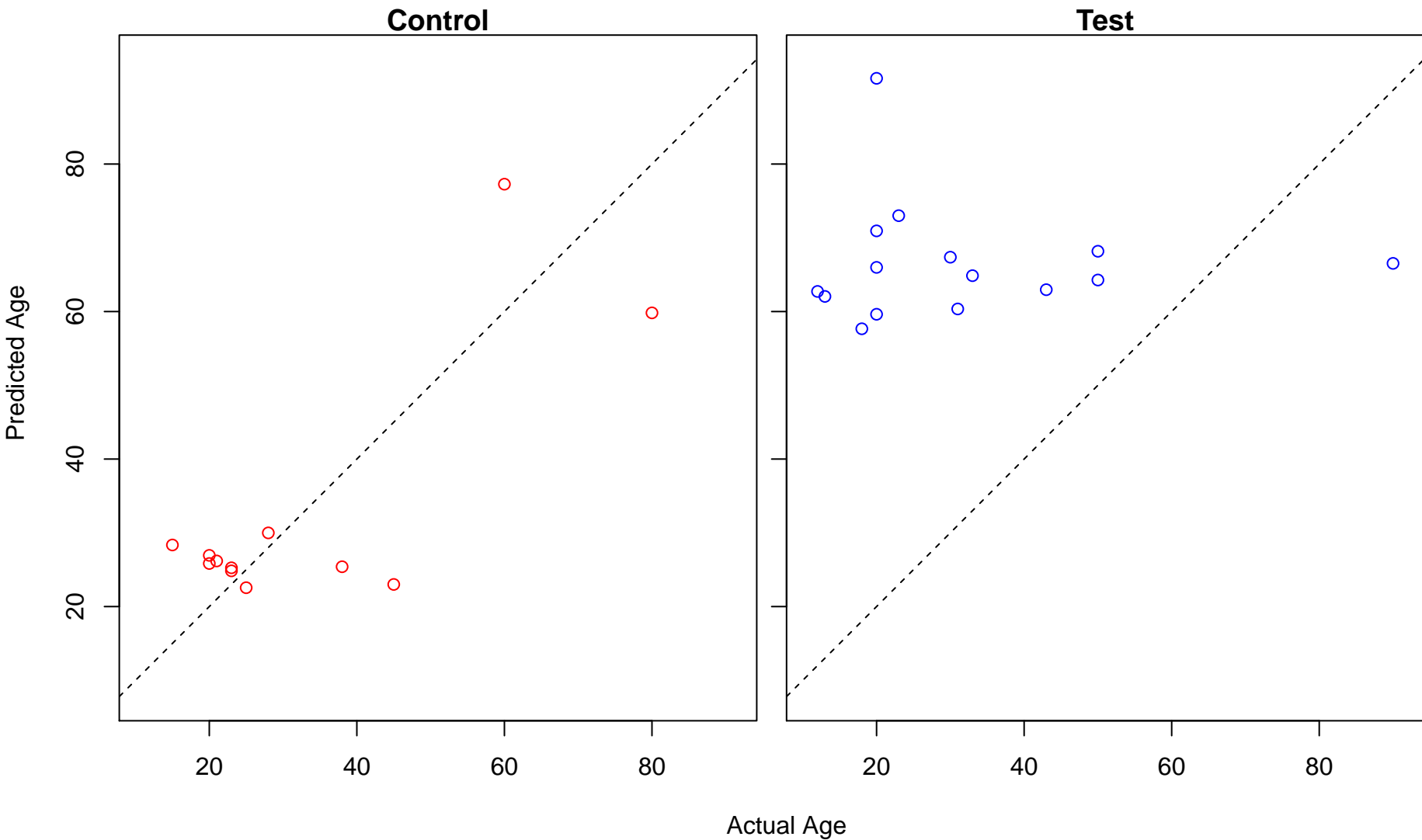
renal tubule development (Score: 4.410443)



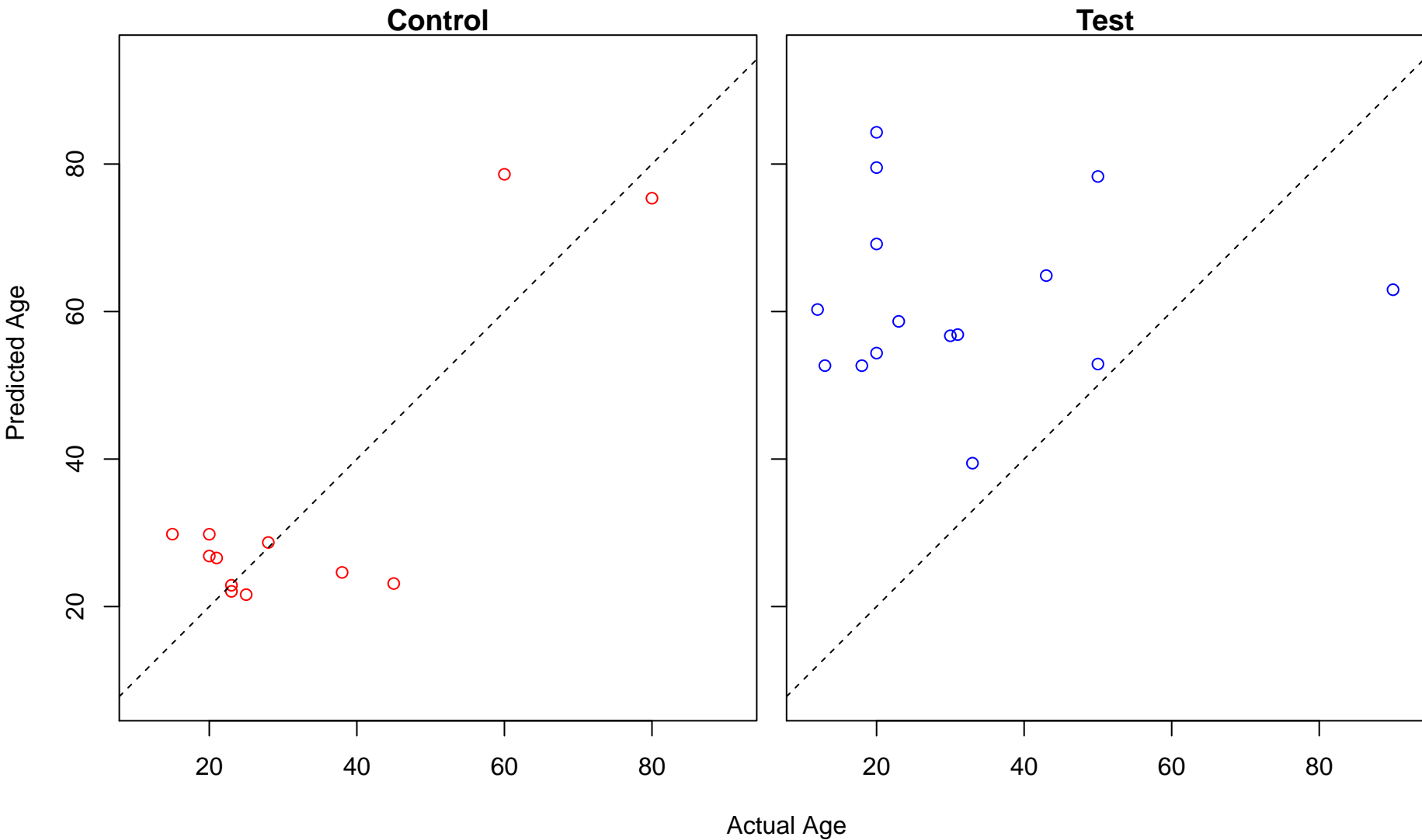
regulation of membrane permeability (Score: 4.408136)



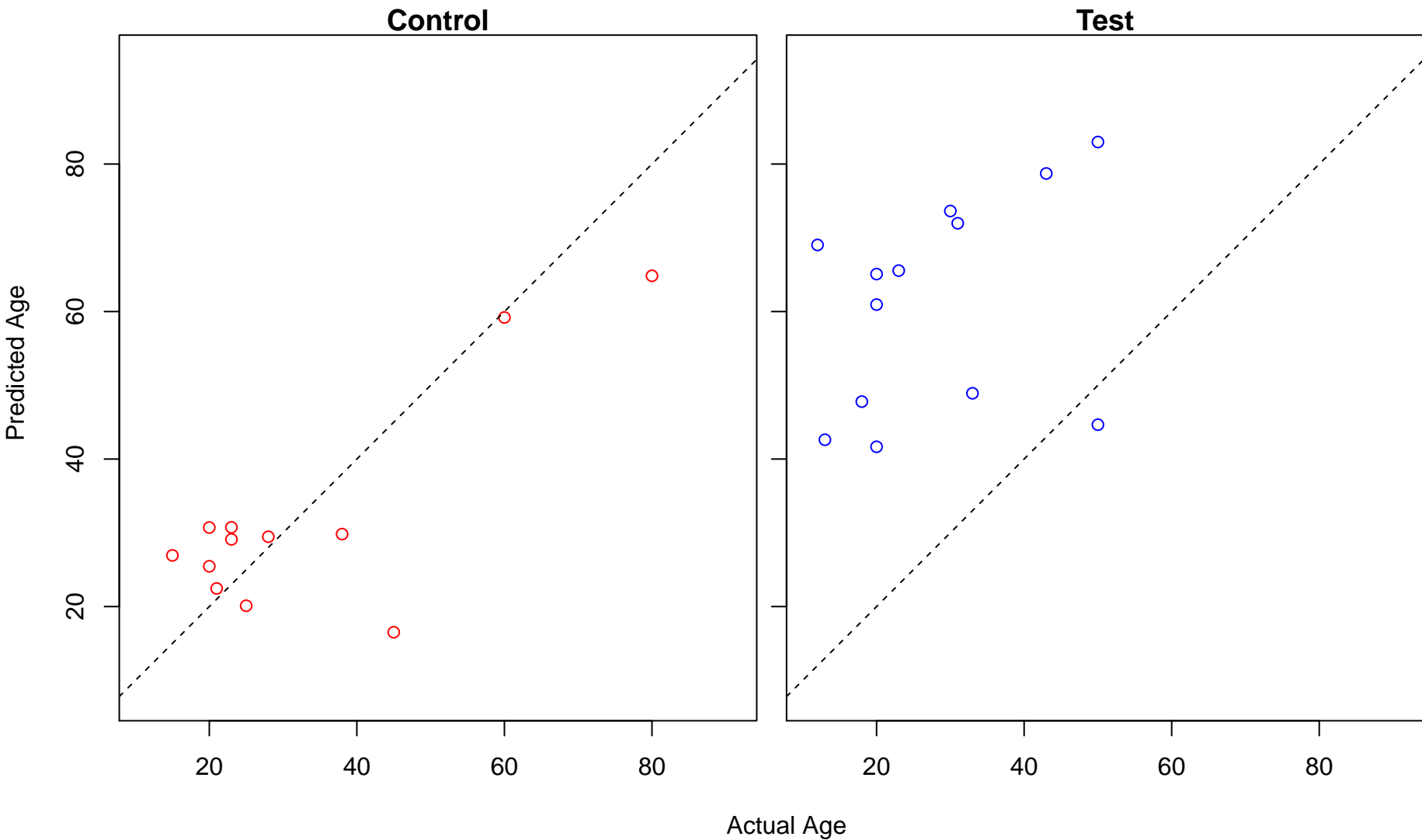
negative regulation of myeloid cell differentiation (Score: 4.407884)



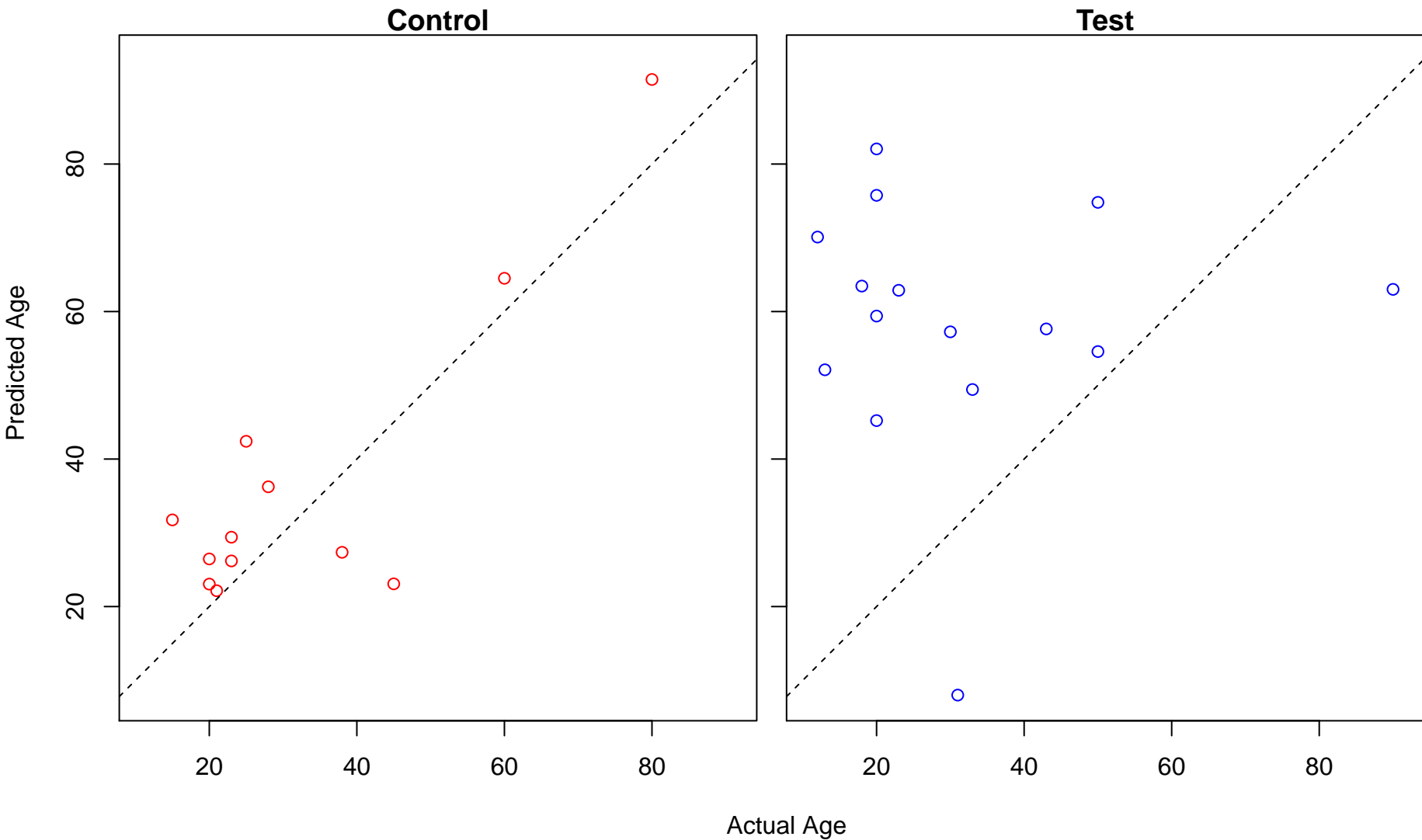
ganglioside metabolic process (Score: 4.404047)



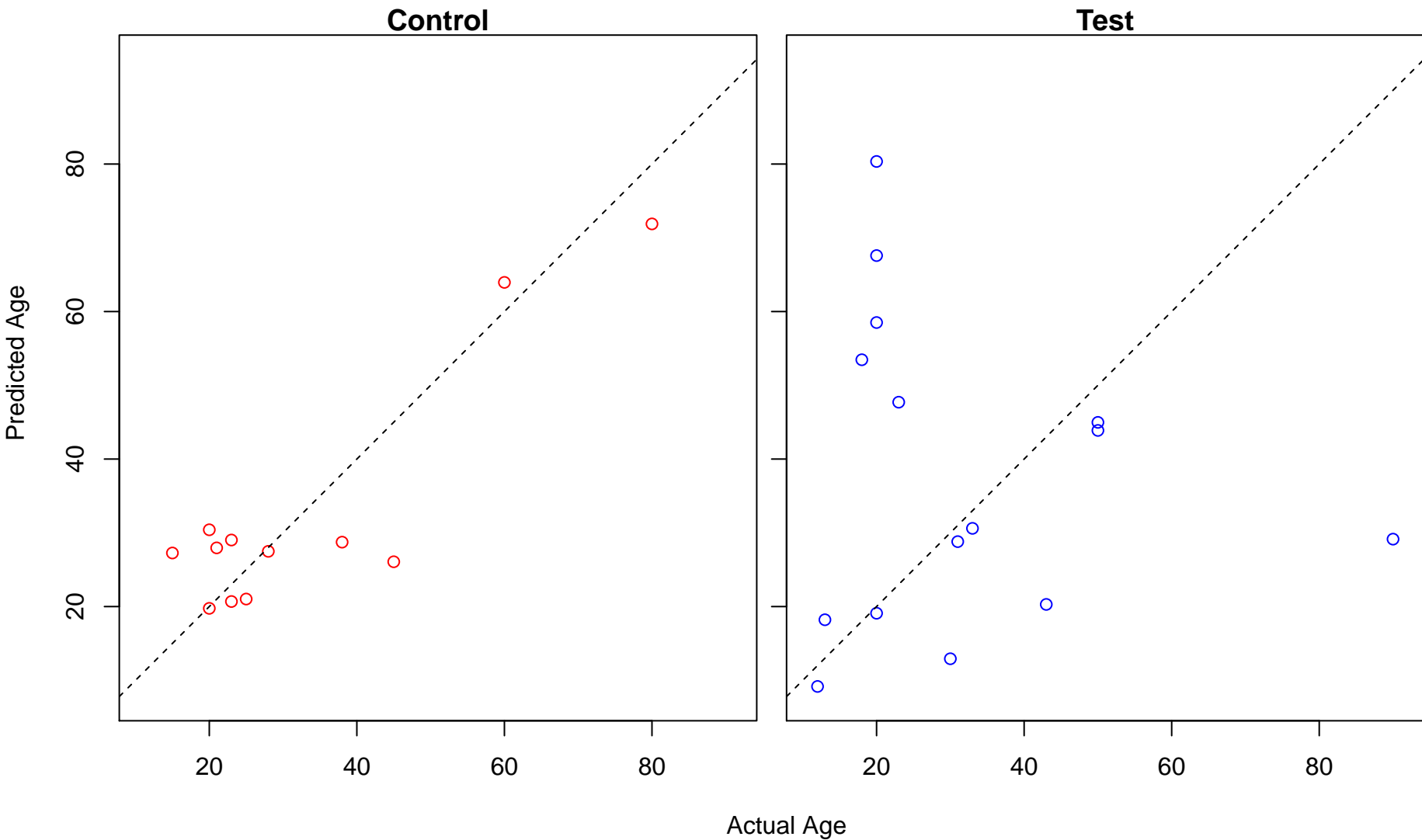
establishment or maintenance of epithelial cell apical/basal polarity (Score: 4.403584)



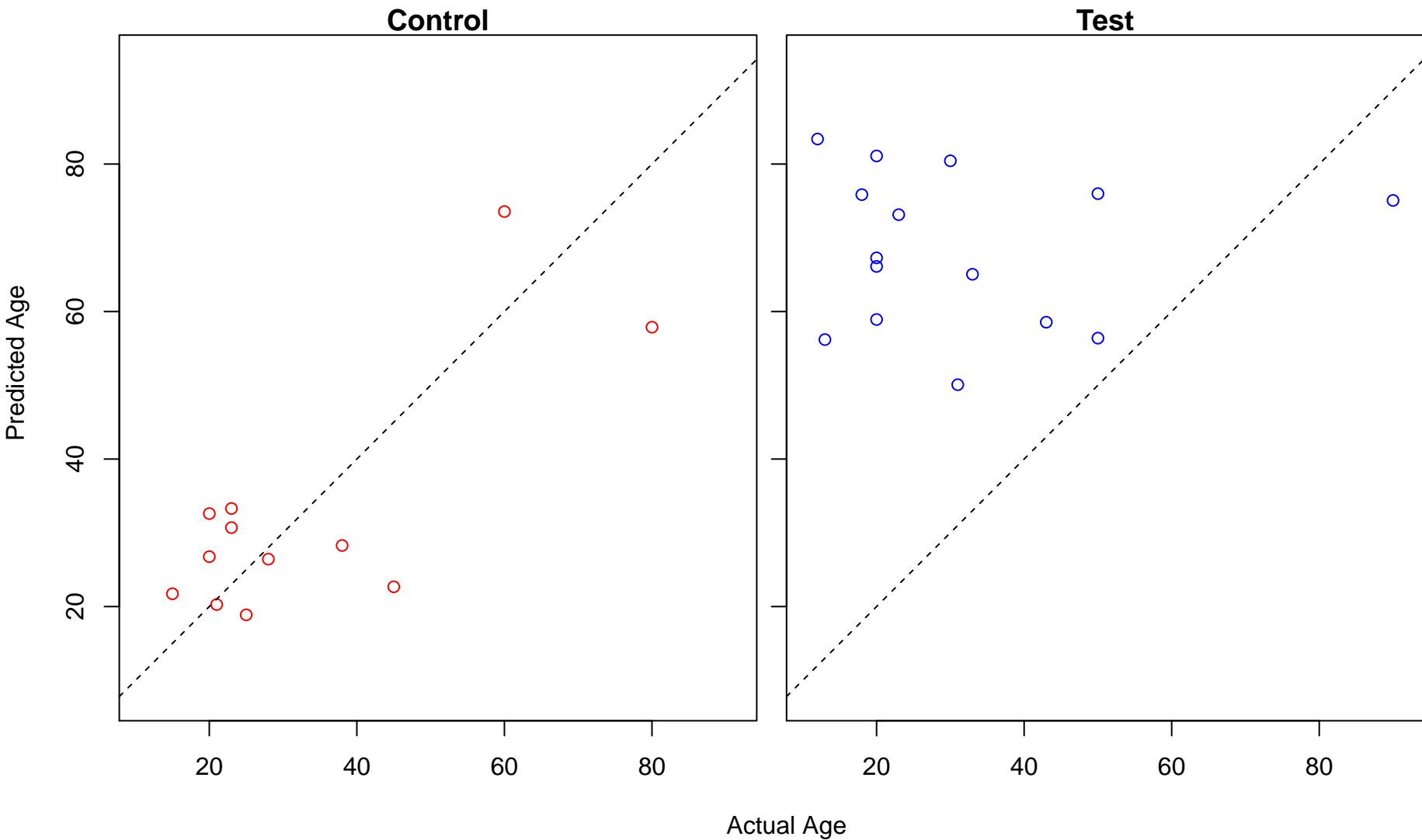
regulation of systemic arterial blood pressure (Score: 4.400952)



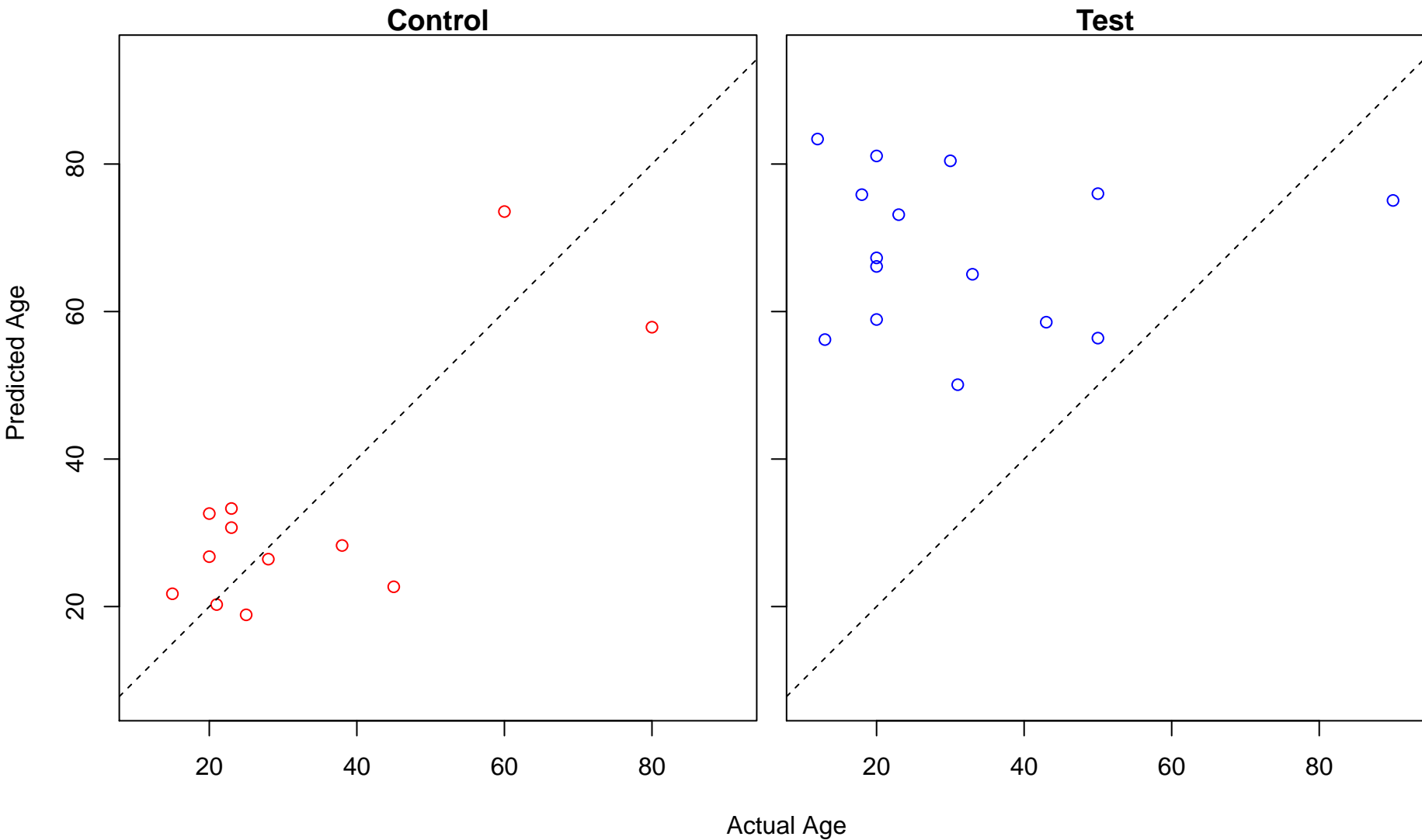
detection of chemical stimulus (Score: 4.400548)



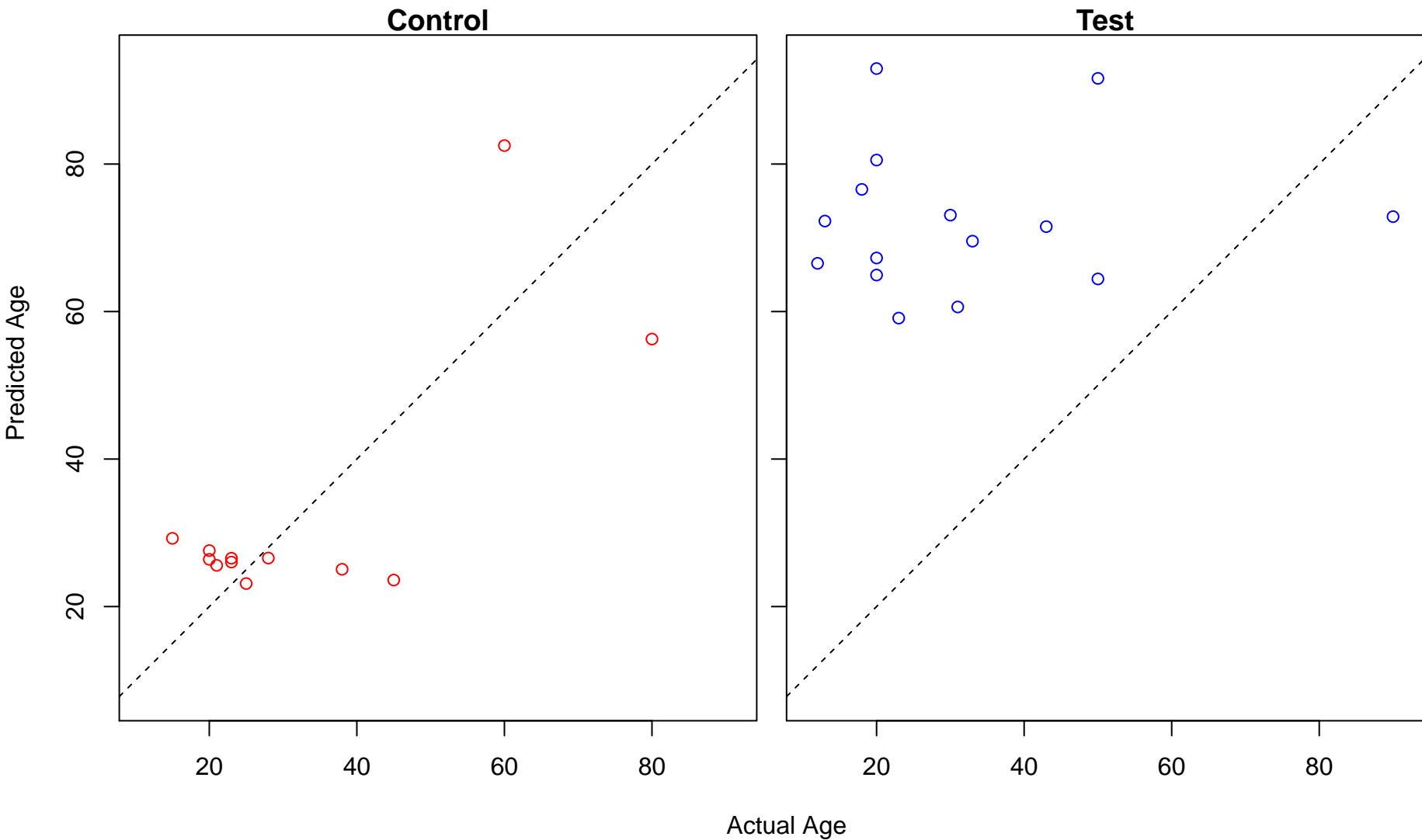
response to forskolin (Score: 4.399085)



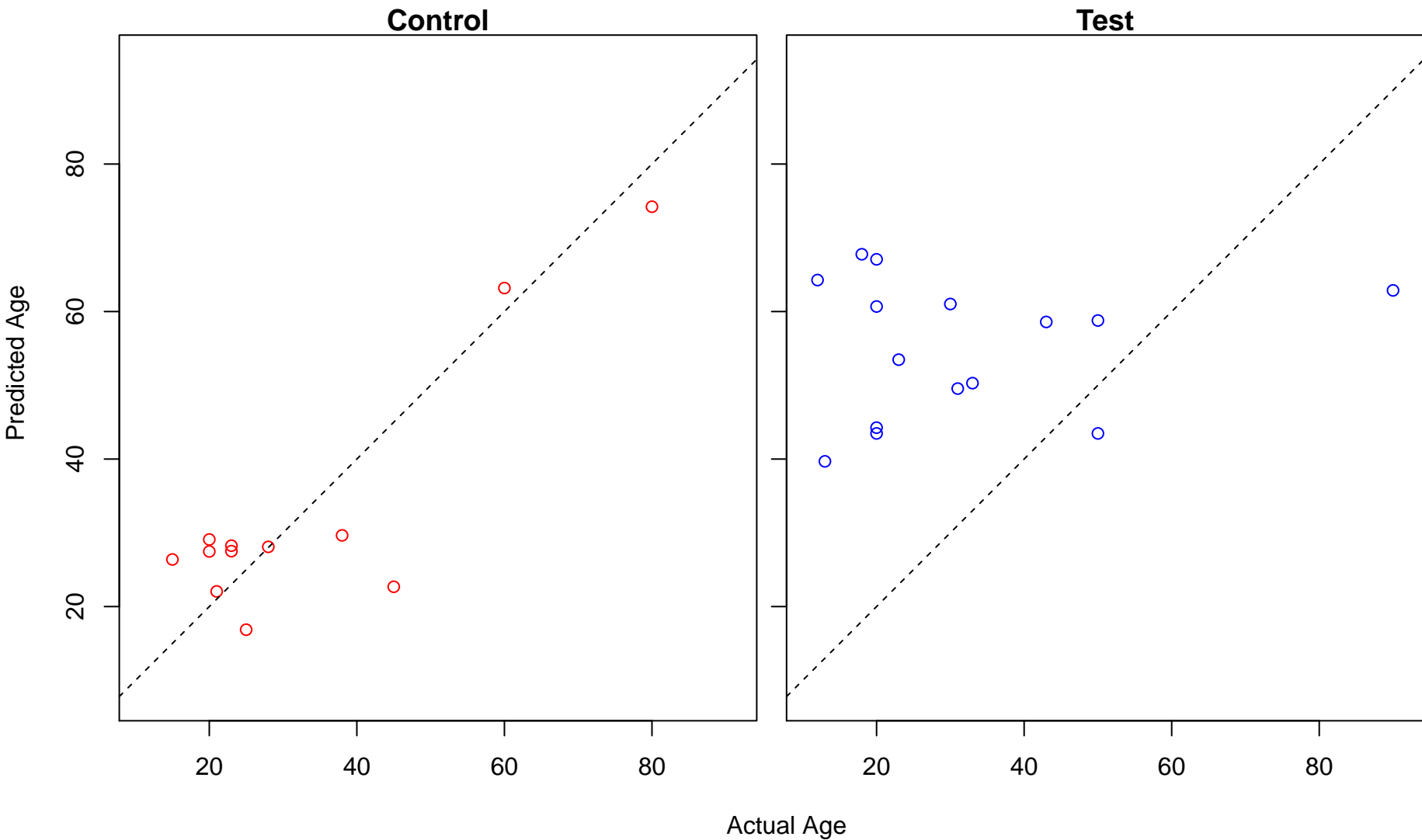
cellular response to forskolin (Score: 4.399085)



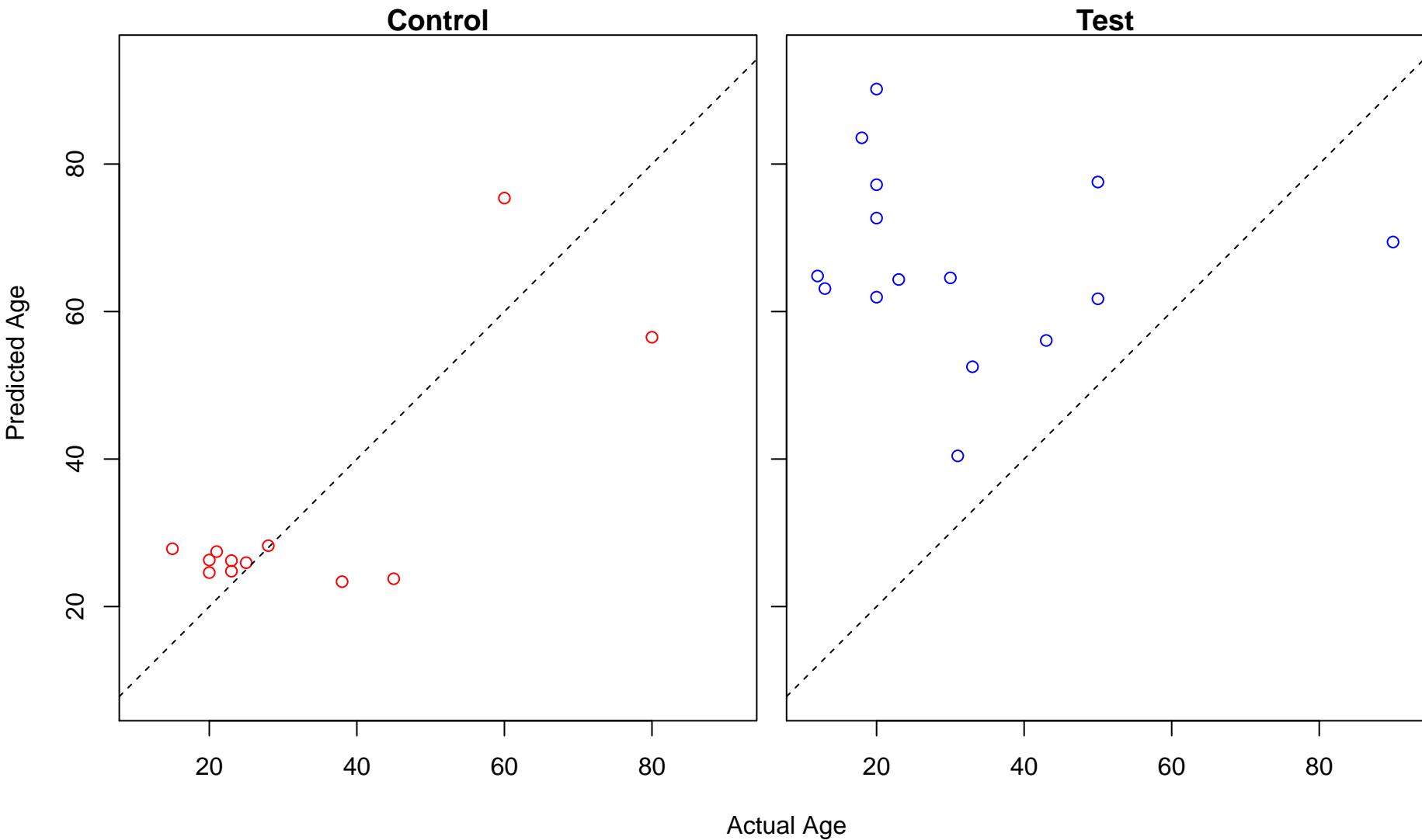
apical junction assembly (Score: 4.396822)



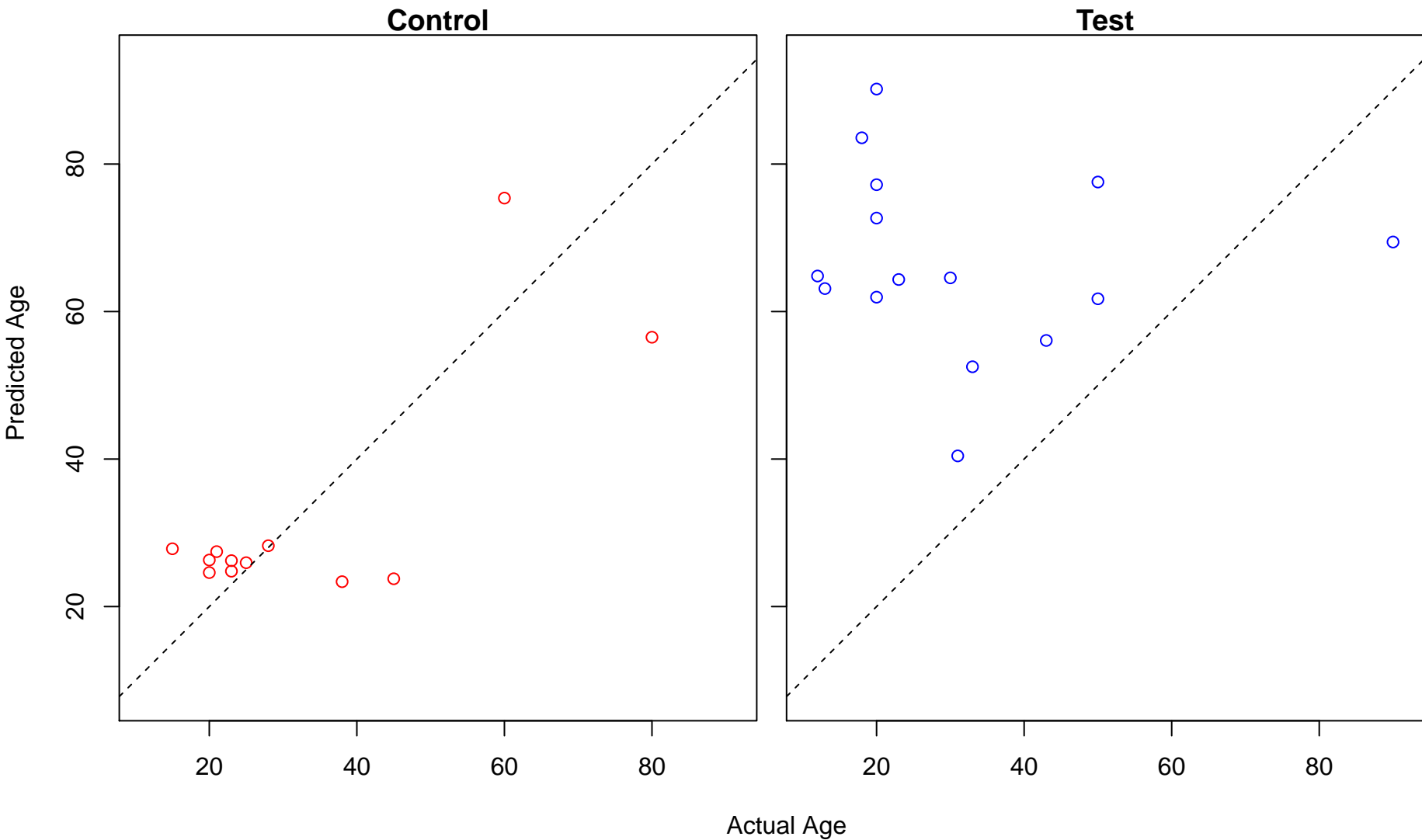
vacuole organization (Score: 4.395591)



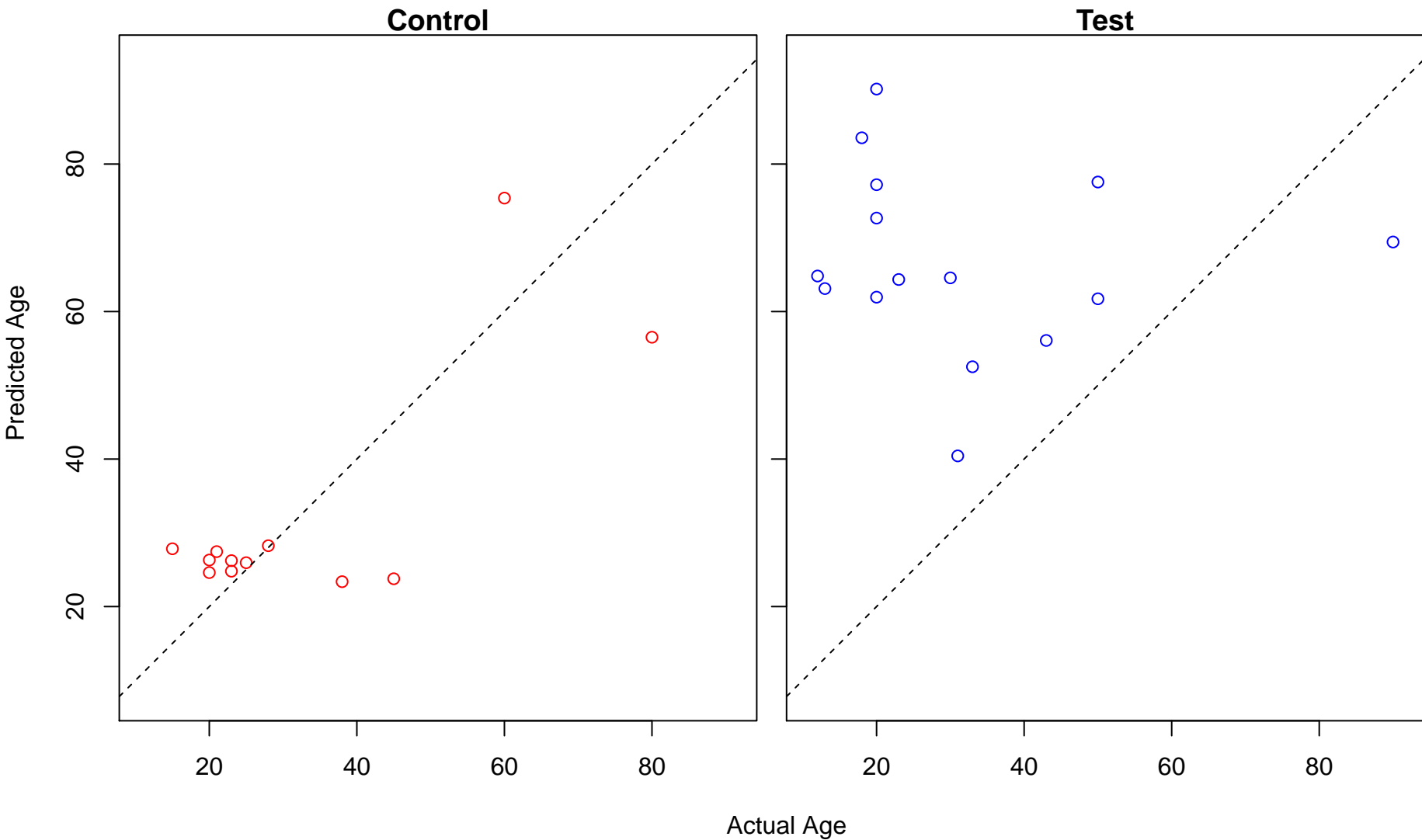
ATP biosynthetic process (Score: 4.393740)



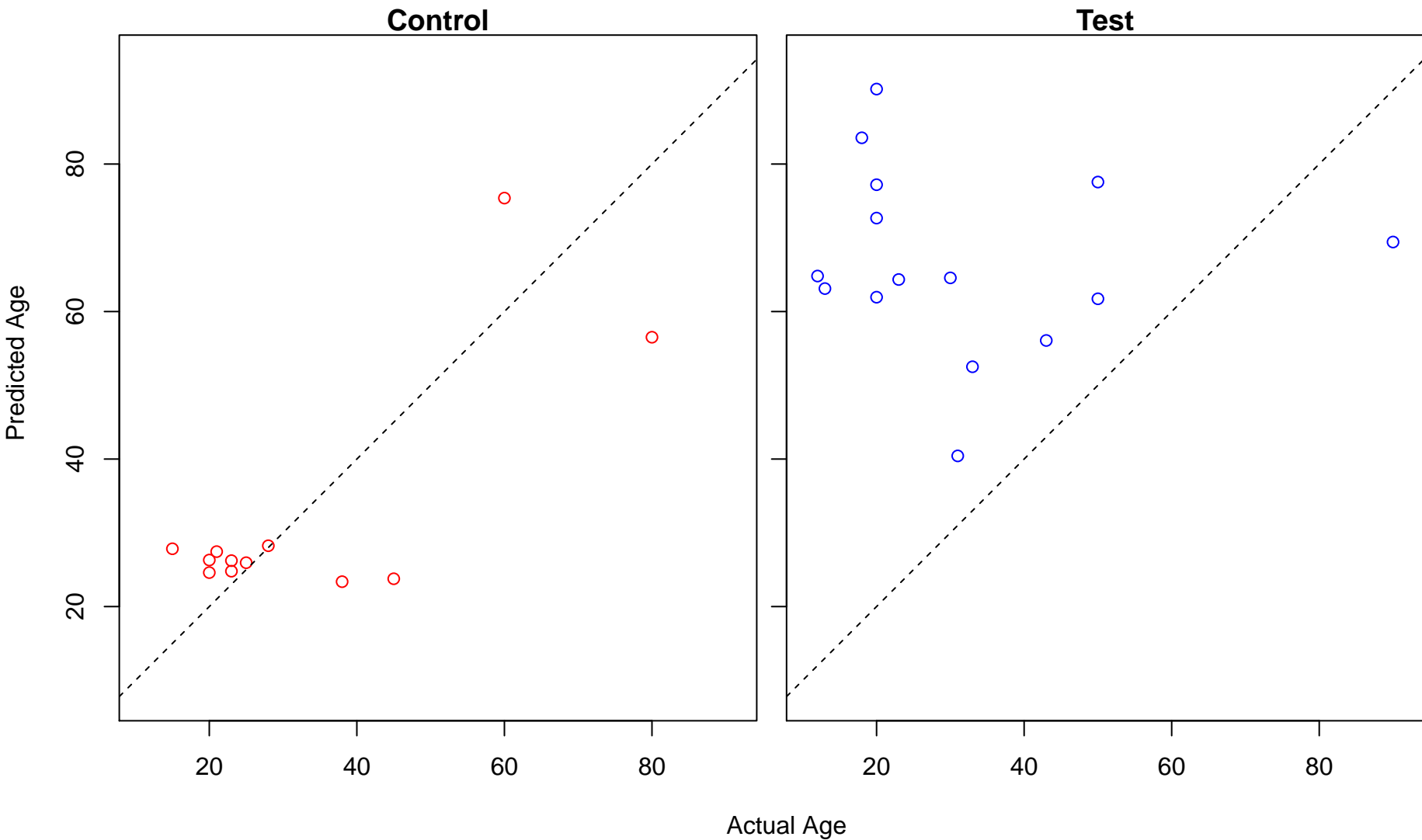
purine nucleoside triphosphate biosynthetic process (Score: 4.393740)



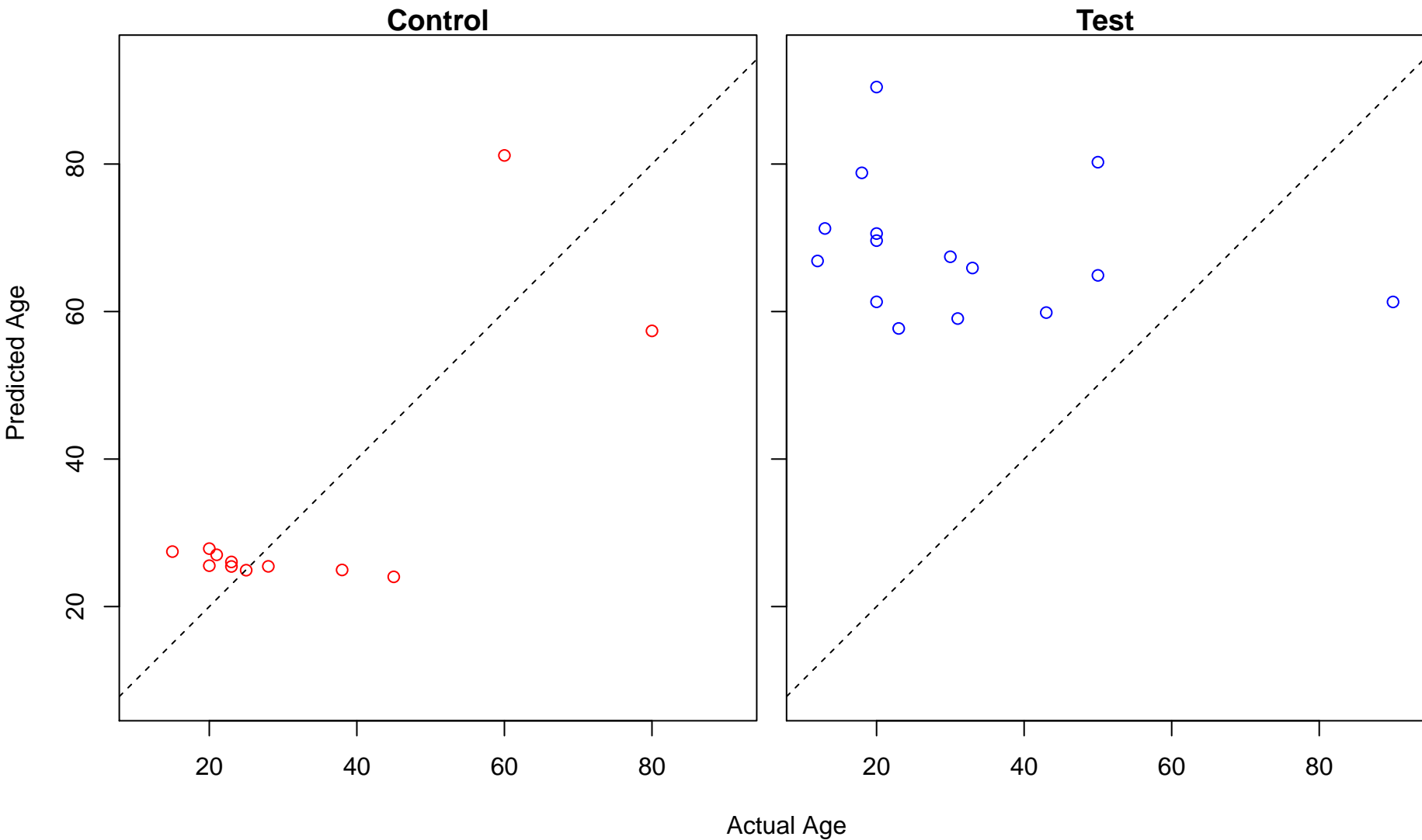
purine ribonucleoside triphosphate biosynthetic process (Score: 4.393740)



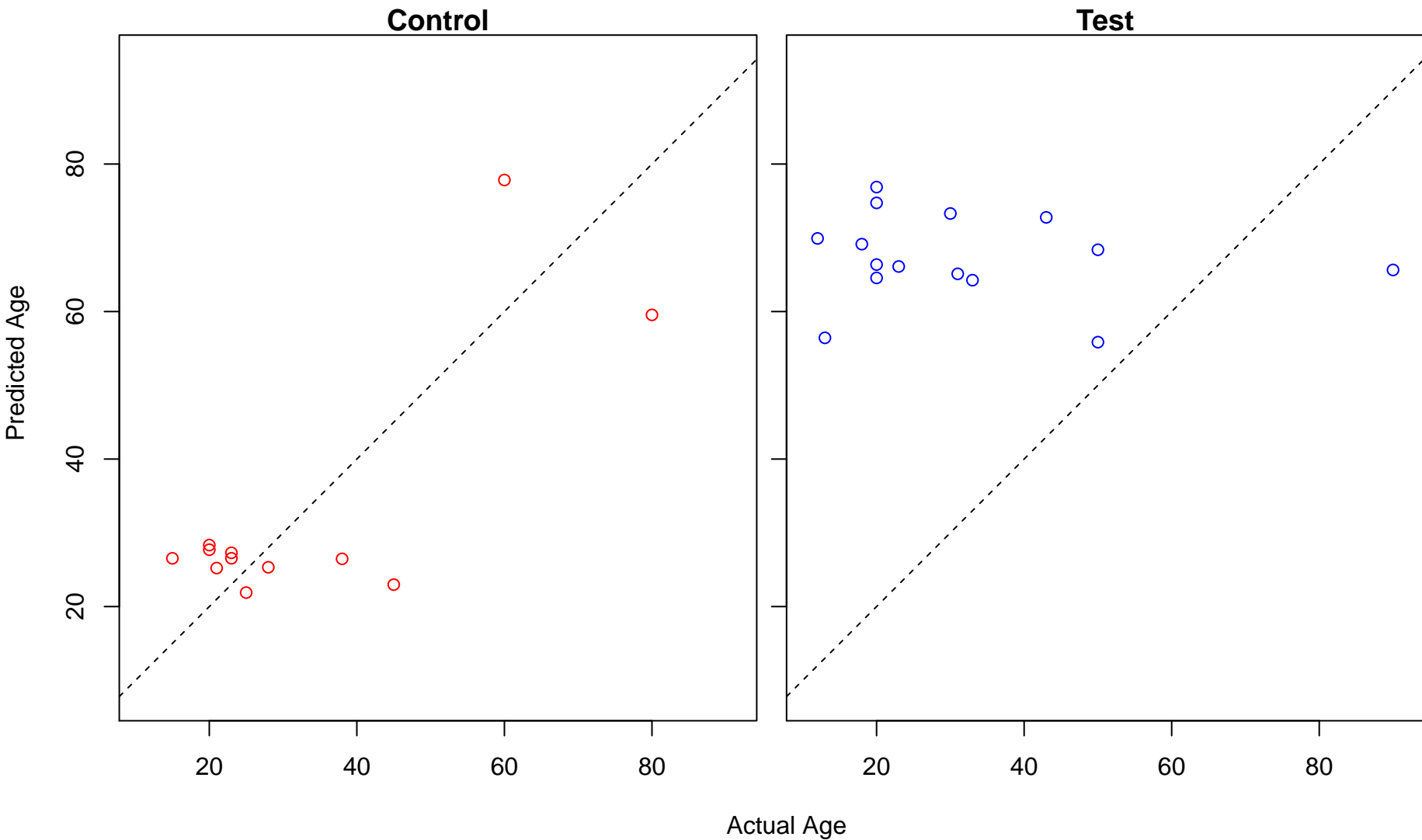
ribonucleoside triphosphate biosynthetic process (Score: 4.393478)



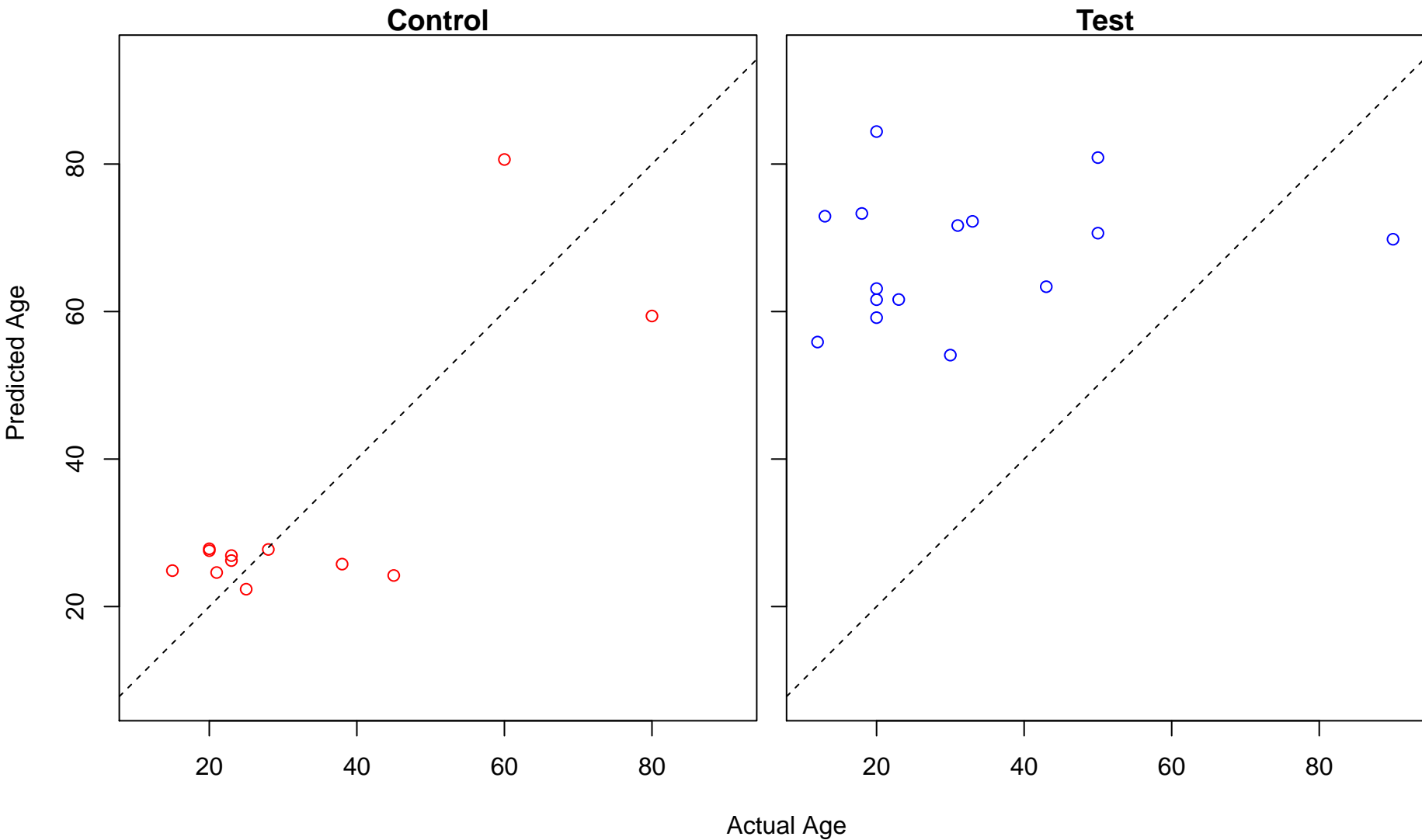
positive regulation of cytoskeleton organization (Score: 4.391272)



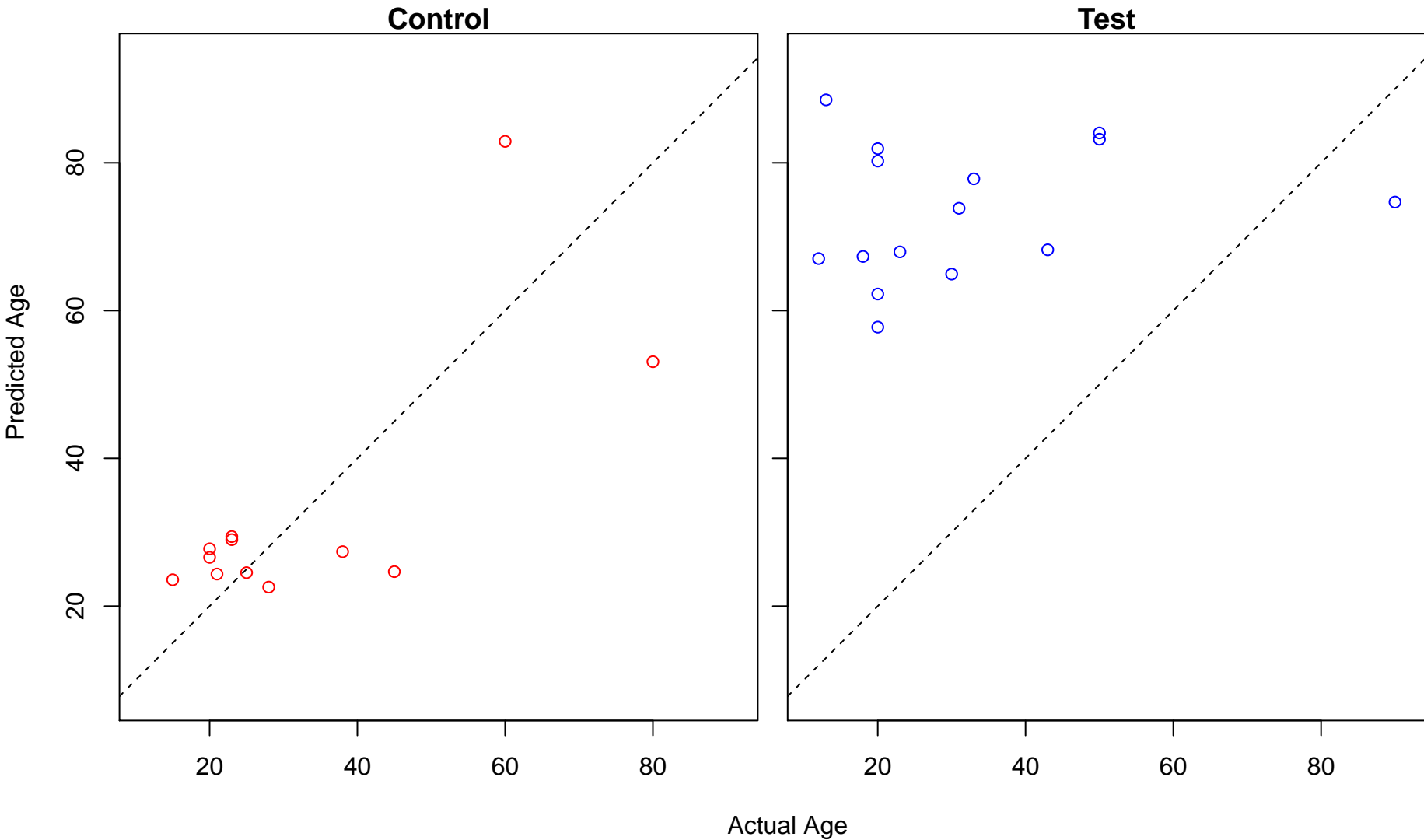
definitive hemopoiesis (Score: 4.391252)



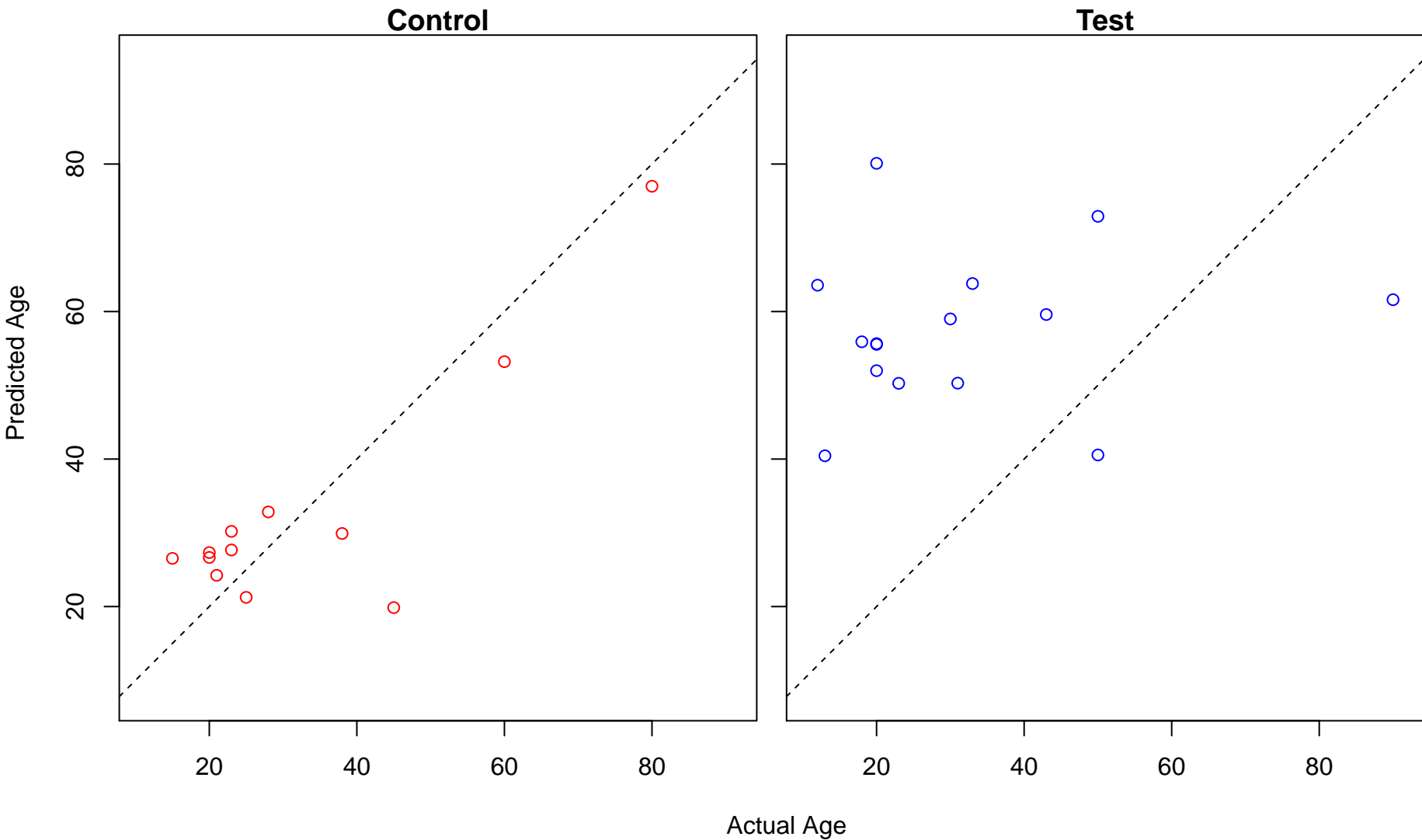
urogenital system development (Score: 4.390697)



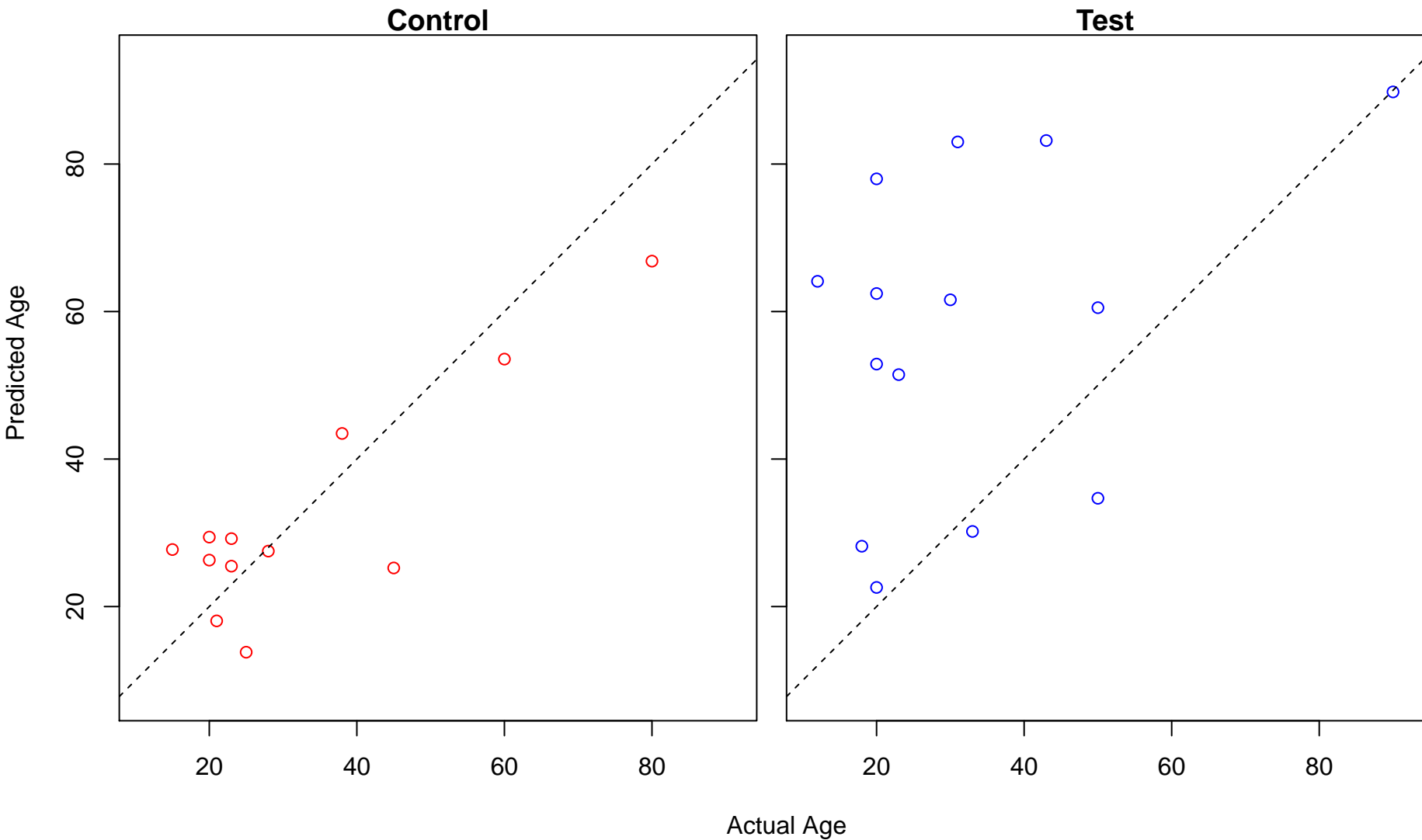
syncytium formation by plasma membrane fusion (Score: 4.390139)



actin filament-based movement (Score: 4.388468)

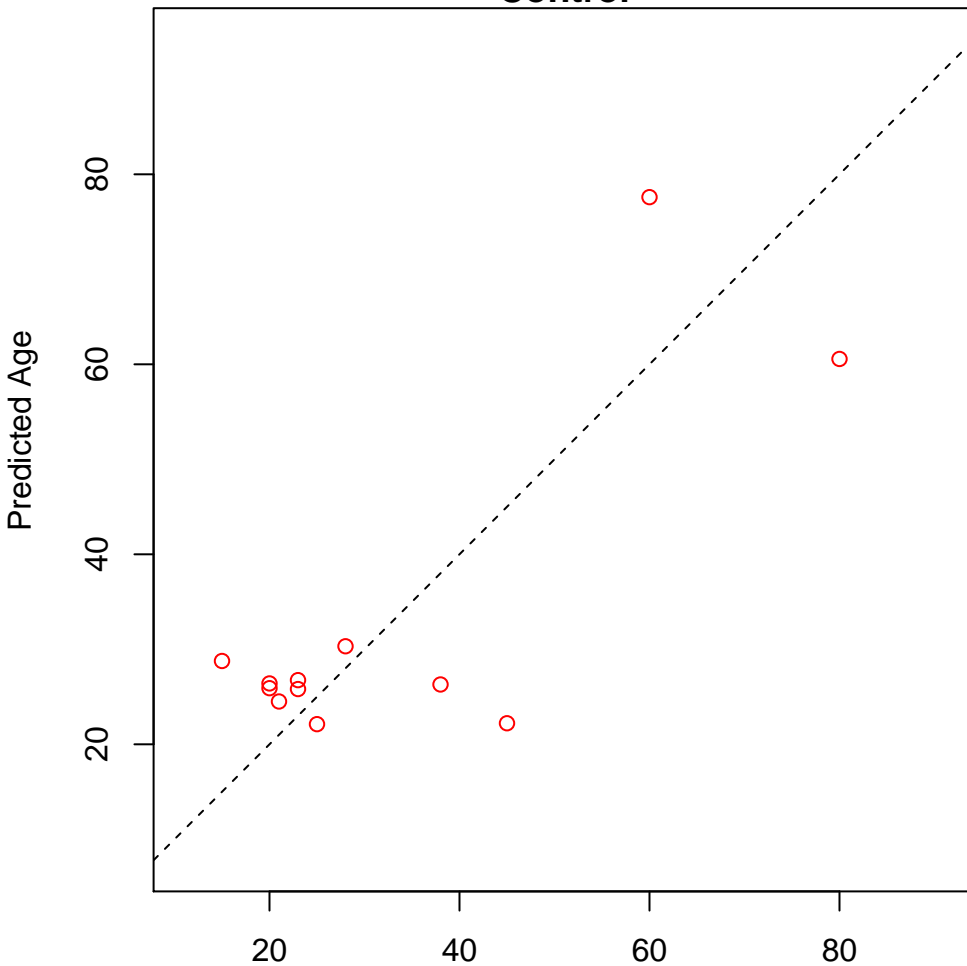


histone deacetylation (Score: 4.386691)

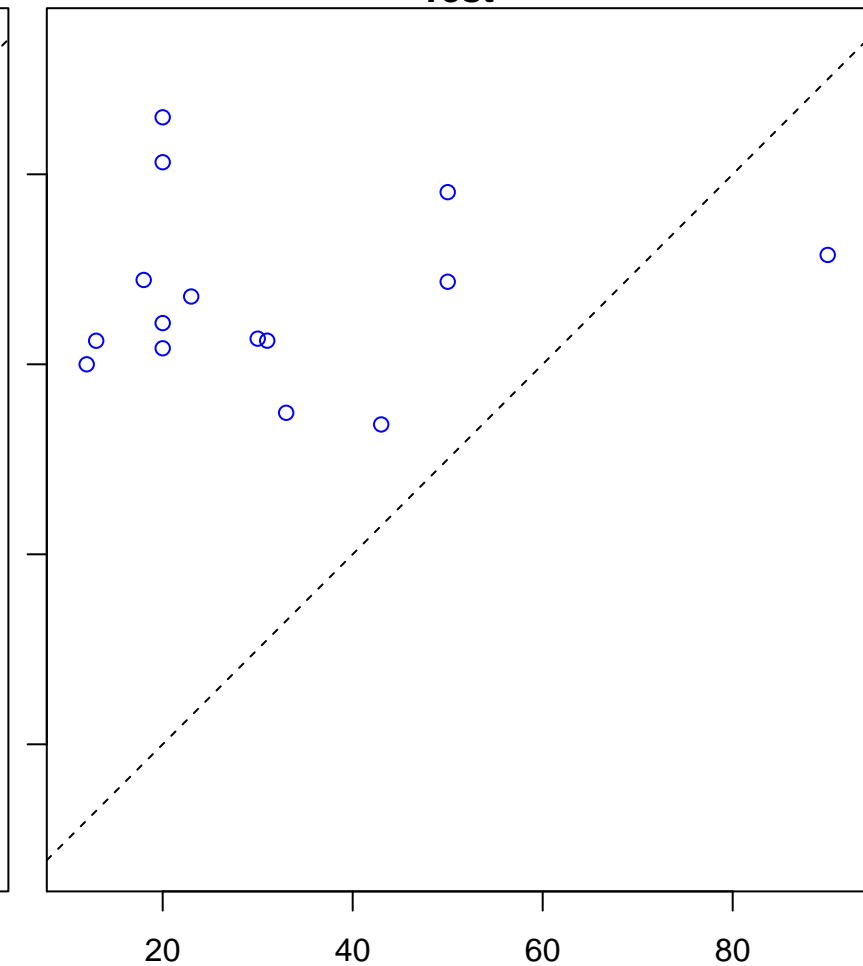


activation of innate immune response (Score: 4.385907)

Control

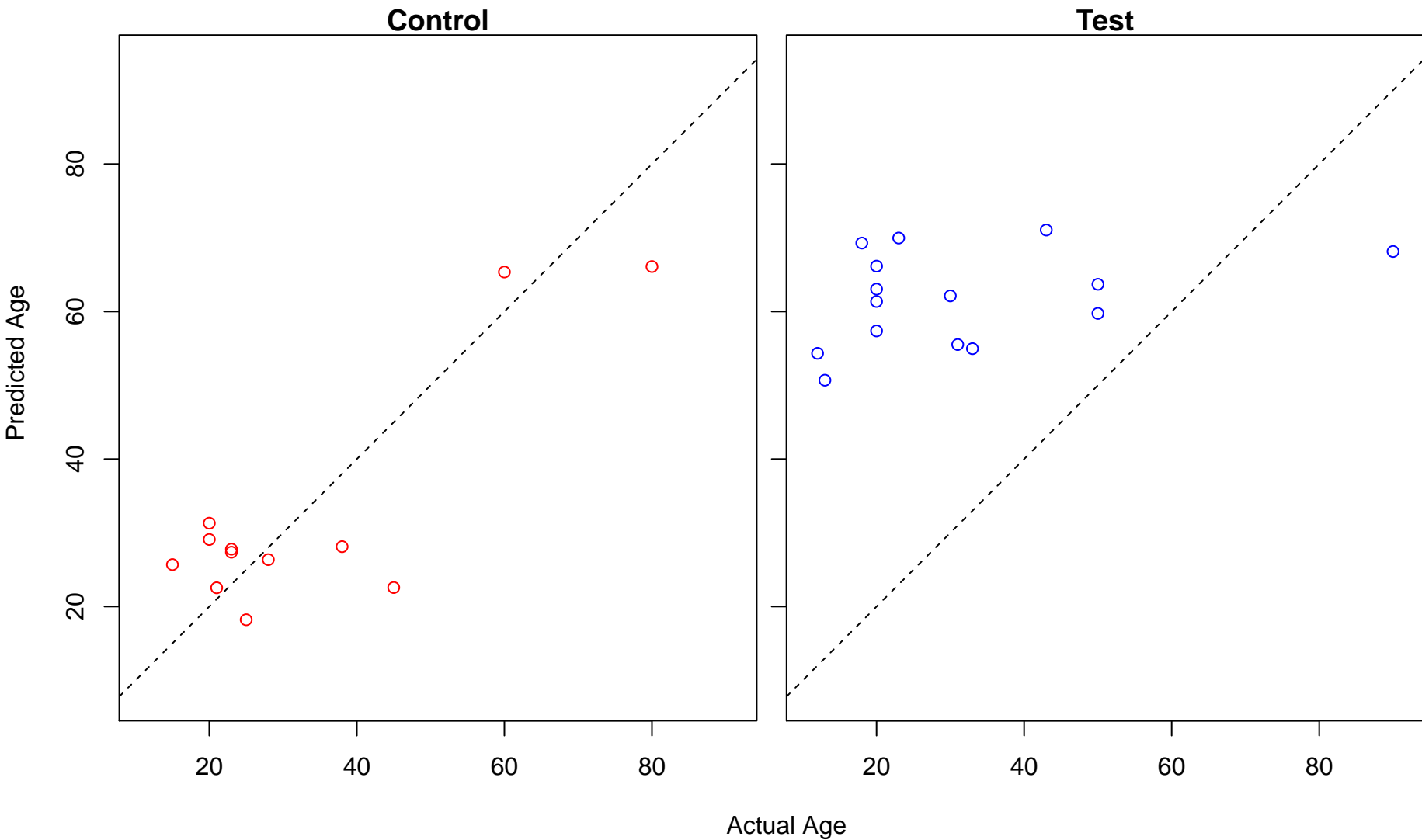


Test

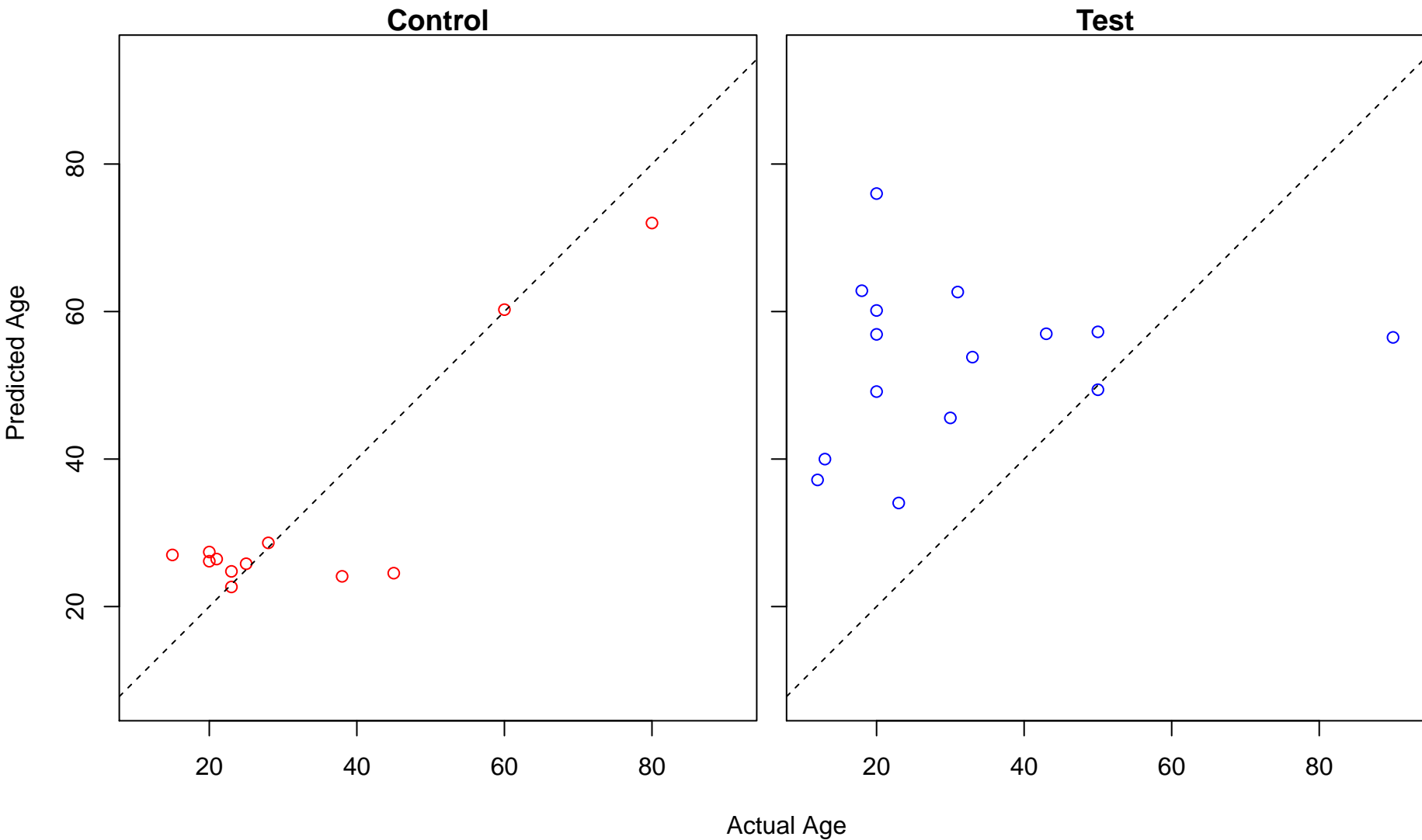


Actual Age

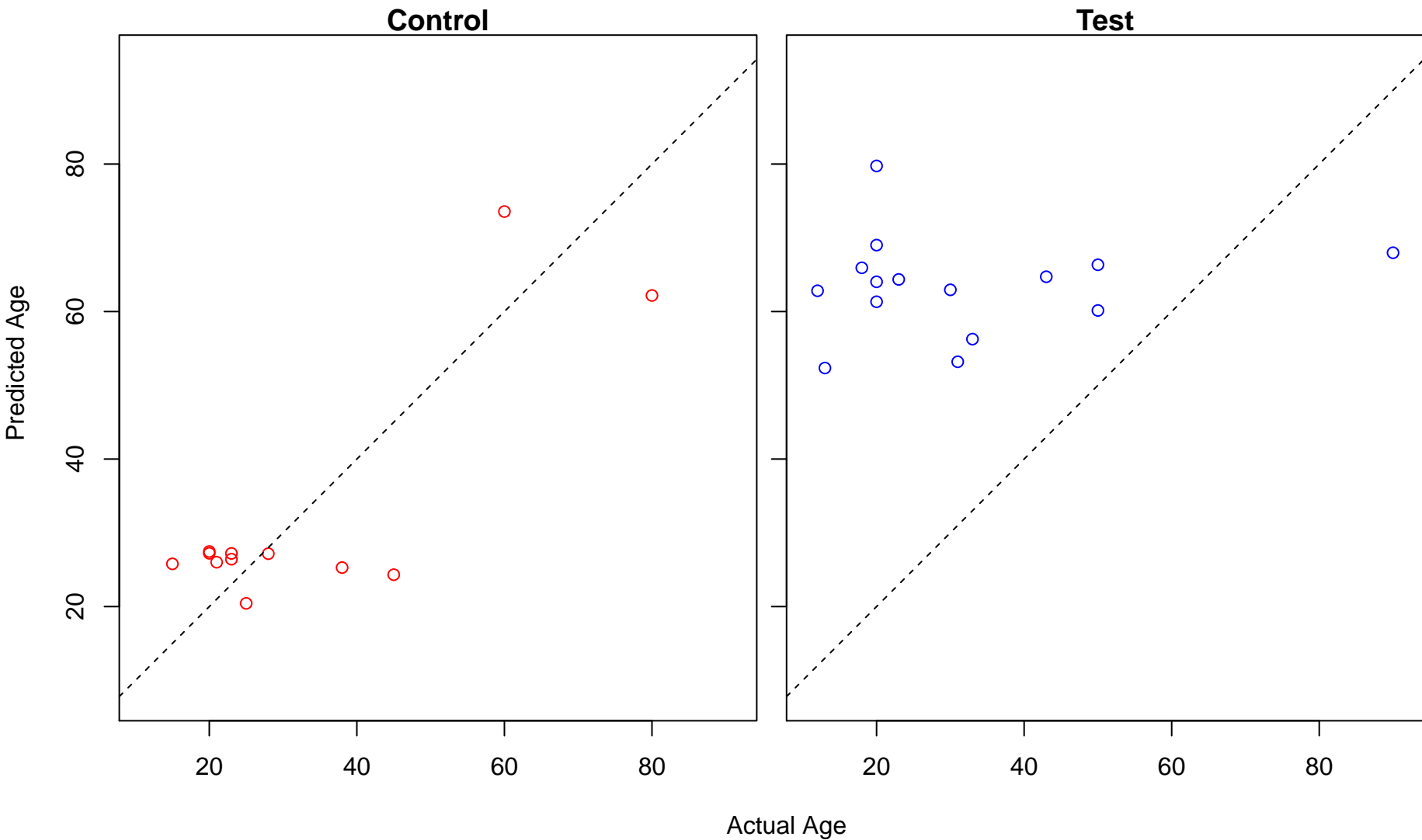
glomerular filtration (Score: 4.384468)



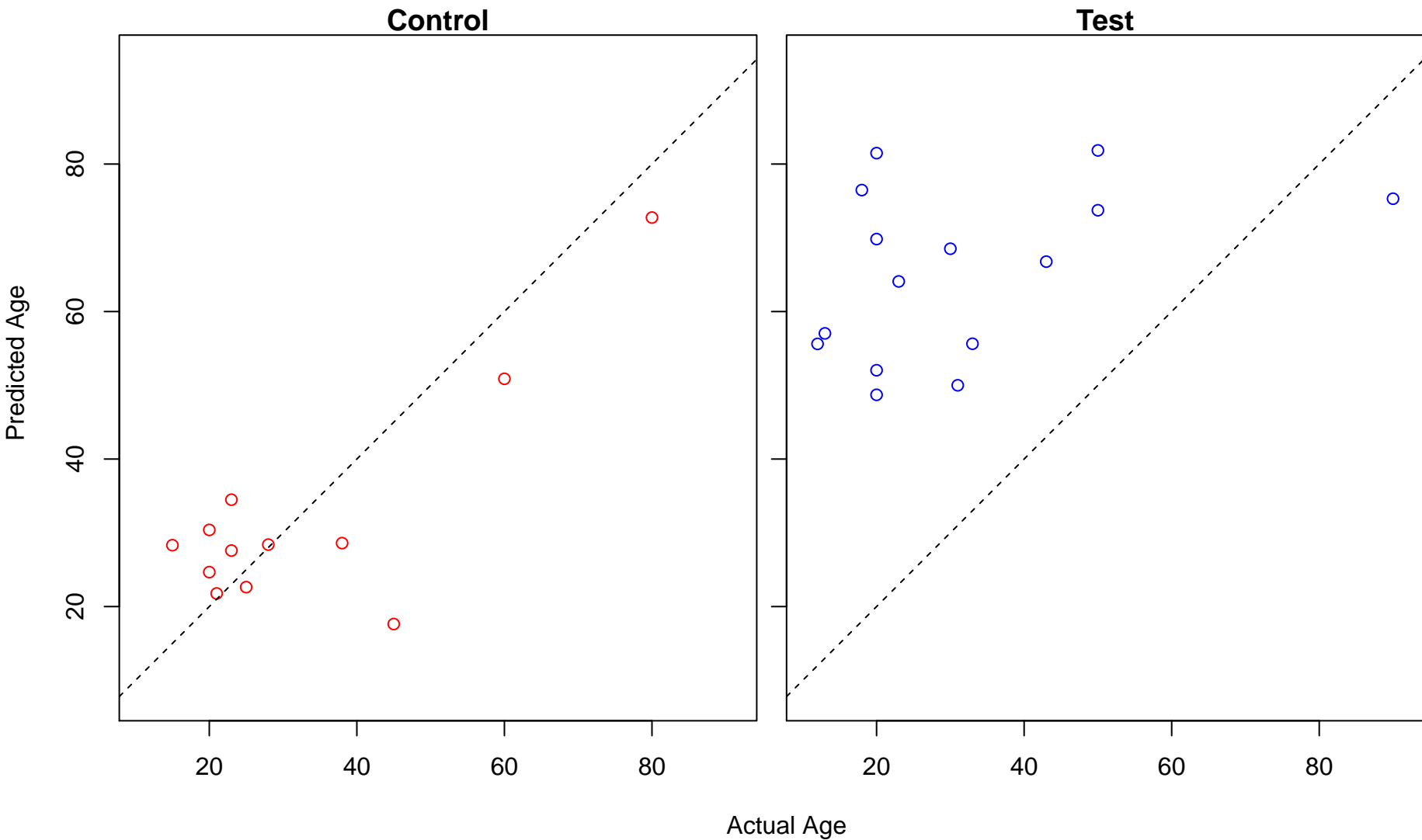
macrophage differentiation (Score: 4.383031)



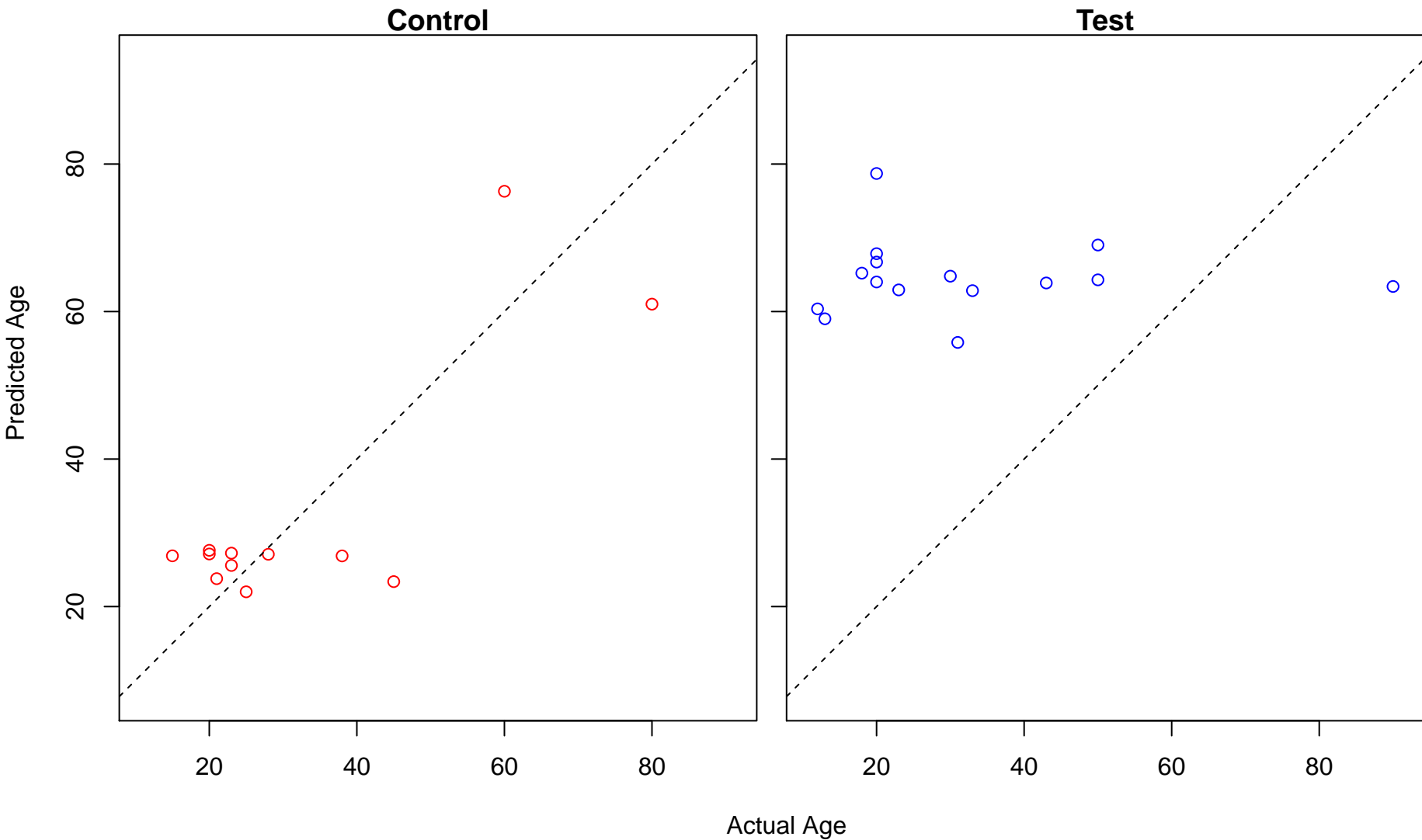
regulation of spindle organization (Score: 4.382967)



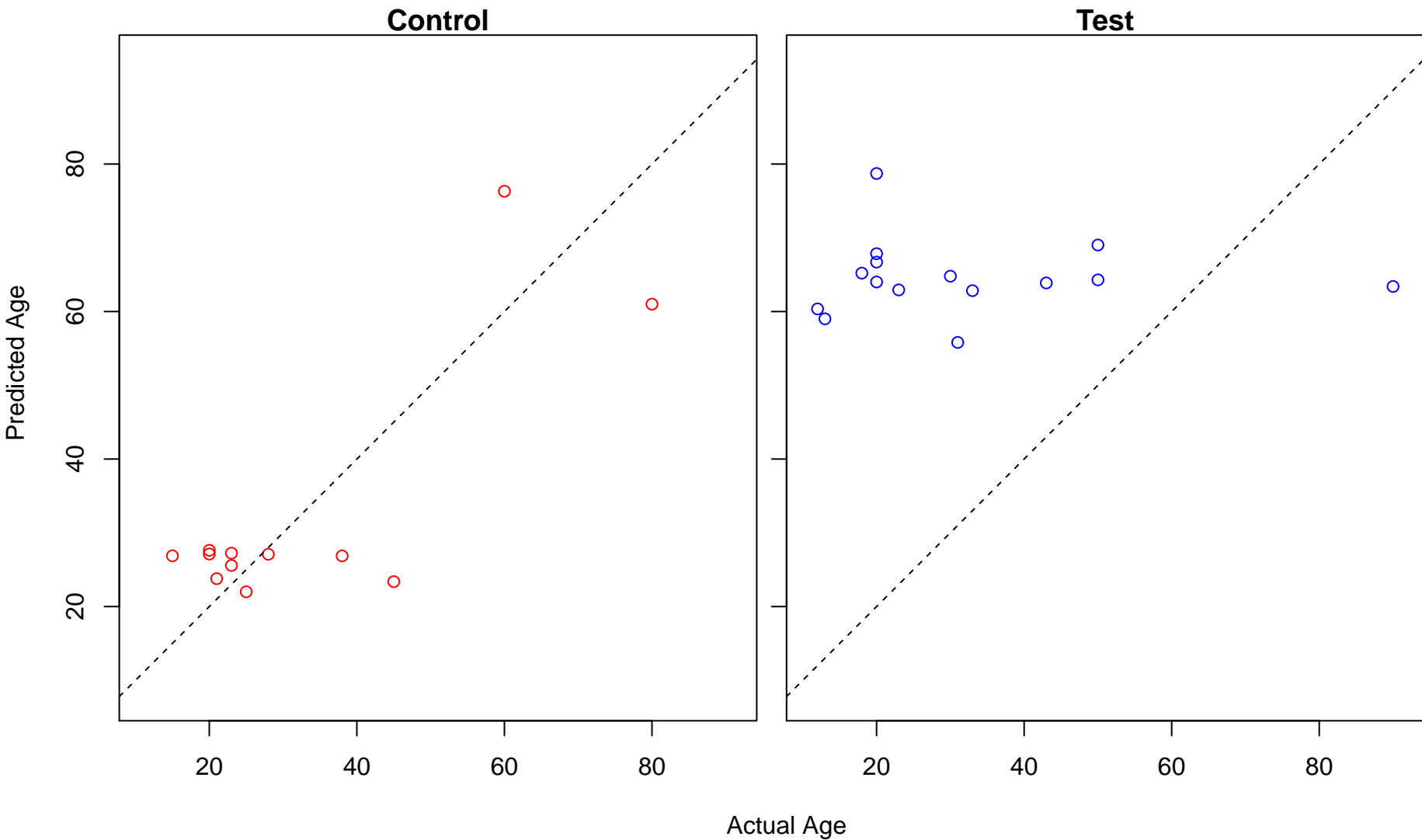
regulation of interleukin-13 secretion (Score: 4.381436)



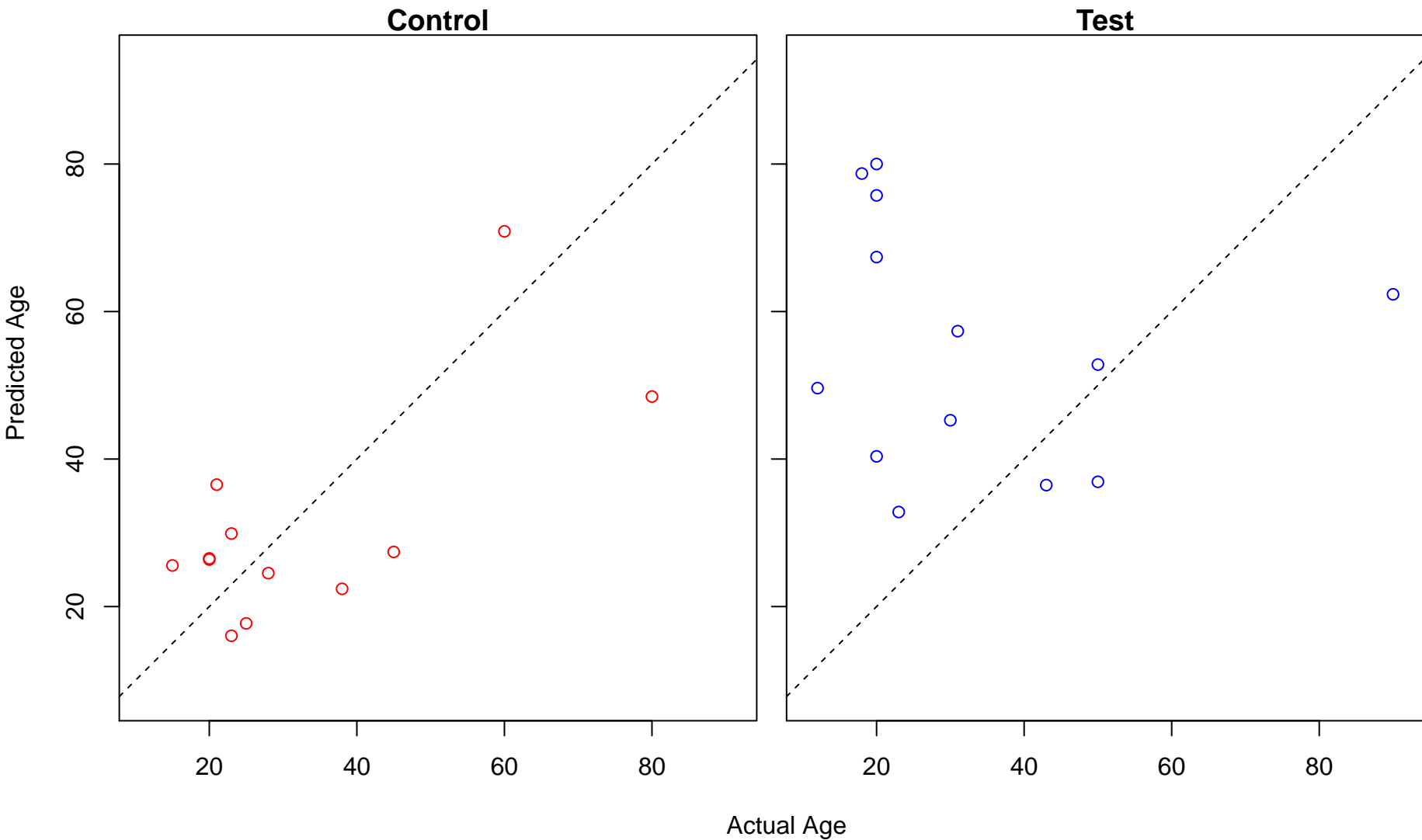
peptidyl-asparagine modification (Score: 4.381200)



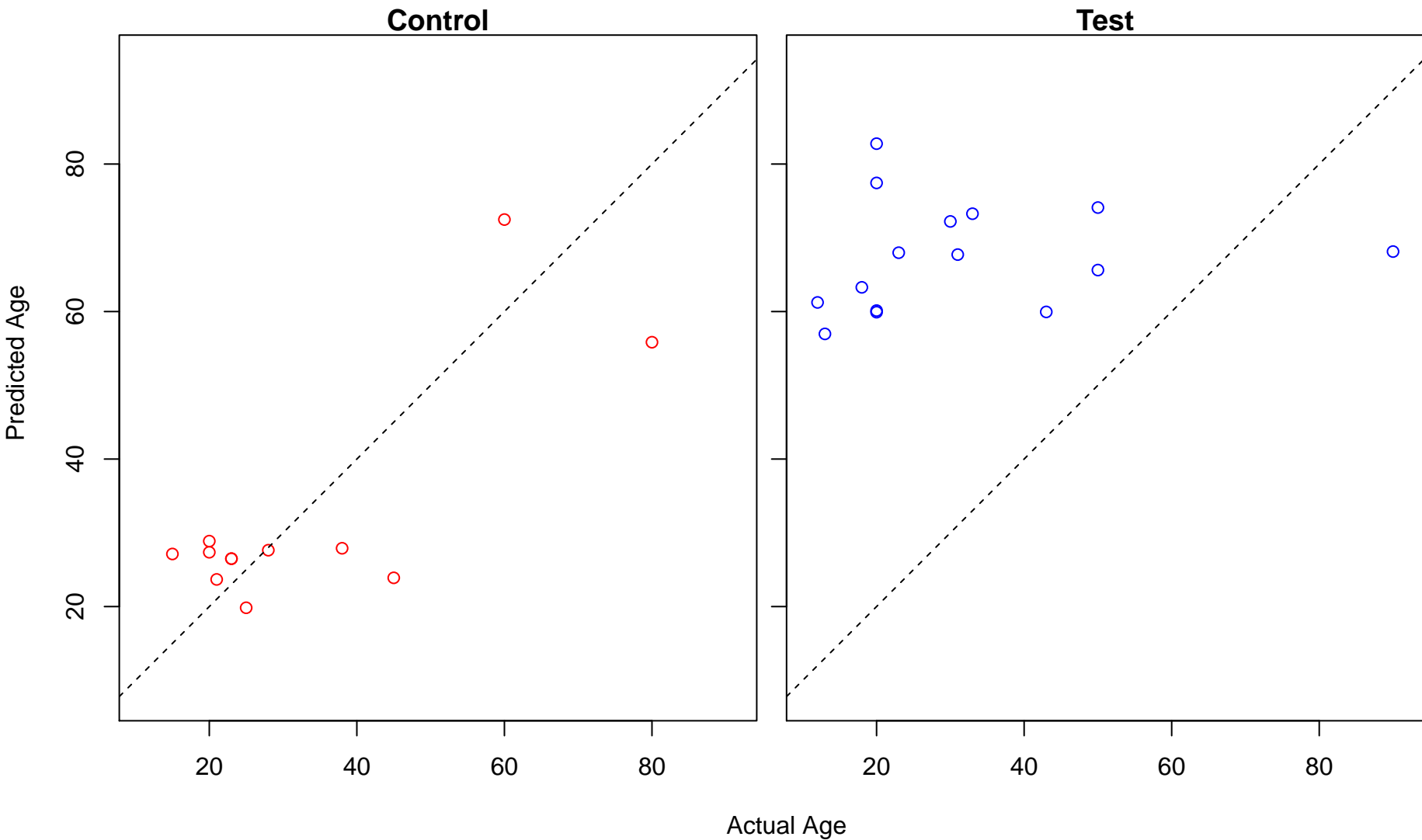
protein N-linked glycosylation via asparagine (Score: 4.380546)



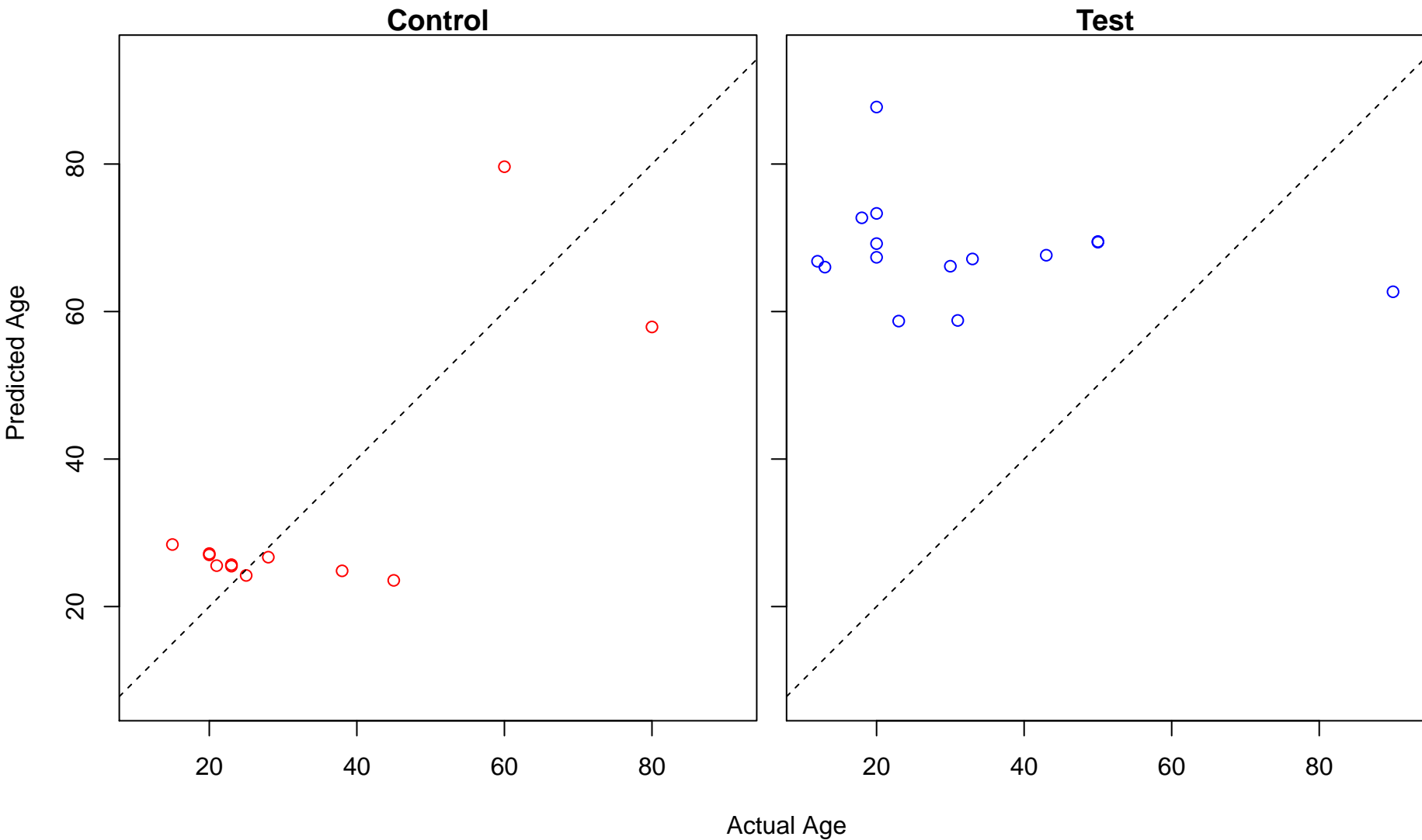
bone growth (Score: 4.377380)



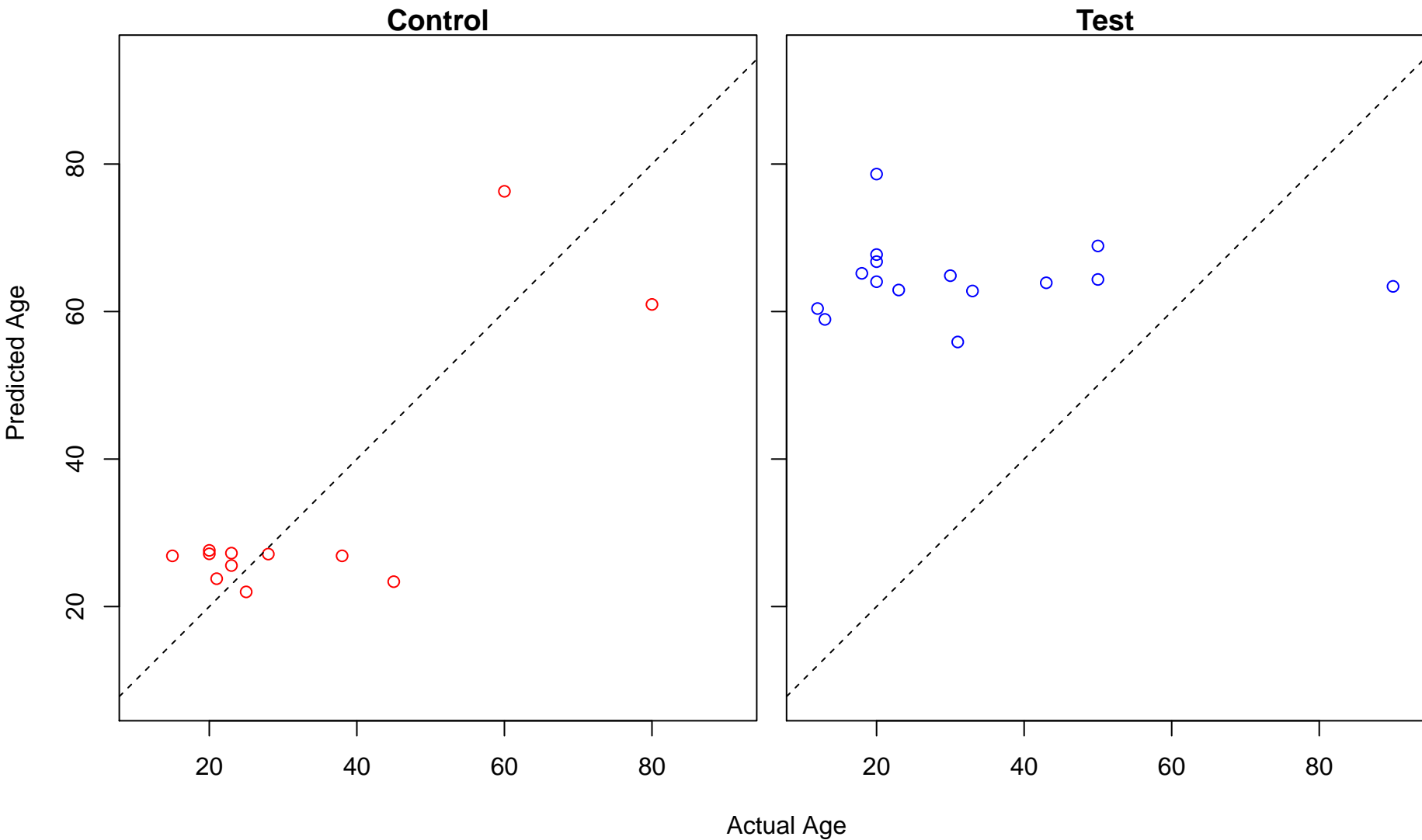
regulation of lipid catabolic process (Score: 4.377367)



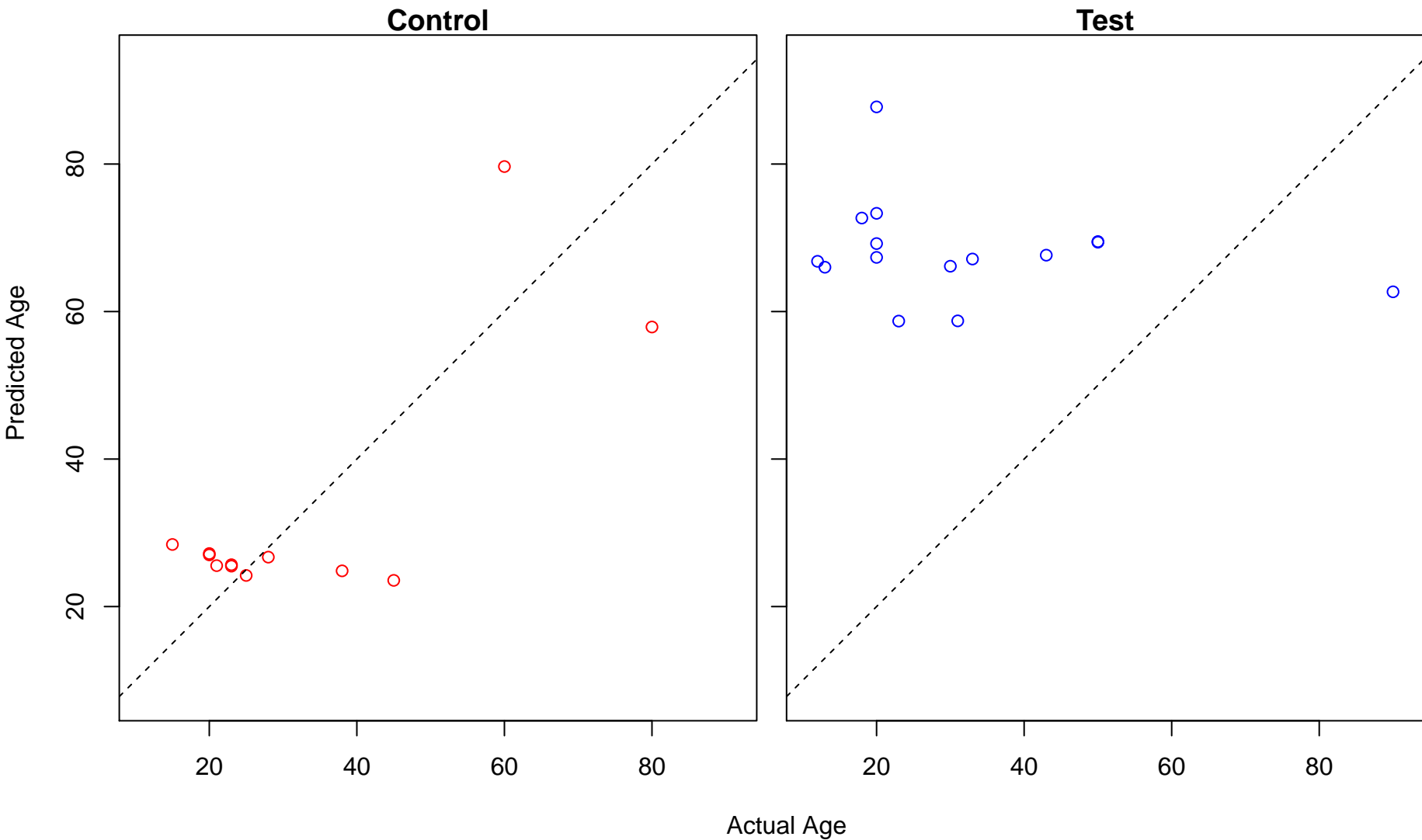
regulation of cellular response to oxidative stress (Score: 4.376973)



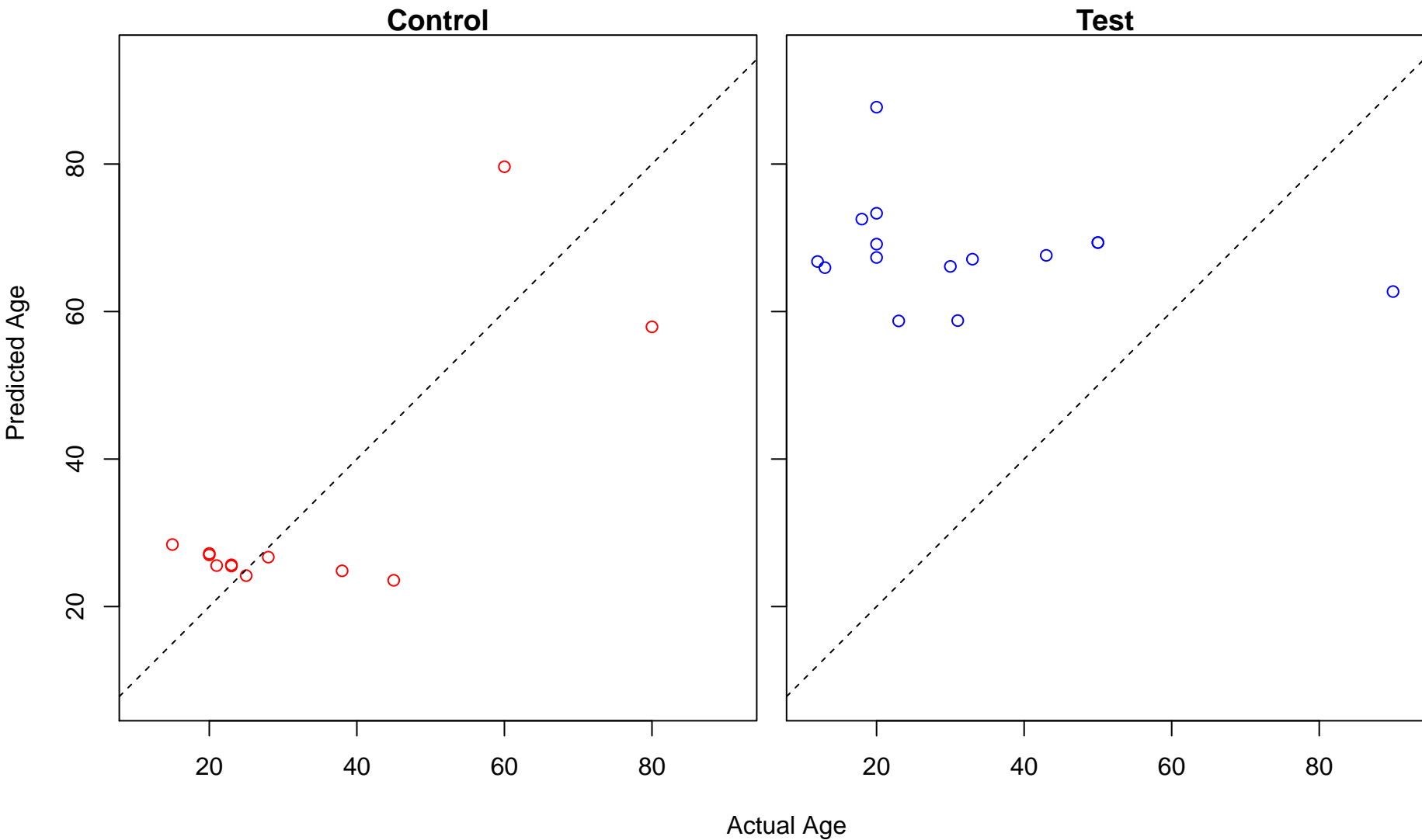
protein N-linked glycosylation (Score: 4.375483)



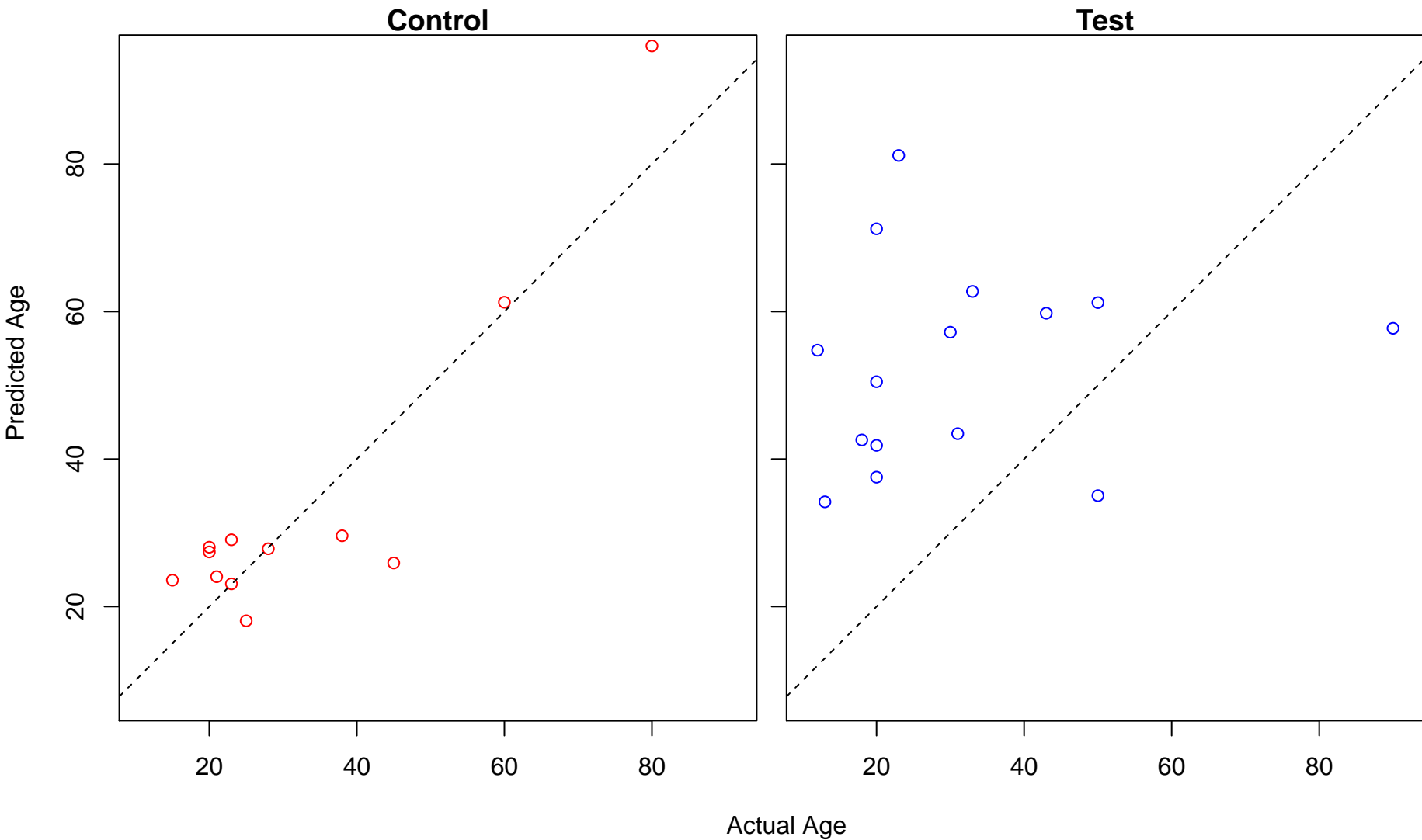
regulation of oxidative stress-induced cell death (Score: 4.374007)



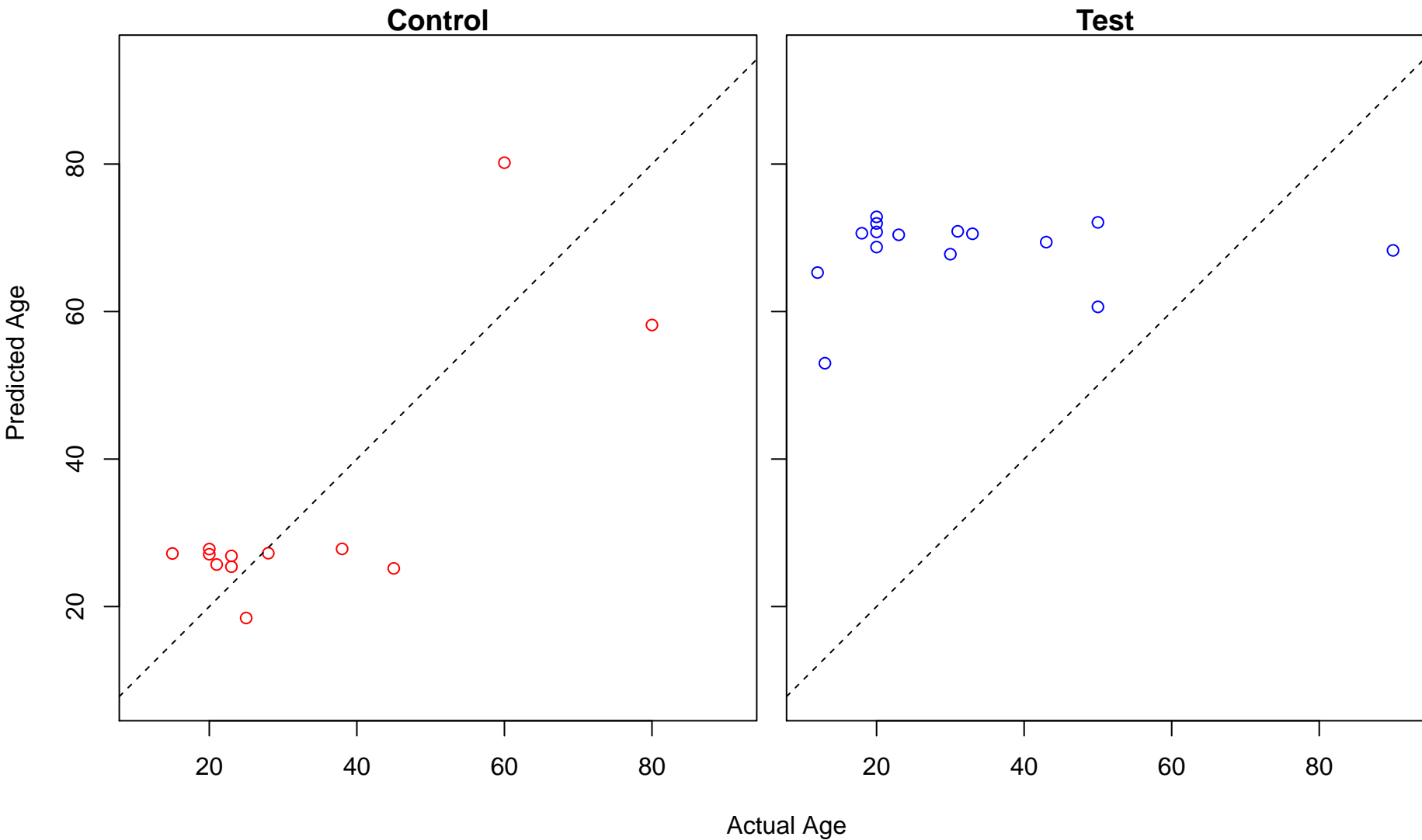
regulation of response to oxidative stress (Score: 4.372569)



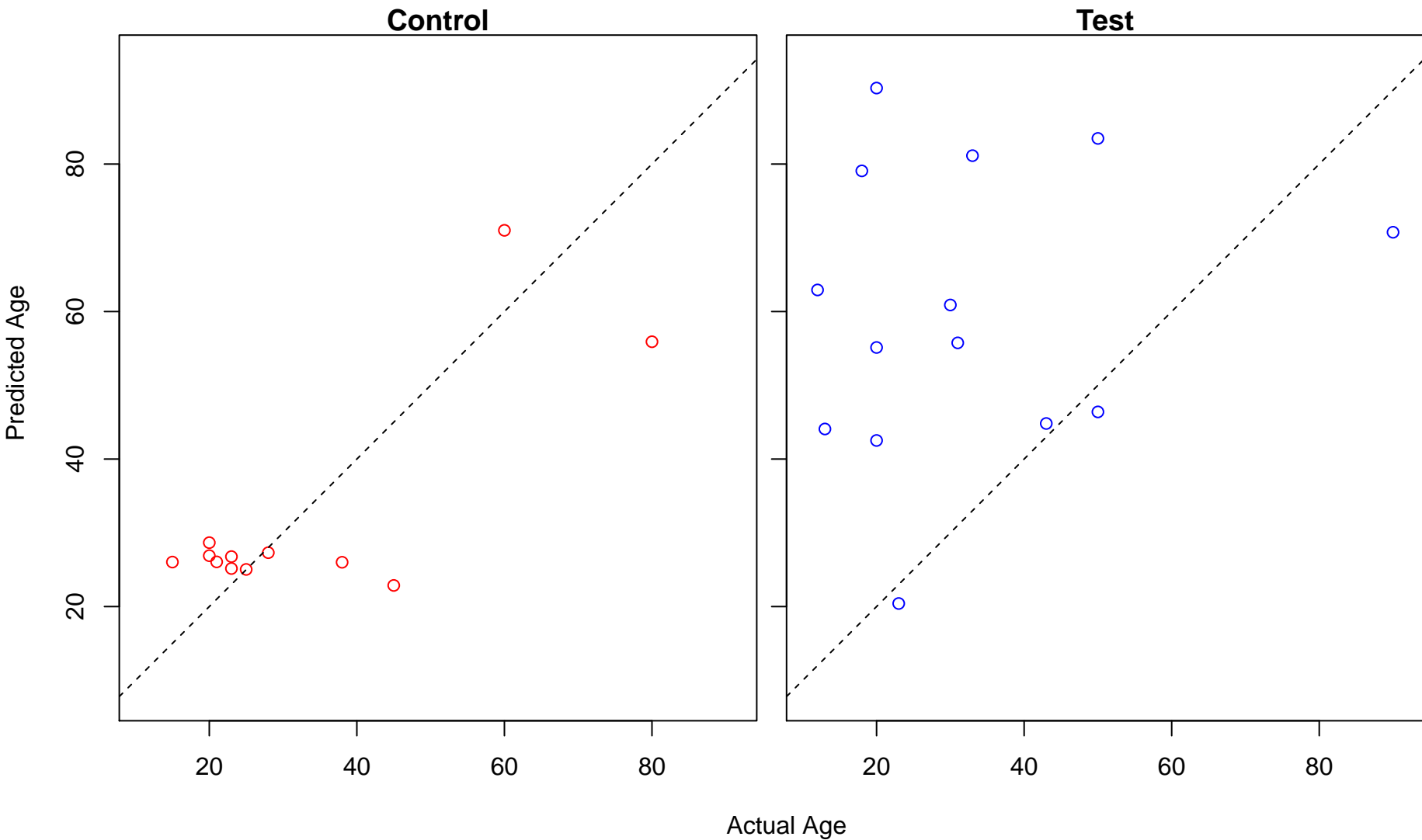
positive regulation of phosphatidylinositol 3-kinase activity (Score: 4.371447)



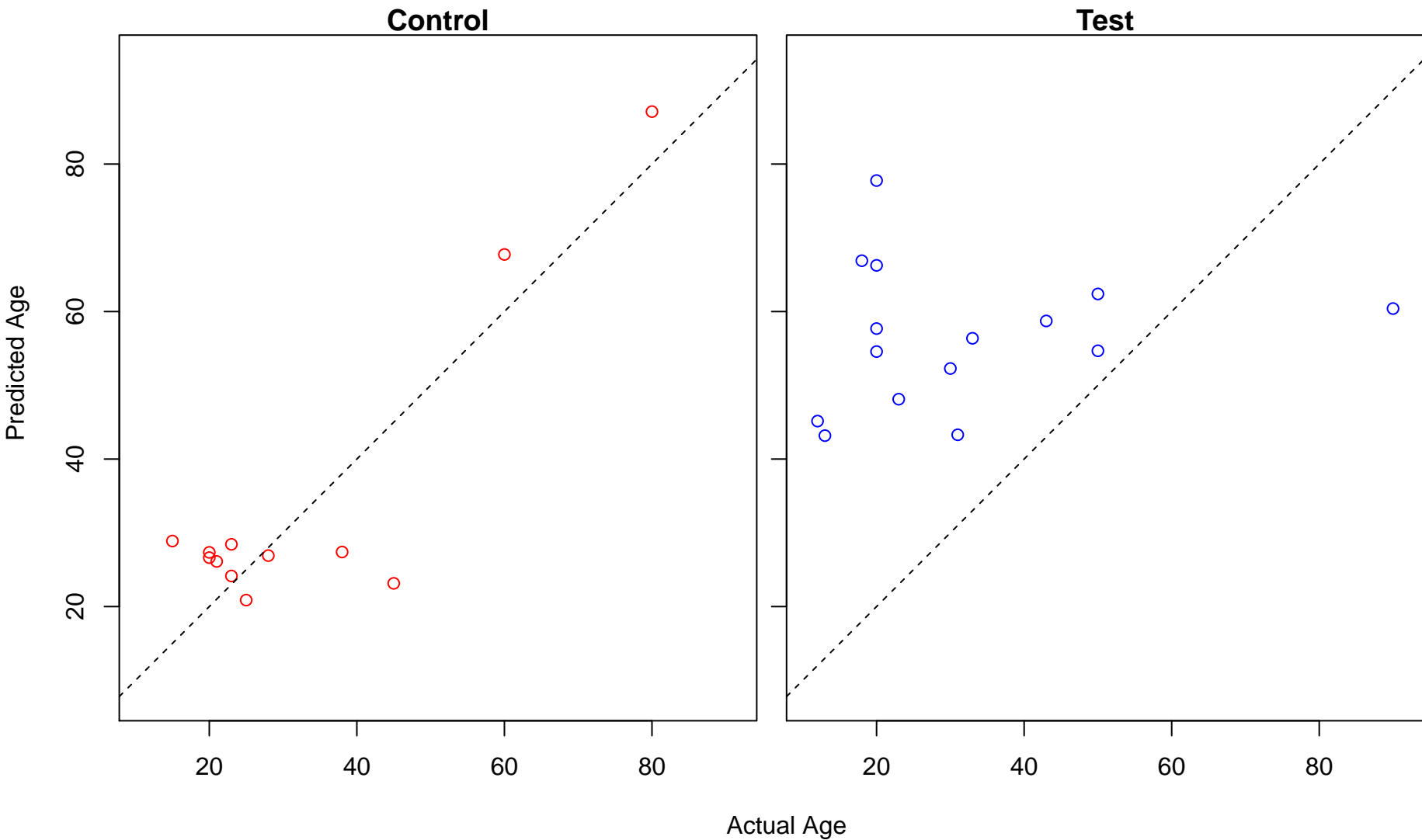
dendrite morphogenesis (Score: 4.371244)



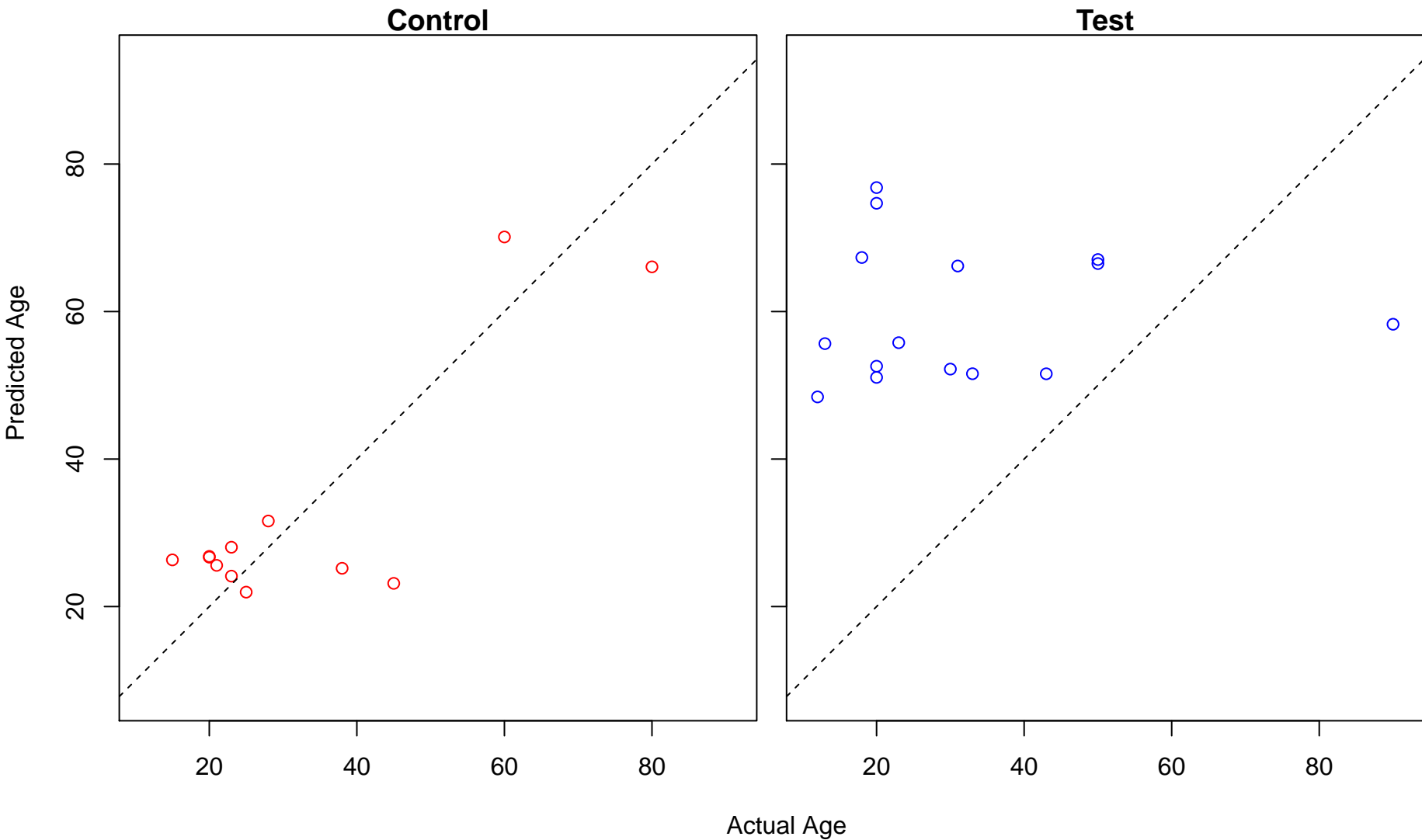
positive regulation of smooth muscle cell differentiation (Score: 4.370450)



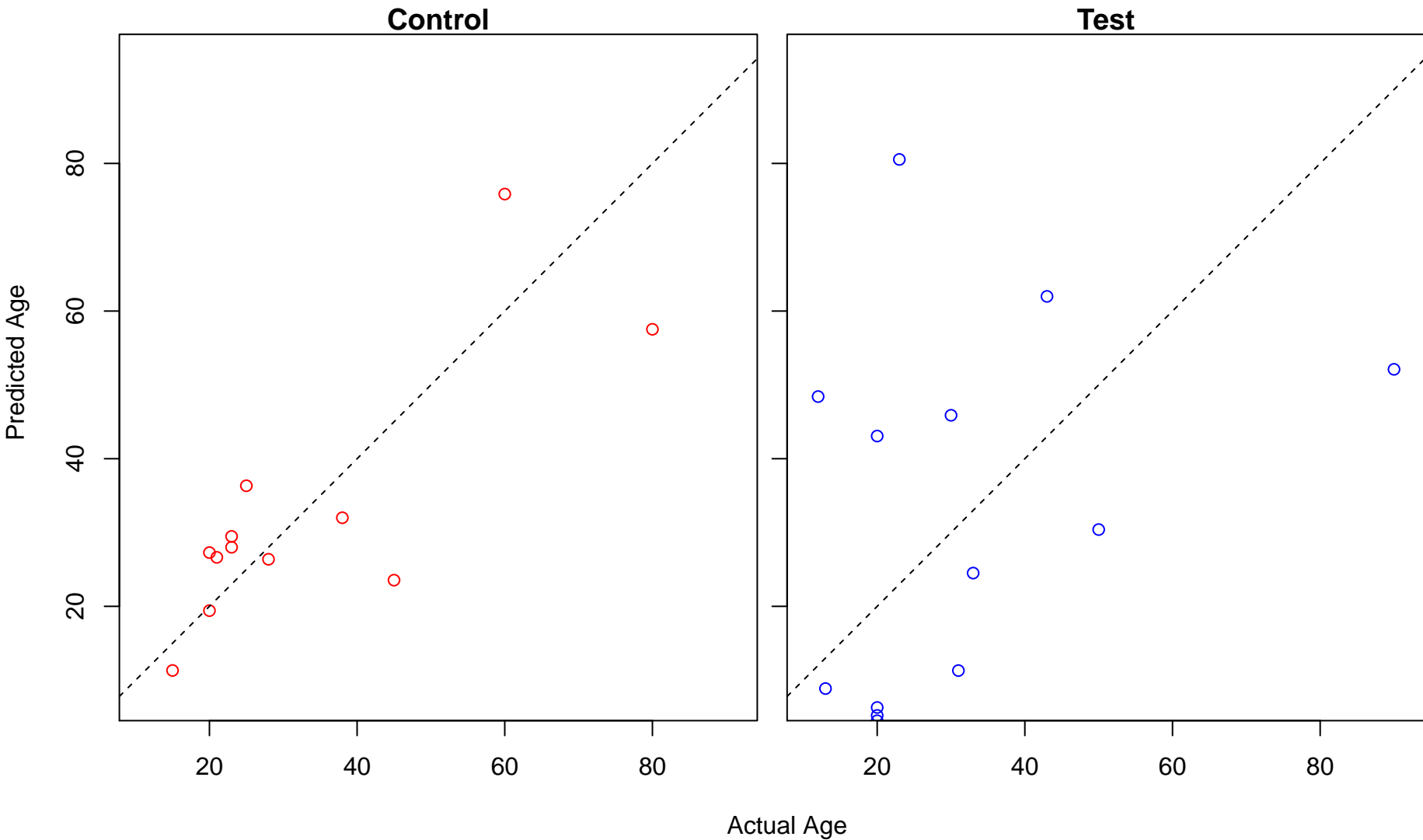
regulation of small GTPase mediated signal transduction (Score: 4.369151)



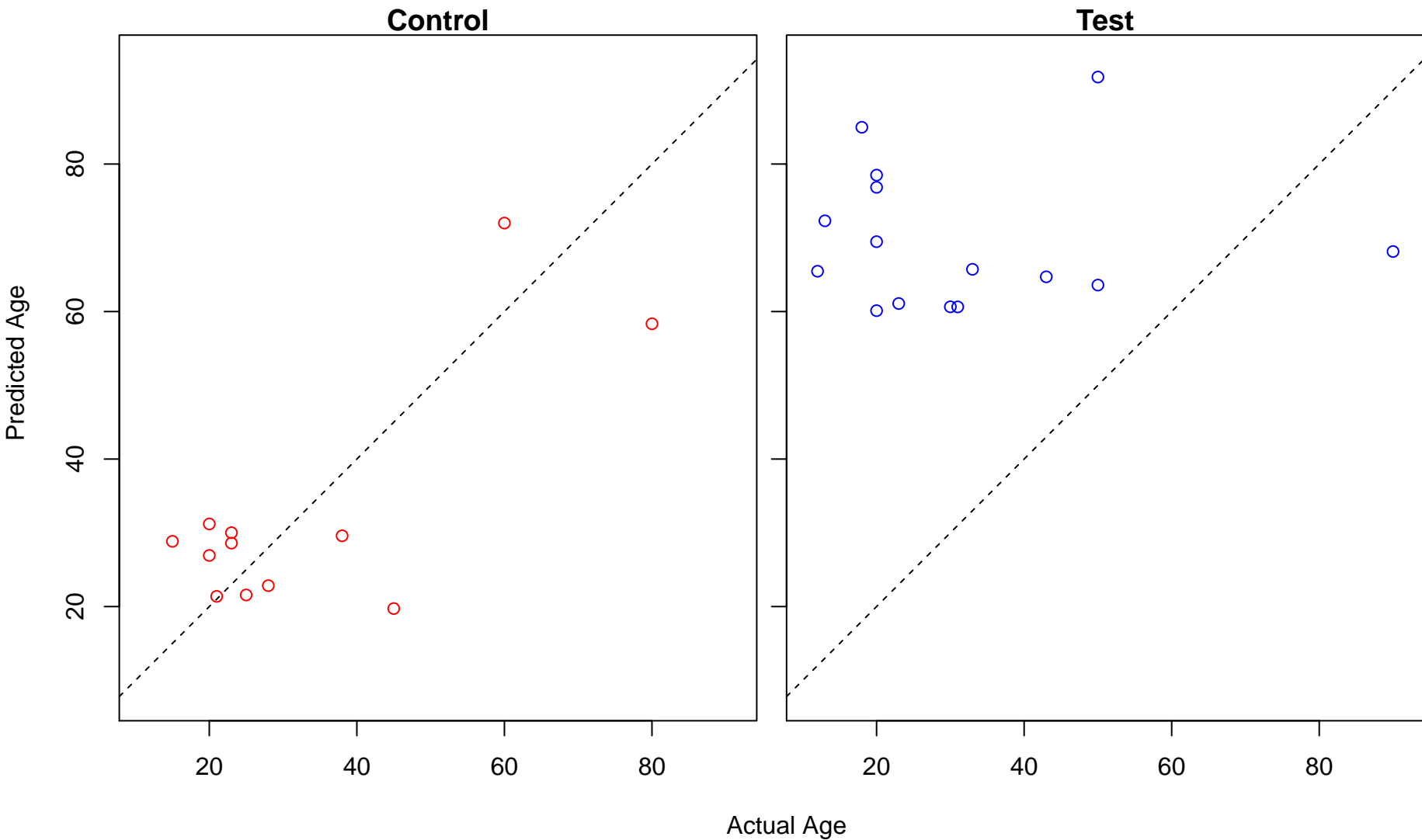
negative regulation of cation transmembrane transport (Score: 4.367885)



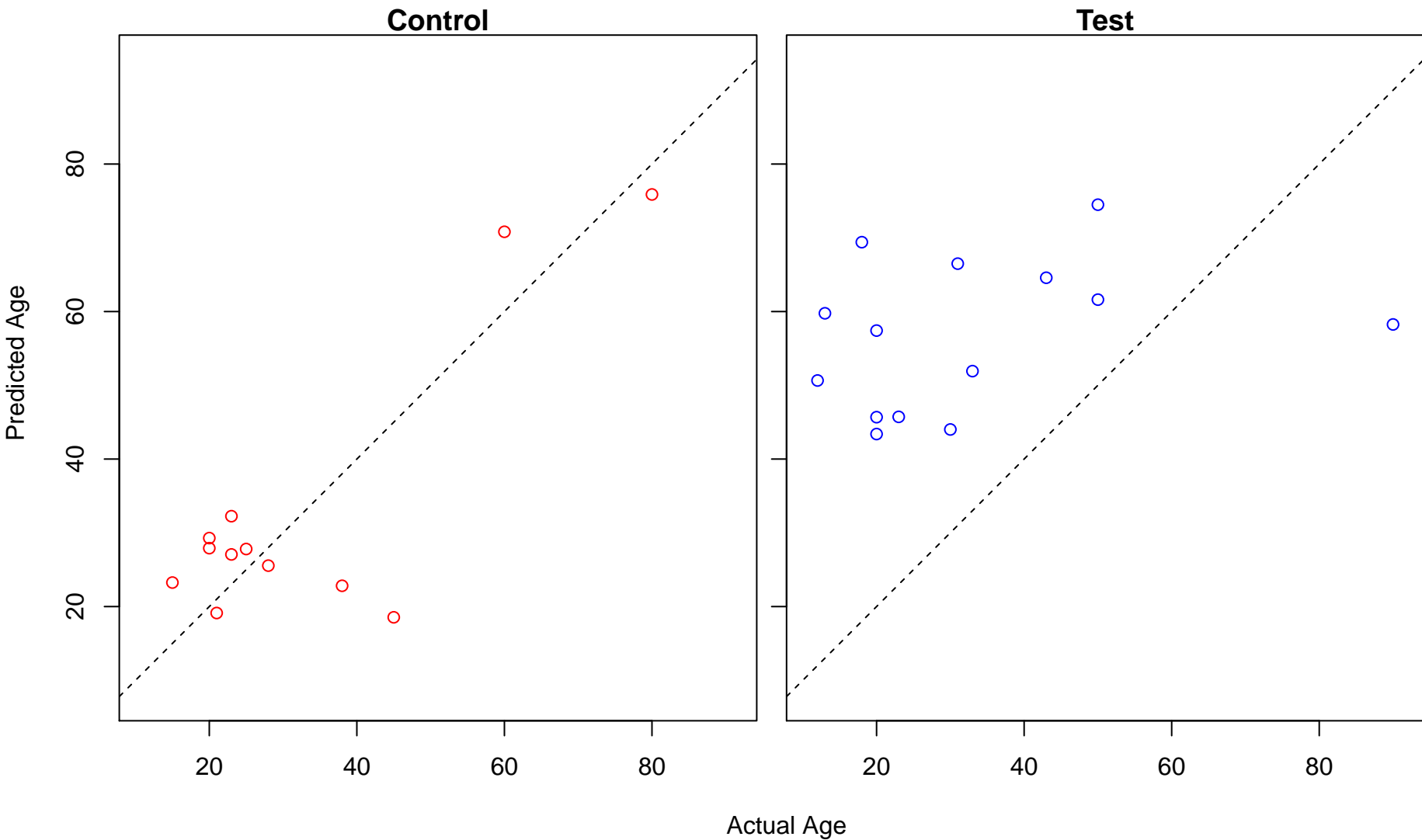
positive regulation of toll-like receptor 4 signaling pathway (Score: 4.366316)



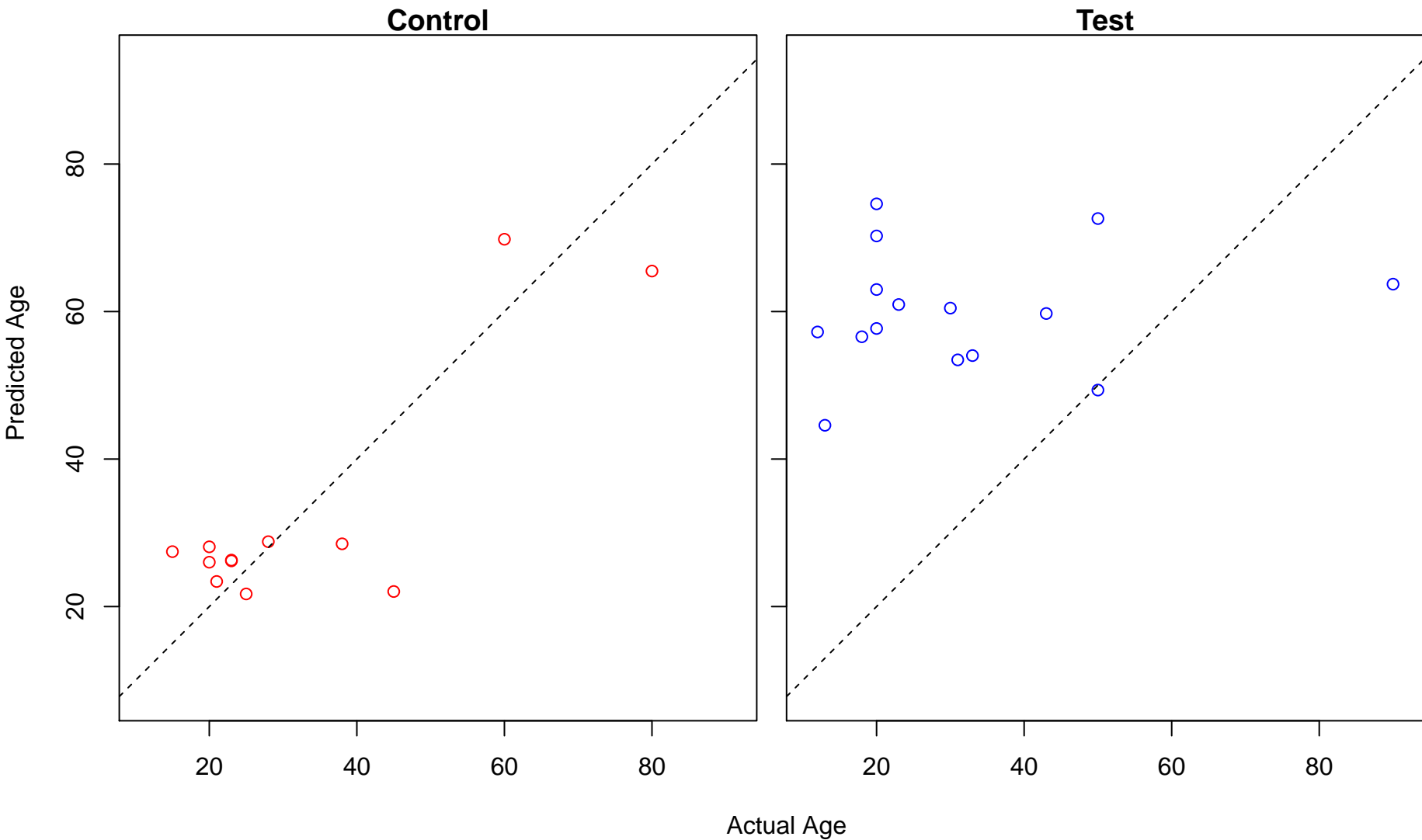
cardiac atrium development (Score: 4.365868)



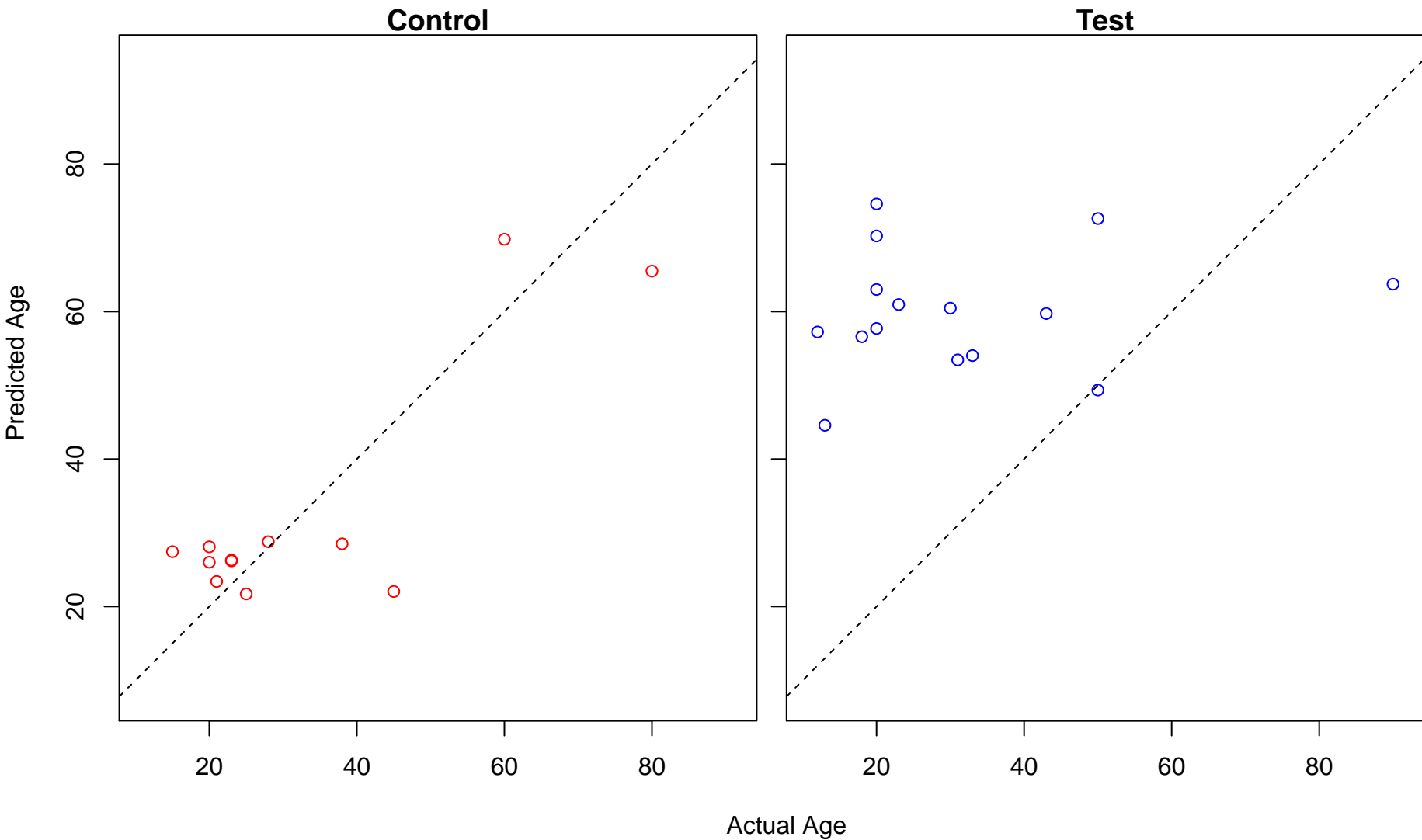
positive regulation of smooth muscle cell migration (Score: 4.364875)



regulation of intracellular pH (Score: 4.363639)

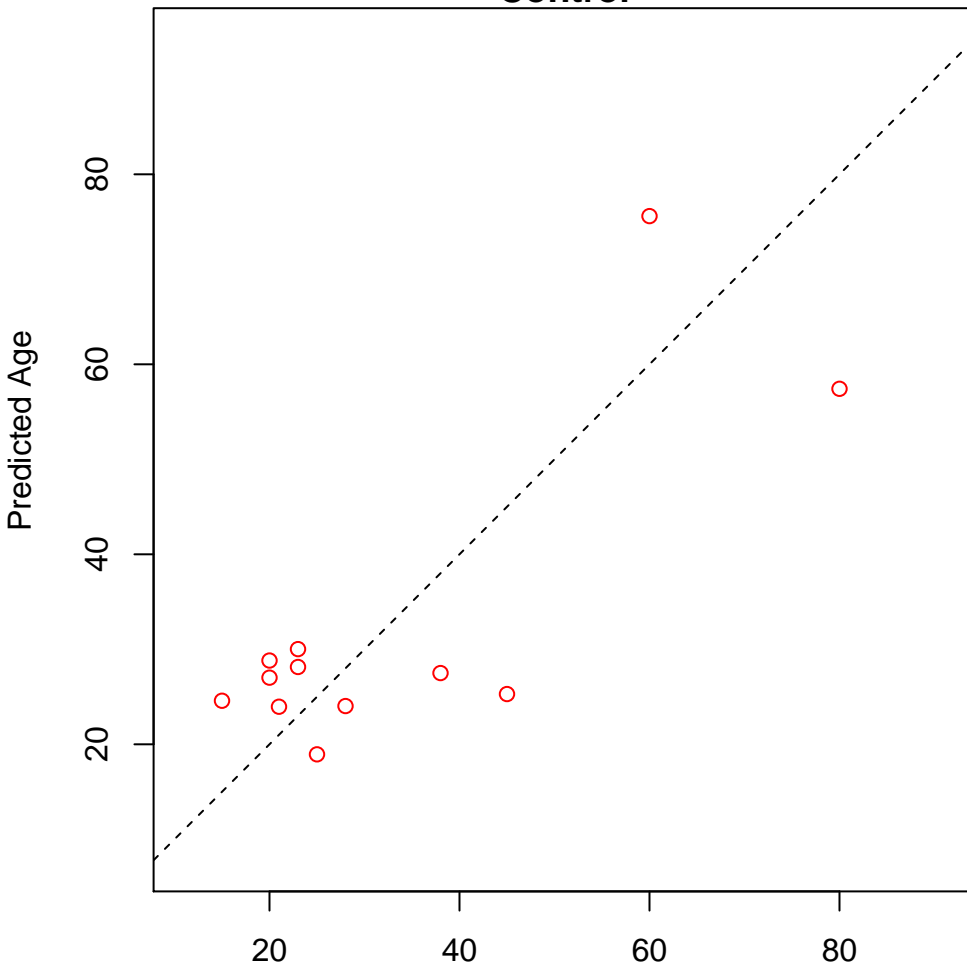


regulation of cellular pH (Score: 4.363602)

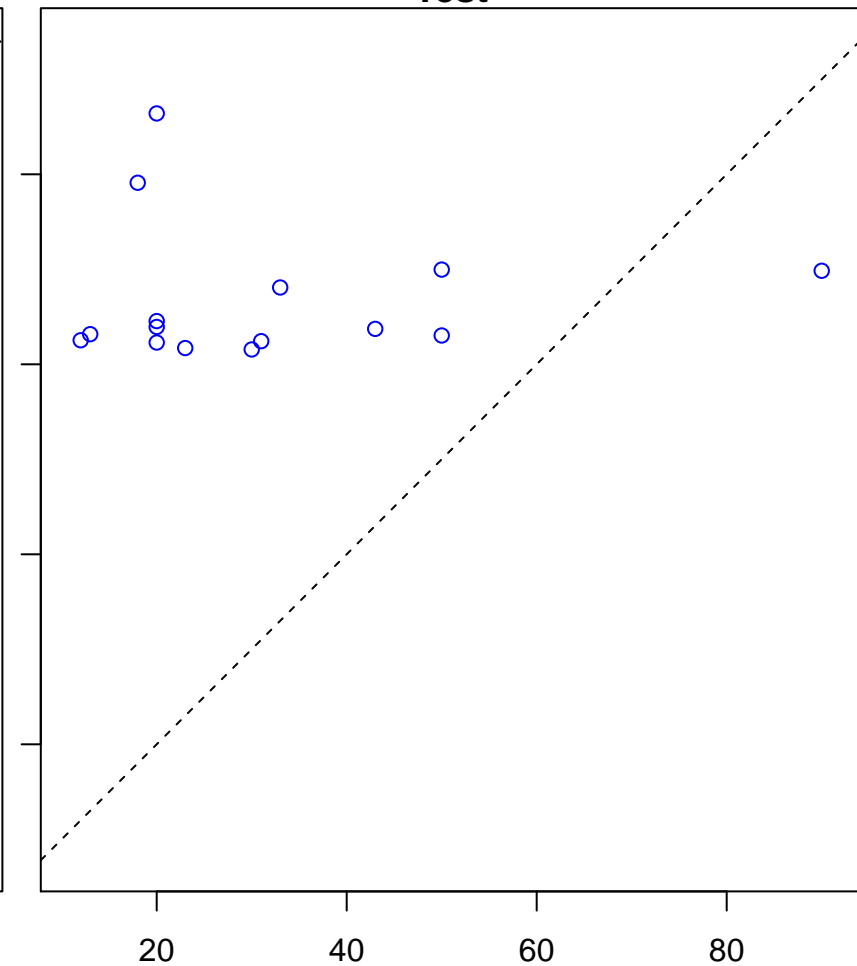


regulation of neurotransmitter transport (Score: 4.362958)

Control

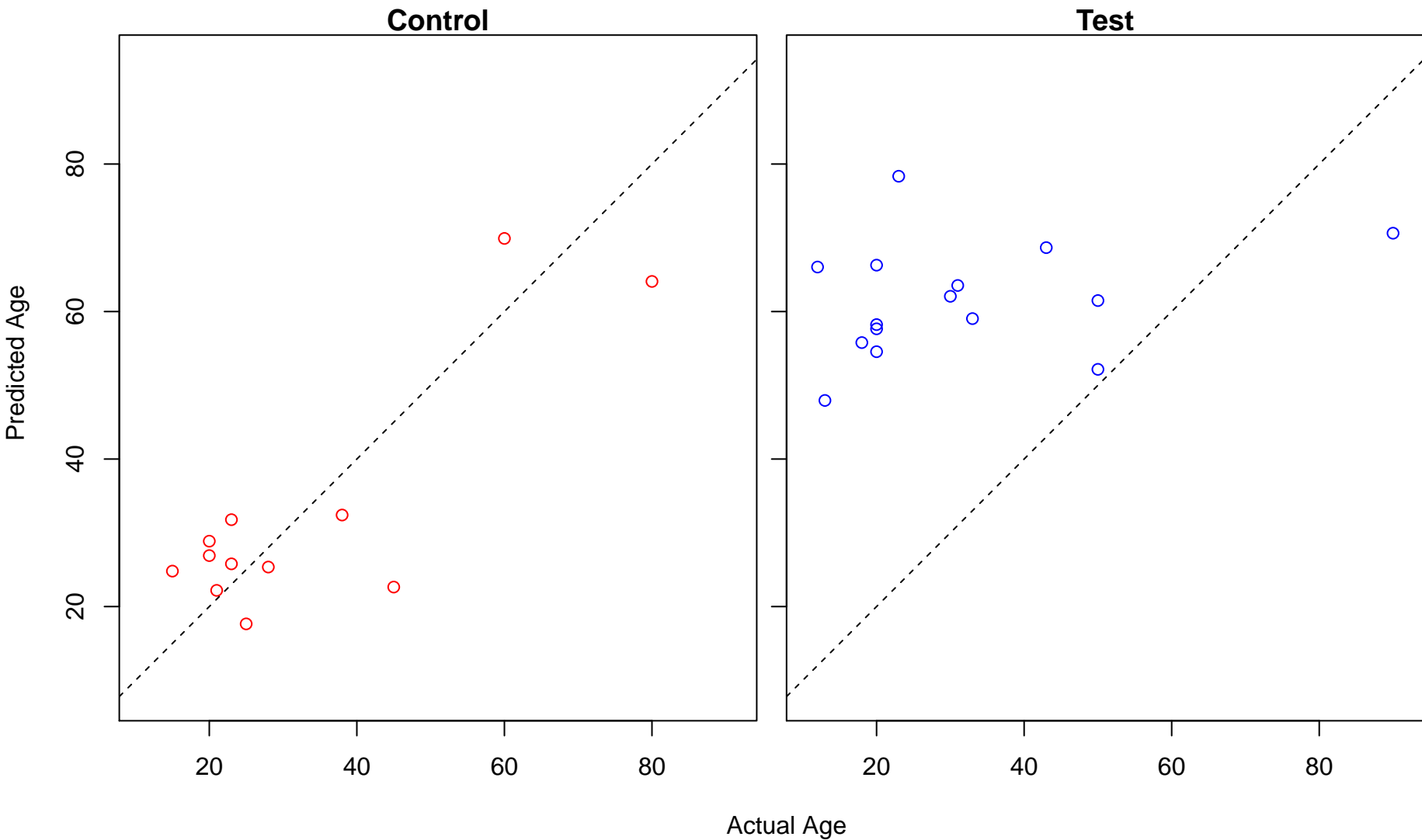


Test

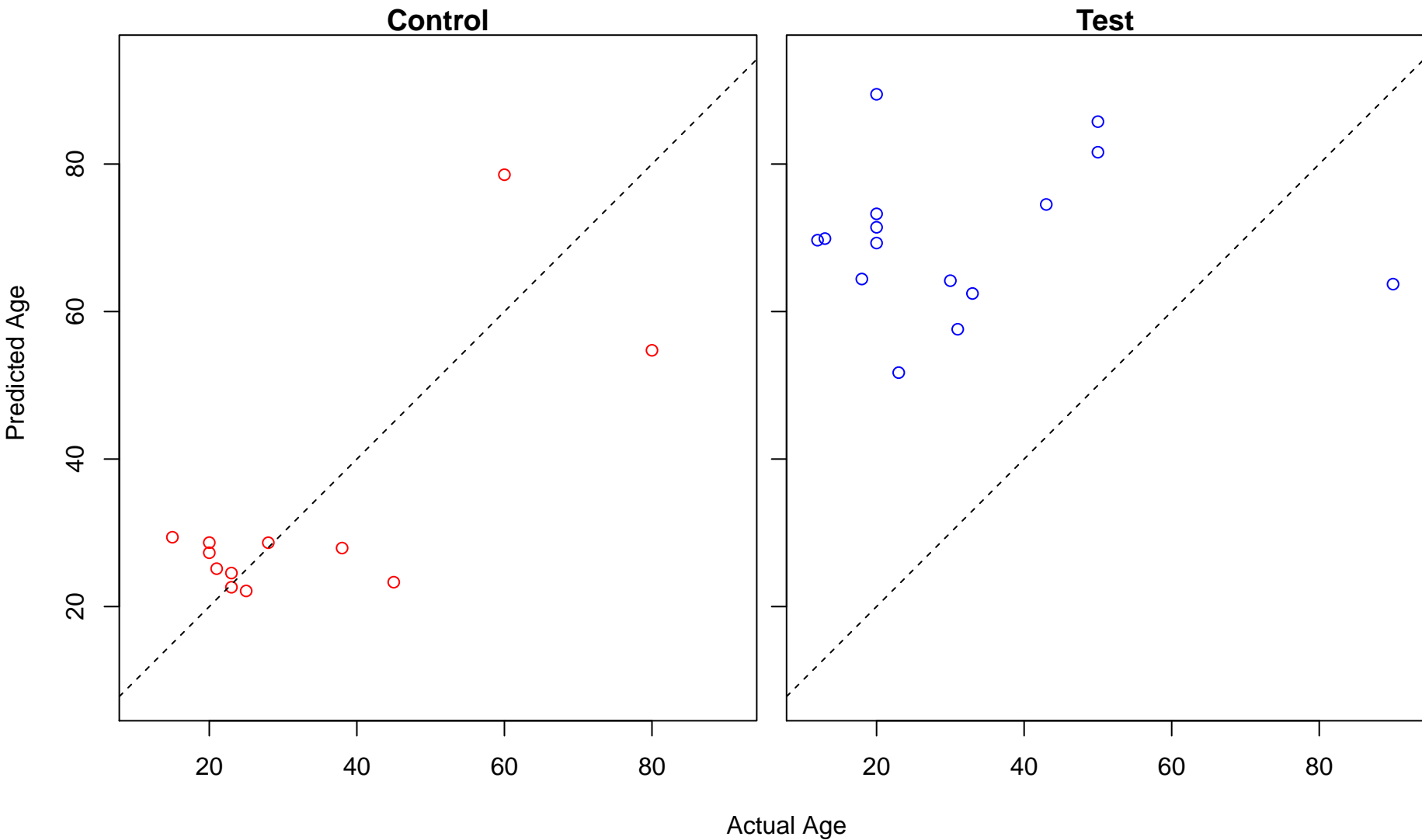


Actual Age

ectoderm development (Score: 4.362265)

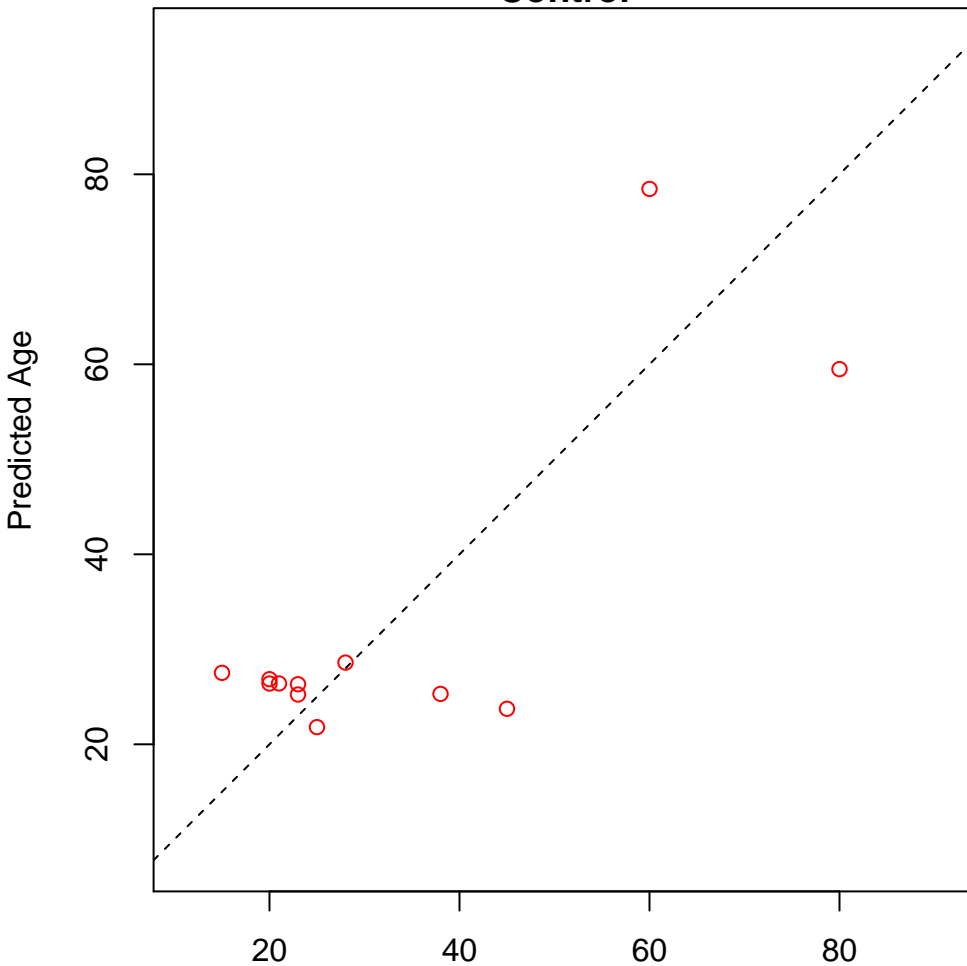


response to xenobiotic stimulus (Score: 4.361437)

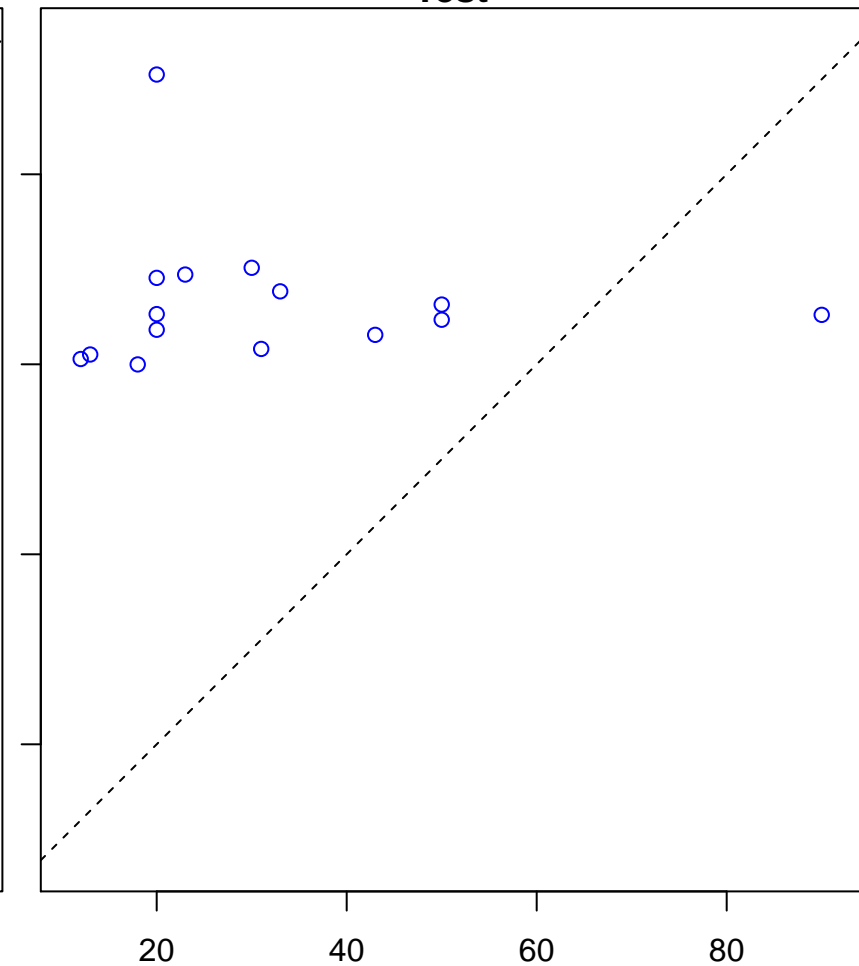


regulation of protein depolymerization (Score: 4.360499)

Control



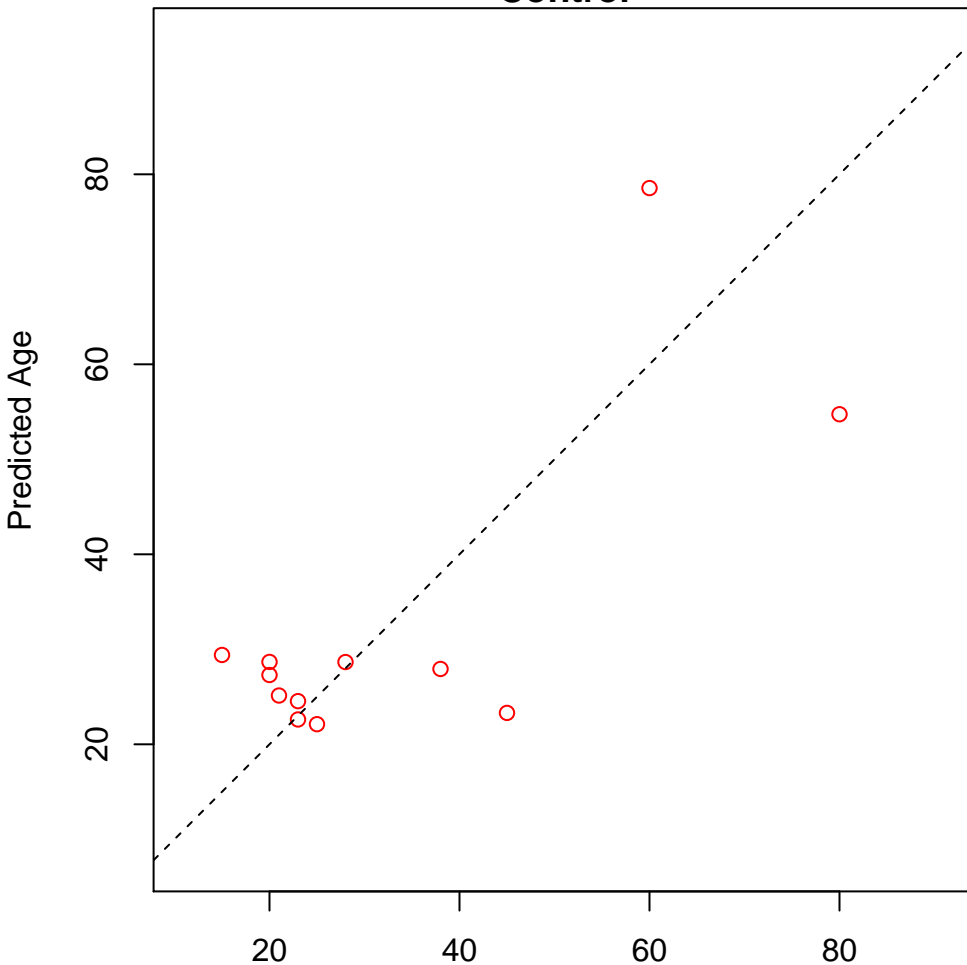
Test



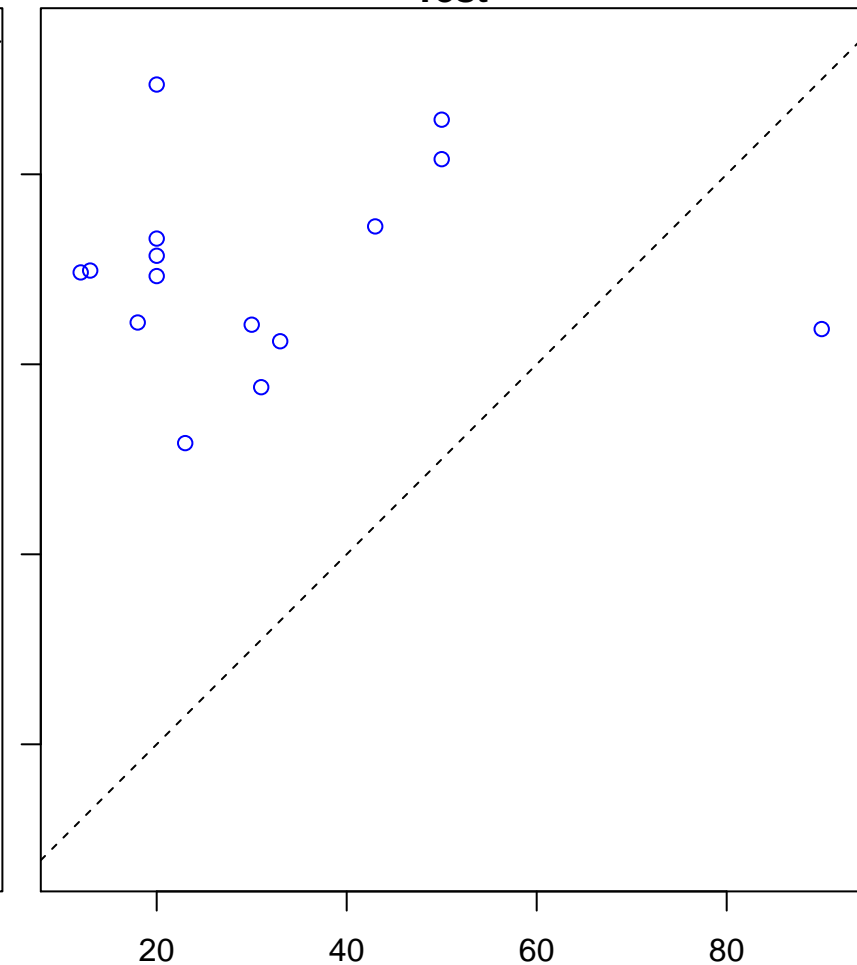
Actual Age

cellular response to xenobiotic stimulus (Score: 4.360394)

Control

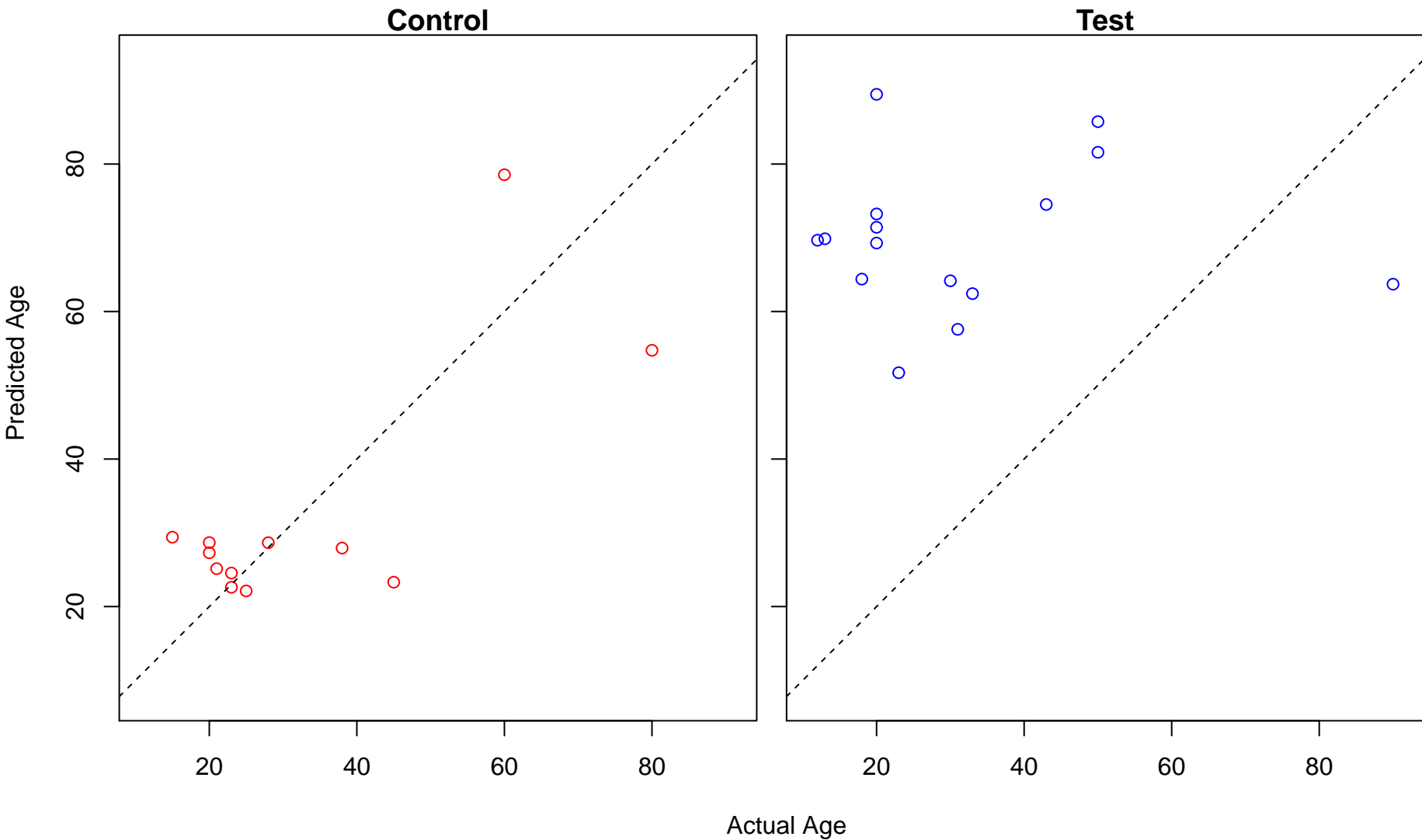


Test

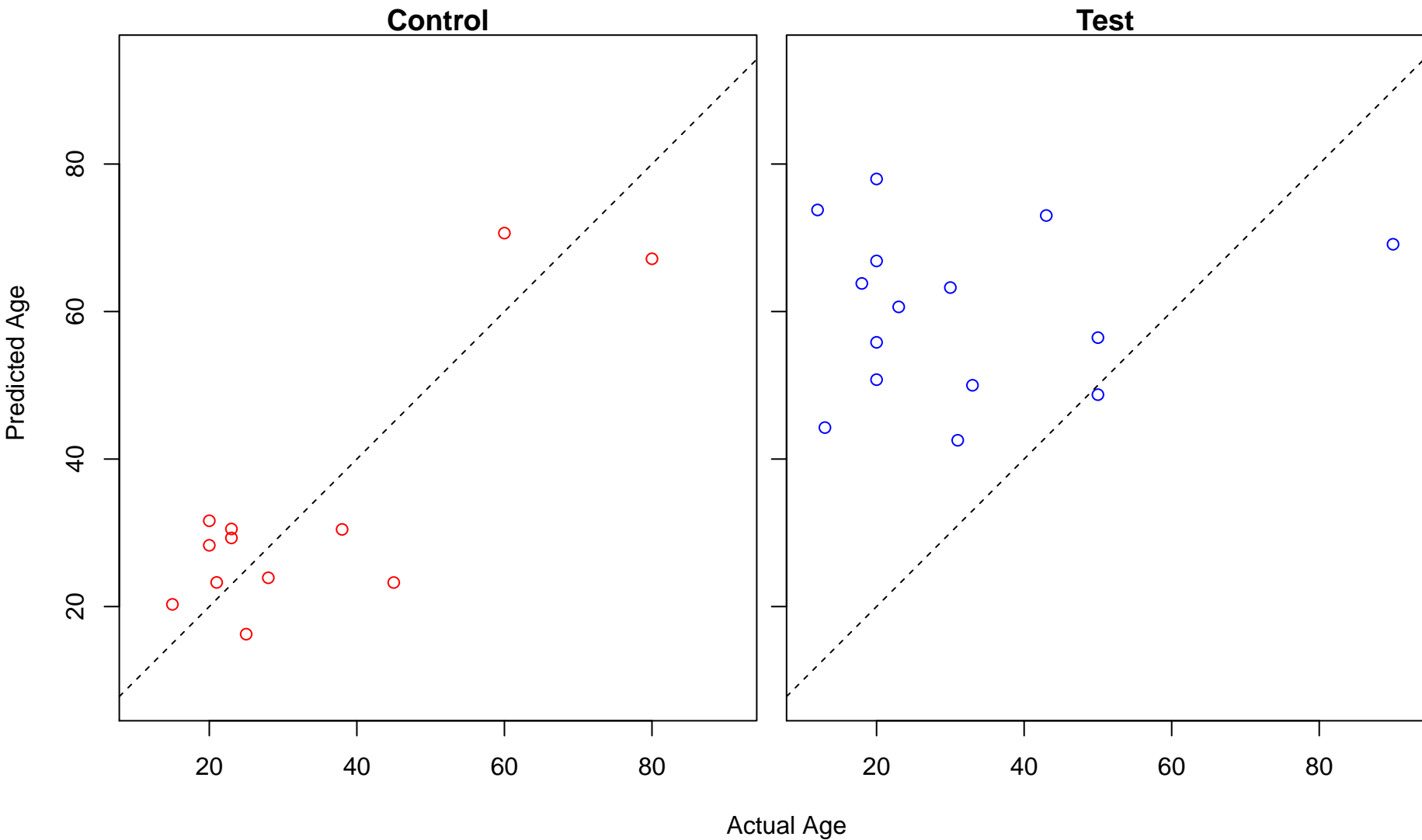


Actual Age

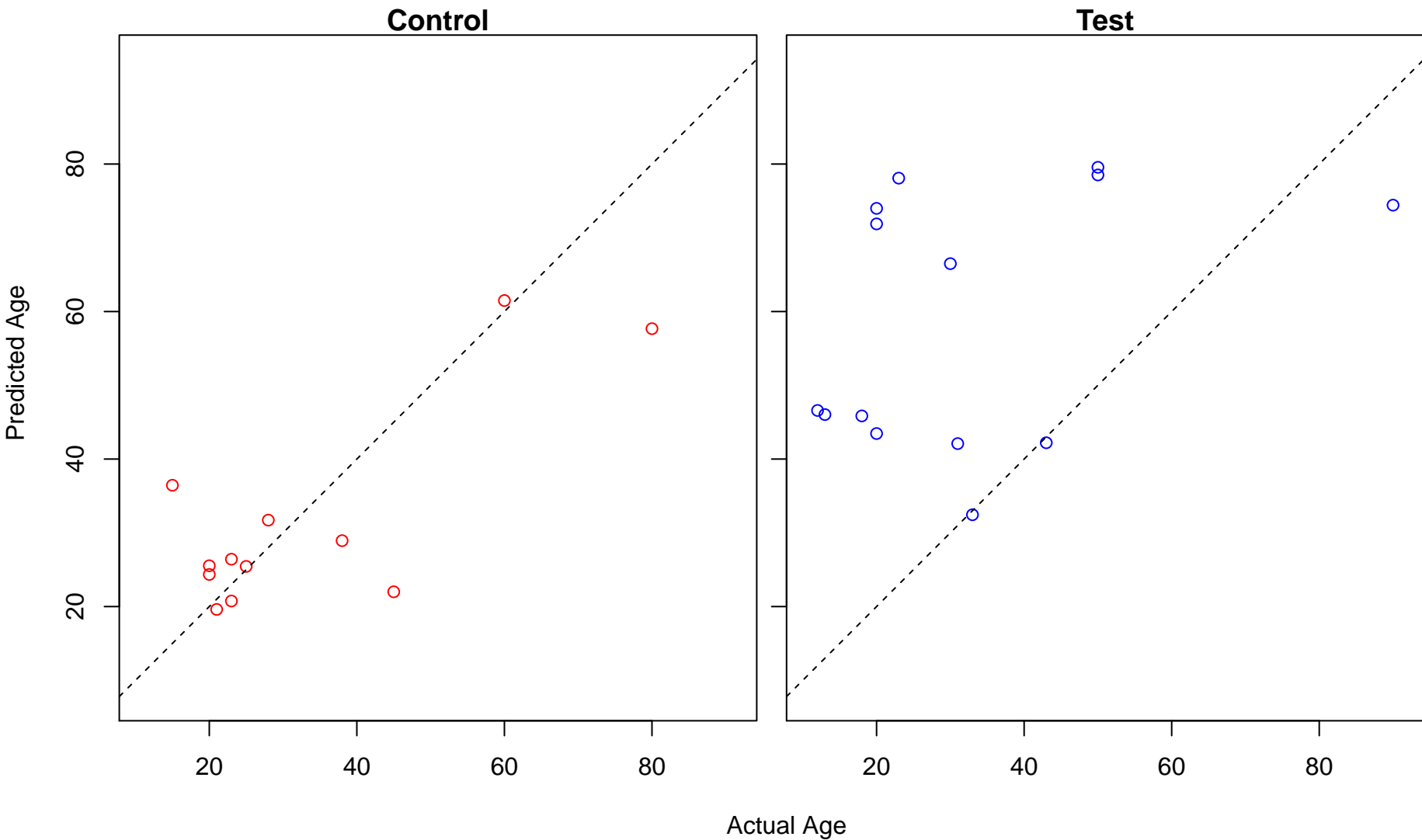
xenobiotic metabolic process (Score: 4.360381)



free ubiquitin chain polymerization (Score: 4.359822)

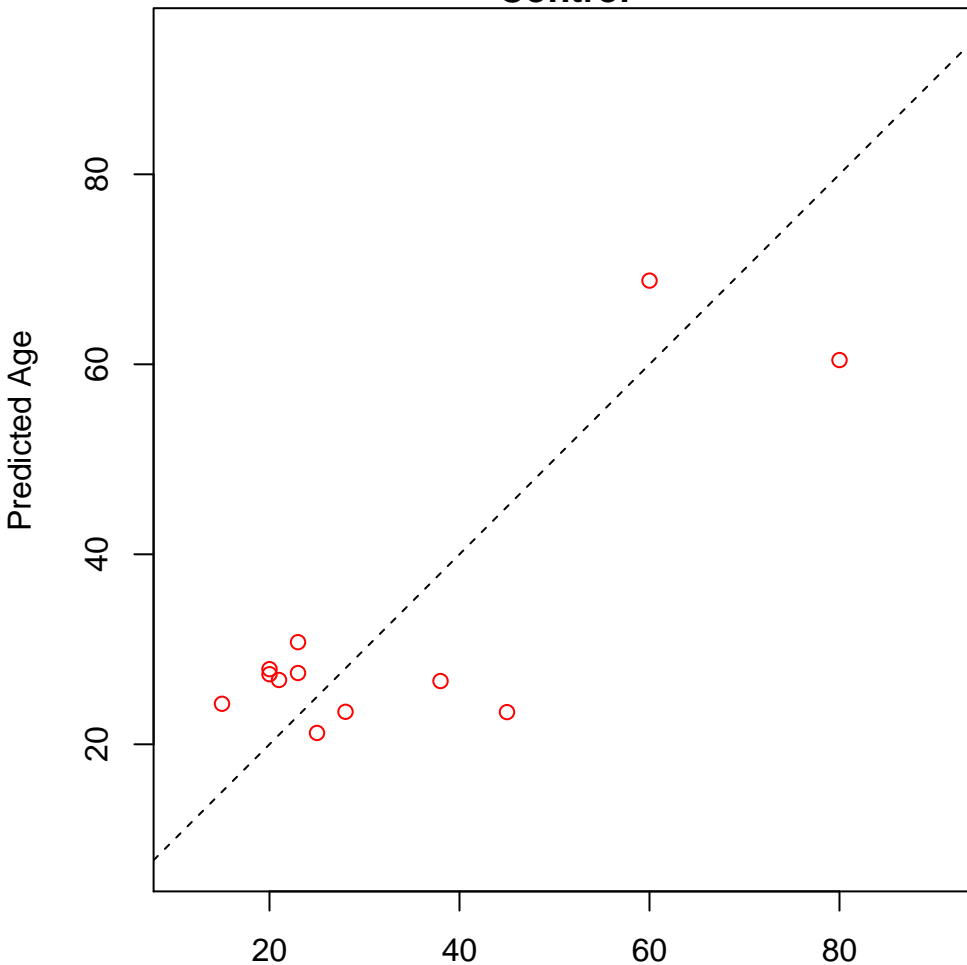


negative regulation of oxidoreductase activity (Score: 4.359232)

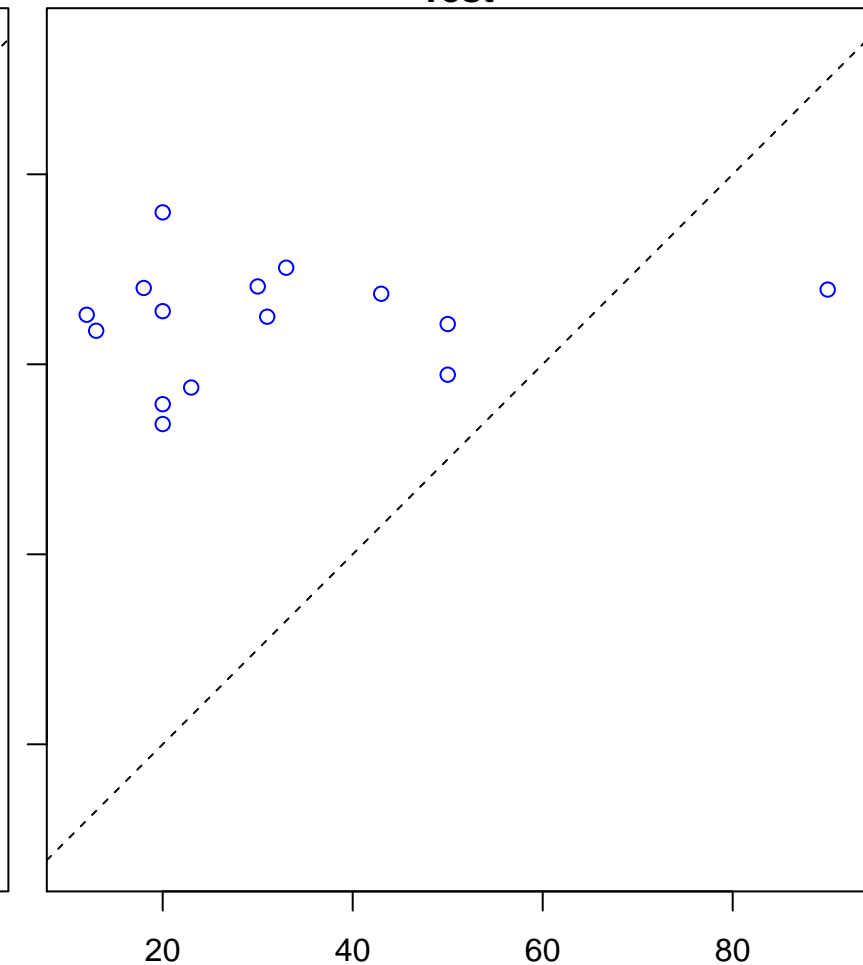


positive regulation of glucose import (Score: 4.357486)

Control

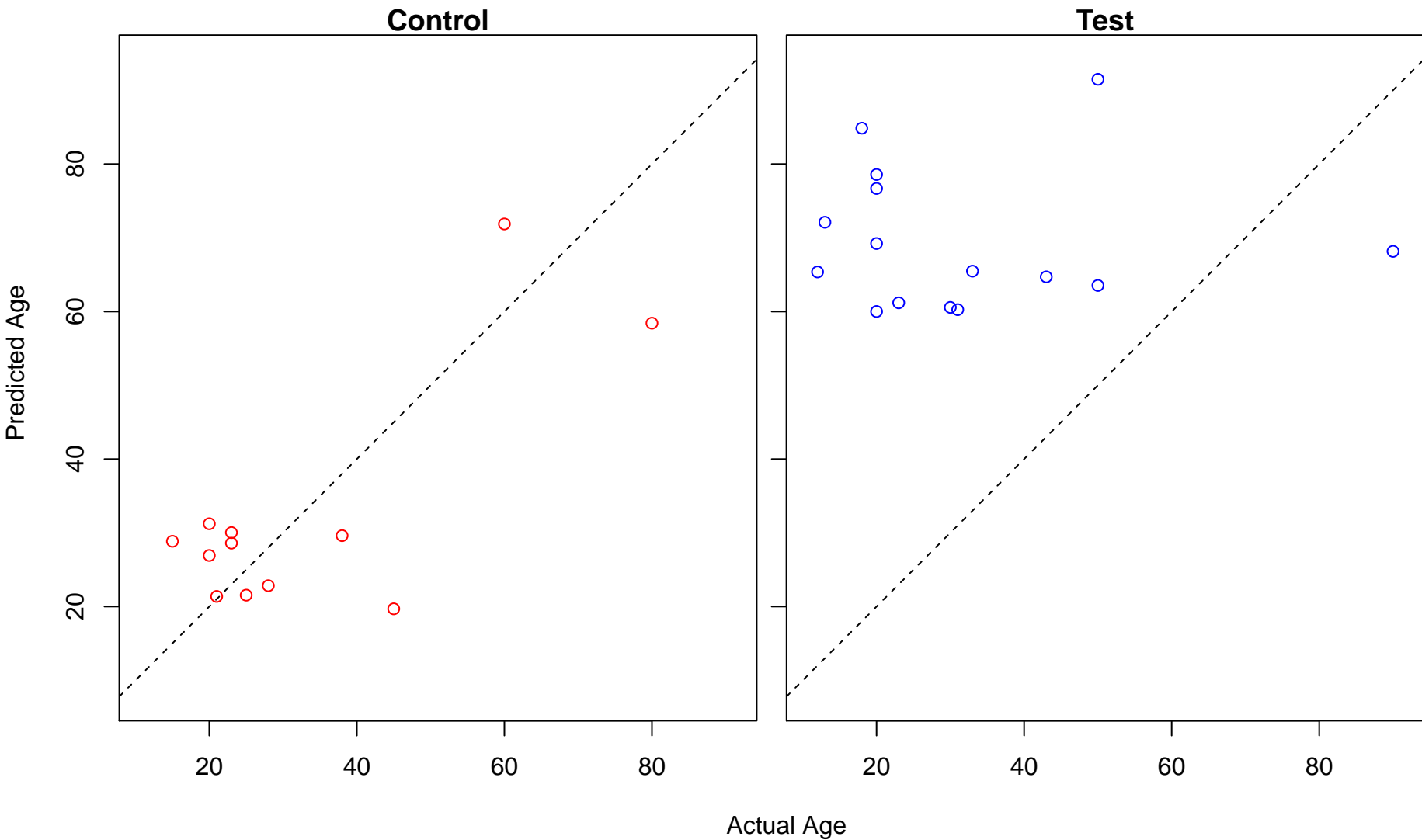


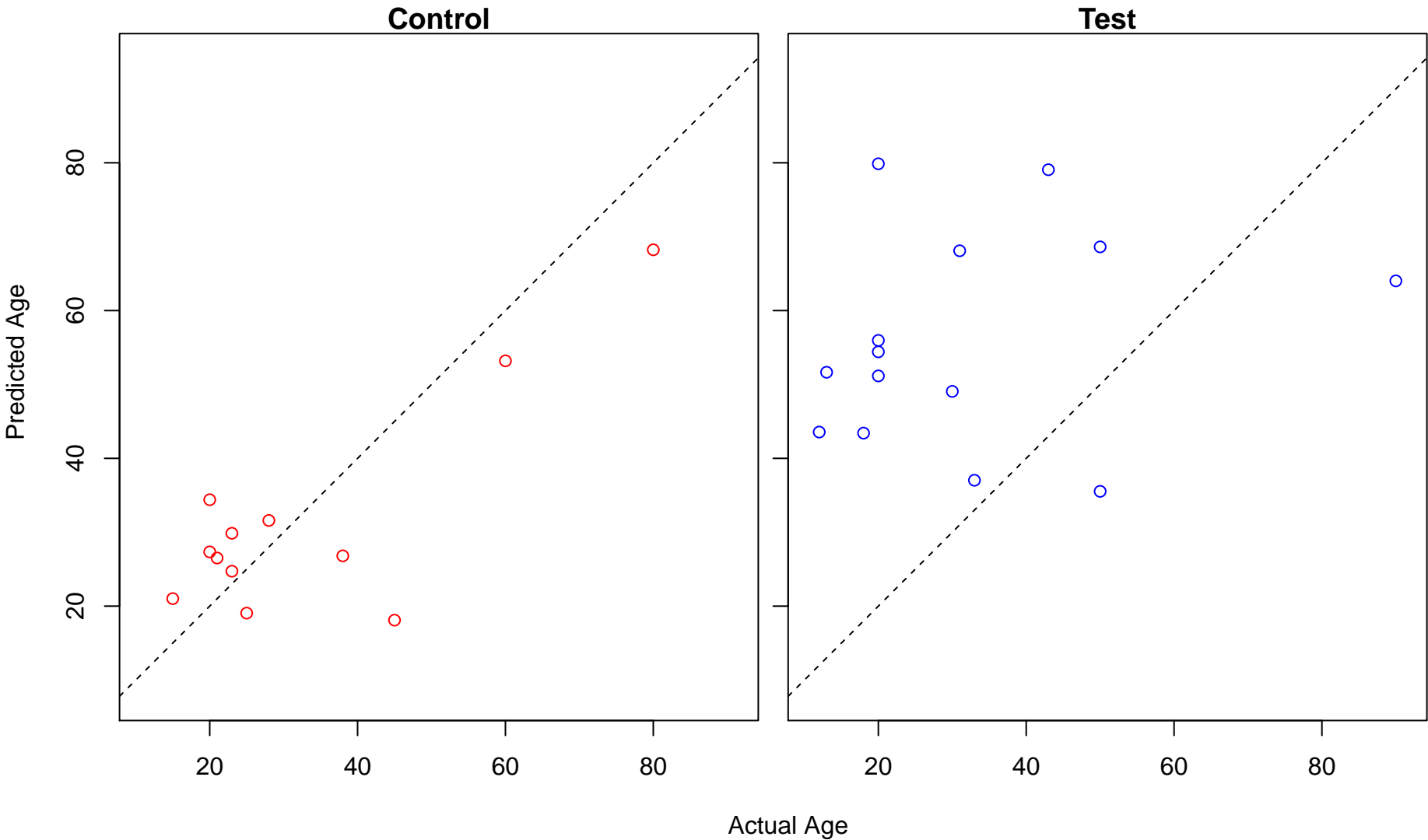
Test



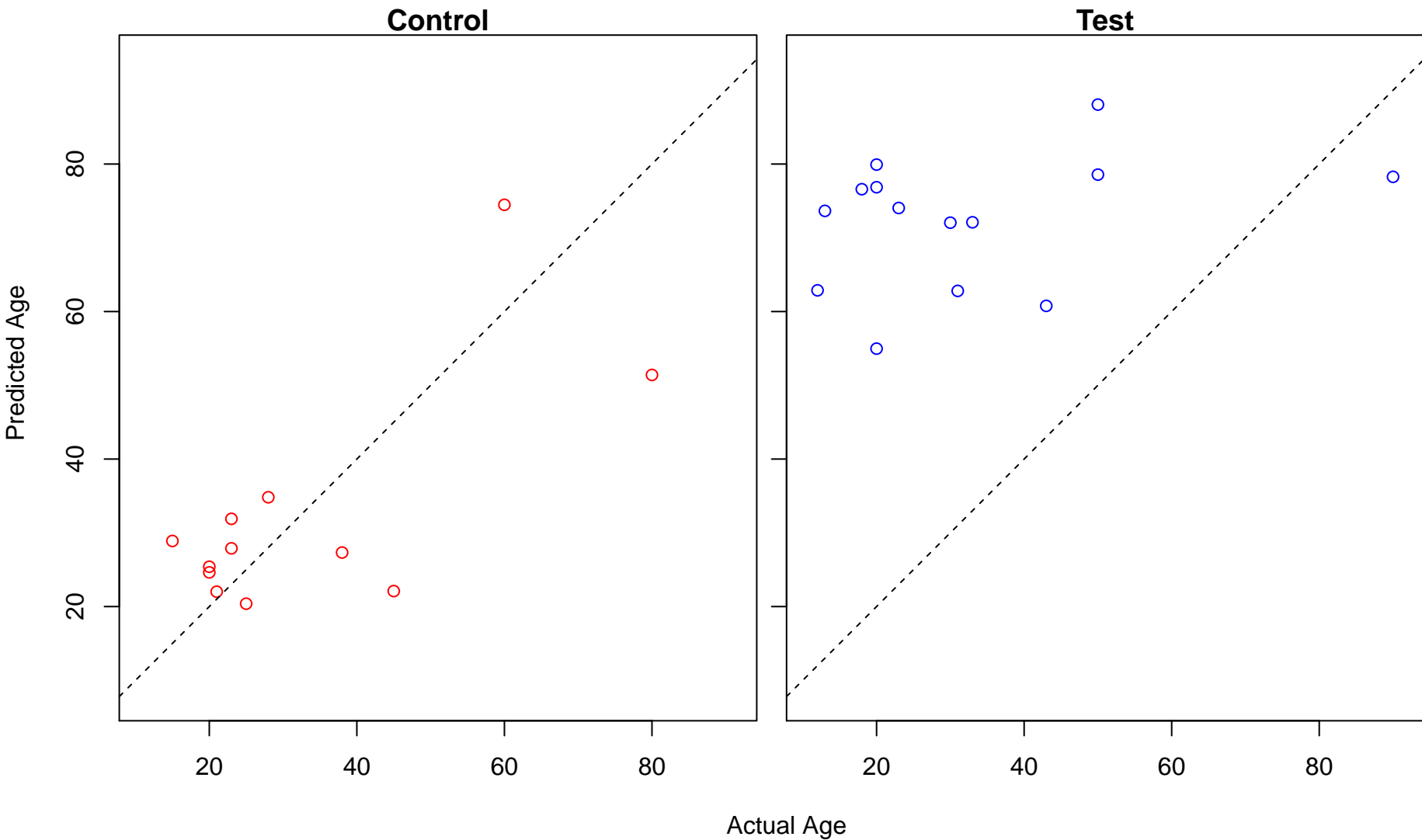
Actual Age

atrial septum development (Score: 4.354406)

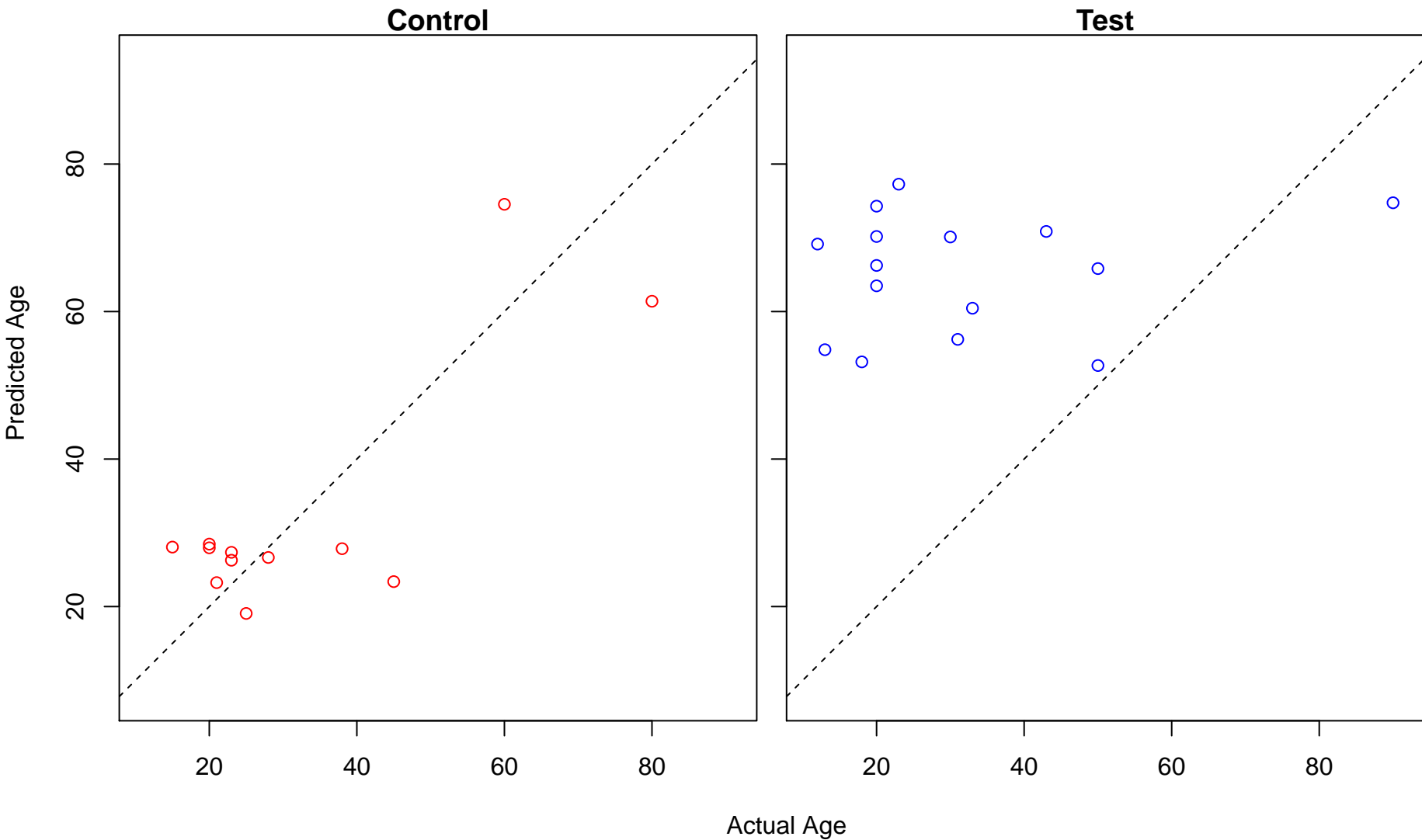




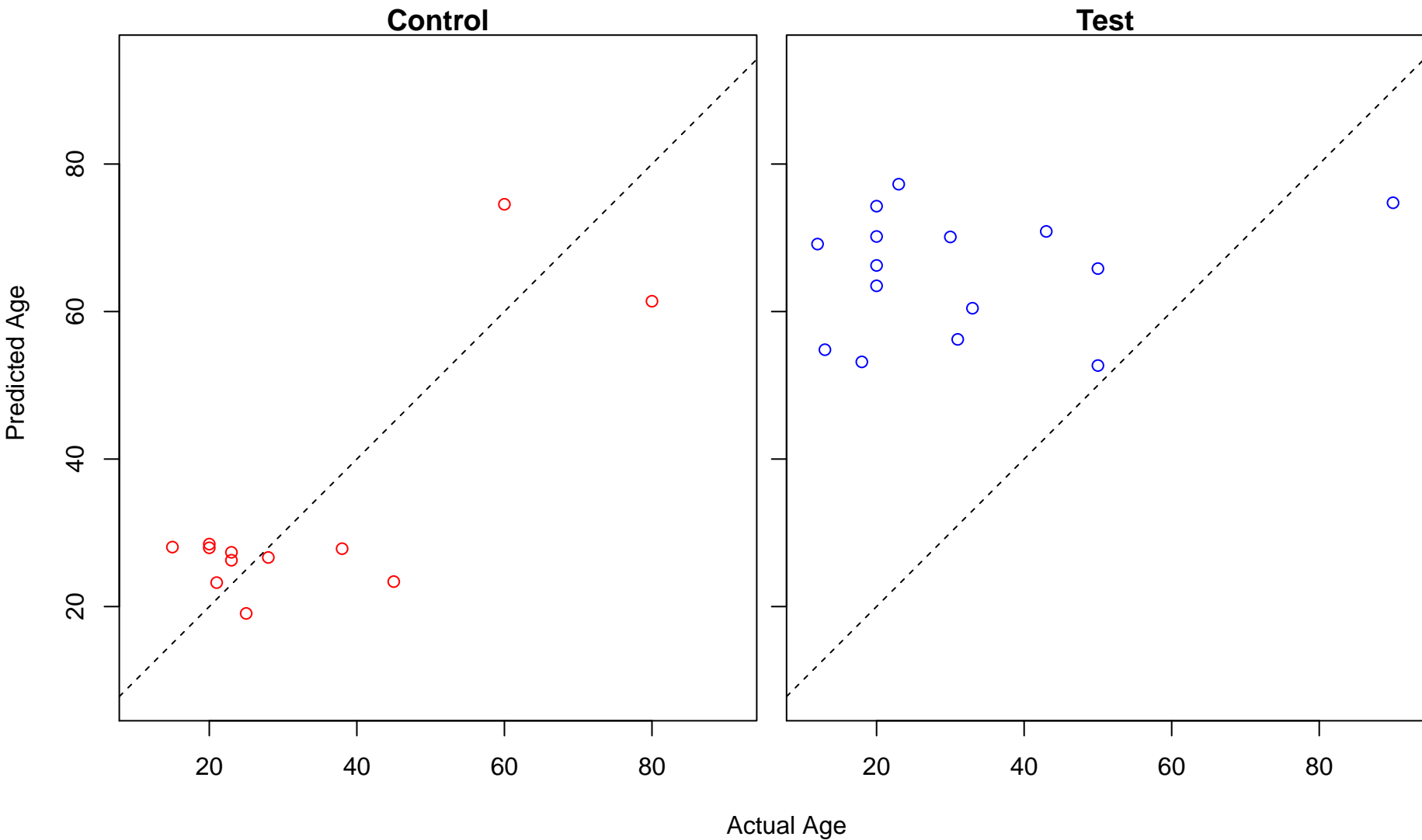
positive regulation of non-canoncal Wnt signaling pathway (Score: 4.353648)



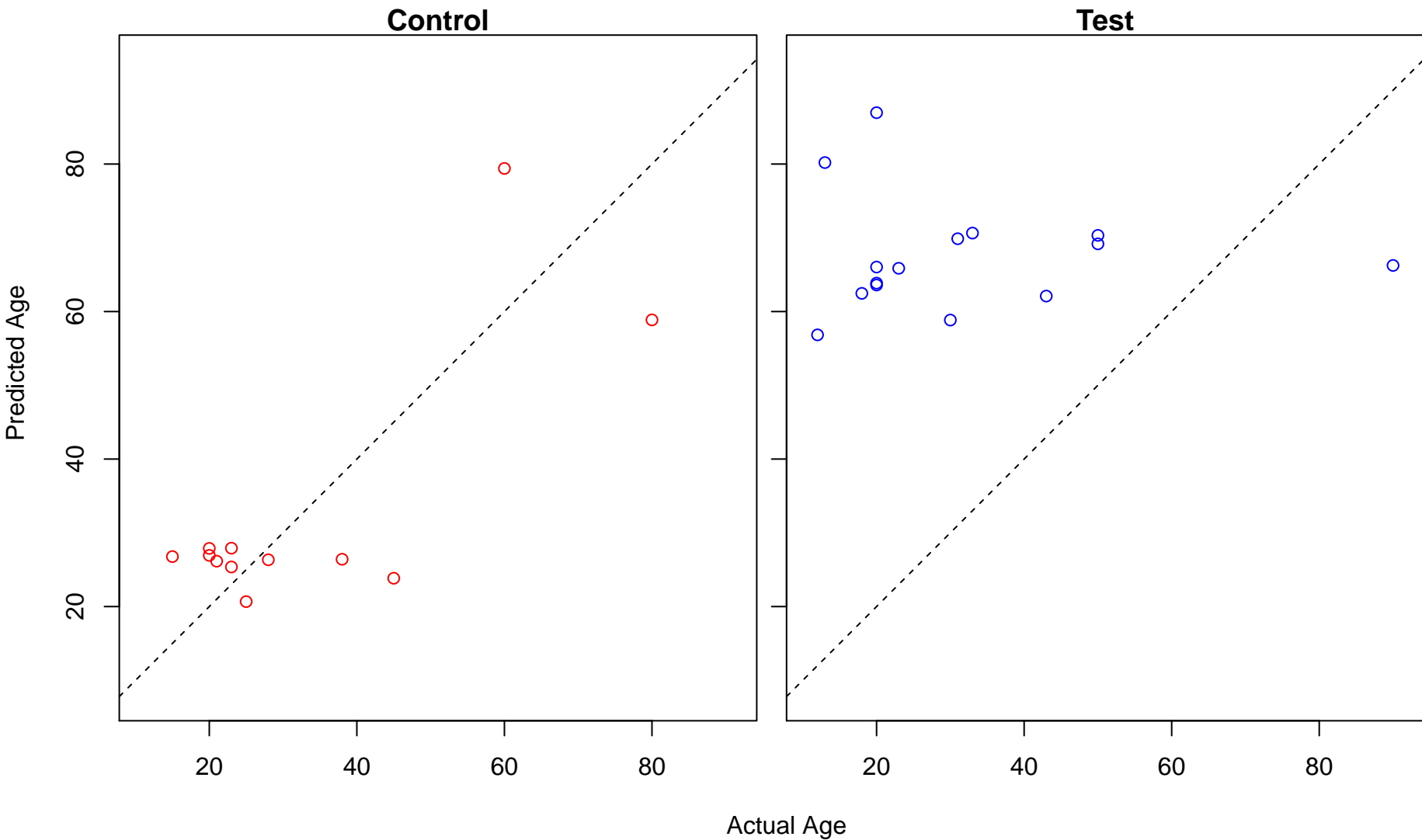
regulation of dendrite extension (Score: 4.353188)



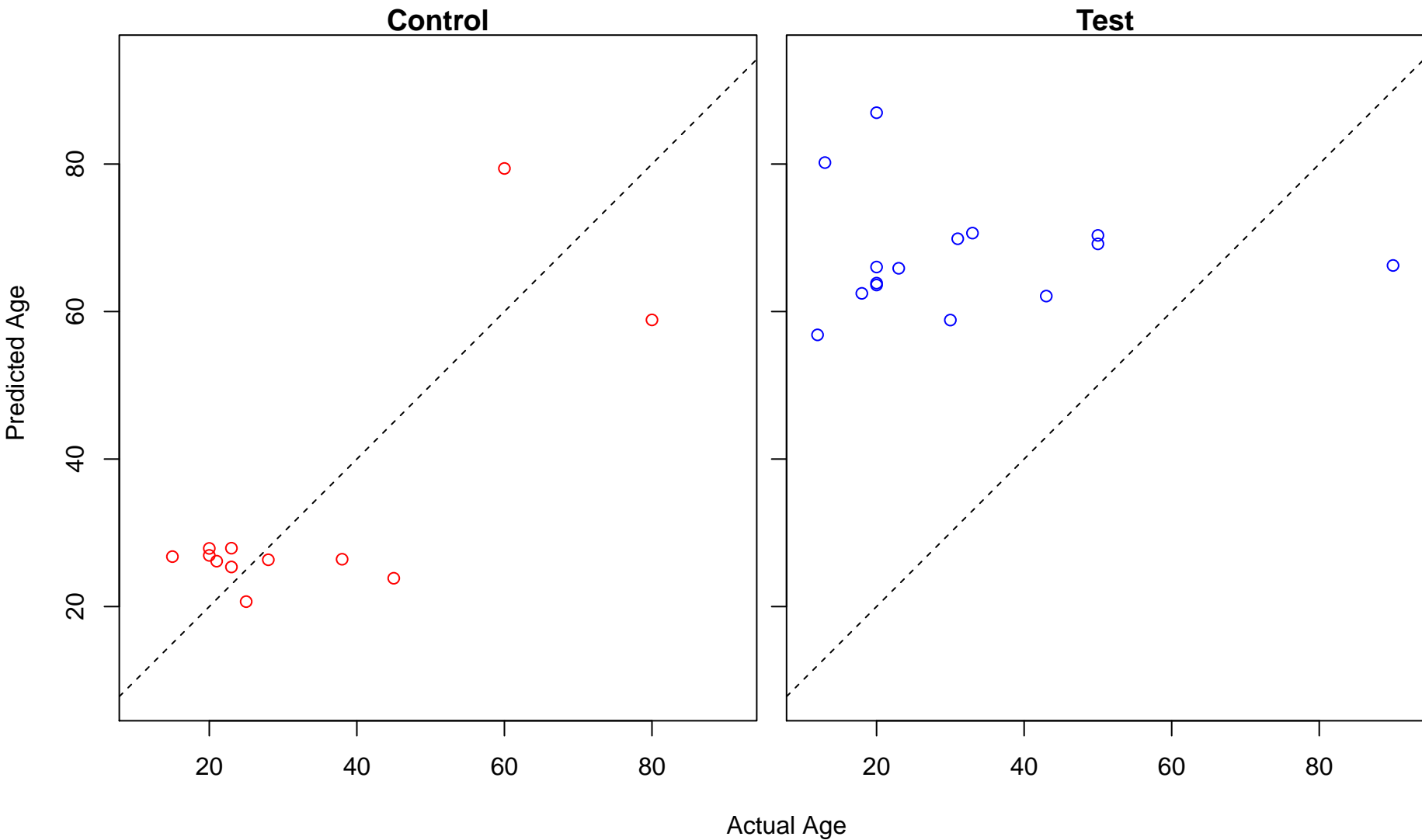
positive regulation of dendrite extension (Score: 4.353188)



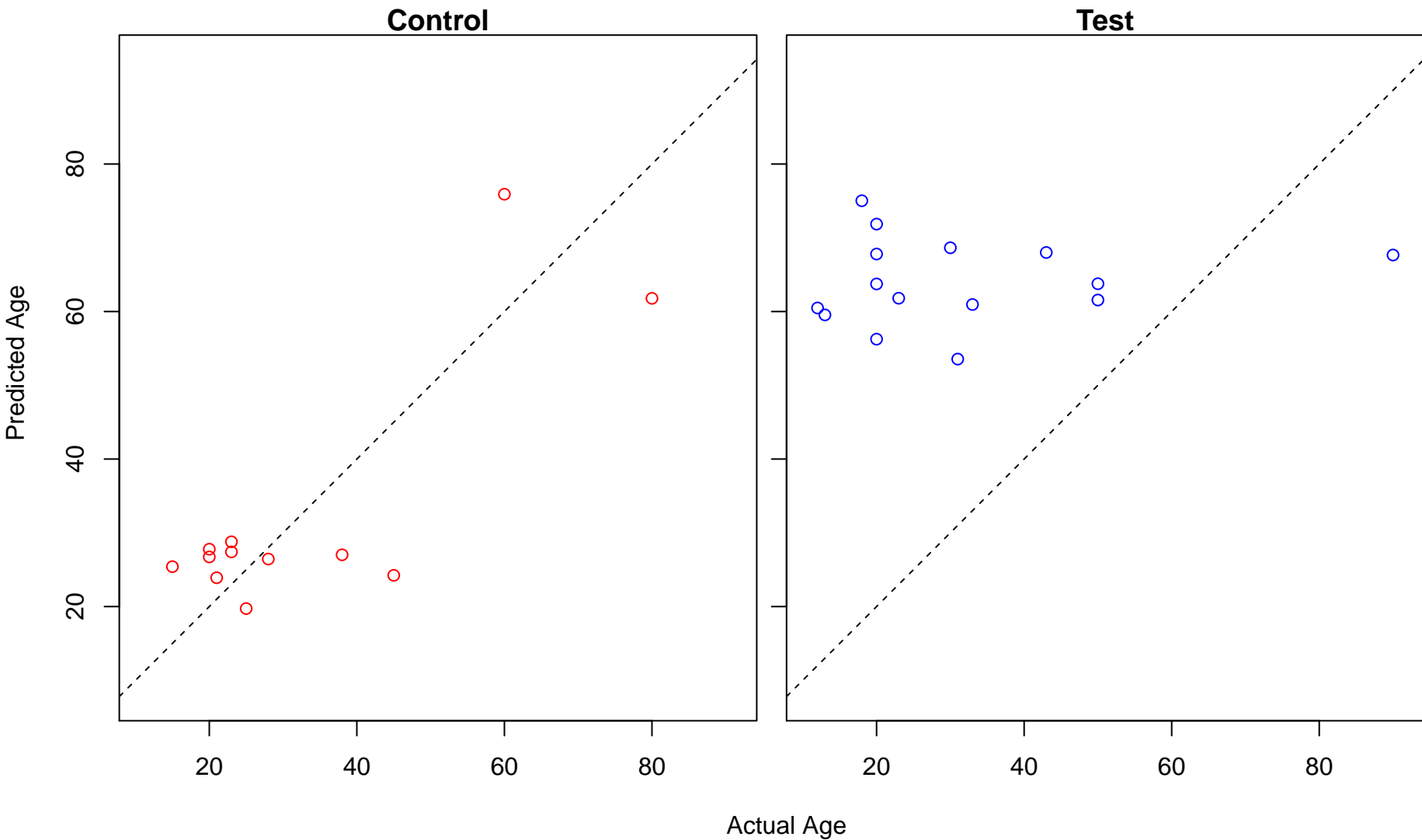
regulation of rhodopsin mediated signaling pathway (Score: 4.349703)



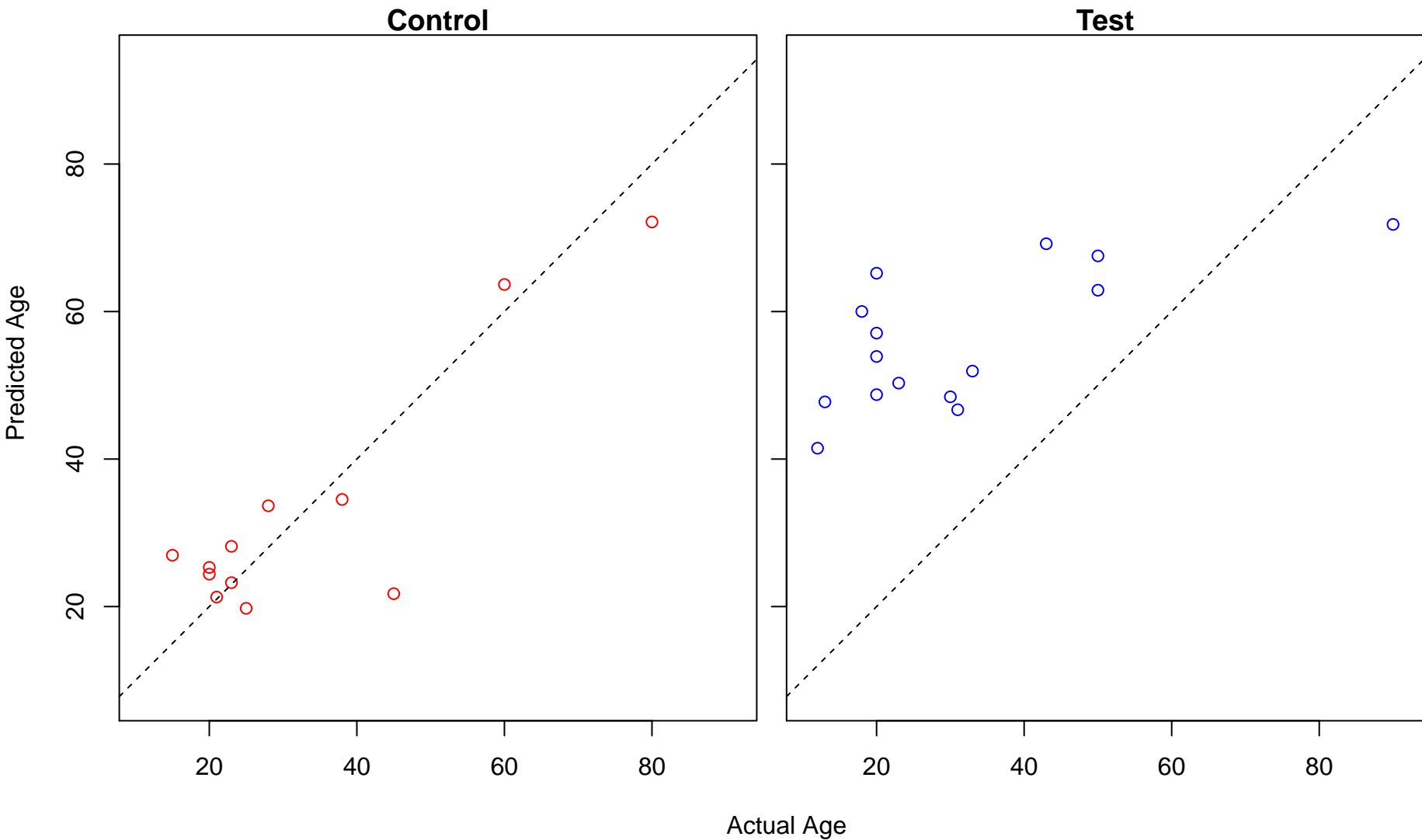
rhodopsin mediated signaling pathway (Score: 4.349534)



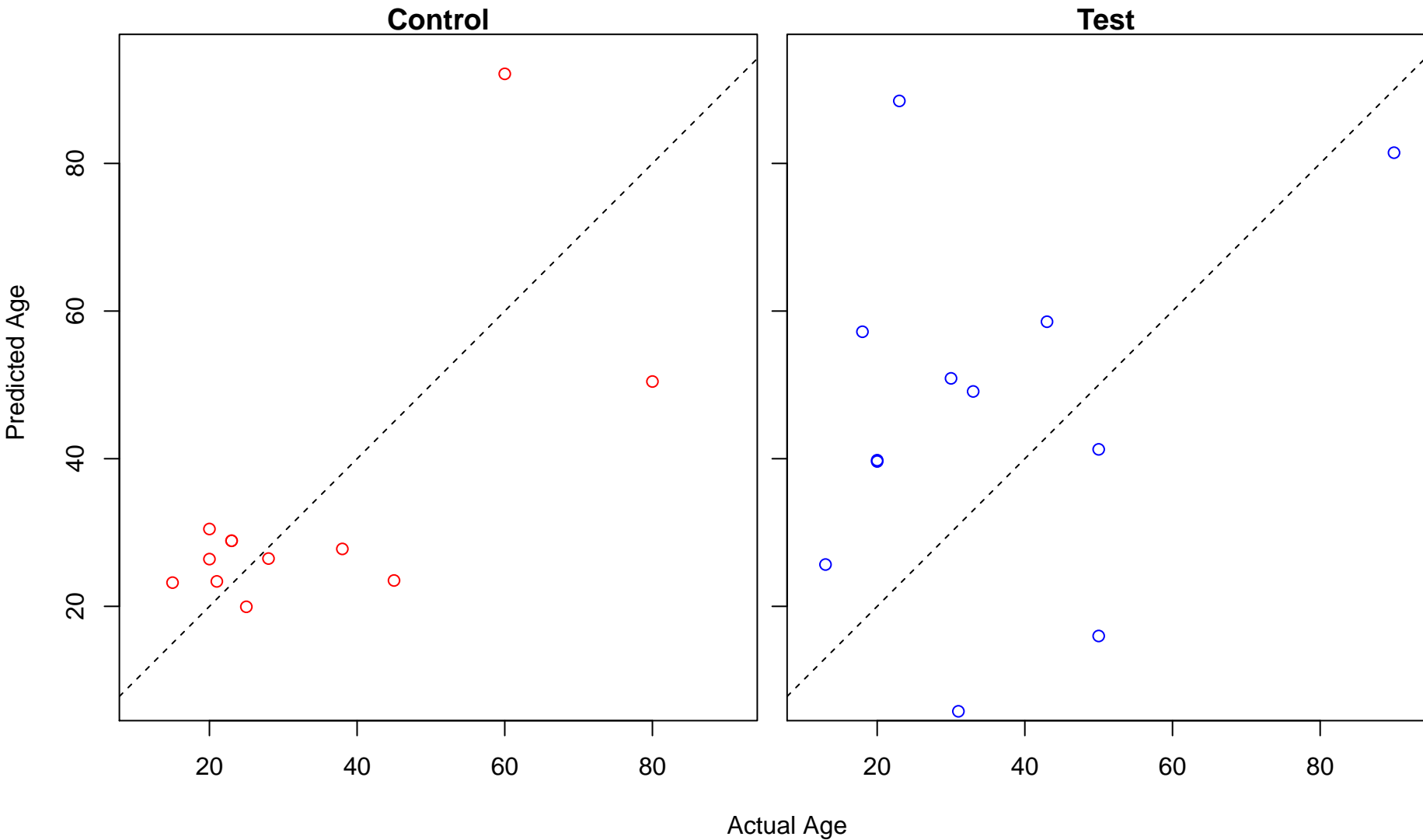
body morphogenesis (Score: 4.347880)



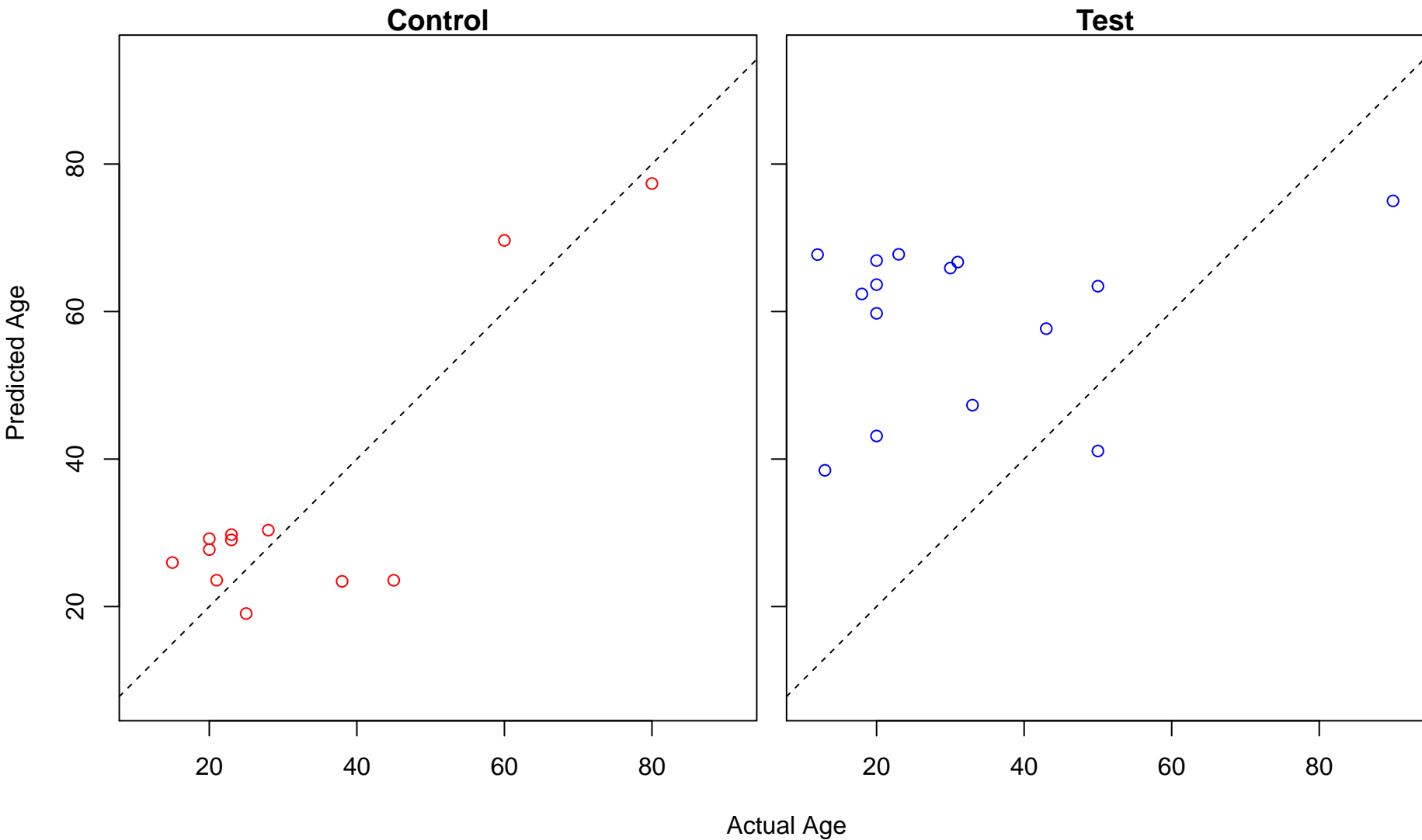
retinoic acid metabolic process (Score: 4.347686)



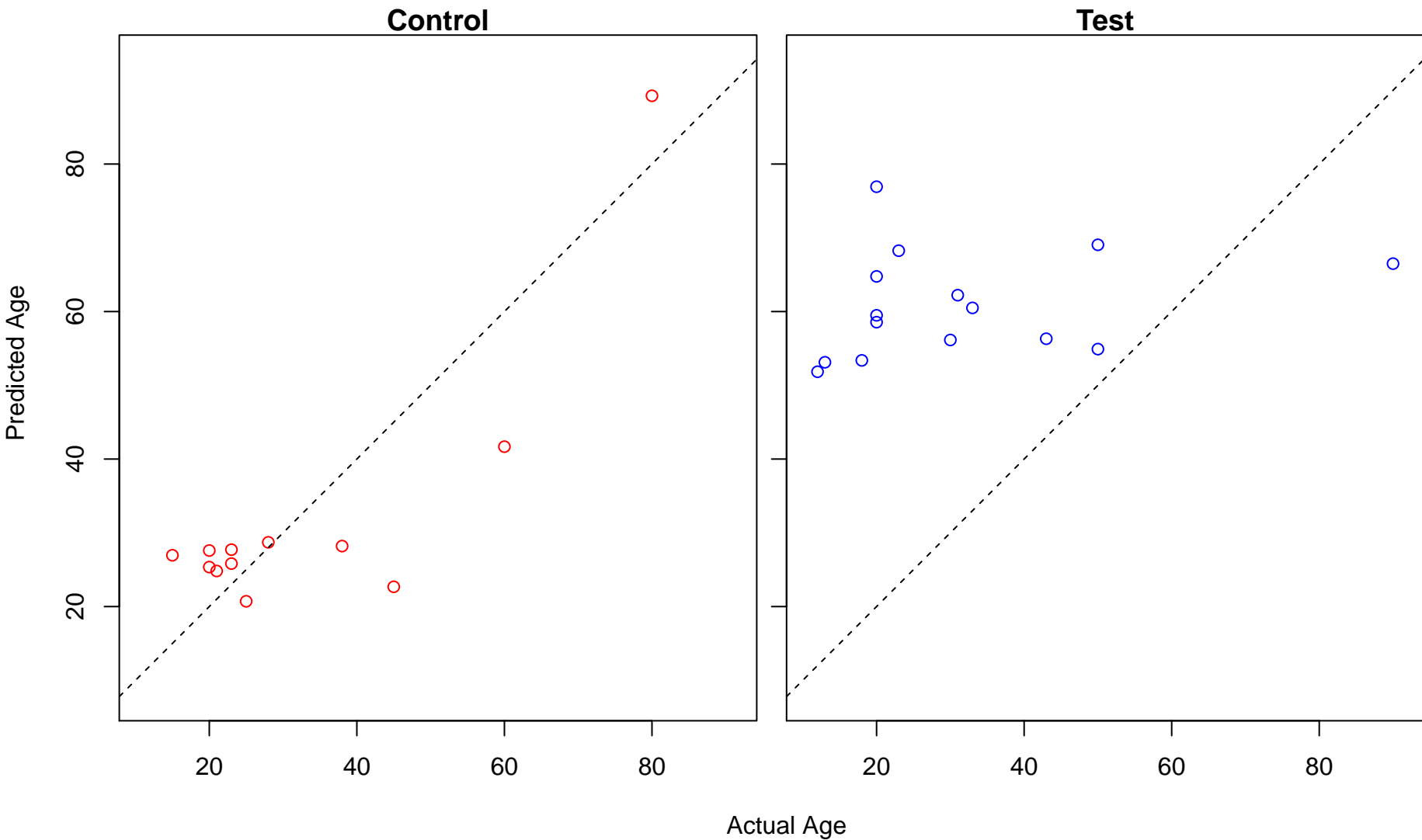
fatty acid beta-oxidation using acyl-CoA dehydrogenase (Score: 4.347429)



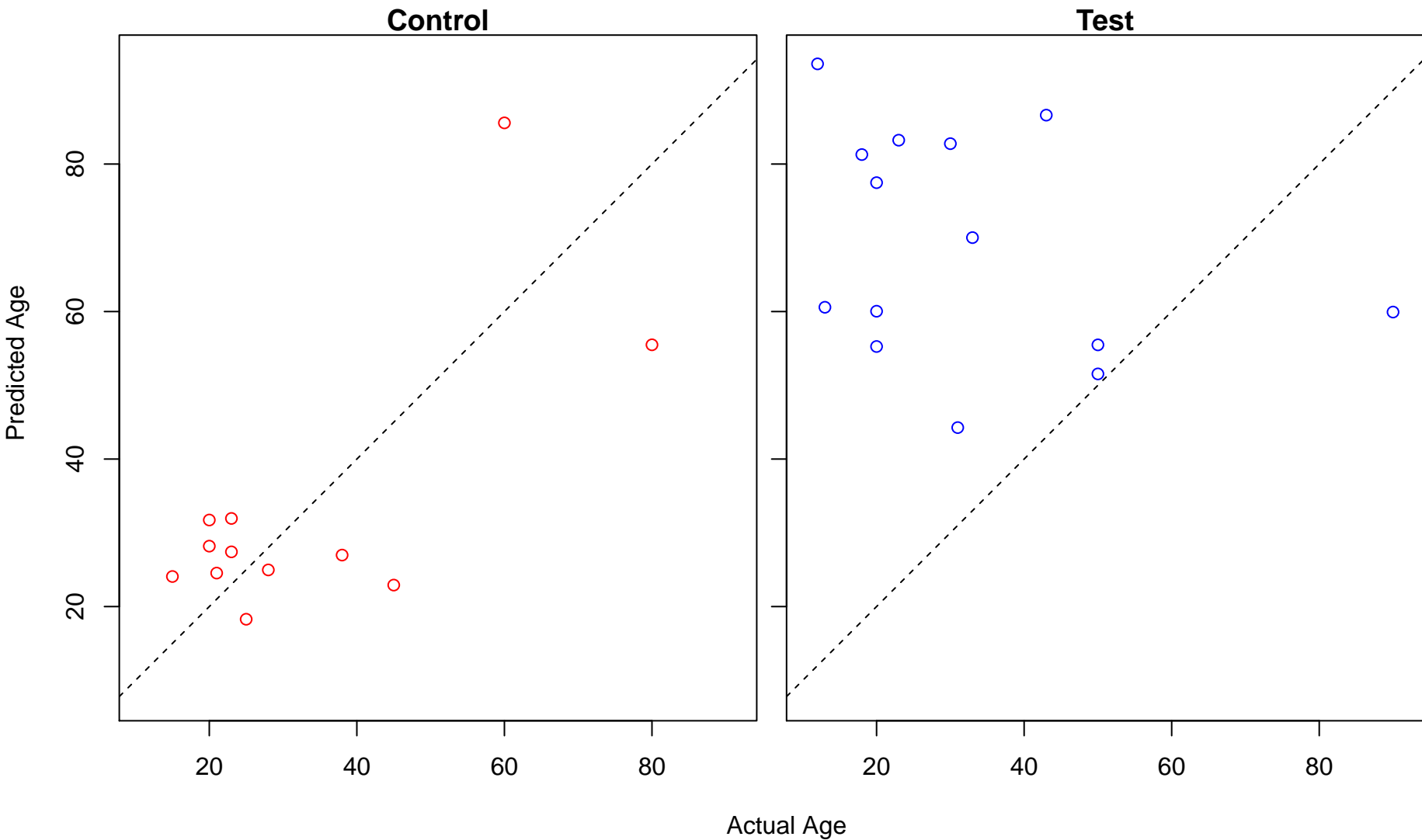
transcription from RNA polymerase III promoter (Score: 4.346092)



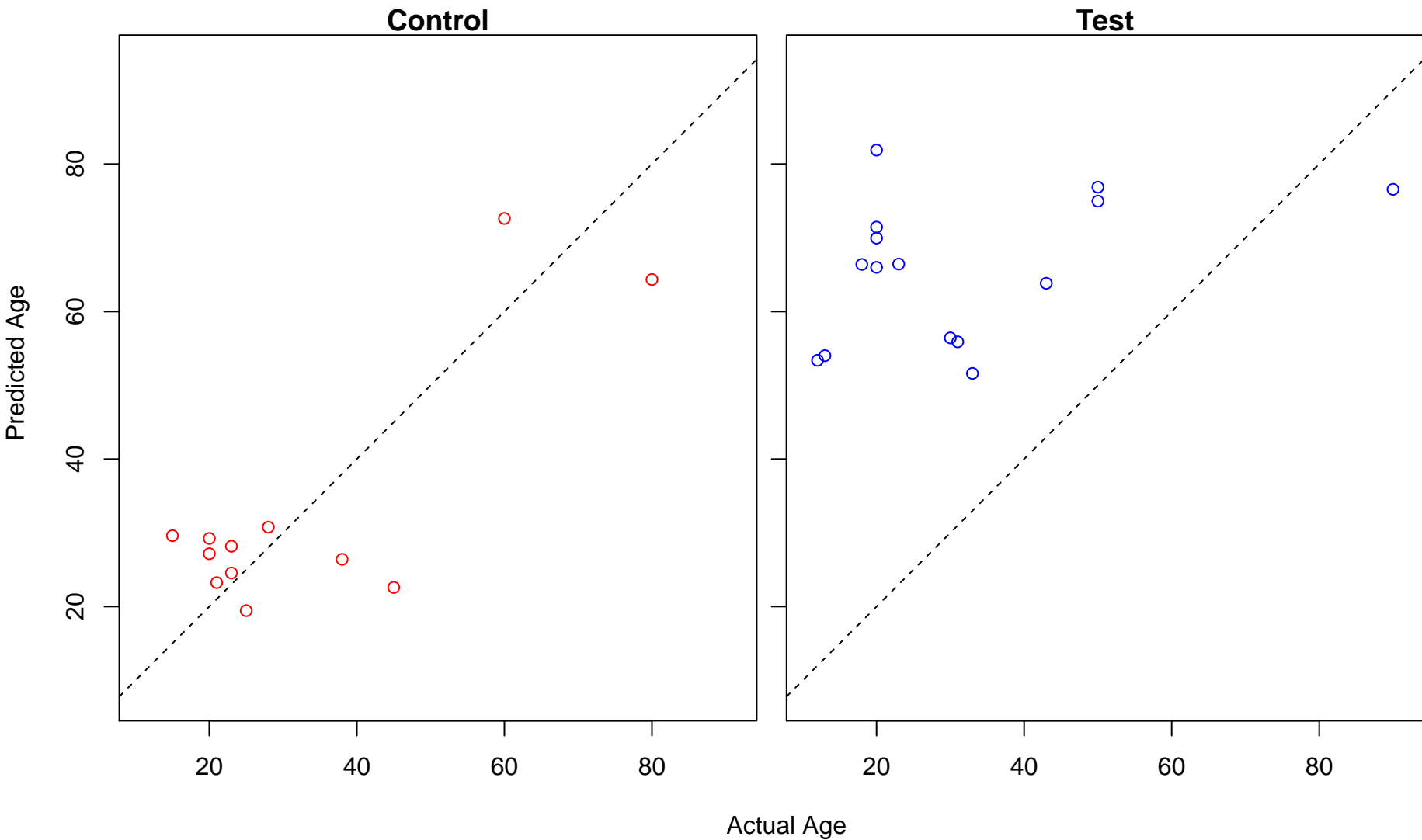
microtubule-based process (Score: 4.345314)



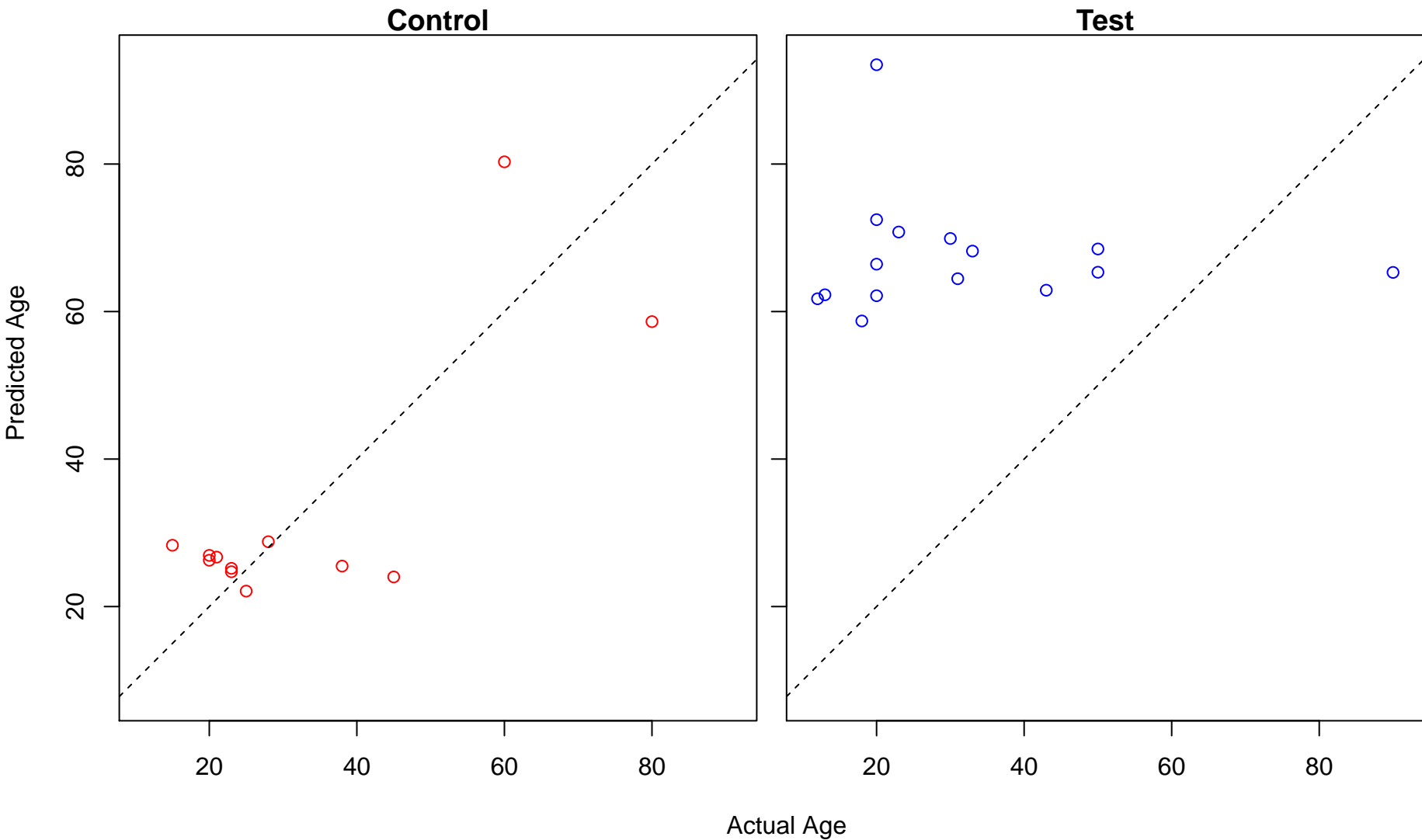
negative regulation of hormone metabolic process (Score: 4.343149)



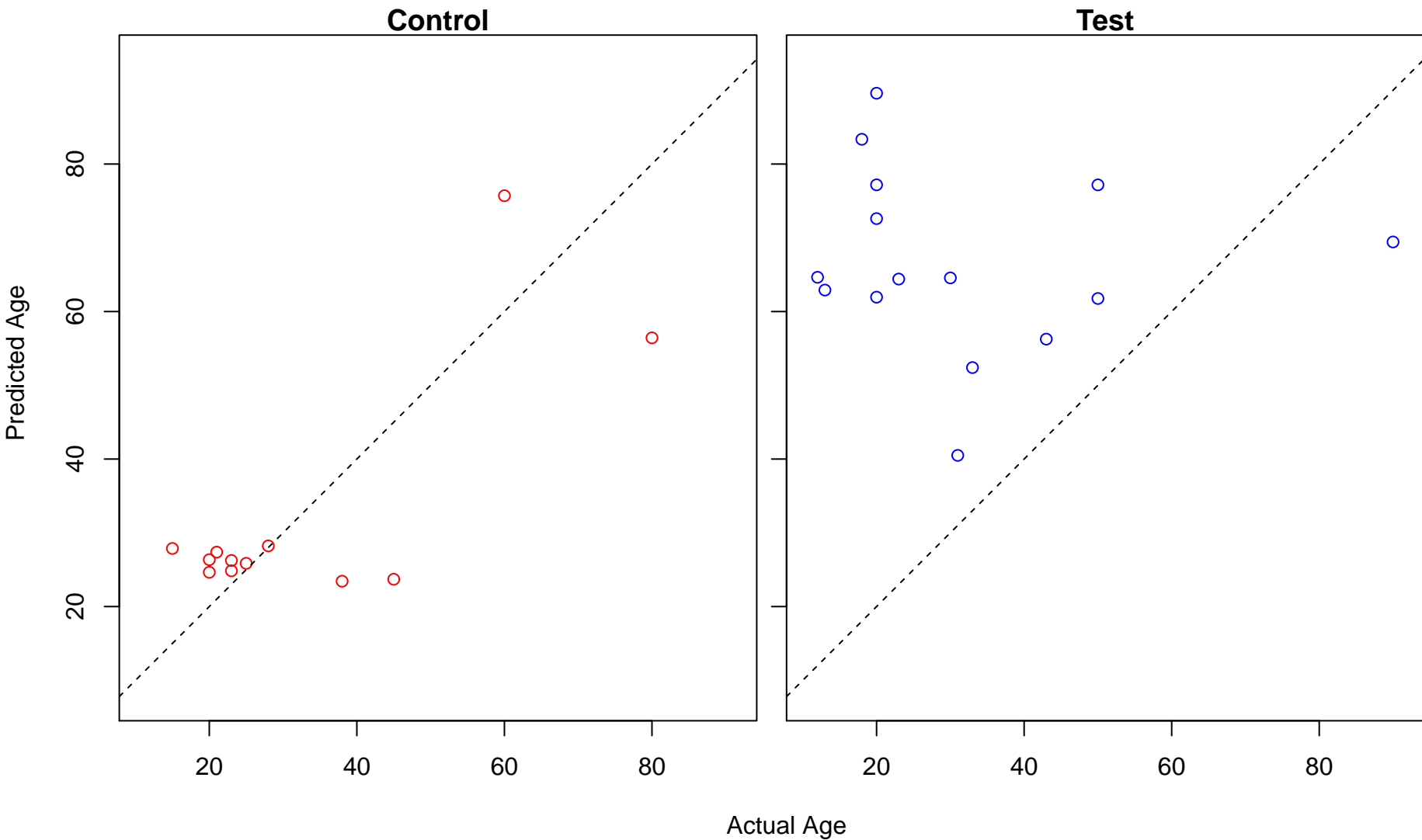
negative regulation of cytokine production (Score: 4.342859)



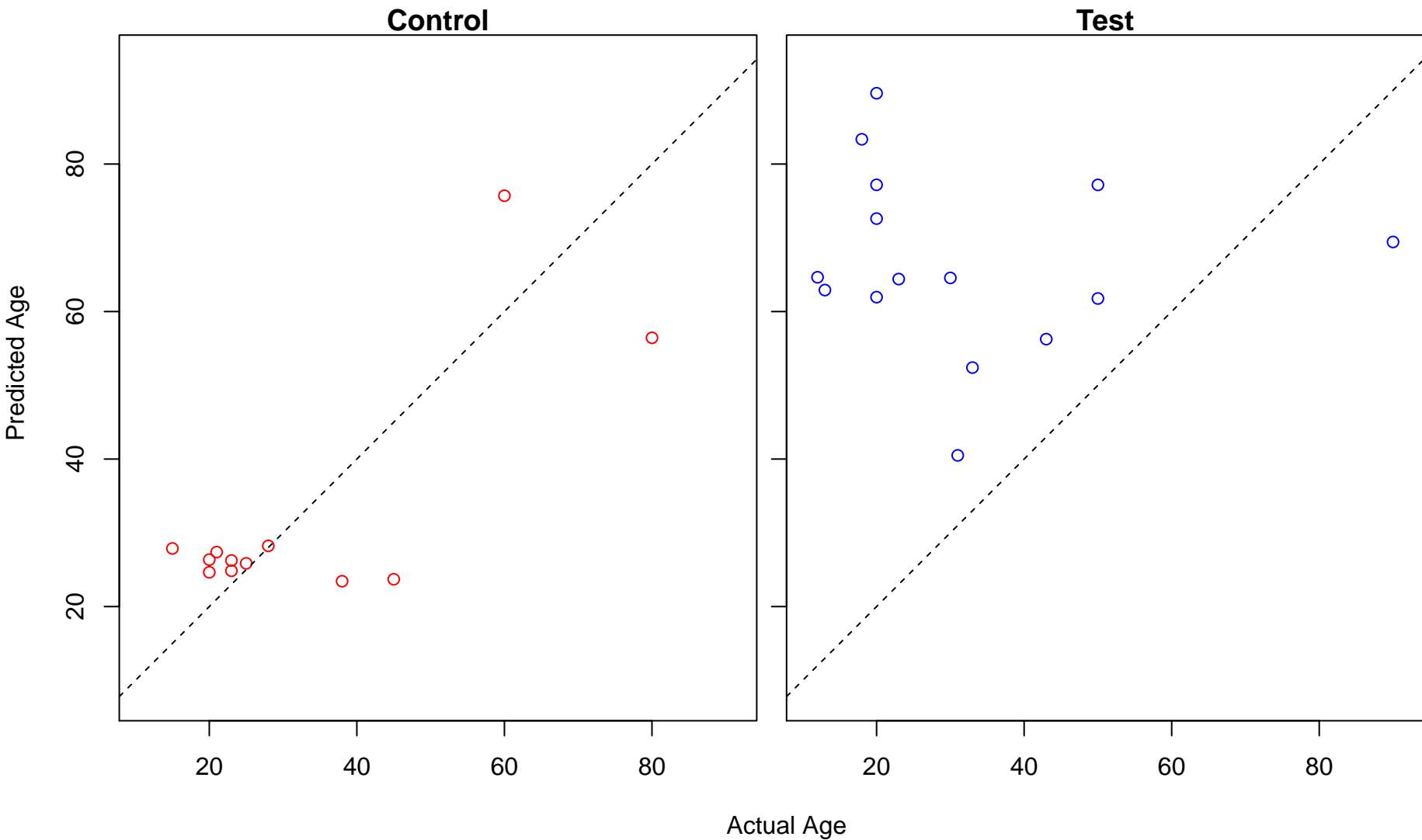
negative regulation of protein complex disassembly (Score: 4.342025)



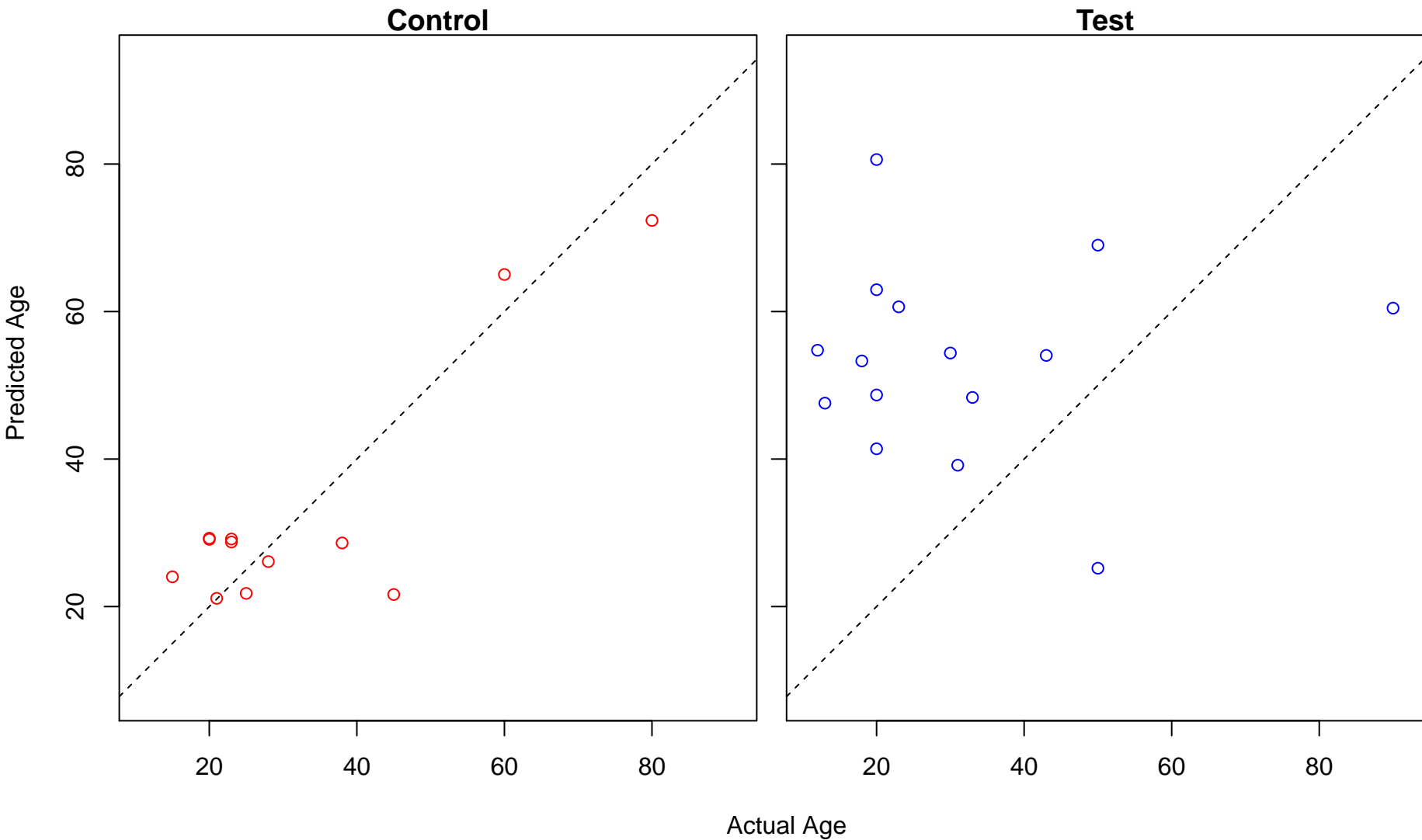
purine nucleoside monophosphate biosynthetic process (Score: 4.341733)



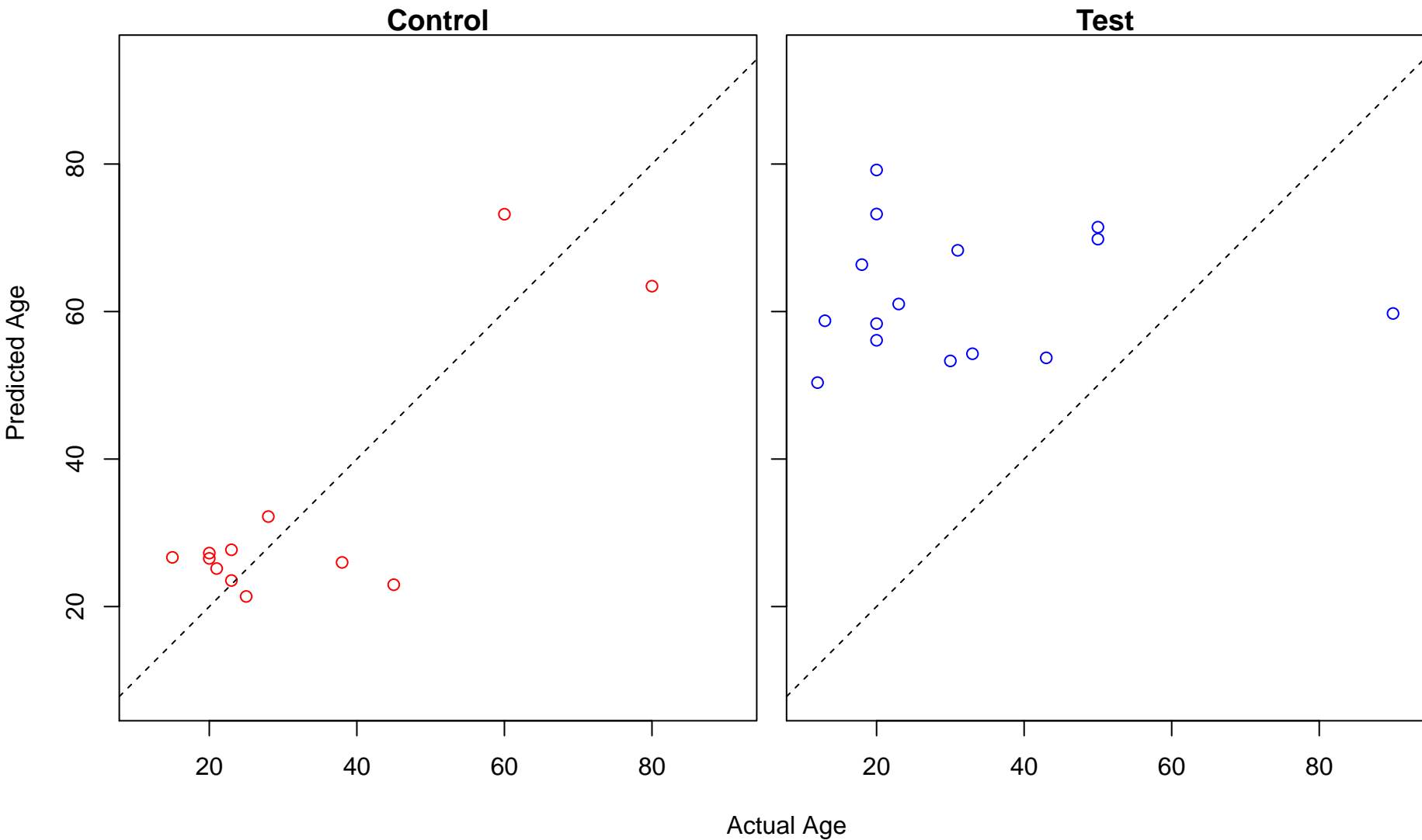
purine ribonucleoside monophosphate biosynthetic process (Score: 4.341733)



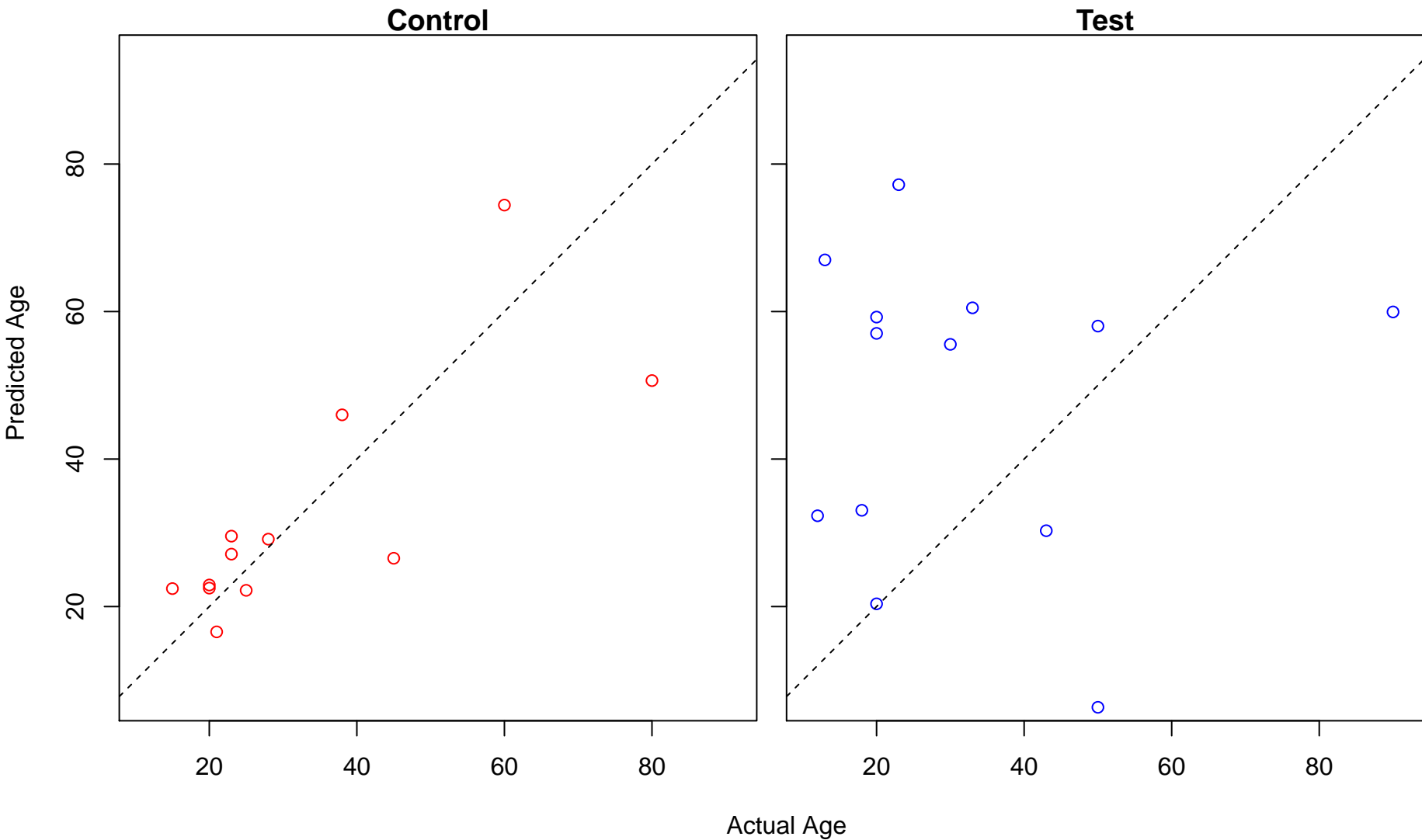
regulation of t-circle formation (Score: 4.339553)



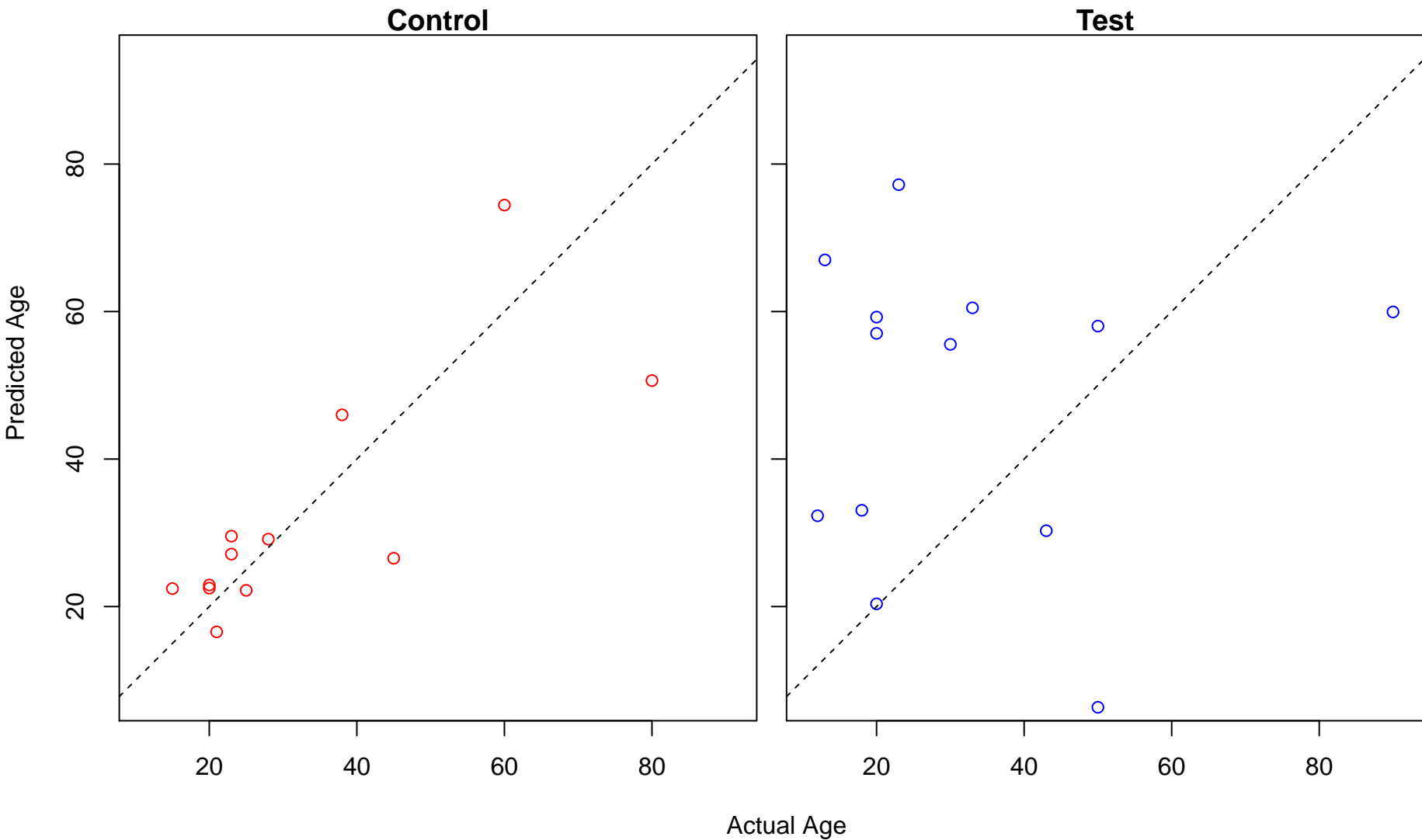
regulation of heart rate (Score: 4.339170)



cochlea development (Score: 4.337413)

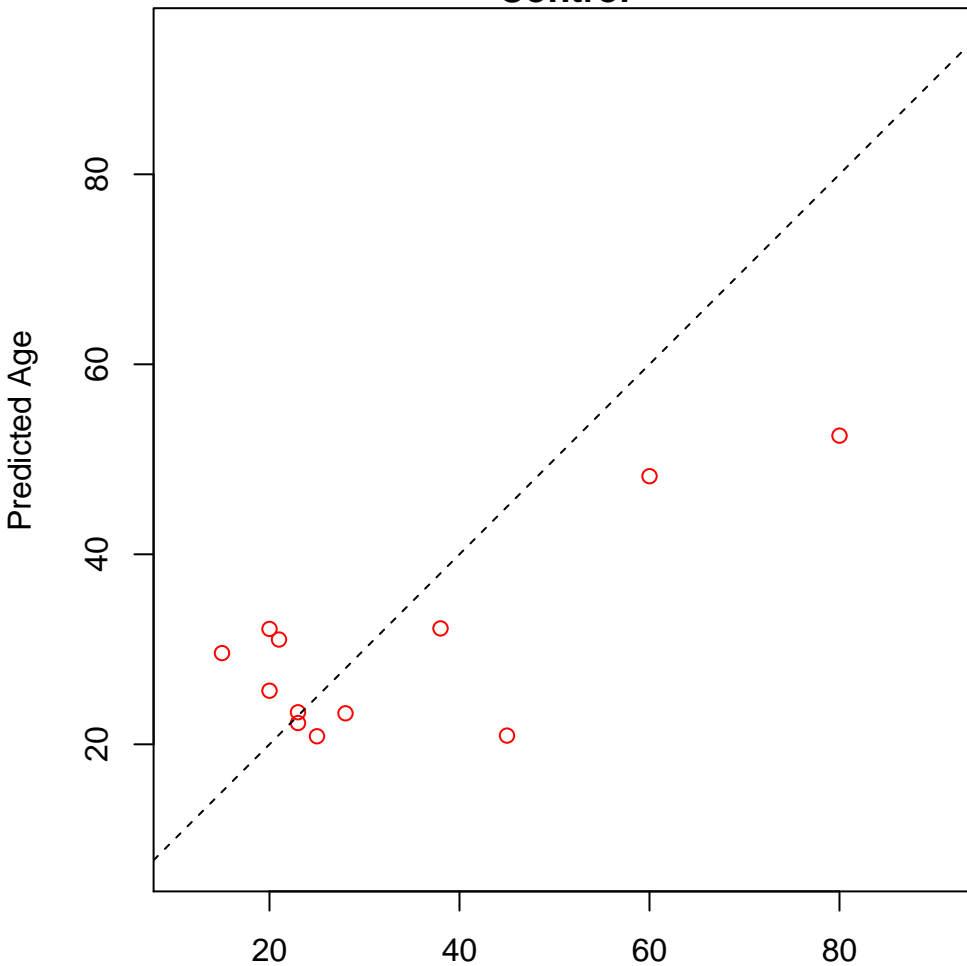


cochlea morphogenesis (Score: 4.337413)

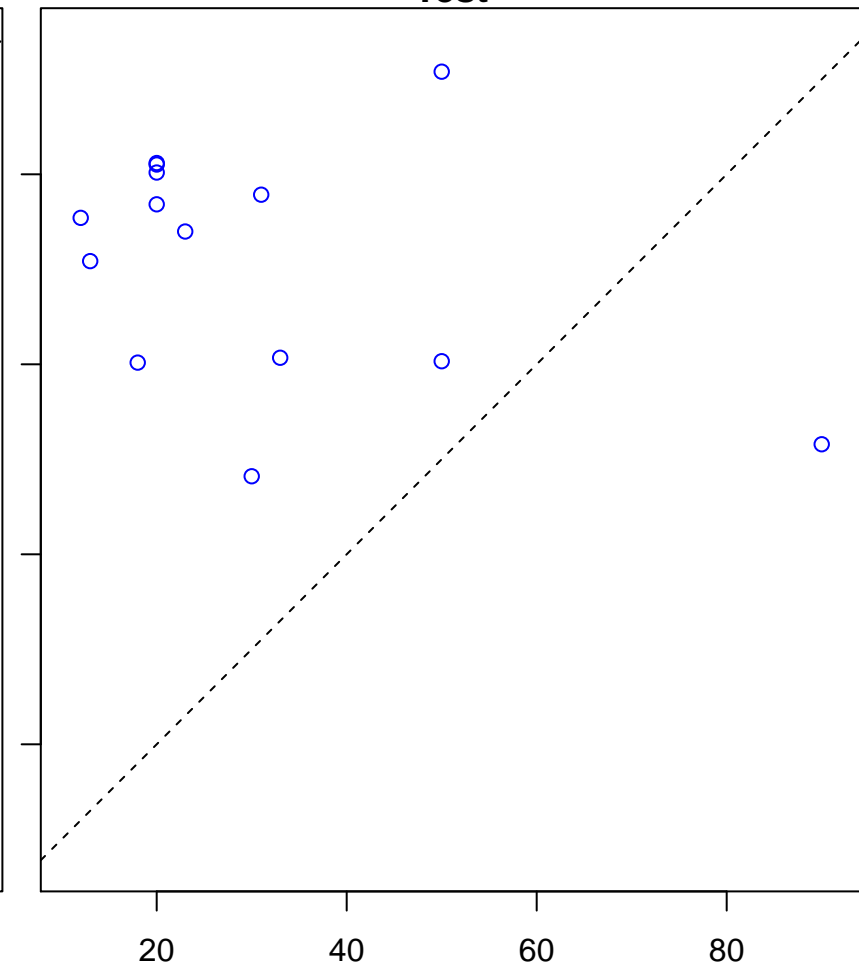


postsynaptic membrane assembly (Score: 4.337073)

Control

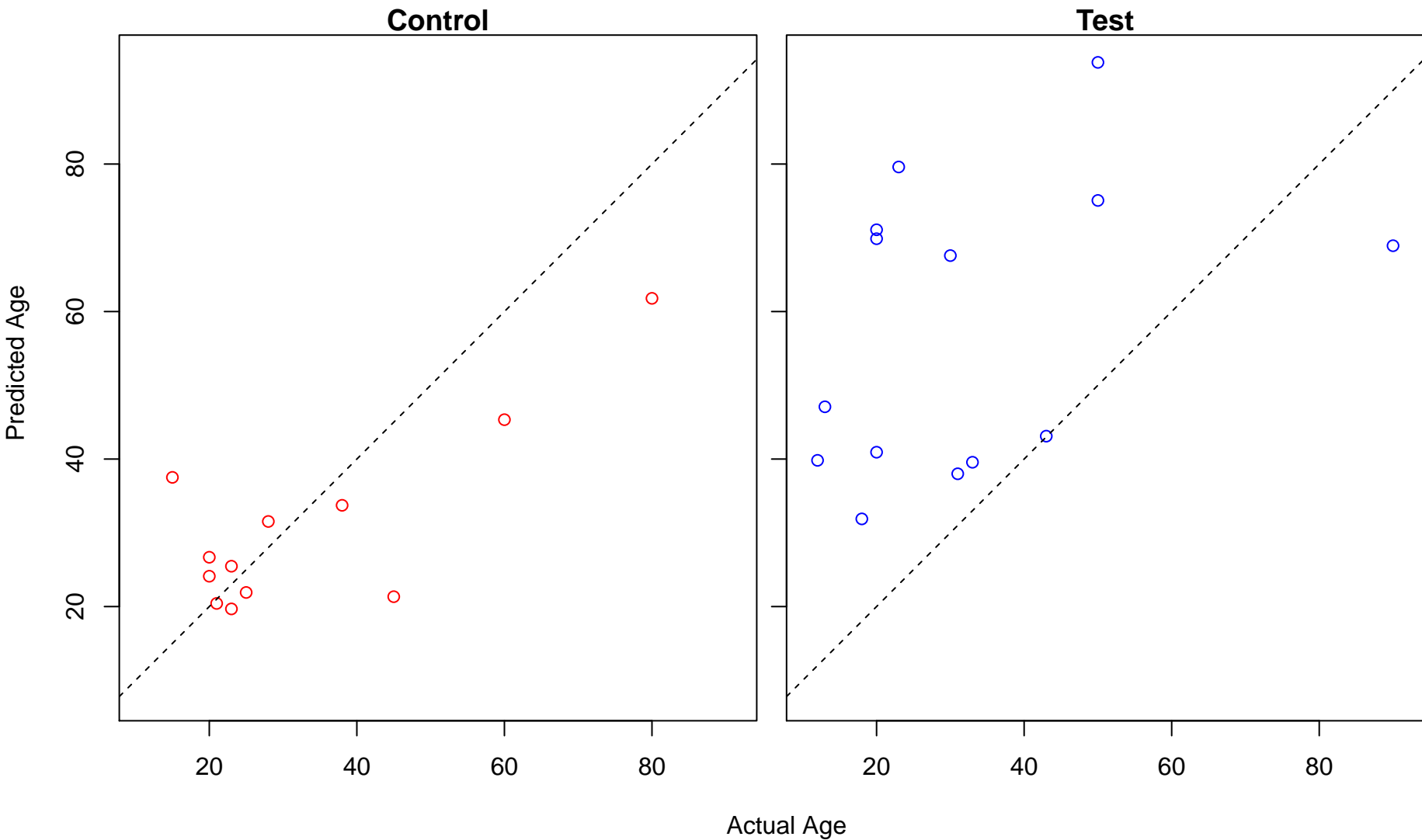


Test

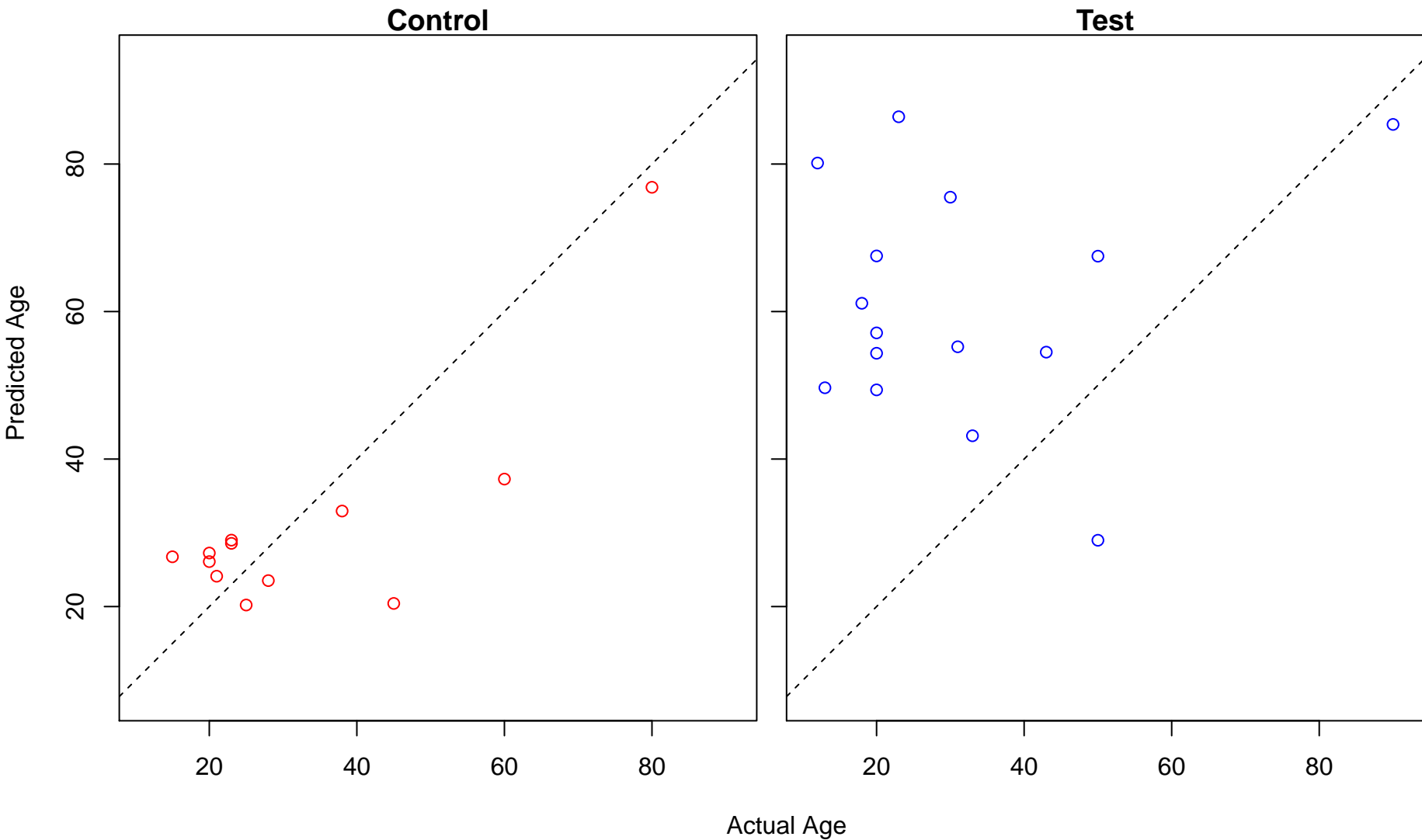


Actual Age

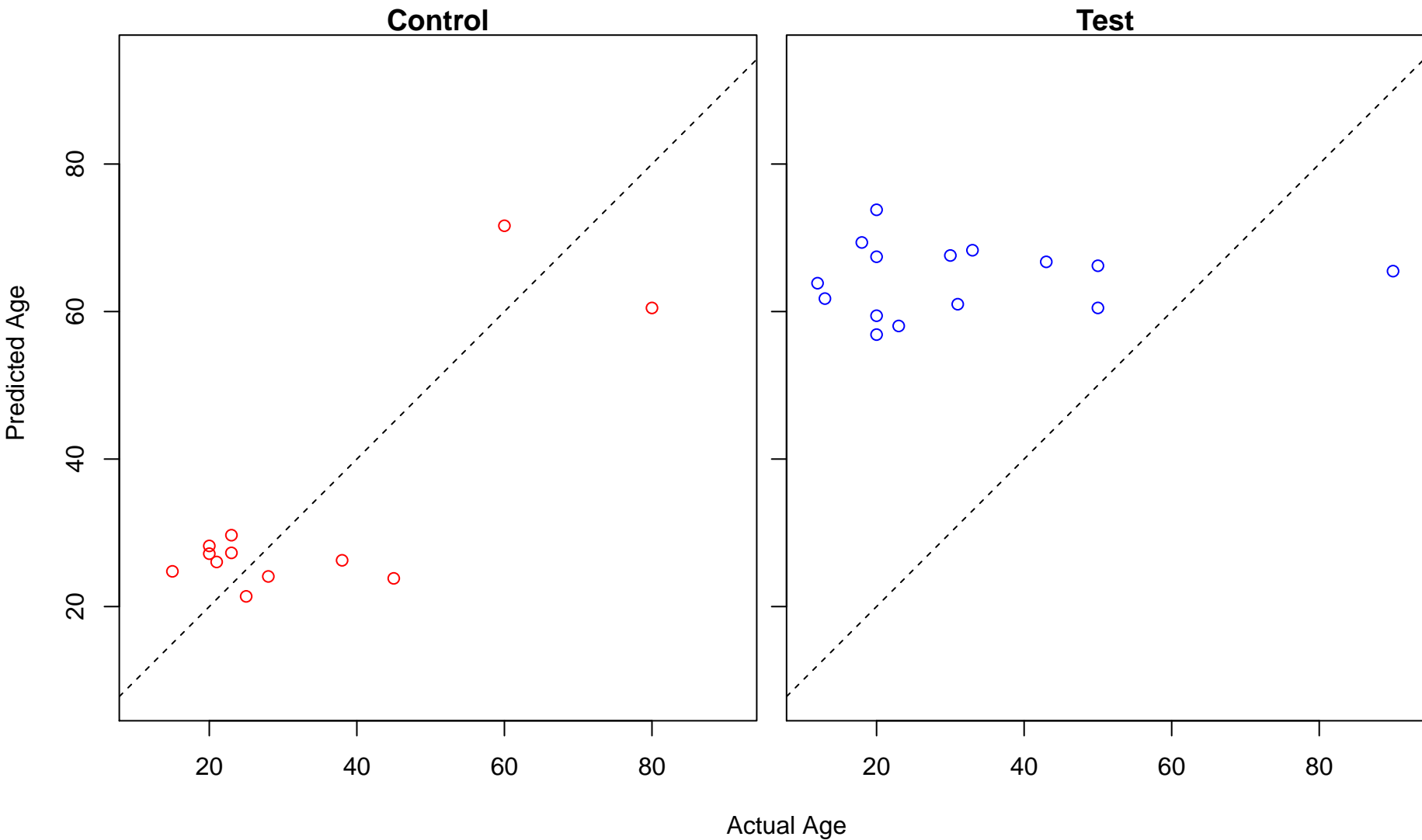
regulation of transcription from RNA polymerase III promoter (Score: 4.336638)



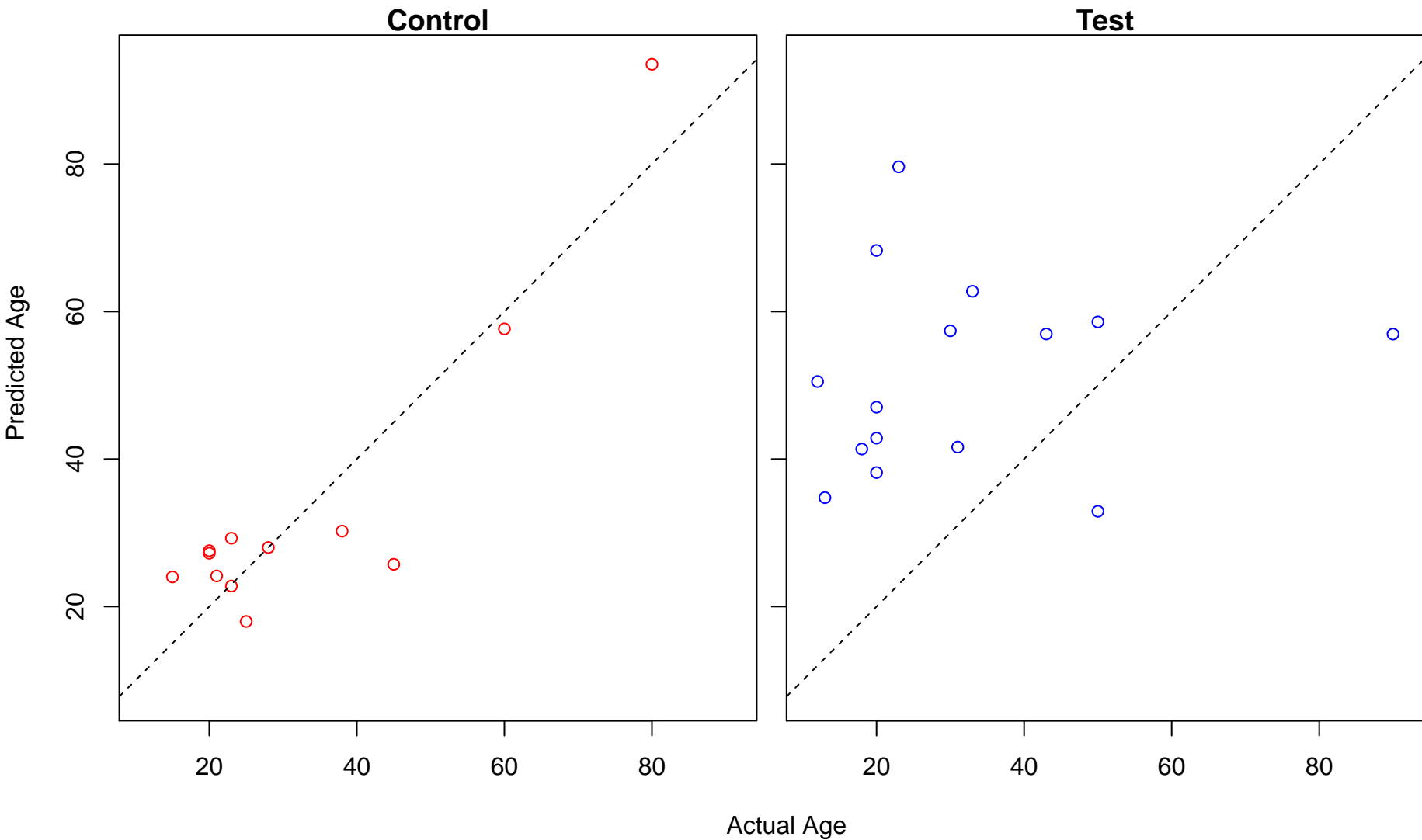
caveolin-mediated endocytosis (Score: 4.335117)



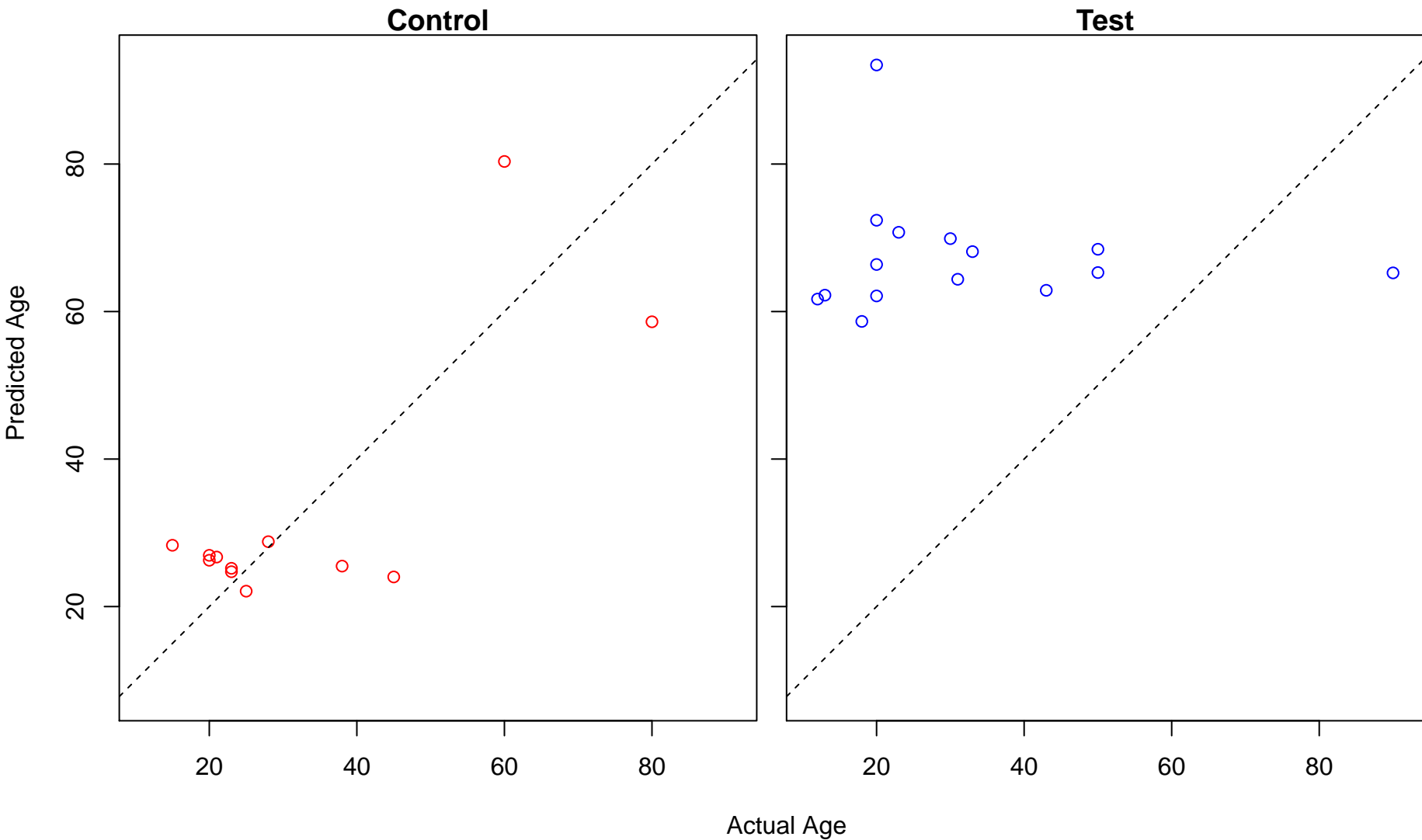
regulation of glucose import (Score: 4.334840)



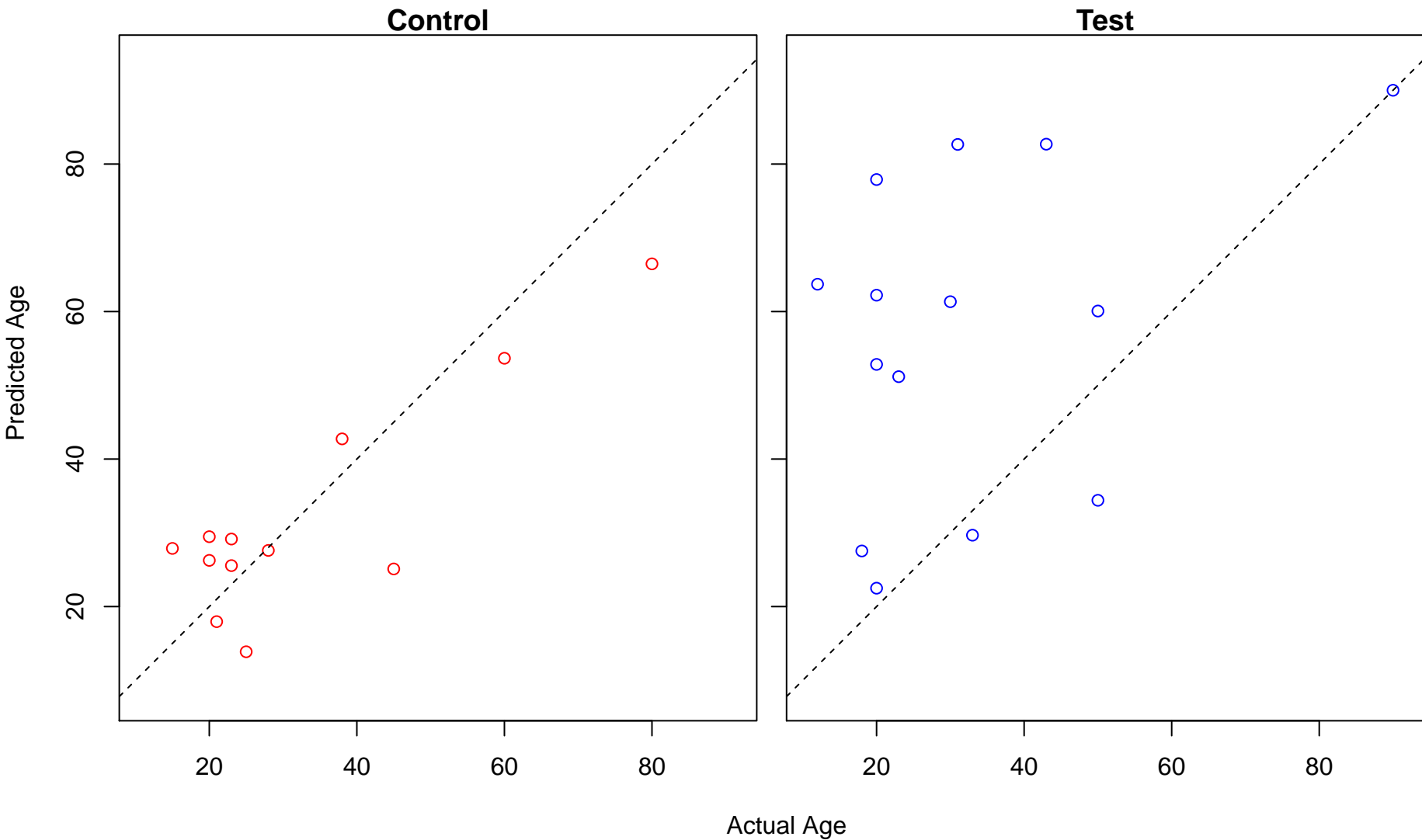
regulation of phosphatidylinositol 3-kinase activity (Score: 4.329953)



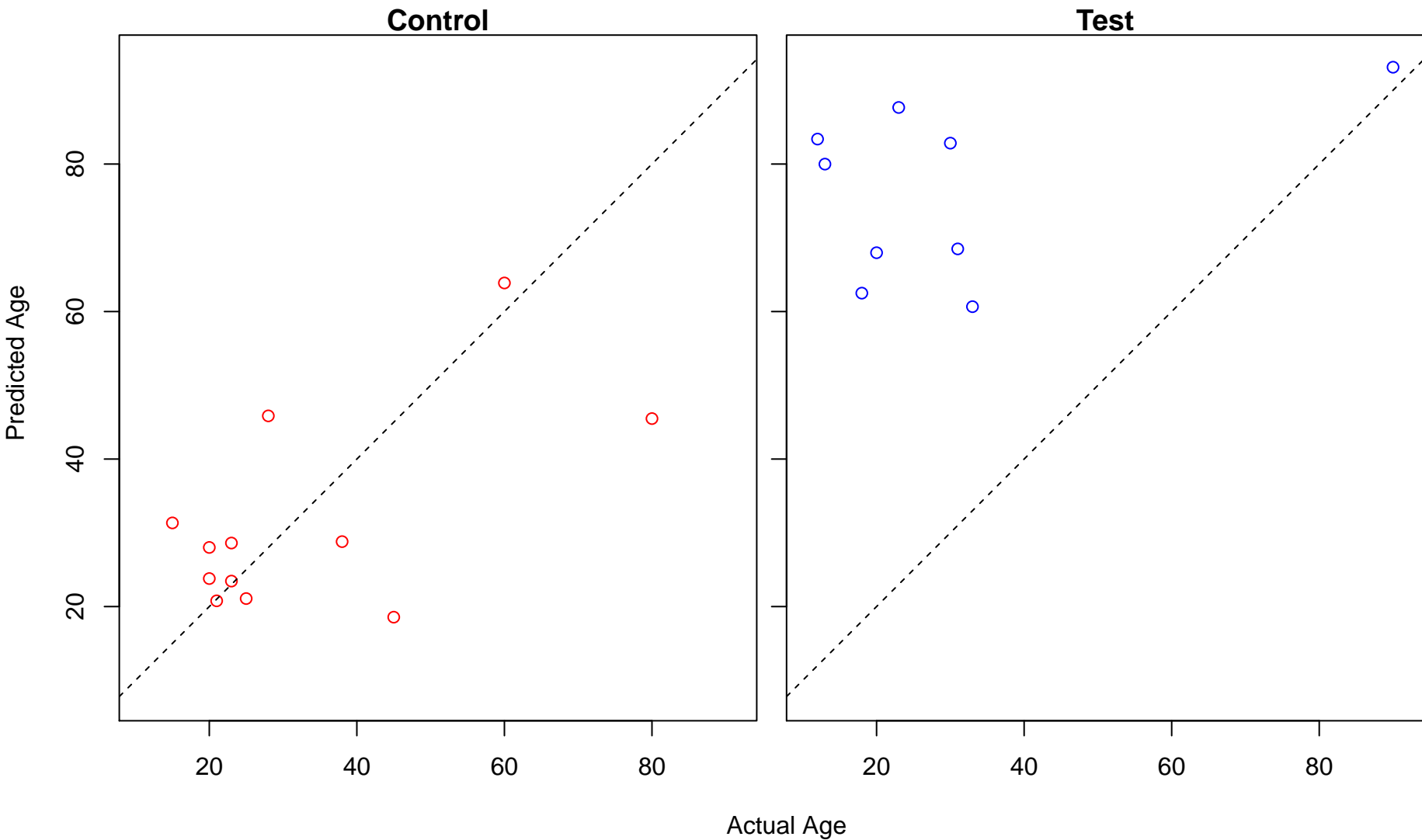
negative regulation of protein depolymerization (Score: 4.328962)



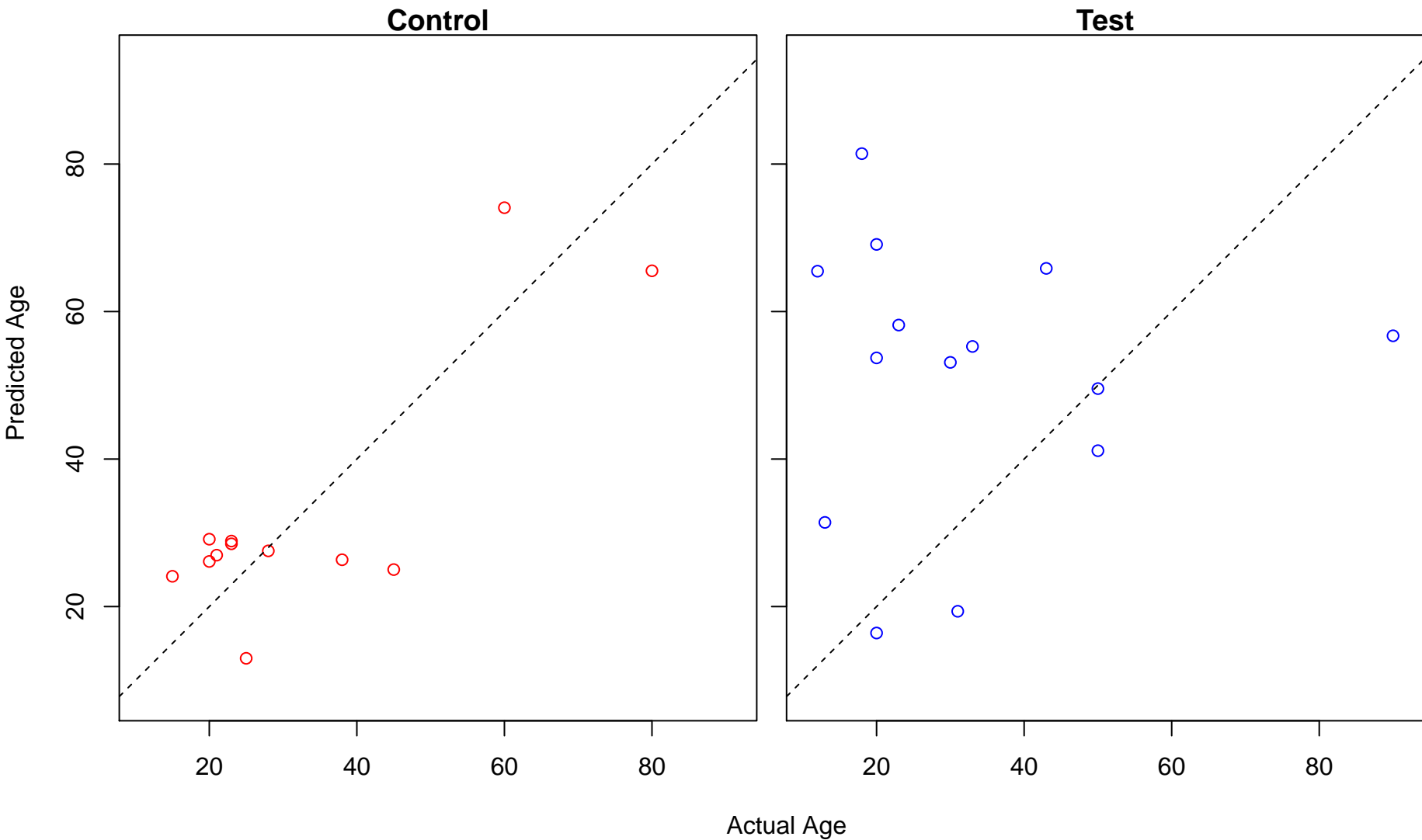
protein deacetylation (Score: 4.328729)



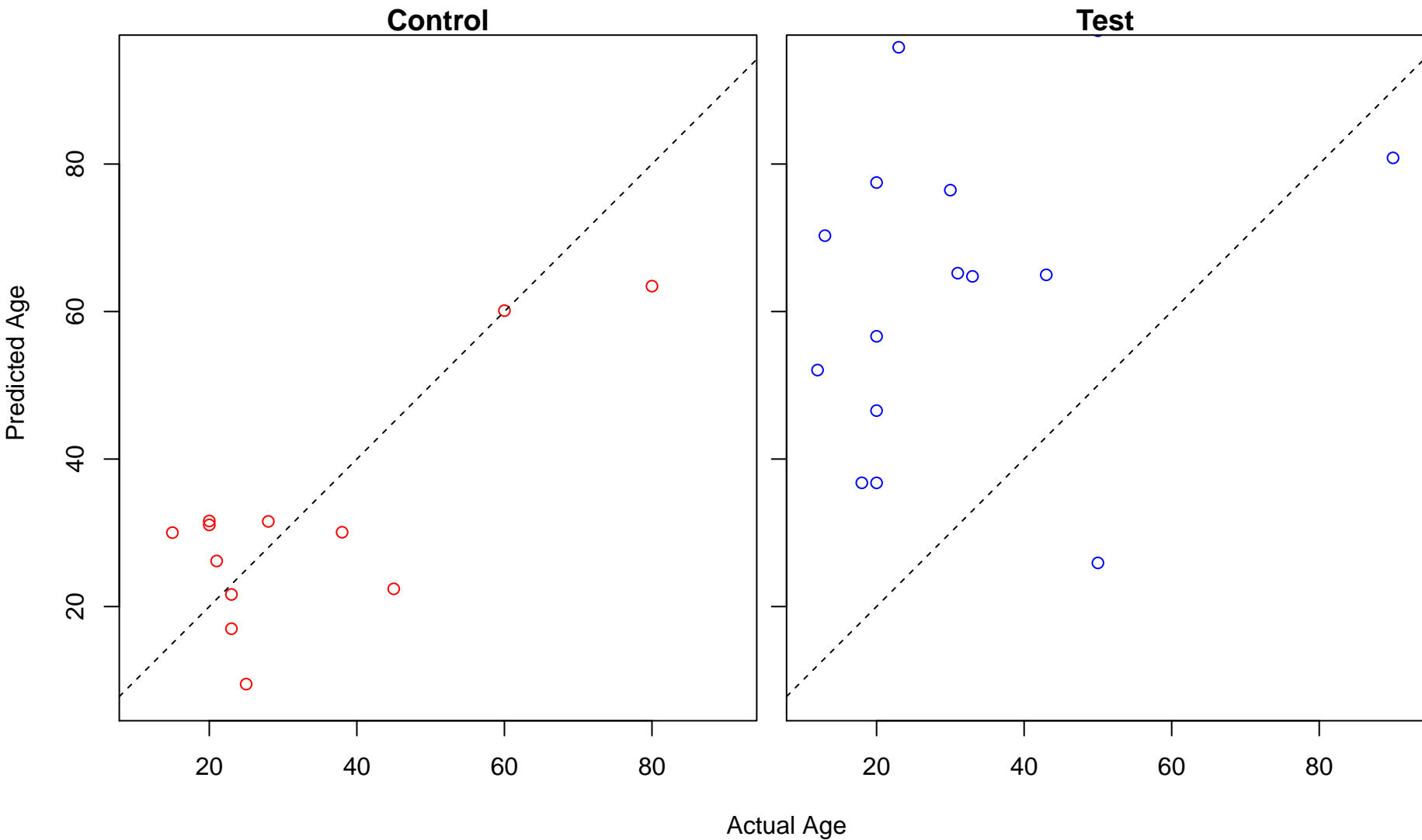
response to misfolded protein (Score: 4.327218)



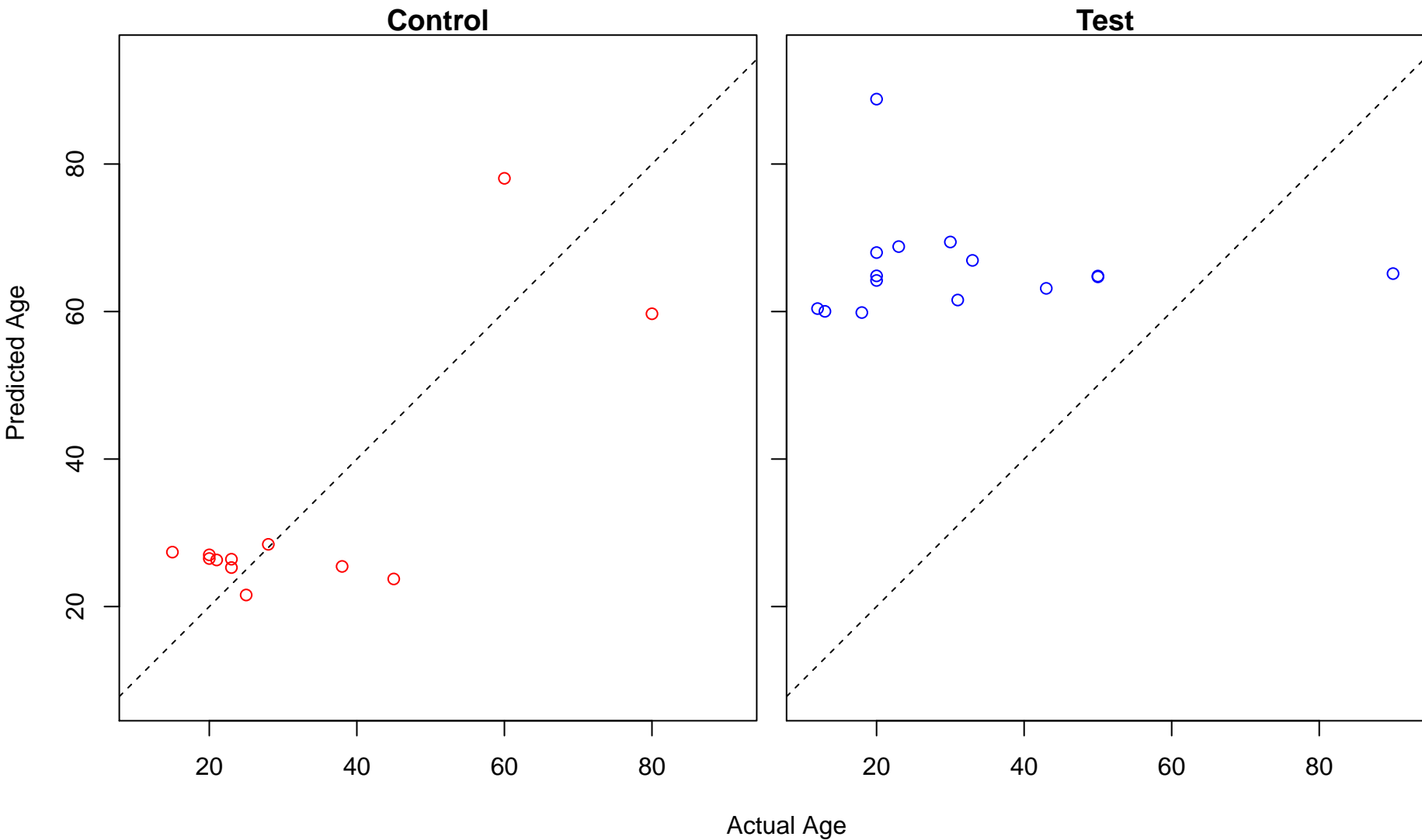
regulation of fibroblast apoptotic process (Score: 4.326705)



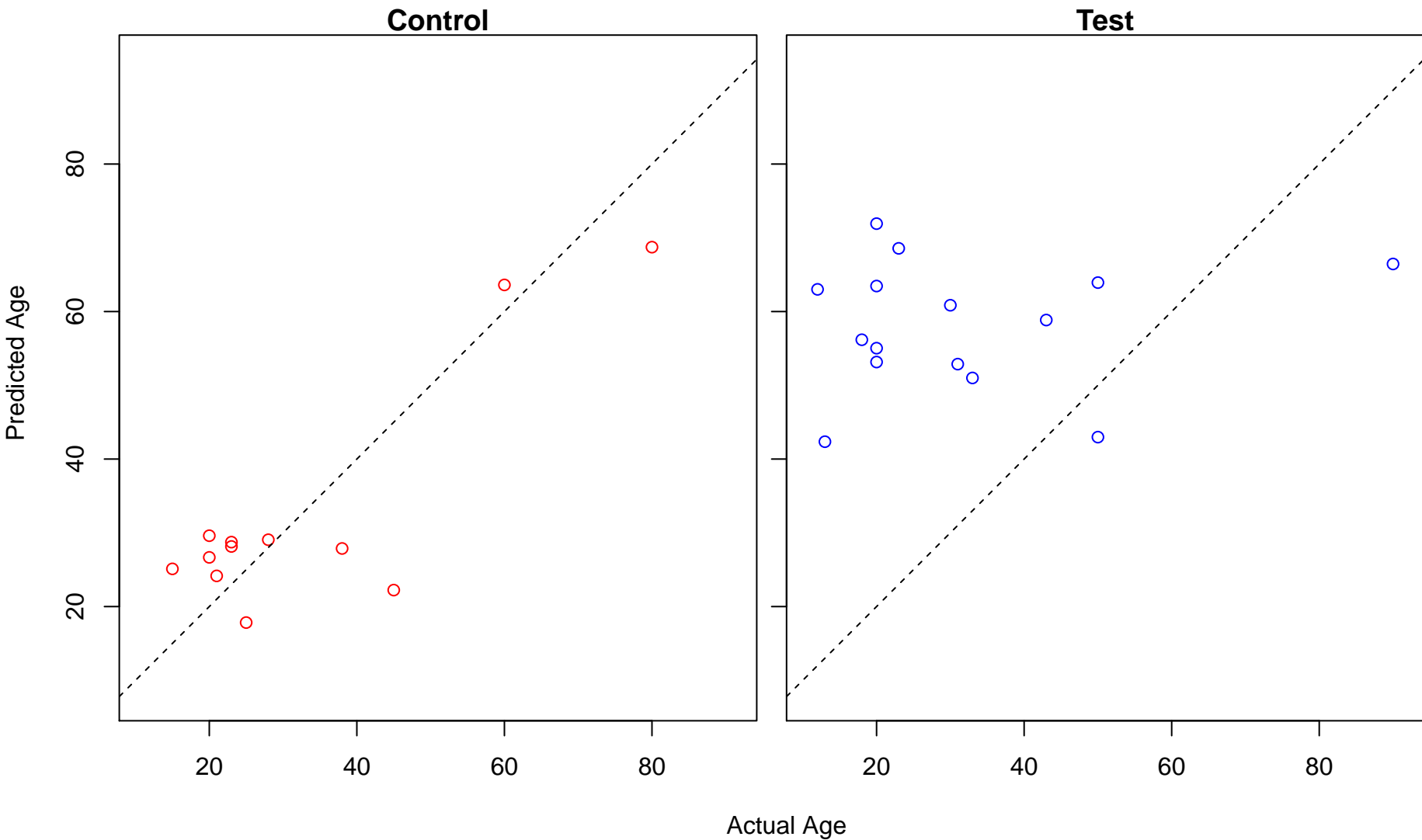
receptor-mediated endocytosis (Score: 4.324994)



regulation of protein complex disassembly (Score: 4.319529)

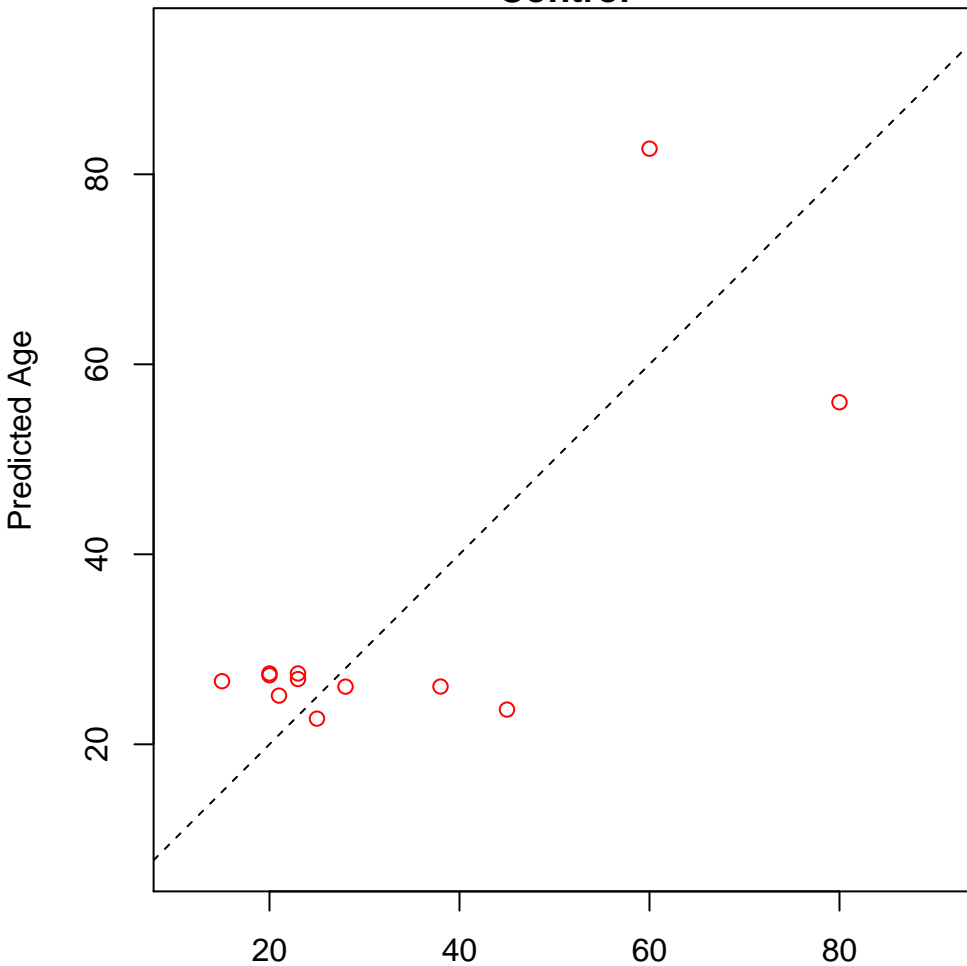


negative regulation of cell growth (Score: 4.317550)

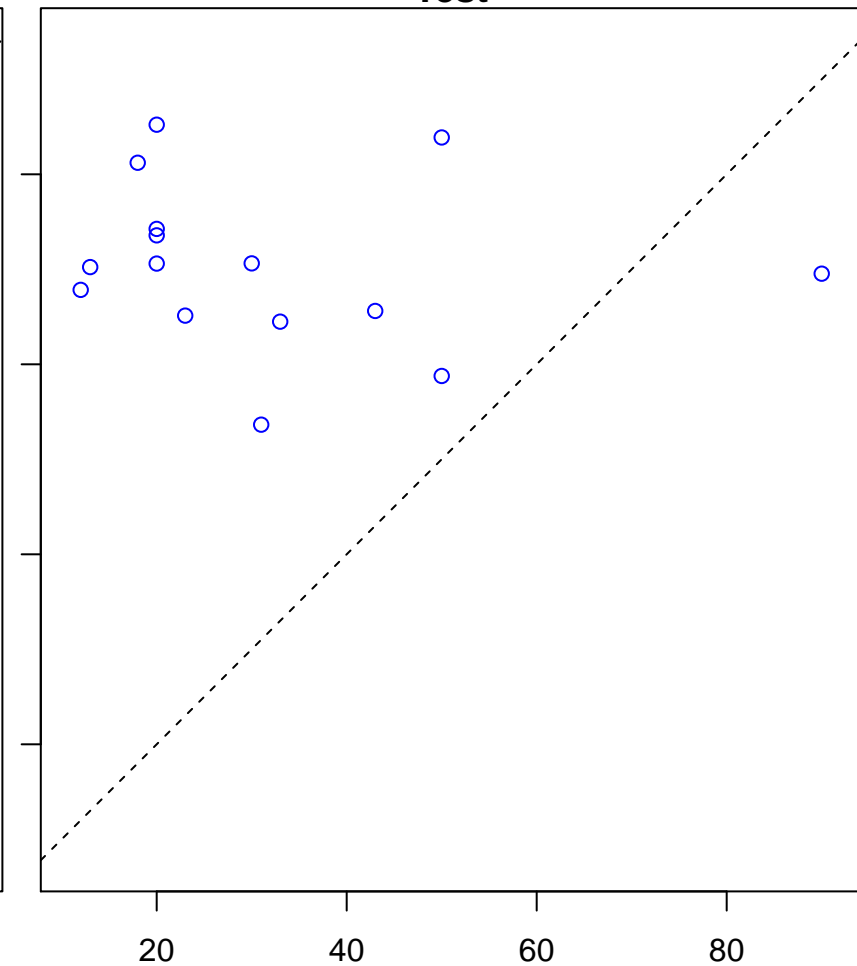


regulation of epithelial cell proliferation (Score: 4.315643)

Control

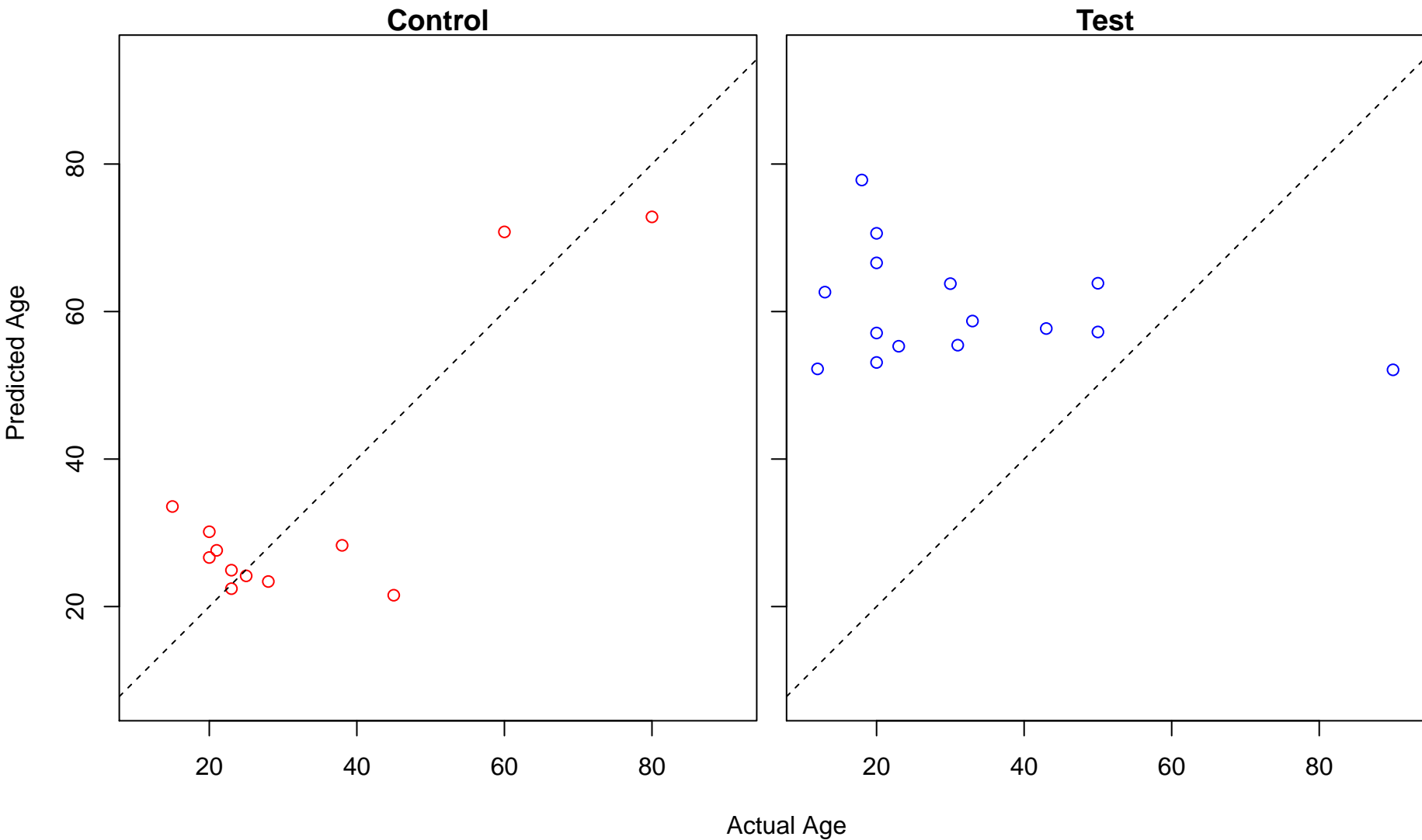


Test

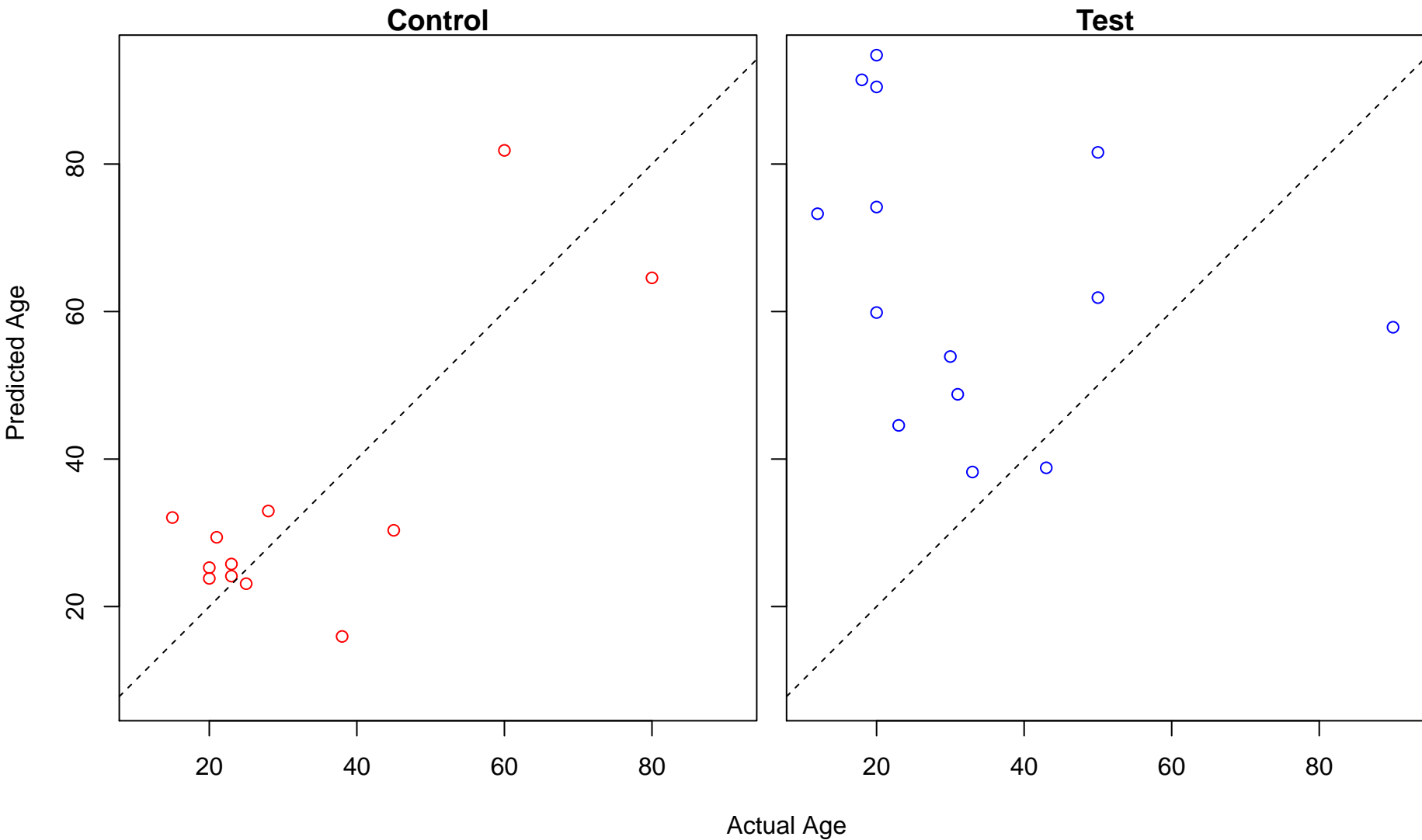


Actual Age

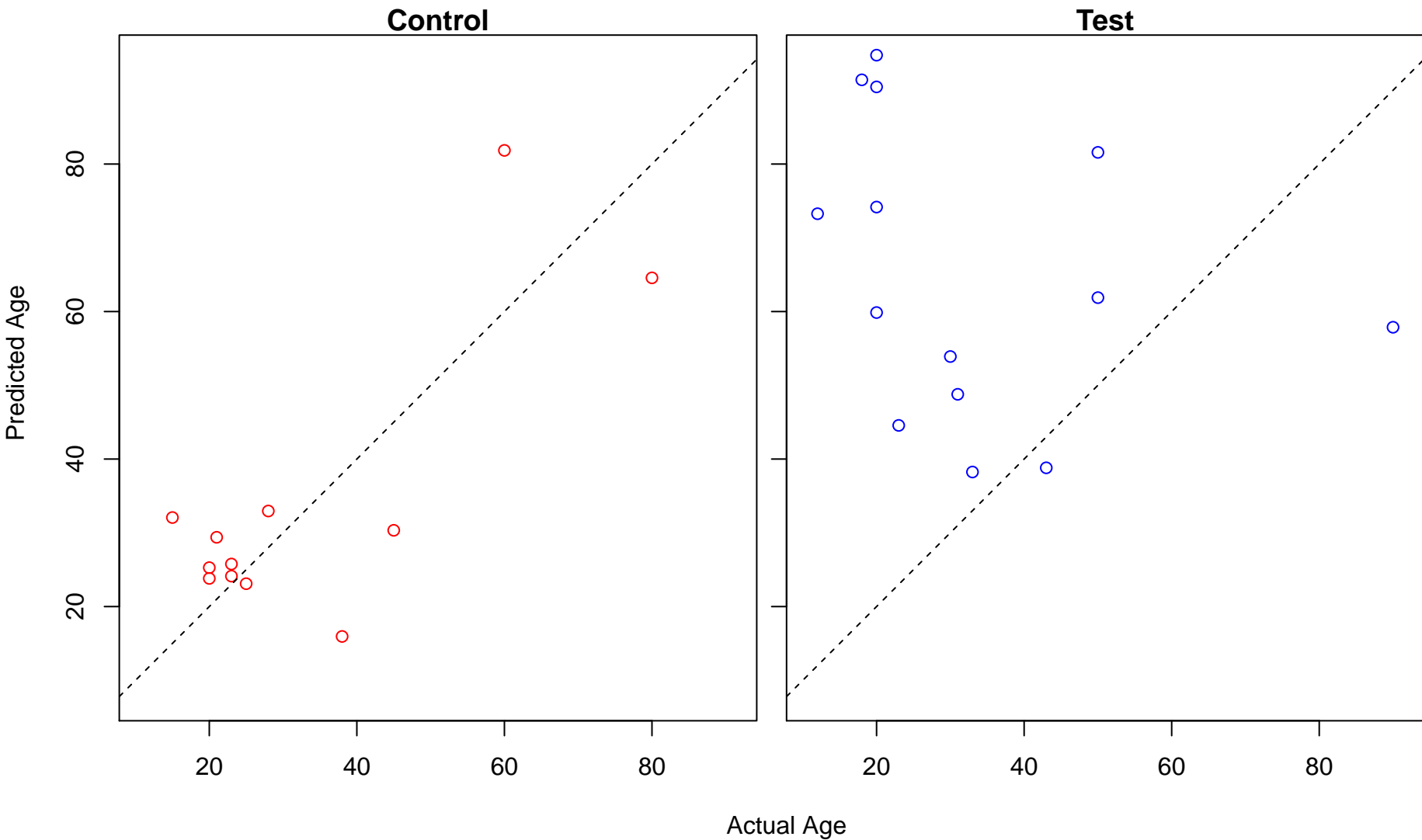
phosphatidylinositol-3-phosphate biosynthetic process (Score: 4.315492)



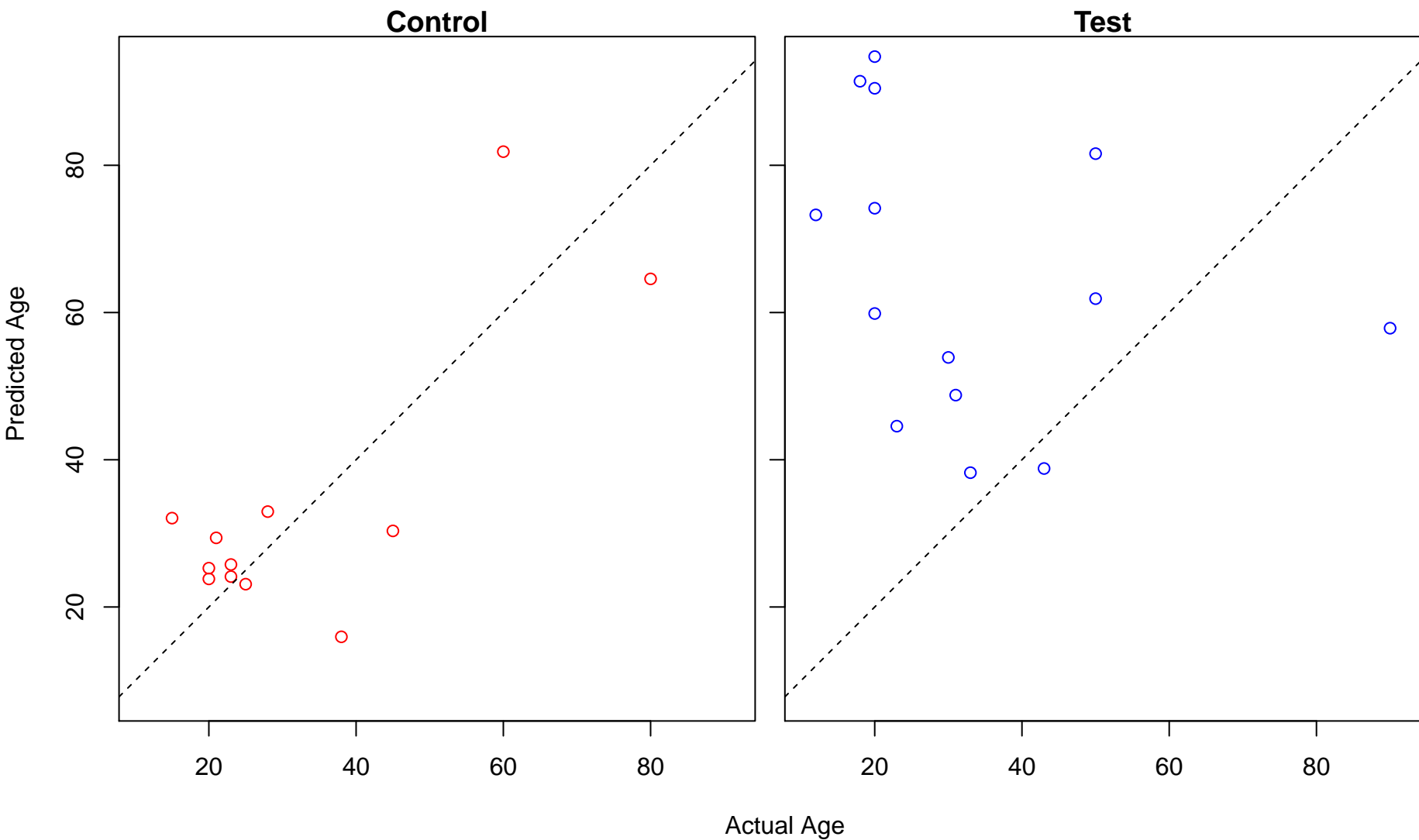
positive regulation of collagen metabolic process (Score: 4.315236)



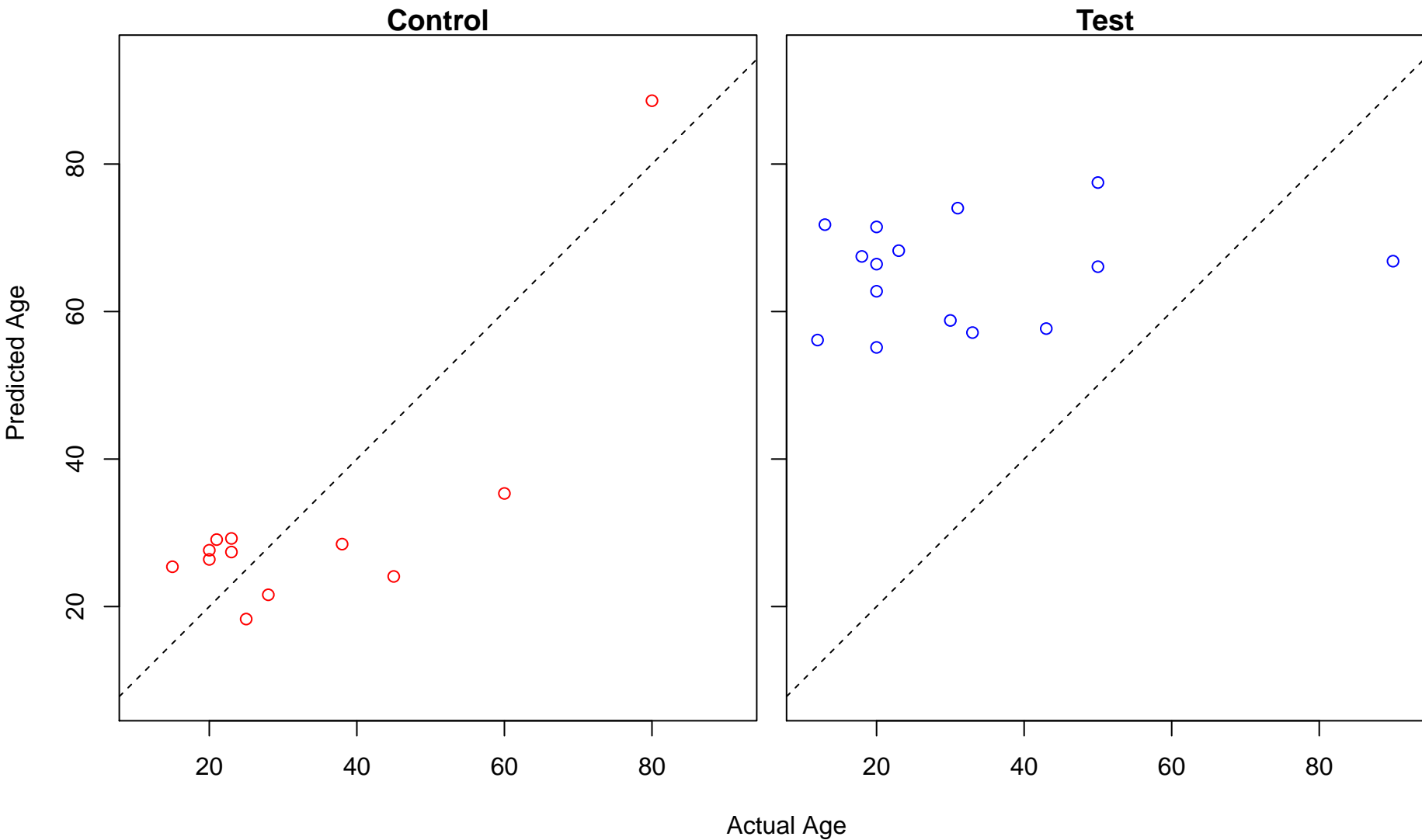
positive regulation of collagen biosynthetic process (Score: 4.315236)



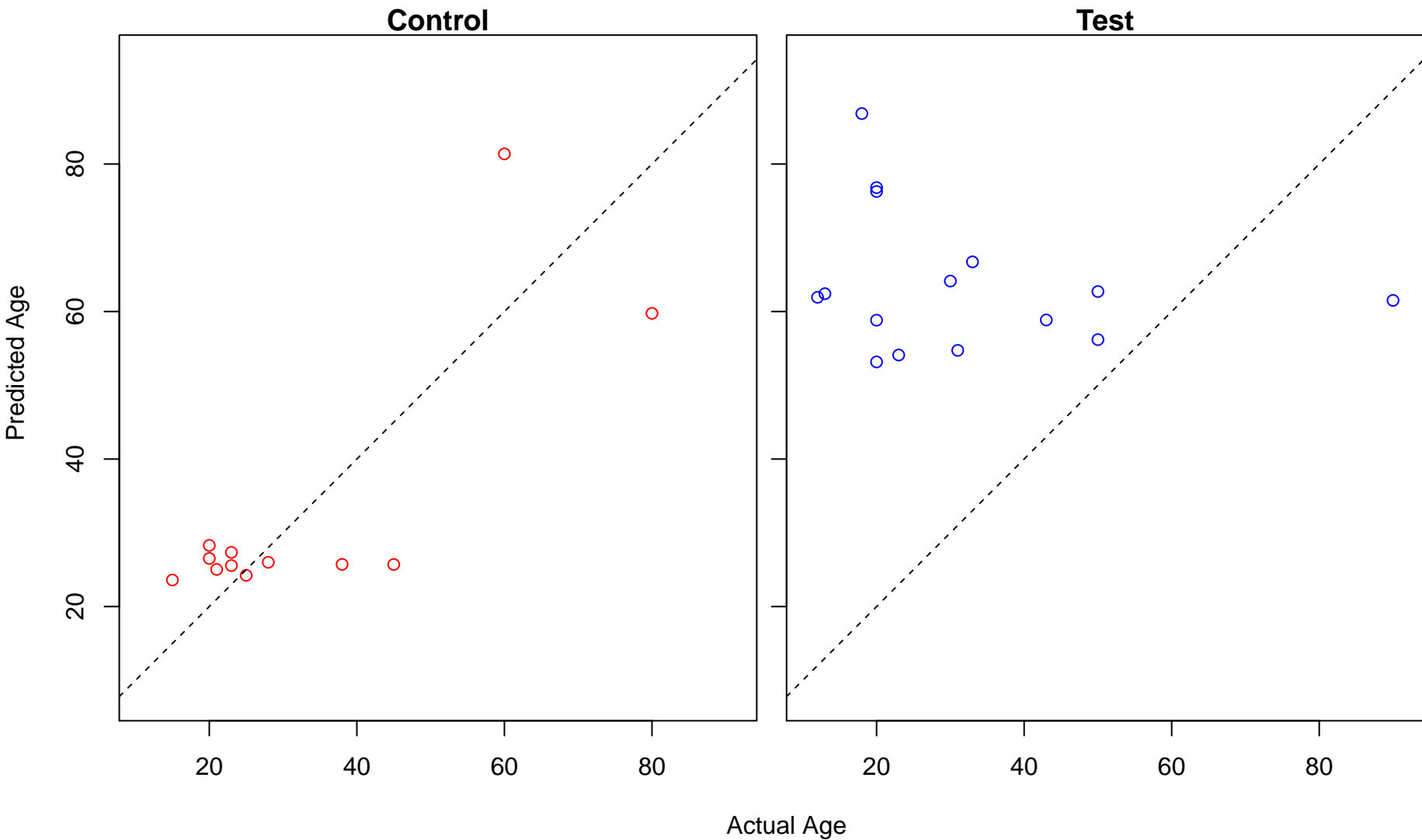
positive regulation of multicellular organismal metabolic process (Score: 4.315236)



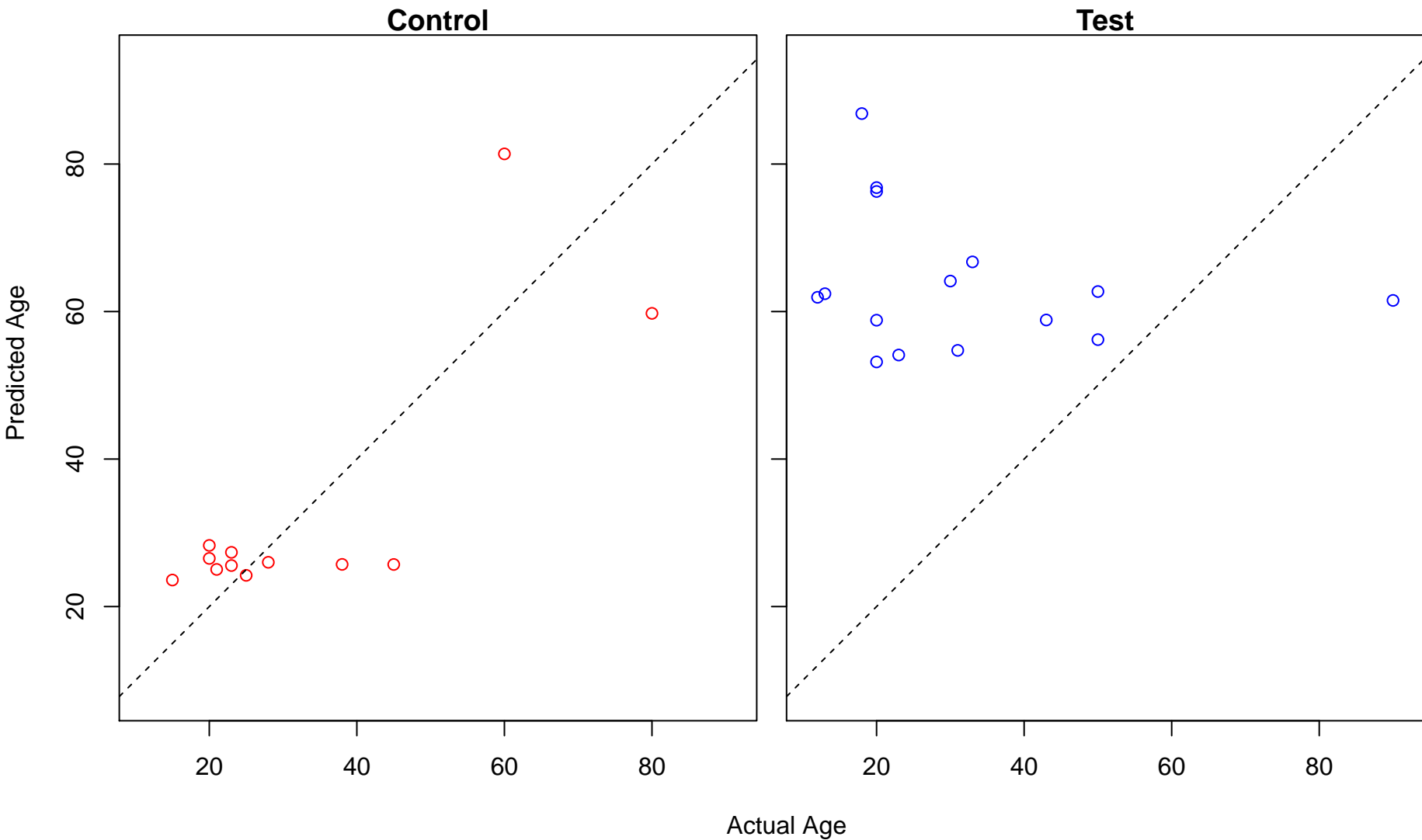
reactive oxygen species metabolic process (Score: 4.314120)



negative regulation of nucleotide biosynthetic process (Score: 4.313760)

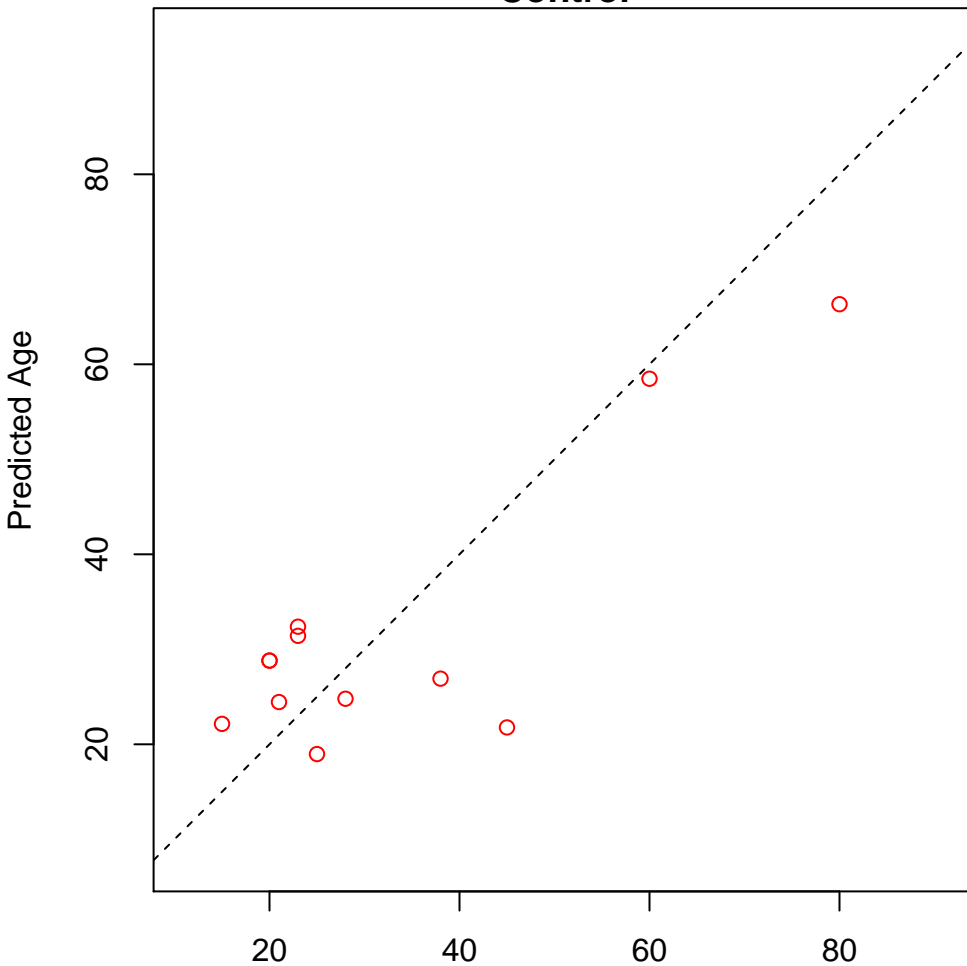


negative regulation of purine nucleotide biosynthetic process (Score: 4.313760)

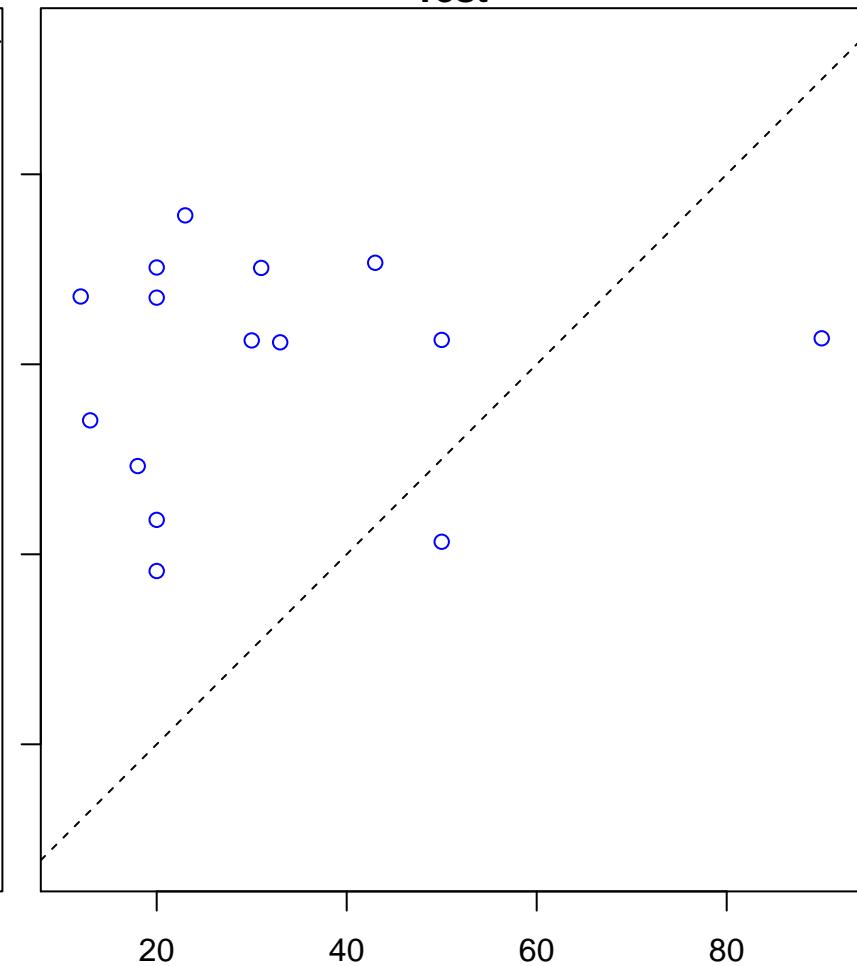


tyrosine phosphorylation of STAT protein (Score: 4.310885)

Control

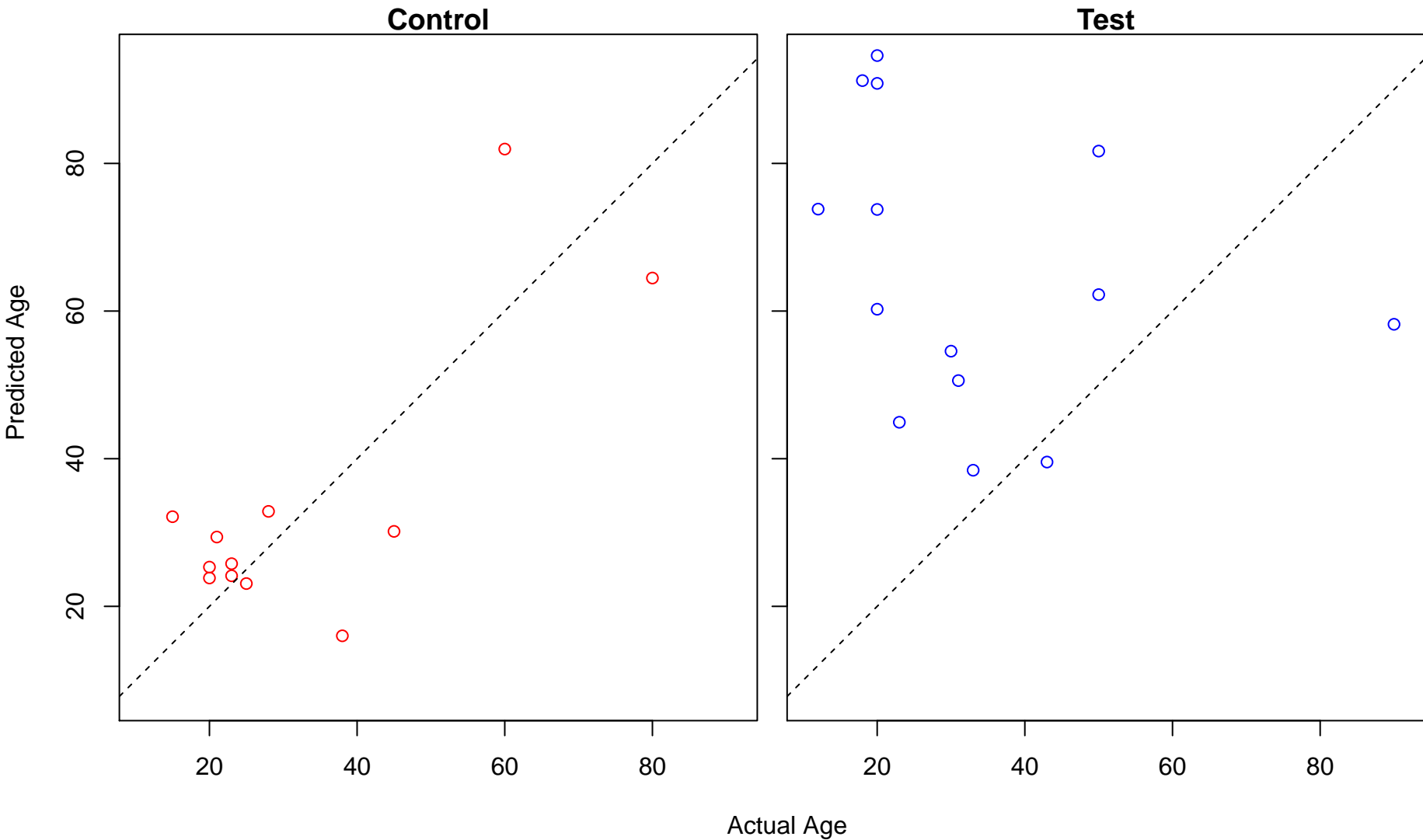


Test

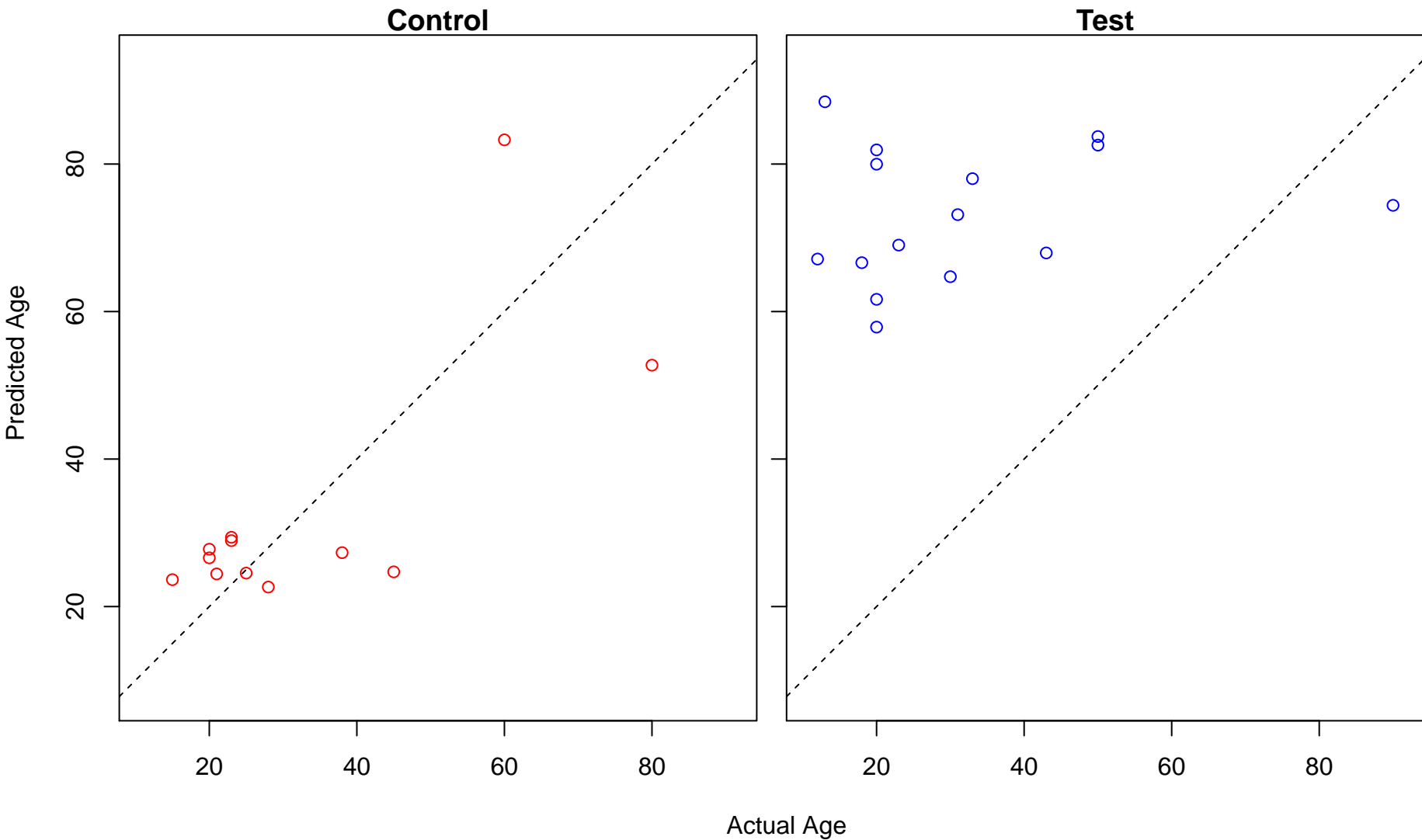


Actual Age

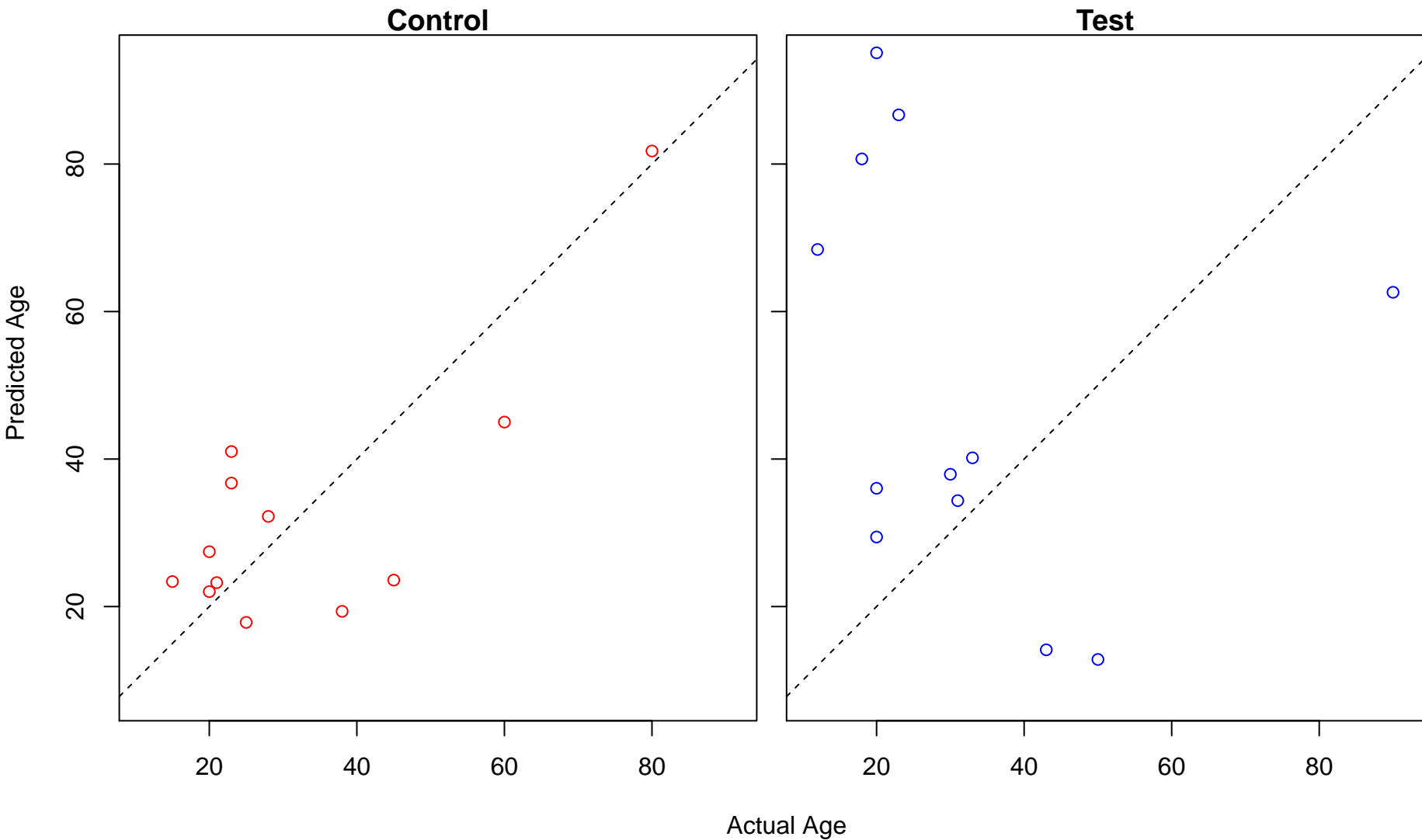
regulation of collagen biosynthetic process (Score: 4.309114)



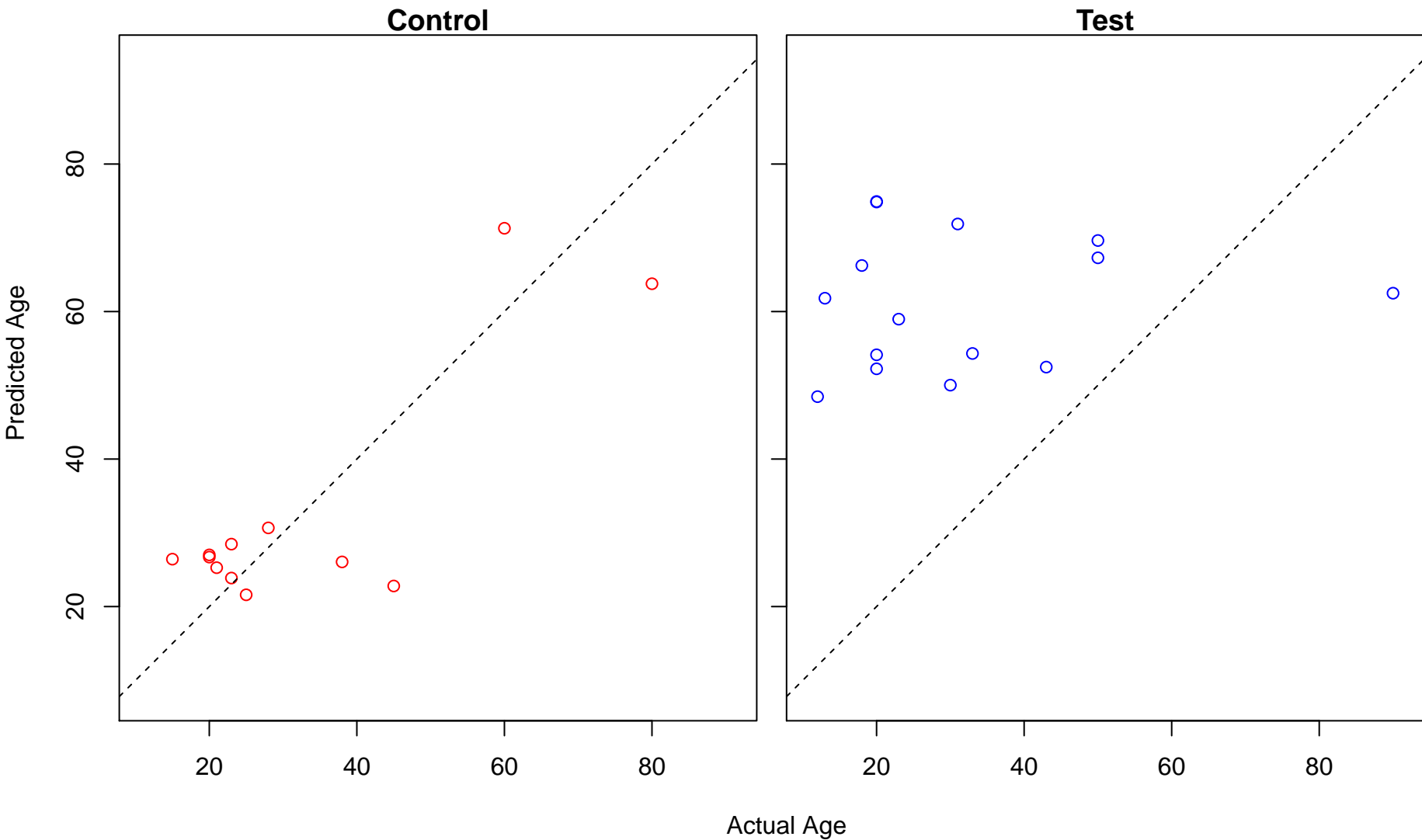
syncytium formation (Score: 4.306575)



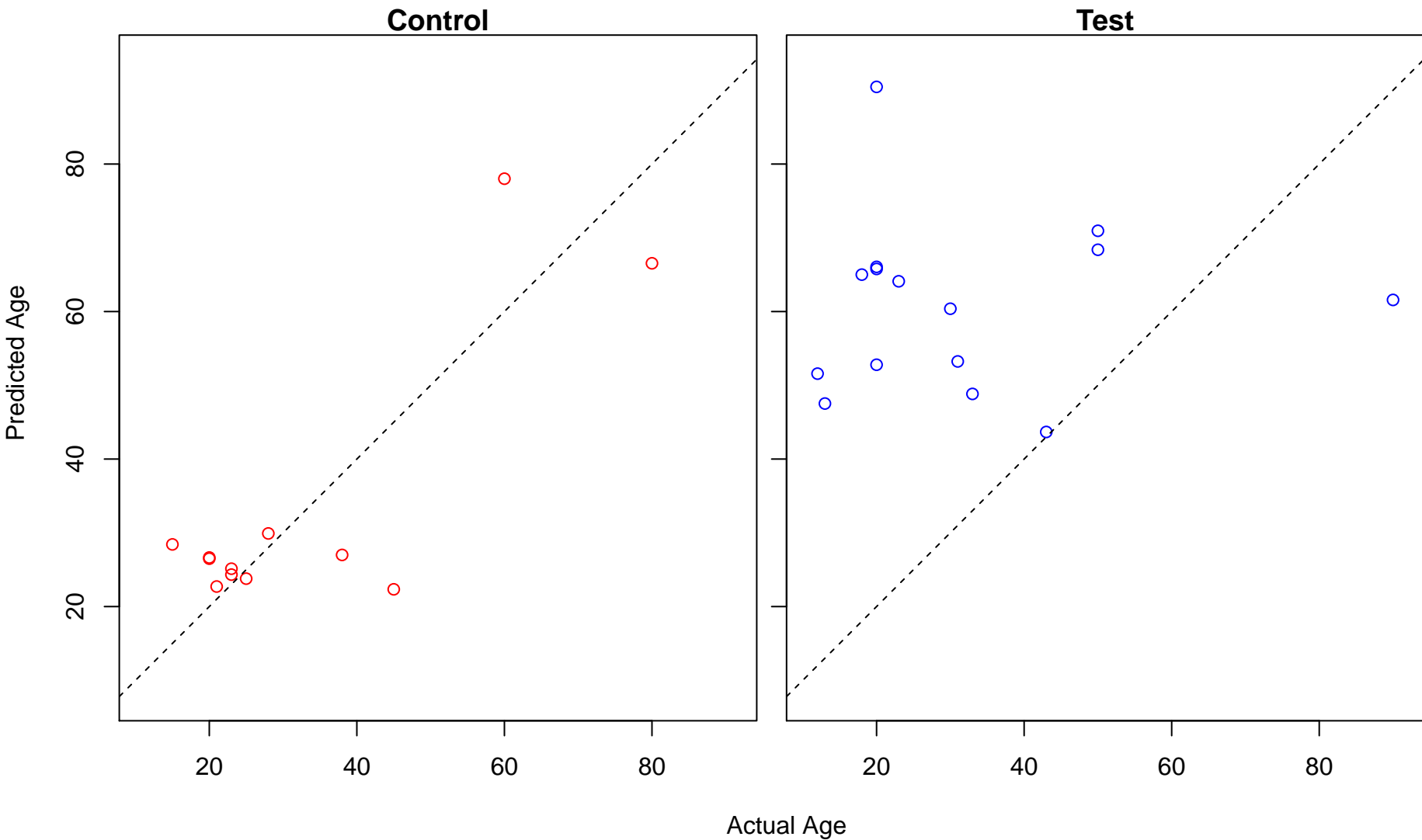
regulation of extent of cell growth (Score: 4.306423)



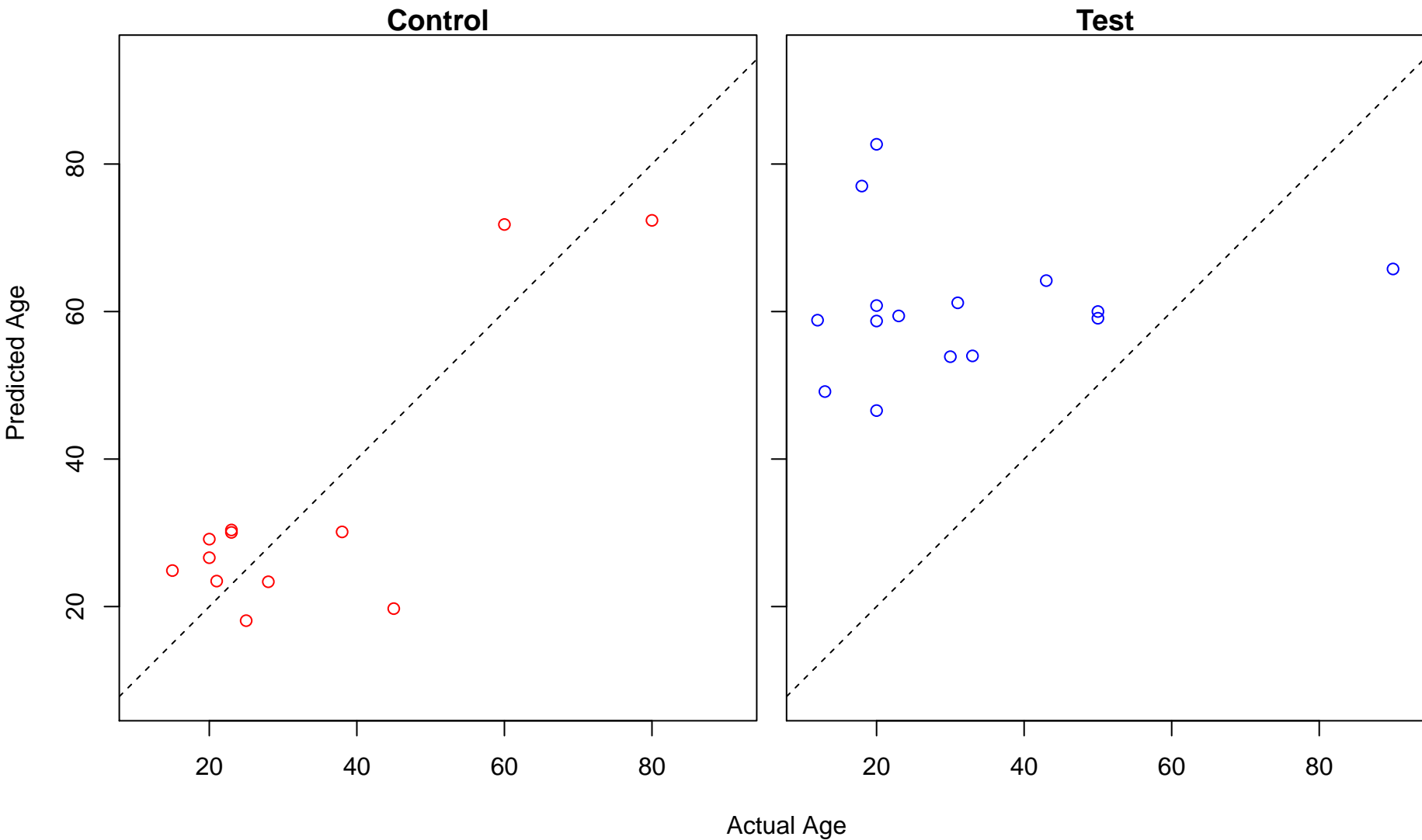
negative regulation of peptidyl–threonine phosphorylation (Score: 4.304832)



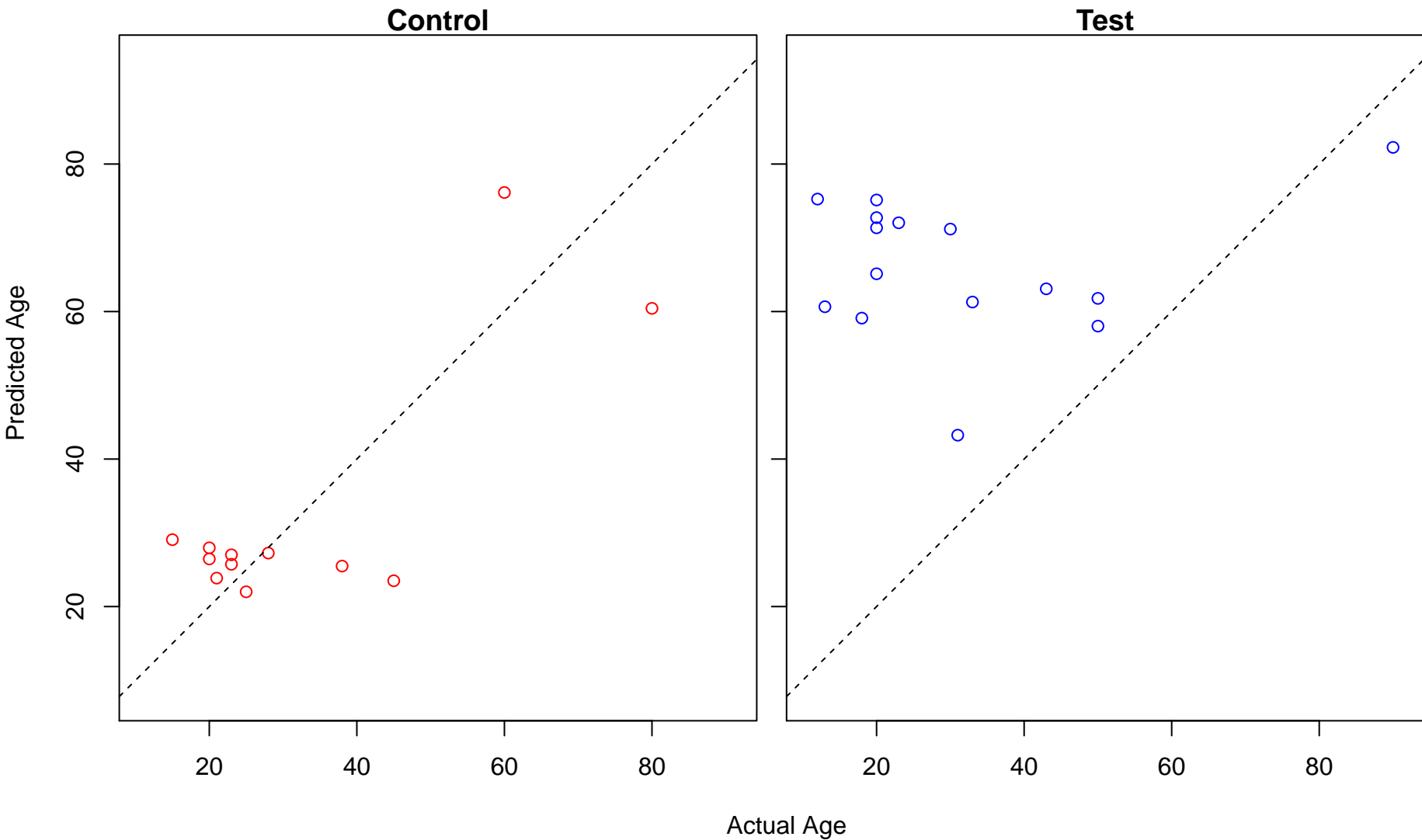
mRNA processing (Score: 4.304322)



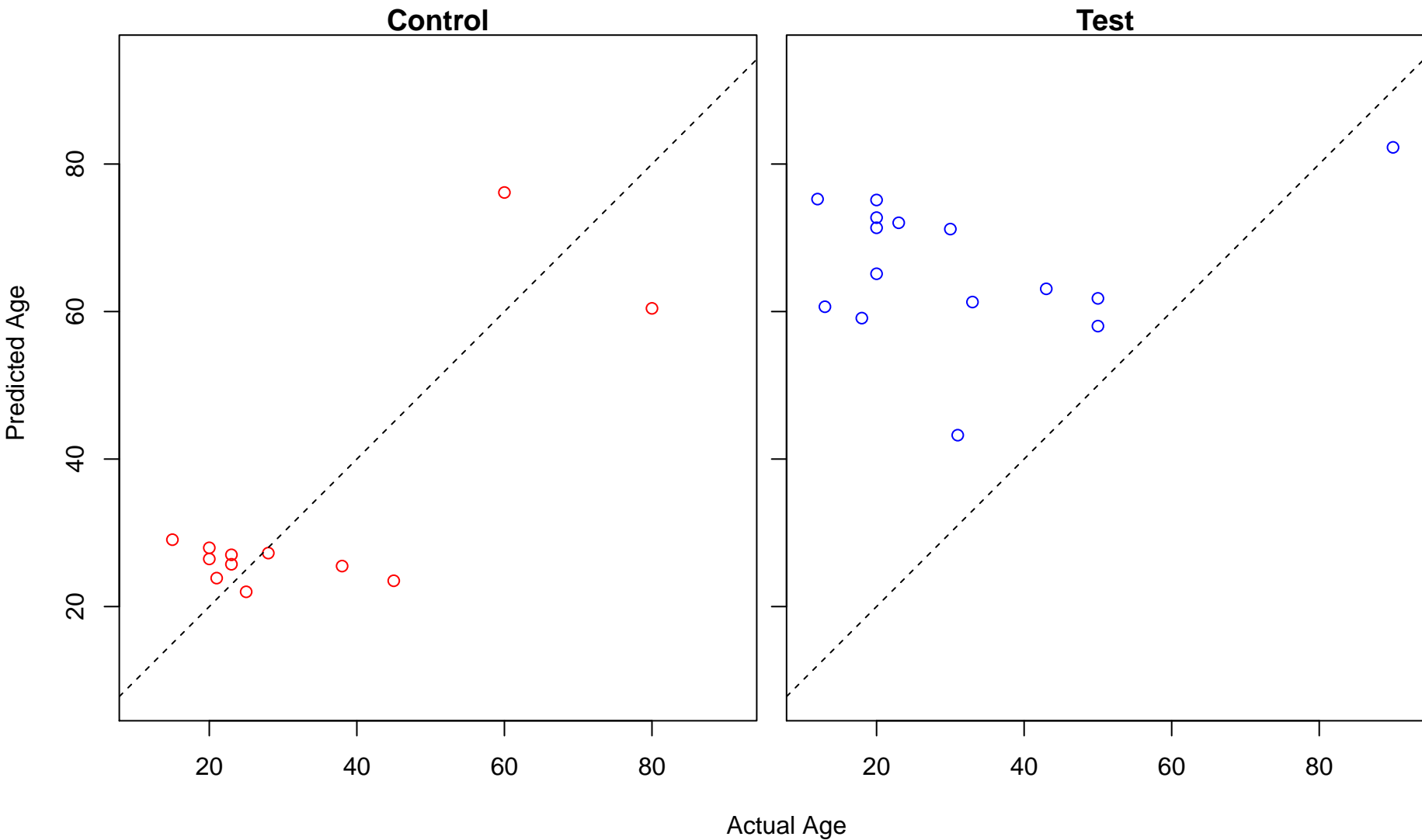
regulation of lymphocyte migration (Score: 4.304057)



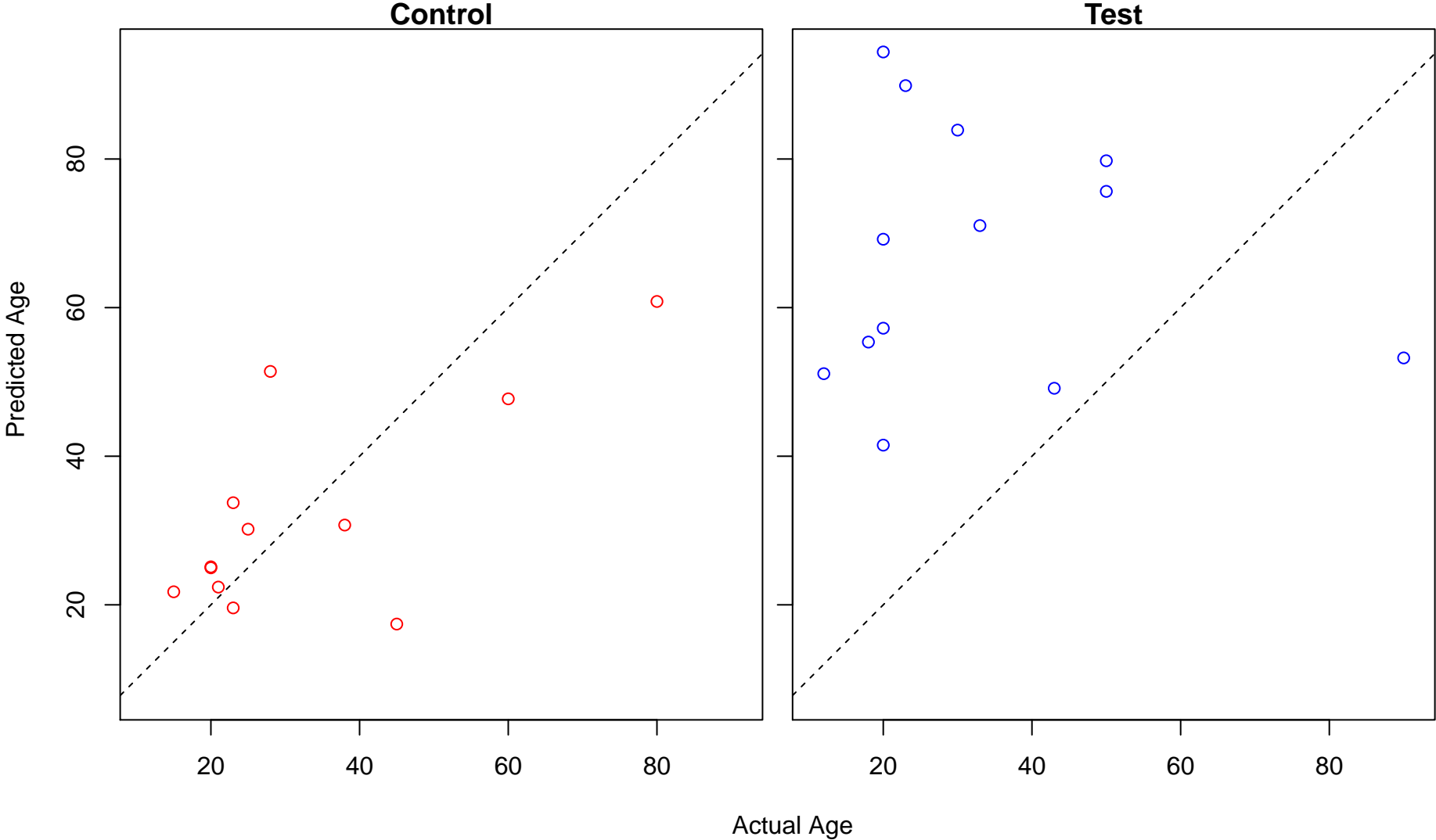
negative regulation of sodium ion transport (Score: 4.303774)



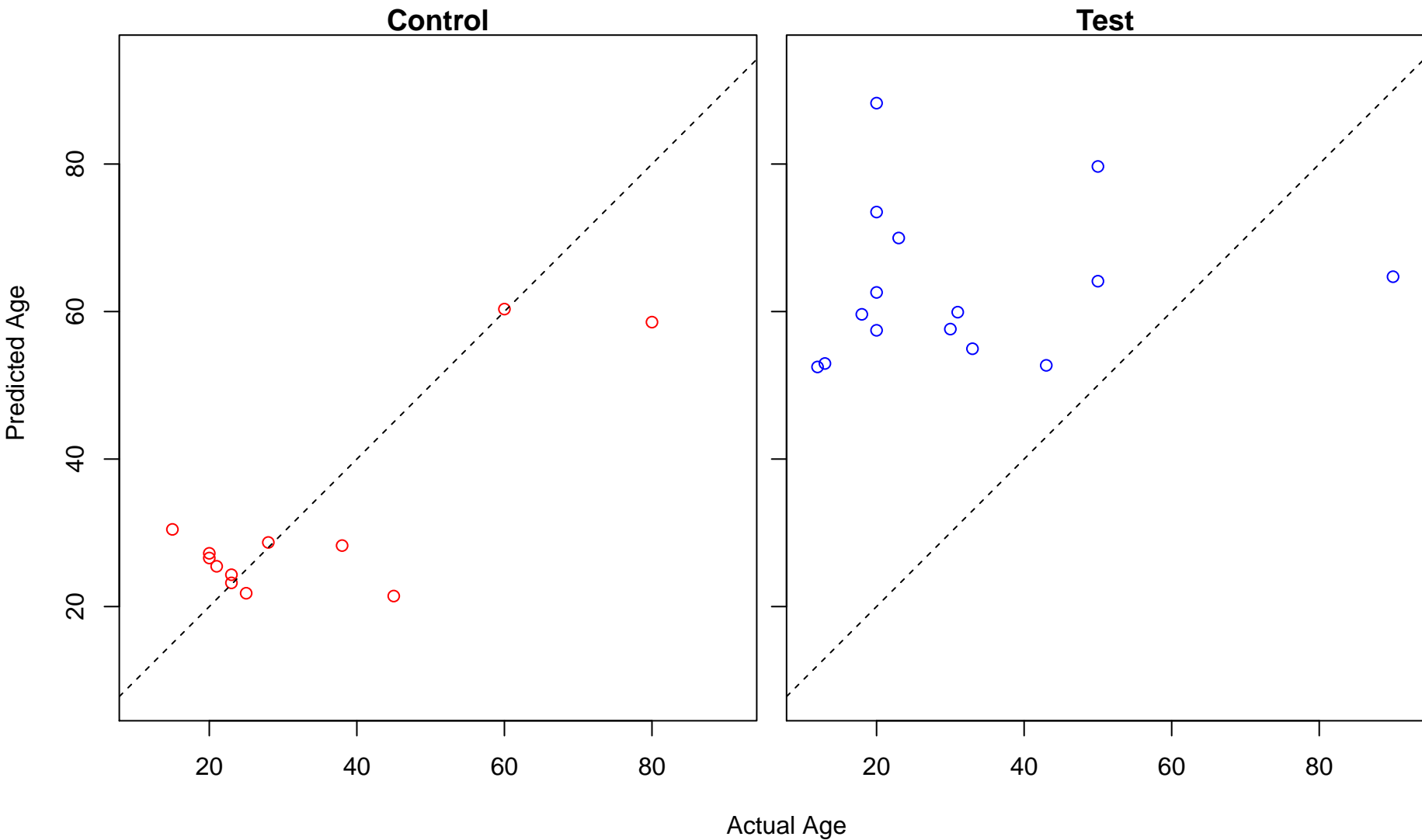
negative regulation of sodium ion transmembrane transport (Score: 4.303774)



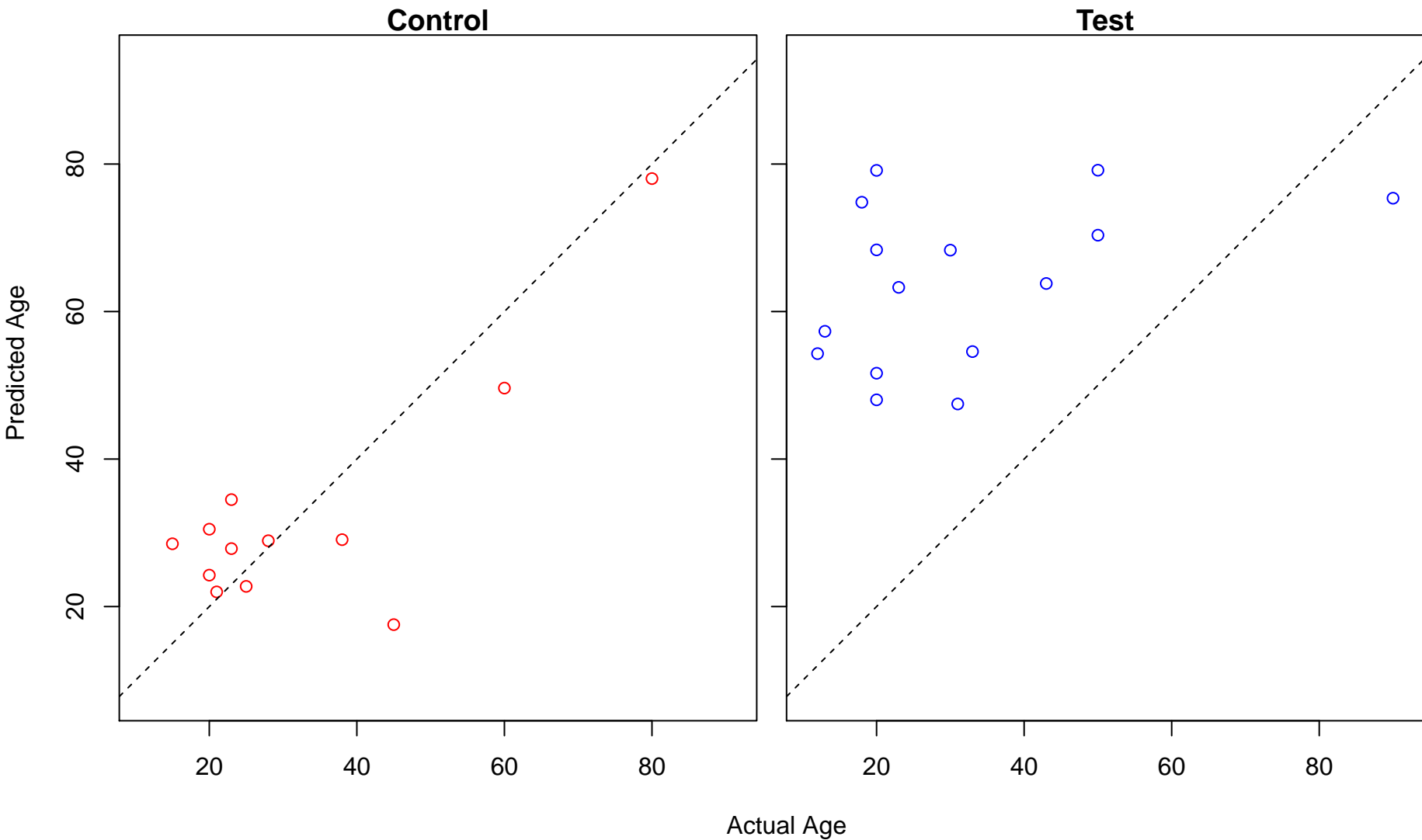
positive regulation of myeloid leukocyte cytokine production involved in immune response (Score: 4.30)



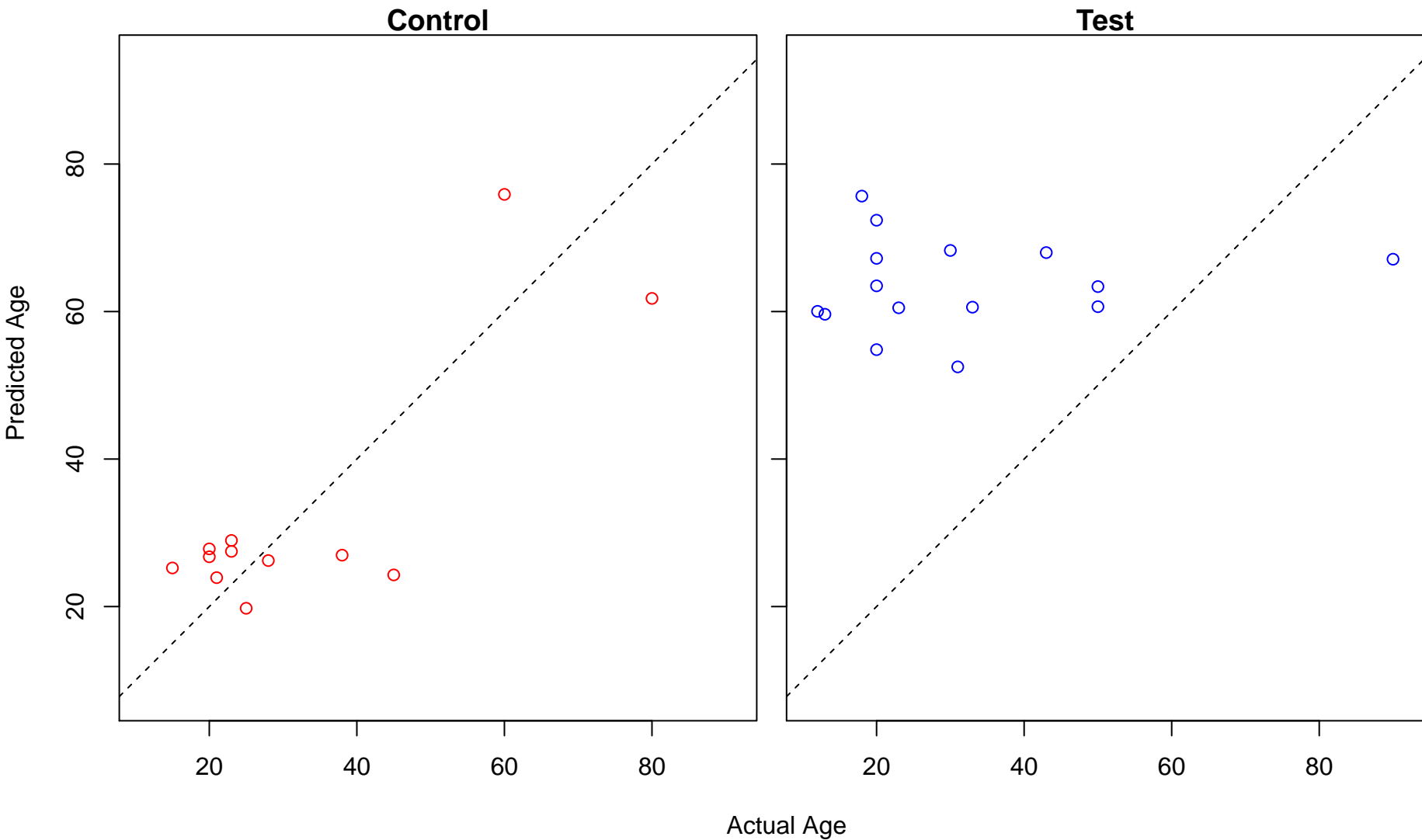
histone demethylation (Score: 4.300690)



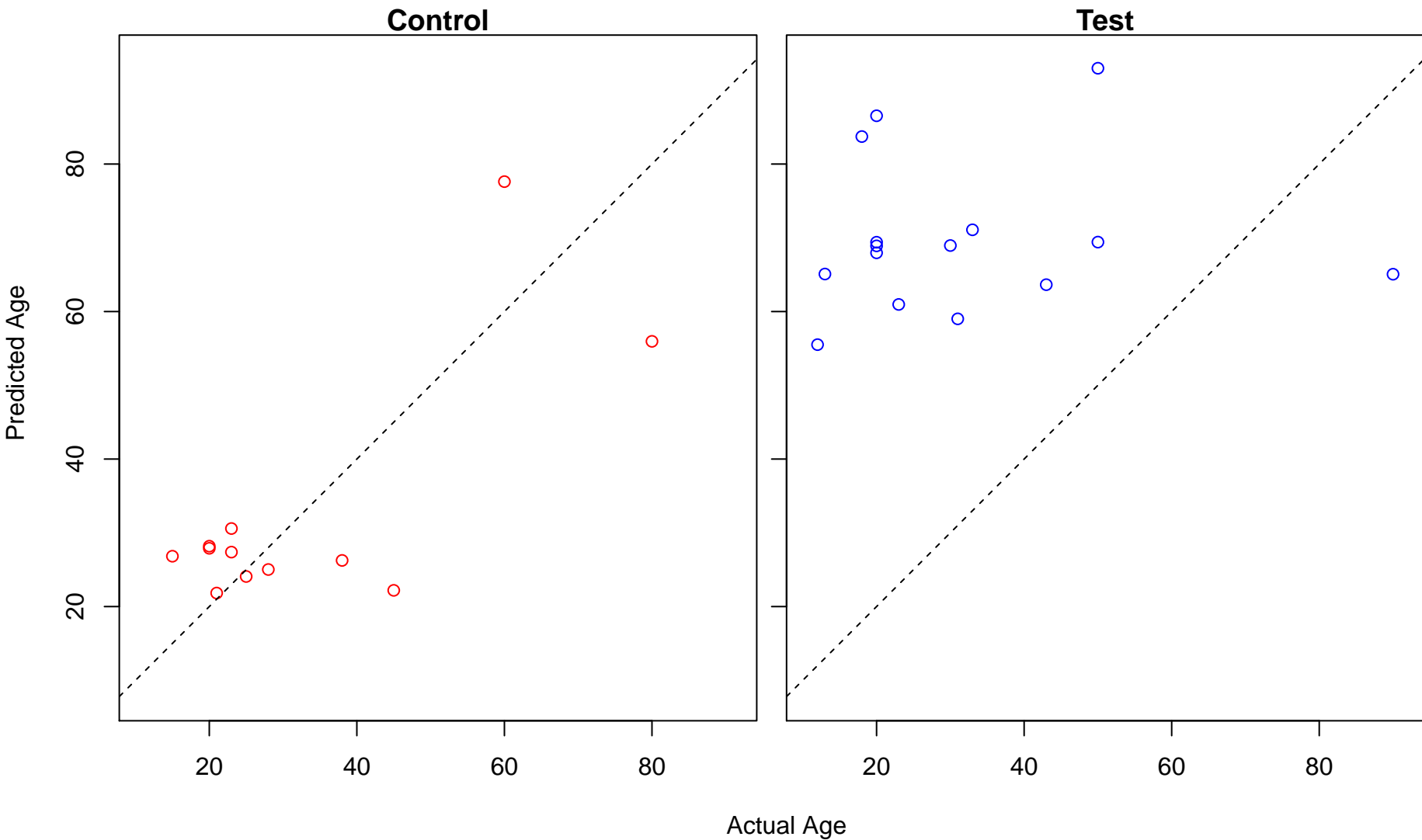
leukocyte apoptotic process (Score: 4.300276)



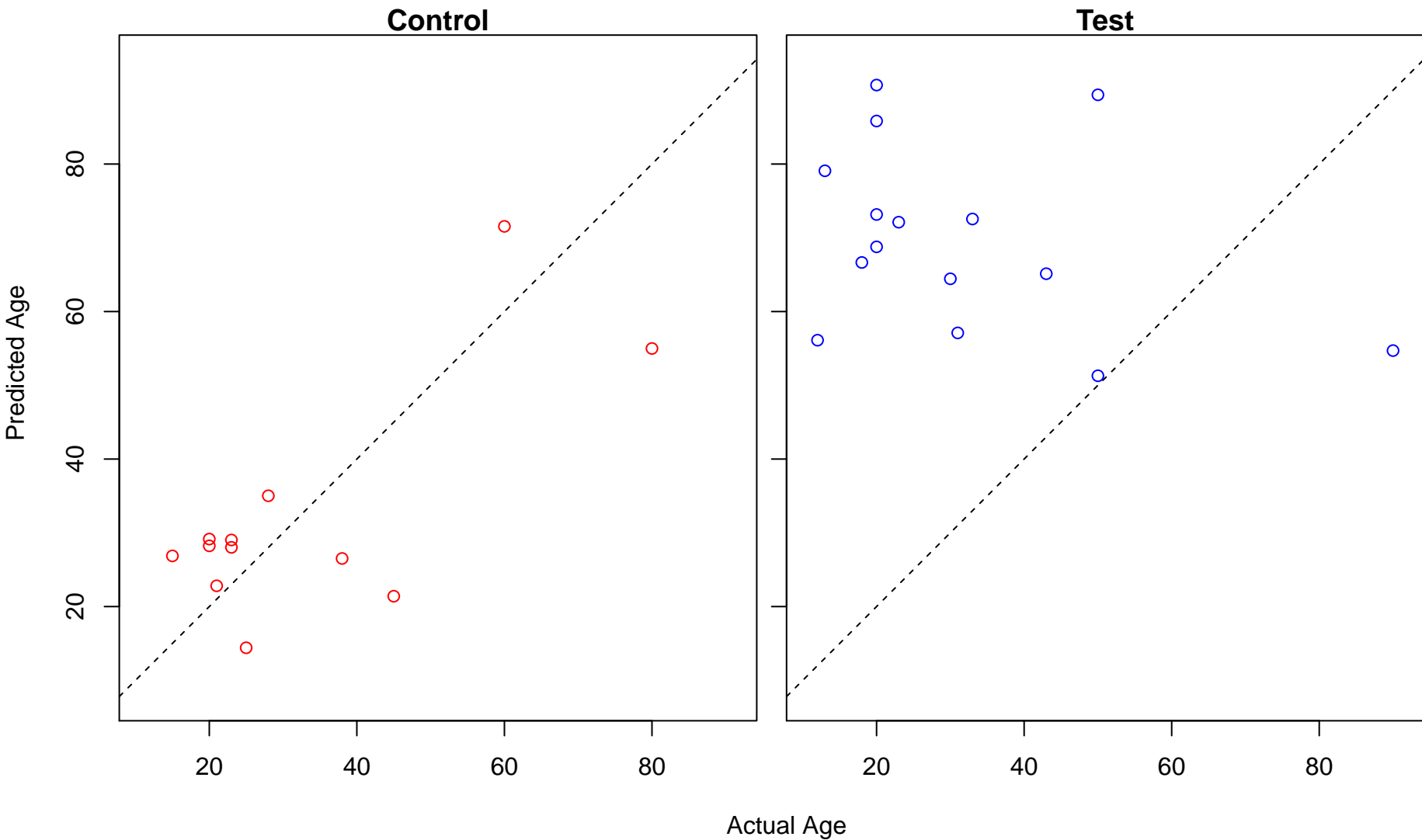
head morphogenesis (Score: 4.298101)



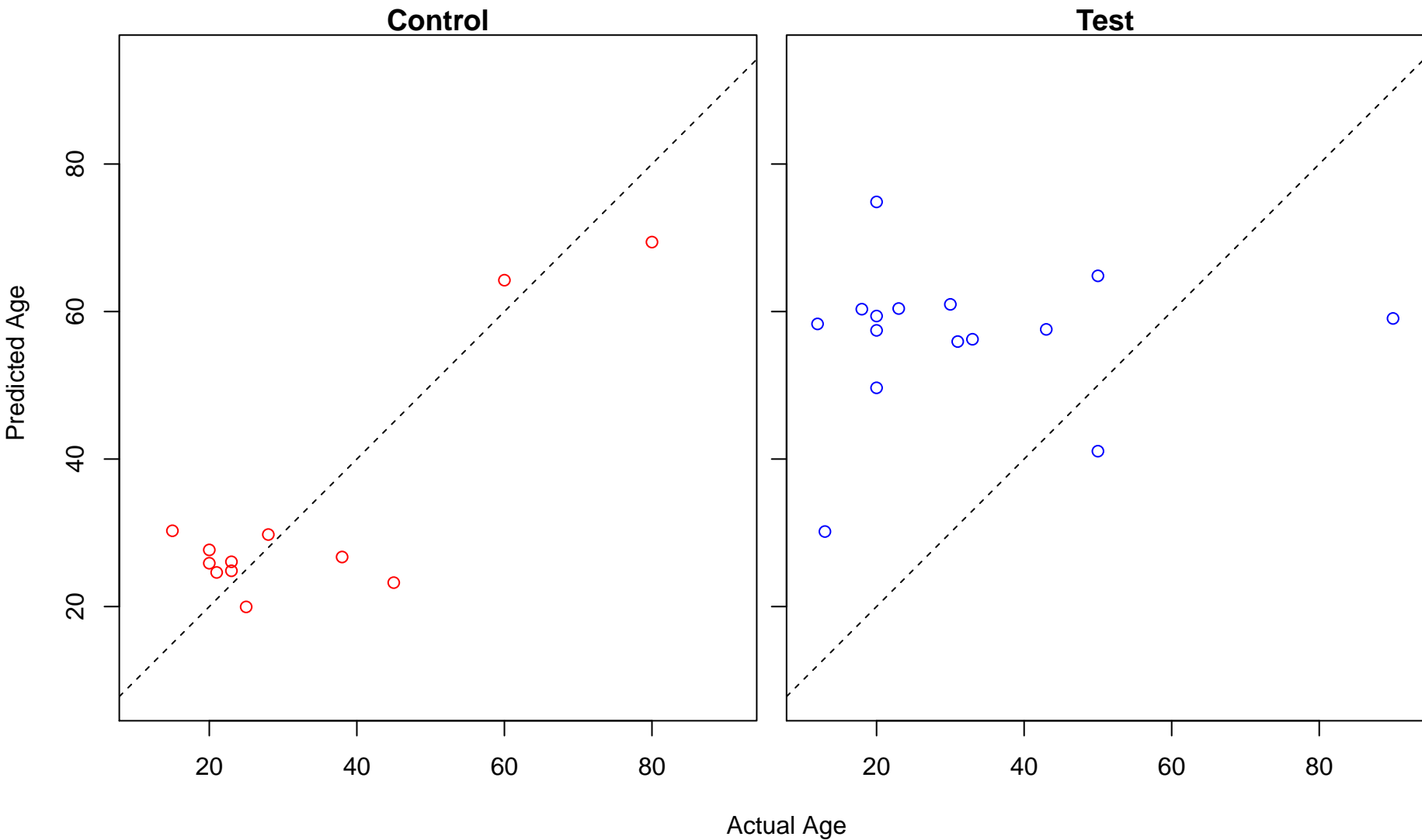
epithelial cell-cell adhesion (Score: 4.291966)



negative regulation of cardiac muscle tissue development (Score: 4.290986)

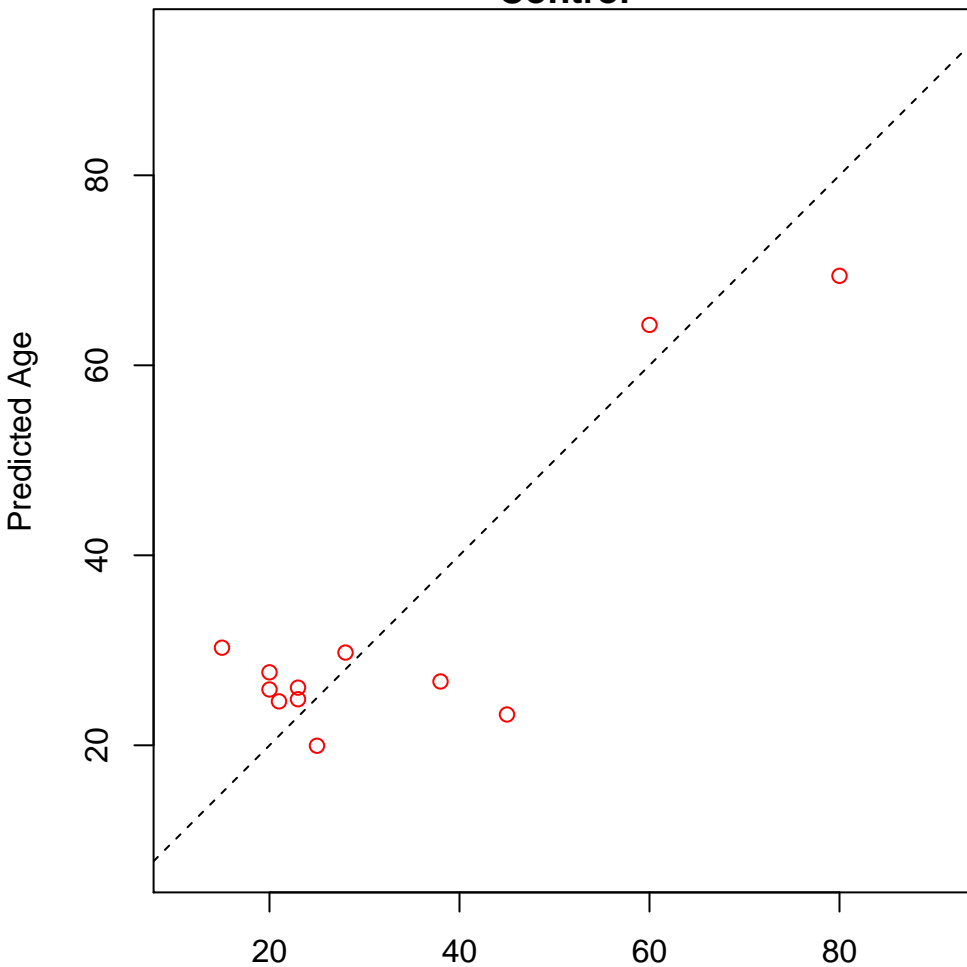


regulation of response to extracellular stimulus (Score: 4.290647)

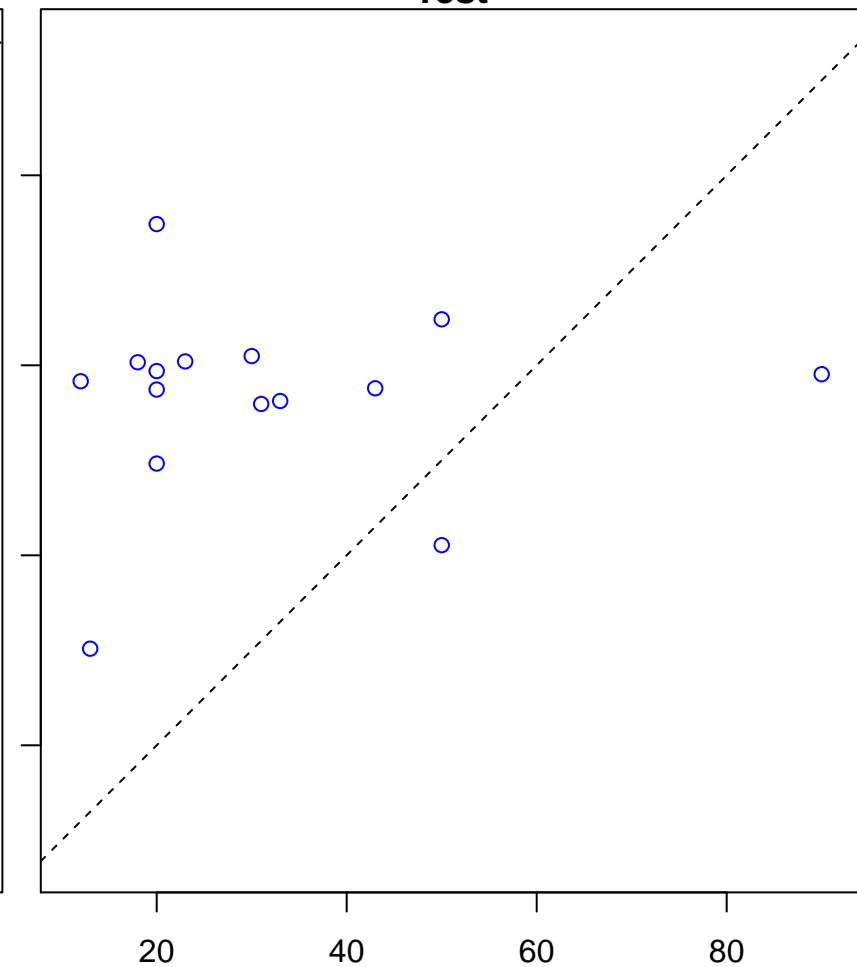


regulation of response to nutrient levels (Score: 4.290647)

Control

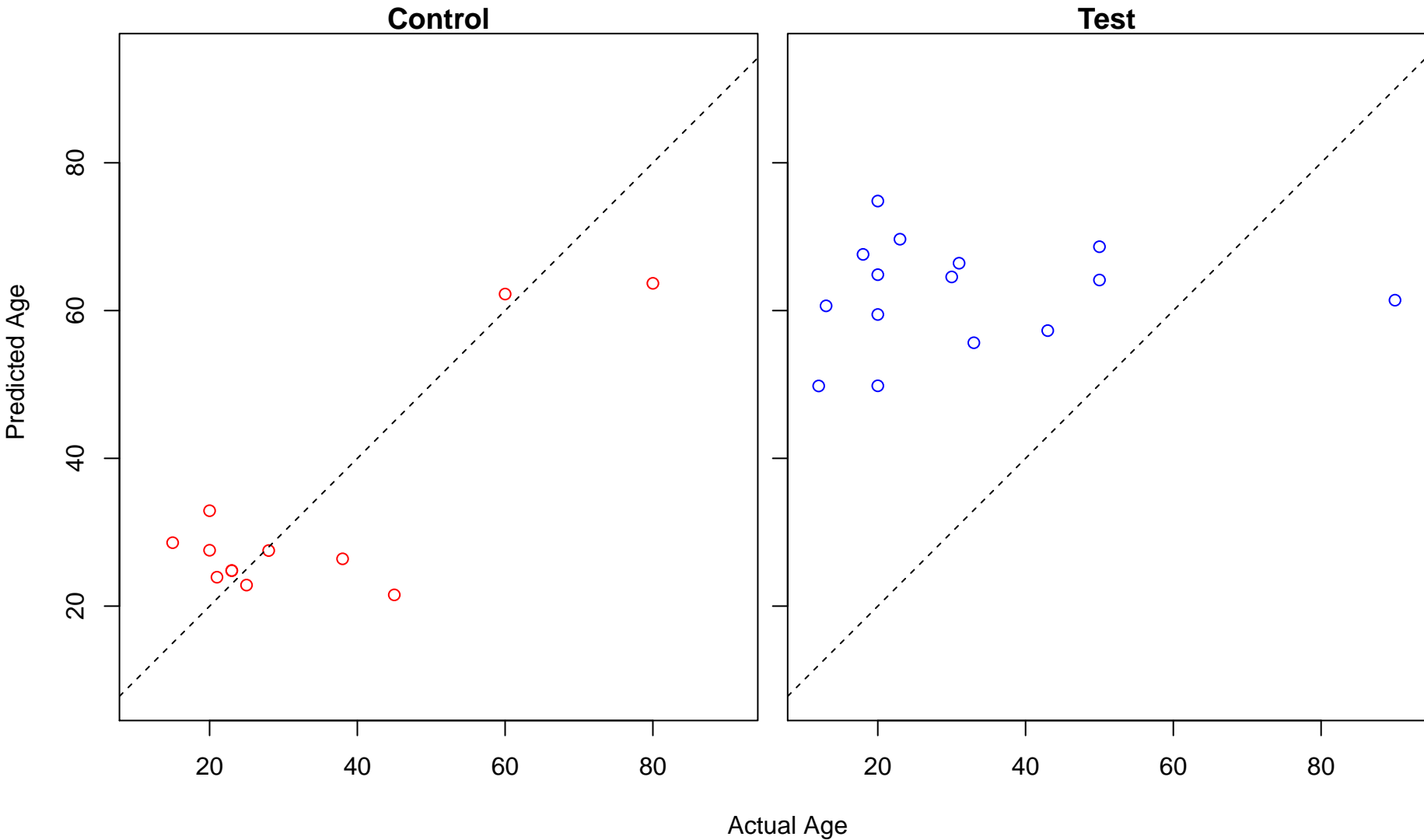


Test



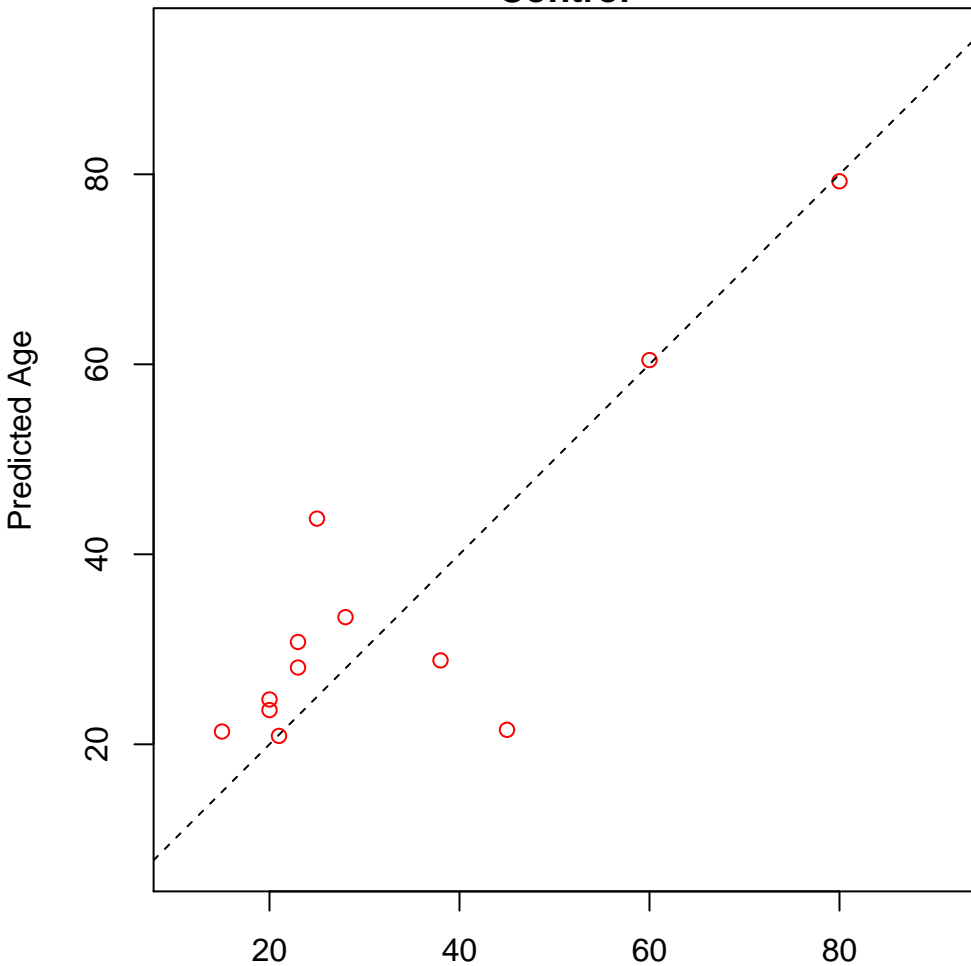
Actual Age

glomerular basement membrane development (Score: 4.289301)

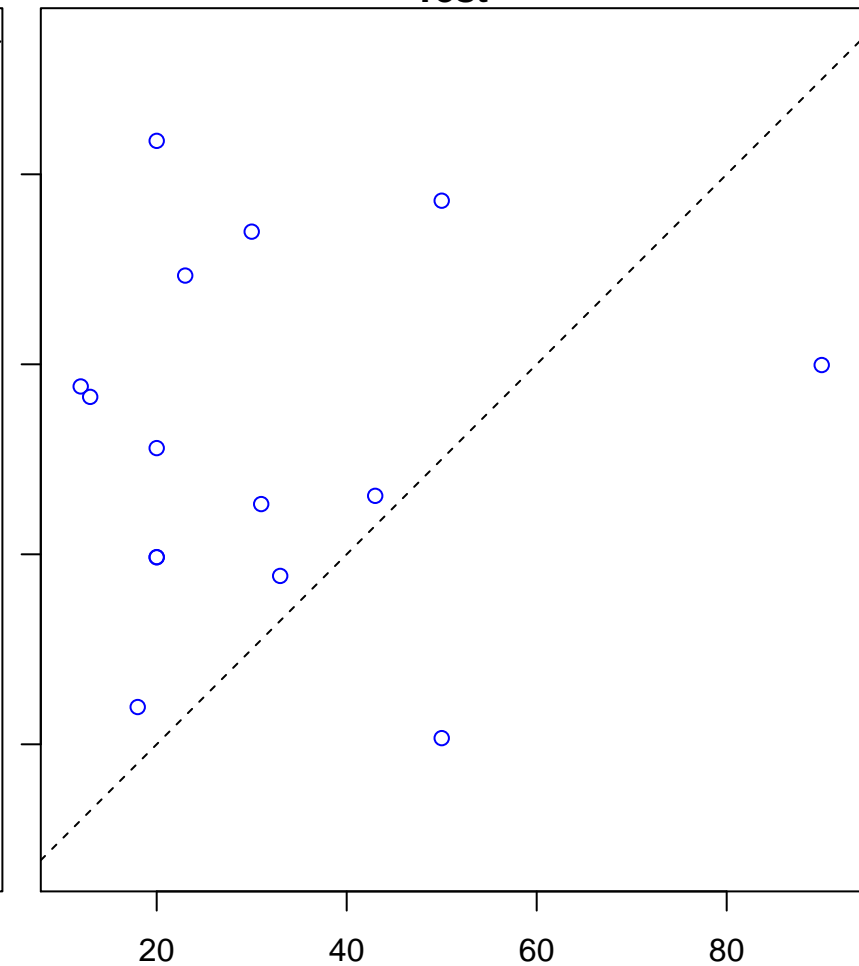


regulation of angiotensin levels in blood (Score: 4.288638)

Control

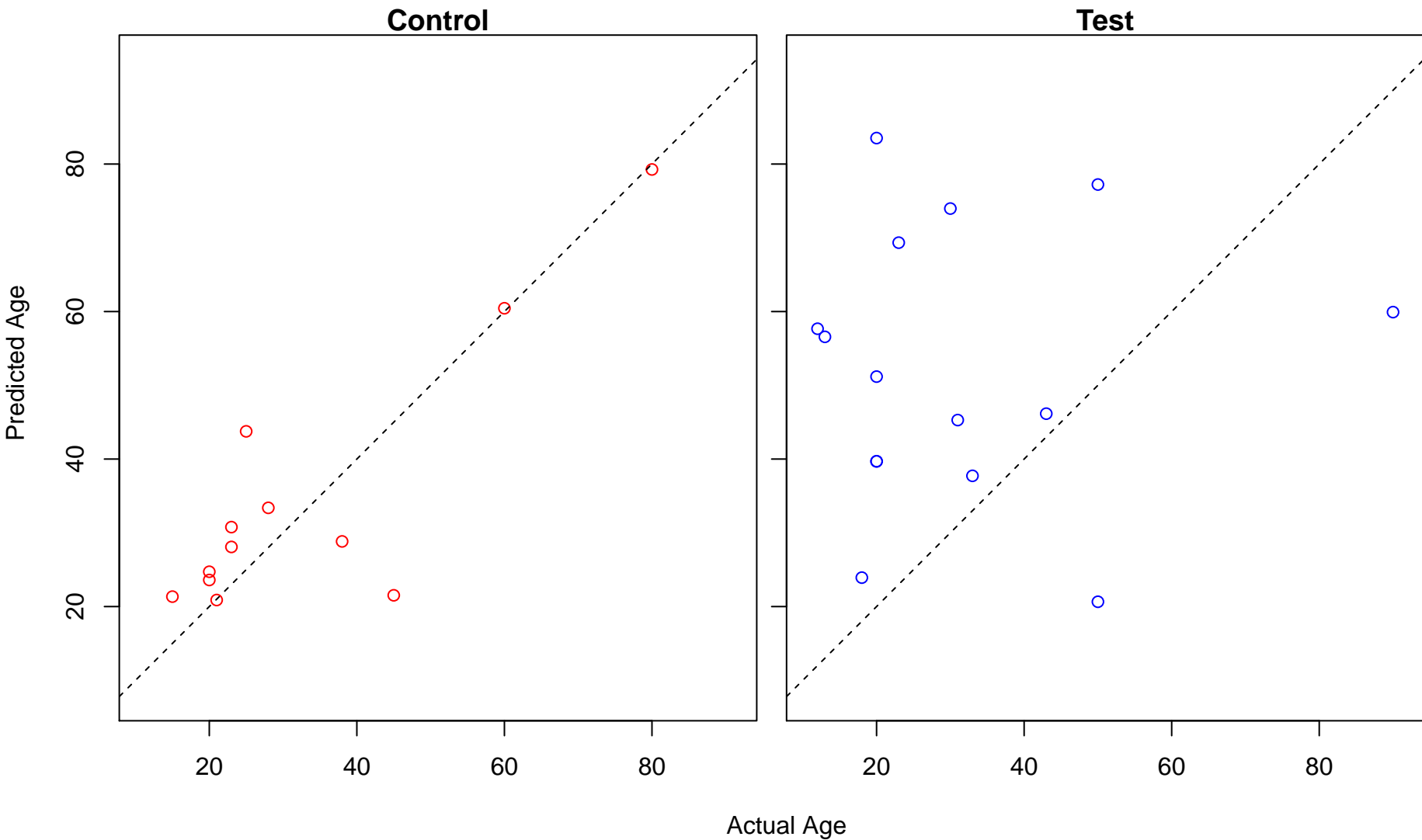


Test

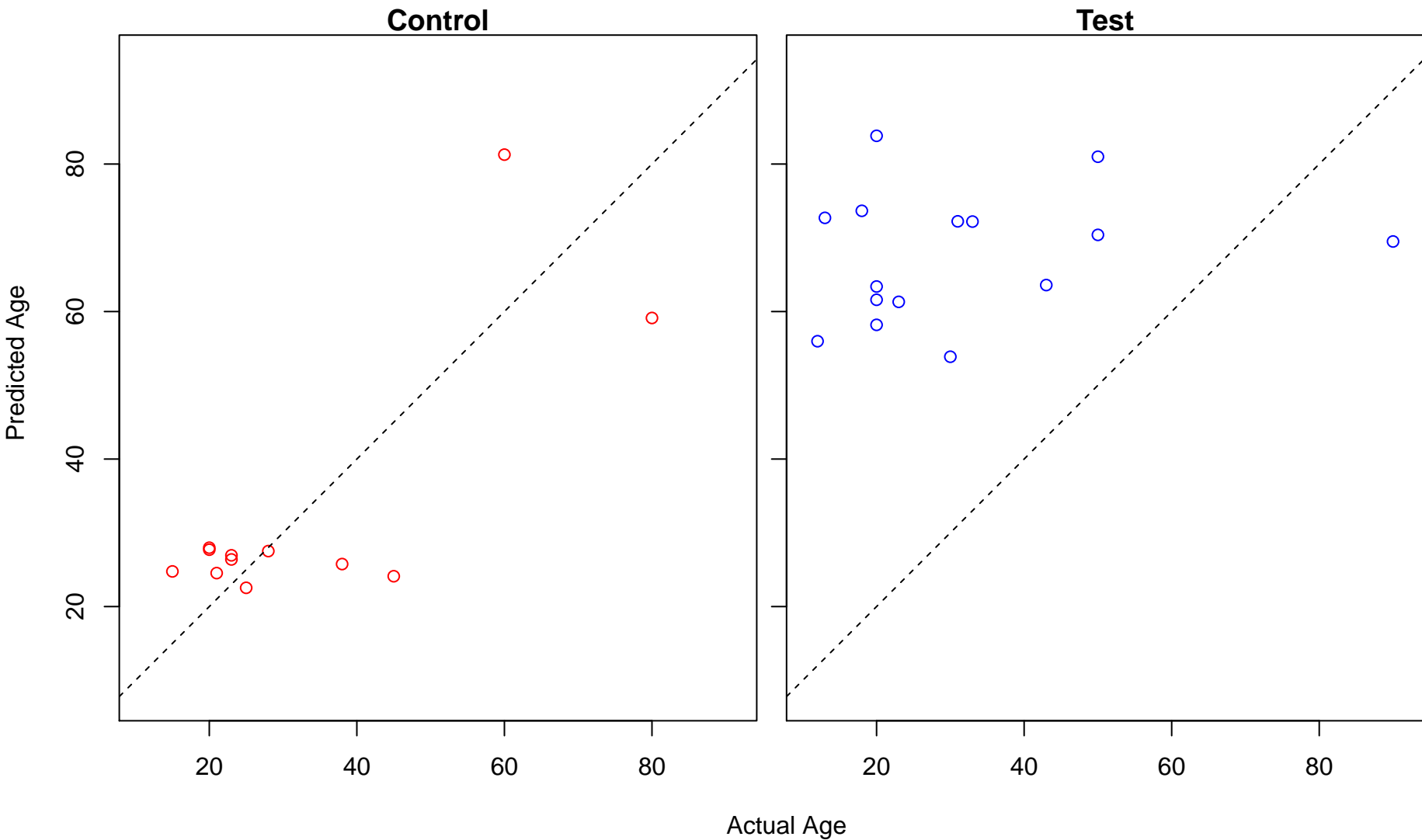


Actual Age

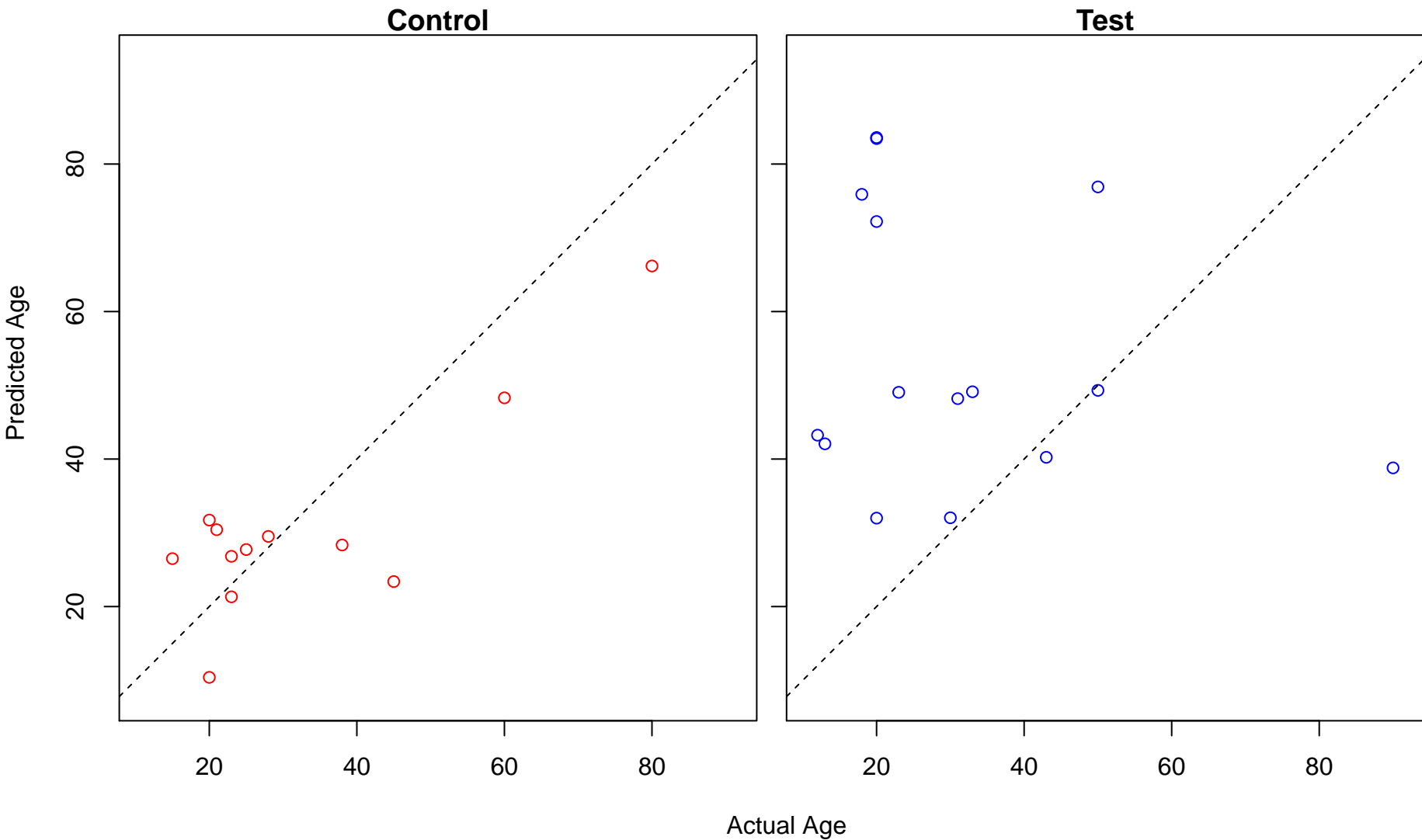
regulation of angiotensin metabolic process (Score: 4.288638)



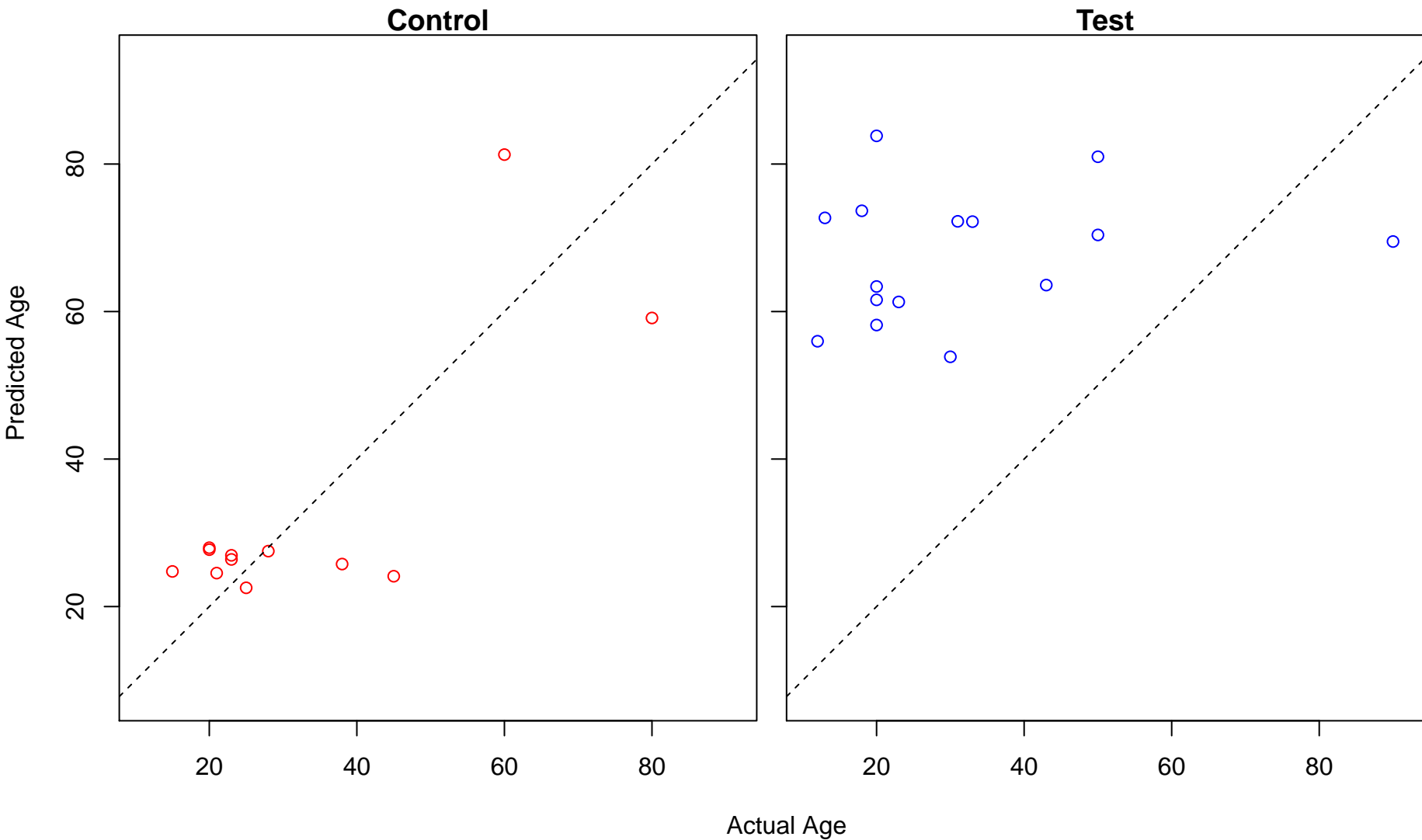
renal system development (Score: 4.288452)



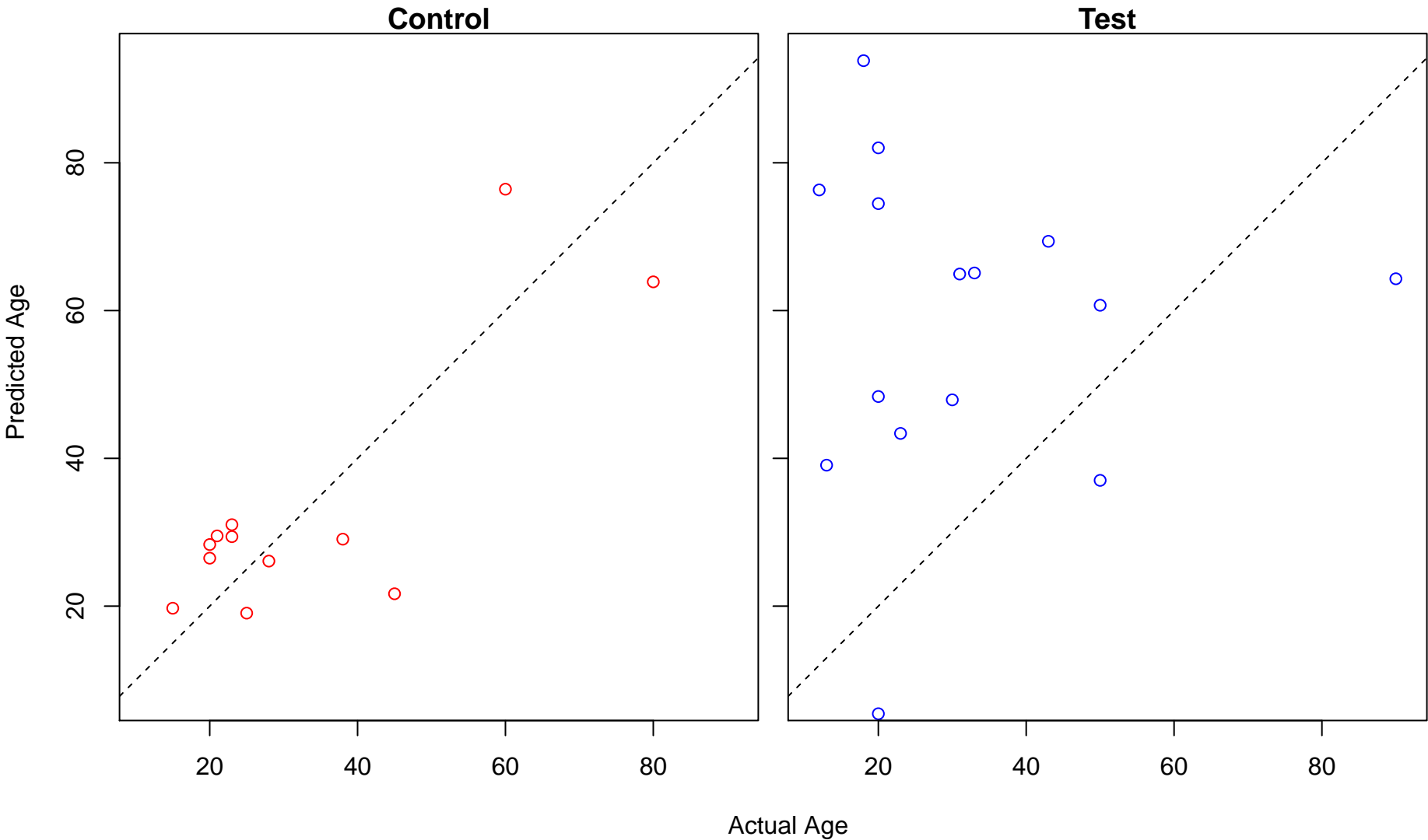
receptor clustering (Score: 4.287963)



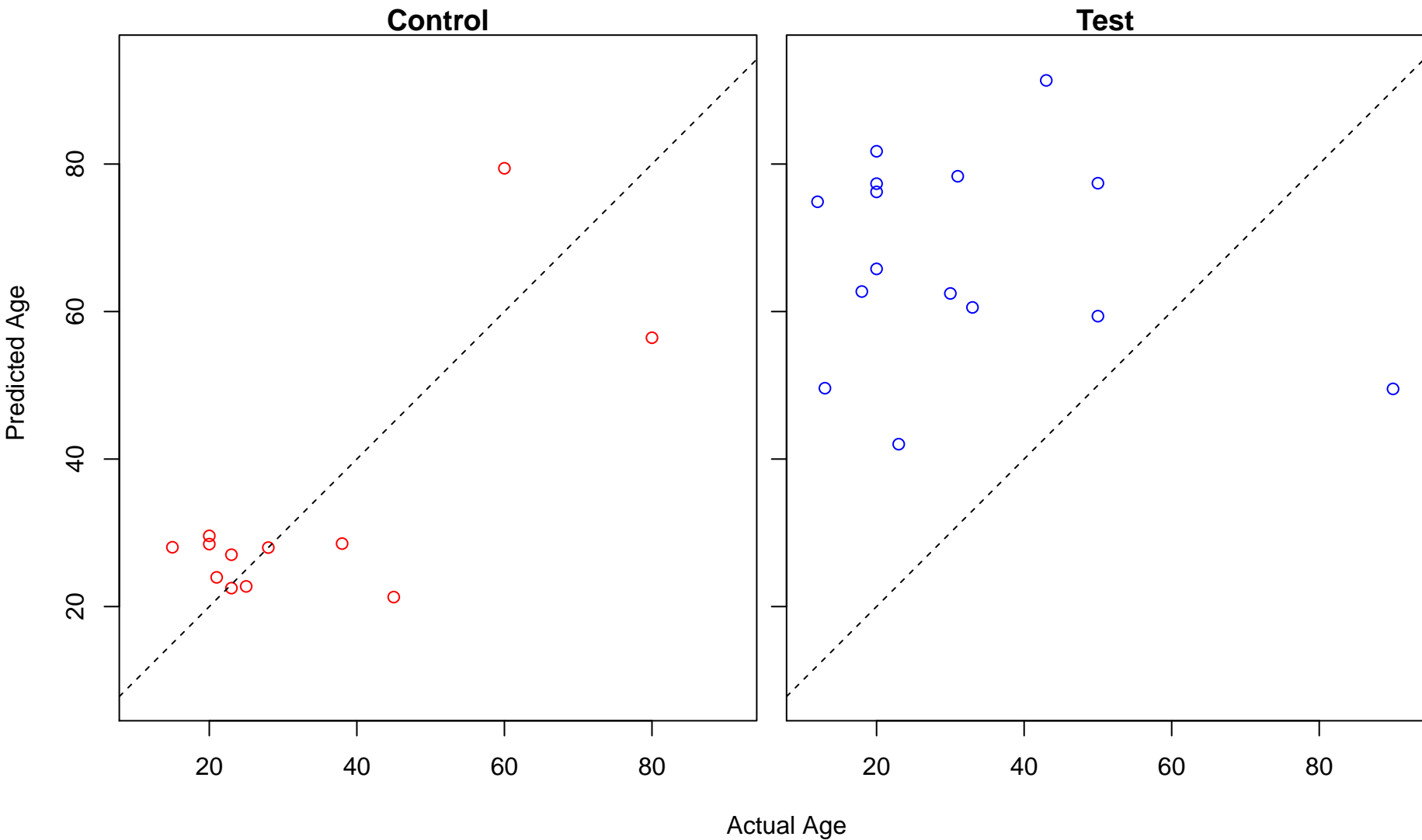
kidney development (Score: 4.287628)



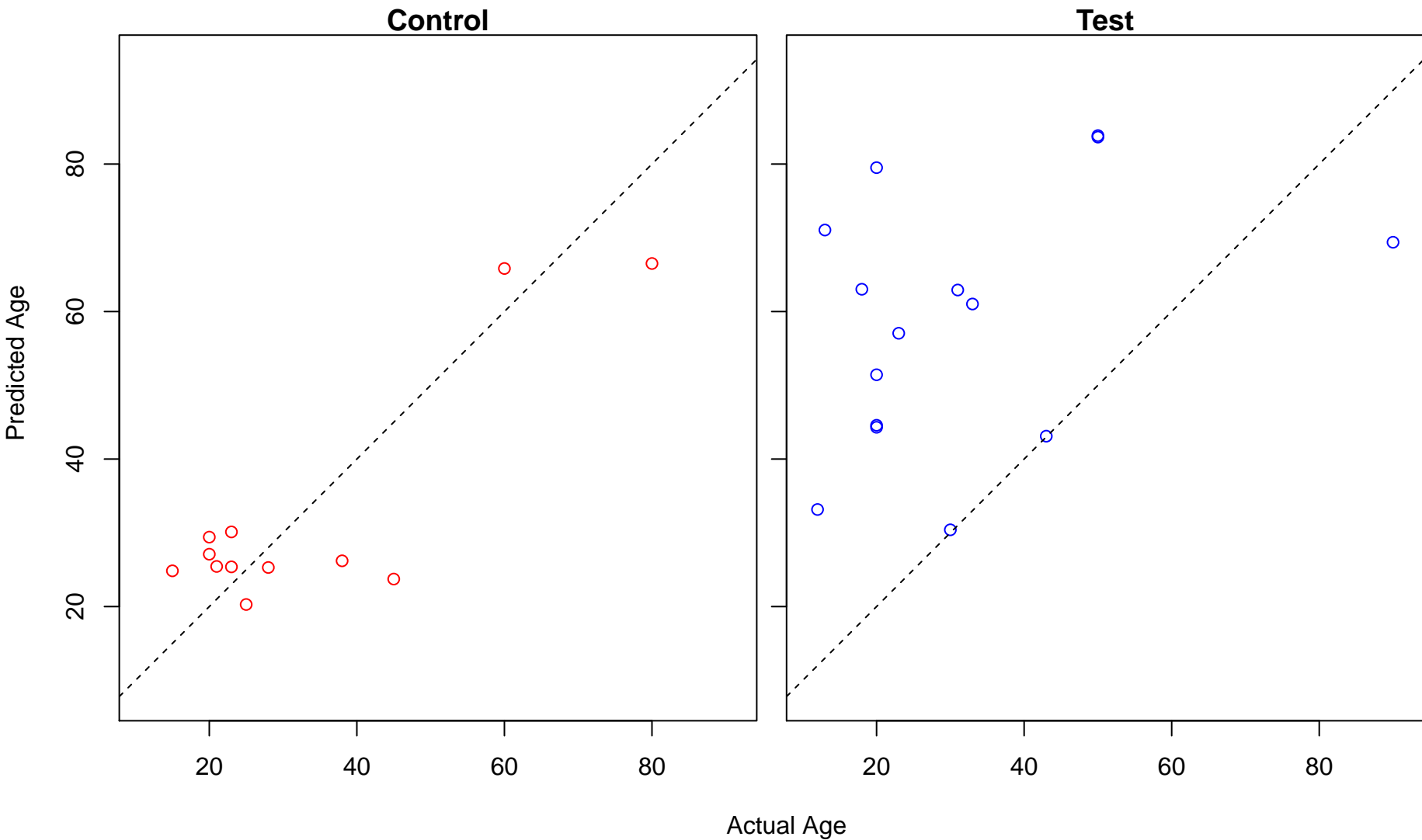
serine family amino acid catabolic process (Score: 4.287373)



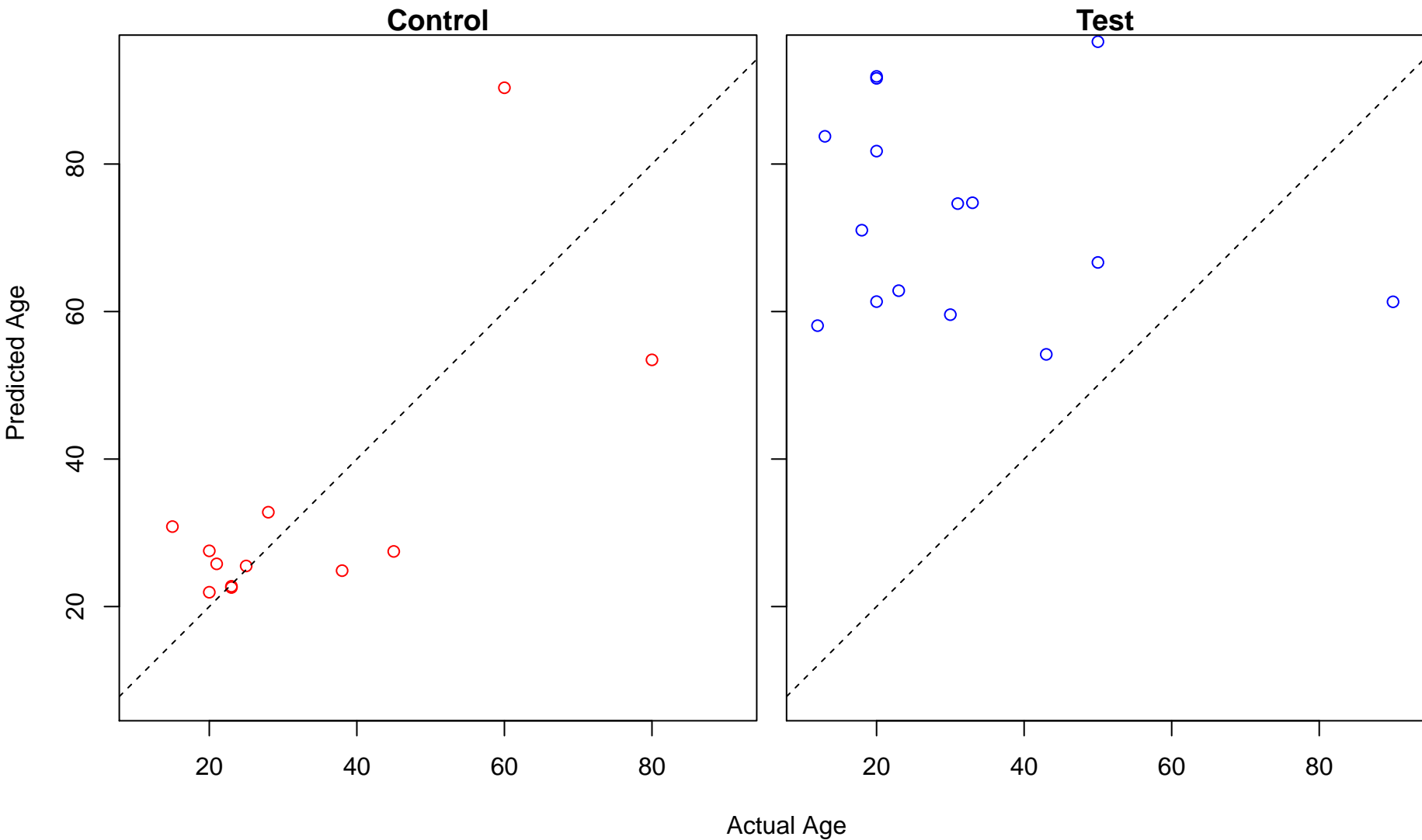
monocyte differentiation (Score: 4.285747)



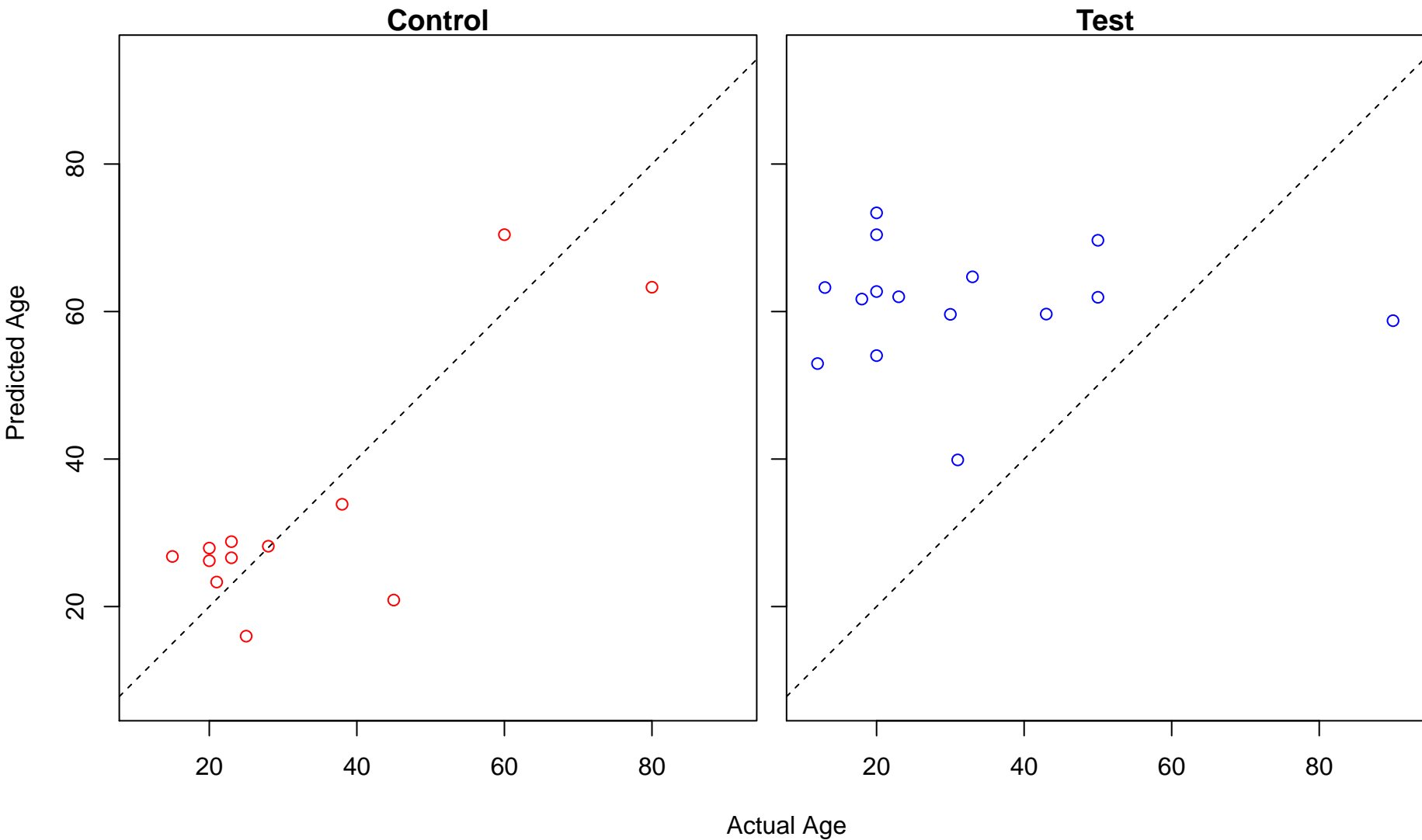
respiratory burst (Score: 4.282267)



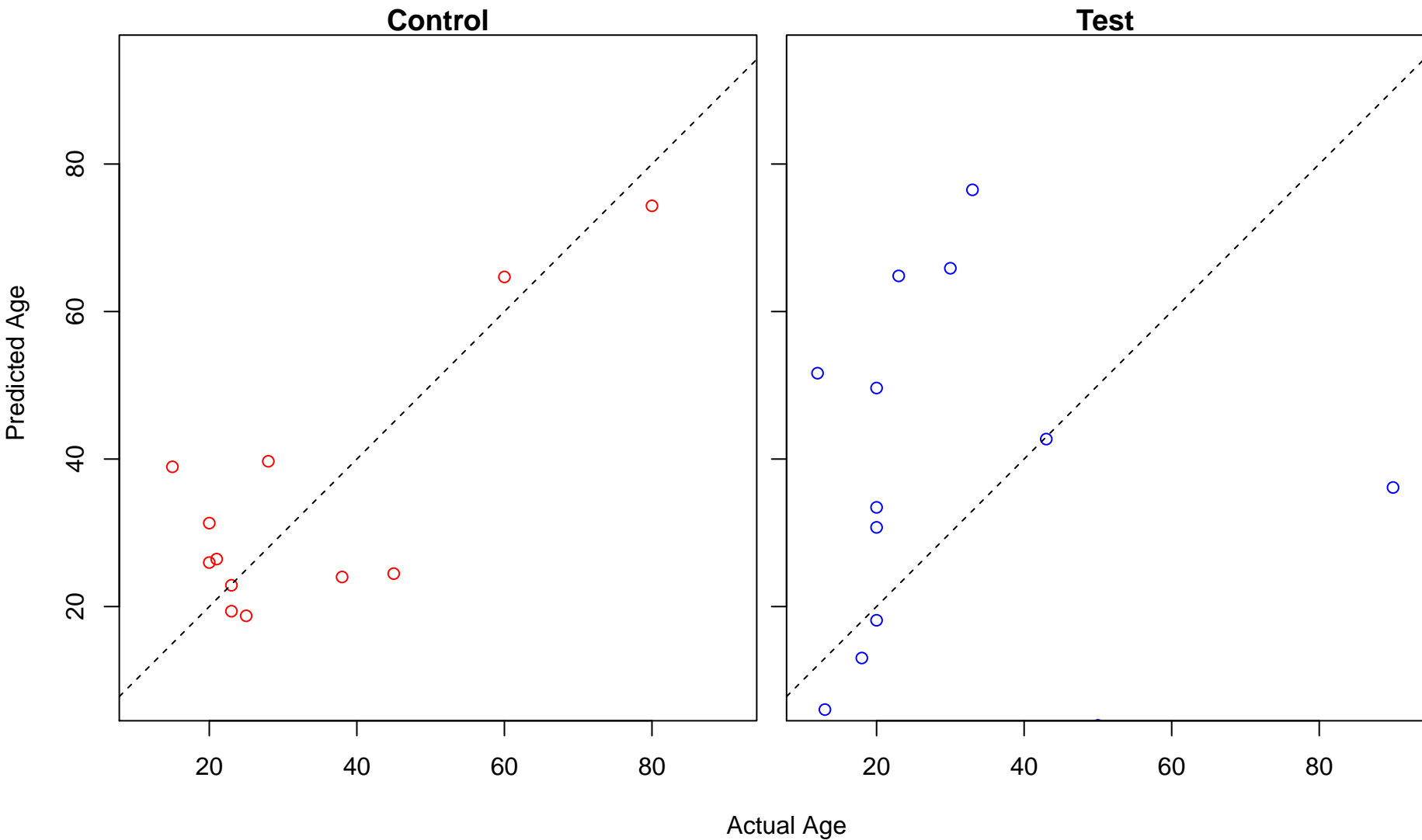
positive regulation of mesonephros development (Score: 4.281472)



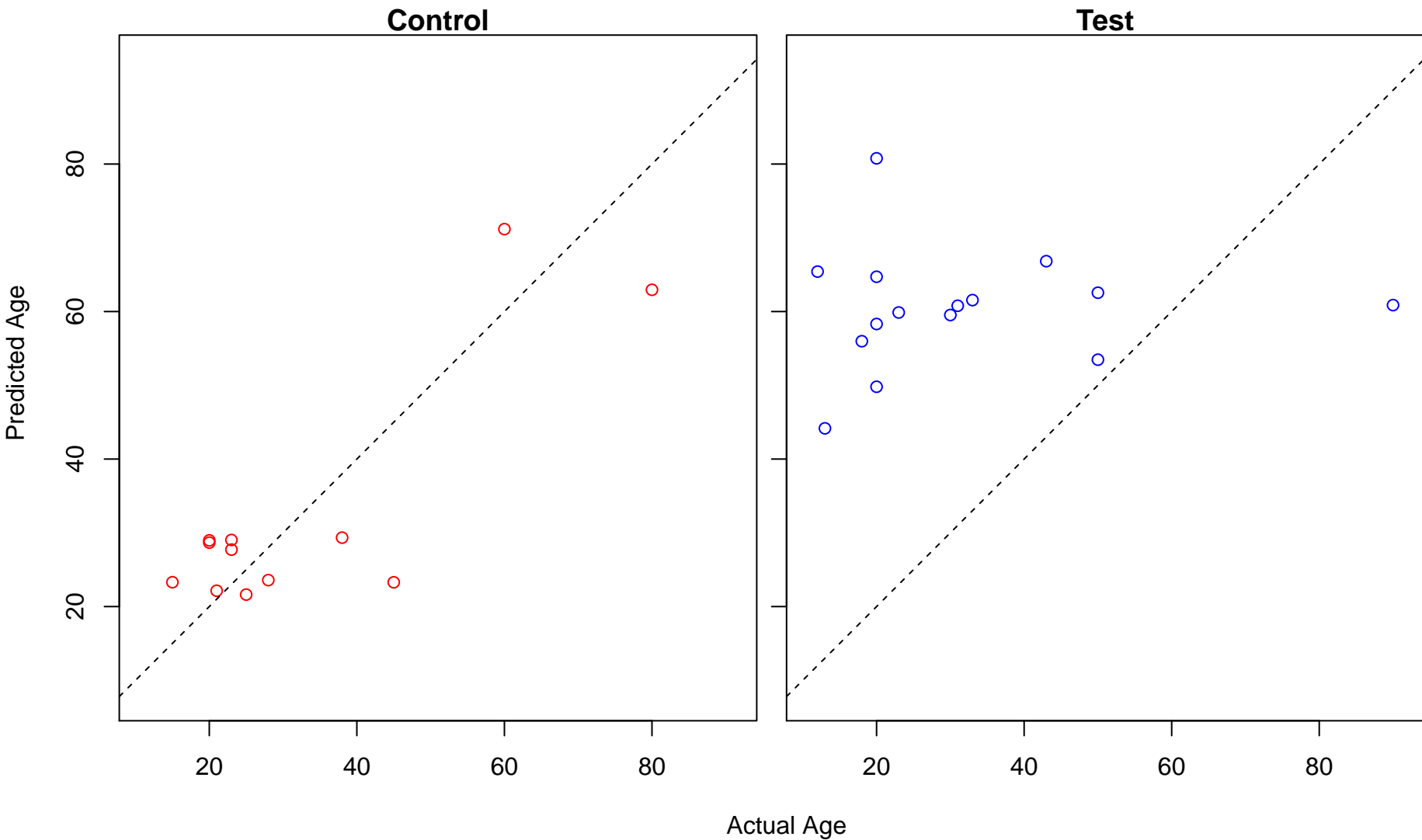
response to lipoprotein particle (Score: 4.281374)



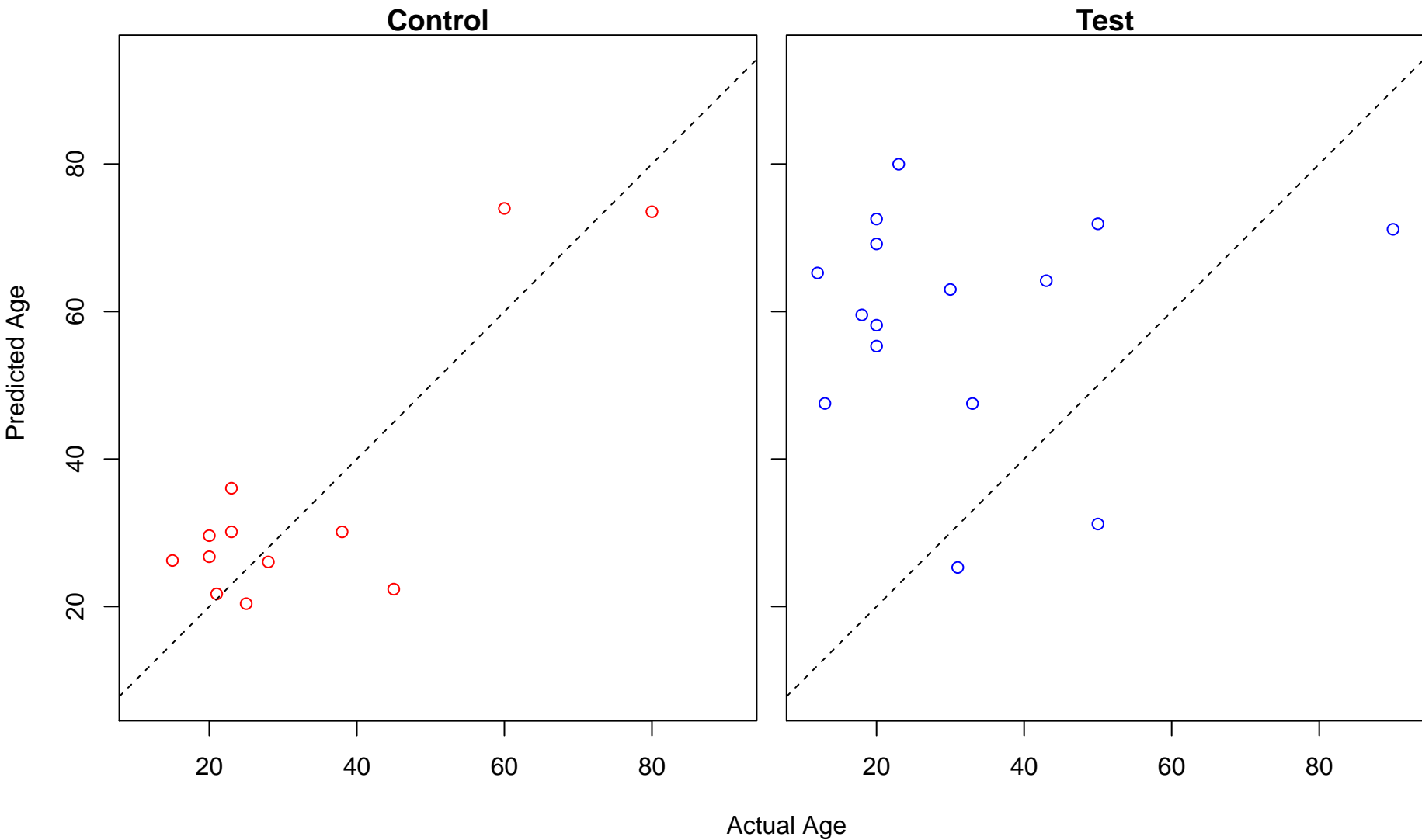
negative regulation of intracellular transport (Score: 4.280805)



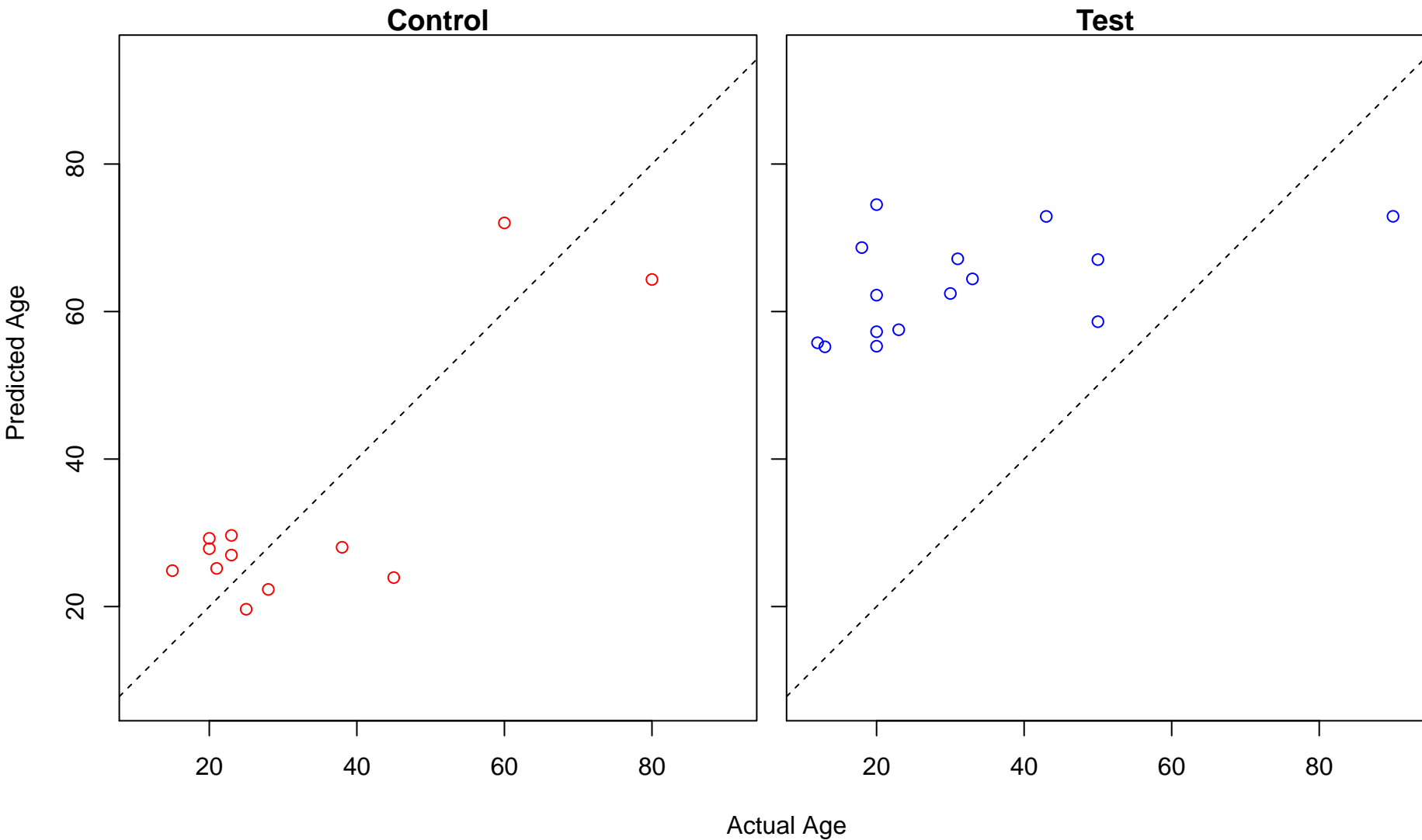
regulation of smooth muscle cell apoptotic process (Score: 4.278825)



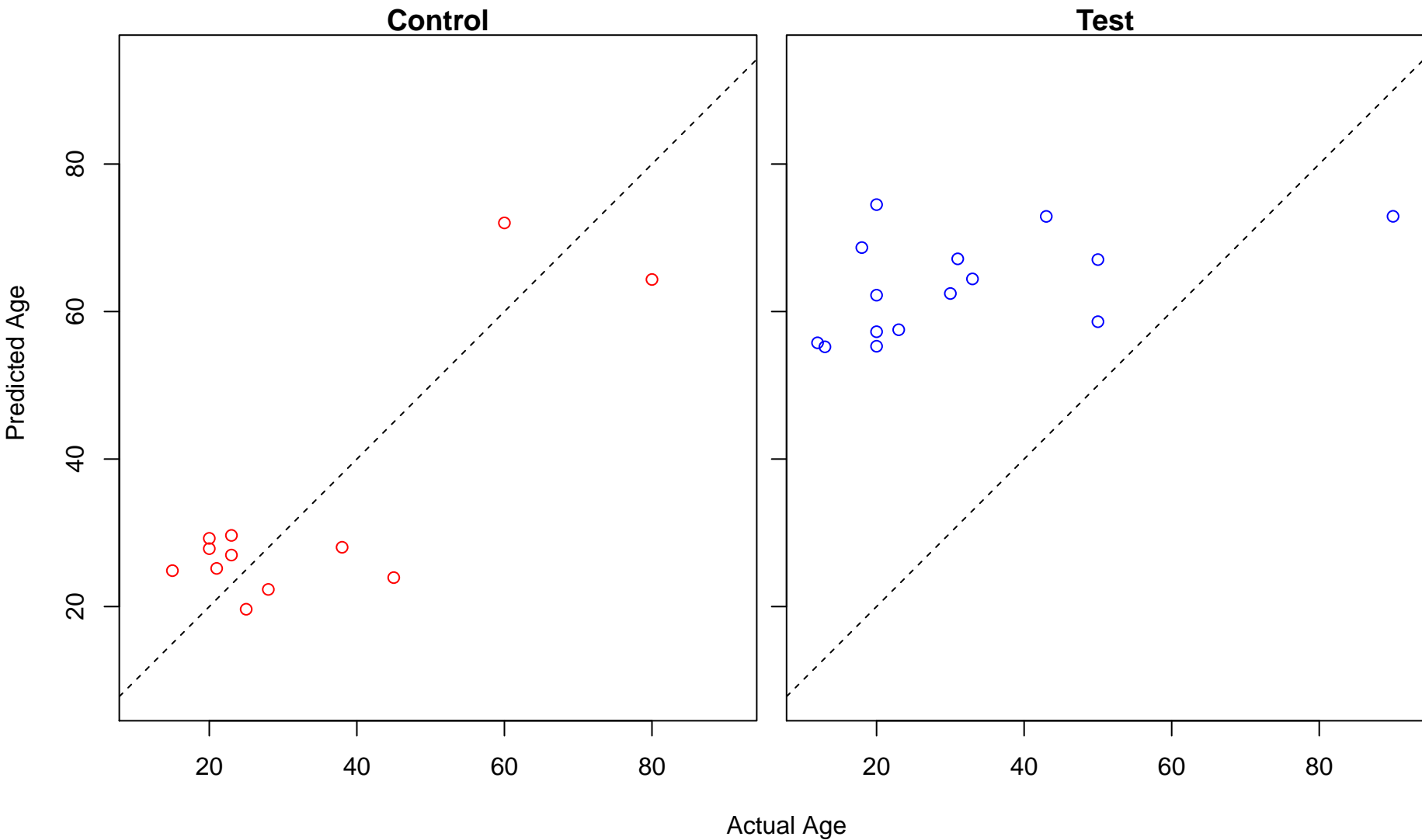
vasculogenesis (Score: 4.277867)



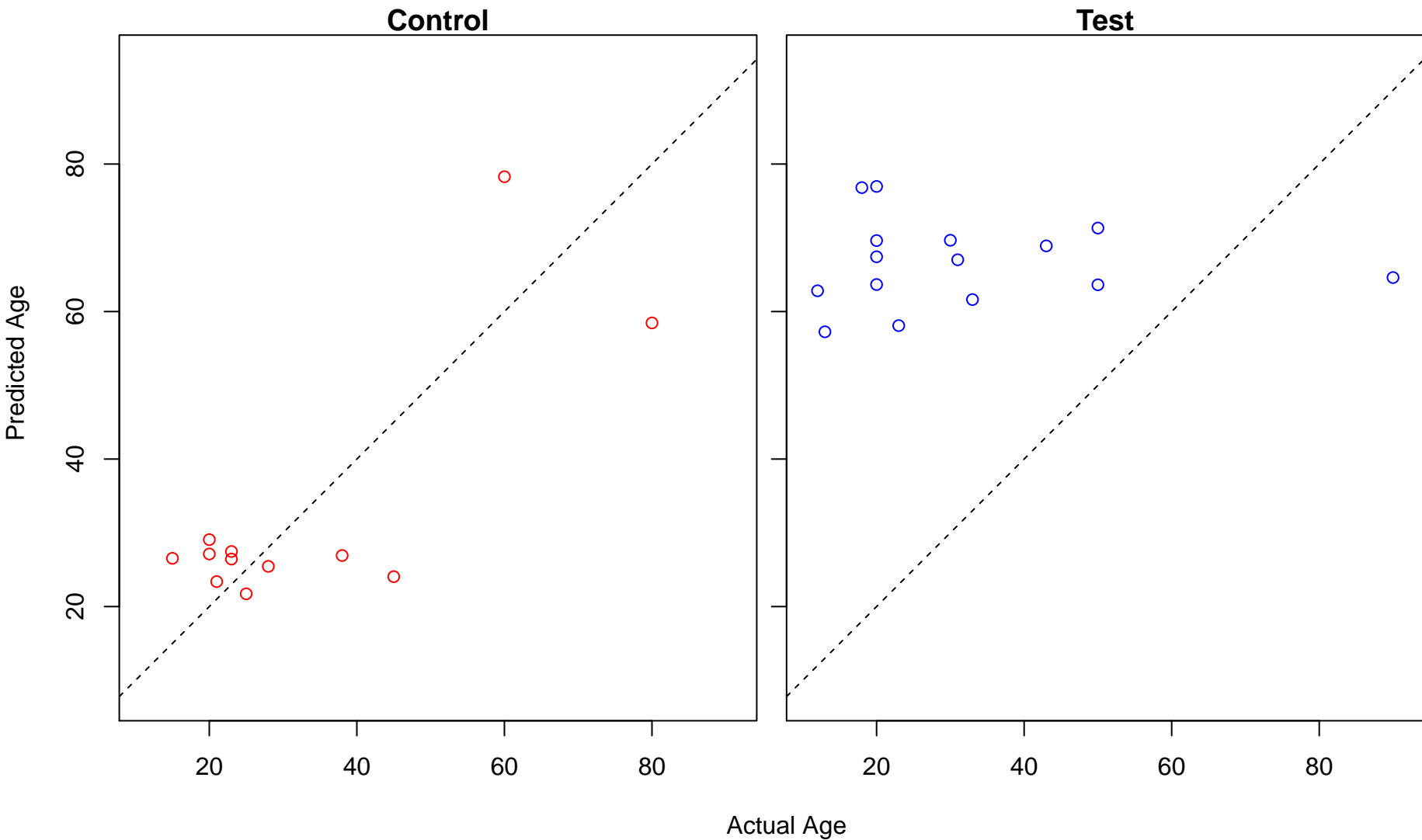
spermatid nucleus differentiation (Score: 4.275168)



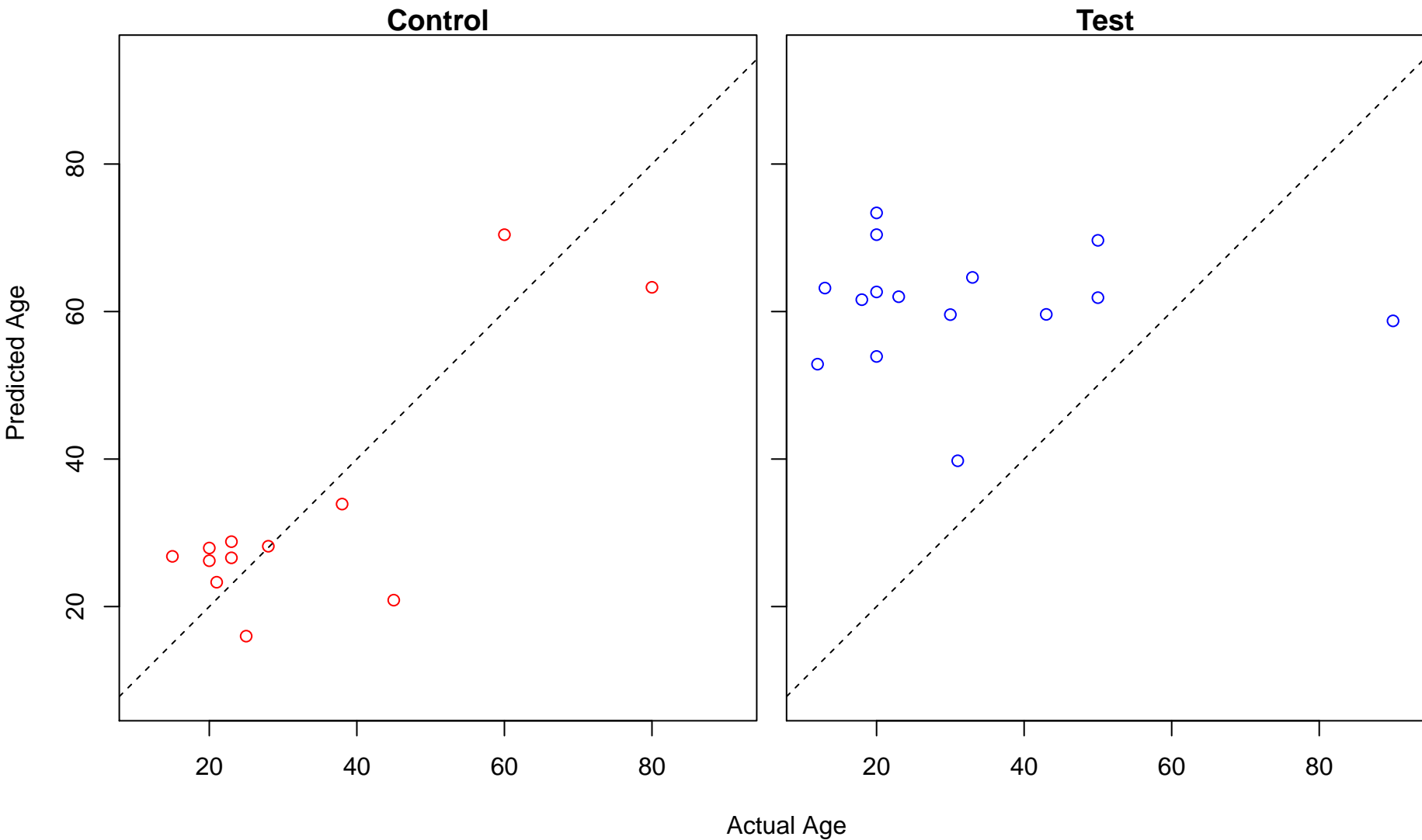
sperm chromatin condensation (Score: 4.274947)



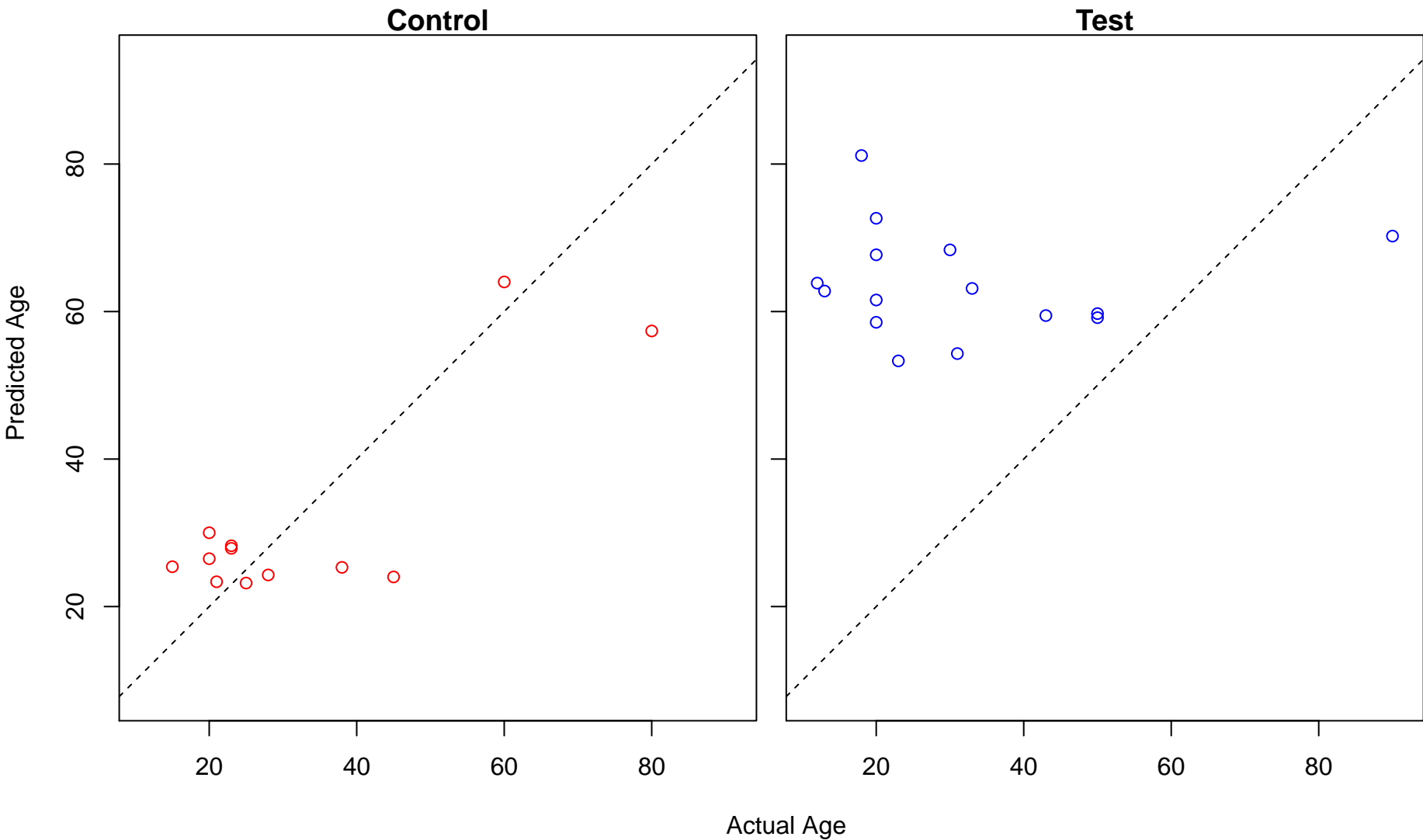
ER-nucleus signaling pathway (Score: 4.273259)



response to low-density lipoprotein particle (Score: 4.271958)

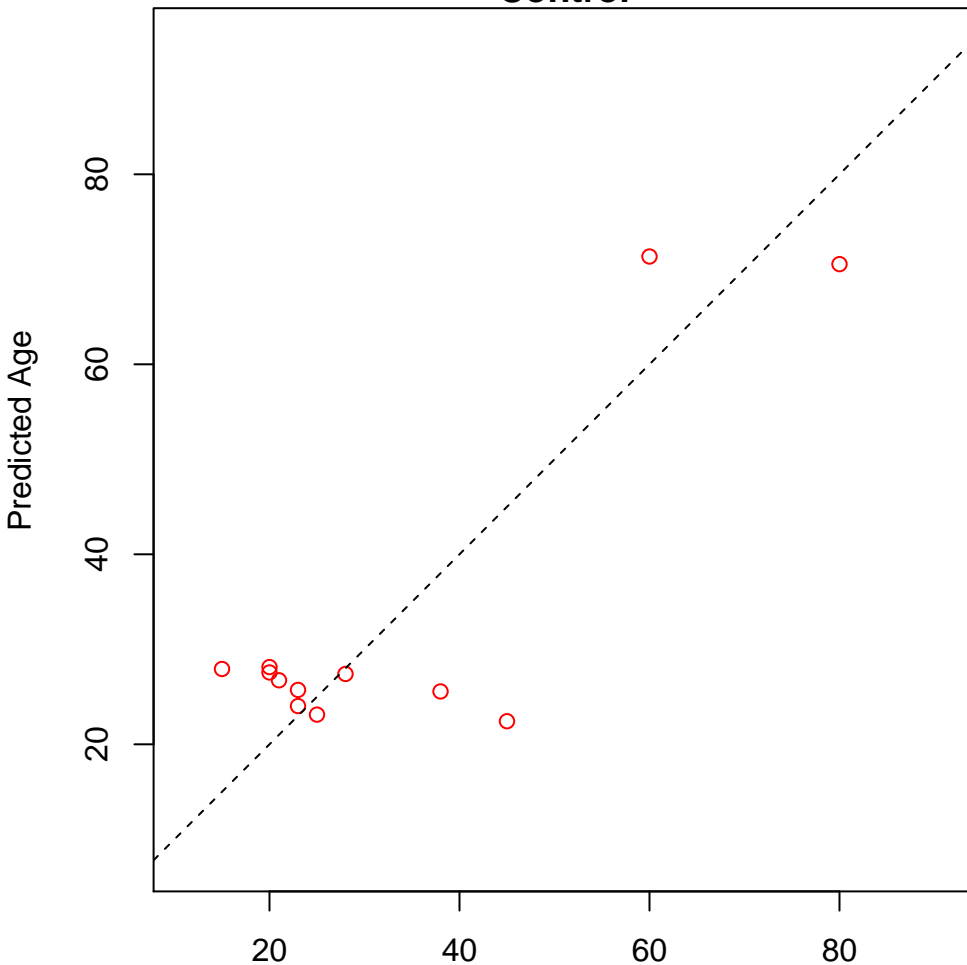


adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway (Score: 4.271886)

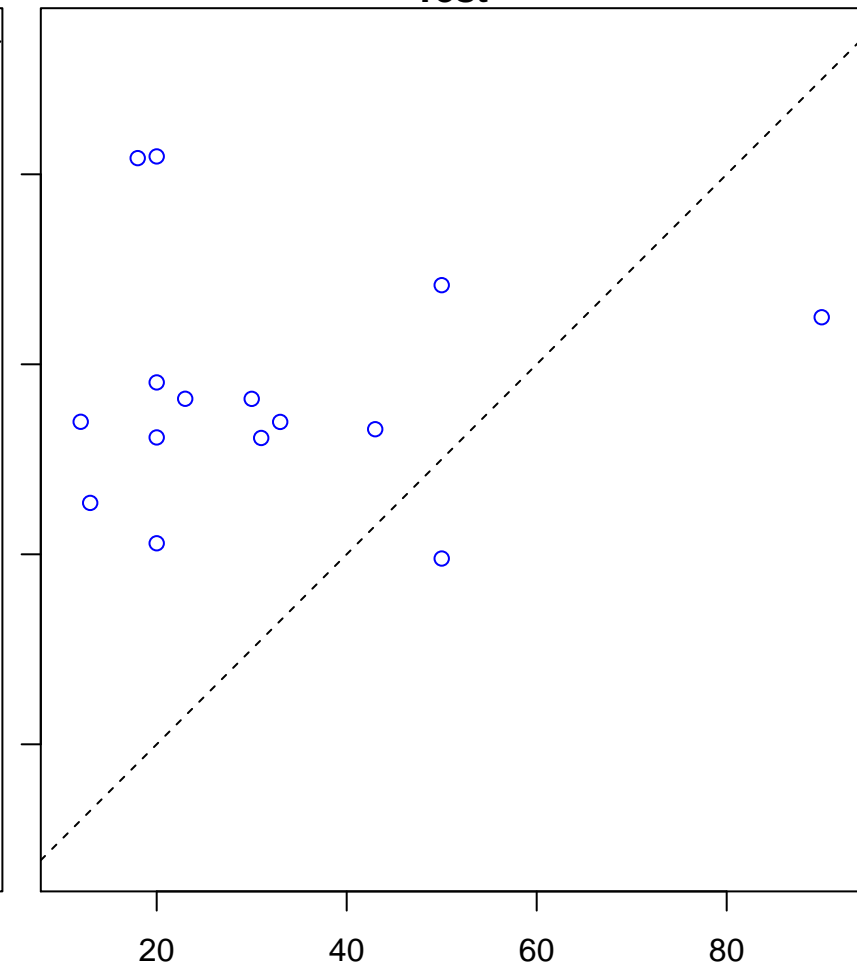


viral budding via host ESCRT complex (Score: 4.271149)

Control

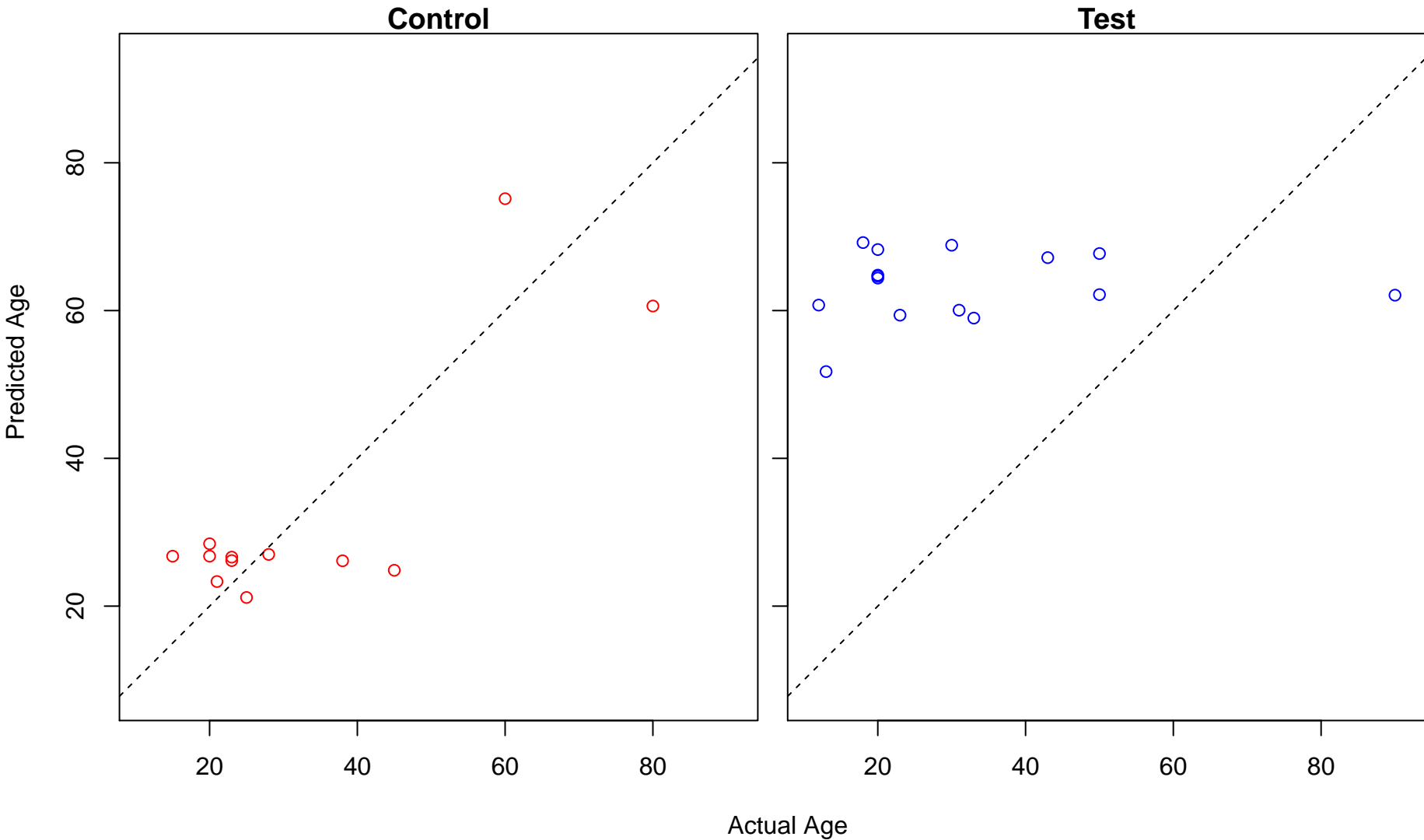


Test

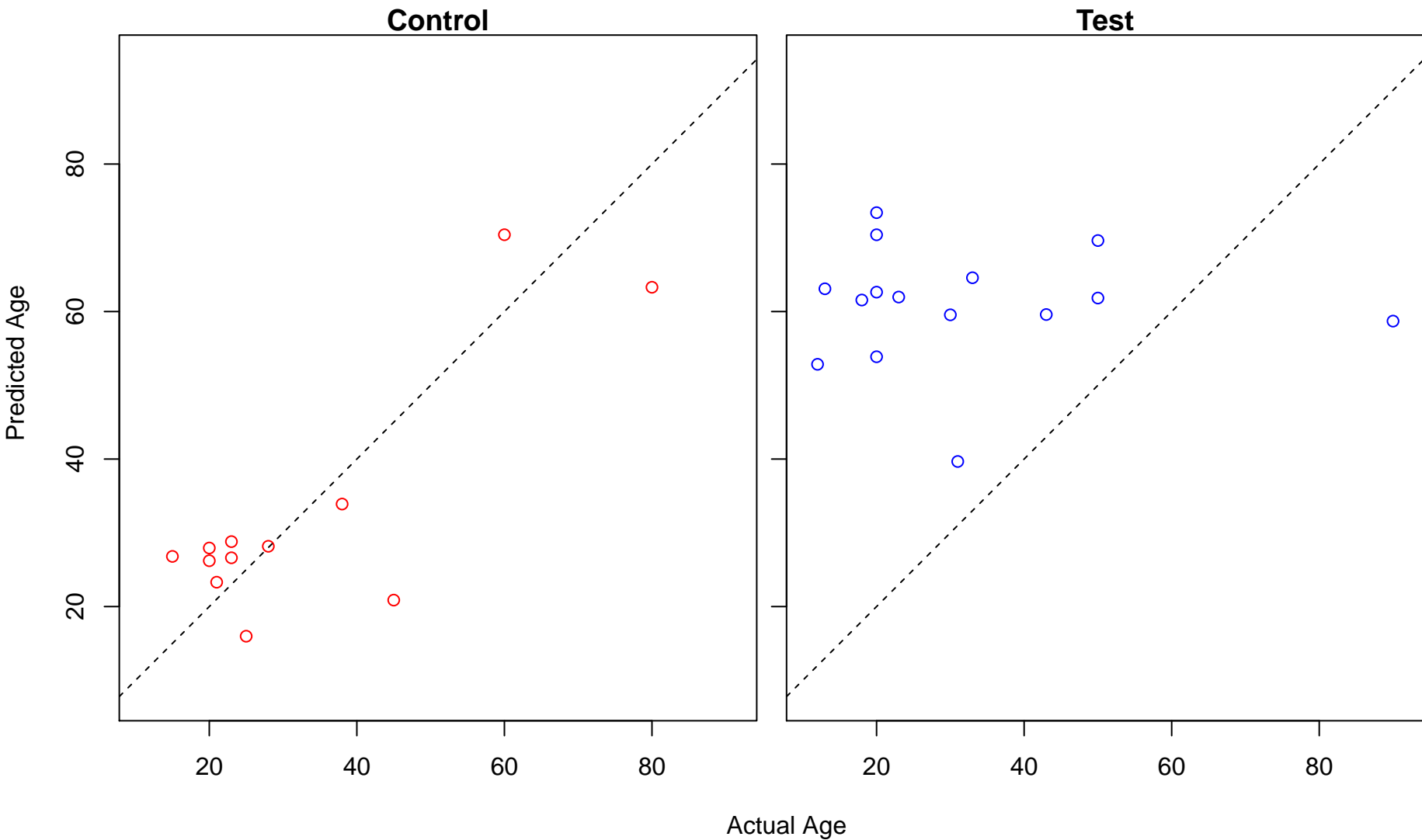


Actual Age

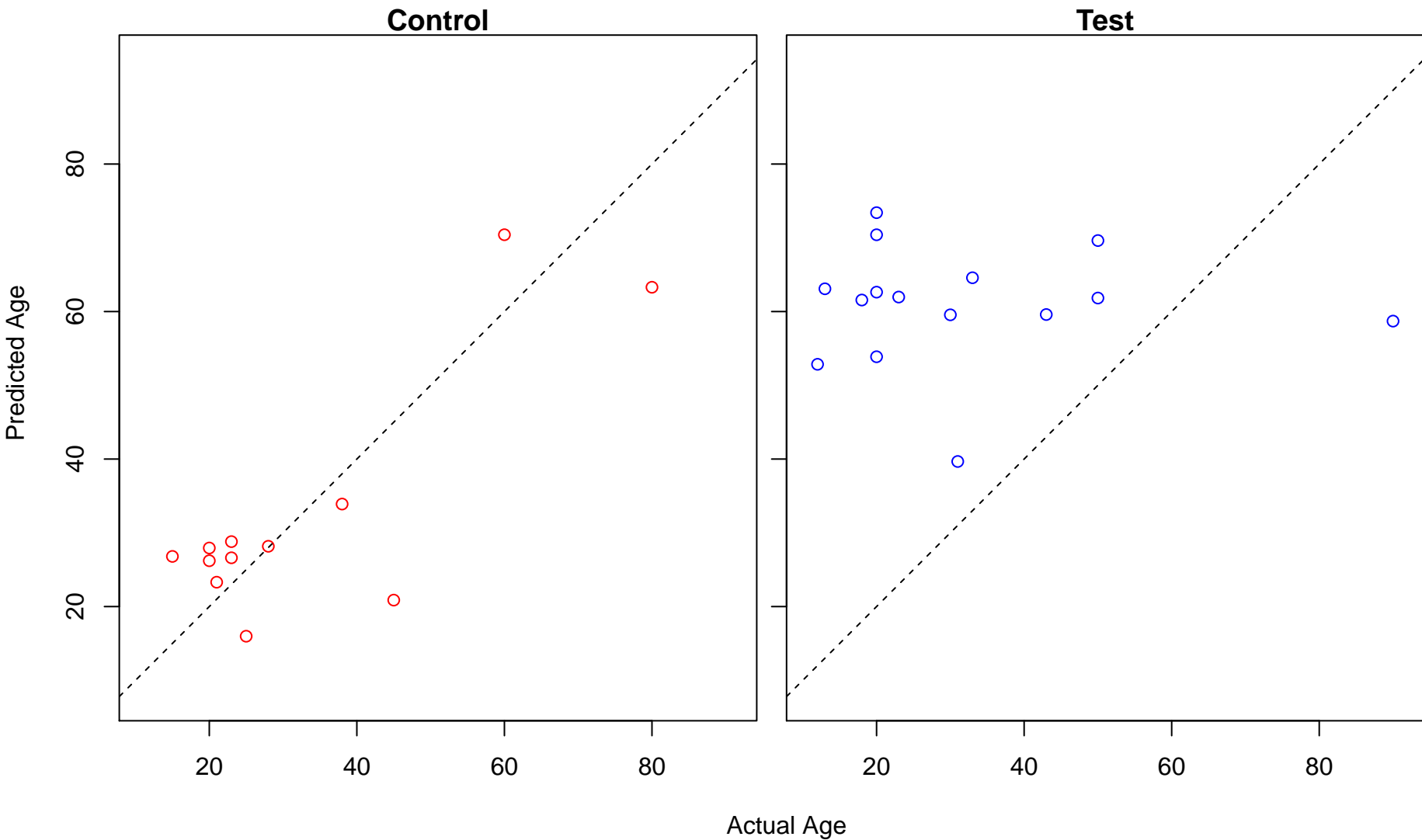
endoplasmic reticulum to cytosol transport (Score: 4.268309)



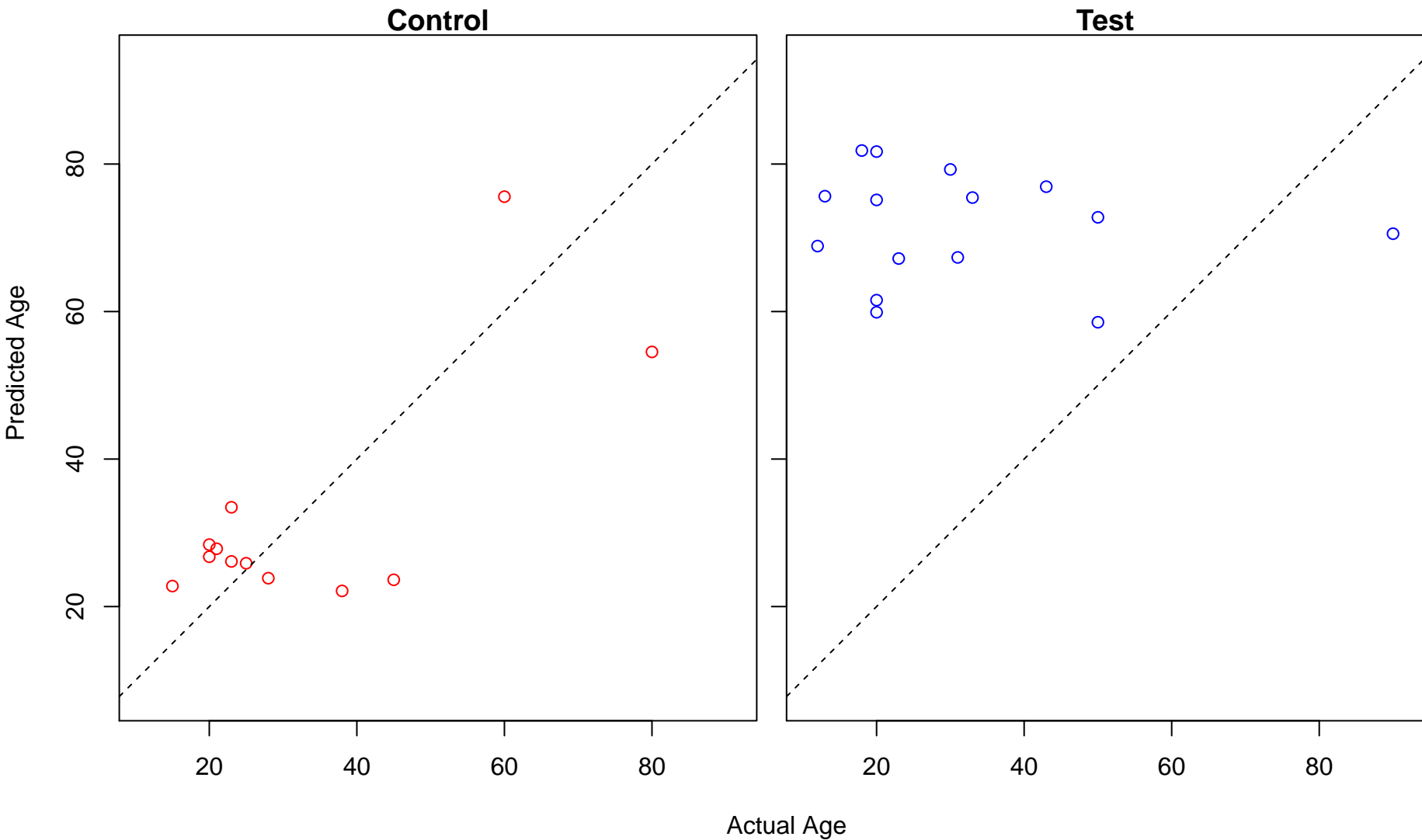
cellular response to lipoprotein particle stimulus (Score: 4.267850)



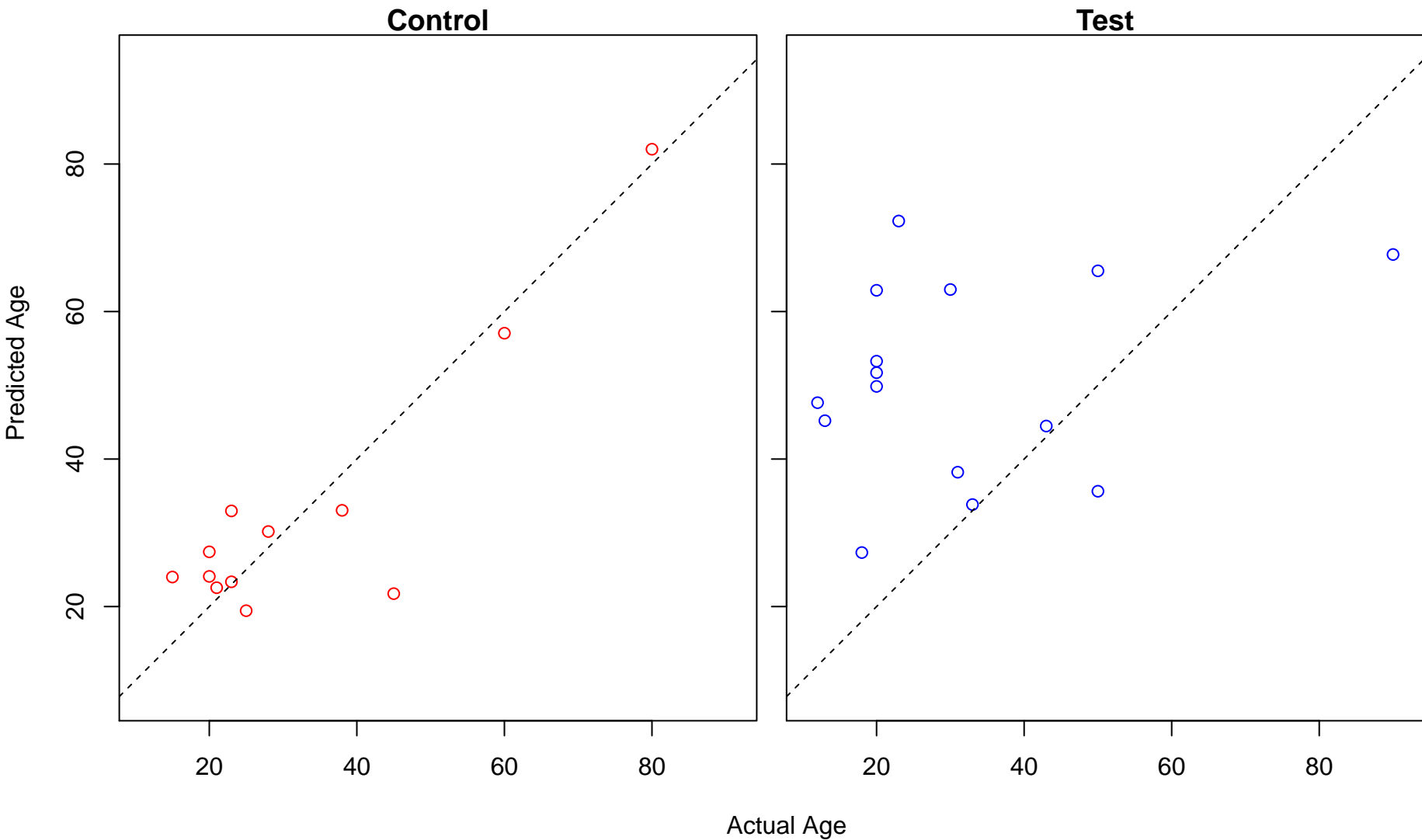
cellular response to low-density lipoprotein particle stimulus (Score: 4.267850)



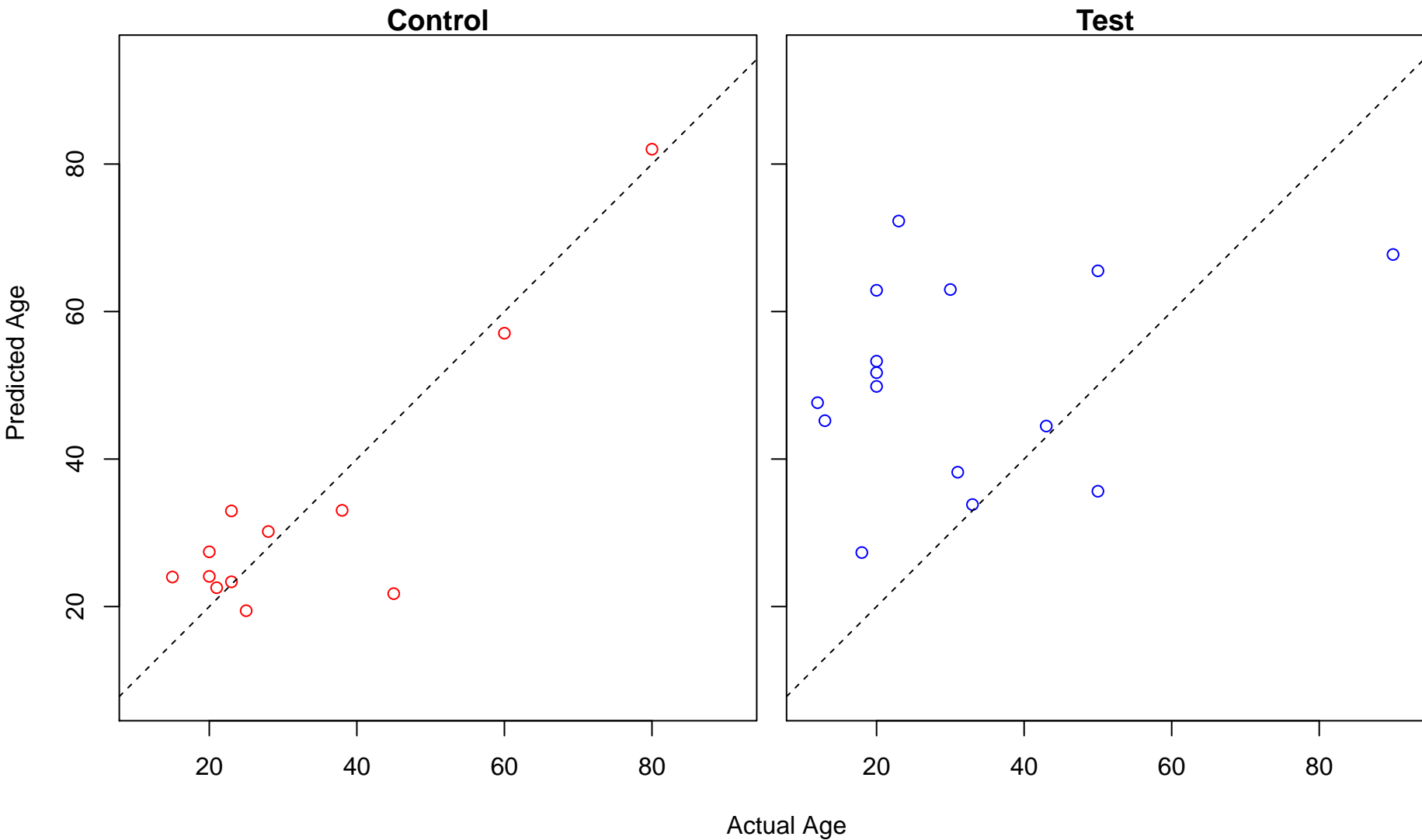
positive regulation of interleukin-17 production (Score: 4.267054)



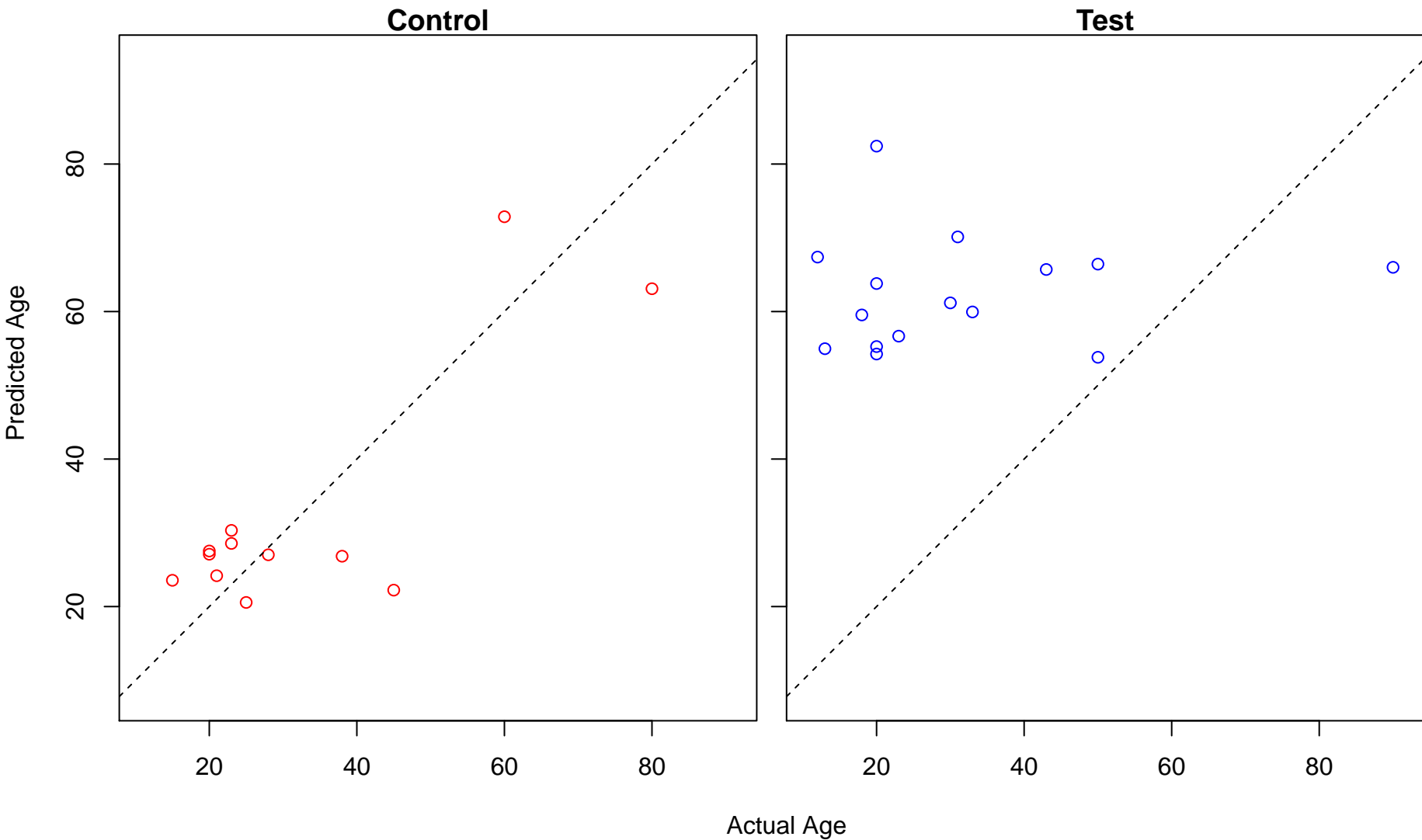
regulation of keratinocyte migration (Score: 4.266497)



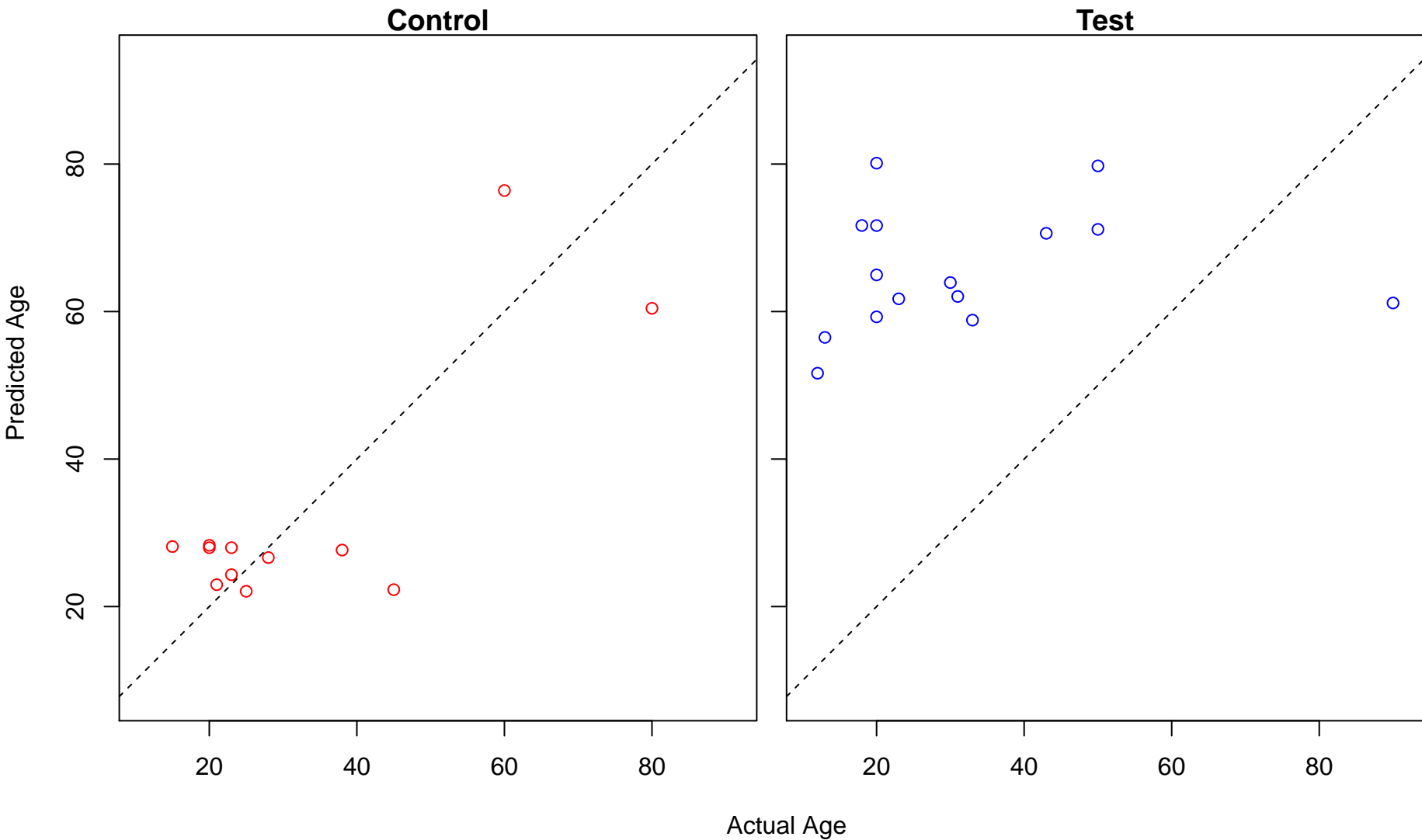
positive regulation of keratinocyte migration (Score: 4.266497)



mitotic G2/M transition checkpoint (Score: 4.266314)

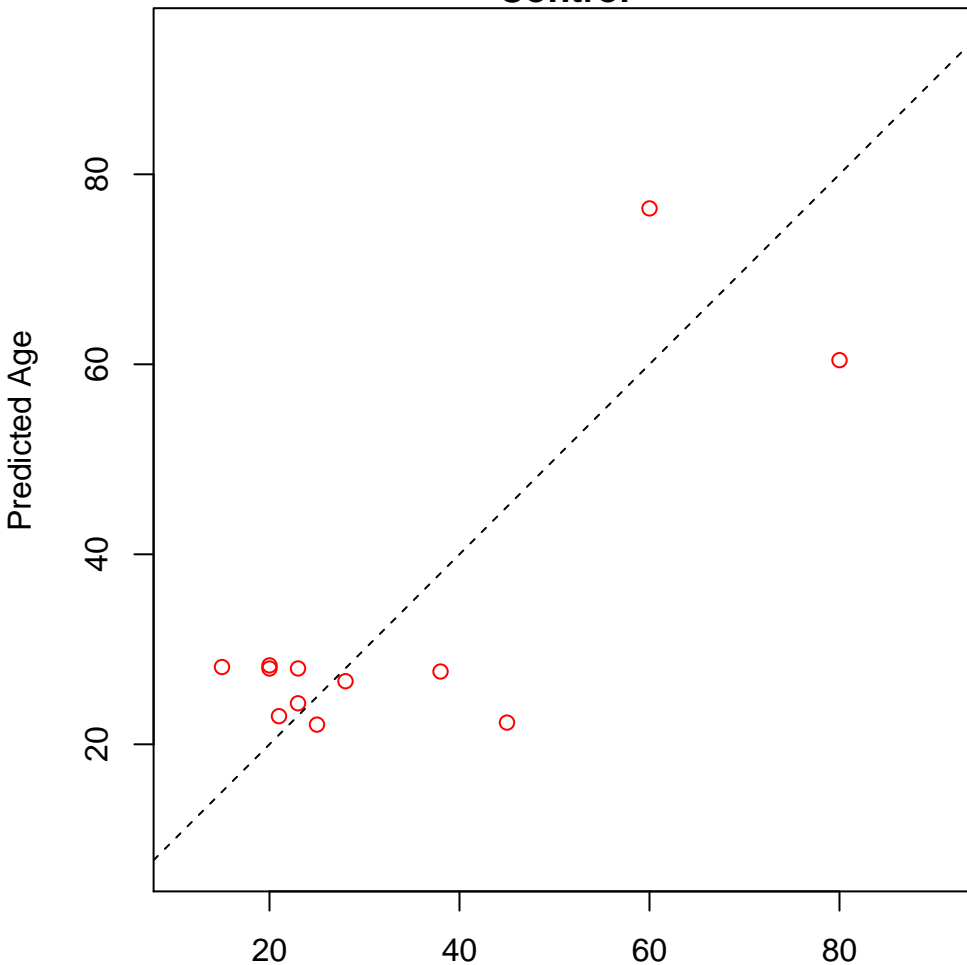


response to indole-3-methanol (Score: 4.264705)

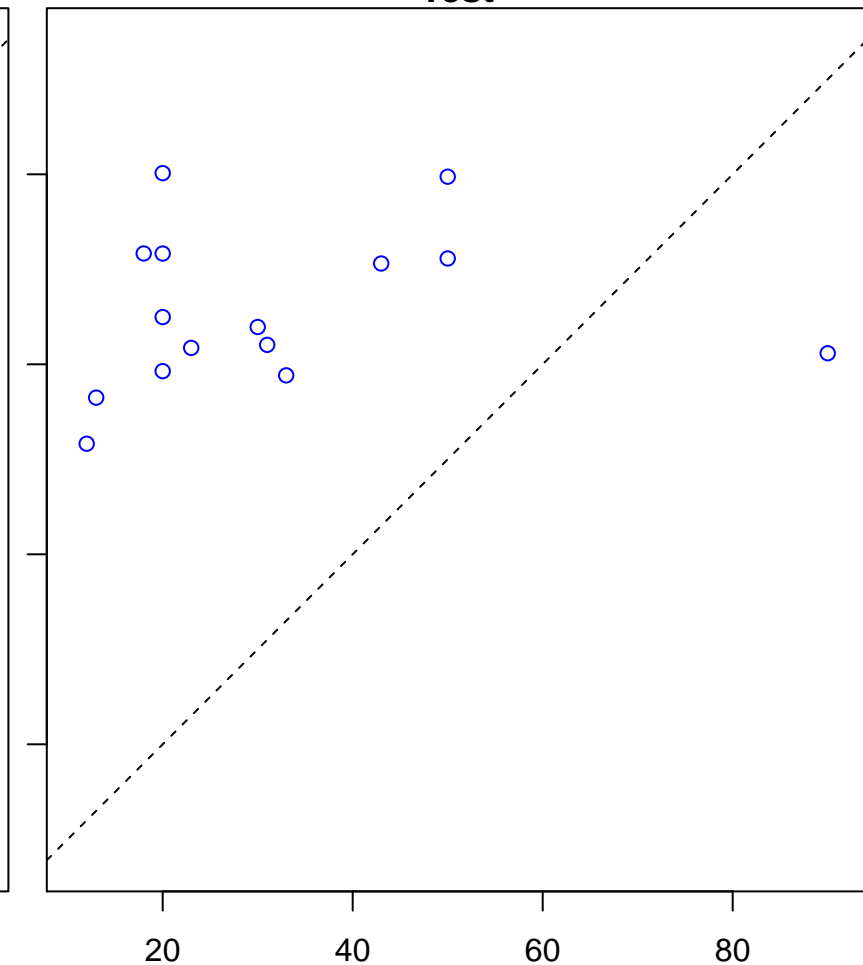


cellular response to indole-3-methanol (Score: 4.264705)

Control

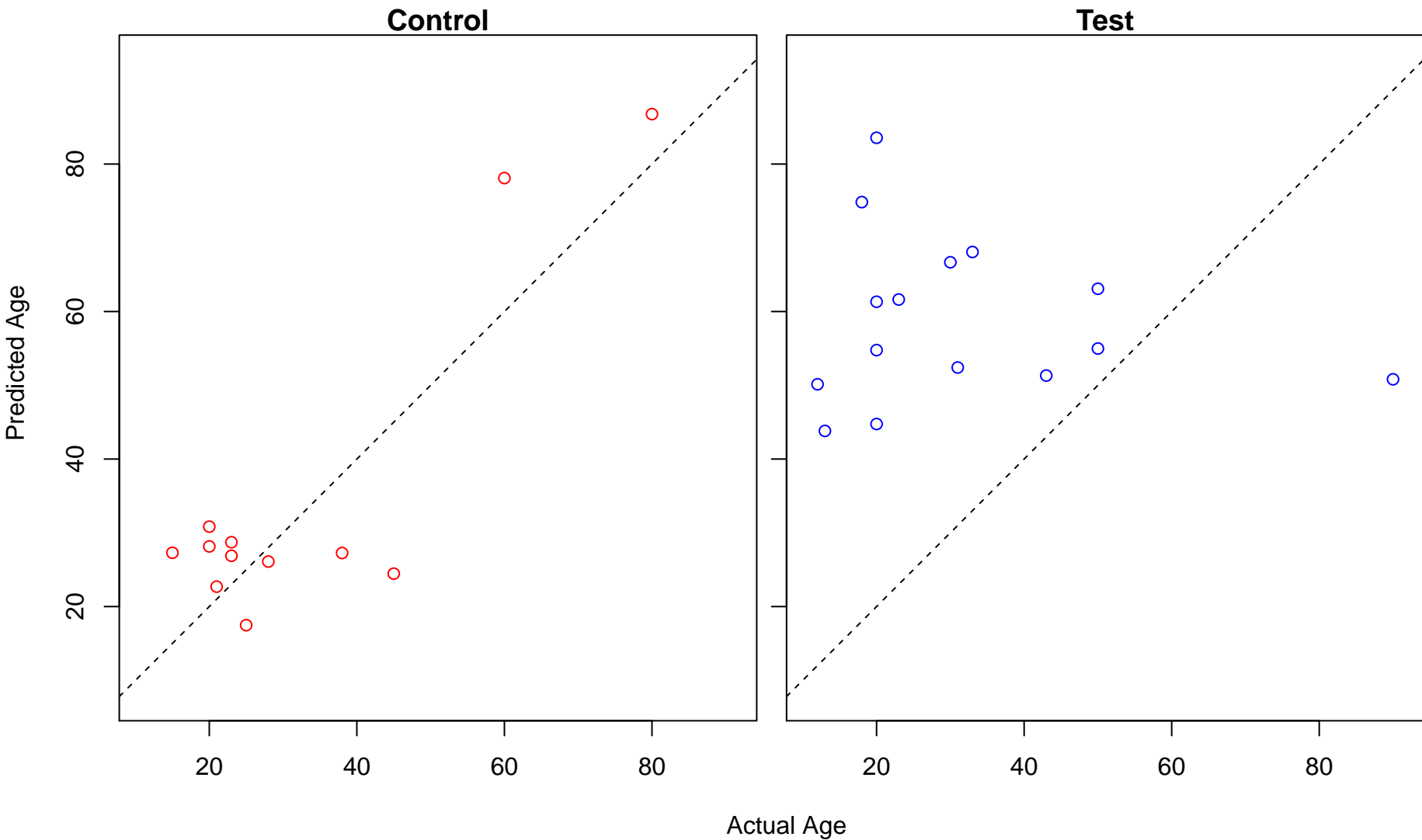


Test

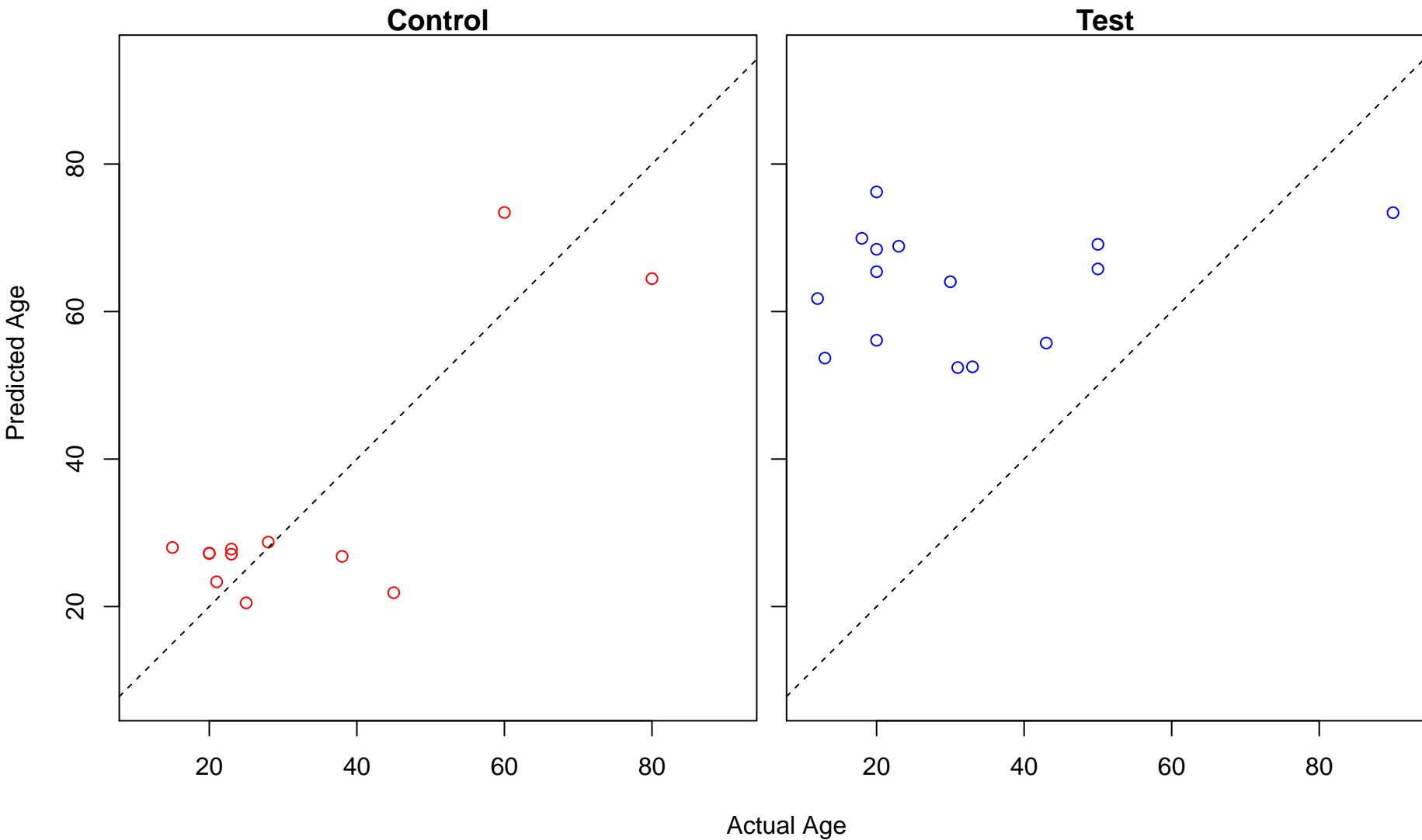


Actual Age

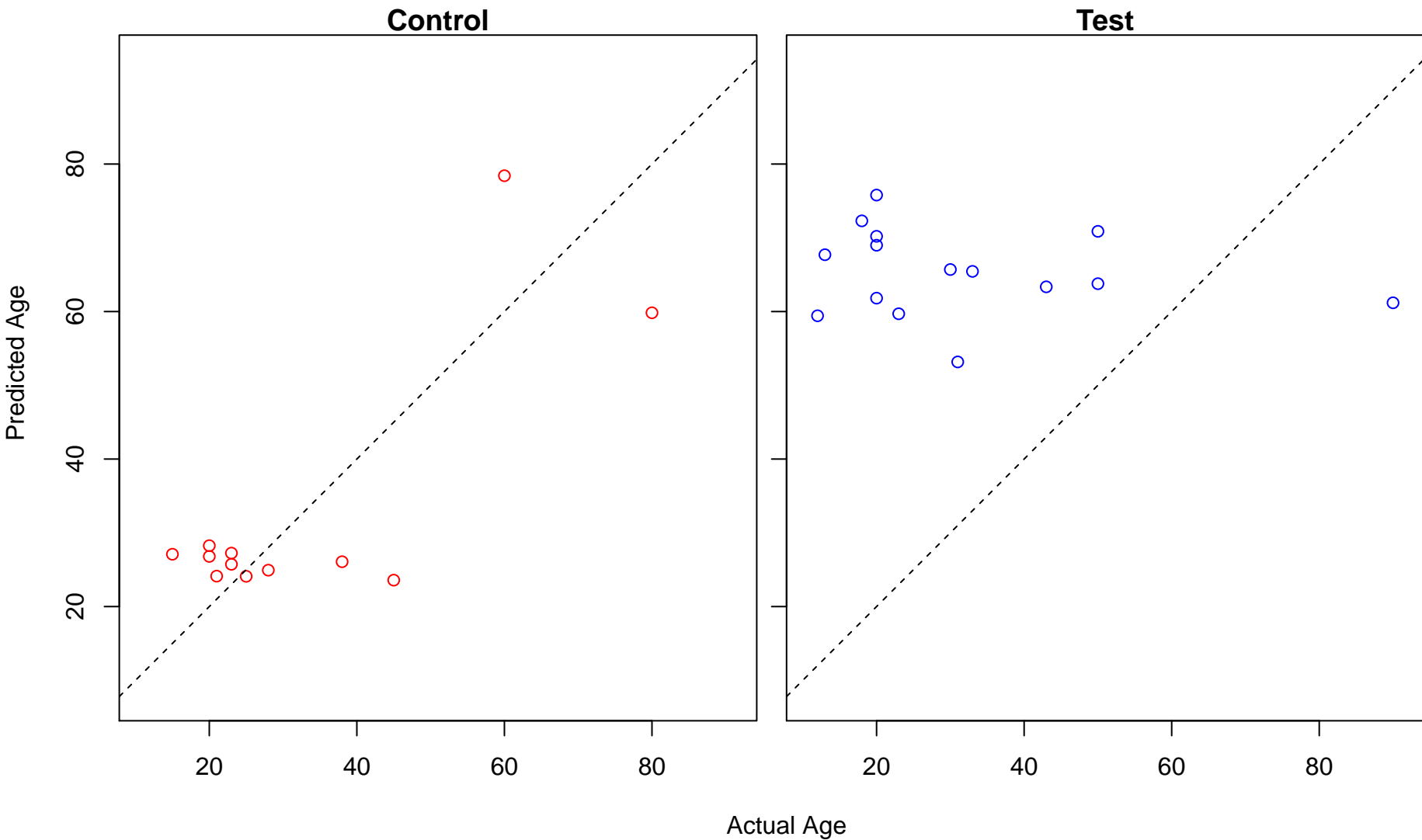
regulation of plasma lipoprotein particle levels (Score: 4.264328)



protein catabolic process (Score: 4.259020)

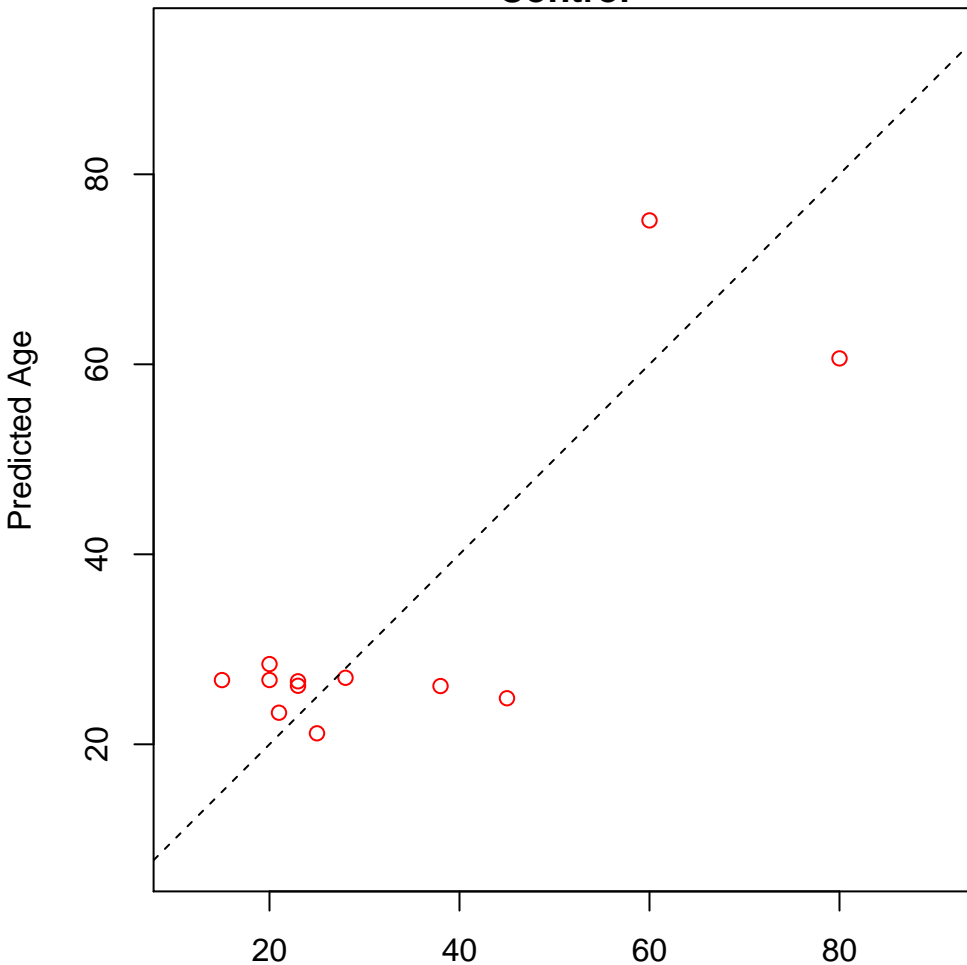


Golgi vesicle budding (Score: 4.256410)

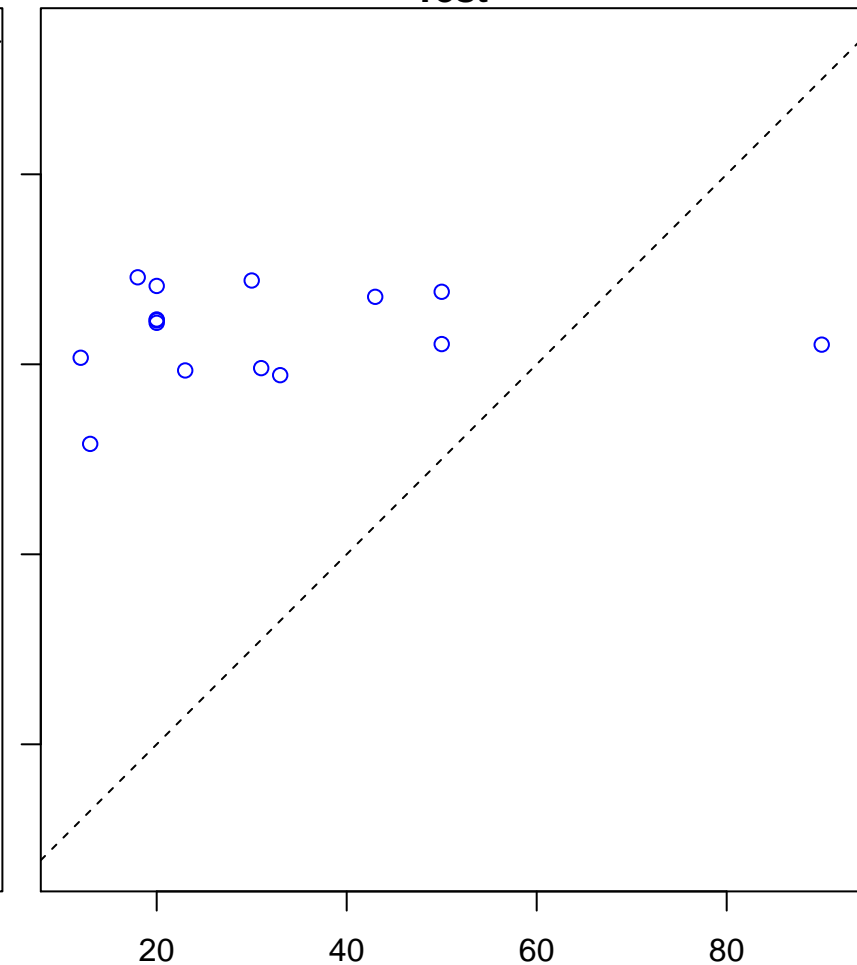


protein exit from endoplasmic reticulum (Score: 4.254854)

Control

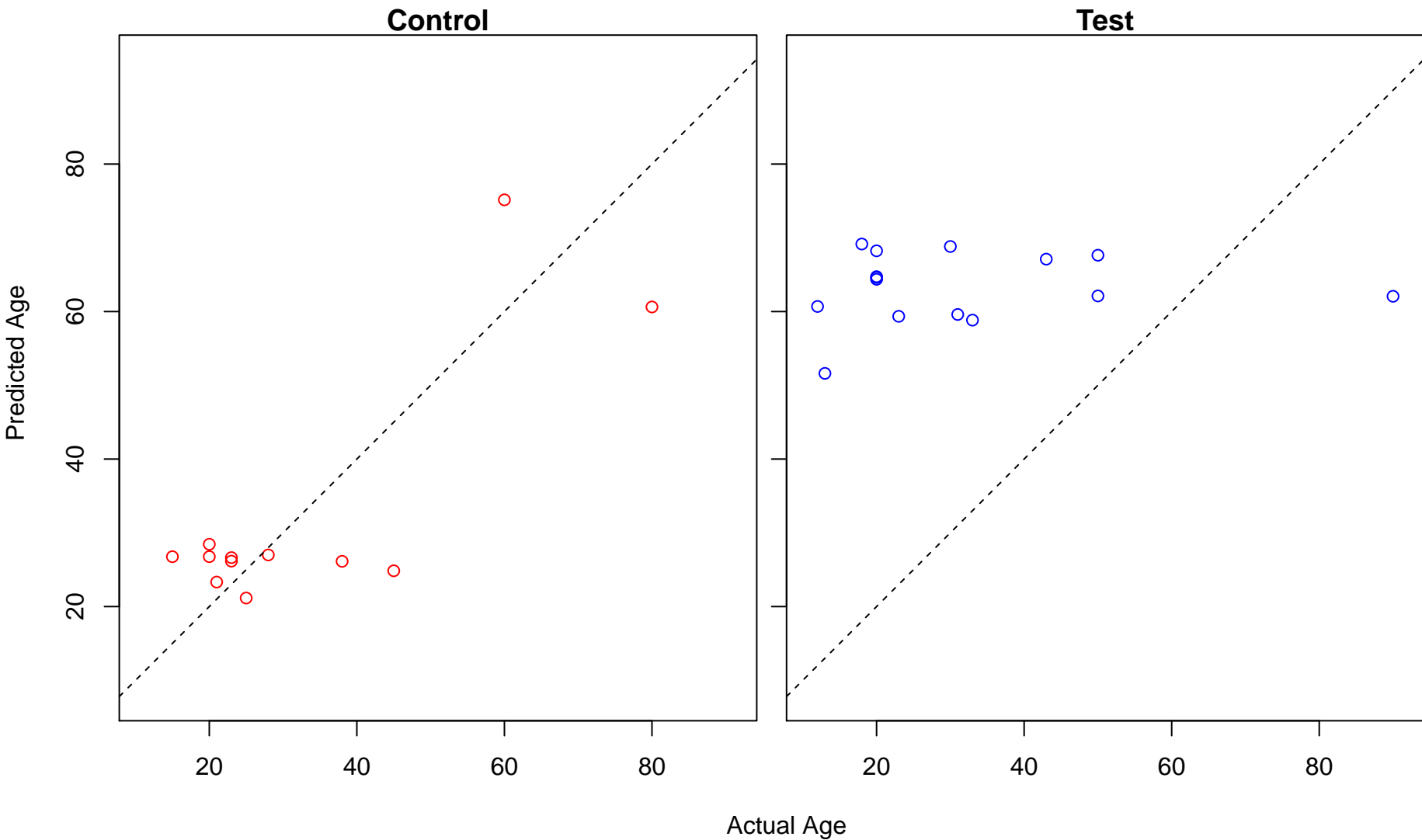


Test



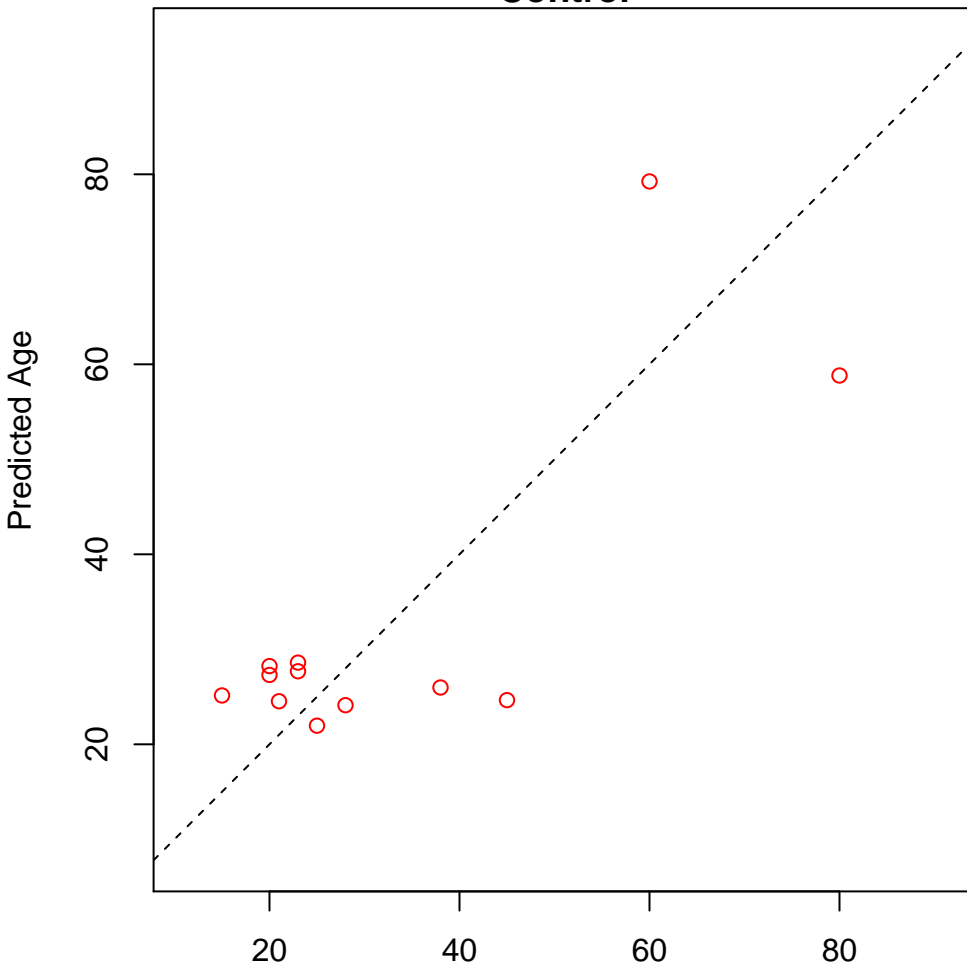
Actual Age

retrograde protein transport, ER to cytosol (Score: 4.254807)

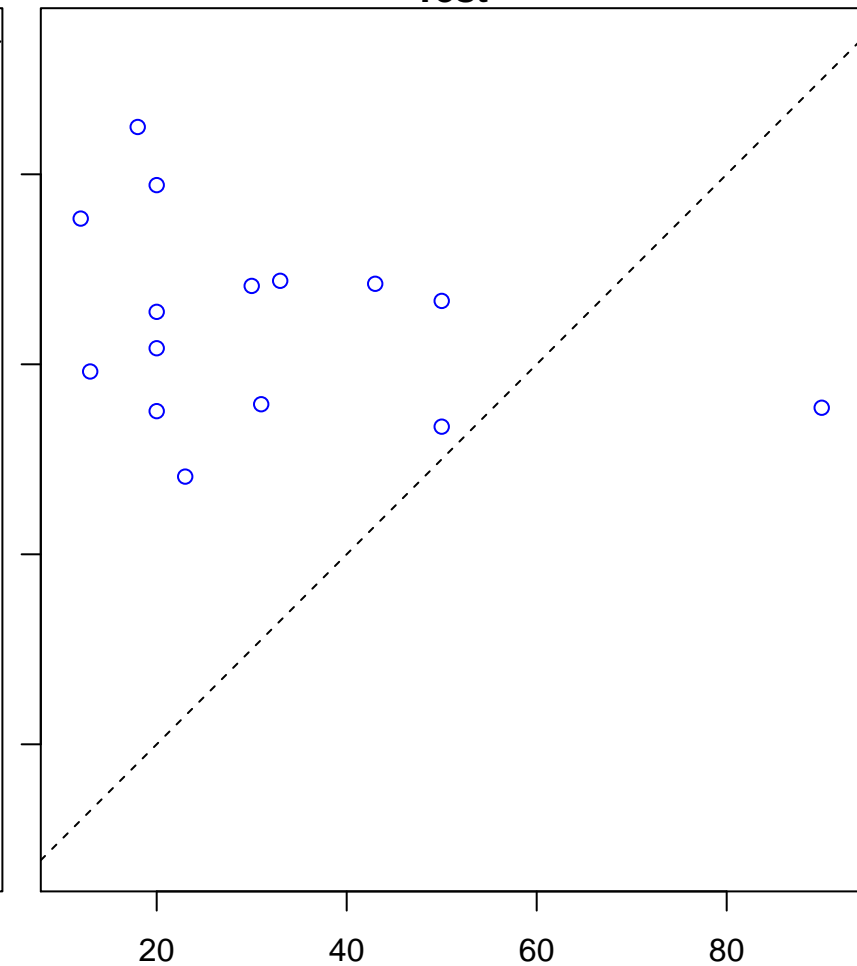


N-terminal protein amino acid acetylation (Score: 4.253337)

Control

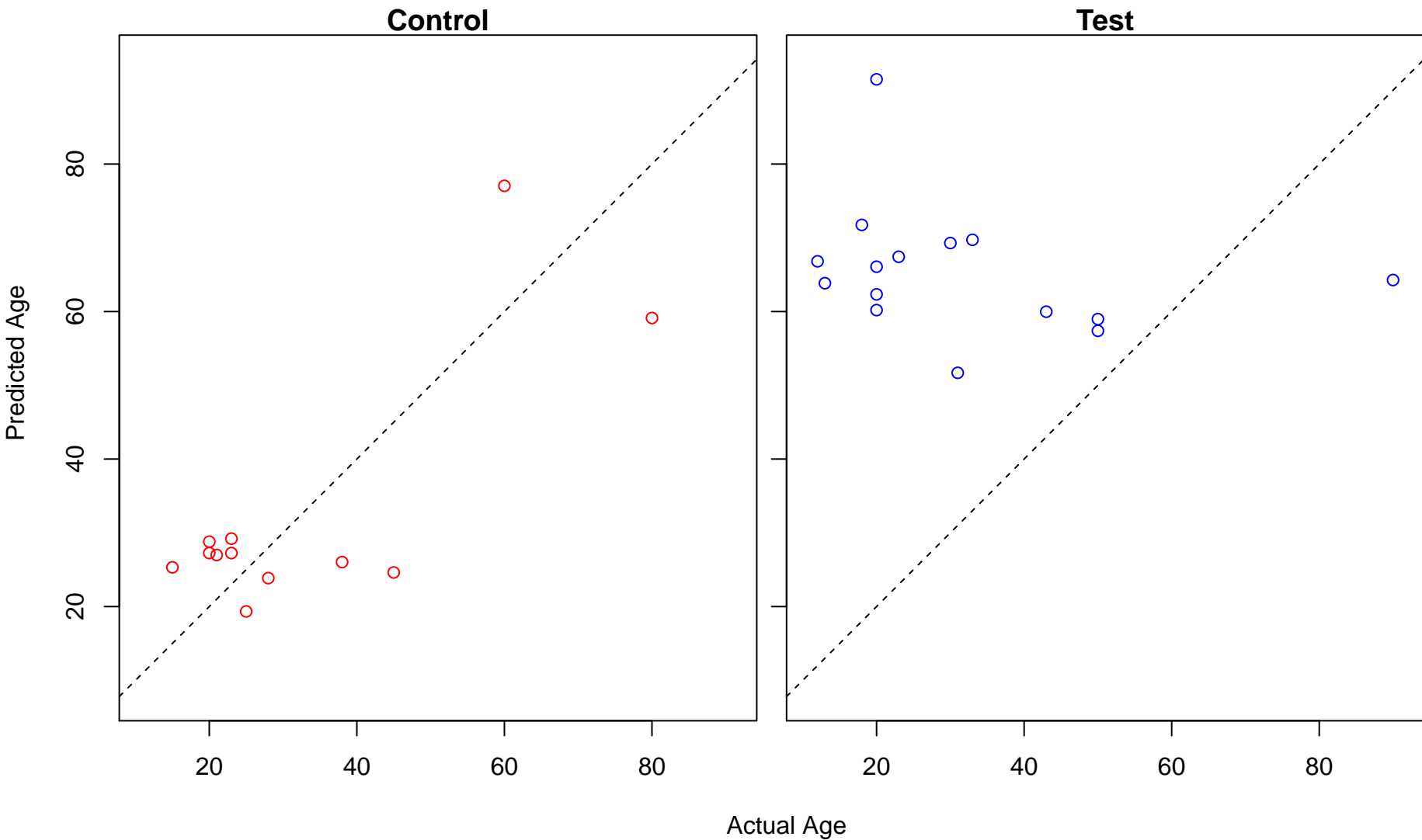


Test

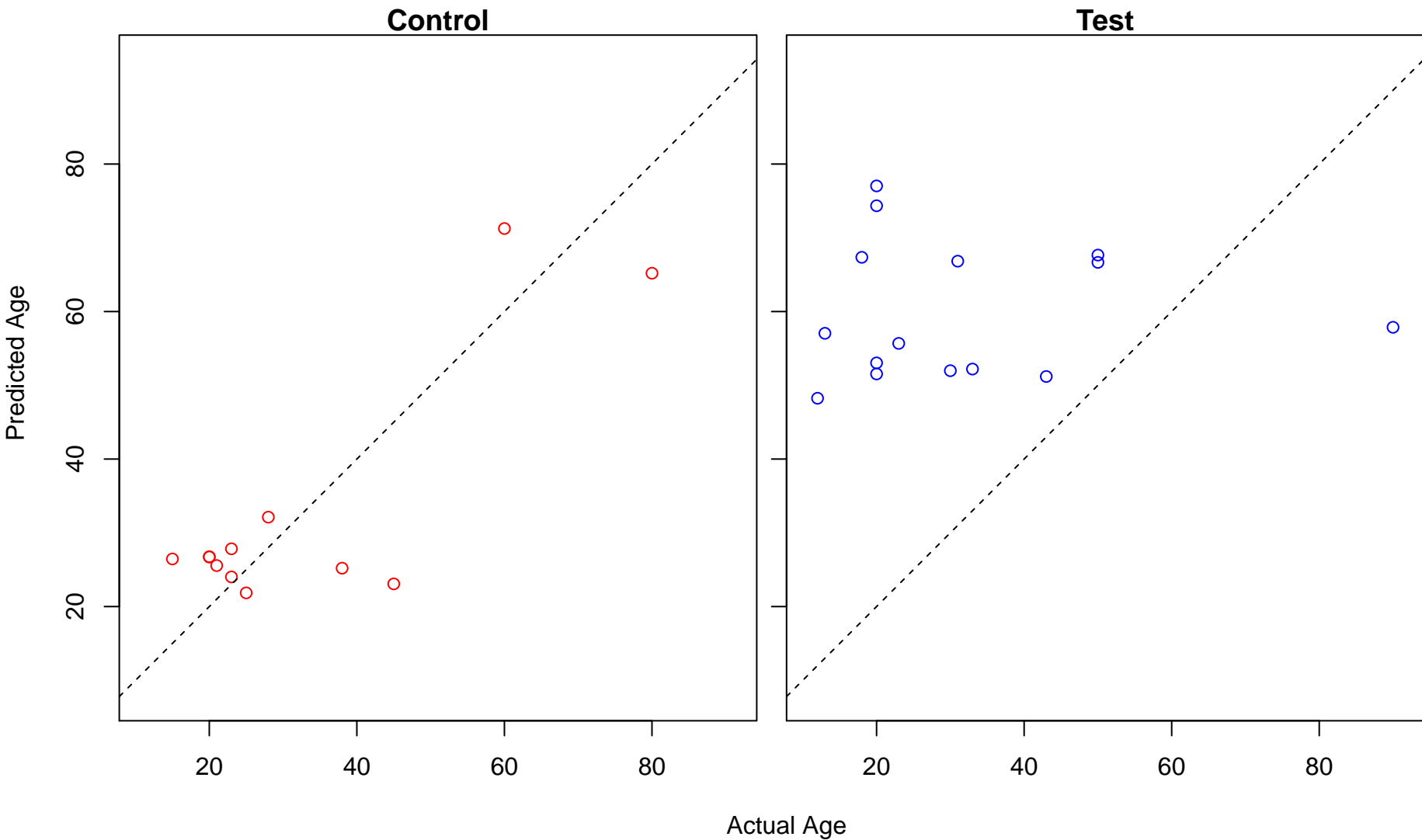


Actual Age

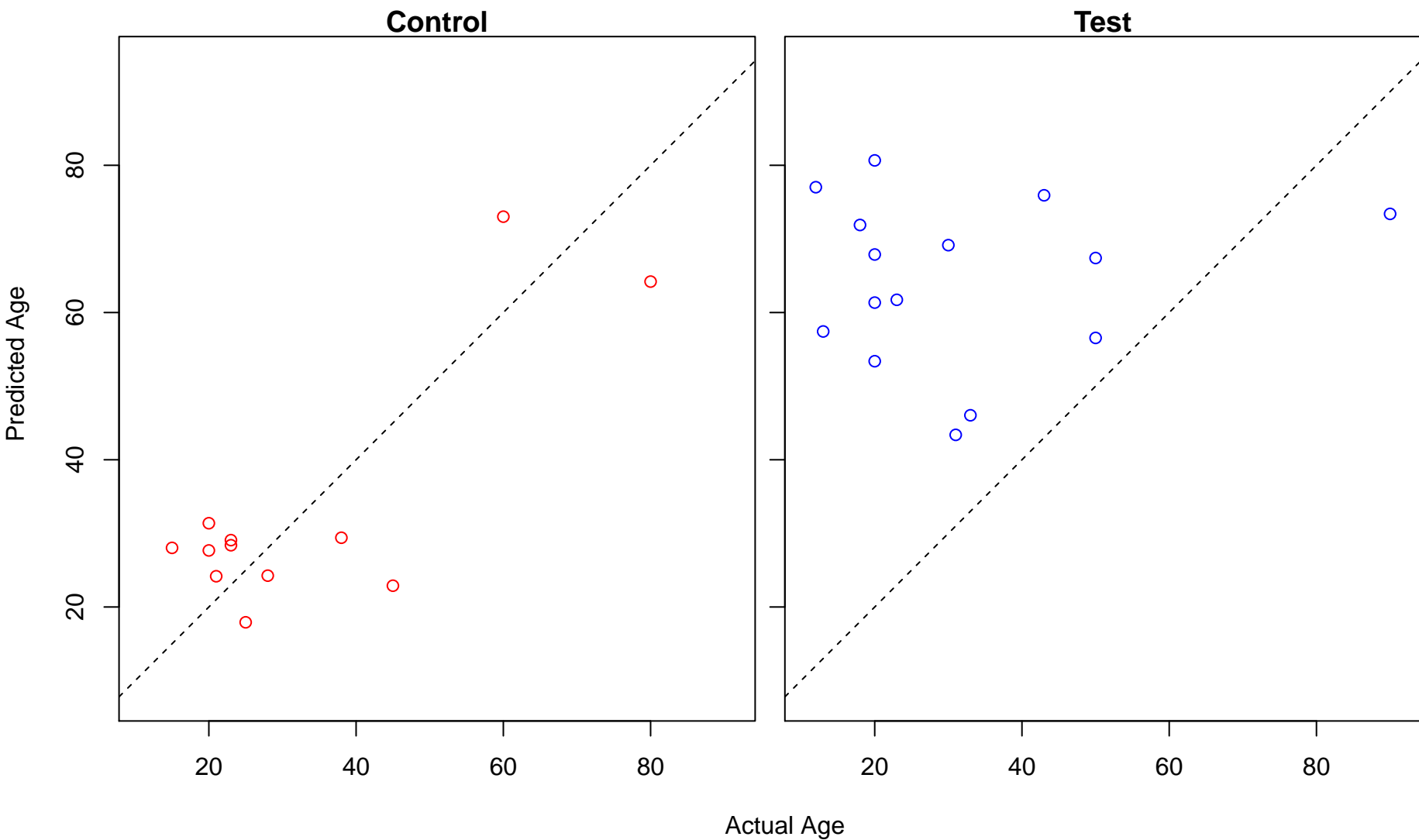
protein depolymerization (Score: 4.253145)



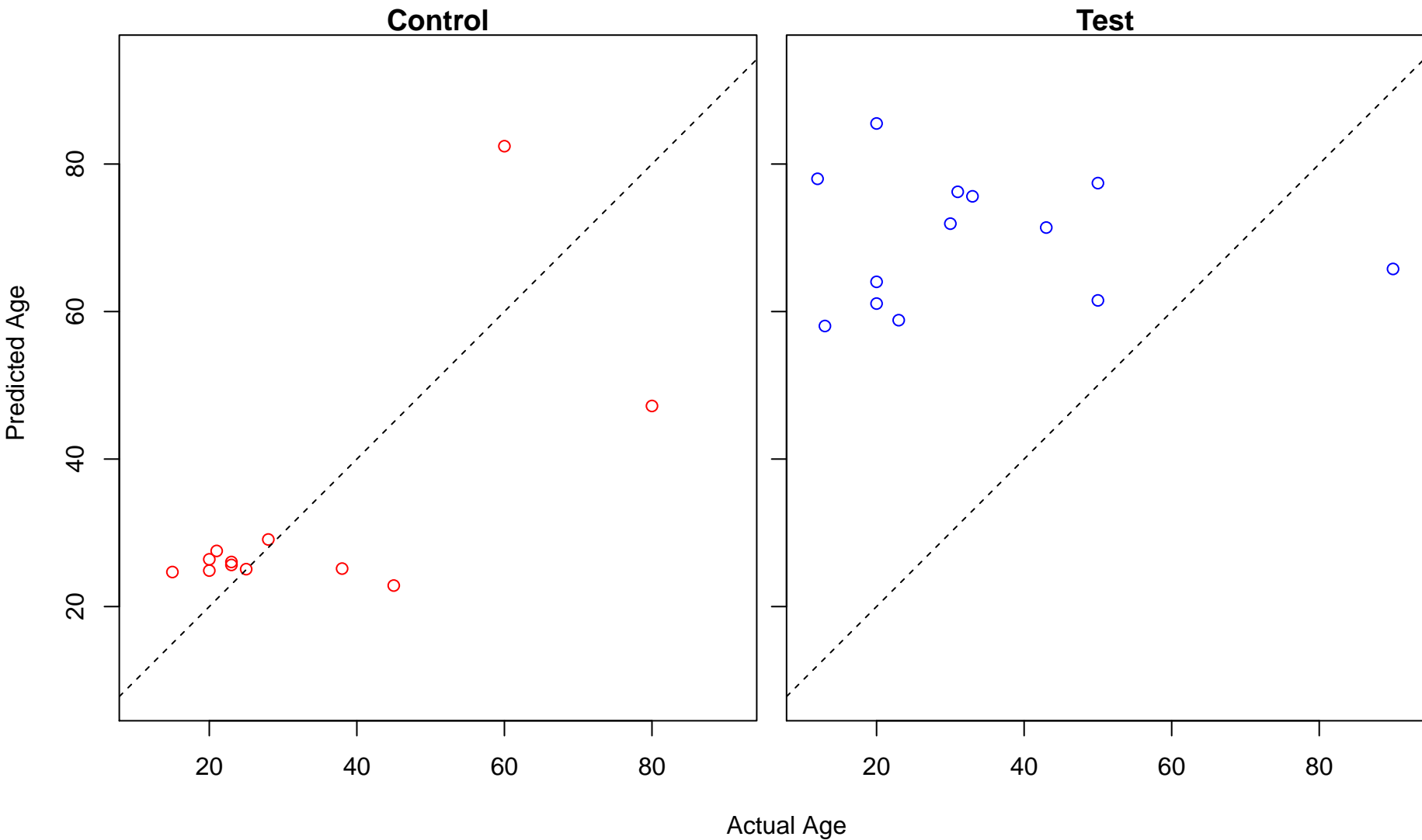
negative regulation of transporter activity (Score: 4.252085)



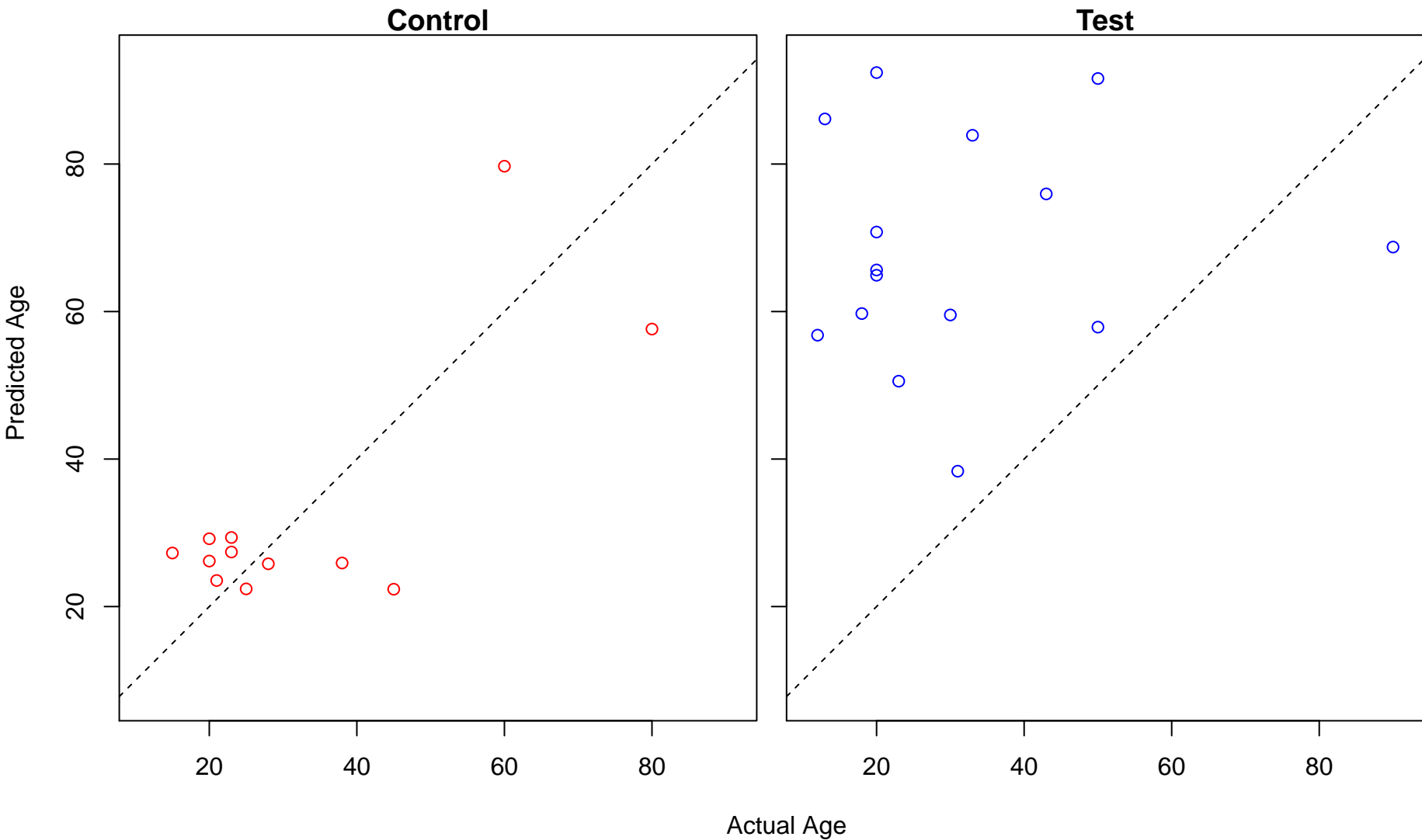
regulation of ubiquitin homeostasis (Score: 4.251006)



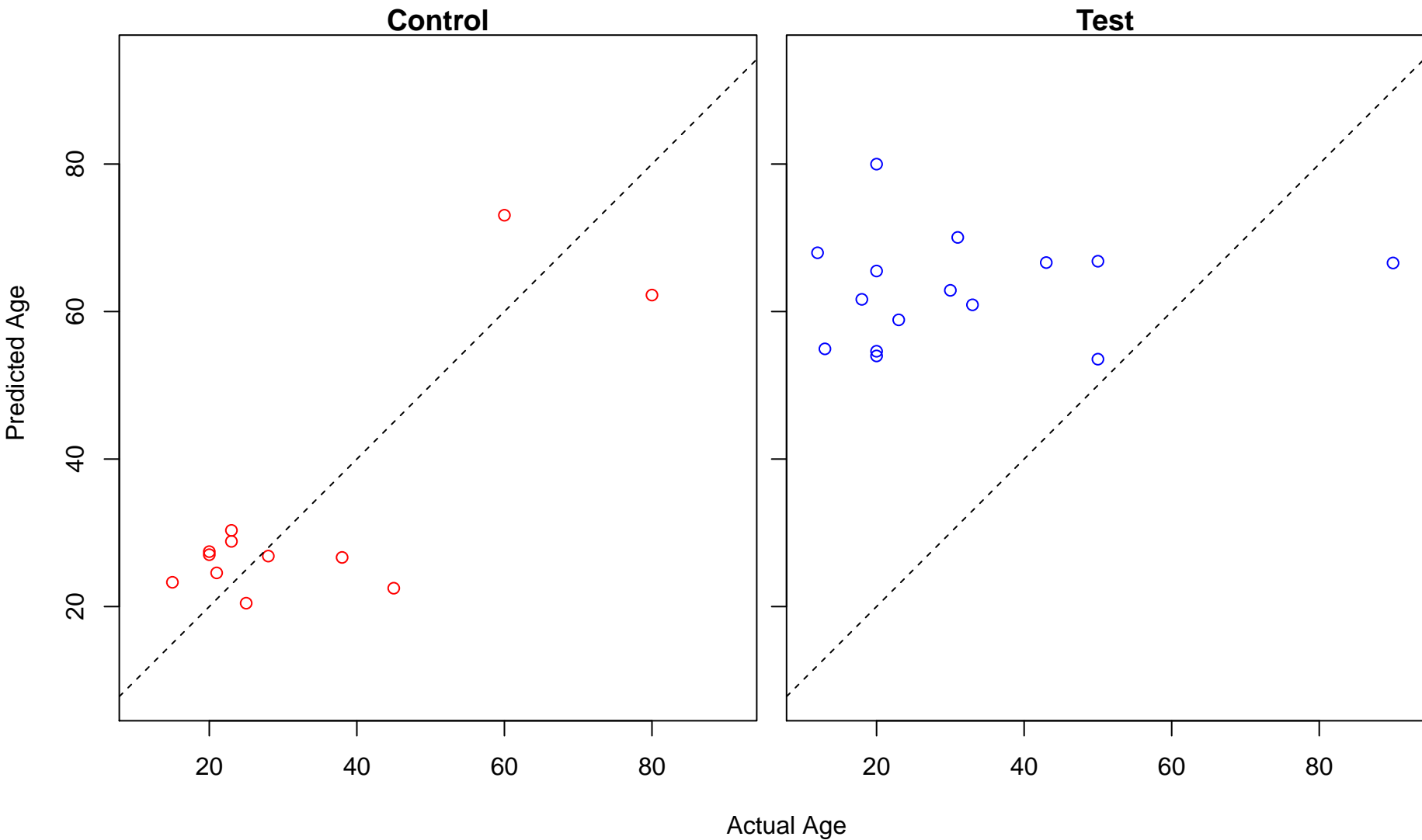
neutrophil activation involved in immune response (Score: 4.250187)



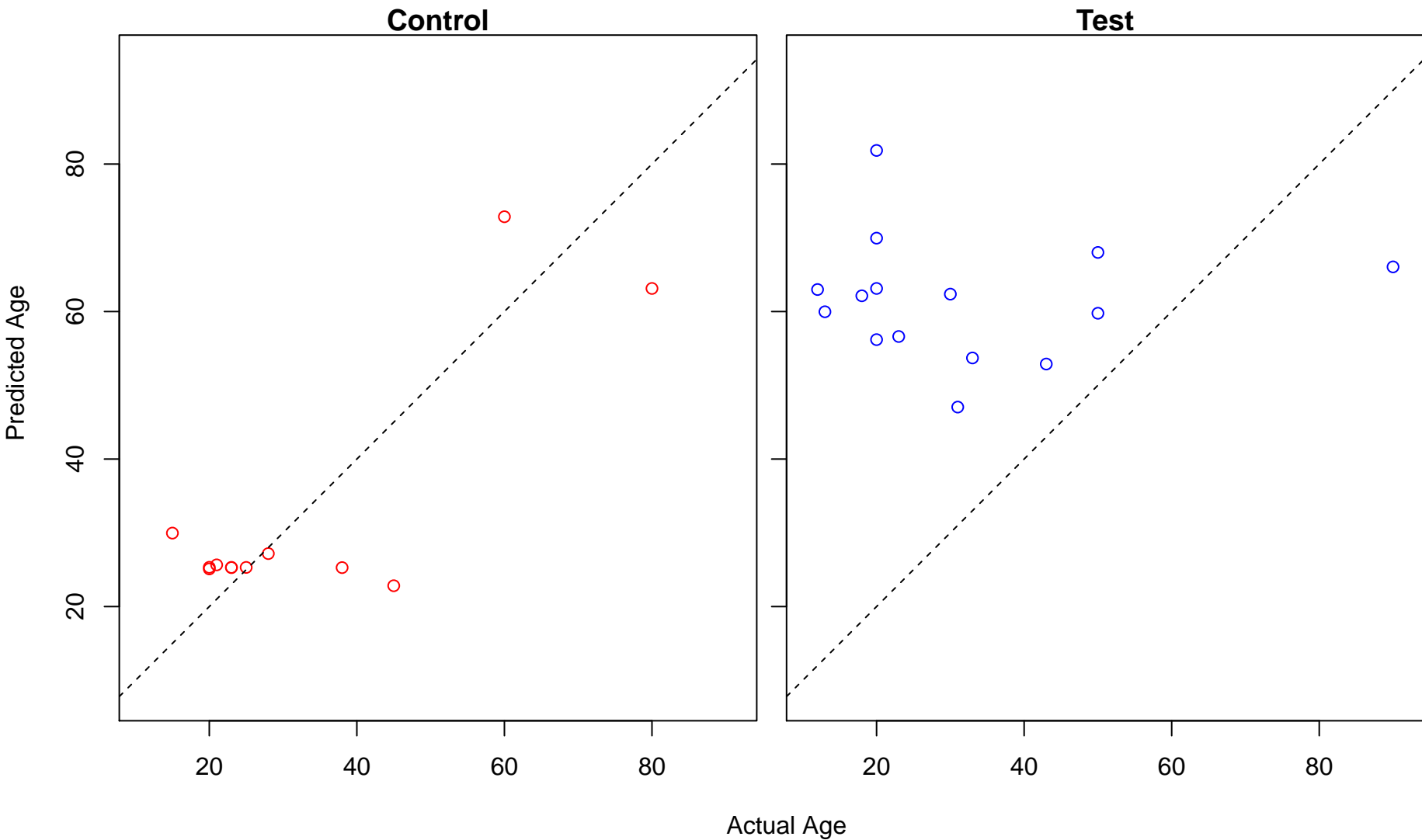
response to yeast (Score: 4.249011)



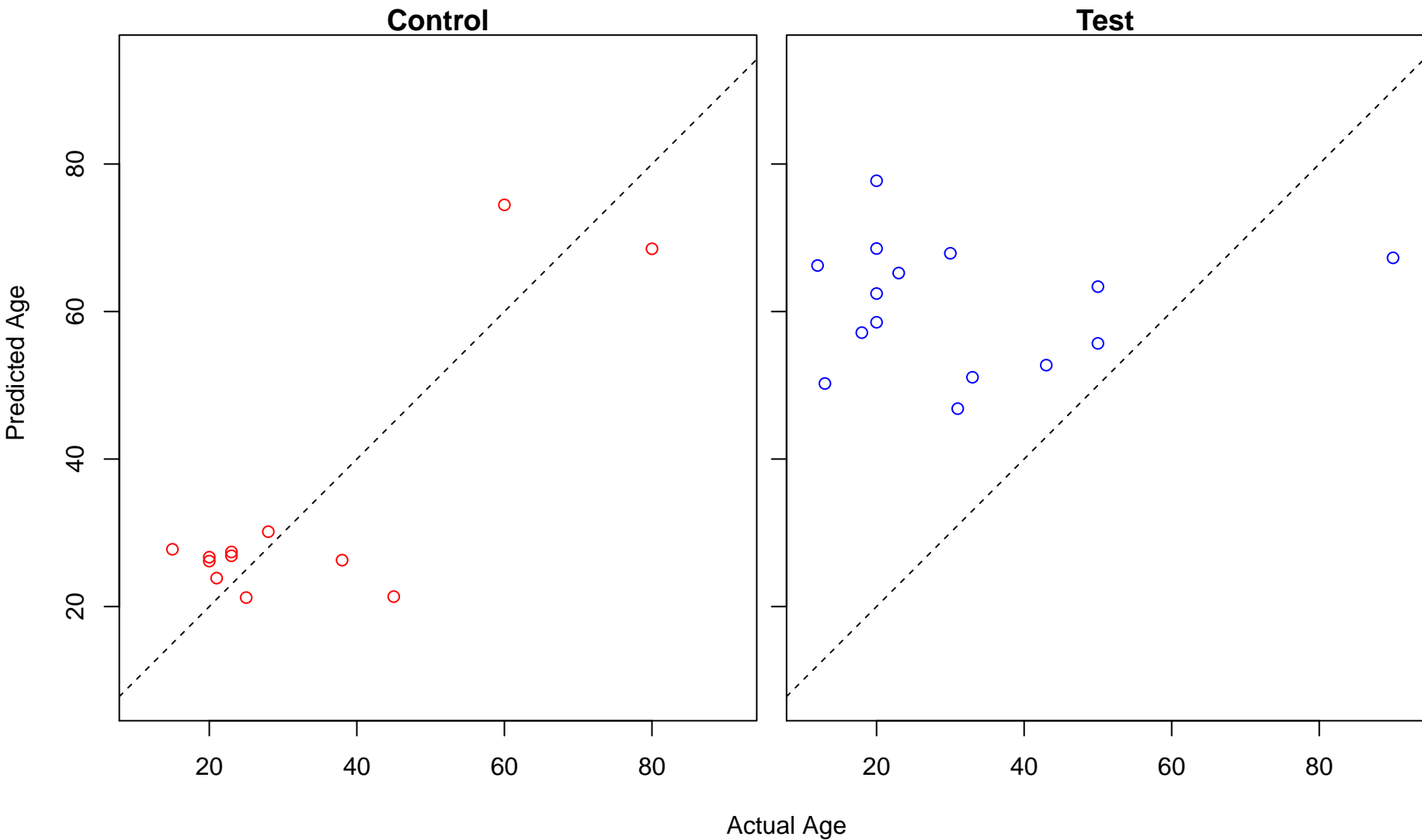
negative regulation of G2/M transition of mitotic cell cycle (Score: 4.247257)



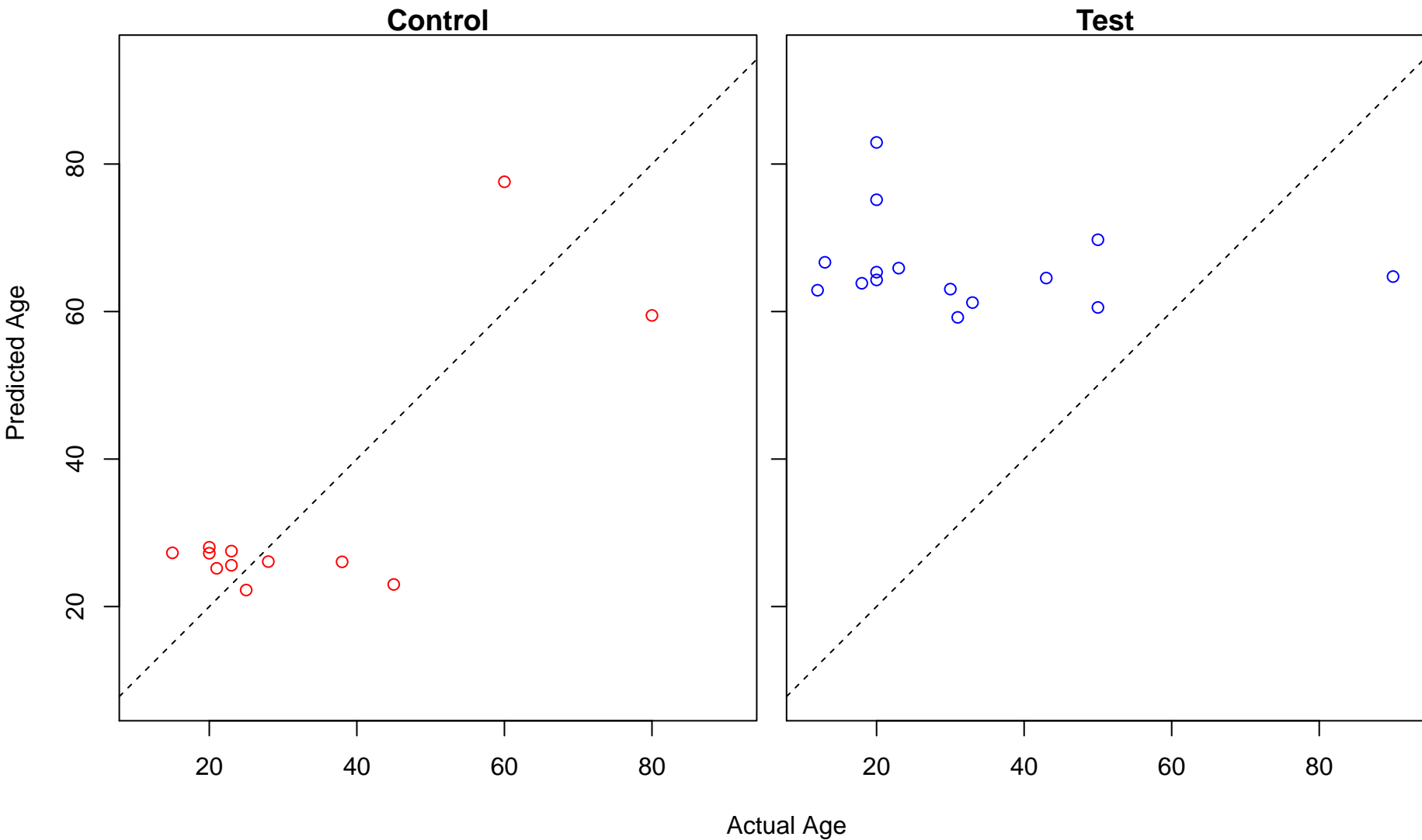
negative regulation of organelle organization (Score: 4.247196)



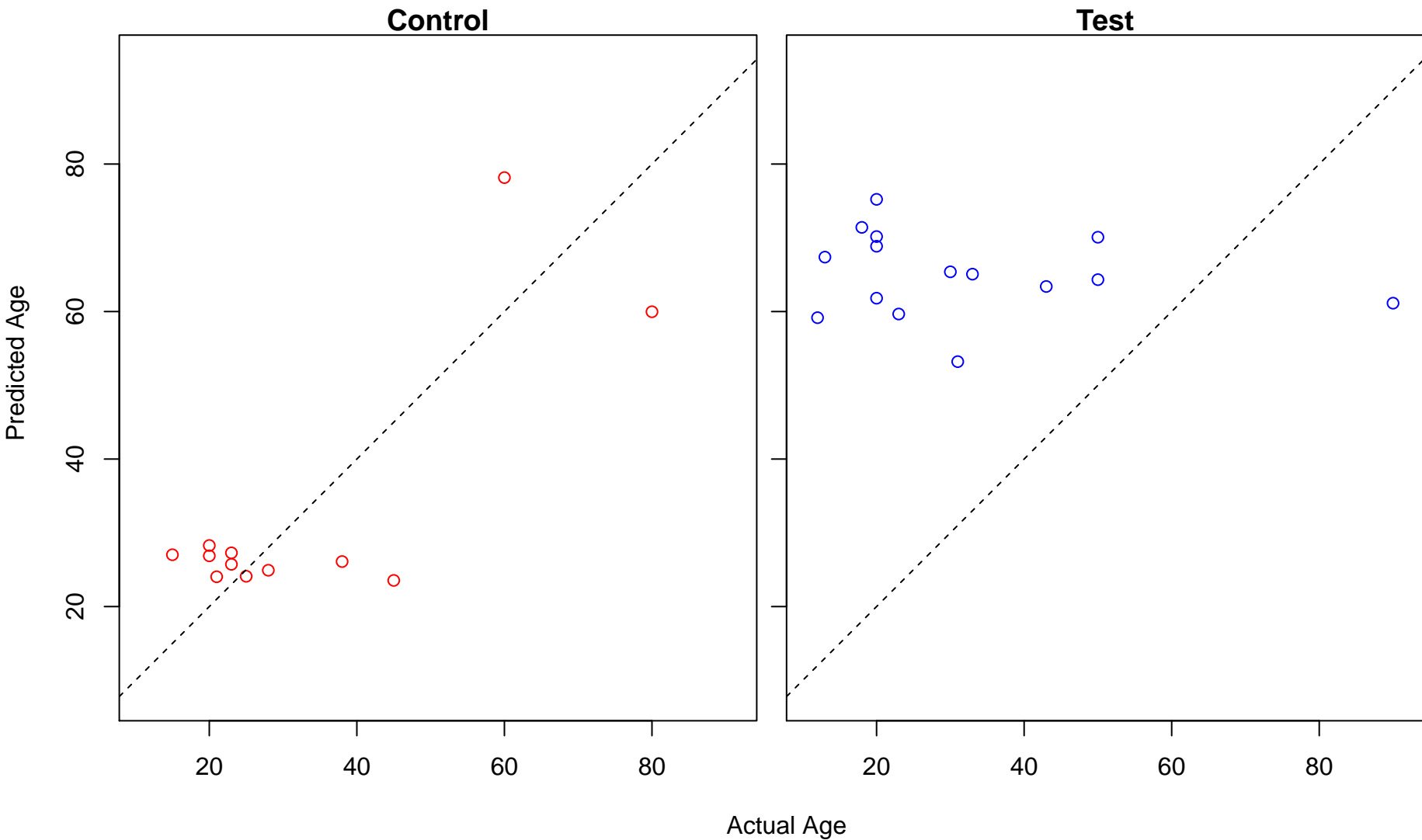
vesicle targeting, to, from or within Golgi (Score: 4.246530)



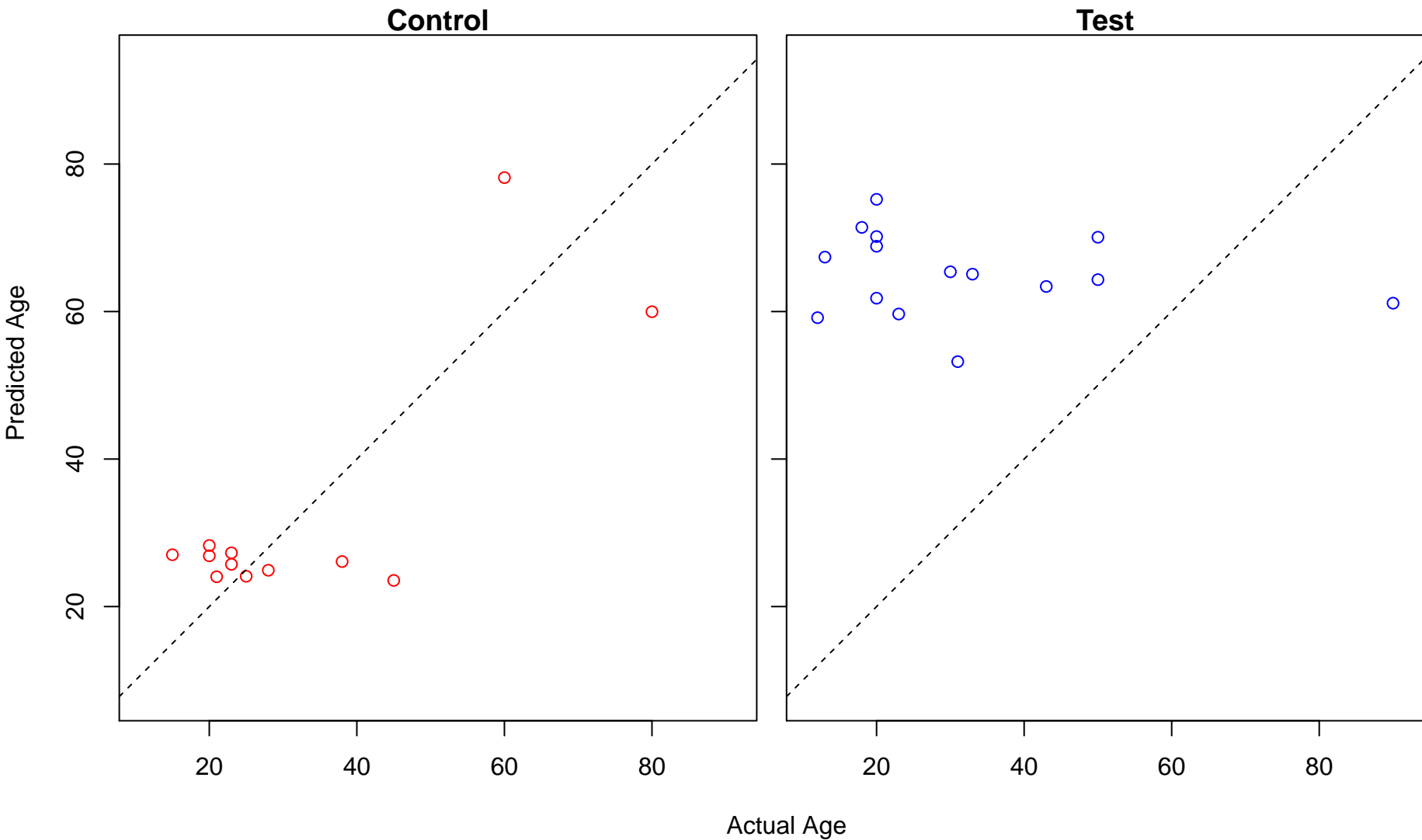
protein sumoylation (Score: 4.246366)



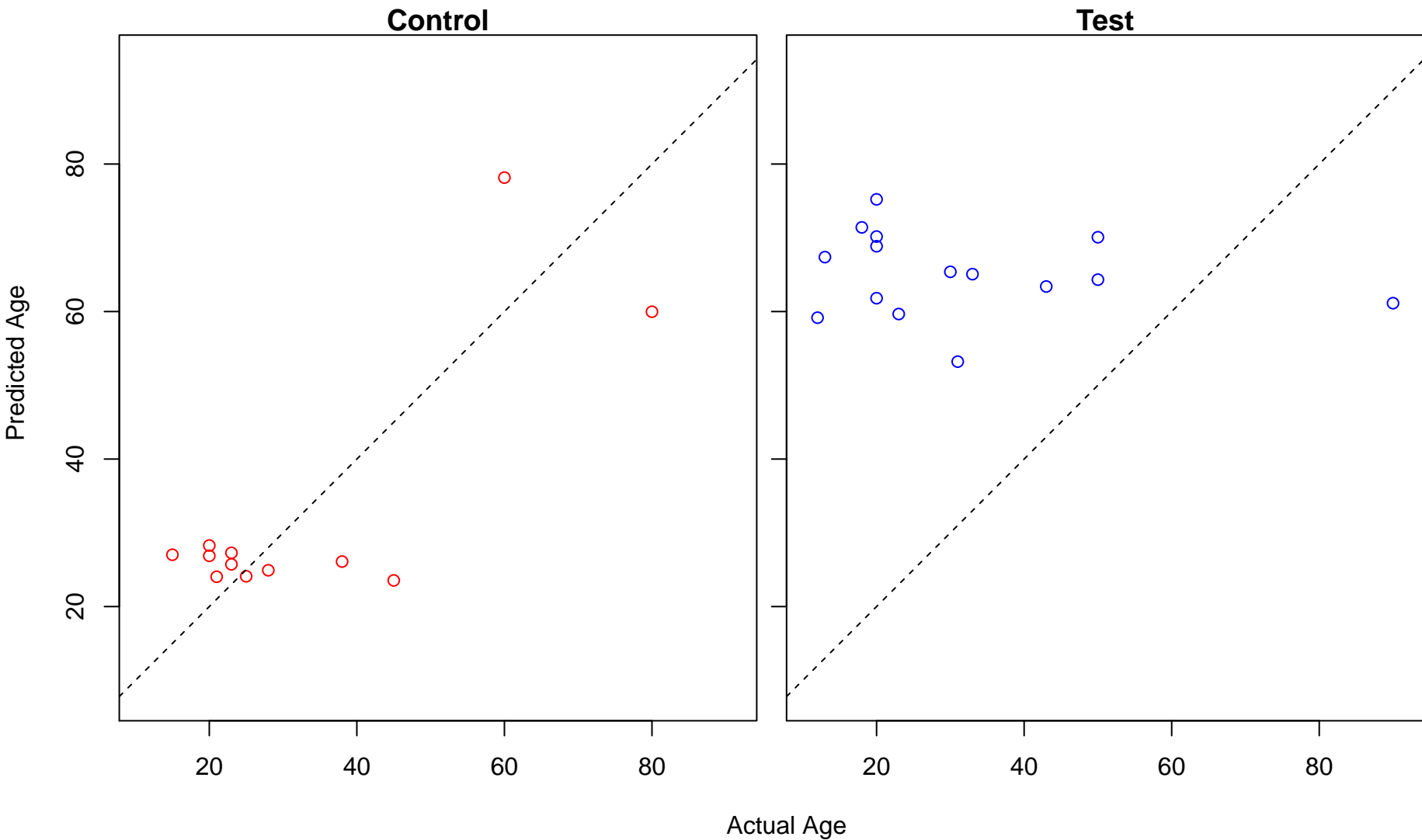
COPI-coated vesicle budding (Score: 4.245379)



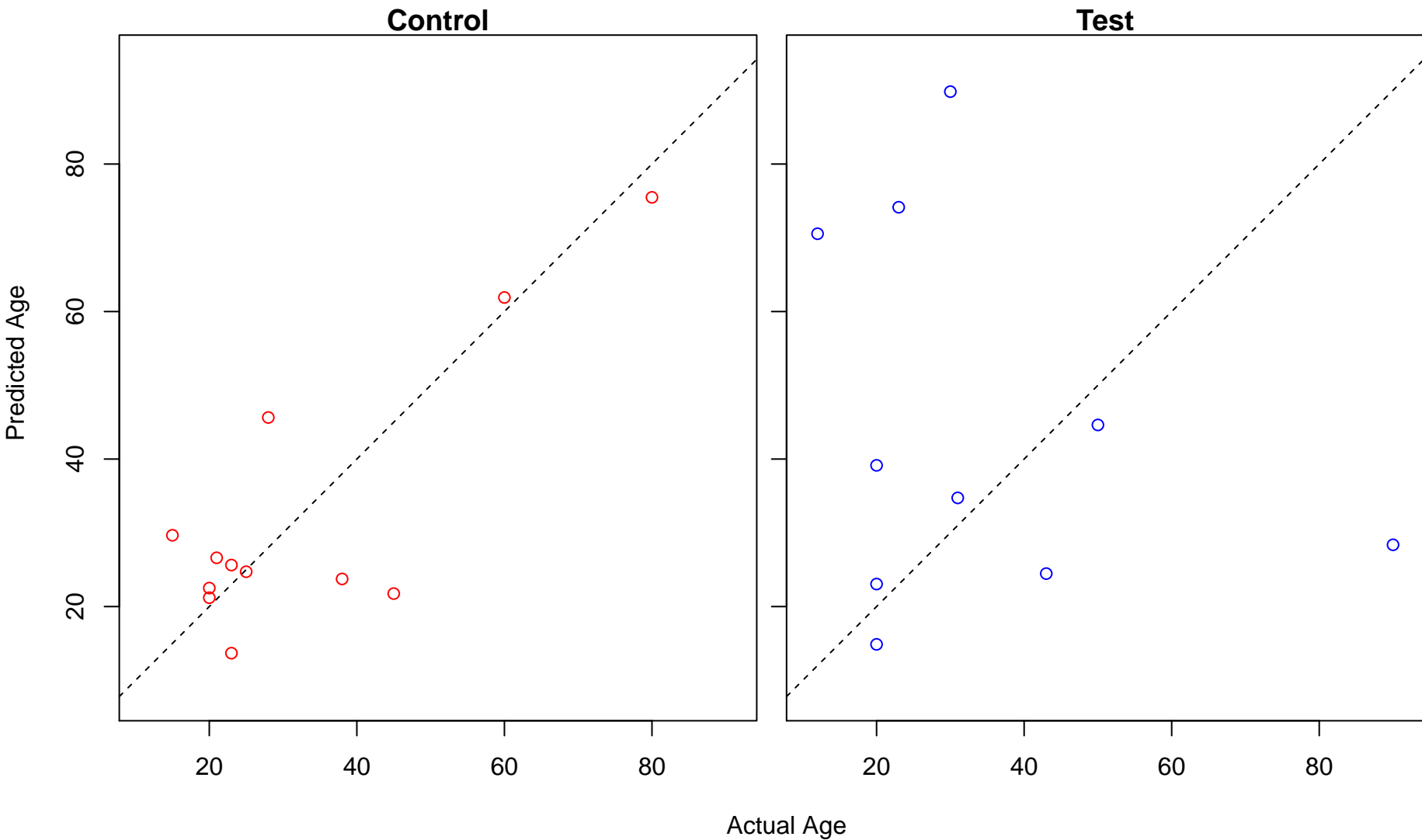
Golgi transport vesicle coating (Score: 4.245379)



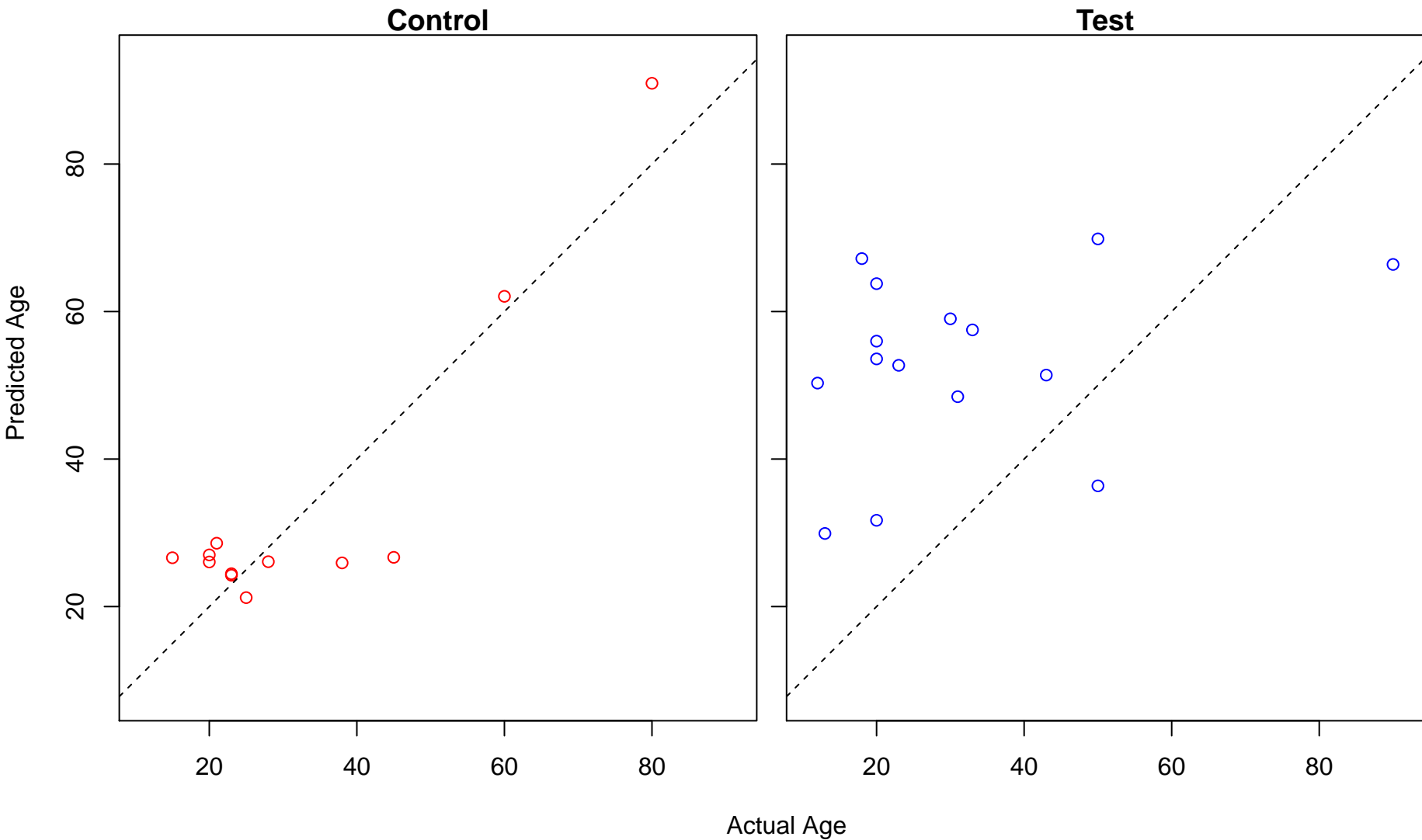
COPI coating of Golgi vesicle (Score: 4.245379)



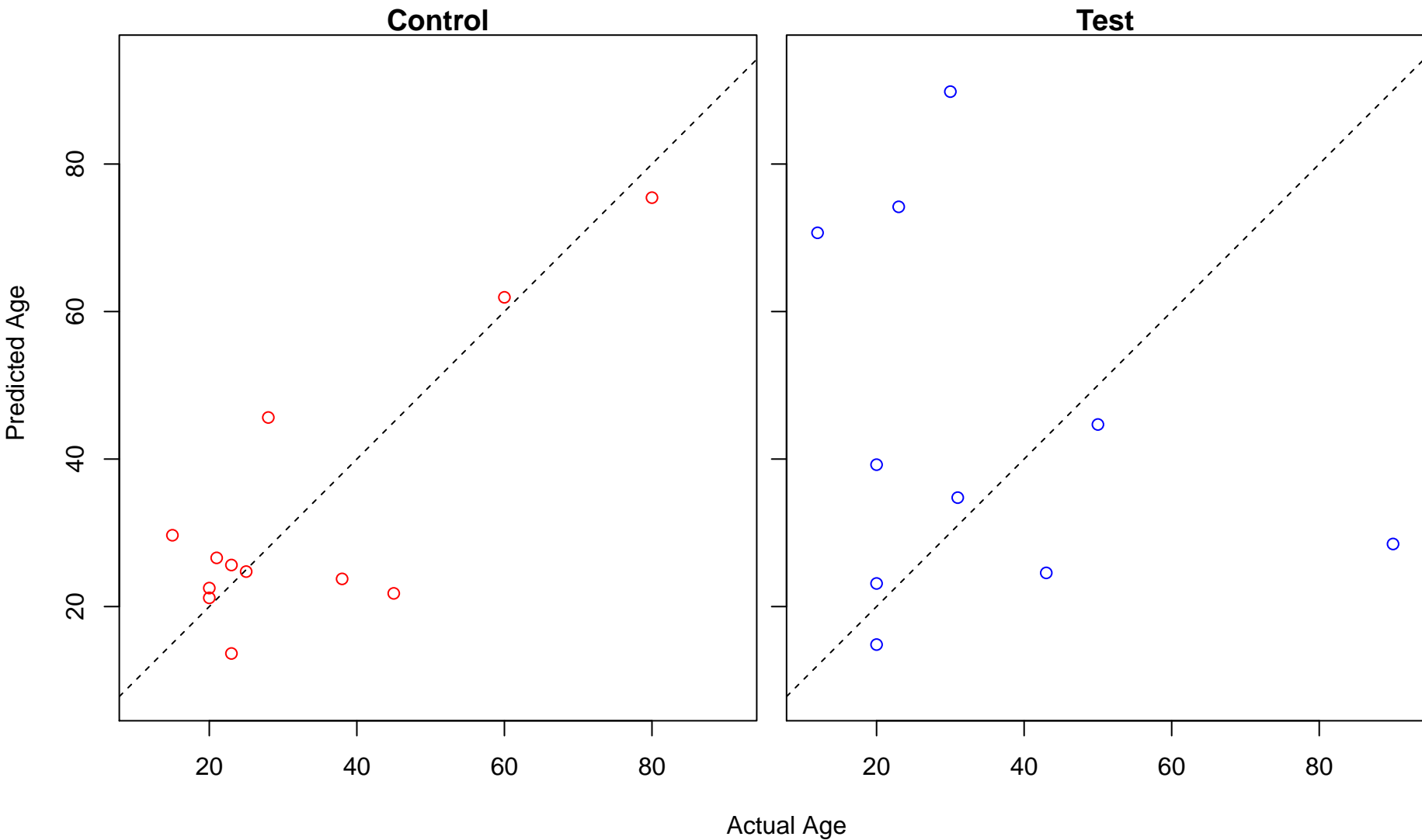
organ maturation (Score: 4.245290)



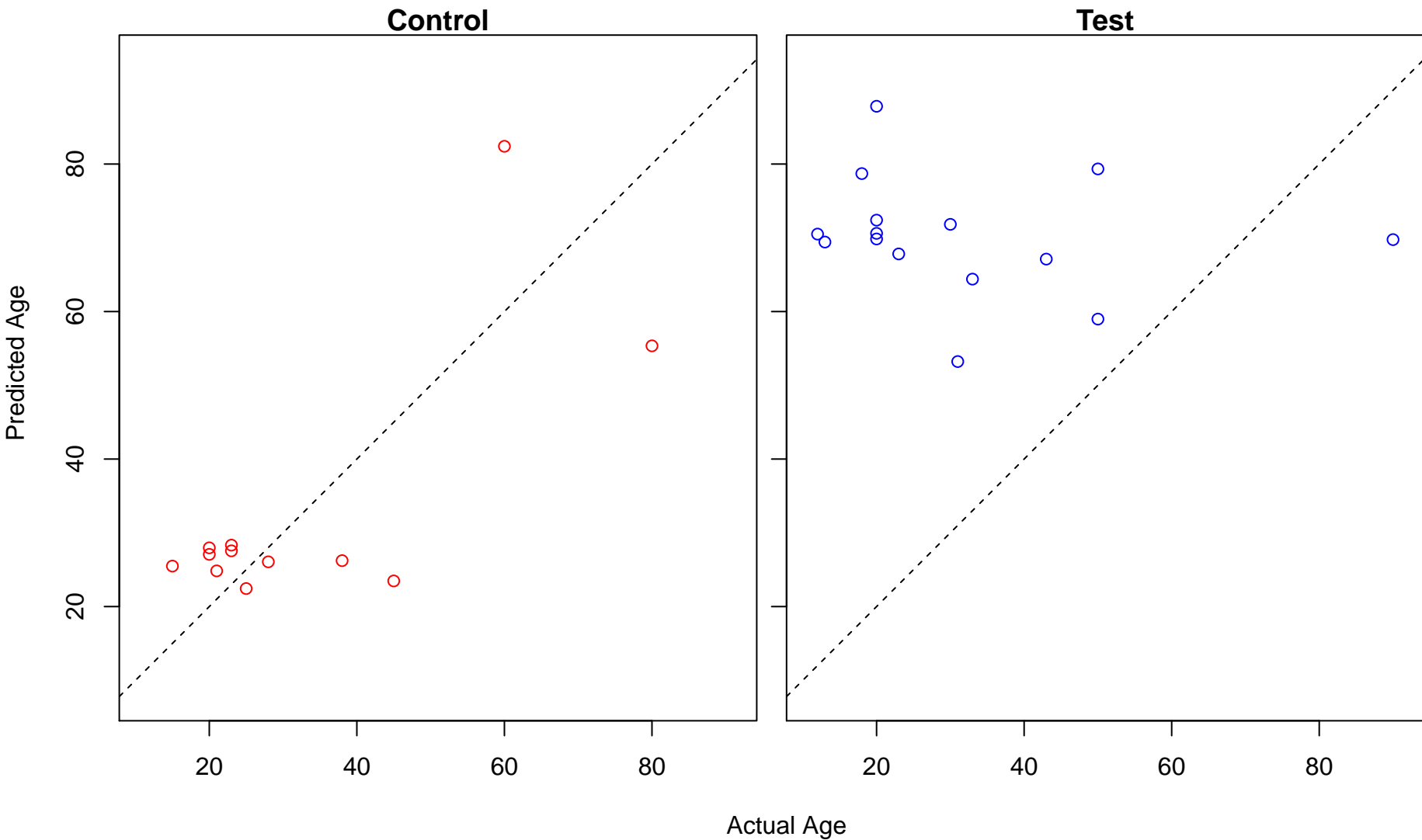
negative regulation of Rho protein signal transduction (Score: 4.244358)



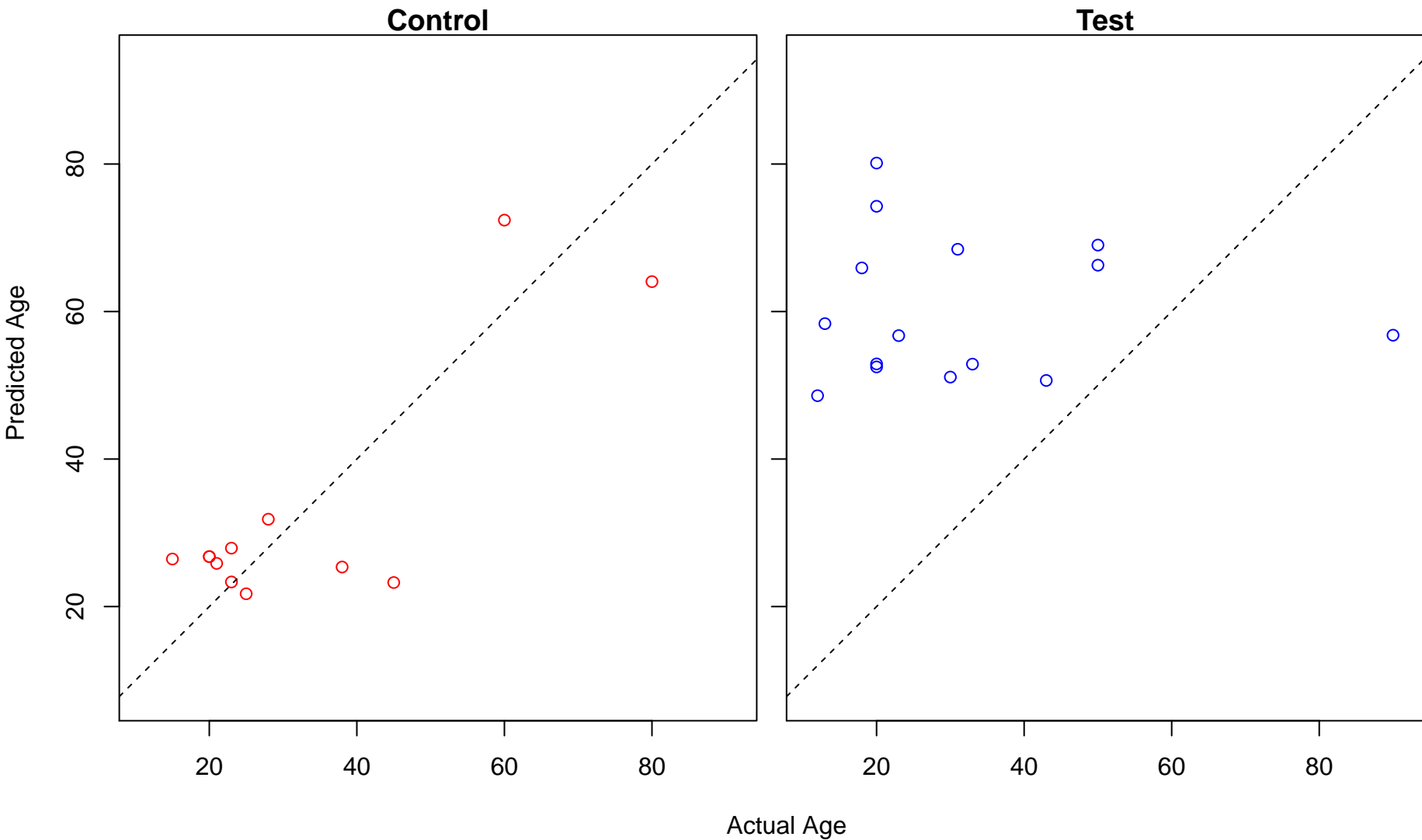
bone maturation (Score: 4.242757)



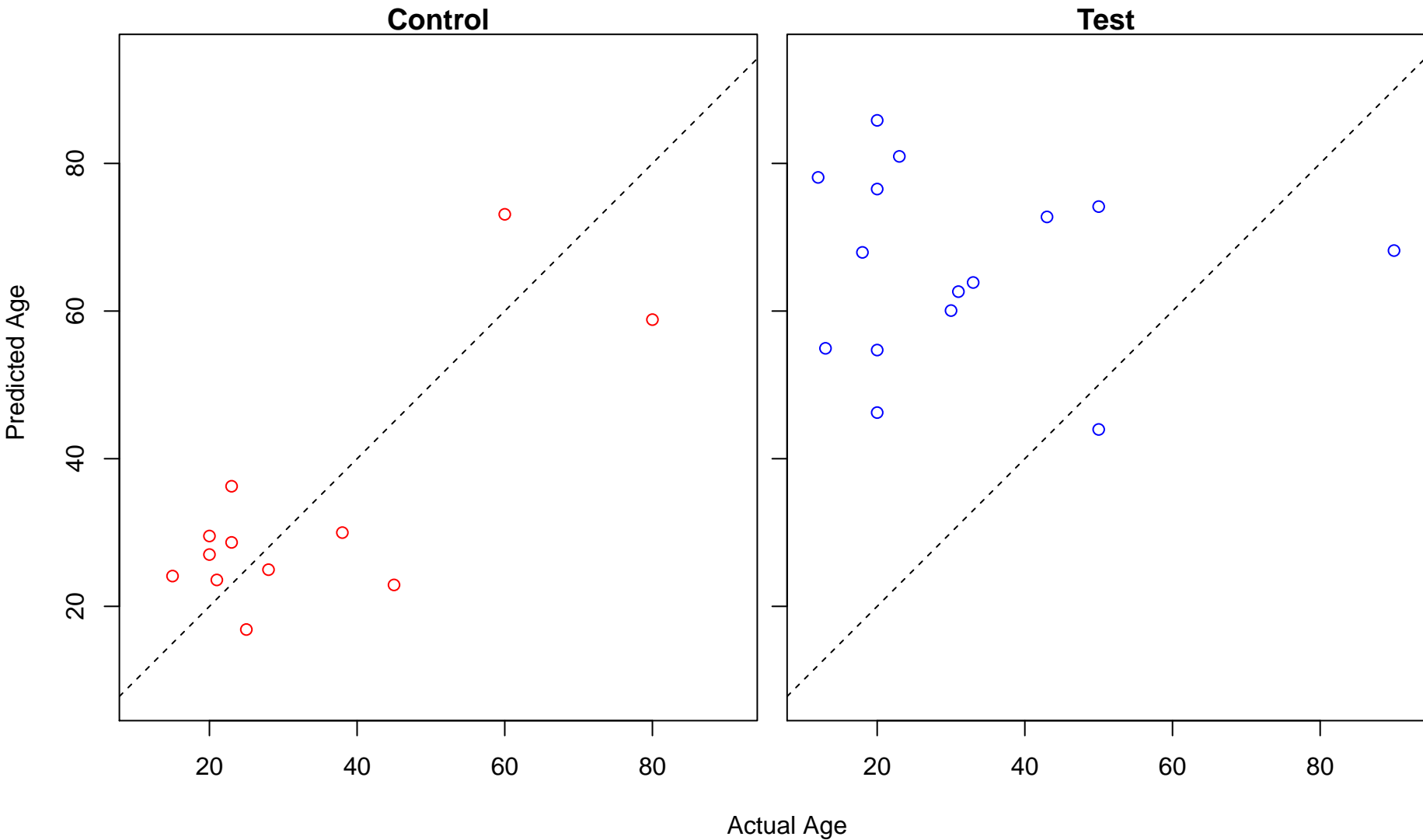
regulation of endothelial cell proliferation (Score: 4.240410)



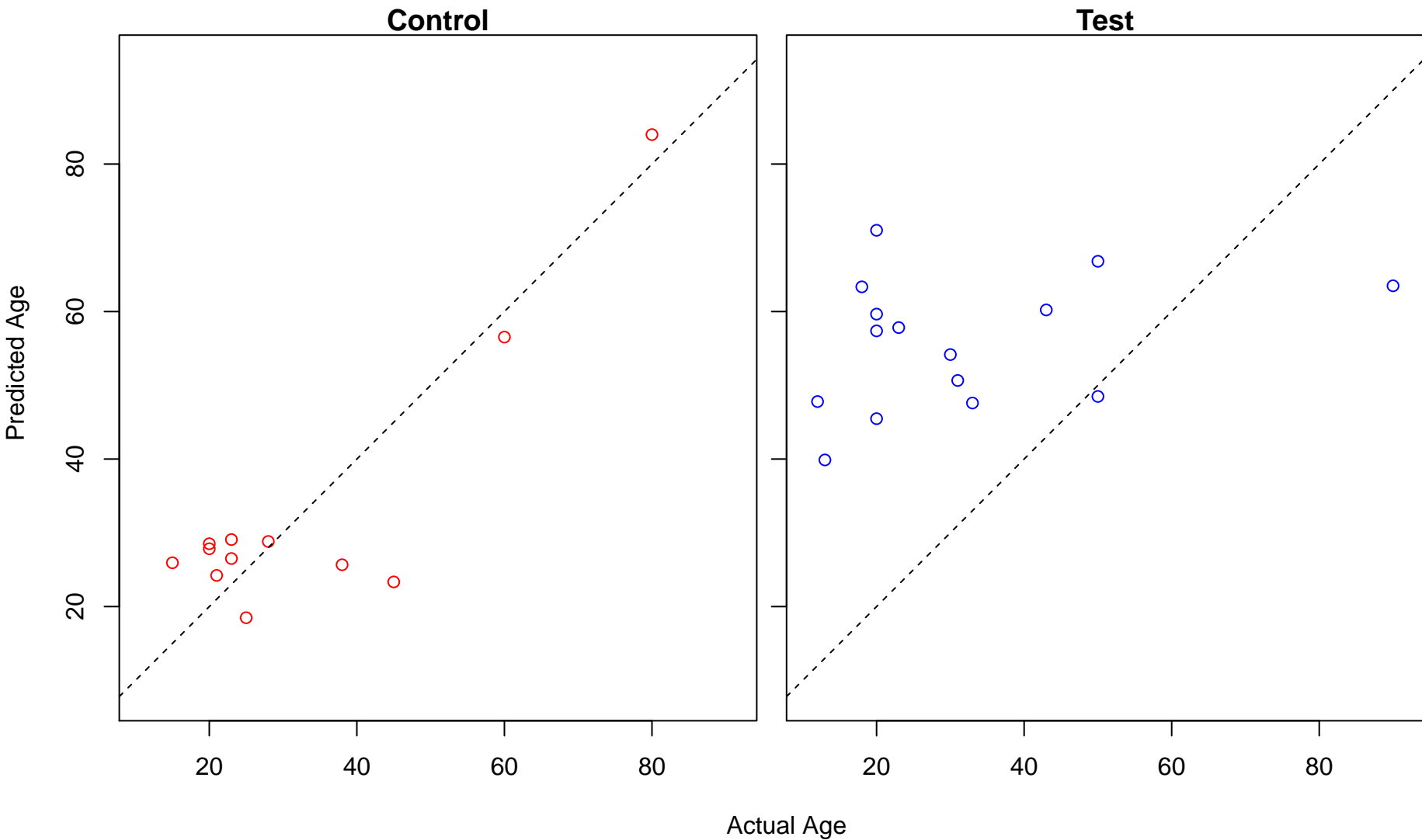
regulation of ryanodine-sensitive calcium-release channel activity (Score: 4.239996)



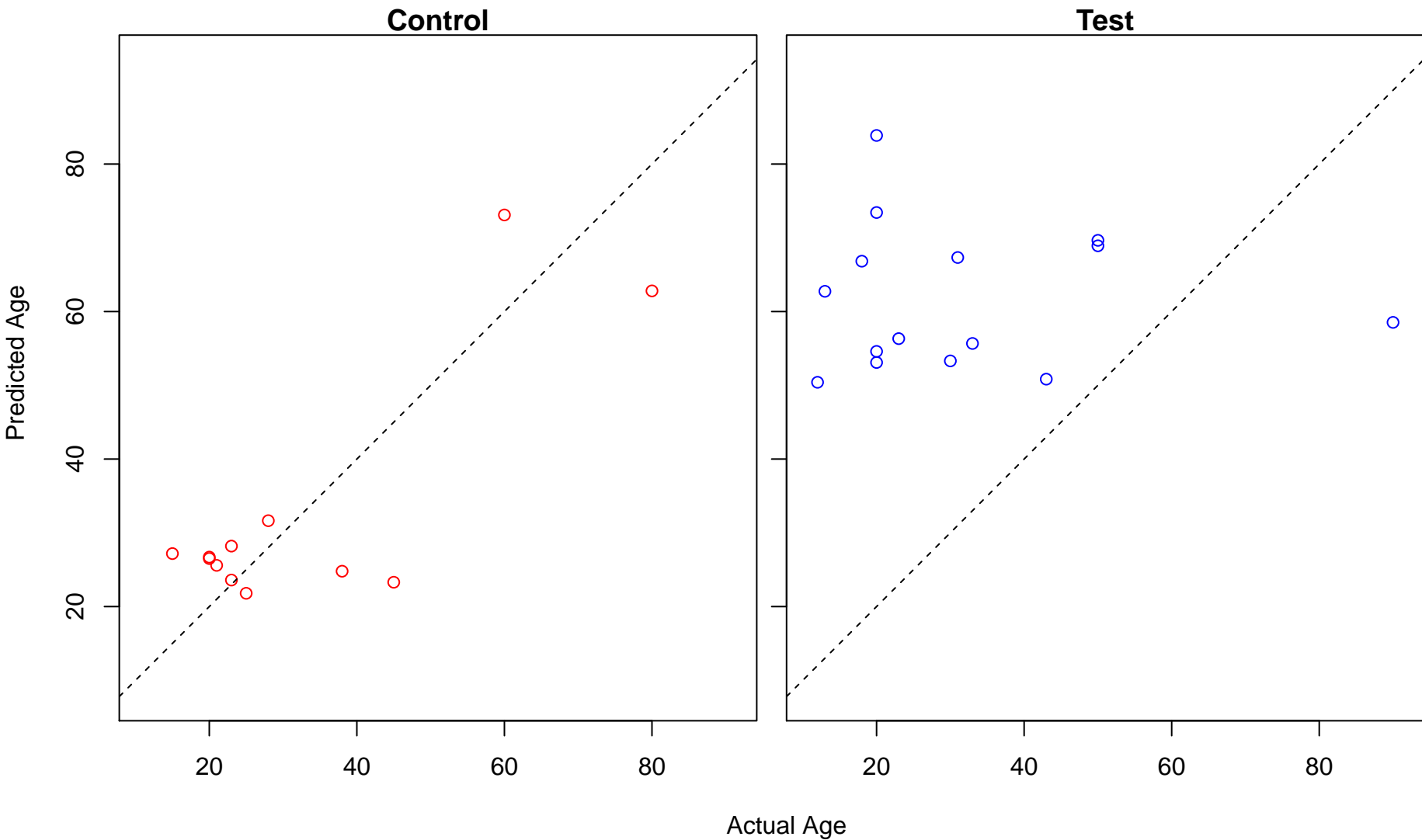
platelet-derived growth factor receptor signaling pathway (Score: 4.239860)



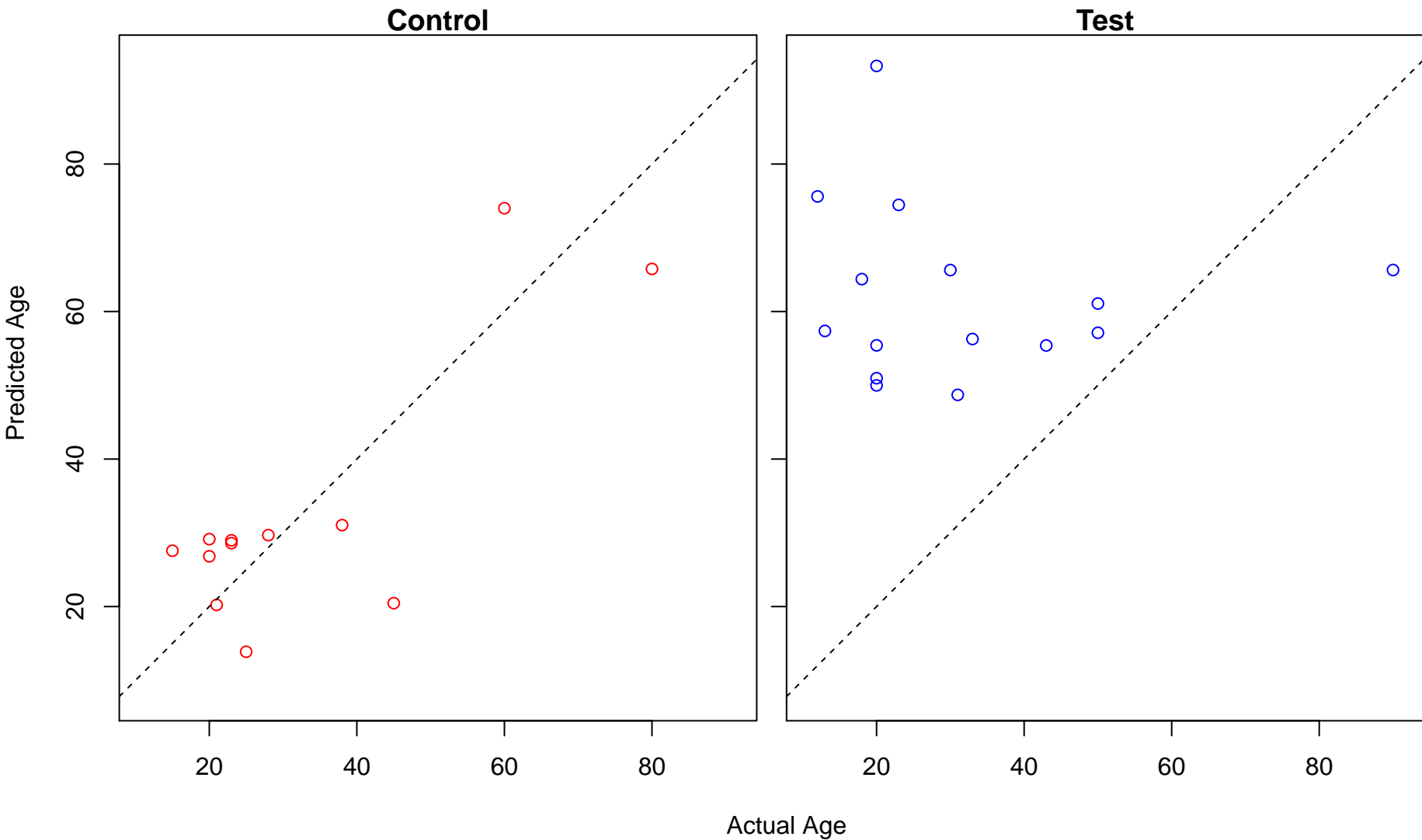
actin cytoskeleton organization (Score: 4.234230)



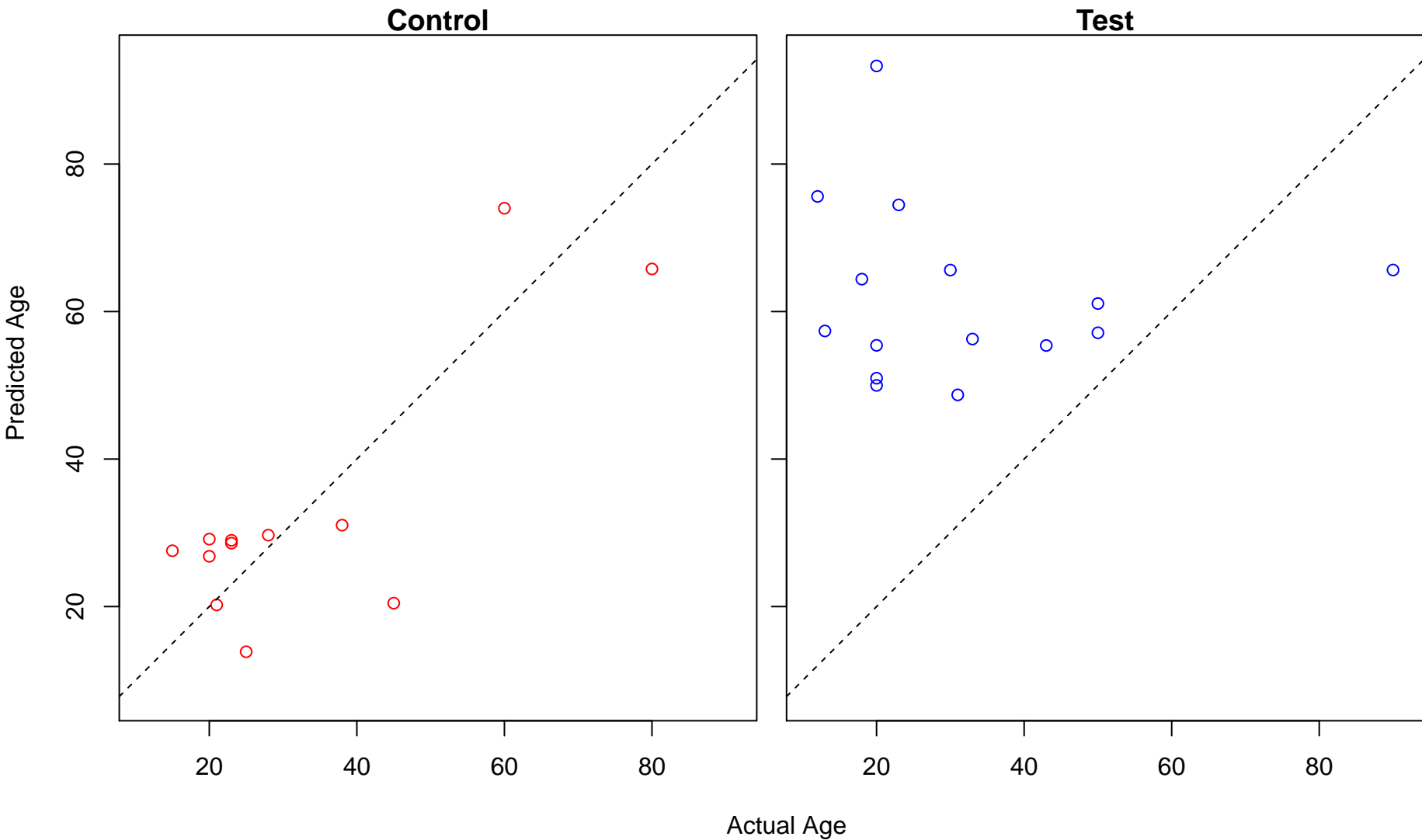
regulation of sequestering of calcium ion (Score: 4.233765)



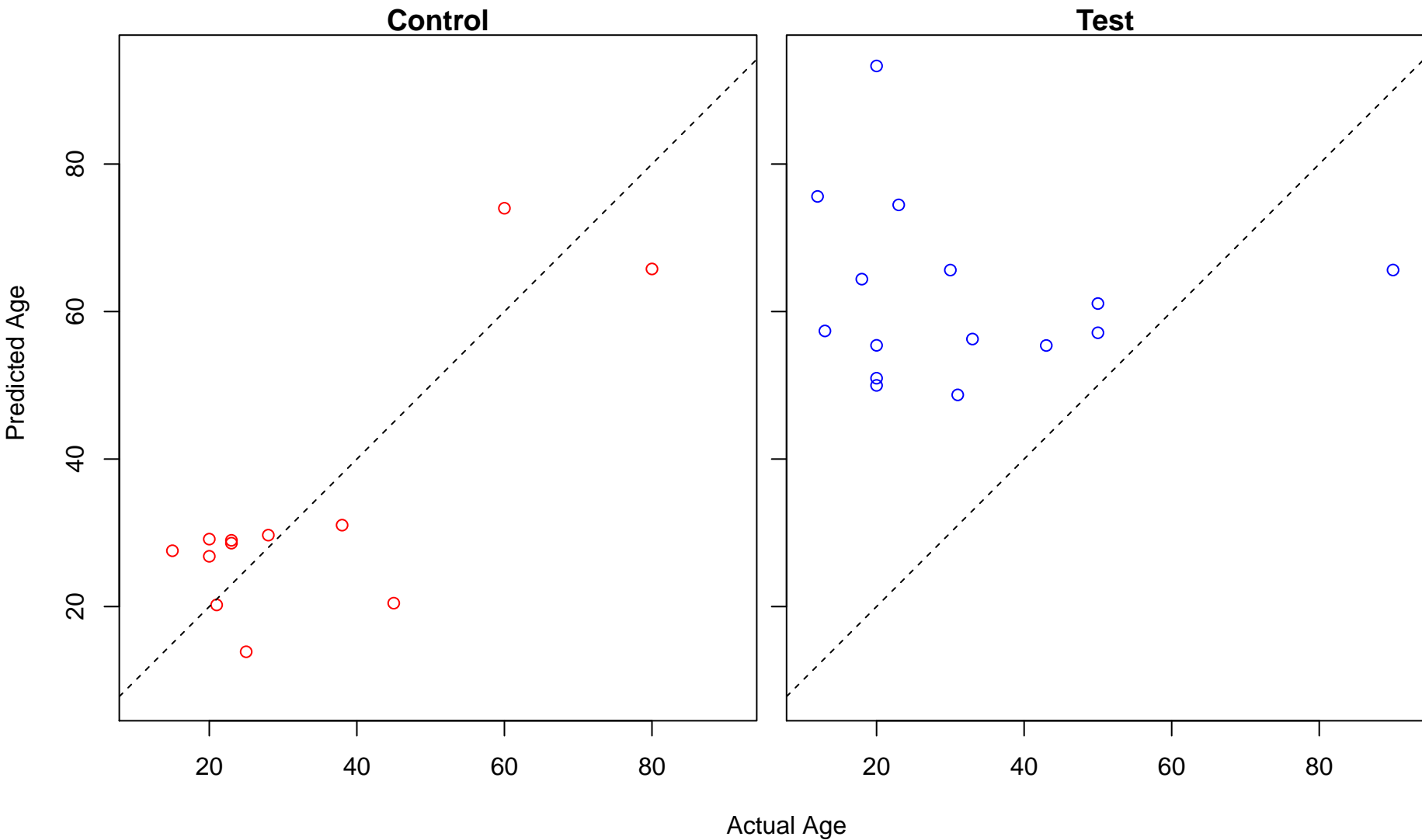
response to defenses of other organism involved in symbiotic interaction (Score: 4.232778)



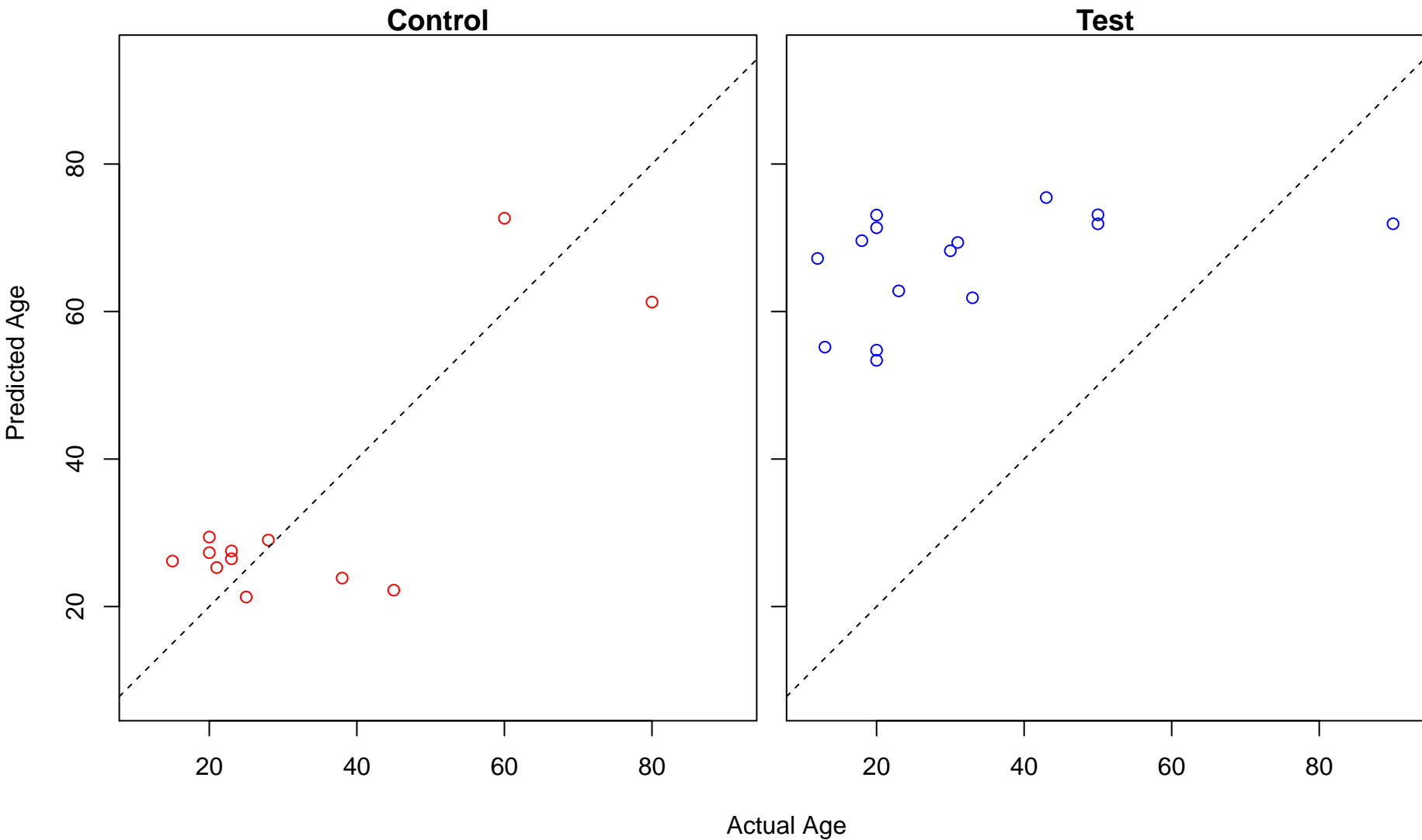
response to host defenses (Score: 4.232778)



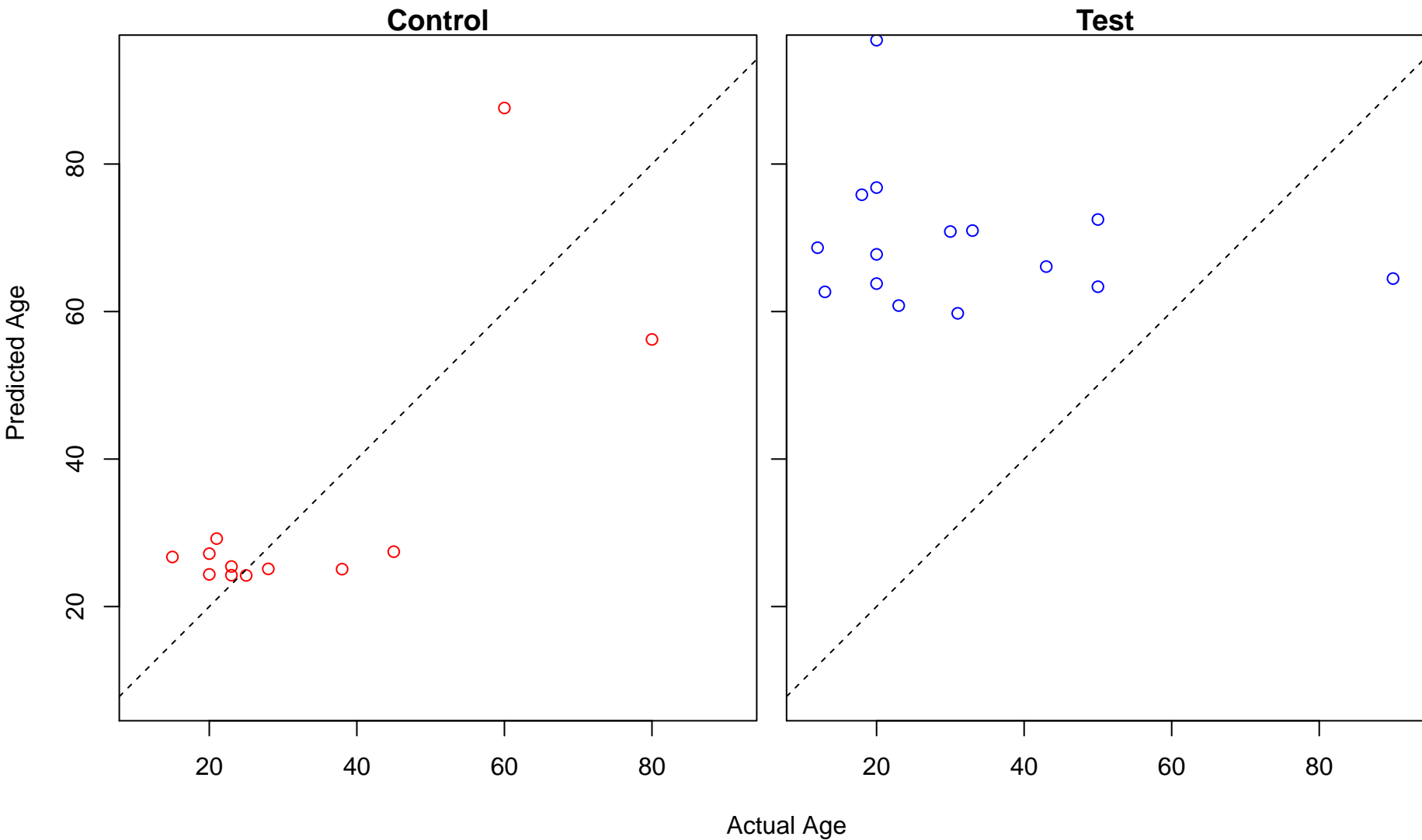
response to host (Score: 4.232778)



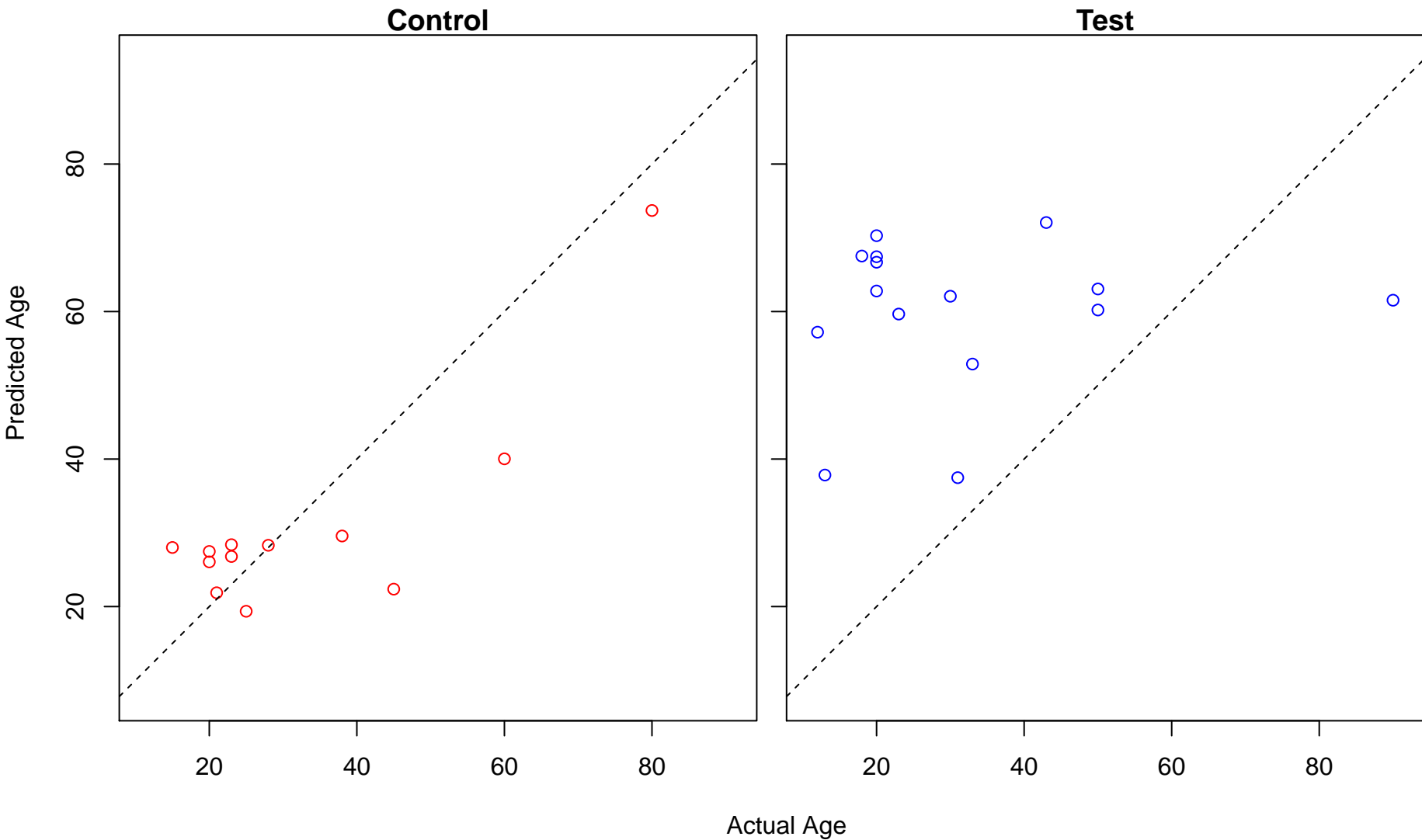
regulation of potassium ion transport (Score: 4.231184)



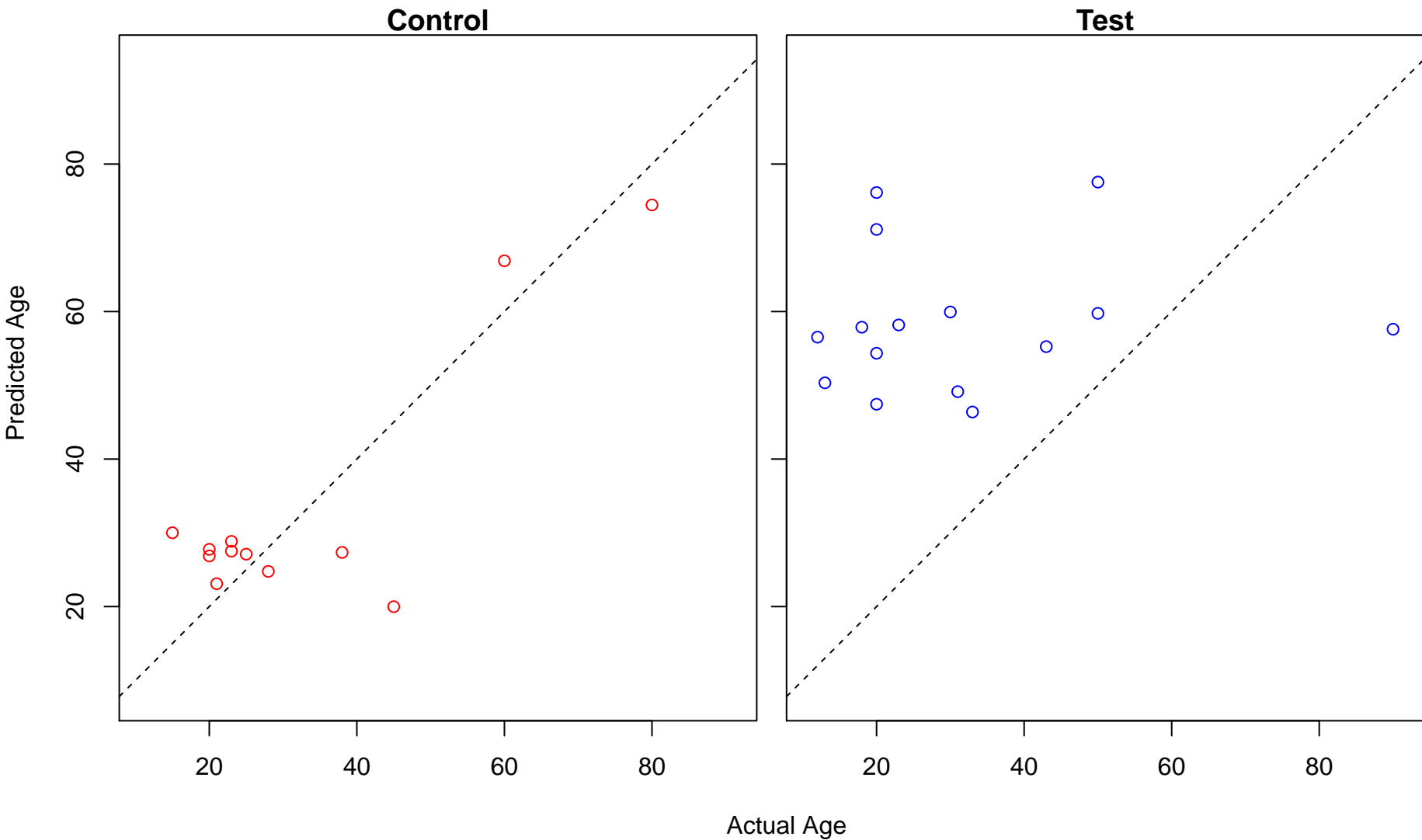
membrane invagination (Score: 4.227855)



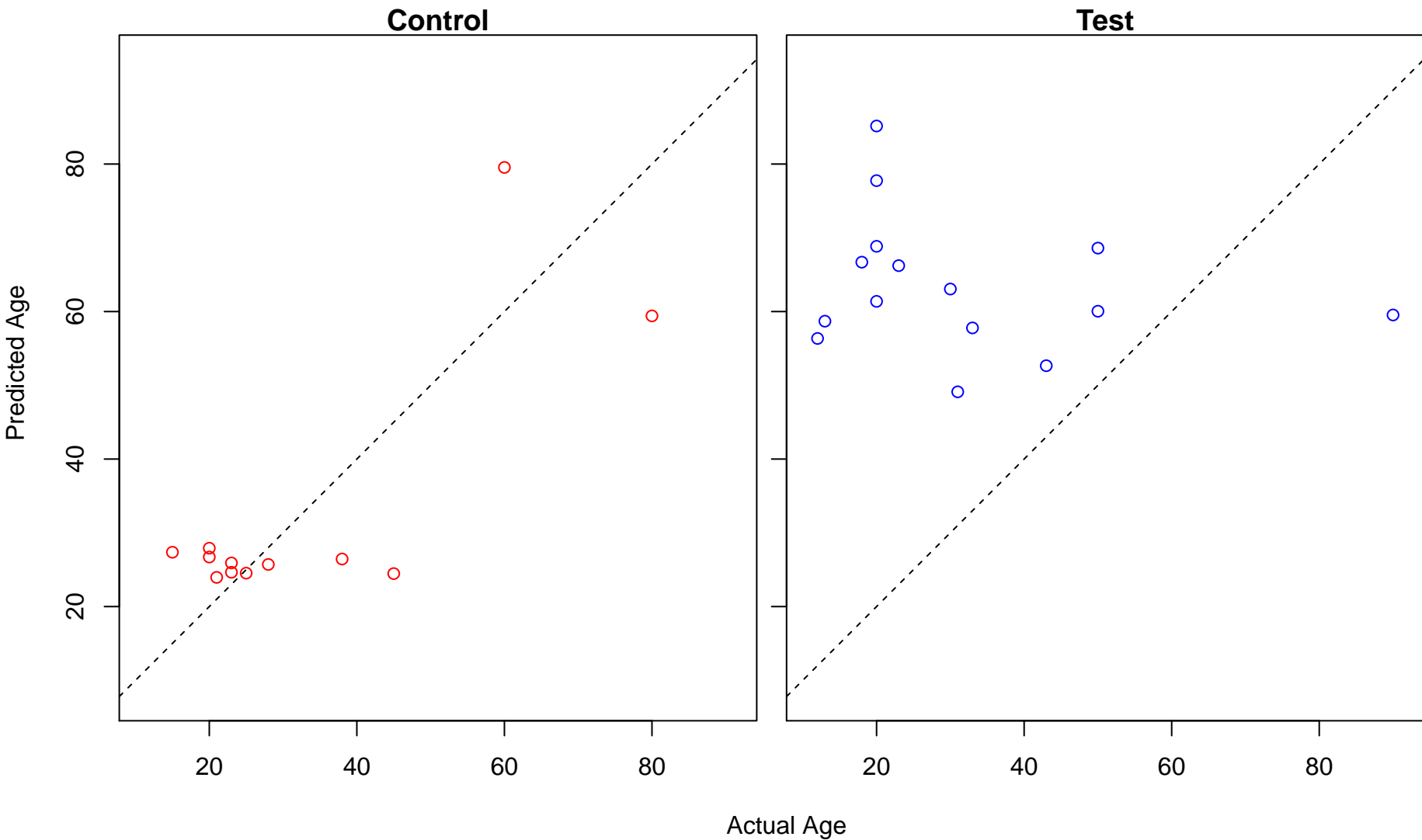
fatty acid beta-oxidation (Score: 4.227396)



beta-amyloid metabolic process (Score: 4.226670)

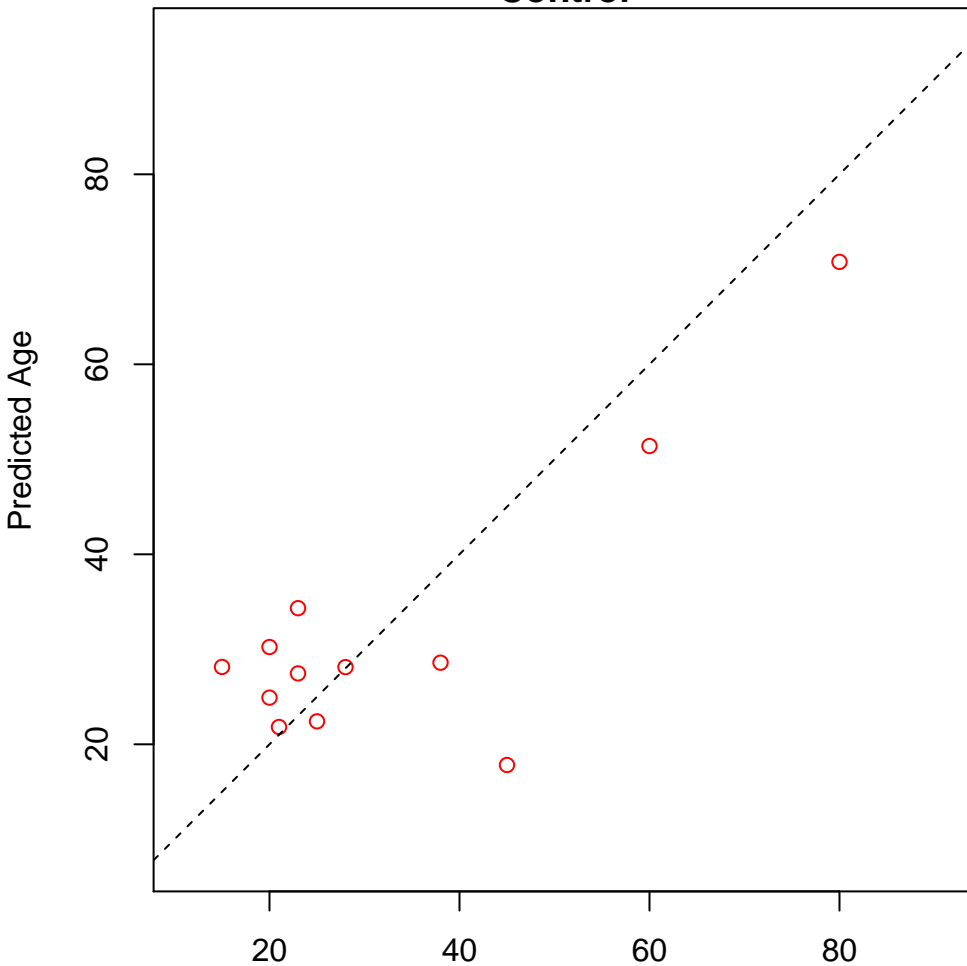


regulation of stem cell population maintenance (Score: 4.226453)

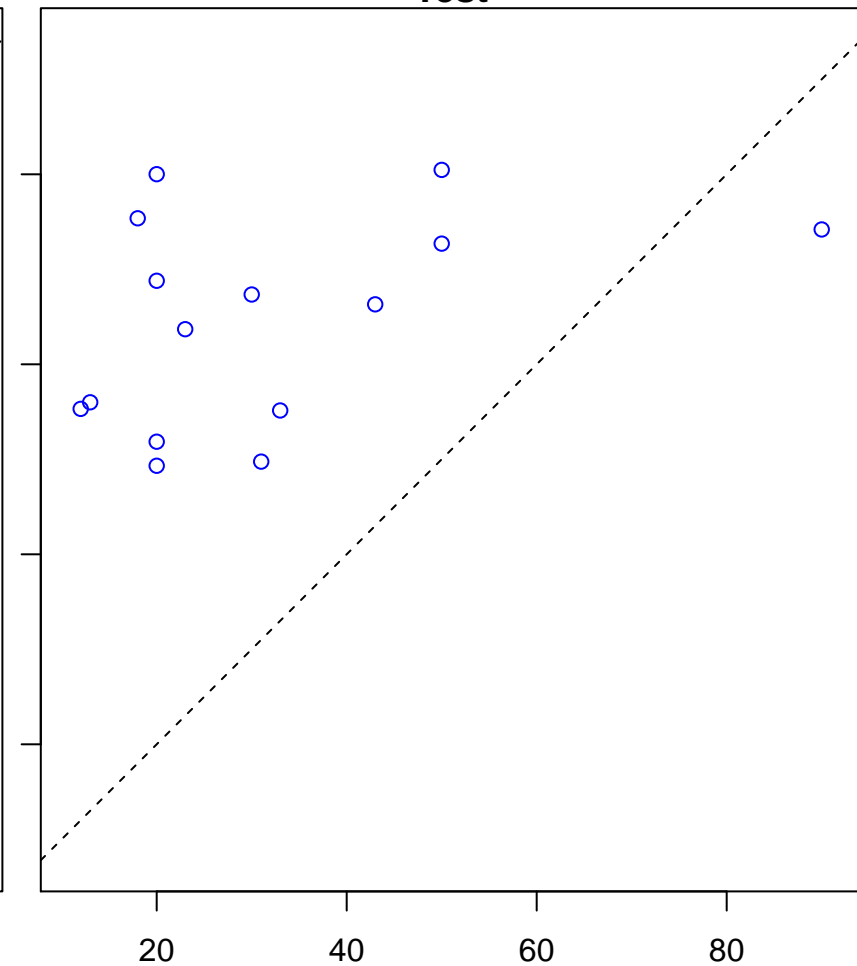


regulation of interleukin-5 production (Score: 4.223664)

Control

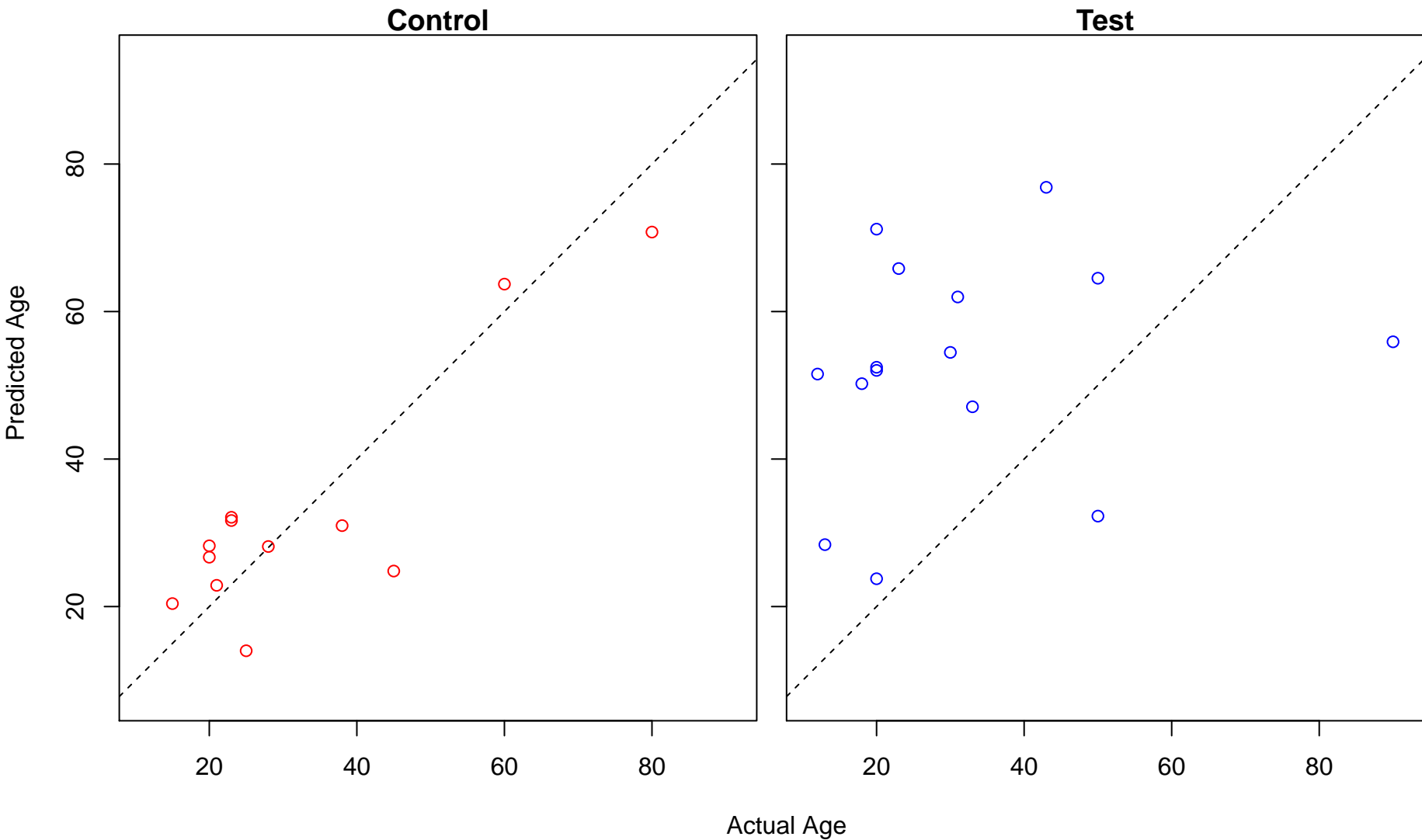


Test



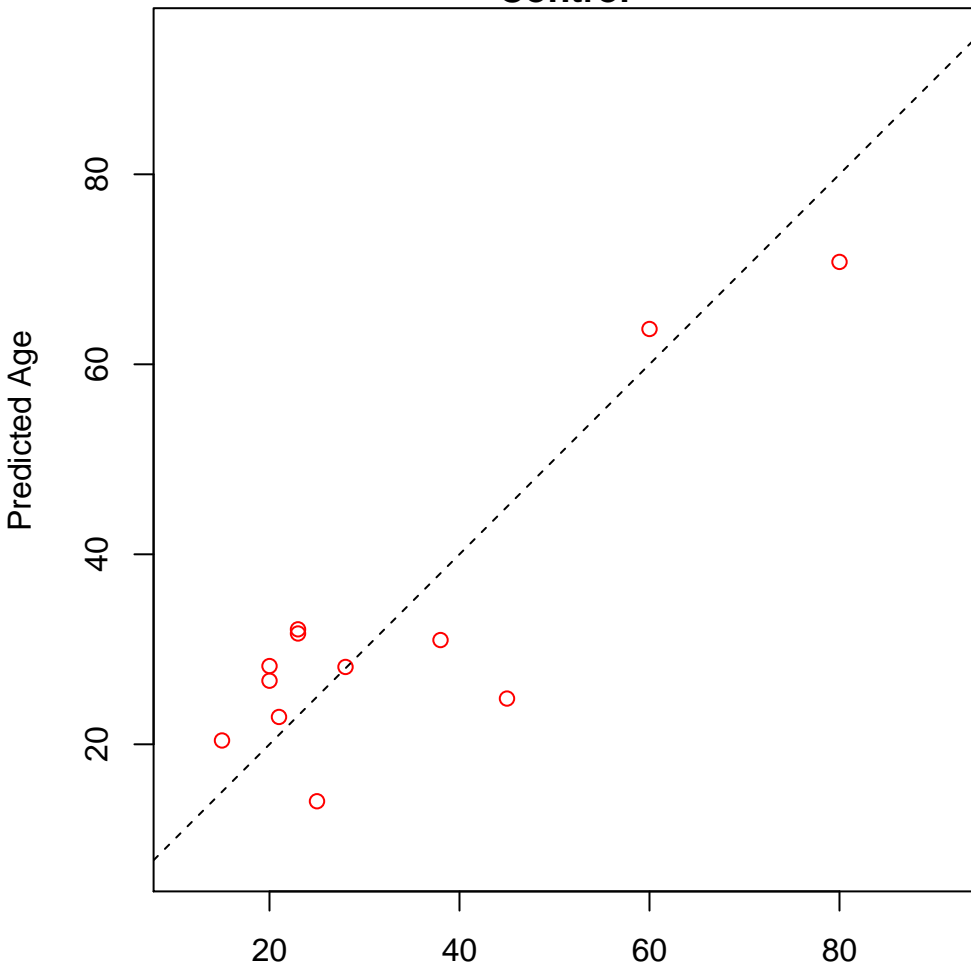
Actual Age

purine nucleoside catabolic process (Score: 4.223011)

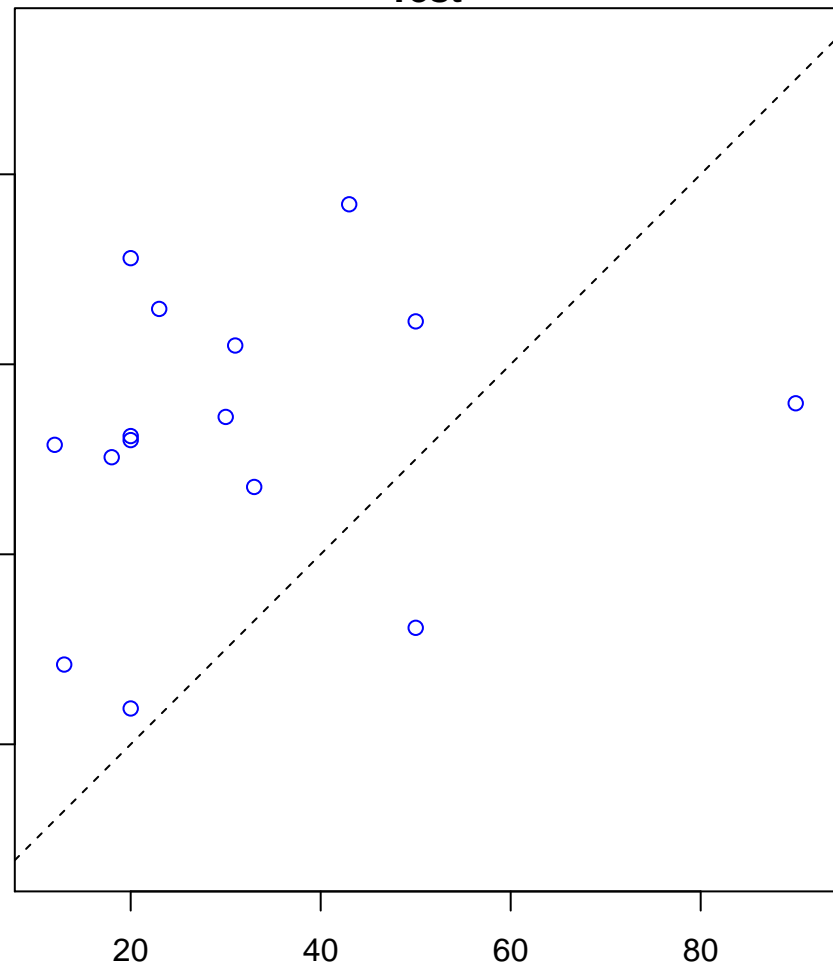


purine ribonucleoside catabolic process (Score: 4.223011)

Control

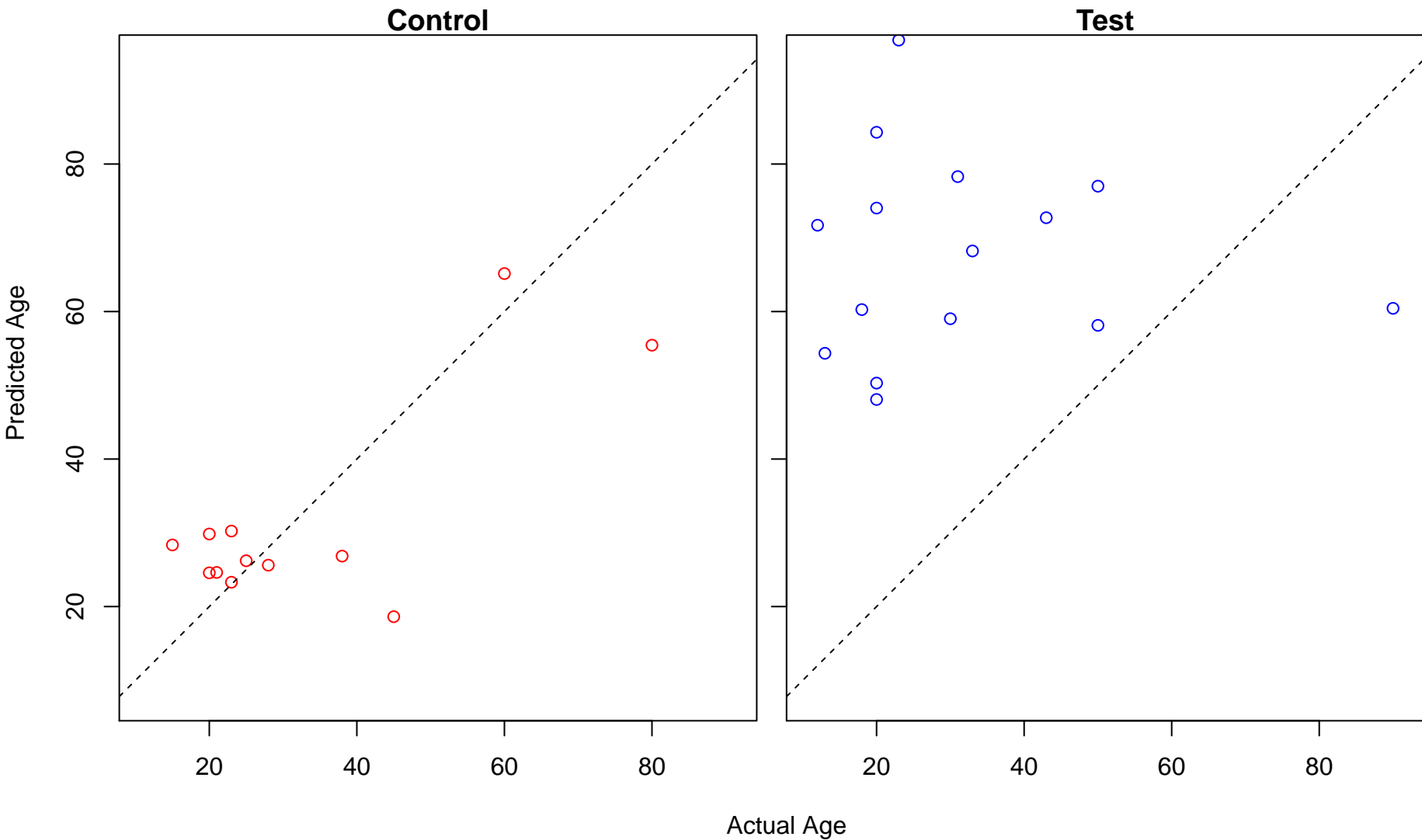


Test

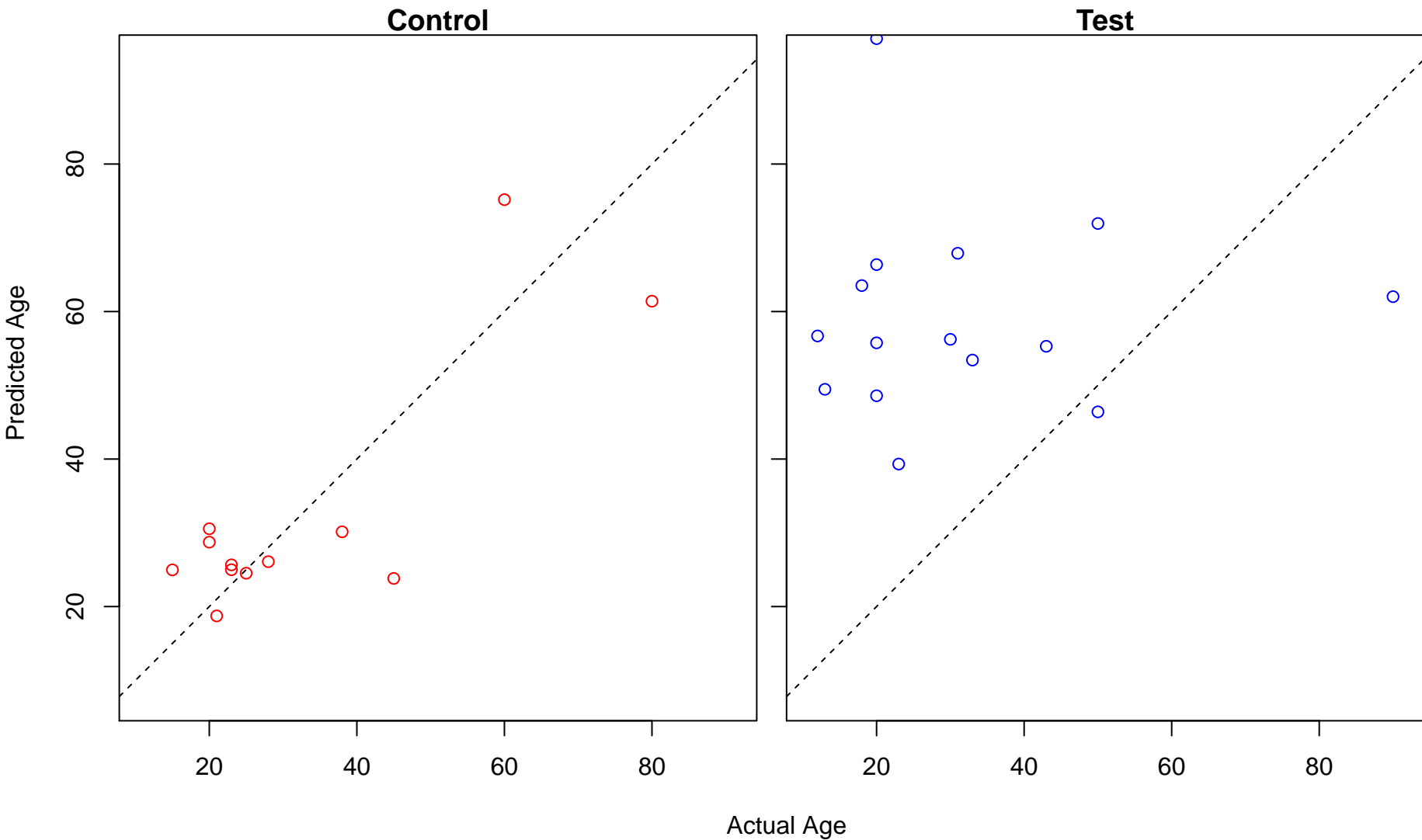


Actual Age

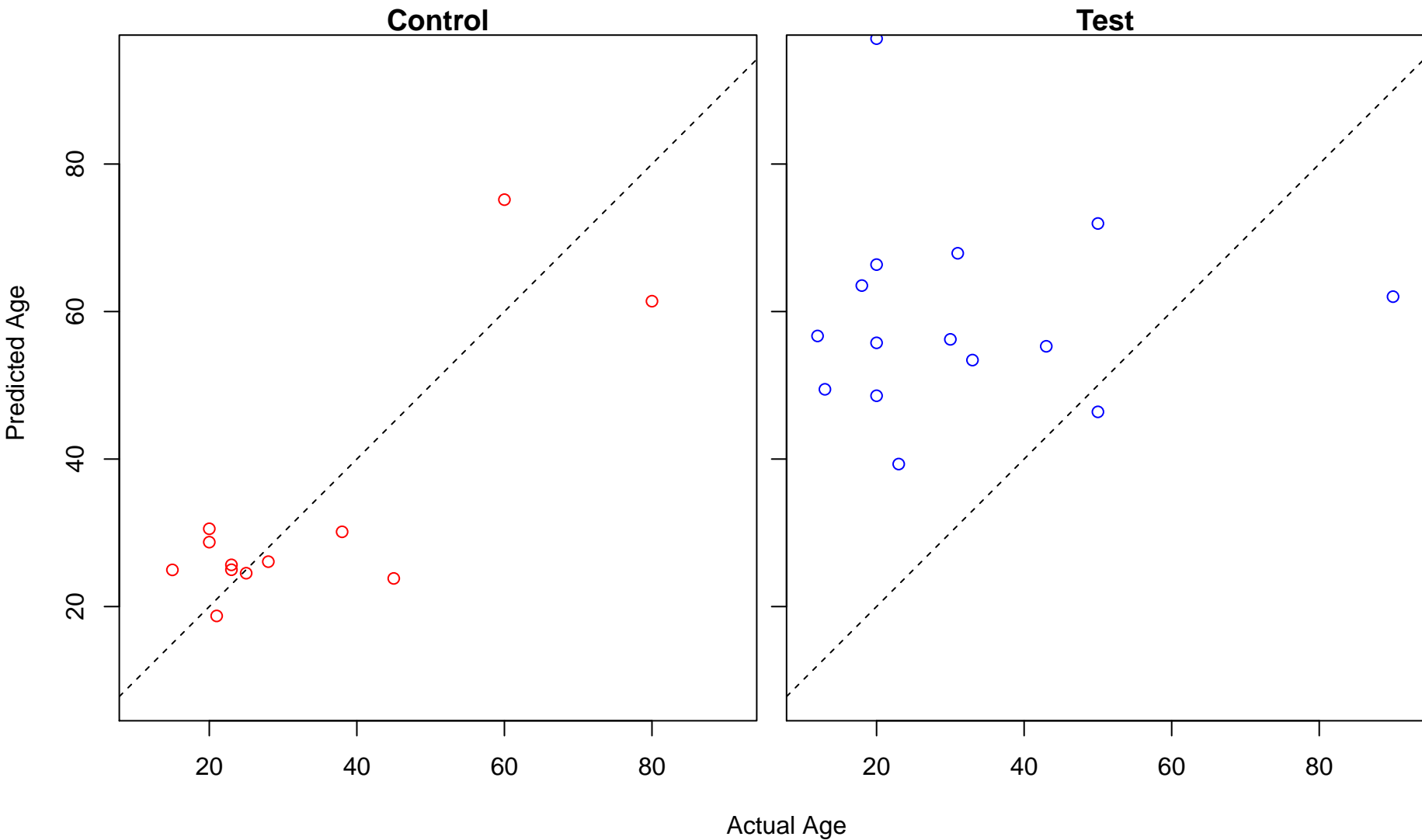
positive regulation of synaptic transmission, glutamatergic (Score: 4.218272)



pH elevation (Score: 4.217533)

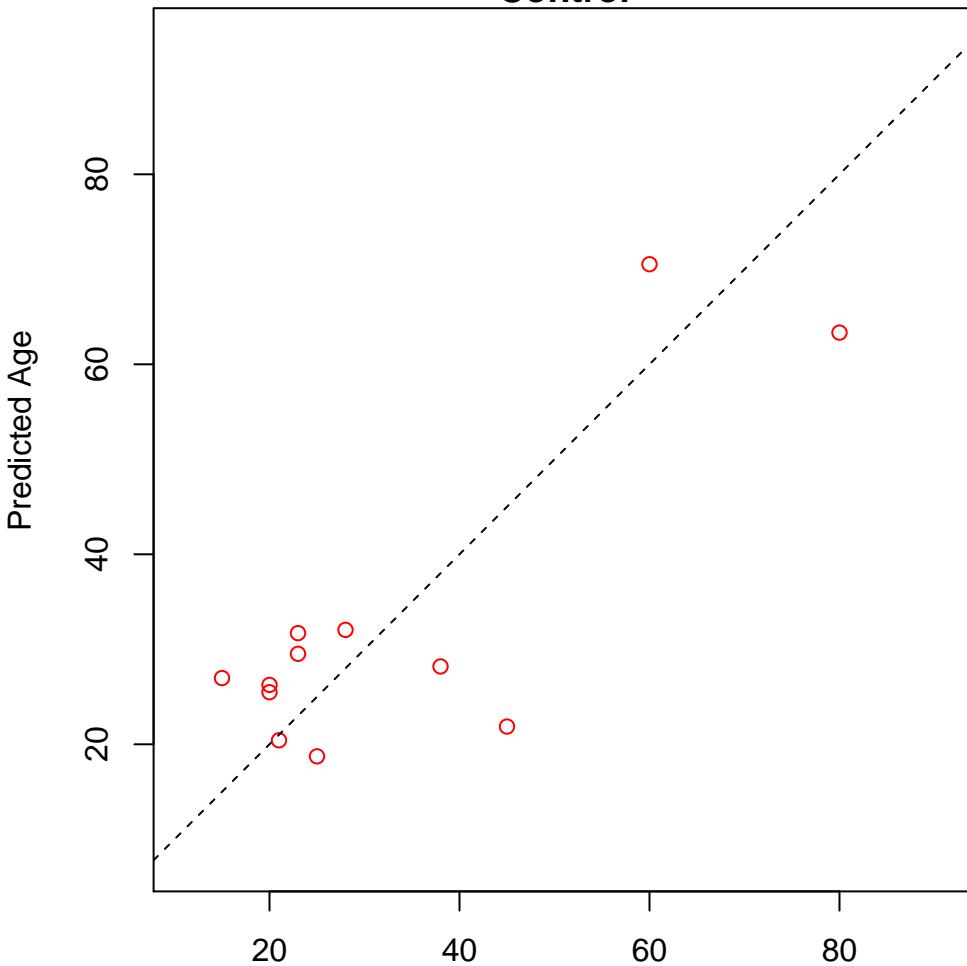


intracellular pH elevation (Score: 4.217533)

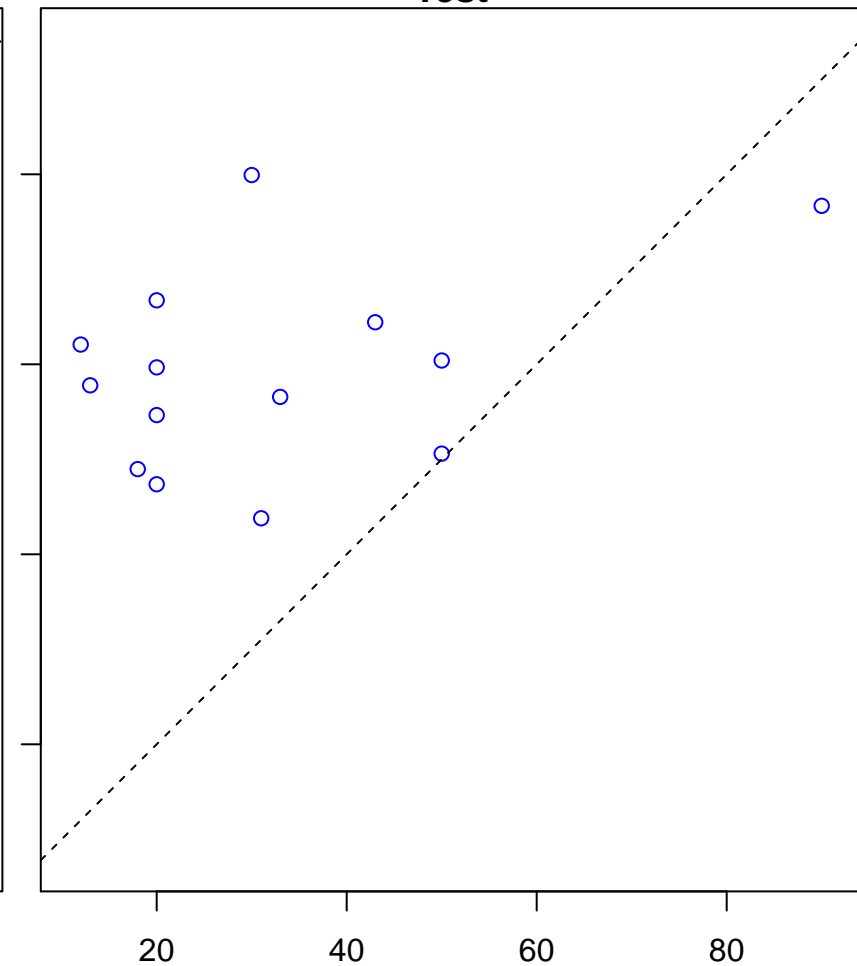


response to organophosphorus (Score: 4.215318)

Control

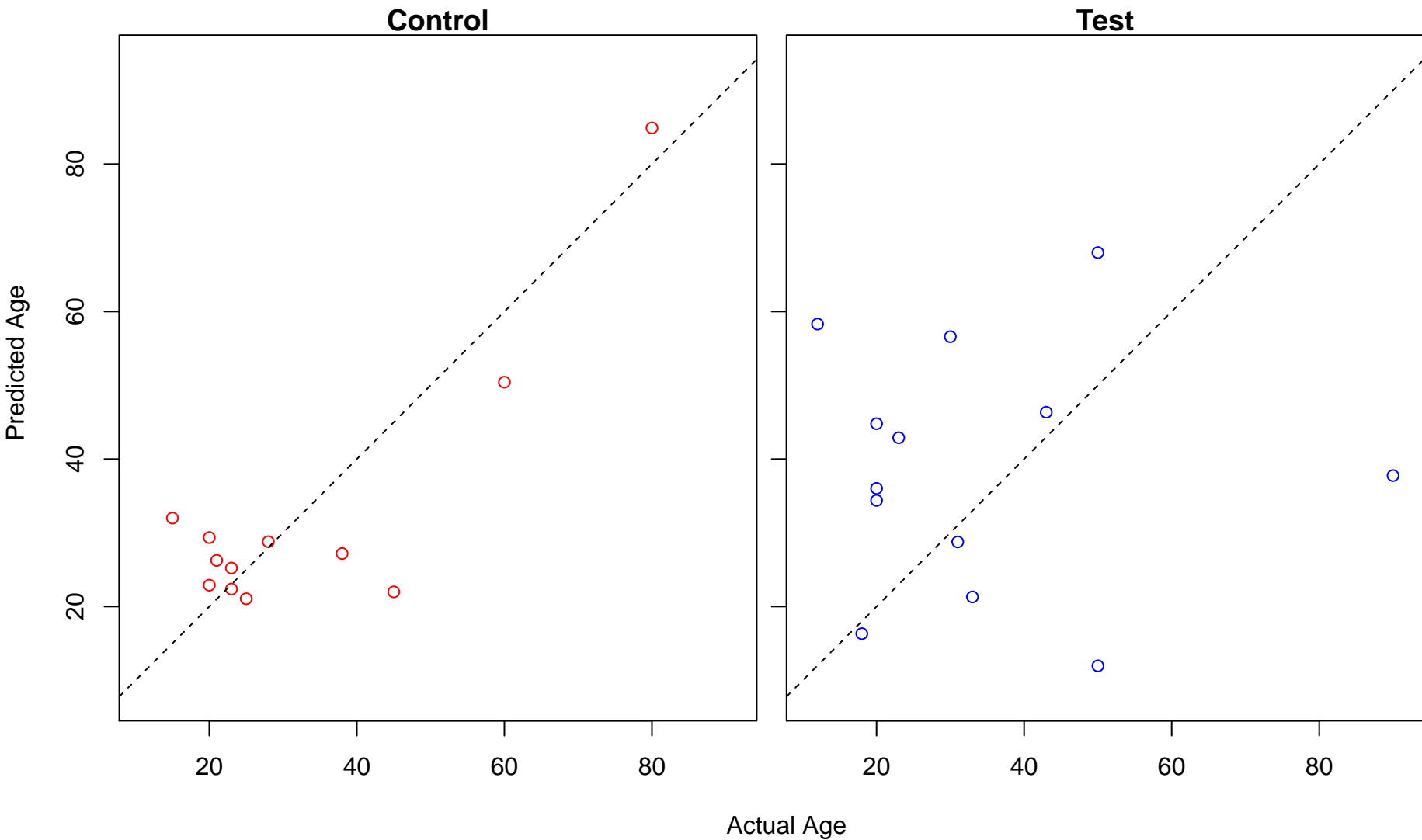


Test

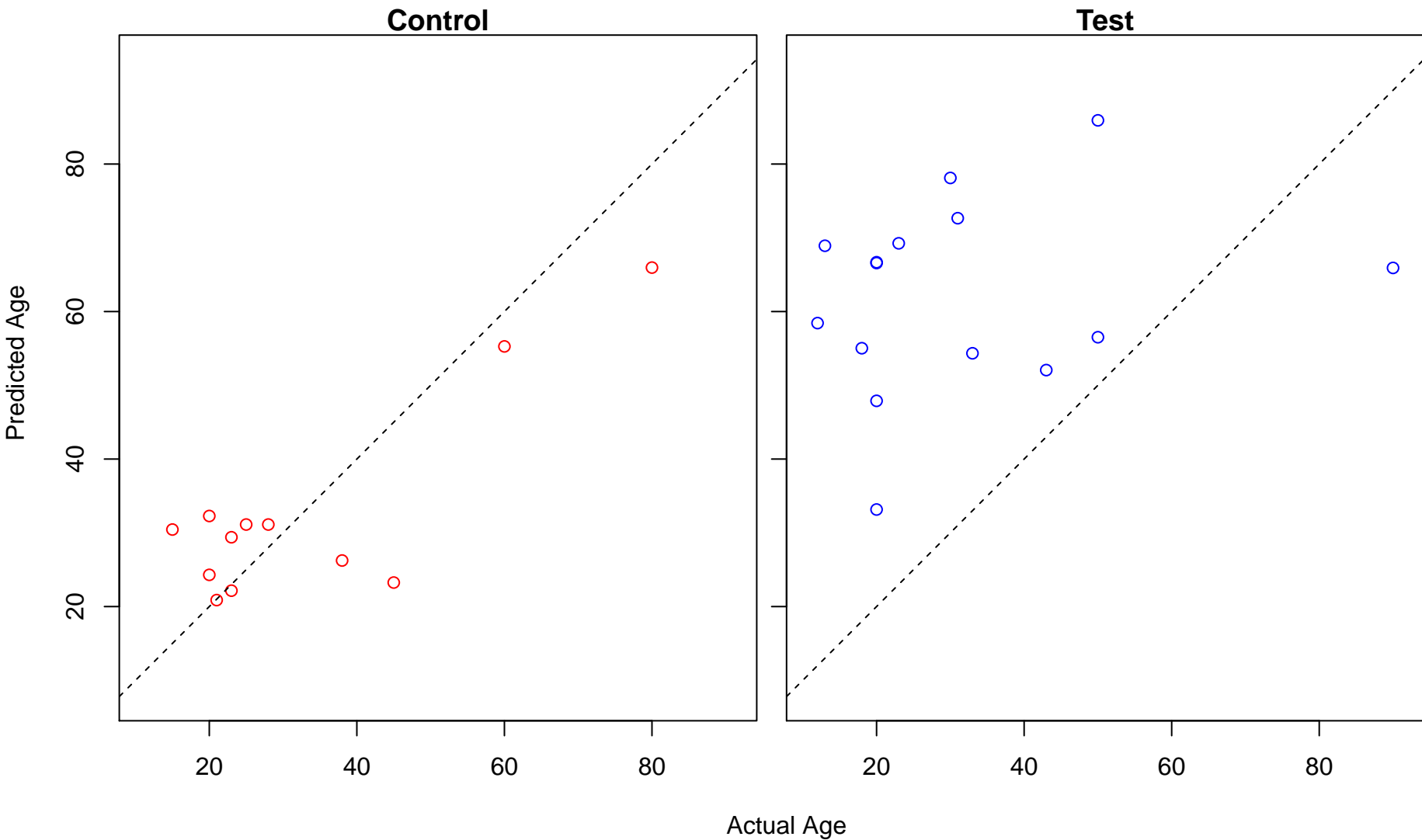


Actual Age

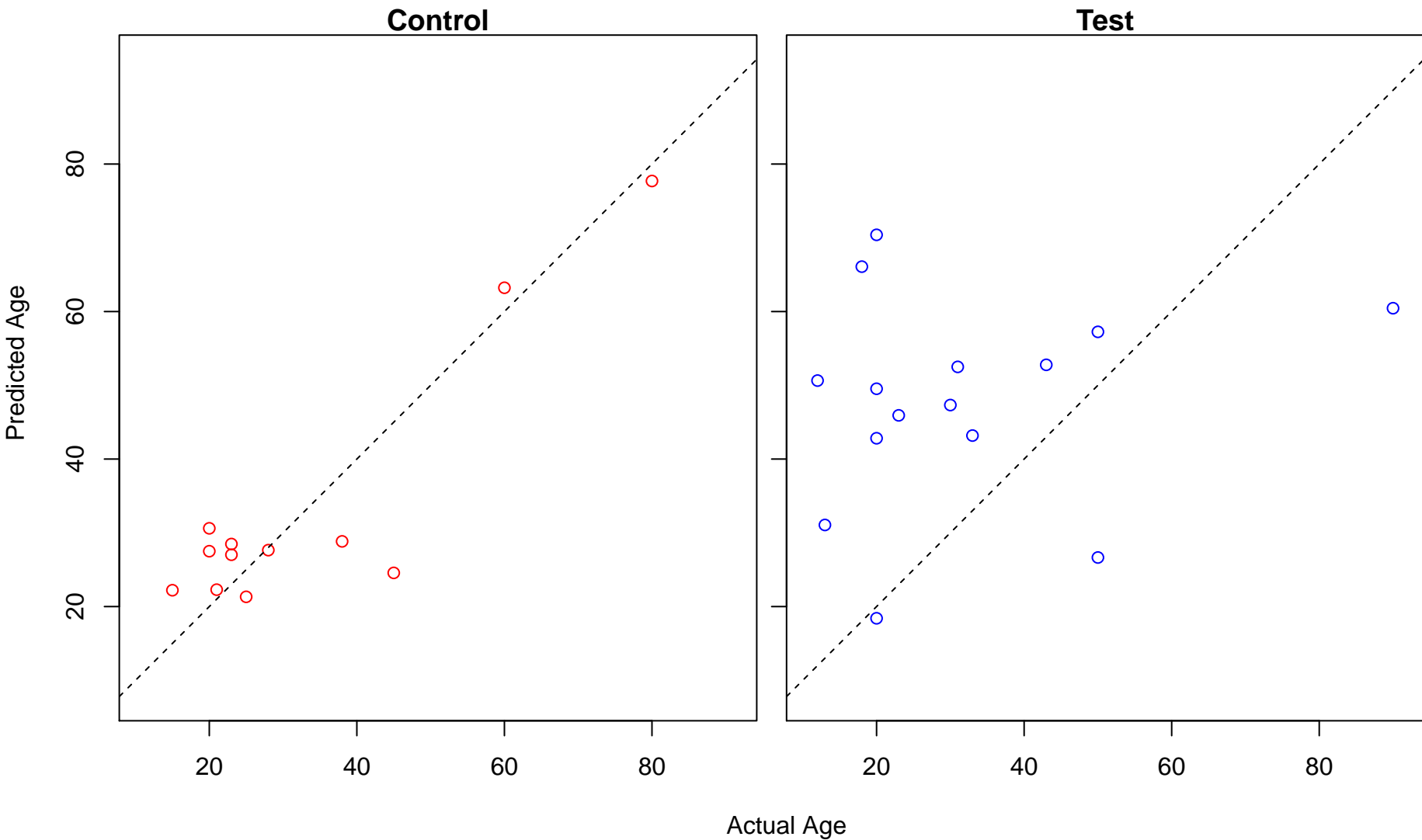
regulation of stress fiber assembly (Score: 4.213912)



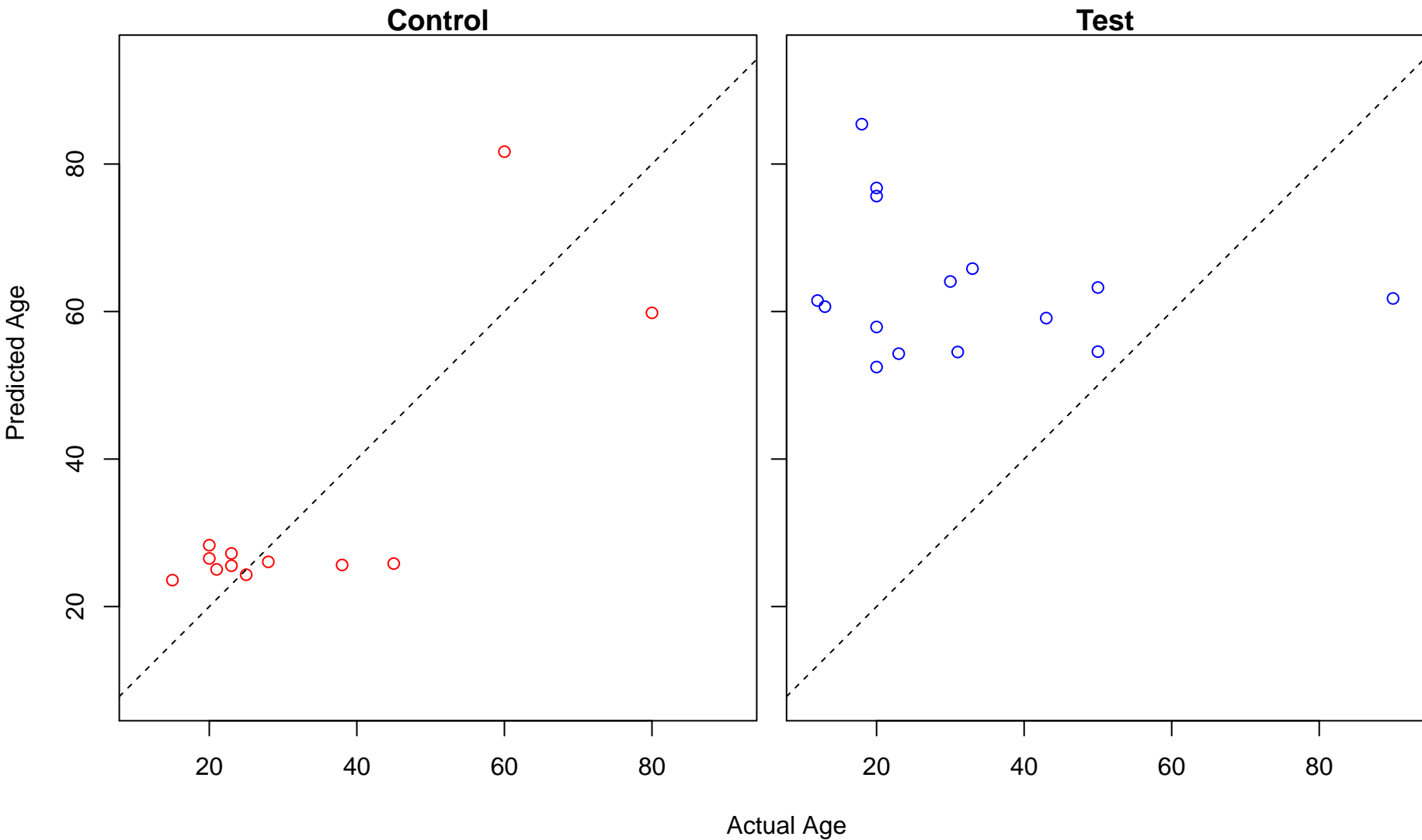
positive regulation of vascular permeability (Score: 4.211499)



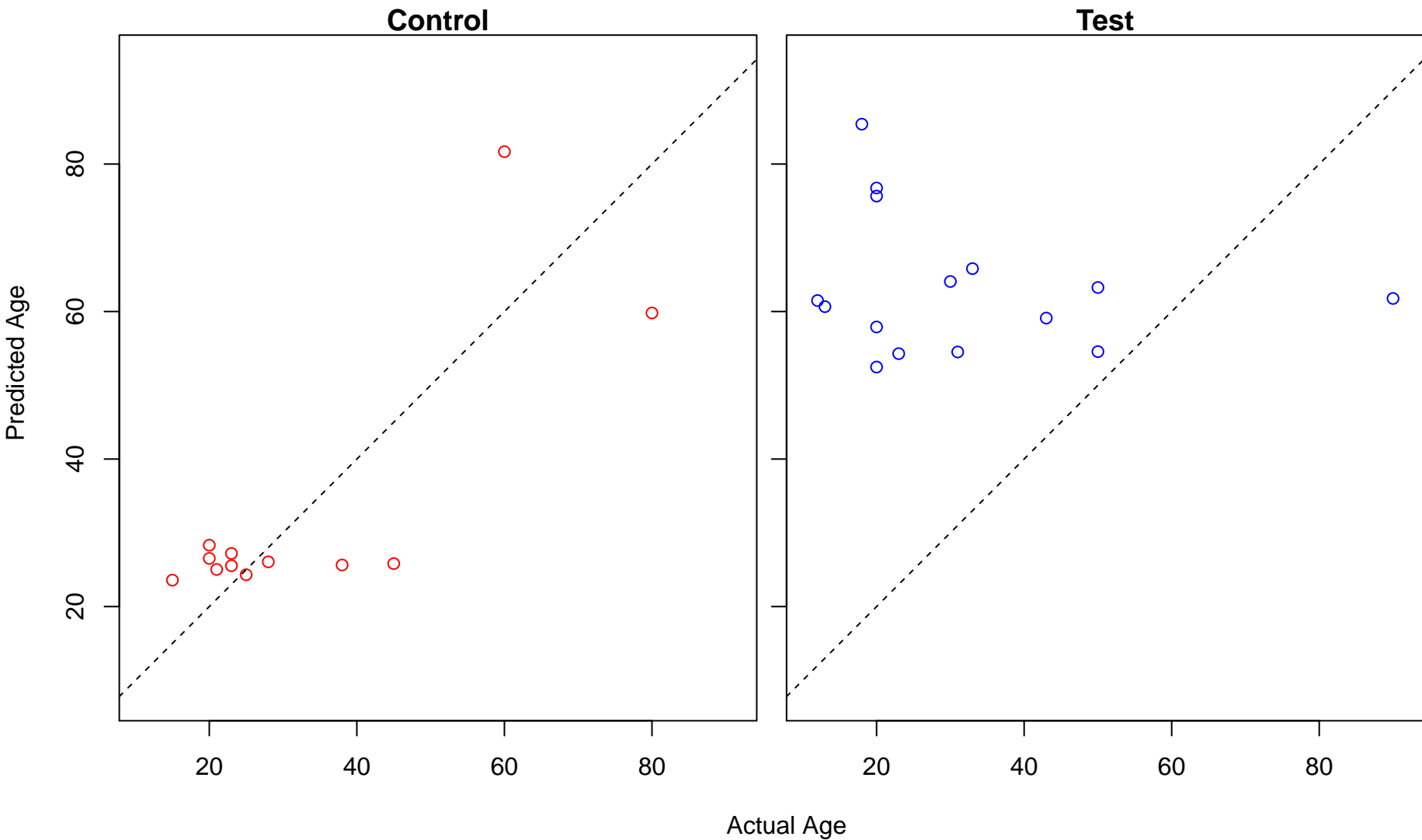
regulation of retrograde protein transport, ER to cytosol (Score: 4.211416)



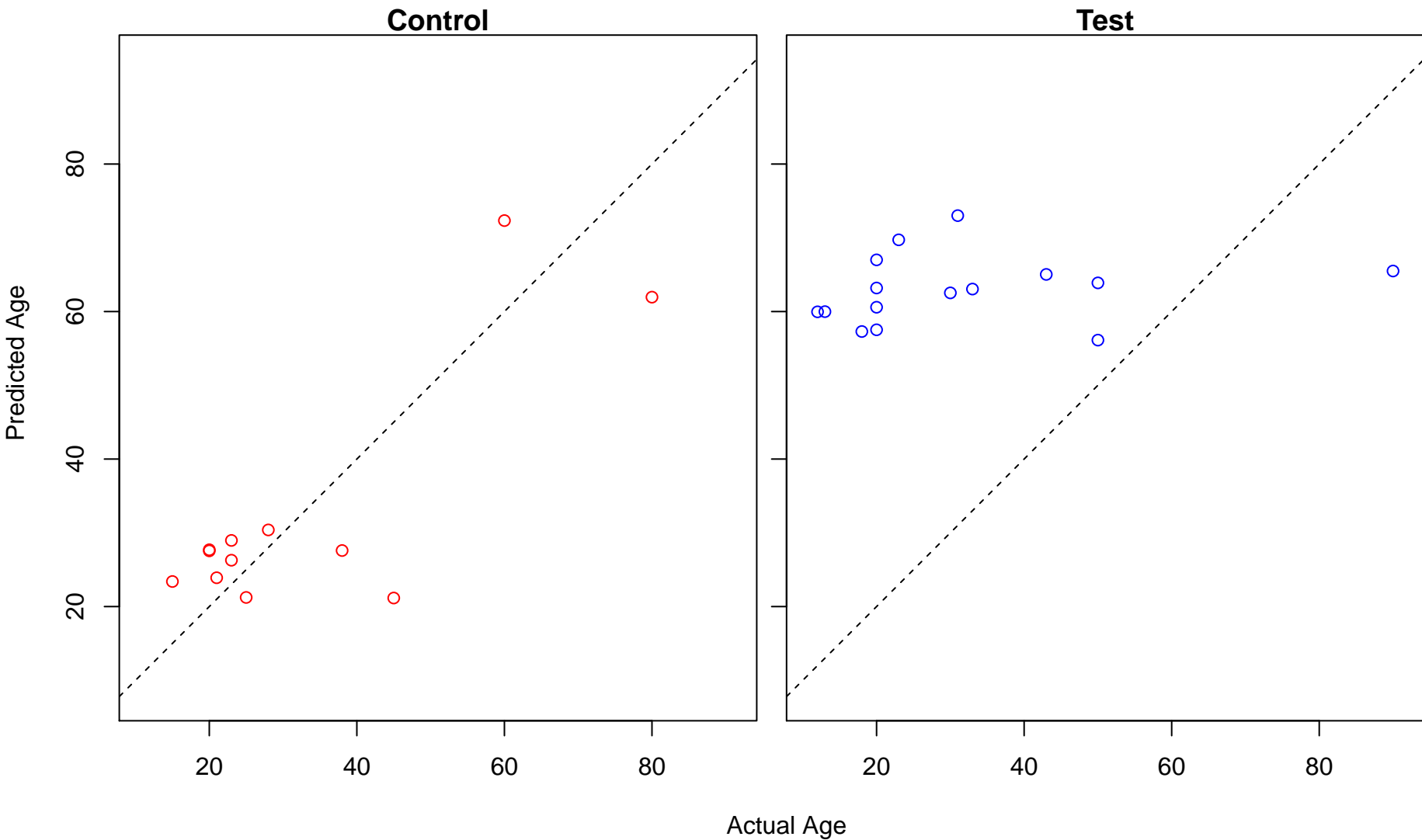
negative regulation of adenylate cyclase activity (Score: 4.210686)



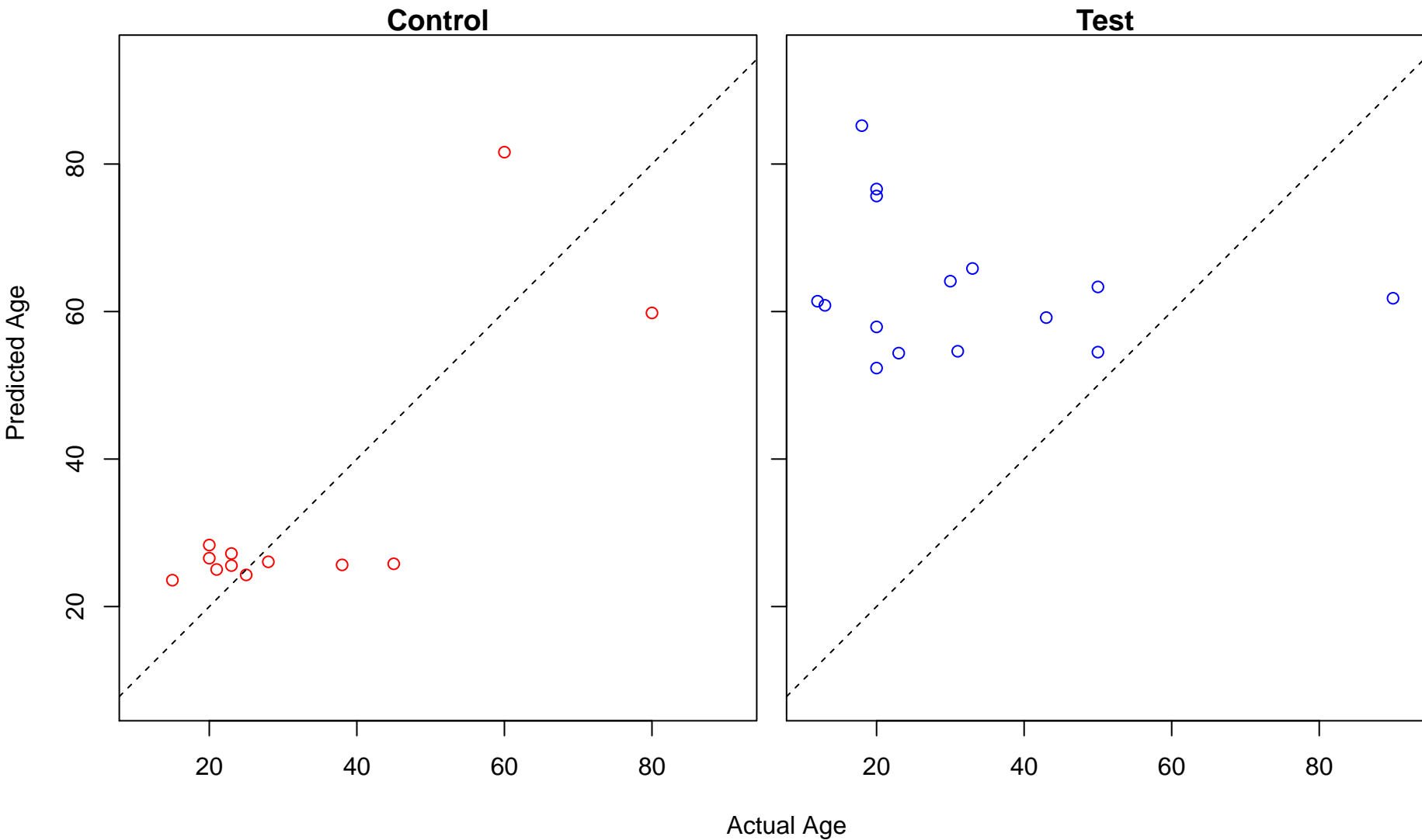
negative regulation of cyclase activity (Score: 4.209630)



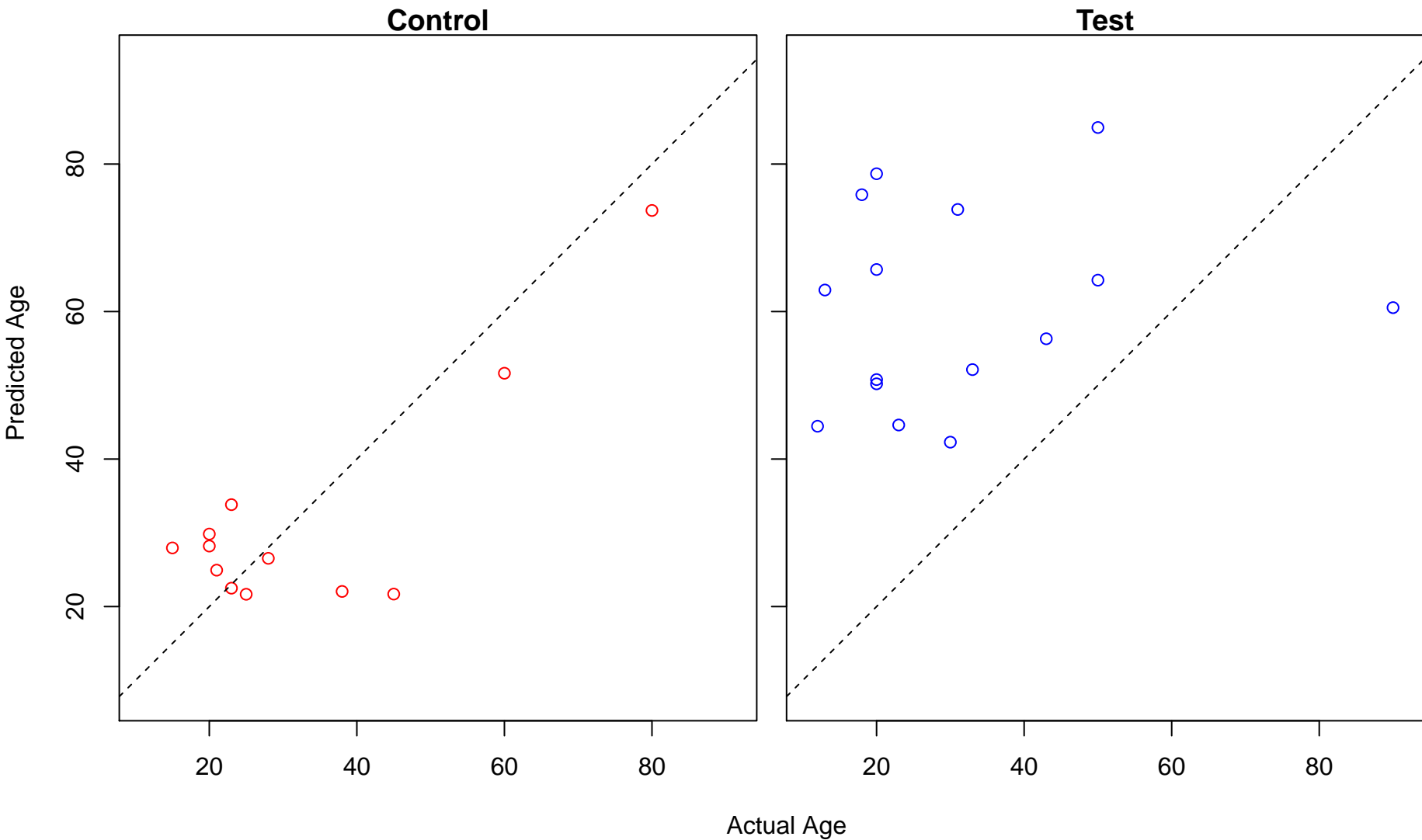
regulation of DNA damage response, signal transduction by p53 class mediator (Score: 4.209015)



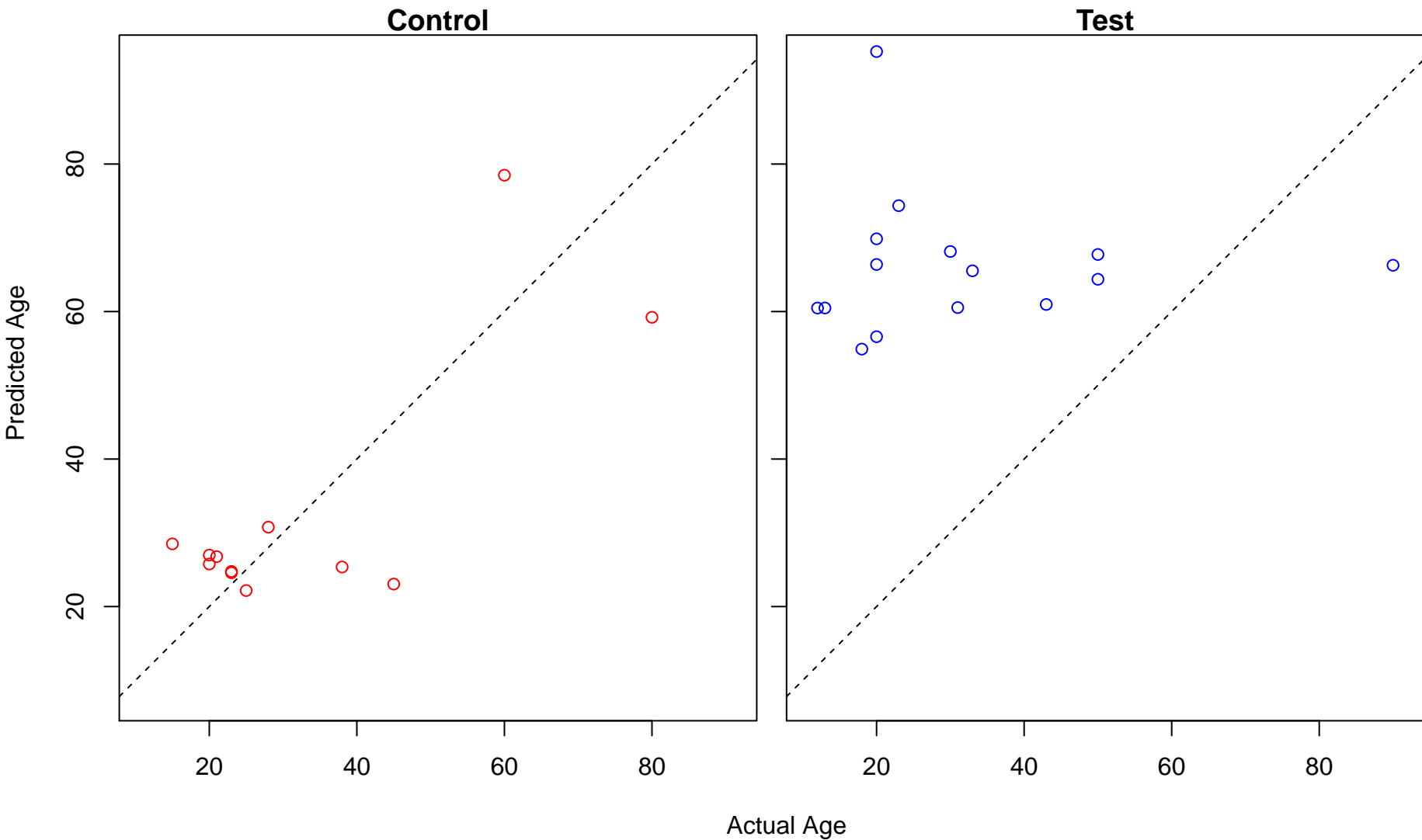
negative regulation of cAMP biosynthetic process (Score: 4.207988)



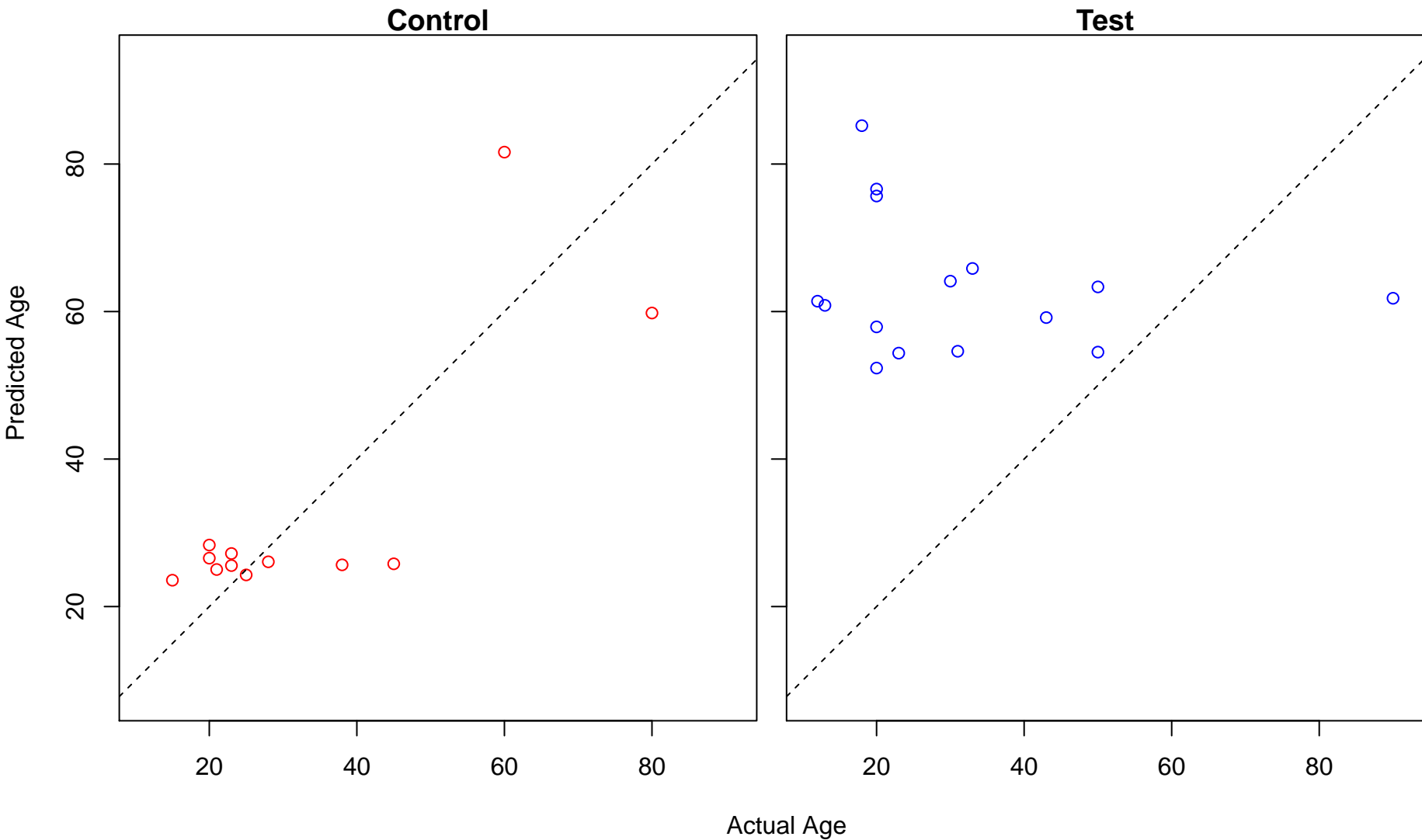
positive regulation of natural killer cell activation (Score: 4.207791)



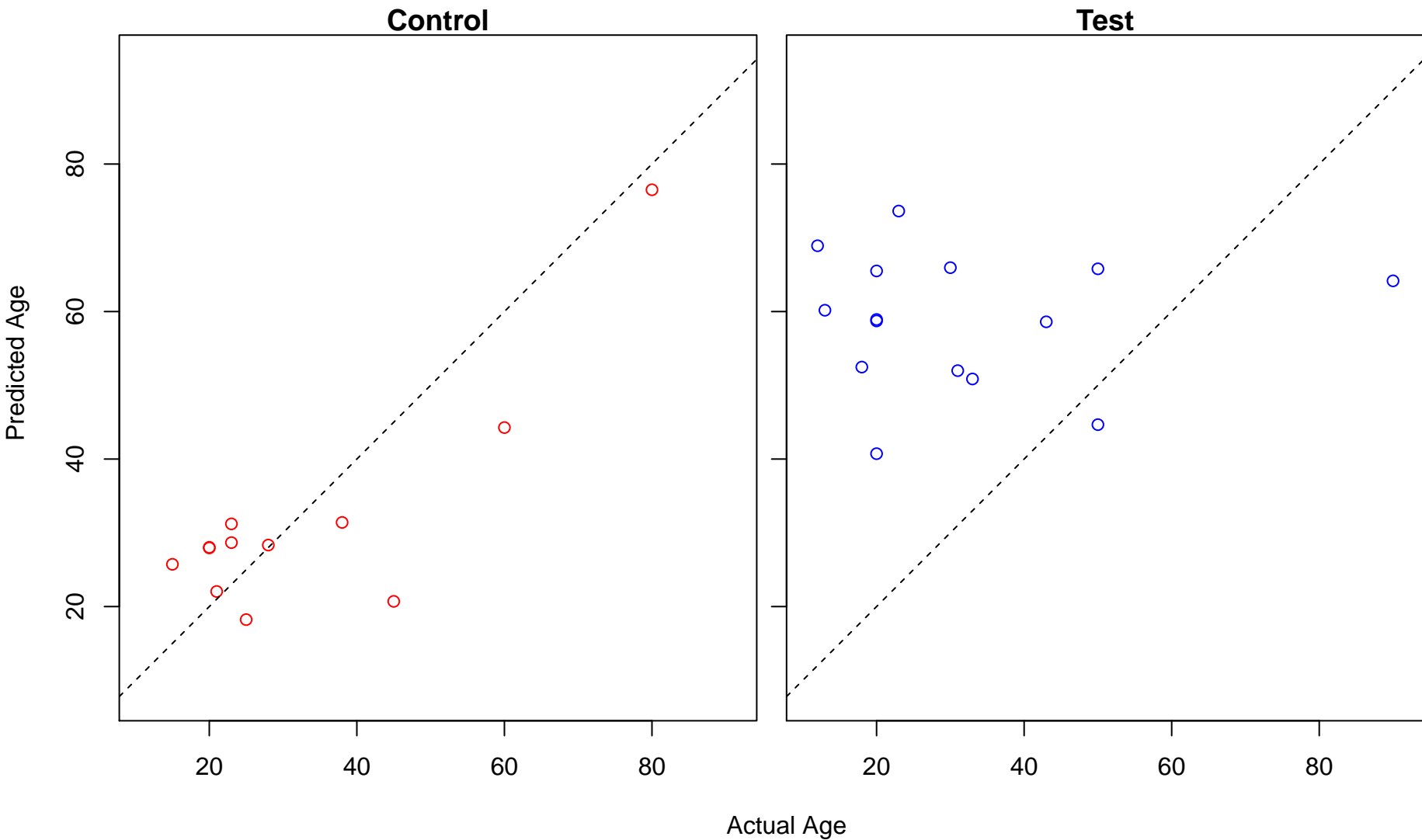
regulation of megakaryocyte differentiation (Score: 4.207391)



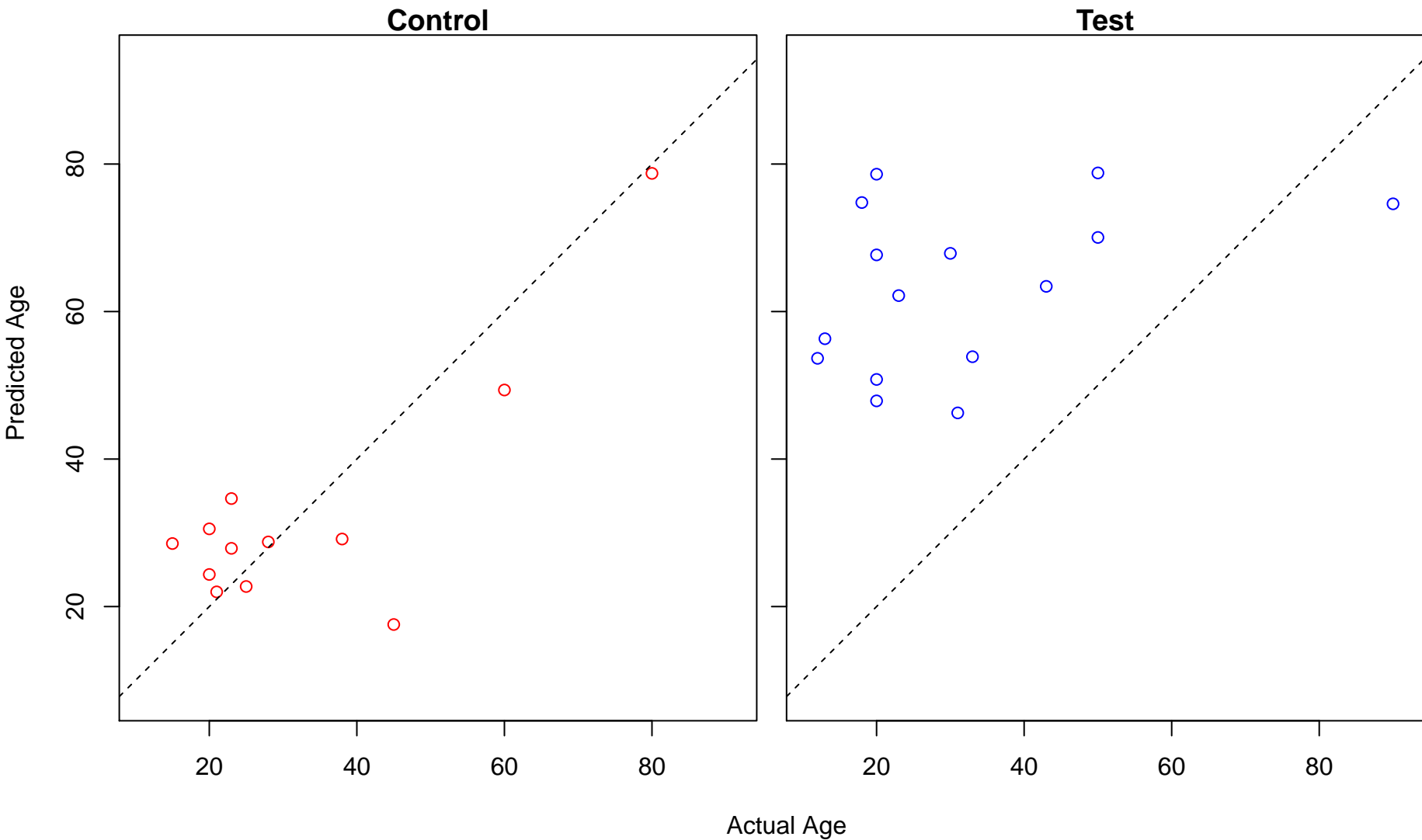
negative regulation of cyclic nucleotide biosynthetic process (Score: 4.206938)



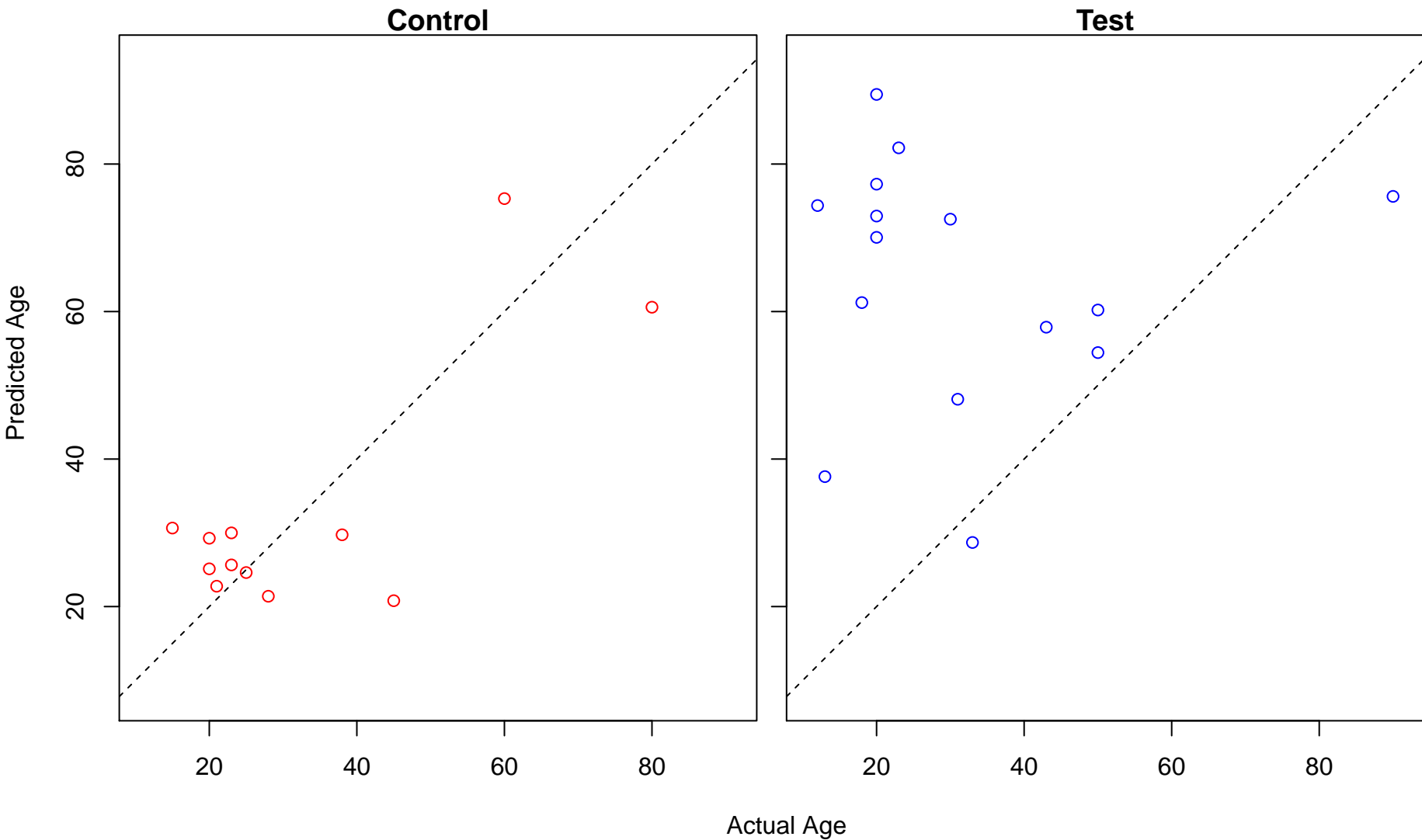
positive regulation of gene silencing by miRNA (Score: 4.206834)



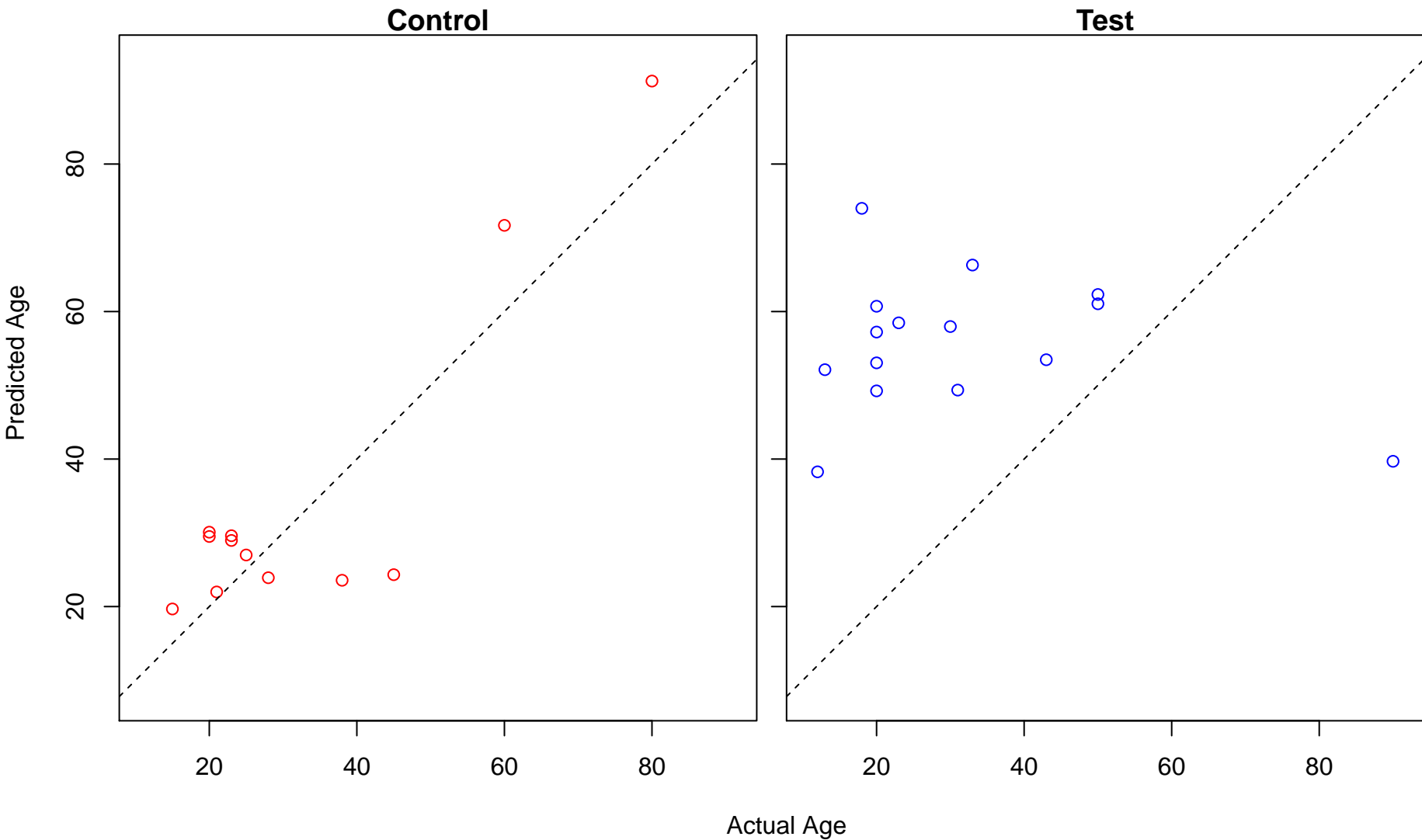
lymphocyte apoptotic process (Score: 4.206603)



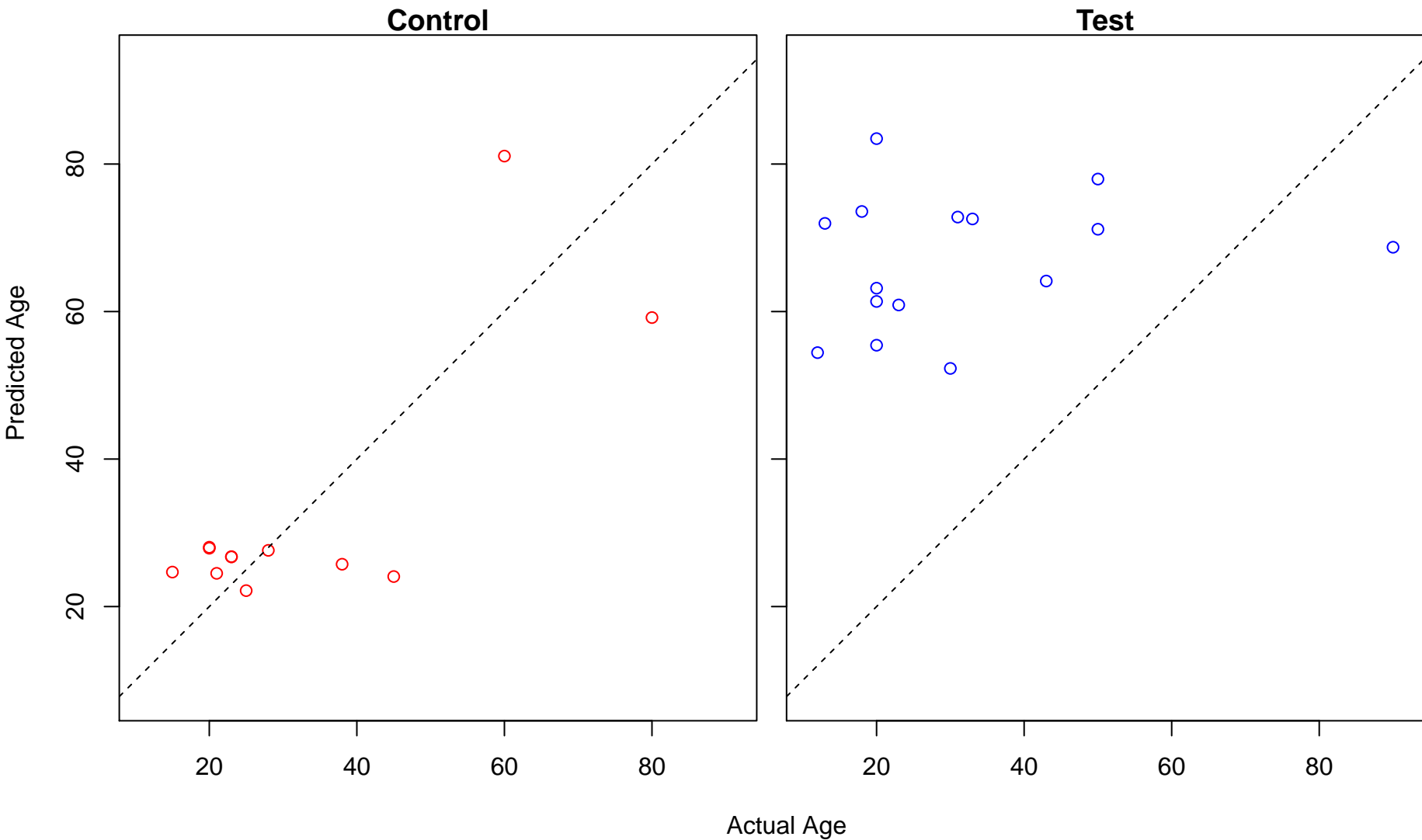
phenol-containing compound metabolic process (Score: 4.206109)



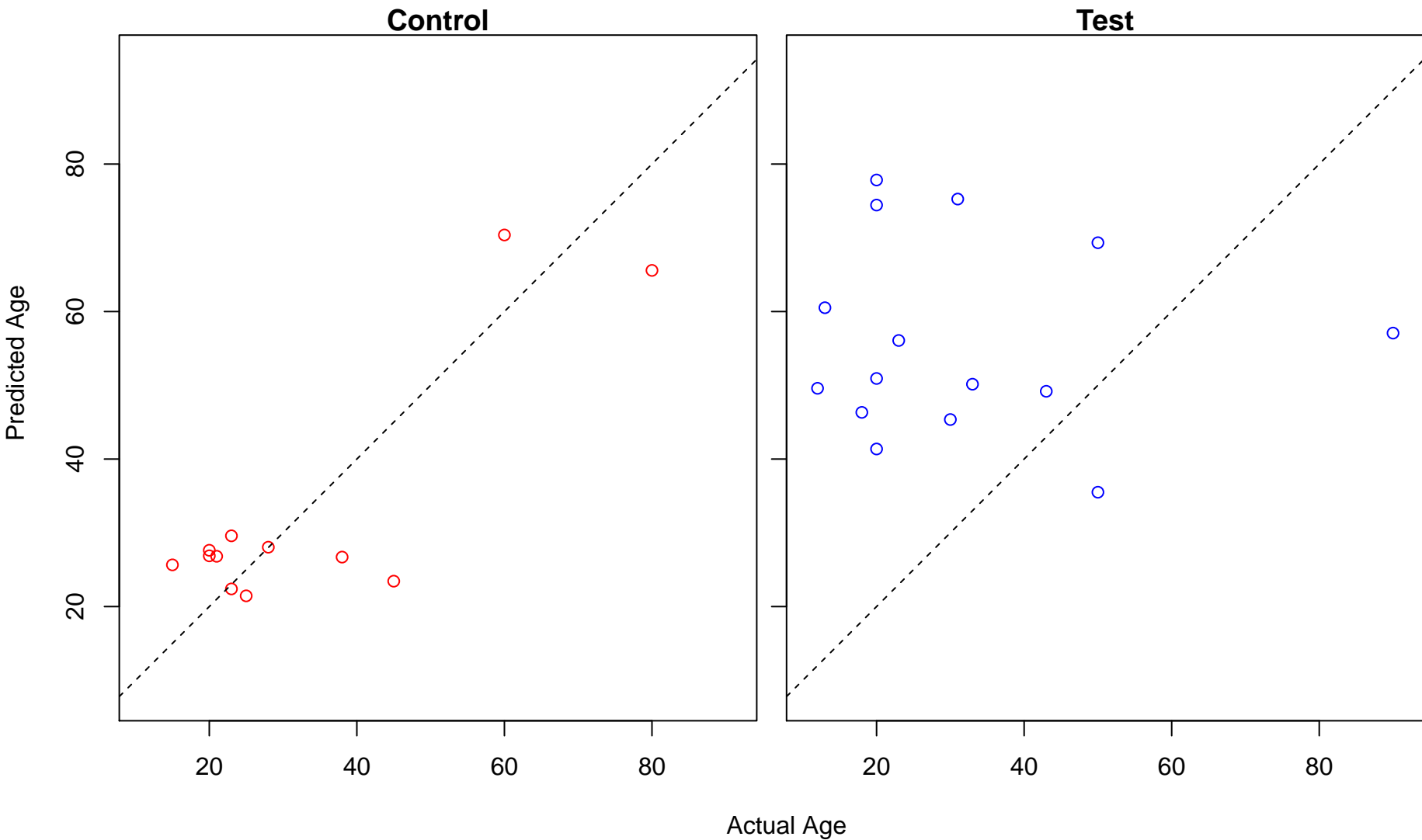
C-terminal protein deglutamylation (Score: 4.204831)



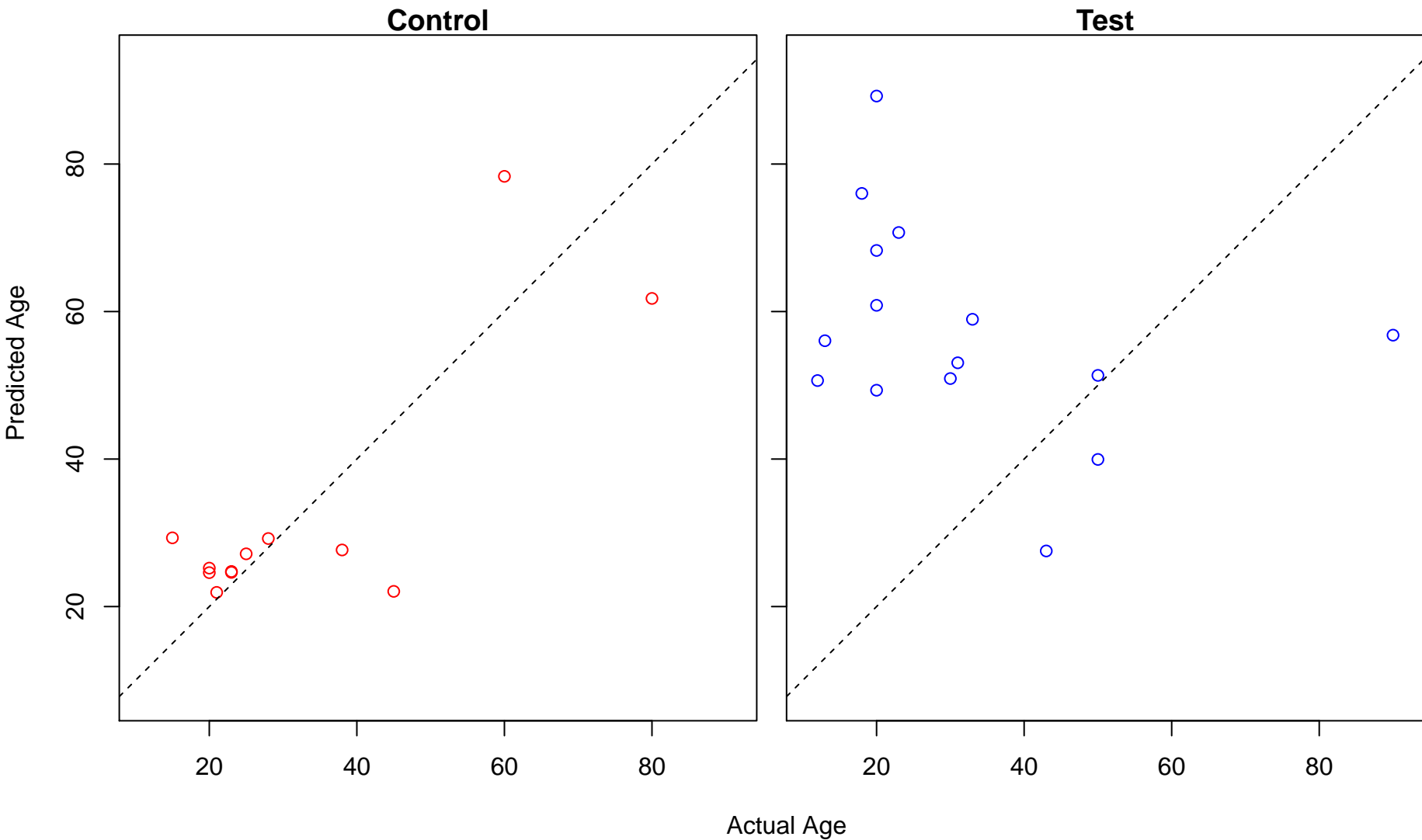
cell differentiation involved in kidney development (Score: 4.202566)



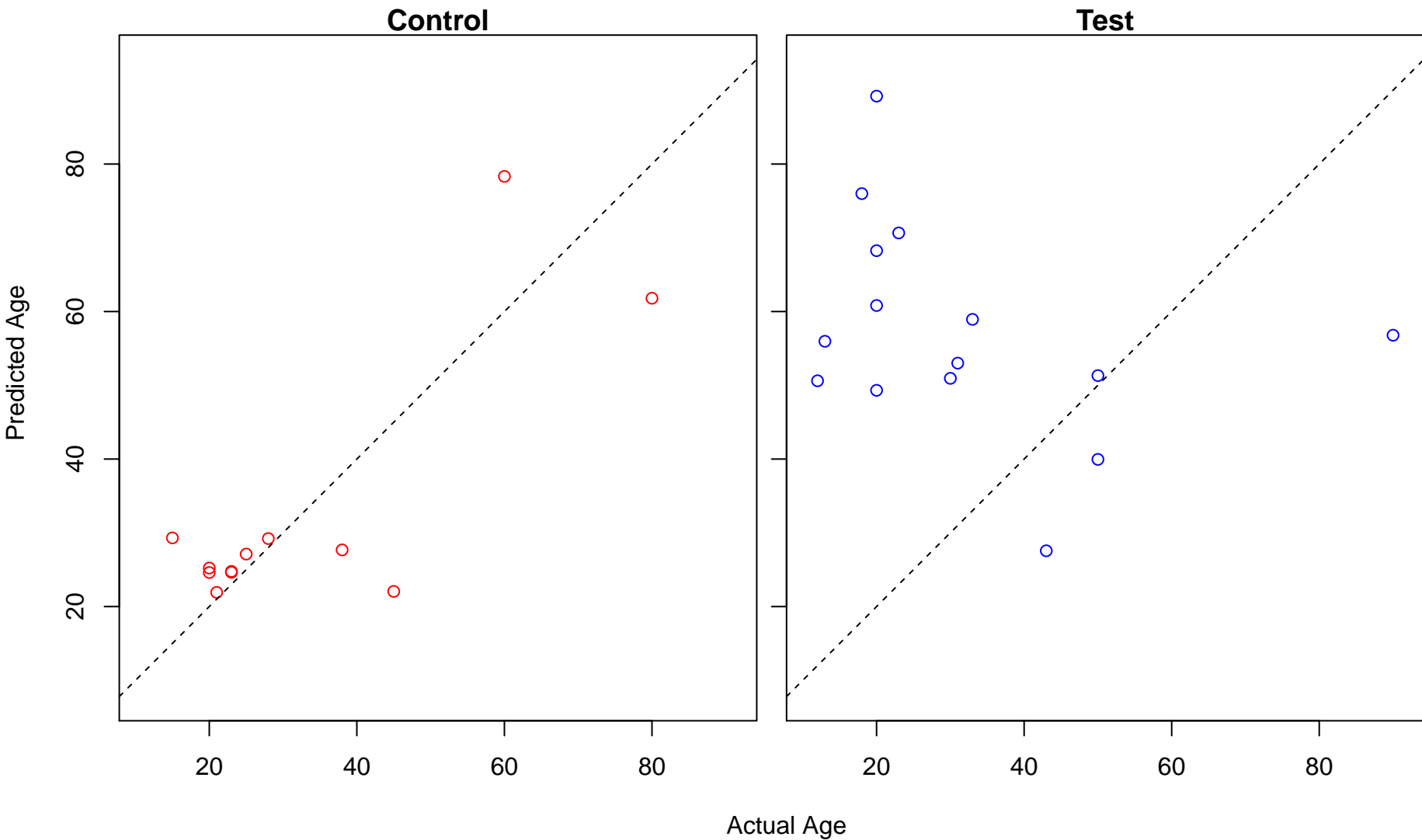
response to calcium ion (Score: 4.202513)



BMP signaling pathway (Score: 4.201329)

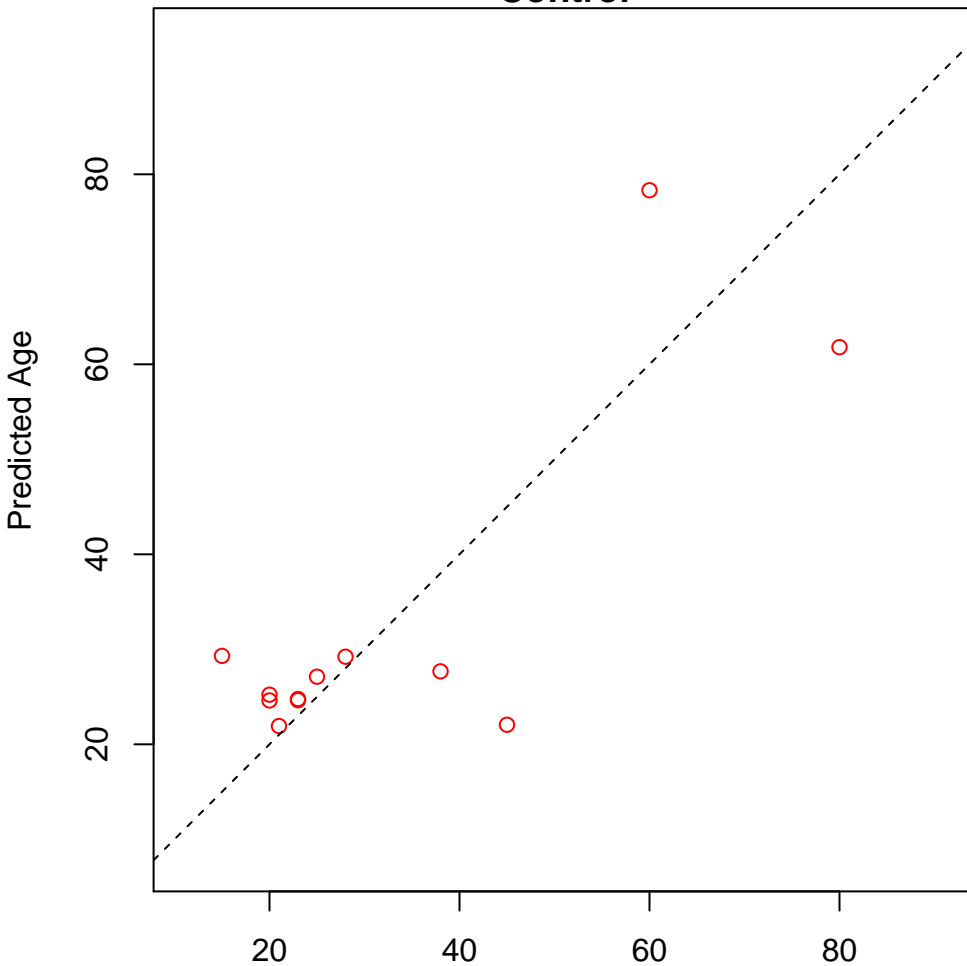


response to BMP (Score: 4.200494)

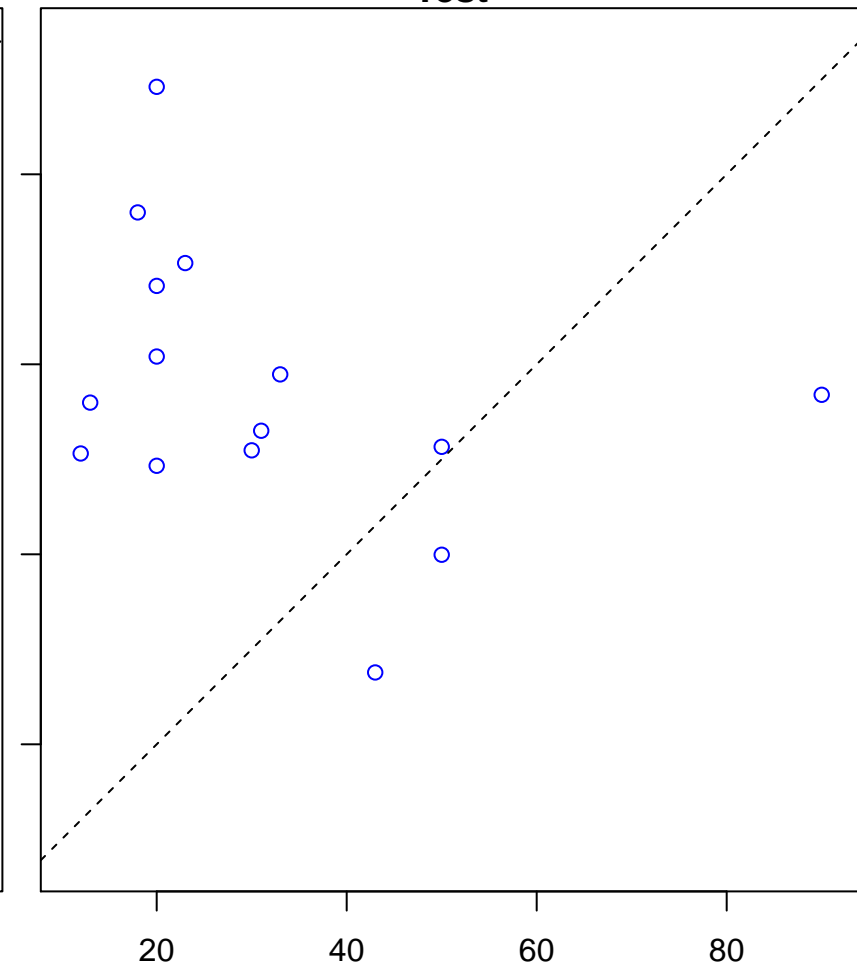


cellular response to BMP stimulus (Score: 4.200494)

Control

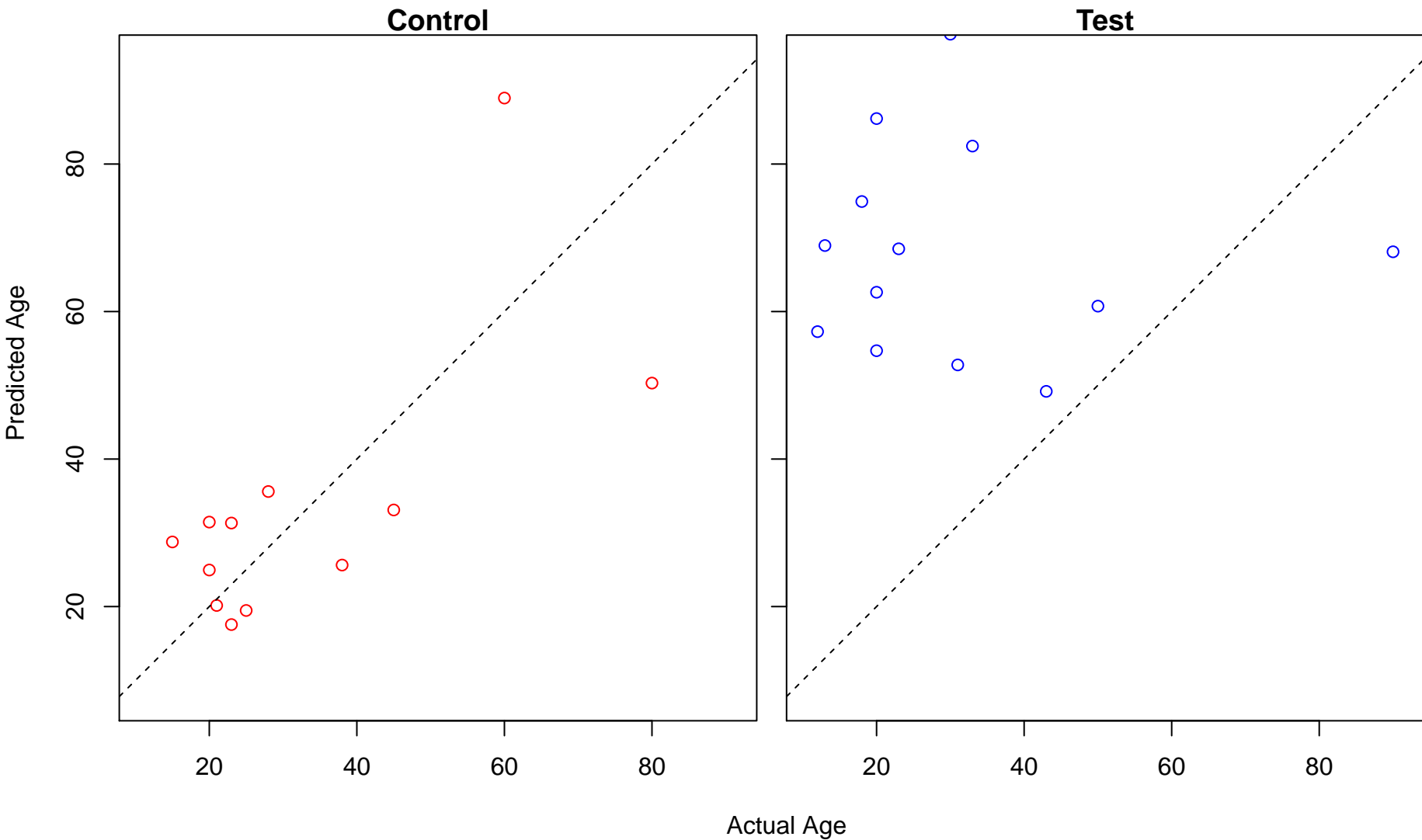


Test

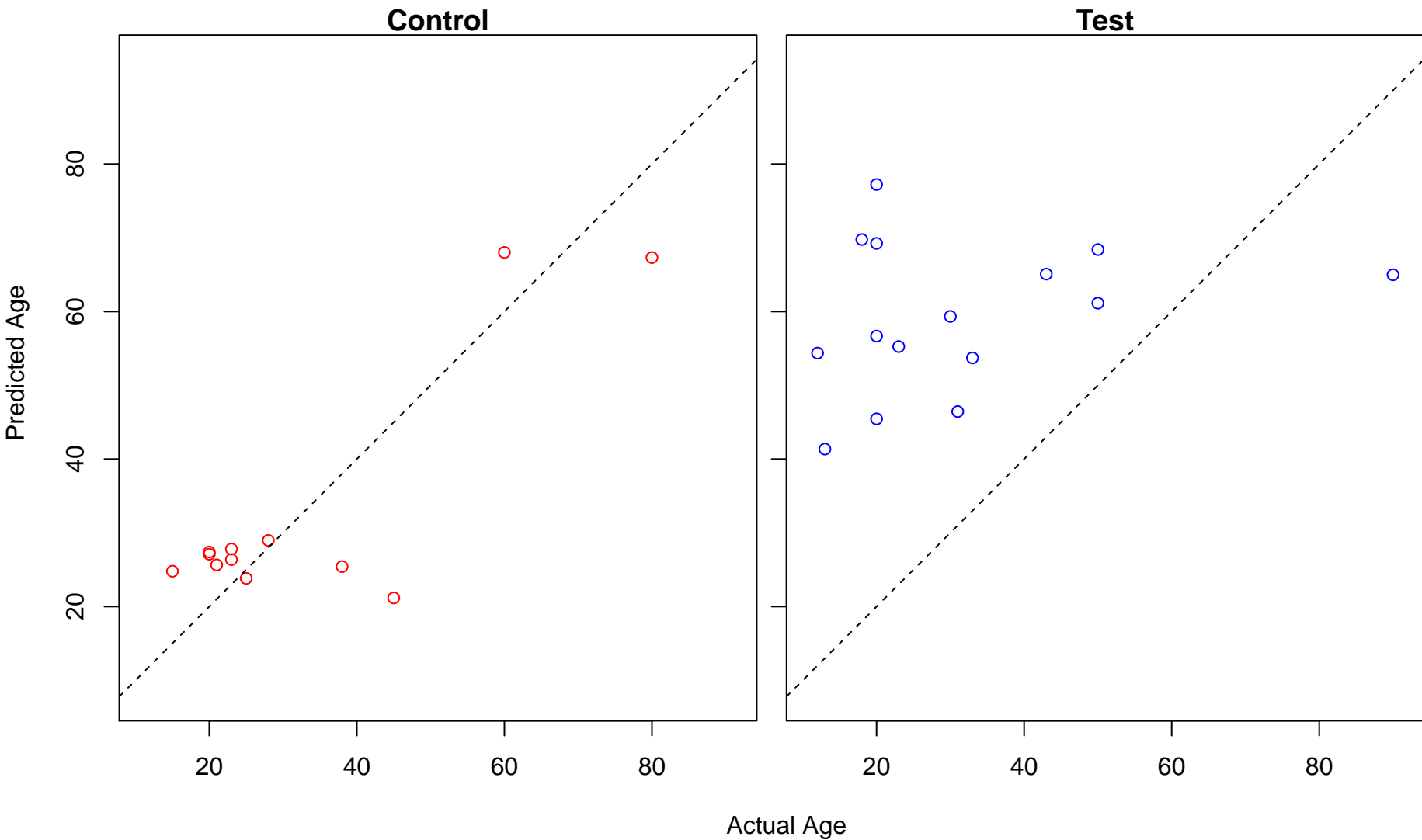


Actual Age

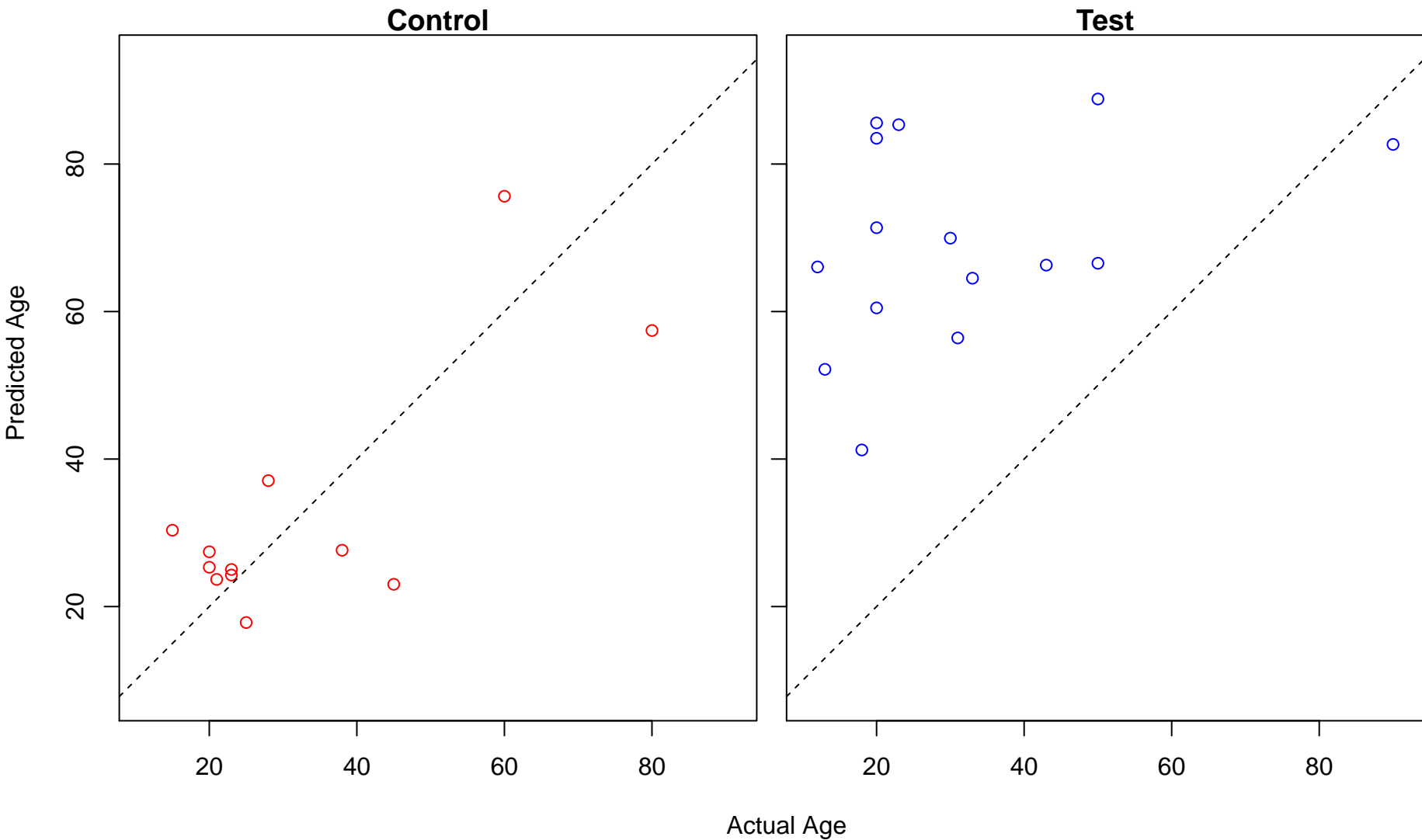
positive regulation of anoikis (Score: 4.200419)



cardiolipin metabolic process (Score: 4.199787)

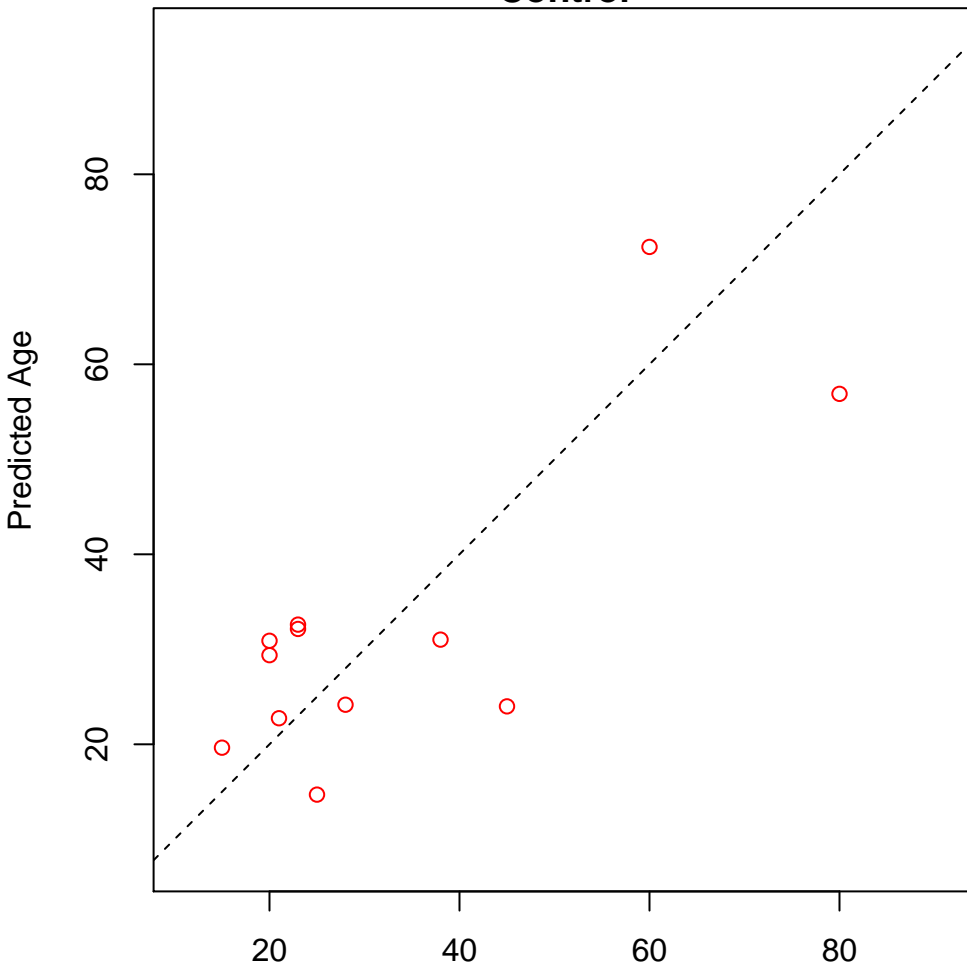


regulation of insulin-like growth factor receptor signaling pathway (Score: 4.198329)

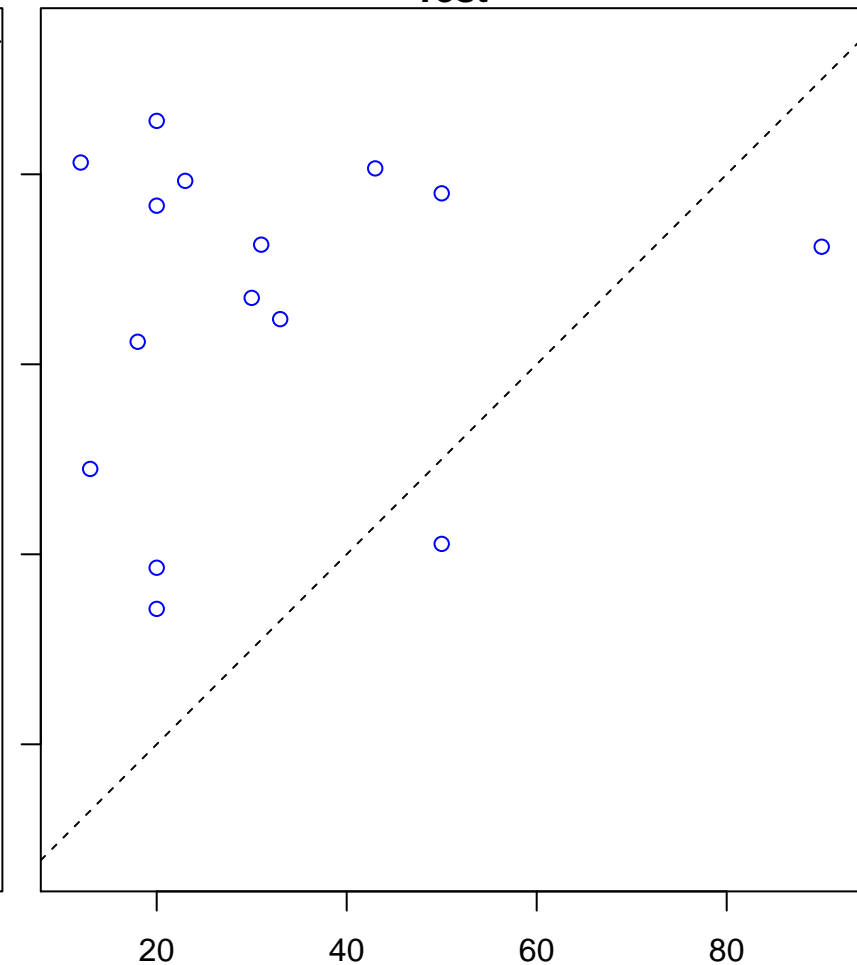


vascular smooth muscle contraction (Score: 4.197442)

Control

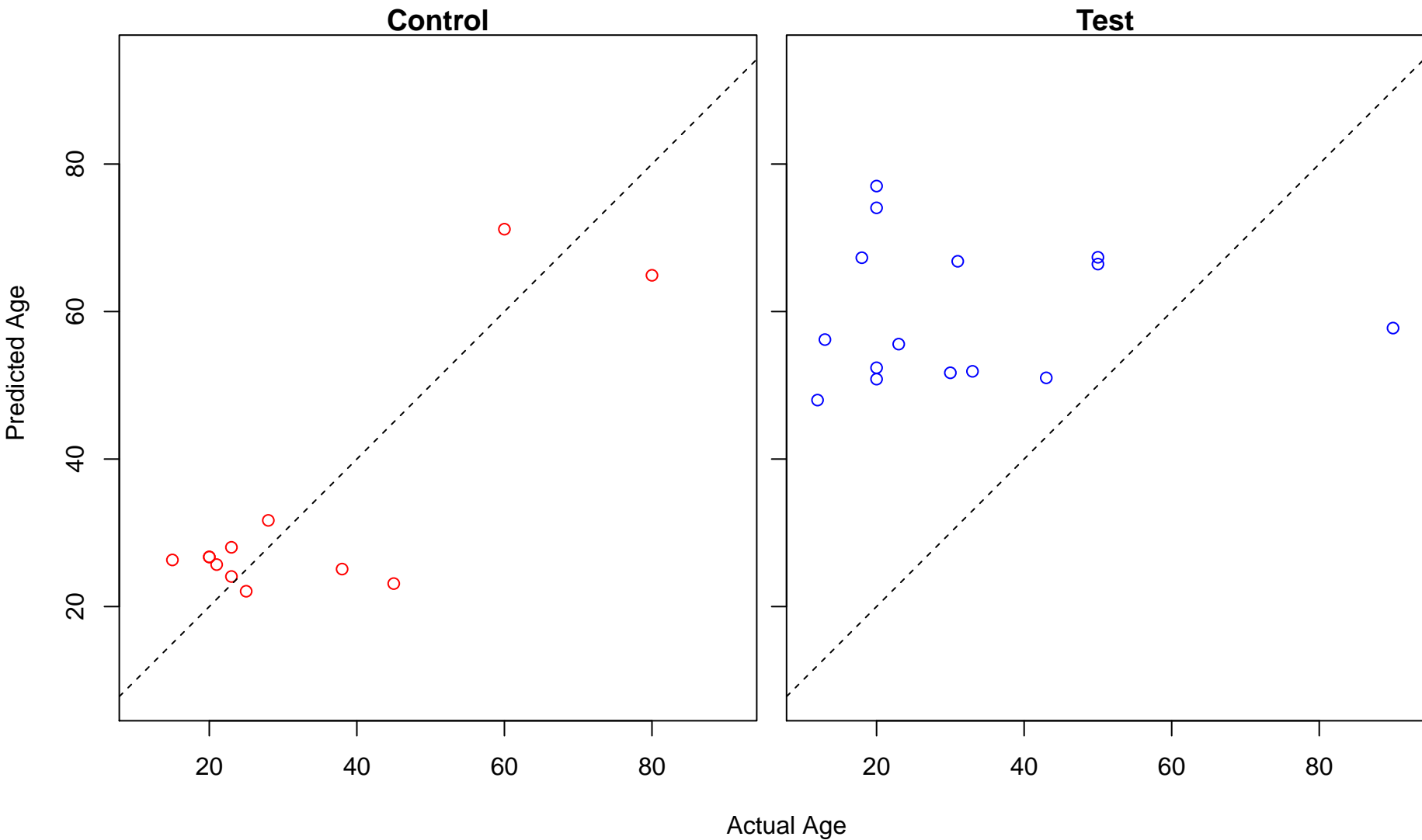


Test

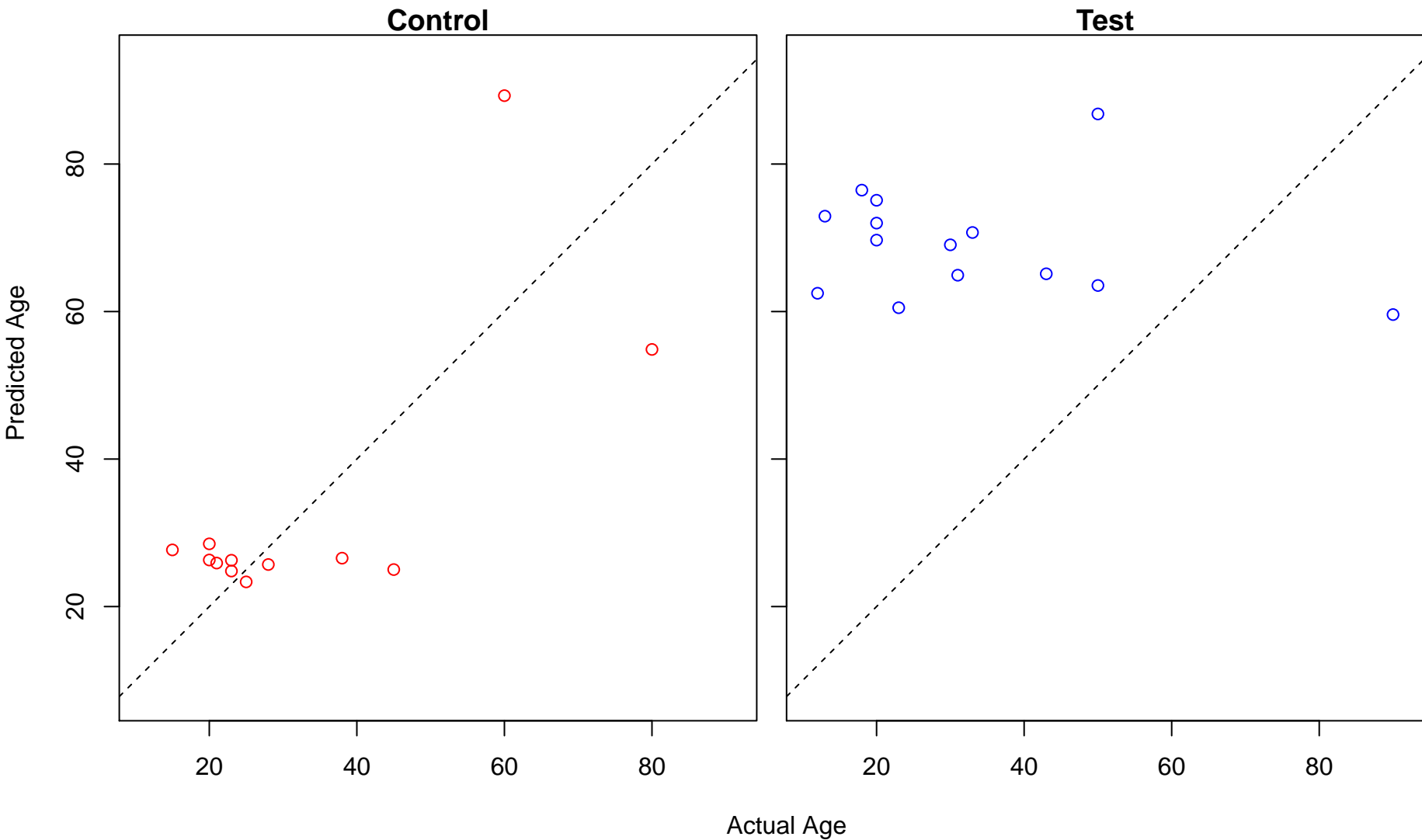


Actual Age

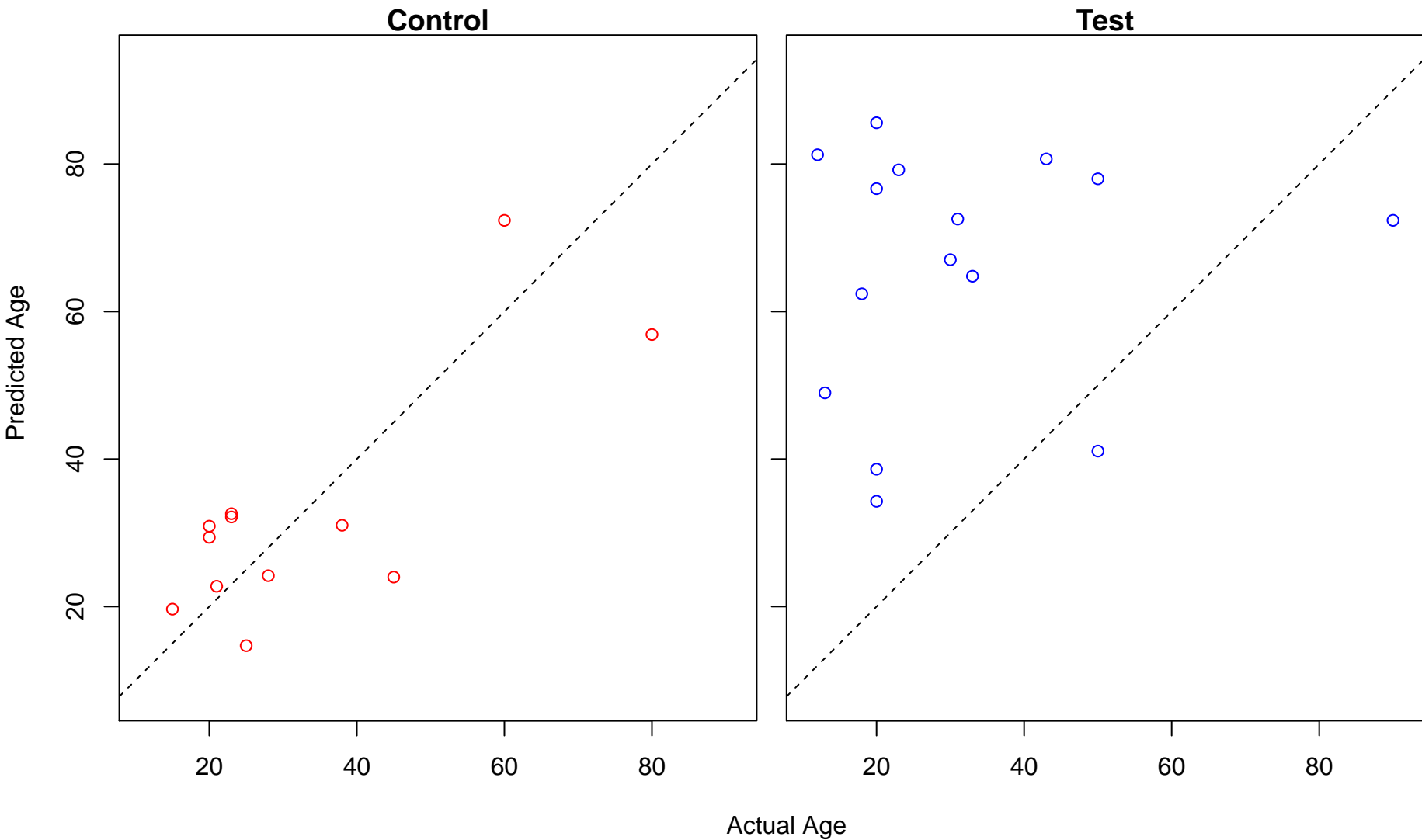
negative regulation of cation channel activity (Score: 4.196864)



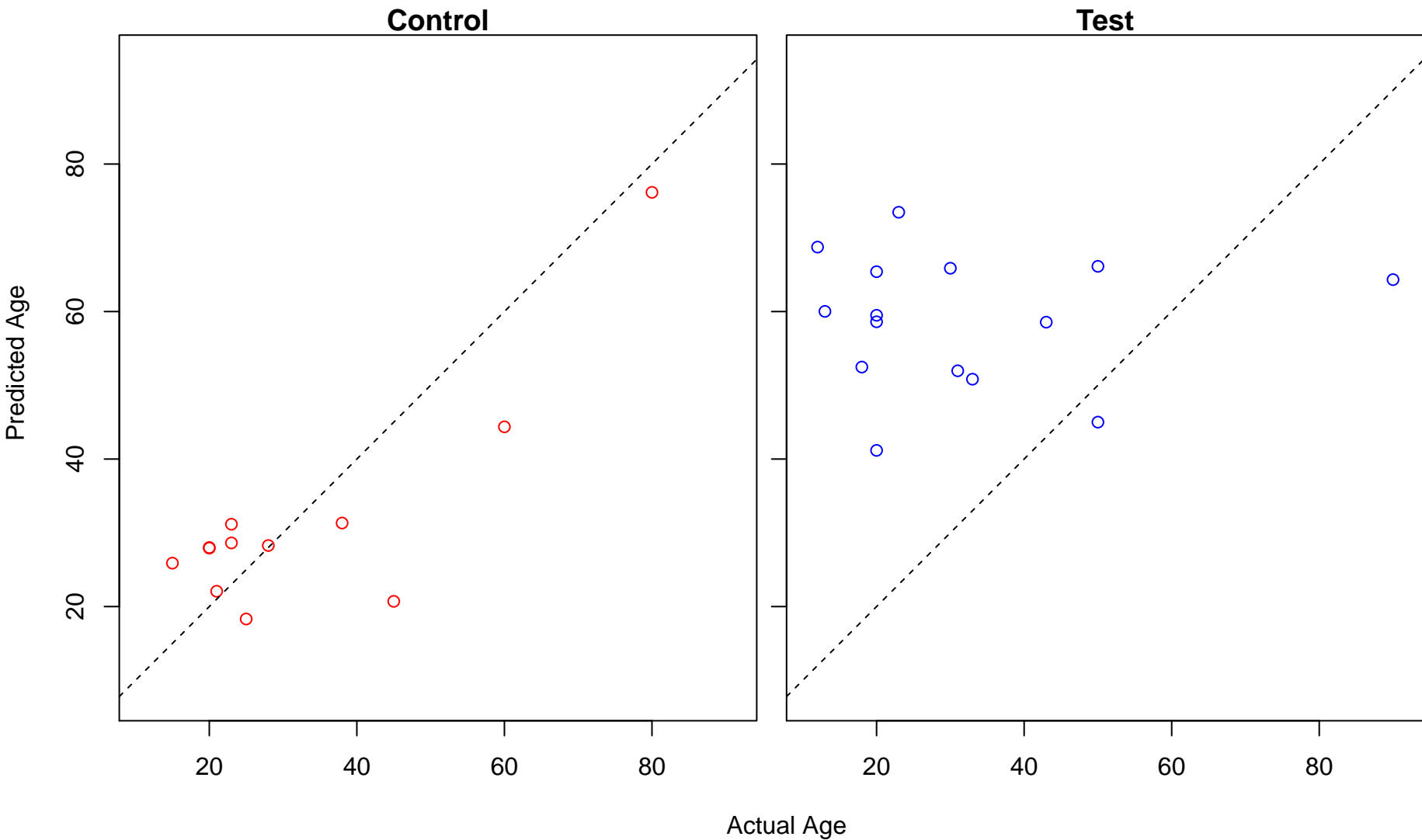
regulation of mitochondrial membrane permeability (Score: 4.195999)



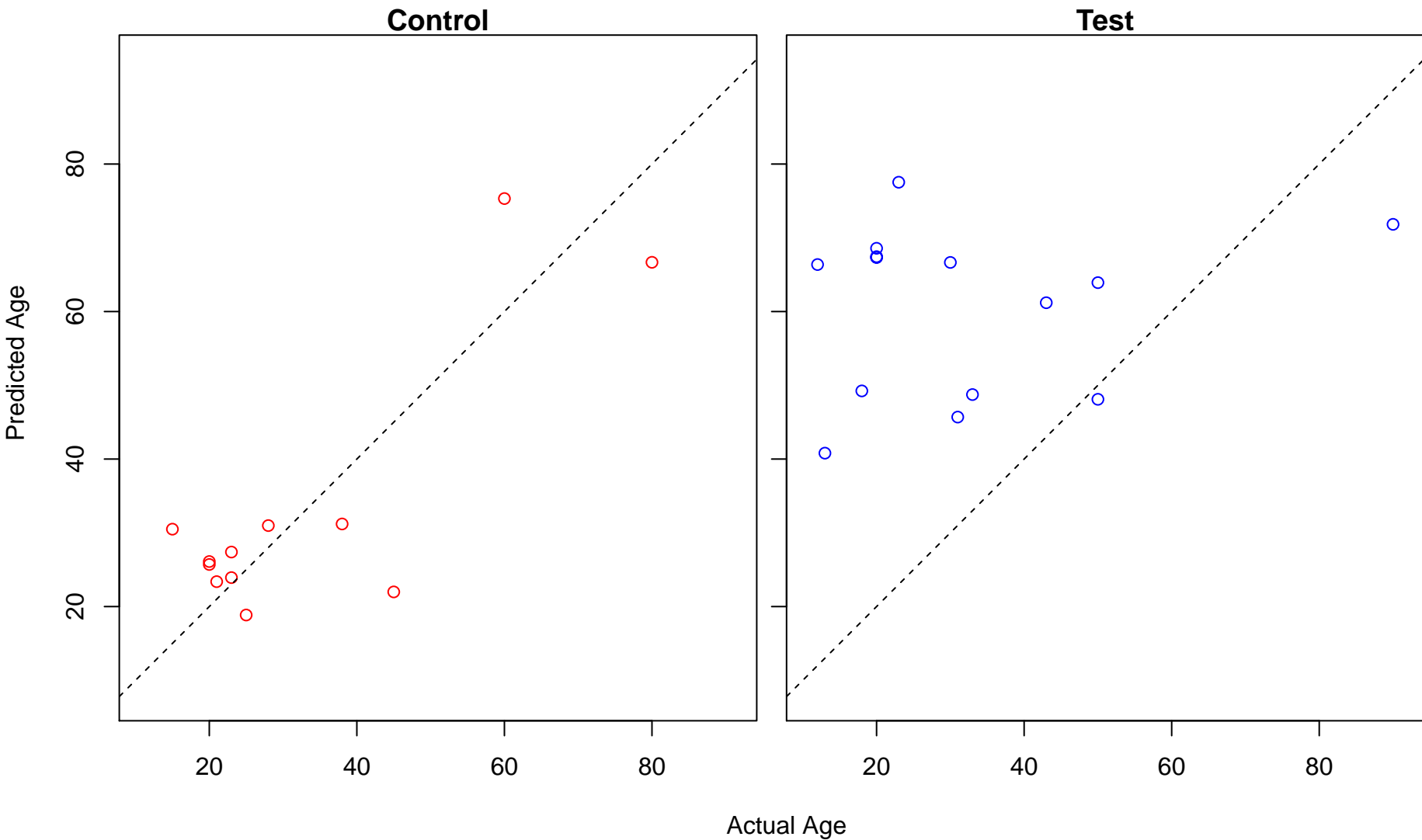
vasoconstriction (Score: 4.195315)



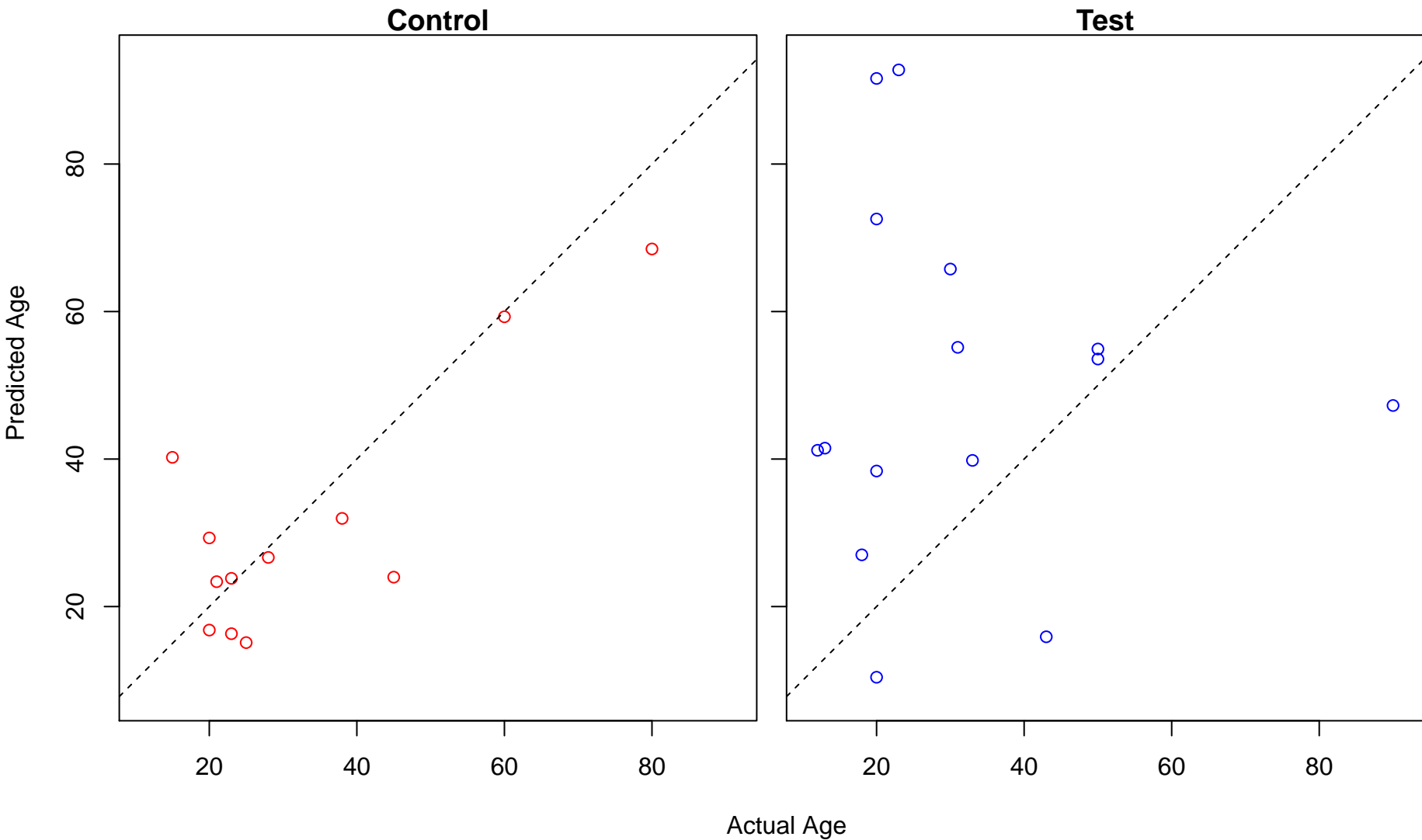
positive regulation of posttranscriptional gene silencing (Score: 4.194655)



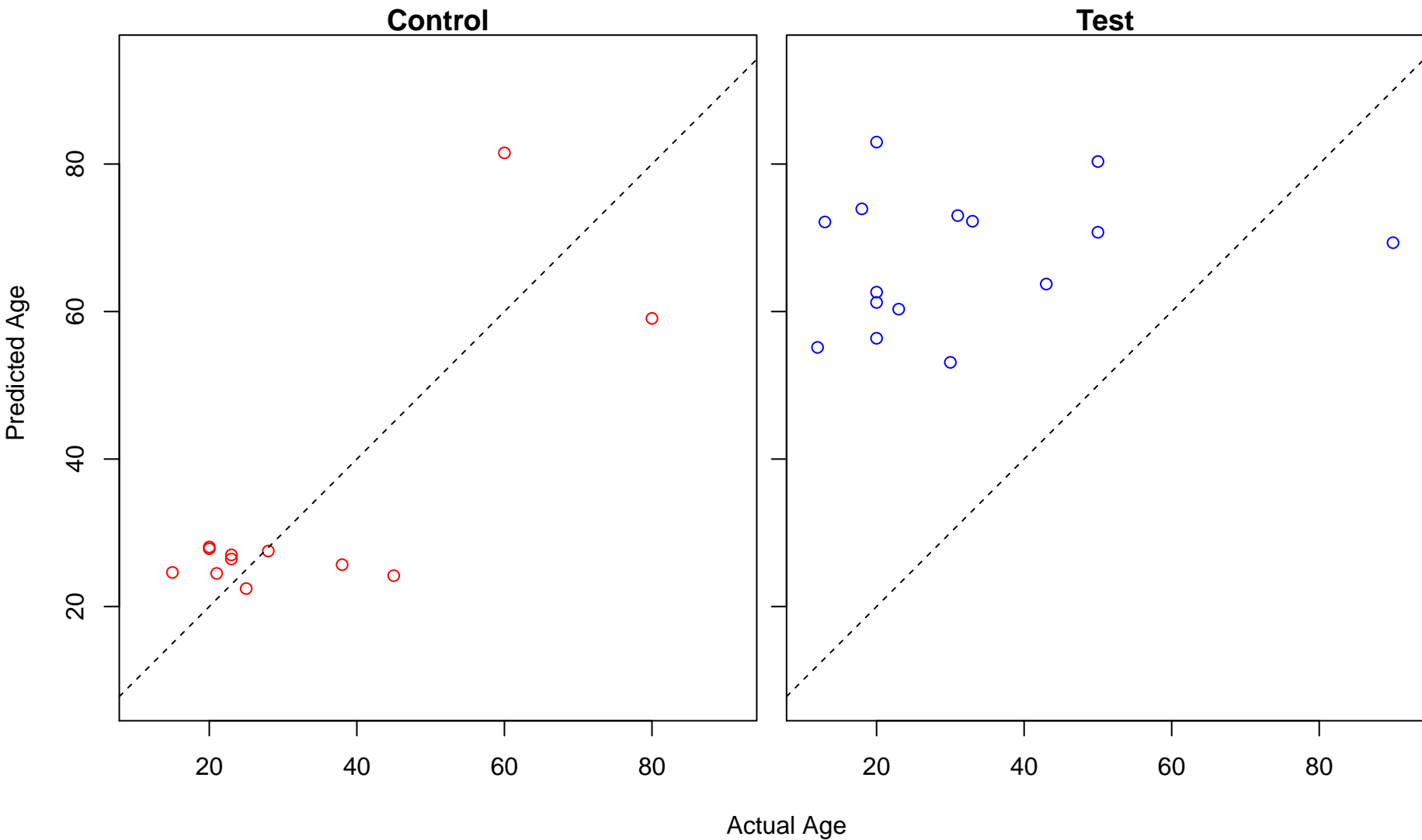
regulation of peptidyl-serine phosphorylation (Score: 4.194596)



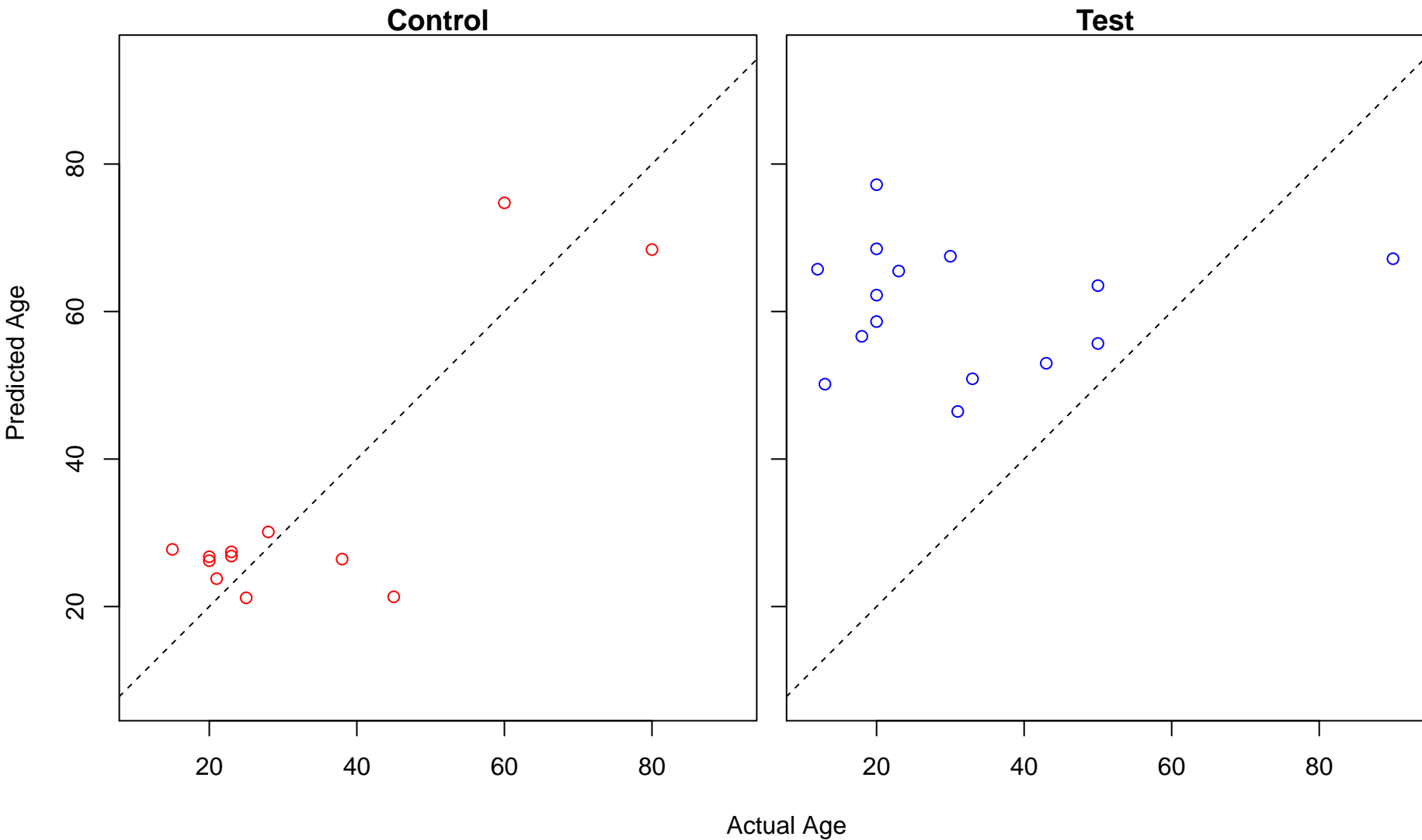
neural retina development (Score: 4.194469)



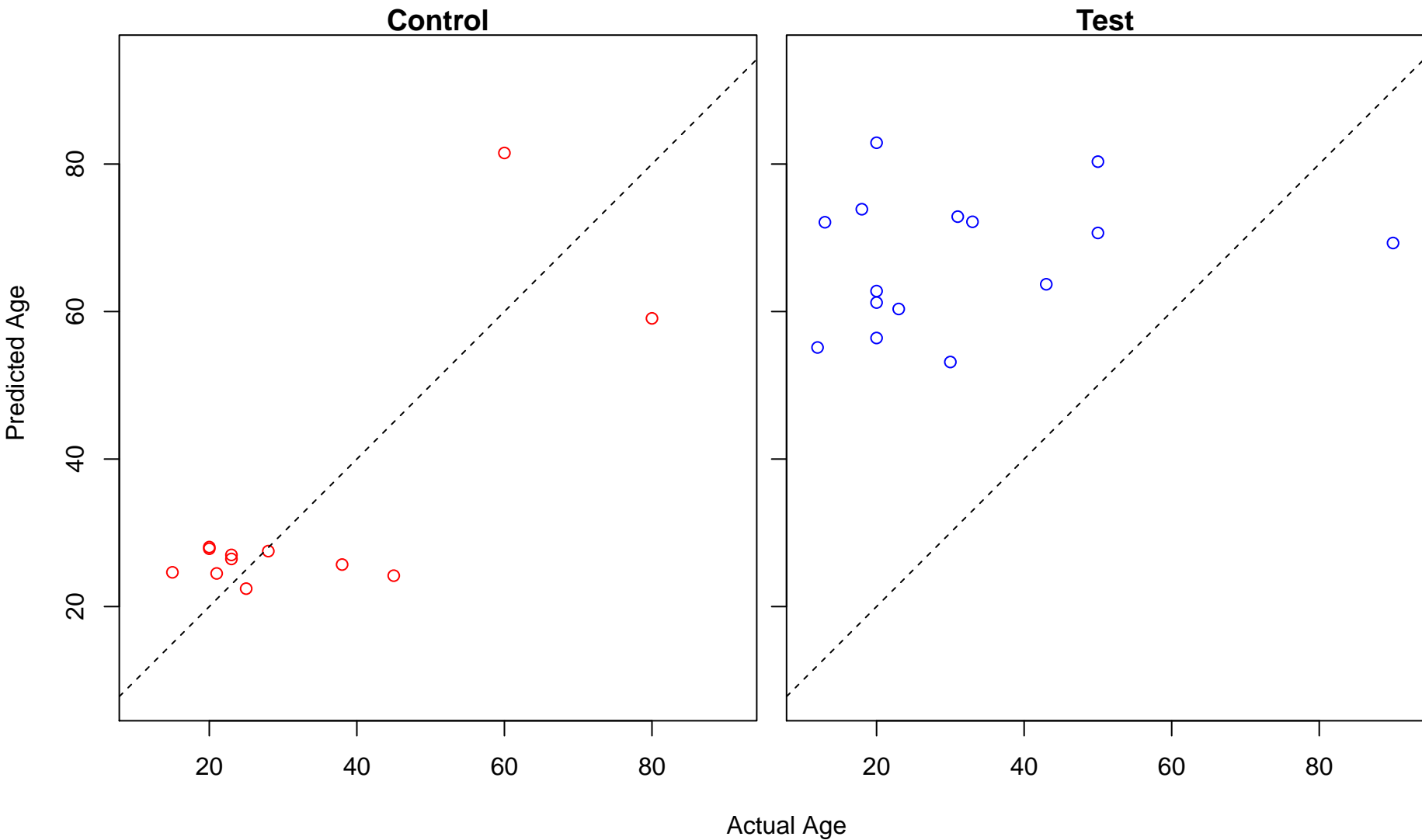
glomerulus development (Score: 4.194422)



vesicle targeting (Score: 4.193594)

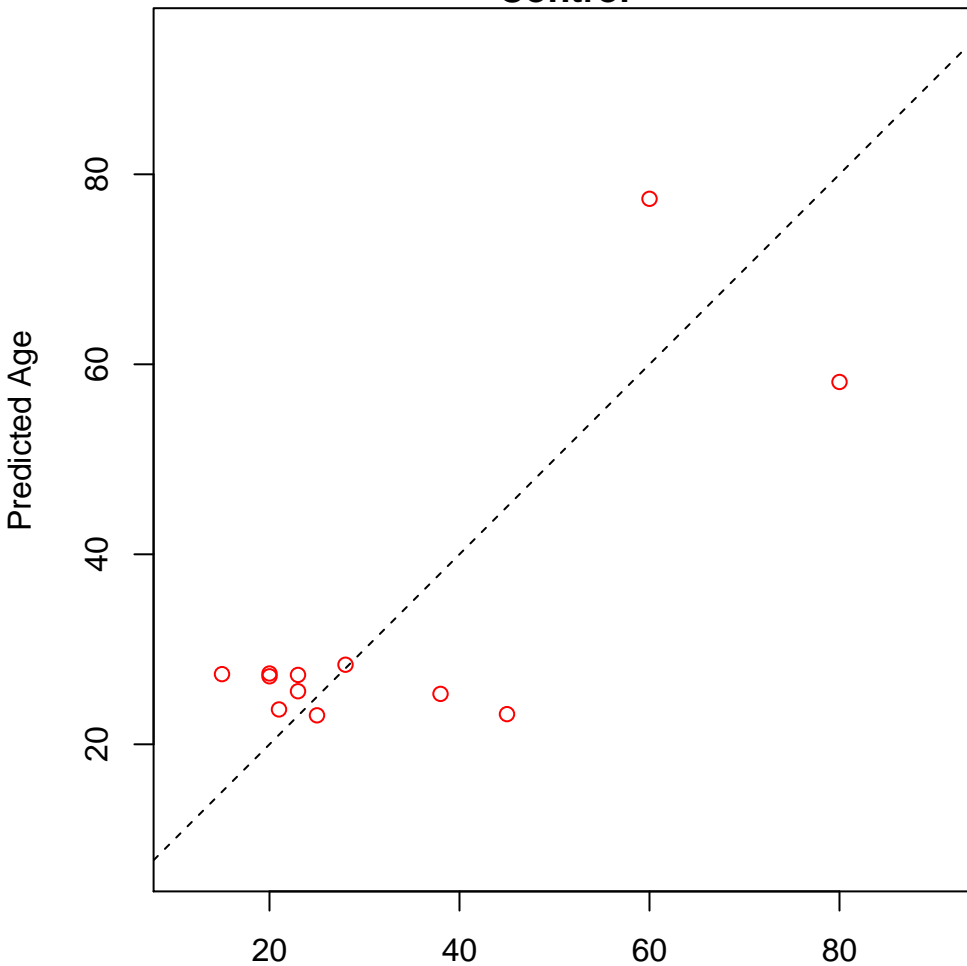


nephron development (Score: 4.192634)

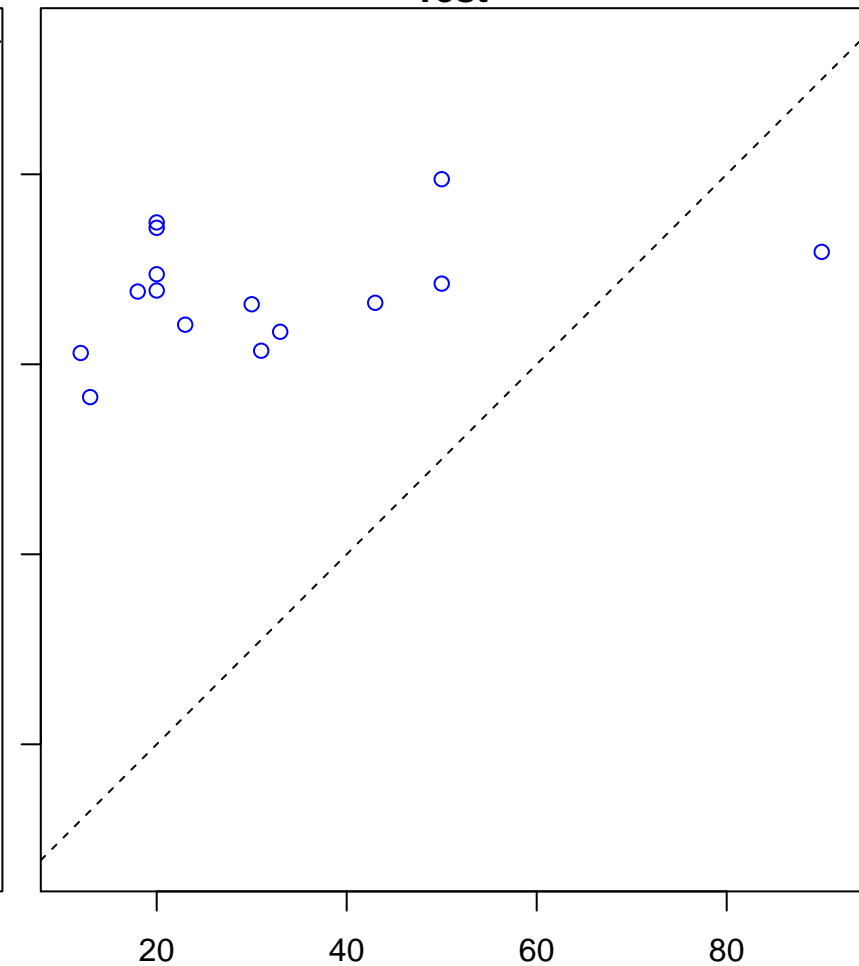


odontogenesis of dentin-containing tooth (Score: 4.190946)

Control



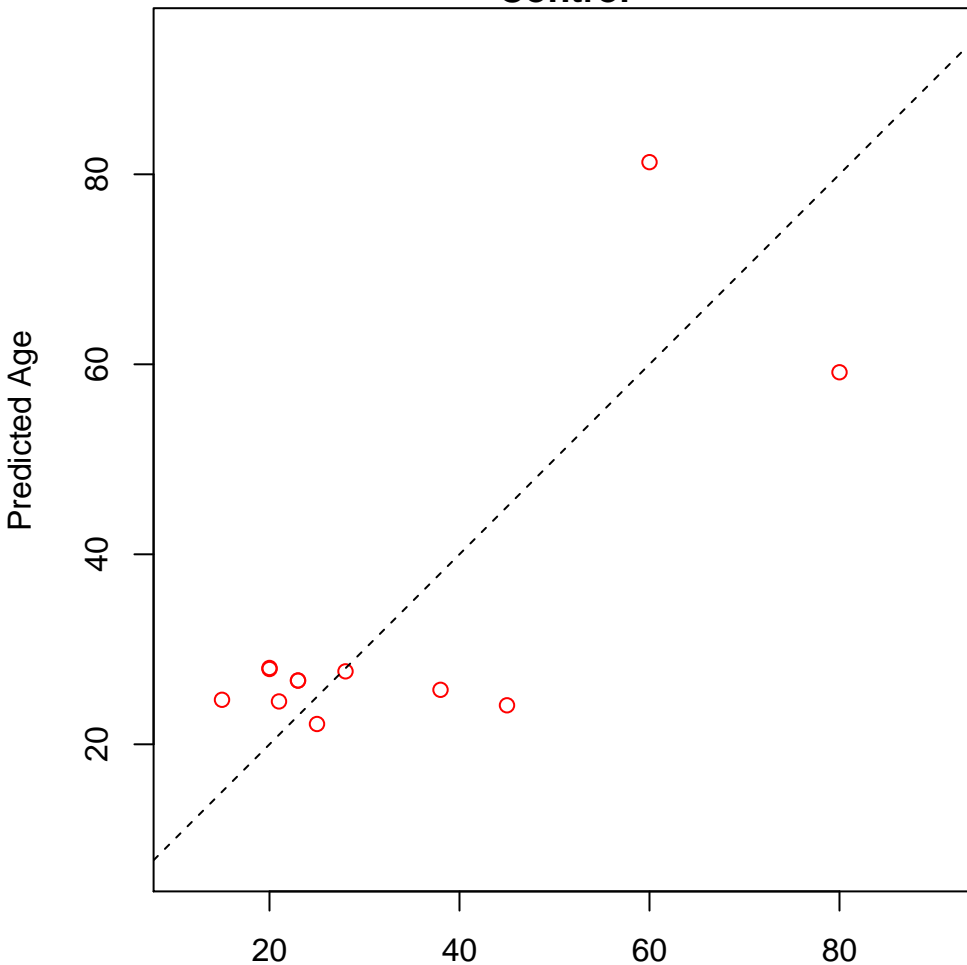
Test



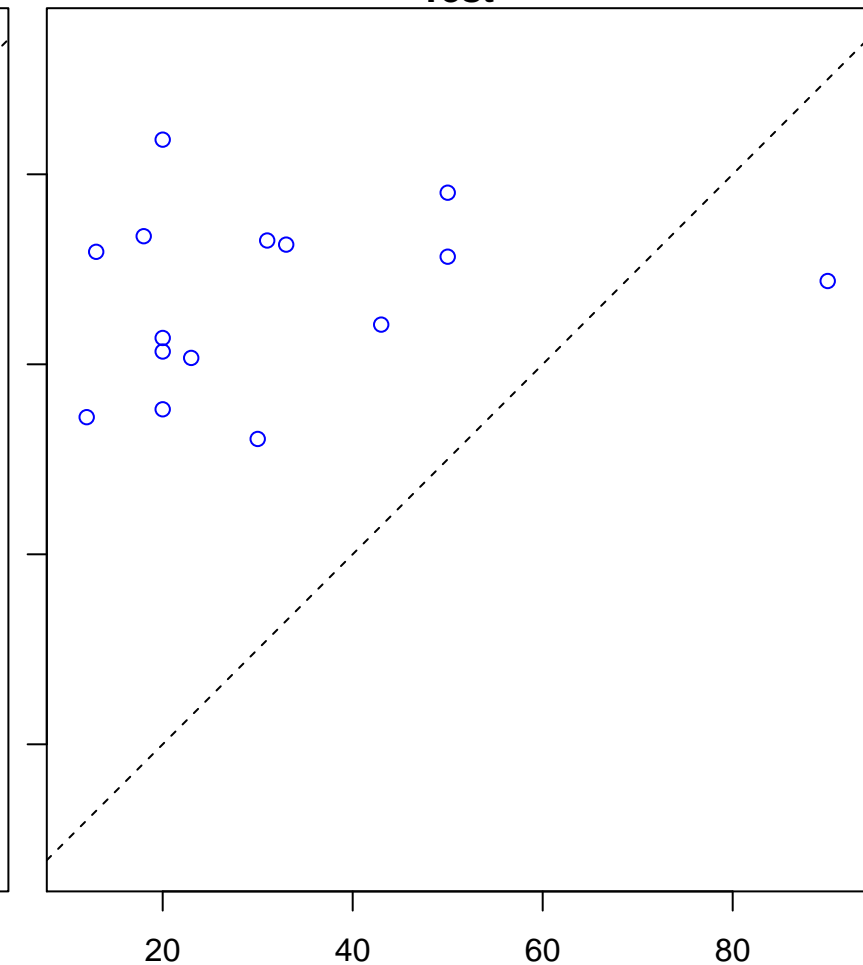
Actual Age

glomerular epithelium development (Score: 4.186104)

Control



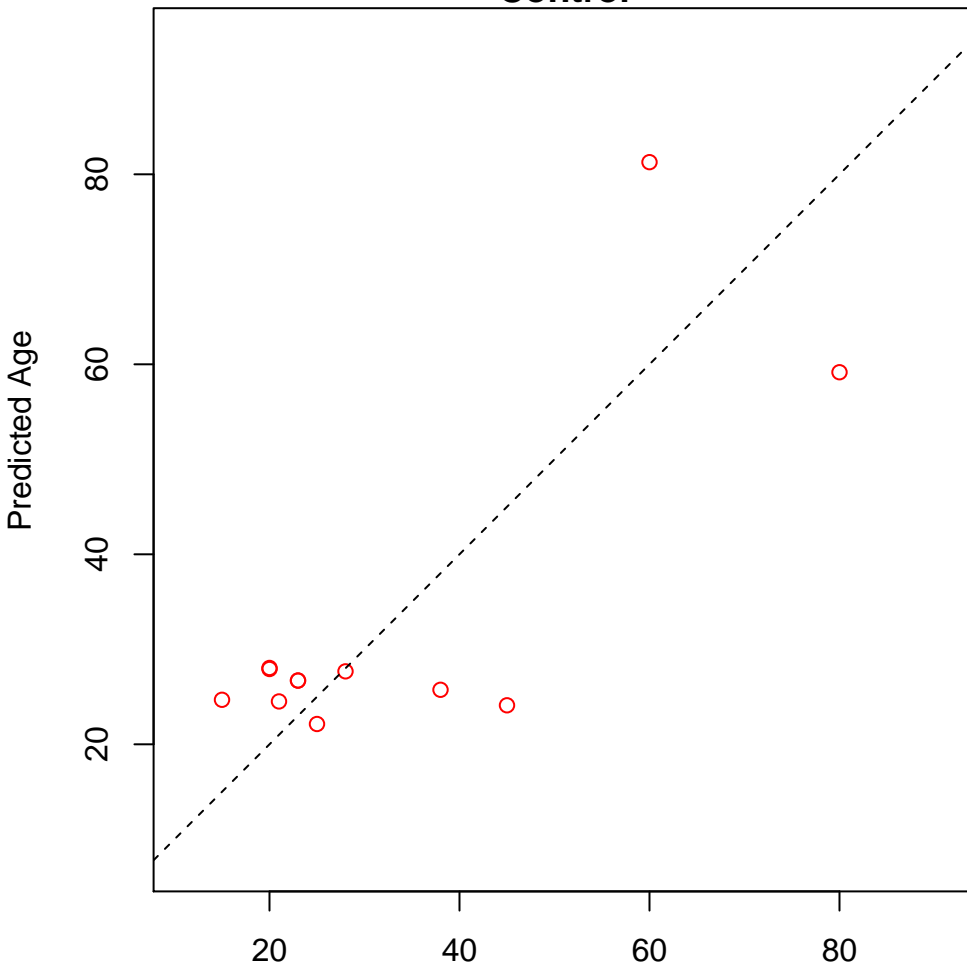
Test



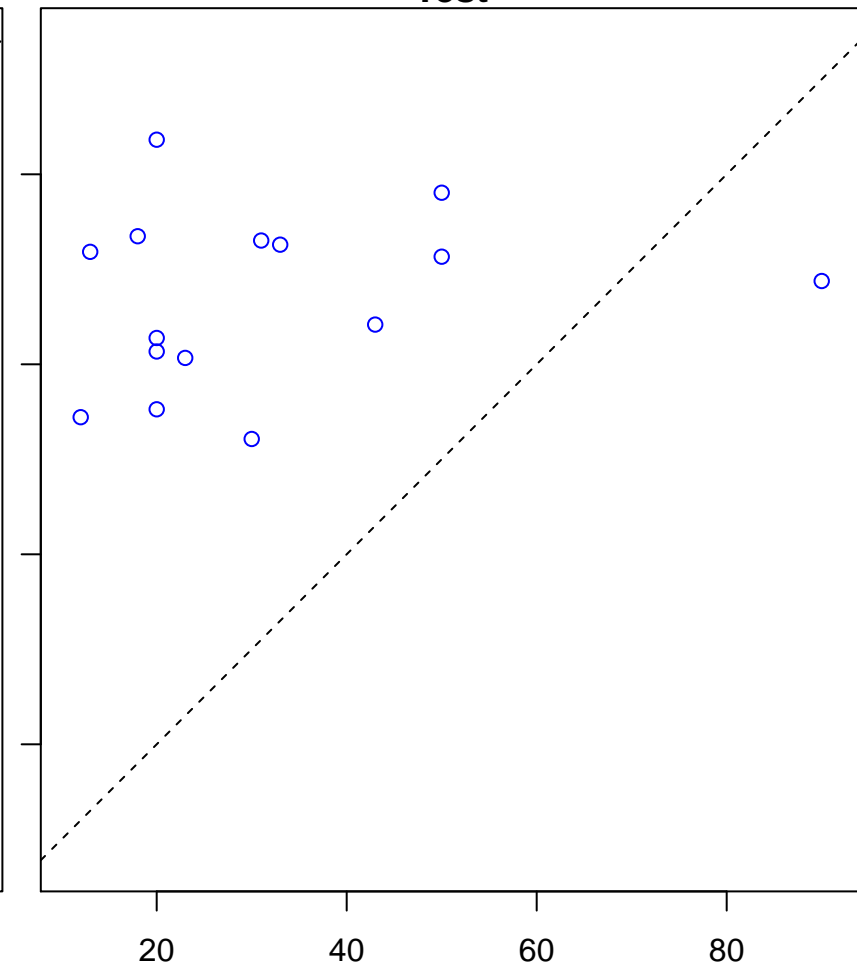
Actual Age

glomerular epithelial cell differentiation (Score: 4.185971)

Control

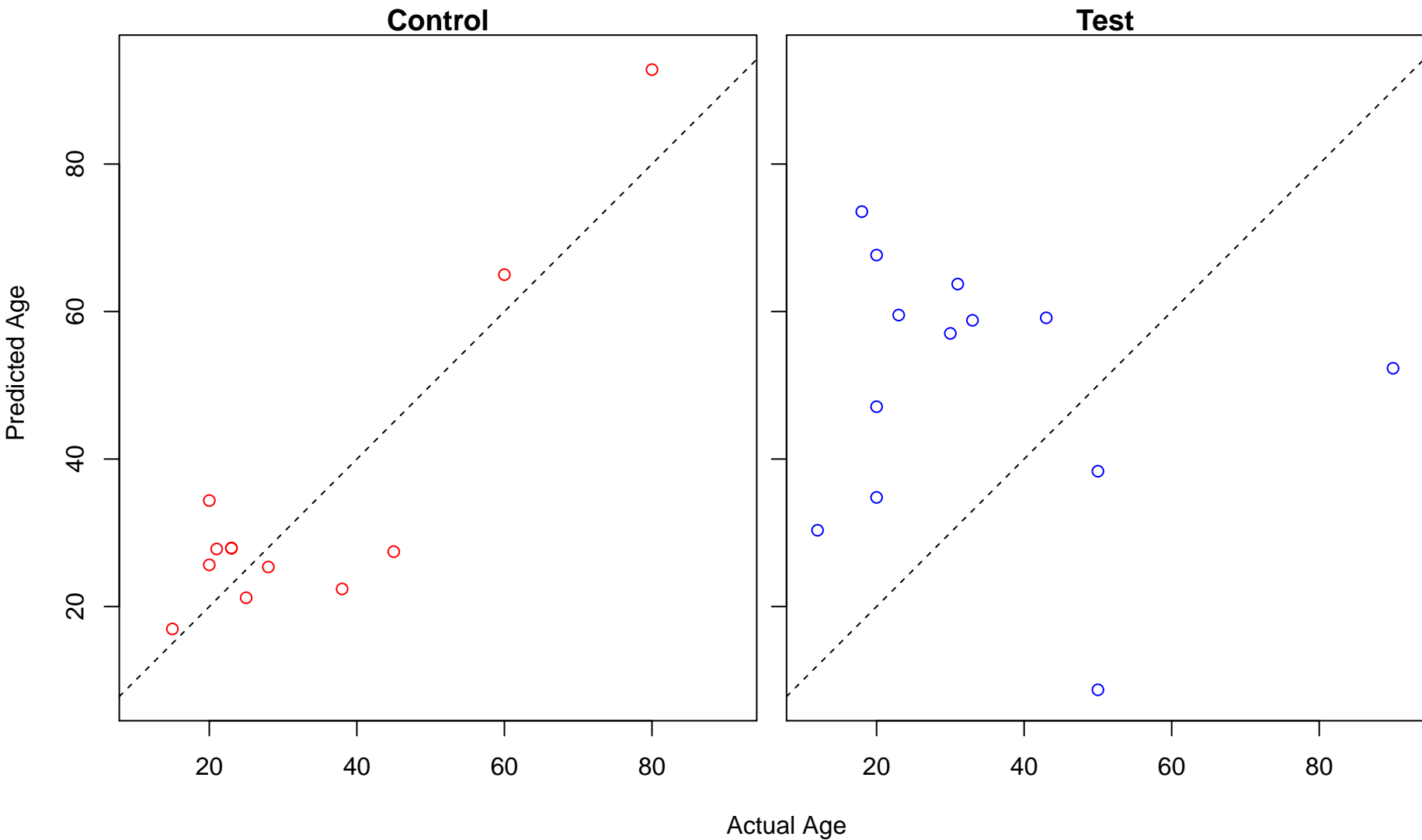


Test

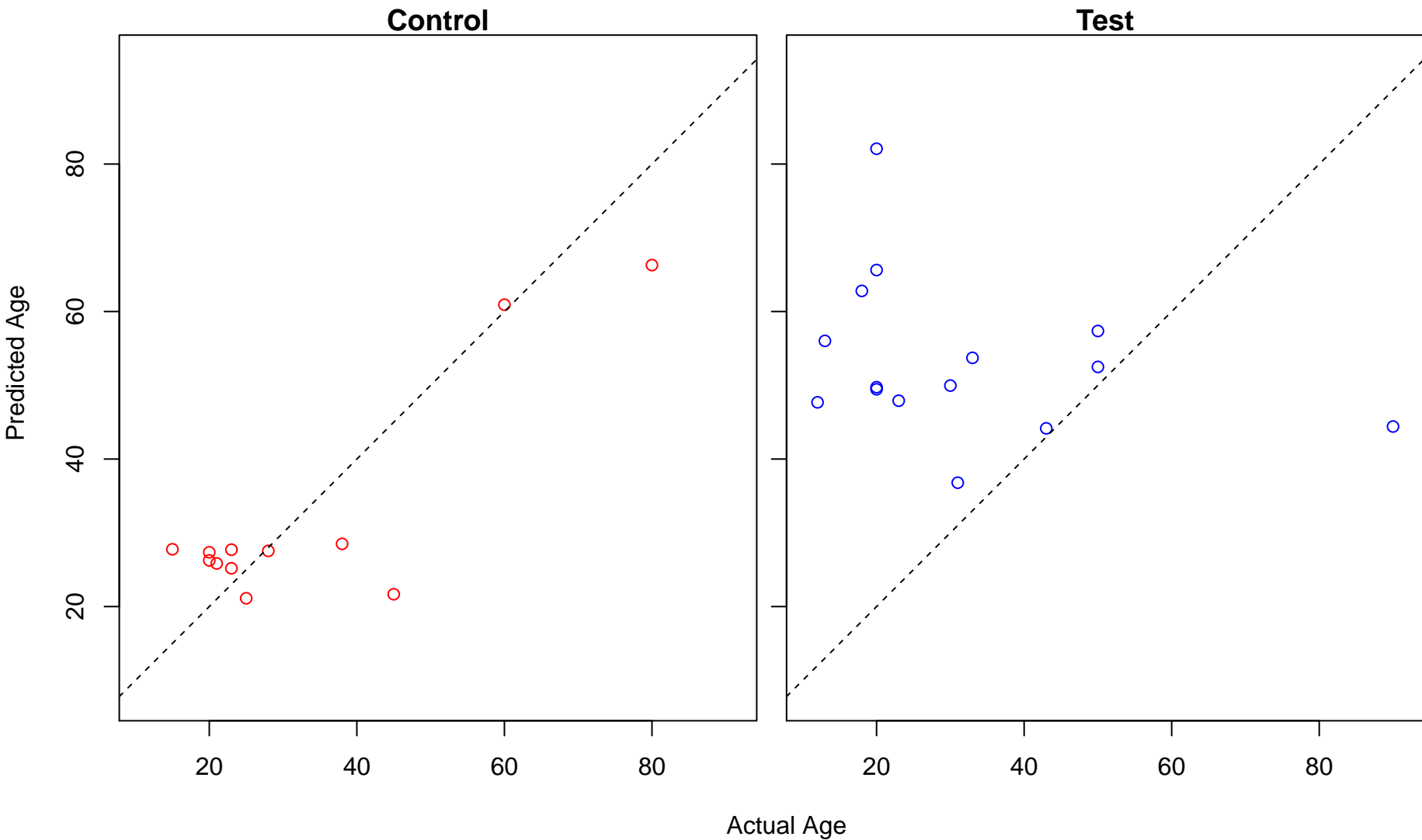


Actual Age

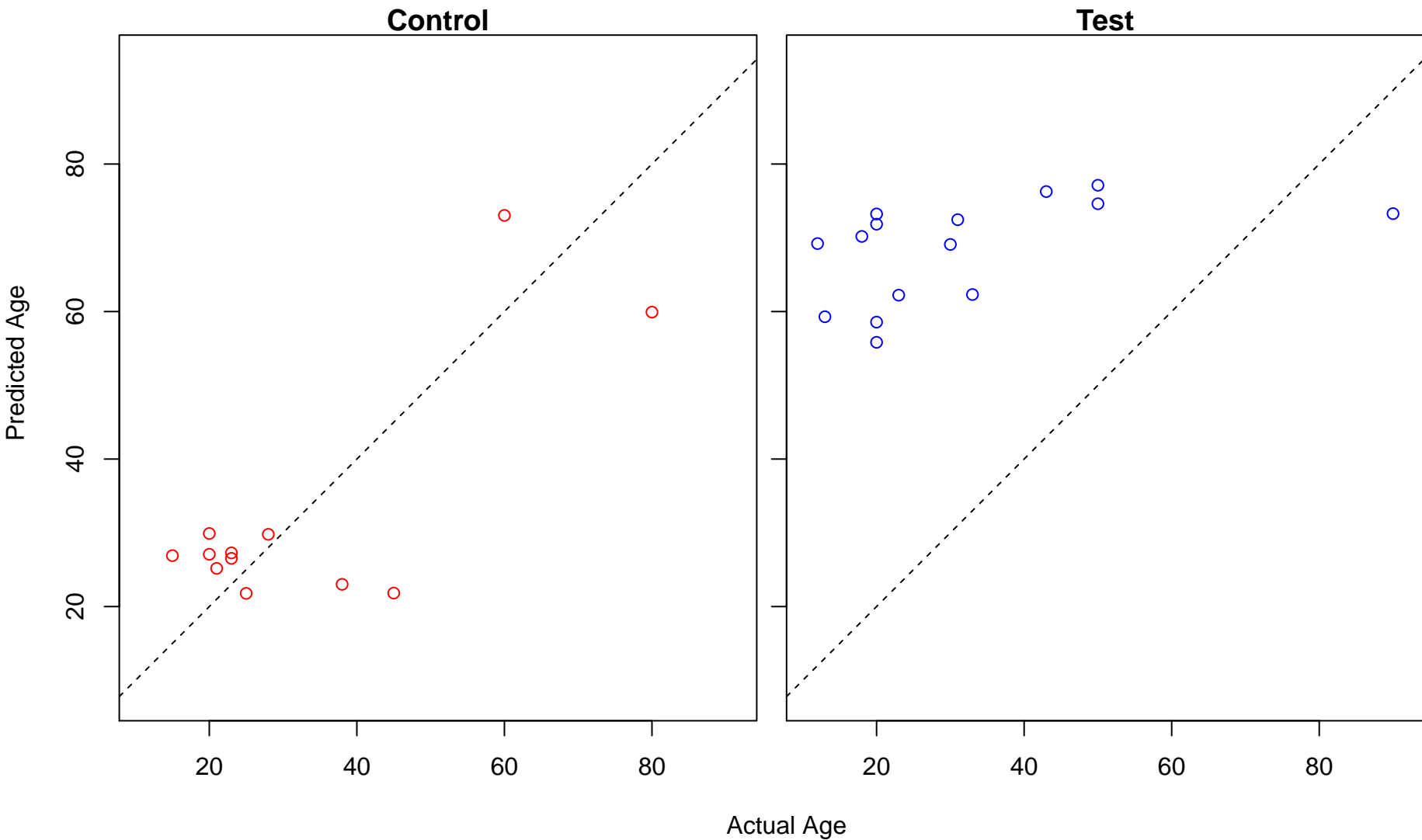
cell differentiation in hindbrain (Score: 4.185674)



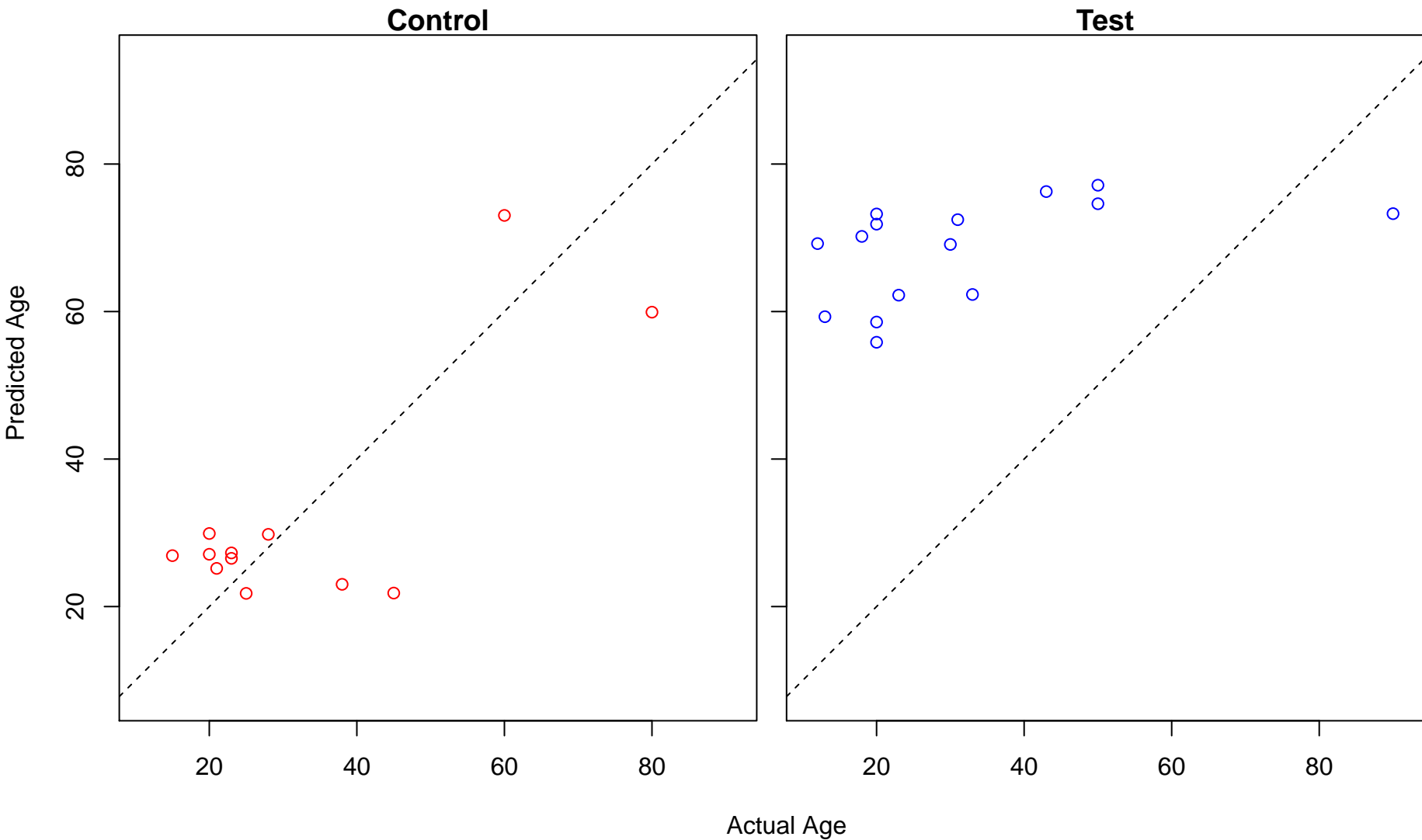
myelination (Score: 4.185610)



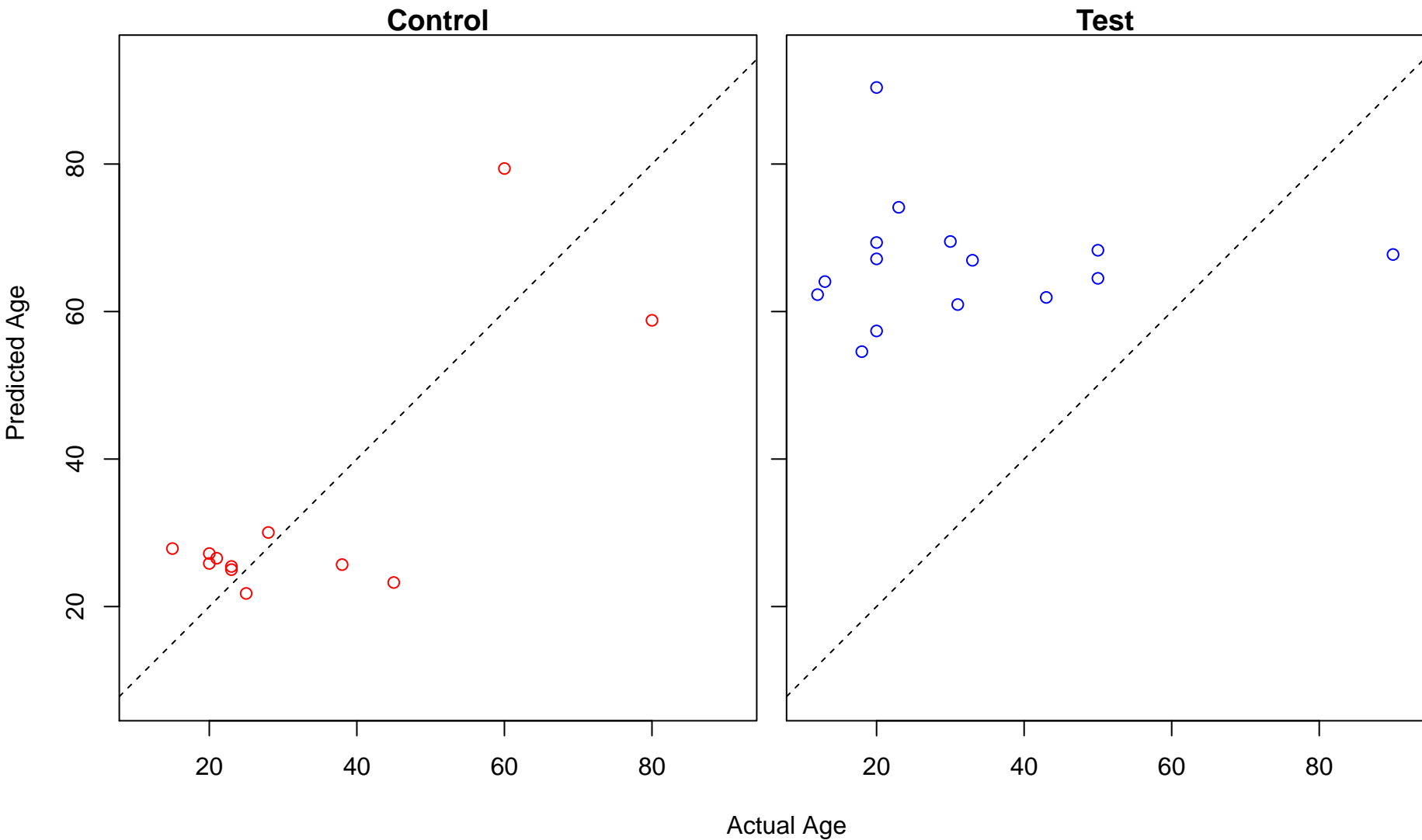
regulation of potassium ion transmembrane transporter activity (Score: 4.181450)



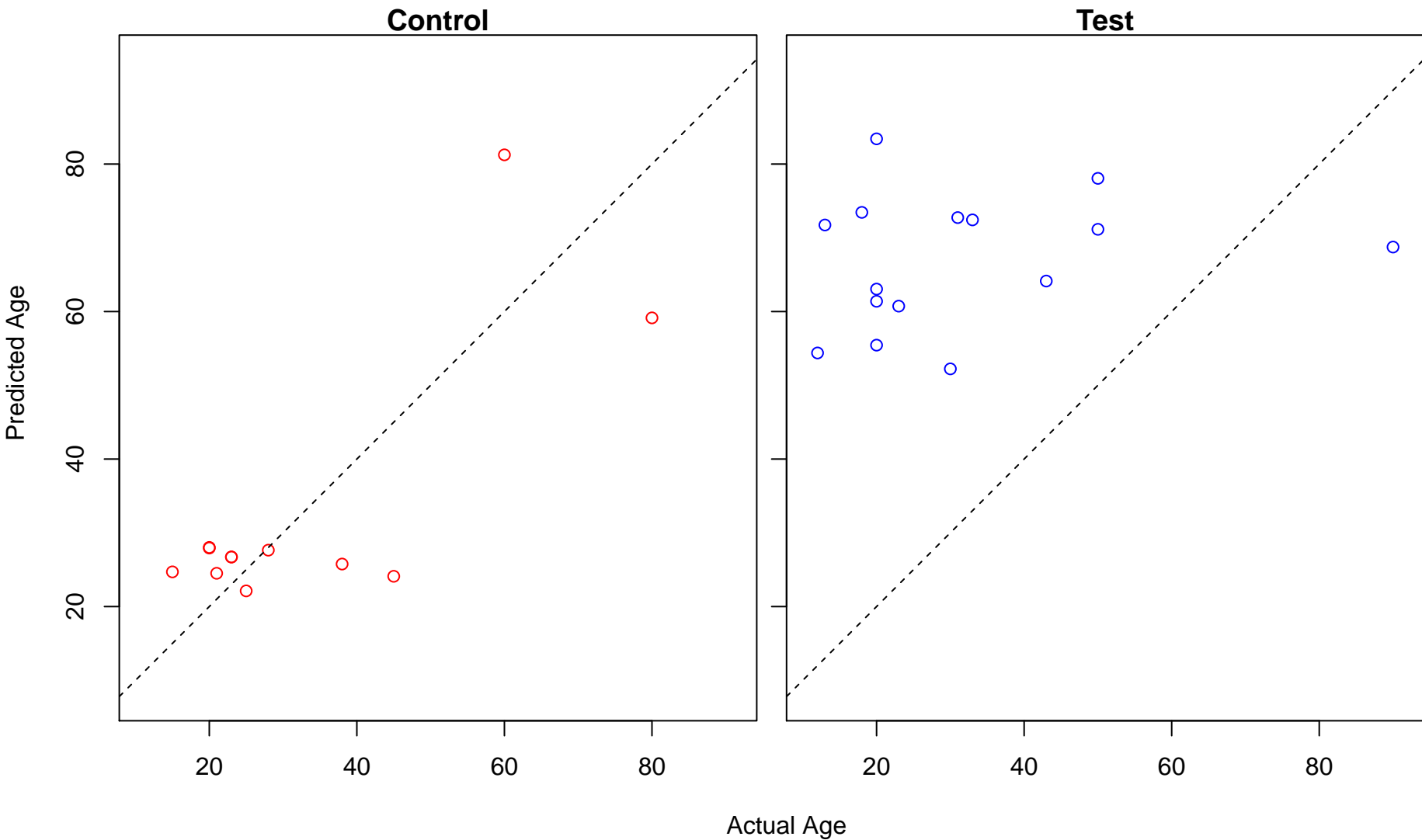
regulation of potassium ion transmembrane transport (Score: 4.181231)



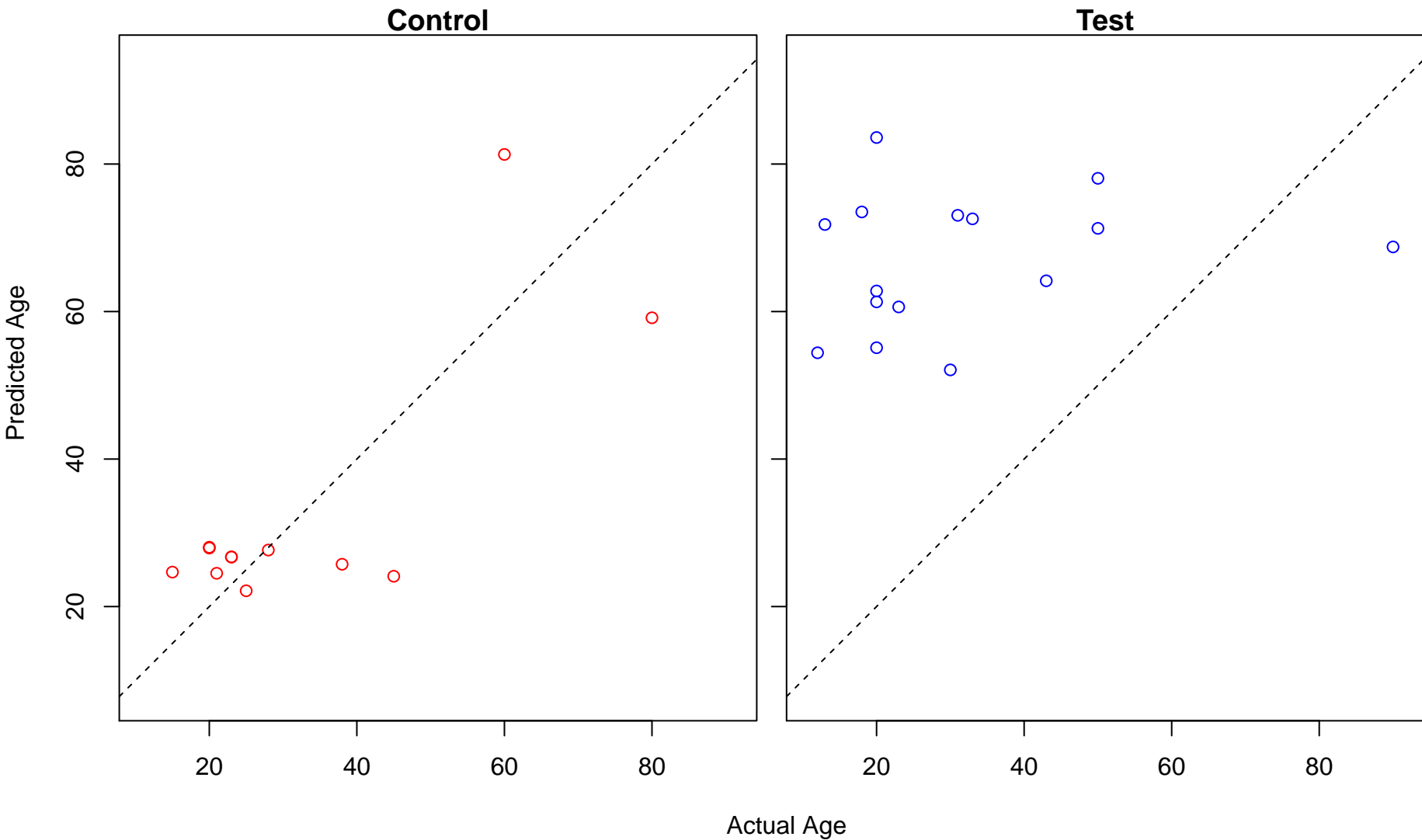
regulation of hematopoietic progenitor cell differentiation (Score: 4.181037)



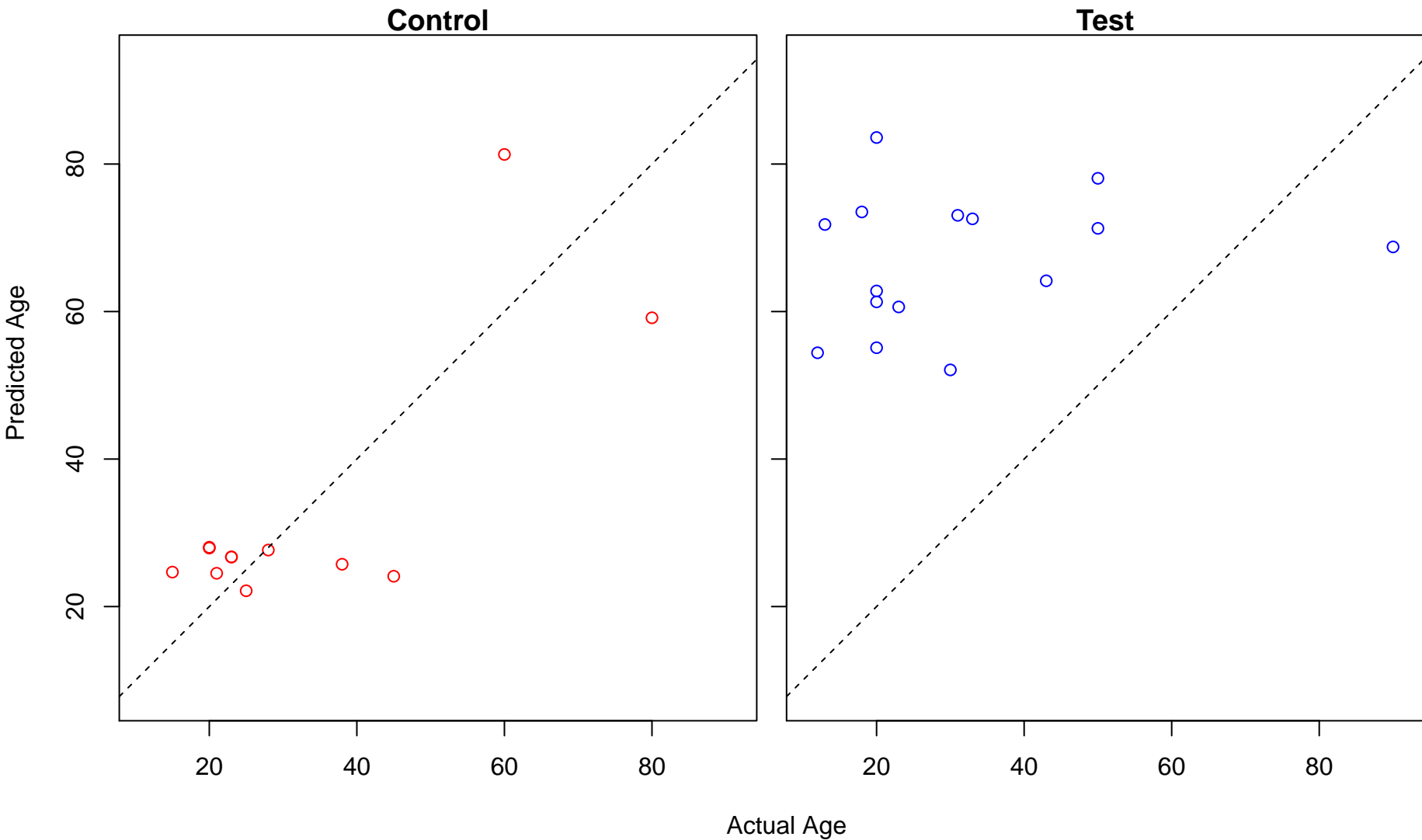
kidney epithelium development (Score: 4.180298)



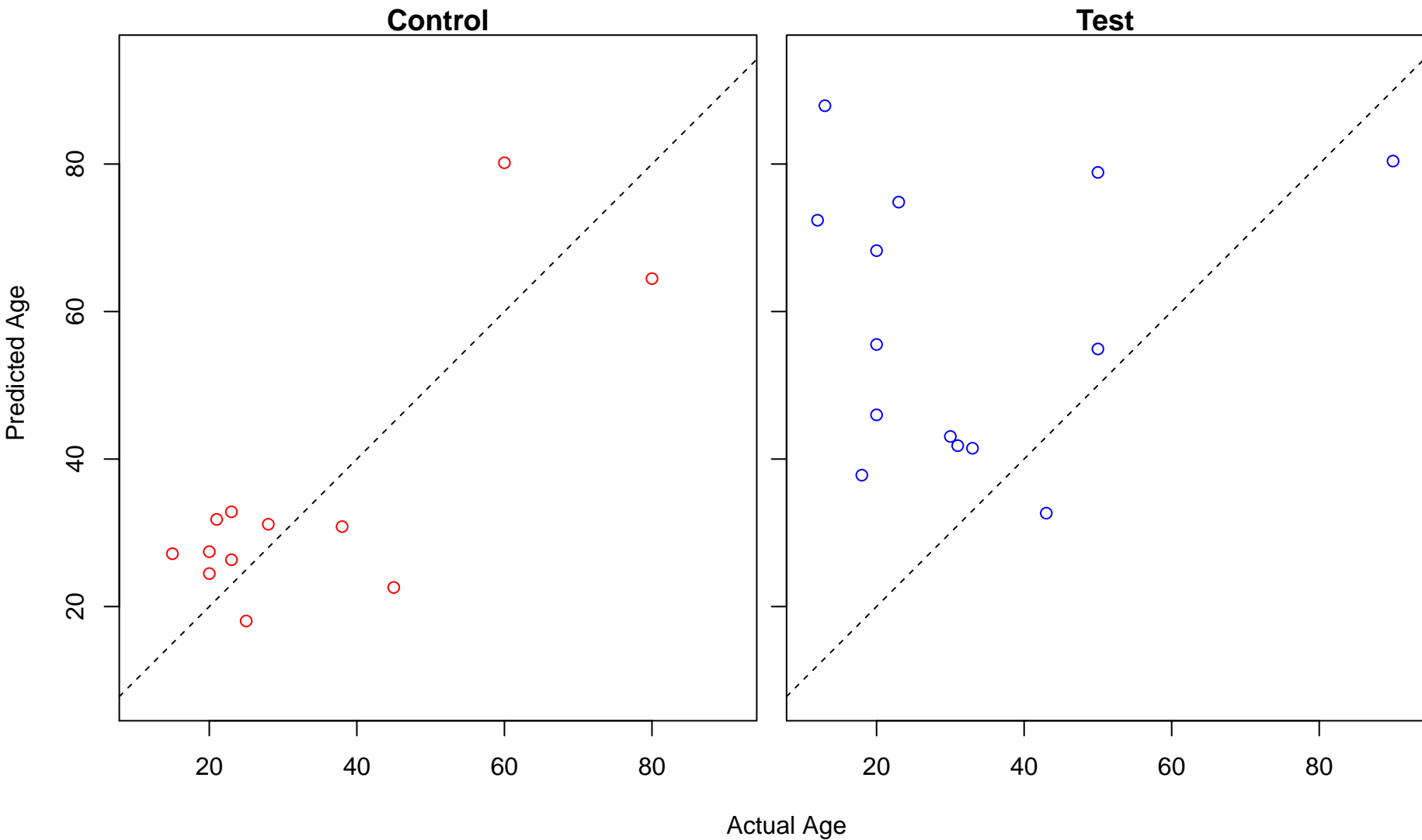
renal filtration cell differentiation (Score: 4.178774)



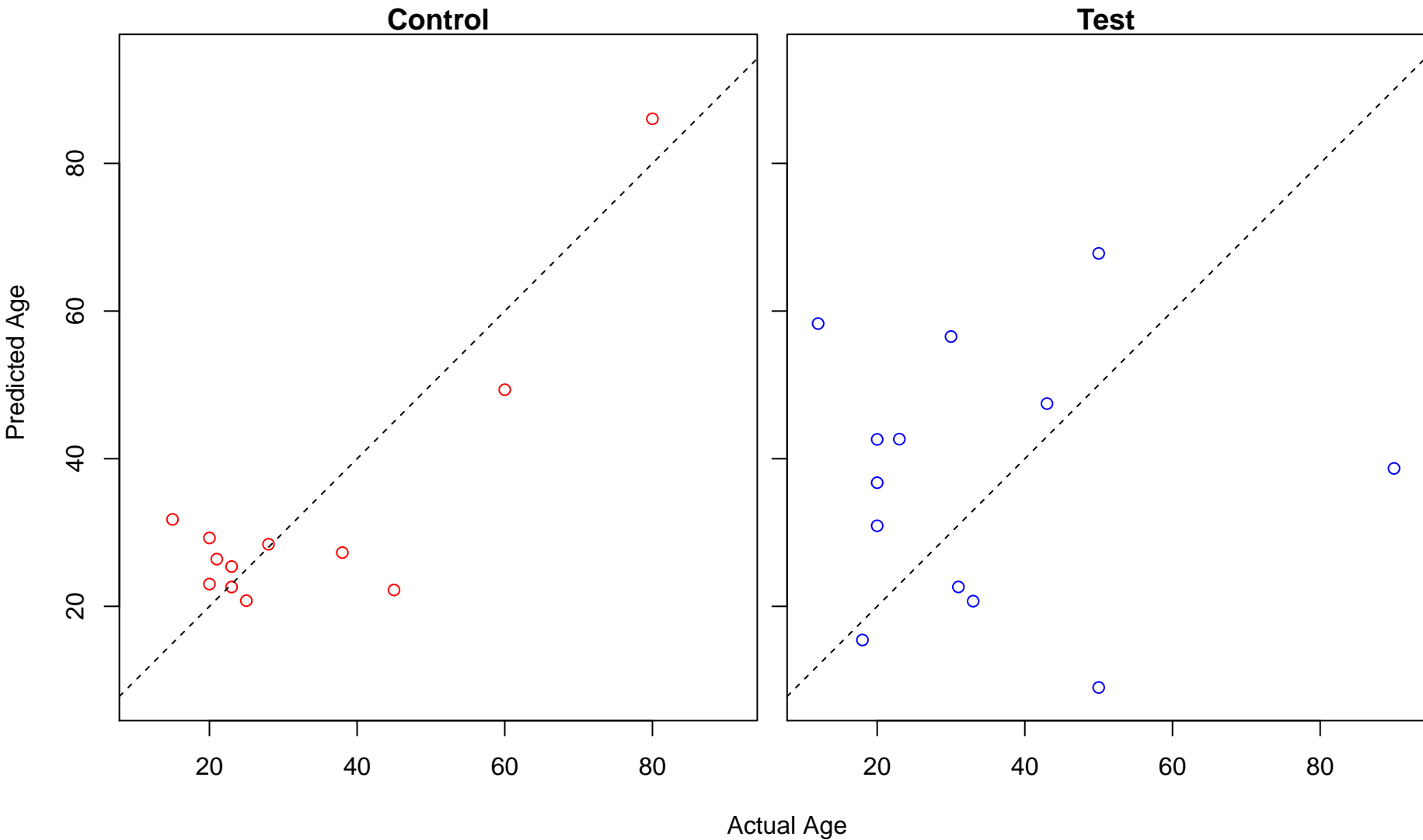
glomerular visceral epithelial cell differentiation (Score: 4.178774)



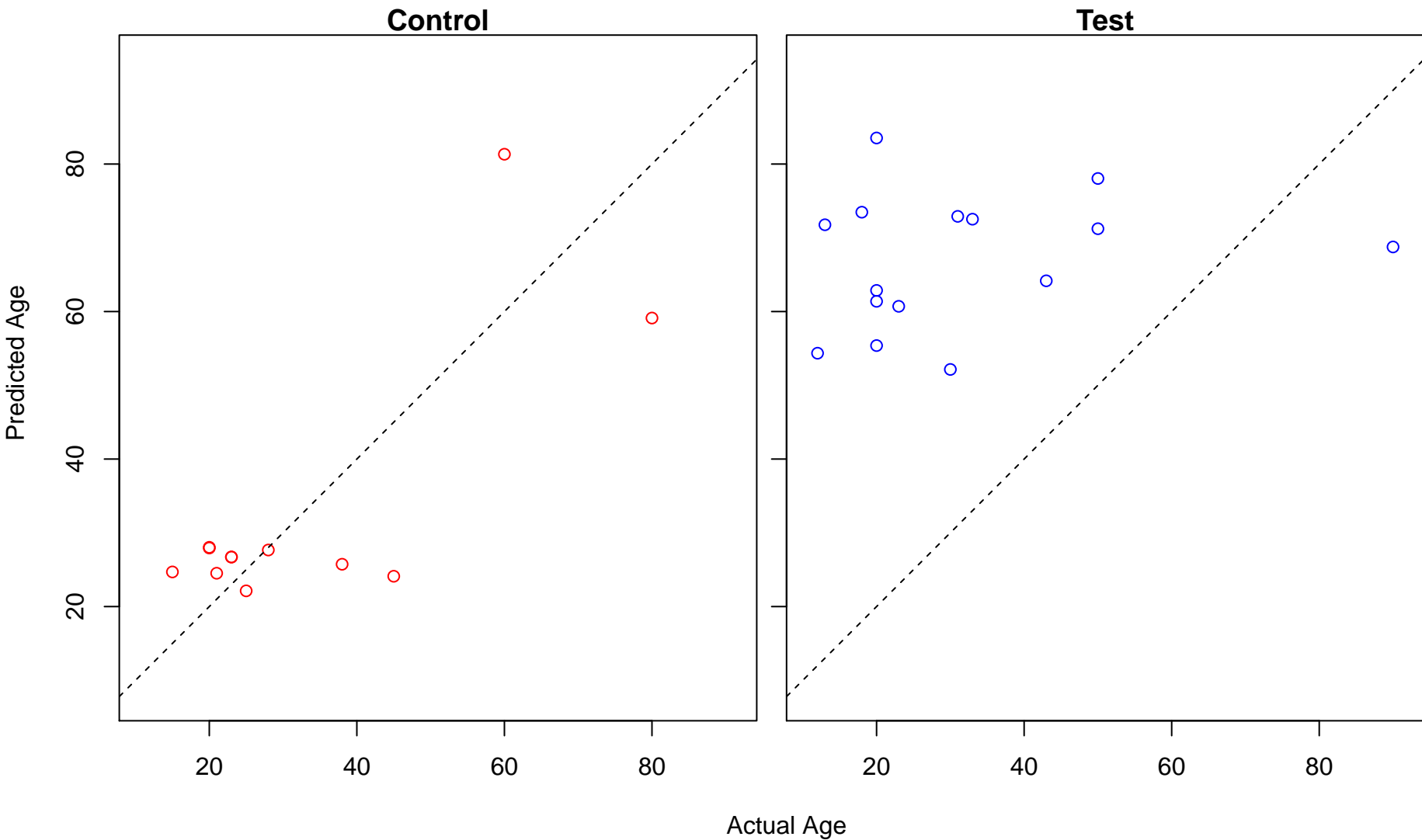
peptide catabolic process (Score: 4.175458)



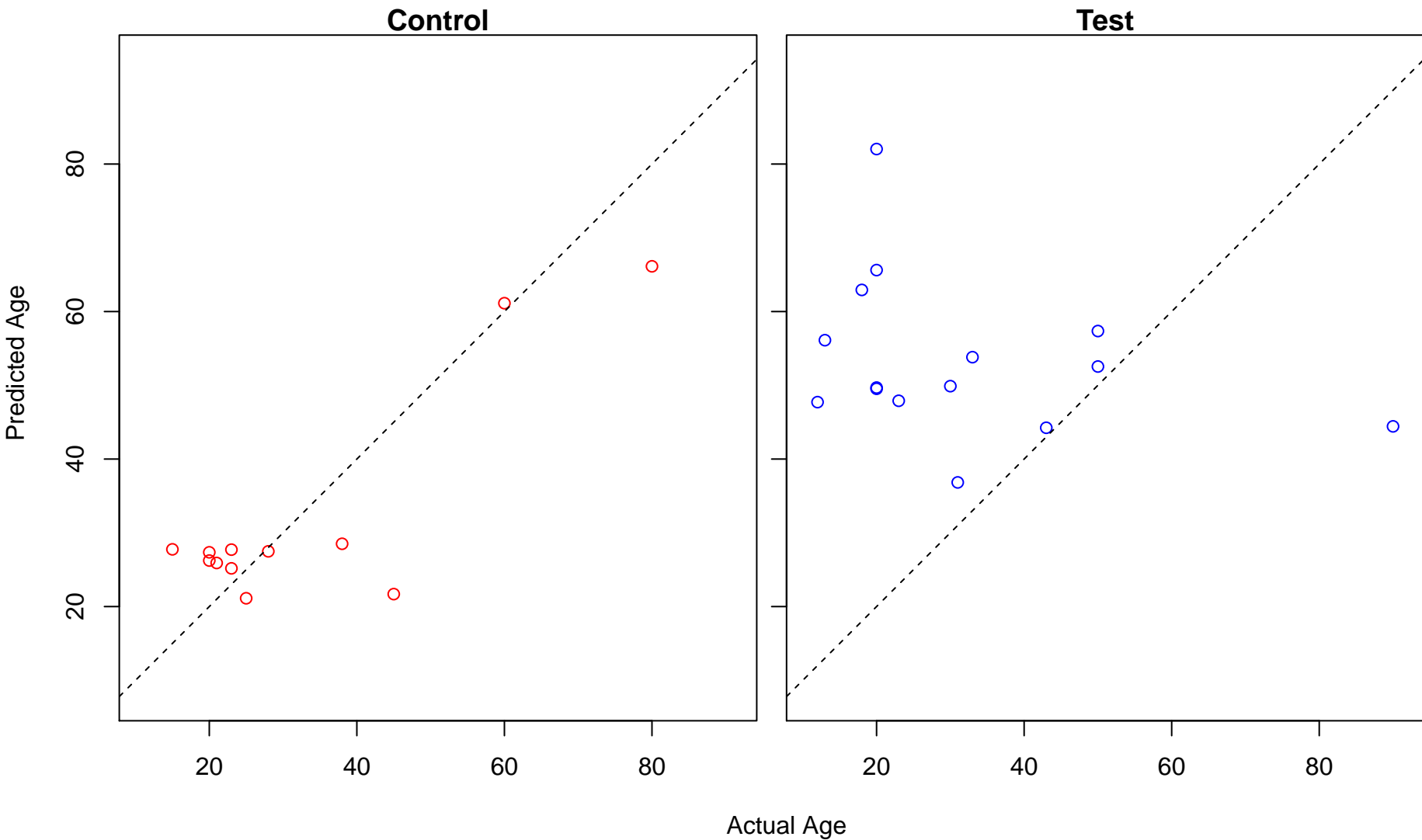
regulation of actin filament bundle assembly (Score: 4.174350)



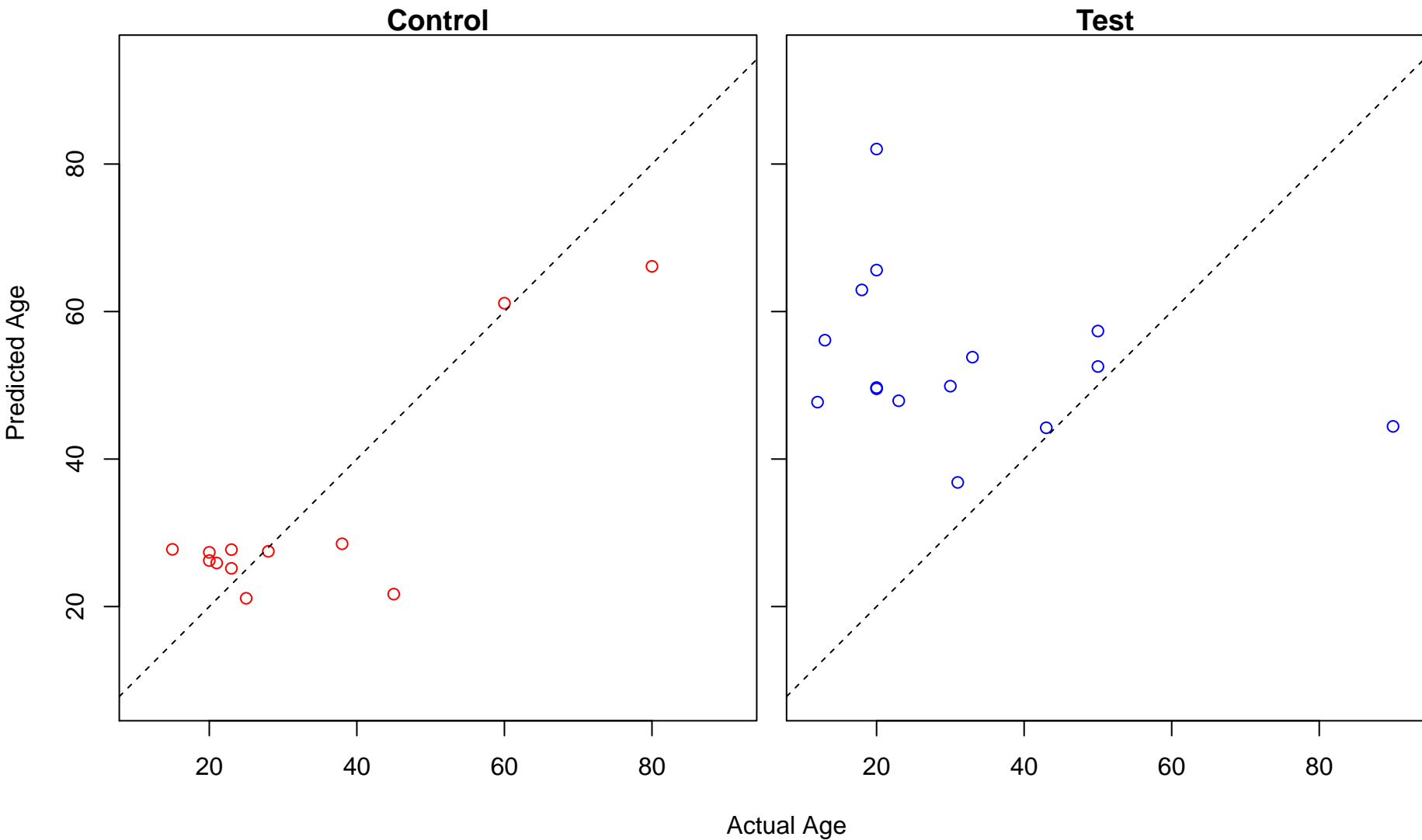
epithelial cell differentiation involved in kidney development (Score: 4.173549)



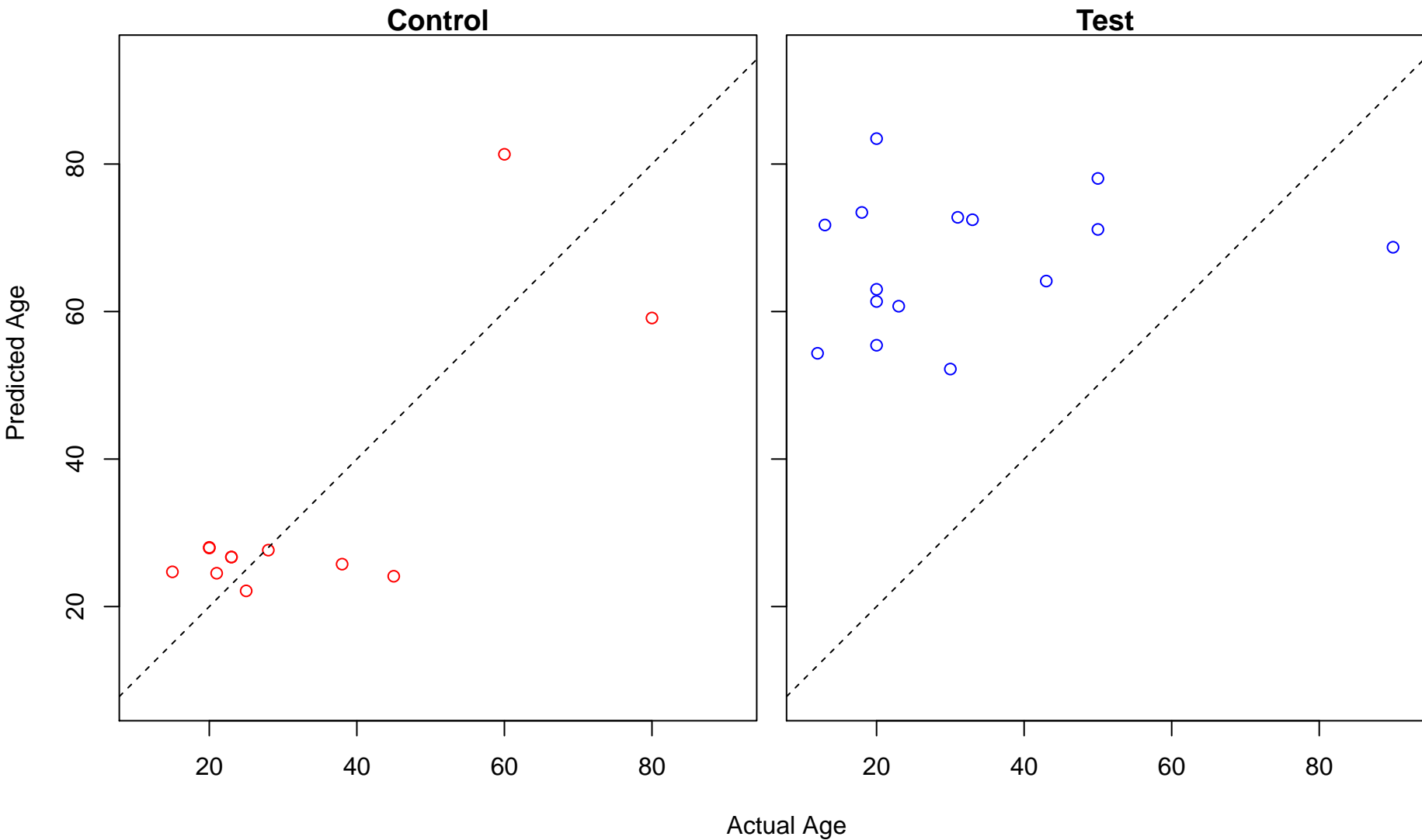
ensheathment of neurons (Score: 4.173092)



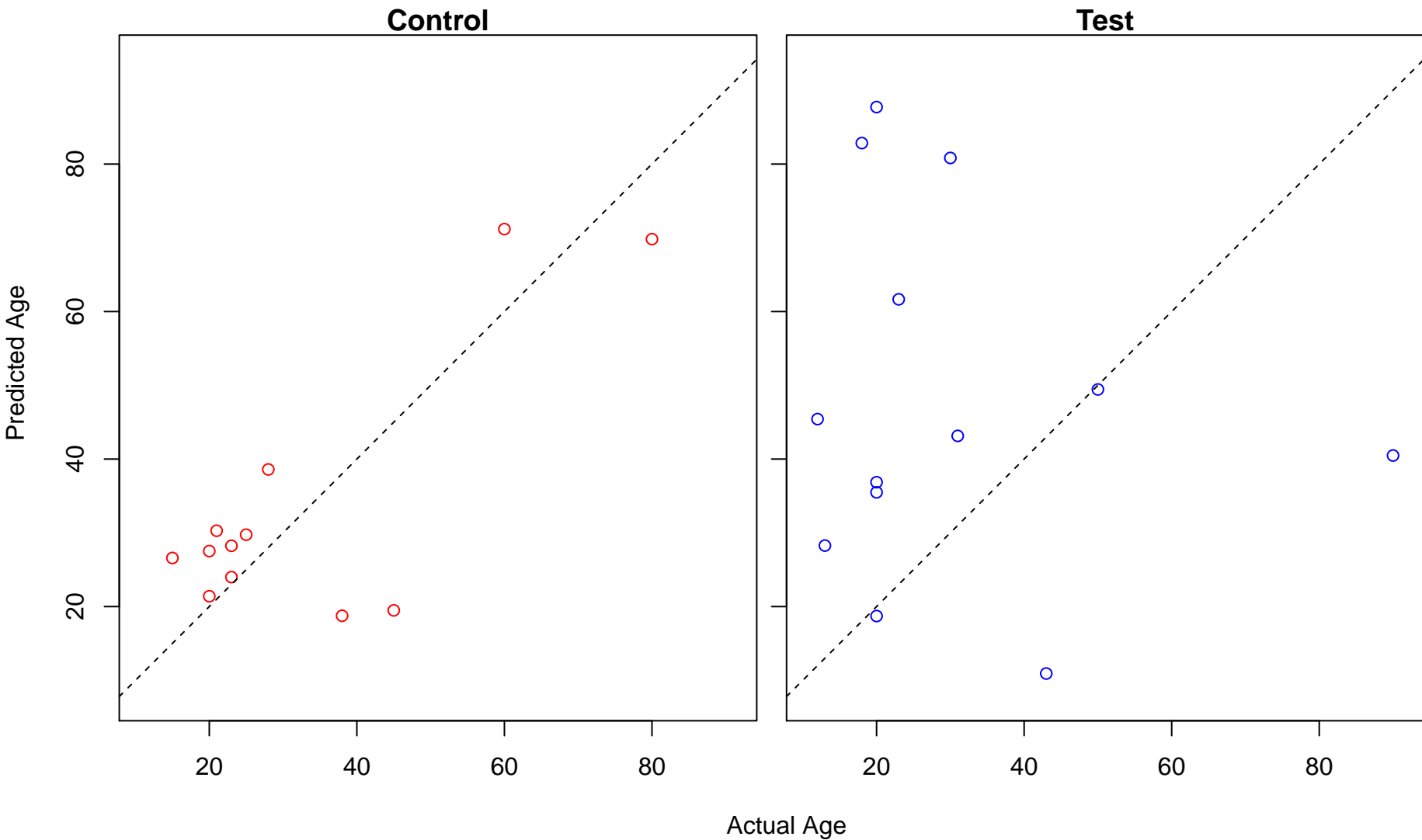
axon ensheathment (Score: 4.173092)



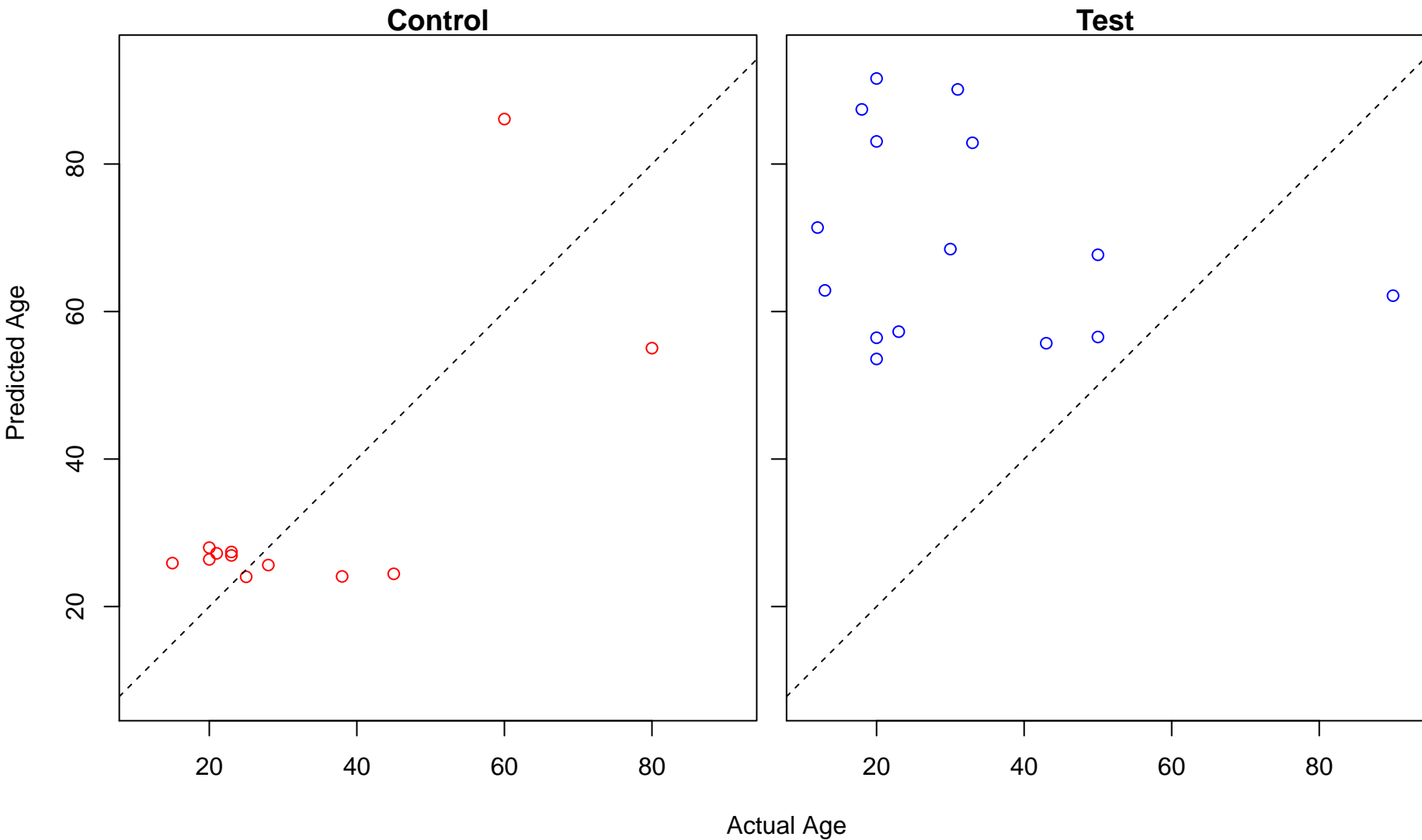
nephron epithelium development (Score: 4.171948)



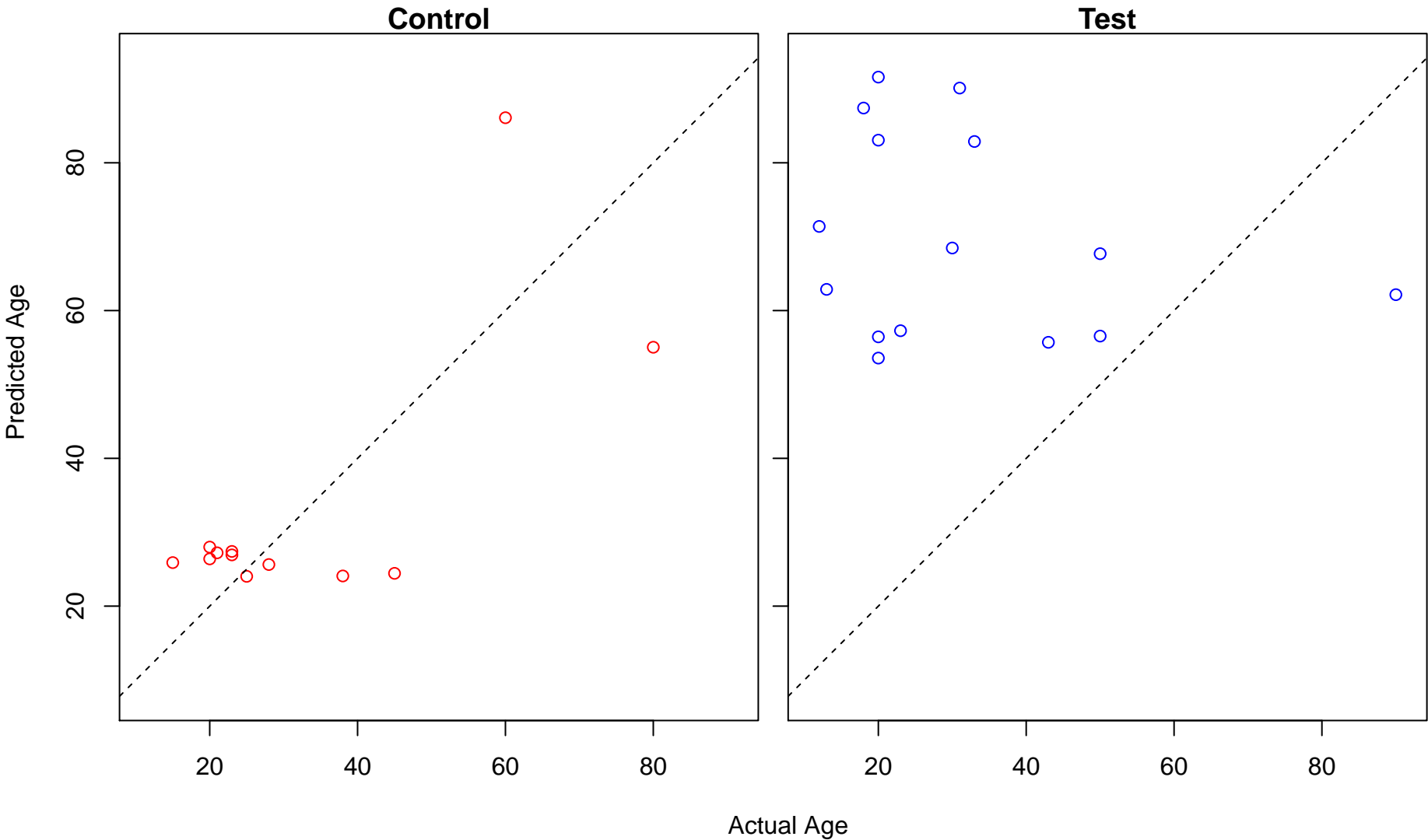
regulation of epidermal growth factor-activated receptor activity (Score: 4.162136)



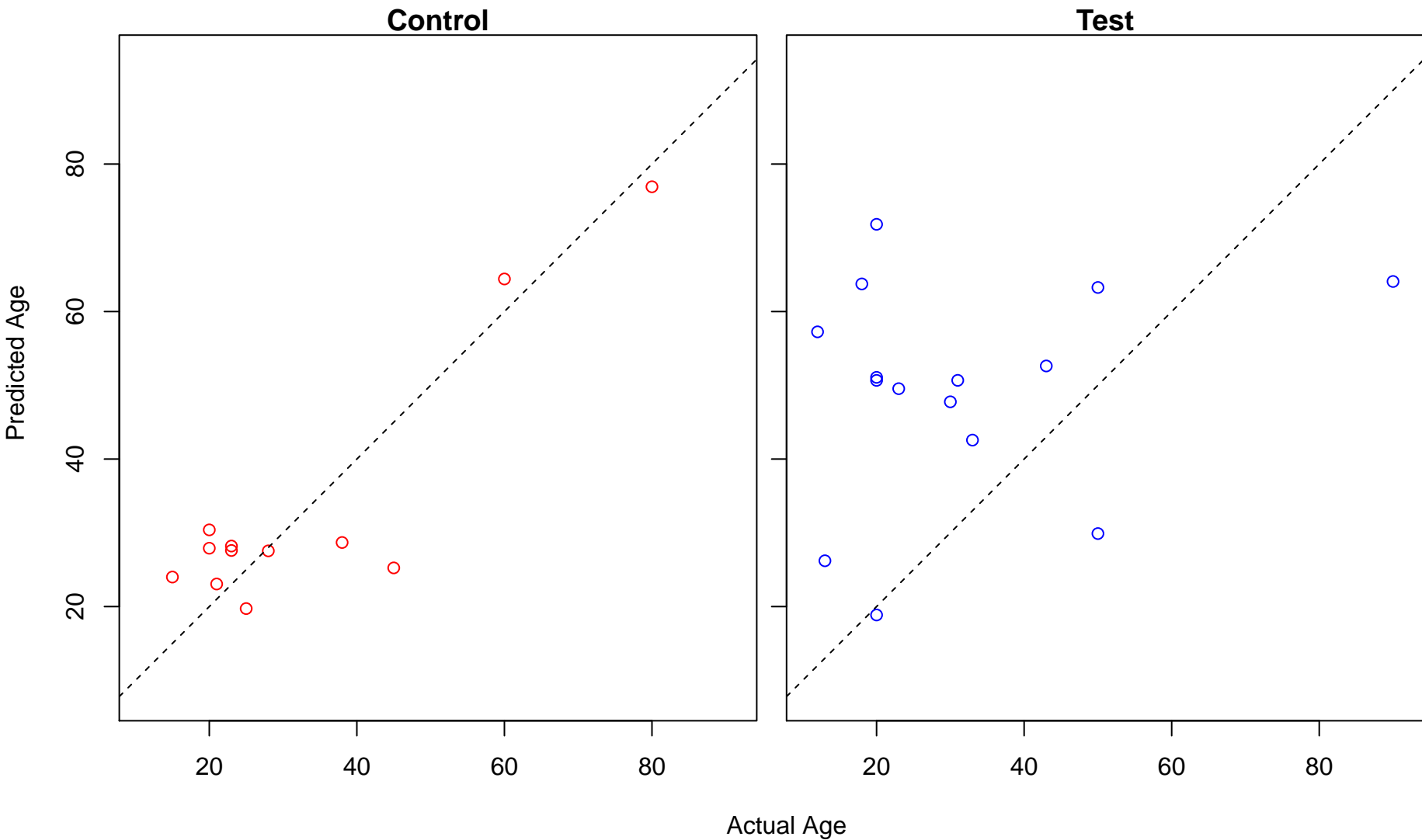
positive regulation of transforming growth factor beta receptor signaling pathway (Score: 4.160893)



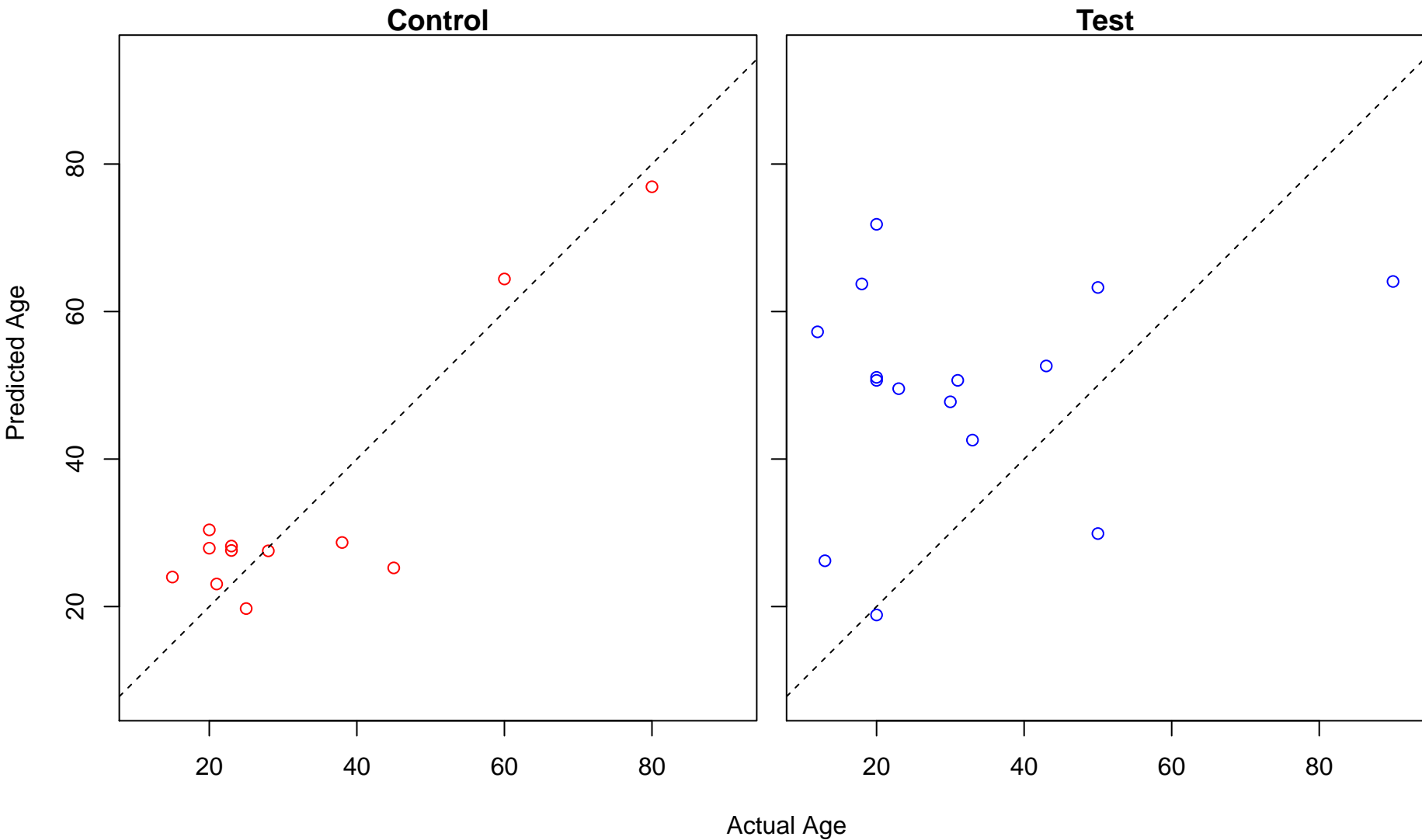
positive regulation of cellular response to transforming growth factor beta stimulus (Score: 4.16089)



negative regulation of protein exit from endoplasmic reticulum (Score: 4.157769)

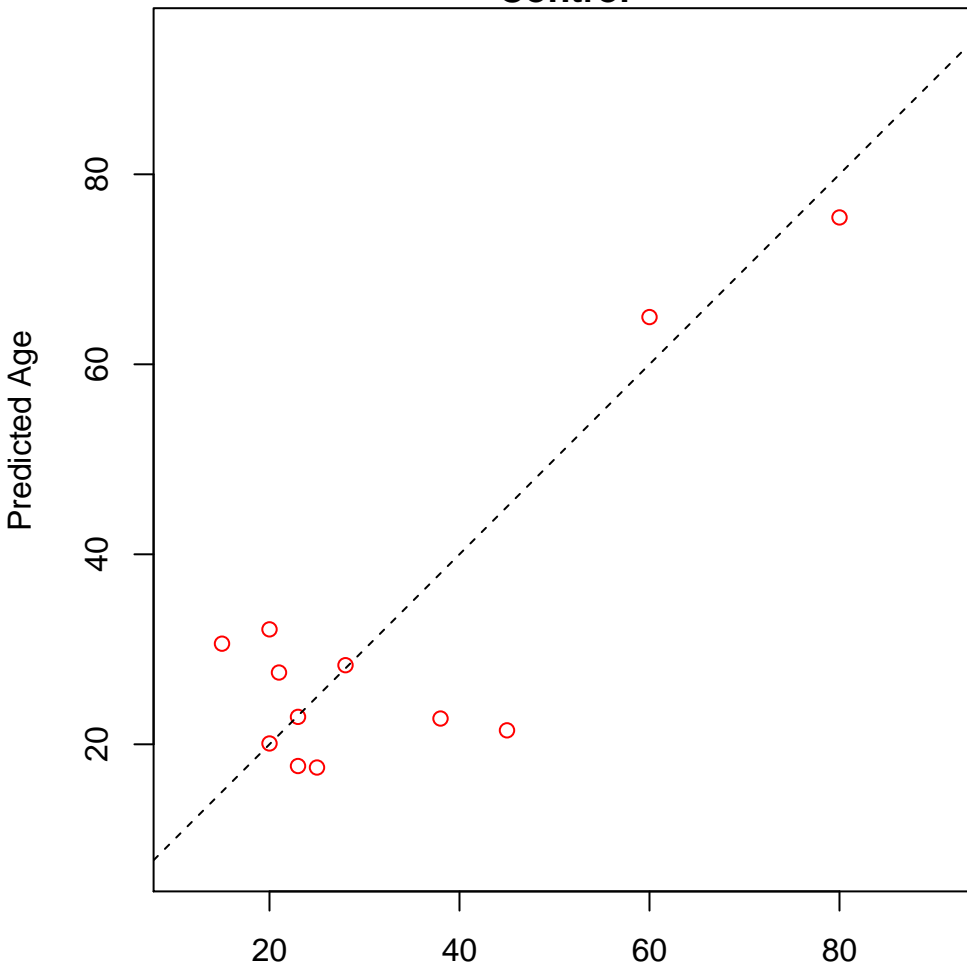


negative regulation of retrograde protein transport, ER to cytosol (Score: 4.157769)

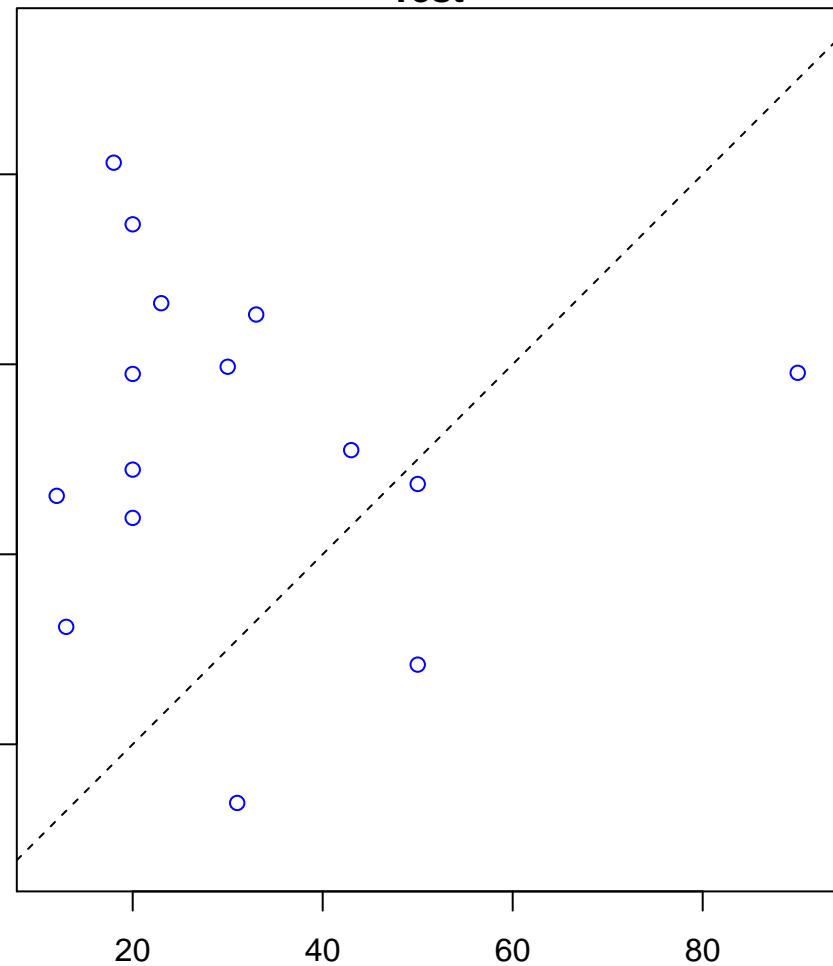


DNA-templated transcription, termination (Score: 4.157641)

Control



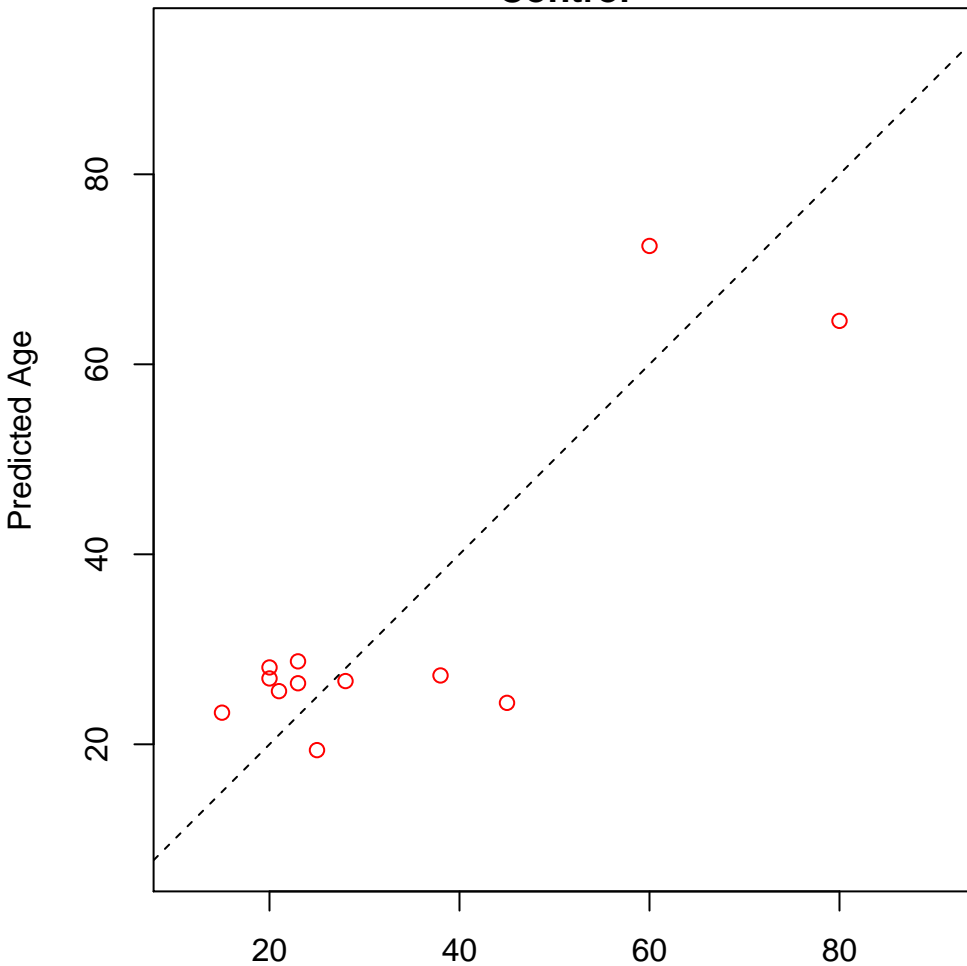
Test



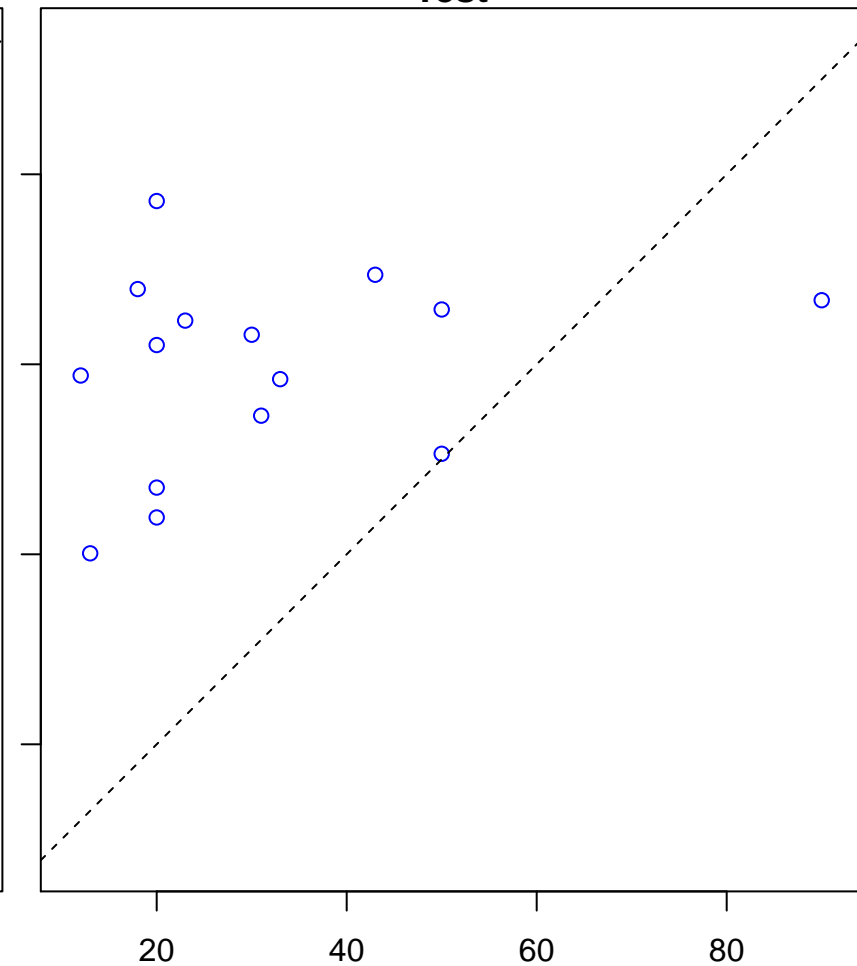
Actual Age

ribonucleoprotein complex disassembly (Score: 4.154738)

Control

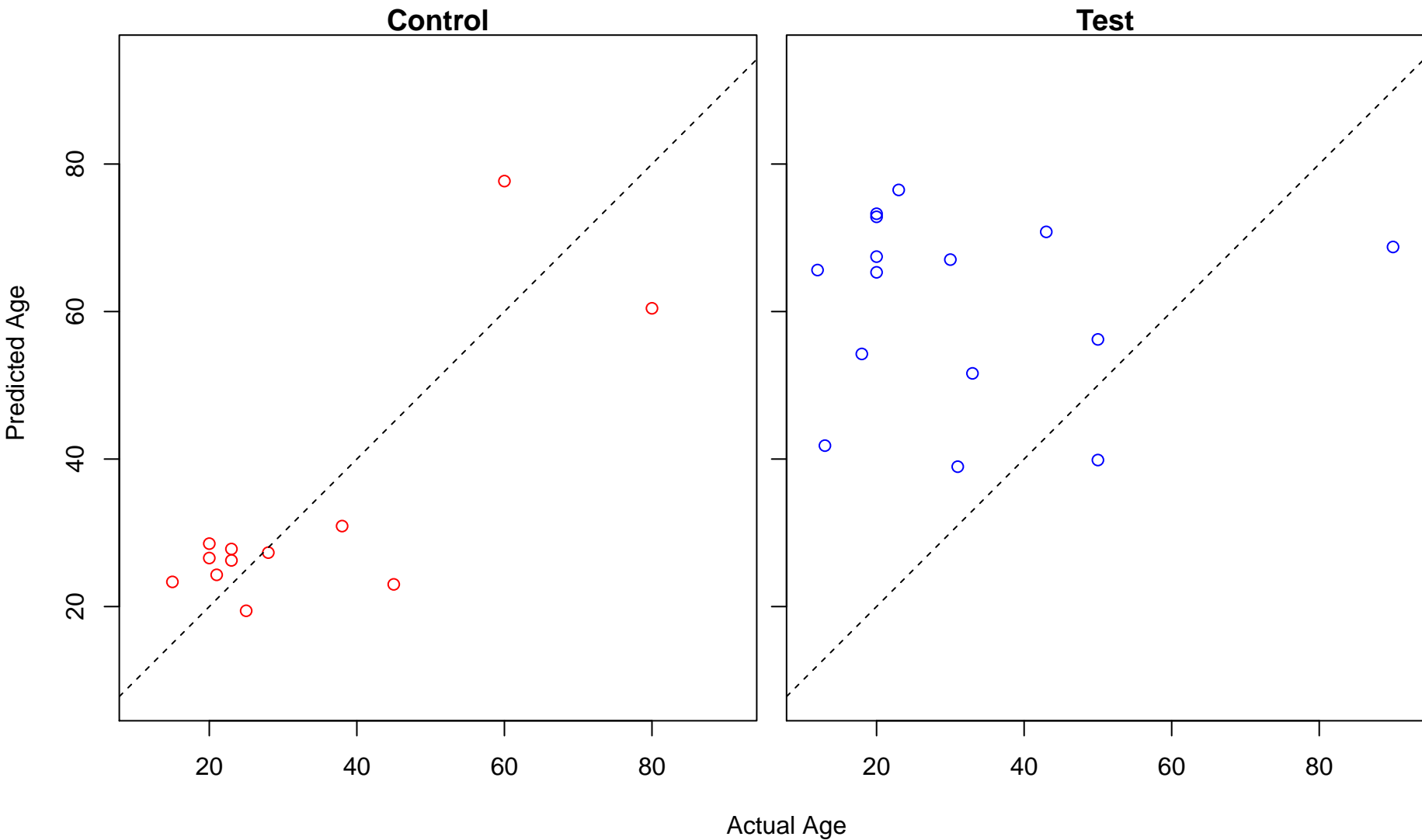


Test

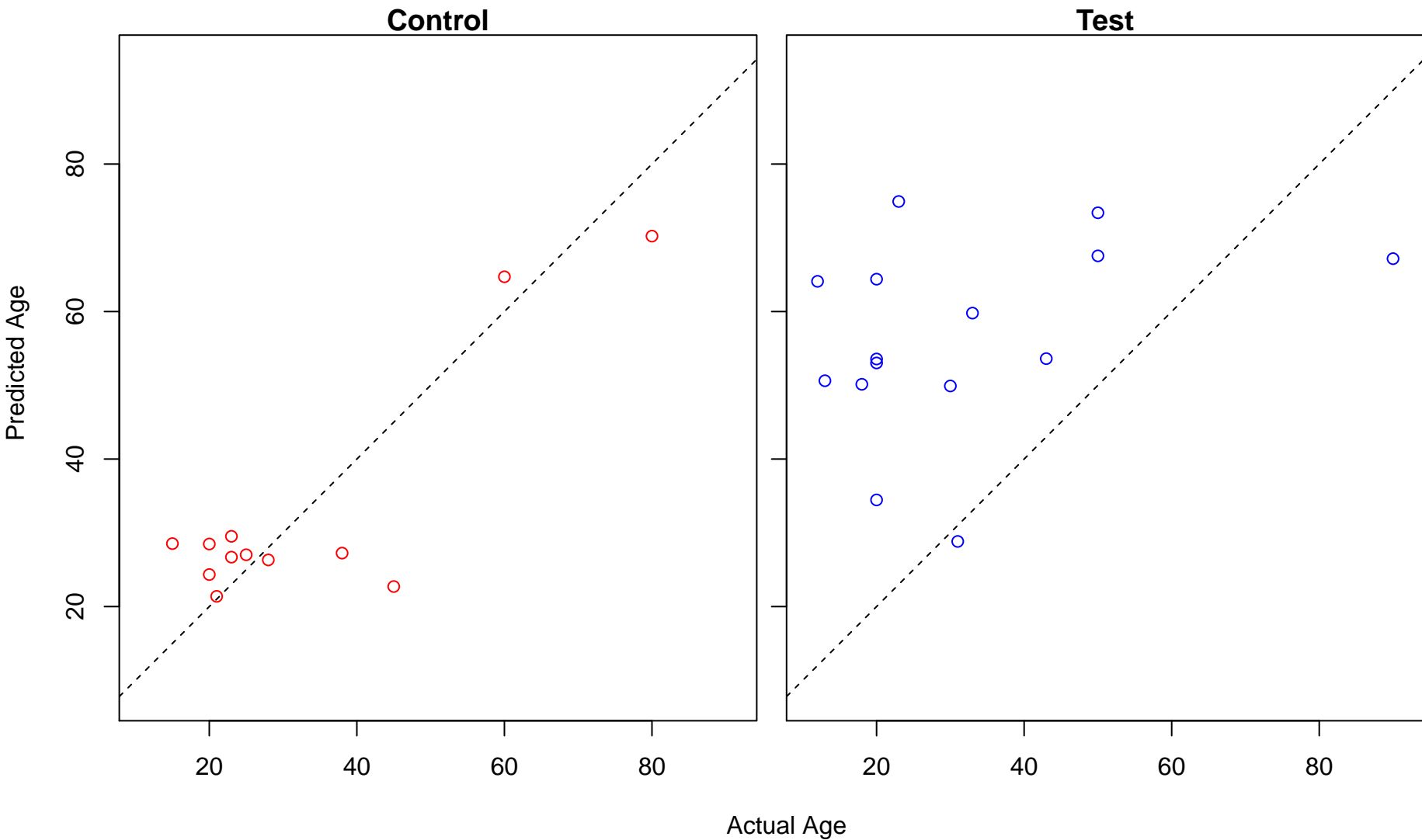


Actual Age

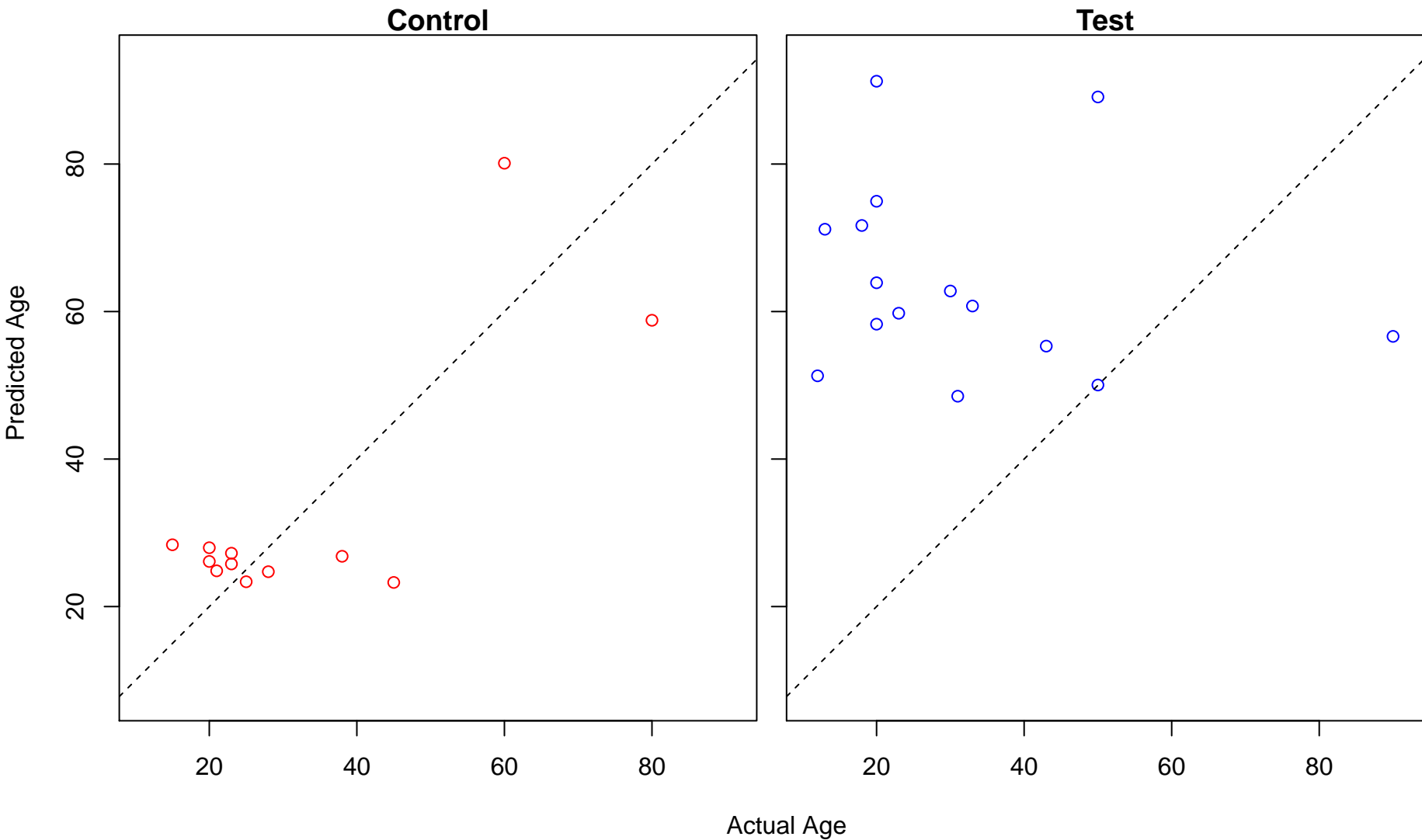
ventricular cardiac muscle cell differentiation (Score: 4.152842)



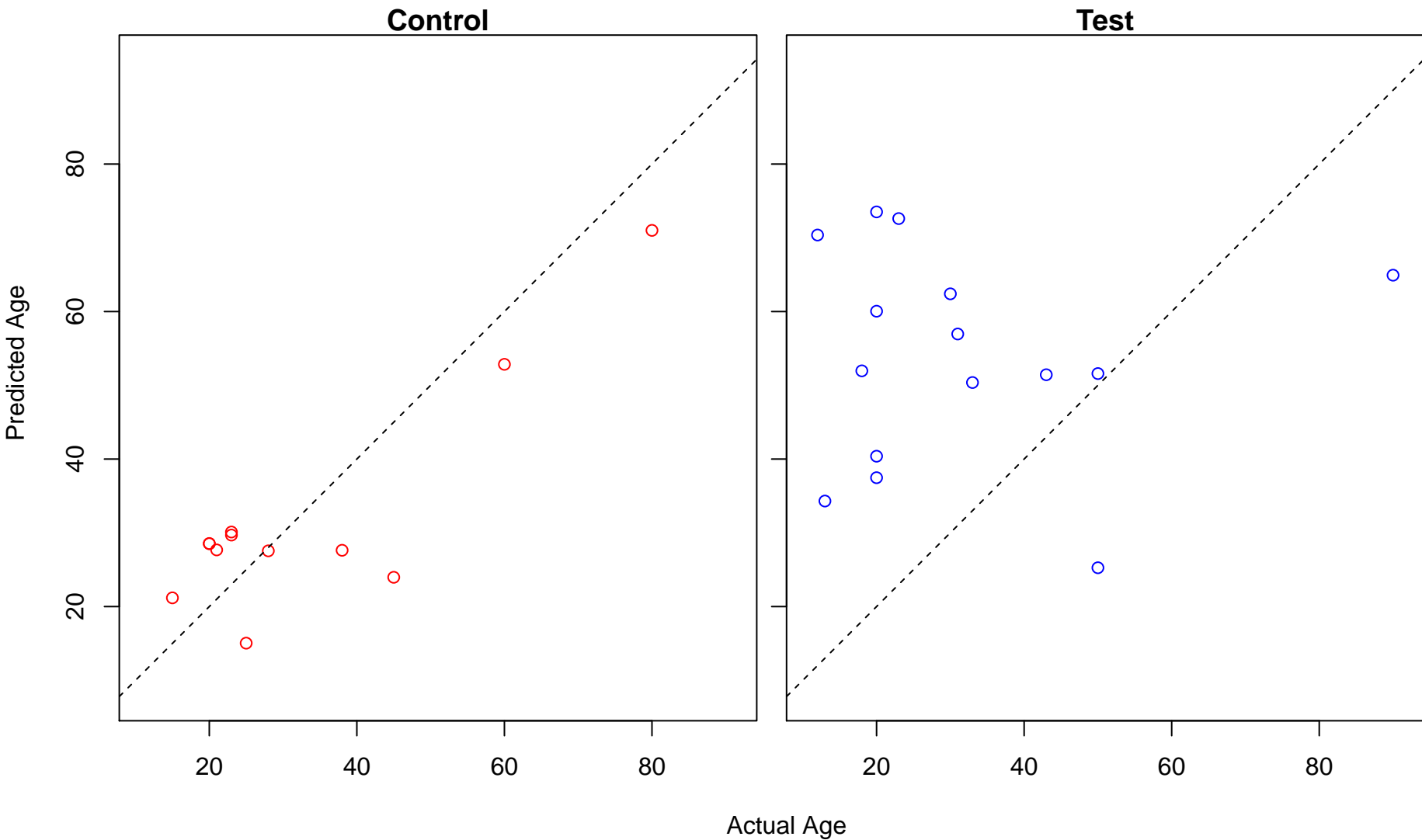
embryonic hindlimb morphogenesis (Score: 4.150660)



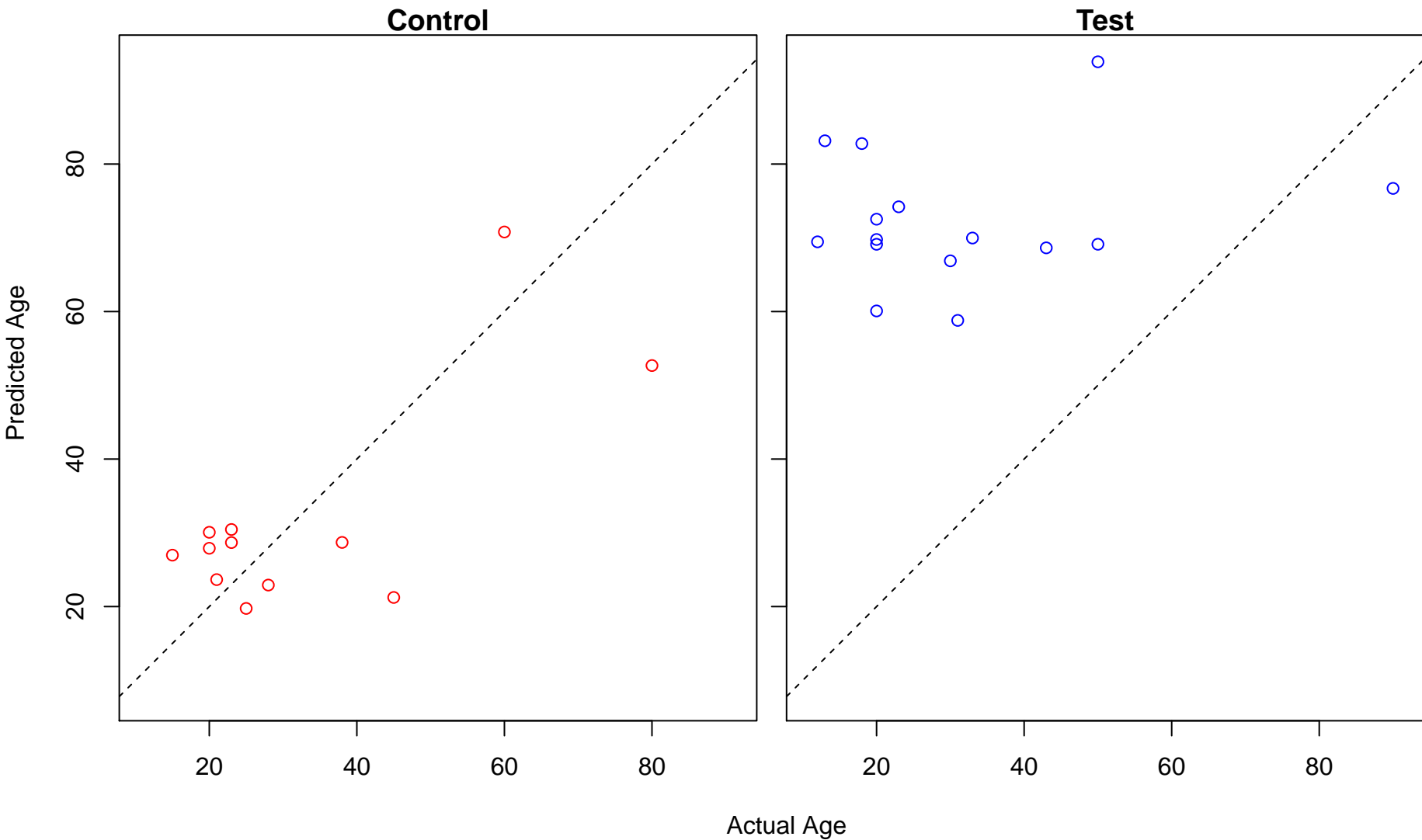
nephron tubule formation (Score: 4.149445)



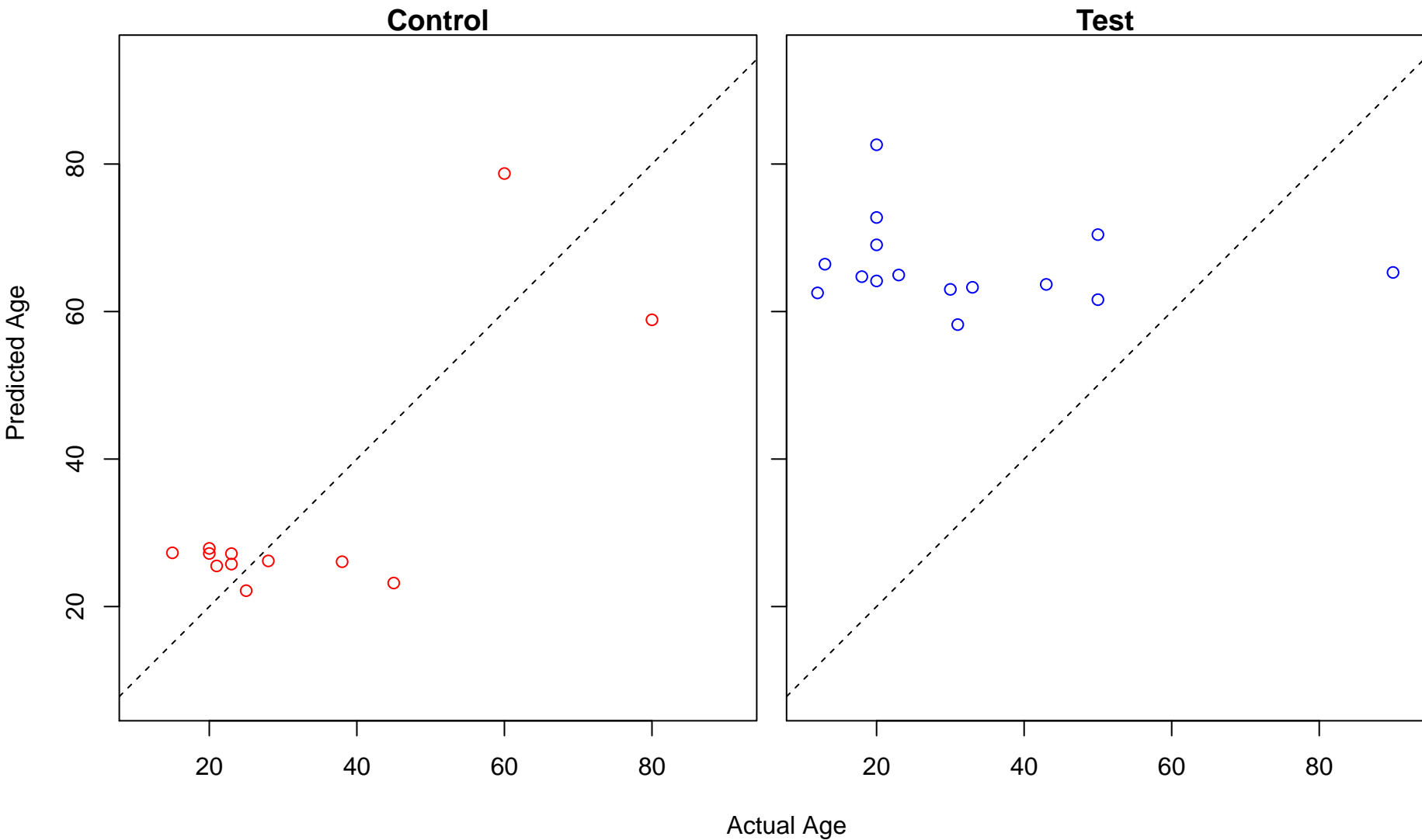
regulation of telomere capping (Score: 4.148721)



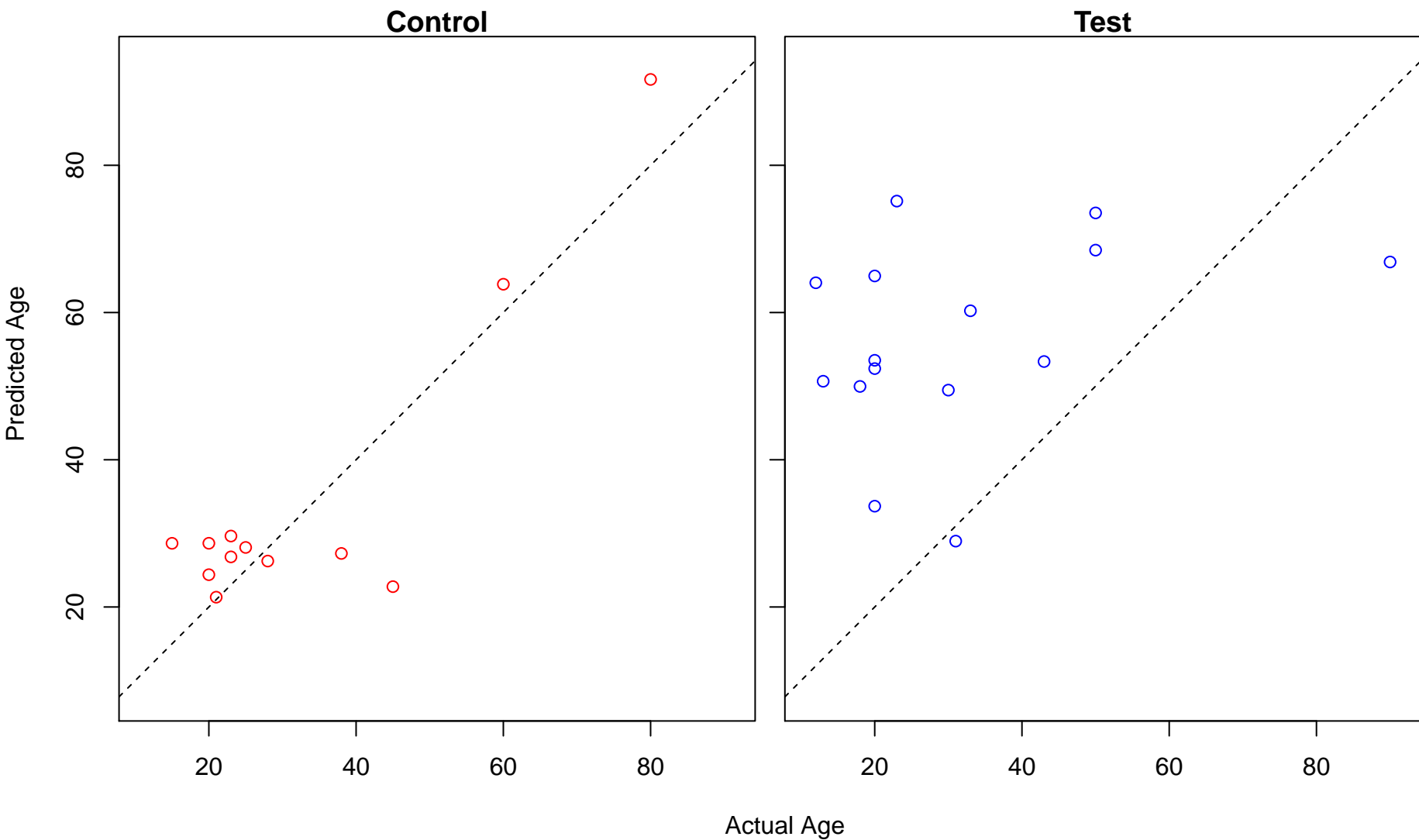
sympathetic nervous system development (Score: 4.148201)



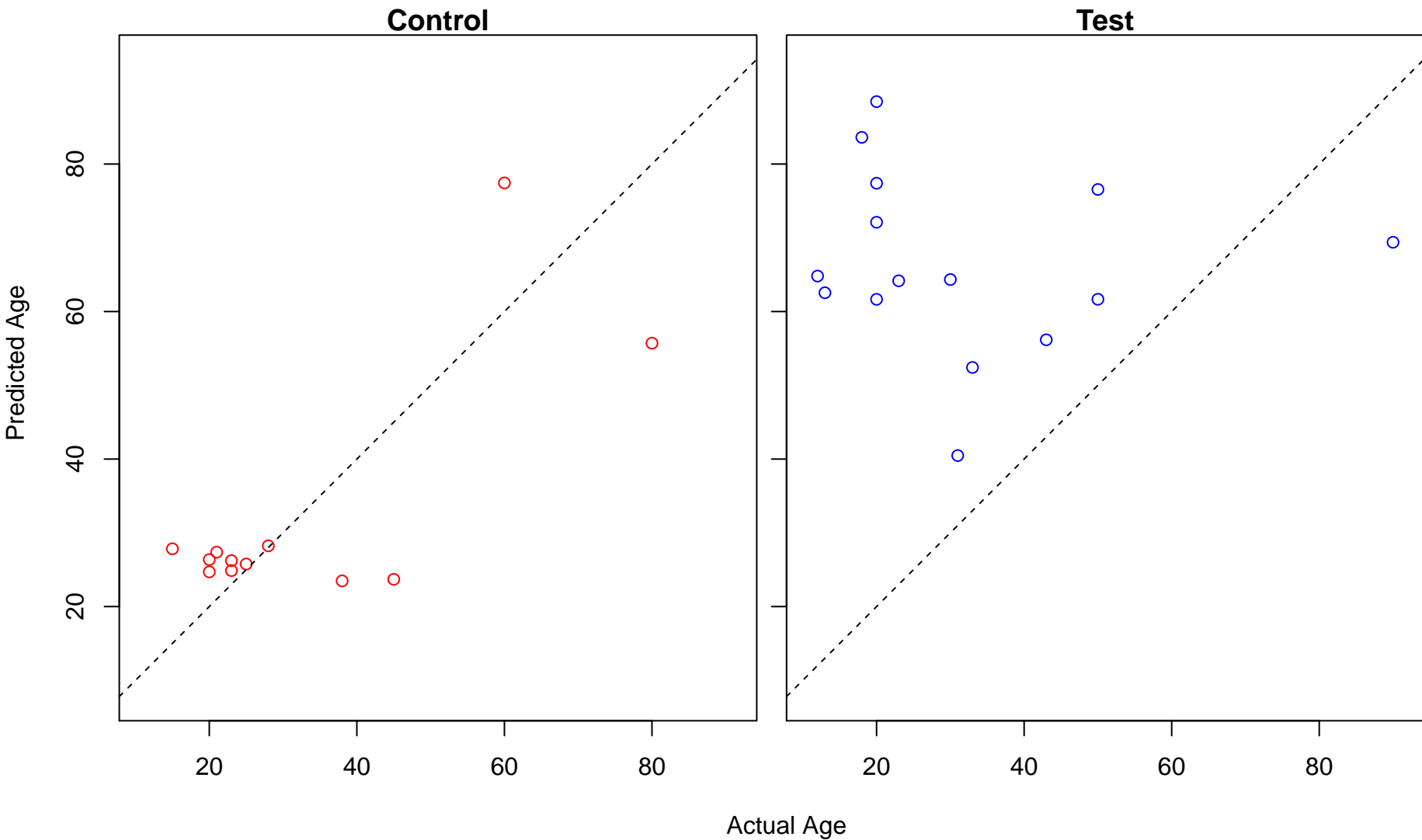
peptidyl-lysine modification (Score: 4.148022)



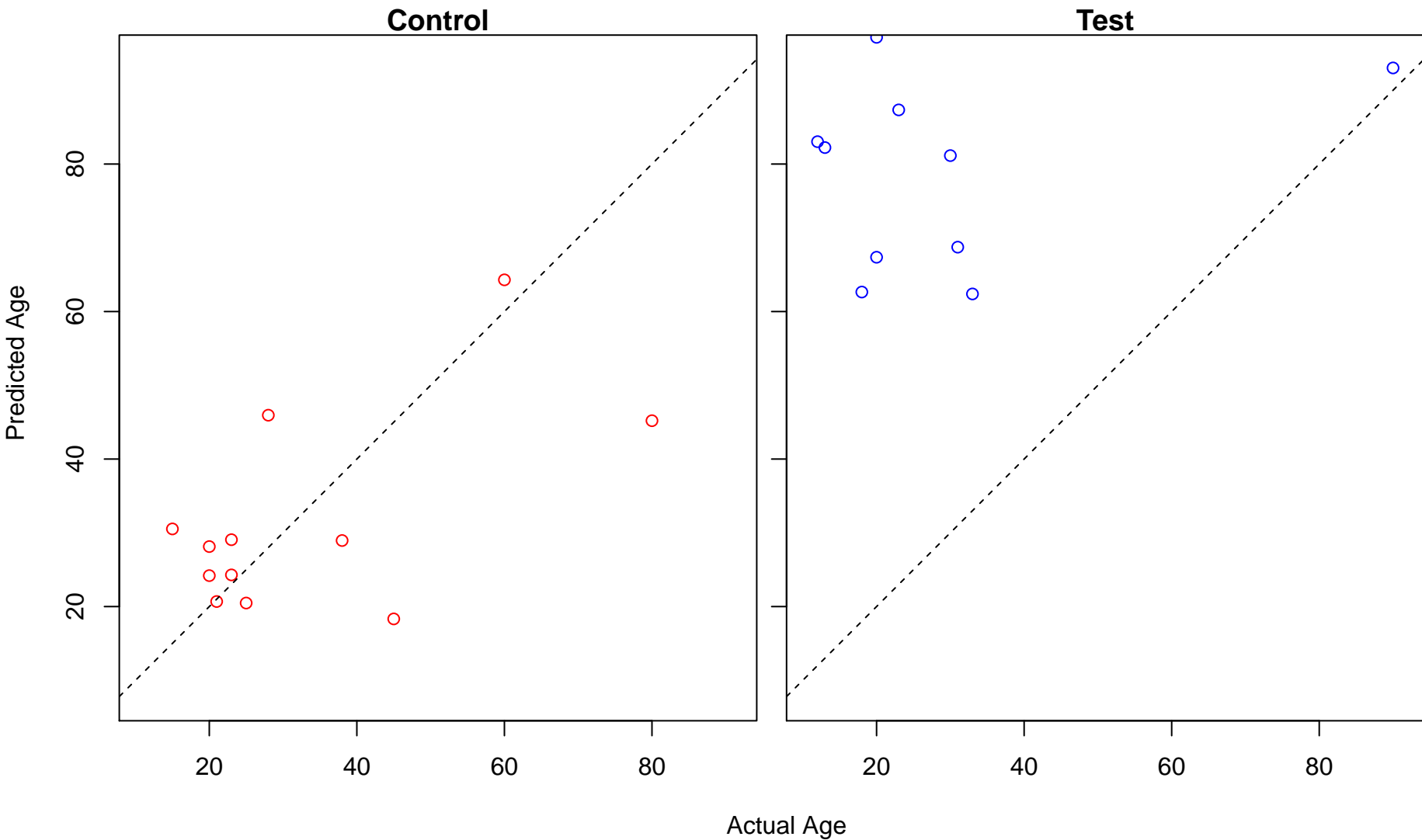
hindlimb morphogenesis (Score: 4.147443)



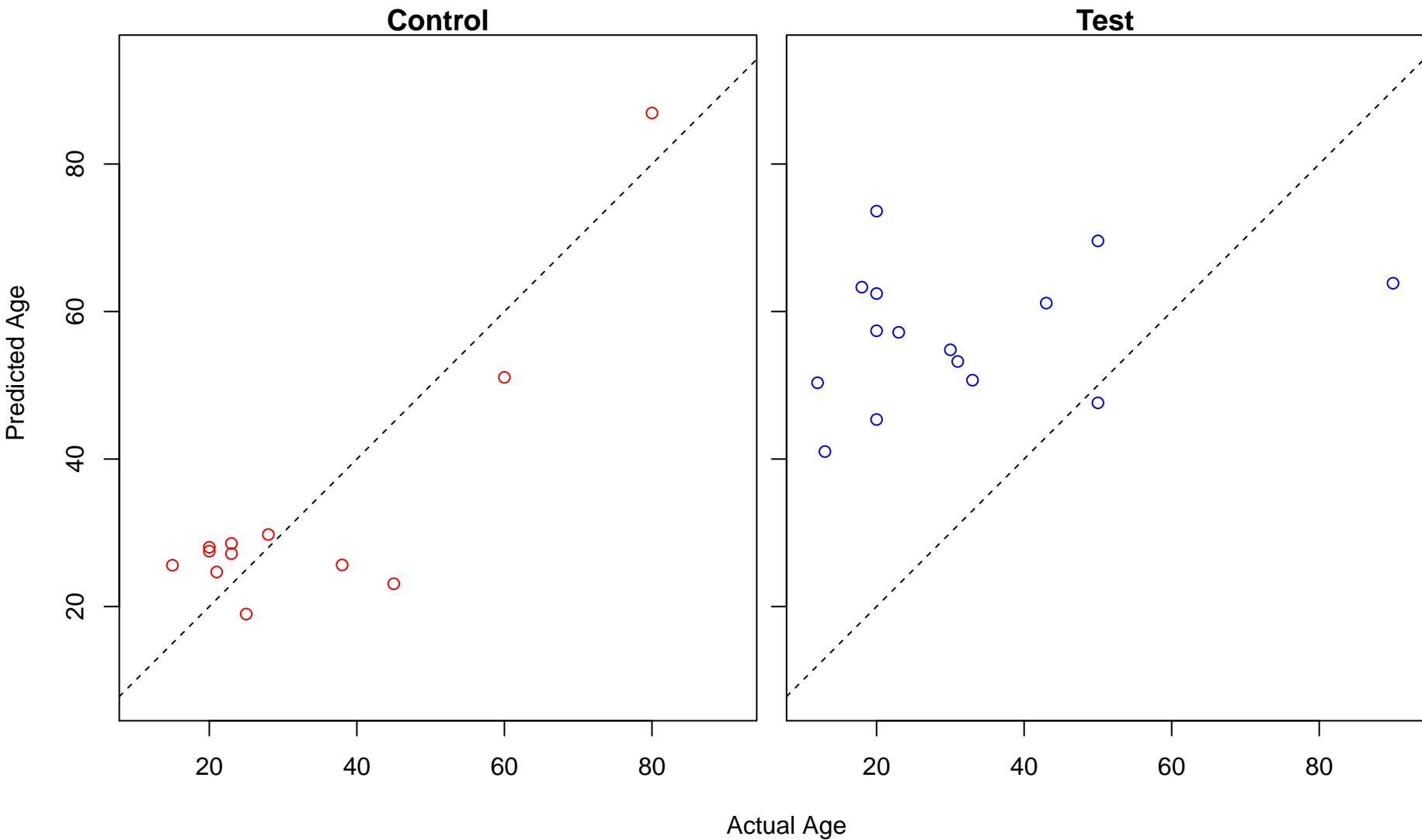
ribonucleoside monophosphate biosynthetic process (Score: 4.146689)



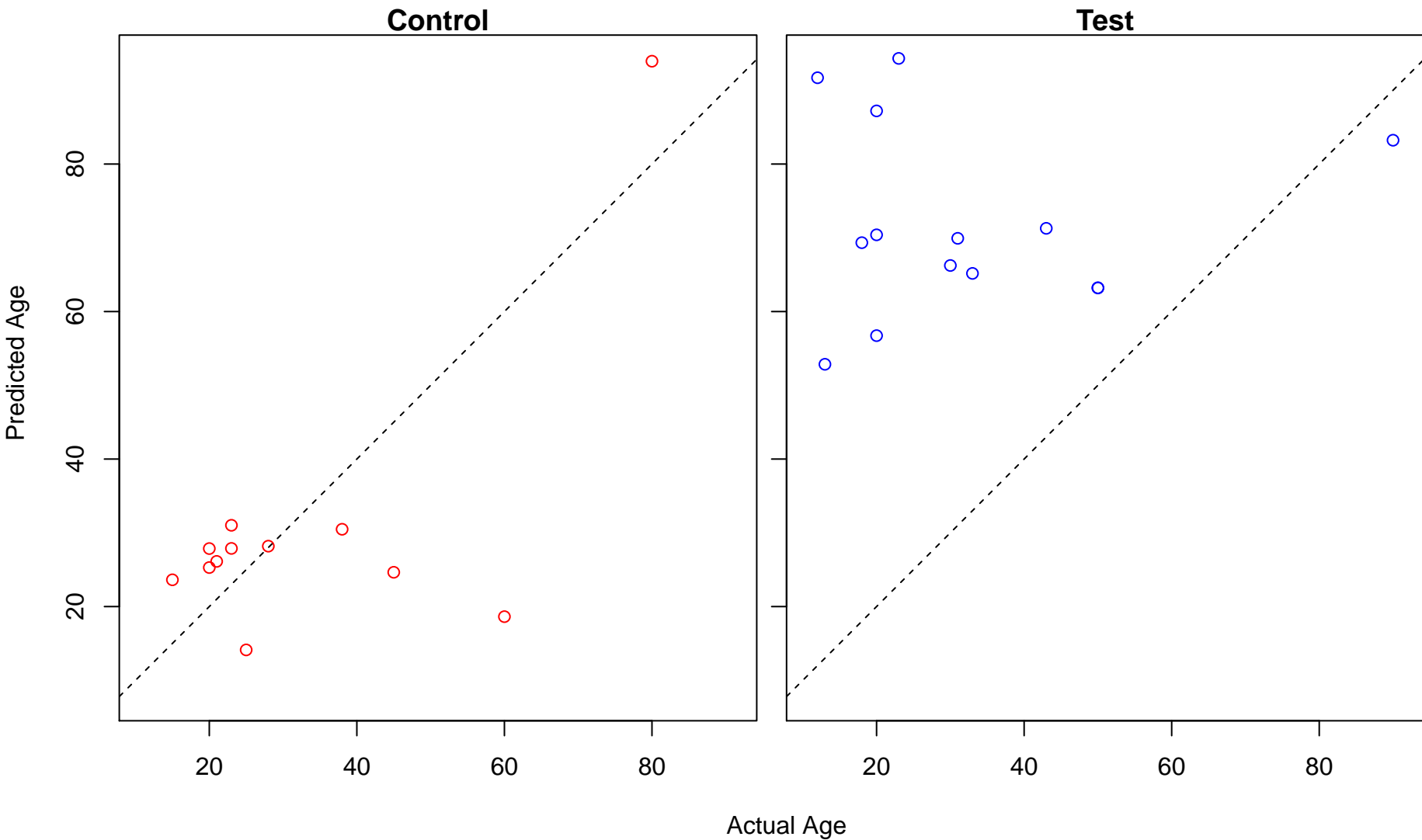
macrophage activation (Score: 4.143513)



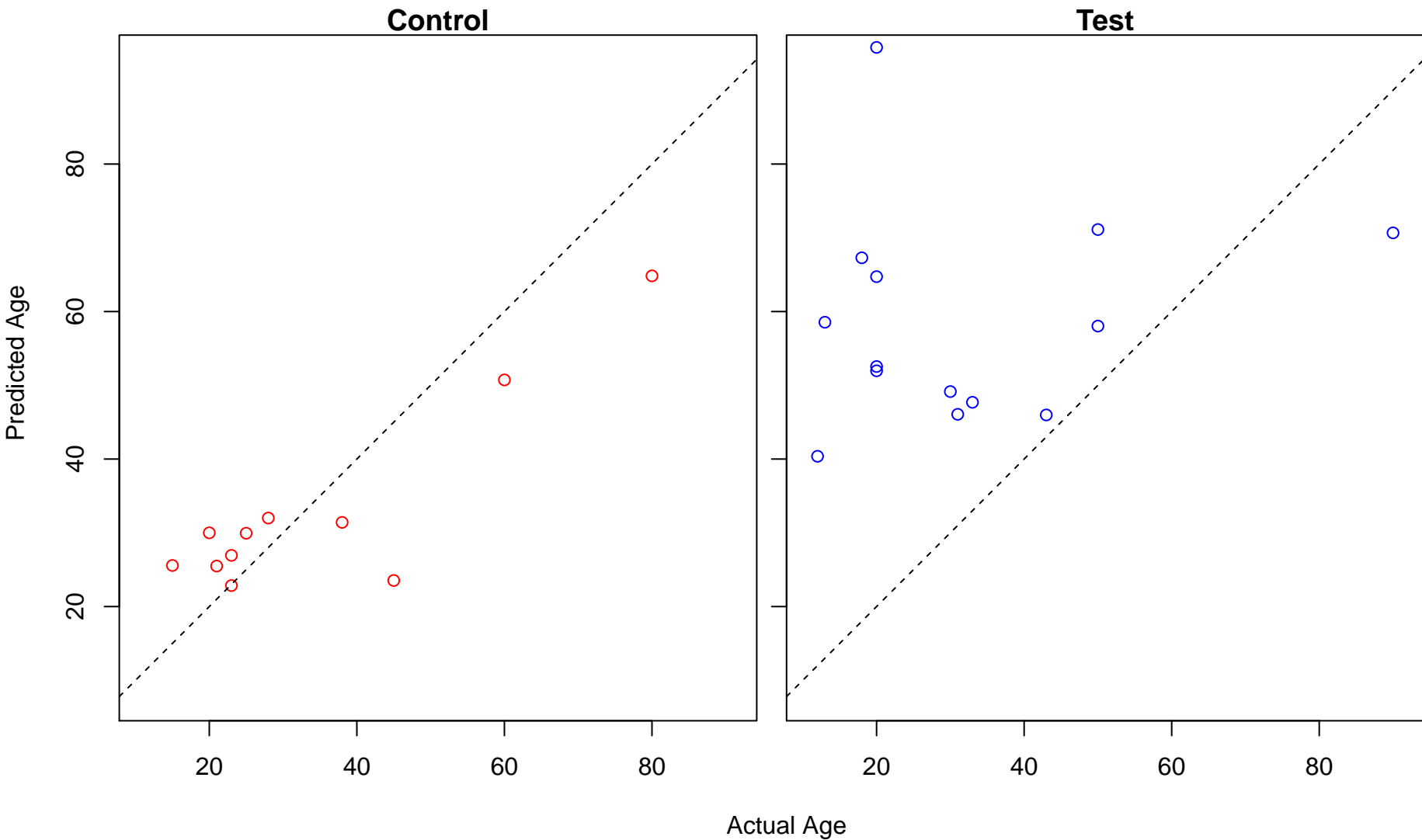
actin filament-based process (Score: 4.142925)



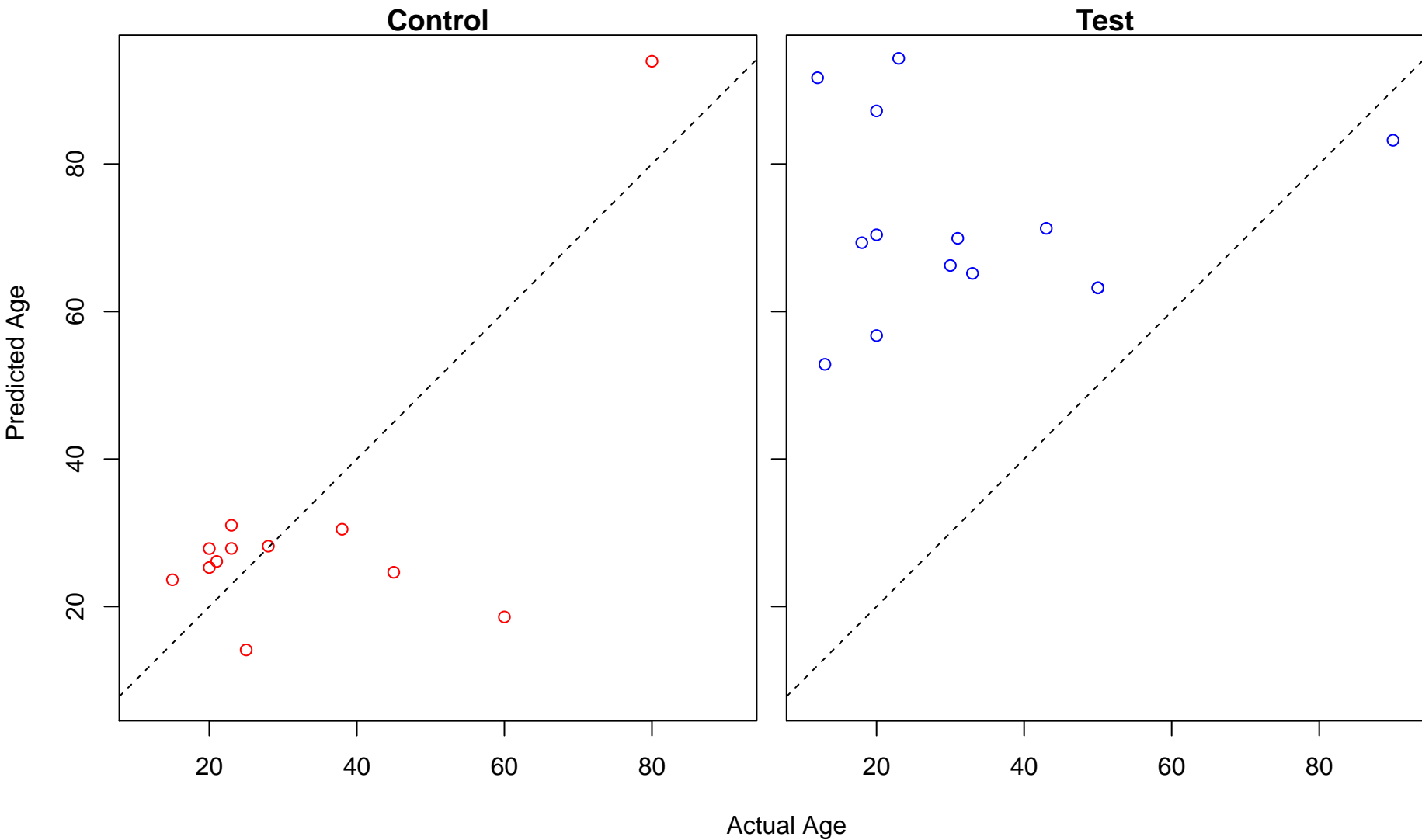
aminoglycan biosynthetic process (Score: 4.142923)



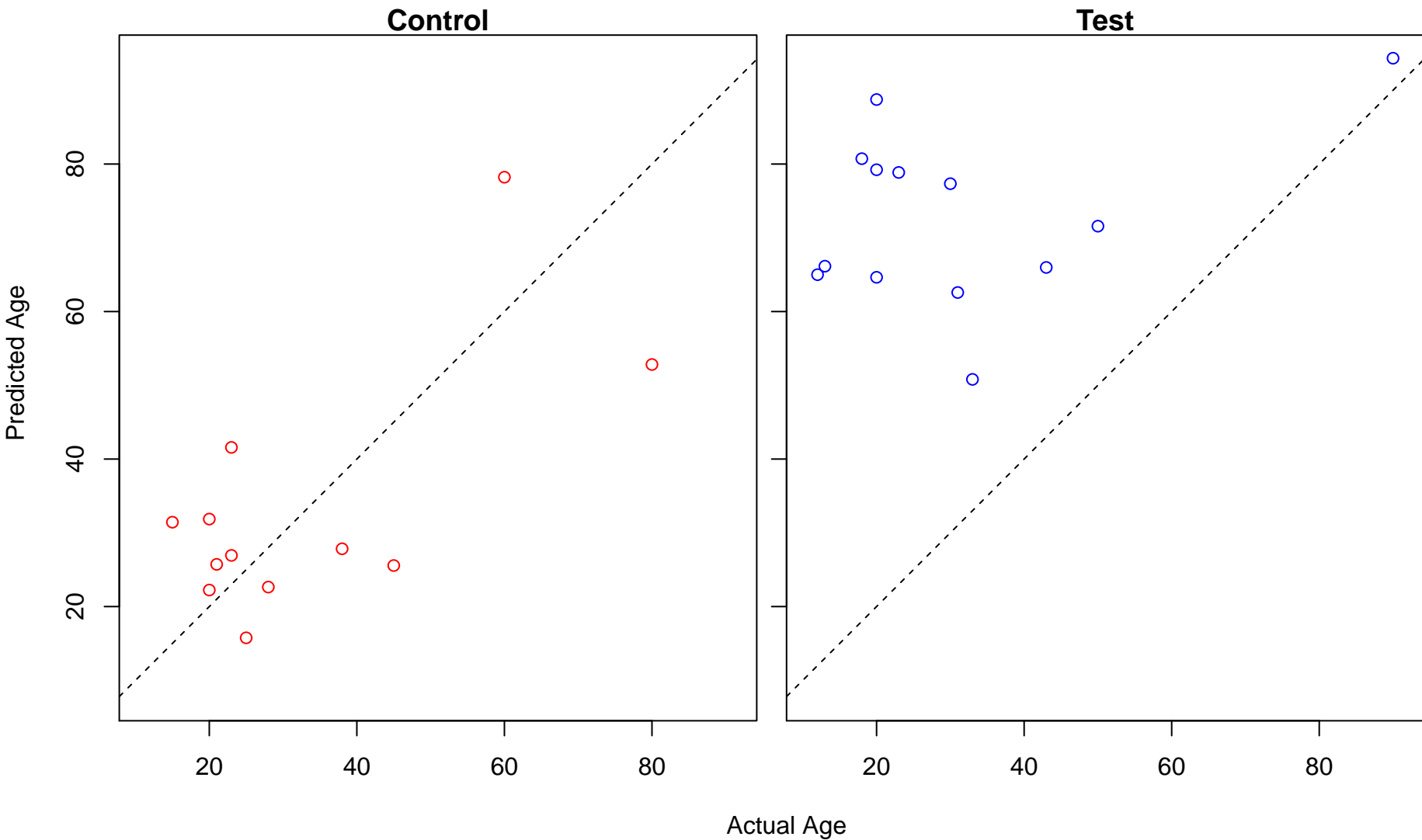
regulation of mitochondrial depolarization (Score: 4.142069)



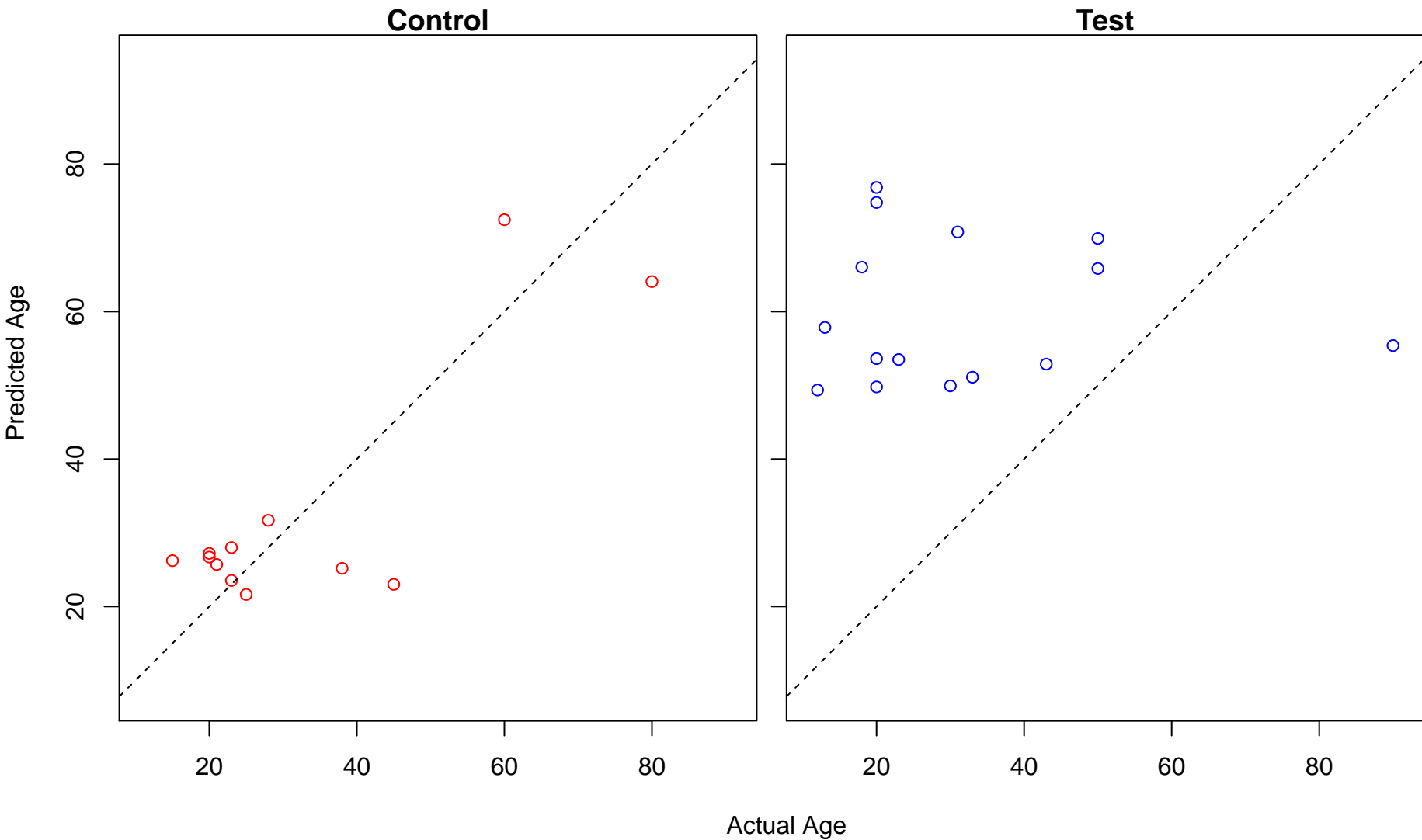
glycosaminoglycan biosynthetic process (Score: 4.139270)



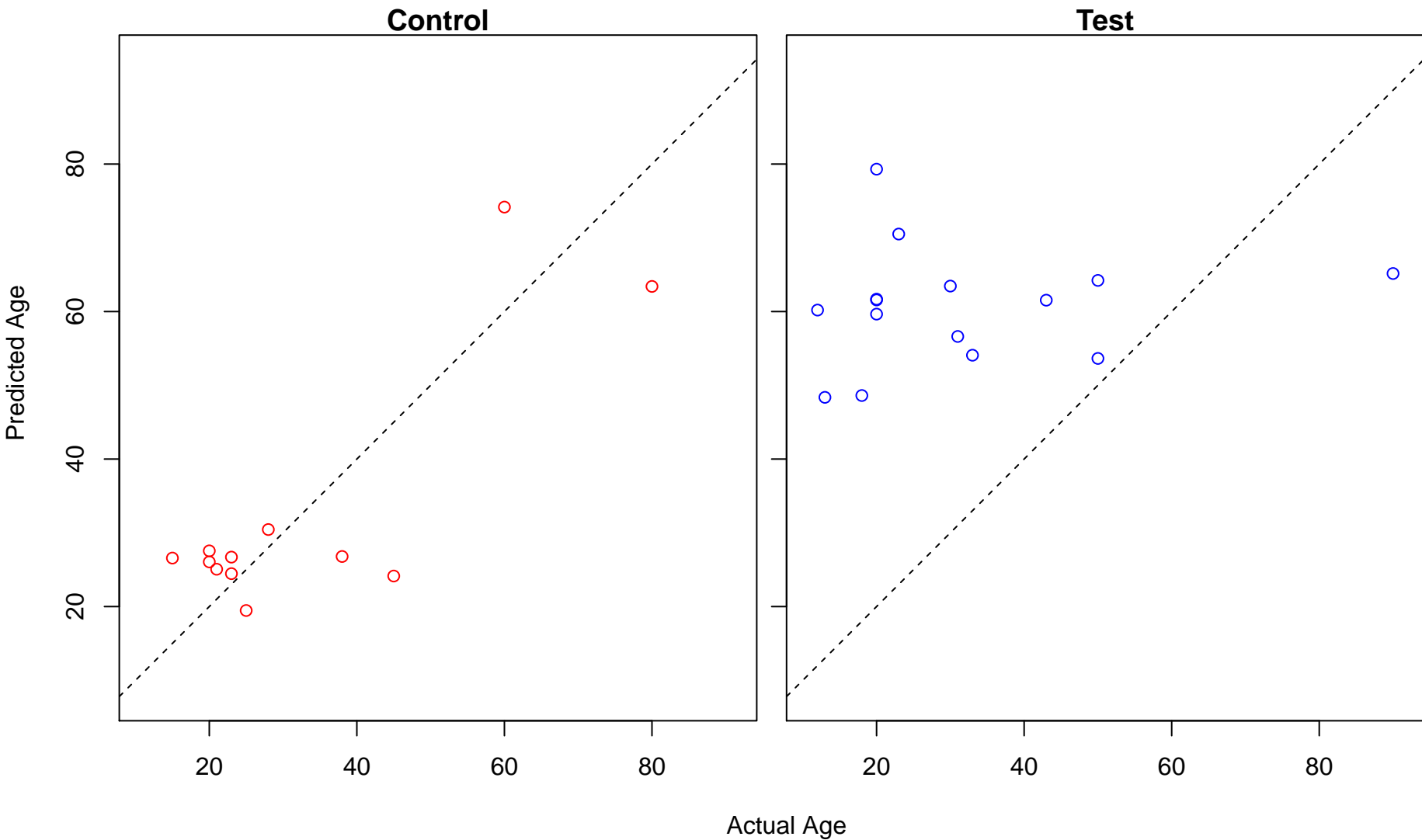
positive regulation of hormone secretion (Score: 4.137943)



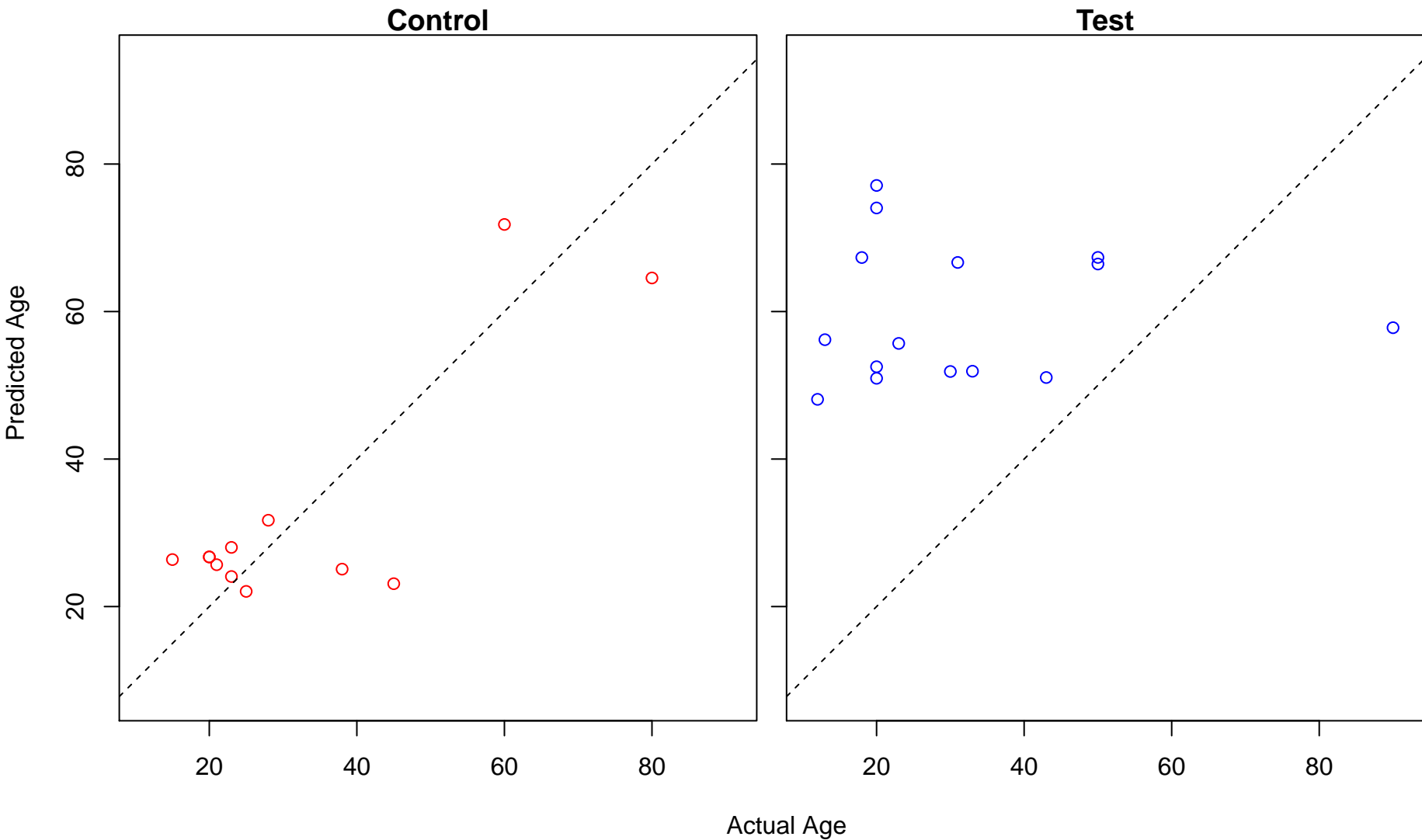
negative regulation of receptor activity (Score: 4.133098)



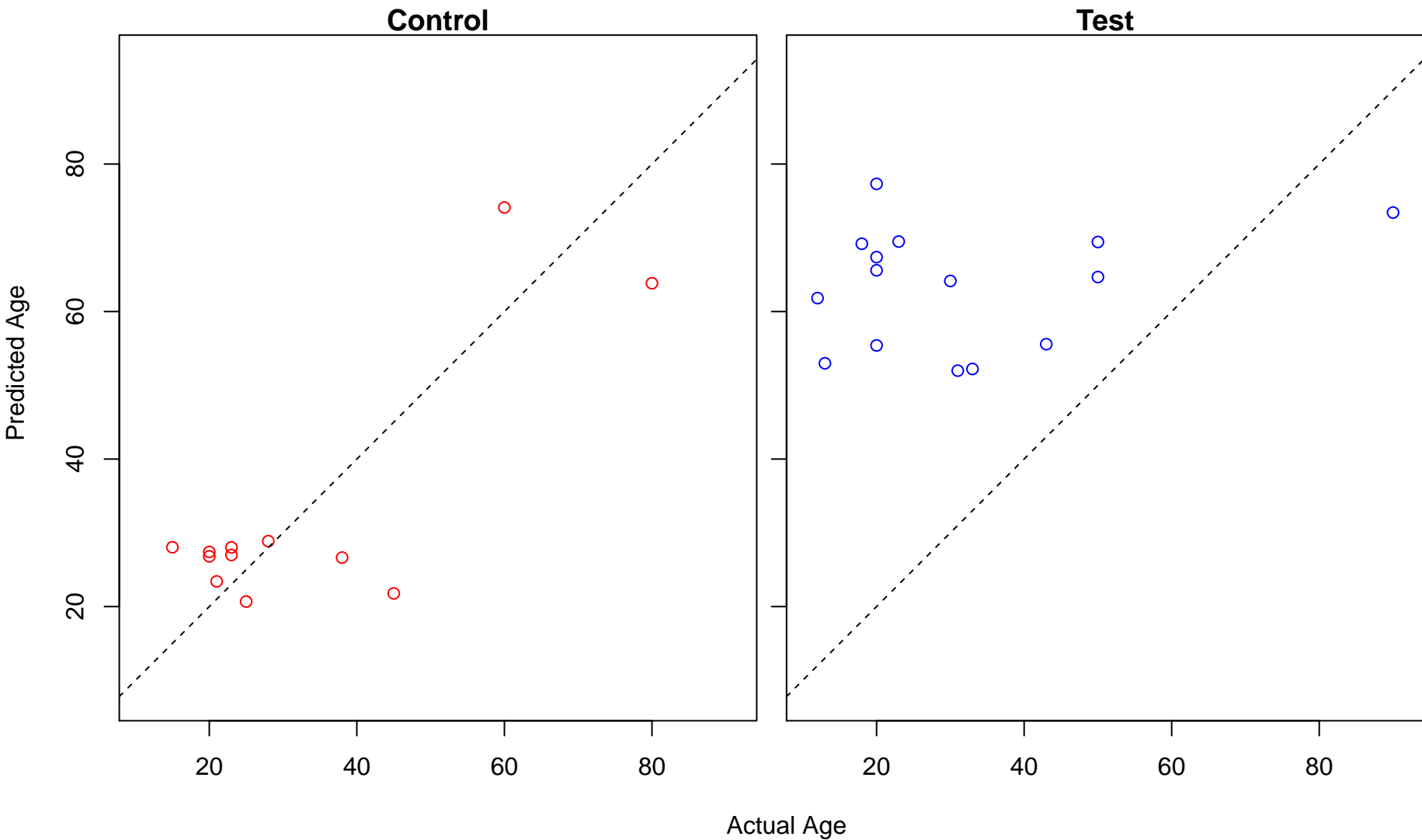
spermatid development (Score: 4.132641)



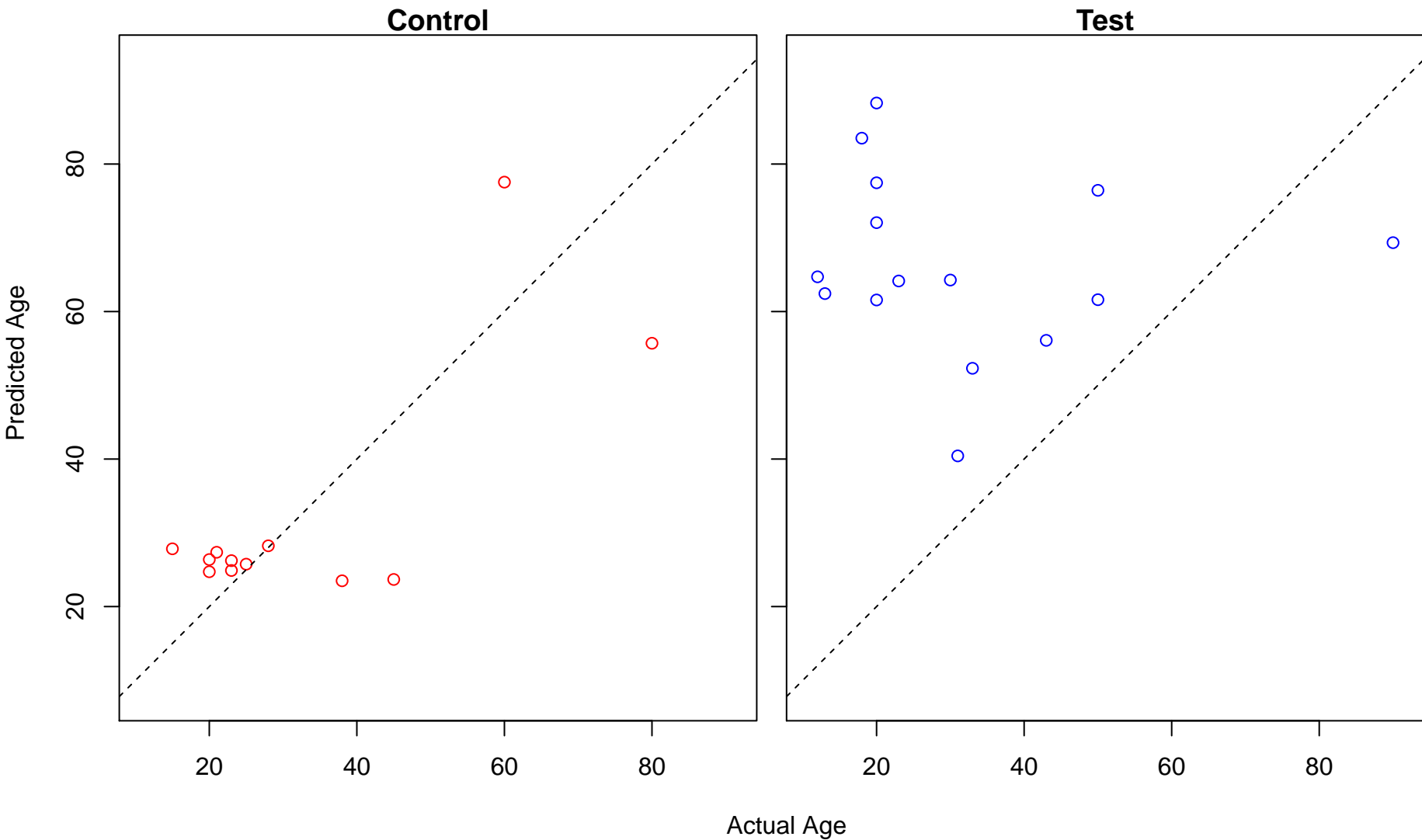
negative regulation of ion transmembrane transporter activity (Score: 4.132022)



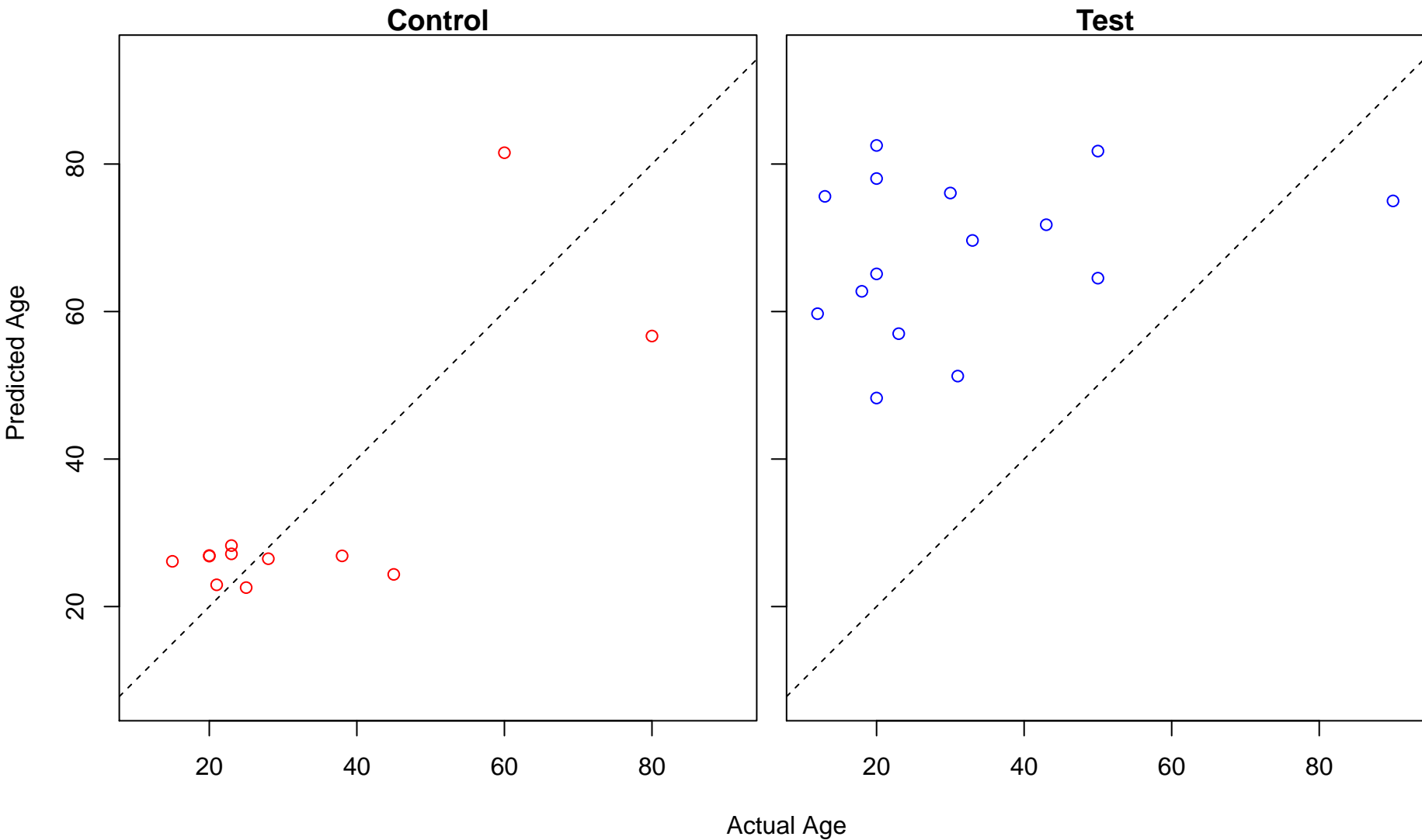
cellular protein catabolic process (Score: 4.131785)



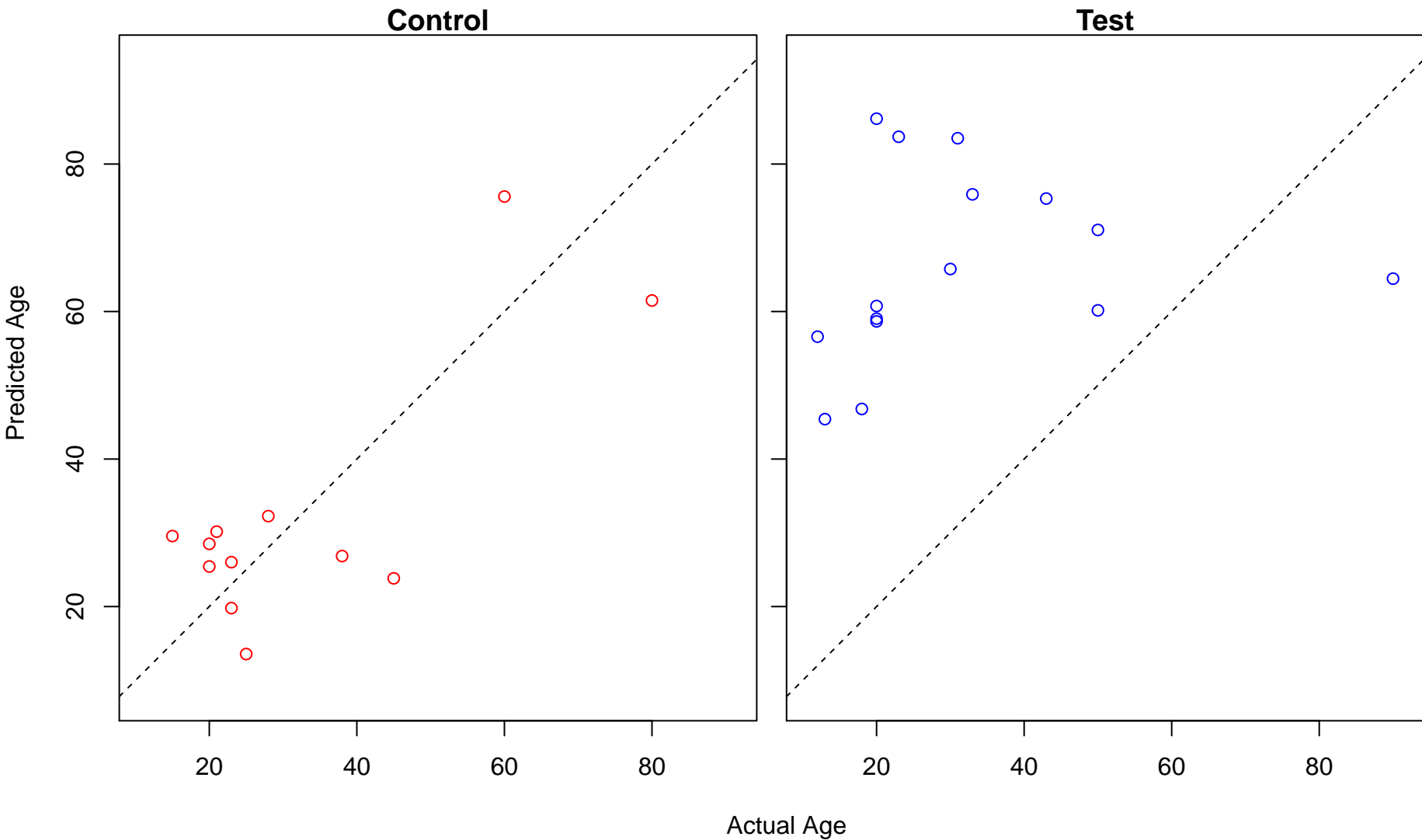
nucleoside monophosphate biosynthetic process (Score: 4.128779)



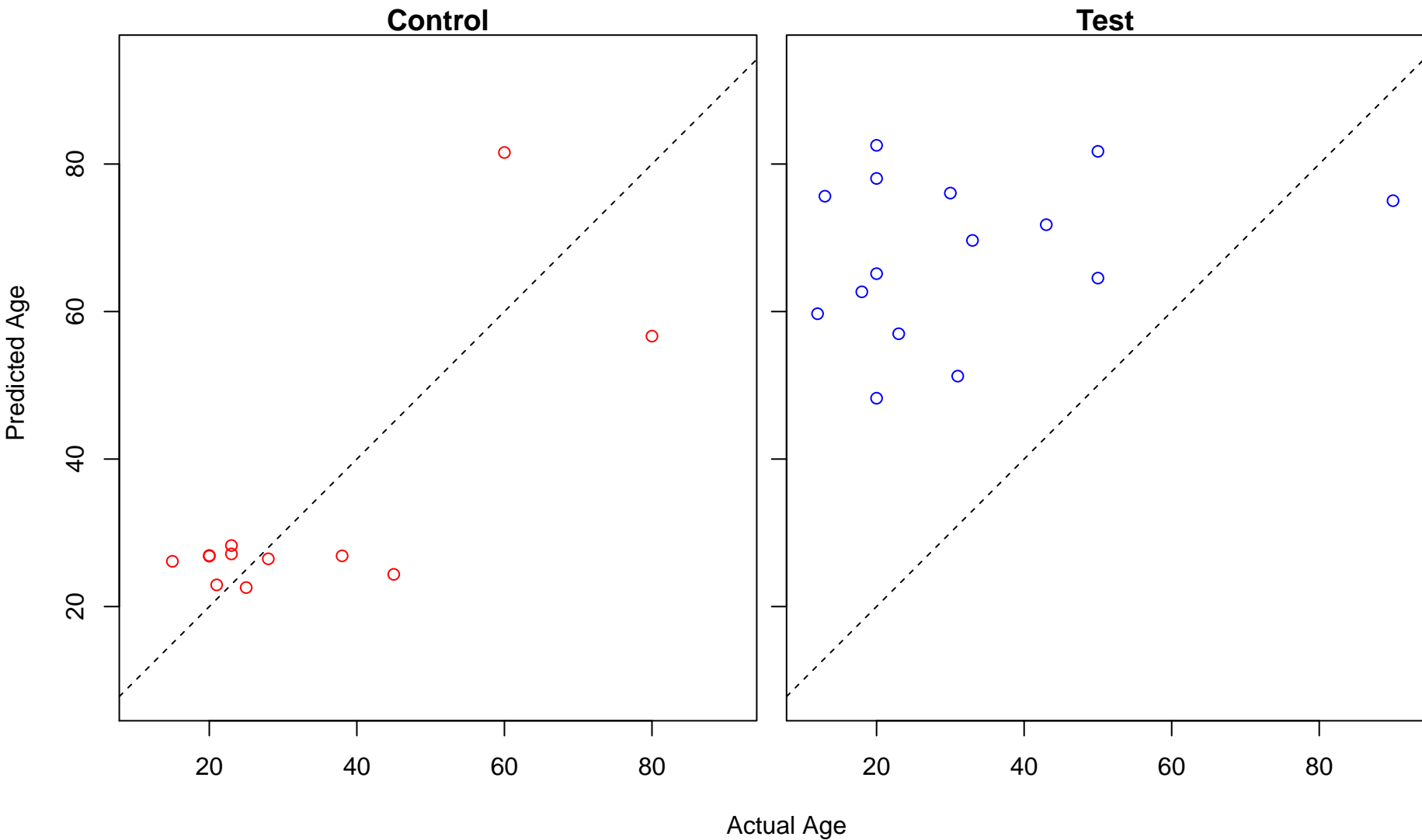
chloride transport (Score: 4.126664)



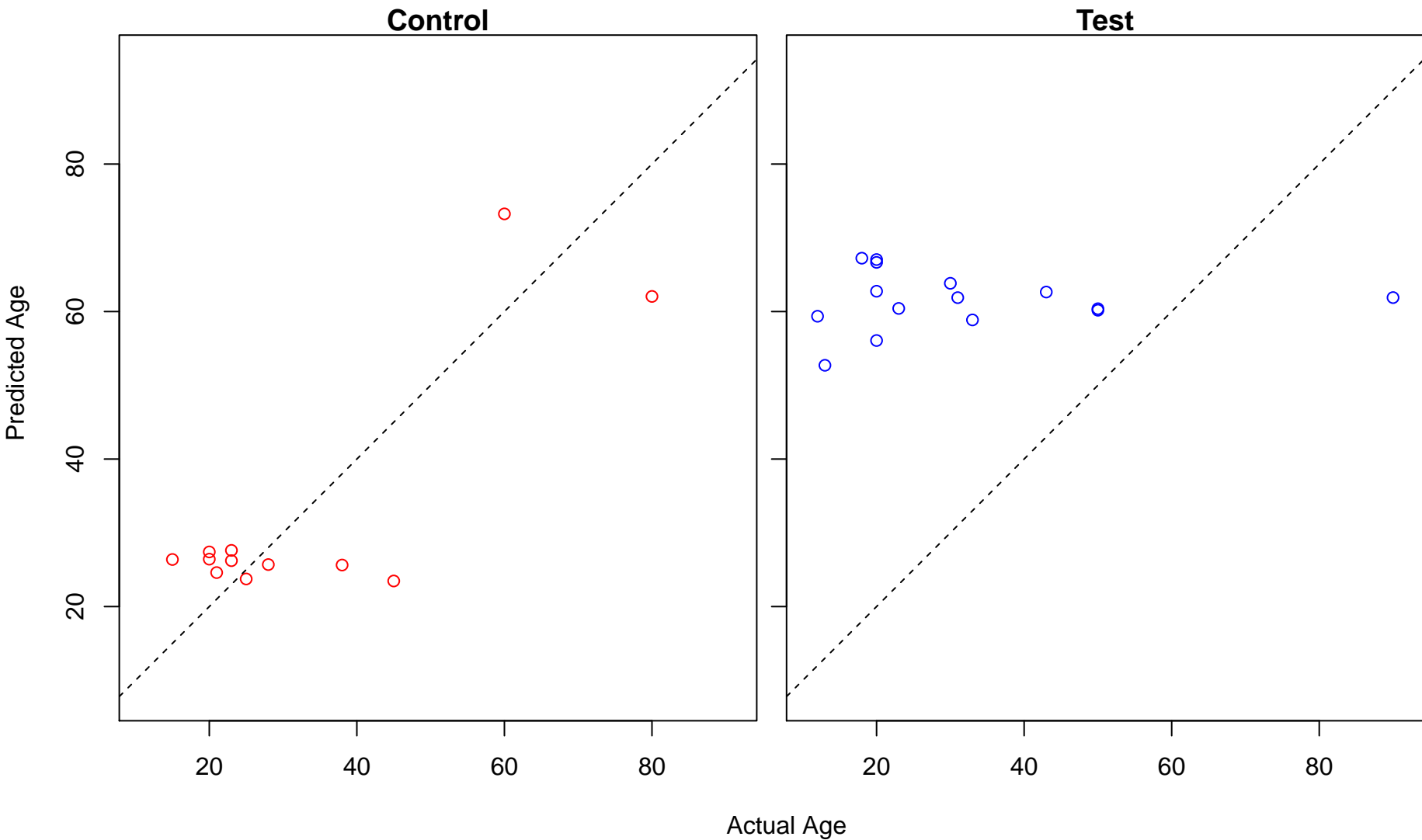
negative regulation of protein kinase B signaling (Score: 4.125589)



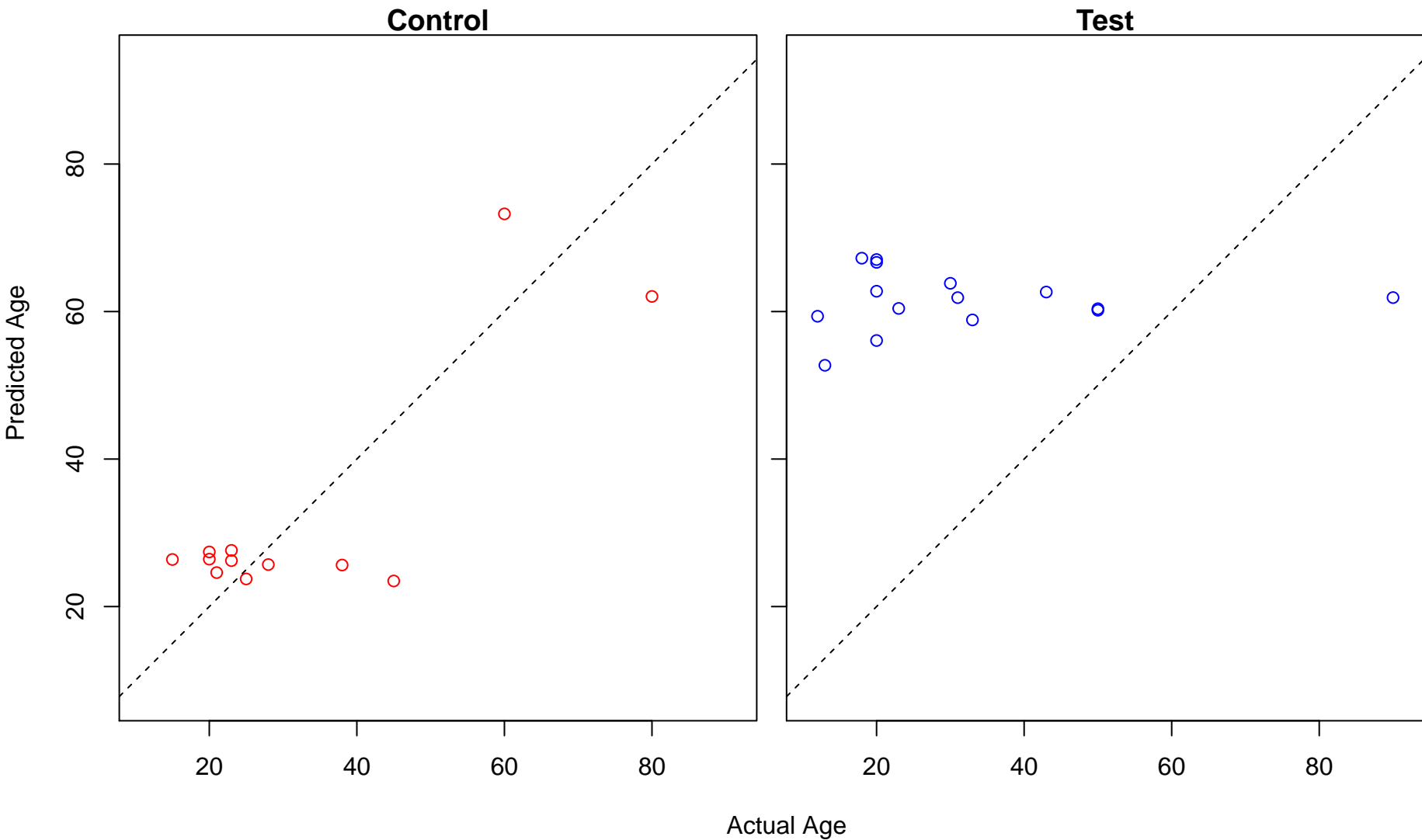
chloride transmembrane transport (Score: 4.123029)



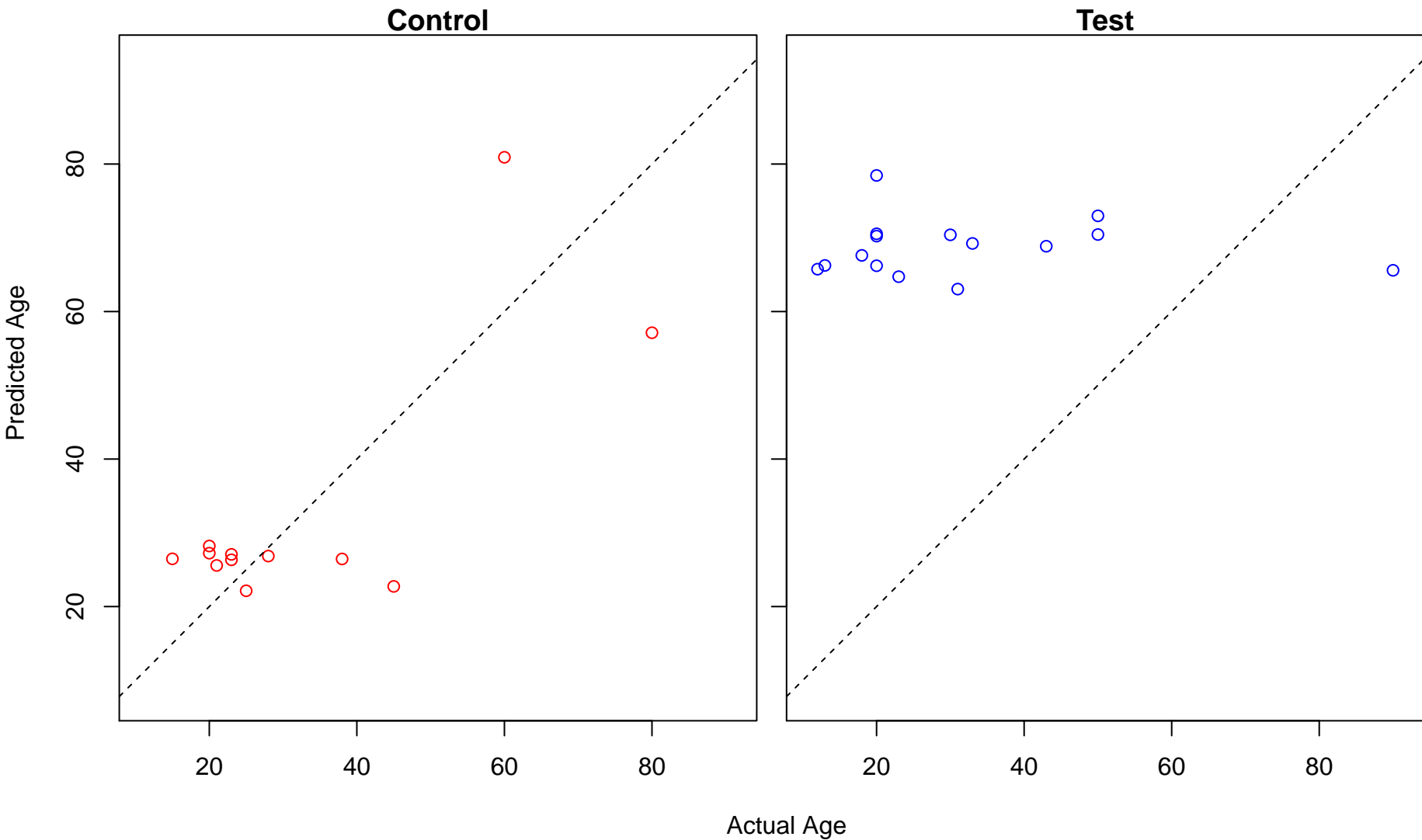
neutral lipid biosynthetic process (Score: 4.121973)



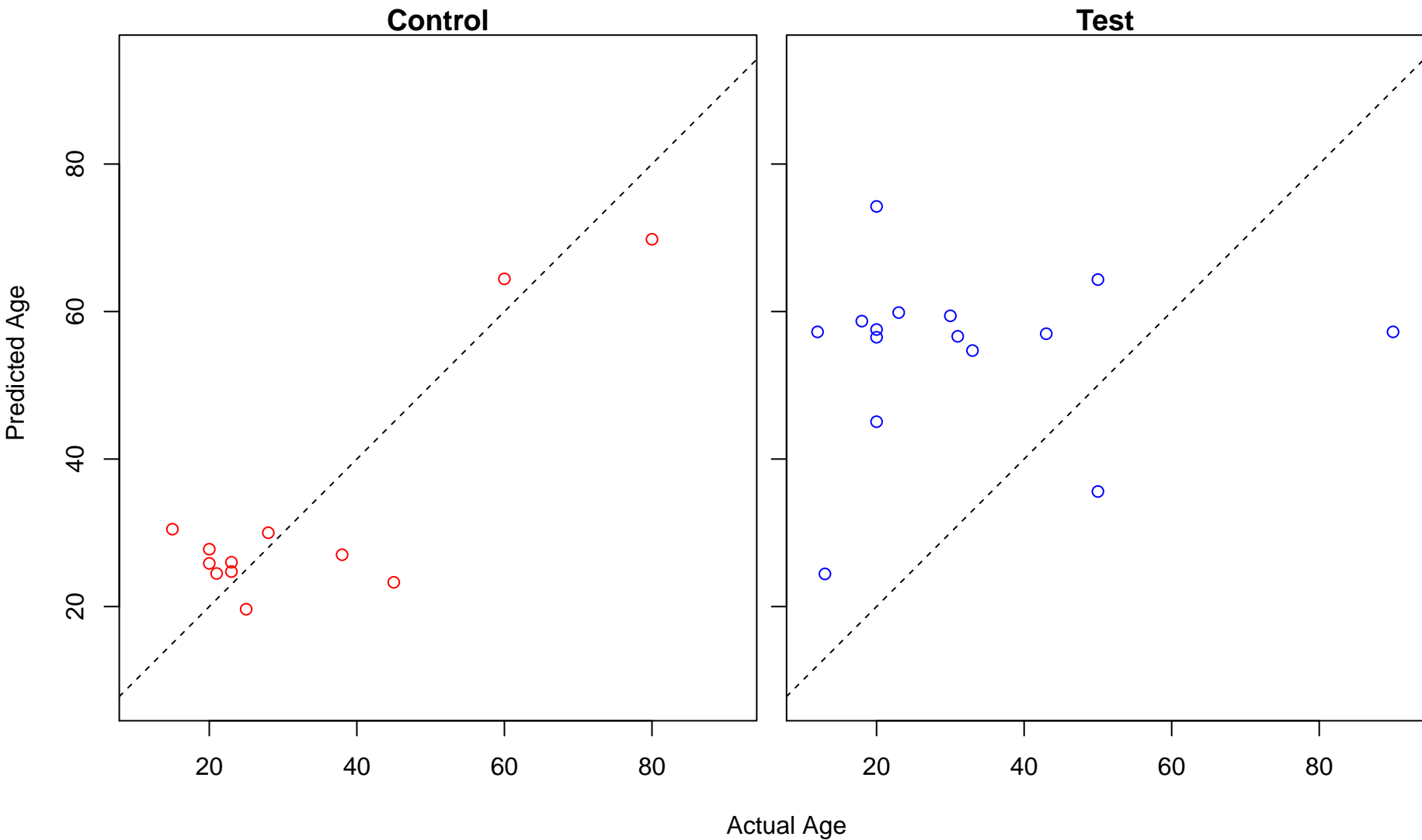
acylglycerol biosynthetic process (Score: 4.121973)



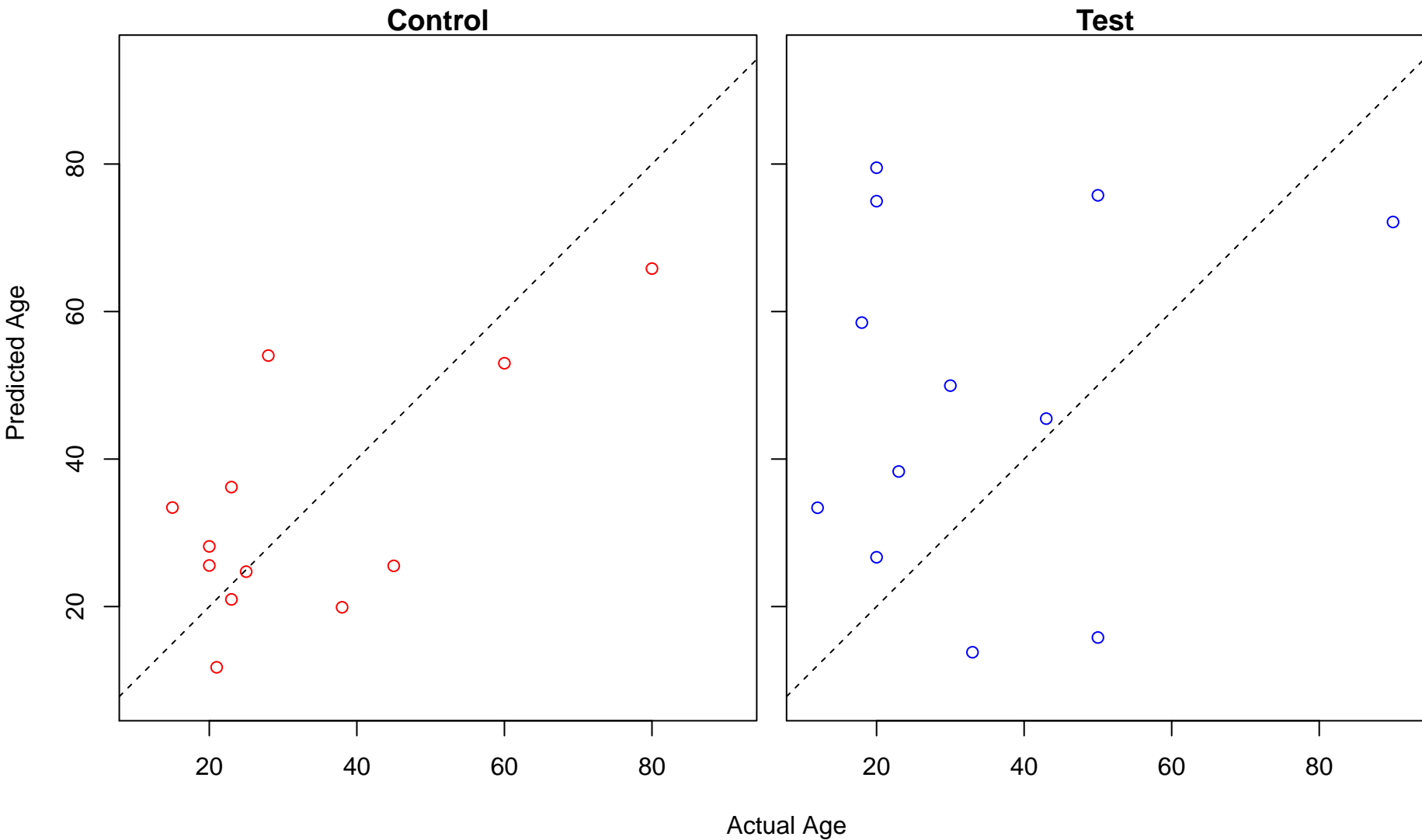
sphingolipid metabolic process (Score: 4.121523)



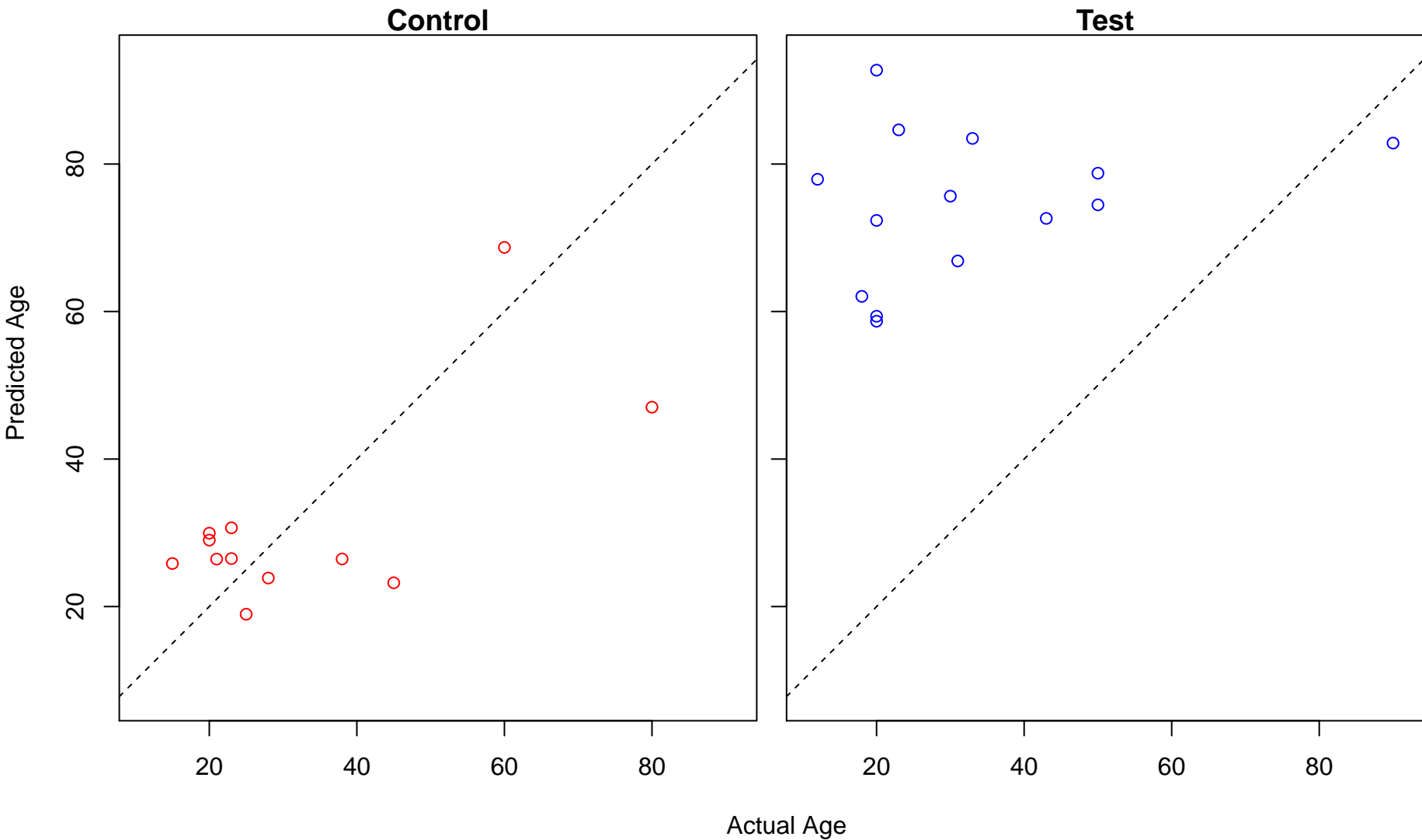
regulation of macroautophagy (Score: 4.120216)



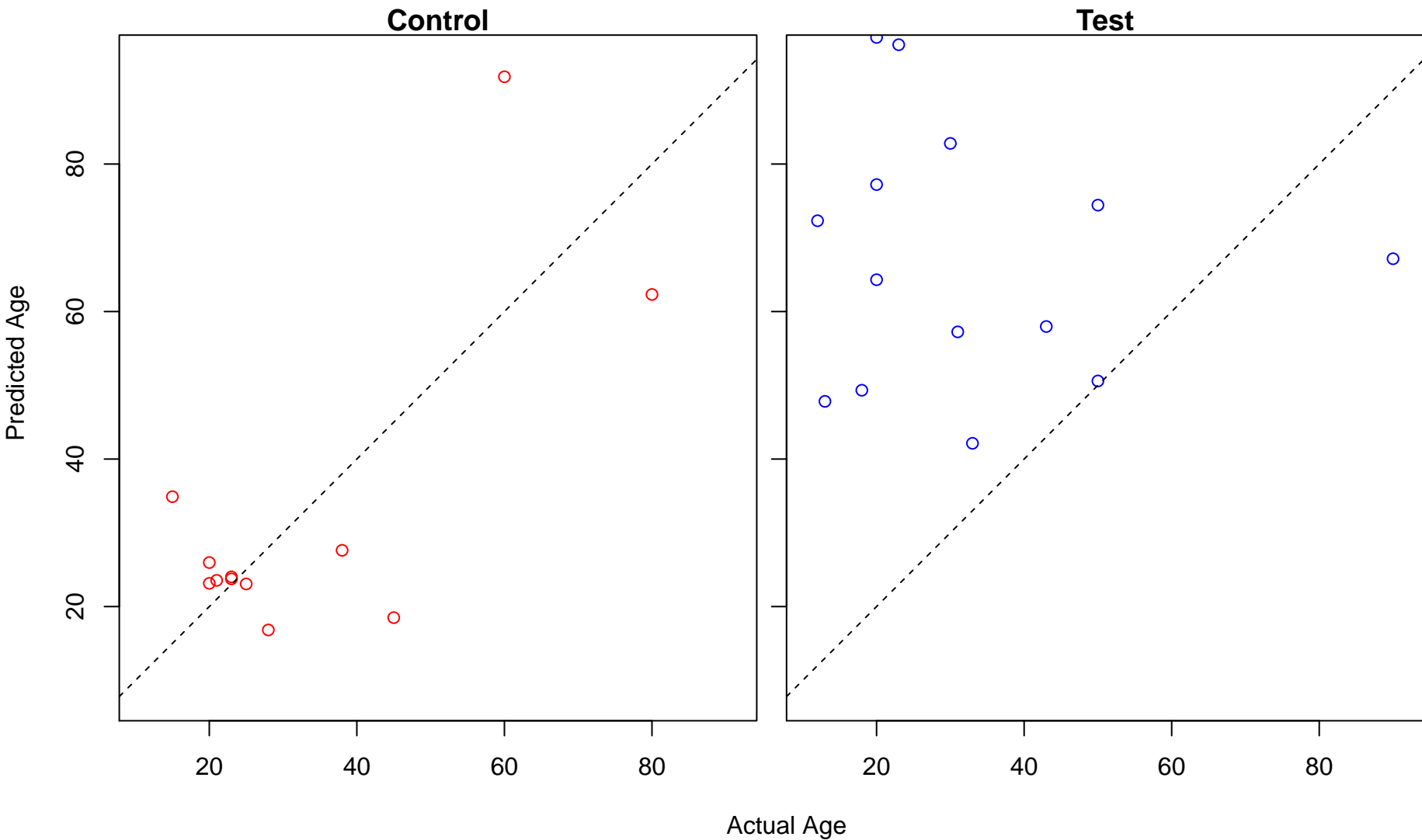
segmentation (Score: 4.116235)



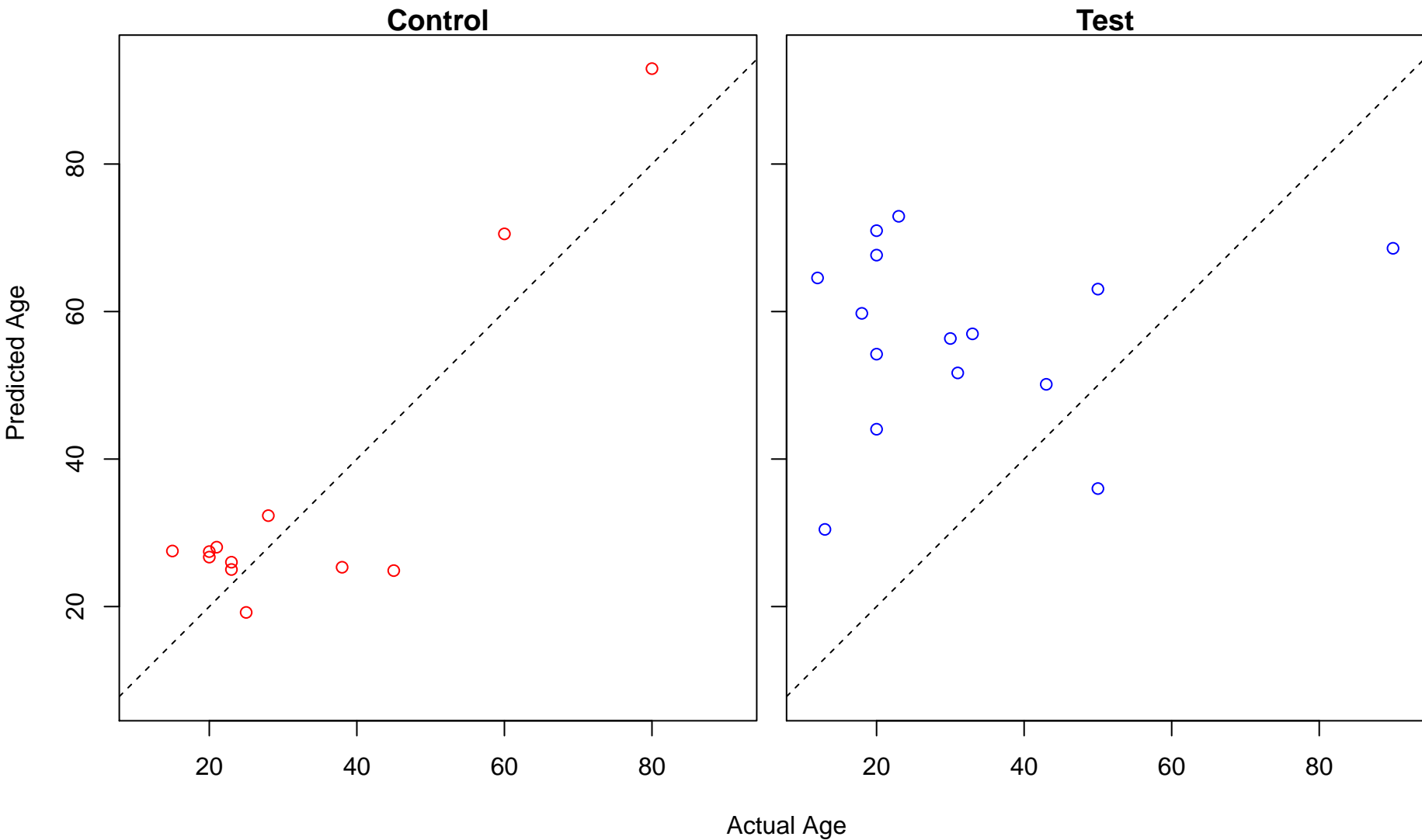
negative regulation of embryonic development (Score: 4.112768)



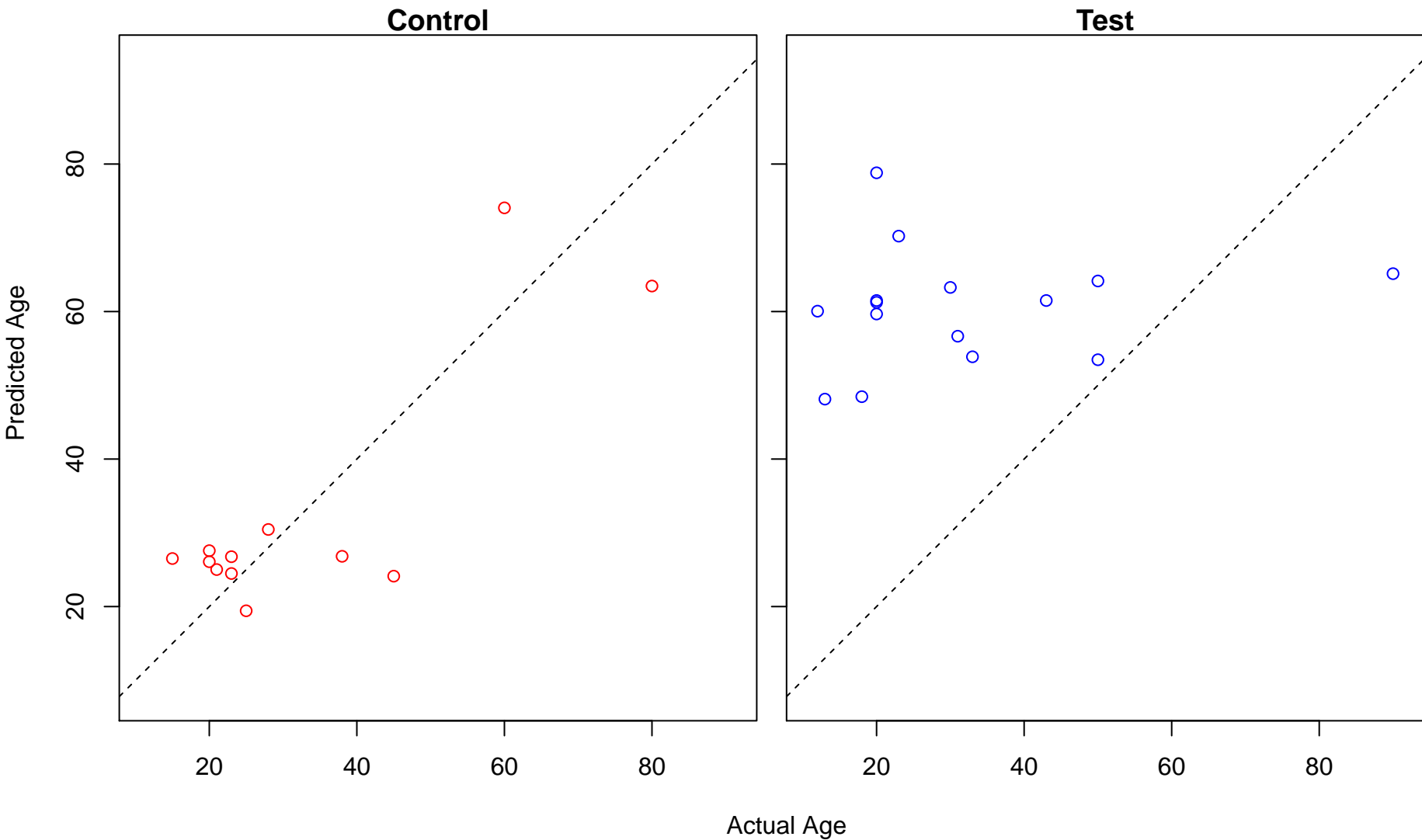
fibril organization (Score: 4.112548)



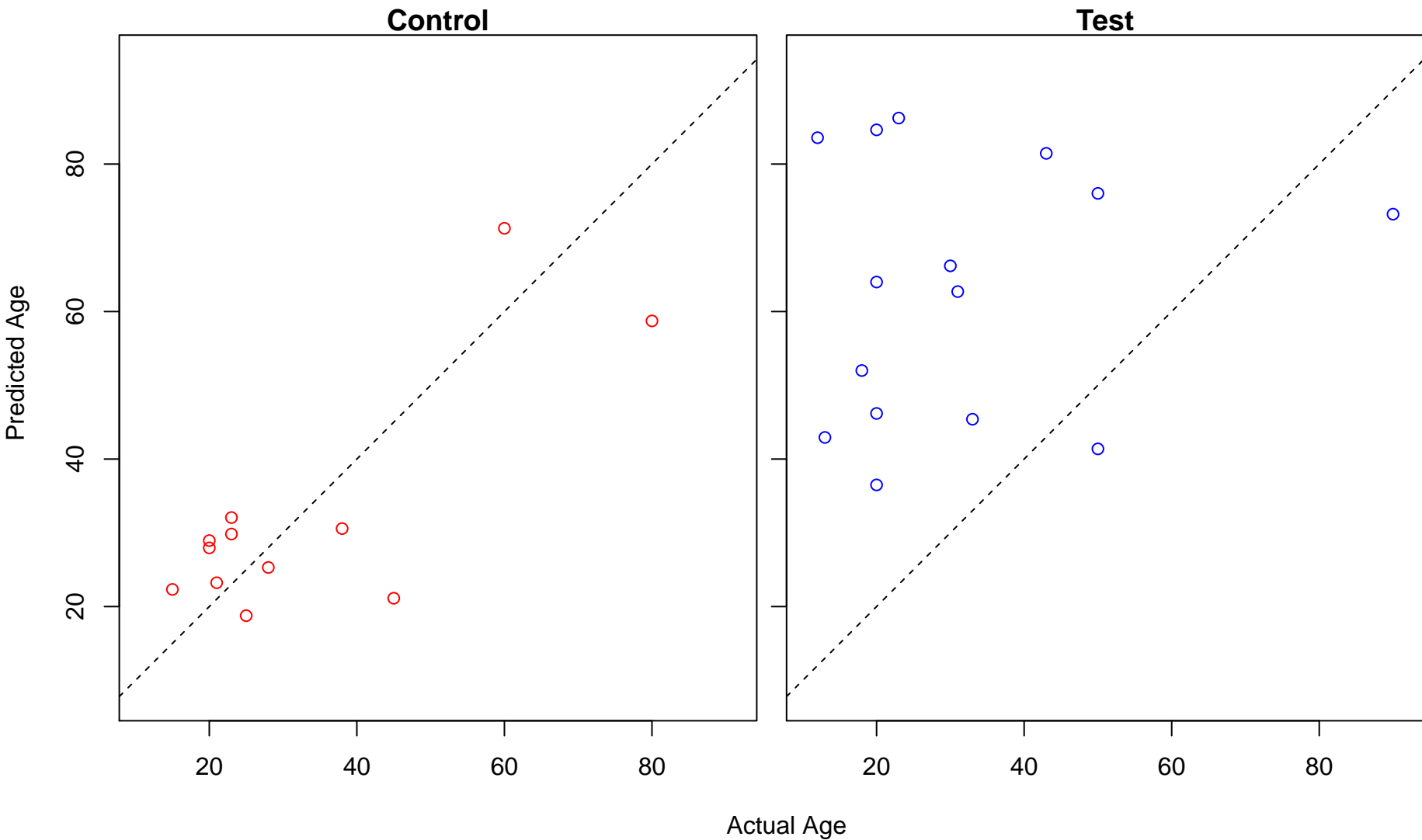
histone deubiquitination (Score: 4.111548)



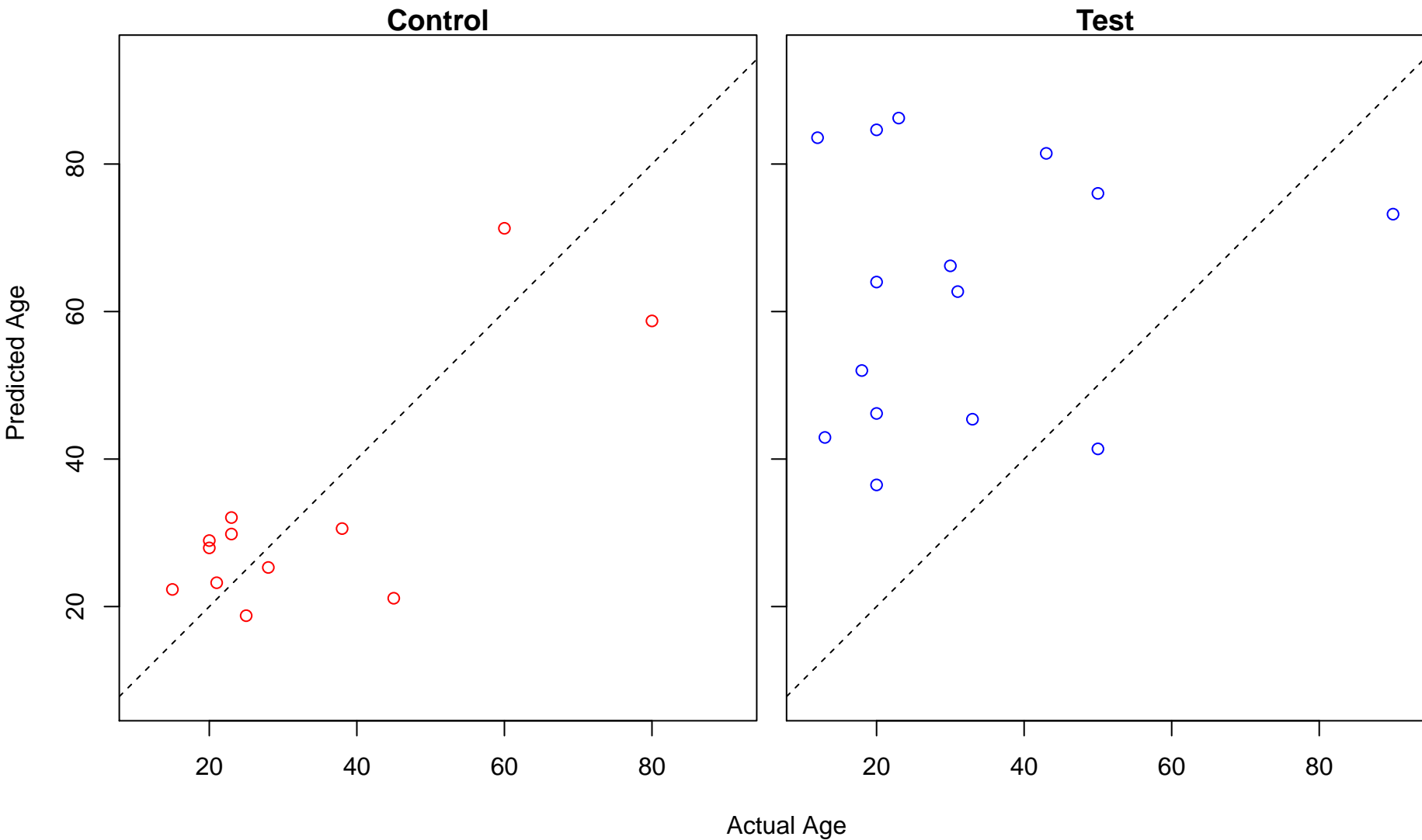
spermatid differentiation (Score: 4.110765)



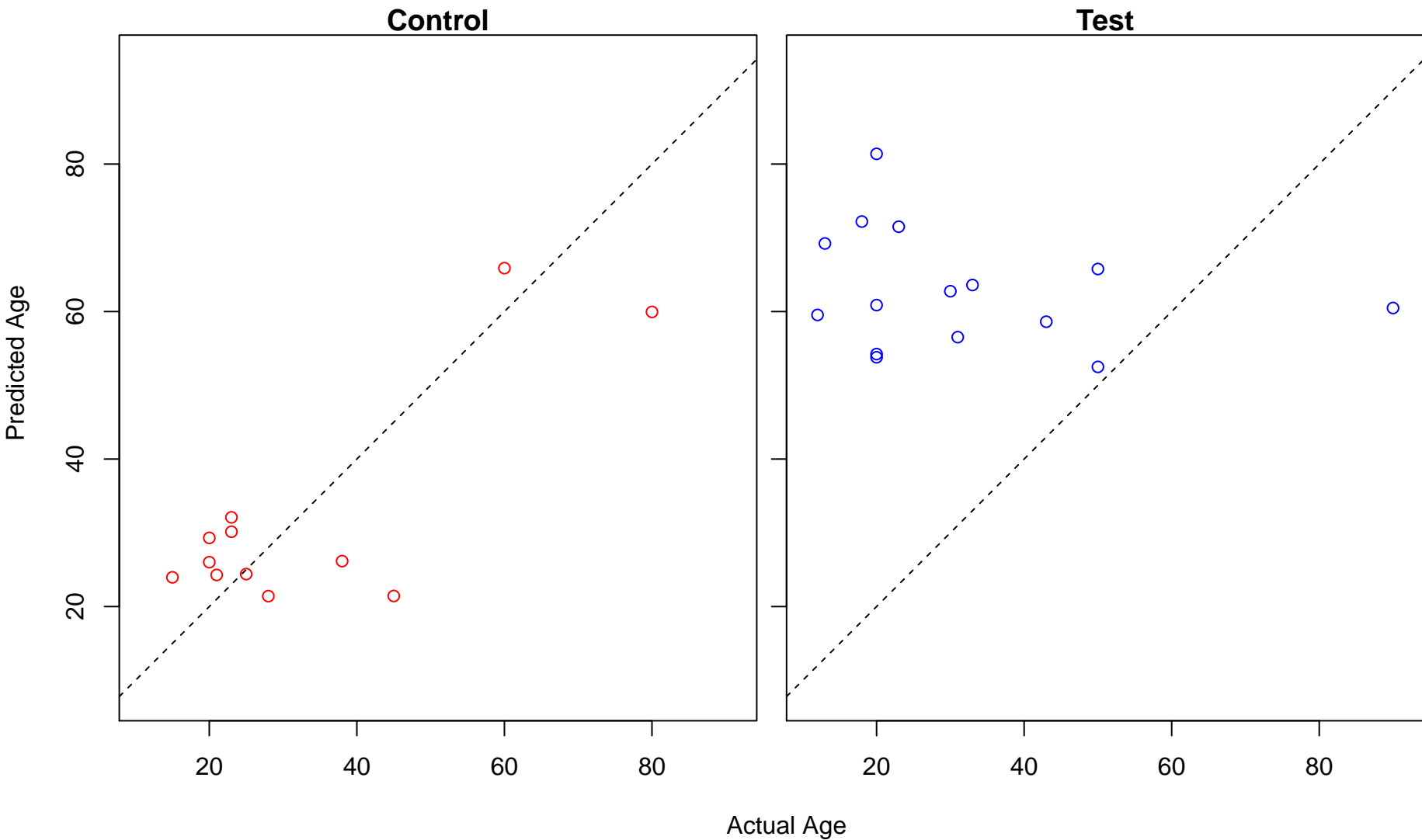
response to potassium ion (Score: 4.110001)



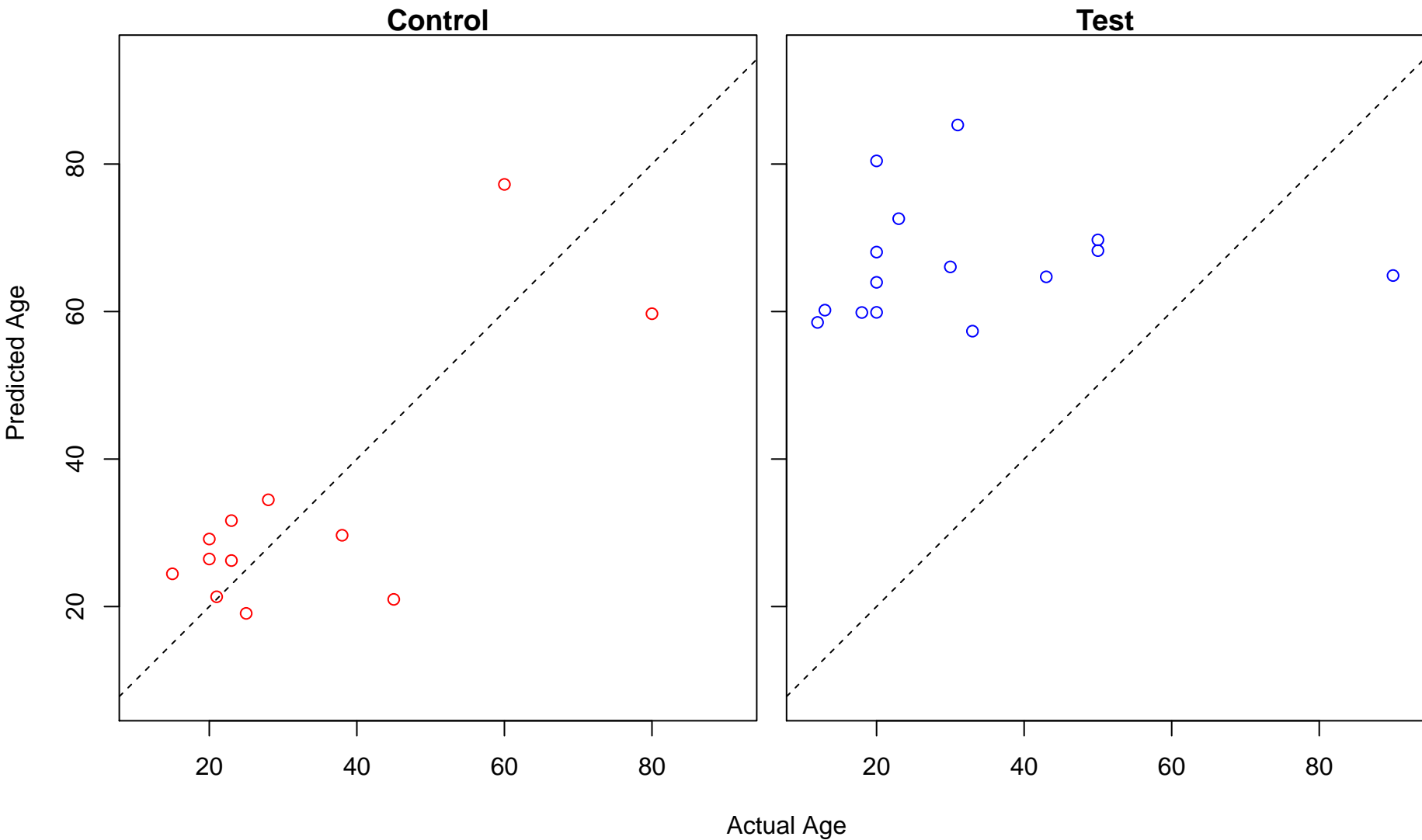
cellular response to potassium ion (Score: 4.110001)



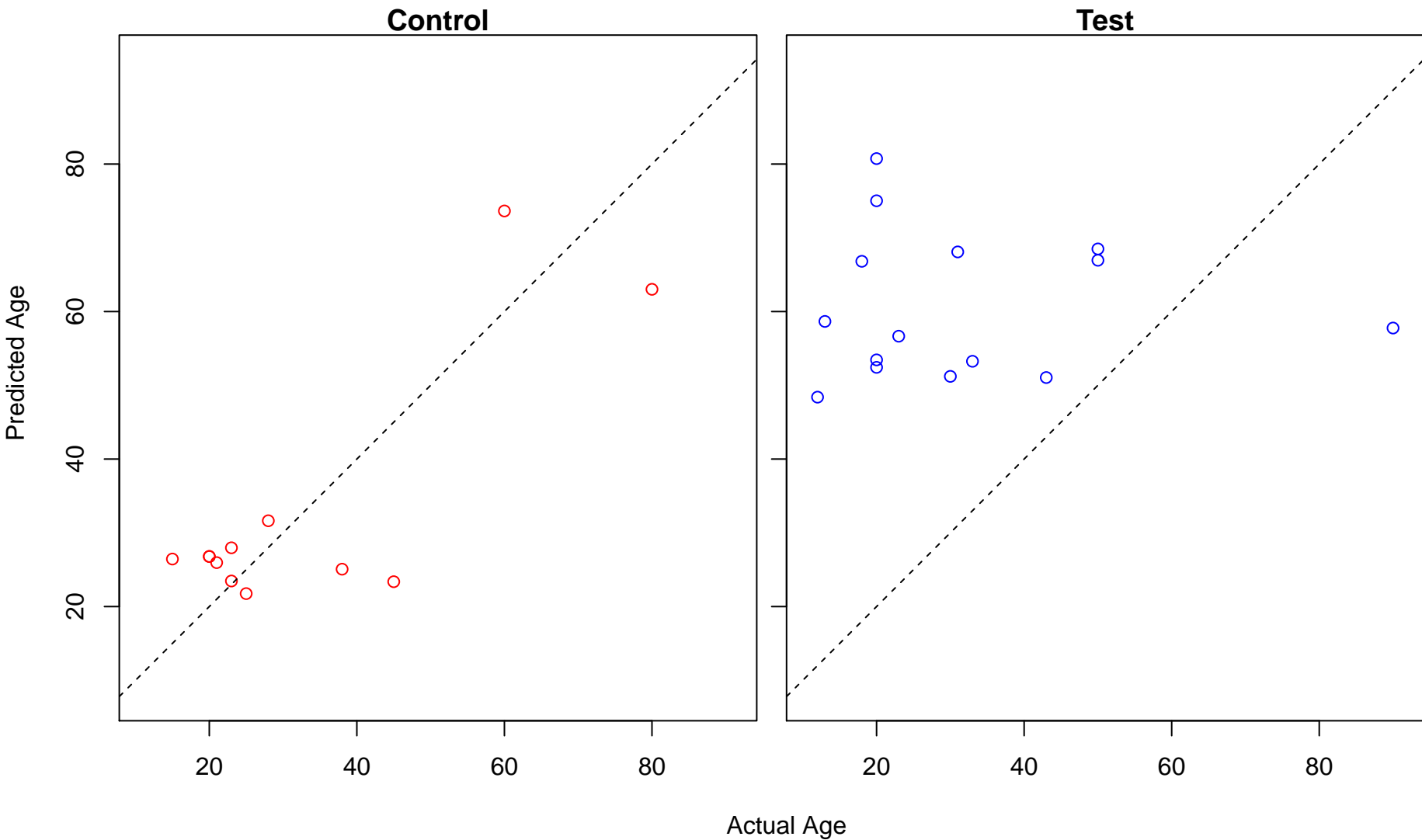
negative regulation of epithelial cell differentiation (Score: 4.108104)



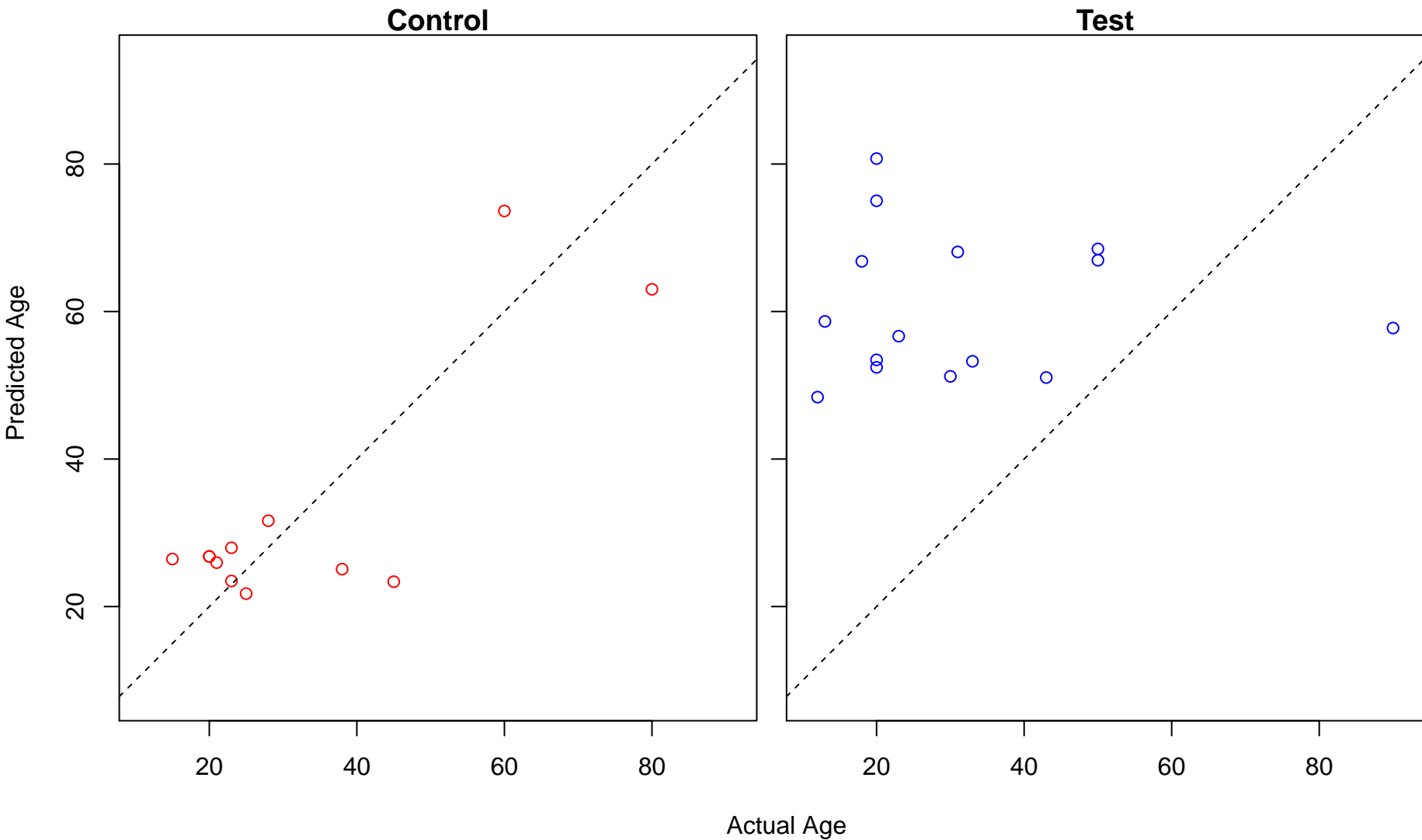
lymphocyte mediated immunity (Score: 4.105481)



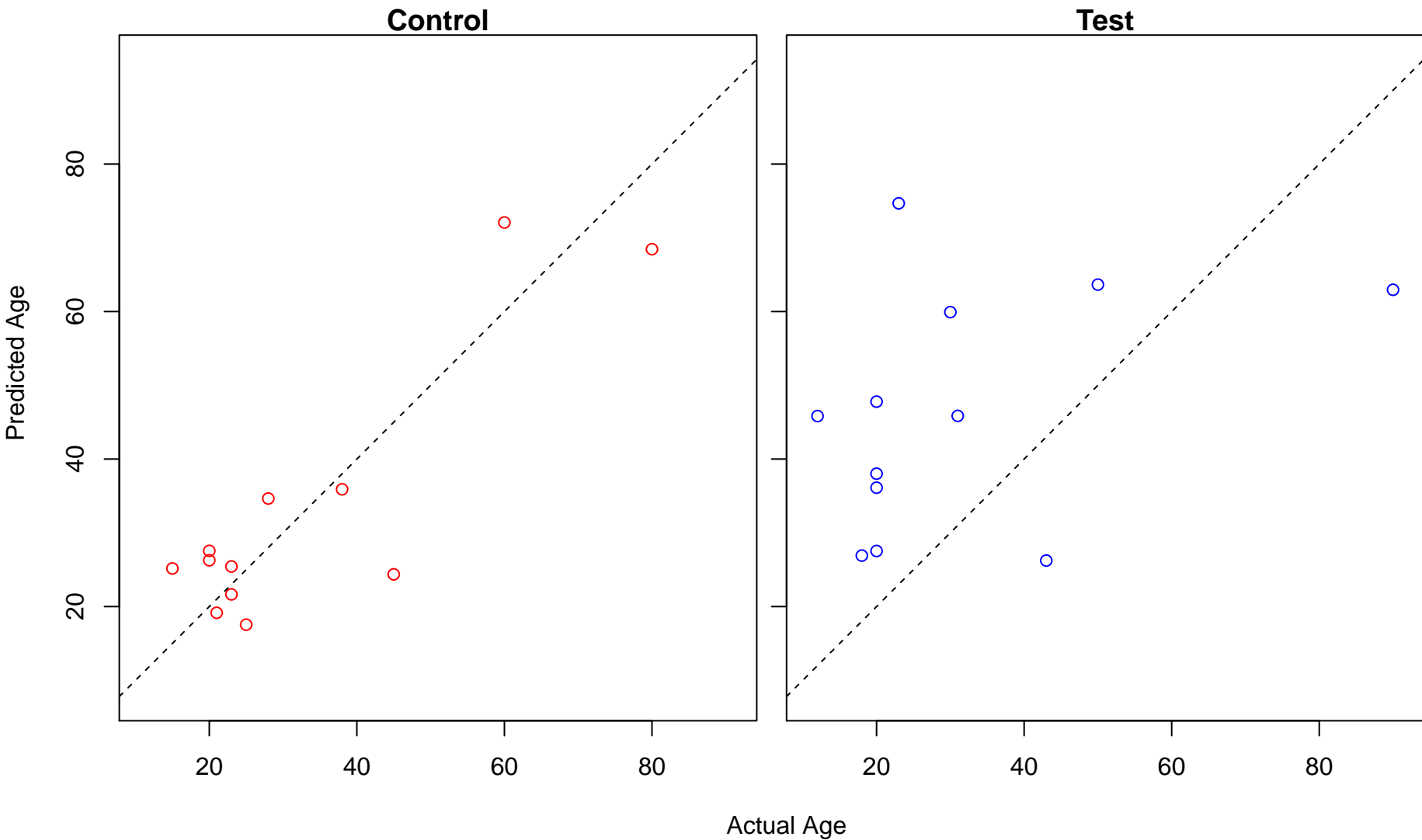
negative regulation of calcium ion transmembrane transporter activity (Score: 4.103554)



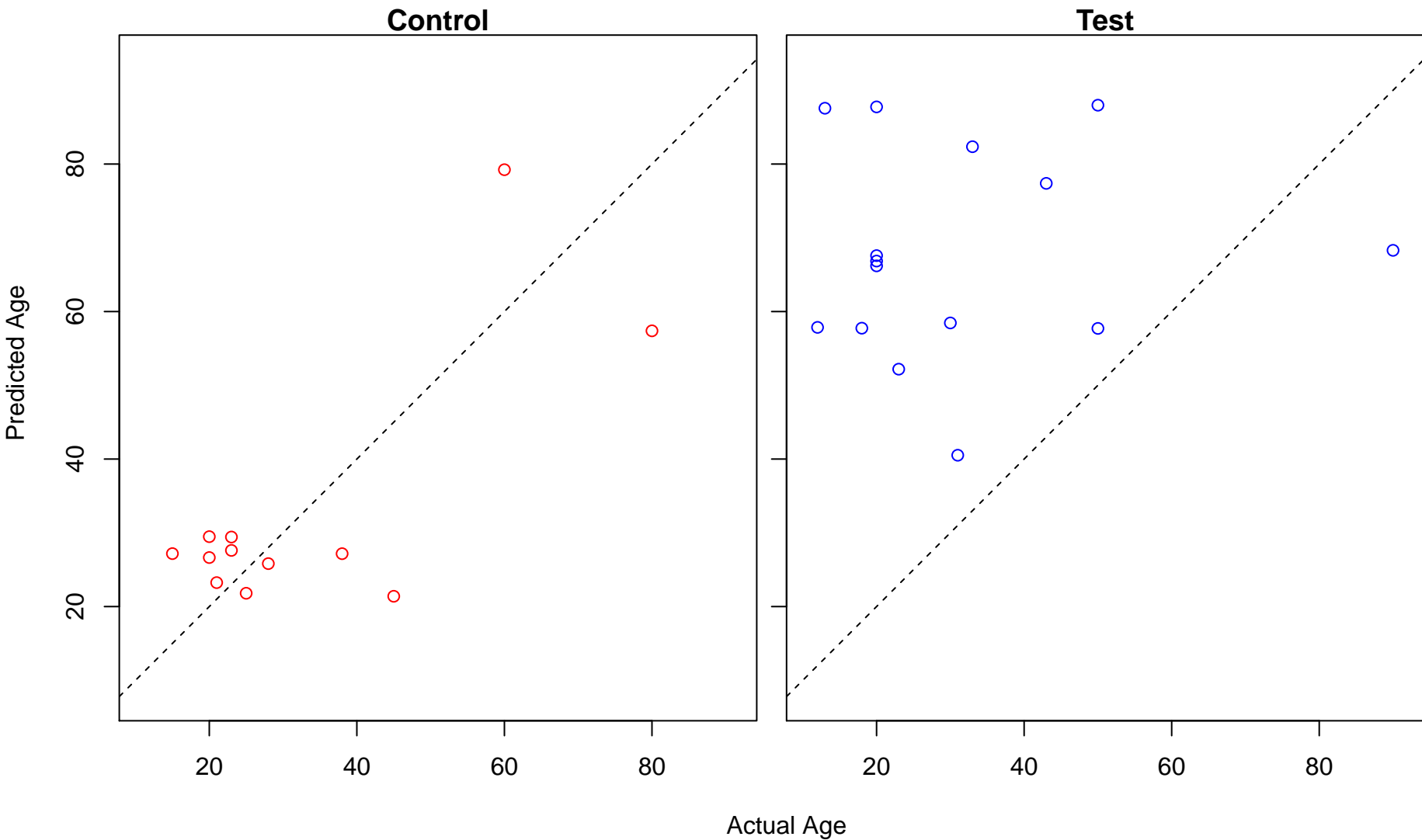
negative regulation of calcium ion transmembrane transport (Score: 4.103554)



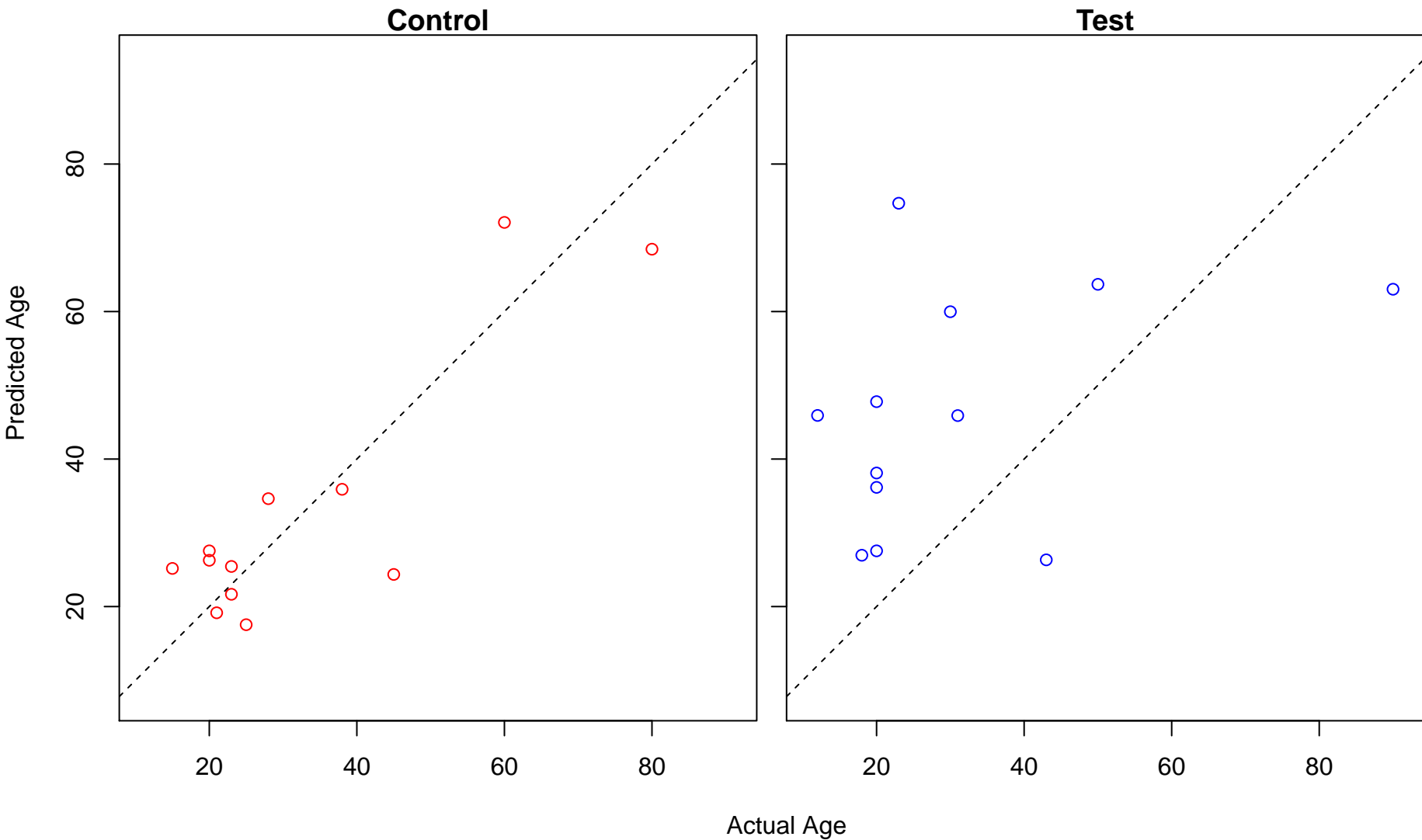
lysosomal transport (Score: 4.102441)



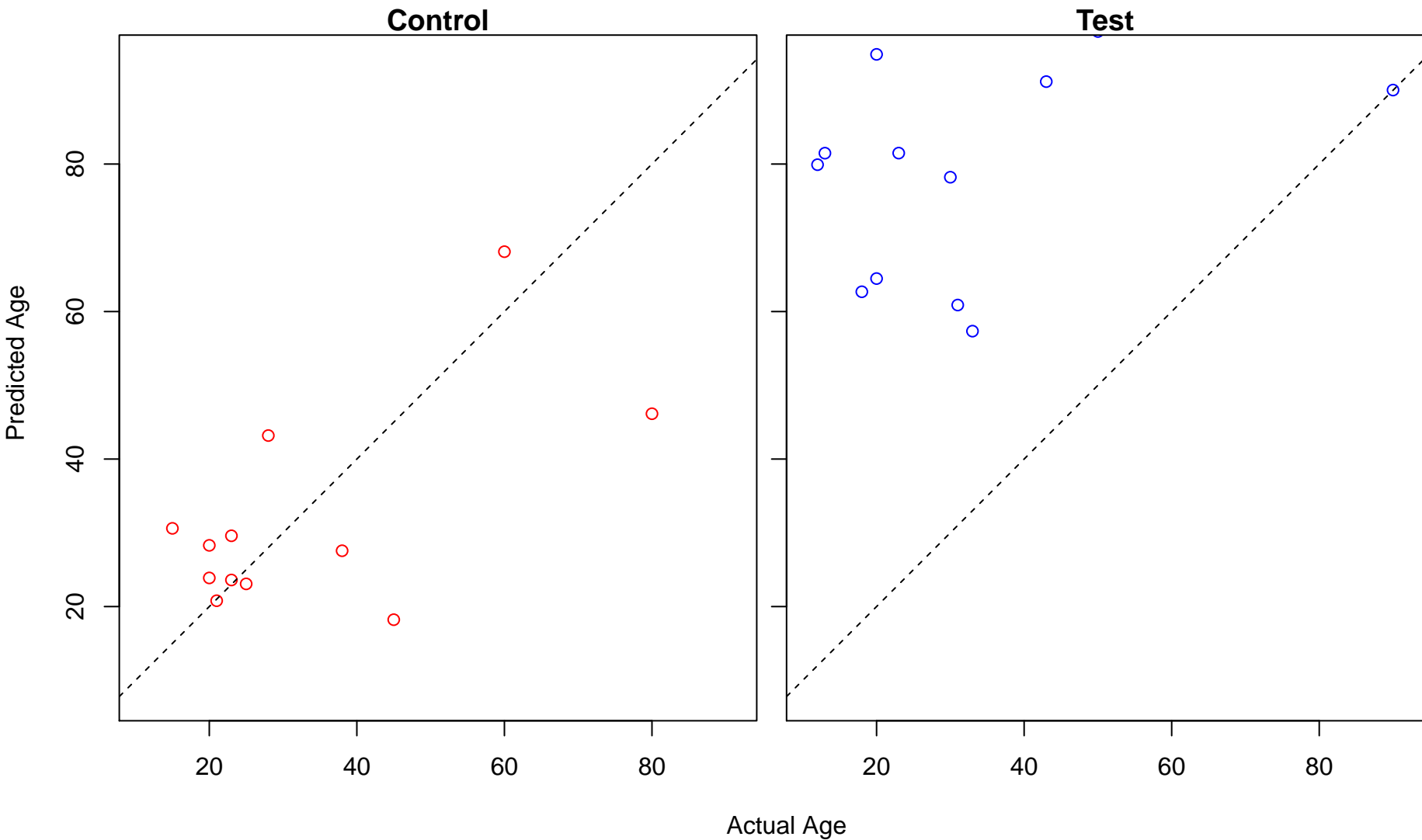
associative learning (Score: 4.101603)



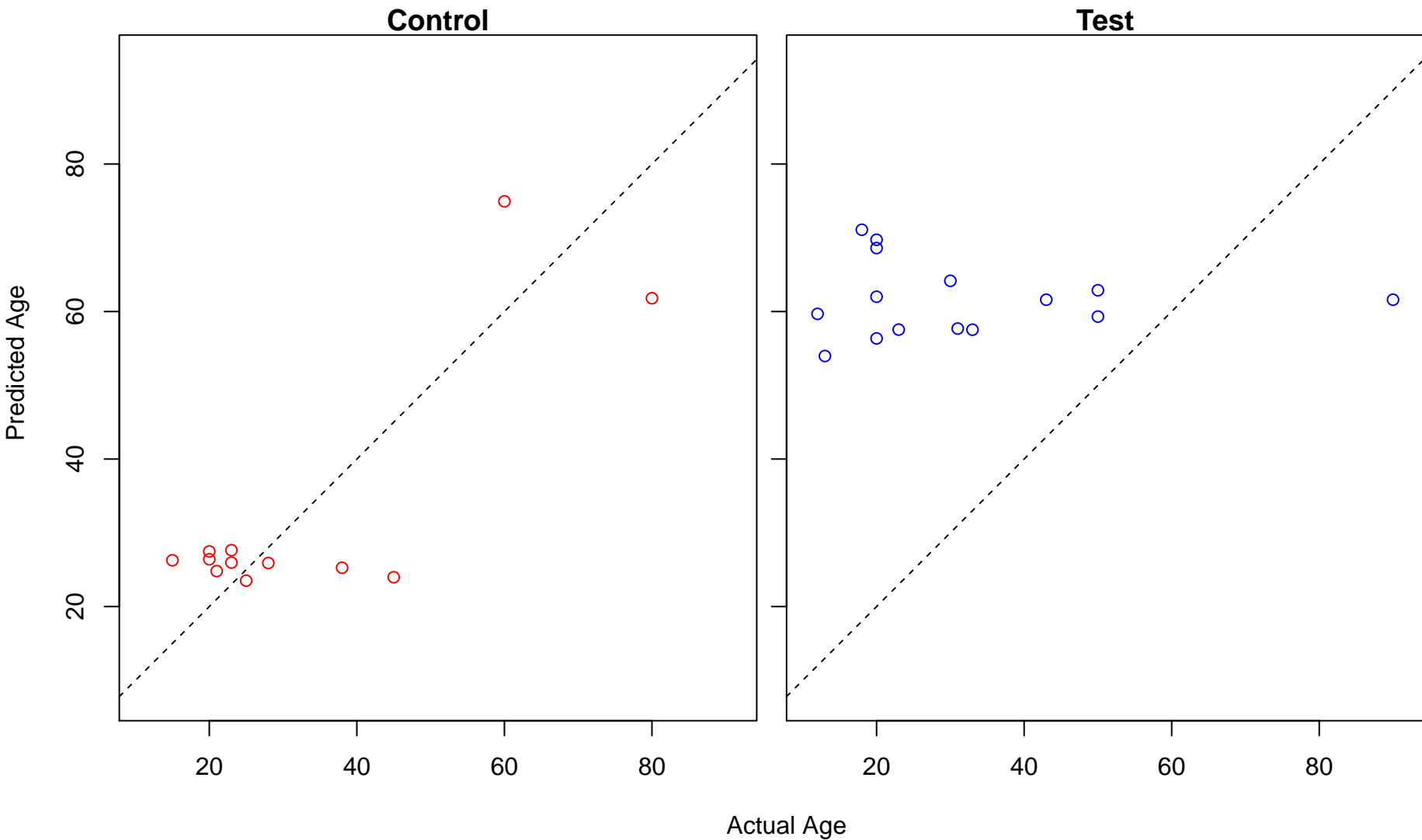
vacuolar transport (Score: 4.098819)



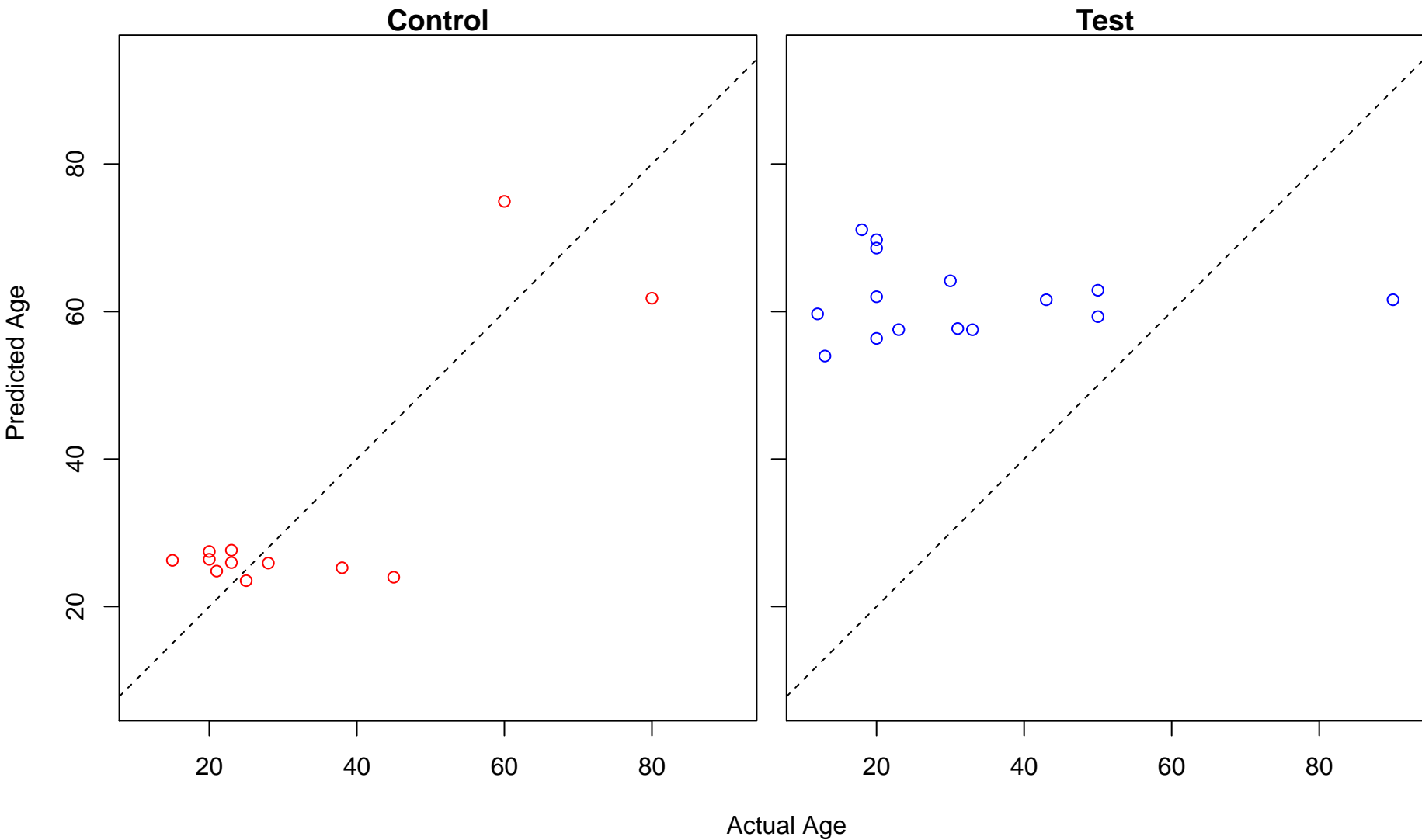
regulation of protein homooligomerization (Score: 4.095775)



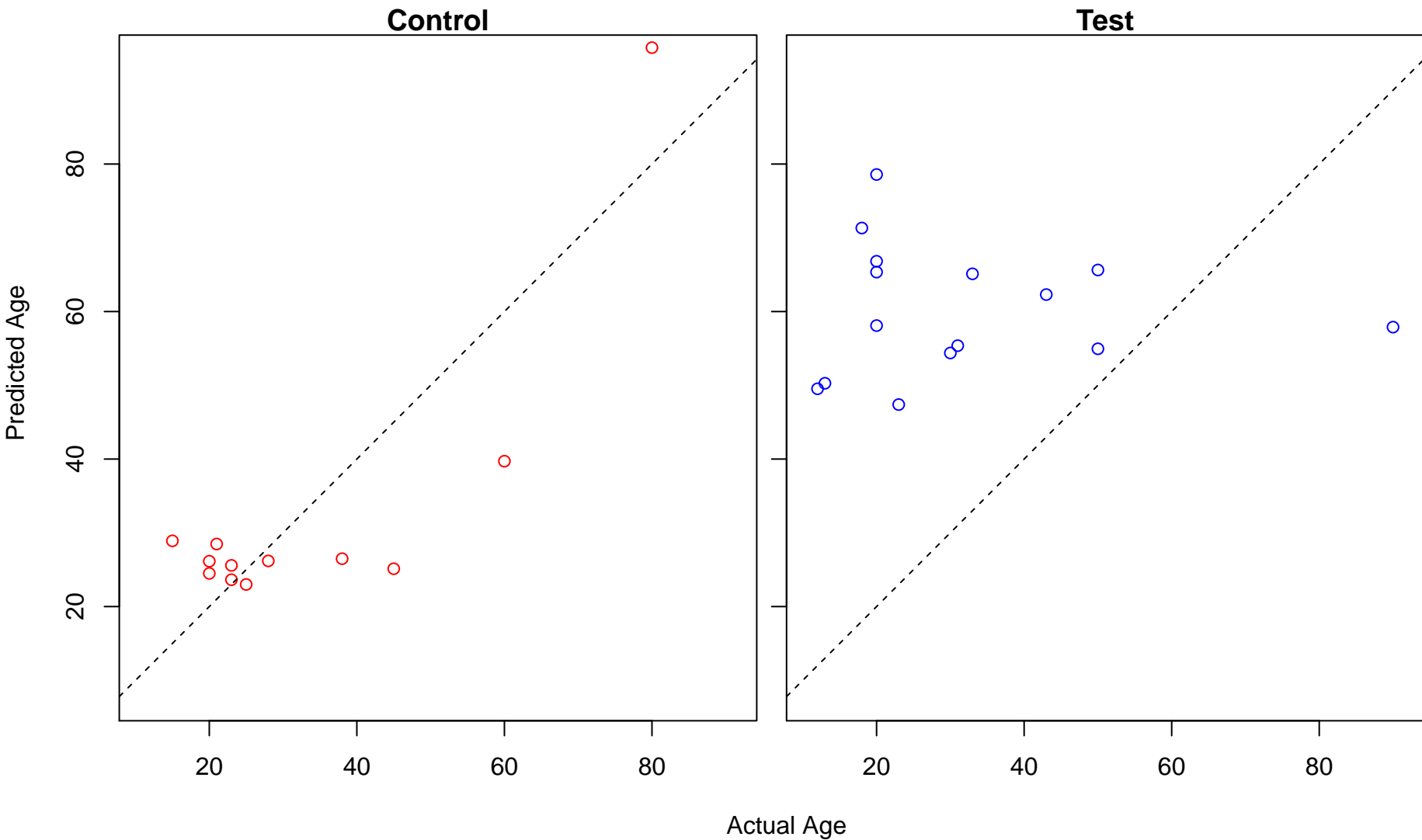
thioester biosynthetic process (Score: 4.094435)



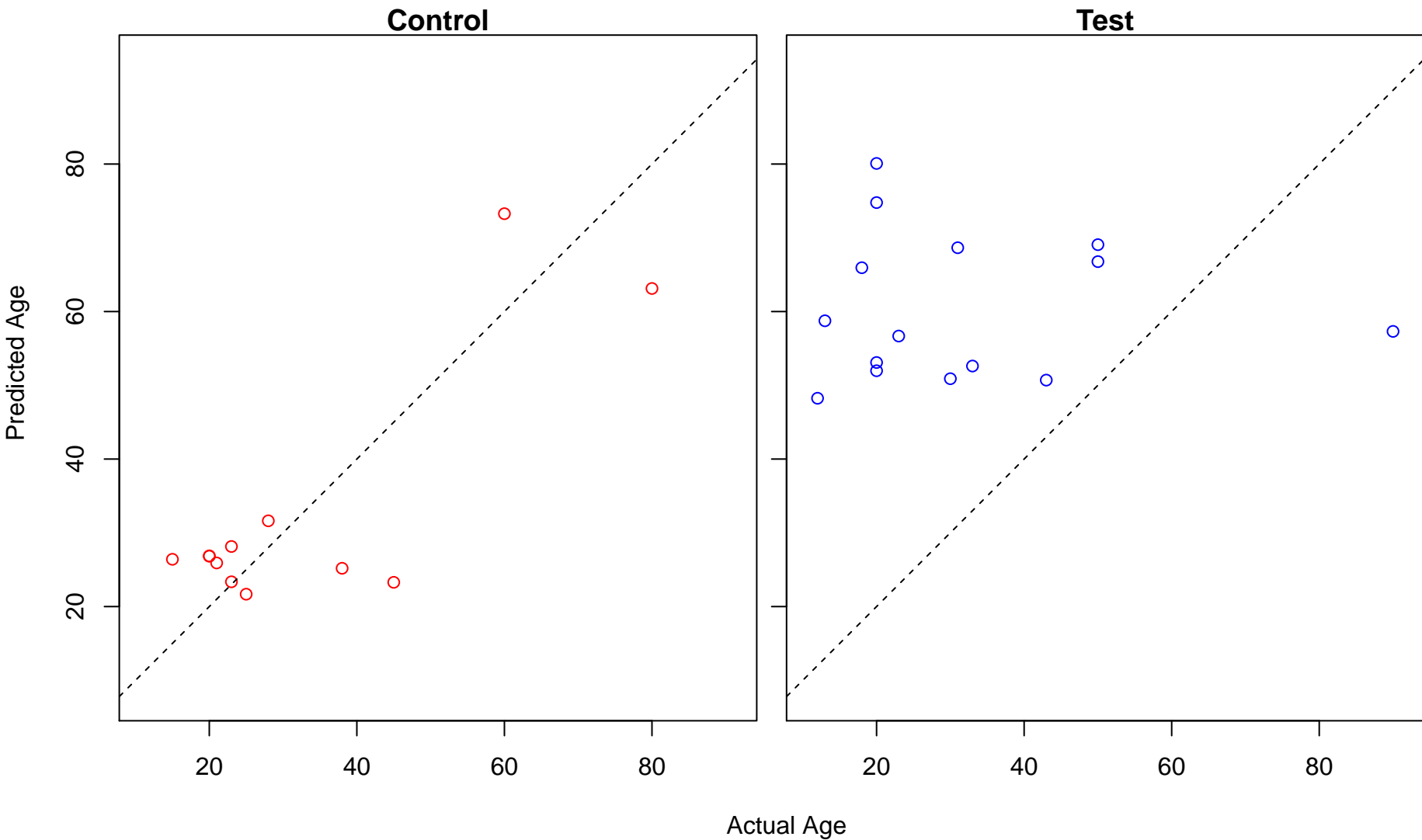
acyl-CoA biosynthetic process (Score: 4.094435)



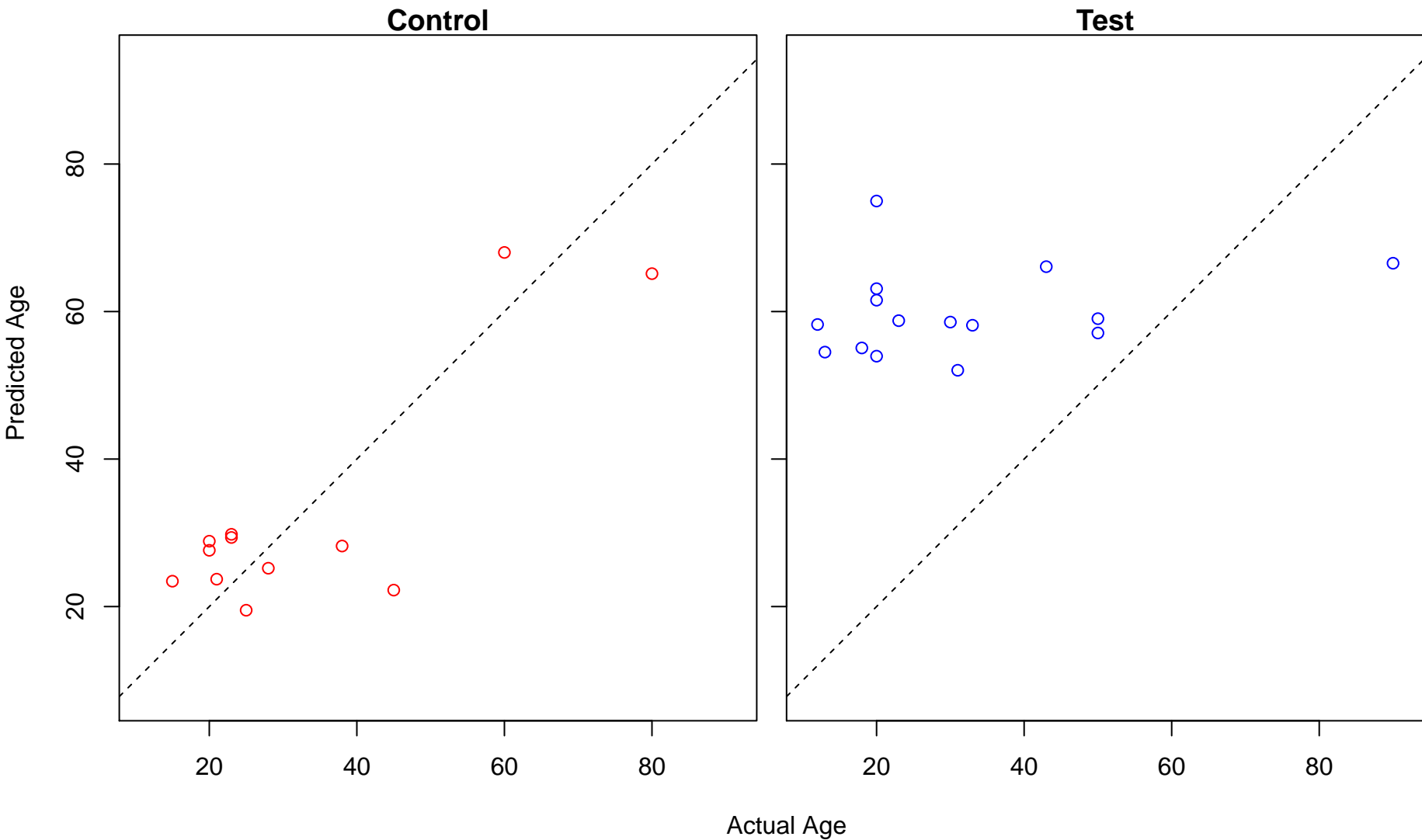
positive regulation of cell division (Score: 4.093438)



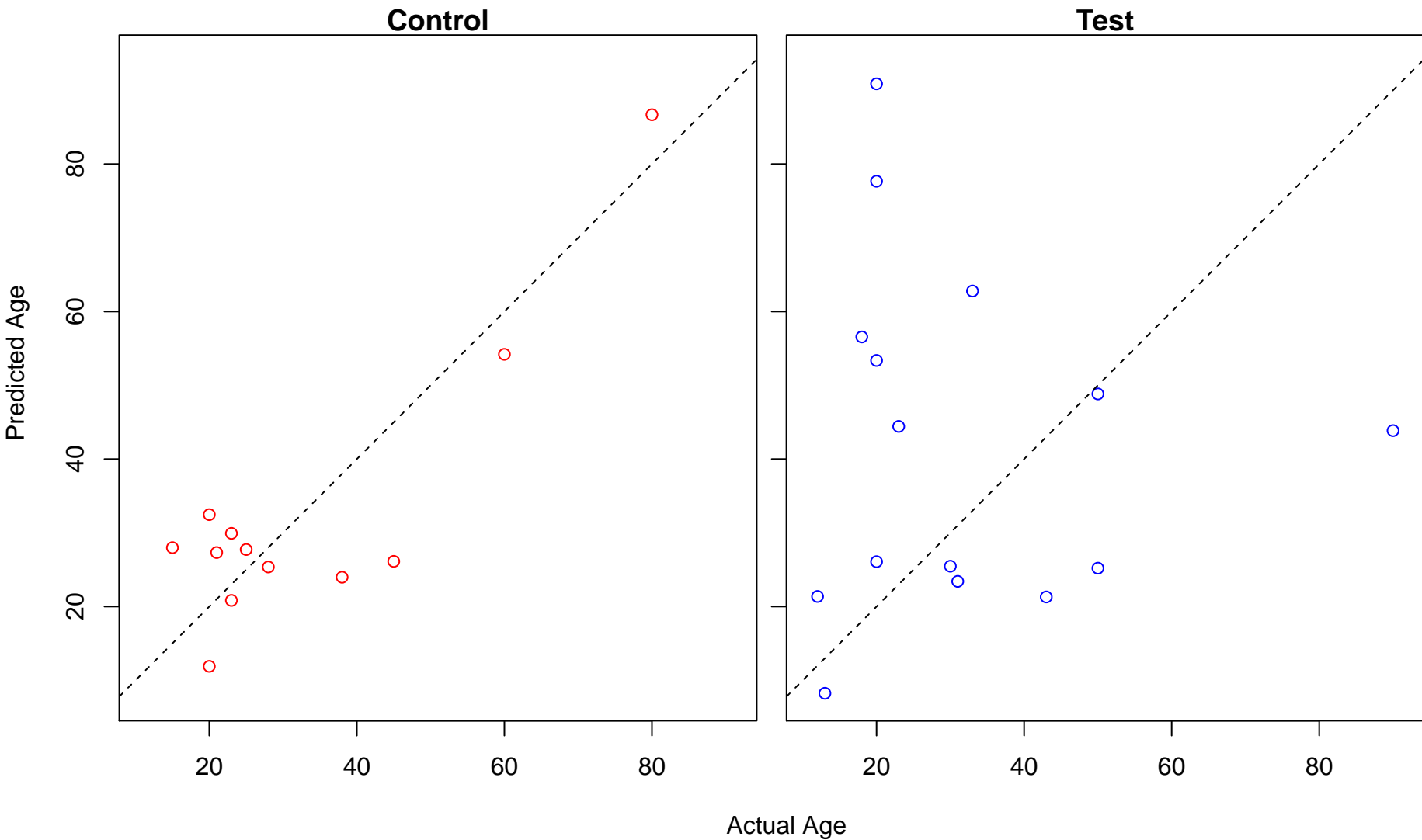
regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum (Score: 4.093)



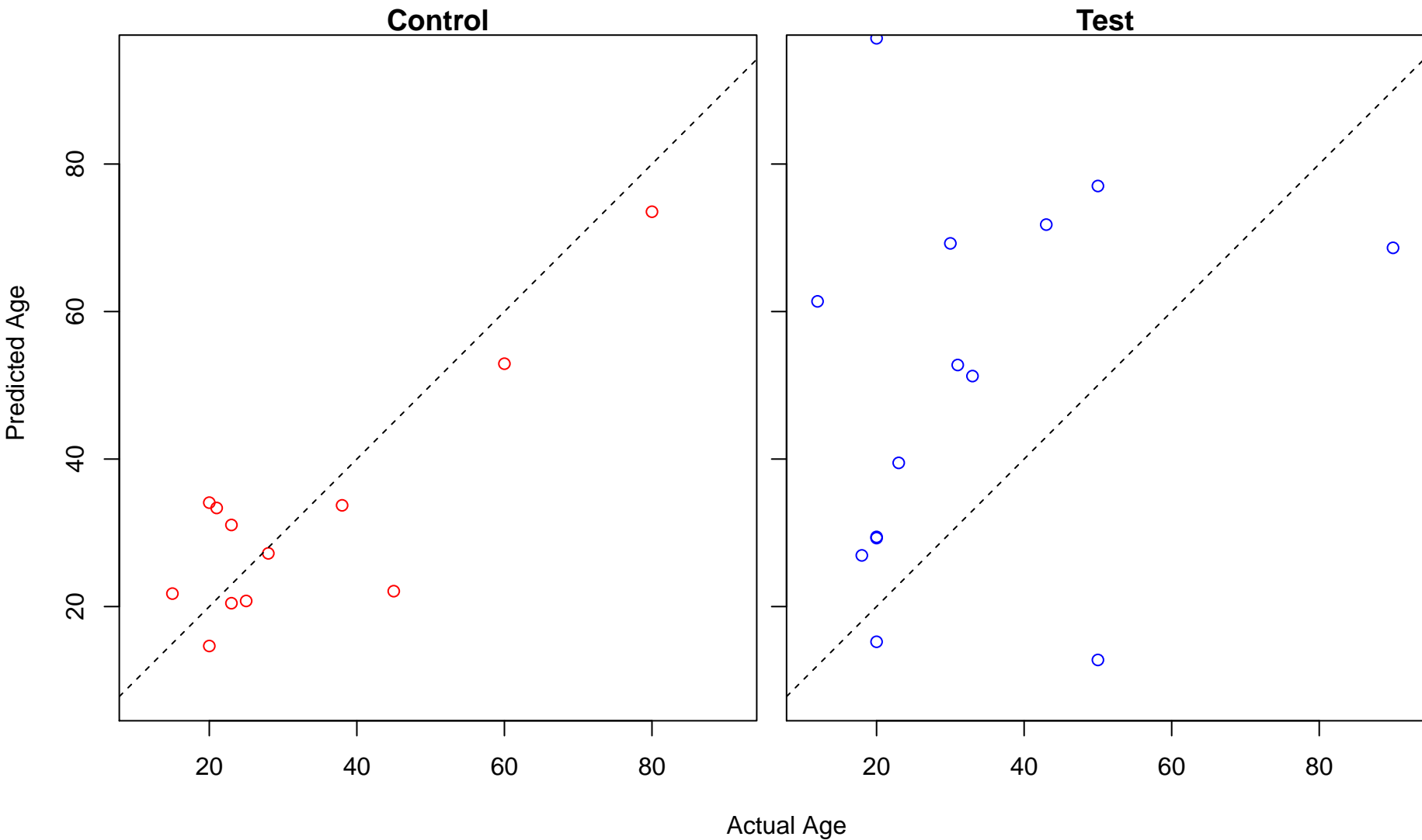
histone H3-K4 trimethylation (Score: 4.091163)



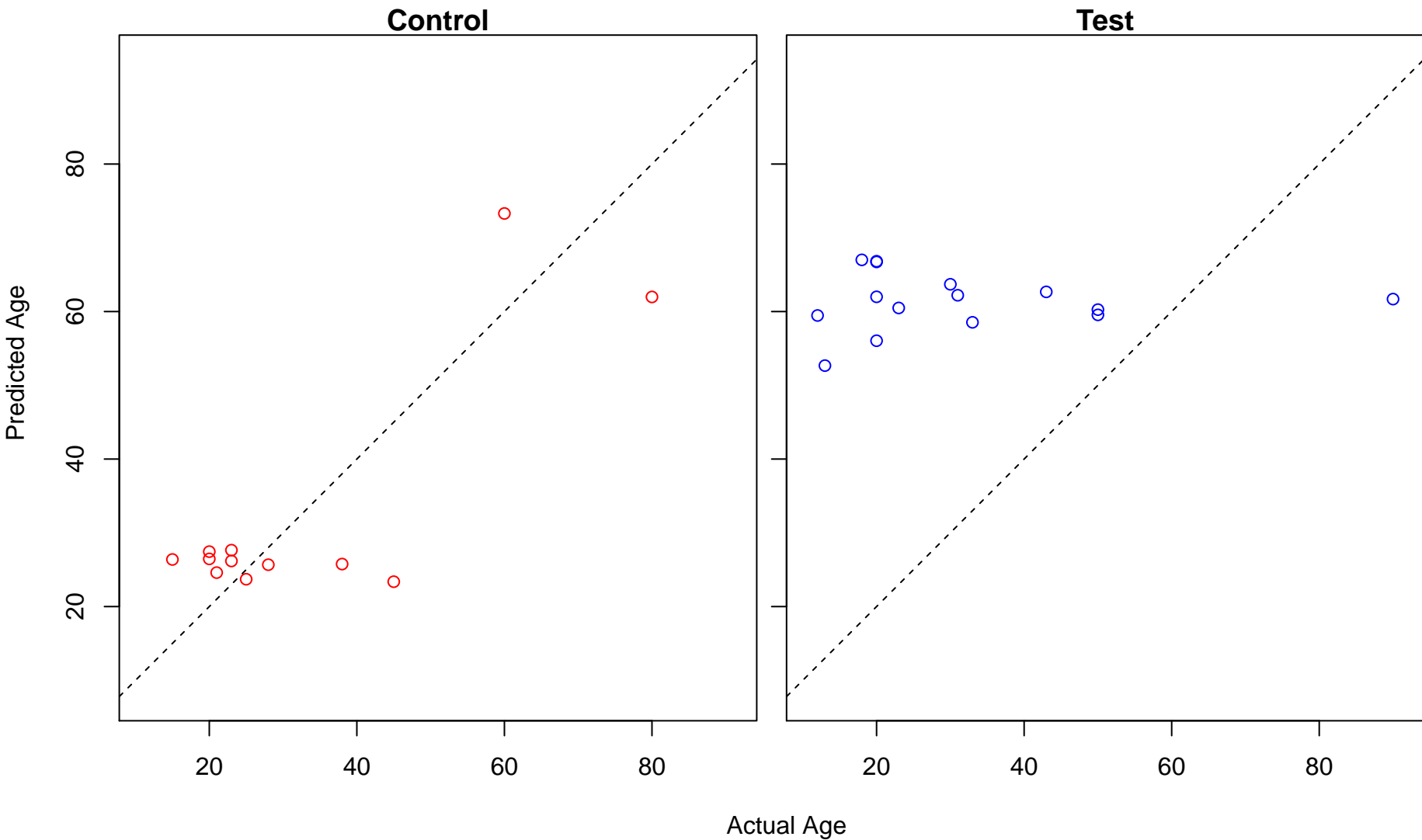
detection of stimulus involved in sensory perception (Score: 4.090119)



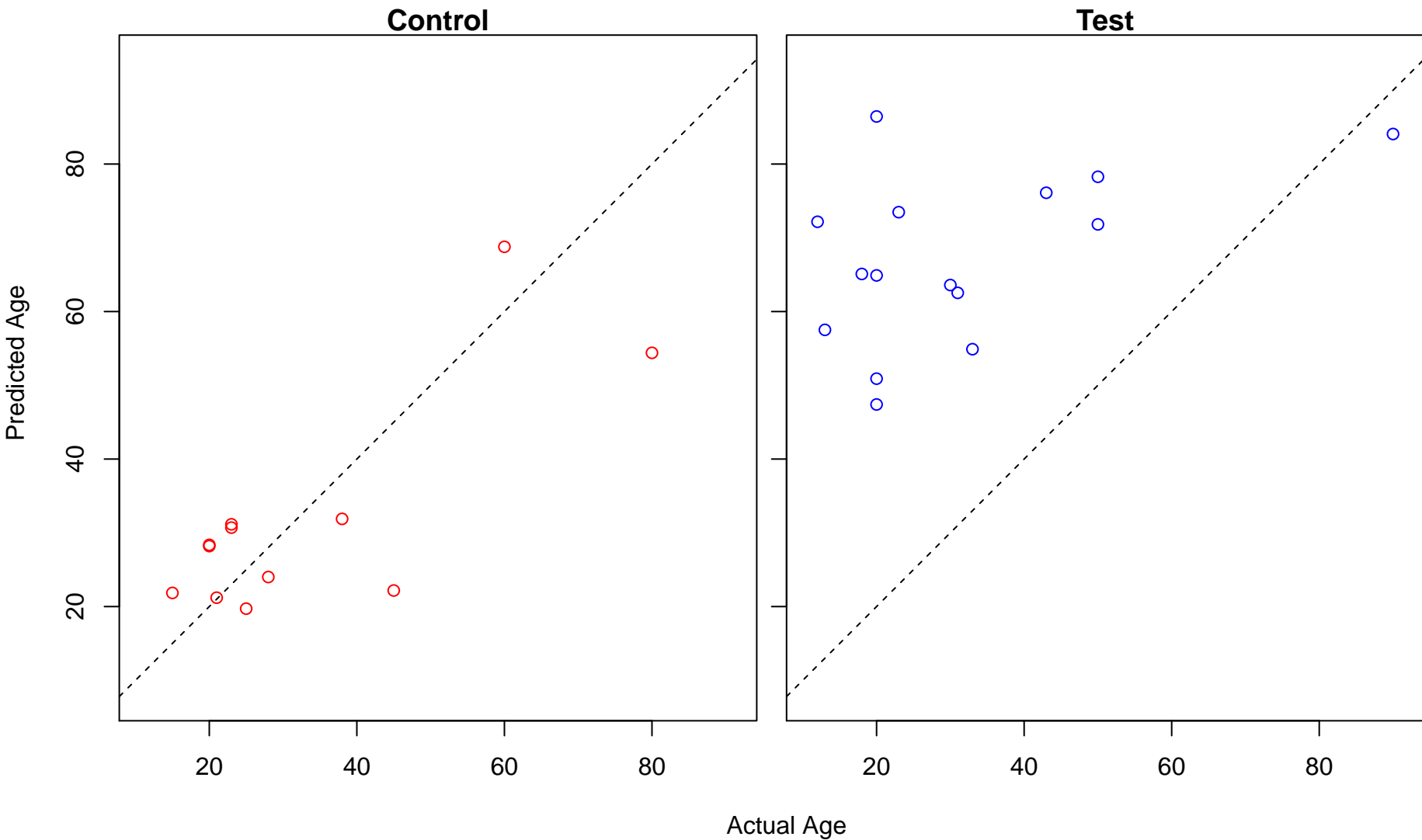
positive regulation of transcription from RNA polymerase III promoter (Score: 4.088875)



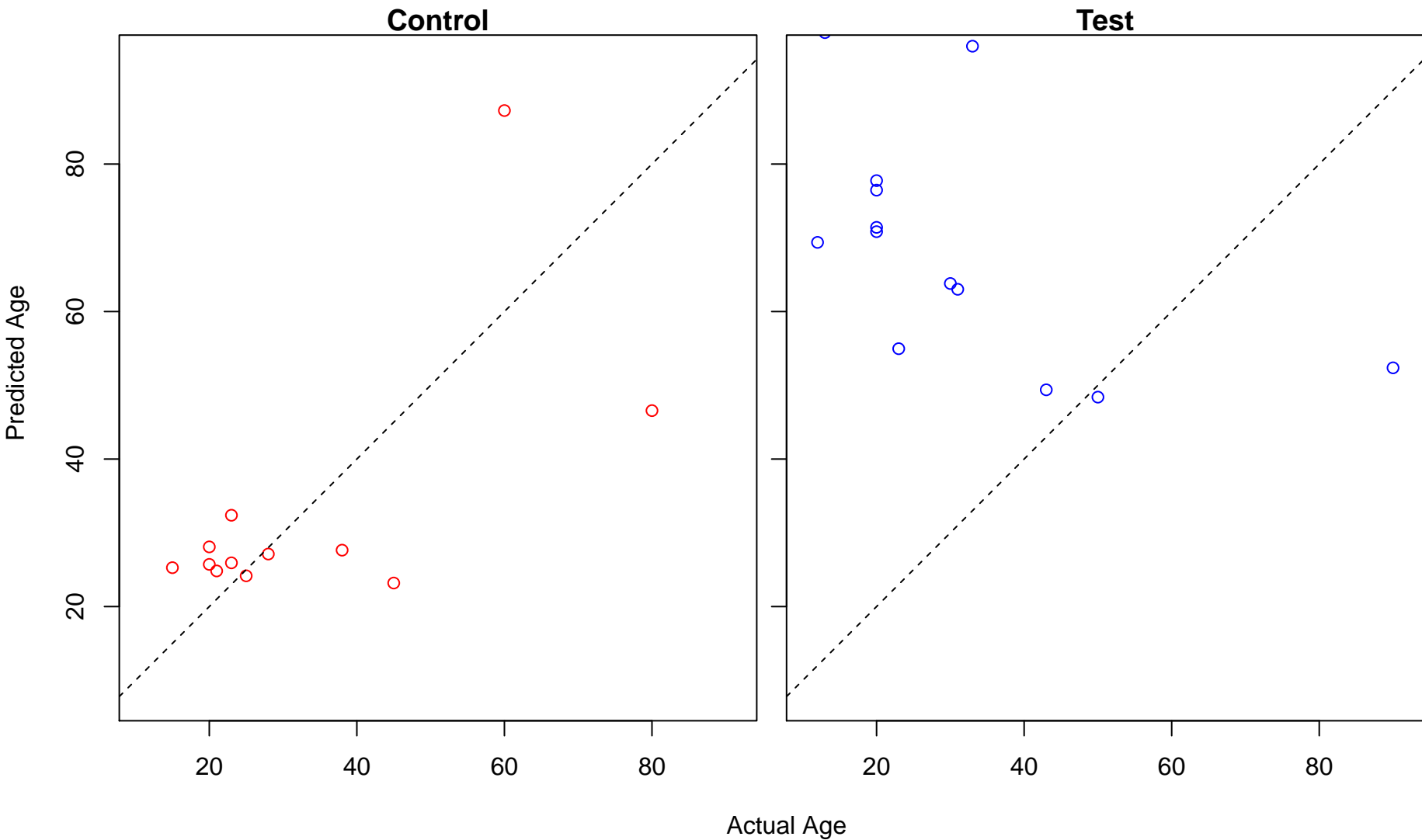
triglyceride biosynthetic process (Score: 4.088767)



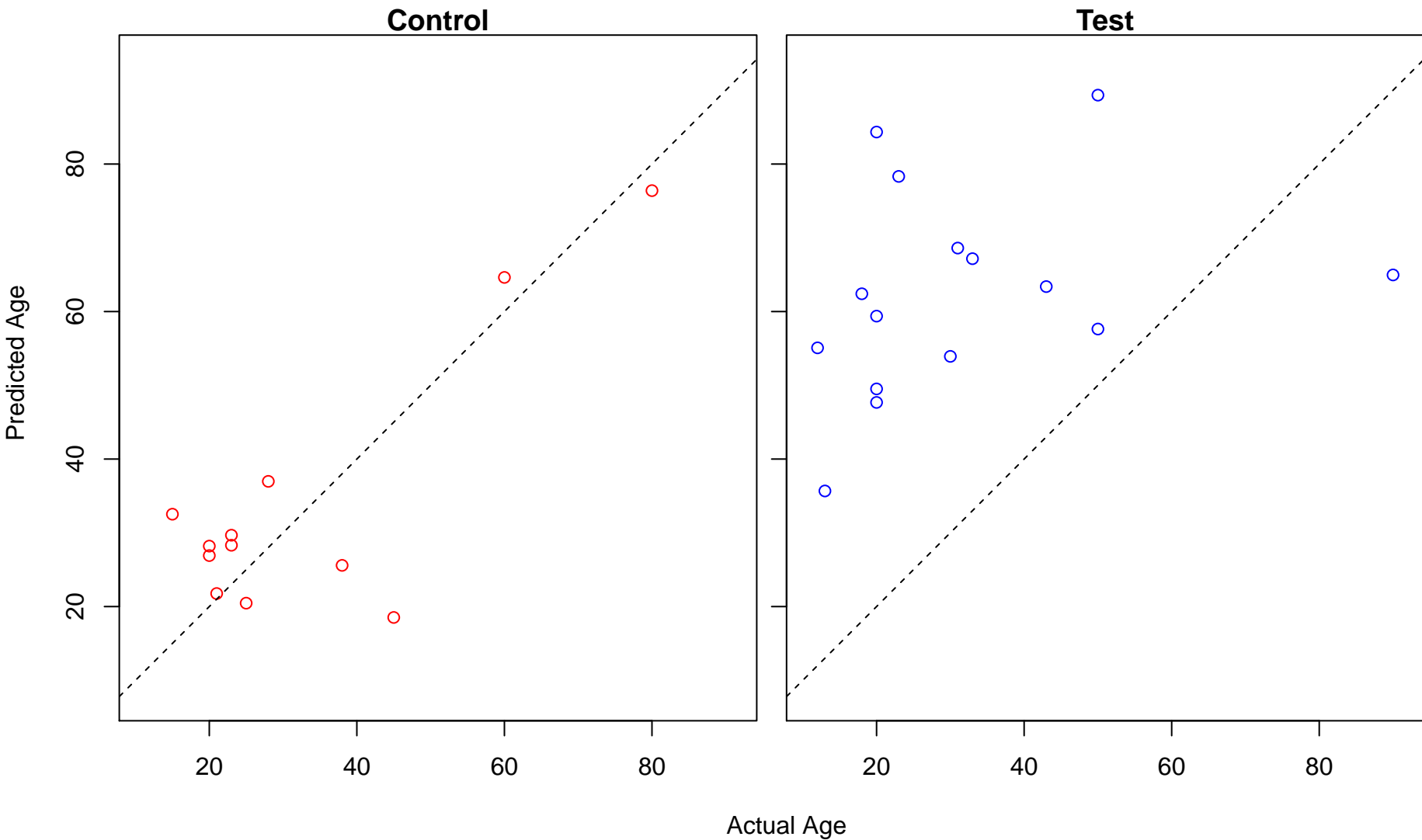
otic vesicle development (Score: 4.084847)



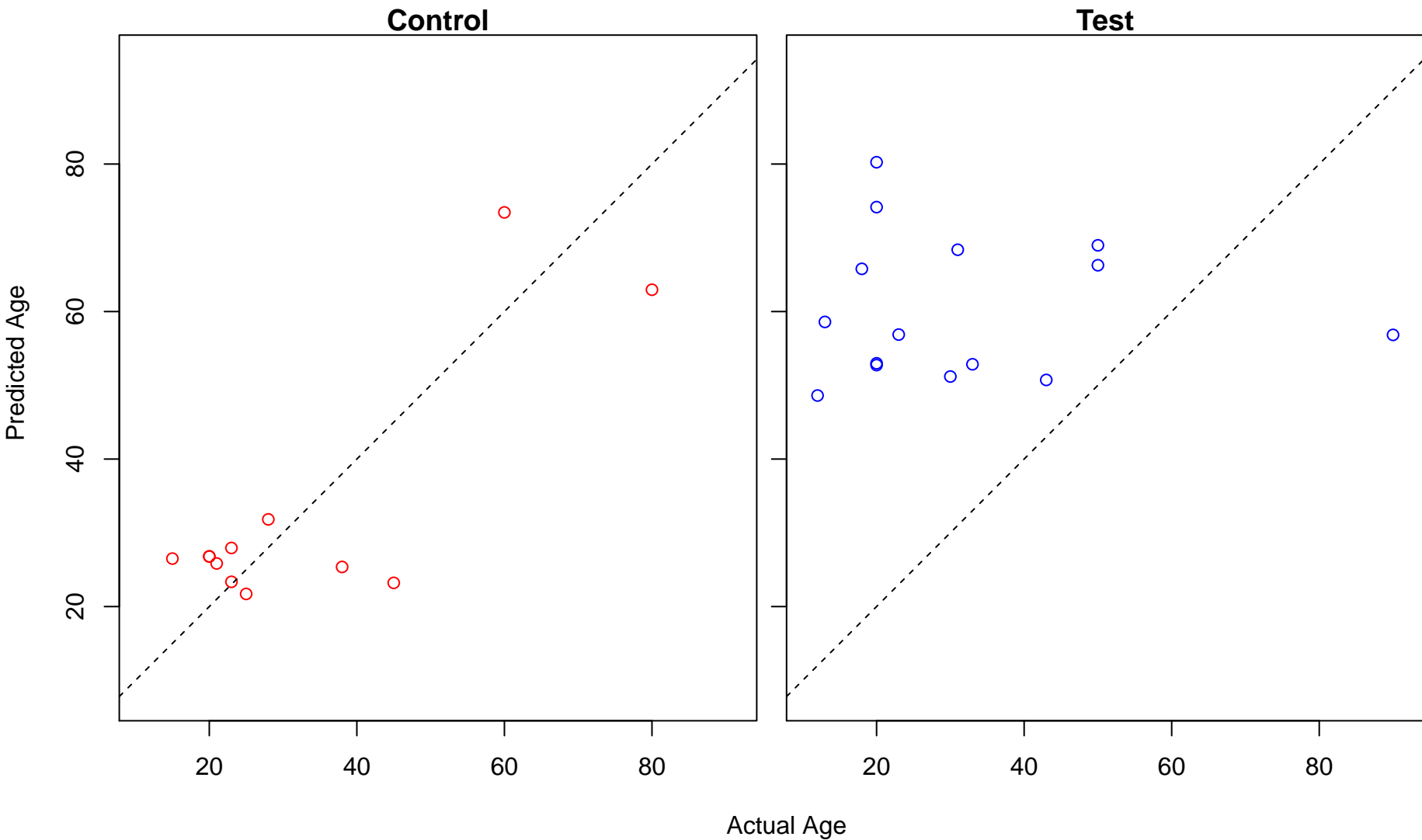
negative regulation of cell proliferation involved in kidney development (Score: 4.082181)



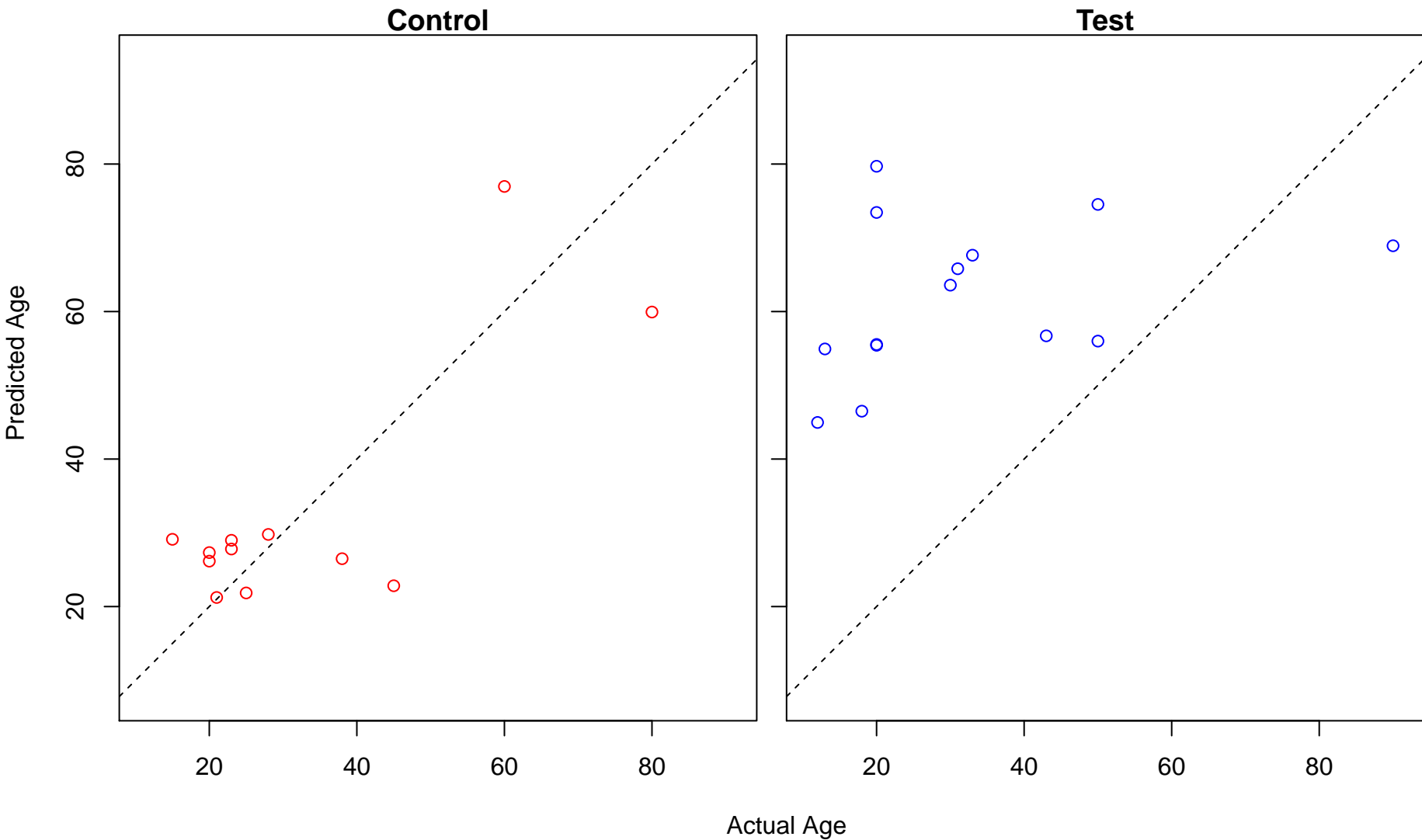
amelogenesis (Score: 4.081506)



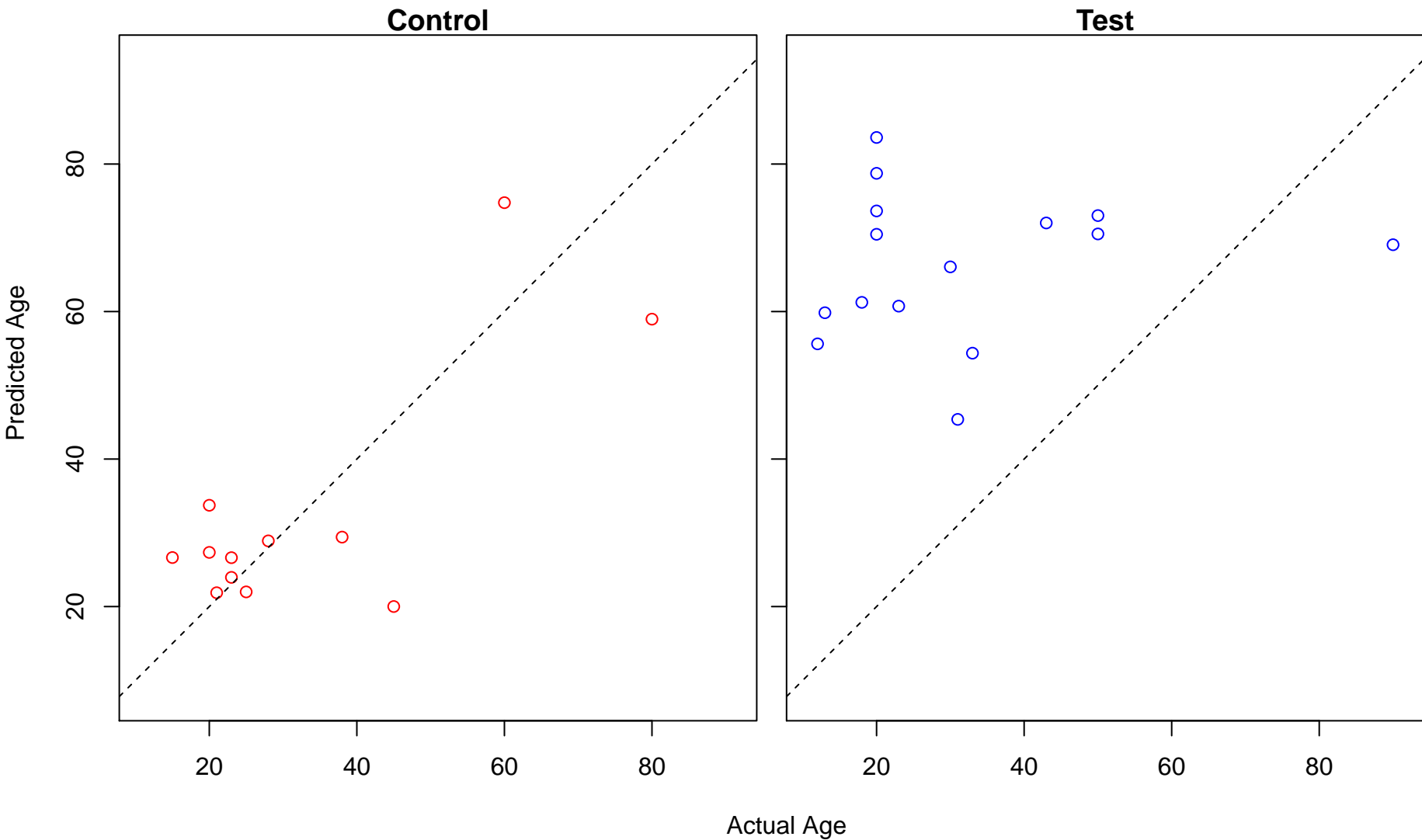
regulation of calcium ion transport into cytosol (Score: 4.079881)



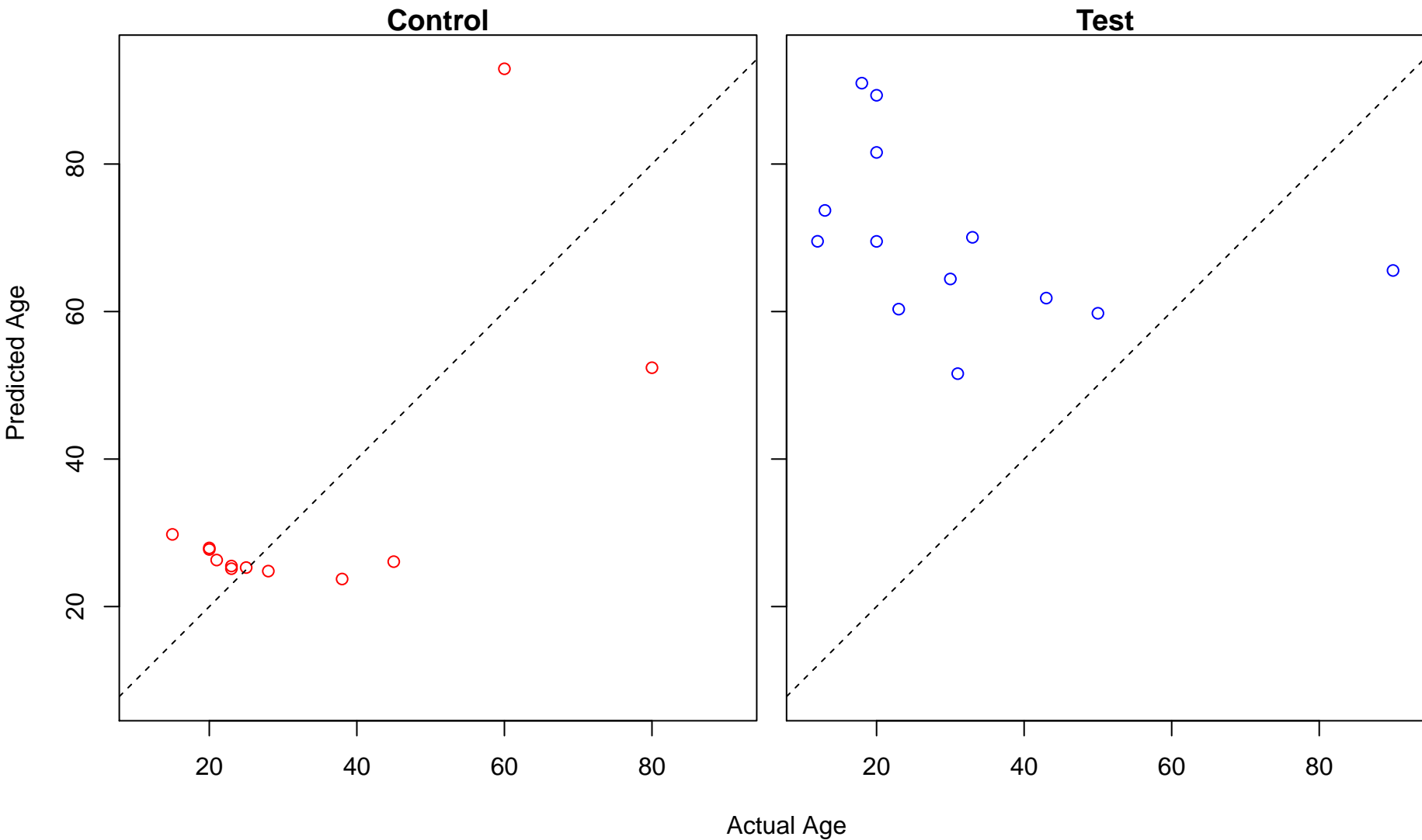
protein deglutamylation (Score: 4.079823)



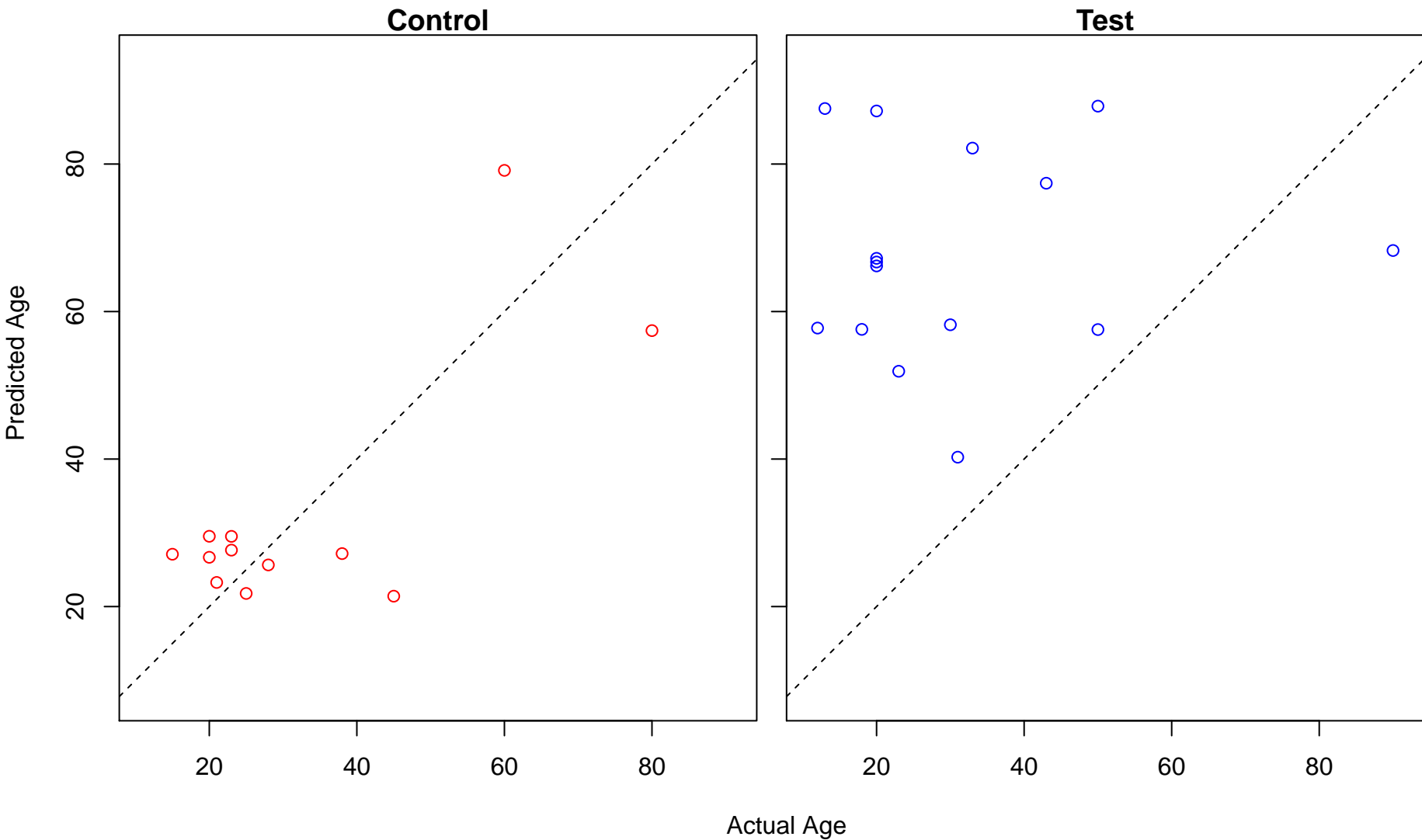
protein oligomerization (Score: 4.079791)



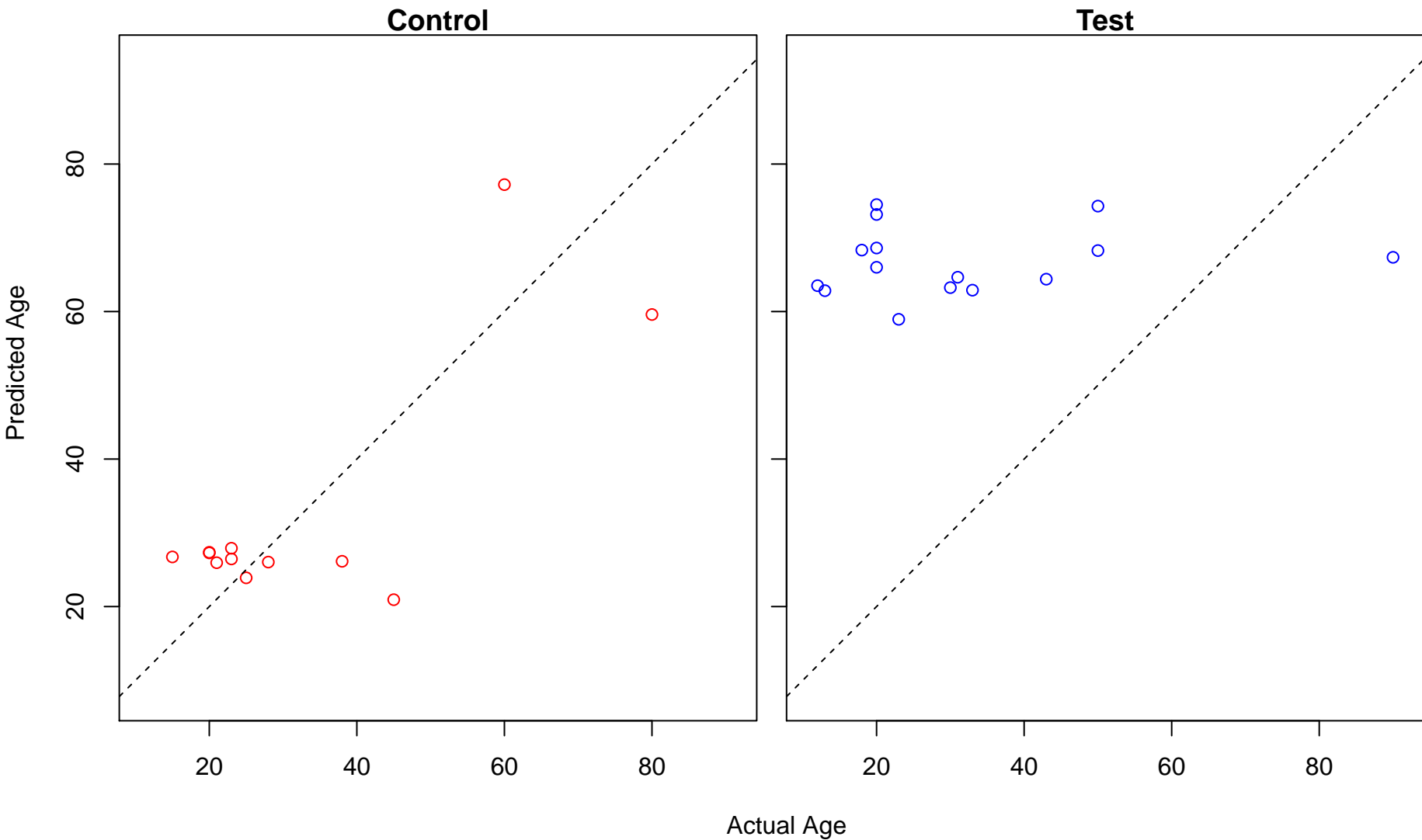
regulation of hydrogen peroxide-mediated programmed cell death (Score: 4.079756)



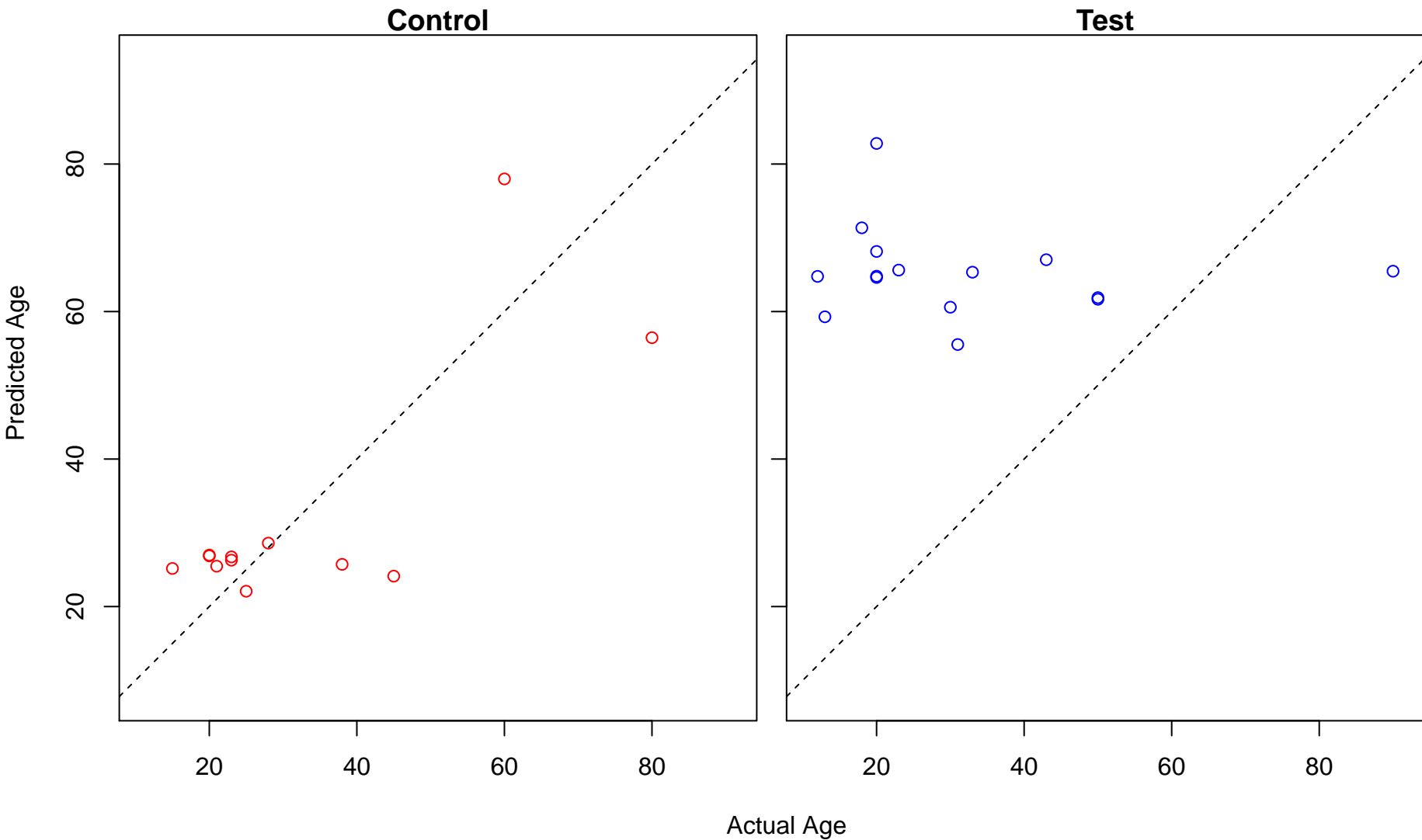
visual learning (Score: 4.078998)



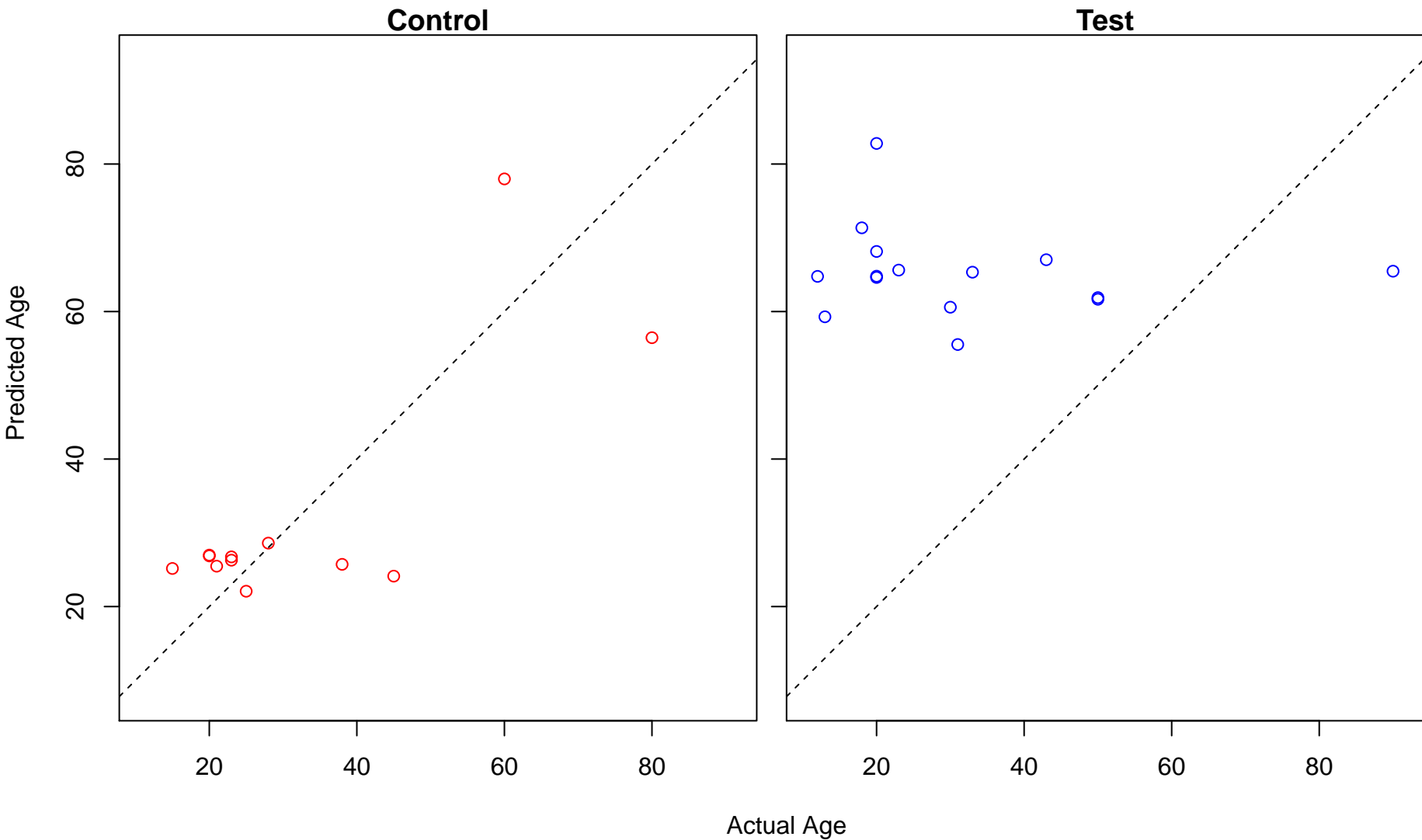
negative regulation of cell cycle G2/M phase transition (Score: 4.078894)



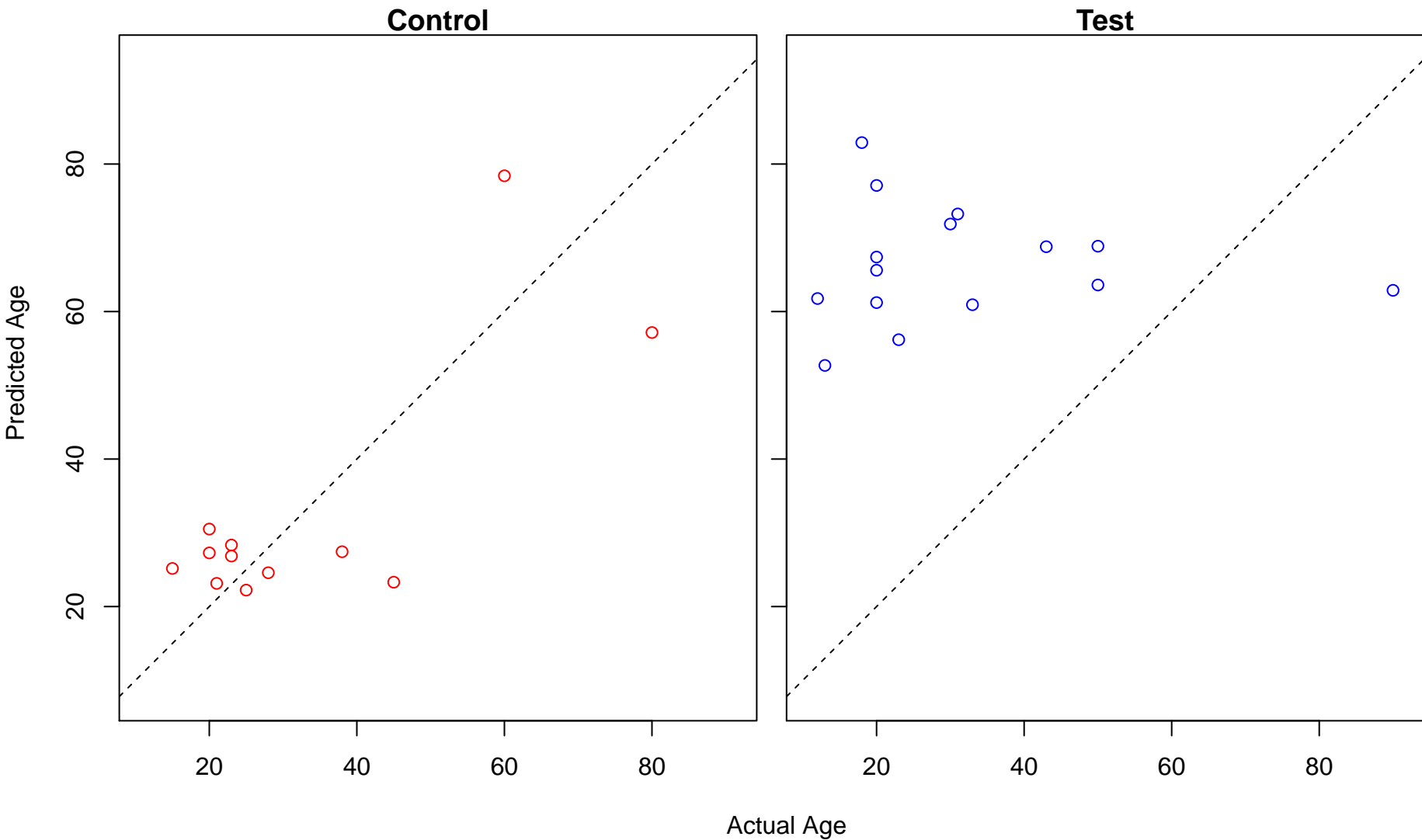
protein lipidation (Score: 4.076254)



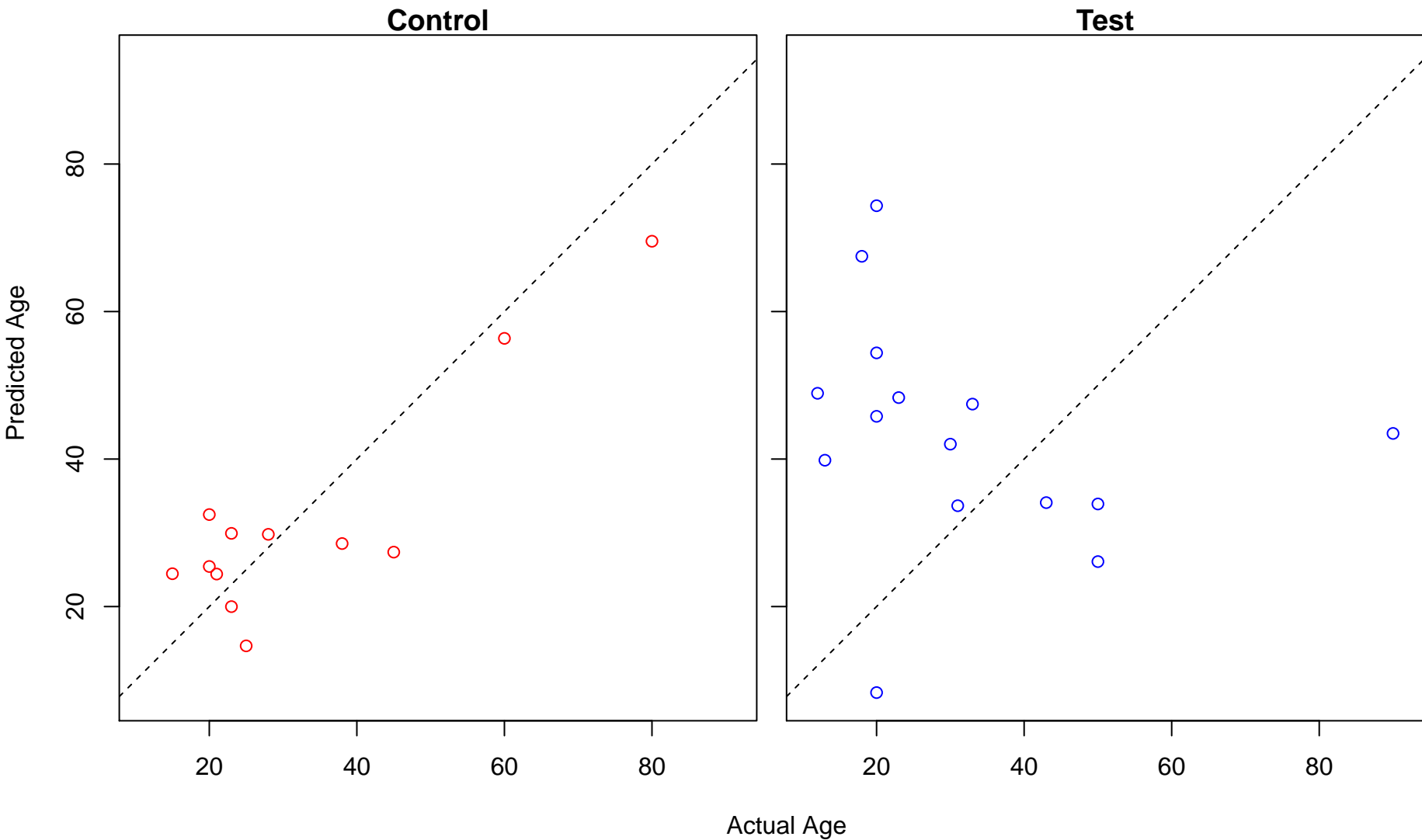
lipoprotein biosynthetic process (Score: 4.076254)



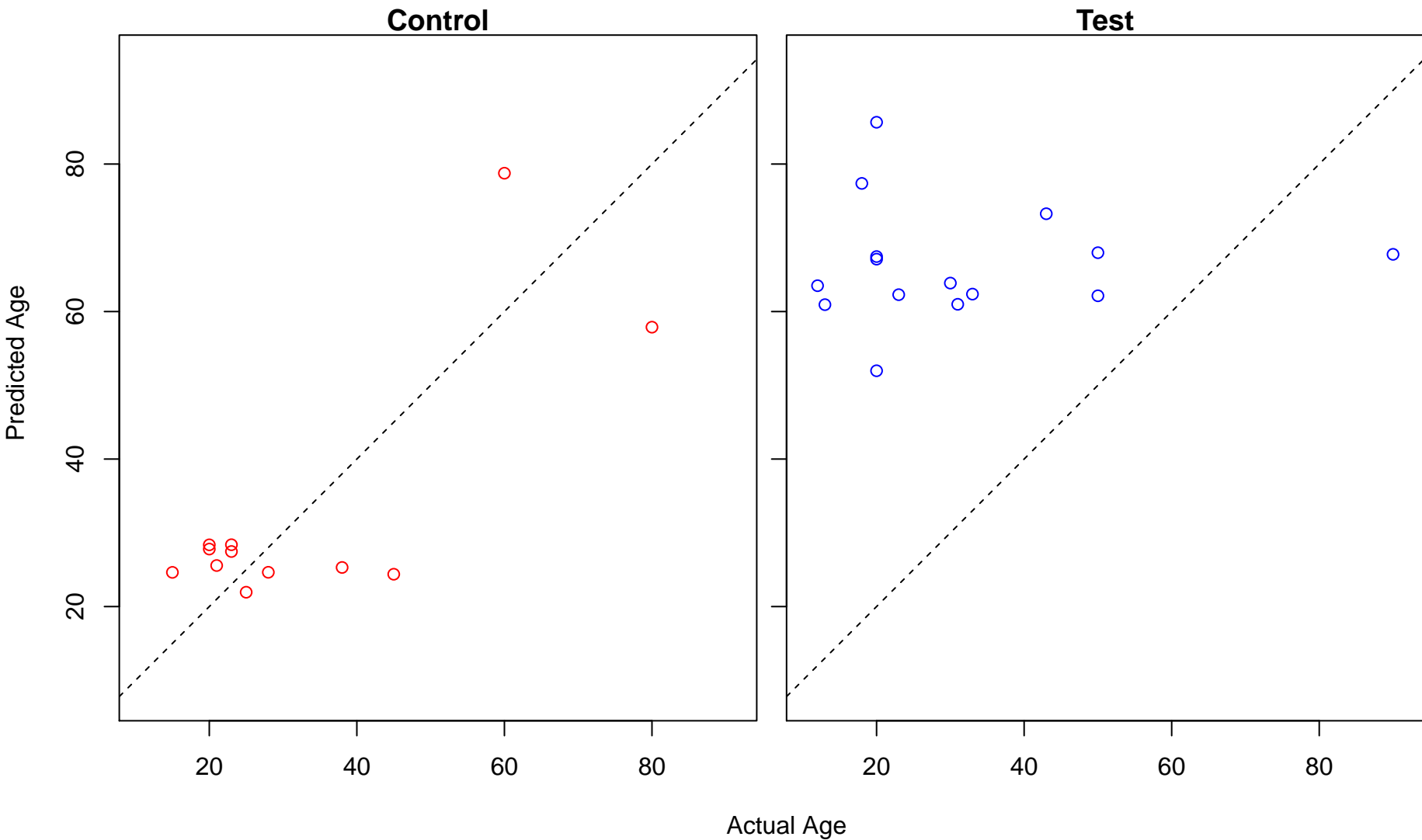
PERK-mediated unfolded protein response (Score: 4.074260)



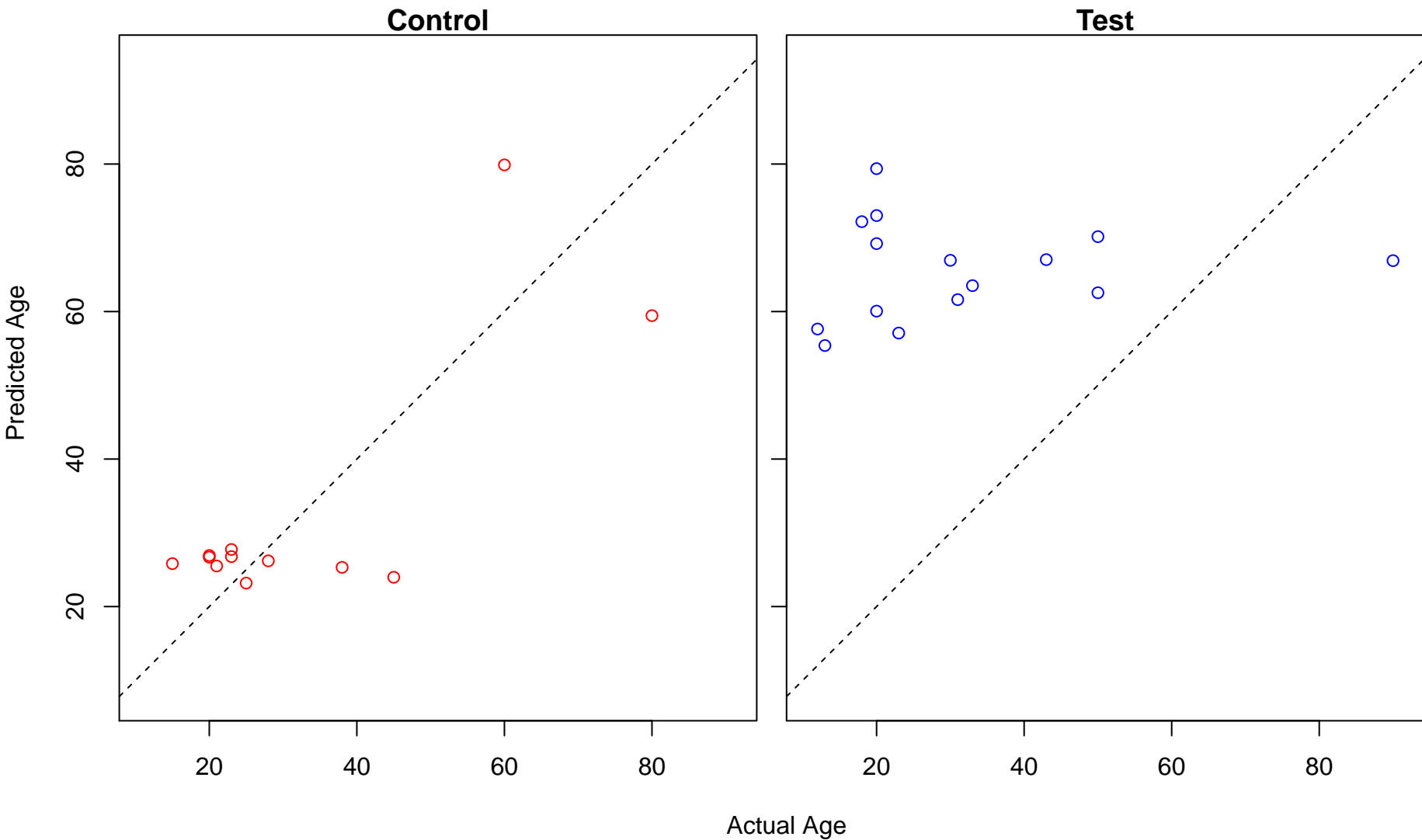
centrosome duplication (Score: 4.071531)



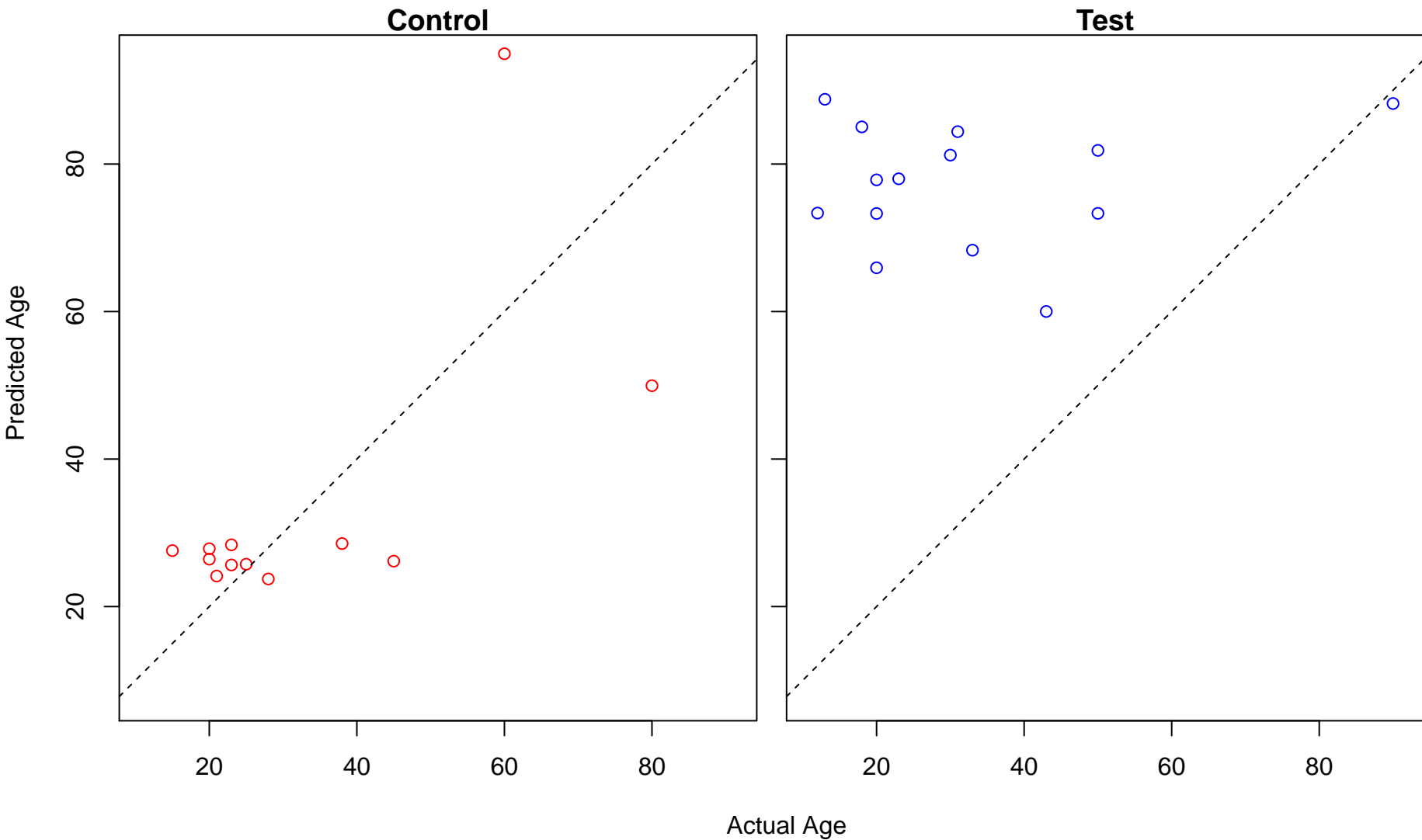
L-amino acid transport (Score: 4.070632)



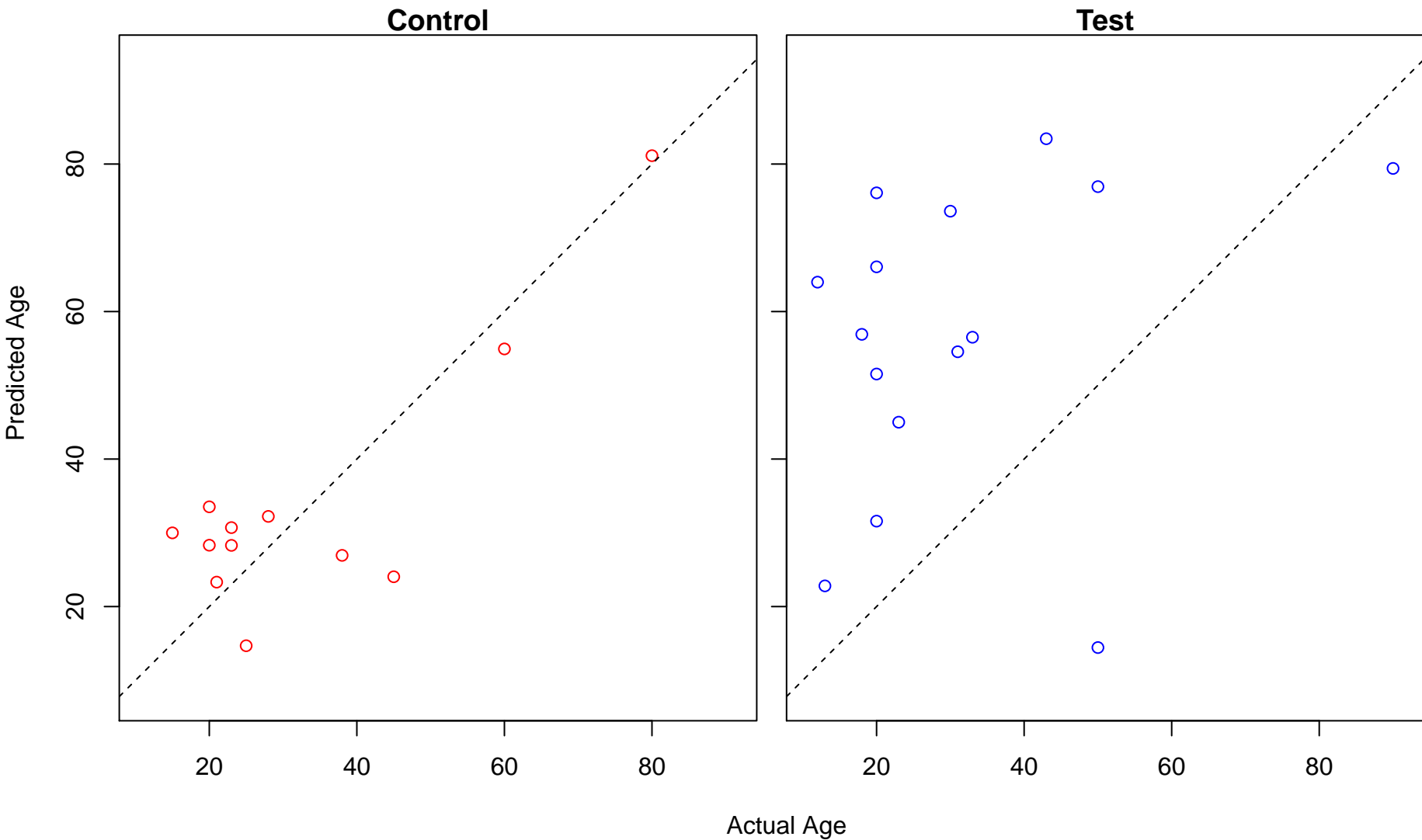
positive regulation of mitotic cell cycle phase transition (Score: 4.069280)



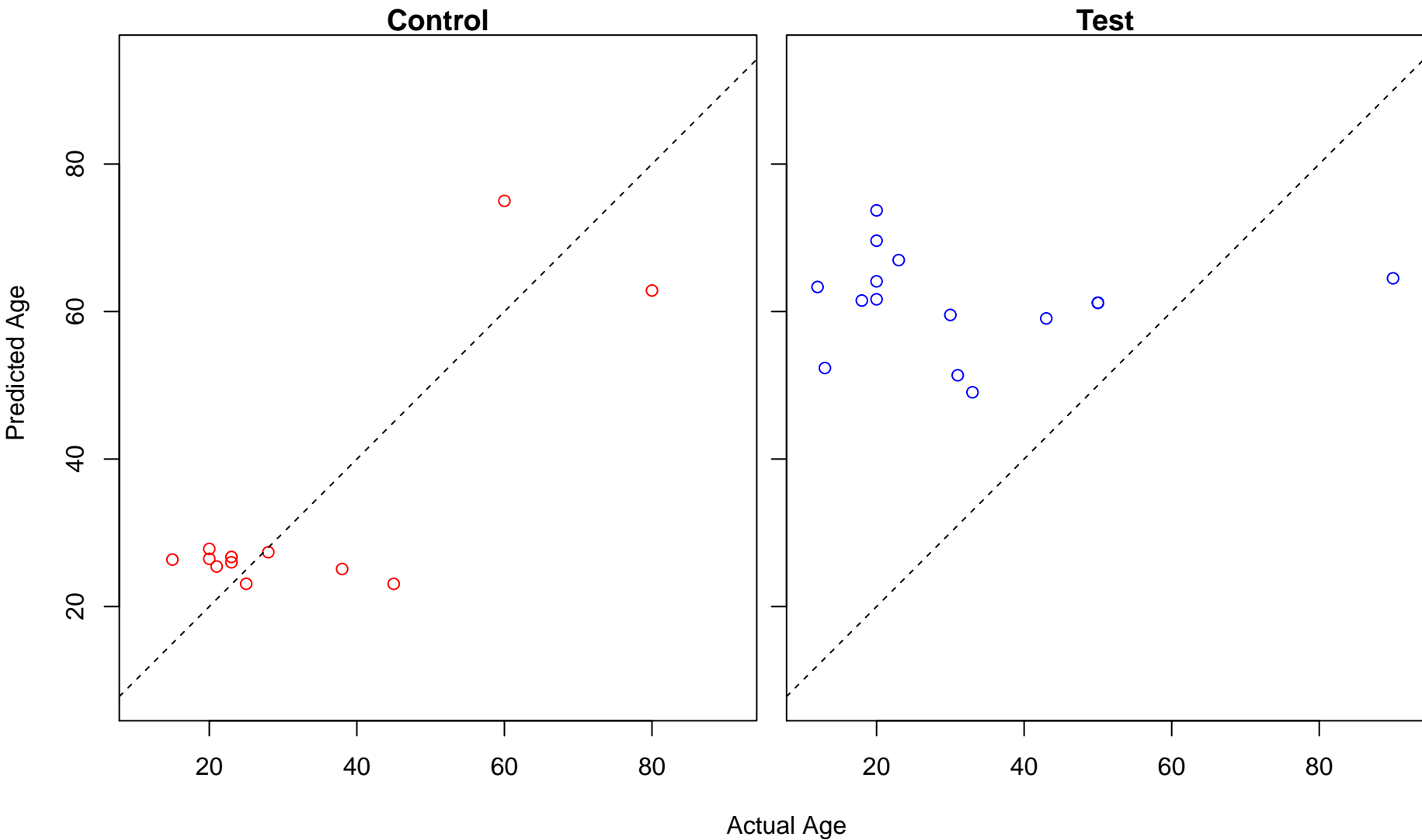
negative regulation of platelet-derived growth factor receptor signaling pathway (Score: 4.067651)



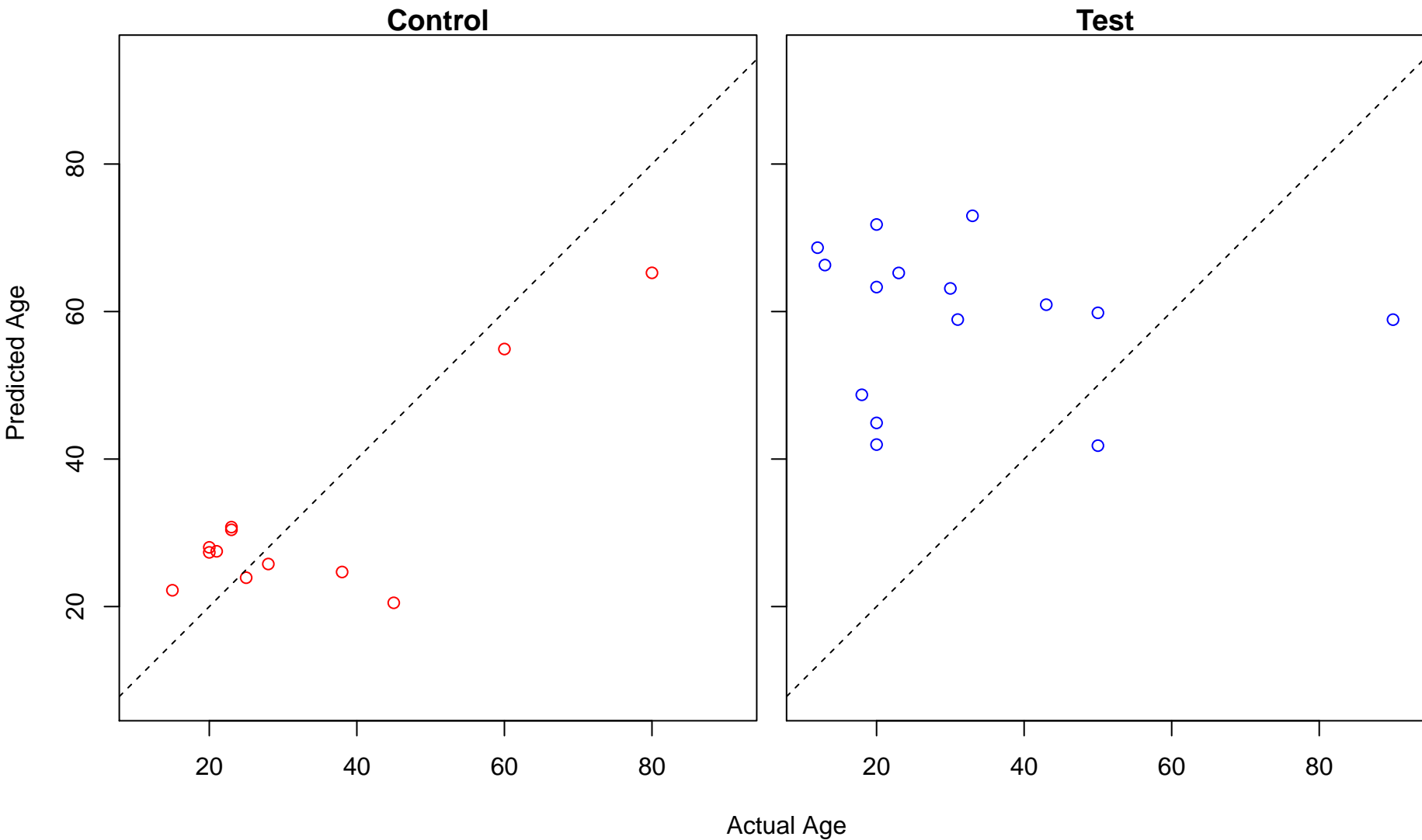
cullin deneddylation (Score: 4.062121)



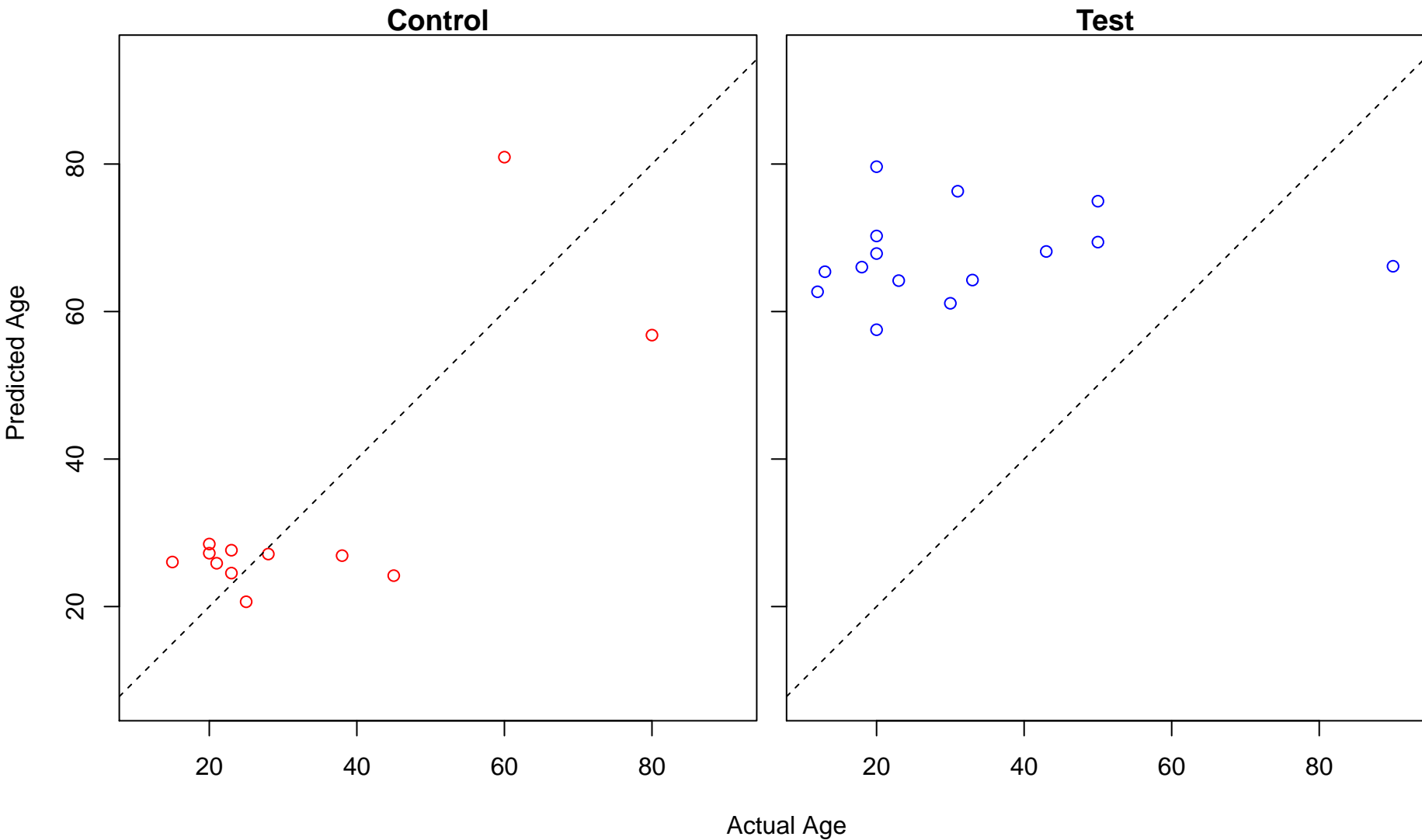
tRNA modification (Score: 4.060481)



negative regulation of mast cell activation (Score: 4.060426)

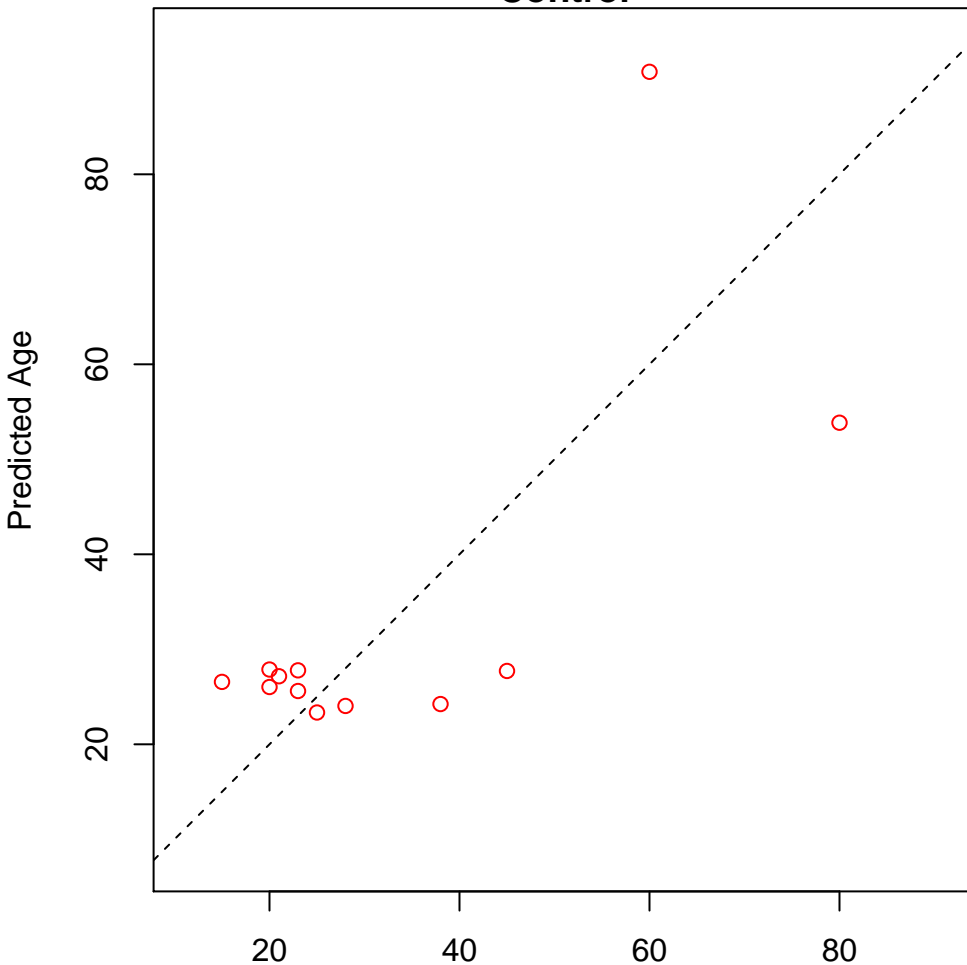


nitric oxide metabolic process (Score: 4.058617)

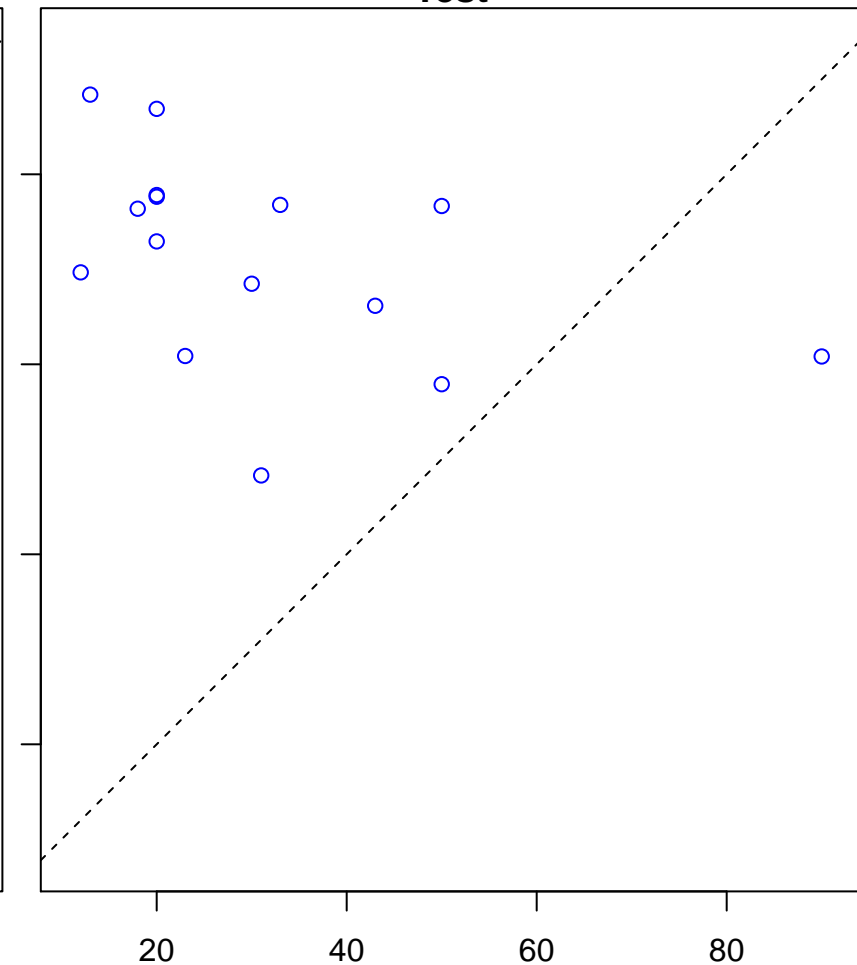


protein localization to microtubule (Score: 4.057678)

Control

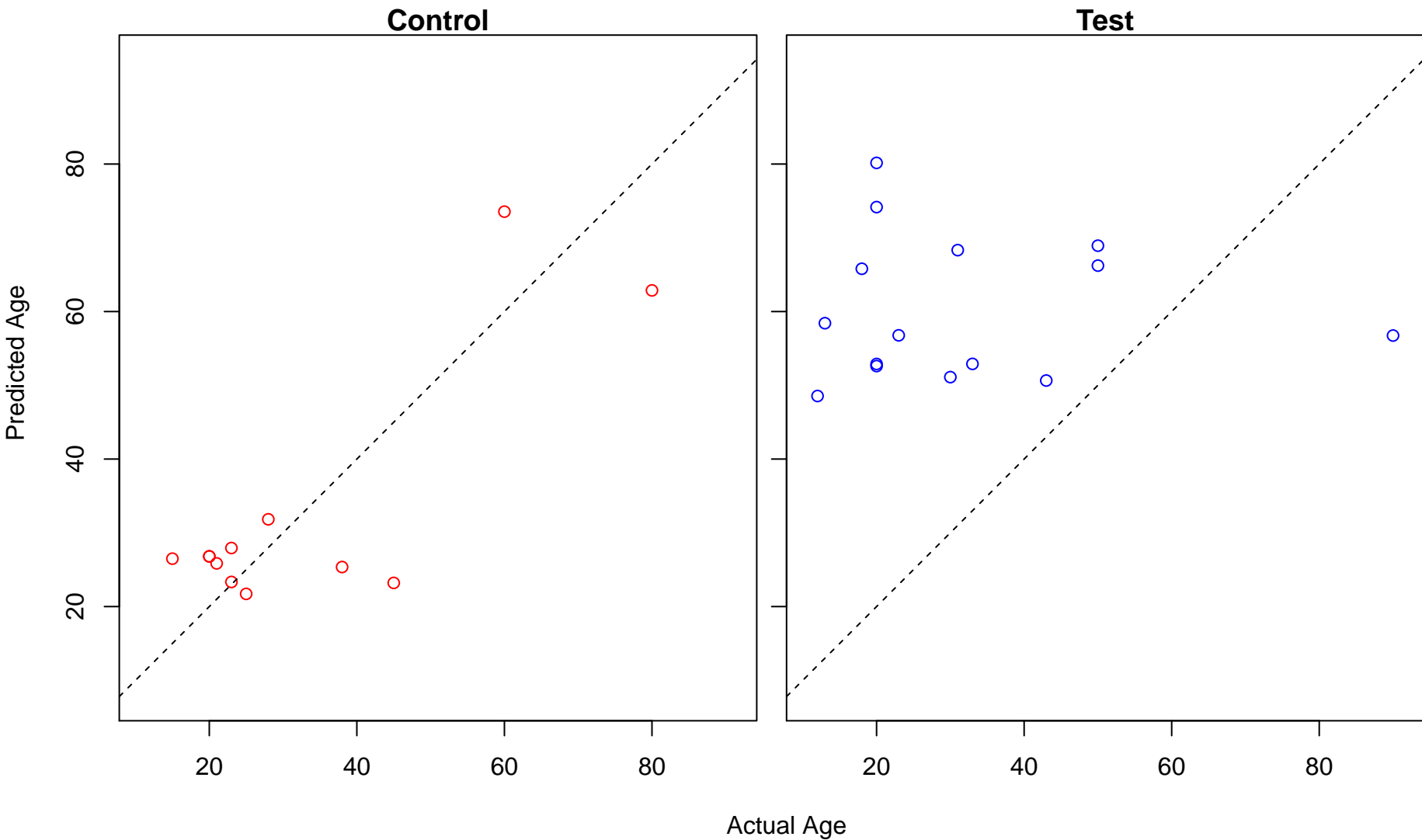


Test

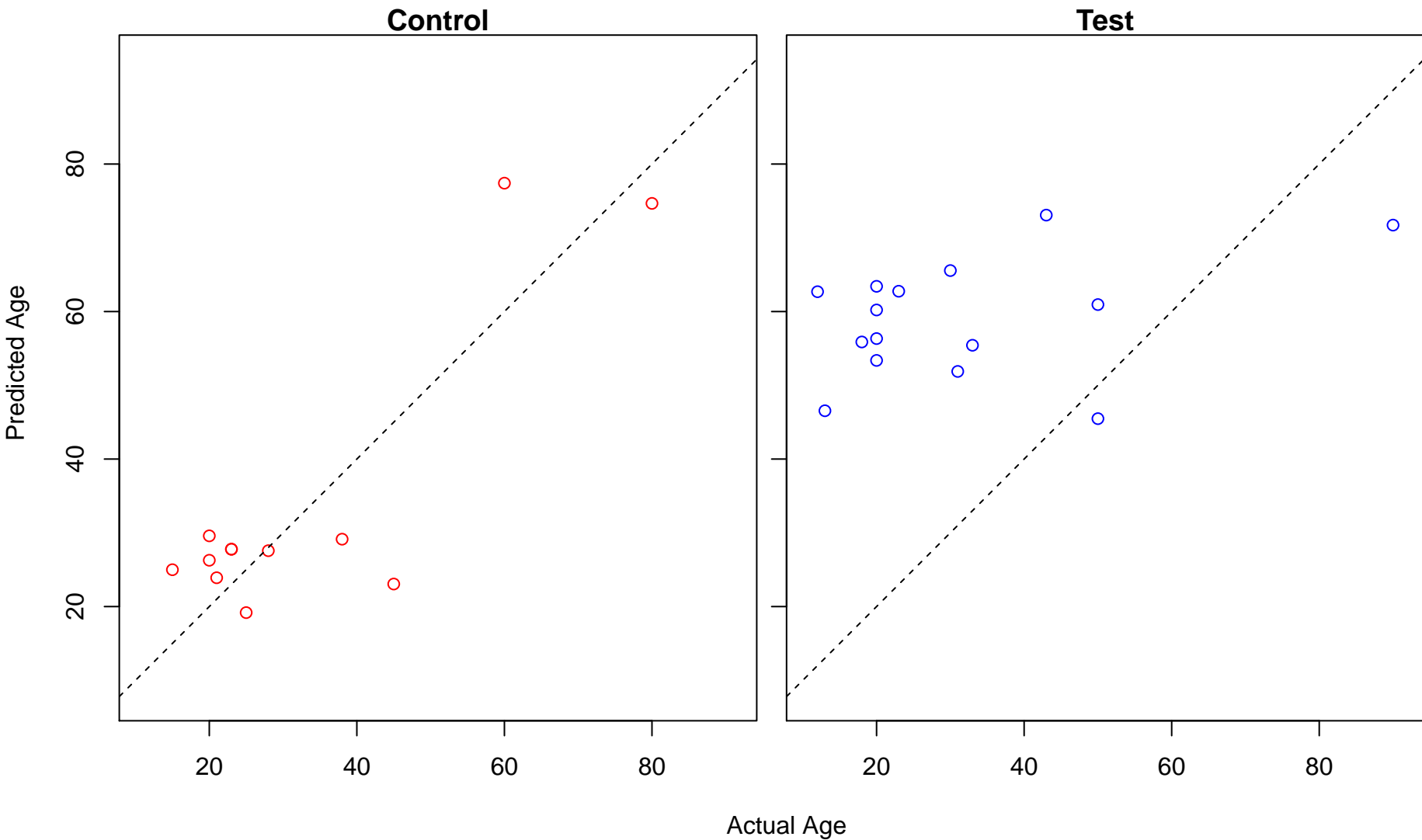


Actual Age

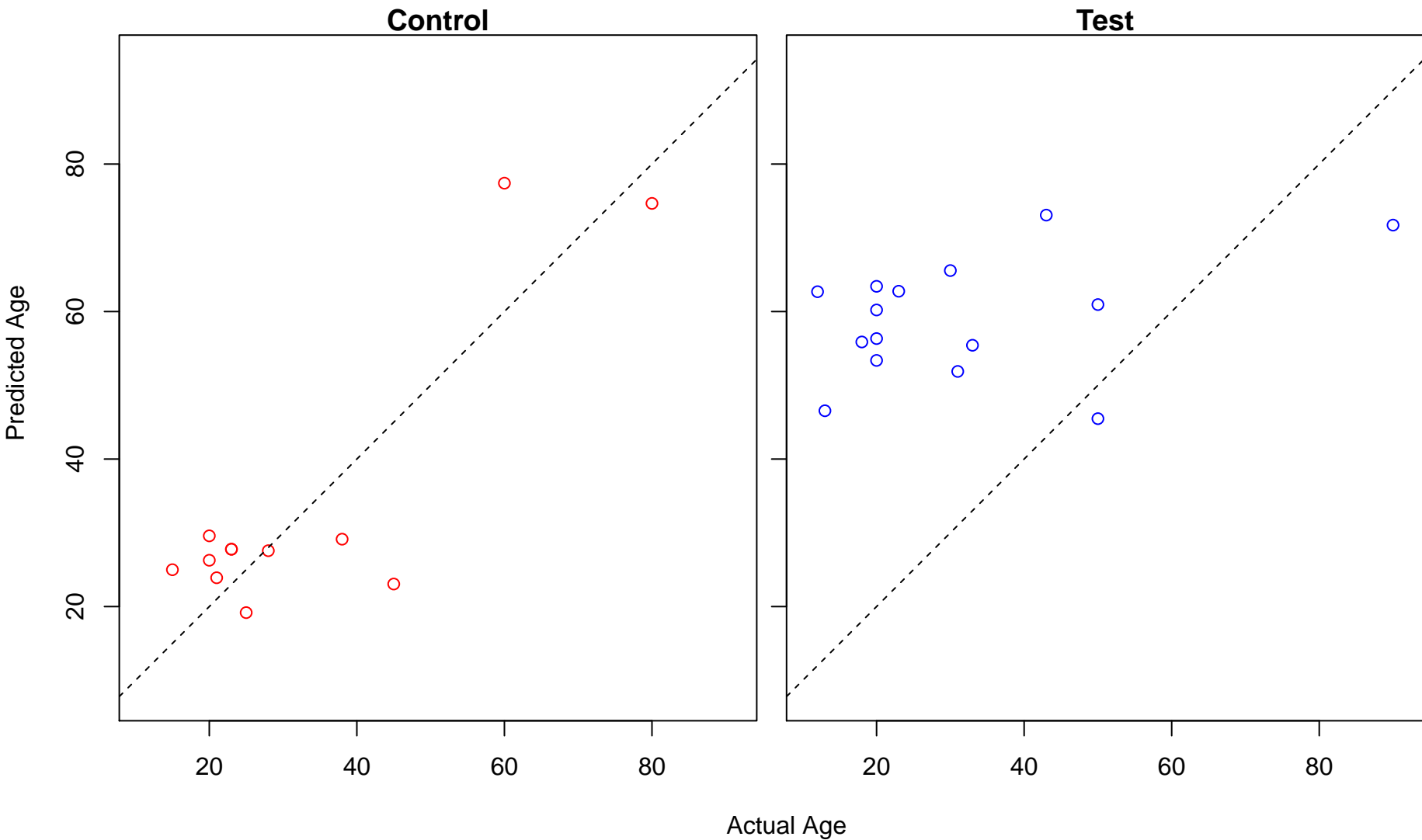
regulation of release of sequestered calcium ion into cytosol (Score: 4.056387)



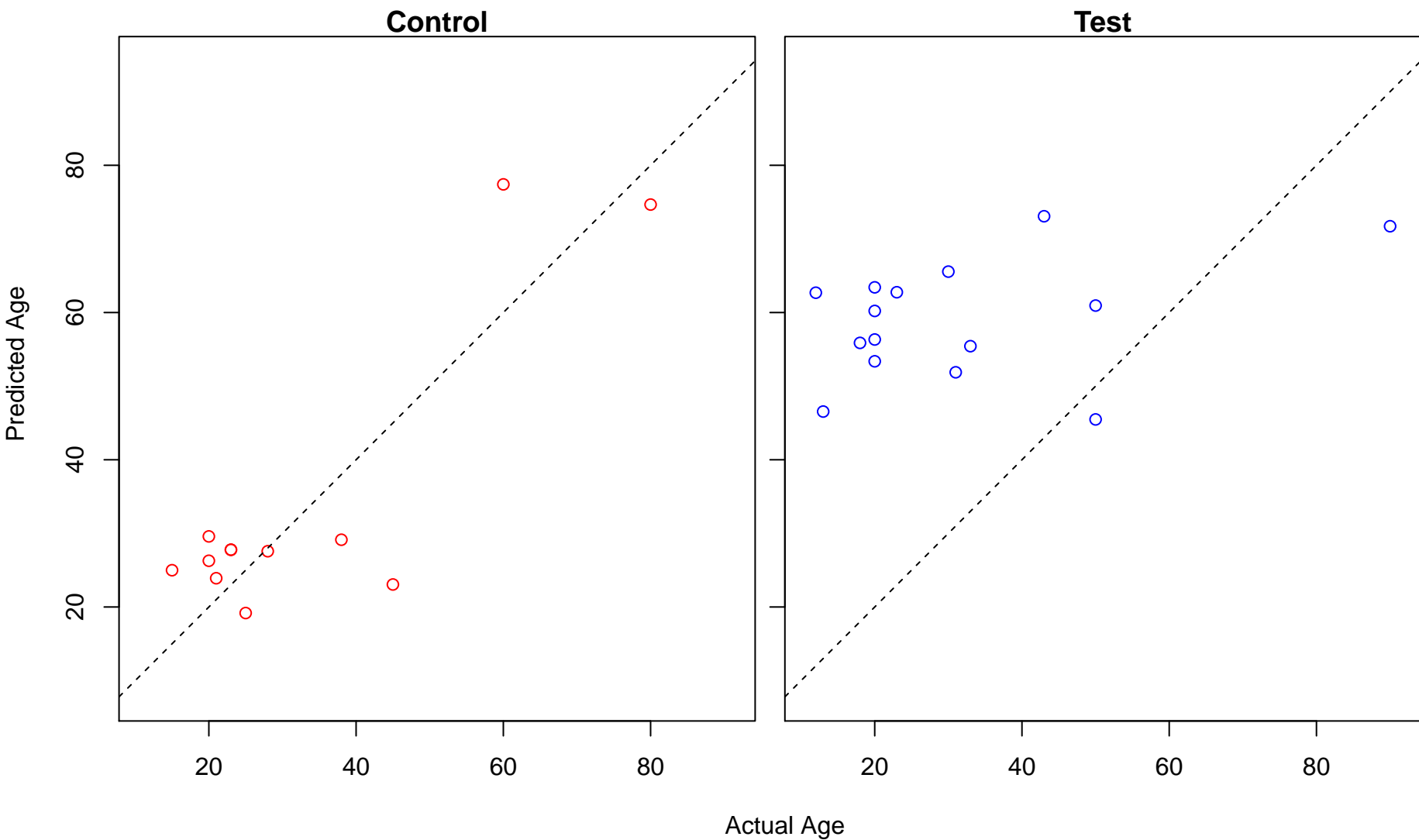
protein targeting to peroxisome (Score: 4.053104)



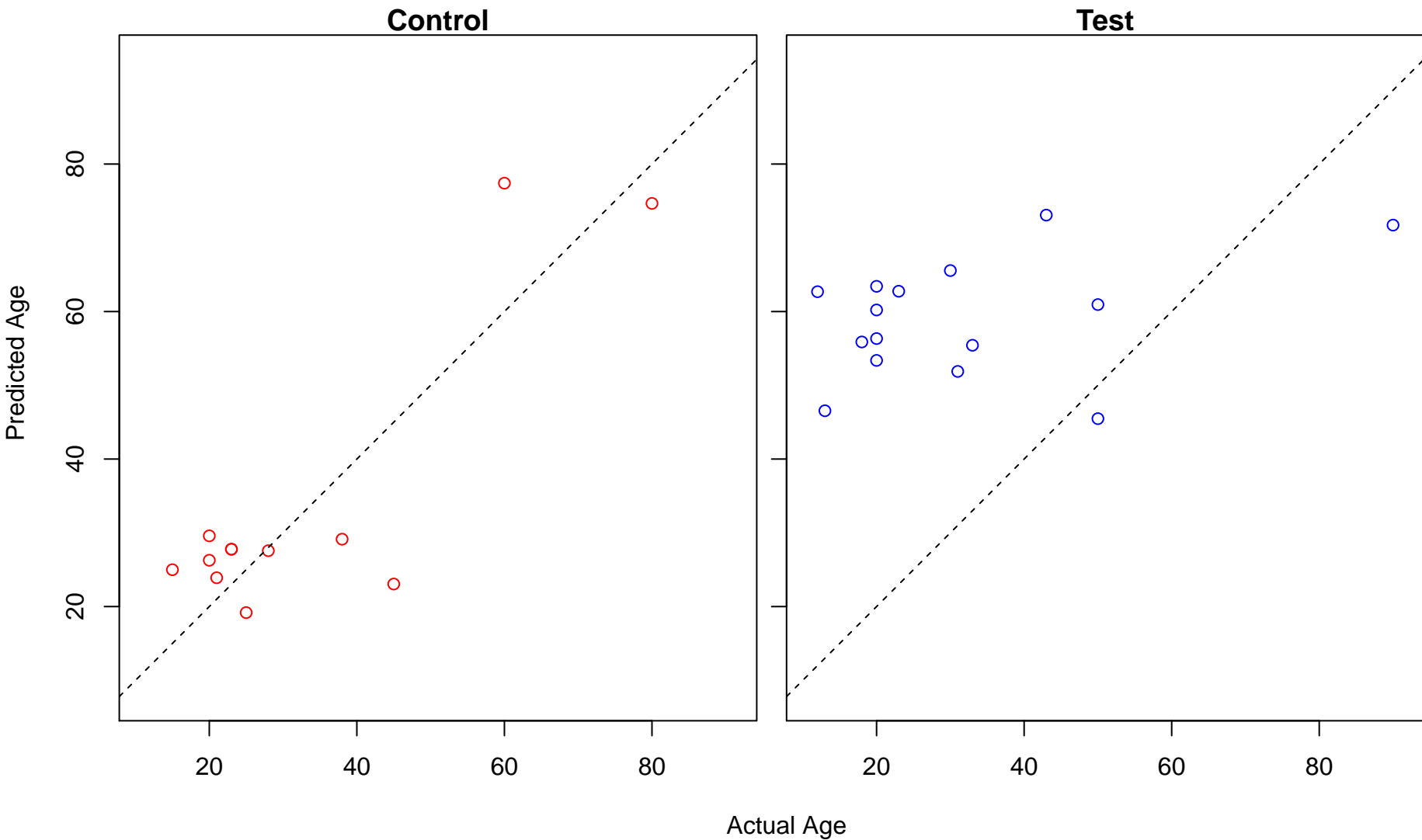
peroxisomal transport (Score: 4.053104)



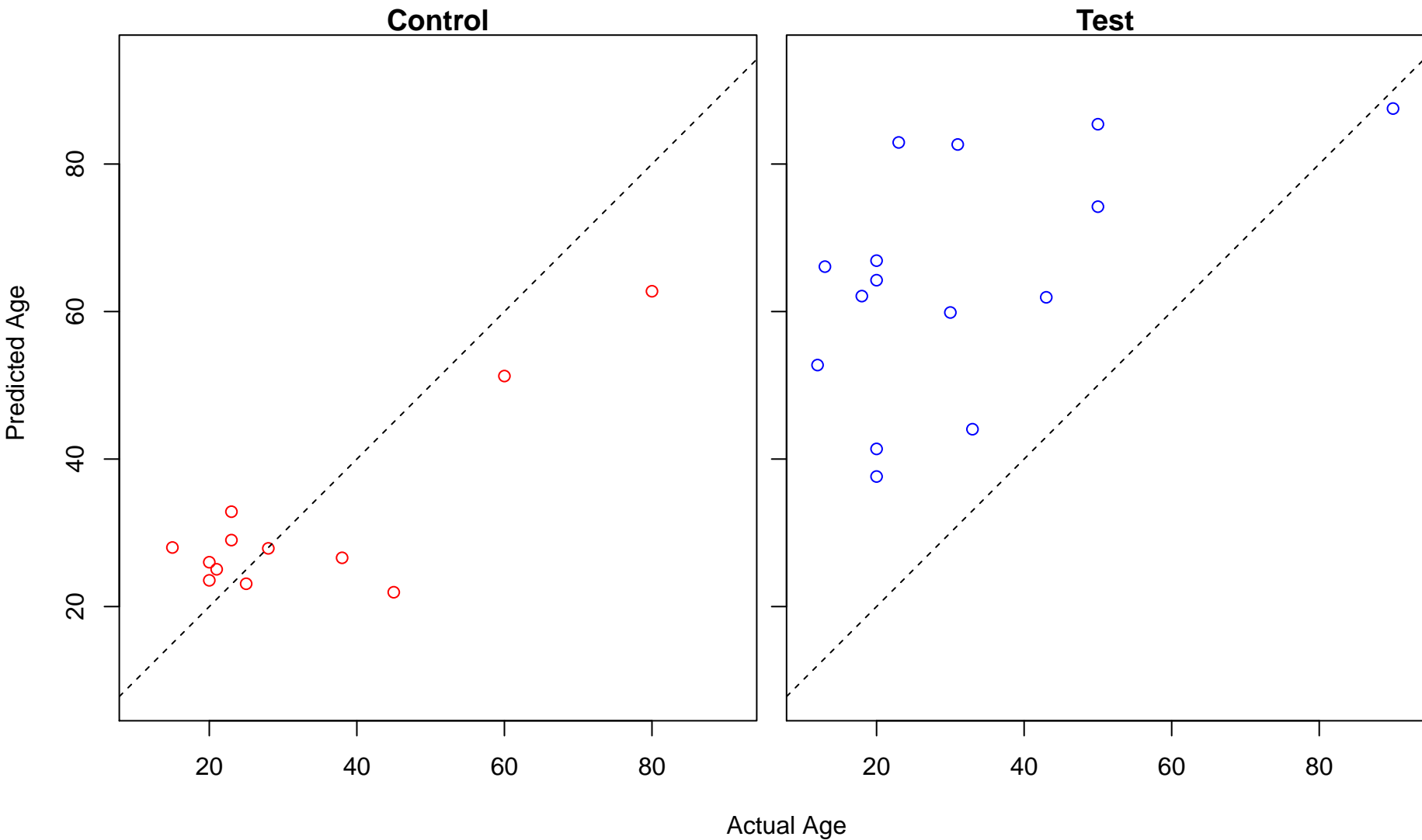
protein localization to peroxisome (Score: 4.053104)



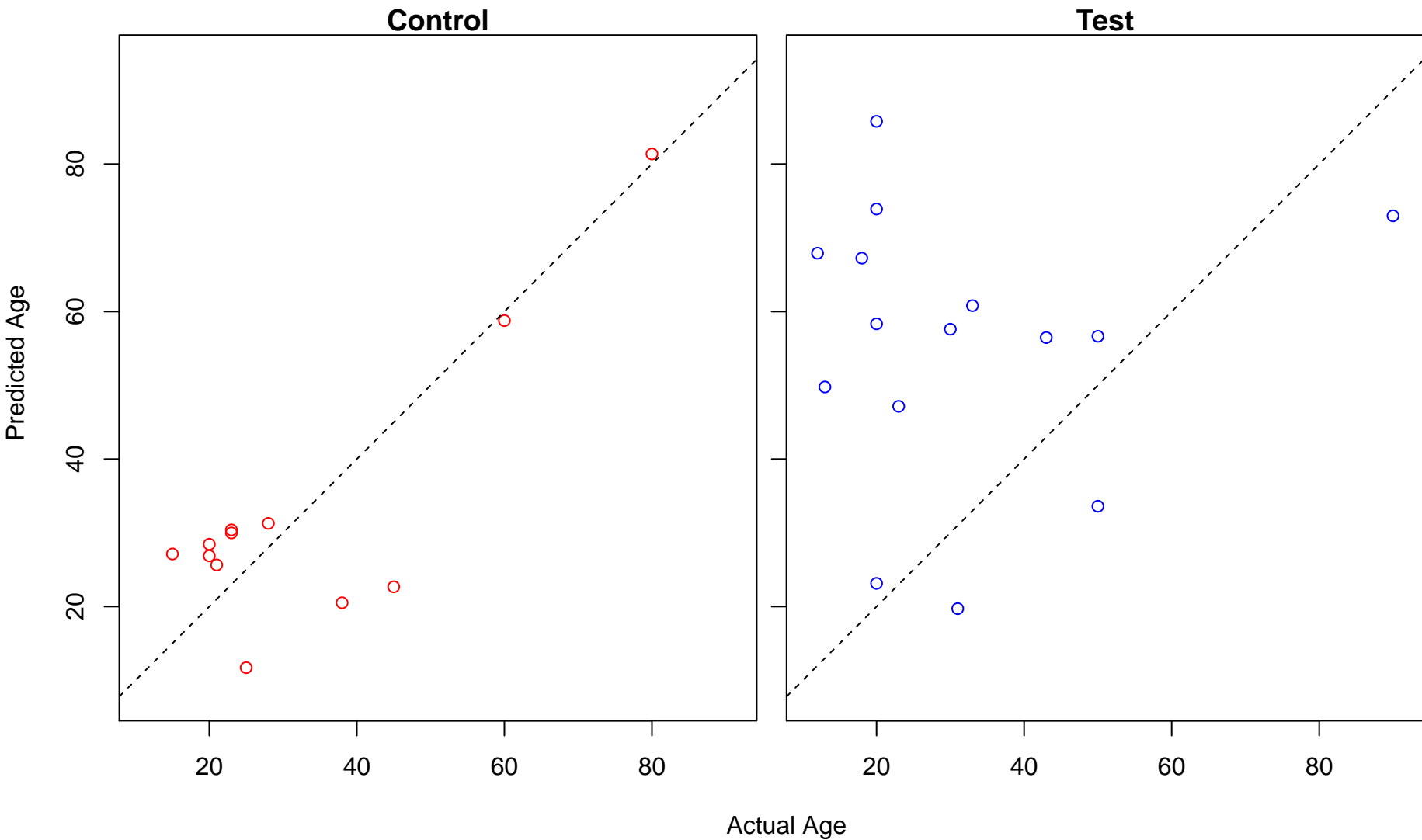
establishment of protein localization to peroxisome (Score: 4.053104)



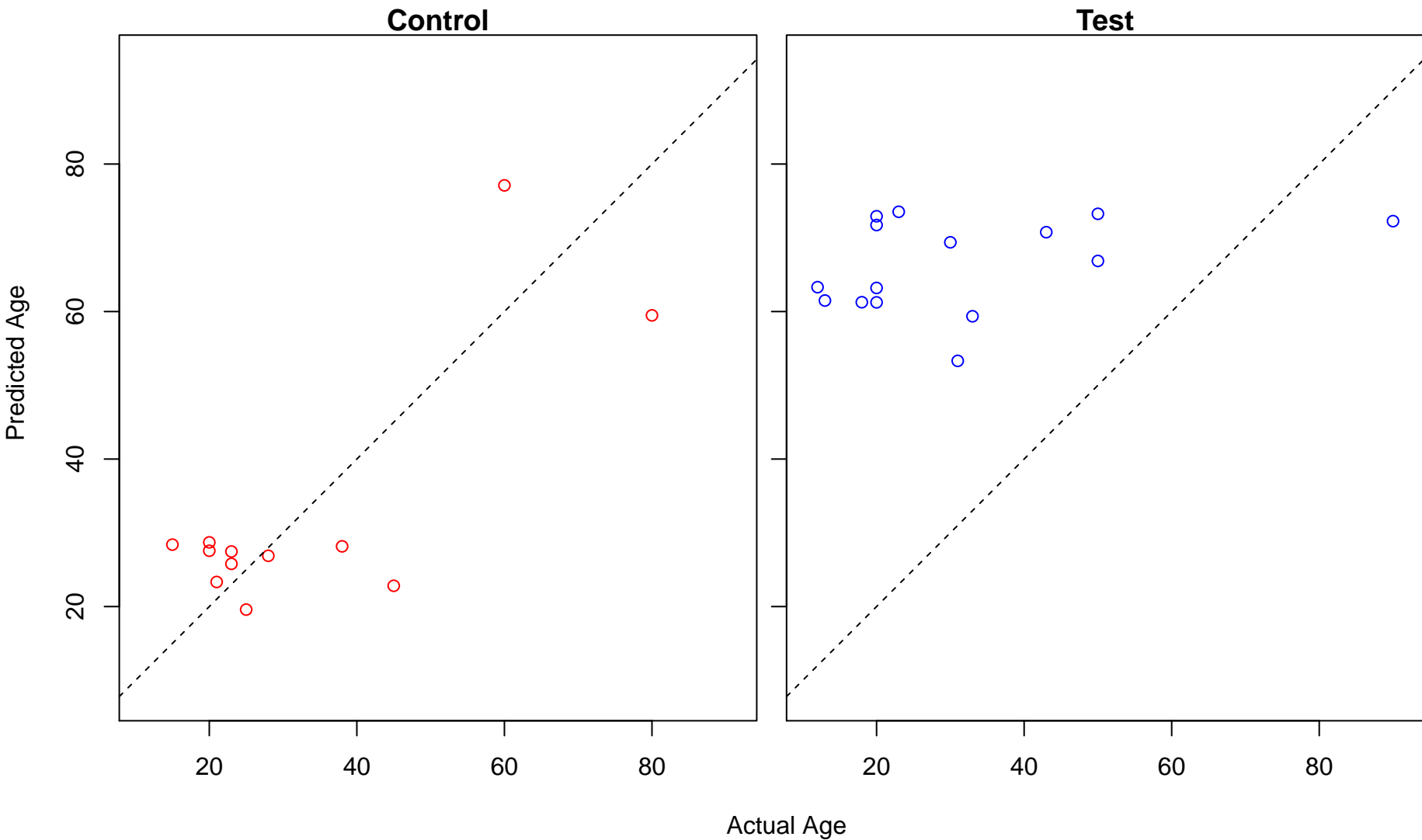
regulation of synapse structural plasticity (Score: 4.052254)



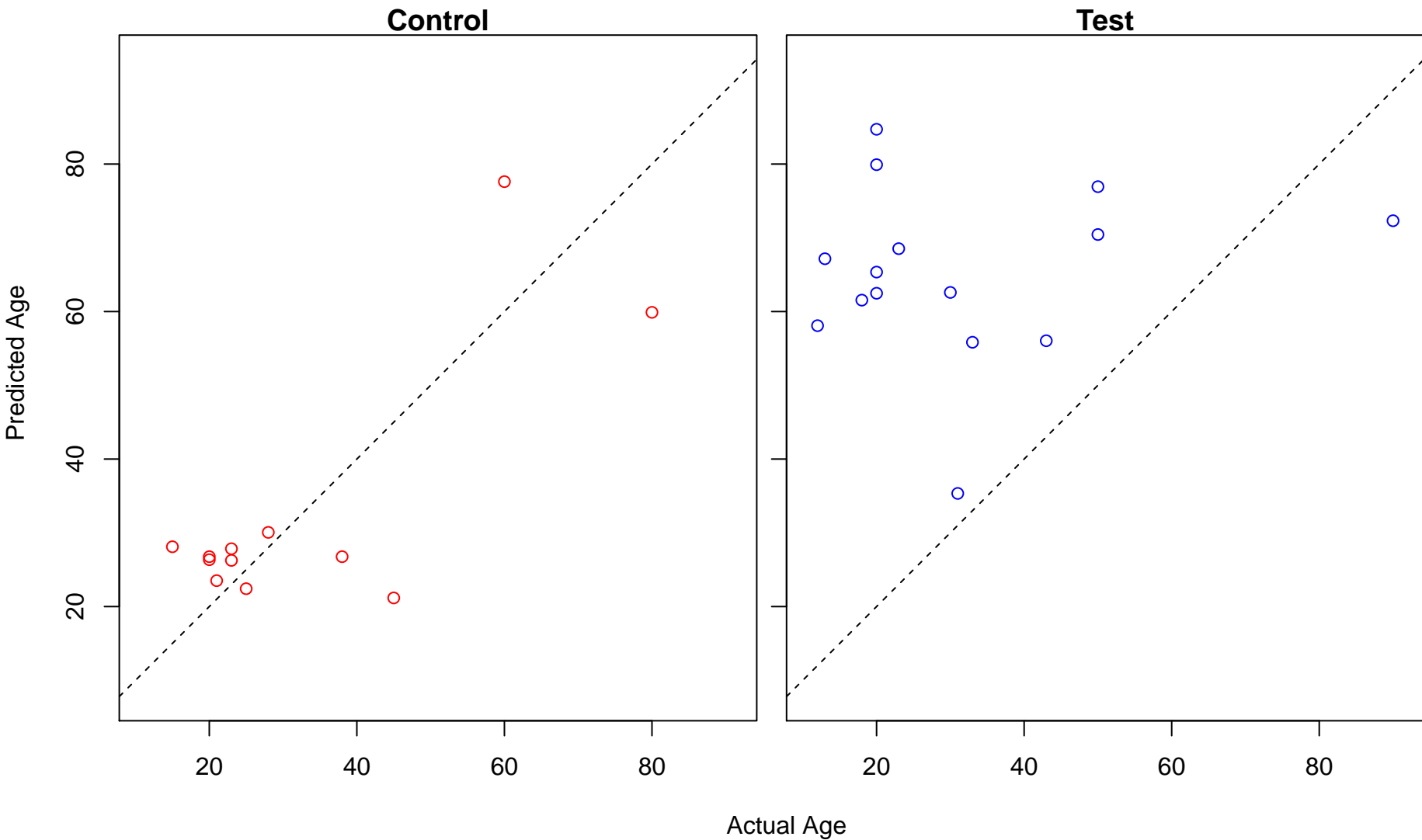
chromatin modification (Score: 4.052138)



endothelial cell development (Score: 4.051686)

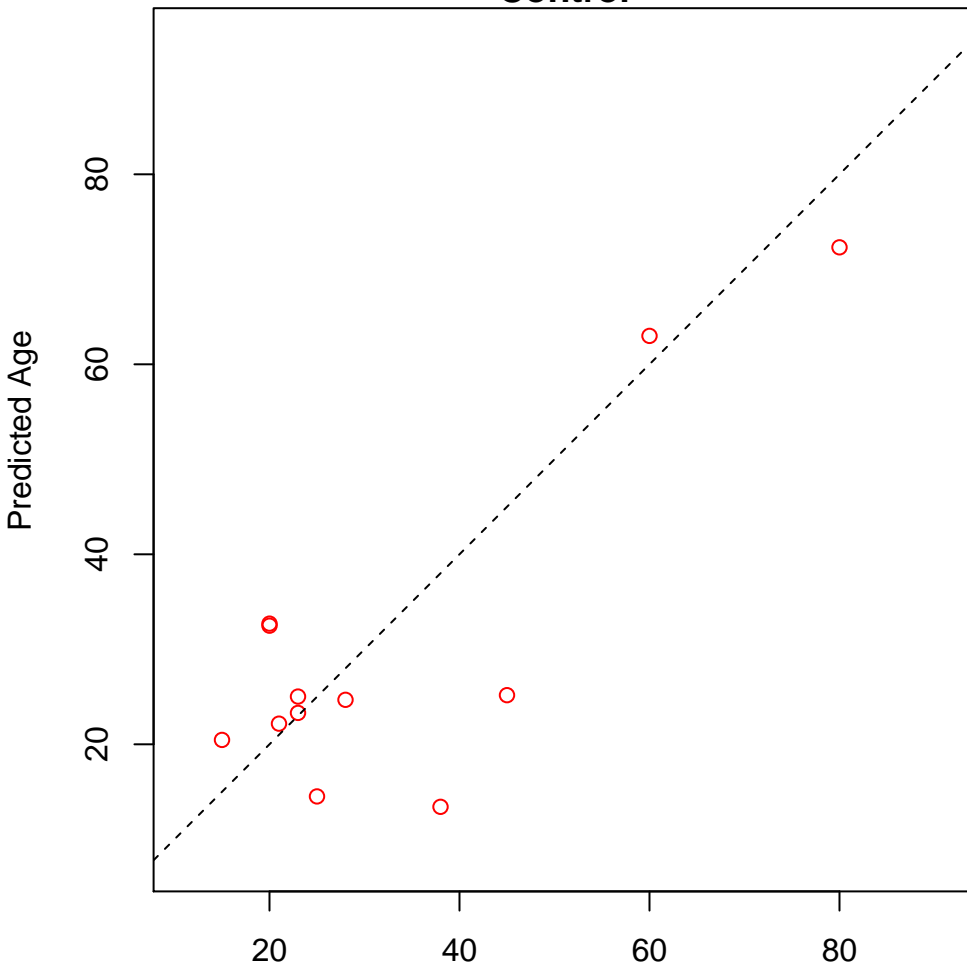


positive regulation of defense response (Score: 4.051287)

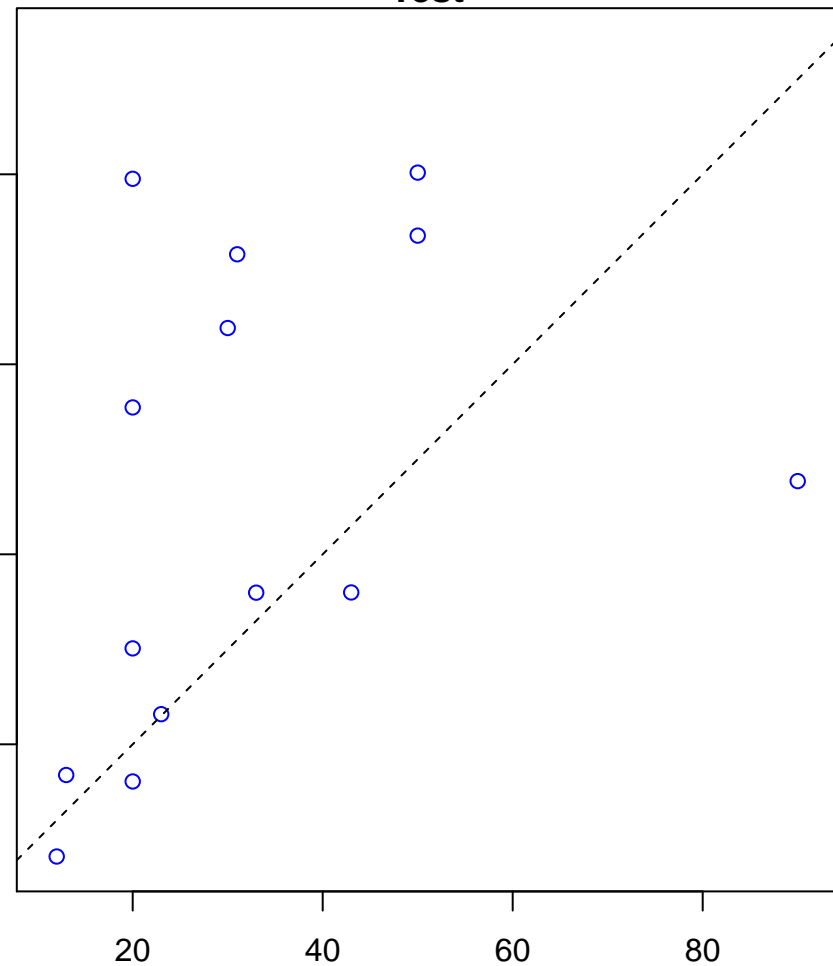


cellular amino acid biosynthetic process (Score: 4.051273)

Control

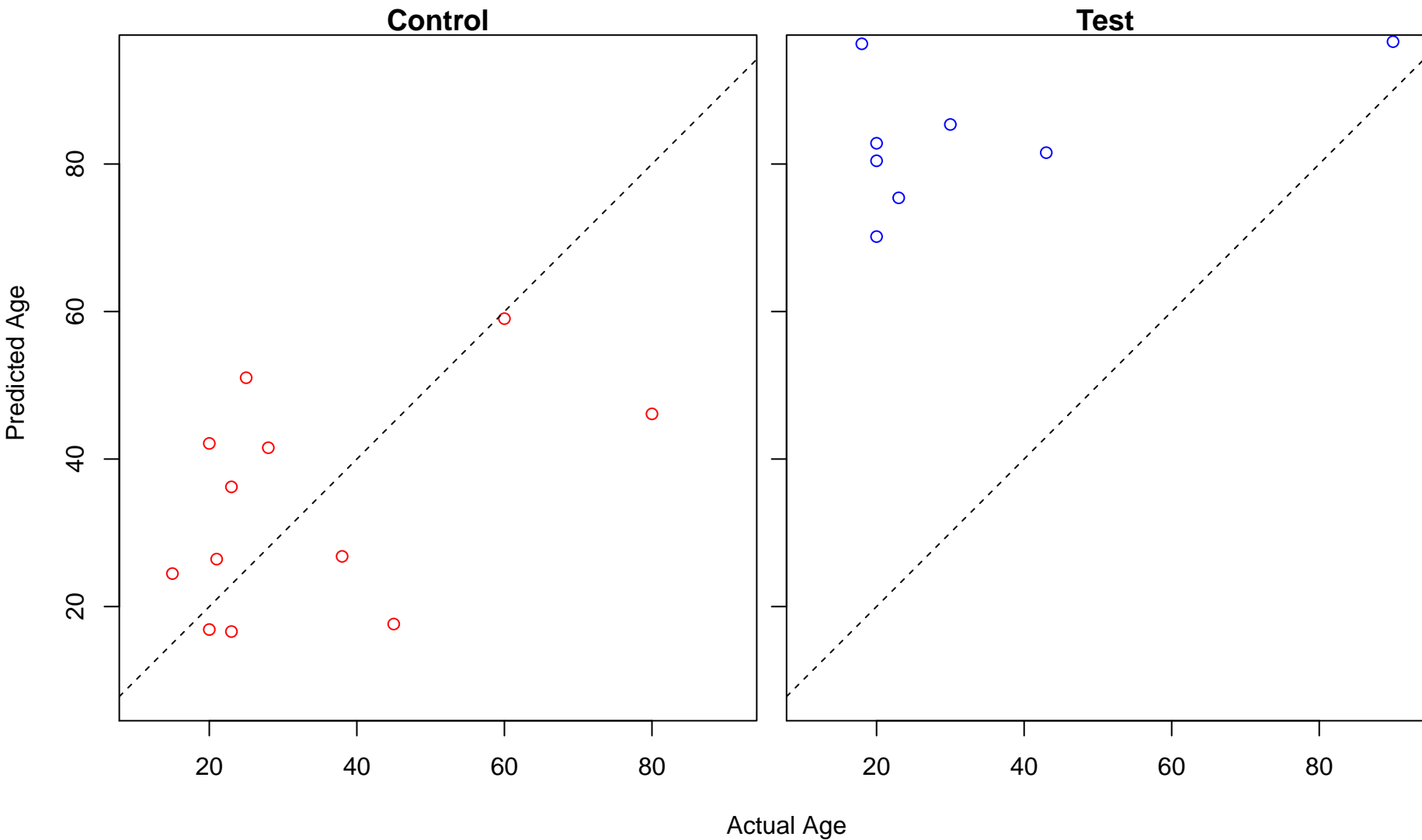


Test

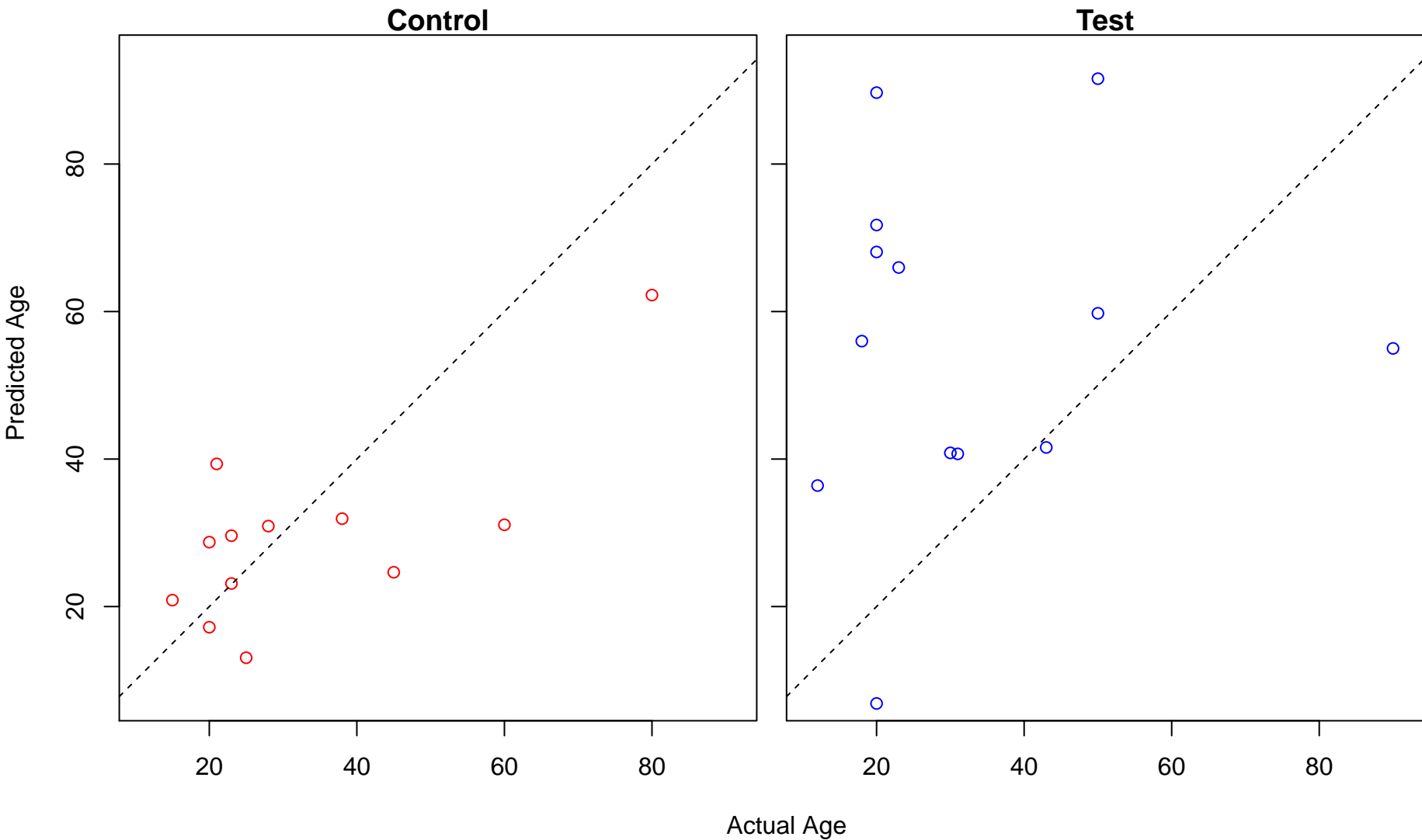


Actual Age

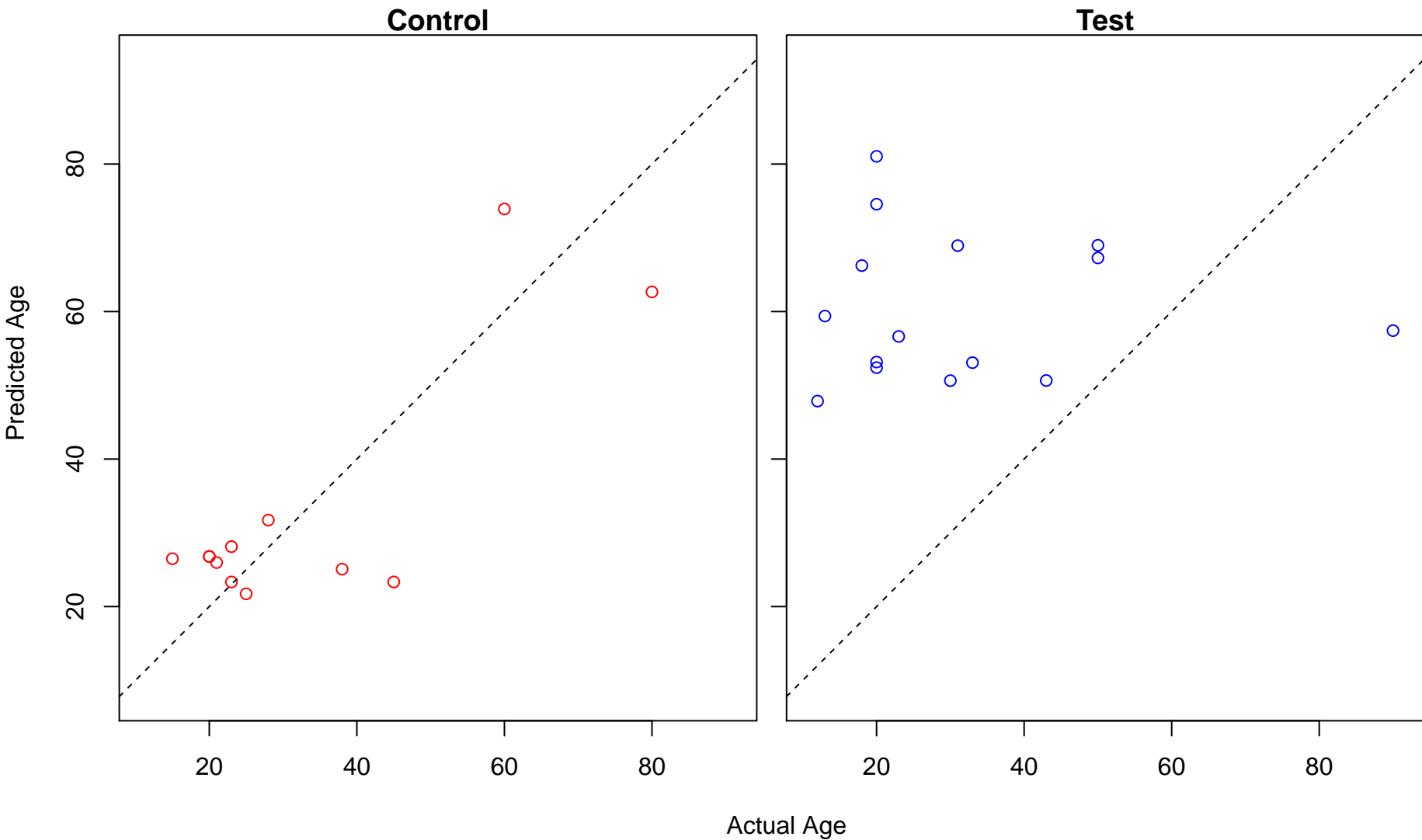
regulation of interferon-gamma secretion (Score: 4.049759)



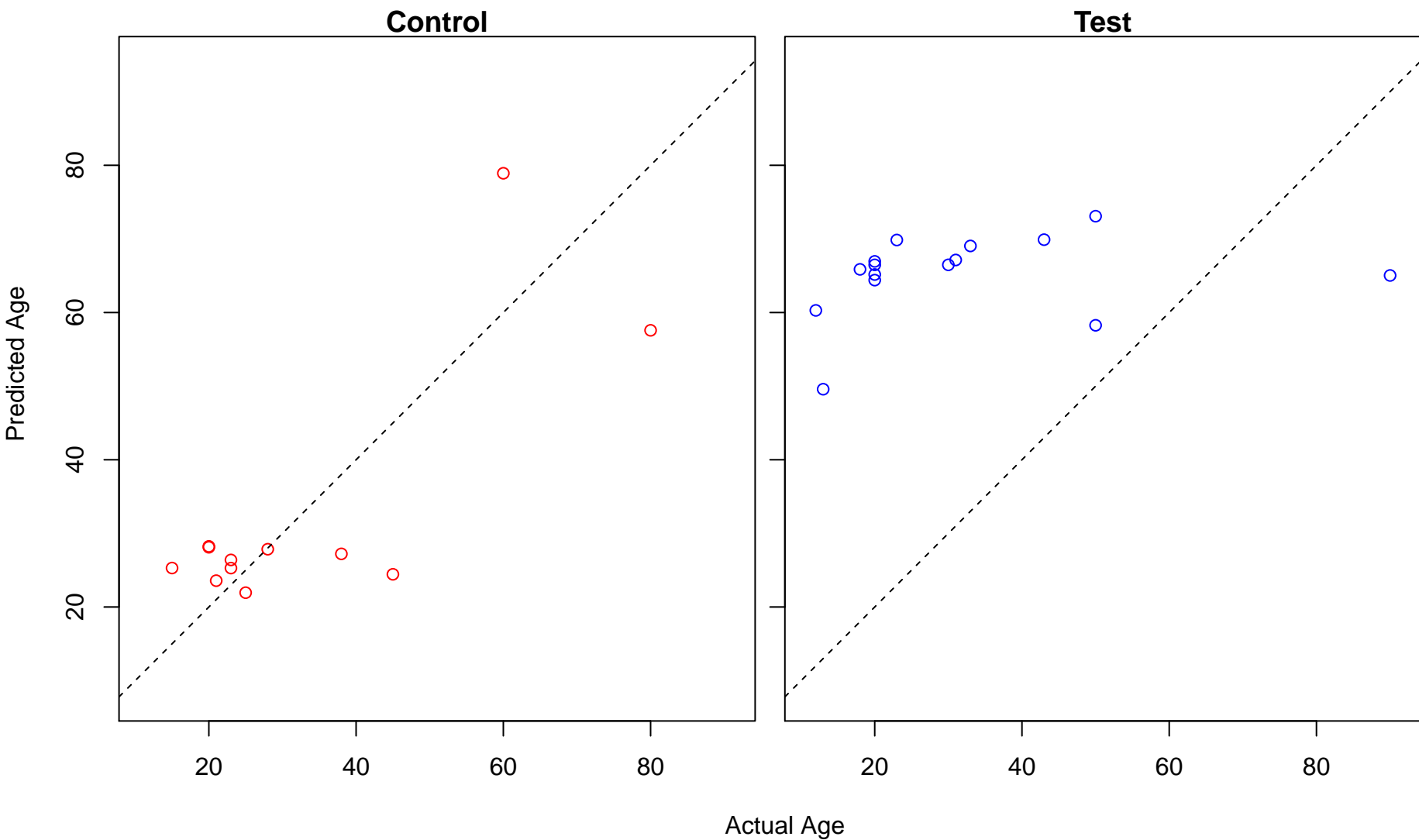
cerebral cortex development (Score: 4.047533)



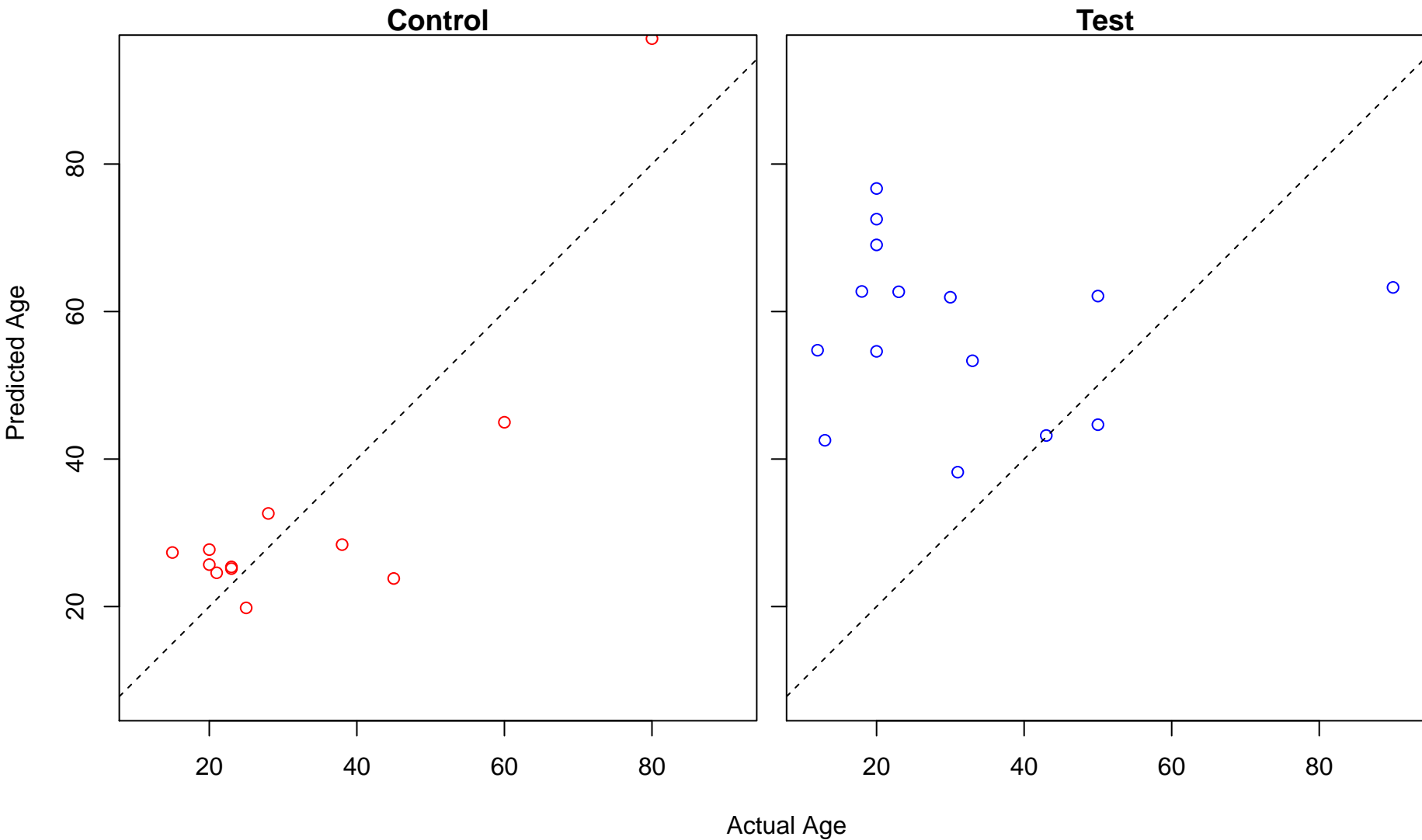
negative regulation of calcium ion transport into cytosol (Score: 4.047490)



intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress (Score: 4.04552)

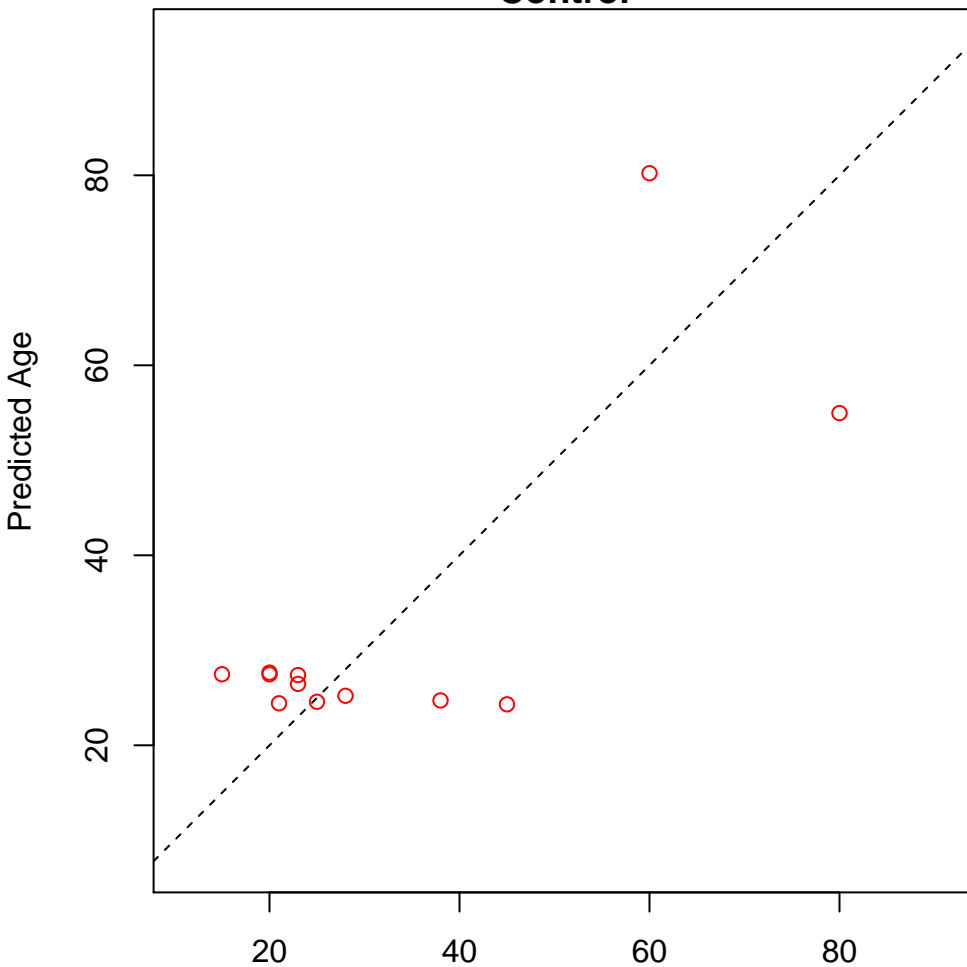


membrane lipid biosynthetic process (Score: 4.045502)

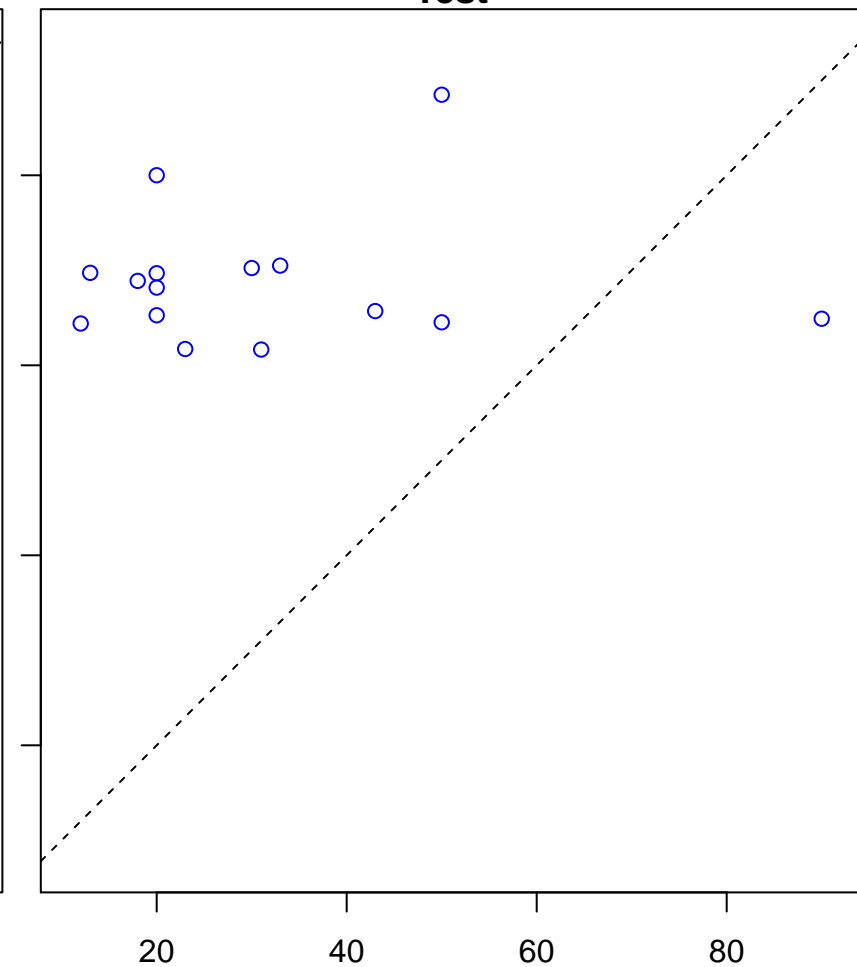


modulation by host of viral transcription (Score: 4.043493)

Control

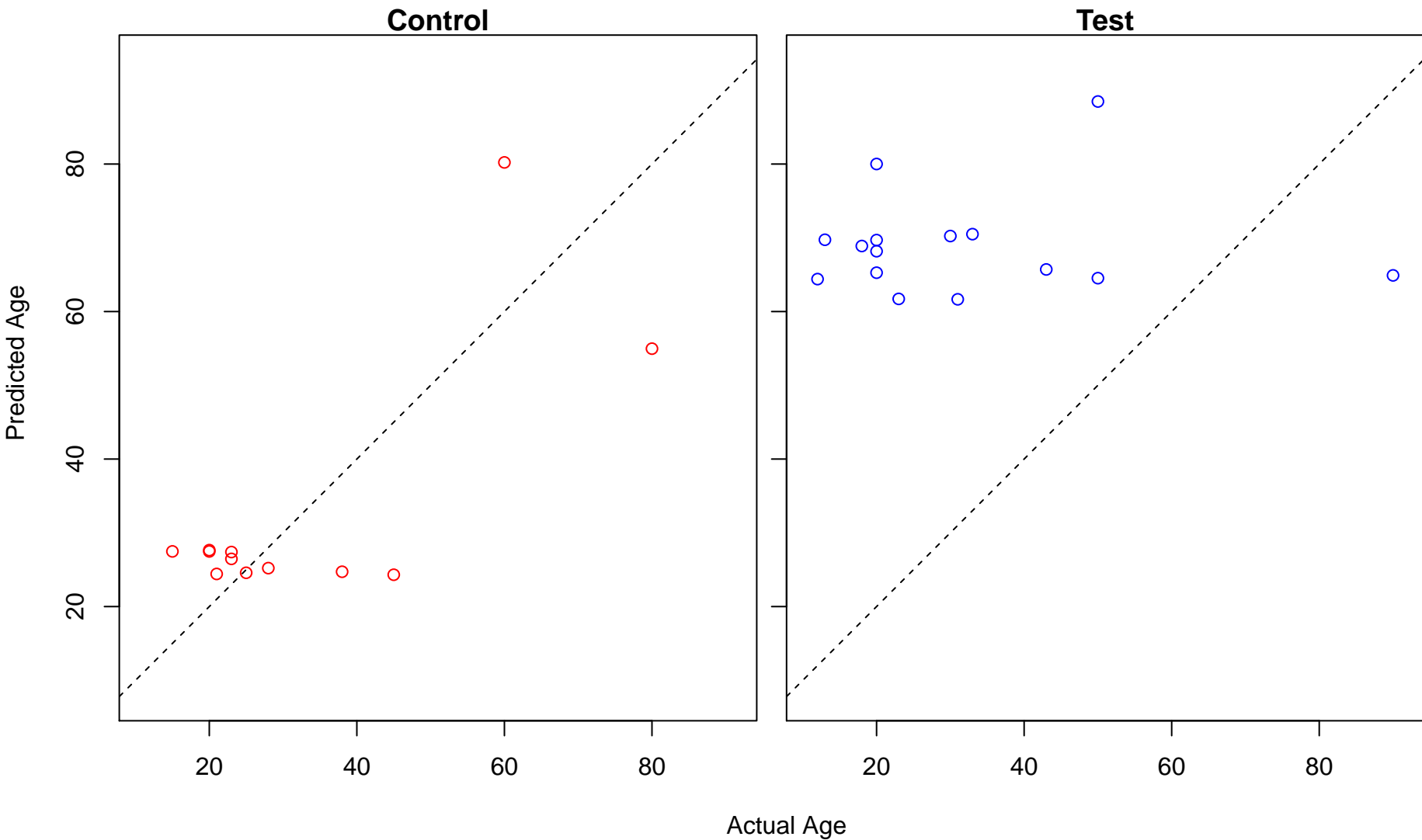


Test

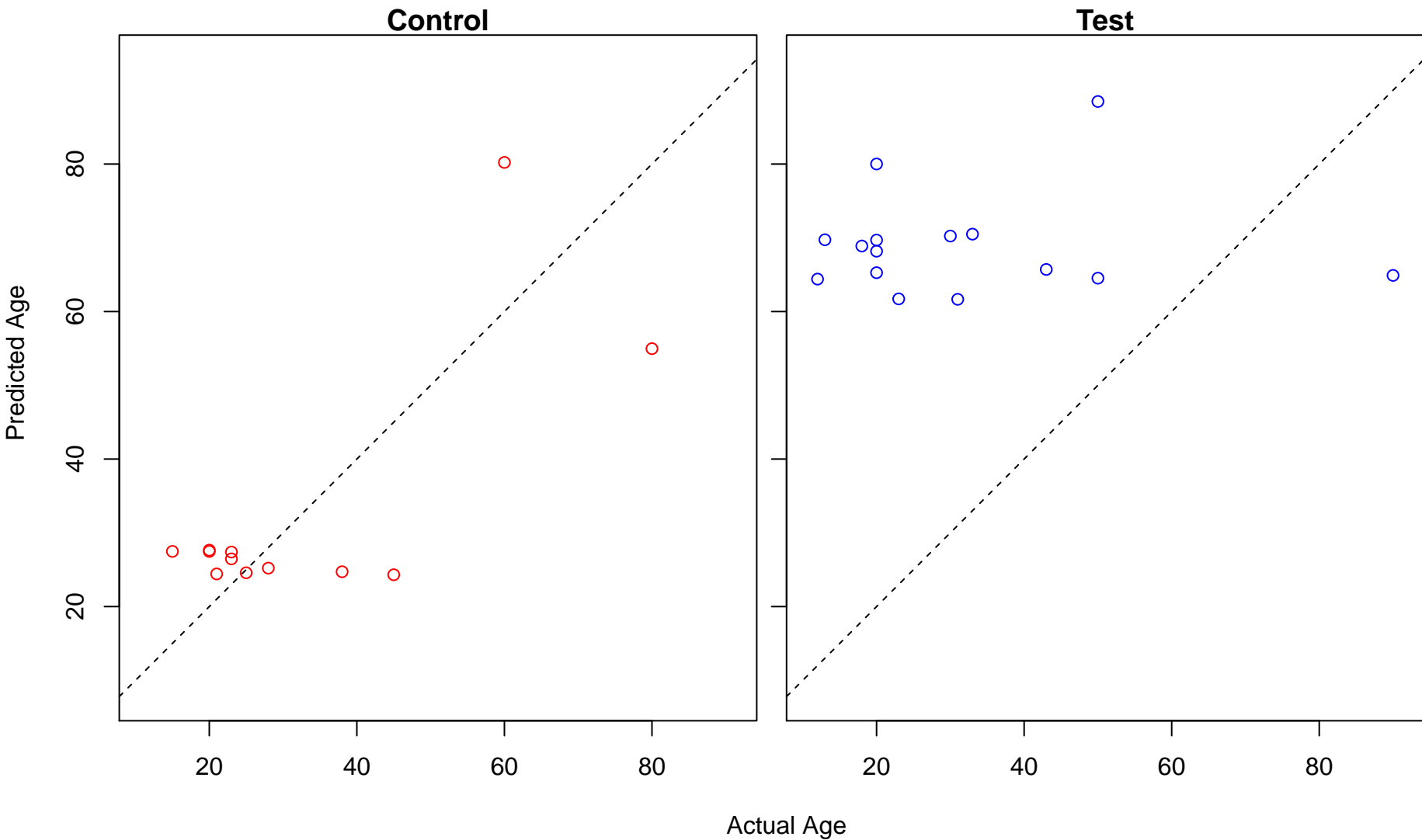


Actual Age

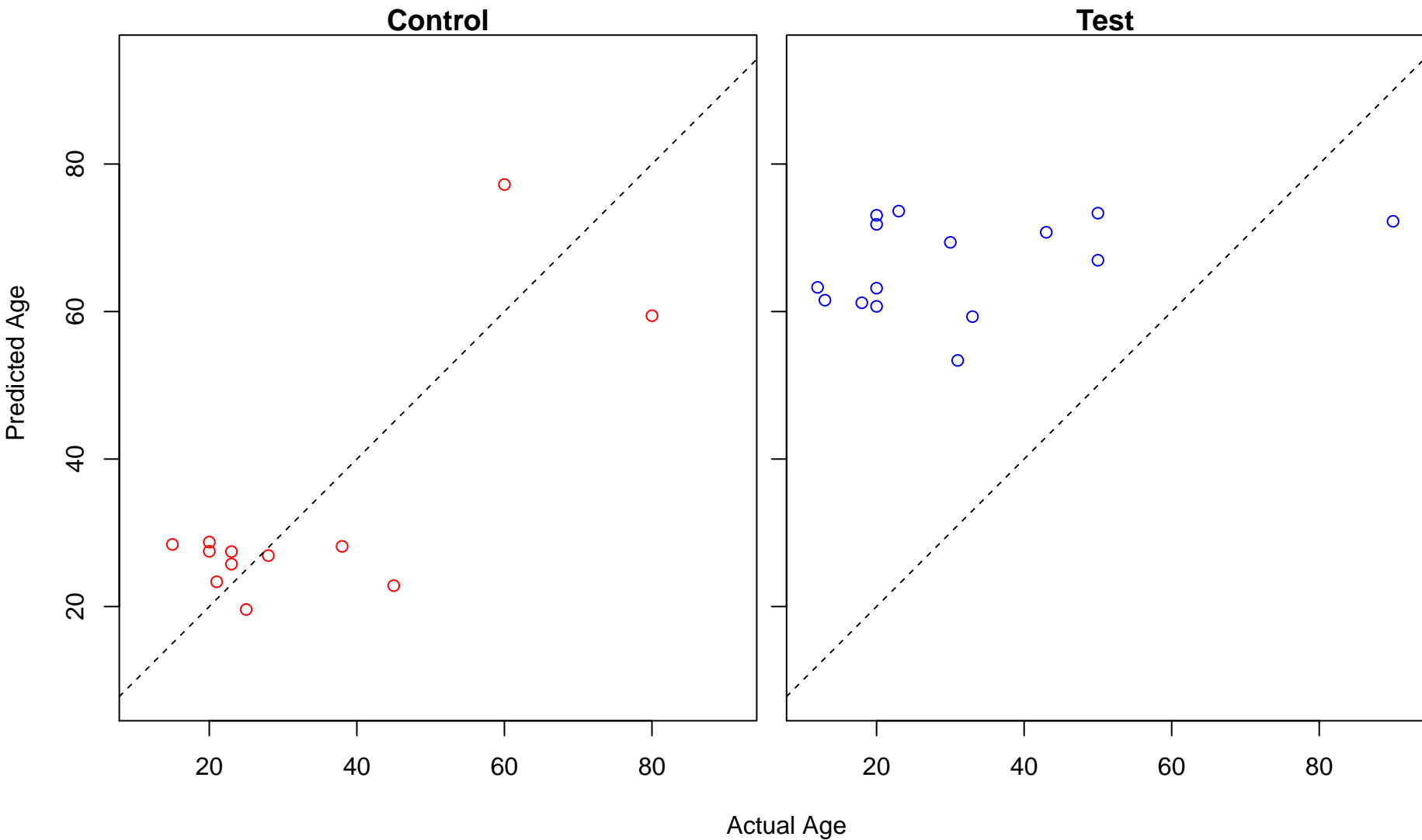
modulation of transcription in other organism involved in symbiotic interaction (Score: 4.043493)



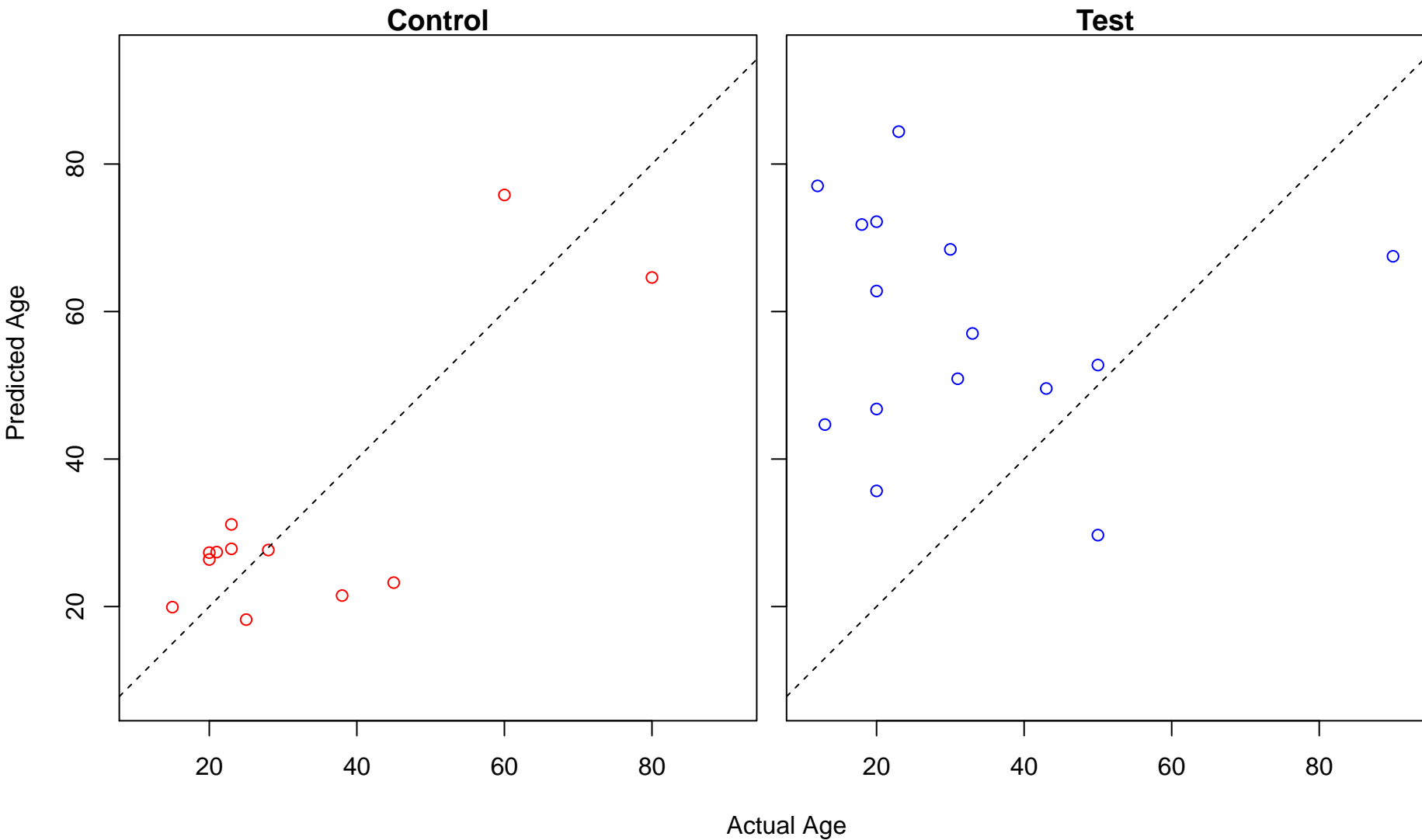
modulation by host of symbiont transcription (Score: 4.043493)



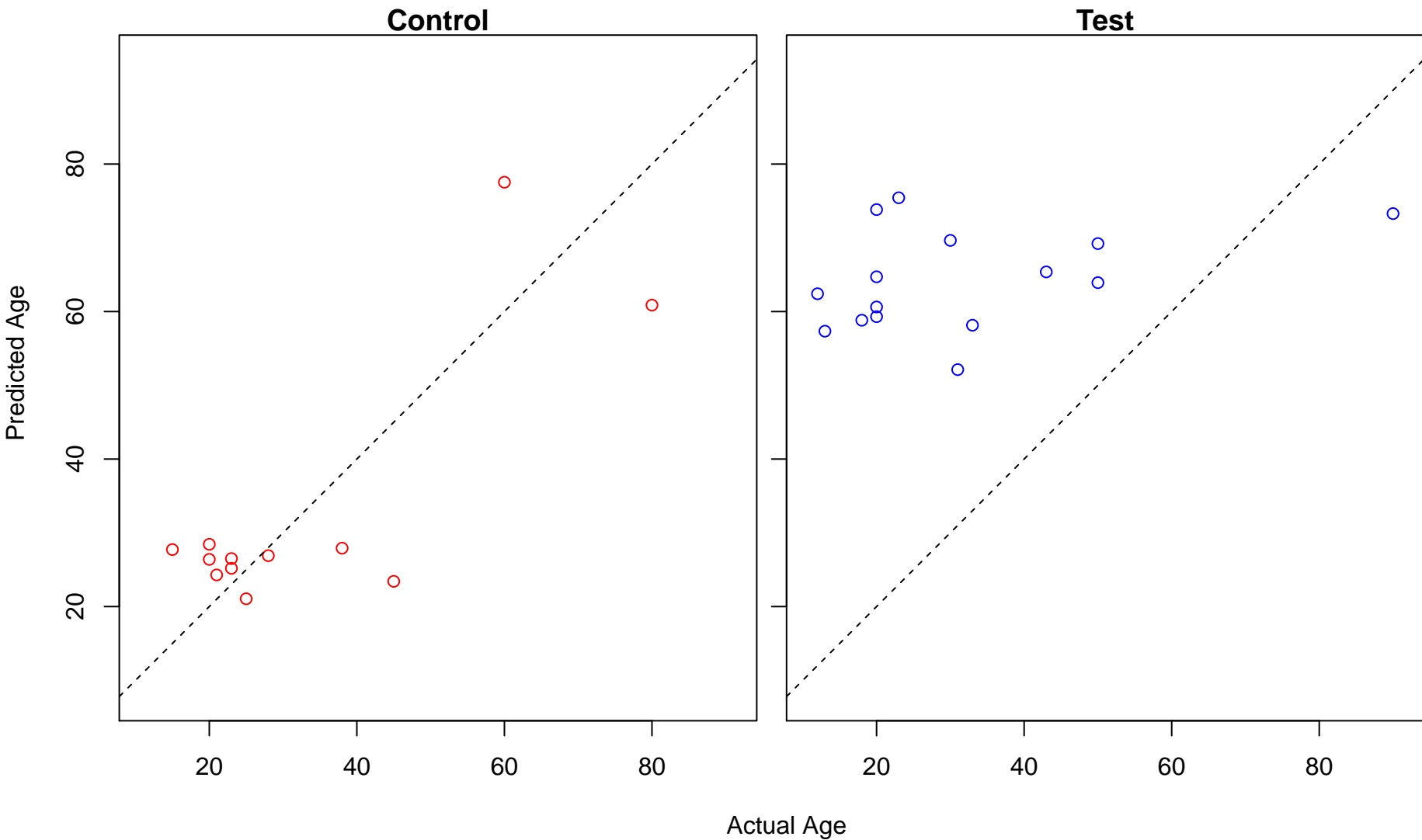
establishment of endothelial barrier (Score: 4.042256)



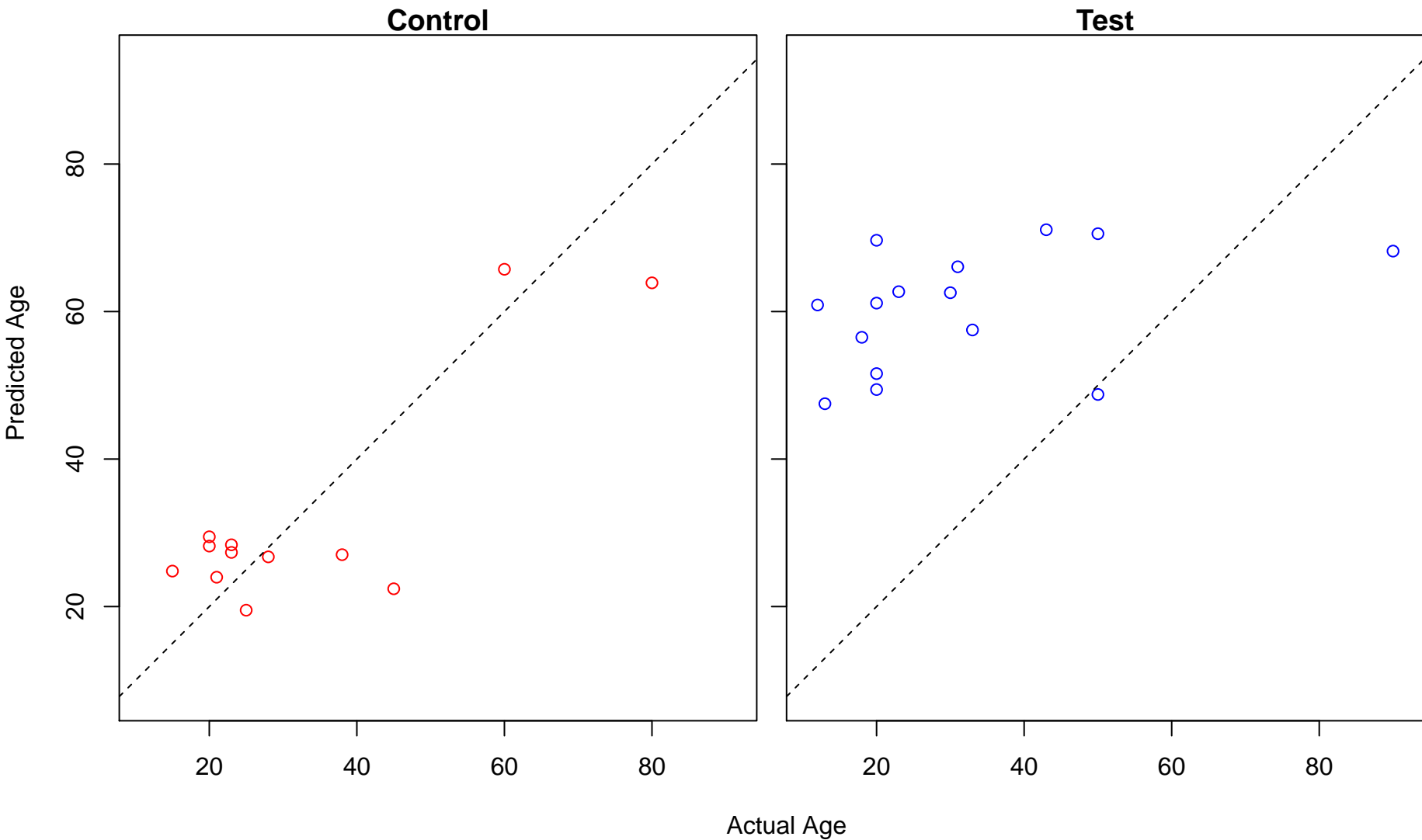
DNA double-strand break processing (Score: 4.037615)



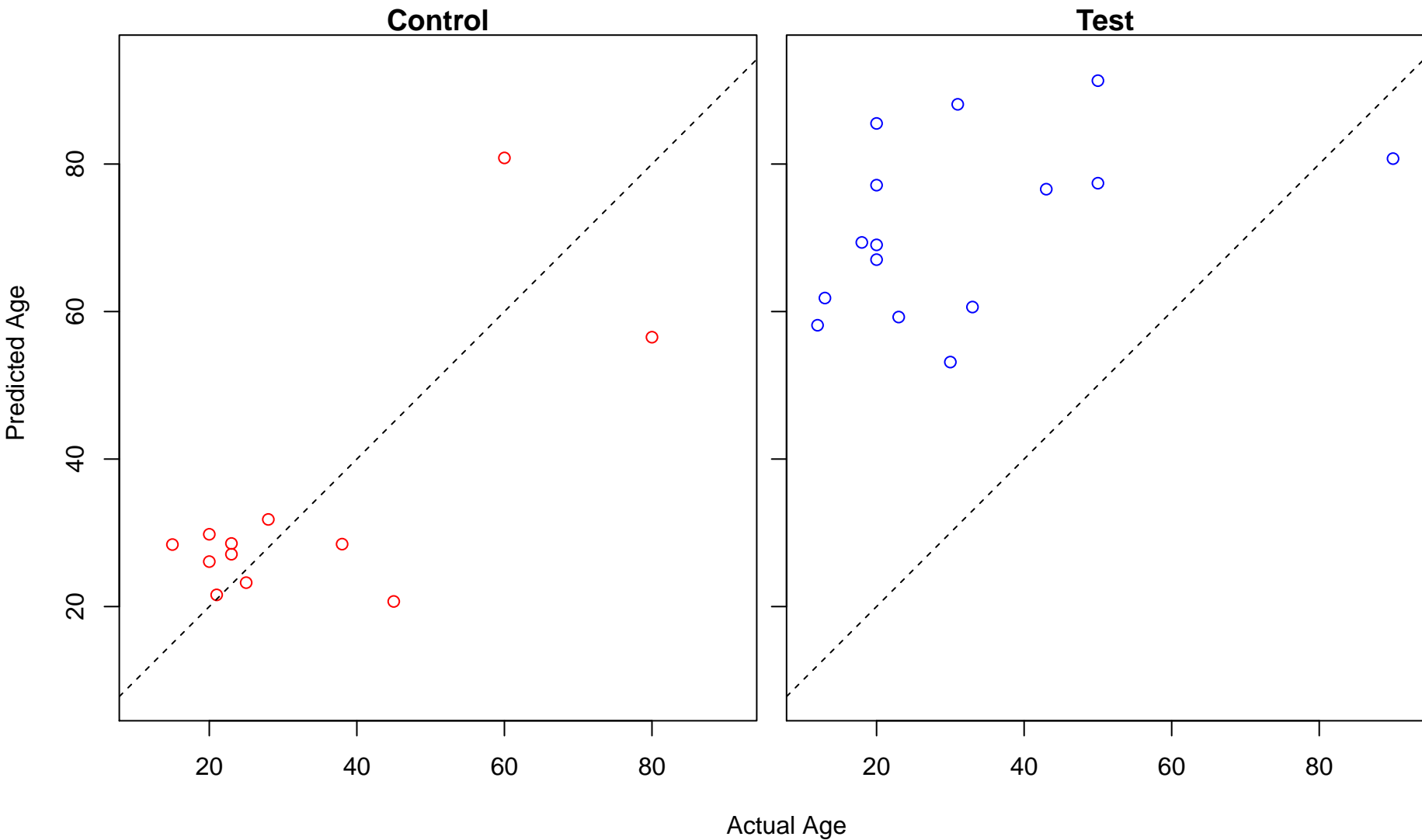
membrane docking (Score: 4.036179)



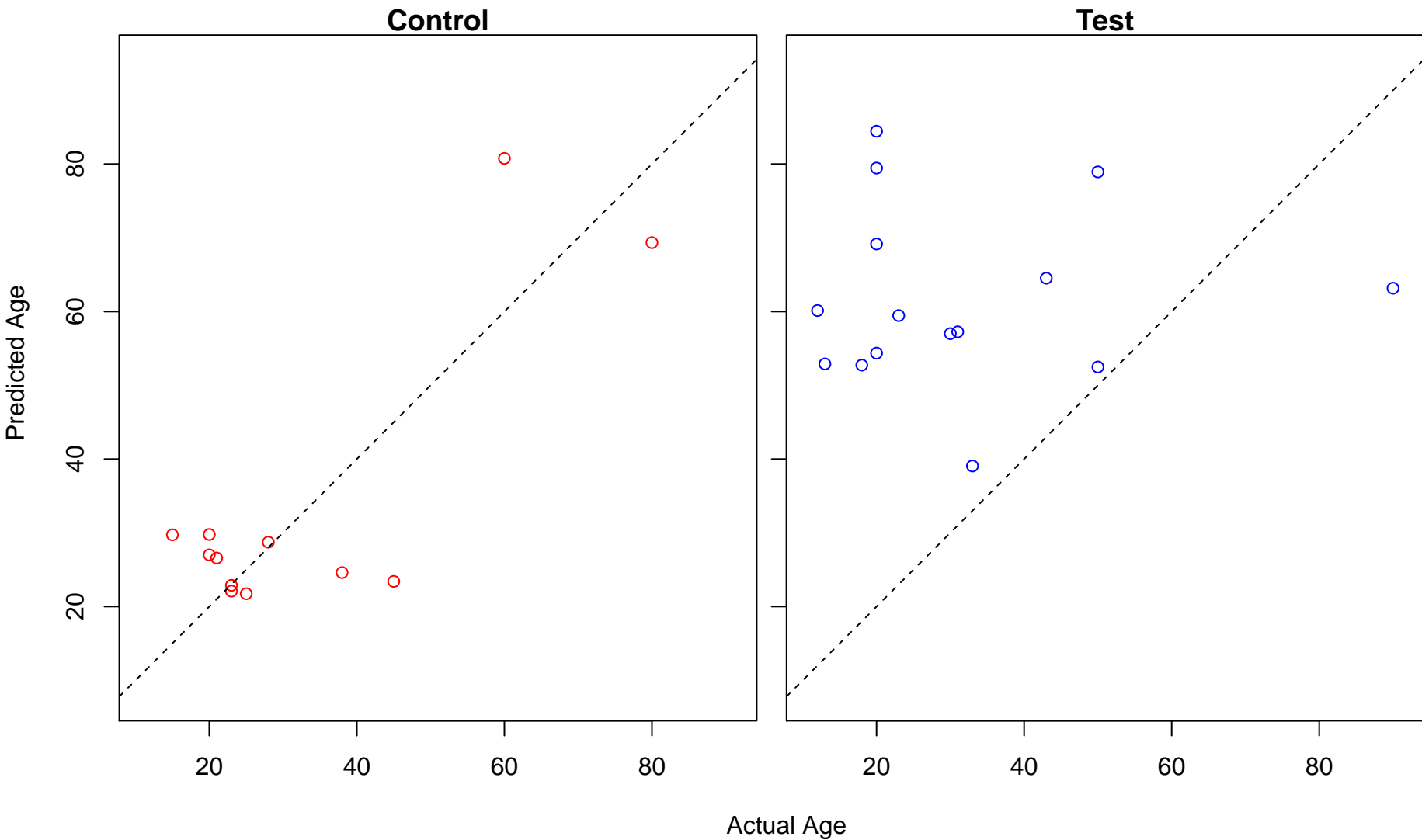
NLS-bearing protein import into nucleus (Score: 4.035209)



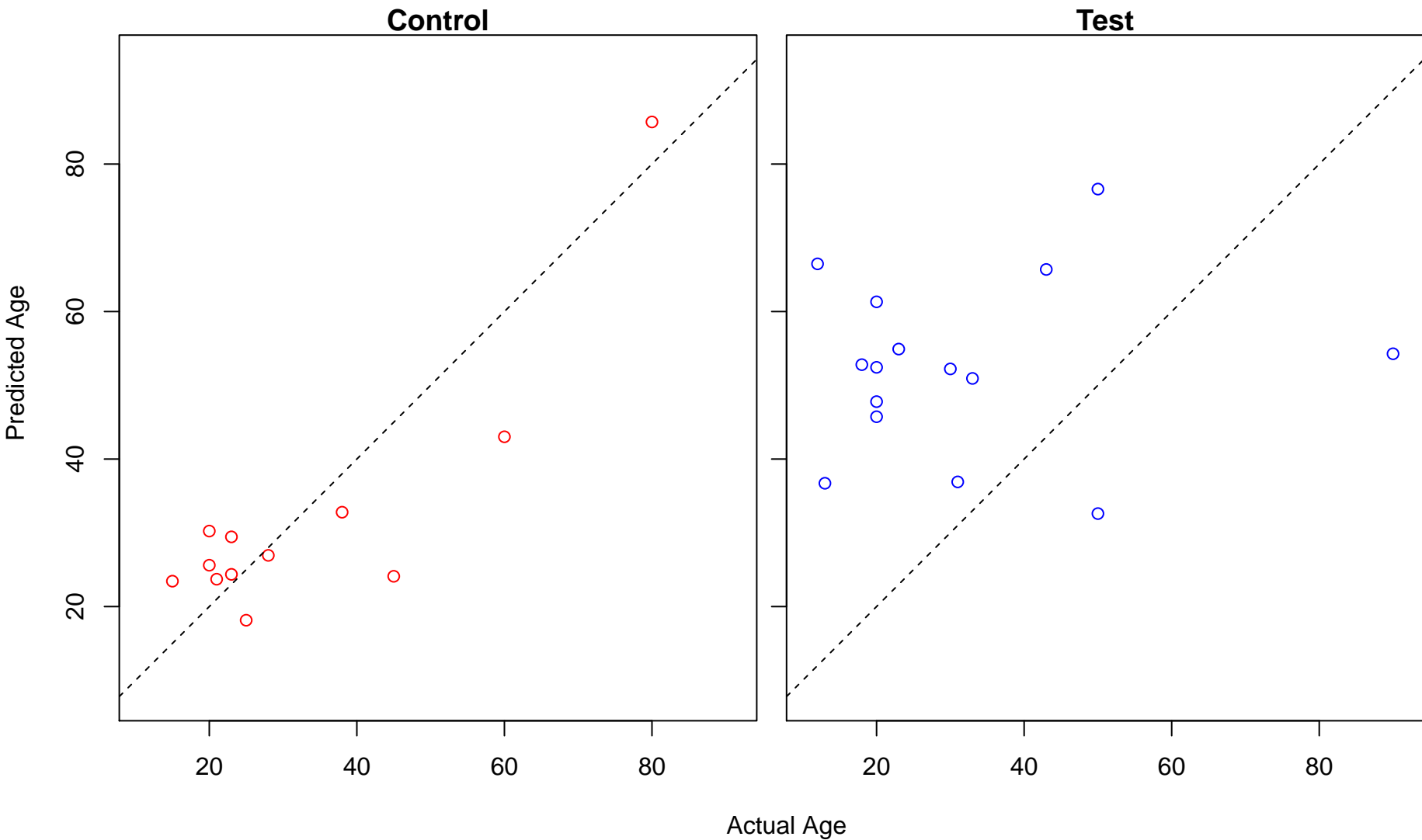
negative regulation of response to external stimulus (Score: 4.034566)



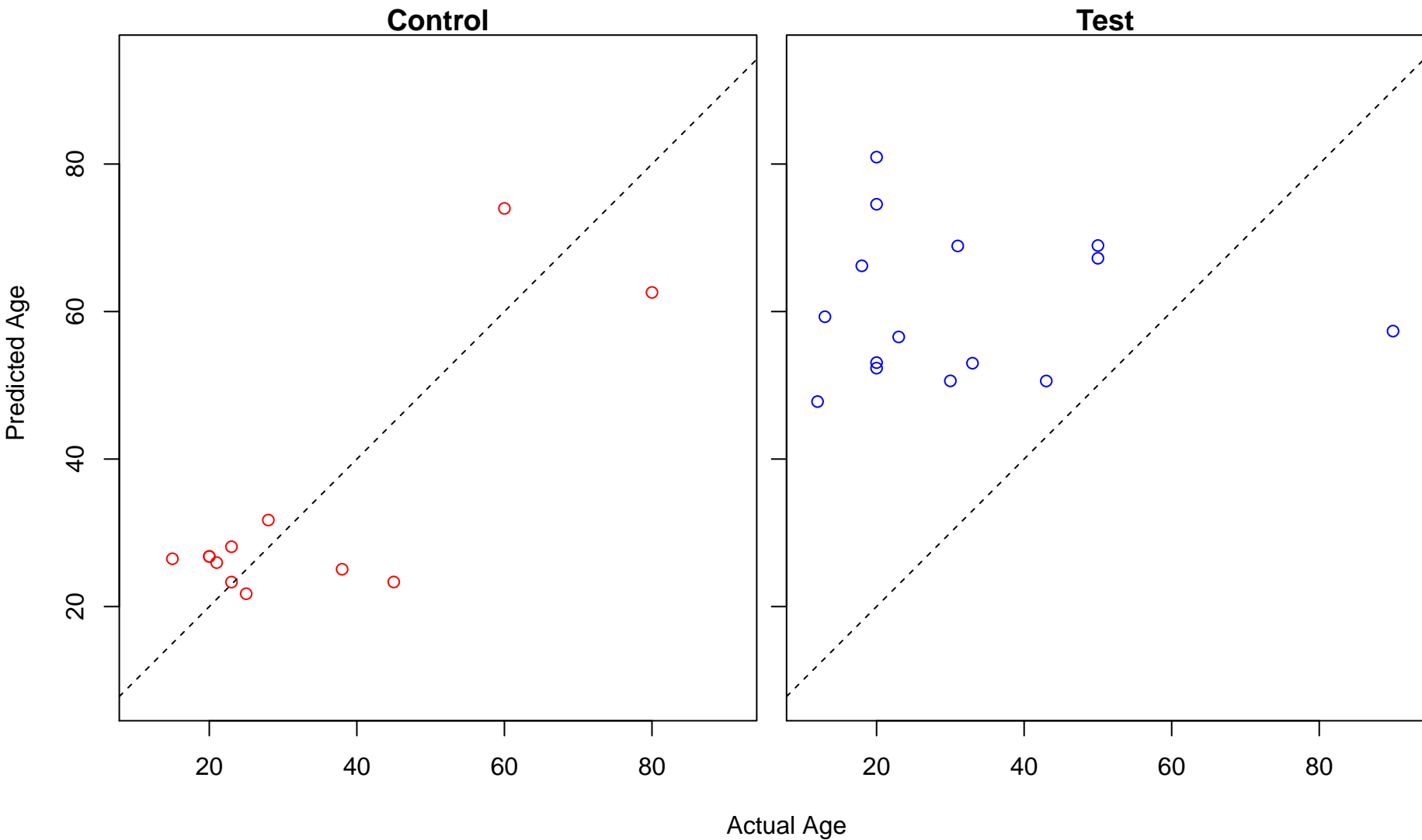
ganglioside biosynthetic process (Score: 4.030891)



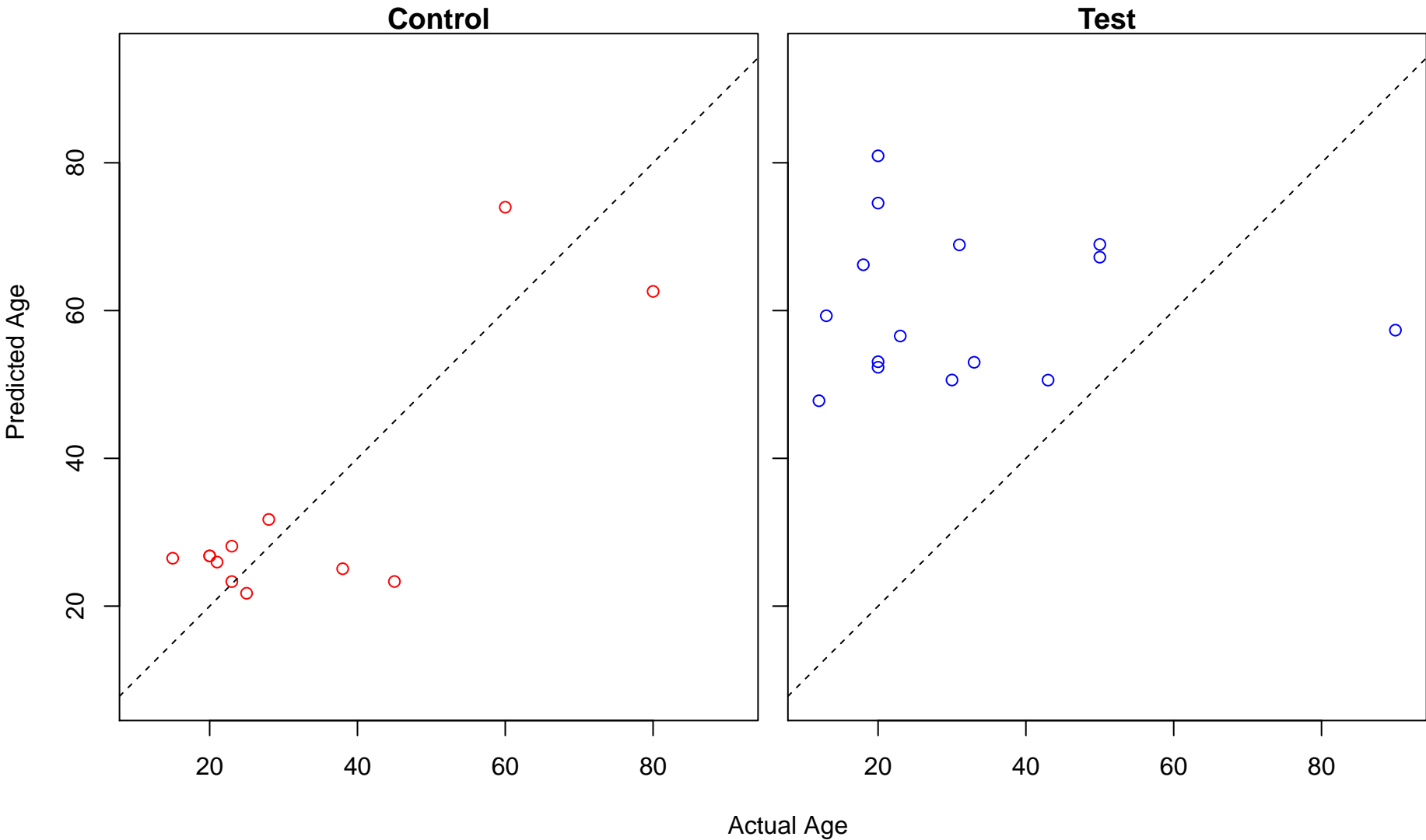
cellular modified amino acid biosynthetic process (Score: 4.030848)



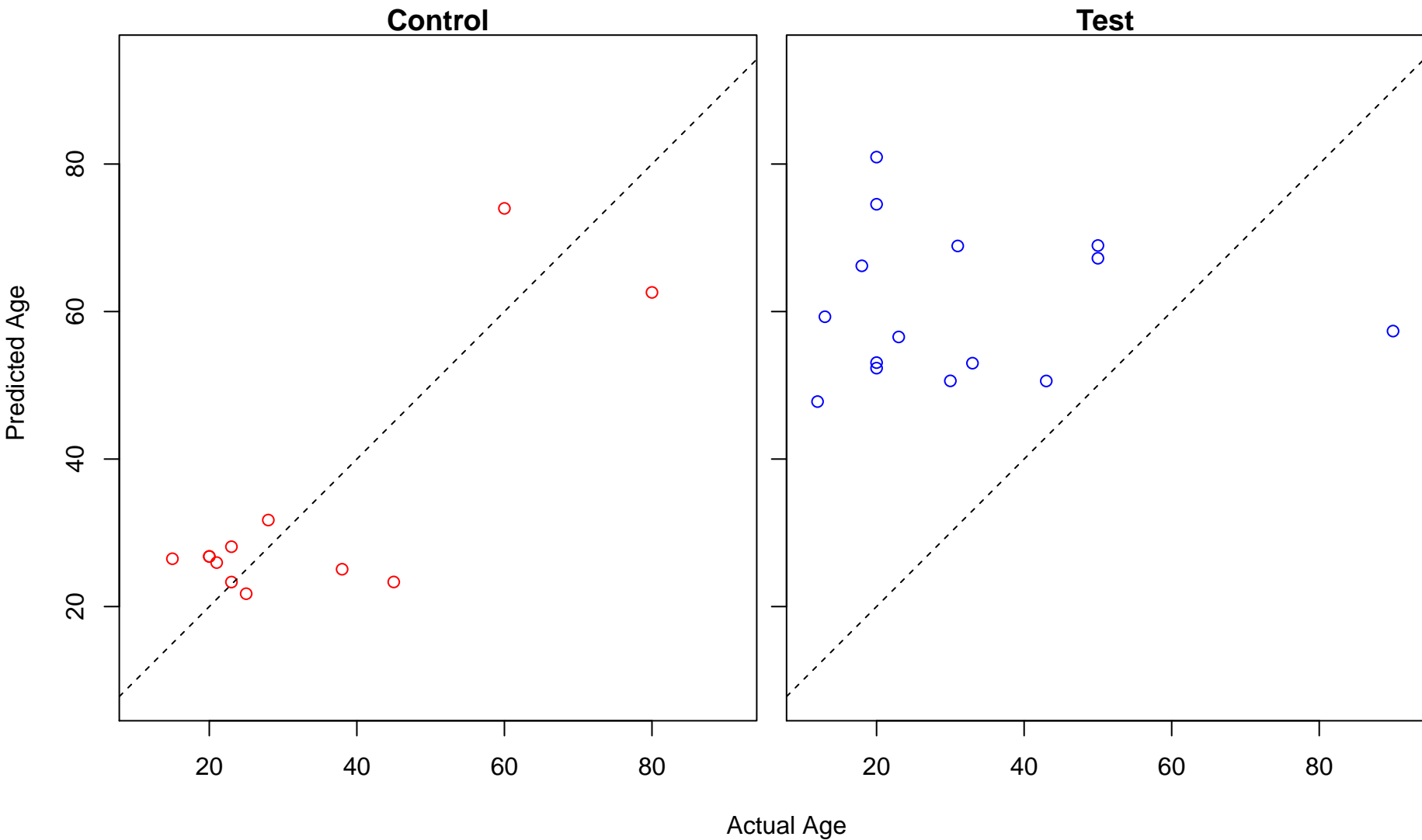
negative regulation of release of sequestered calcium ion into cytosol (Score: 4.027902)



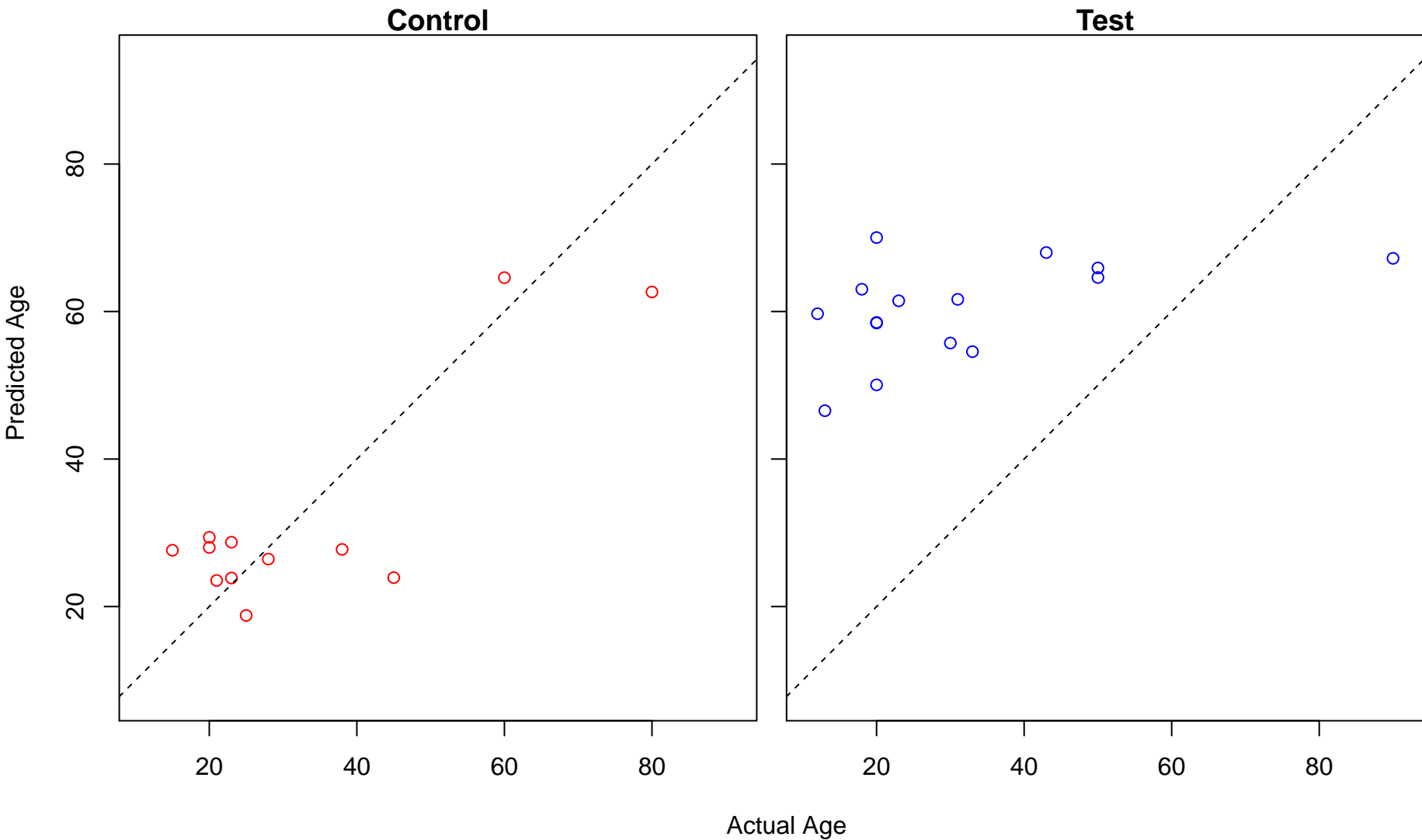
negative regulation of ryanodine-sensitive calcium-release channel activity (Score: 4.027902)



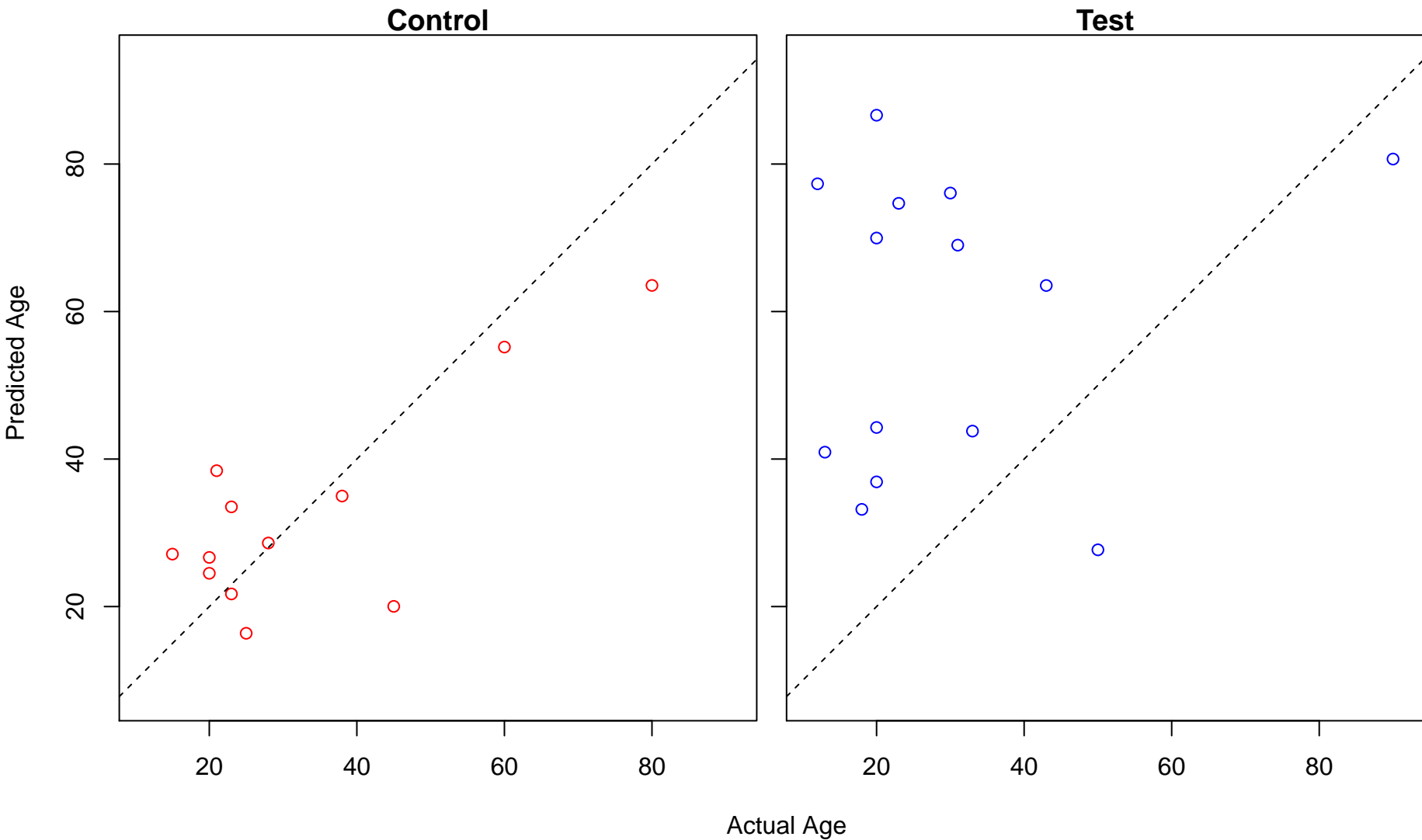
positive regulation of sequestering of calcium ion (Score: 4.027883)



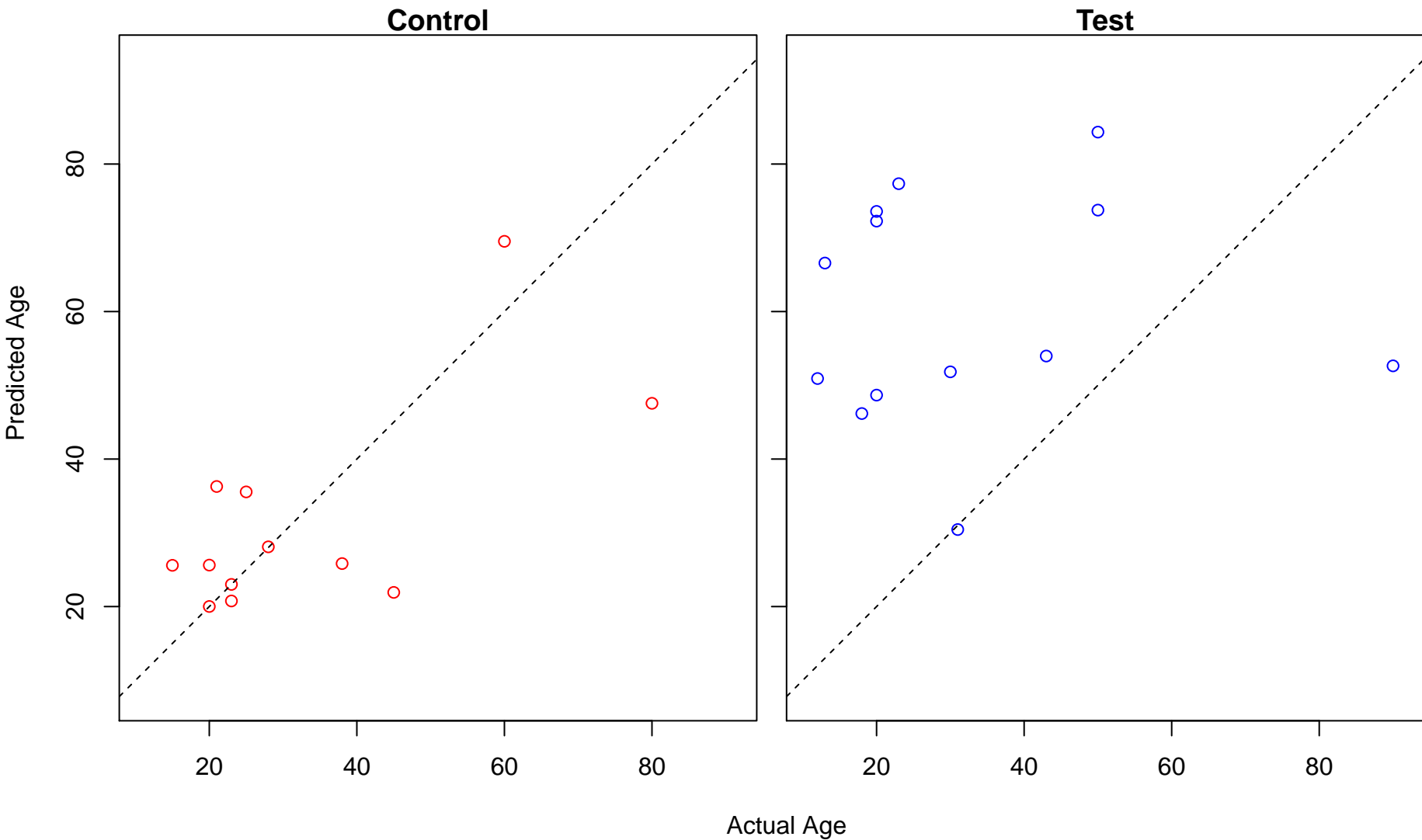
protein deacylation (Score: 4.026833)



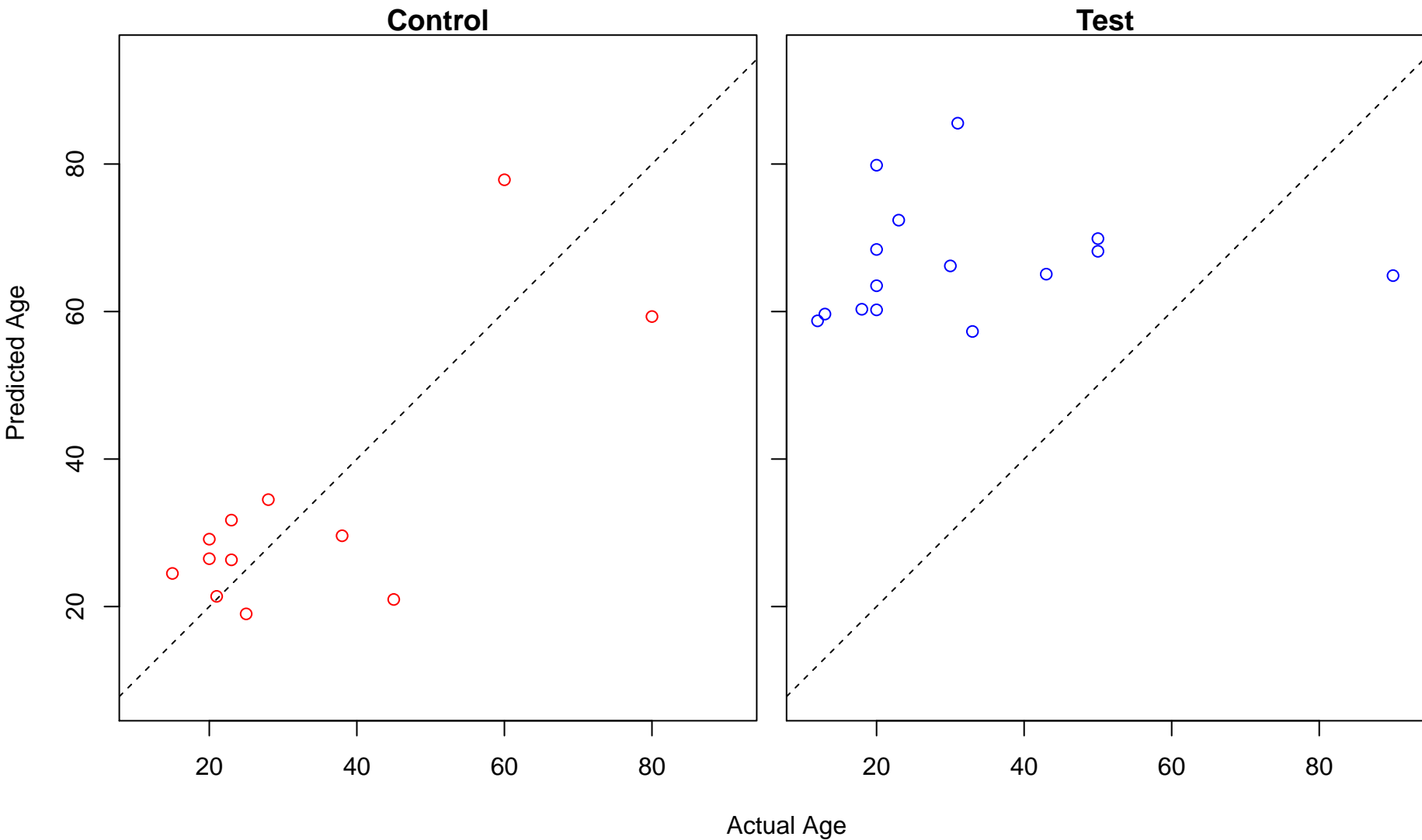
embryonic digestive tract morphogenesis (Score: 4.024950)



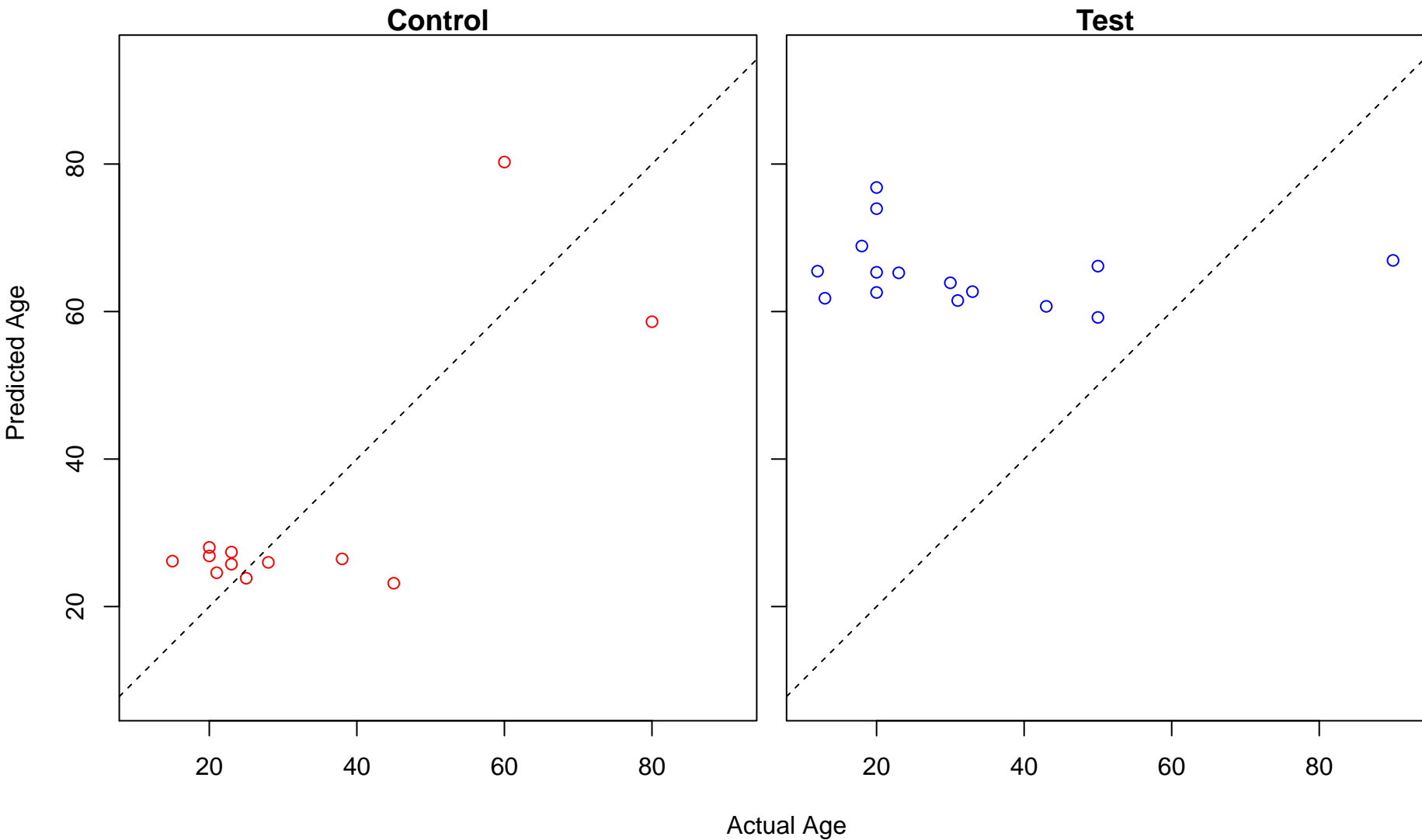
phagocytosis, recognition (Score: 4.022585)



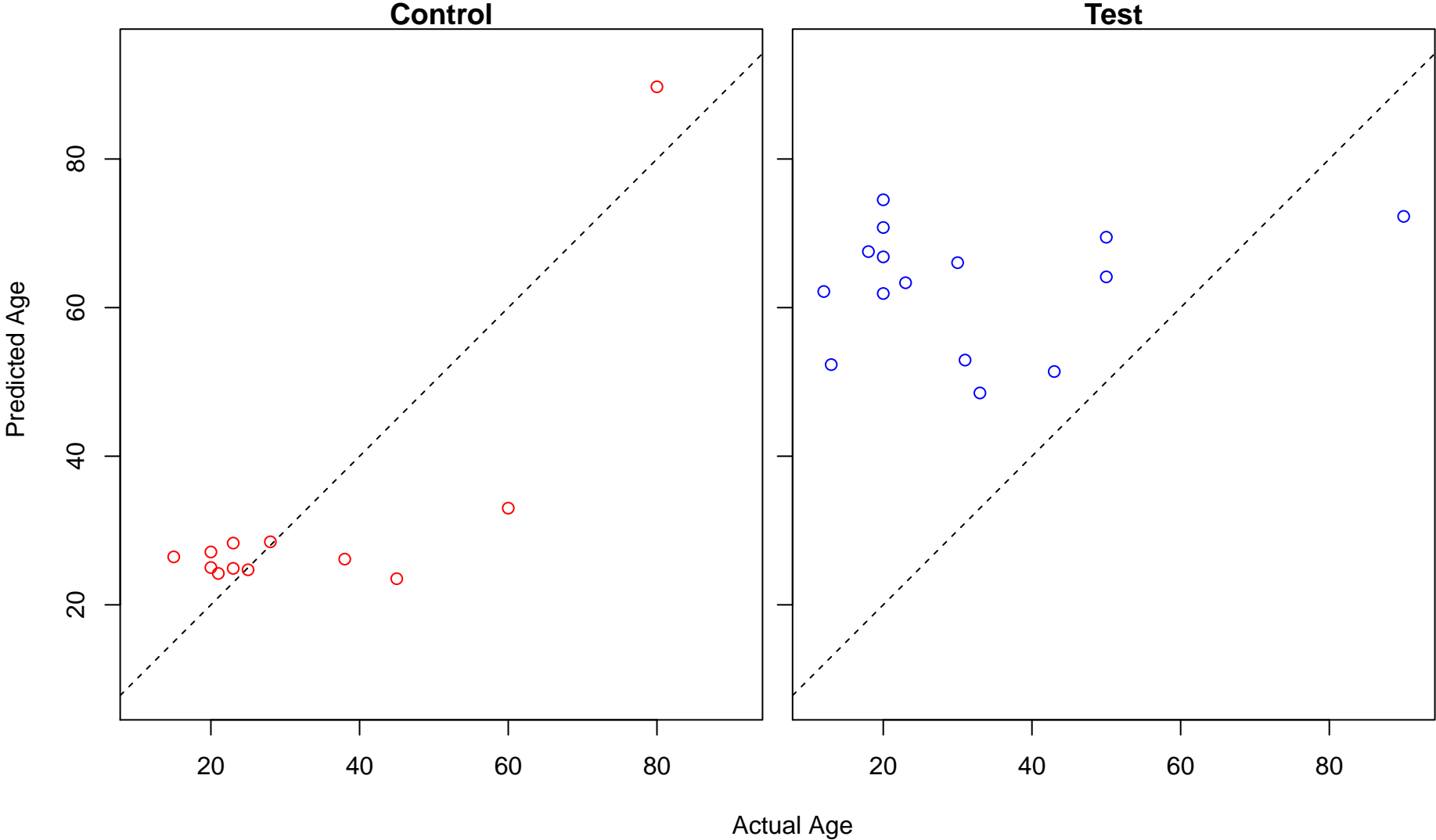
leukocyte mediated immunity (Score: 4.021985)



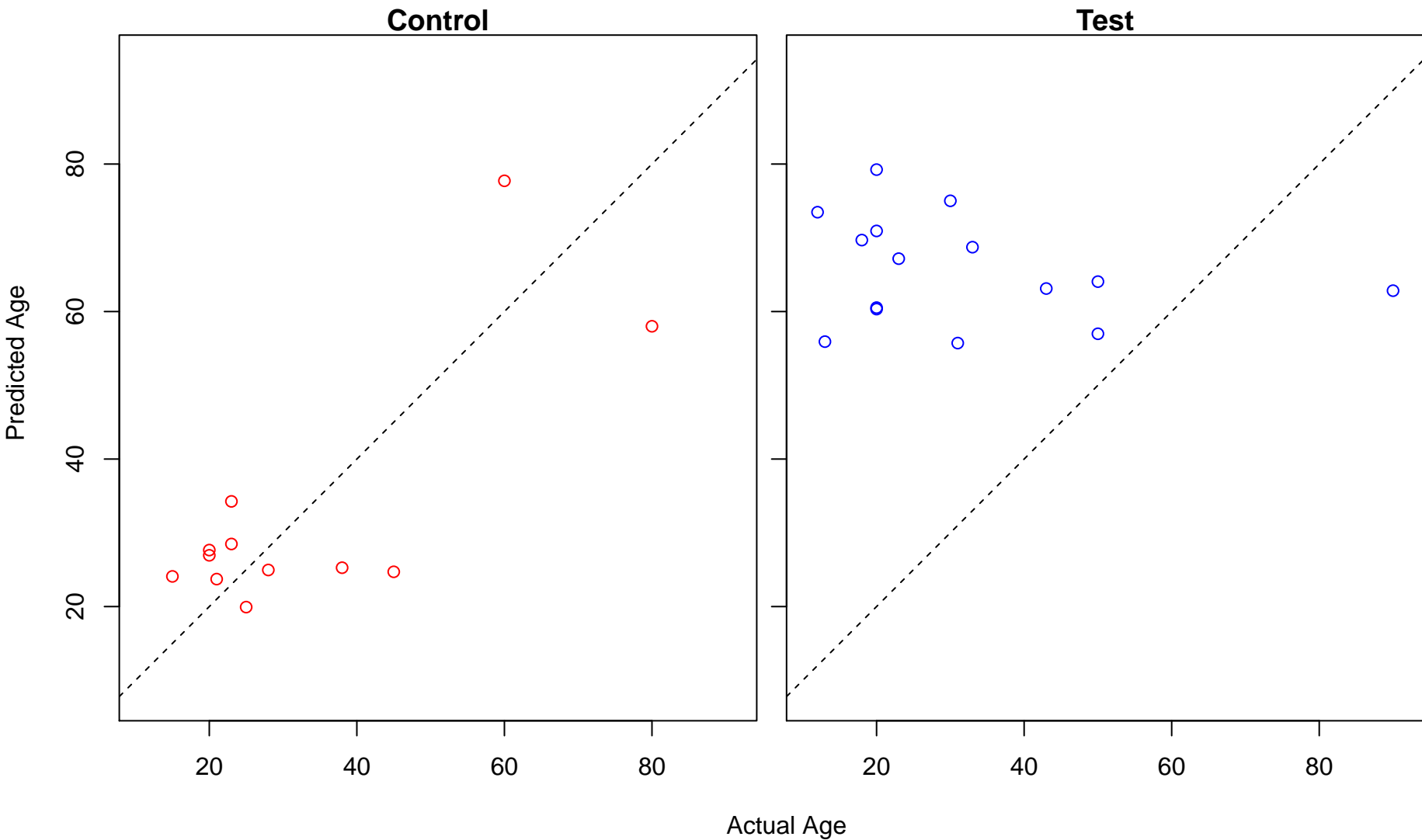
protein K11-linked ubiquitination (Score: 4.021818)



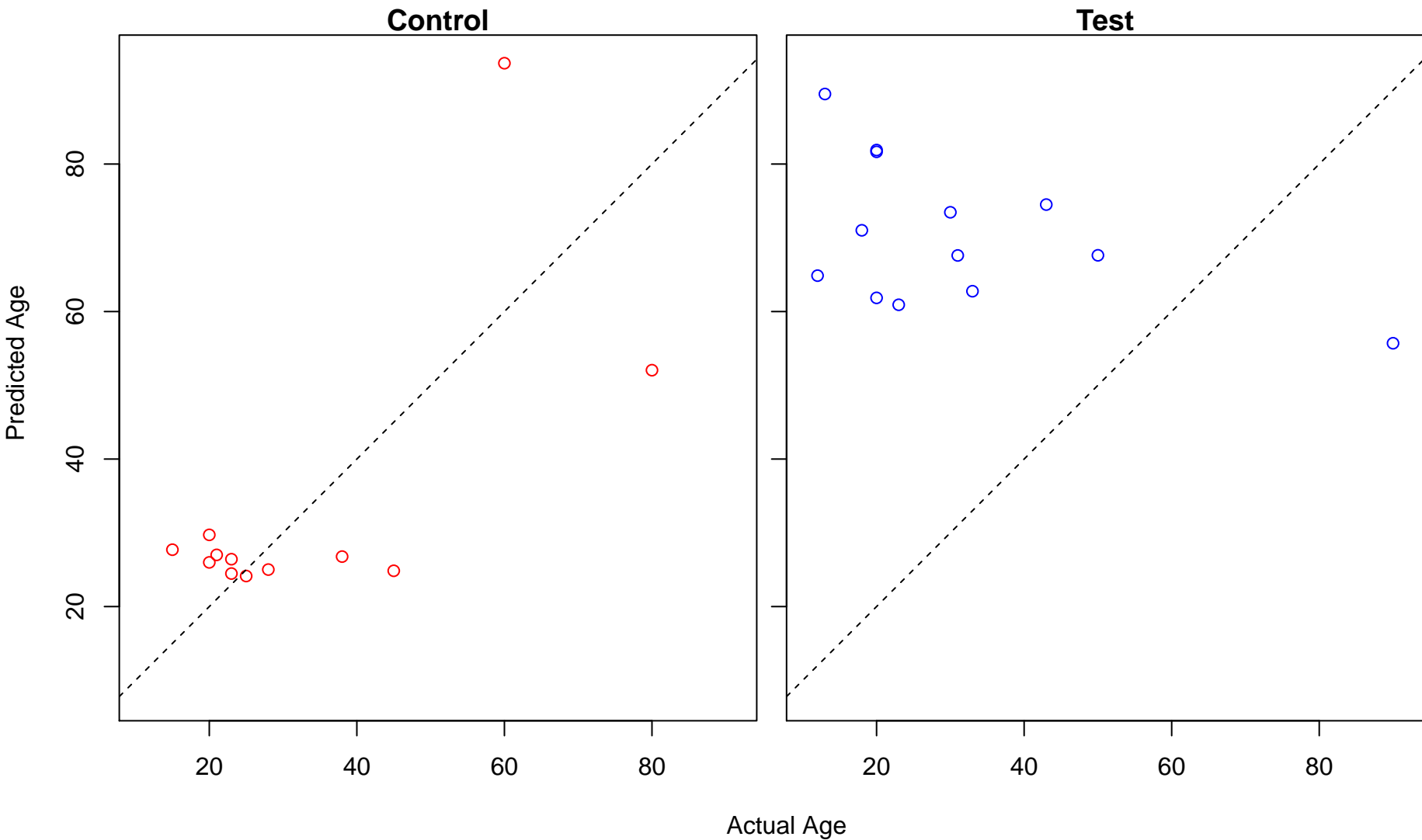
aspartate family amino acid metabolic process (Score: 4.020497)



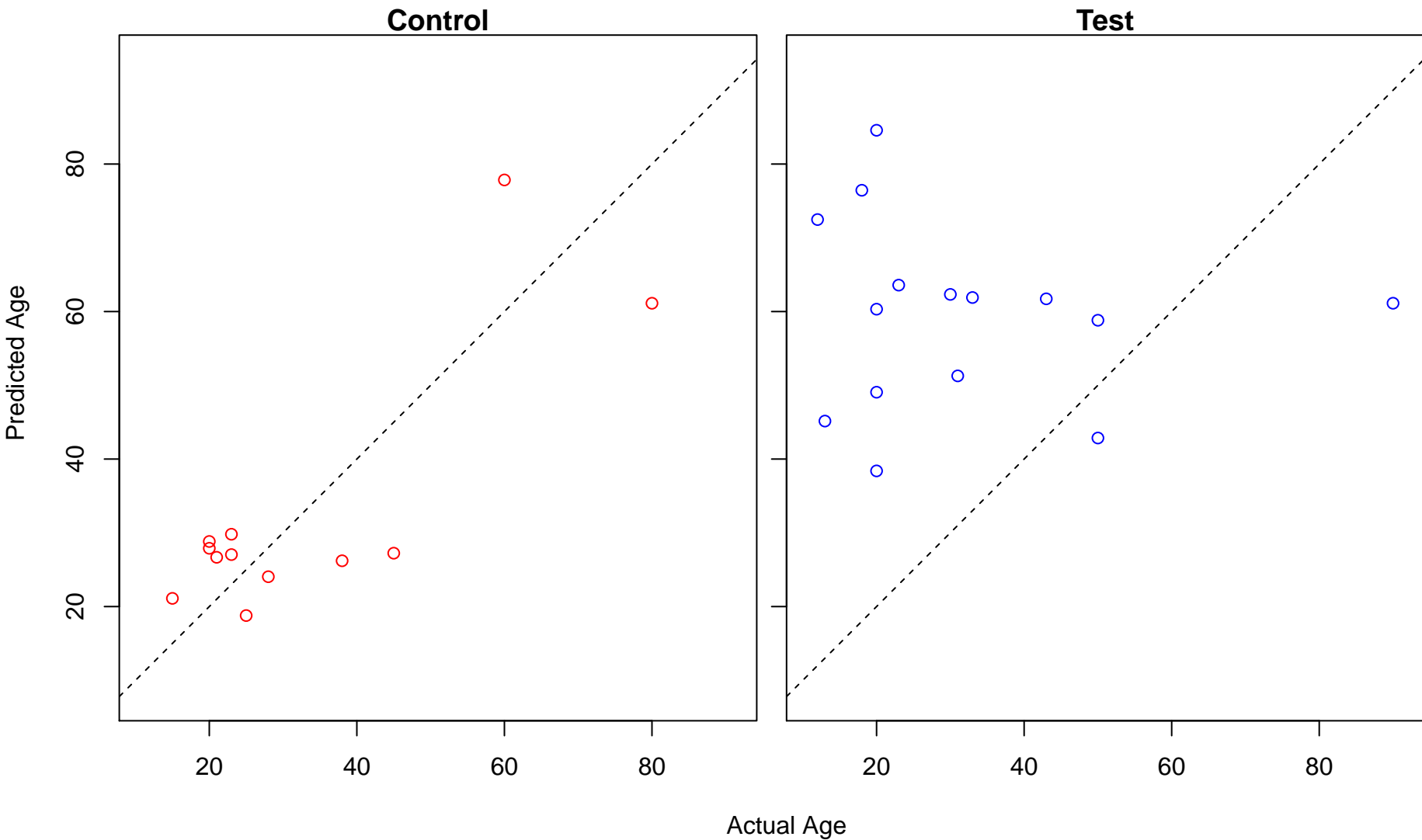
calcineurin-NFAT signaling cascade (Score: 4.016409)



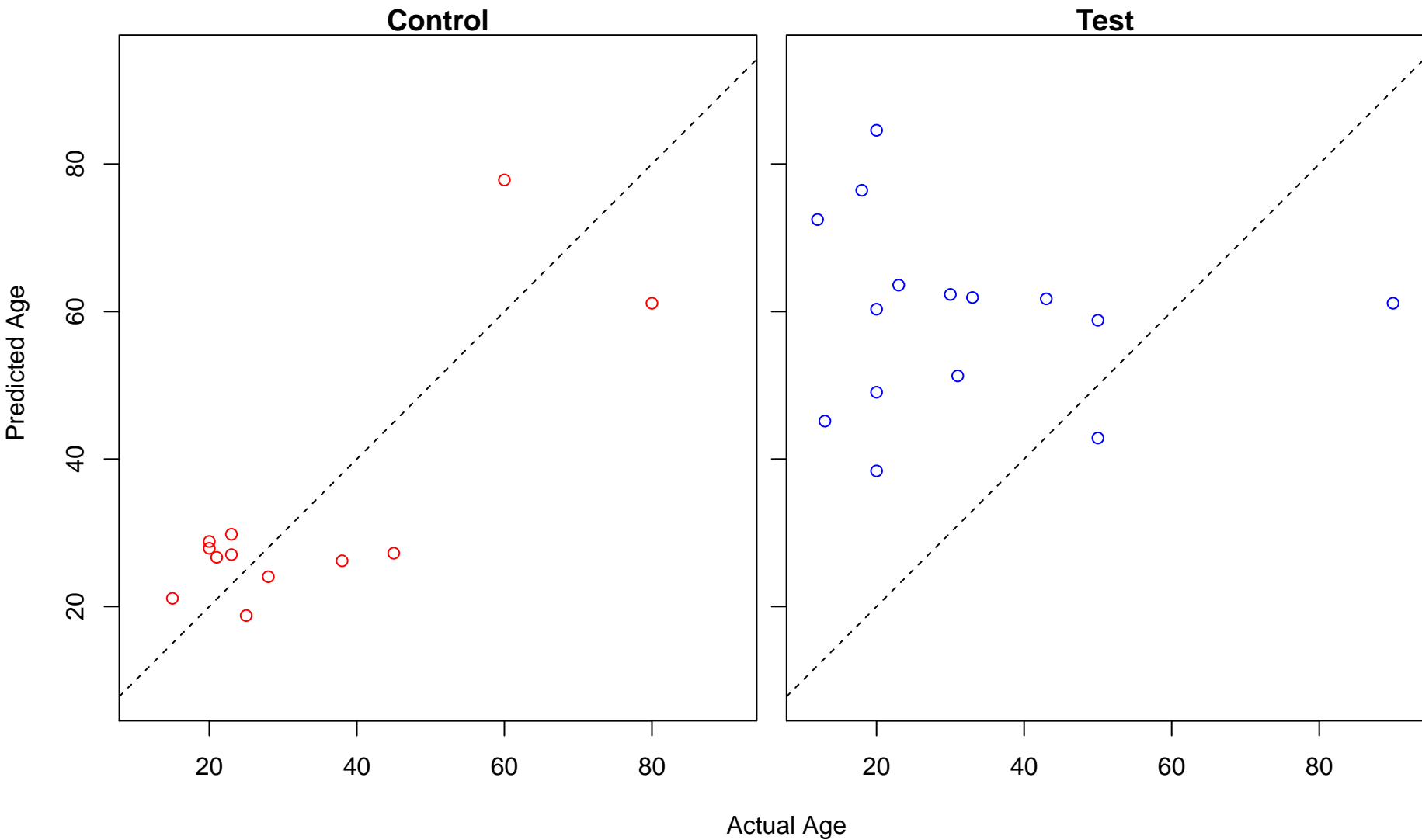
positive regulation of nuclease activity (Score: 4.016404)



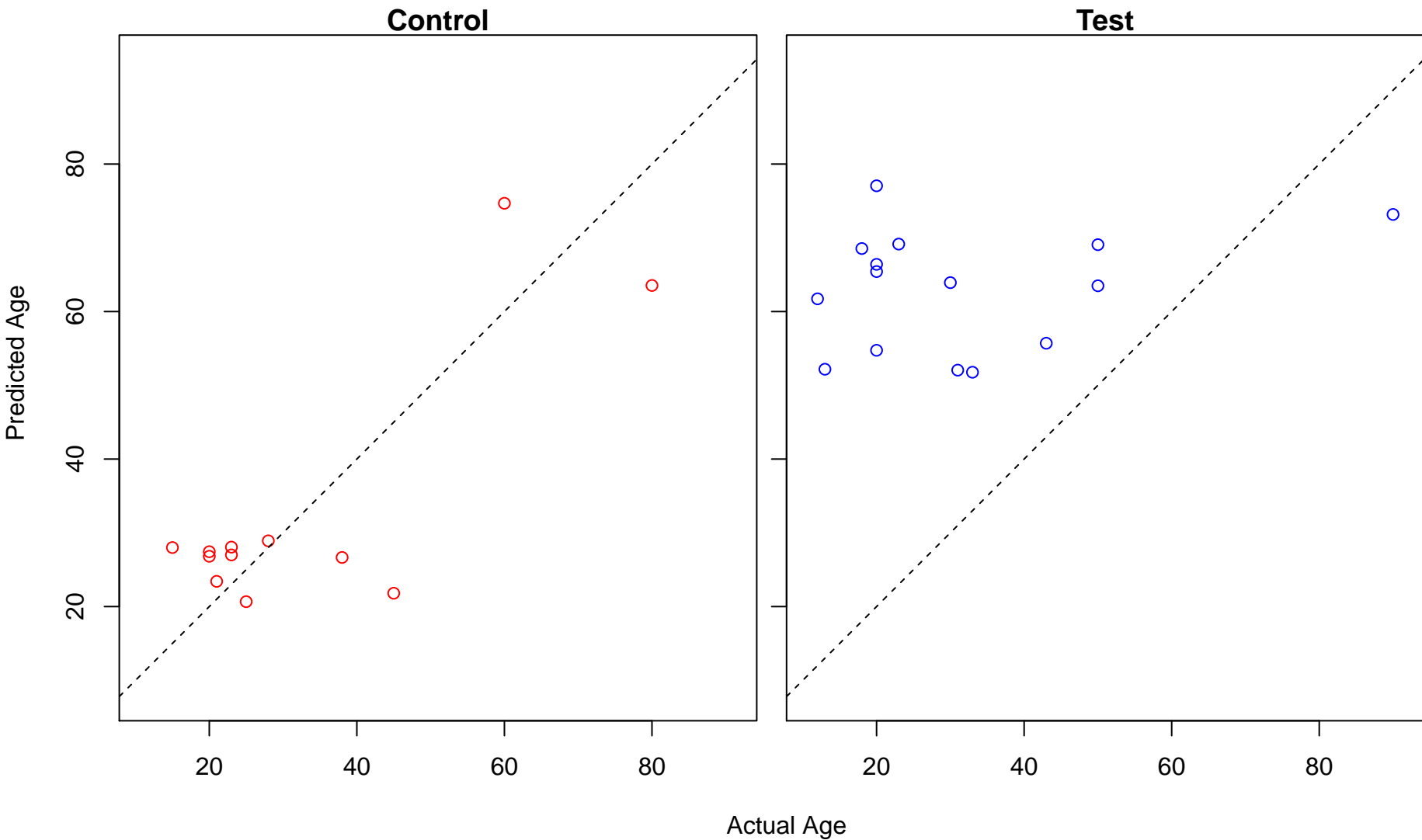
DNA double-strand break processing involved in repair via single-strand annealing (Score: 4.01557)



double-strand break repair via single-strand annealing (Score: 4.015576)

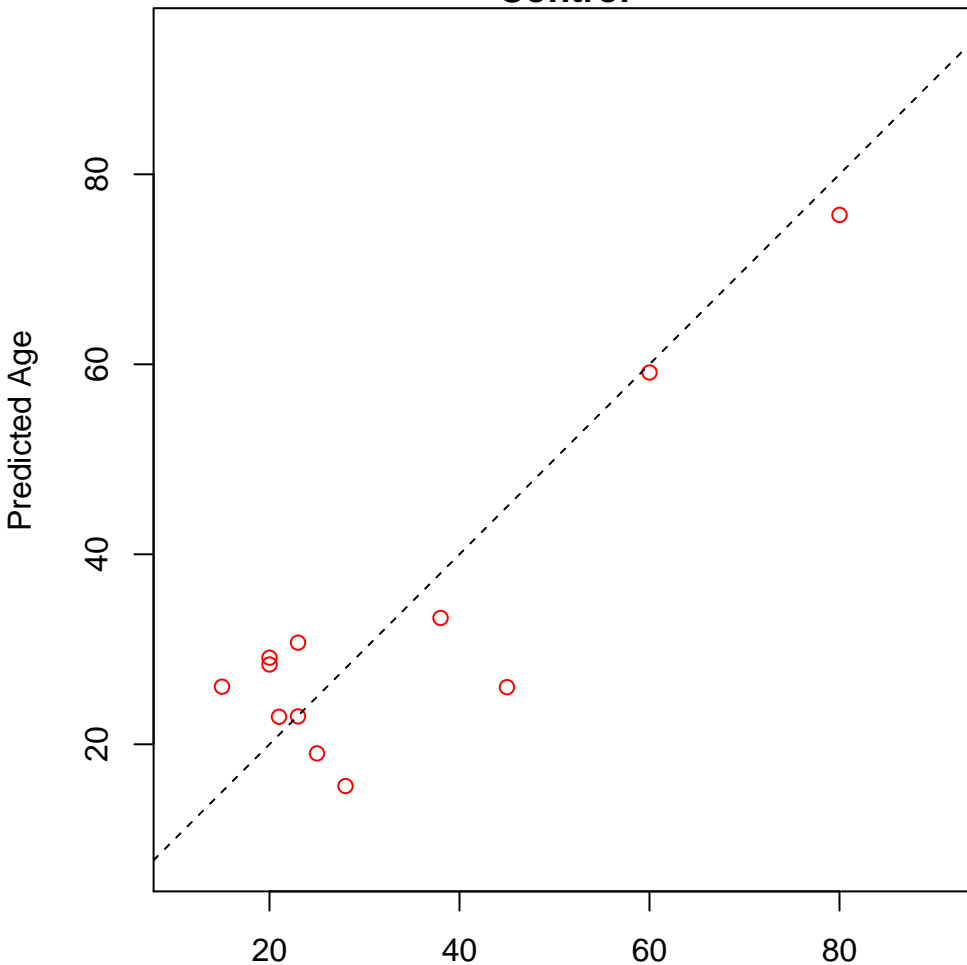


proteolysis involved in cellular protein catabolic process (Score: 4.010911)

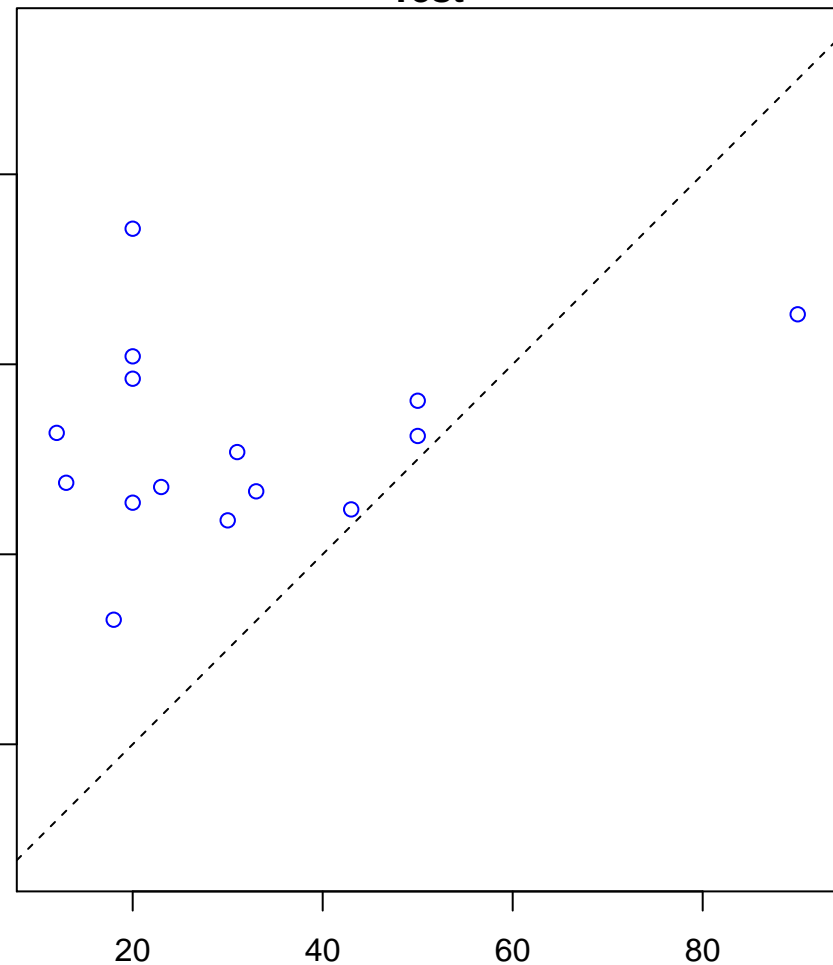


organic acid transmembrane transport (Score: 4.010757)

Control

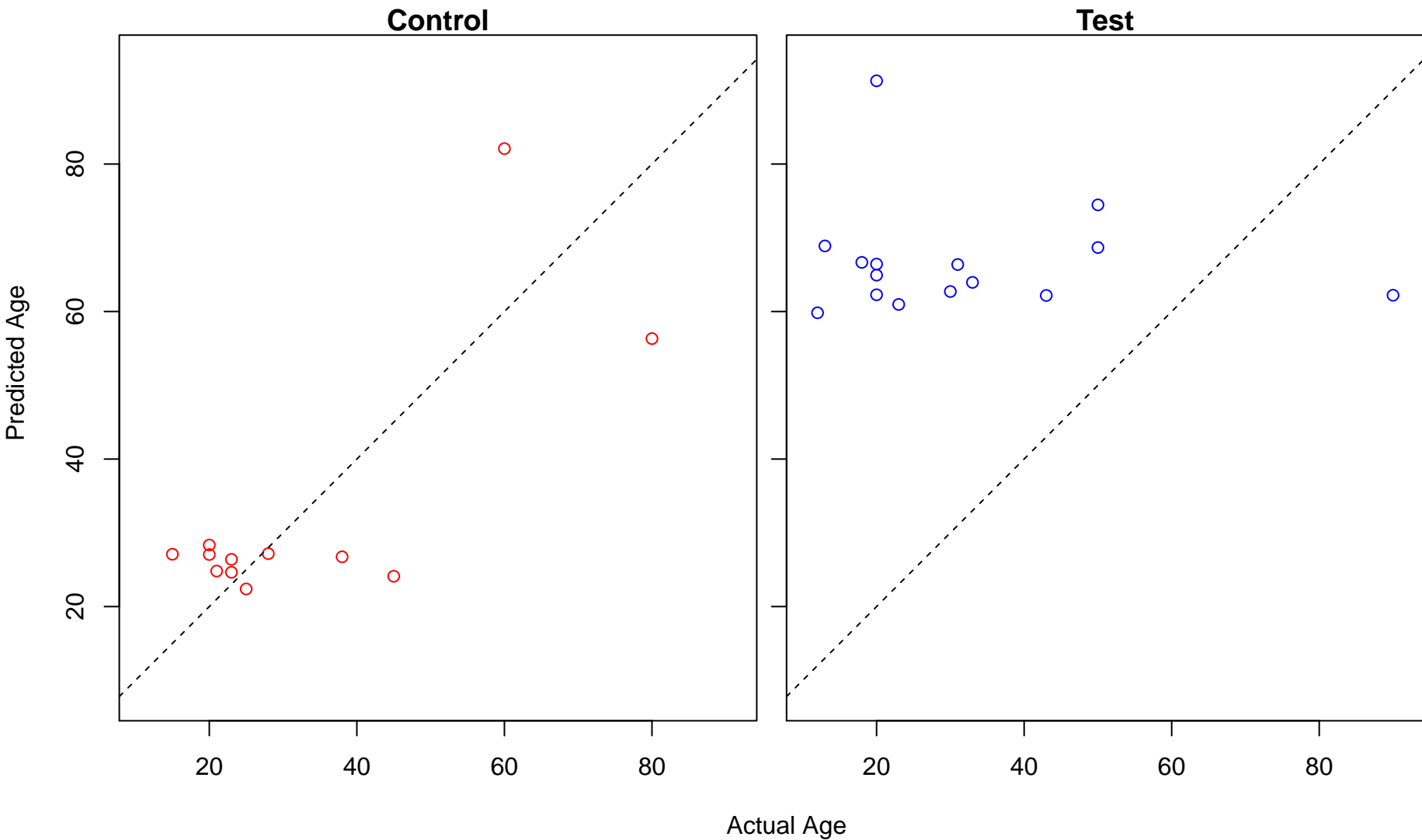


Test

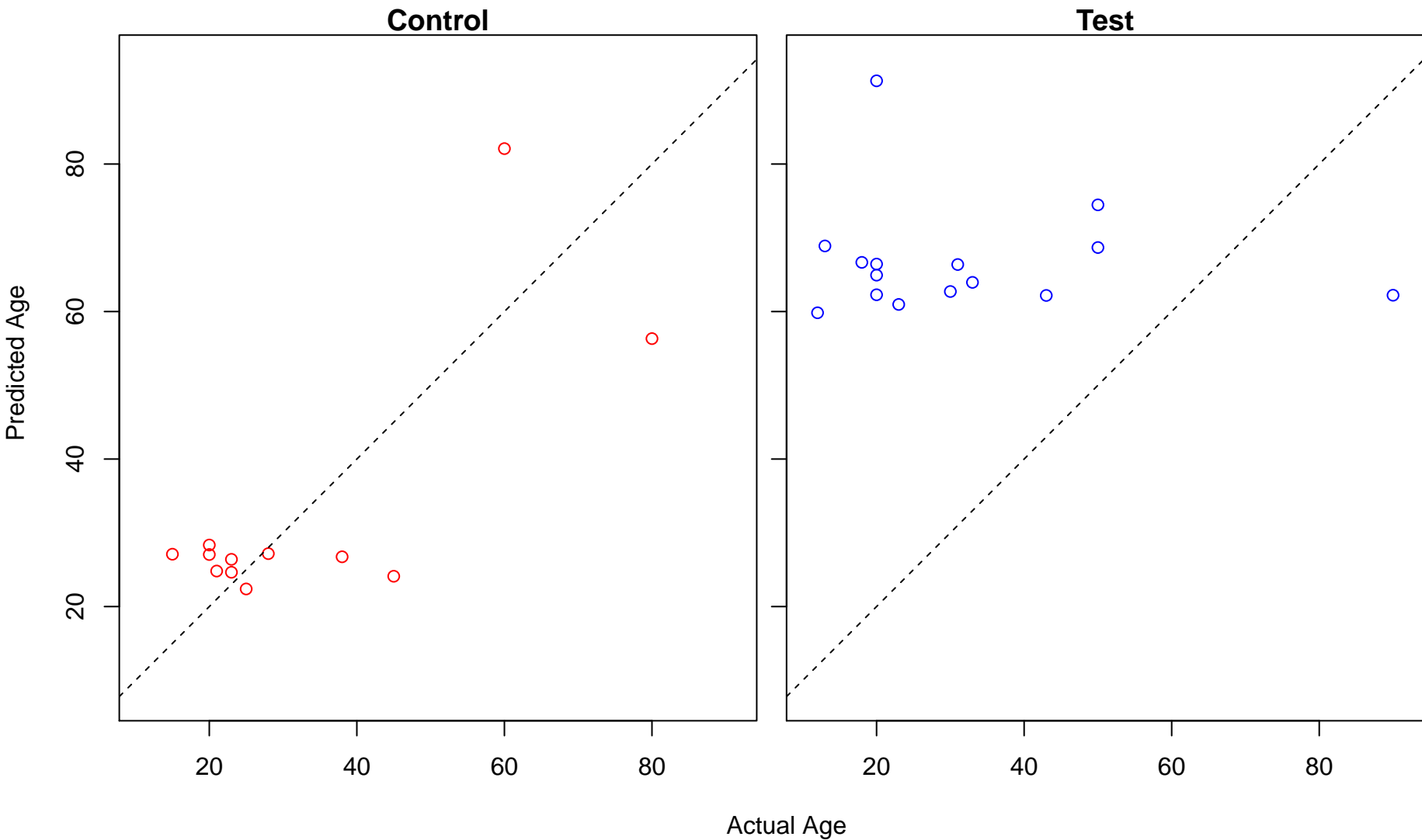


Actual Age

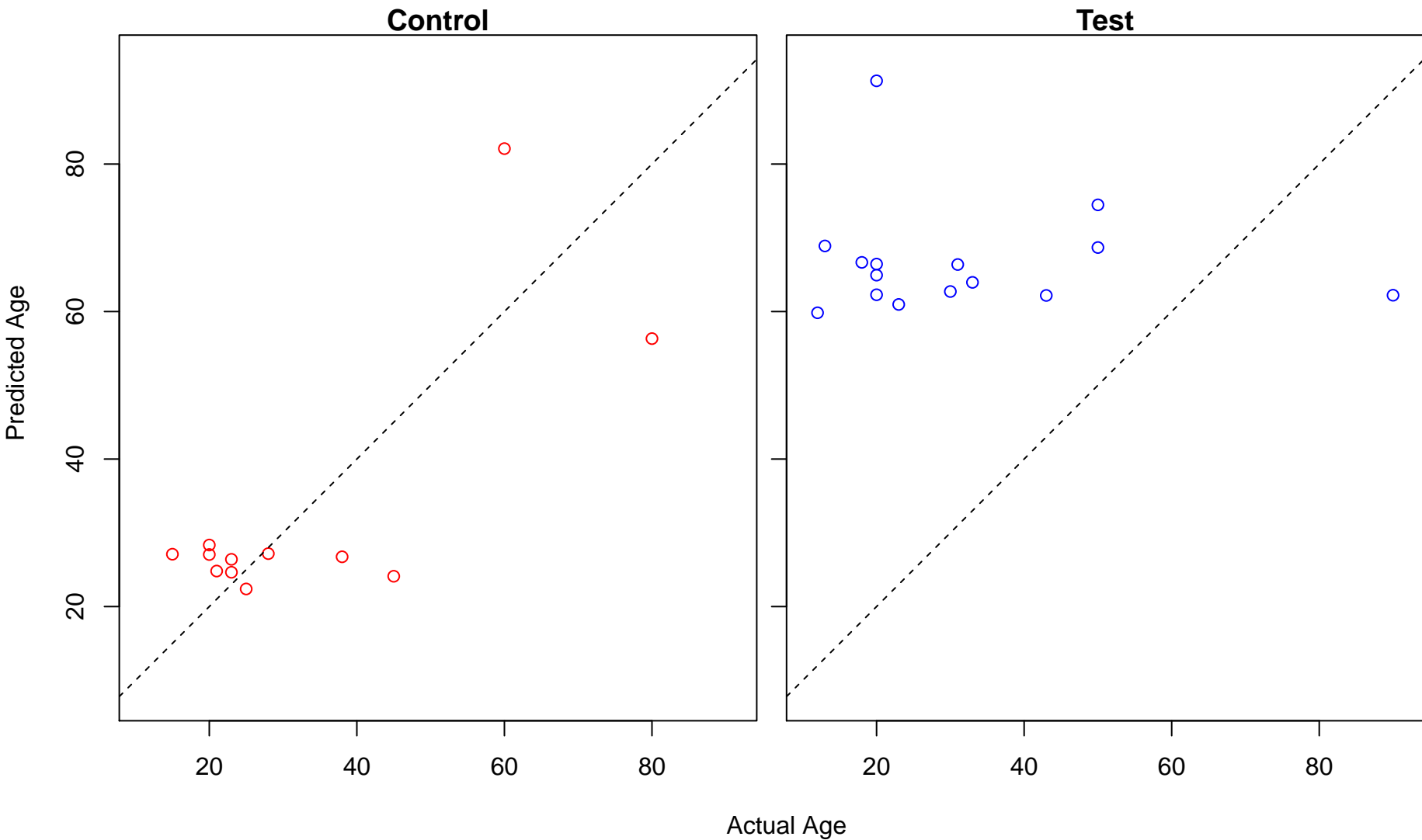
synaptic transmission (Score: 4.010110)



synaptic signaling (Score: 4.010110)

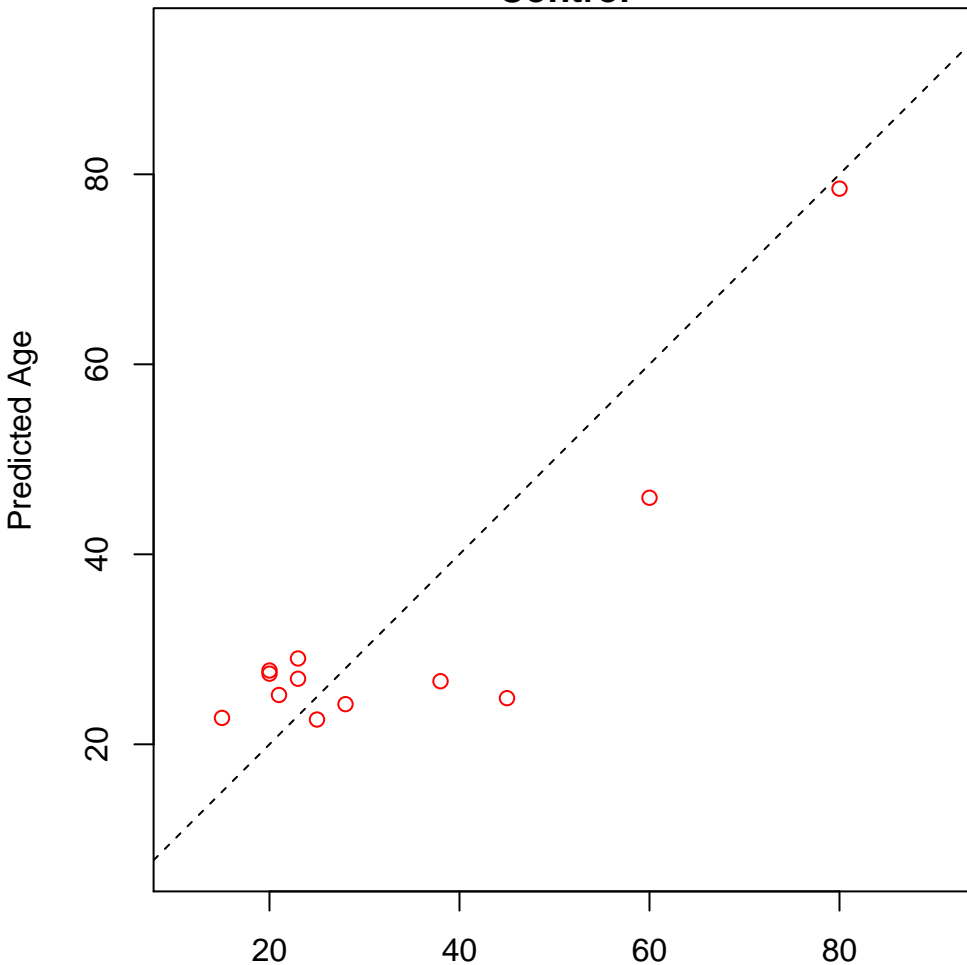


trans-synaptic signaling (Score: 4.010110)

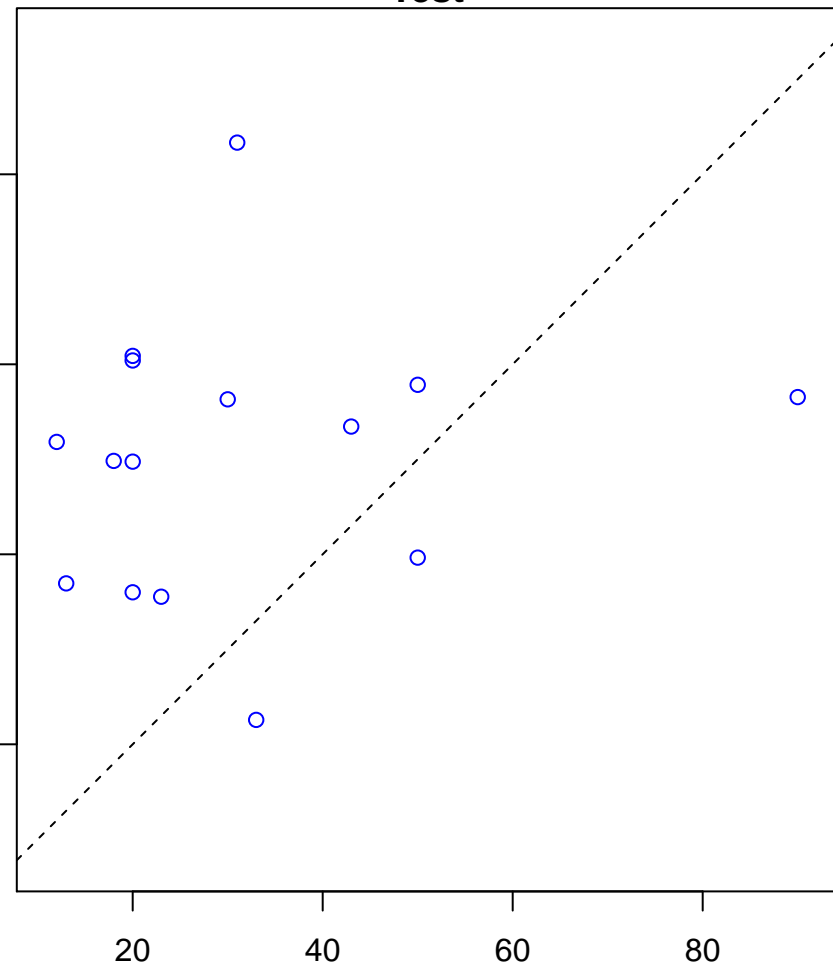


DNA replication, synthesis of RNA primer (Score: 4.007240)

Control

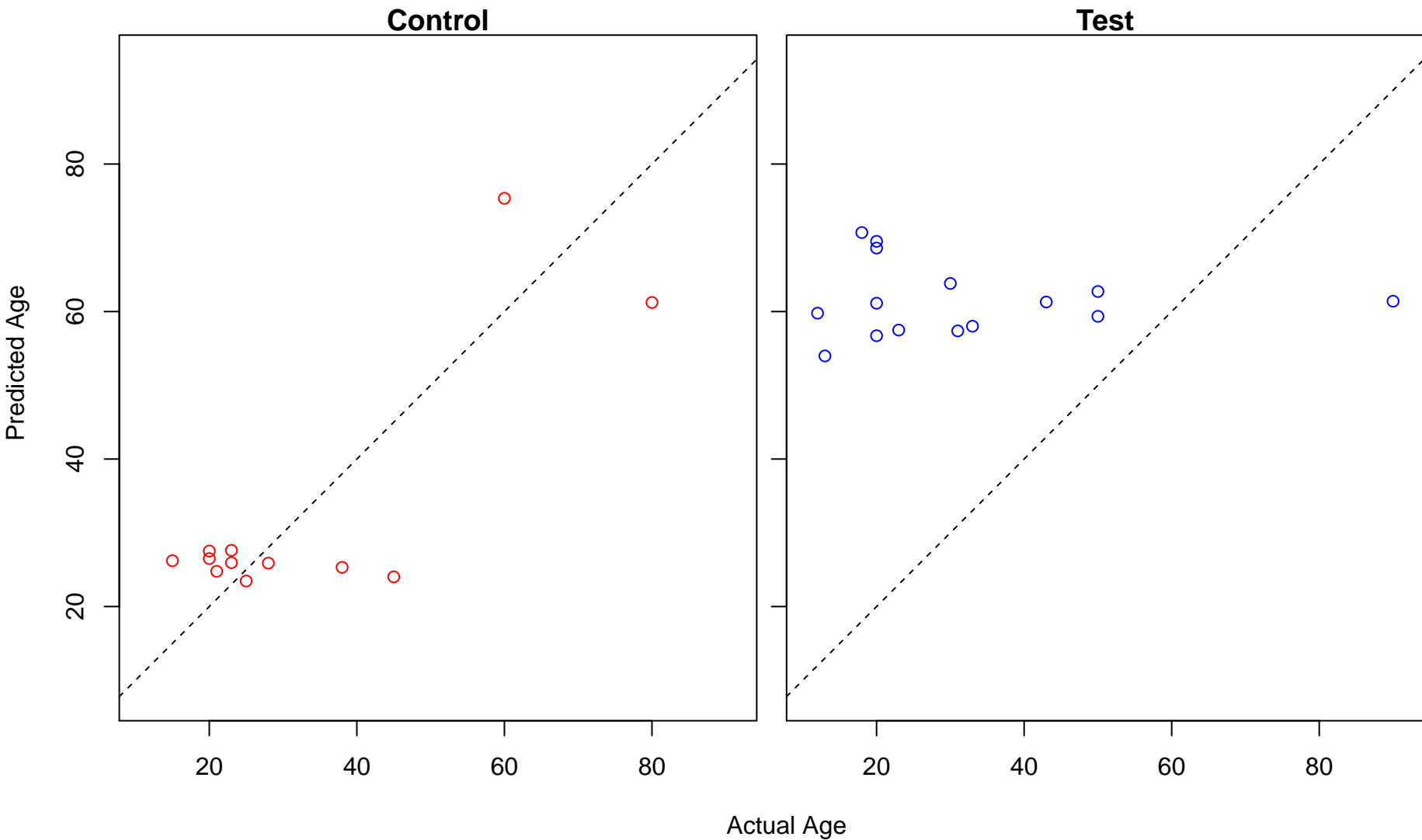


Test

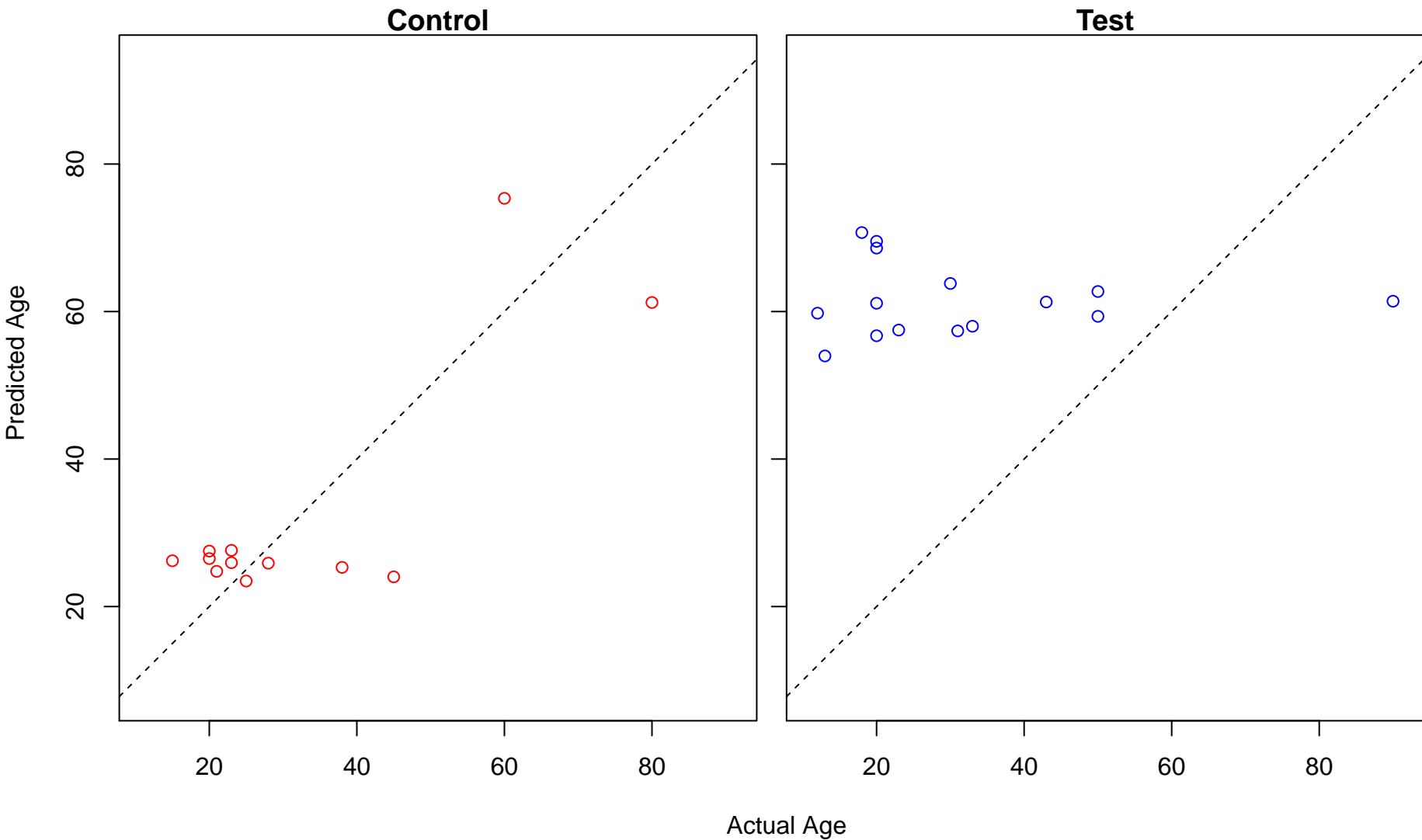


Actual Age

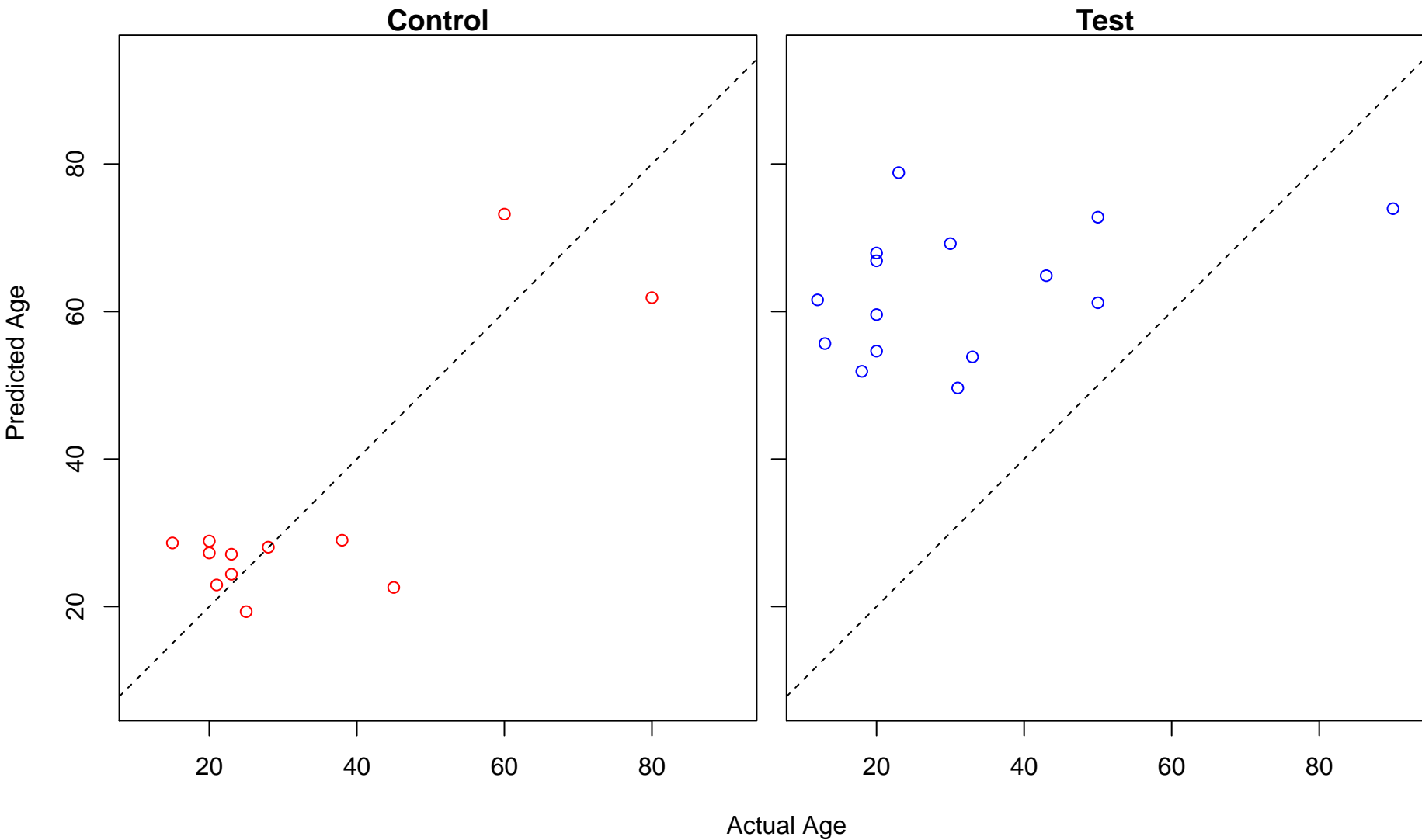
acyl-CoA metabolic process (Score: 4.005975)



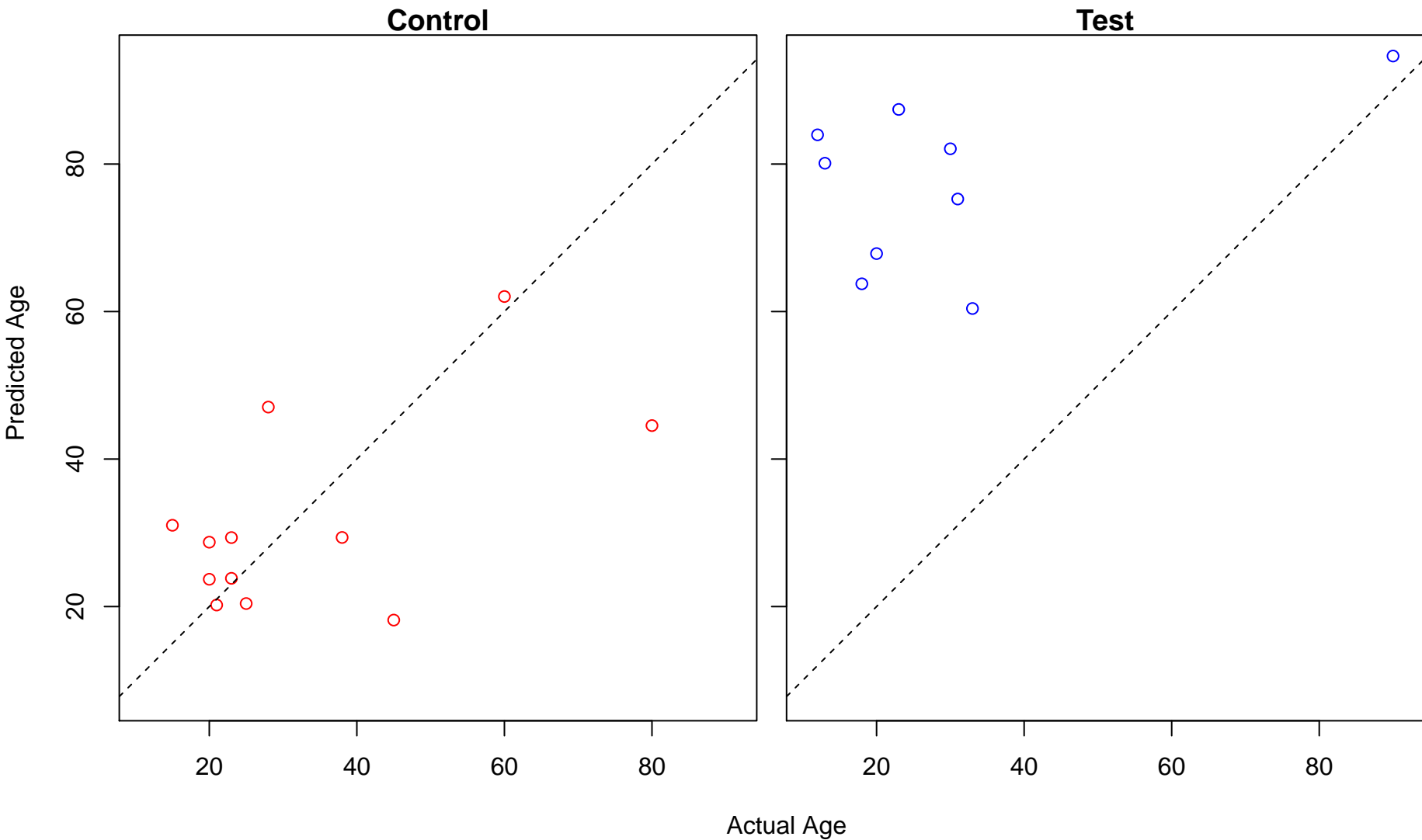
thioester metabolic process (Score: 4.005975)



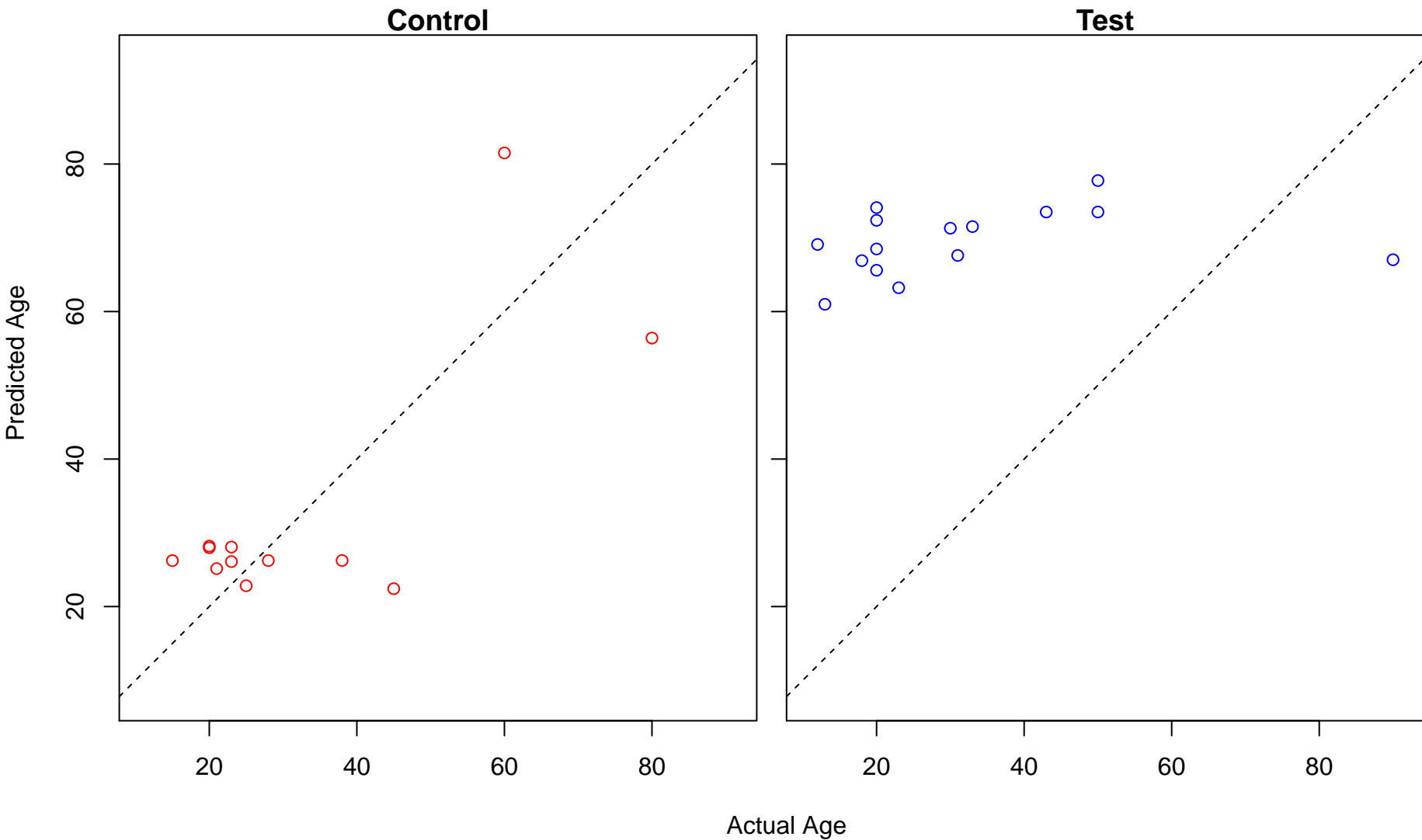
astral microtubule organization (Score: 4.005062)



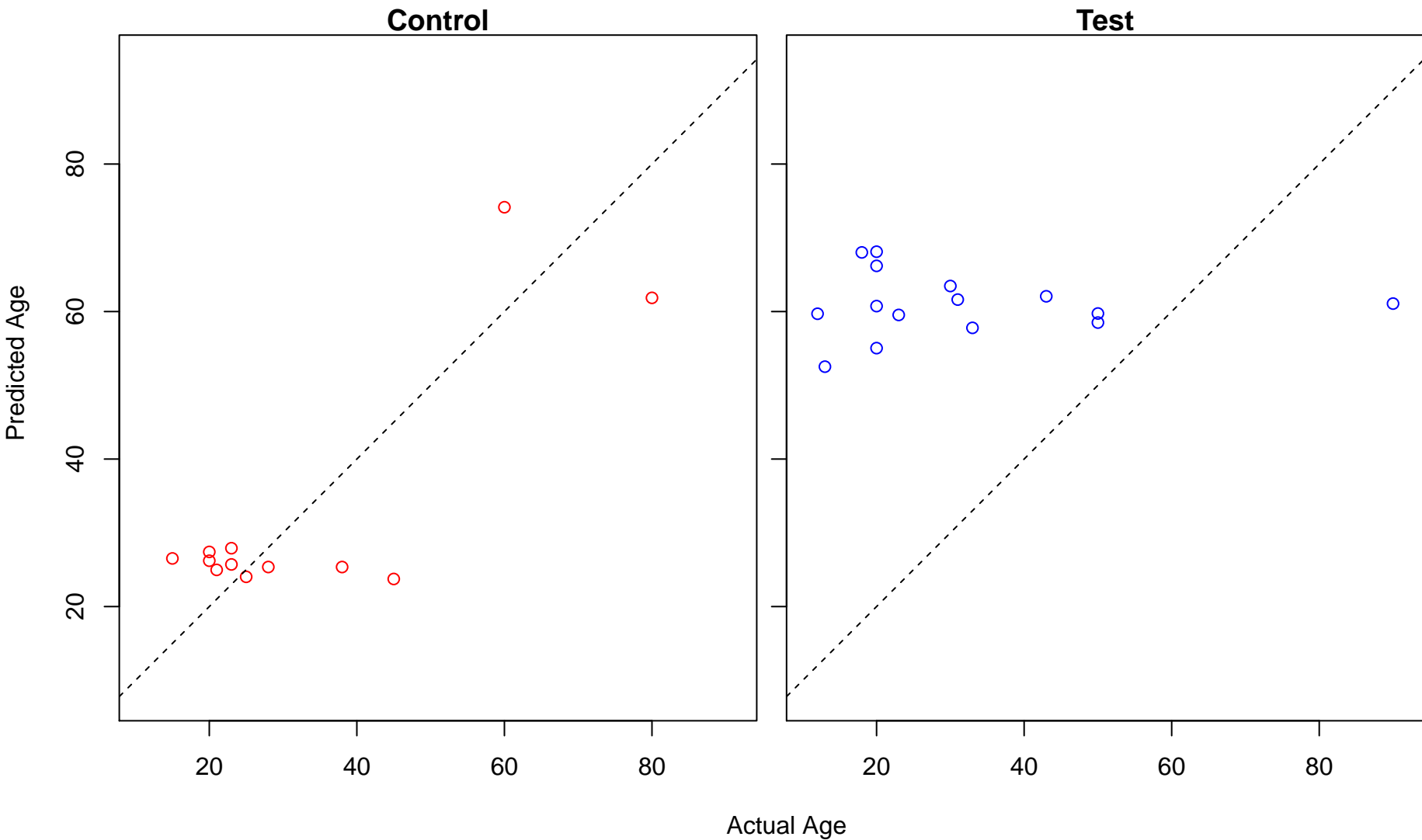
negative regulation of amyloid precursor protein catabolic process (Score: 4.003498)



glycosphingolipid metabolic process (Score: 4.001892)

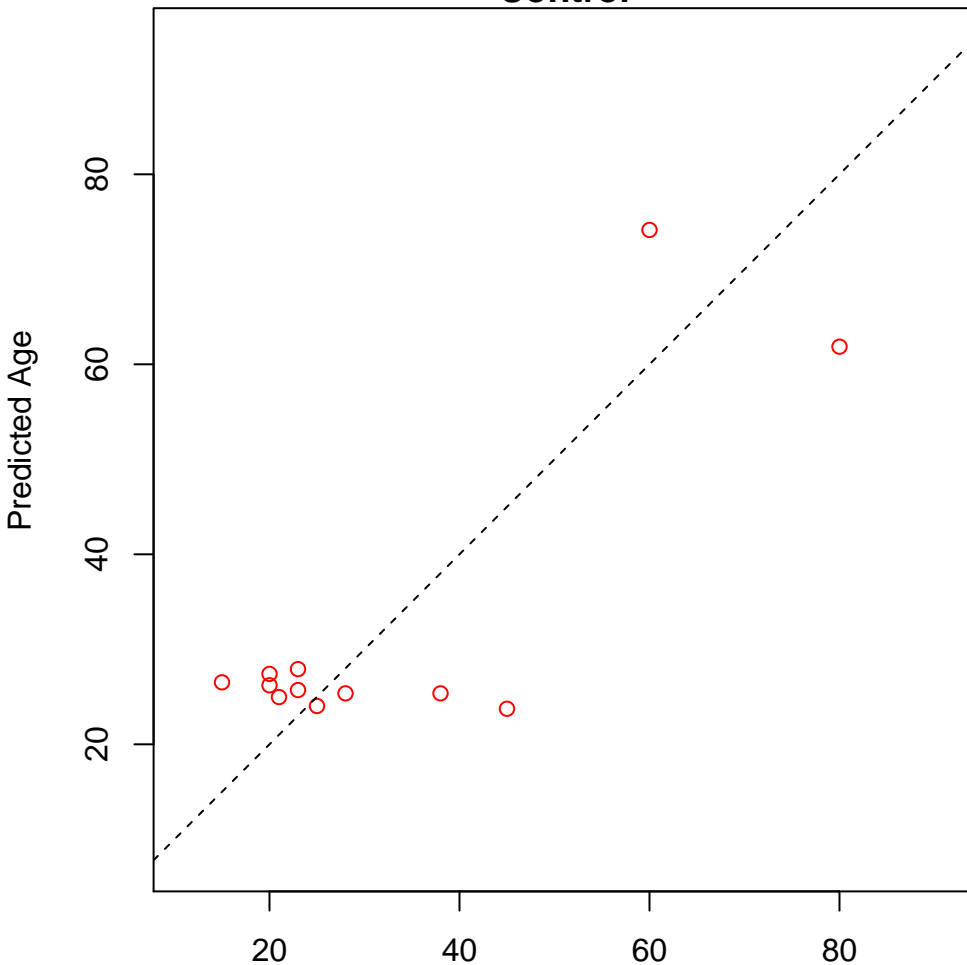


long-chain fatty-acyl-CoA biosynthetic process (Score: 4.001642)

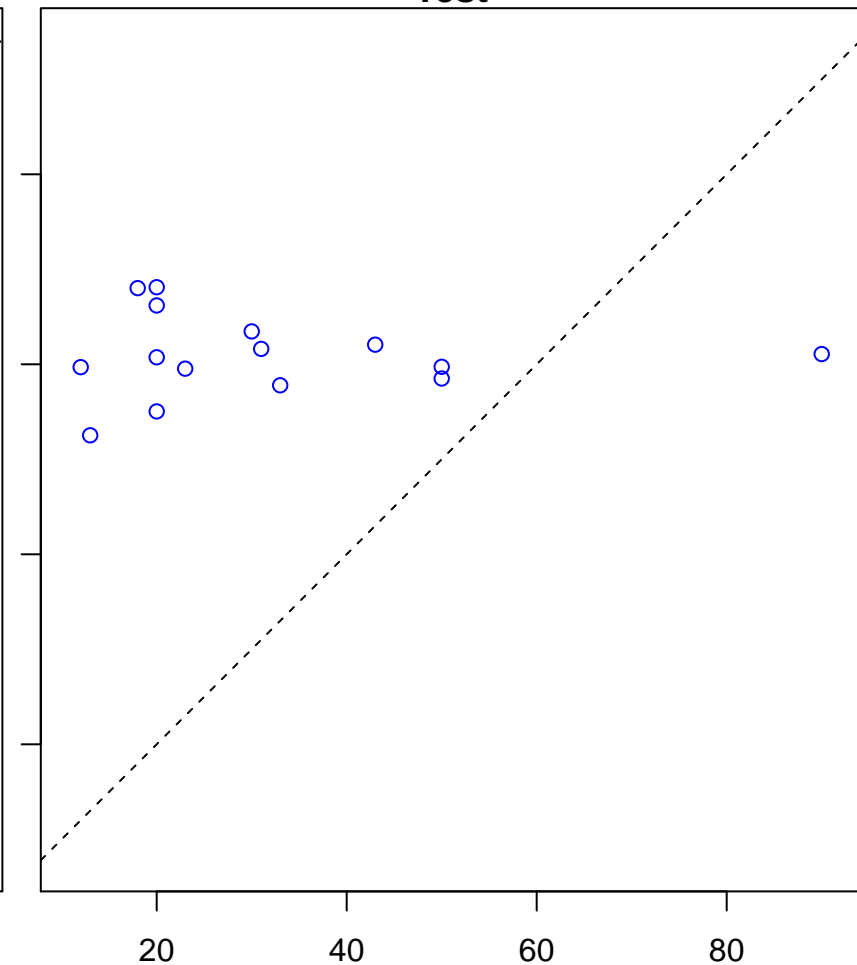


fatty-acyl-CoA biosynthetic process (Score: 4.001642)

Control



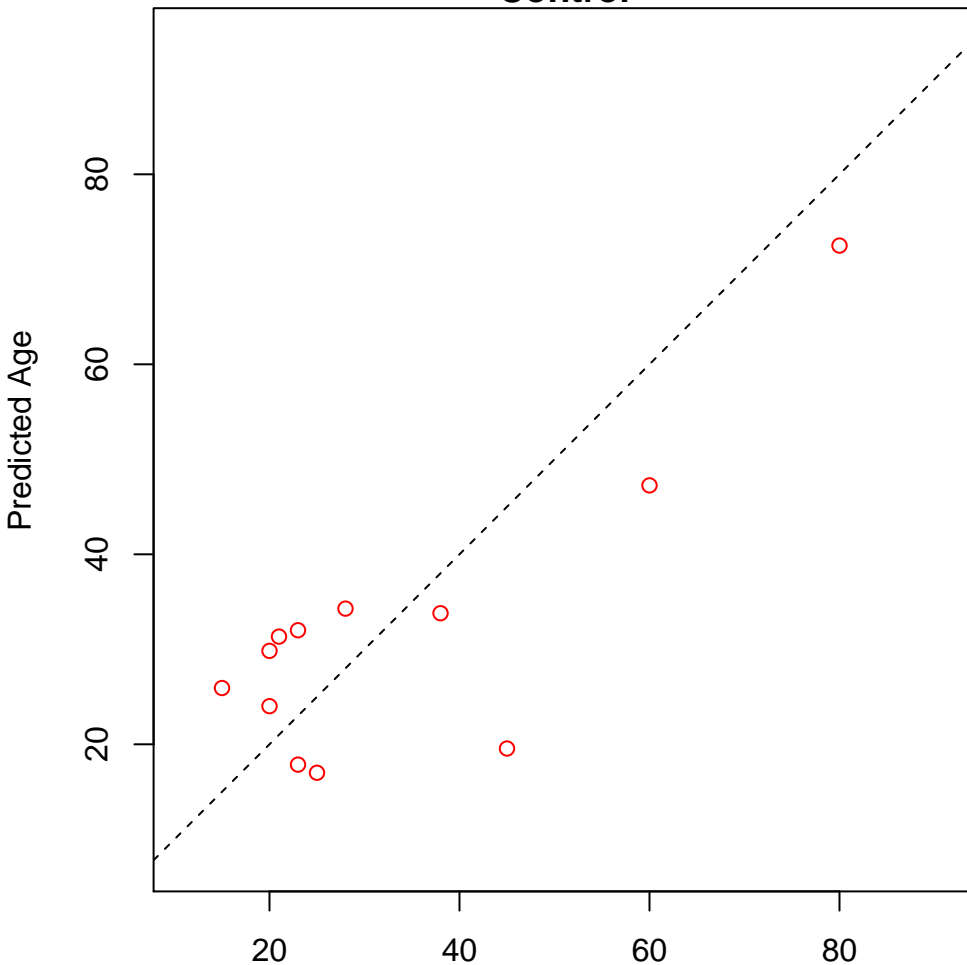
Test



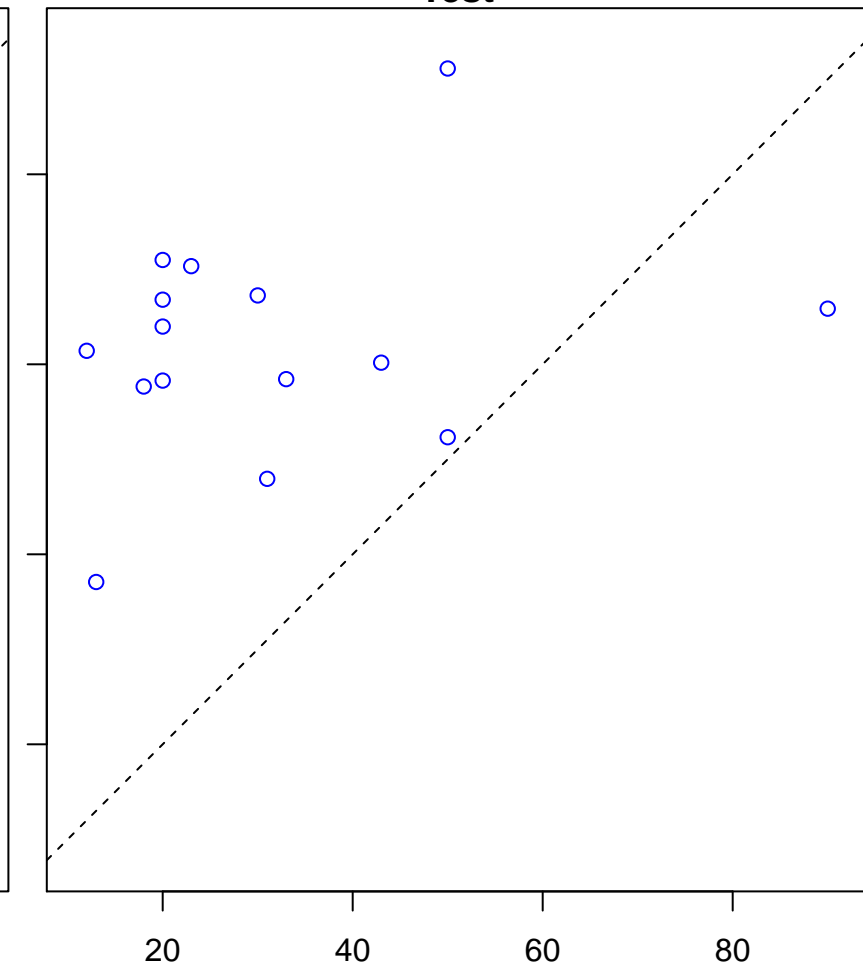
Actual Age

embryonic digestive tract development (Score: 3.997745)

Control



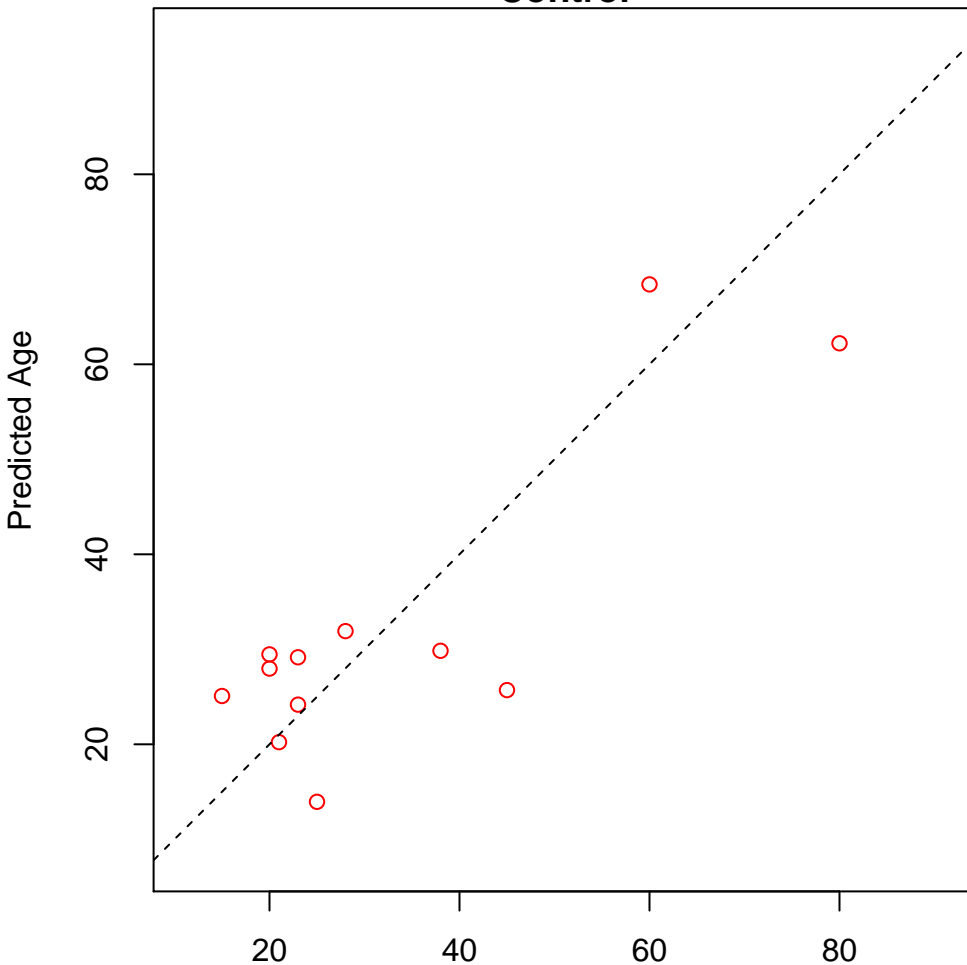
Test



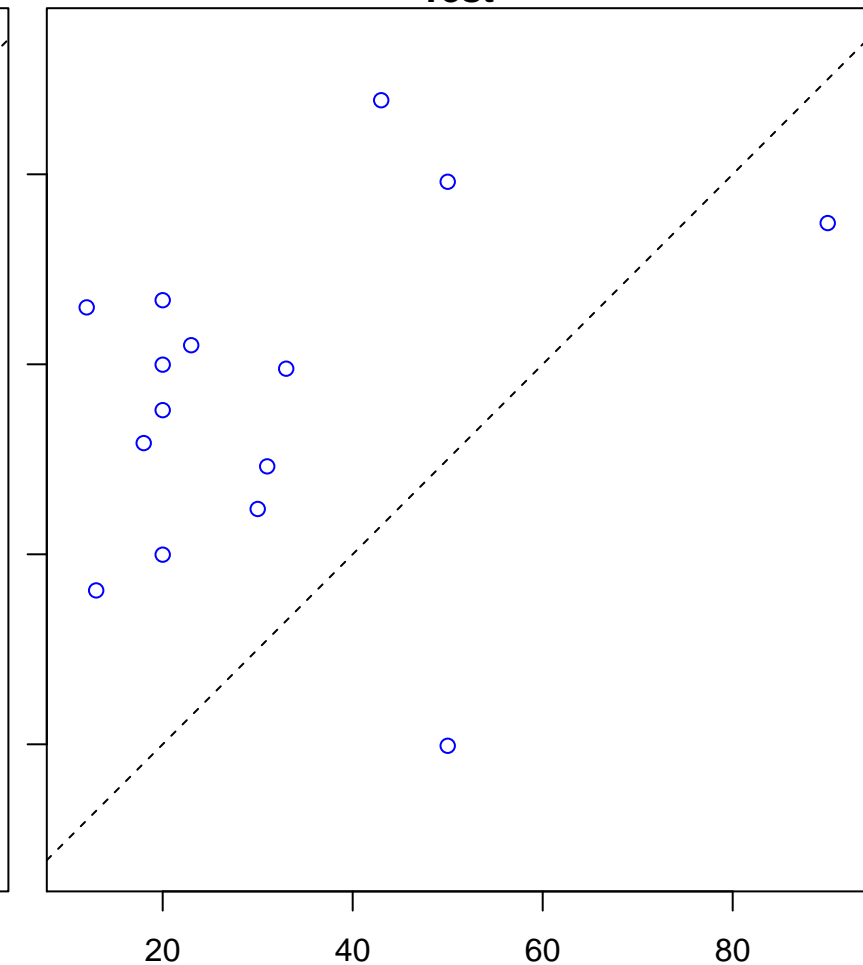
Actual Age

smooth muscle tissue development (Score: 3.996087)

Control

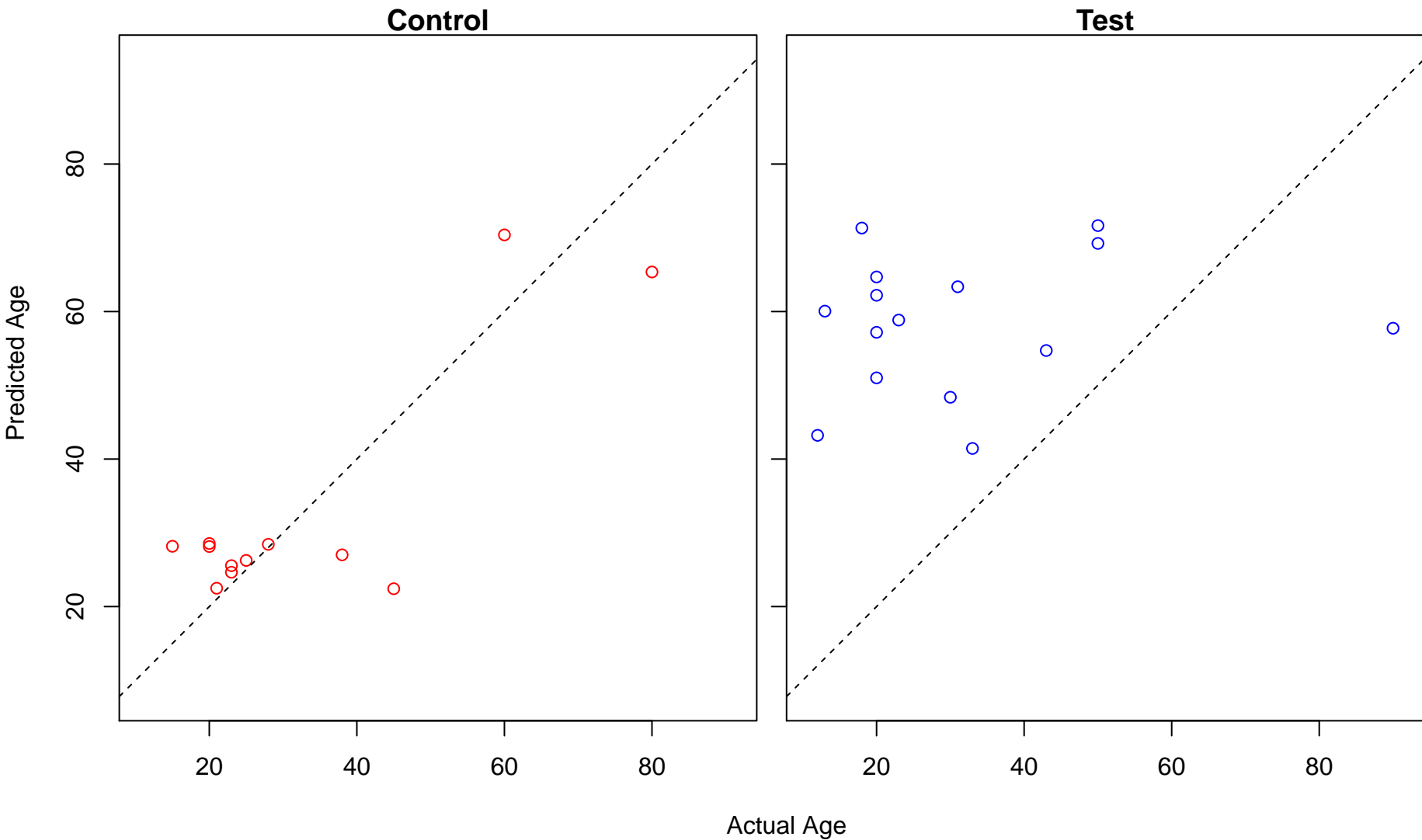


Test

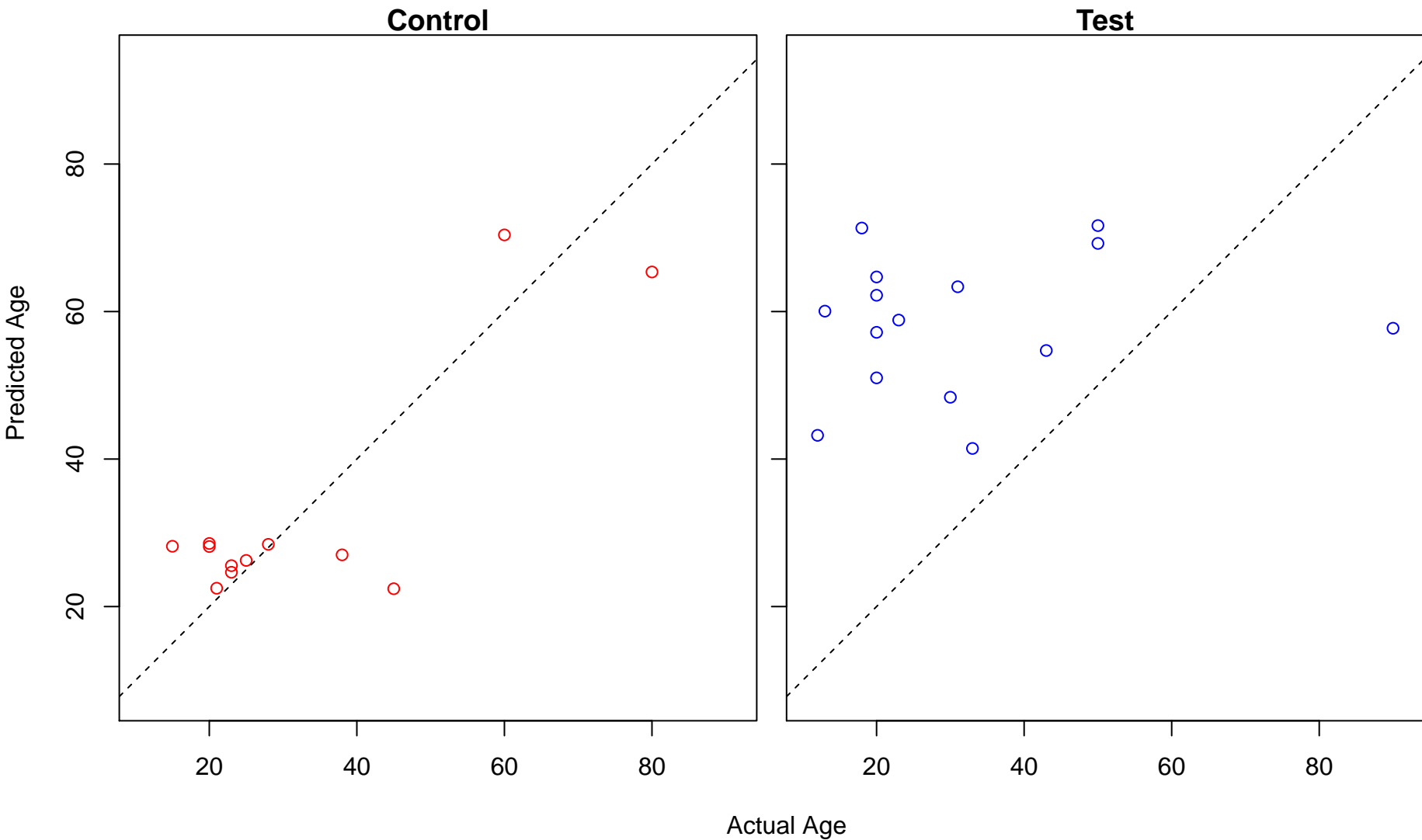


Actual Age

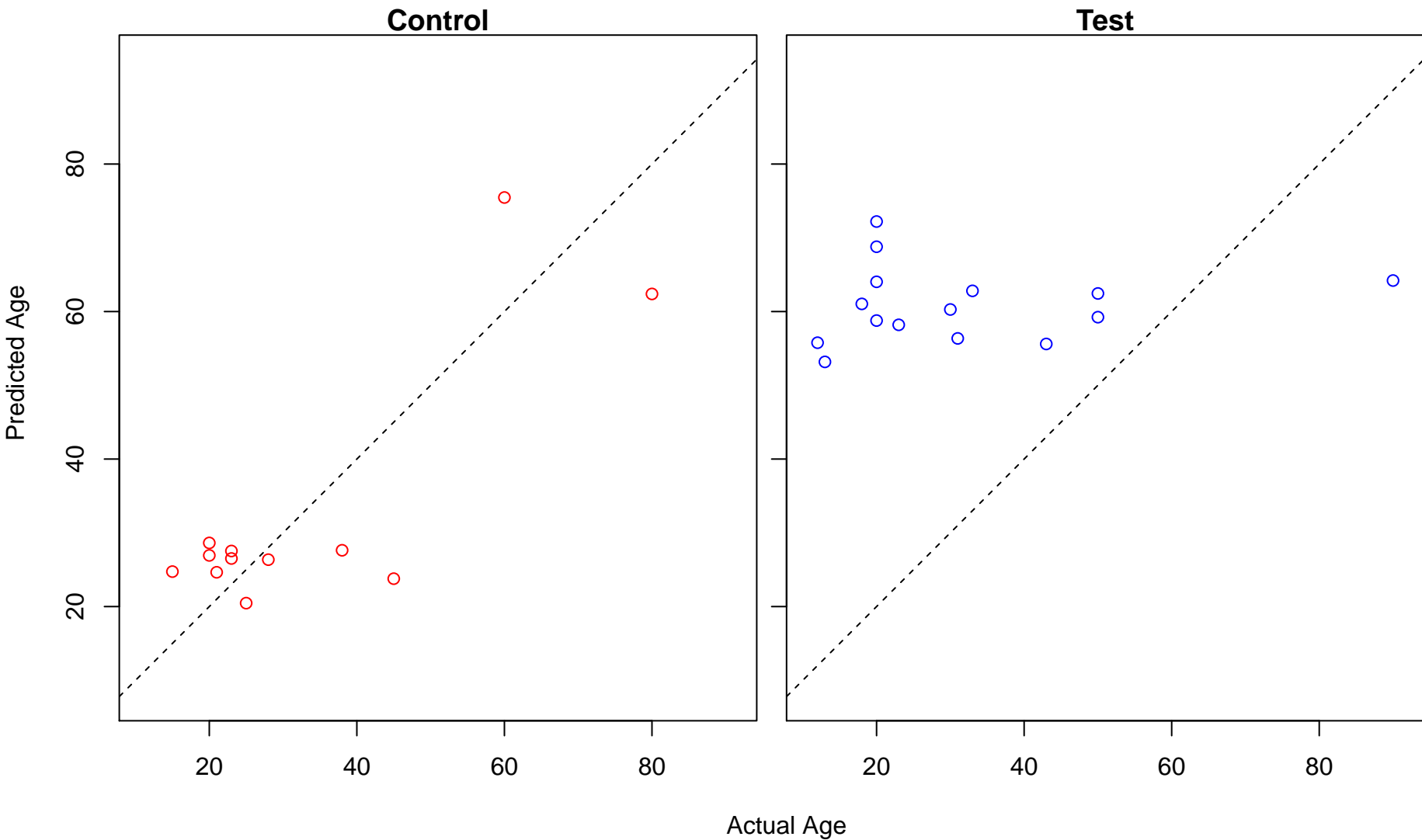
purine nucleoside diphosphate metabolic process (Score: 3.994396)



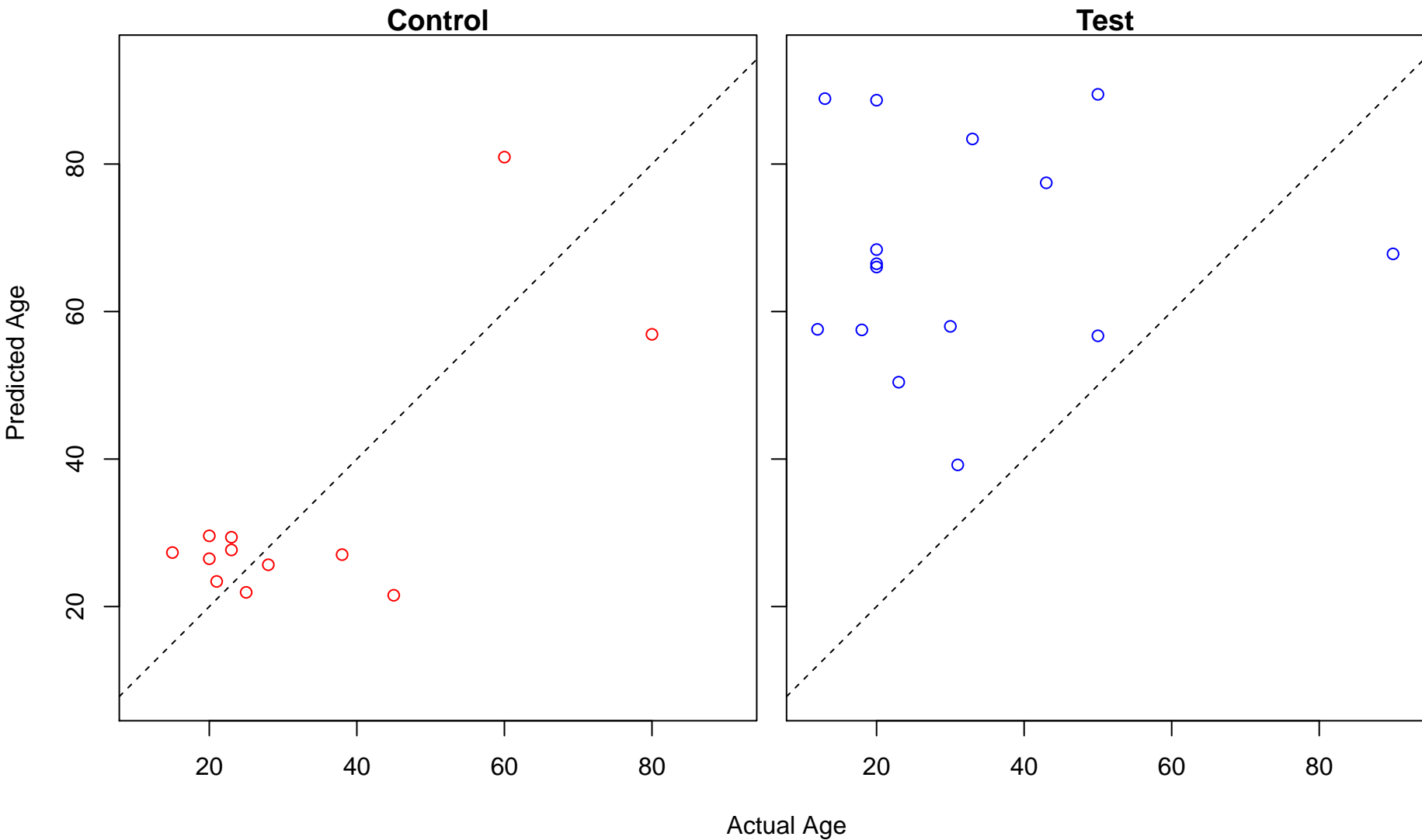
purine ribonucleoside diphosphate metabolic process (Score: 3.994396)



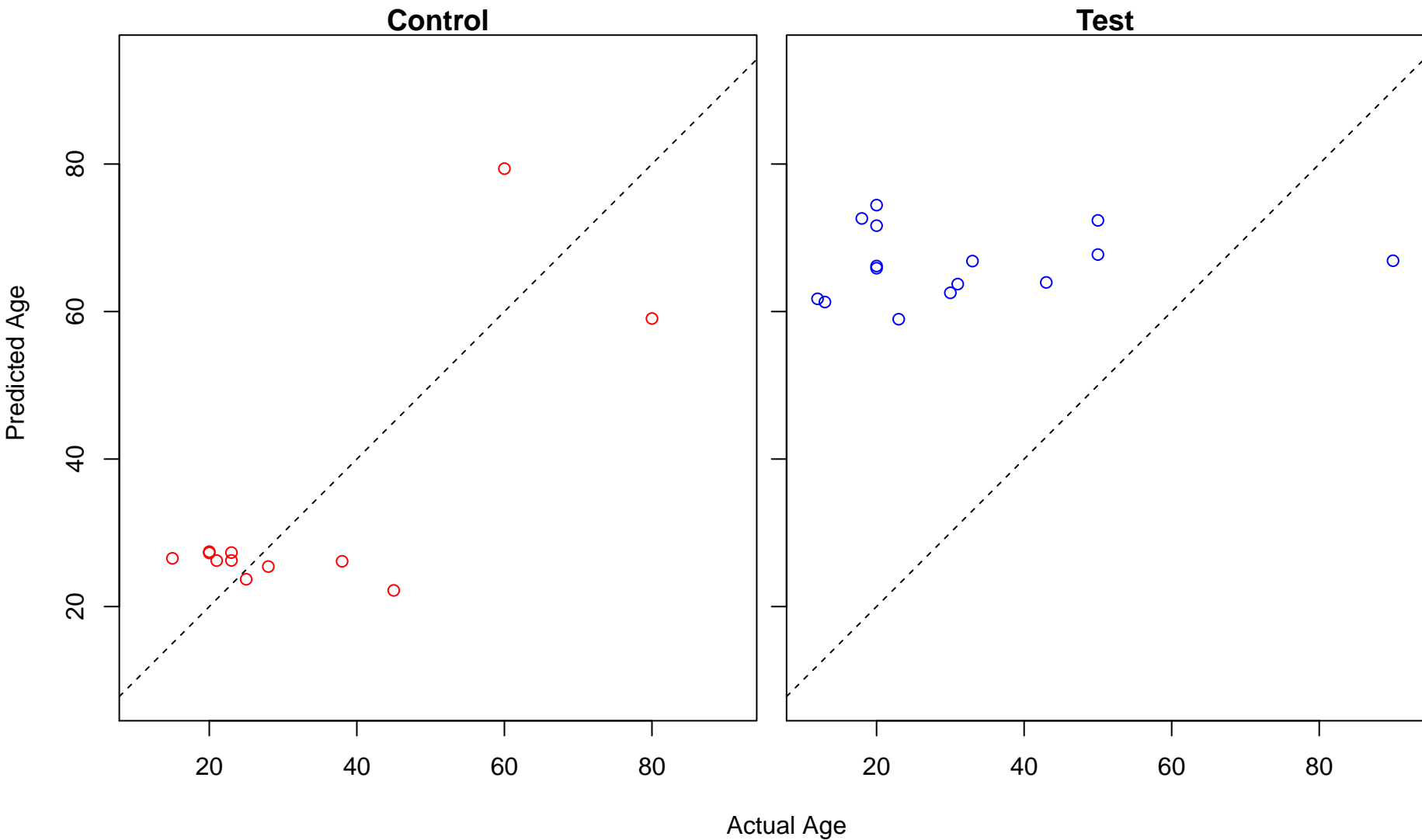
regulation of cilium assembly (Score: 3.992519)



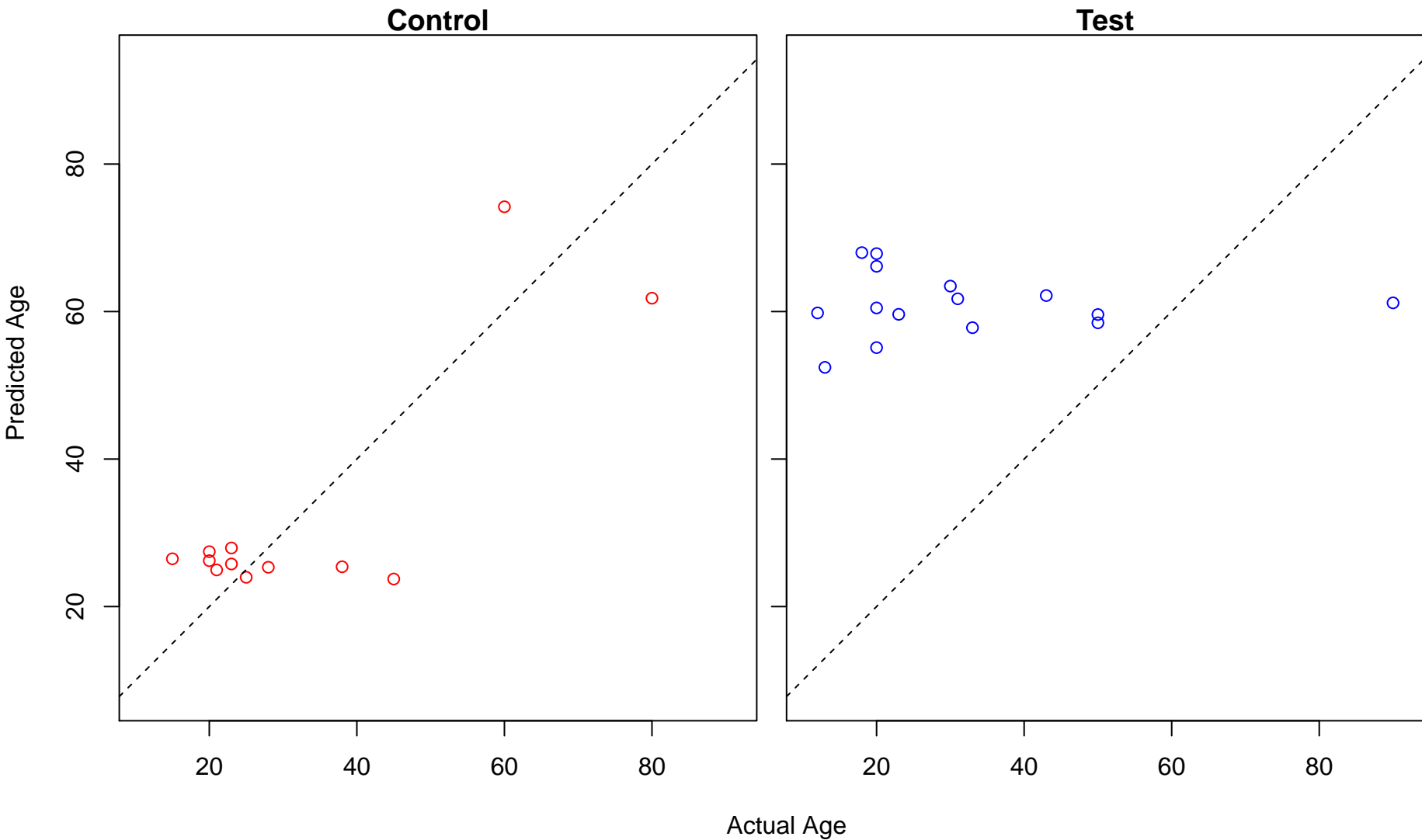
dating (Score: 3.992427)



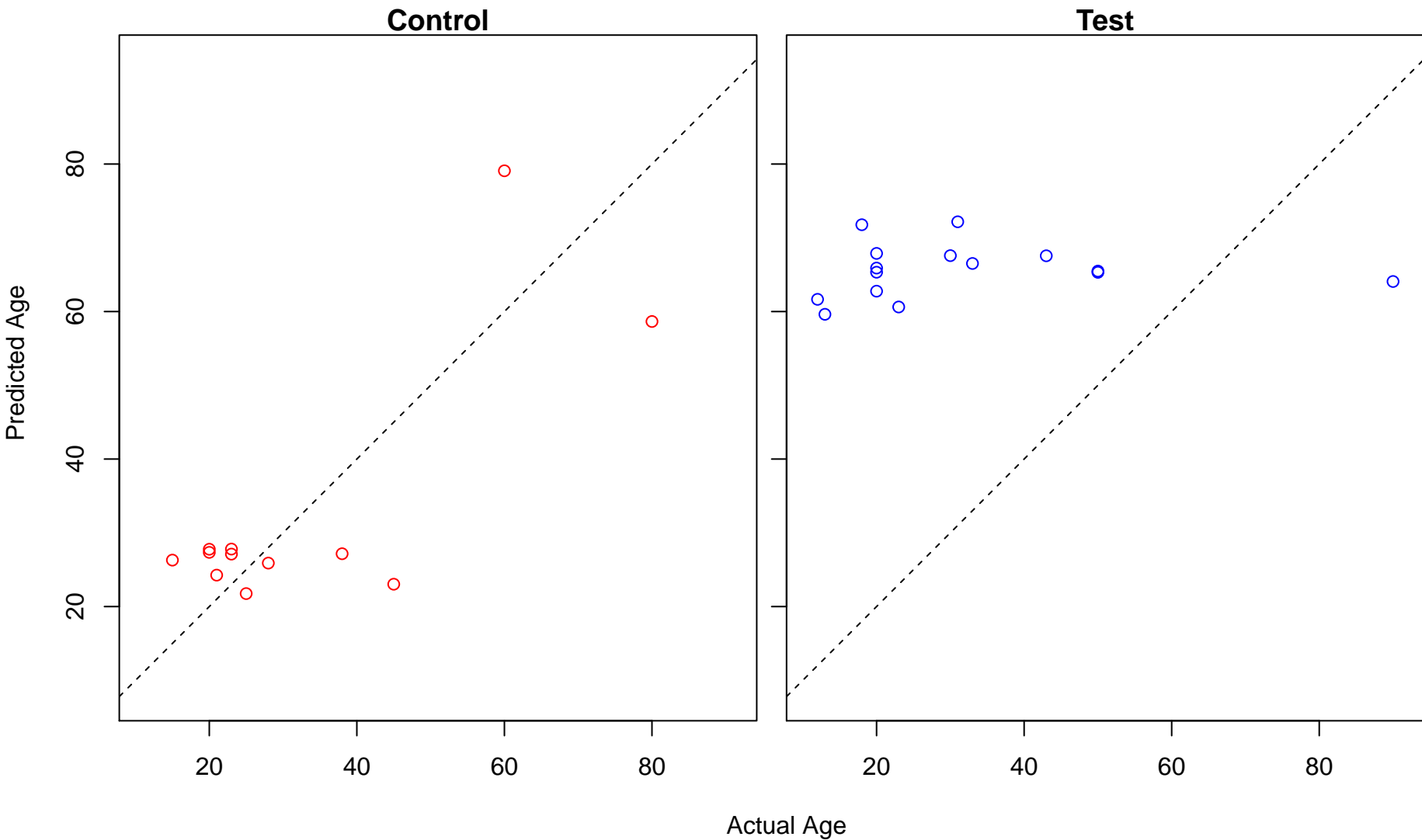
positive regulation of chromosome segregation (Score: 3.989793)



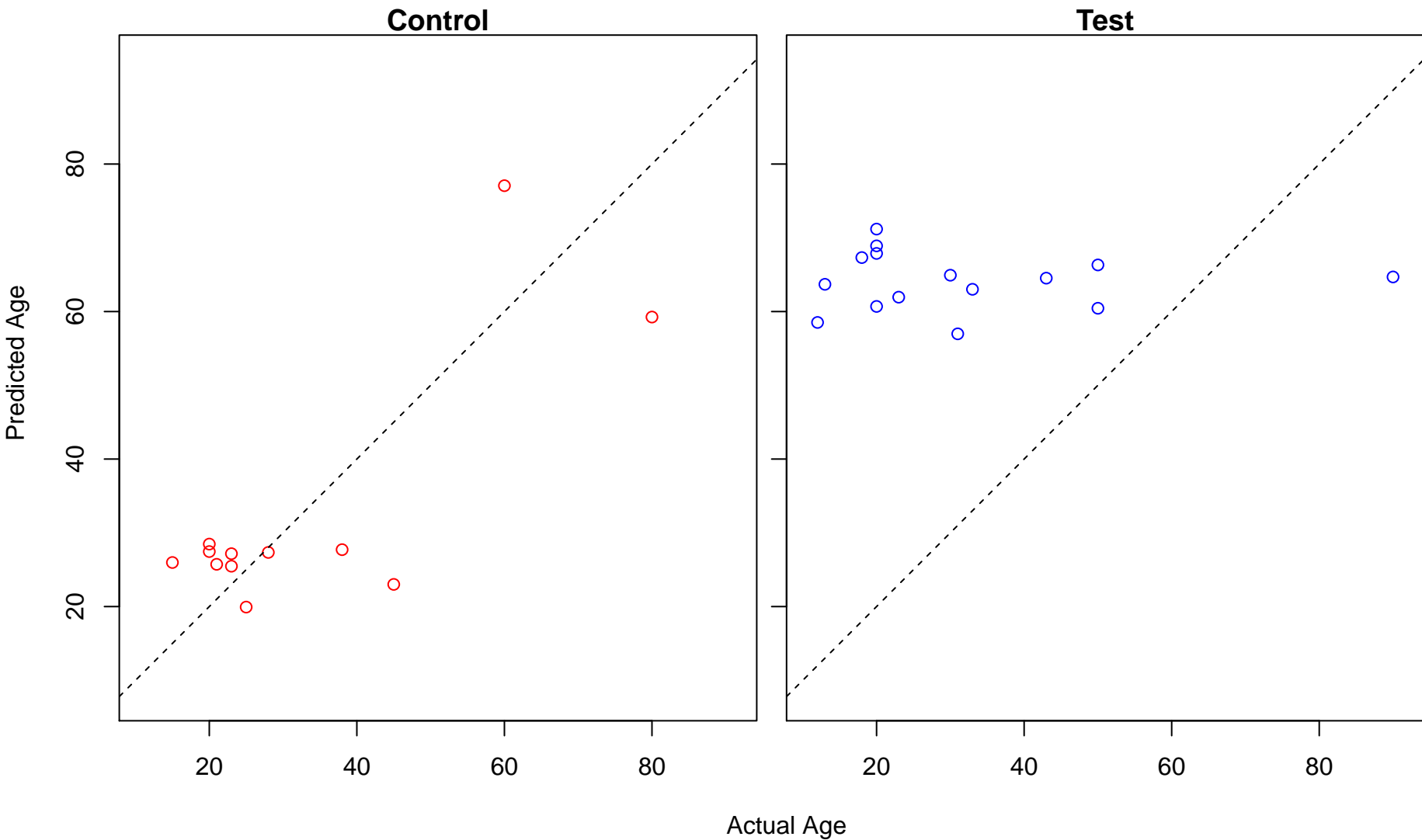
long-chain fatty-acyl-CoA metabolic process (Score: 3.985949)



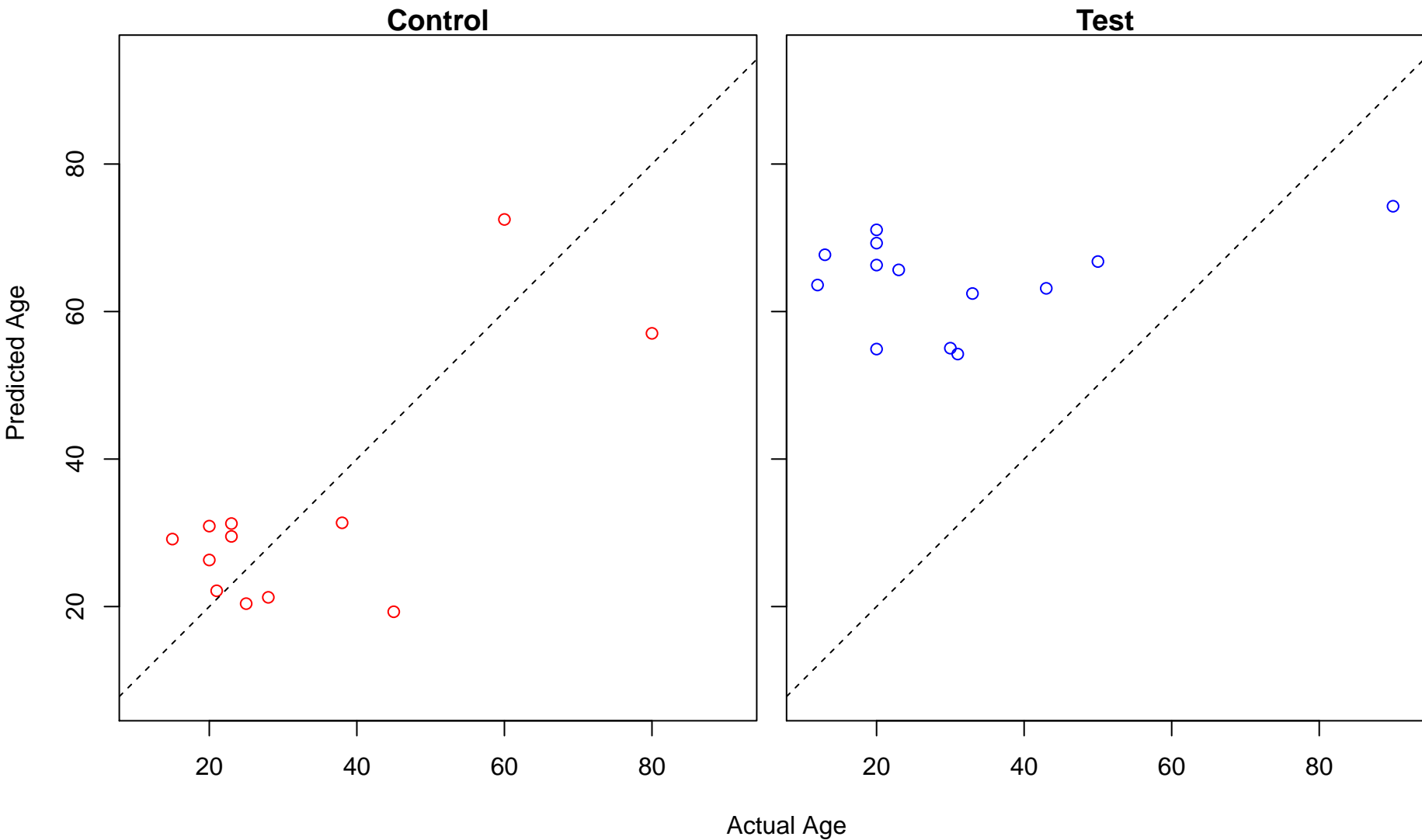
maintenance of protein location (Score: 3.983874)



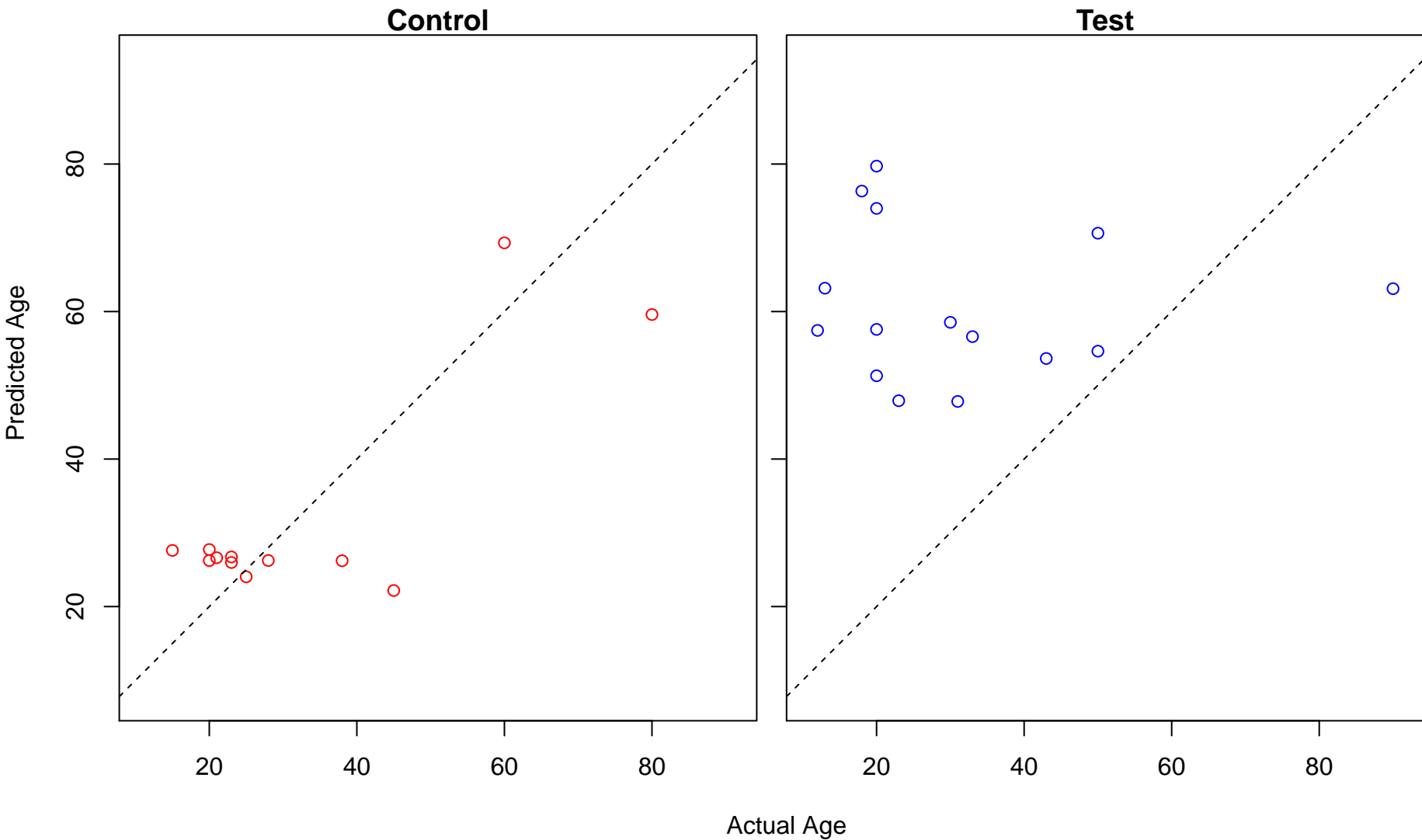
sphingolipid biosynthetic process (Score: 3.979301)



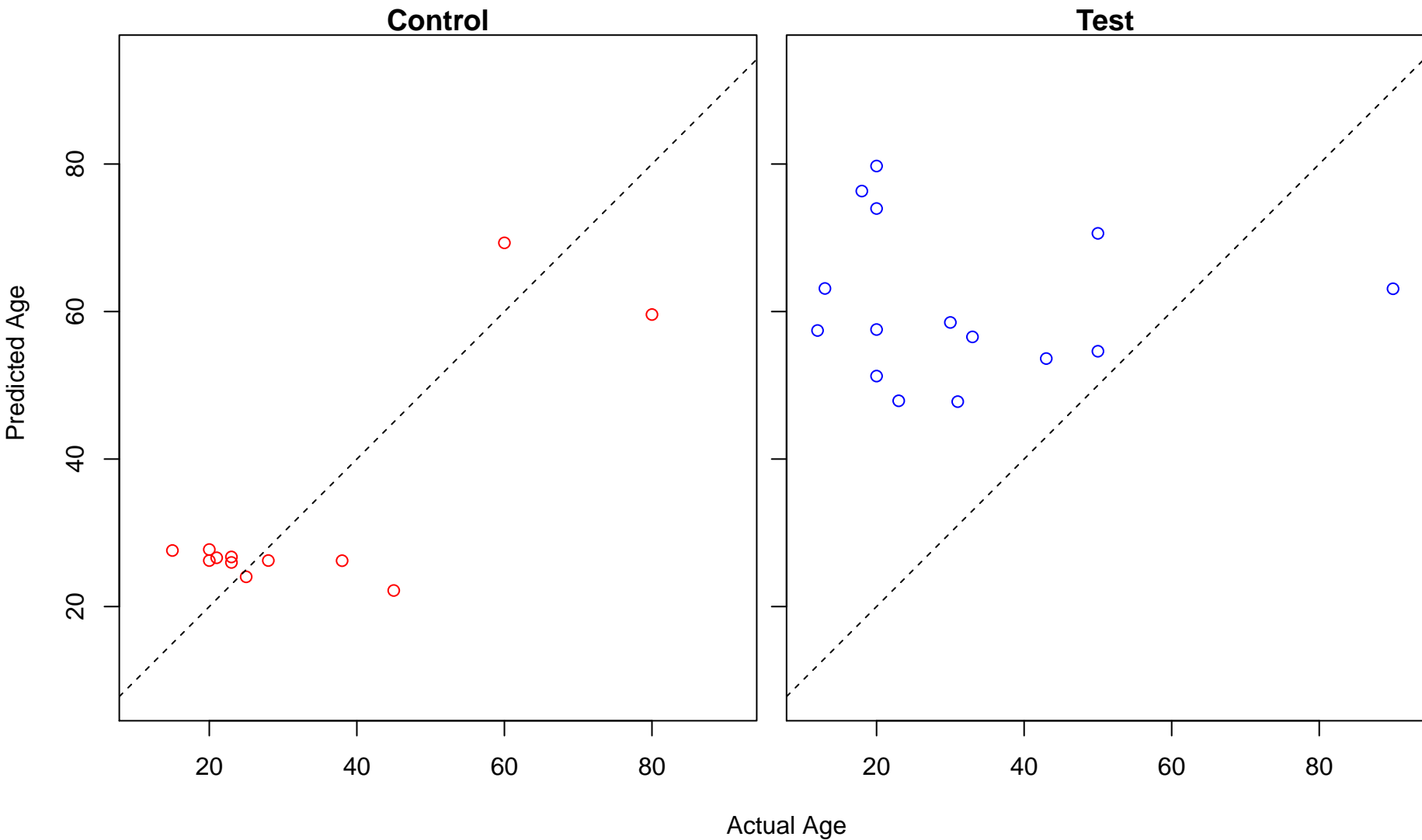
cardiac chamber formation (Score: 3.977154)



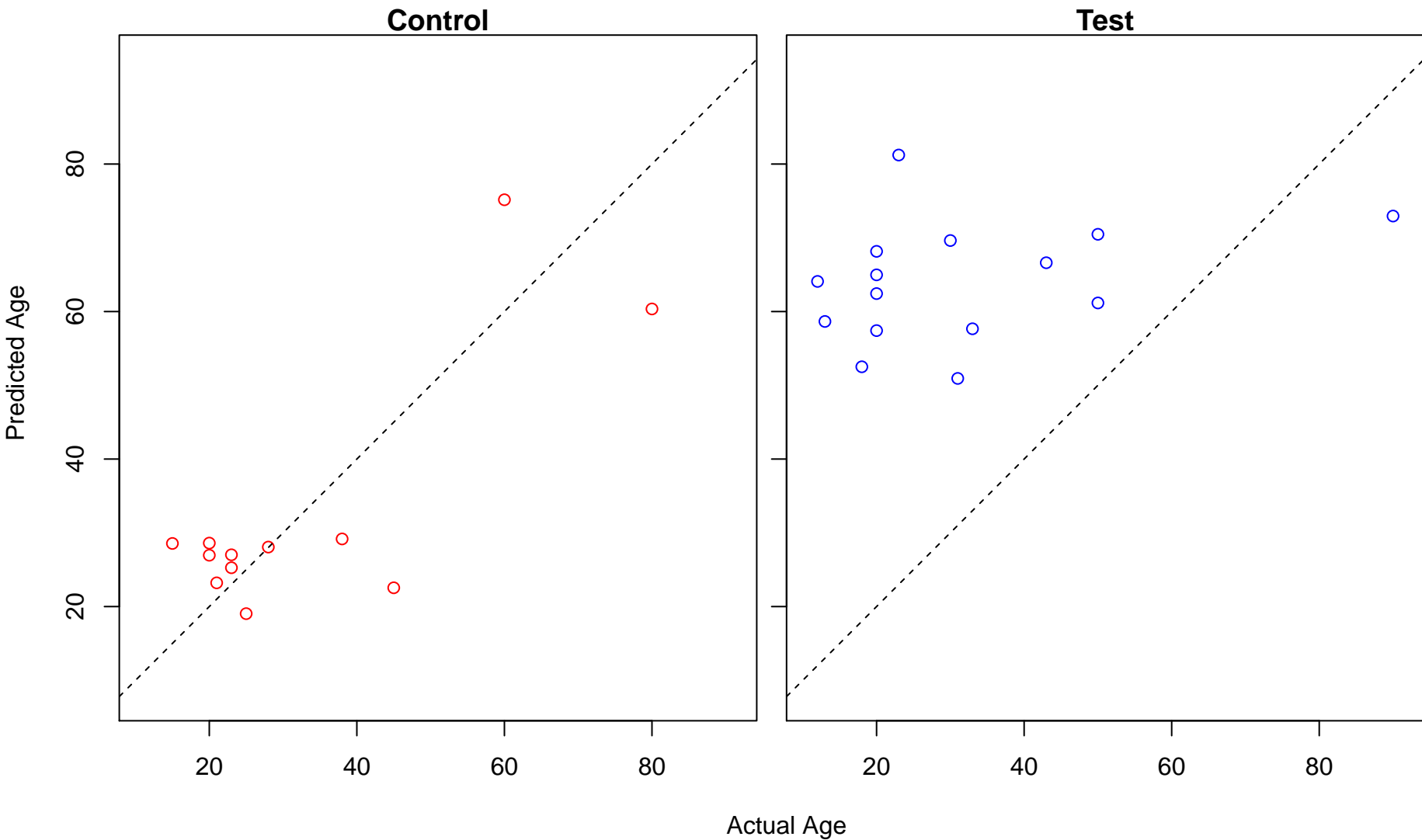
positive regulation of proteasomal protein catabolic process (Score: 3.976949)



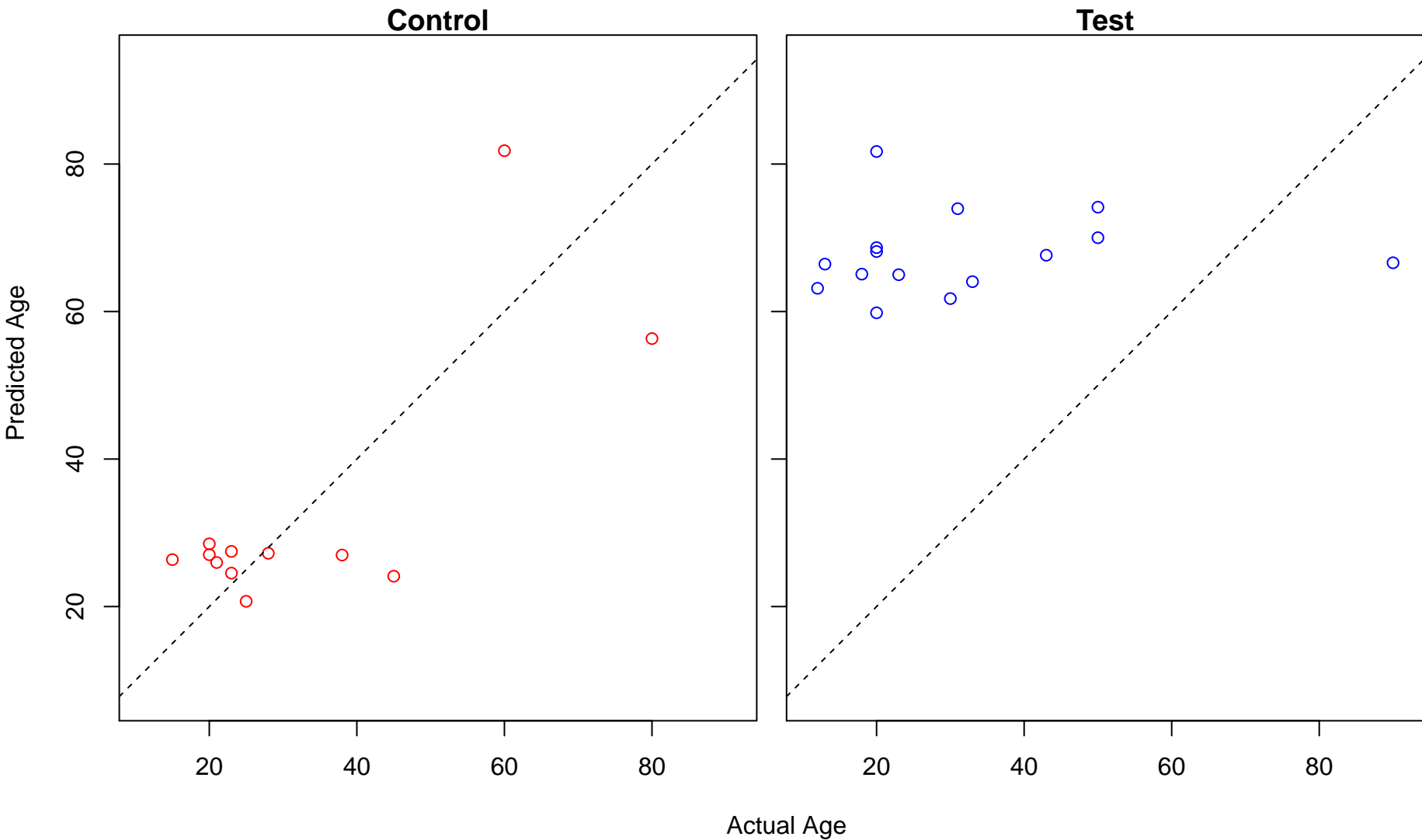
positive regulation of proteasomal ubiquitin-dependent protein catabolic process (Score: 3.975485)



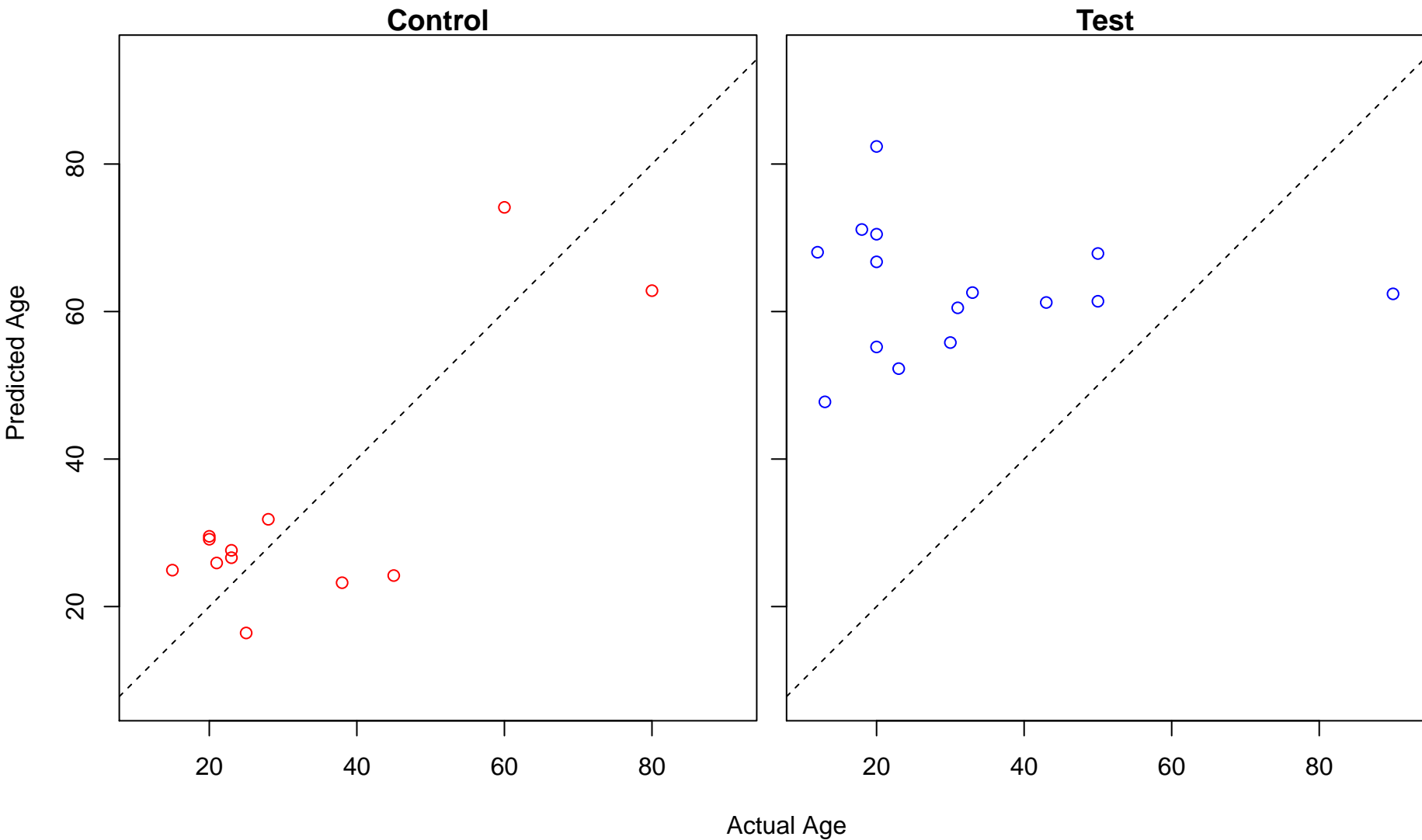
response to cAMP (Score: 3.974597)



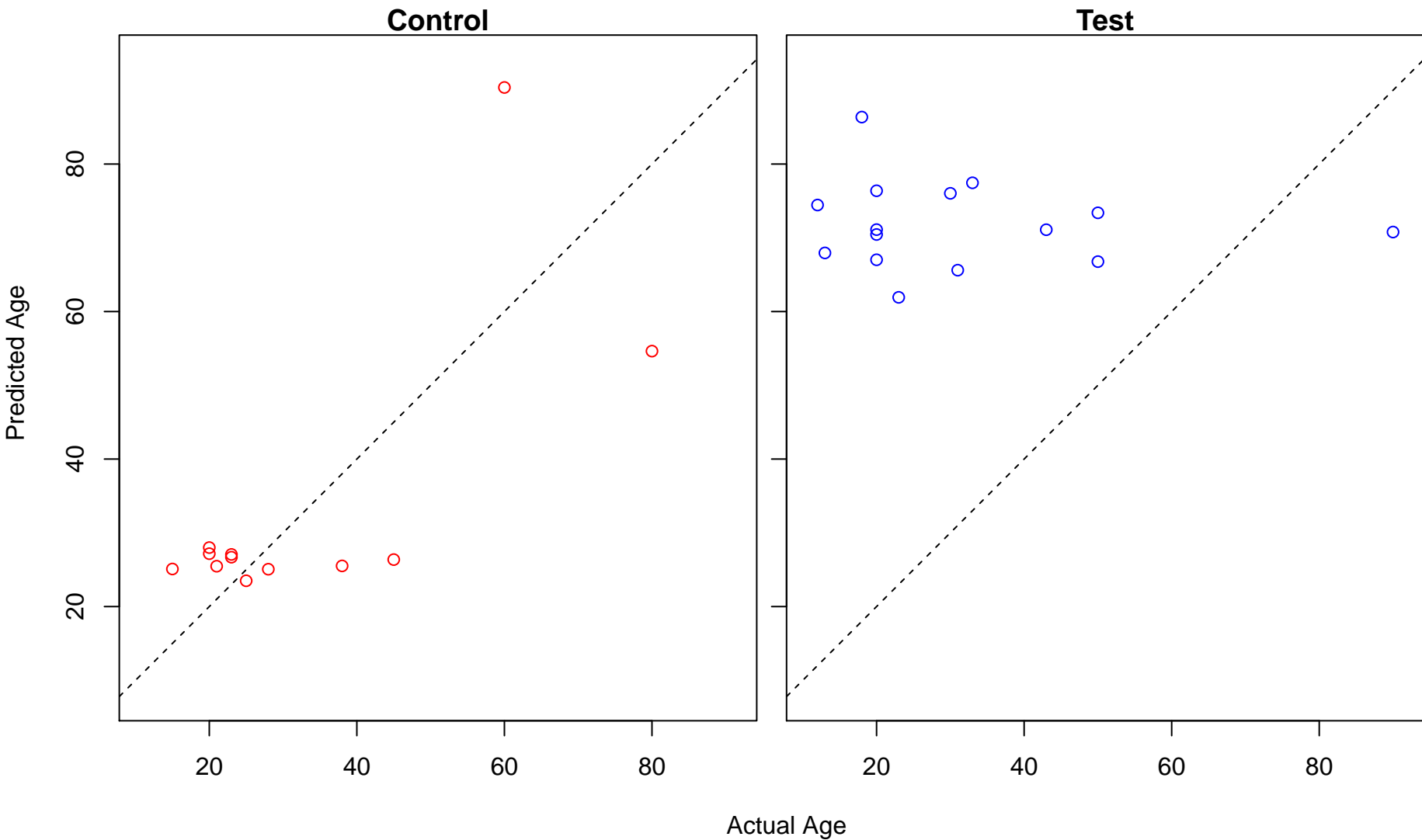
reactive nitrogen species metabolic process (Score: 3.973237)



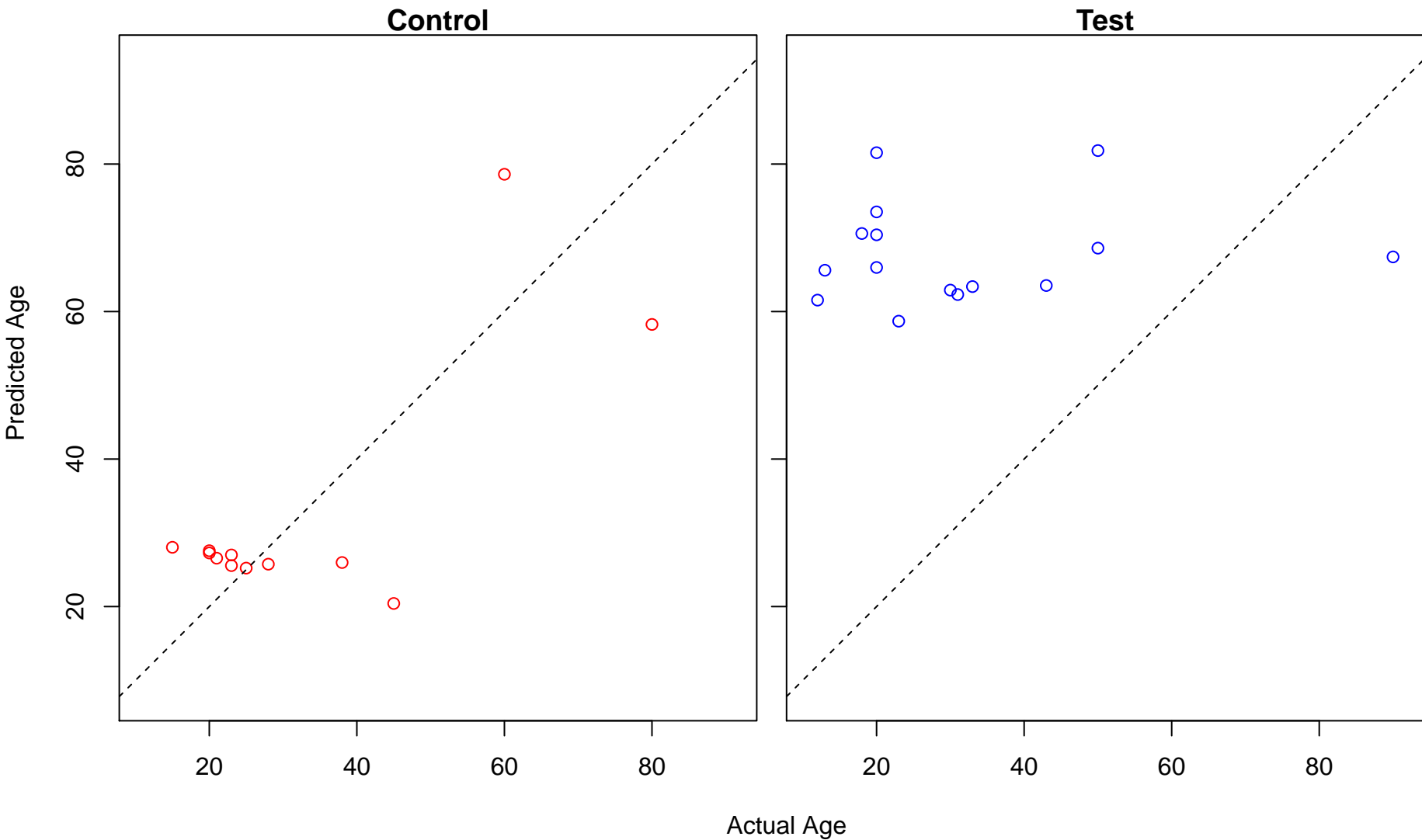
positive regulation of extracellular matrix organization (Score: 3.972490)



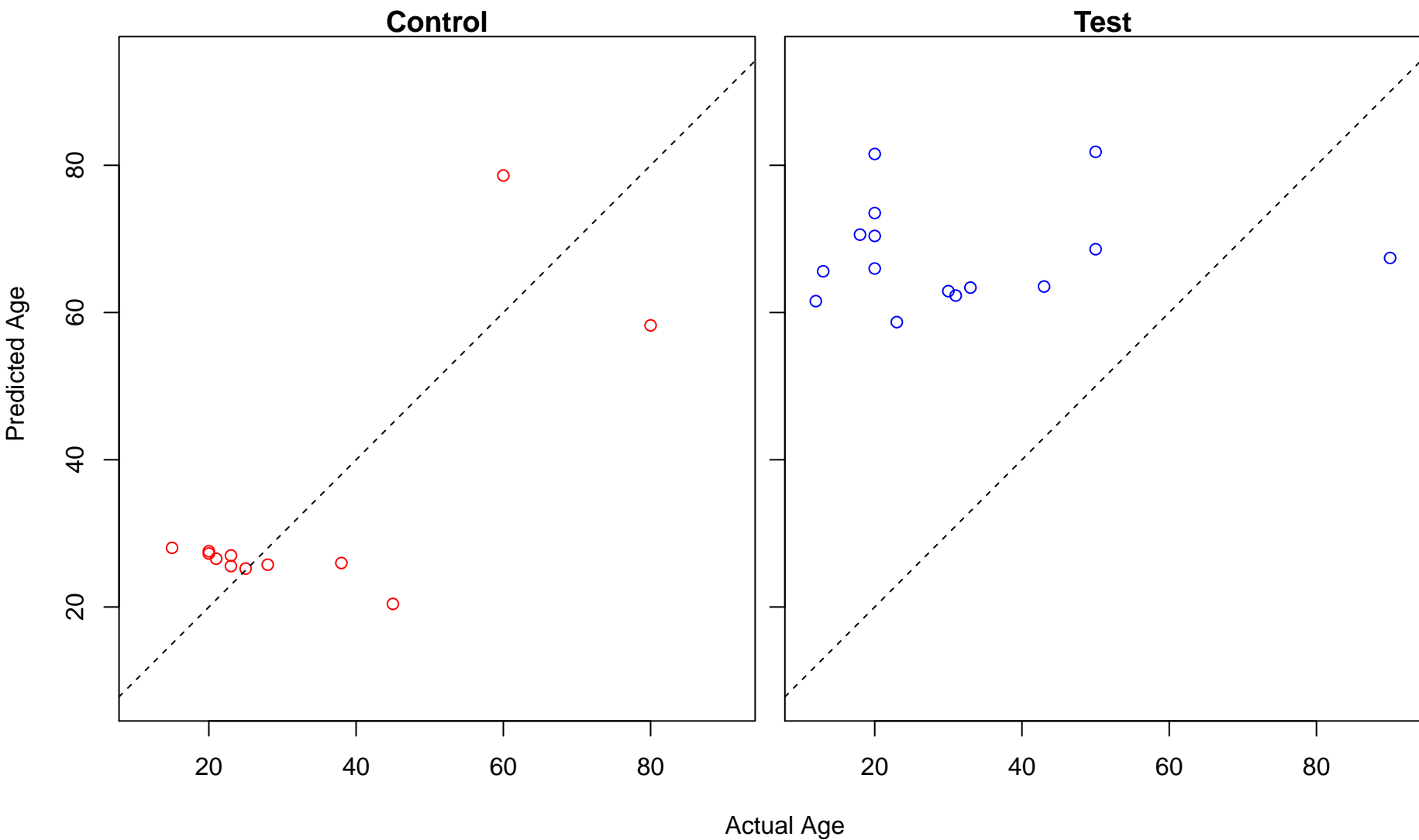
negative regulation of translation in response to stress (Score: 3.972080)



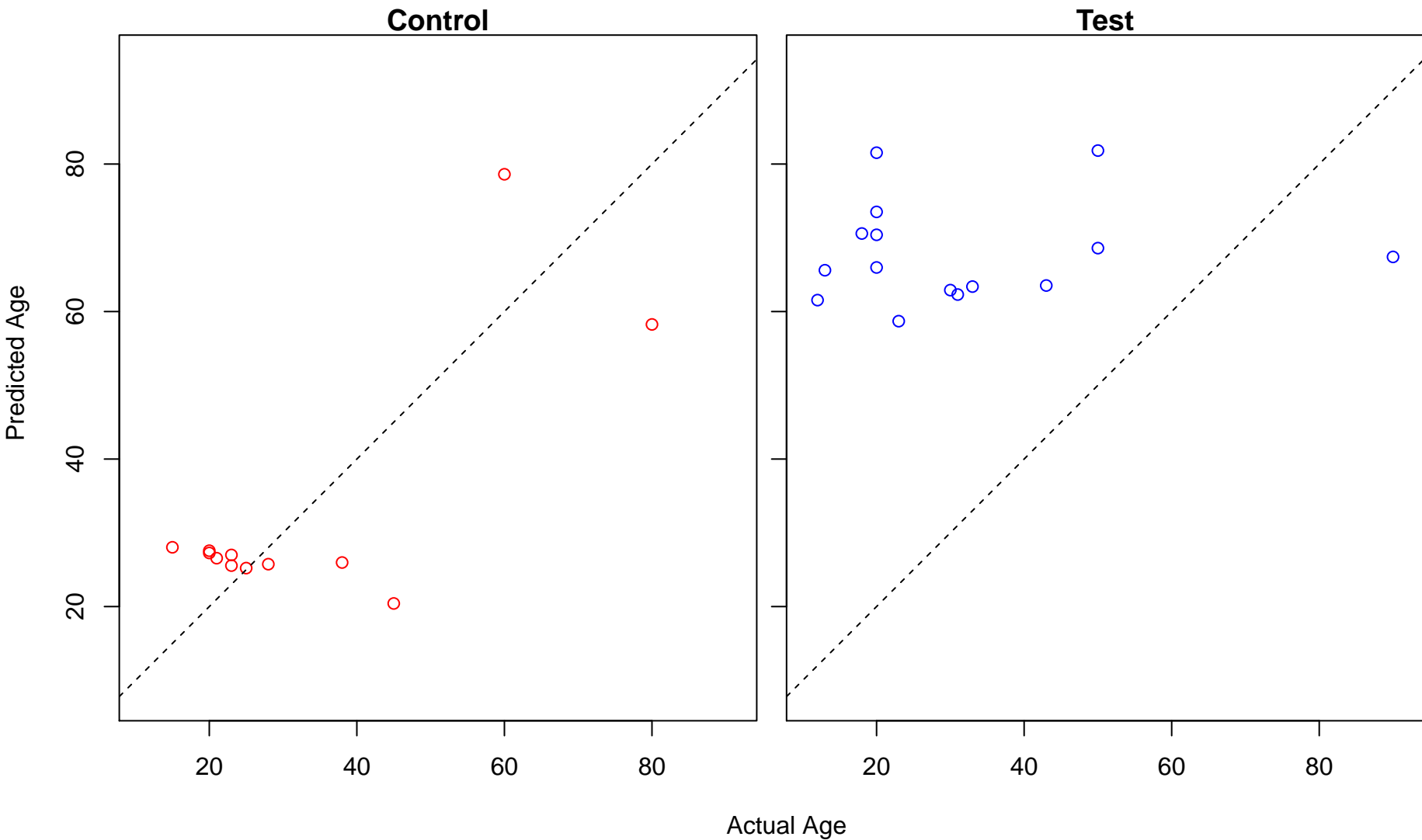
positive regulation of maintenance of sister chromatid cohesion (Score: 3.971700)



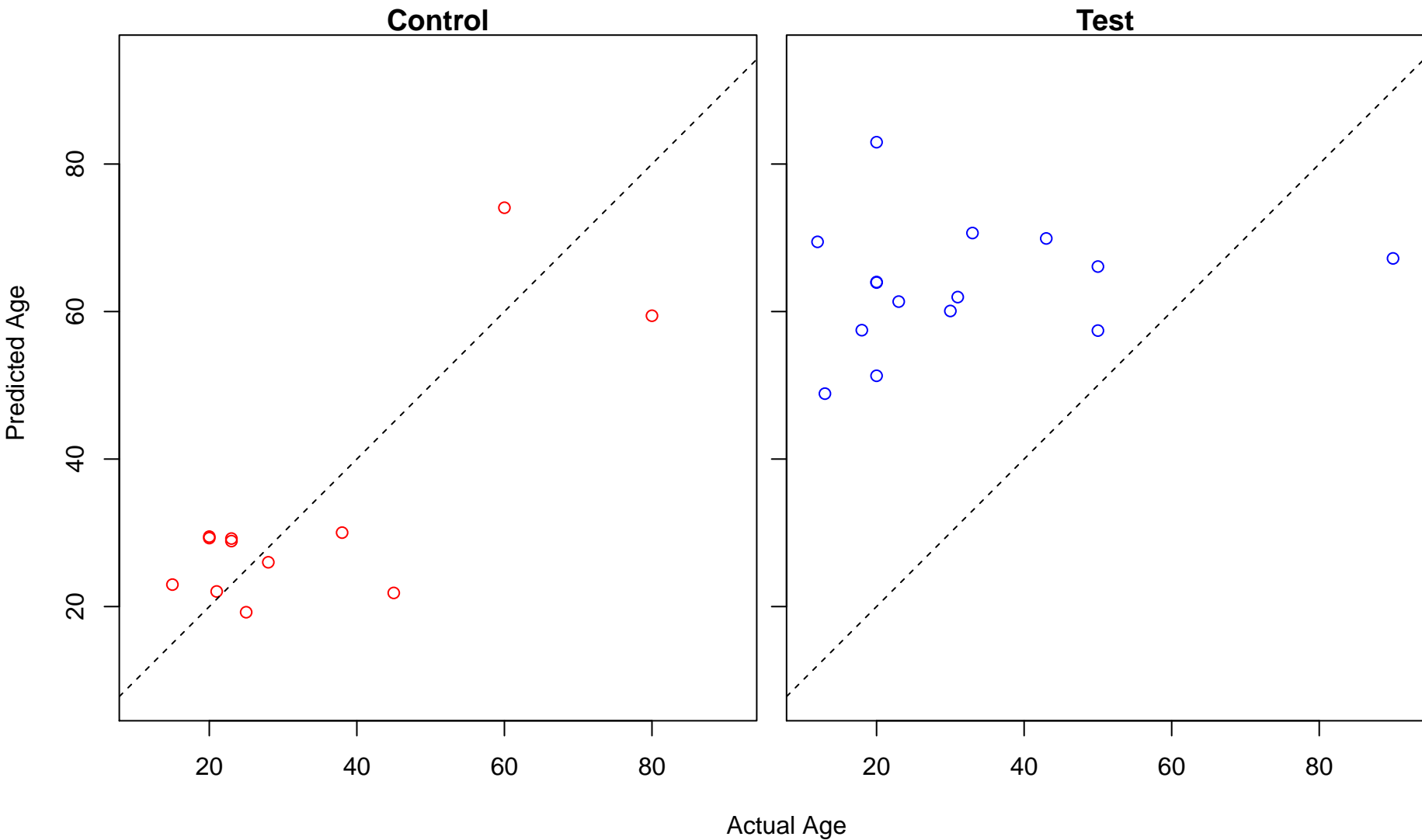
positive regulation of maintenance of mitotic sister chromatid cohesion (Score: 3.971700)



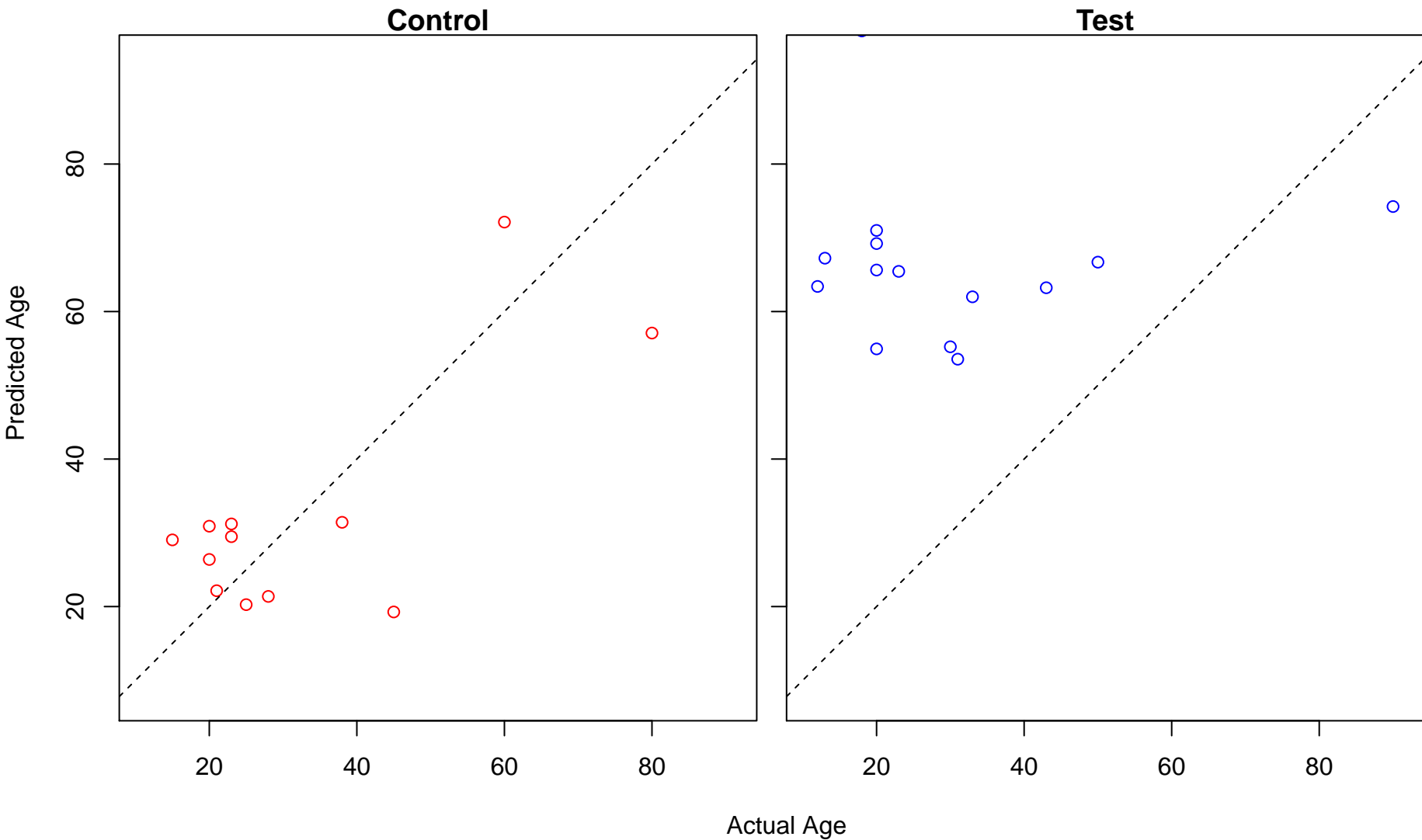
positive regulation of sister chromatid cohesion (Score: 3.971700)



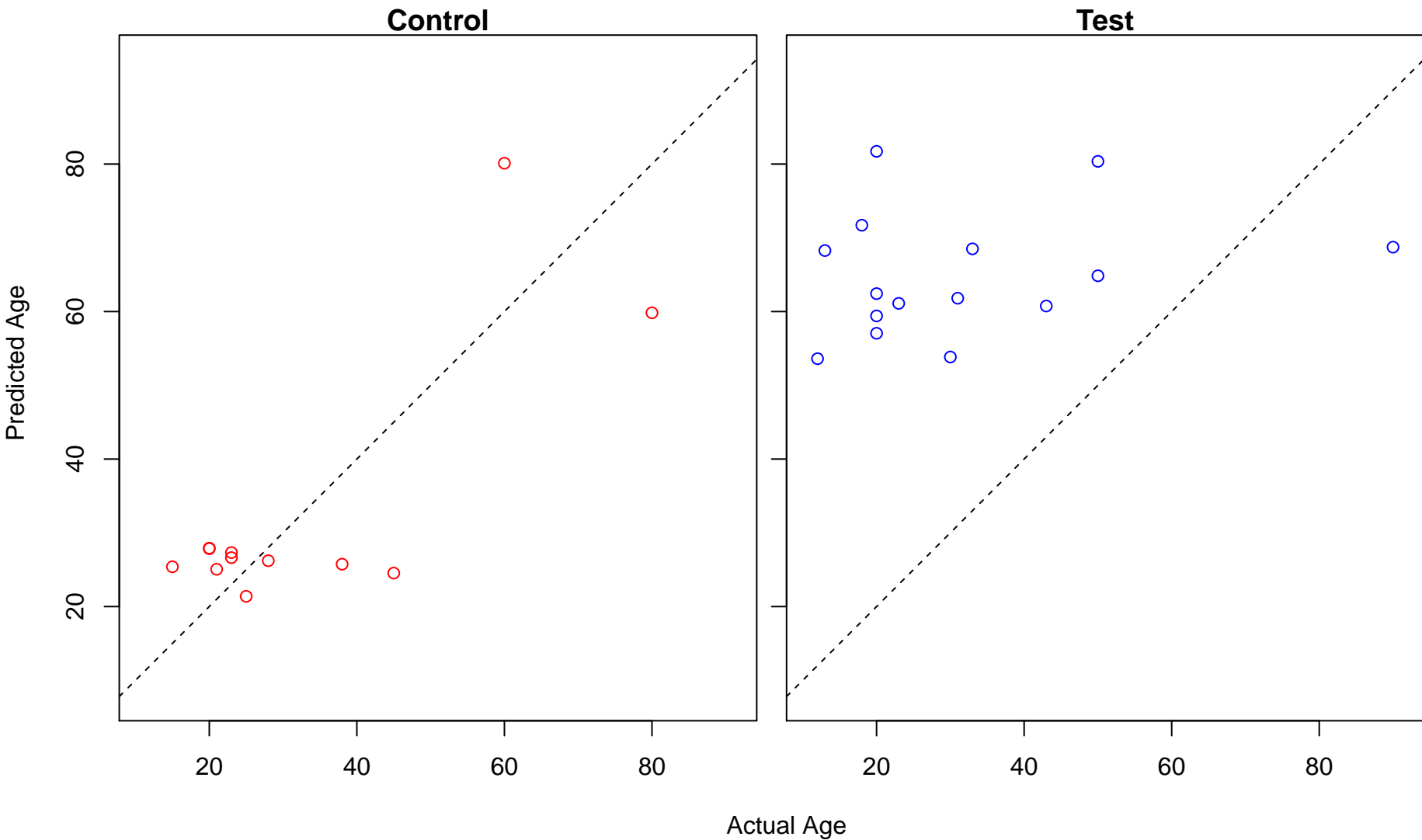
cellular response to cholesterol (Score: 3.967803)



ventral spinal cord development (Score: 3.966907)

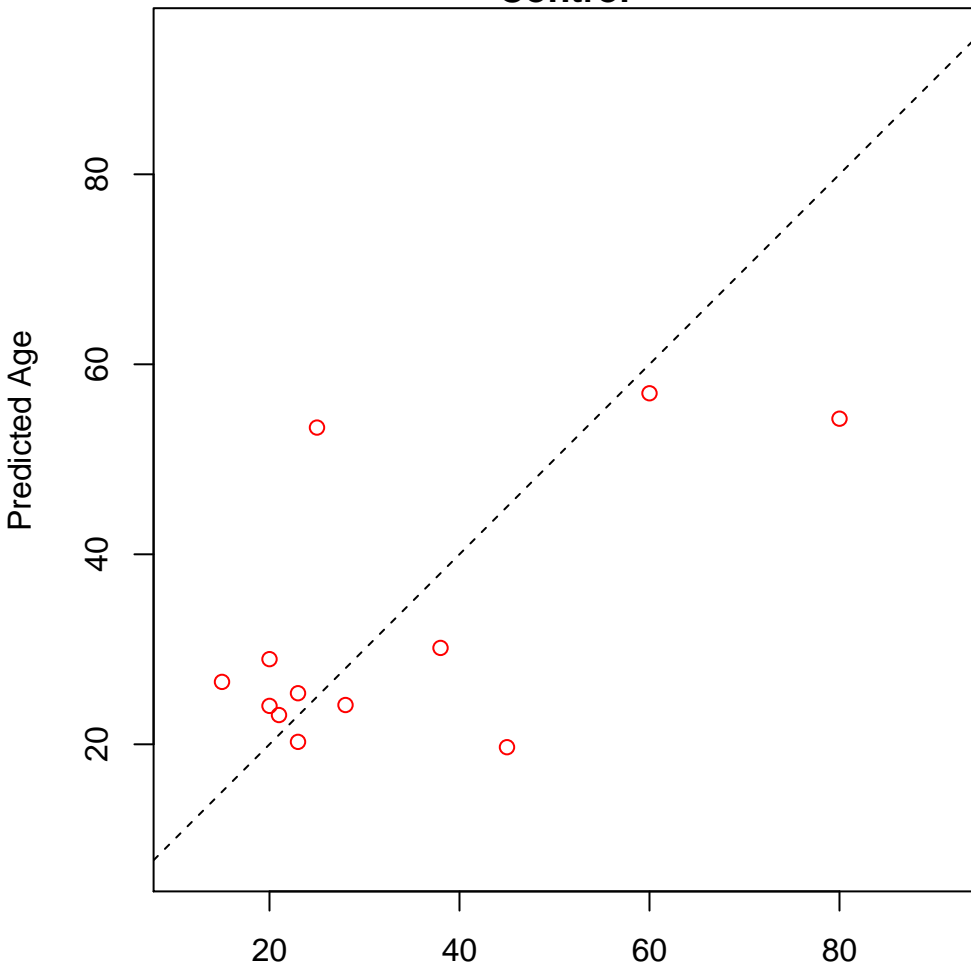


positive regulation of kidney development (Score: 3.964901)

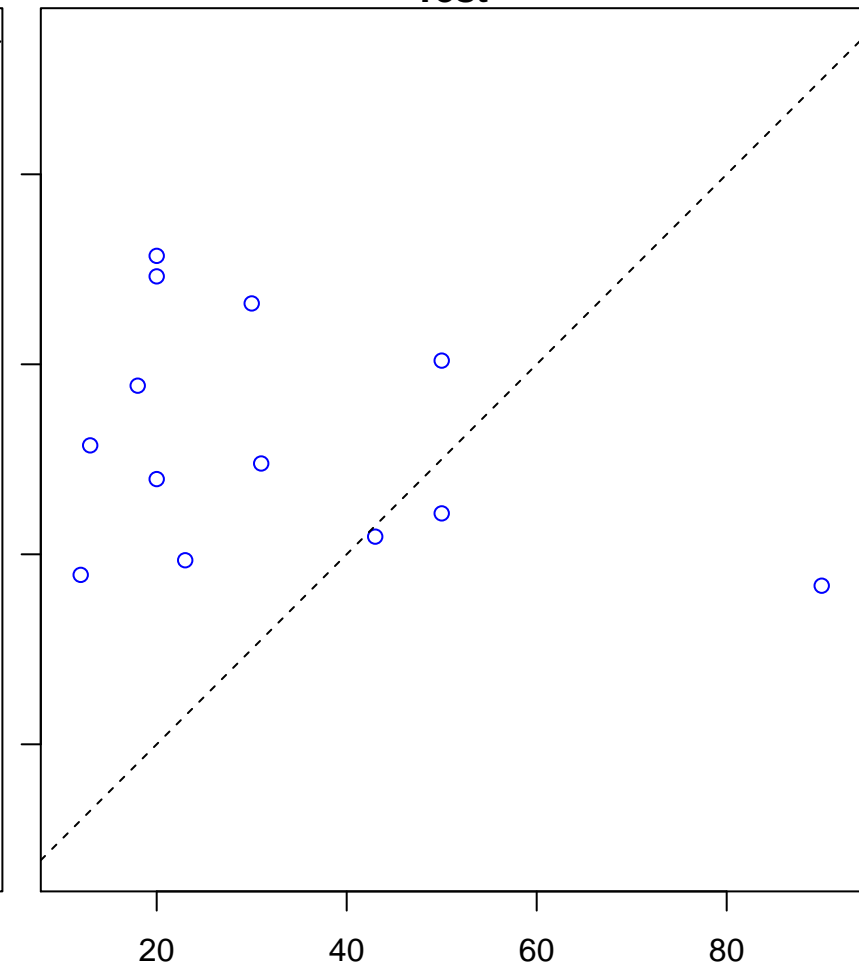


regulation of steroid hormone secretion (Score: 3.955292)

Control

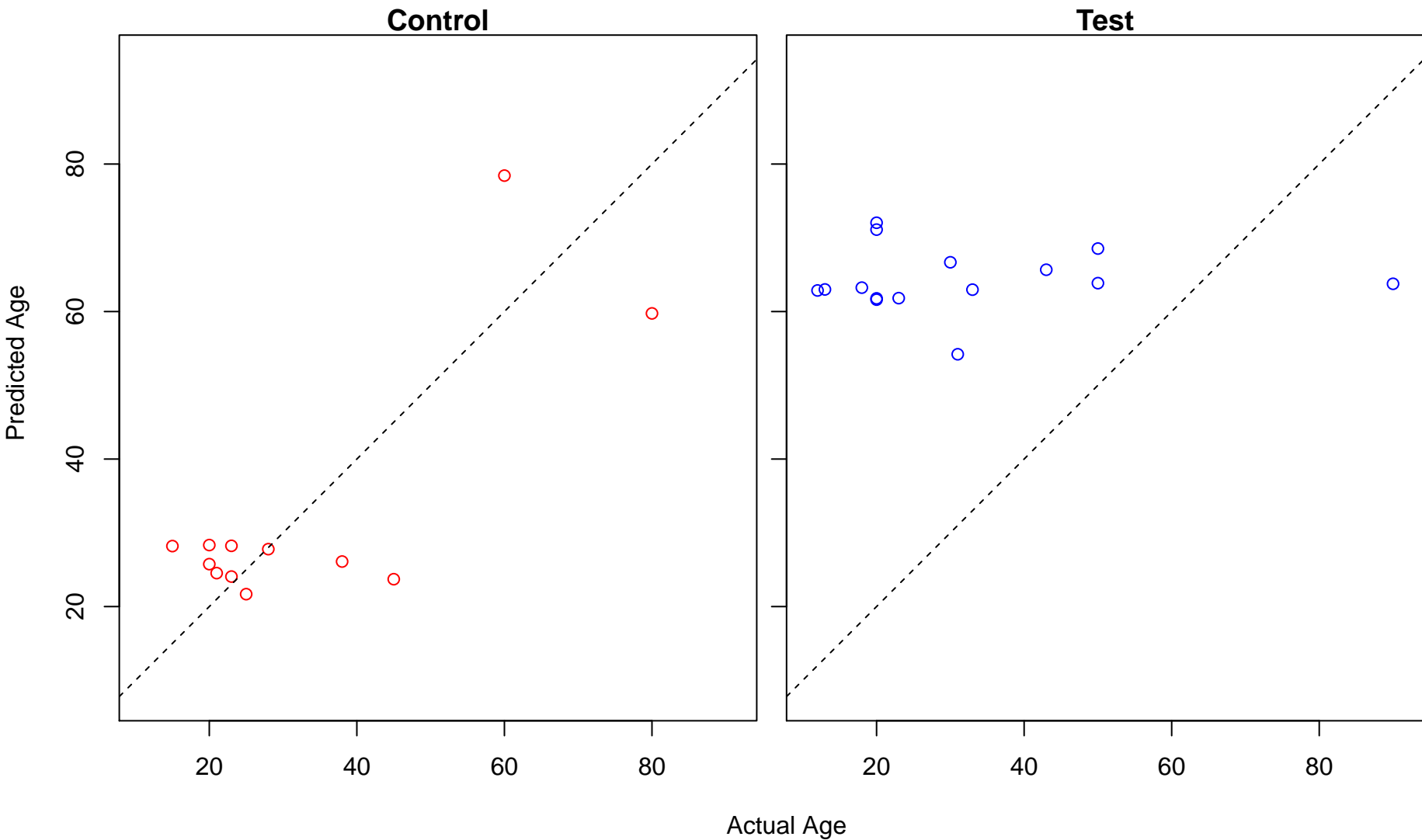


Test

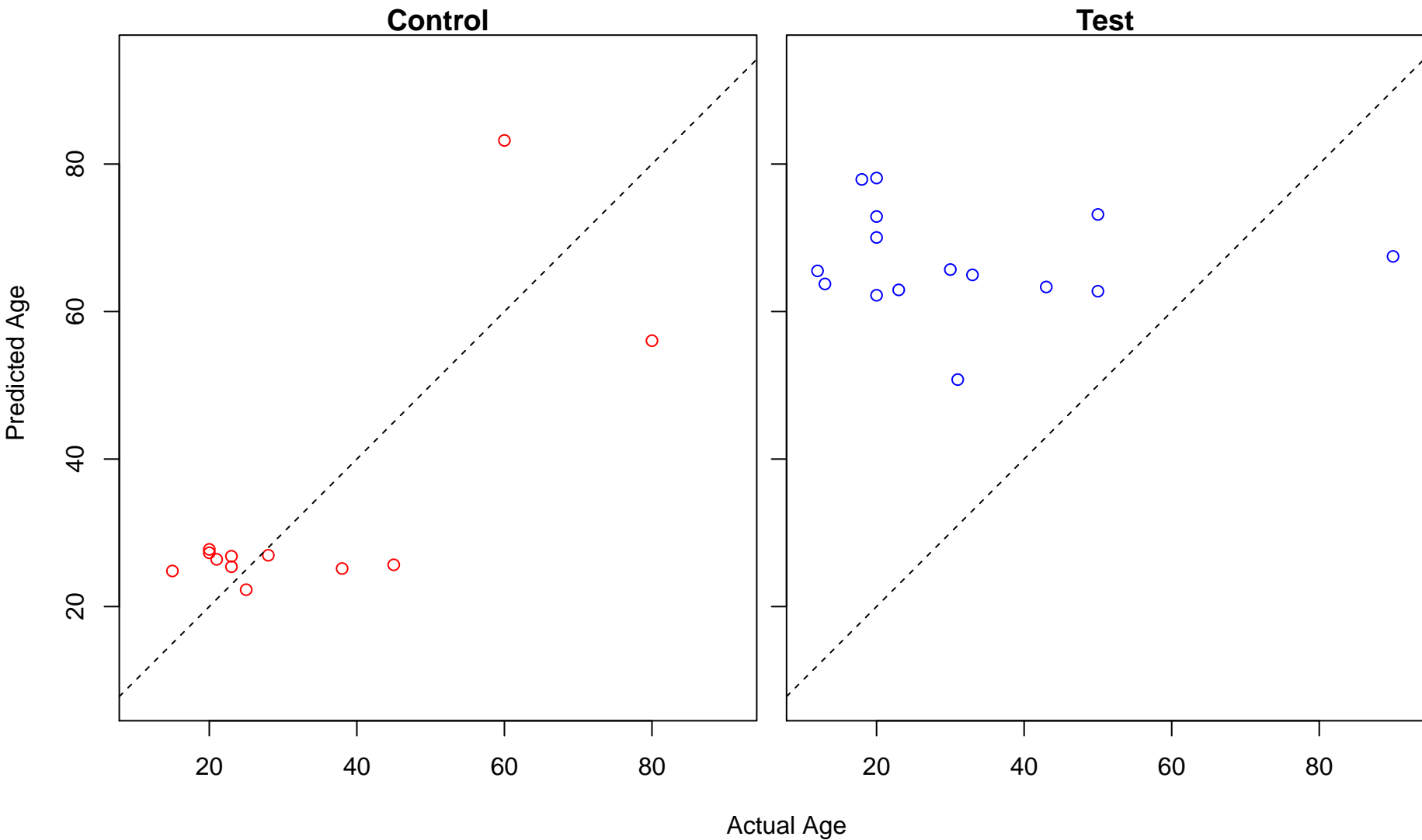


Actual Age

negative regulation of viral release from host cell (Score: 3.954297)

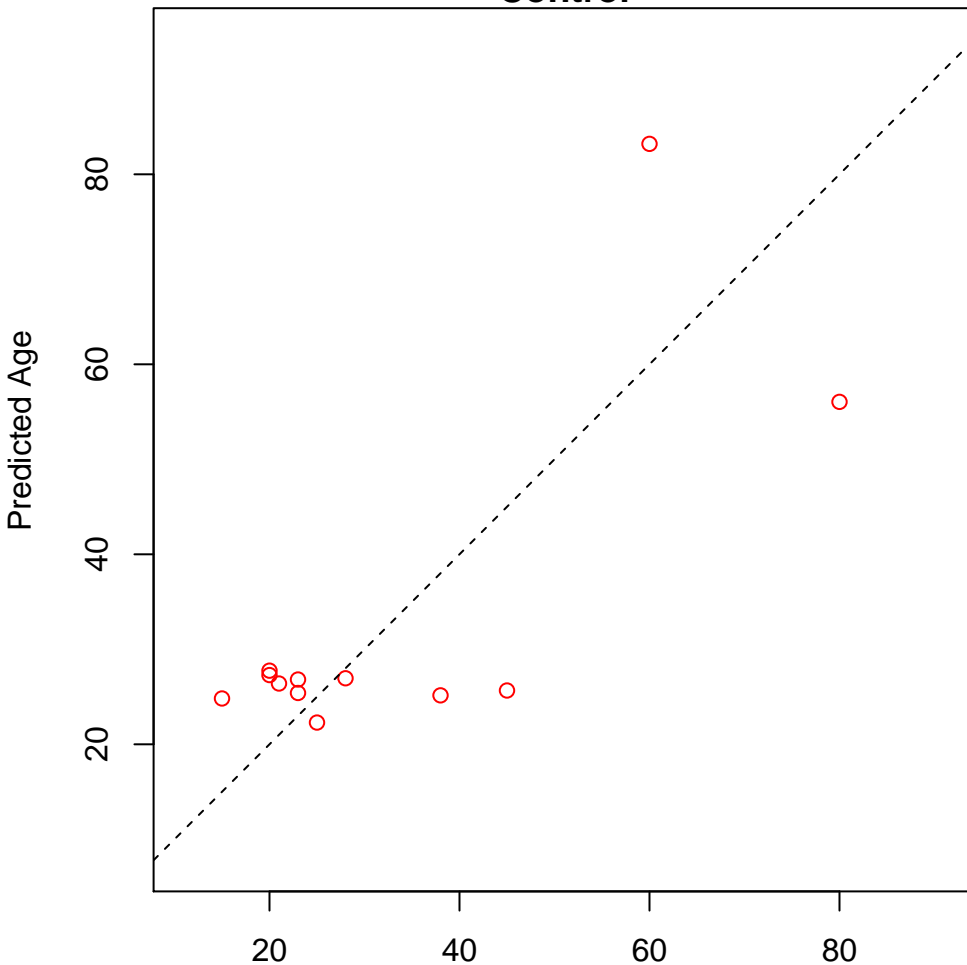


regulation of centrosome cycle (Score: 3.953397)

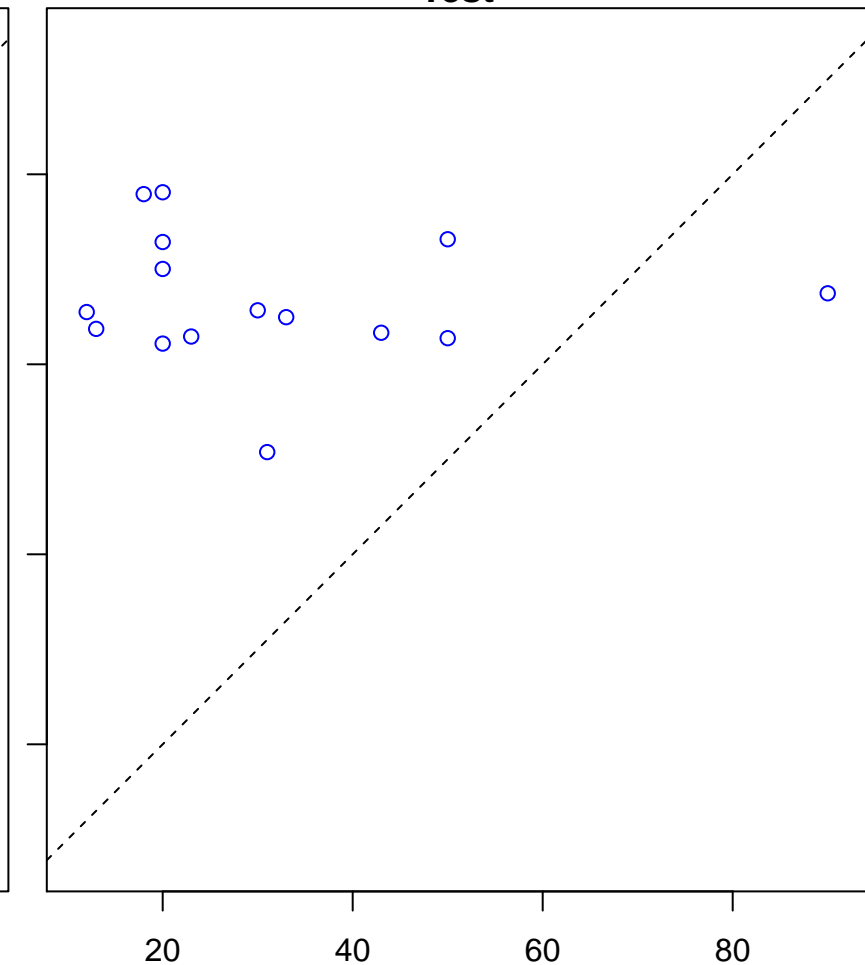


regulation of centrosome duplication (Score: 3.951786)

Control

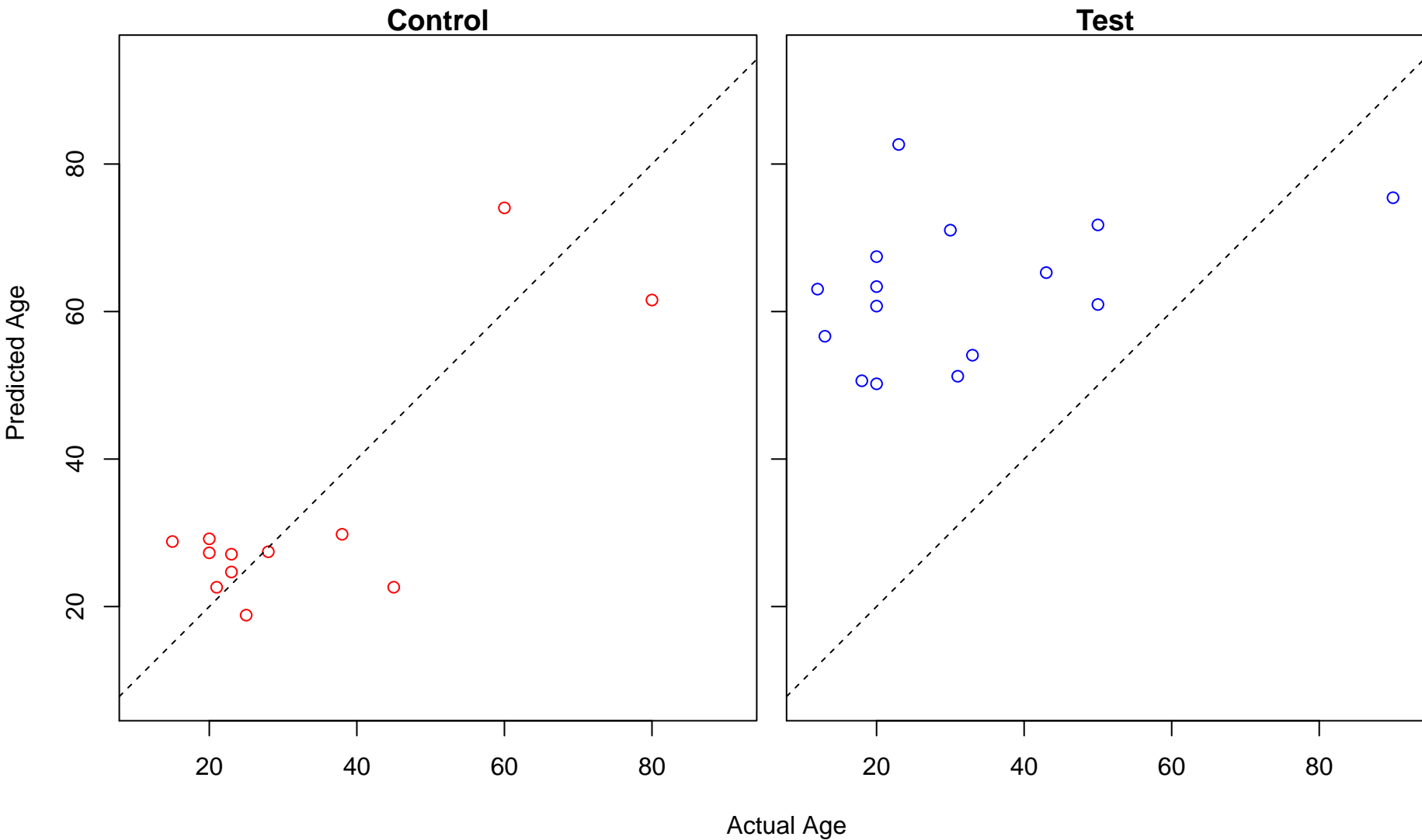


Test

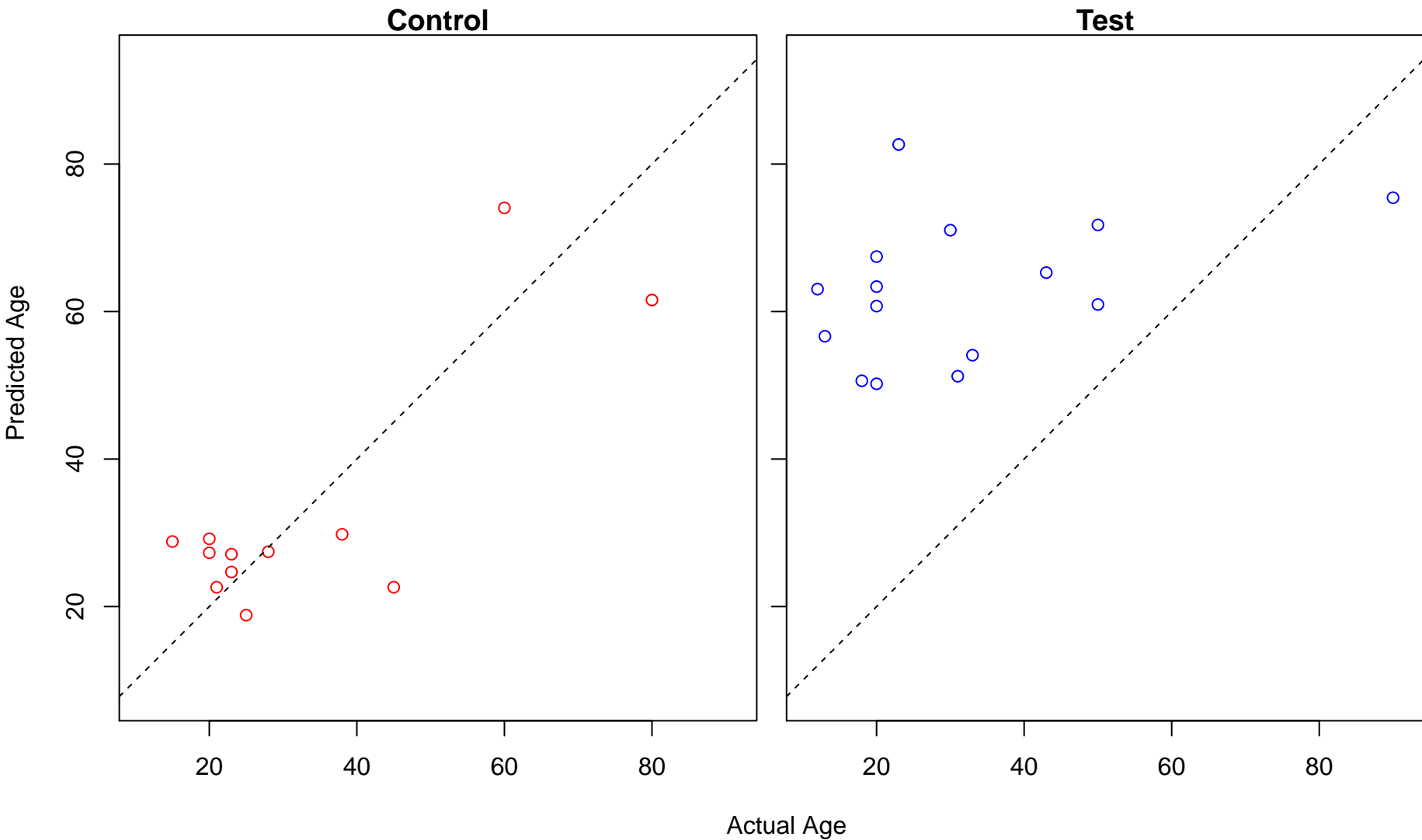


Actual Age

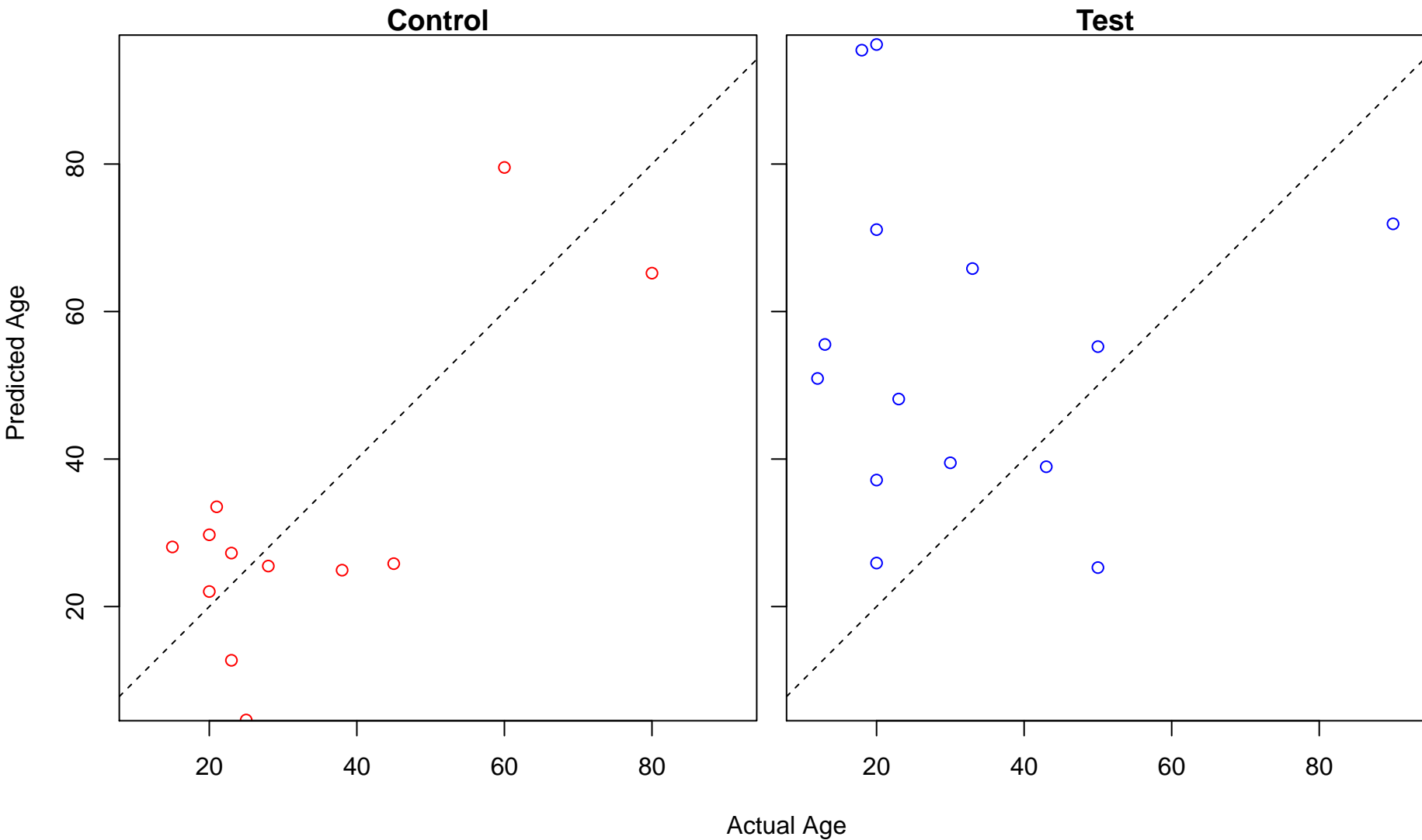
regulation of protein localization to early endosome (Score: 3.951615)



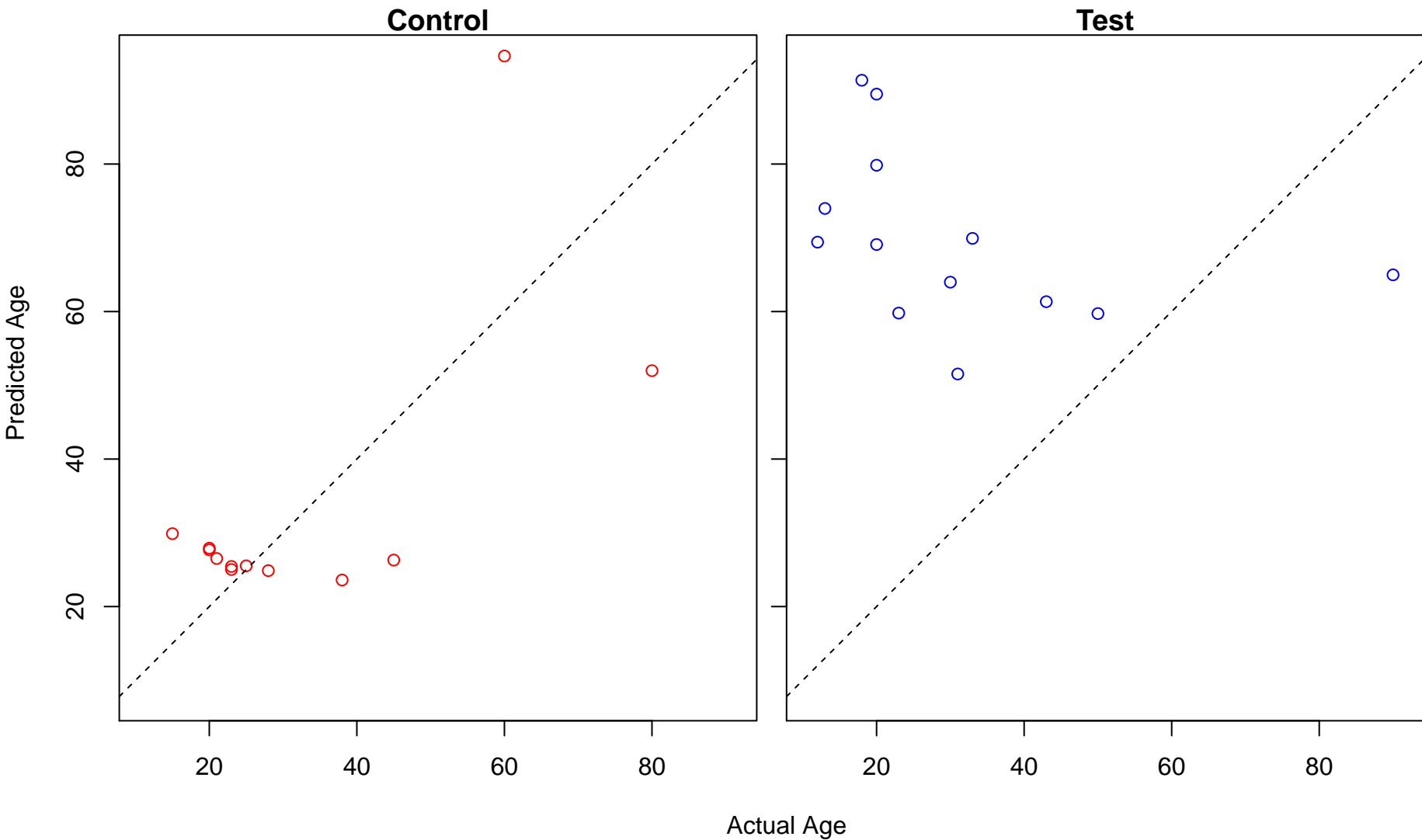
positive regulation of protein localization to early endosome (Score: 3.951615)



pantothenate metabolic process (Score: 3.950528)

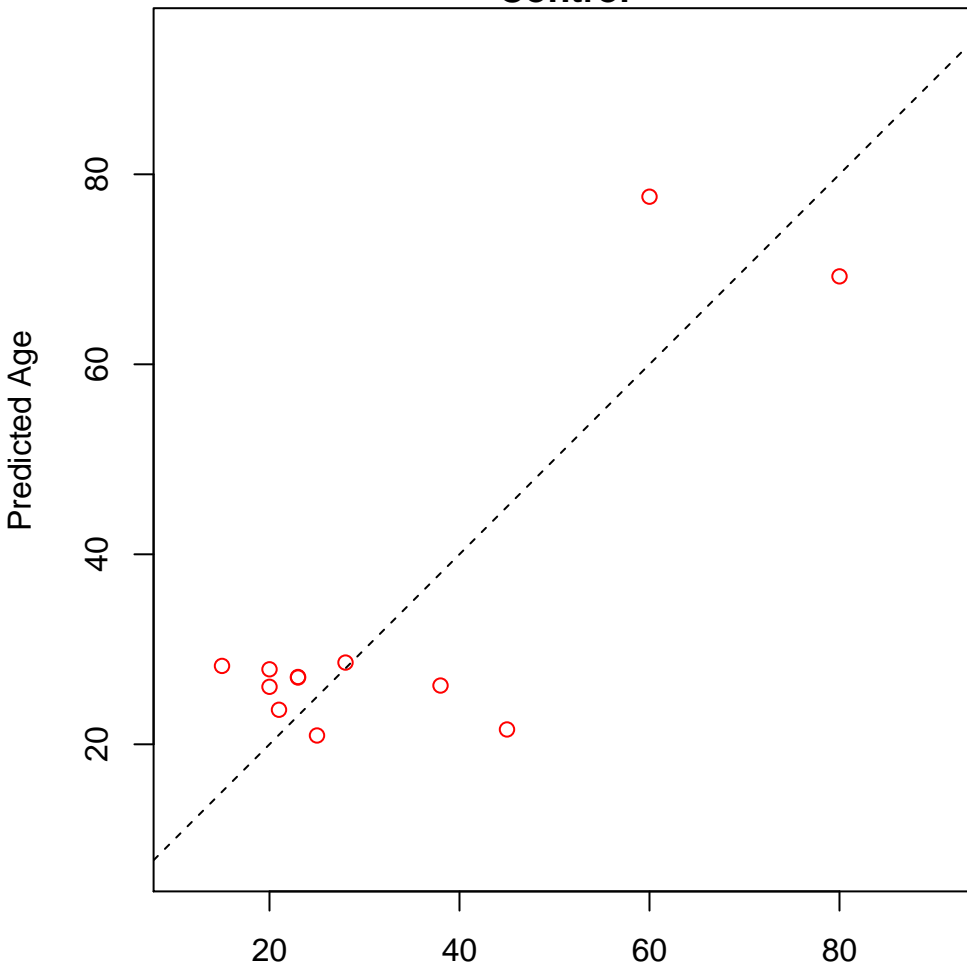


positive regulation of transcription regulatory region DNA binding (Score: 3.946837)

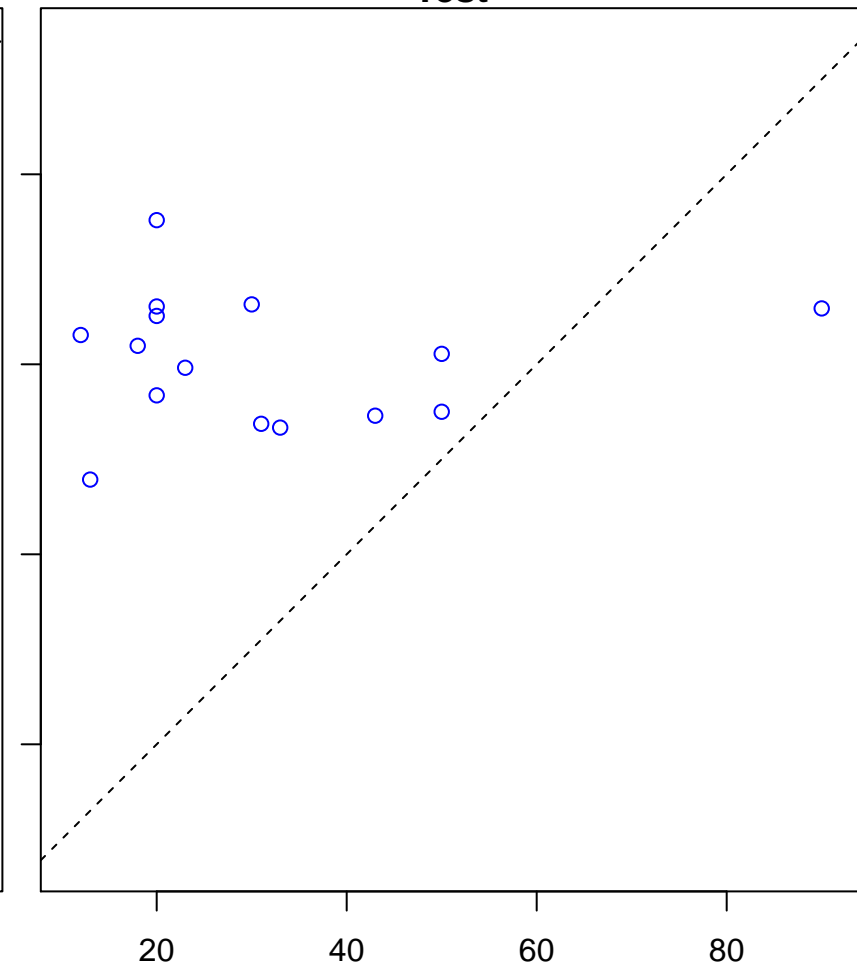


ER to Golgi vesicle-mediated transport (Score: 3.946761)

Control

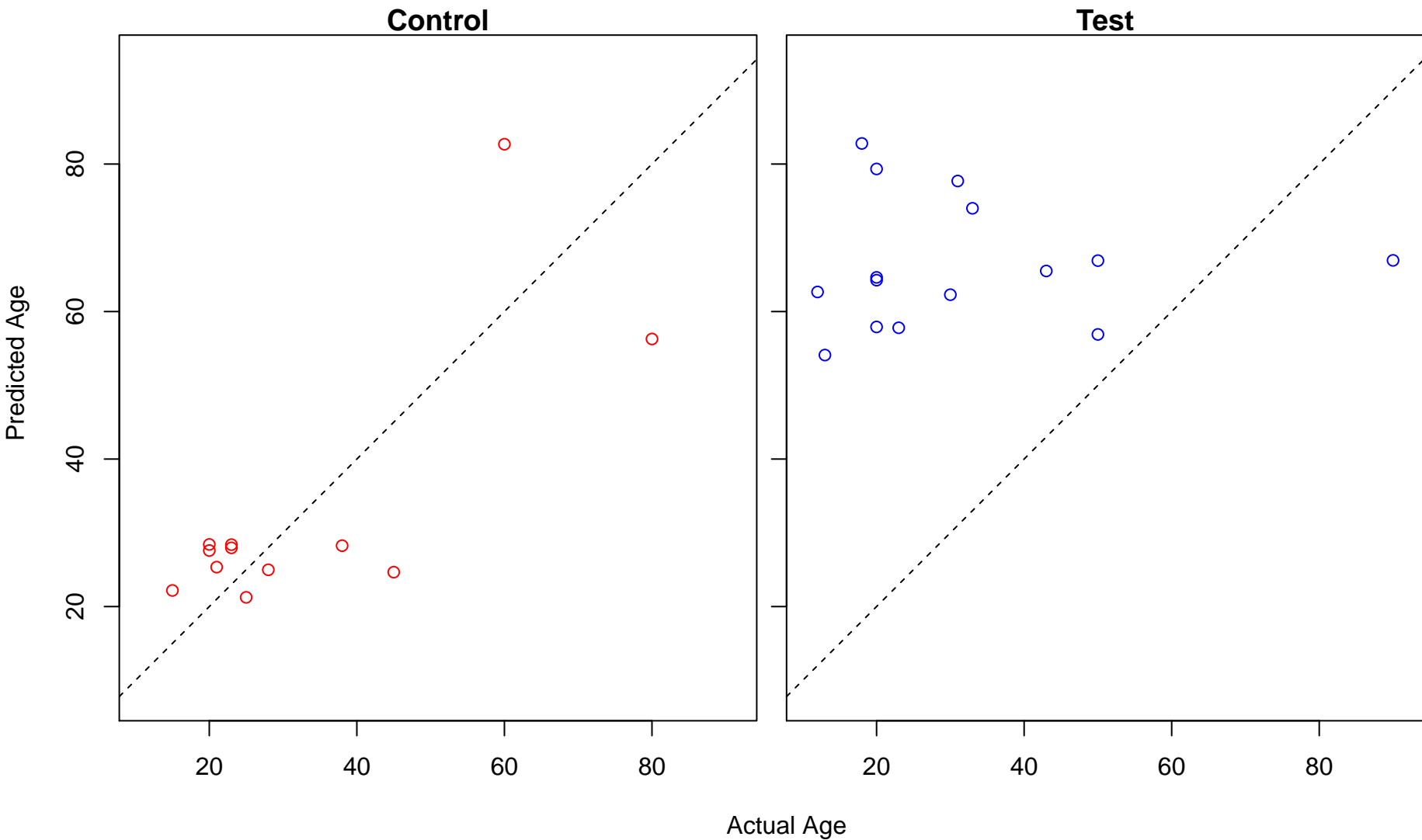


Test

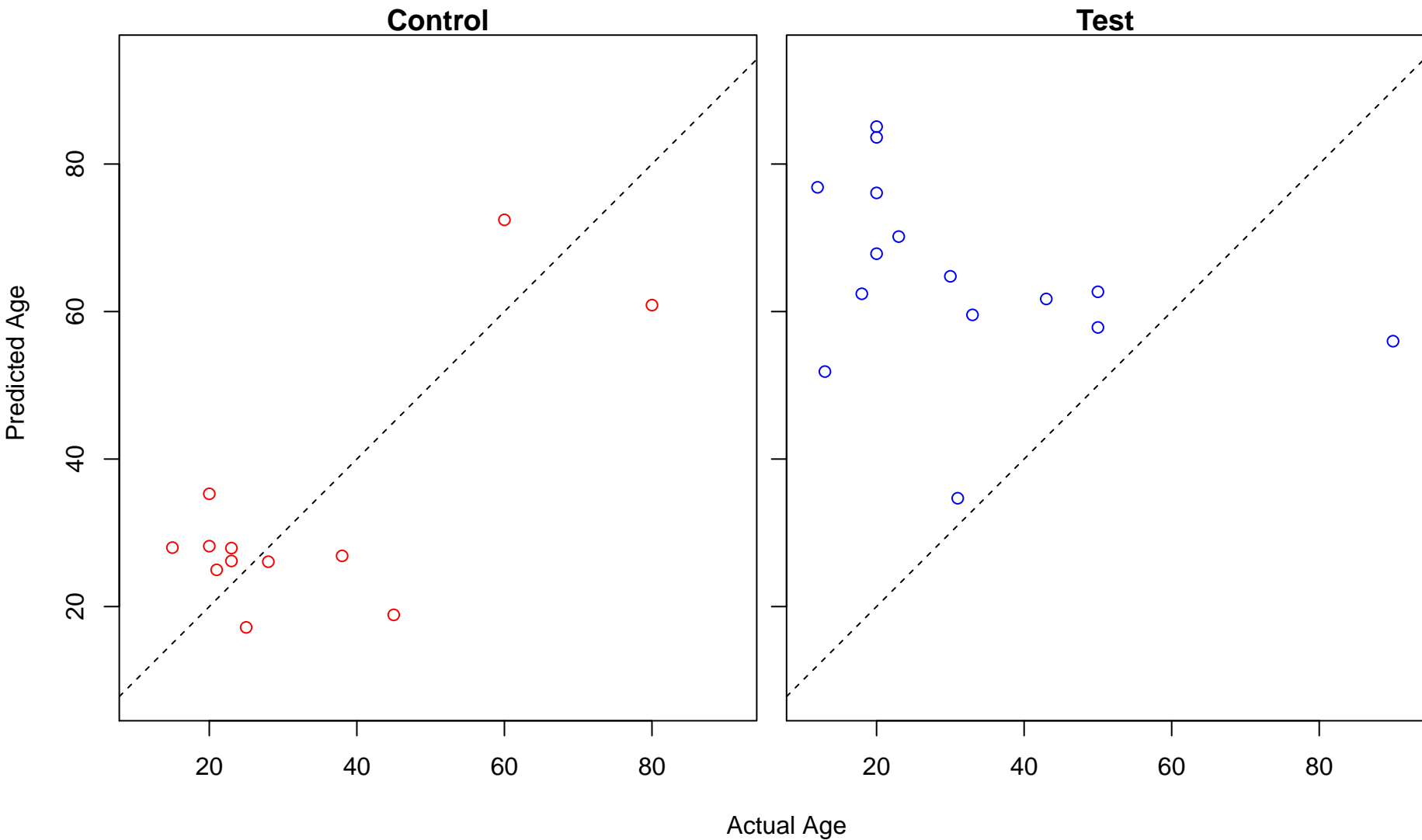


Actual Age

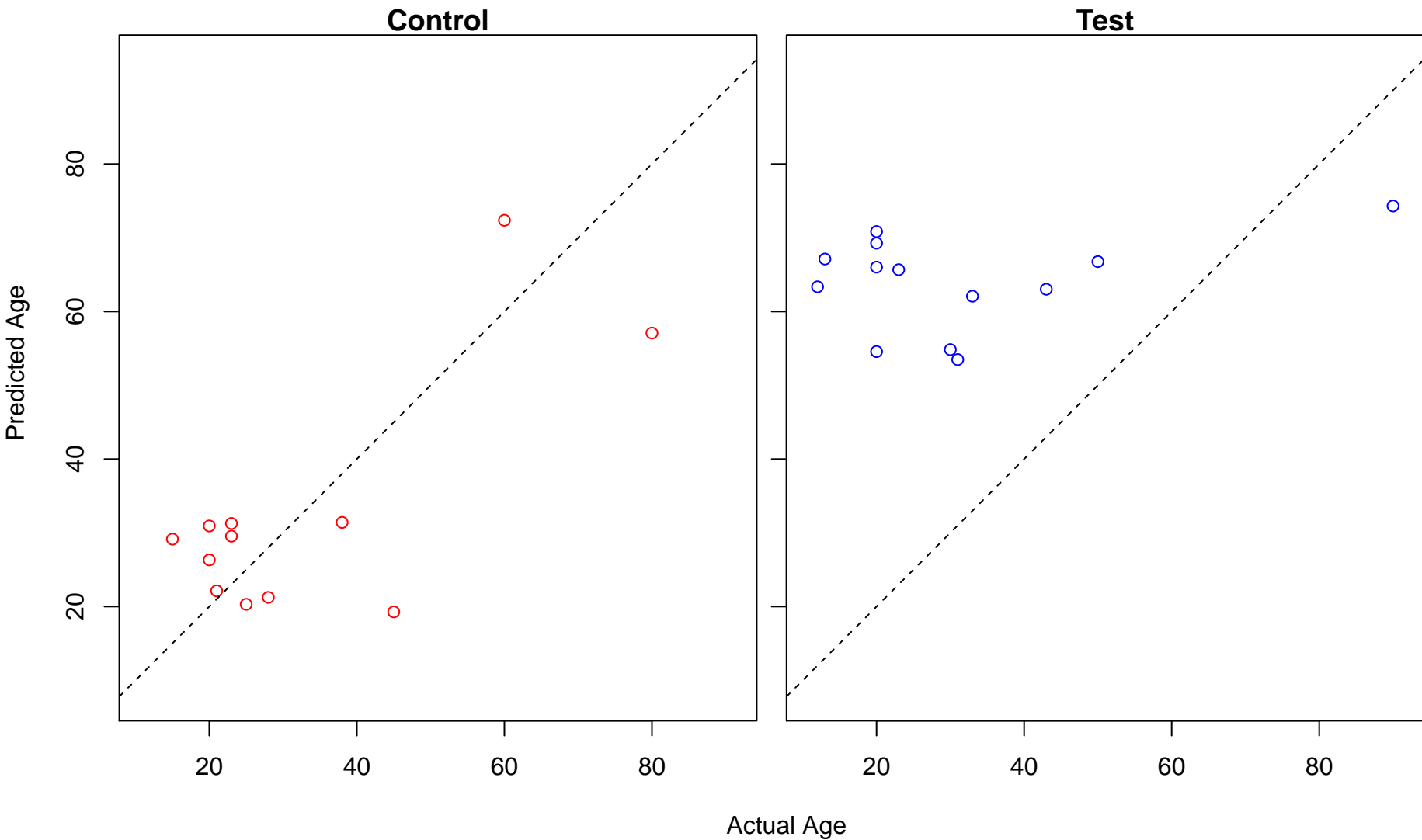
neuromuscular process (Score: 3.946152)



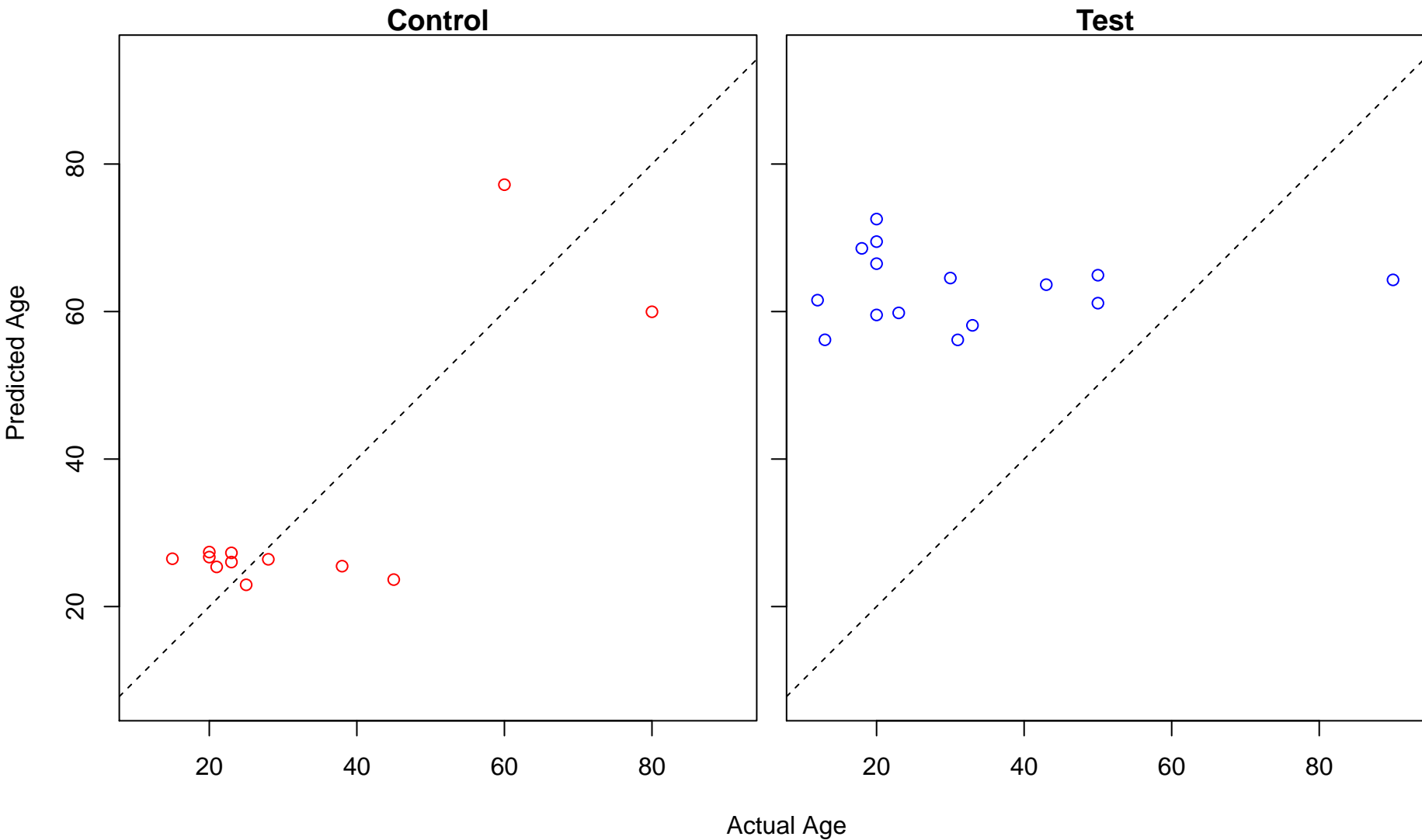
L-serine metabolic process (Score: 3.945337)



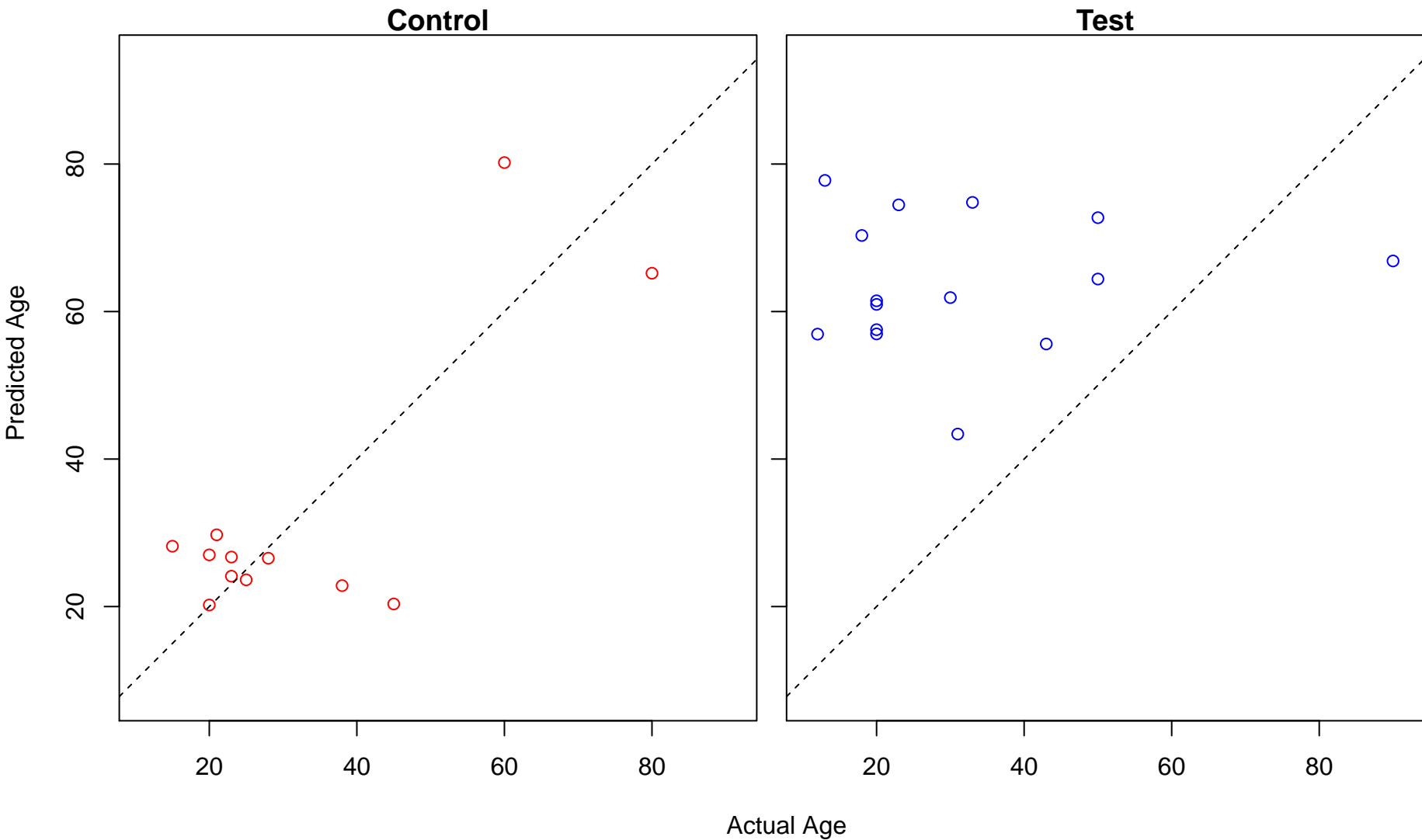
cardiac ventricle formation (Score: 3.944494)



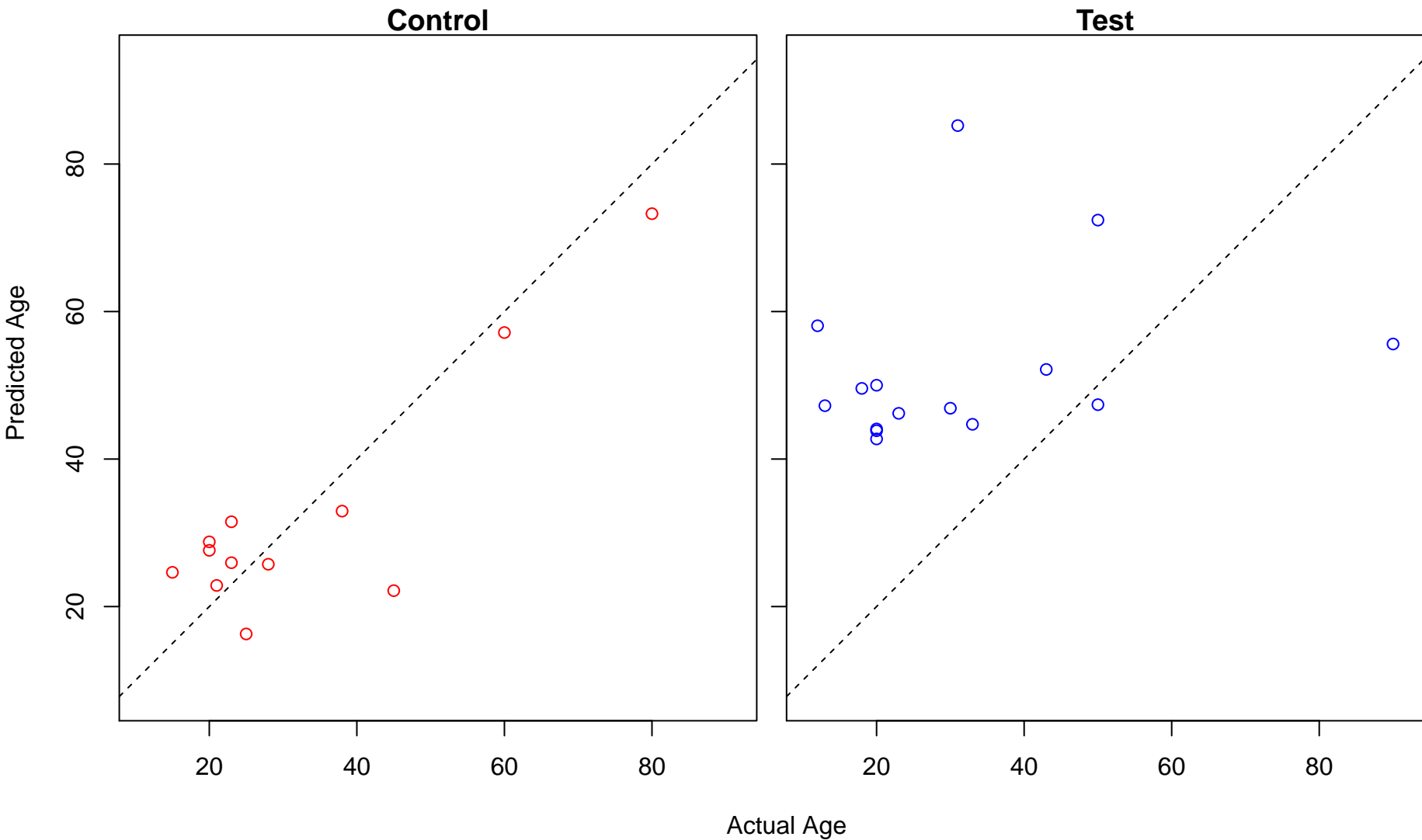
cofactor biosynthetic process (Score: 3.943652)



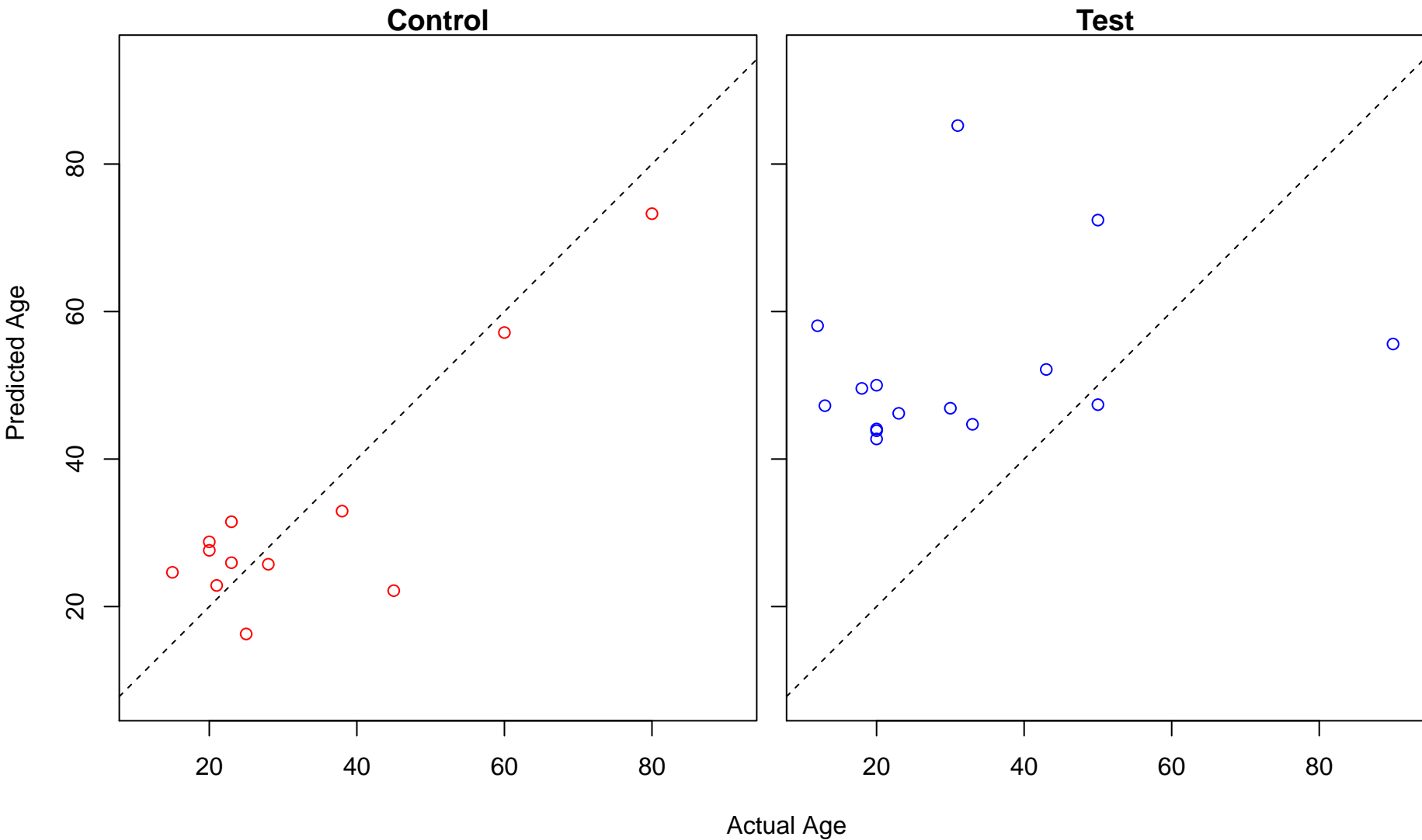
activation of JUN kinase activity (Score: 3.942693)



inorganic cation import into cell (Score: 3.942585)

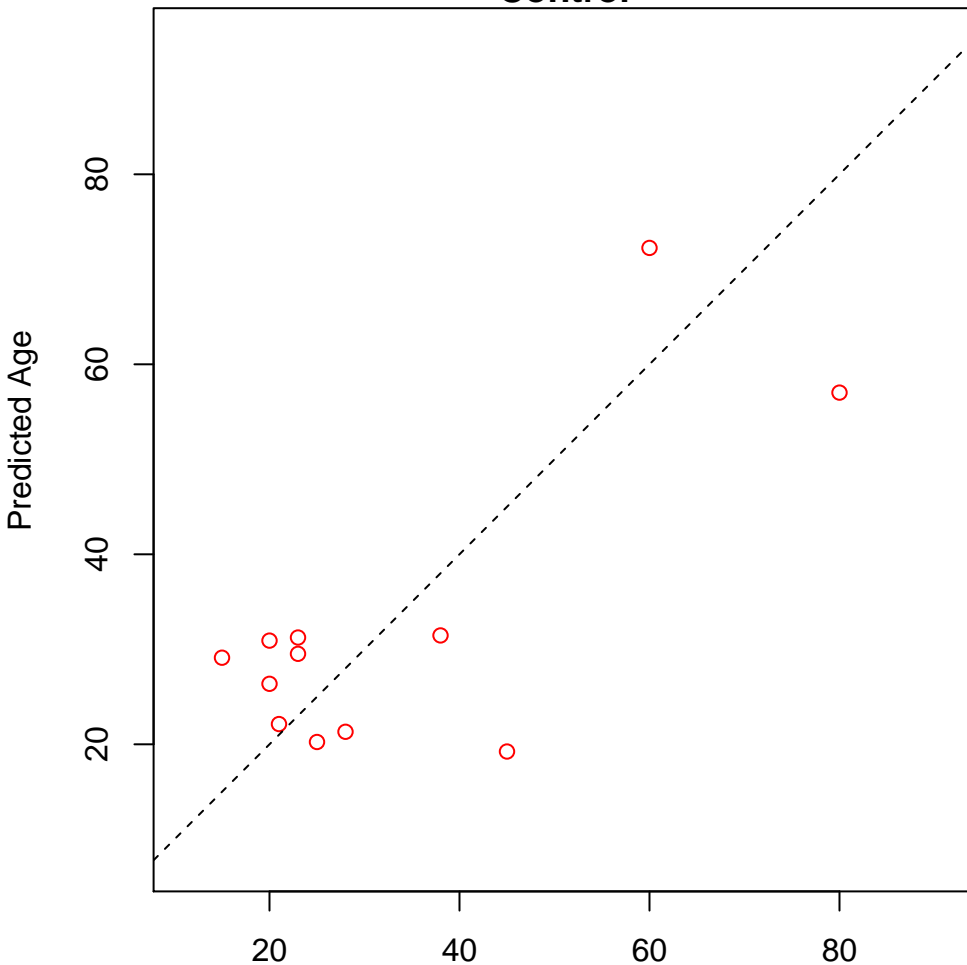


inorganic ion import into cell (Score: 3.942585)

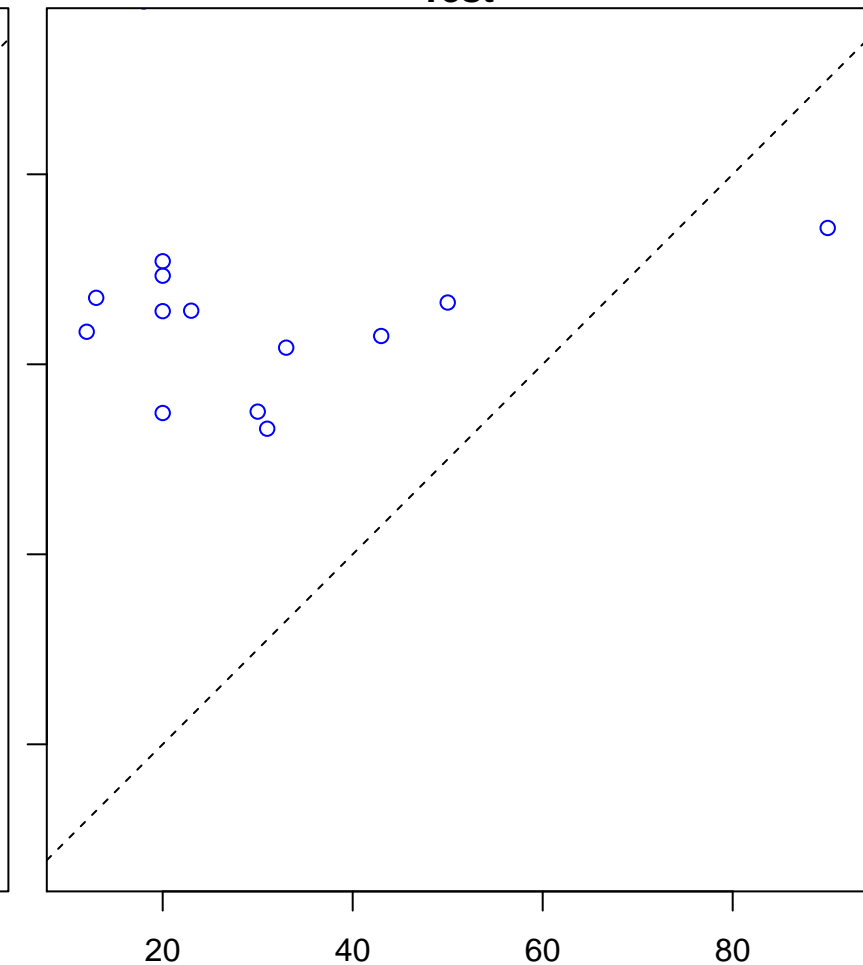


spinal cord motor neuron differentiation (Score: 3.939742)

Control

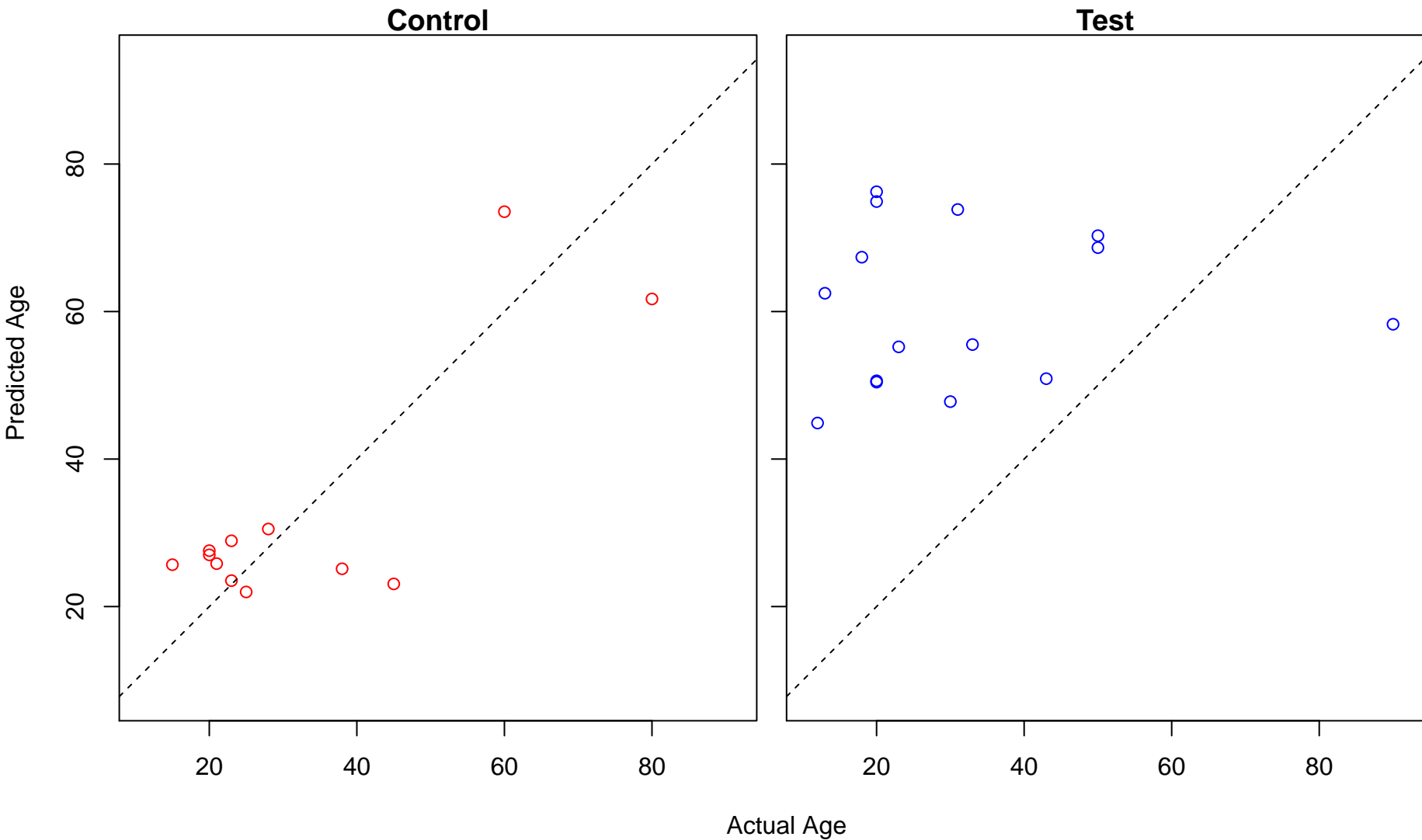


Test

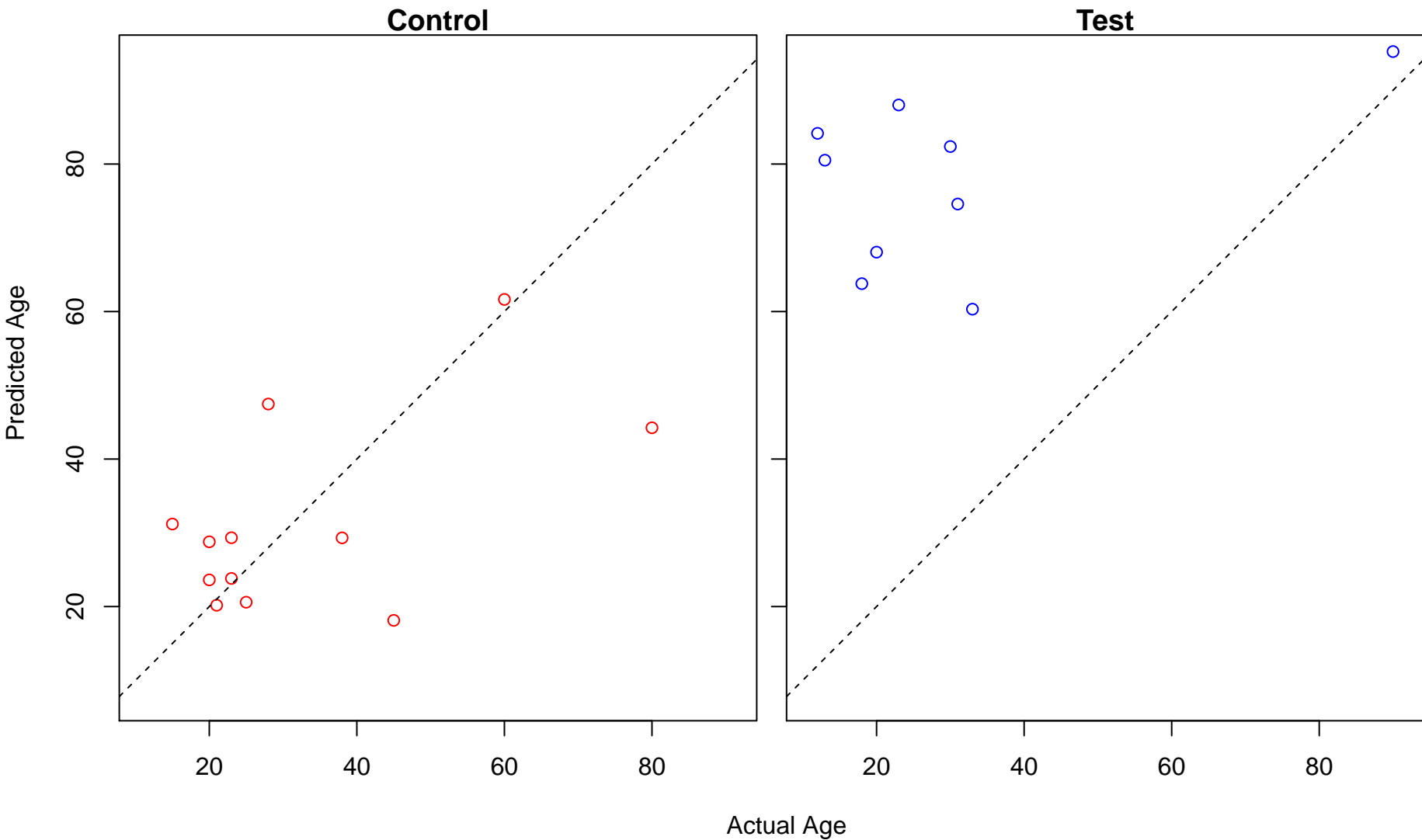


Actual Age

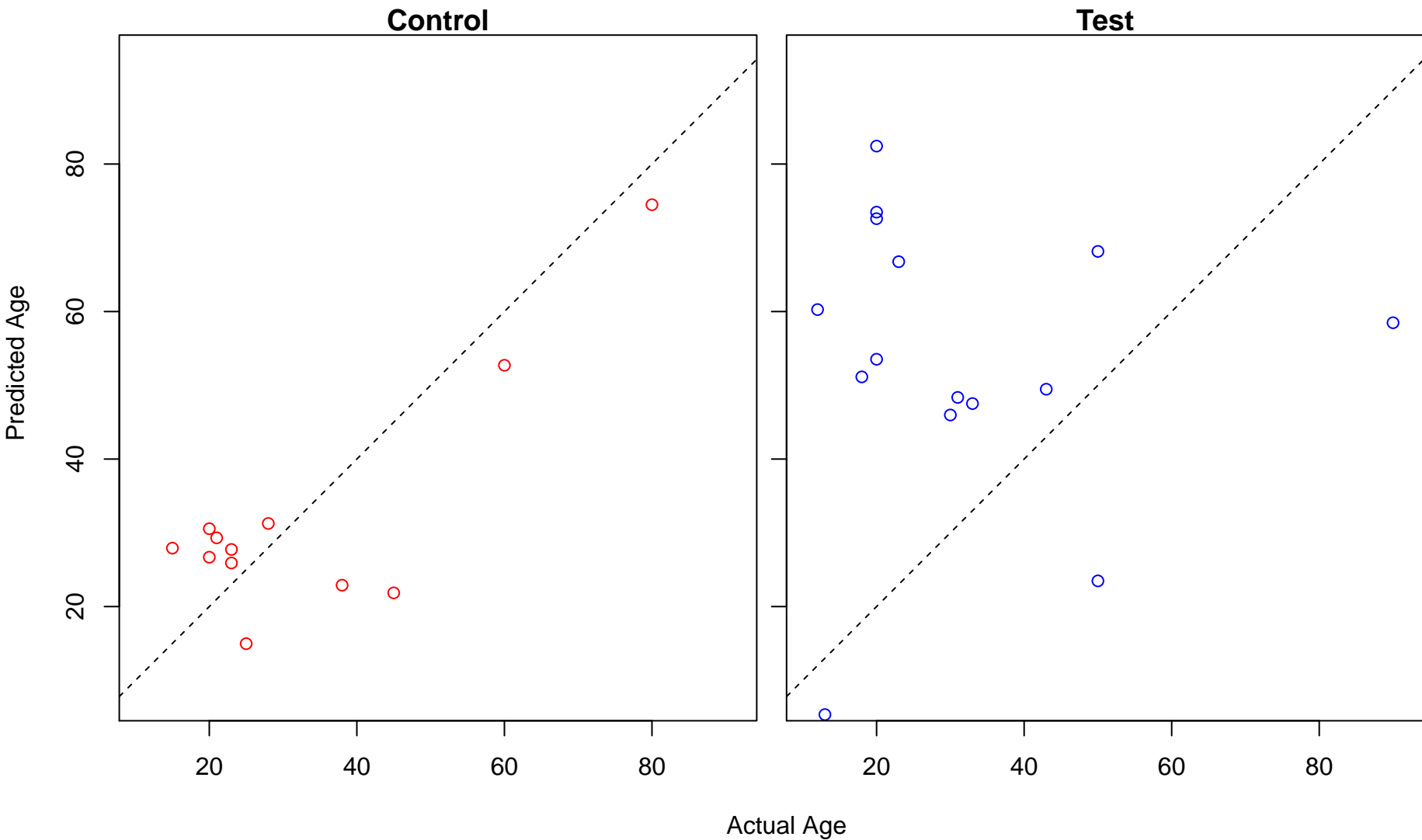
regulation of protein autophosphorylation (Score: 3.938674)



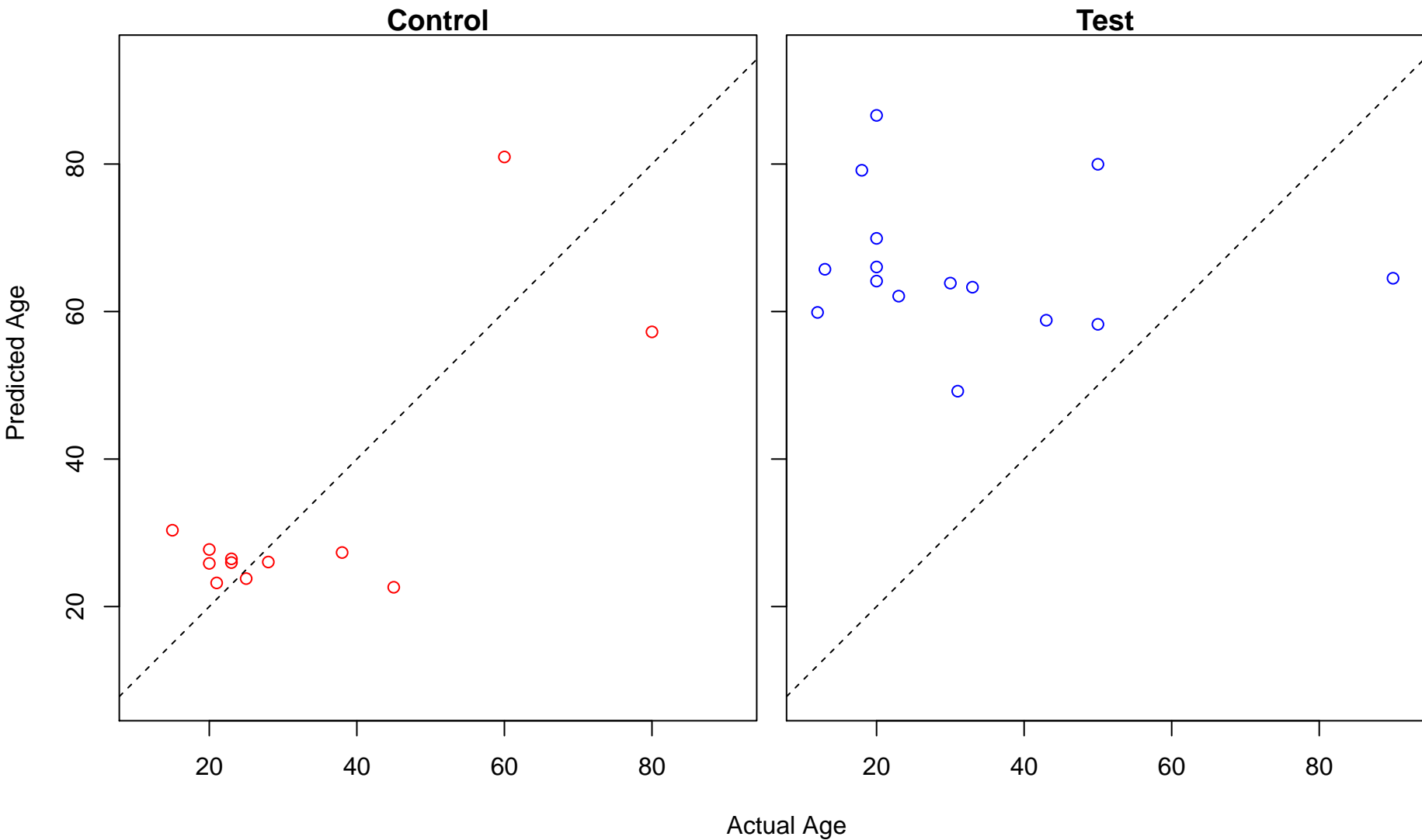
negative regulation of protein oligomerization (Score: 3.937540)



organonitrogen compound catabolic process (Score: 3.935608)

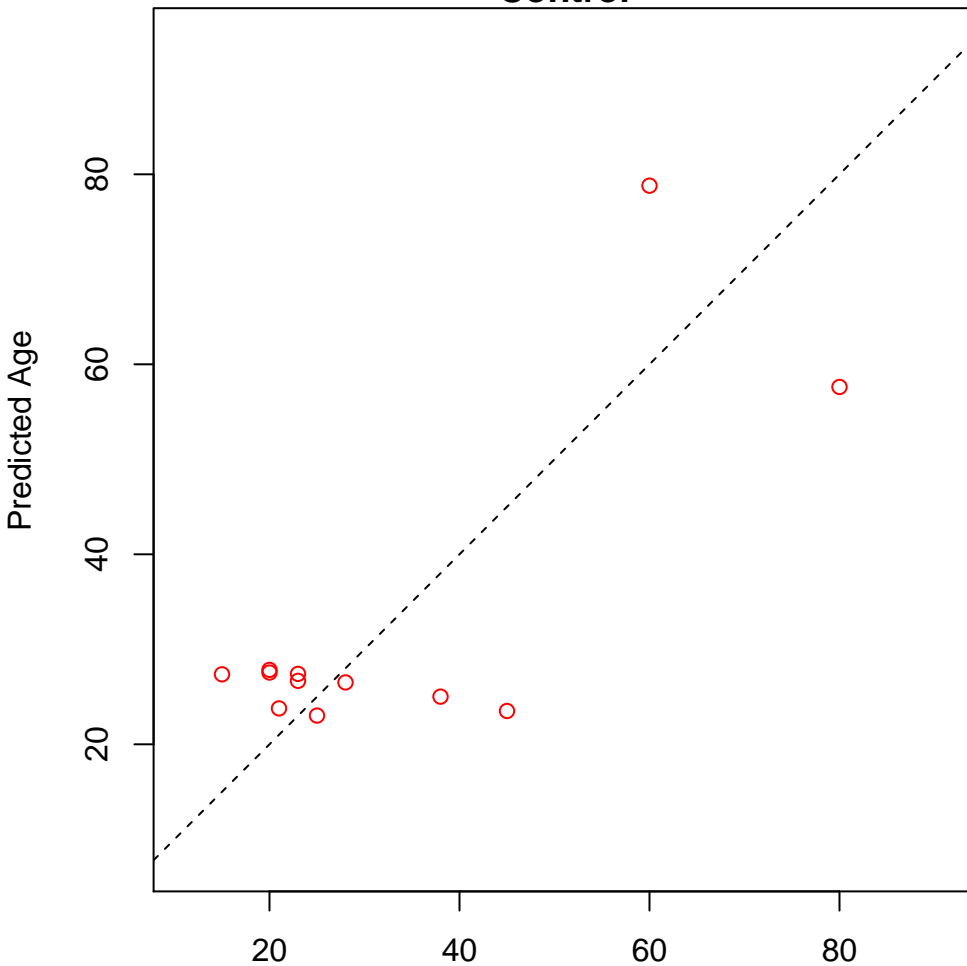


small molecule catabolic process (Score: 3.935556)

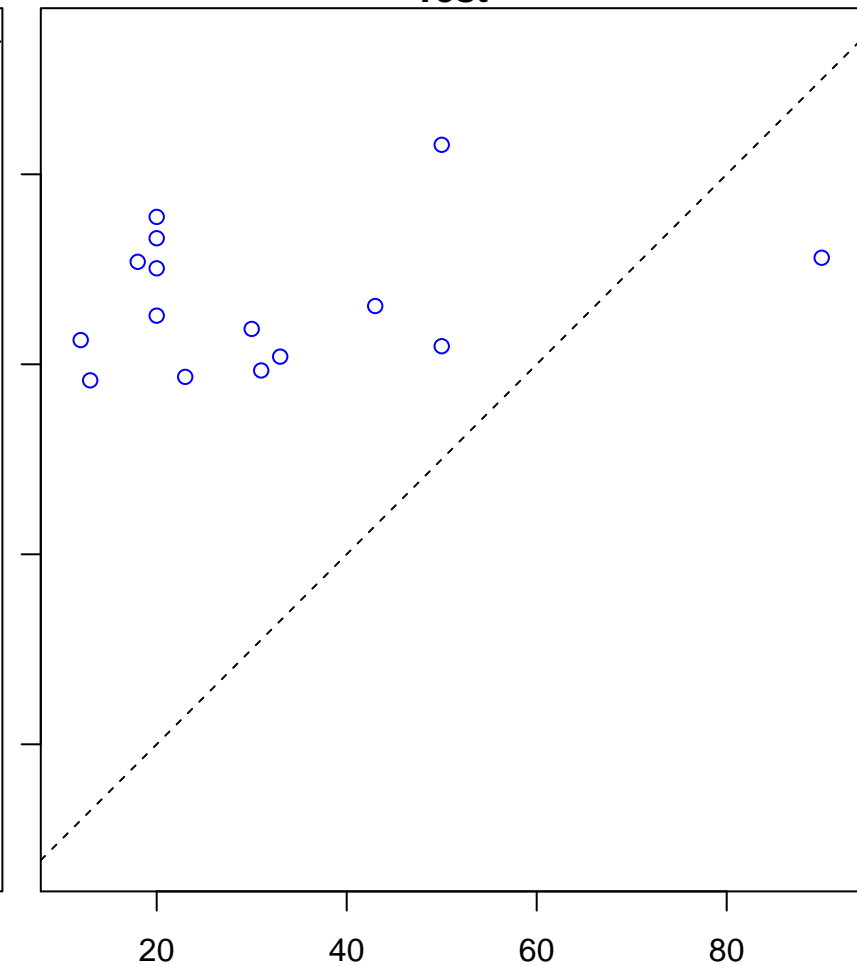


embryonic digit morphogenesis (Score: 3.931657)

Control

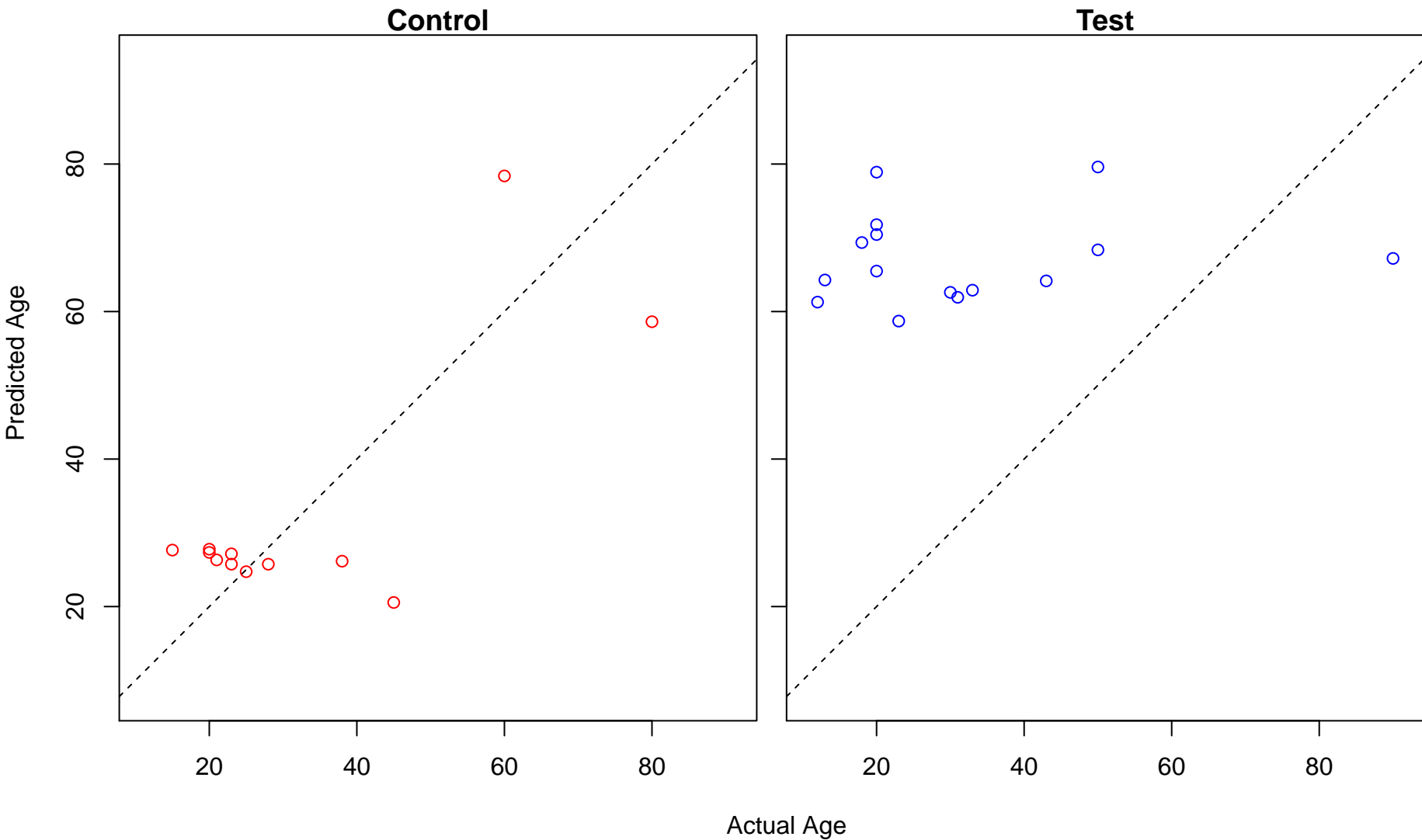


Test

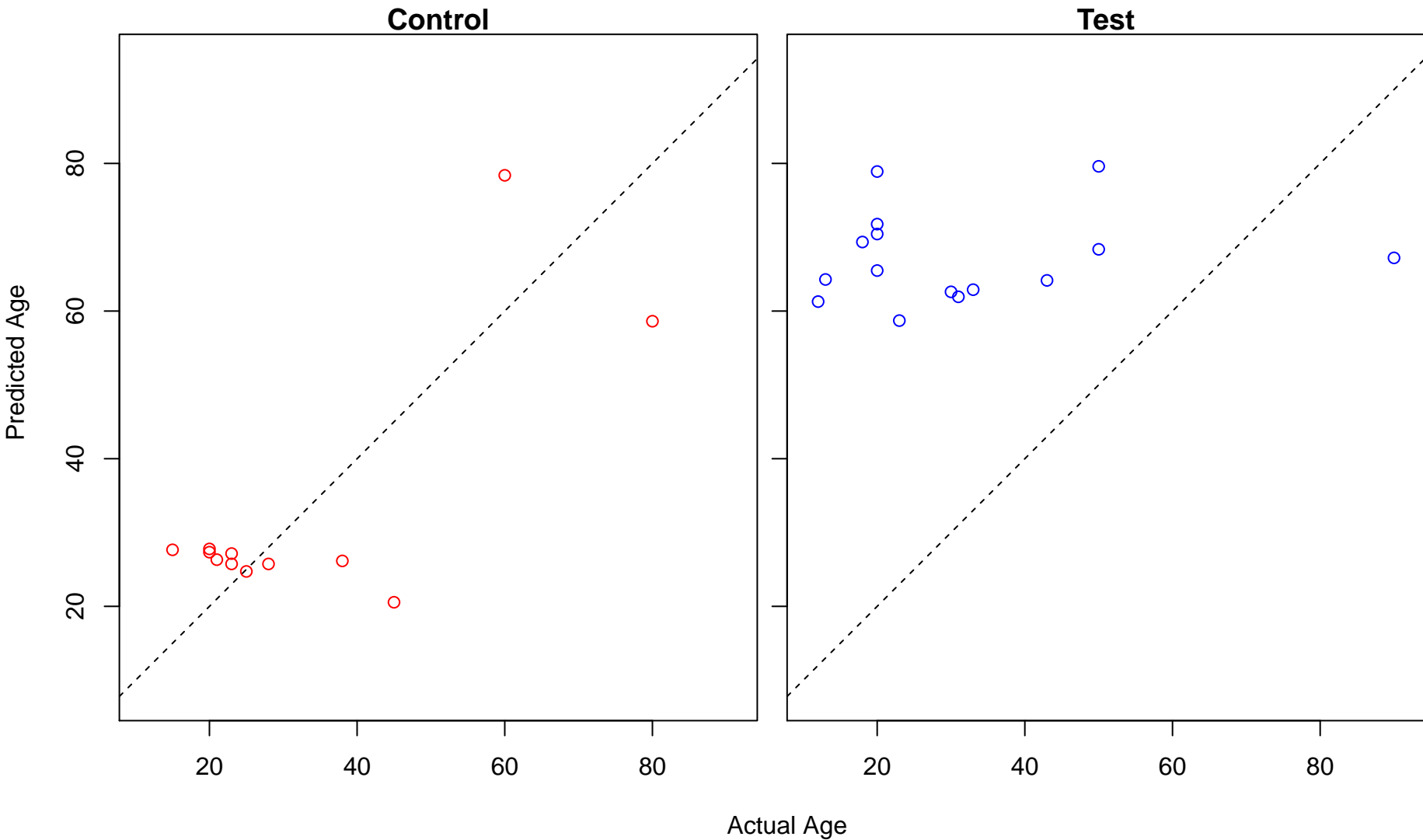


Actual Age

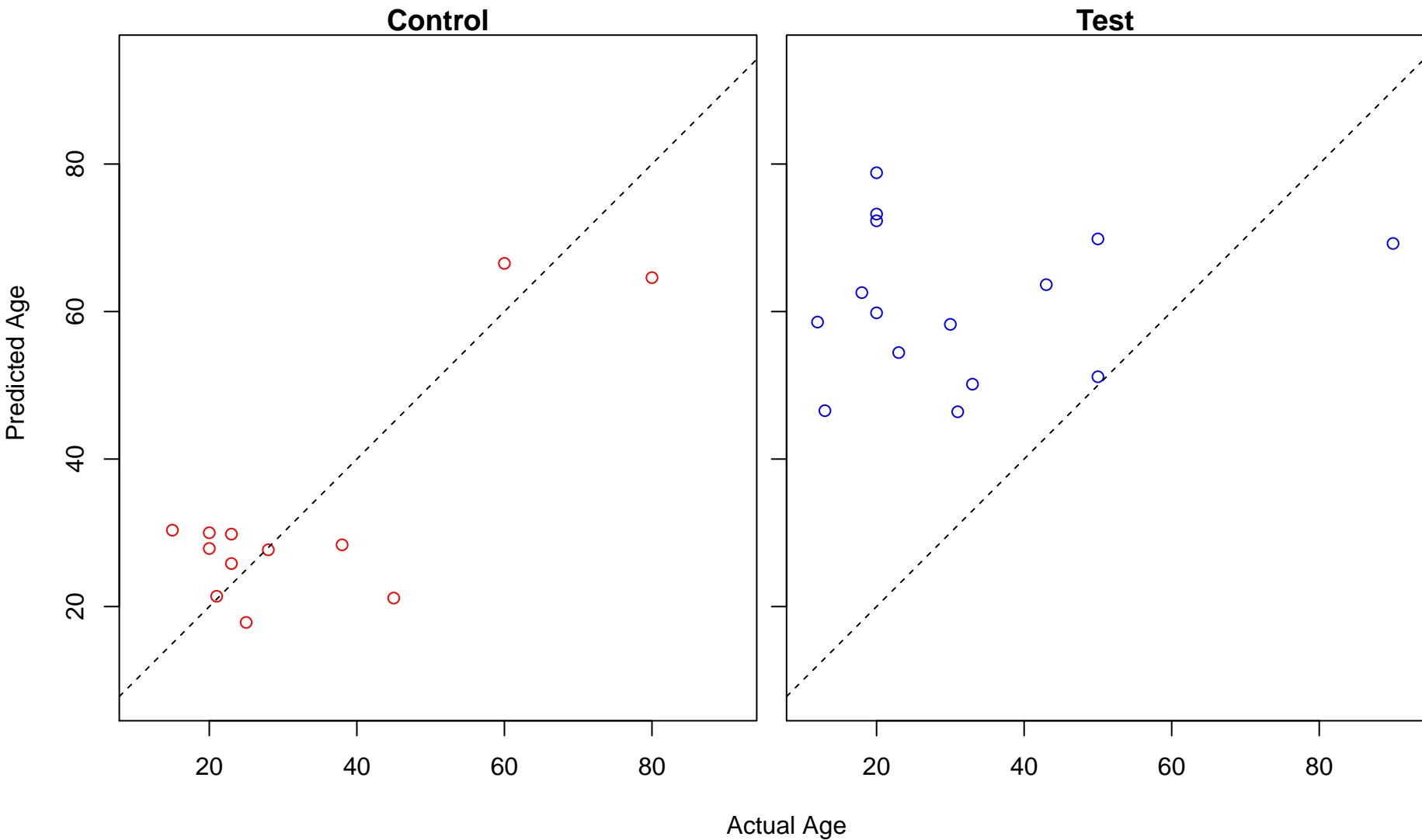
regulation of maintenance of sister chromatid cohesion (Score: 3.929699)



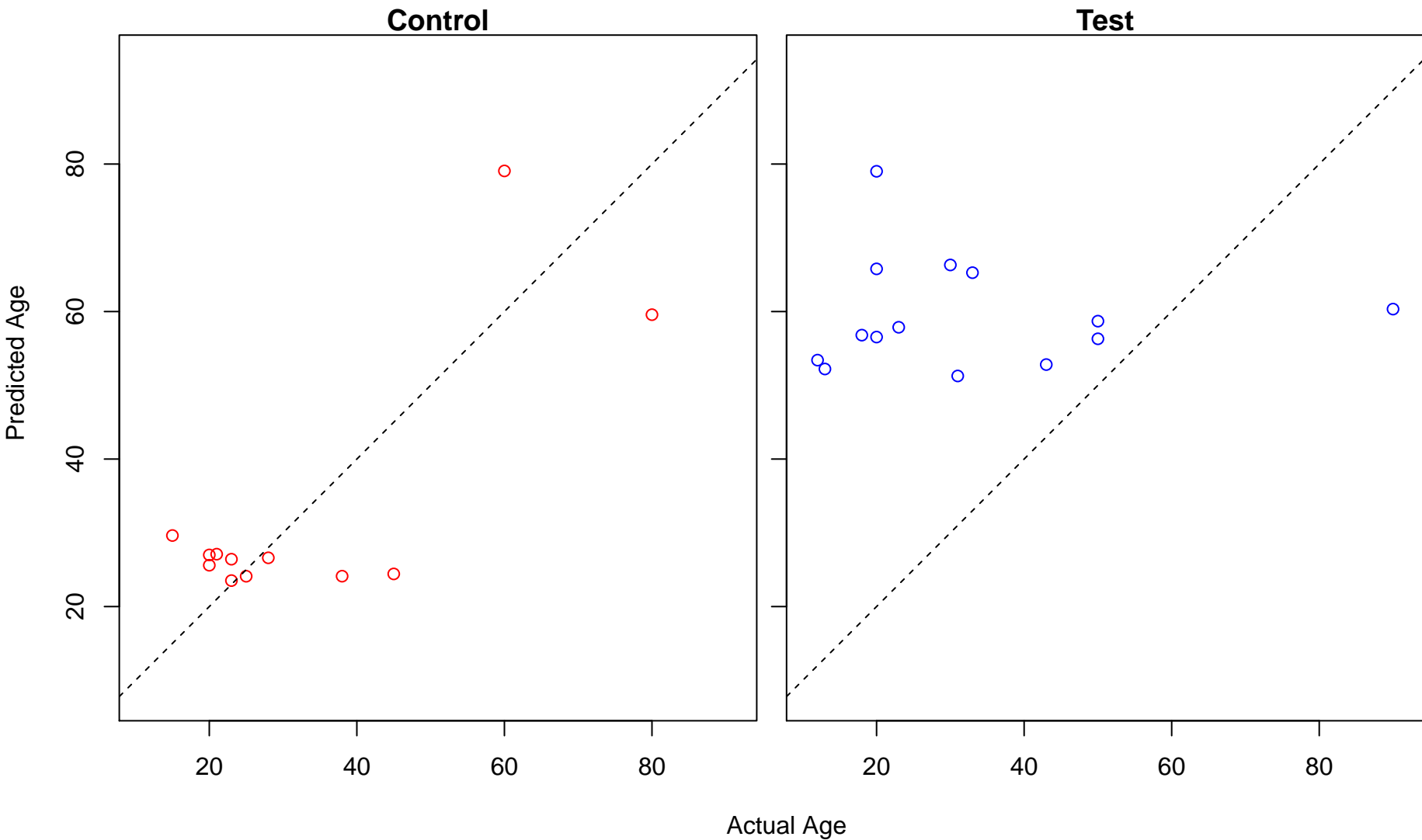
regulation of maintenance of mitotic sister chromatid cohesion (Score: 3.929699)



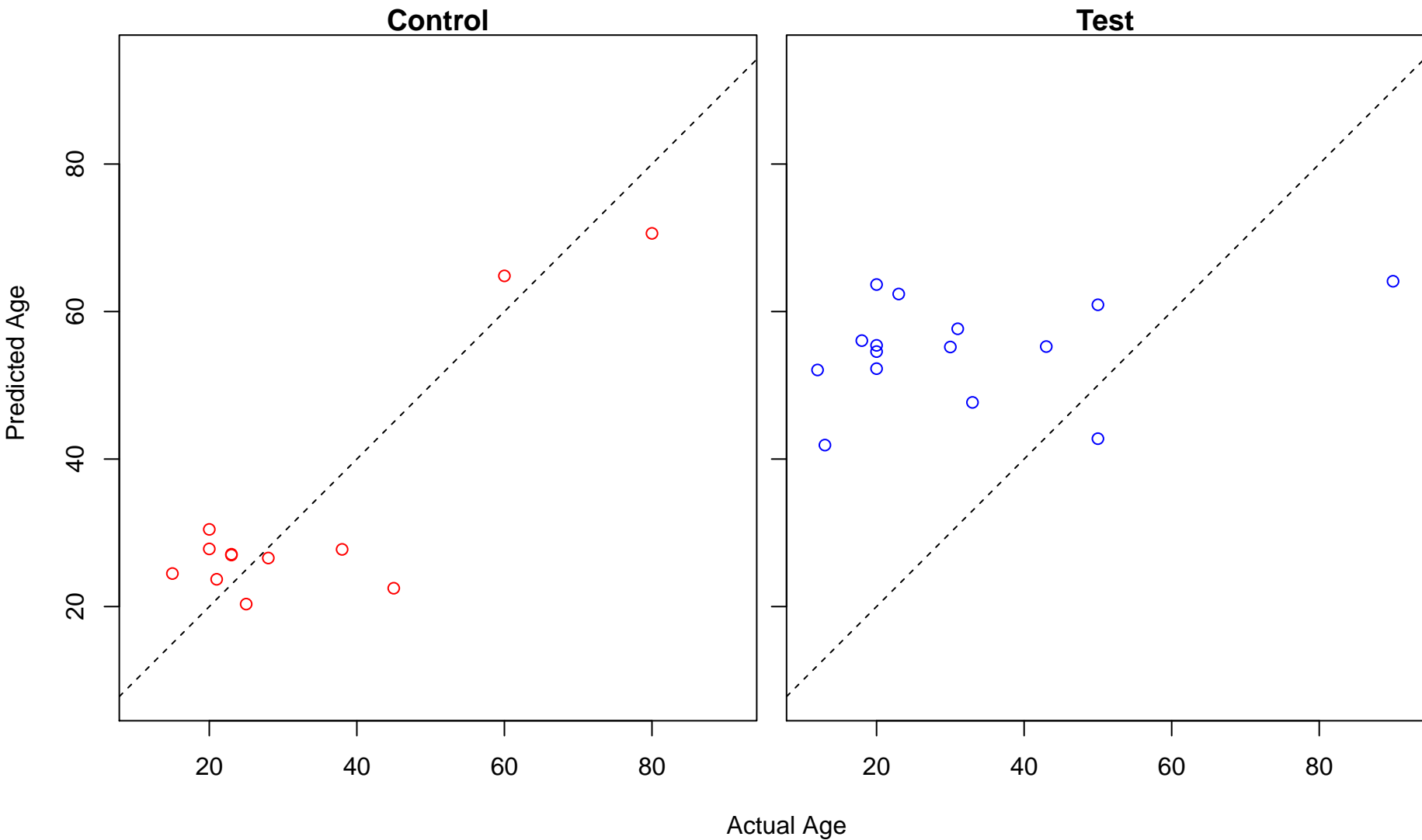
cellular glucose homeostasis (Score: 3.928437)



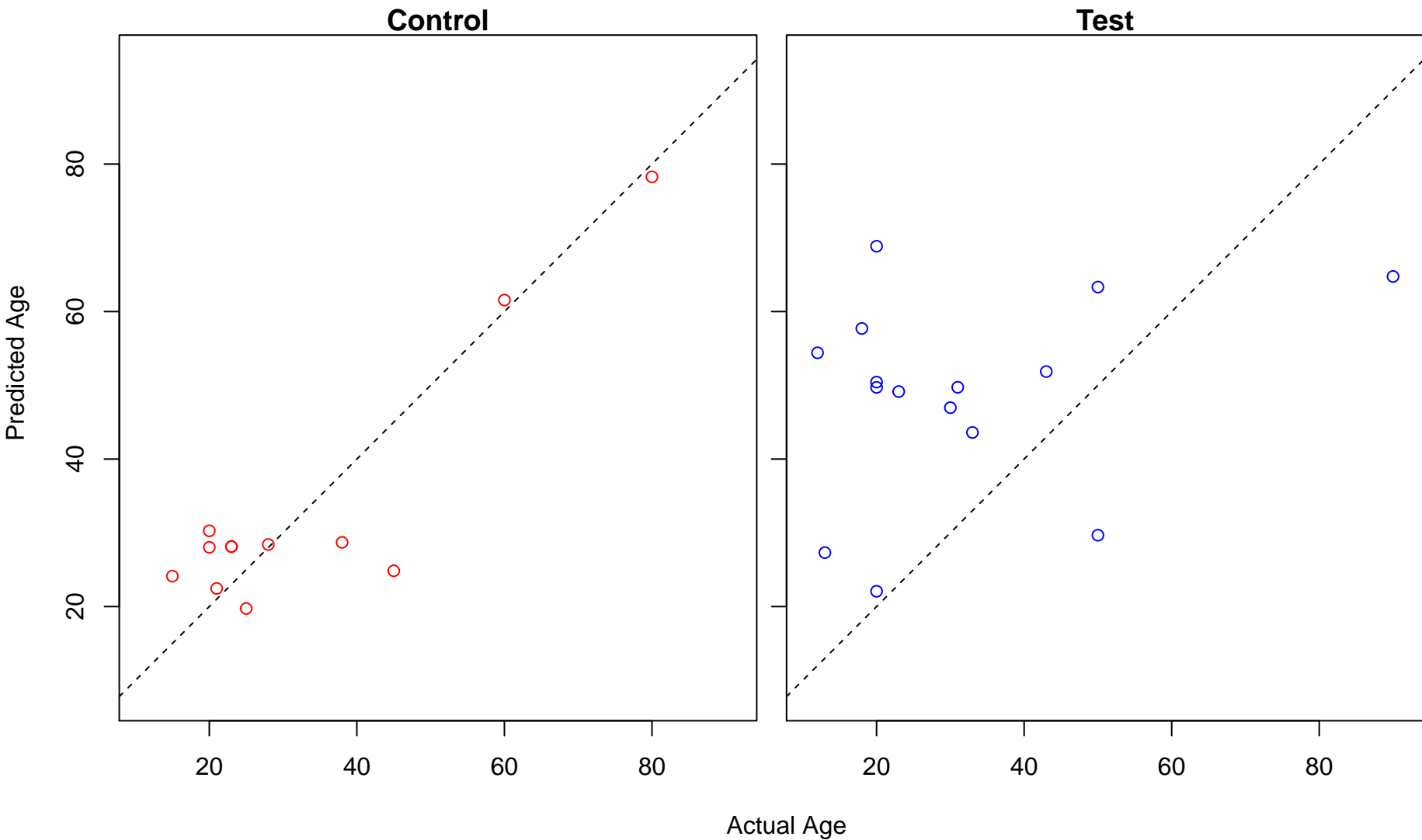
regulation of viral budding via host ESCRT complex (Score: 3.926021)



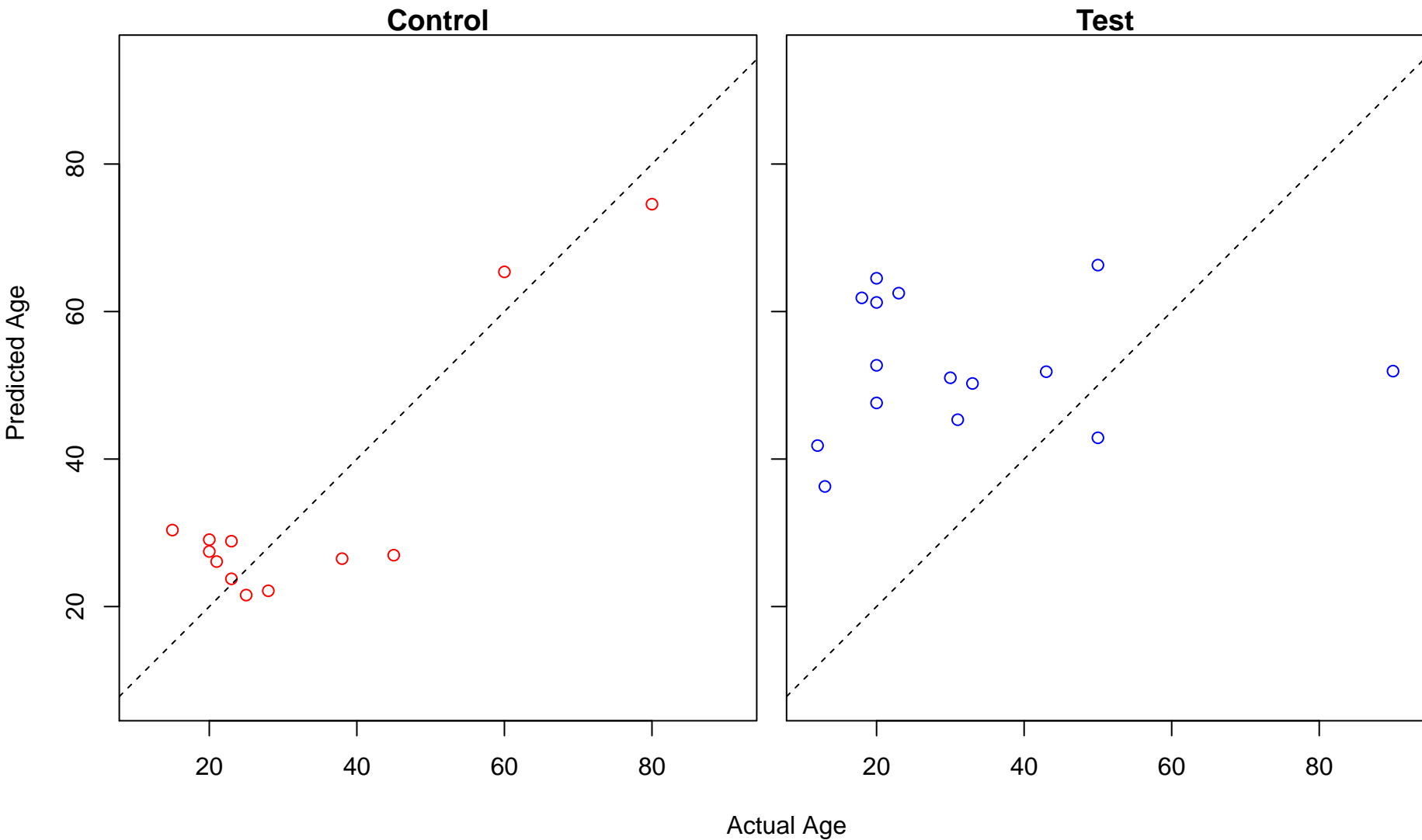
regulation of translational termination (Score: 3.925006)



negative regulation of ERAD pathway (Score: 3.921773)

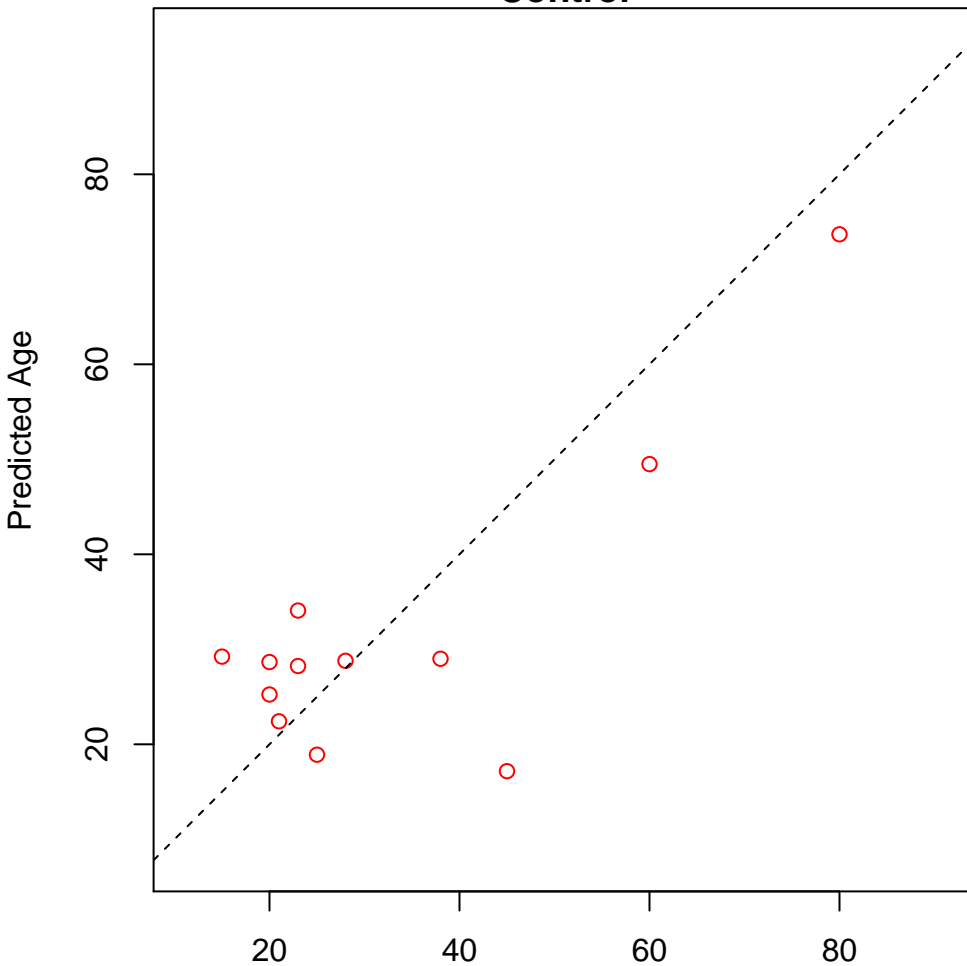


cardiac cell development (Score: 3.921768)

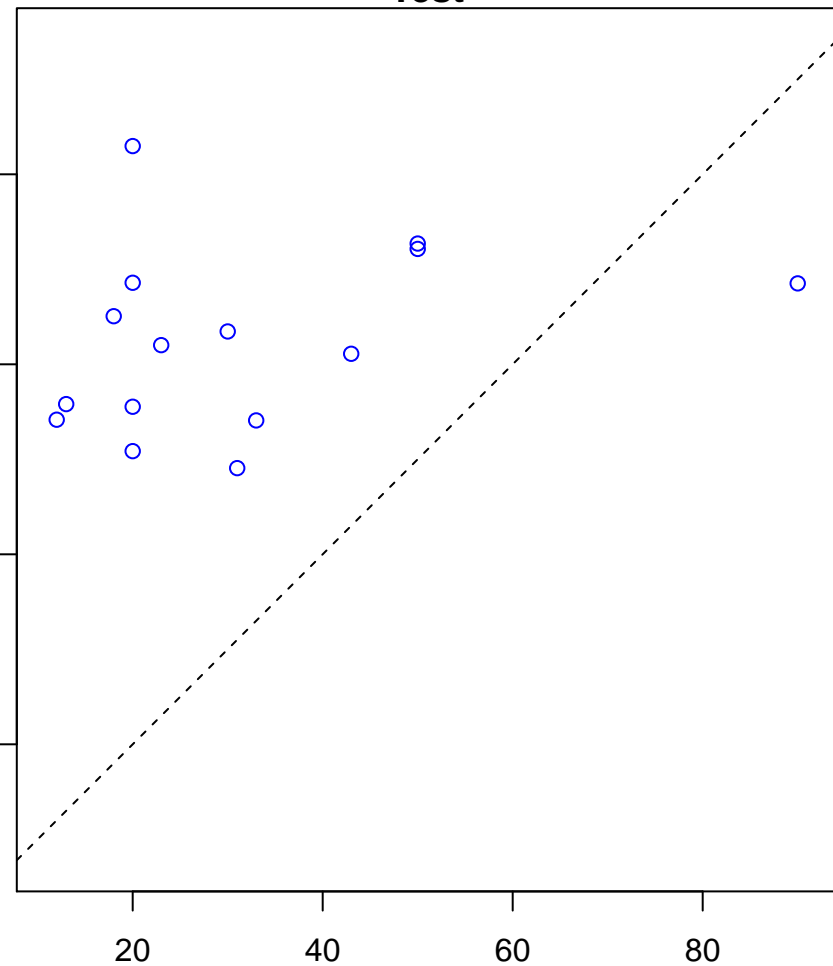


regulation of interleukin-13 production (Score: 3.920696)

Control

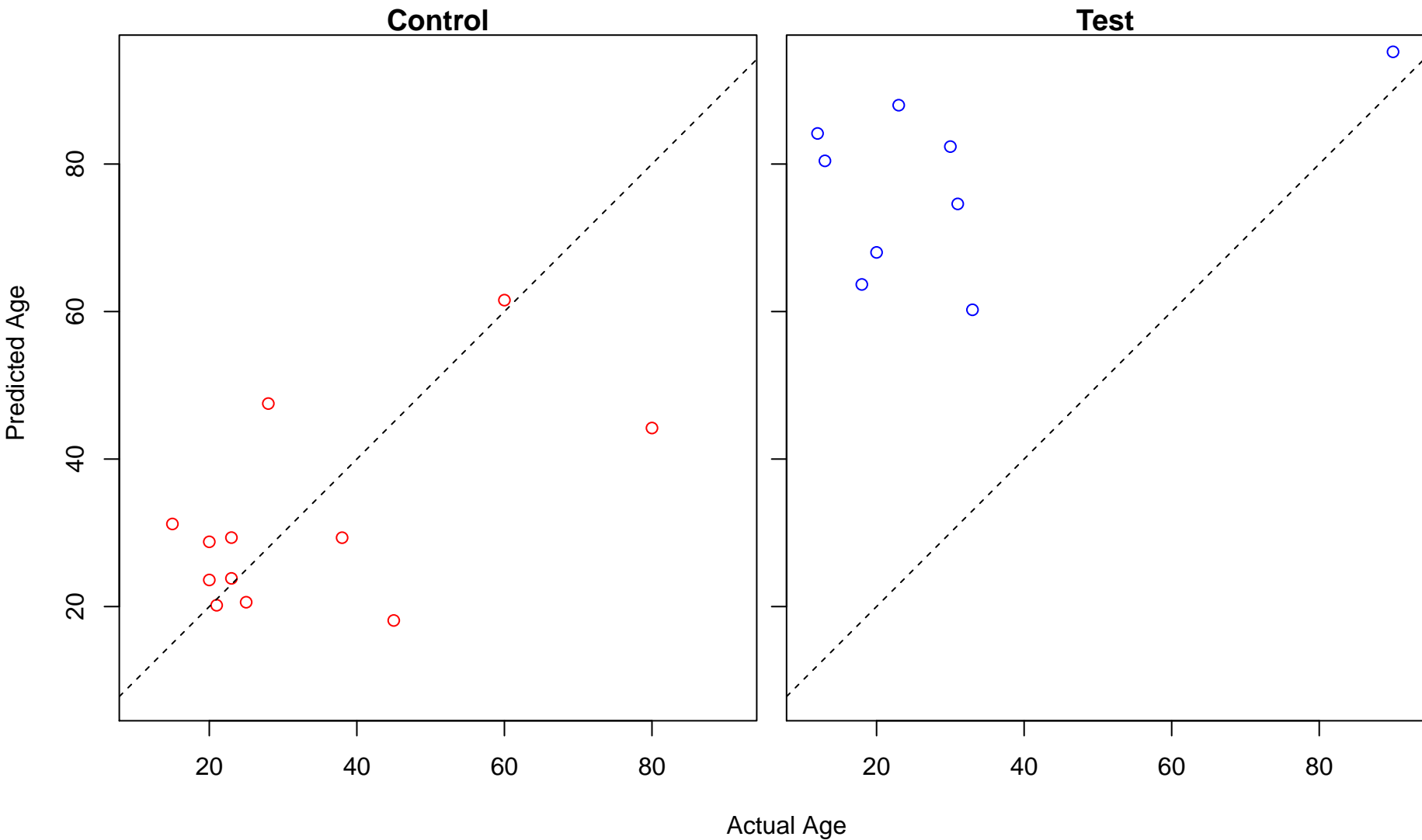


Test

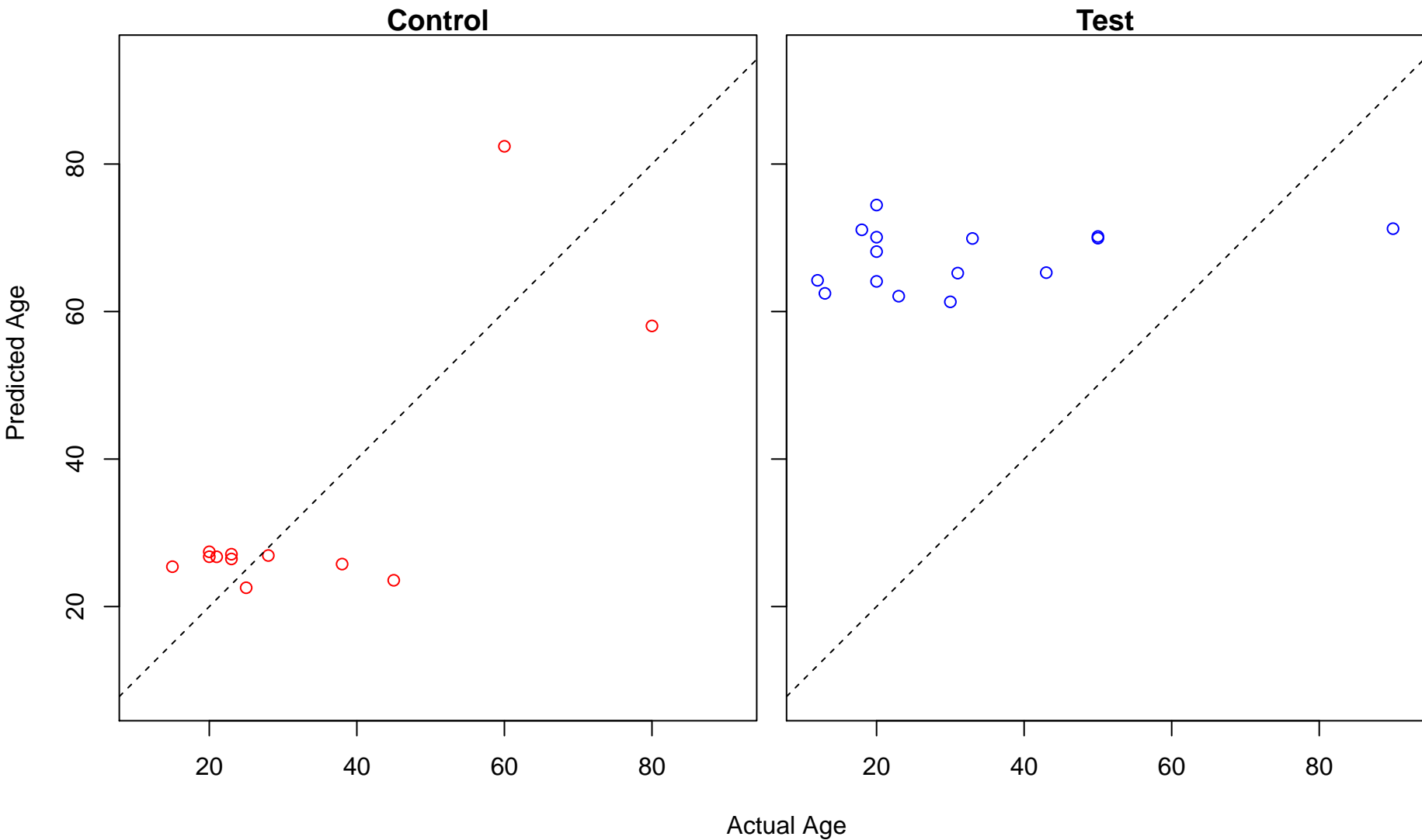


Actual Age

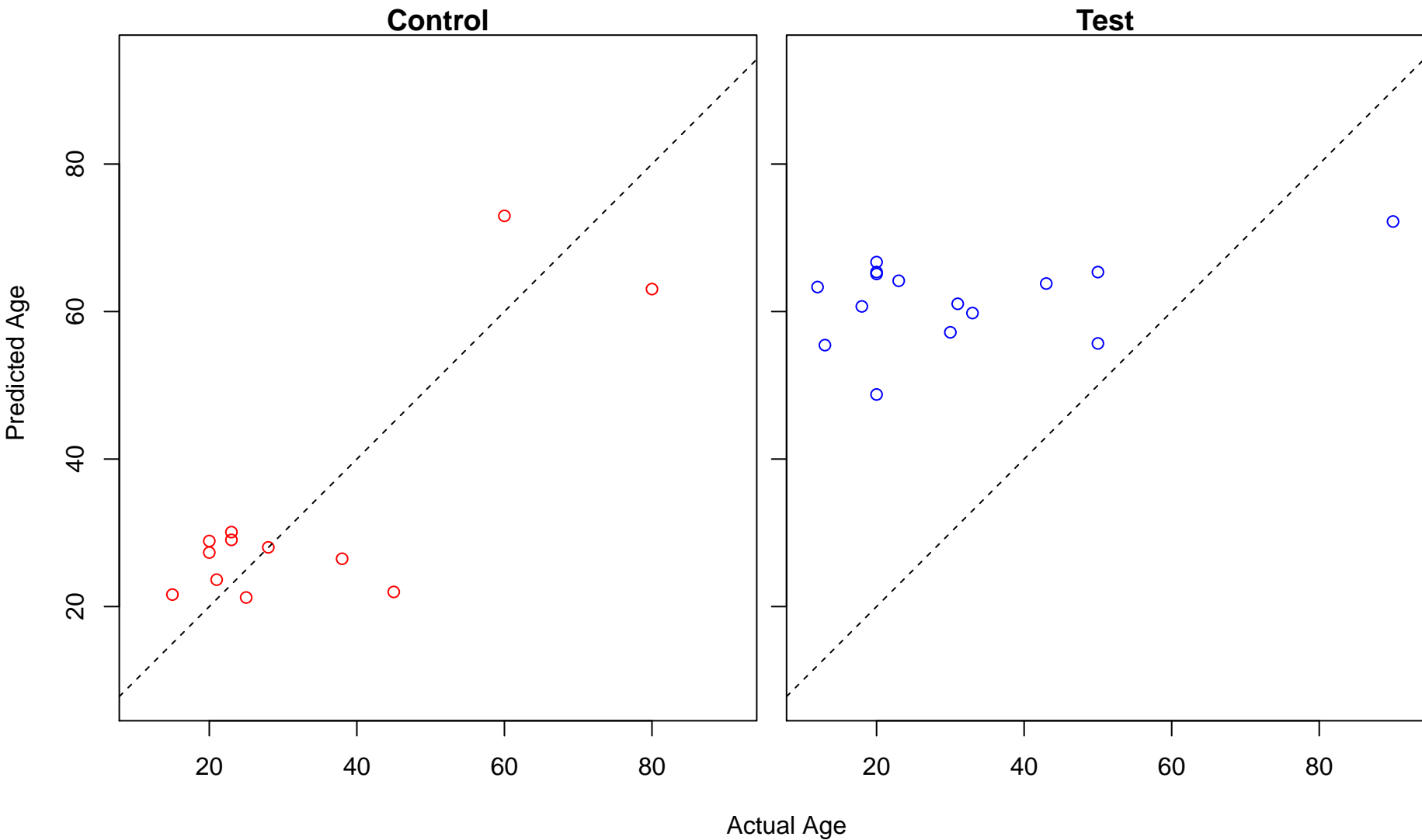
negative regulation of beta-amyloid formation (Score: 3.920446)



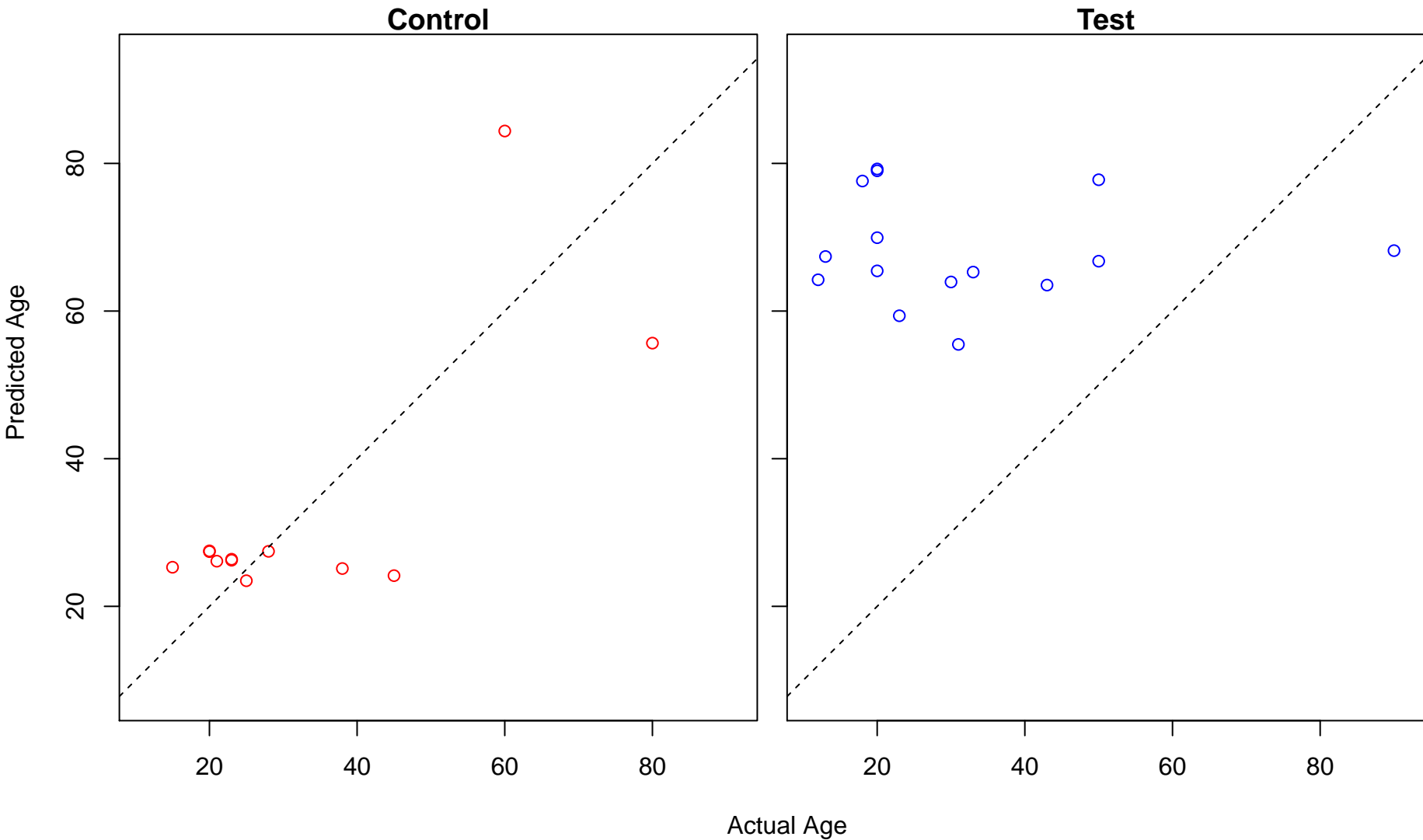
positive regulation of mitotic nuclear division (Score: 3.918352)



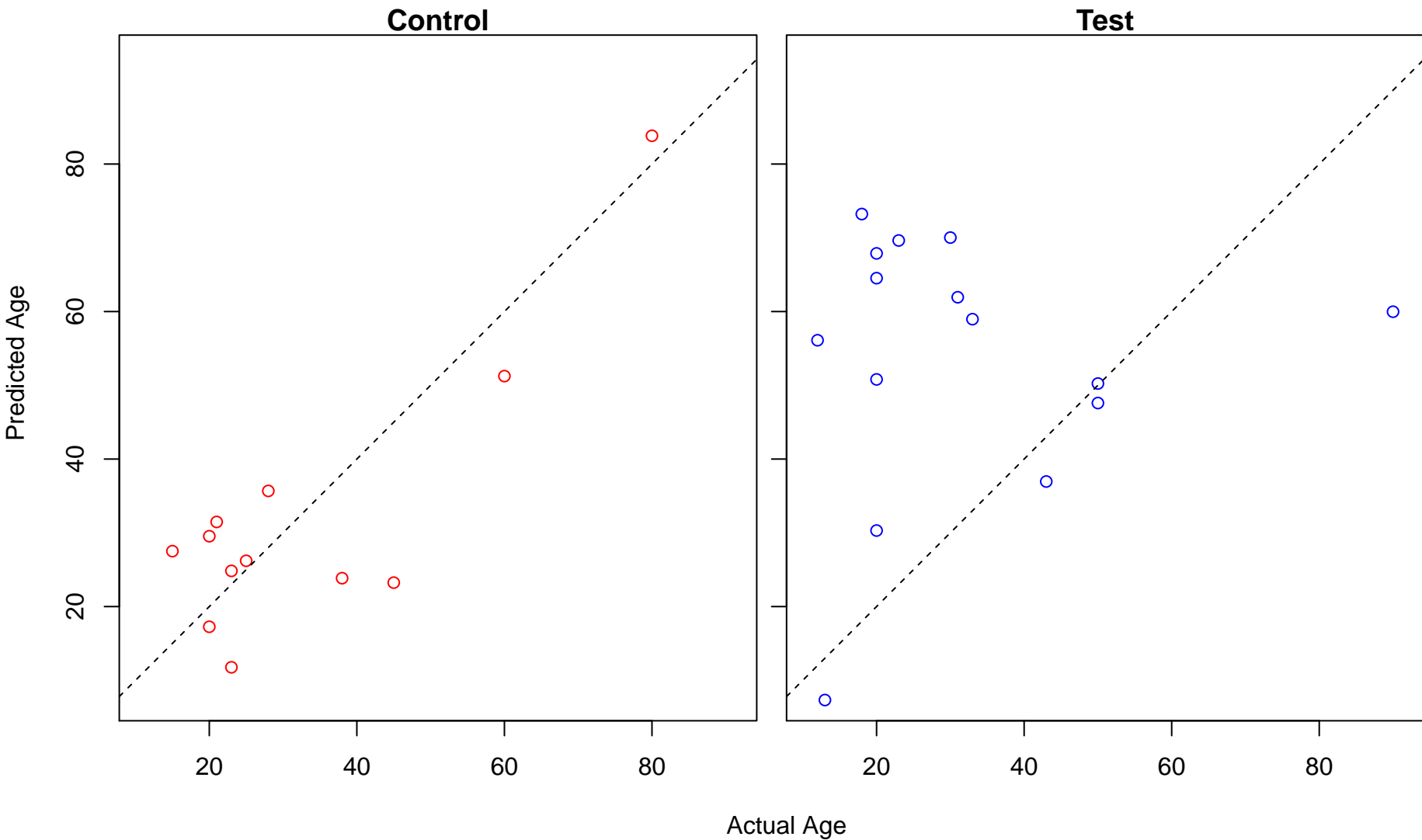
regulation of skeletal muscle tissue development (Score: 3.918294)



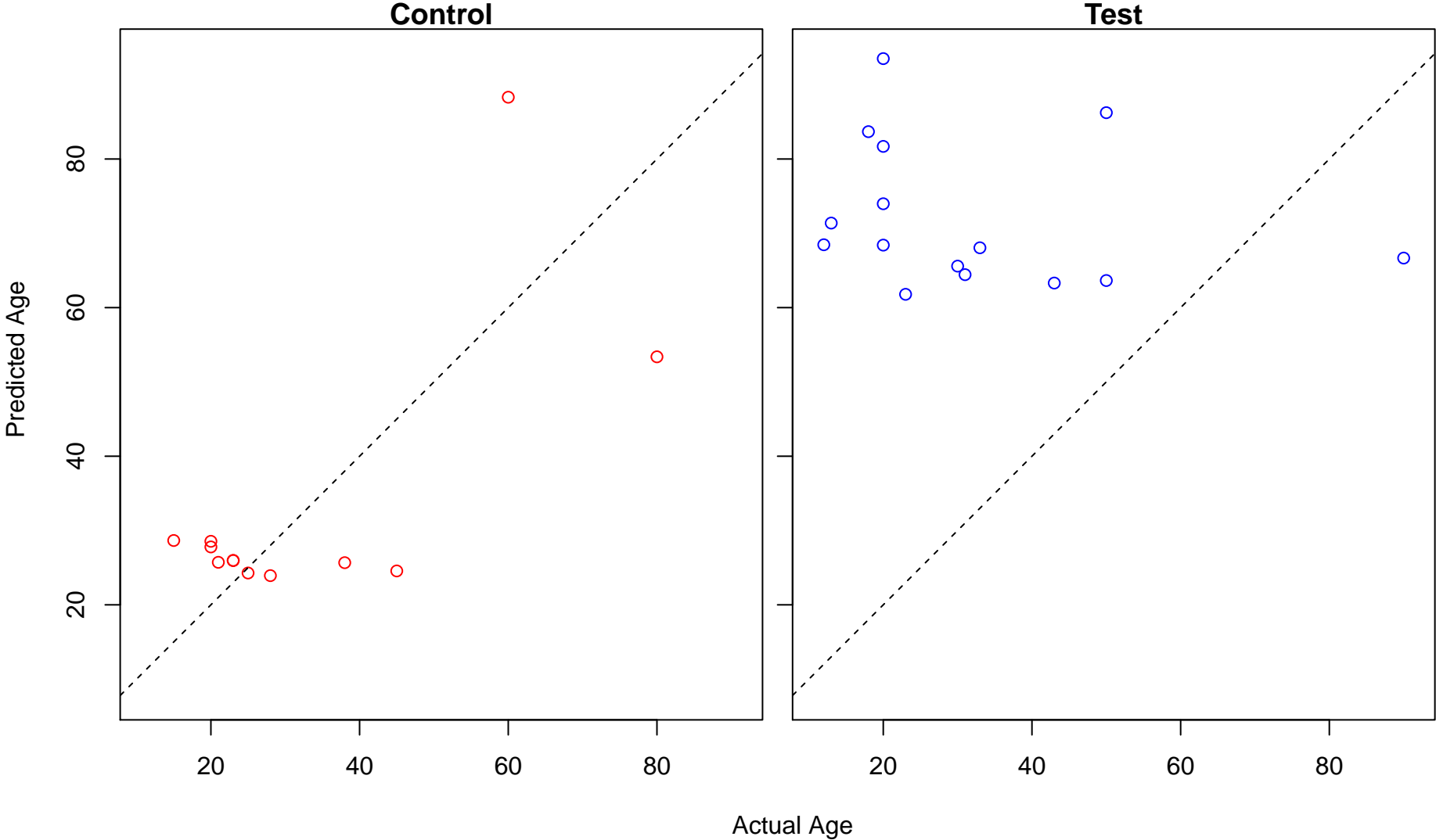
regulation of cell cycle G2/M phase transition (Score: 3.918016)



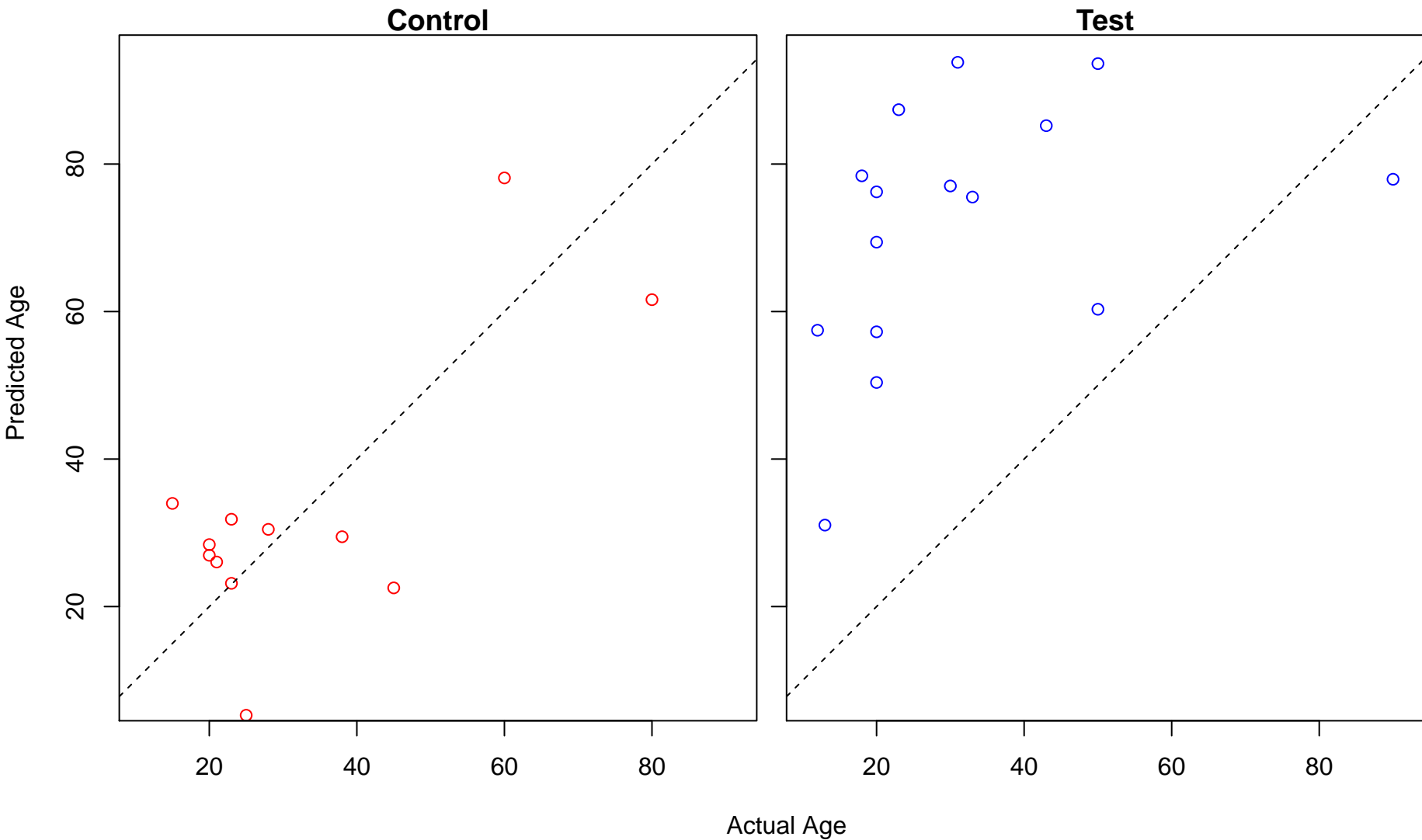
peptidyl-proline modification (Score: 3.916924)



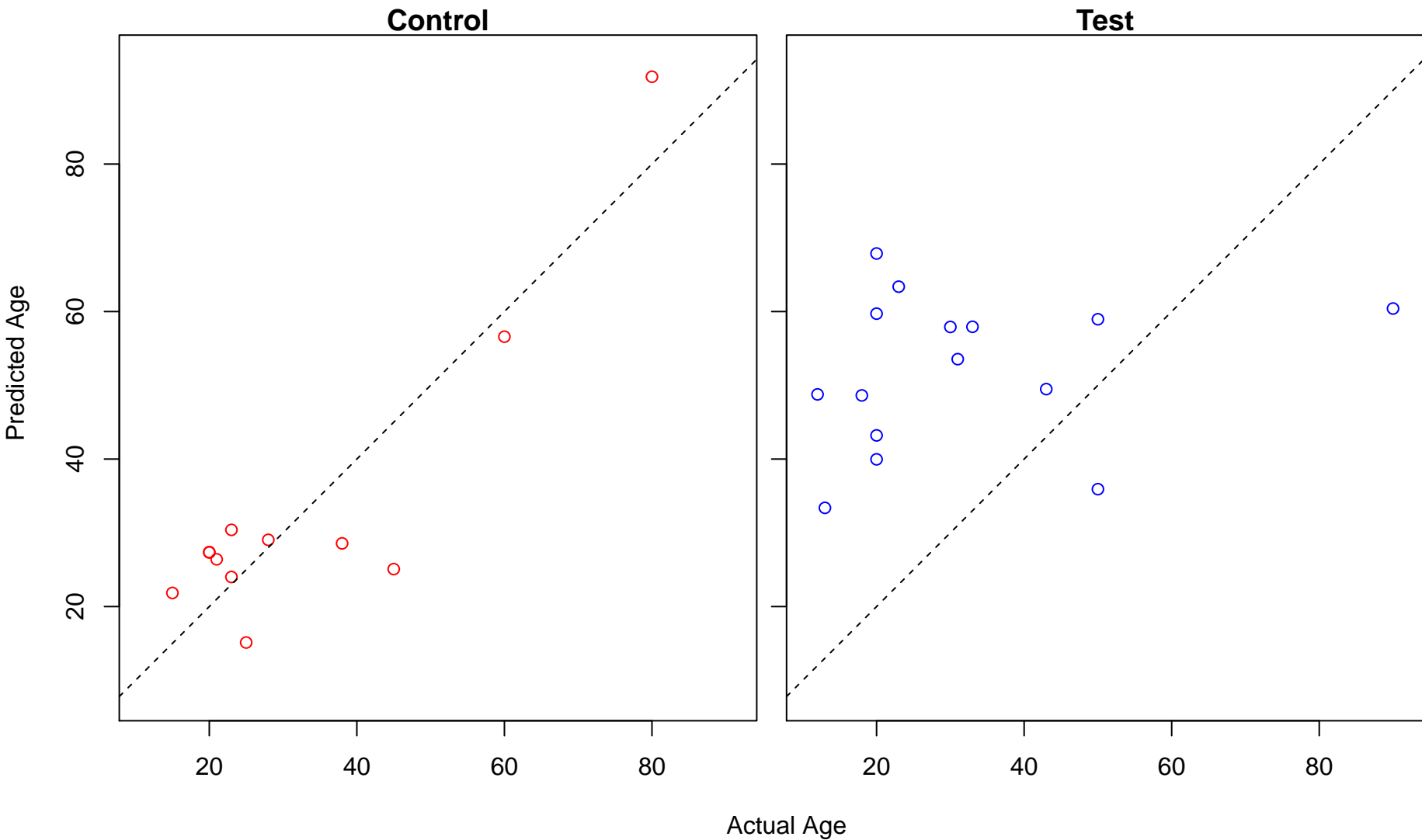
negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway (Score: 3.9167)



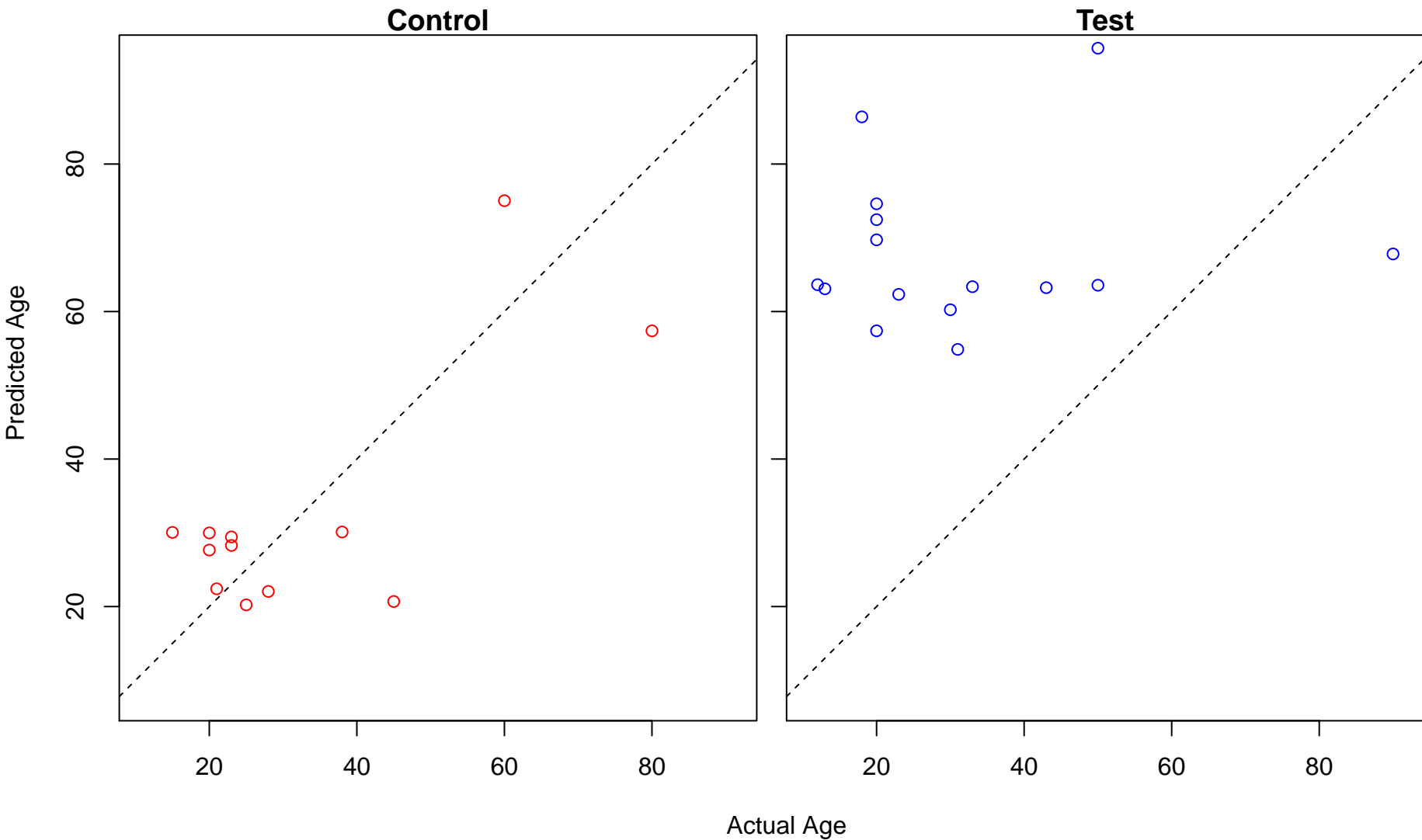
negative regulation of protein tyrosine kinase activity (Score: 3.916212)



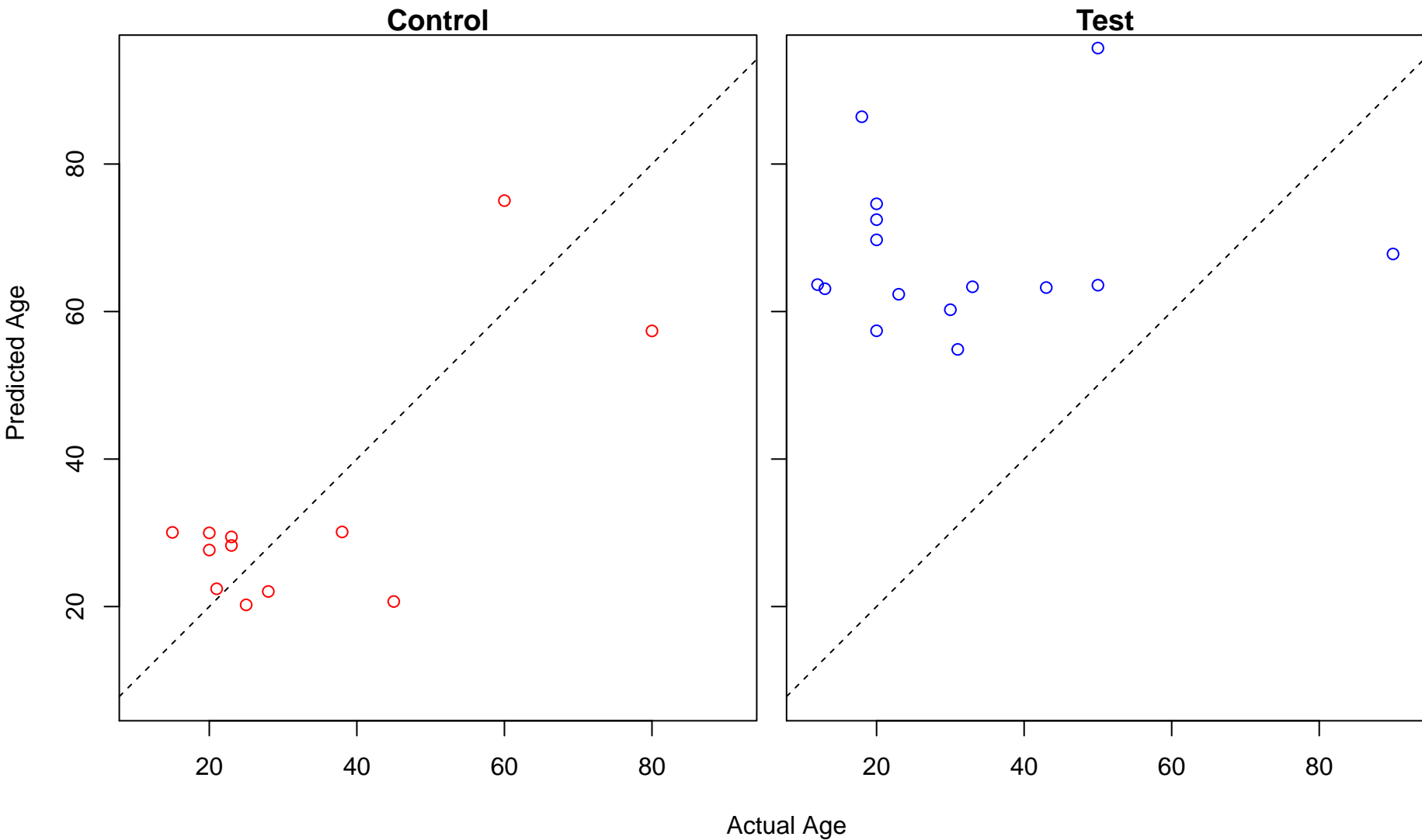
regulation of myosin–light–chain–phosphatase activity (Score: 3.914732)



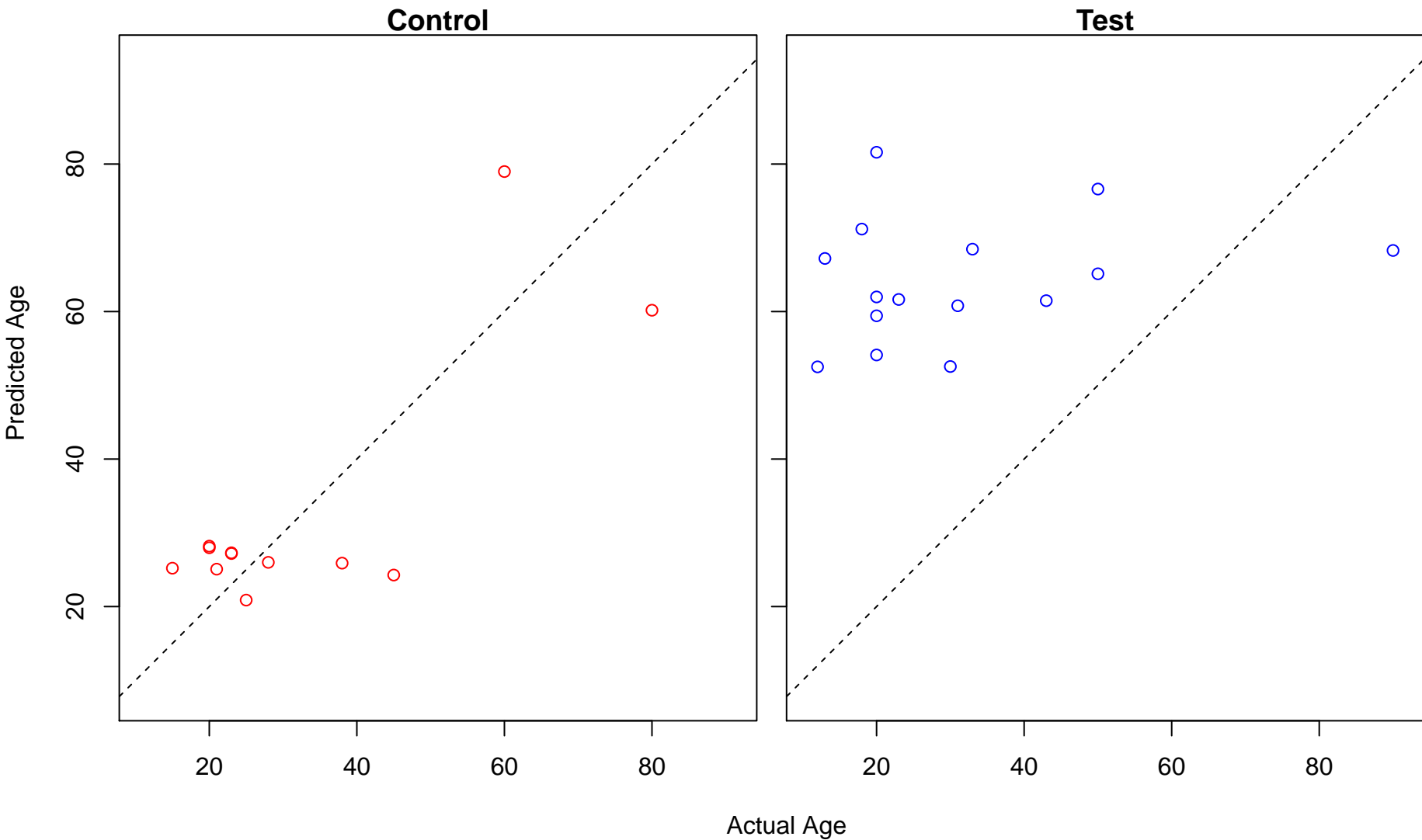
mitral valve development (Score: 3.914599)



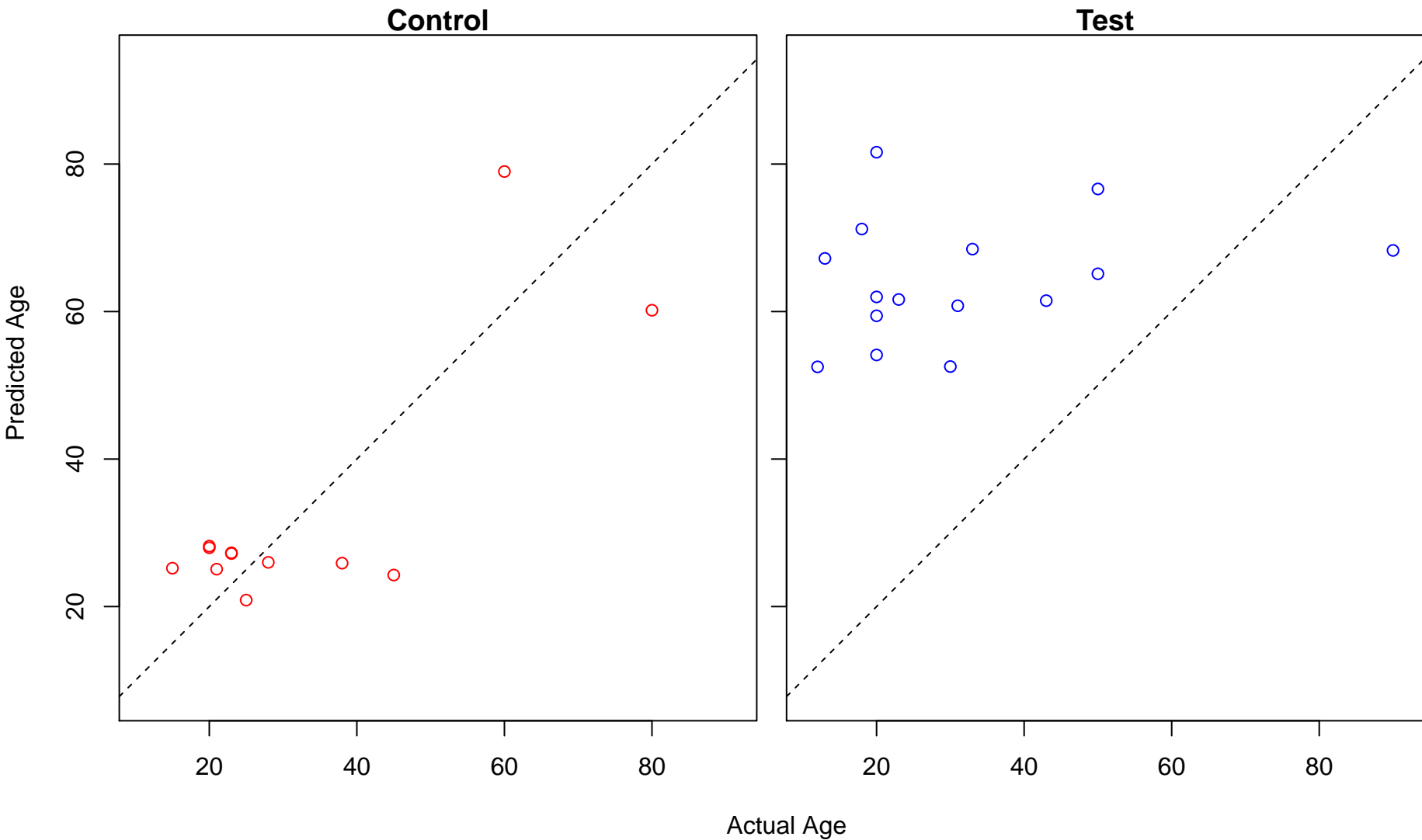
mitral valve morphogenesis (Score: 3.914158)



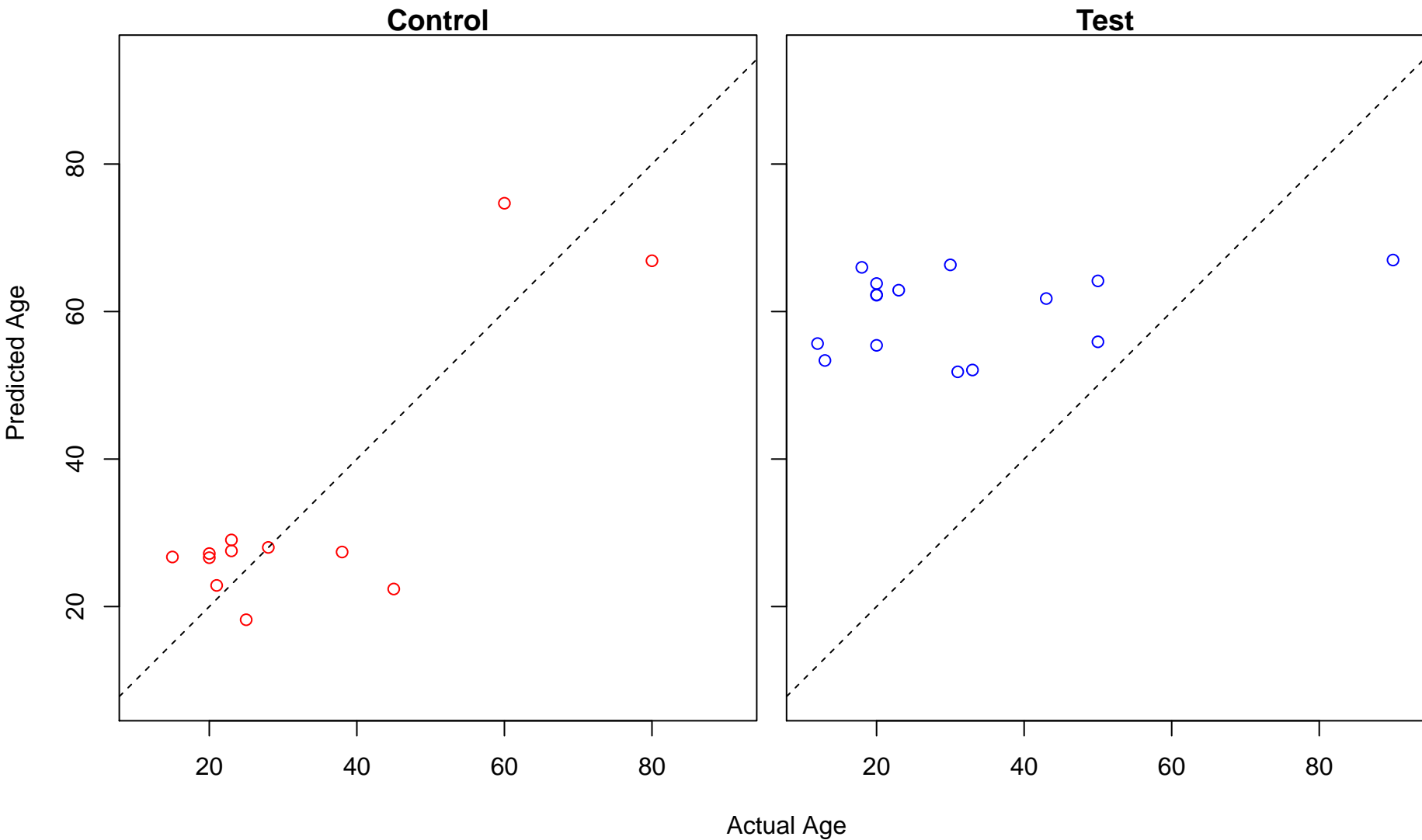
regulation of epithelial cell differentiation involved in kidney development (Score: 3.913346)



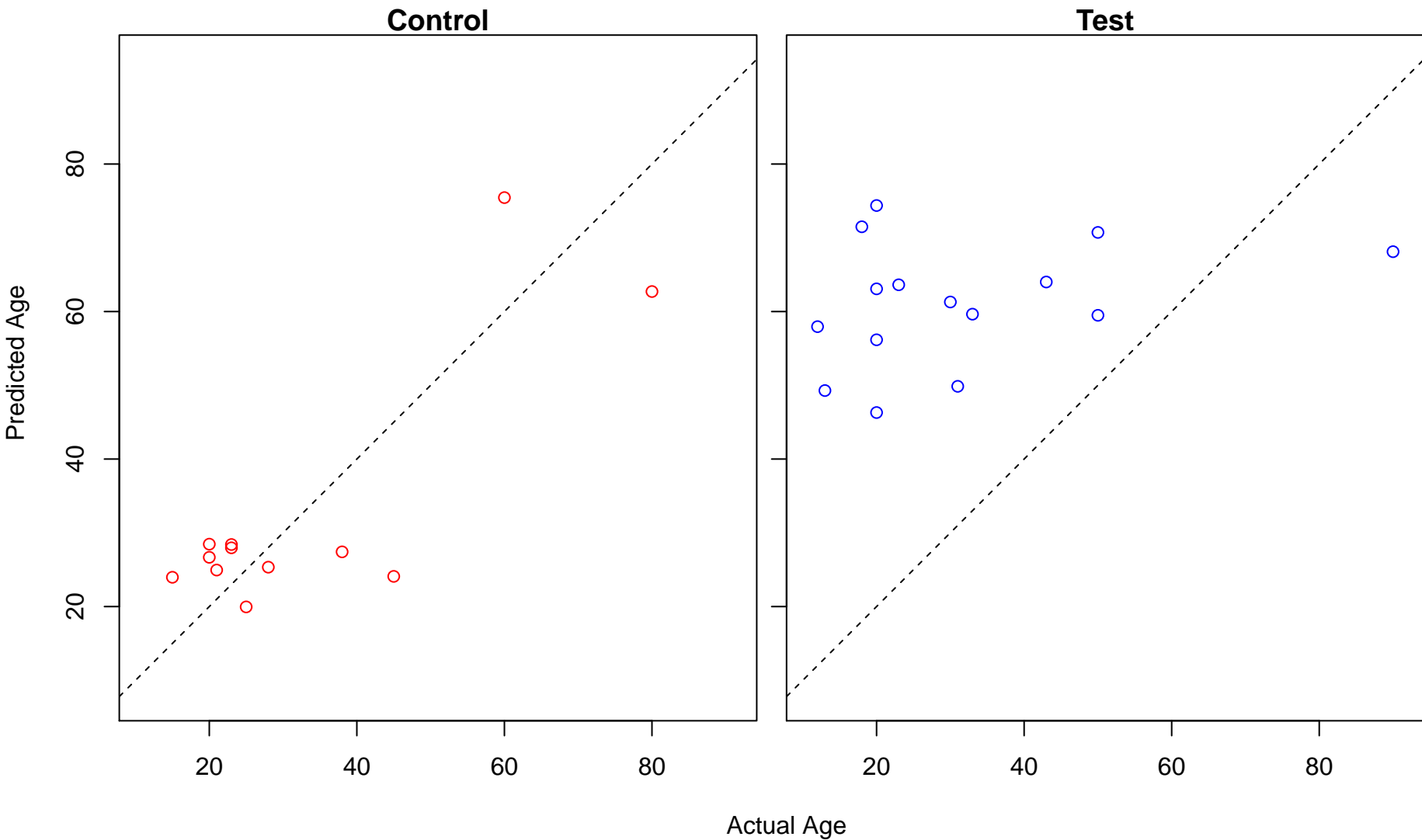
regulation of nephron tubule epithelial cell differentiation (Score: 3.913222)



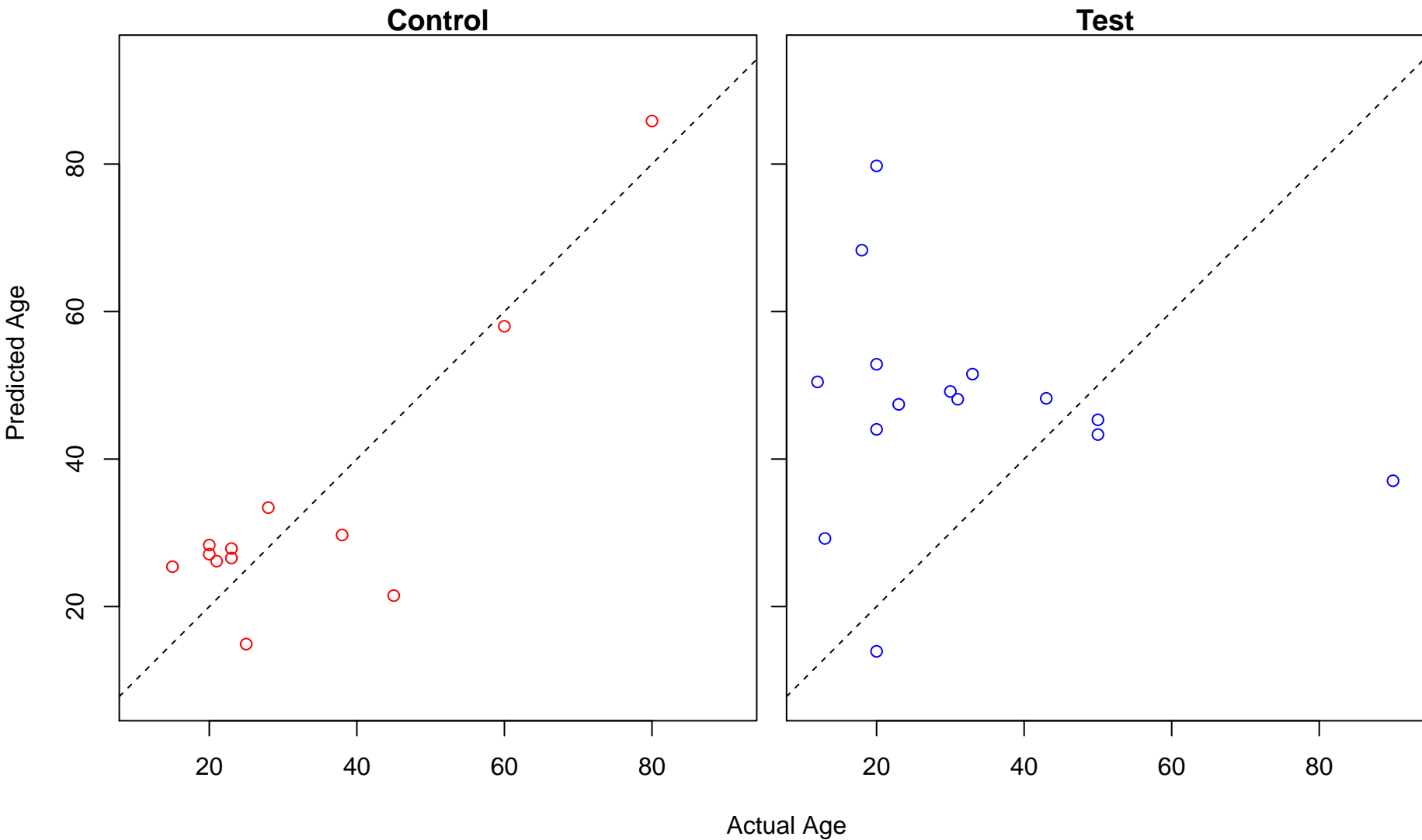
developmental pigmentation (Score: 3.911992)



heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules (Score: 3.909947)

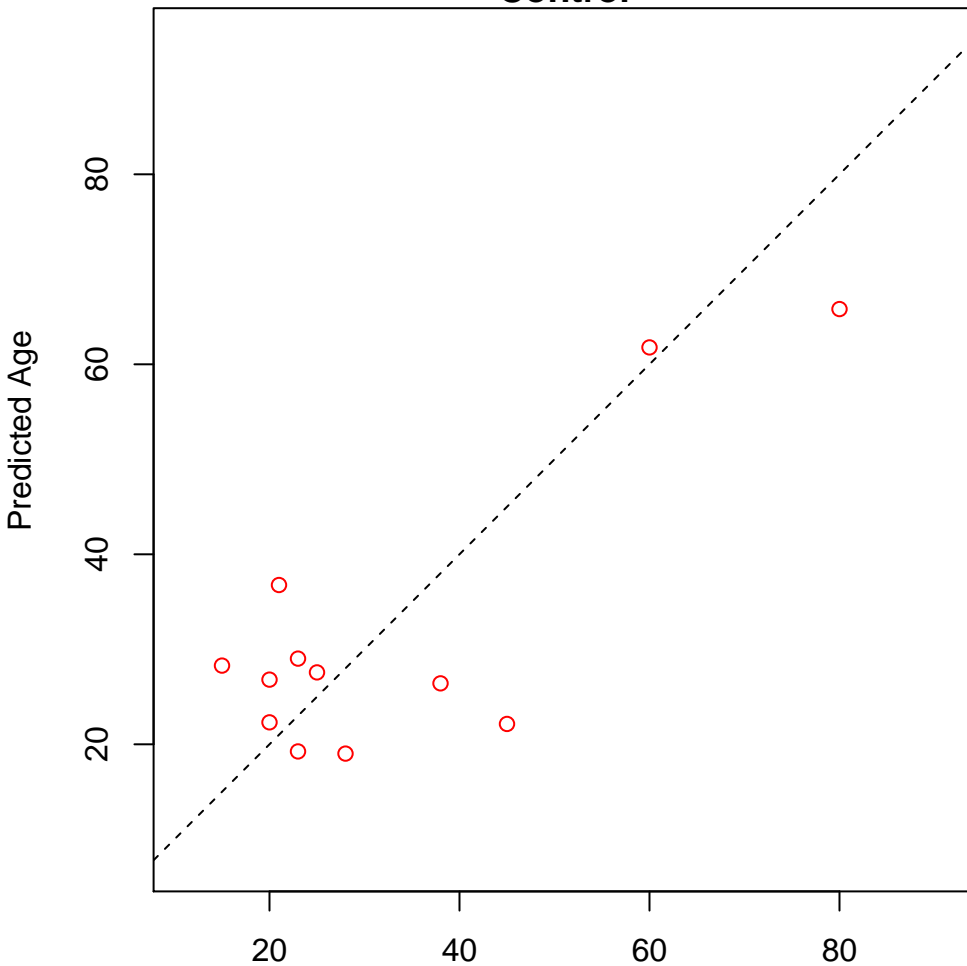


negative regulation of phosphoprotein phosphatase activity (Score: 3.907794)

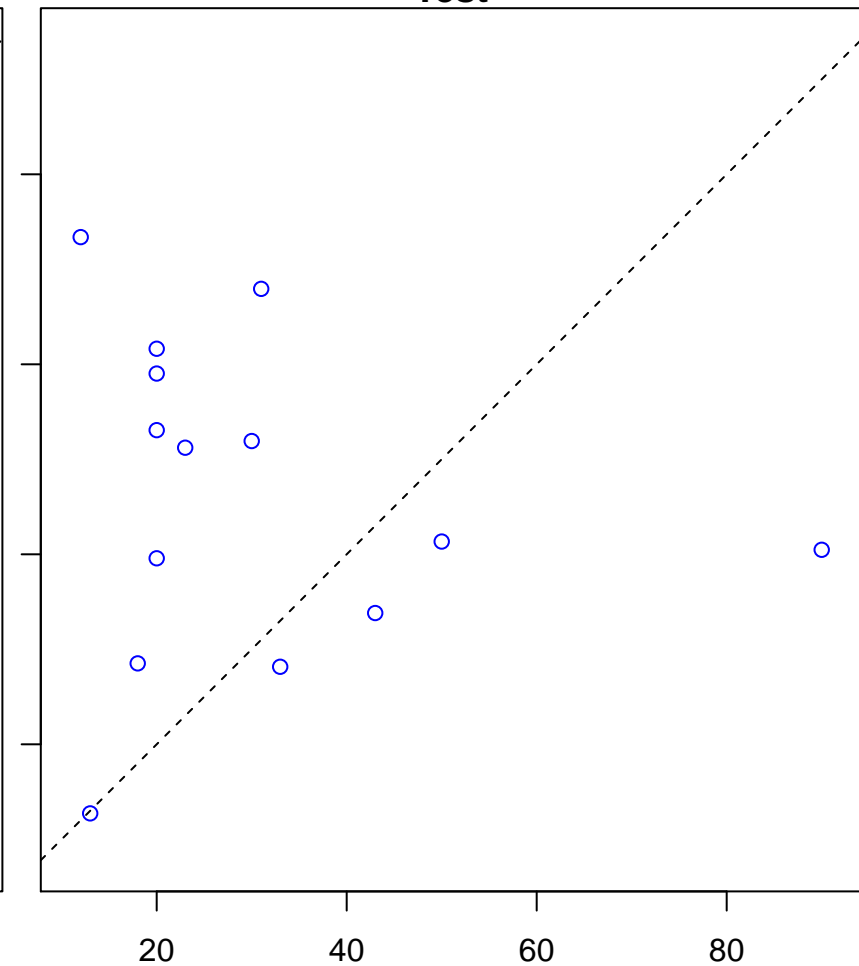


regulation of epidermal cell differentiation (Score: 3.907145)

Control



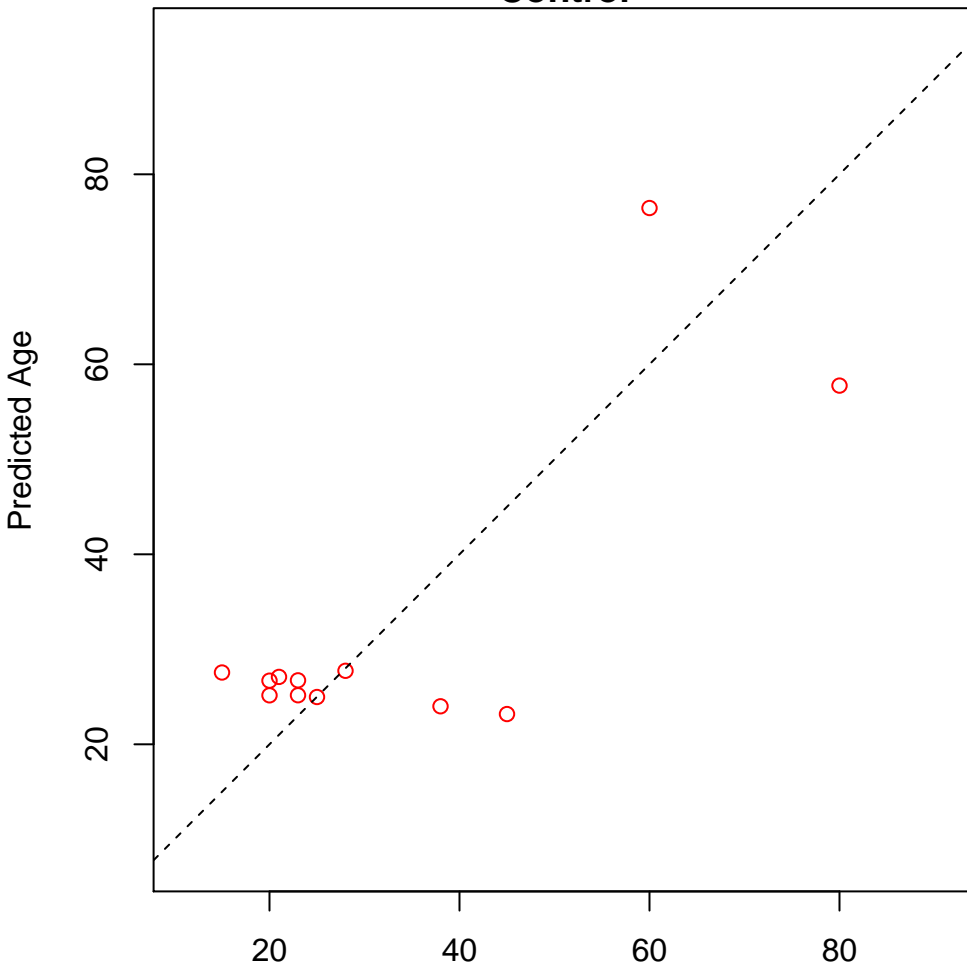
Test



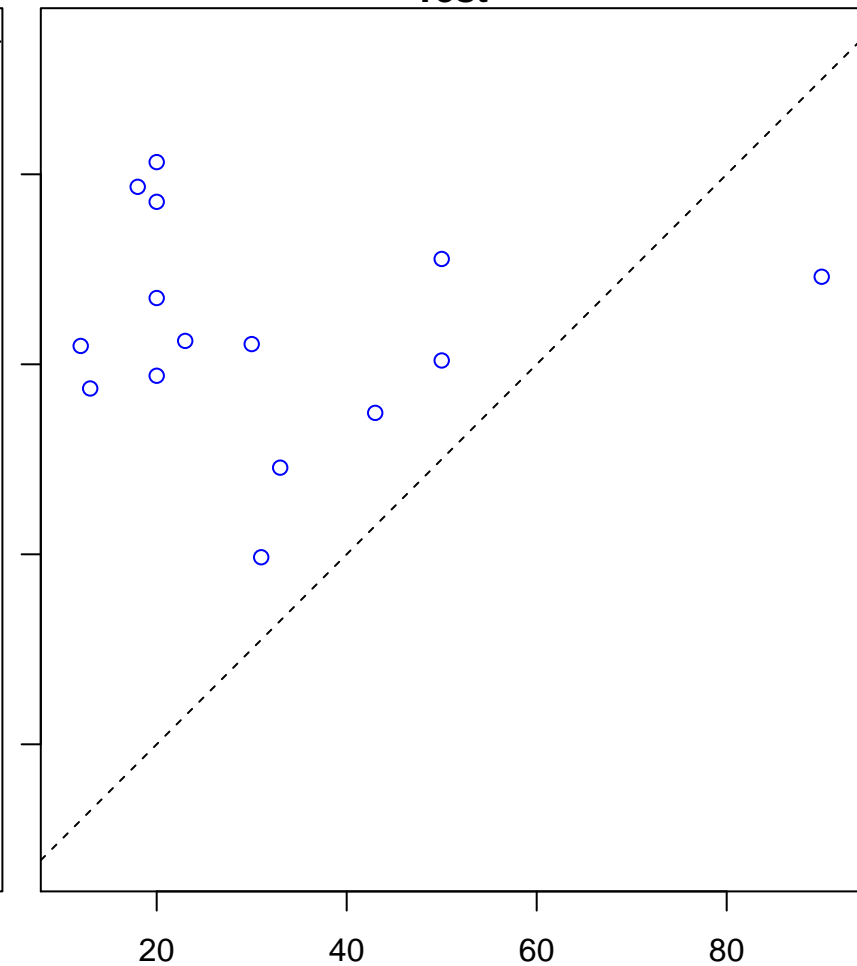
Actual Age

purine nucleoside biosynthetic process (Score: 3.906765)

Control

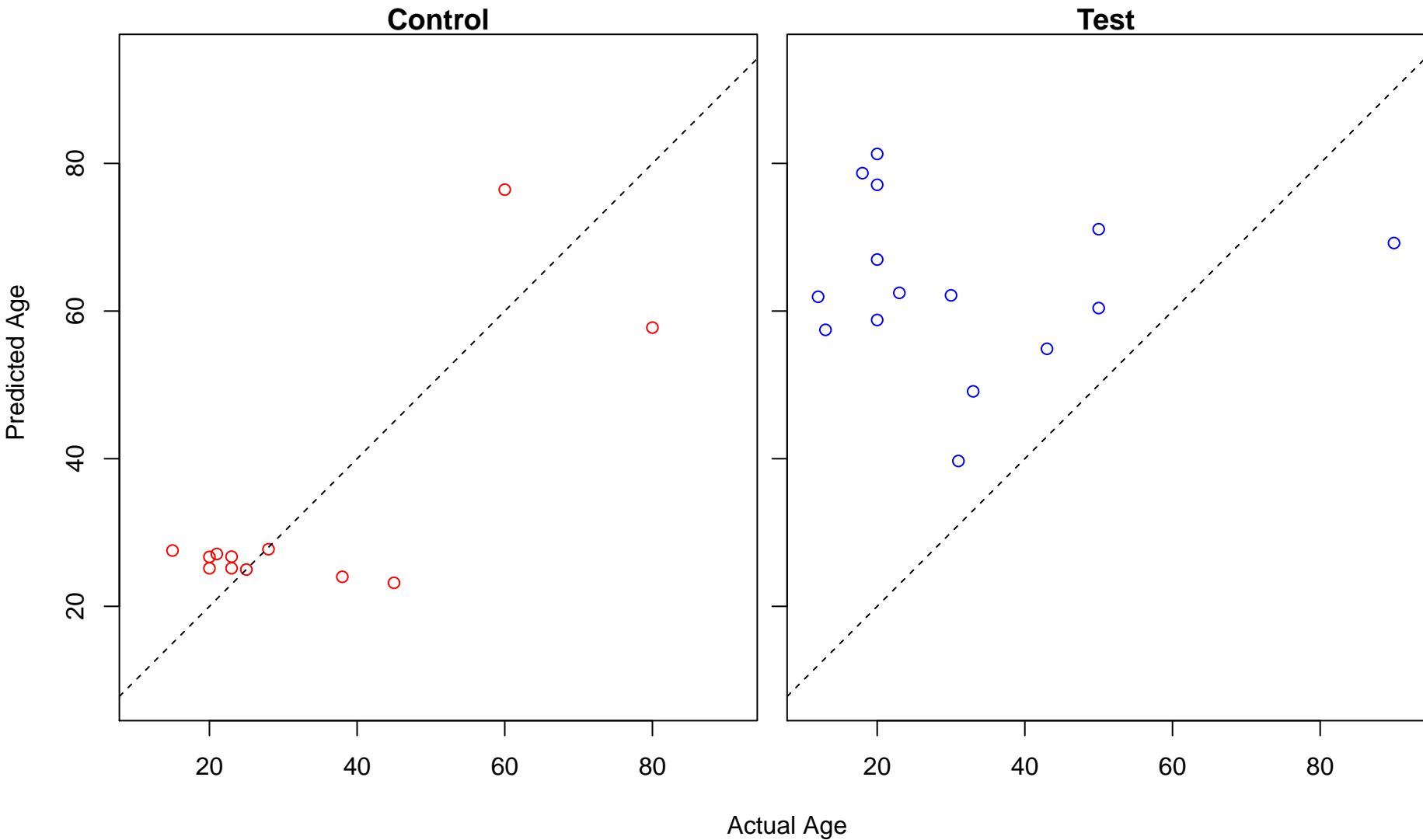


Test

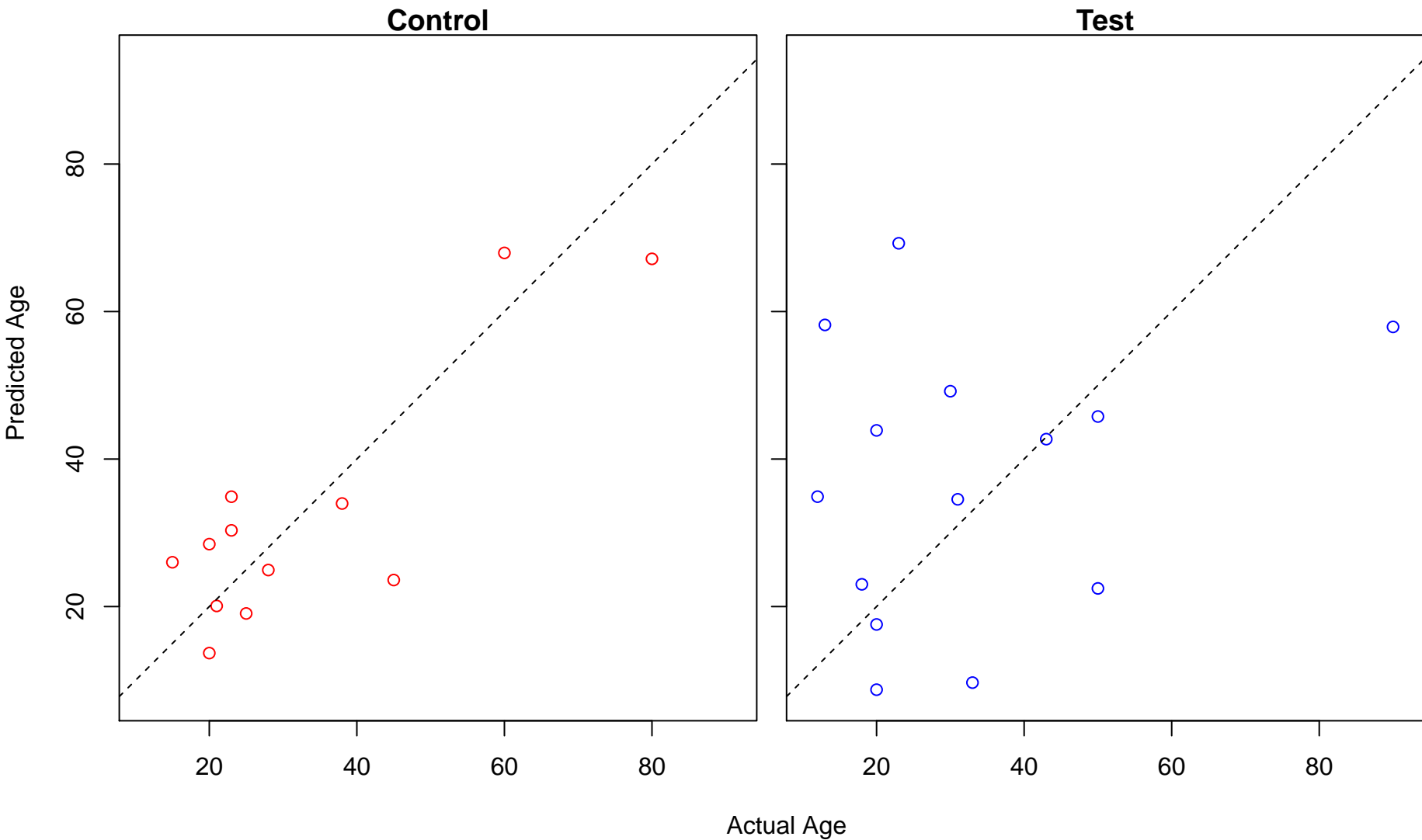


Actual Age

purine ribonucleoside biosynthetic process (Score: 3.906765)

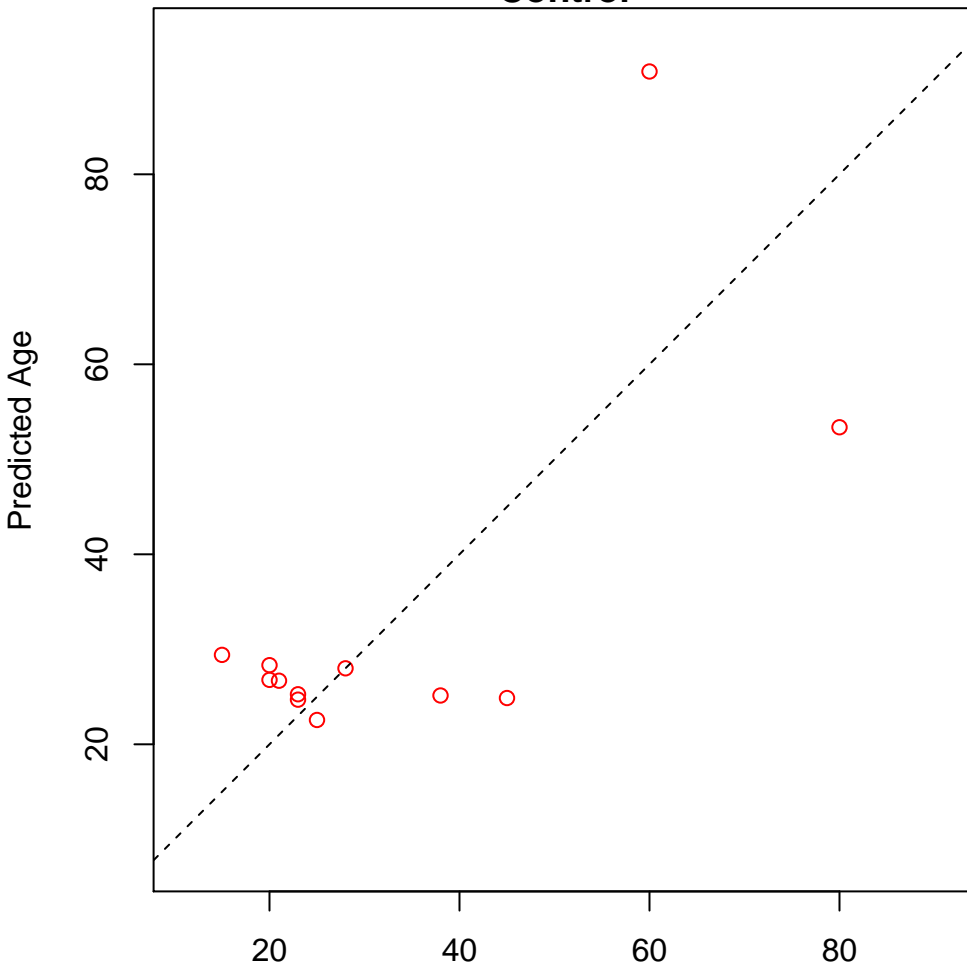


regulation of organ formation (Score: 3.904836)

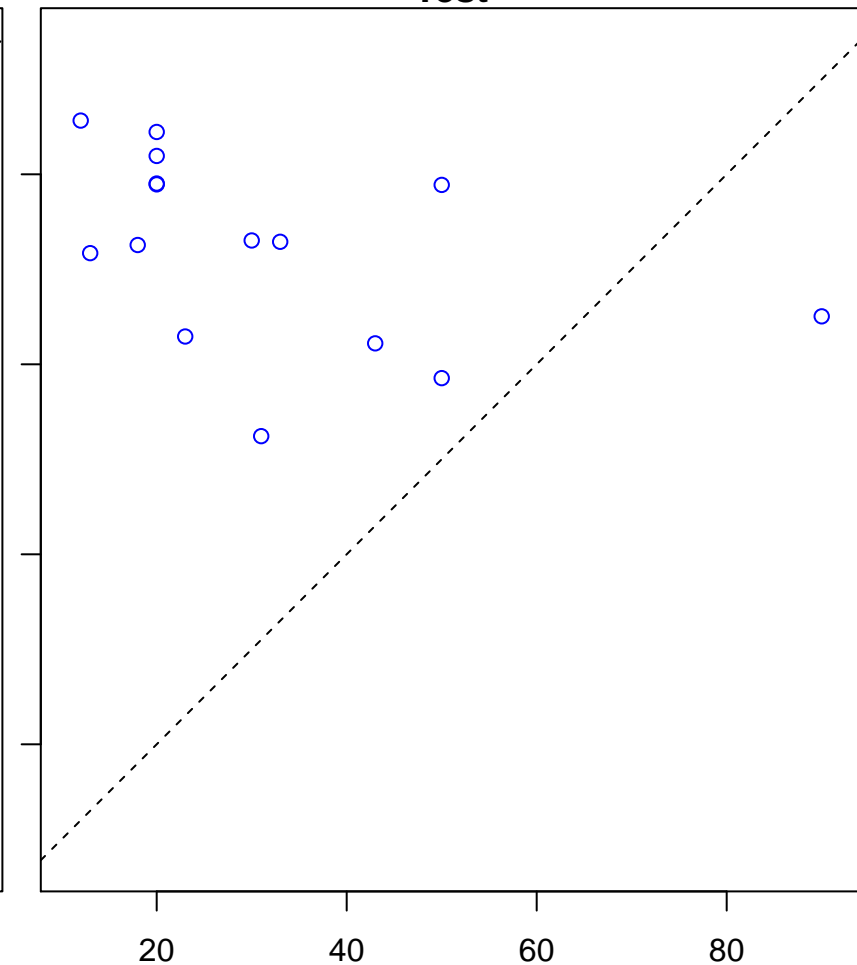


amino-acid betaine metabolic process (Score: 3.904579)

Control

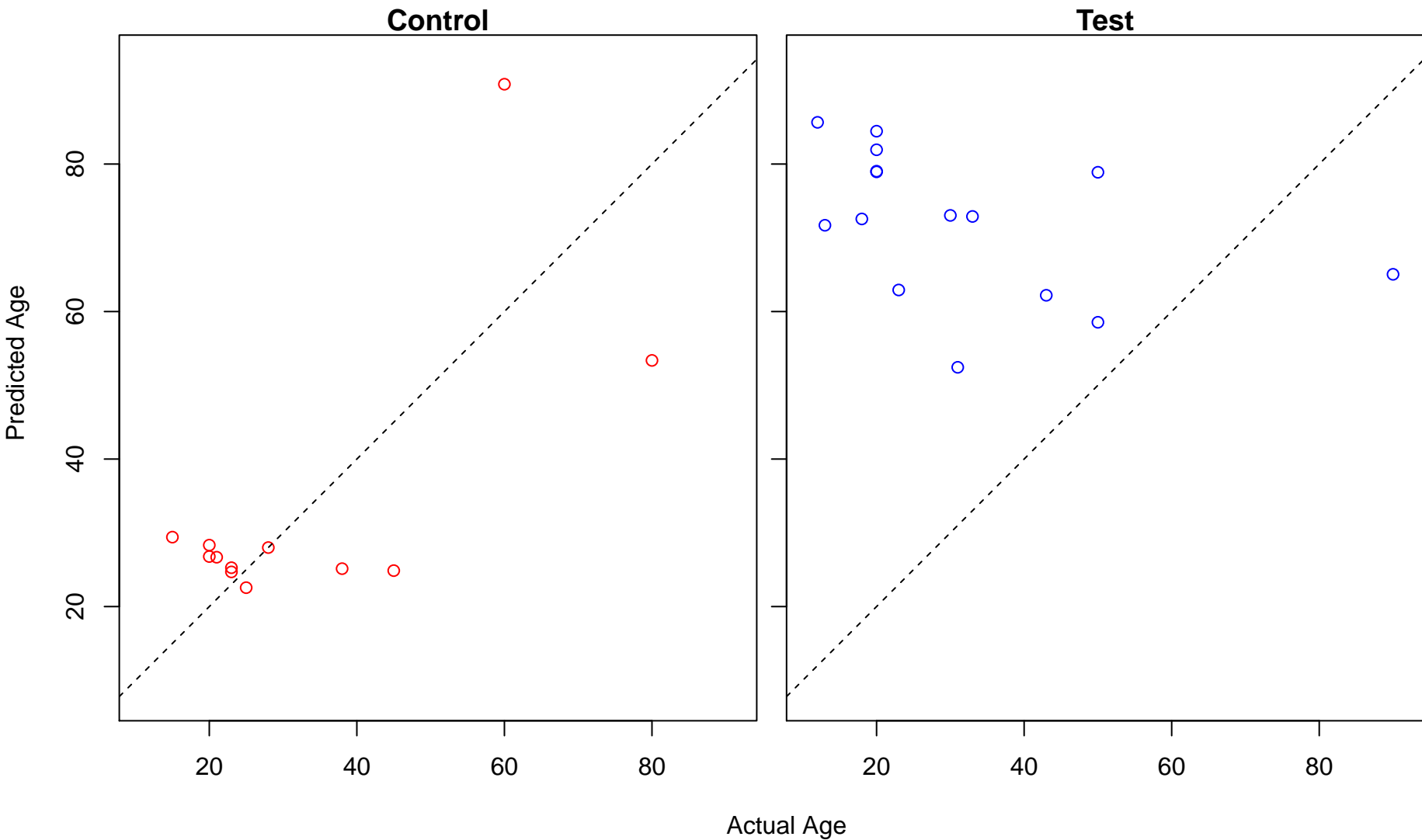


Test

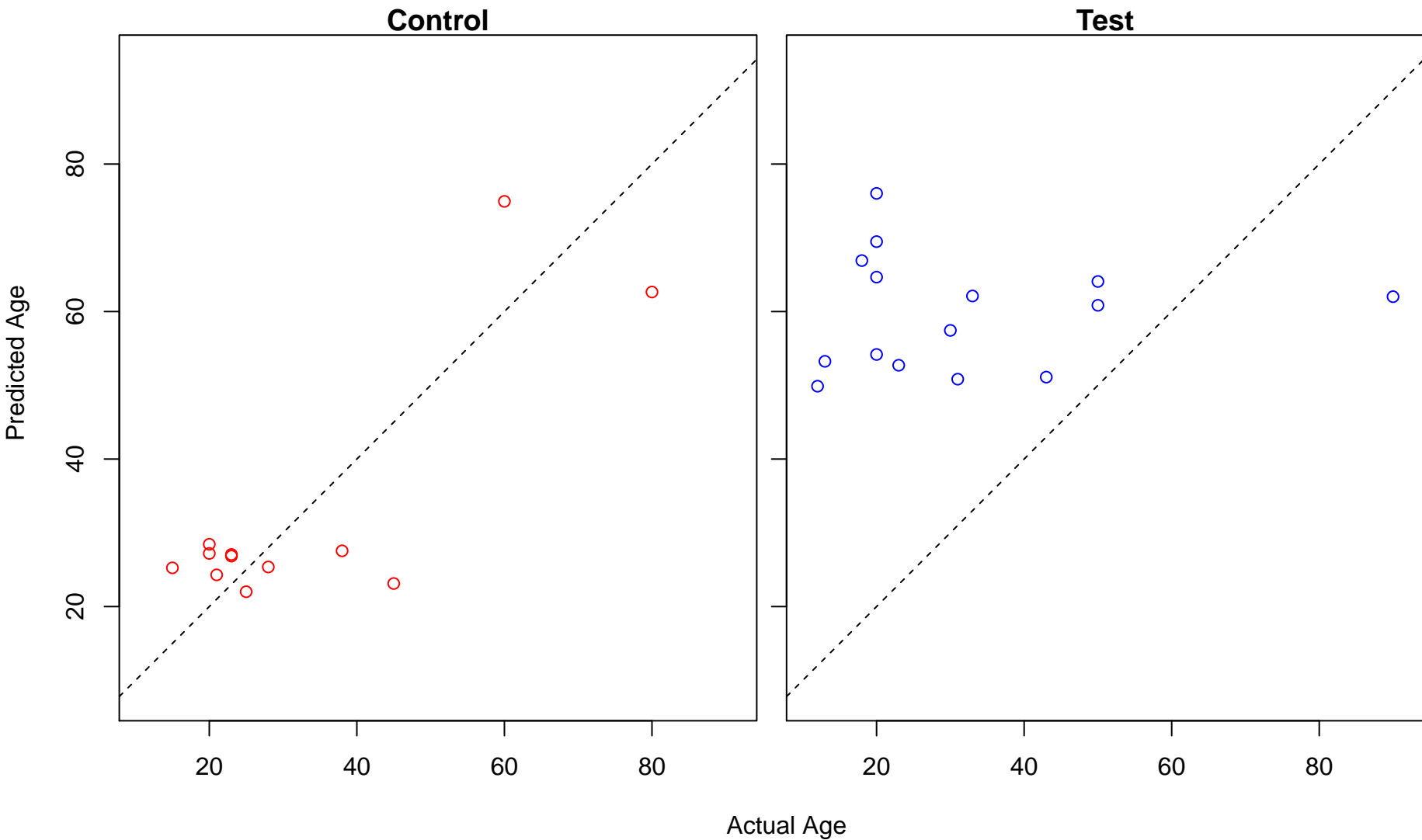


Actual Age

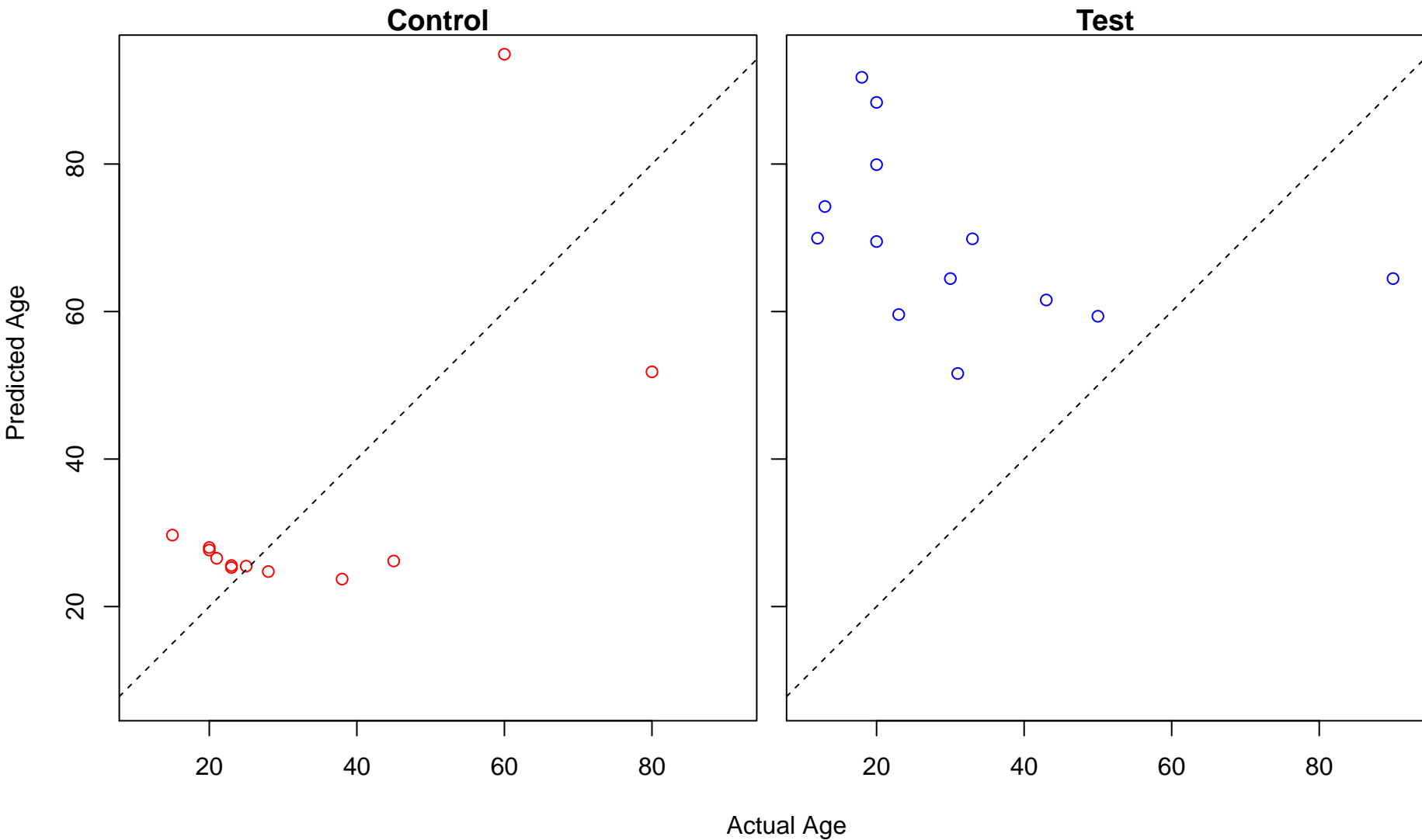
carnitine metabolic process (Score: 3.904474)



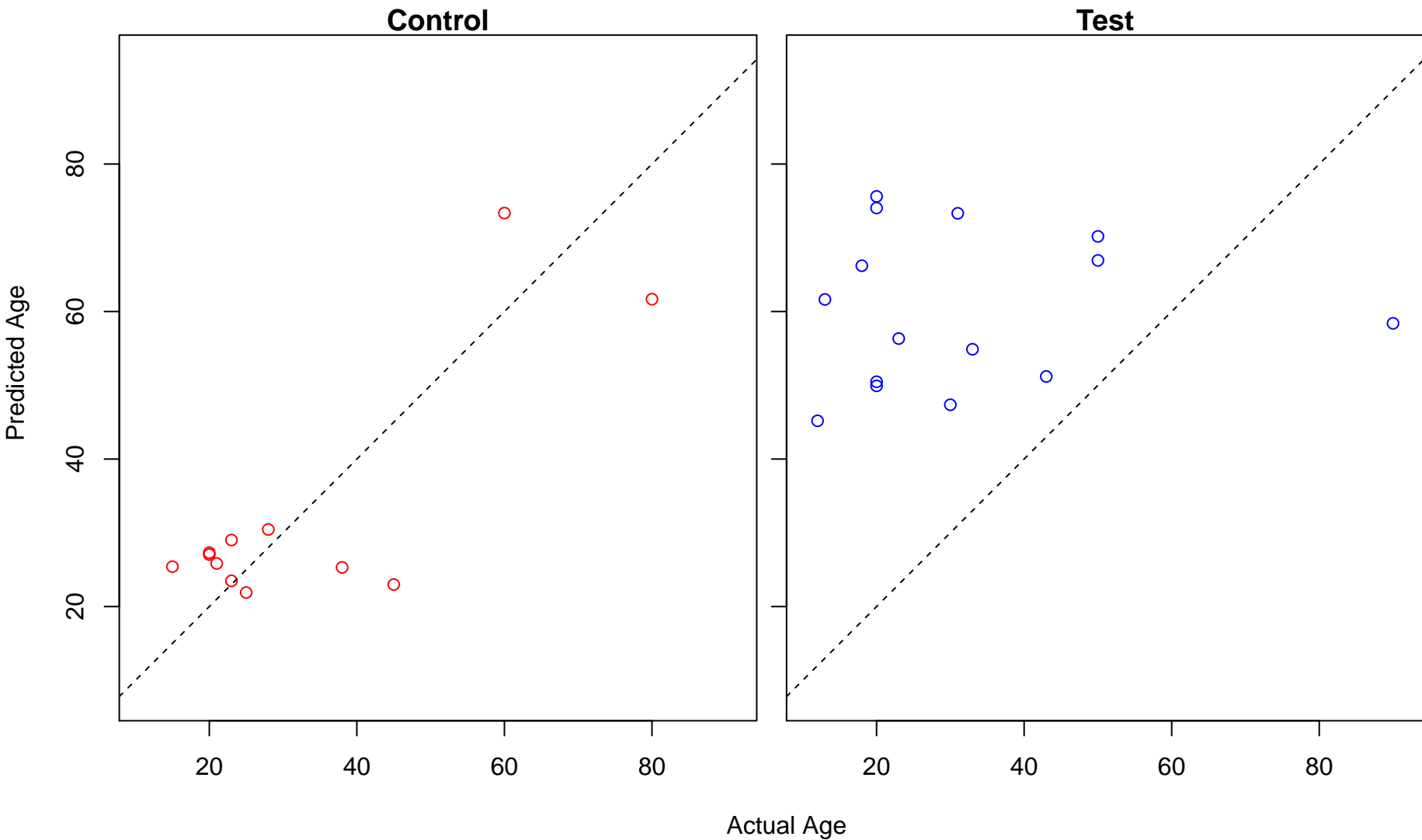
positive regulation of cilium assembly (Score: 3.901714)



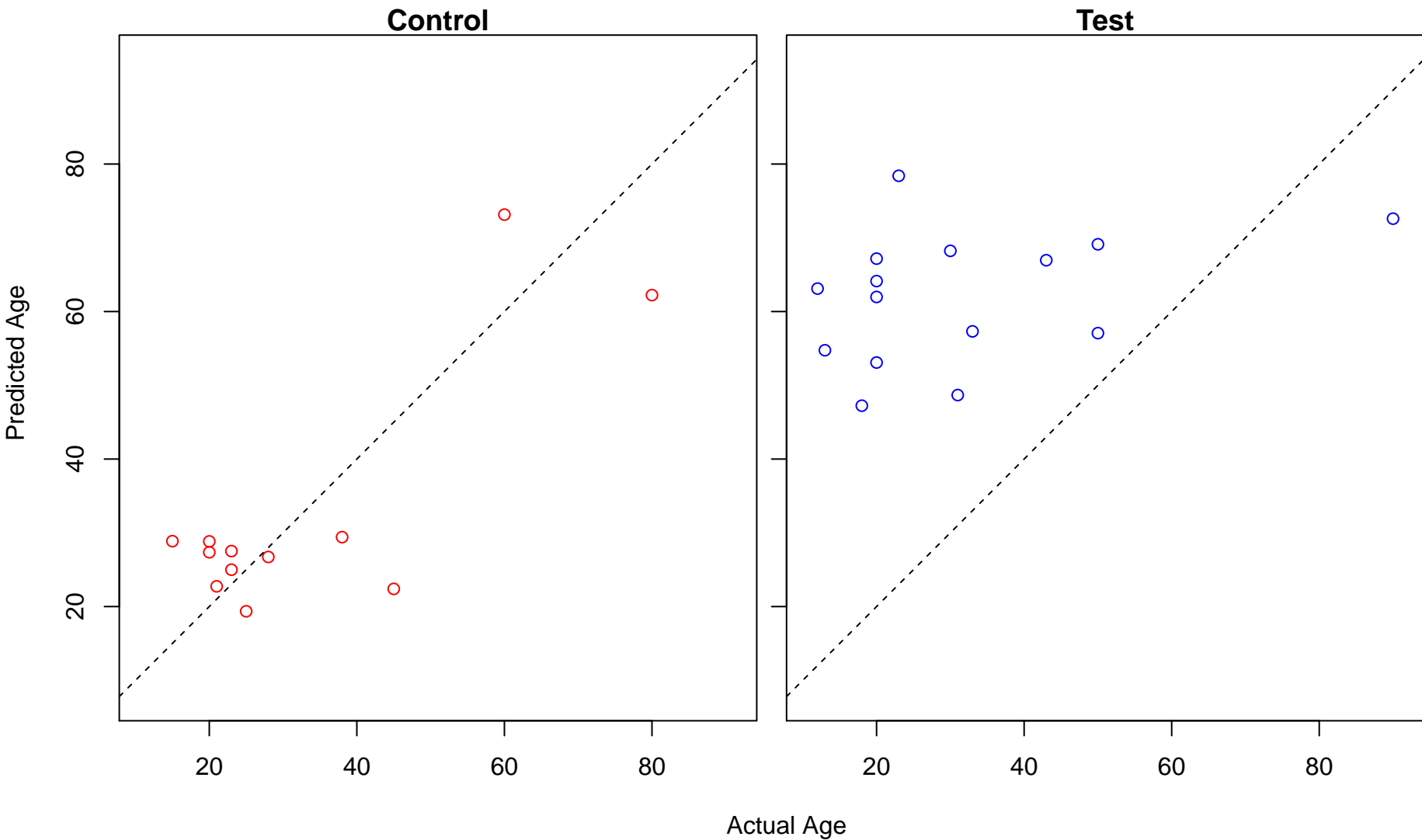
response to copper ion (Score: 3.900751)



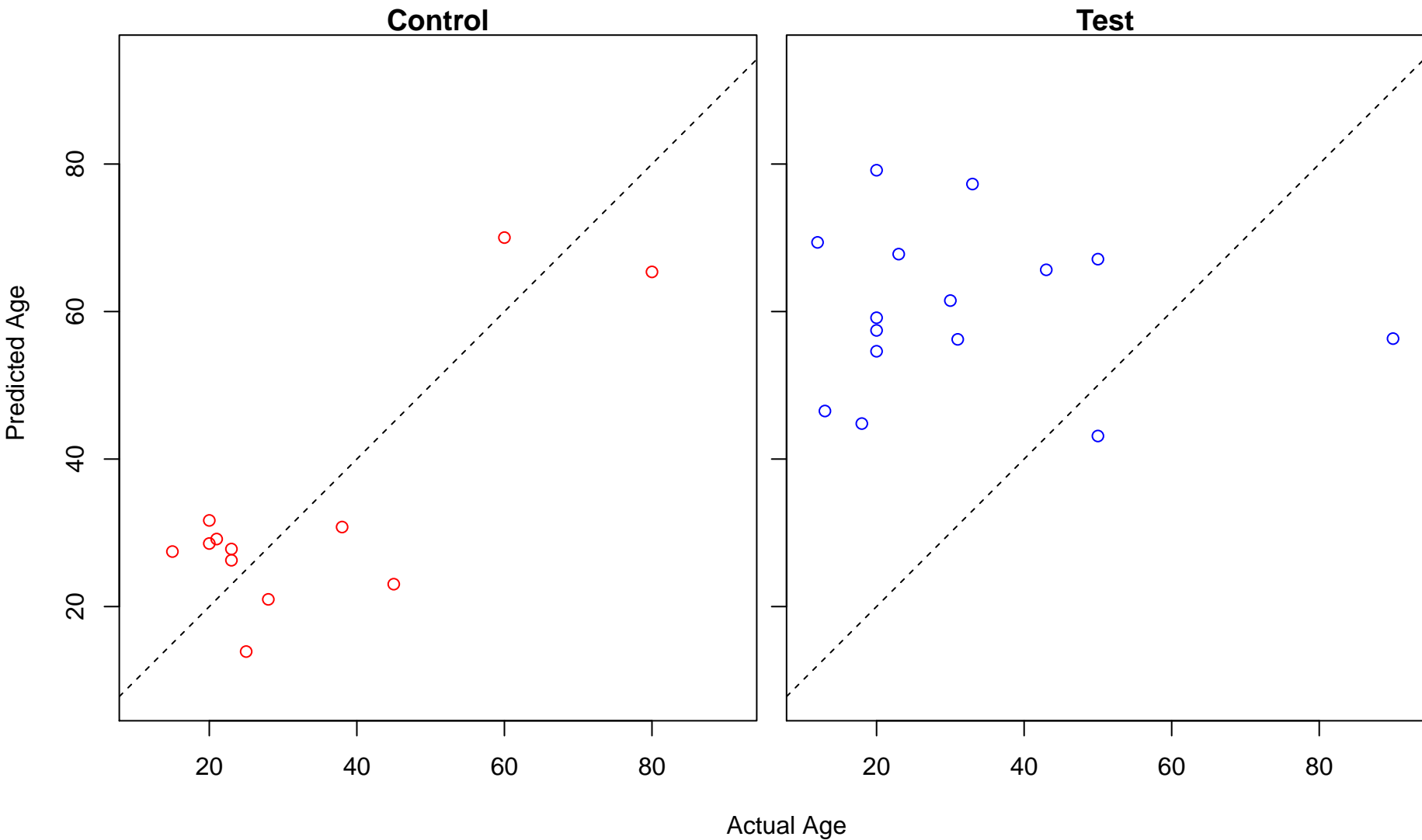
positive regulation of peptidyl–threonine phosphorylation (Score: 3.900534)



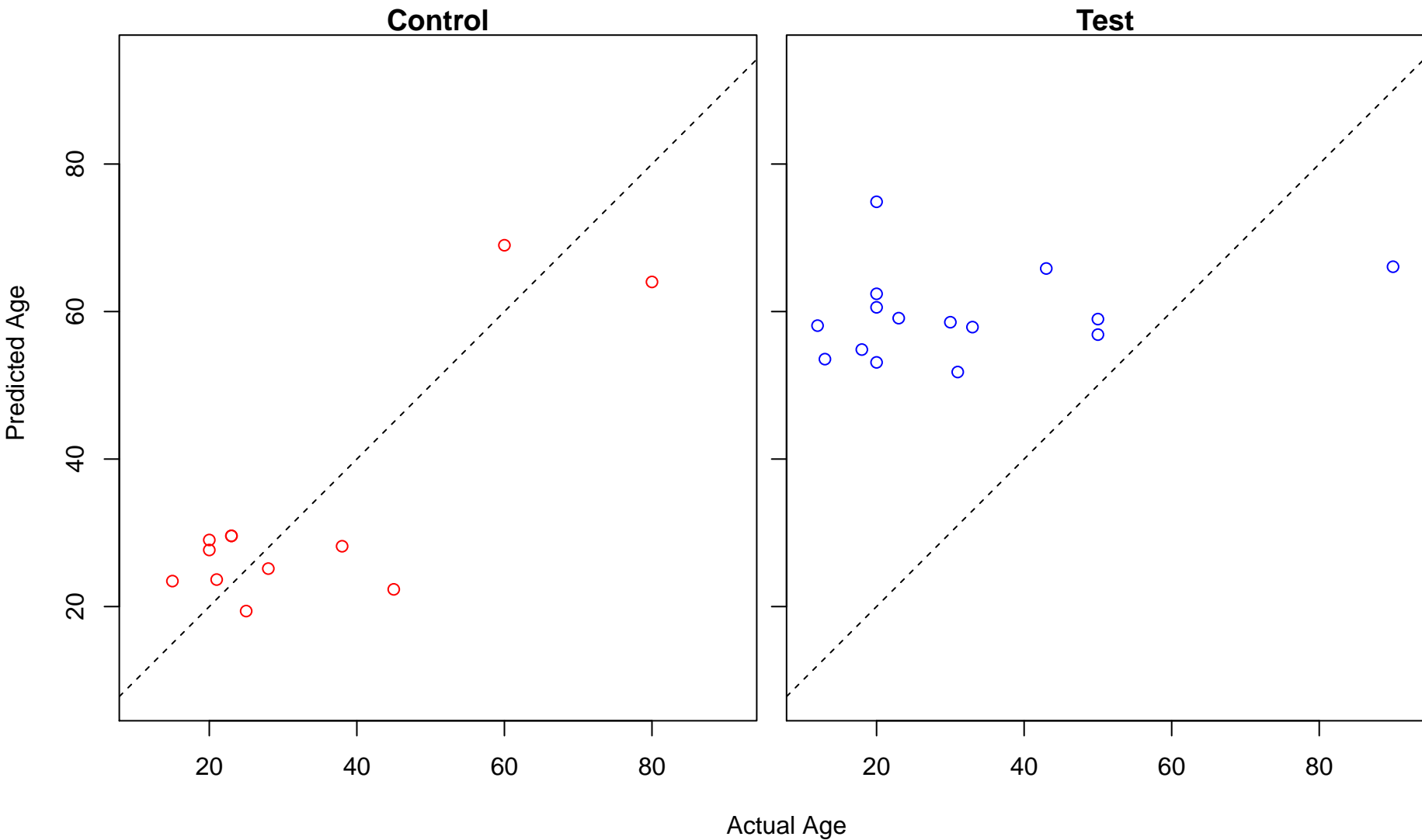
regulation of interleukin-2 secretion (Score: 3.900370)



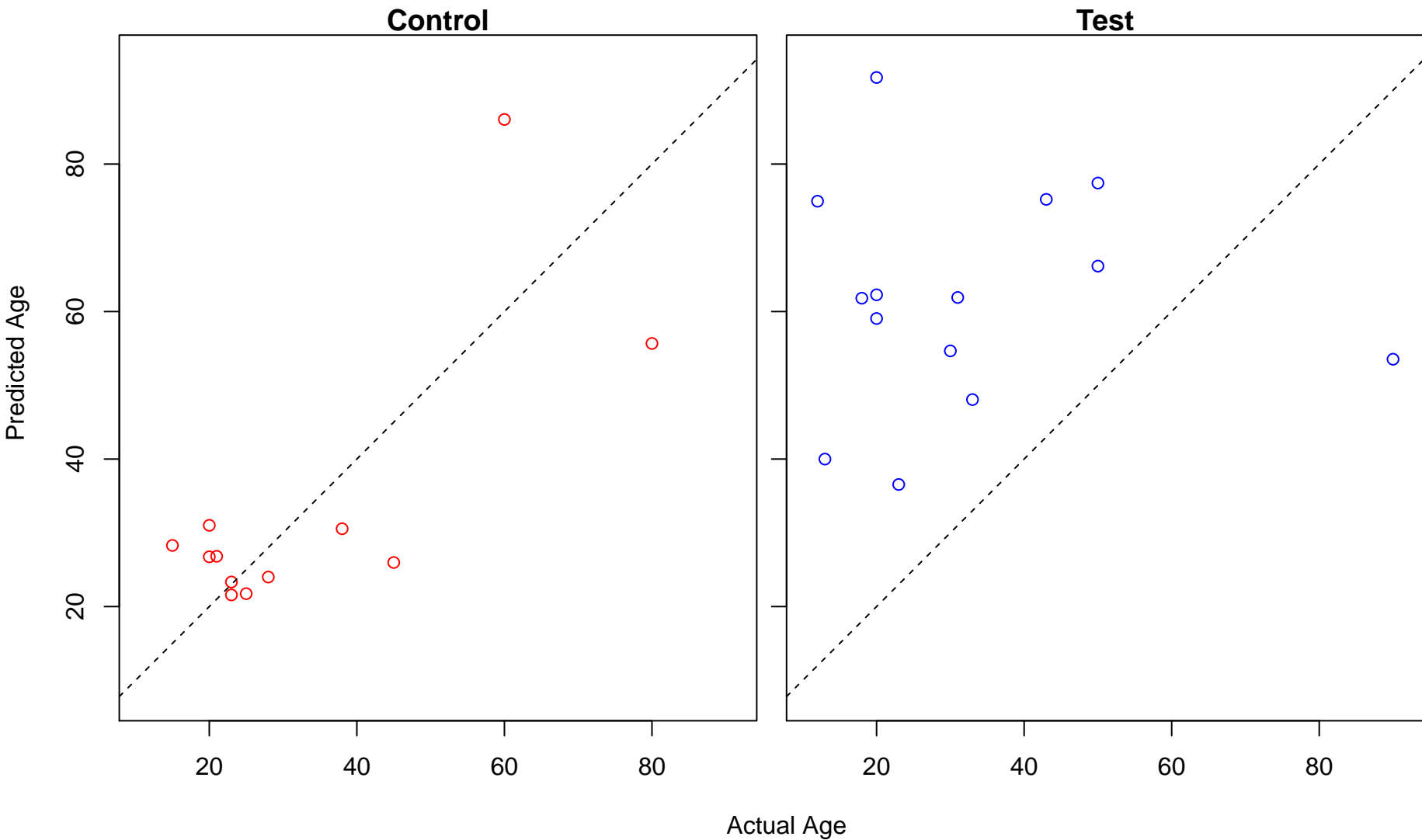
cellular modified amino acid catabolic process (Score: 3.899722)



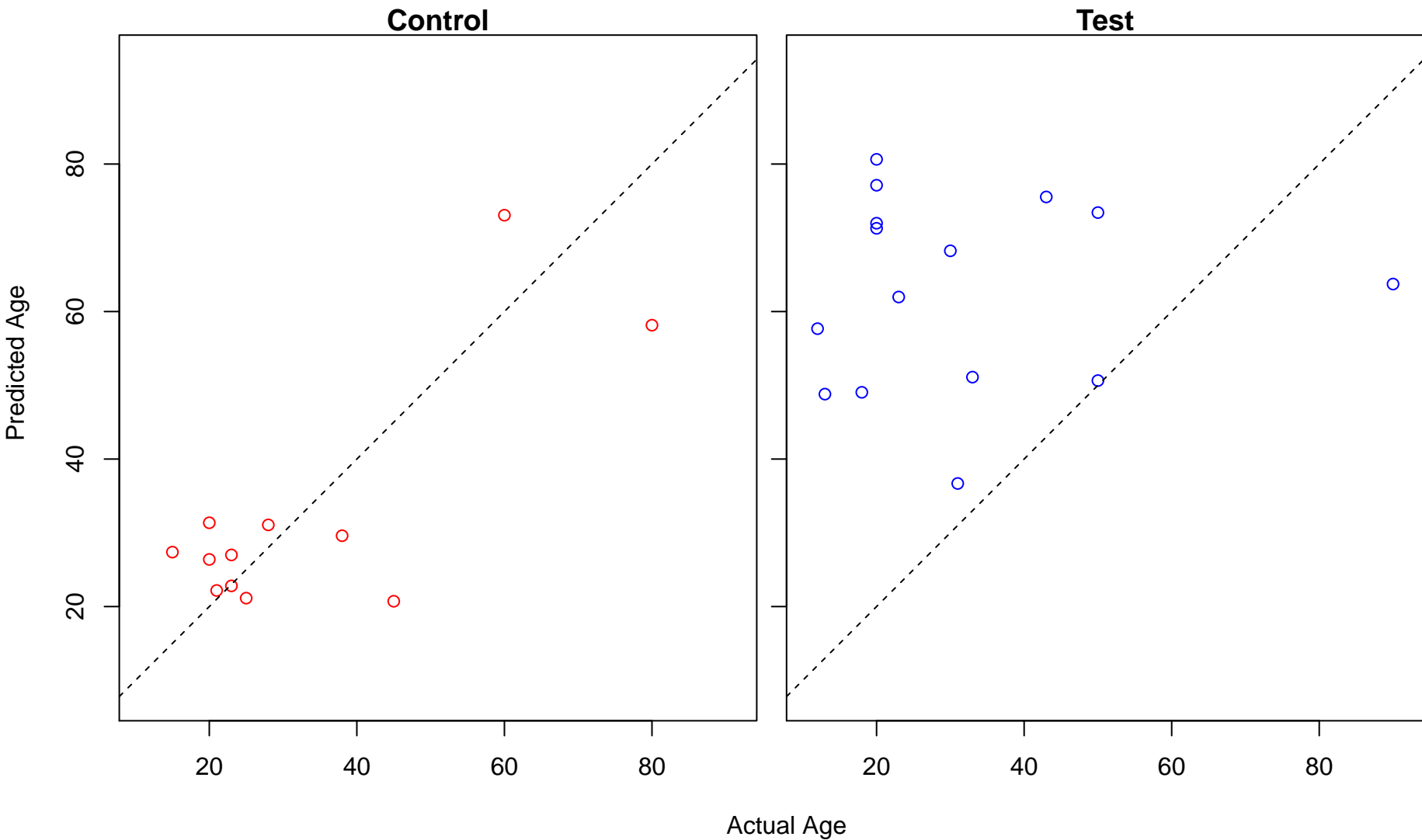
peptidyl-lysine trimethylation (Score: 3.894847)



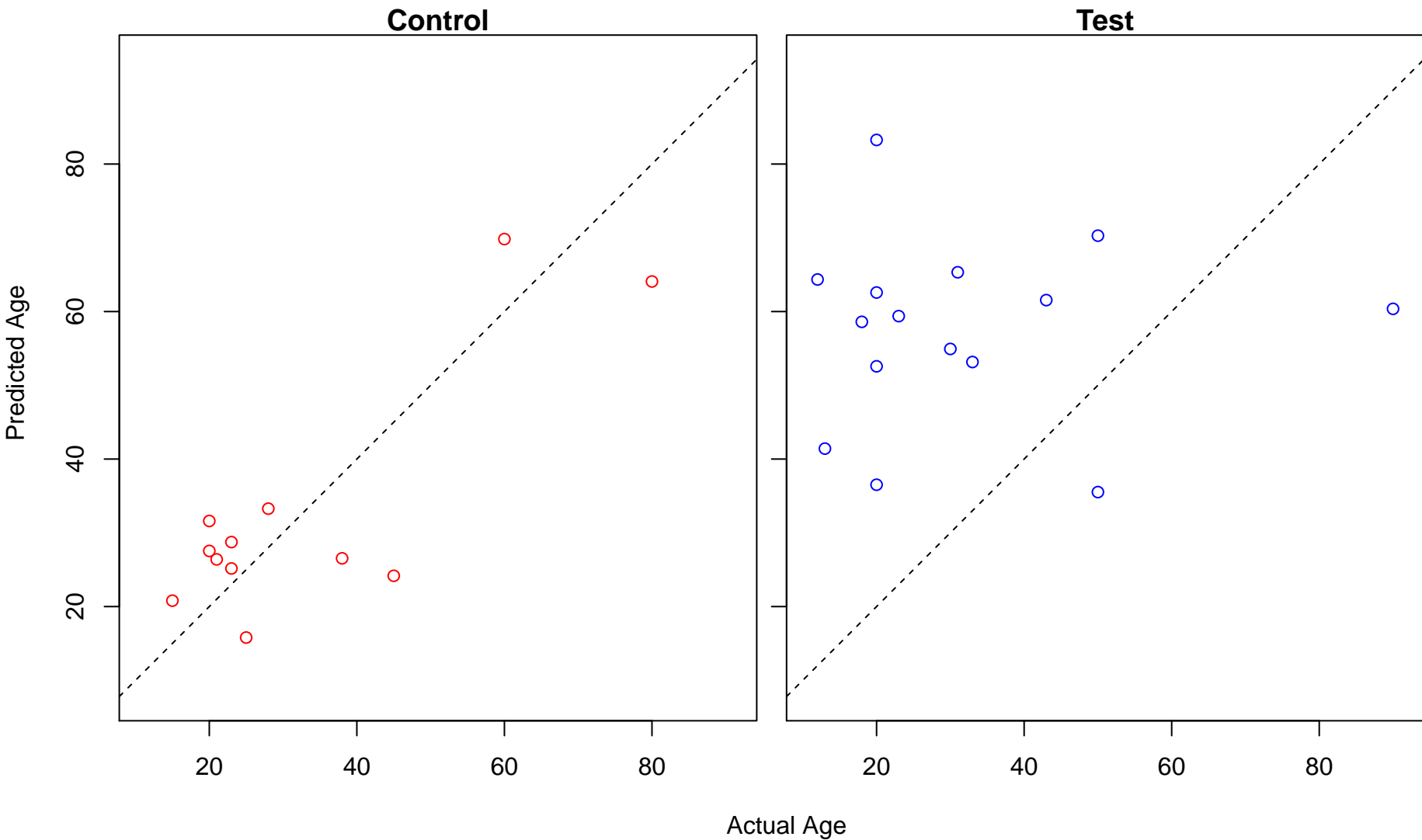
positive regulation of endothelial cell apoptotic process (Score: 3.891338)



detoxification (Score: 3.891120)

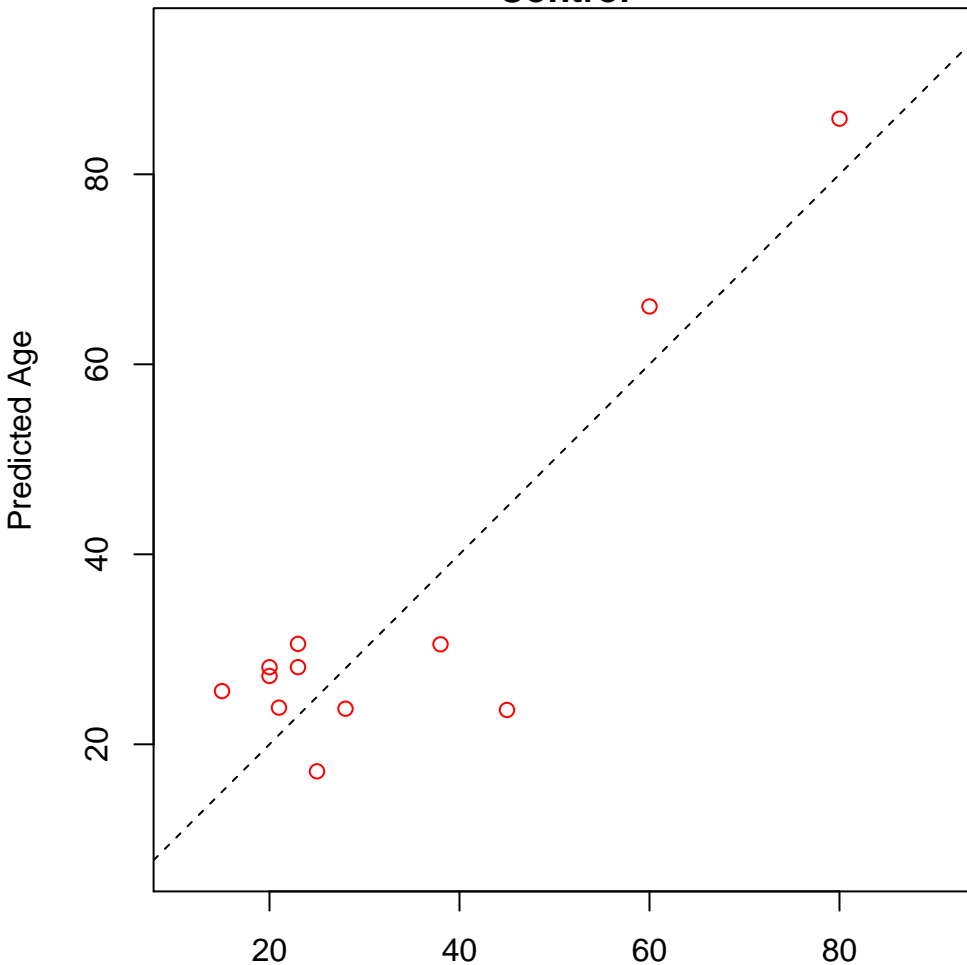


axonal fasciculation (Score: 3.891085)

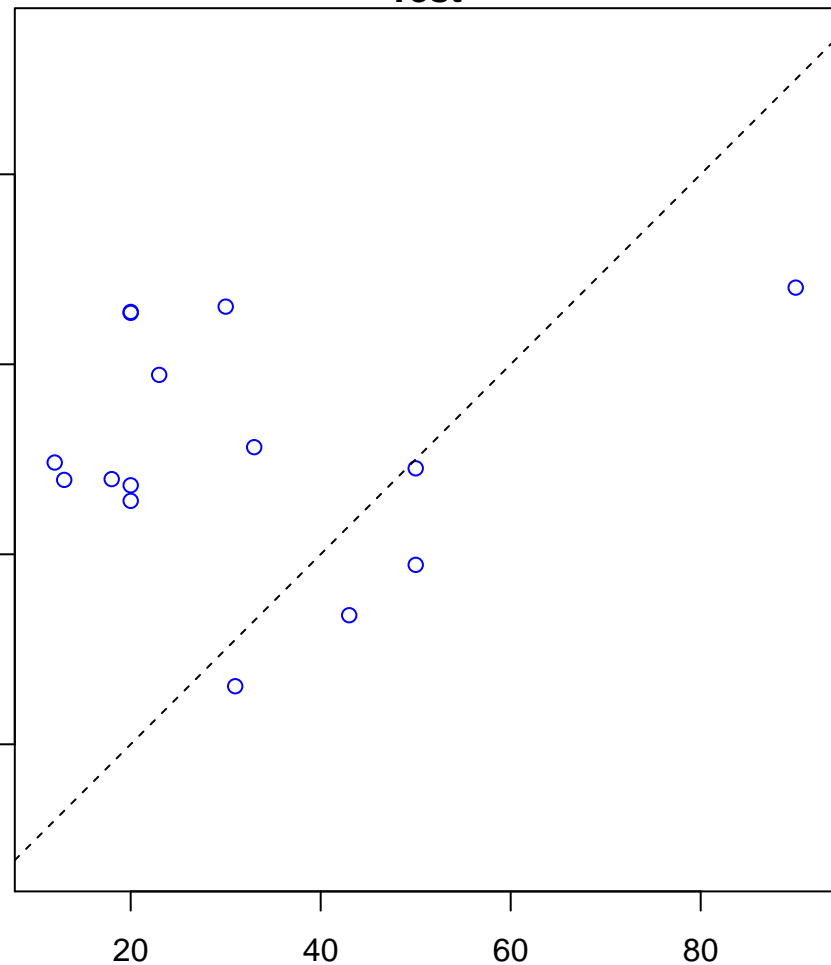


amino acid transmembrane transport (Score: 3.890876)

Control

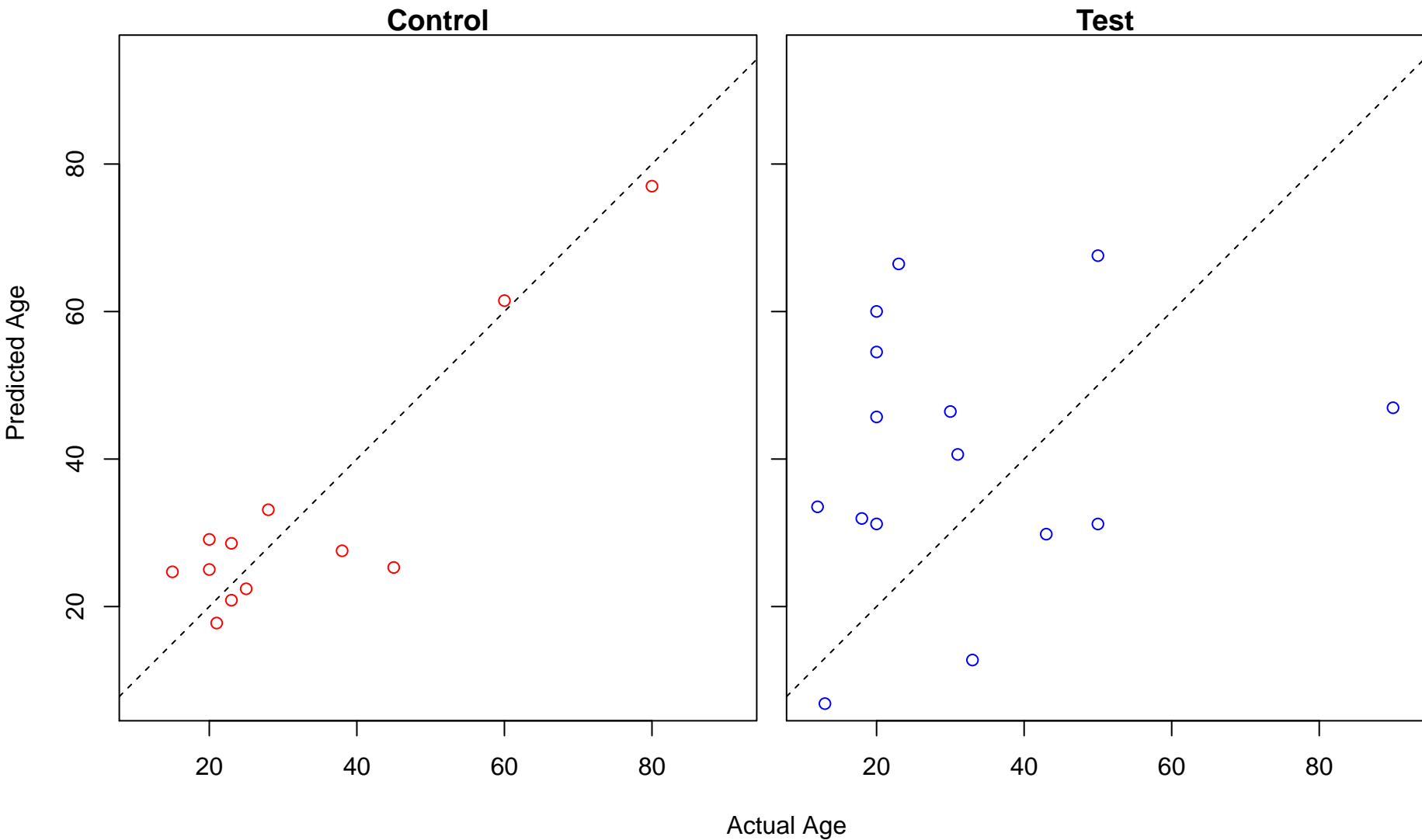


Test

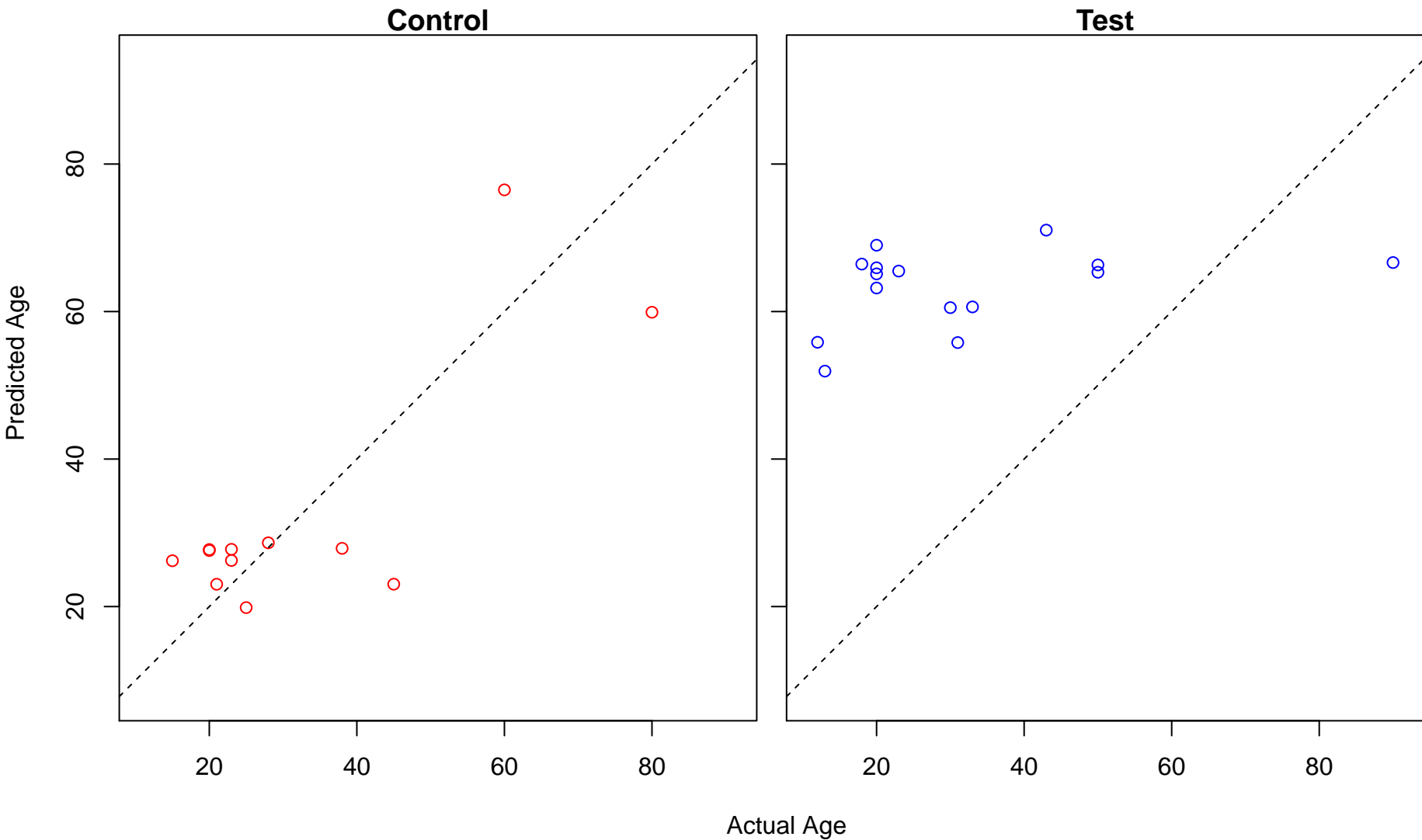


Actual Age

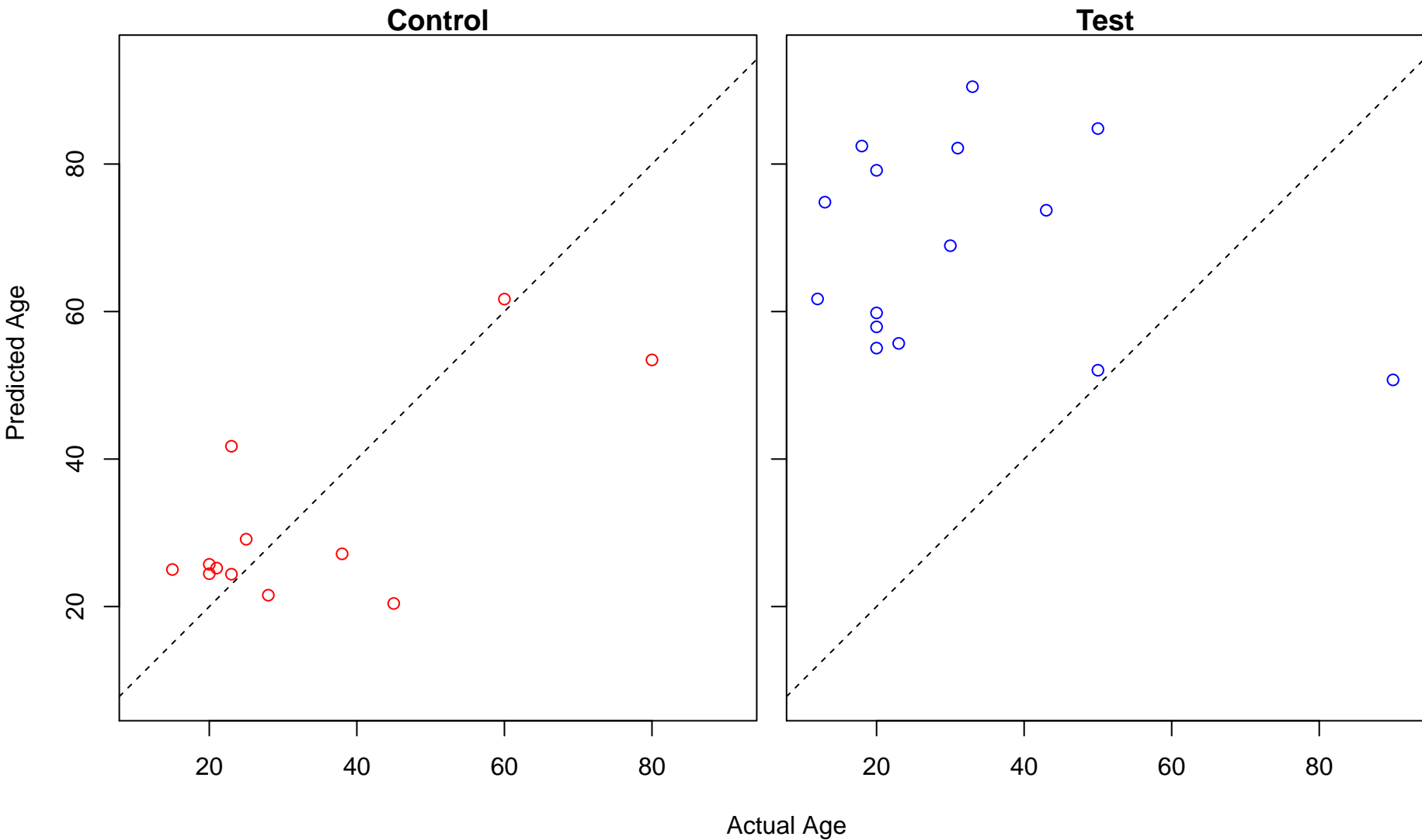
neurotransmitter transport (Score: 3.884582)



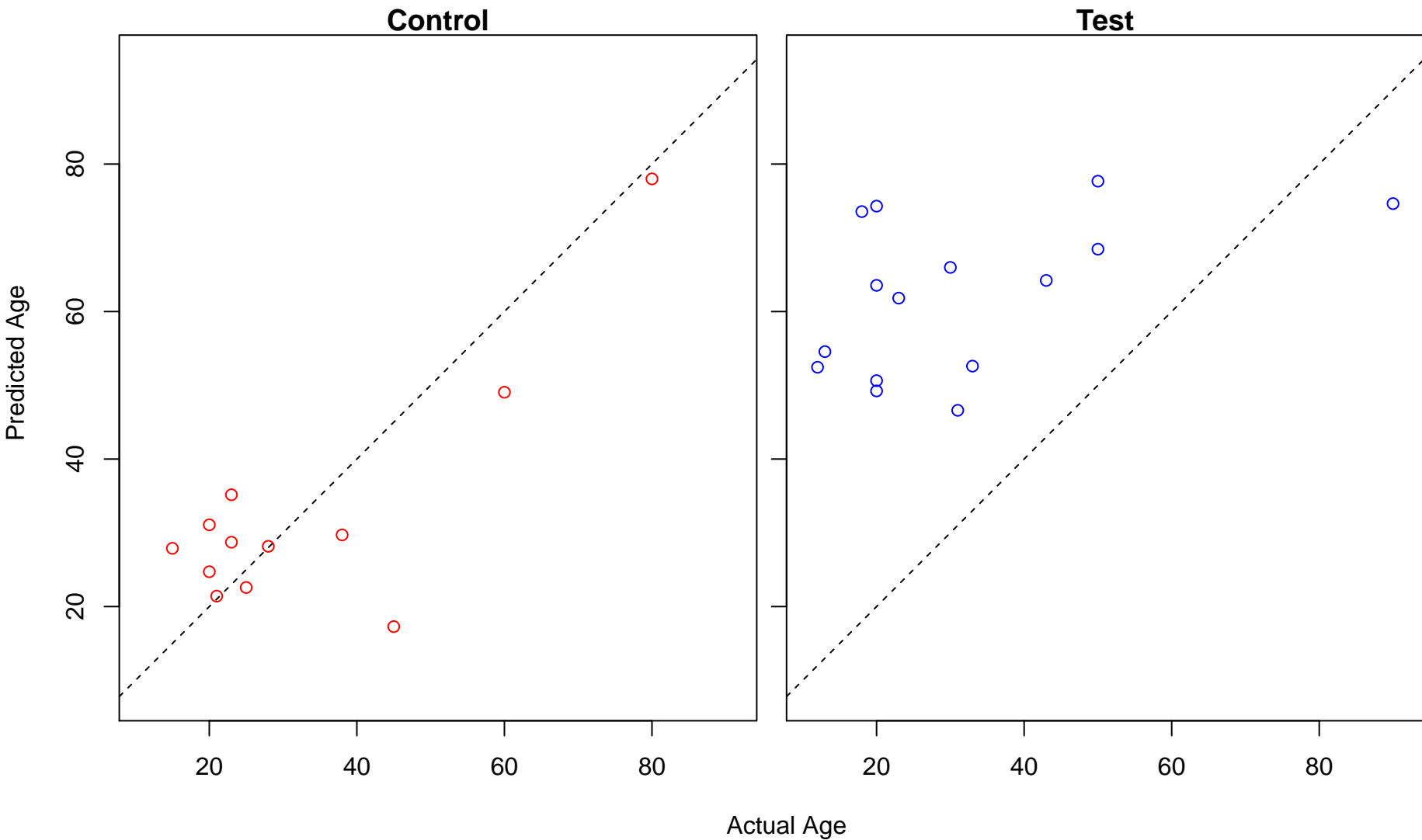
regulation of cardiac muscle cell action potential (Score: 3.880363)



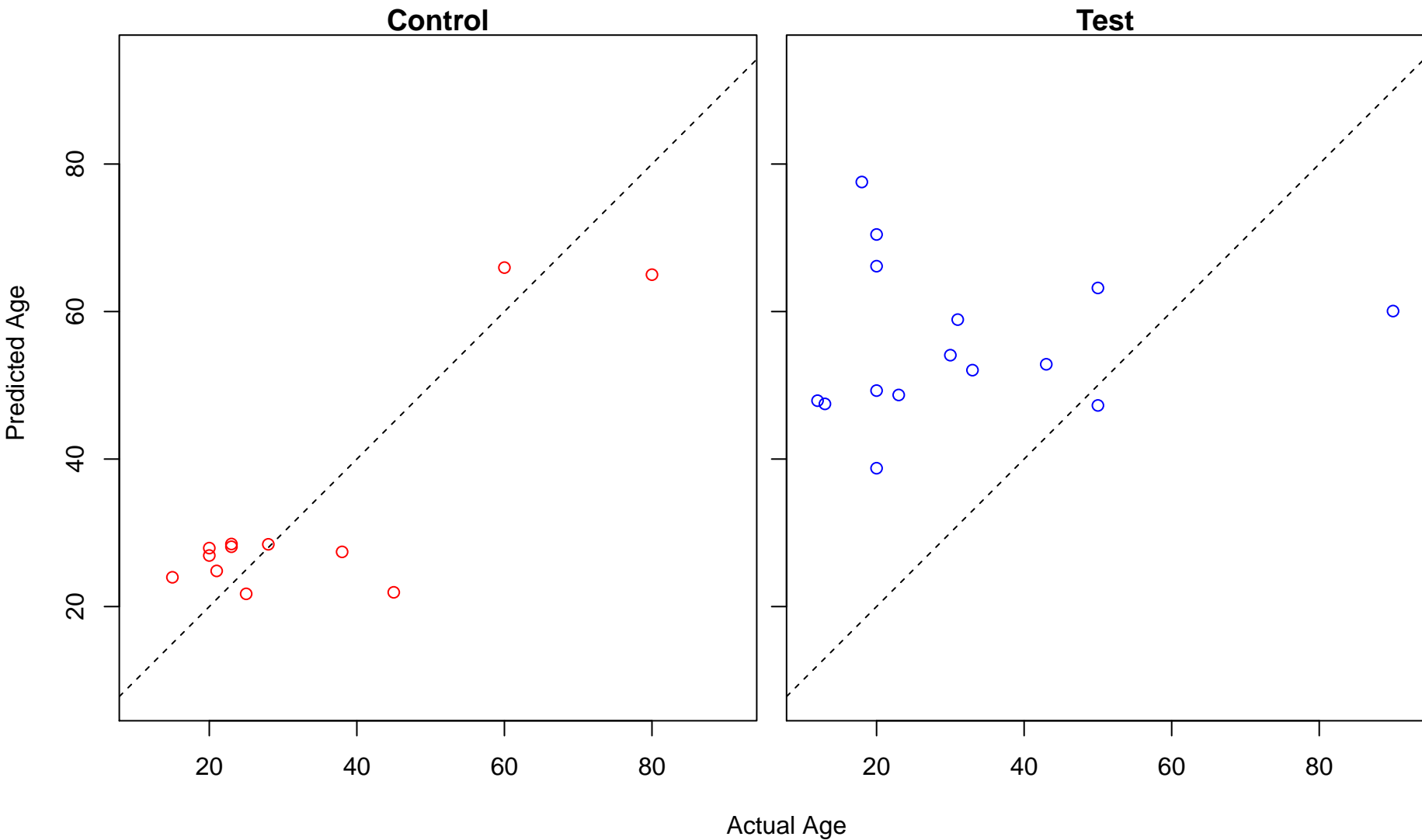
T cell proliferation (Score: 3.879202)



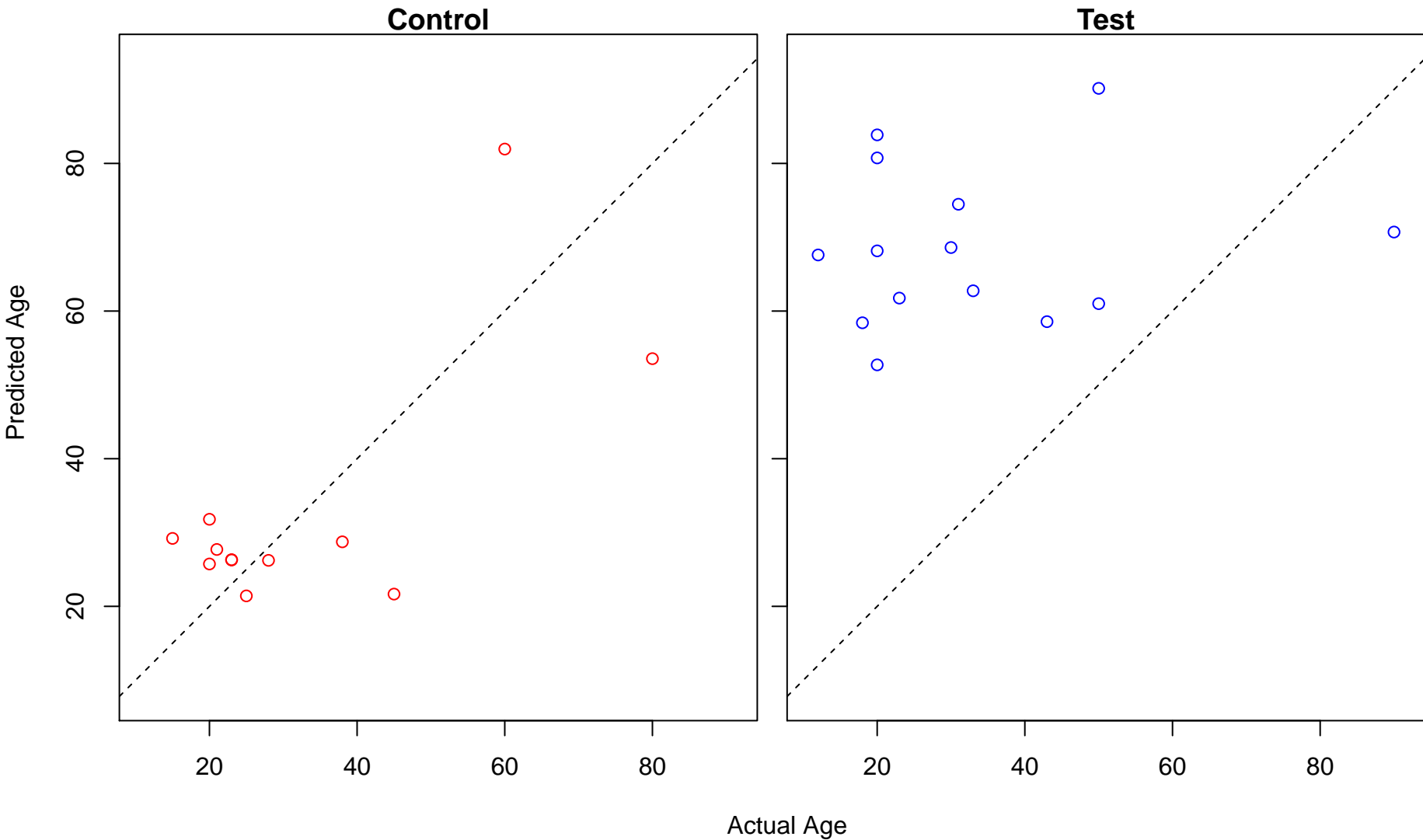
negative regulation of interleukin-10 production (Score: 3.878051)



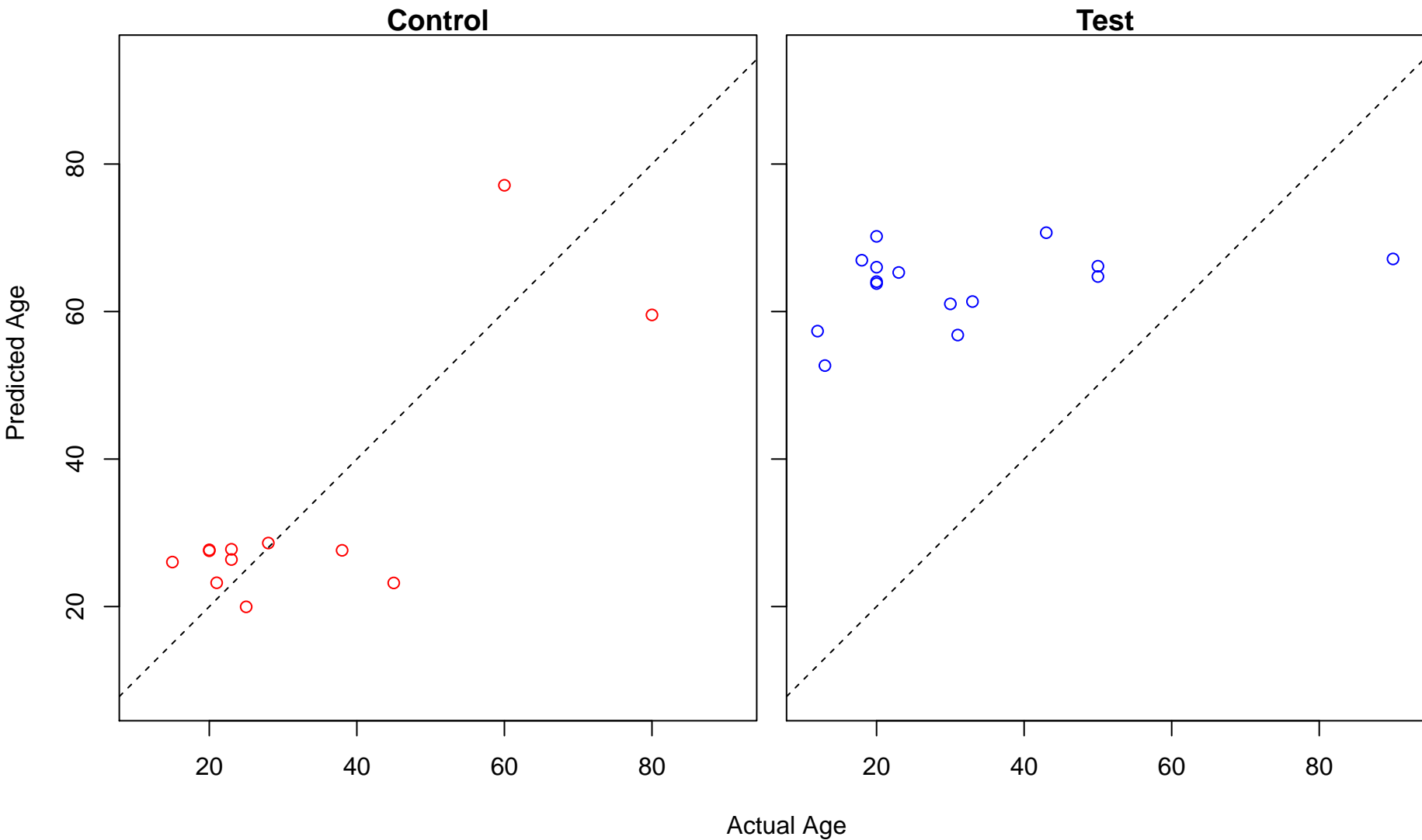
leukocyte activation (Score: 3.876145)



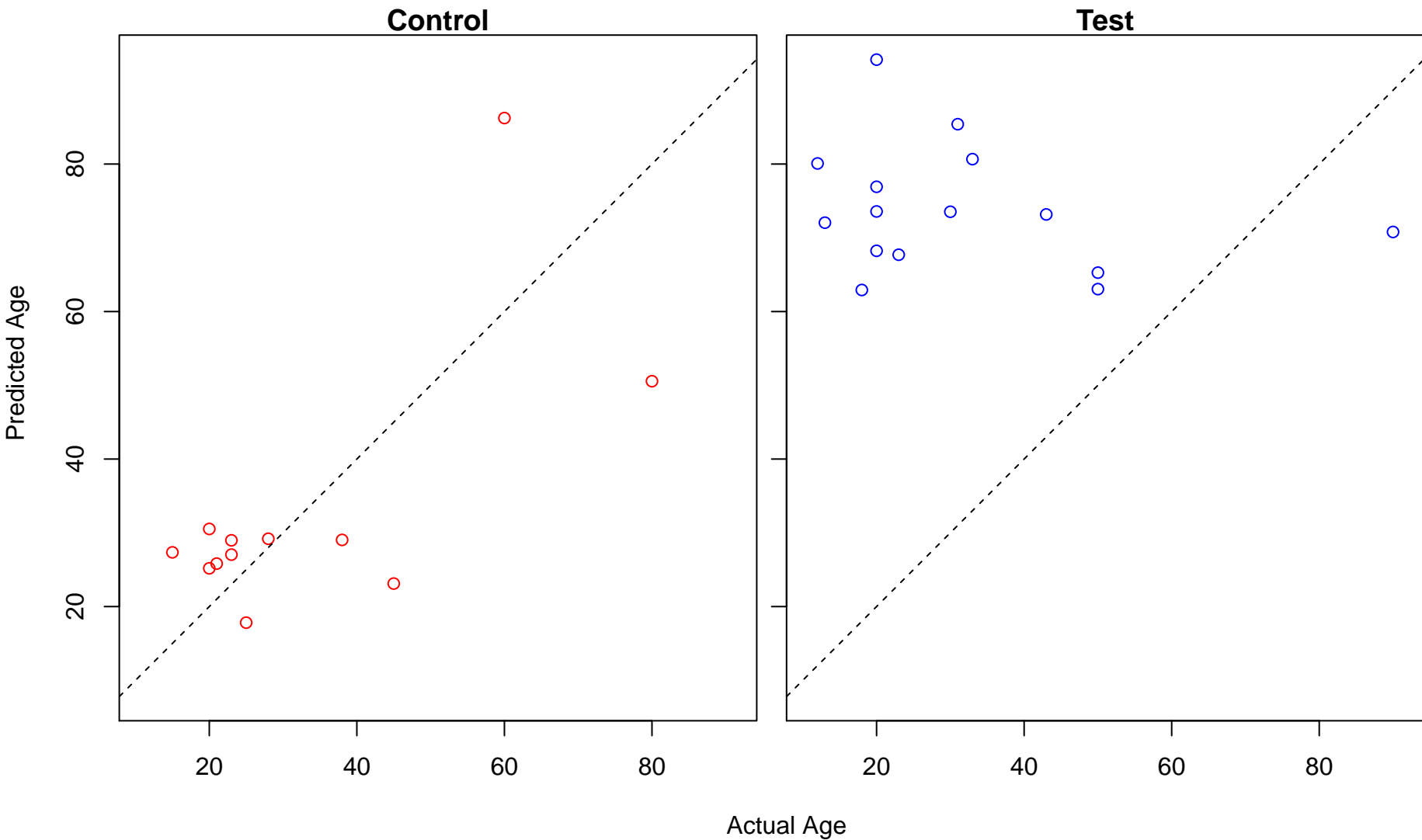
cellular response to gonadotropin stimulus (Score: 3.876066)



regulation of action potential (Score: 3.874878)

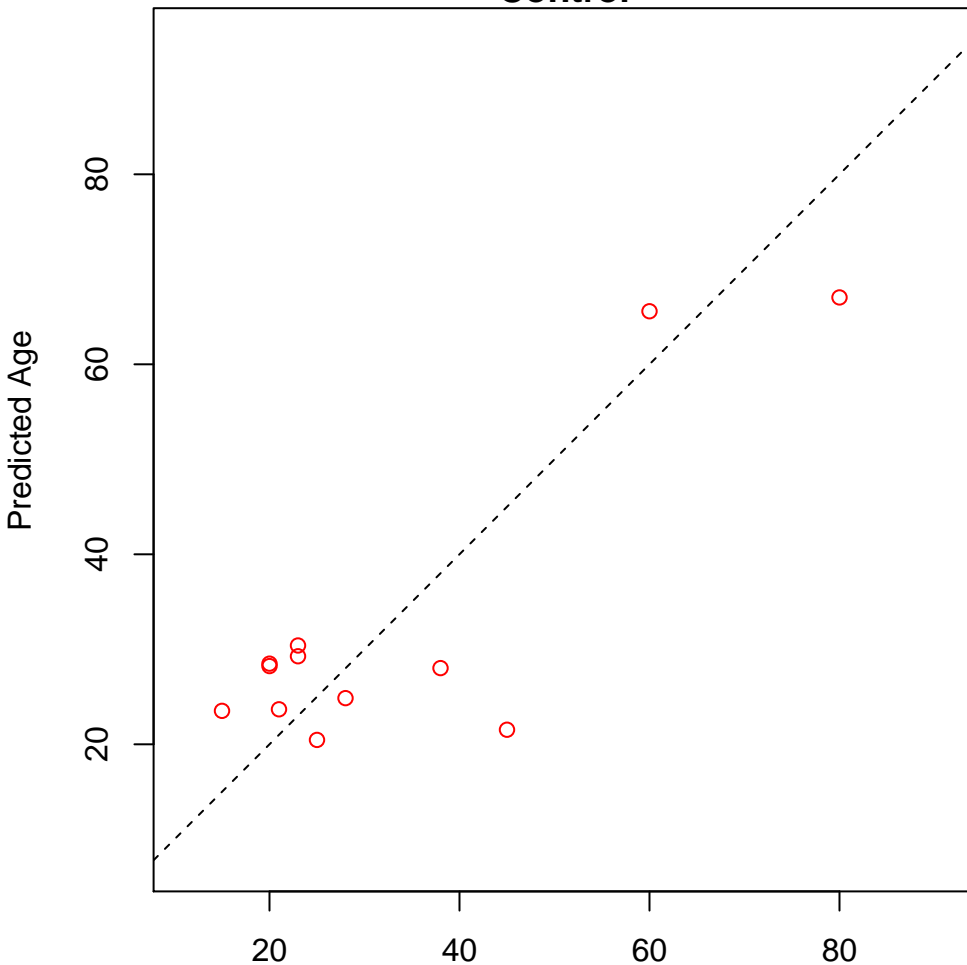


sodium-independent organic anion transport (Score: 3.873681)

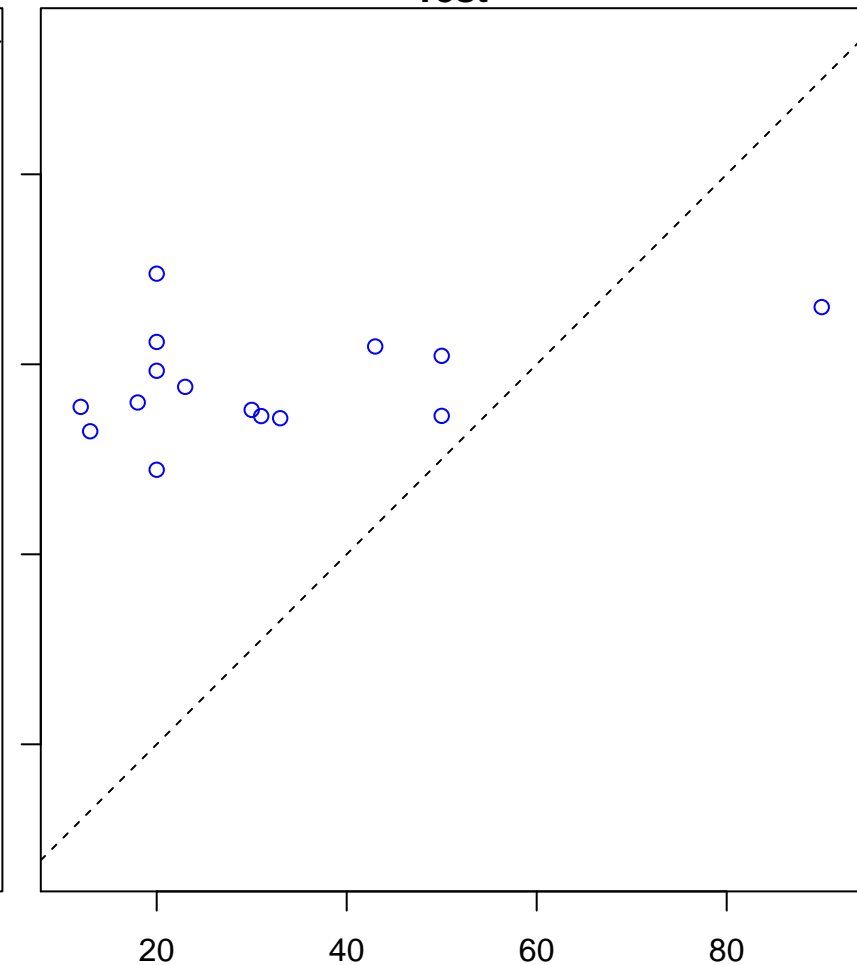


regulation of granulocyte differentiation (Score: 3.871067)

Control

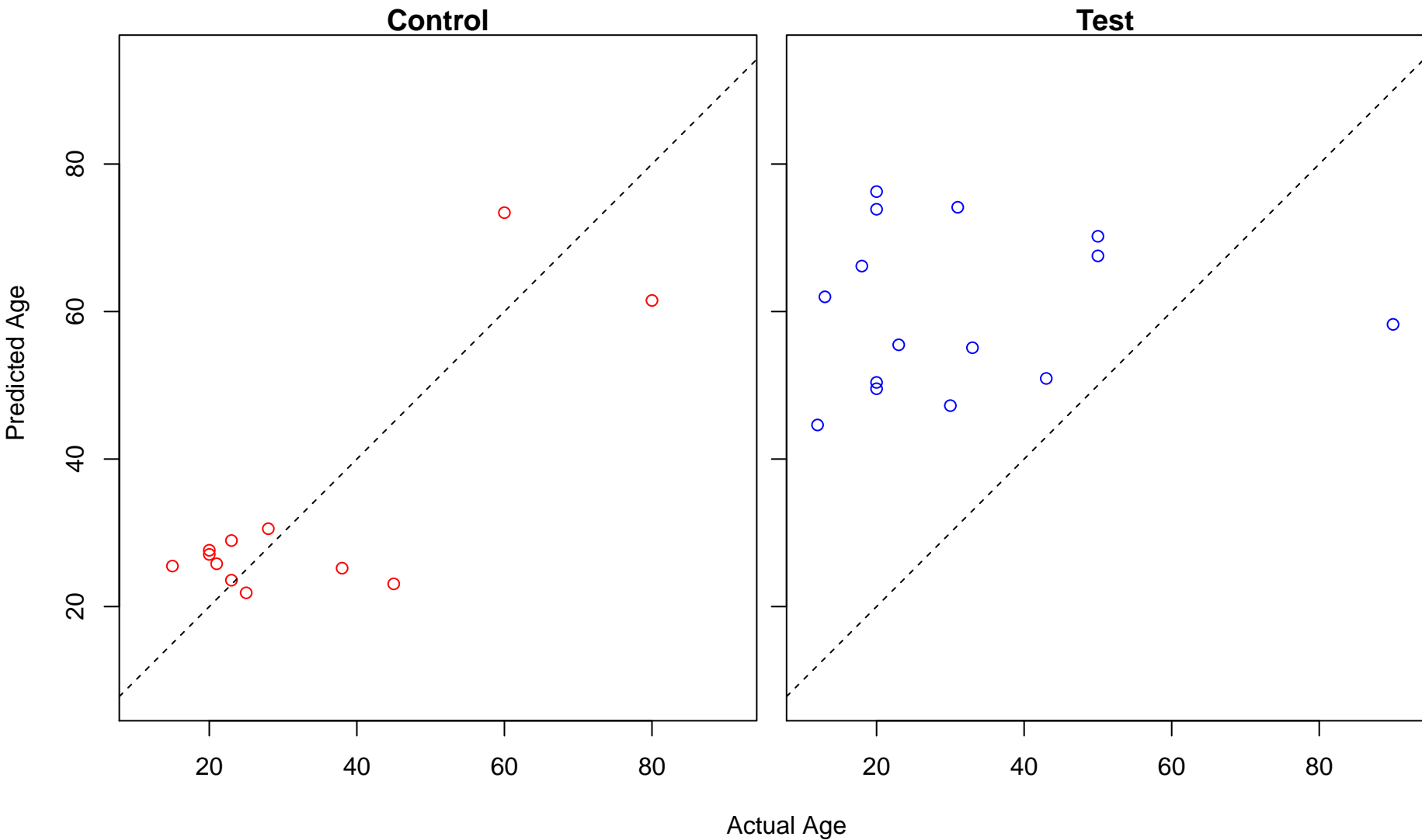


Test

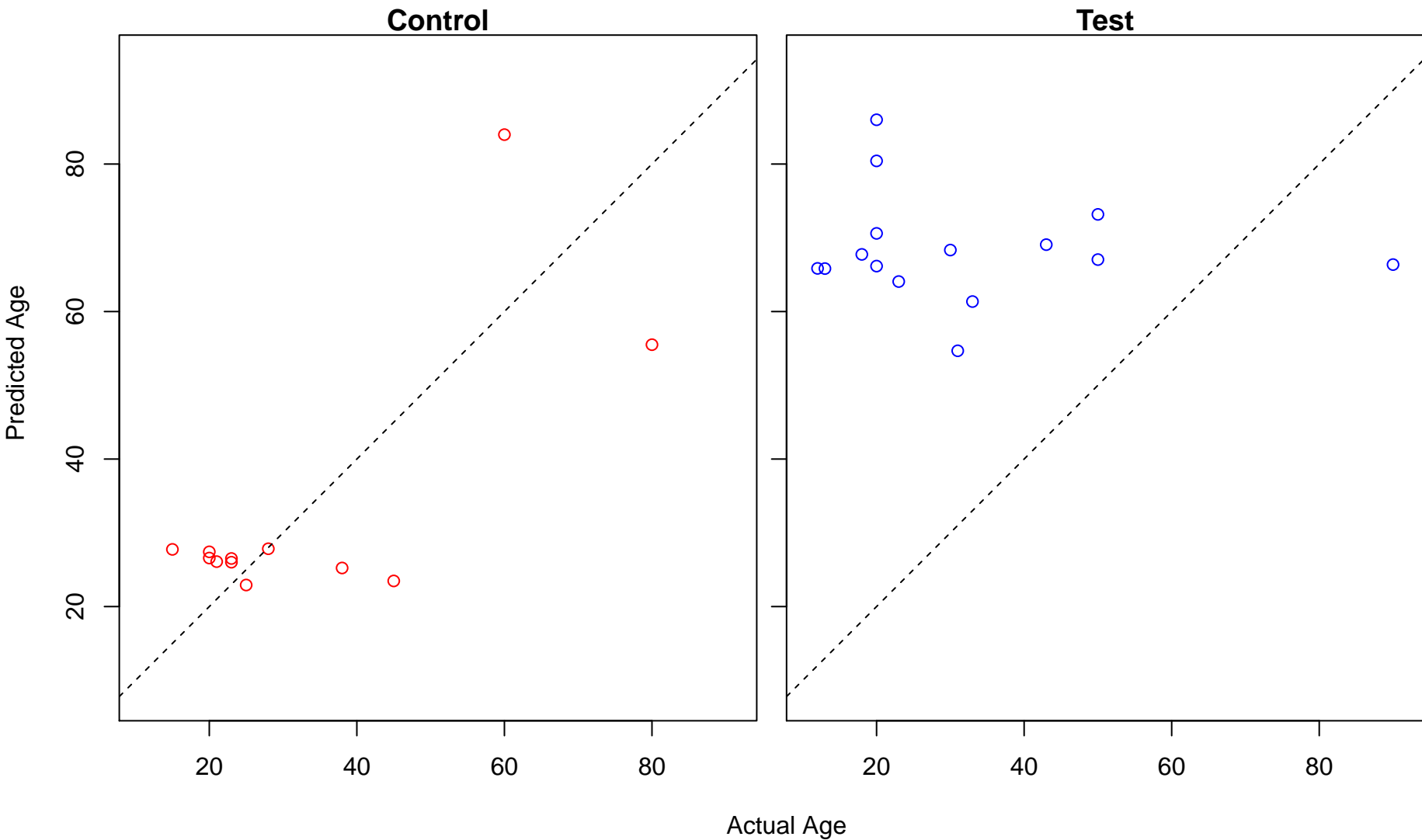


Actual Age

positive regulation of protein autophosphorylation (Score: 3.870730)

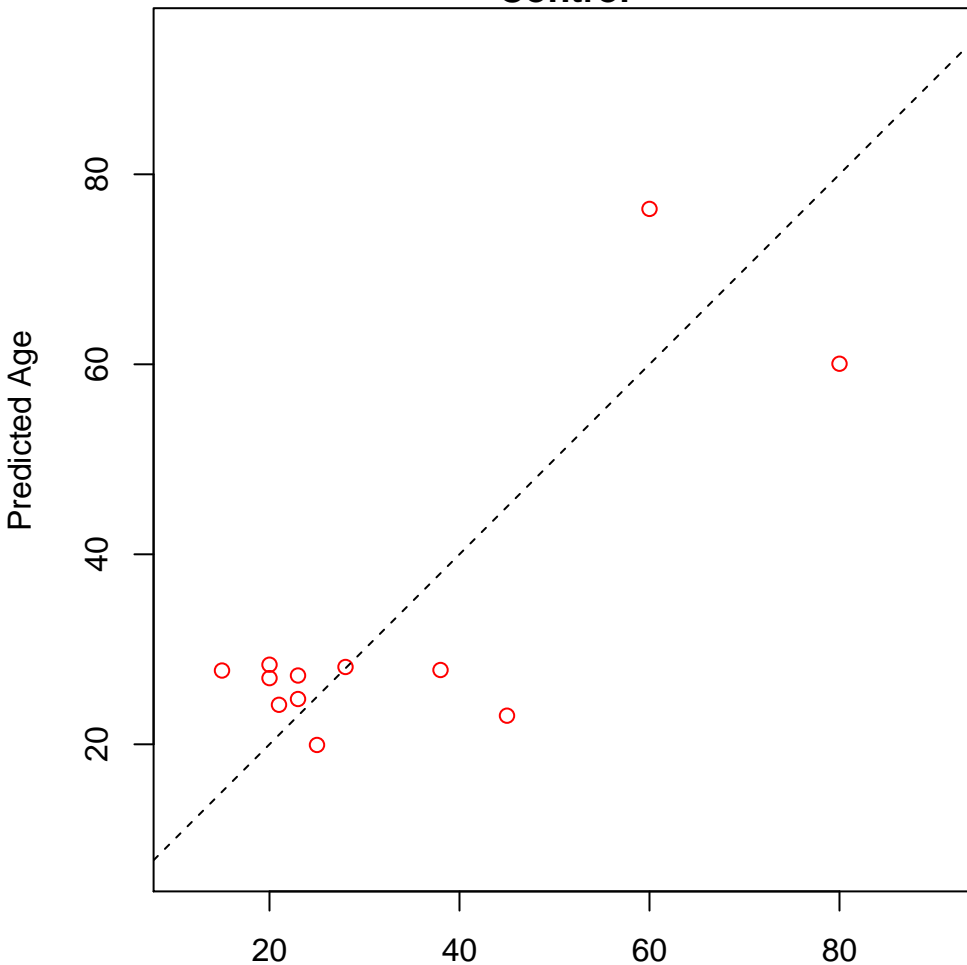


pigment metabolic process (Score: 3.868945)

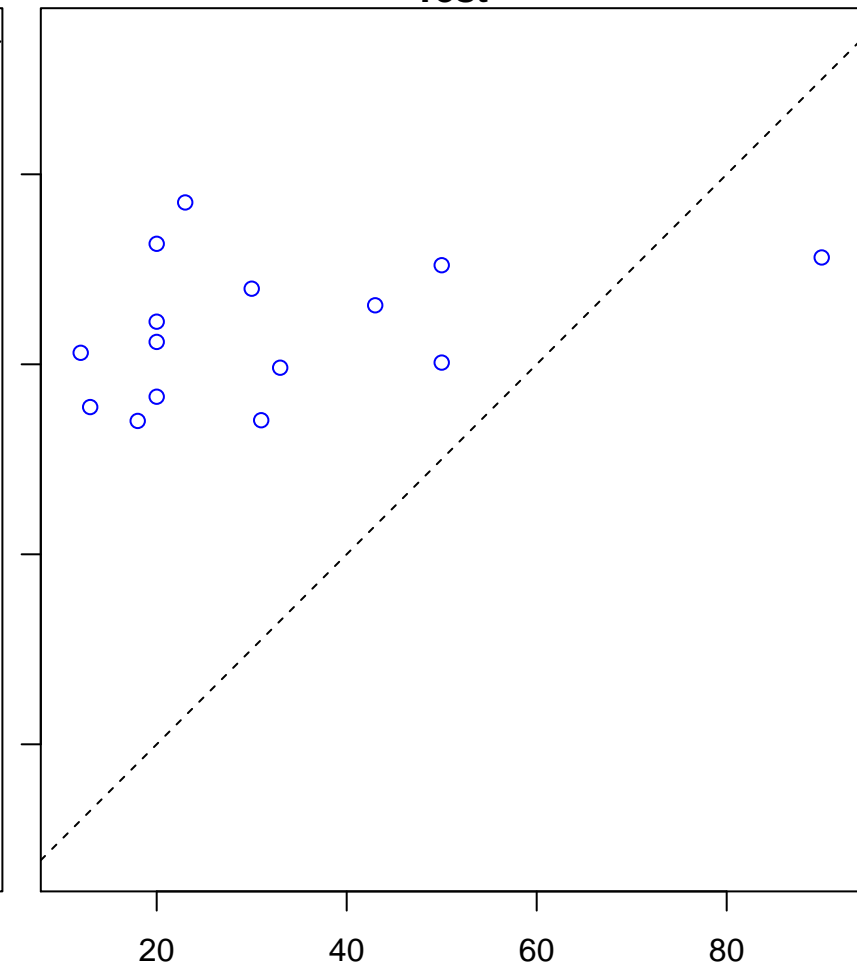


cytoplasmic microtubule organization (Score: 3.867010)

Control

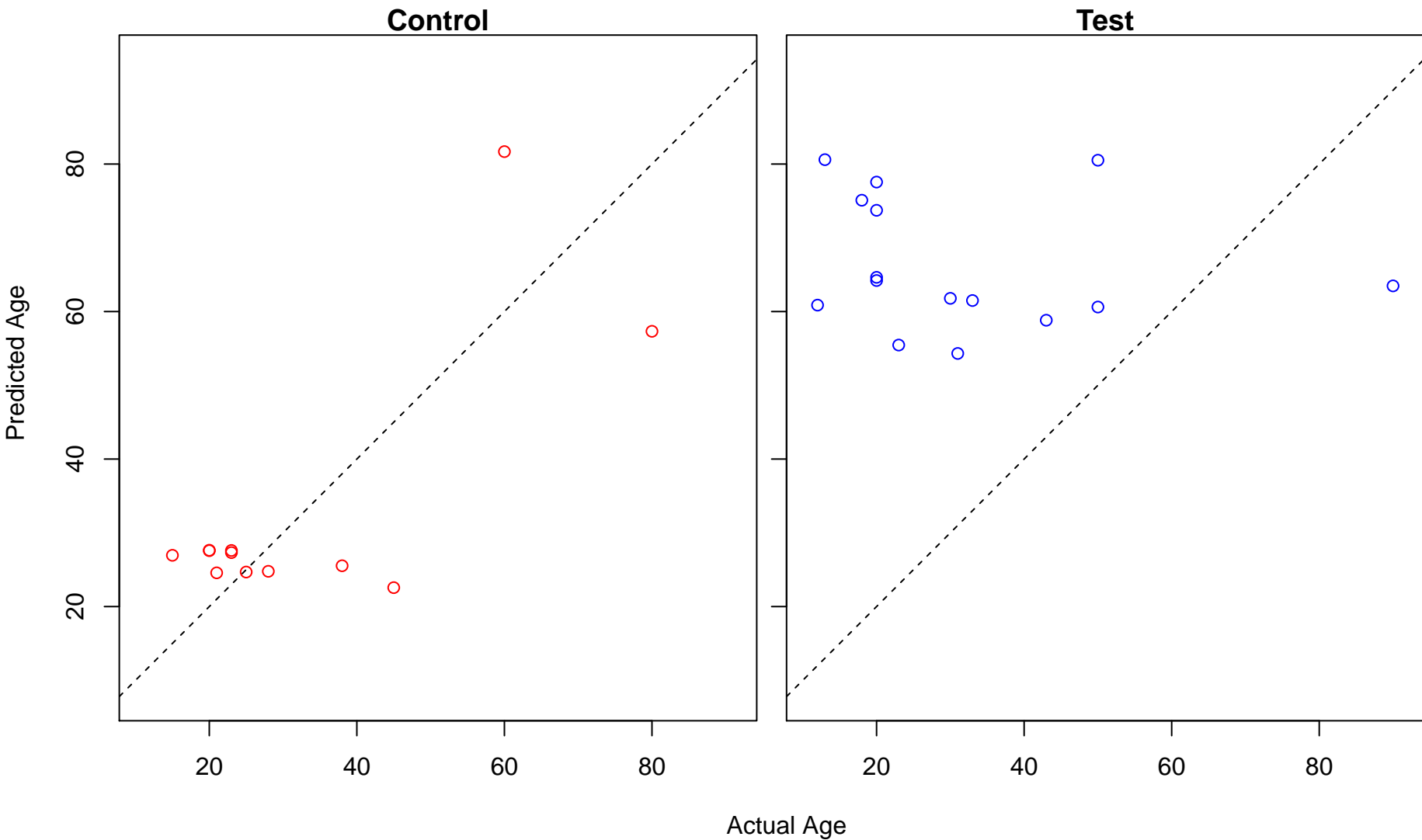


Test

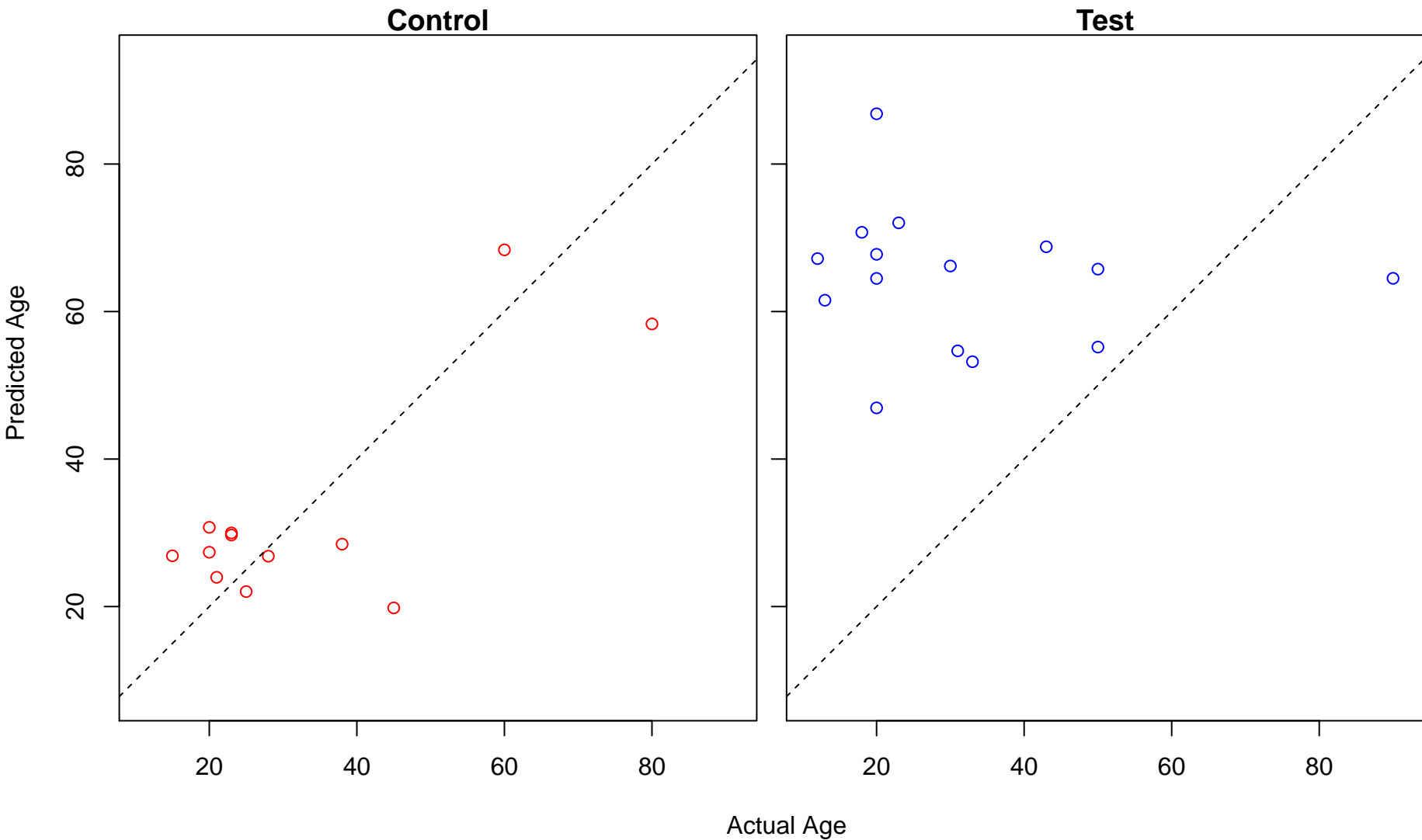


Actual Age

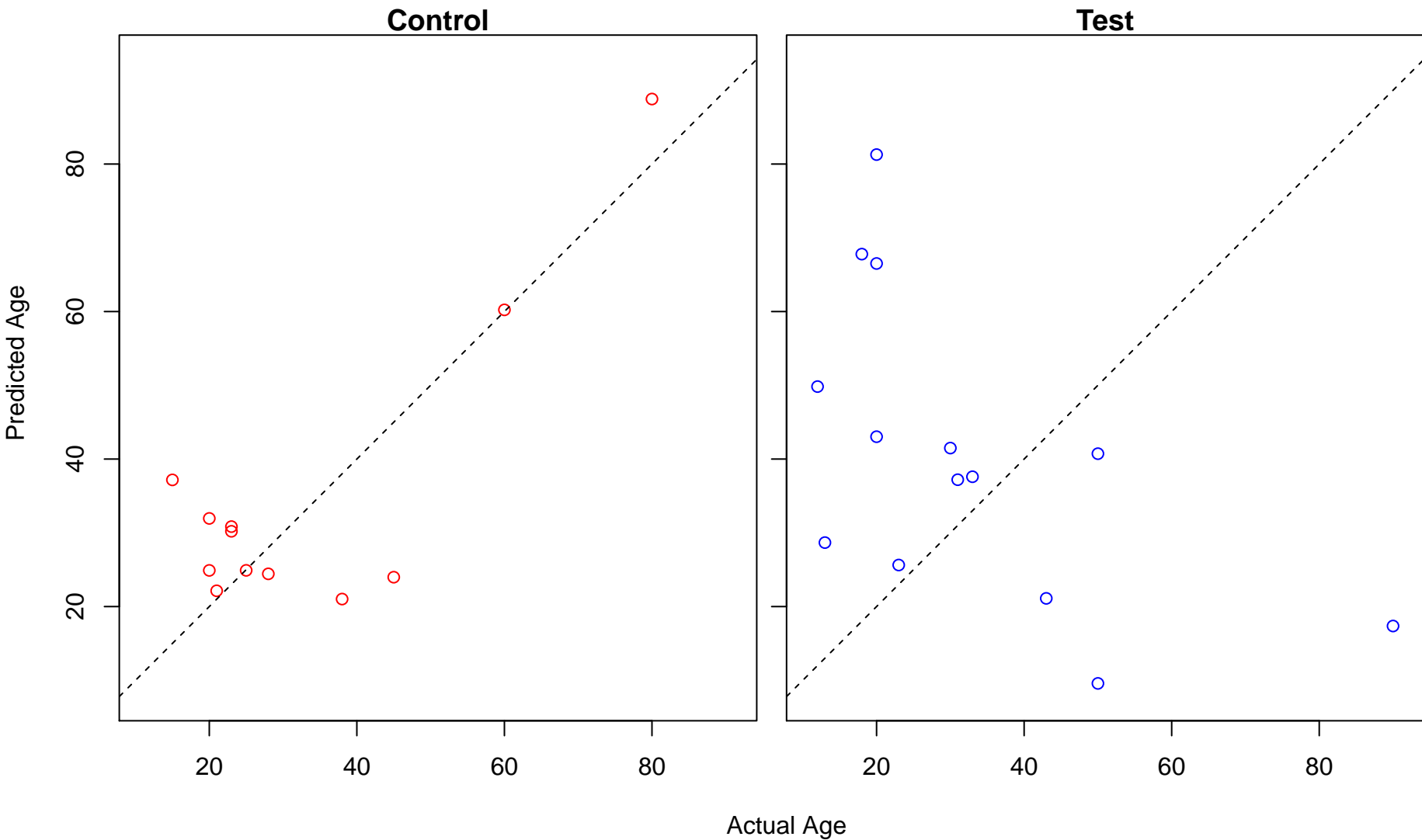
negative regulation of telomere maintenance (Score: 3.865189)



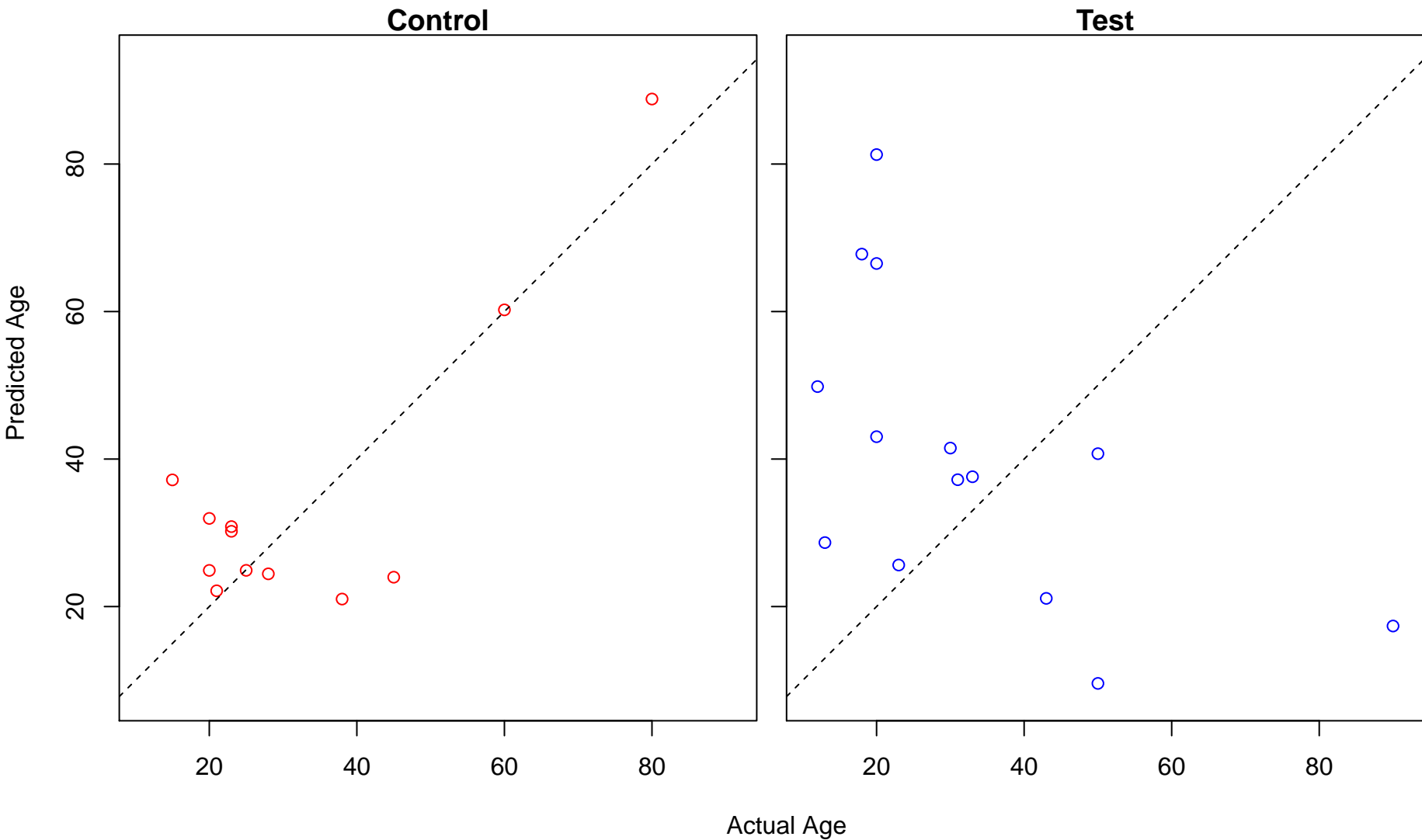
regulation of axon extension involved in axon guidance (Score: 3.865025)



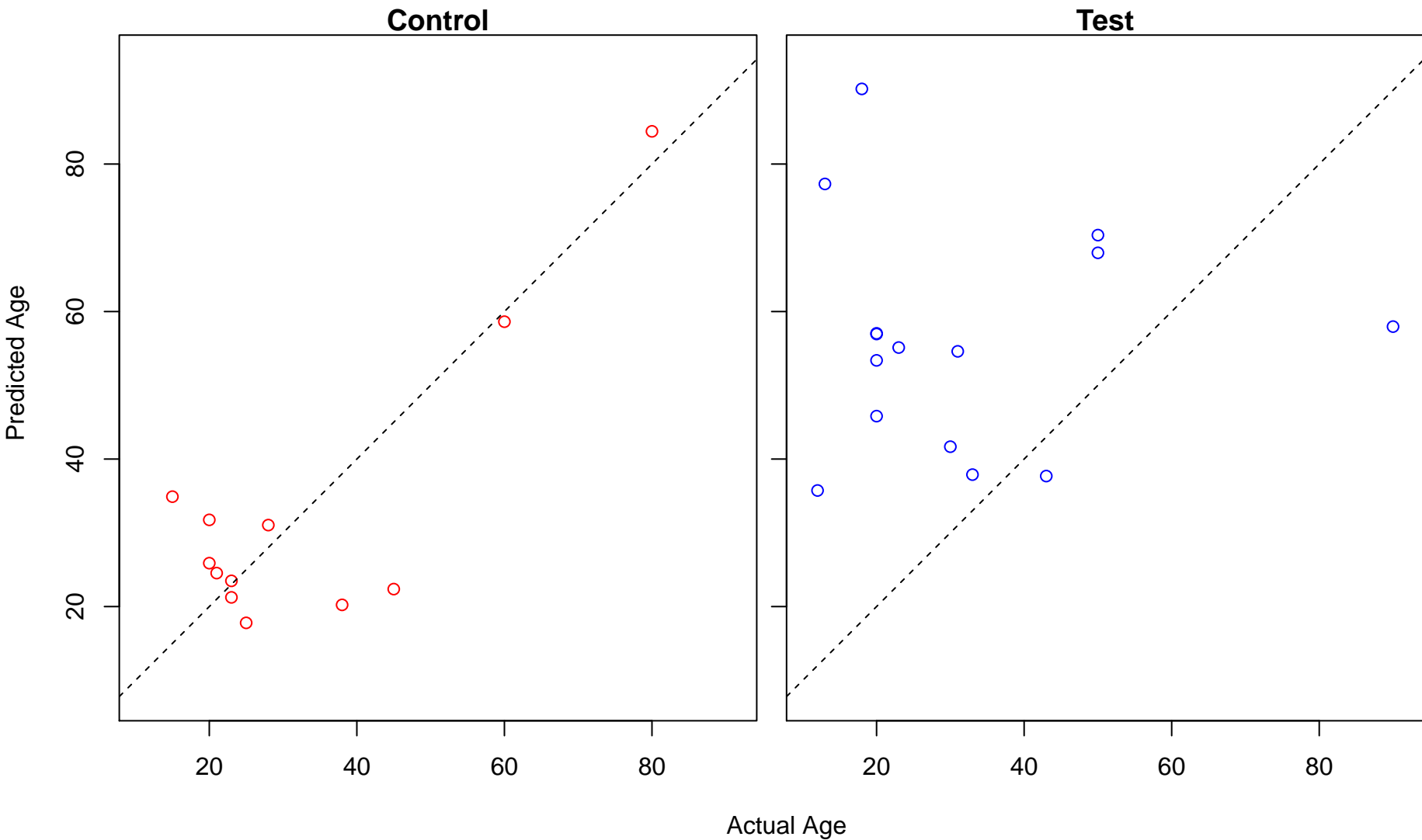
regulation of telomerase RNA localization to Cajal body (Score: 3.862296)



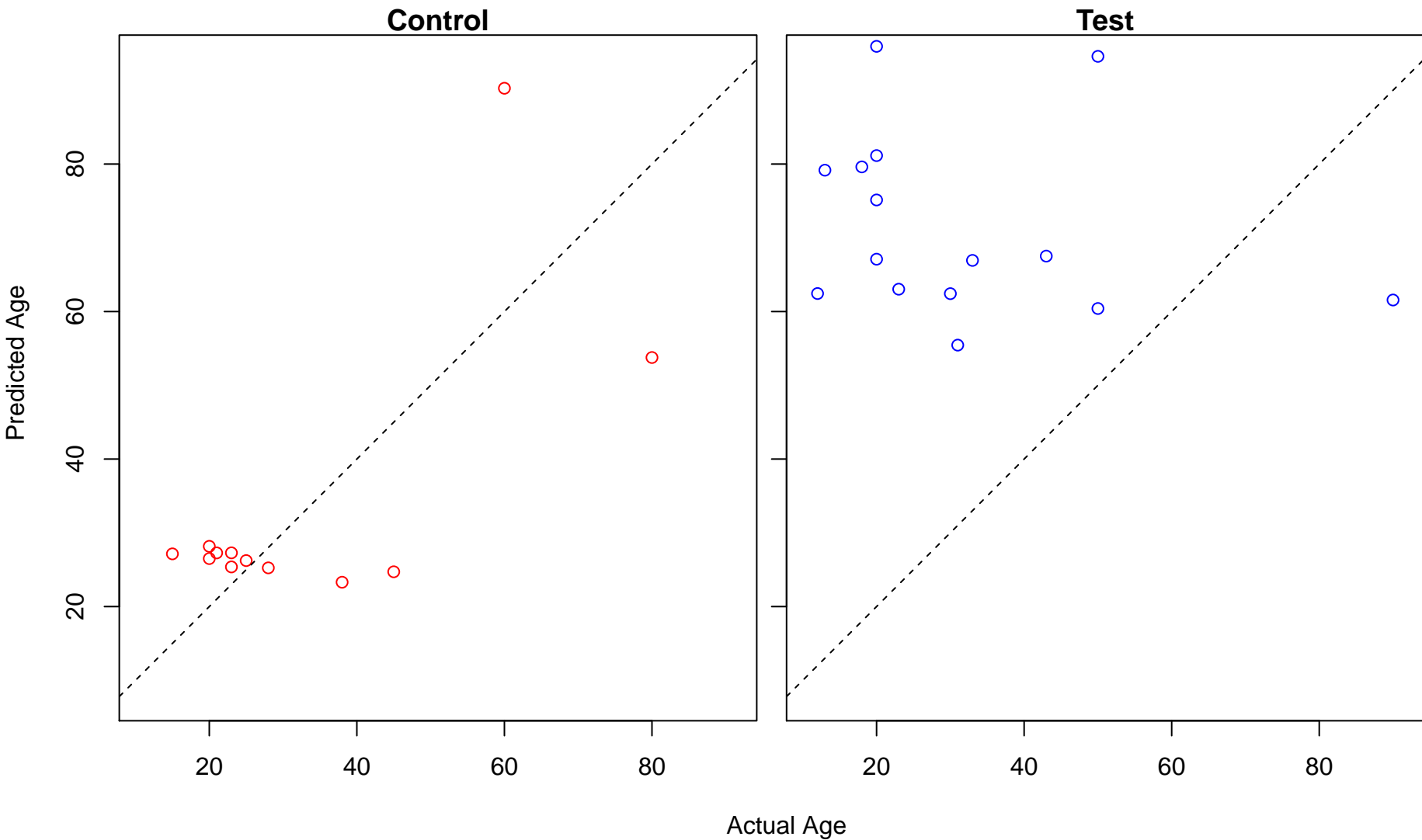
positive regulation of telomerase RNA localization to Cajal body (Score: 3.862296)



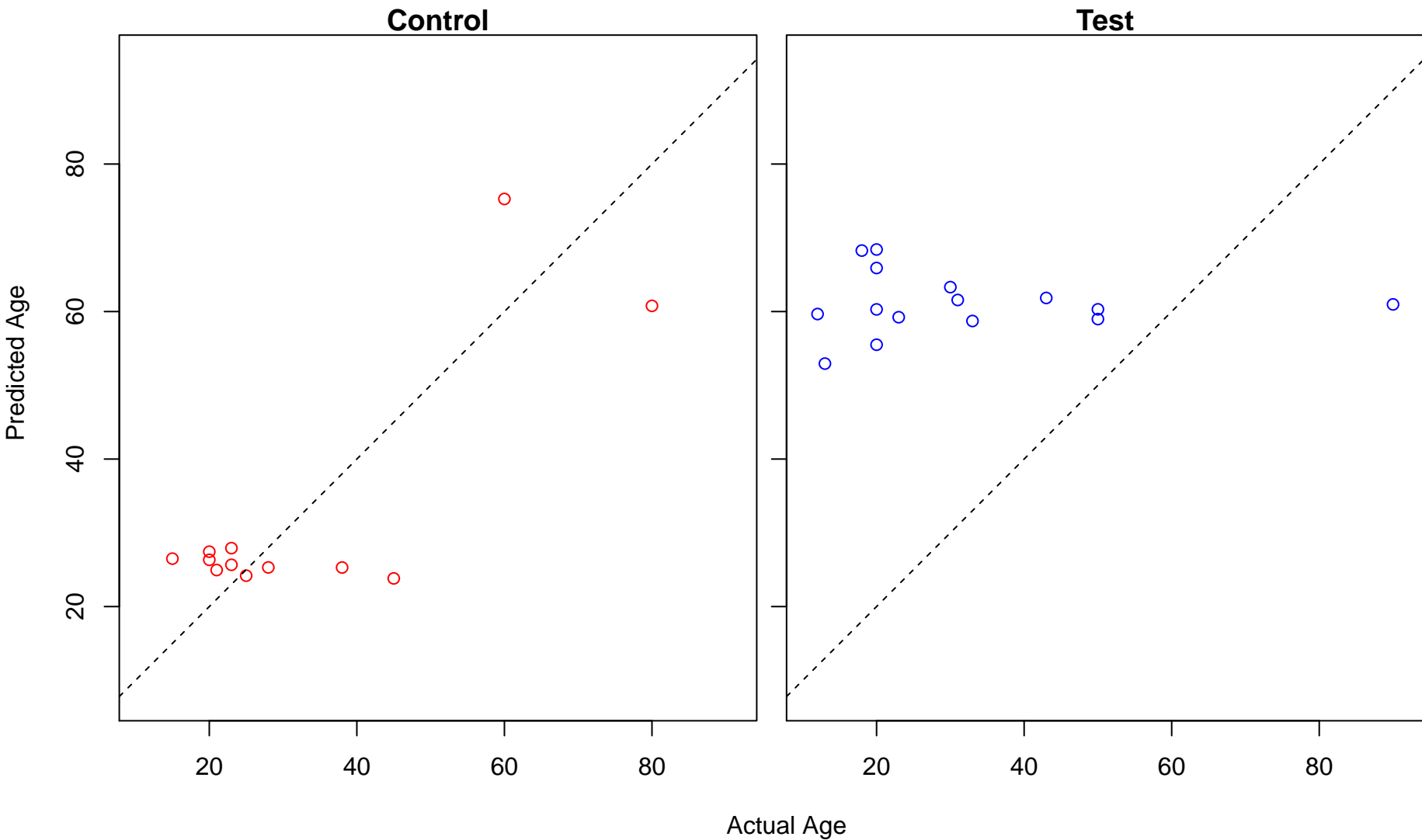
nucleoside diphosphate metabolic process (Score: 3.861964)



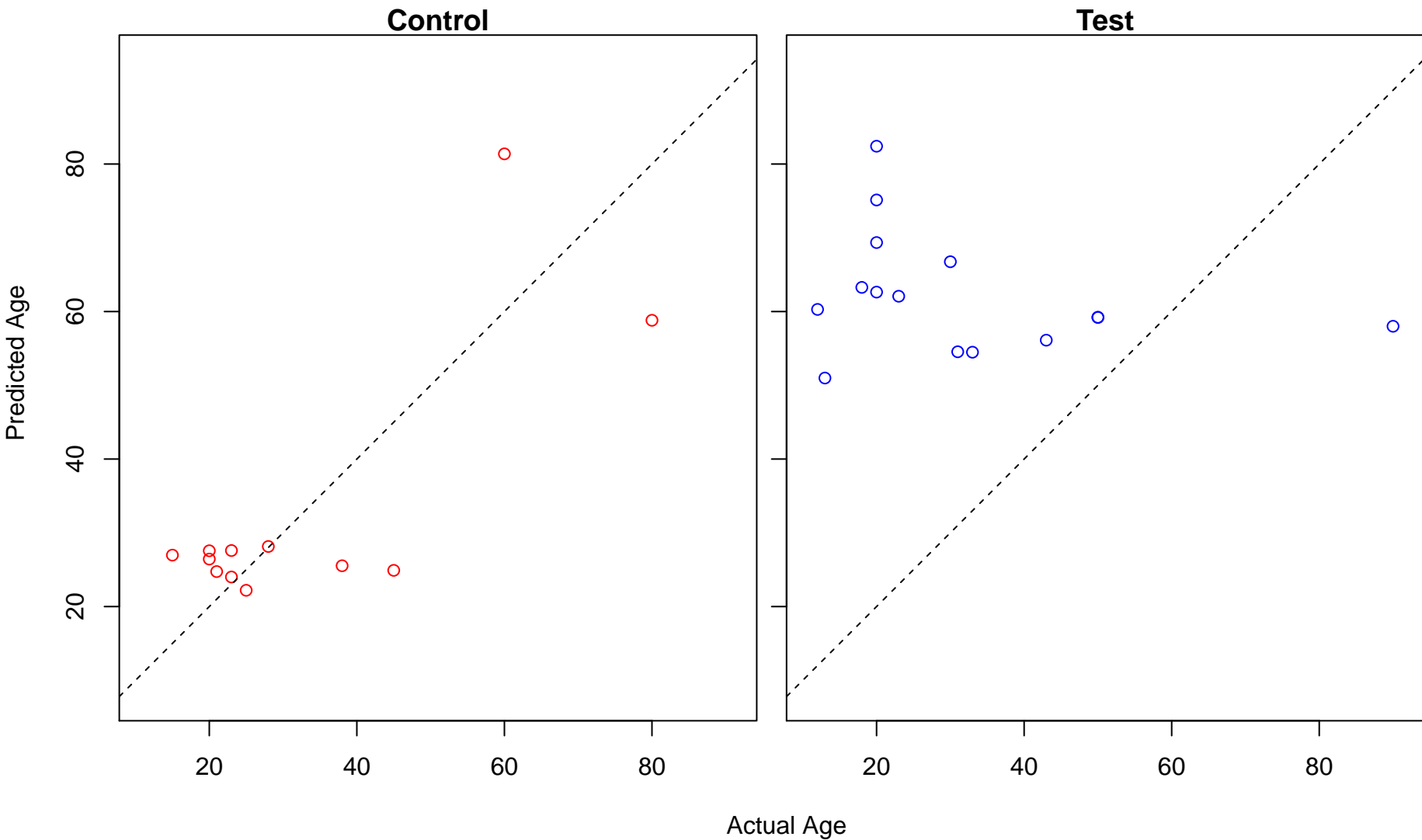
adenine transport (Score: 3.860337)



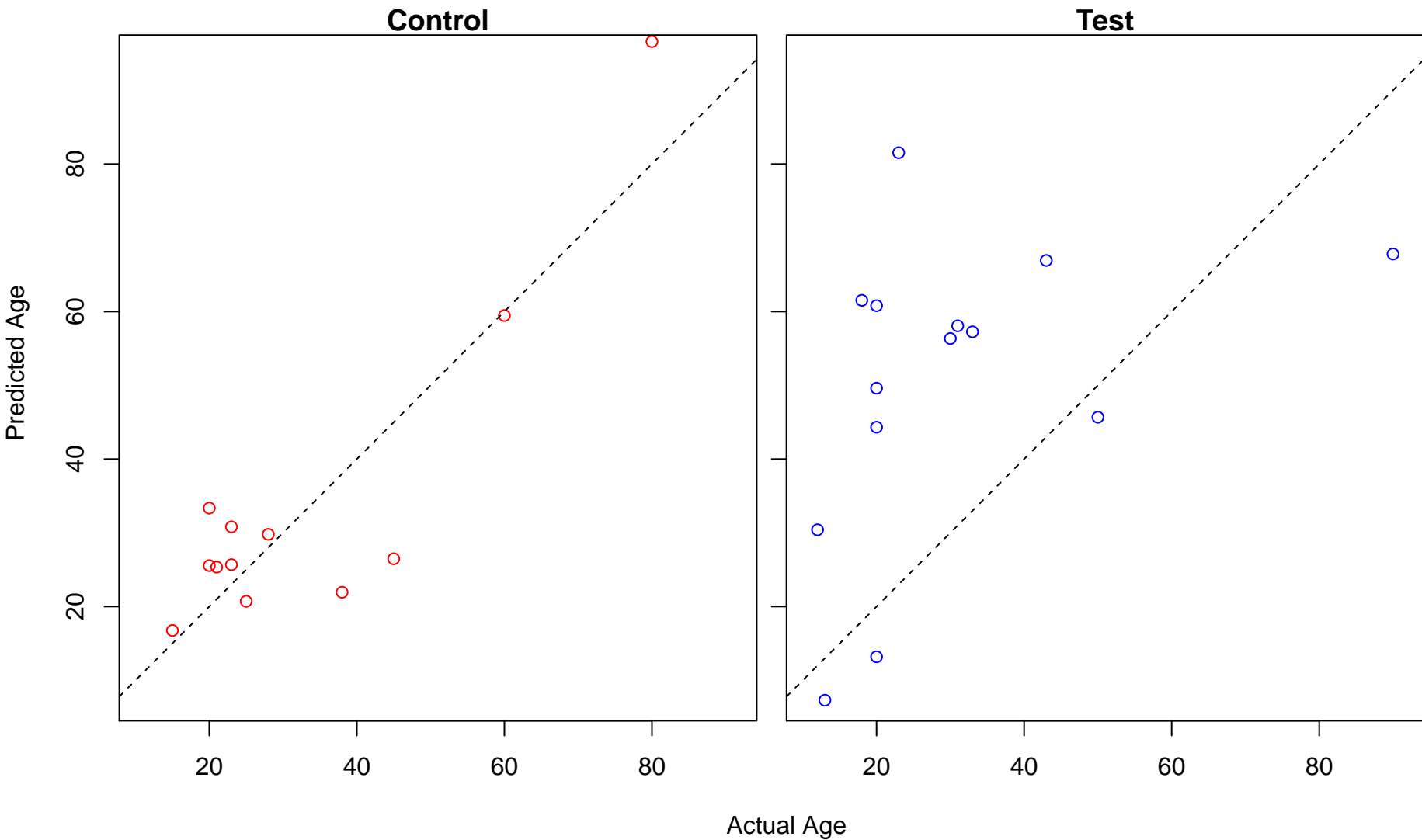
fatty-acyl-CoA metabolic process (Score: 3.858853)



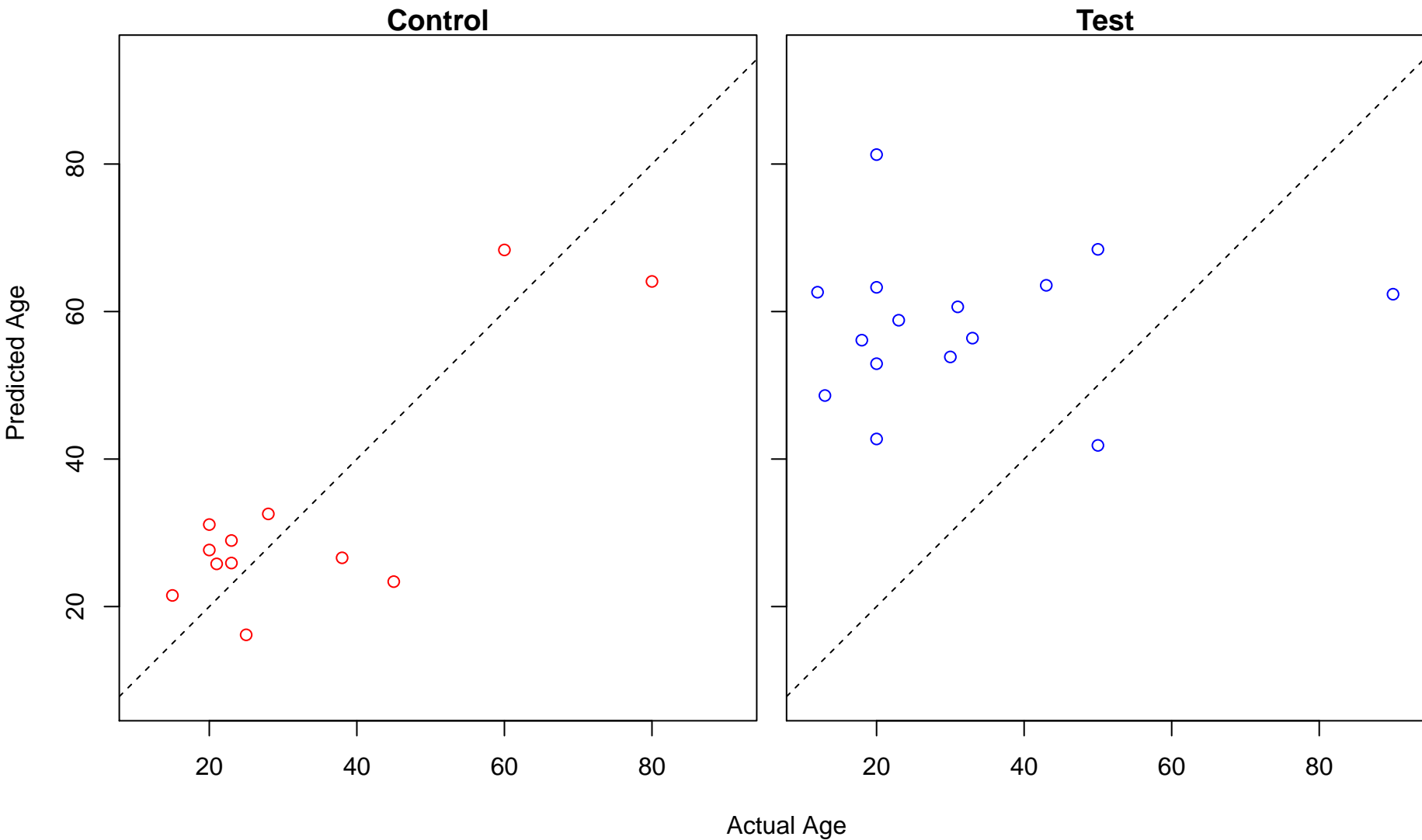
positive regulation of protein localization to chromosome, telomeric region (Score: 3.858131)



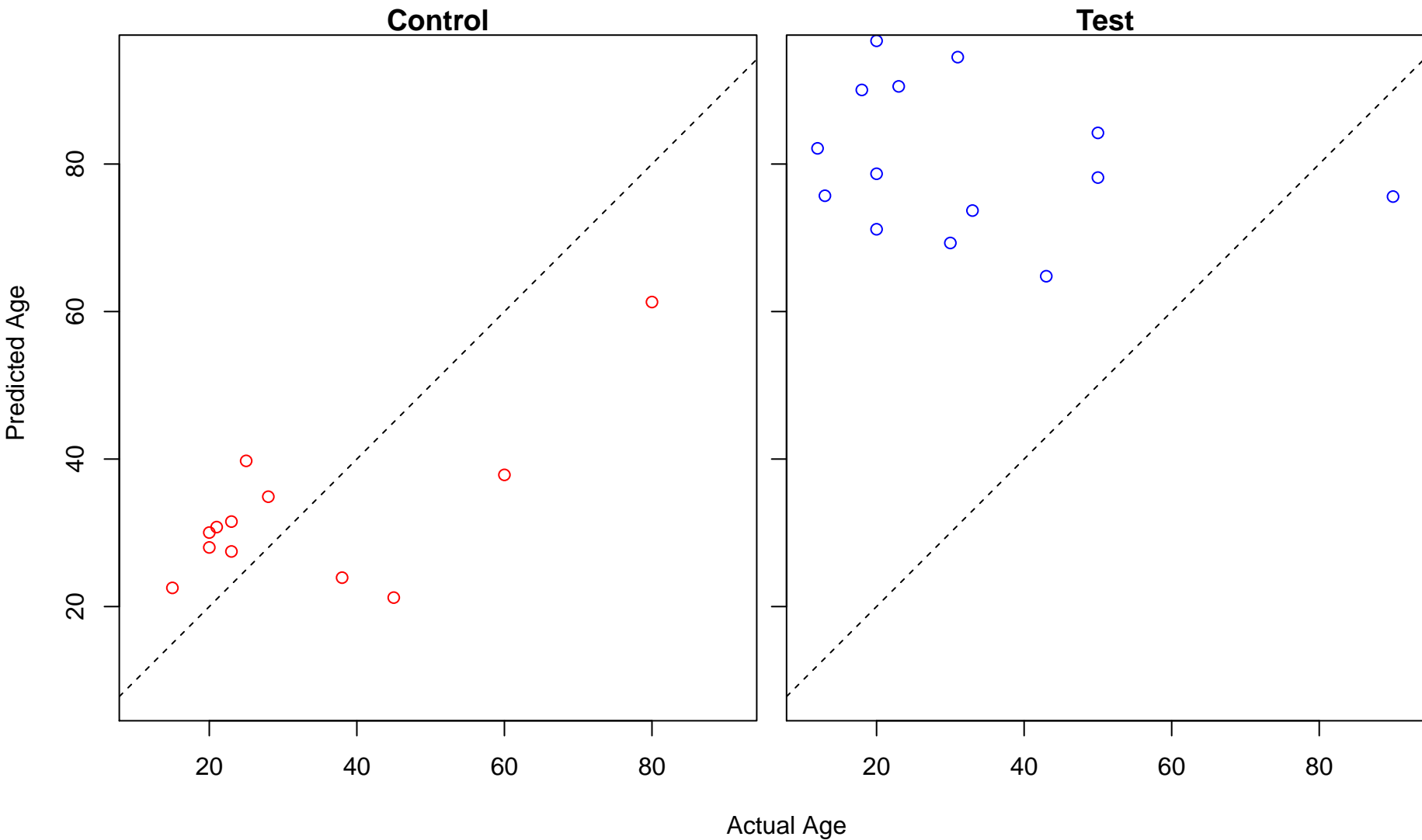
cerebellar cortex formation (Score: 3.856129)



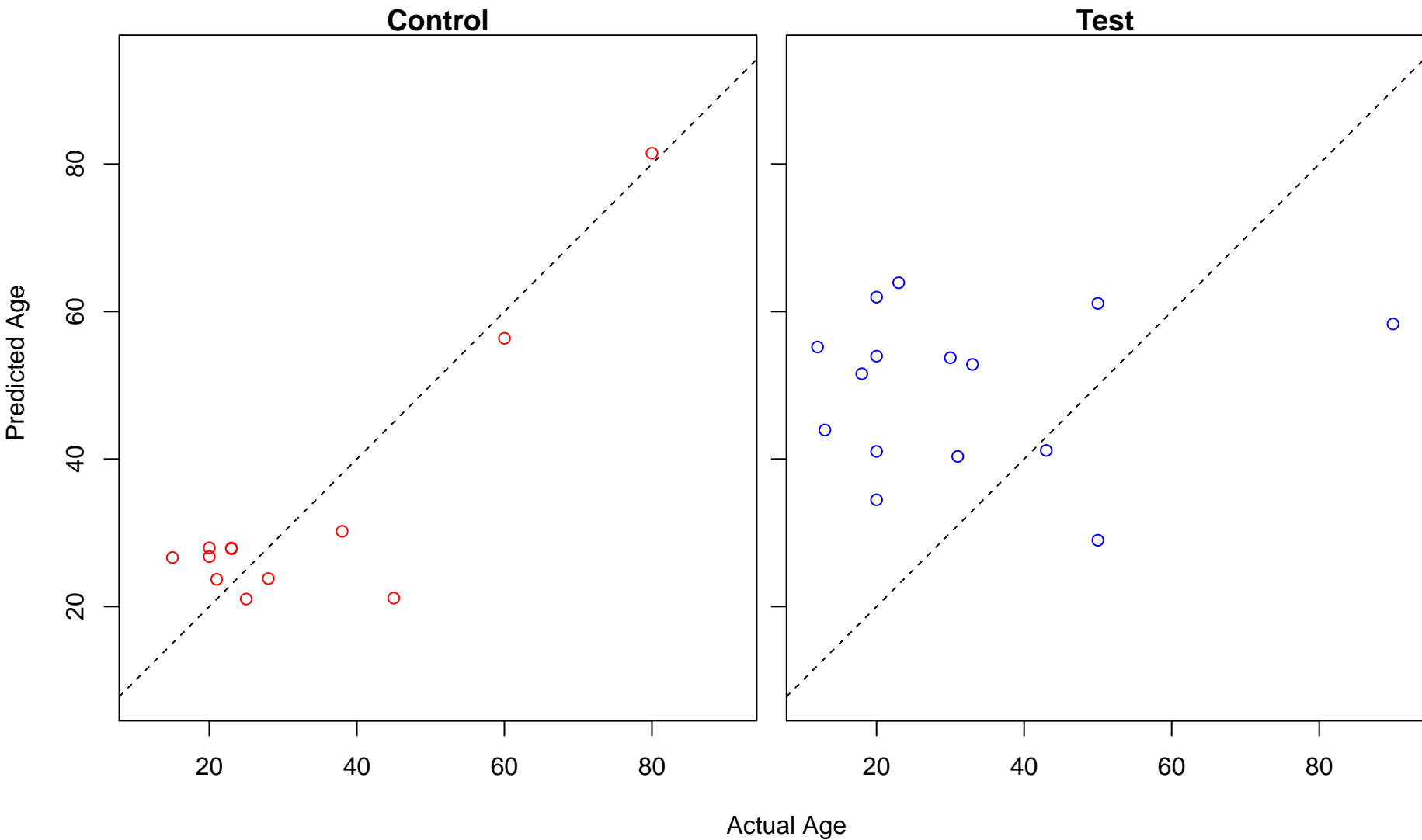
neuron recognition (Score: 3.856039)



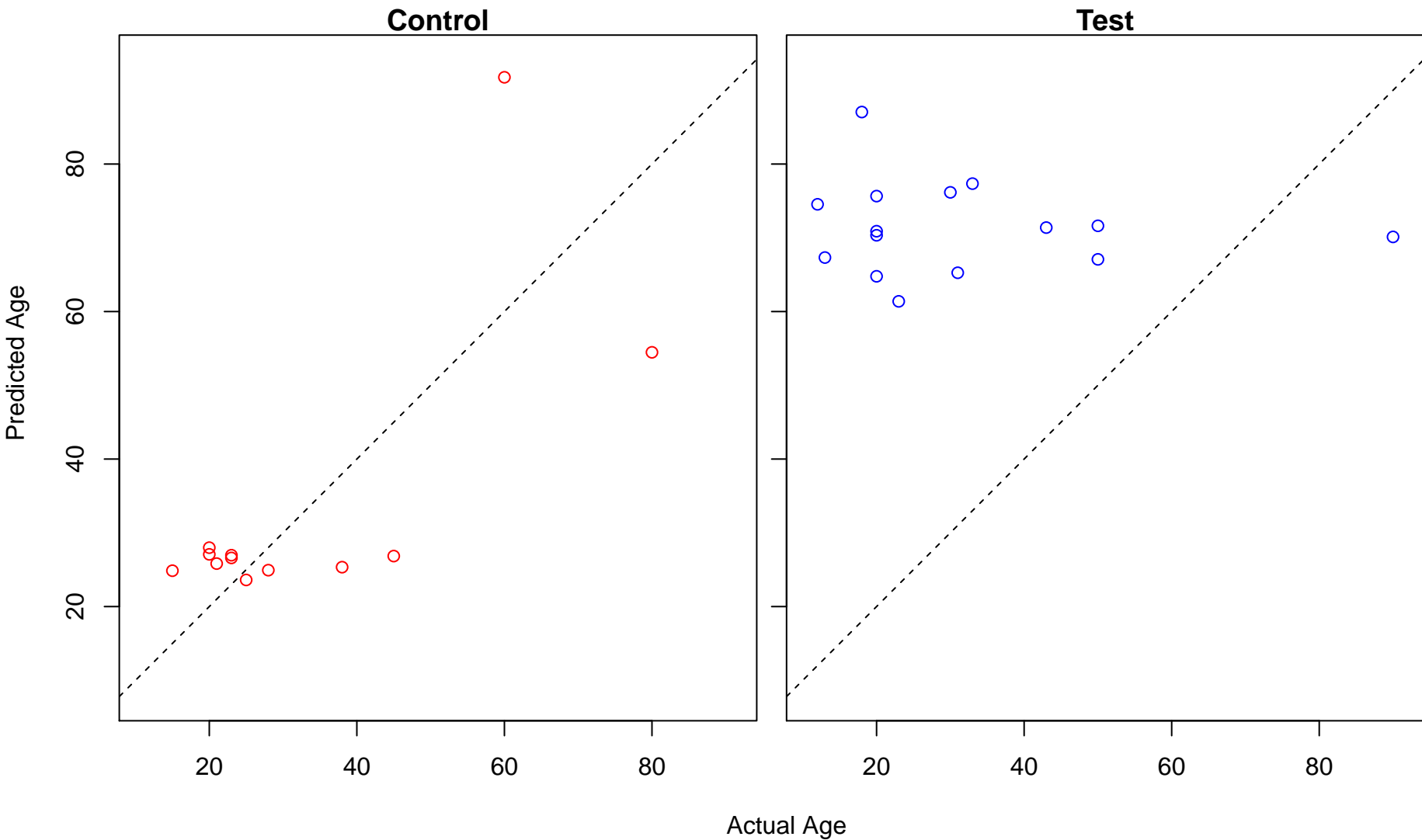
tion of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity (S



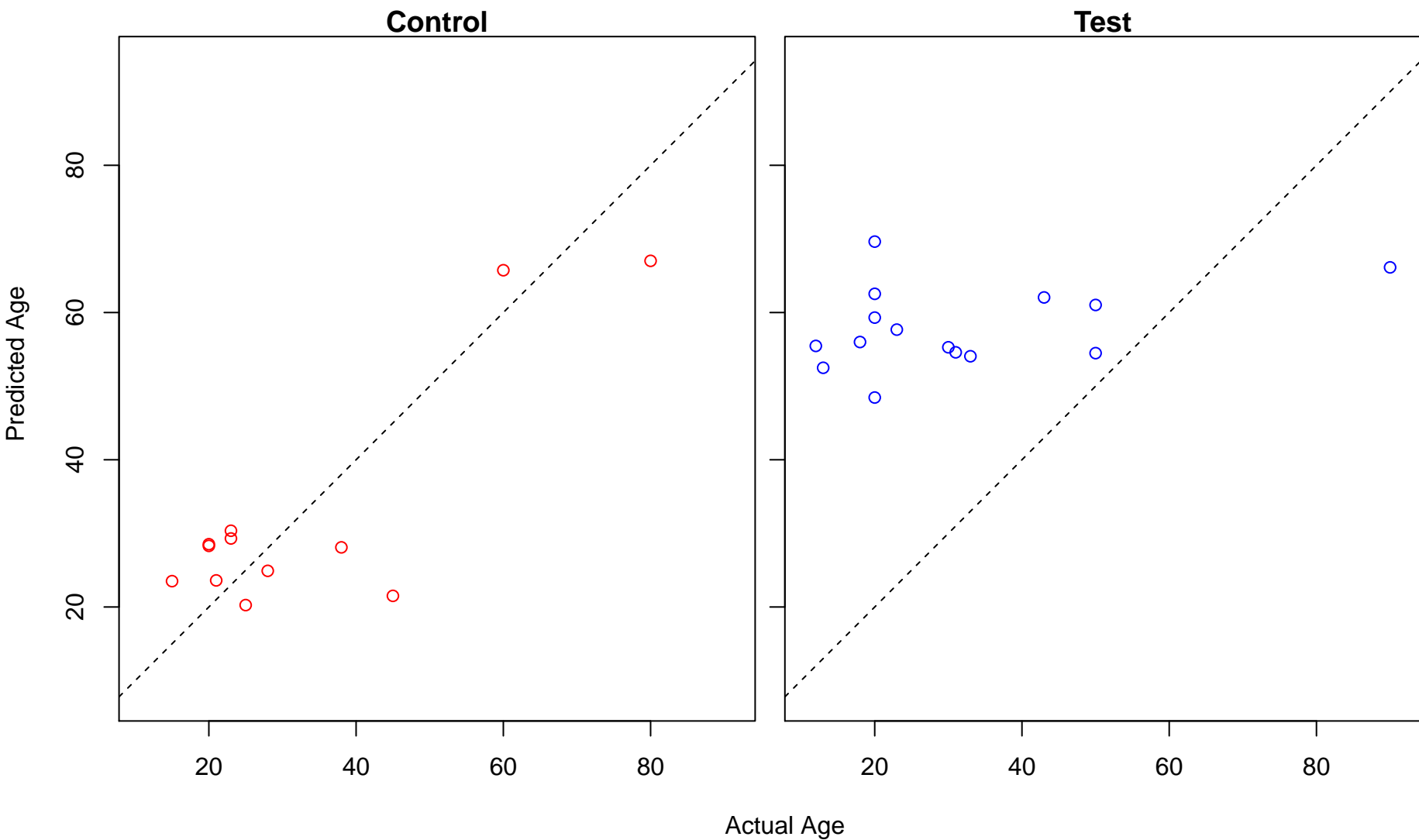
negative regulation of GTPase activity (Score: 3.855377)



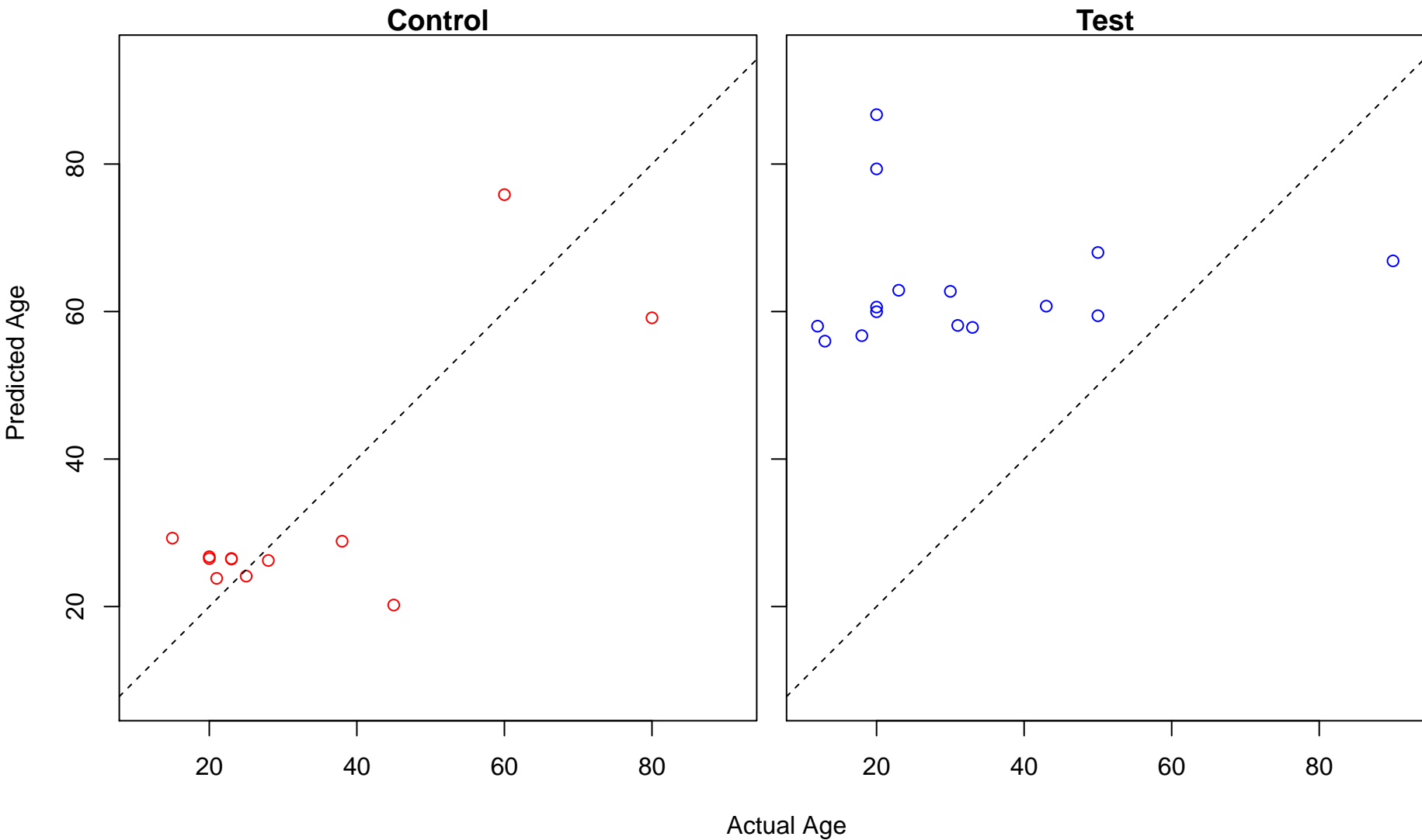
negative regulation of translational initiation in response to stress (Score: 3.853085)



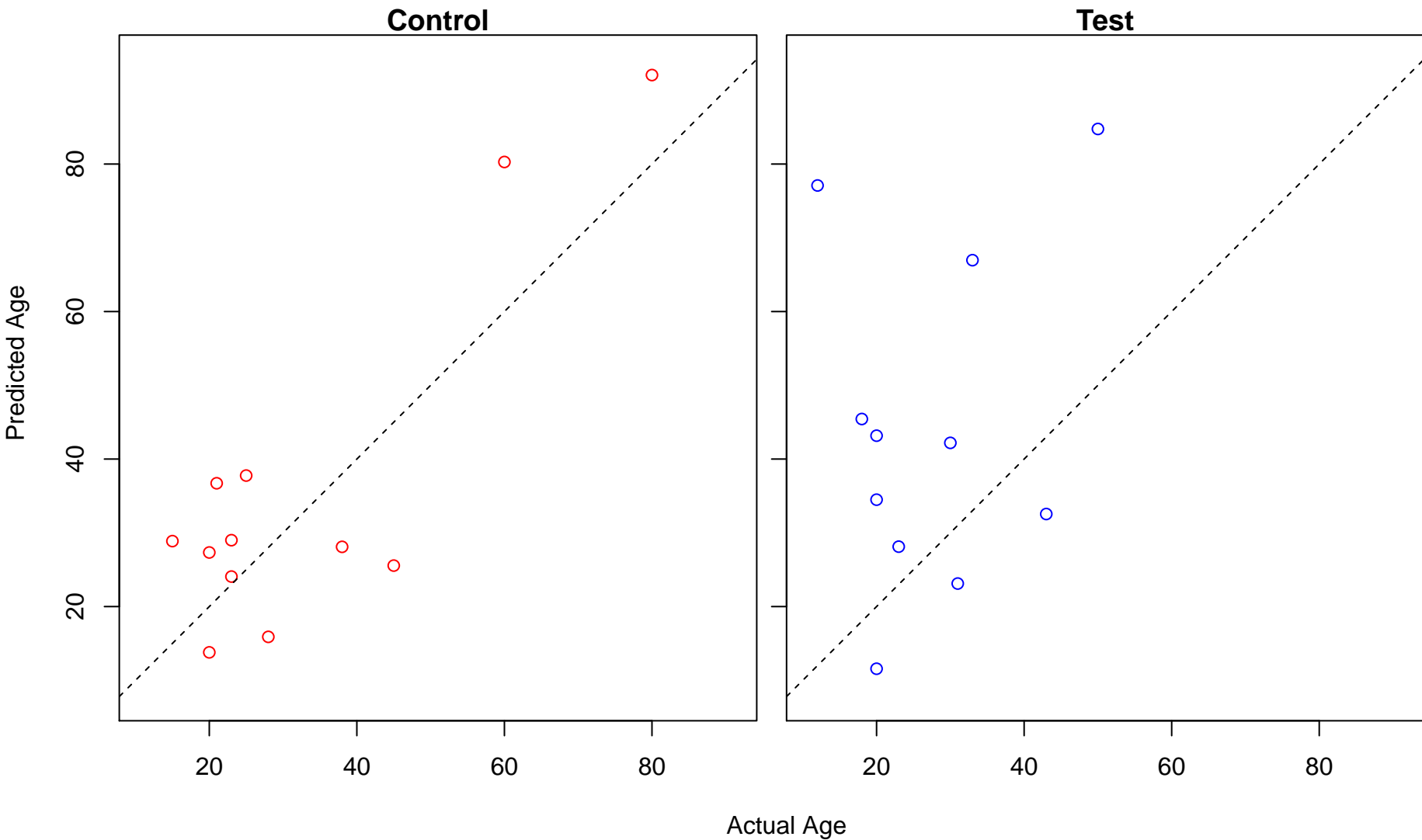
positive regulation of granulocyte differentiation (Score: 3.852317)



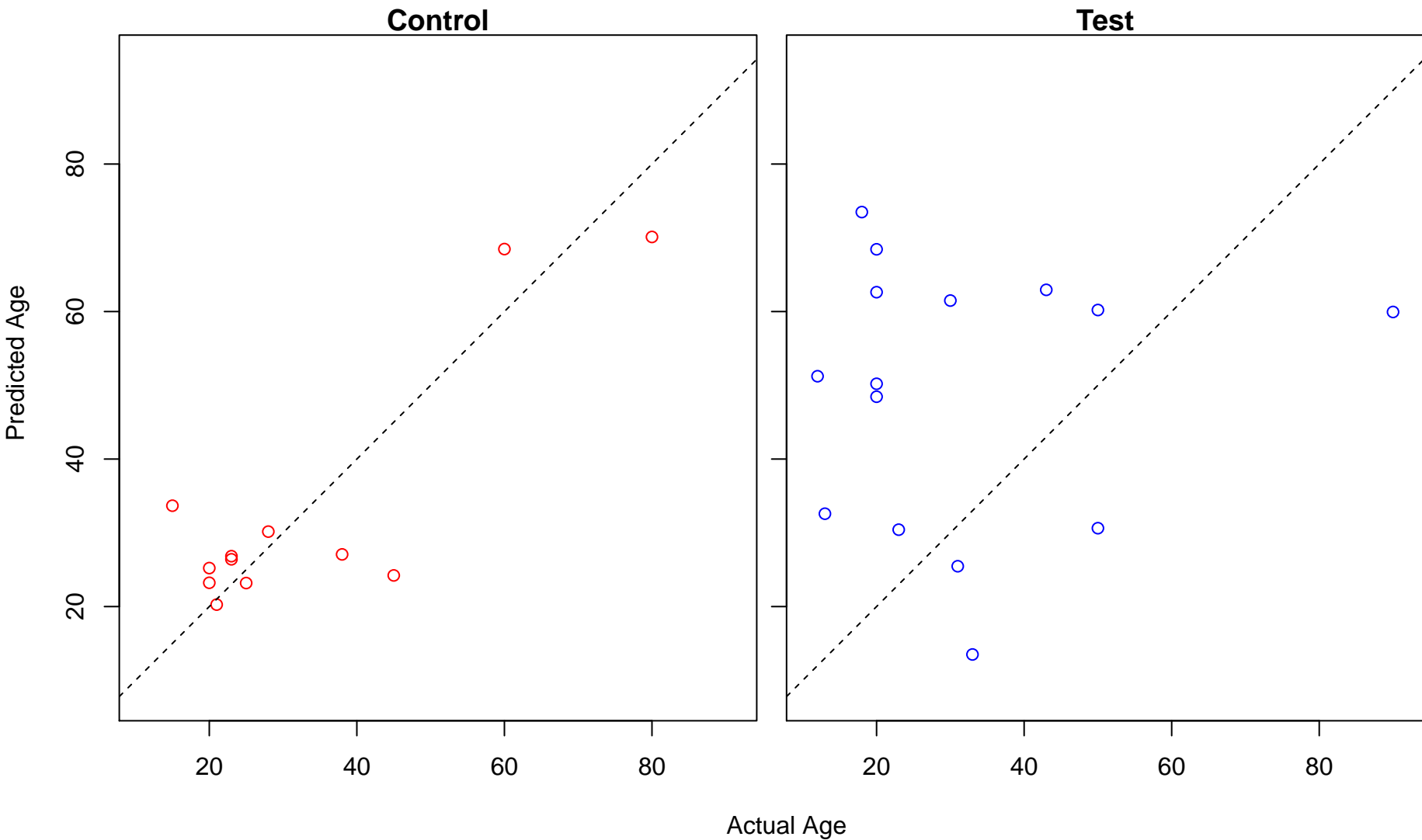
negative regulation of response to biotic stimulus (Score: 3.852037)



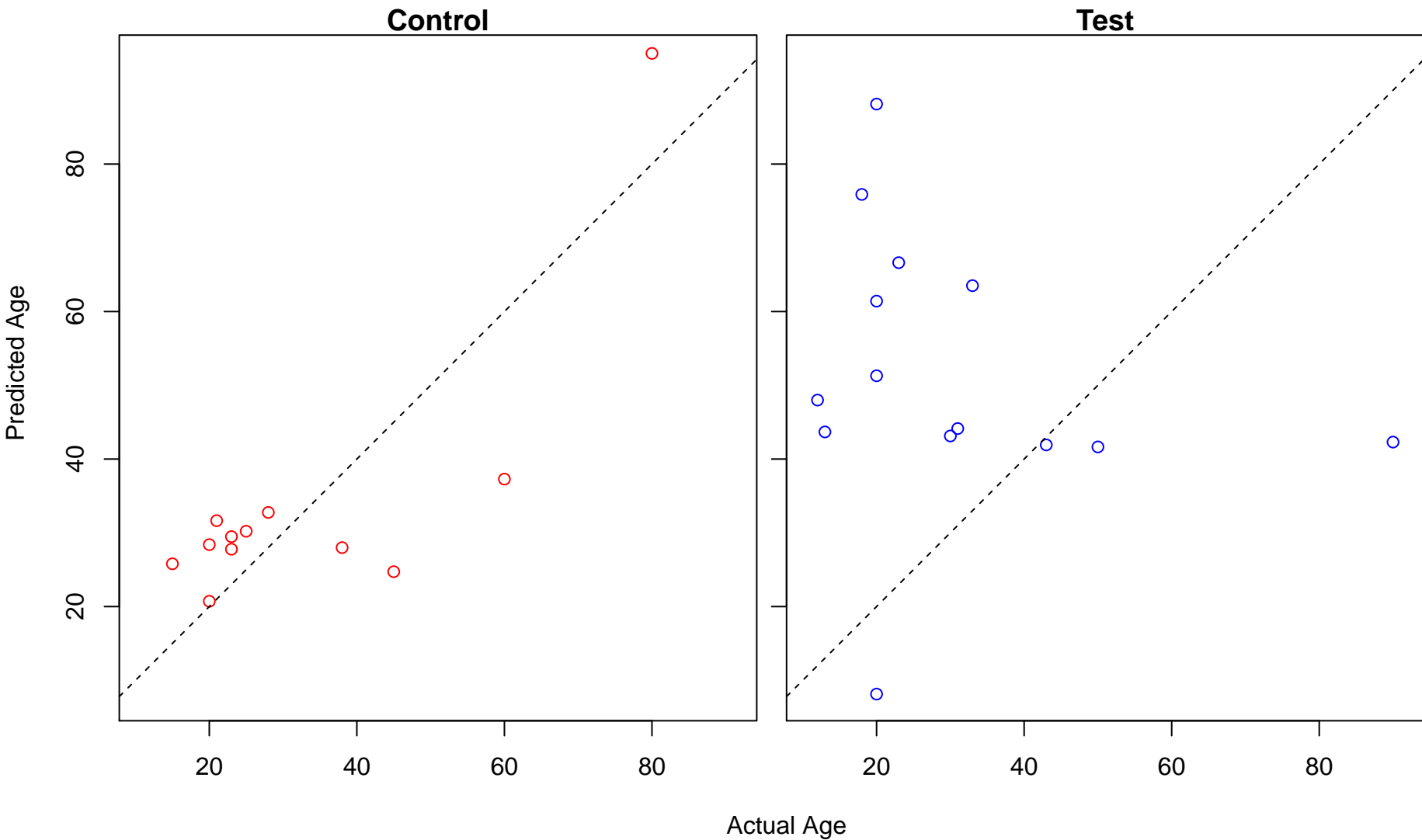
bicarbonate transport (Score: 3.851998)



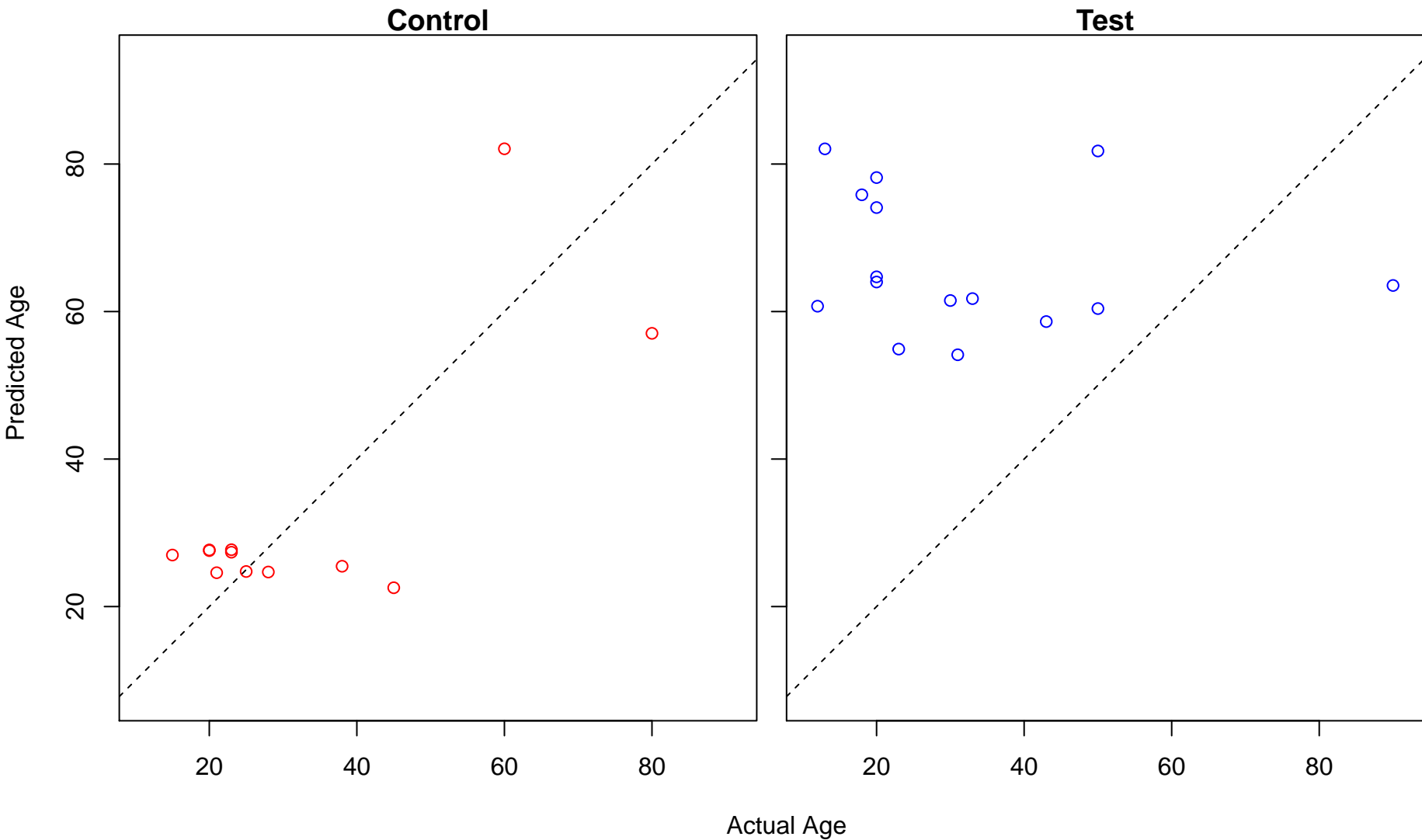
positive regulation of action potential (Score: 3.851566)



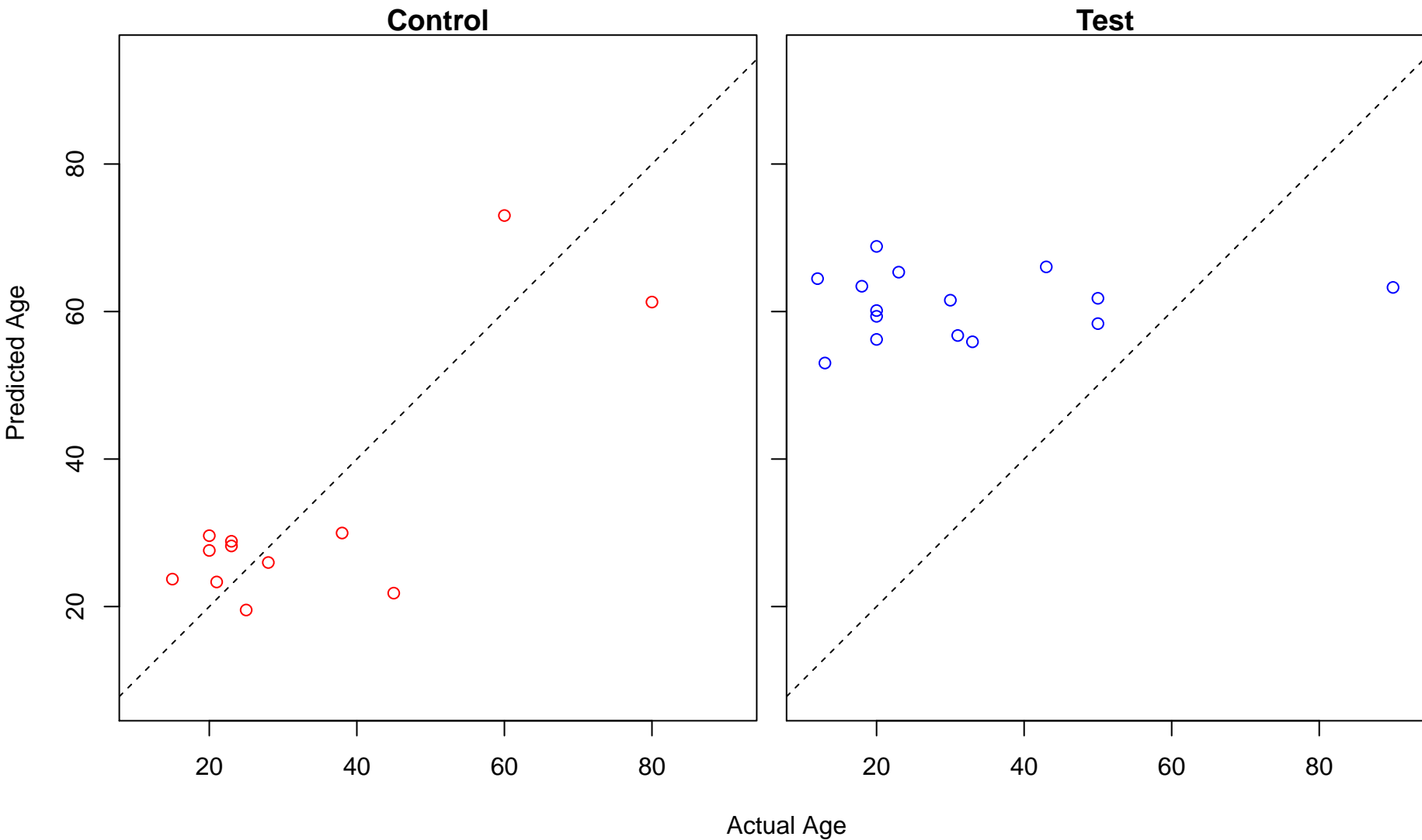
regulation of neuron projection development (Score: 3.849282)



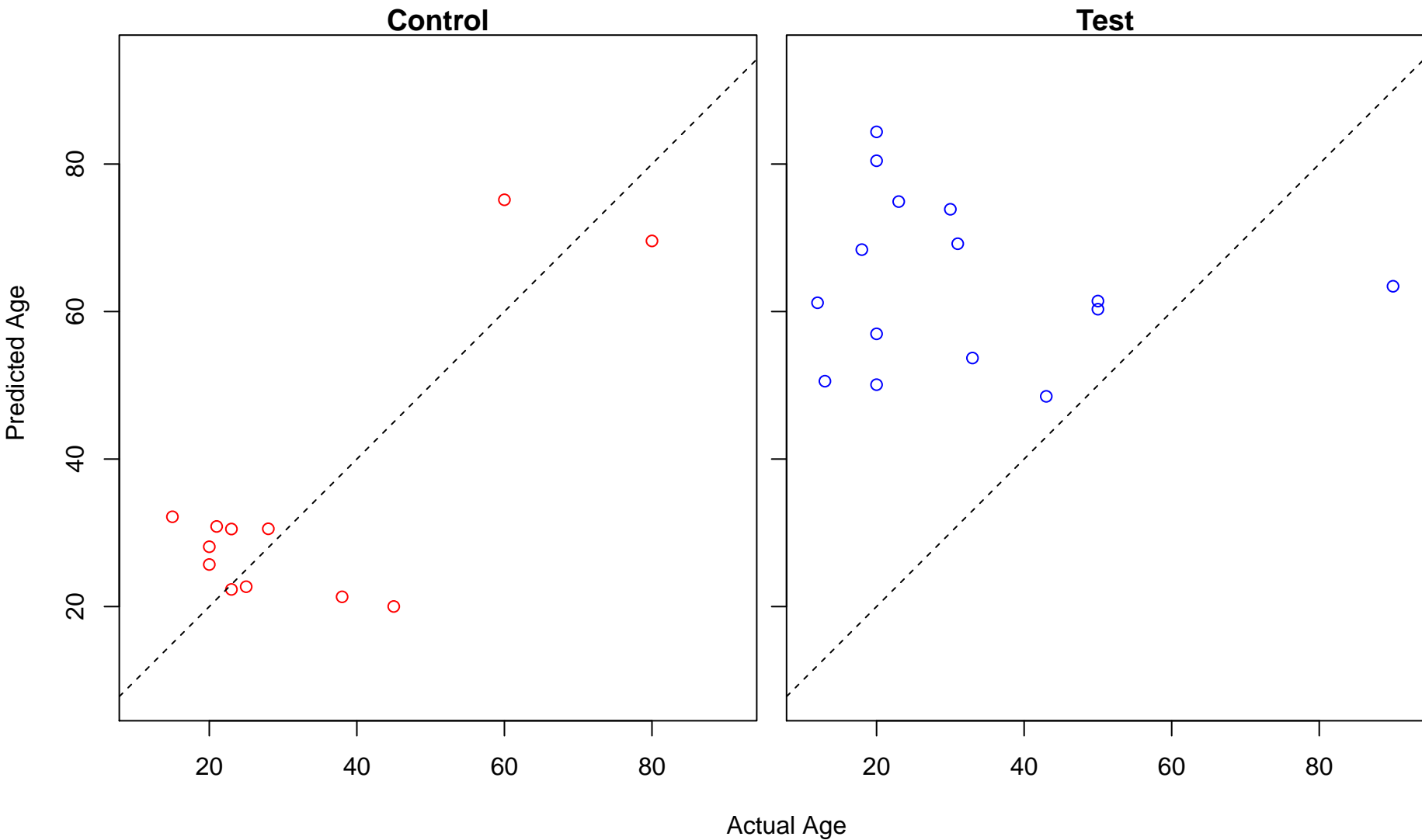
negative regulation of telomere maintenance via telomerase (Score: 3.848855)



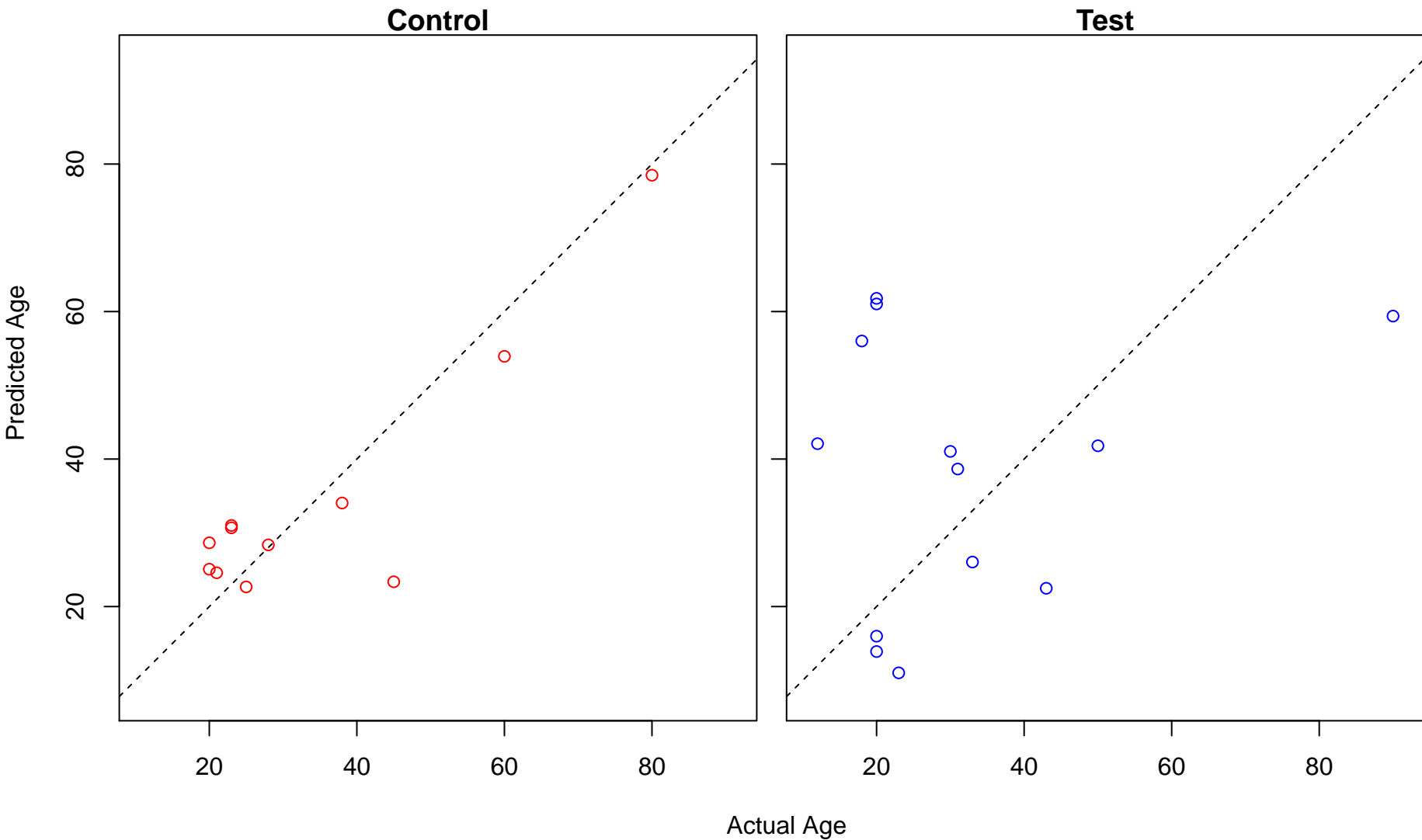
negative regulation of fat cell differentiation (Score: 3.848174)



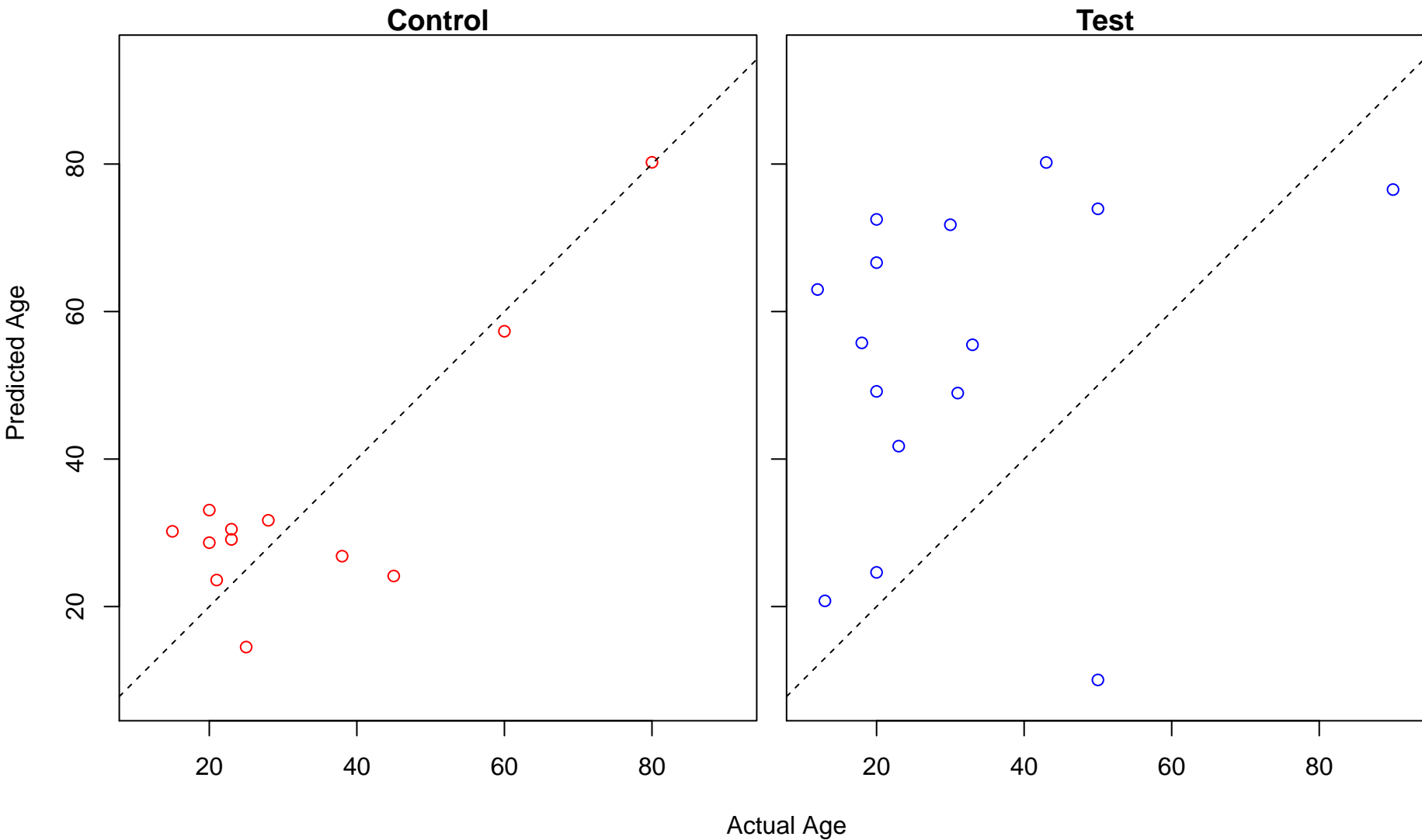
regulation of release of cytochrome c from mitochondria (Score: 3.847246)



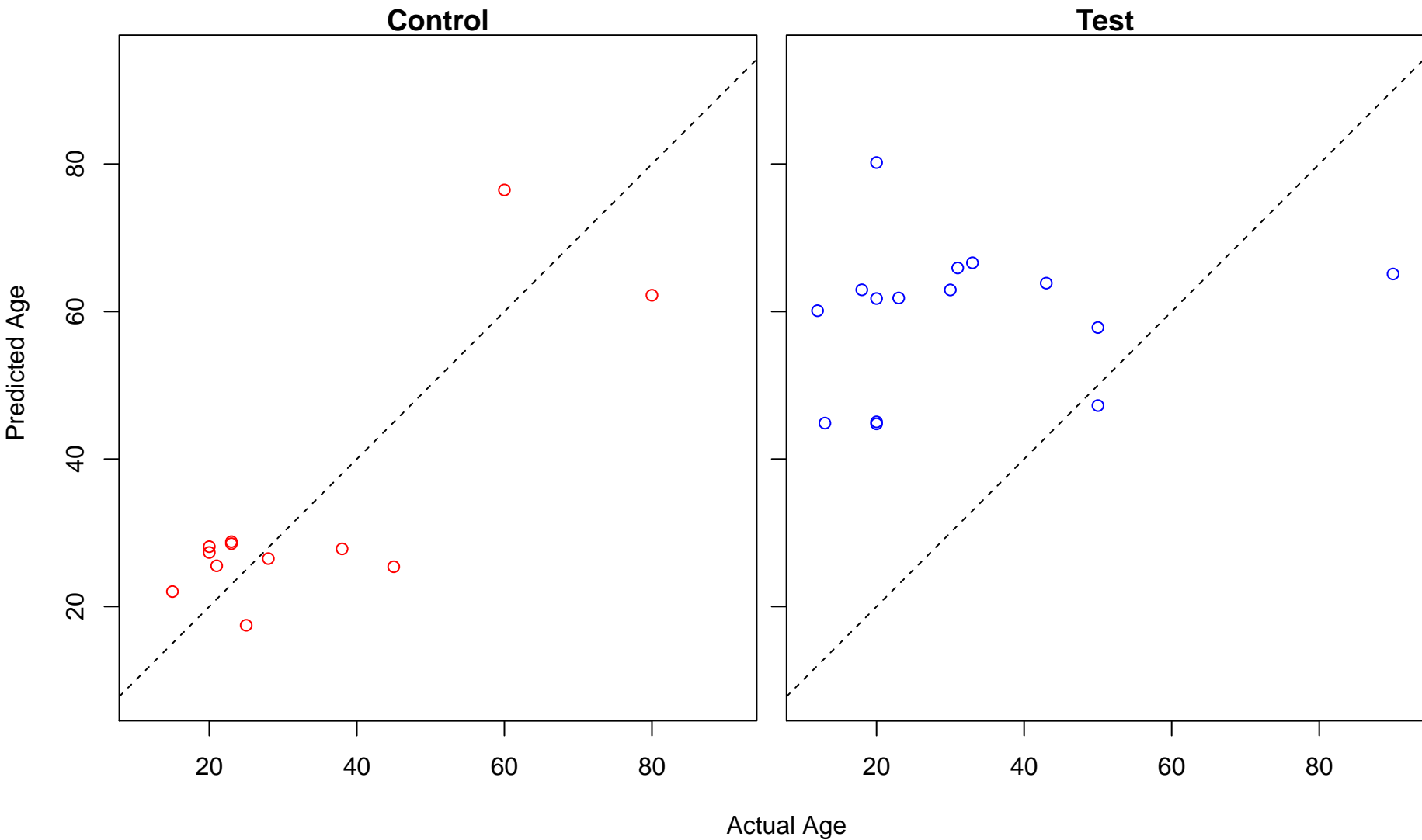
skeletal myofibril assembly (Score: 3.845596)



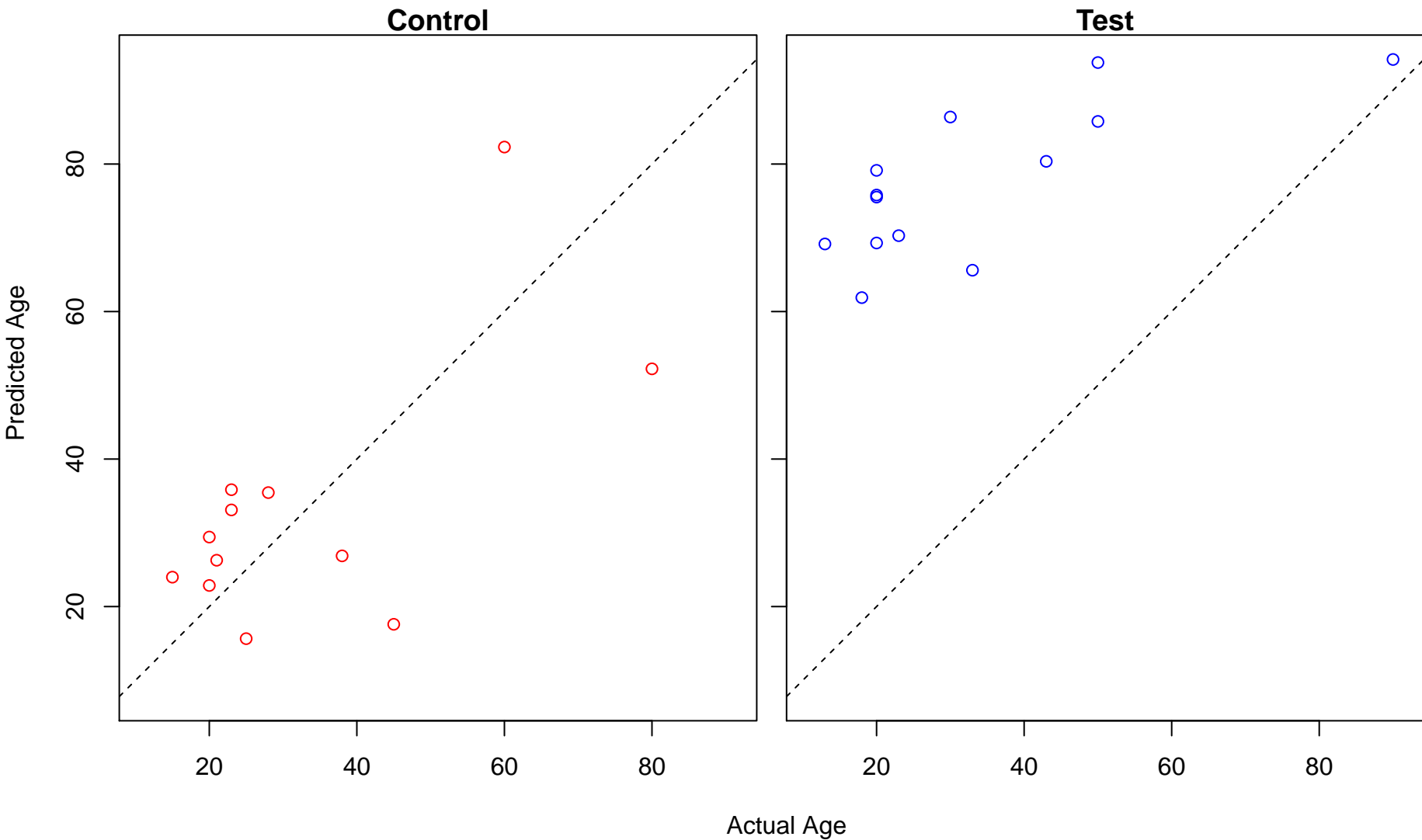
protein deneddylation (Score: 3.843997)



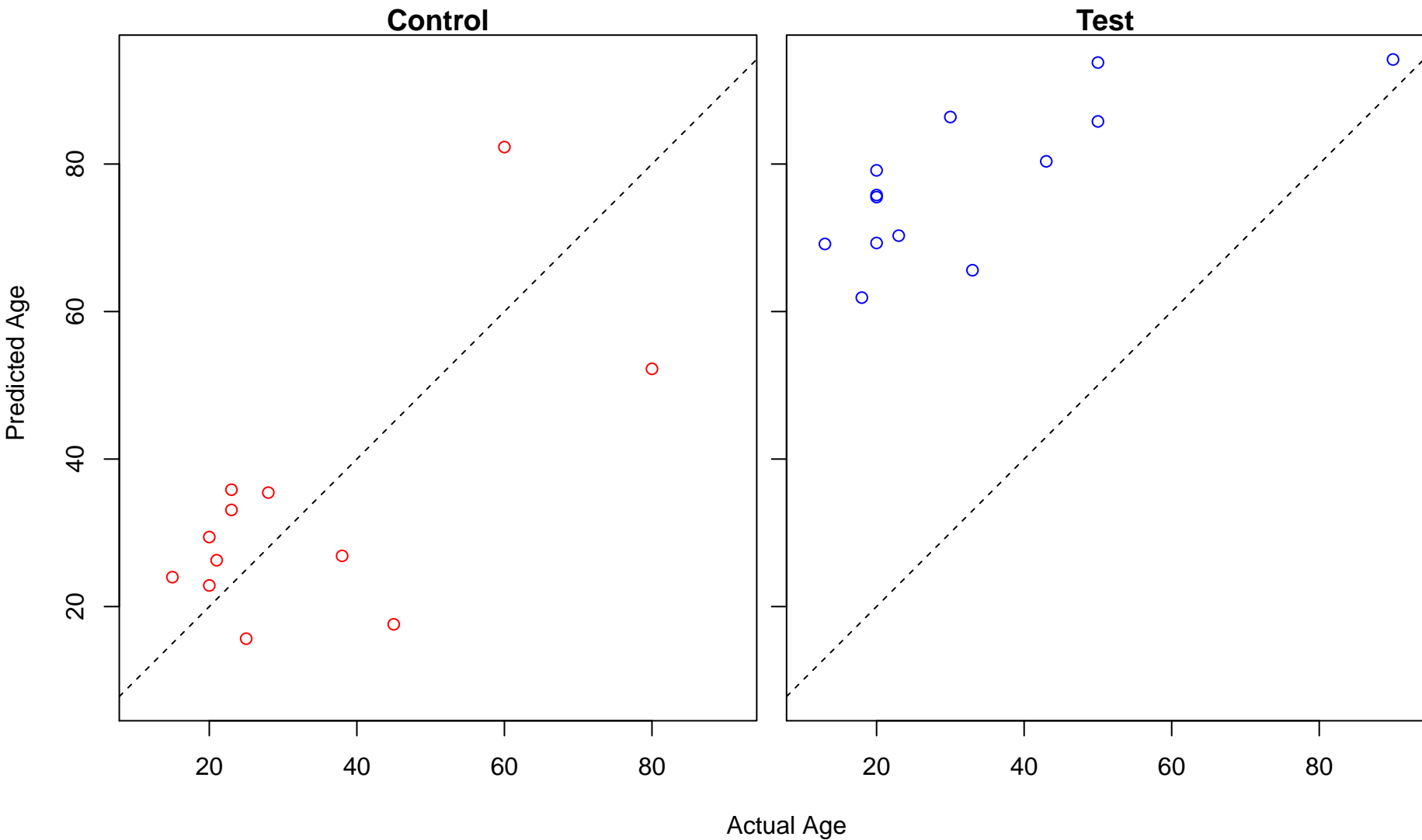
regulation of bicellular tight junction assembly (Score: 3.842826)



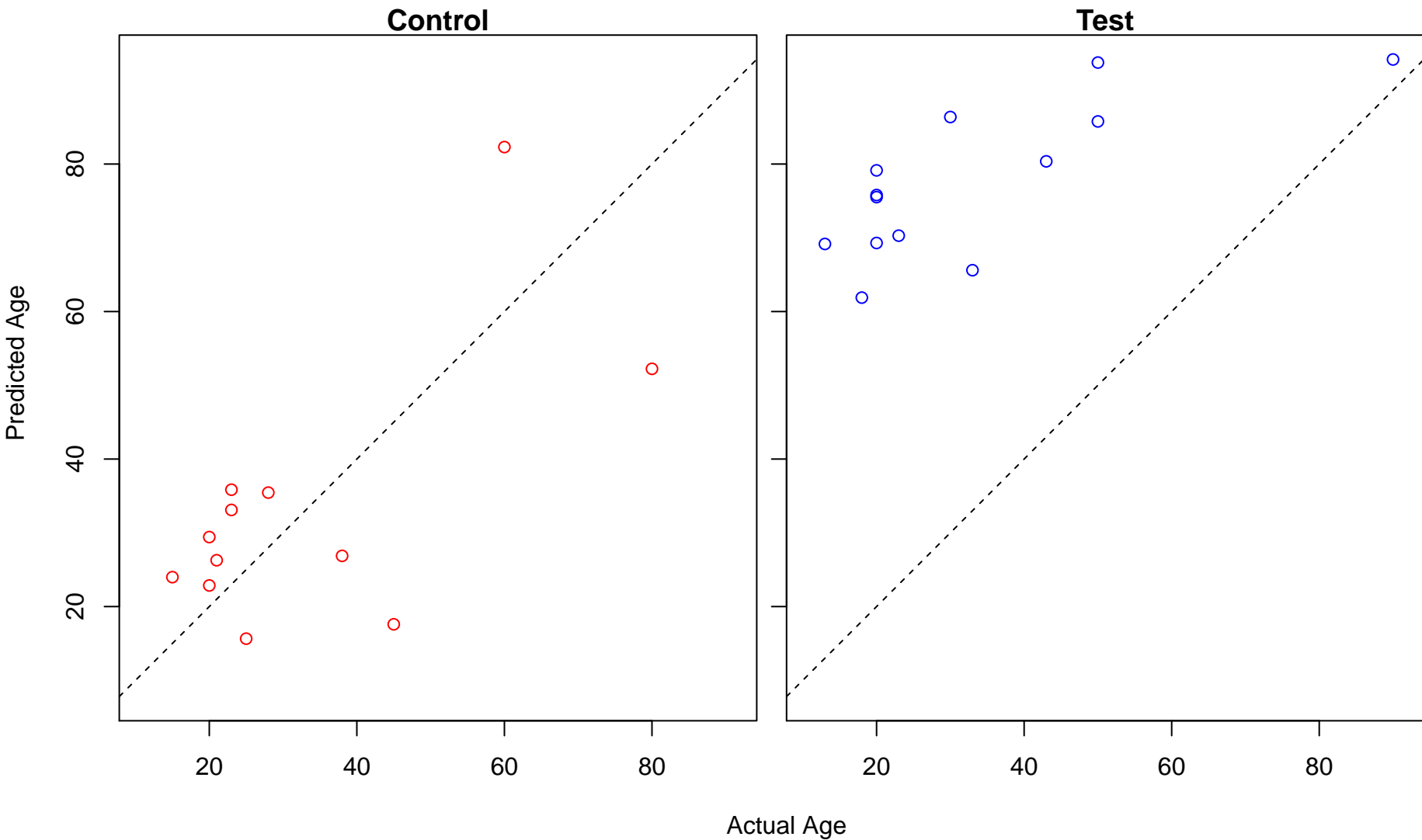
desensitization of G-protein coupled receptor protein signaling pathway (Score: 3.837875)



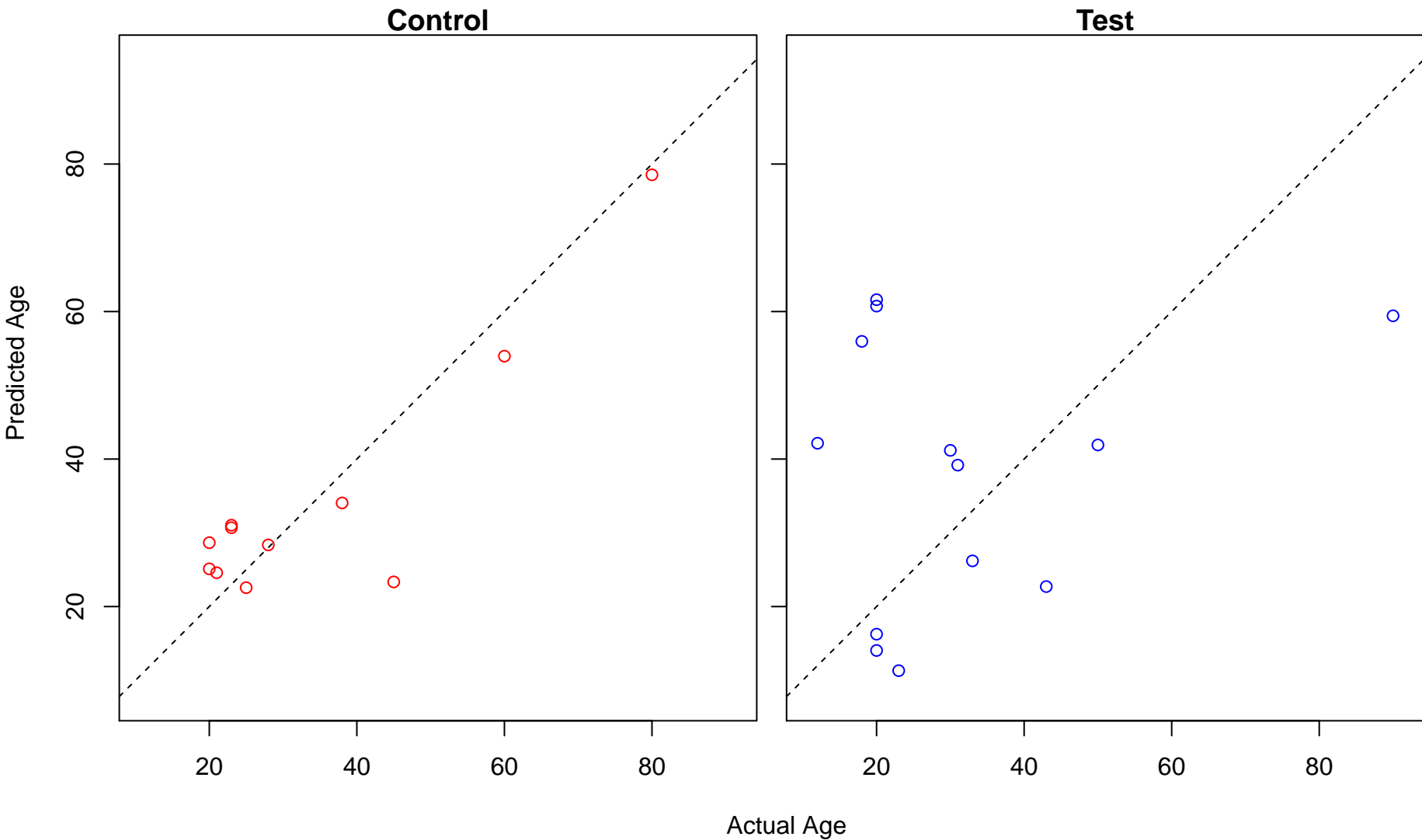
negative adaptation of signaling pathway (Score: 3.837875)



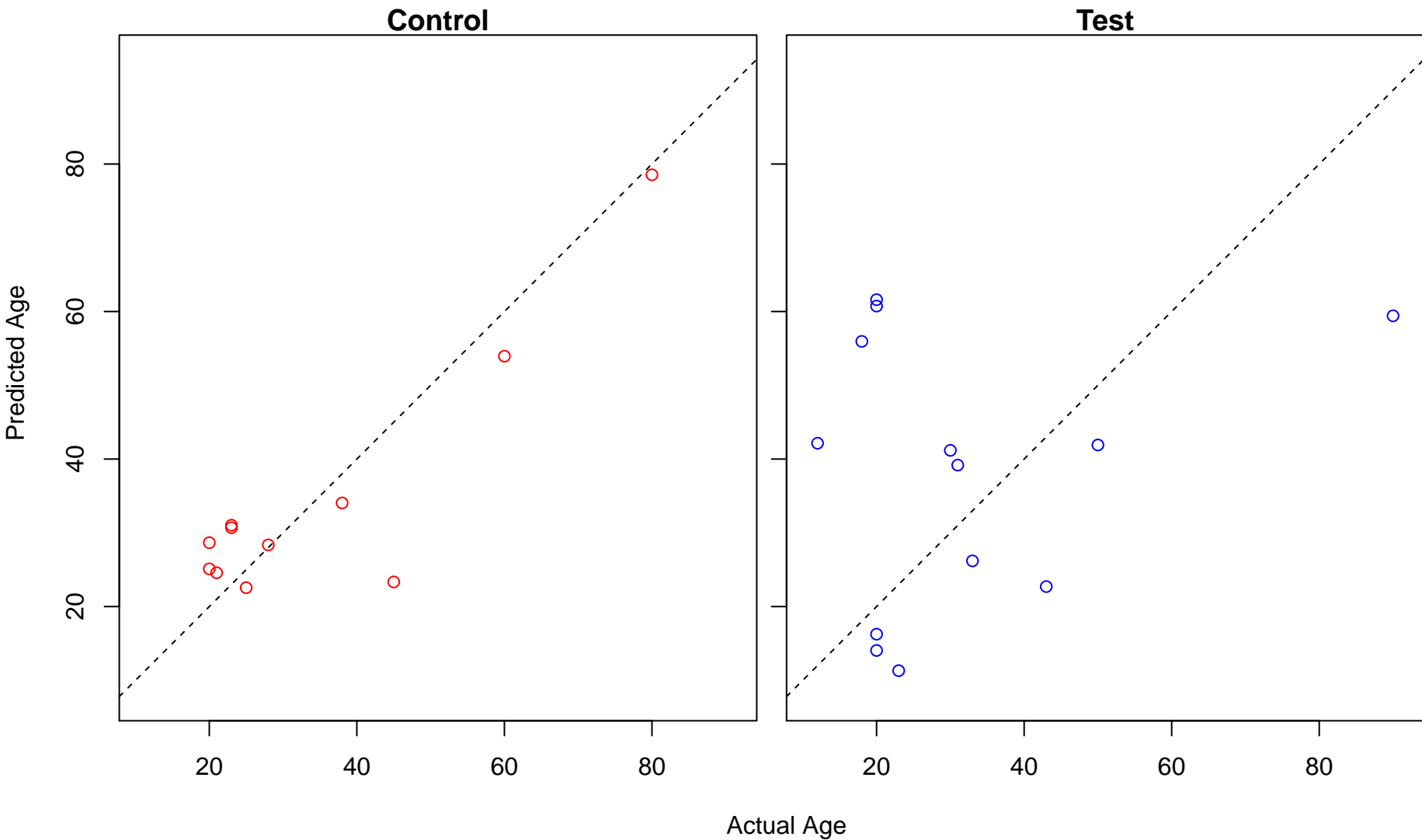
adaptation of signaling pathway (Score: 3.837875)



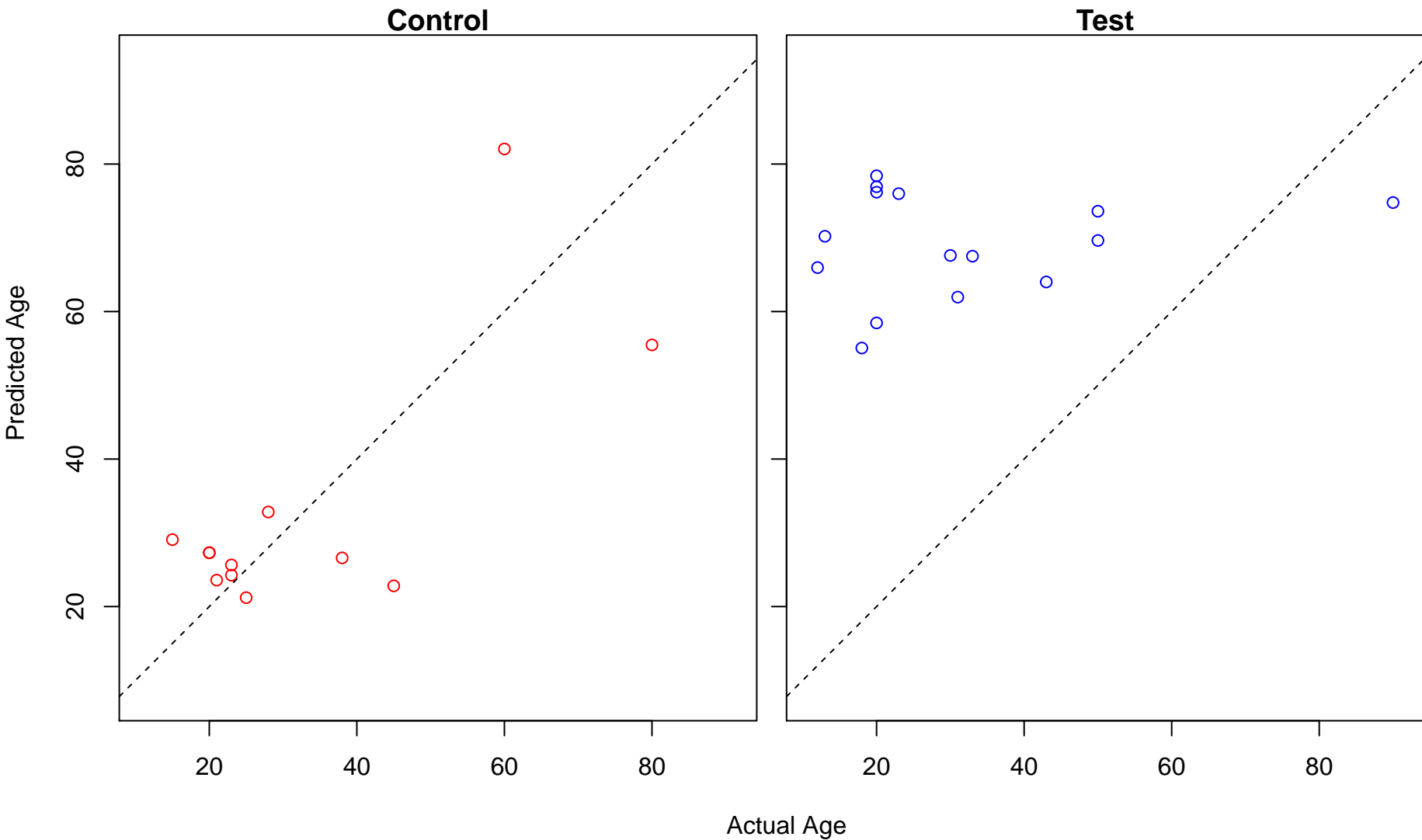
regulation of skeletal muscle satellite cell proliferation (Score: 3.836574)



regulation of skeletal muscle cell proliferation (Score: 3.836574)

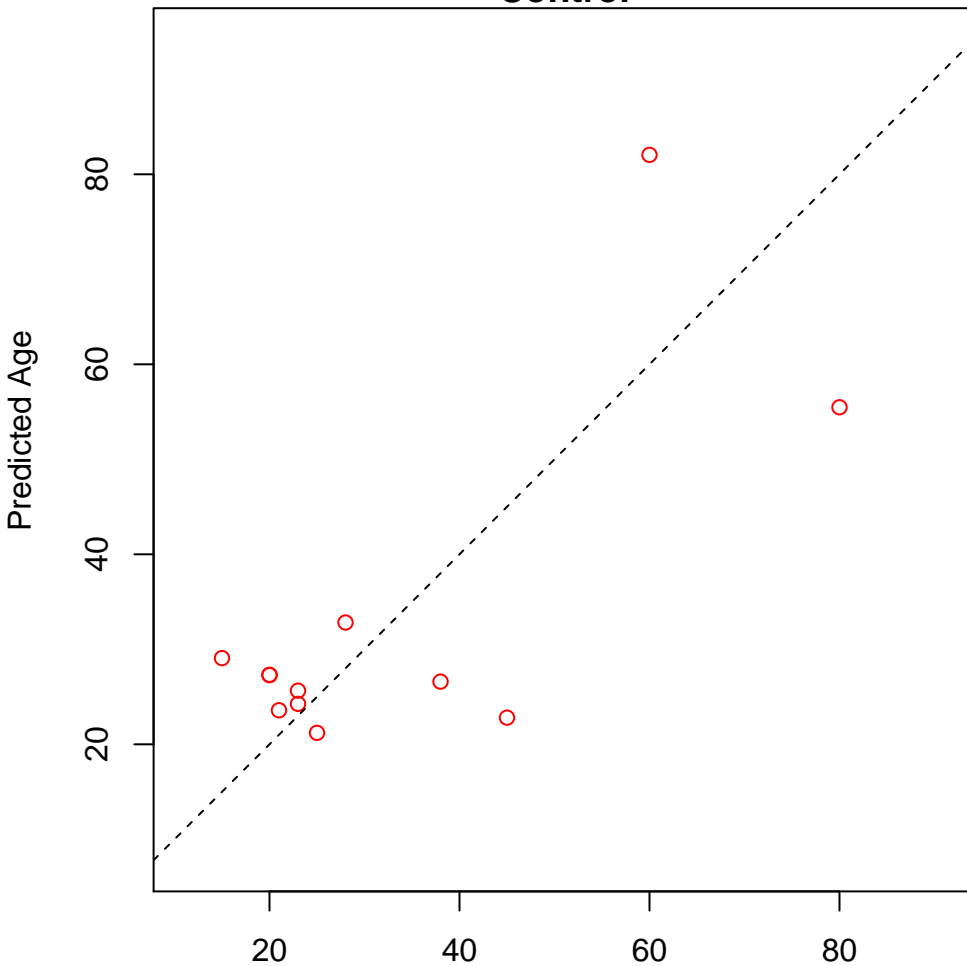


mitophagy in response to mitochondrial depolarization (Score: 3.835477)

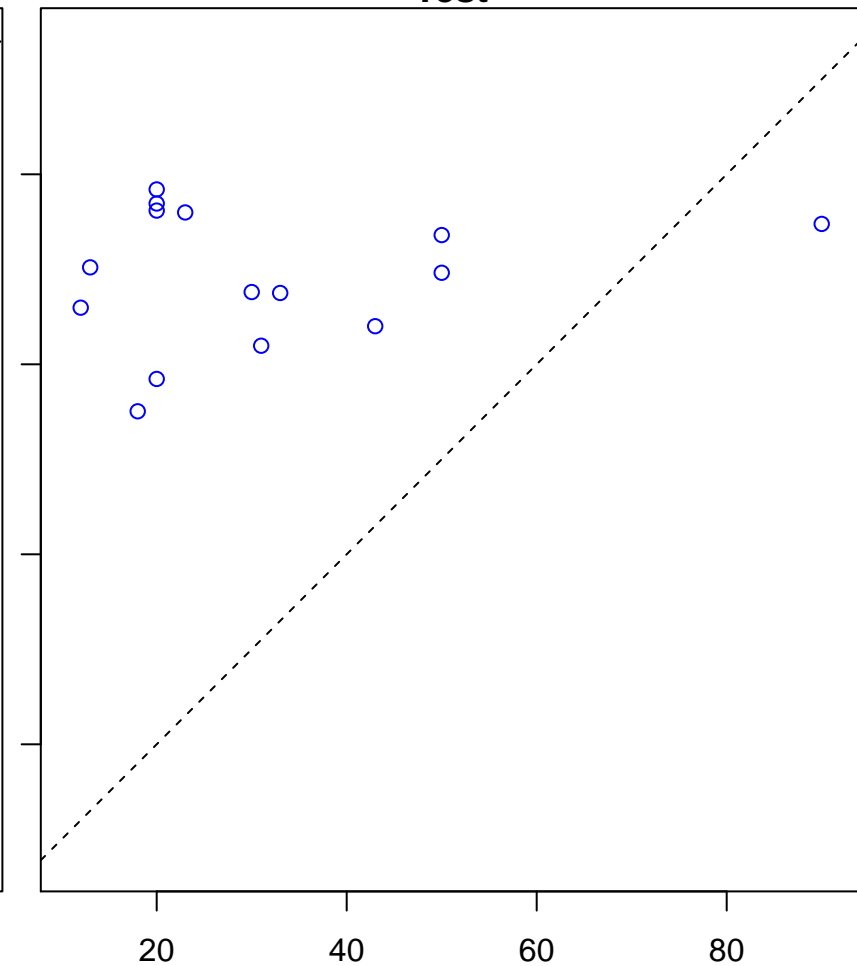


response to mitochondrial depolarisation (Score: 3.835477)

Control

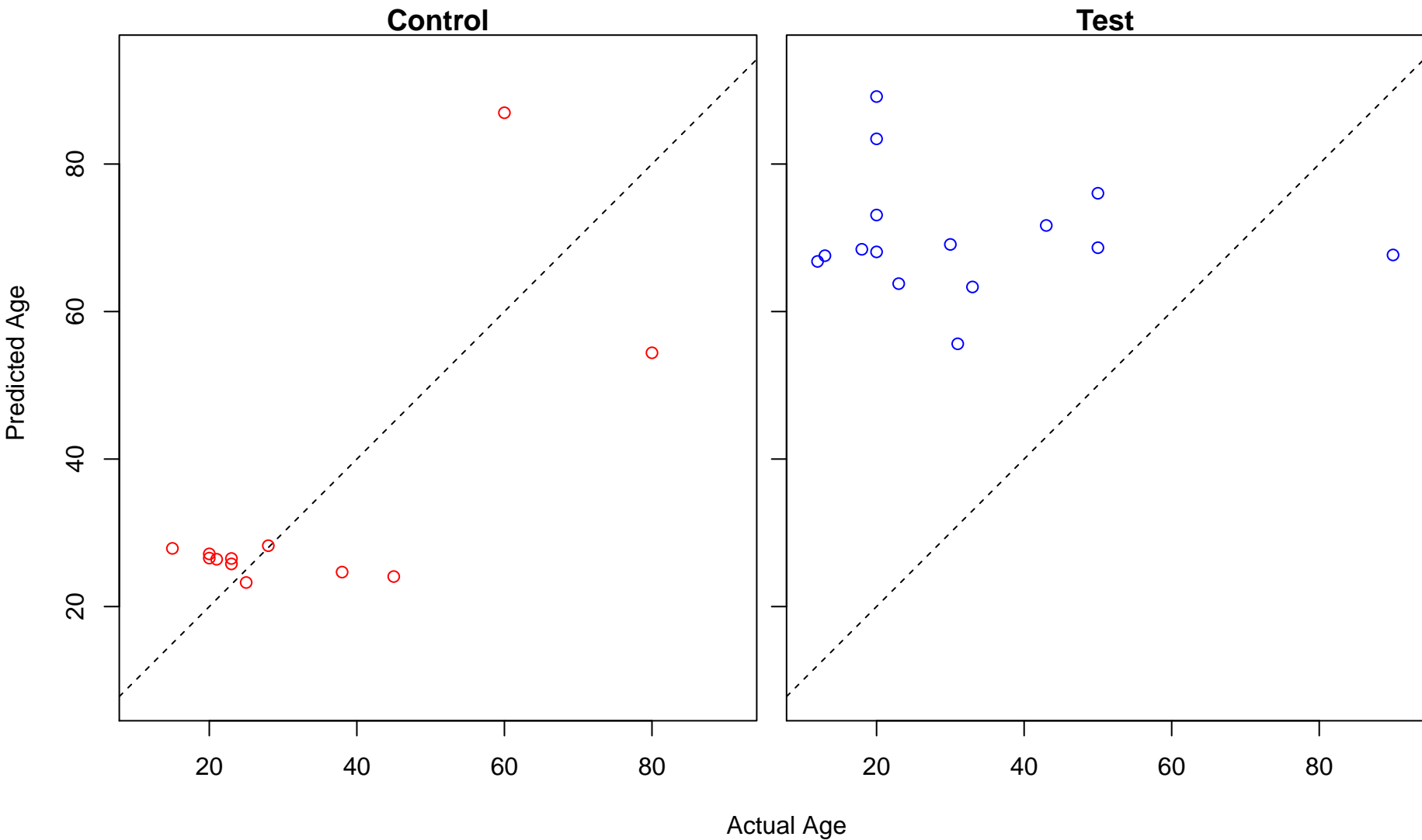


Test

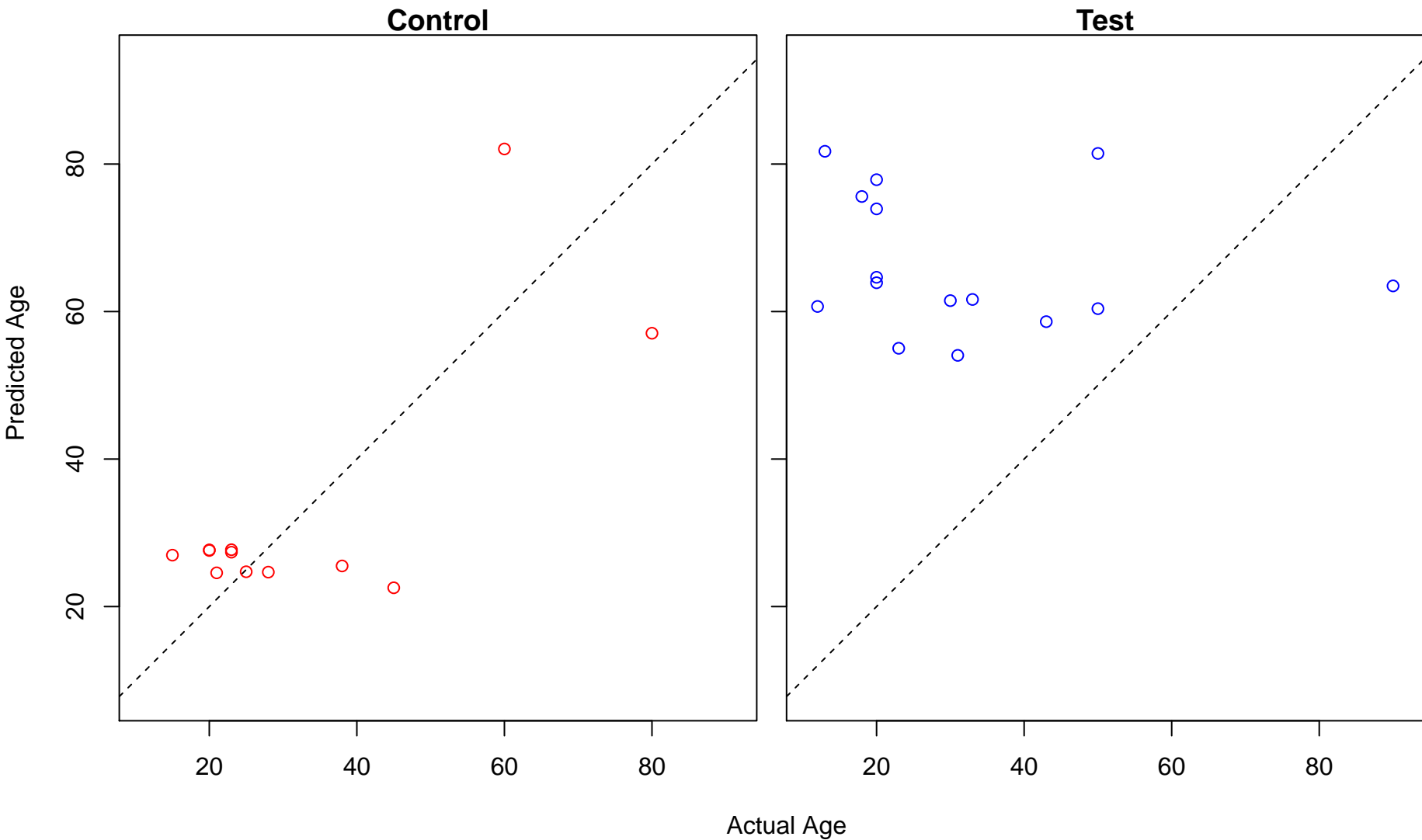


Actual Age

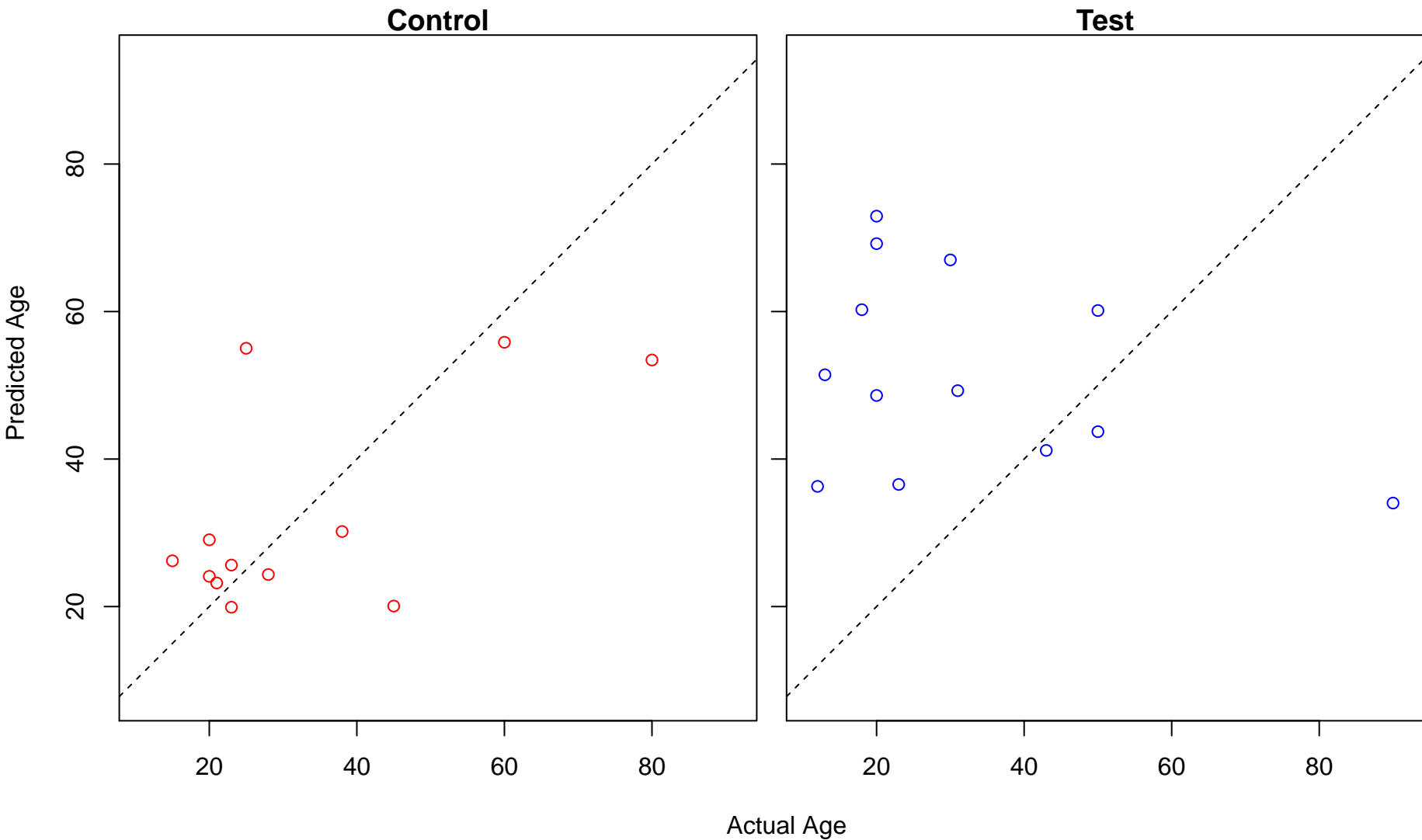
heme metabolic process (Score: 3.834597)



negative regulation of telomere maintenance via telomere lengthening (Score: 3.834221)

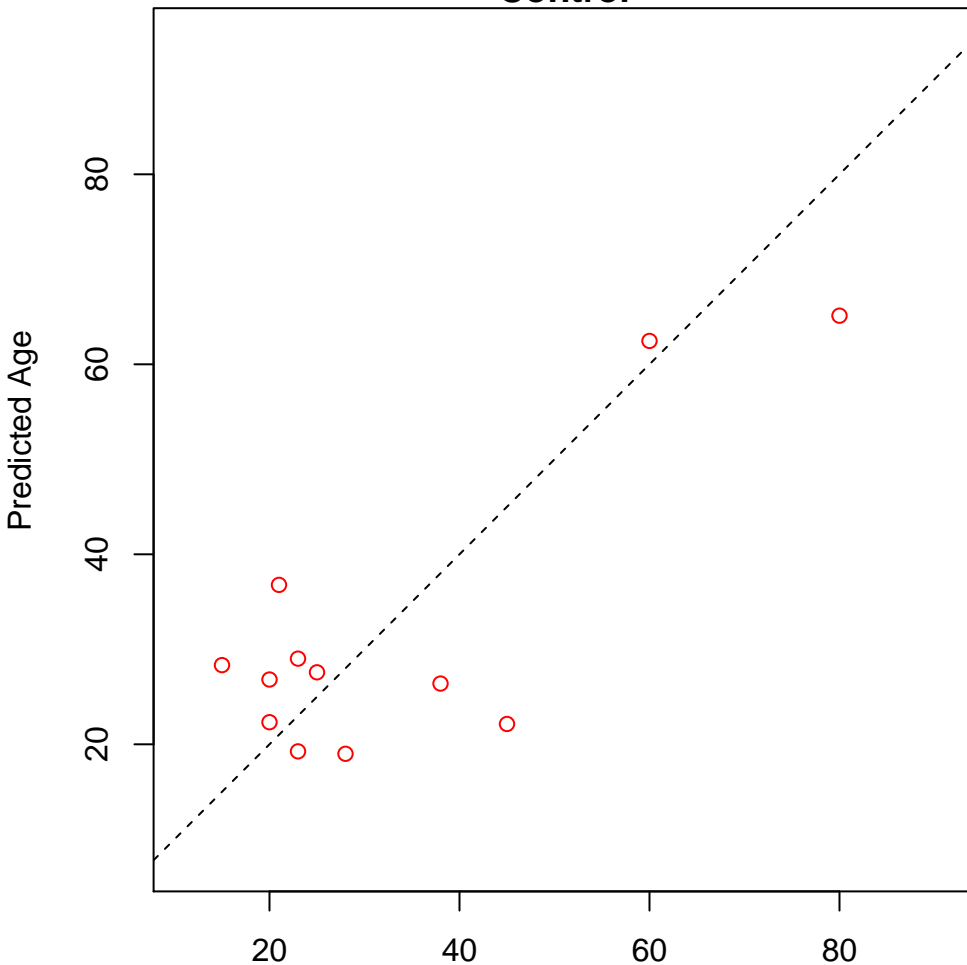


positive regulation of steroid hormone secretion (Score: 3.834190)

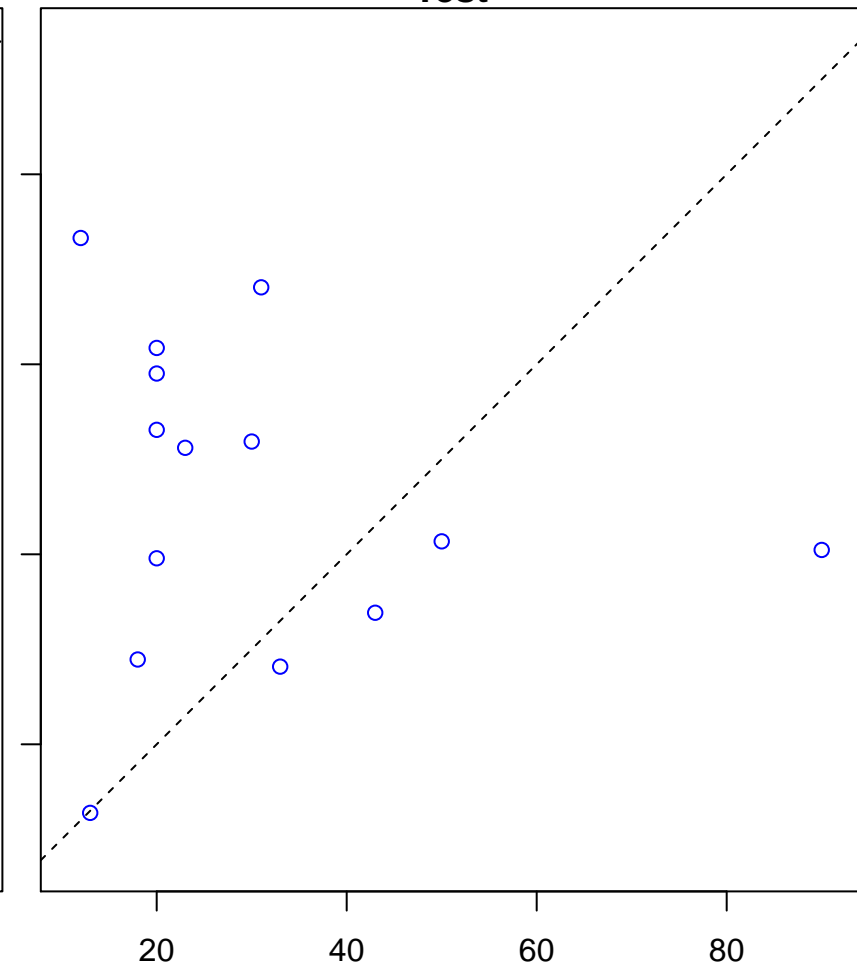


regulation of epidermis development (Score: 3.833696)

Control

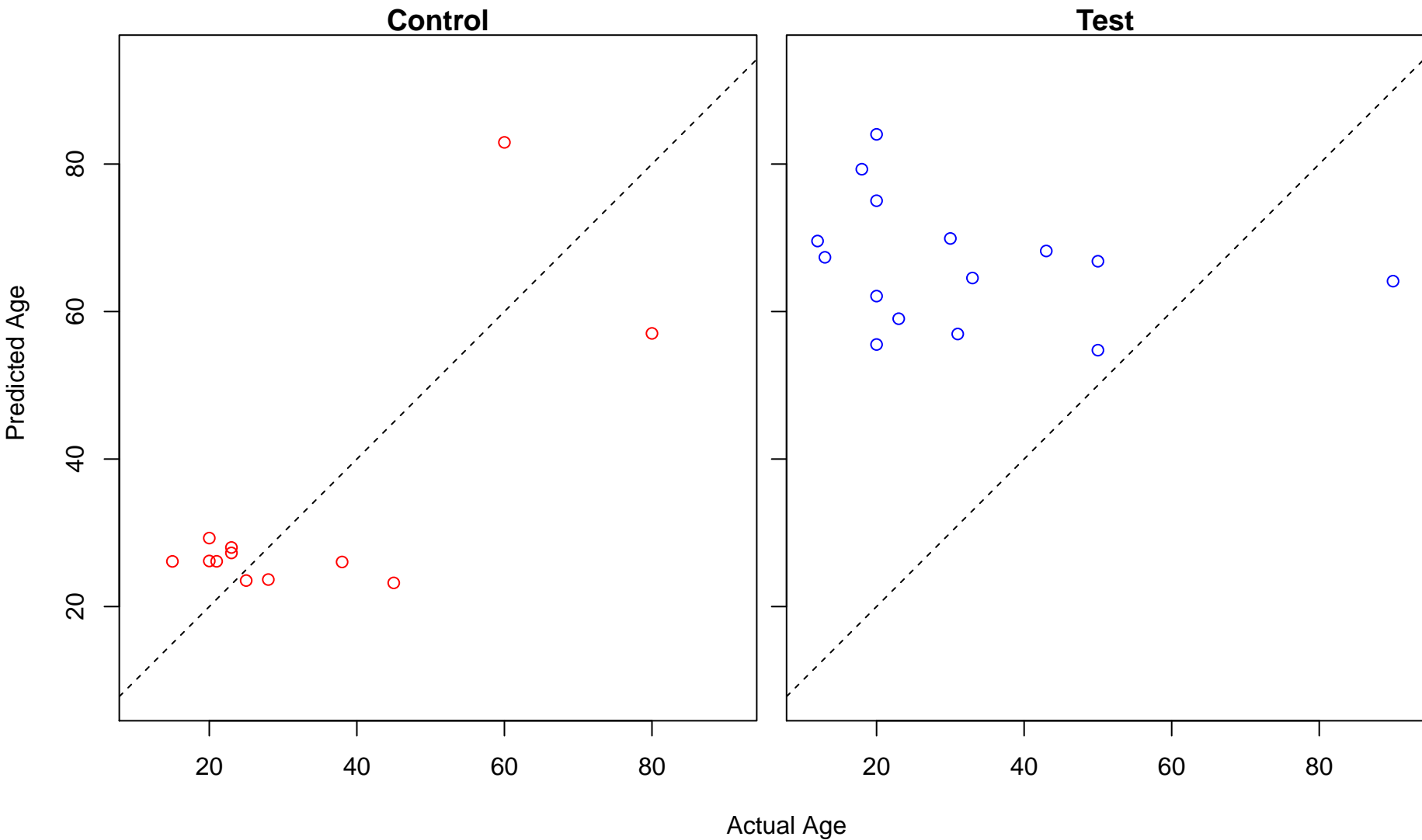


Test

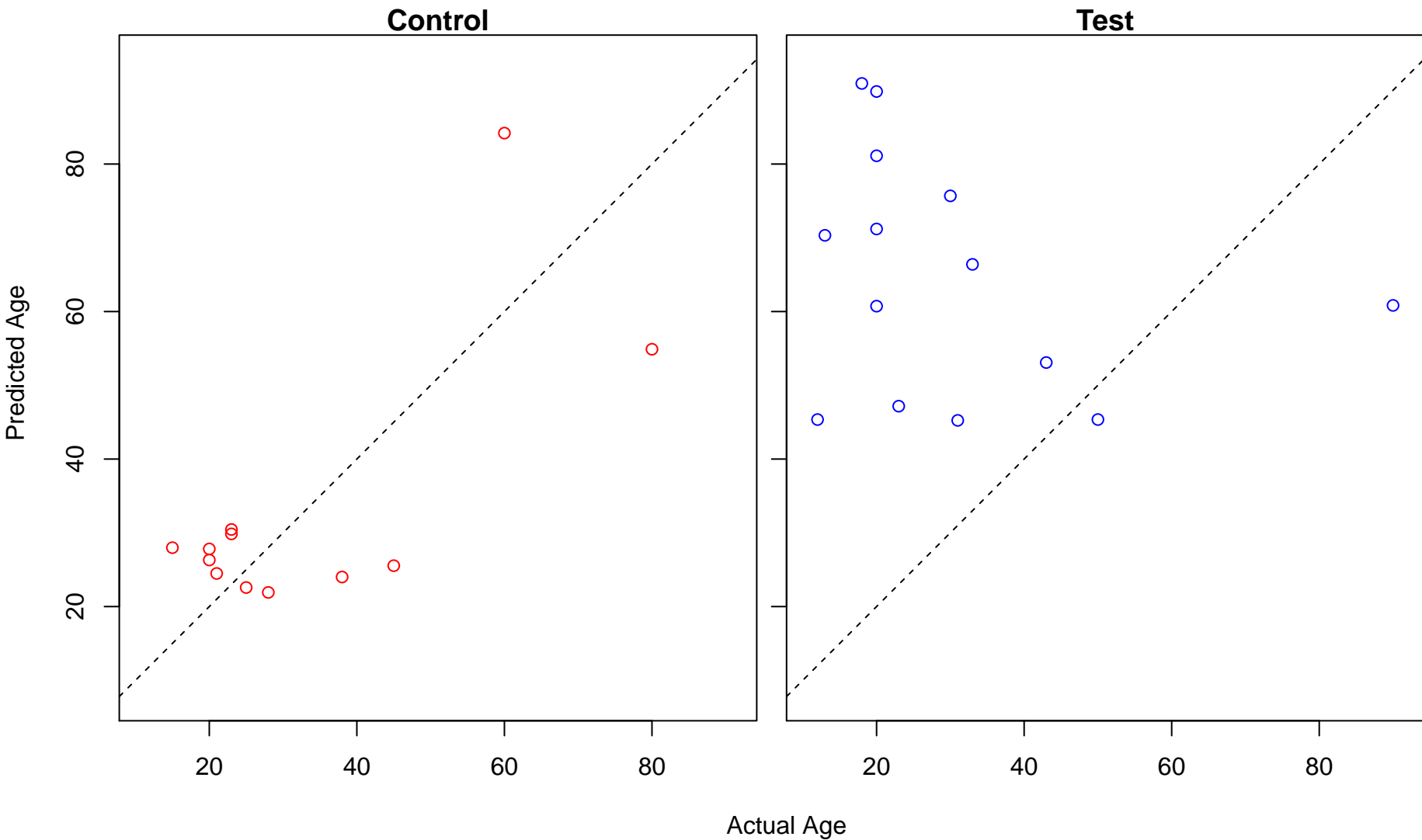


Actual Age

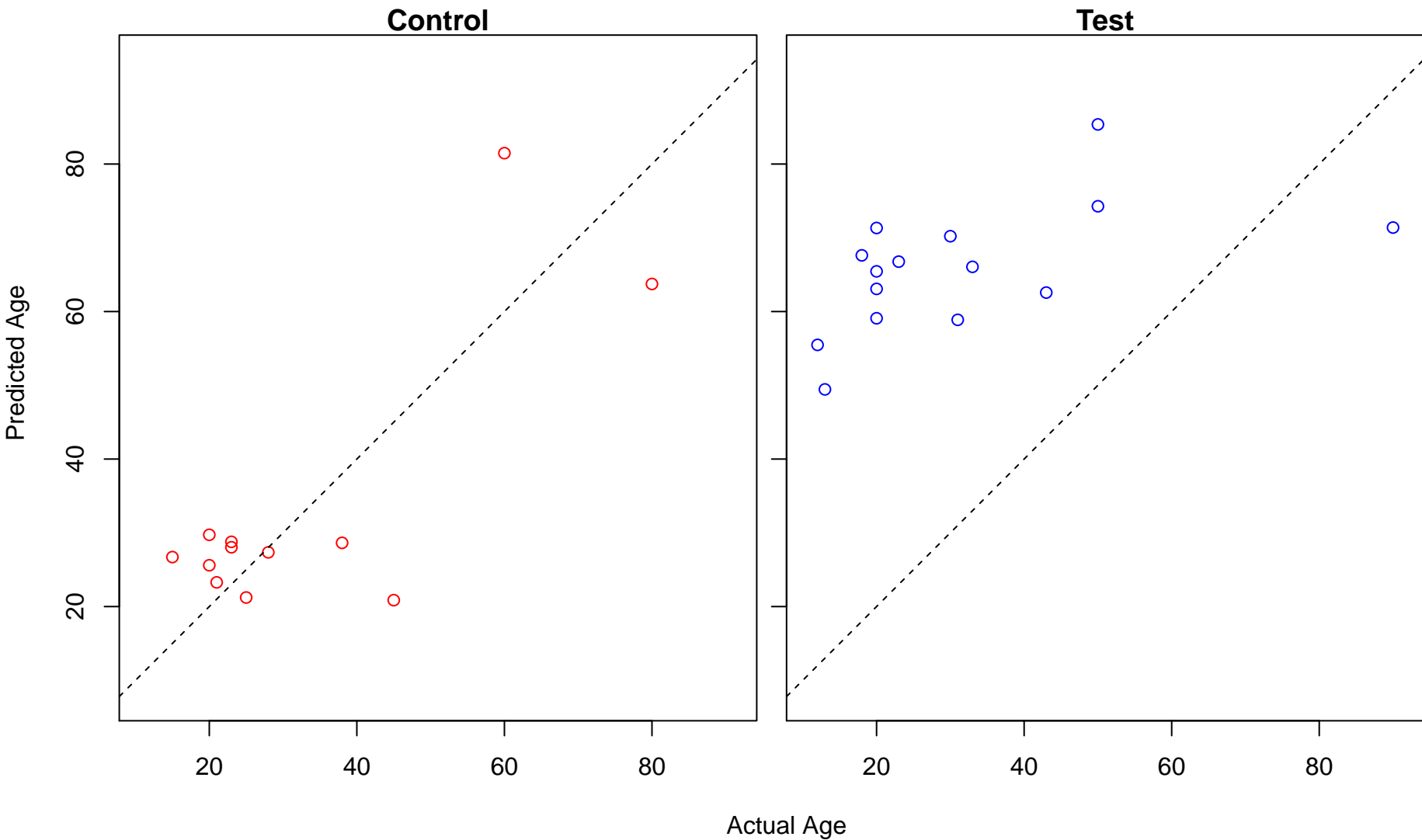
response to UV-C (Score: 3.832333)



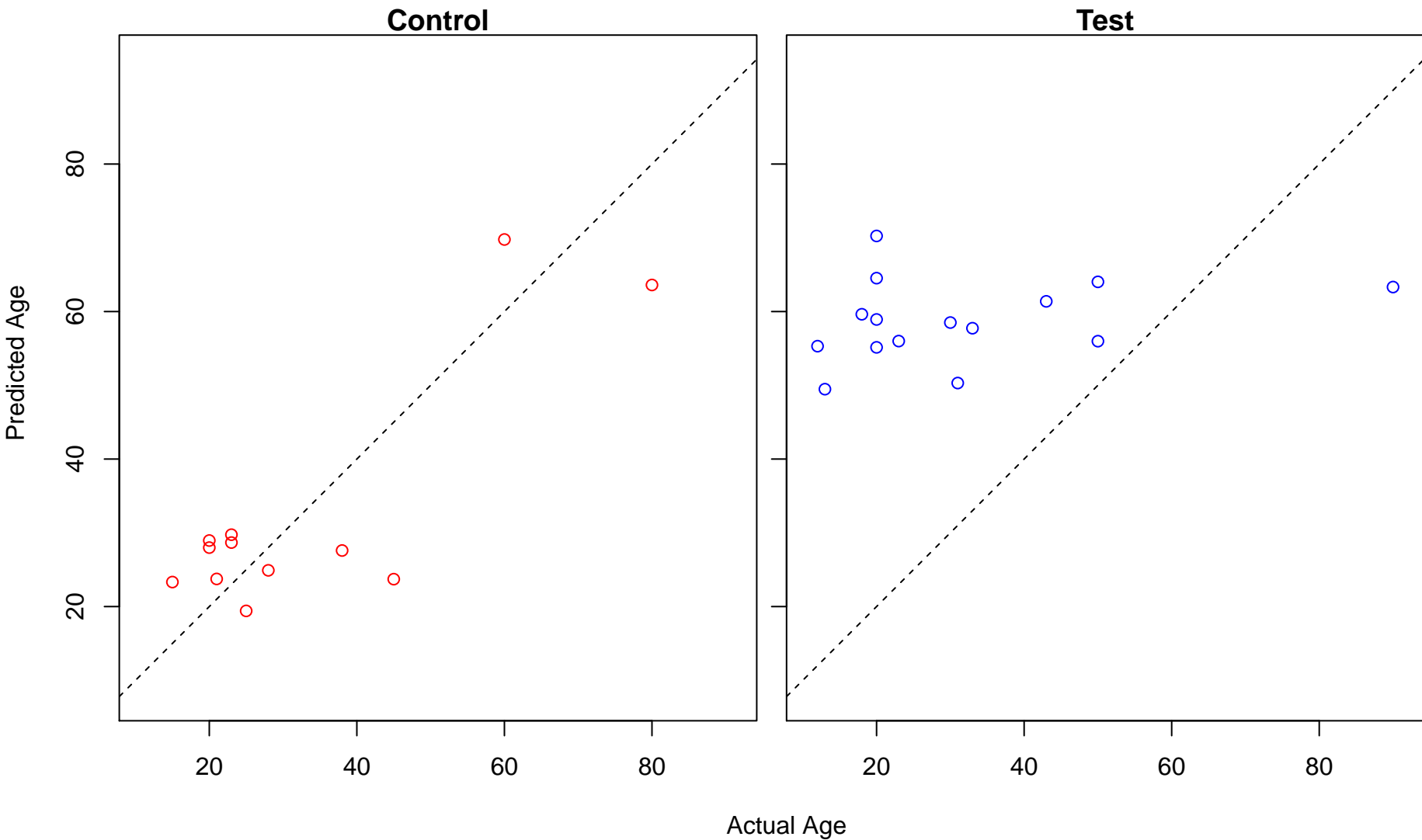
keratinocyte proliferation (Score: 3.832236)



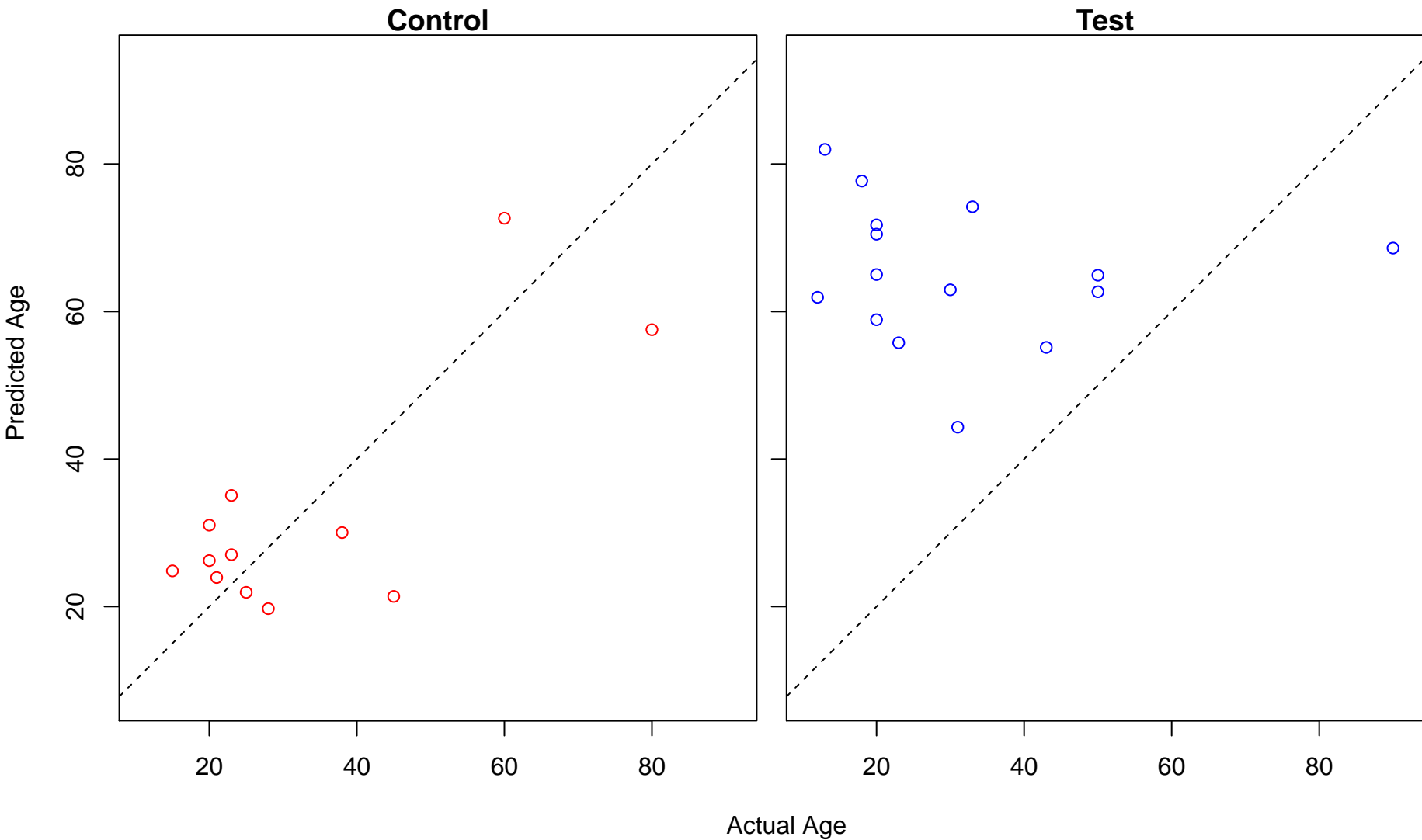
O-glycan processing (Score: 3.830029)



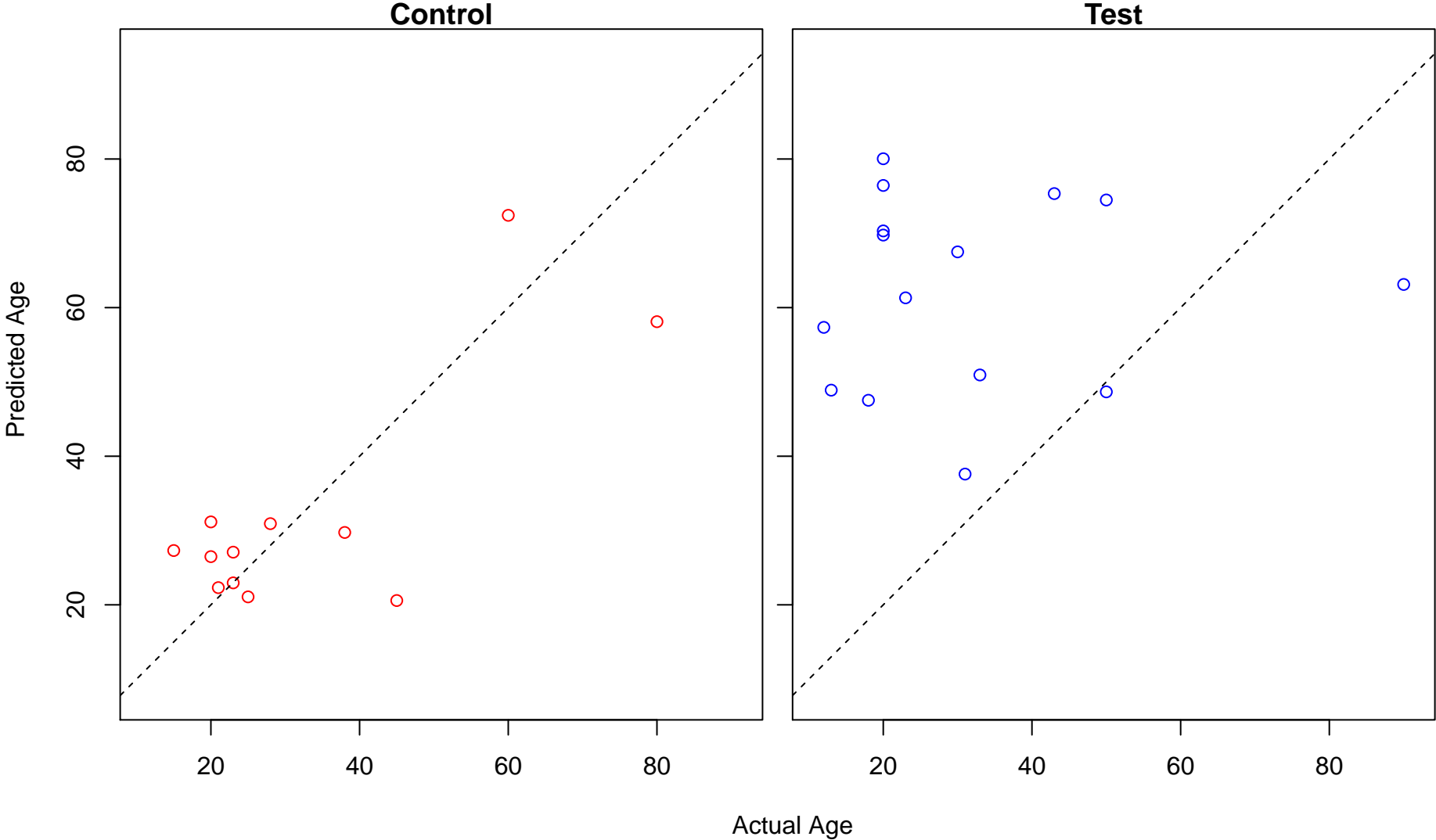
regulation of gluconeogenesis (Score: 3.830000)



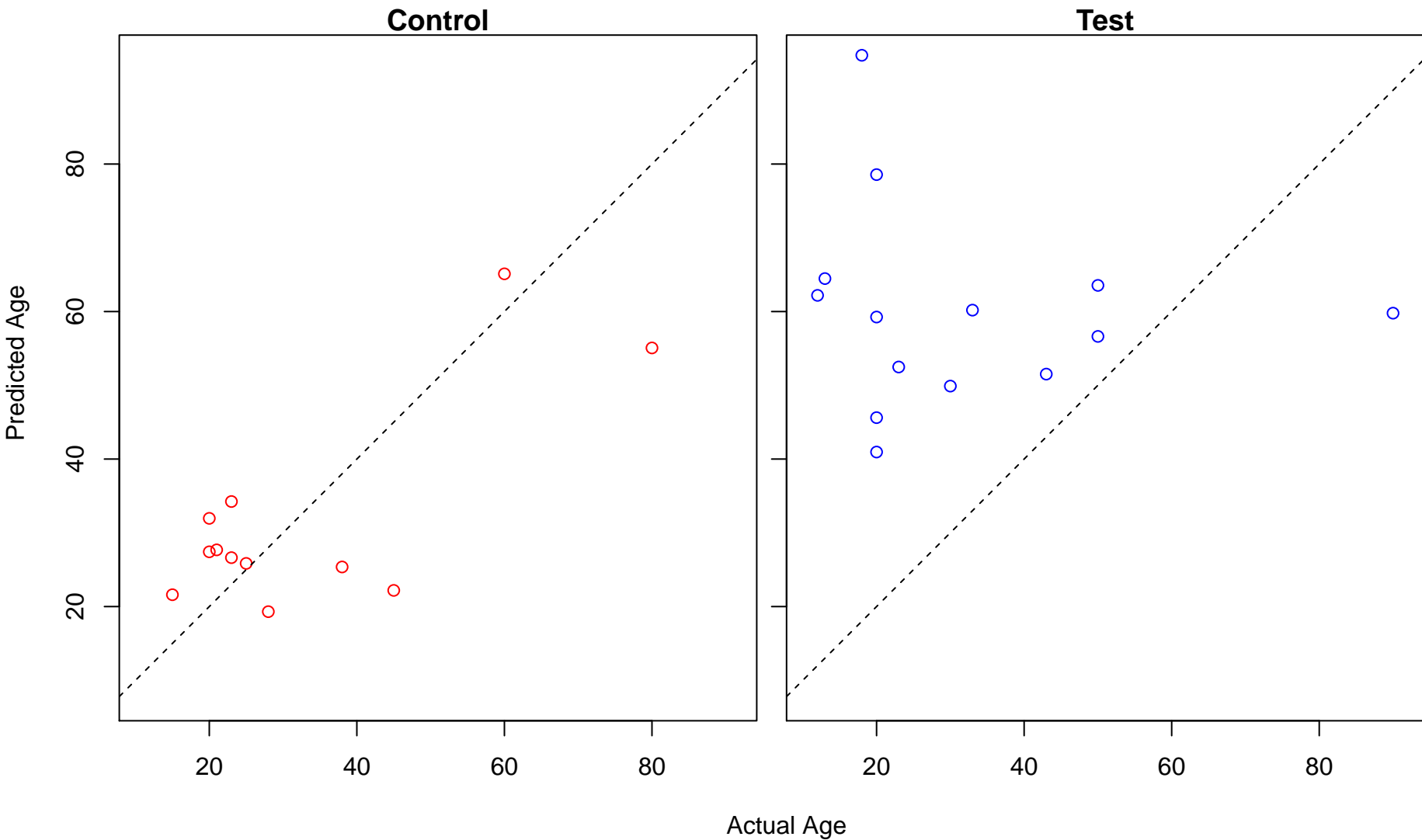
dicarboxylic acid biosynthetic process (Score: 3.829637)



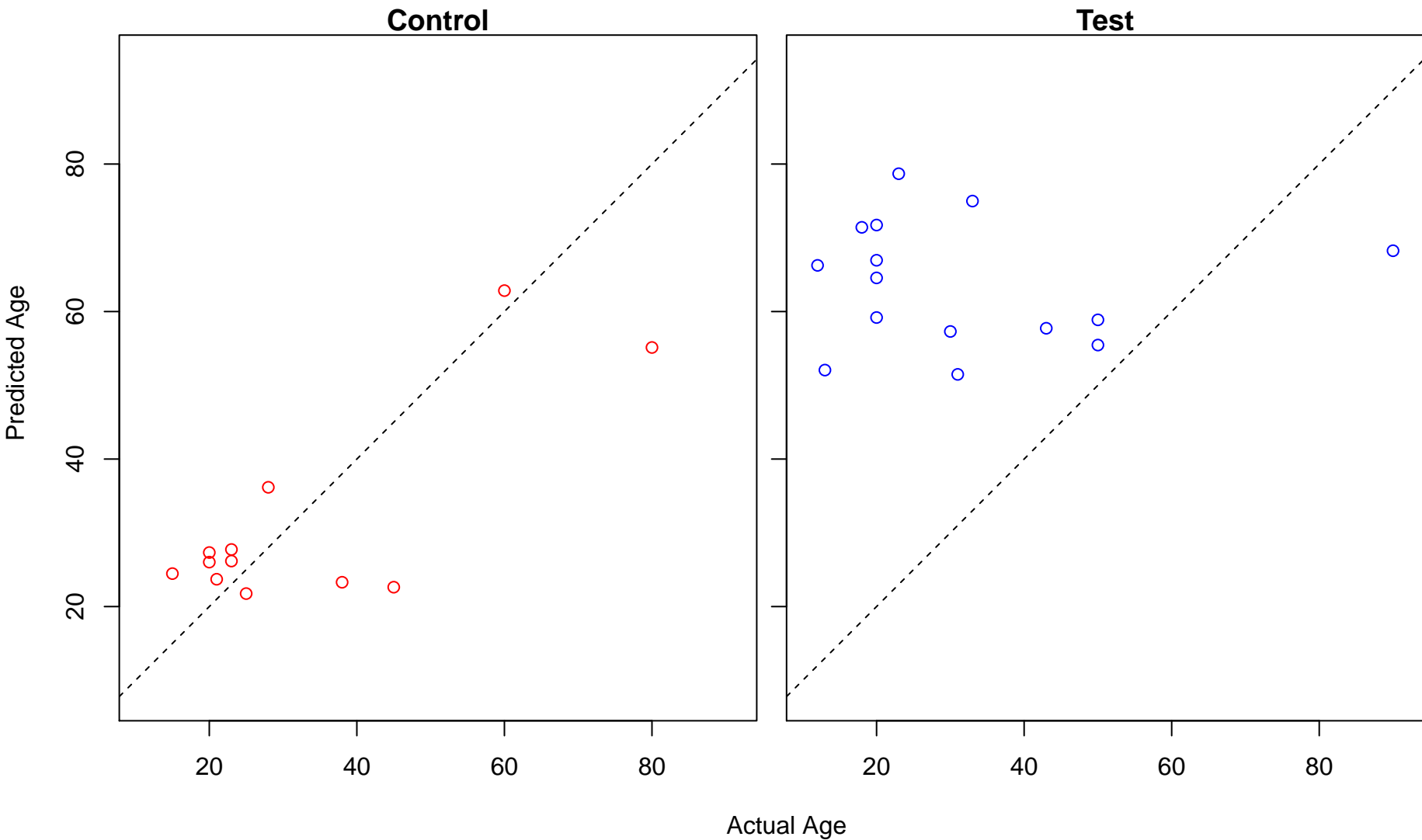
cellular detoxification (Score: 3.829322)



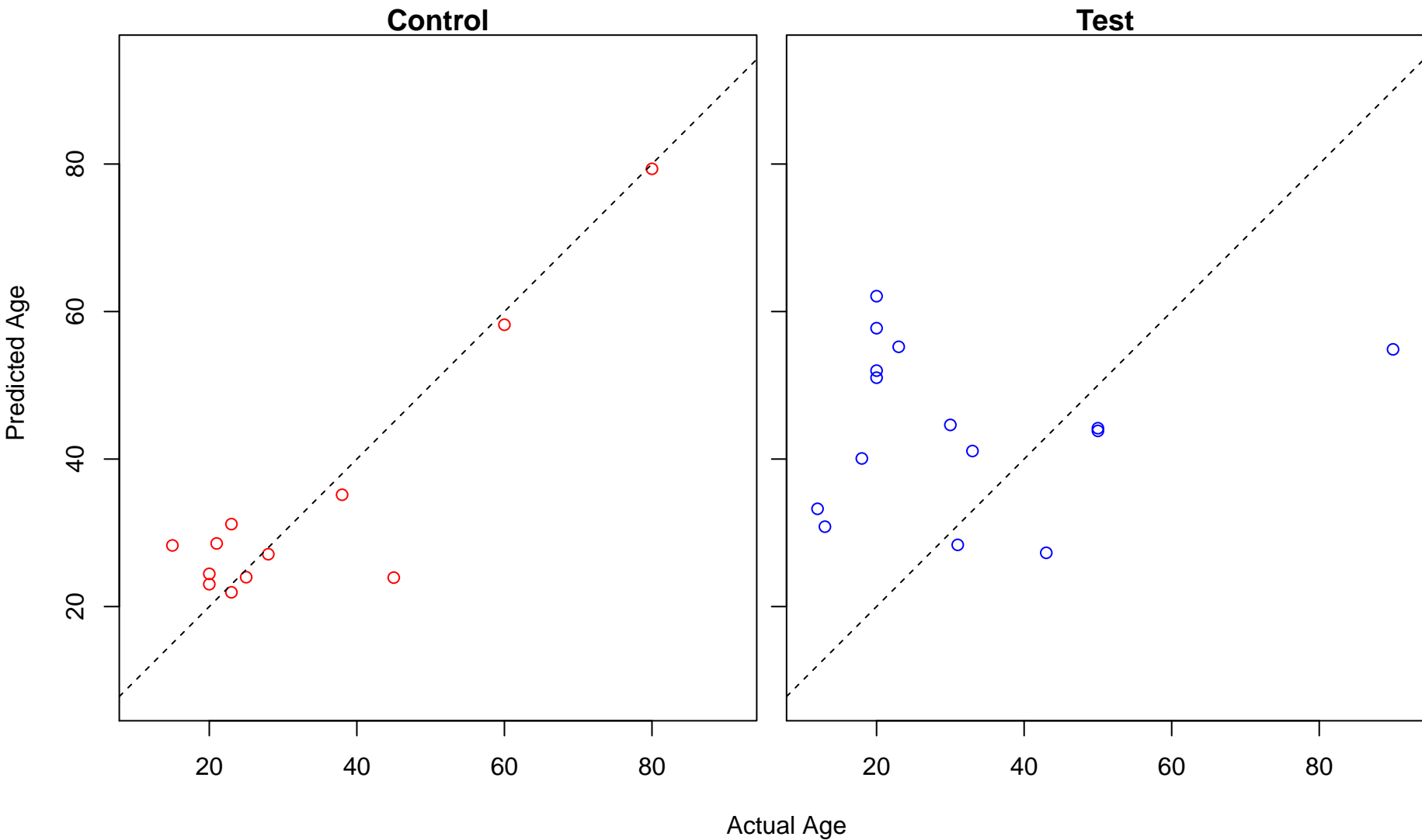
phenol-containing compound biosynthetic process (Score: 3.828871)



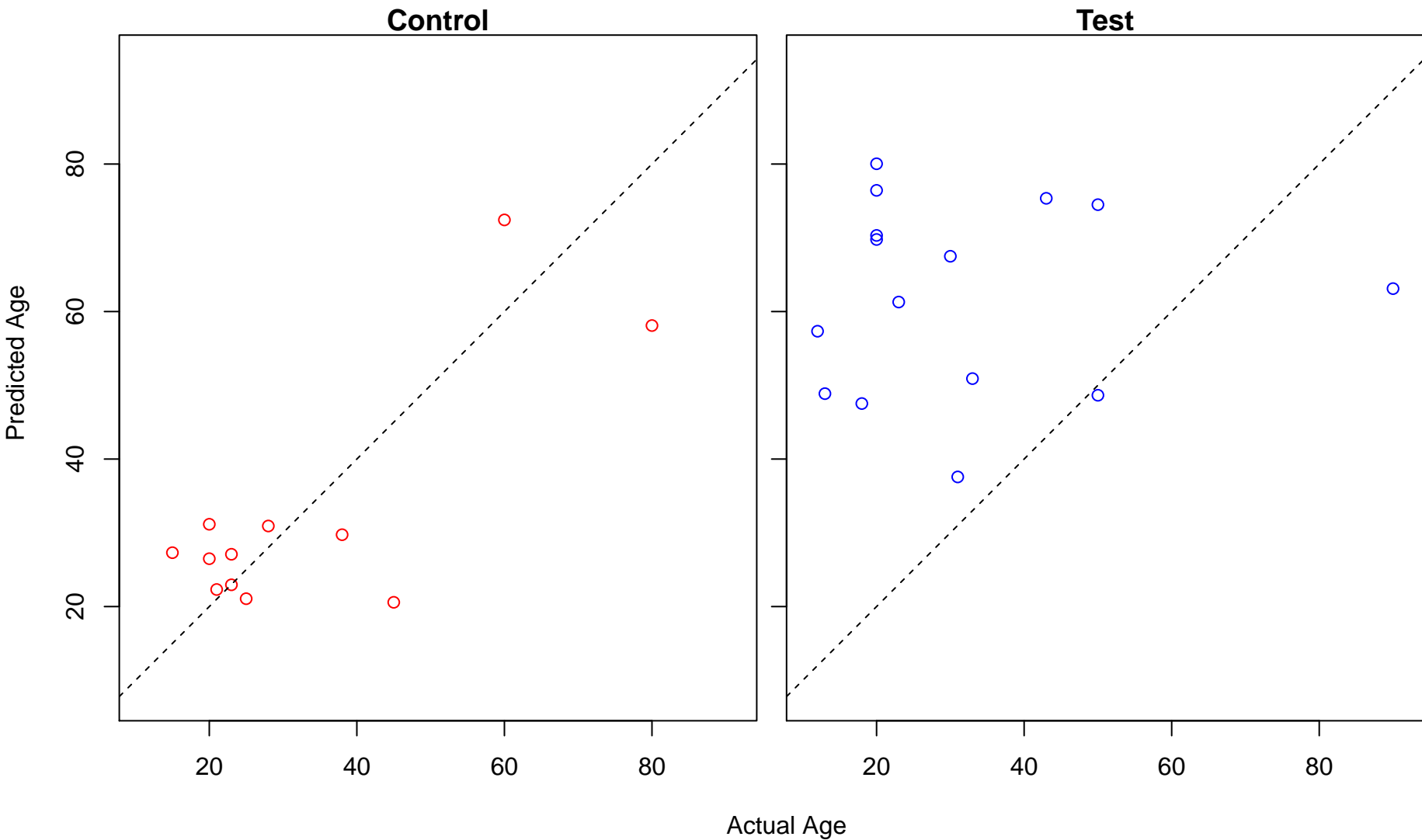
succinate metabolic process (Score: 3.828783)



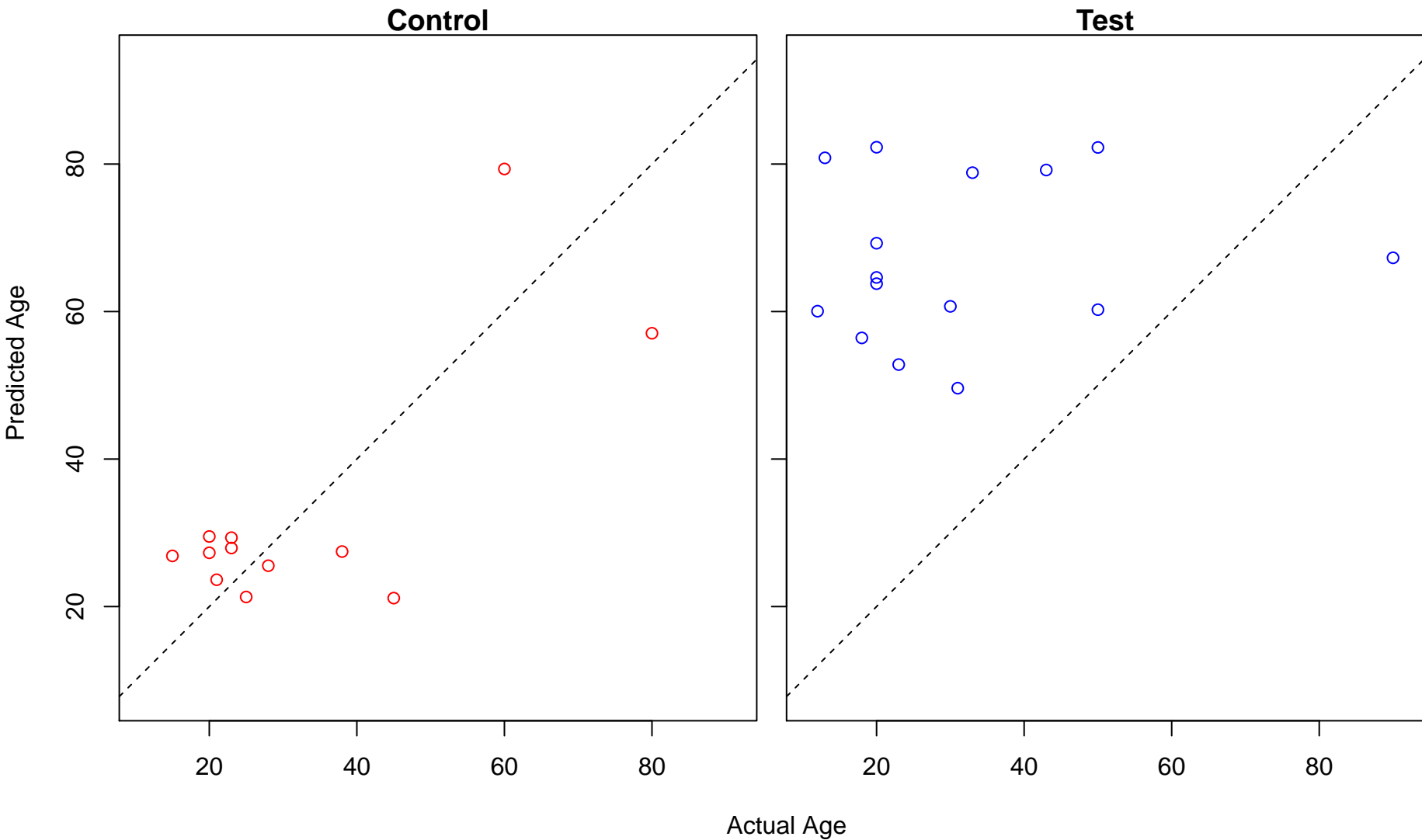
mRNA methylation (Score: 3.827968)



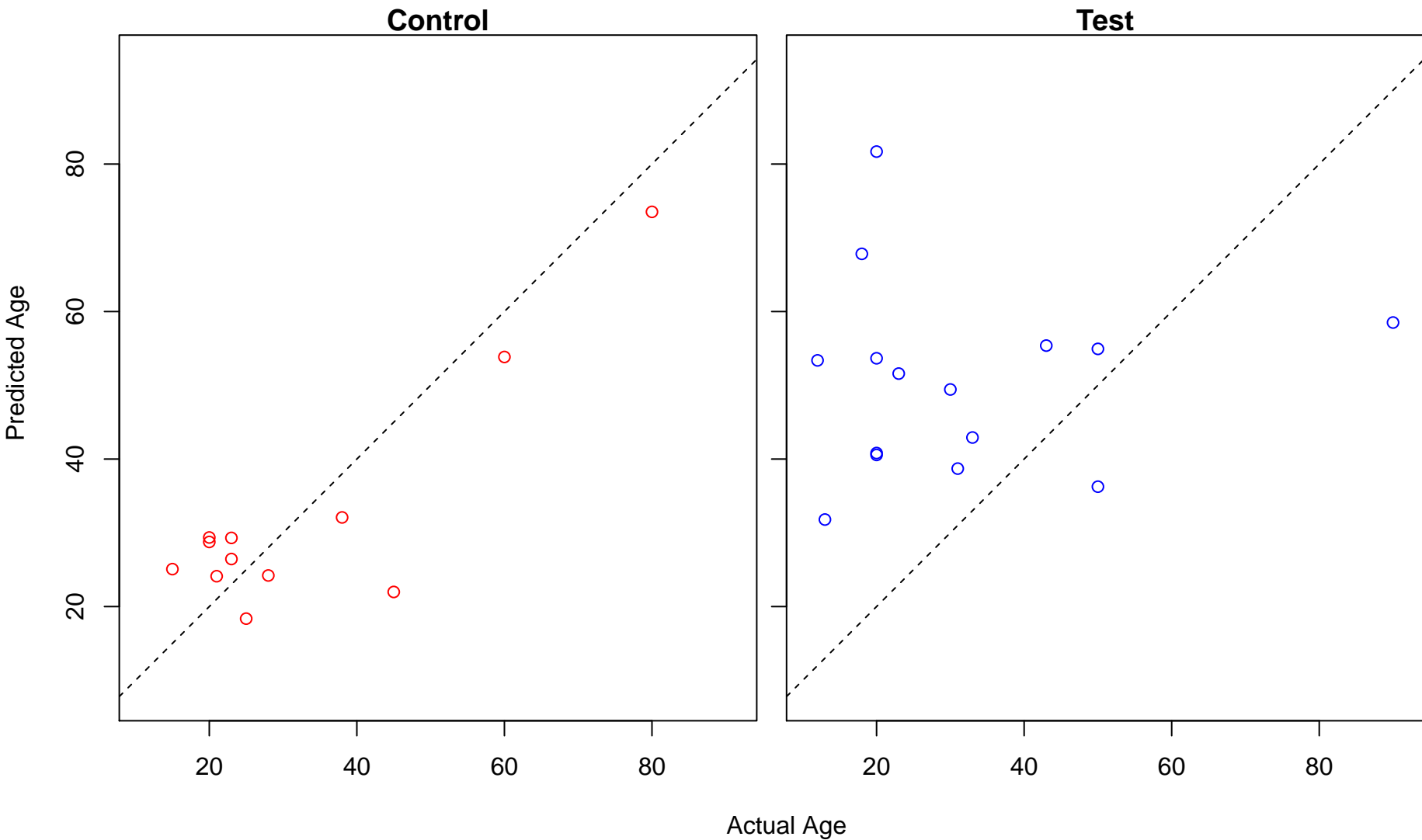
cellular oxidant detoxification (Score: 3.827928)



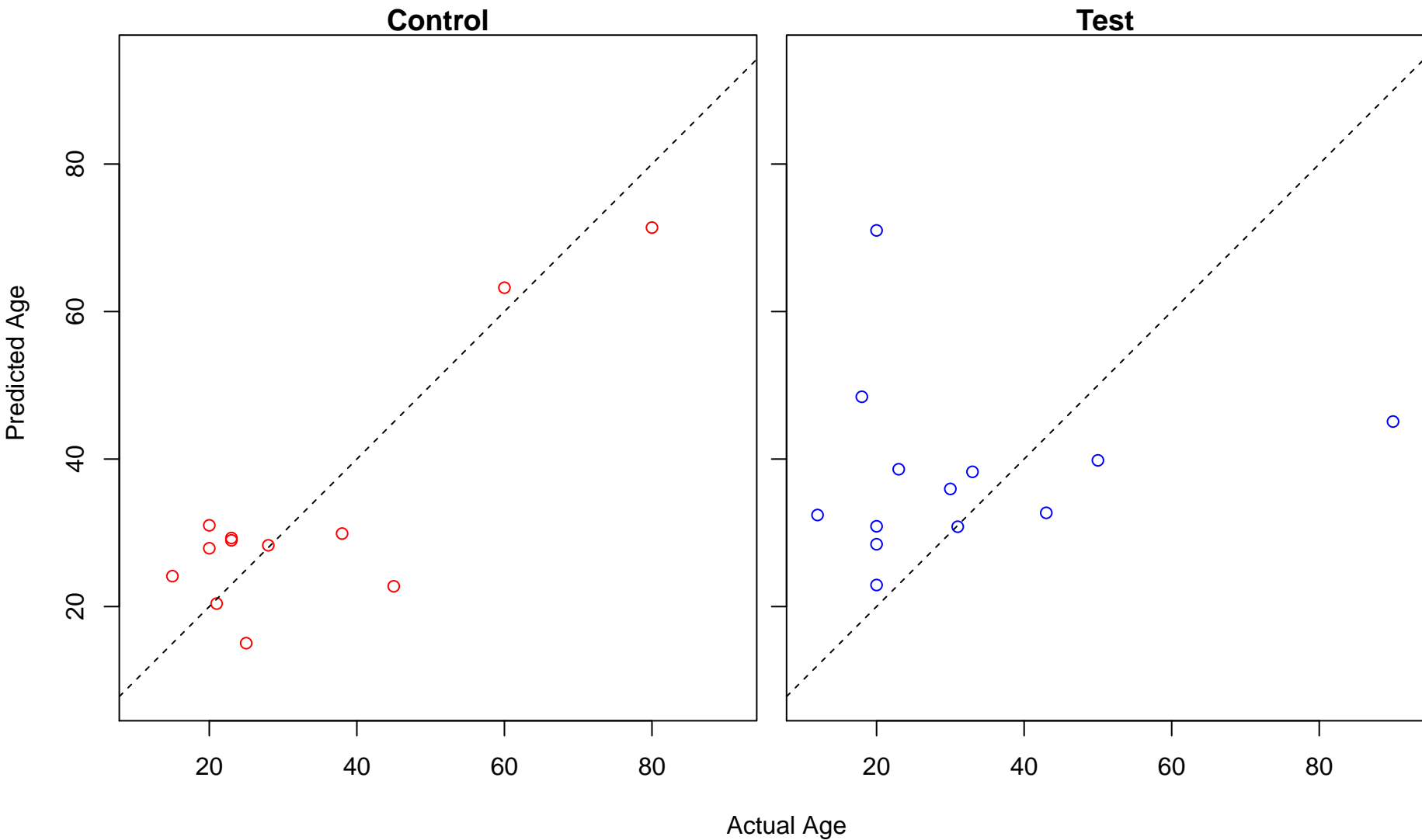
ionotropic glutamate receptor signaling pathway (Score: 3.827500)



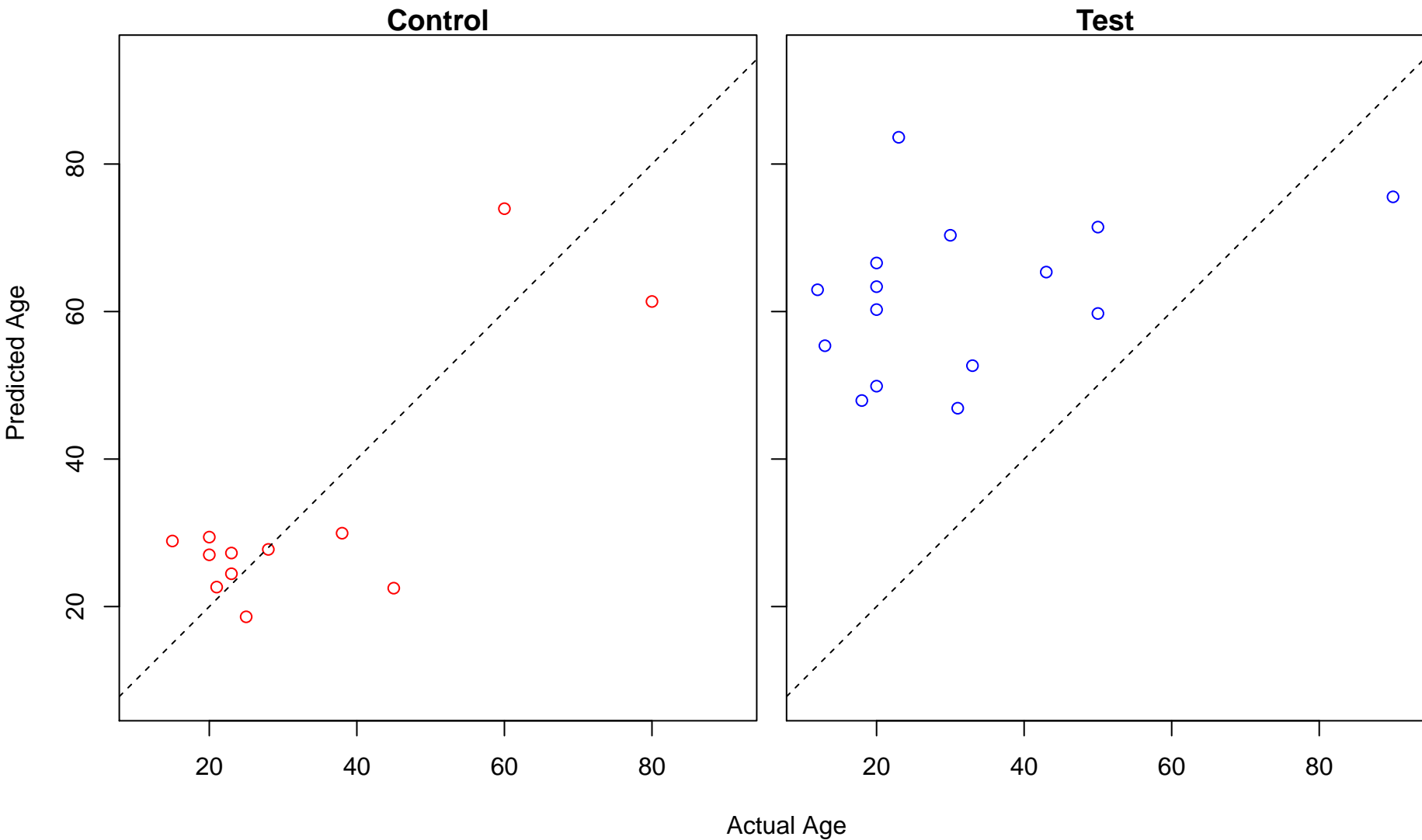
regulation of clathrin-mediated endocytosis (Score: 3.826545)



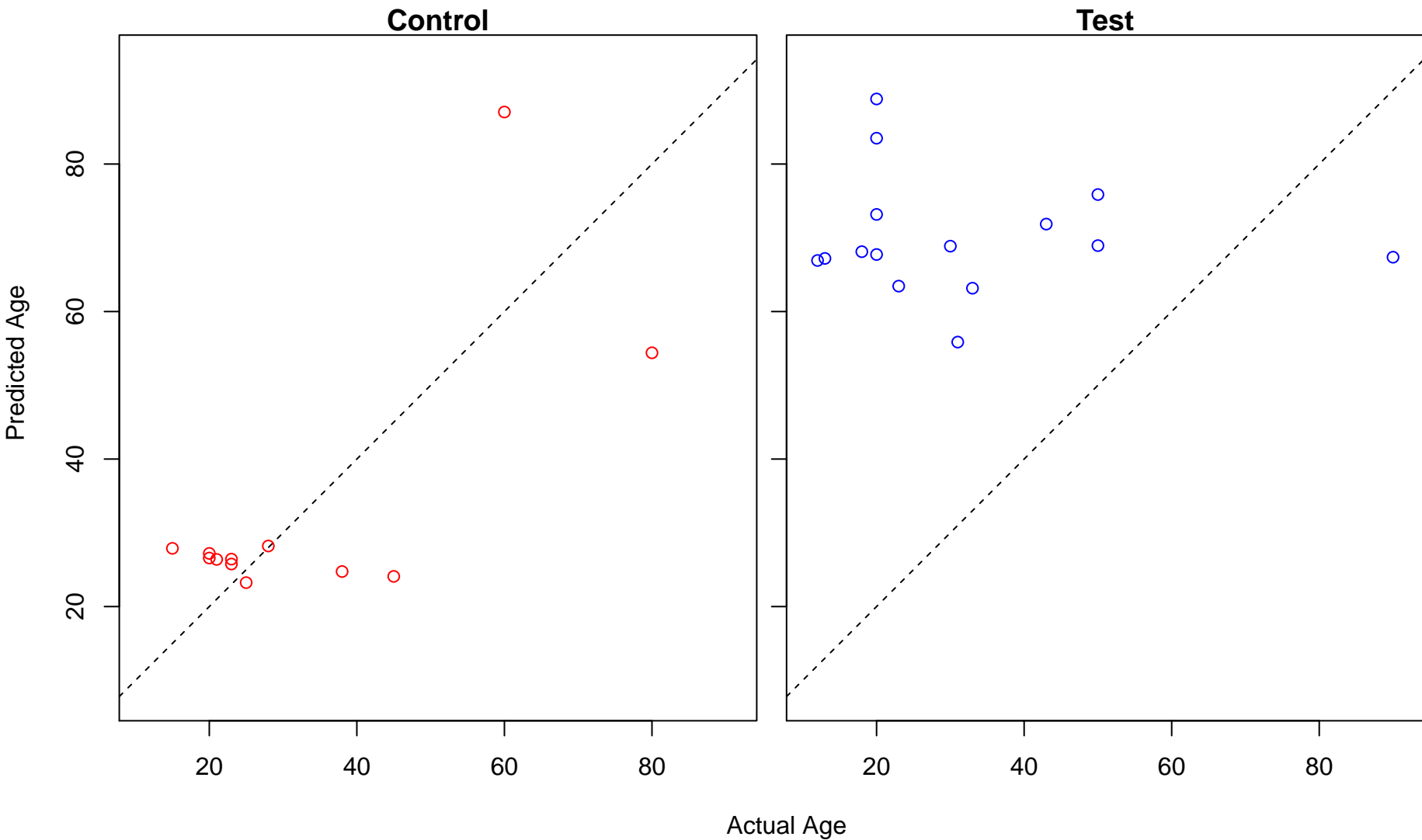
regulation of membrane lipid distribution (Score: 3.824973)



positive regulation of early endosome to late endosome transport (Score: 3.822259)

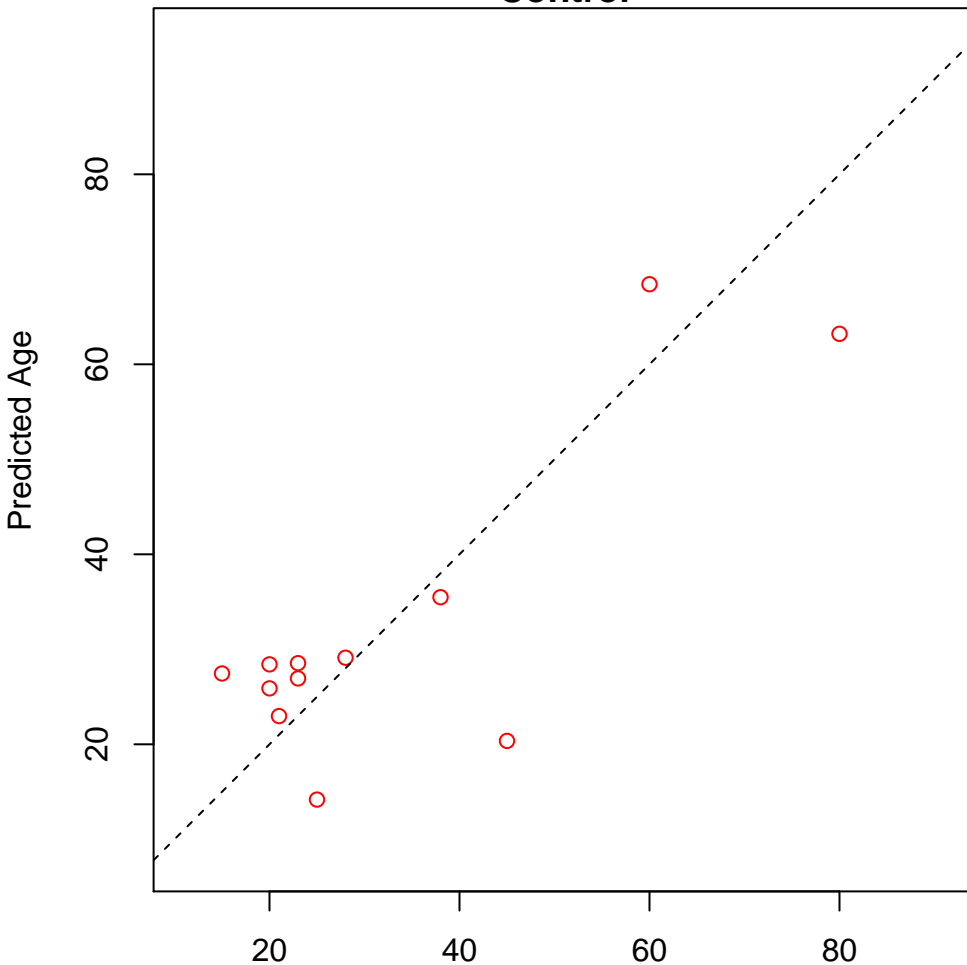


porphyrin-containing compound metabolic process (Score: 3.819746)

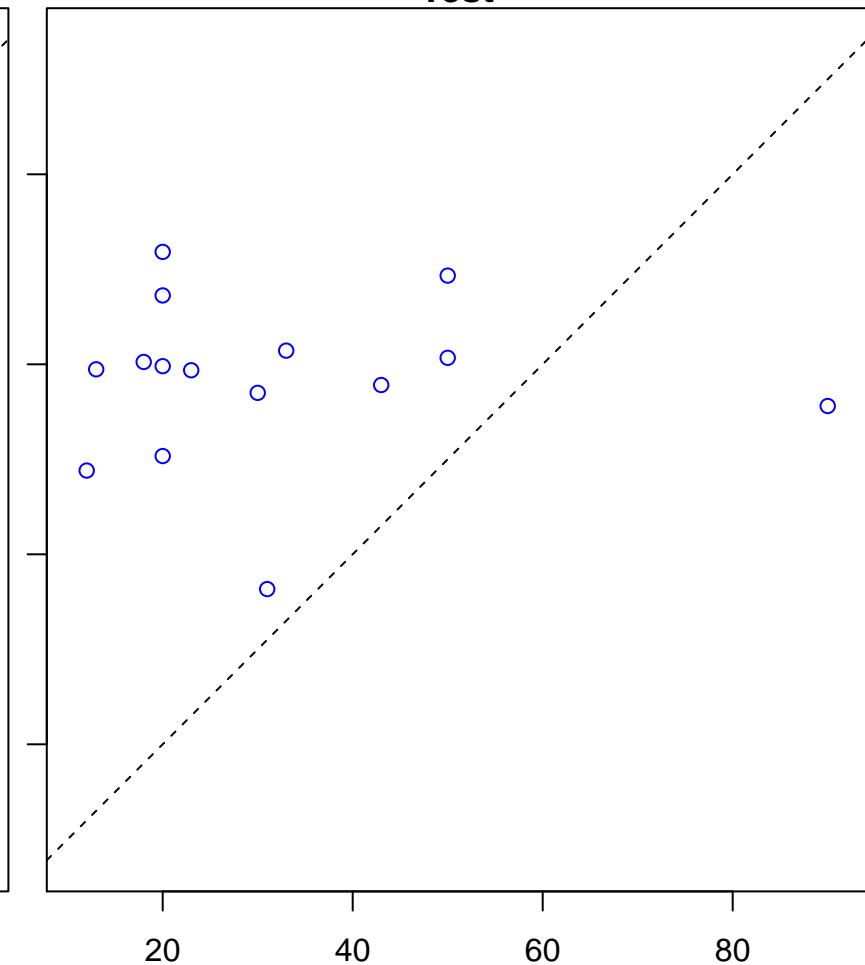


fusion of sperm to egg plasma membrane (Score: 3.818432)

Control

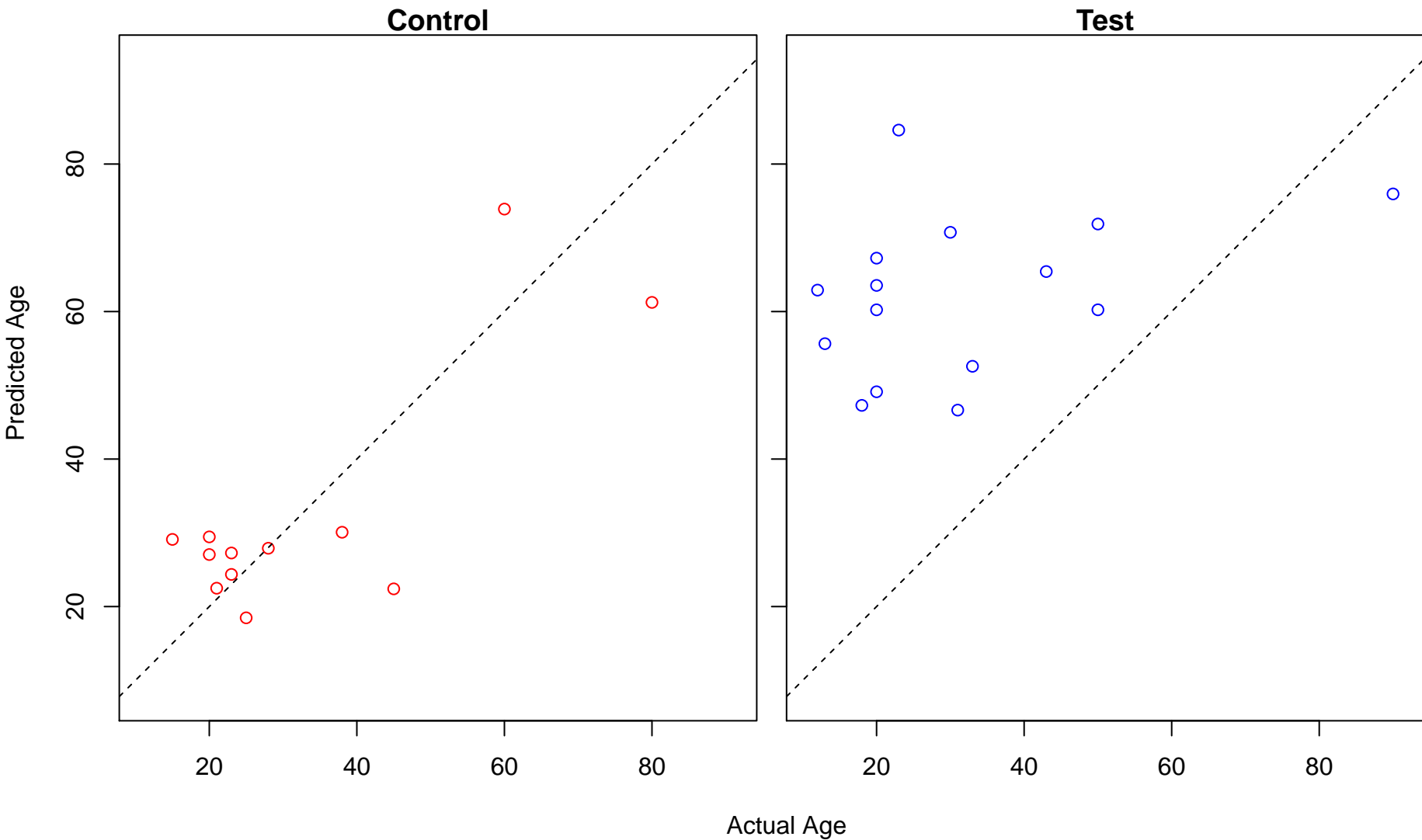


Test

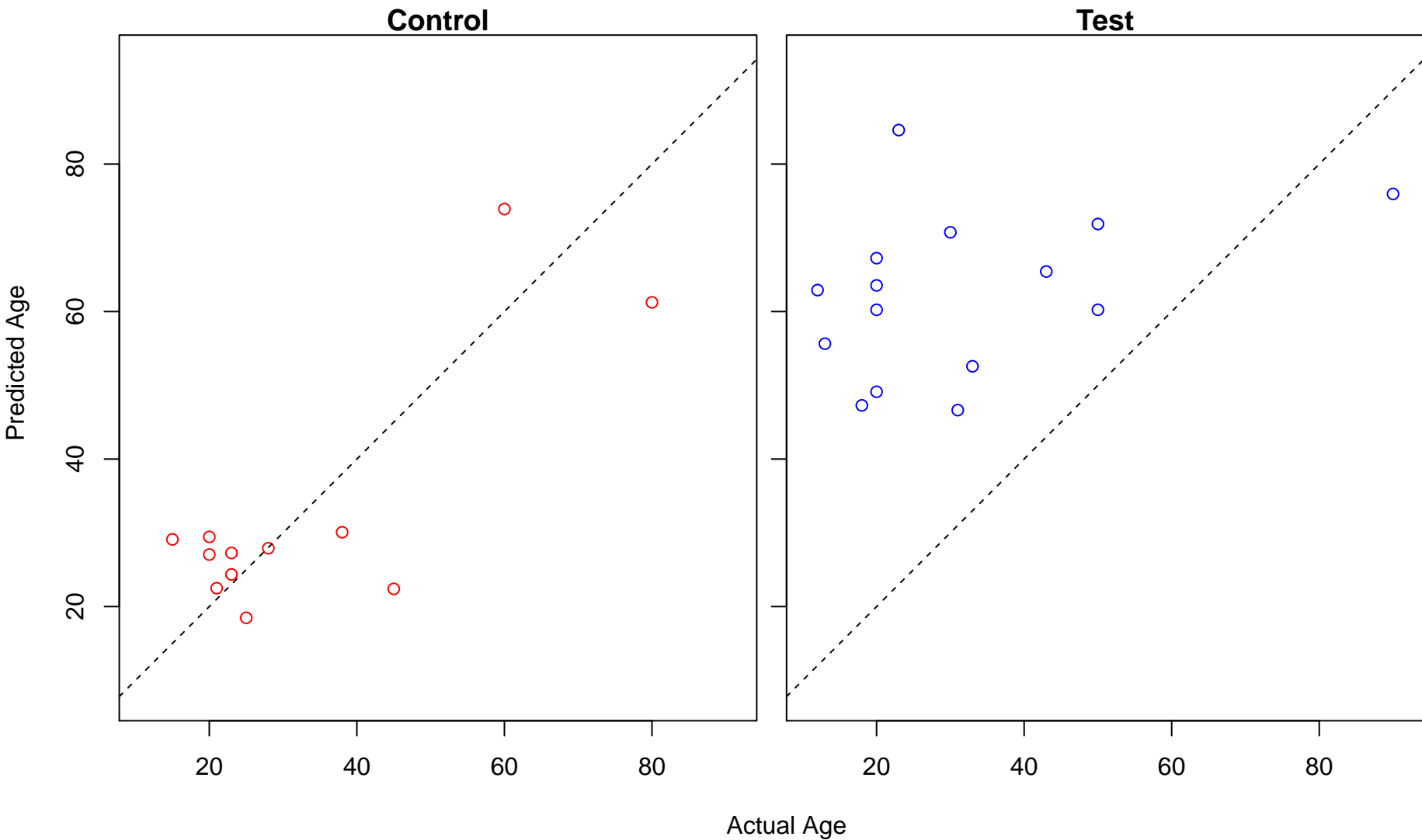


Actual Age

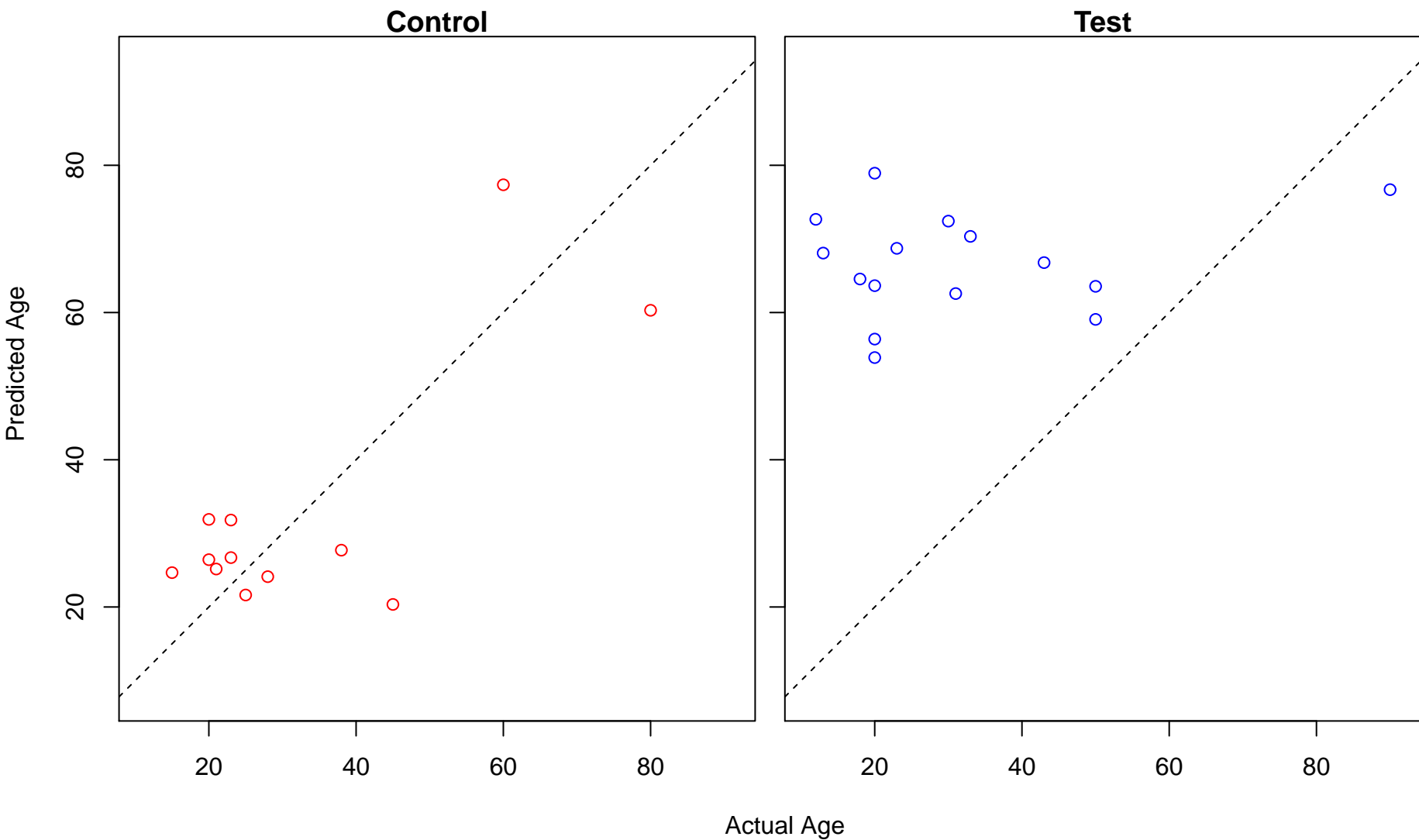
sphingosine-1-phosphate signaling pathway (Score: 3.818249)



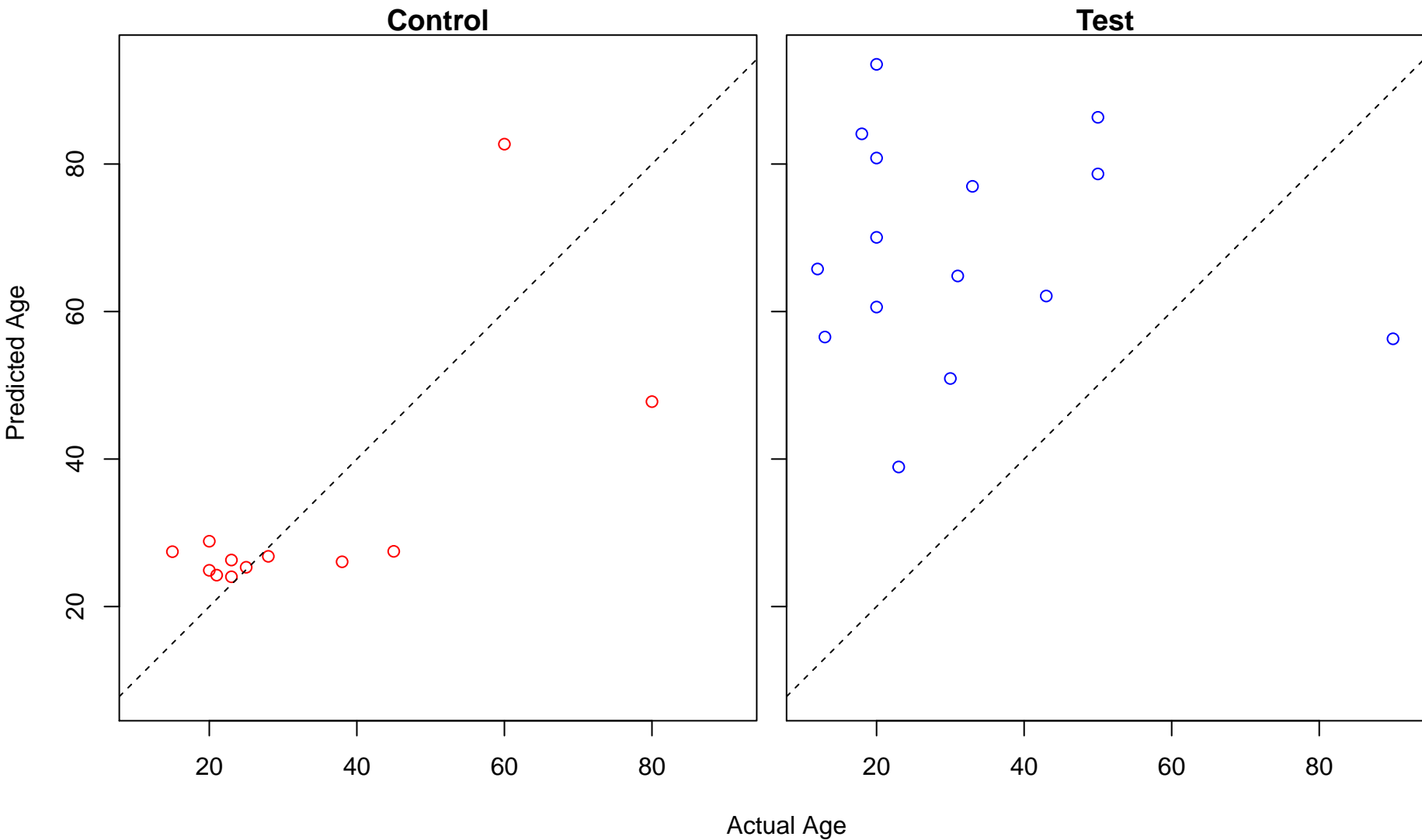
sphingolipid mediated signaling pathway (Score: 3.818249)



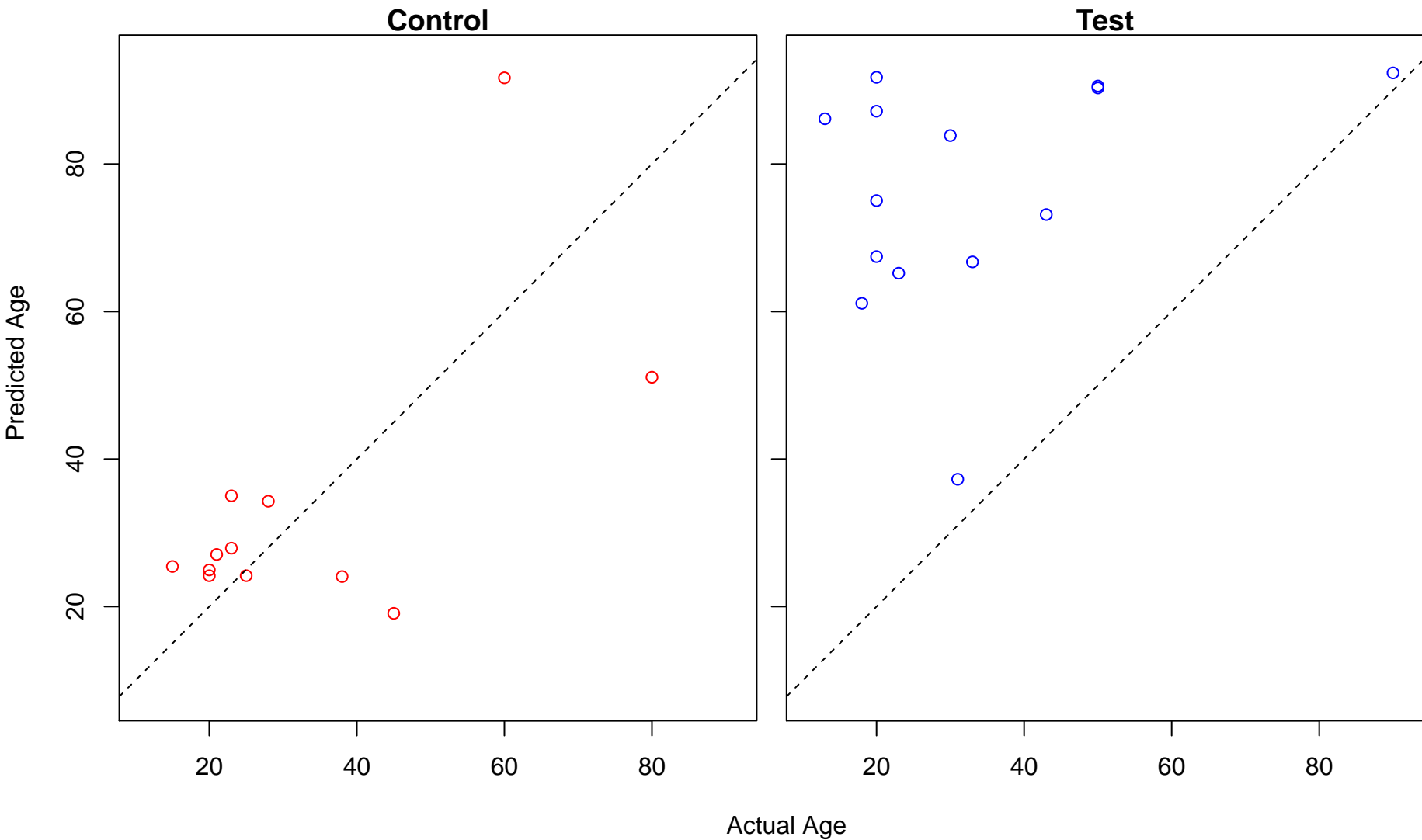
positive regulation of glucose transport (Score: 3.817293)



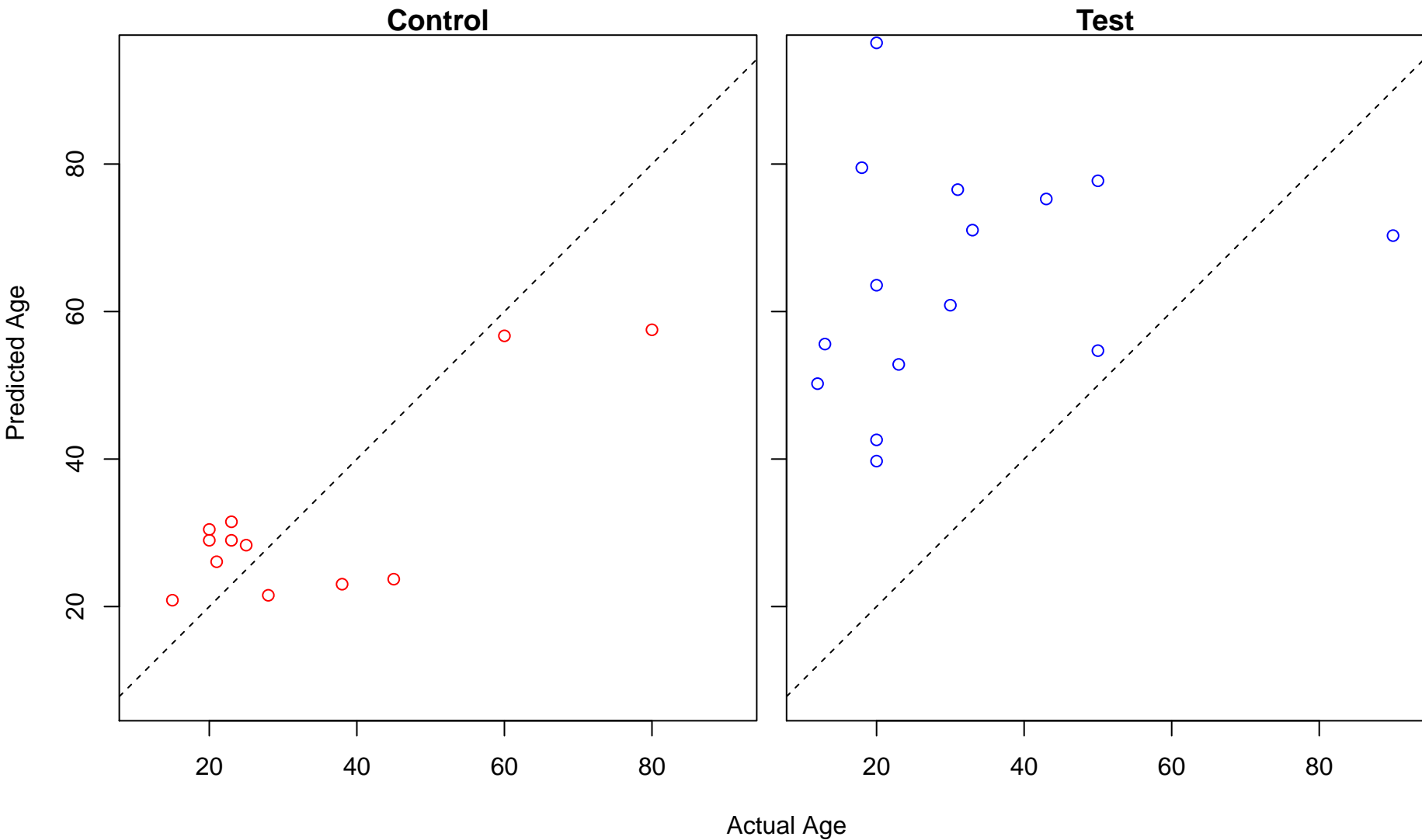
regulation of cell fate specification (Score: 3.814250)



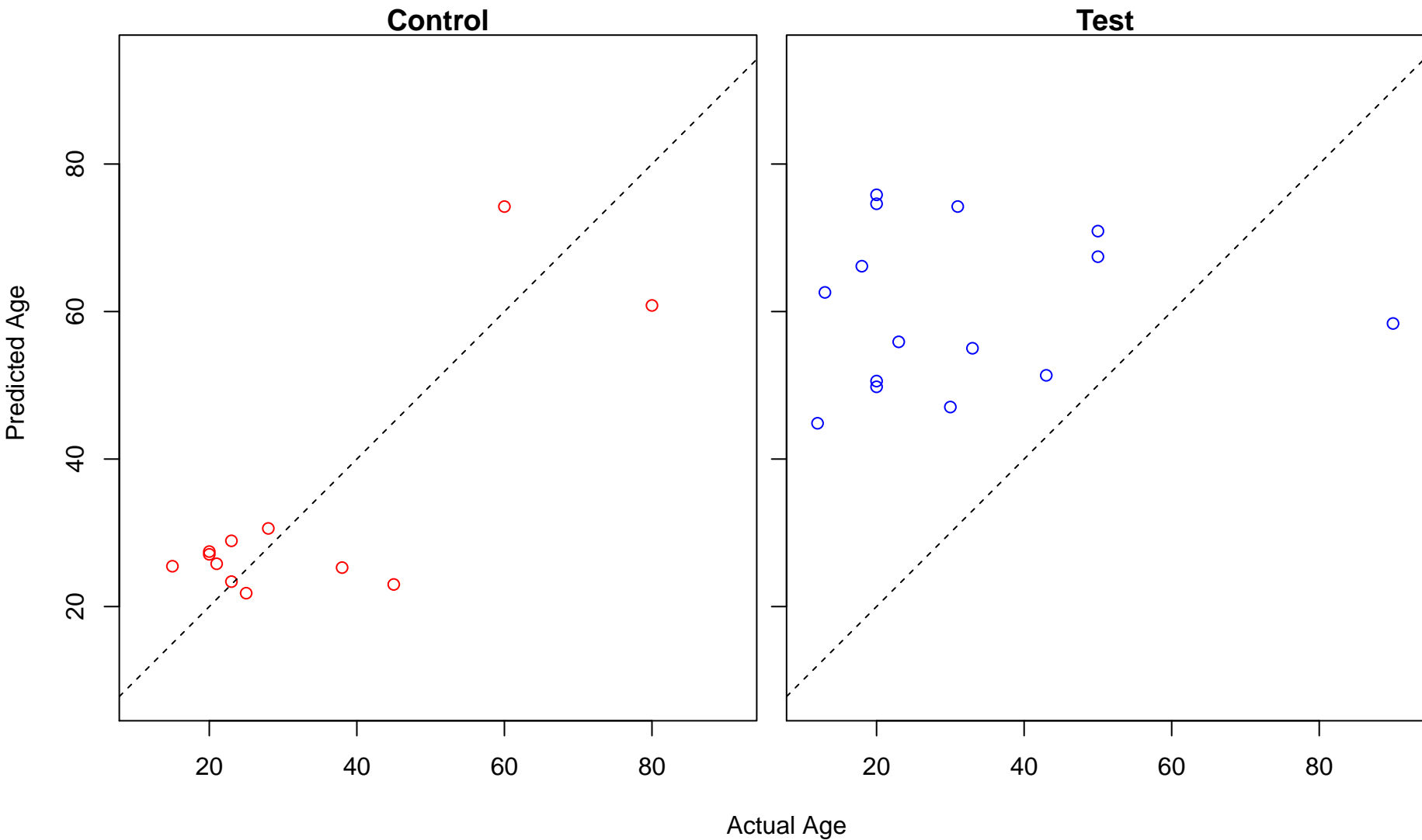
G-protein coupled receptor internalization (Score: 3.812921)



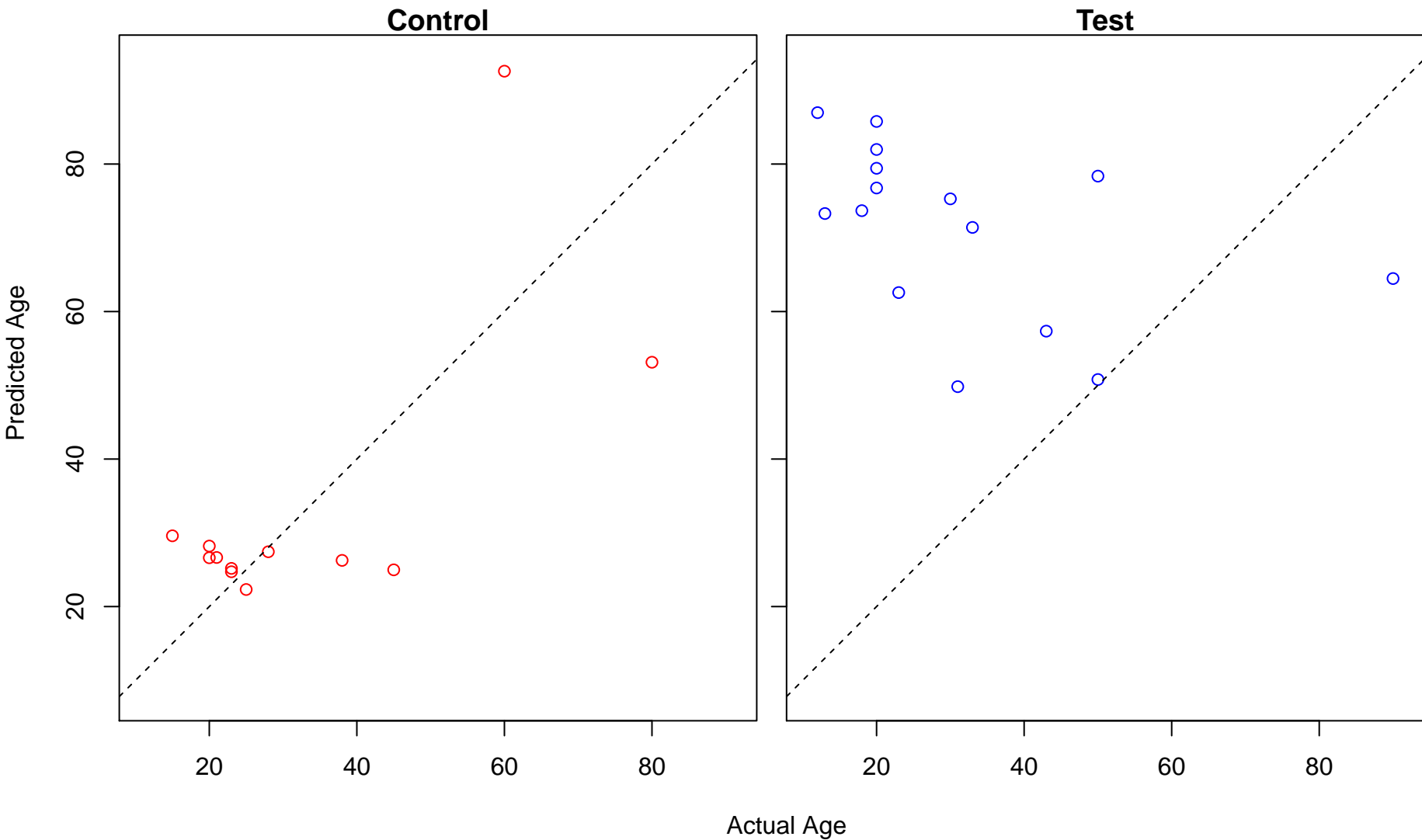
monoterpenoid metabolic process (Score: 3.812860)



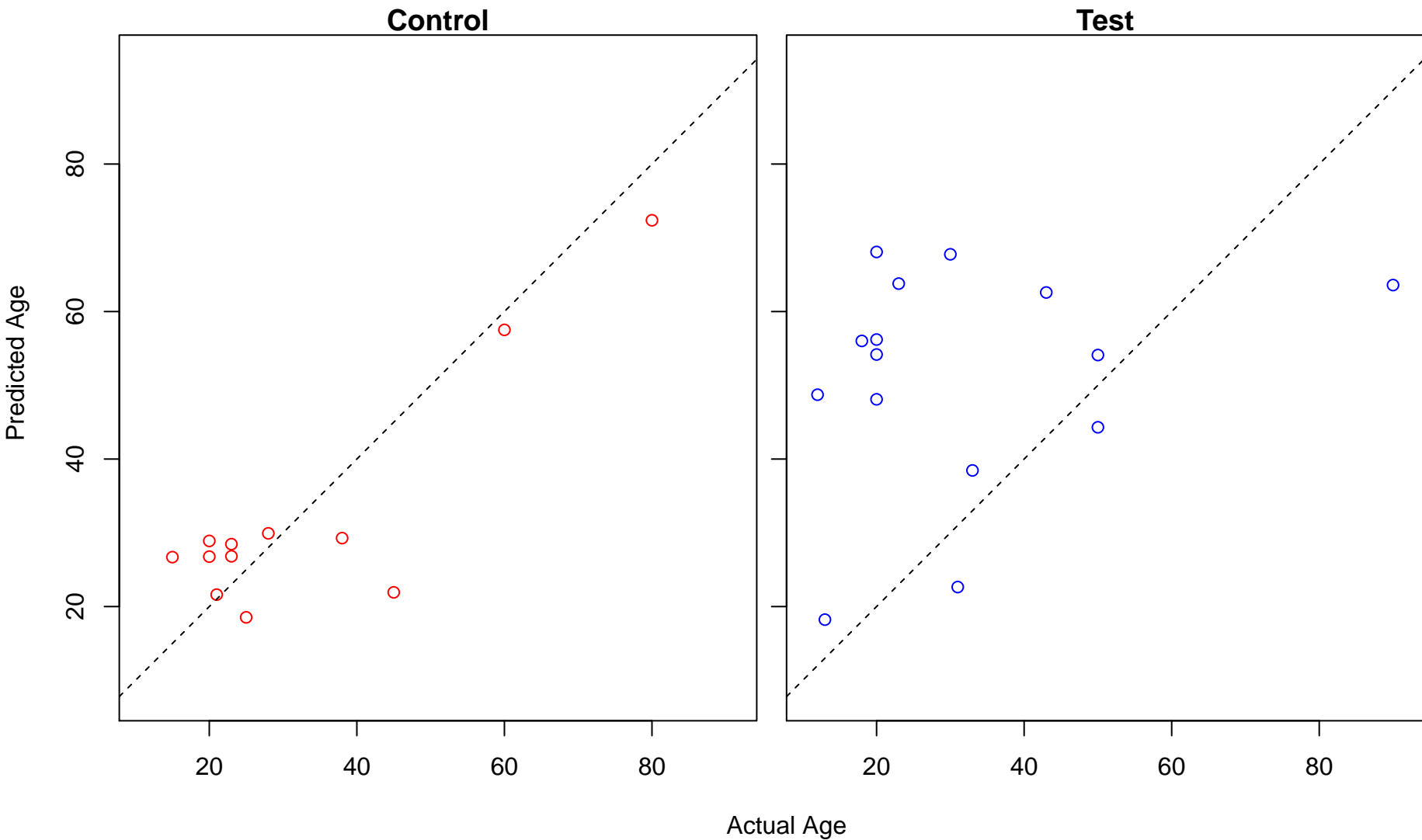
detection of calcium ion (Score: 3.812515)



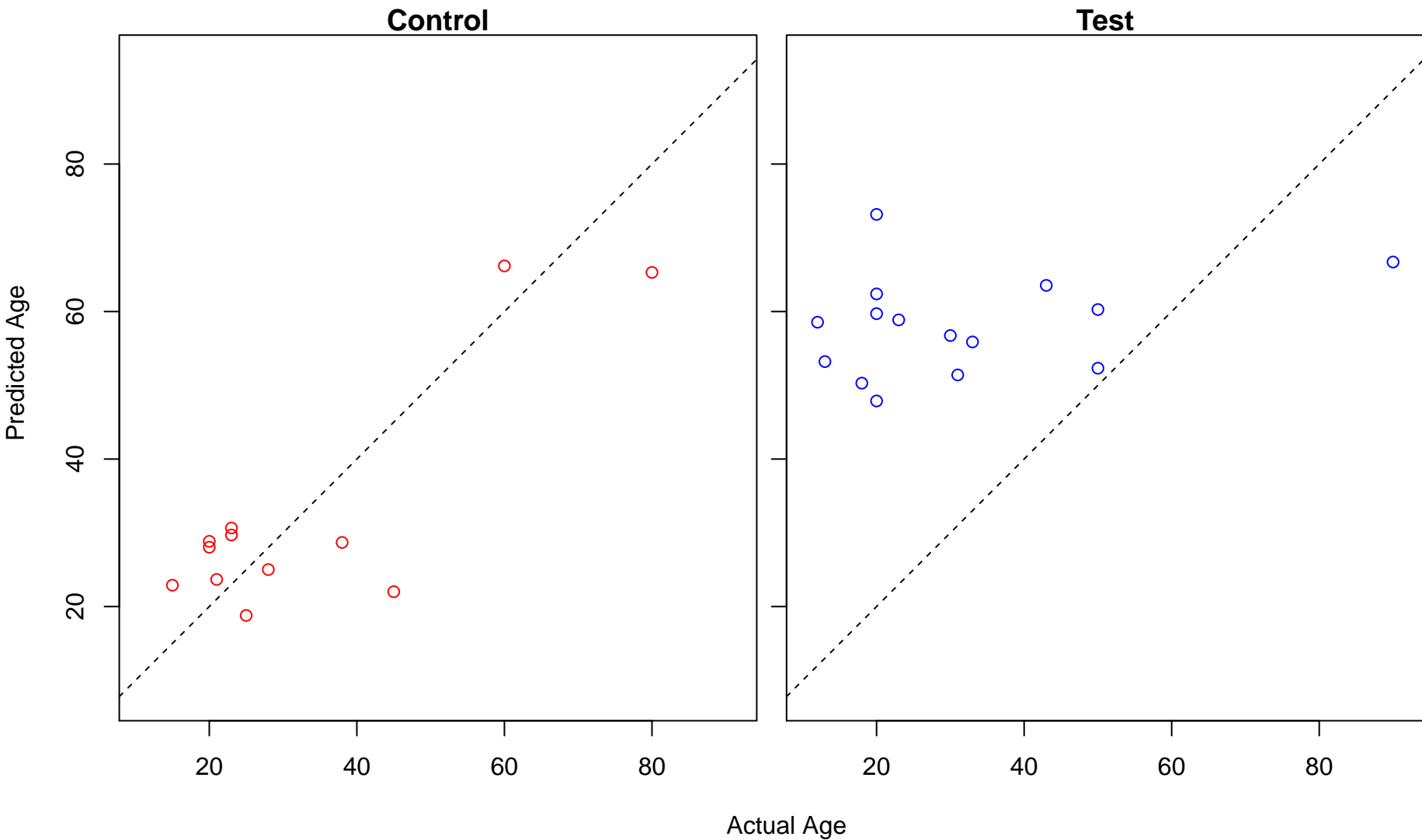
carnitine biosynthetic process (Score: 3.811982)



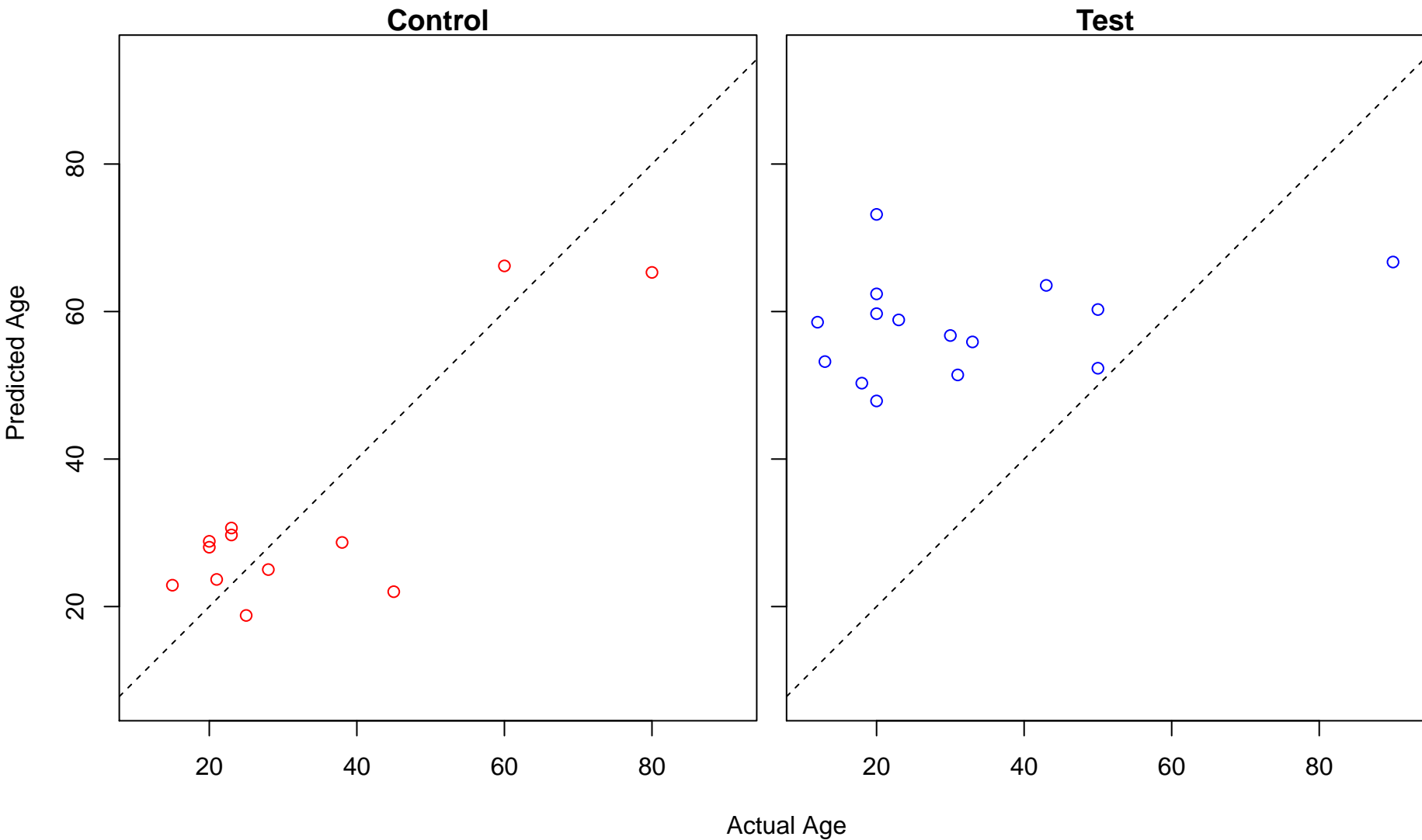
maintenance of location in cell (Score: 3.811058)



histone H4-K5 acetylation (Score: 3.810925)

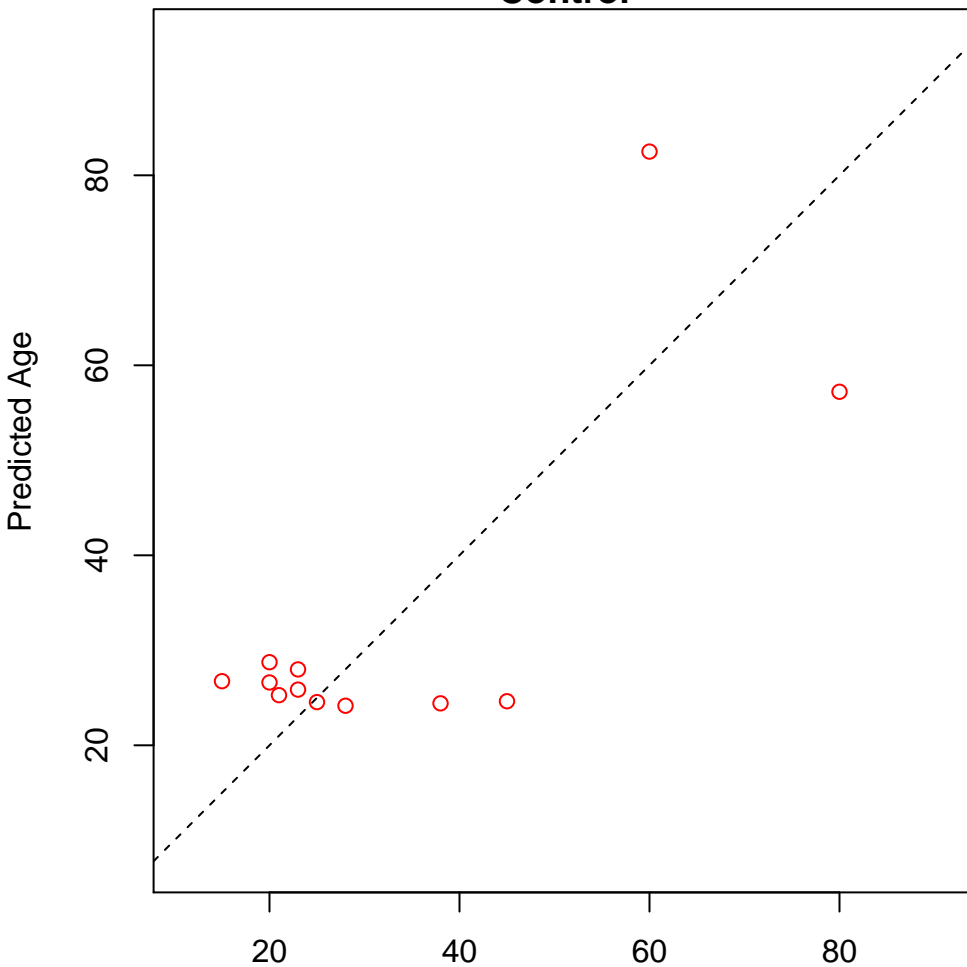


histone H4-K8 acetylation (Score: 3.810925)

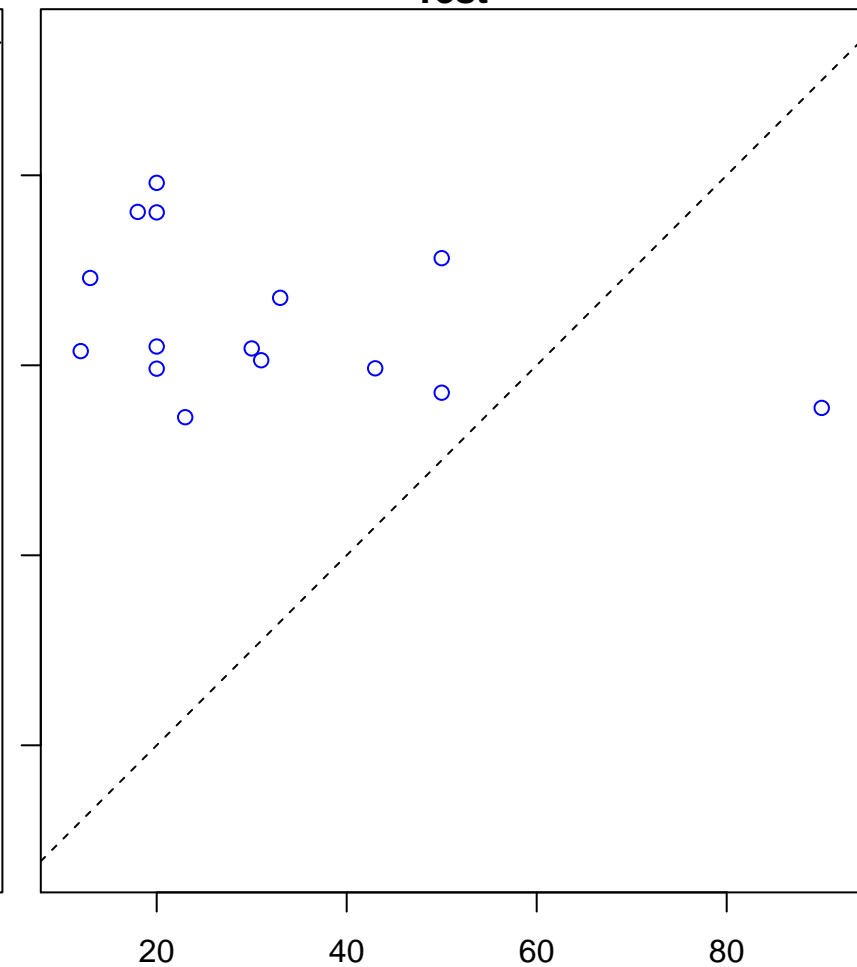


intra-Golgi vesicle-mediated transport (Score: 3.810263)

Control

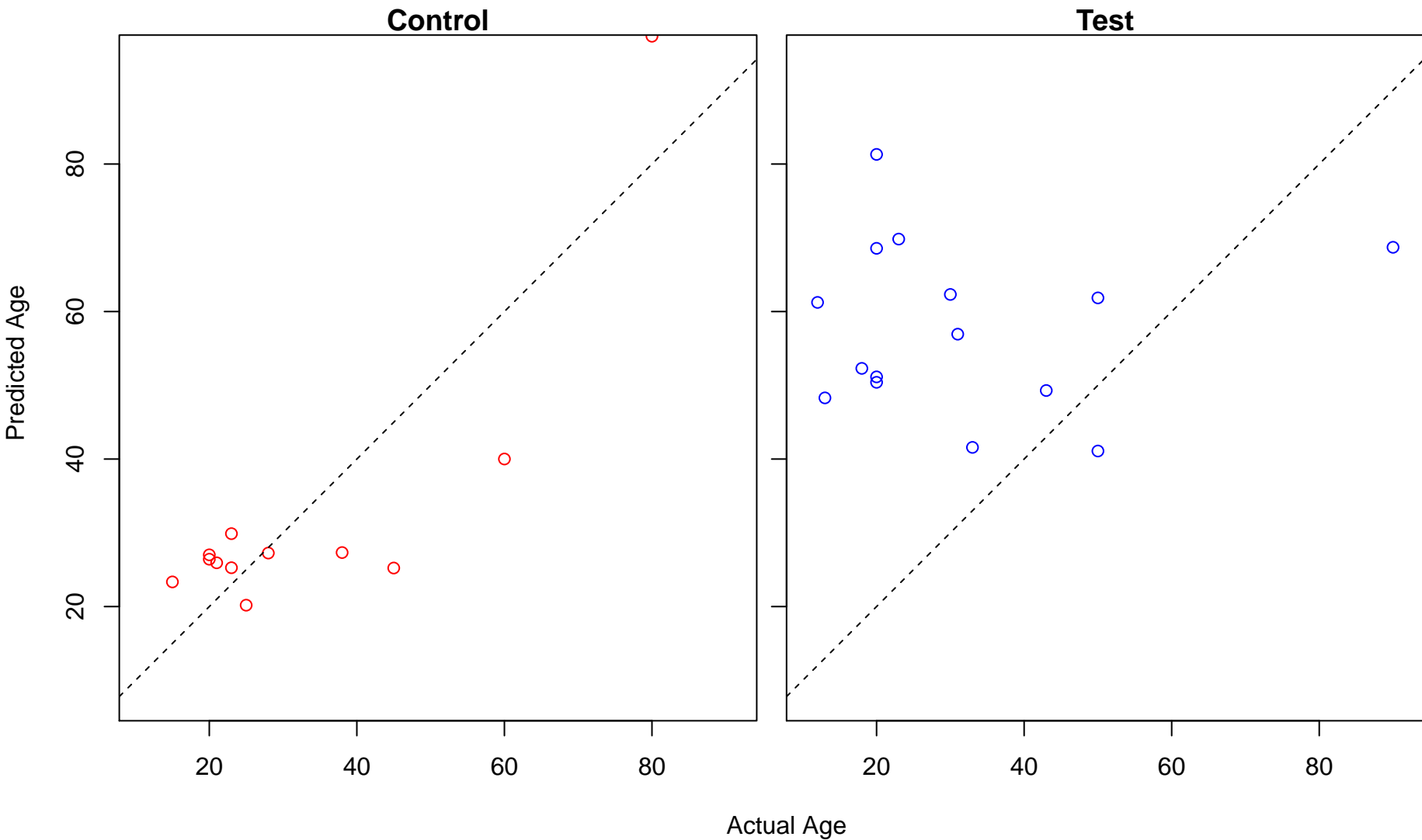


Test

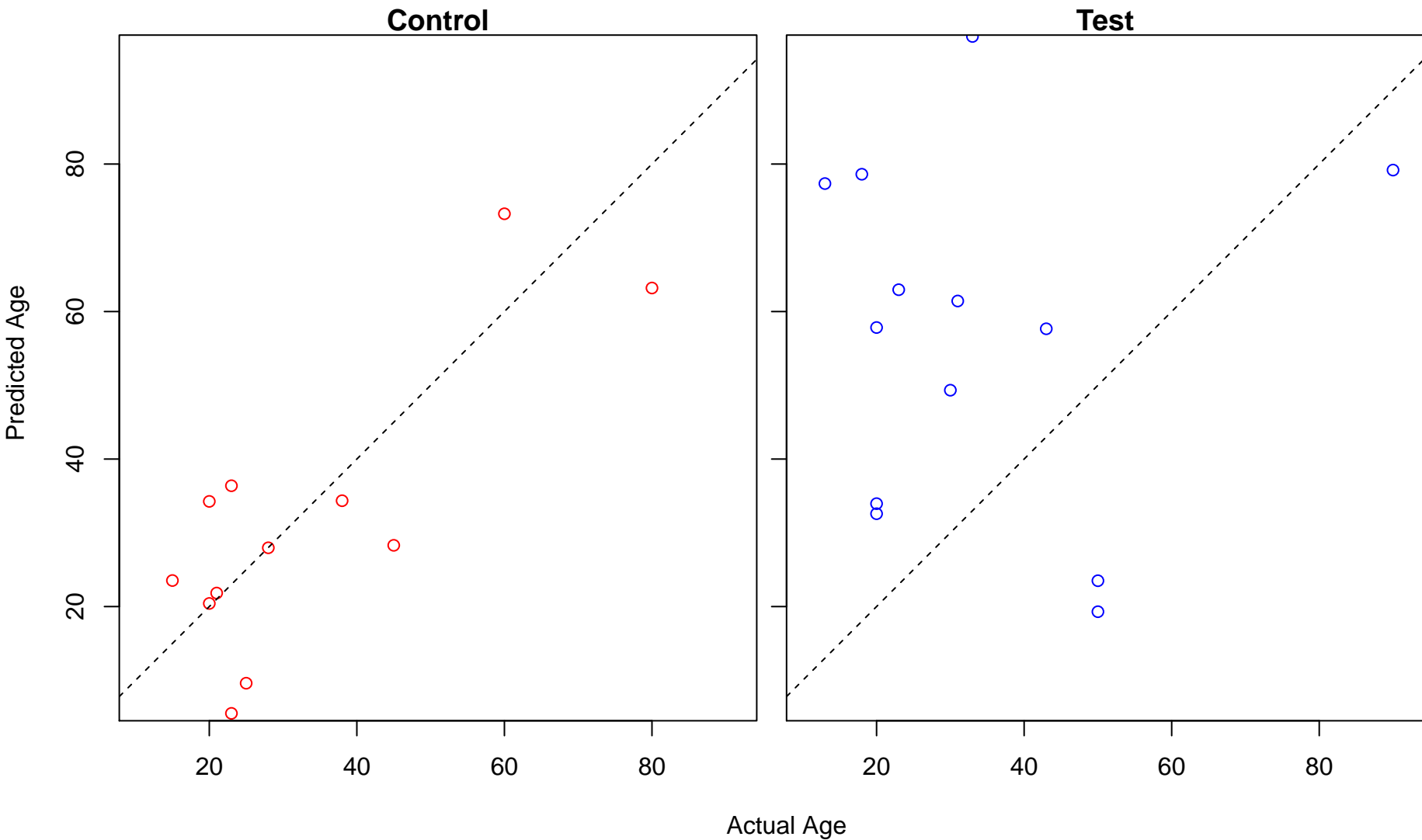


Actual Age

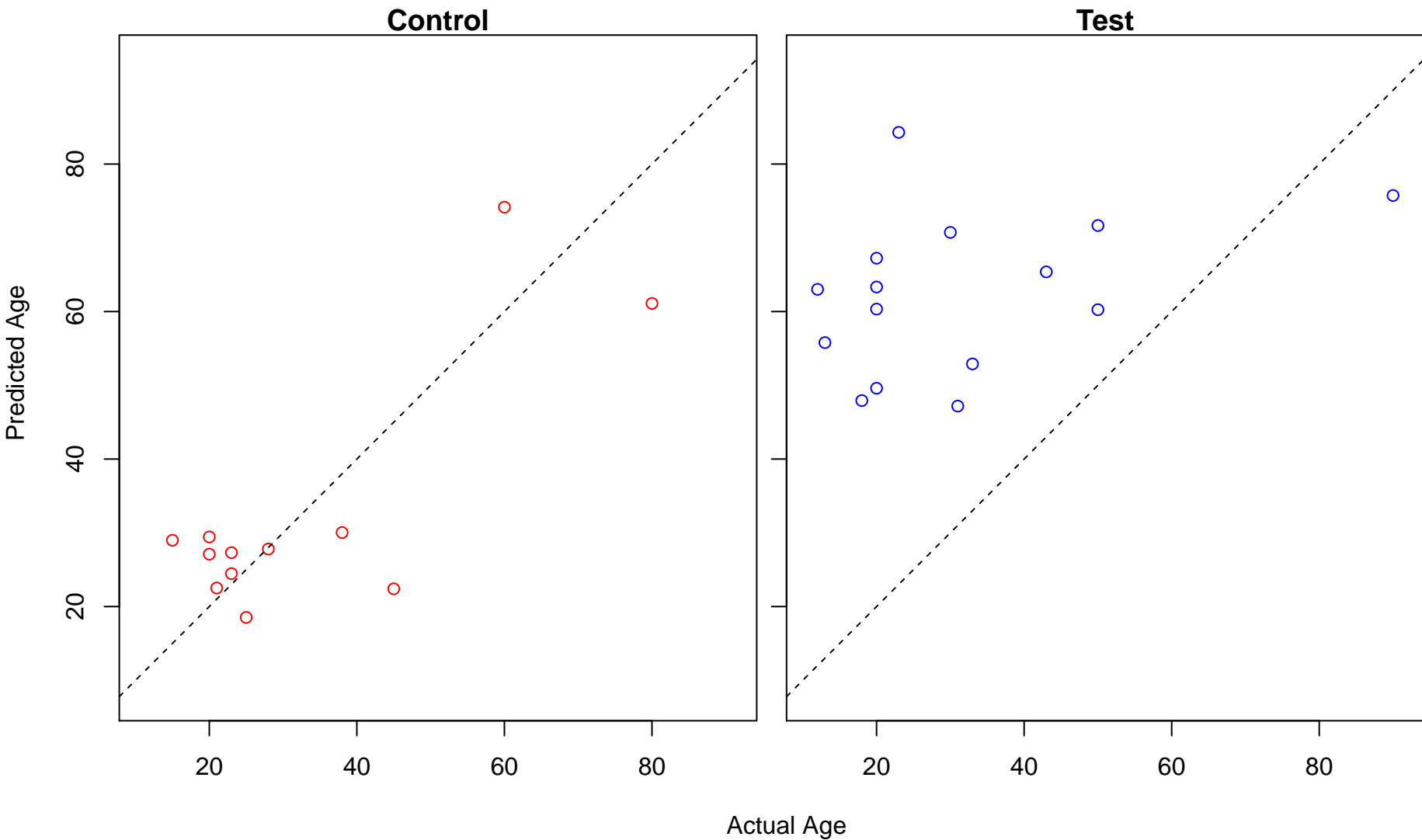
methionine metabolic process (Score: 3.809891)



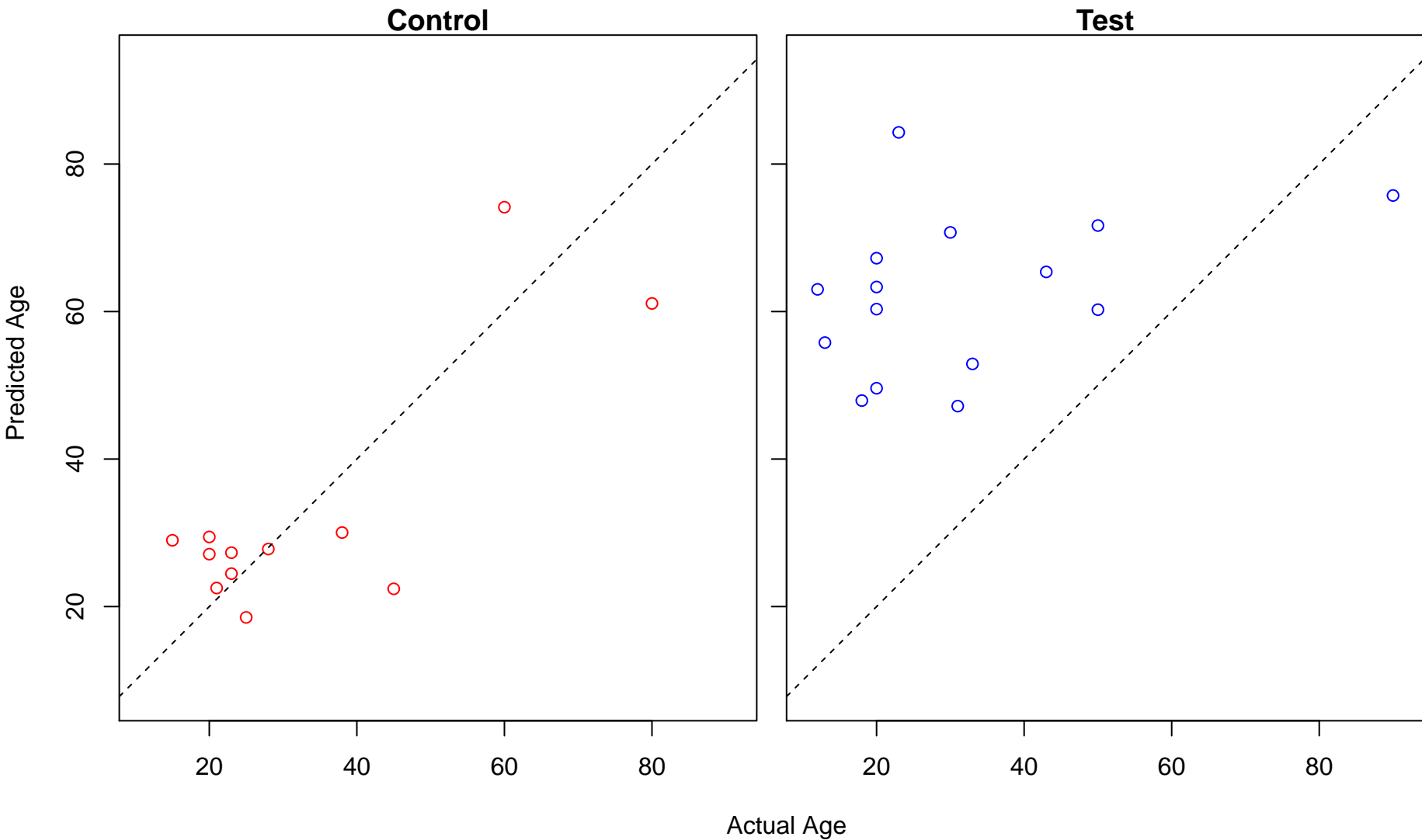
regulation of secondary metabolic process (Score: 3.808868)



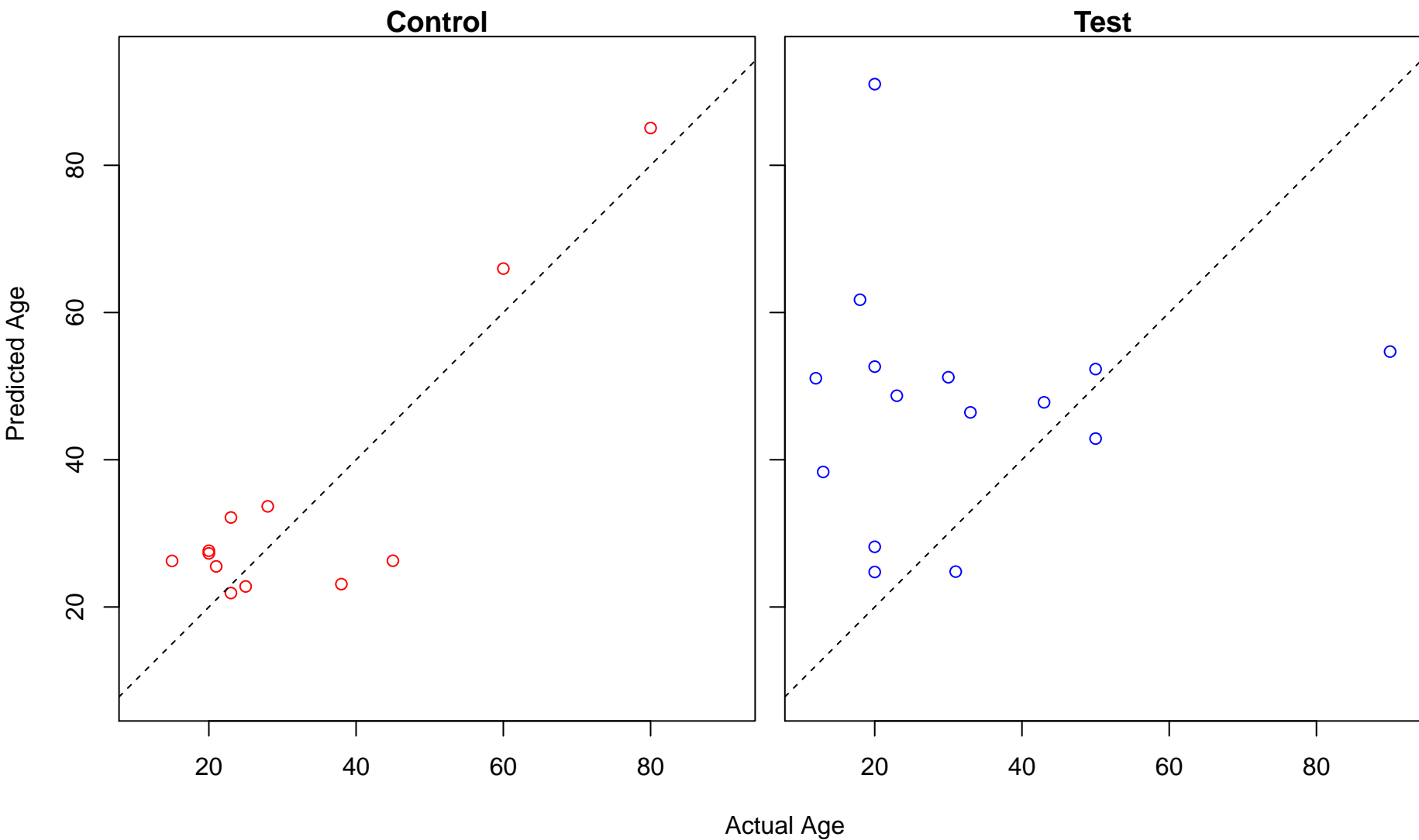
microvillus assembly (Score: 3.808109)



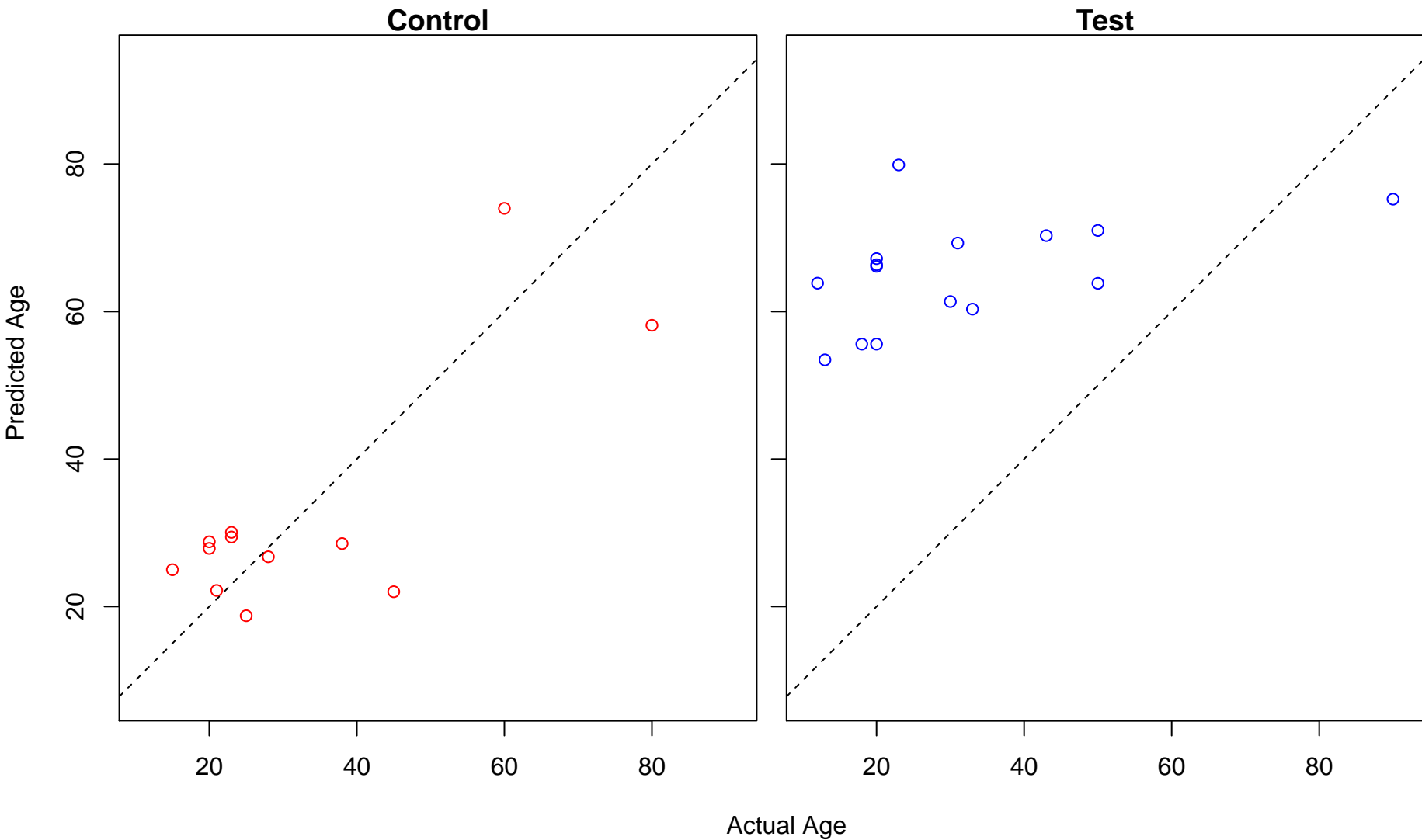
microvillus organization (Score: 3.808109)



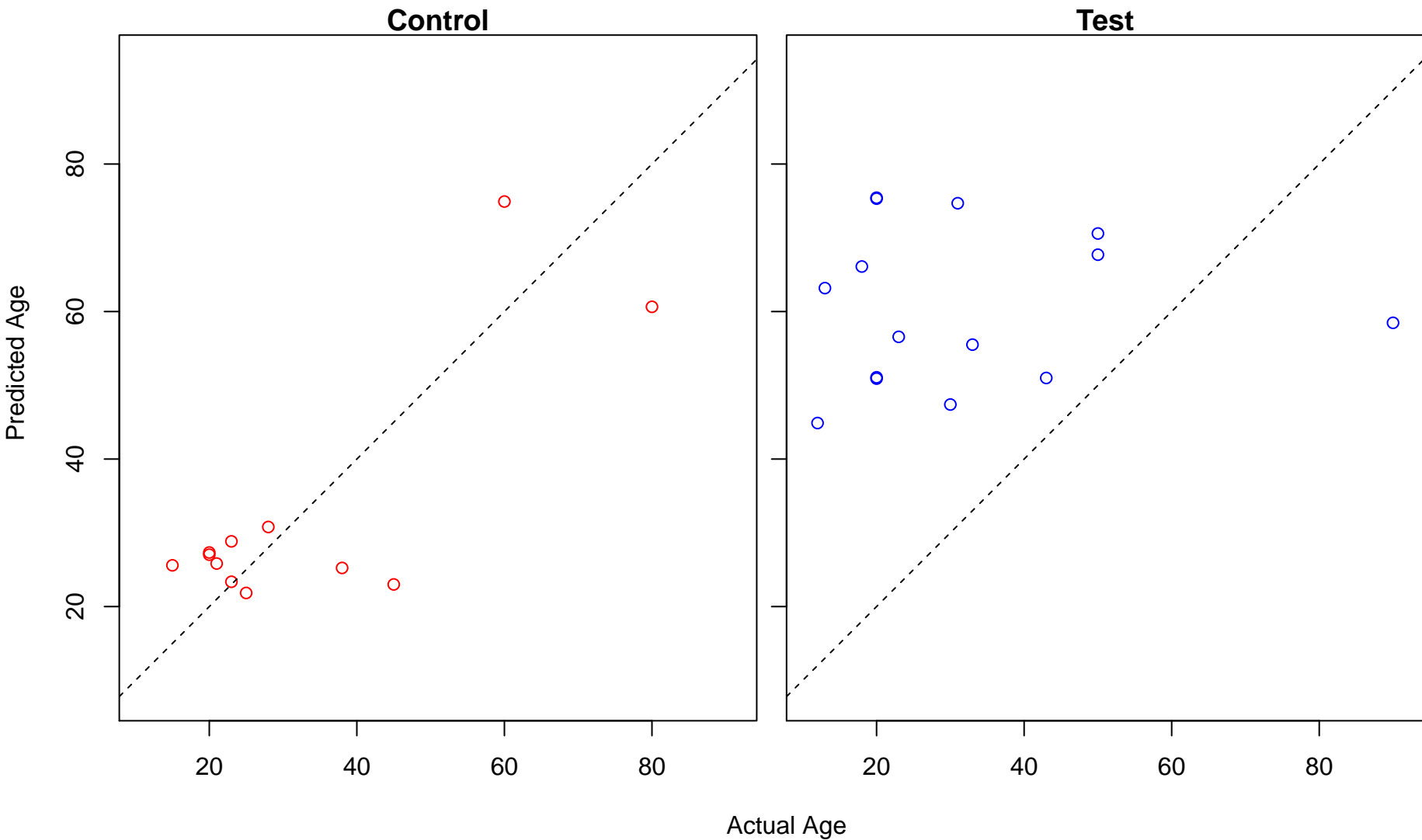
centrosome cycle (Score: 3.802119)



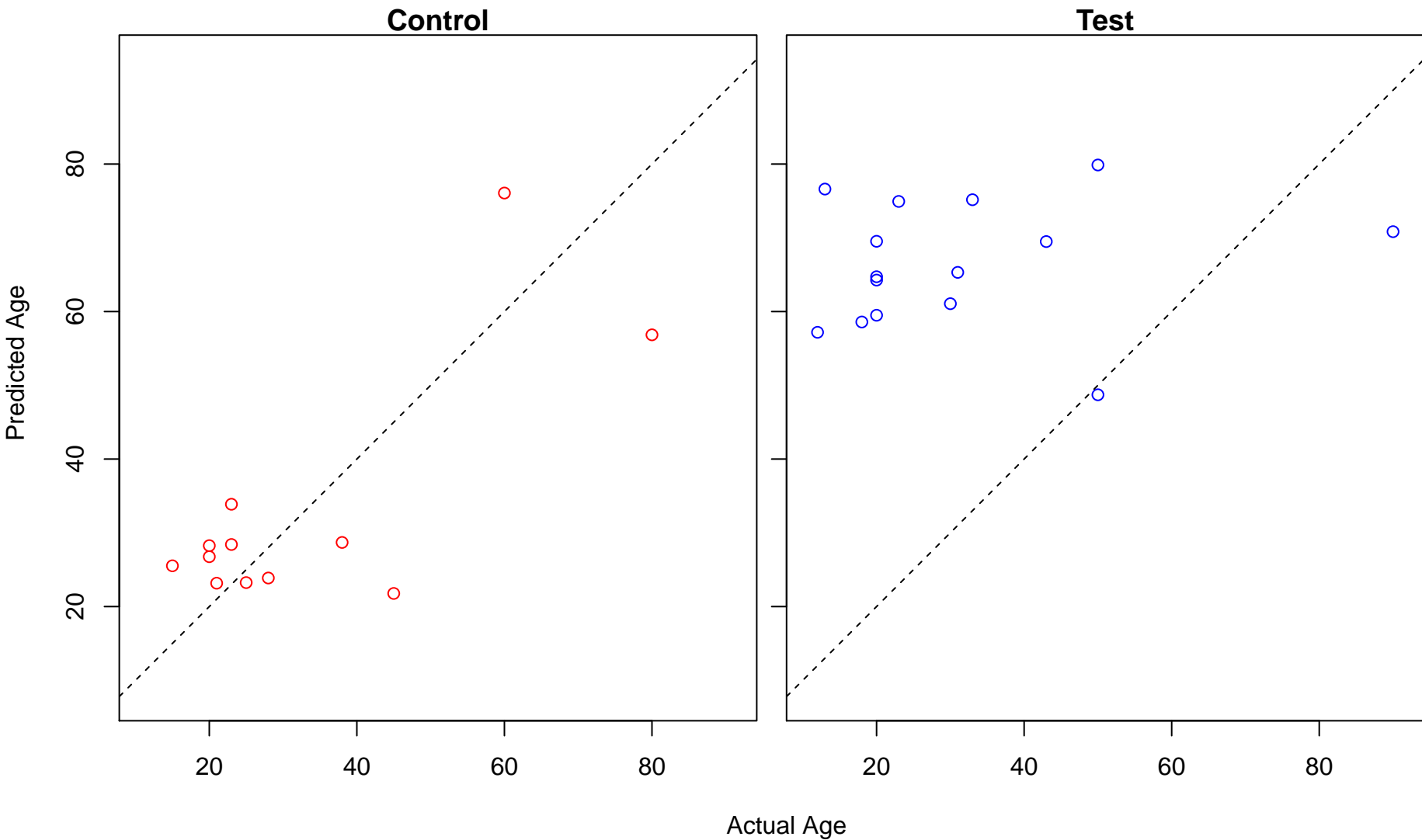
regulation of smoothened signaling pathway (Score: 3.801623)



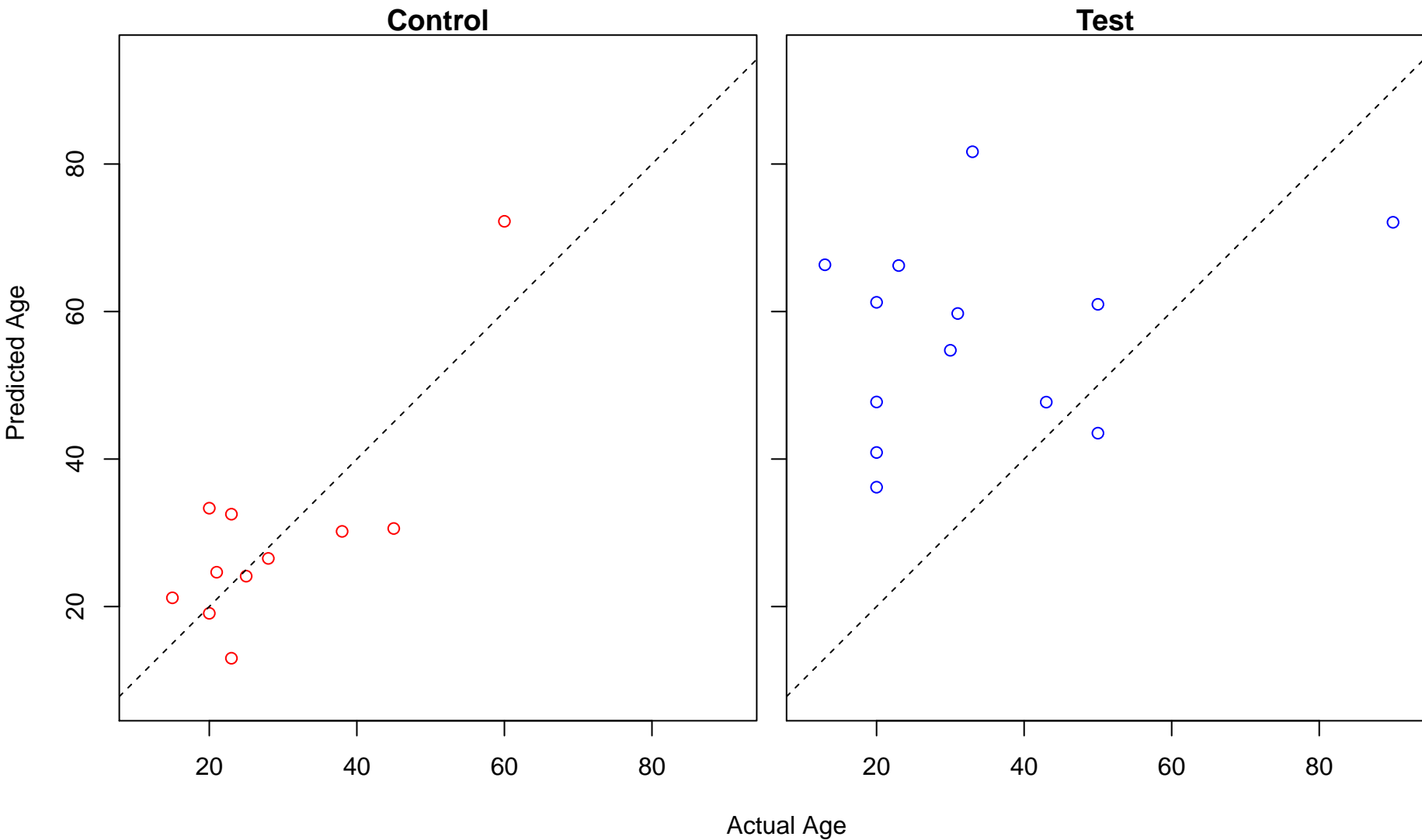
positive regulation of phosphoprotein phosphatase activity (Score: 3.801439)



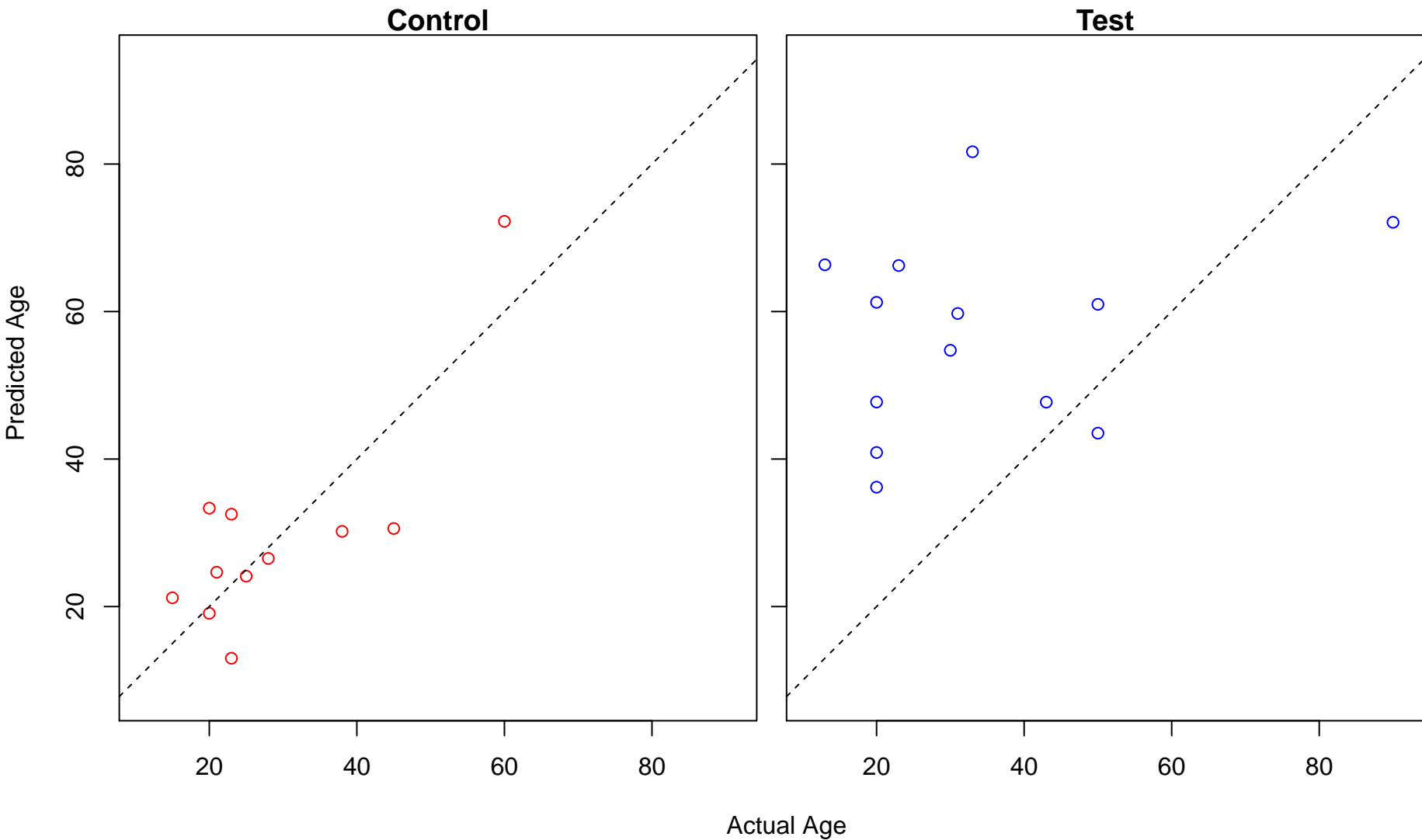
embryonic hemopoiesis (Score: 3.800369)



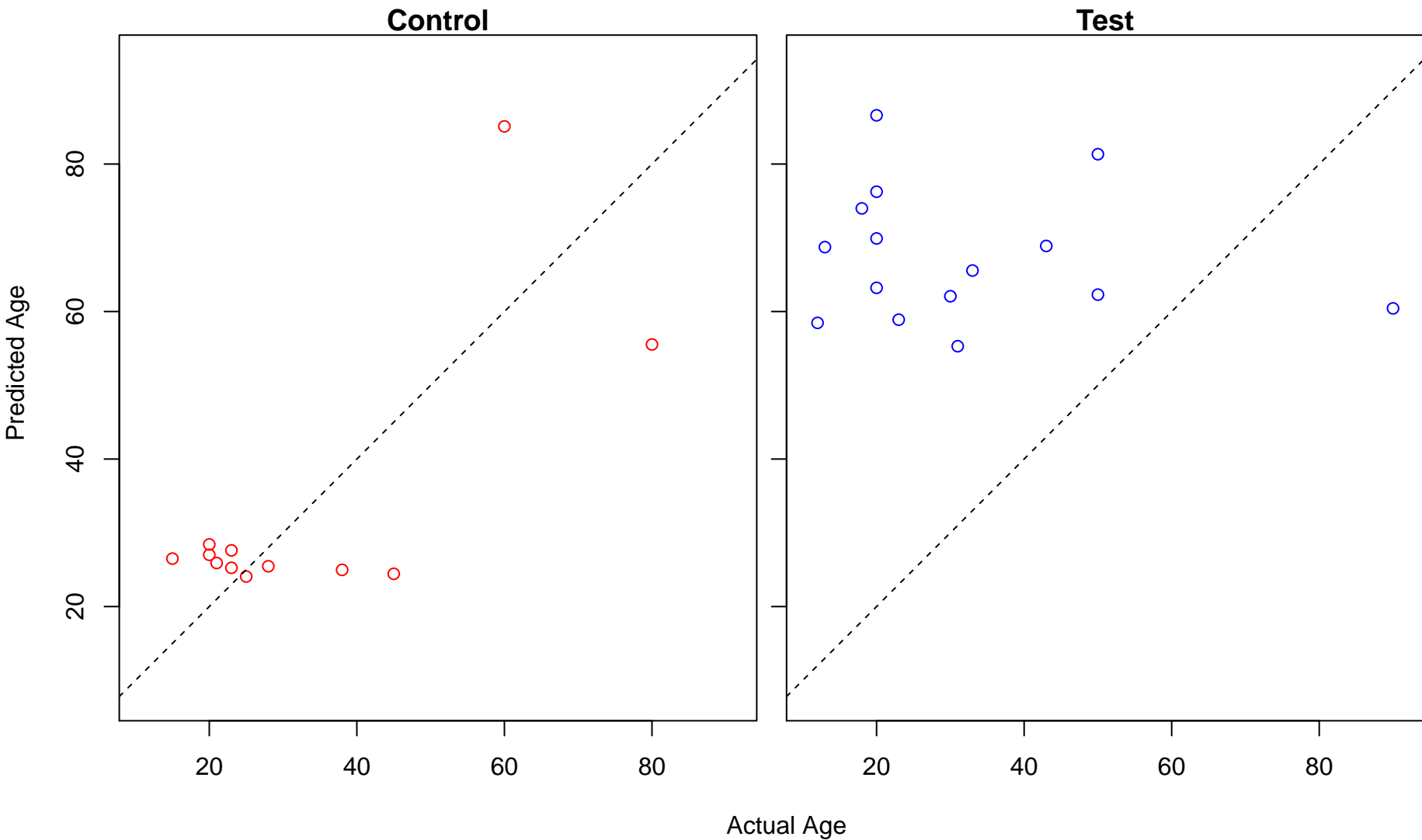
response to cGMP (Score: 3.799511)



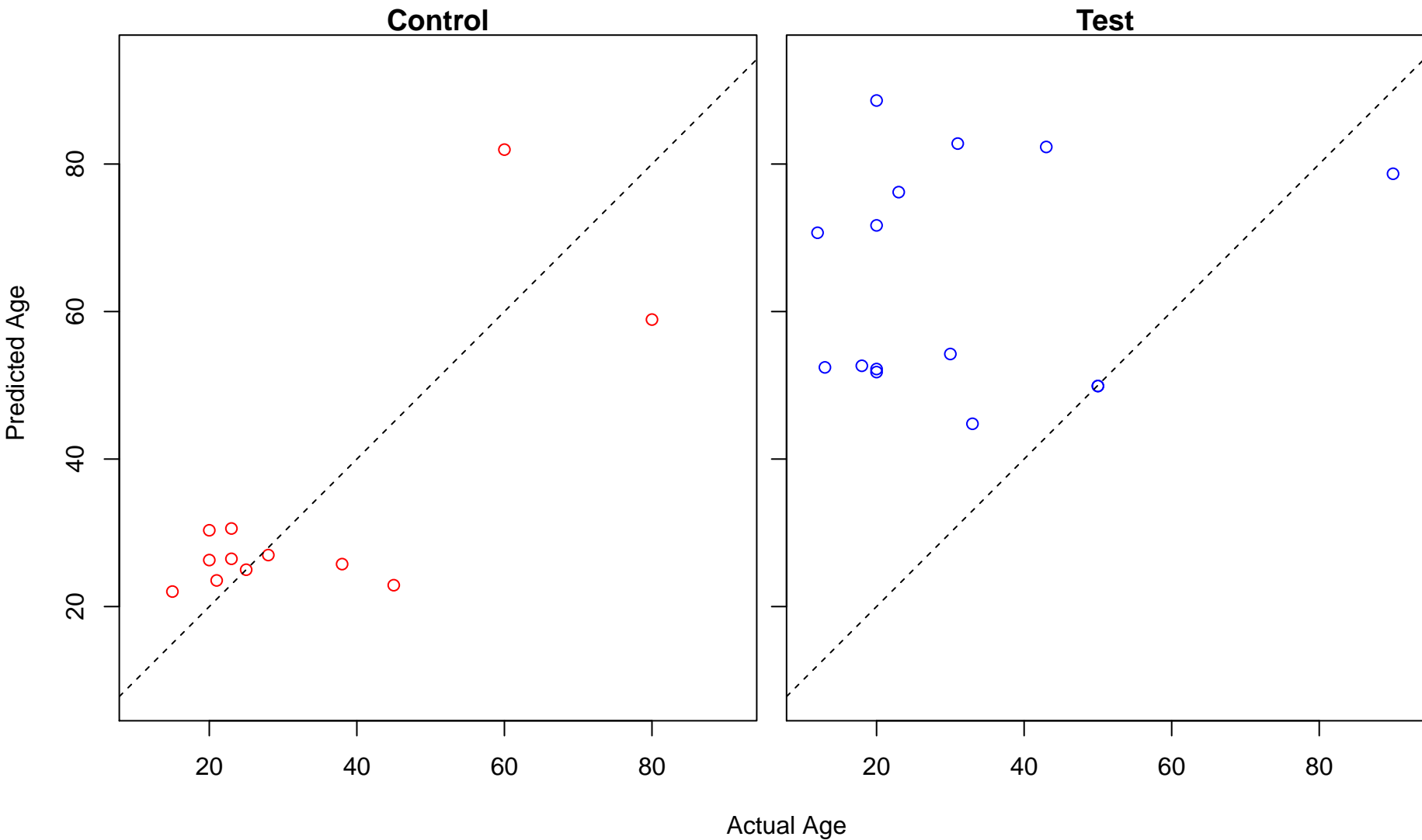
cellular response to cGMP (Score: 3.799511)



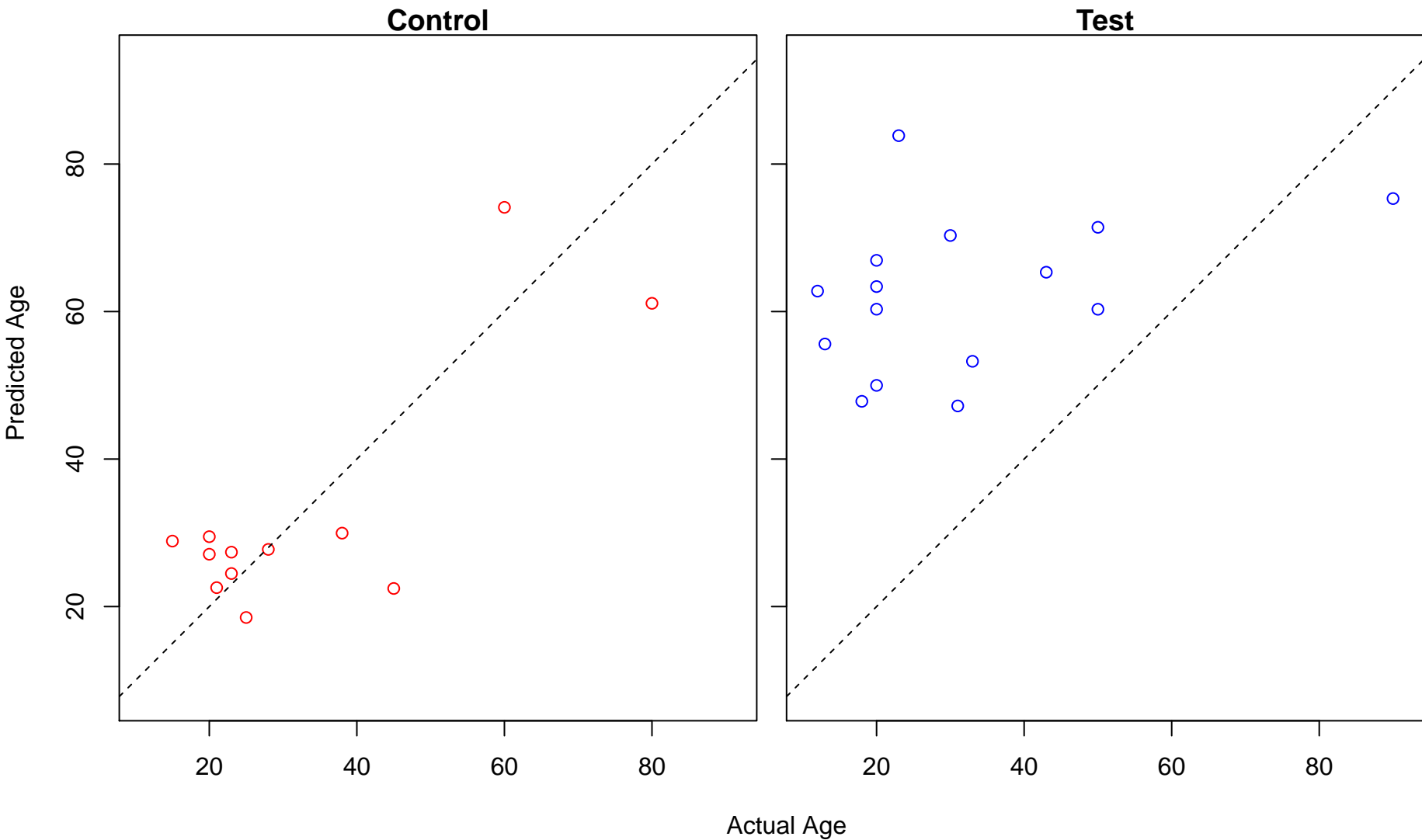
regulation of anion transmembrane transport (Score: 3.798851)



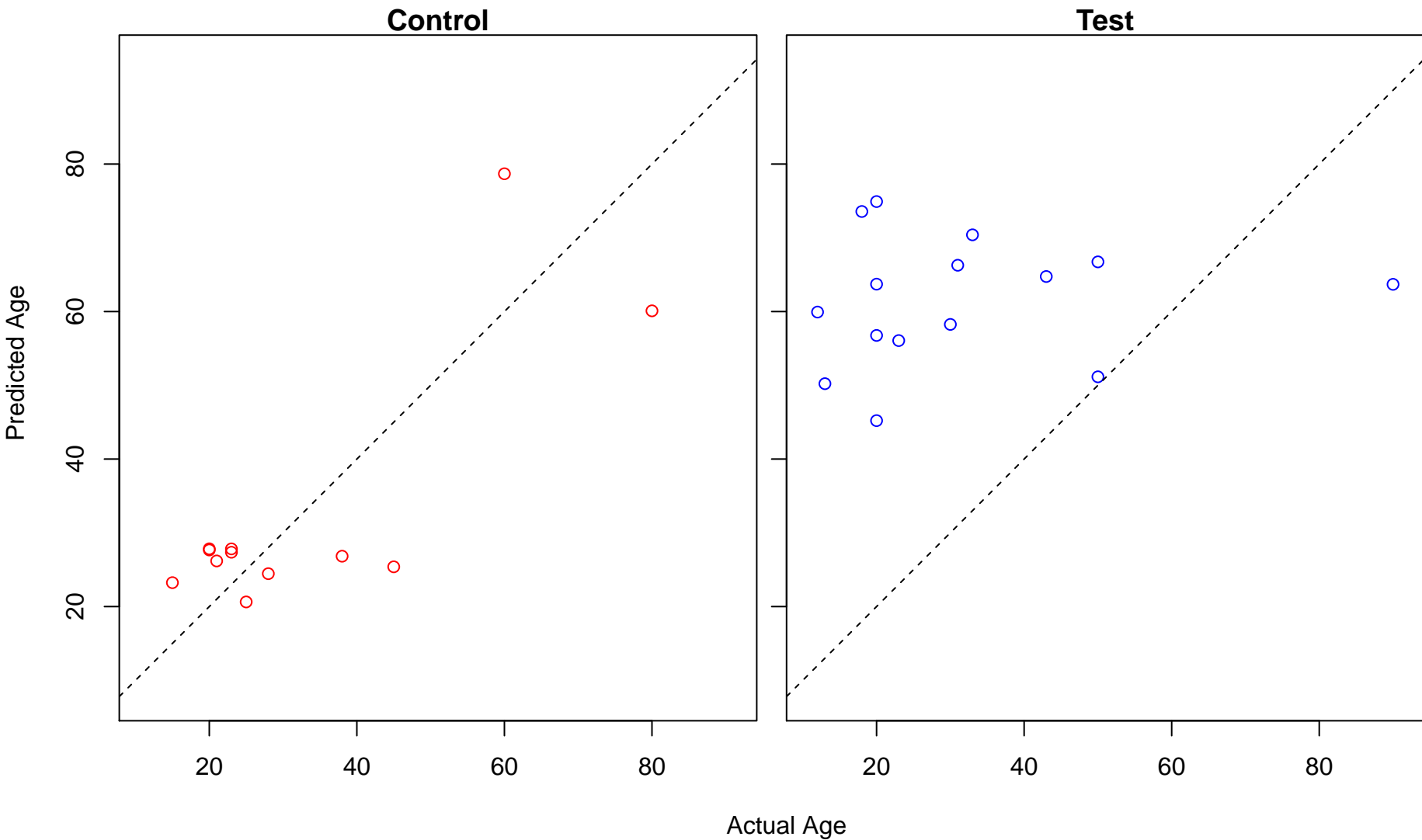
regulation of myoblast proliferation (Score: 3.798553)



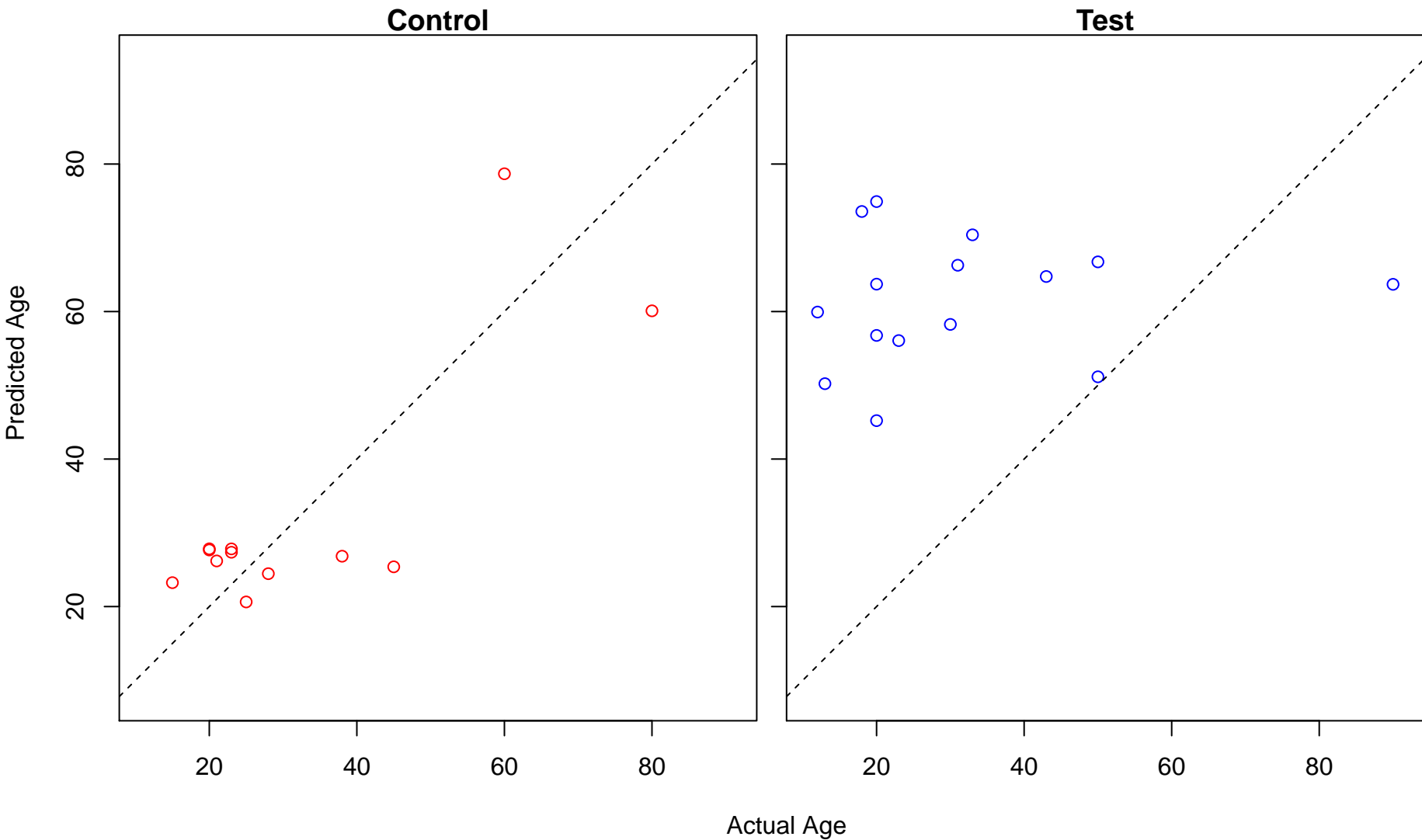
cellular protein complex localization (Score: 3.798027)



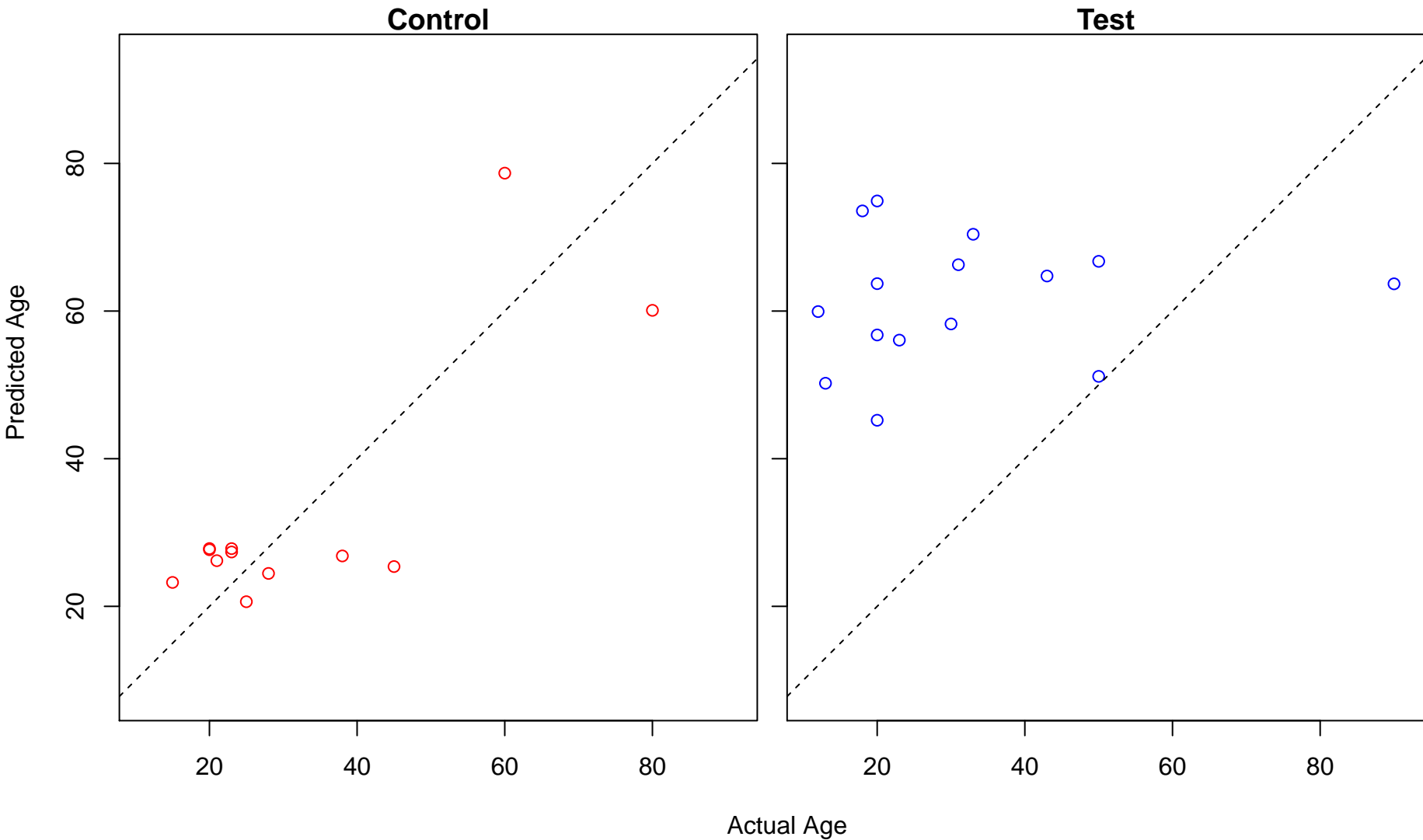
positive regulation of mitotic metaphase/anaphase transition (Score: 3.796046)



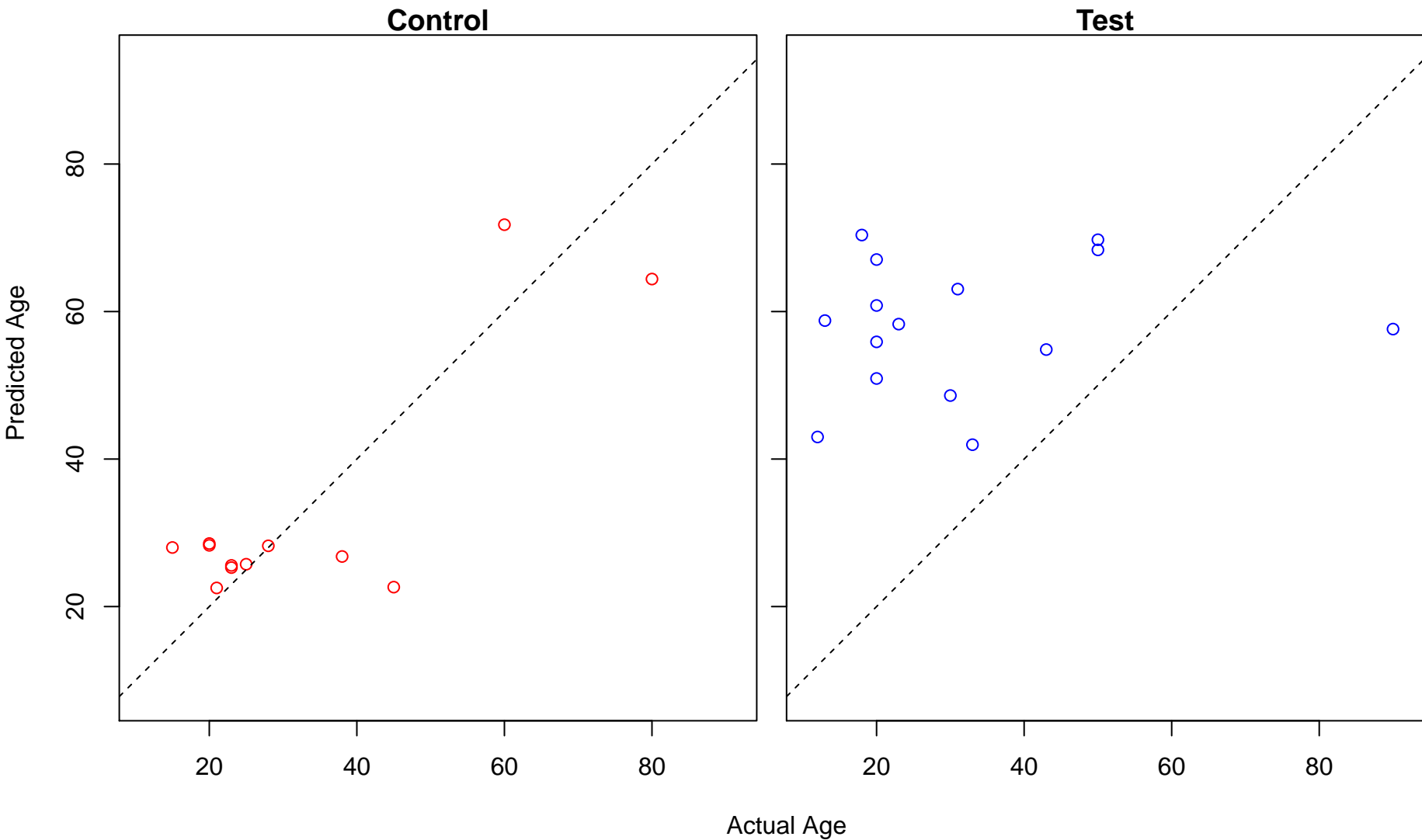
positive regulation of mitotic sister chromatid separation (Score: 3.796046)



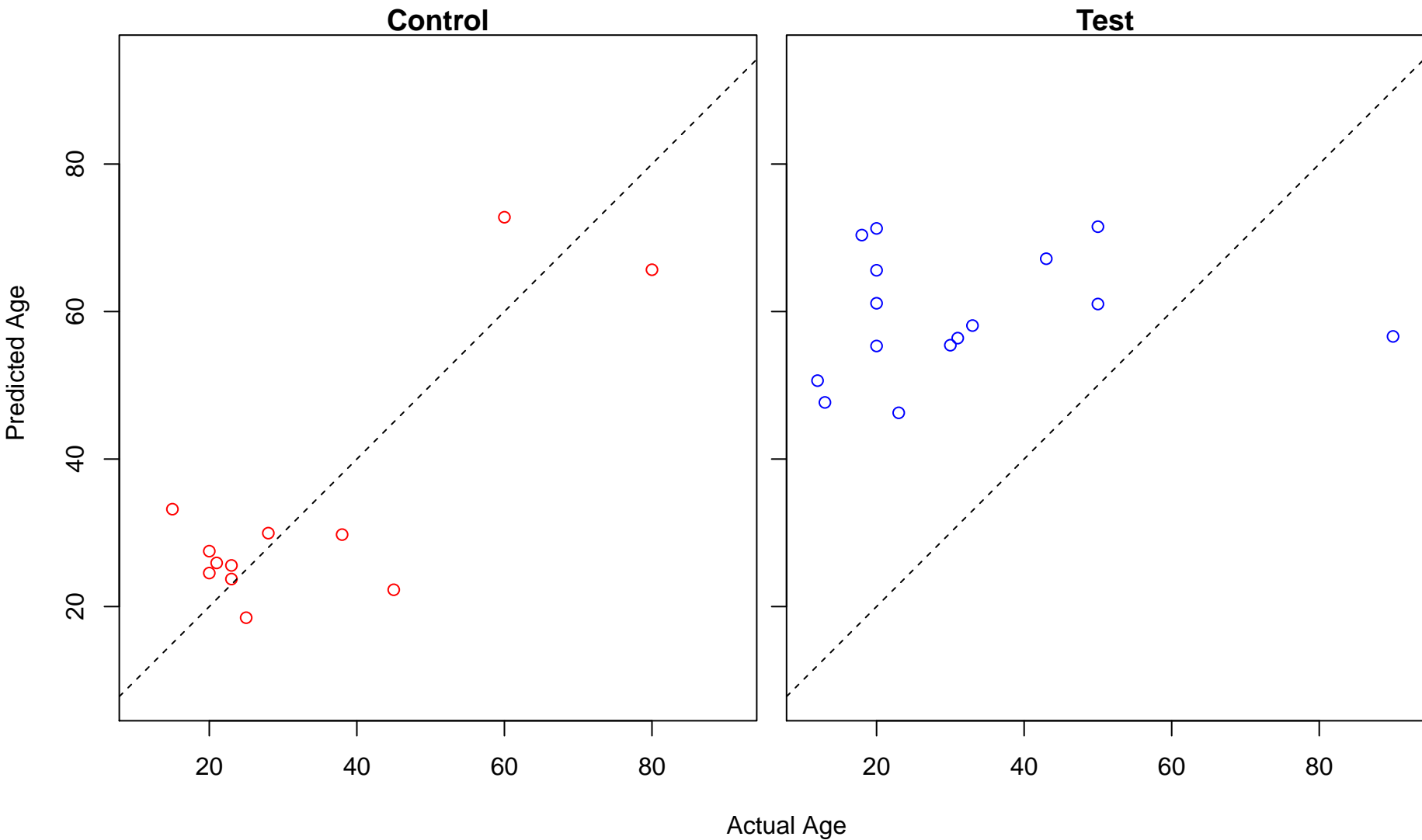
positive regulation of metaphase/anaphase transition of cell cycle (Score: 3.796046)



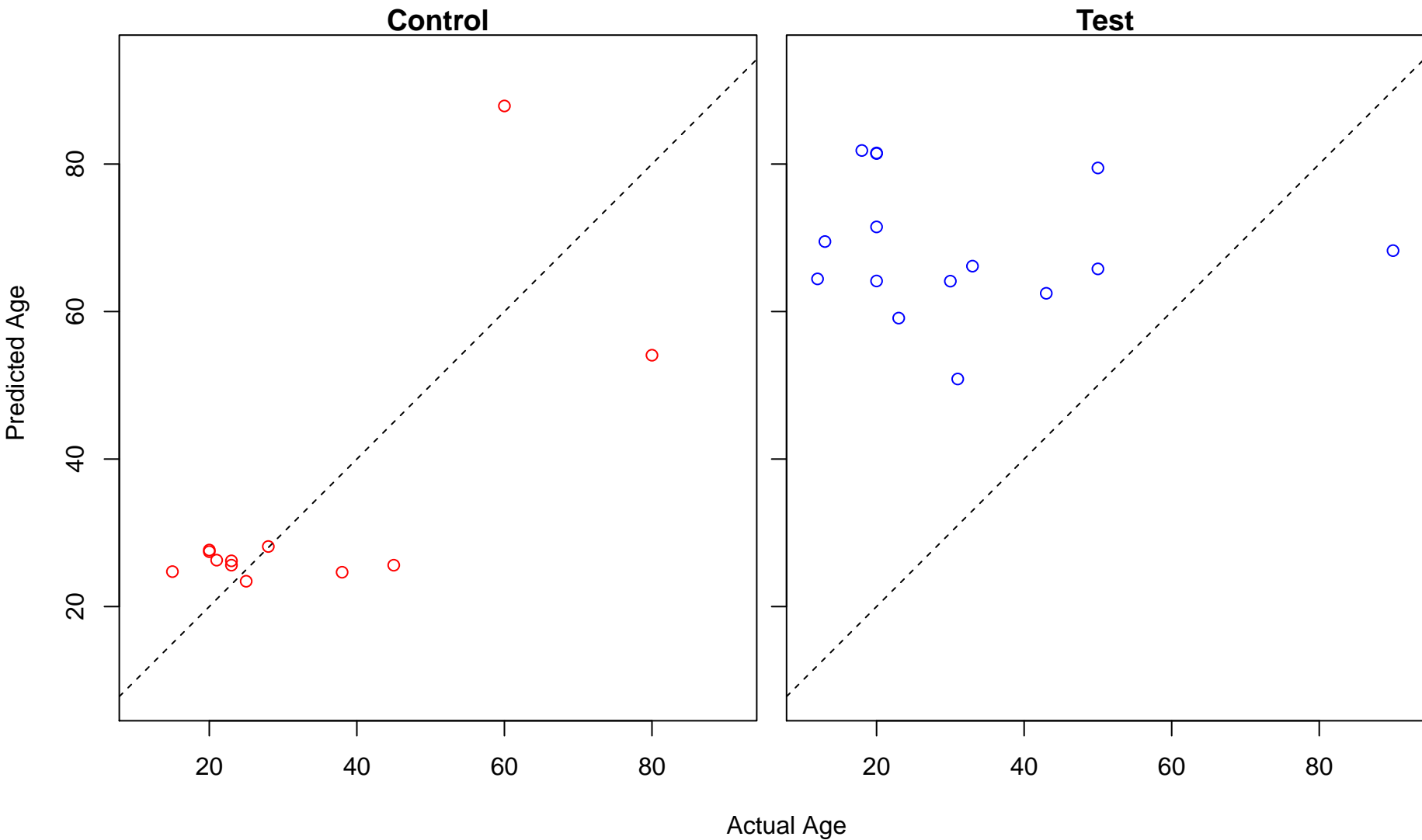
ribonucleoside diphosphate metabolic process (Score: 3.795097)



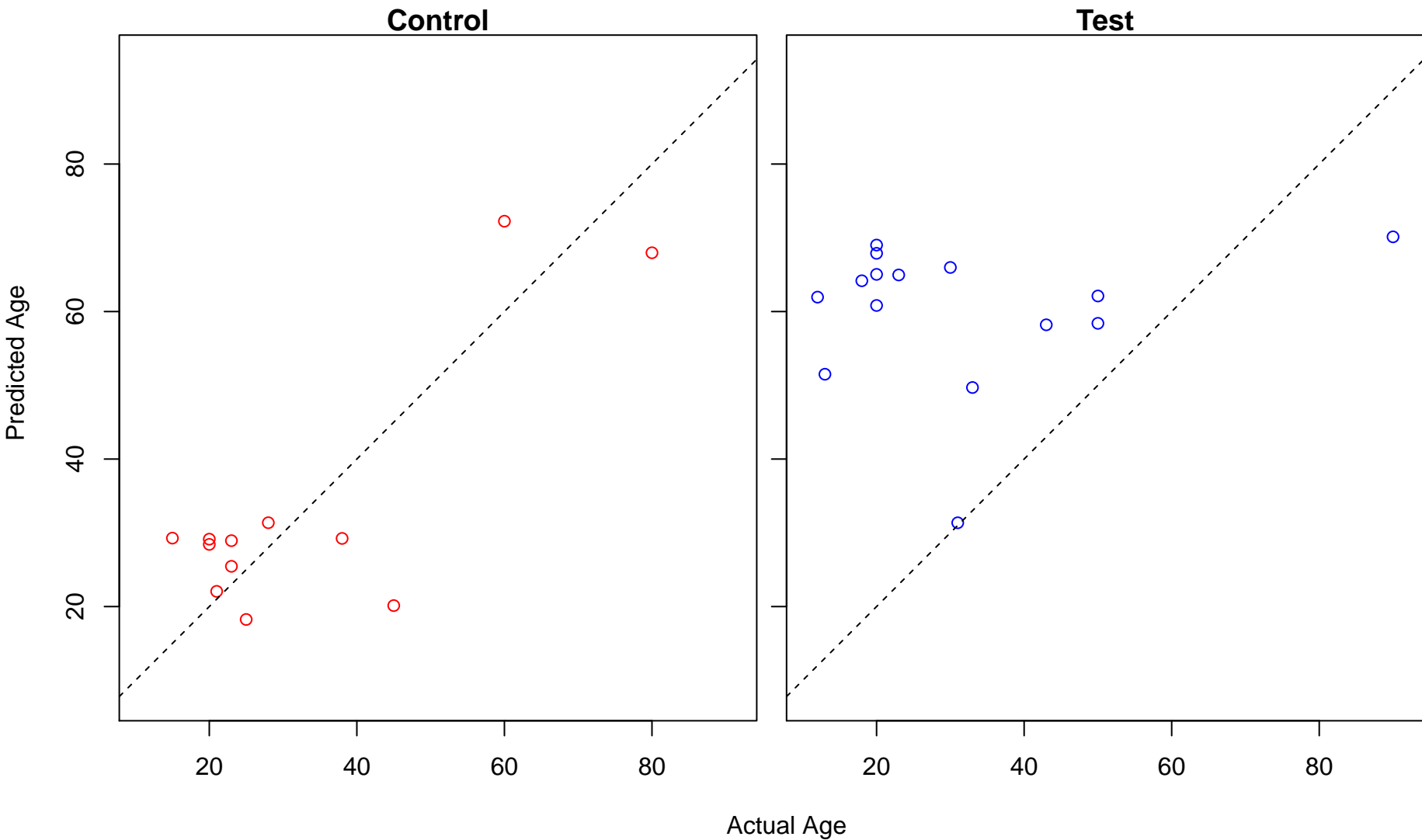
regulation of vasculogenesis (Score: 3.794599)



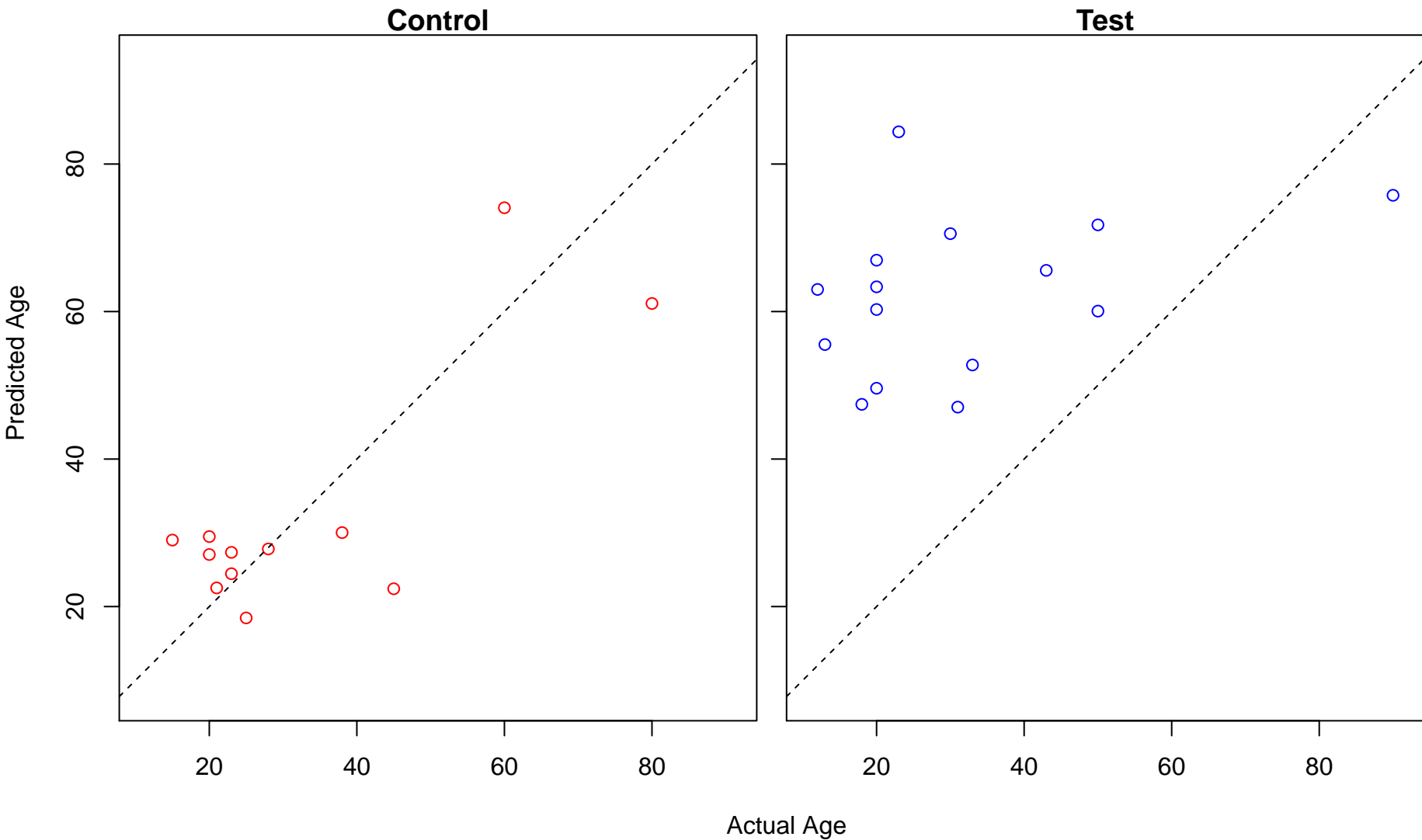
positive regulation of cell cycle G2/M phase transition (Score: 3.794535)



positive regulation of cell cycle G1/S phase transition (Score: 3.793775)

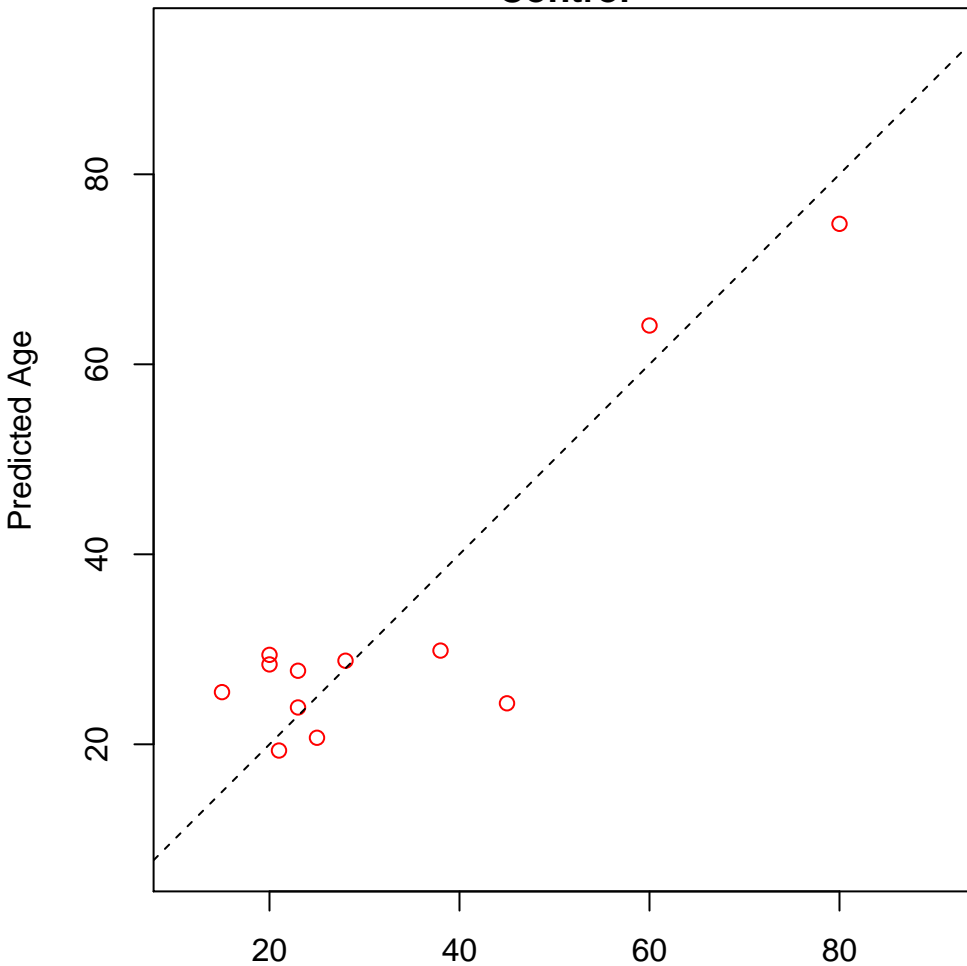


filopodium assembly (Score: 3.792895)

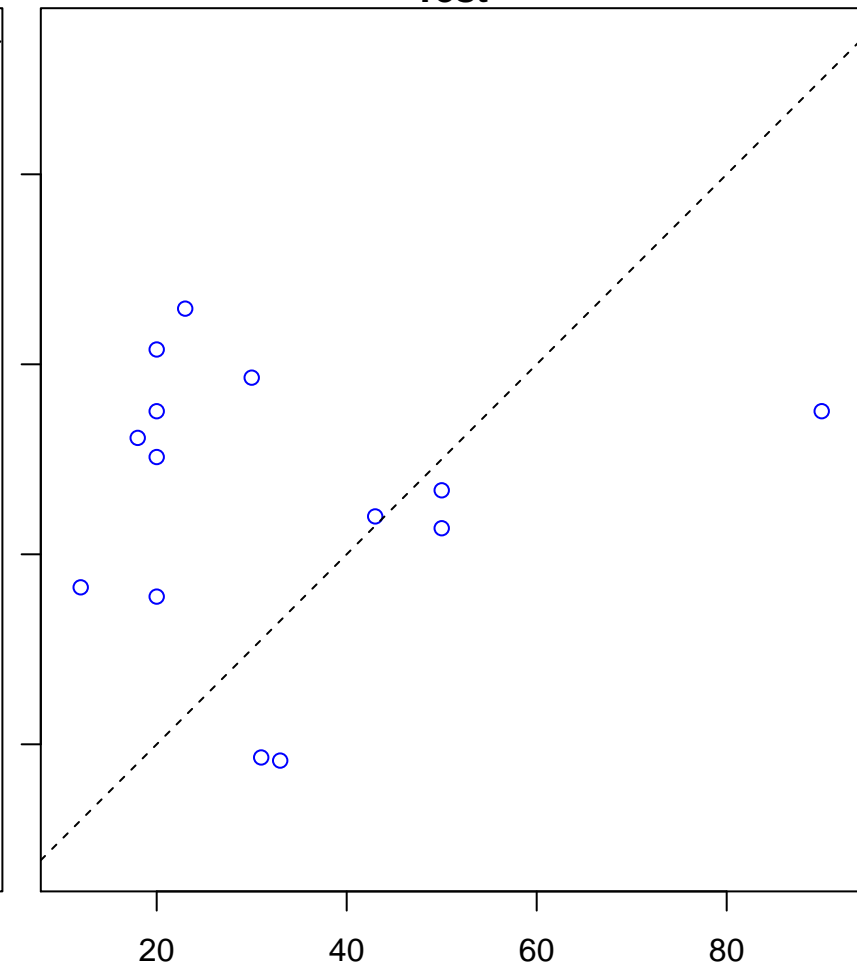


post-Golgi vesicle-mediated transport (Score: 3.791540)

Control

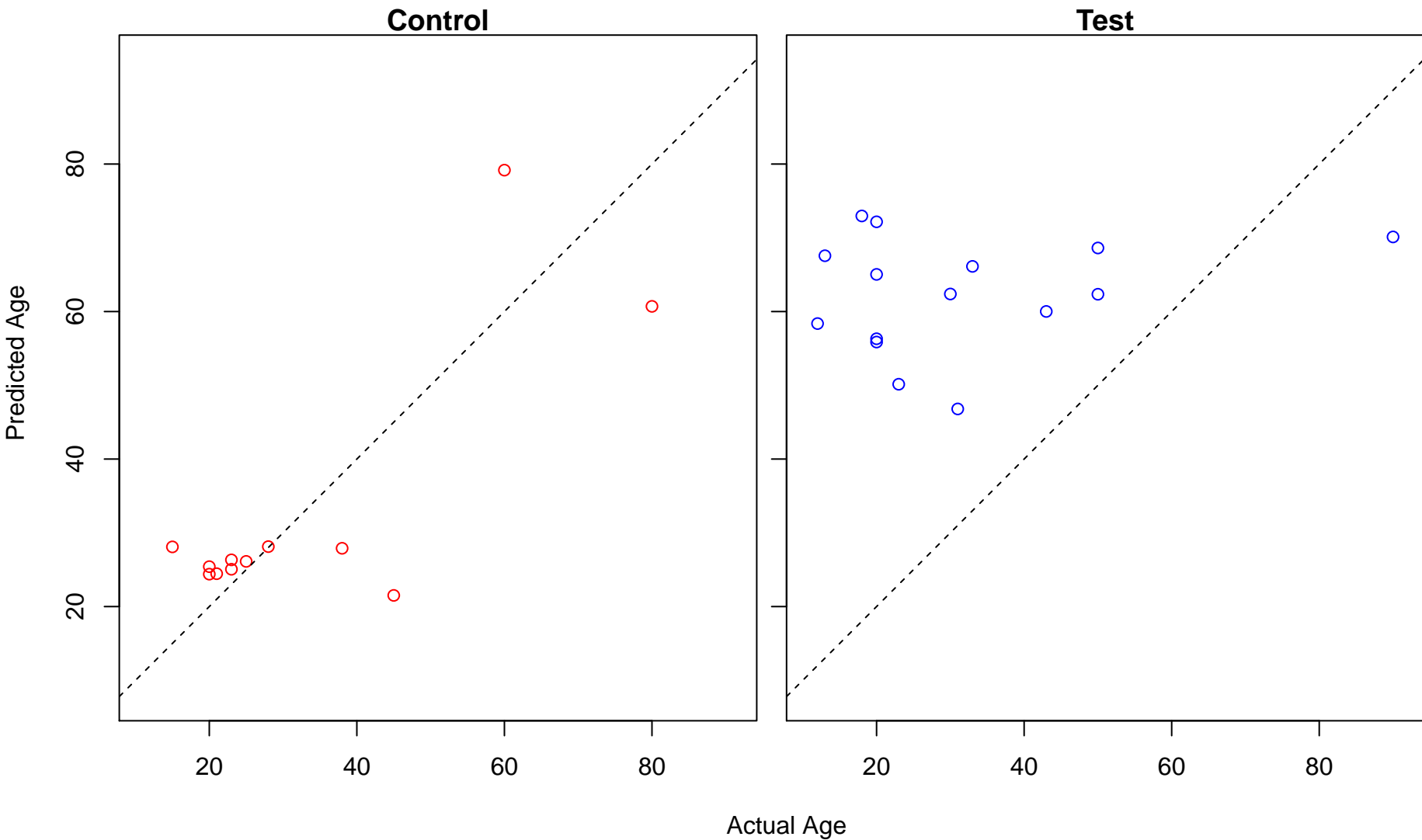


Test

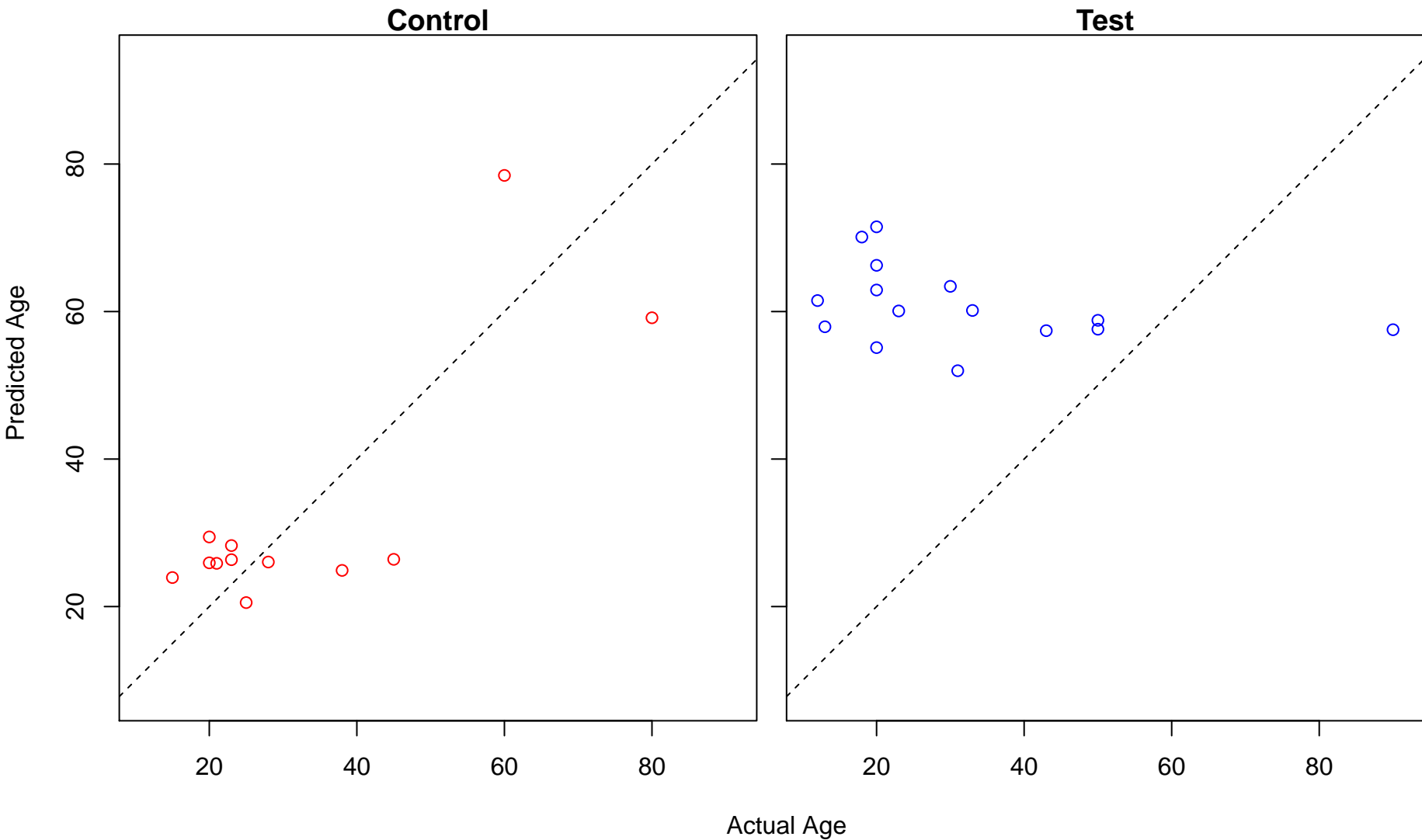


Actual Age

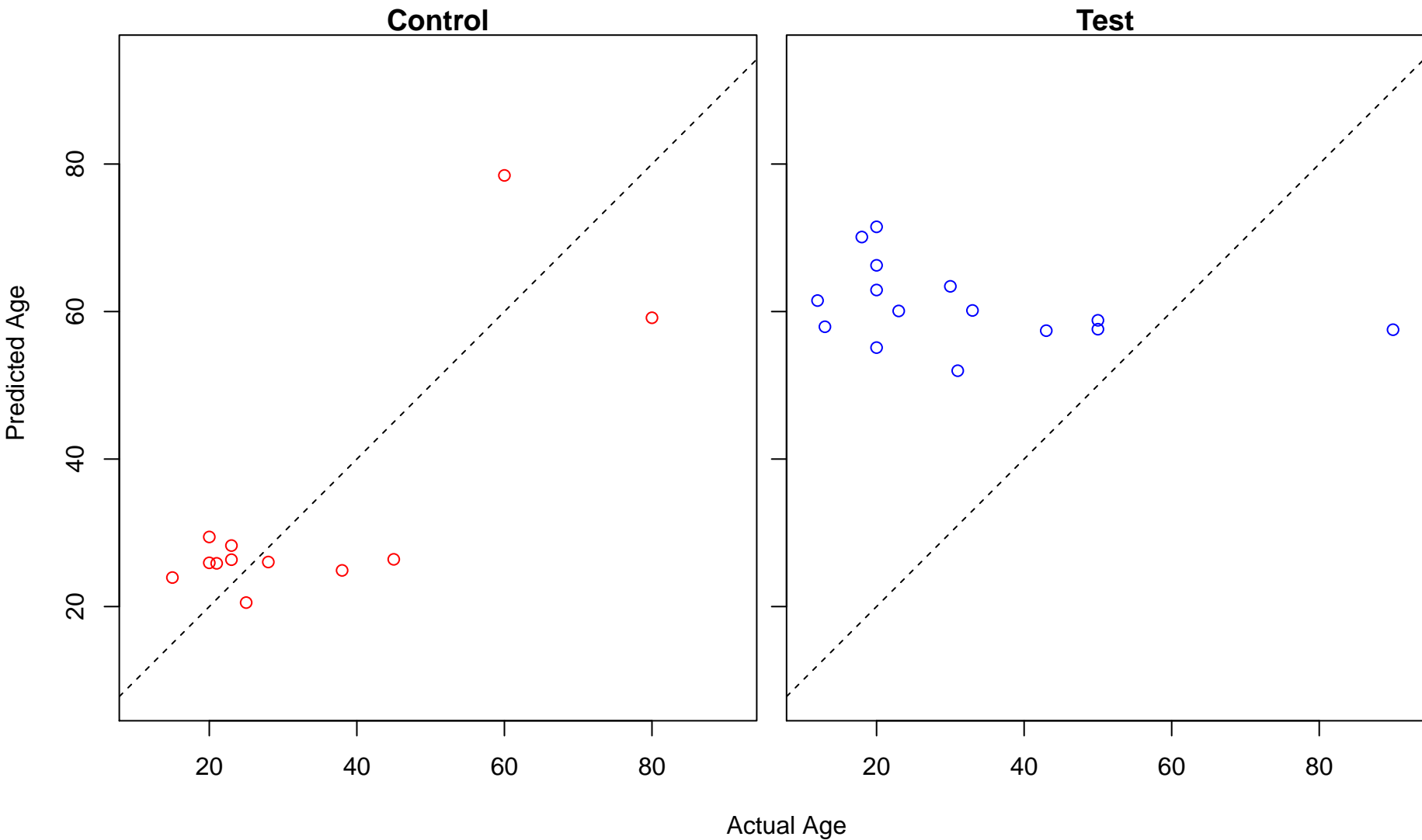
negative regulation of protein acetylation (Score: 3.789523)



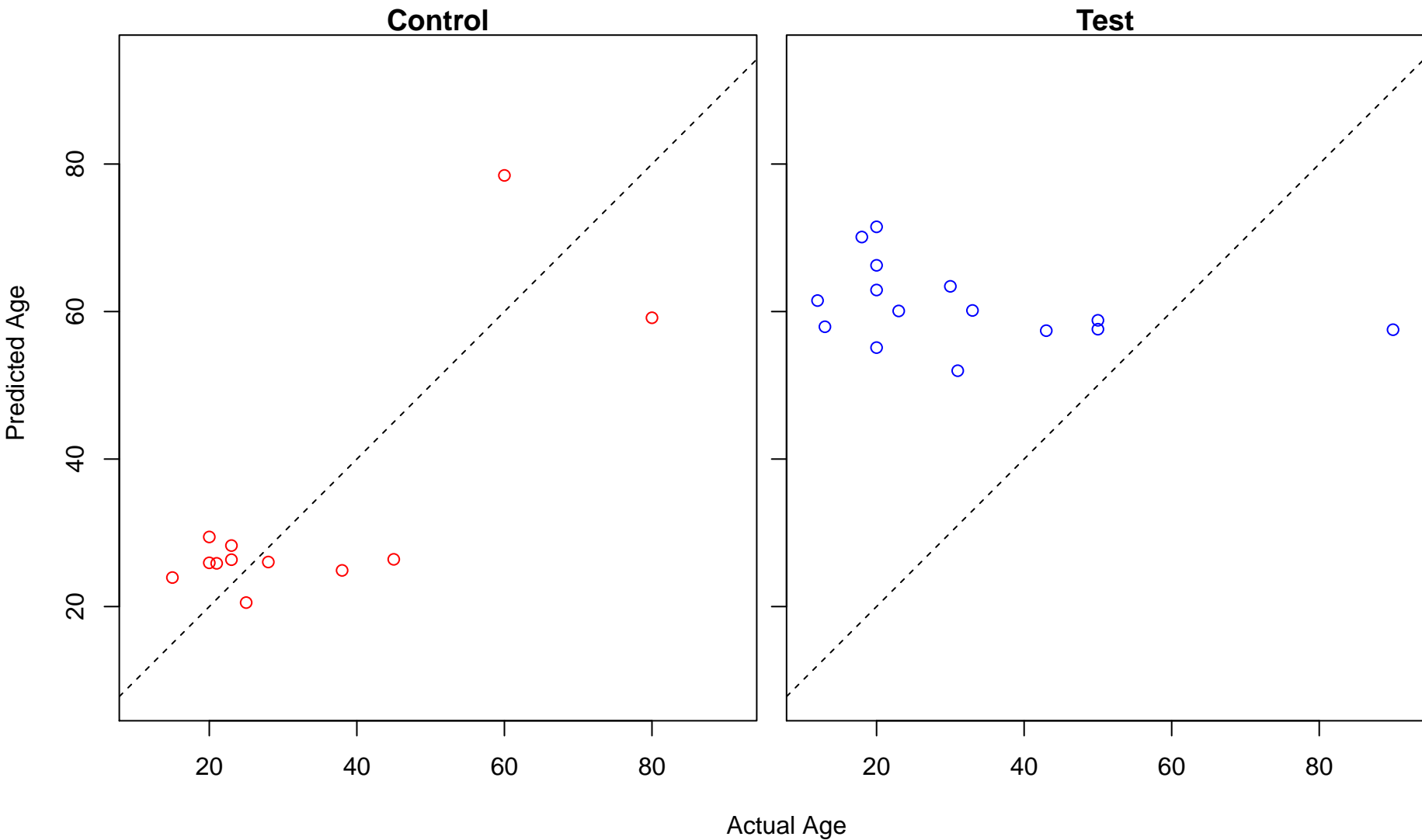
ether lipid biosynthetic process (Score: 3.789149)



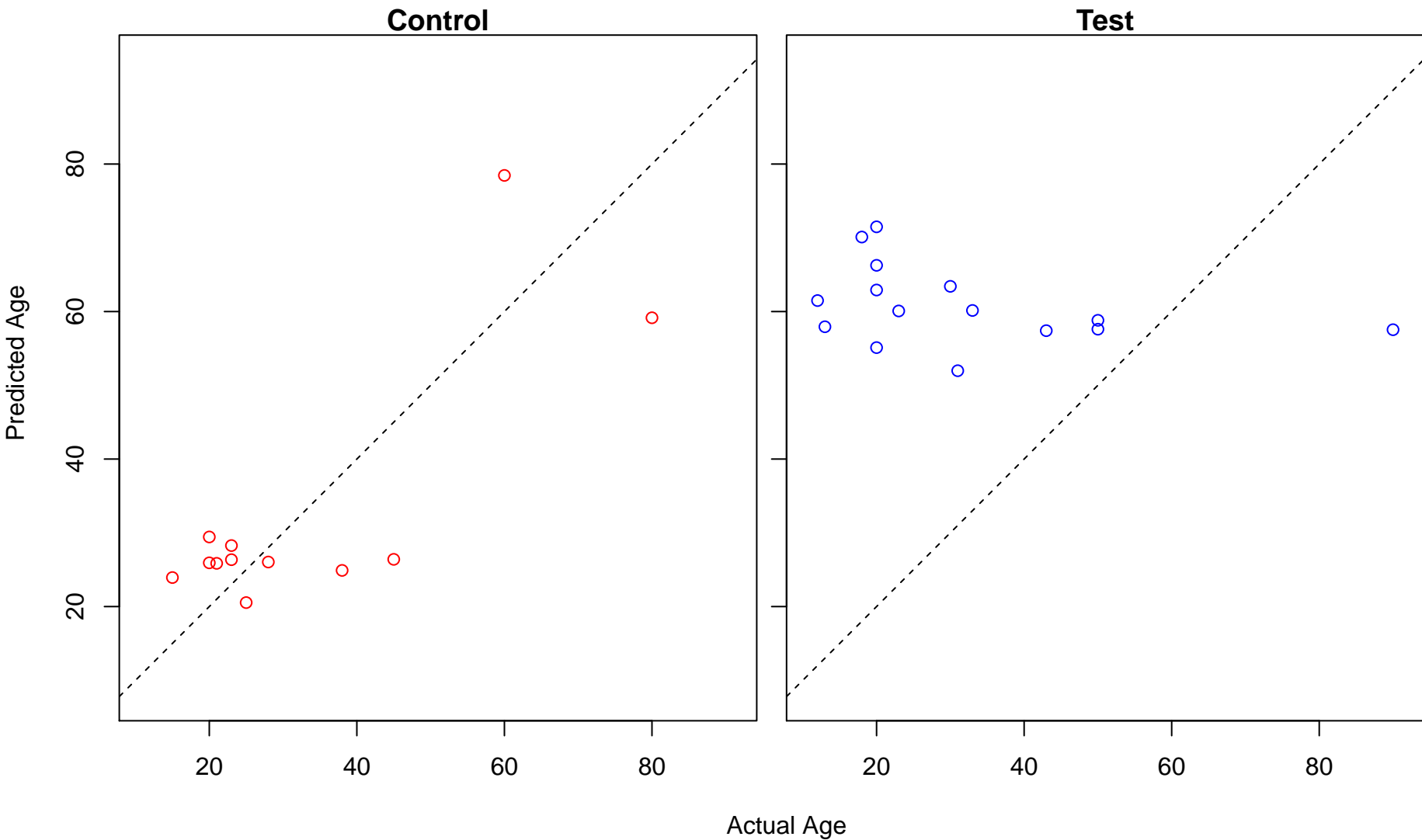
glycerol ether biosynthetic process (Score: 3.789149)



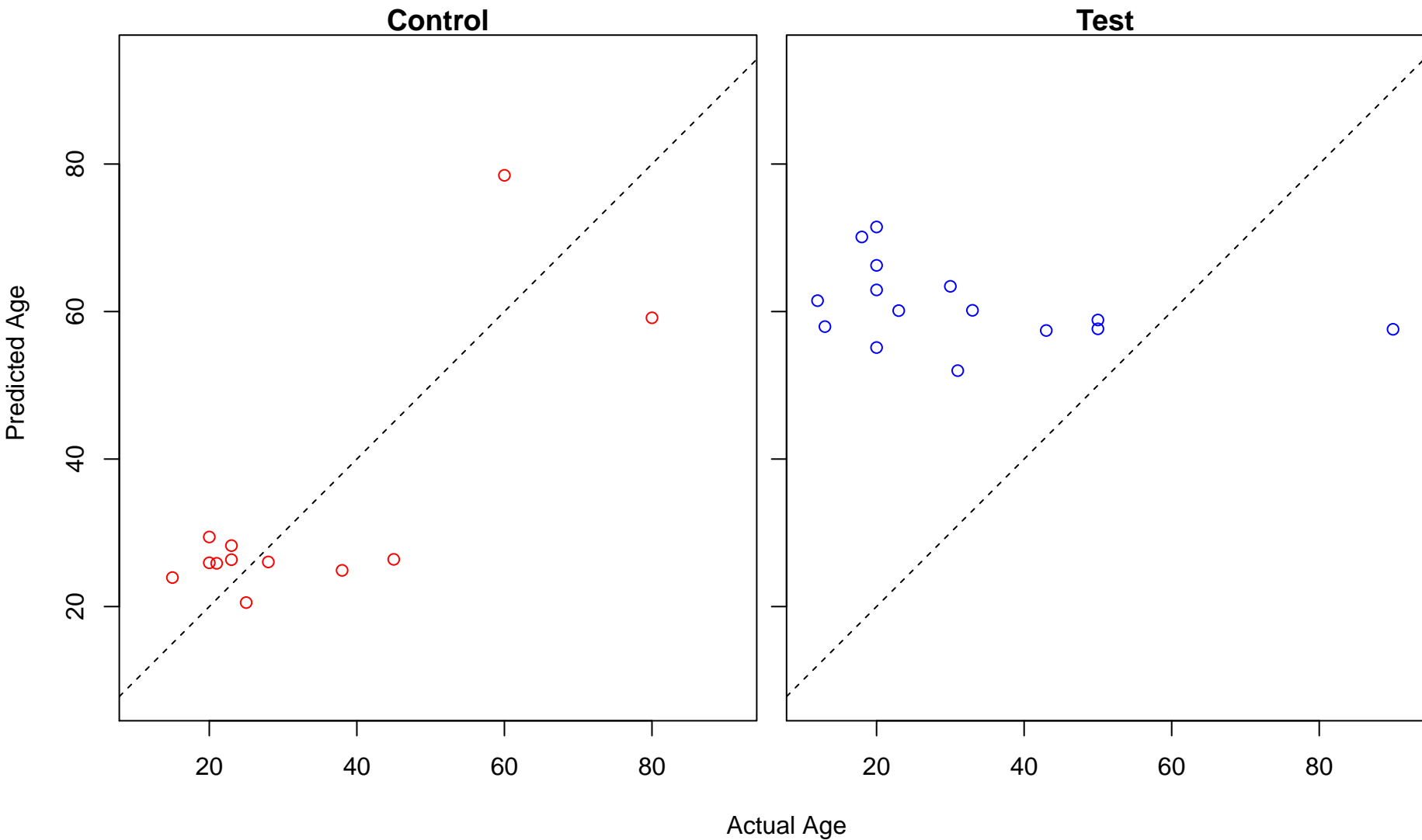
cellular lipid biosynthetic process (Score: 3.789149)



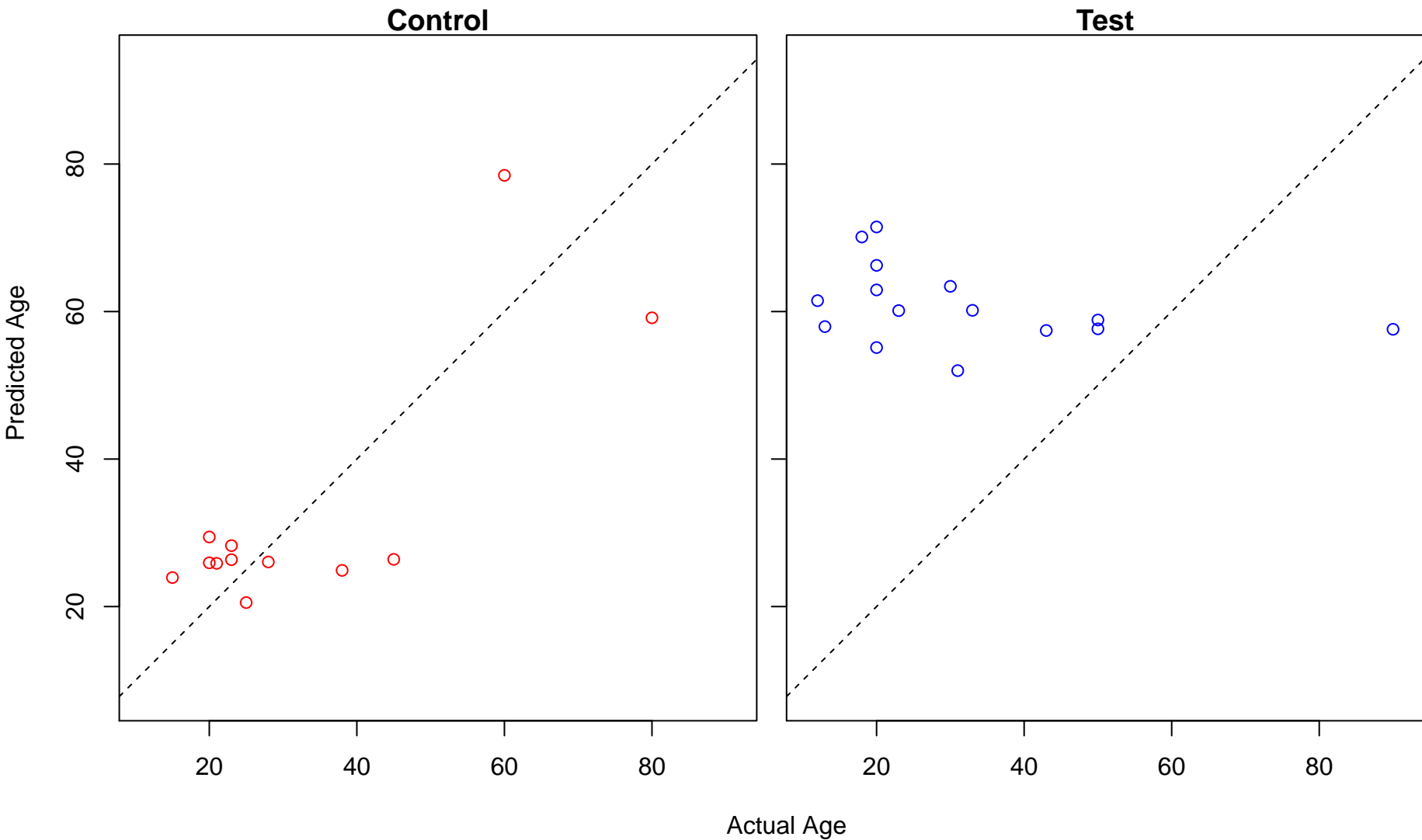
ether biosynthetic process (Score: 3.789149)



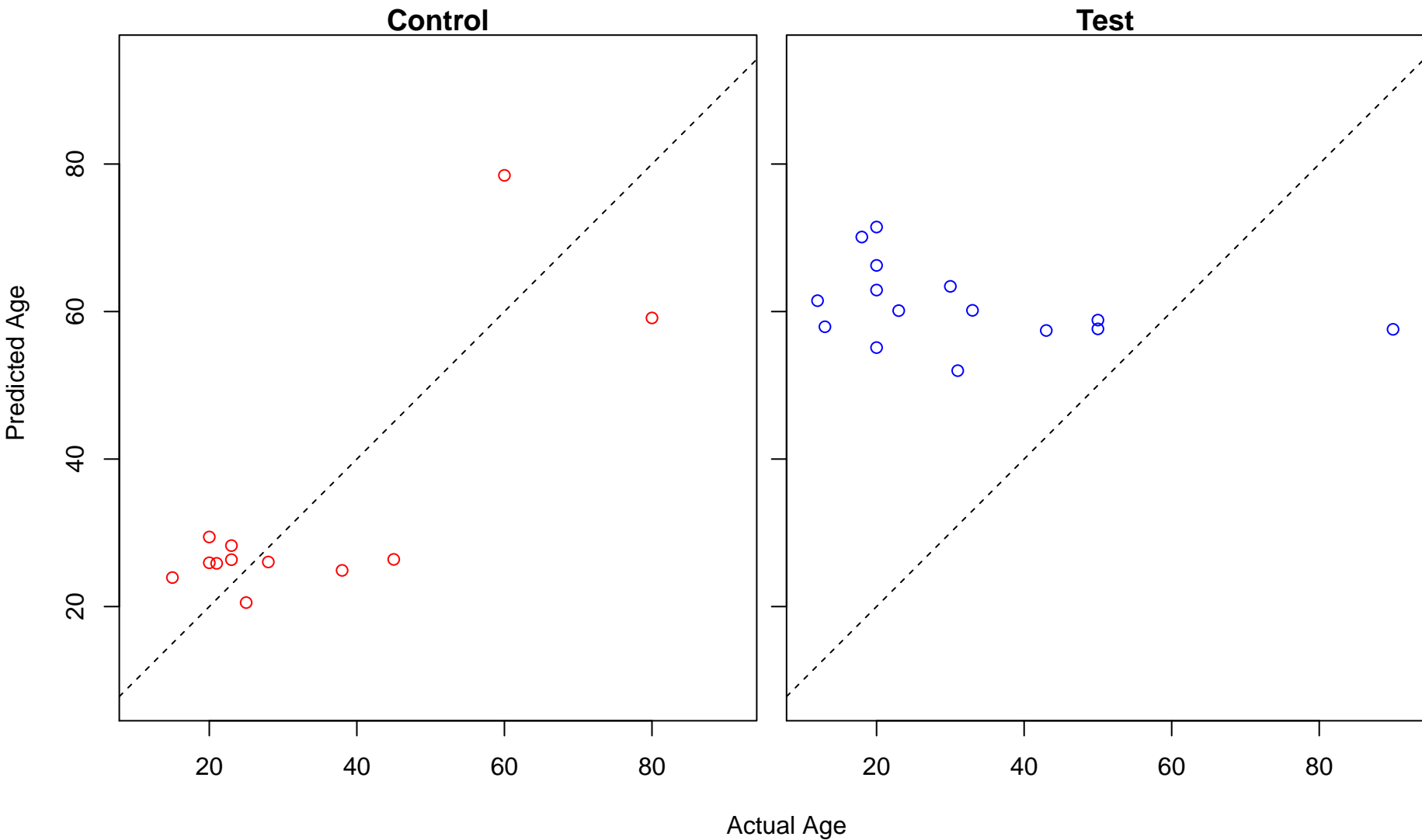
glycerol ether metabolic process (Score: 3.789075)



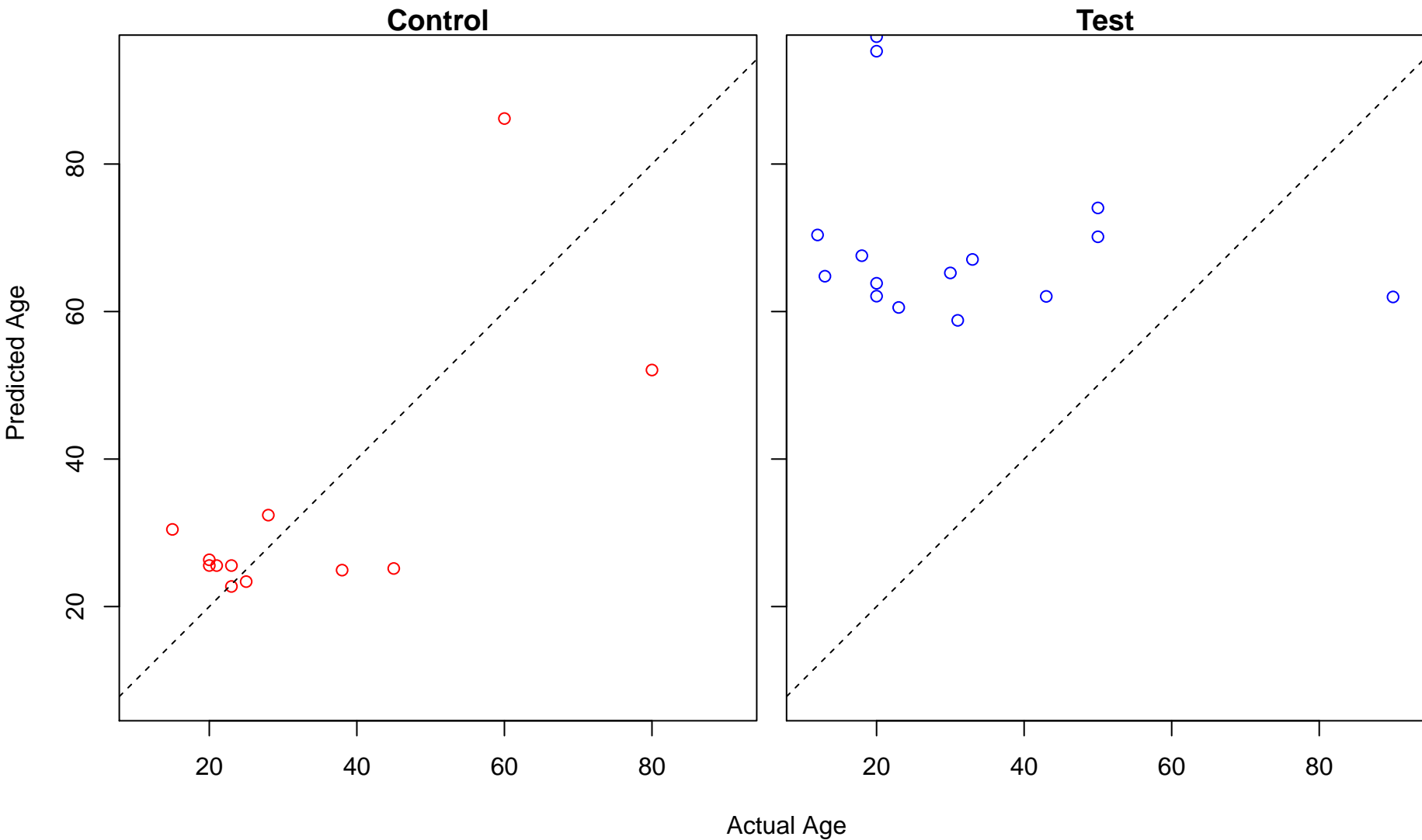
ether lipid metabolic process (Score: 3.789075)



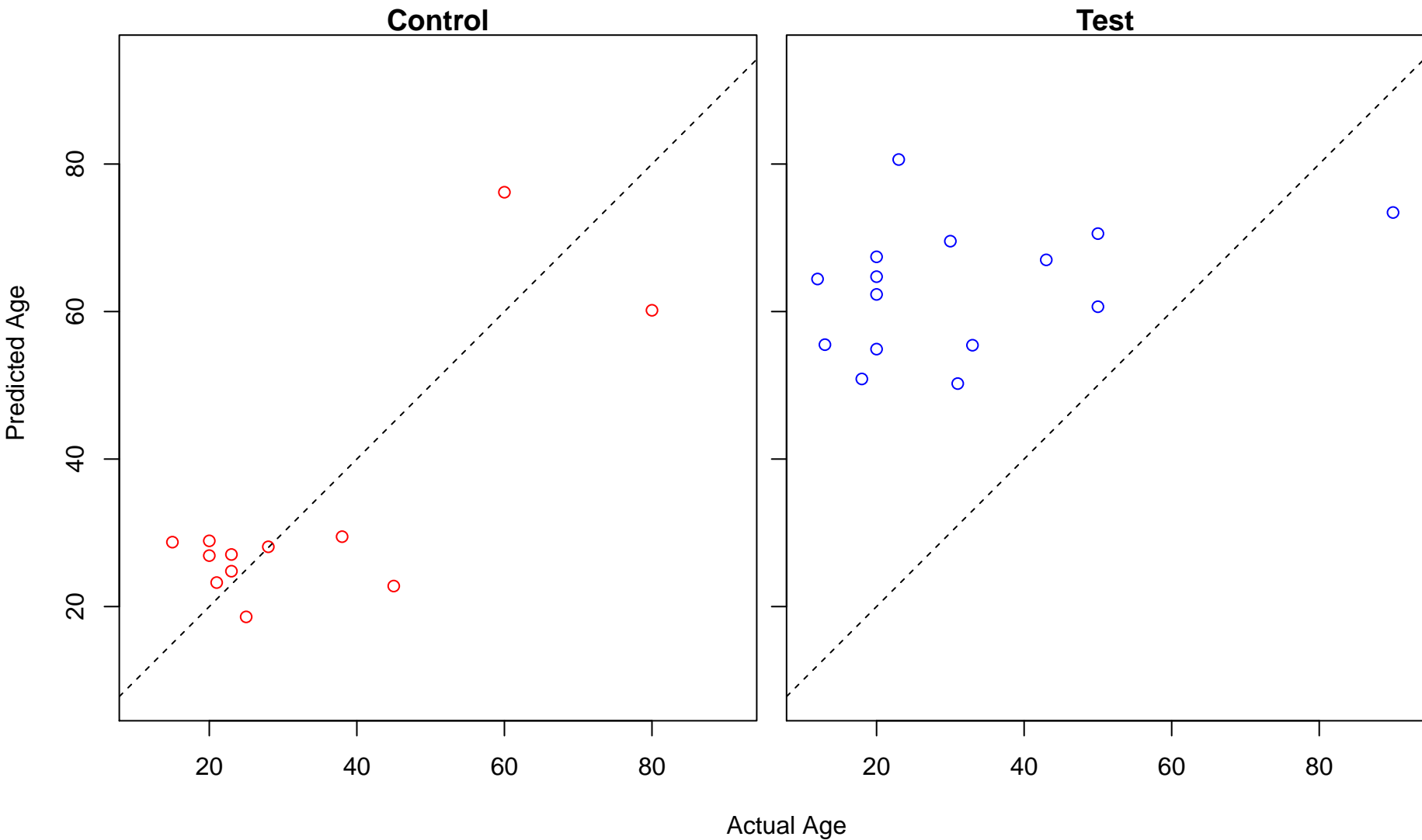
ether metabolic process (Score: 3.786767)



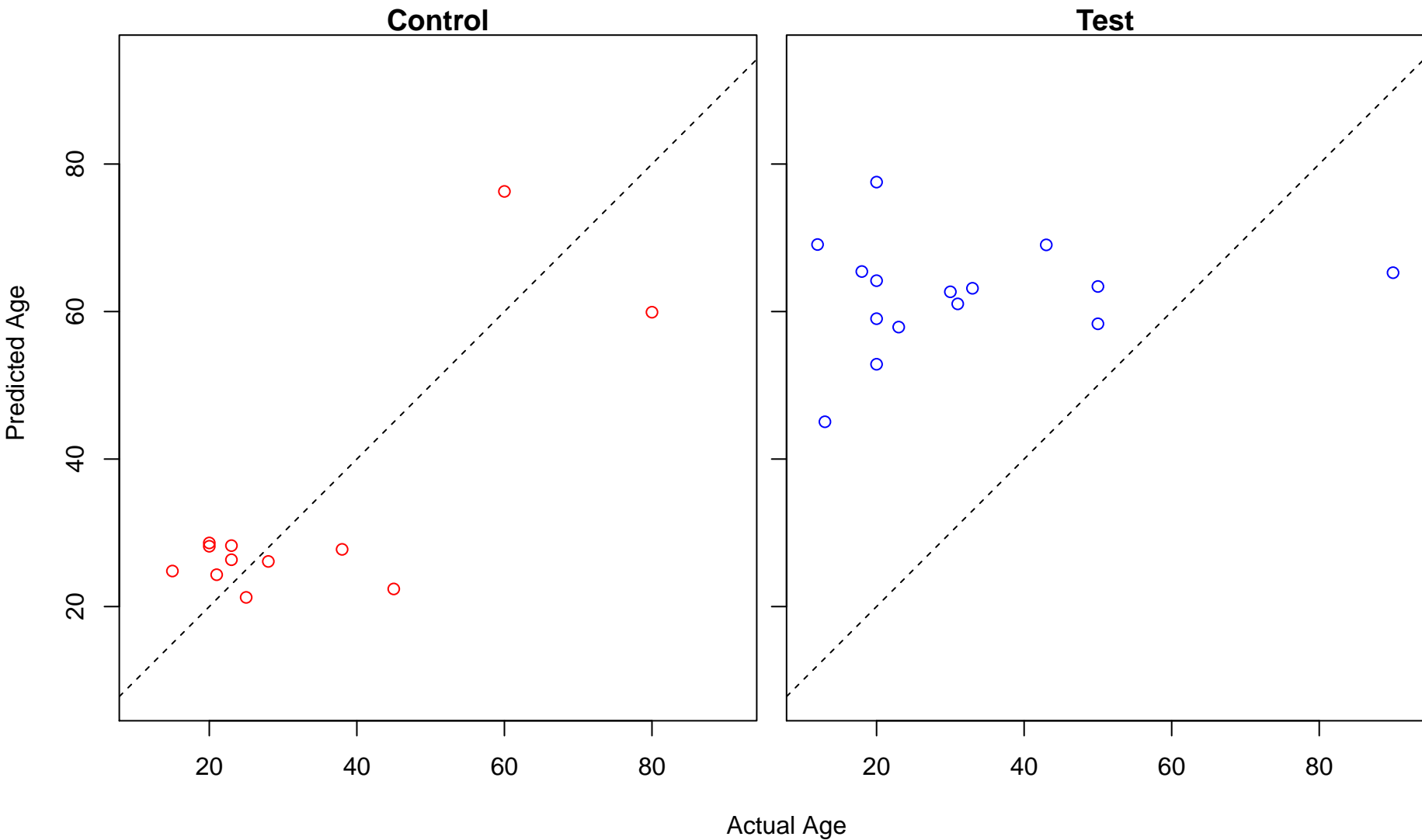
cristae formation (Score: 3.785962)



cellular response to cAMP (Score: 3.785189)

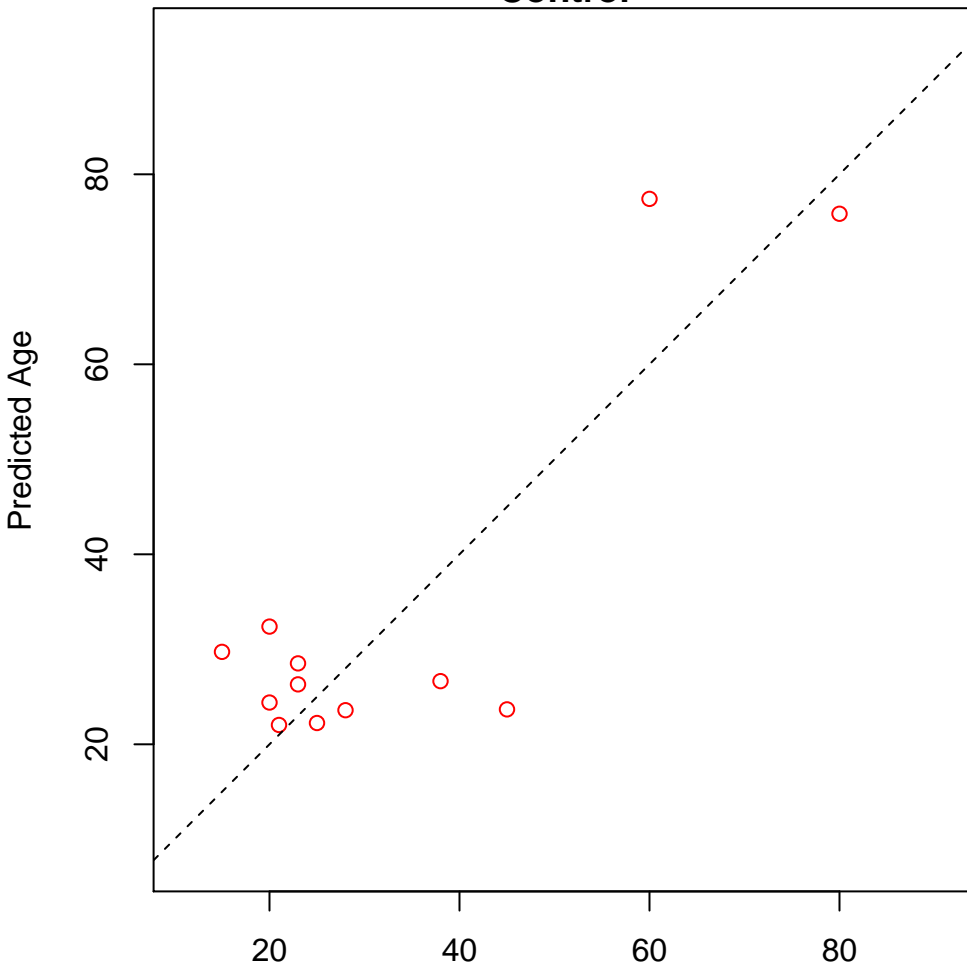


ceramide metabolic process (Score: 3.779900)

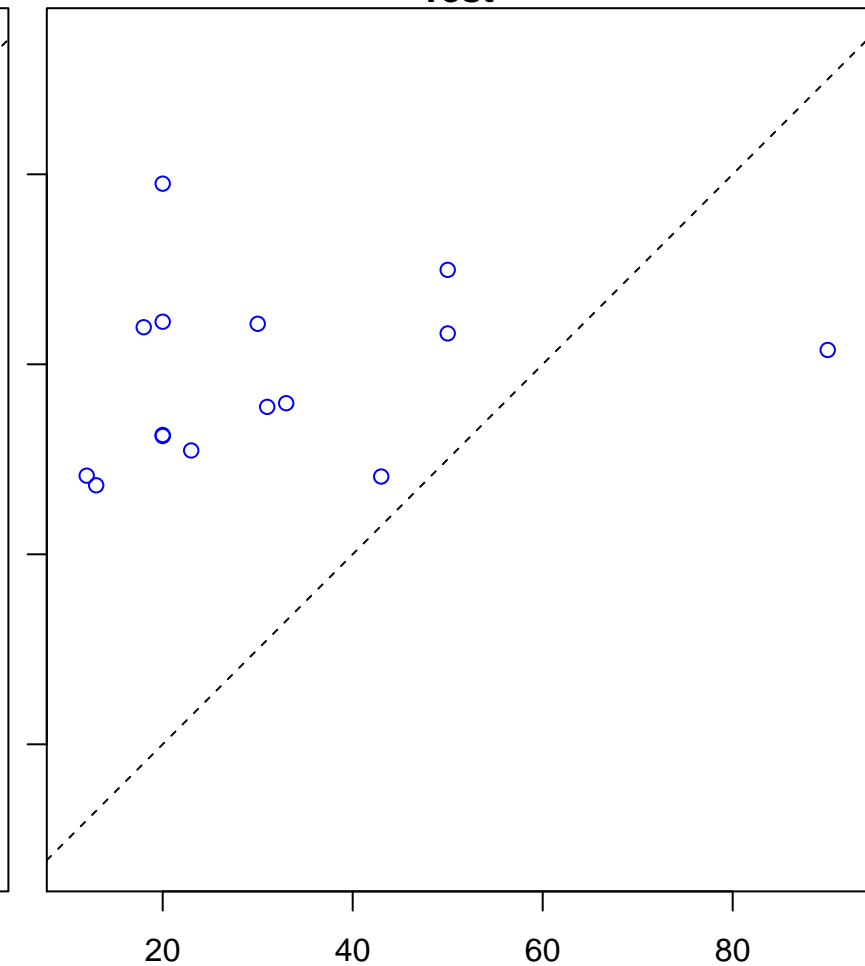


nucleotide-sugar biosynthetic process (Score: 3.779287)

Control

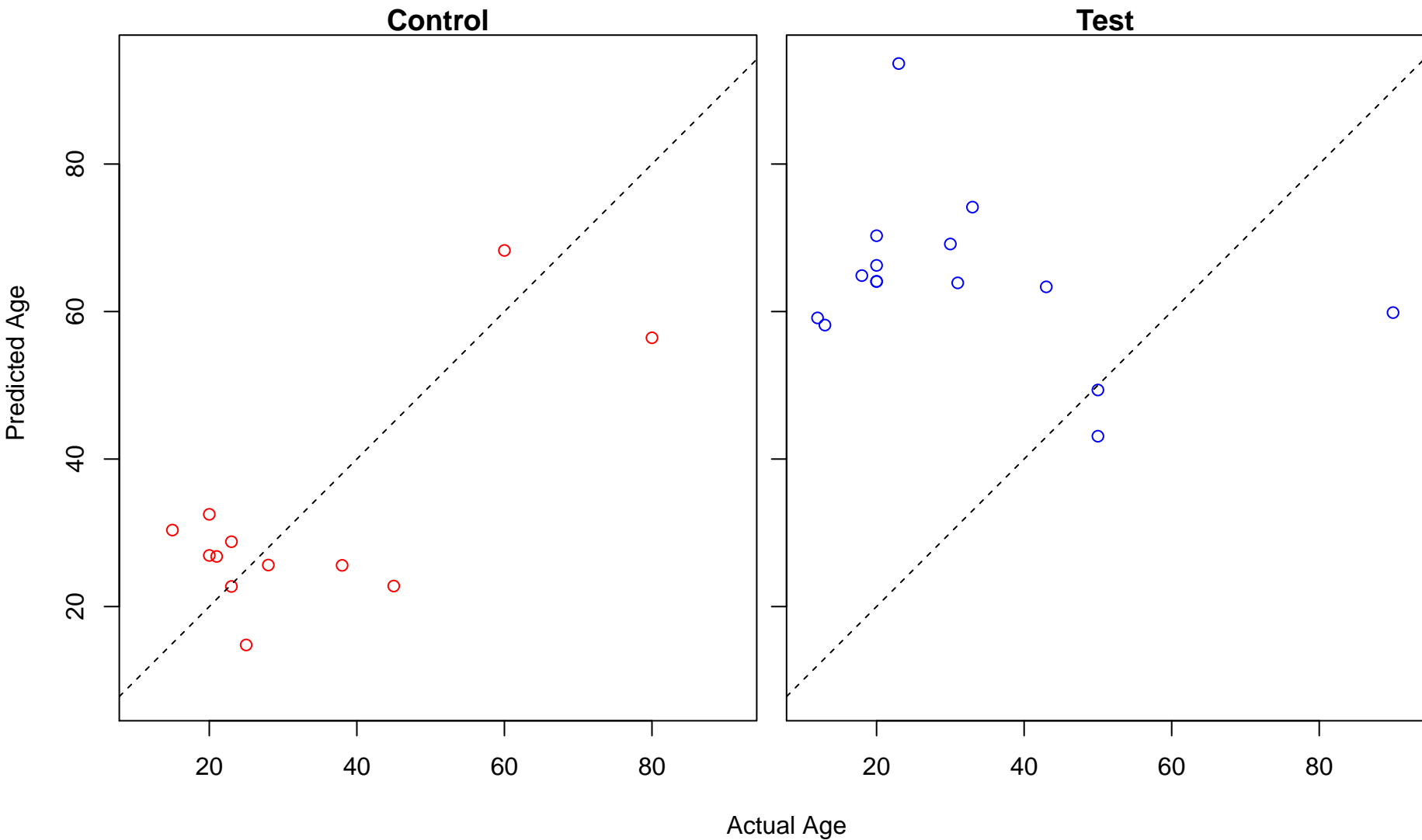


Test

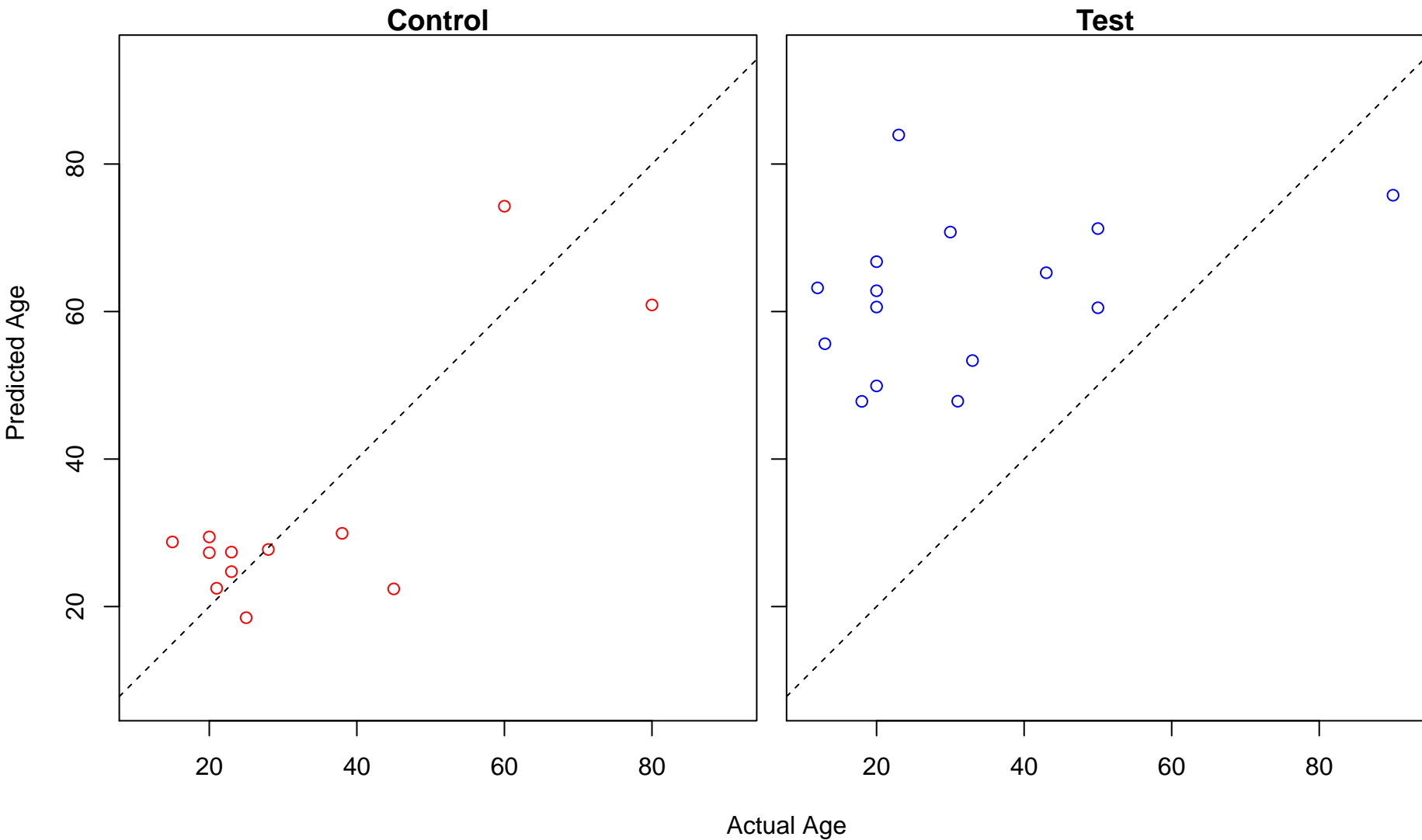


Actual Age

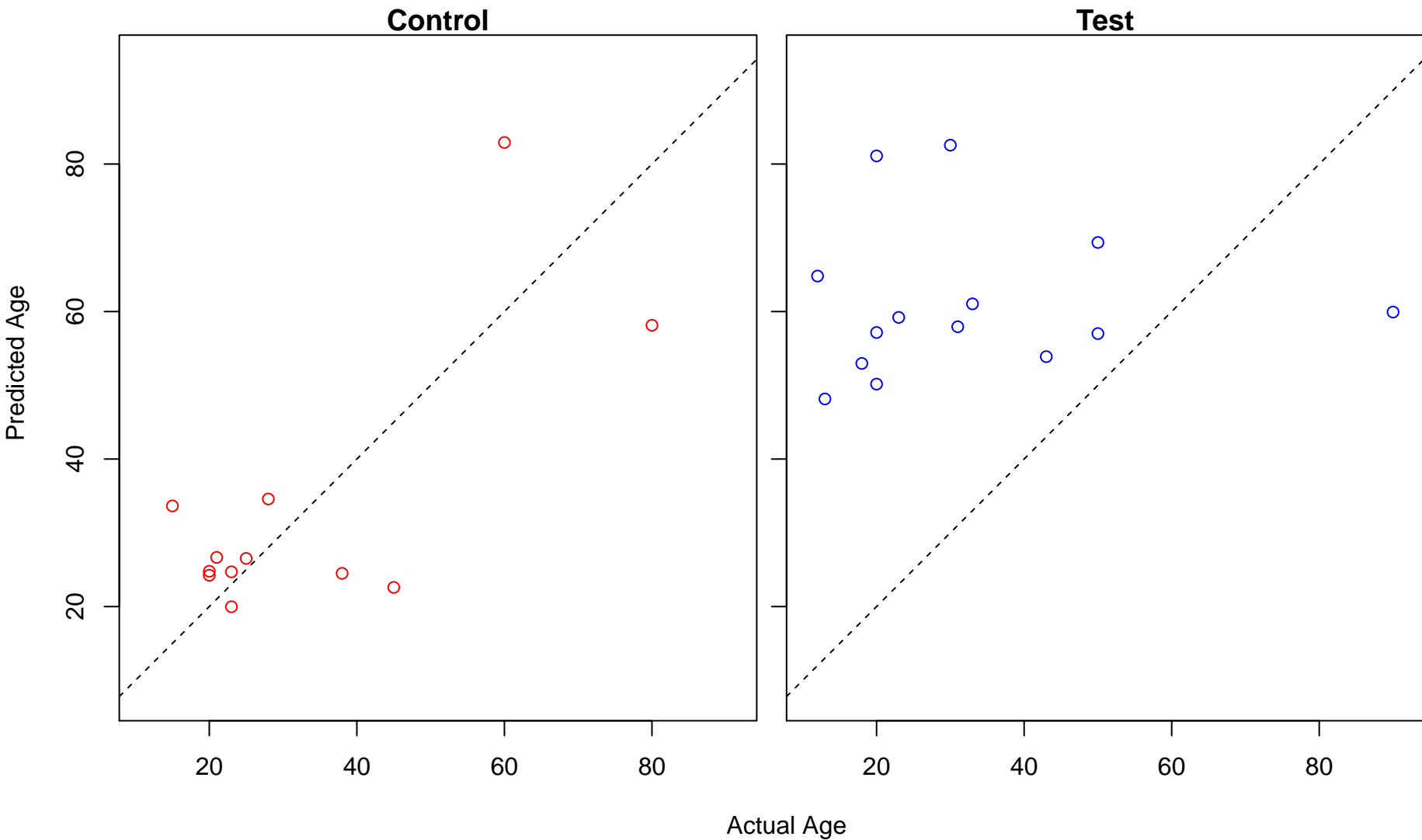
neuron cell-cell adhesion (Score: 3.774995)



regulation of p38MAPK cascade (Score: 3.770477)

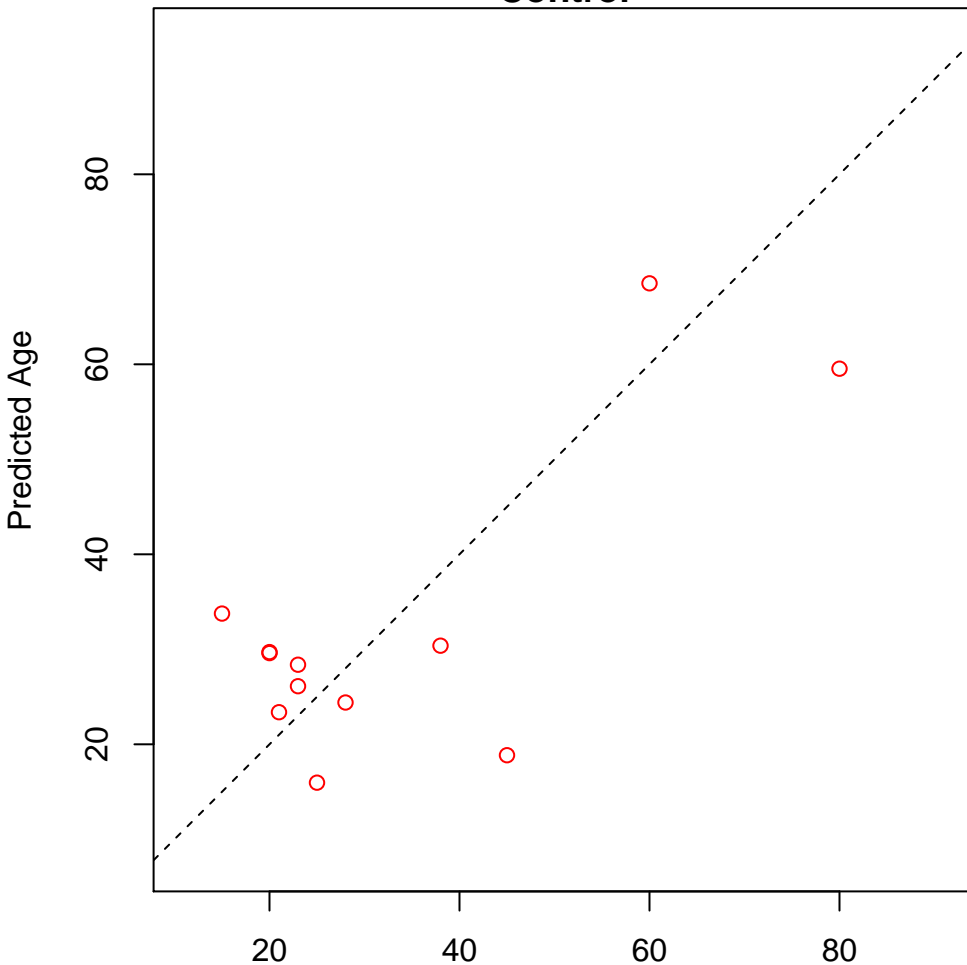


regulation of blood vessel endothelial cell migration (Score: 3.769506)

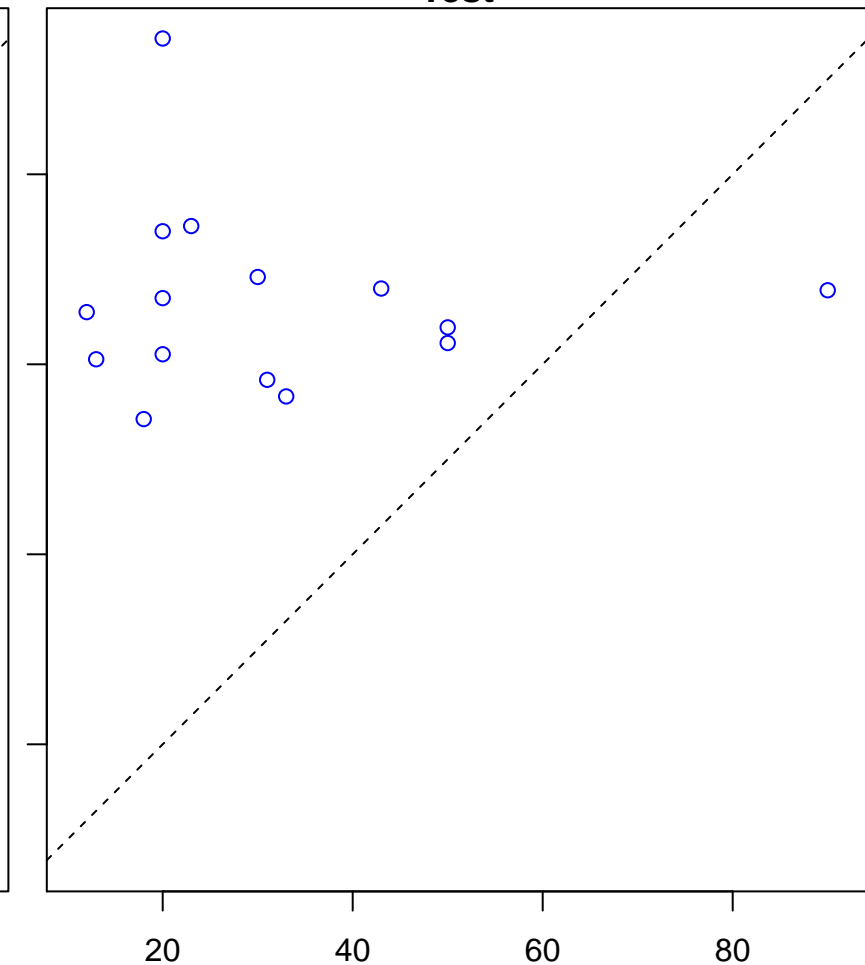


atrioventricular valve morphogenesis (Score: 3.767062)

Control



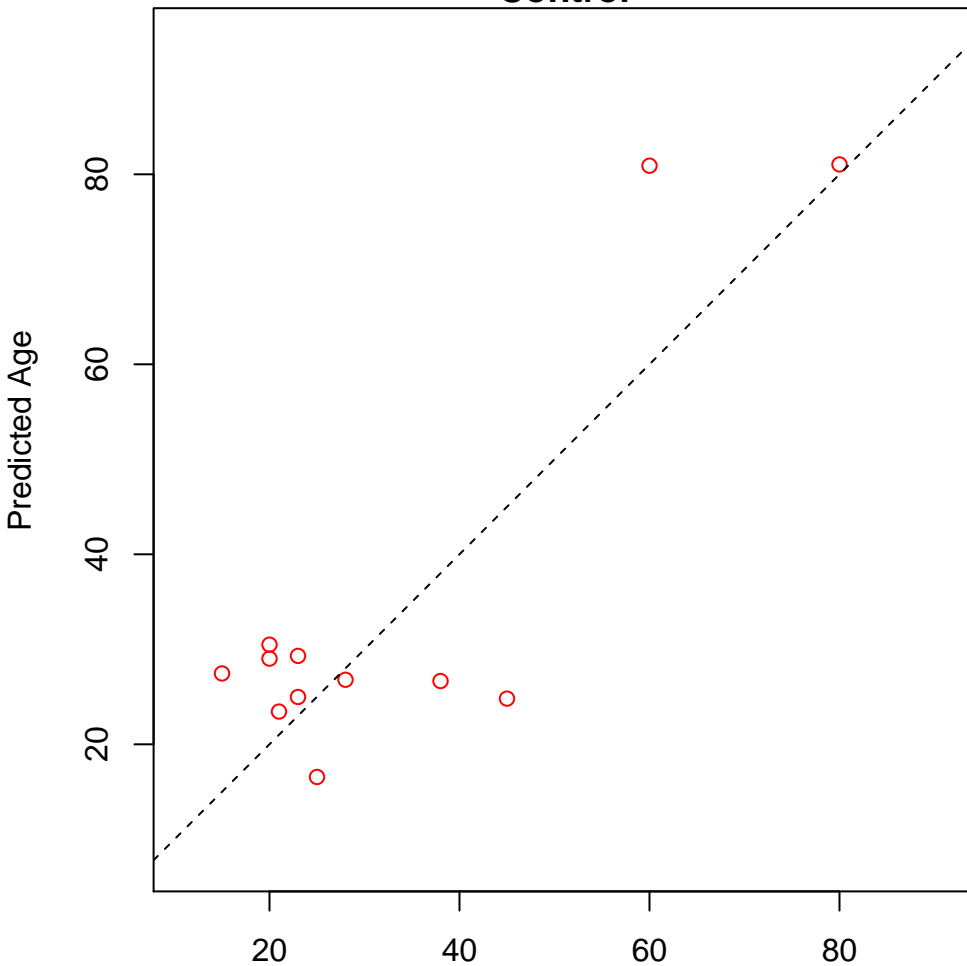
Test



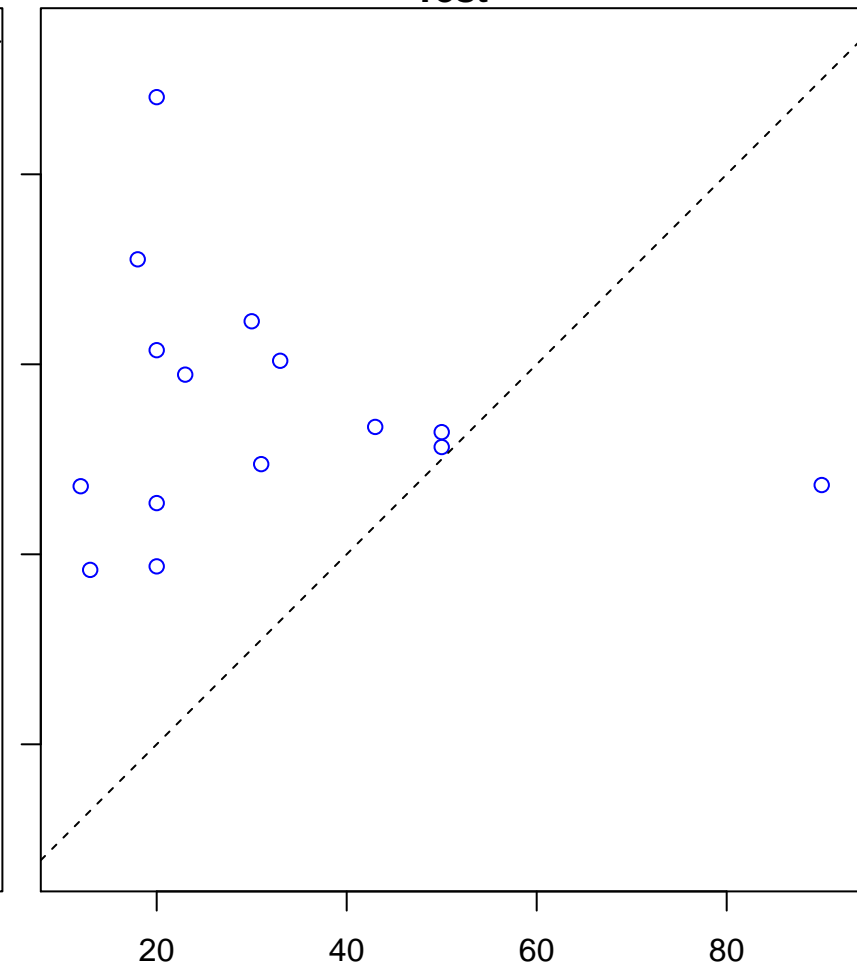
Actual Age

plasma lipoprotein particle organization (Score: 3.766436)

Control

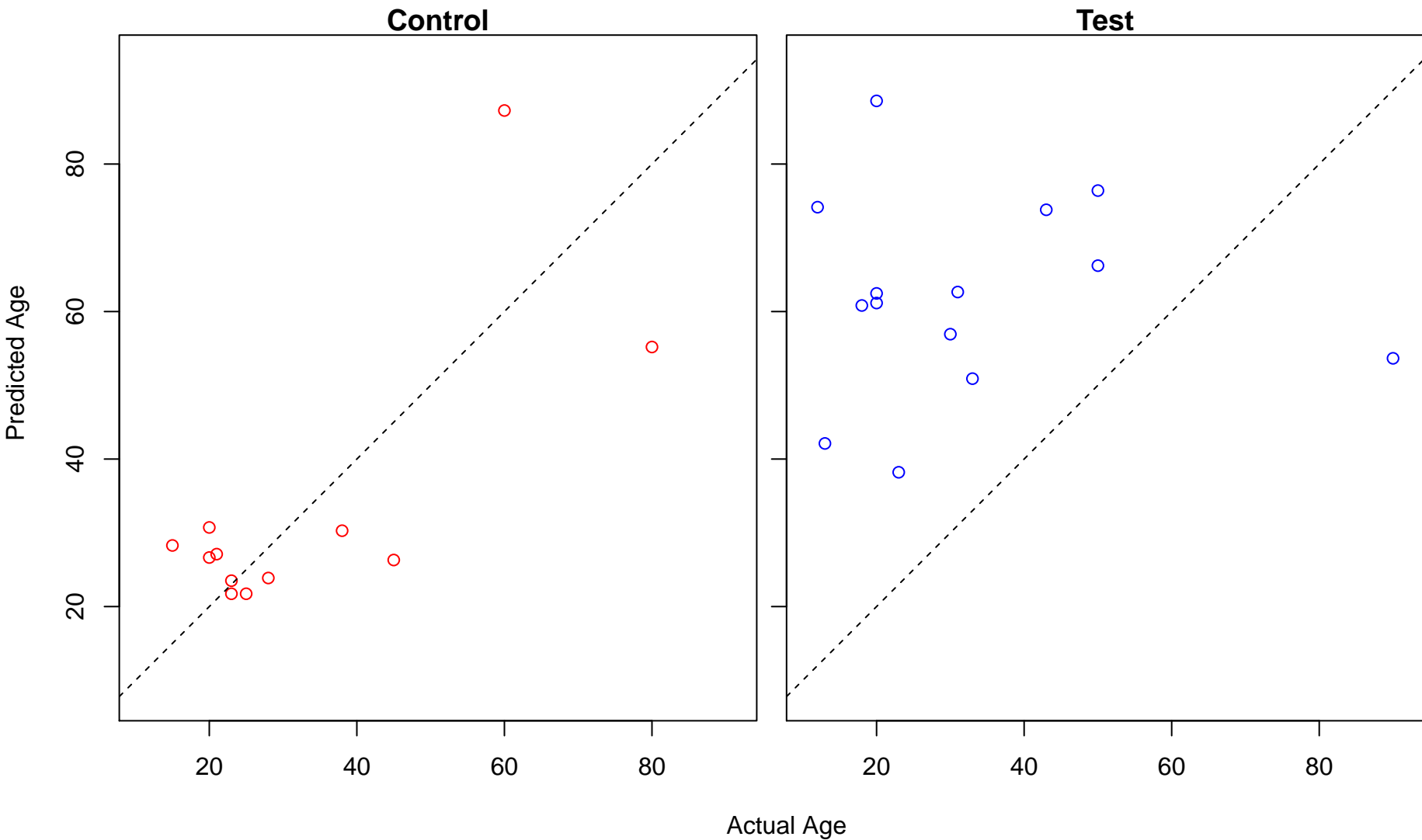


Test

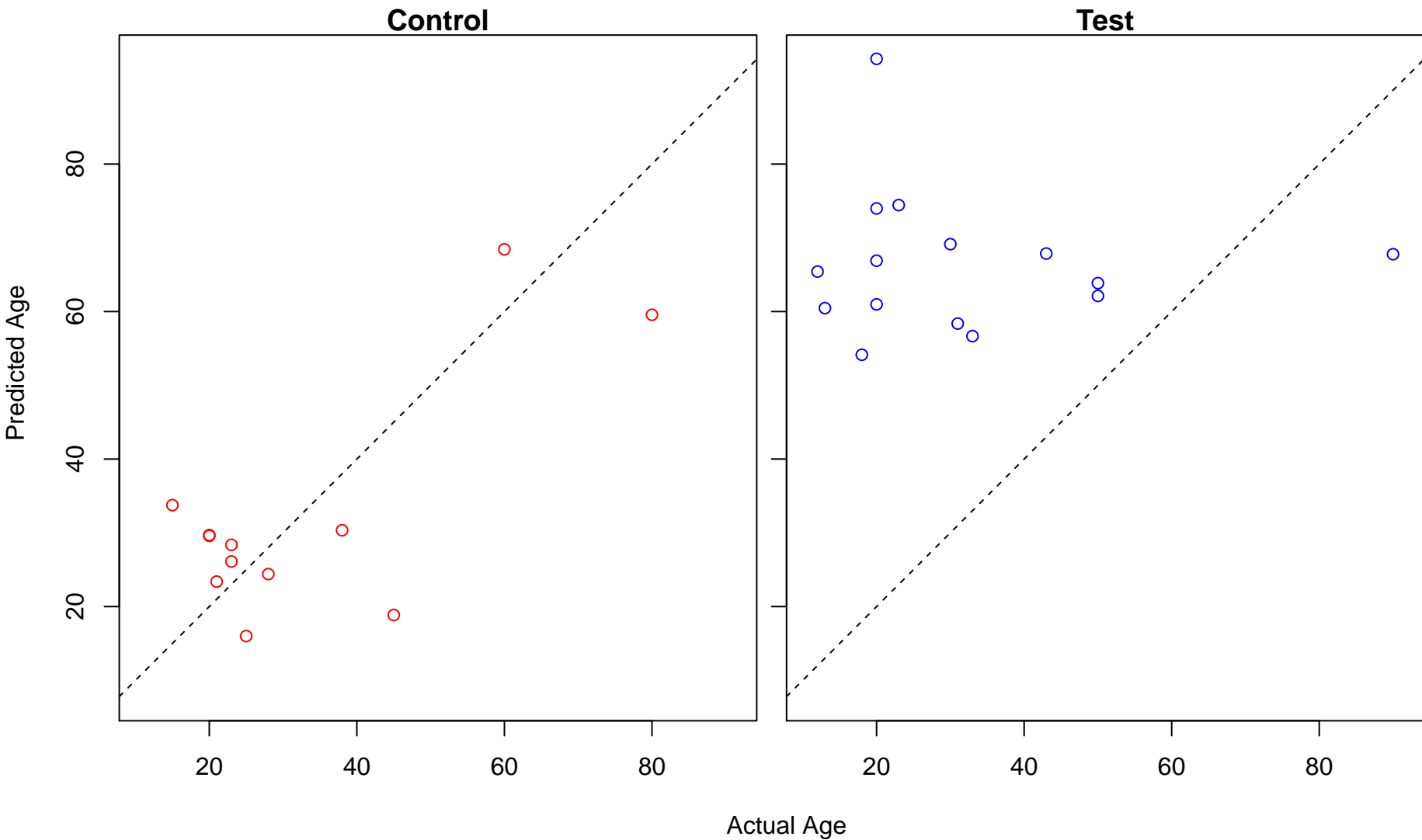


Actual Age

positive regulation of epithelial cell apoptotic process (Score: 3.765911)

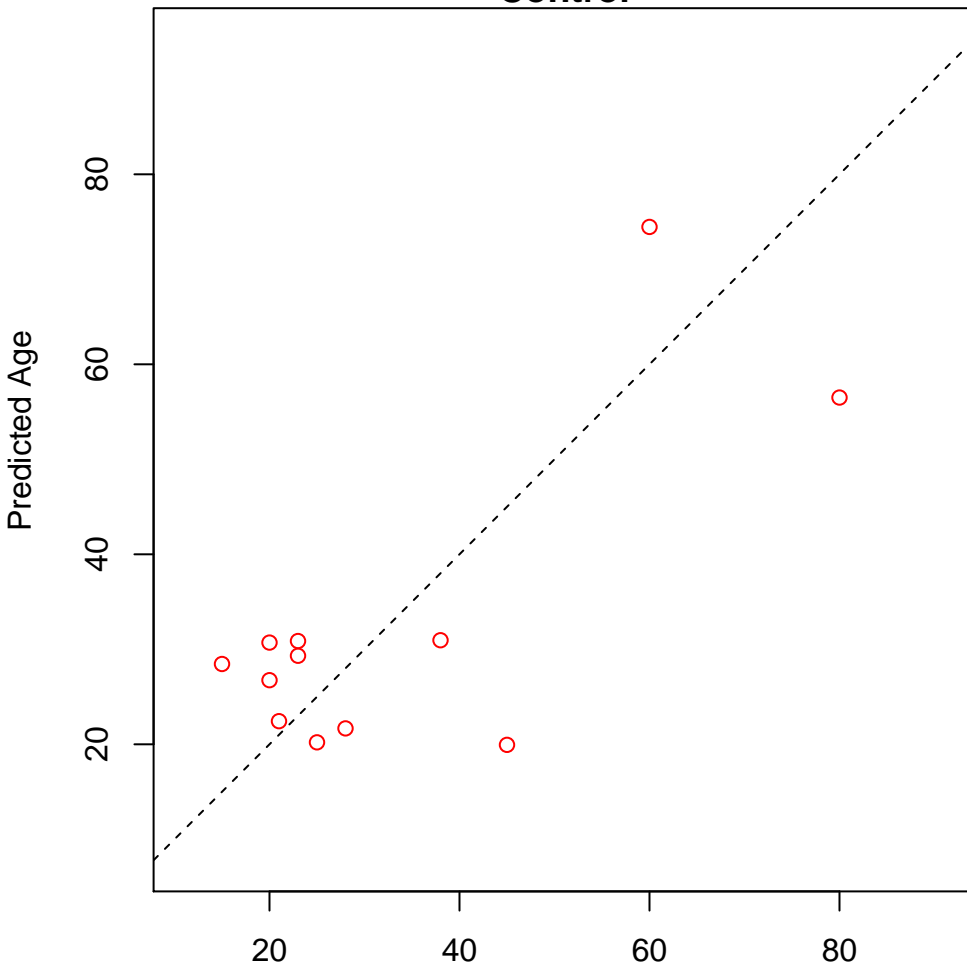


atrioventricular valve development (Score: 3.765492)

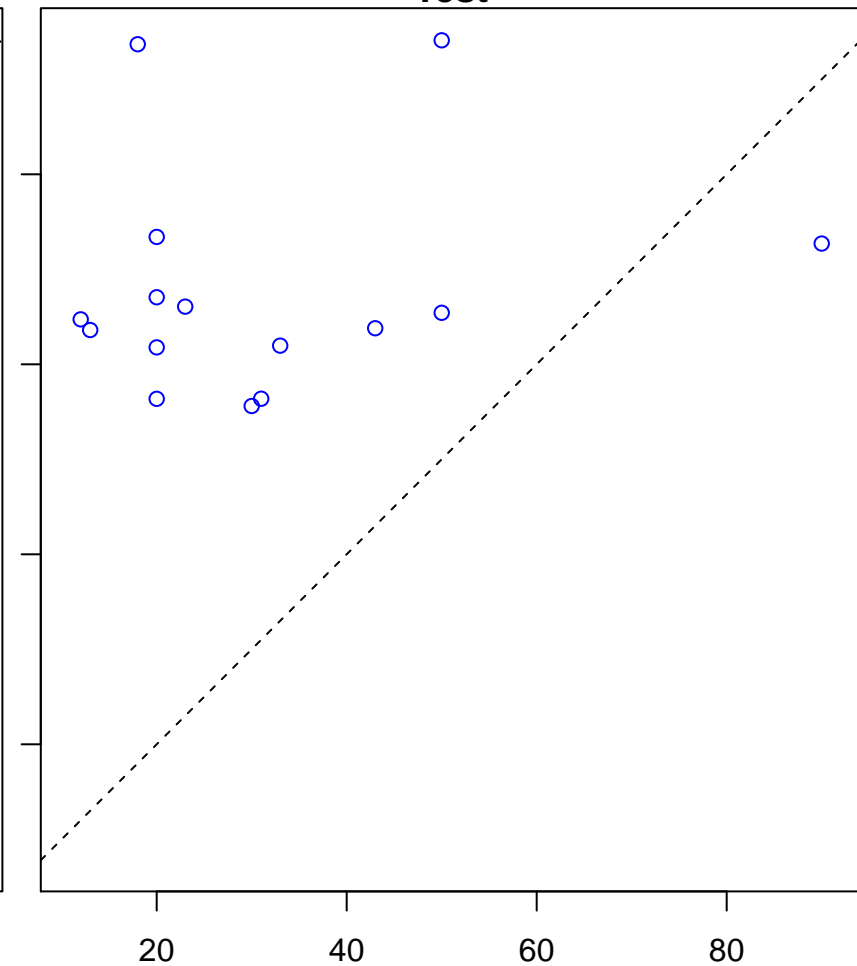


lymphoid progenitor cell differentiation (Score: 3.764853)

Control

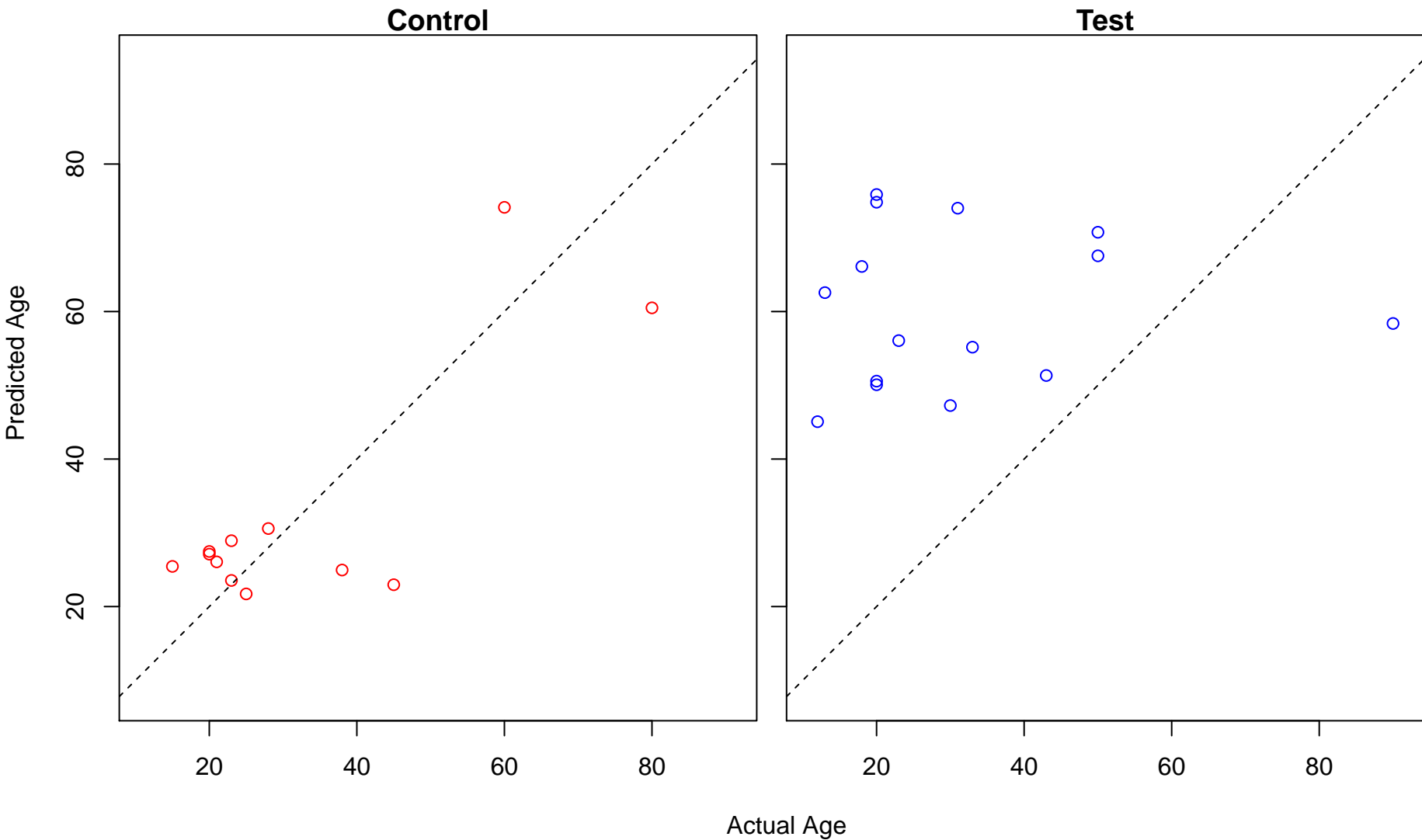


Test

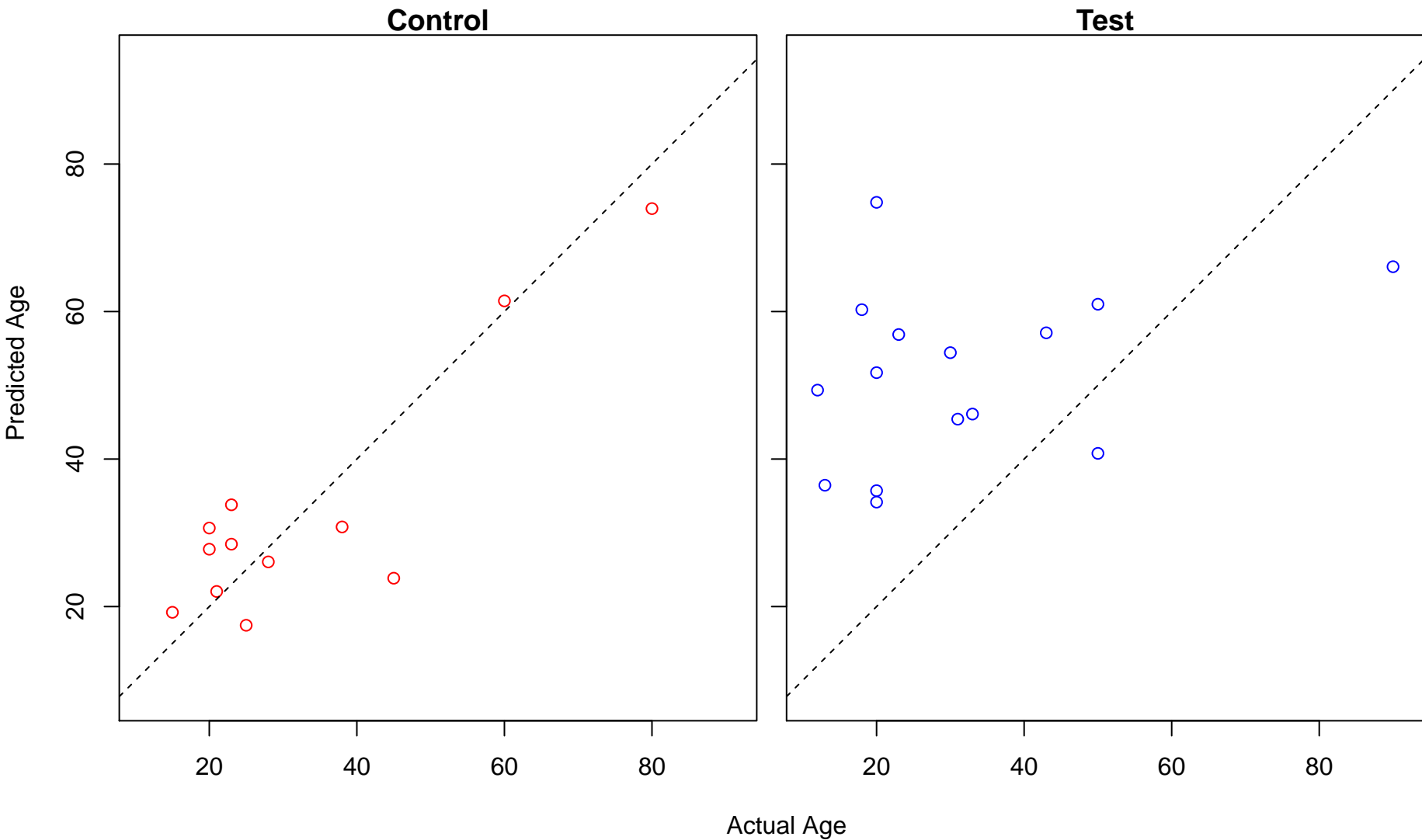


Actual Age

positive regulation of ryanodine-sensitive calcium-release channel activity (Score: 3.764825)

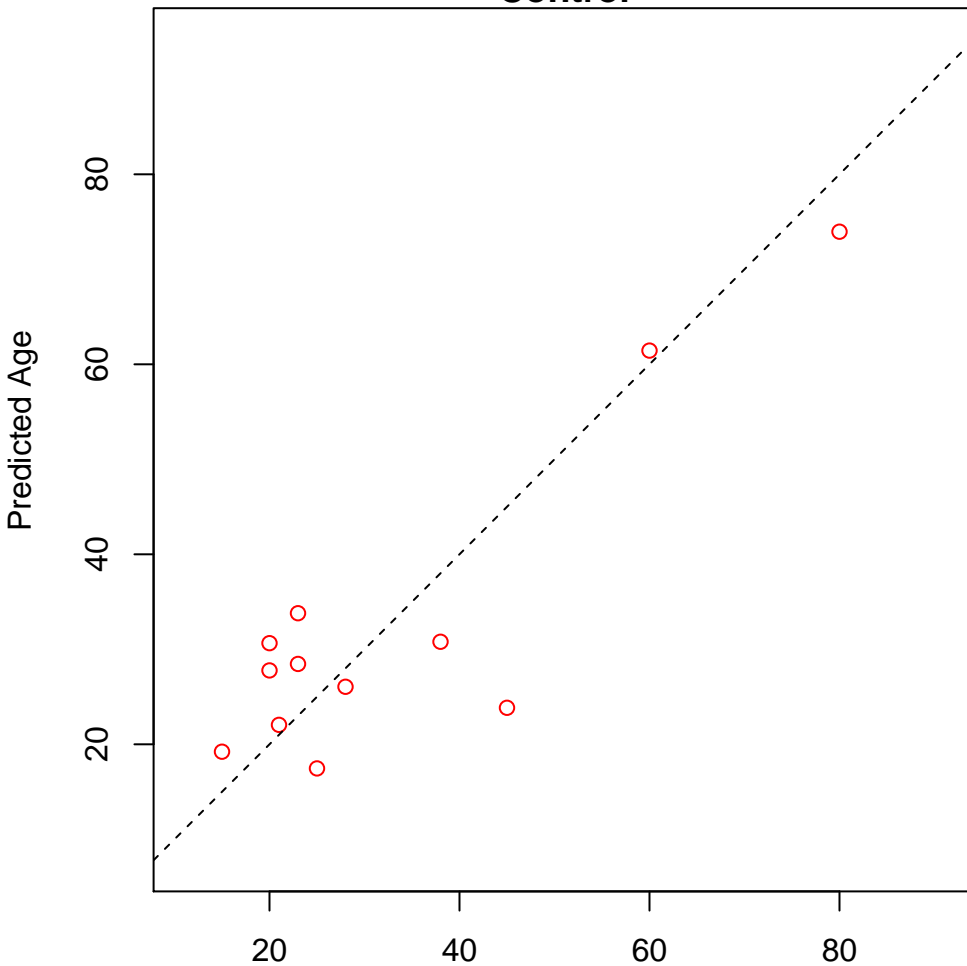


protein demannosylation (Score: 3.764407)

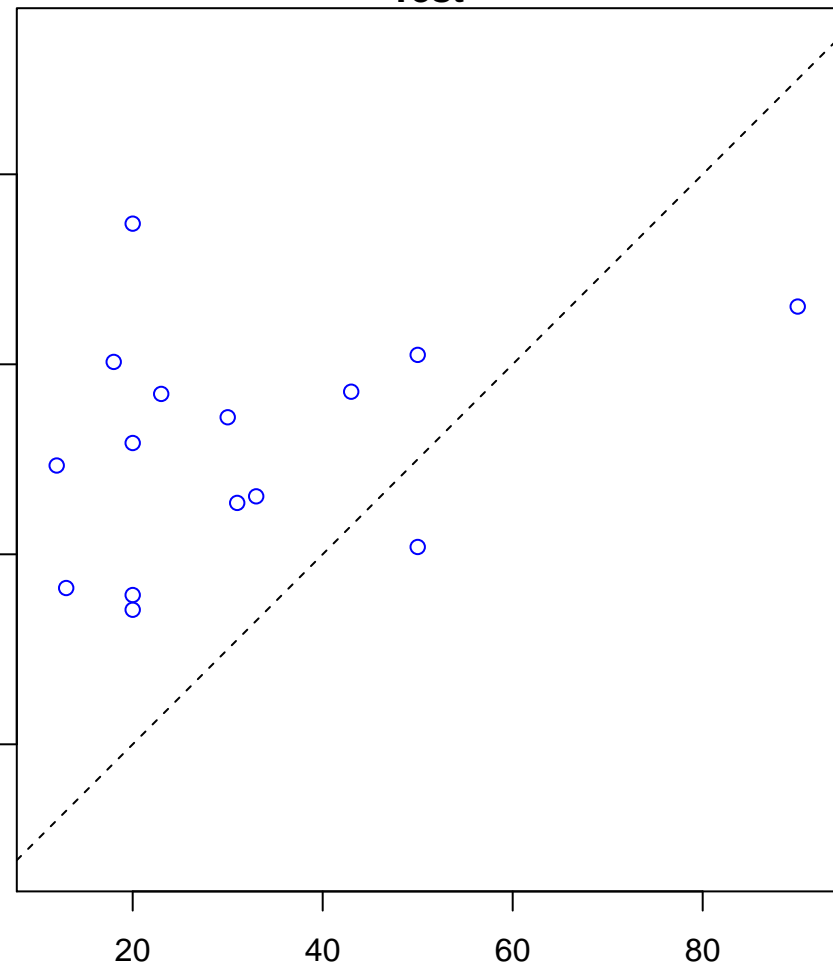


protein alpha-1,2-demannosylation (Score: 3.764407)

Control

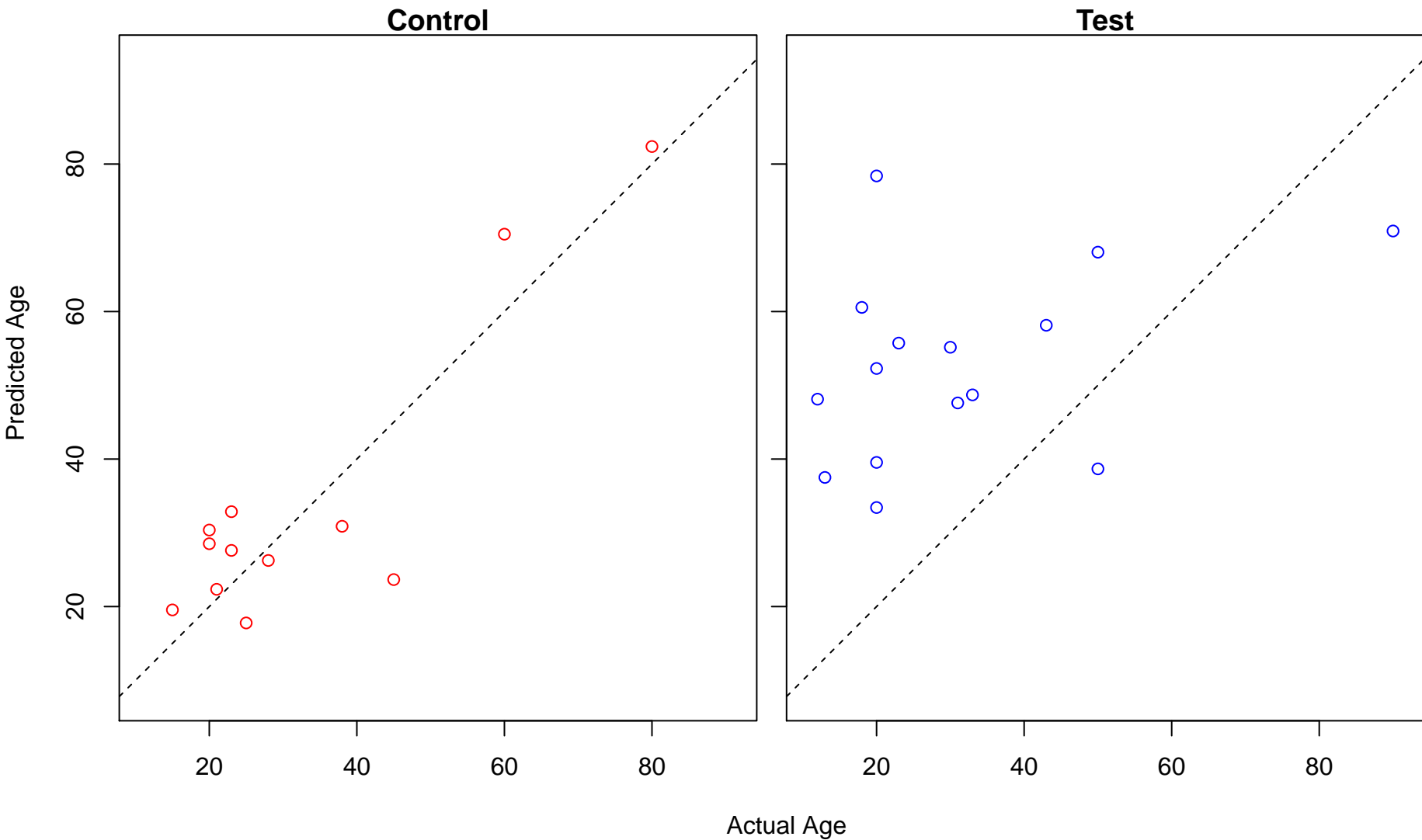


Test

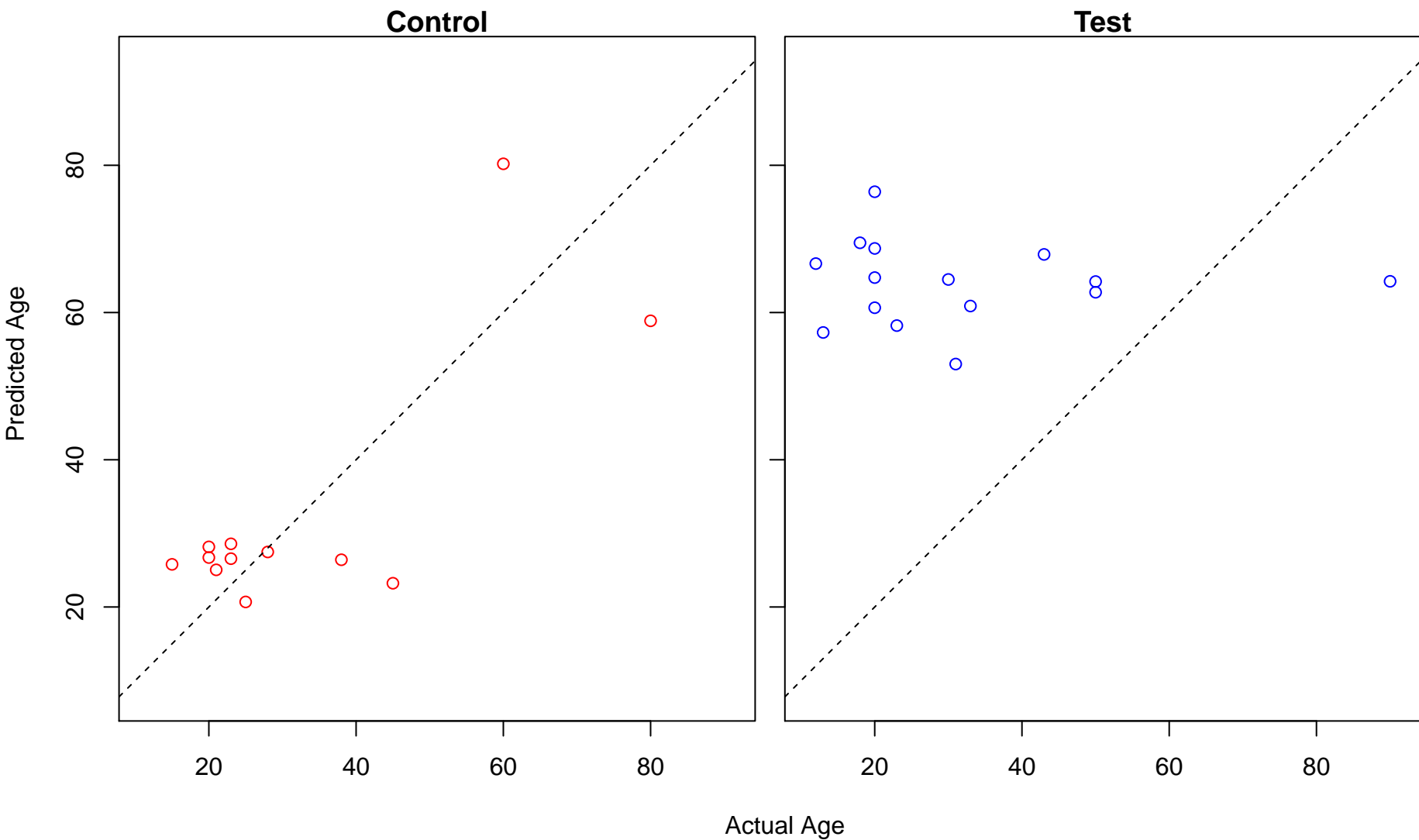


Actual Age

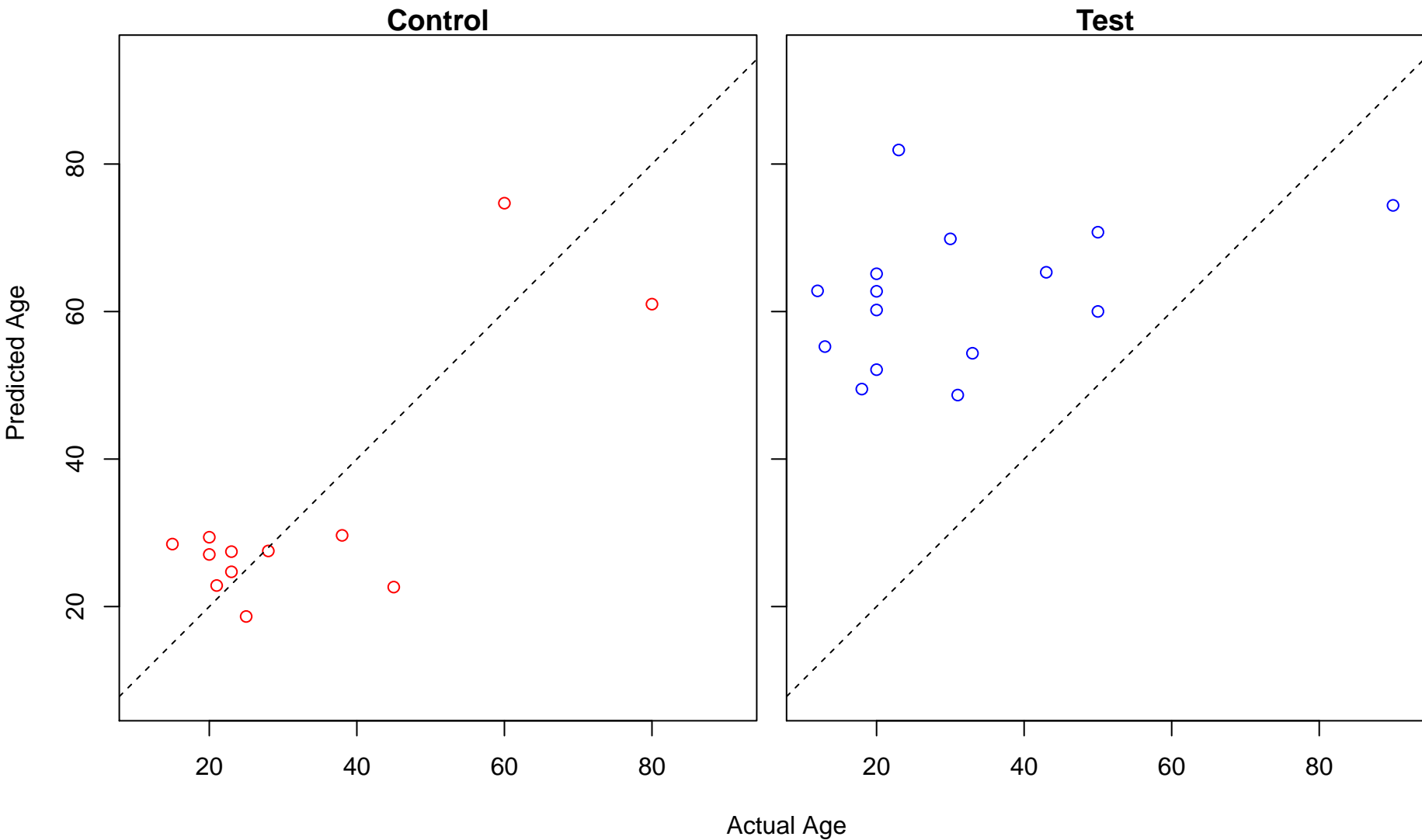
N-glycan processing (Score: 3.762950)



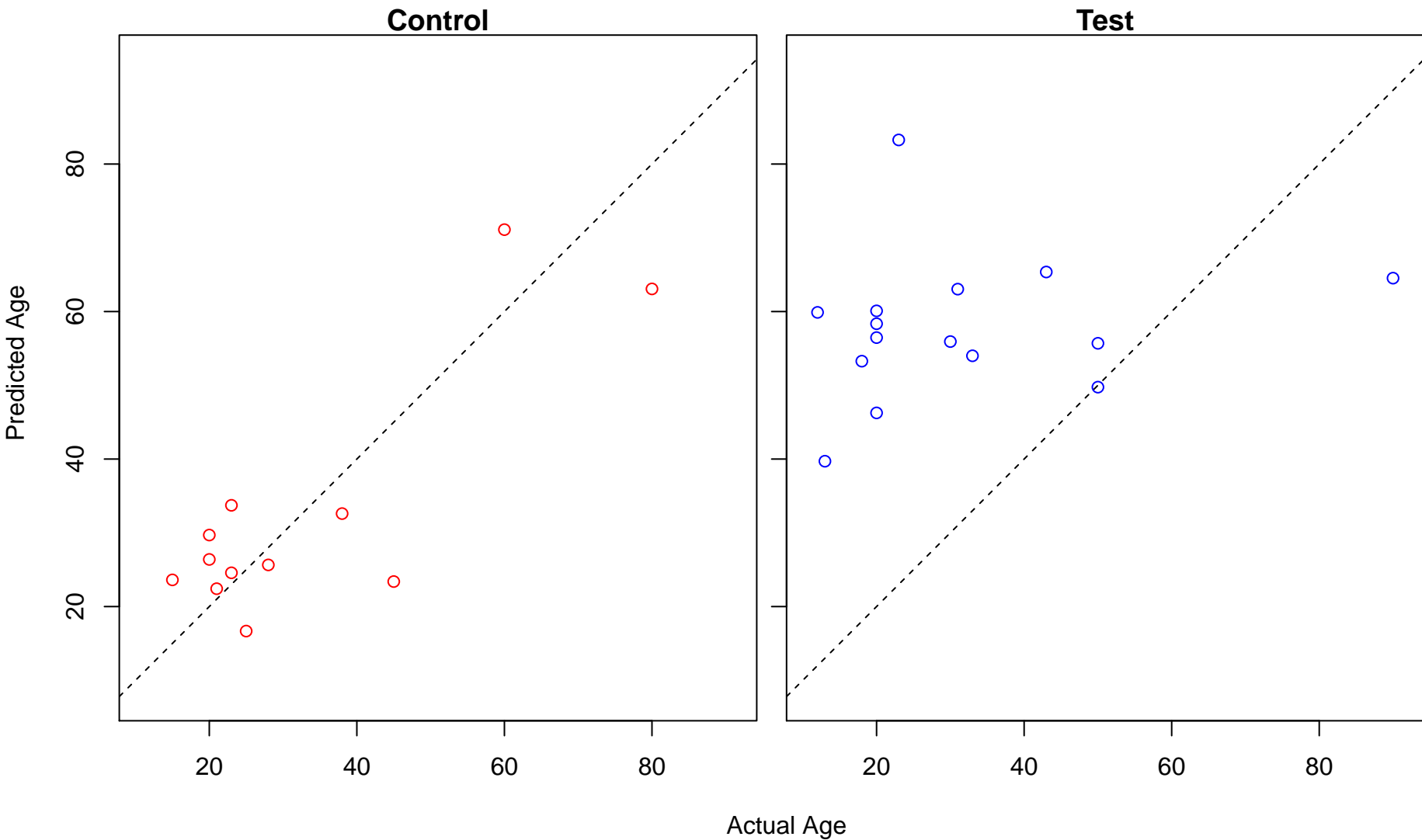
regulation of transcription elongation from RNA polymerase II promoter (Score: 3.762365)



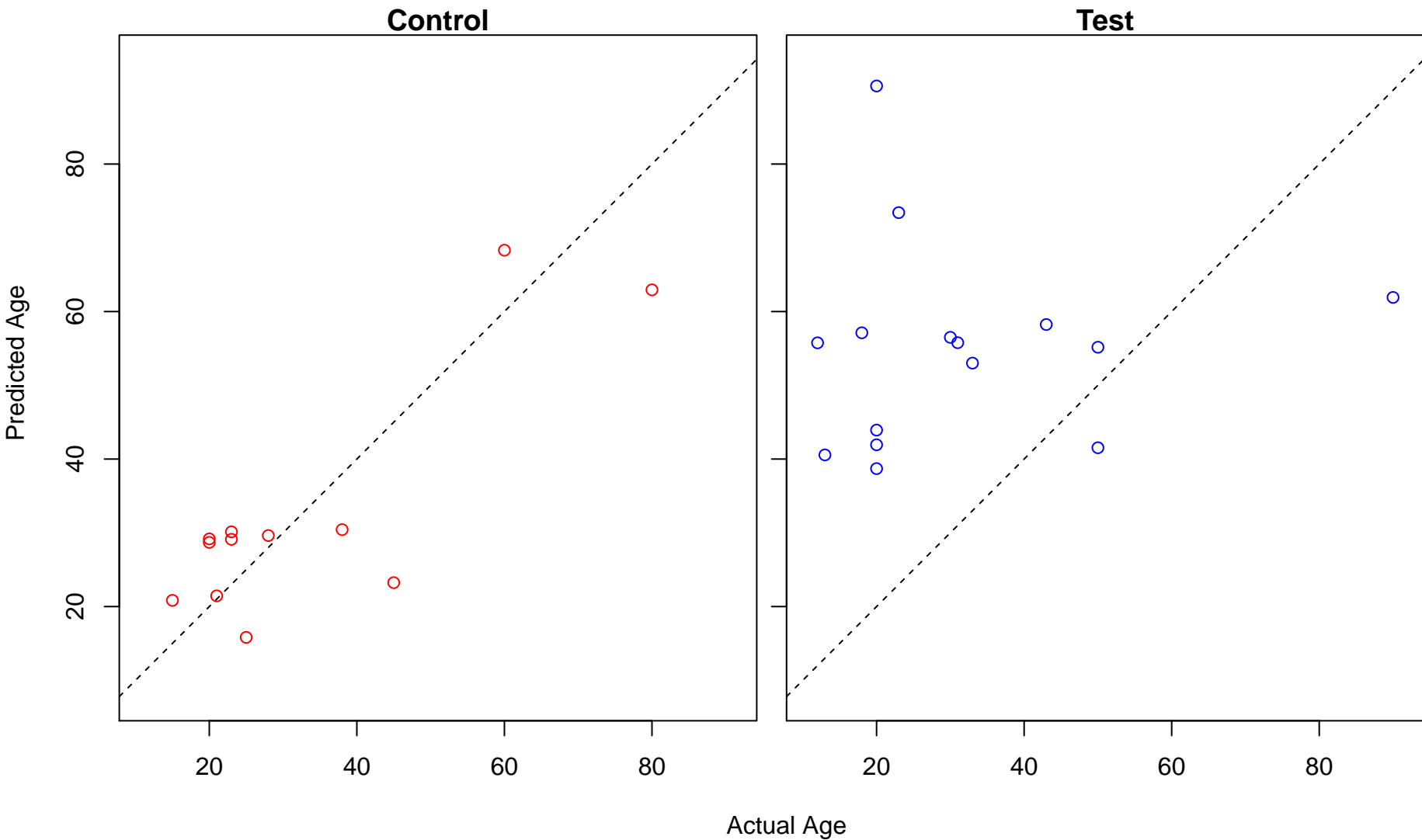
cortical cytoskeleton organization (Score: 3.759948)



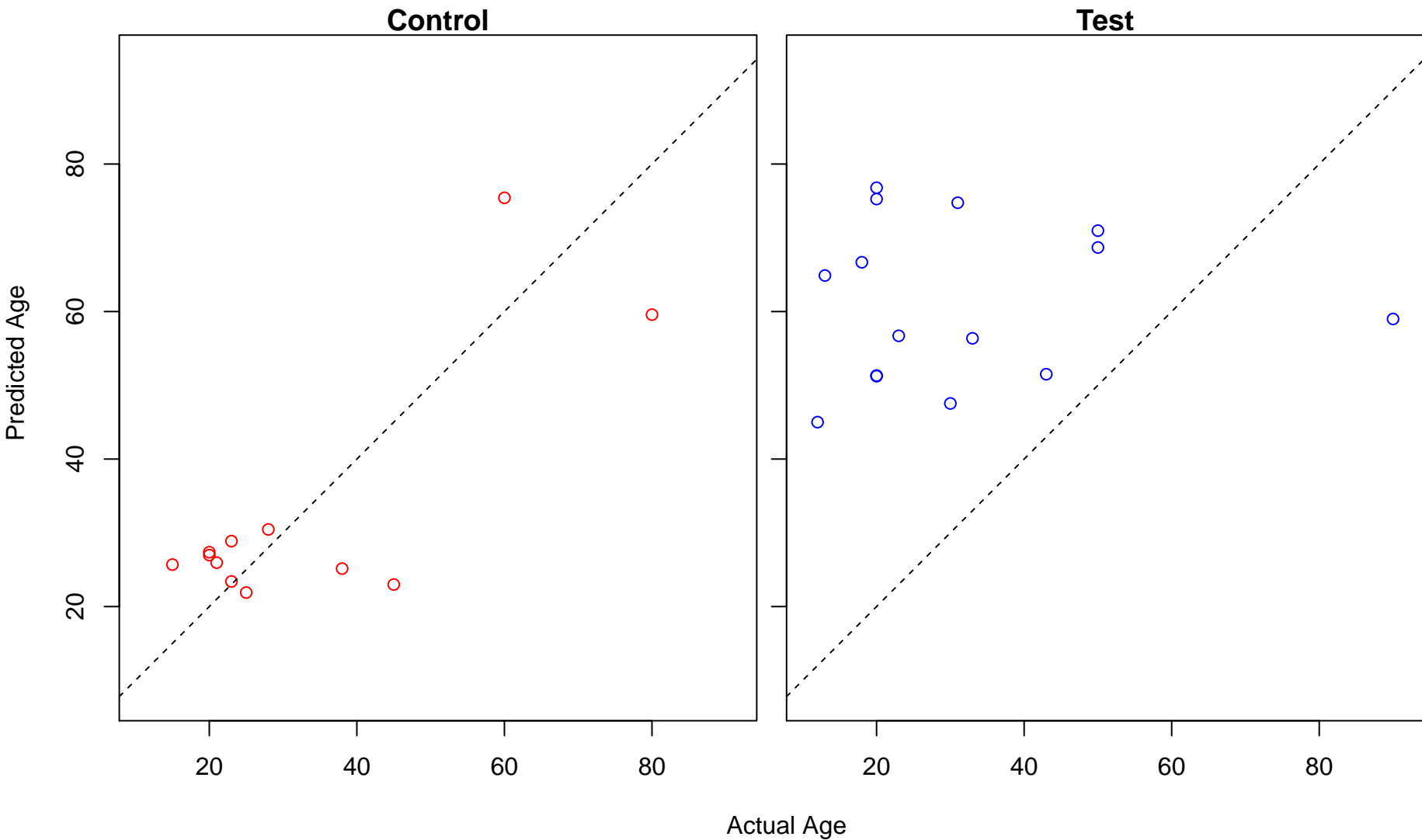
acrosome reaction (Score: 3.758491)



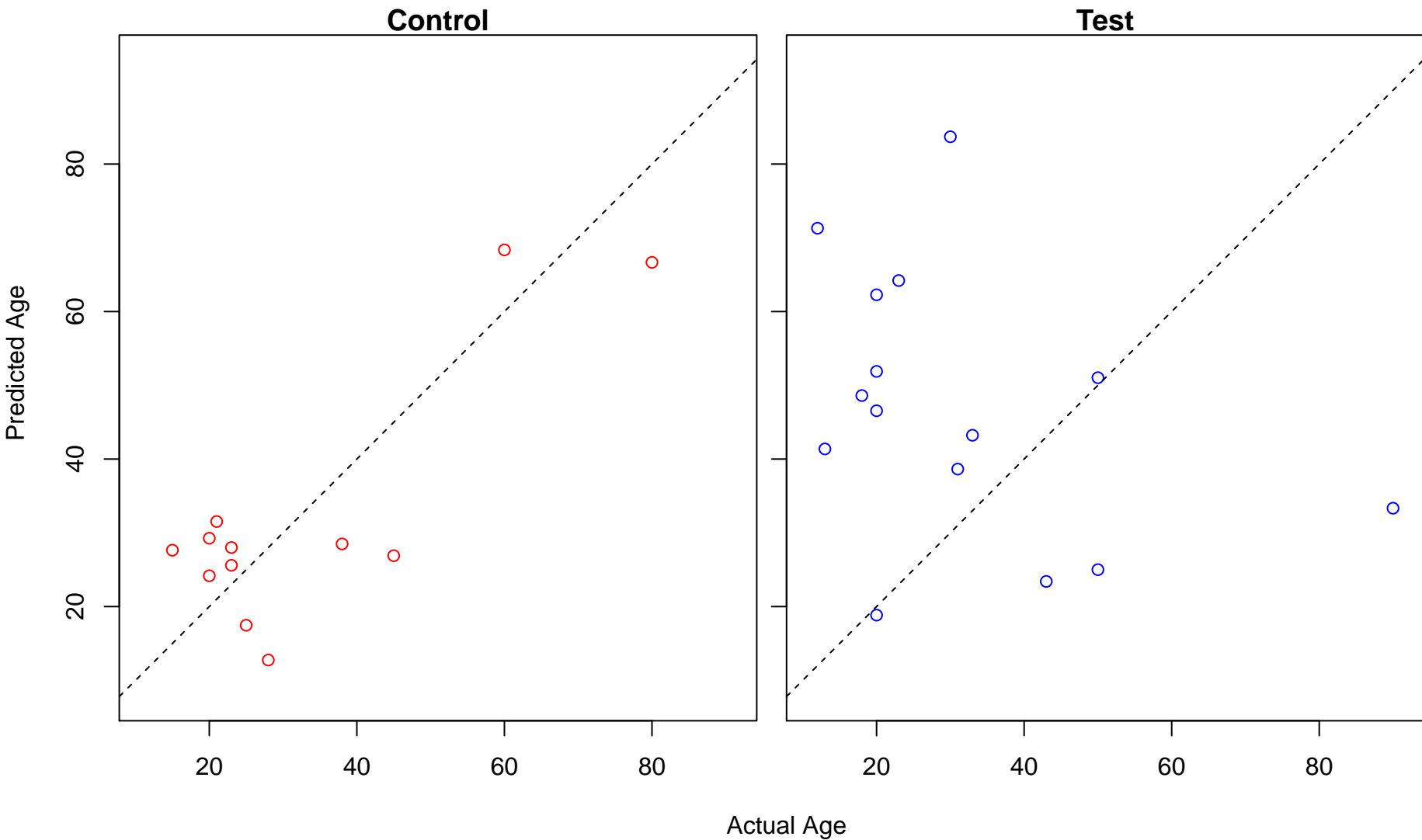
regulation of NLRP3 inflammasome complex assembly (Score: 3.758016)



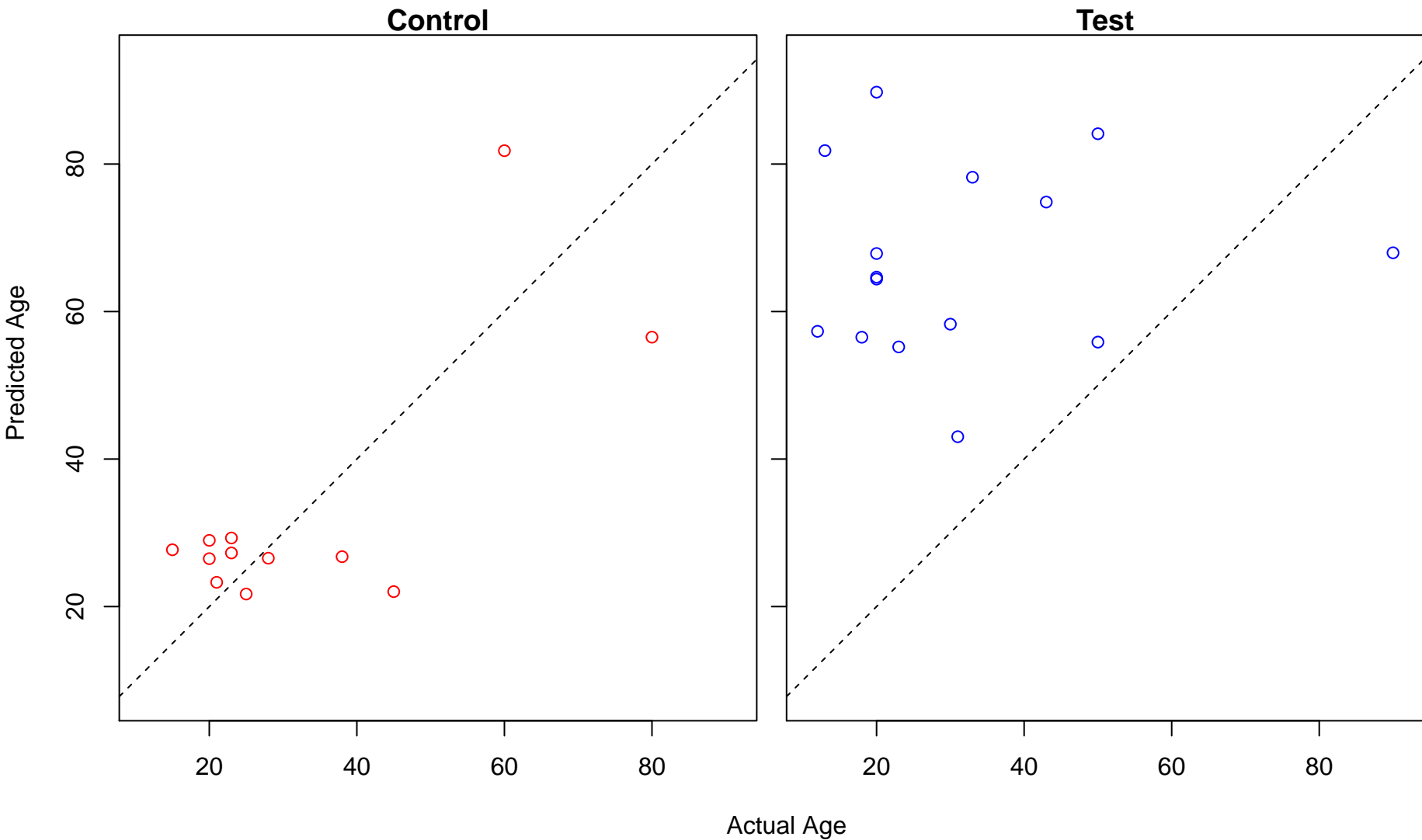
glycogen catabolic process (Score: 3.755267)



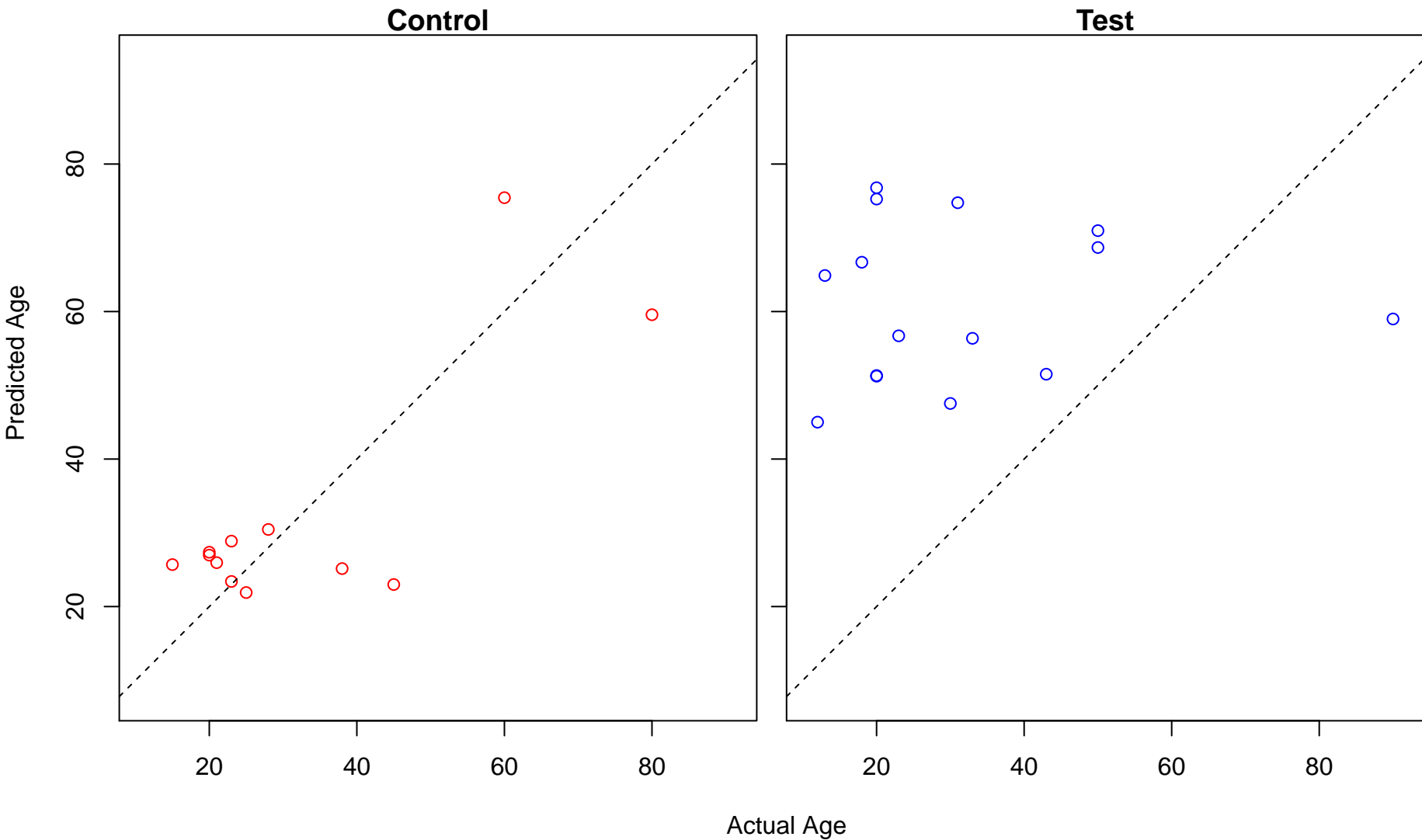
maintenance of organelle location (Score: 3.755097)



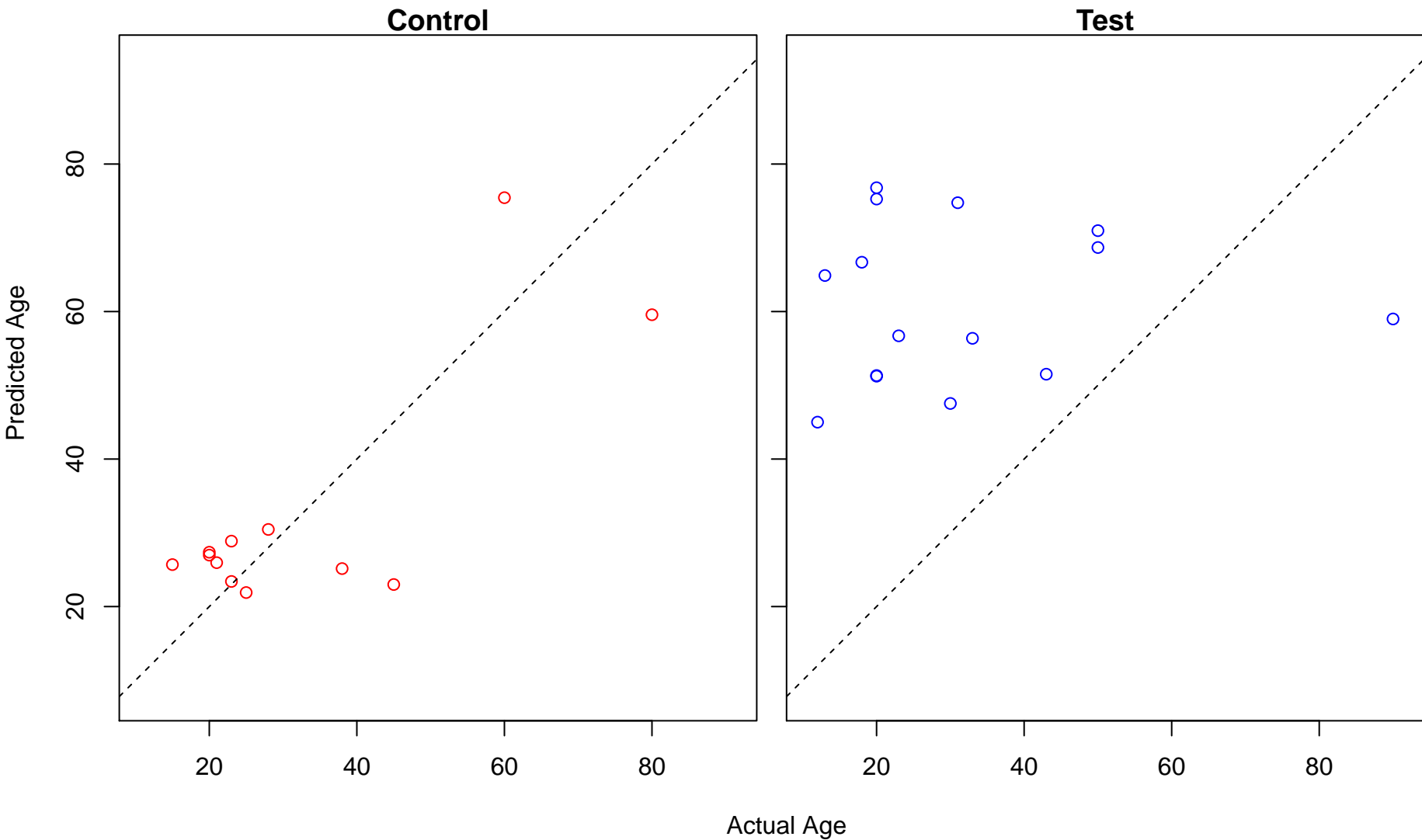
neuron maturation (Score: 3.753756)



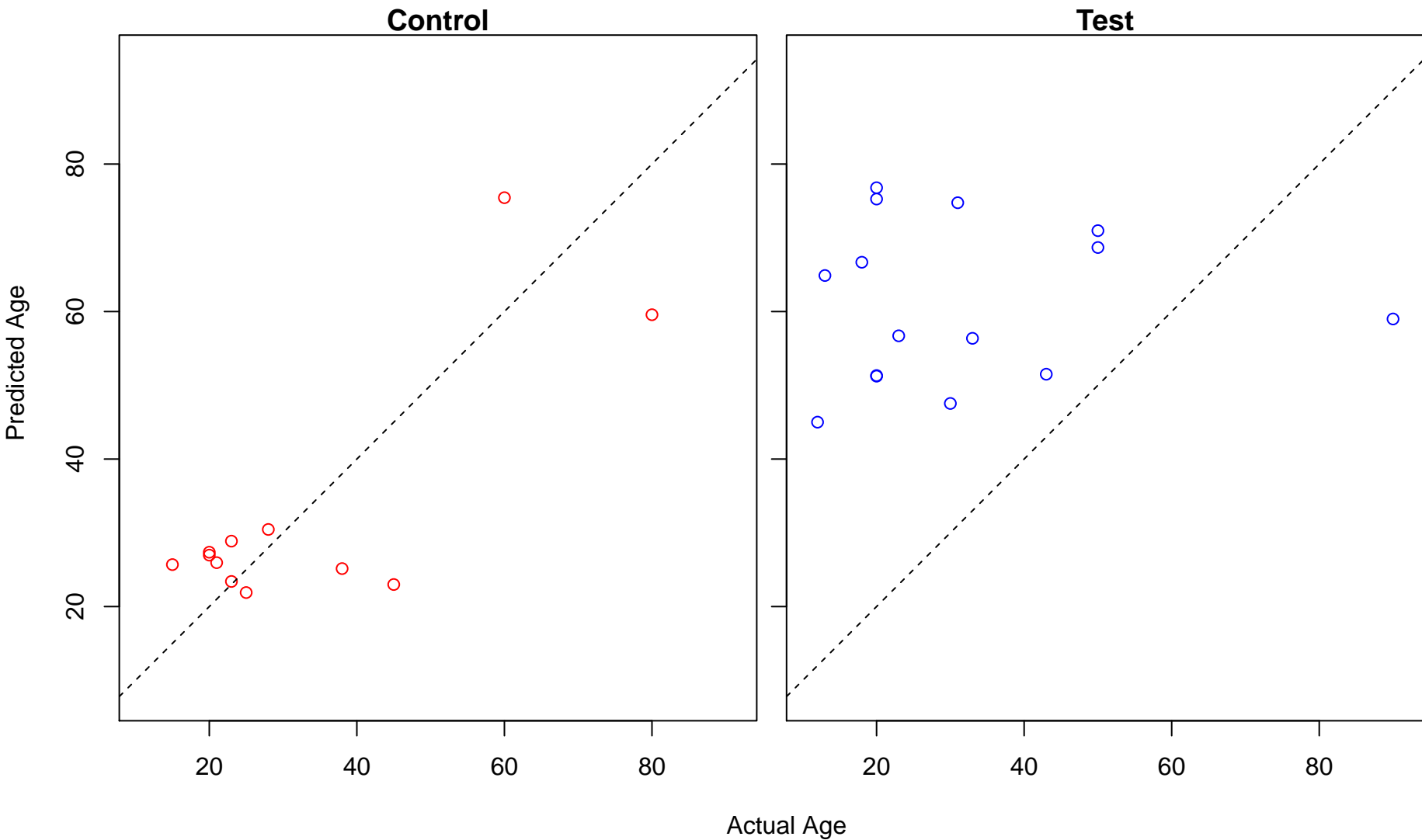
polysaccharide catabolic process (Score: 3.753707)



glucan catabolic process (Score: 3.753707)

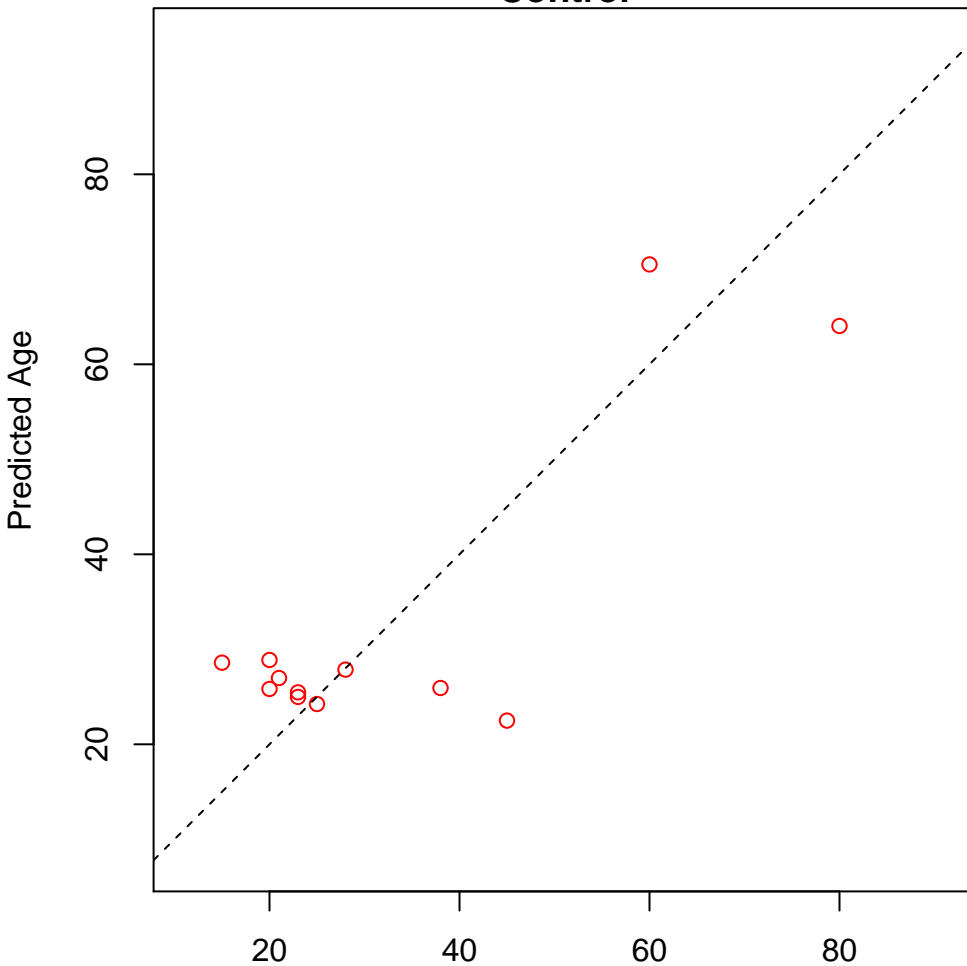


cellular polysaccharide catabolic process (Score: 3.753707)

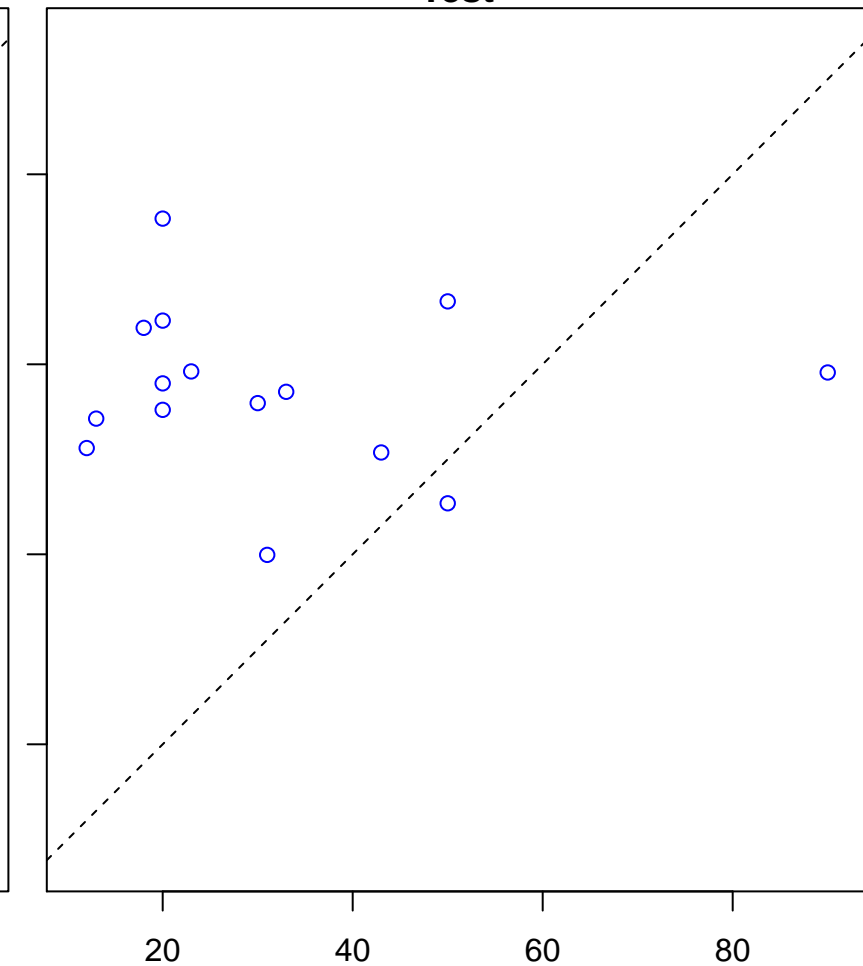


phosphatidic acid biosynthetic process (Score: 3.752625)

Control



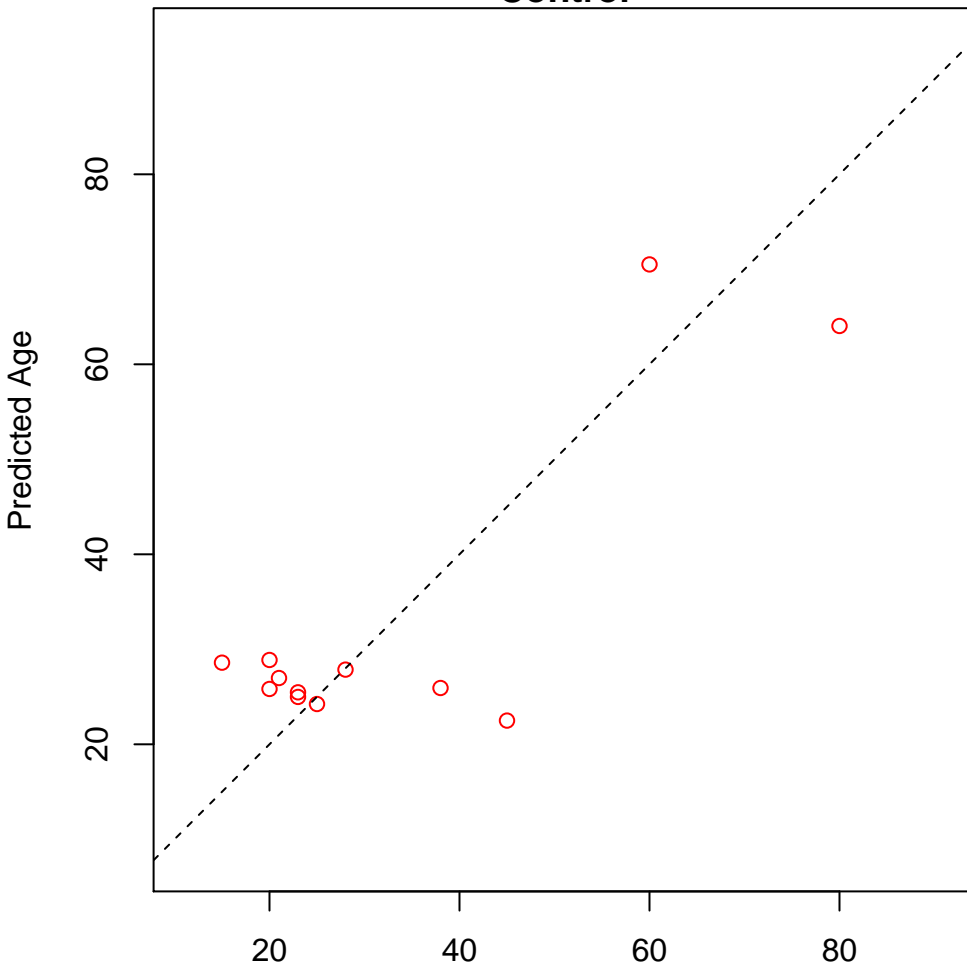
Test



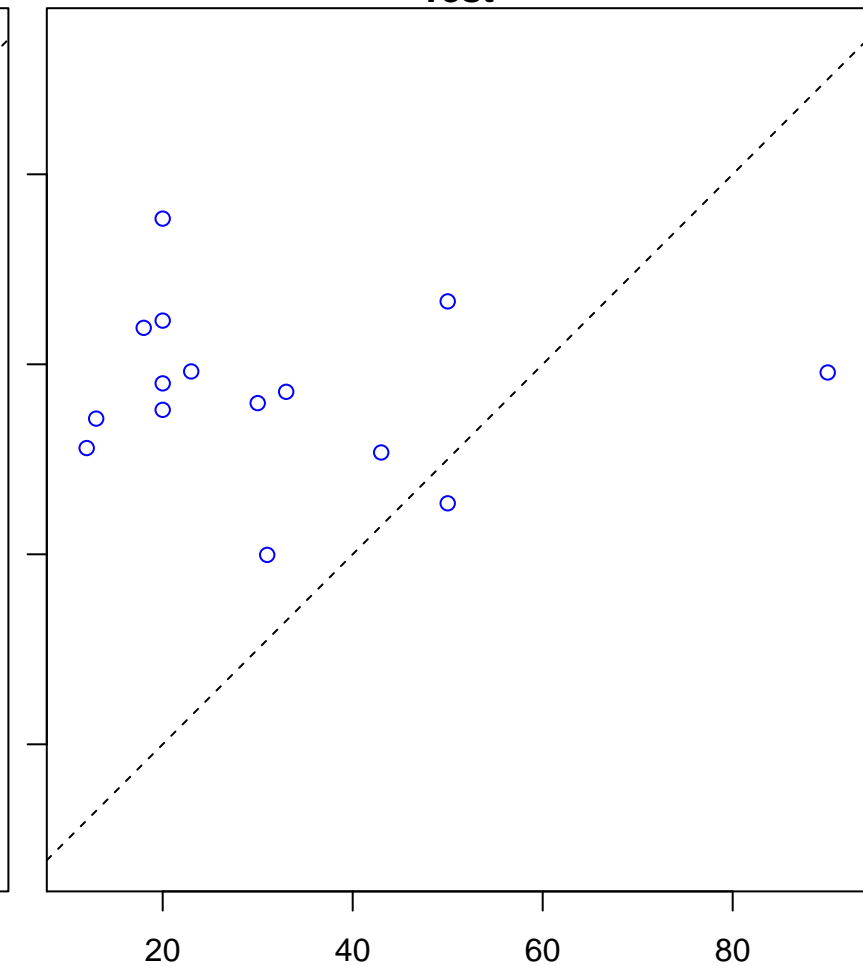
Actual Age

phosphatidic acid metabolic process (Score: 3.752625)

Control

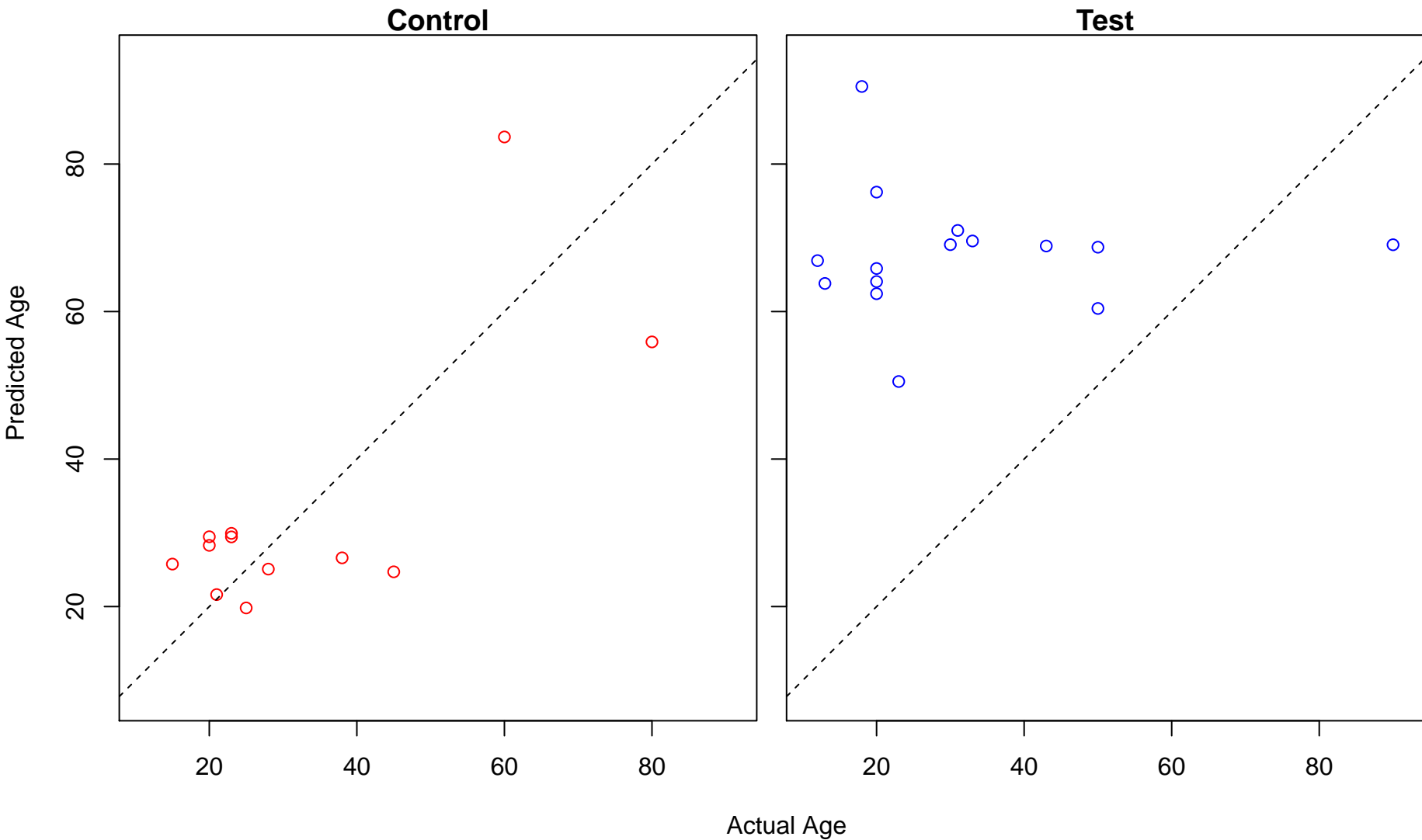


Test

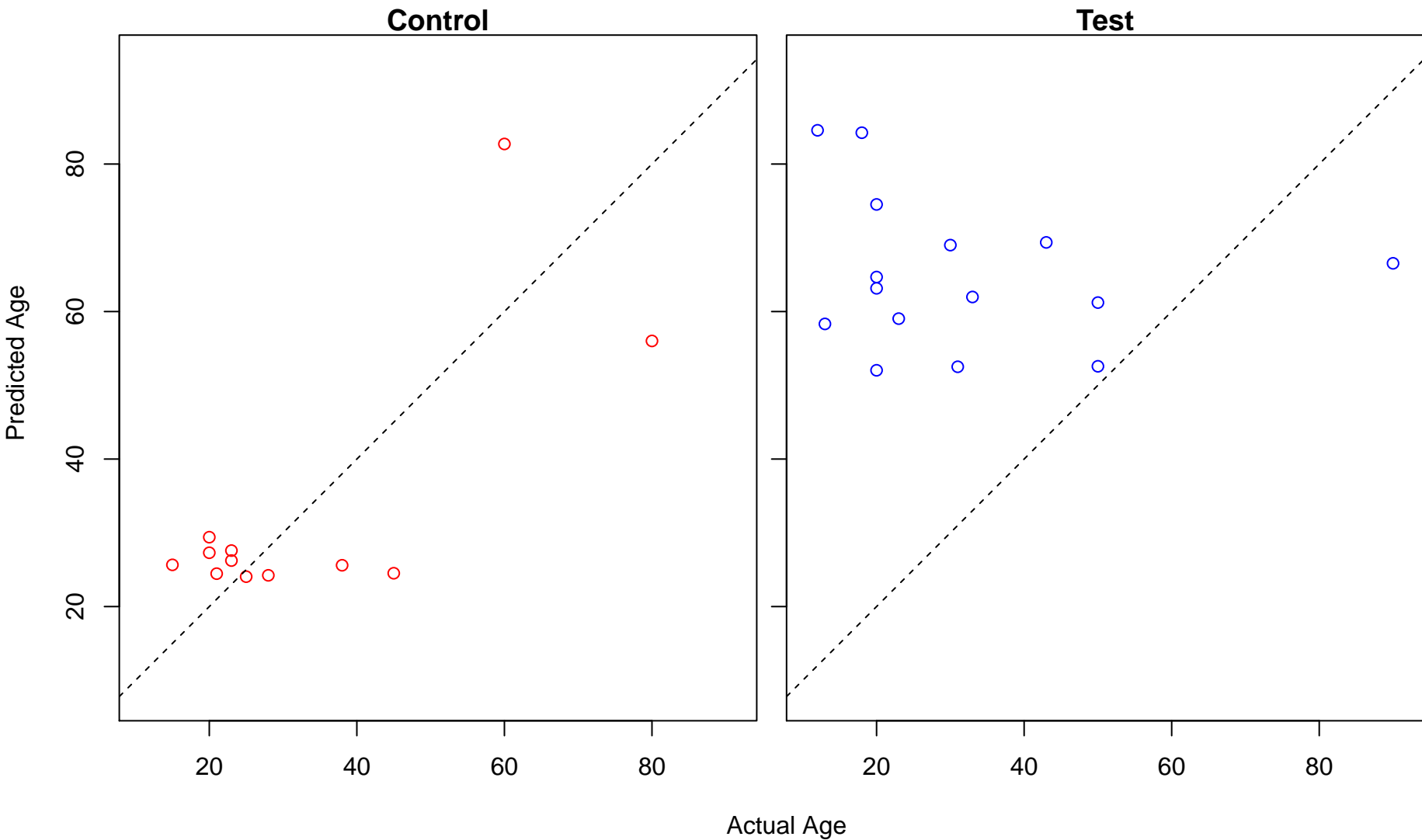


Actual Age

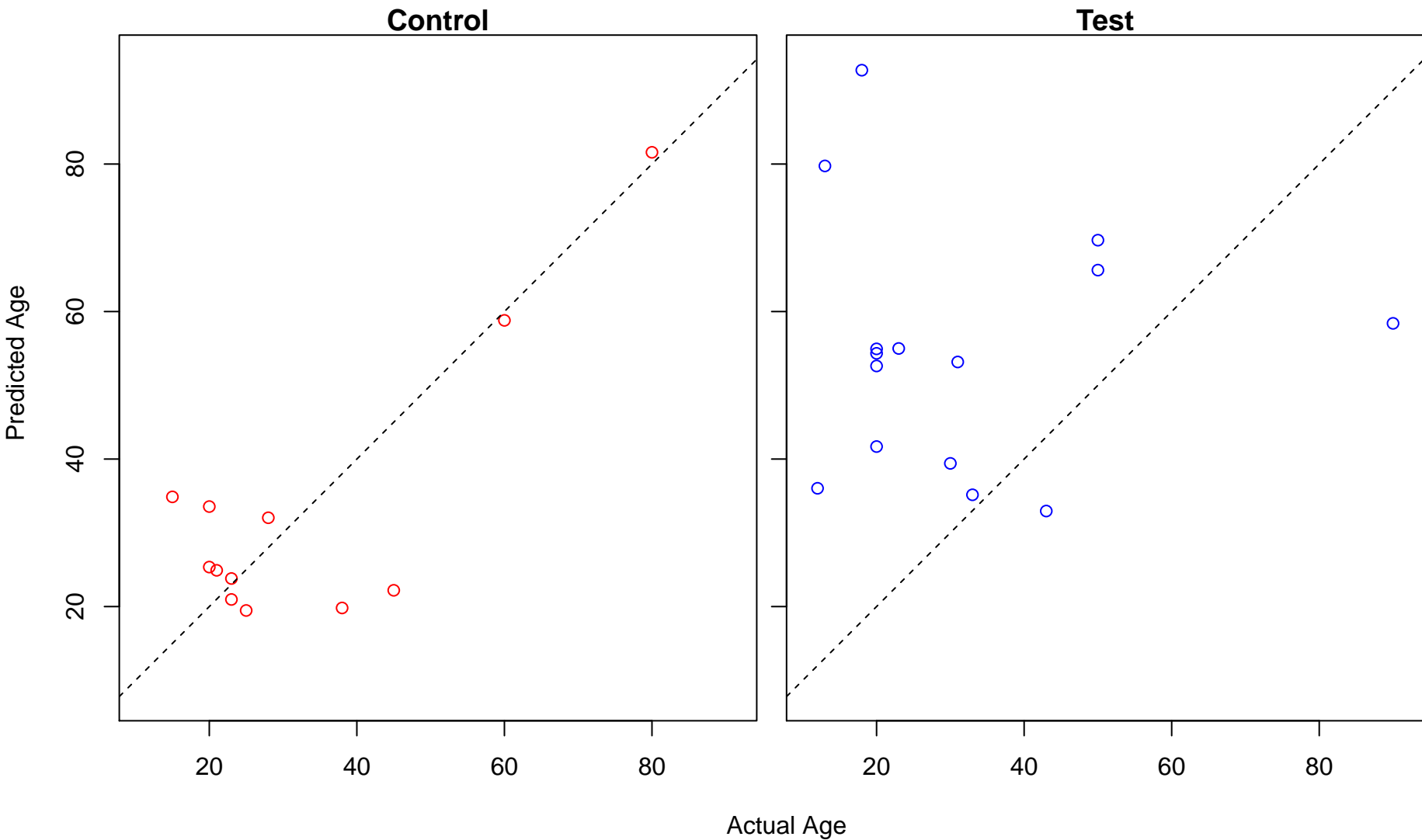
mitochondrial DNA replication (Score: 3.748765)



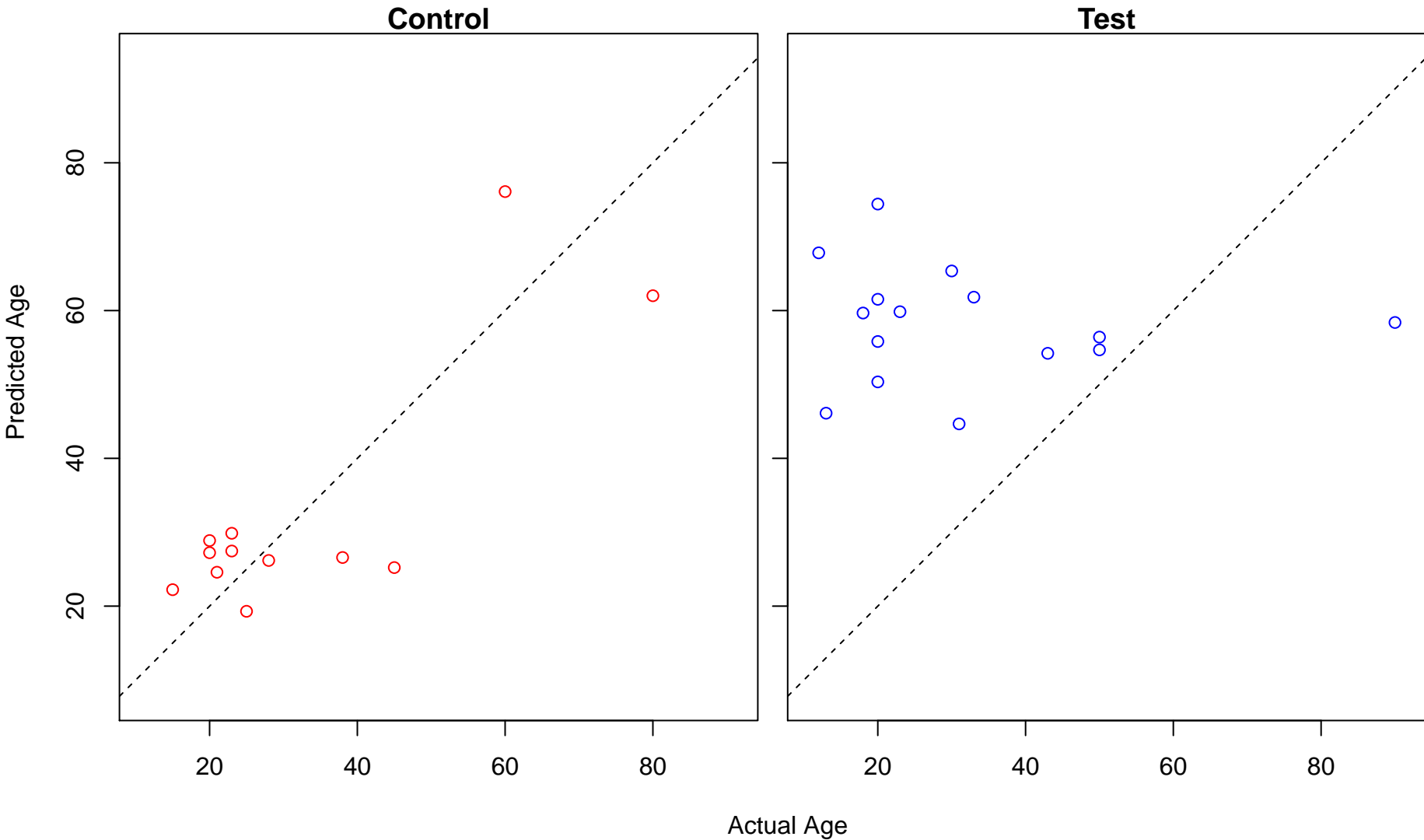
UDP-glucose metabolic process (Score: 3.743943)



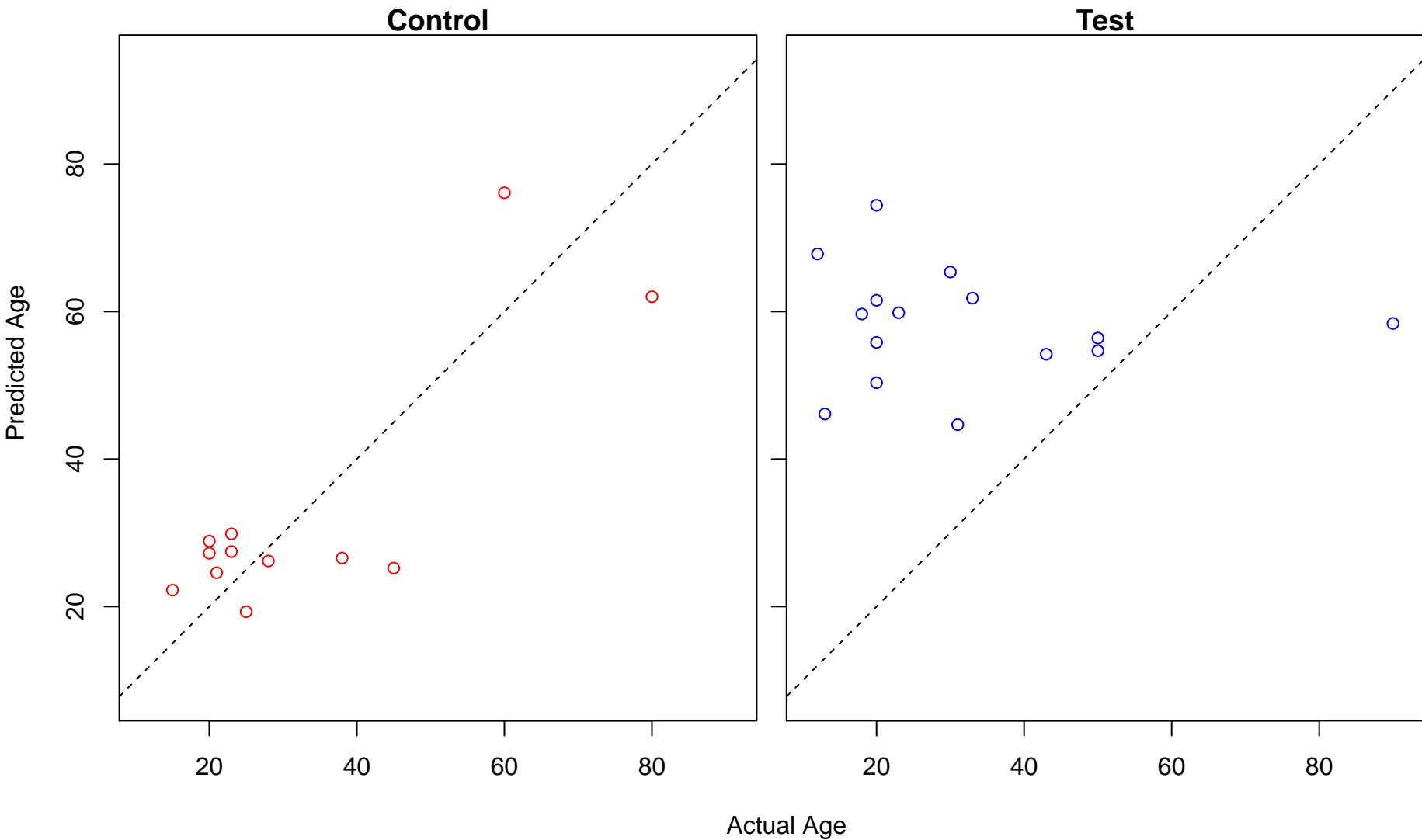
nucleotide phosphorylation (Score: 3.743058)



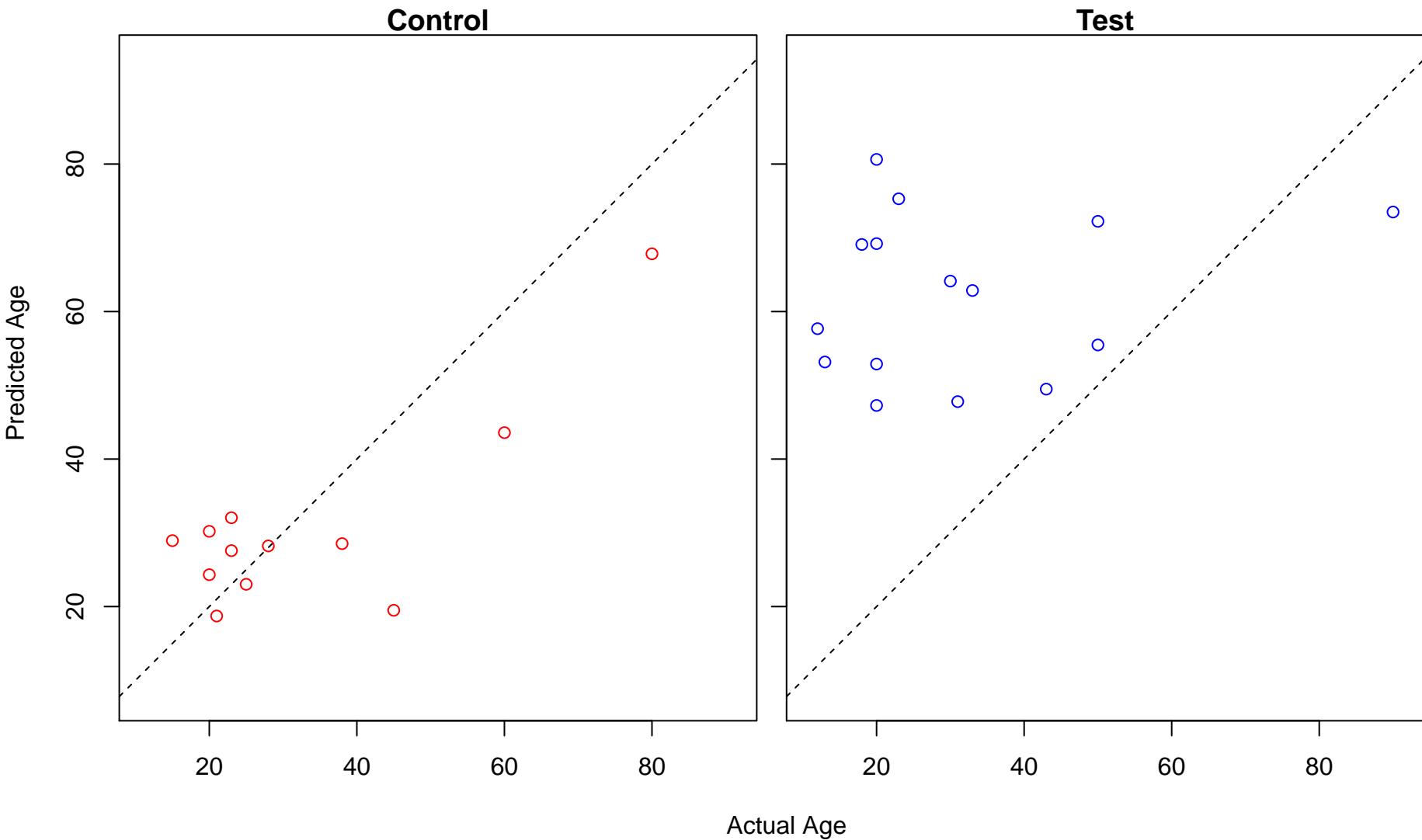
regulation of protein localization to synapse (Score: 3.739900)



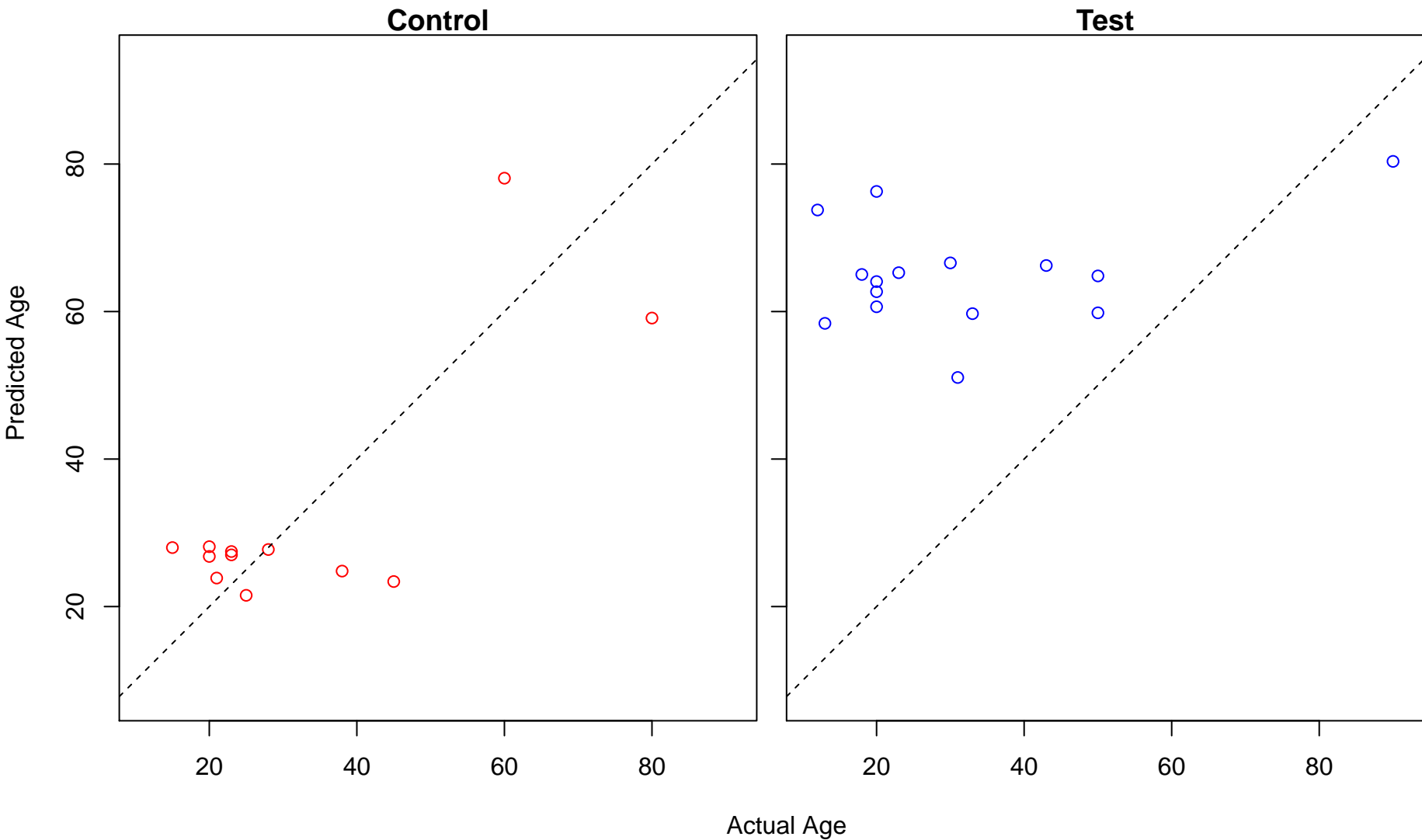
positive regulation of protein localization to synapse (Score: 3.739900)



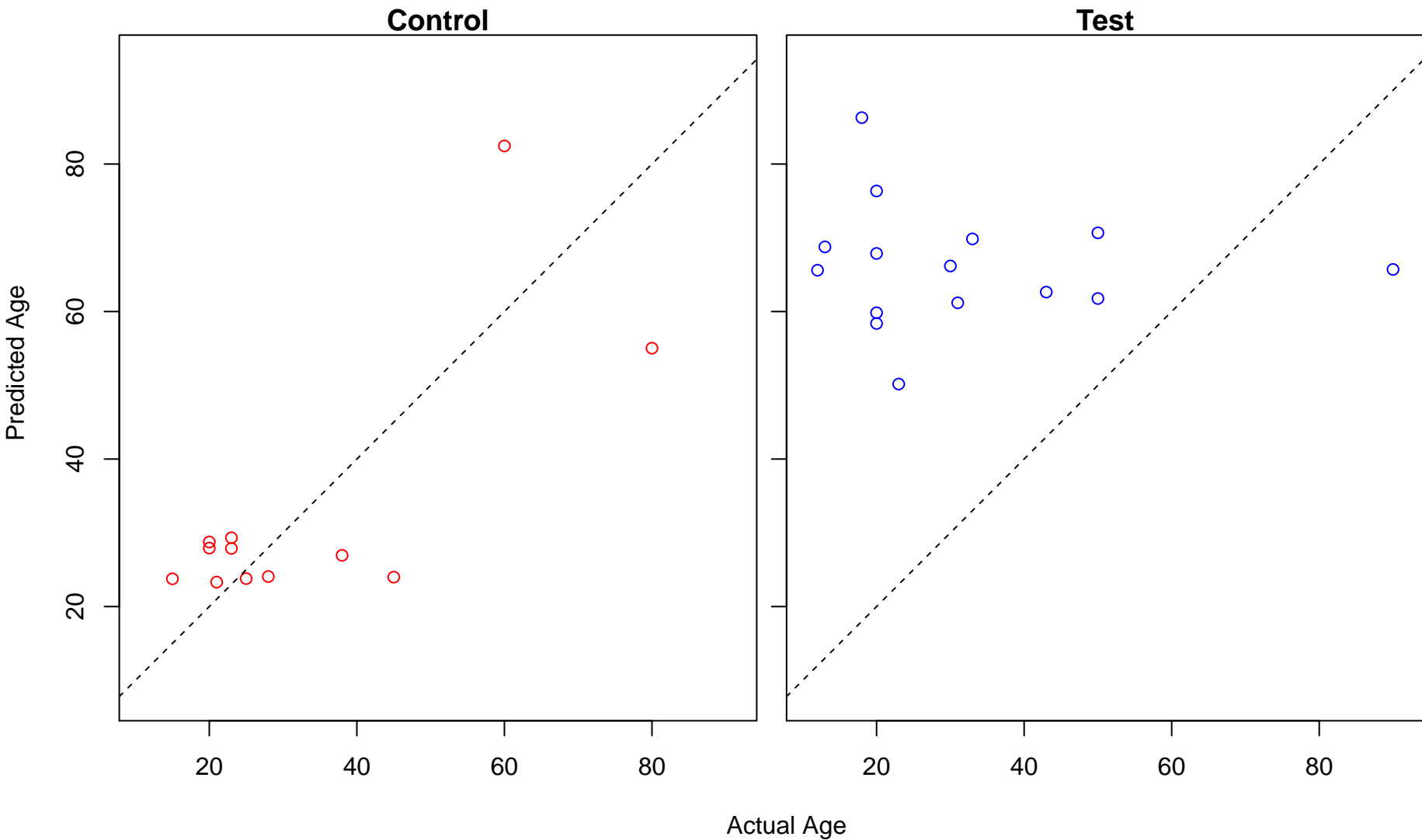
regulation of neurological system process (Score: 3.739663)



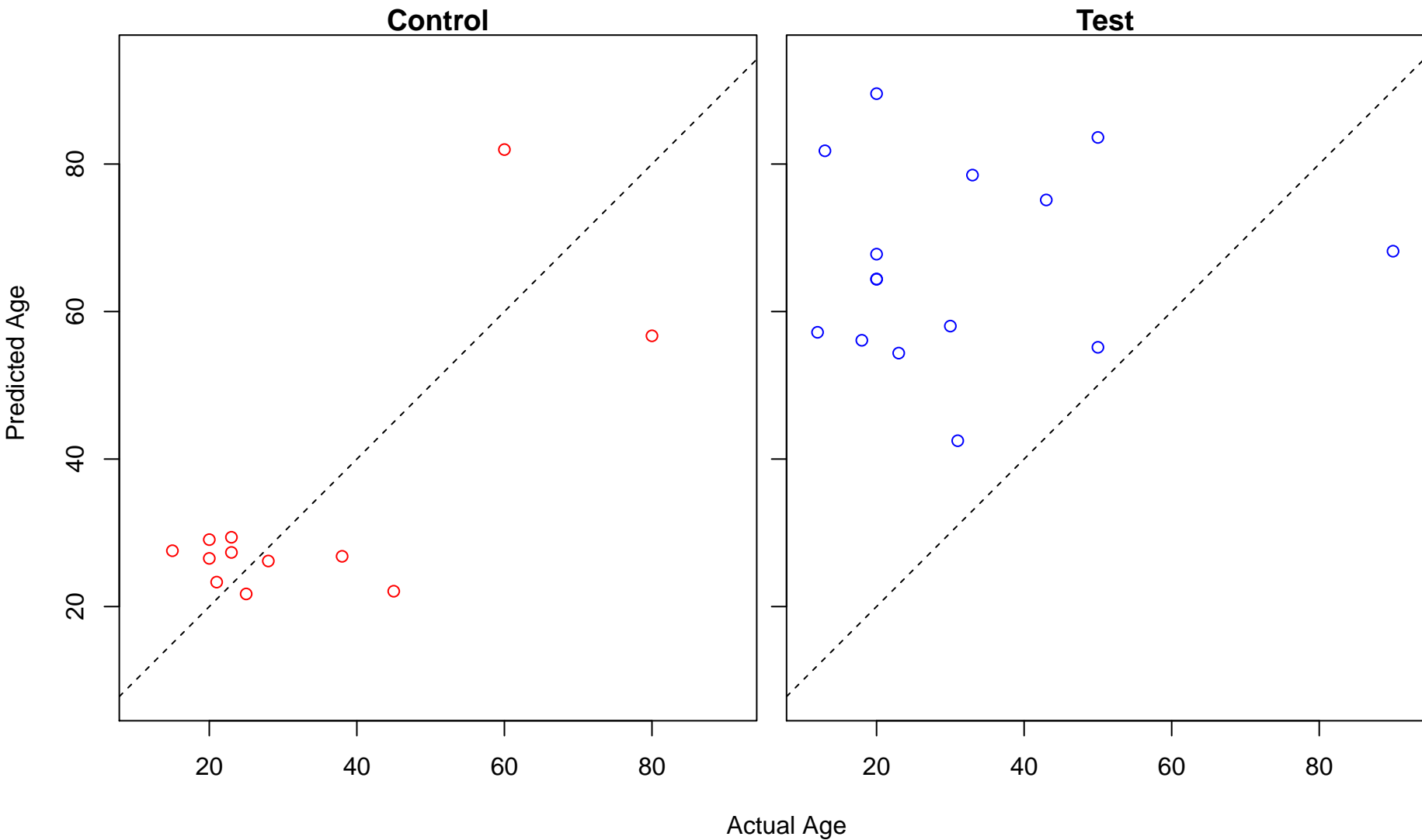
regulation of the force of heart contraction (Score: 3.739227)



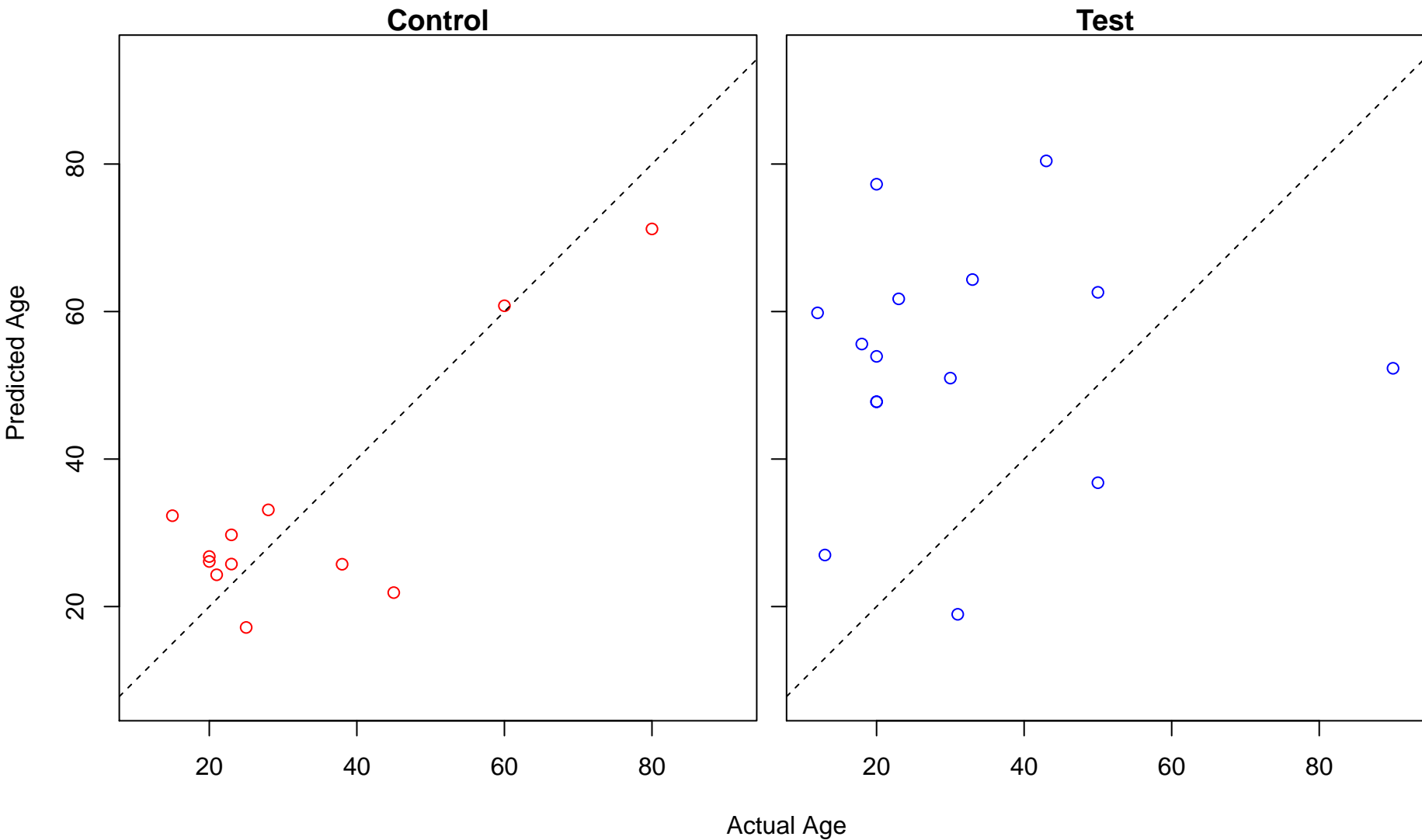
B cell differentiation (Score: 3.734381)



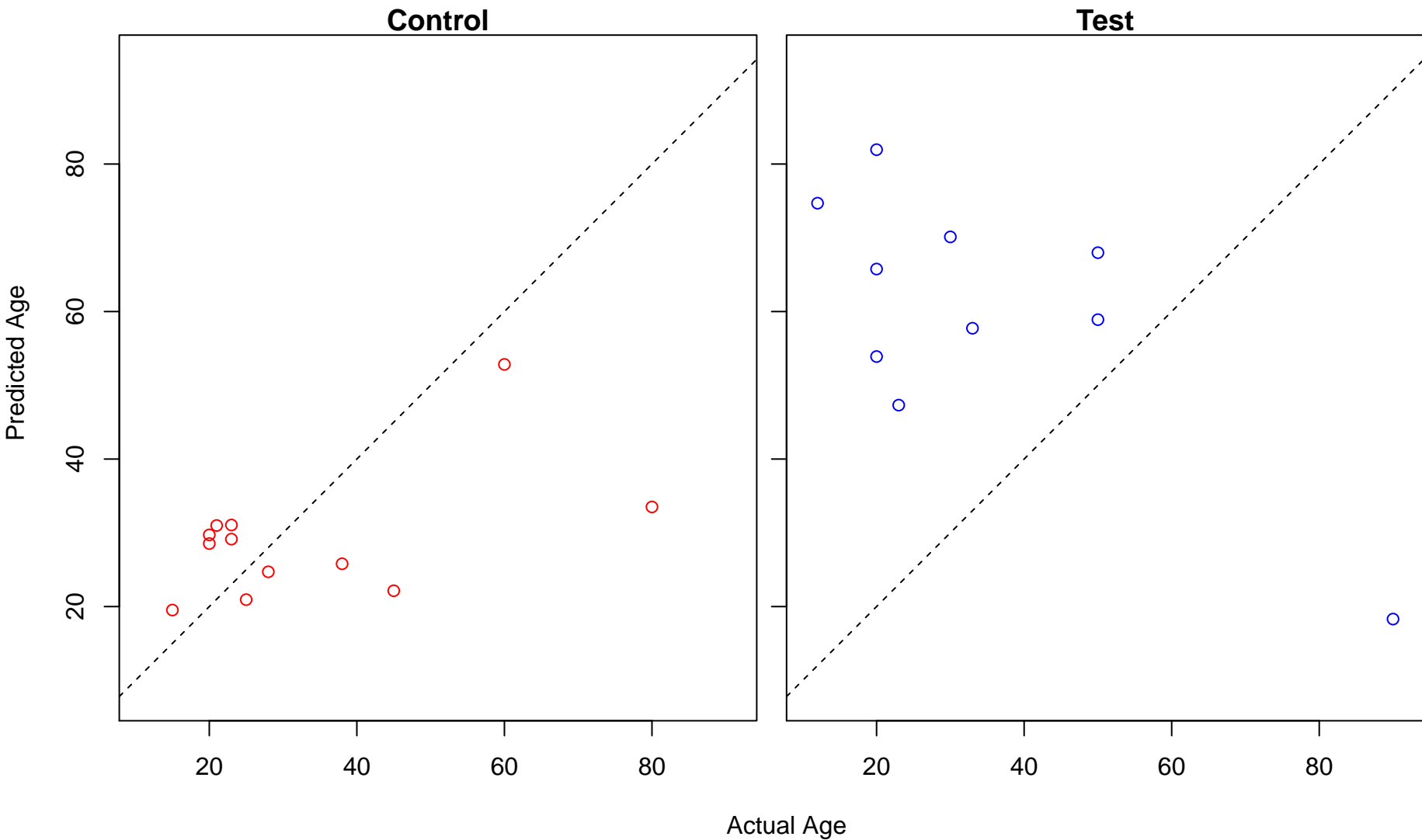
neuron remodeling (Score: 3.733334)



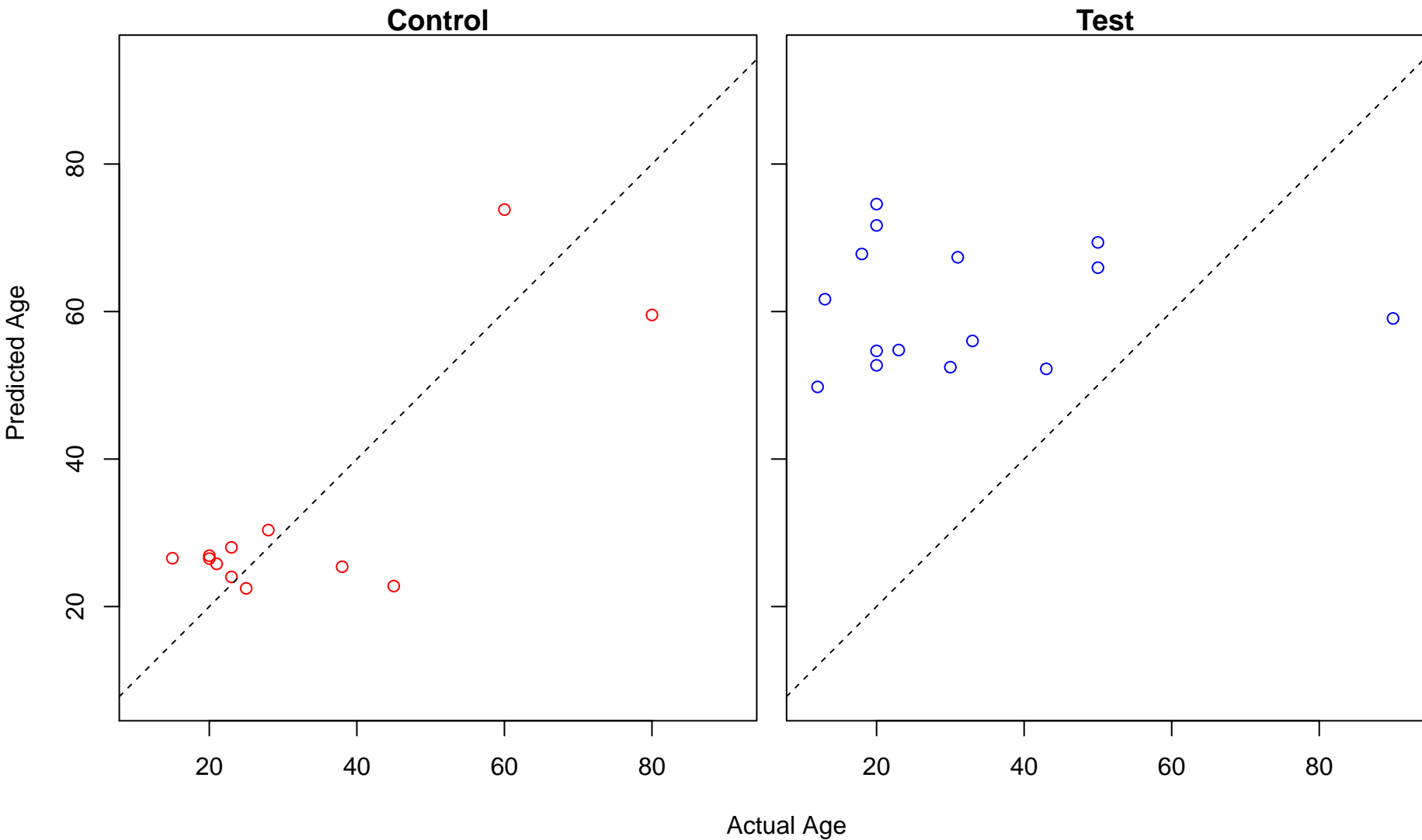
regulation of stem cell proliferation (Score: 3.726703)



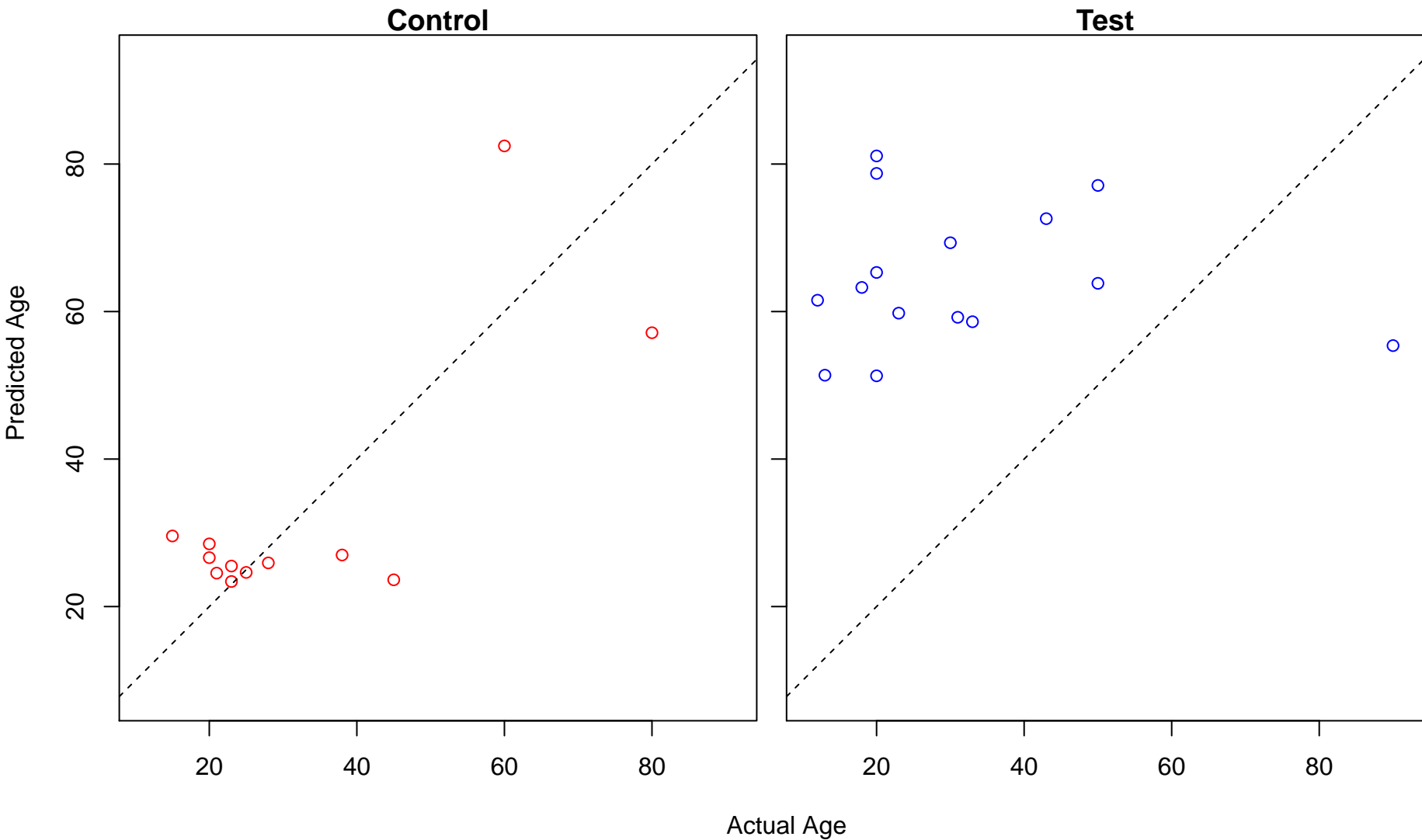
G-protein coupled purinergic receptor signaling pathway (Score: 3.726591)



regulation of phosphoprotein phosphatase activity (Score: 3.726427)

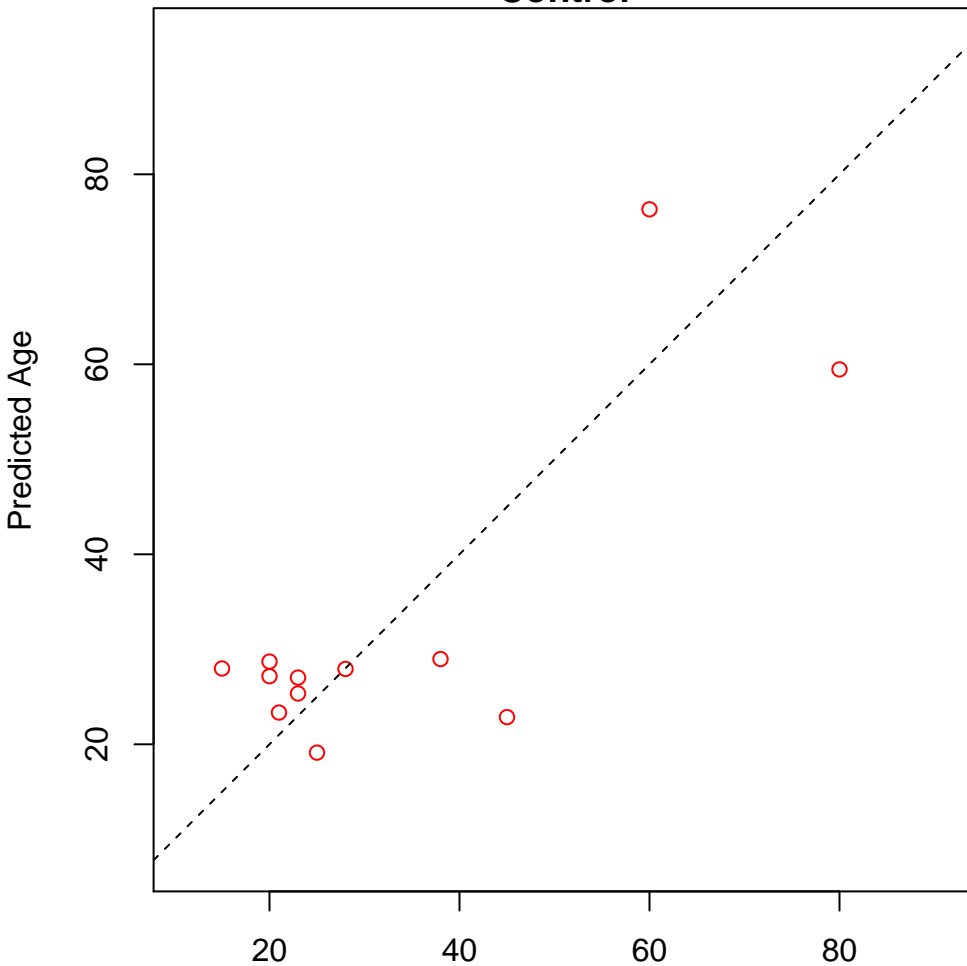


coenzyme catabolic process (Score: 3.725915)

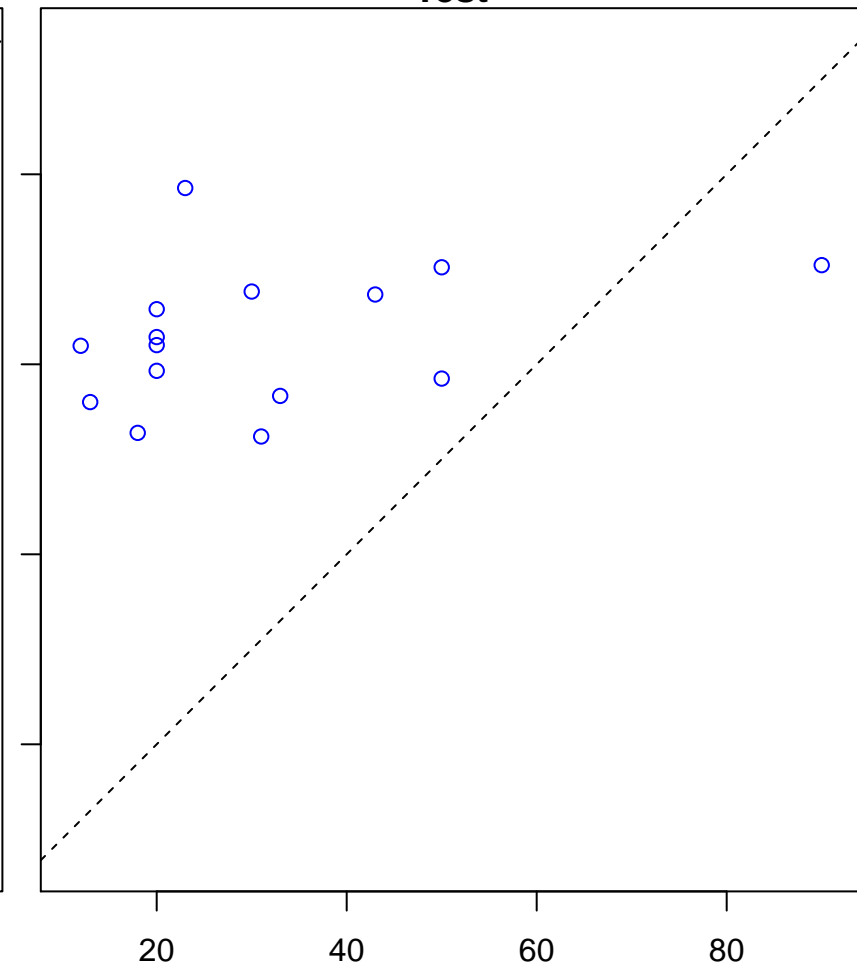


response to purine-containing compound (Score: 3.722547)

Control



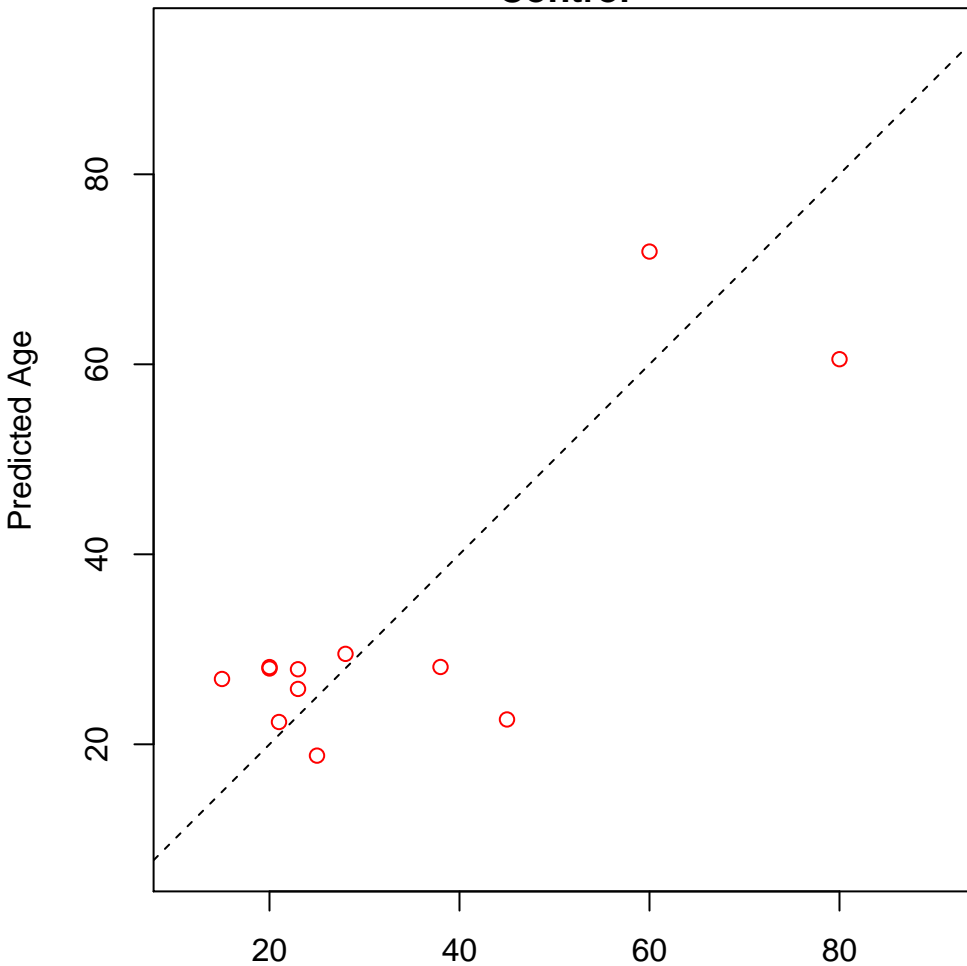
Test



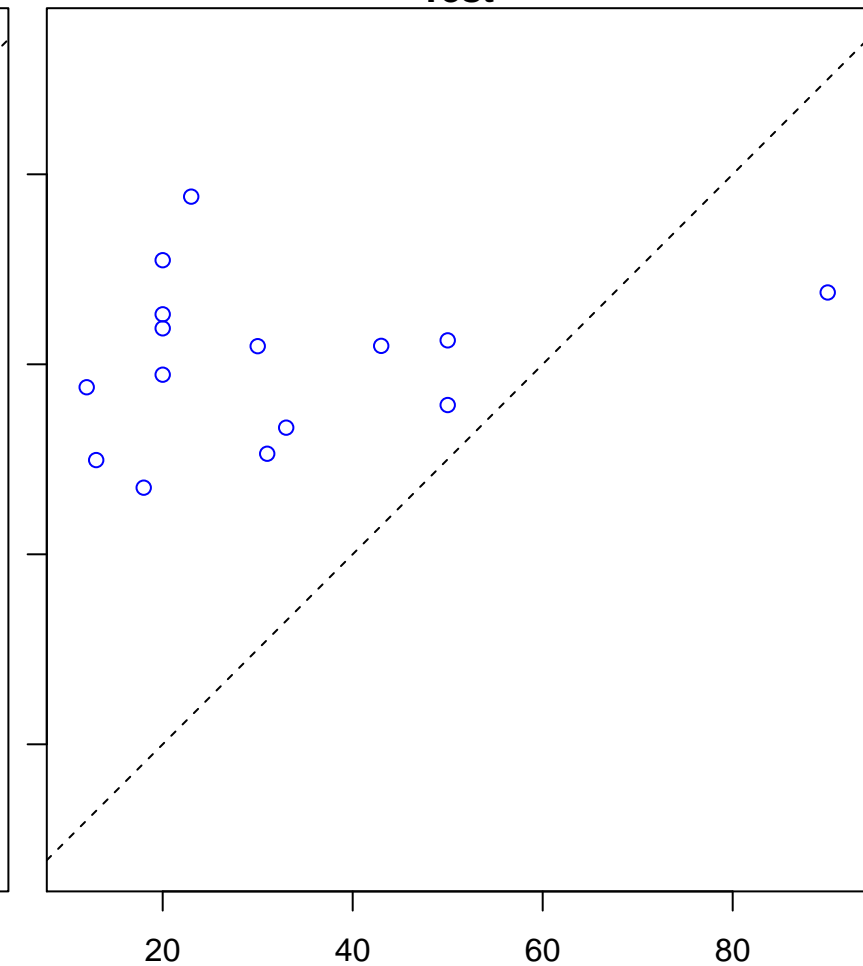
Actual Age

regulation of humoral immune response (Score: 3.722503)

Control

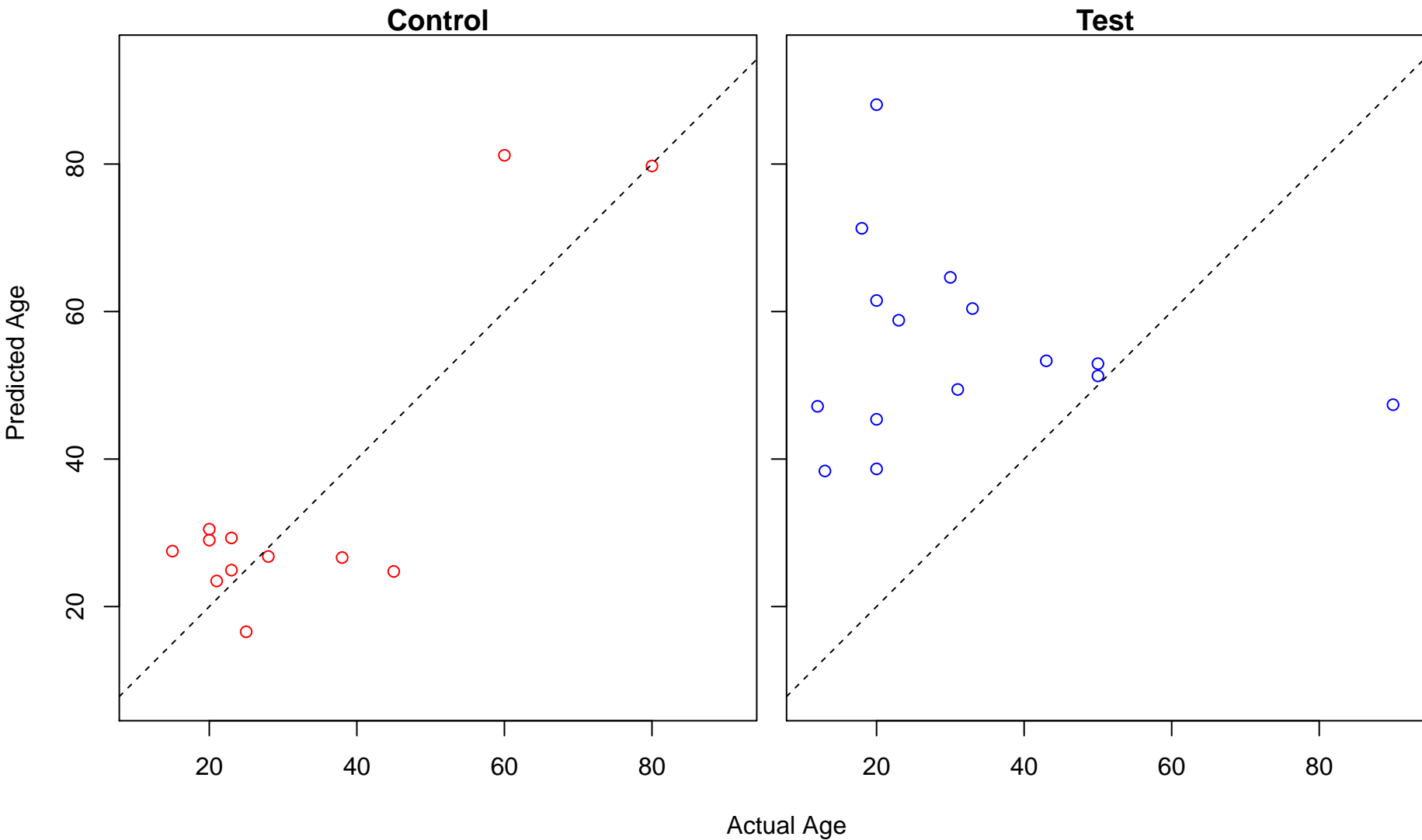


Test

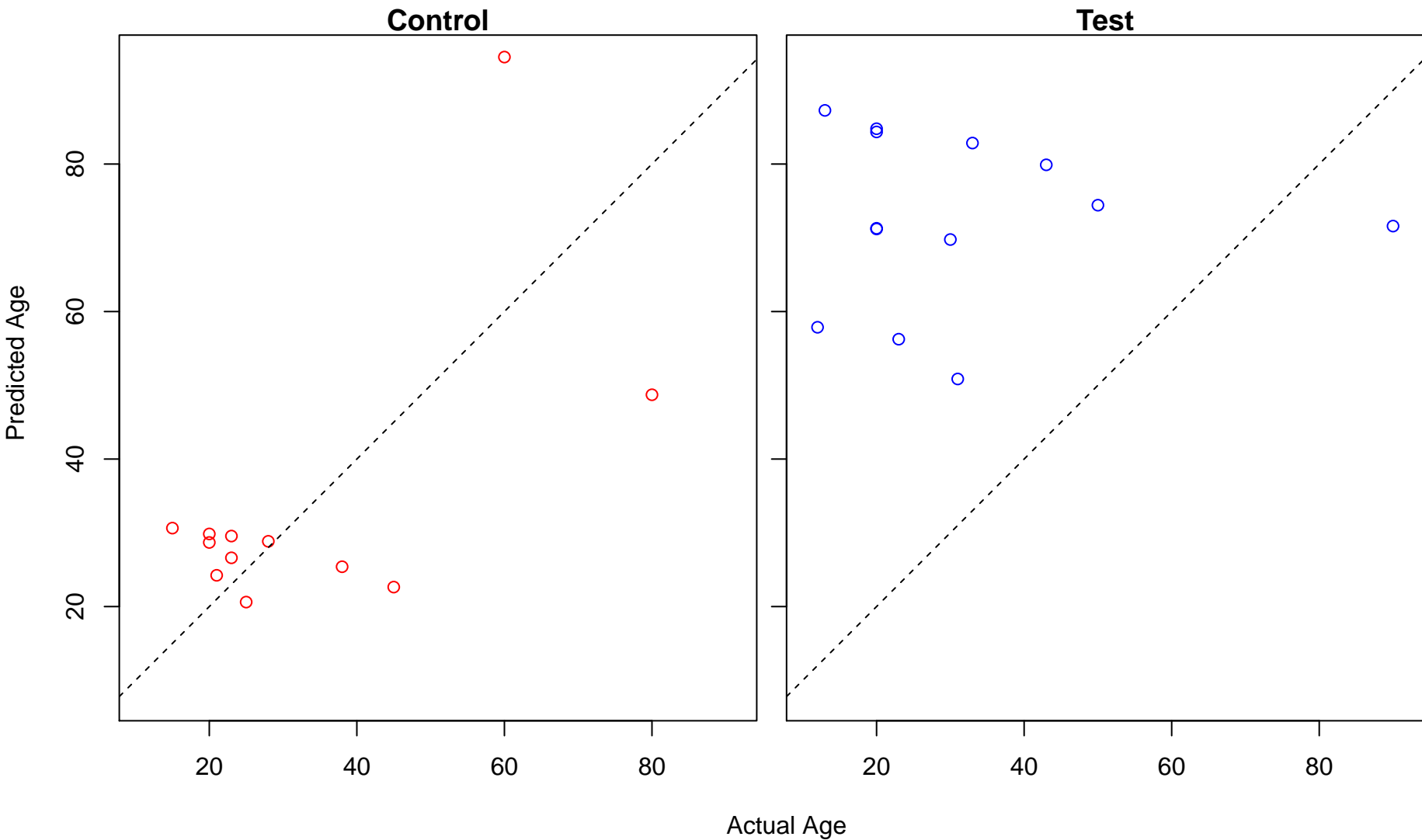


Actual Age

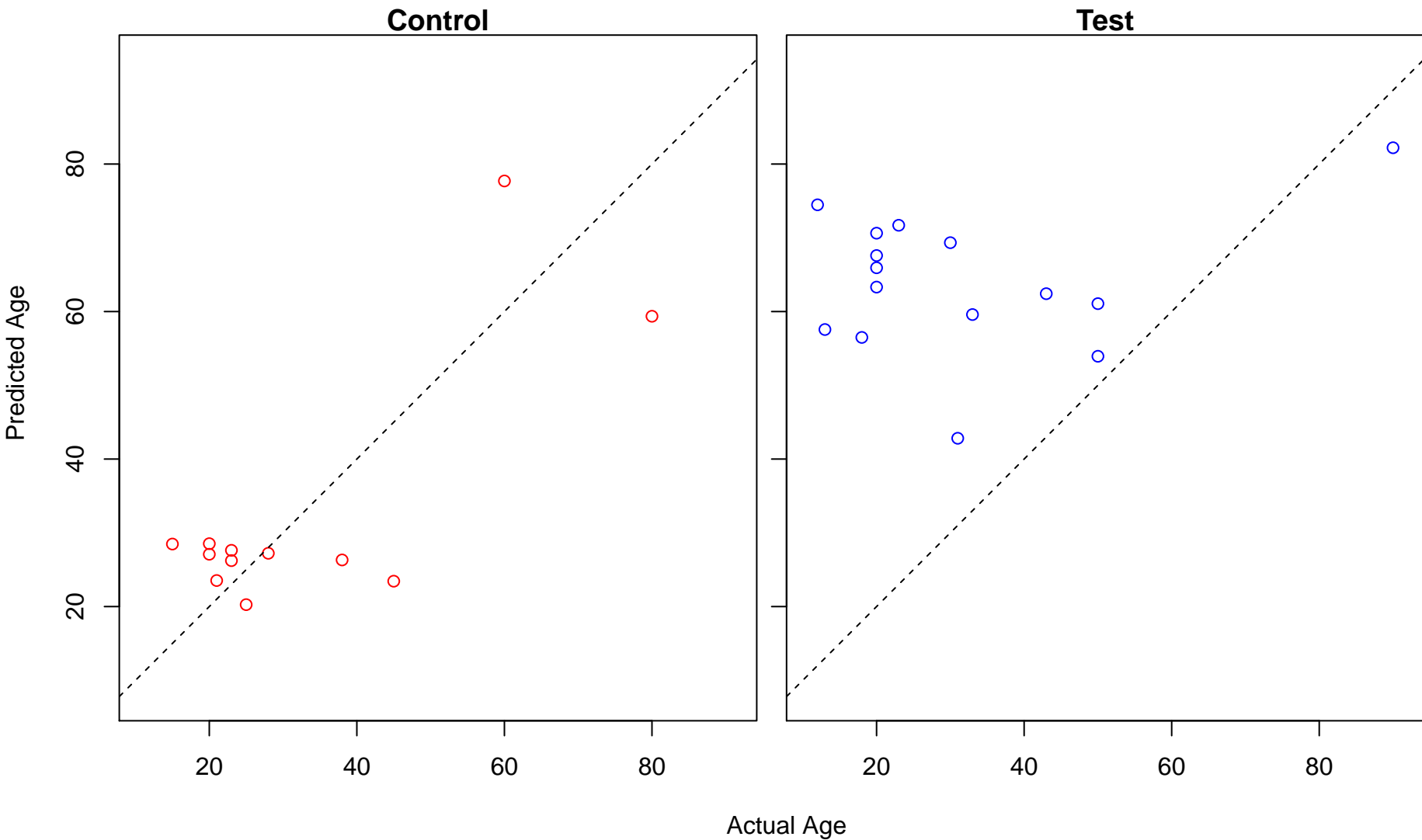
protein-lipid complex subunit organization (Score: 3.722257)



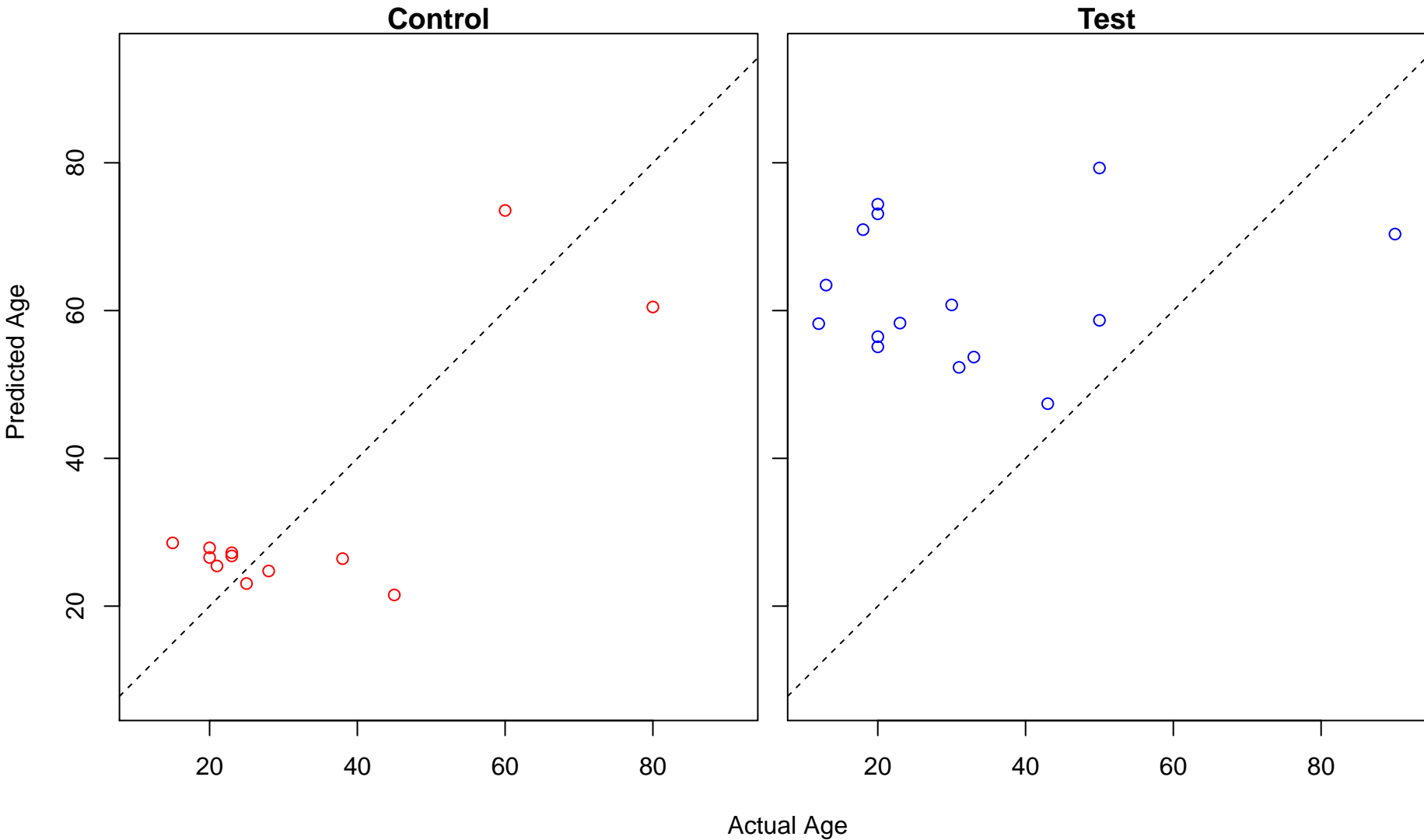
response to vitamin D (Score: 3.722104)



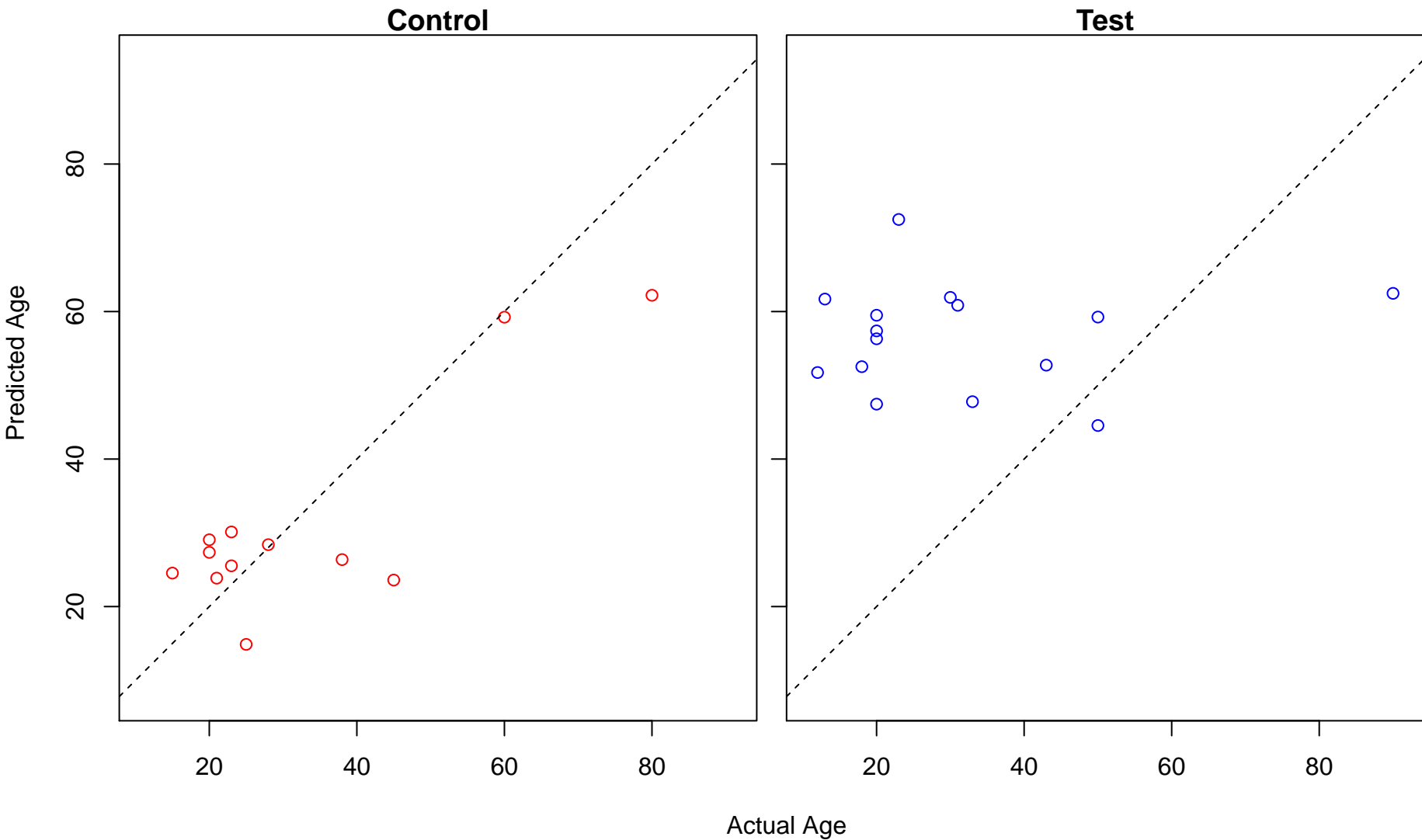
negative regulation of sodium ion transmembrane transporter activity (Score: 3.719273)



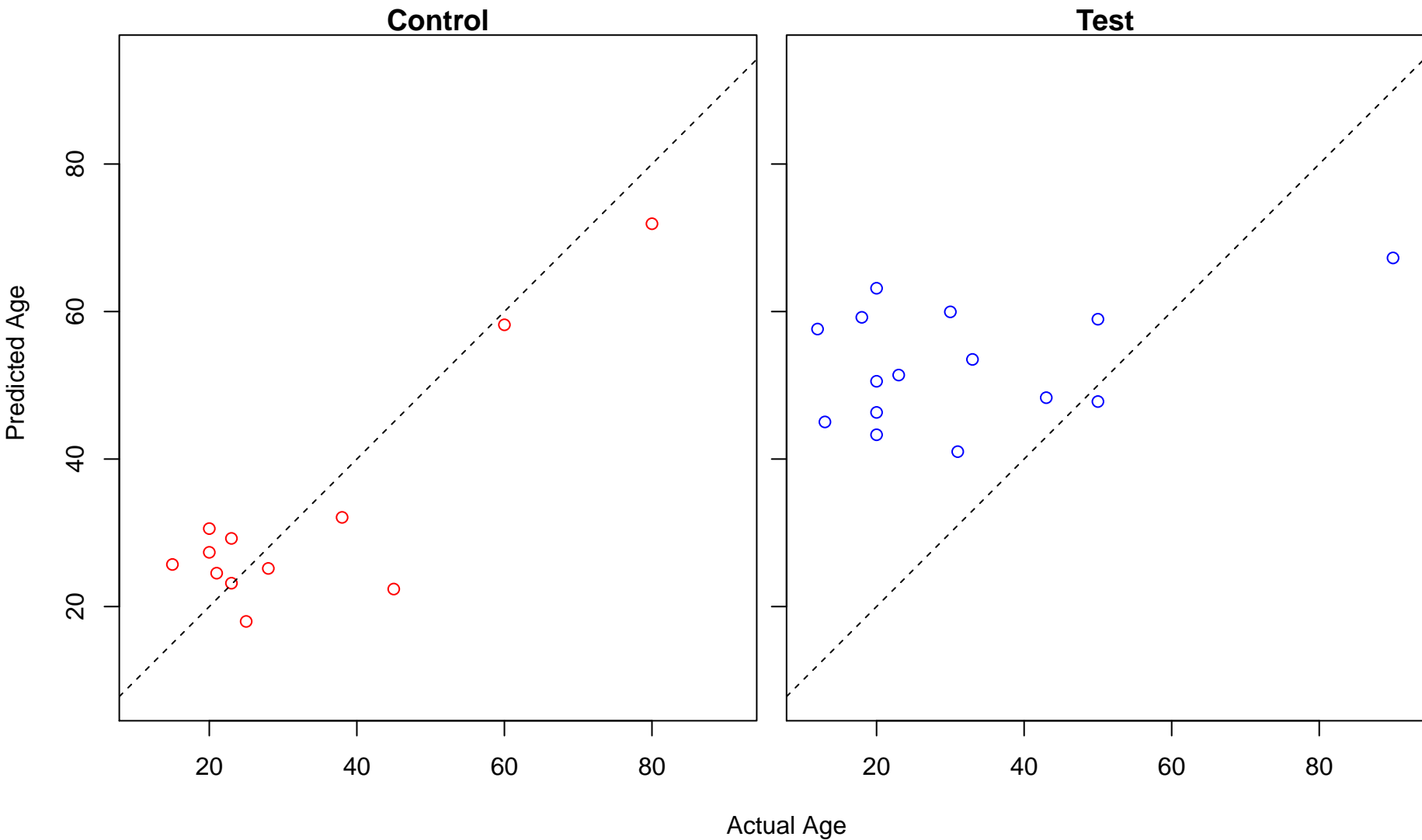
regulation of cellular protein catabolic process (Score: 3.718166)



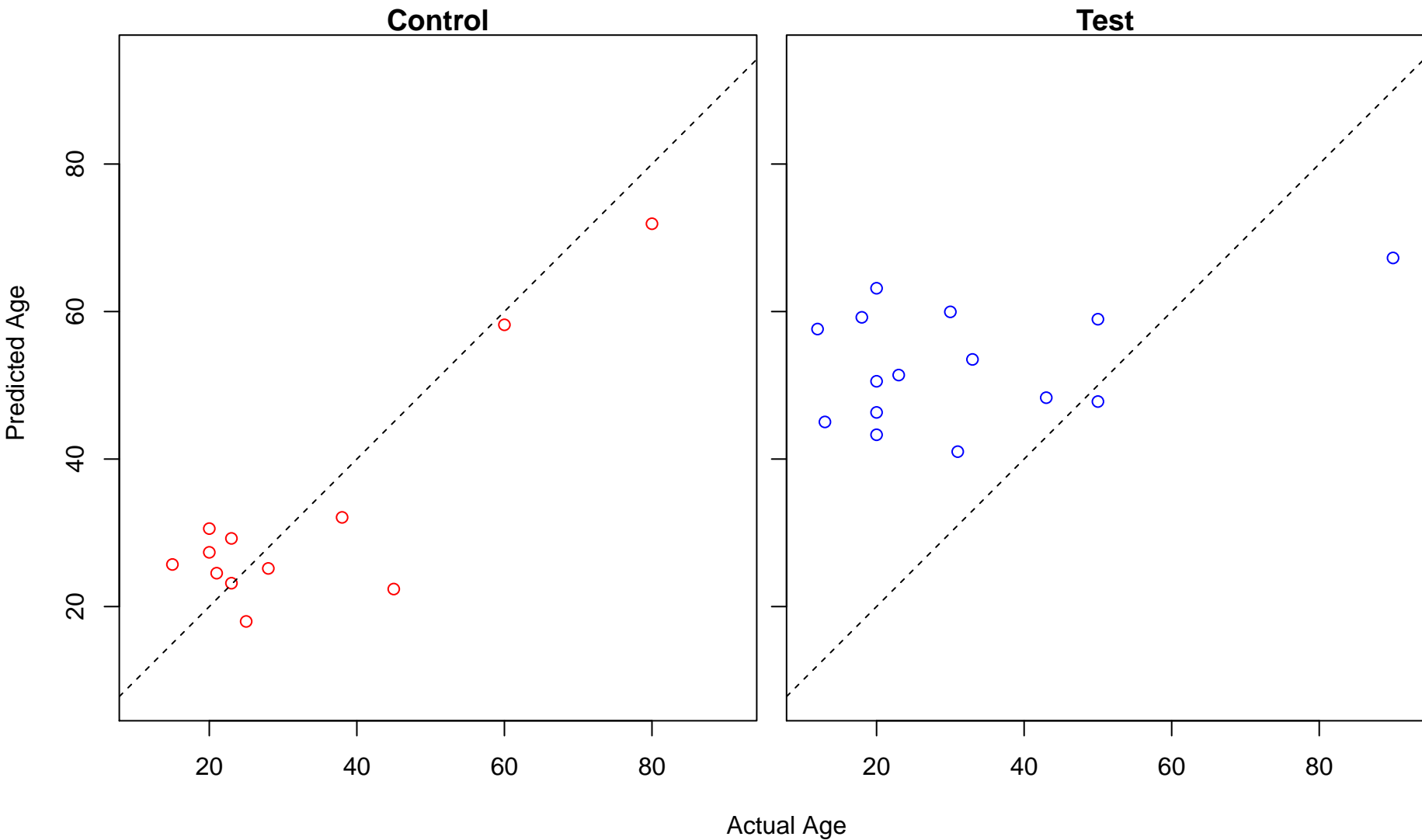
positive regulation of microtubule polymerization or depolymerization (Score: 3.716959)



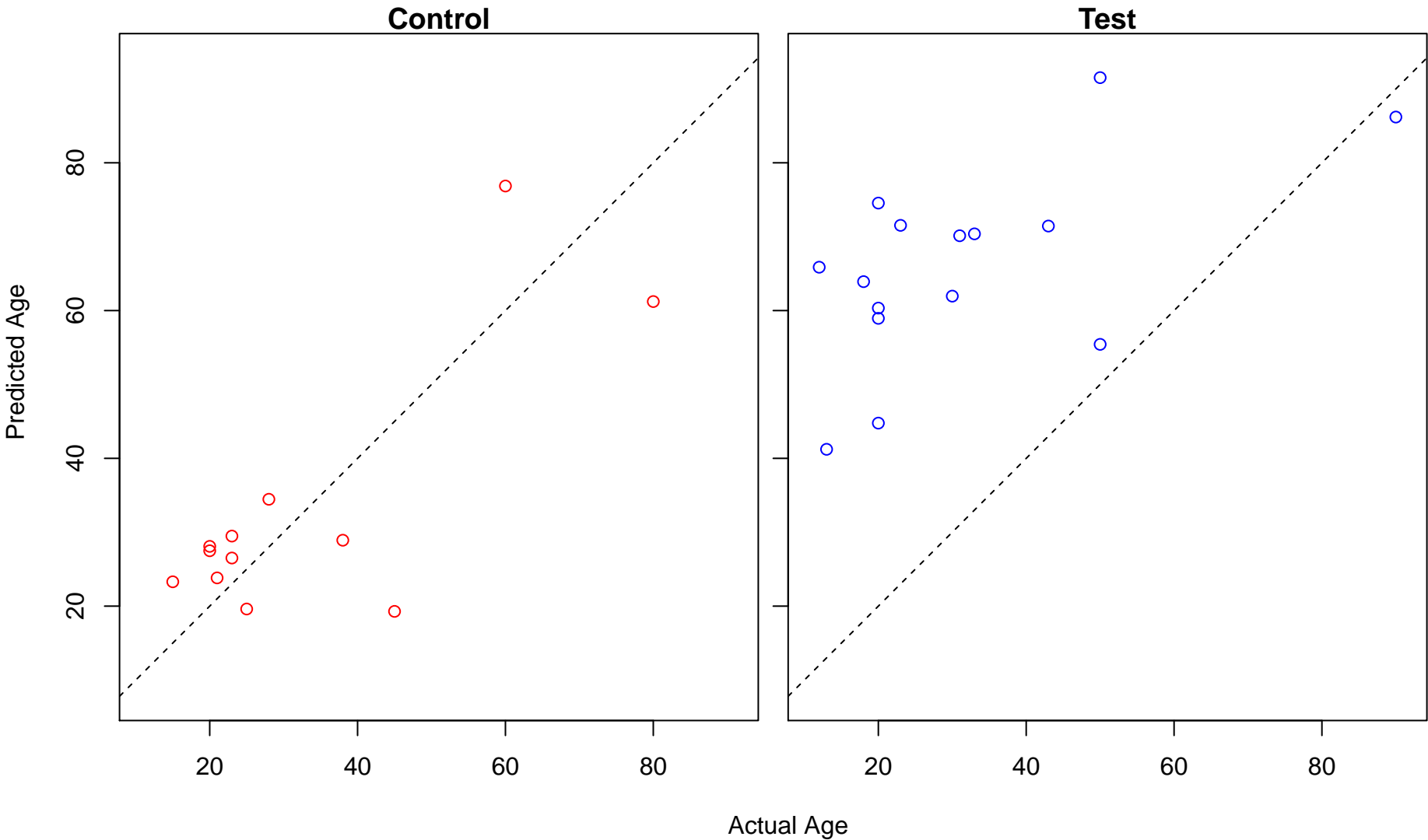
poly-N-acetyllactosamine metabolic process (Score: 3.716772)



poly-N-acetyllactosamine biosynthetic process (Score: 3.716772)

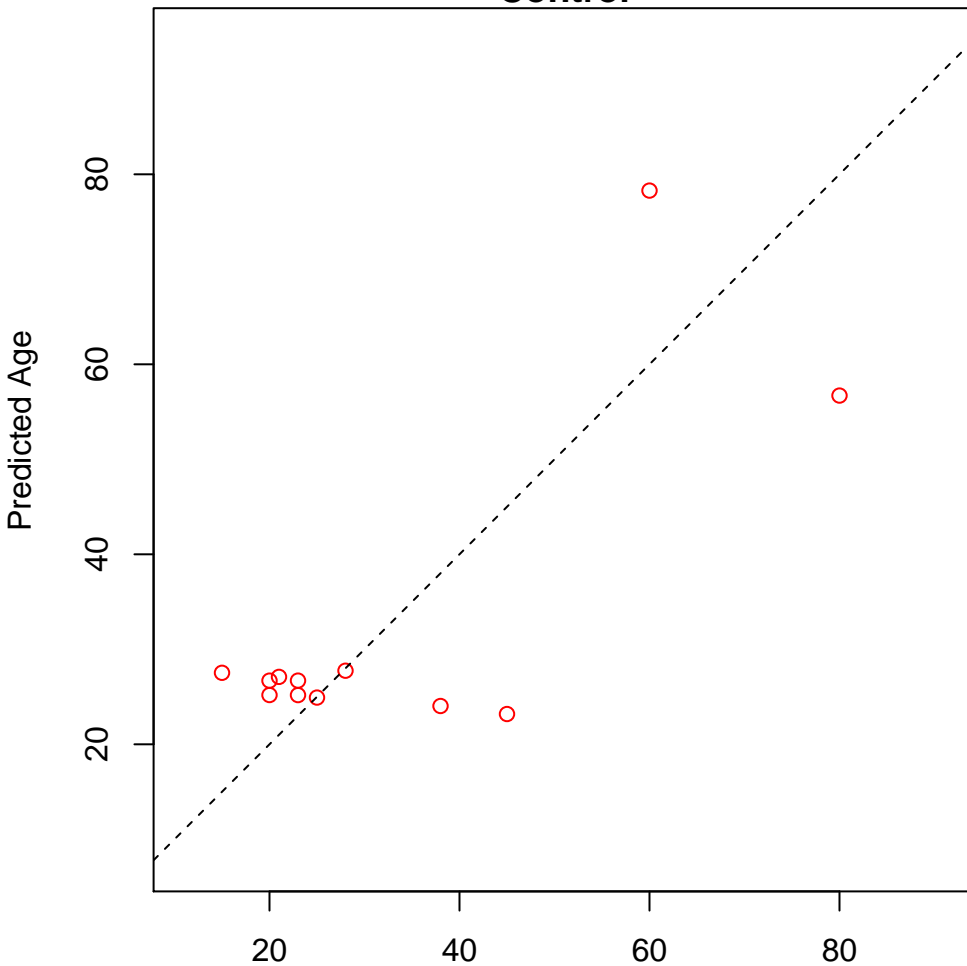


phosphatidylglycerol biosynthetic process (Score: 3.715076)

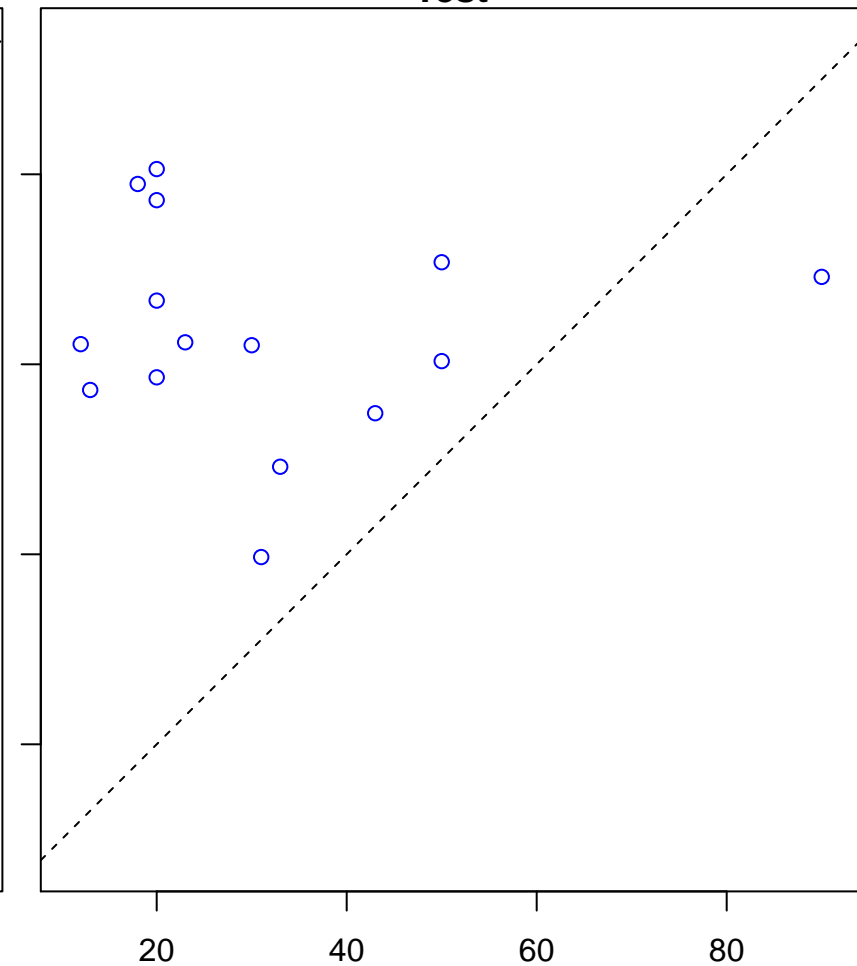


ribonucleoside biosynthetic process (Score: 3.713763)

Control

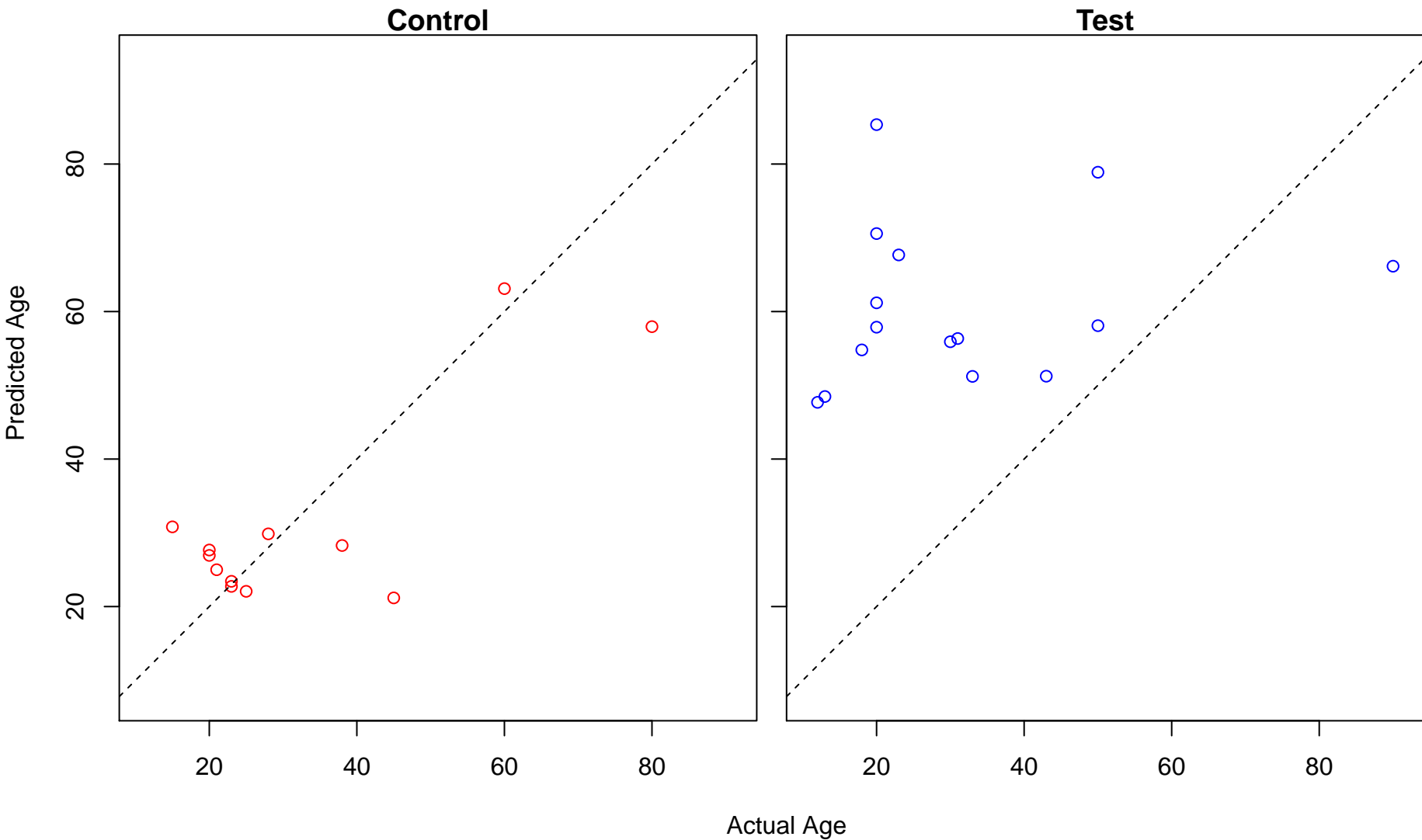


Test

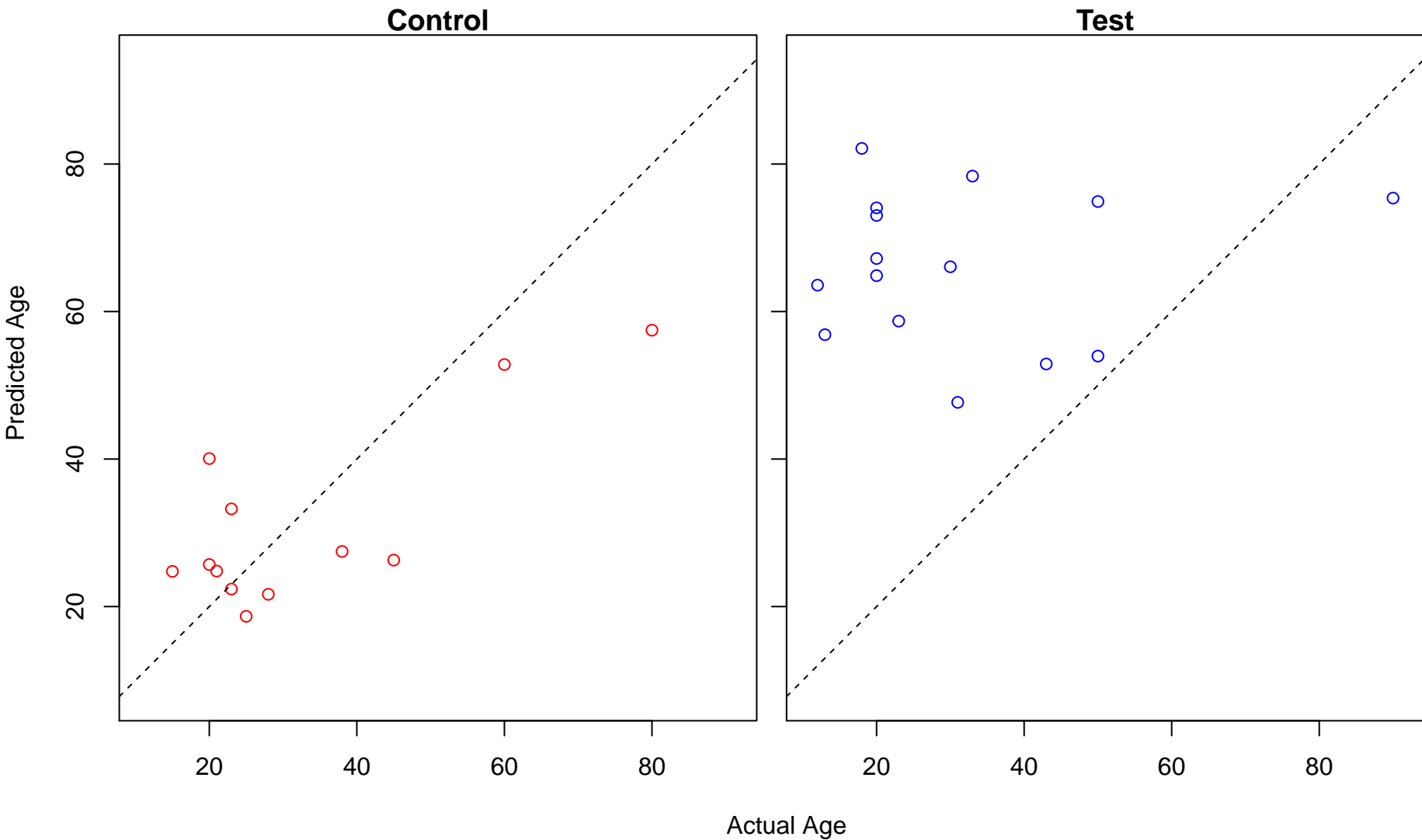


Actual Age

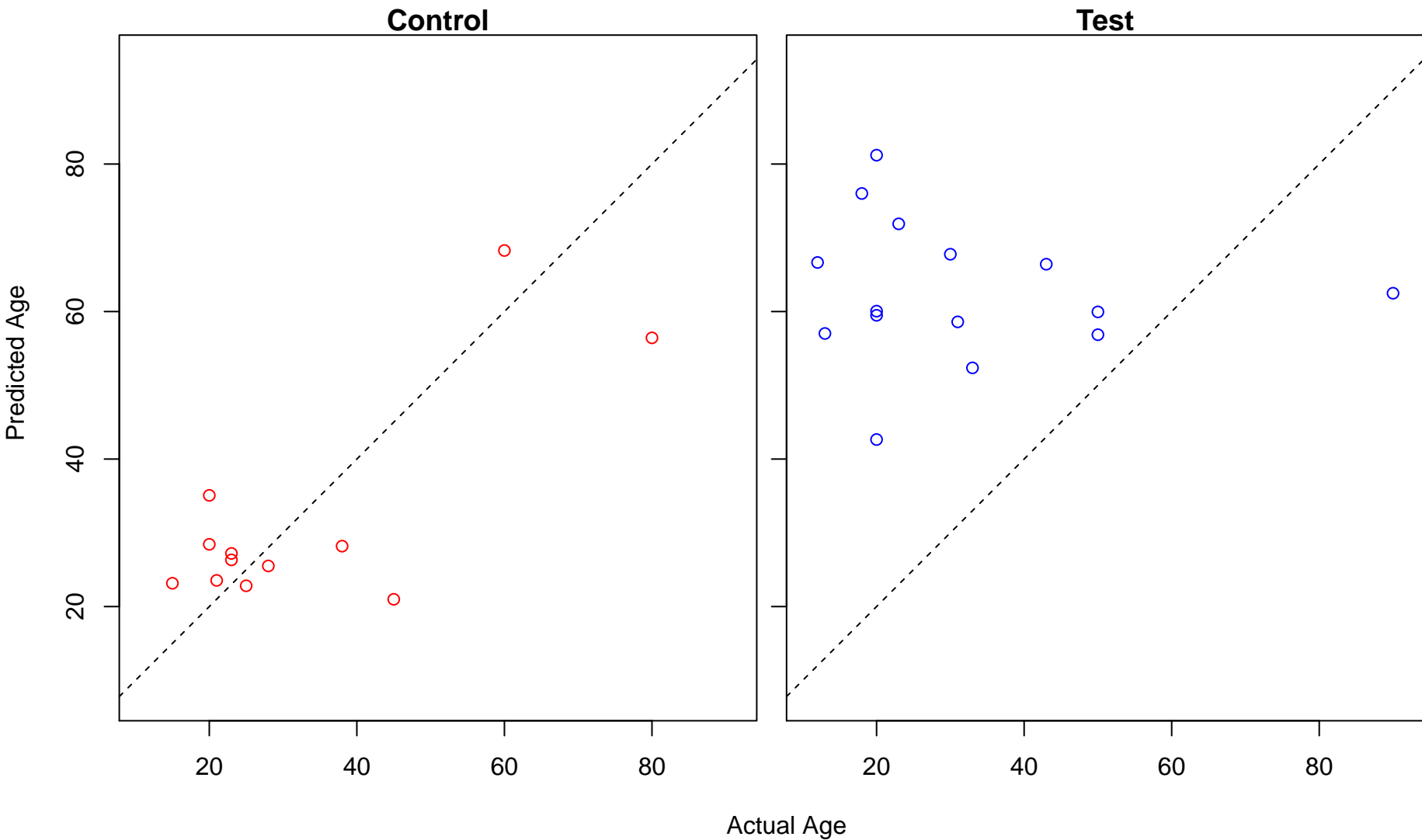
histone lysine demethylation (Score: 3.711045)



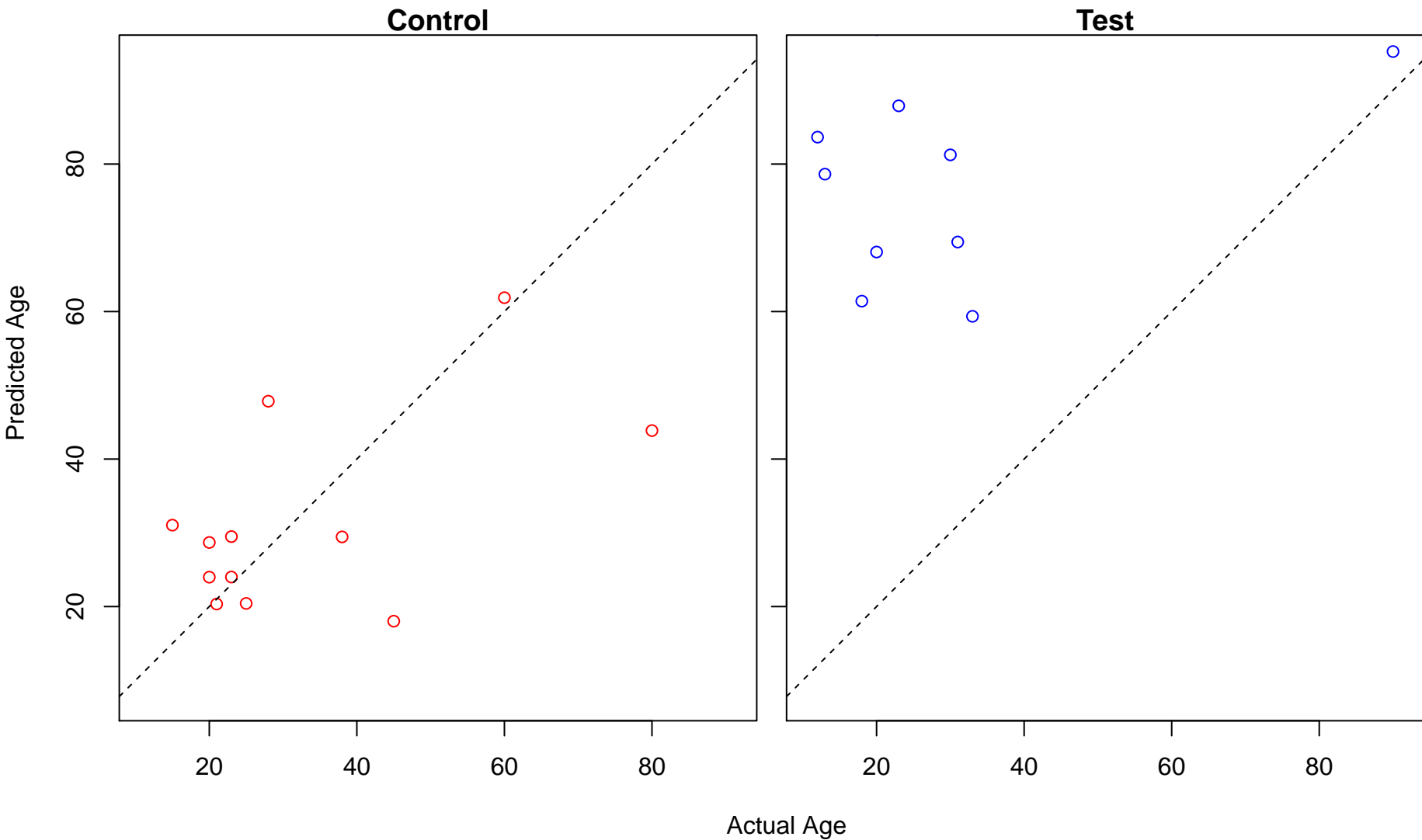
negative regulation of anion transport (Score: 3.710374)



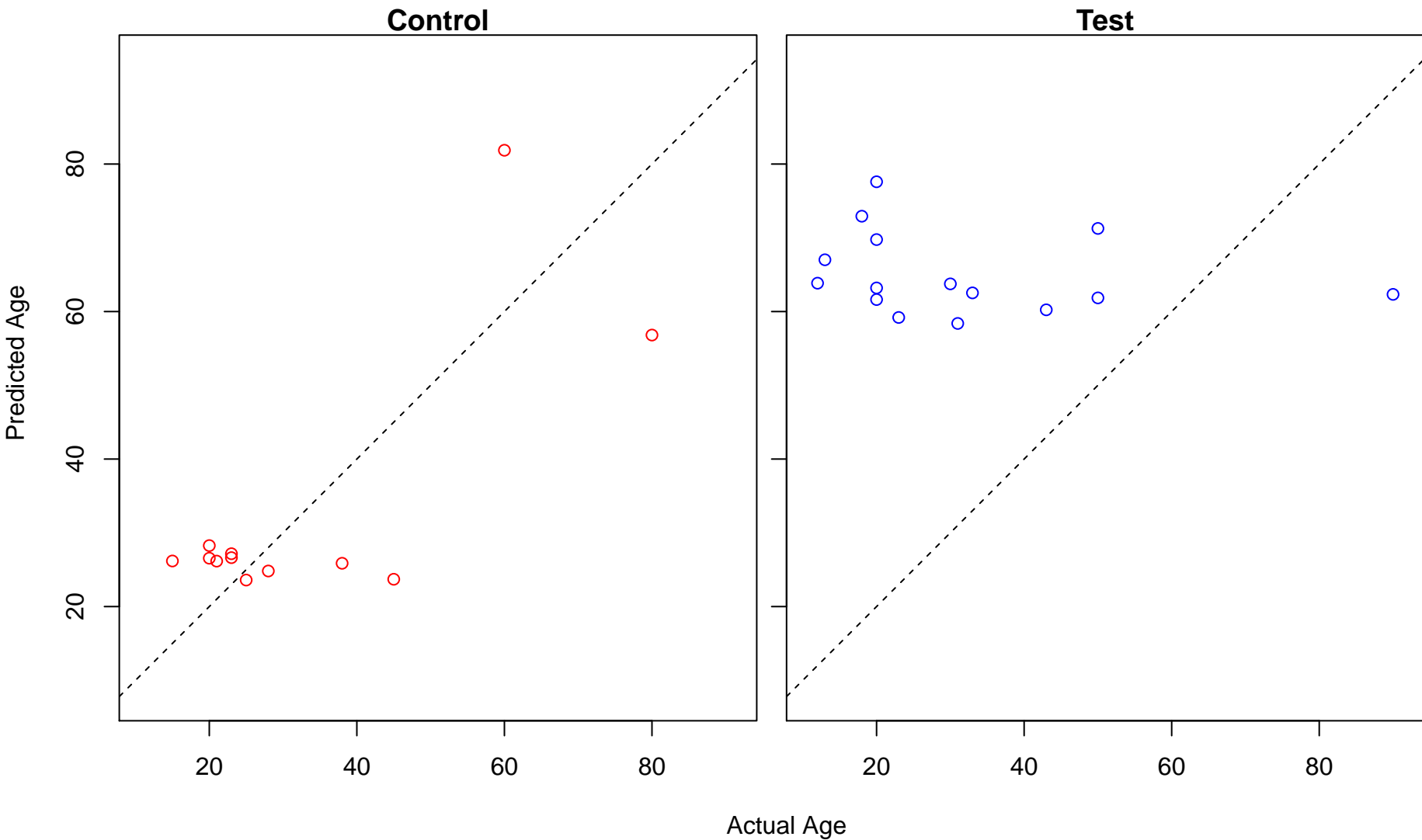
innervation (Score: 3.709218)



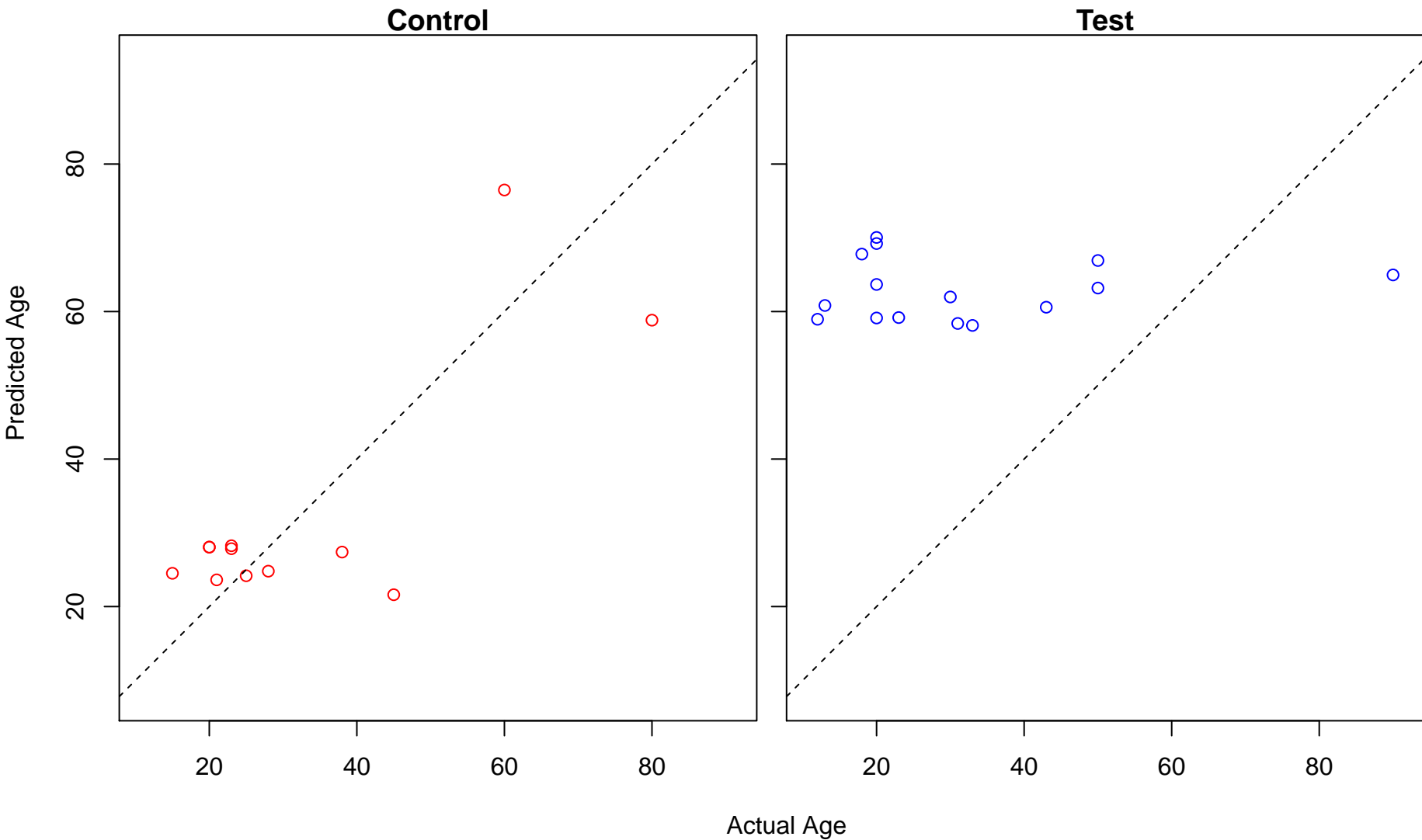
oligodendrocyte differentiation (Score: 3.708761)



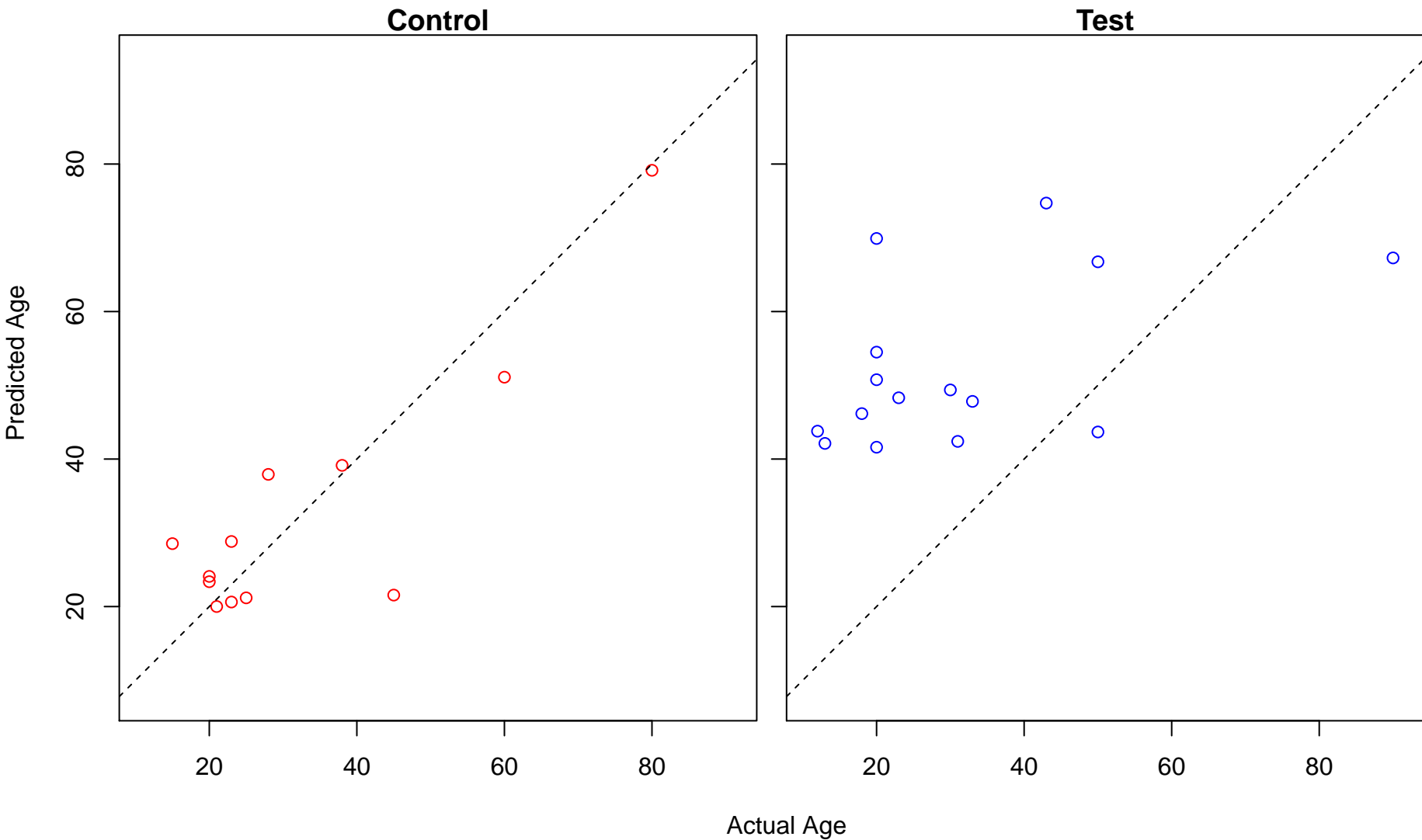
regulation of protein polymerization (Score: 3.707107)



nuclear-transcribed mRNA poly(A) tail shortening (Score: 3.705751)

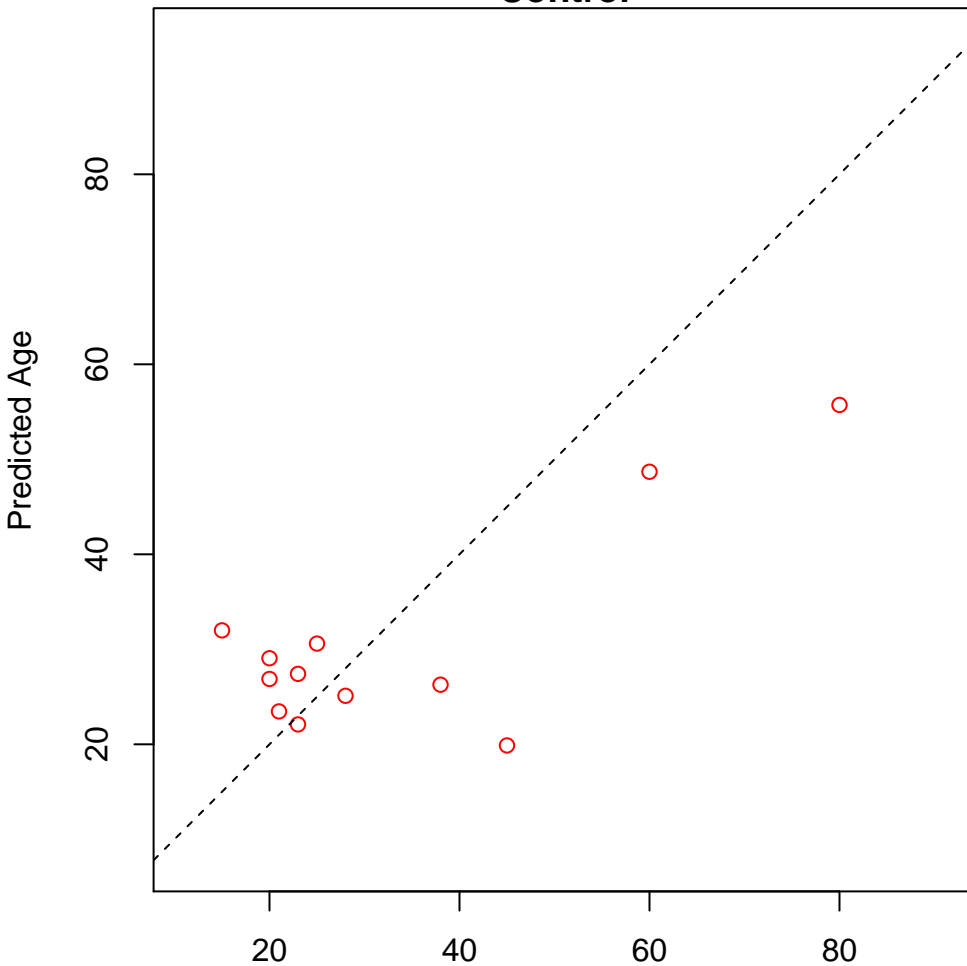


regulation of vasodilation (Score: 3.705055)

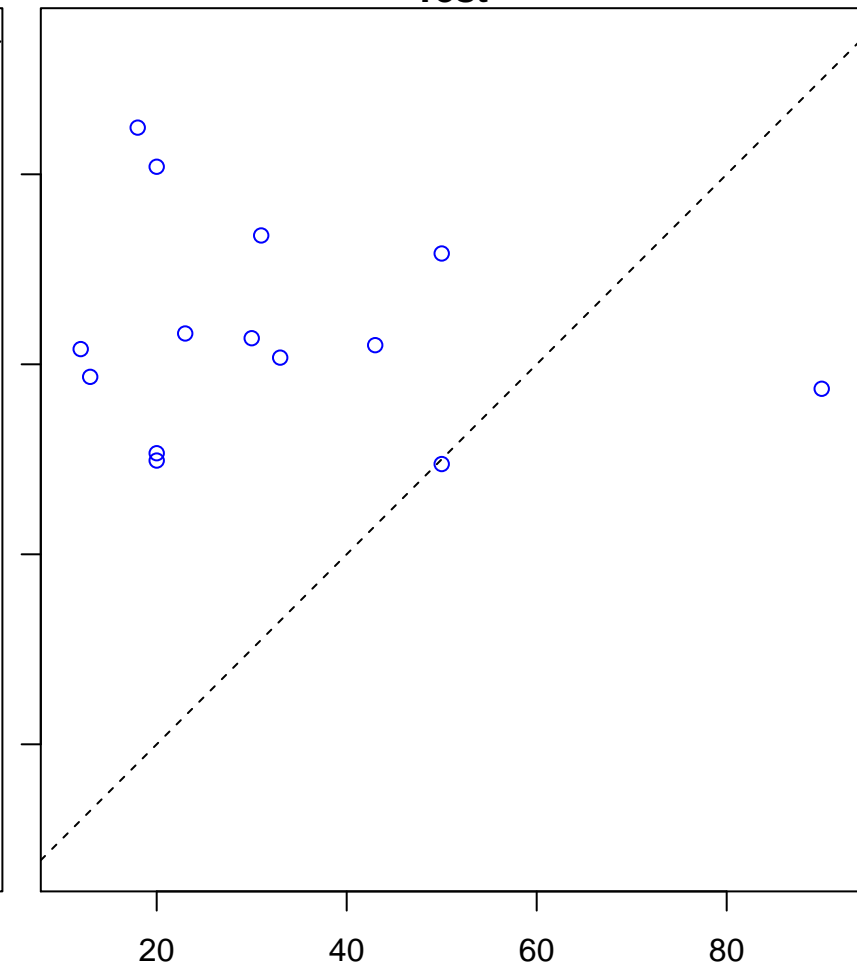


positive regulation of acrosome reaction (Score: 3.705041)

Control

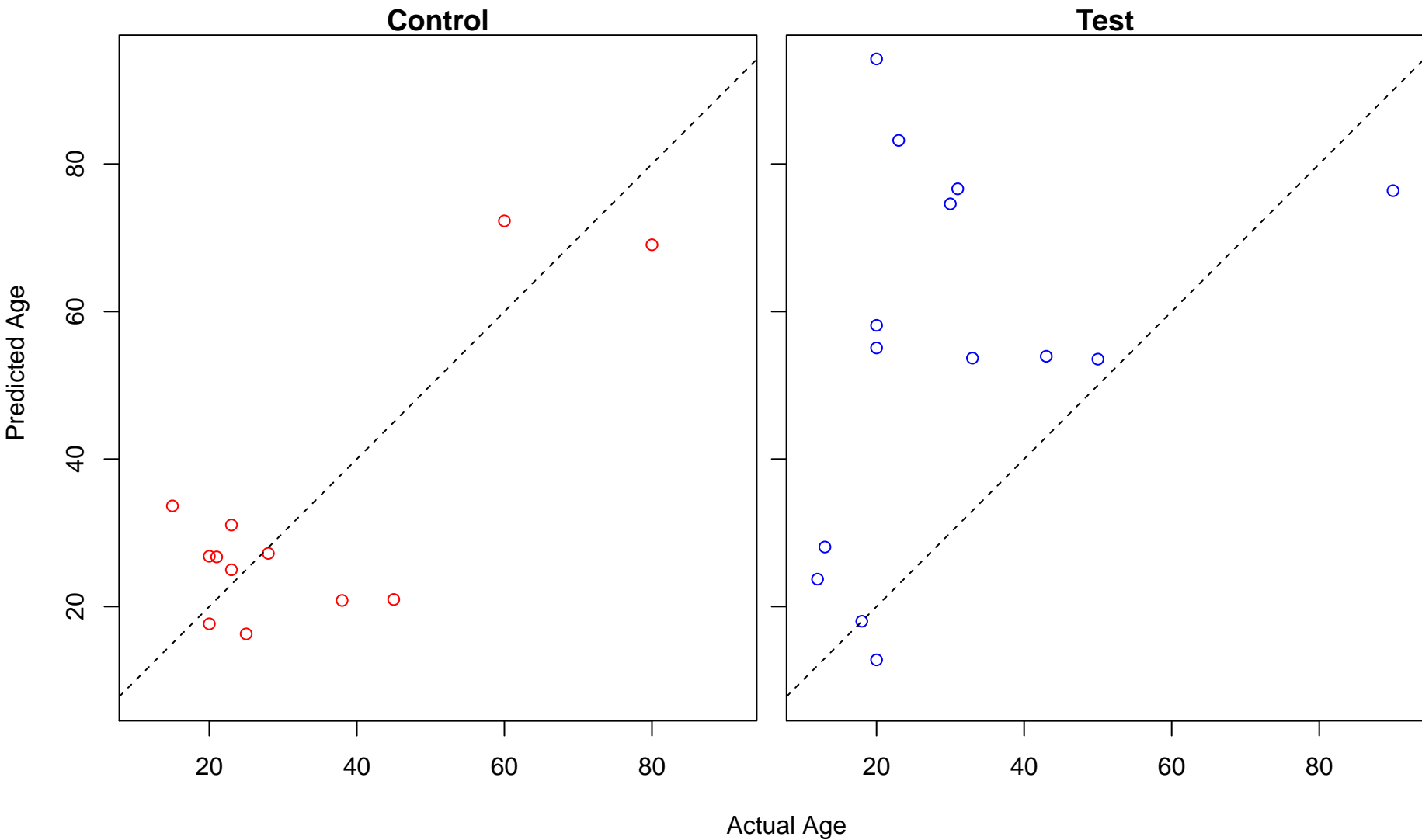


Test

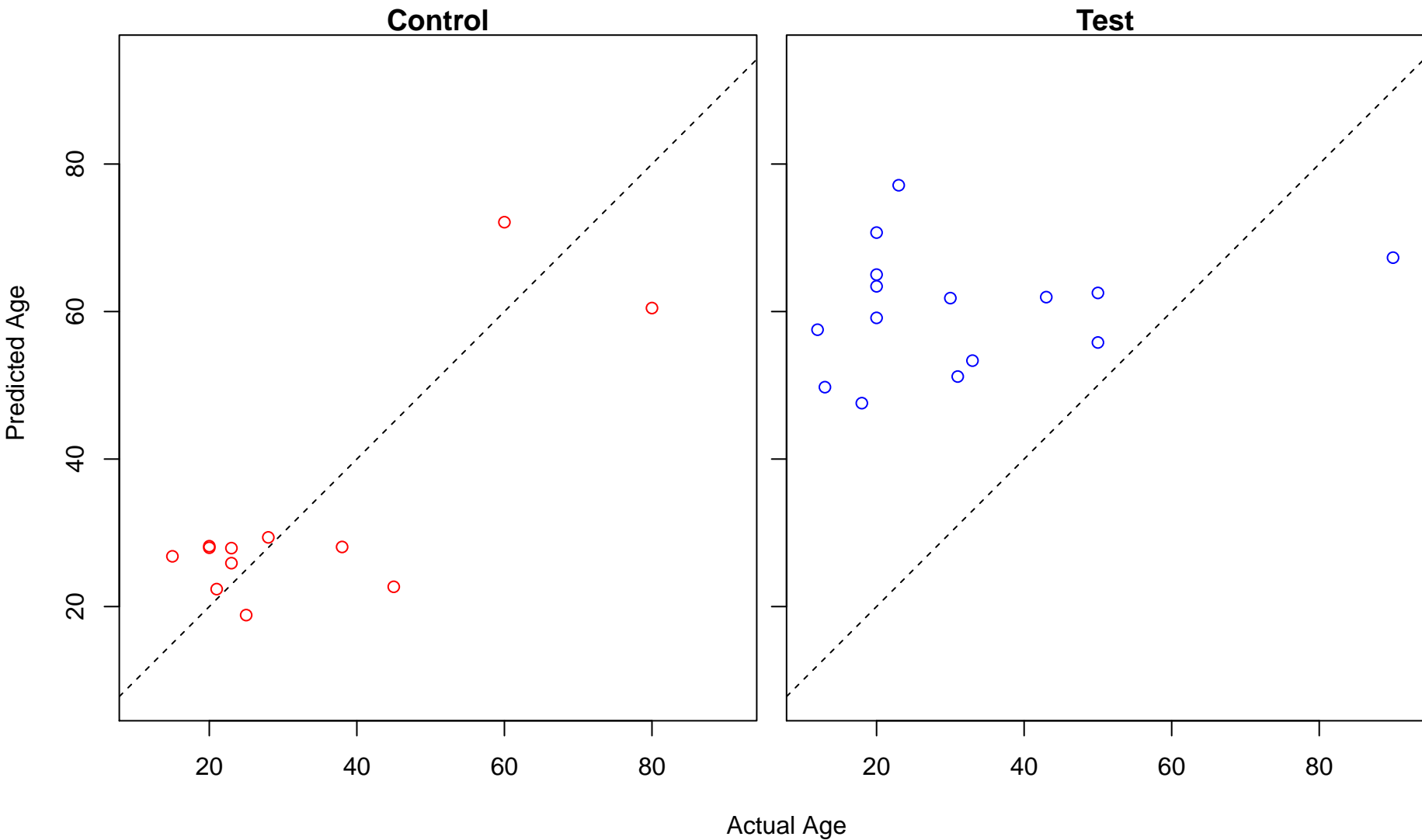


Actual Age

regulation of macrophage activation (Score: 3.702350)

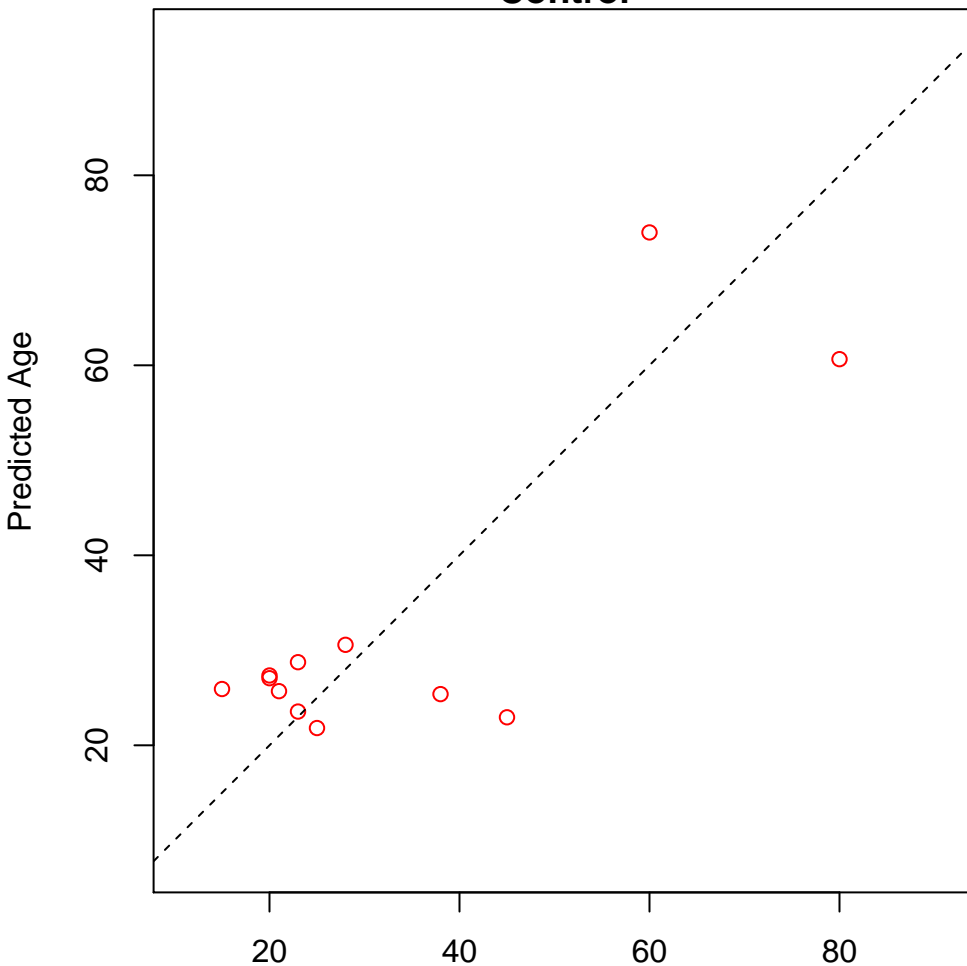


regulation of acute inflammatory response (Score: 3.702329)

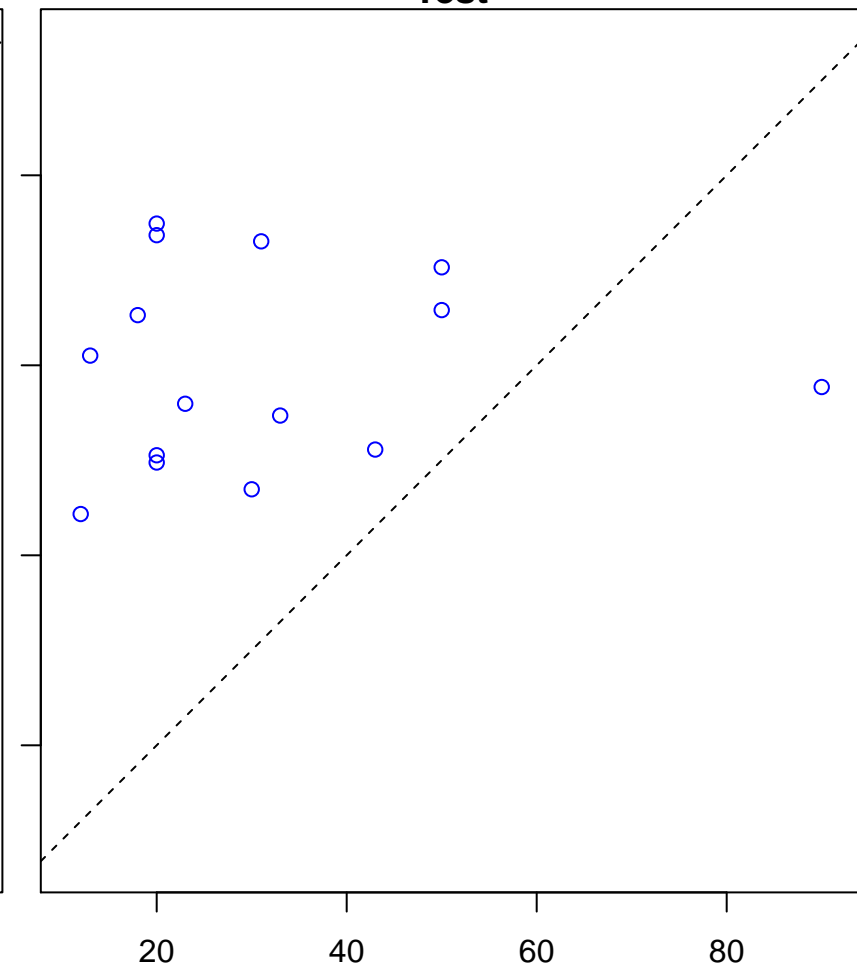


inositol phosphate metabolic process (Score: 3.701969)

Control

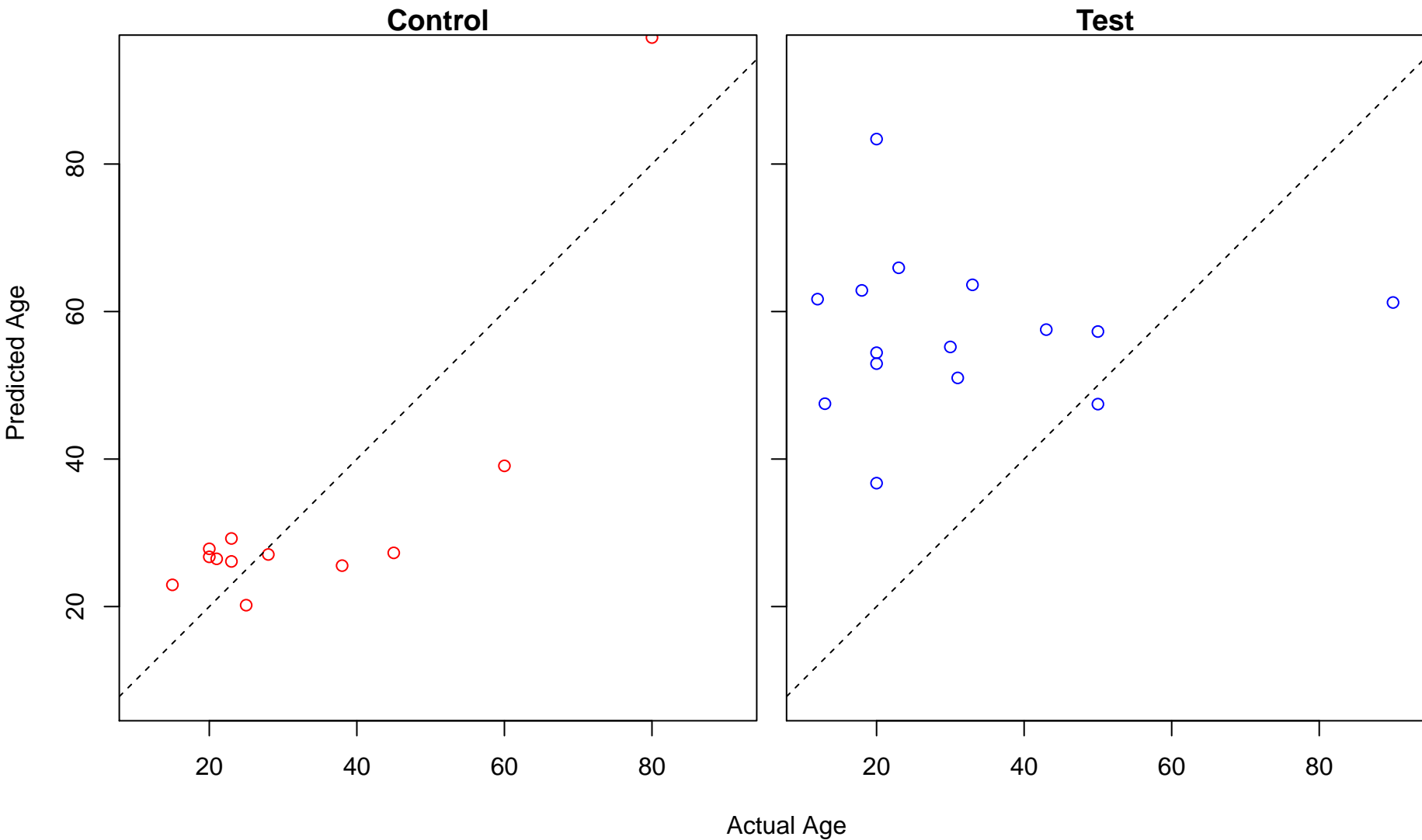


Test



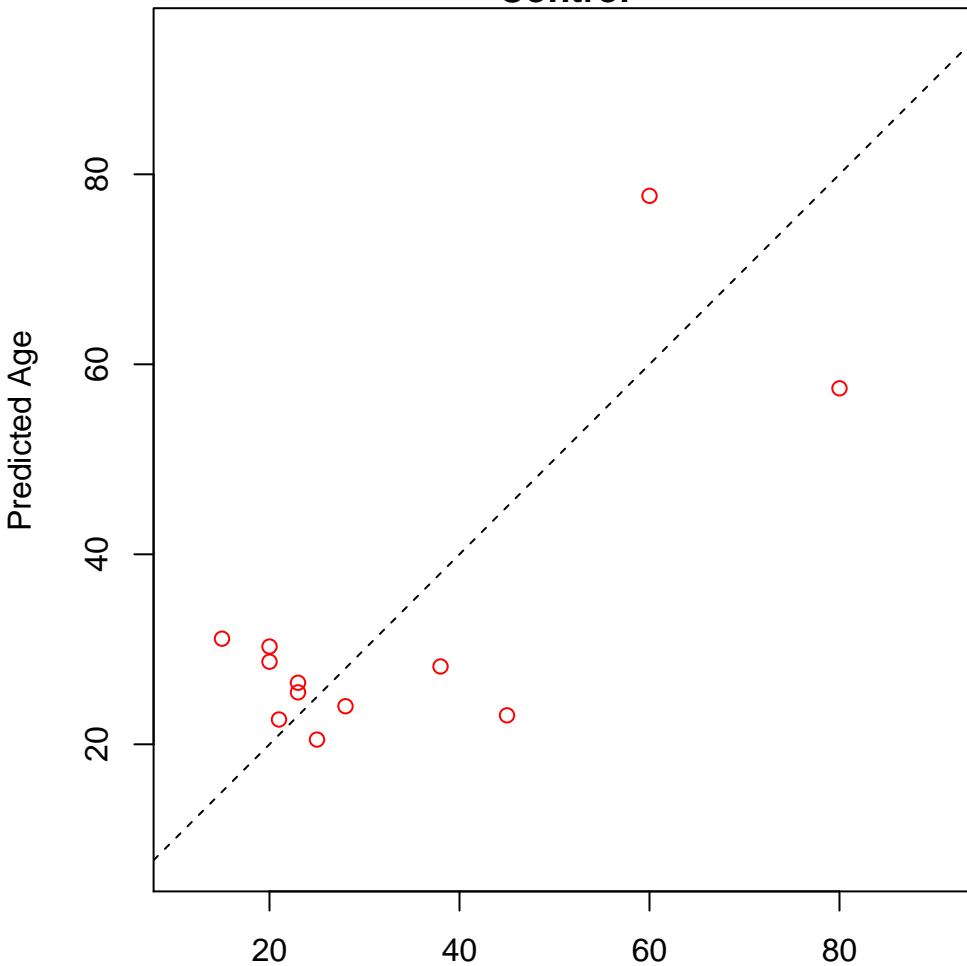
Actual Age

mitochondrial fission (Score: 3.701625)

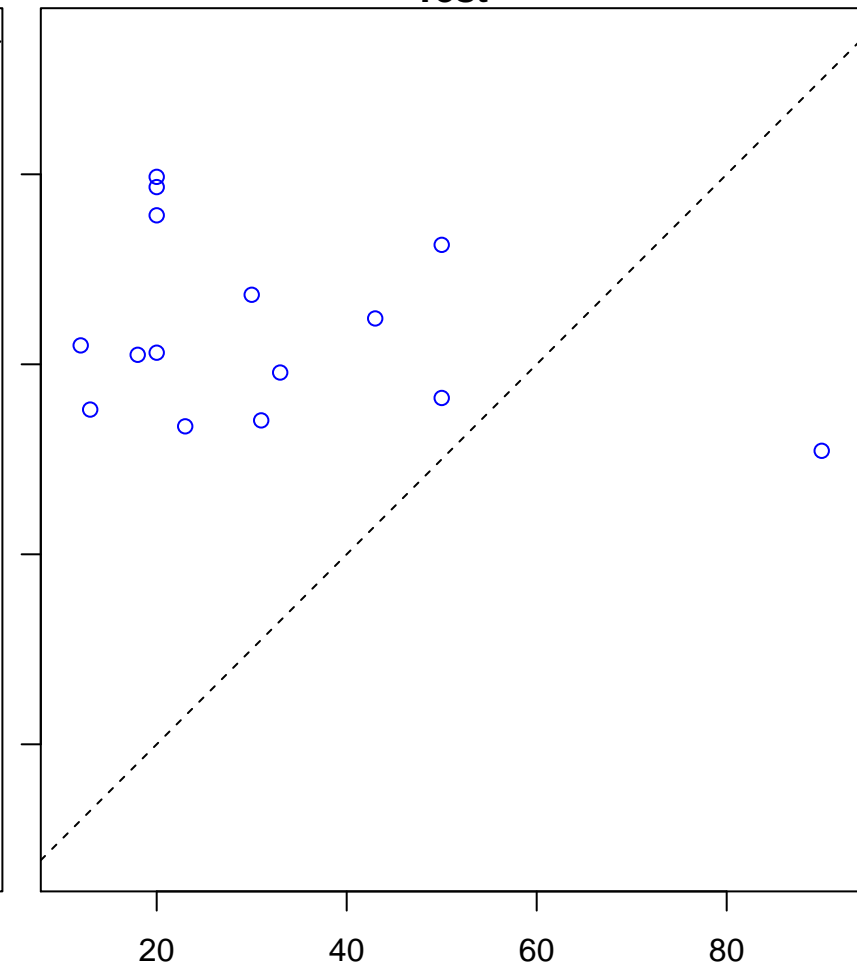


cardiac endothelial cell differentiation (Score: 3.700808)

Control

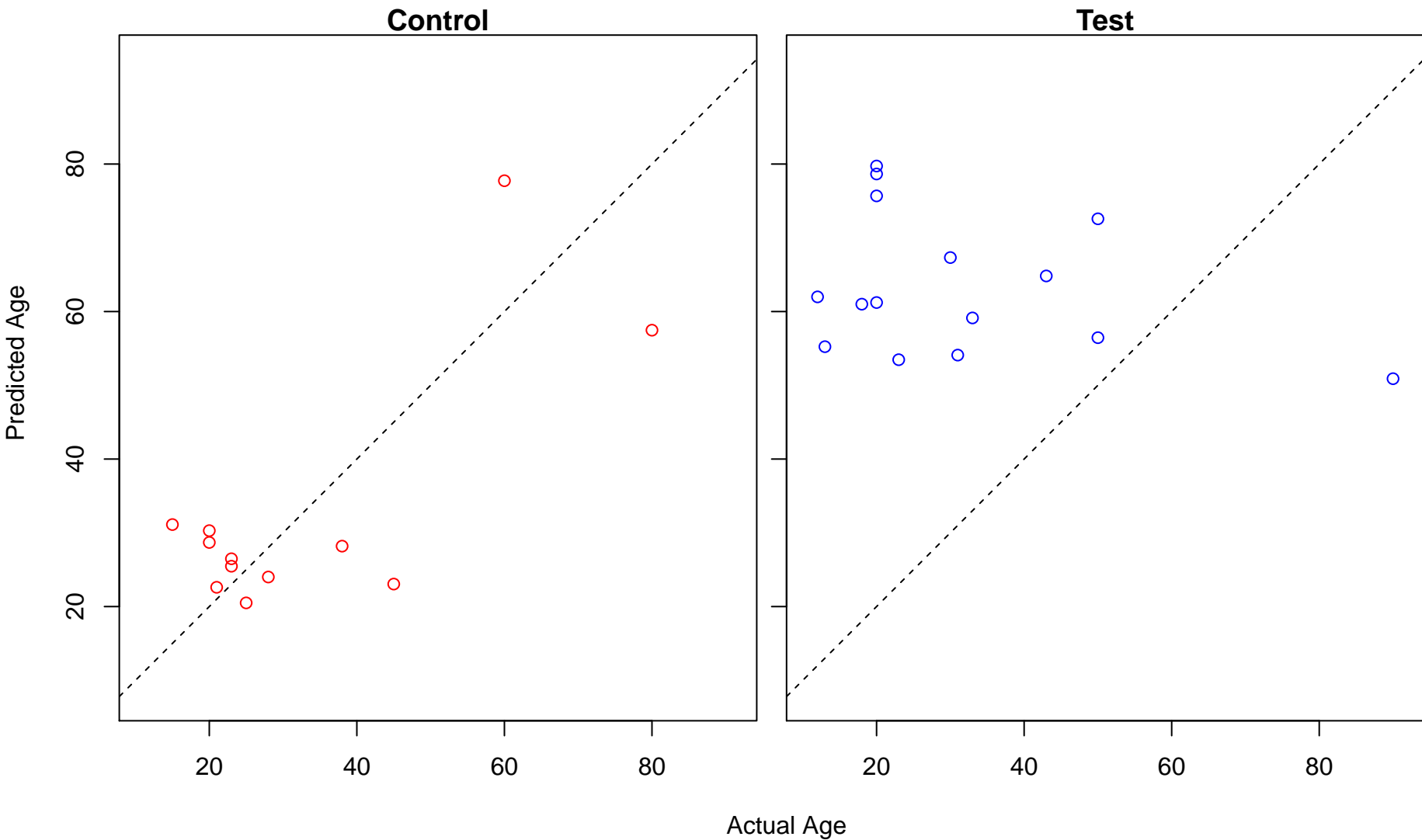


Test

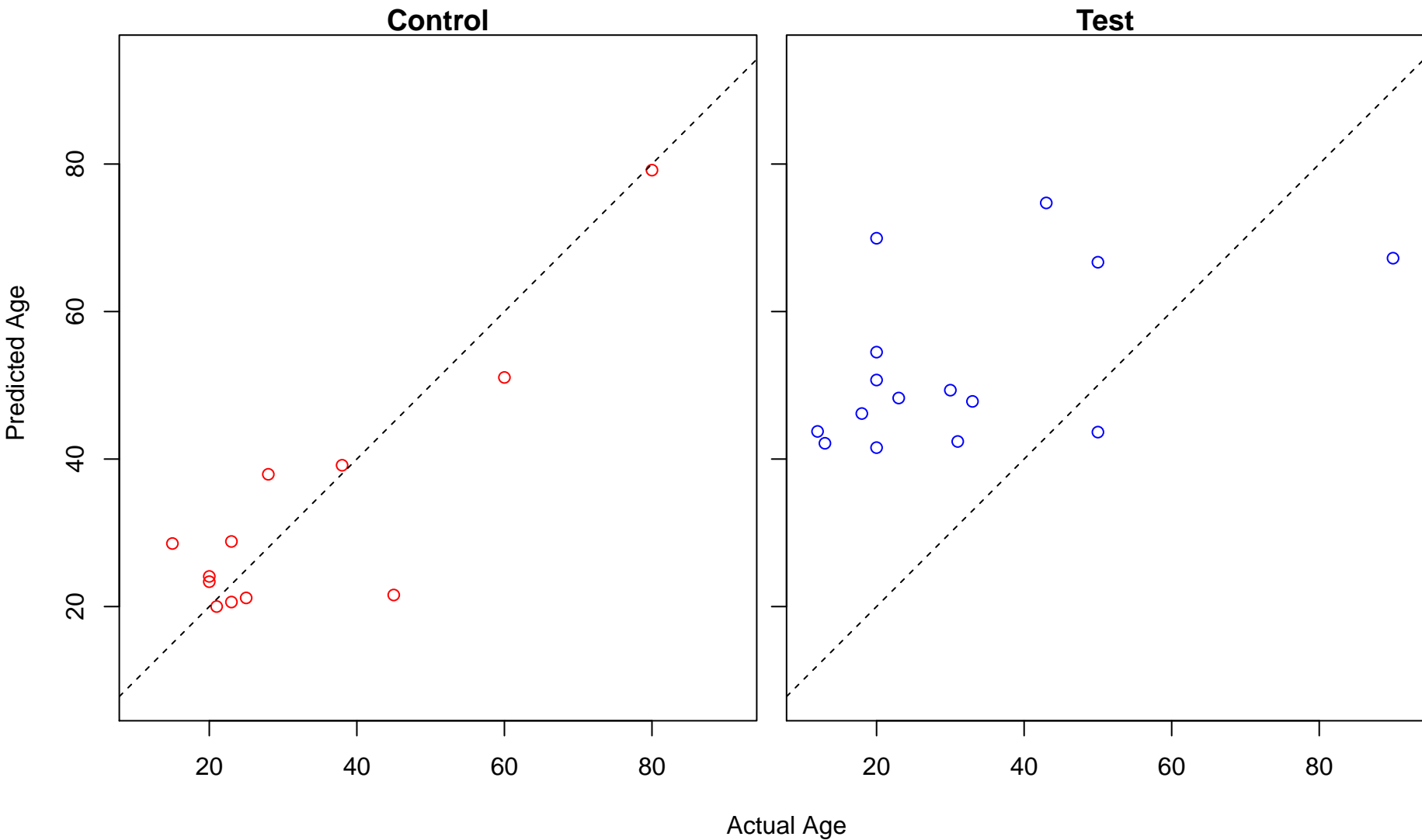


Actual Age

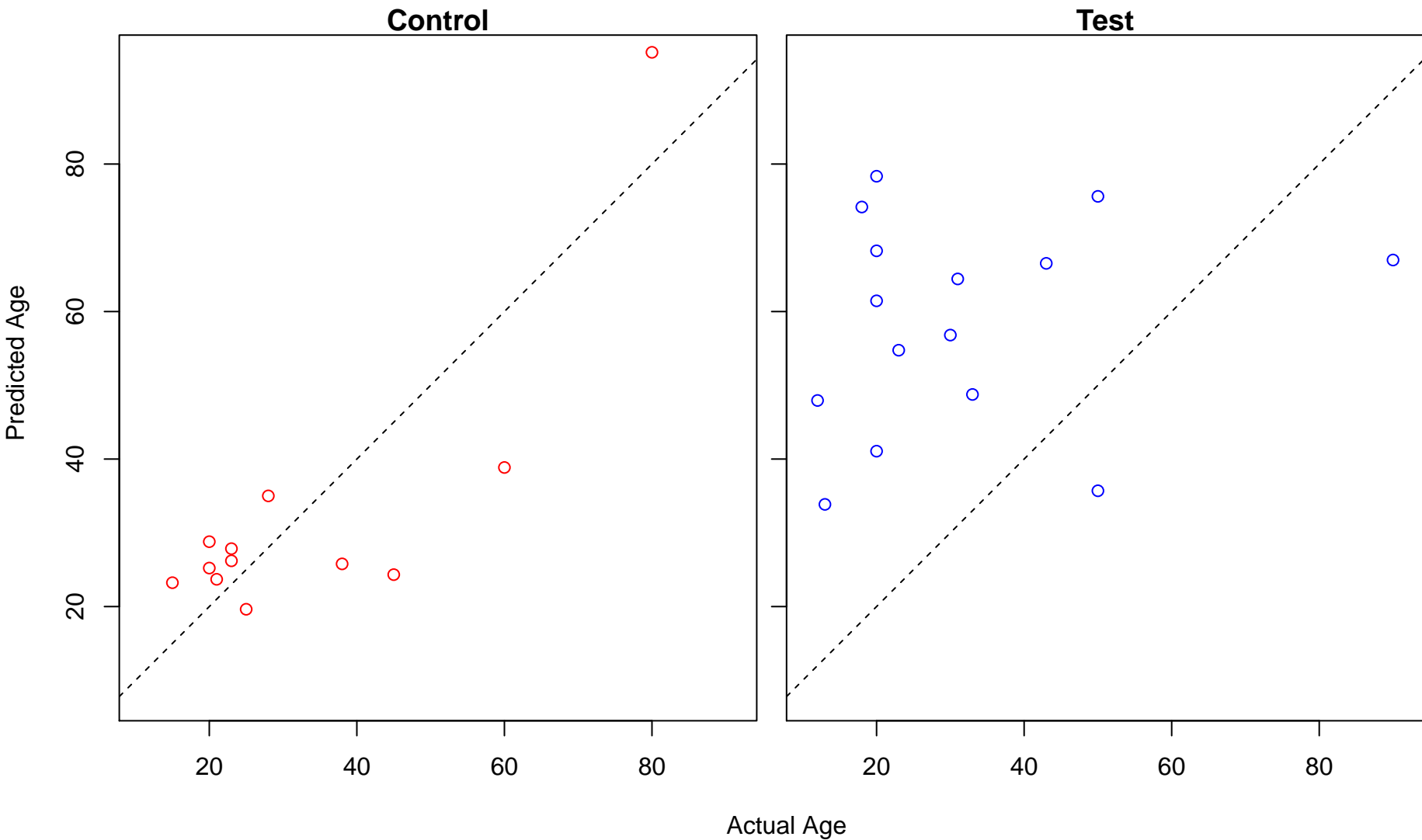
endocardial cell differentiation (Score: 3.700808)



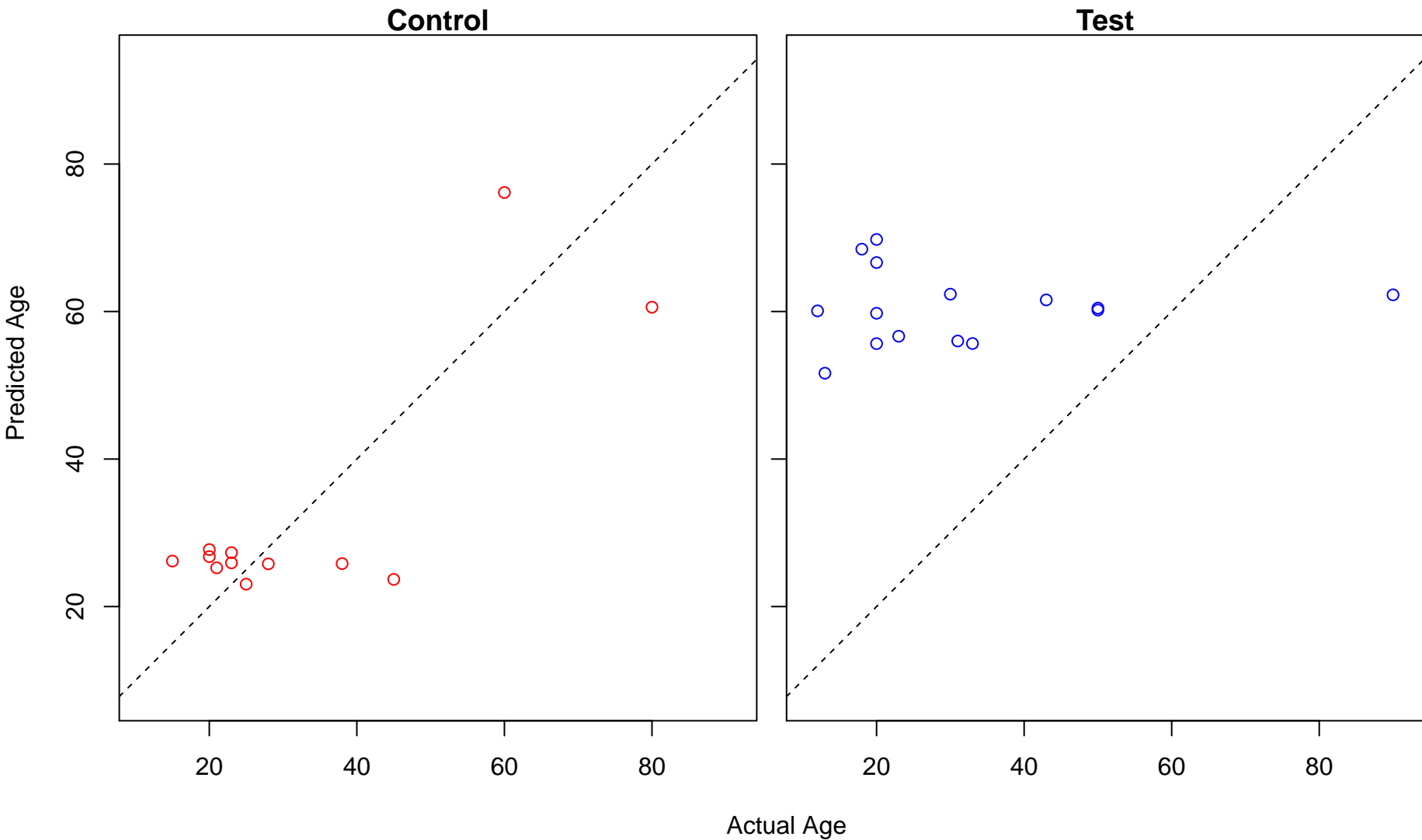
positive regulation of vasodilation (Score: 3.700580)



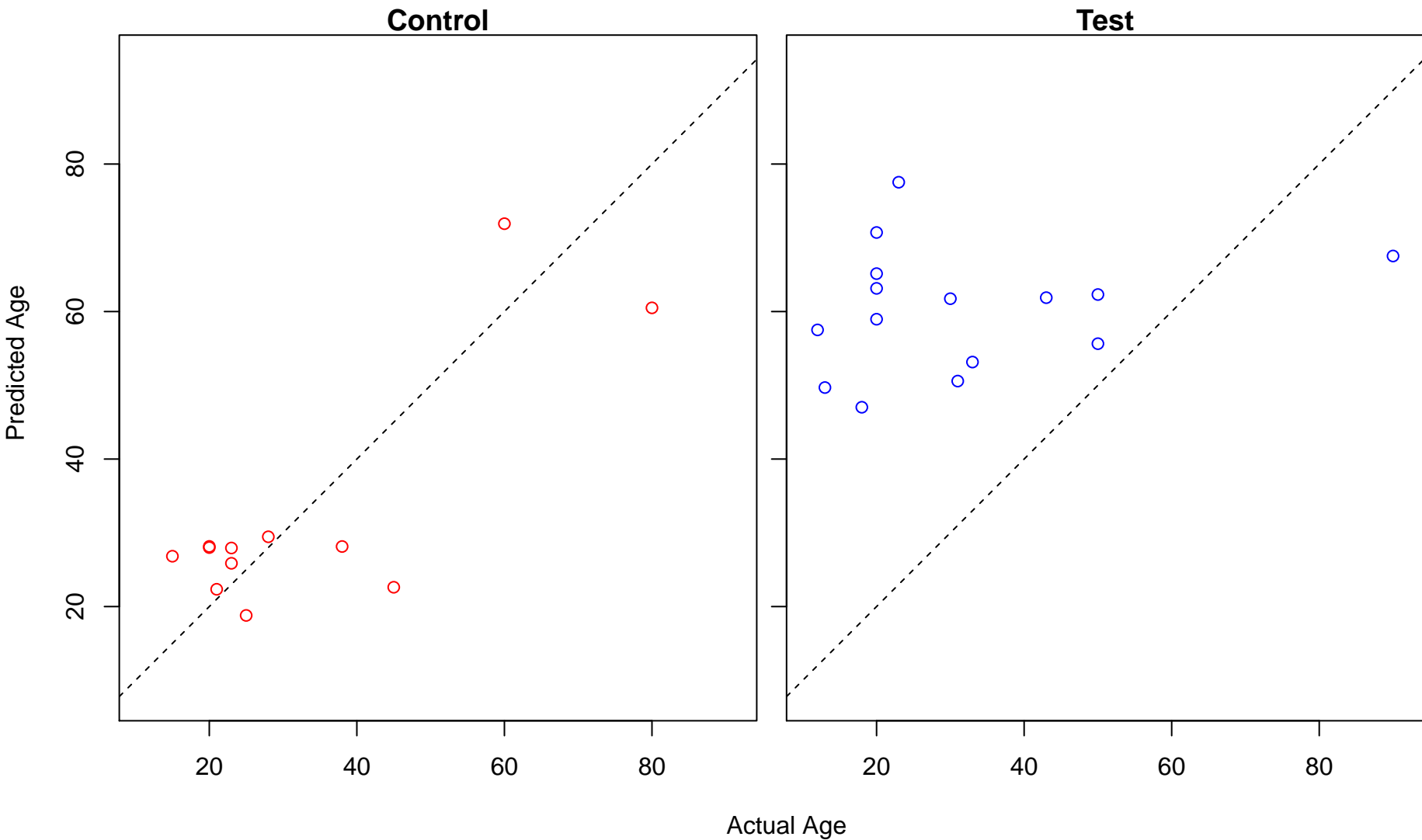
leukocyte homeostasis (Score: 3.700516)



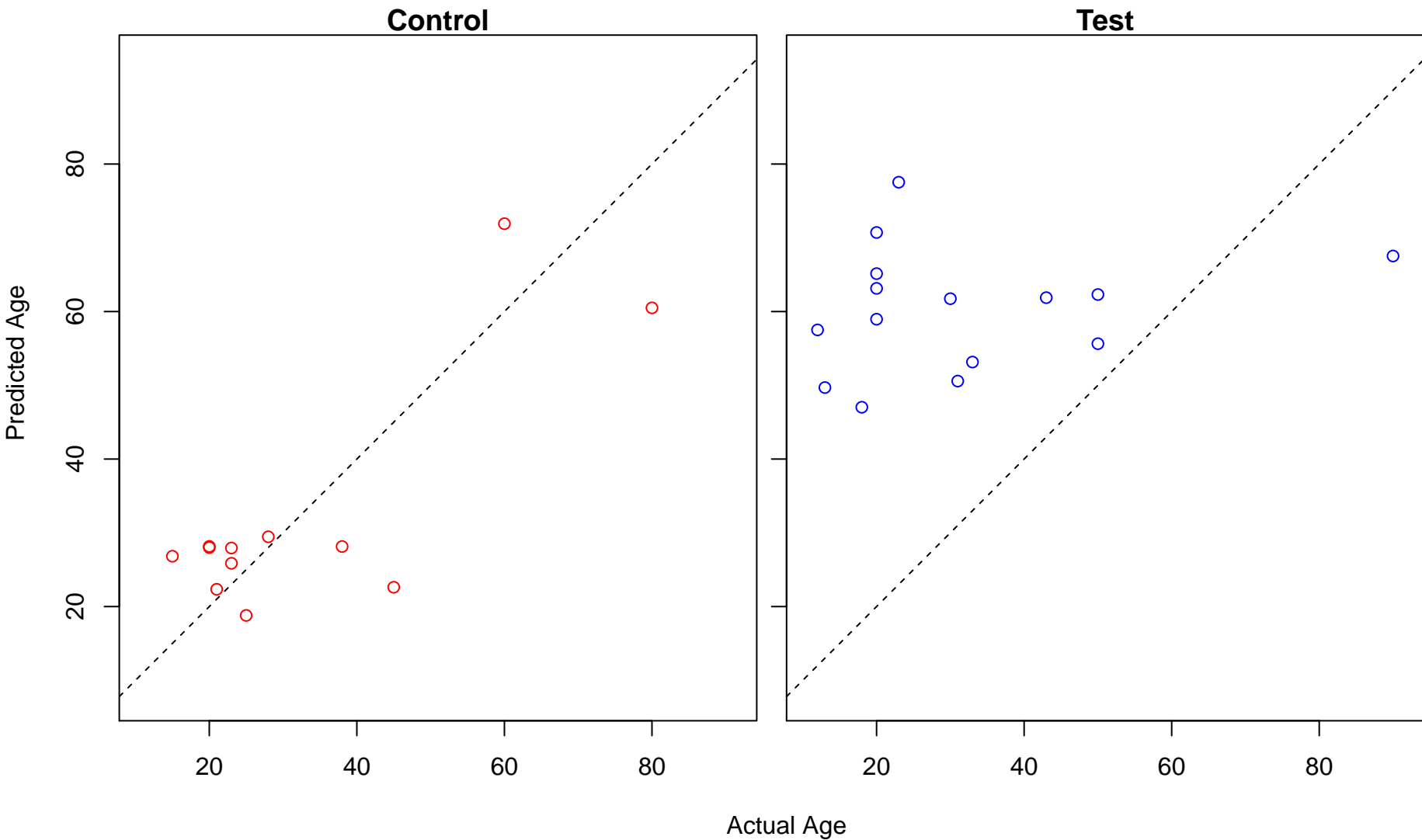
coenzyme biosynthetic process (Score: 3.697200)



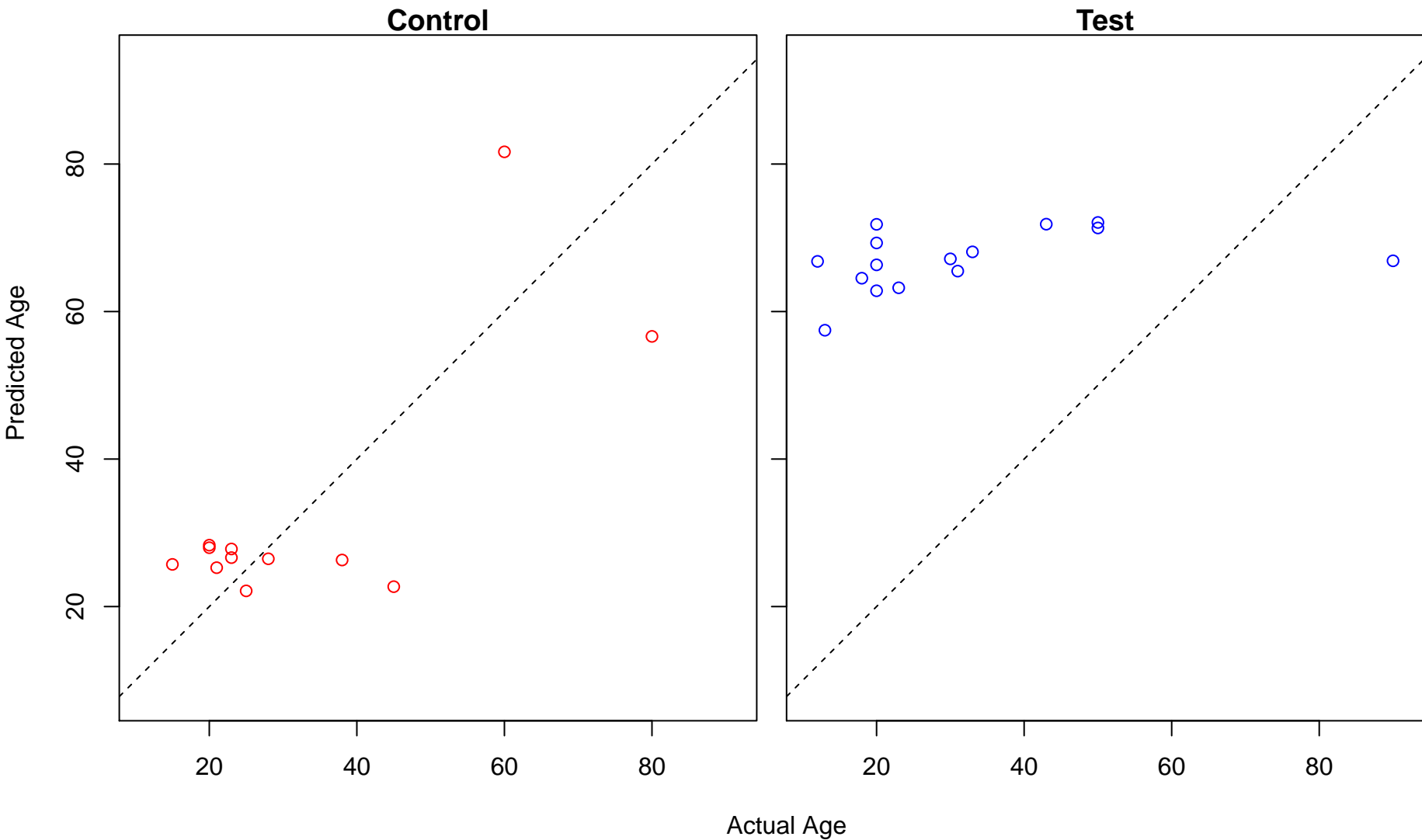
regulation of protein activation cascade (Score: 3.694508)



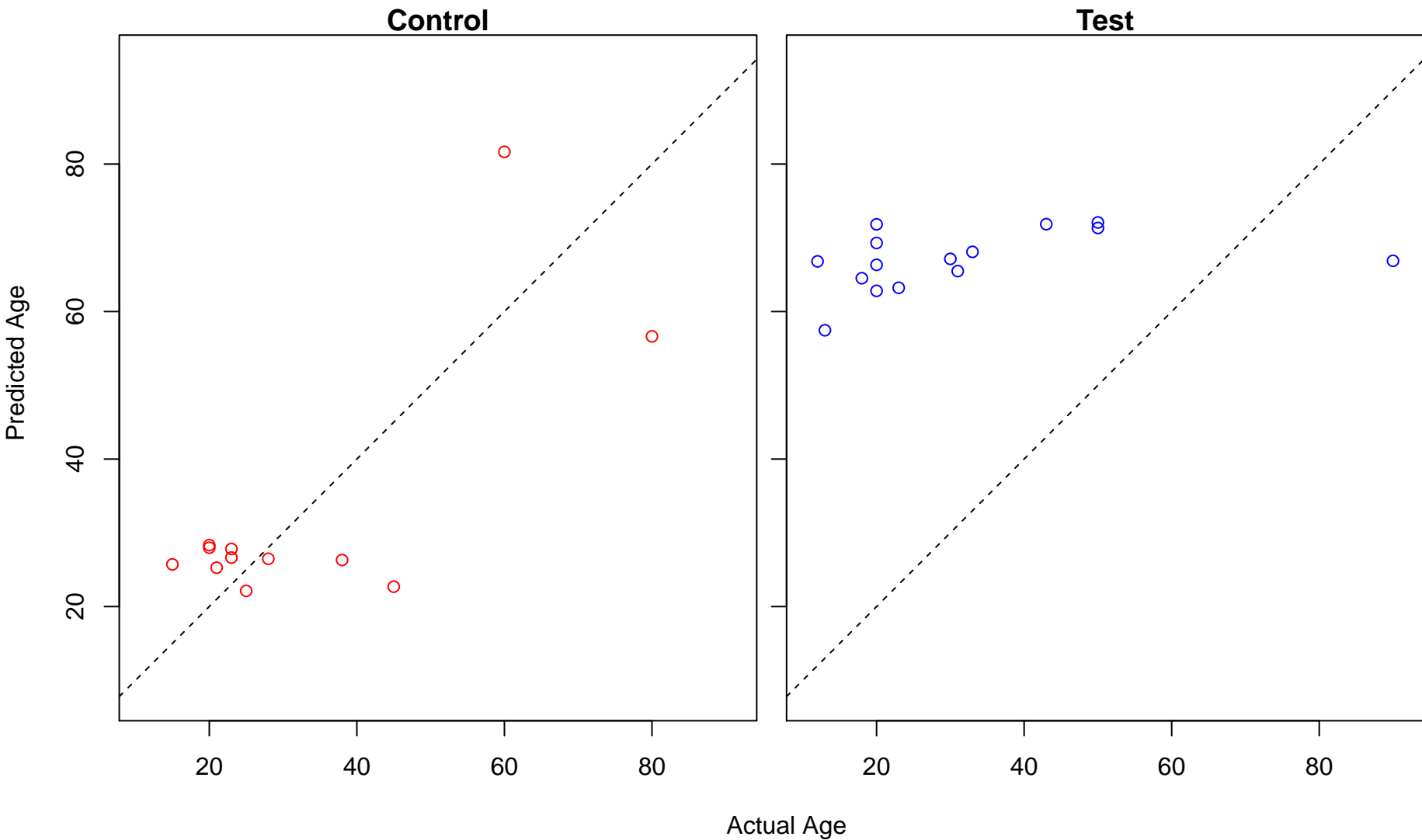
regulation of complement activation (Score: 3.694492)



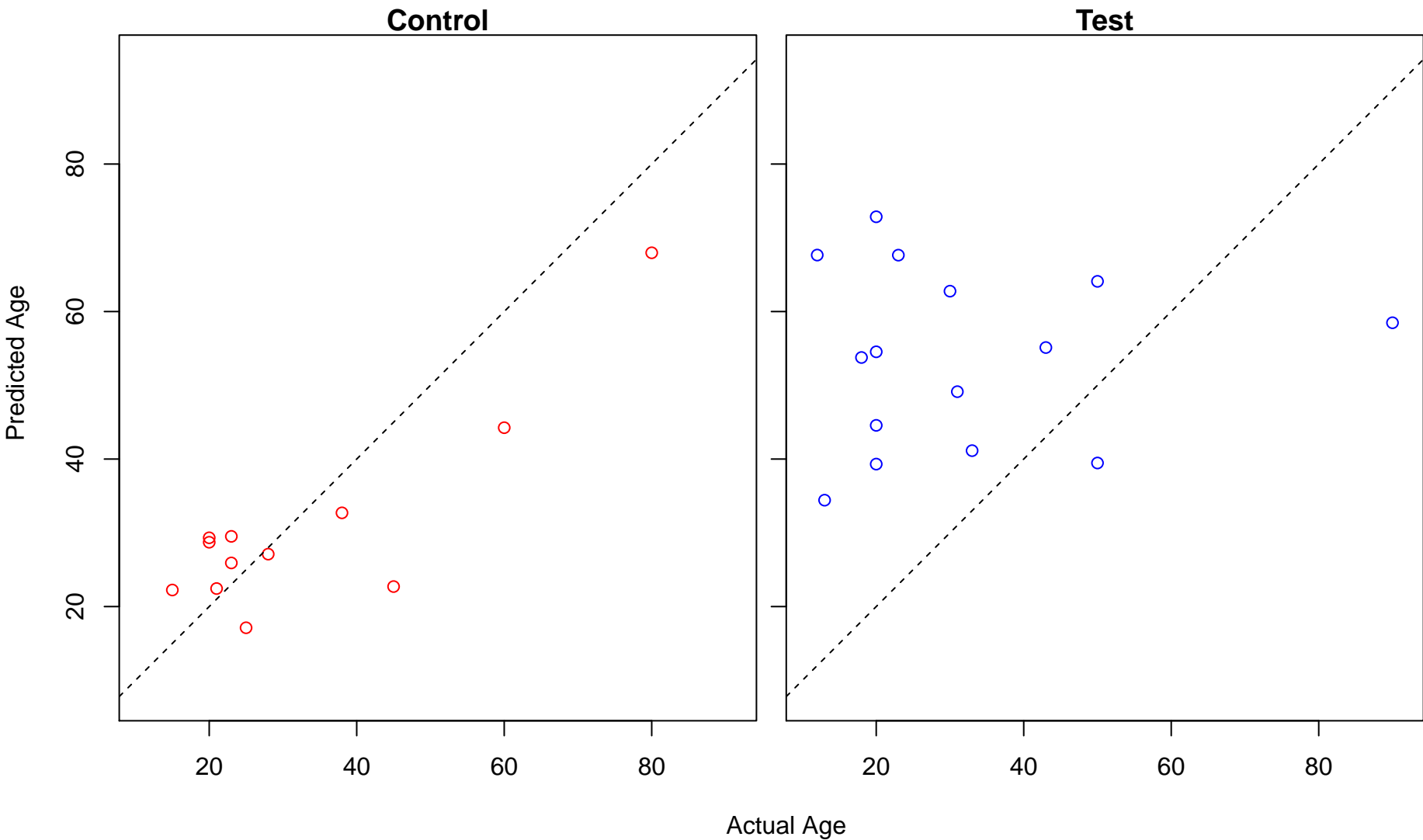
liposaccharide metabolic process (Score: 3.690691)



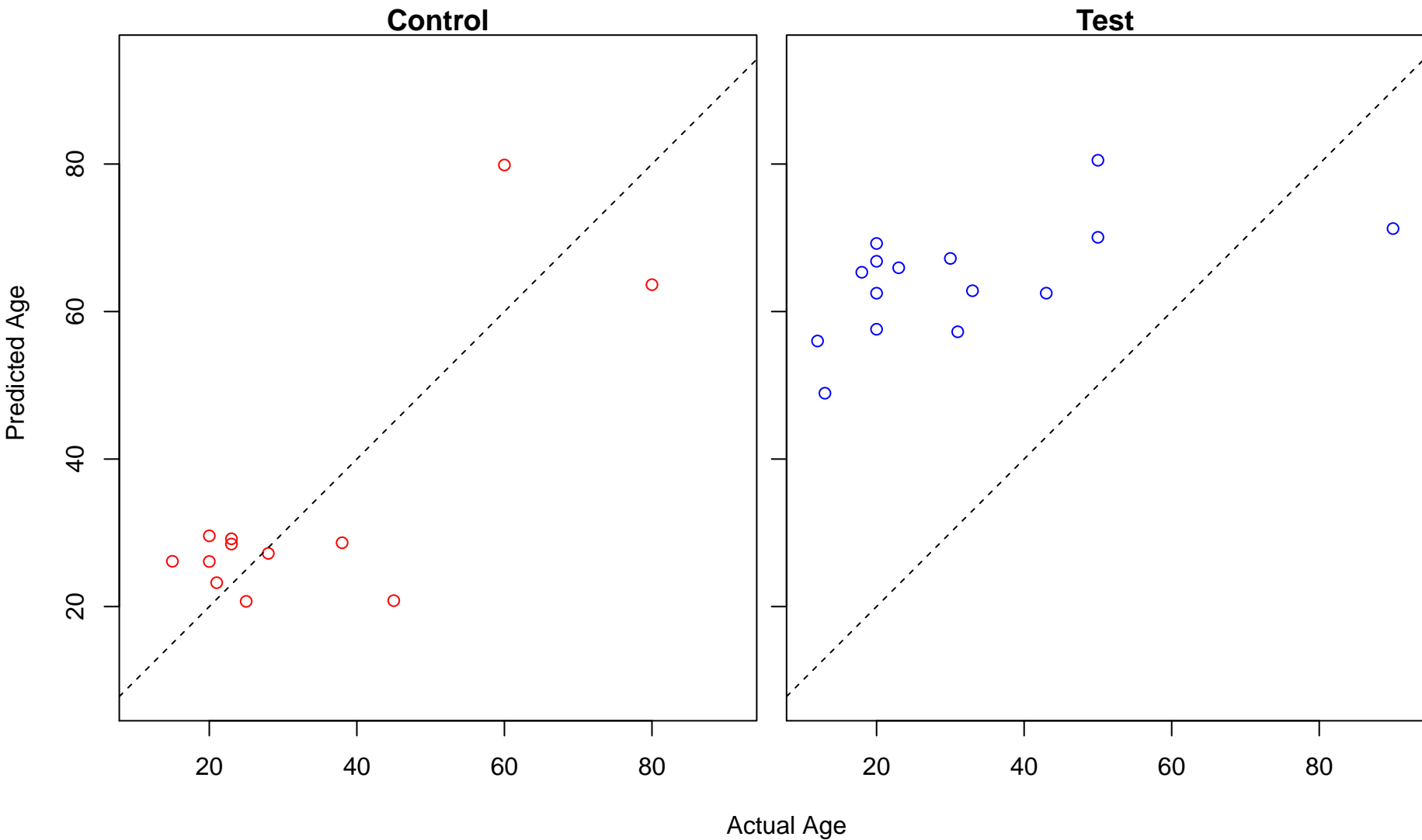
glycolipid metabolic process (Score: 3.690682)



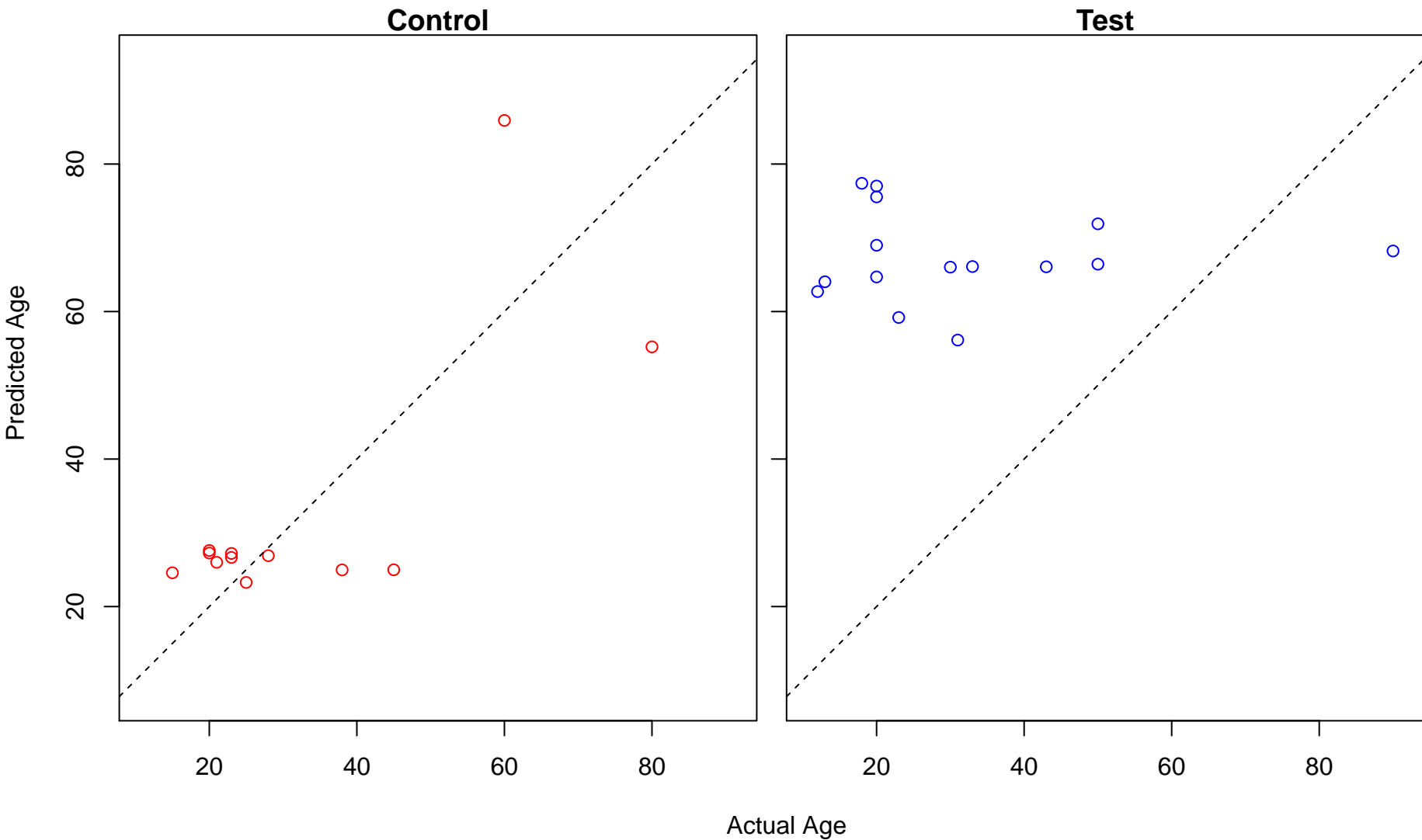
regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion (Score: 3



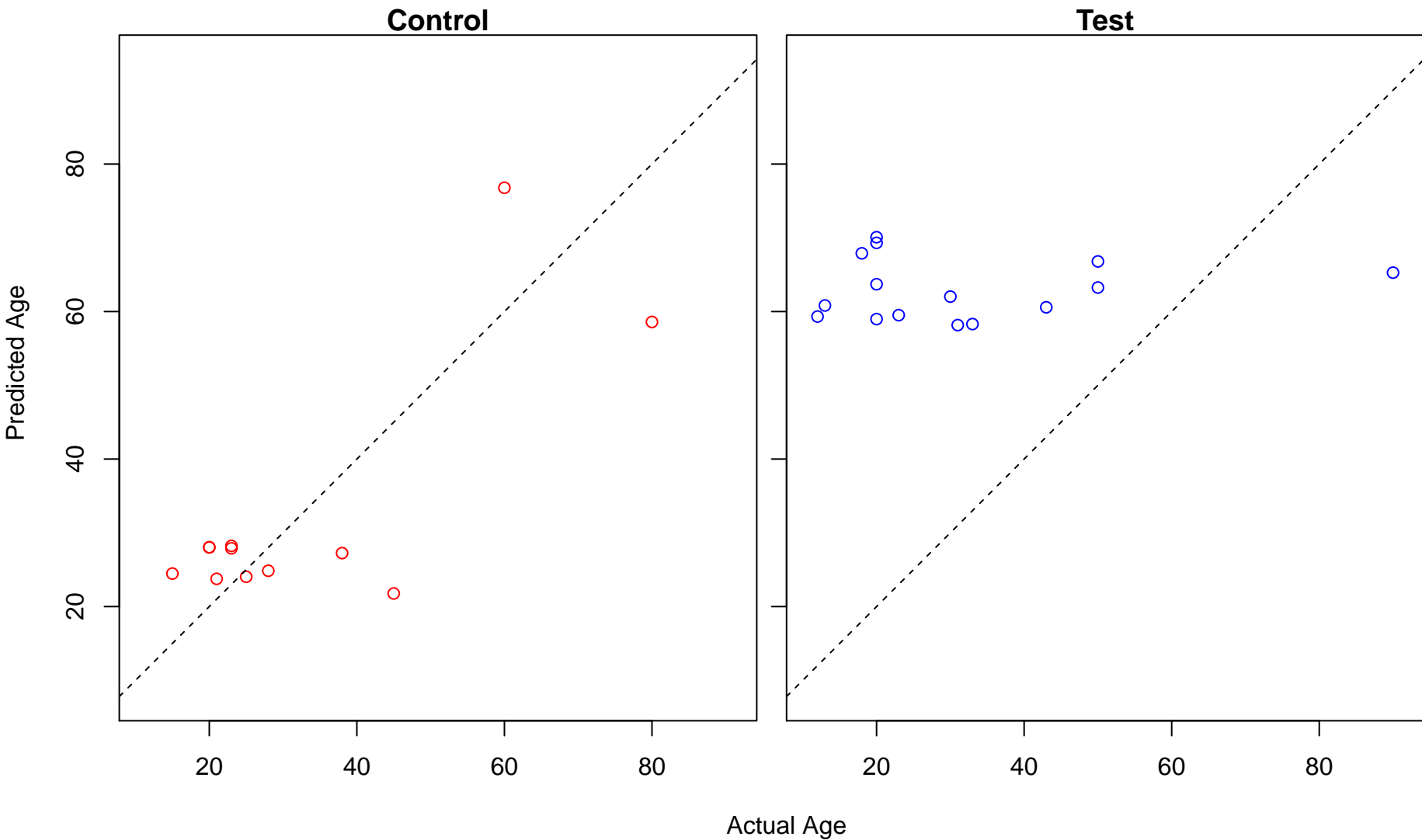
protein O-linked glycosylation (Score: 3.687488)



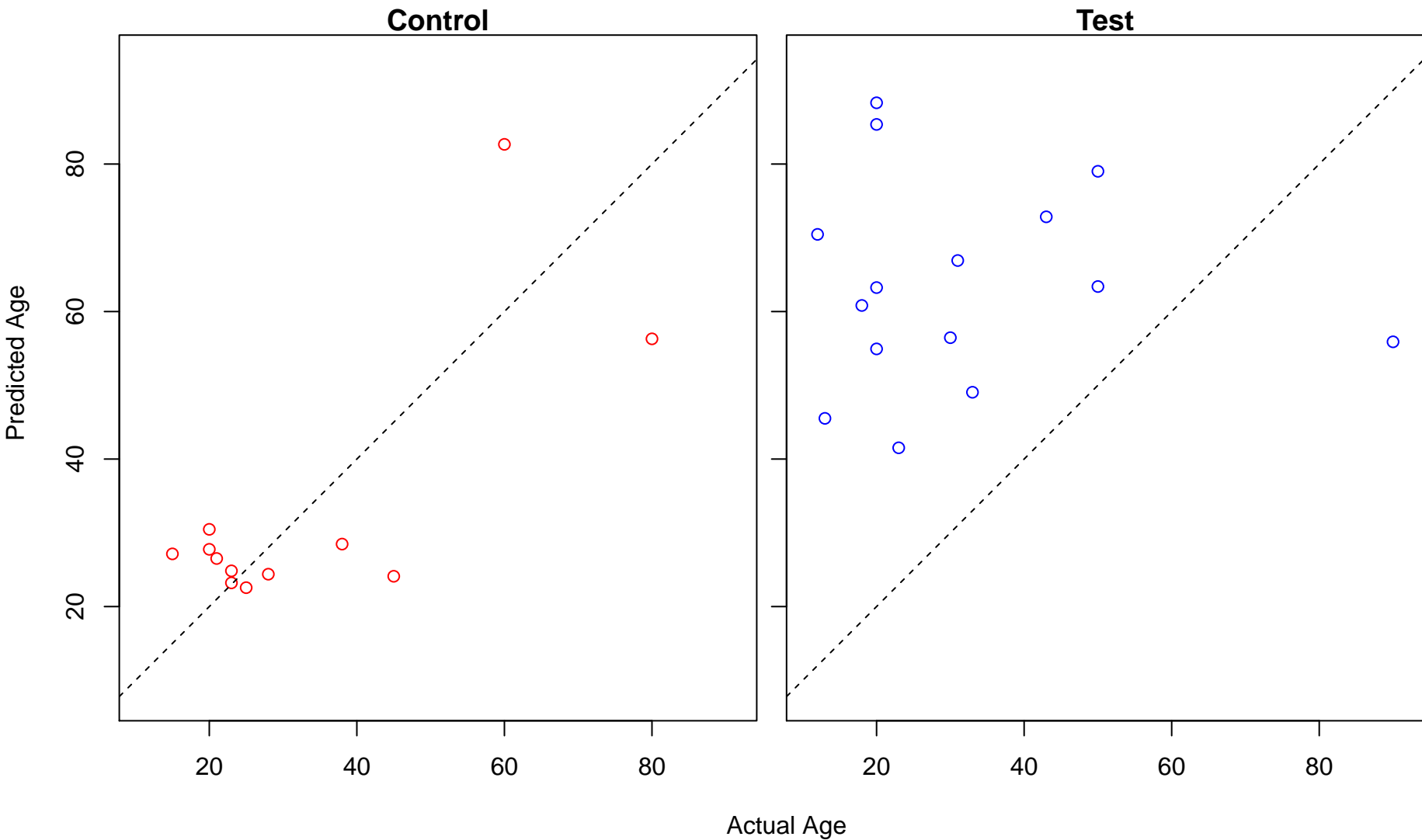
positive regulation of cell cycle phase transition (Score: 3.685827)



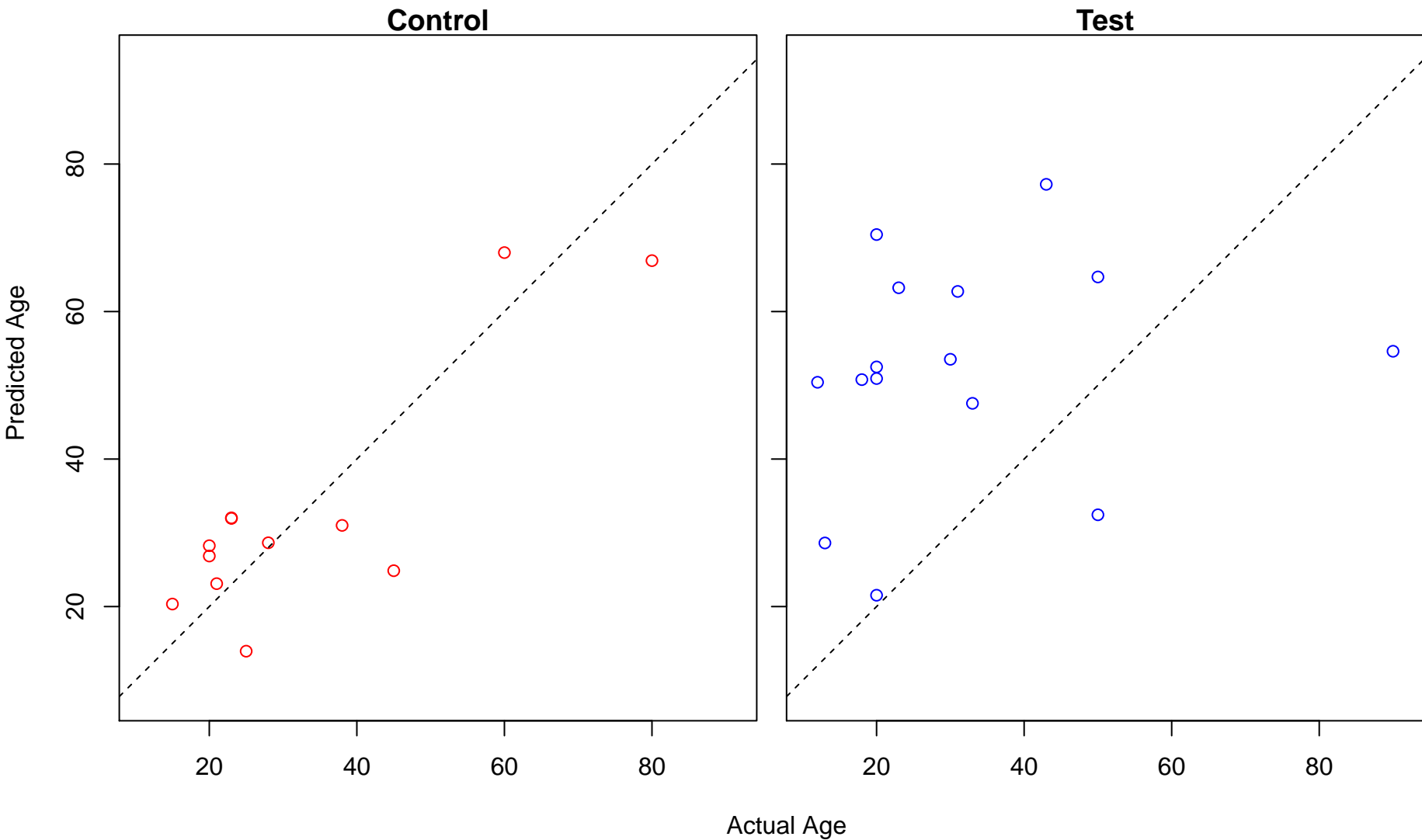
nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay (Score: 3.683854)



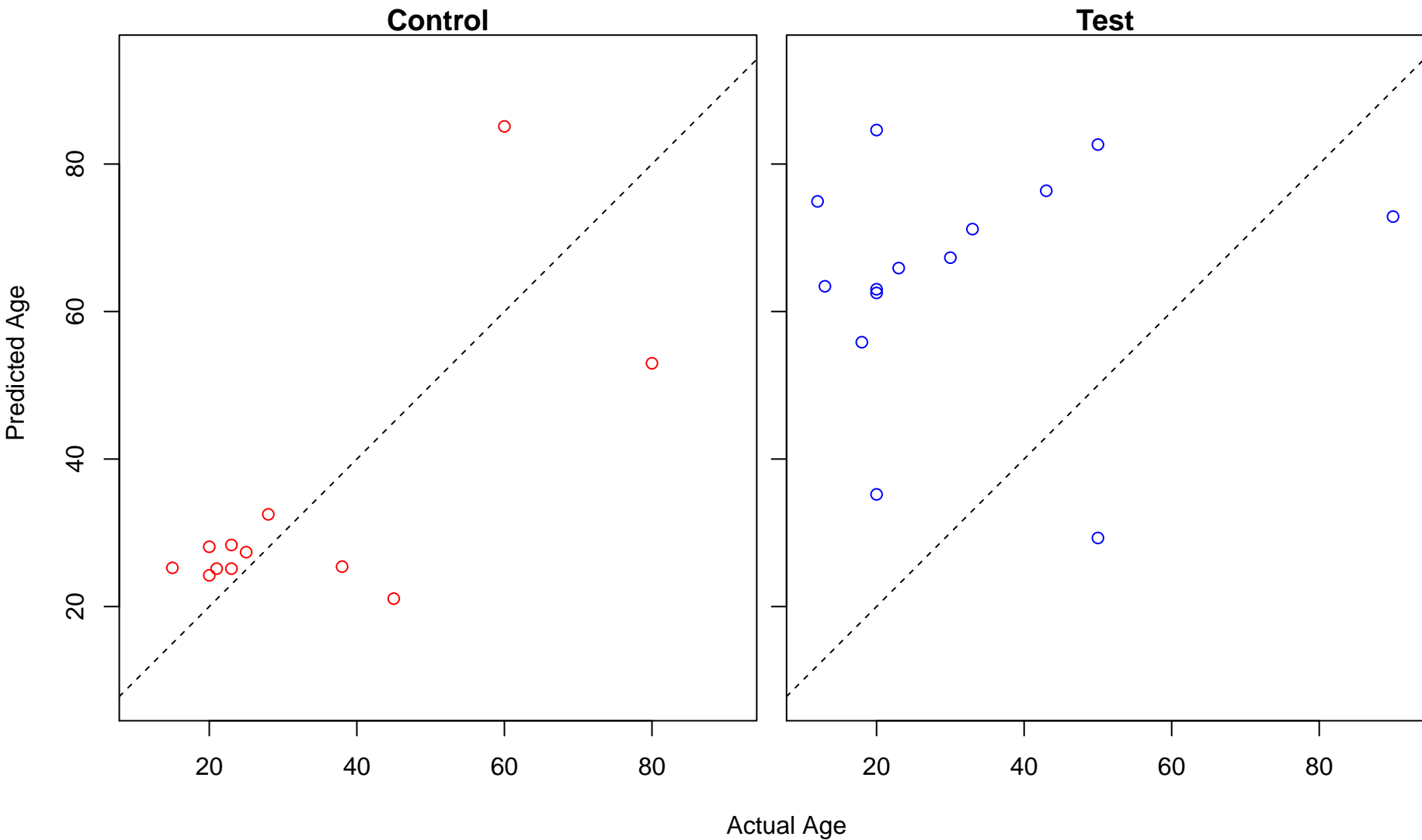
protein import into nucleus, translocation (Score: 3.681334)



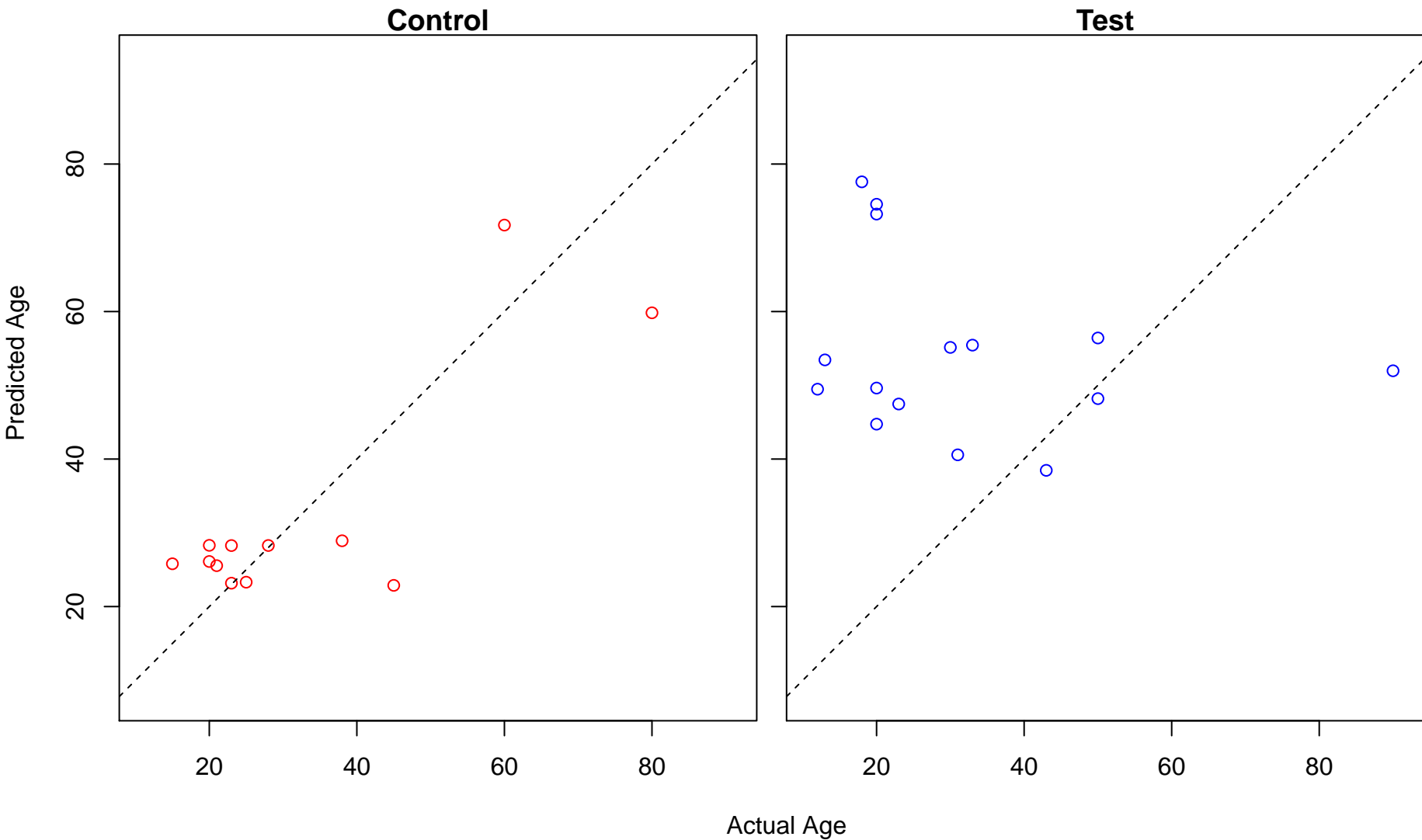
ribonucleoside catabolic process (Score: 3.671885)



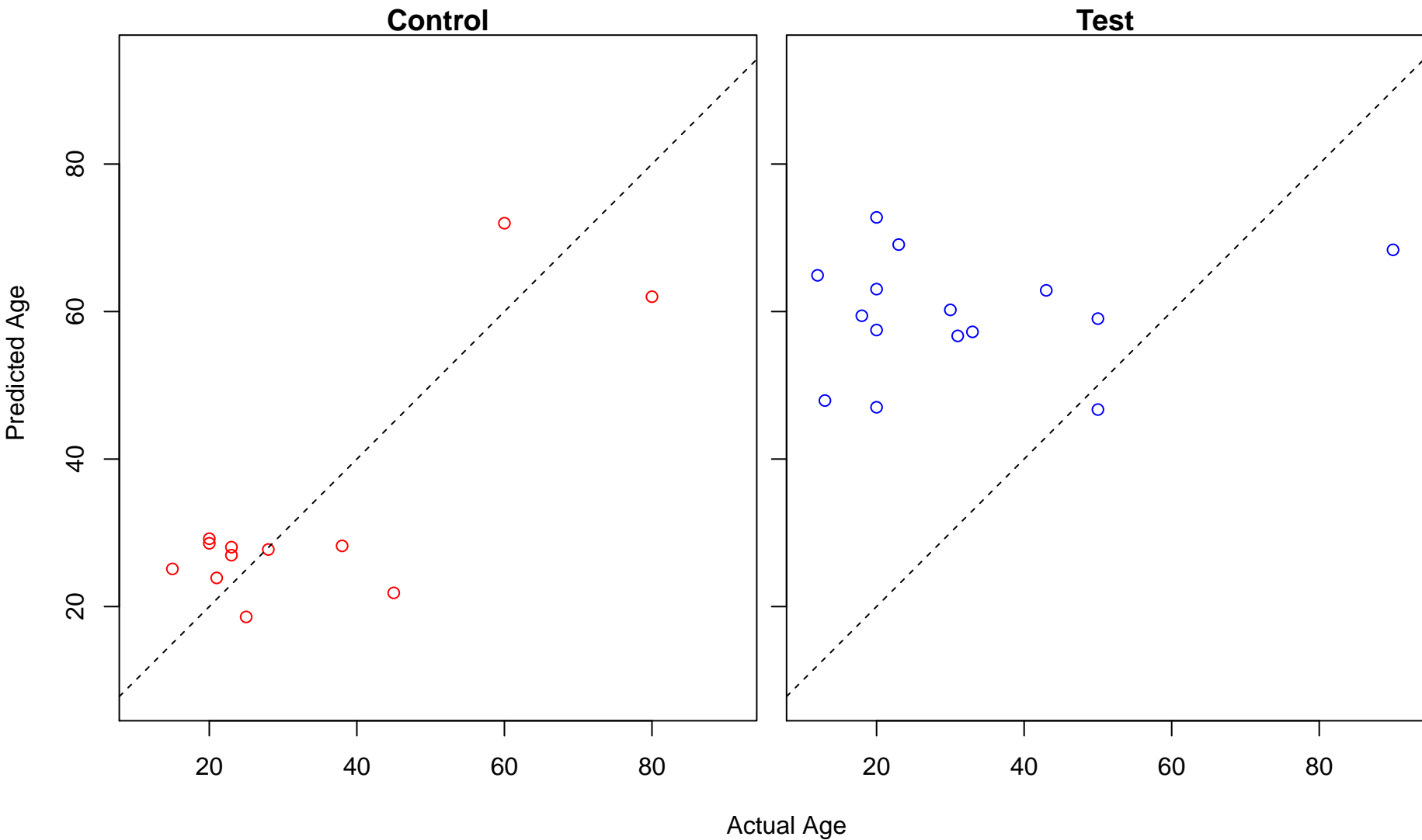
negative regulation of cell morphogenesis involved in differentiation (Score: 3.671884)



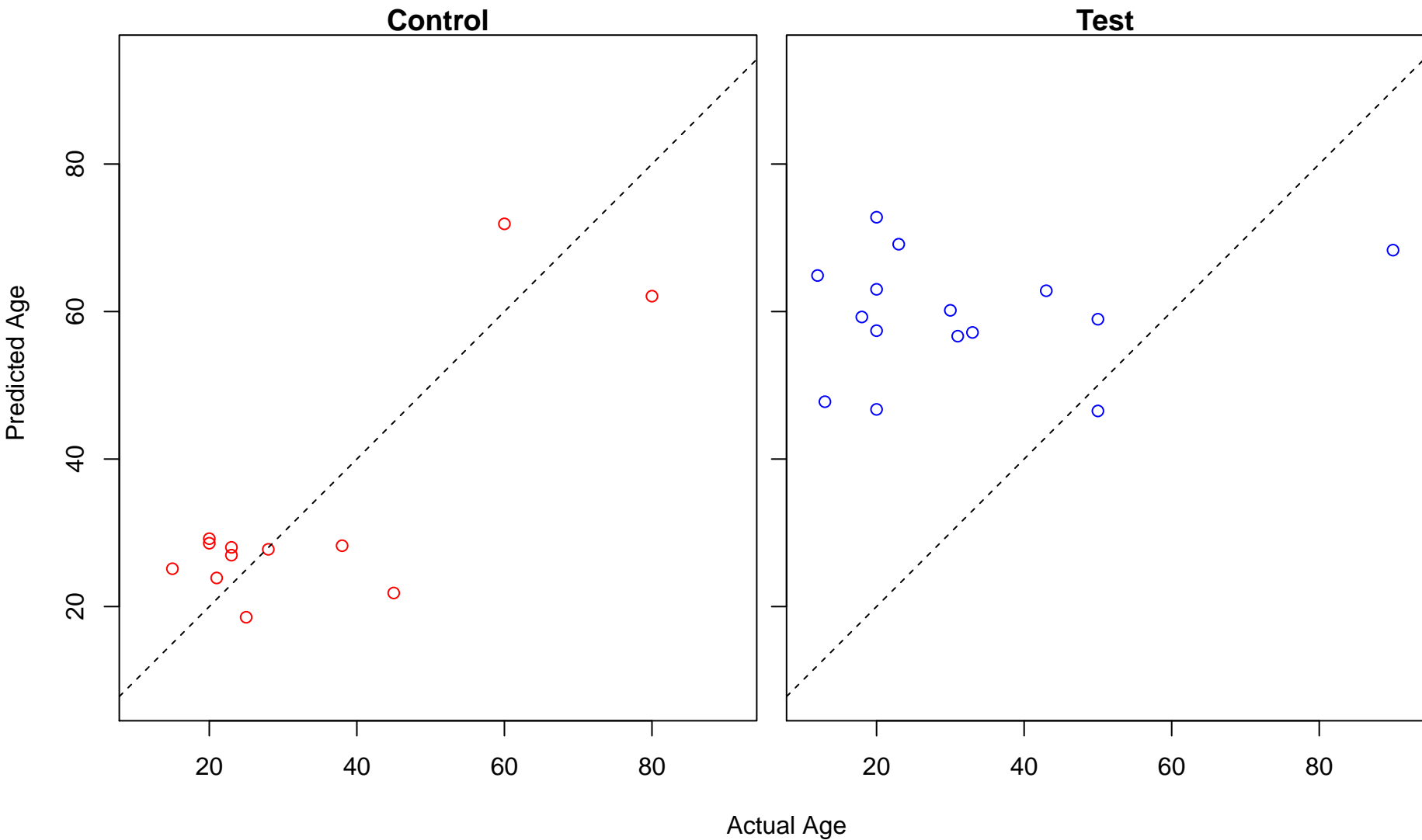
chaperone-mediated protein folding (Score: 3.671541)



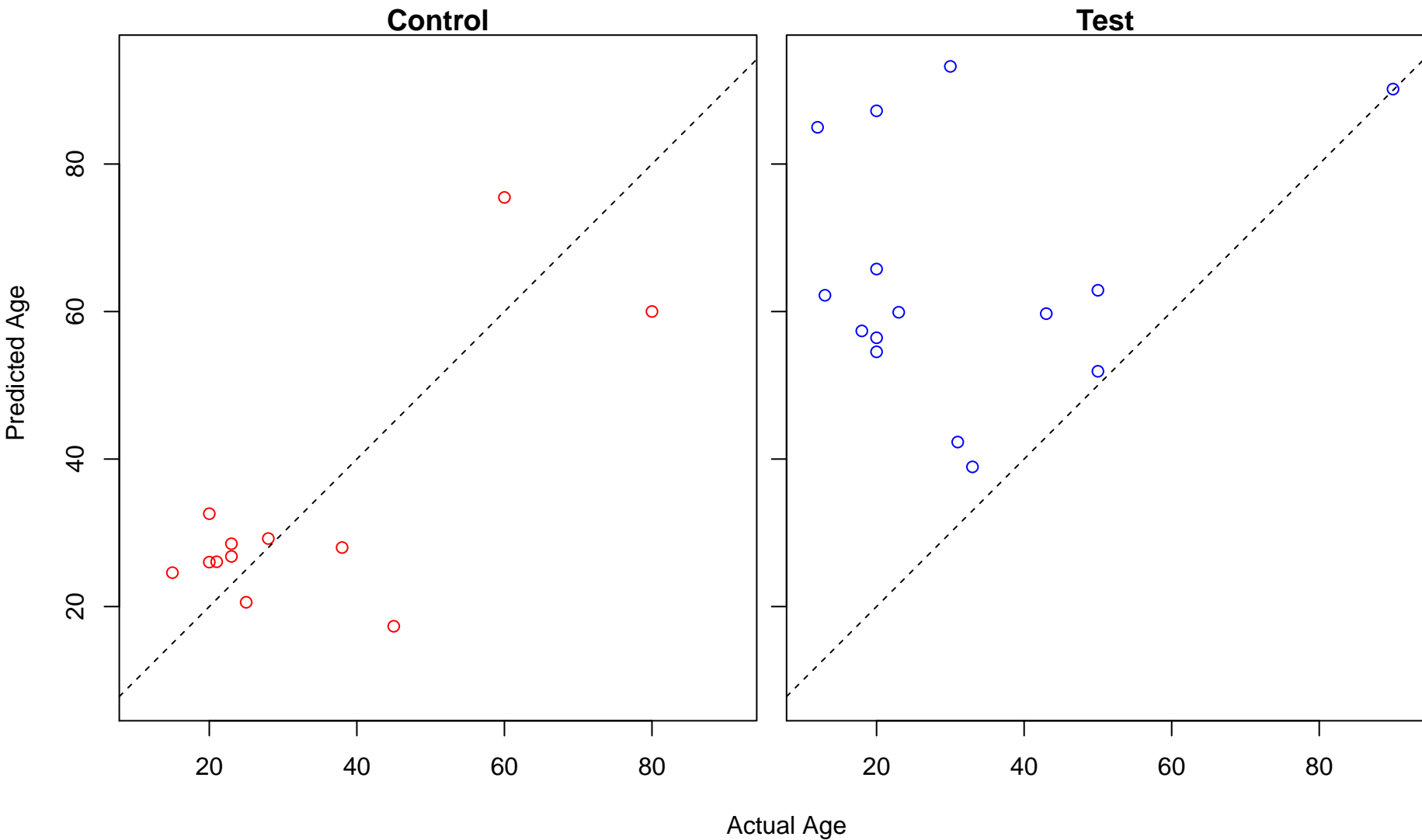
activation of protein kinase A activity (Score: 3.671109)



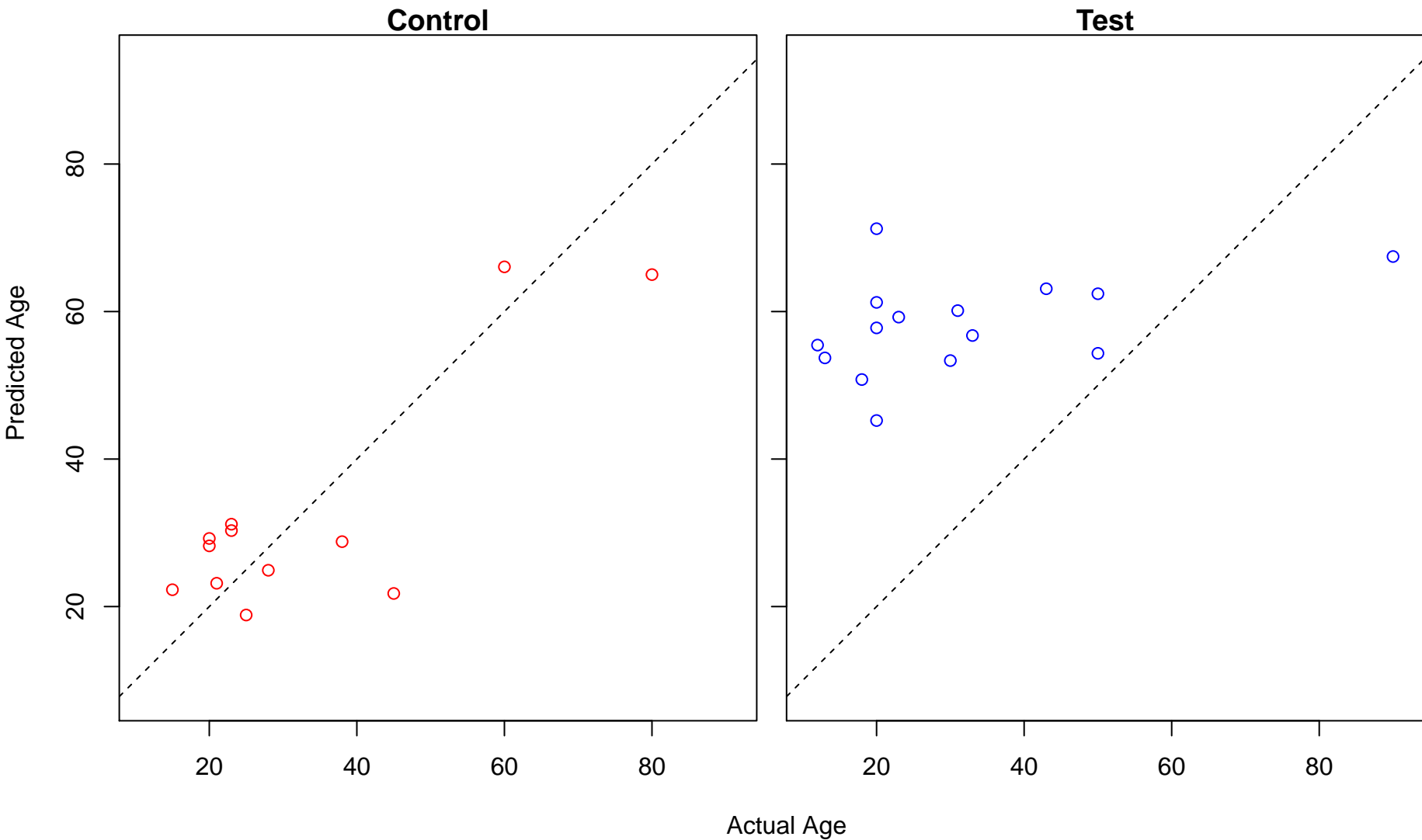
negative regulation of cAMP-dependent protein kinase activity (Score: 3.670123)



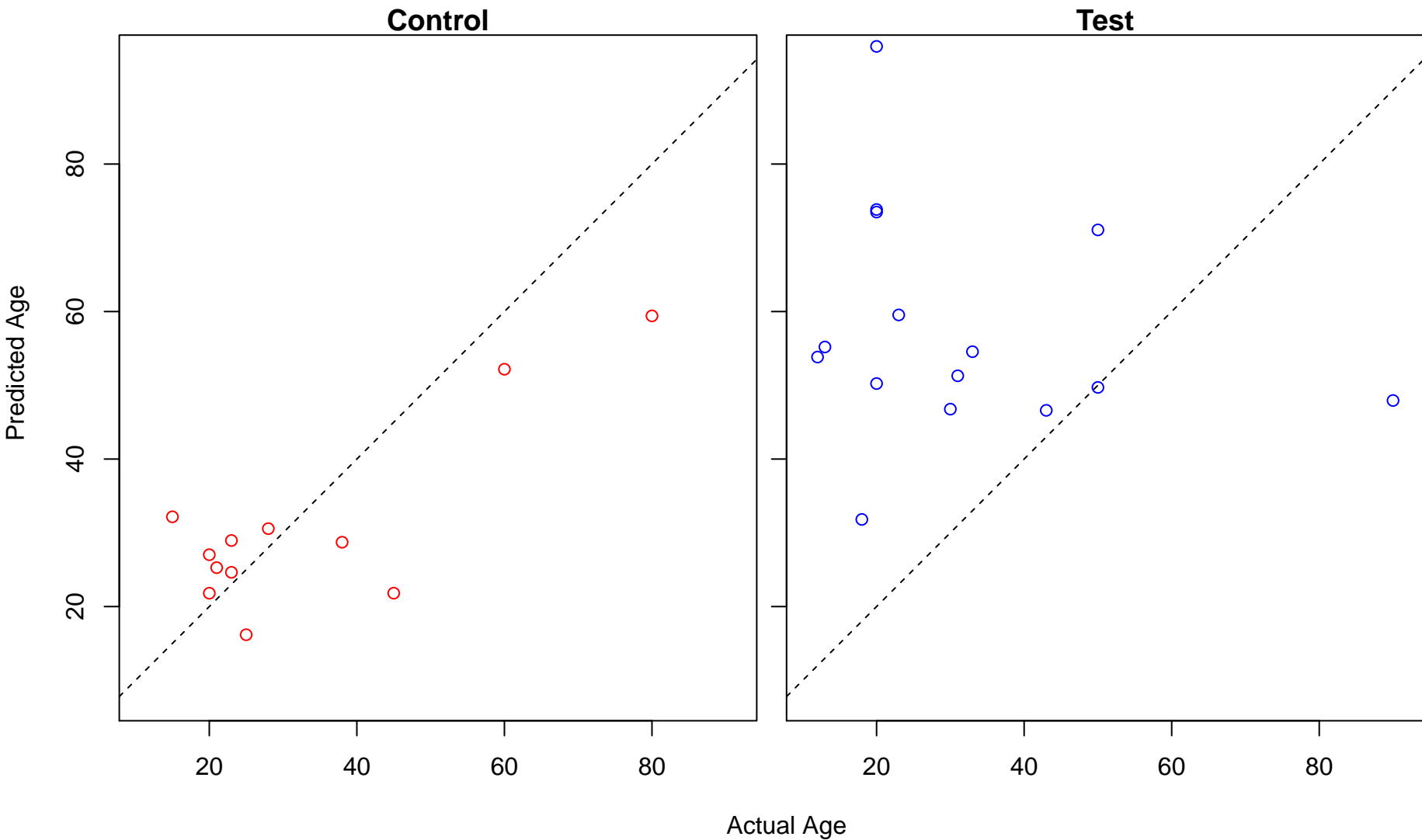
calcium-mediated signaling using intracellular calcium source (Score: 3.670092)



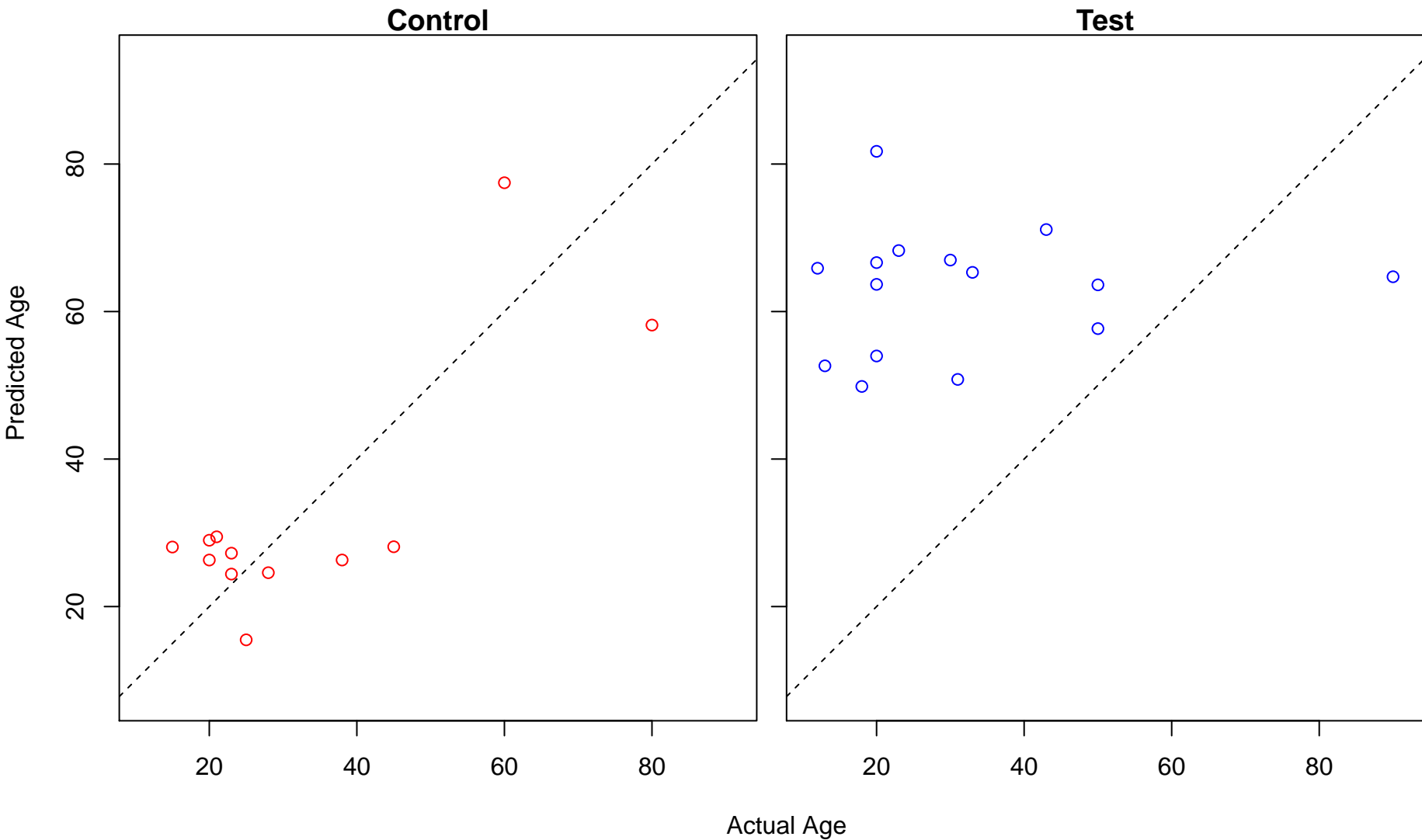
histone H4-K16 acetylation (Score: 3.668103)



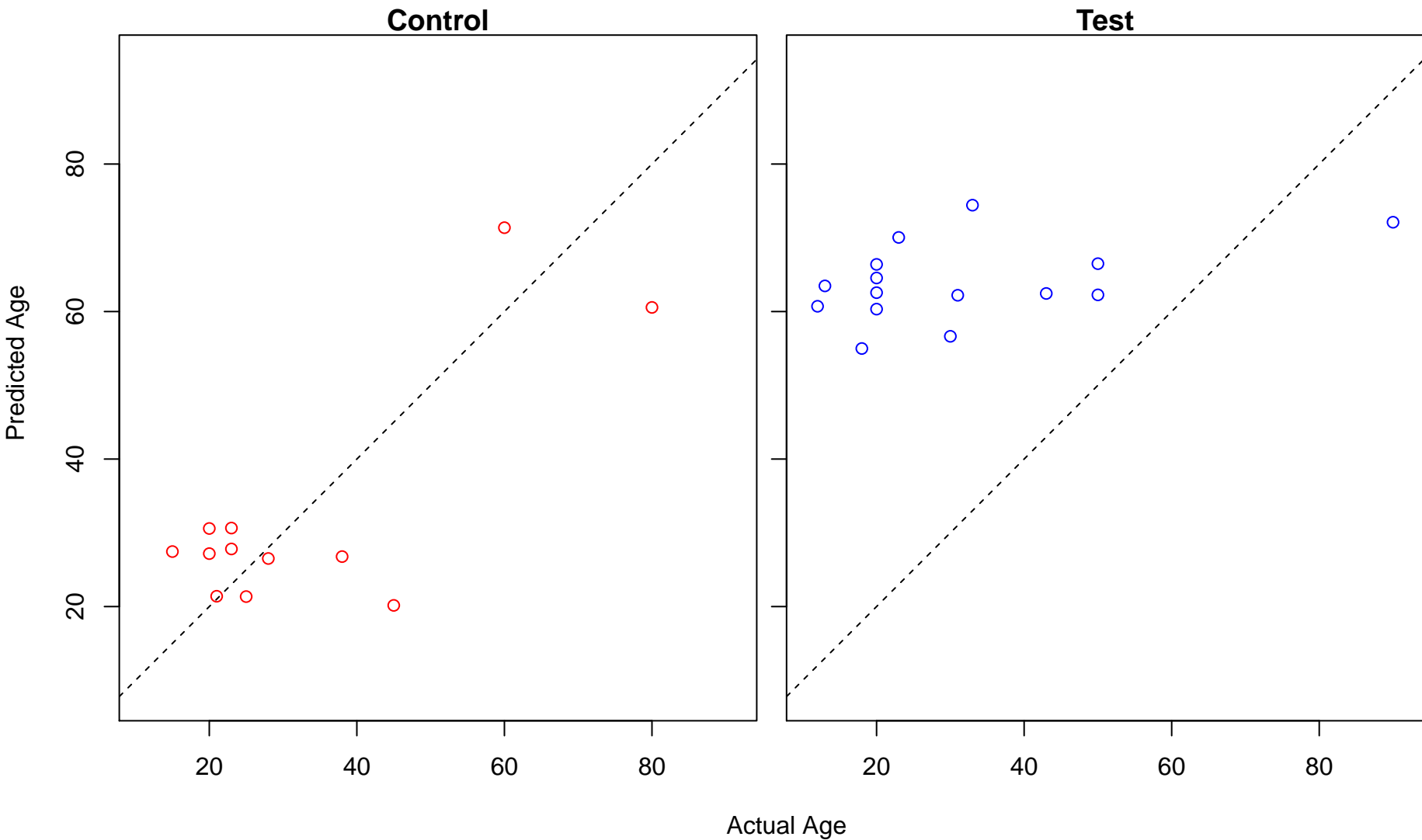
positive regulation of interleukin-13 production (Score: 3.667069)



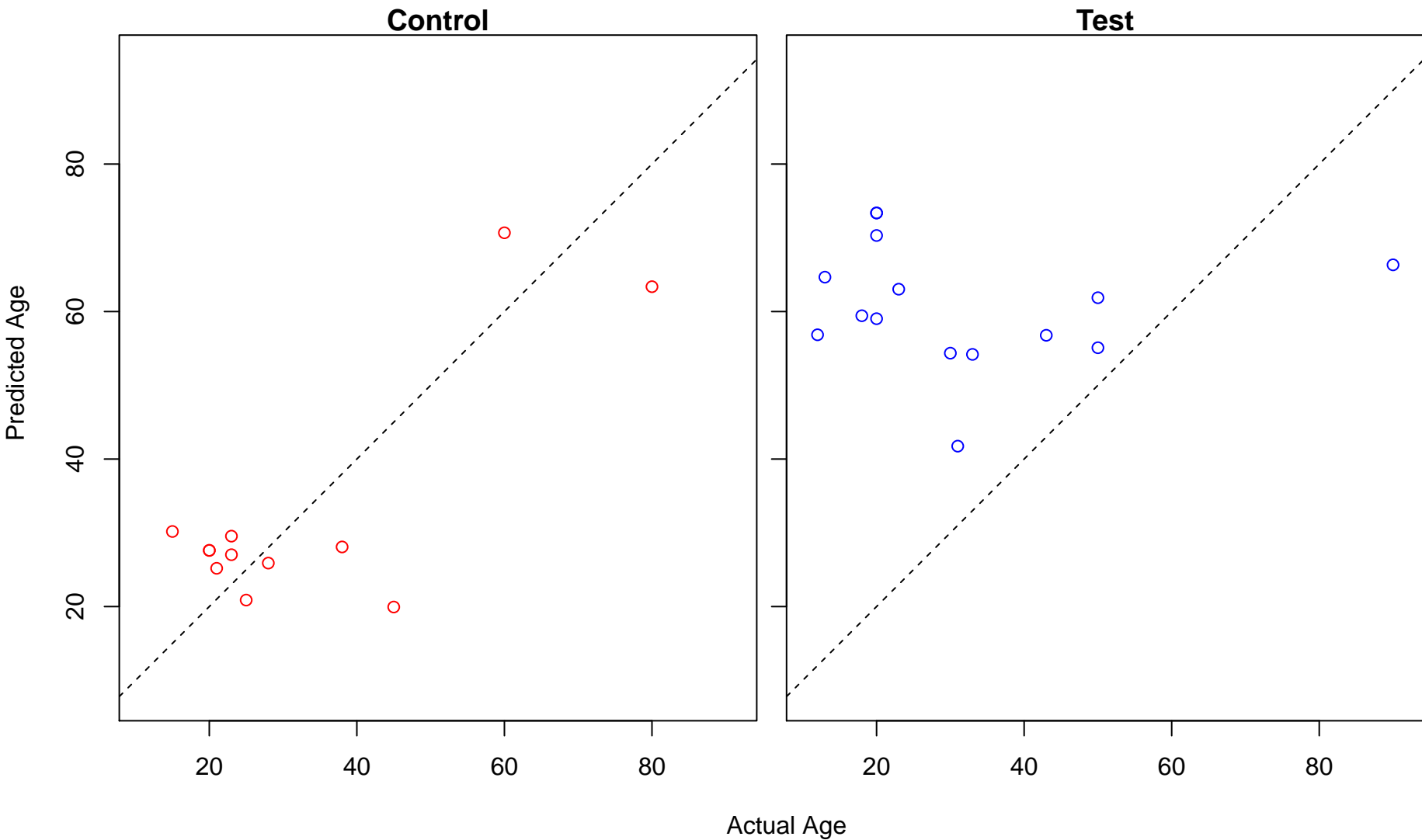
histone-serine phosphorylation (Score: 3.665973)



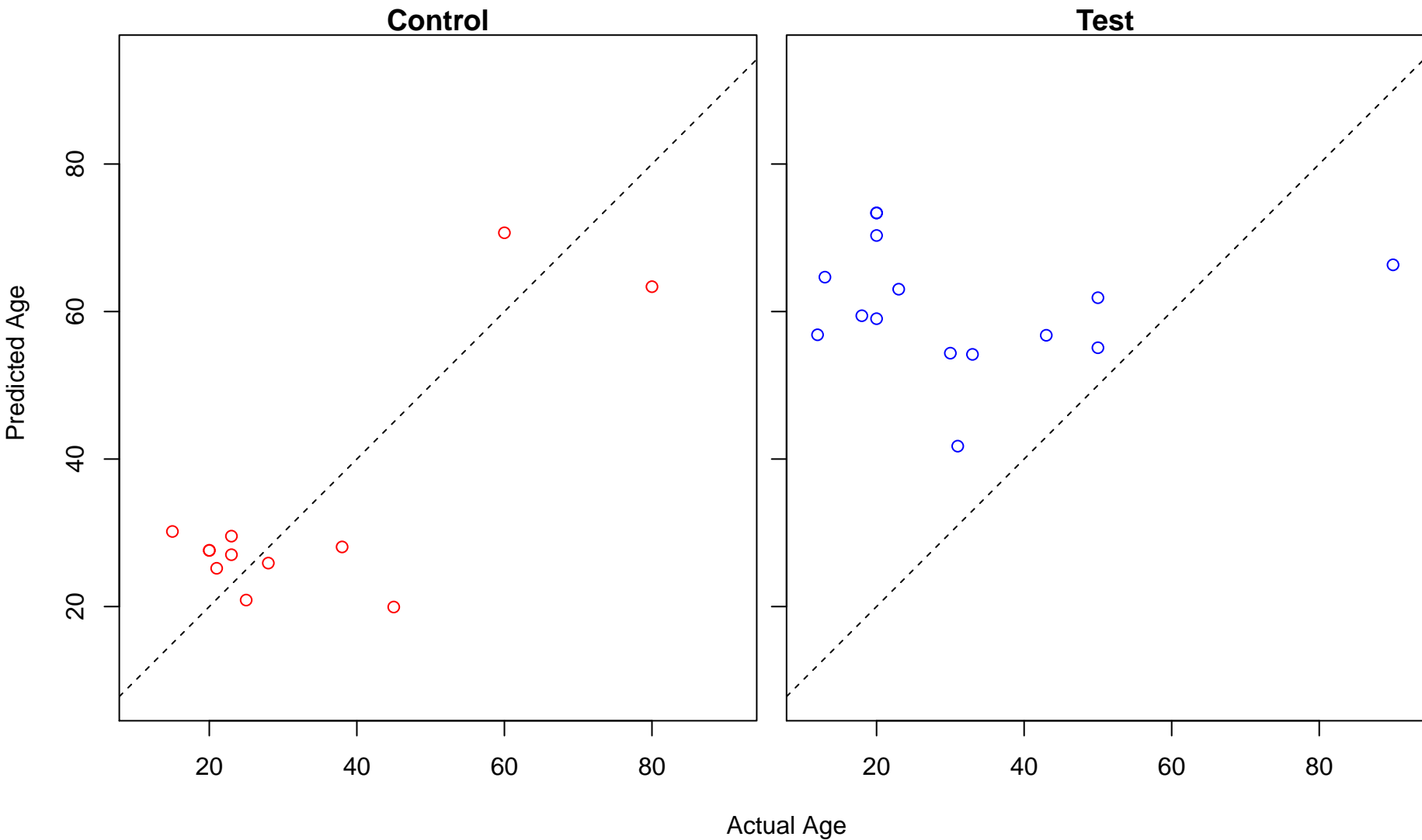
eye morphogenesis (Score: 3.665495)



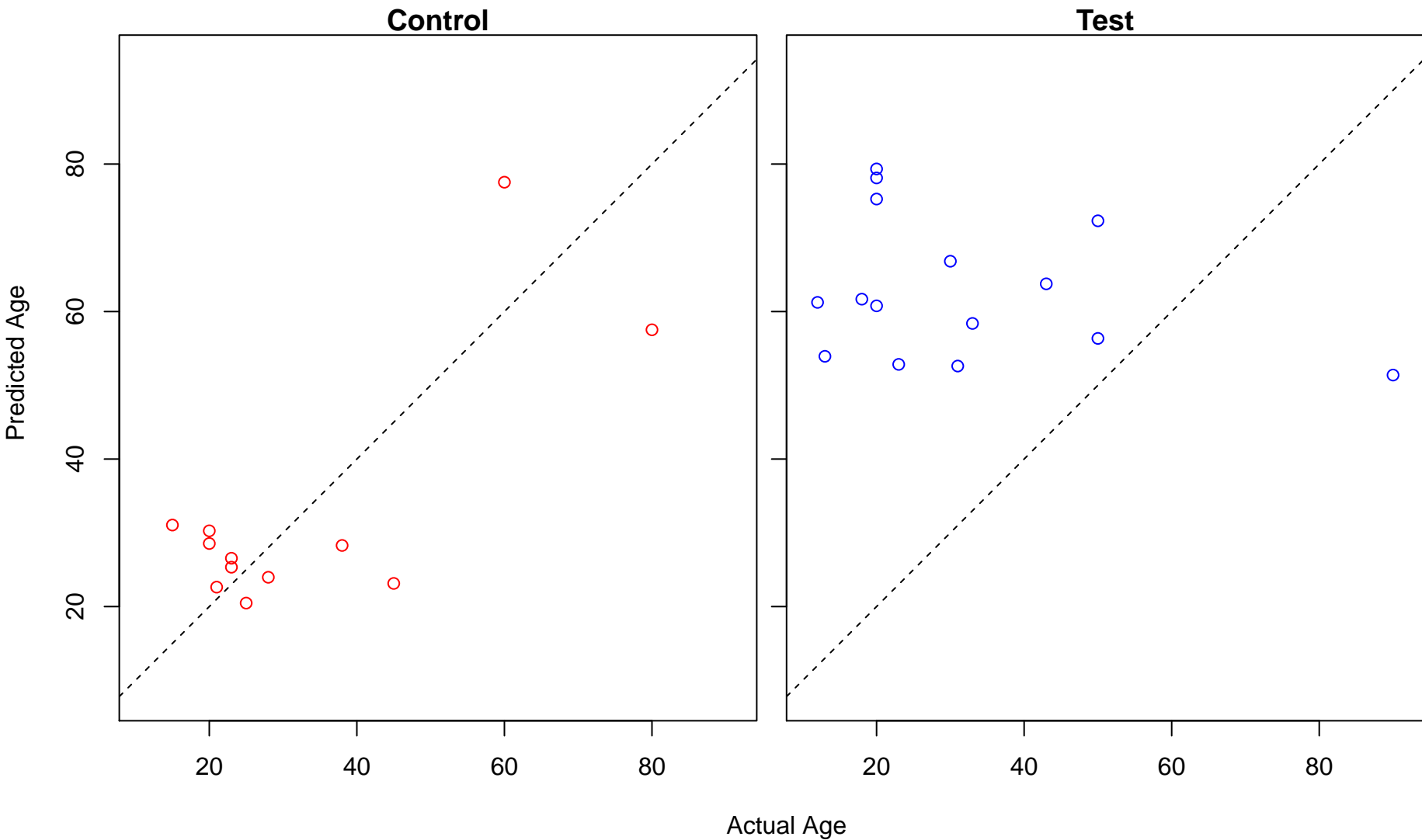
carbohydrate homeostasis (Score: 3.664829)



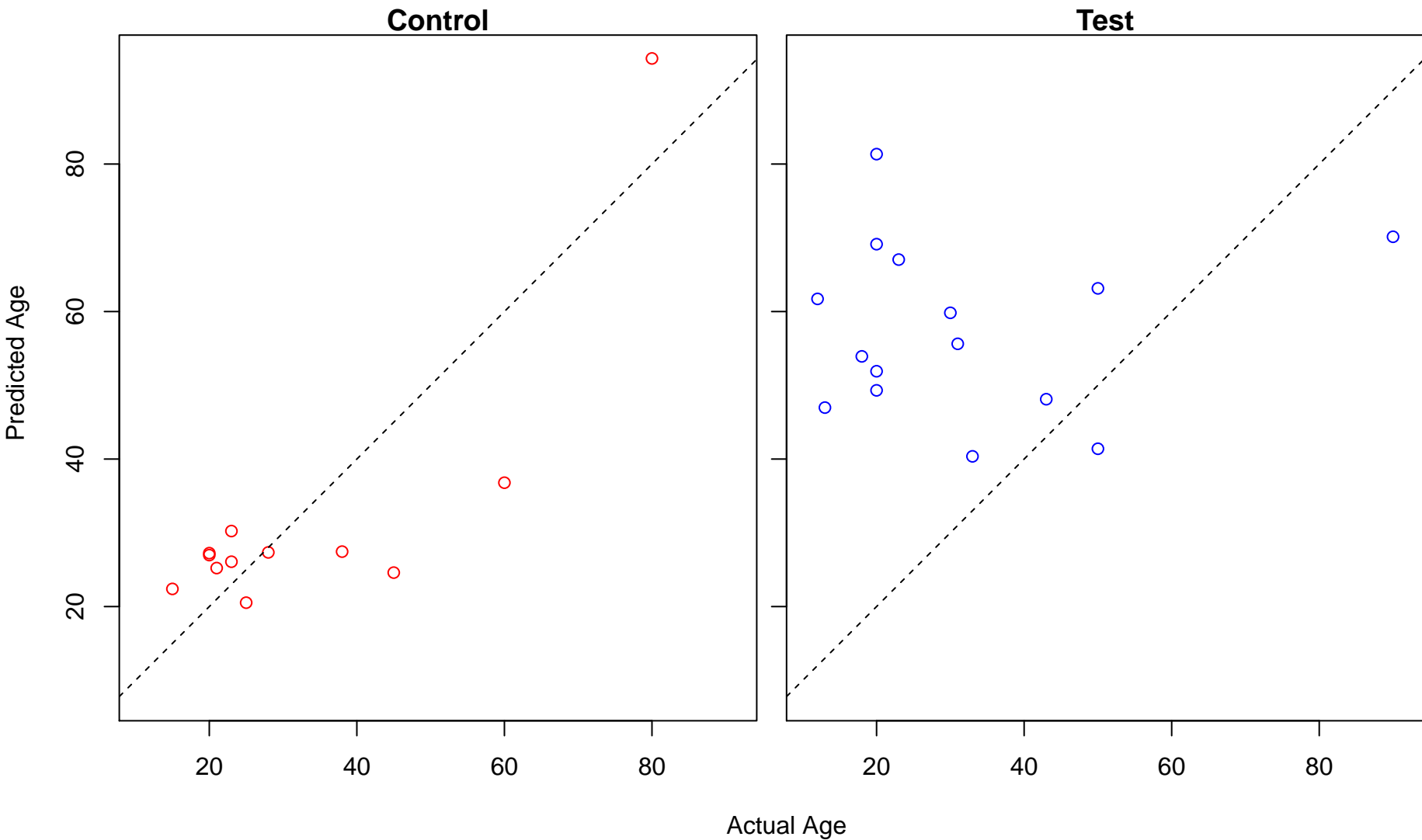
glucose homeostasis (Score: 3.664829)



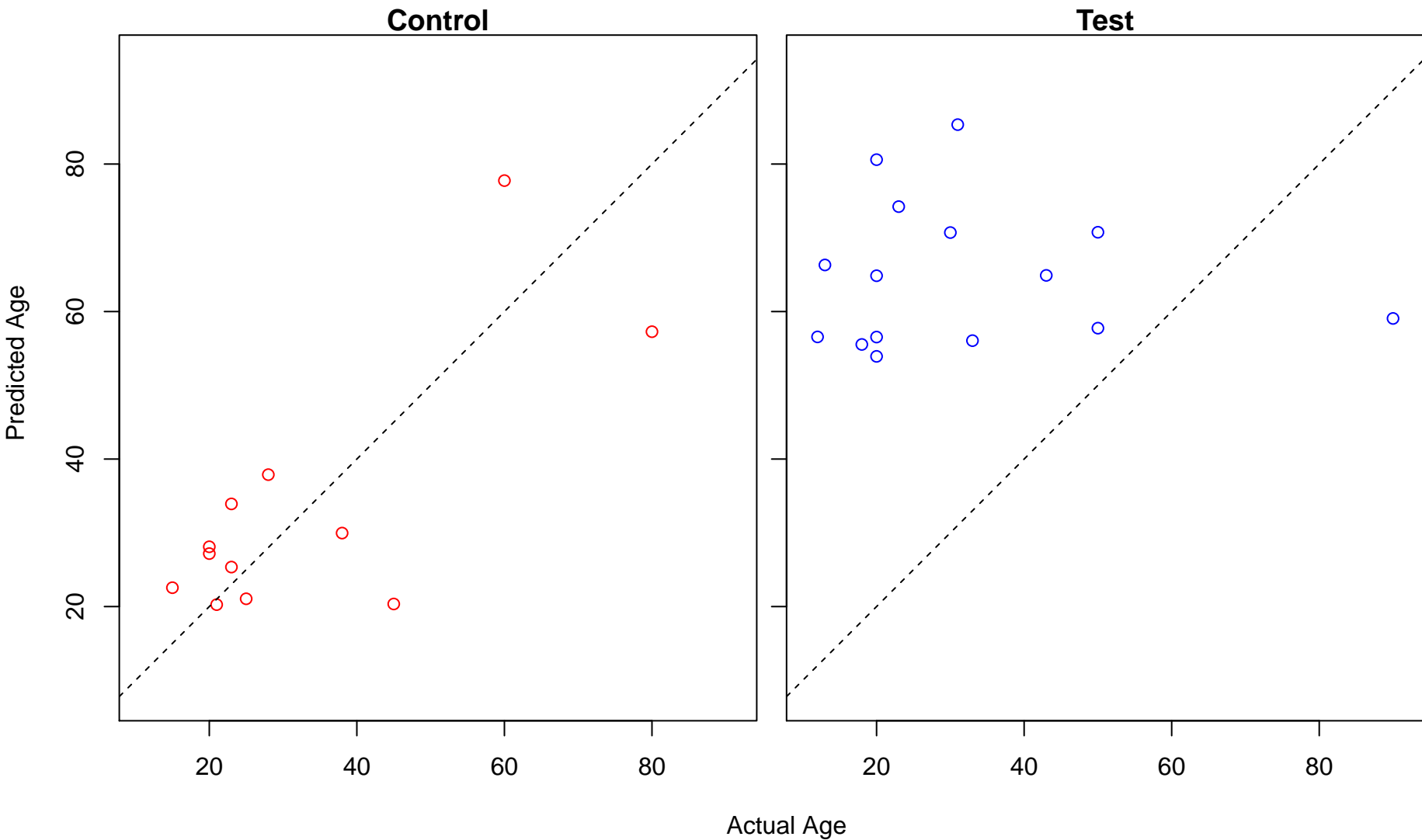
cardiac cell fate commitment (Score: 3.662636)



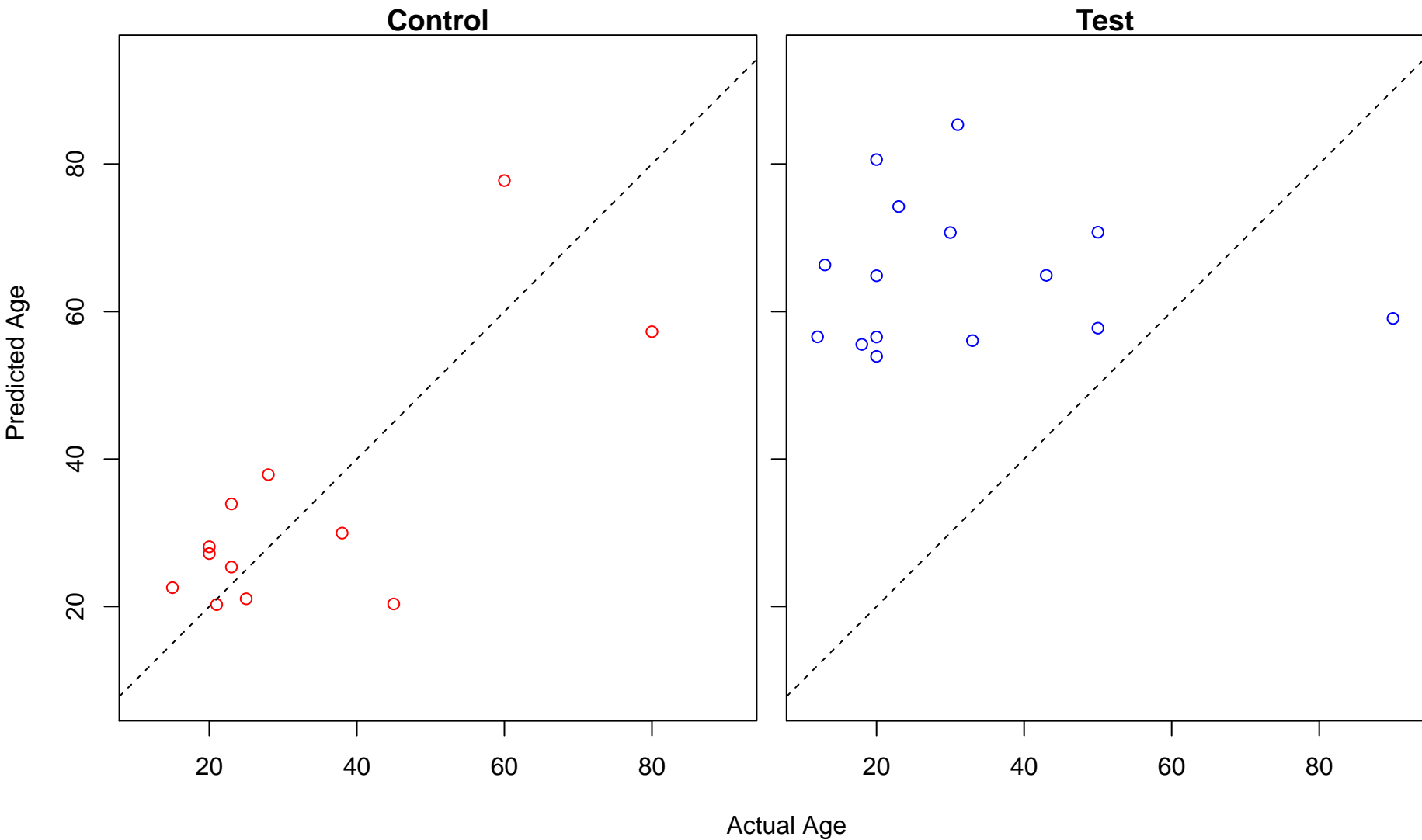
aspartate family amino acid biosynthetic process (Score: 3.662240)



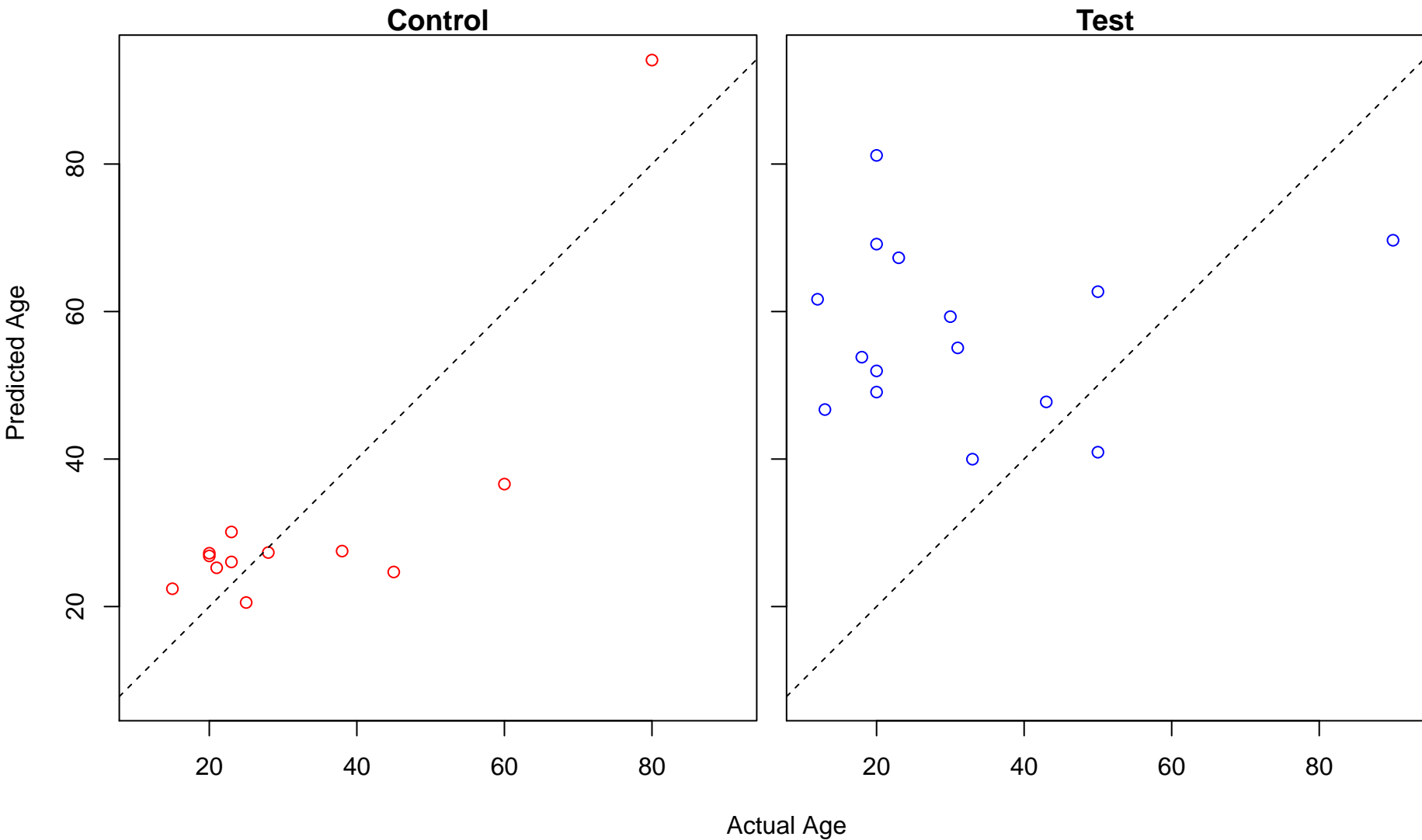
B cell mediated immunity (Score: 3.661992)



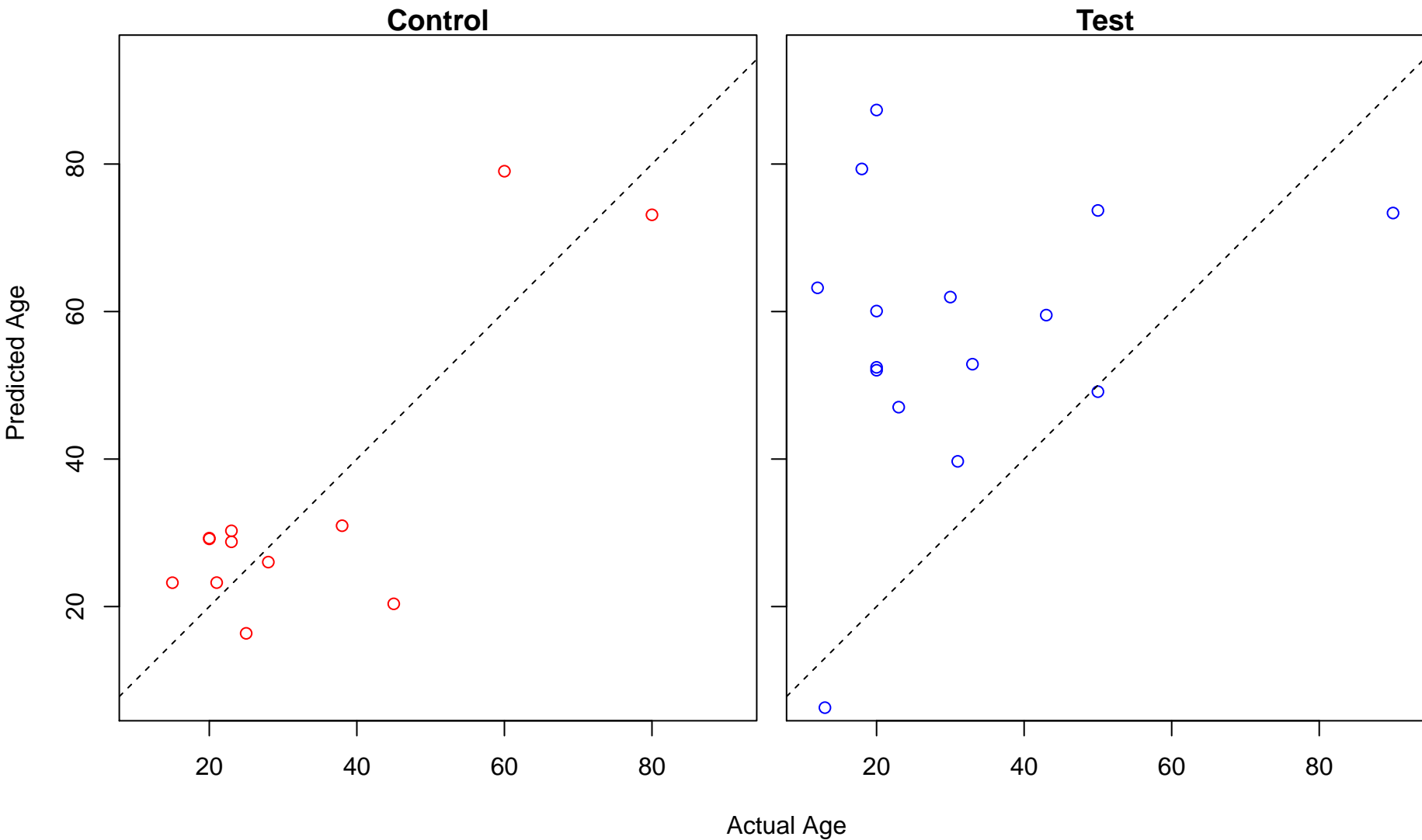
immunoglobulin mediated immune response (Score: 3.661924)



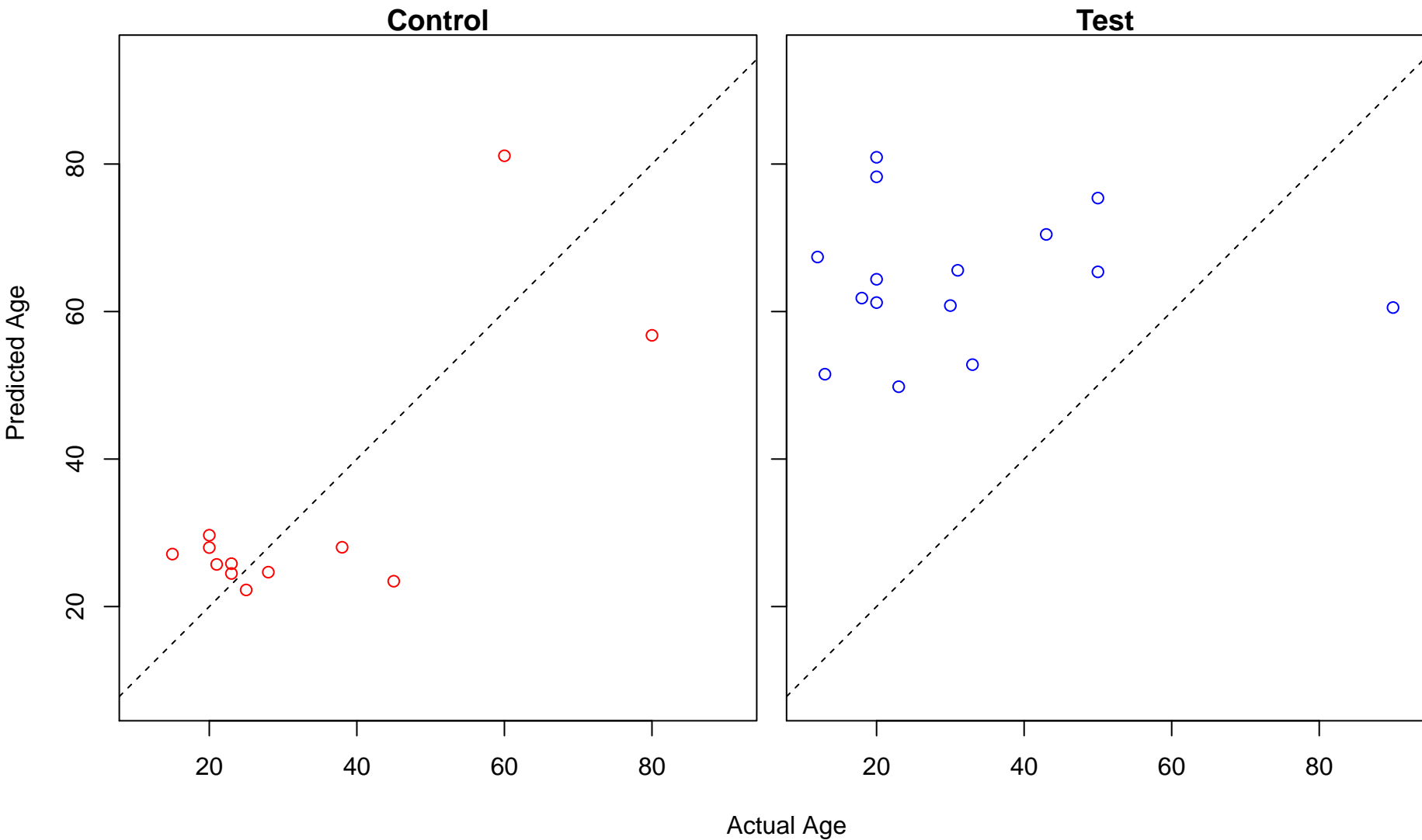
methionine biosynthetic process (Score: 3.661003)



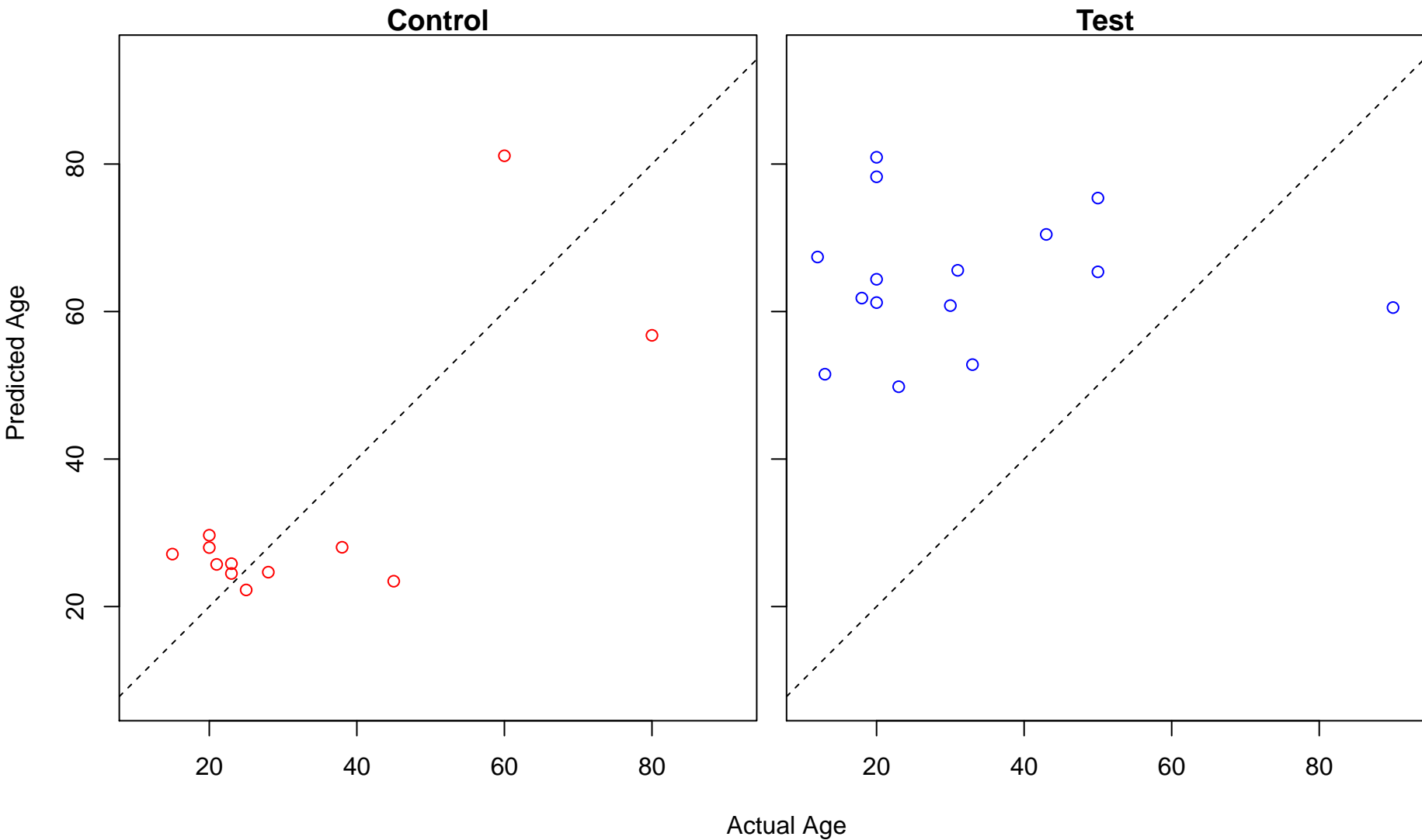
neuroblast proliferation (Score: 3.658382)



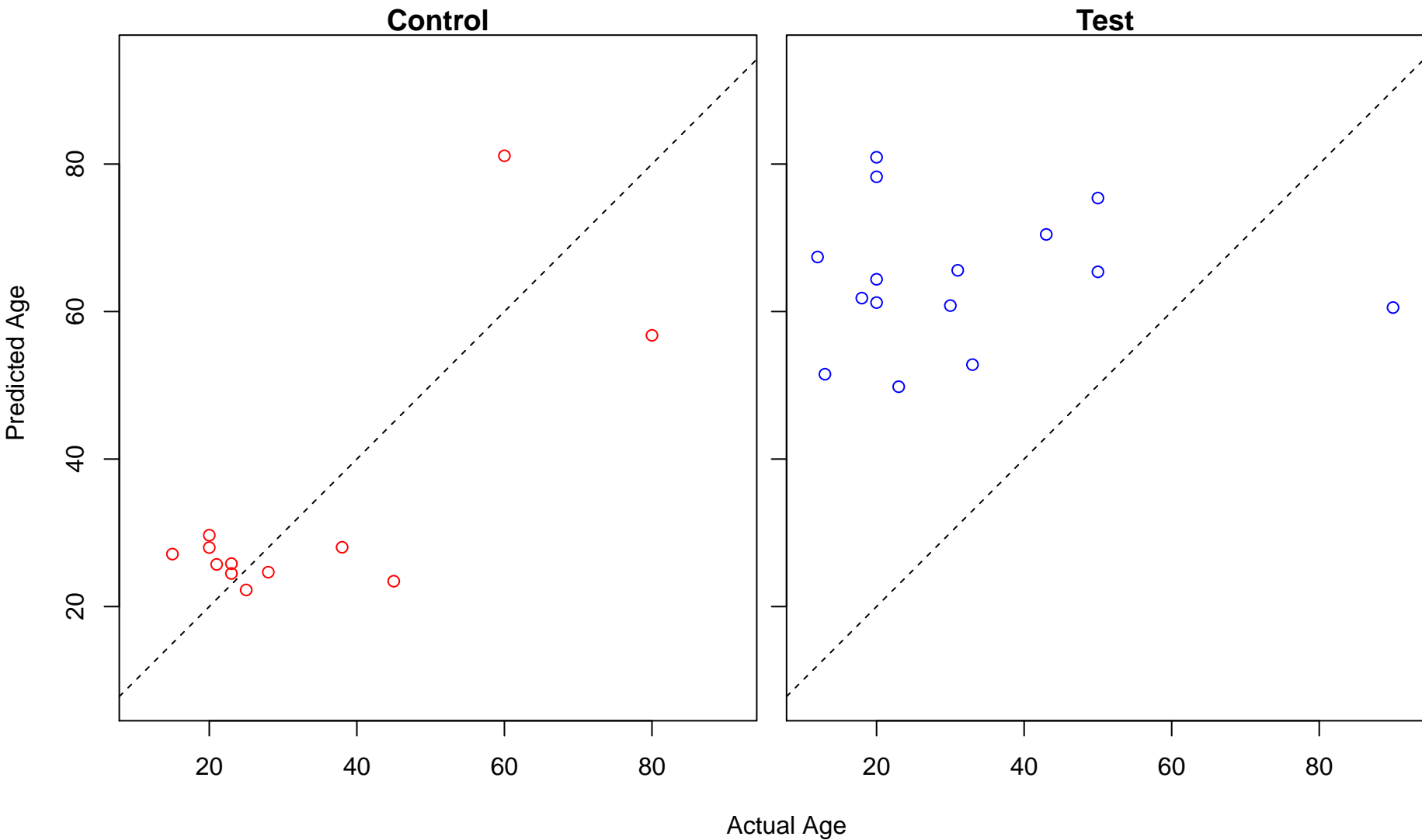
protein import into nucleus (Score: 3.657544)



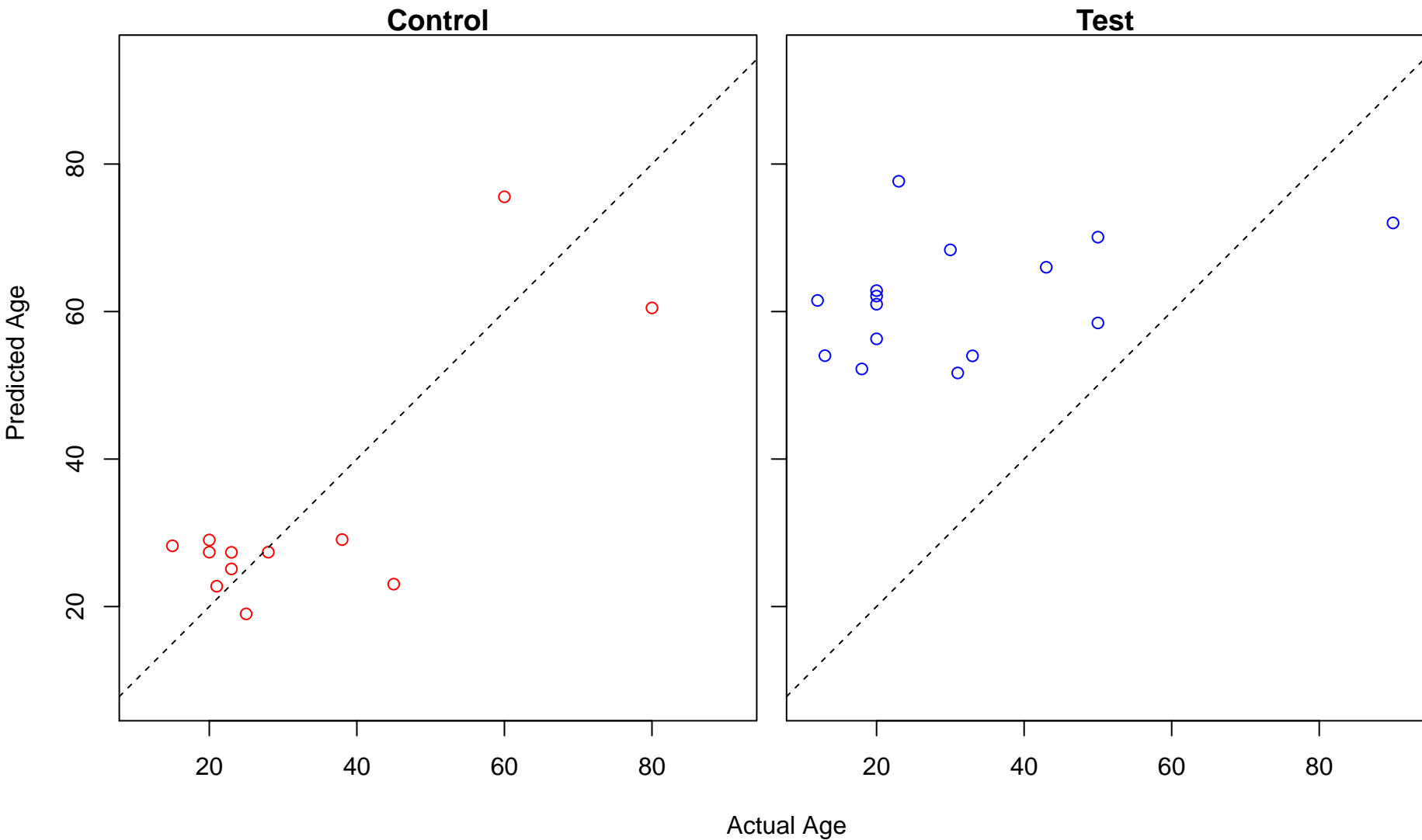
protein targeting to nucleus (Score: 3.657544)



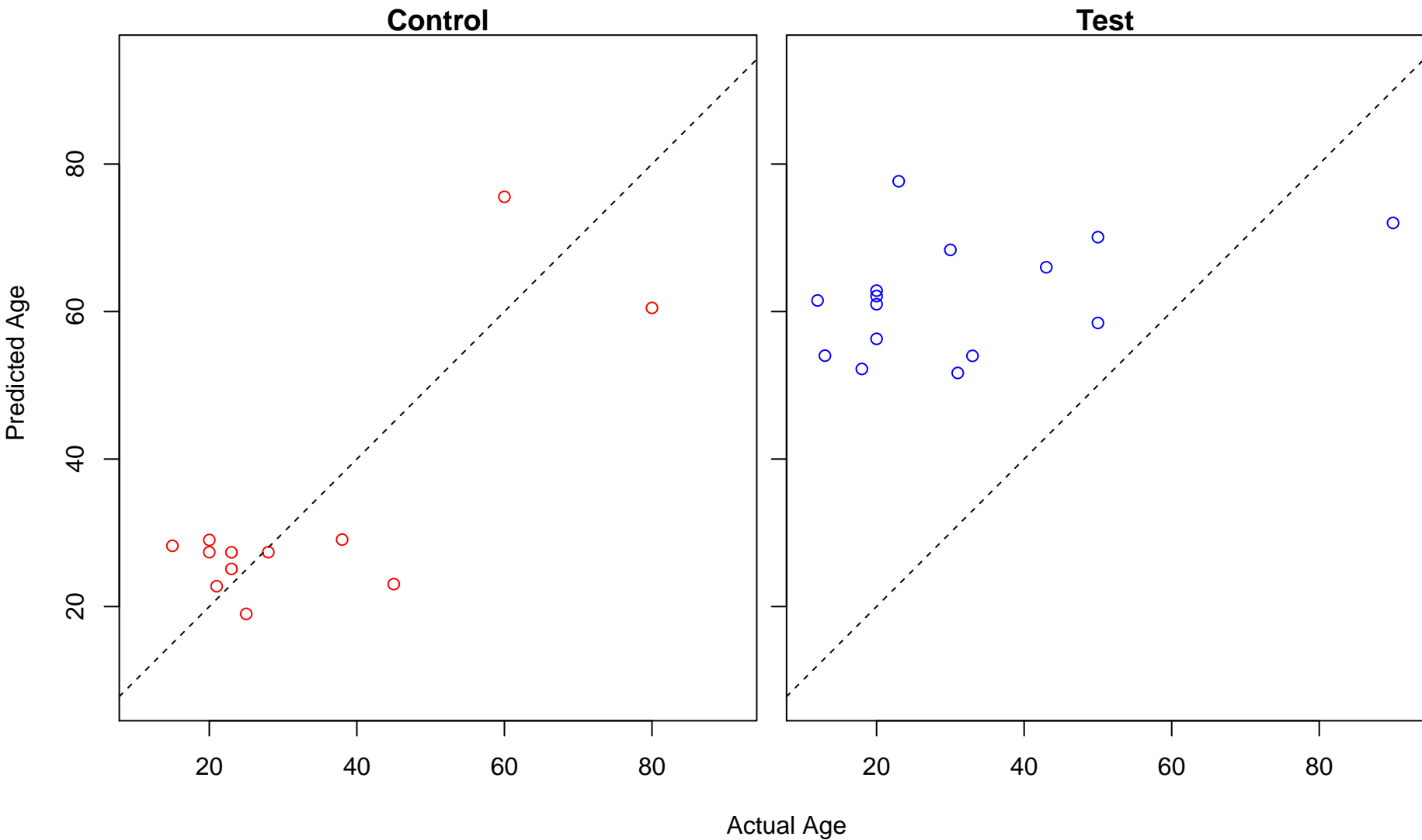
single-organism nuclear import (Score: 3.657544)



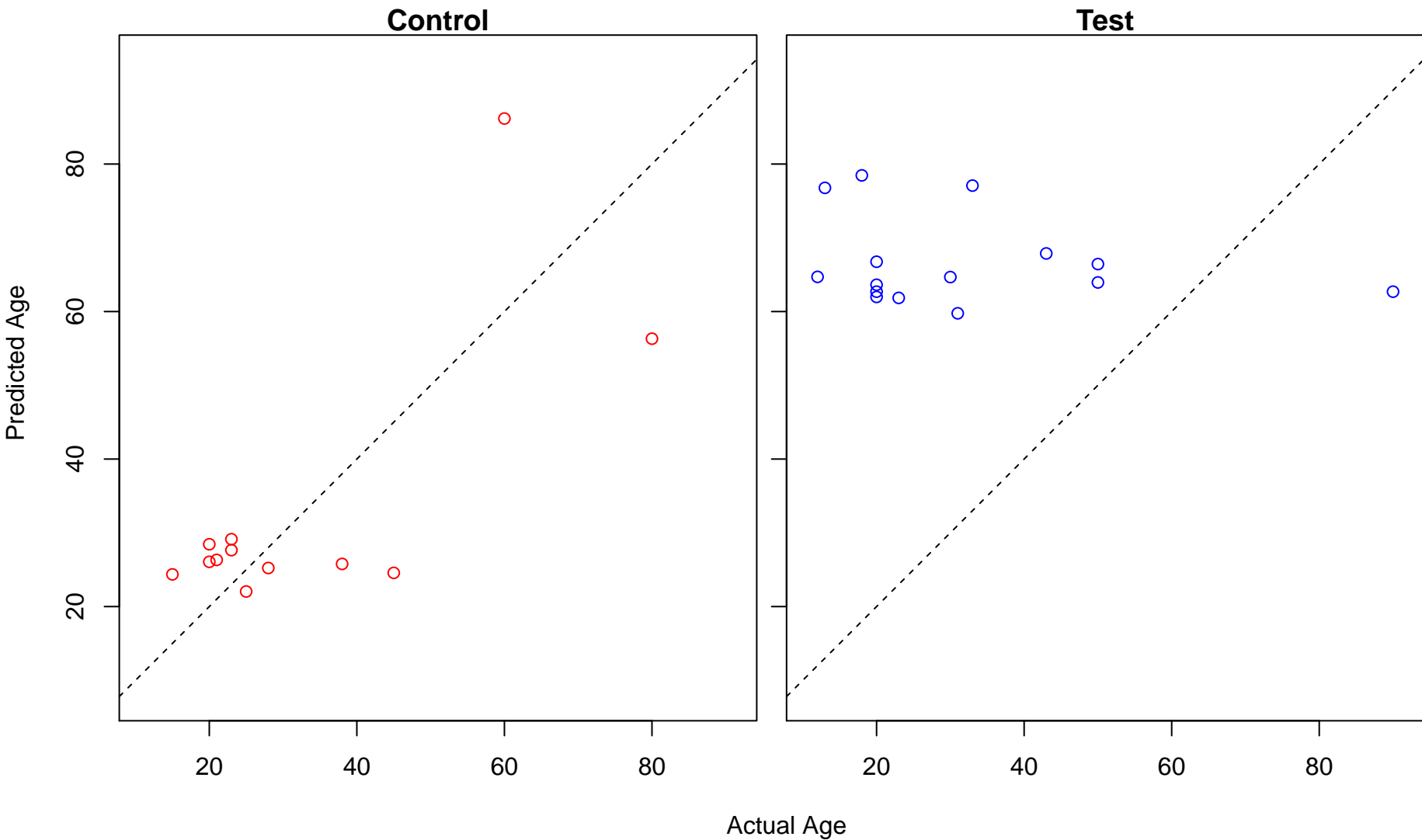
actin filament bundle assembly (Score: 3.656177)



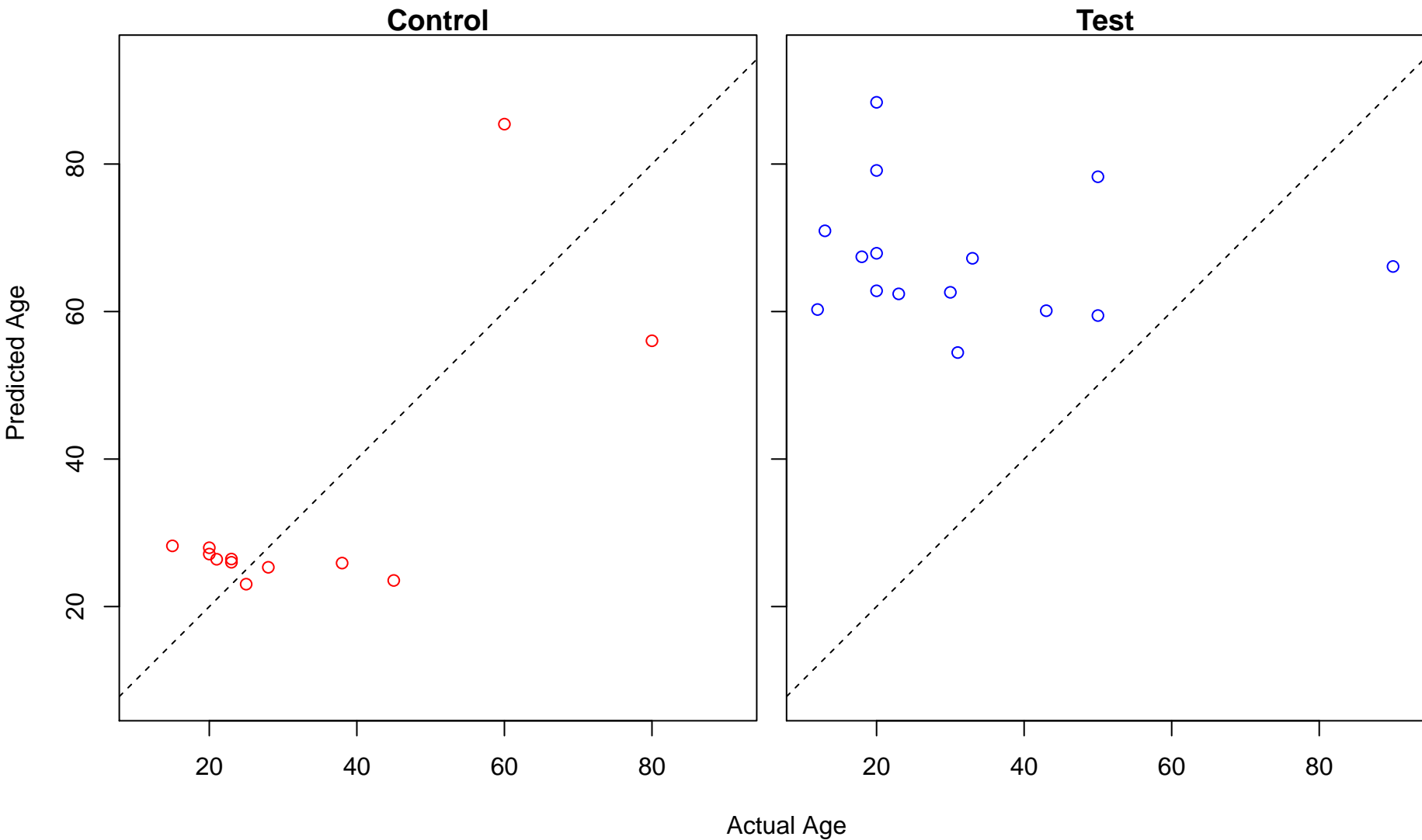
actin filament bundle organization (Score: 3.656177)



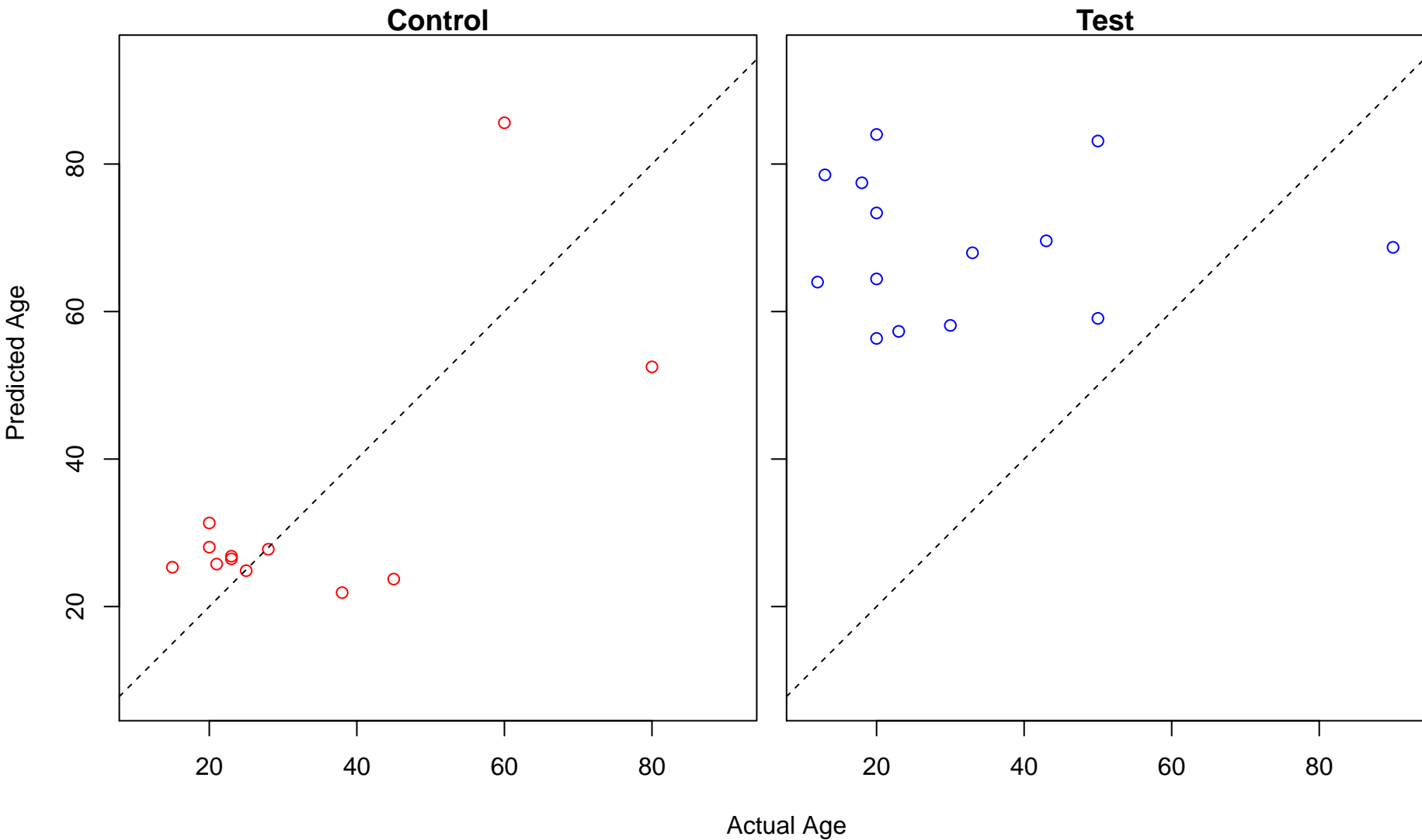
monocyte activation (Score: 3.653593)



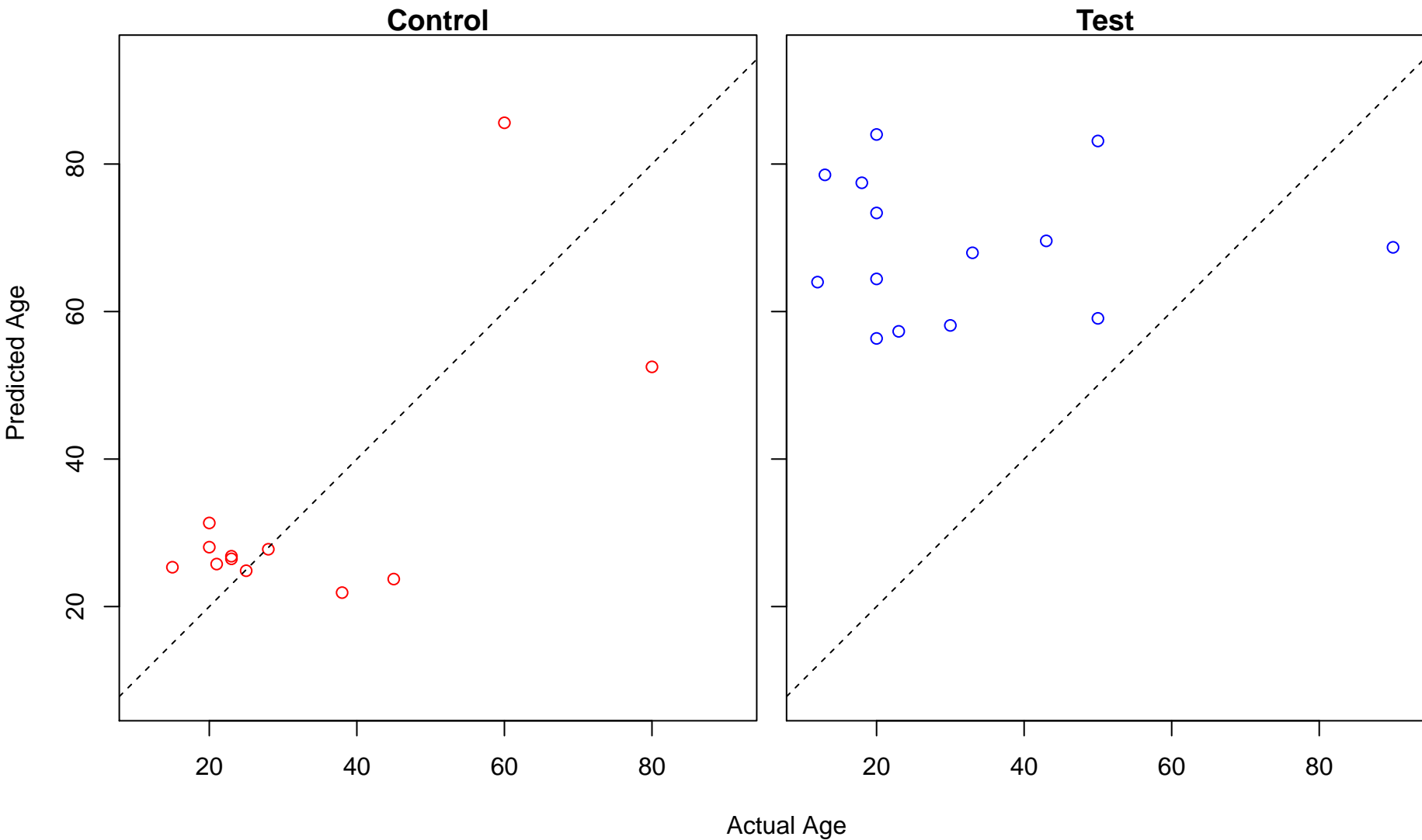
histone H2A acetylation (Score: 3.653137)



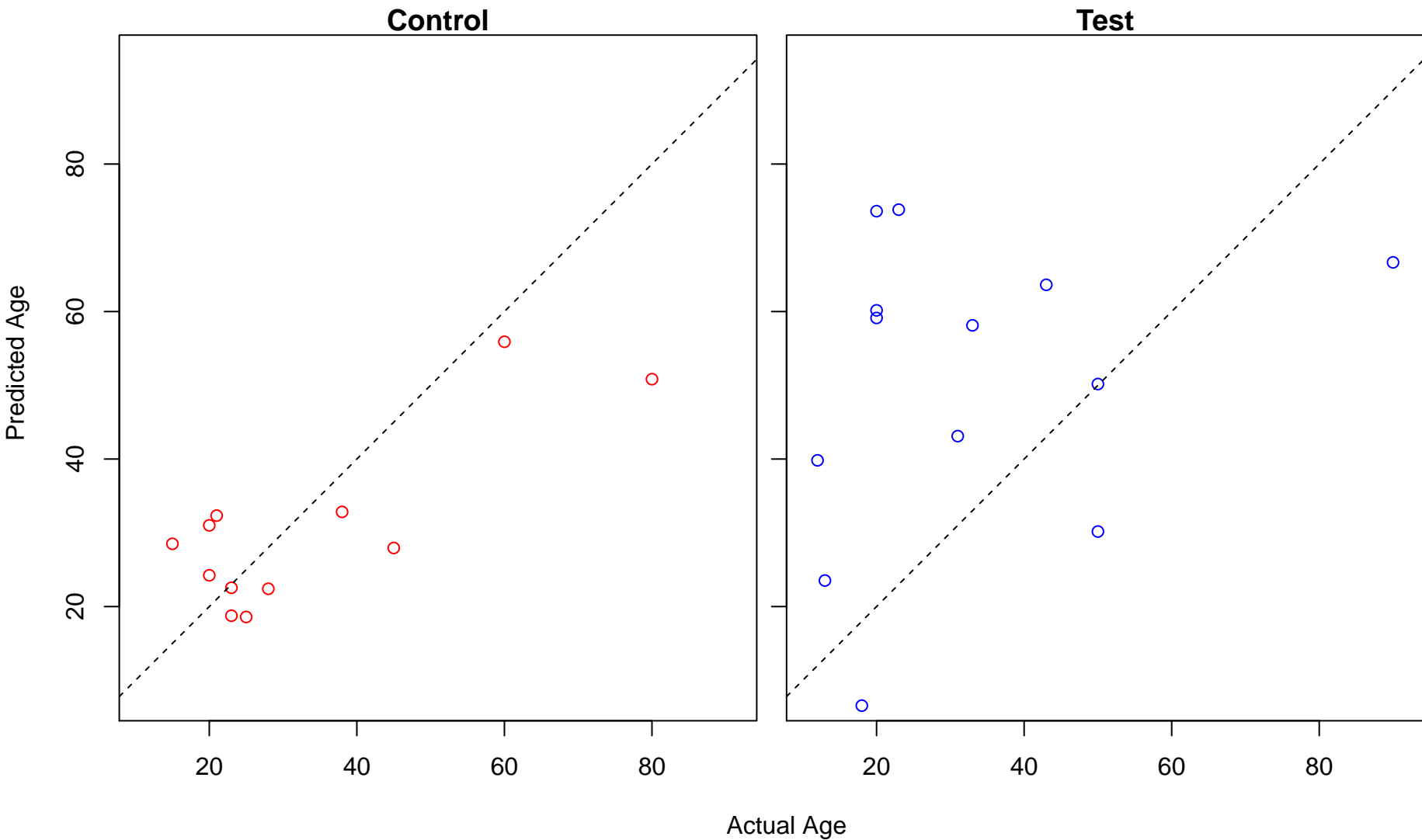
cellular biogenic amine biosynthetic process (Score: 3.652443)



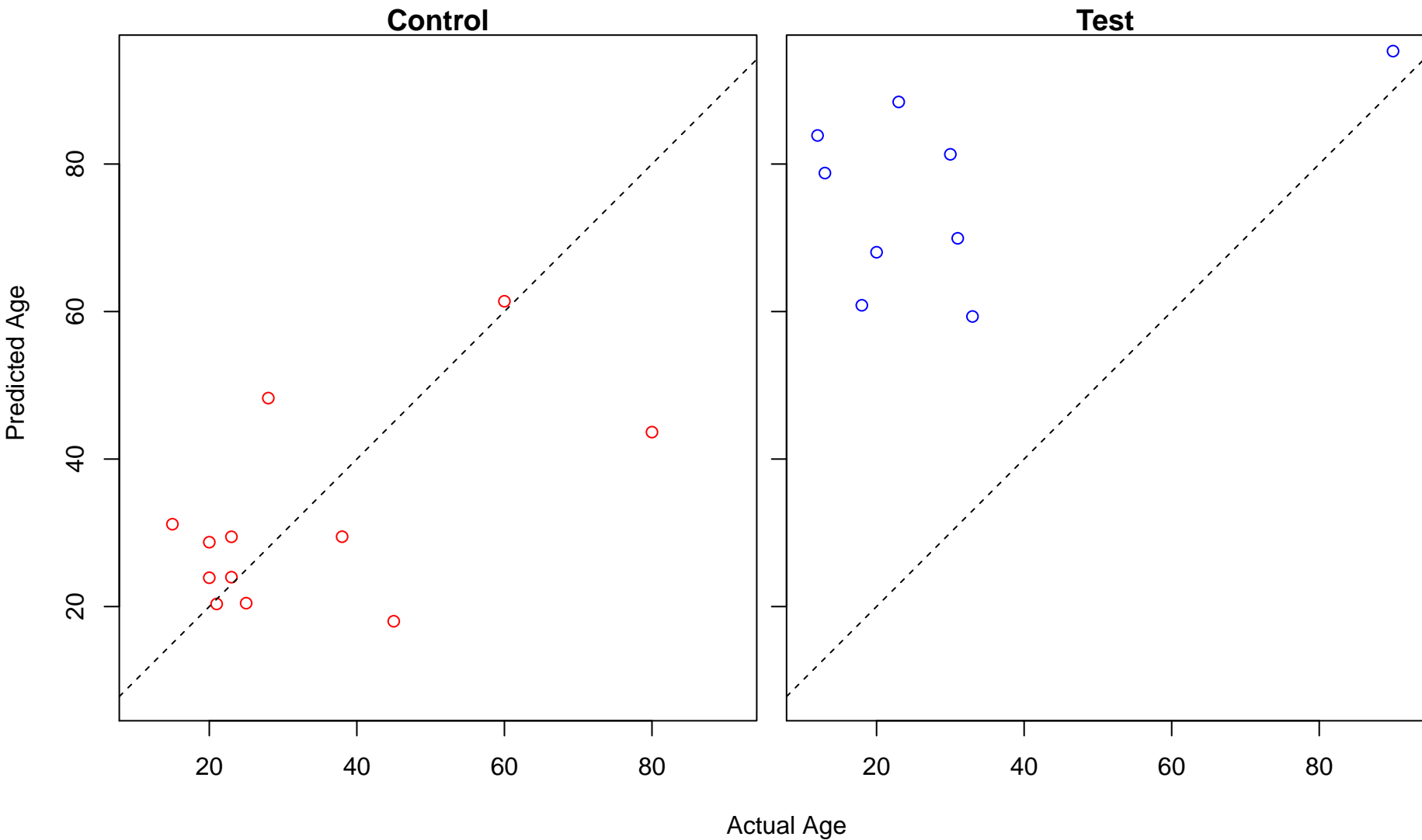
polyamine biosynthetic process (Score: 3.652441)



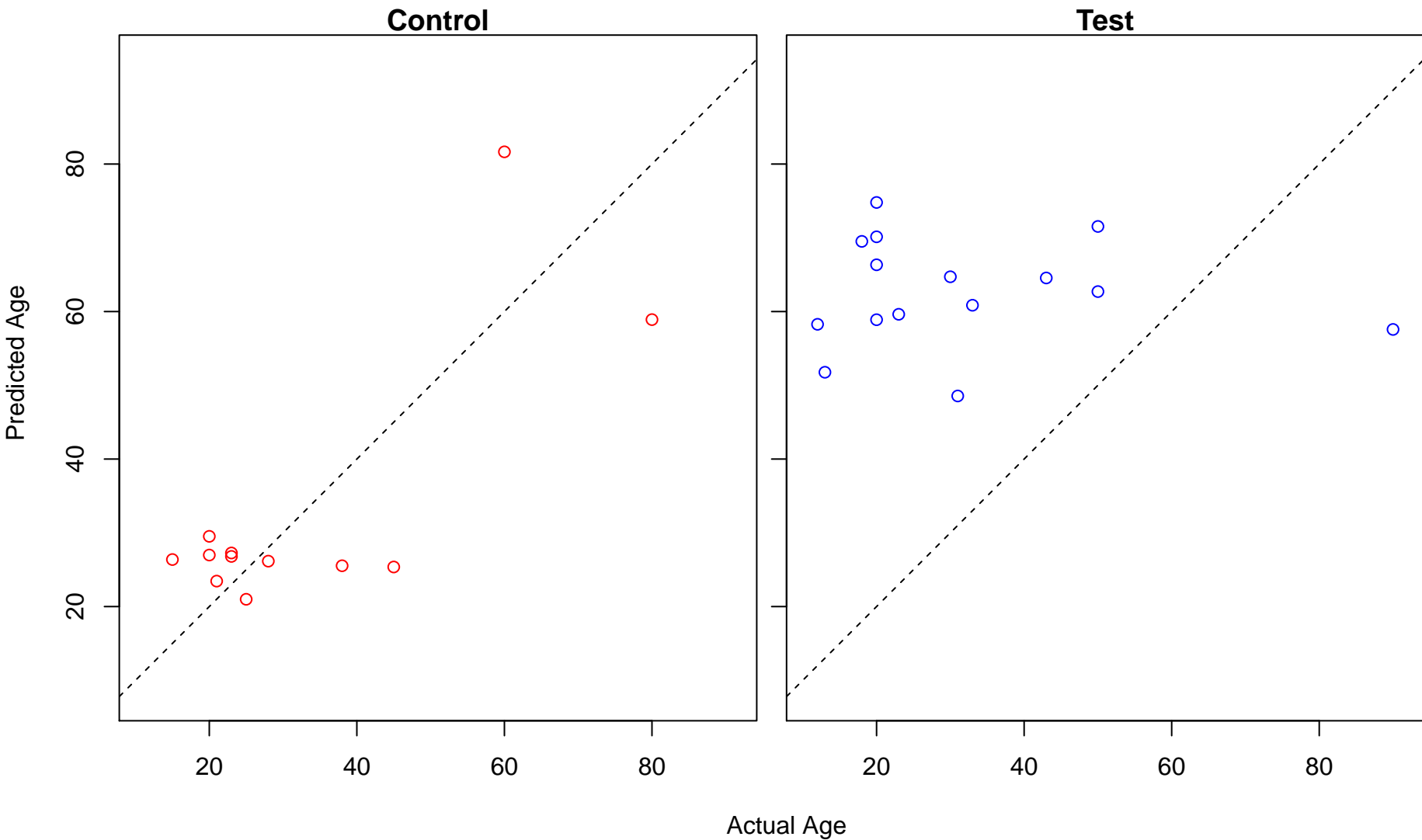
renal absorption (Score: 3.651695)



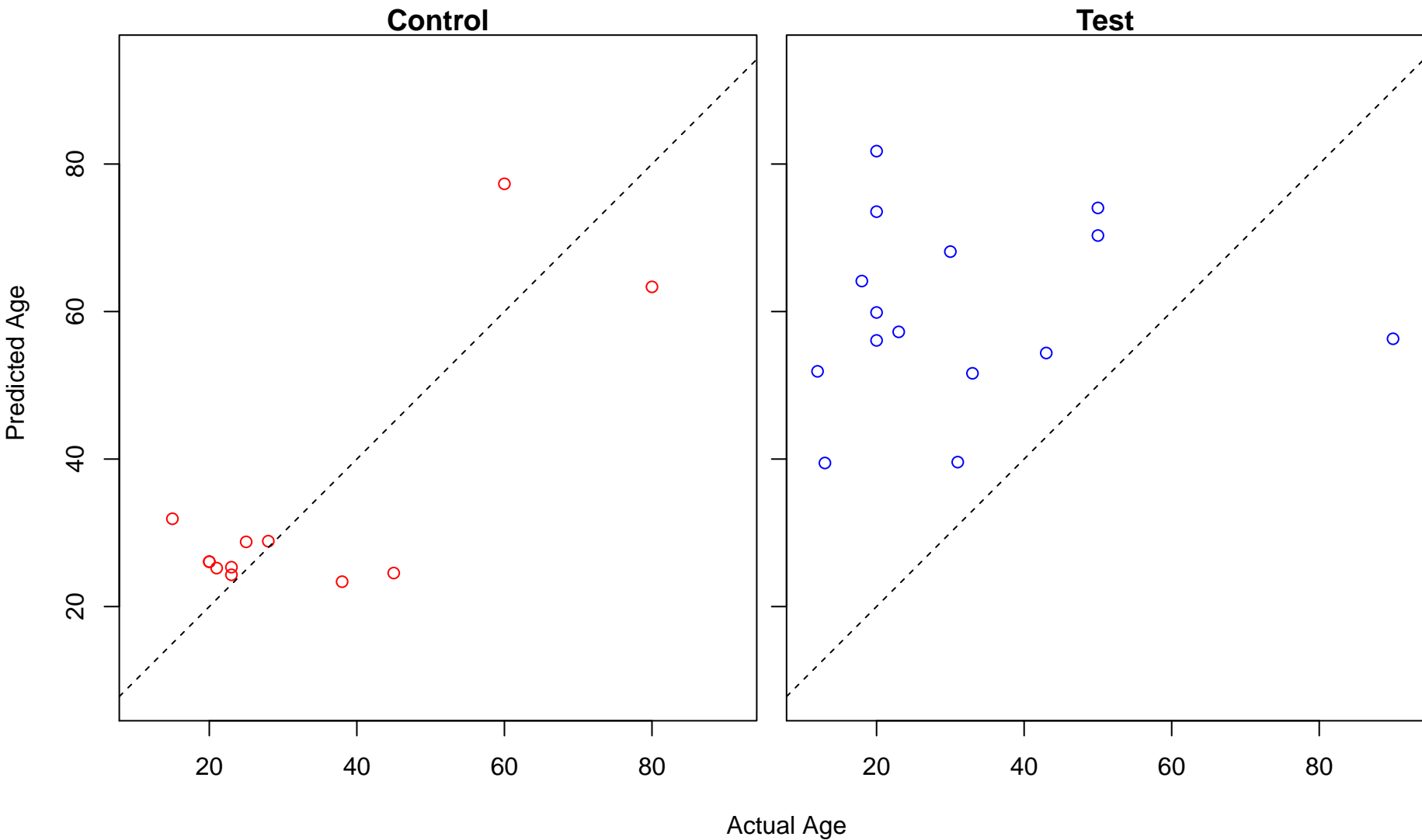
oligodendrocyte development (Score: 3.650930)



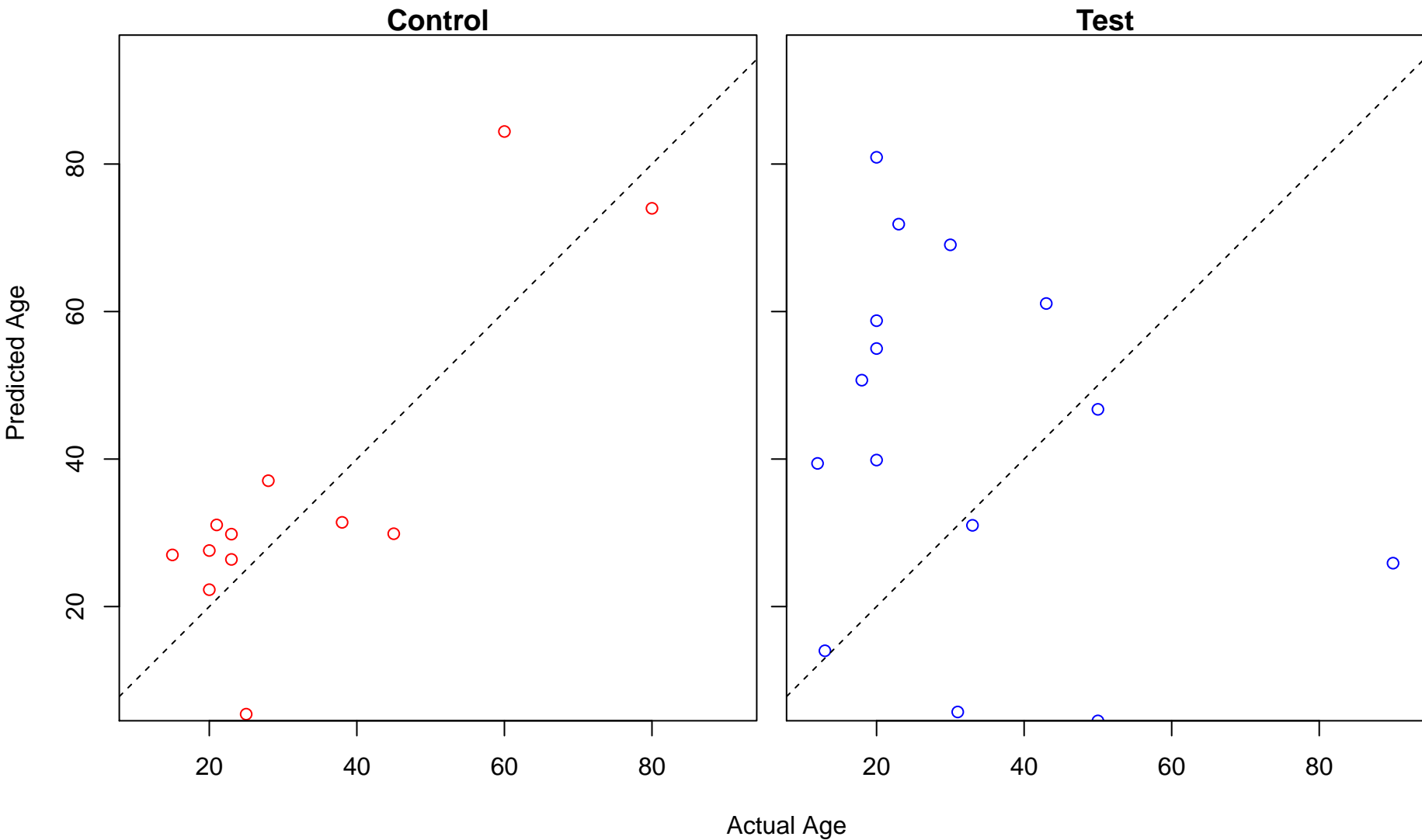
regulation of macrophage apoptotic process (Score: 3.648760)



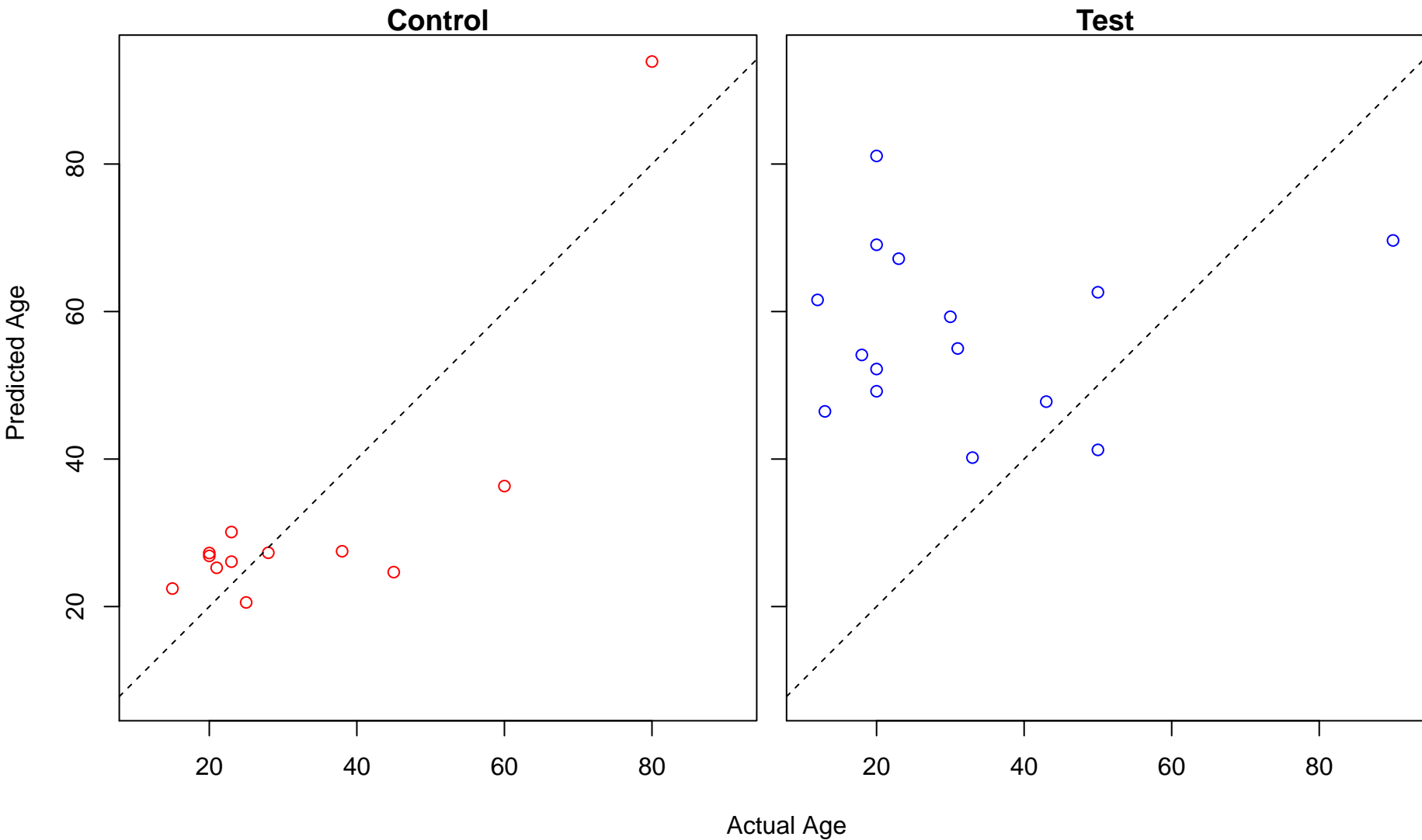
cellular response to misfolded protein (Score: 3.647695)



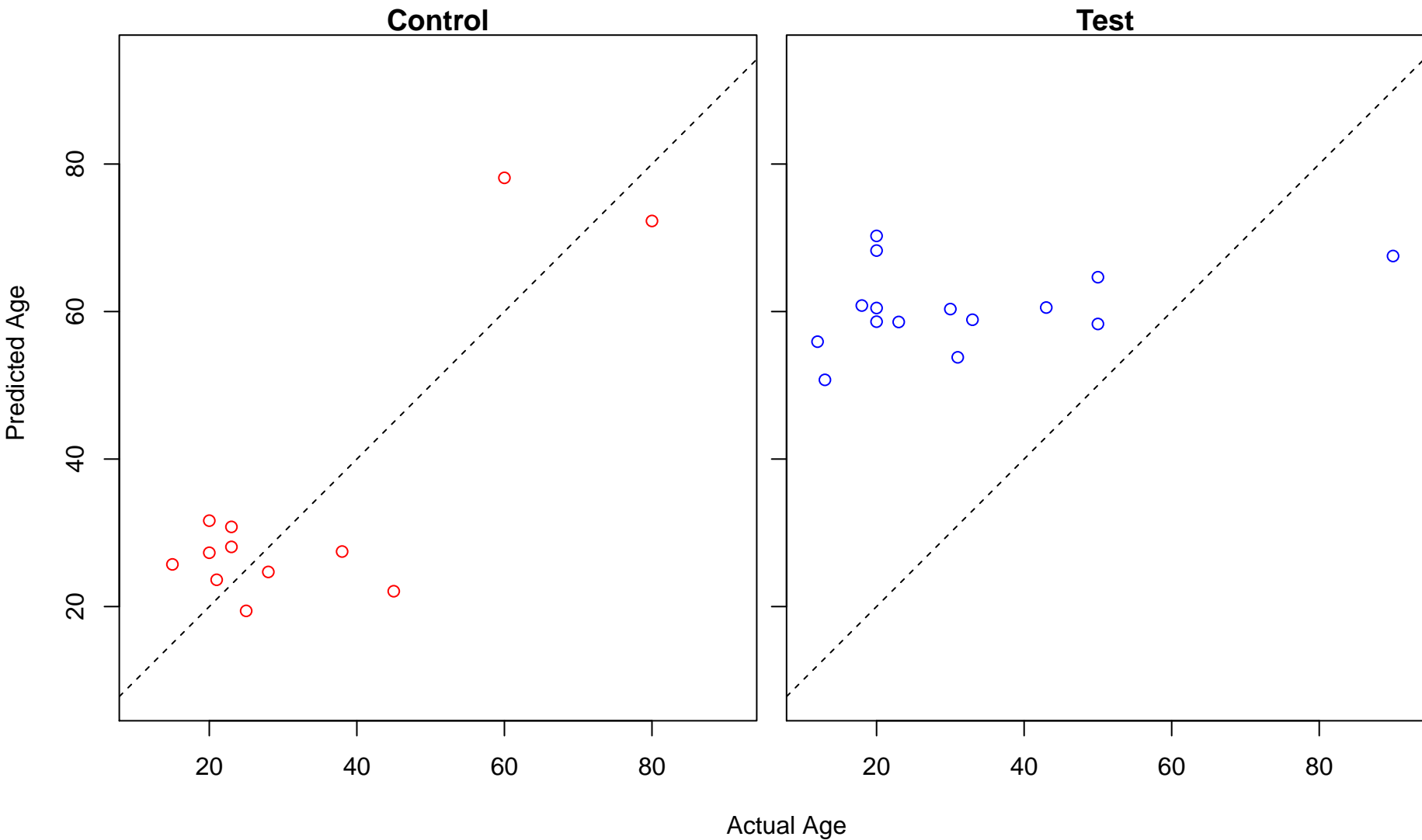
photoreceptor cell maintenance (Score: 3.644985)



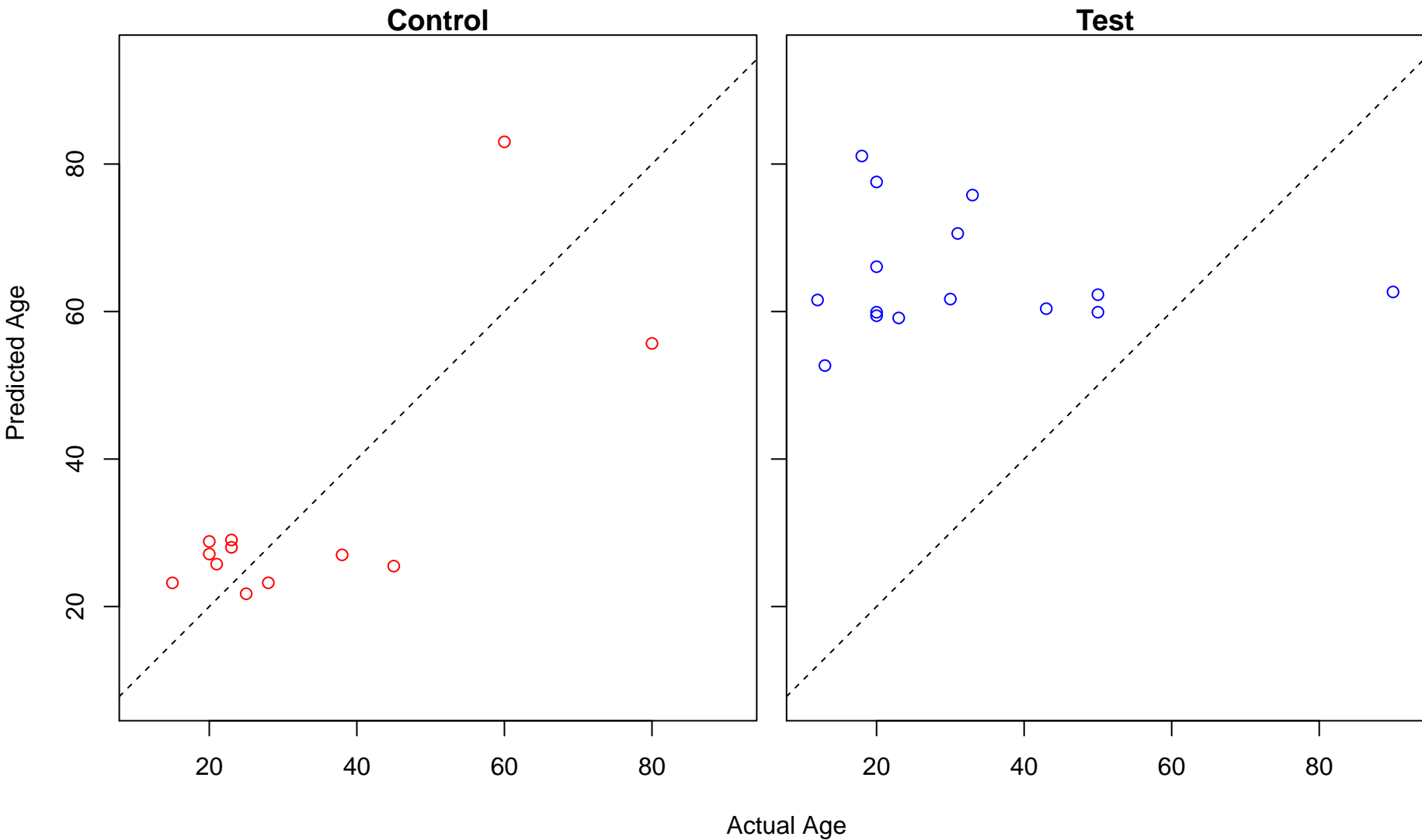
sulfur amino acid biosynthetic process (Score: 3.644528)



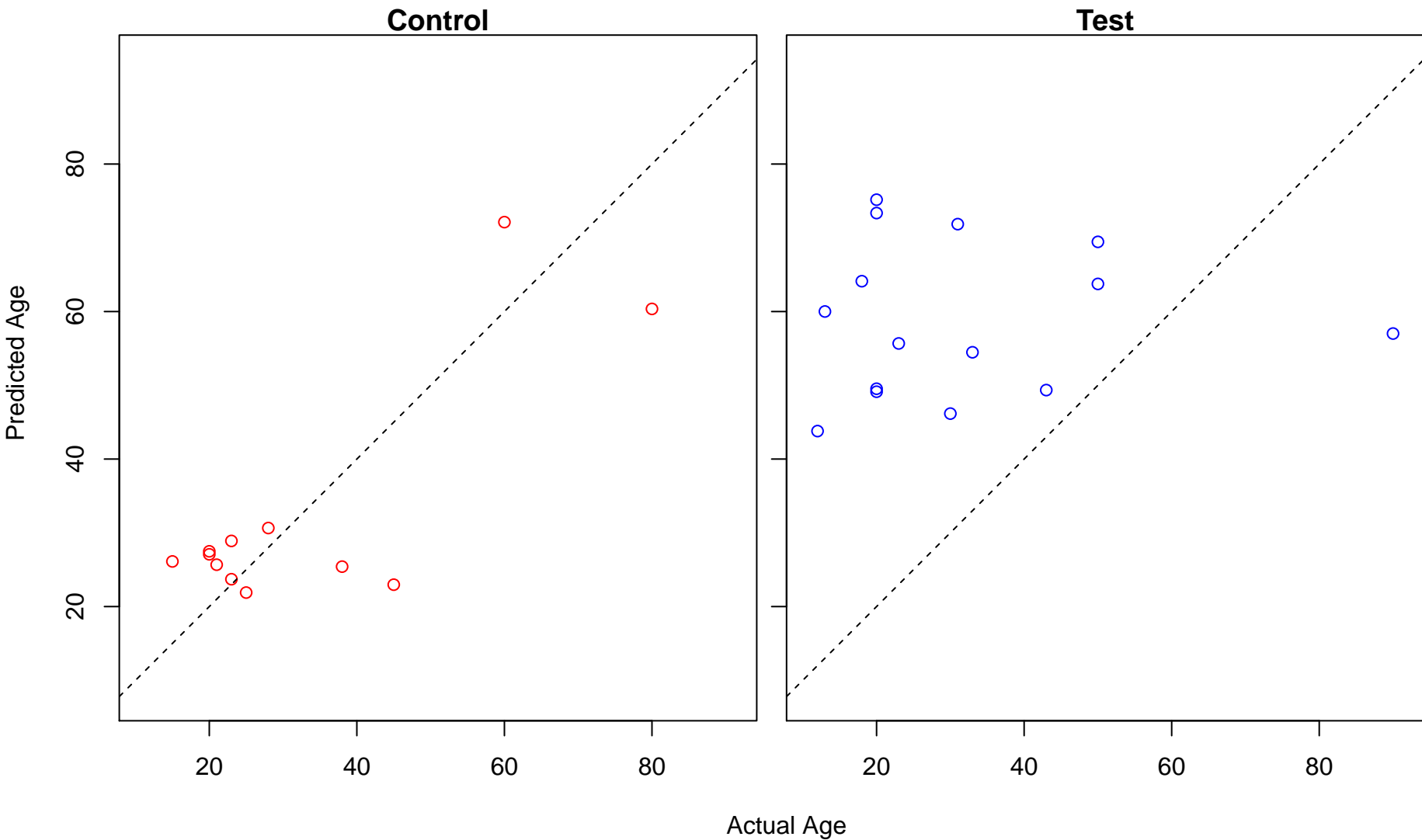
regulation of generation of precursor metabolites and energy (Score: 3.642557)



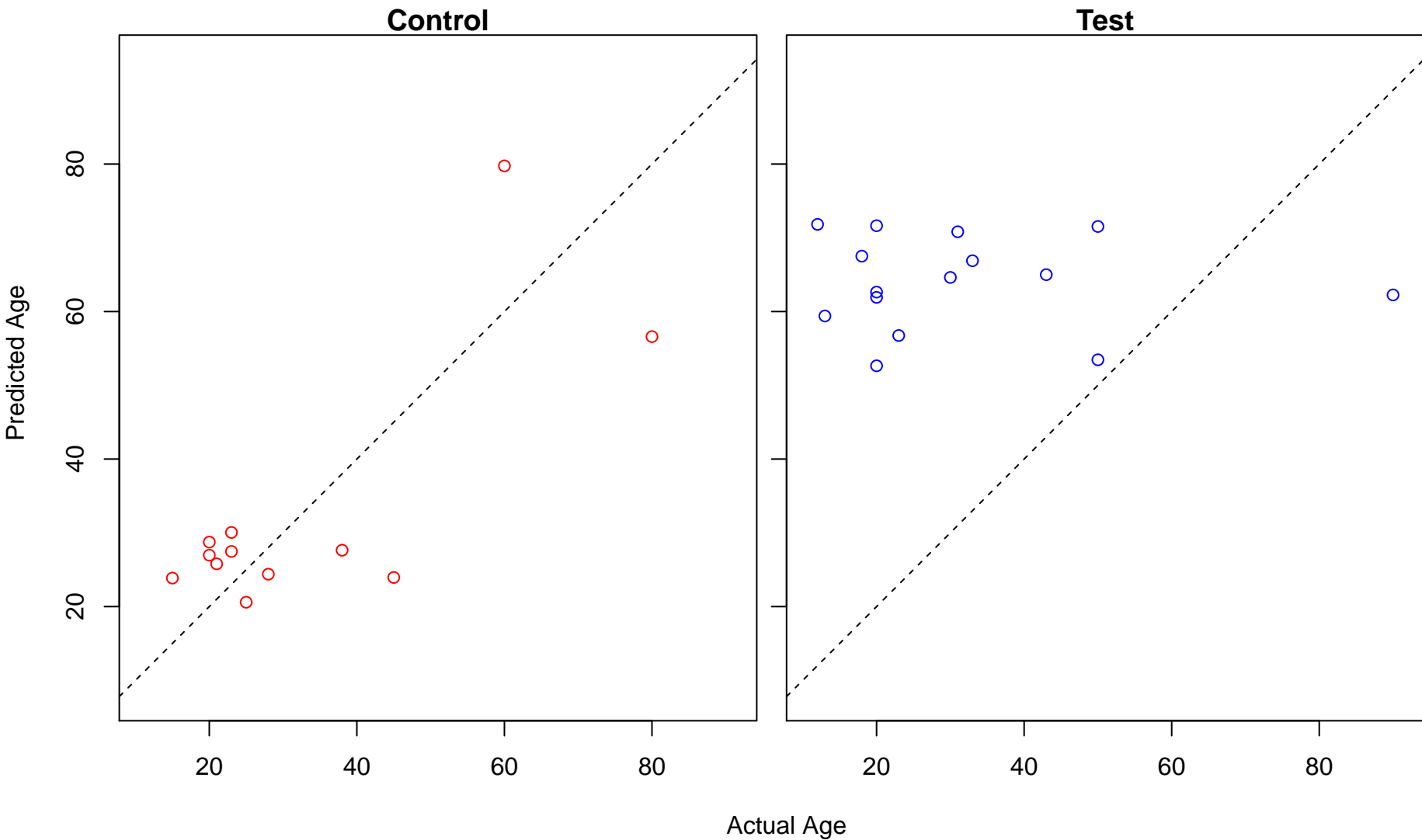
negative regulation of cell-matrix adhesion (Score: 3.638768)



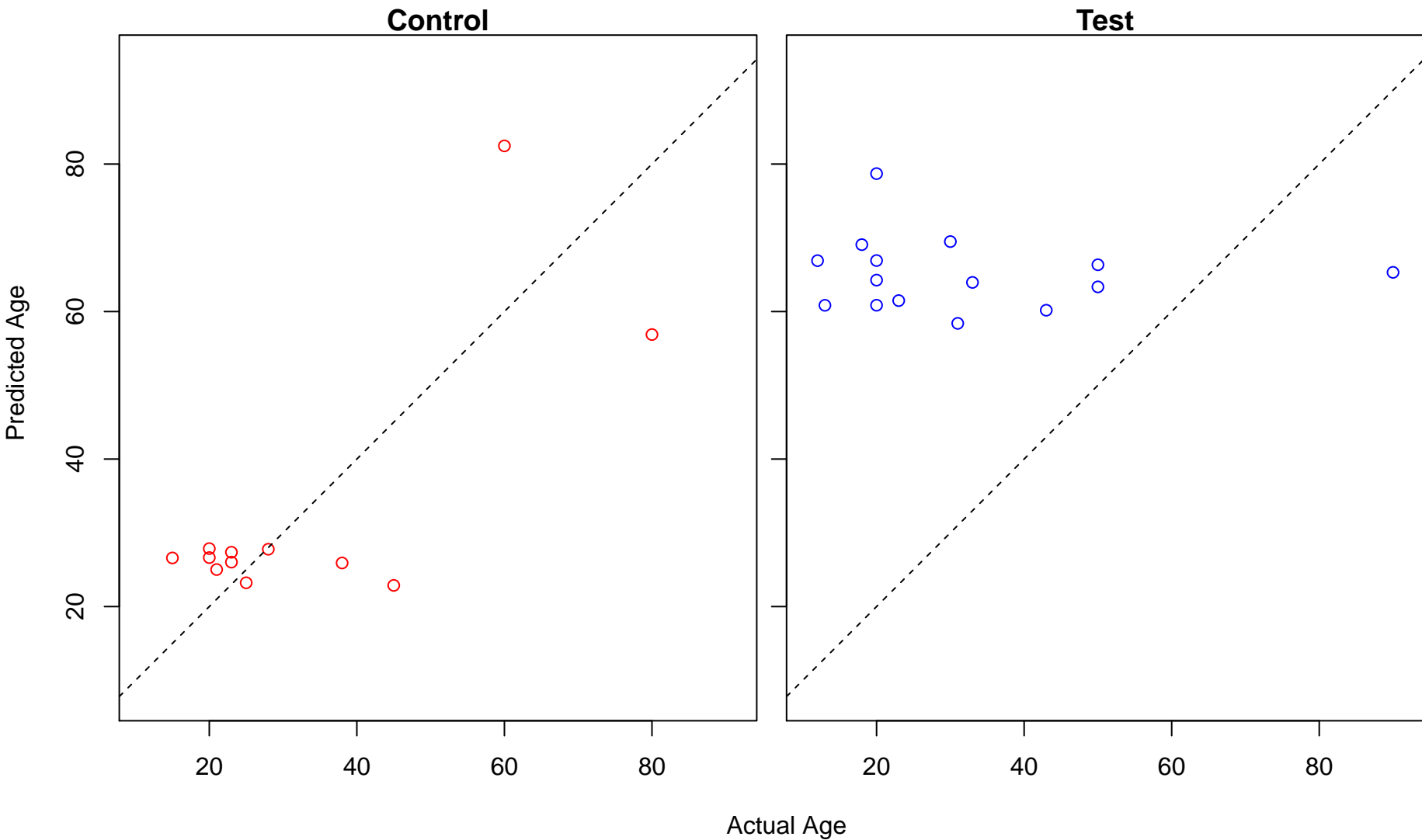
polyol metabolic process (Score: 3.637653)



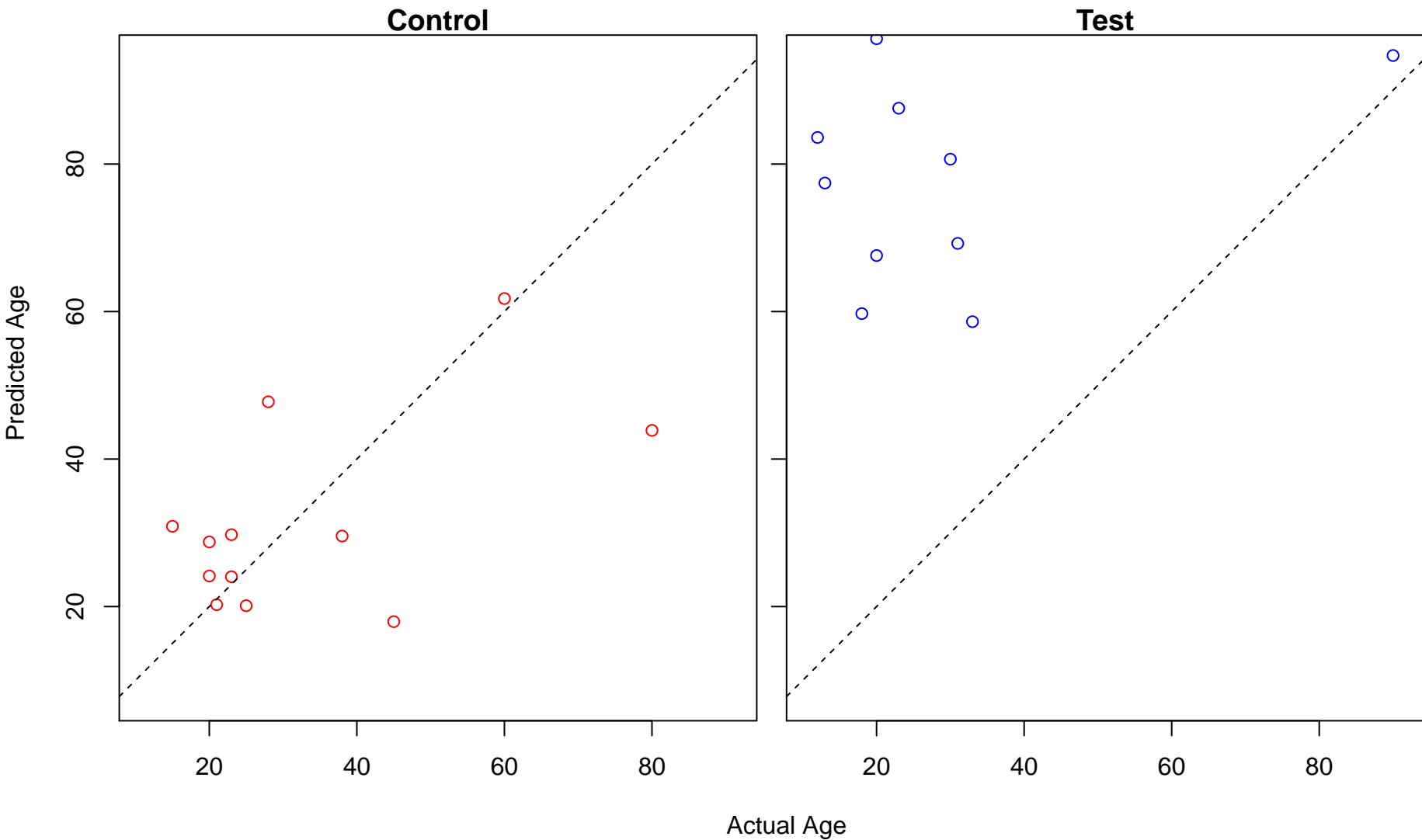
clathrin coat assembly (Score: 3.637201)



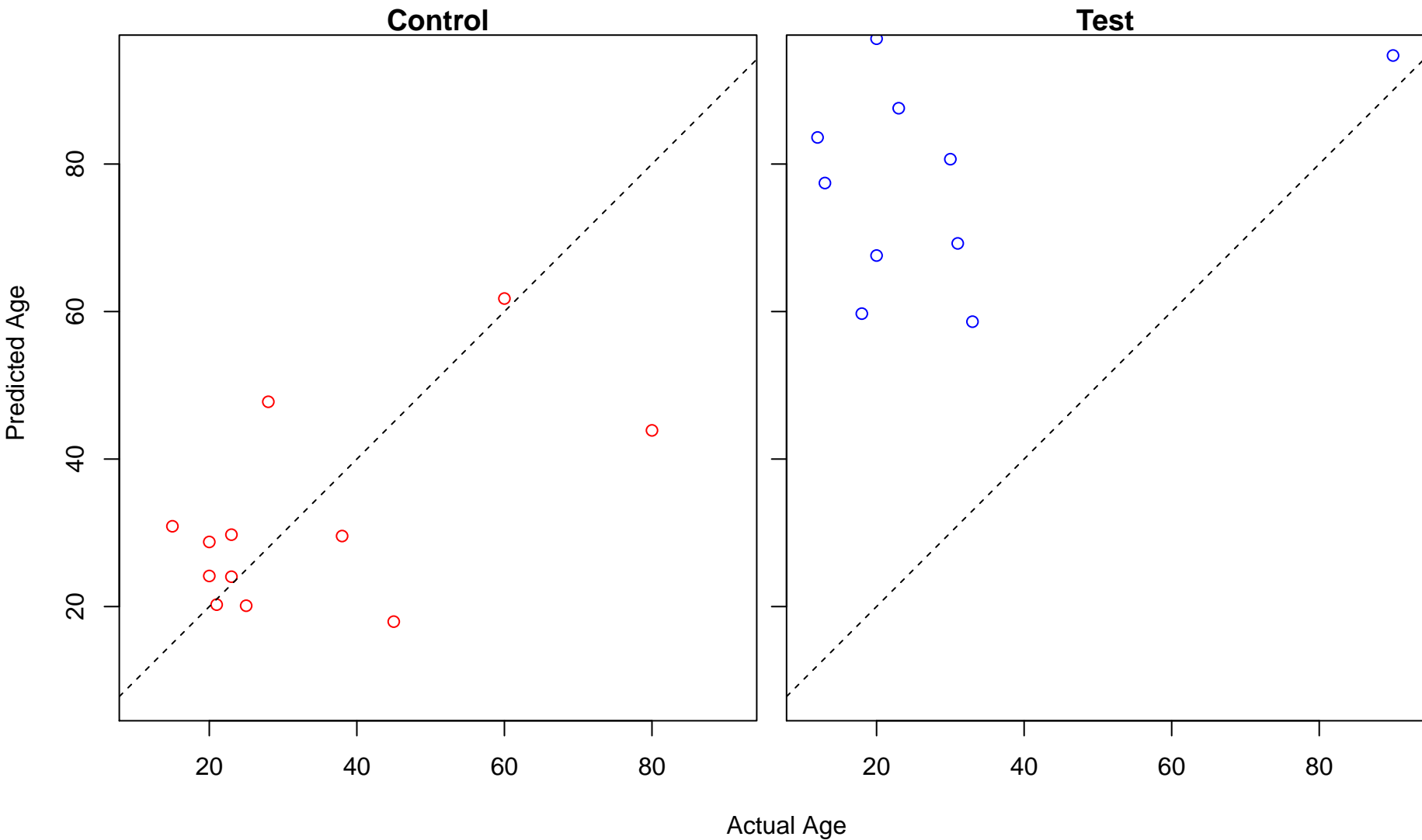
negative regulation of vasculature development (Score: 3.635168)



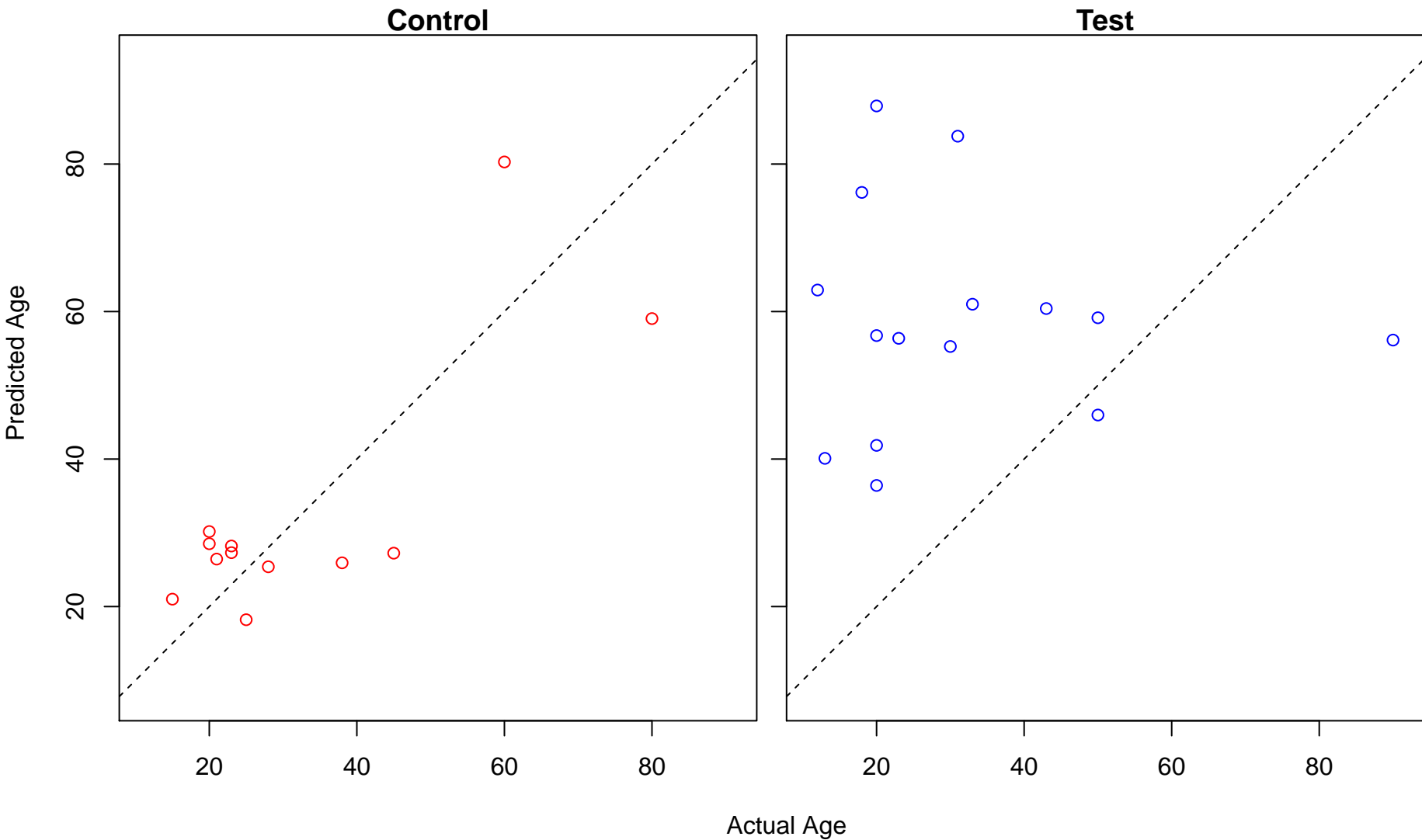
positive regulation of beta-amyloid formation (Score: 3.634899)



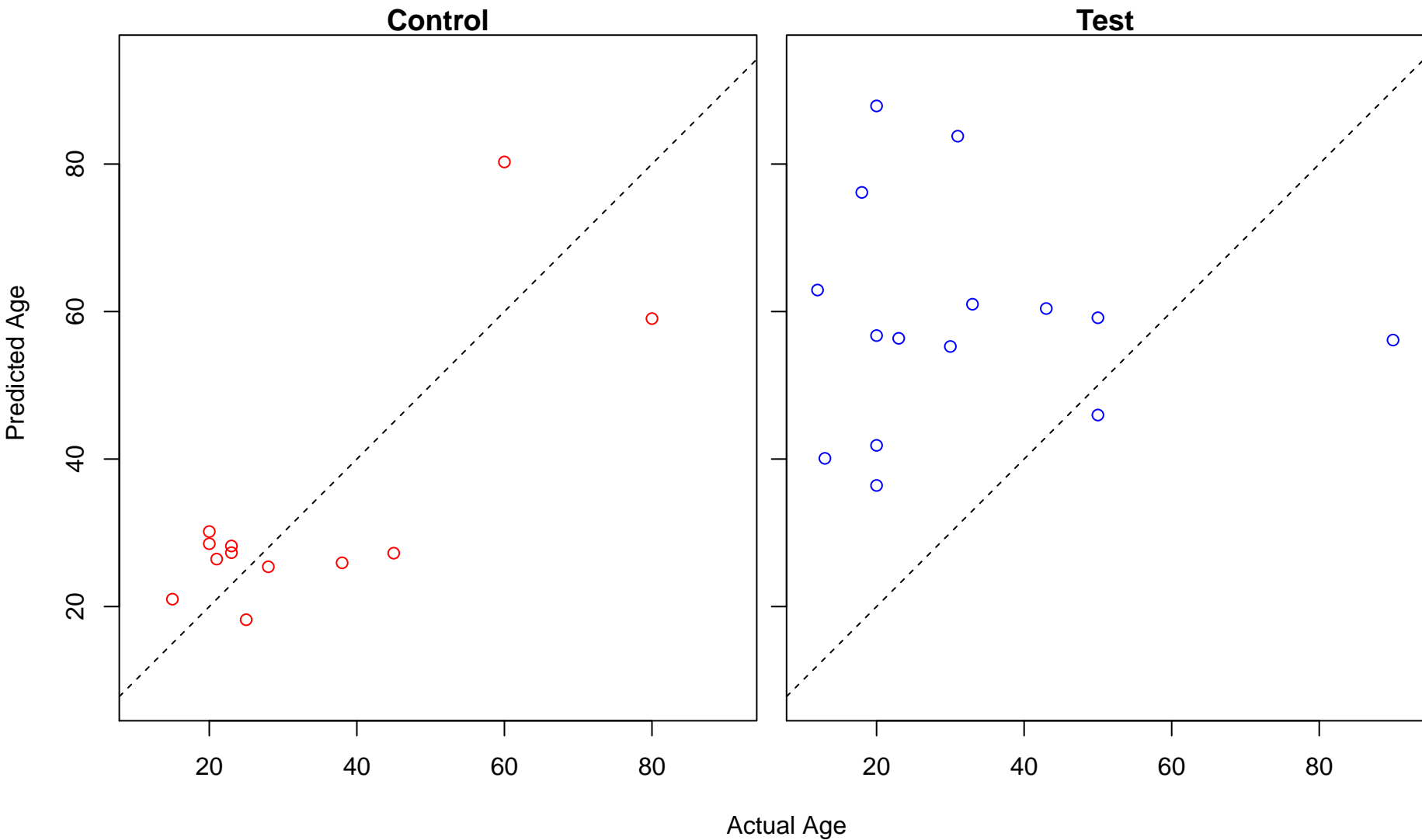
positive regulation of amyloid precursor protein catabolic process (Score: 3.634899)



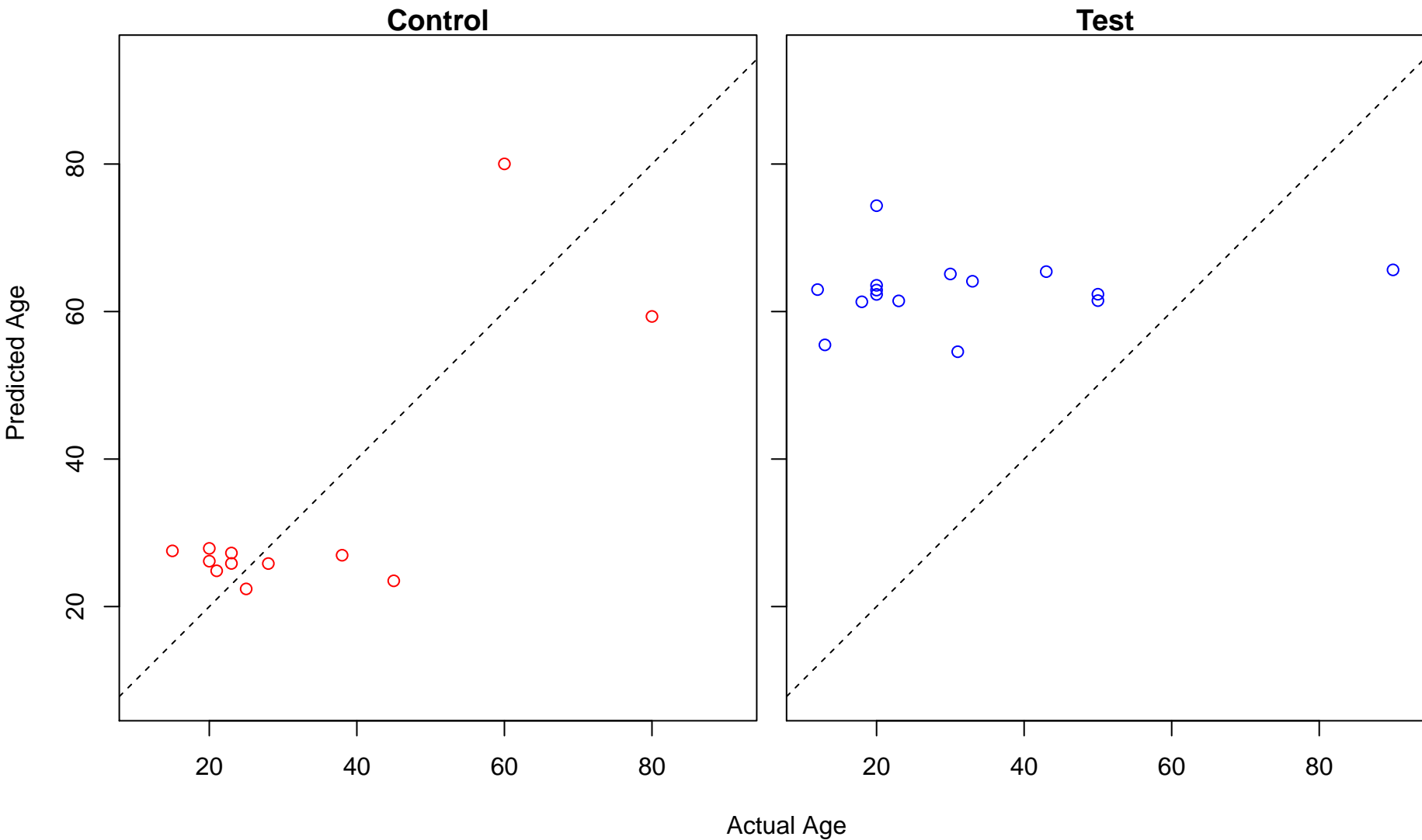
arachidonic acid secretion (Score: 3.634645)



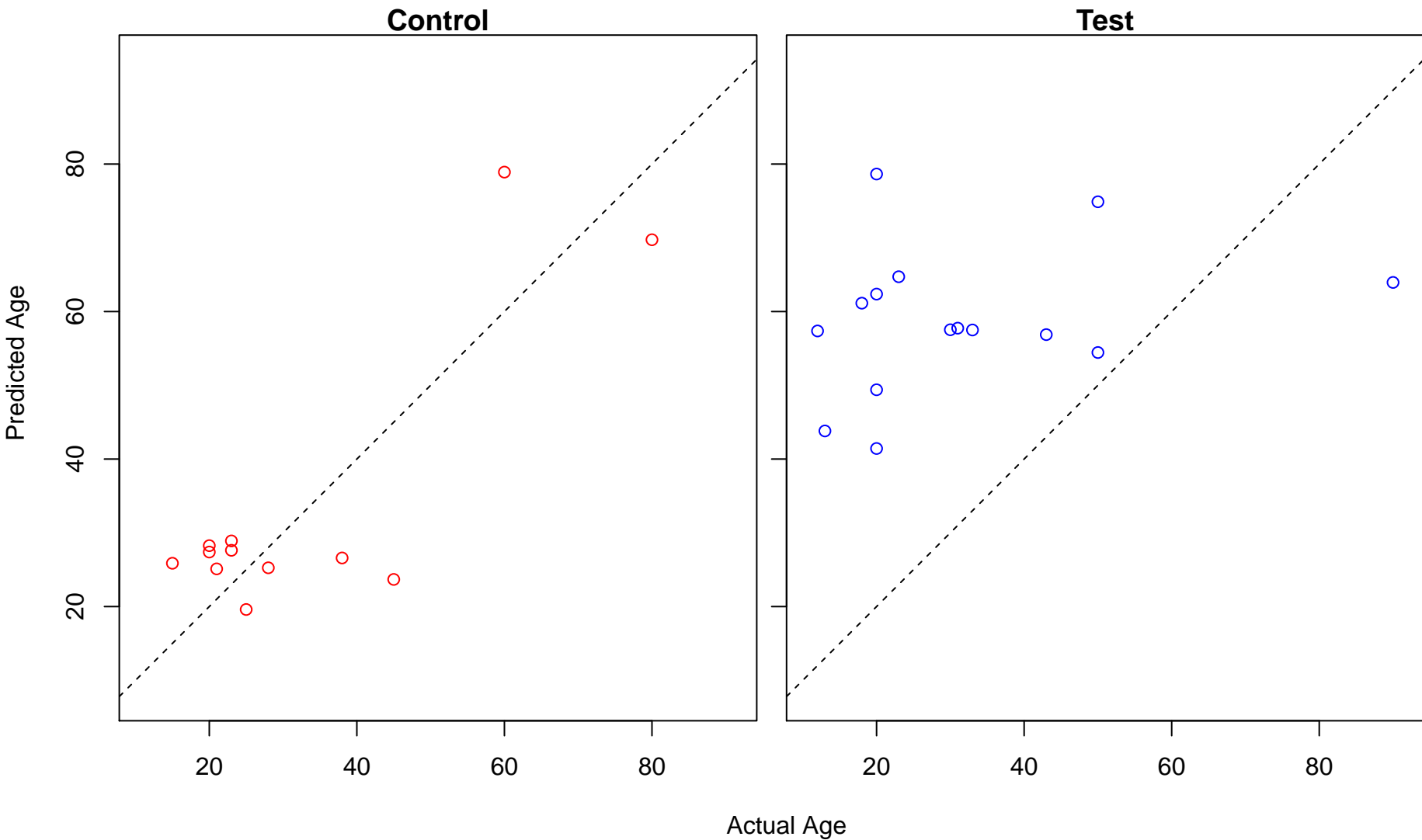
arachidonate transport (Score: 3.634645)



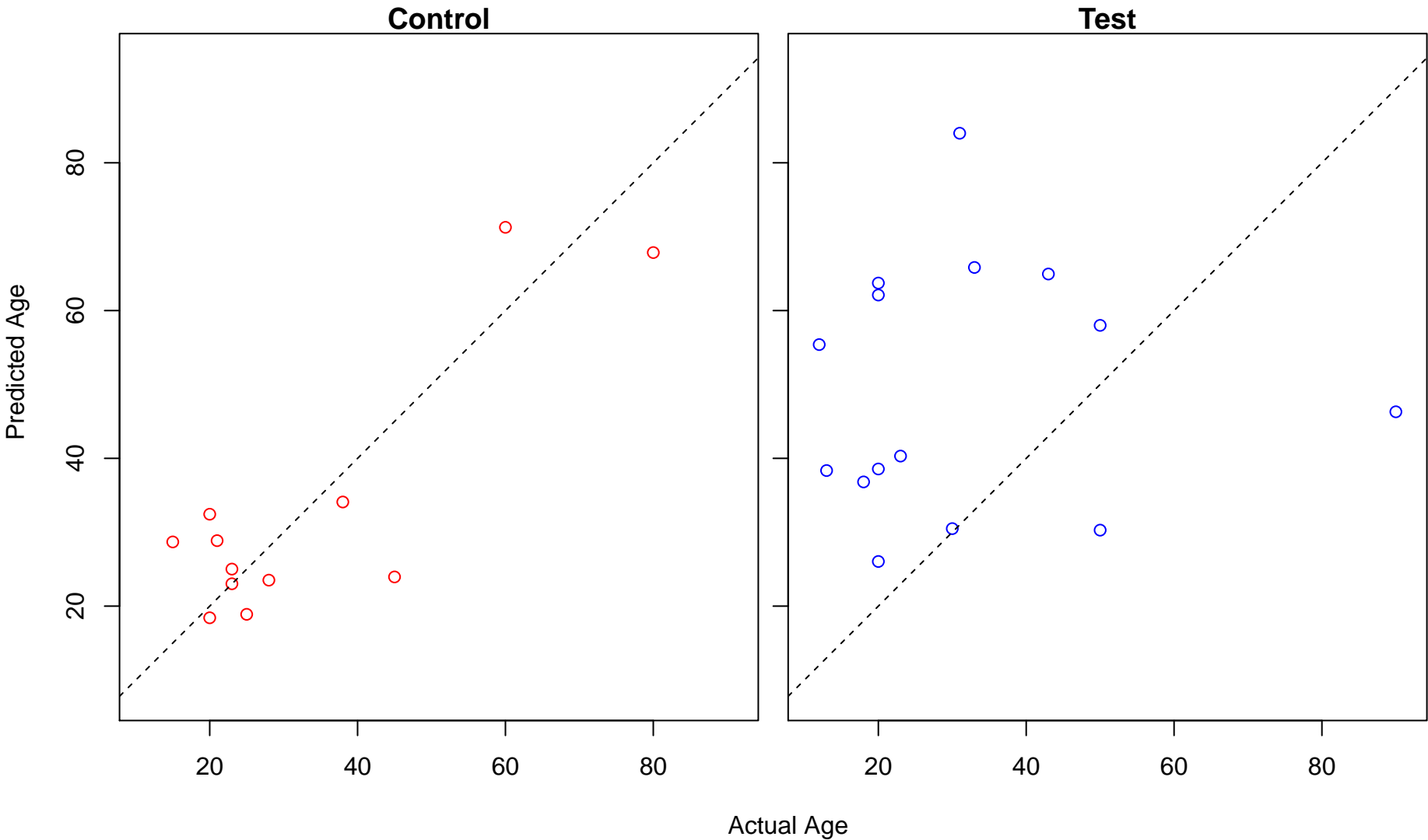
cytoskeleton-dependent cytokinesis (Score: 3.634385)



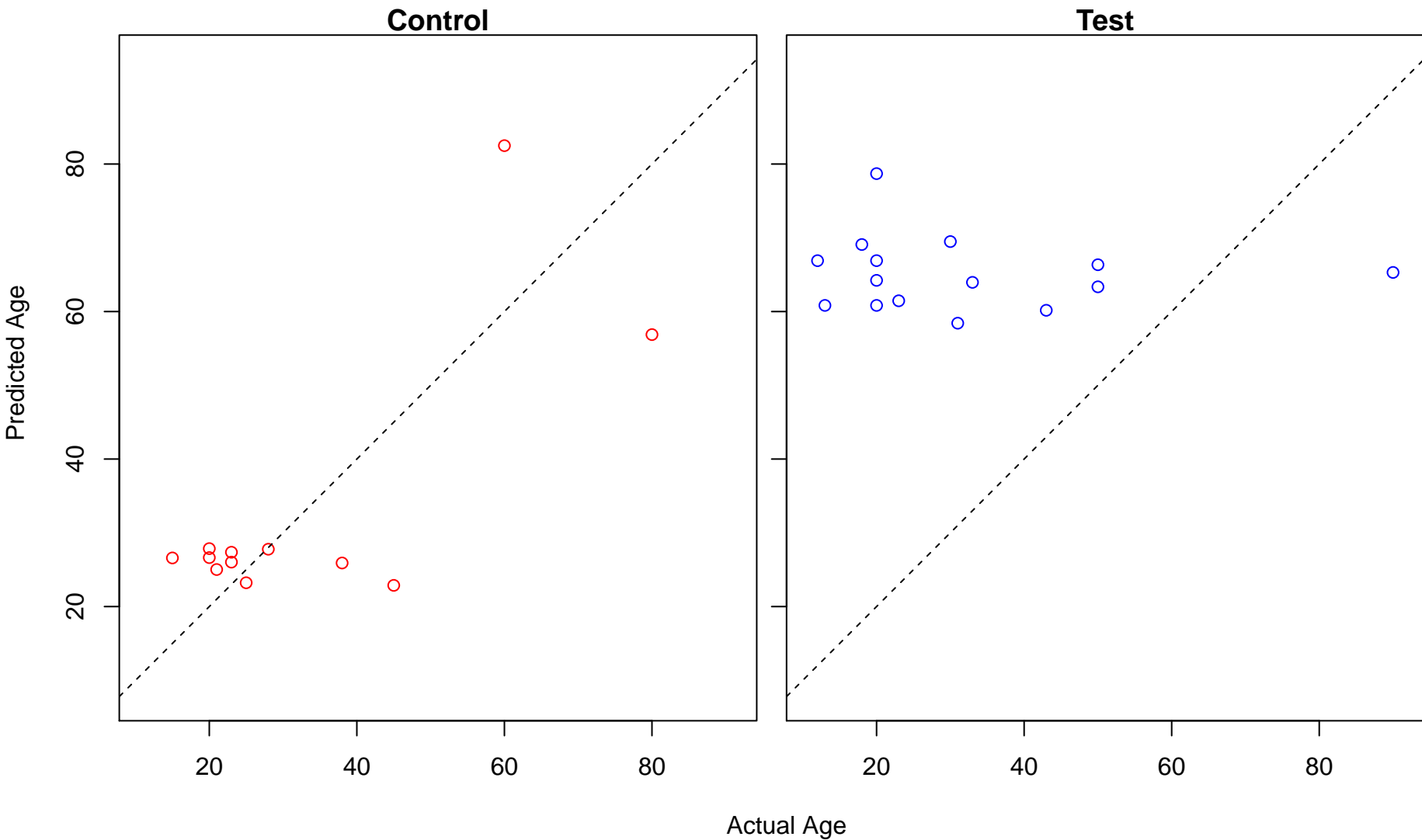
cell growth (Score: 3.633172)



regulation of intracellular steroid hormone receptor signaling pathway (Score: 3.633137)

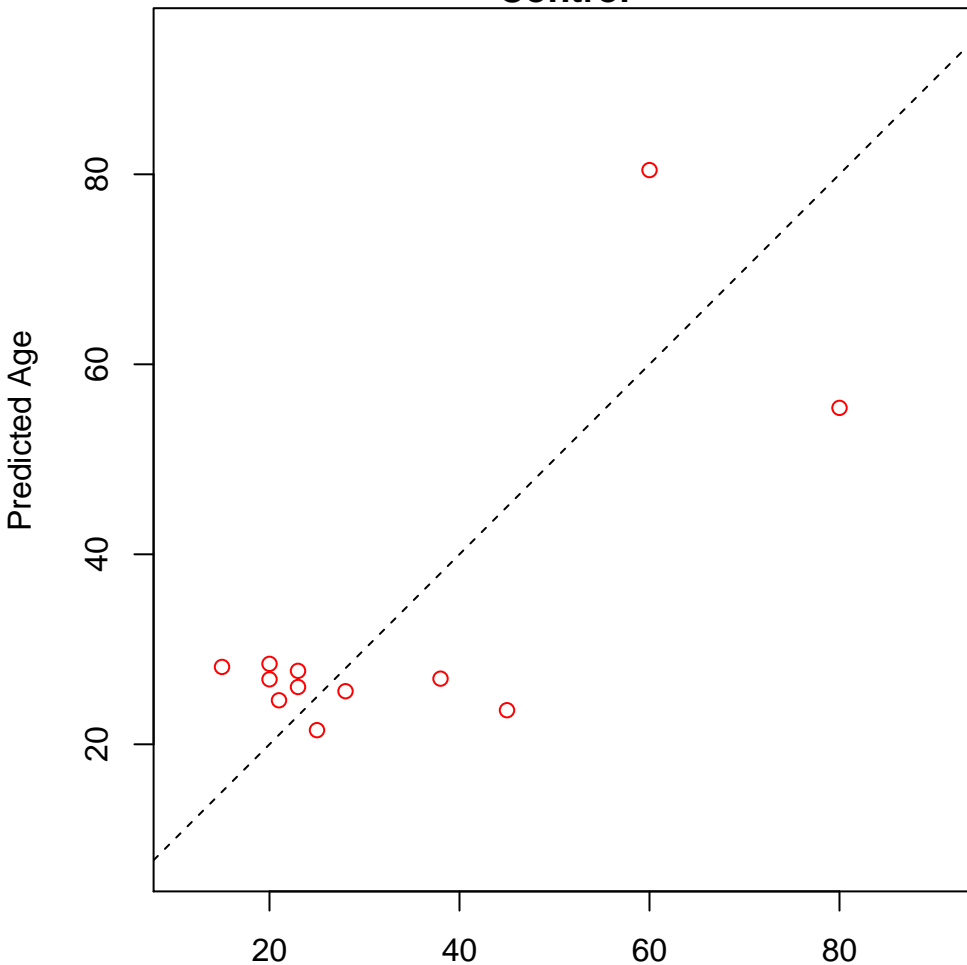


negative regulation of blood vessel morphogenesis (Score: 3.632439)

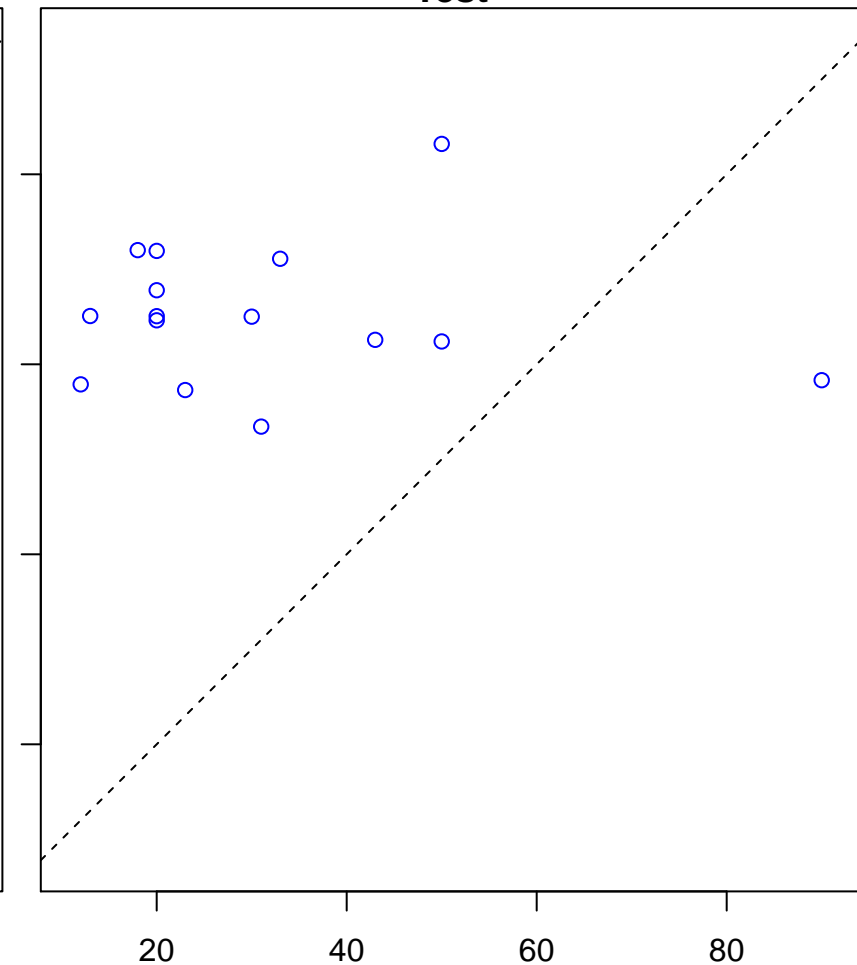


protein localization to cell surface (Score: 3.632209)

Control

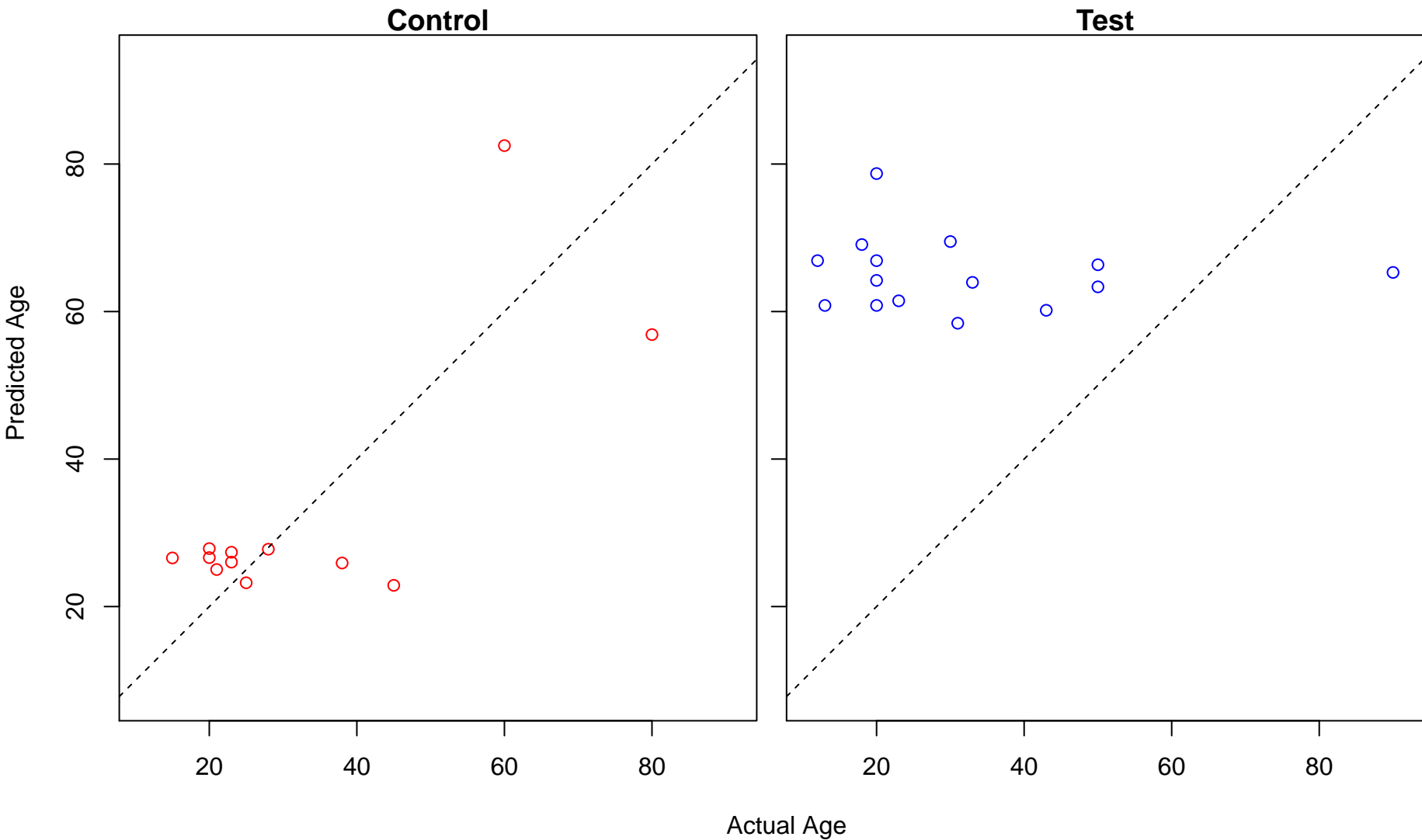


Test

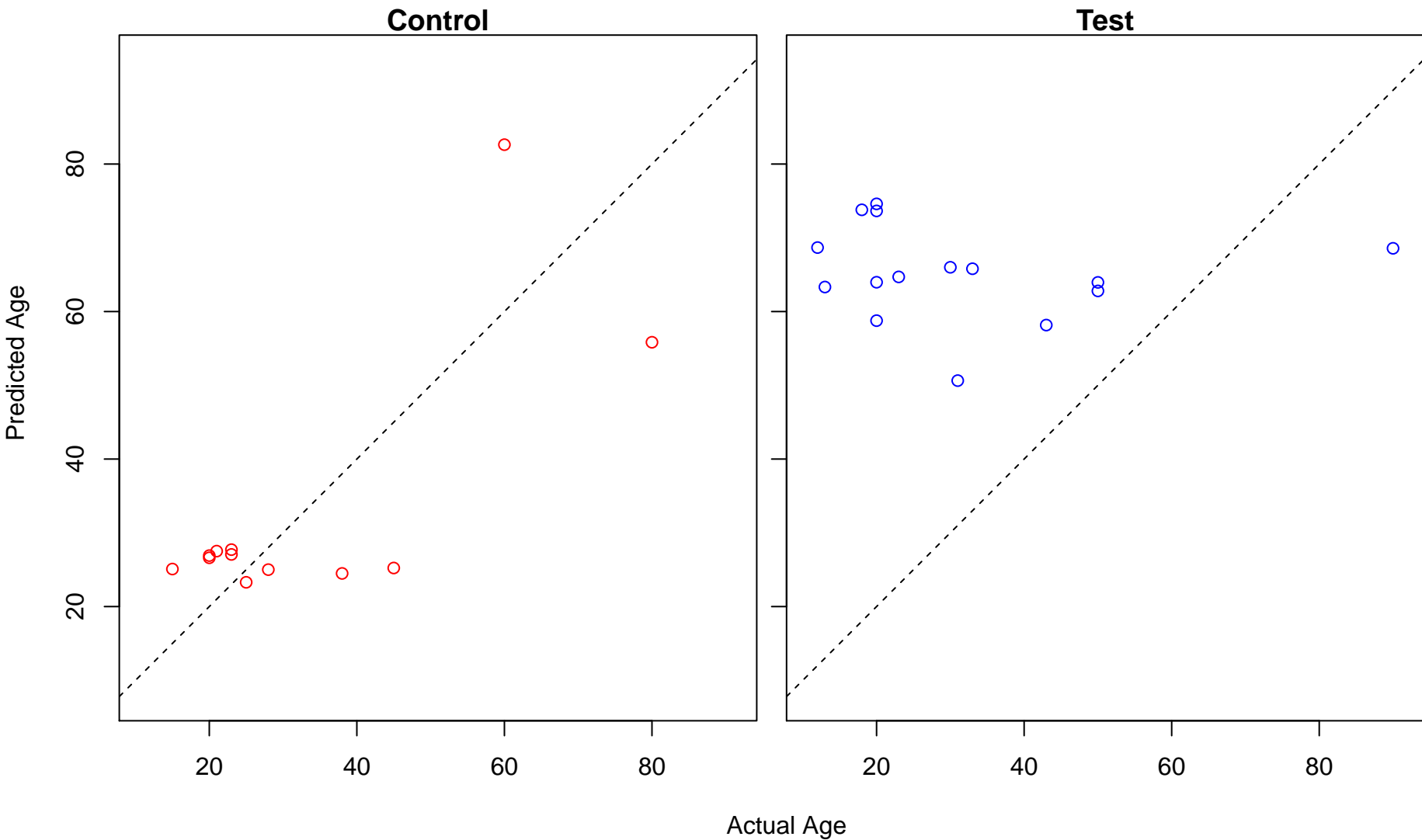


Actual Age

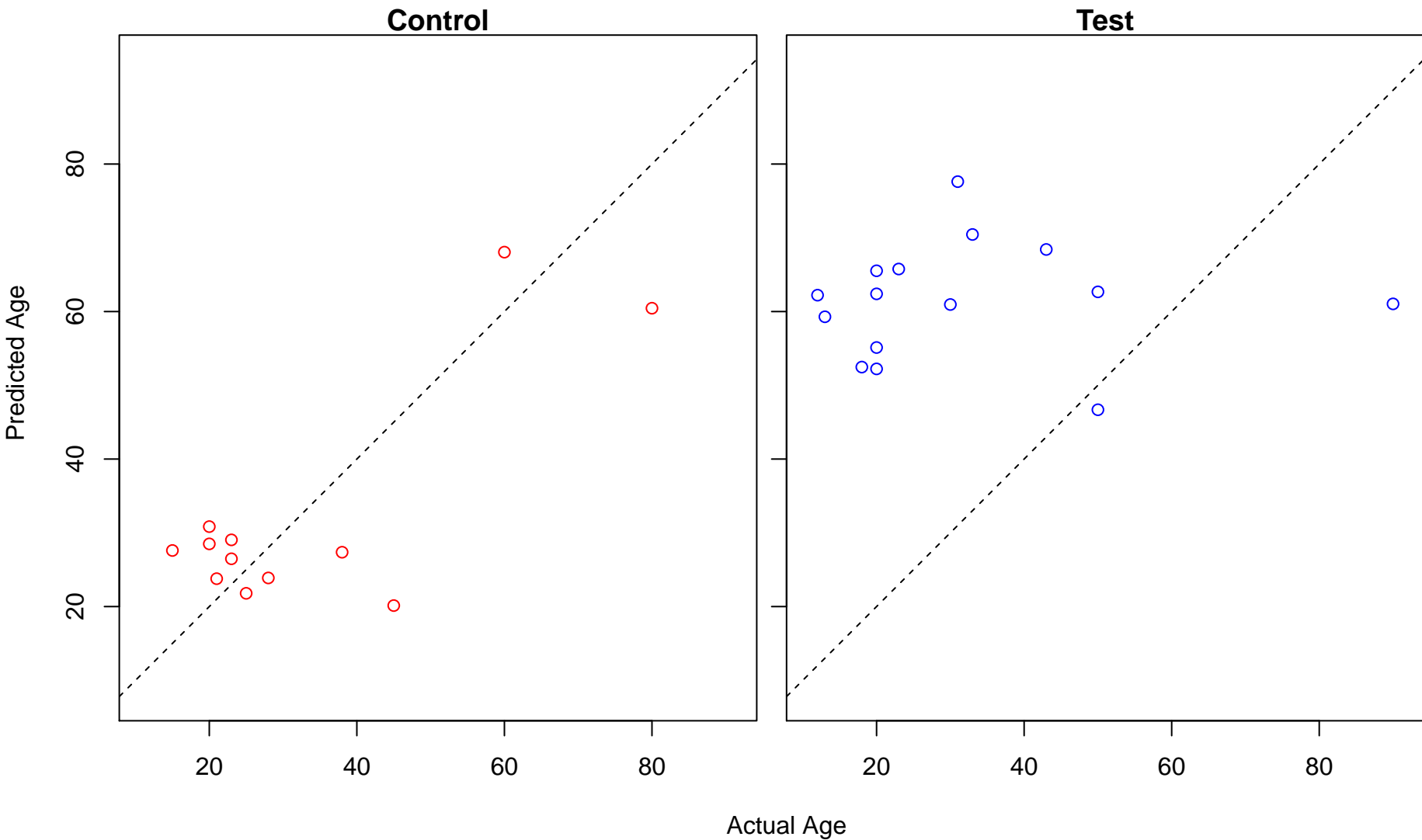
negative regulation of angiogenesis (Score: 3.632026)



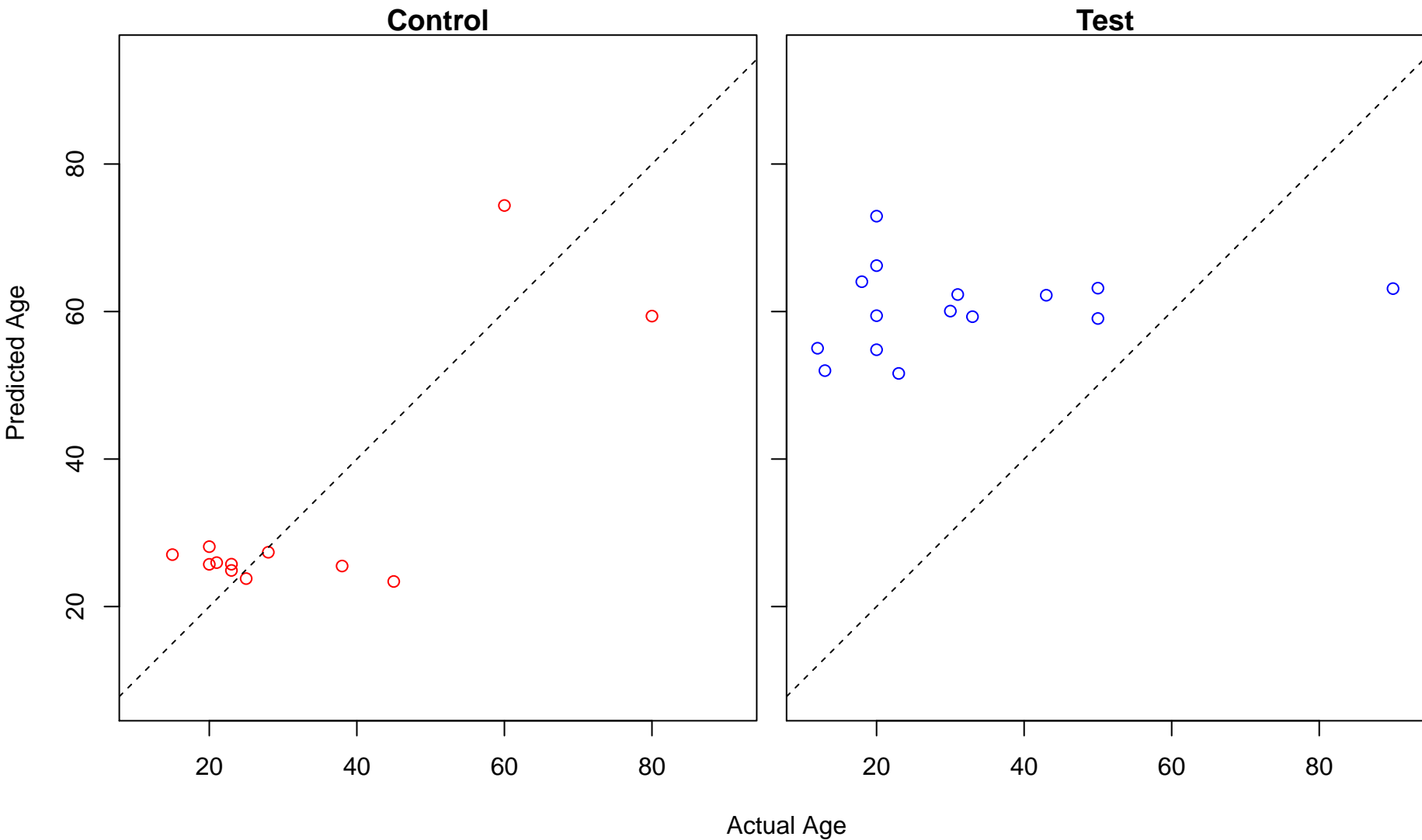
nuclear-transcribed mRNA catabolic process, exonucleolytic (Score: 3.630919)



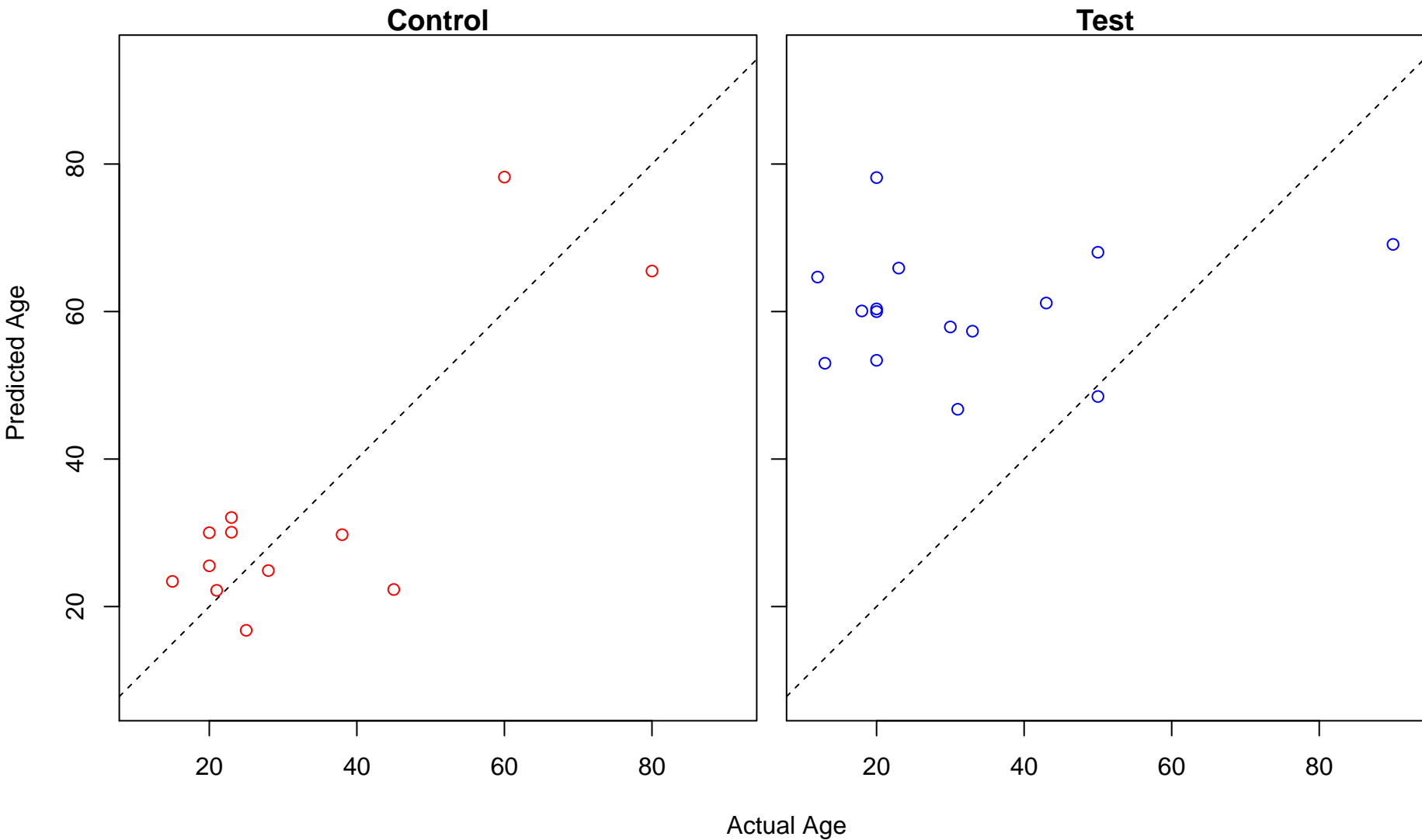
nuclear body organization (Score: 3.630468)



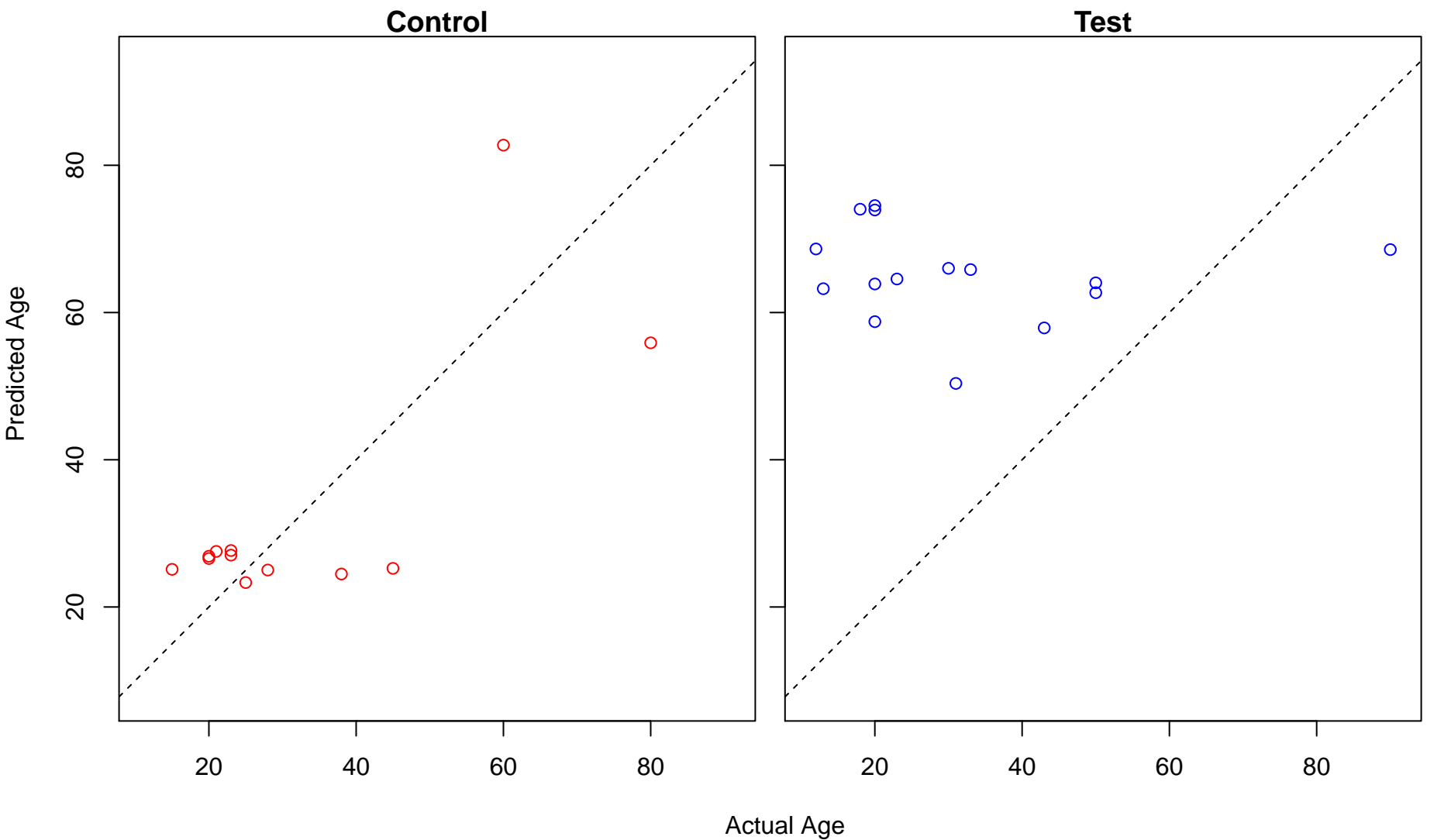
positive regulation of cytokinesis (Score: 3.630319)



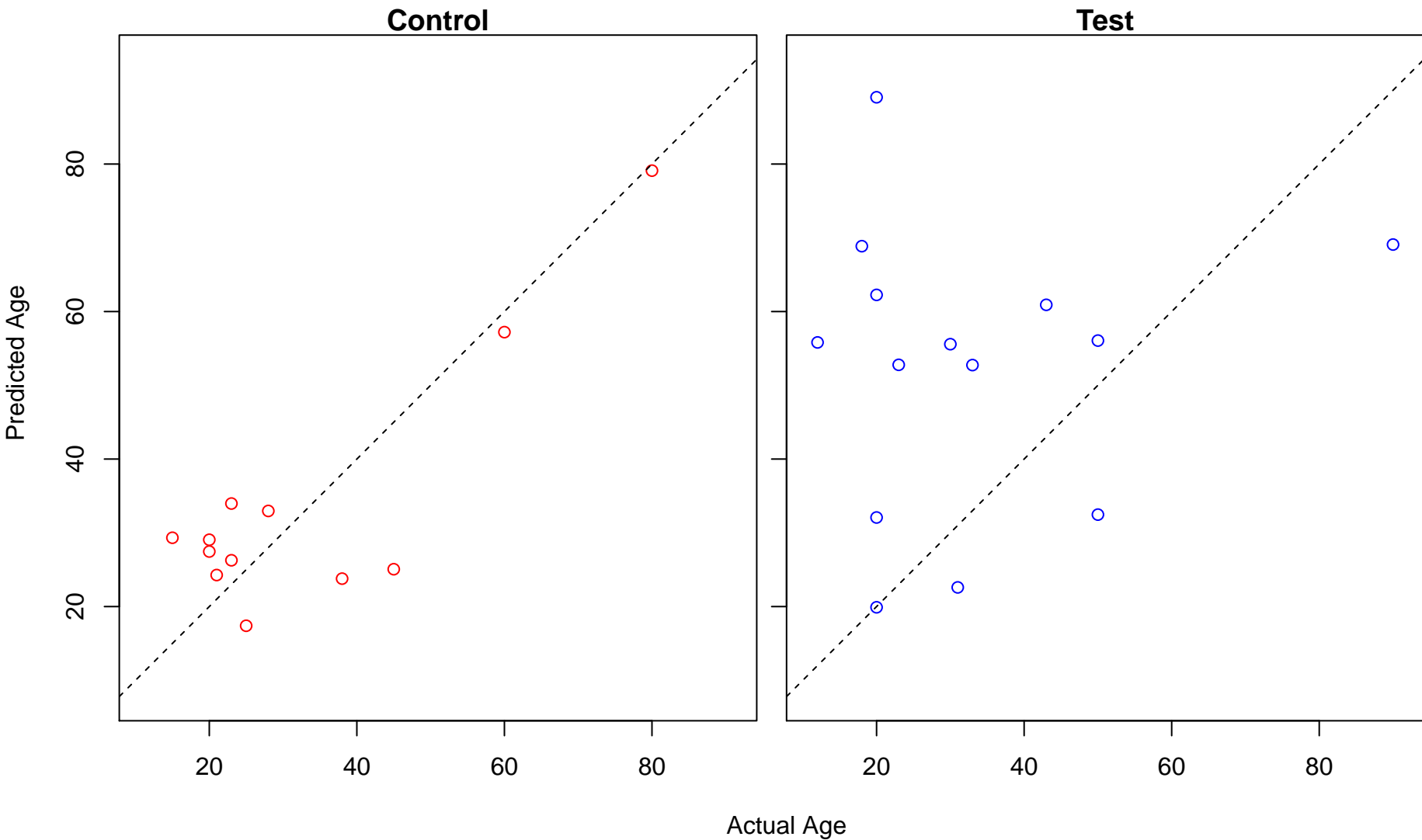
negative regulation of glycogen biosynthetic process (Score: 3.630048)



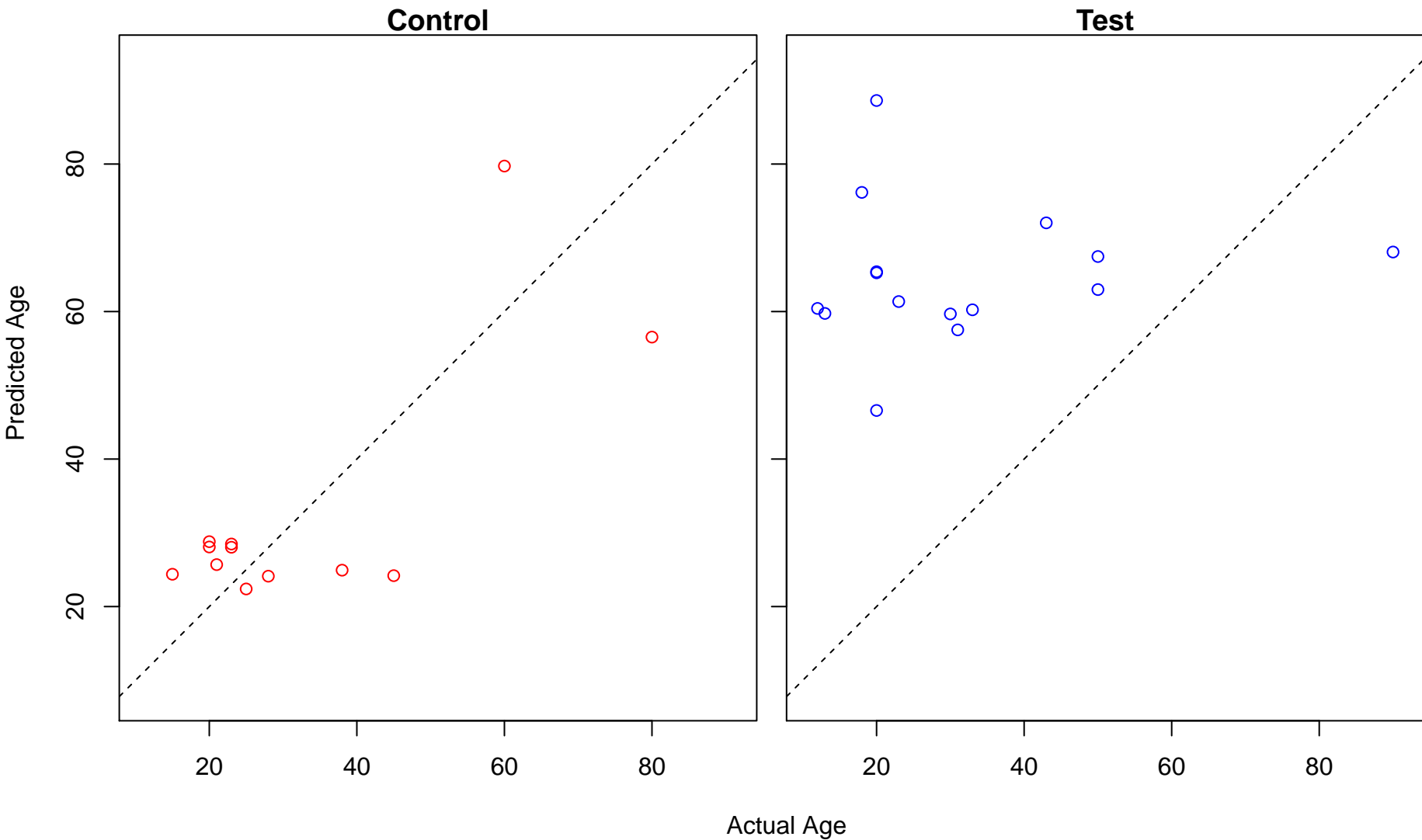
nucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay (Scor



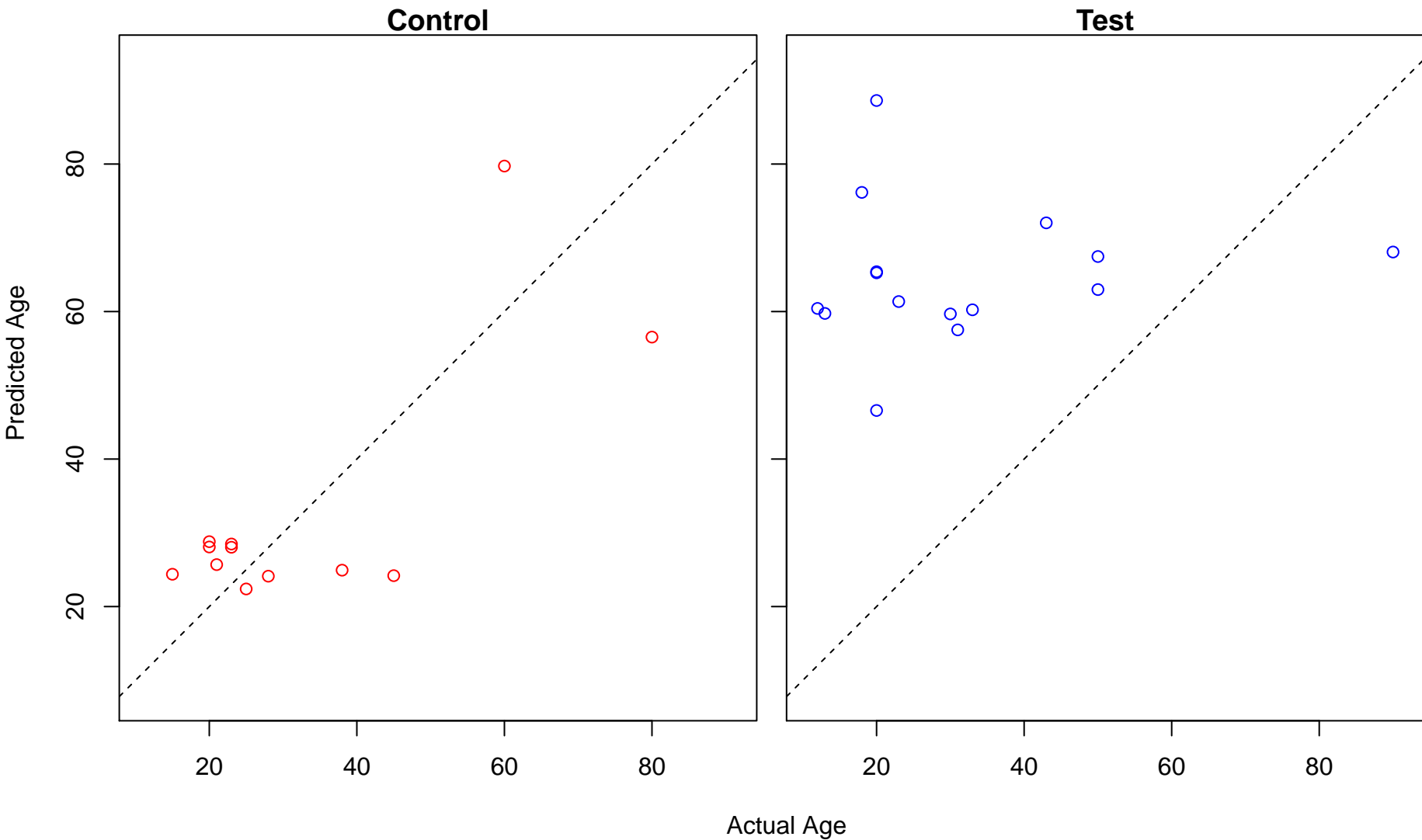
microtubule organizing center organization (Score: 3.623805)



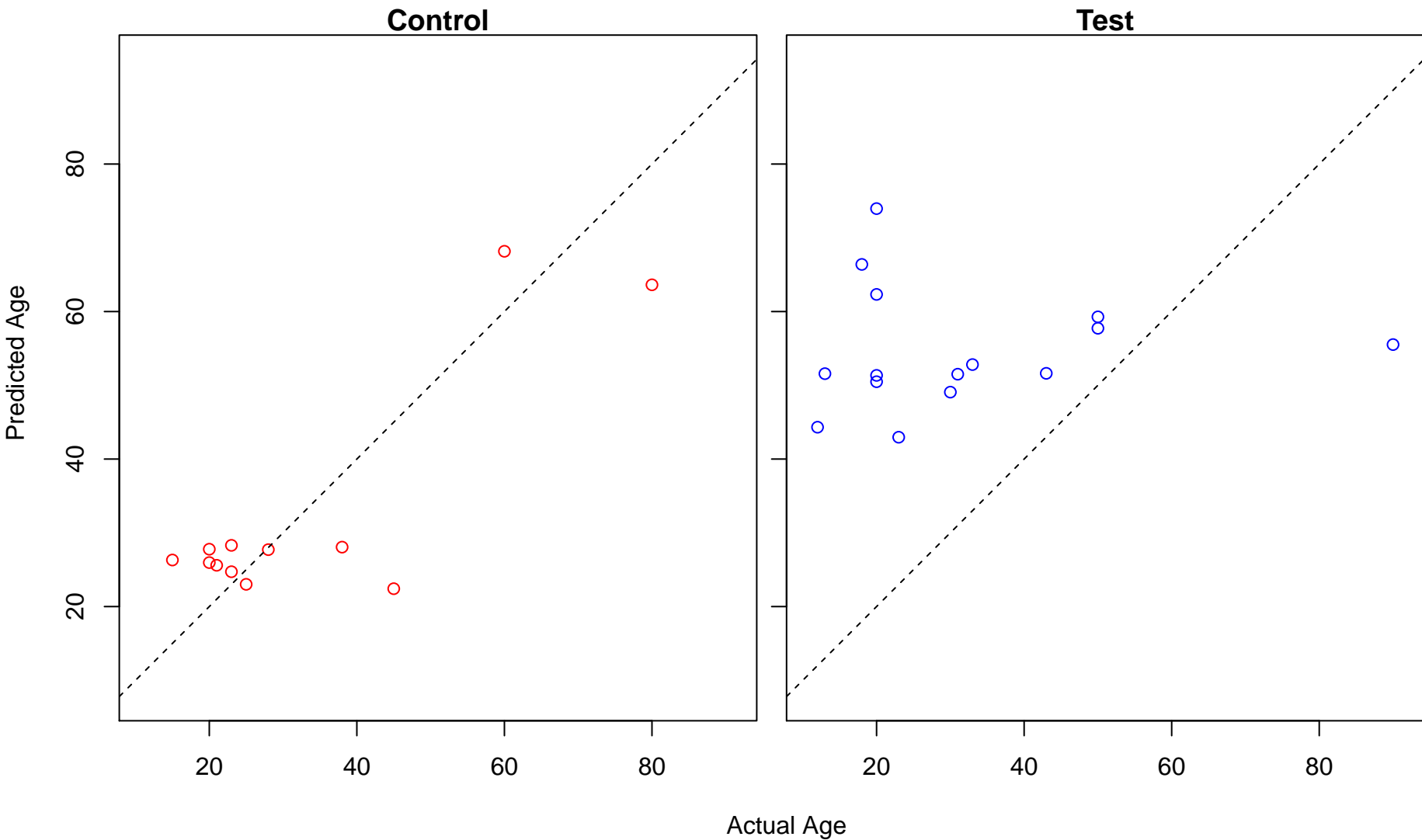
acidic amino acid transport (Score: 3.622587)



L-glutamate transport (Score: 3.622587)

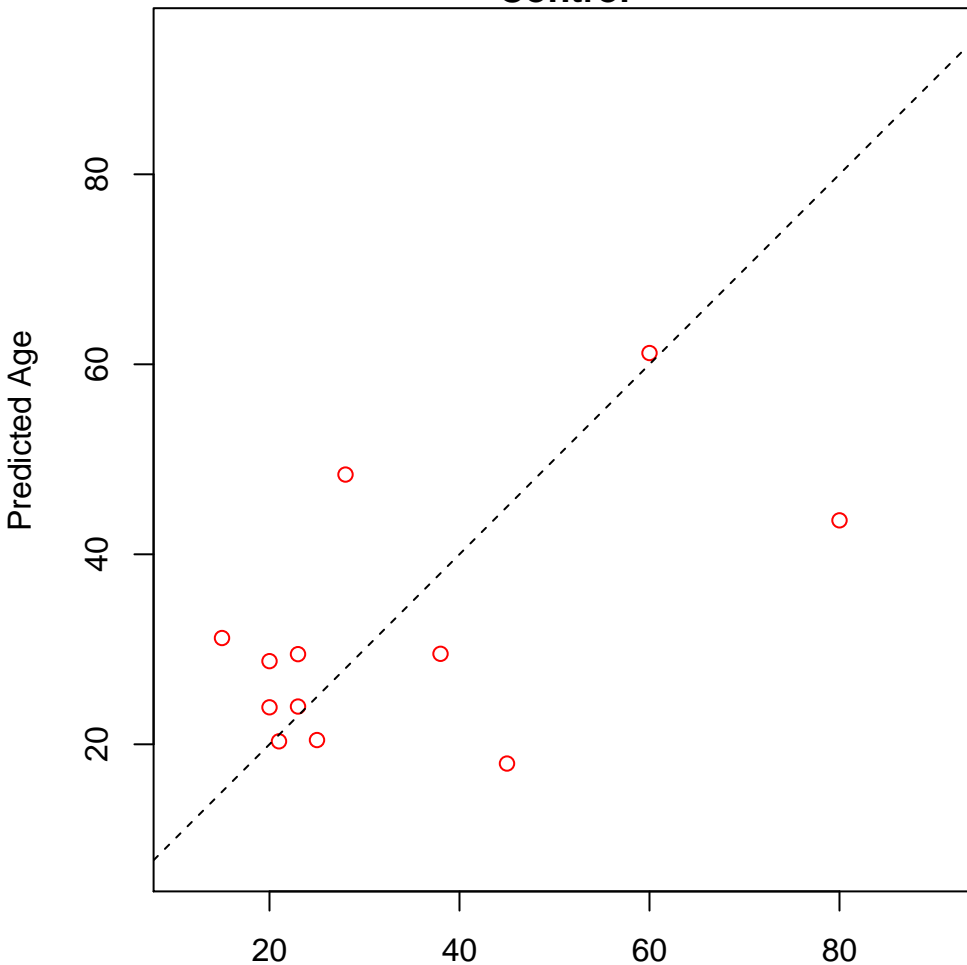


negative regulation of protein complex assembly (Score: 3.621034)

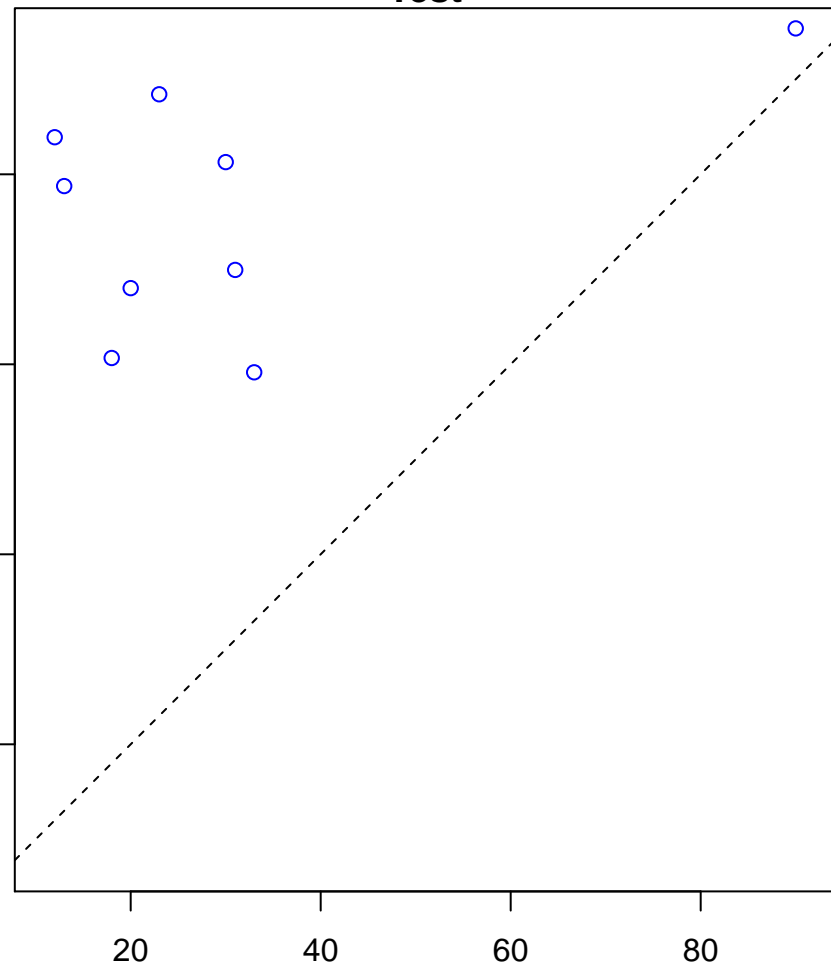


central nervous system myelination (Score: 3.620104)

Control

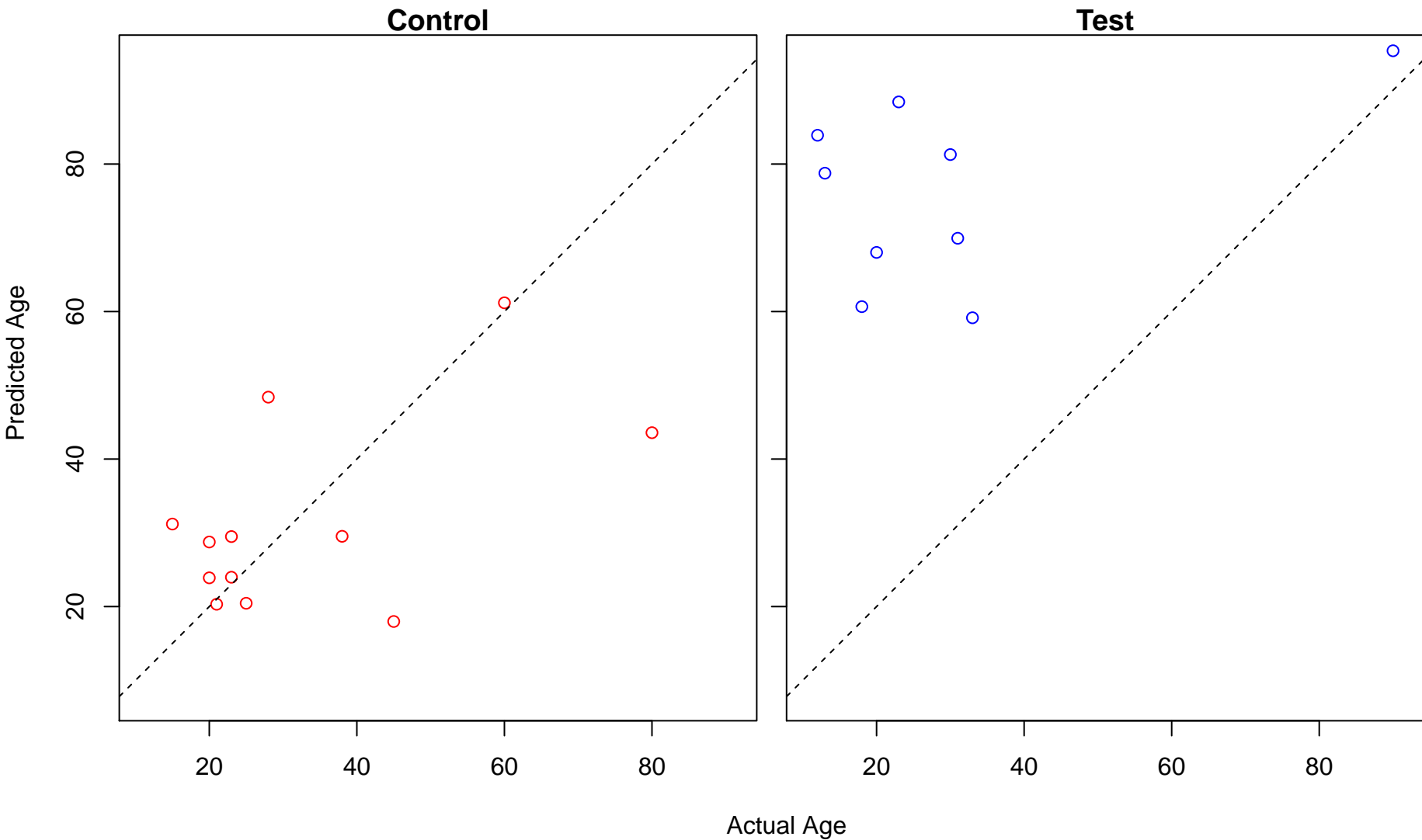


Test

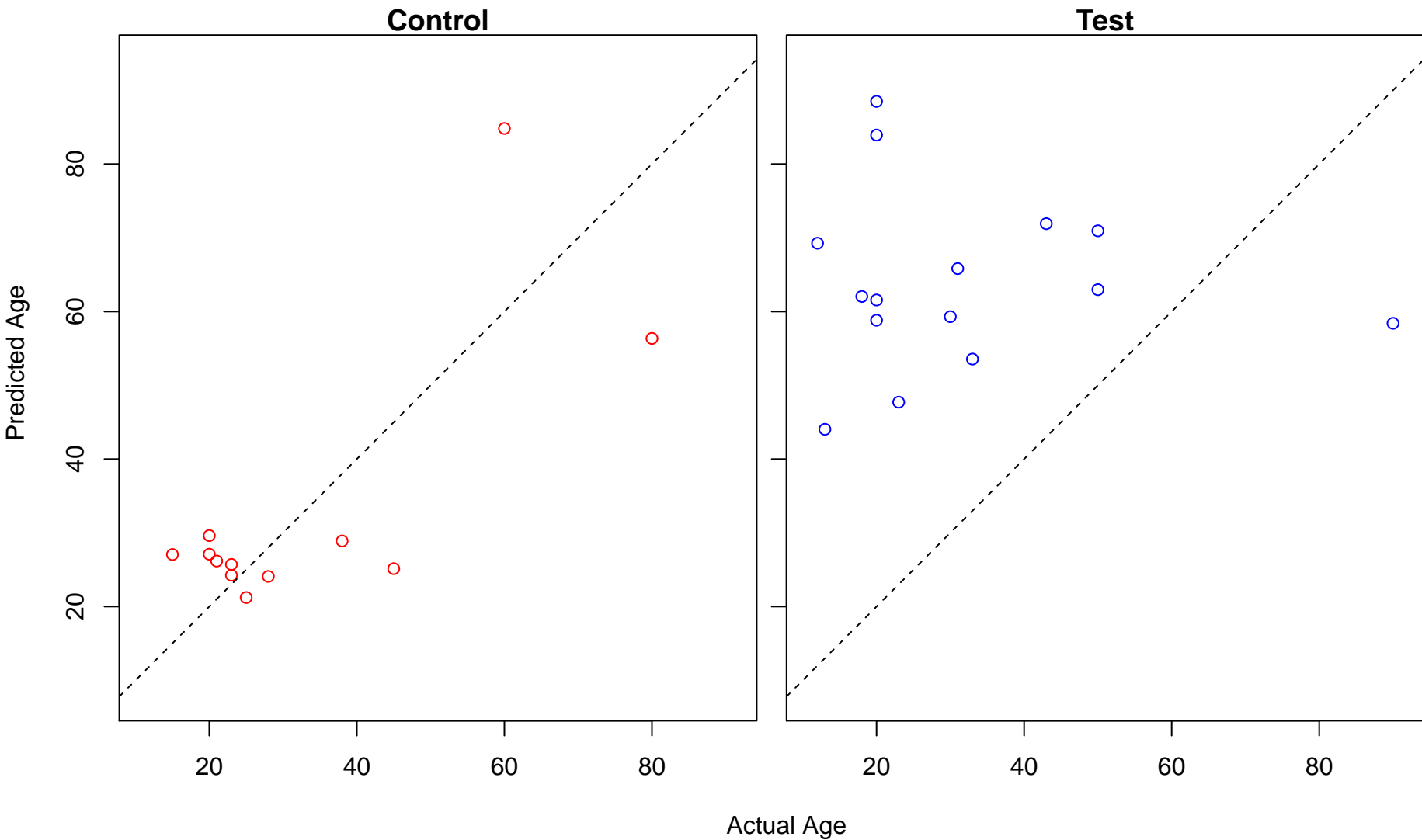


Actual Age

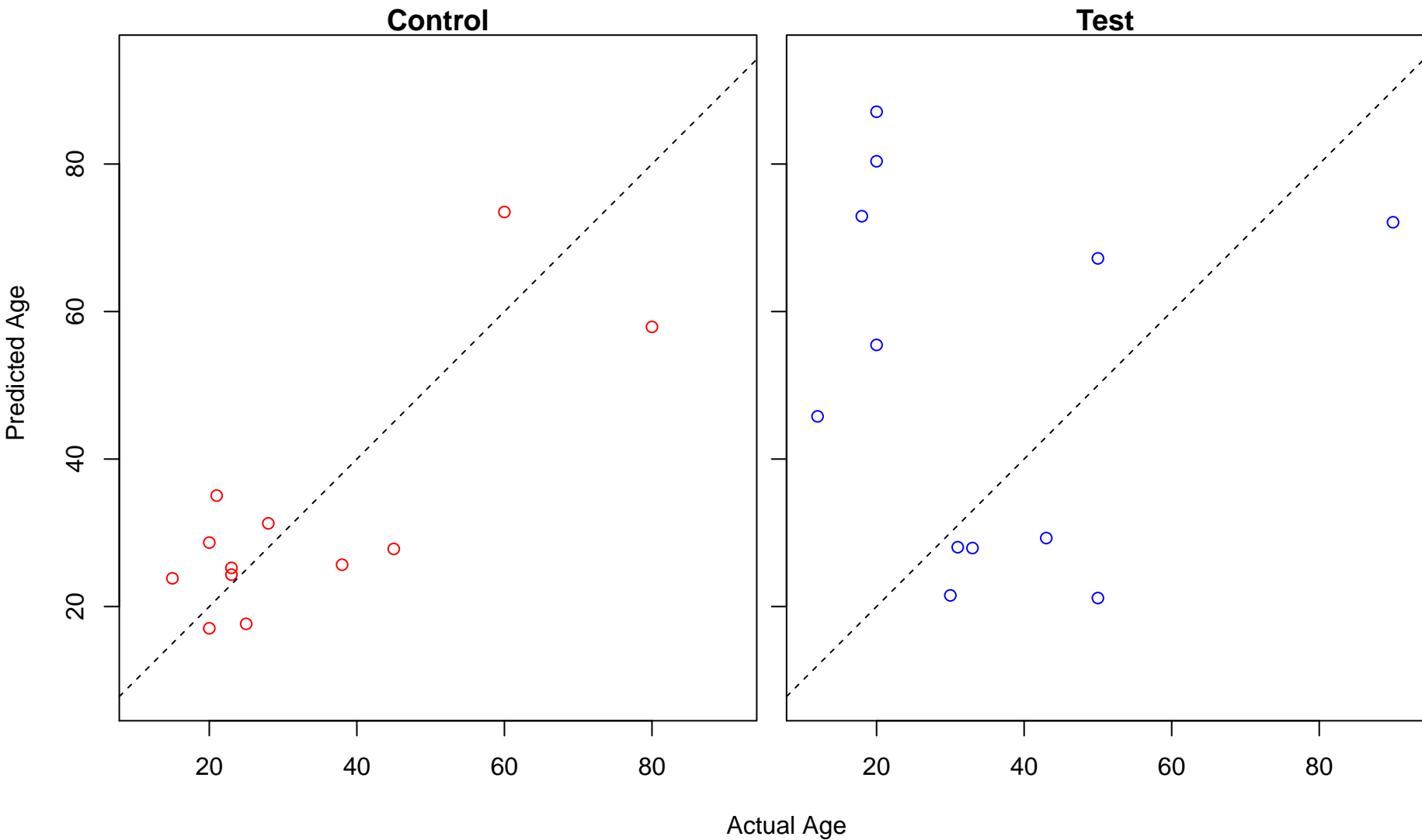
axon ensheathment in central nervous system (Score: 3.620104)



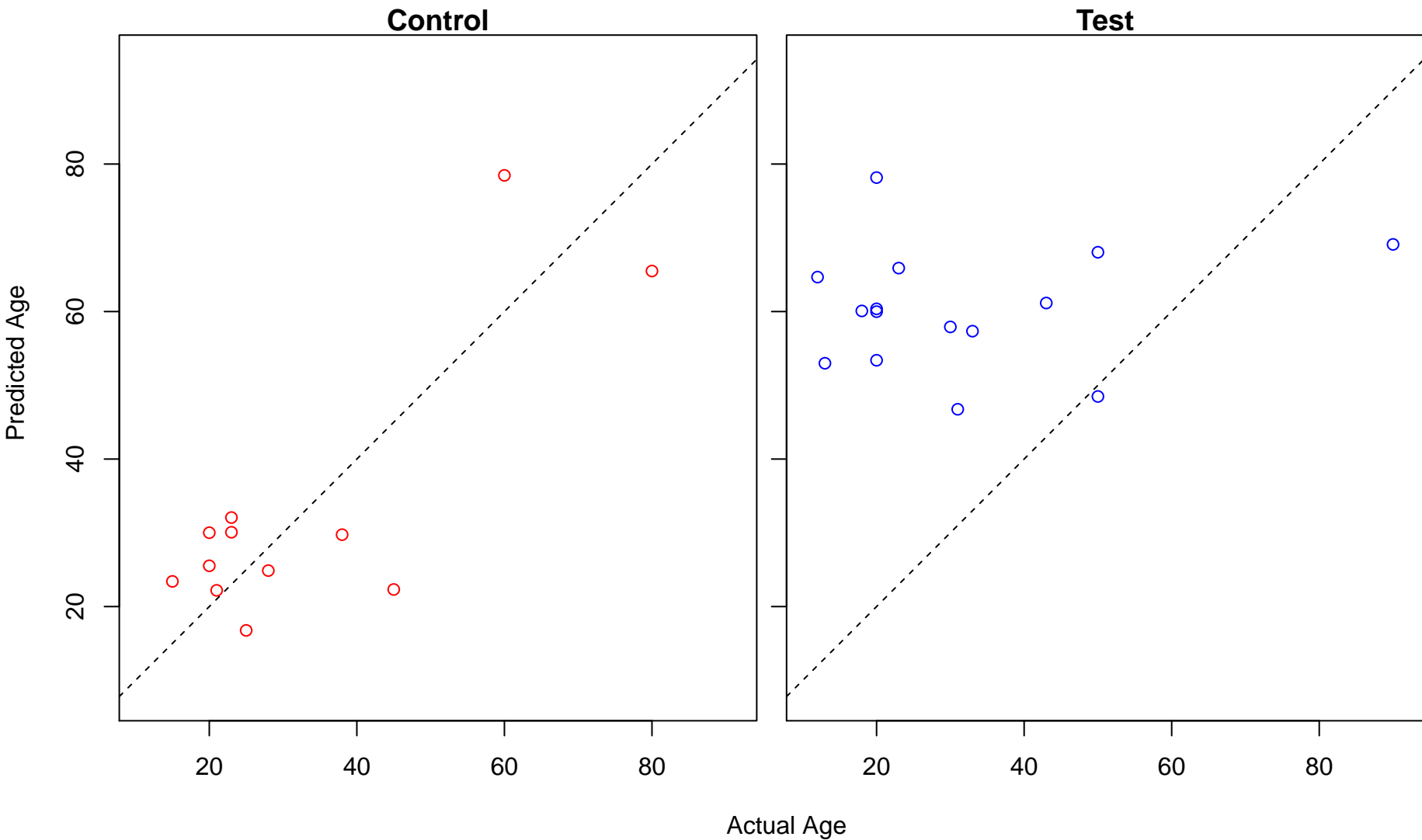
regulation of epithelial cell apoptotic process (Score: 3.620096)



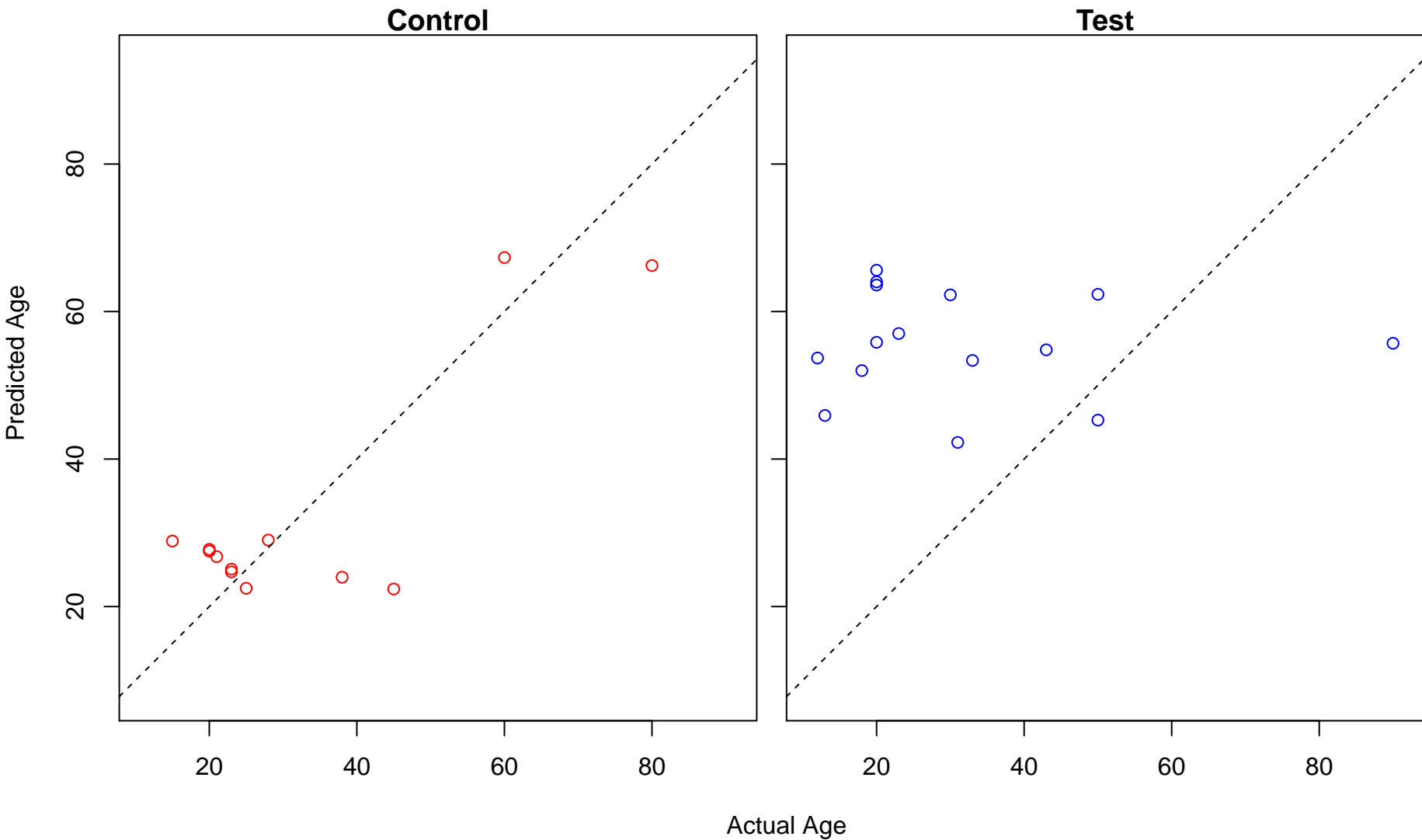
protein homotetramerization (Score: 3.615819)



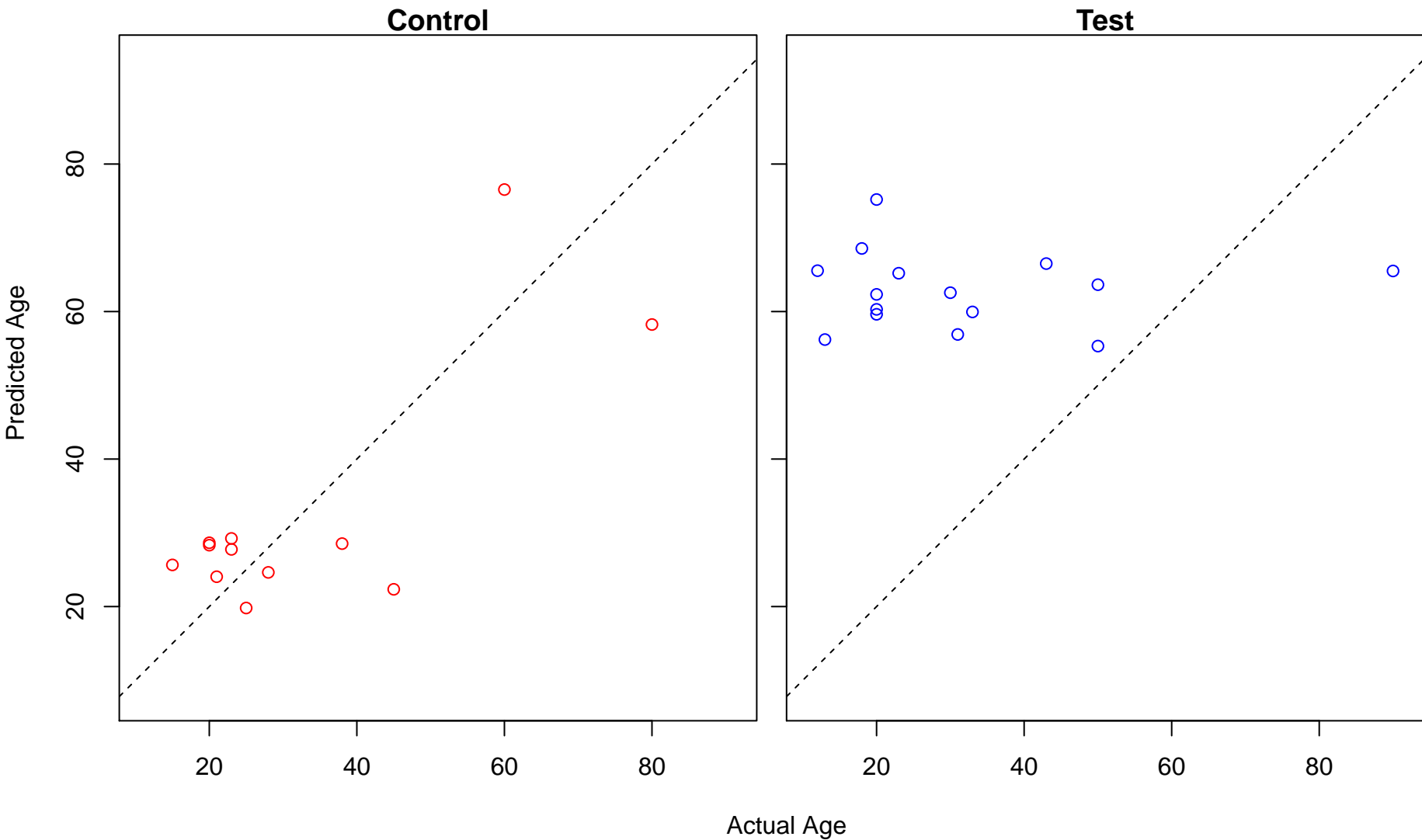
negative regulation of glycogen metabolic process (Score: 3.615709)



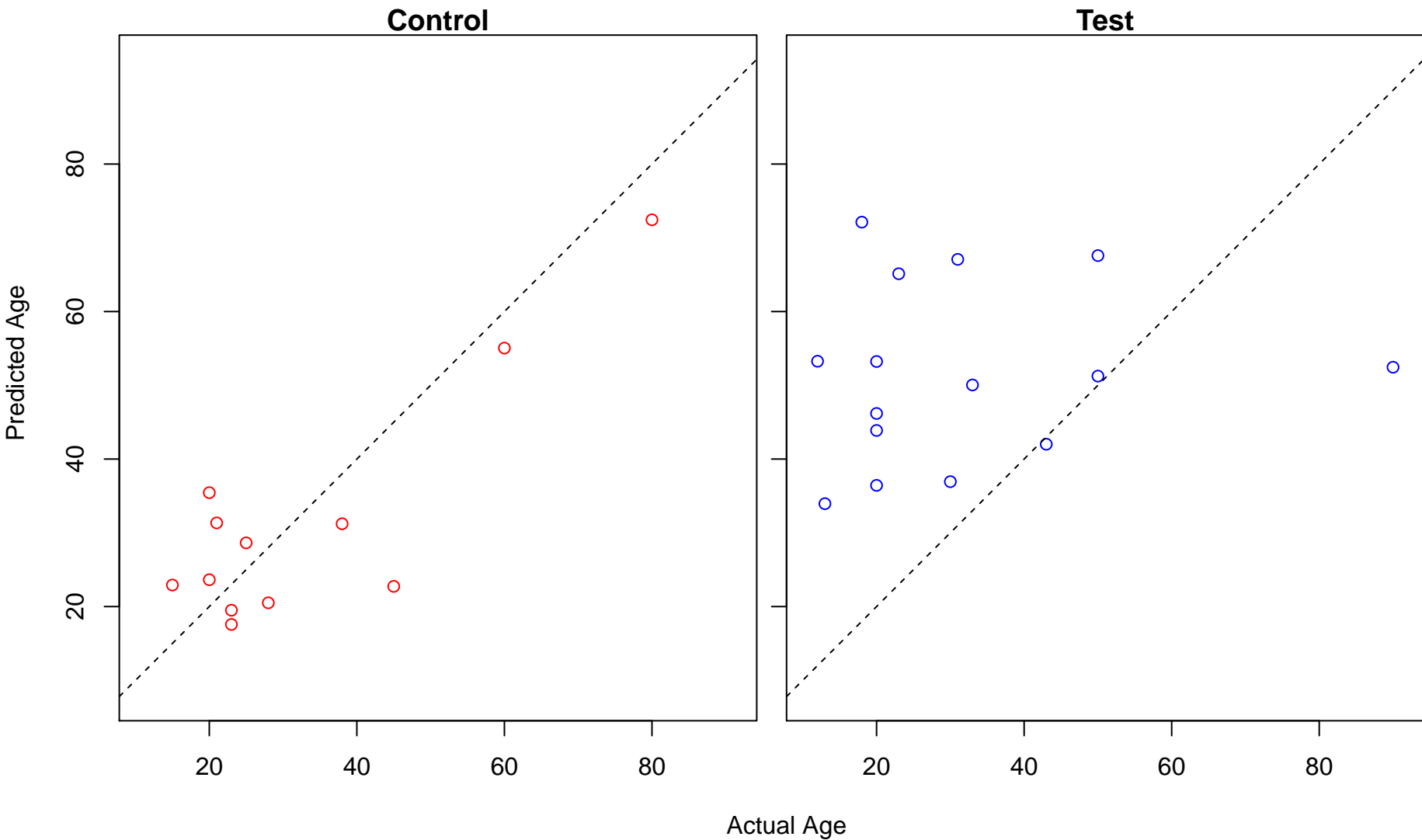
transcription from mitochondrial promoter (Score: 3.609886)



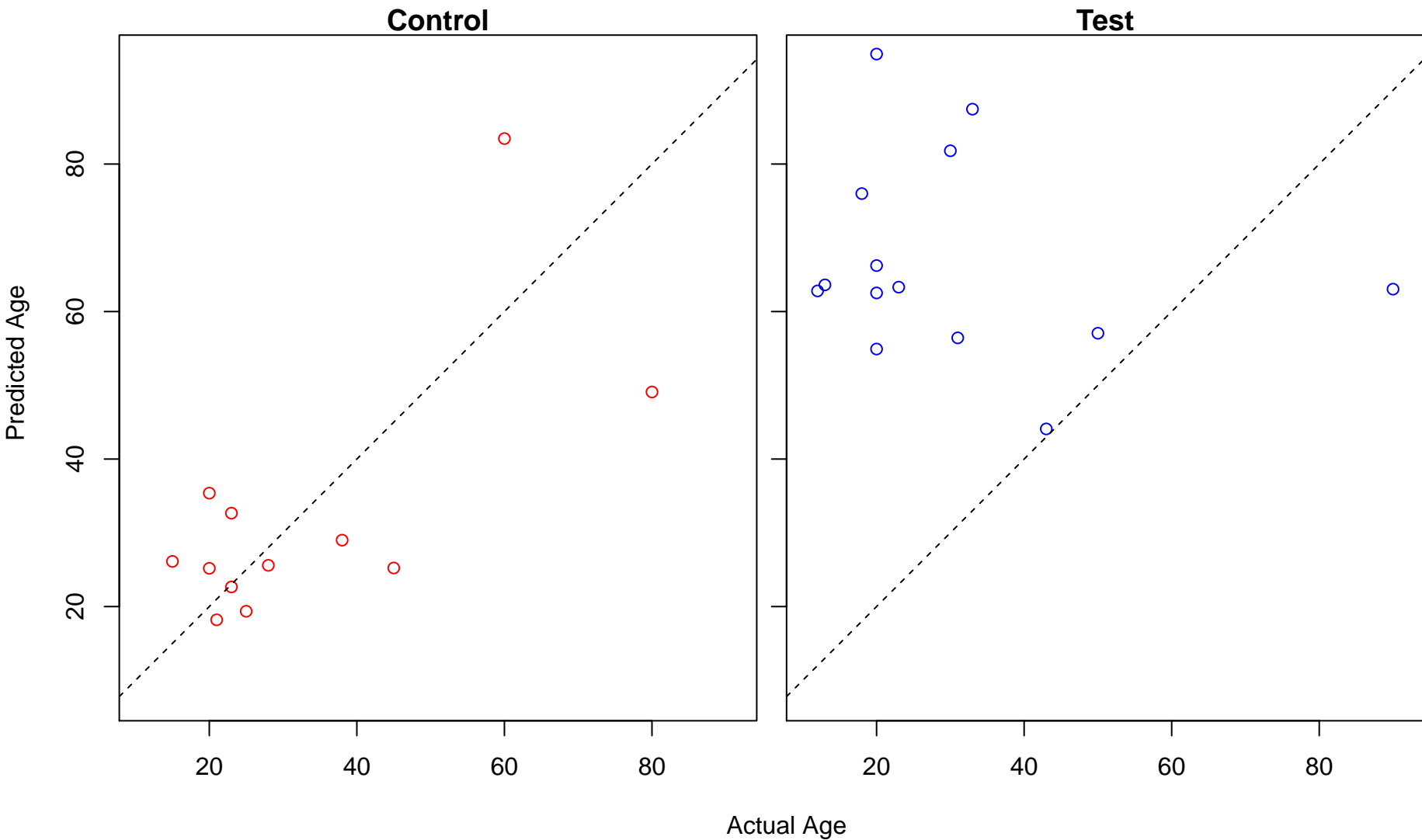
regulation of RIG-I signaling pathway (Score: 3.607667)



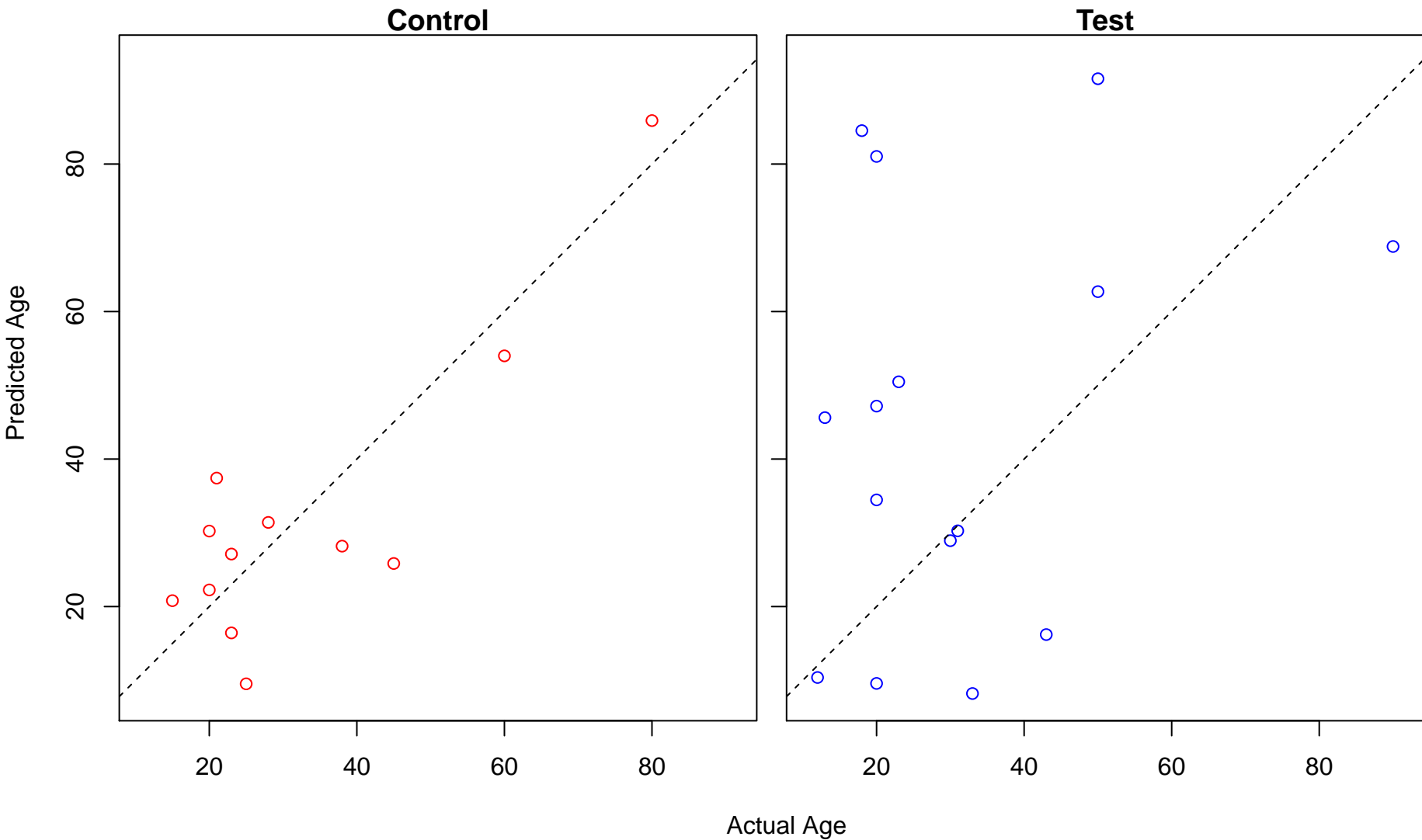
bone remodeling (Score: 3.607463)



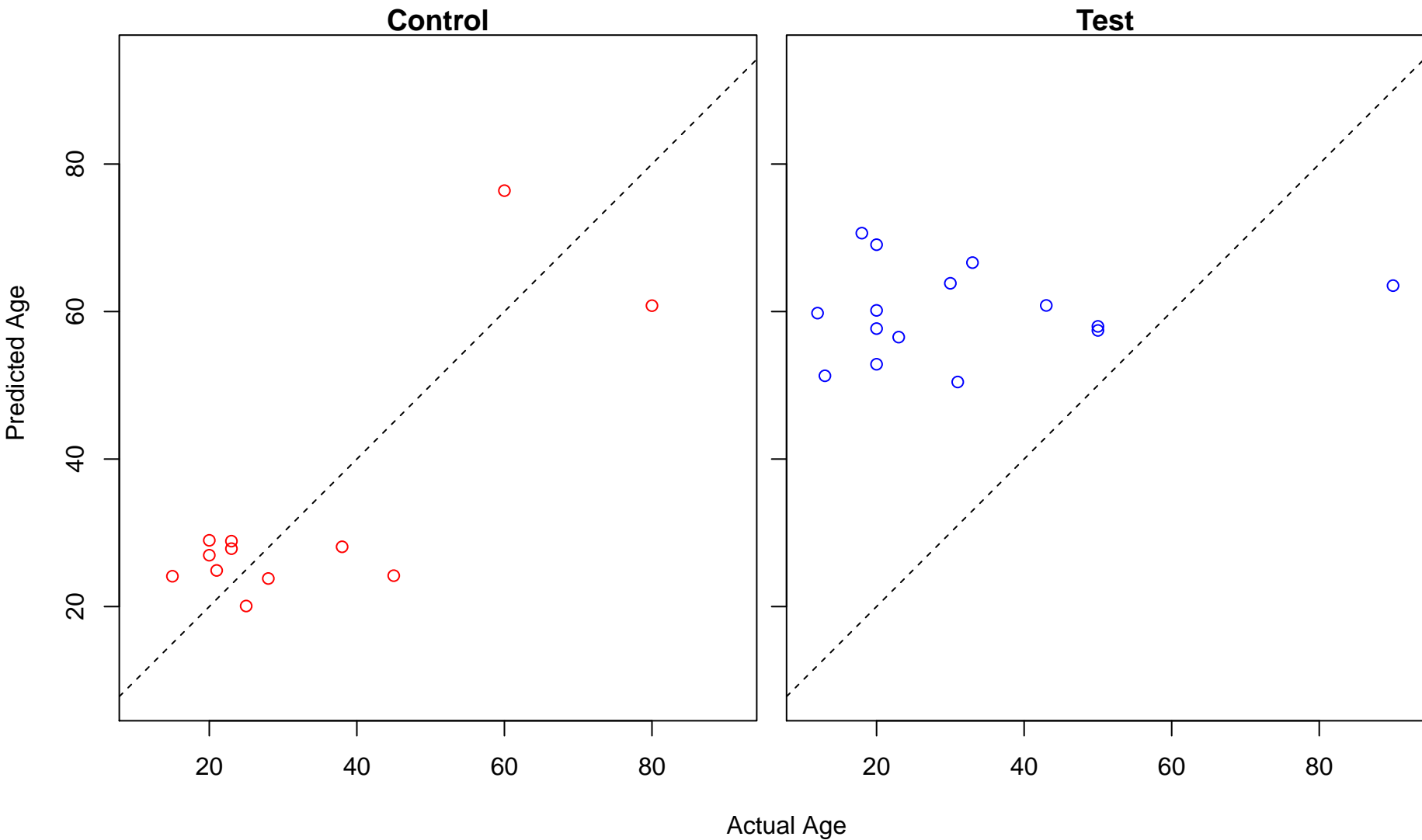
regulation of triglyceride biosynthetic process (Score: 3.606922)



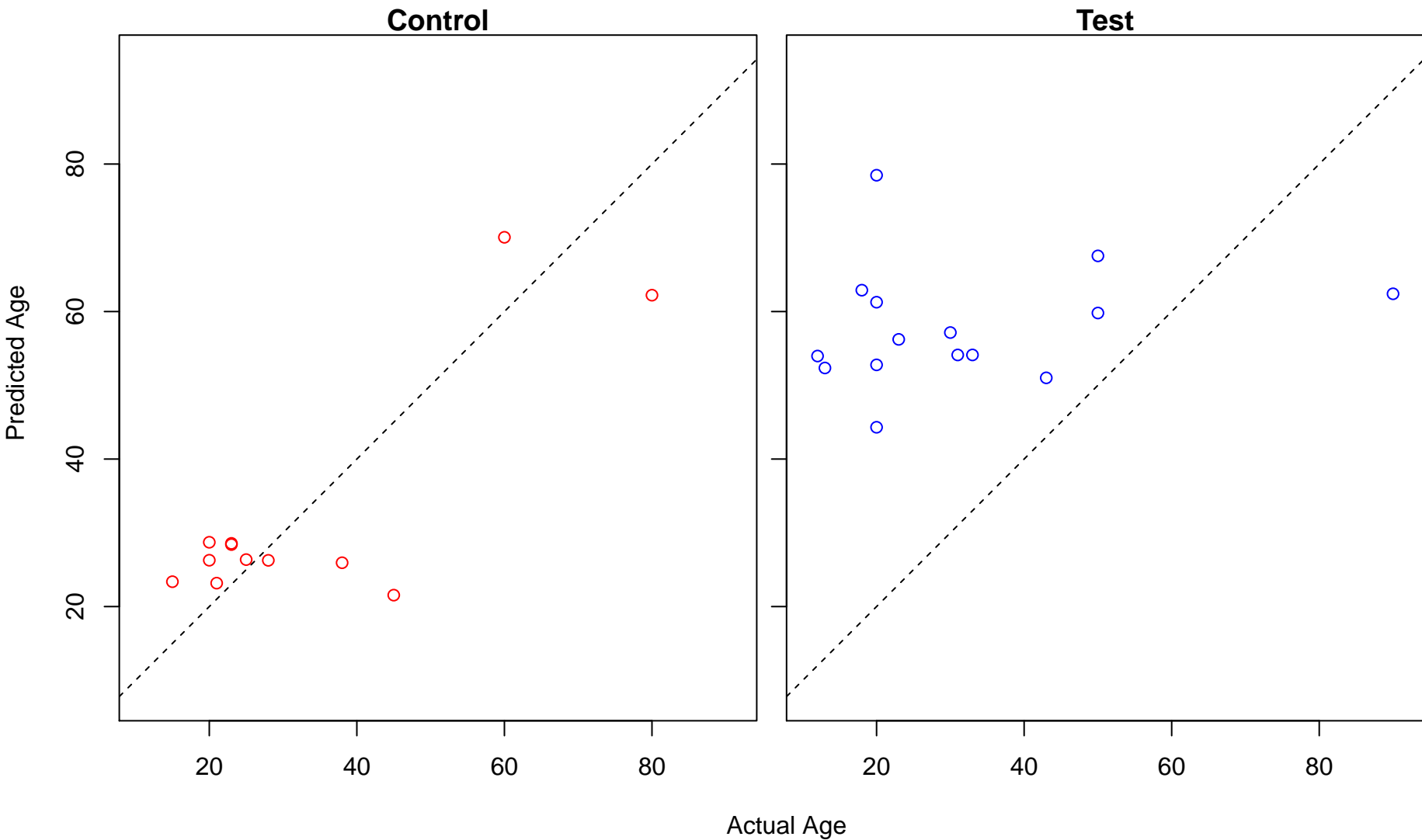
positive regulation of epithelial cell differentiation (Score: 3.605885)



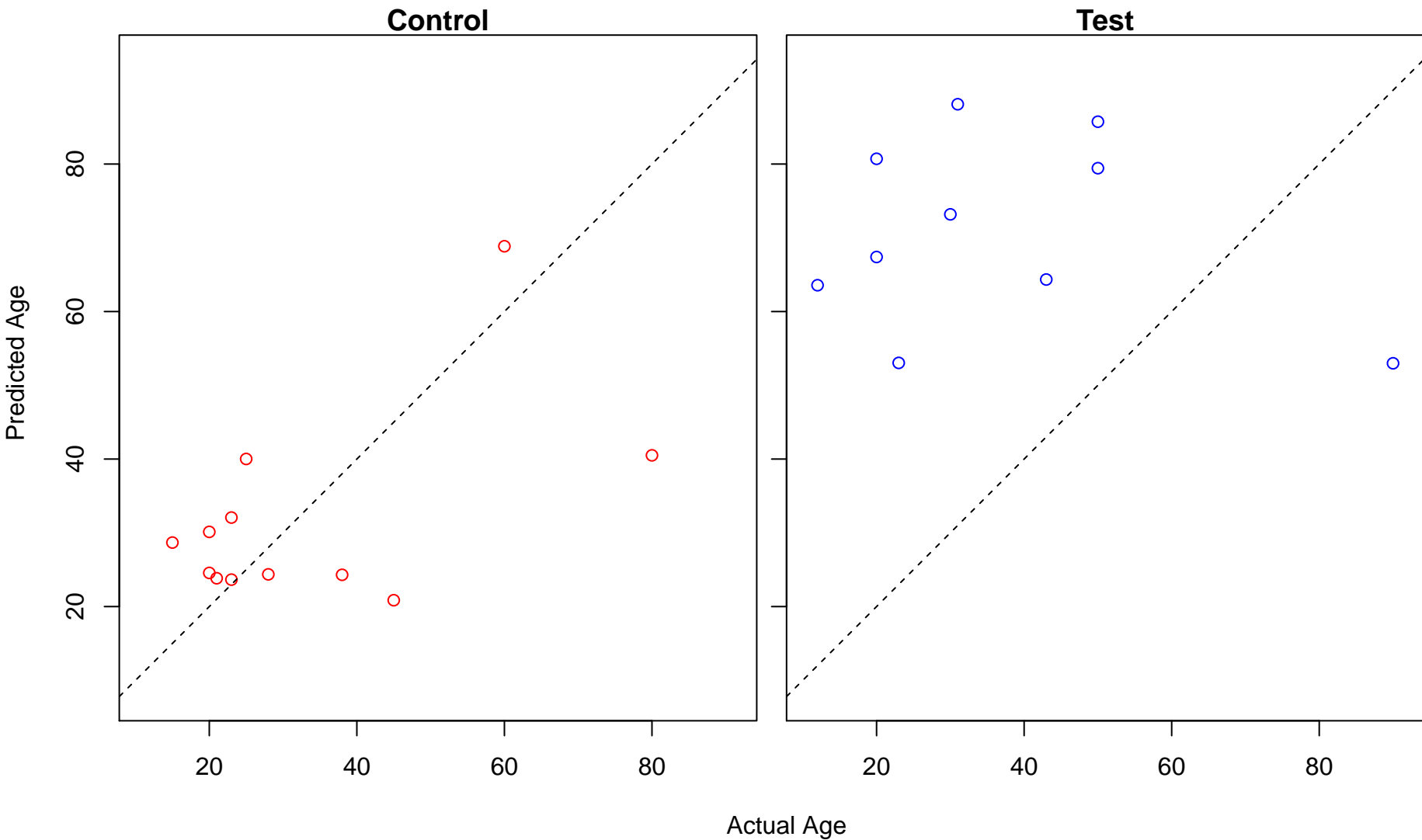
cellular extravasation (Score: 3.605232)



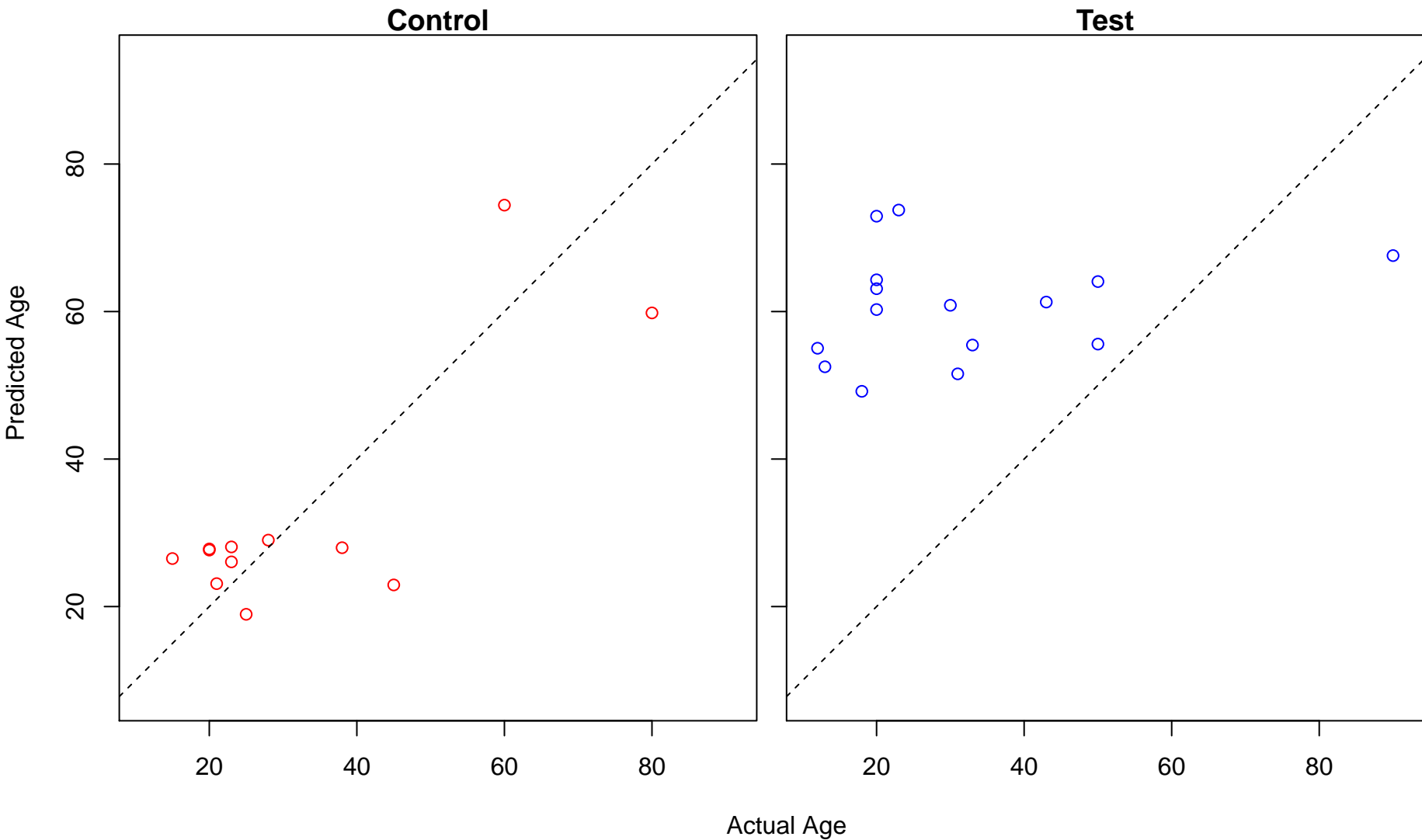
positive regulation of translation (Score: 3.603305)



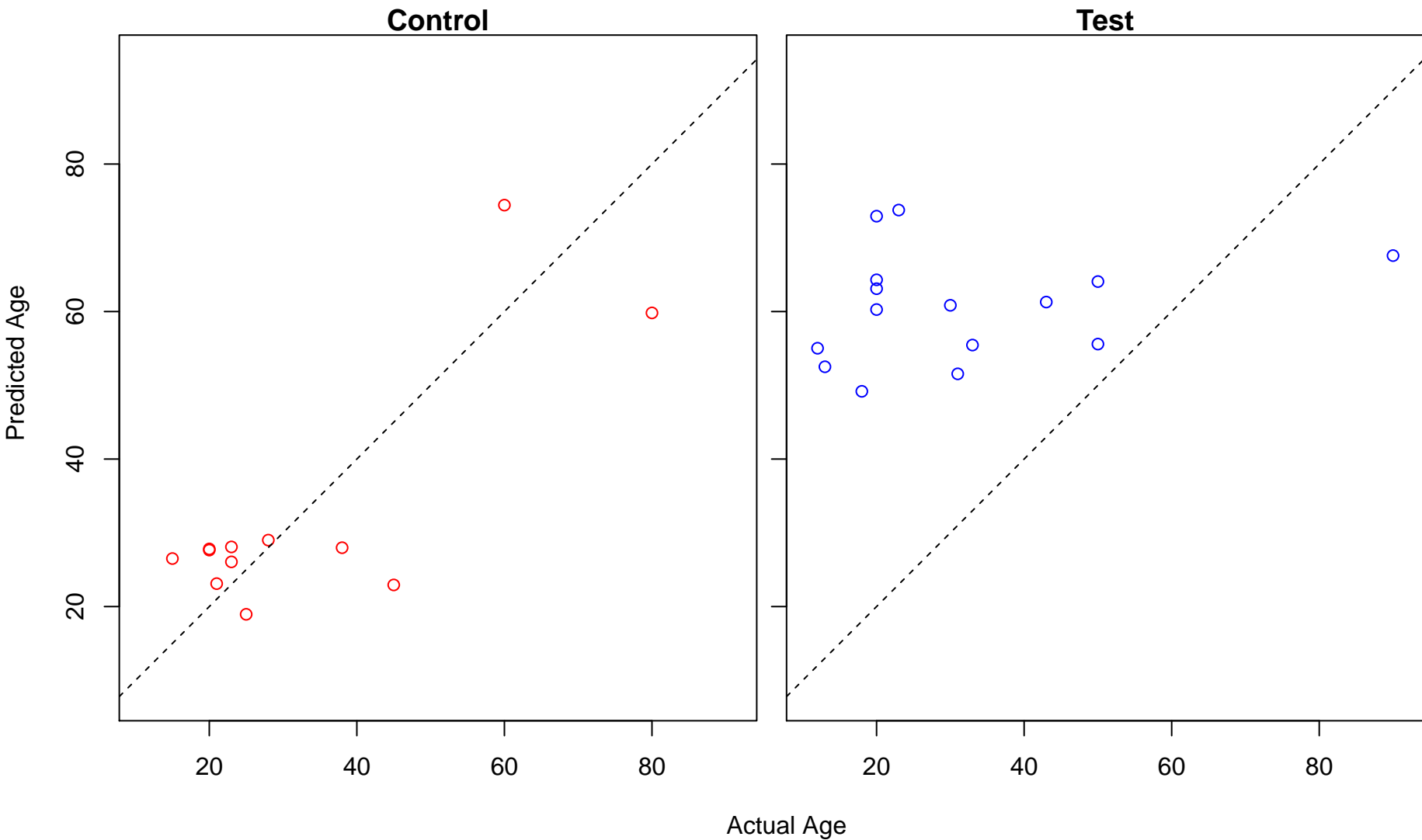
blastocyst formation (Score: 3.597015)



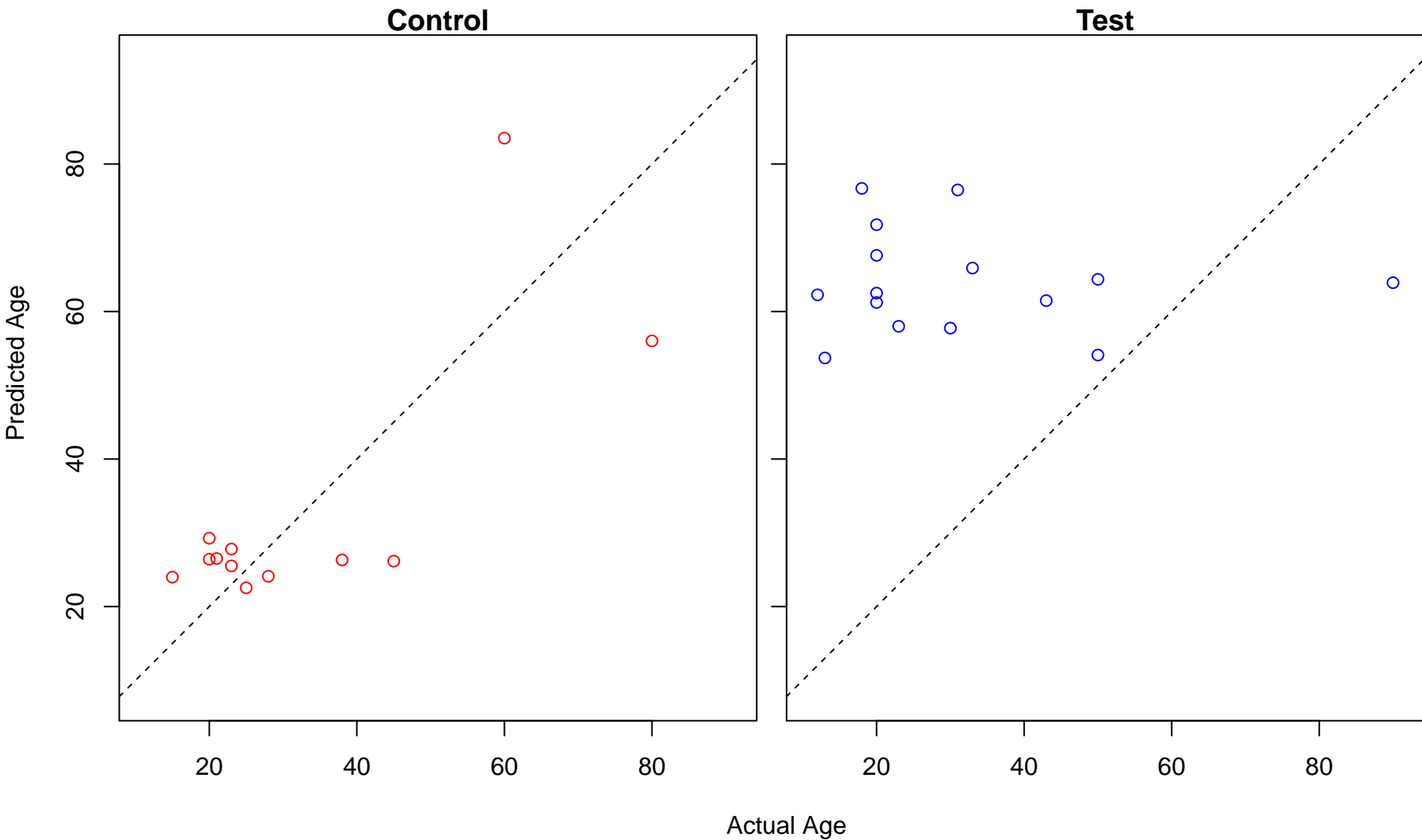
regulation of protein processing (Score: 3.593238)



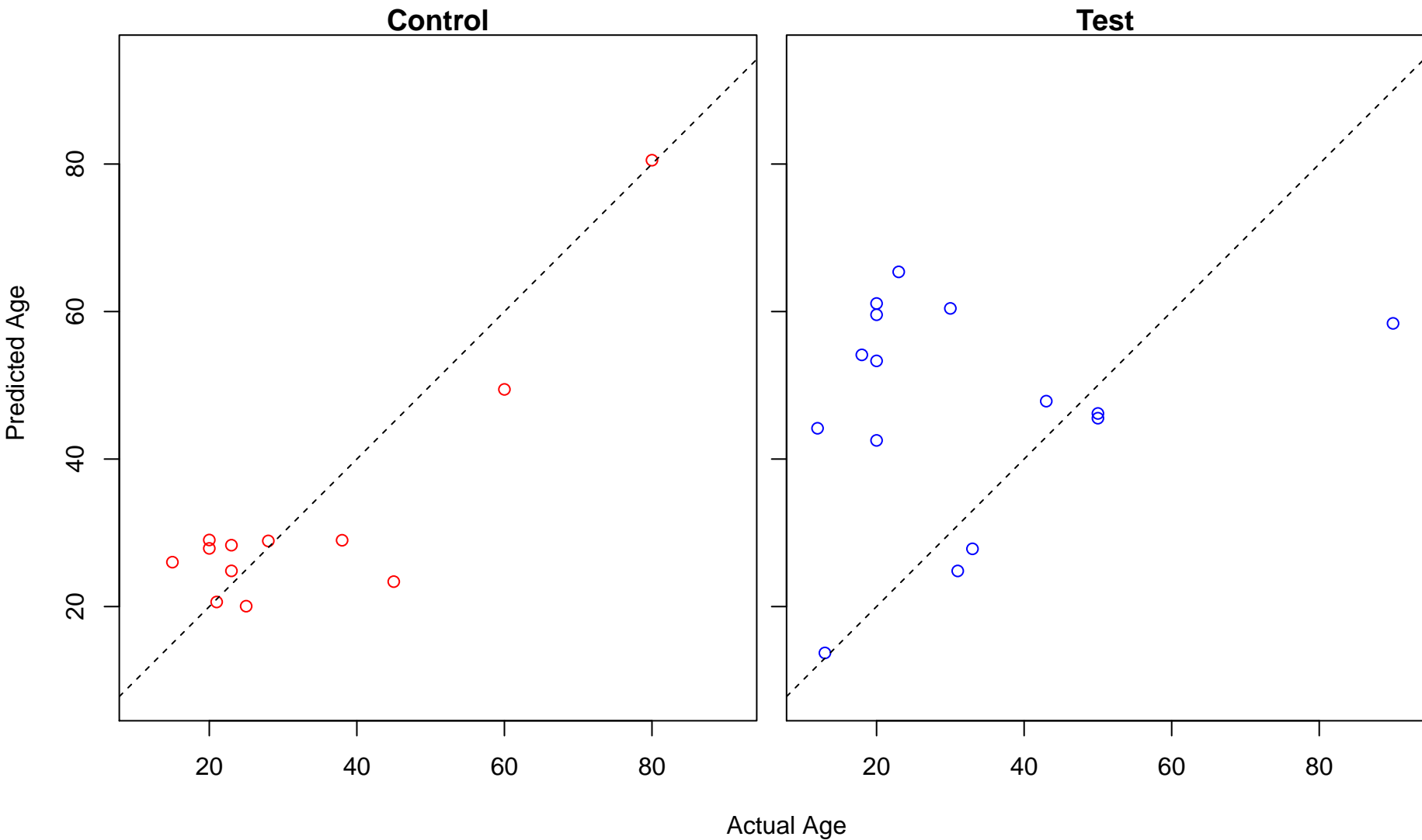
regulation of protein maturation (Score: 3.593166)



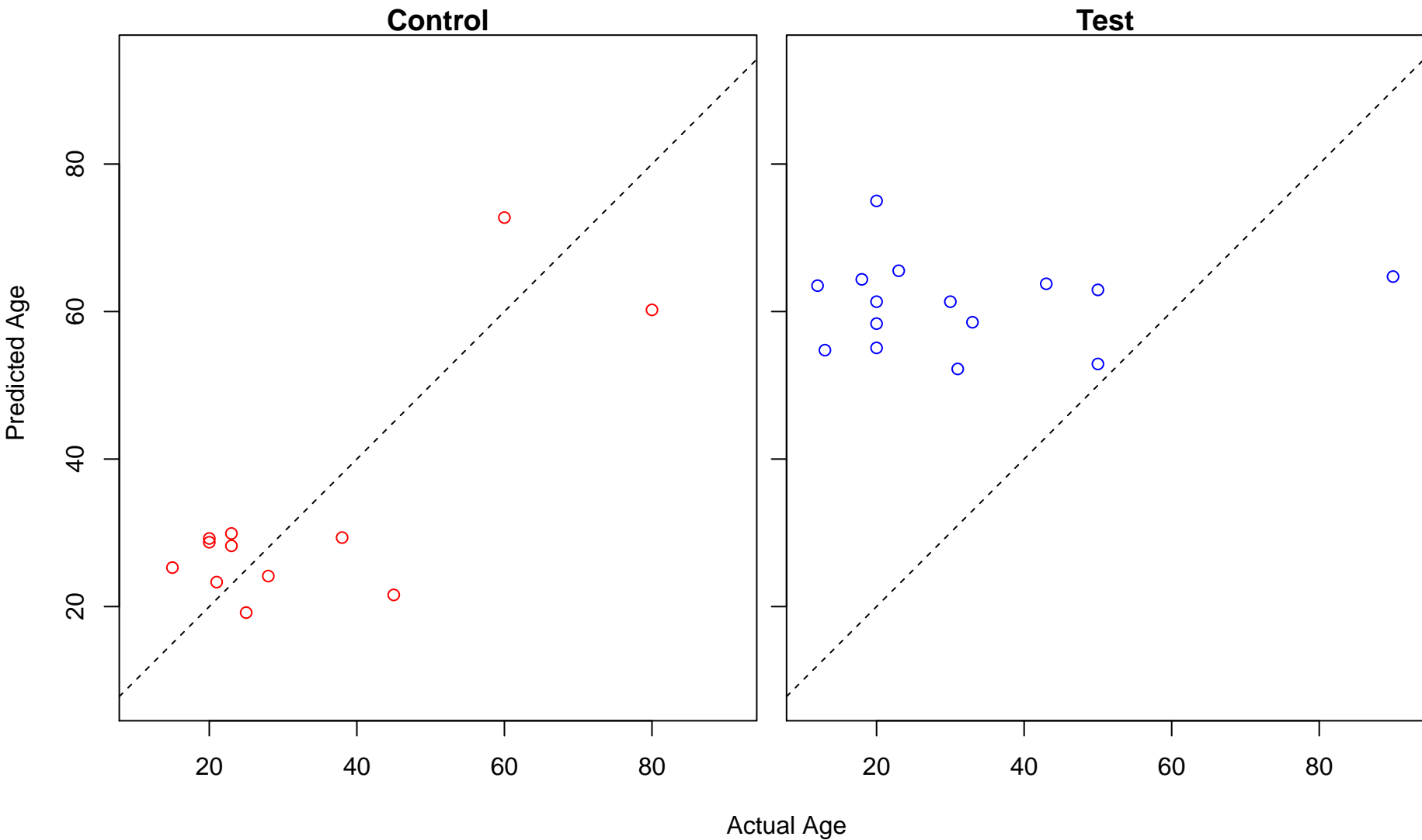
modulation of excitatory postsynaptic potential (Score: 3.592236)



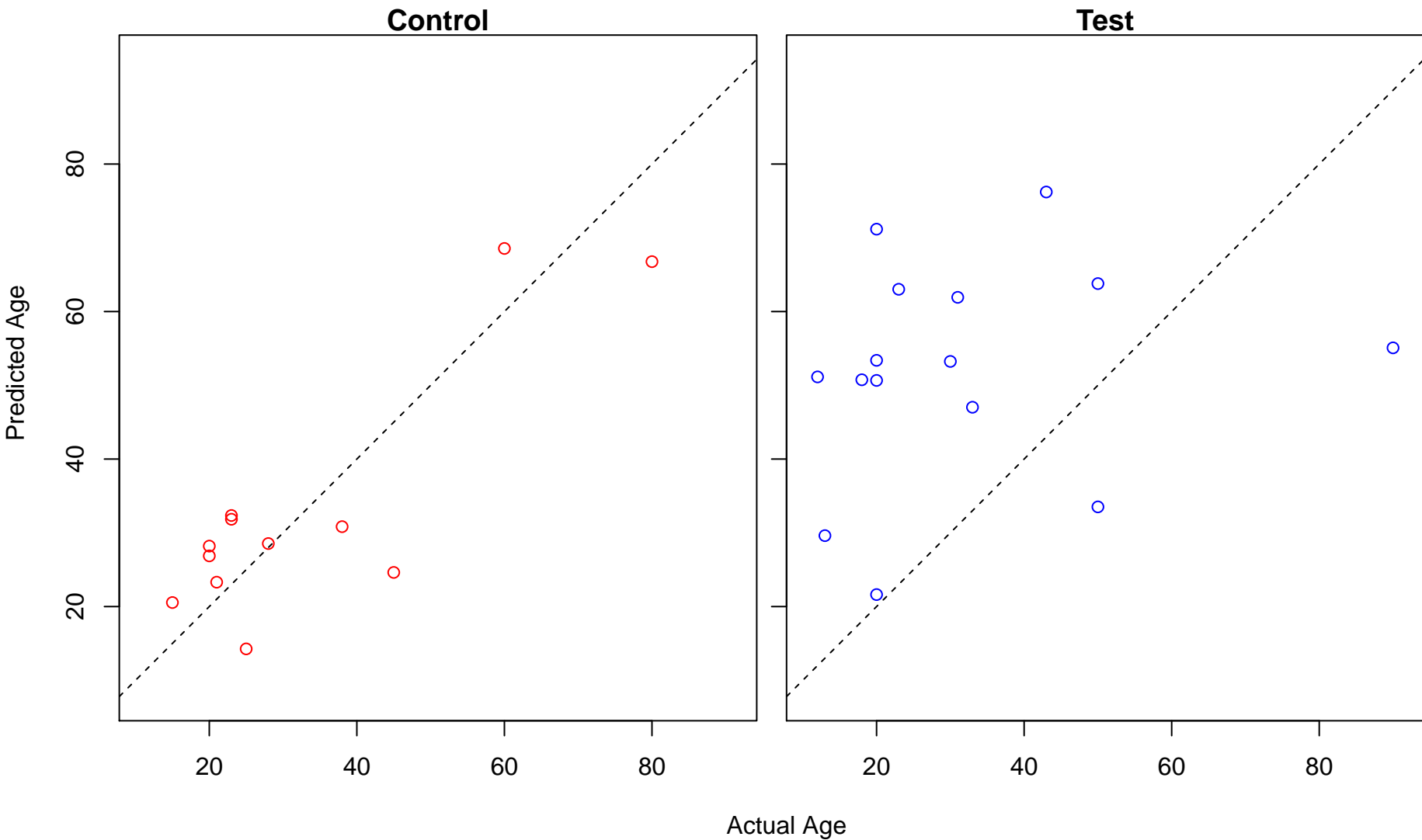
Golgi vesicle transport (Score: 3.591047)



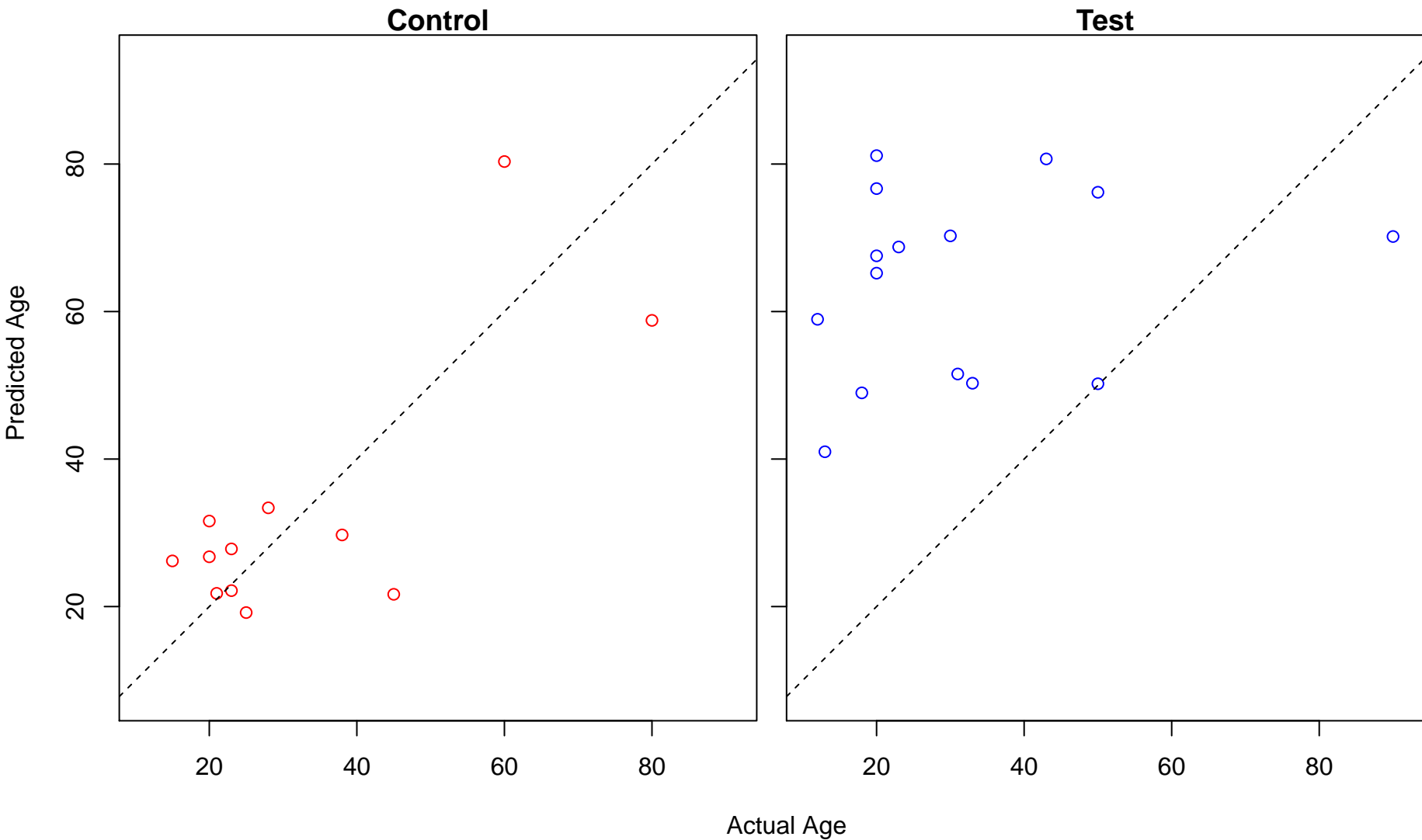
positive regulation of RIG-I signaling pathway (Score: 3.590936)



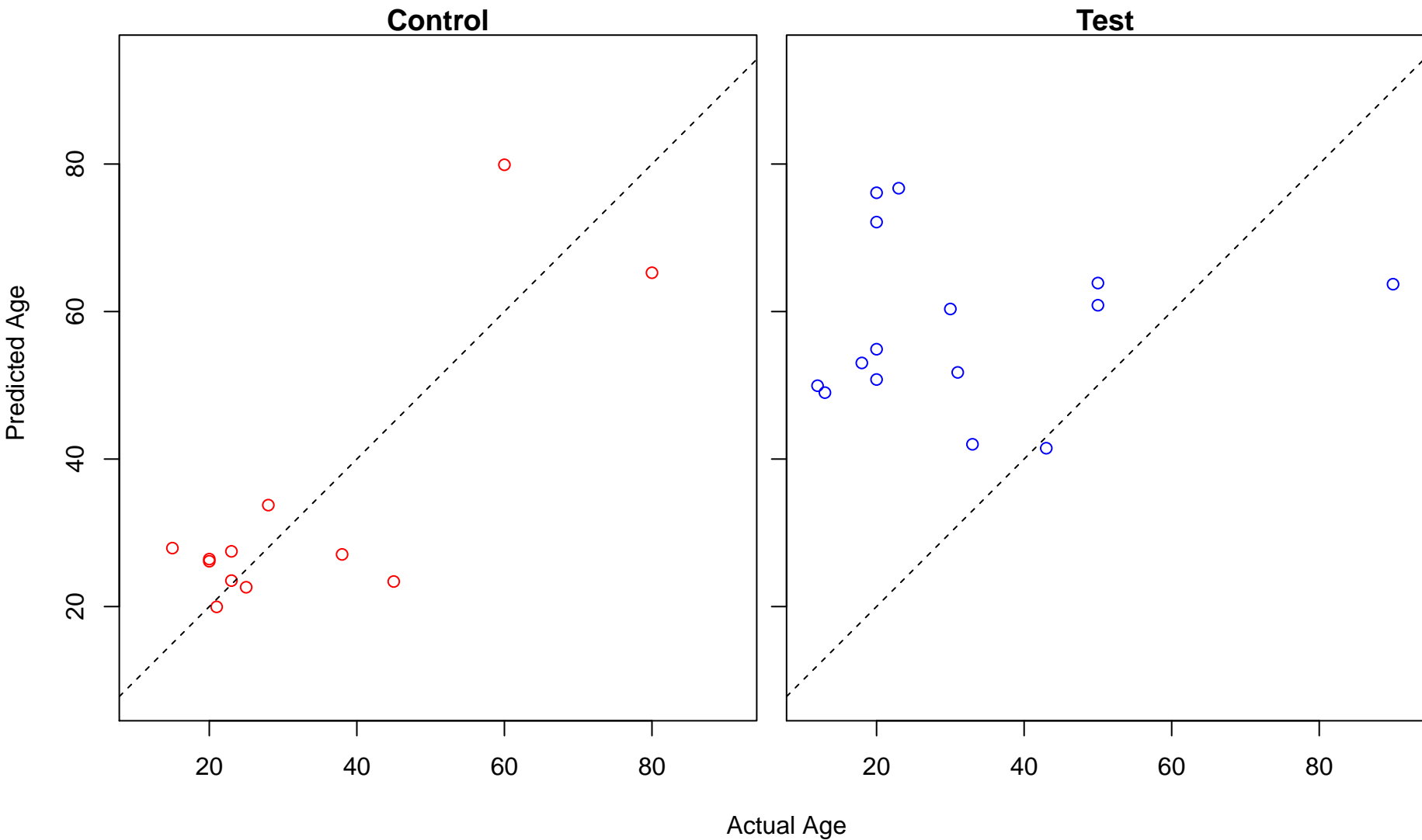
nucleoside catabolic process (Score: 3.590599)



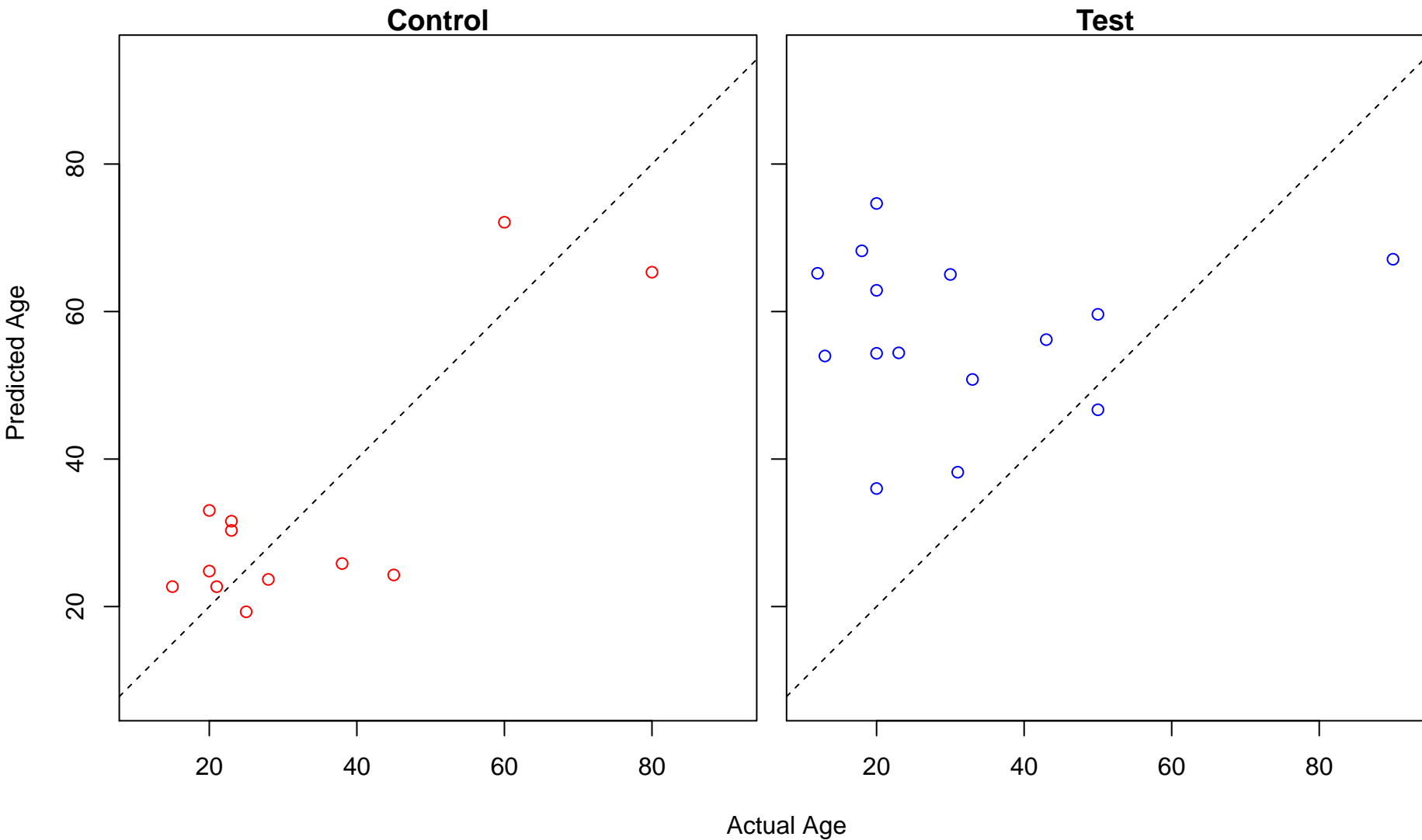
response to toxic substance (Score: 3.589723)



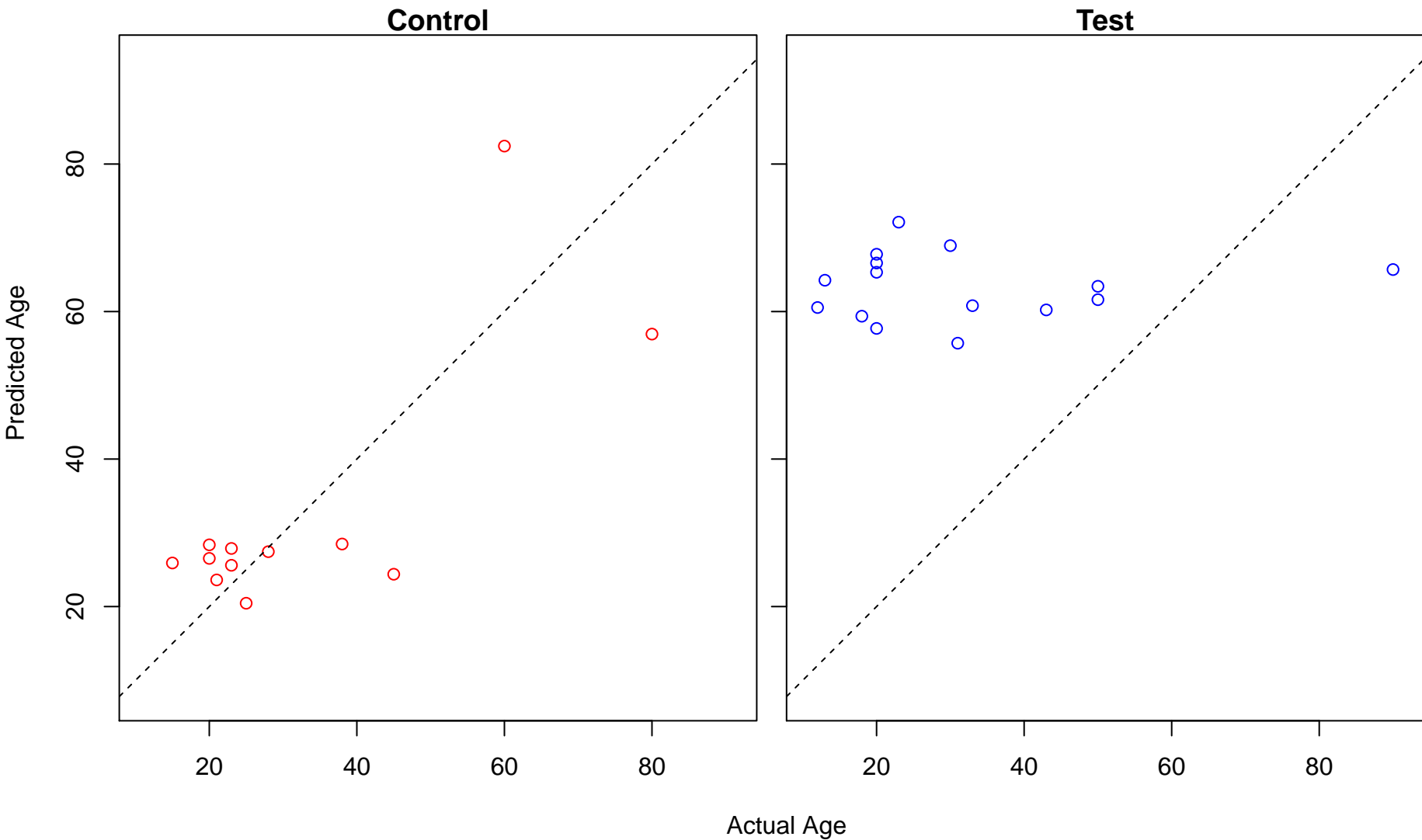
cellular response to extracellular stimulus (Score: 3.584274)



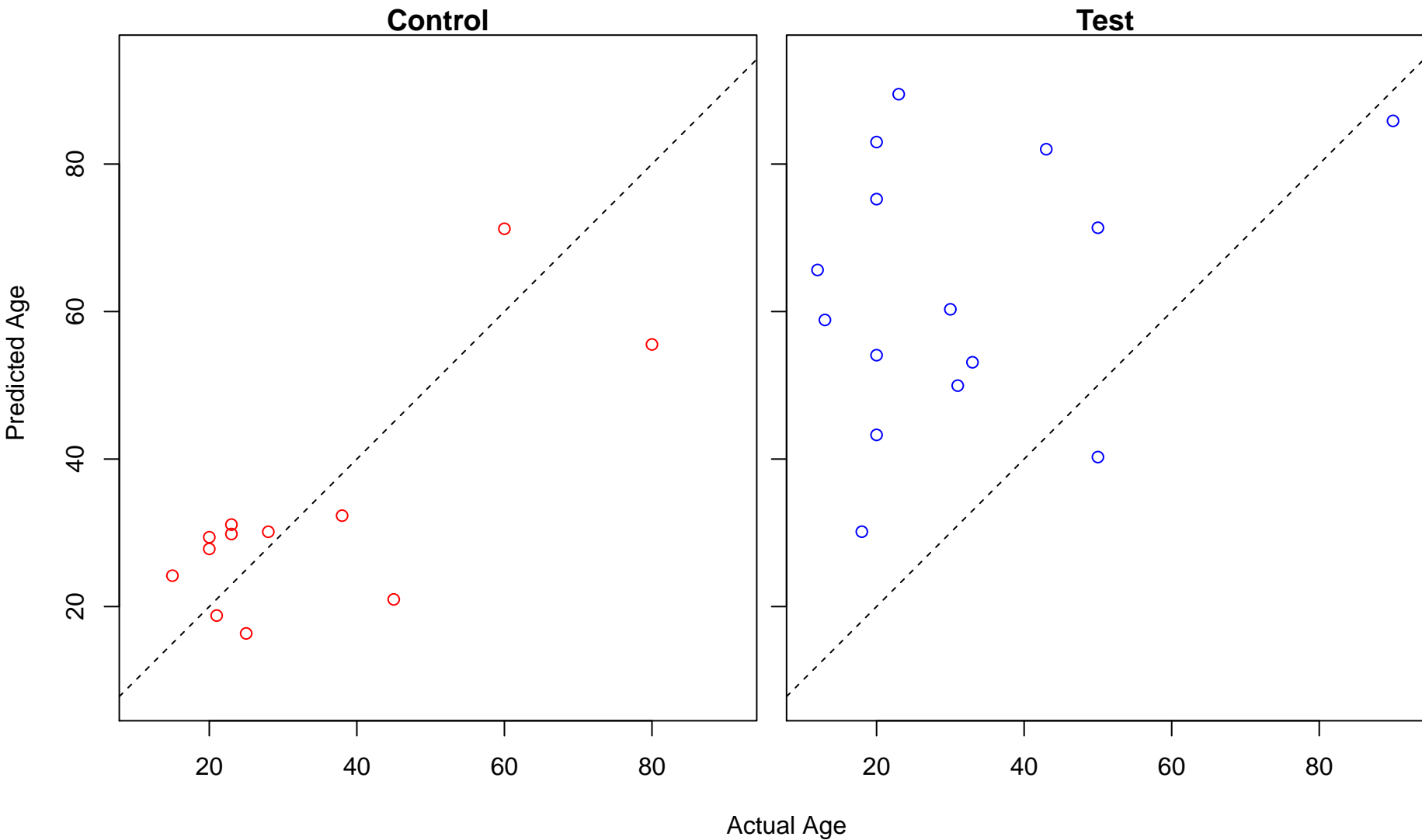
ER overload response (Score: 3.576790)



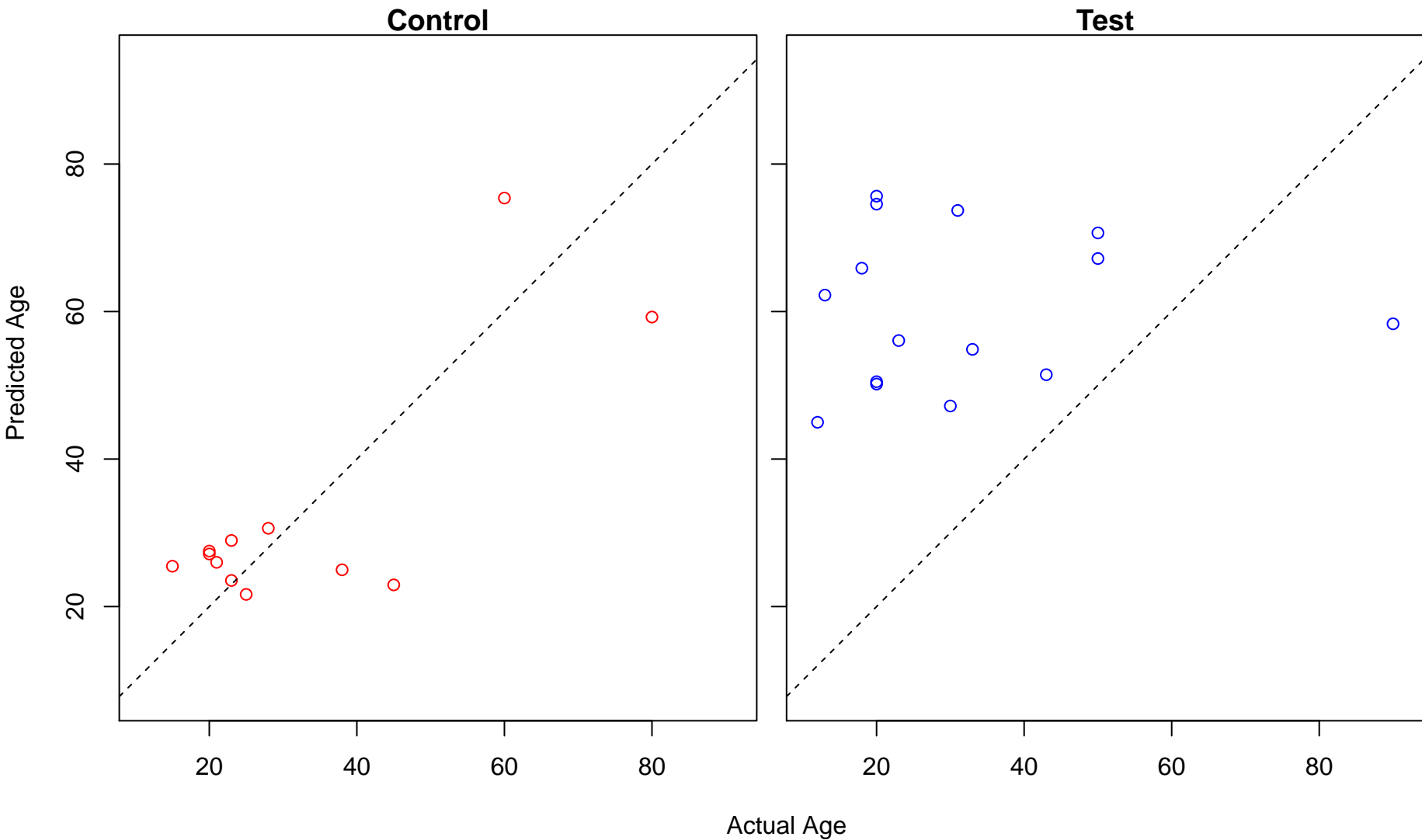
peptidyl-arginine N-methylation (Score: 3.576150)



proximal/distal pattern formation (Score: 3.574800)

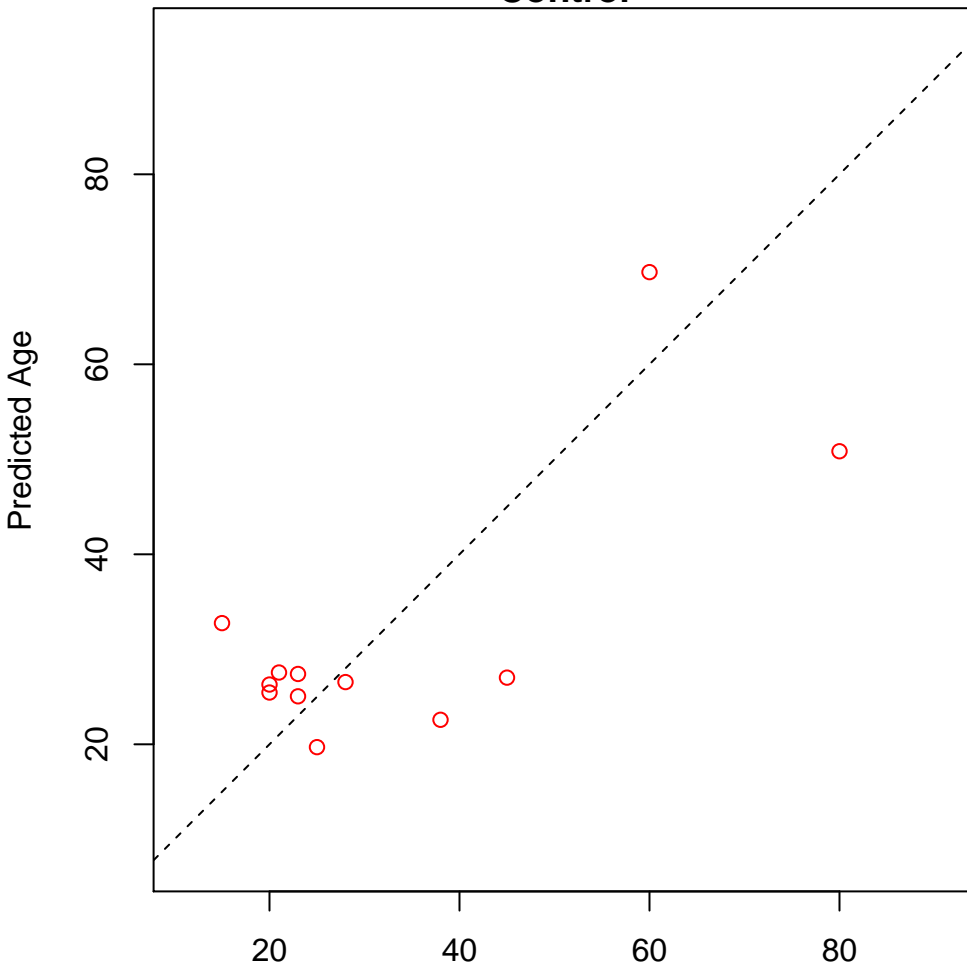


positive regulation of calcium ion transport into cytosol (Score: 3.574579)

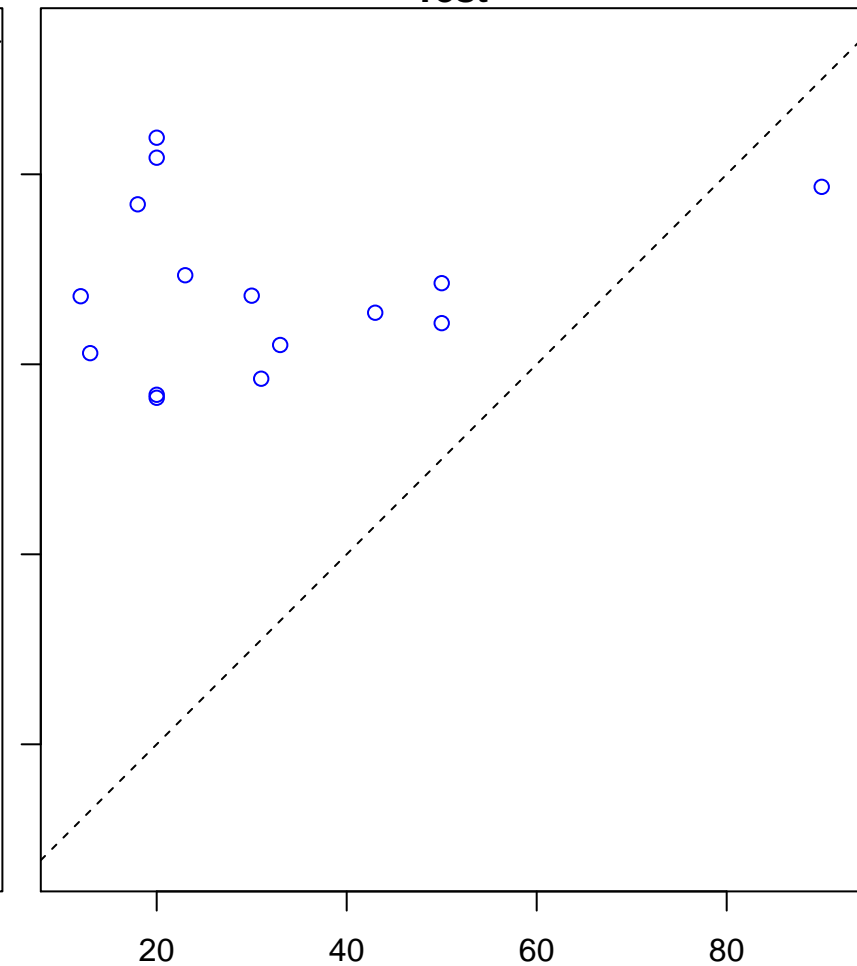


cellular ketone body metabolic process (Score: 3.572304)

Control

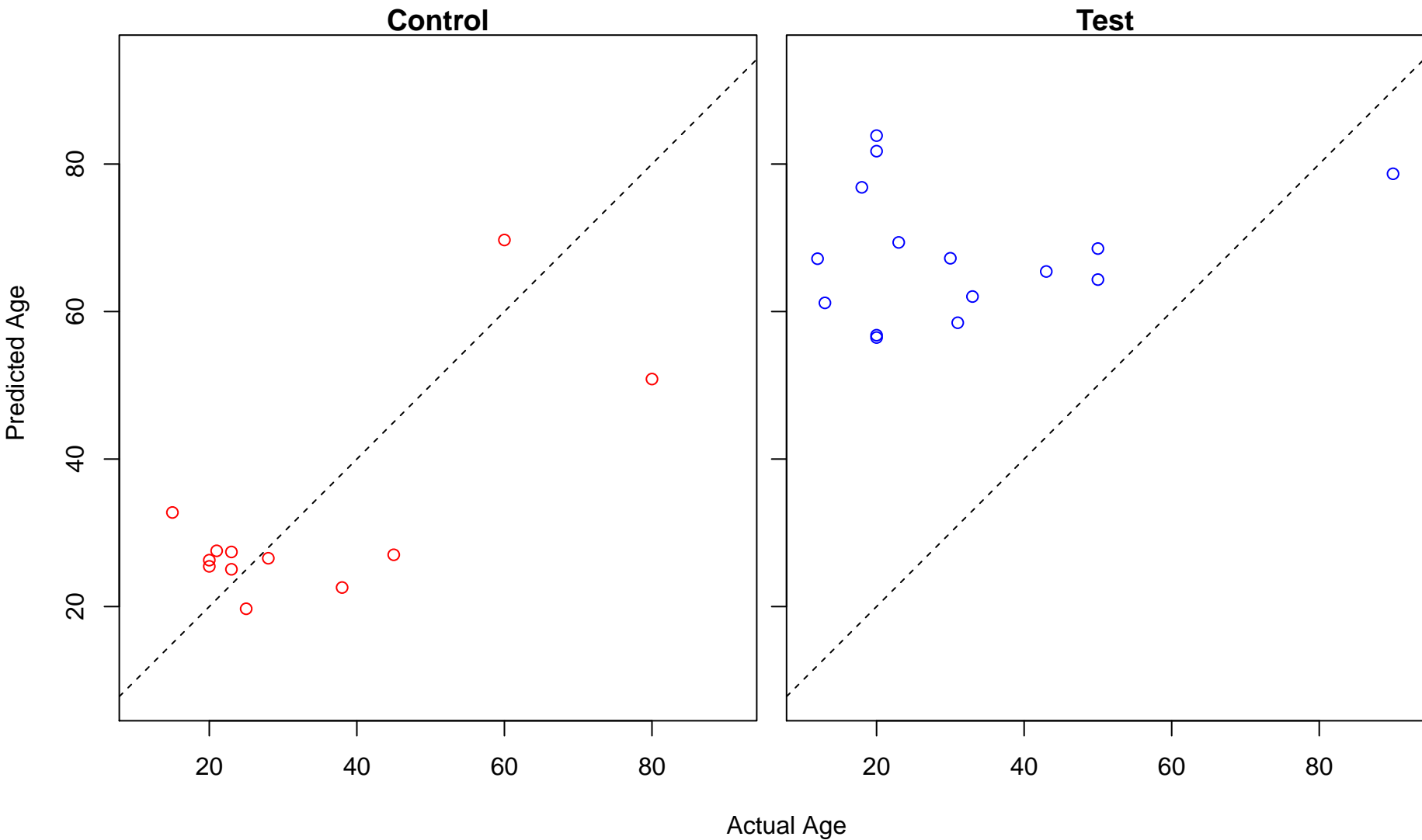


Test

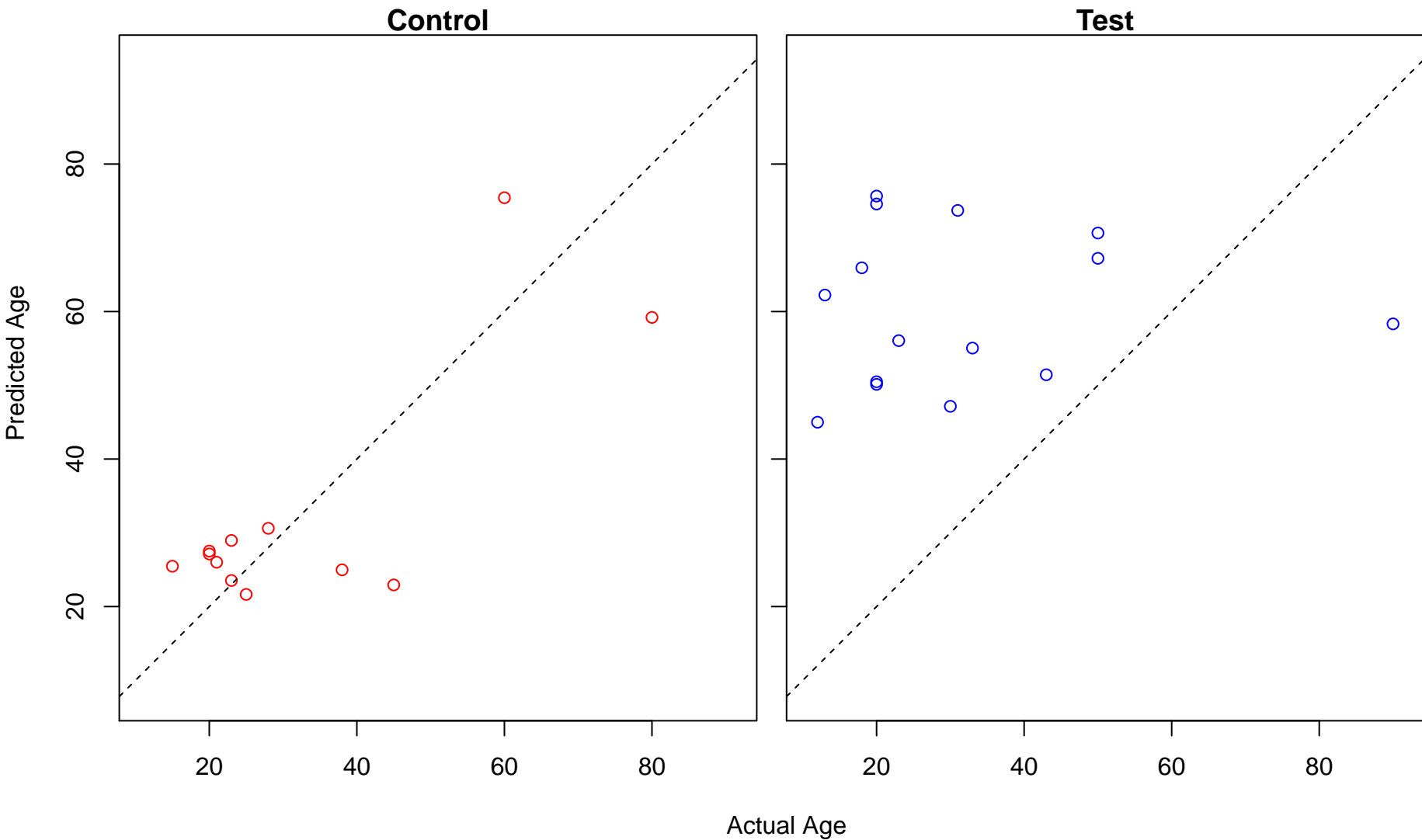


Actual Age

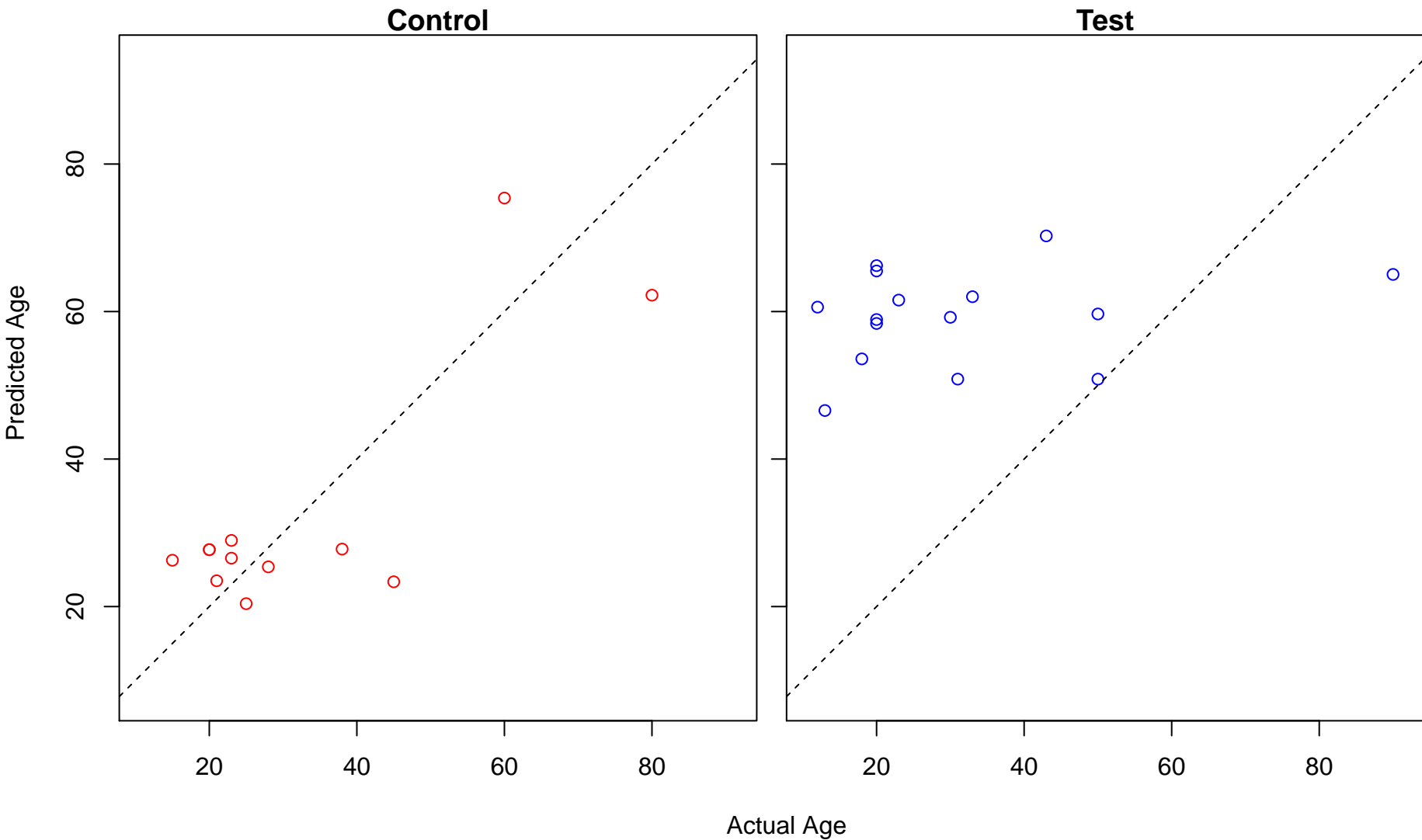
ketone body metabolic process (Score: 3.572304)



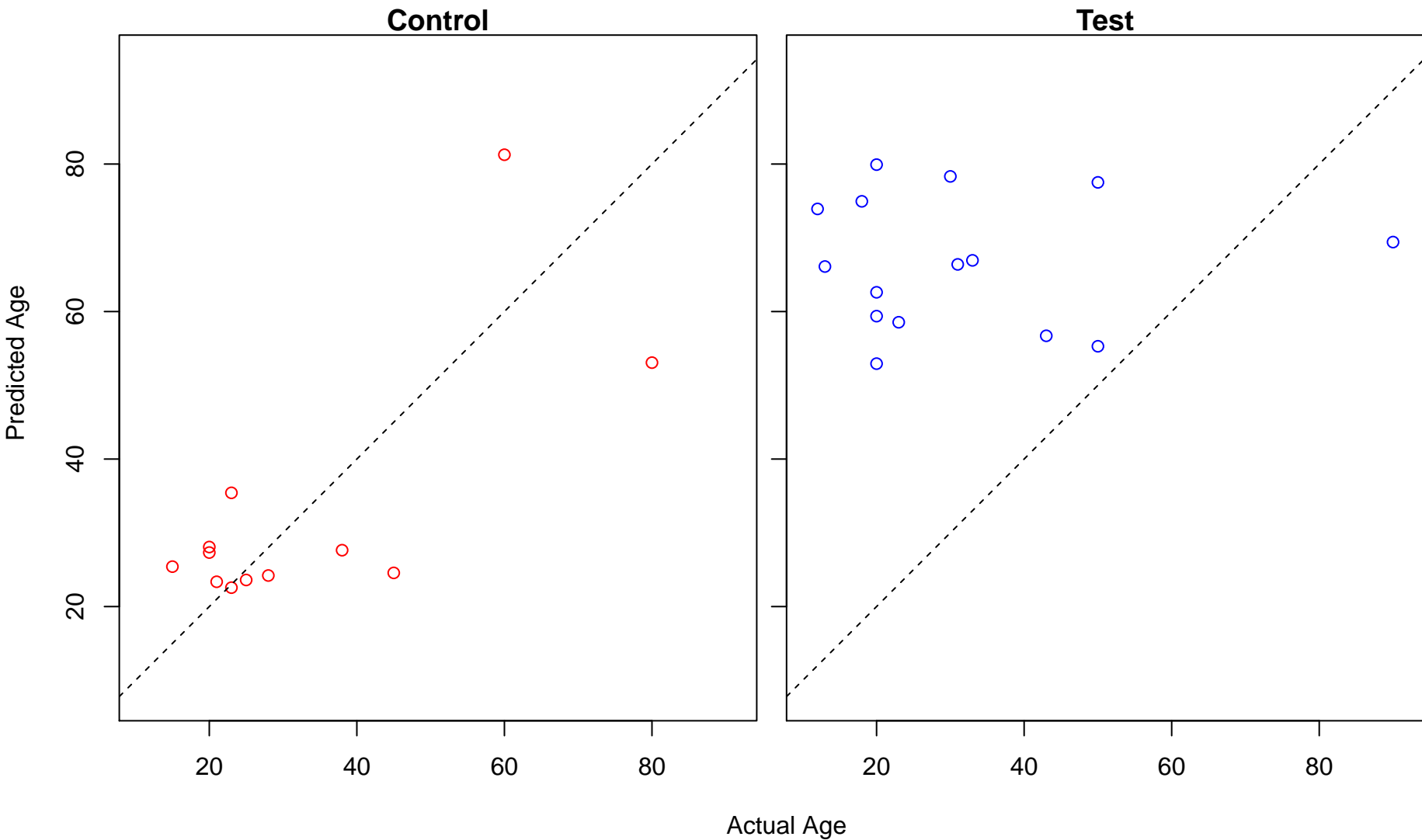
positive regulation of release of sequestered calcium ion into cytosol (Score: 3.570429)



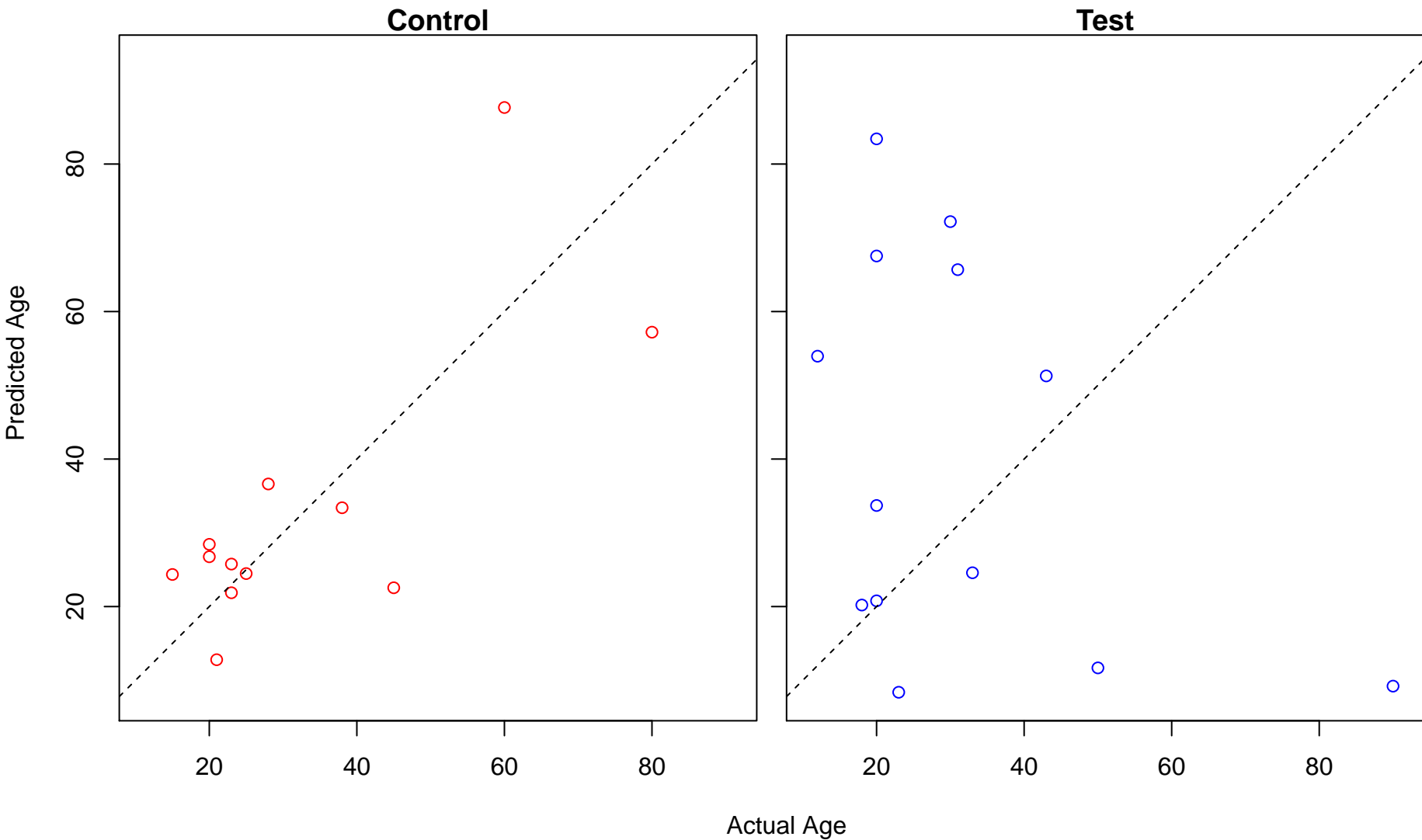
mitotic cytokinesis (Score: 3.563411)



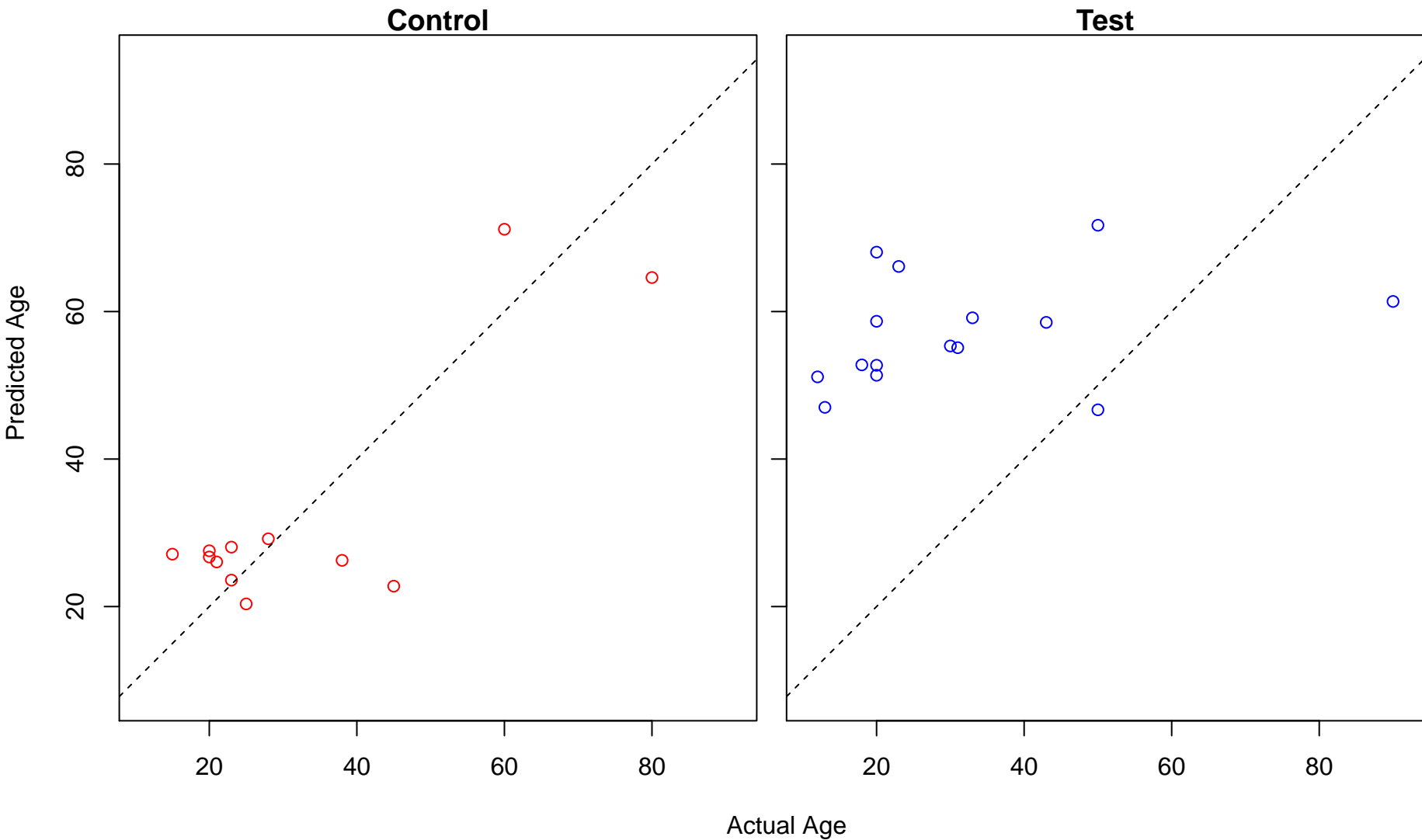
regulation of pri-miRNA transcription from RNA polymerase II promoter (Score: 3.560863)



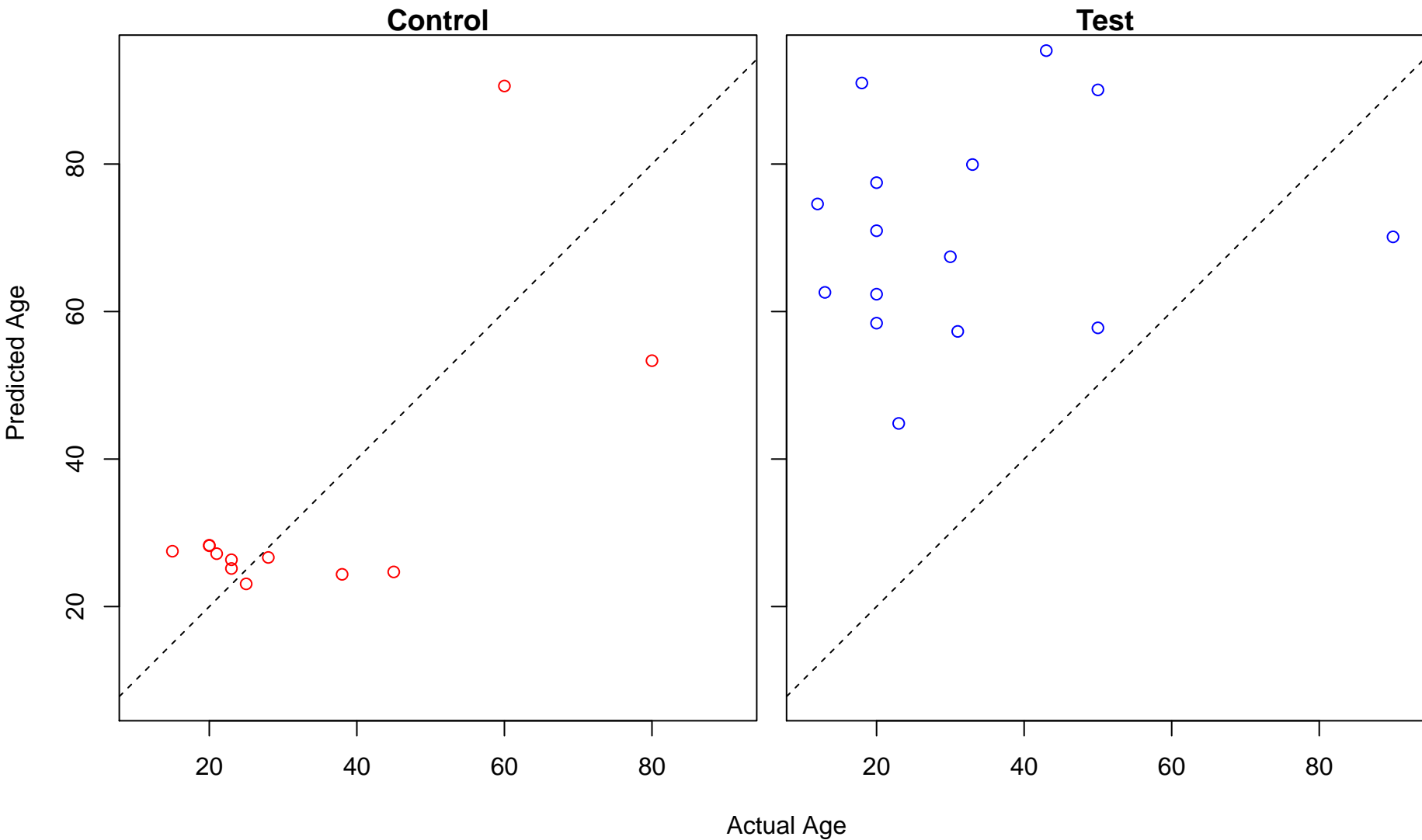
lymphocyte activation involved in immune response (Score: 3.55516)



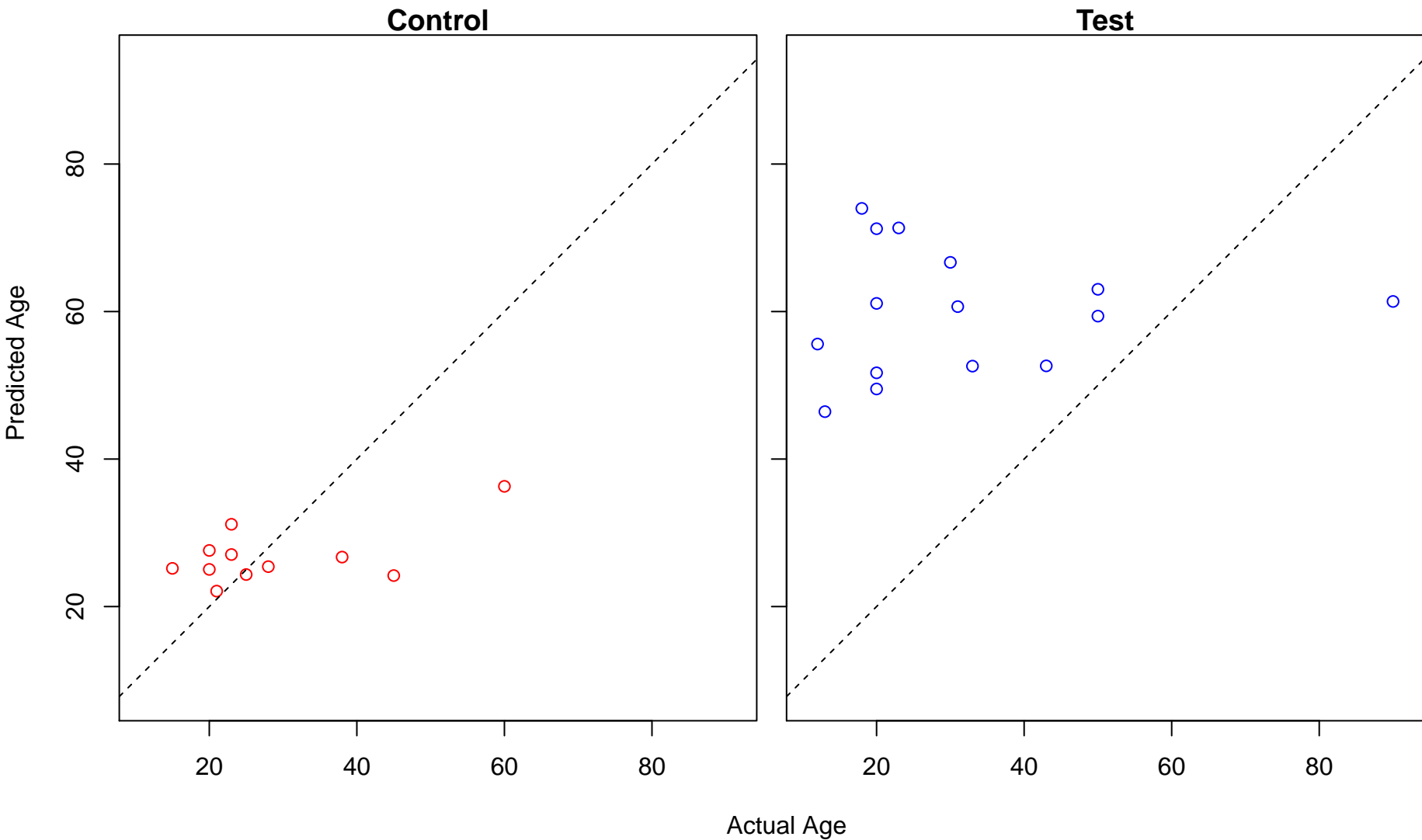
peptidyl-lysine dimethylation (Score: 3.553700)



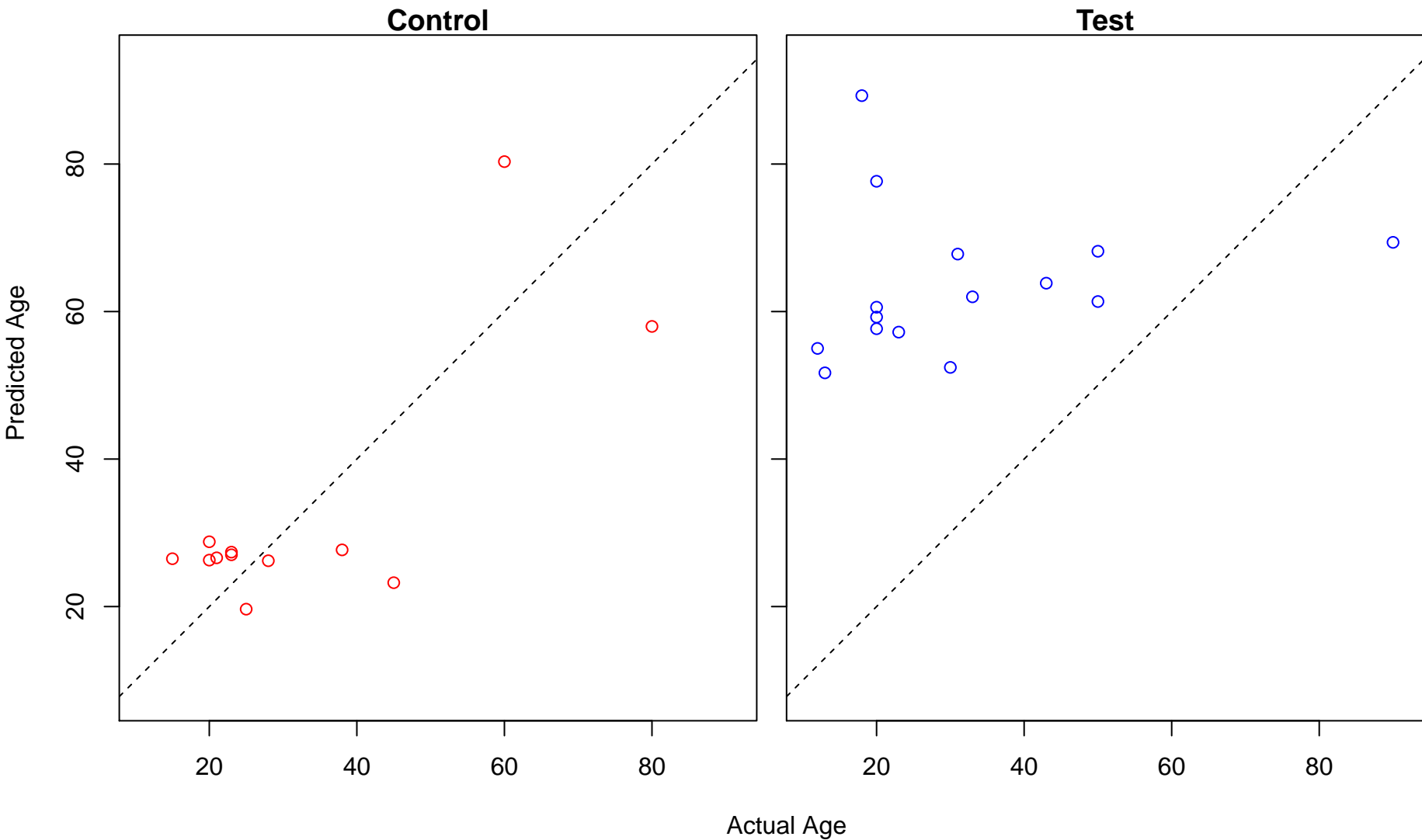
regulation of protein import into nucleus, translocation (Score: 3.549843)



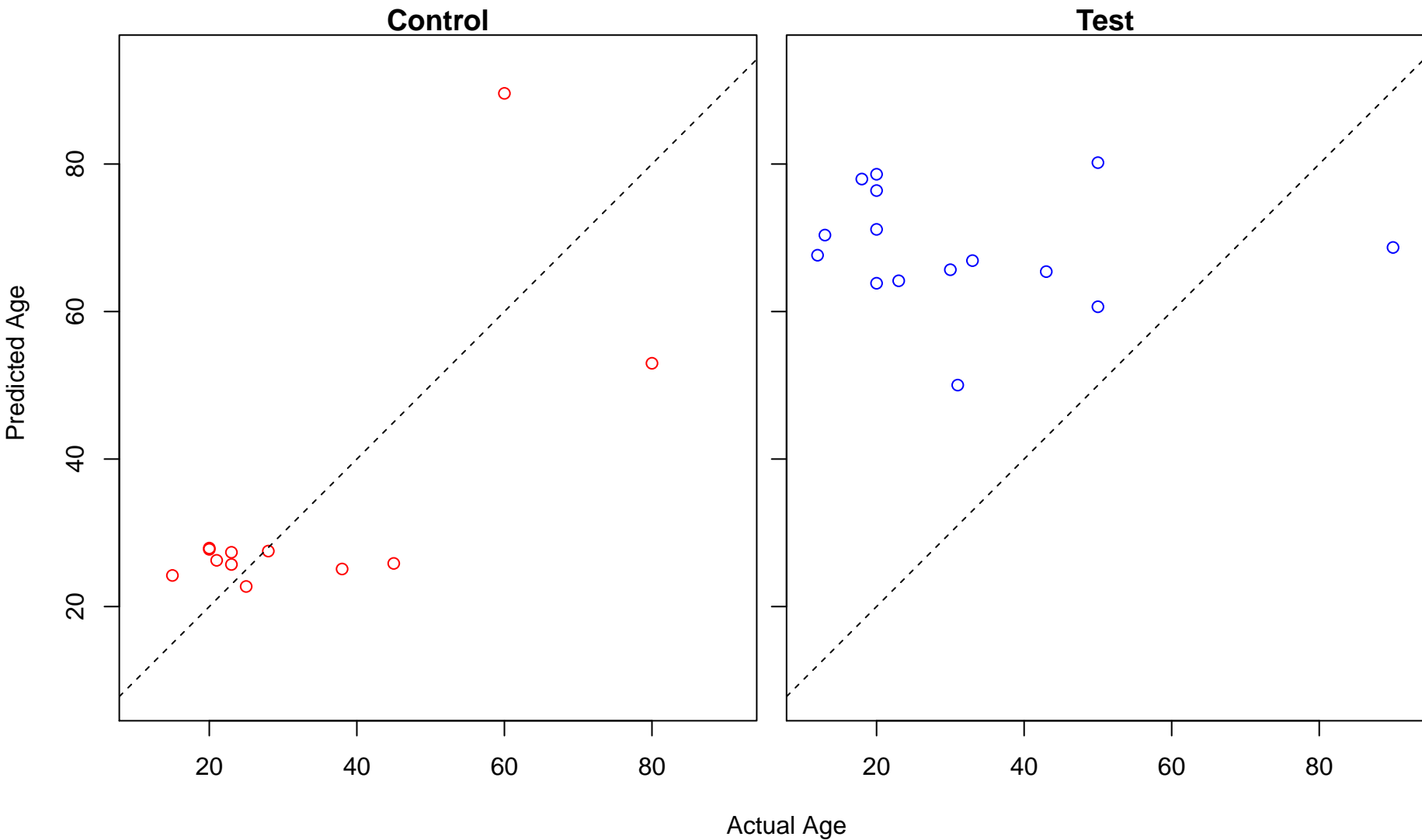
very long-chain fatty acid metabolic process (Score: 3.548319)



polyol catabolic process (Score: 3.548081)

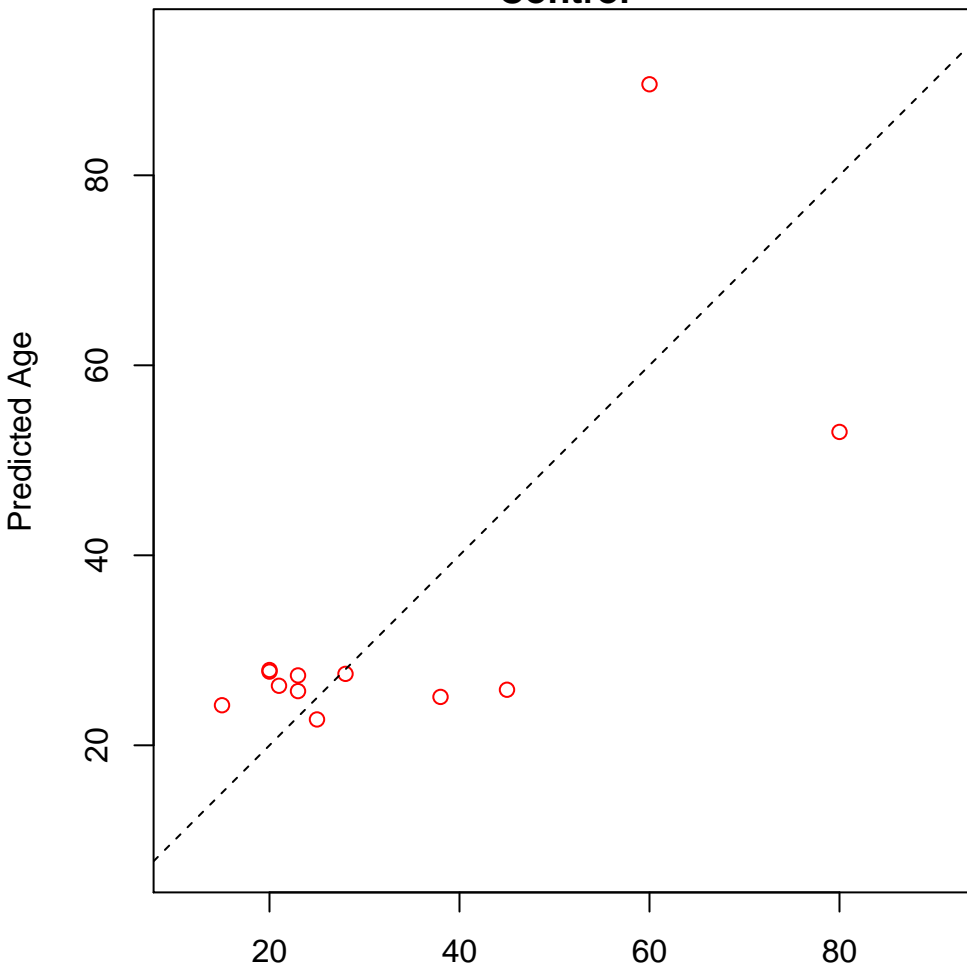


negative regulation of centrosome duplication (Score: 3.547317)

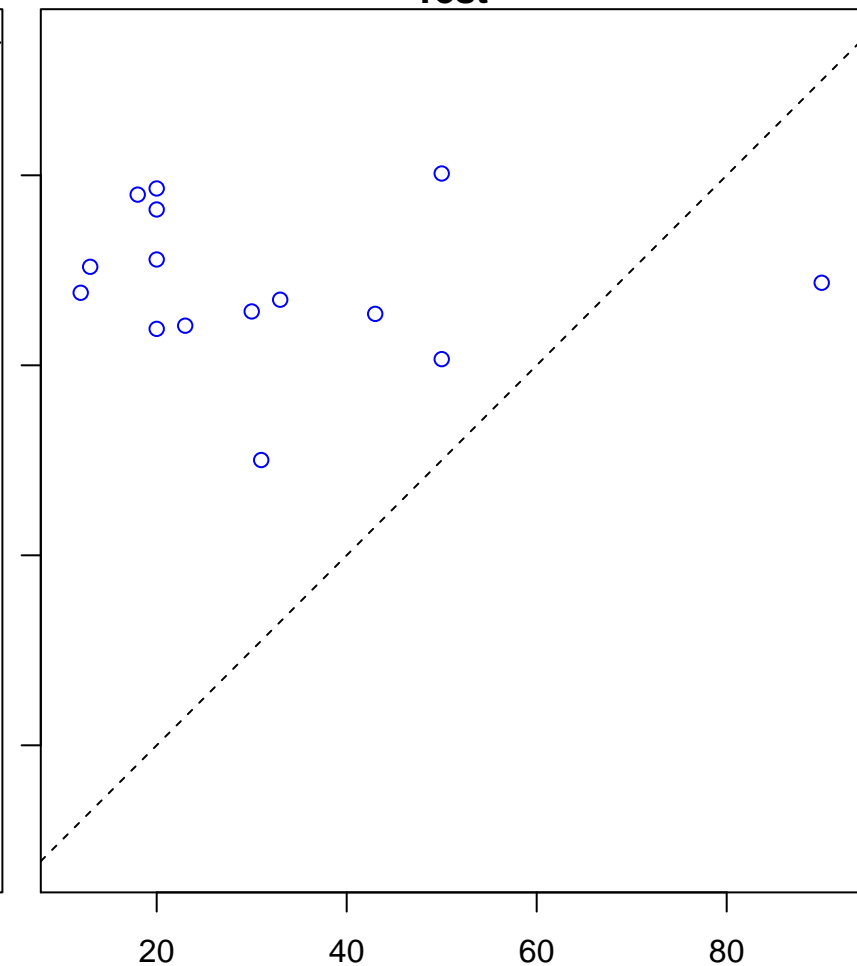


negative regulation of centrosome cycle (Score: 3.547317)

Control

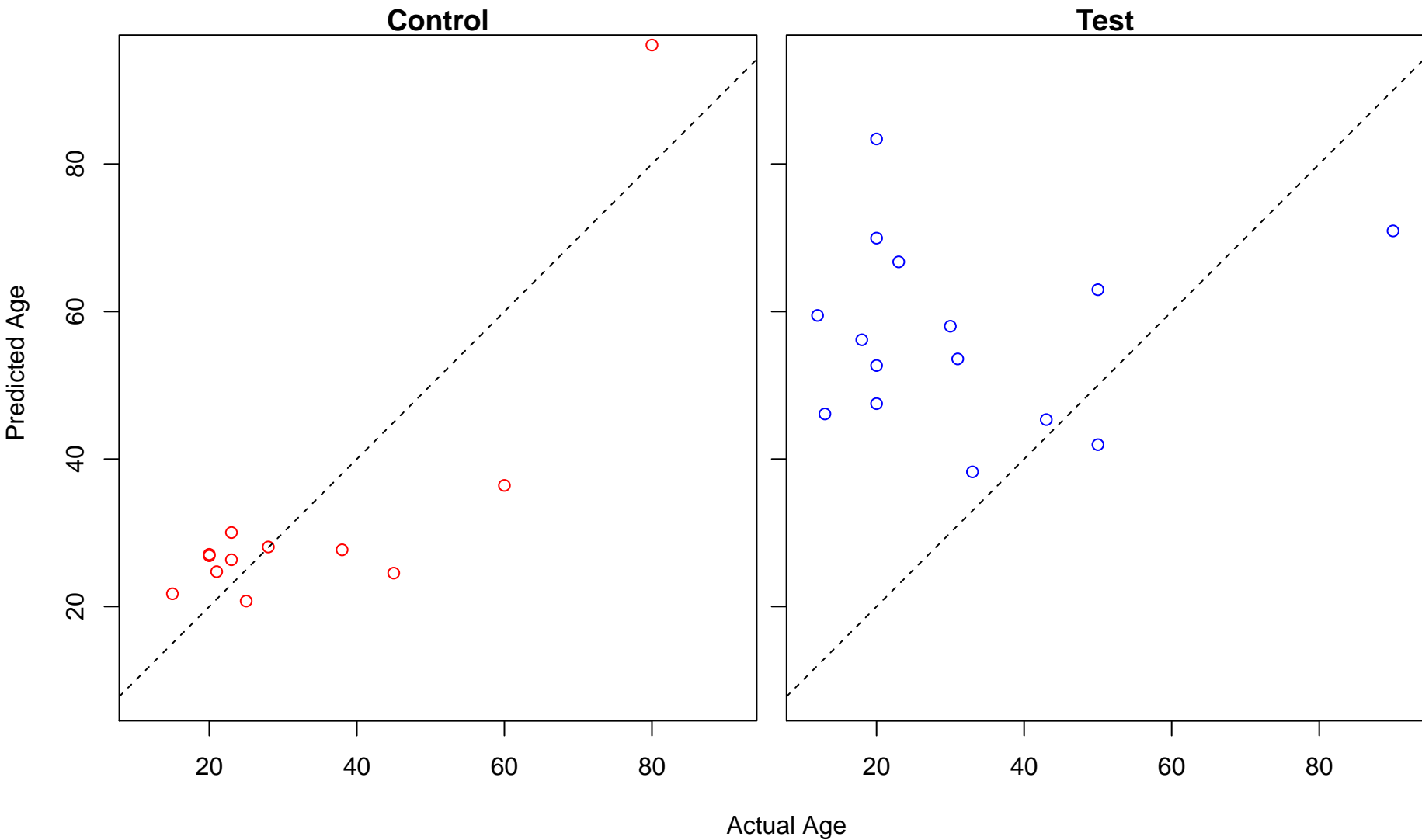


Test

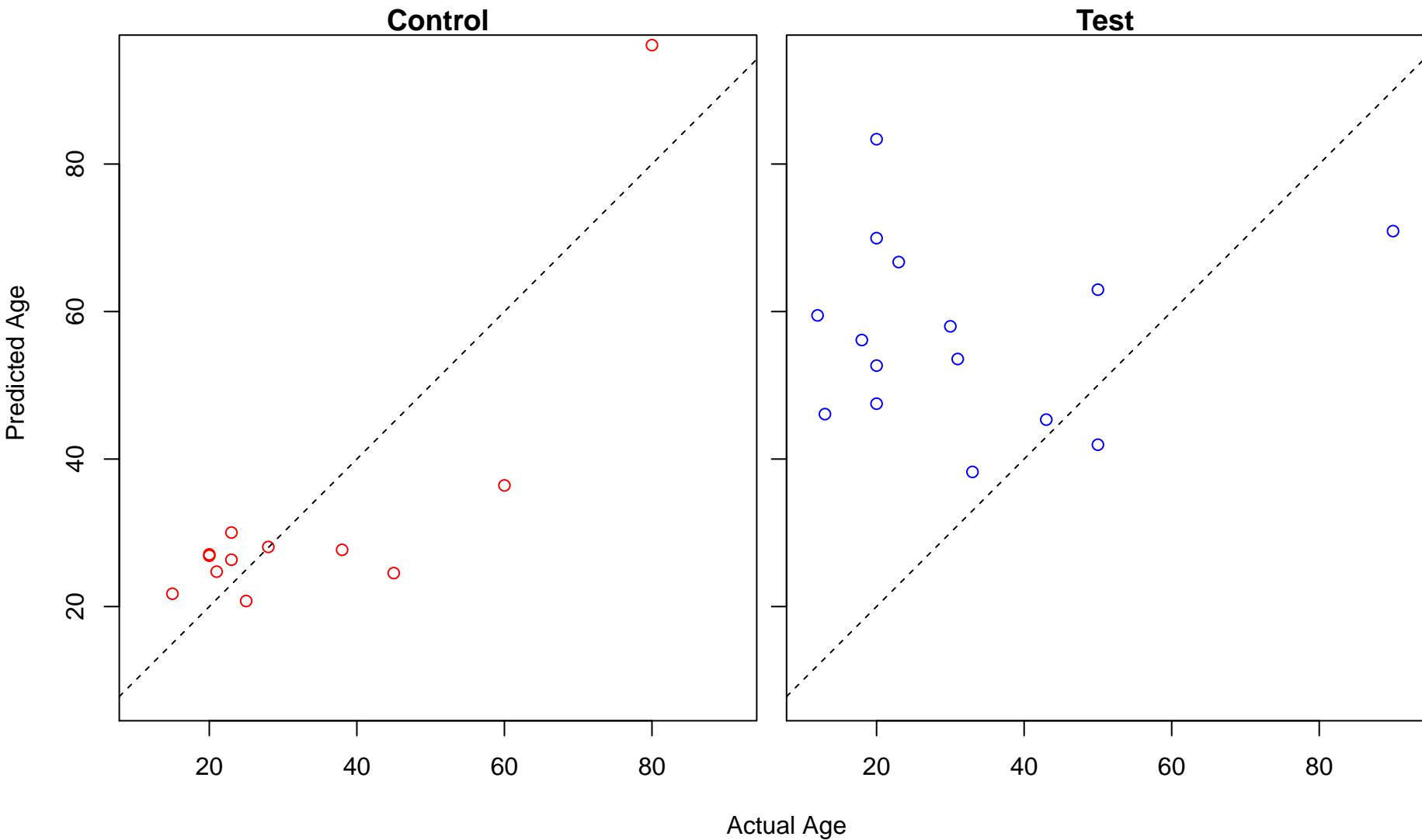


Actual Age

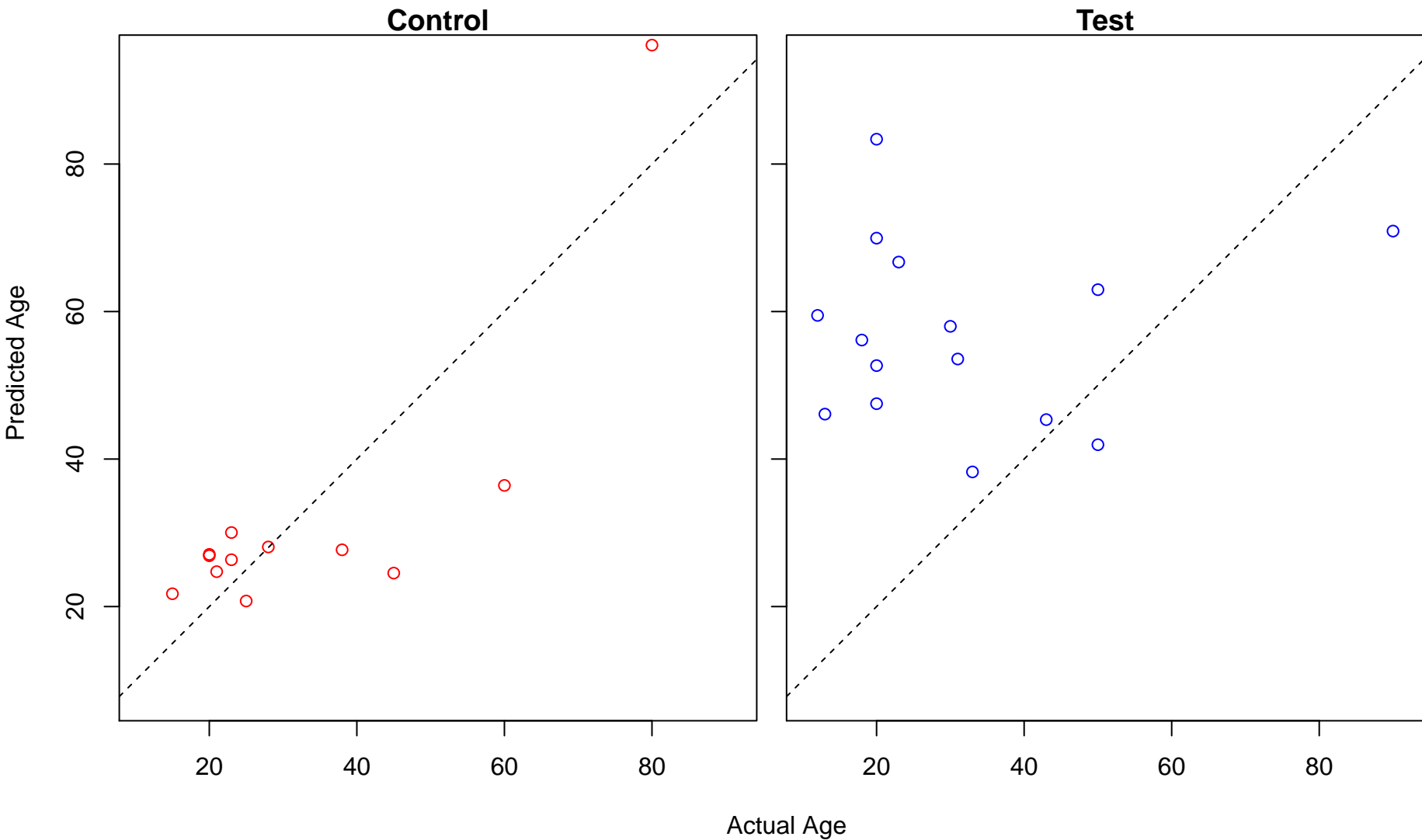
L-methionine biosynthetic process from methylthioadenosine (Score: 3.546779)



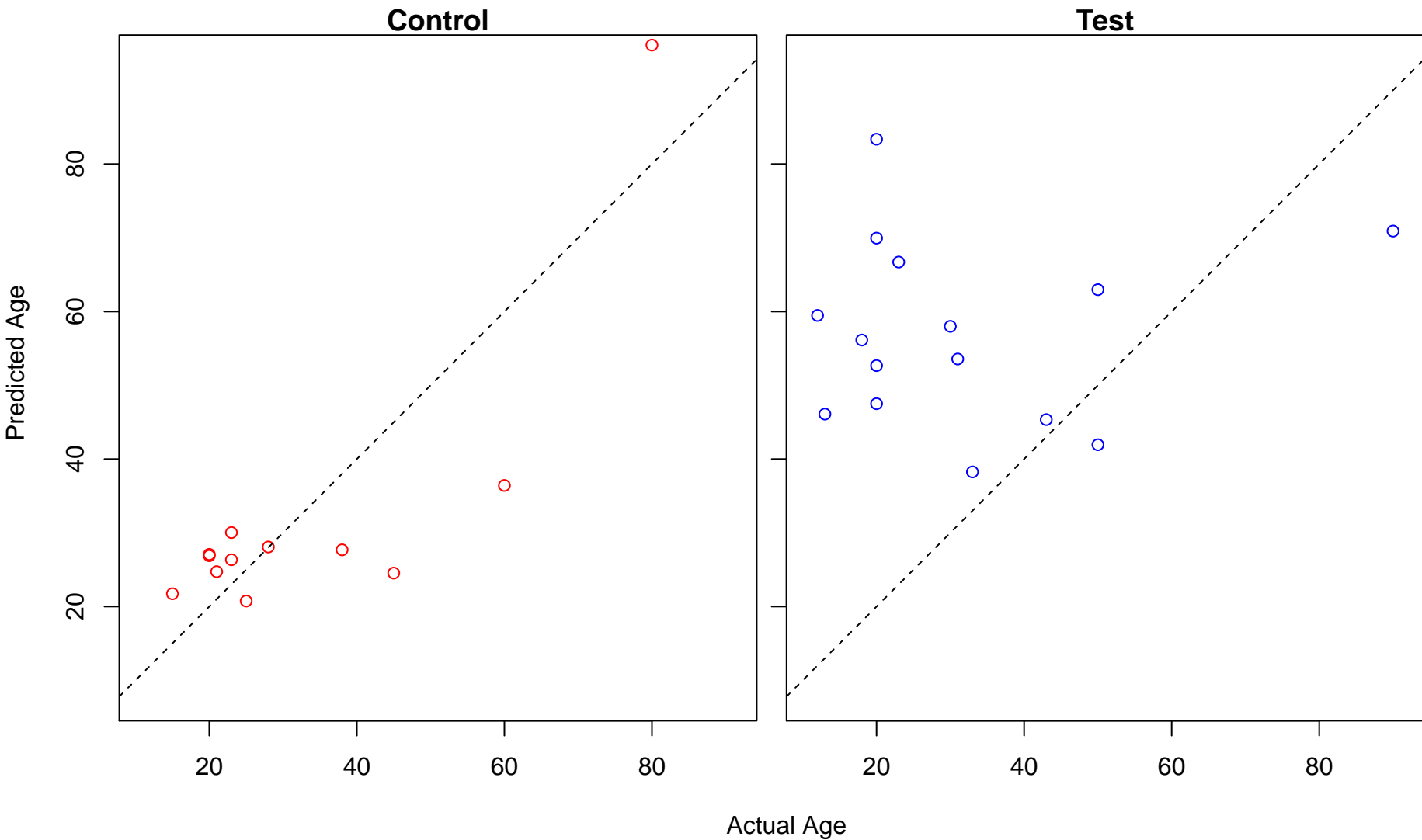
amino acid salvage (Score: 3.545103)



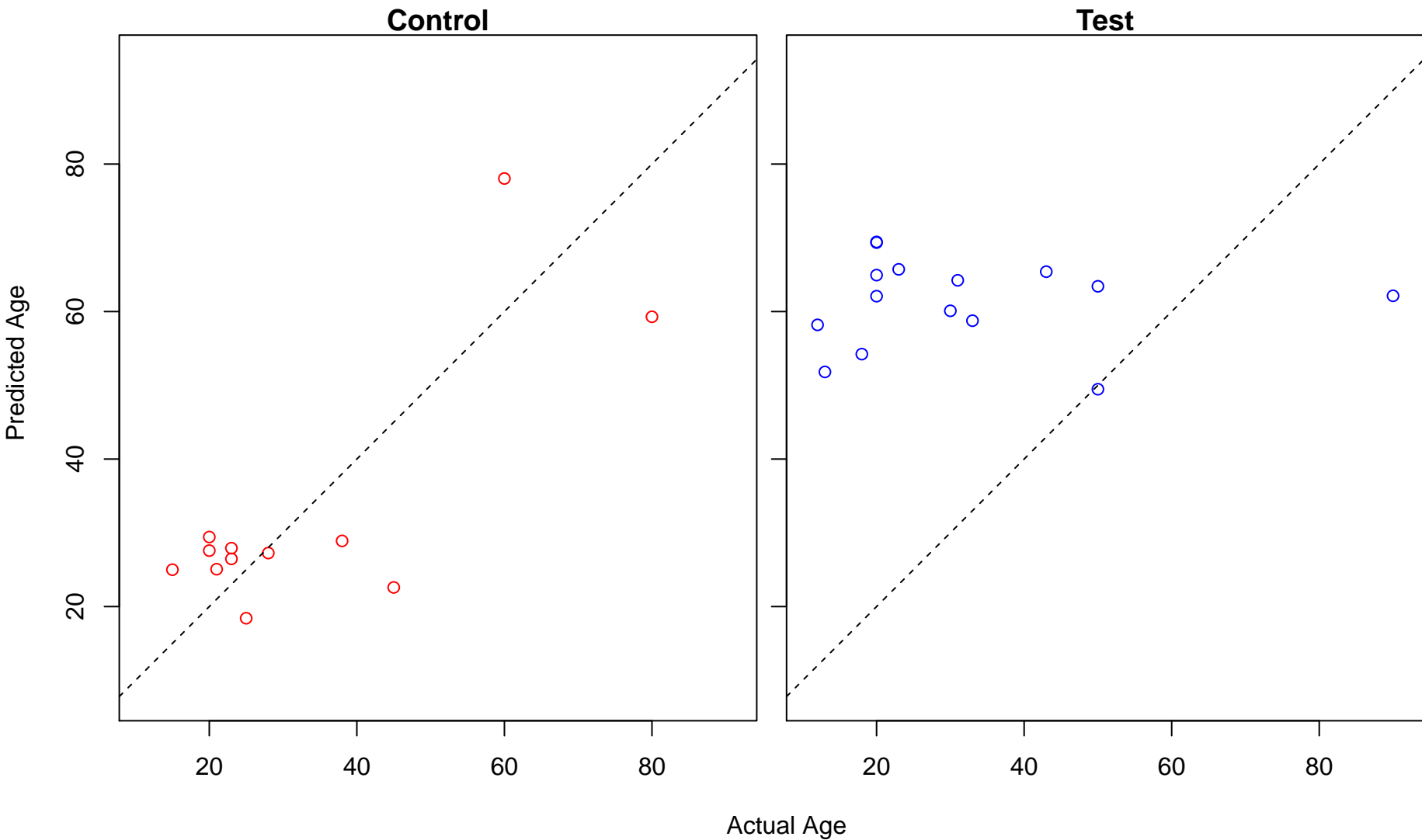
L-methionine biosynthetic process (Score: 3.545103)



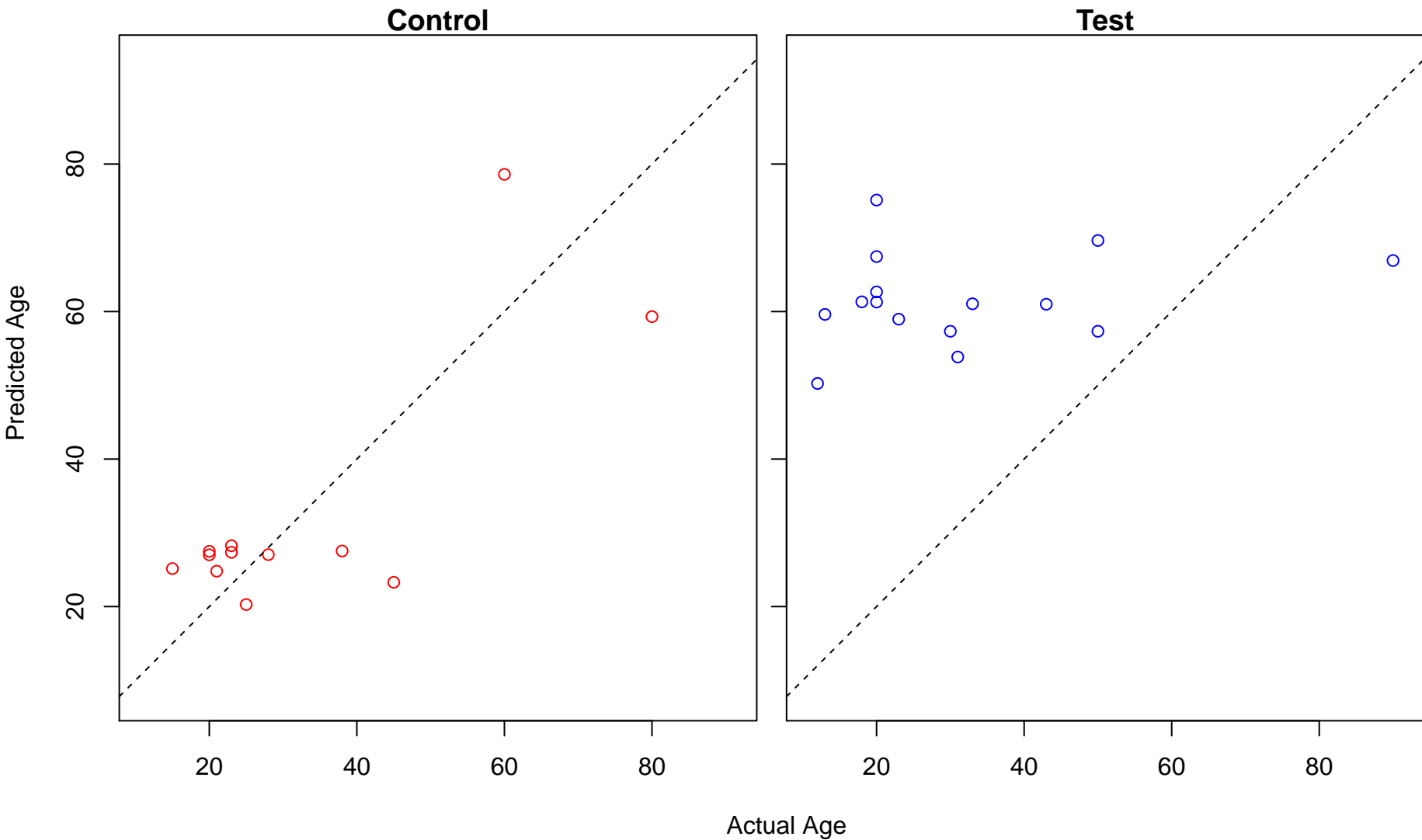
L-methionine salvage (Score: 3.545103)



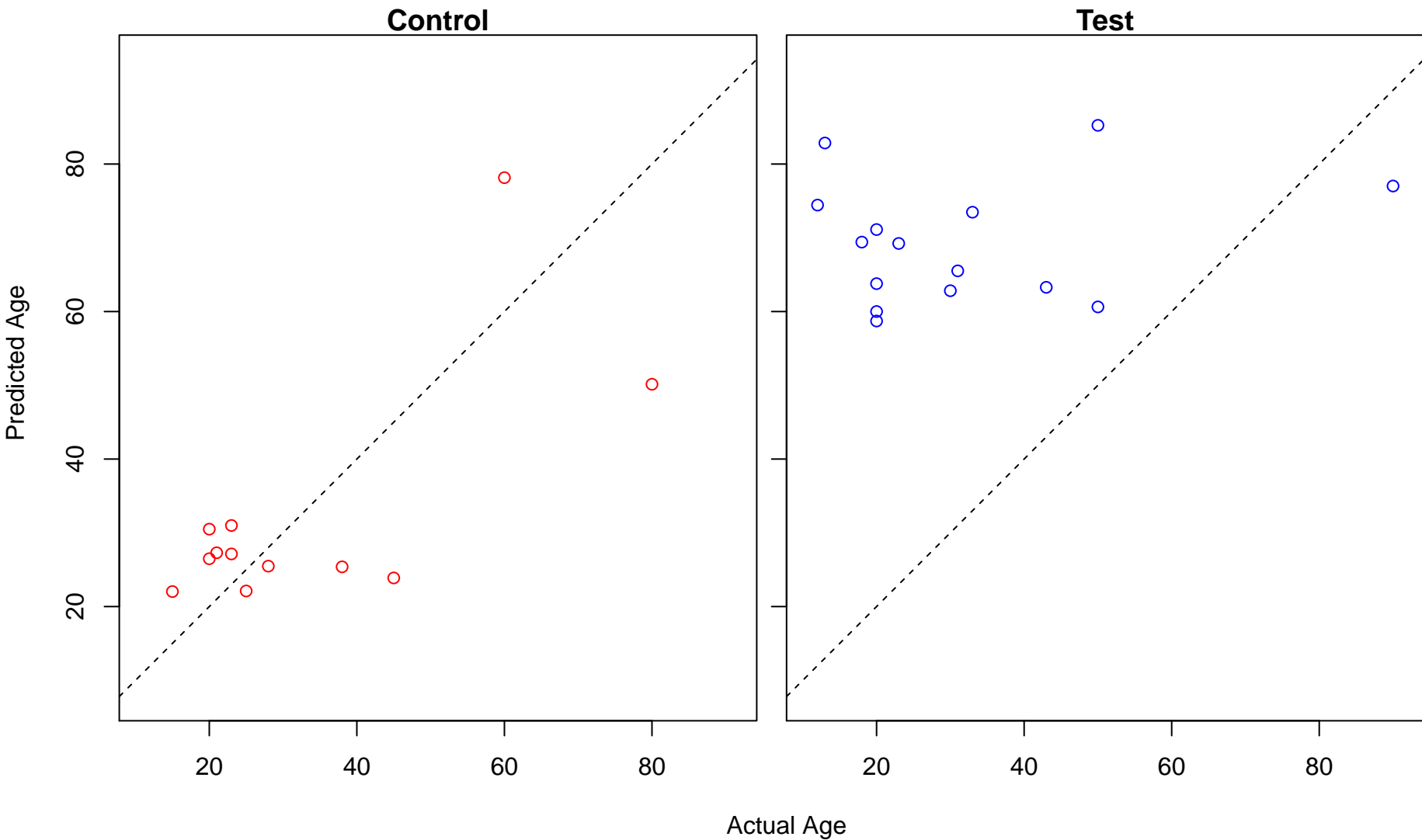
histone H3-K9 demethylation (Score: 3.543376)



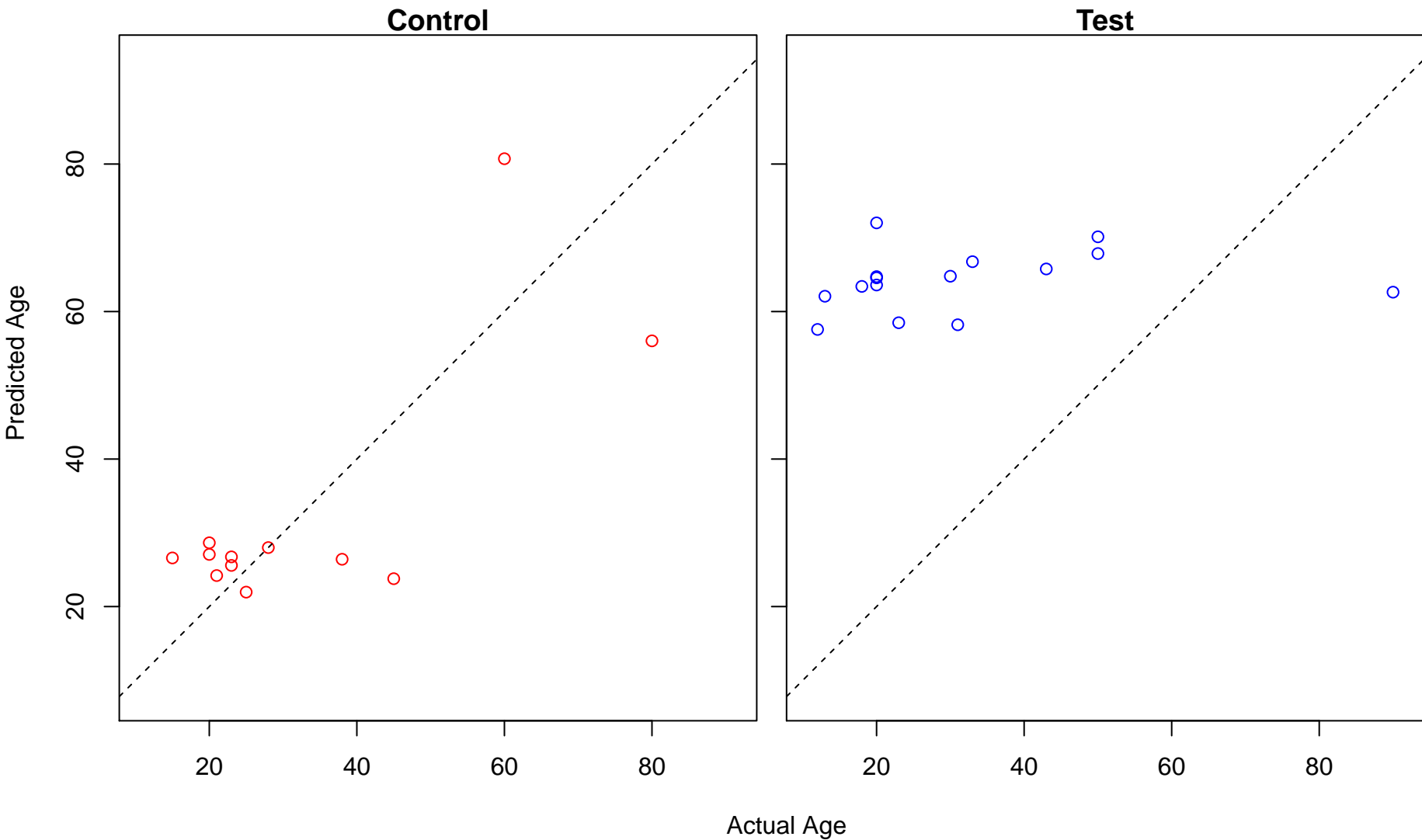
regulation of cellular carbohydrate metabolic process (Score: 3.541365)



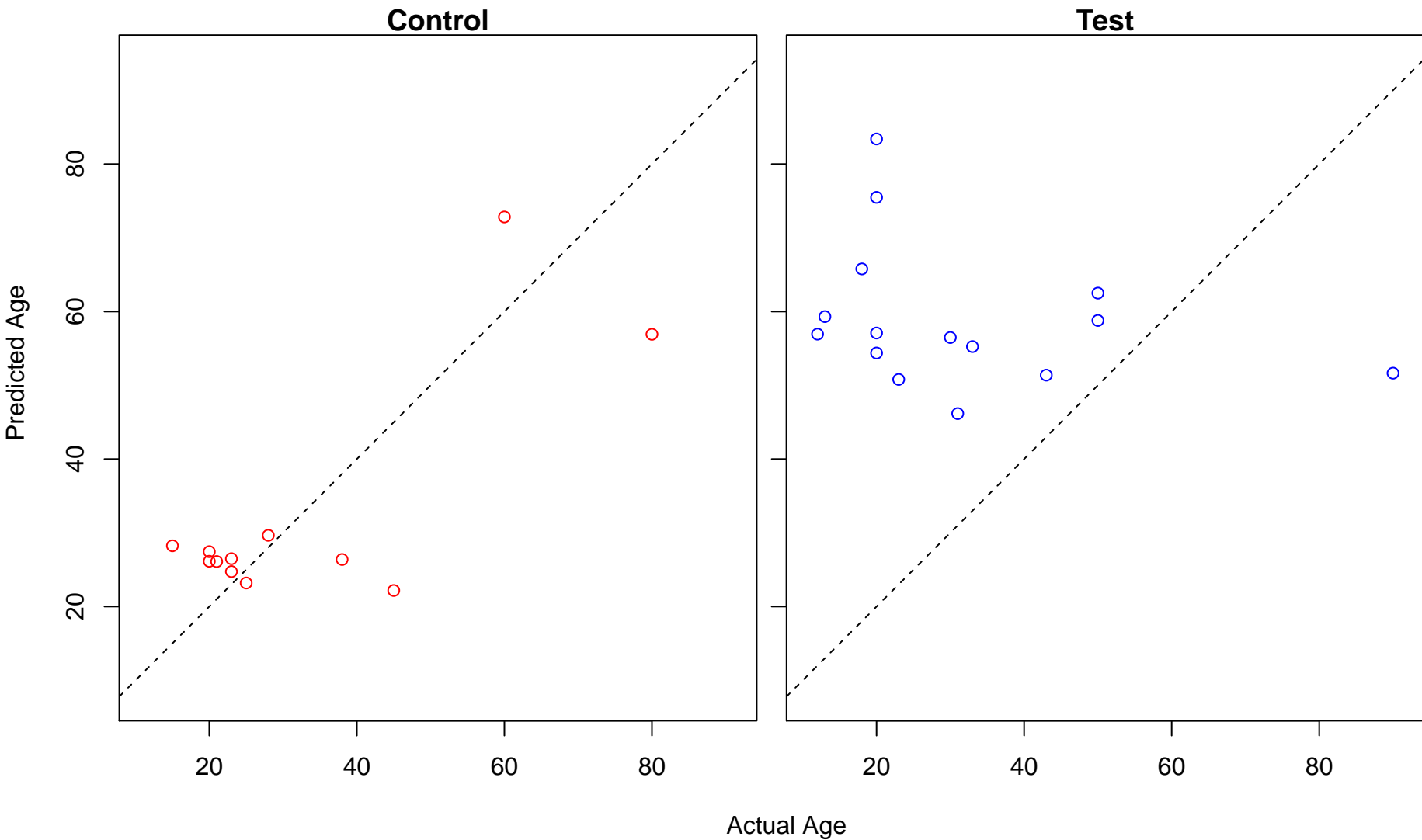
microtubule depolymerization (Score: 3.538602)



glycoprotein metabolic process (Score: 3.538001)

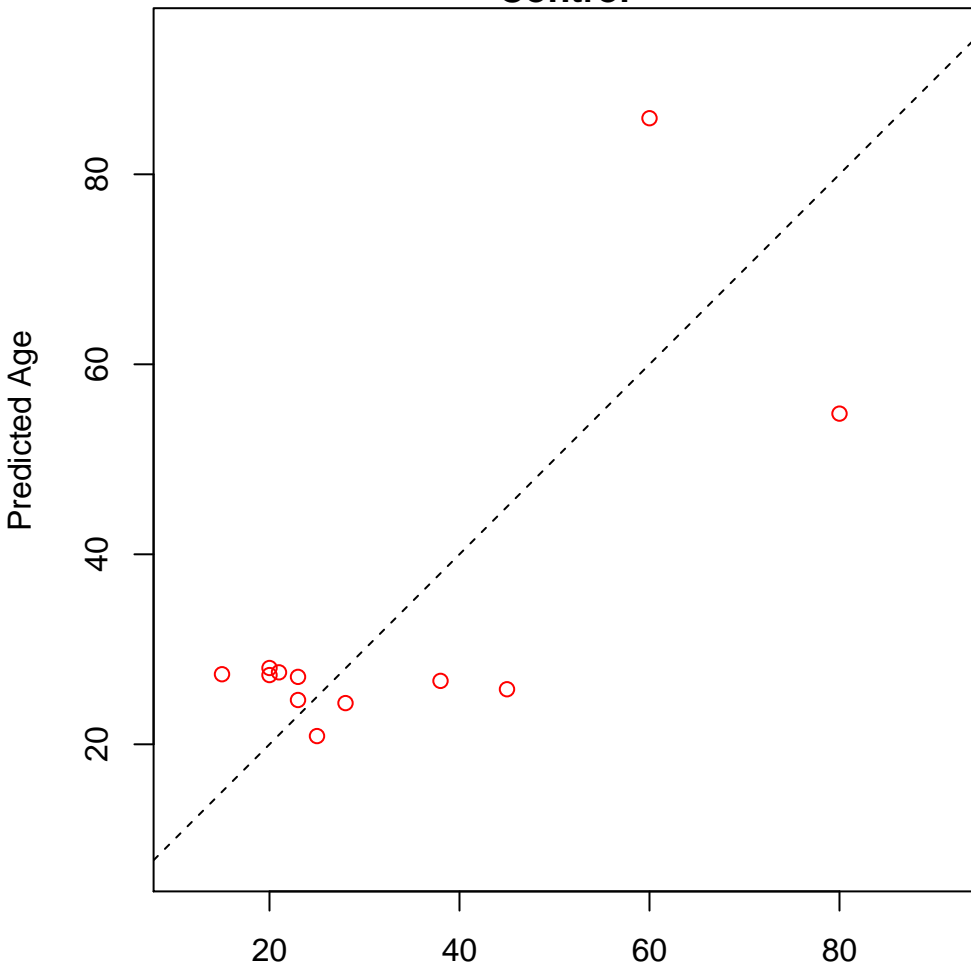


gliogenesis (Score: 3.537133)

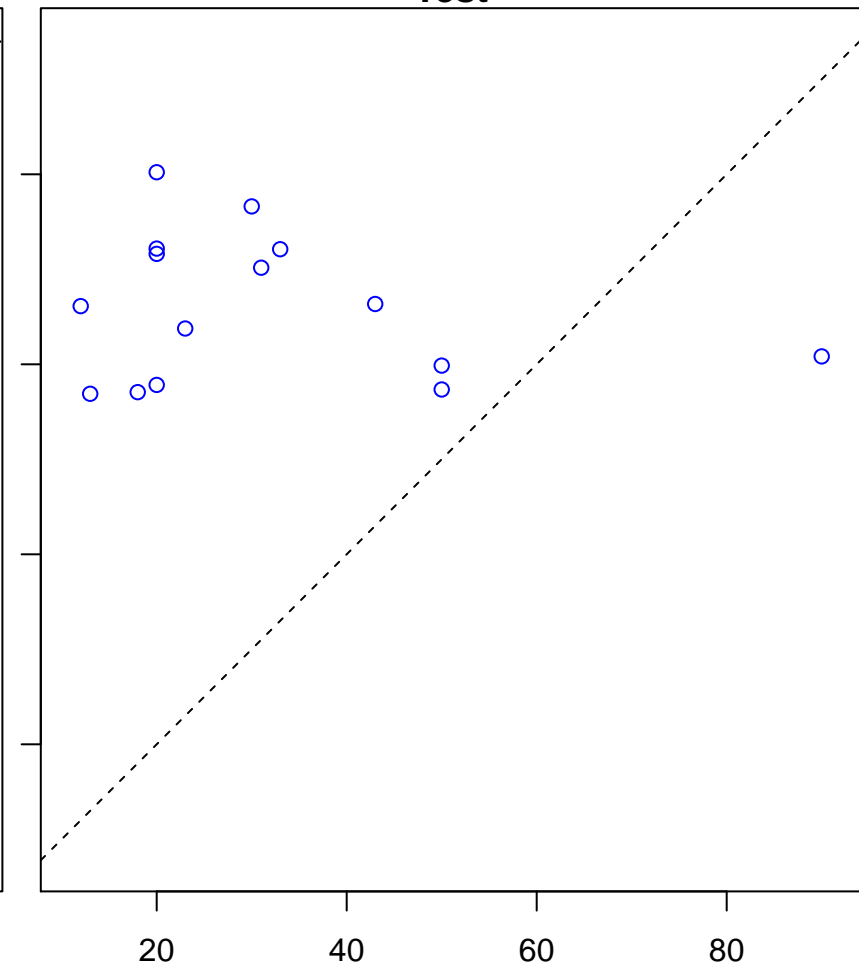


epithelial cell apoptotic process (Score: 3.535546)

Control

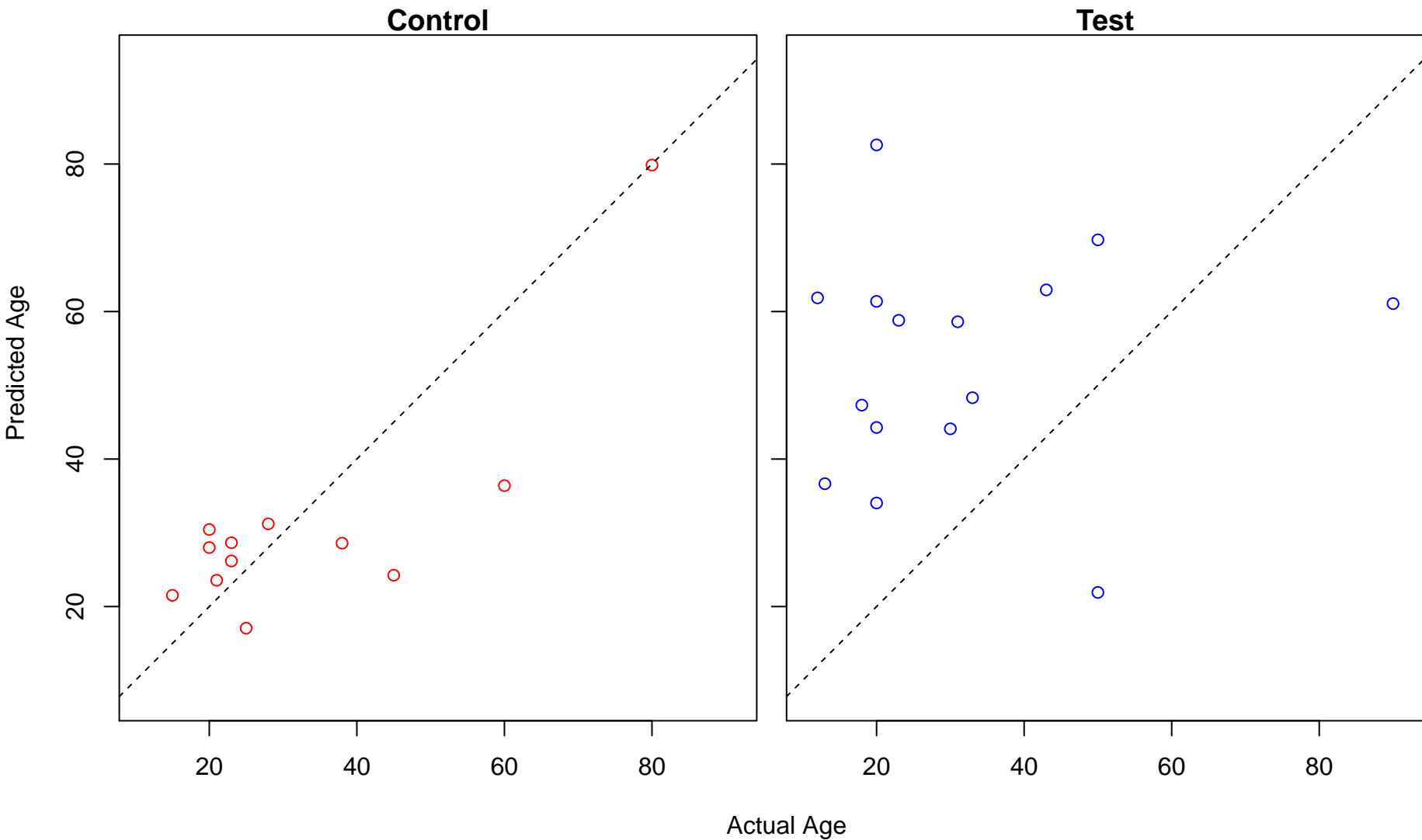


Test



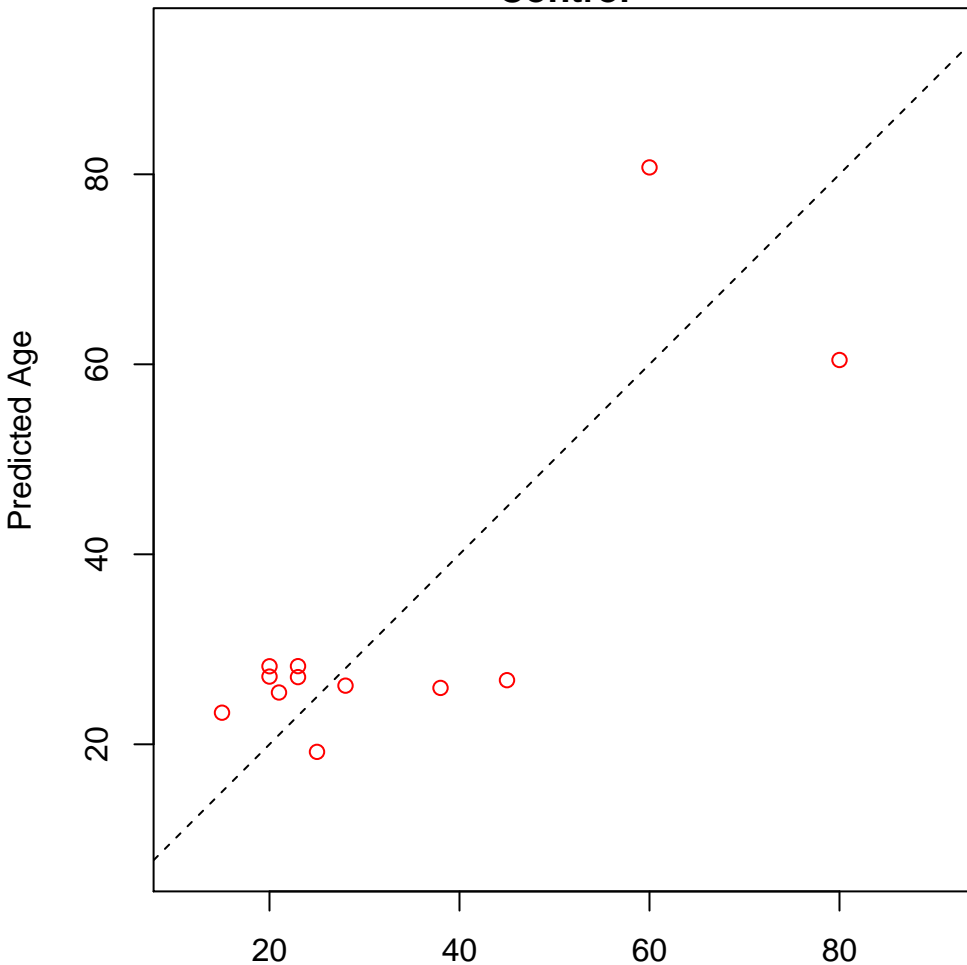
Actual Age

endoplasmic reticulum tubular network organization (Score: 3.535277)

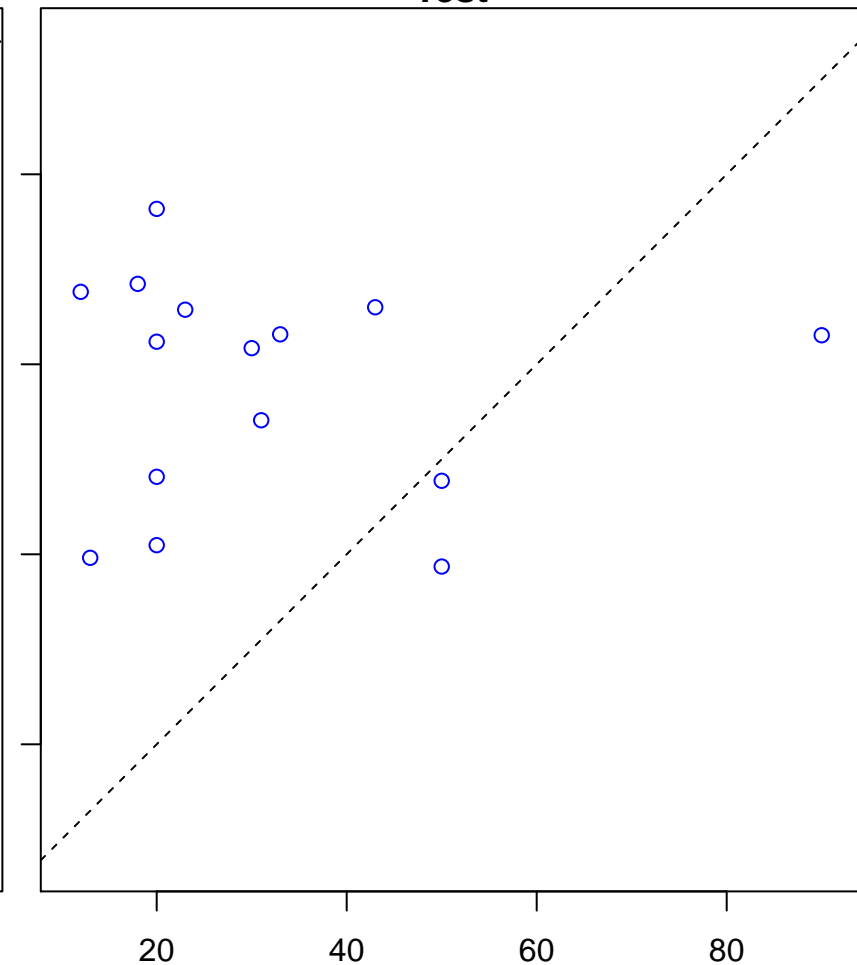


protein K6-linked ubiquitination (Score: 3.531162)

Control

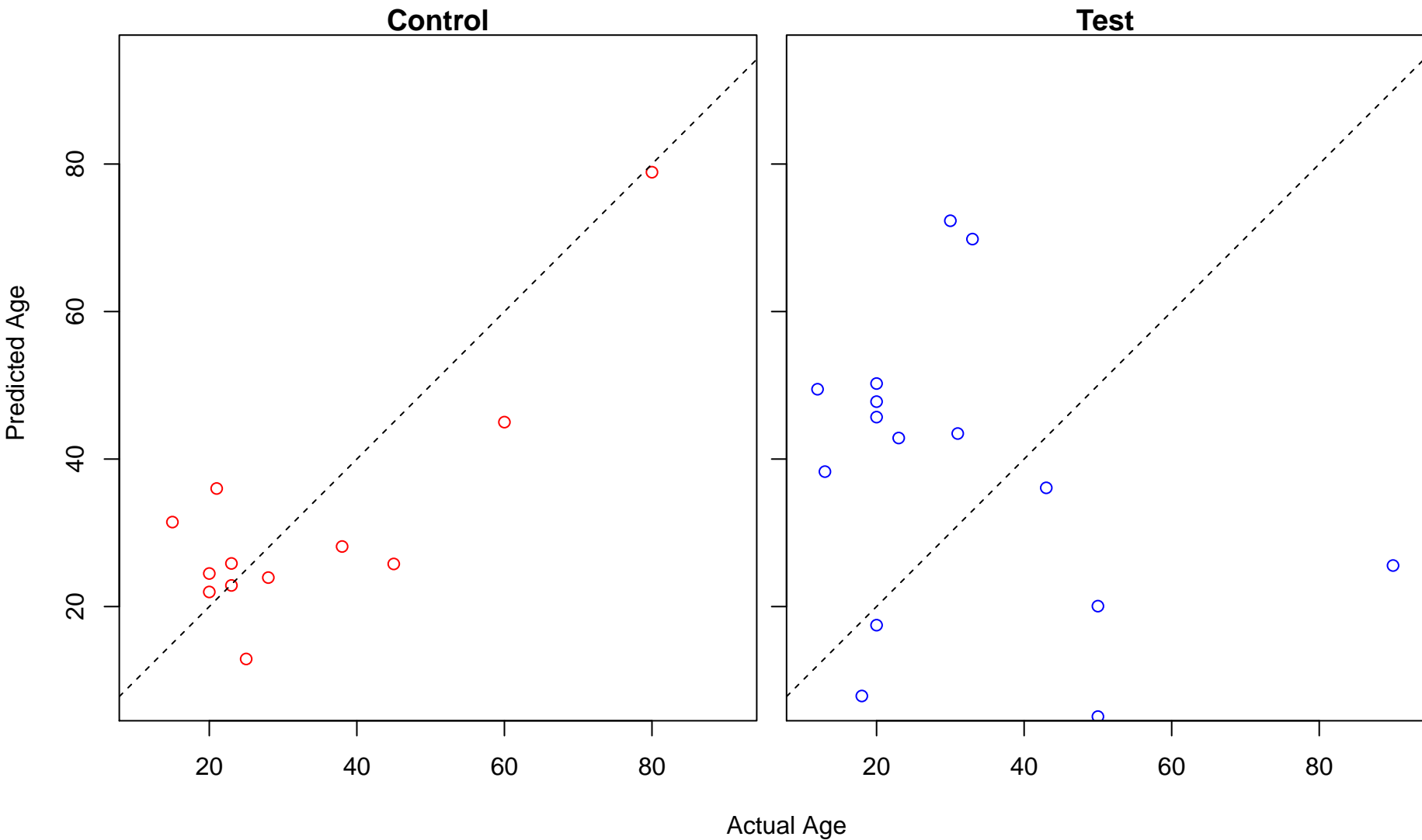


Test

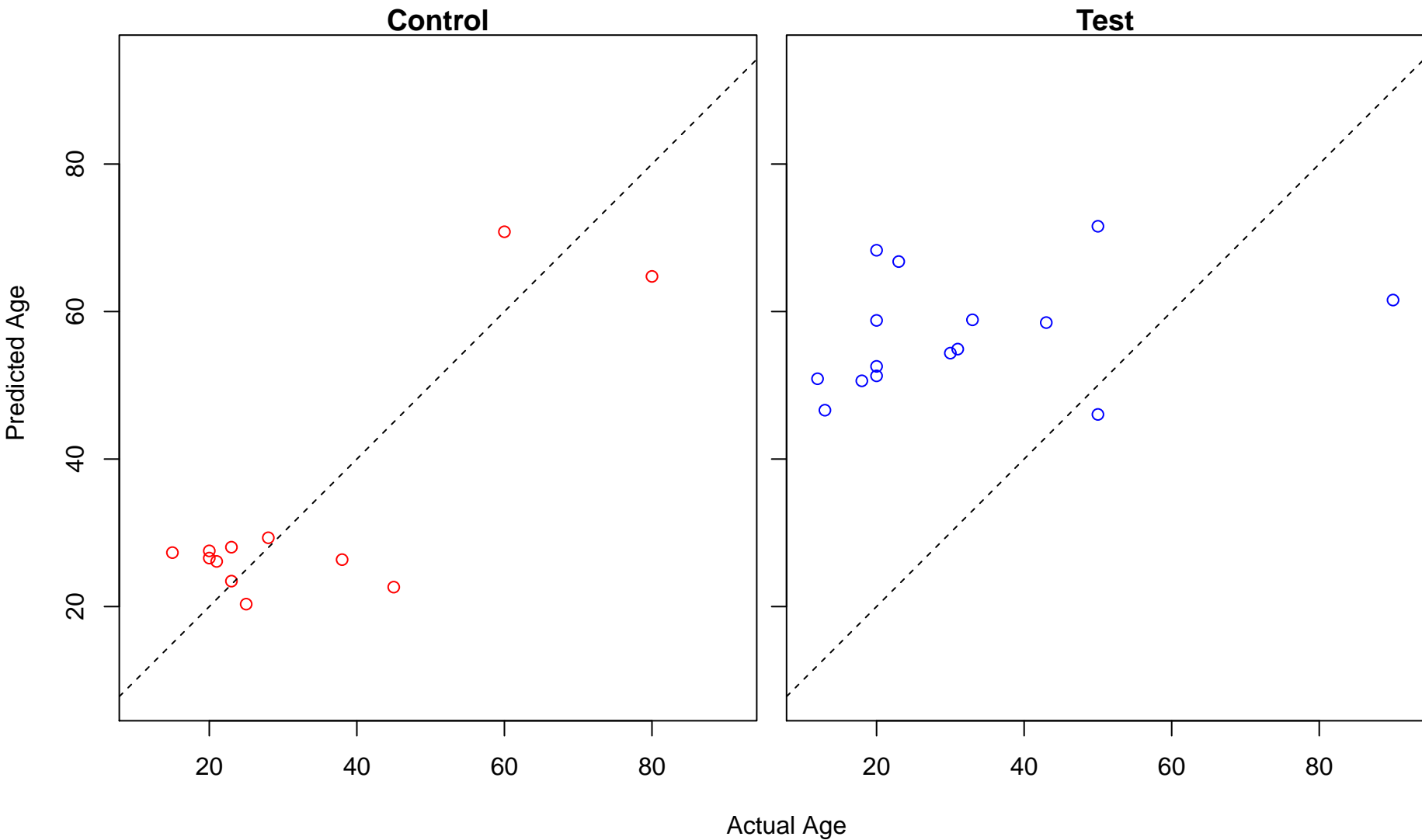


Actual Age

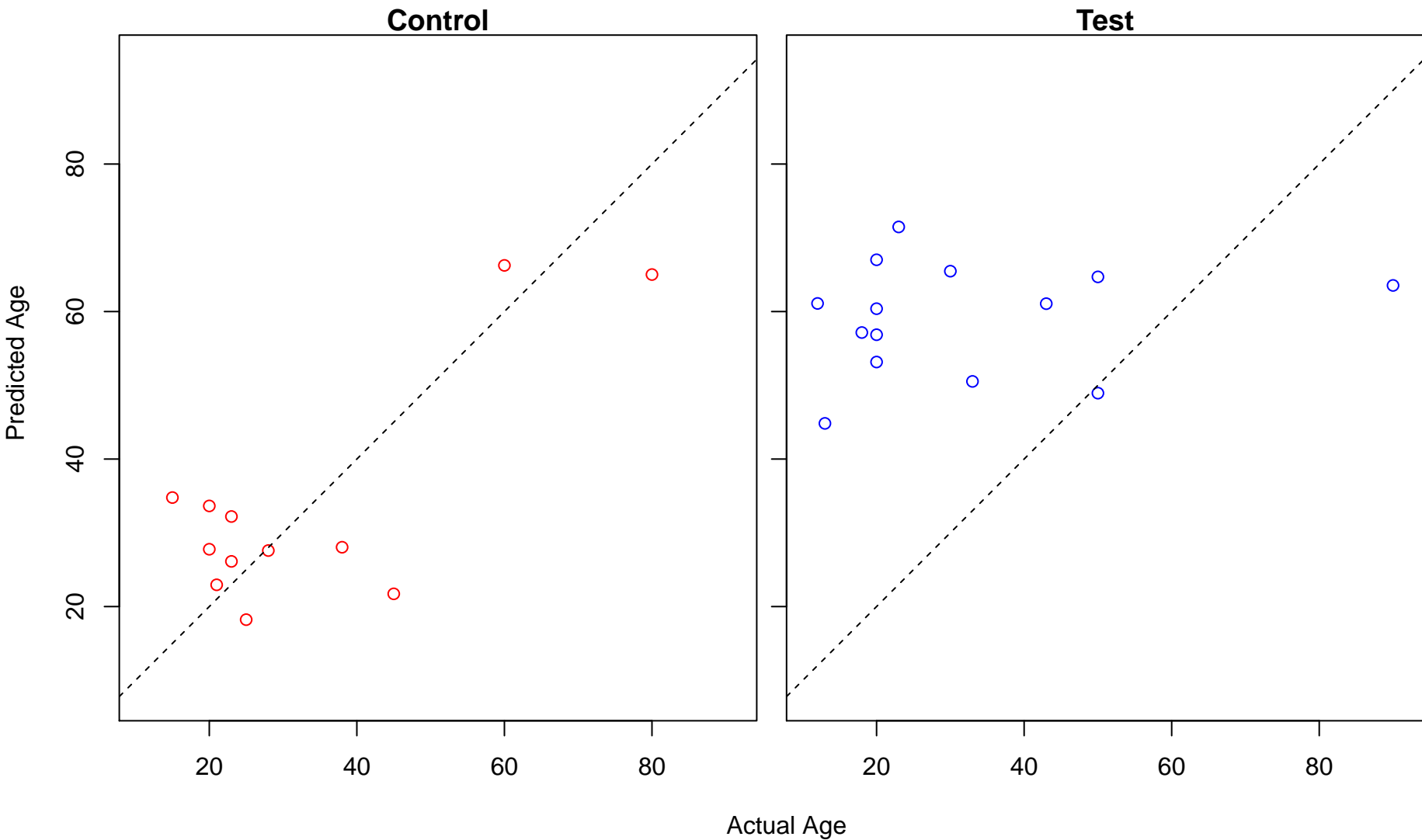
execution phase of apoptosis (Score: 3.531125)



histone H3-K36 methylation (Score: 3.528878)

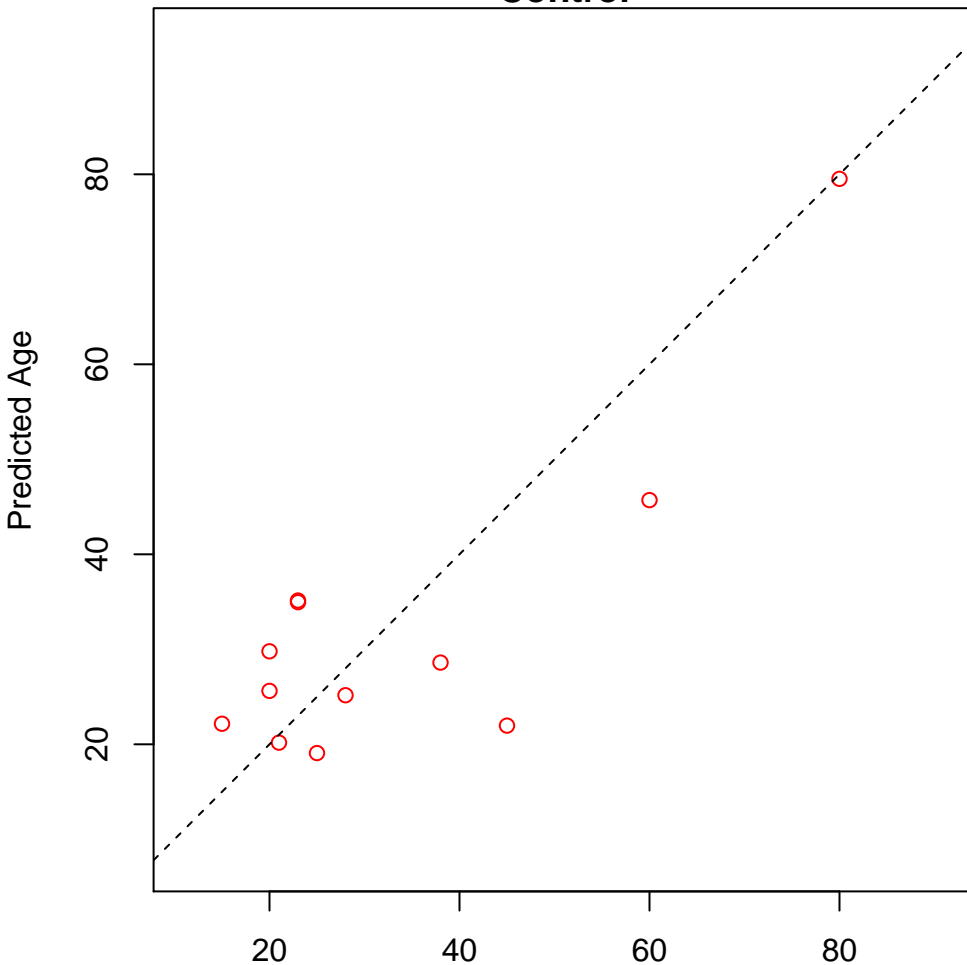


alditol metabolic process (Score: 3.524909)

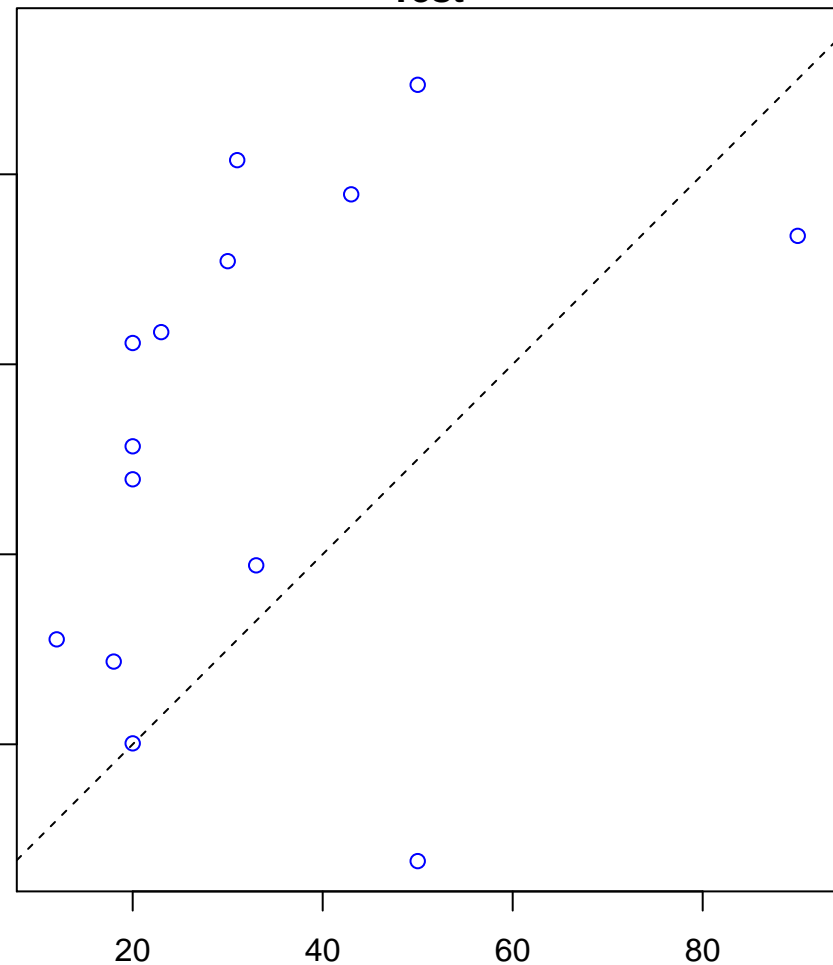


cellular response to osmotic stress (Score: 3.523905)

Control

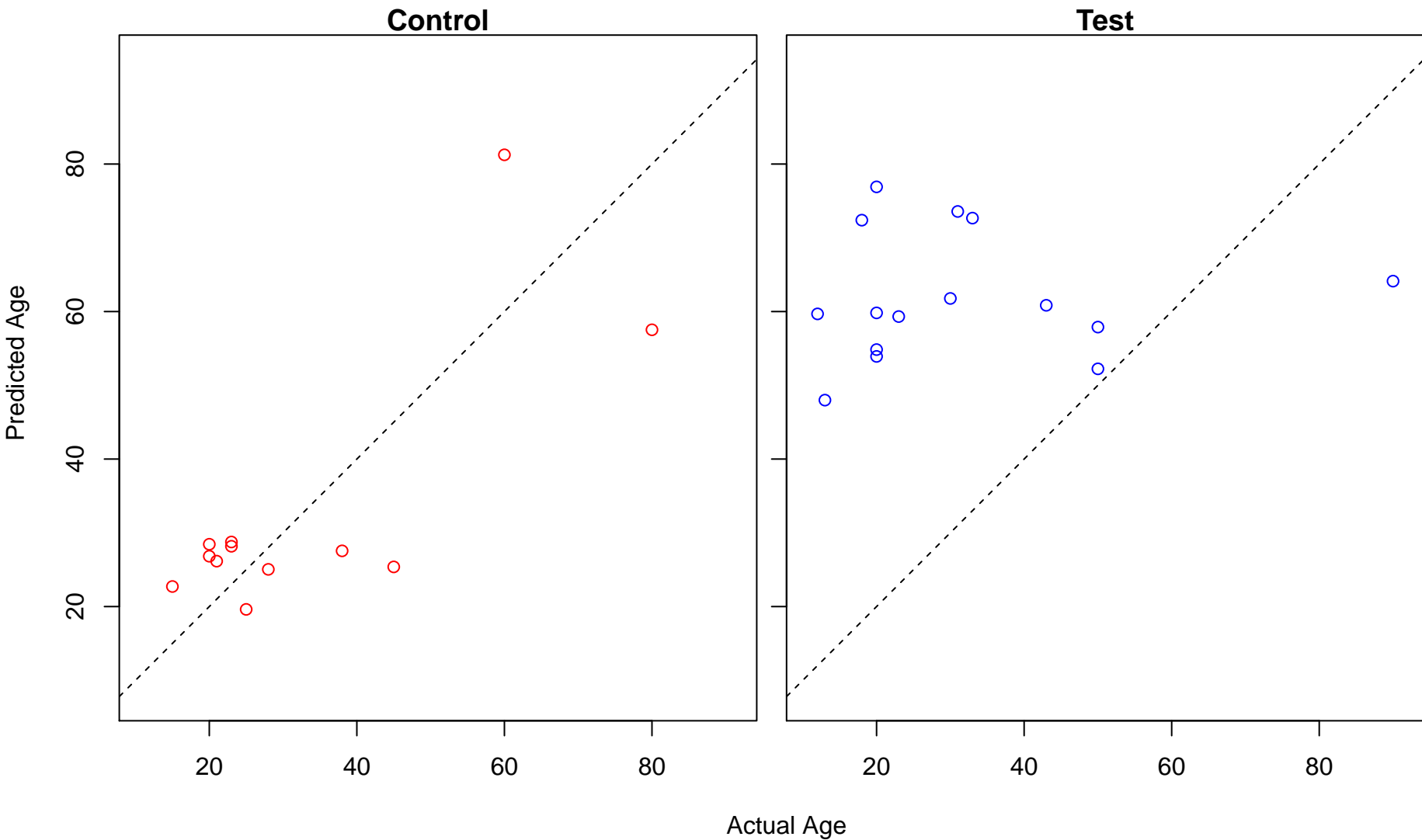


Test

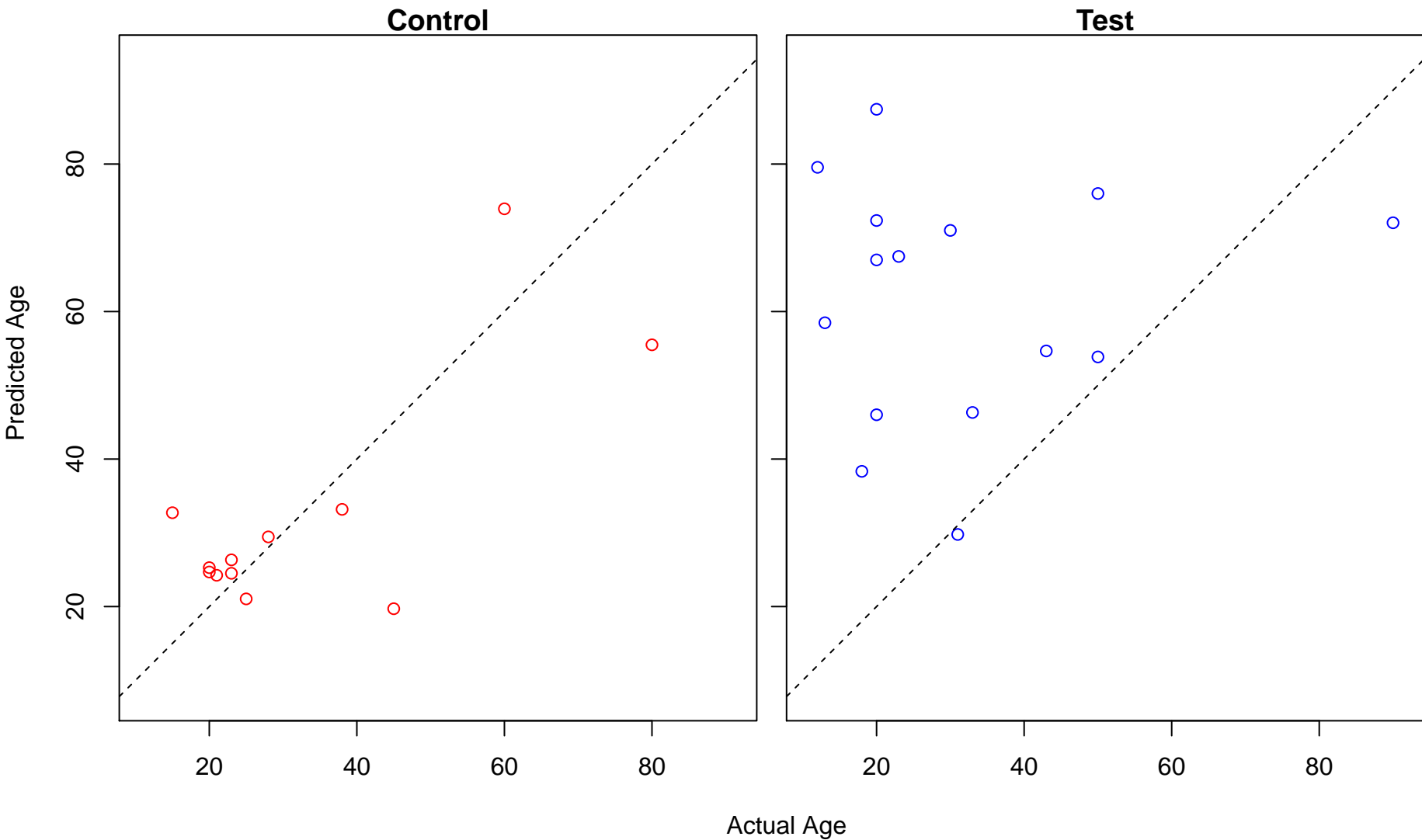


Actual Age

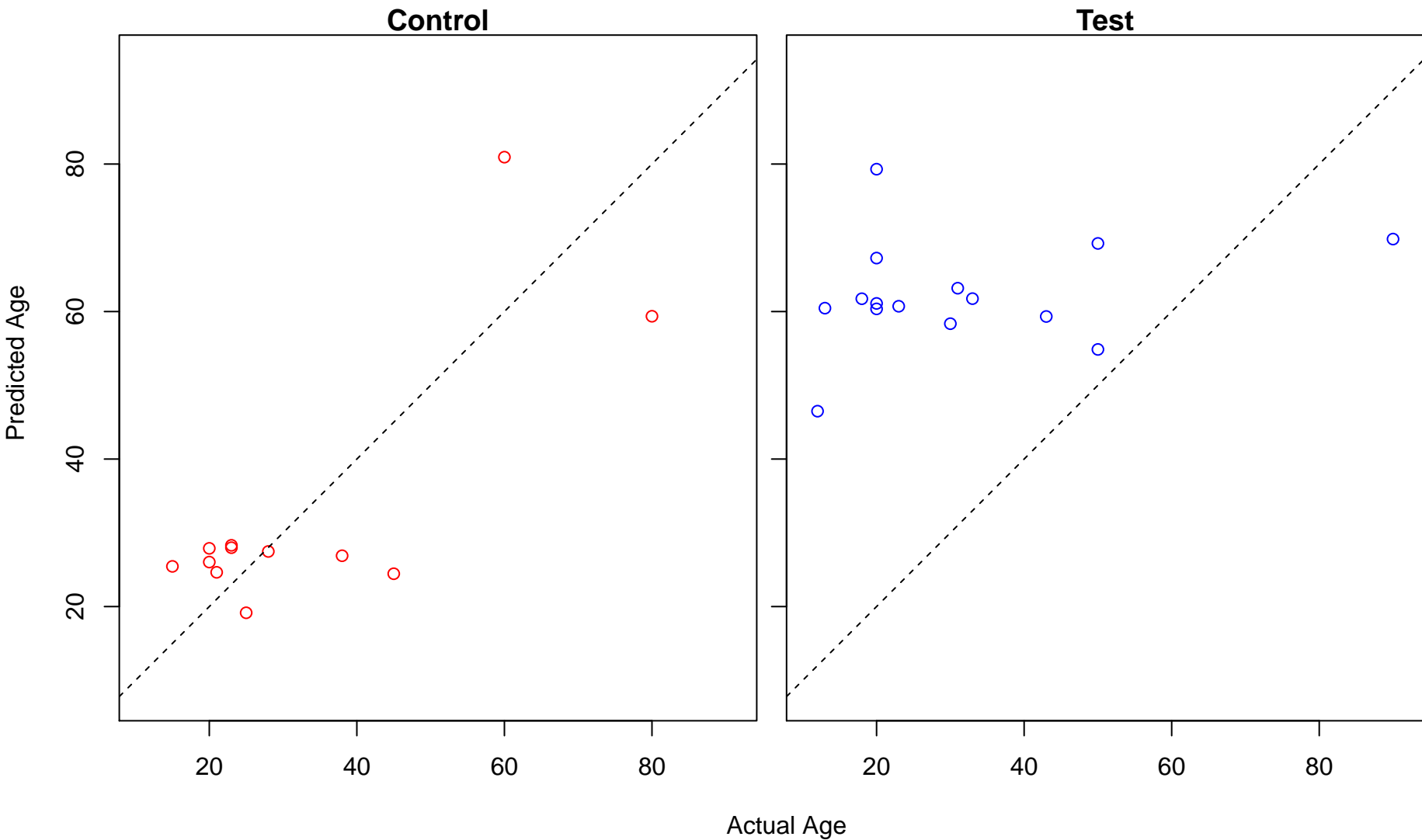
negative regulation of cell junction assembly (Score: 3.522914)



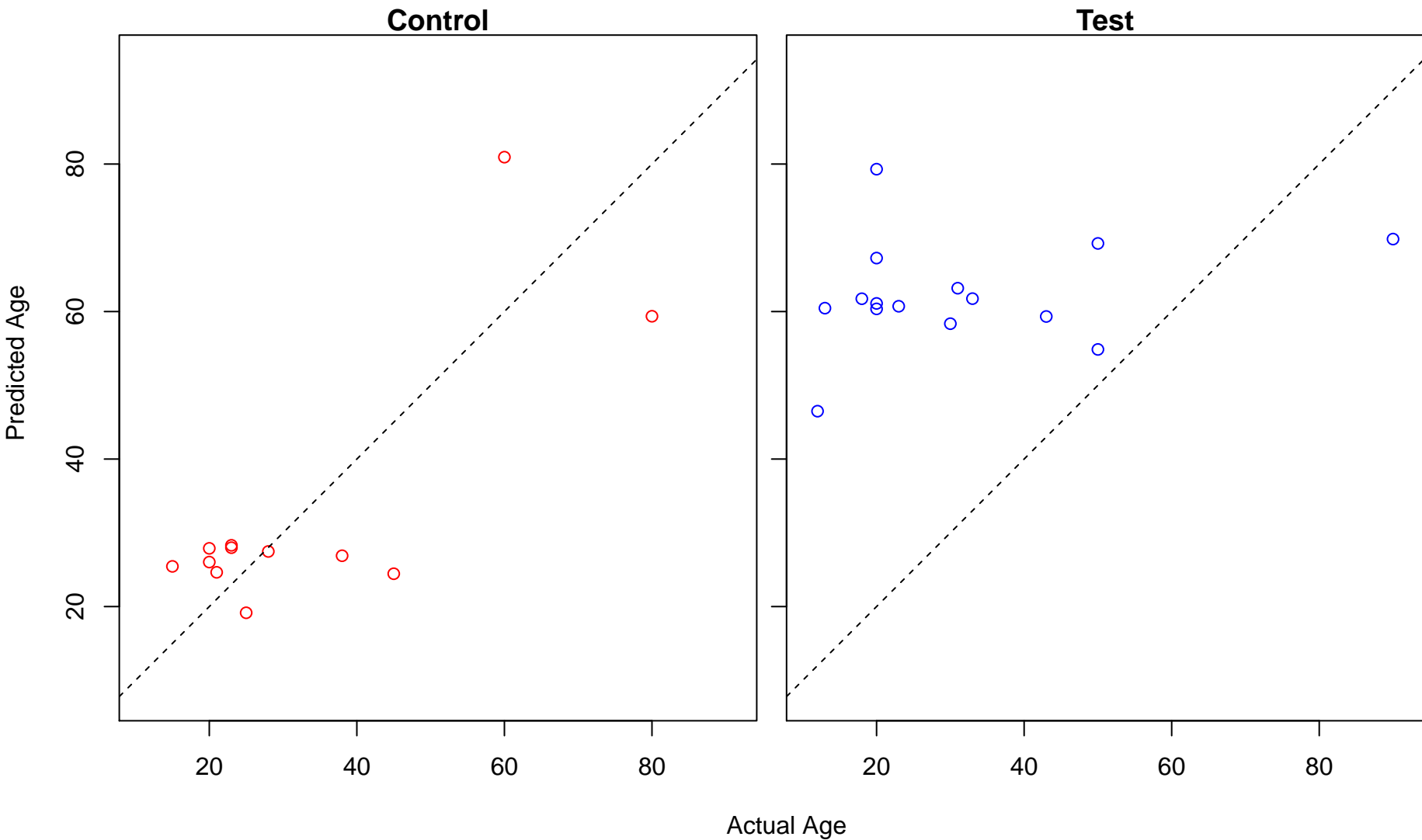
NADP metabolic process (Score: 3.515313)



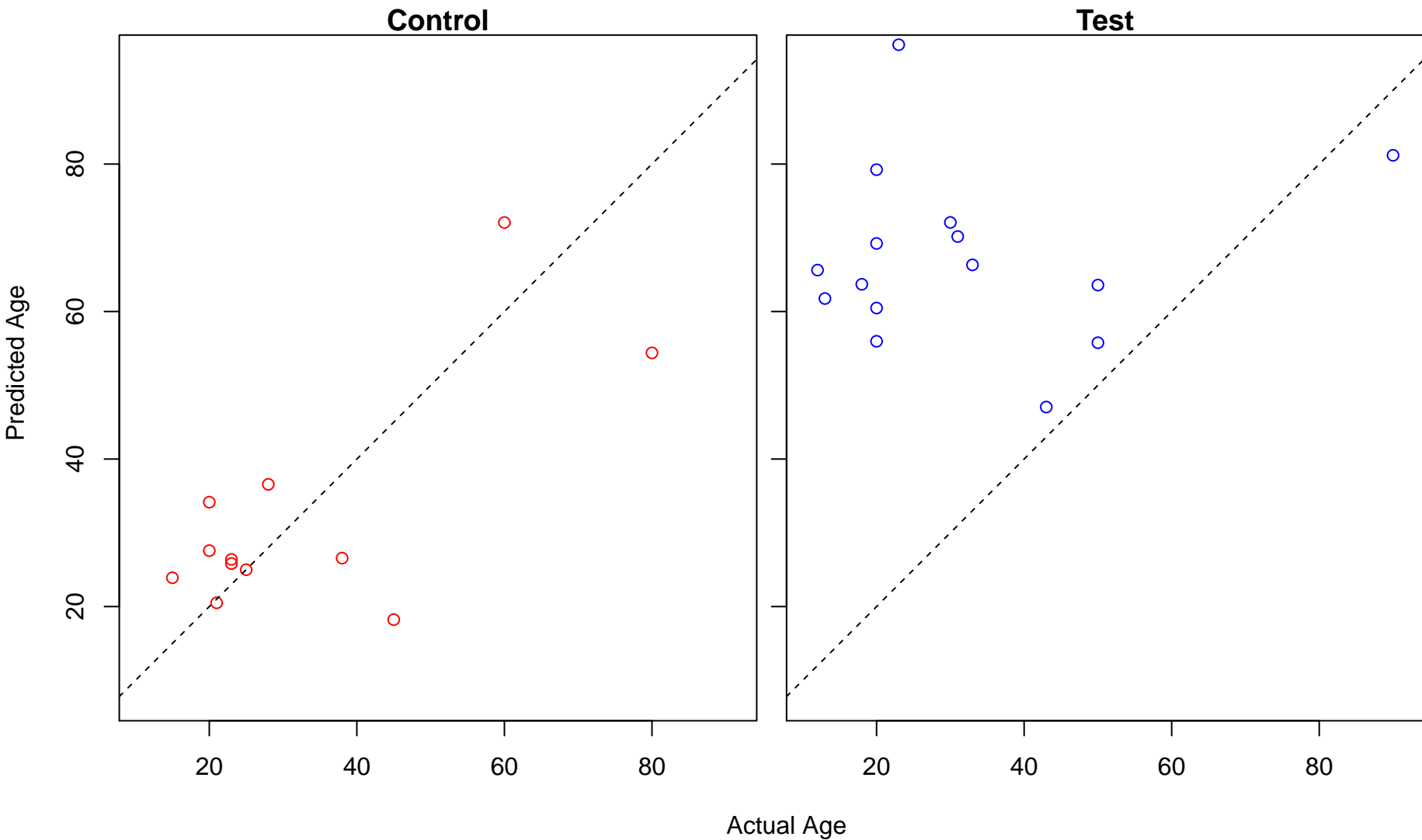
negative regulation of protein processing (Score: 3.511544)



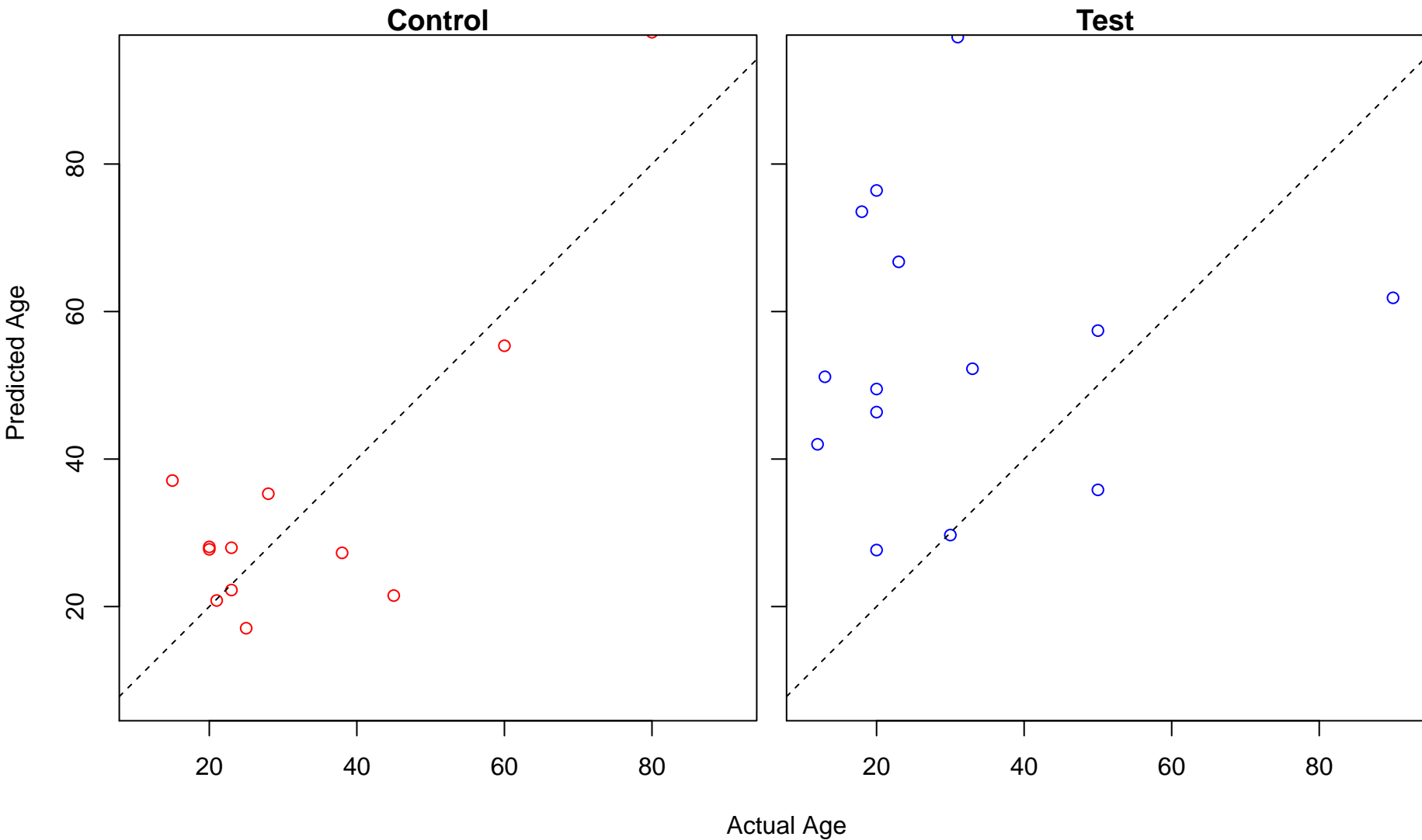
negative regulation of protein maturation (Score: 3.511544)



negative regulation of fibroblast growth factor receptor signaling pathway (Score: 3.510453)

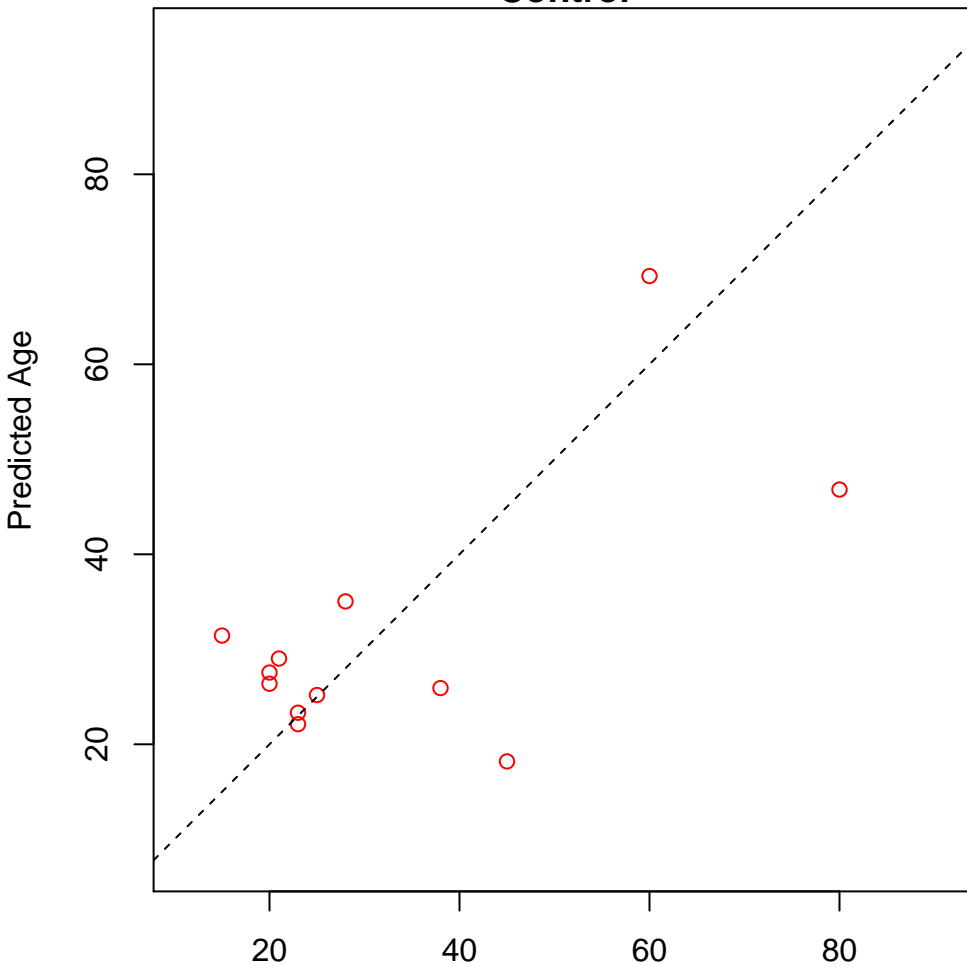


negative regulation of axonogenesis (Score: 3.510412)

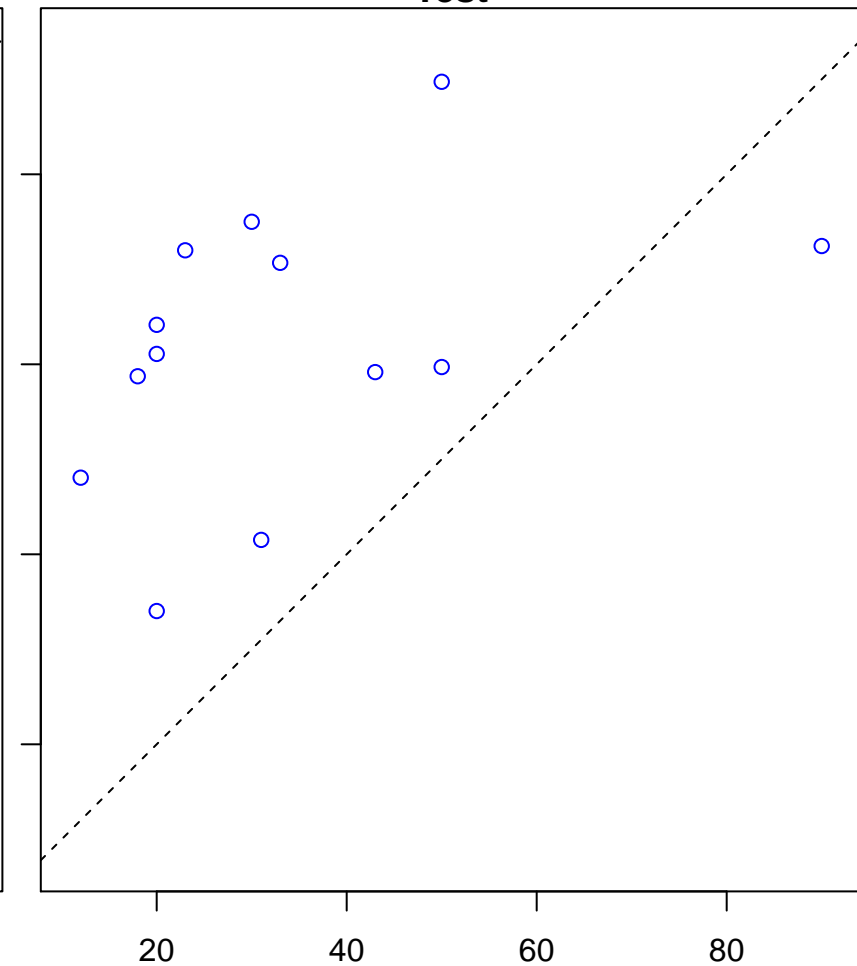


sensory perception of sour taste (Score: 3.501783)

Control

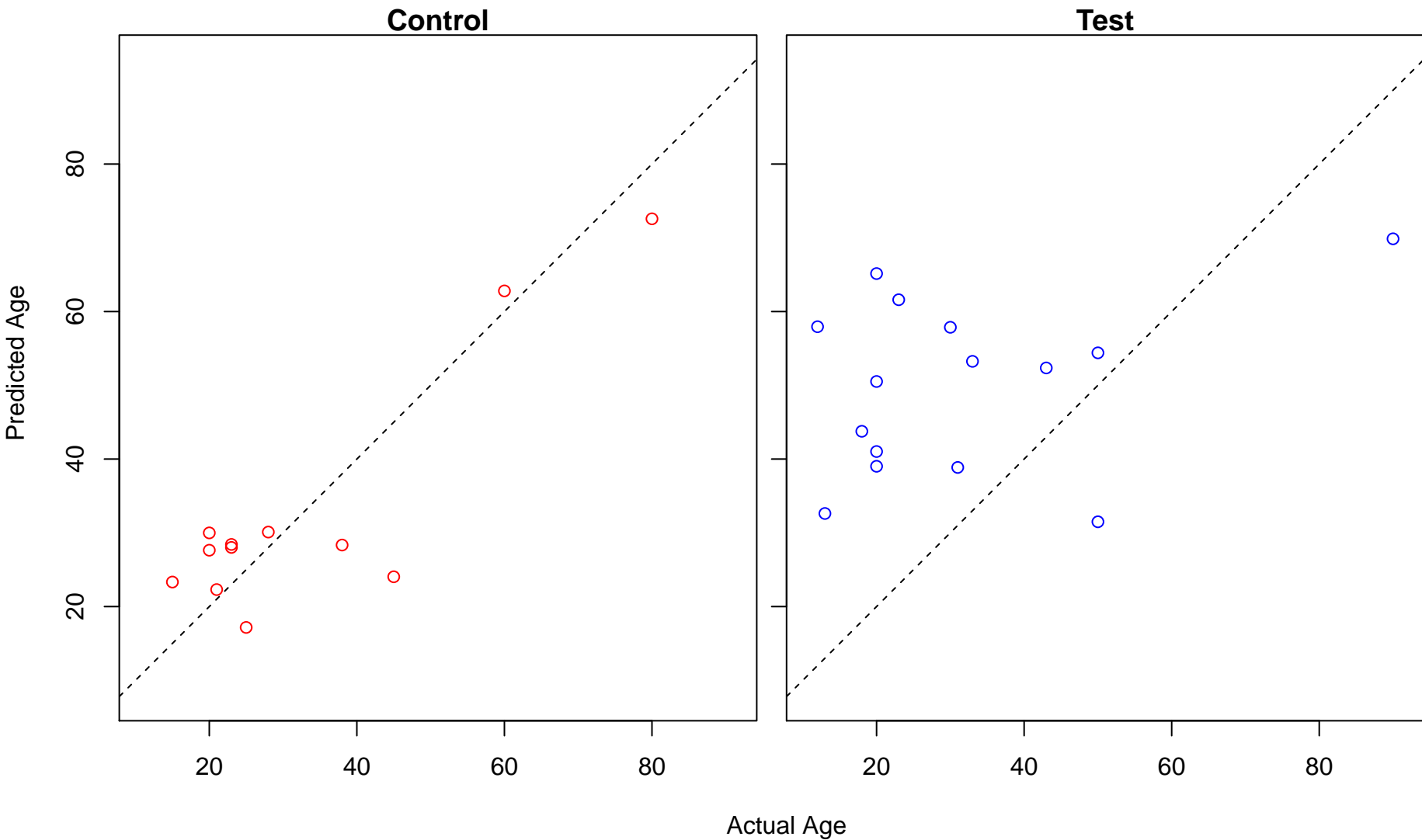


Test

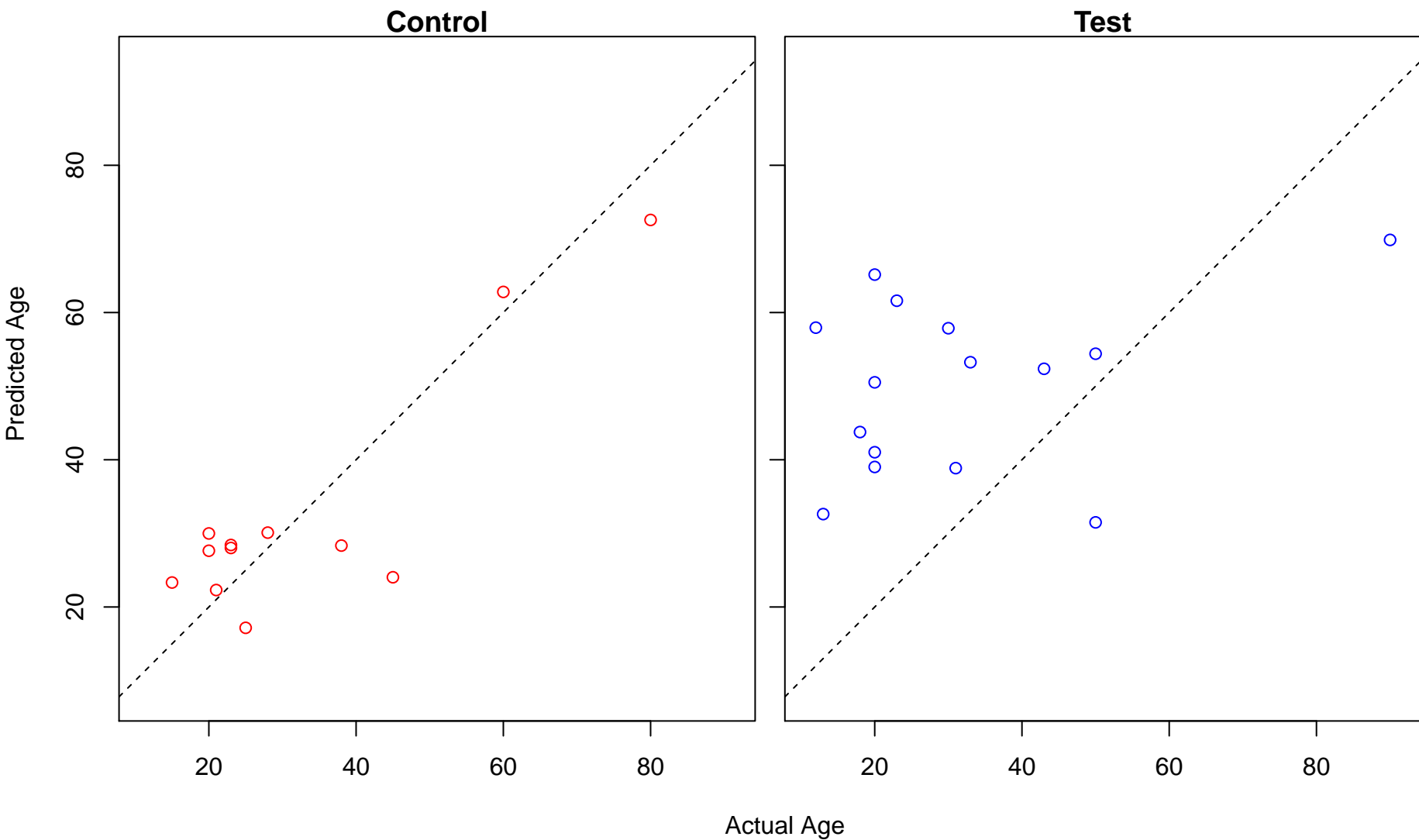


Actual Age

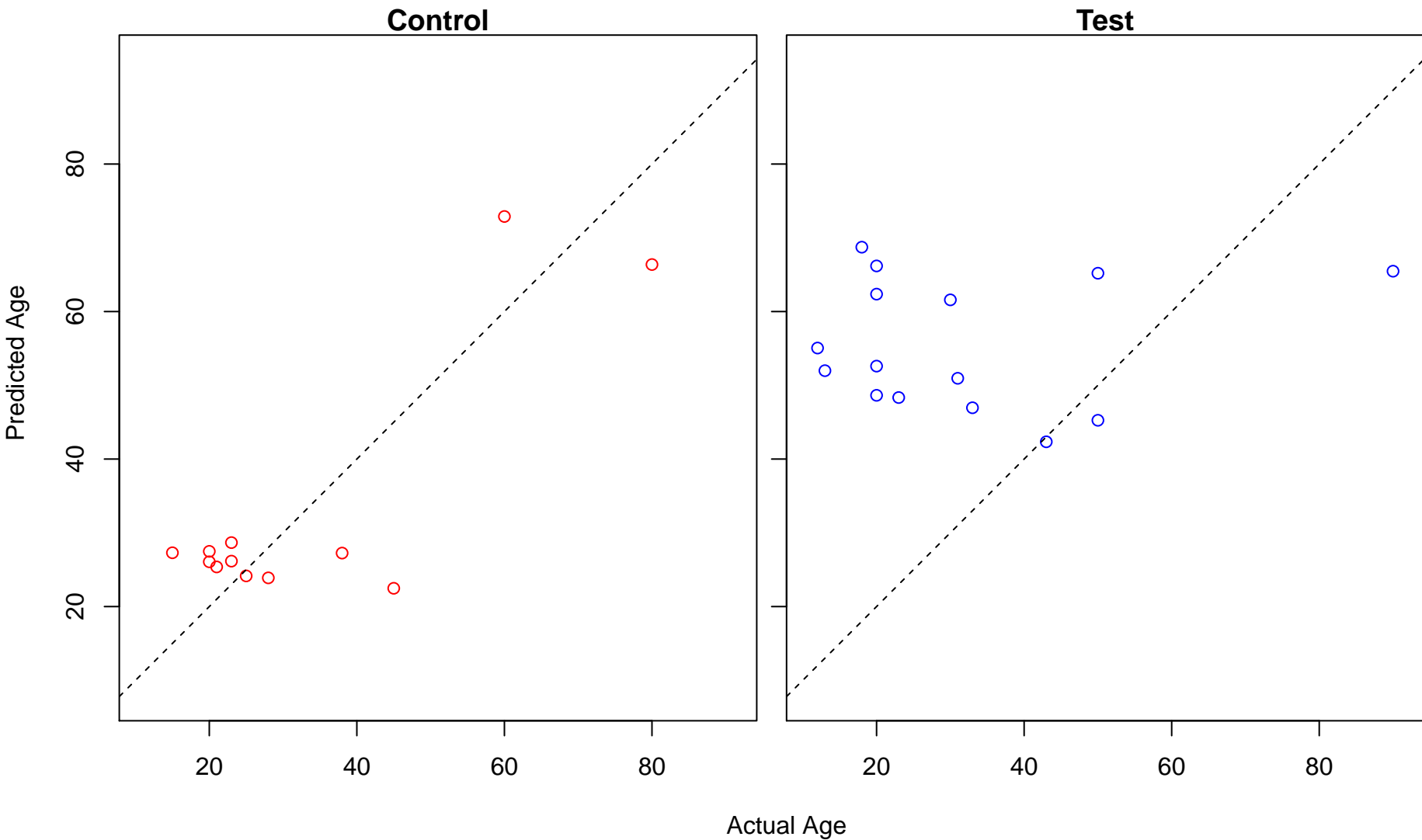
peroxisomal membrane transport (Score: 3.494580)



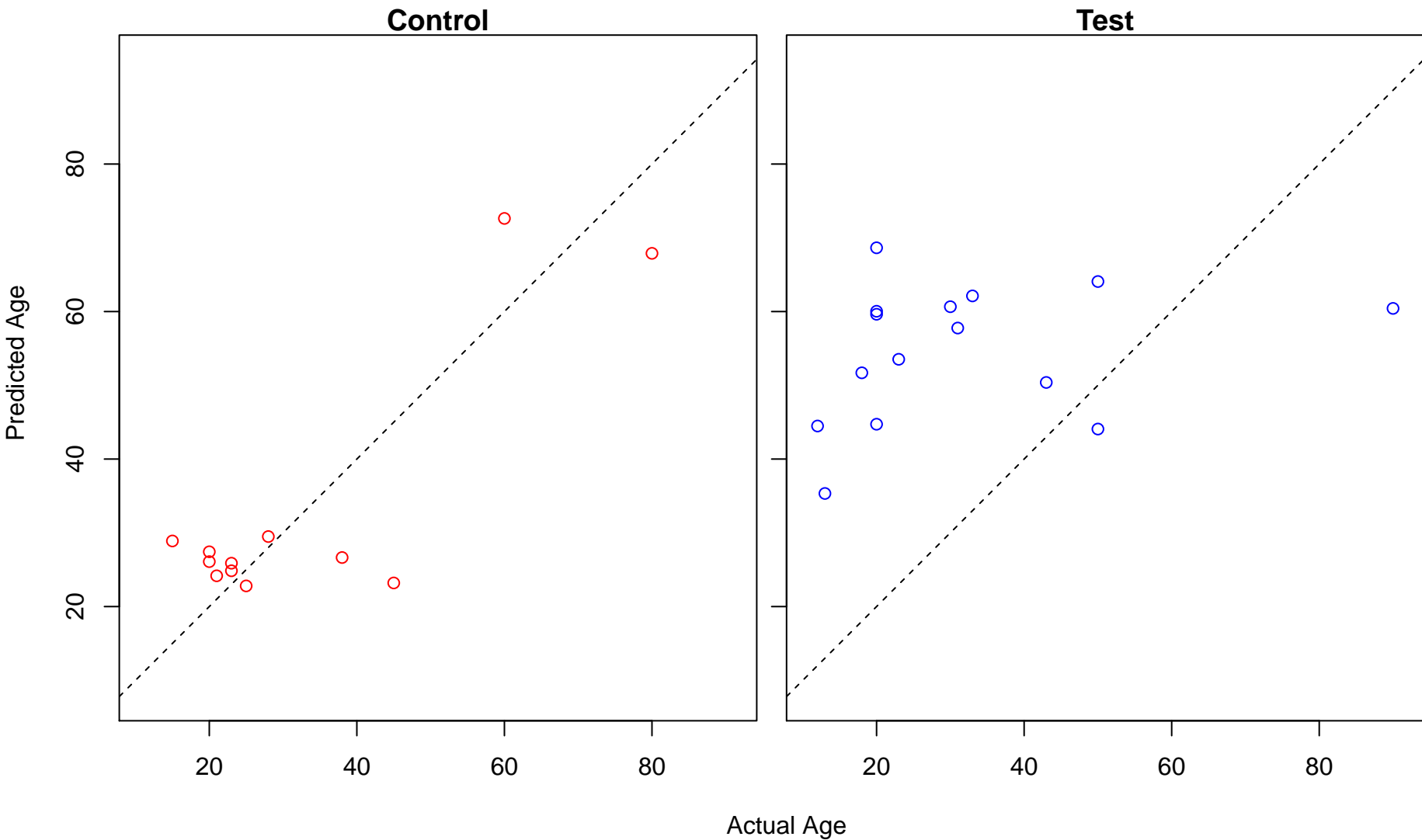
protein import into peroxisome membrane (Score: 3.494580)



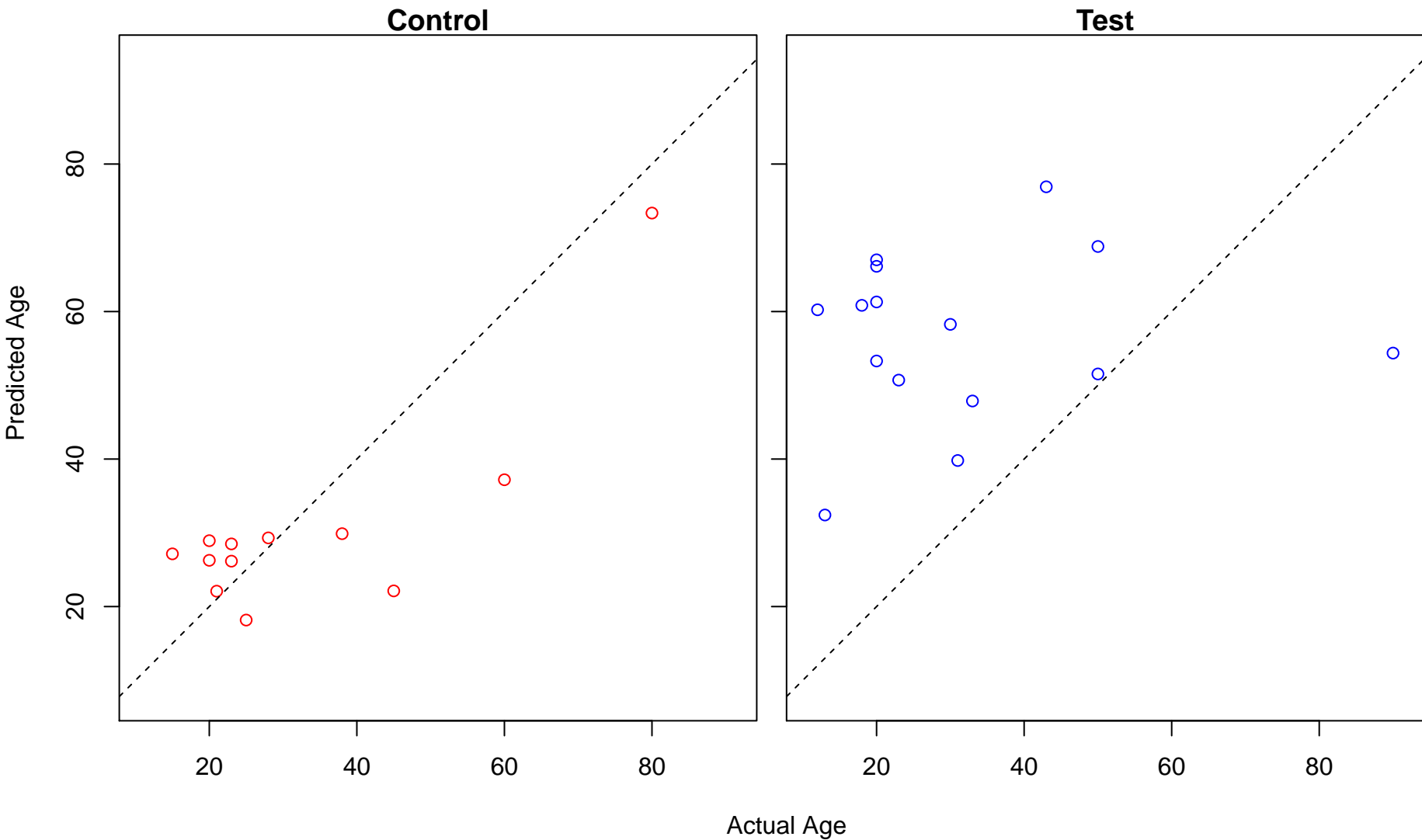
regulation of proteasomal ubiquitin-dependent protein catabolic process (Score: 3.492494)



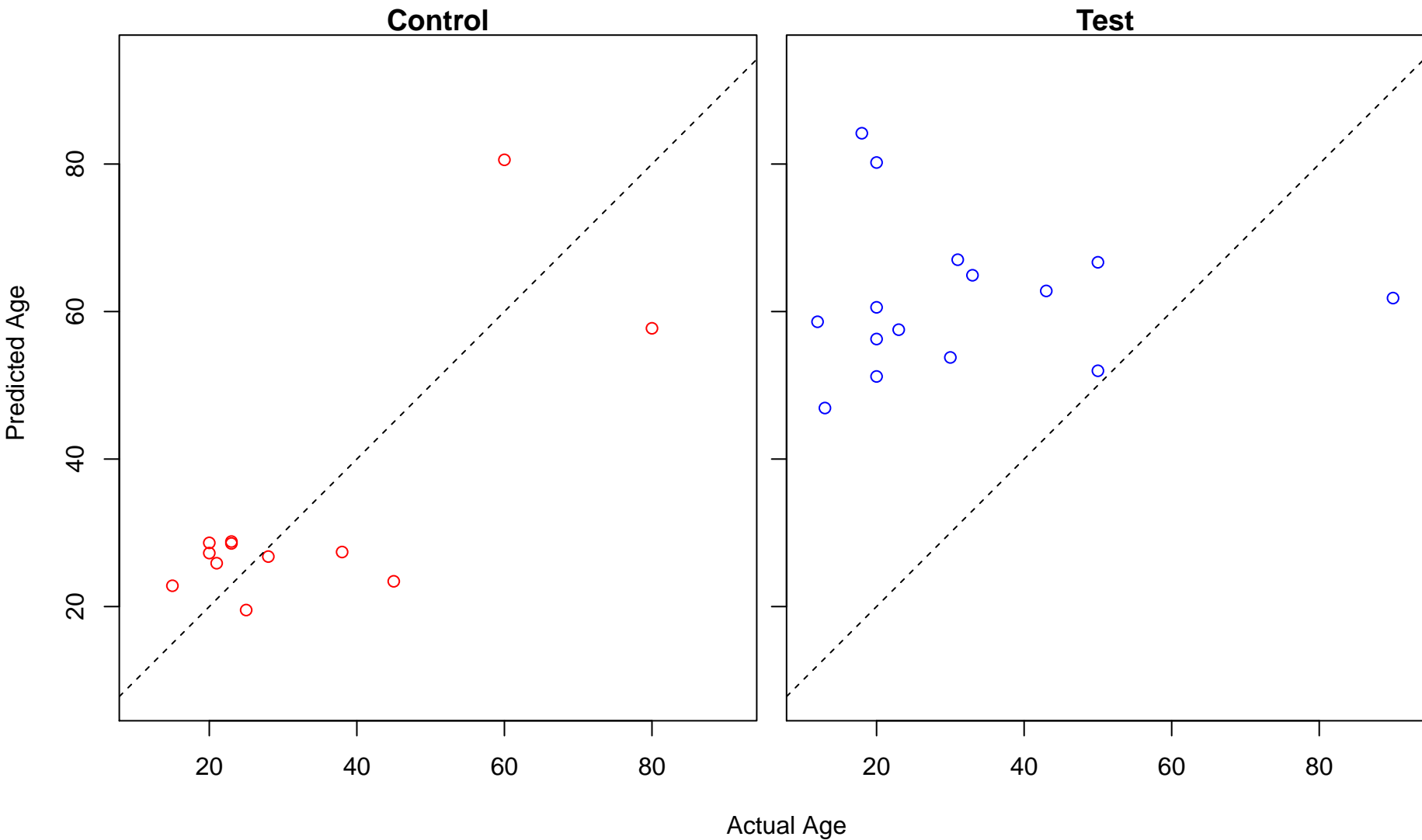
lipoprotein metabolic process (Score: 3.489113)



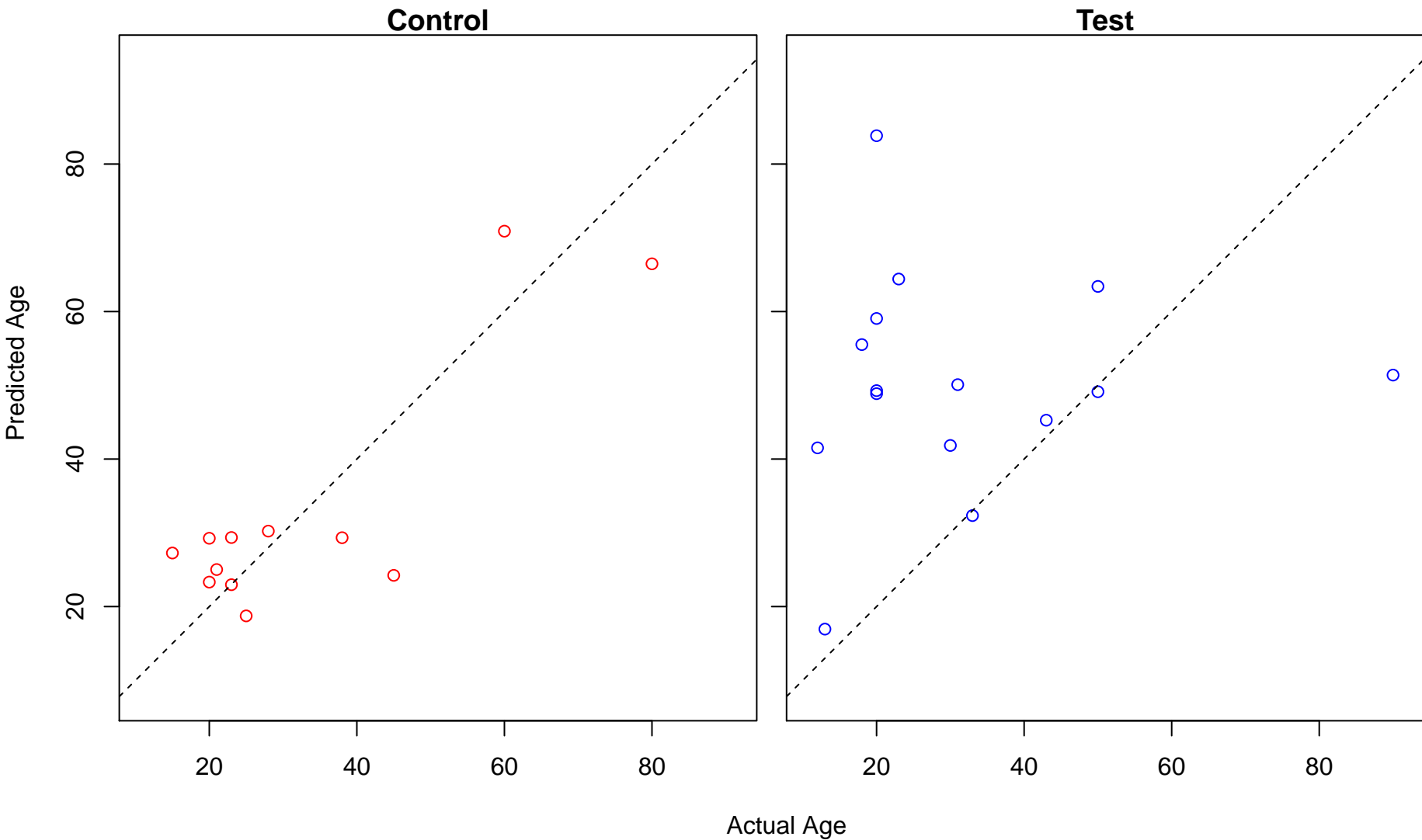
fatty acid oxidation (Score: 3.487619)



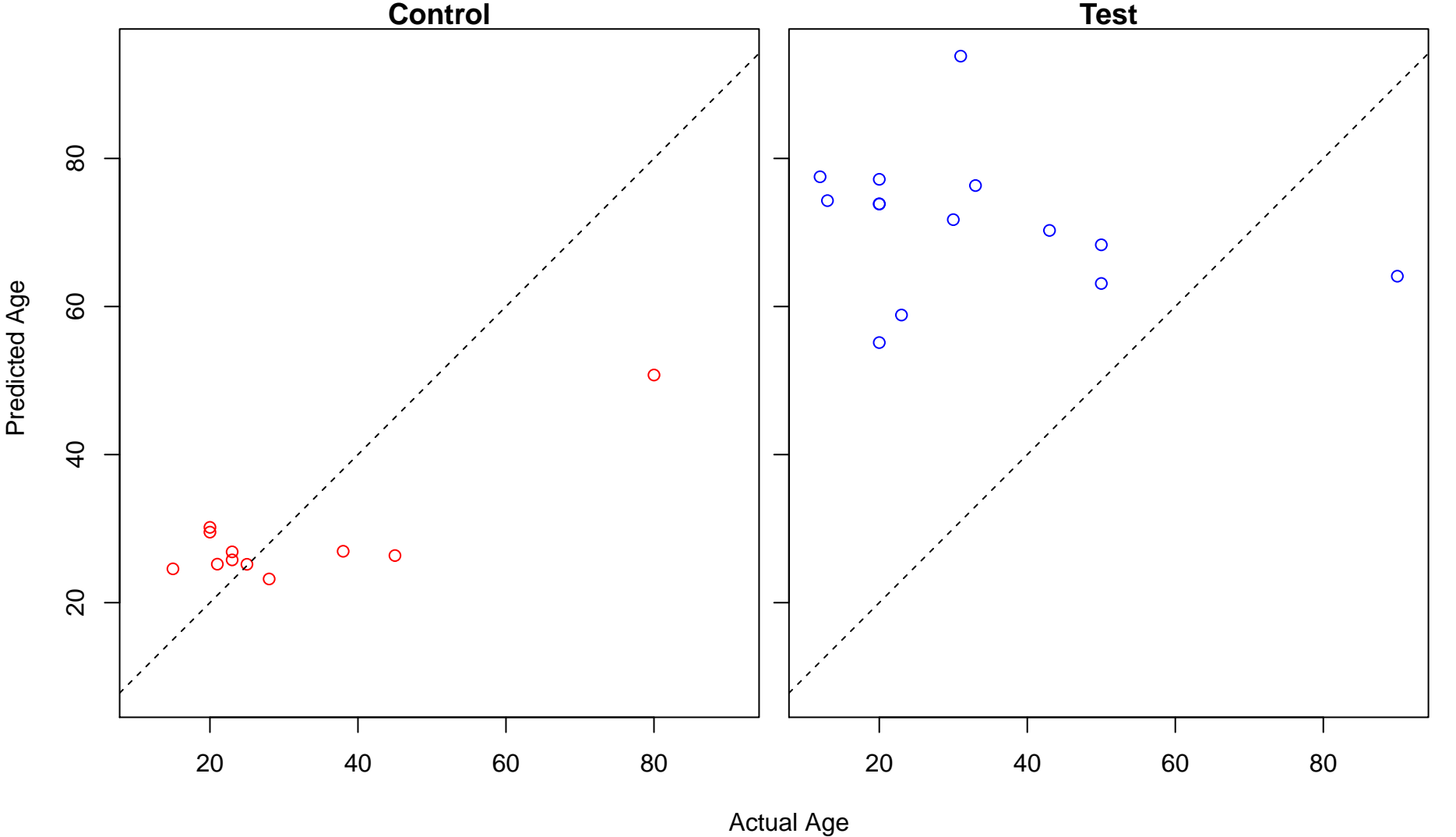
inositol phosphate catabolic process (Score: 3.485914)



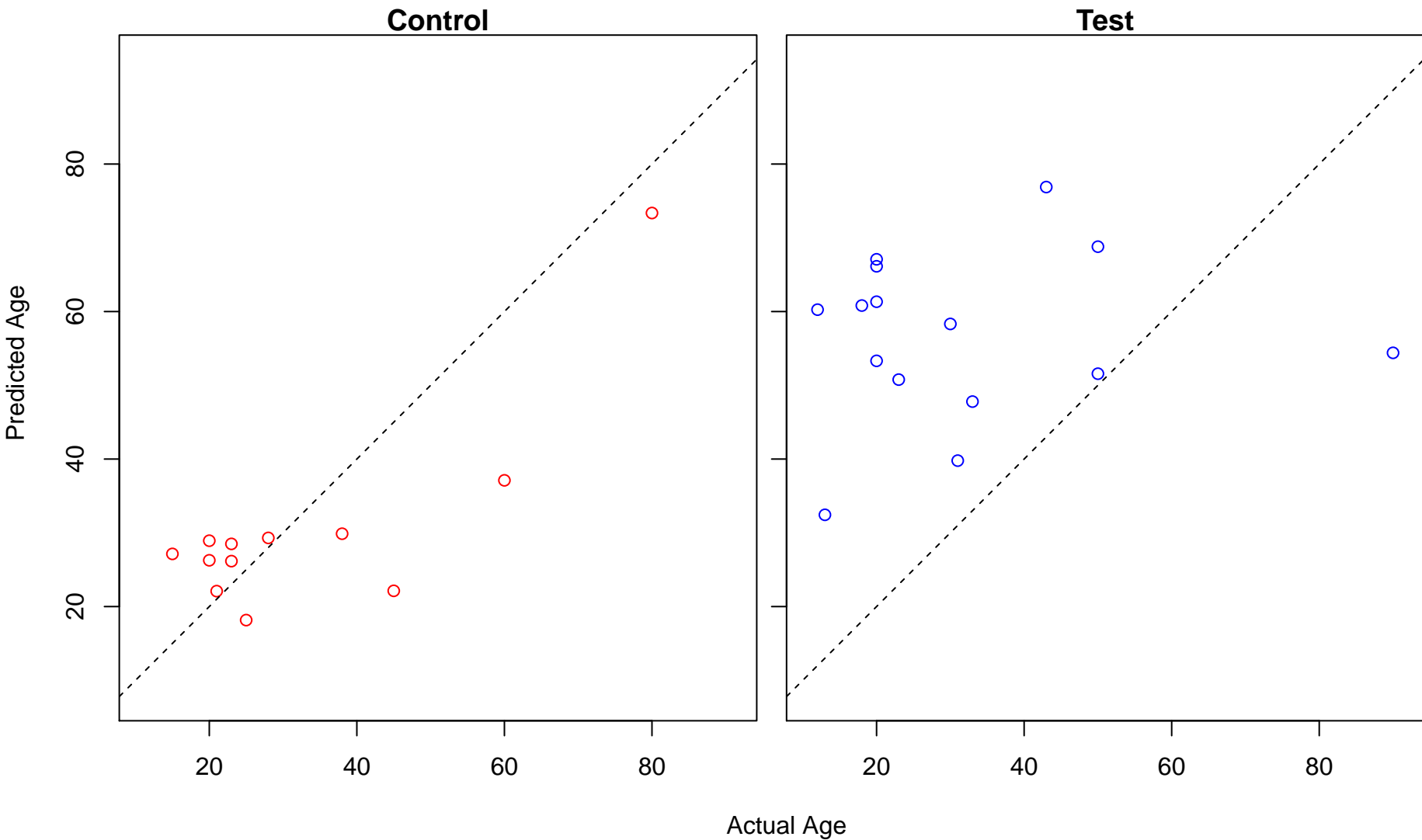
Fc receptor signaling pathway (Score: 3.484758)



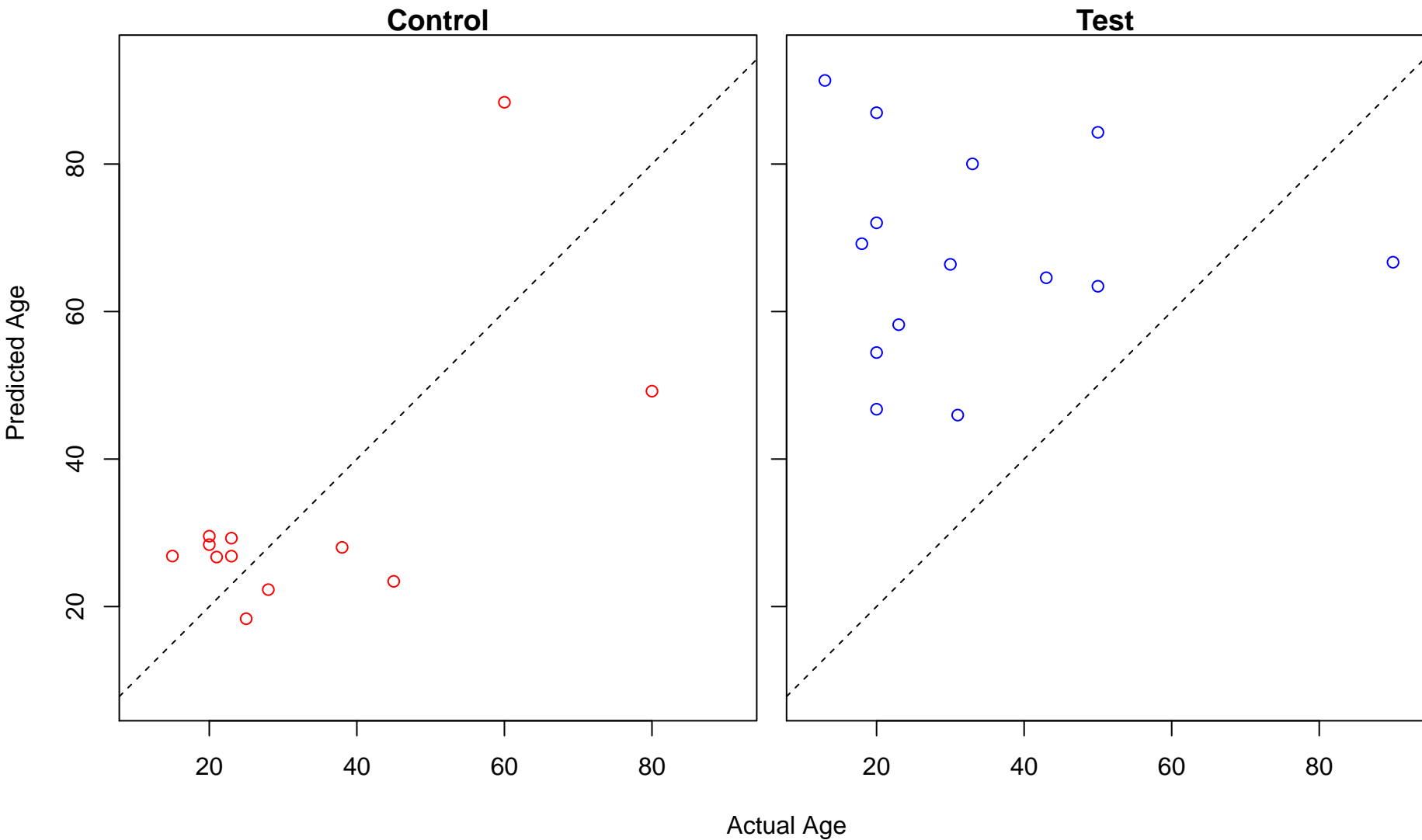
regulation of transcription from RNA polymerase II promoter in response to oxidative stress (Score: 3.4)



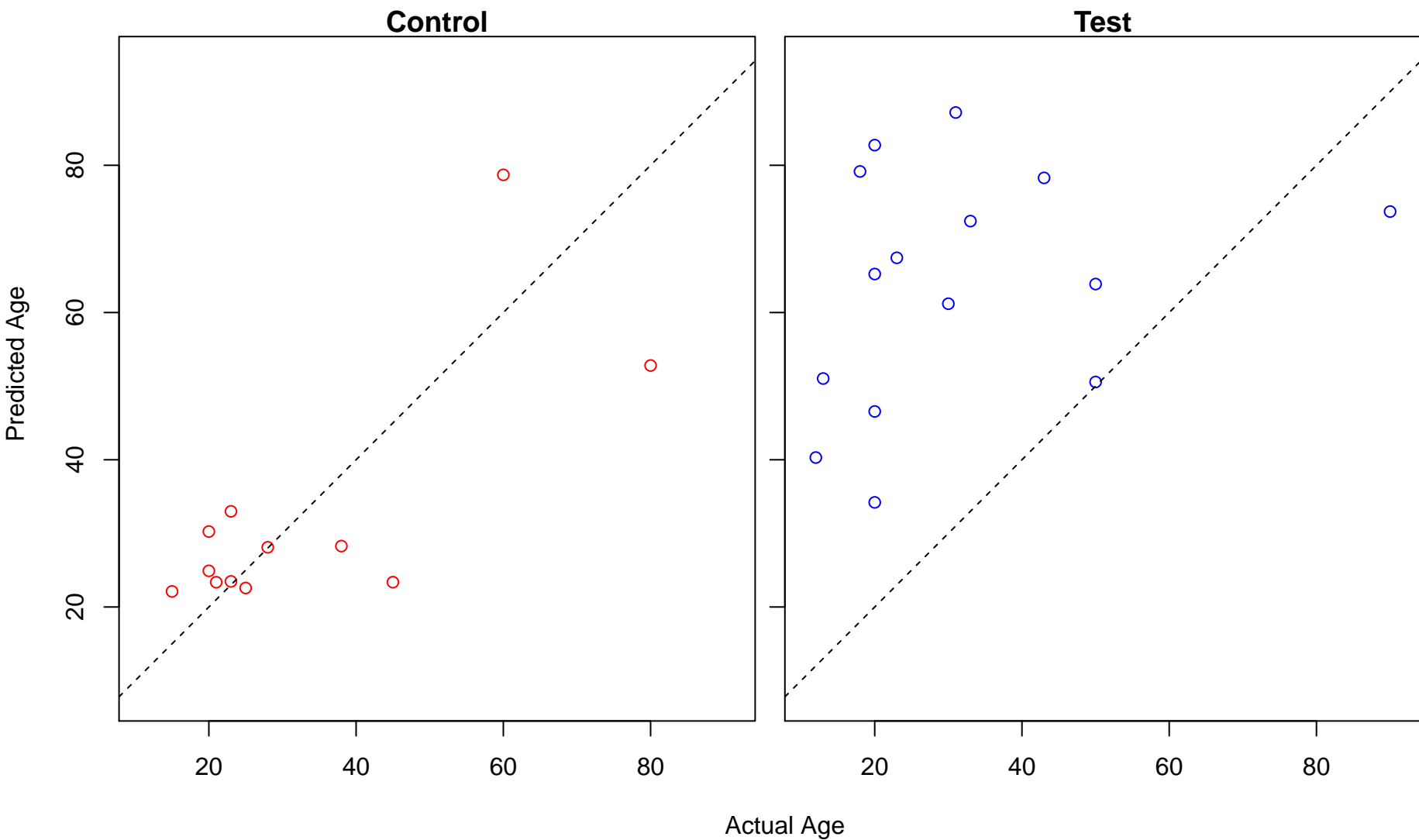
lipid oxidation (Score: 3.483374)



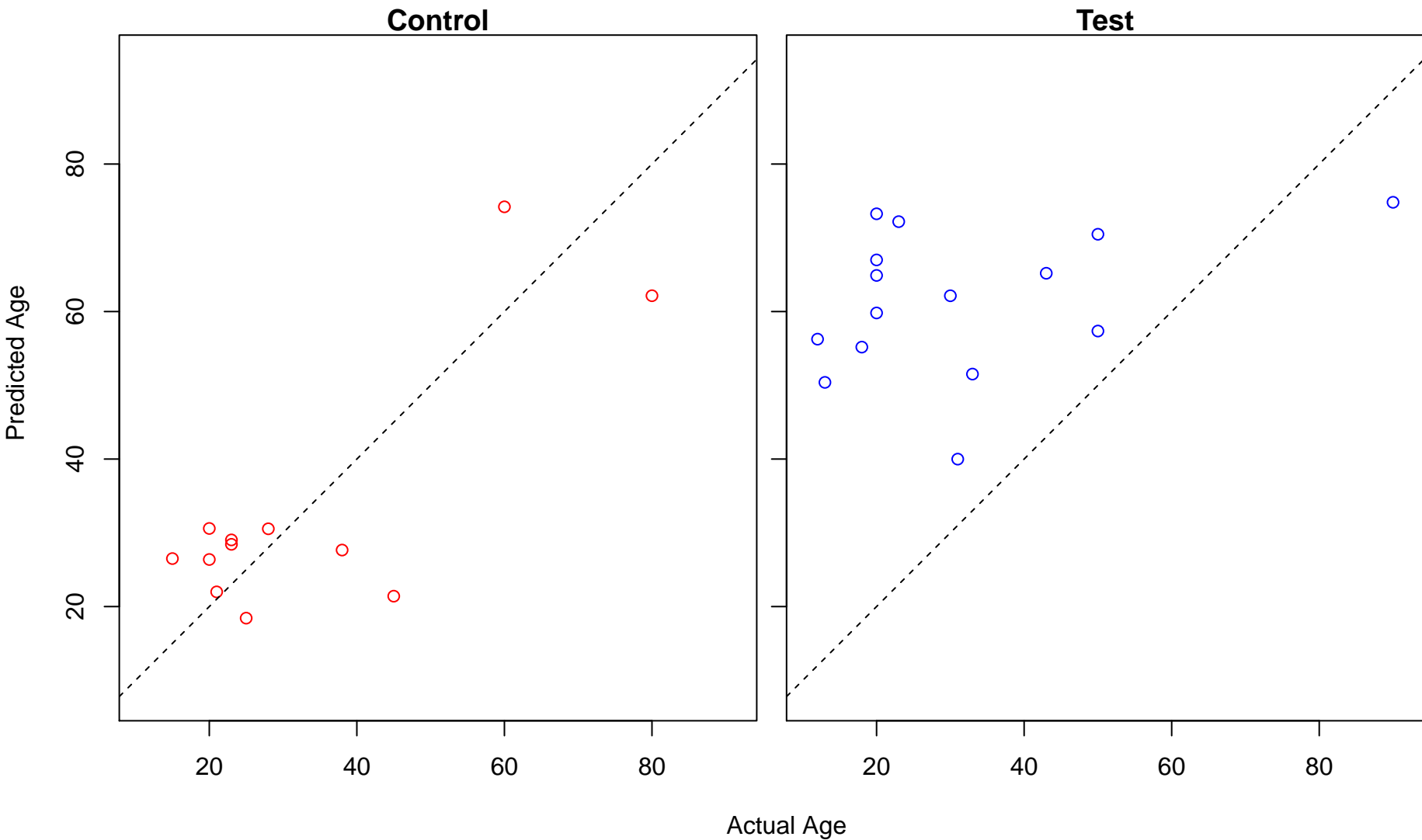
positive regulation of urine volume (Score: 3.482245)



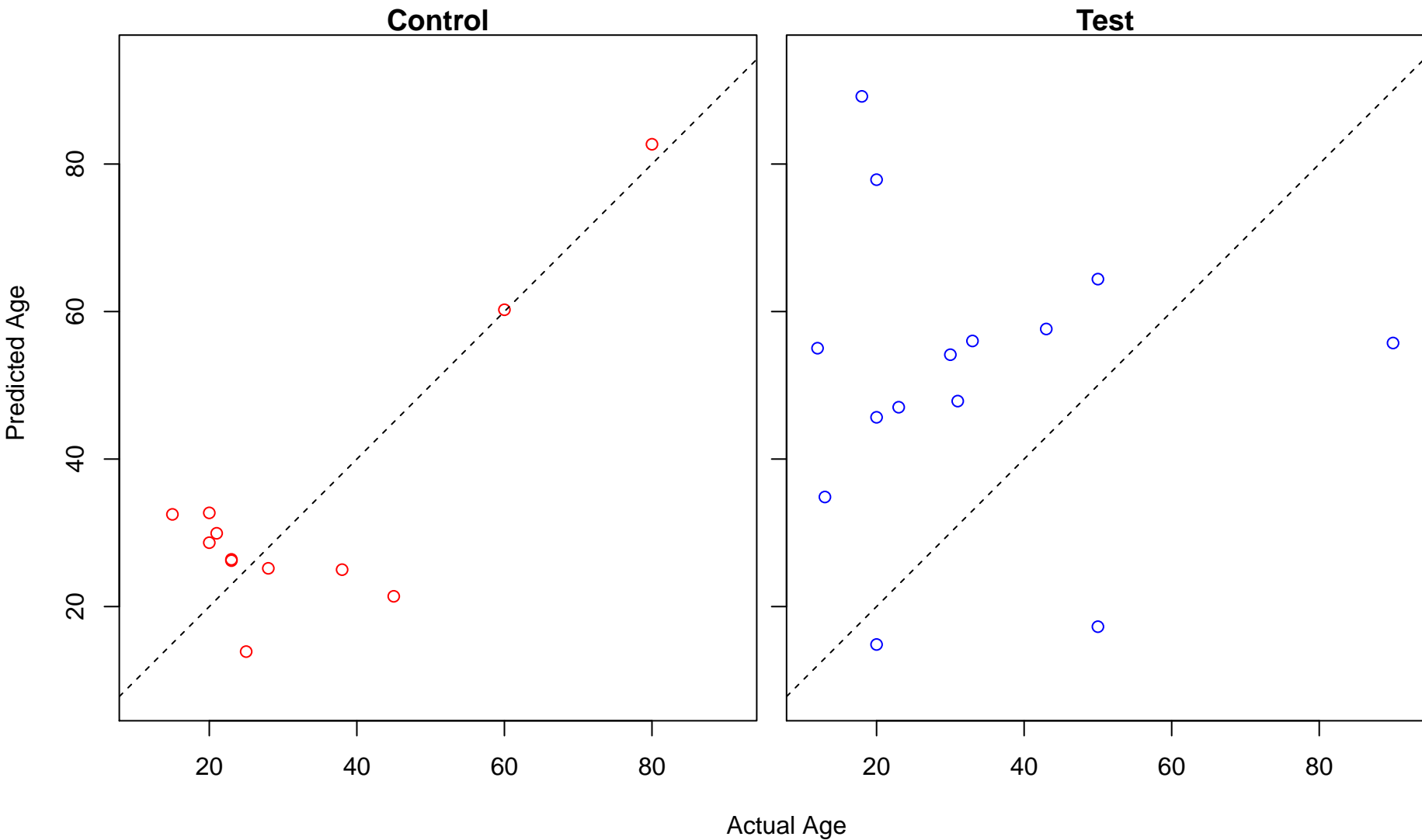
positive regulation of neuron migration (Score: 3.480990)



regulation of inflammatory response (Score: 3.480122)

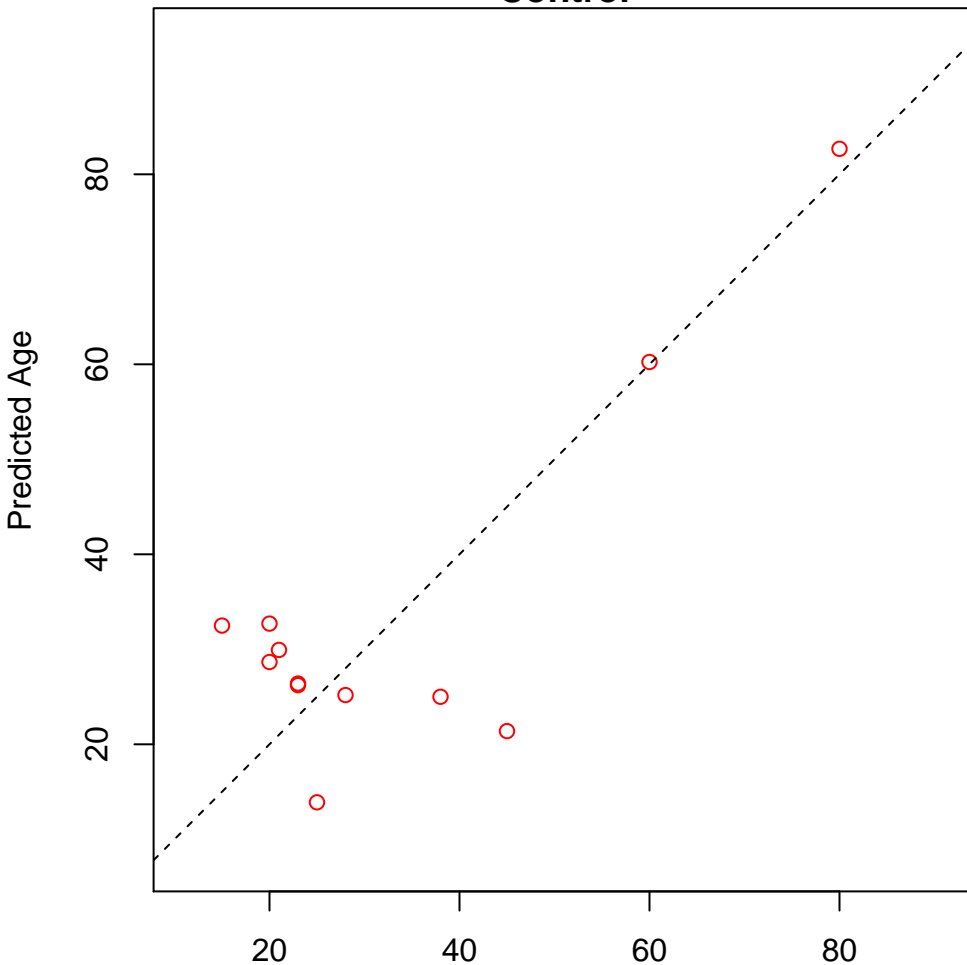


viral budding (Score: 3.480075)

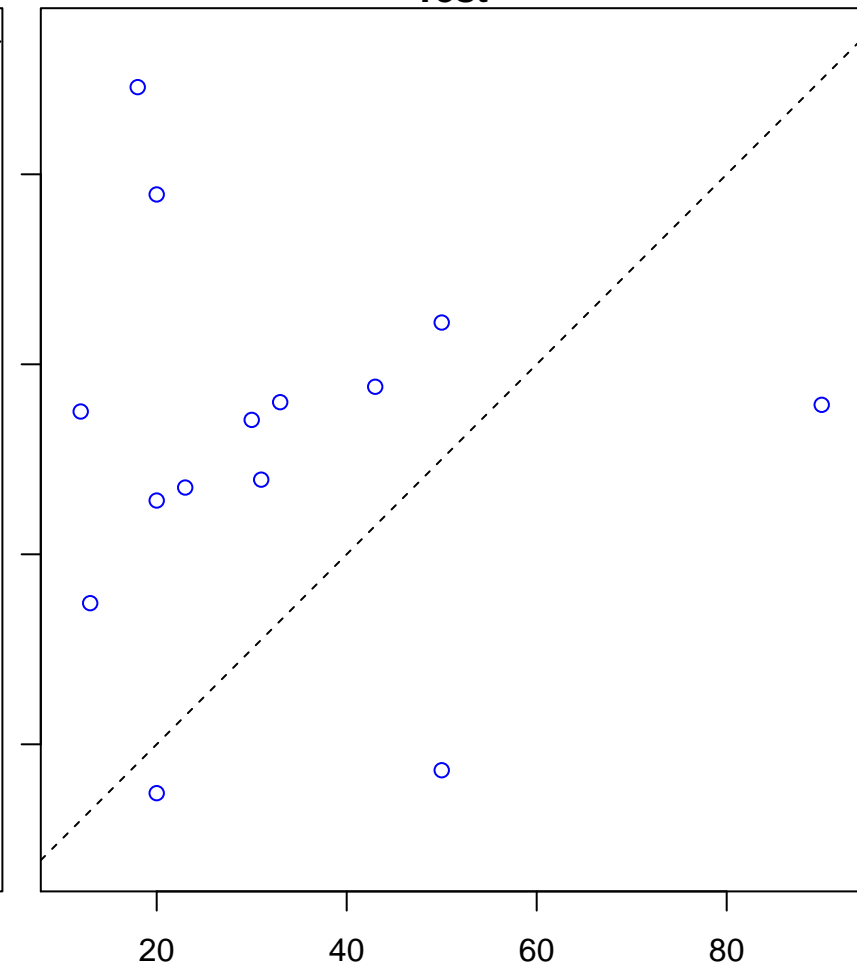


multi-organism organelle organization (Score: 3.480075)

Control

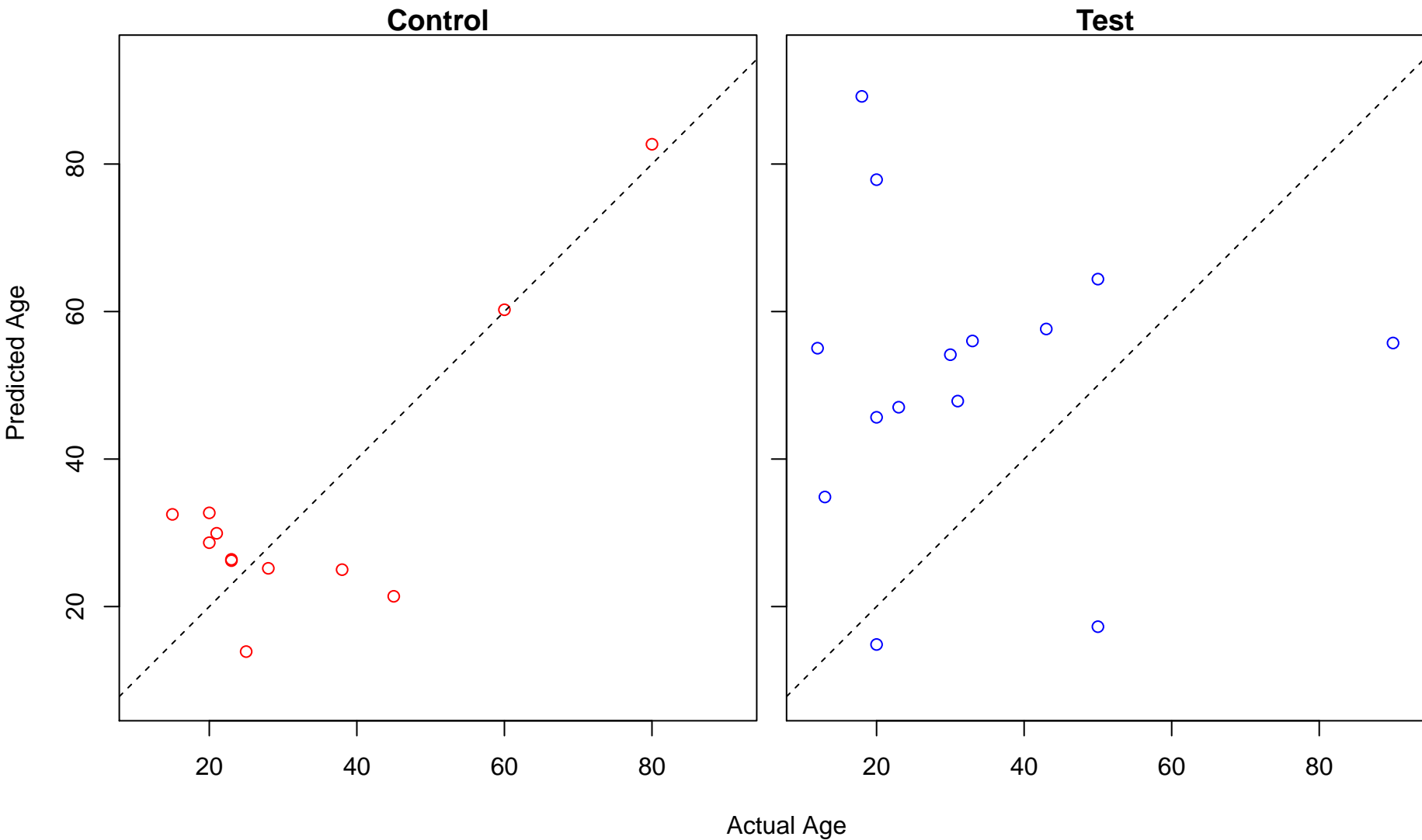


Test

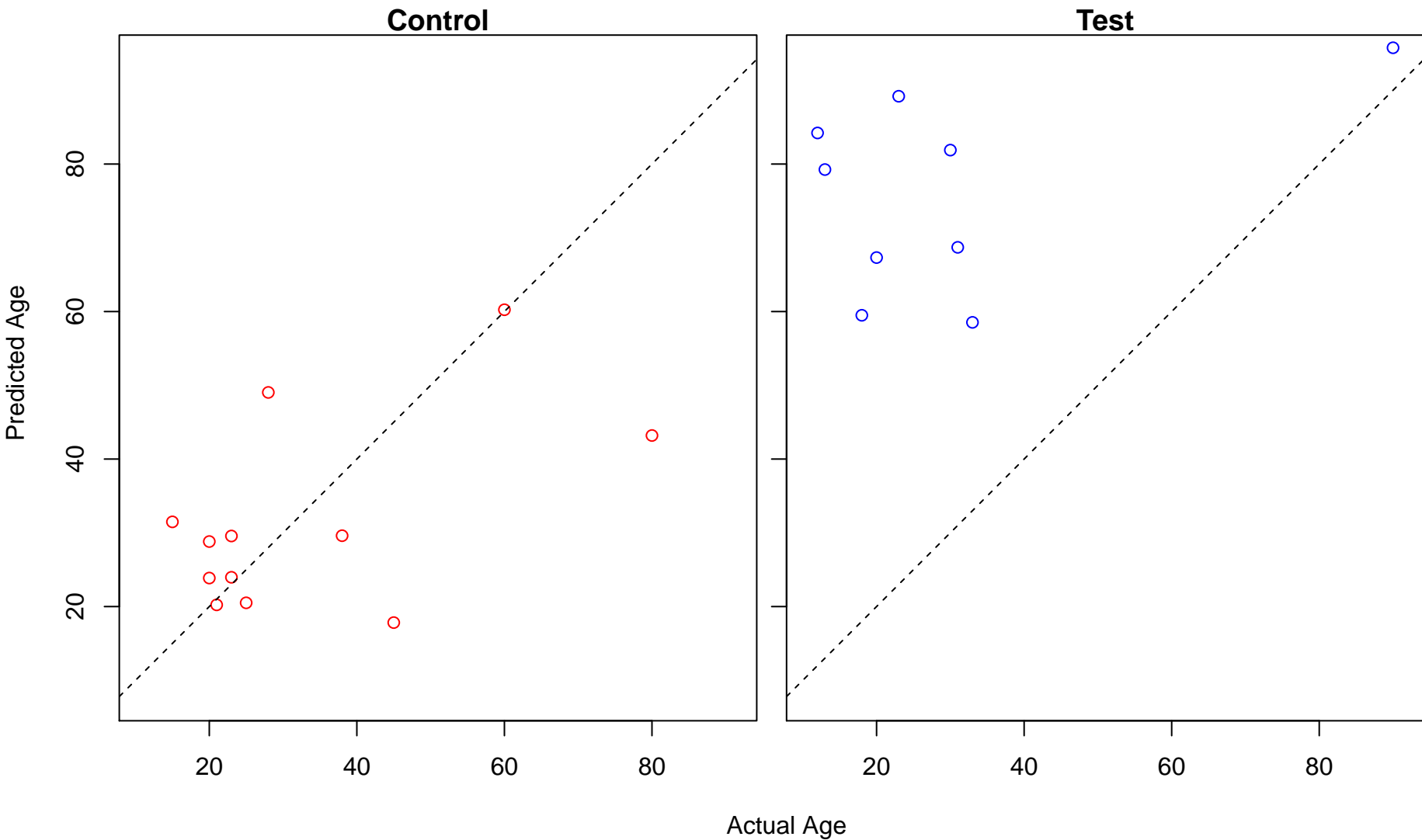


Actual Age

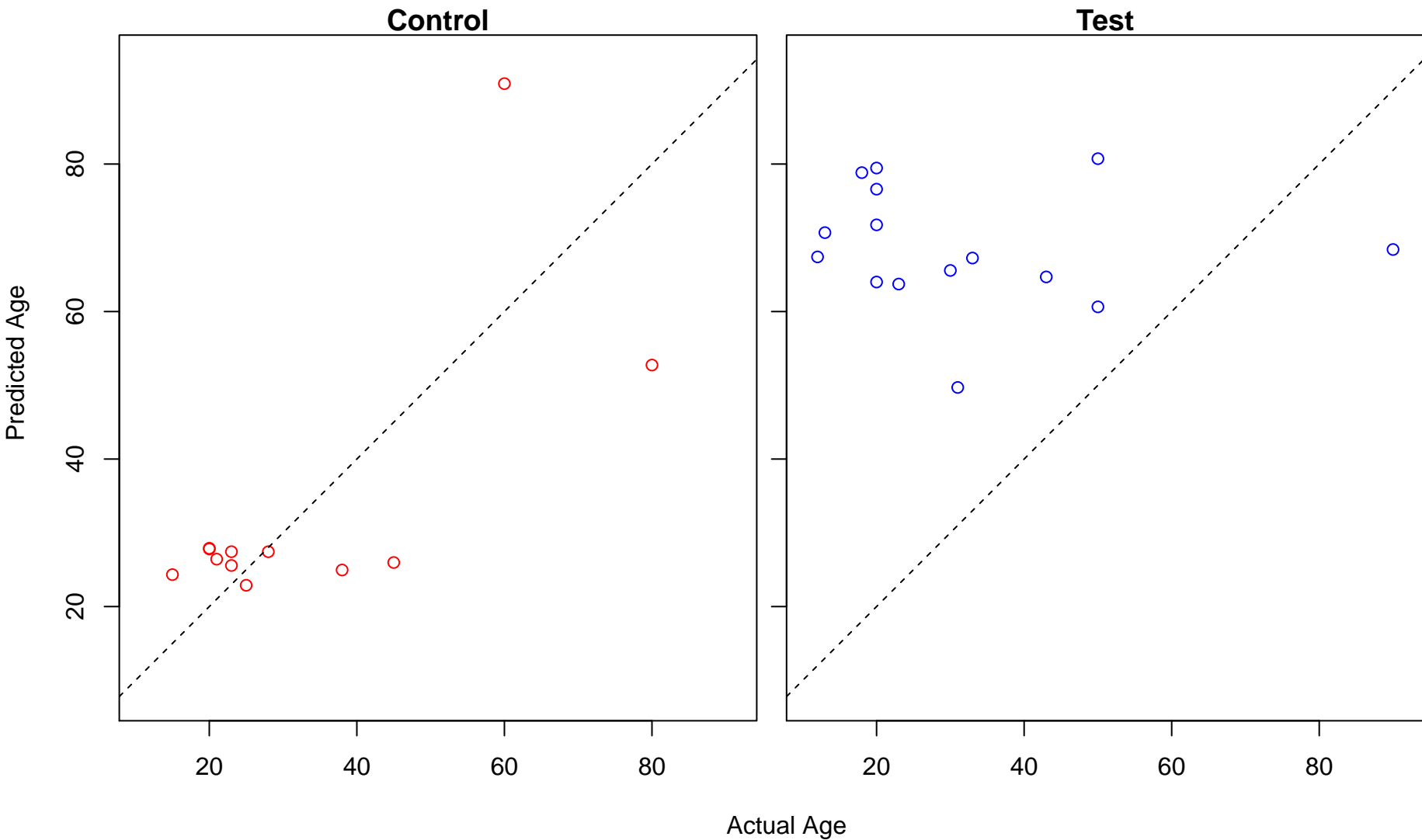
multi-organism membrane budding (Score: 3.480075)



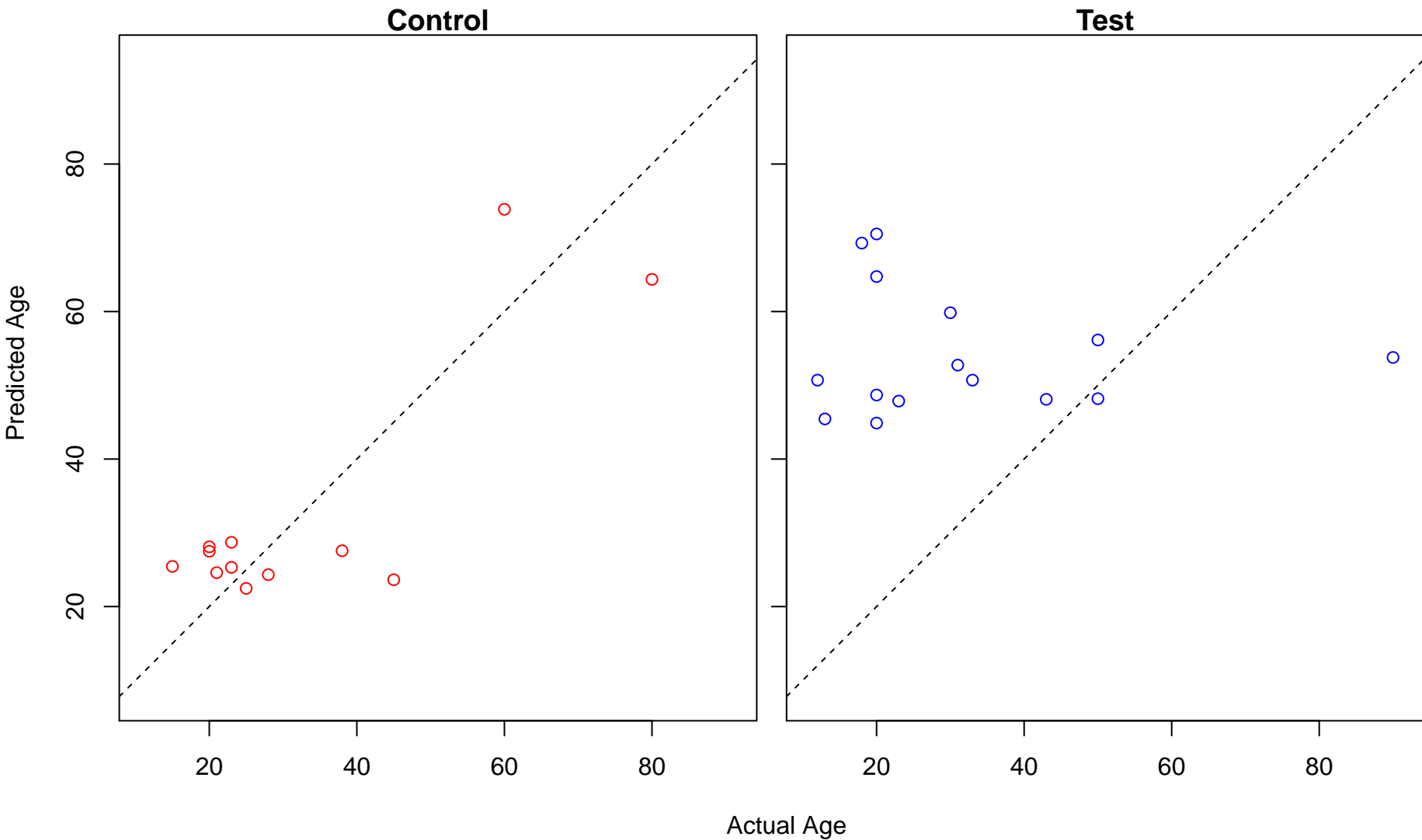
regulation of beta-amyloid clearance (Score: 3.479319)



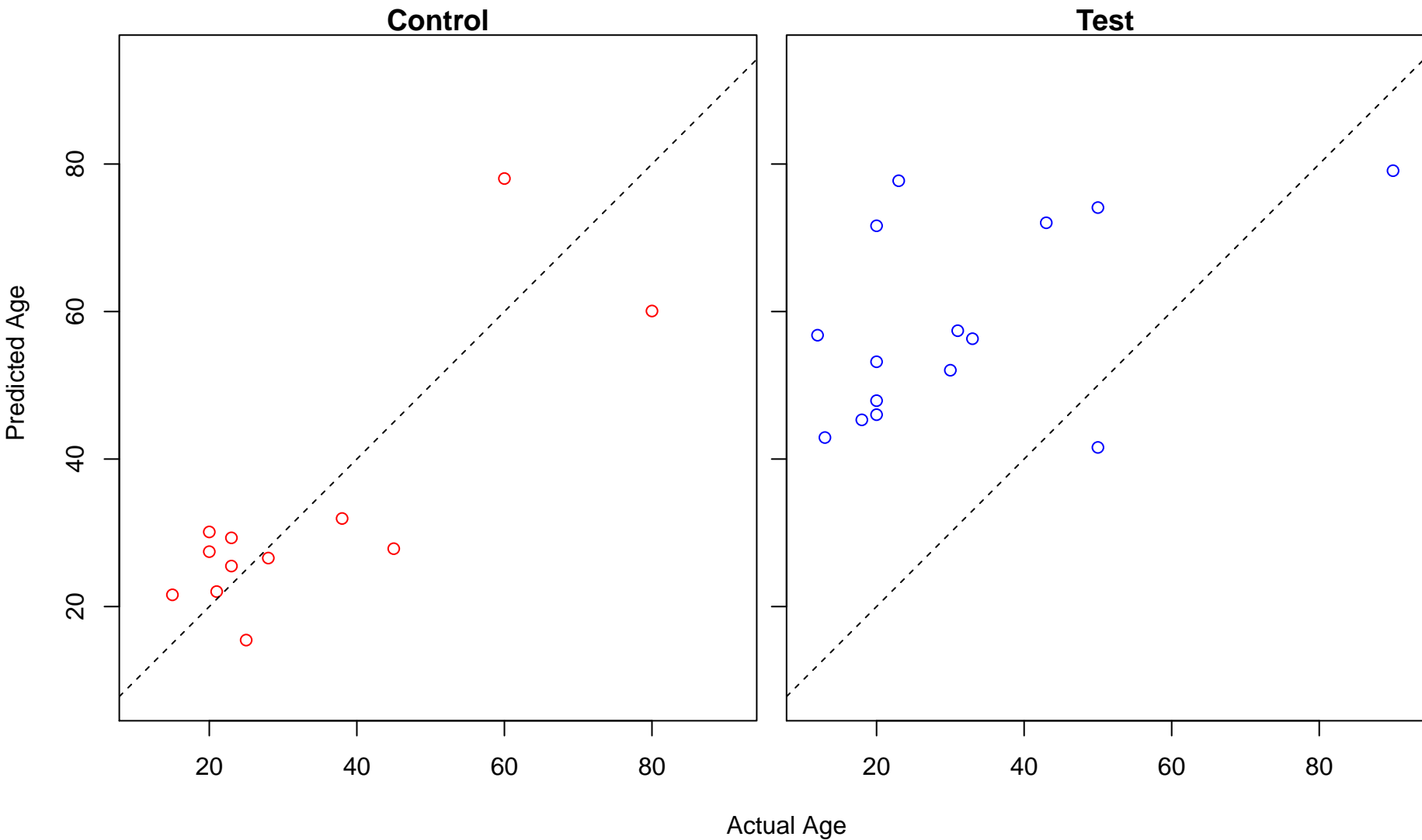
regulation of centriole replication (Score: 3.475009)



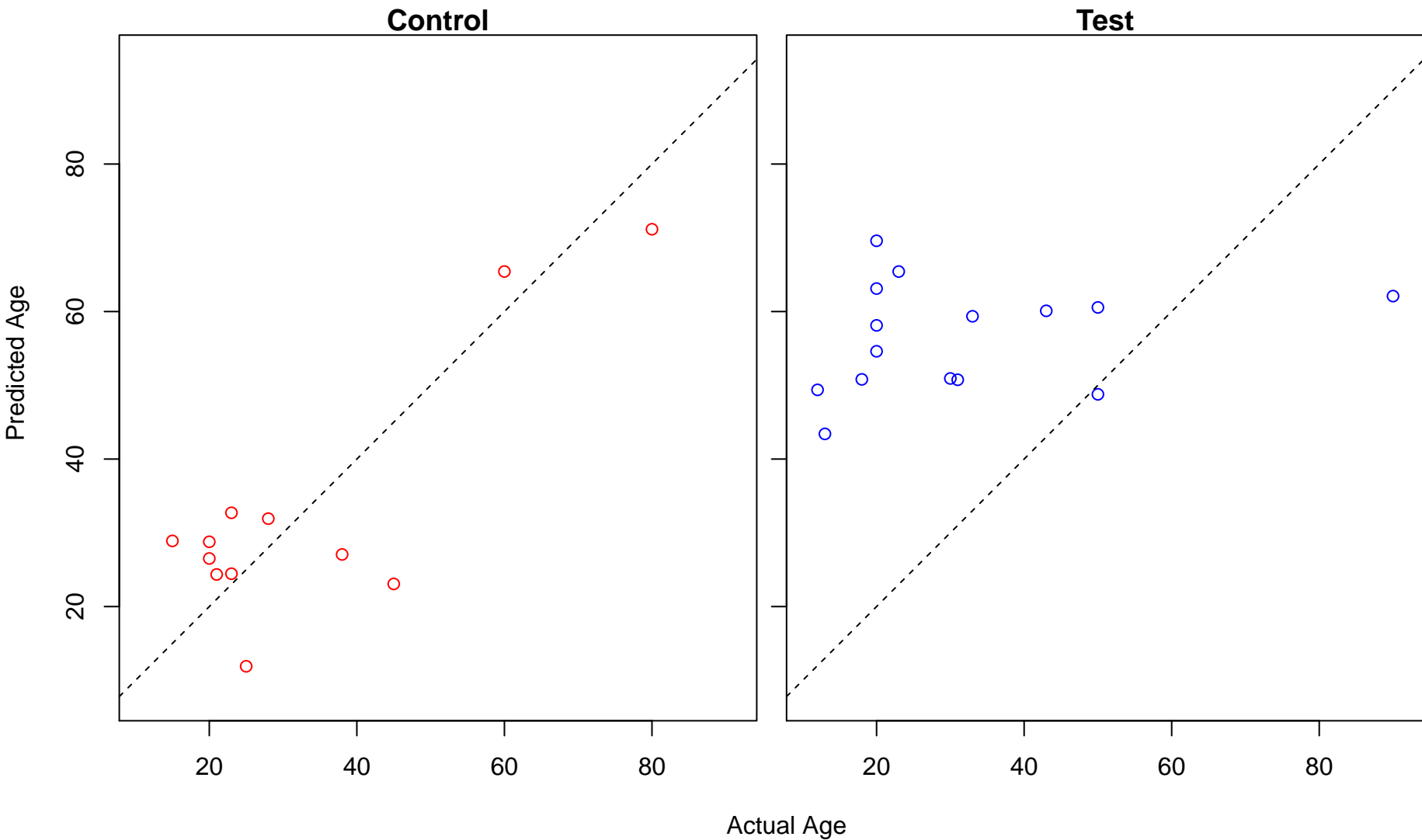
response to topologically incorrect protein (Score: 3.473014)



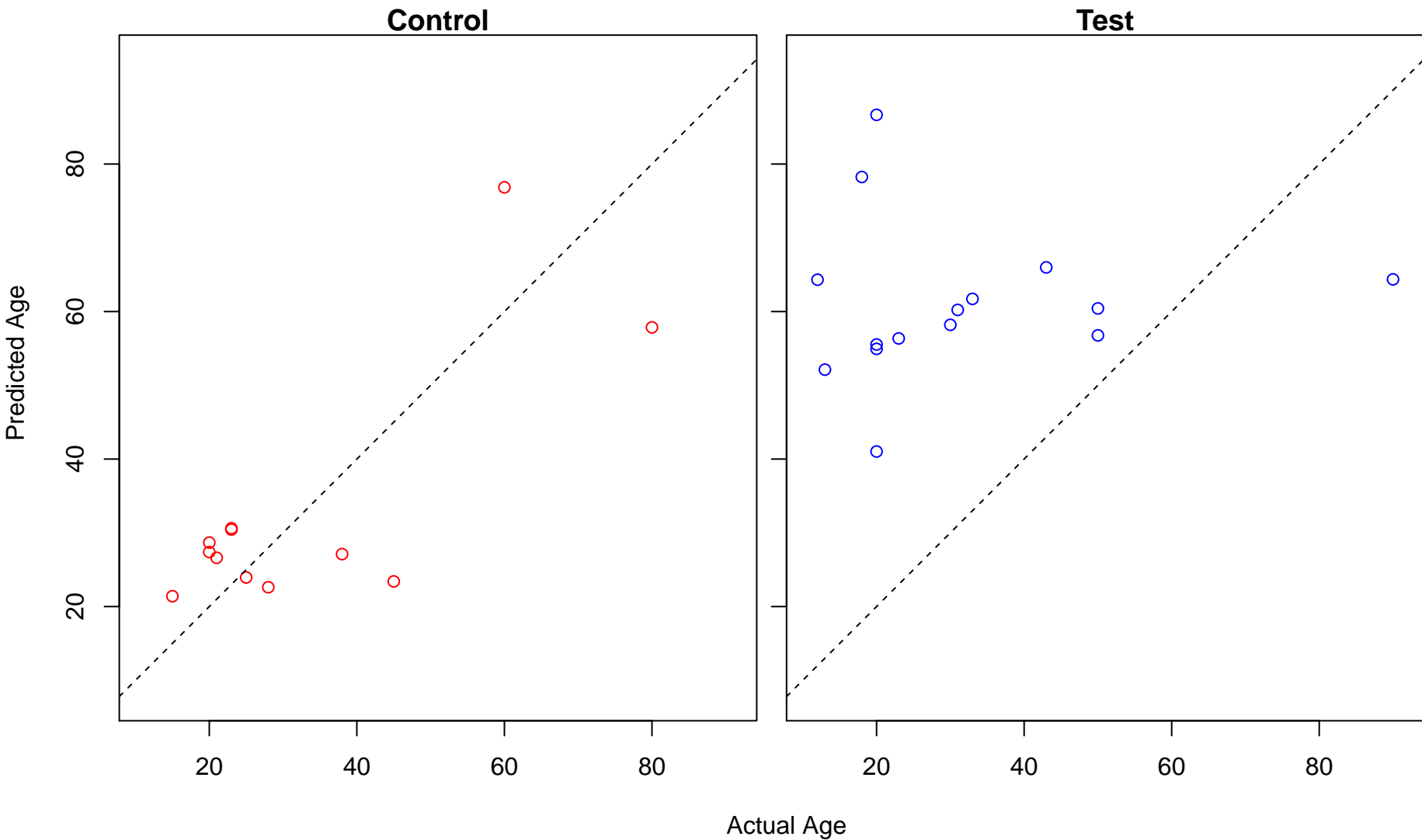
nephric duct development (Score: 3.471612)



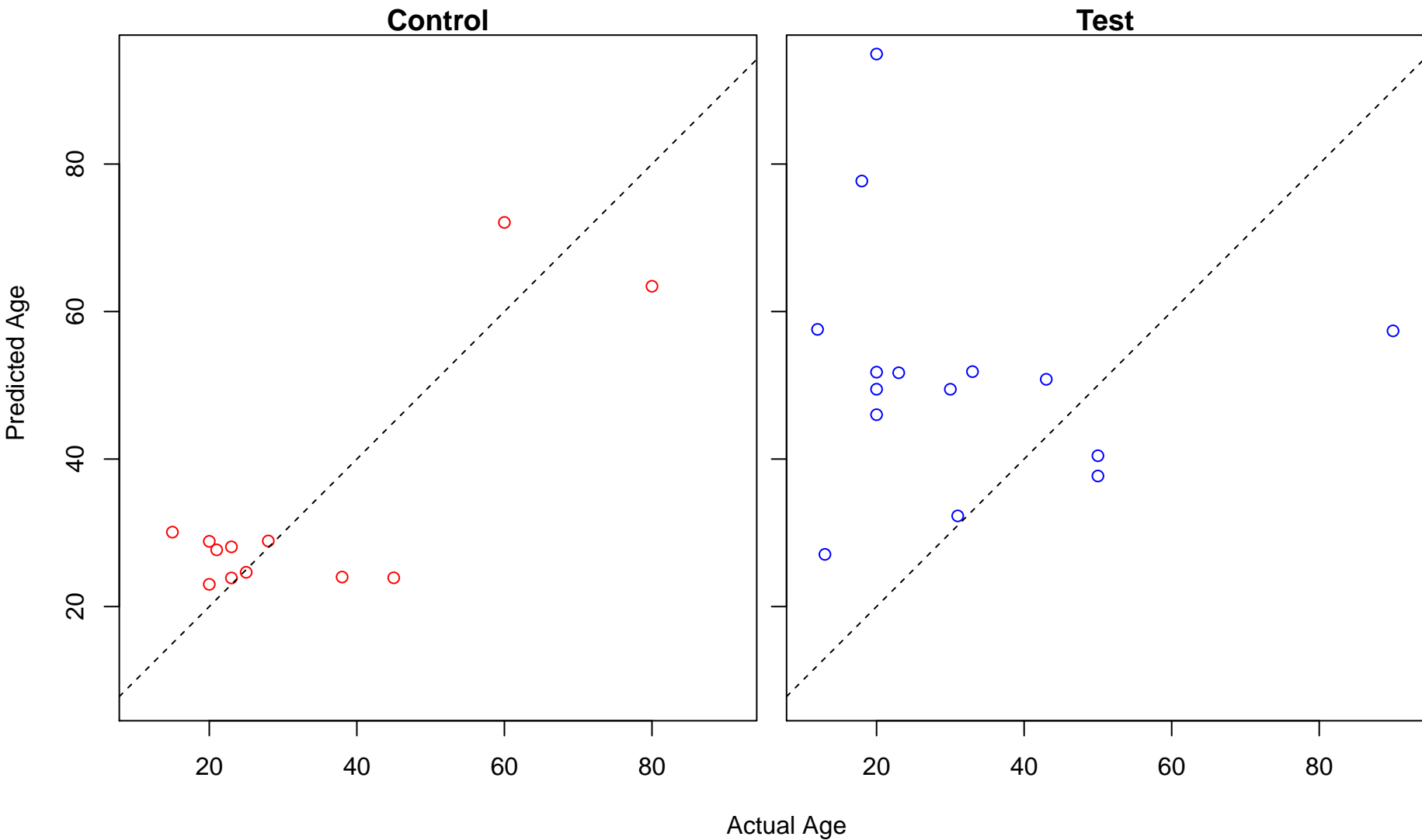
head development (Score: 3.470407)



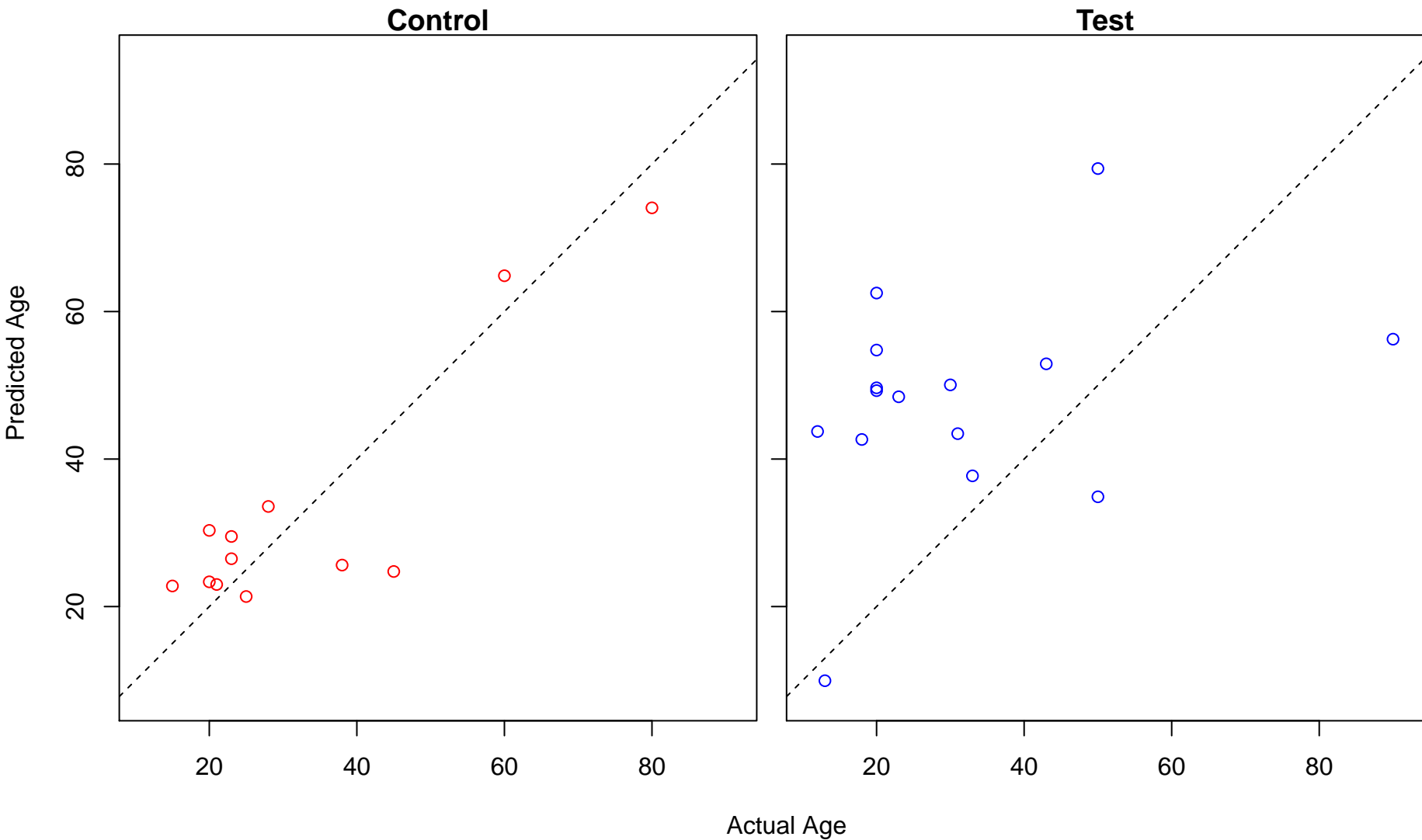
positive regulation of T cell migration (Score: 3.469748)



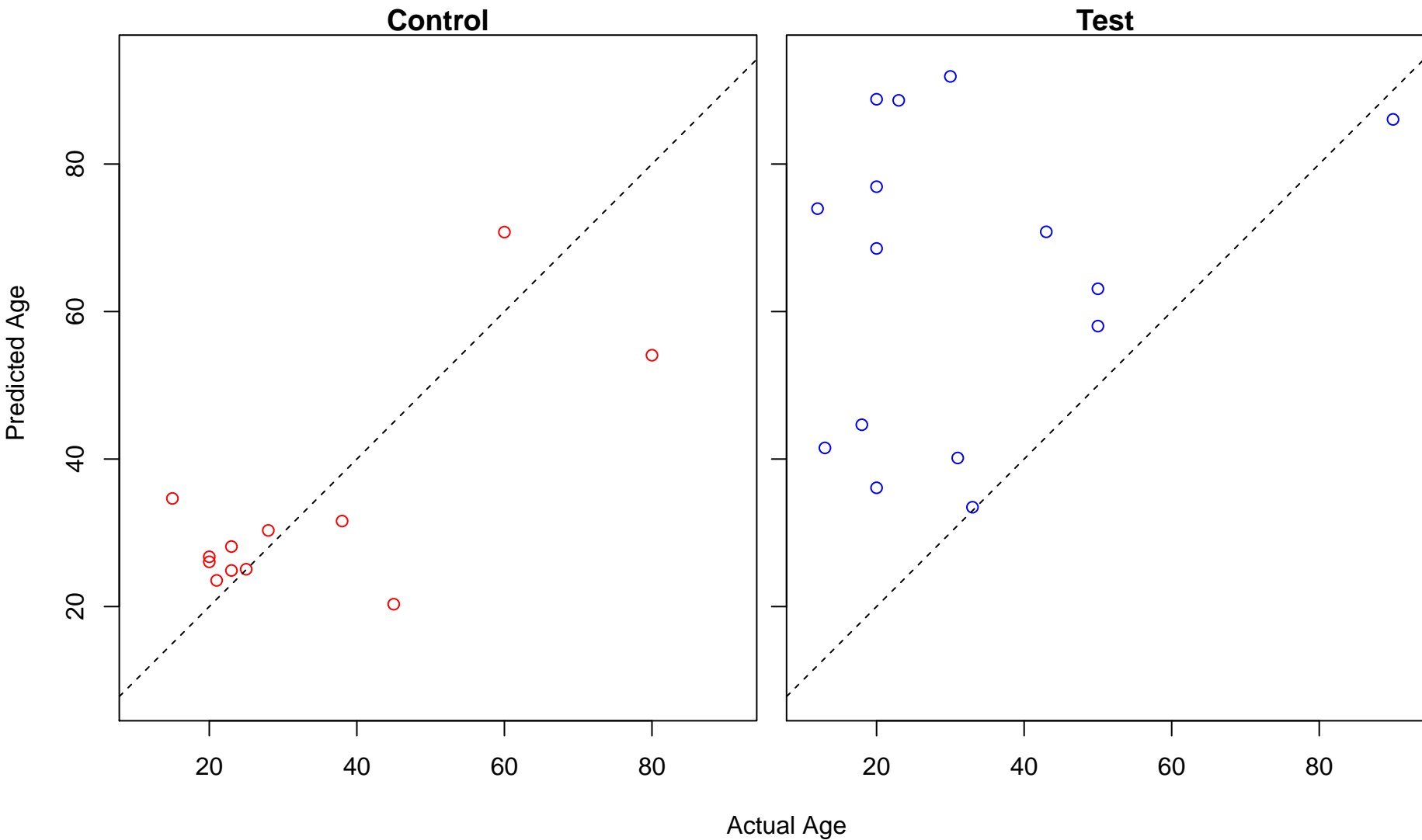
protein K29-linked ubiquitination (Score: 3.468383)



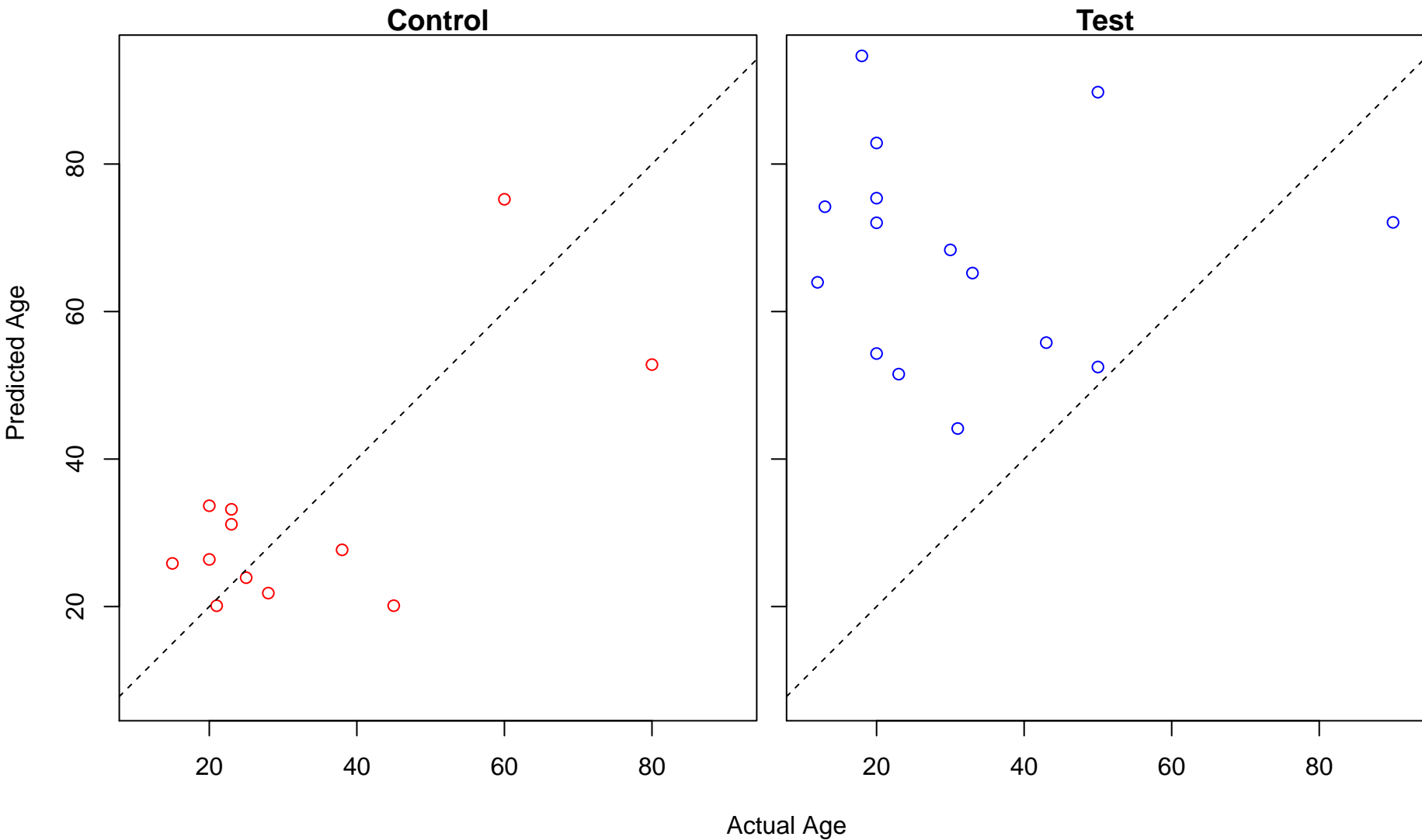
polyol biosynthetic process (Score: 3.467318)



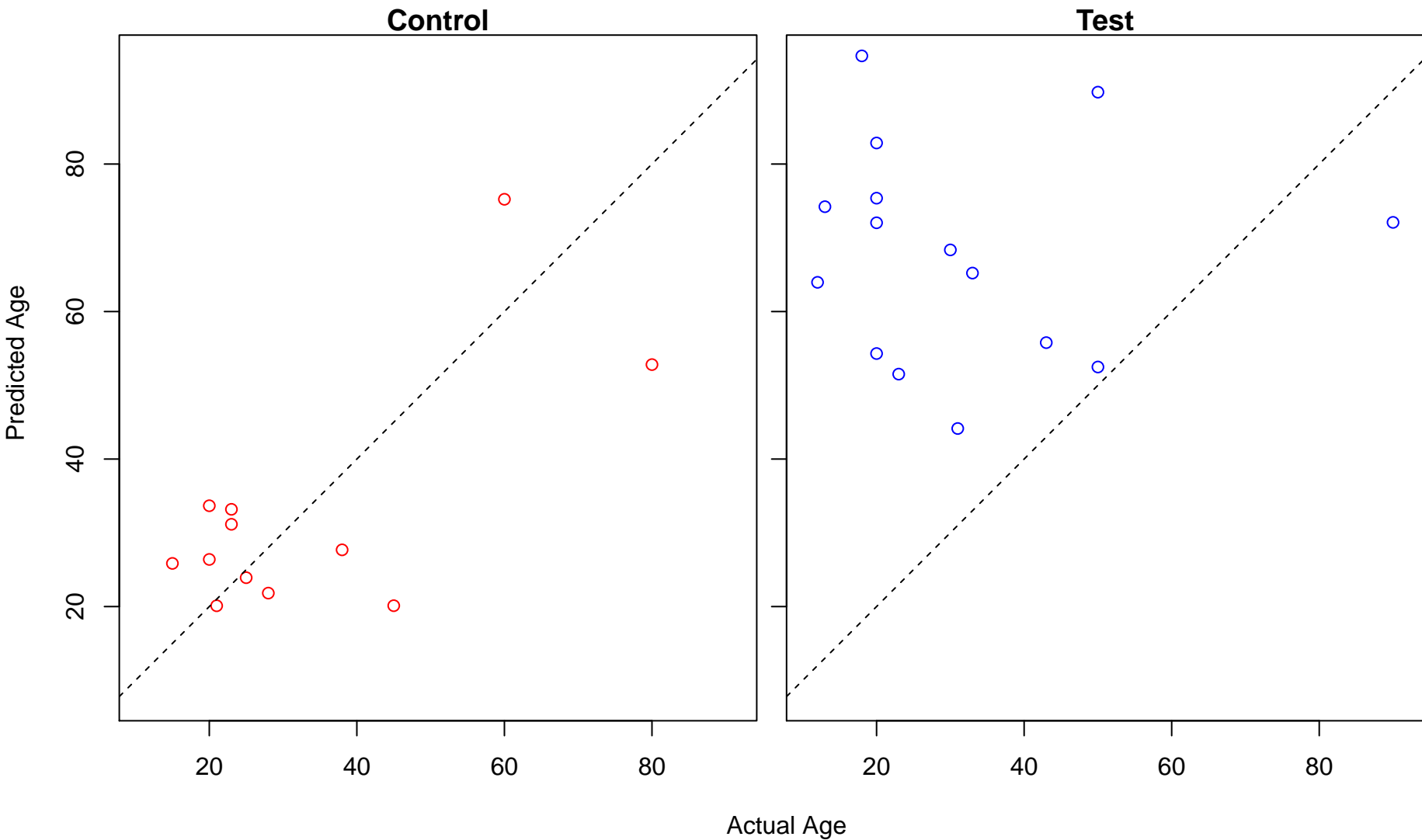
middle ear morphogenesis (Score: 3.463107)



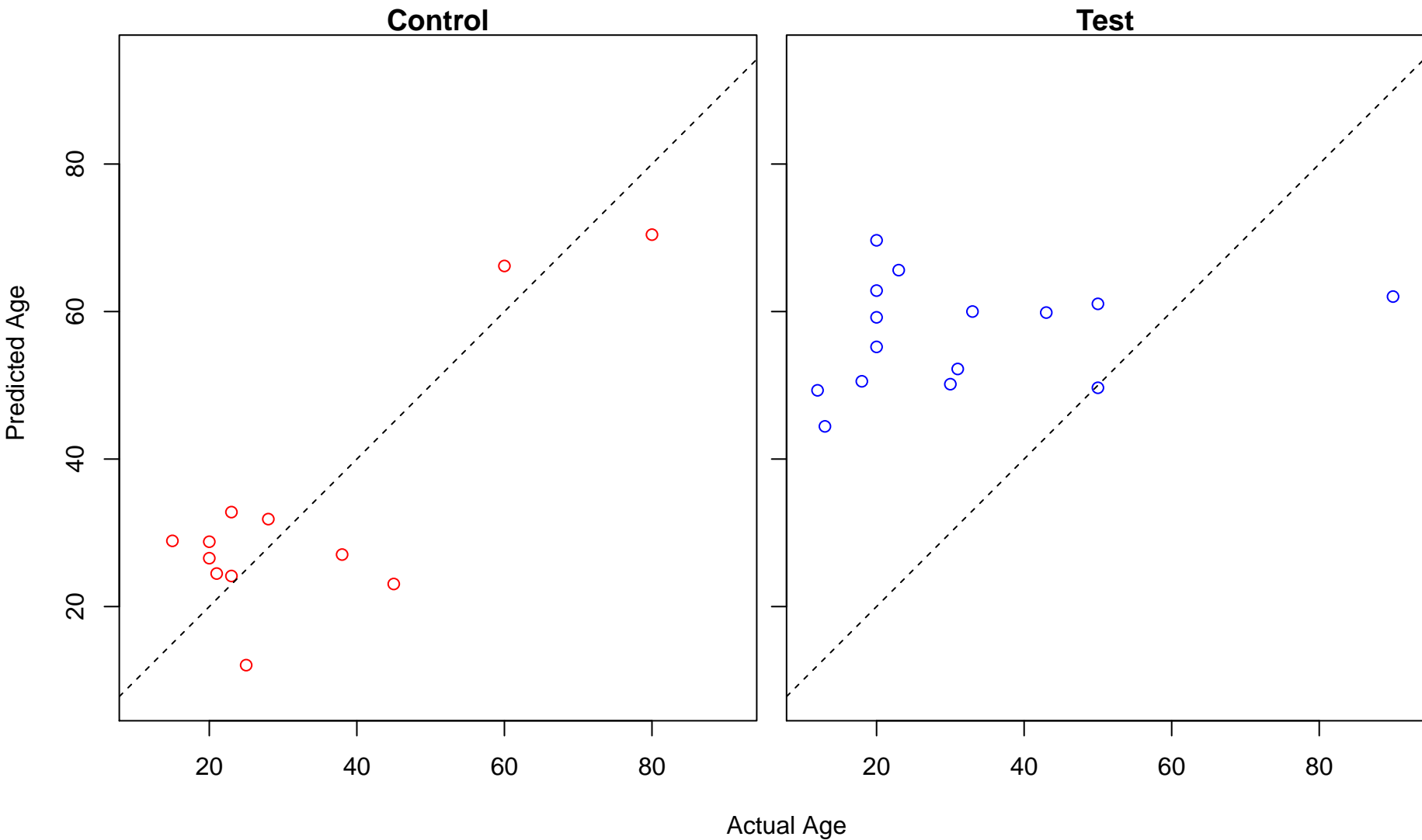
pulmonary valve development (Score: 3.461302)



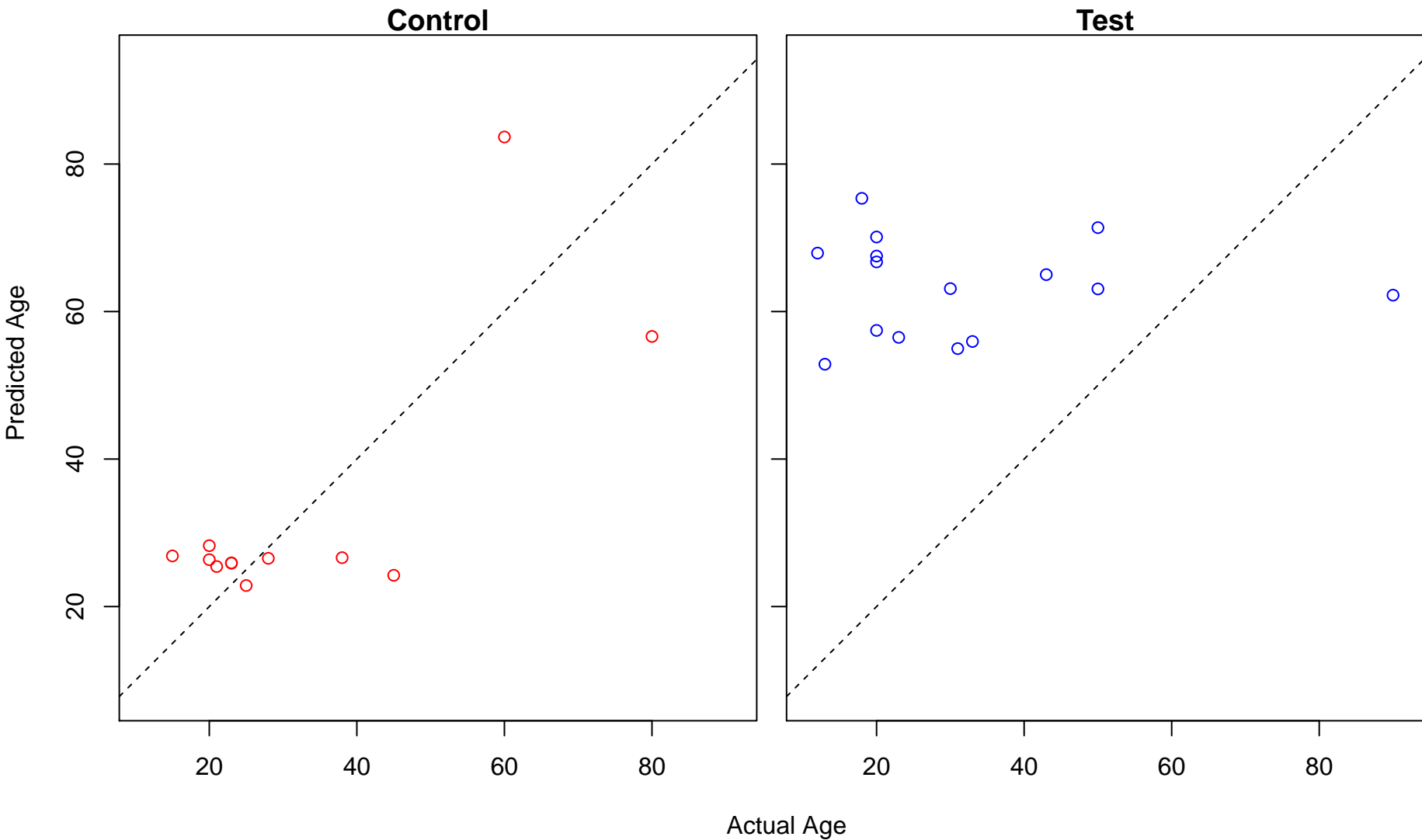
pulmonary valve morphogenesis (Score: 3.461302)



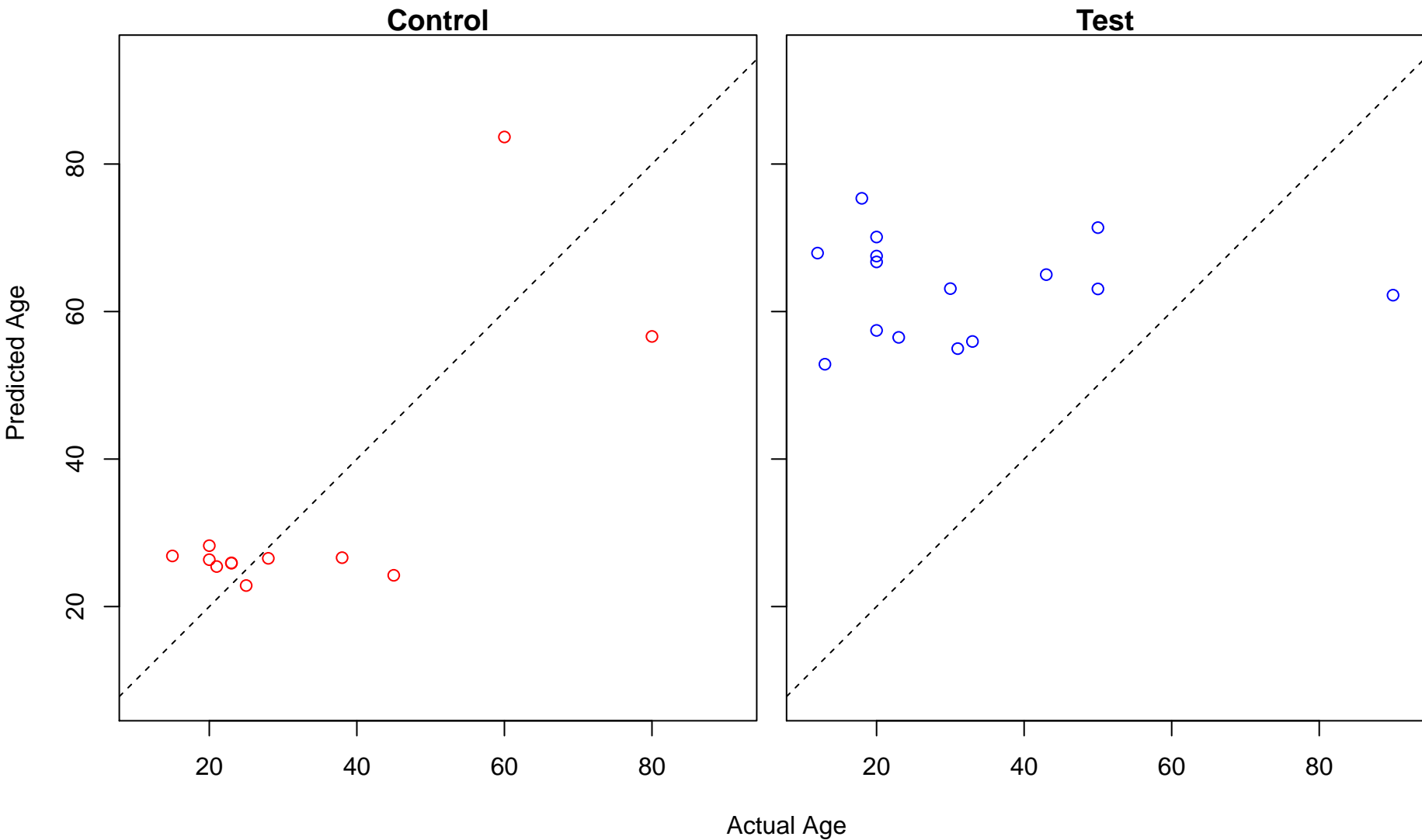
brain development (Score: 3.459077)



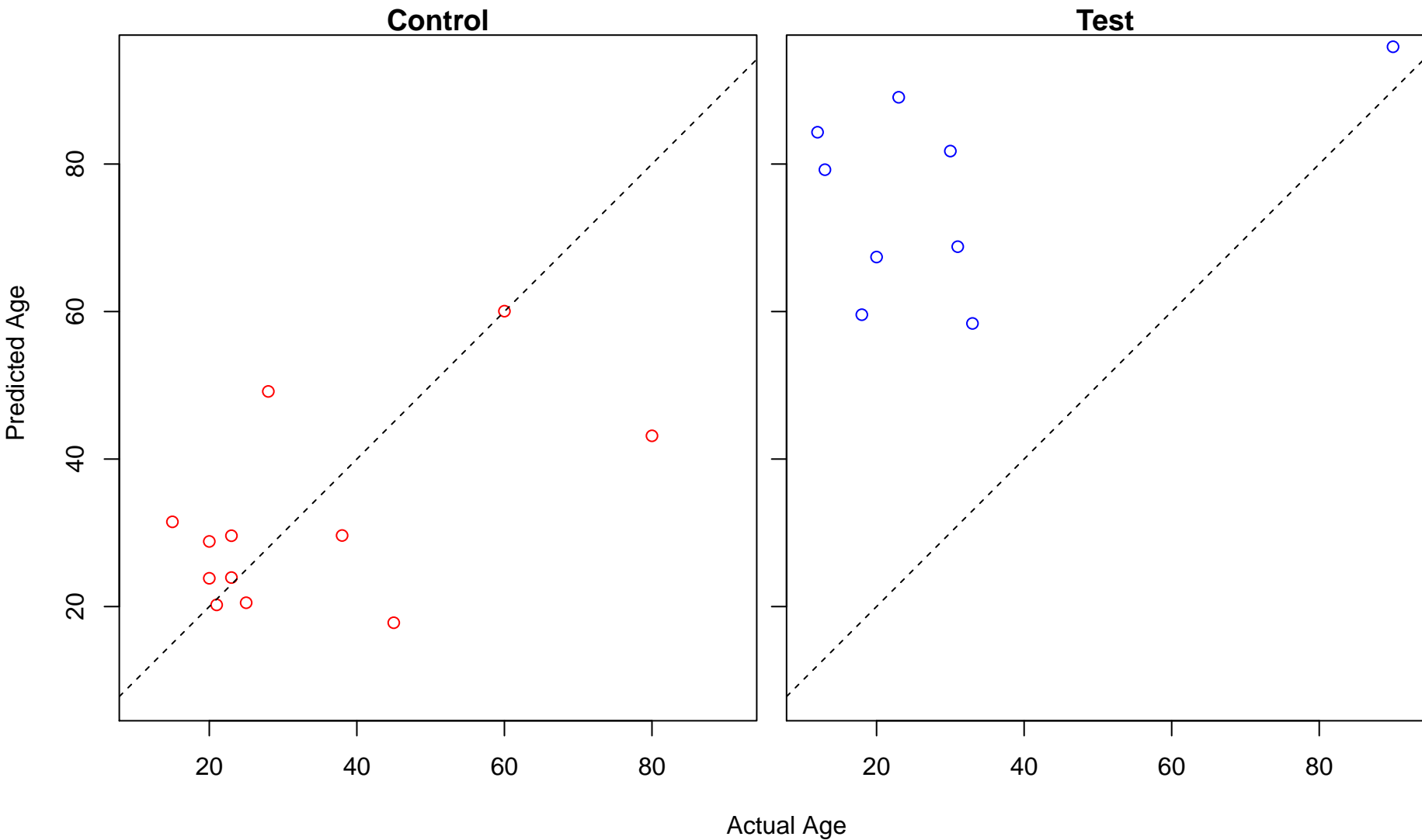
uronic acid metabolic process (Score: 3.455480)



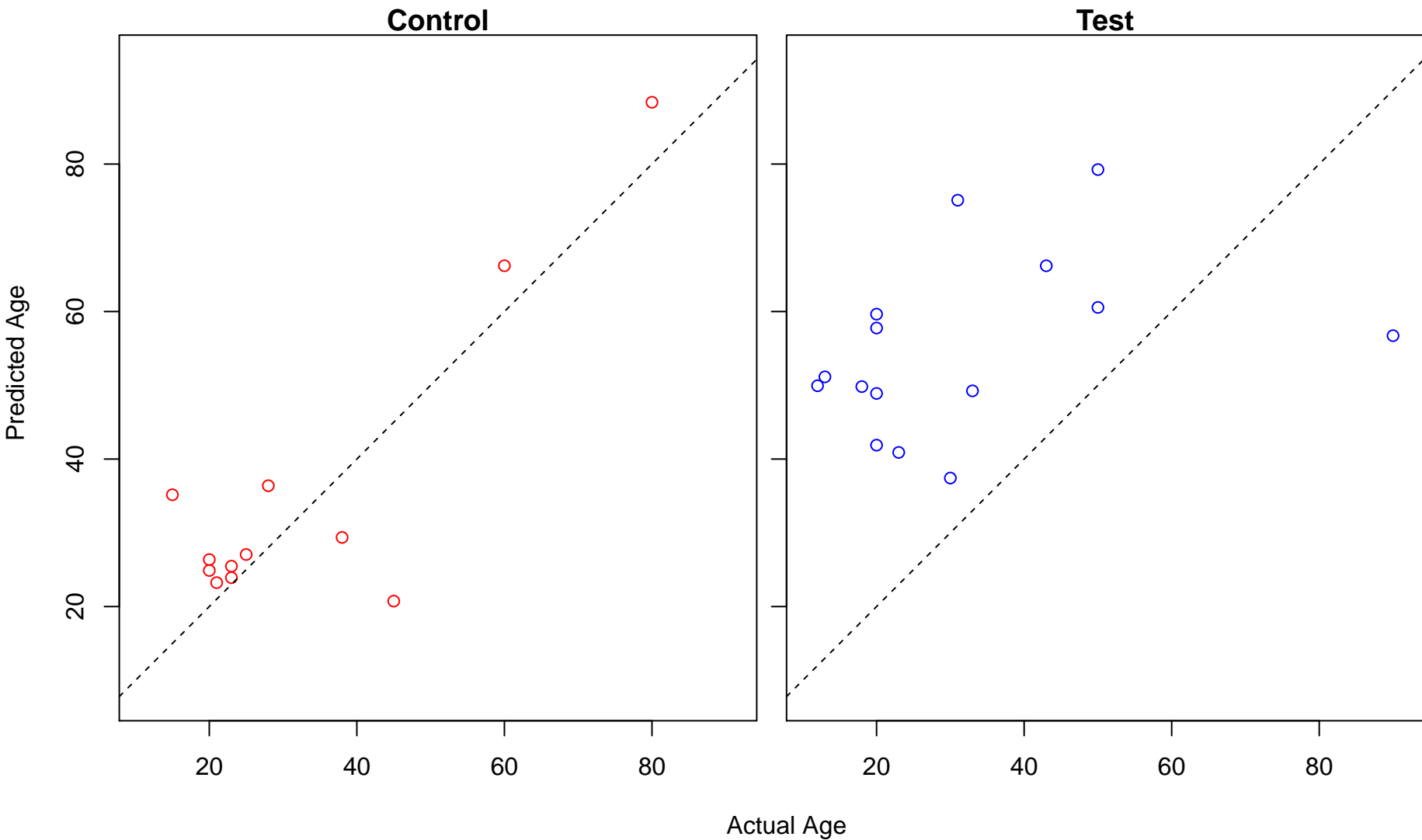
glucuronate metabolic process (Score: 3.455480)



reverse cholesterol transport (Score: 3.454482)

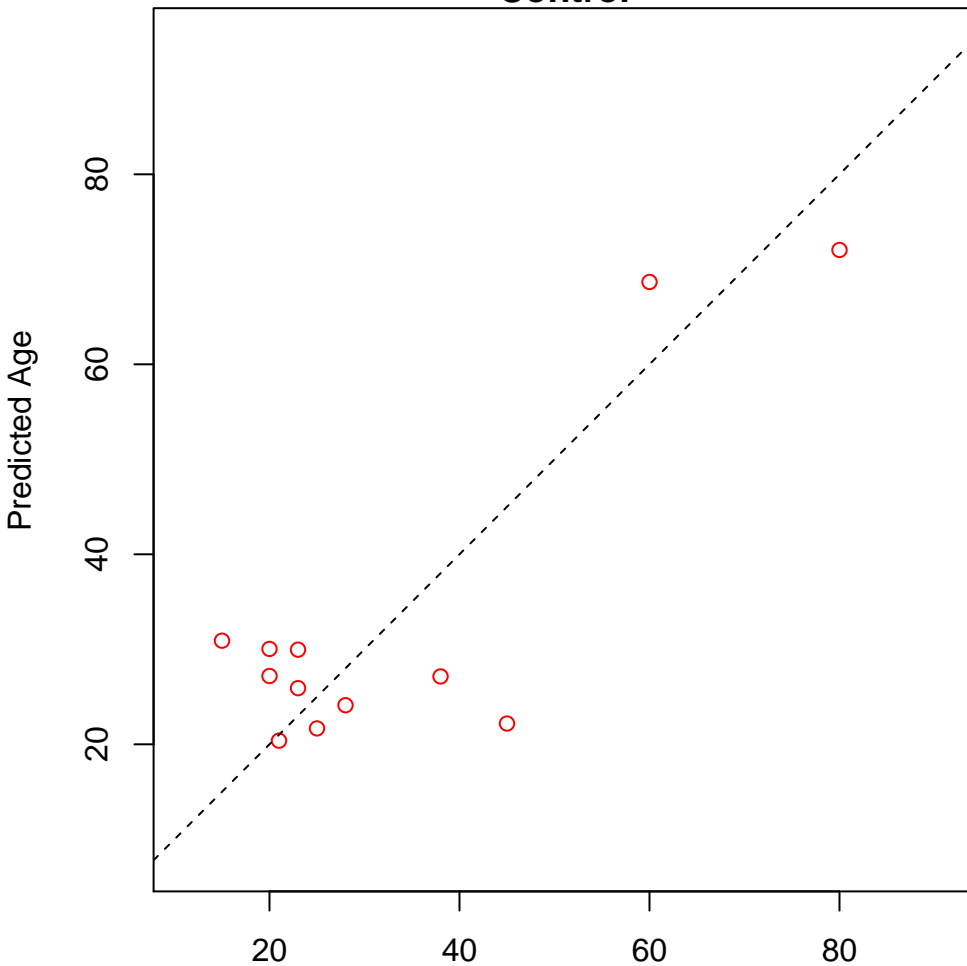


renal system process involved in regulation of systemic arterial blood pressure (Score: 3.451673)

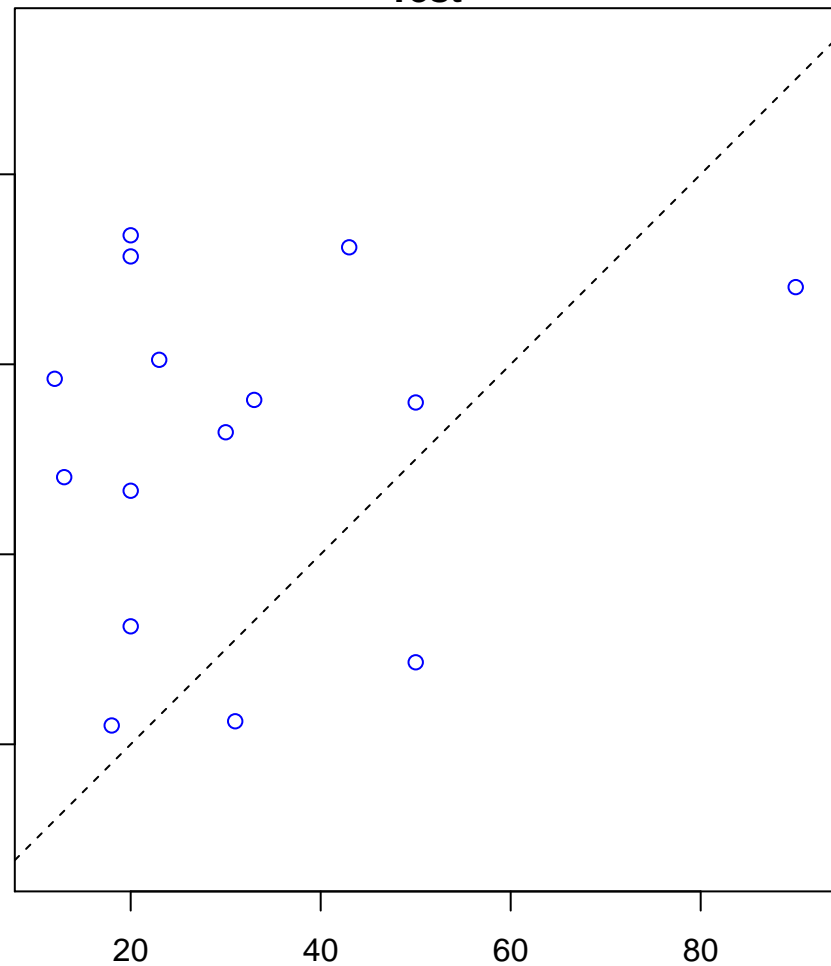


protein targeting to plasma membrane (Score: 3.450888)

Control

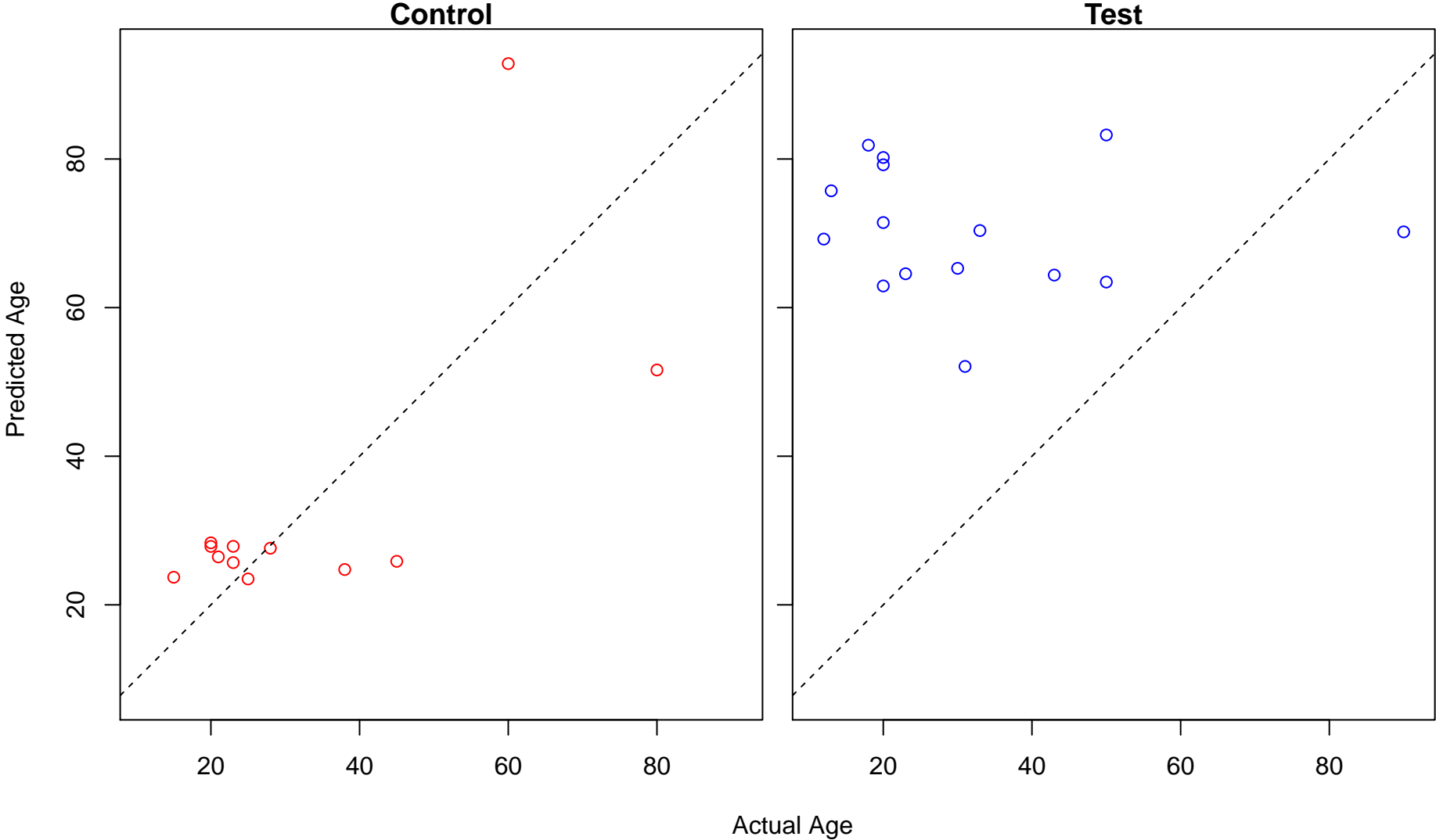


Test

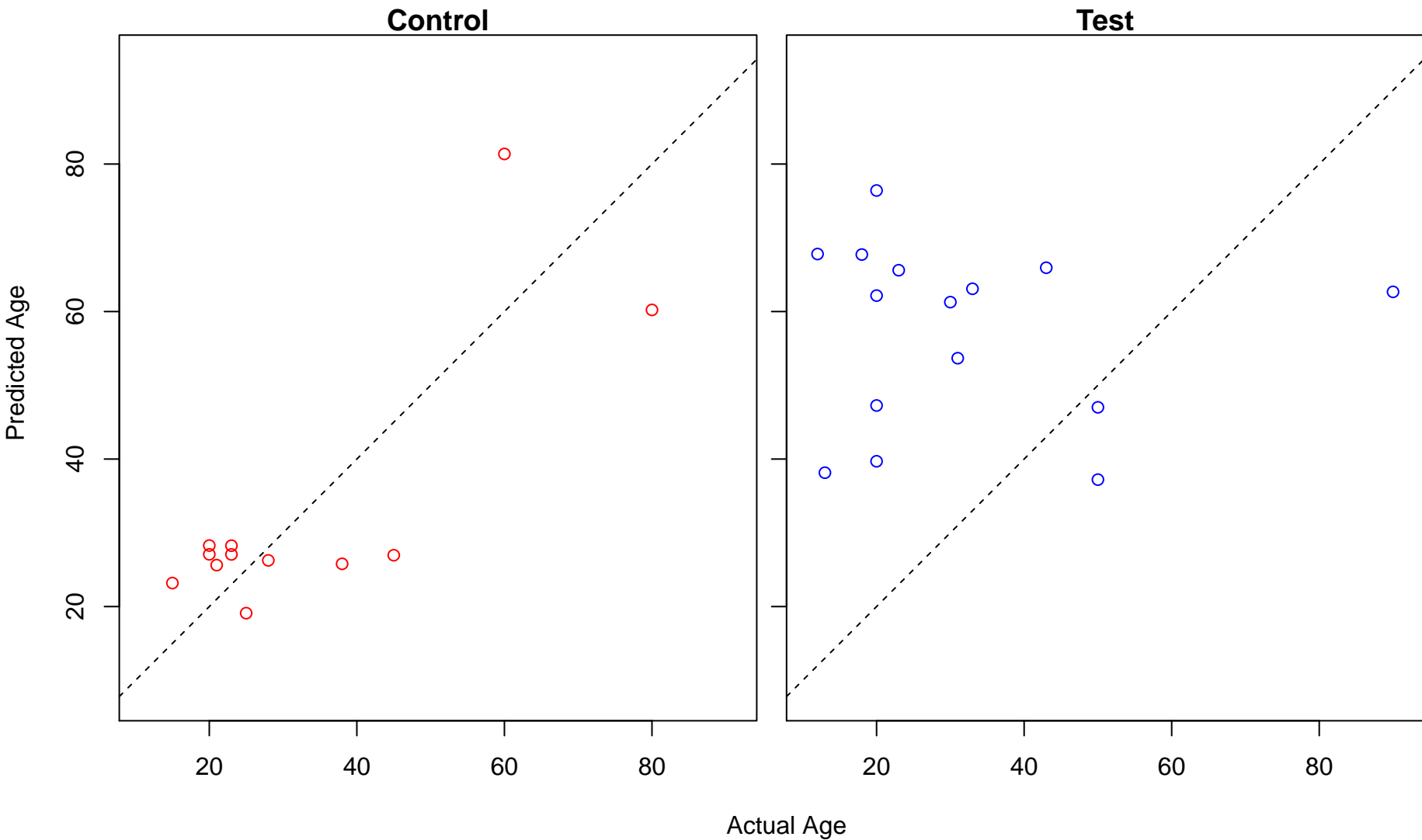


Actual Age

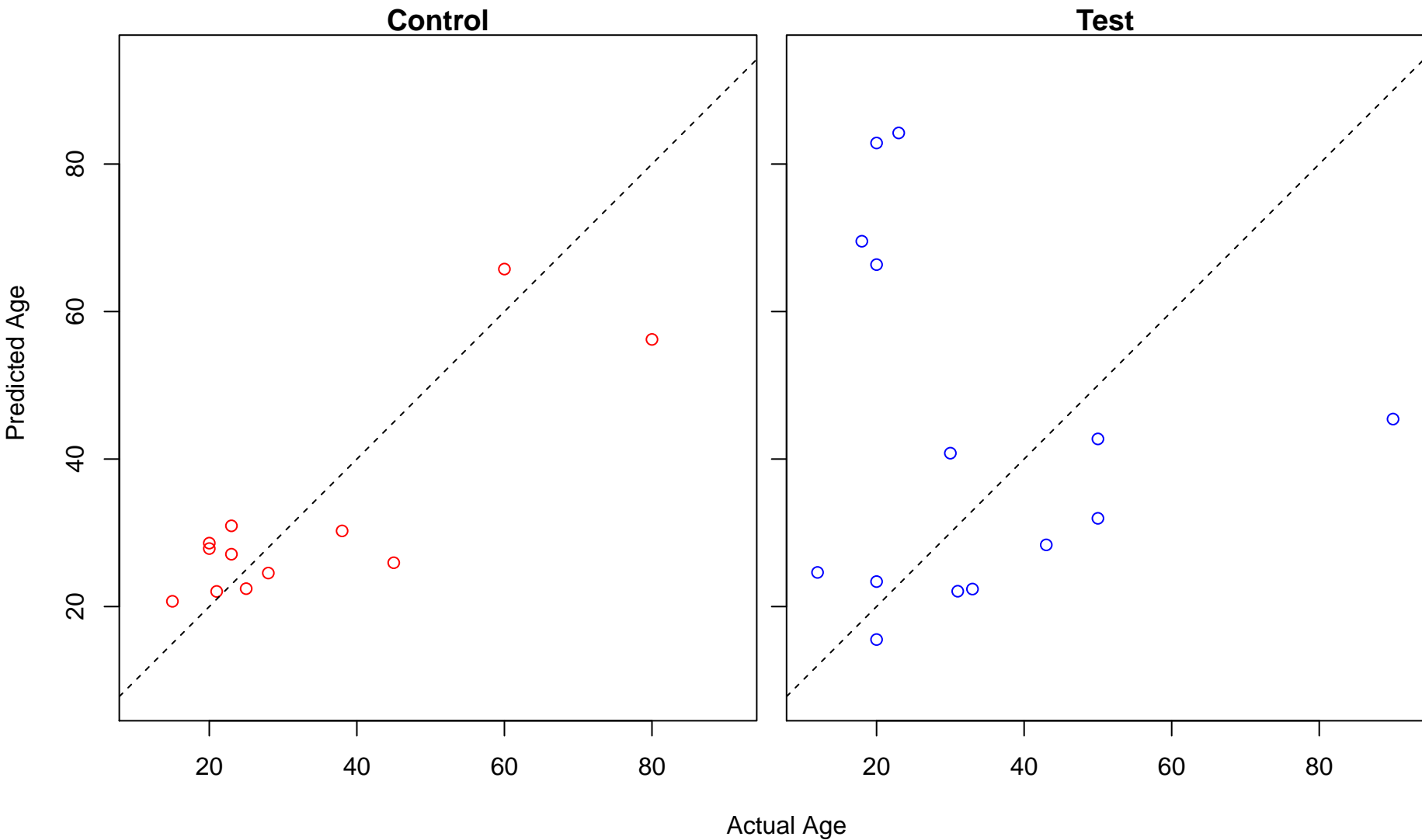
negative regulation of protein kinase activity by regulation of protein phosphorylation (Score: 3.4499)



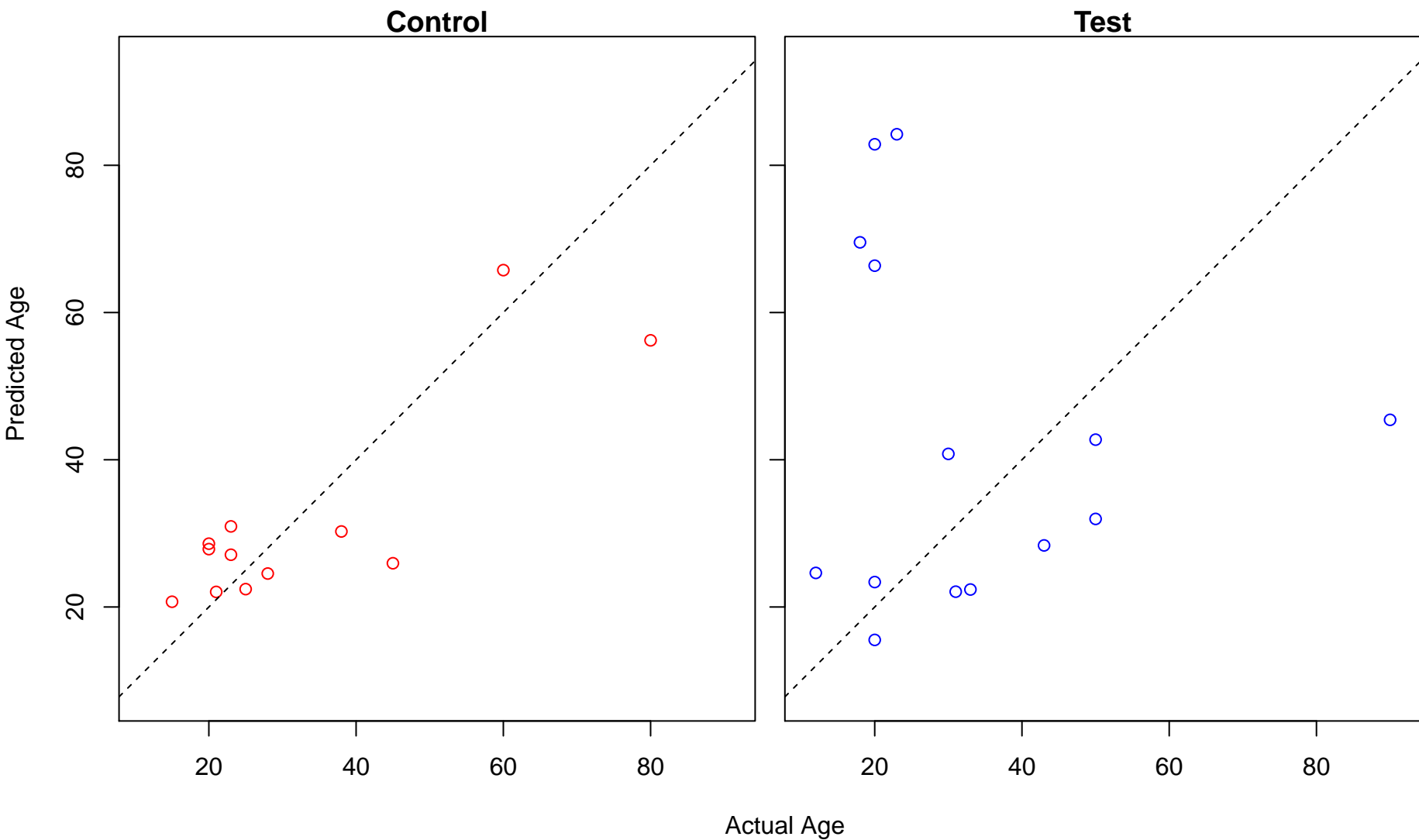
protein K27-linked ubiquitination (Score: 3.445528)



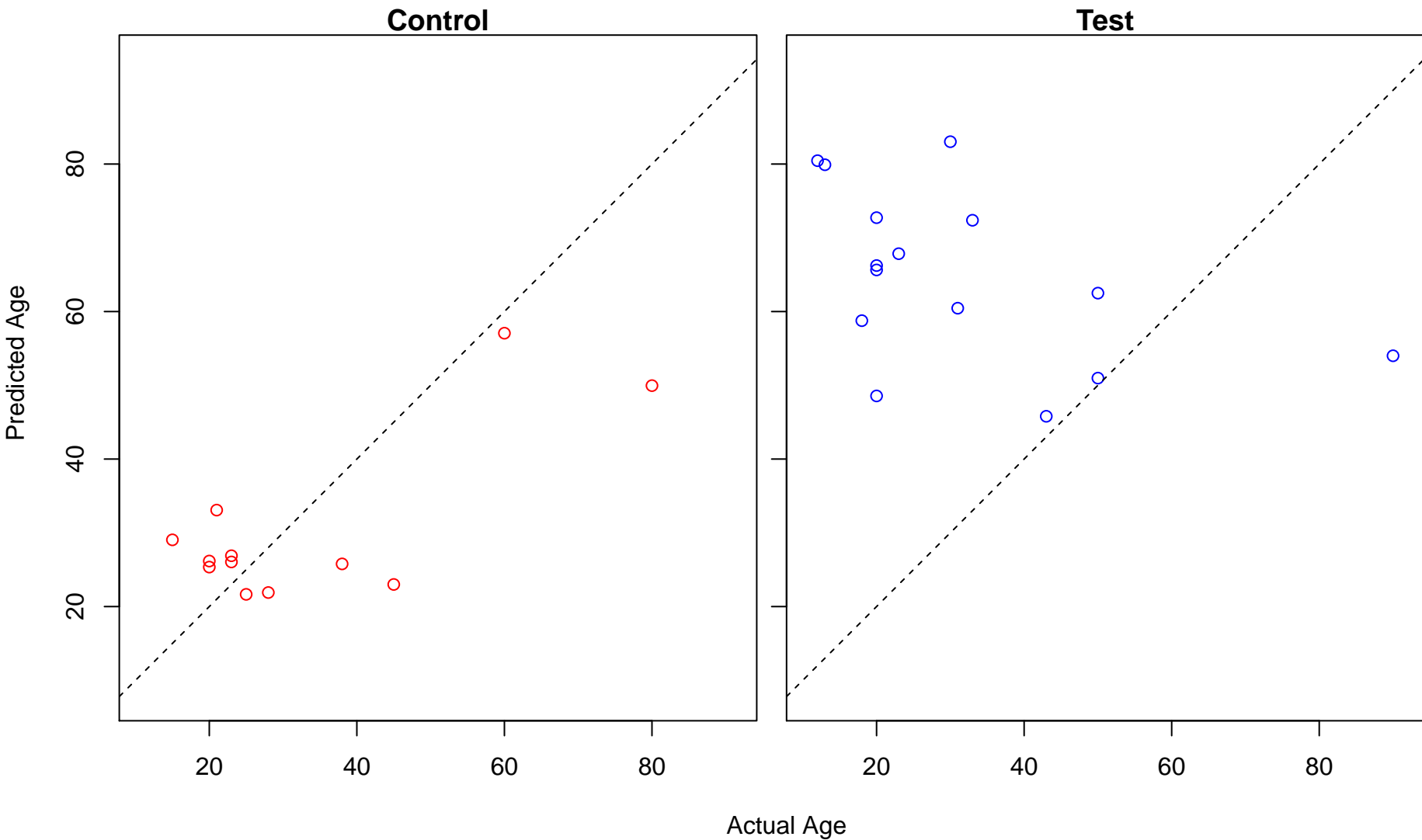
regulation of cell chemotaxis to fibroblast growth factor (Score: 3.444155)



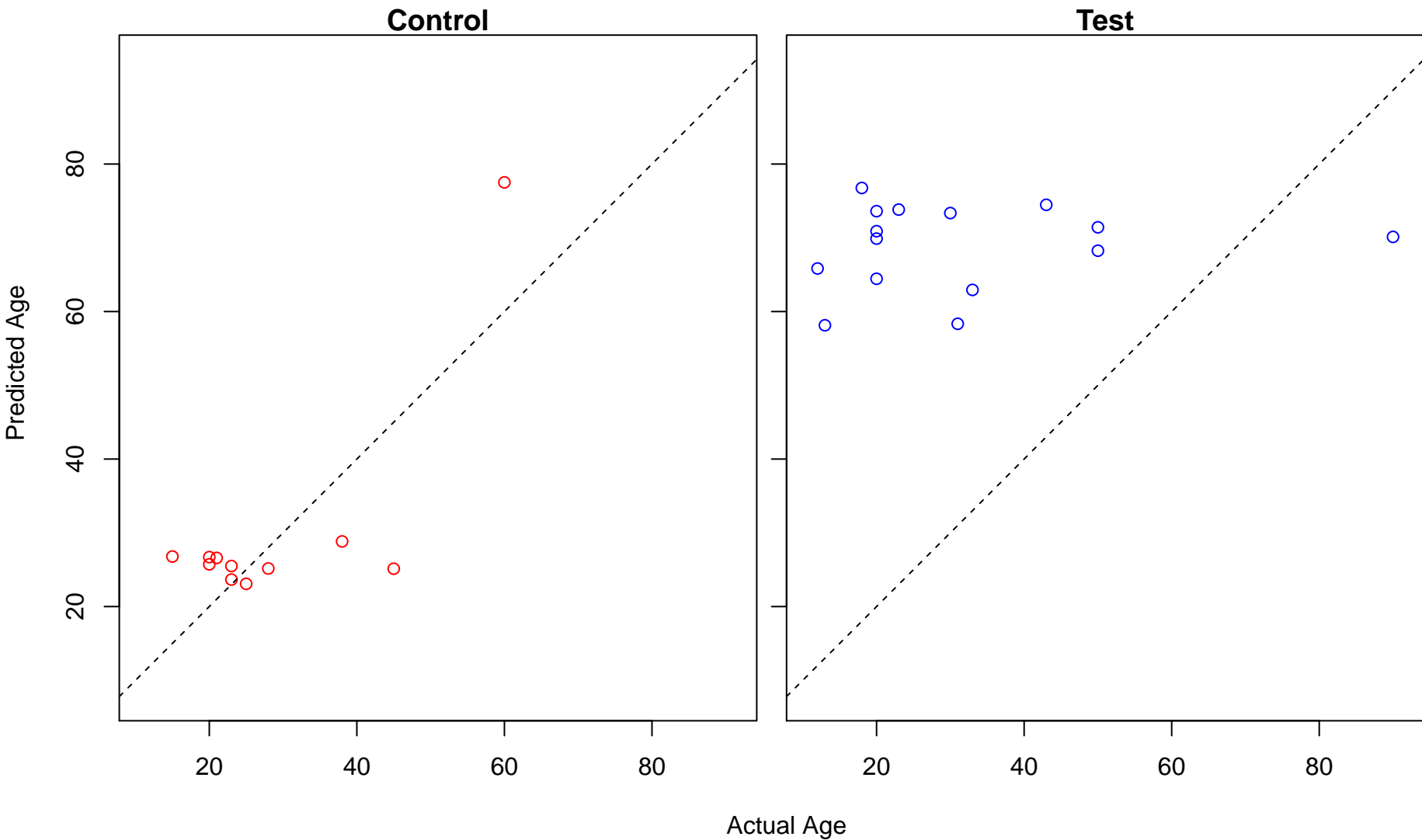
regulation of endothelial cell chemotaxis to fibroblast growth factor (Score: 3.444155)



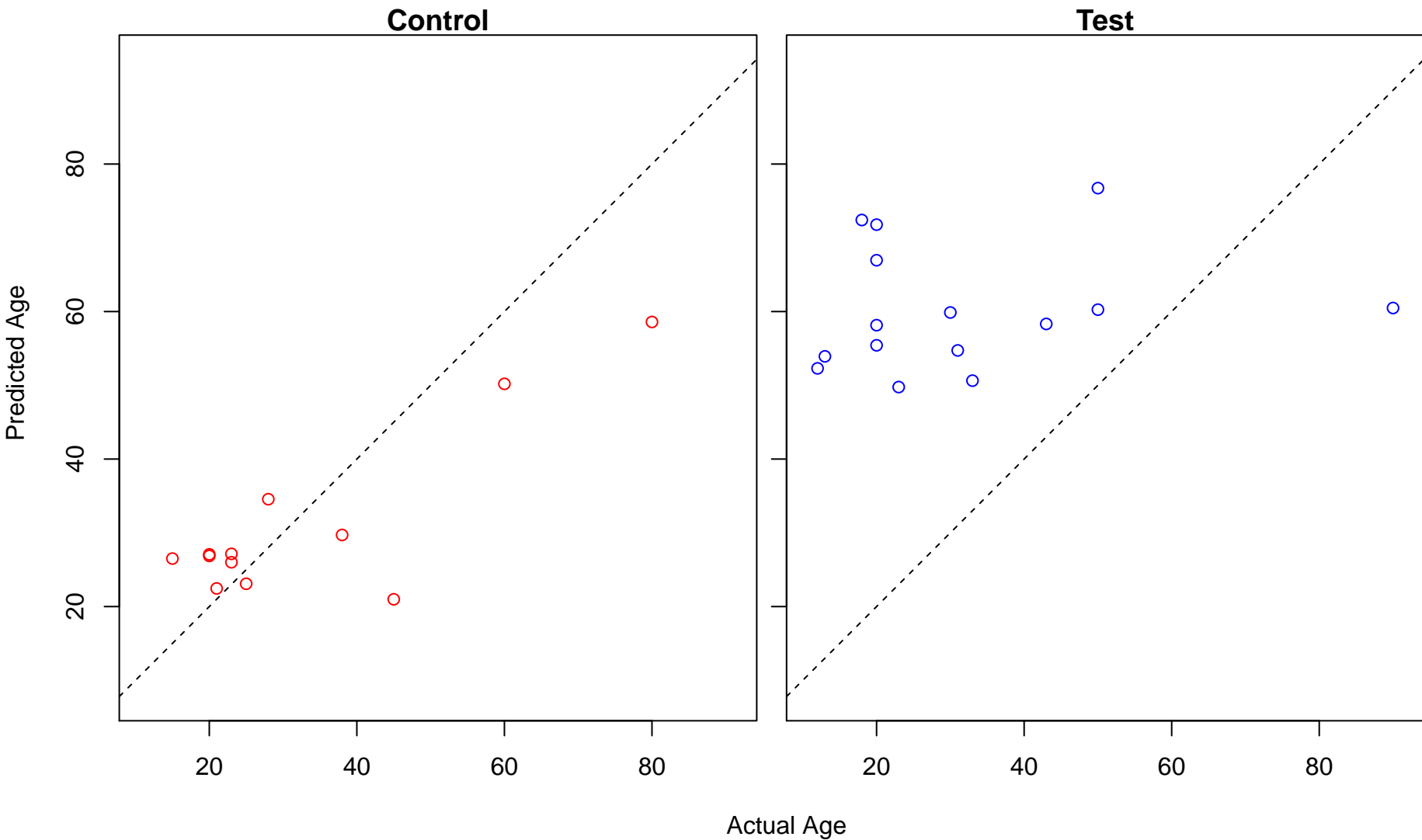
cGMP biosynthetic process (Score: 3.443471)



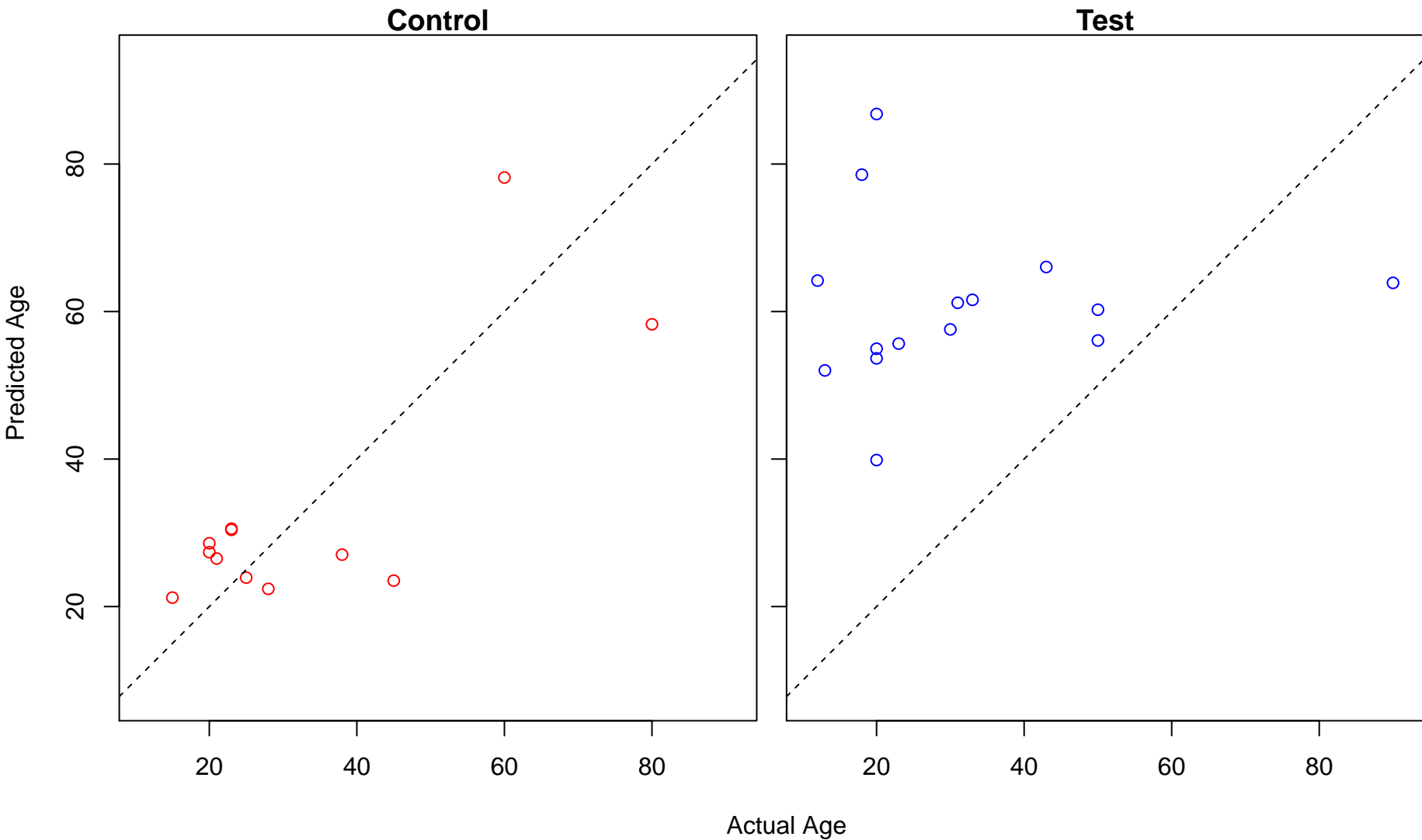
mitochondrion distribution (Score: 3.439810)



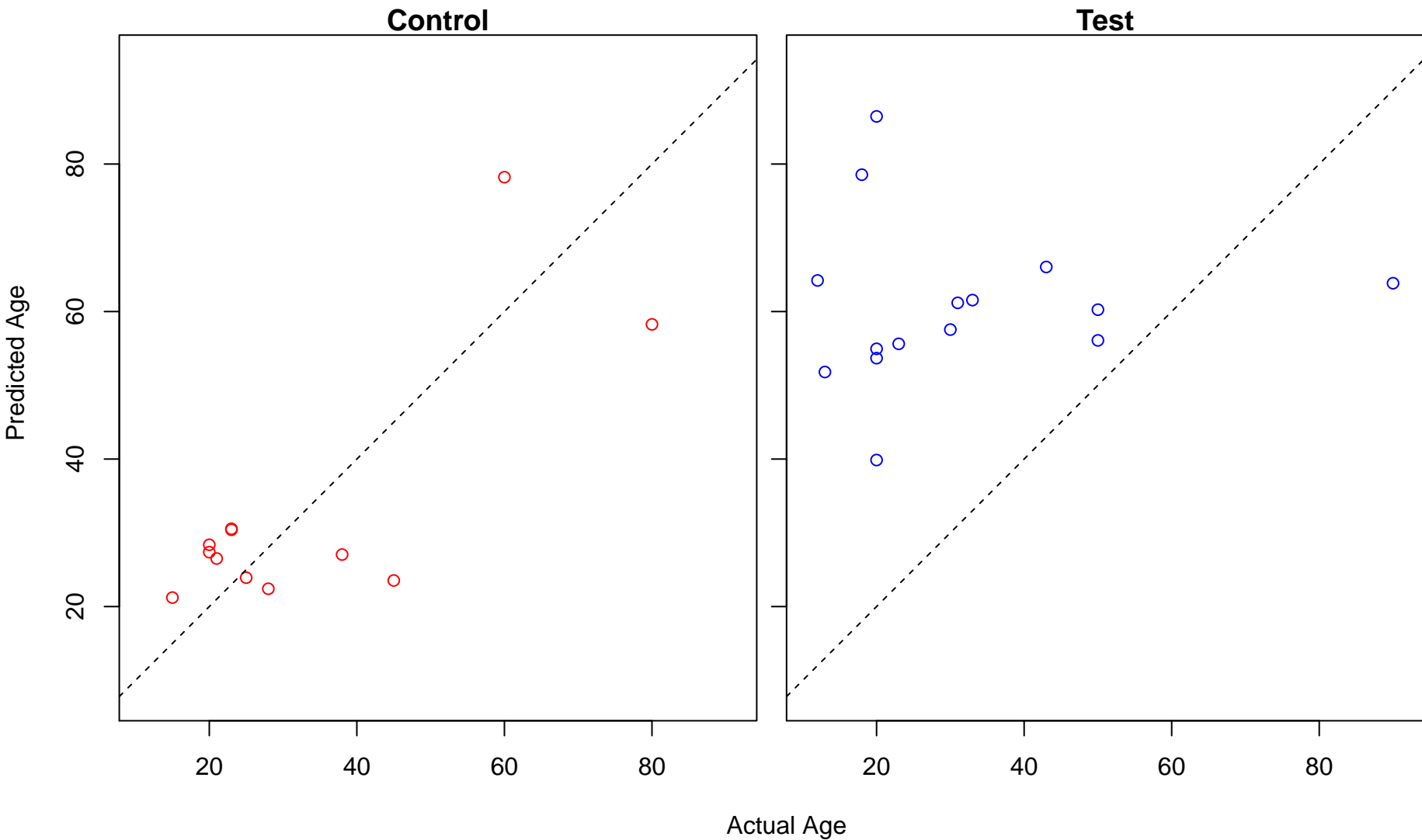
regulation of amyloid precursor protein catabolic process (Score: 3.439237)



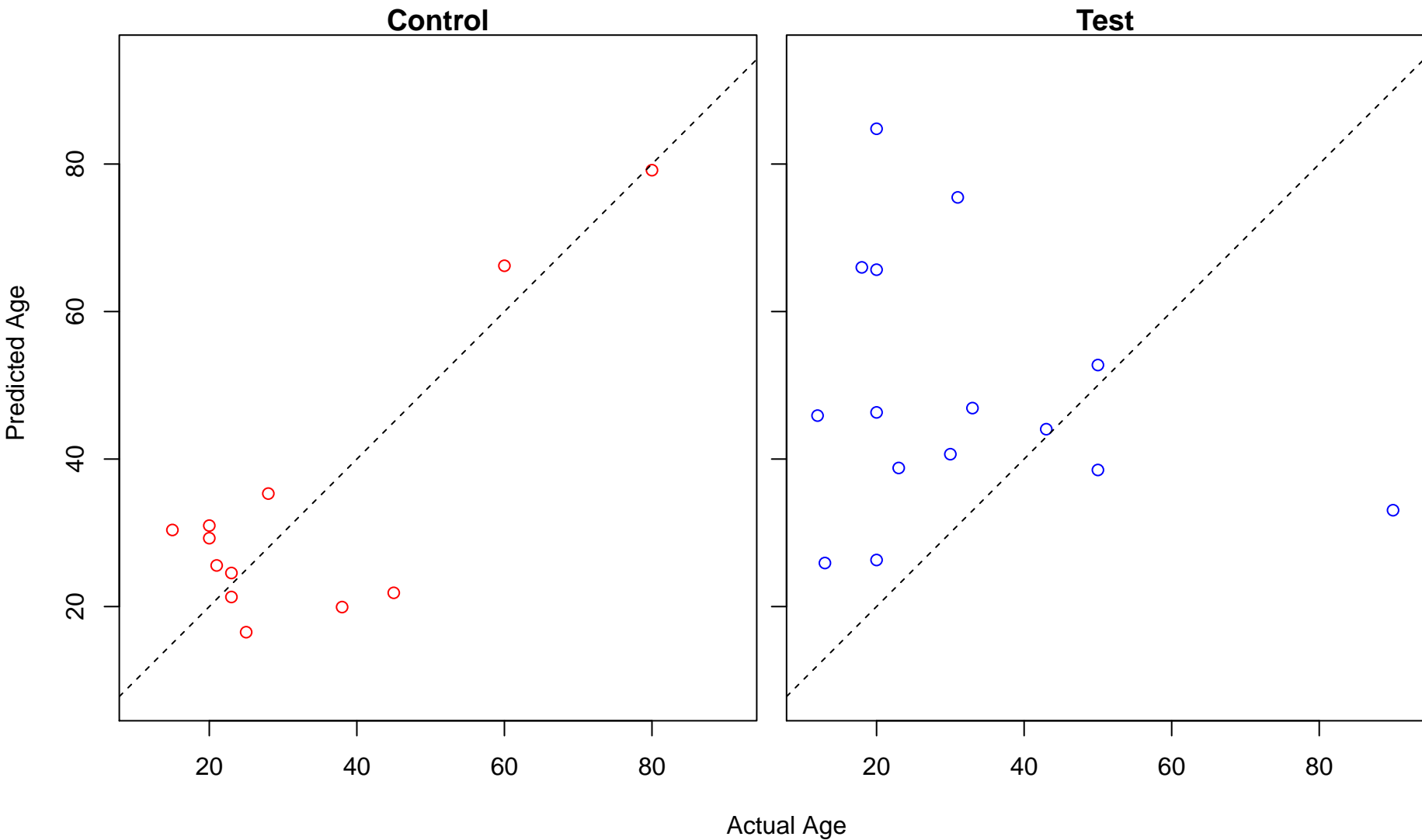
regulation of T cell chemotaxis (Score: 3.436397)



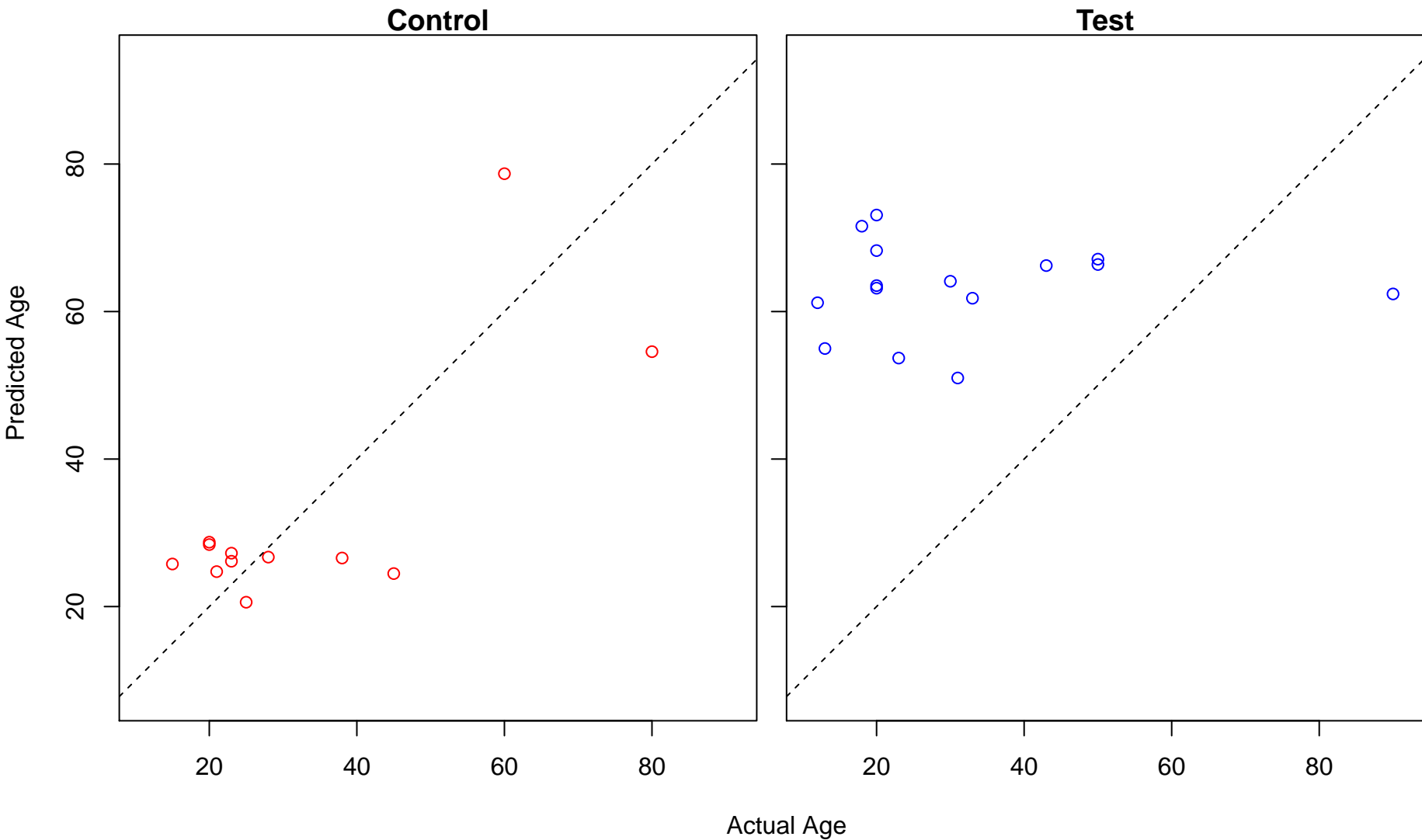
positive regulation of T cell chemotaxis (Score: 3.436216)



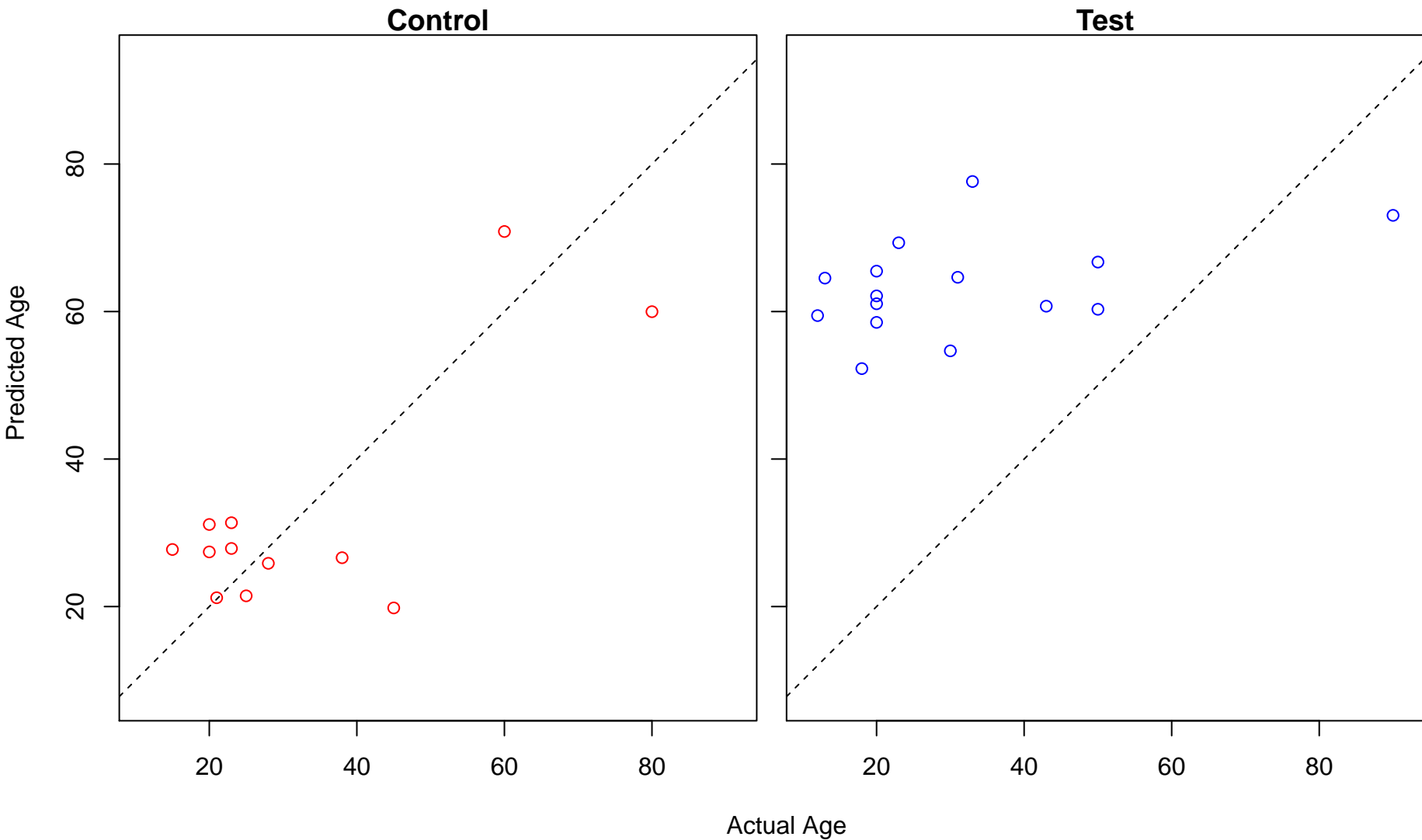
regulation of mitochondrion organization (Score: 3.434744)



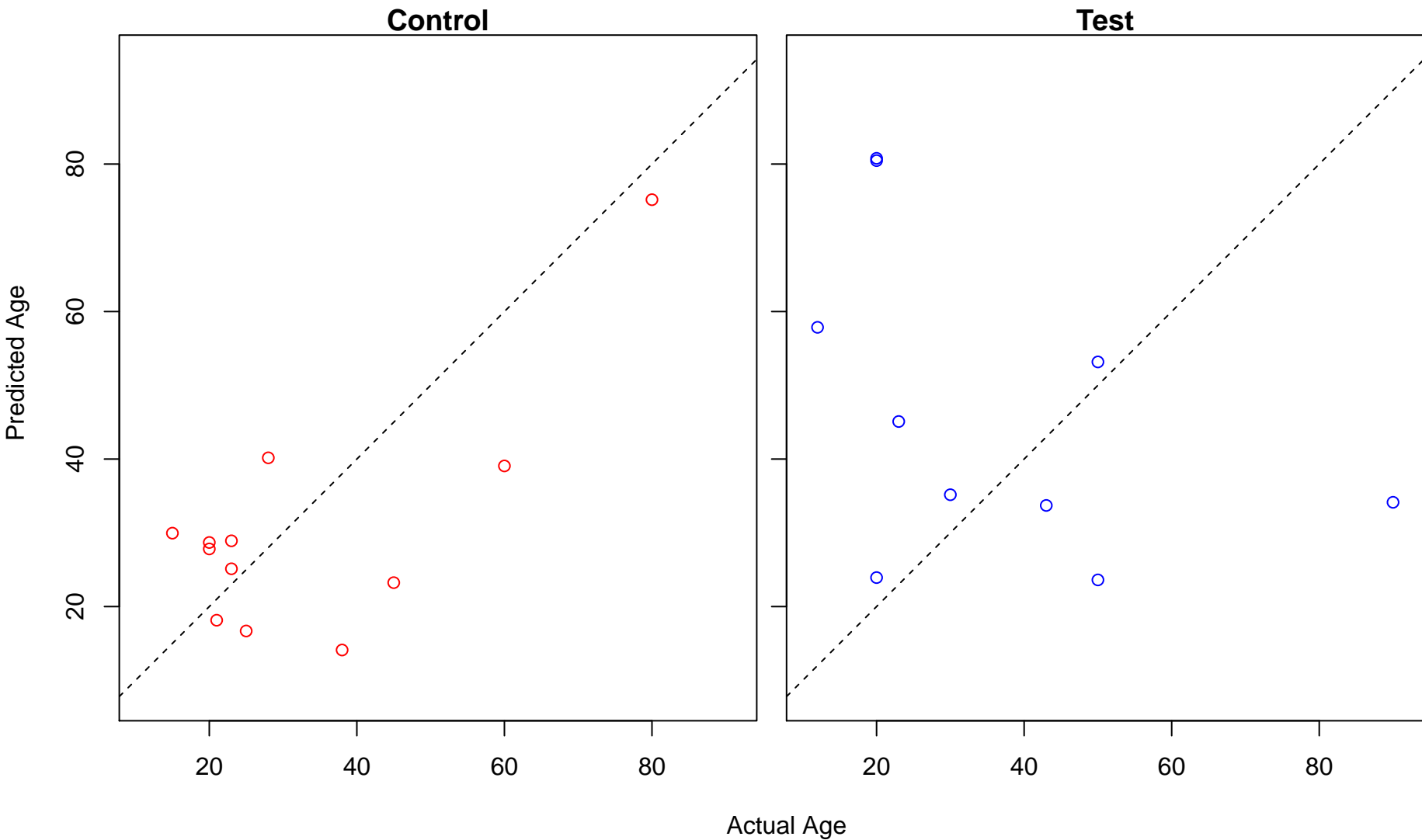
regulation of fatty acid metabolic process (Score: 3.434315)



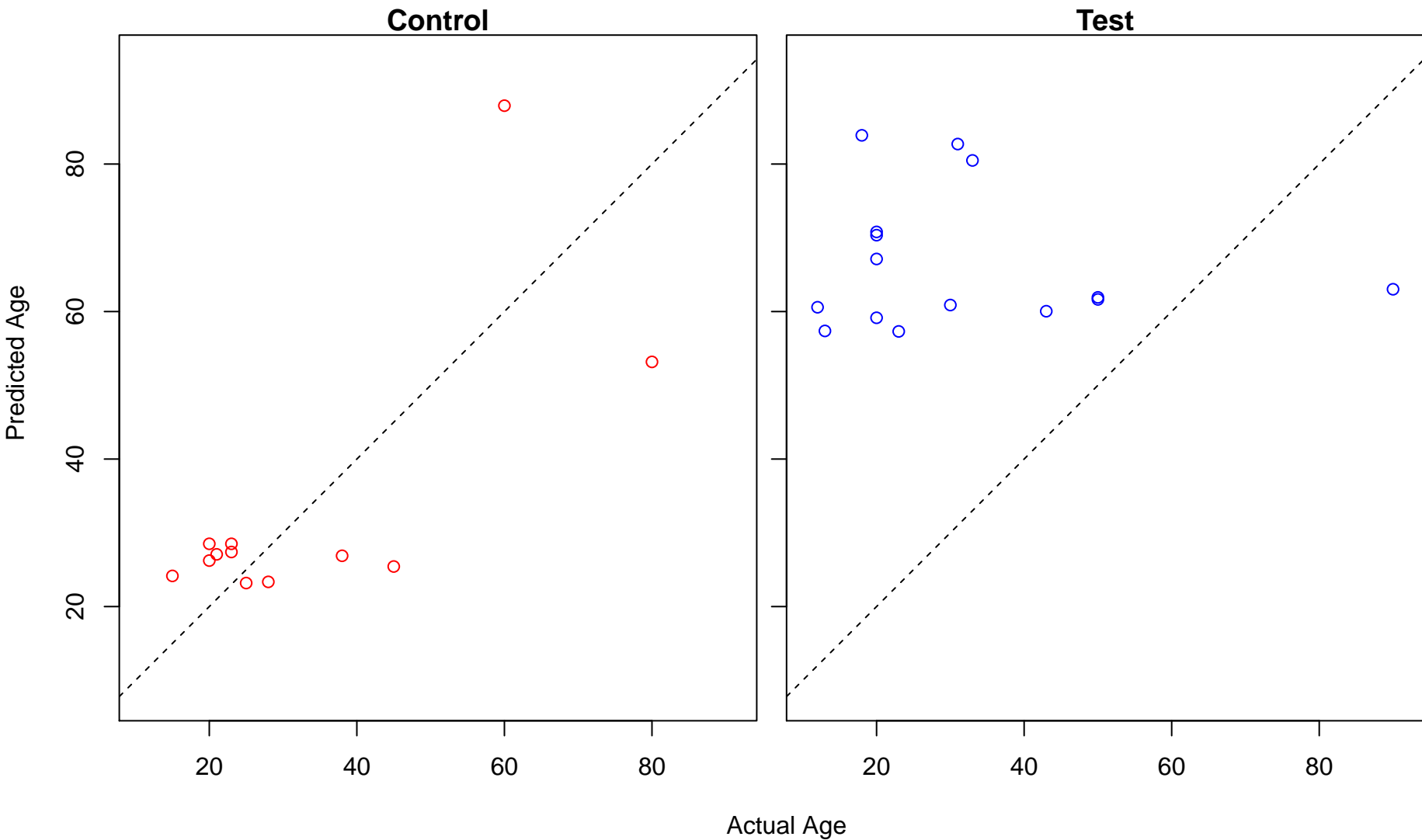
eye photoreceptor cell differentiation (Score: 3.432797)



glycoprotein catabolic process (Score: 3.428353)

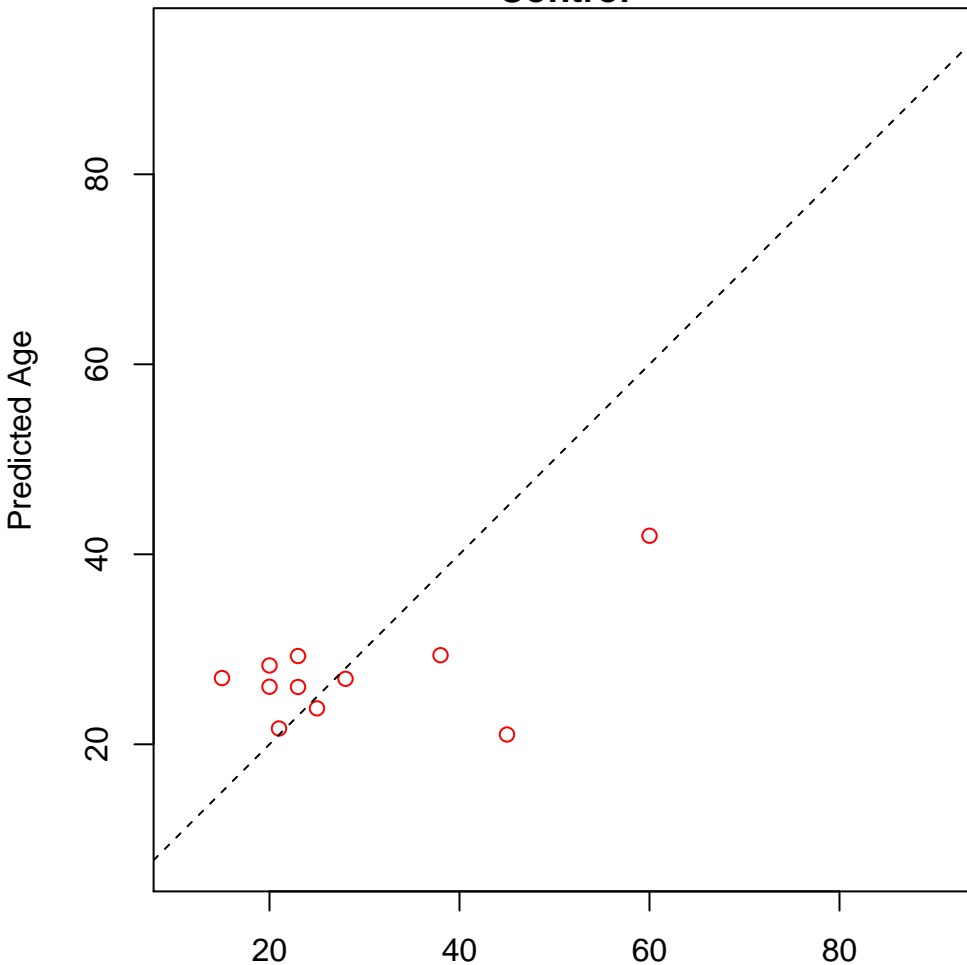


negative regulation of focal adhesion assembly (Score: 3.423968)

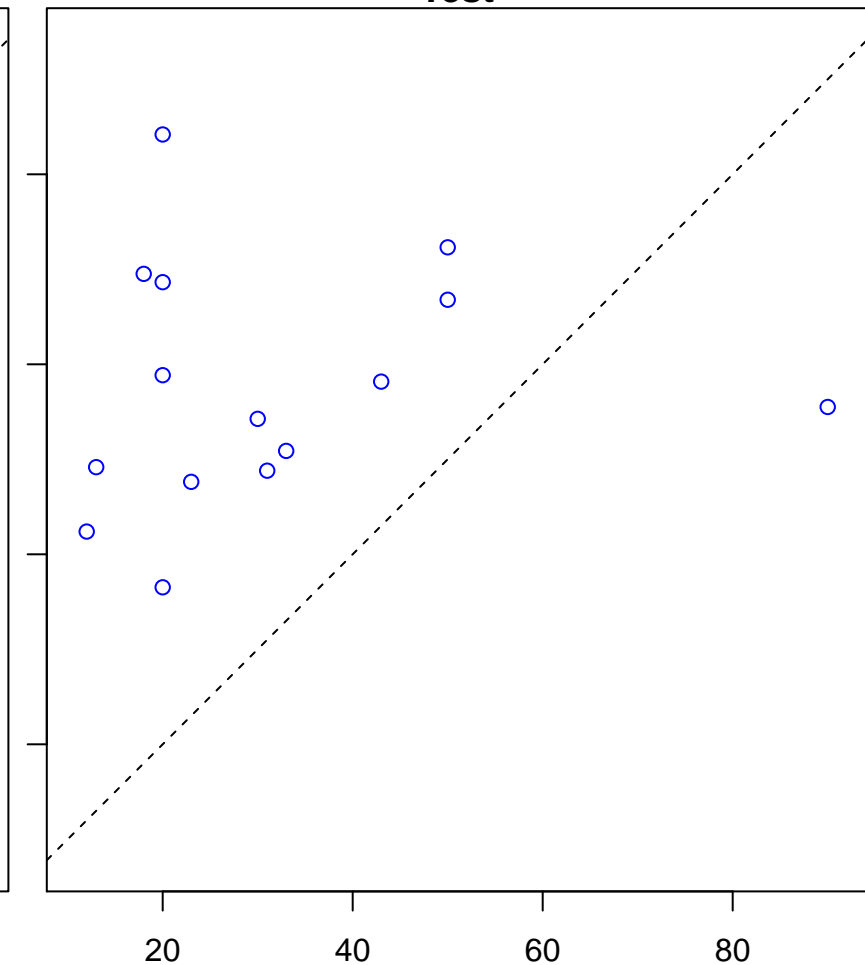


embryonic skeletal system development (Score: 3.423518)

Control

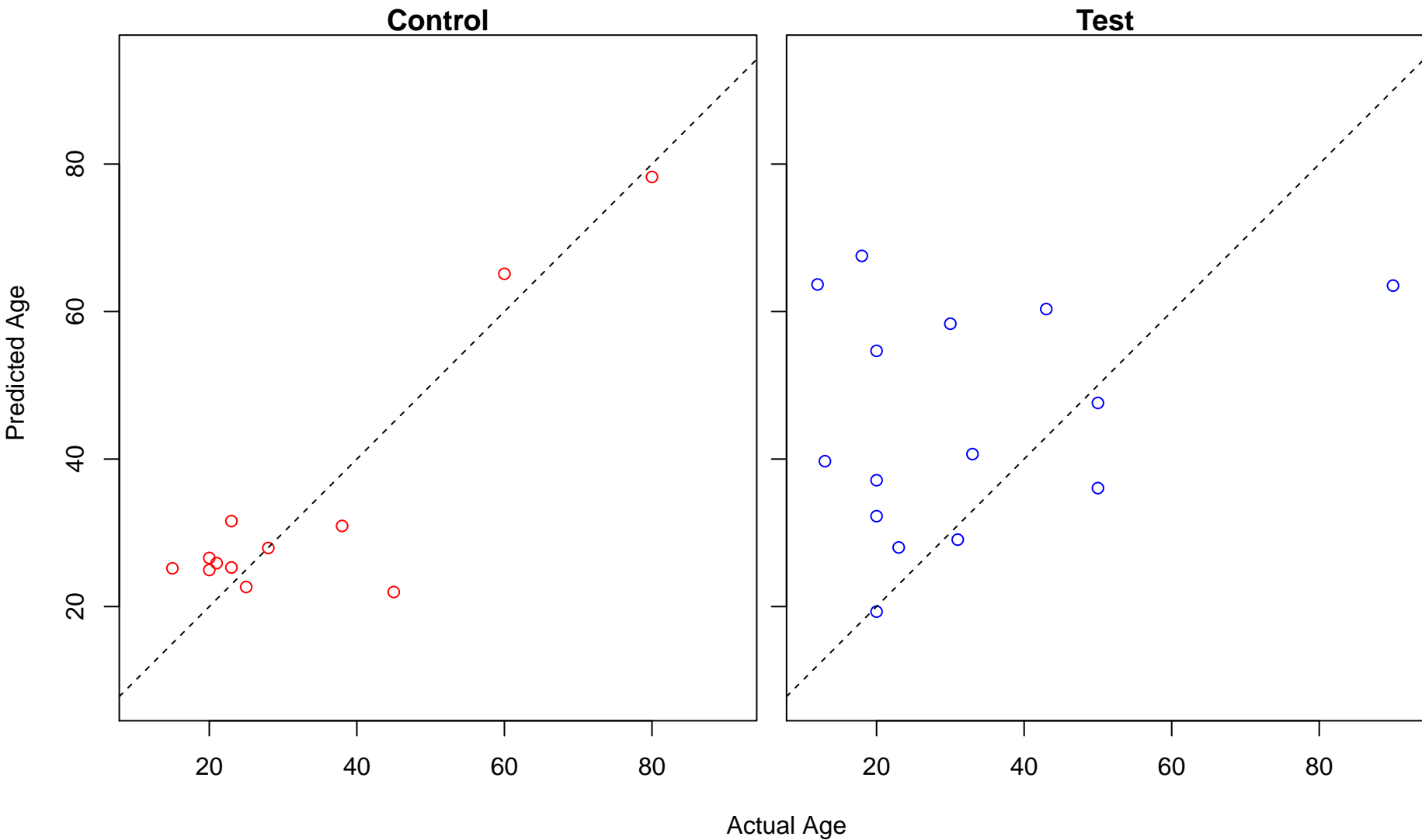


Test

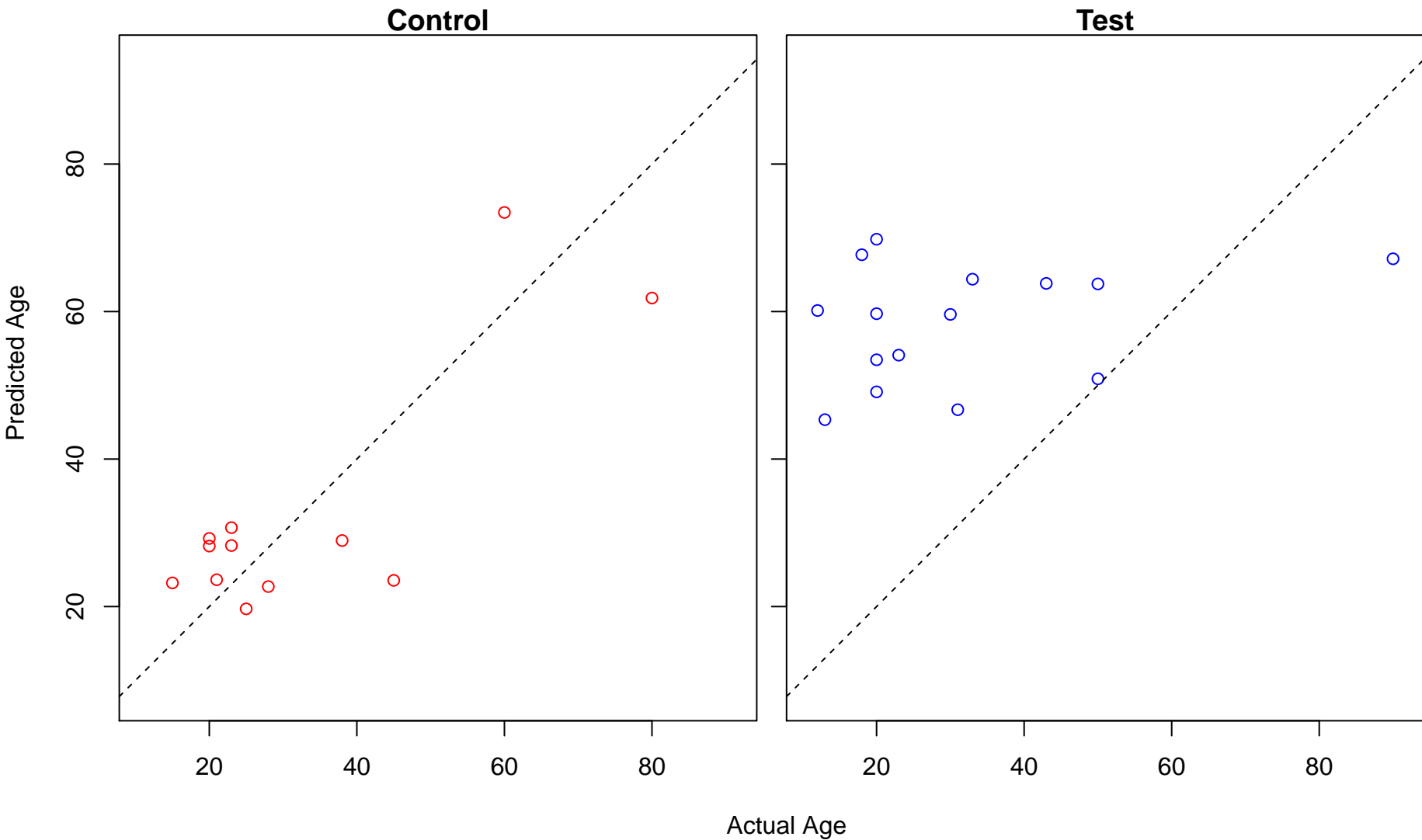


Actual Age

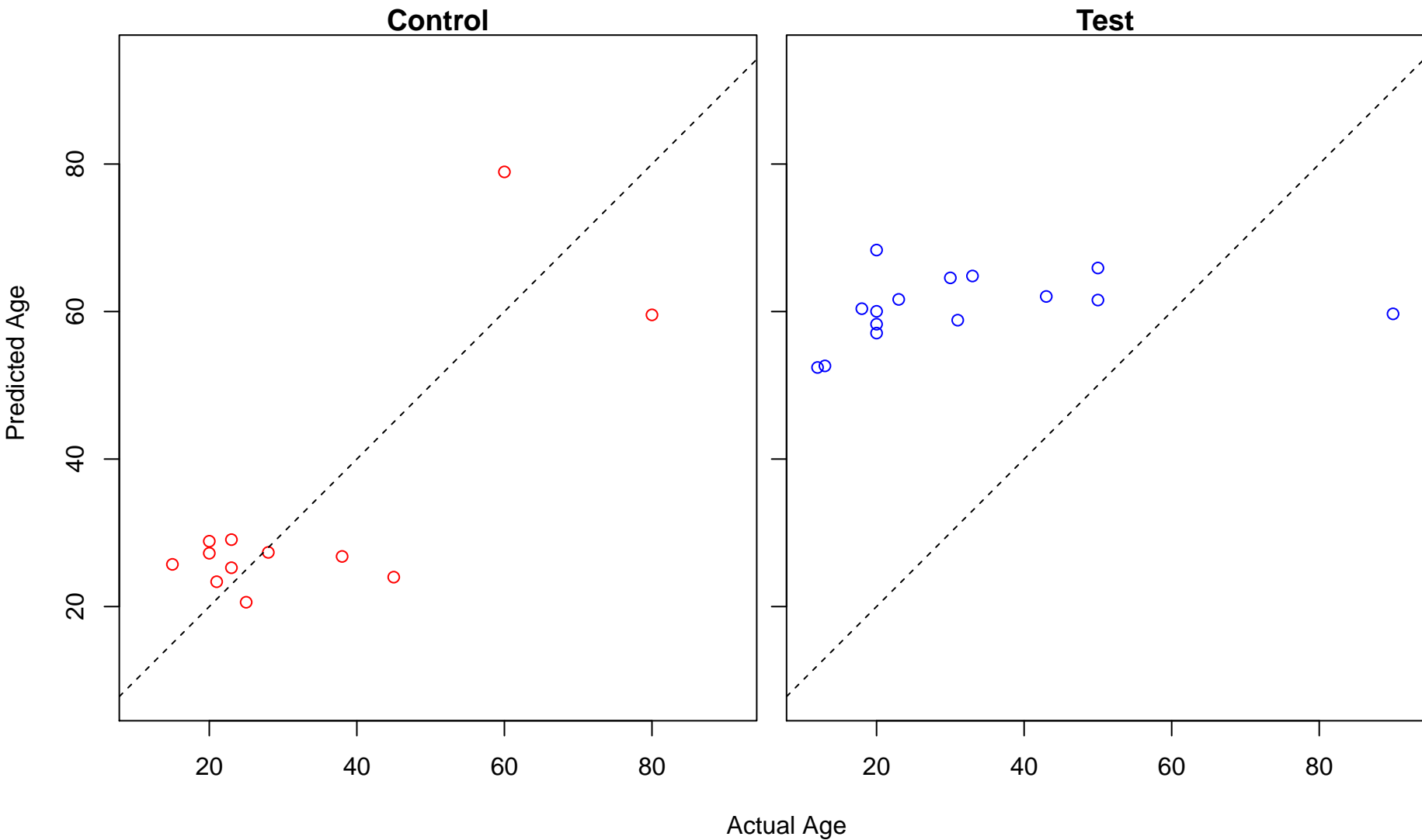
positive regulation of DNA-templated transcription, elongation (Score: 3.423310)



cell adhesion mediated by integrin (Score: 3.421152)

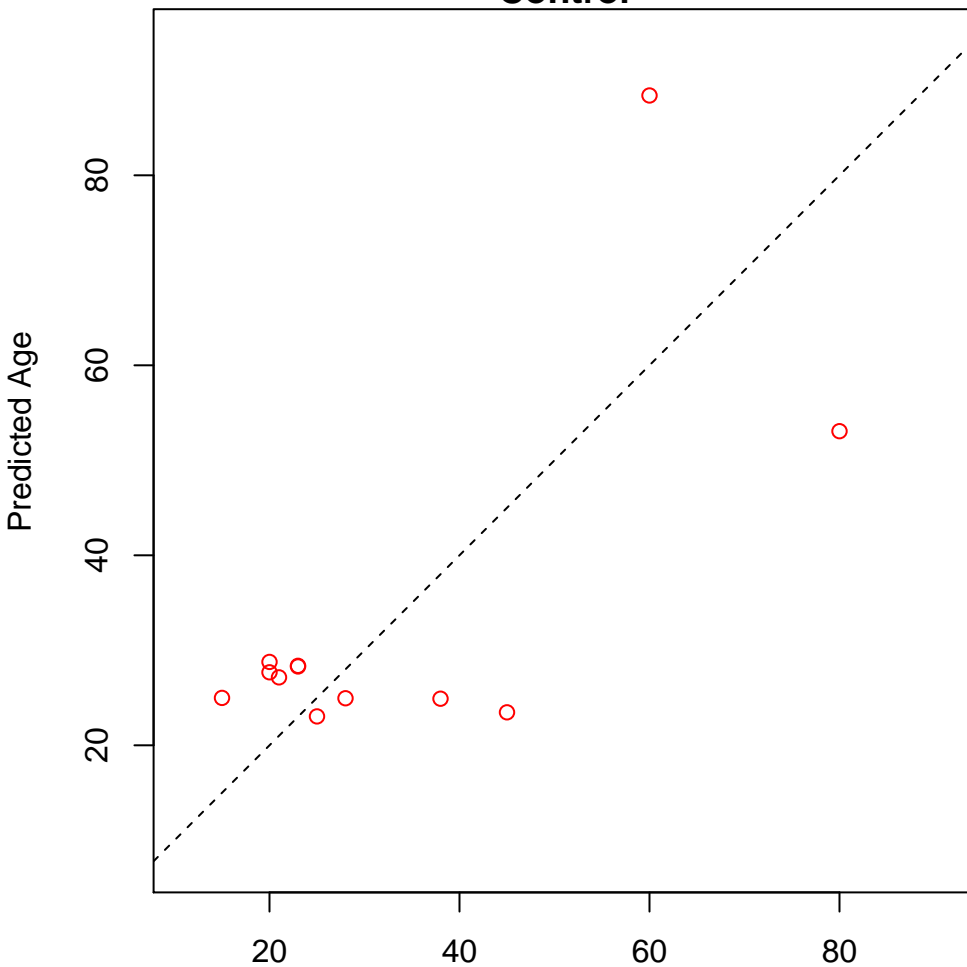


retrograde transport, endosome to plasma membrane (Score: 3.420189)

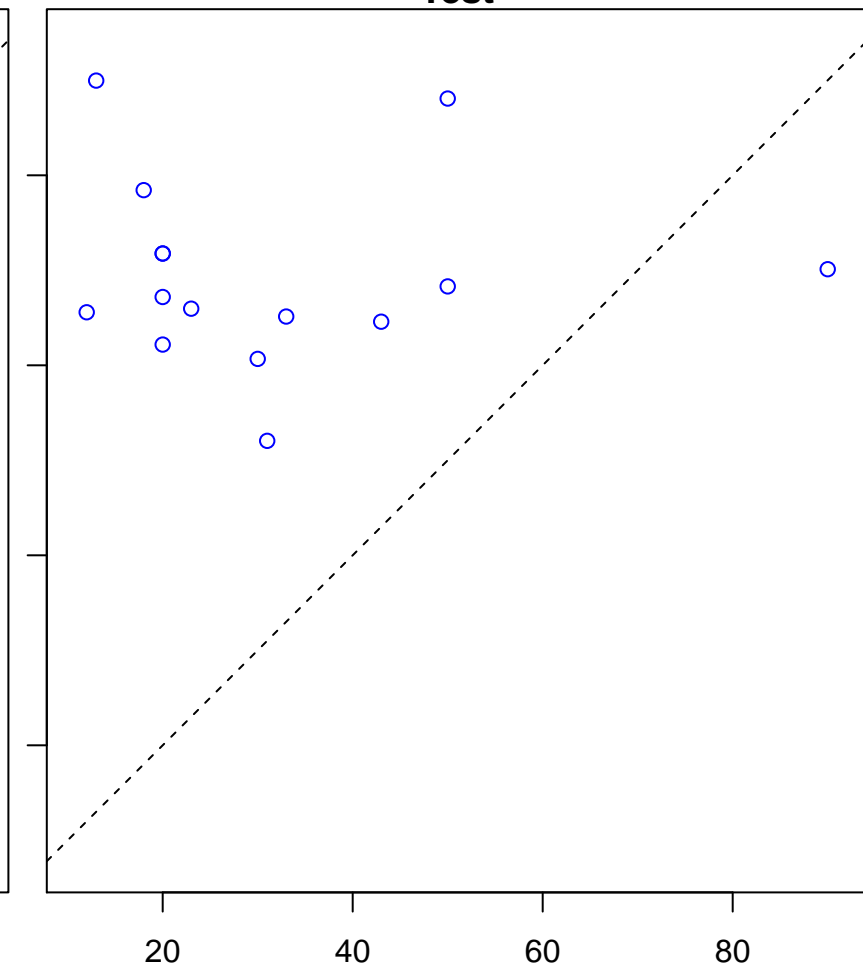


regulation of deoxyribonuclease activity (Score: 3.419798)

Control

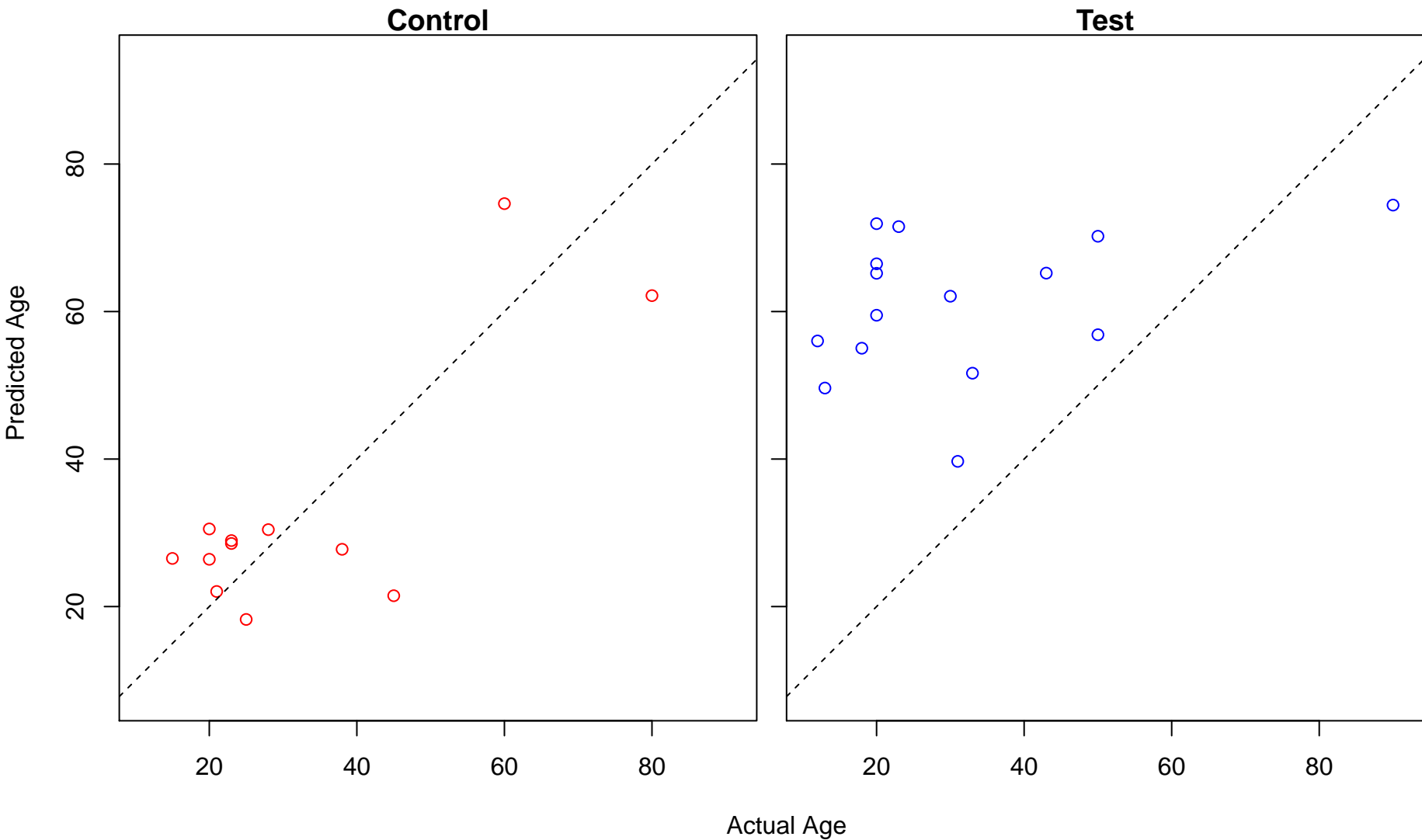


Test

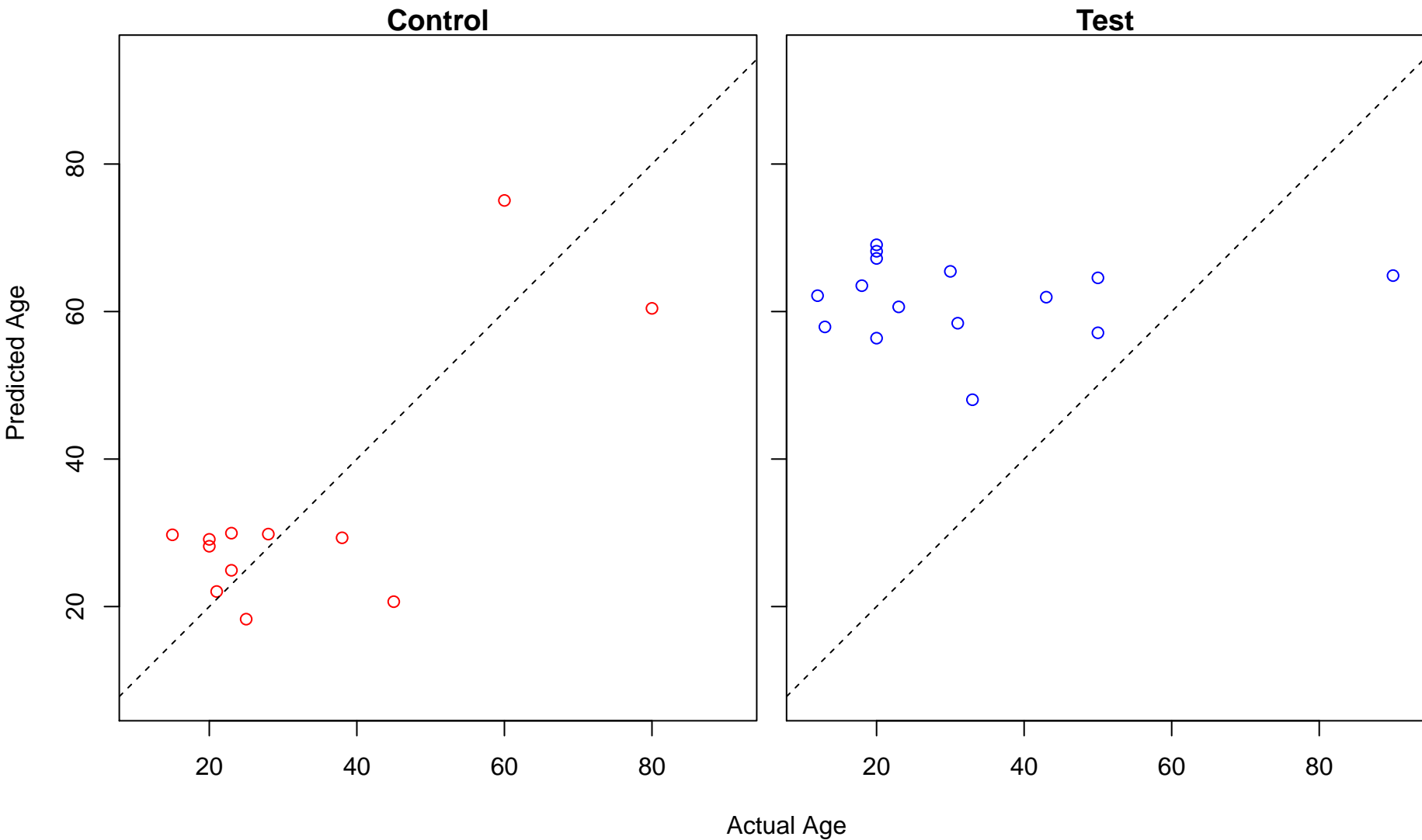


Actual Age

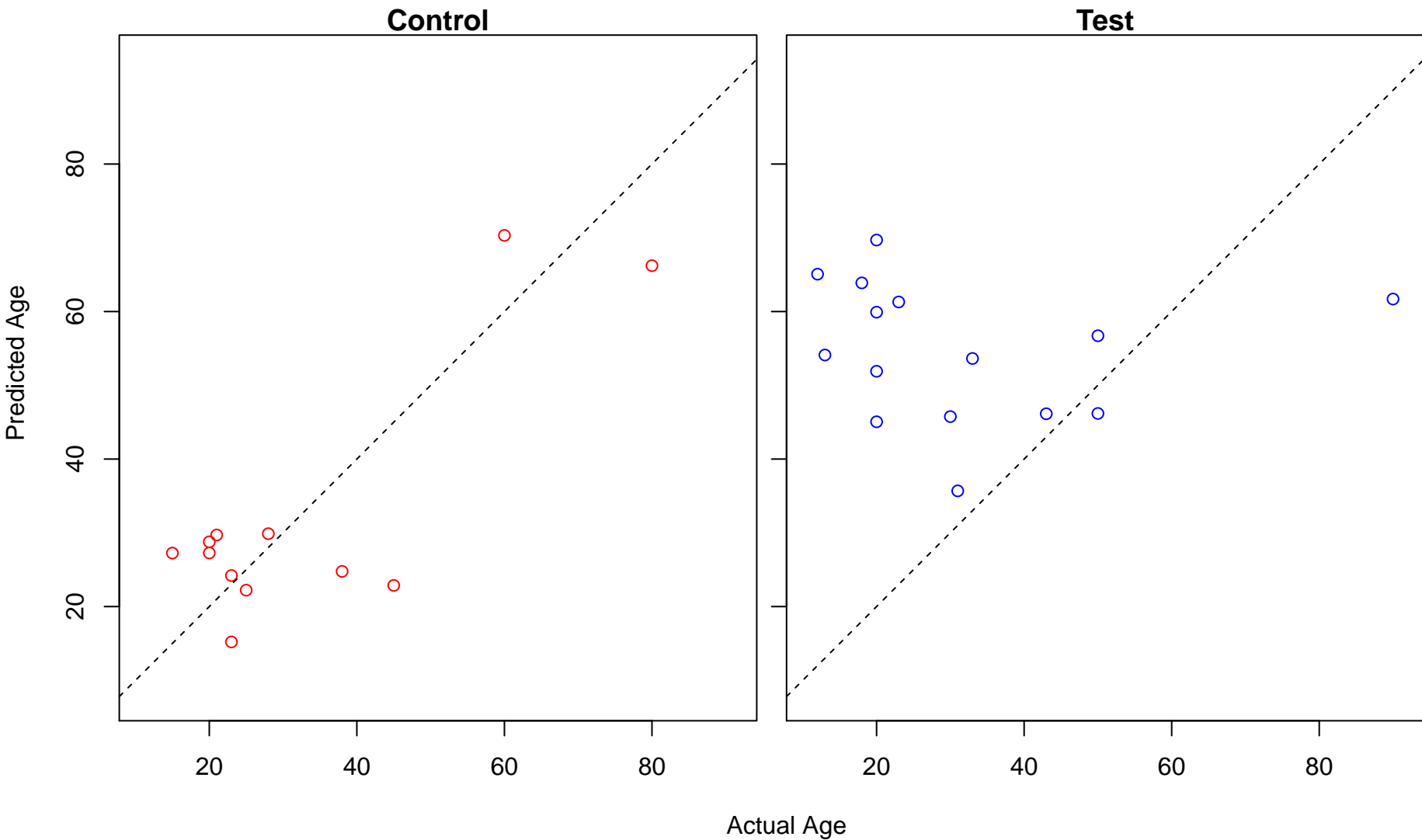
regulation of response to wounding (Score: 3.419291)



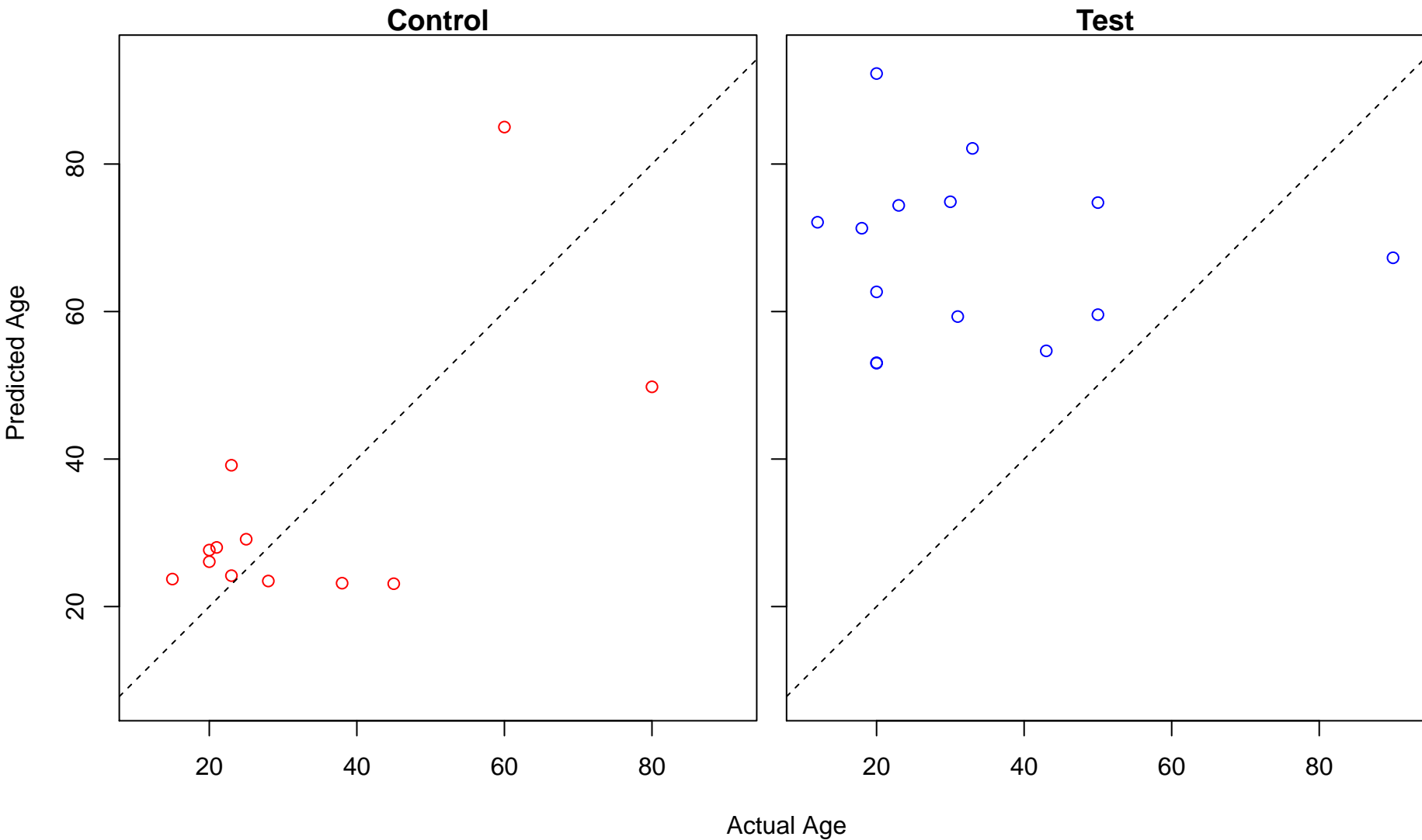
regulation of SMAD protein import into nucleus (Score: 3.417104)



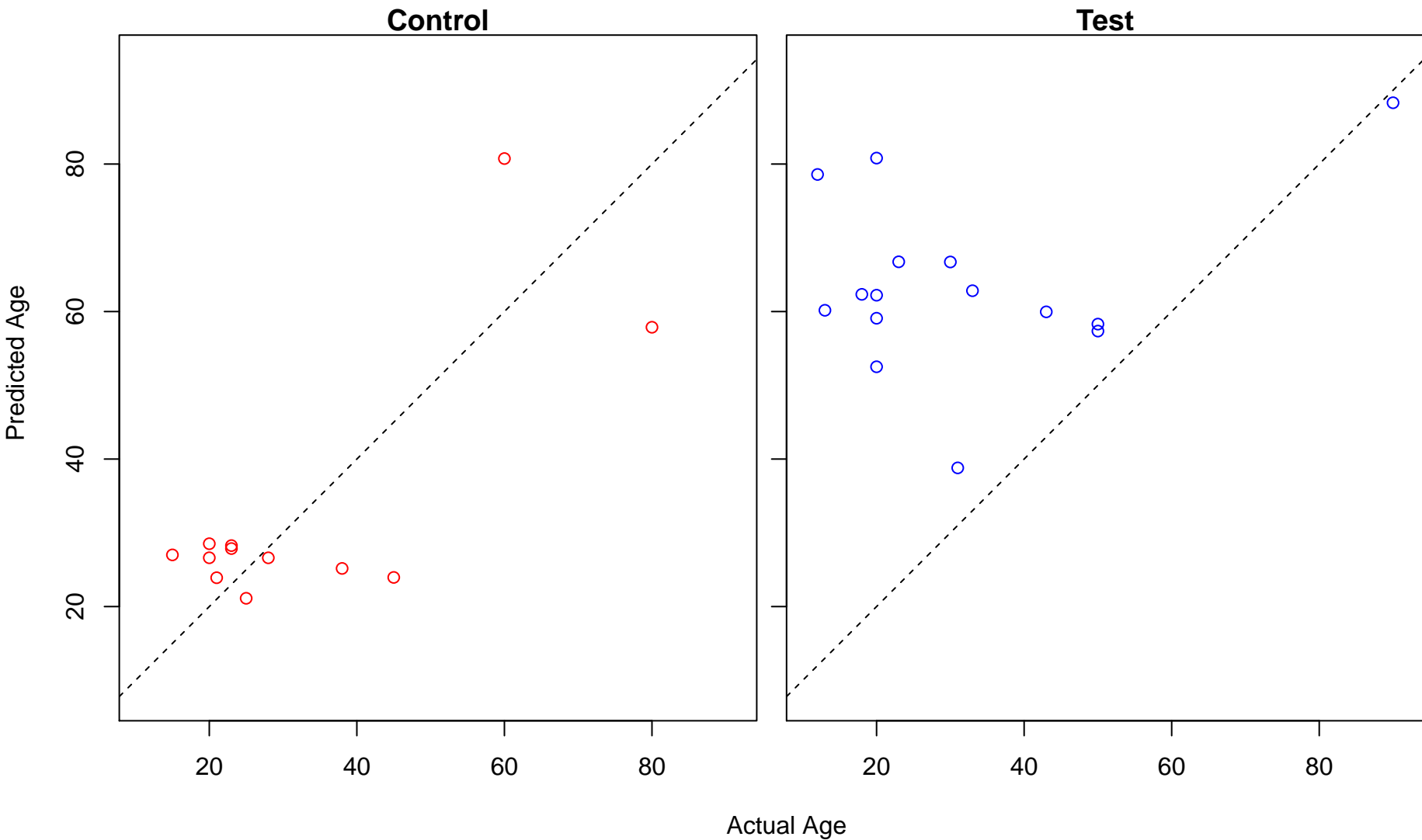
positive regulation of G1/S transition of mitotic cell cycle (Score: 3.411803)



negative regulation of interferon-gamma production (Score: 3.409858)

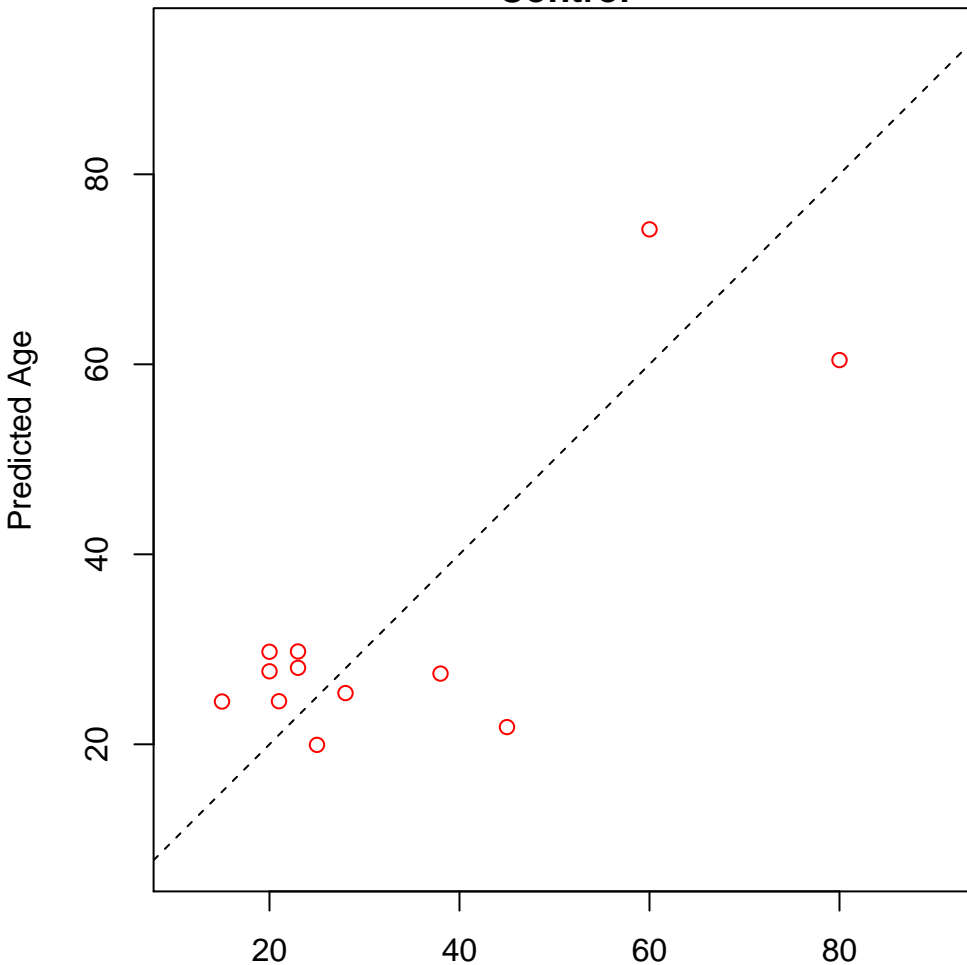


regulation of generation of L-type calcium current (Score: 3.409332)

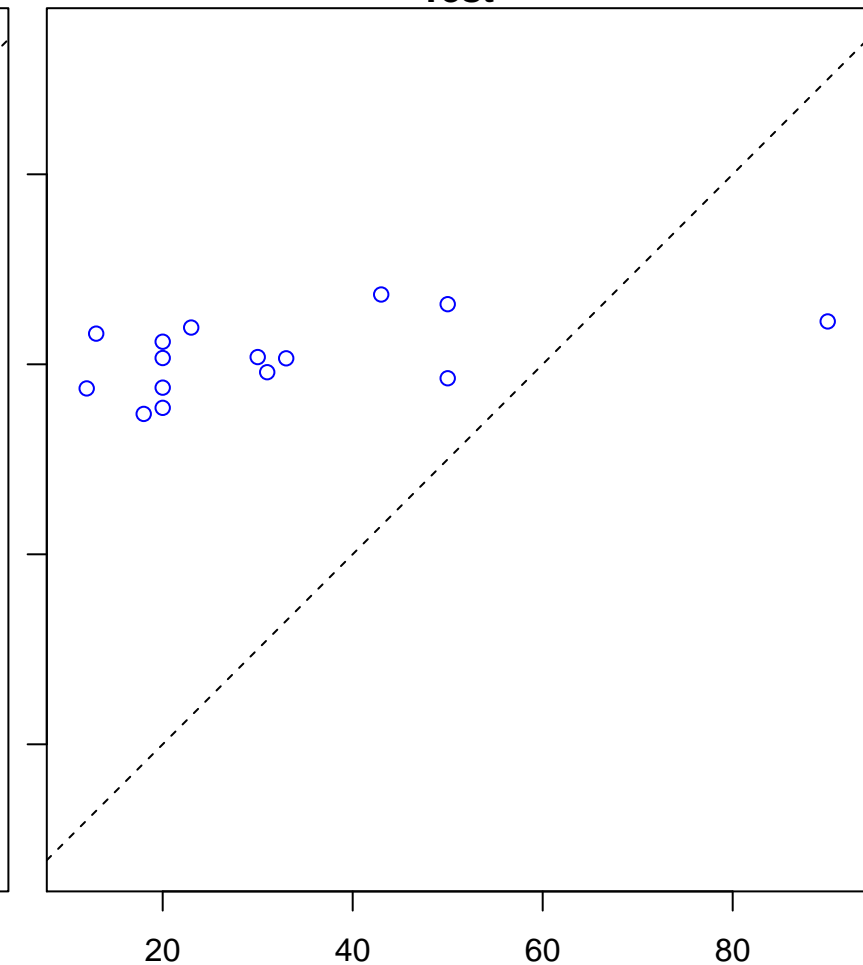


regulation of histone H3-K9 acetylation (Score: 3.408039)

Control

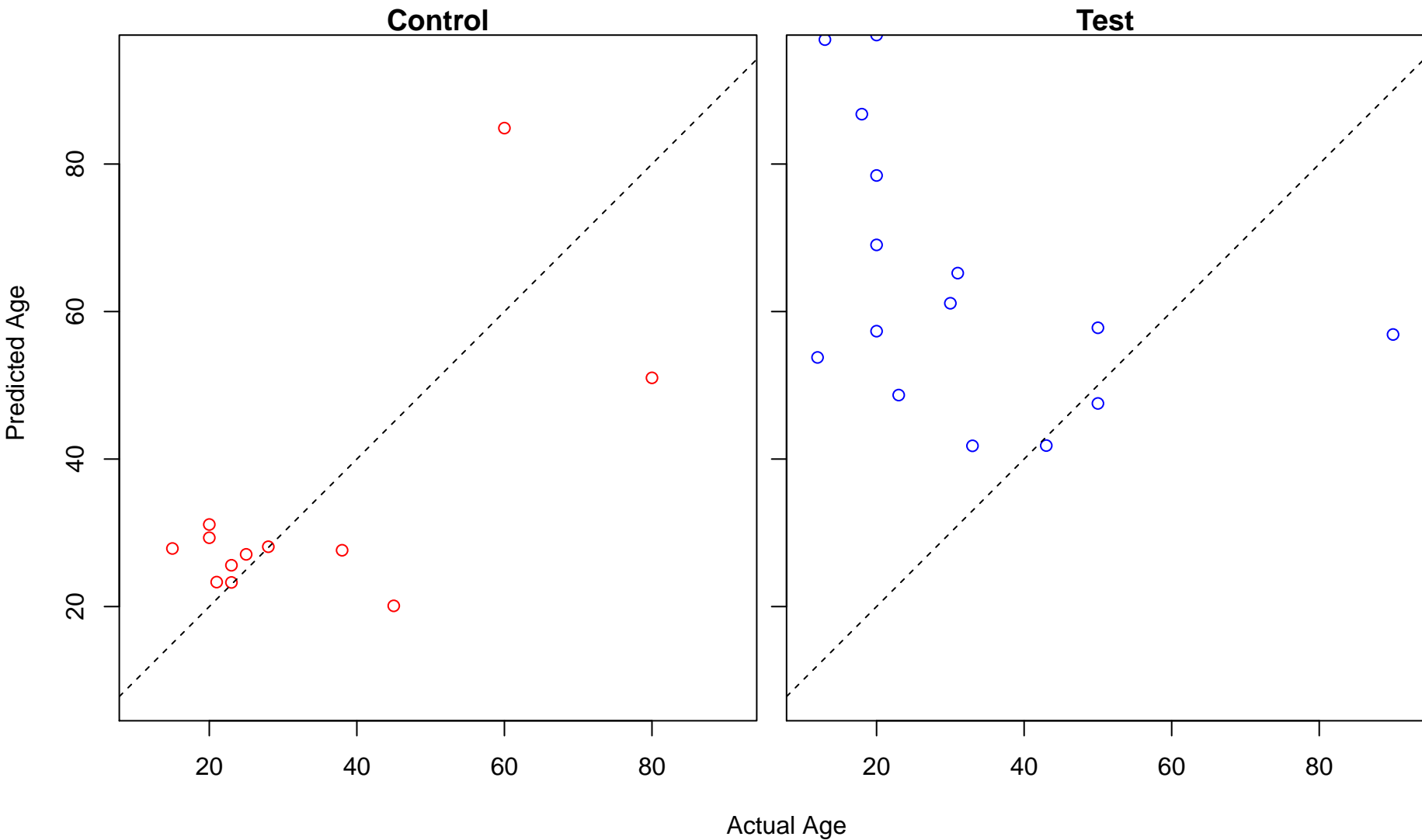


Test

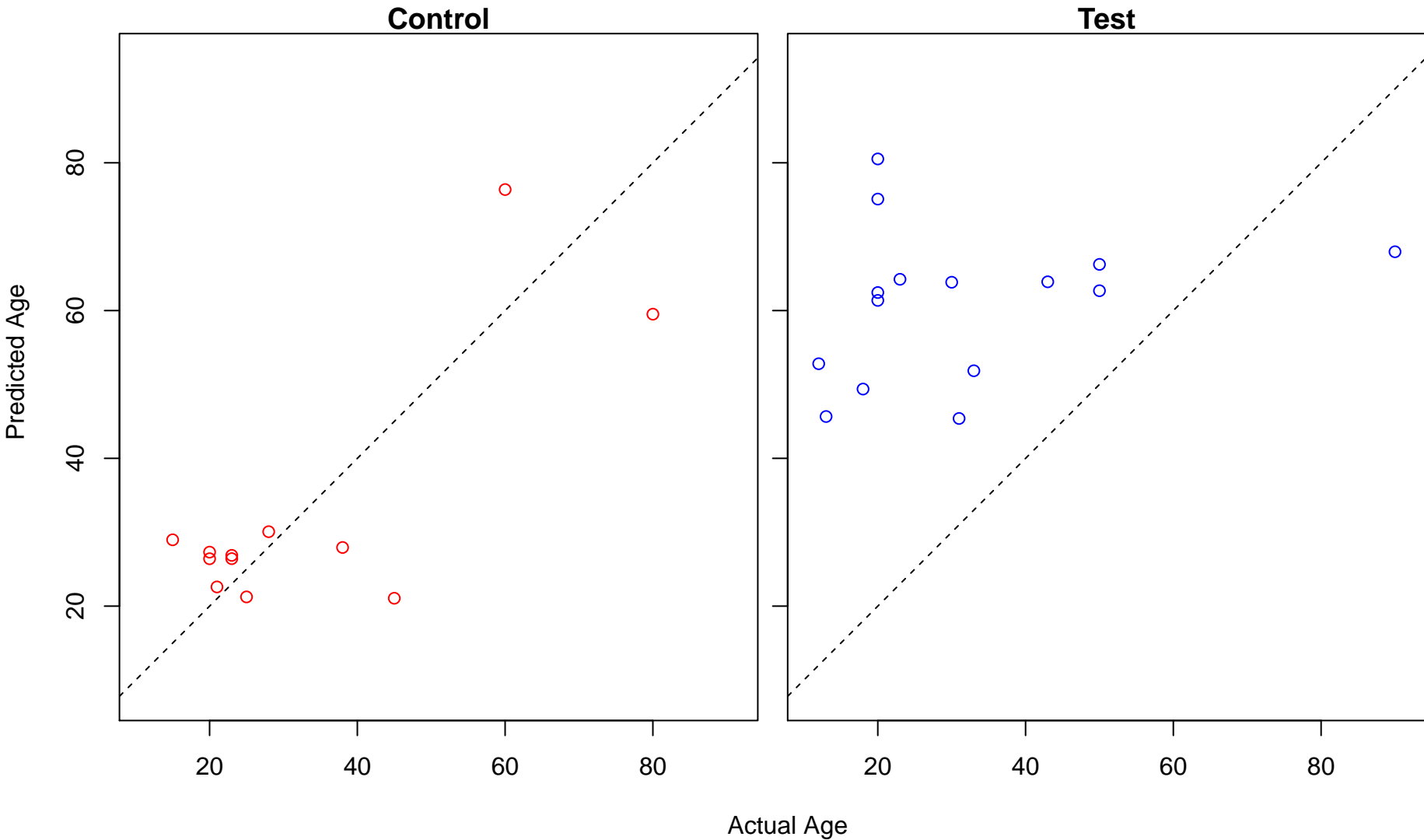


Actual Age

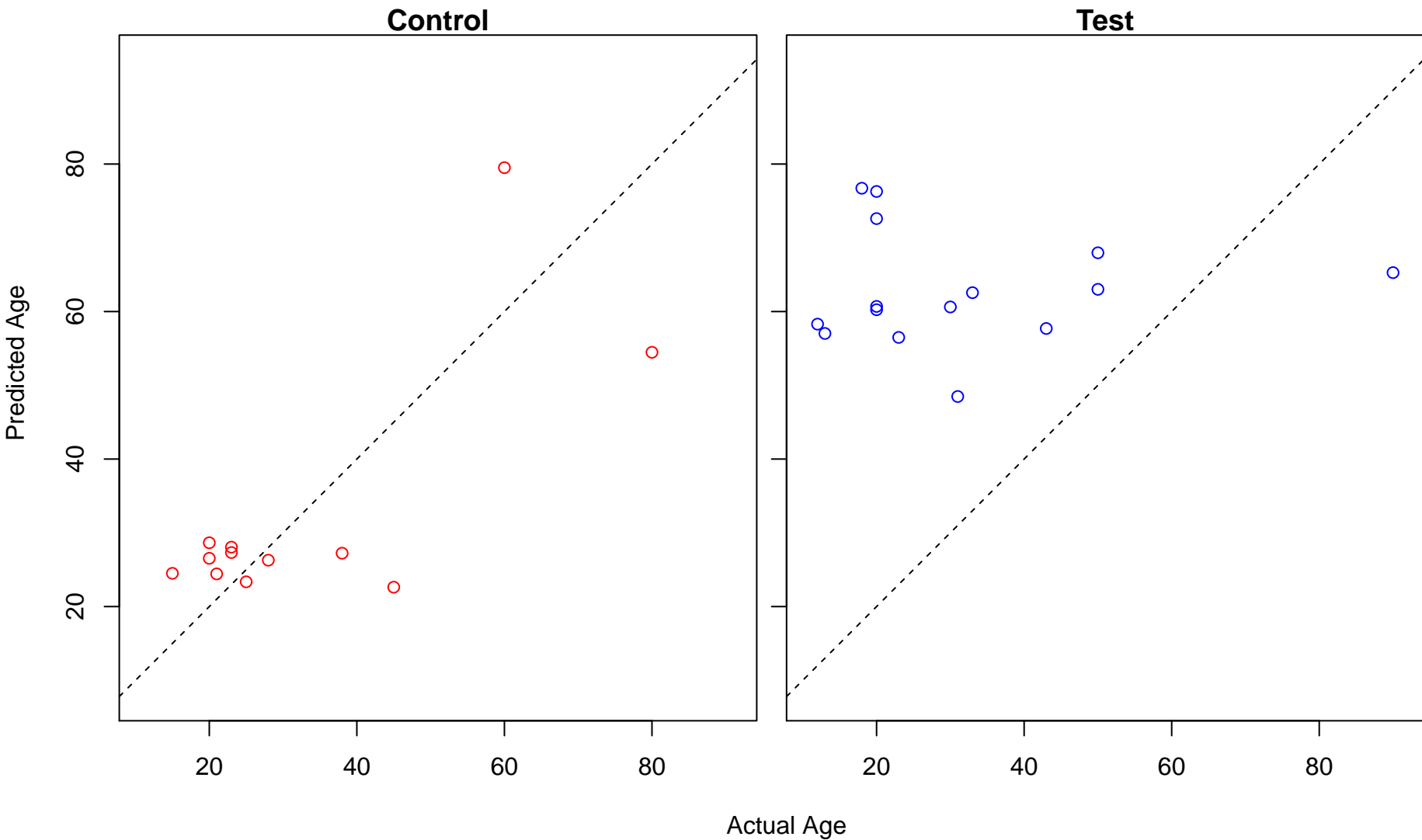
renal vesicle development (Score: 3.407086)



negative regulation of NIK/NF-kappaB signaling (Score: 3.406711)

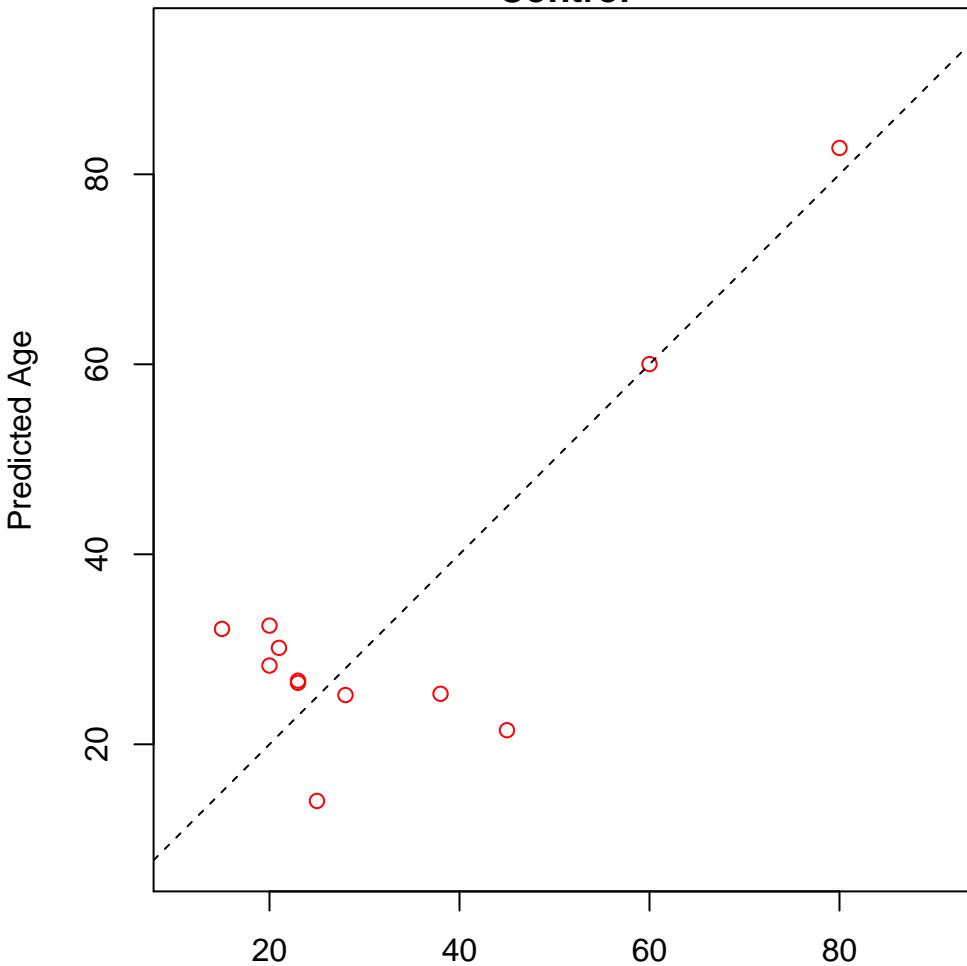


cellular metabolic compound salvage (Score: 3.404518)

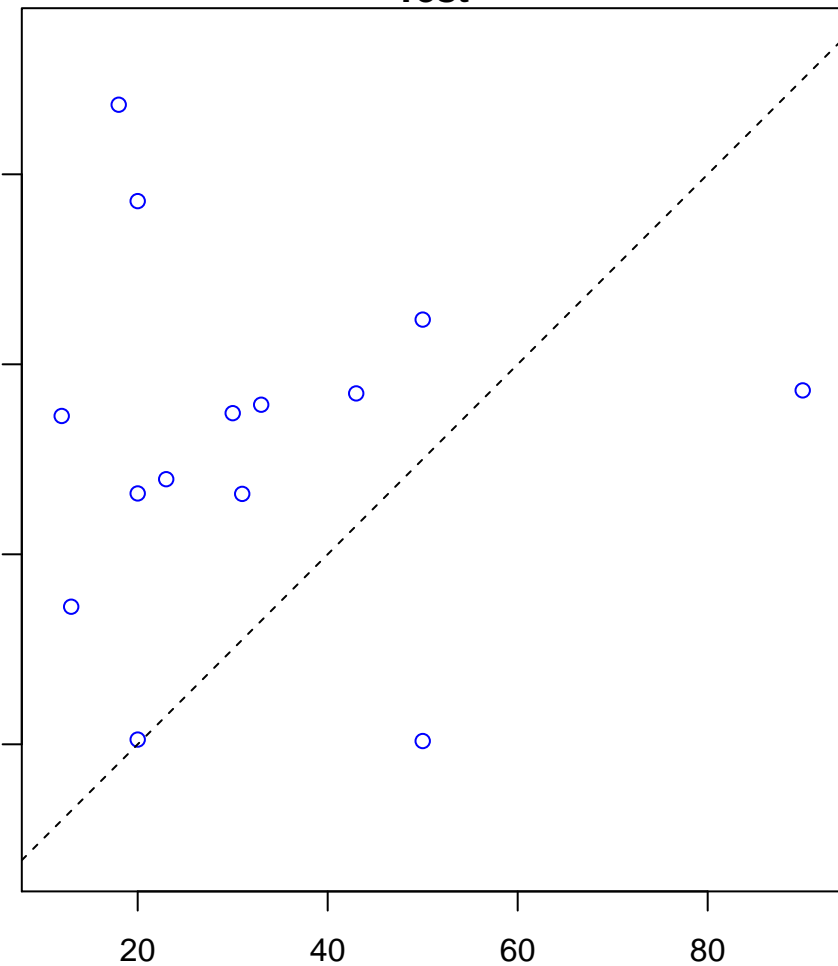


multi-organism membrane organization (Score: 3.401521)

Control

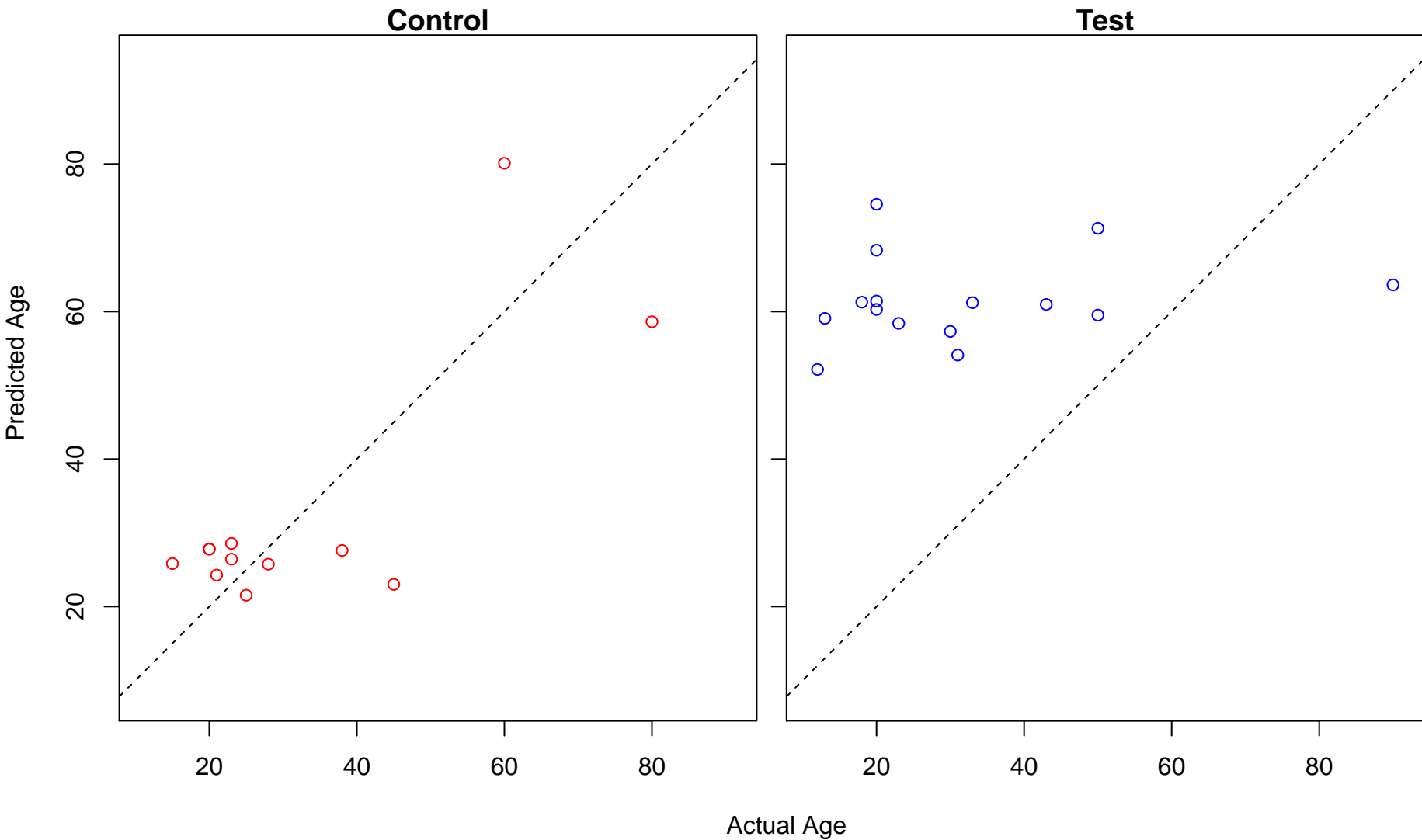


Test

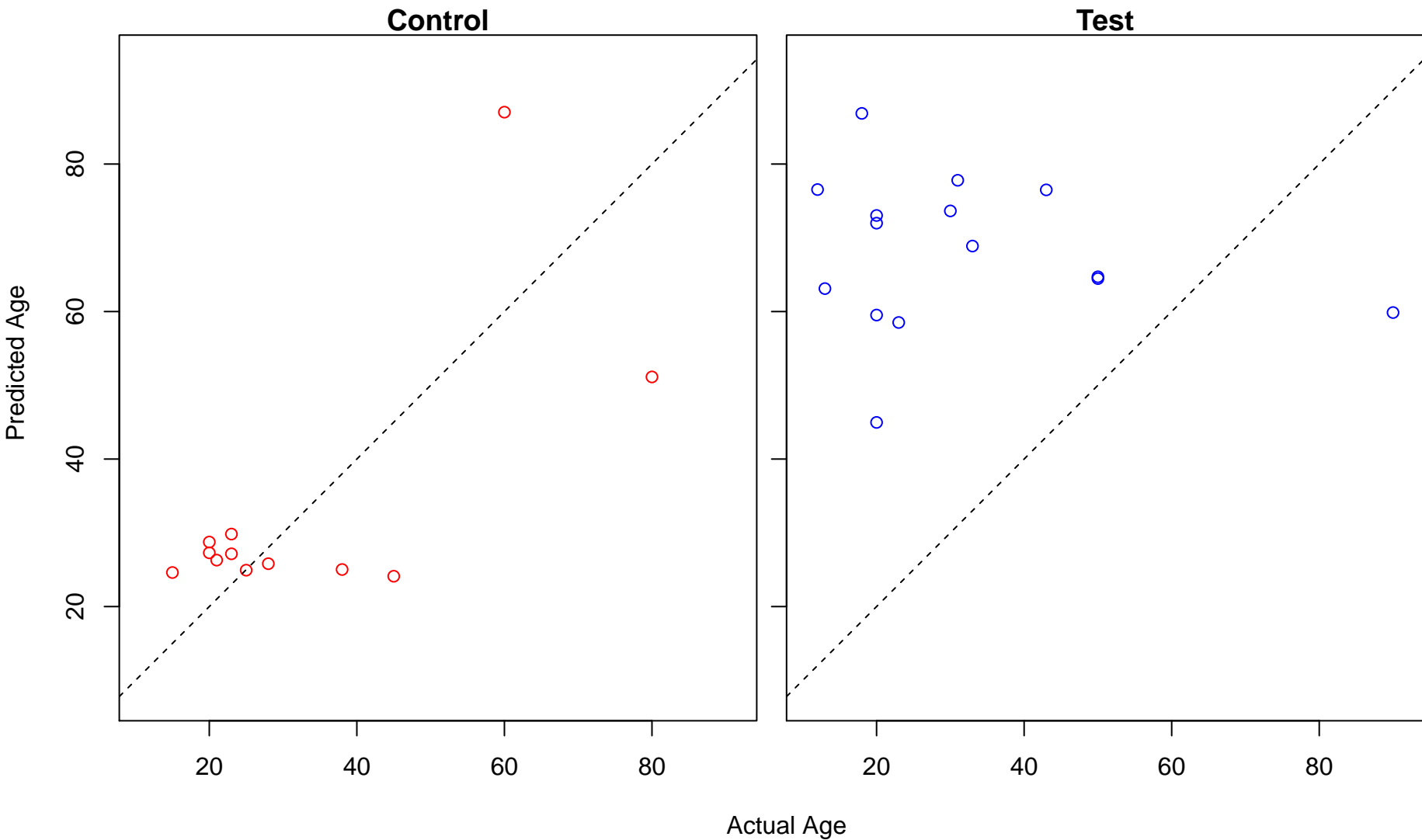


Actual Age

regulation of carbohydrate metabolic process (Score: 3.390555)

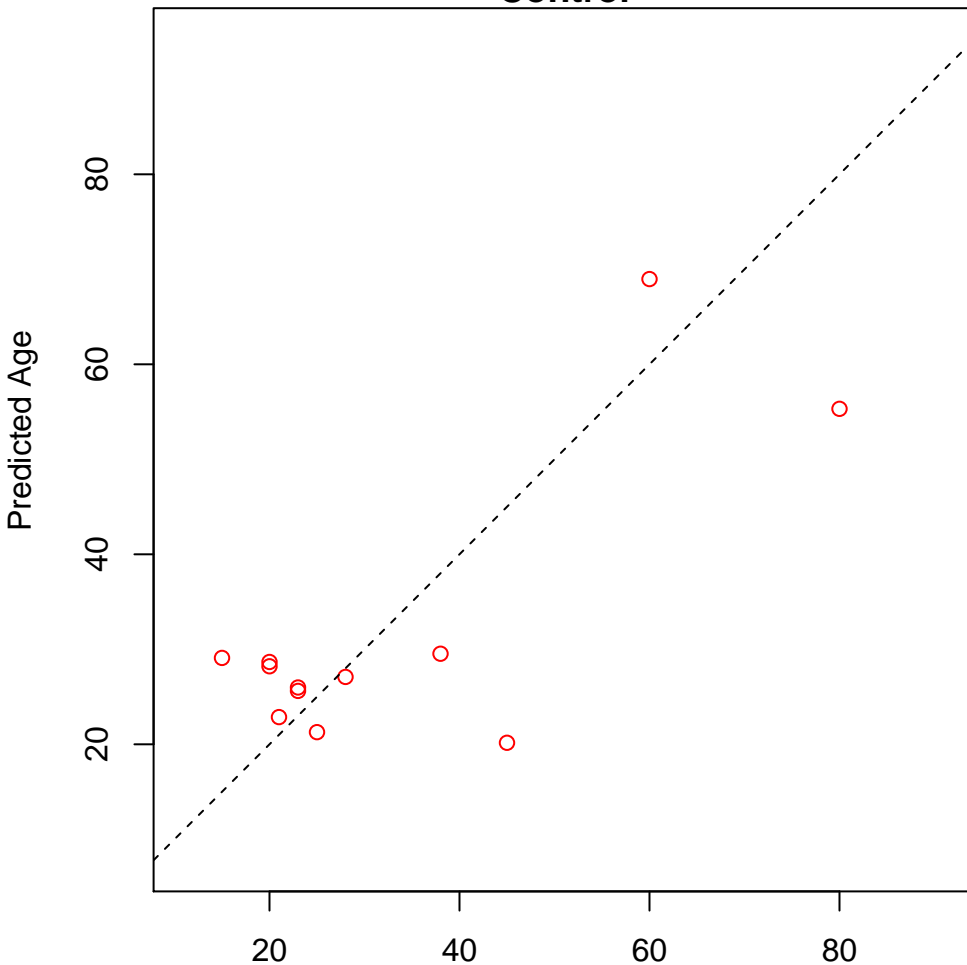


granulocyte activation (Score: 3.381933)

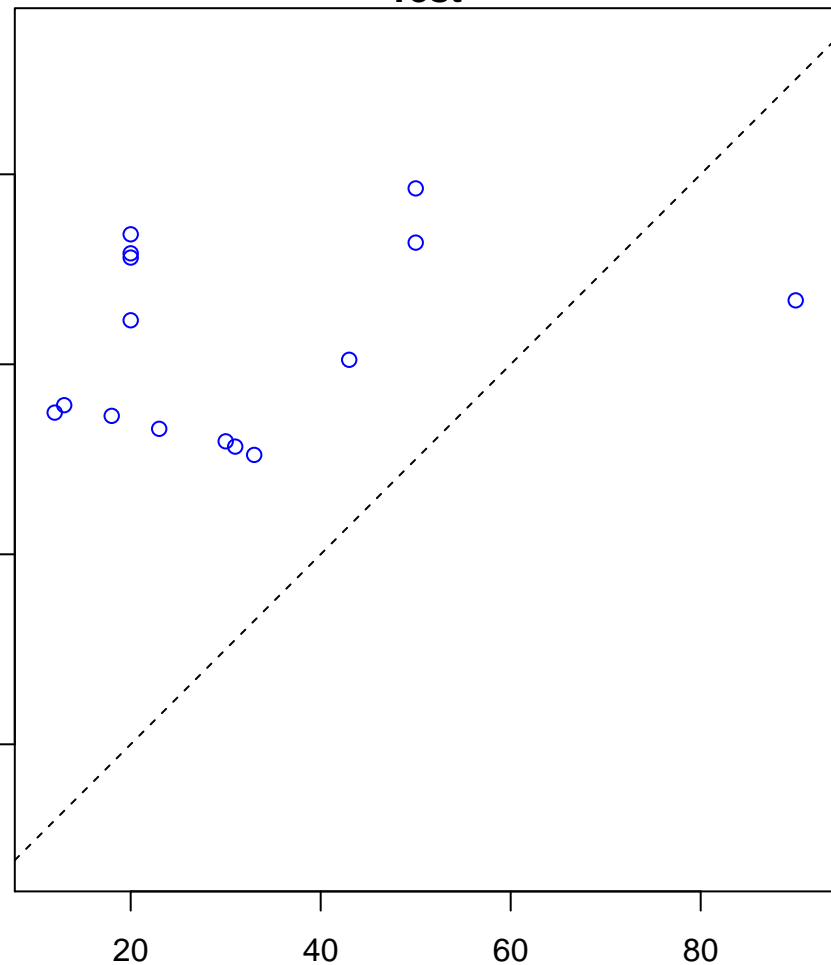


organic hydroxy compound transport (Score: 3.381933)

Control



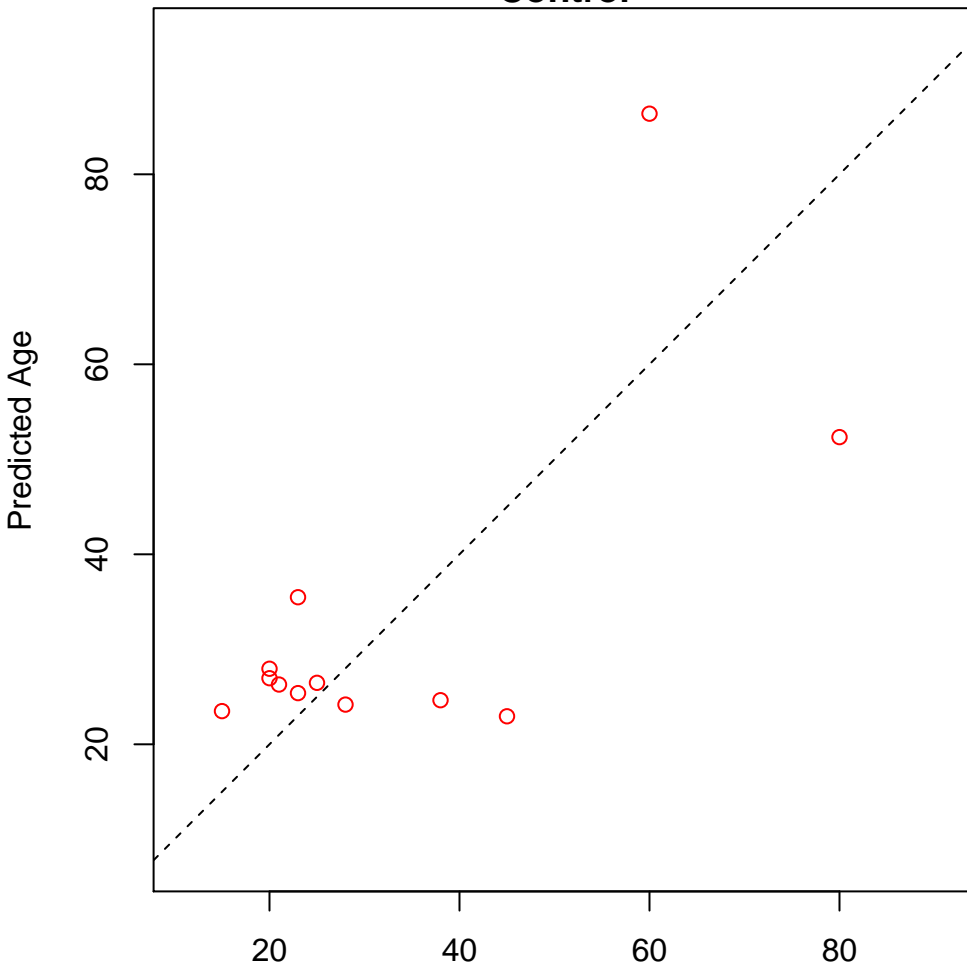
Test



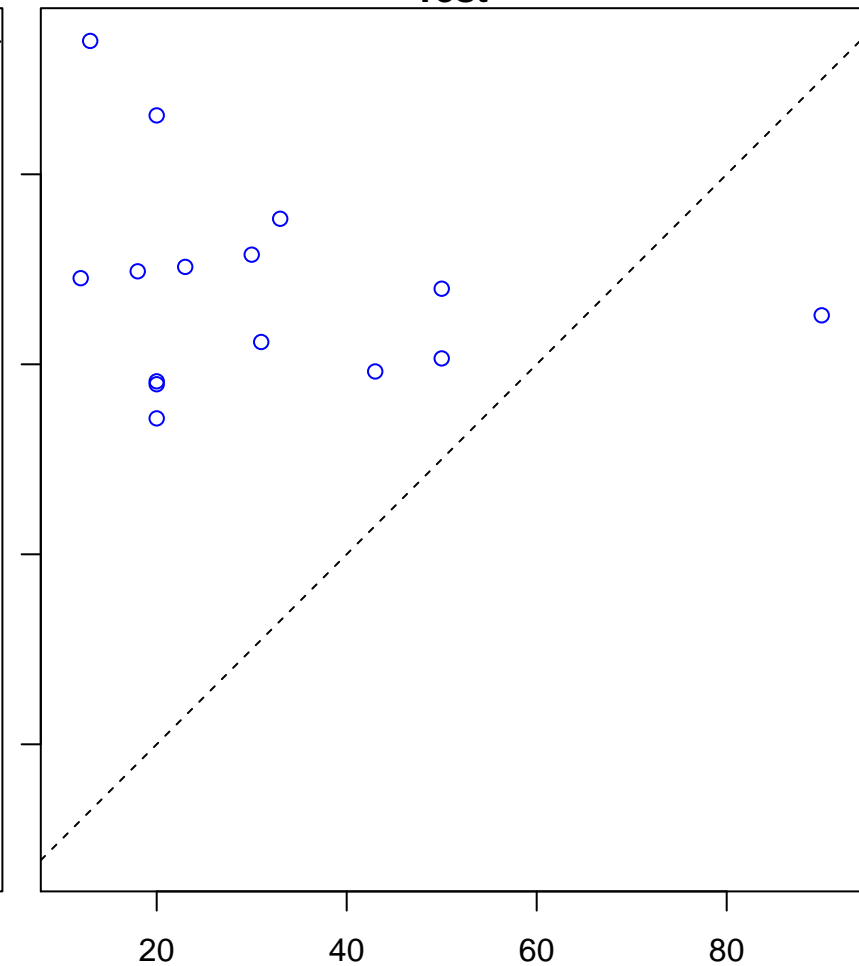
Actual Age

regulation of interleukin-10 production (Score: 3.380605)

Control

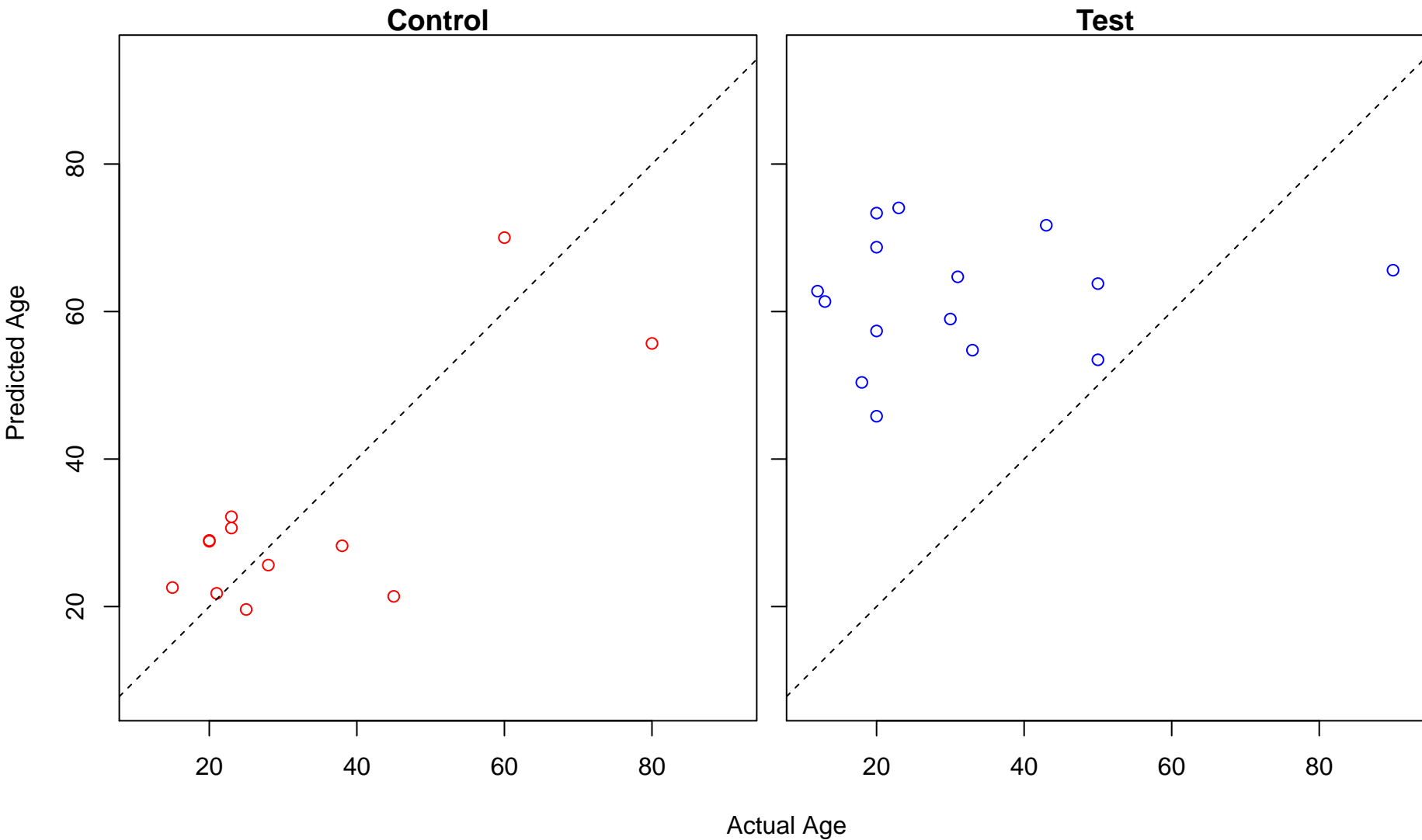


Test

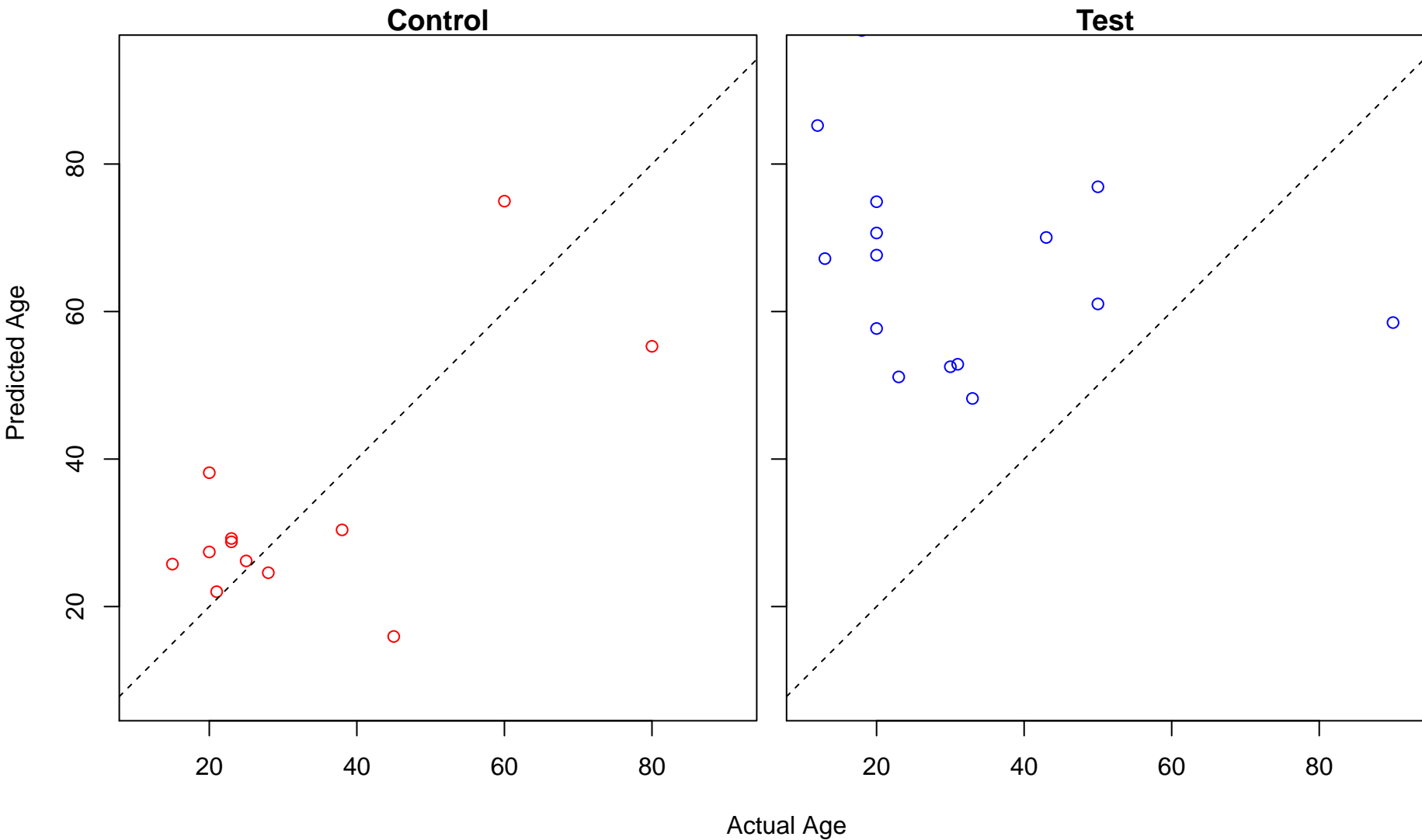


Actual Age

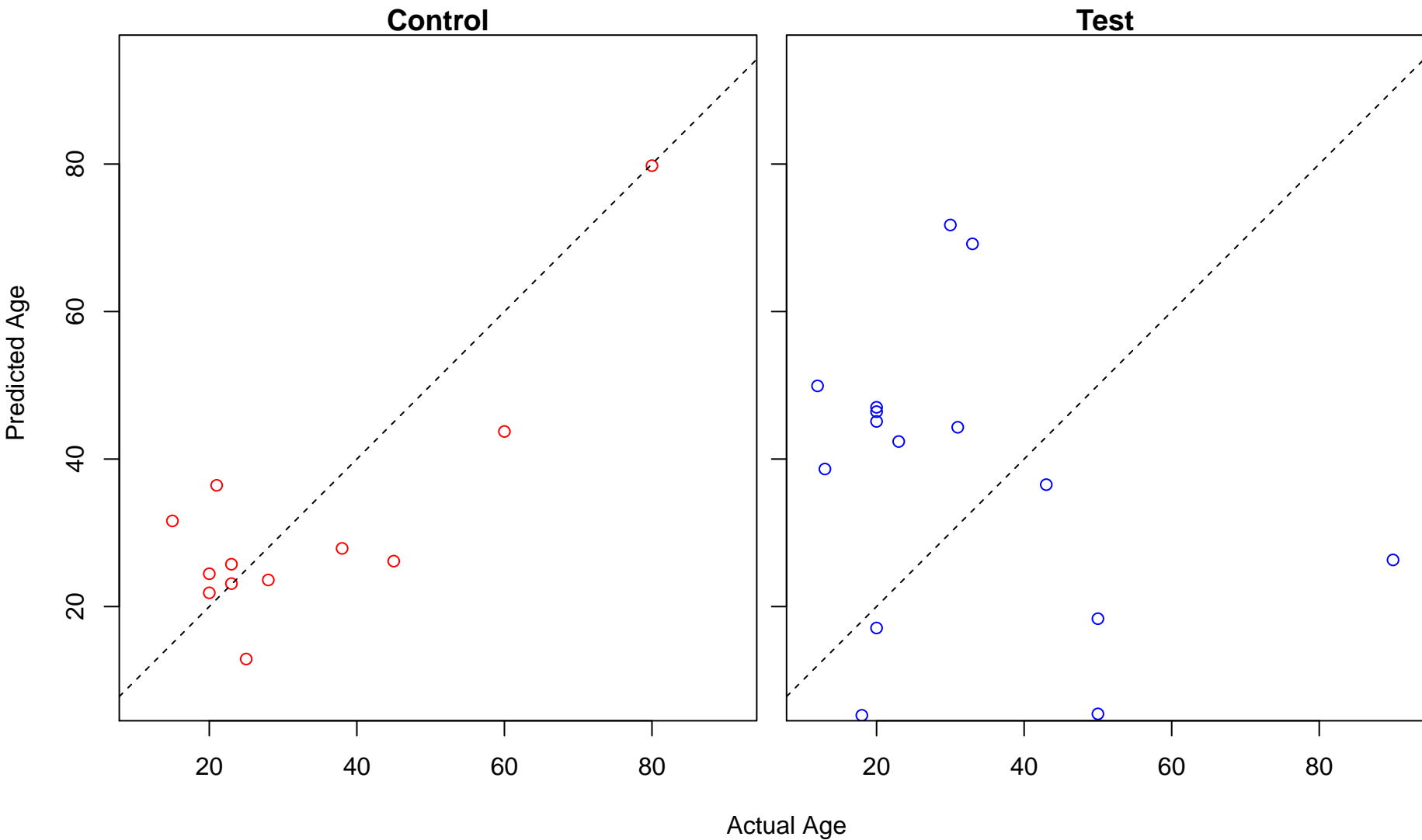
miRNA metabolic process (Score: 3.380196)



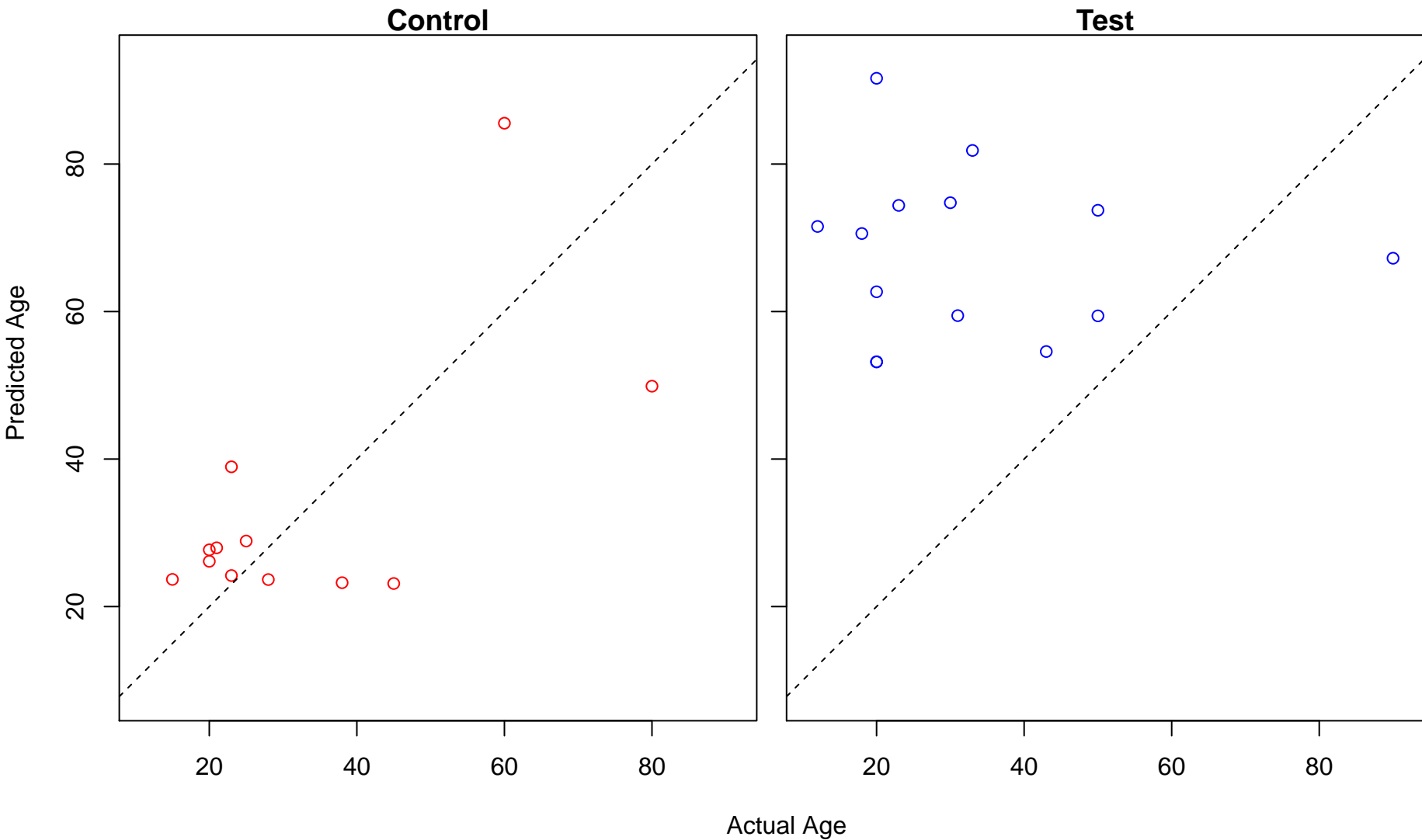
positive regulation of protein kinase C signaling (Score: 3.378651)



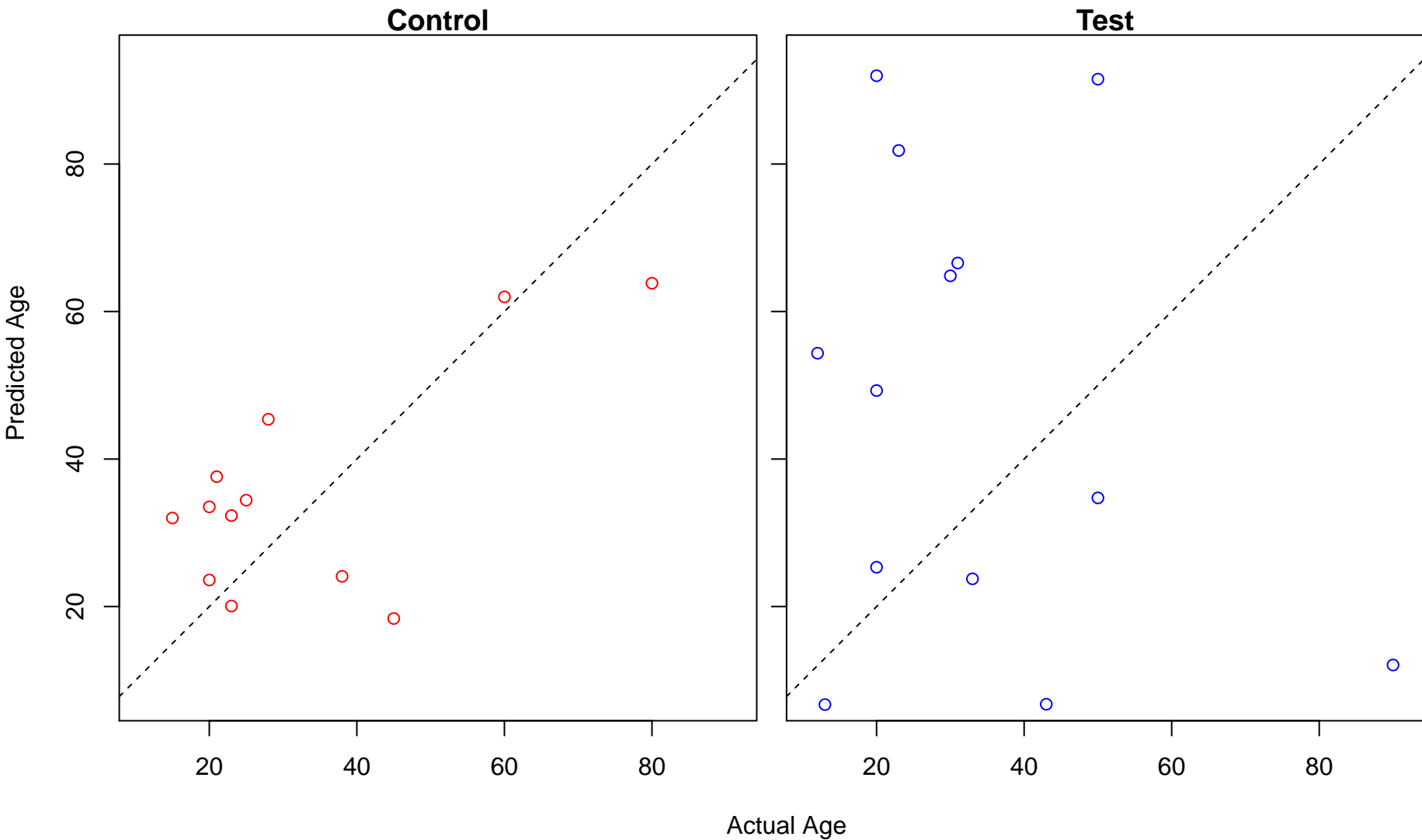
cellular component disassembly involved in execution phase of apoptosis (Score: 3.378257)



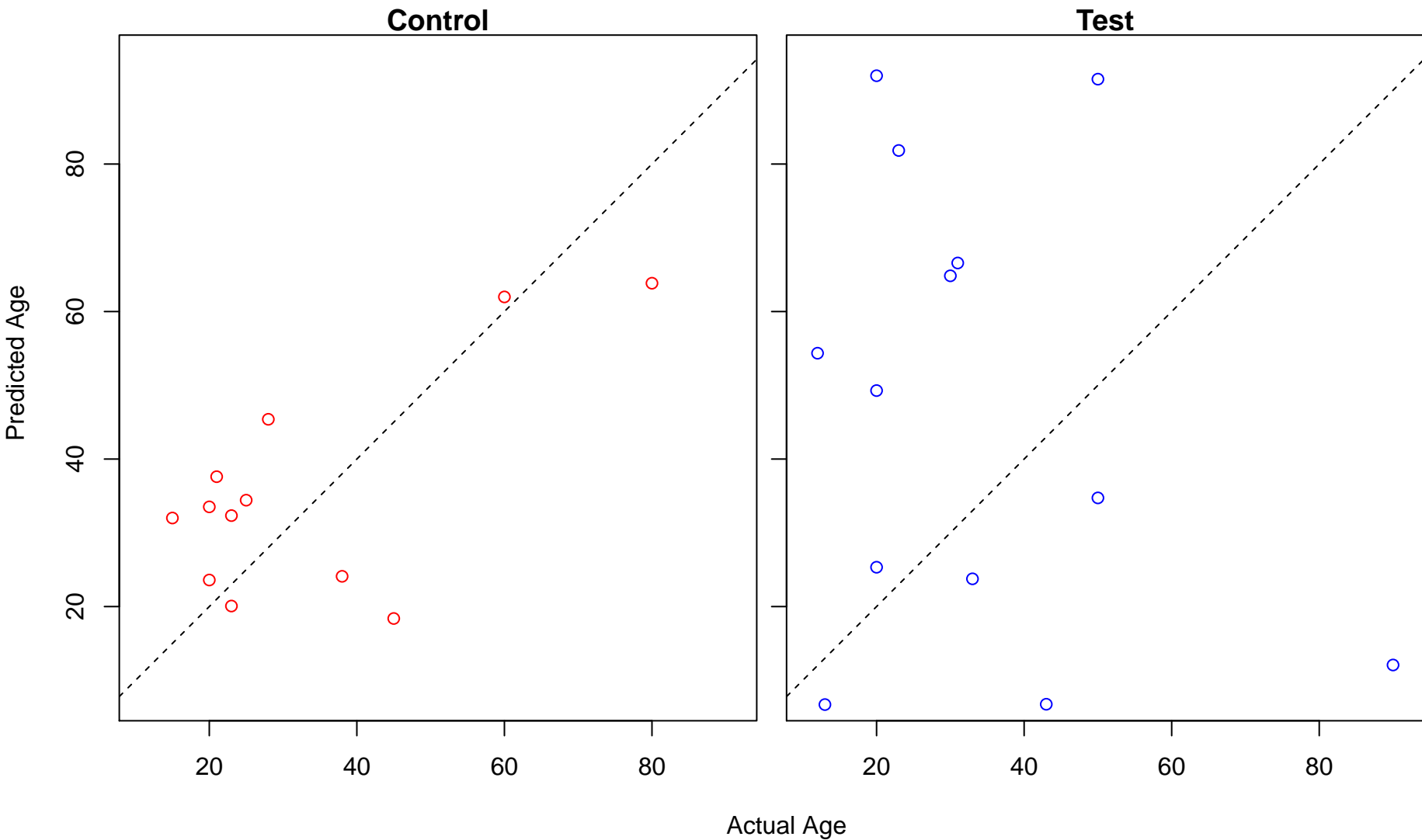
inflammatory response to antigenic stimulus (Score: 3.376638)



mesenchymal to epithelial transition involved in metanephros morphogenesis (Score: 3.374401)

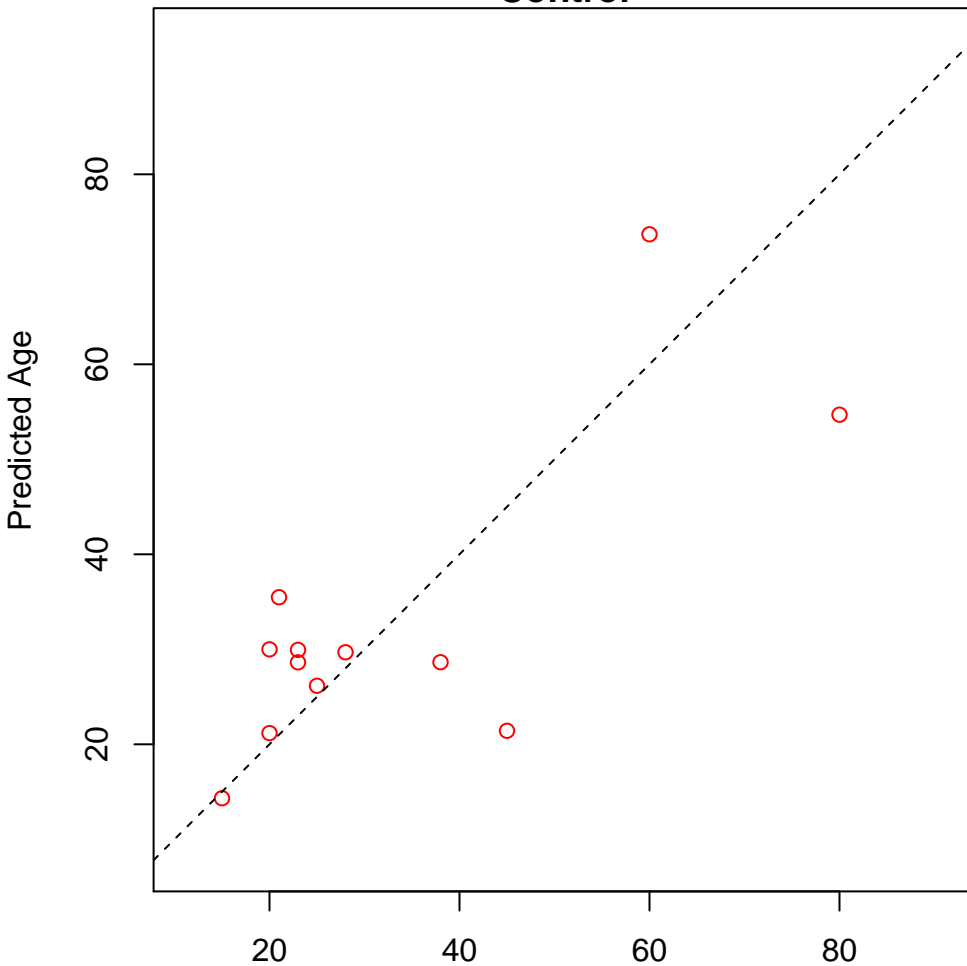


metanephric renal vesicle morphogenesis (Score: 3.374401)

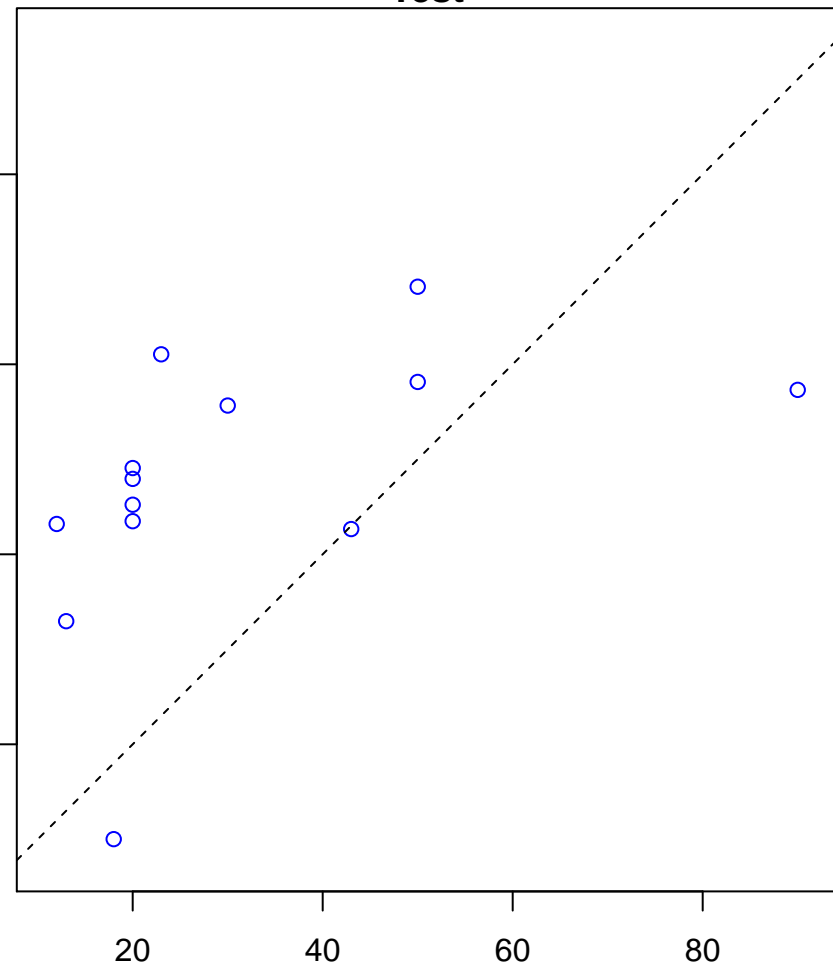


complement activation, lectin pathway (Score: 3.373737)

Control

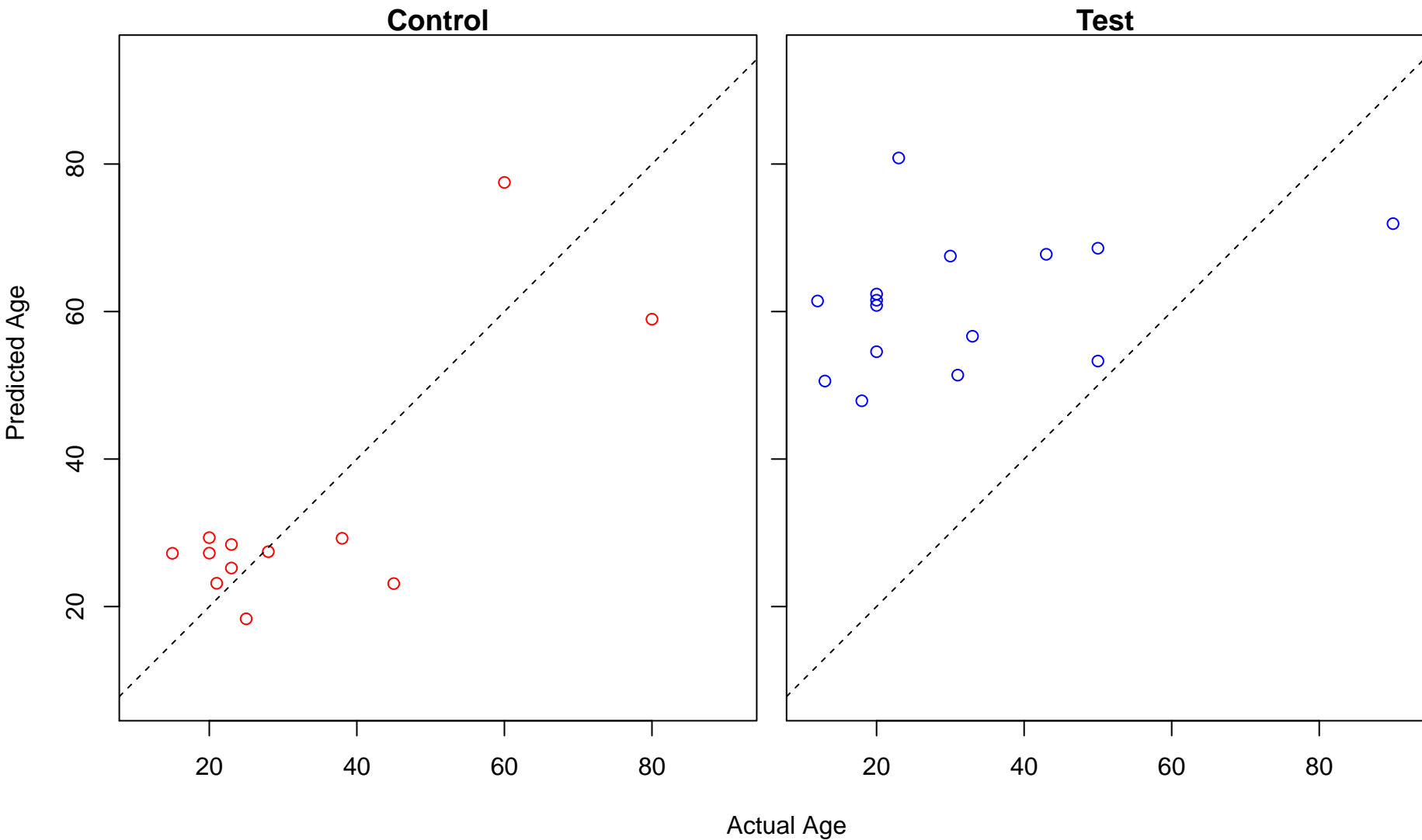


Test

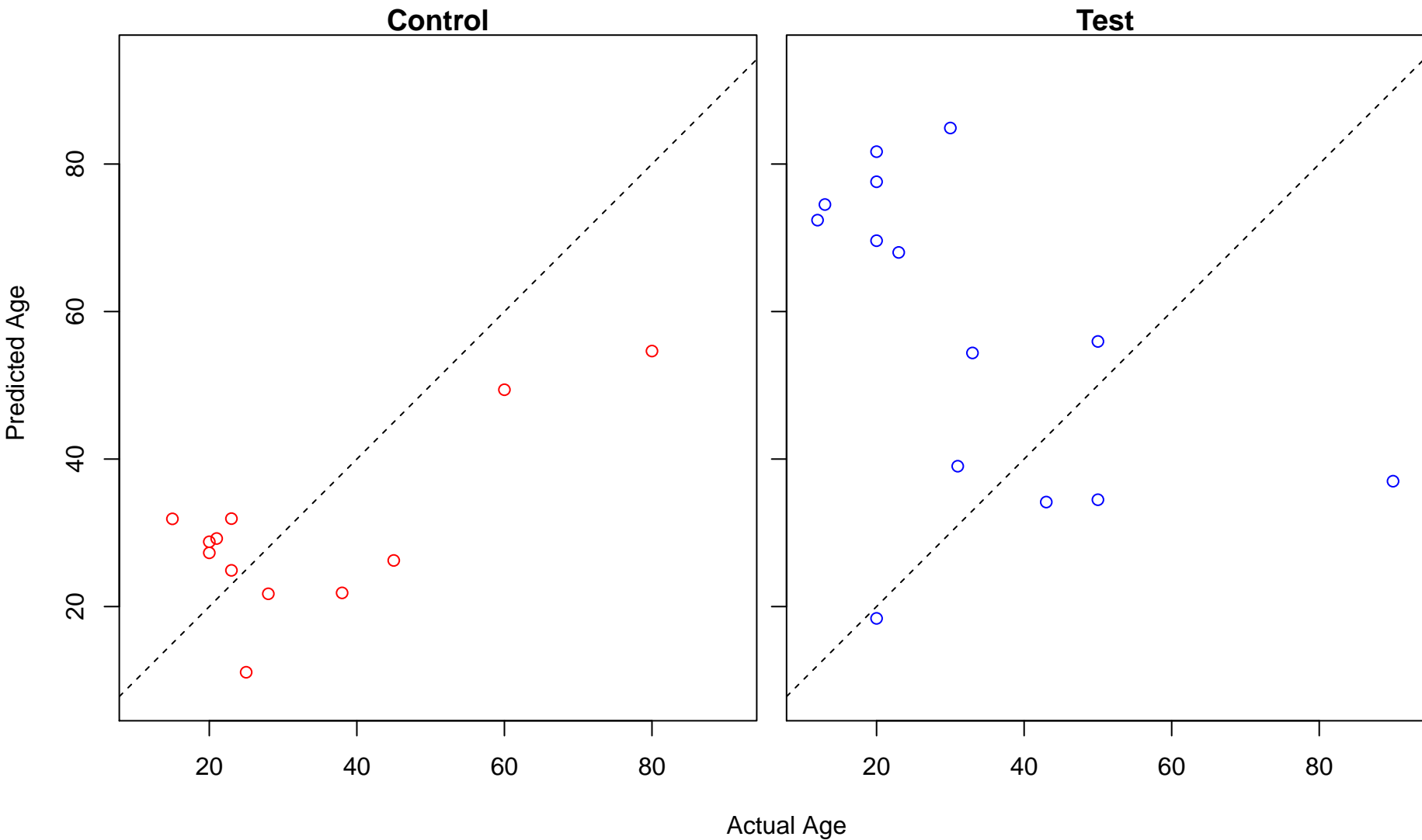


Actual Age

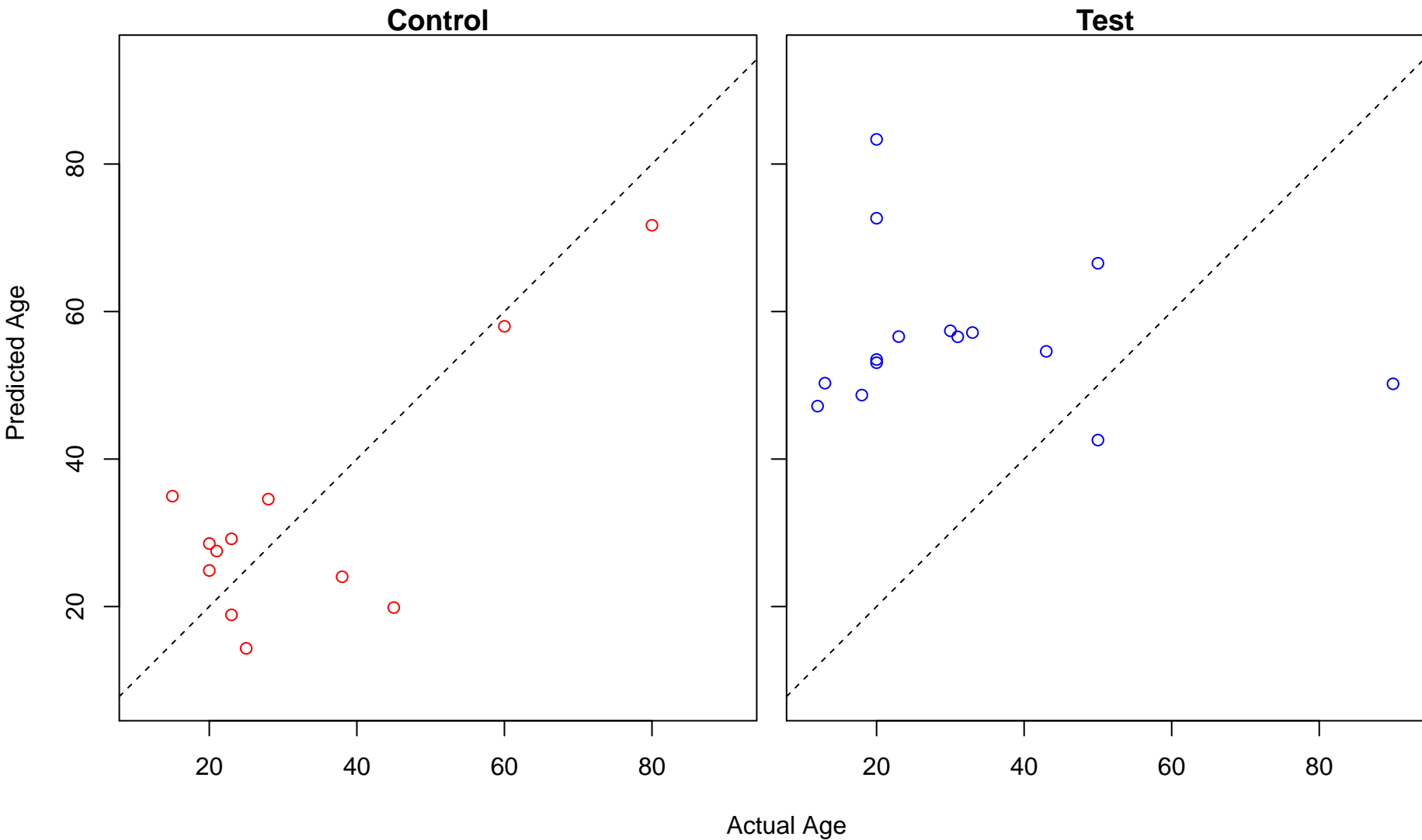
protein complex localization (Score: 3.372375)



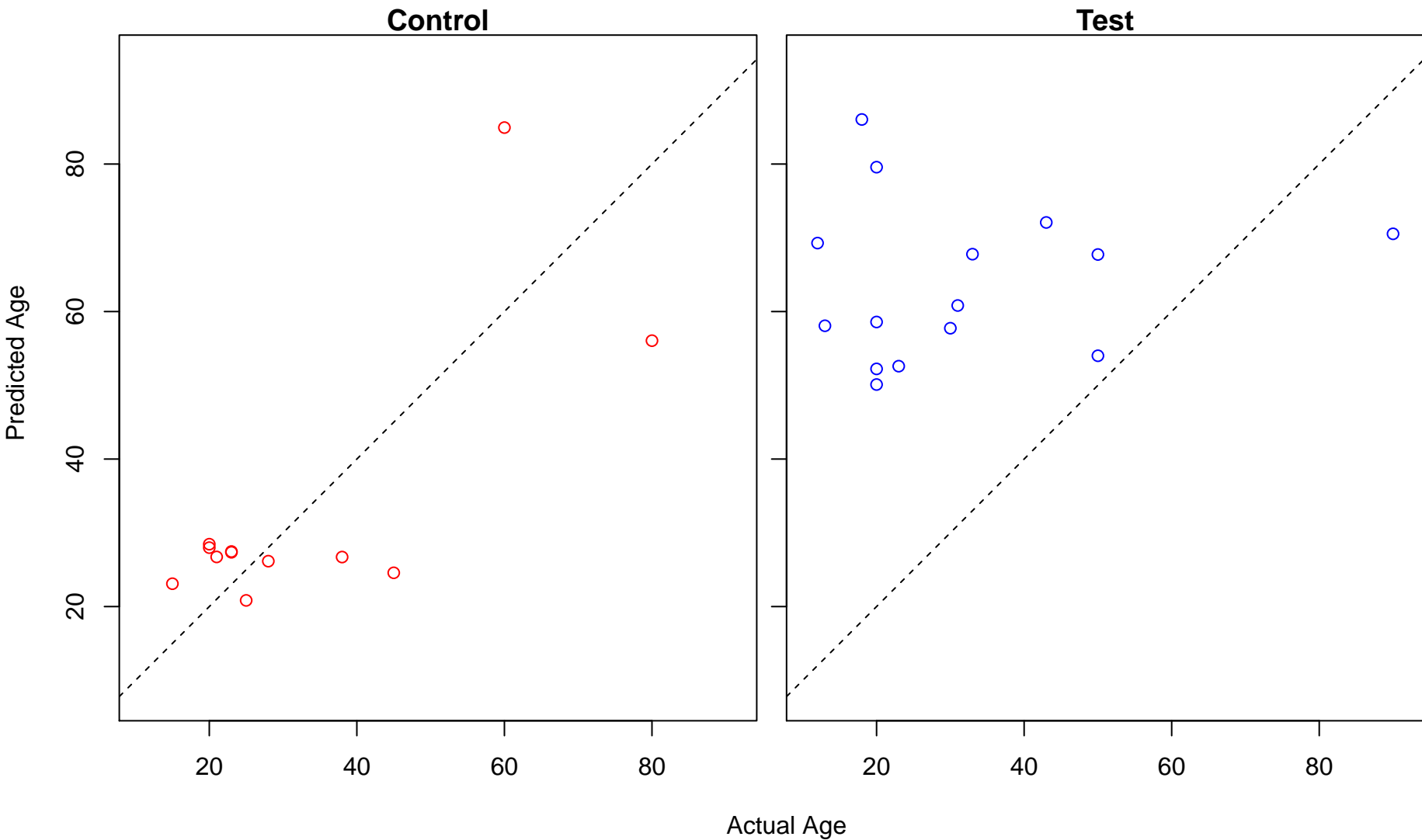
regulation of T-helper 17 cell differentiation (Score: 3.371527)



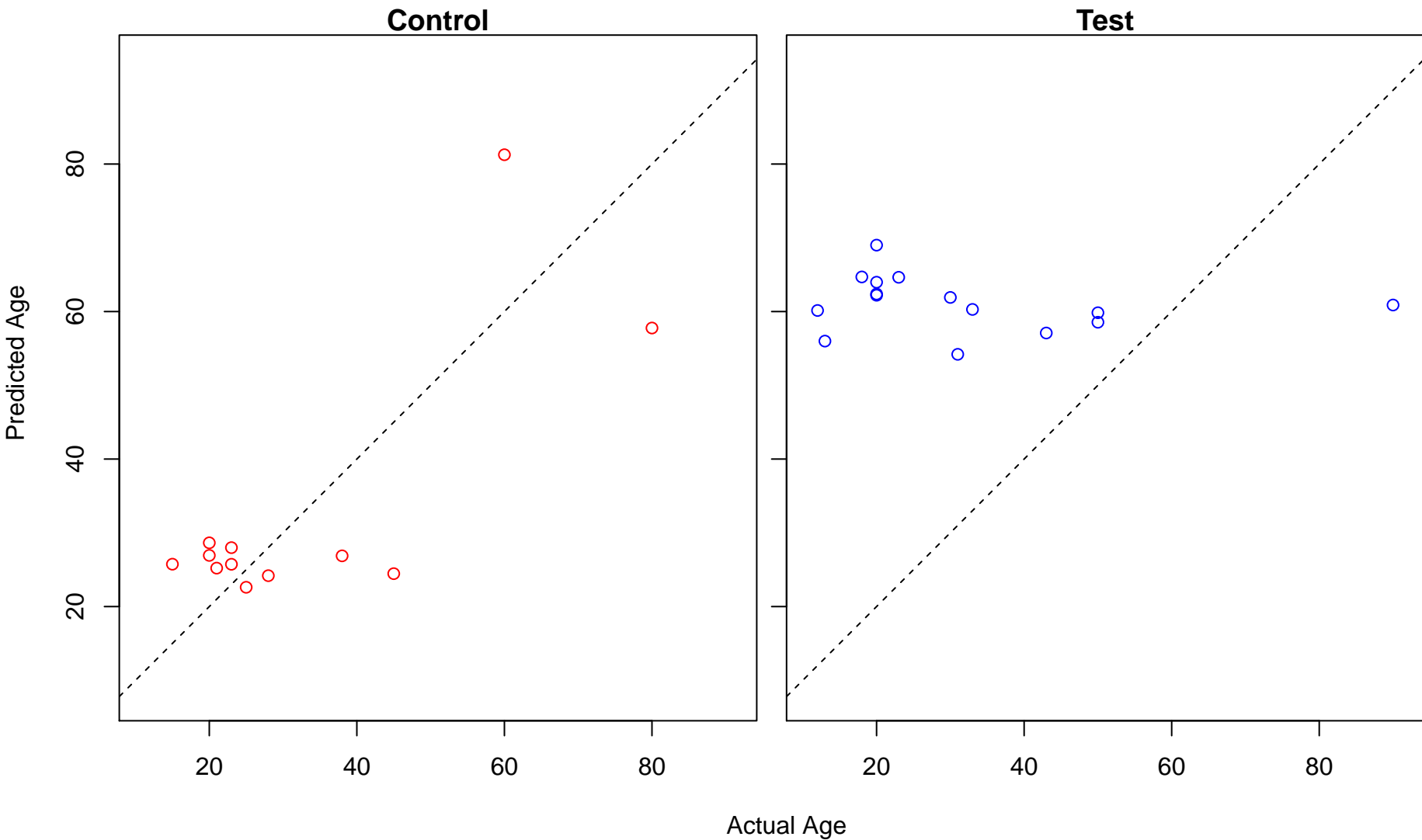
regulation of ion homeostasis (Score: 3.371489)



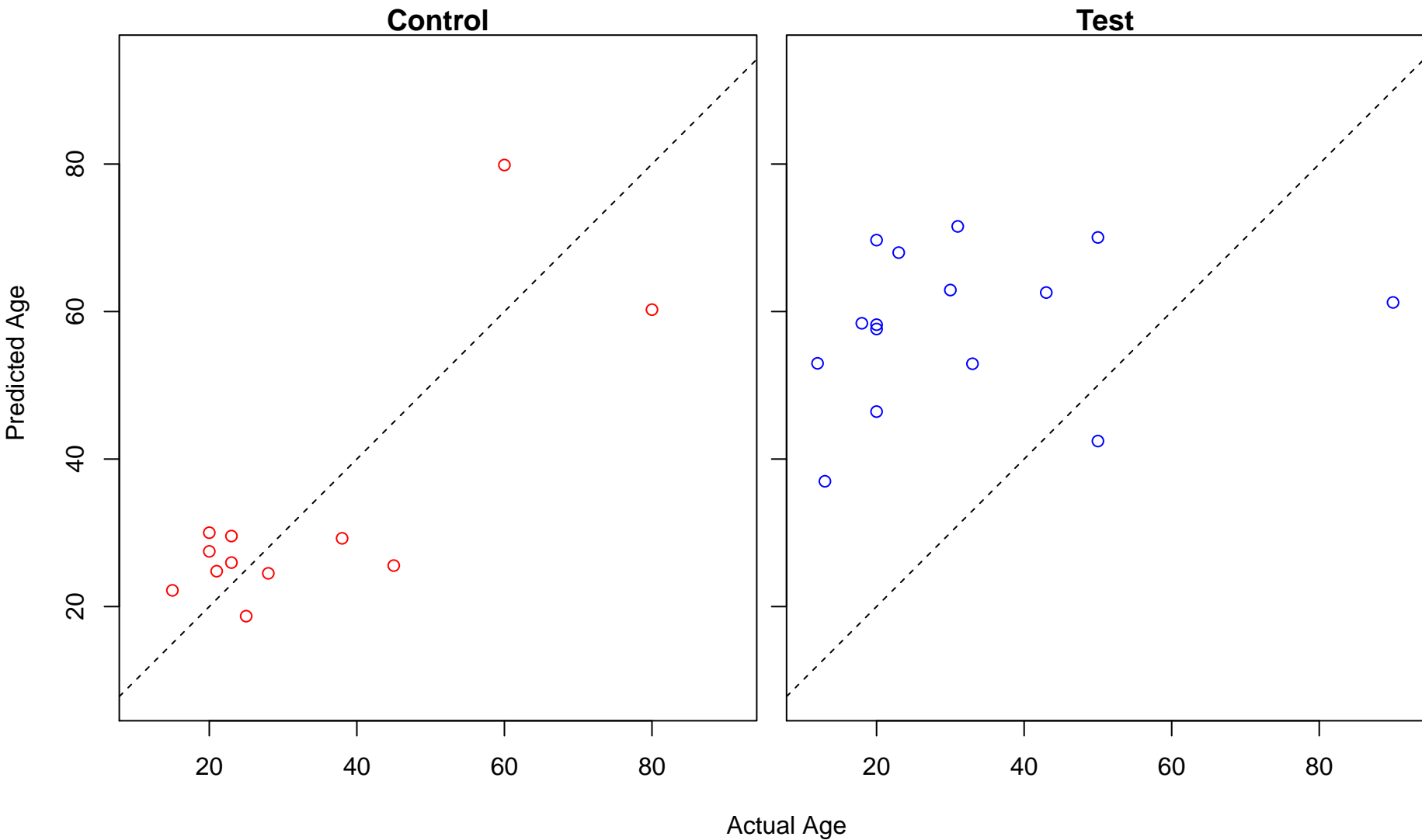
pyrimidine ribonucleoside metabolic process (Score: 3.370246)



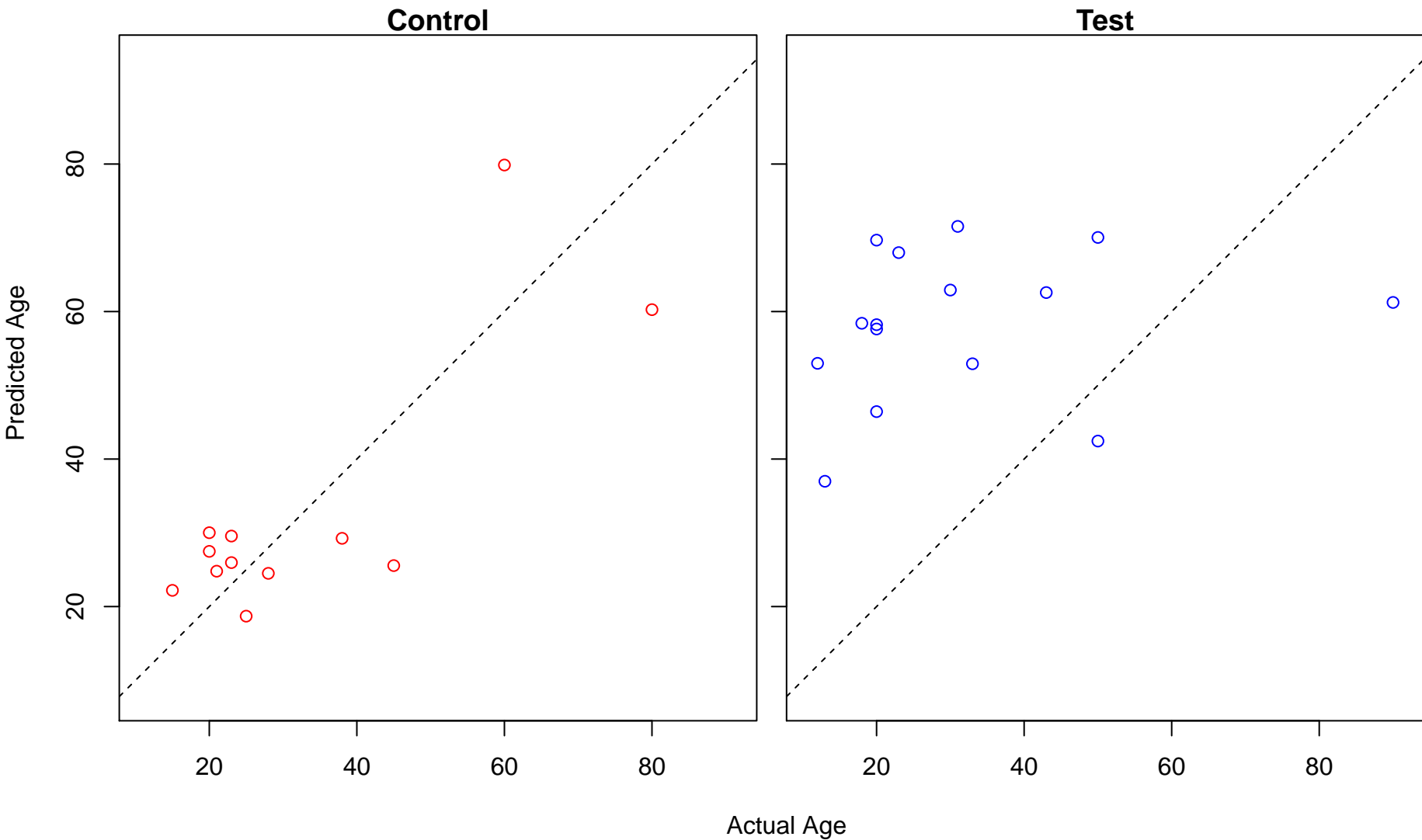
RNA phosphodiester bond hydrolysis, exonucleolytic (Score: 3.368658)



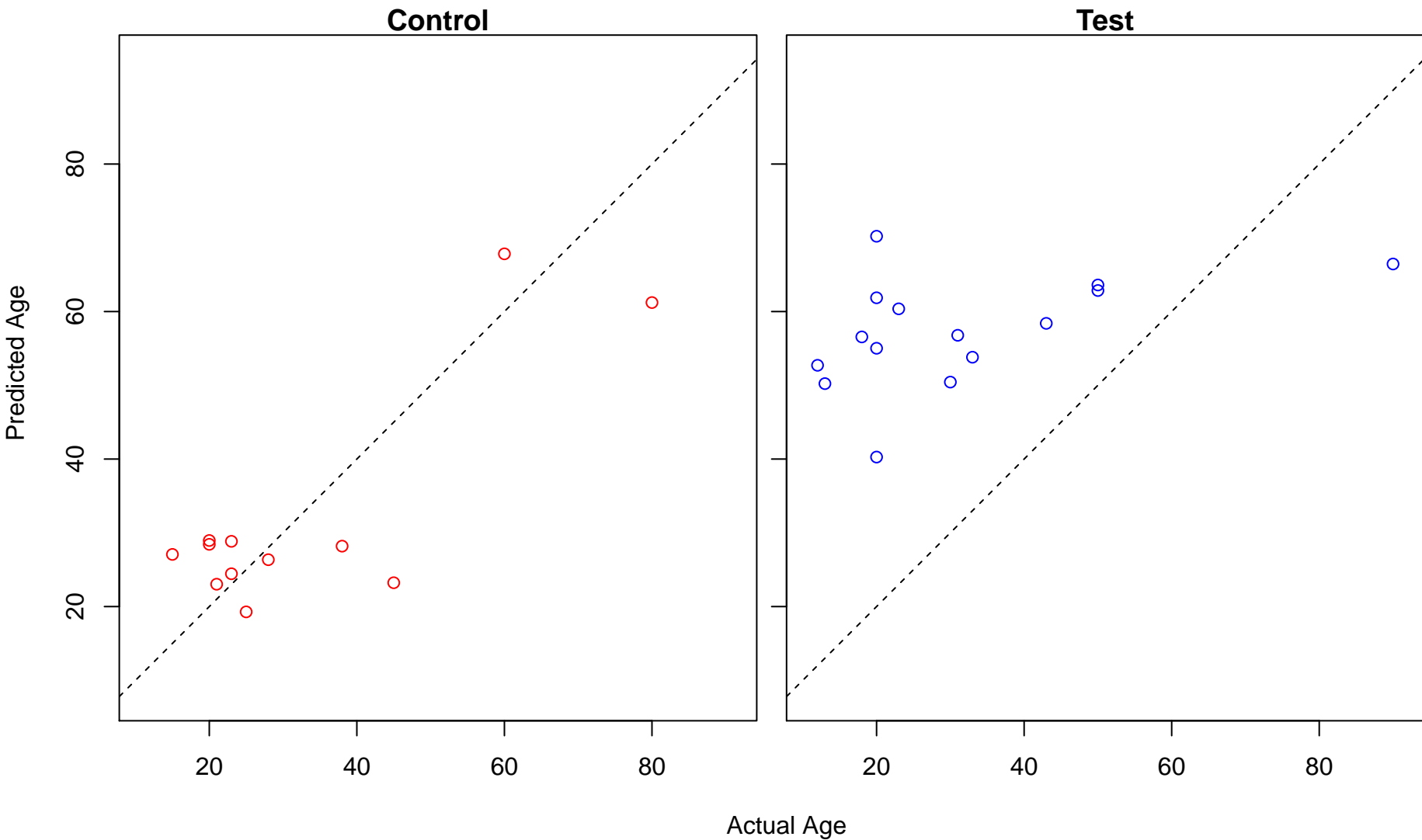
regulation of MHC class I biosynthetic process (Score: 3.365367)



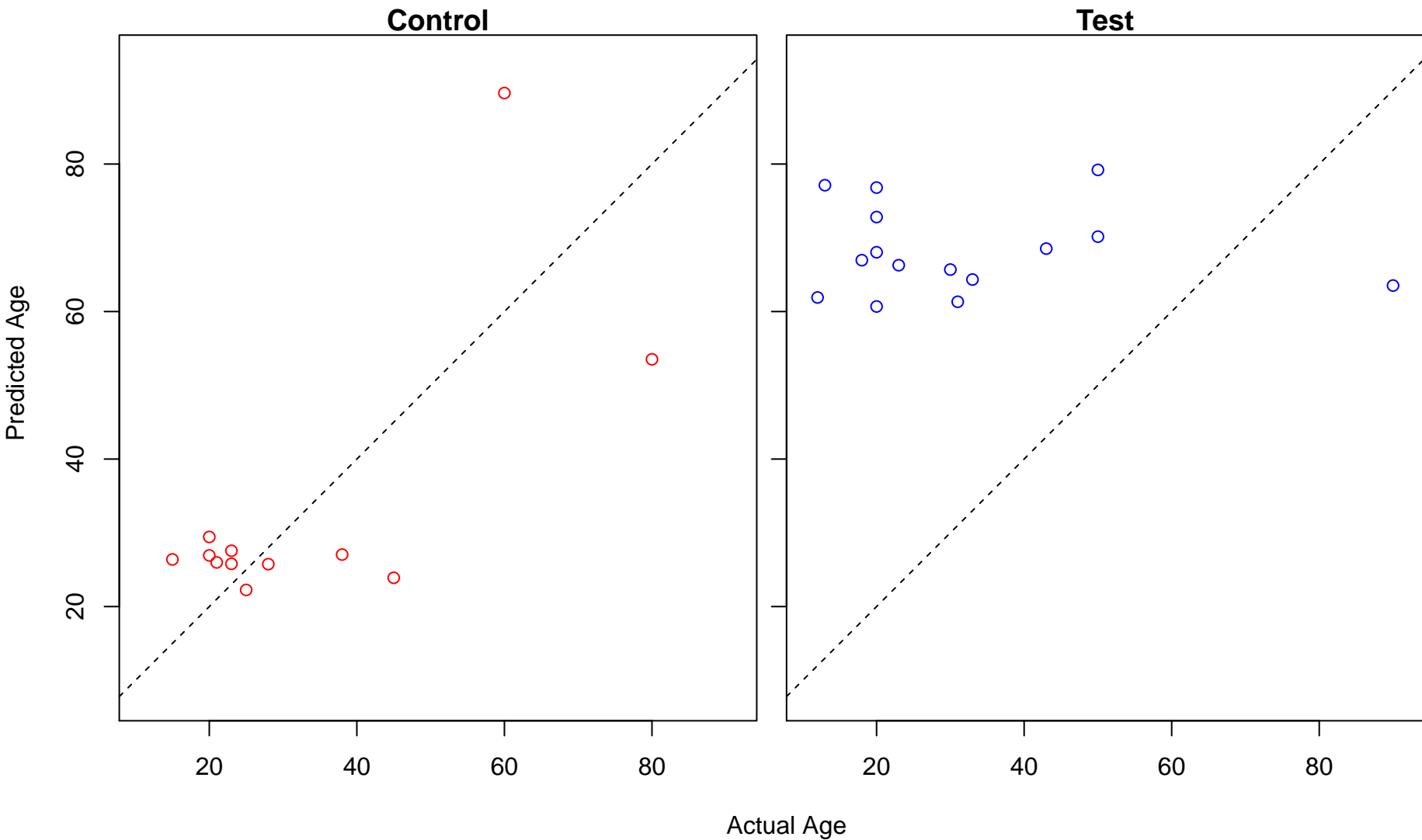
positive regulation of MHC class I biosynthetic process (Score: 3.365367)



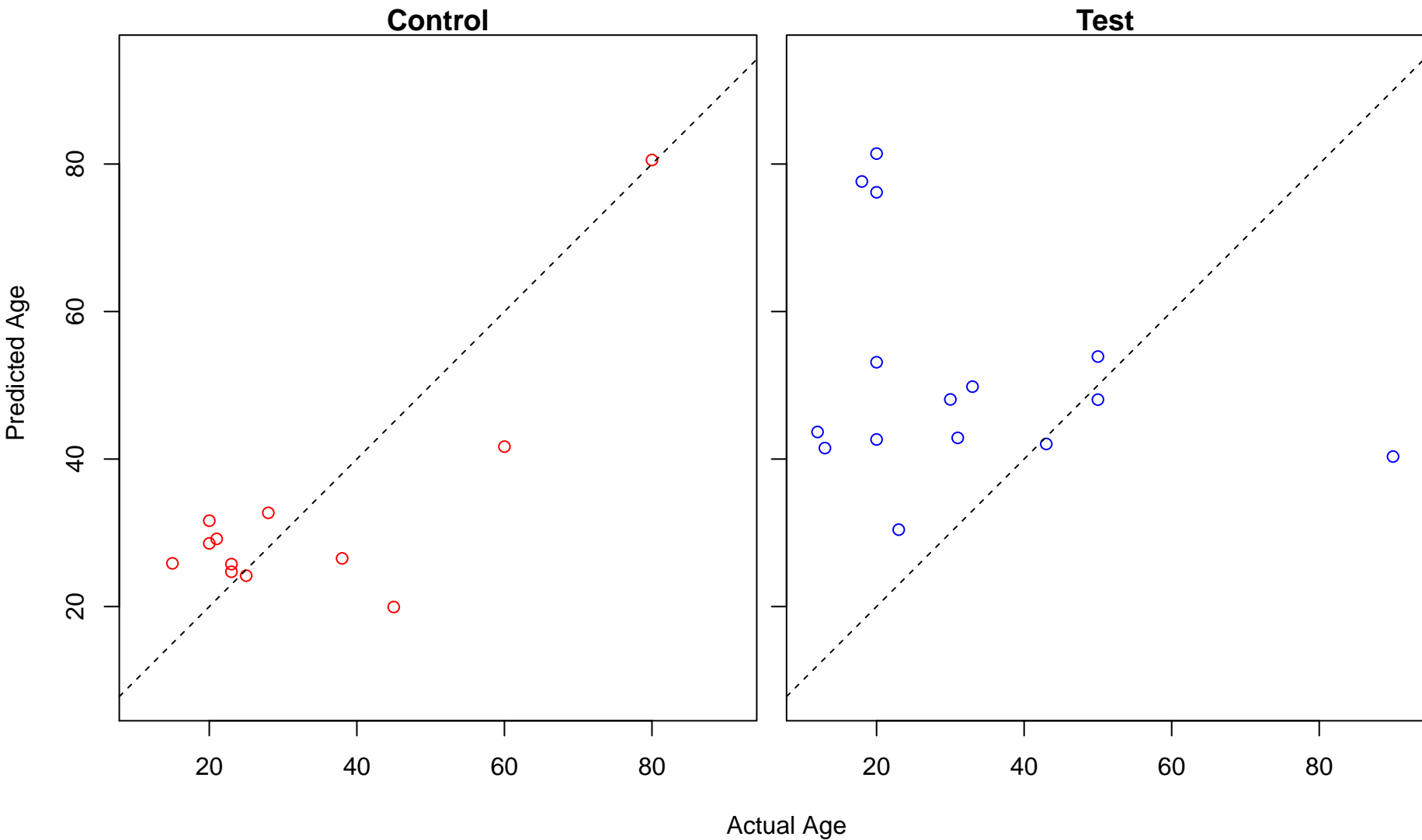
macromolecule deacylation (Score: 3.365199)



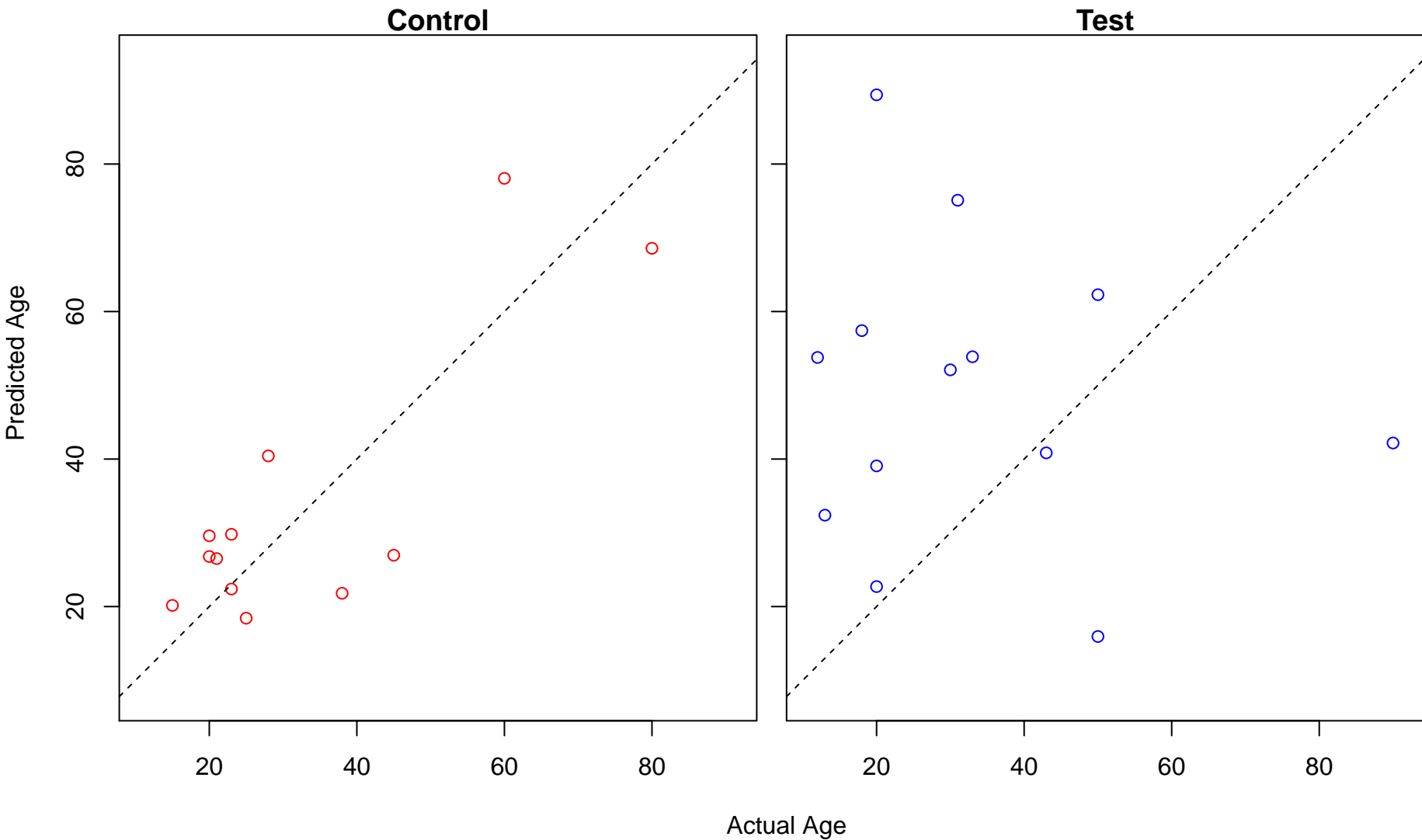
regulation of nuclease activity (Score: 3.362008)



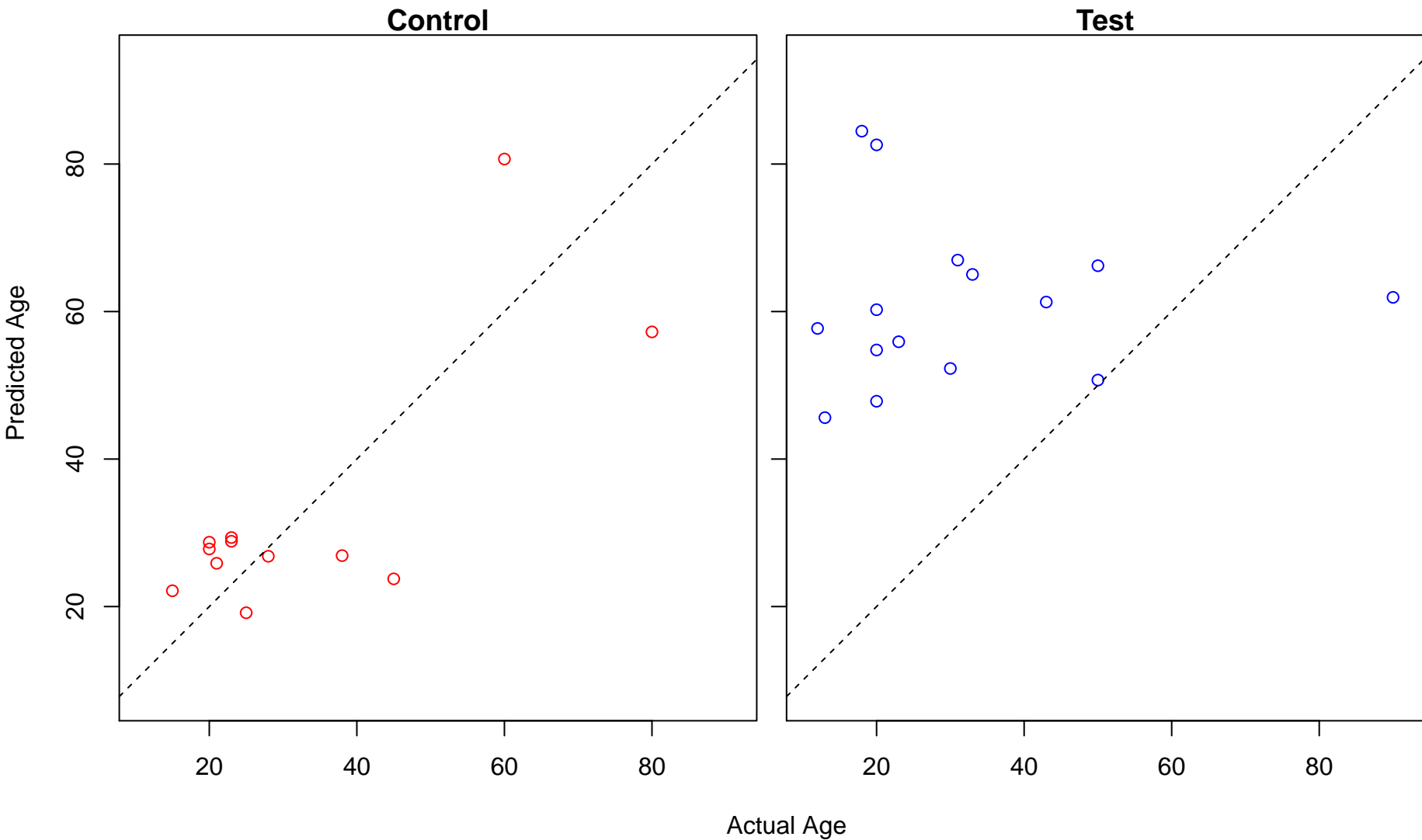
protein activation cascade (Score: 3.360952)



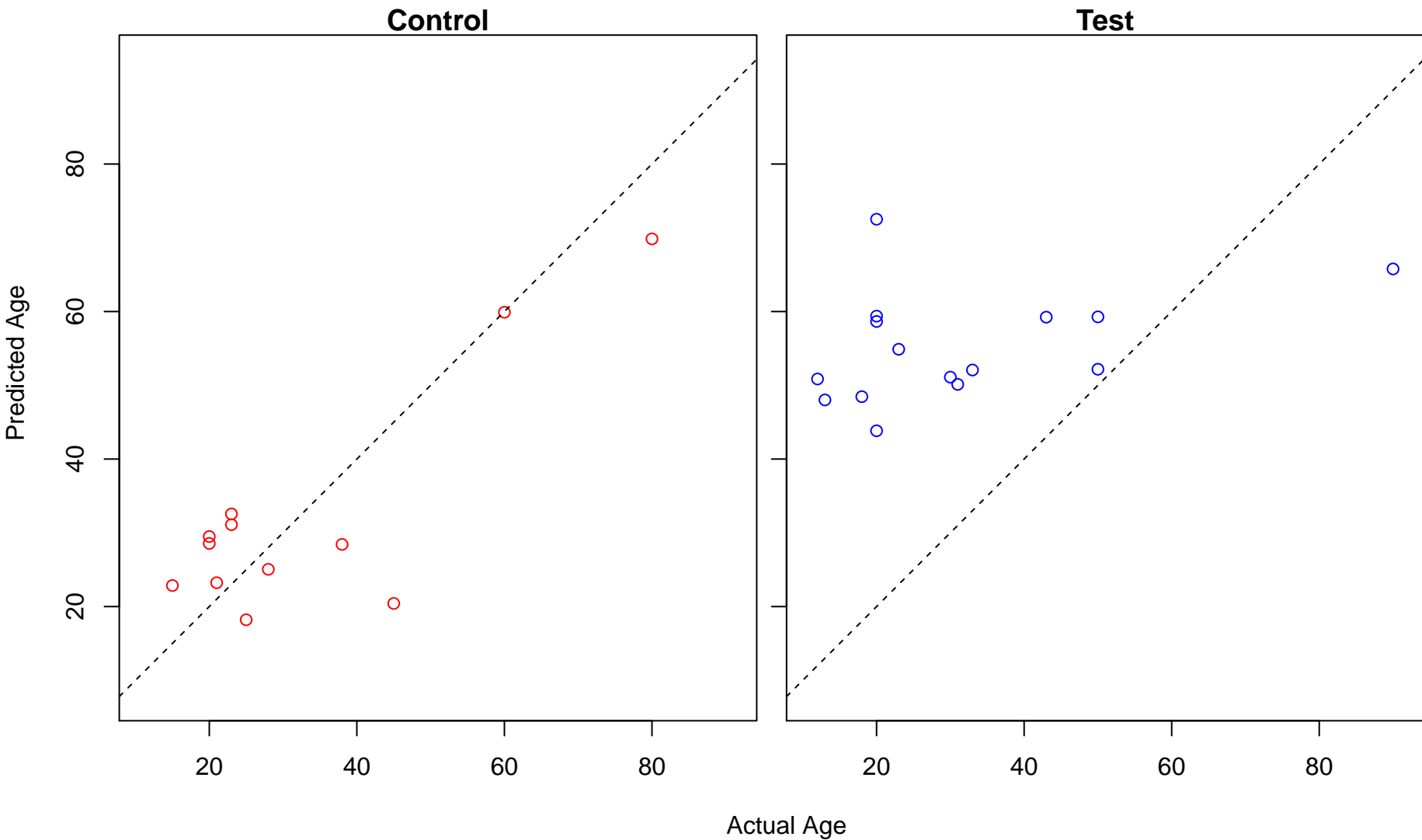
regulation of double-strand break repair via homologous recombination (Score: 3.360105)



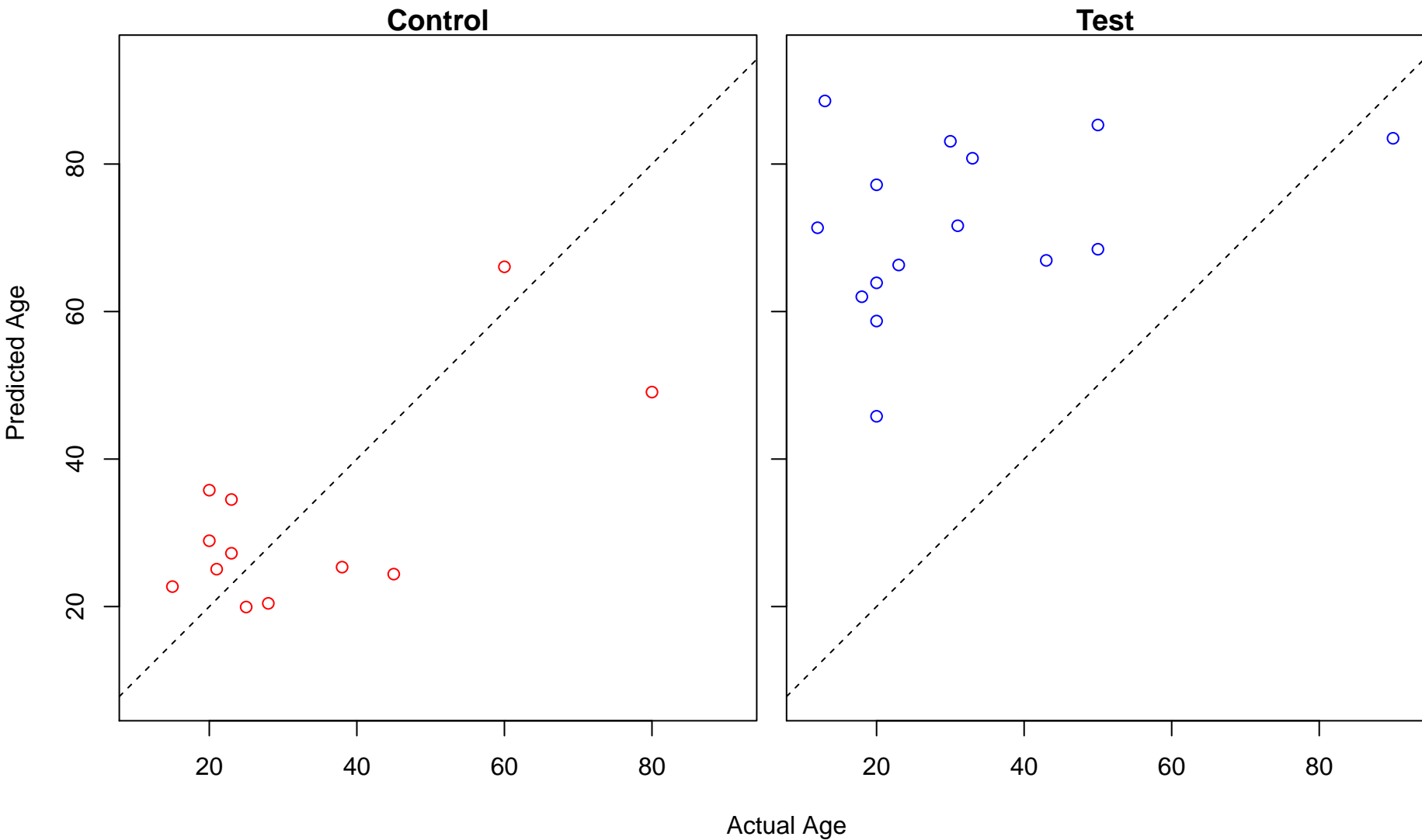
phosphorylated carbohydrate dephosphorylation (Score: 3.357838)



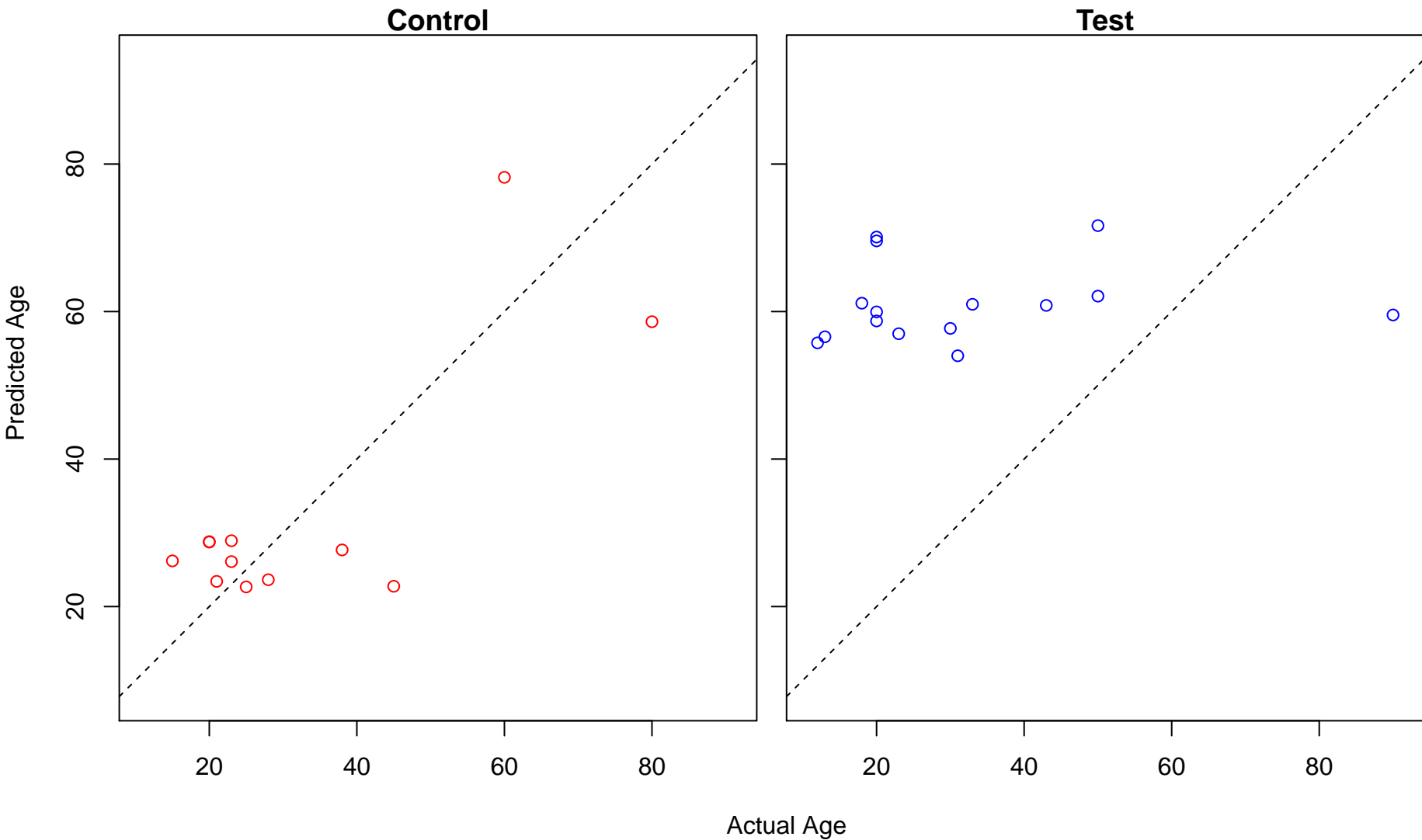
regulation of histone H3-K27 methylation (Score: 3.354068)



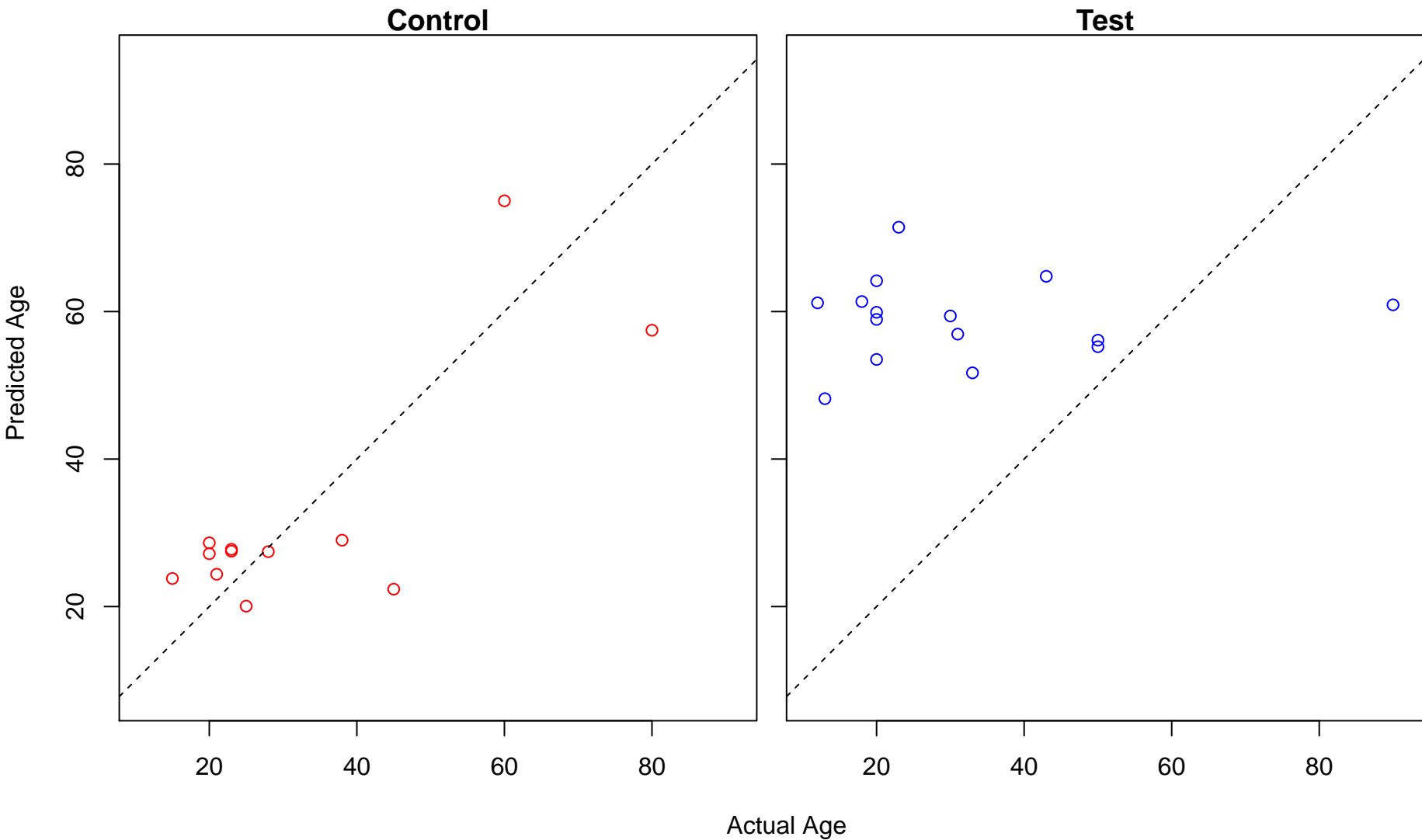
regulation of neuroblast proliferation (Score: 3.352094)



regulation of carbohydrate biosynthetic process (Score: 3.351460)

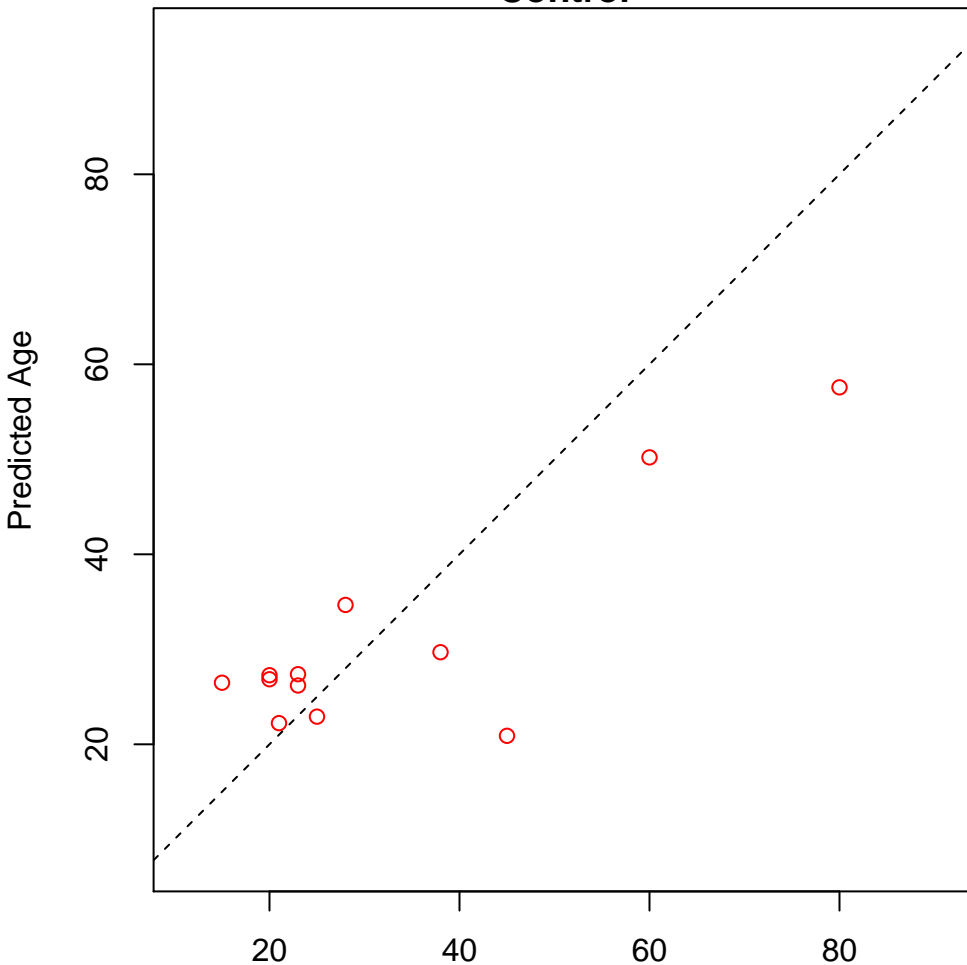


phosphatidylethanolamine metabolic process (Score: 3.351040)

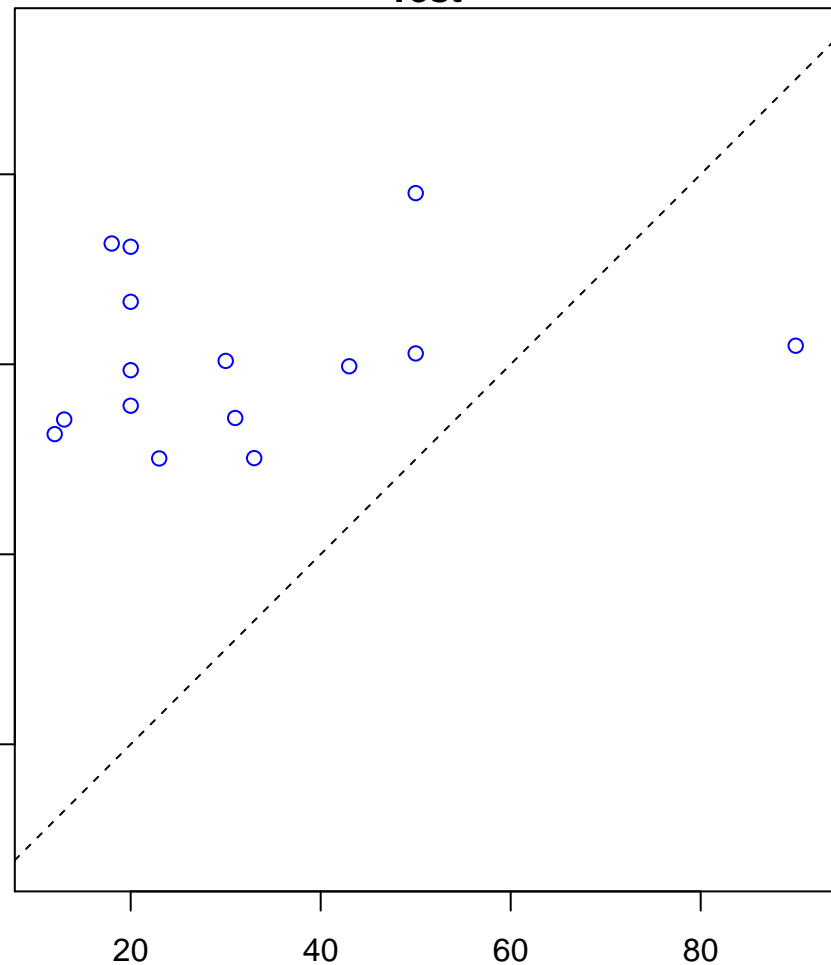


regulation of beta-amyloid formation (Score: 3.350512)

Control



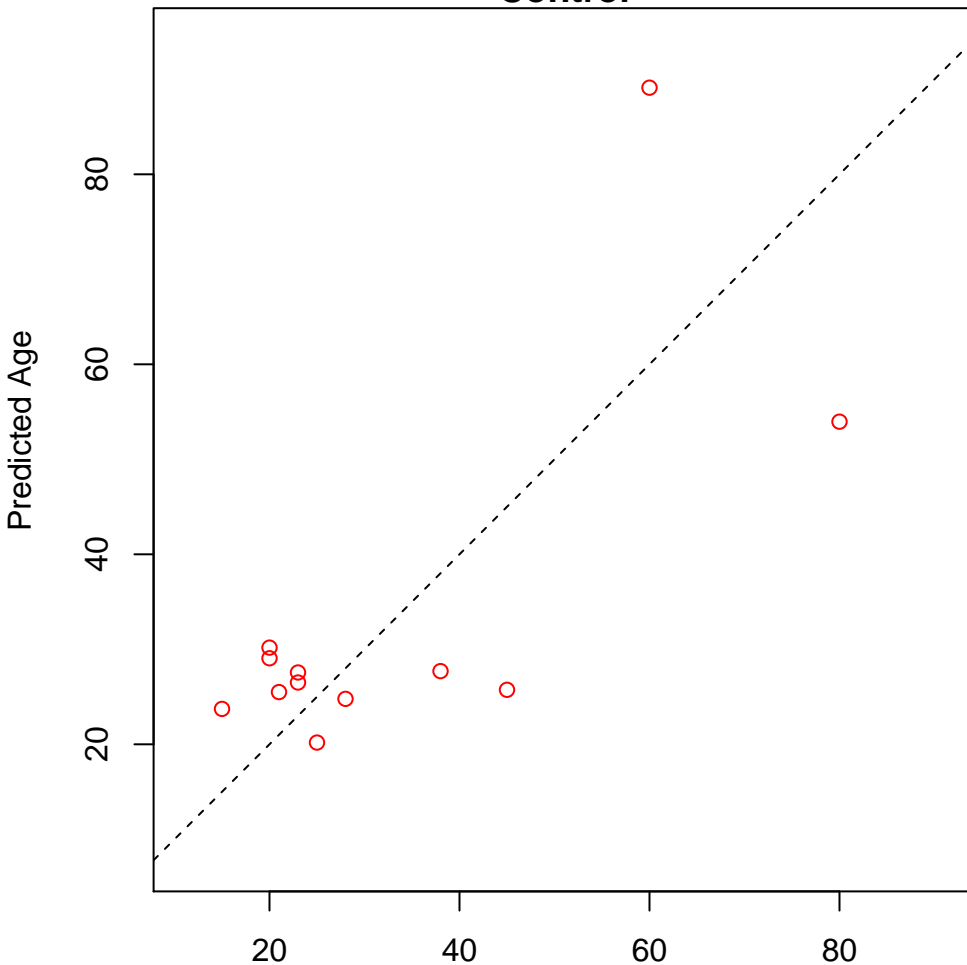
Test



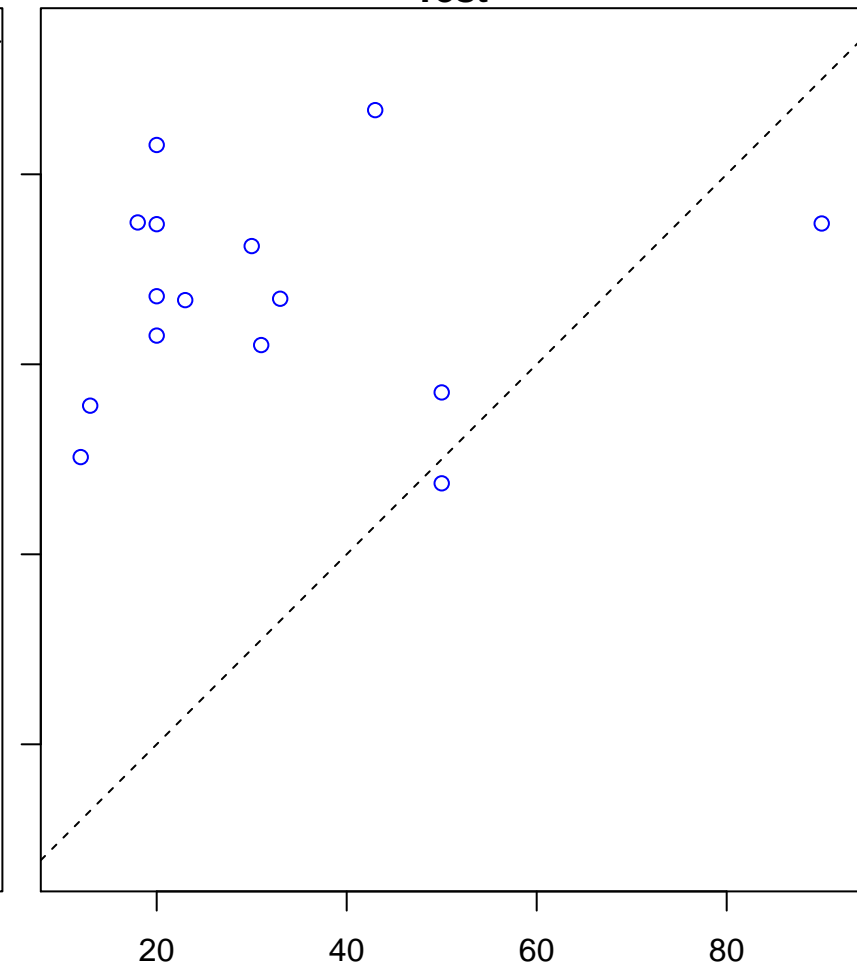
Actual Age

craniofacial suture morphogenesis (Score: 3.349377)

Control

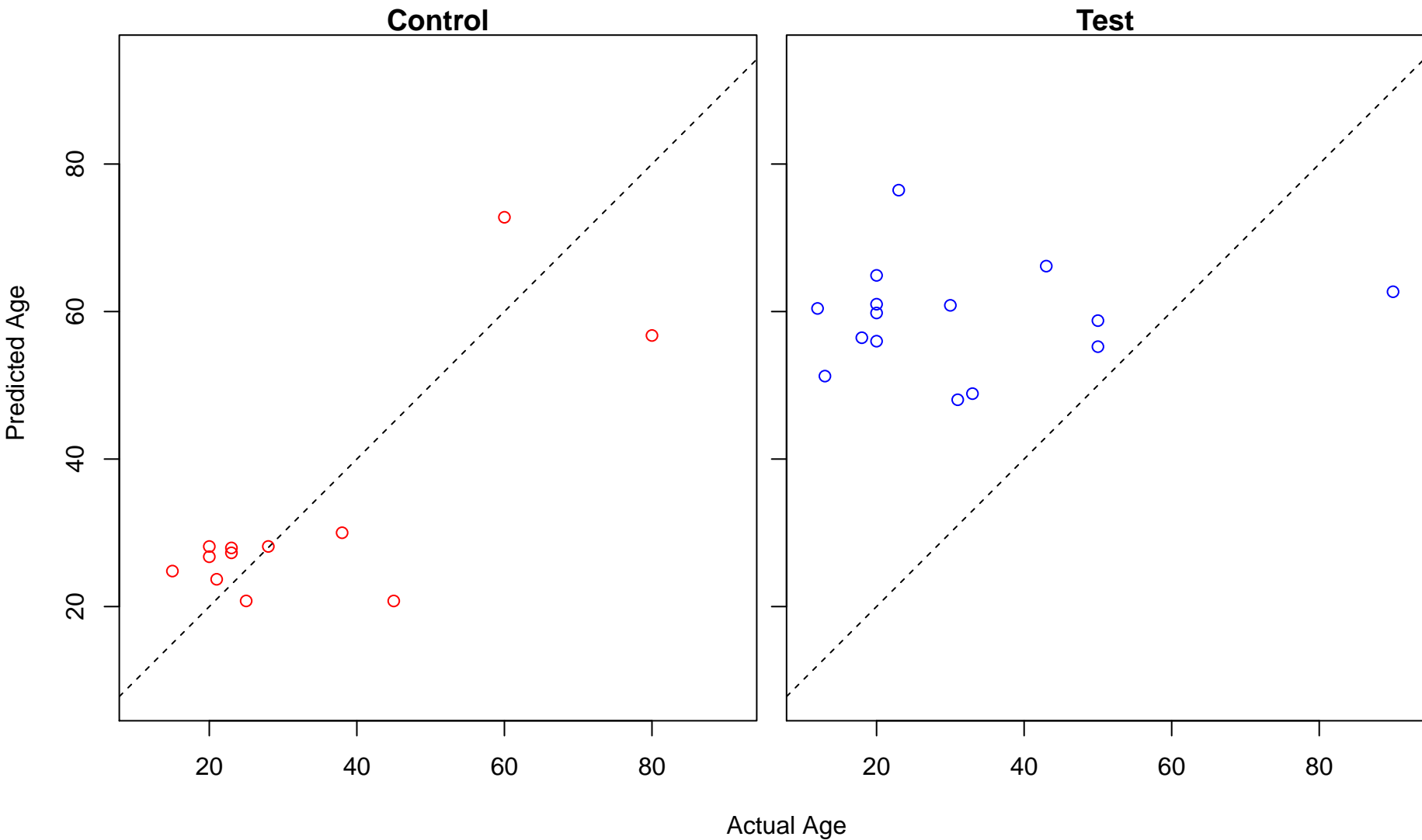


Test

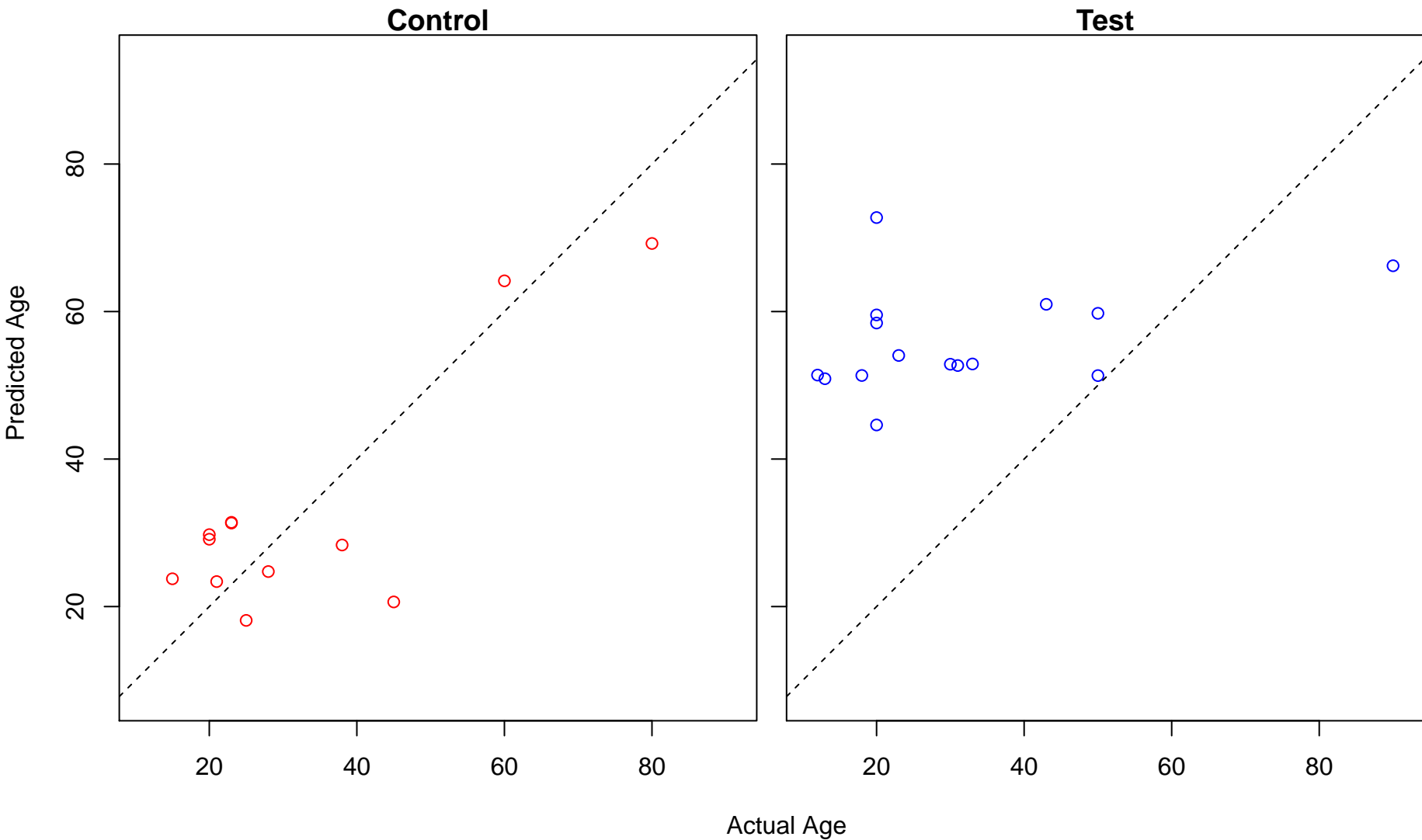


Actual Age

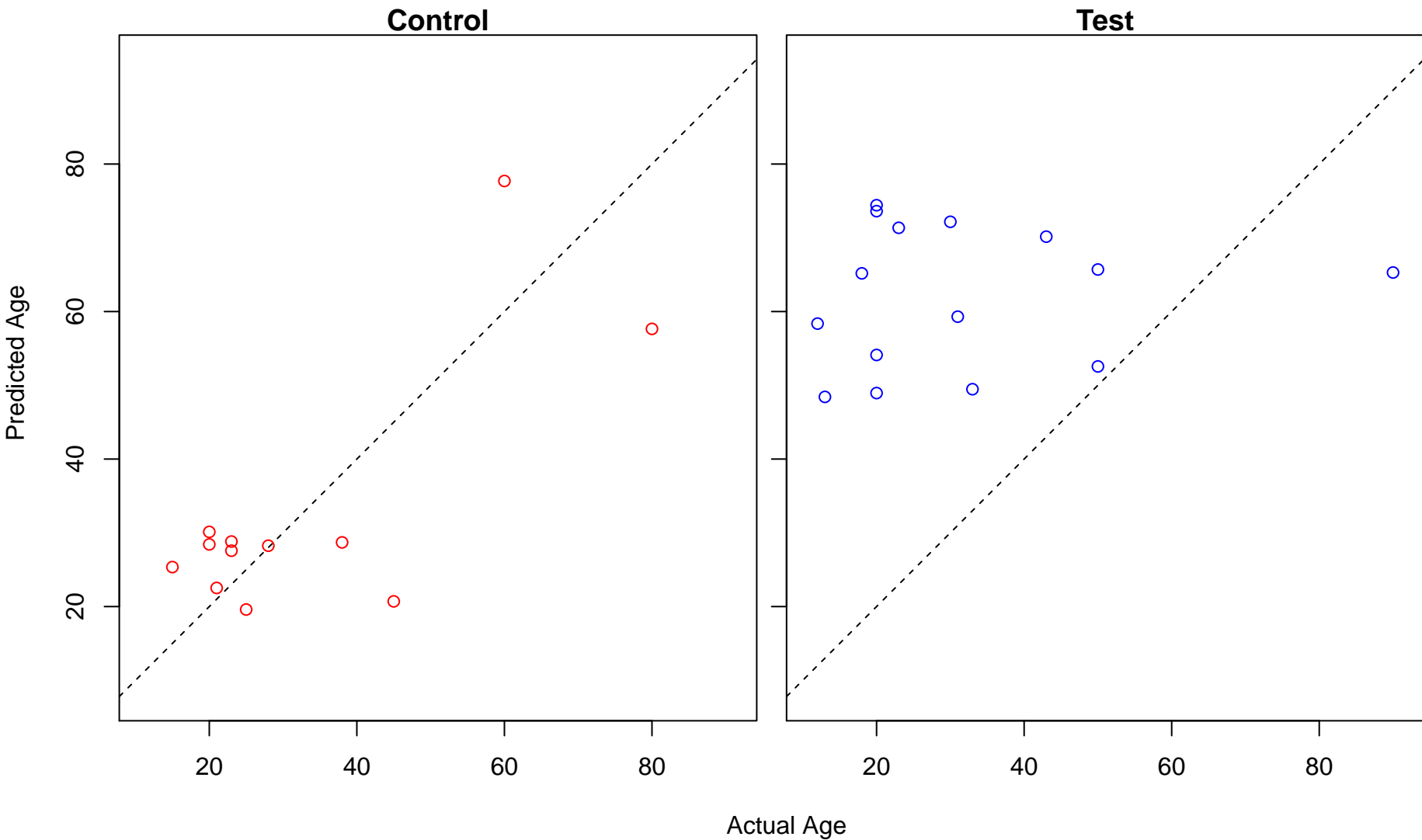
phosphatidylethanolamine biosynthetic process (Score: 3.335917)



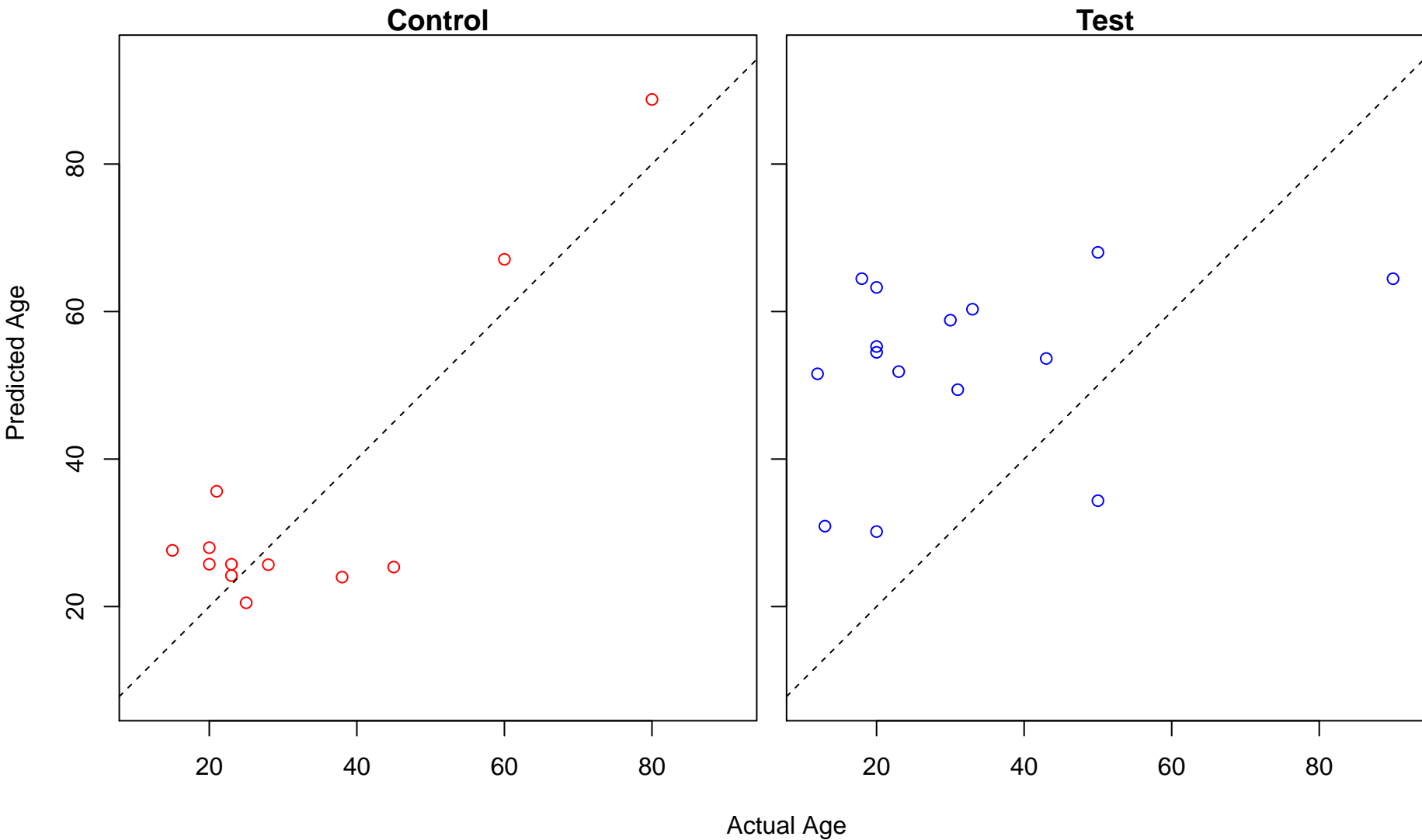
regulation of nucleotide catabolic process (Score: 3.333490)



response to UV-A (Score: 3.331526)

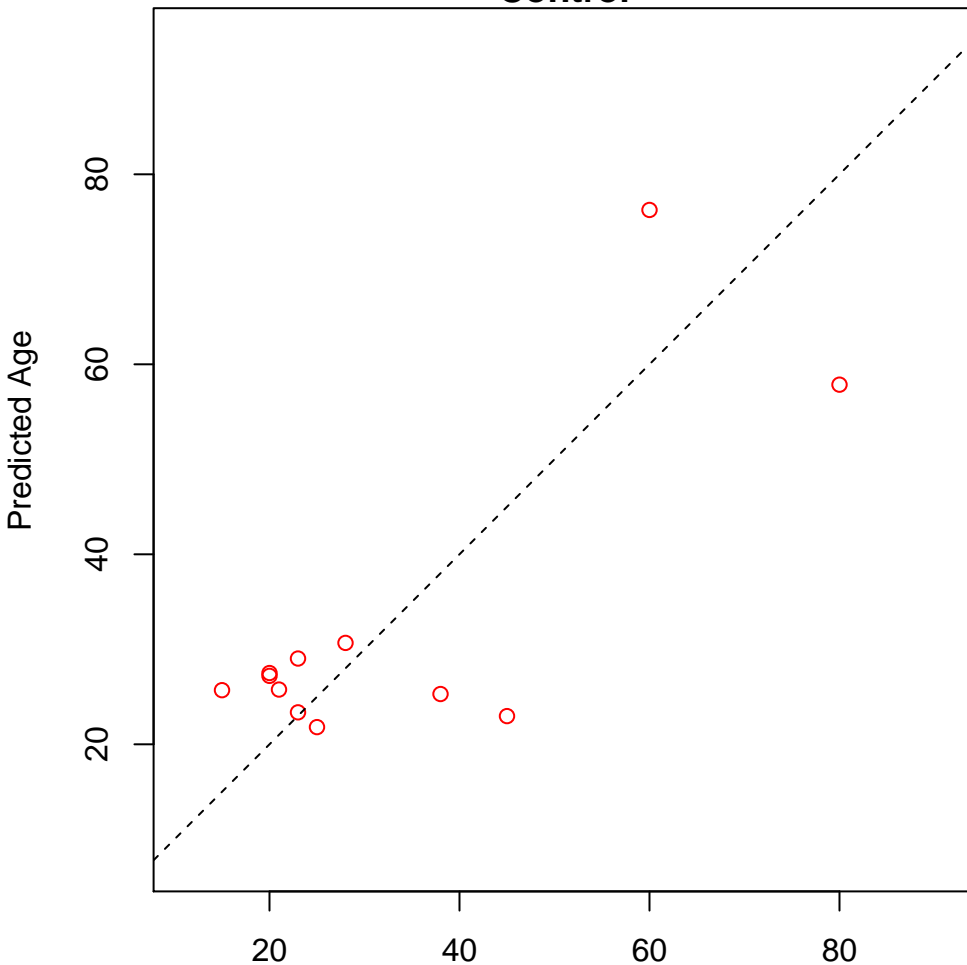


negative regulation of Ras protein signal transduction (Score: 3.330586)

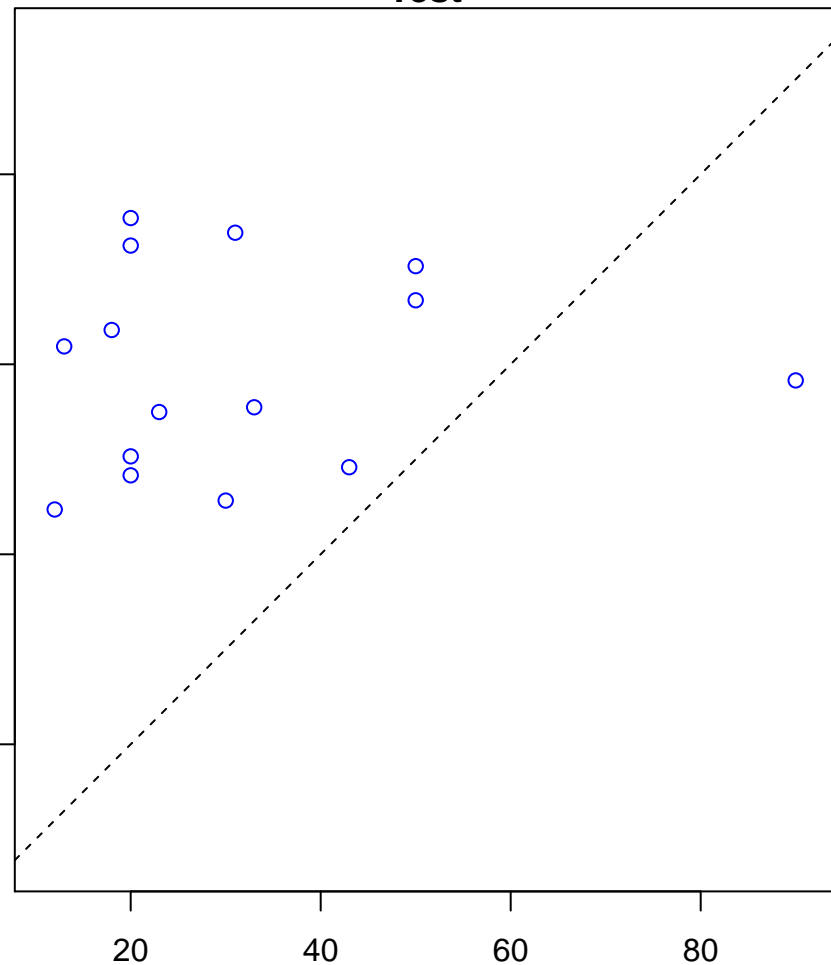


cellular carbohydrate catabolic process (Score: 3.328256)

Control

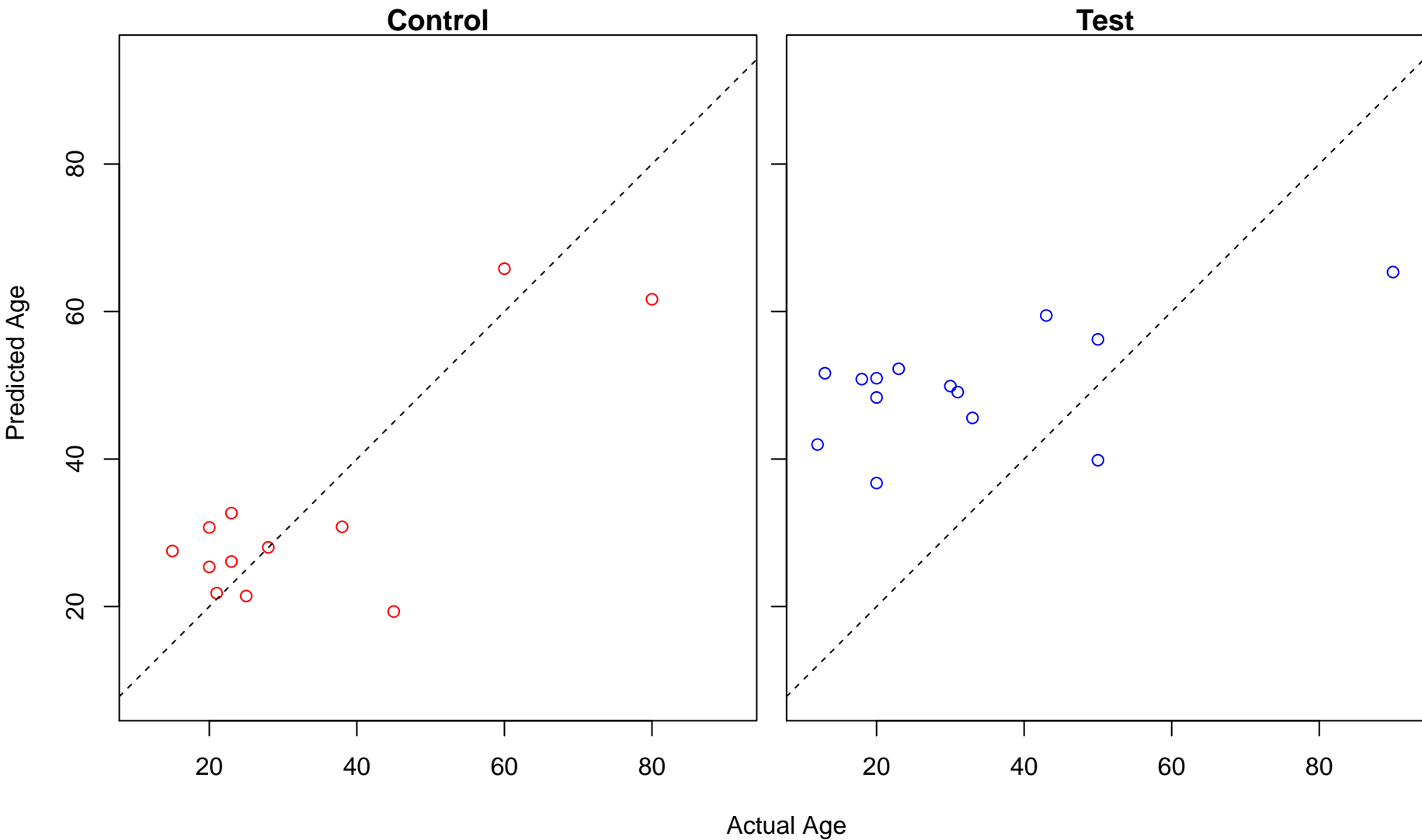


Test

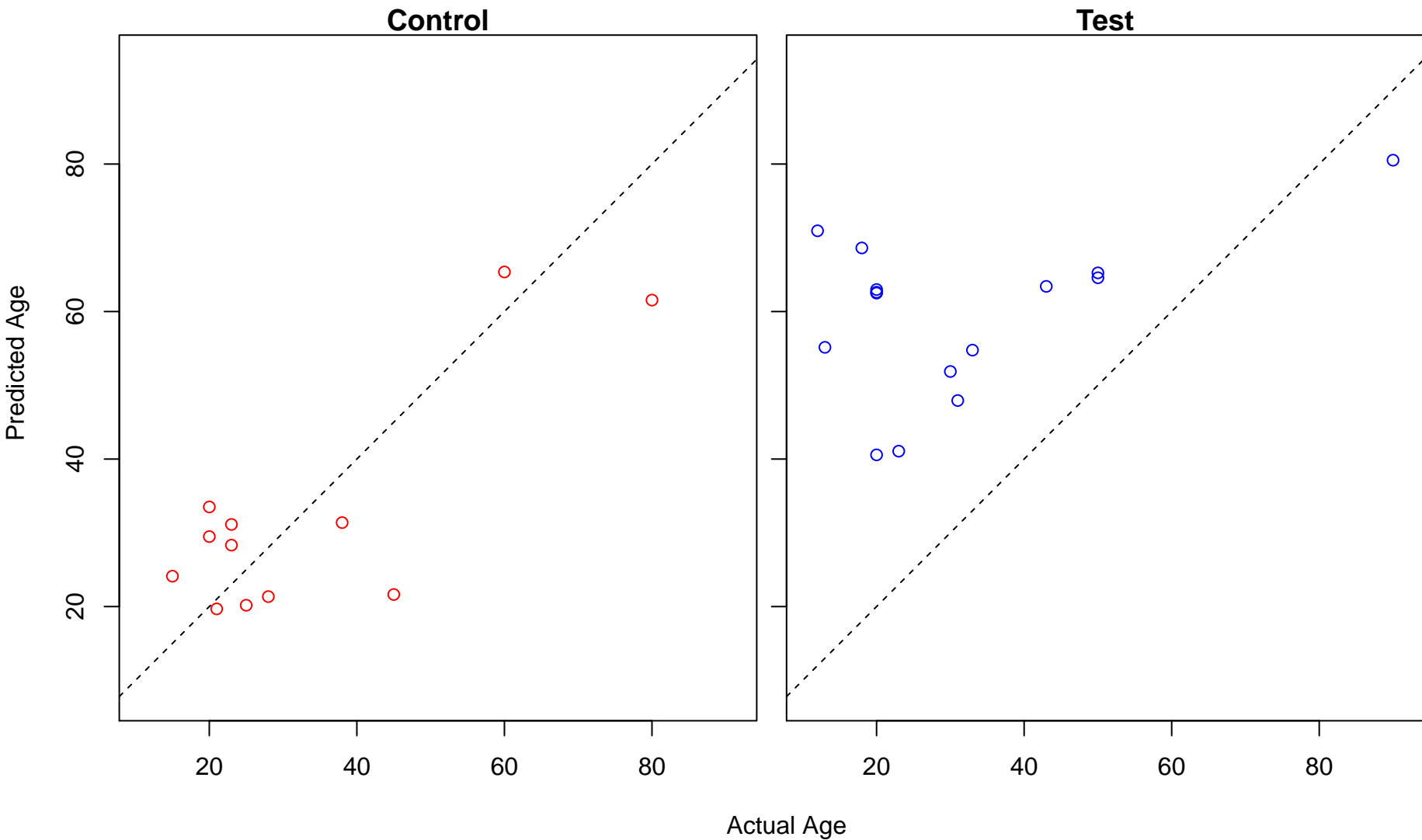


Actual Age

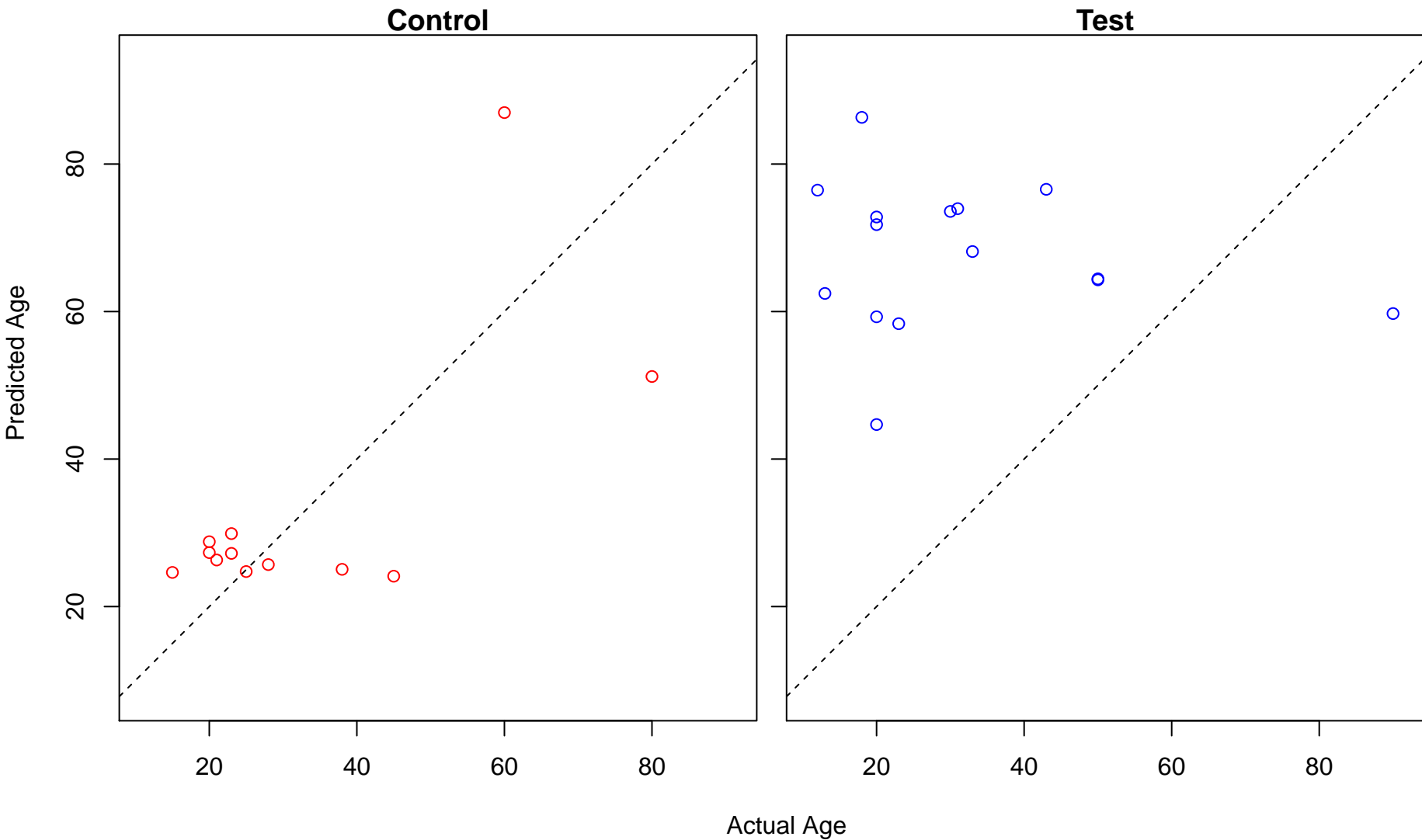
regulation of antigen processing and presentation (Score: 3.325899)



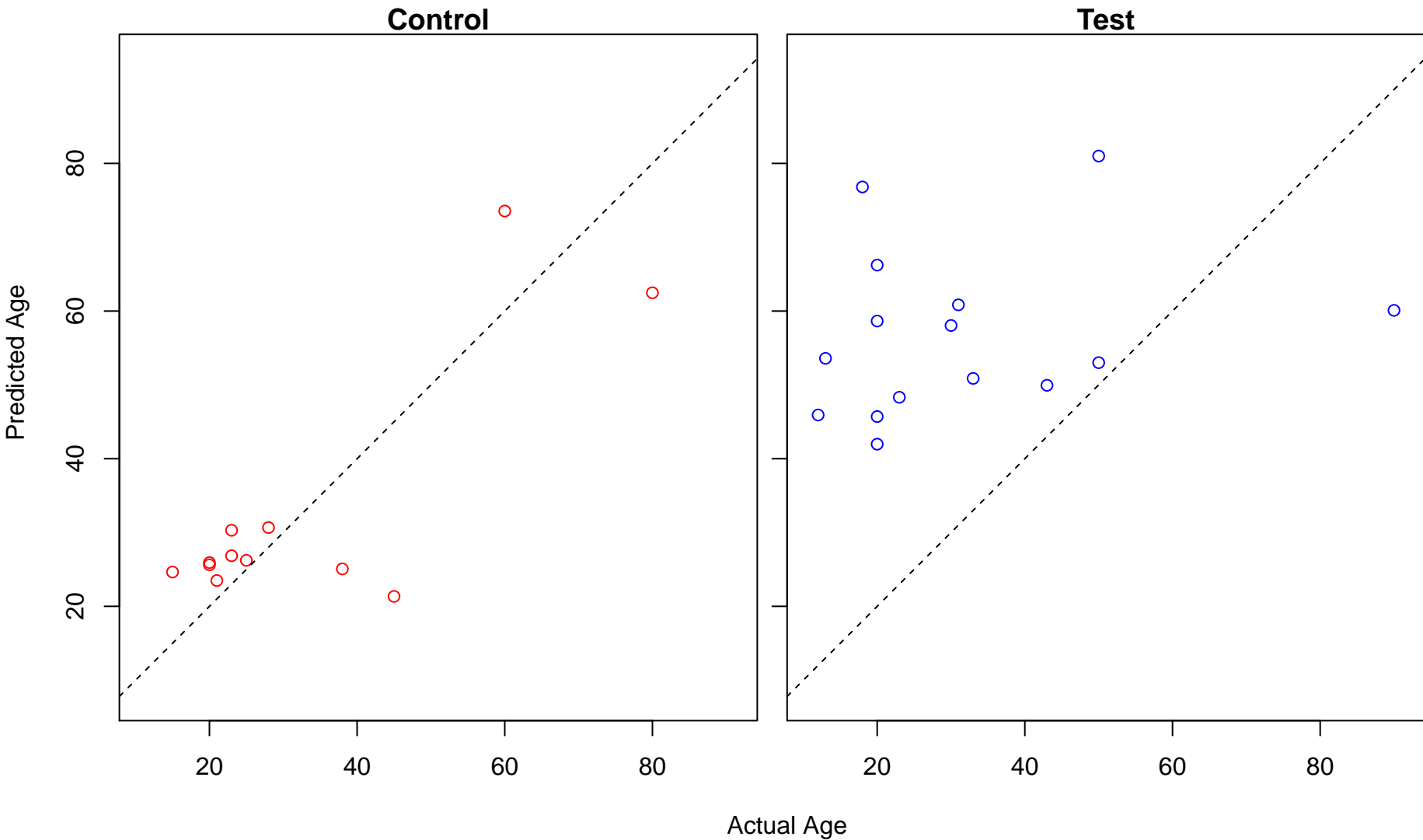
regulation of cardiac muscle cell differentiation (Score: 3.325686)



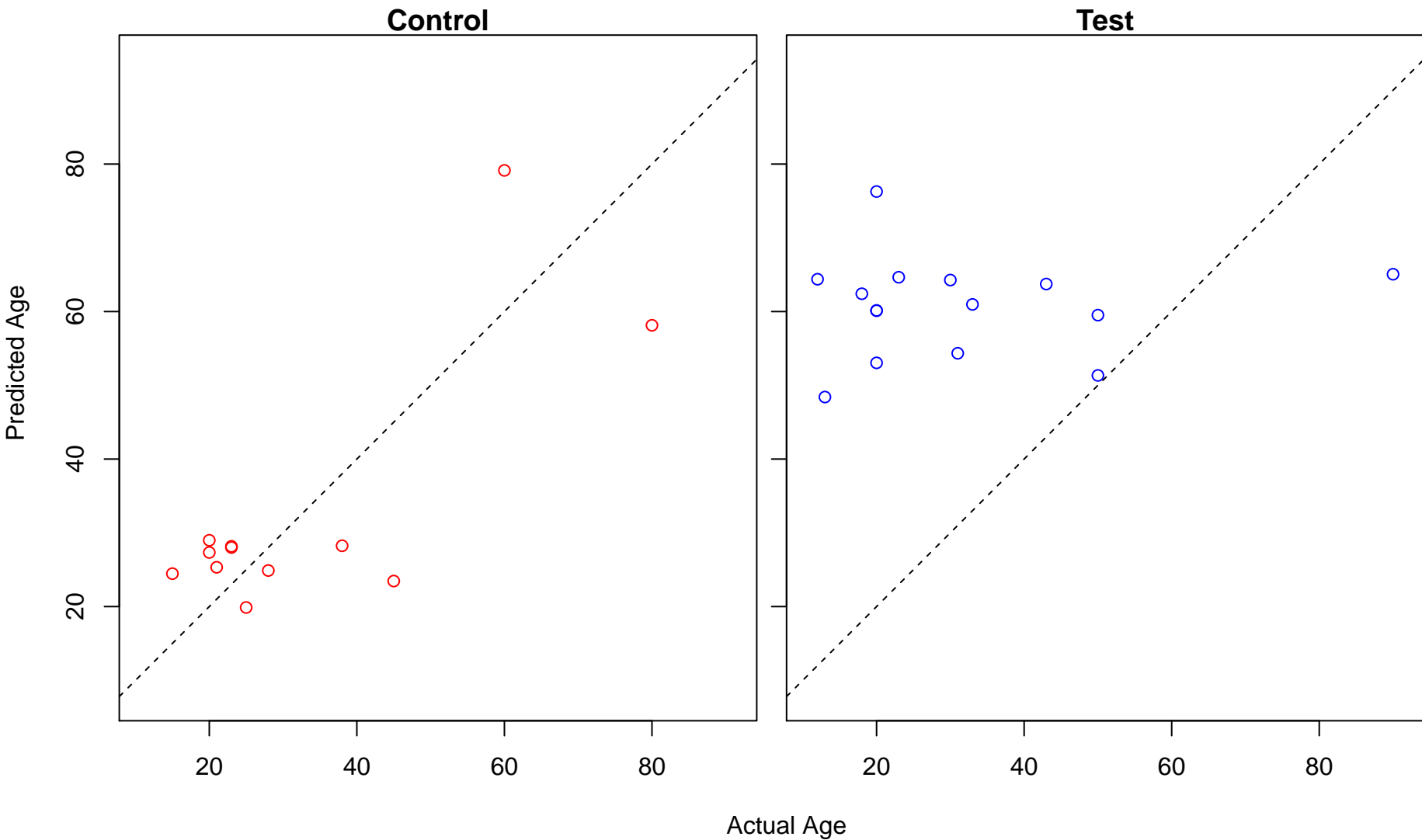
neutrophil activation (Score: 3.324915)



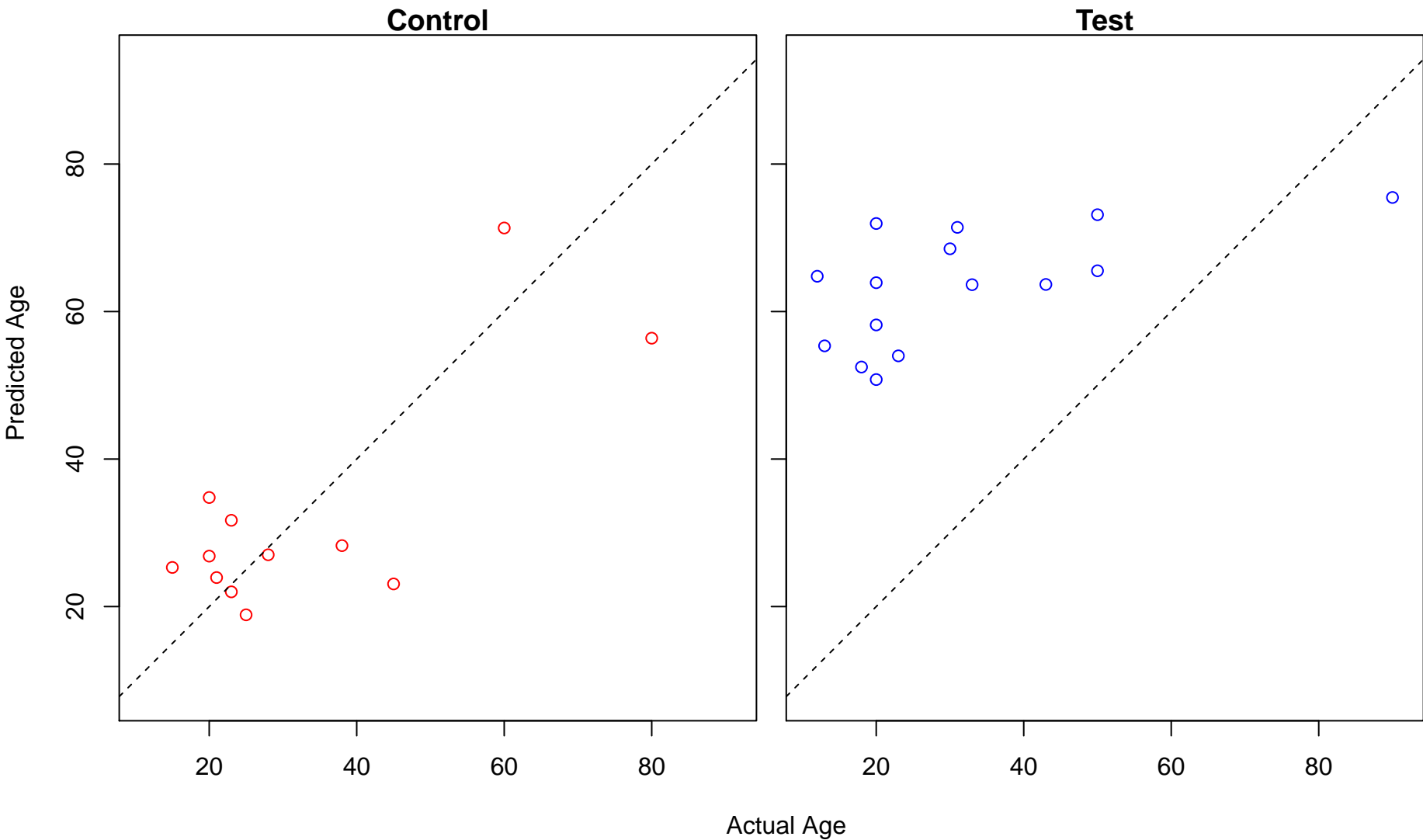
regulation of delayed rectifier potassium channel activity (Score: 3.323876)



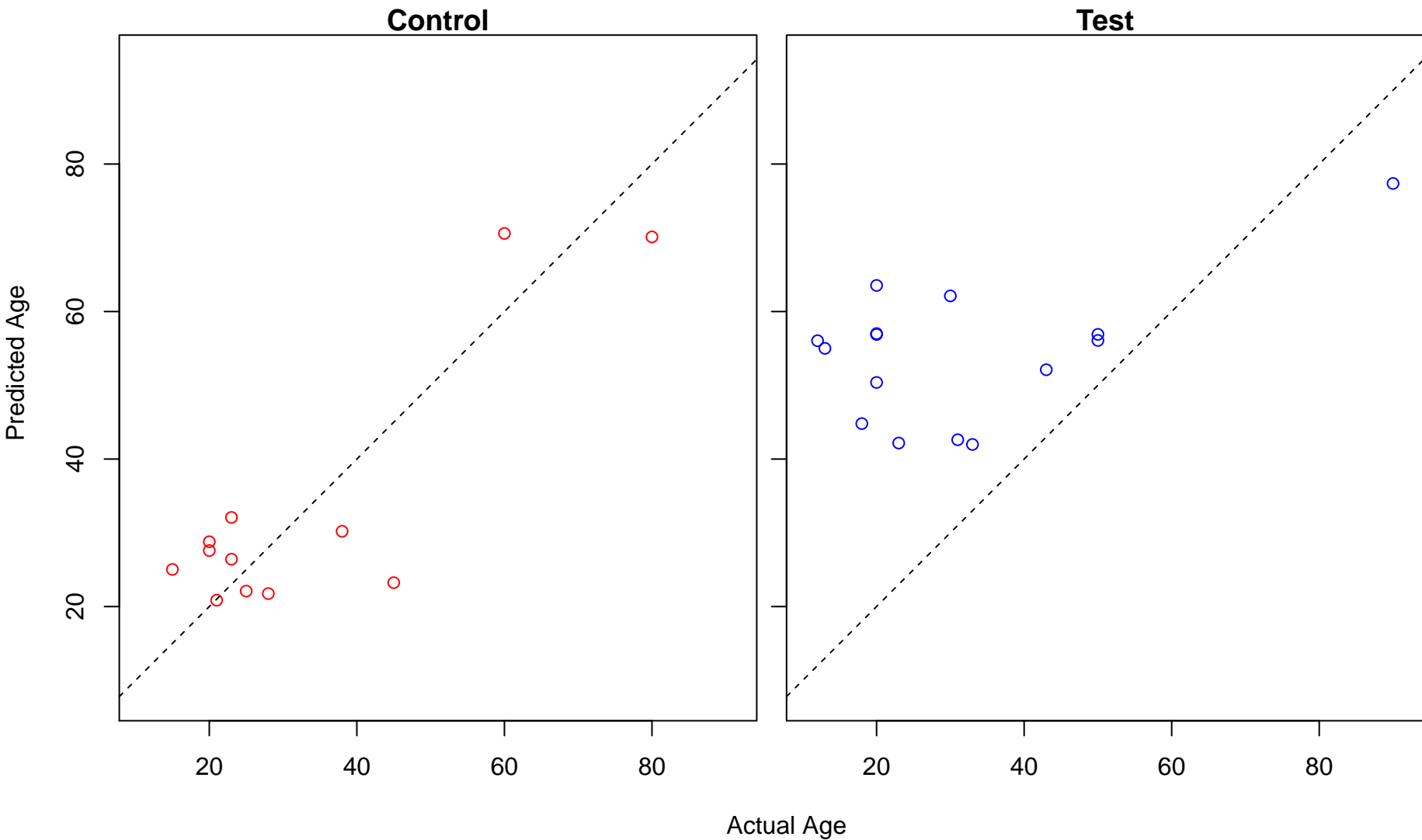
regulation of double-strand break repair (Score: 3.323134)



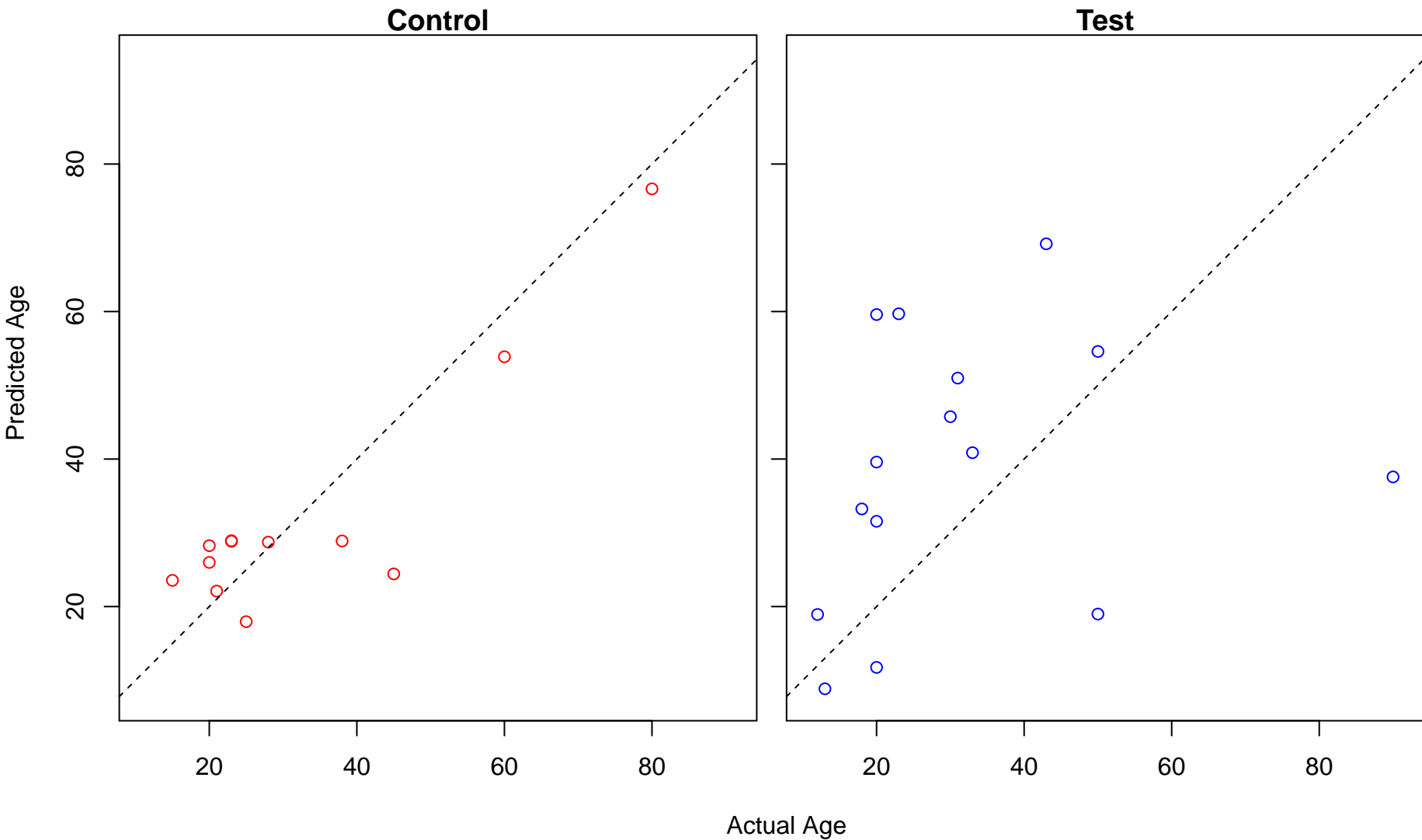
regulation of vascular endothelial growth factor receptor signaling pathway (Score: 3.318420)



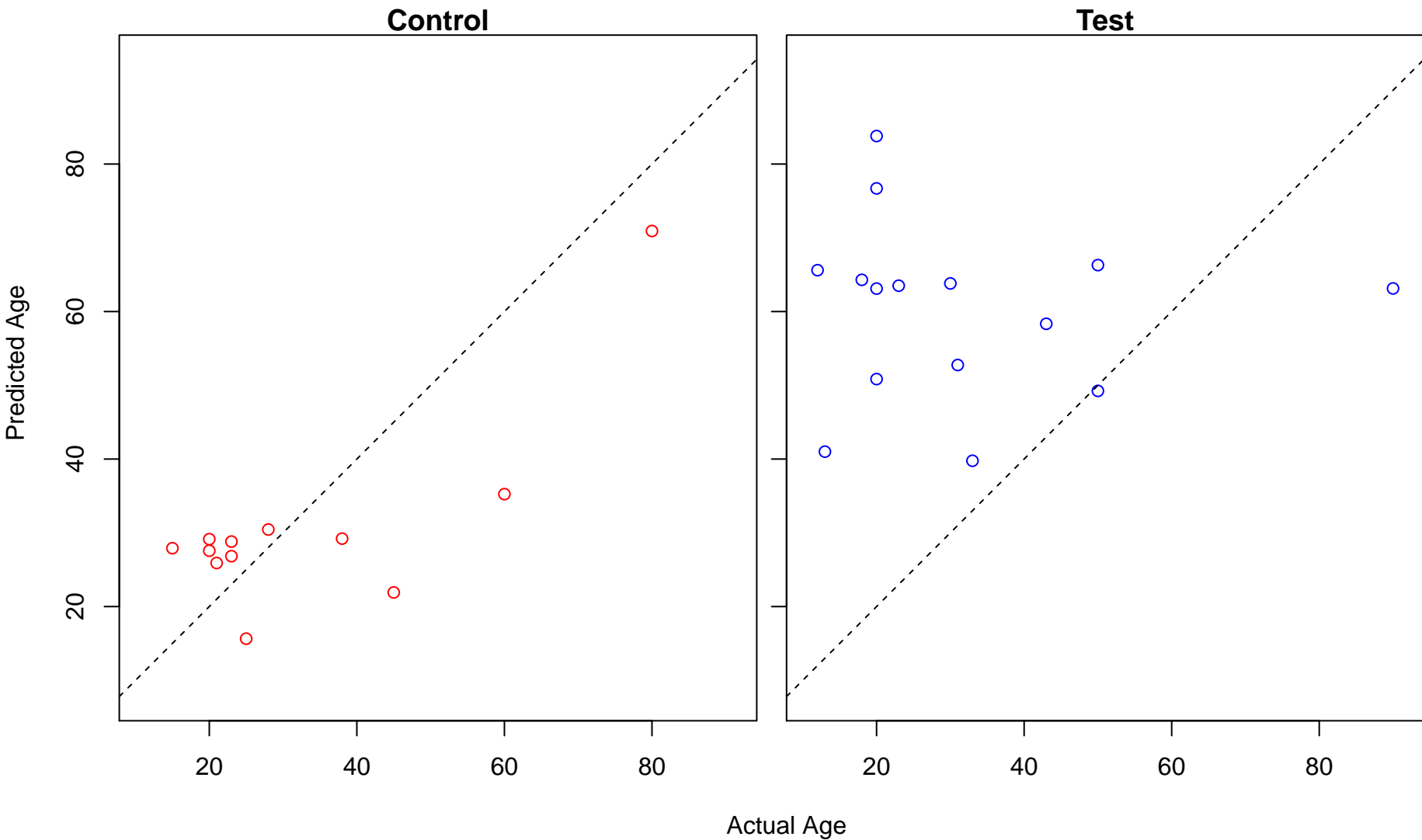
anion transmembrane transport (Score: 3.316583)



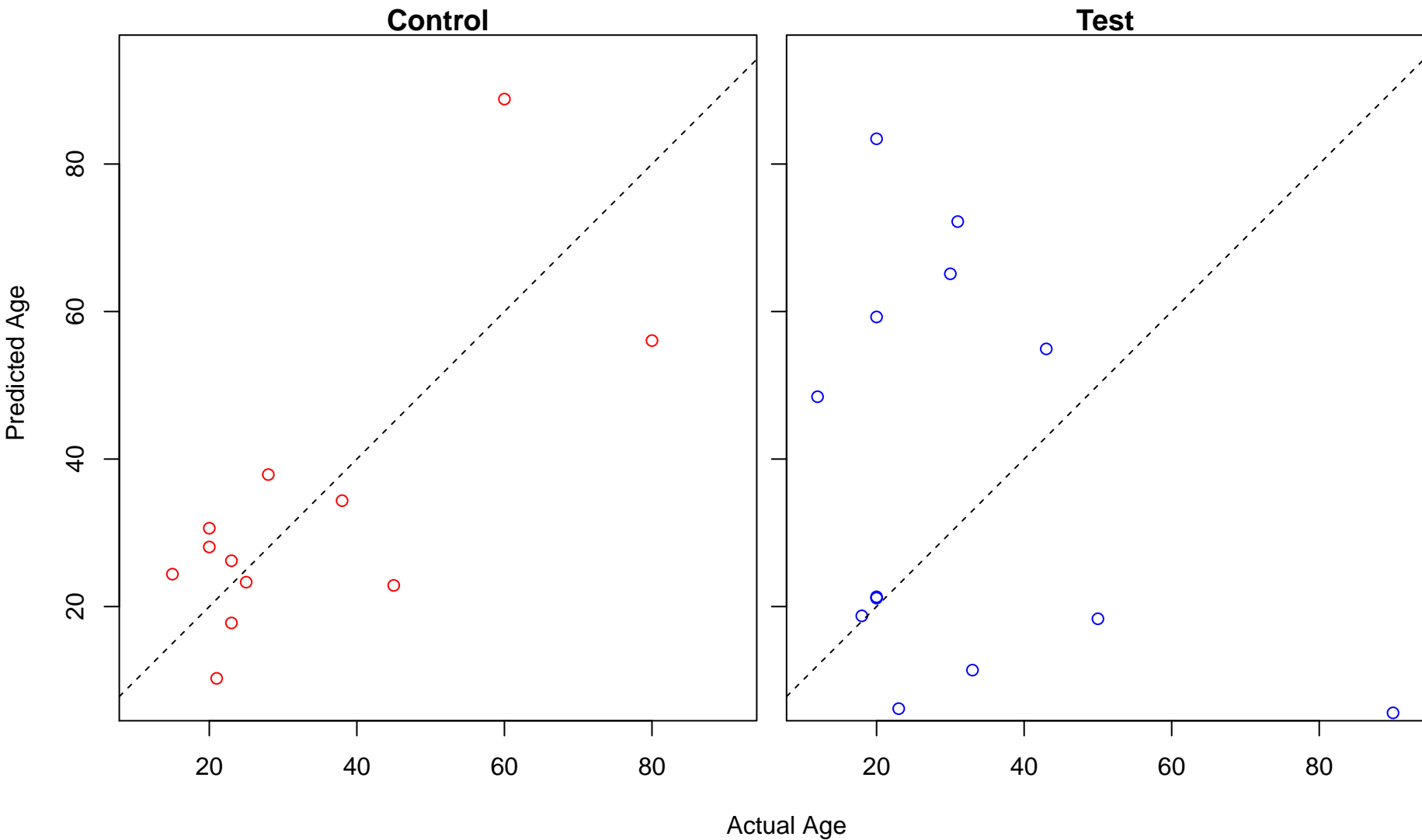
ganglion development (Score: 3.316251)



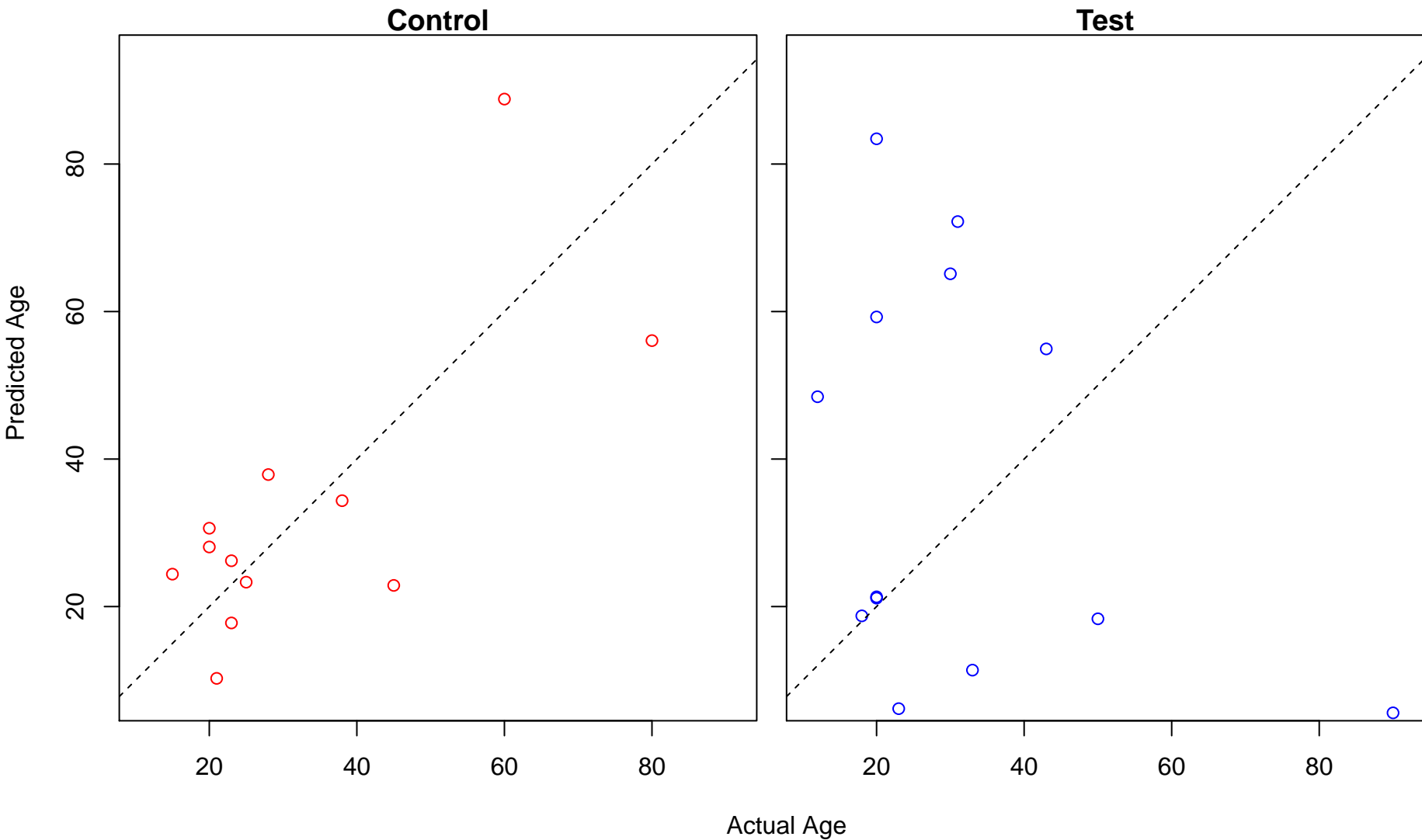
cerebral cortex cell migration (Score: 3.312233)



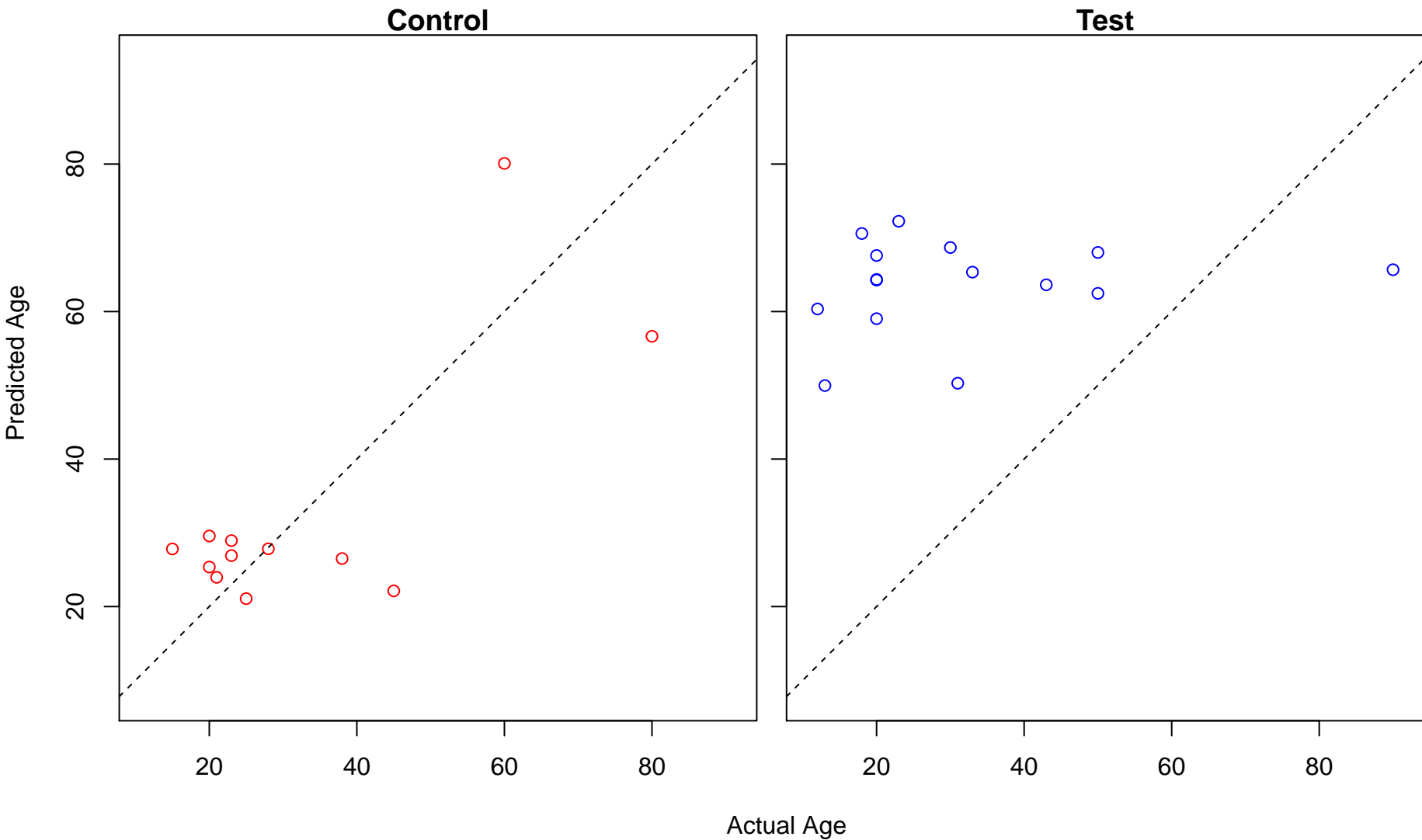
regulation of response to tumor cell (Score: 3.312088)



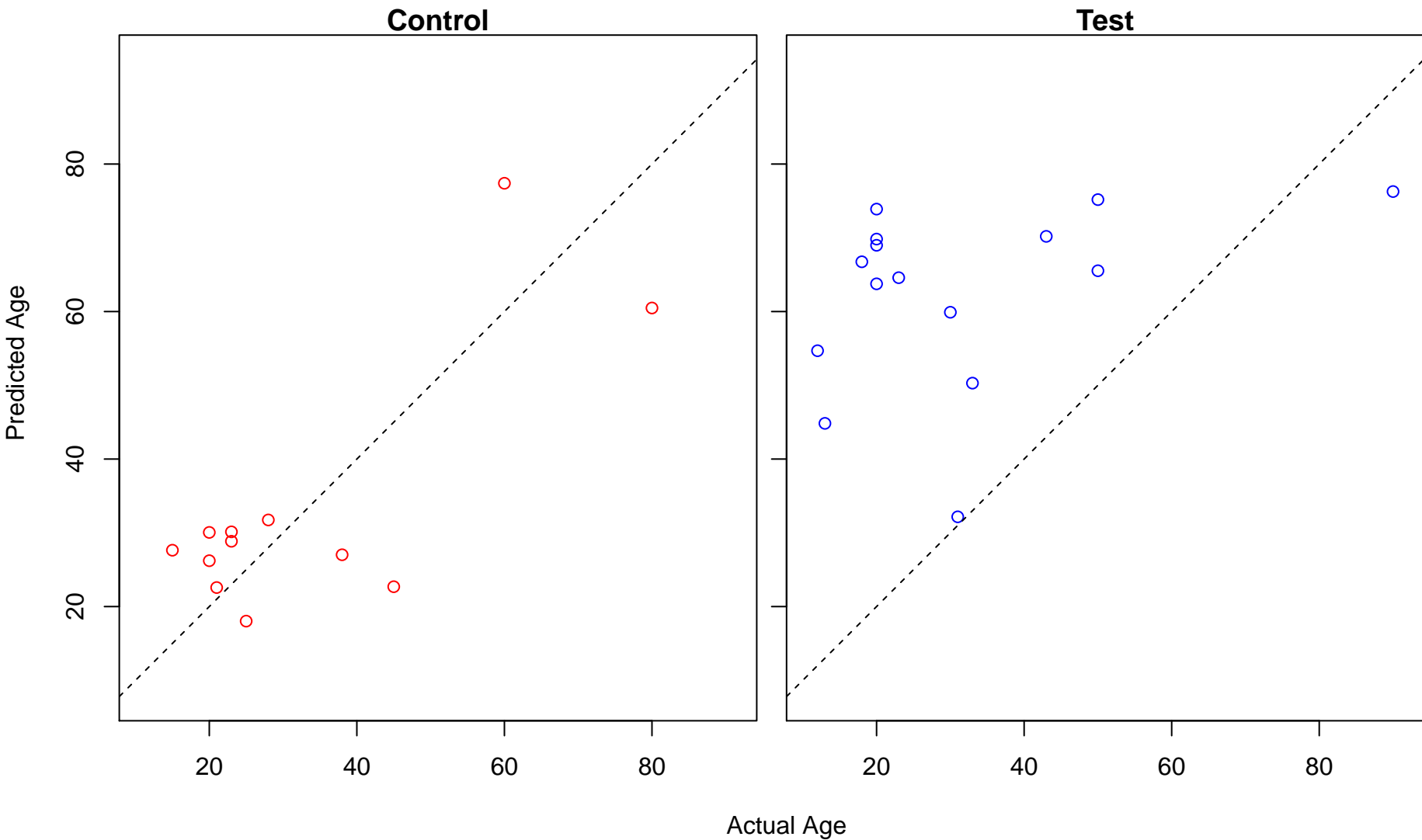
regulation of immune response to tumor cell (Score: 3.312088)



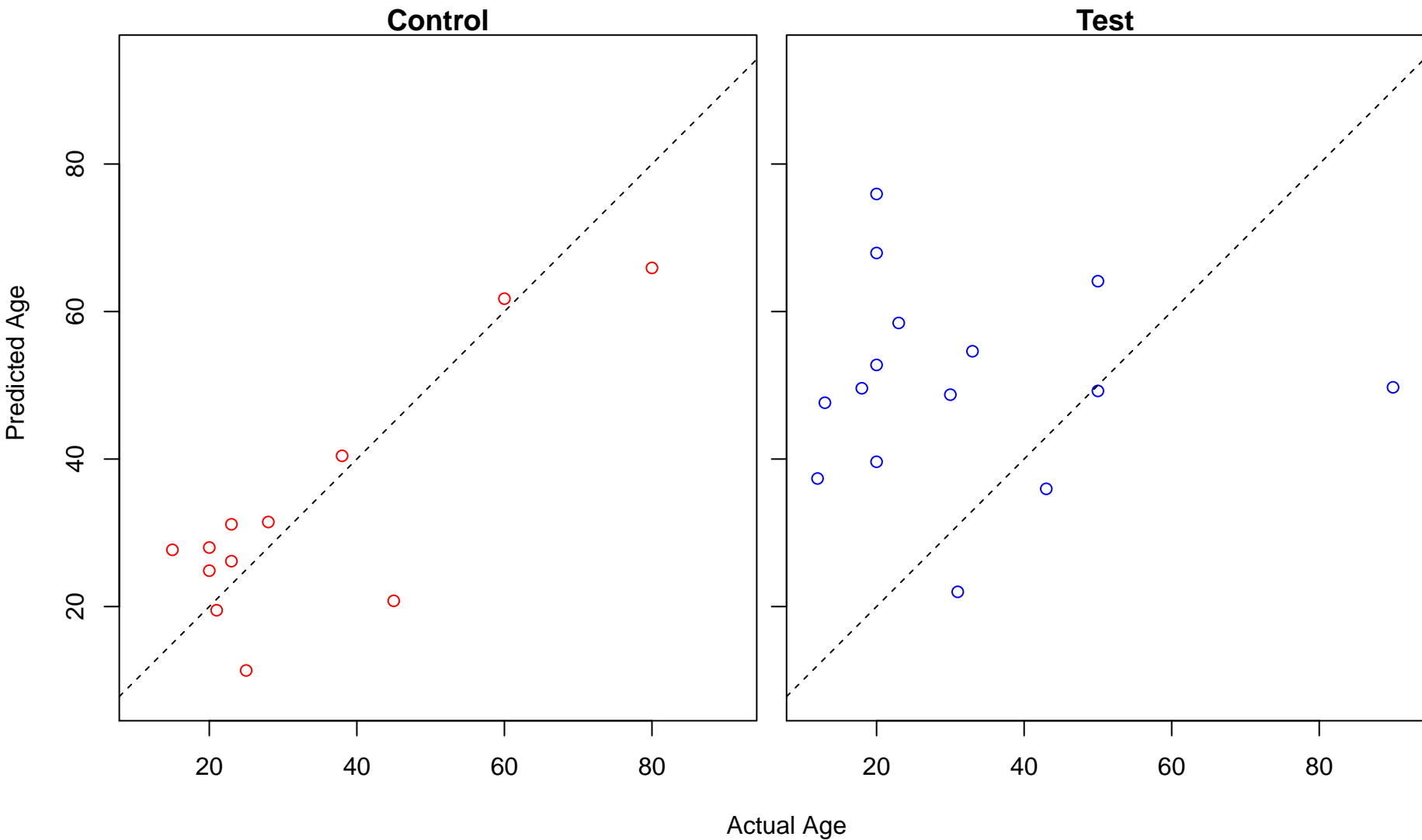
negative regulation of protein localization to cell surface (Score: 3.310748)



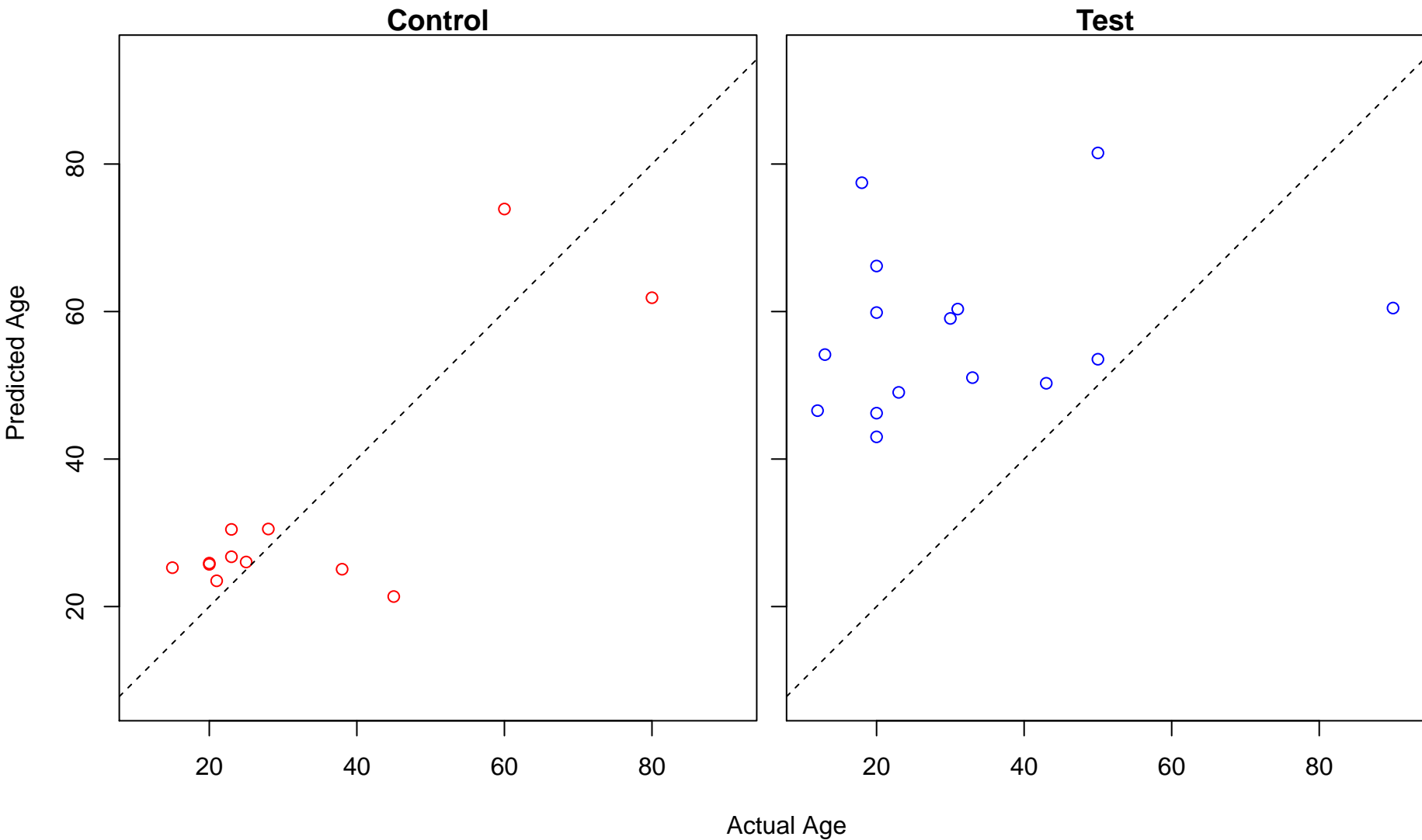
inflammatory response (Score: 3.310337)



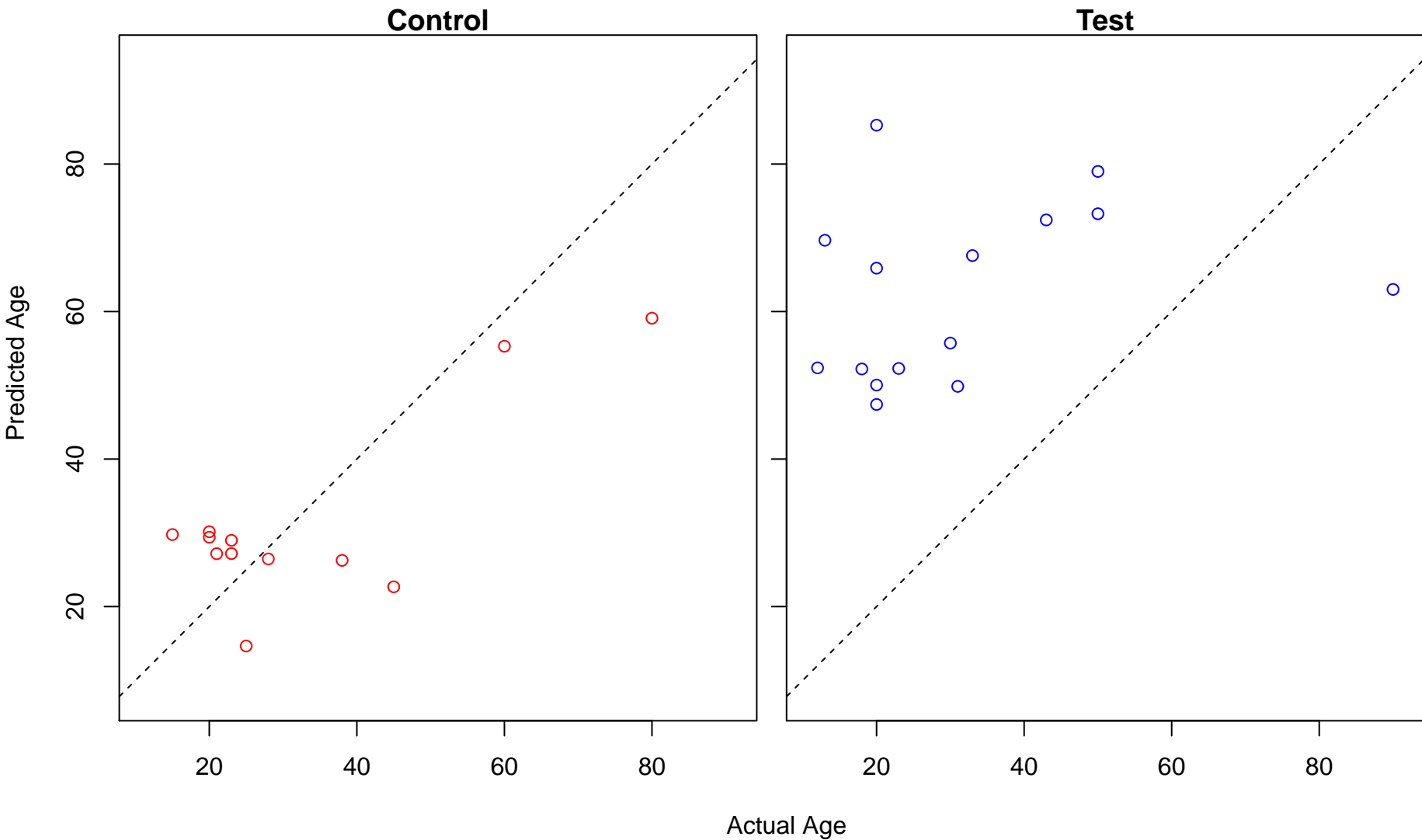
myelin assembly (Score: 3.308479)



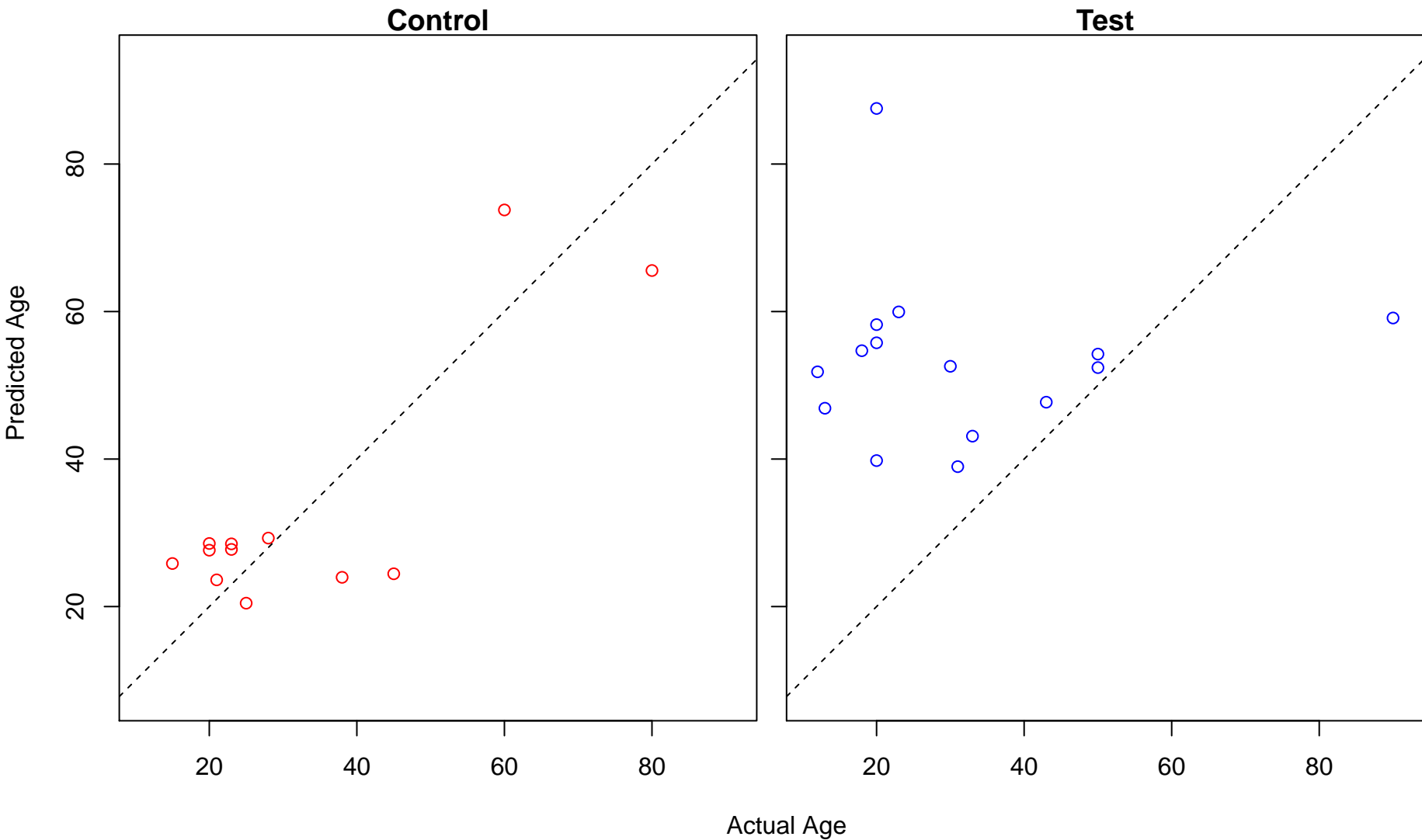
negative regulation of potassium ion transmembrane transporter activity (Score: 3.307737)



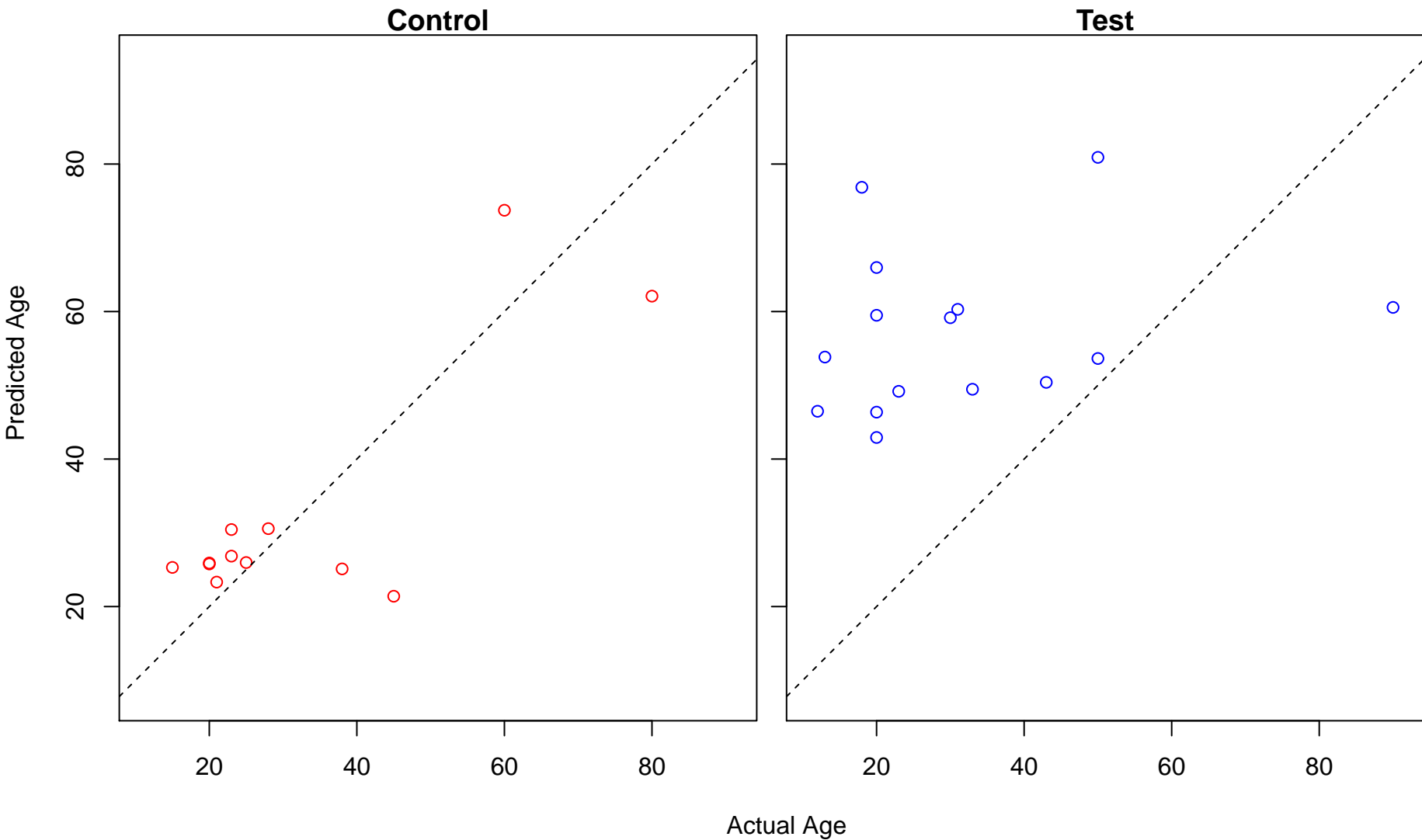
cerebral cortex neuron differentiation (Score: 3.299242)



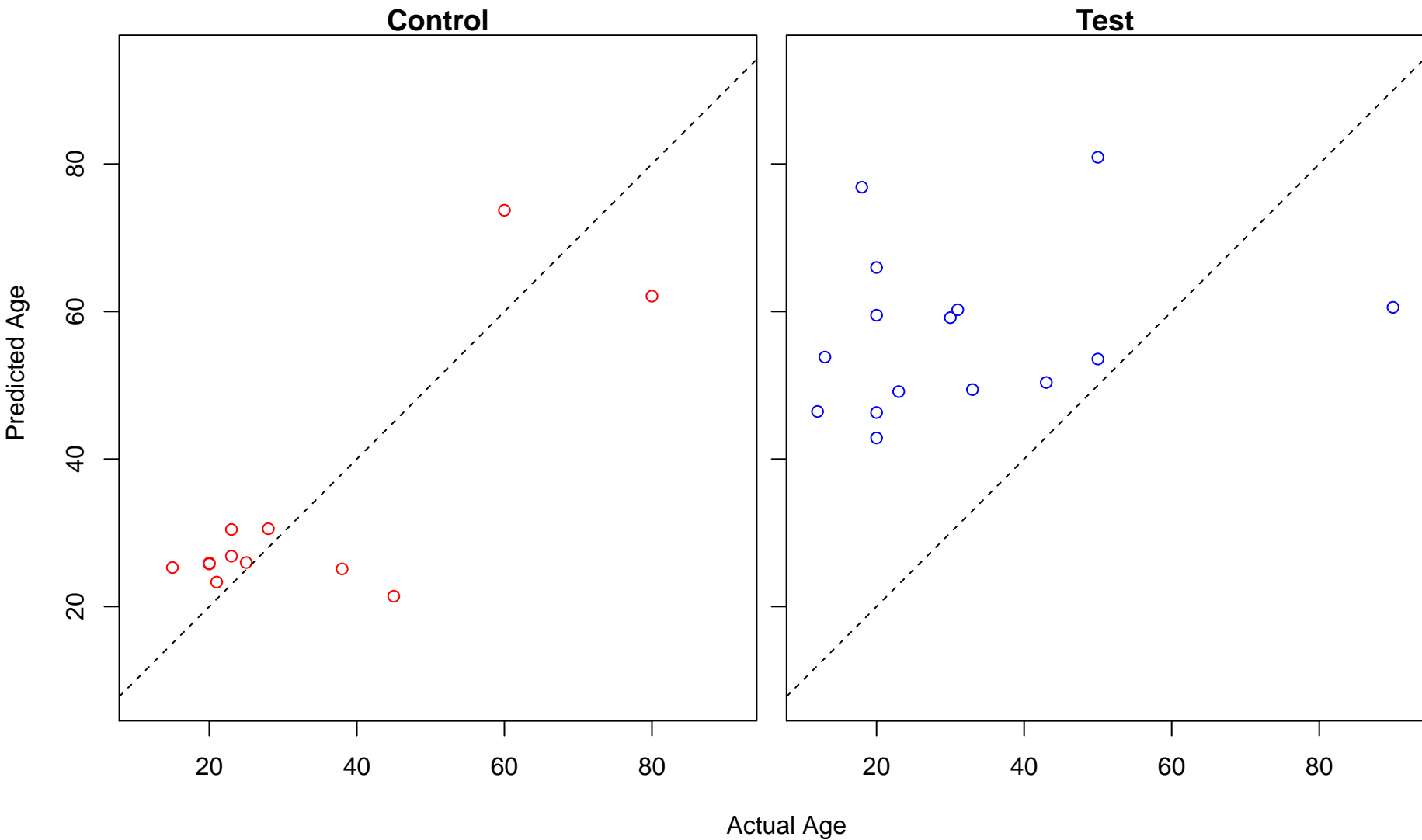
pyruvate metabolic process (Score: 3.298841)



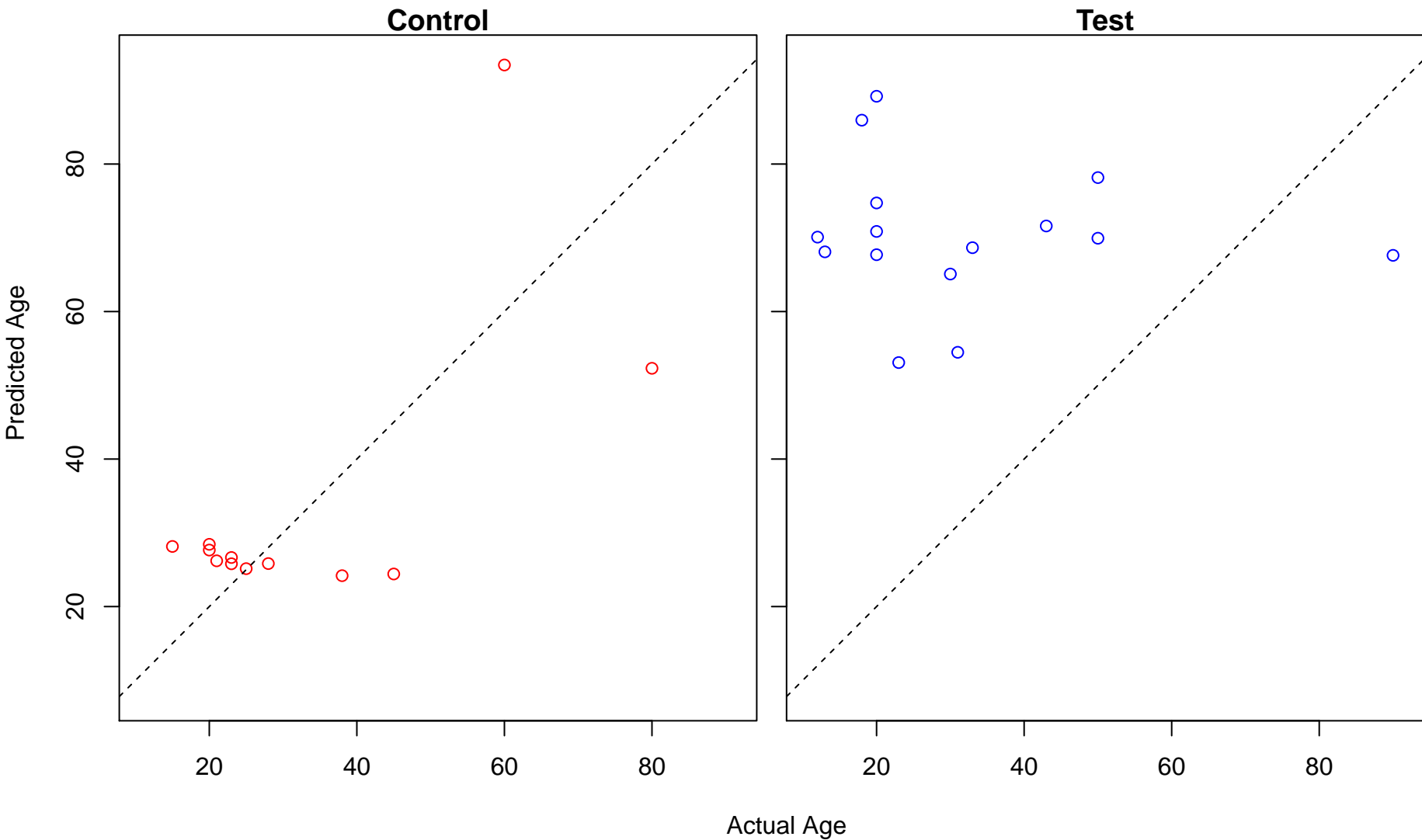
negative regulation of potassium ion transport (Score: 3.297548)



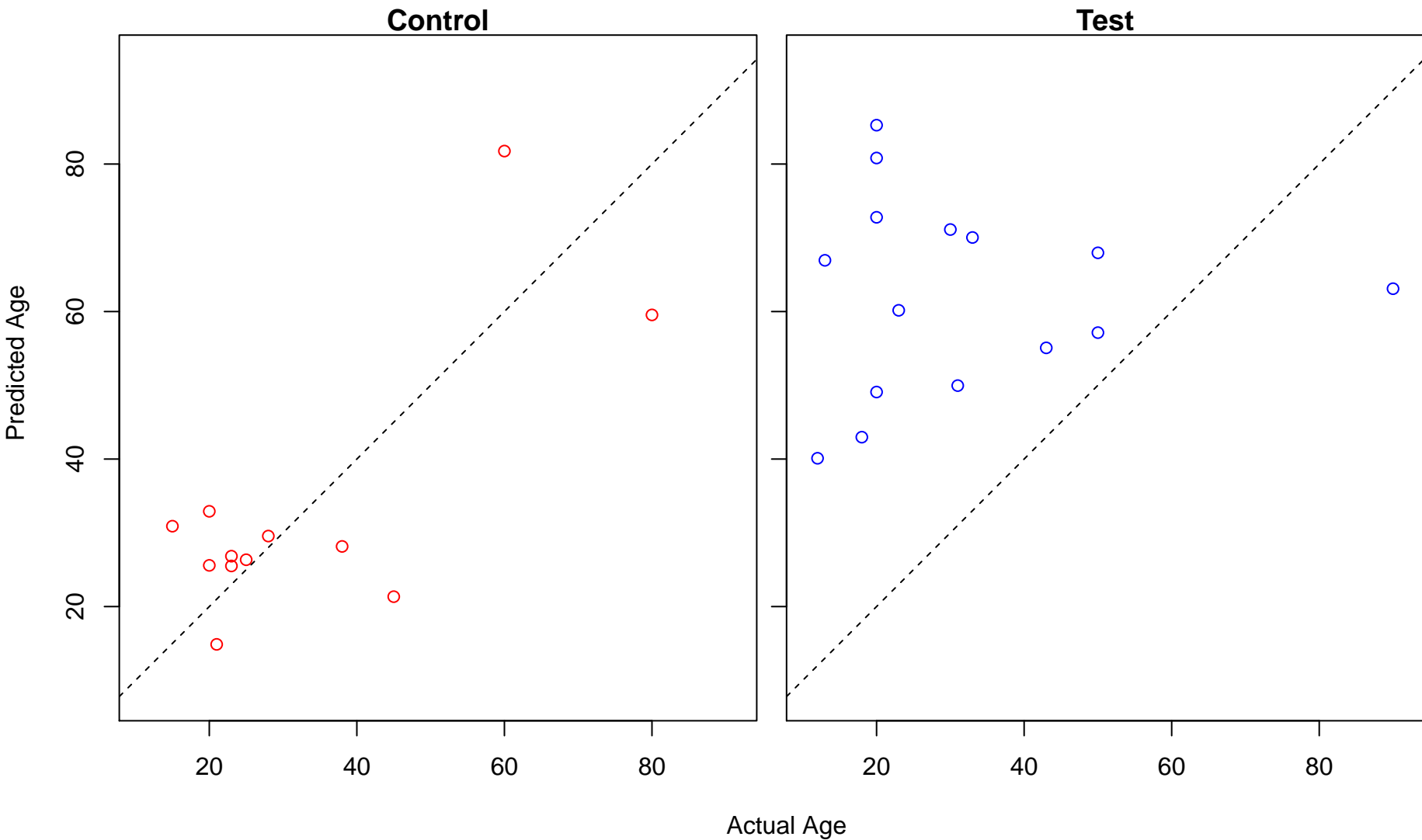
negative regulation of potassium ion transmembrane transport (Score: 3.295498)



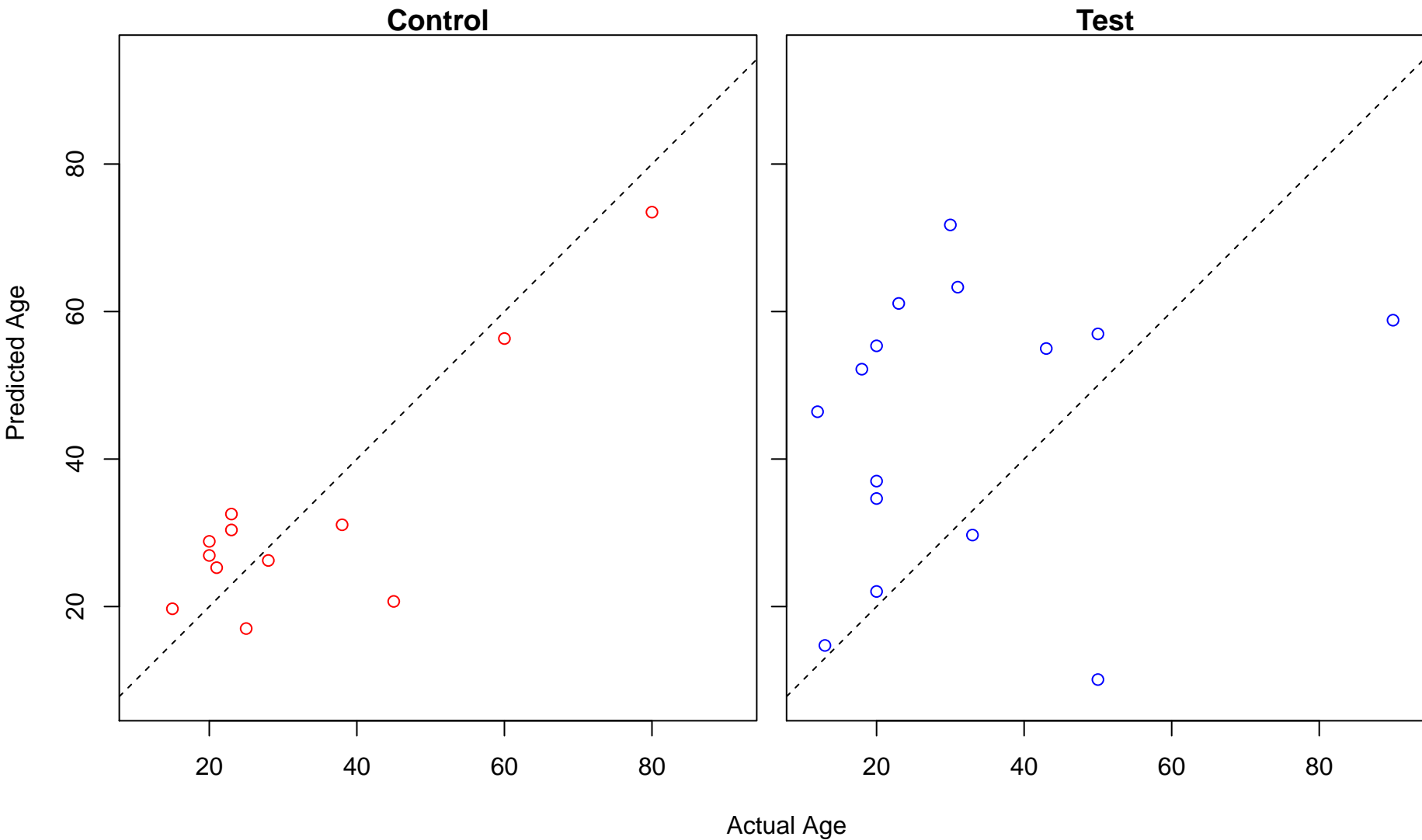
regulation of response to reactive oxygen species (Score: 3.292846)



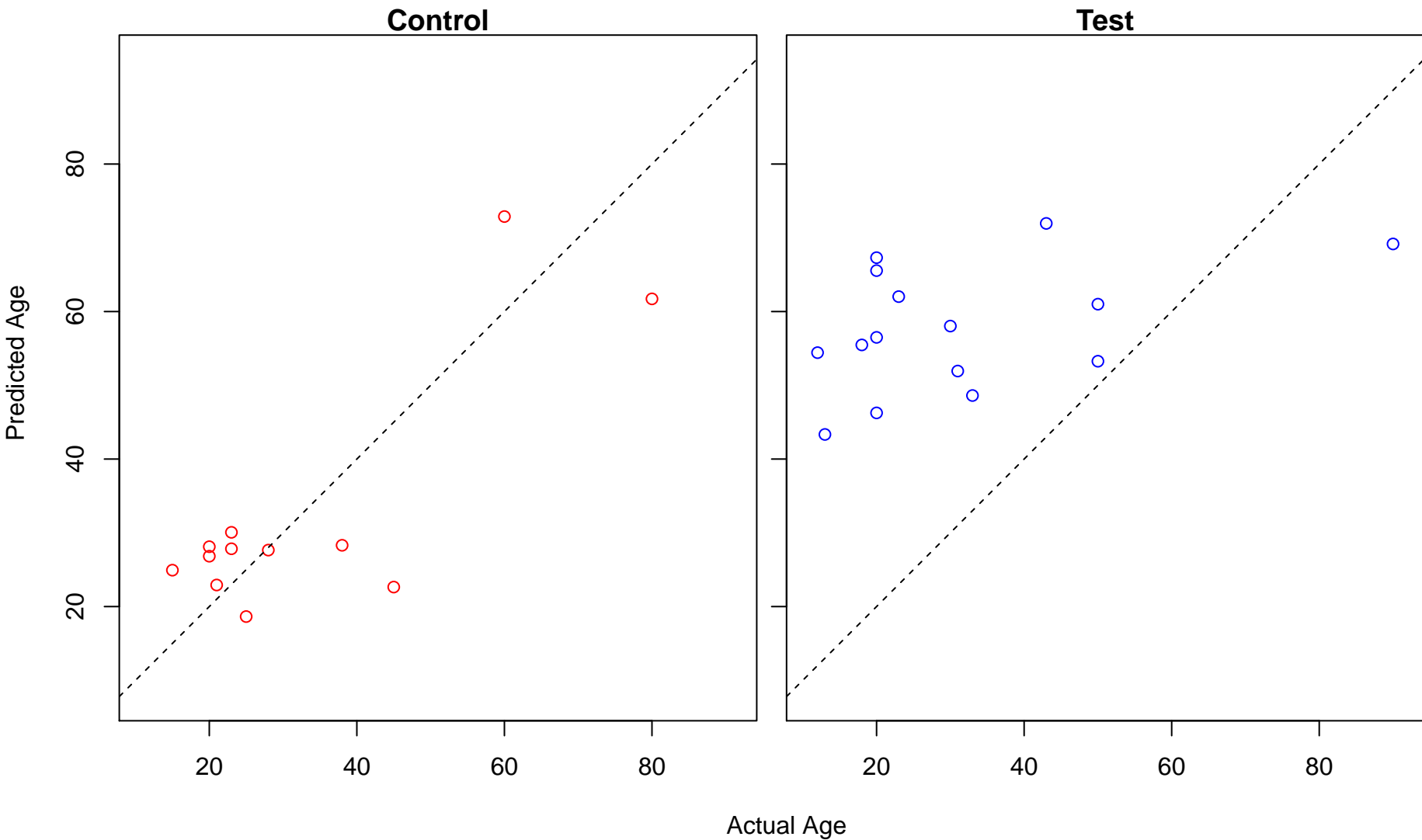
negative regulation of microtubule polymerization (Score: 3.292699)



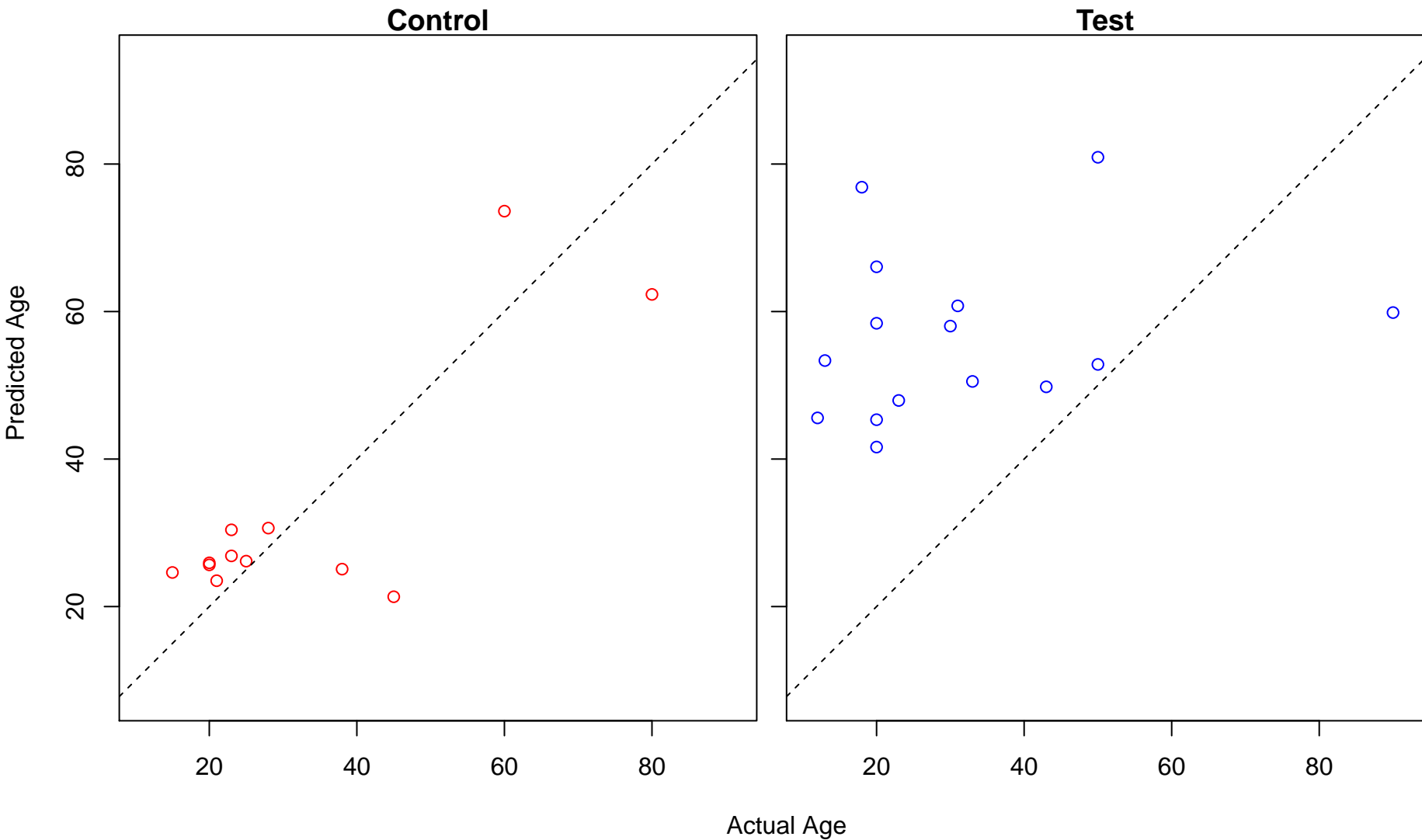
collagen metabolic process (Score: 3.291222)



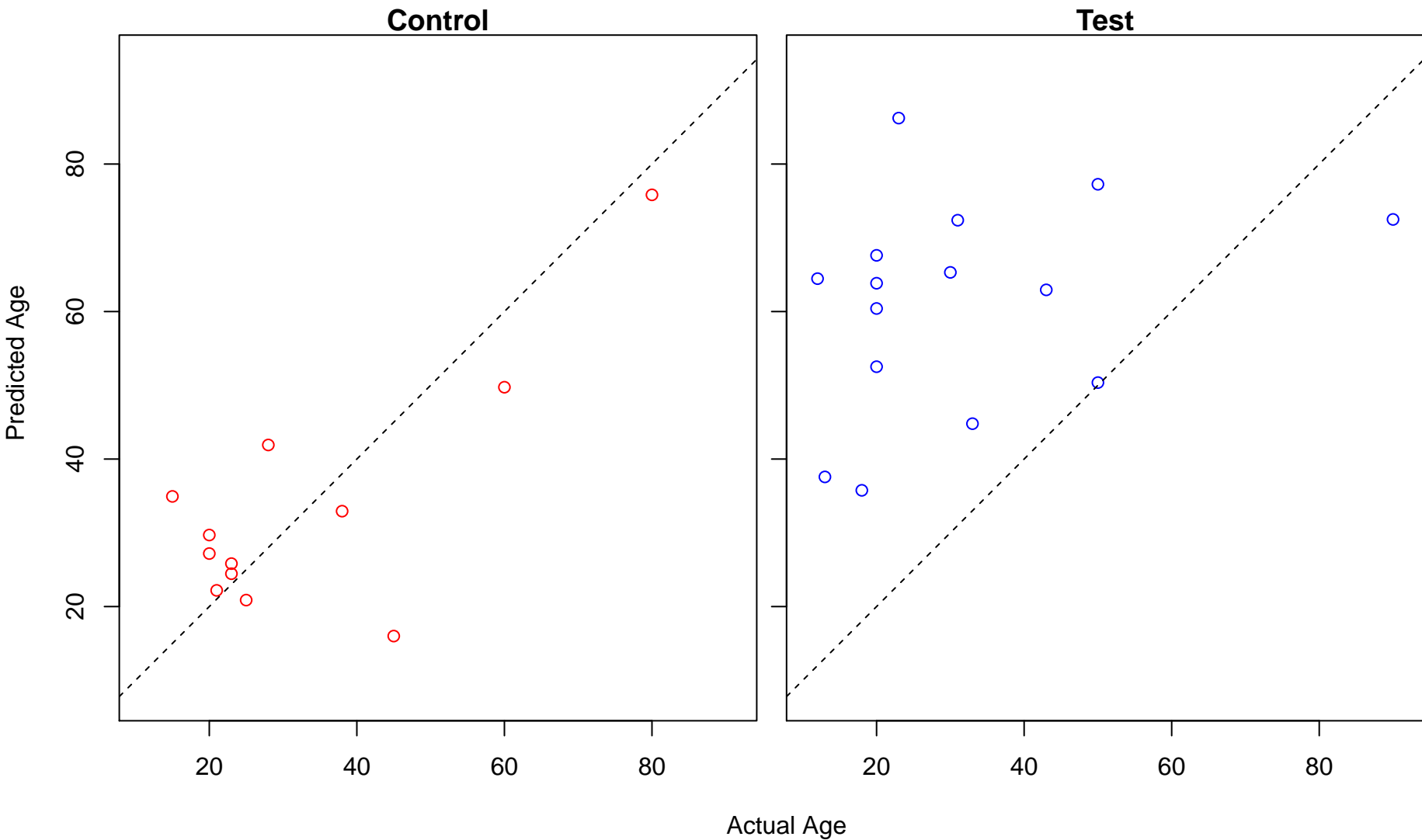
cytoskeletal anchoring at plasma membrane (Score: 3.287336)



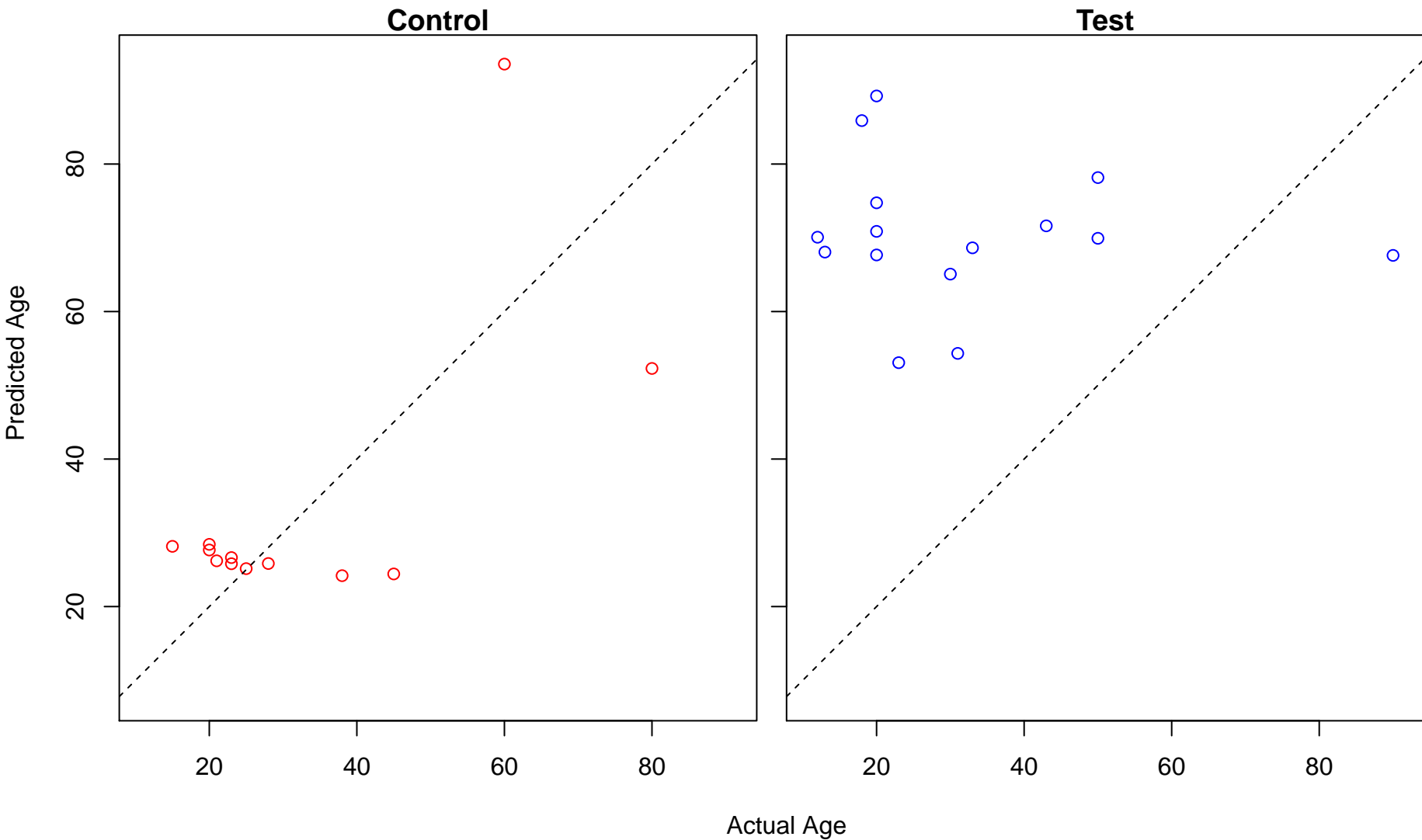
negative regulation of delayed rectifier potassium channel activity (Score: 3.285027)



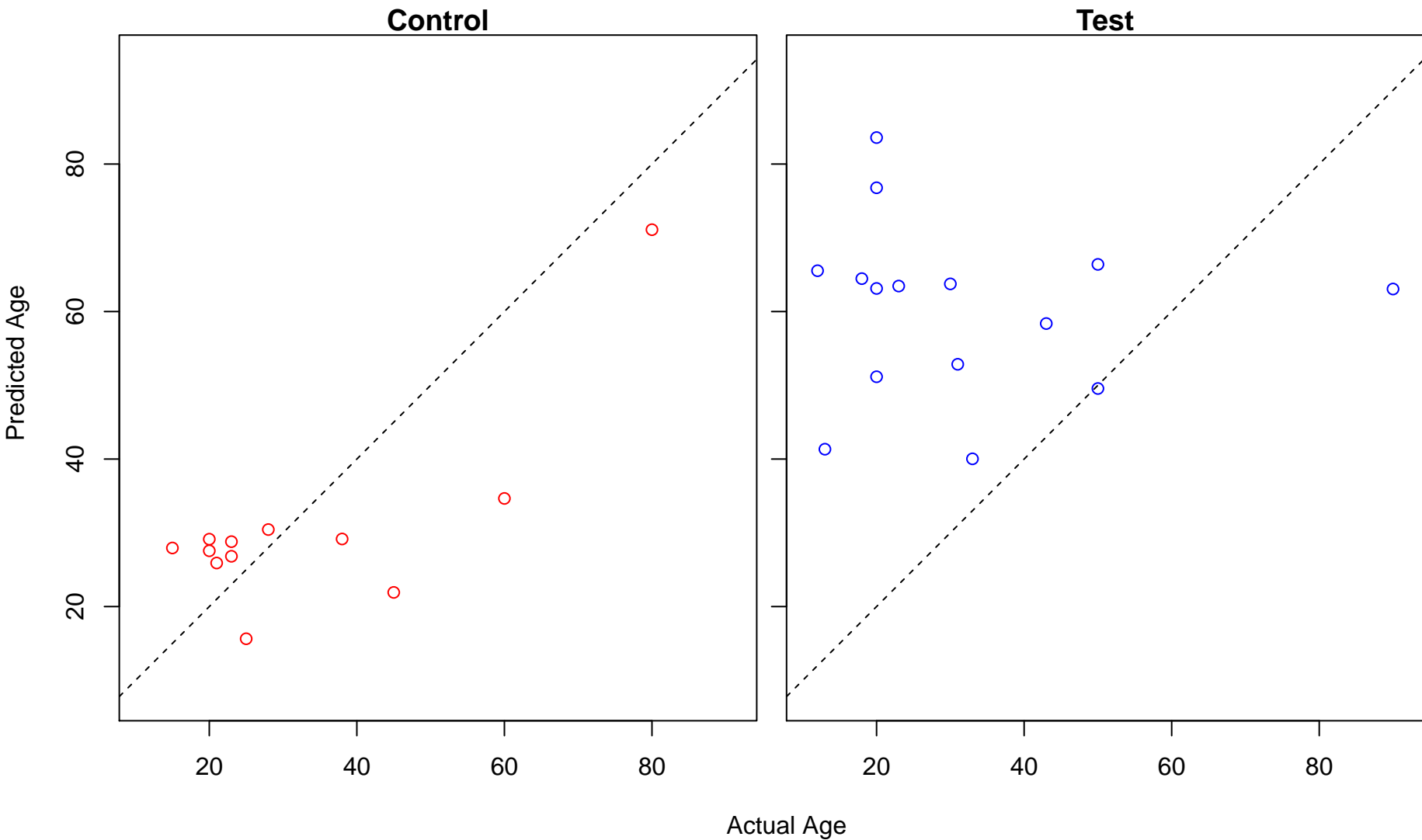
barbed-end actin filament capping (Score: 3.284759)



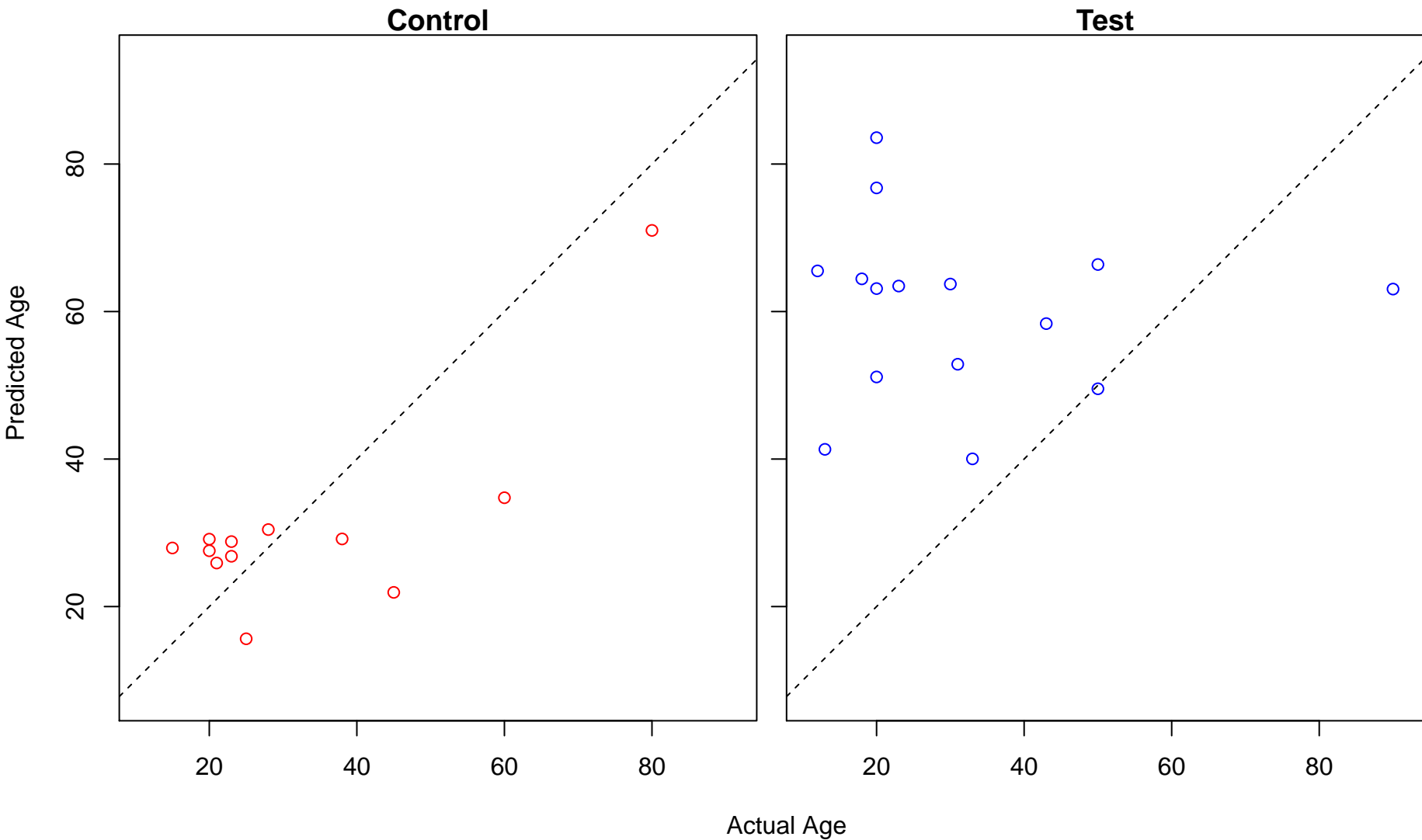
regulation of hydrogen peroxide-induced cell death (Score: 3.284086)



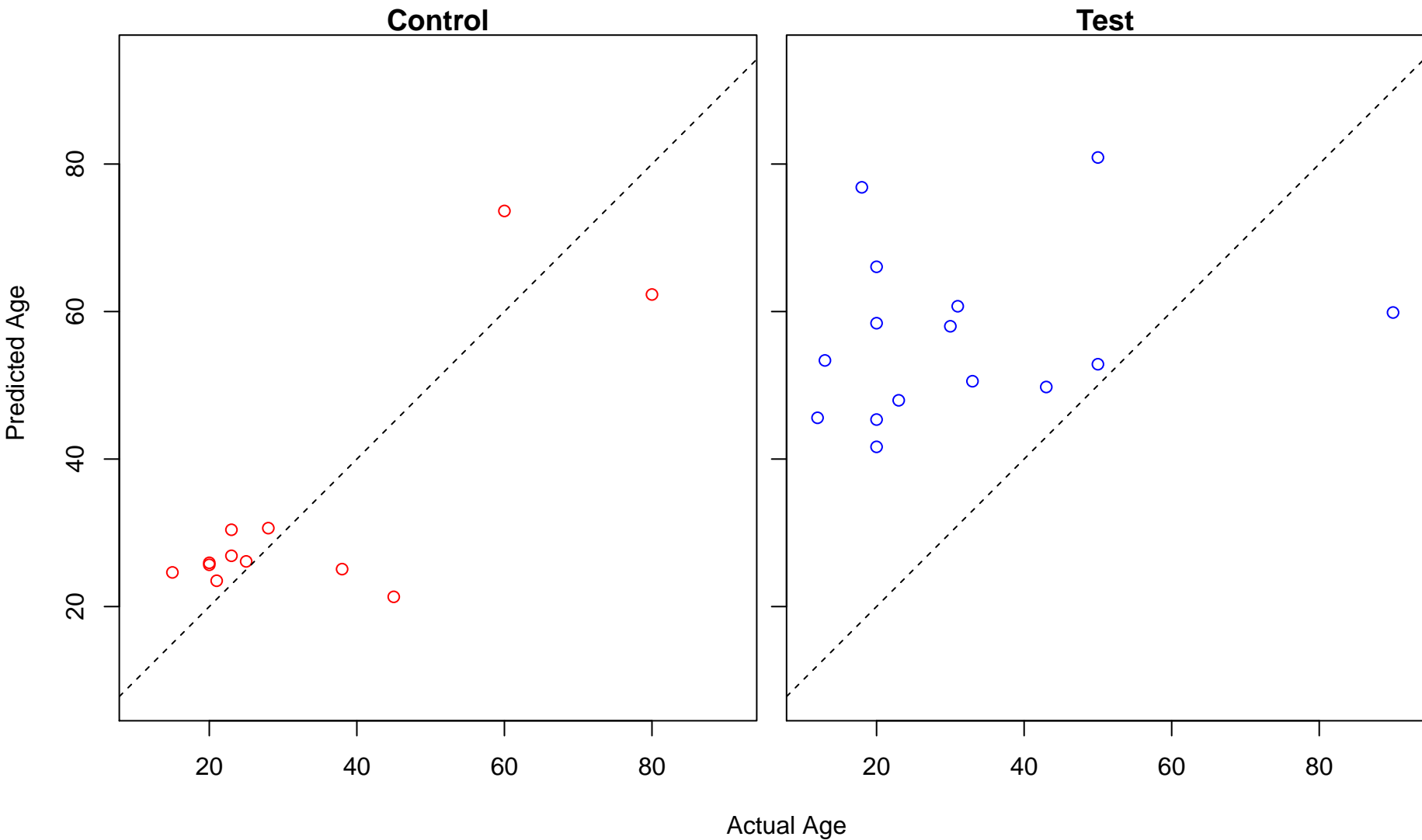
forebrain cell migration (Score: 3.282727)



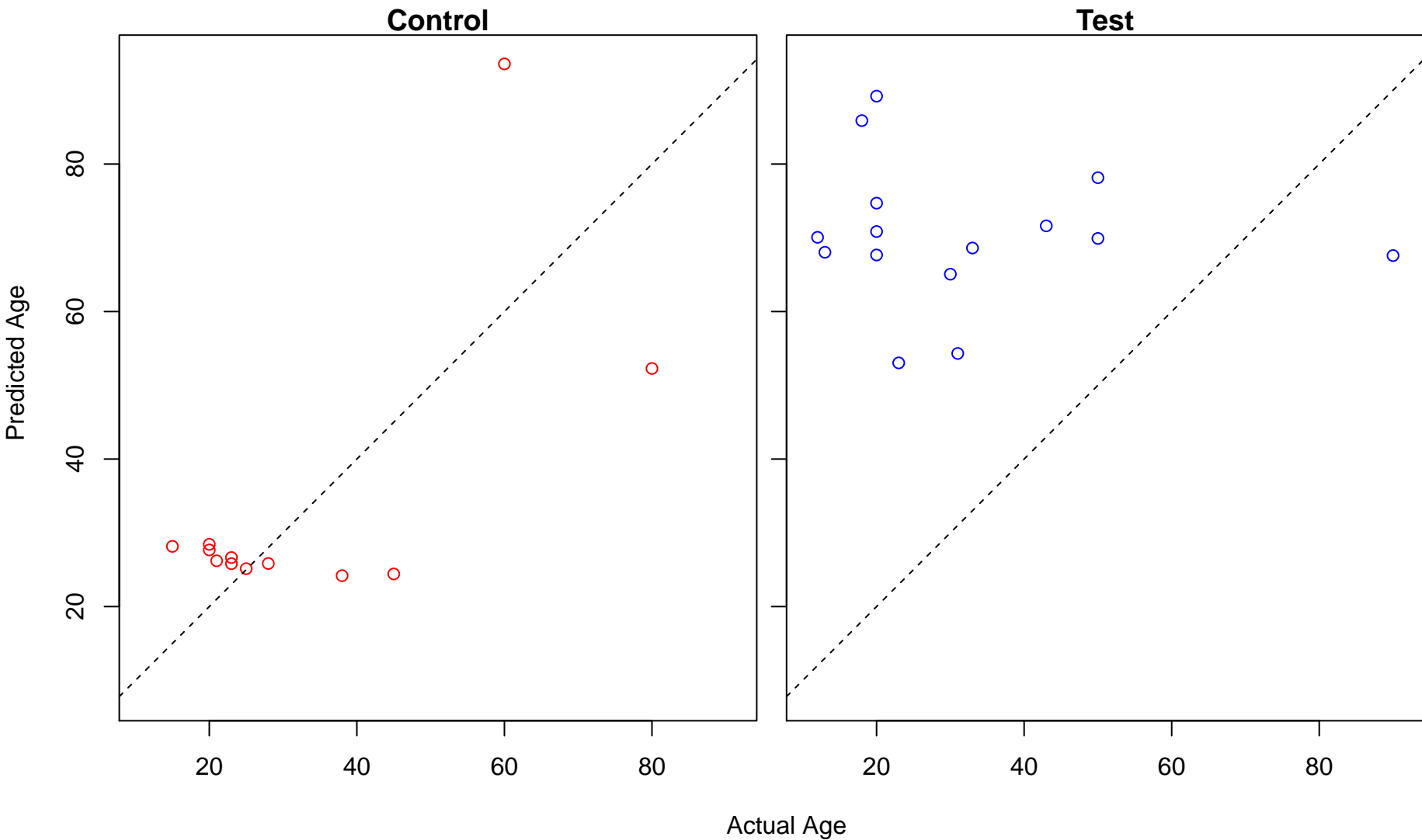
telencephalon cell migration (Score: 3.282562)



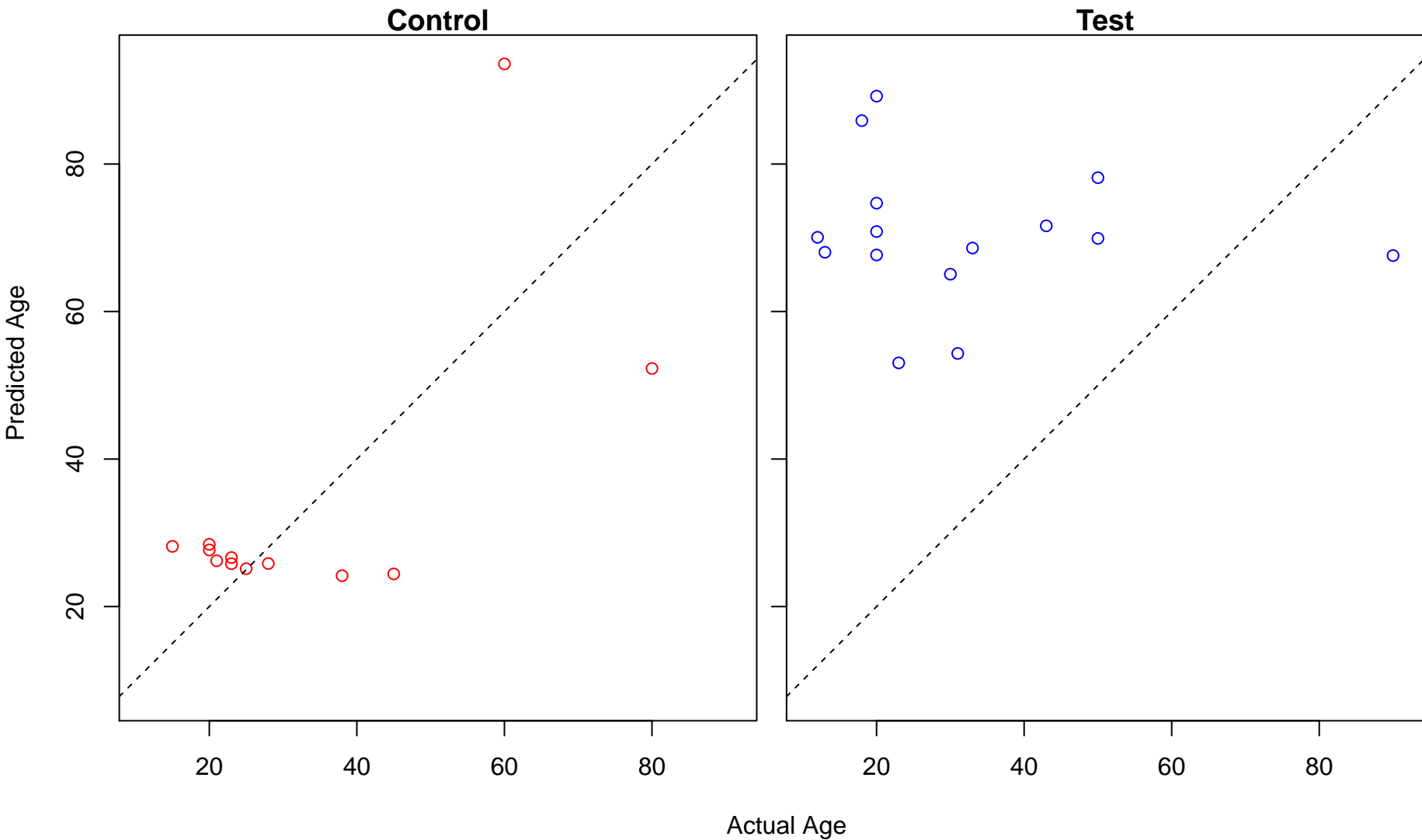
negative regulation of voltage-gated potassium channel activity (Score: 3.281688)



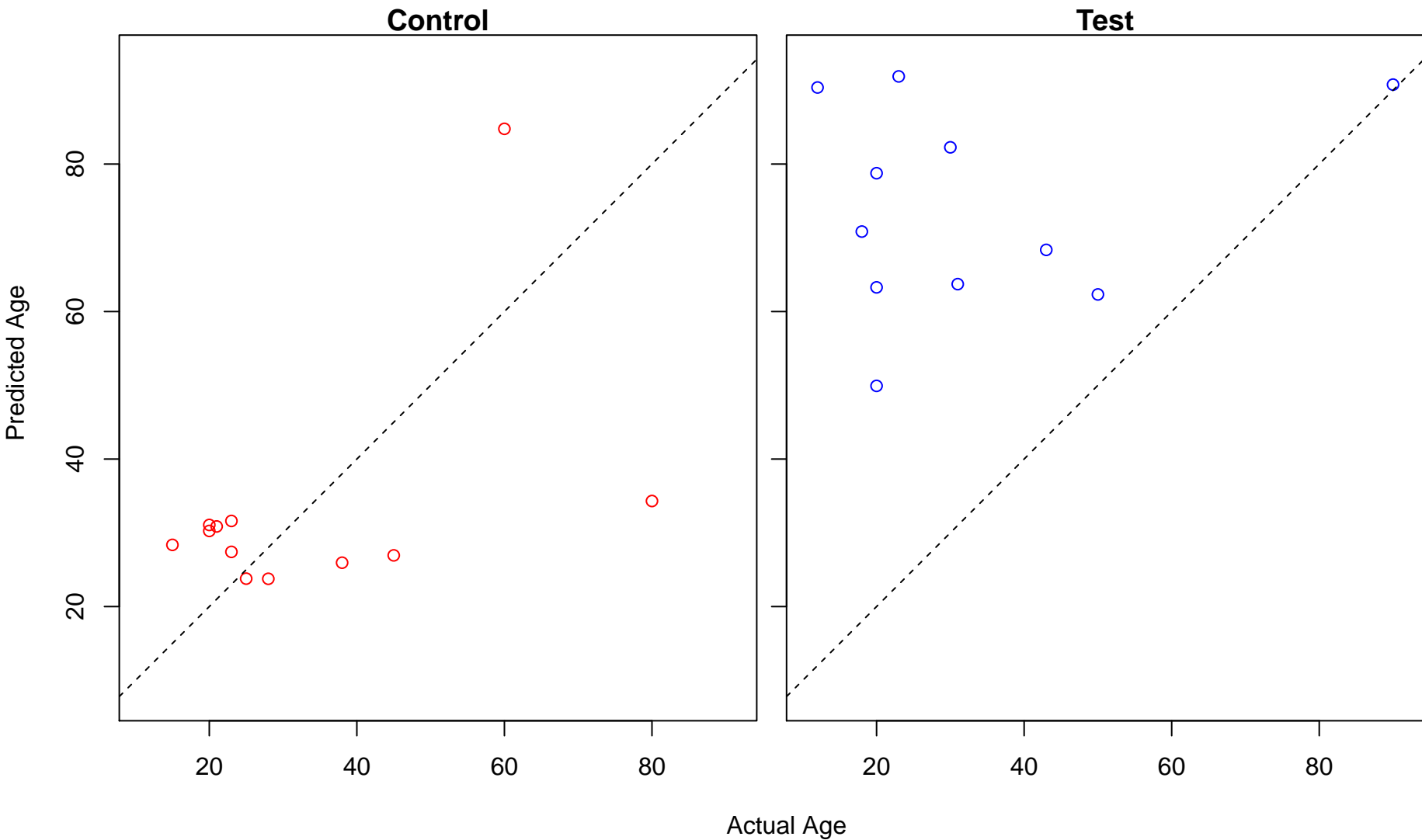
negative regulation of hydrogen peroxide-induced cell death (Score: 3.280475)



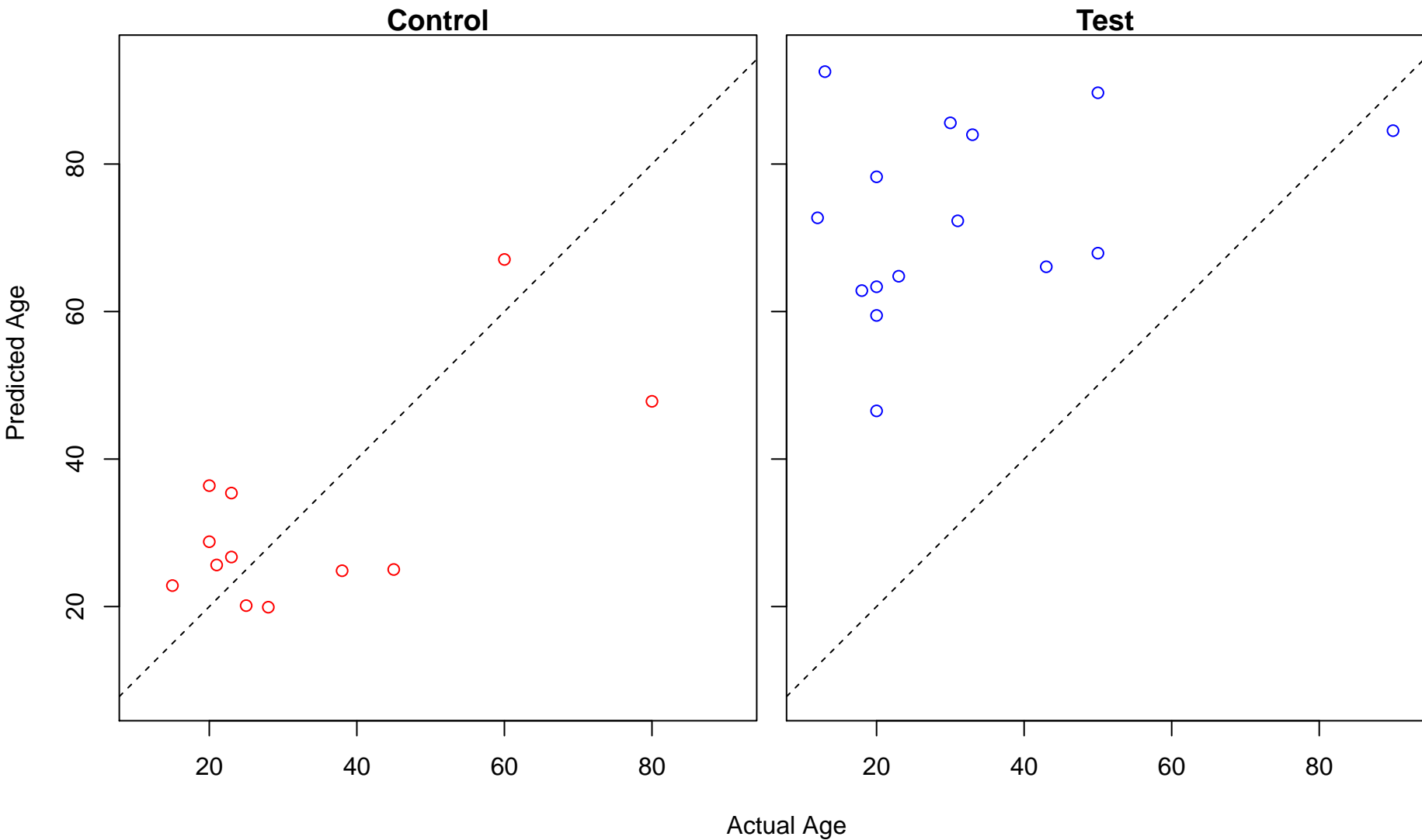
negative regulation of response to reactive oxygen species (Score: 3.280441)



embryonic skeletal joint development (Score: 3.279496)

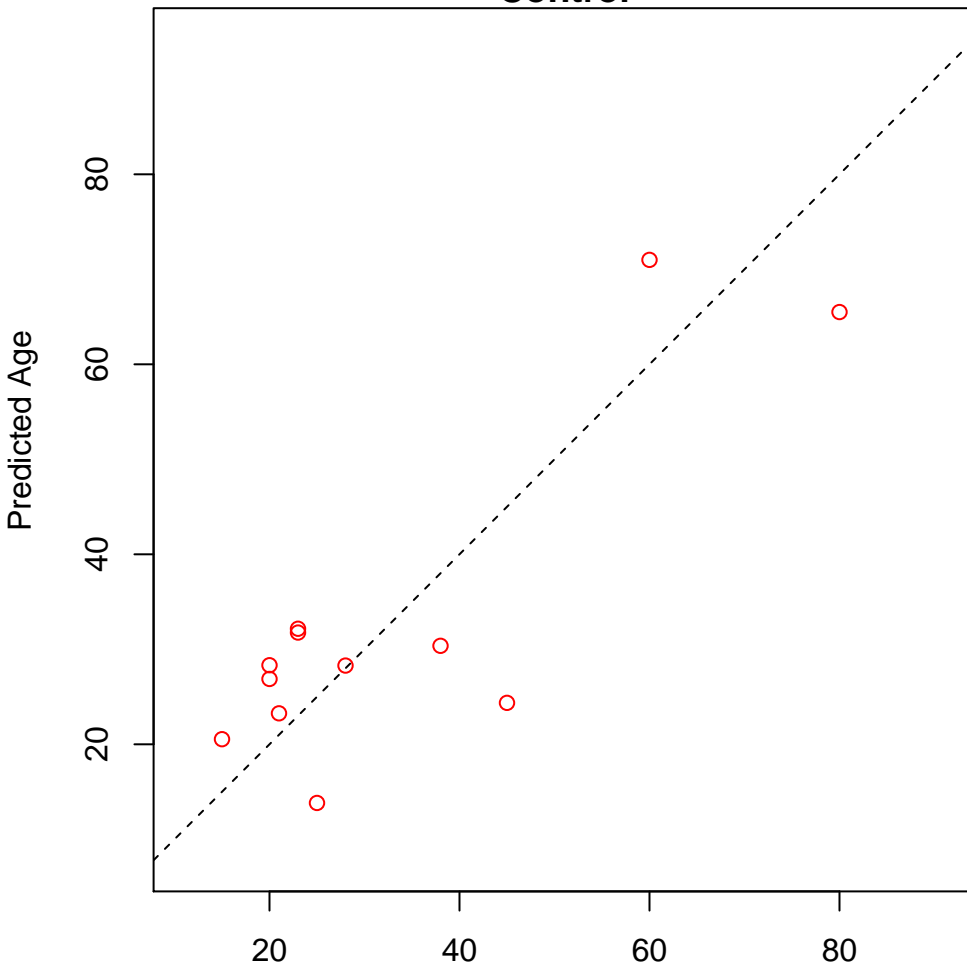


positive regulation of neuroblast proliferation (Score: 3.276612)

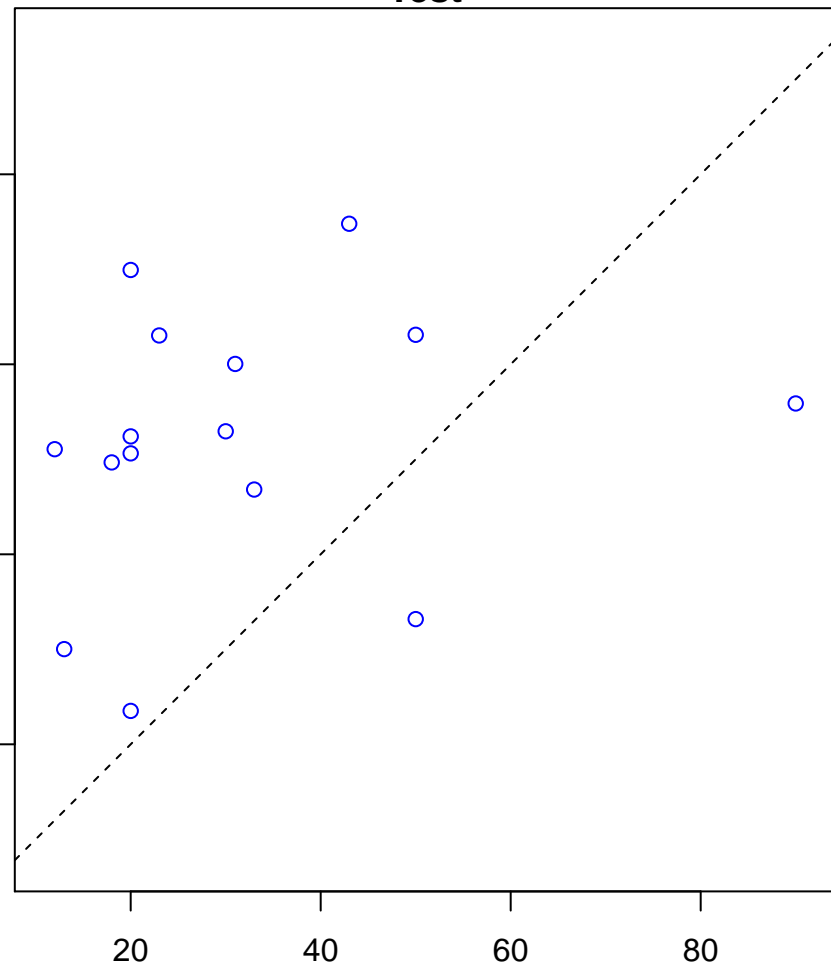


glycosyl compound catabolic process (Score: 3.275416)

Control

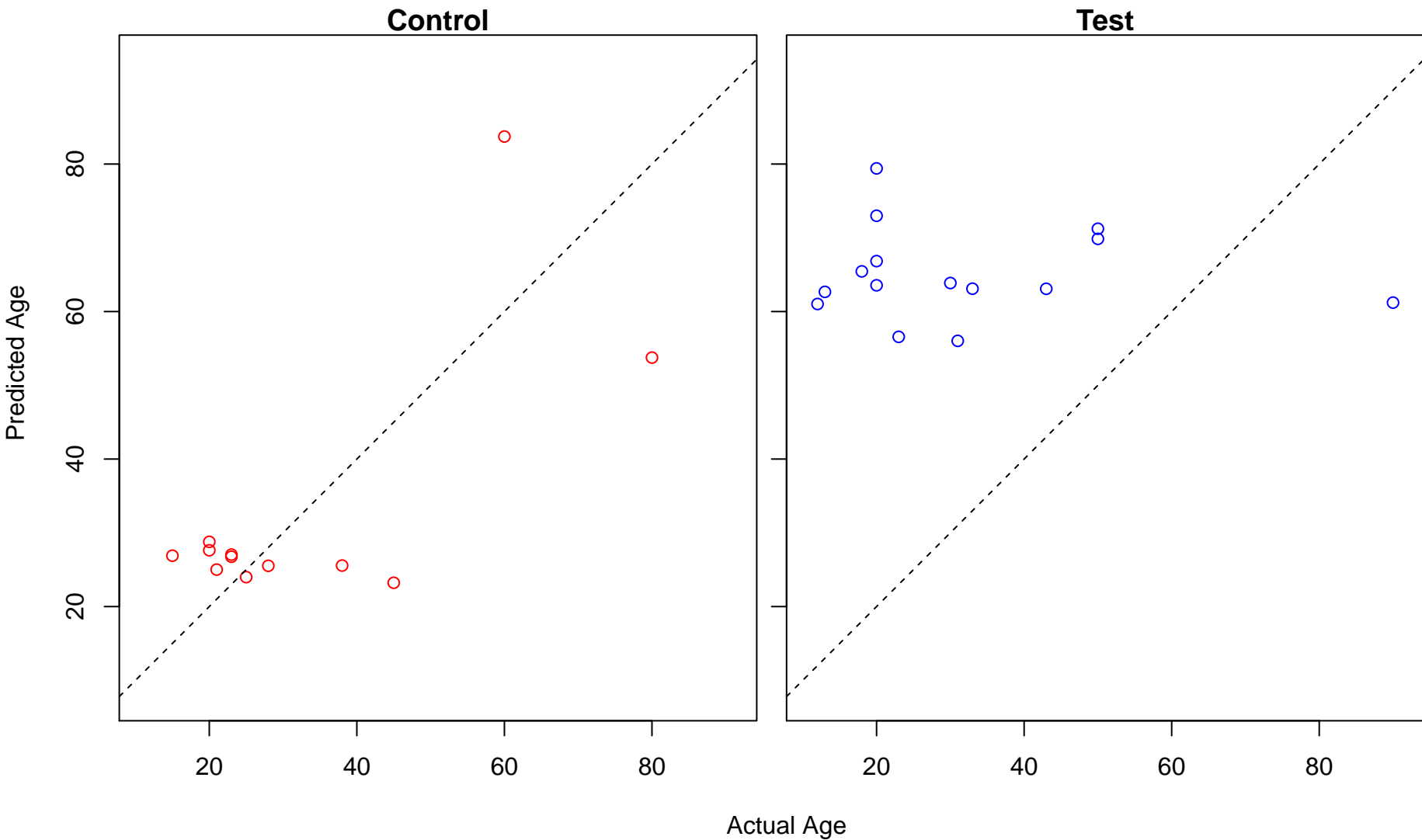


Test

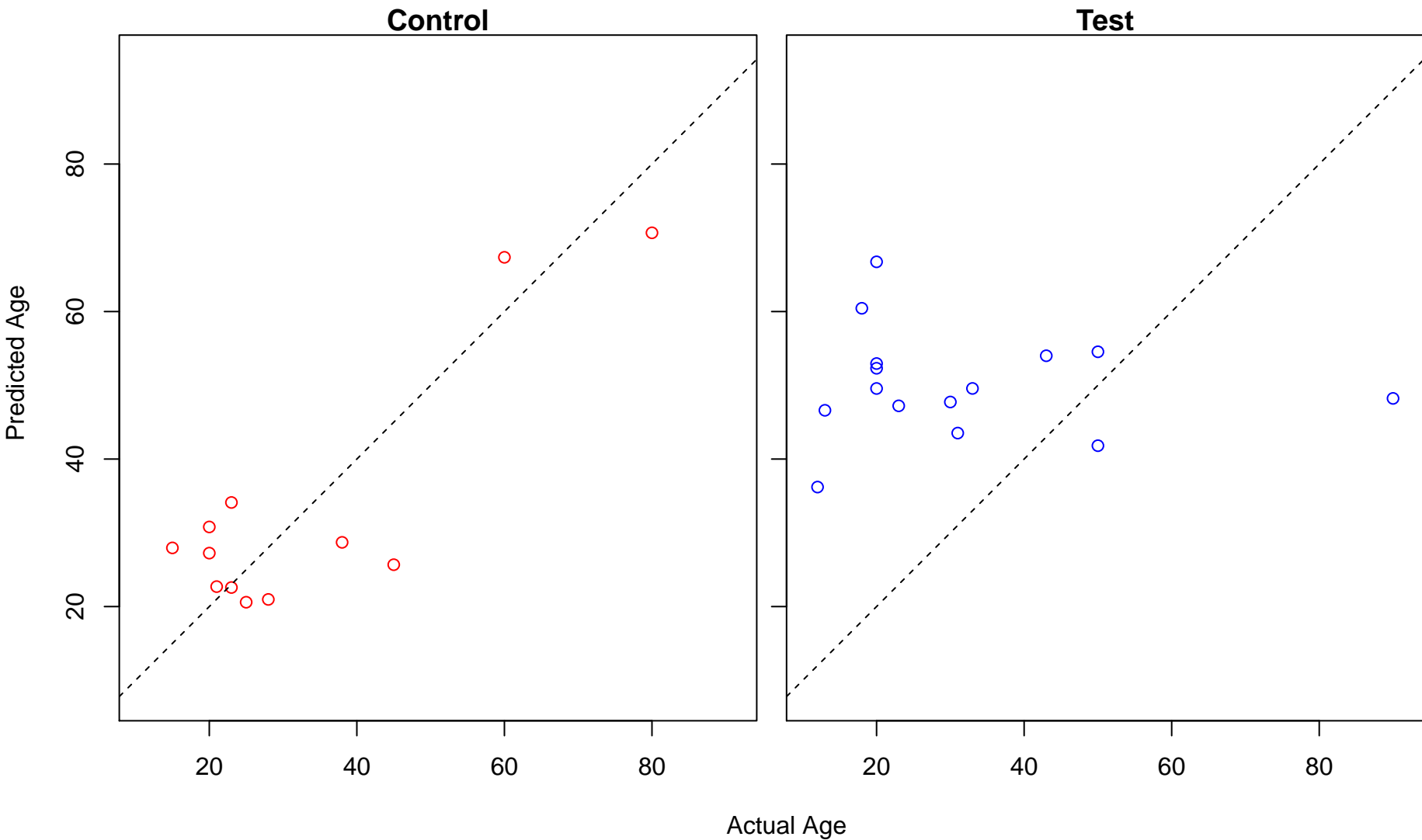


Actual Age

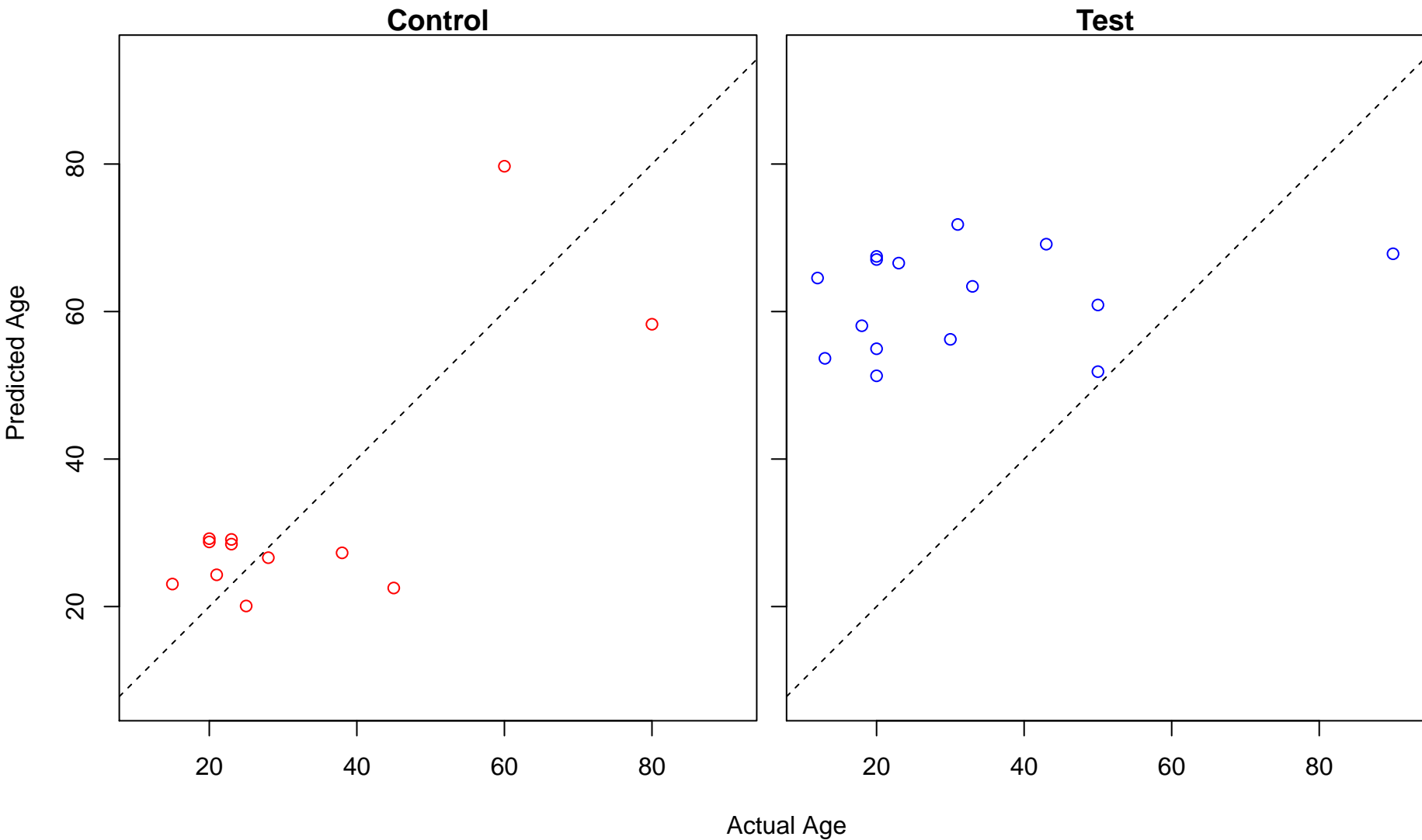
transition metal ion transport (Score: 3.275322)



muscle hypertrophy (Score: 3.273639)

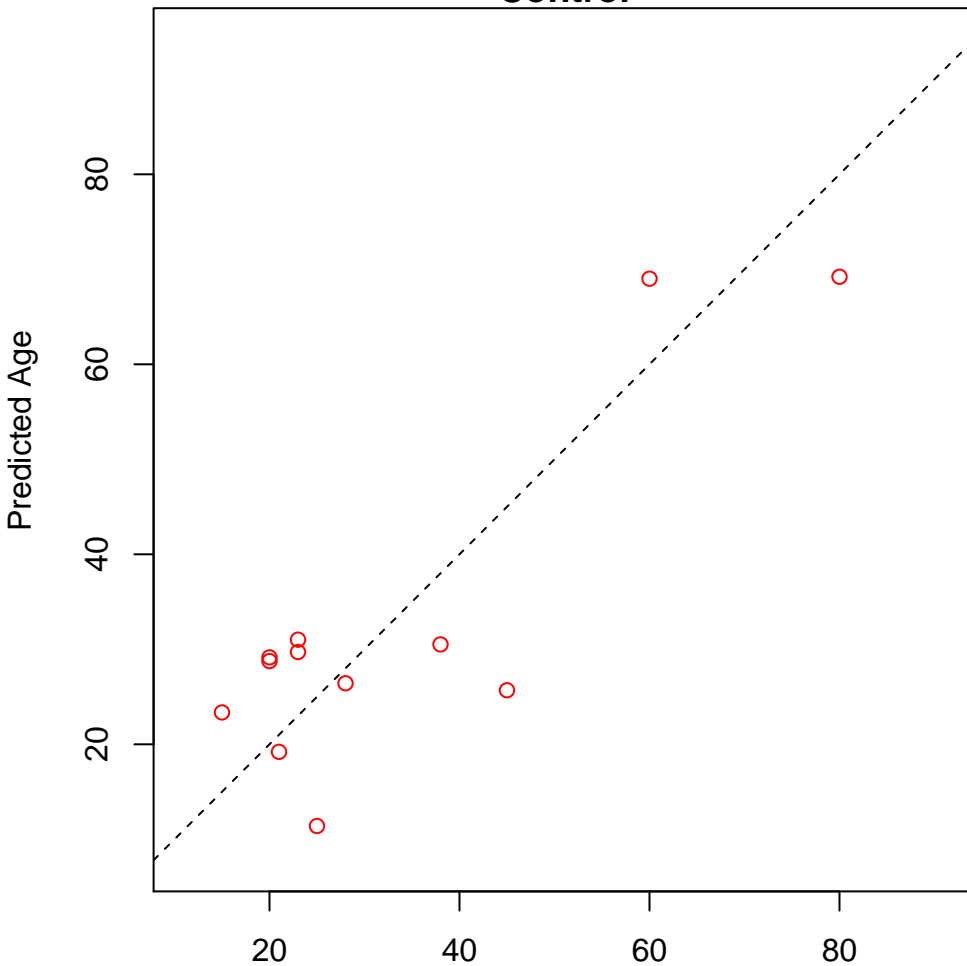


mRNA transcription (Score: 3.272892)

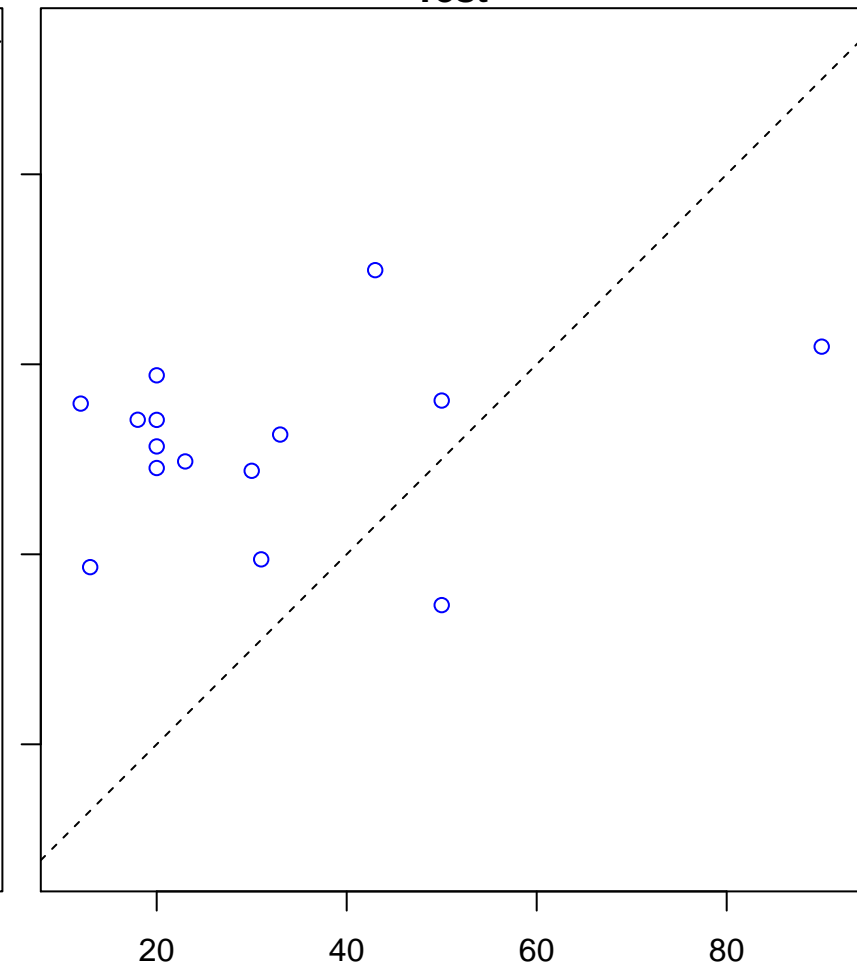


mesonephric tubule morphogenesis (Score: 3.265281)

Control

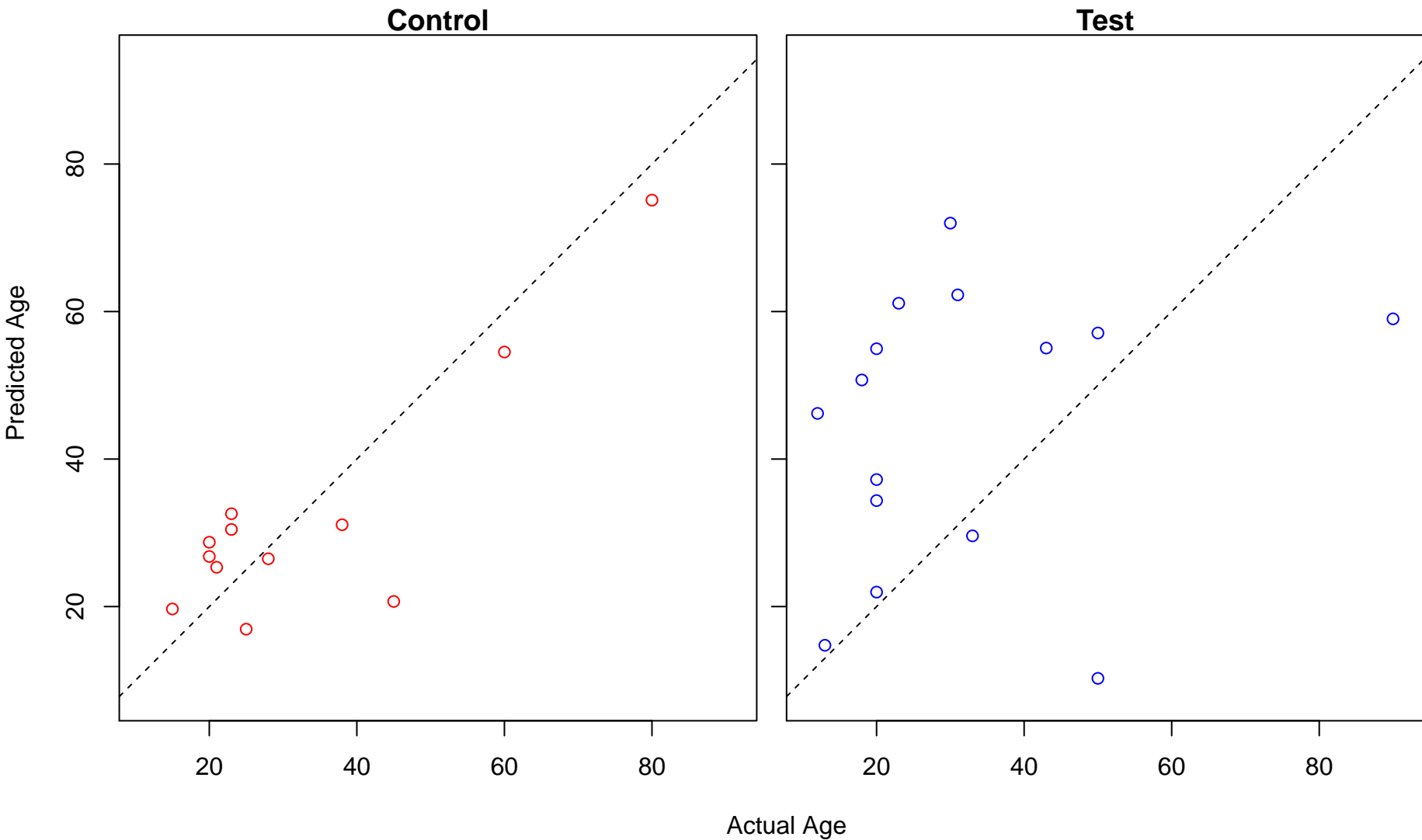


Test

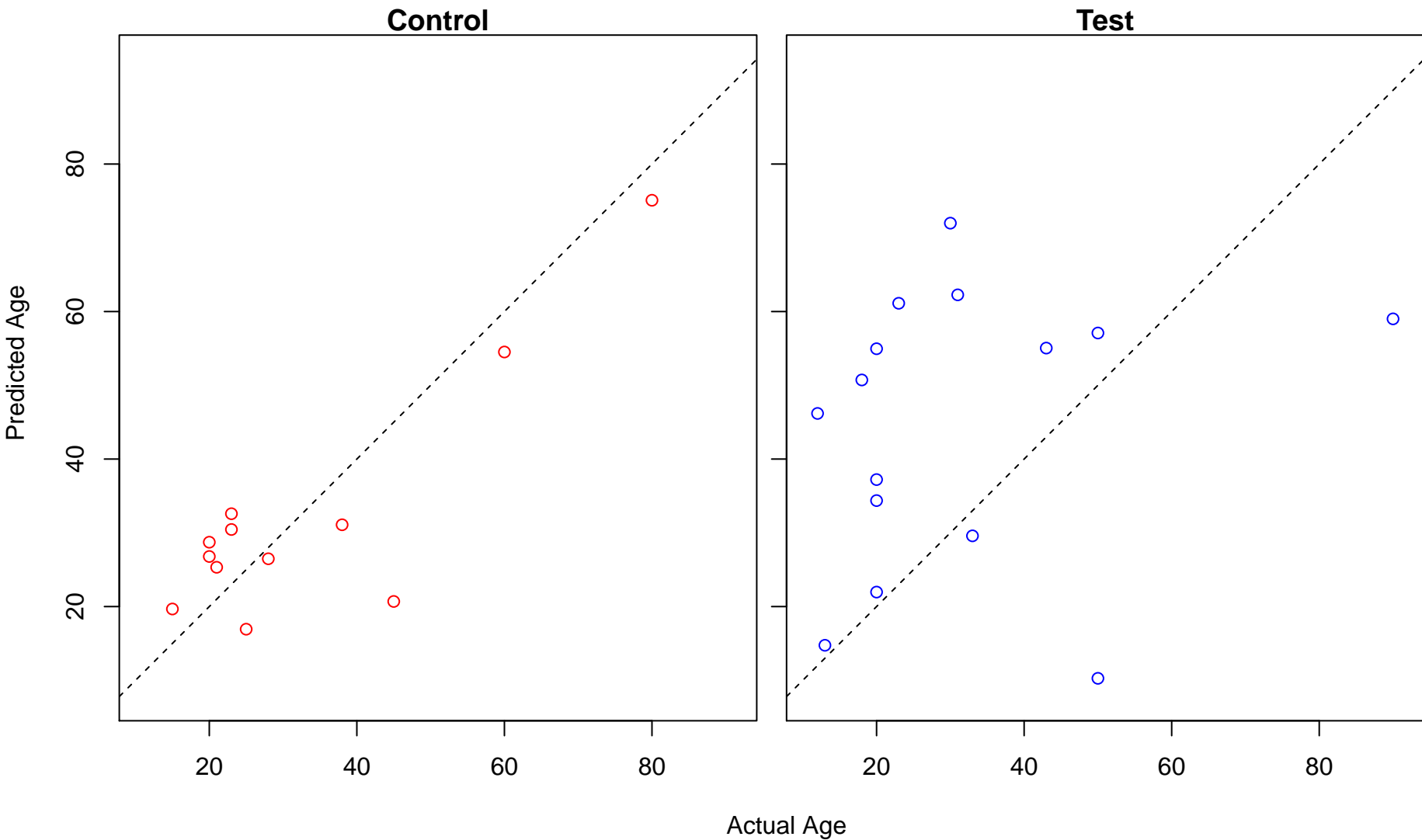


Actual Age

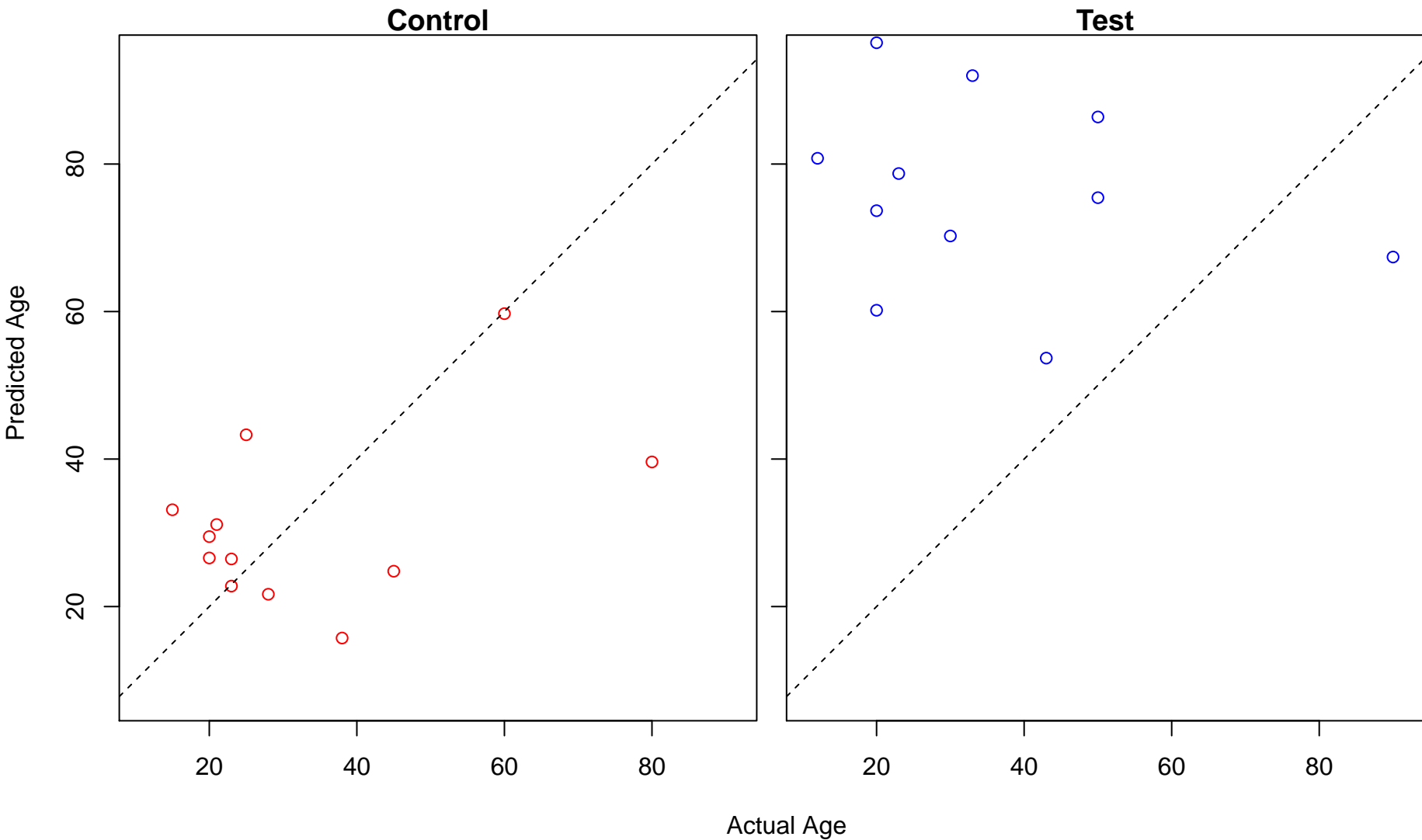
collagen catabolic process (Score: 3.264244)



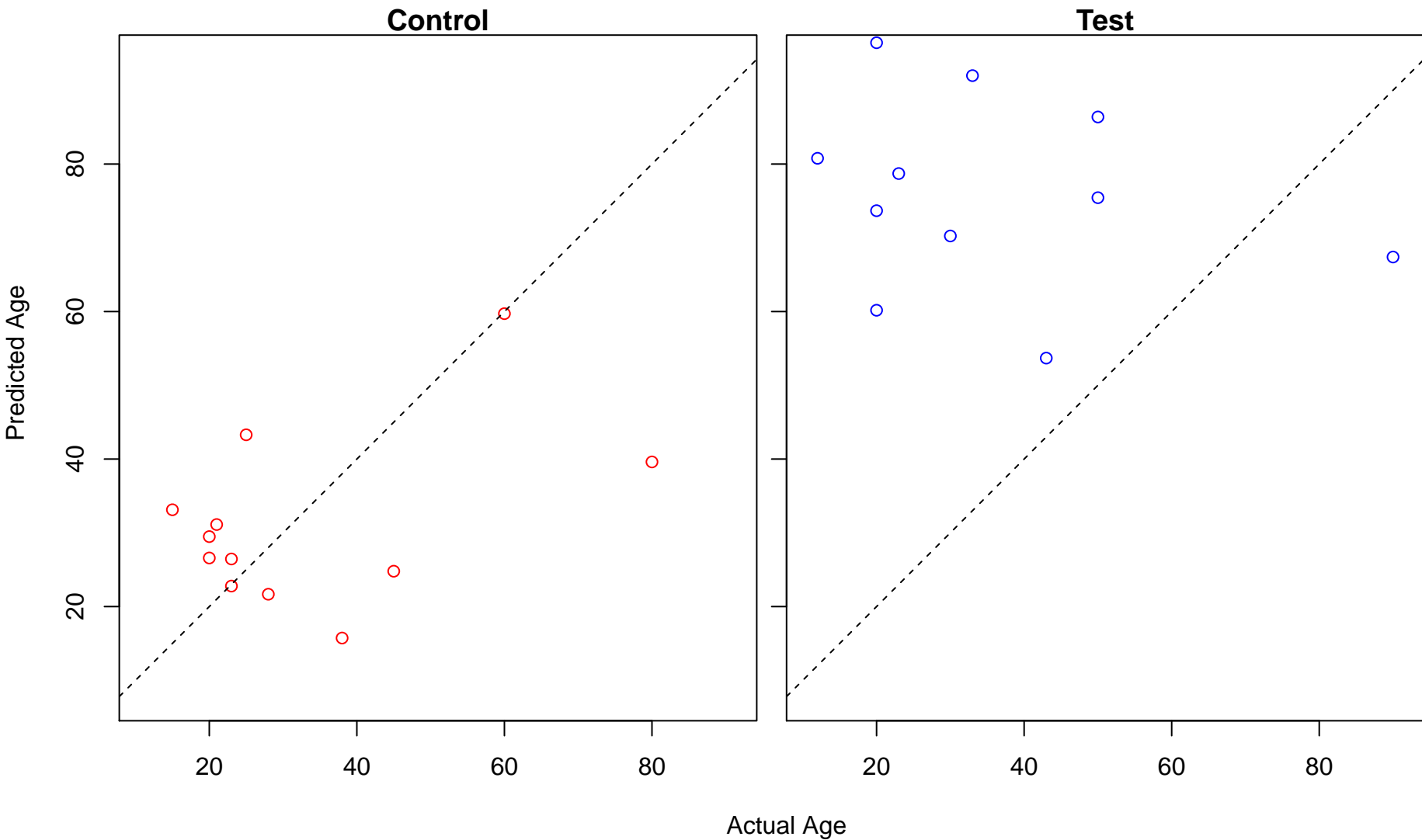
multicellular organismal catabolic process (Score: 3.26327)



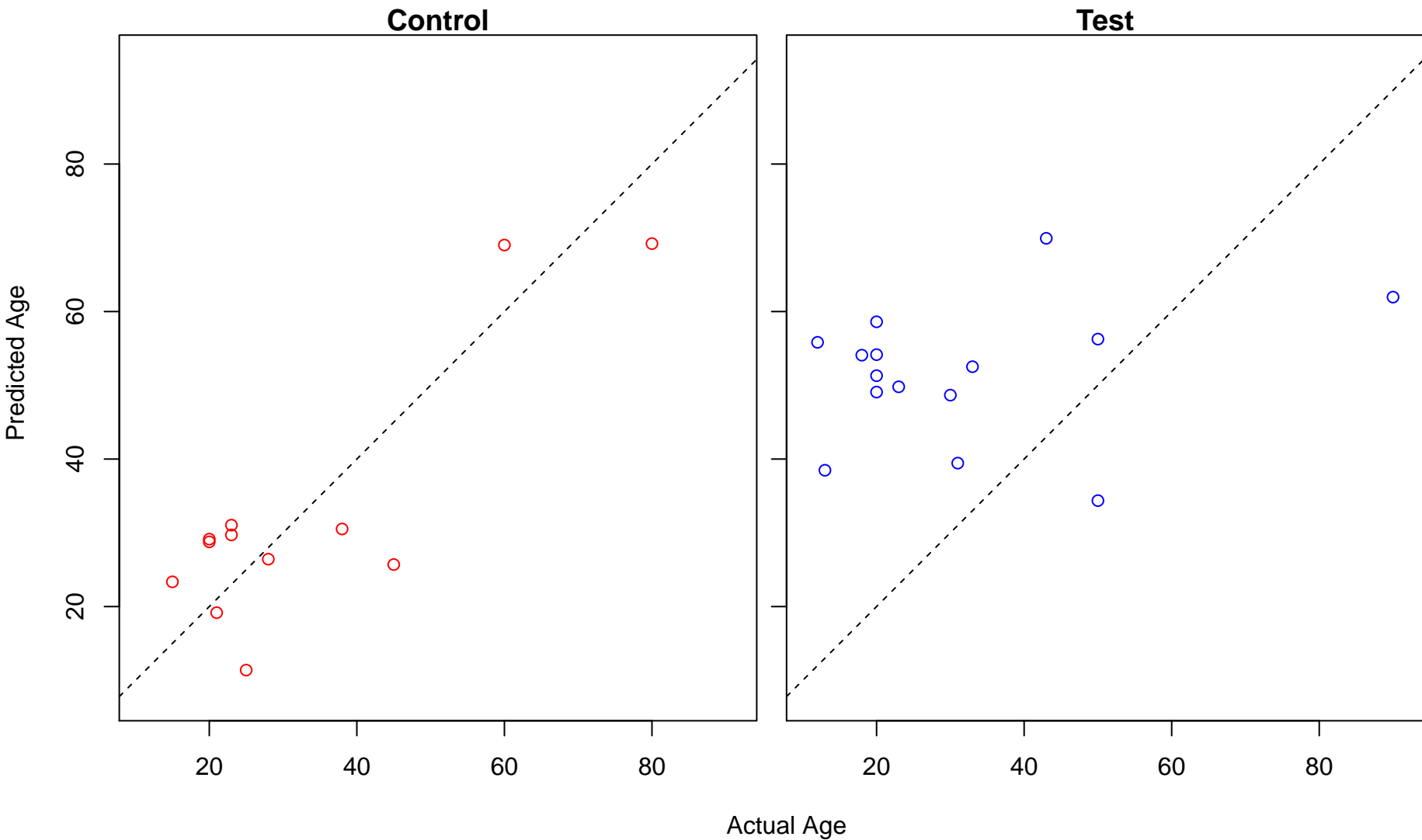
T cell lineage commitment (Score: 3.259148)



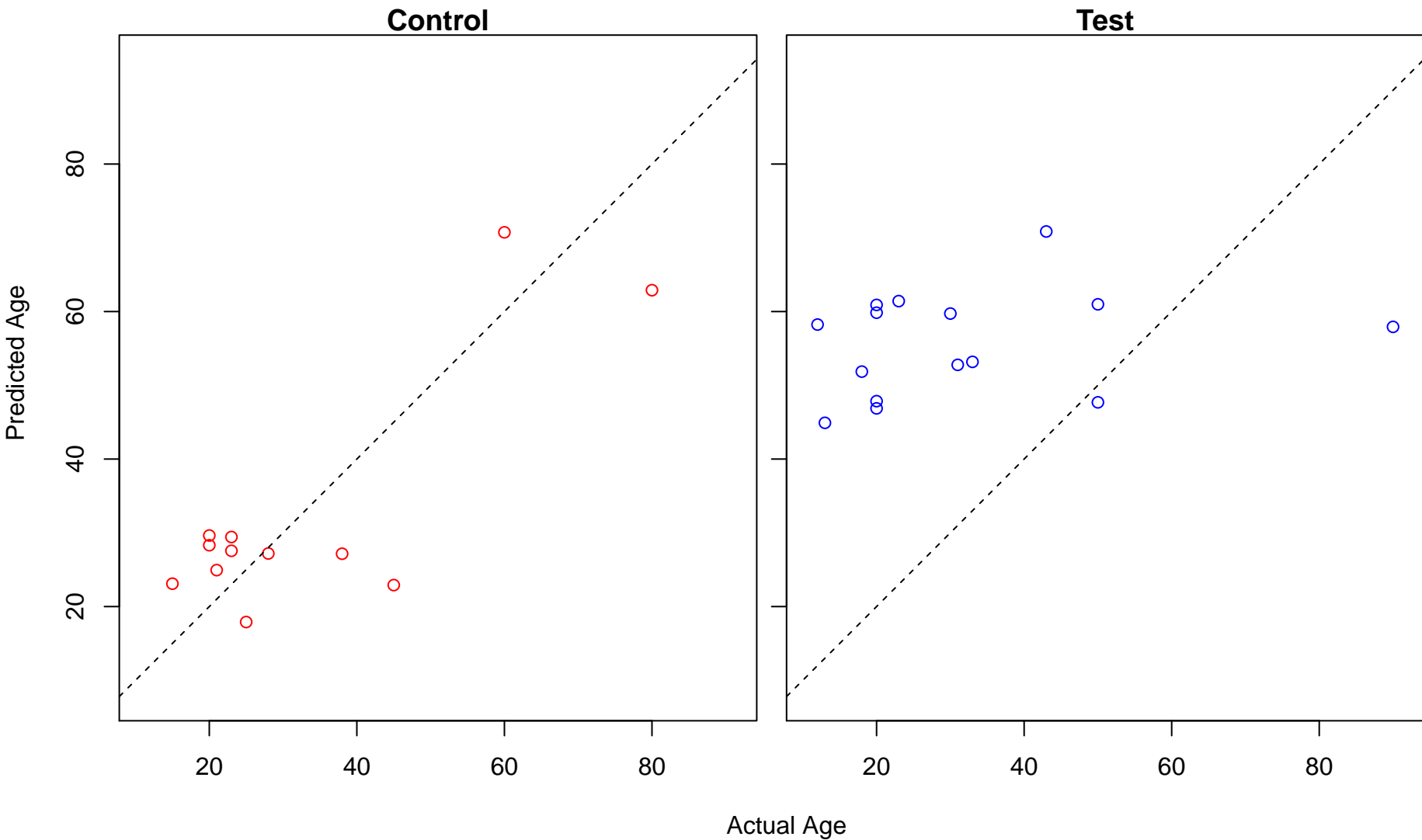
CD4-positive or CD8-positive, alpha-beta T cell lineage commitment (Score: 3.259148)



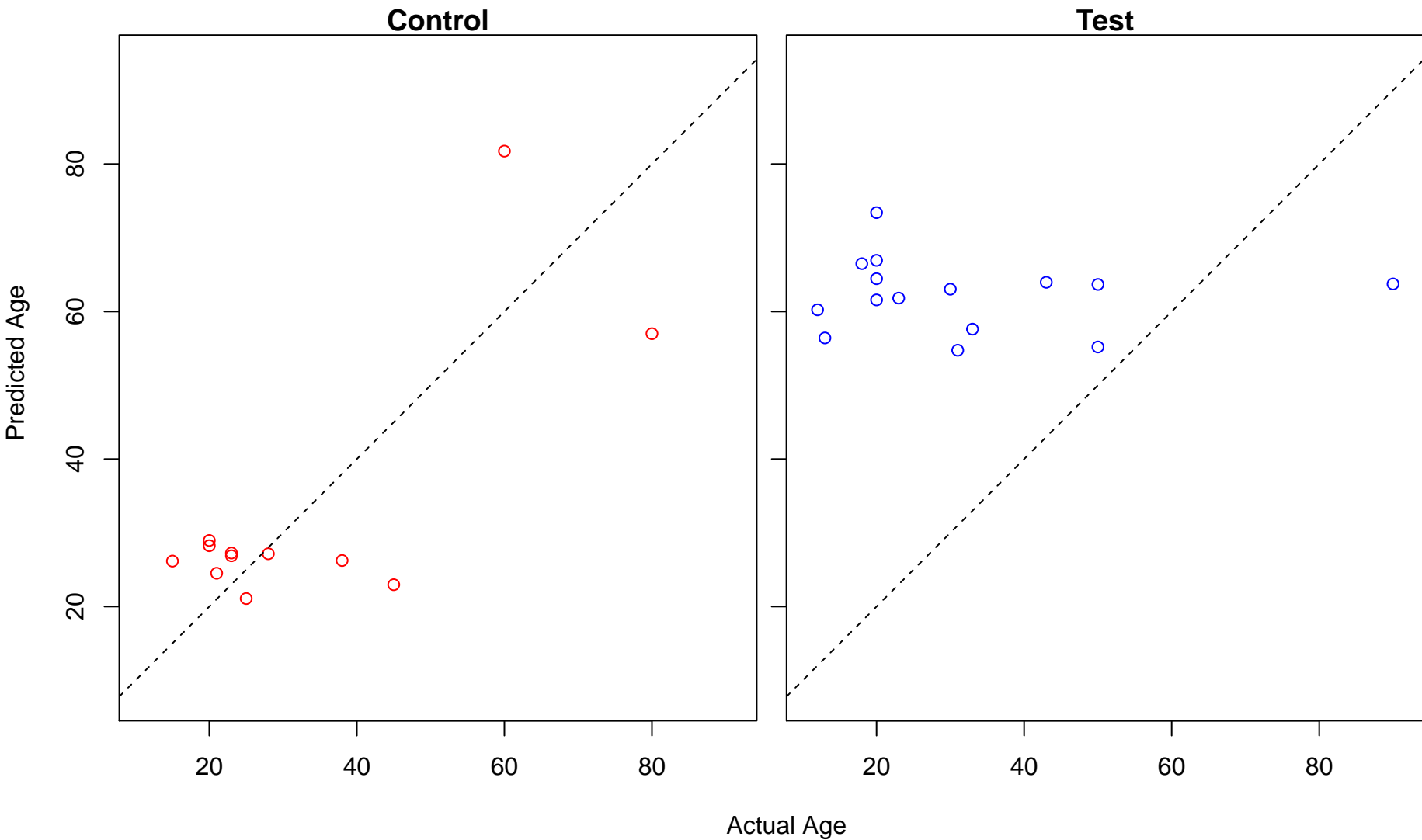
ureteric bud morphogenesis (Score: 3.255432)



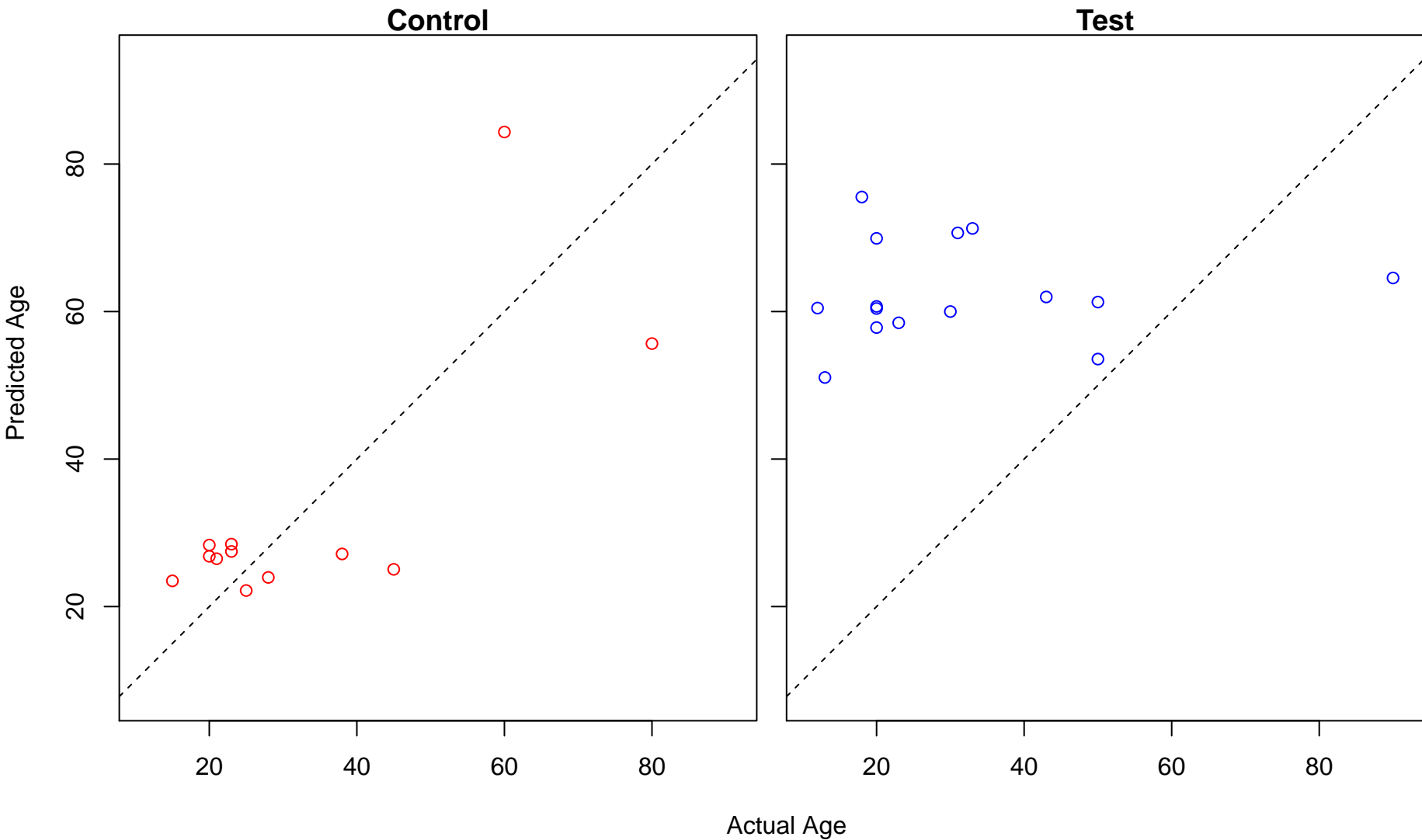
muscle cell proliferation (Score: 3.252392)



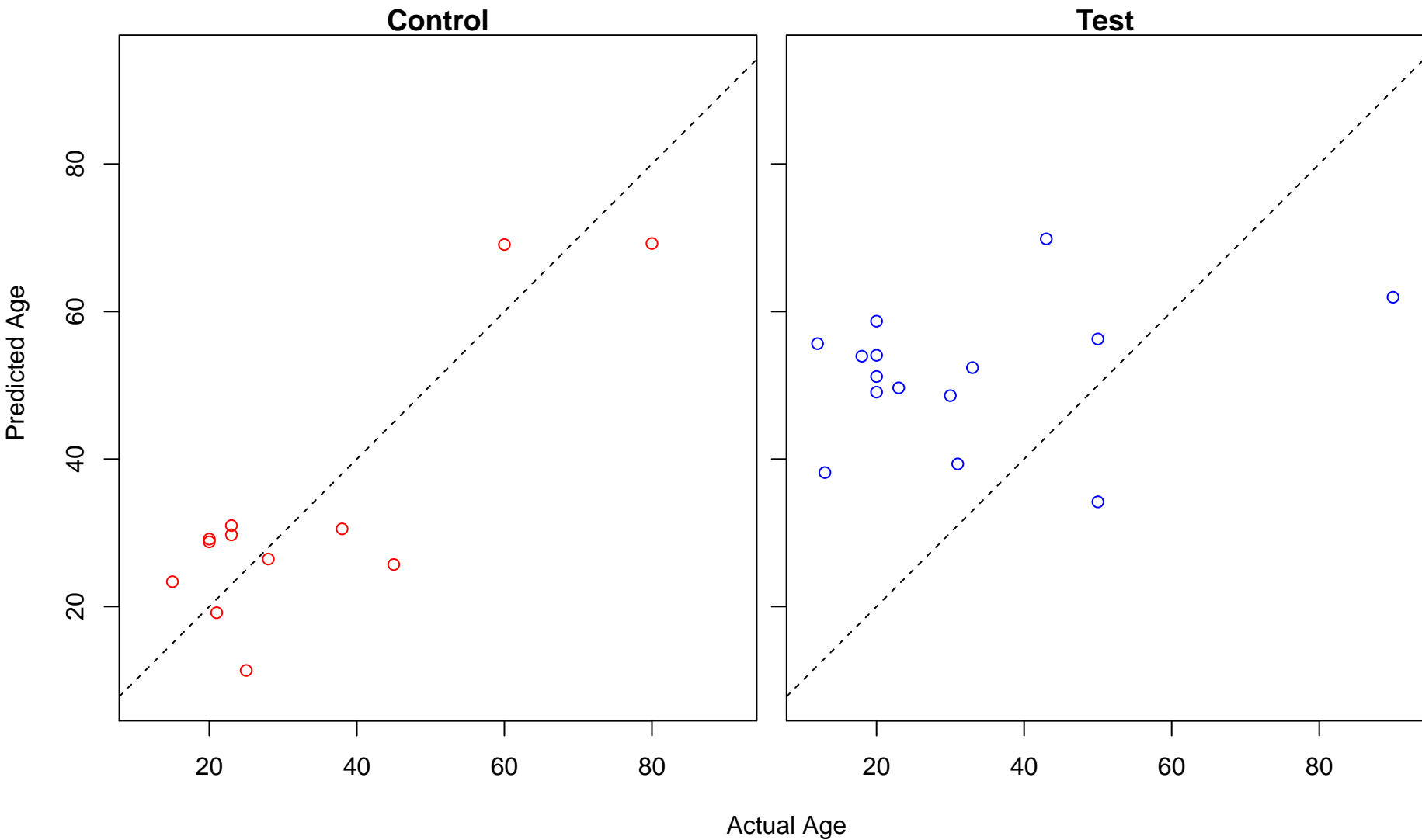
negative regulation of epithelial to mesenchymal transition (Score: 3.248233)



negative regulation of adherens junction organization (Score: 3.243182)

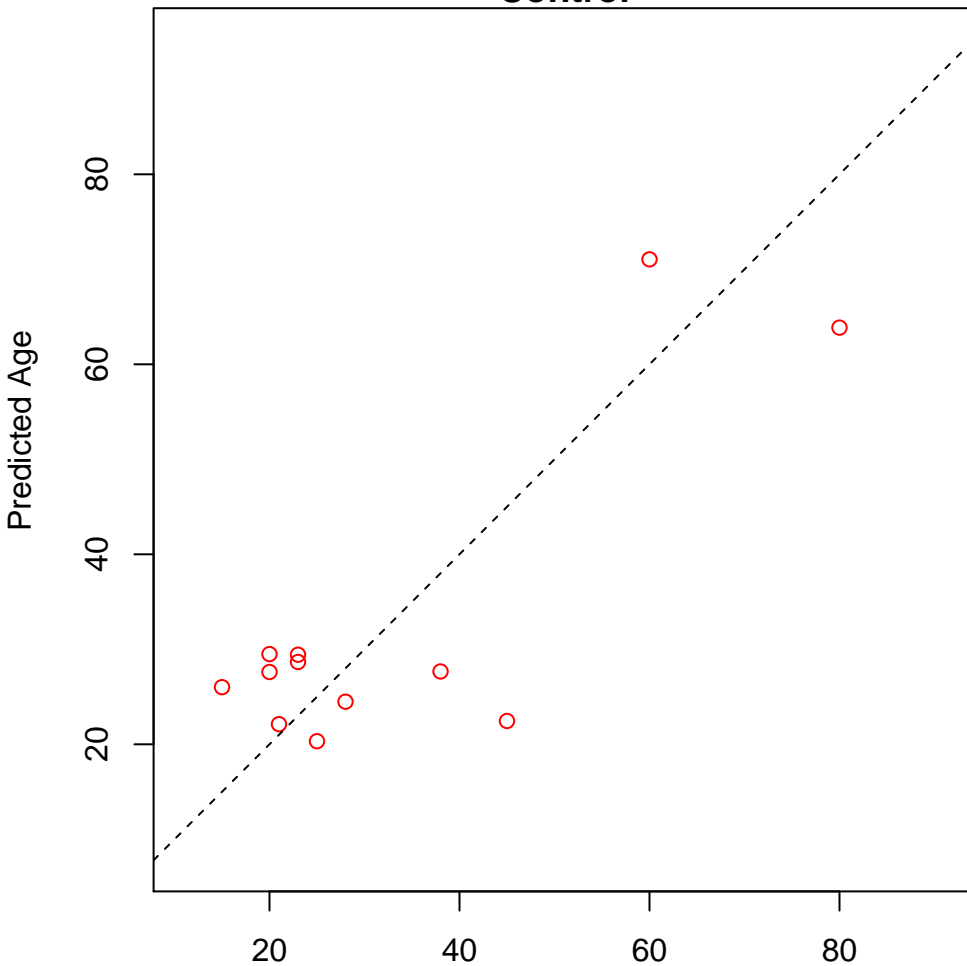


branching involved in ureteric bud morphogenesis (Score: 3.240878)

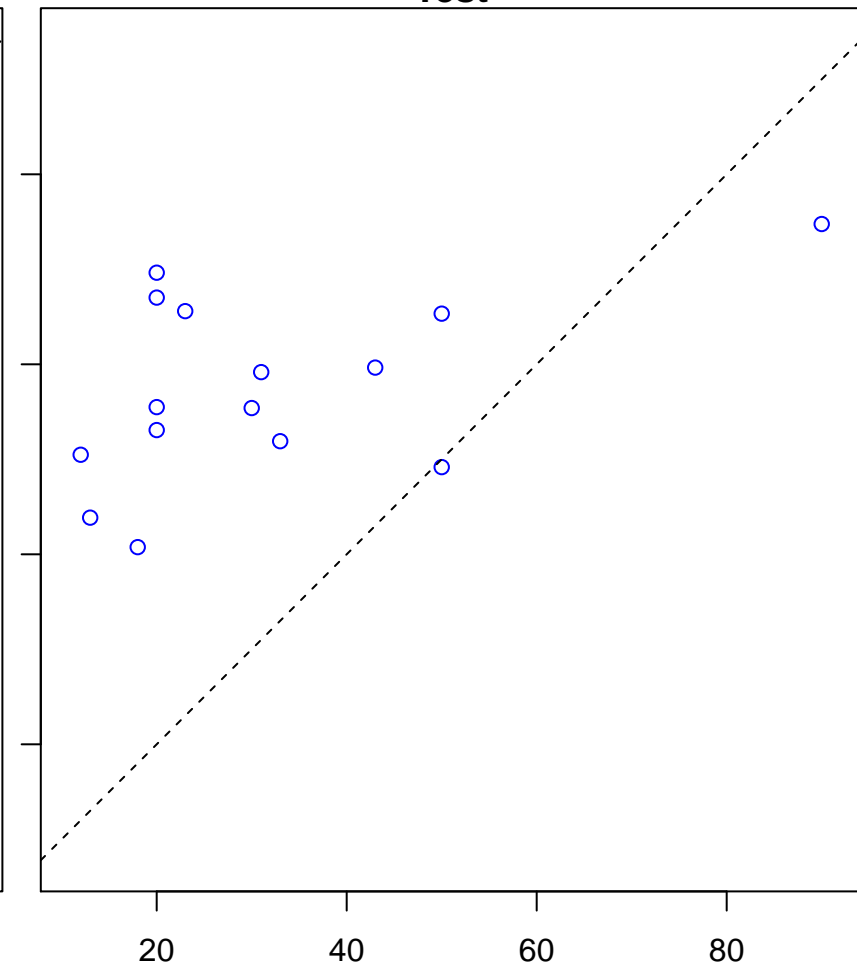


regulation of histone H3-K9 methylation (Score: 3.240073)

Control

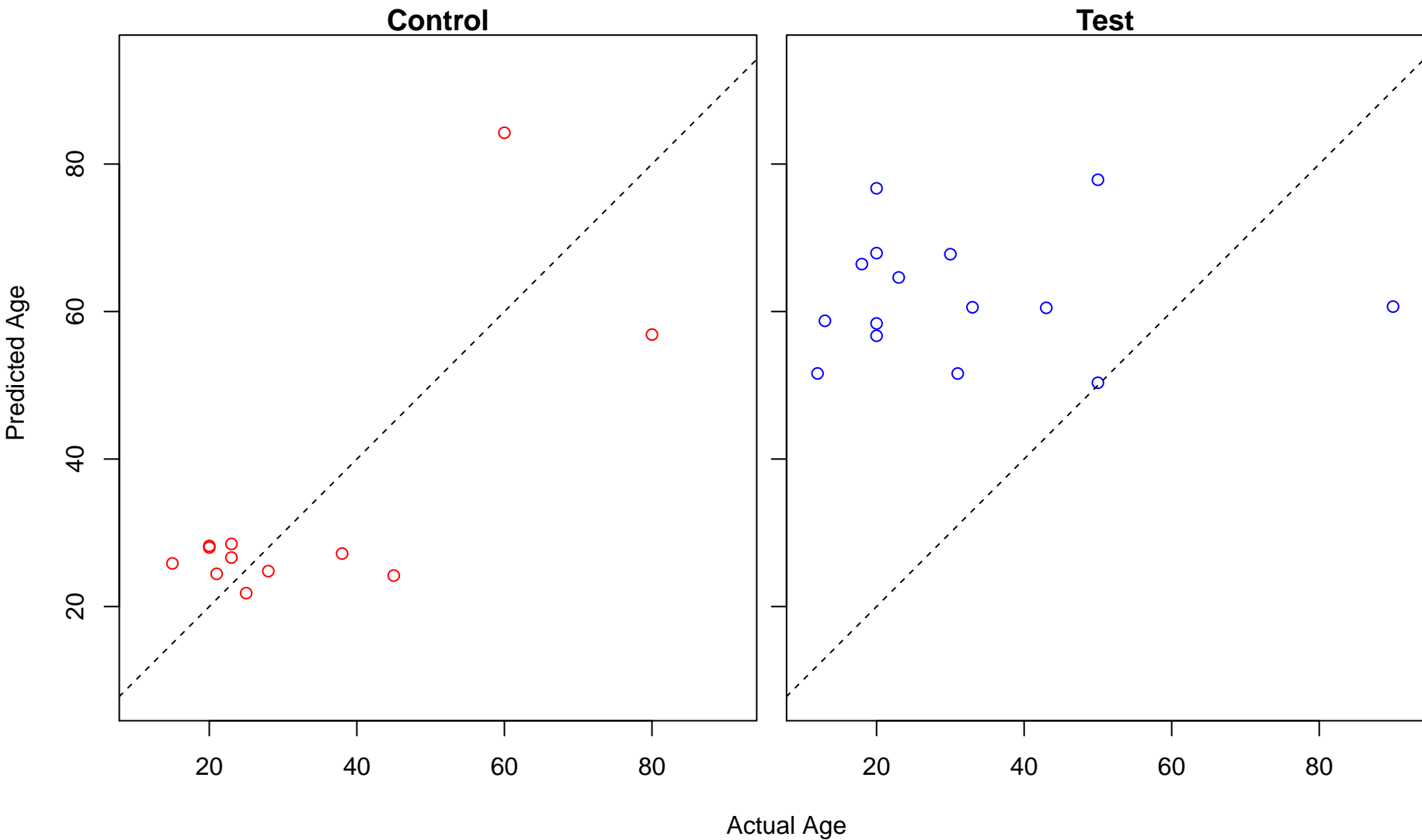


Test

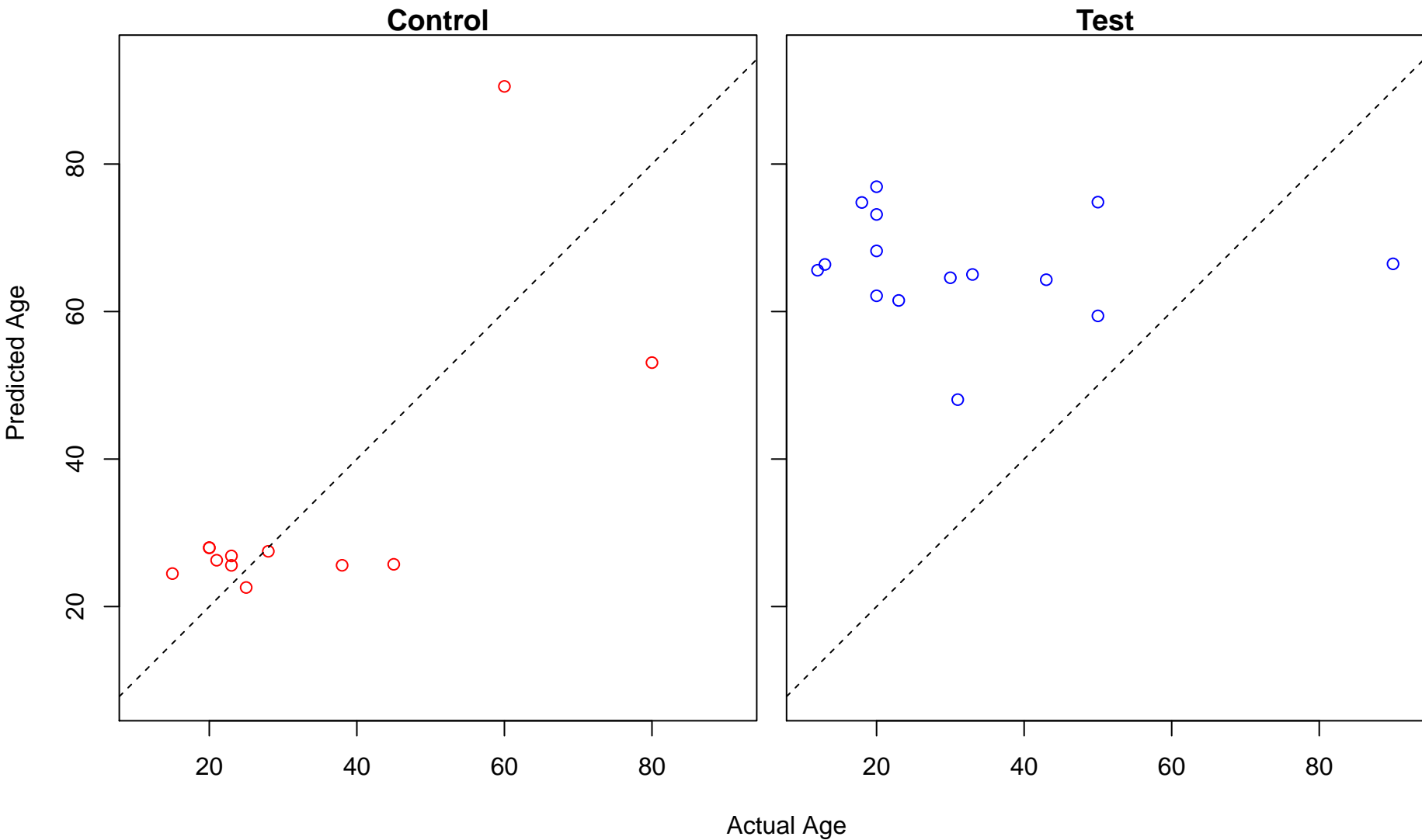


Actual Age

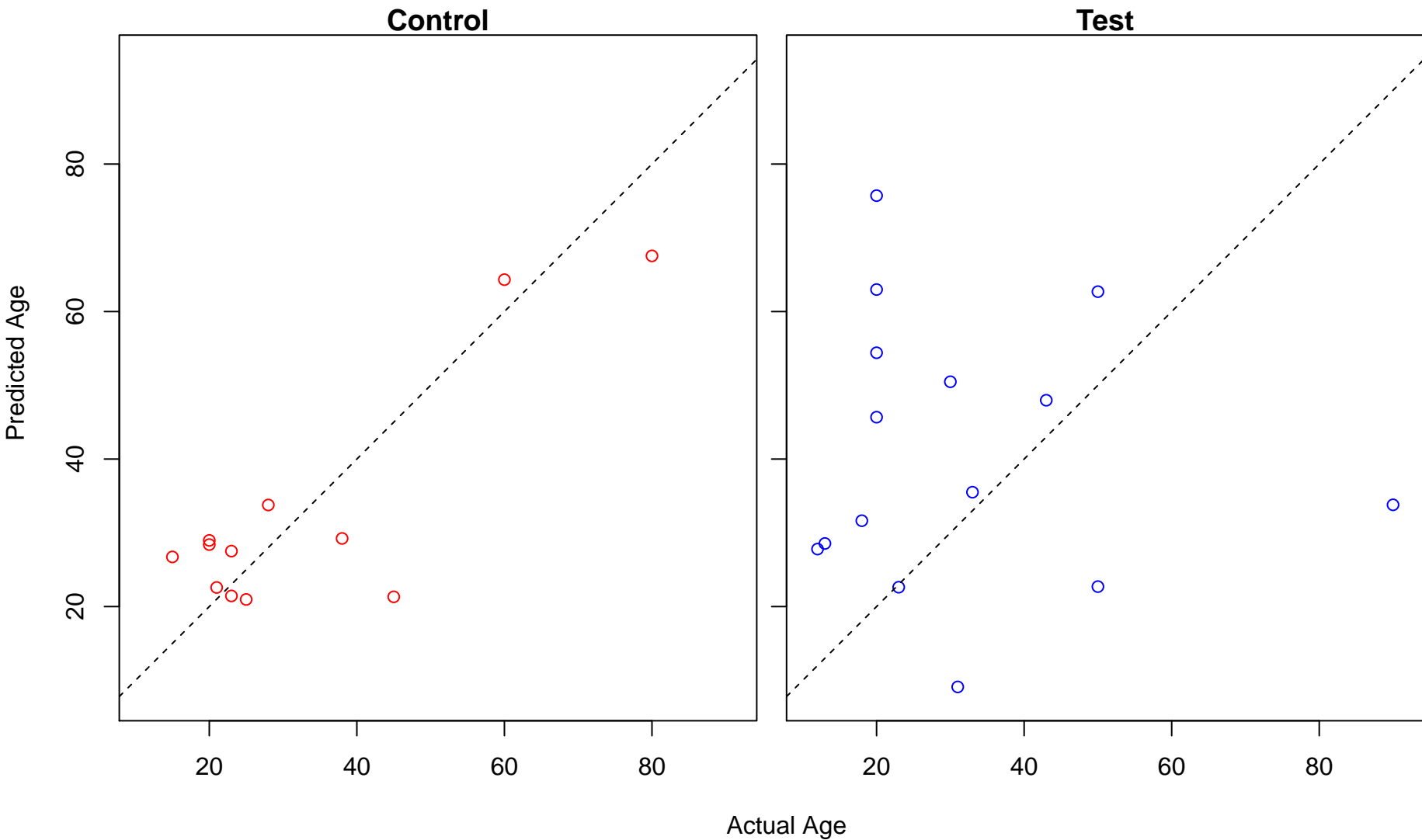
positive regulation of branching involved in ureteric bud morphogenesis (Score: 3.239425)



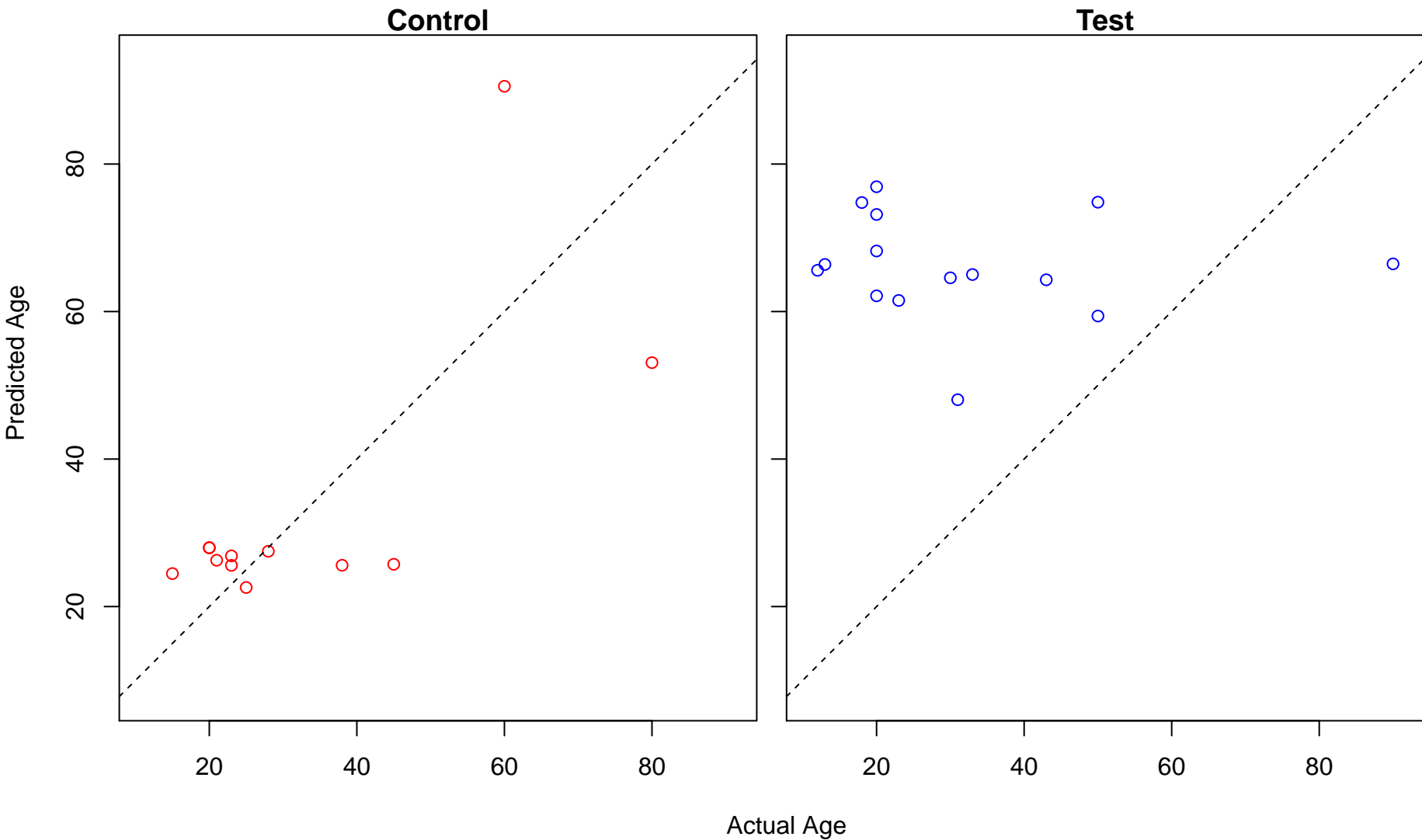
chromatin remodeling at centromere (Score: 3.238888)



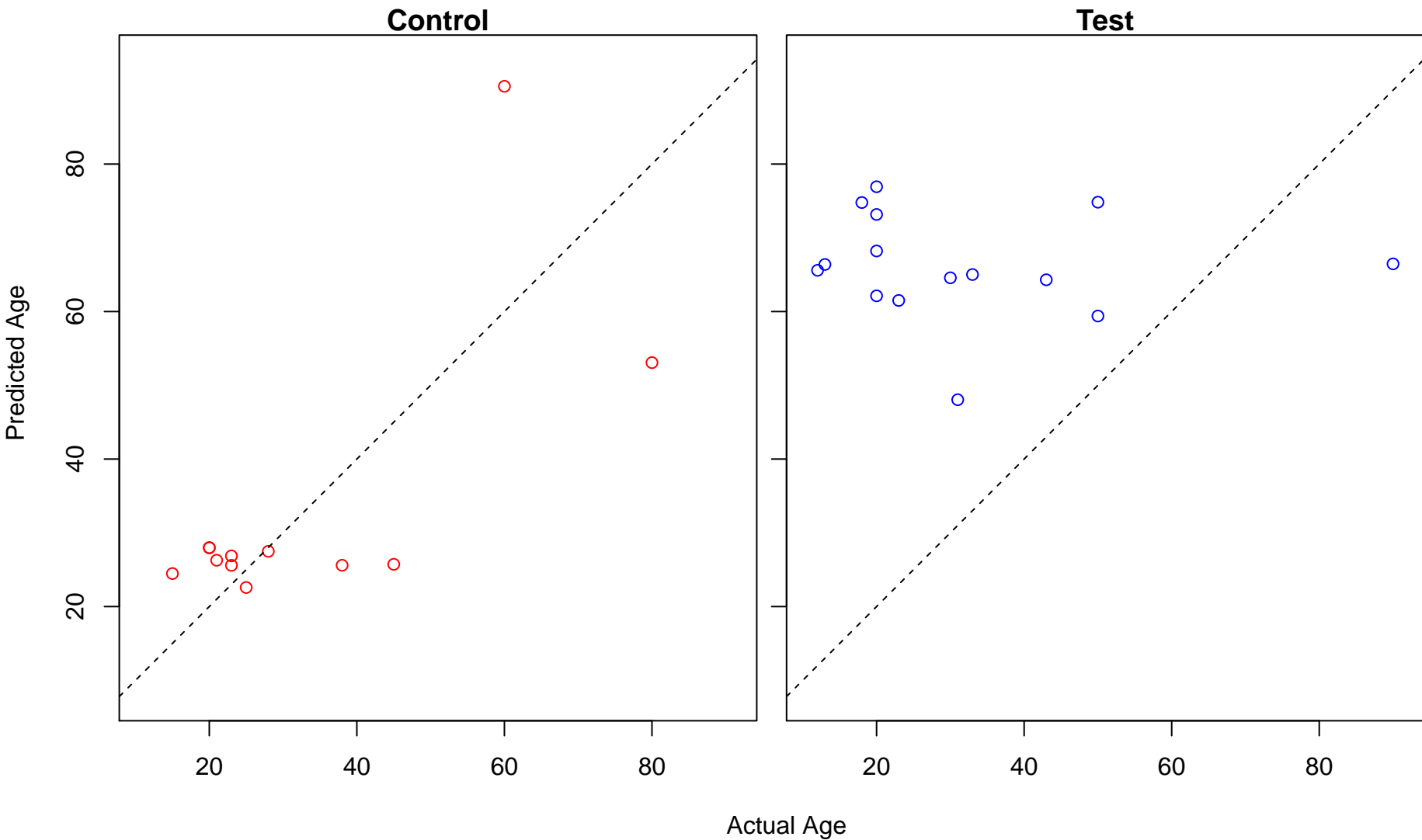
regulation of cytolysis (Score: 3.237960)



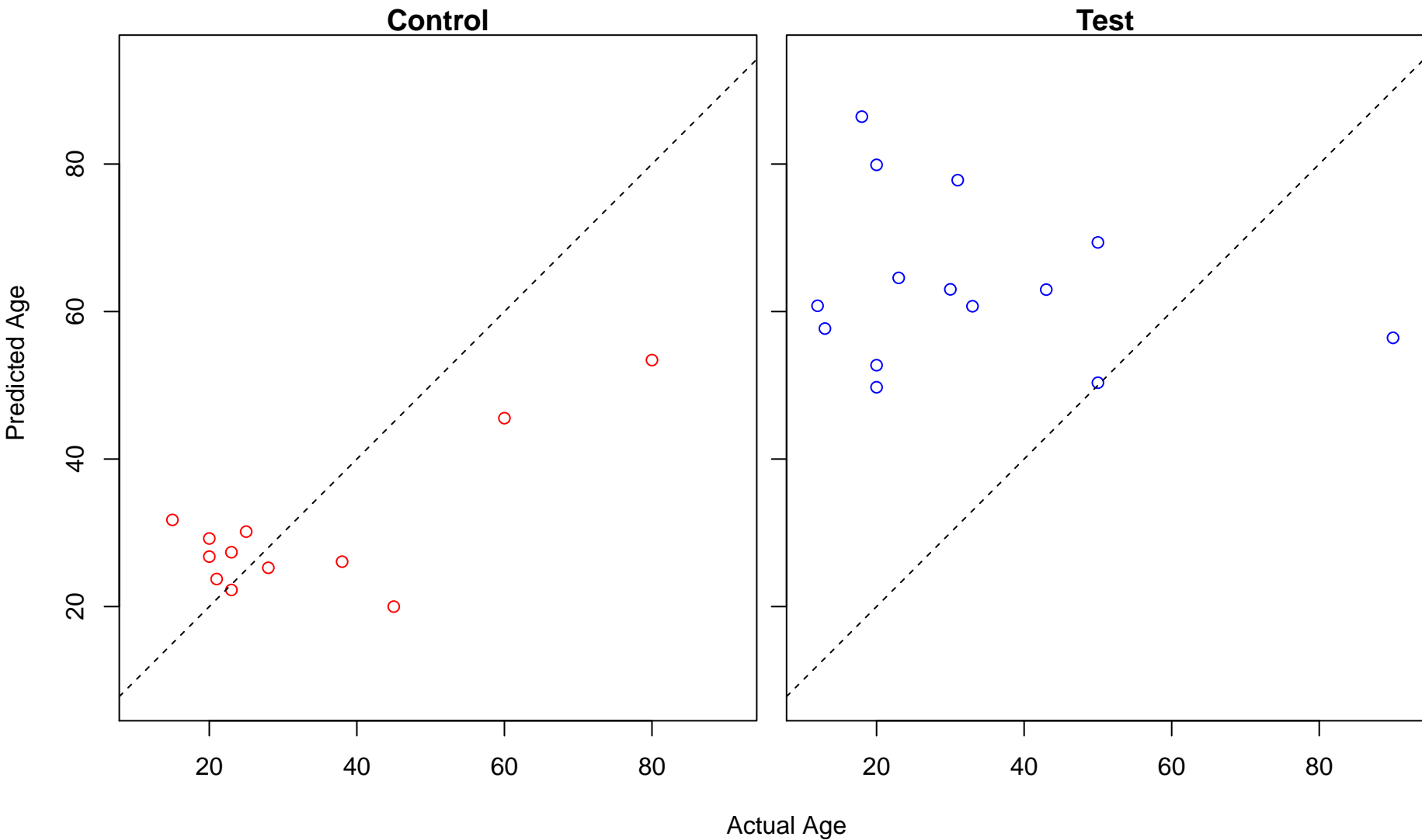
CENP-A containing nucleosome assembly (Score: 3.237034)



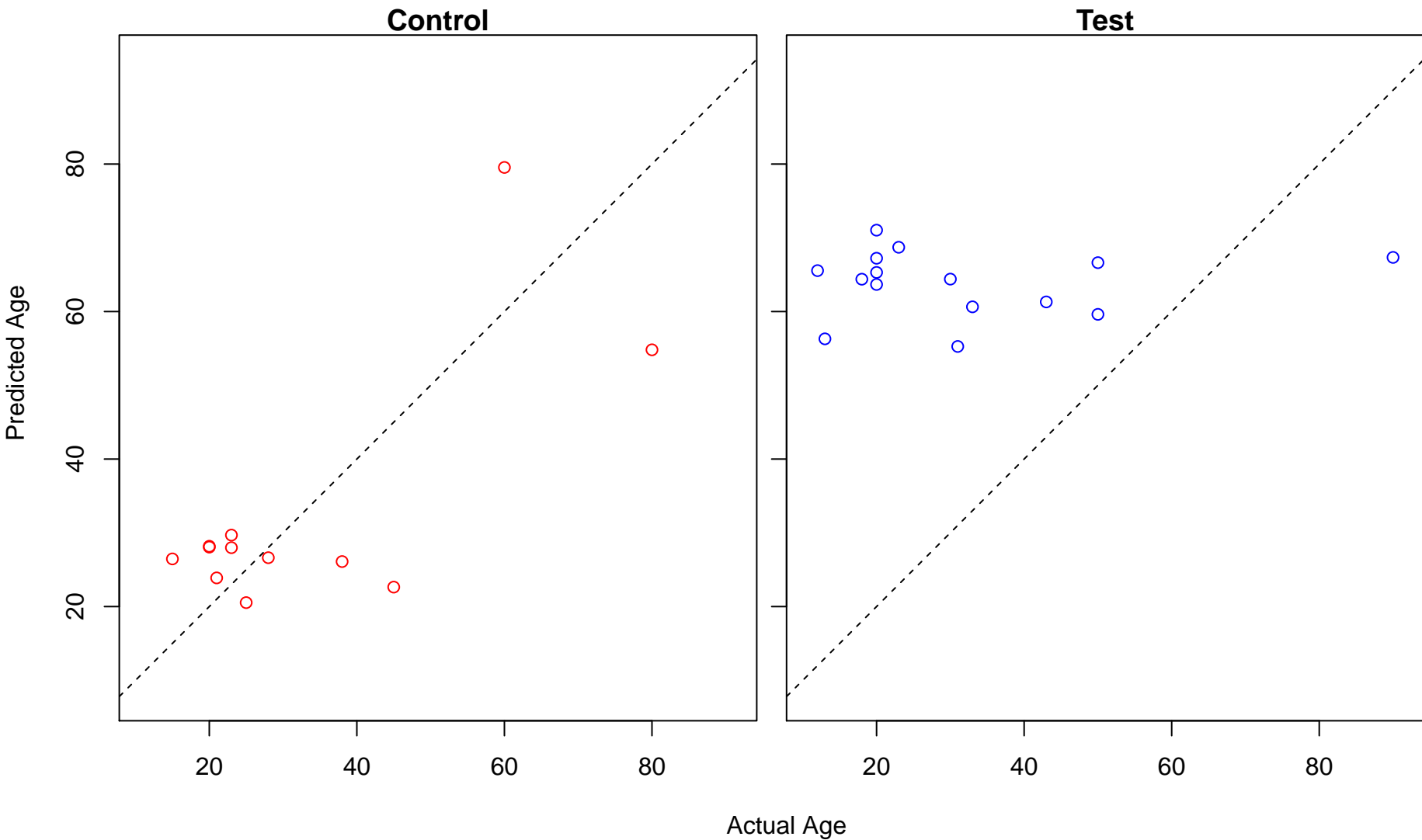
CENP-A containing chromatin organization (Score: 3.237034)



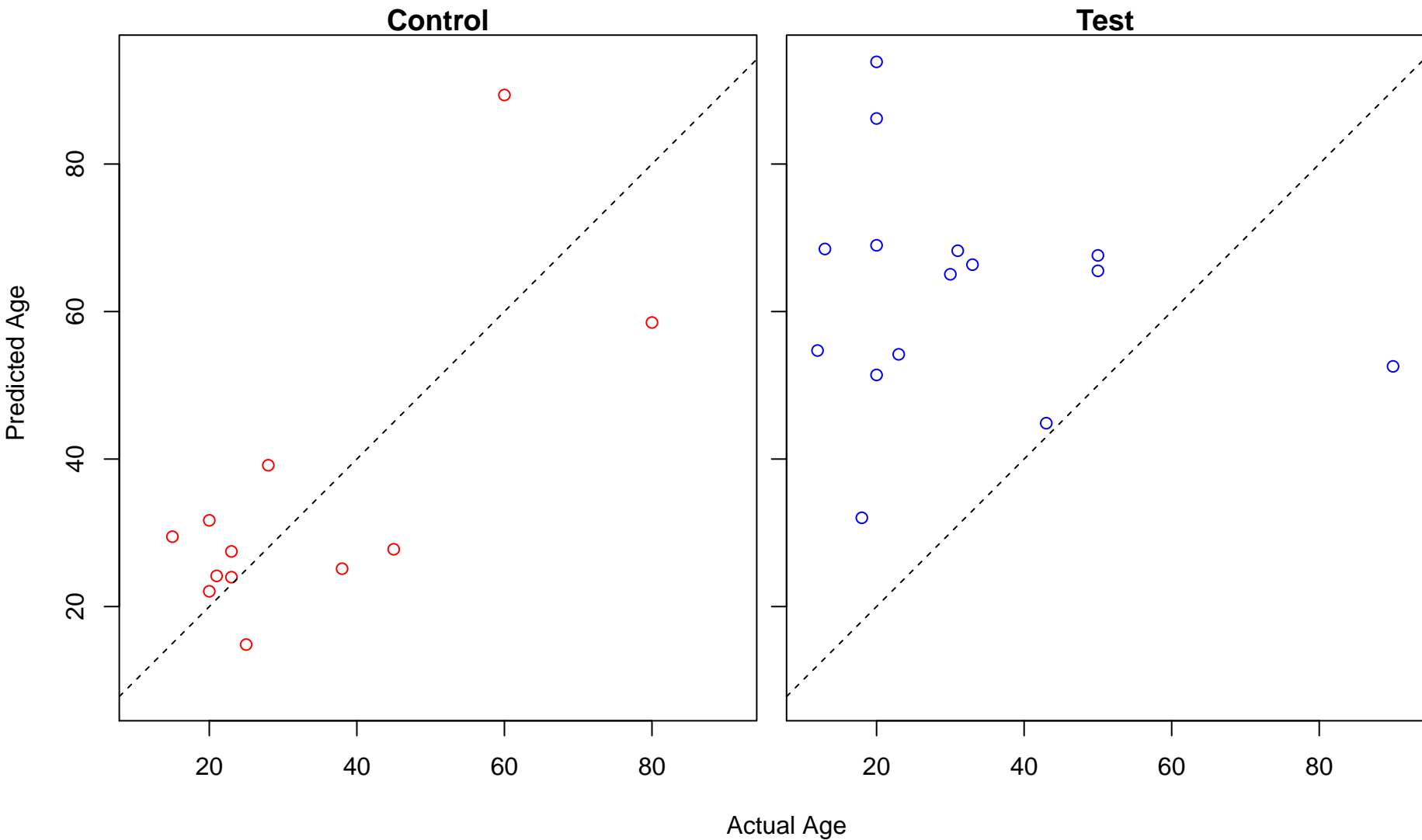
regulation of acrosome reaction (Score: 3.234979)



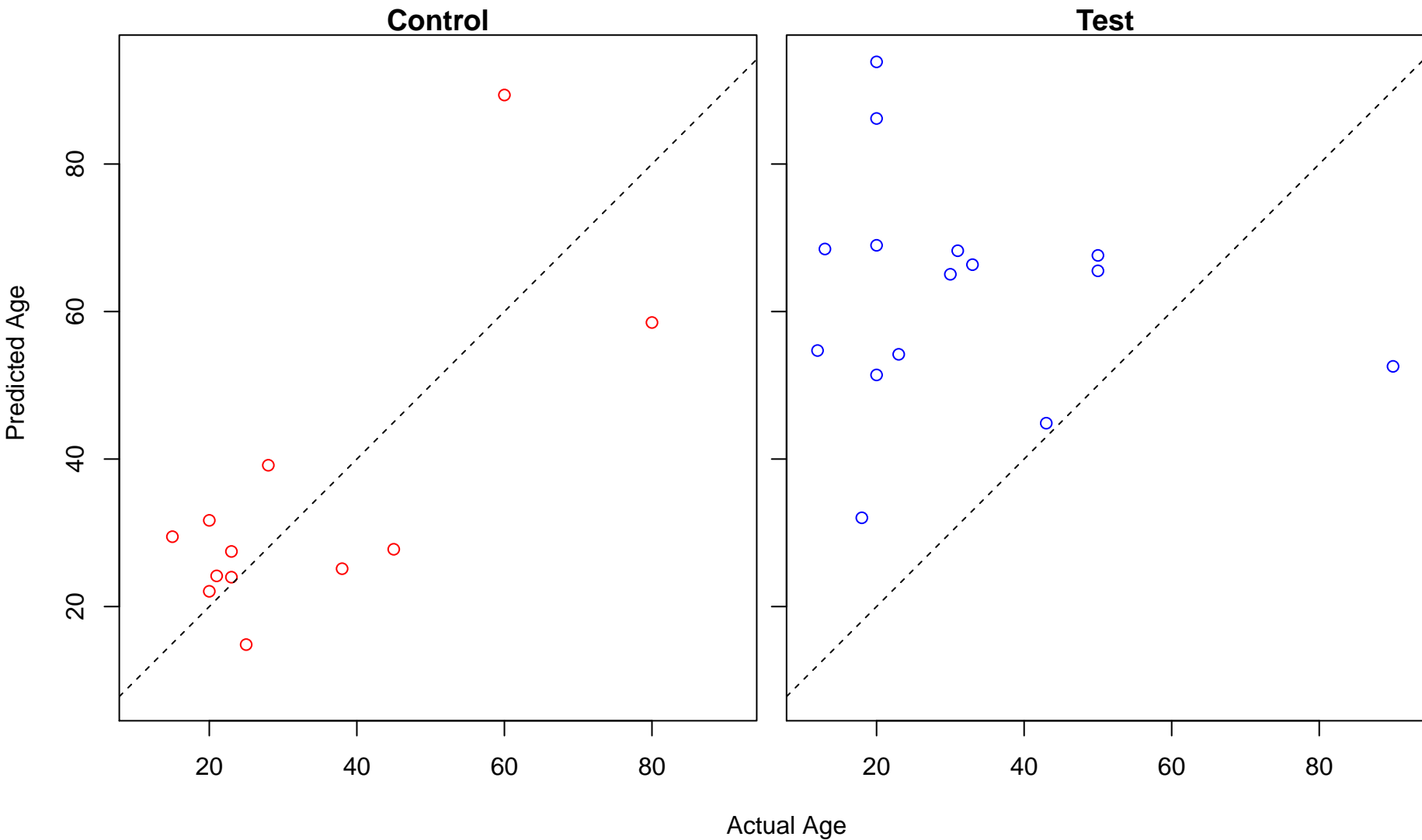
mRNA cleavage (Score: 3.232443)



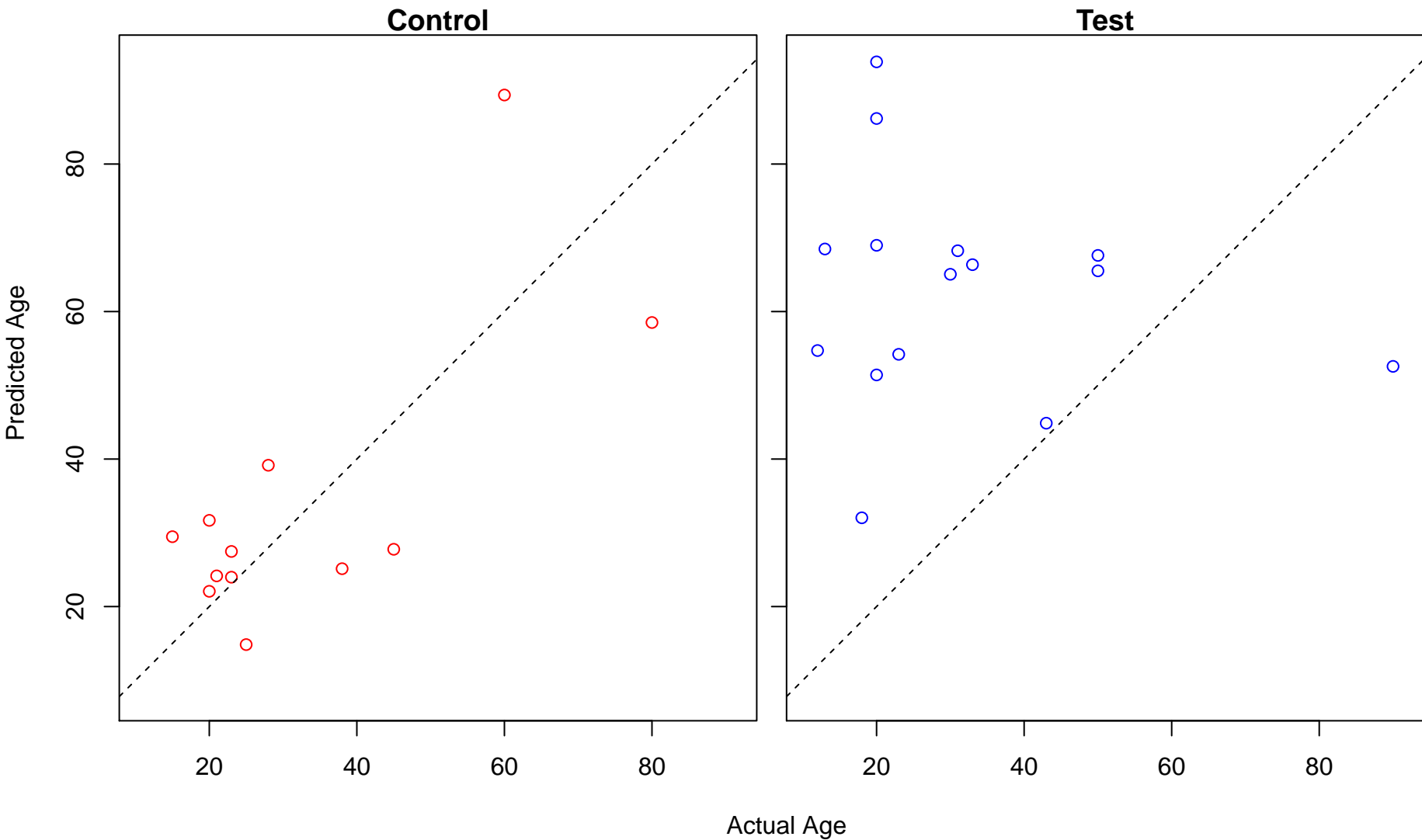
blastoderm segmentation (Score: 3.231852)



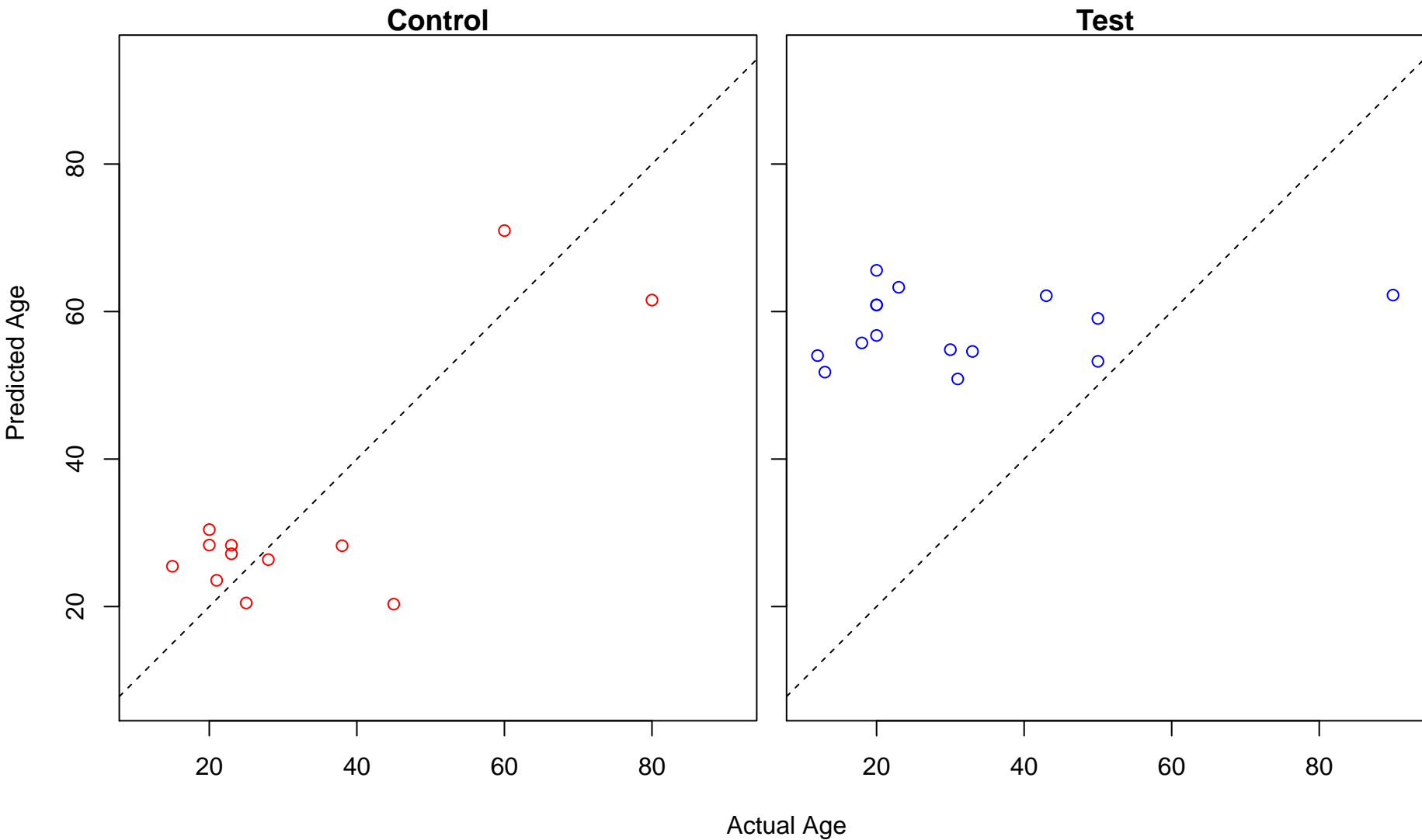
tripartite regional subdivision (Score: 3.231852)



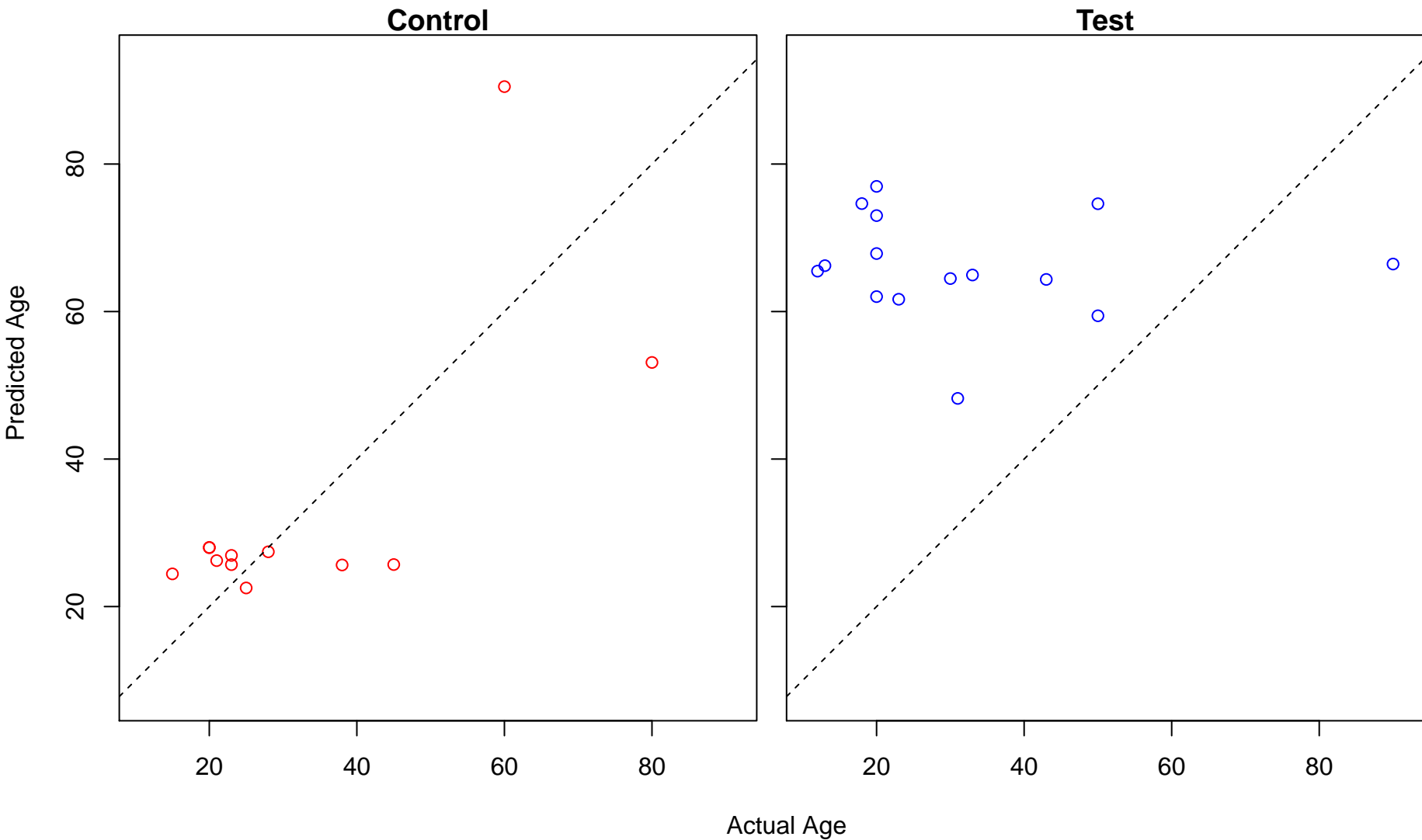
anterior/posterior axis specification, embryo (Score: 3.231852)



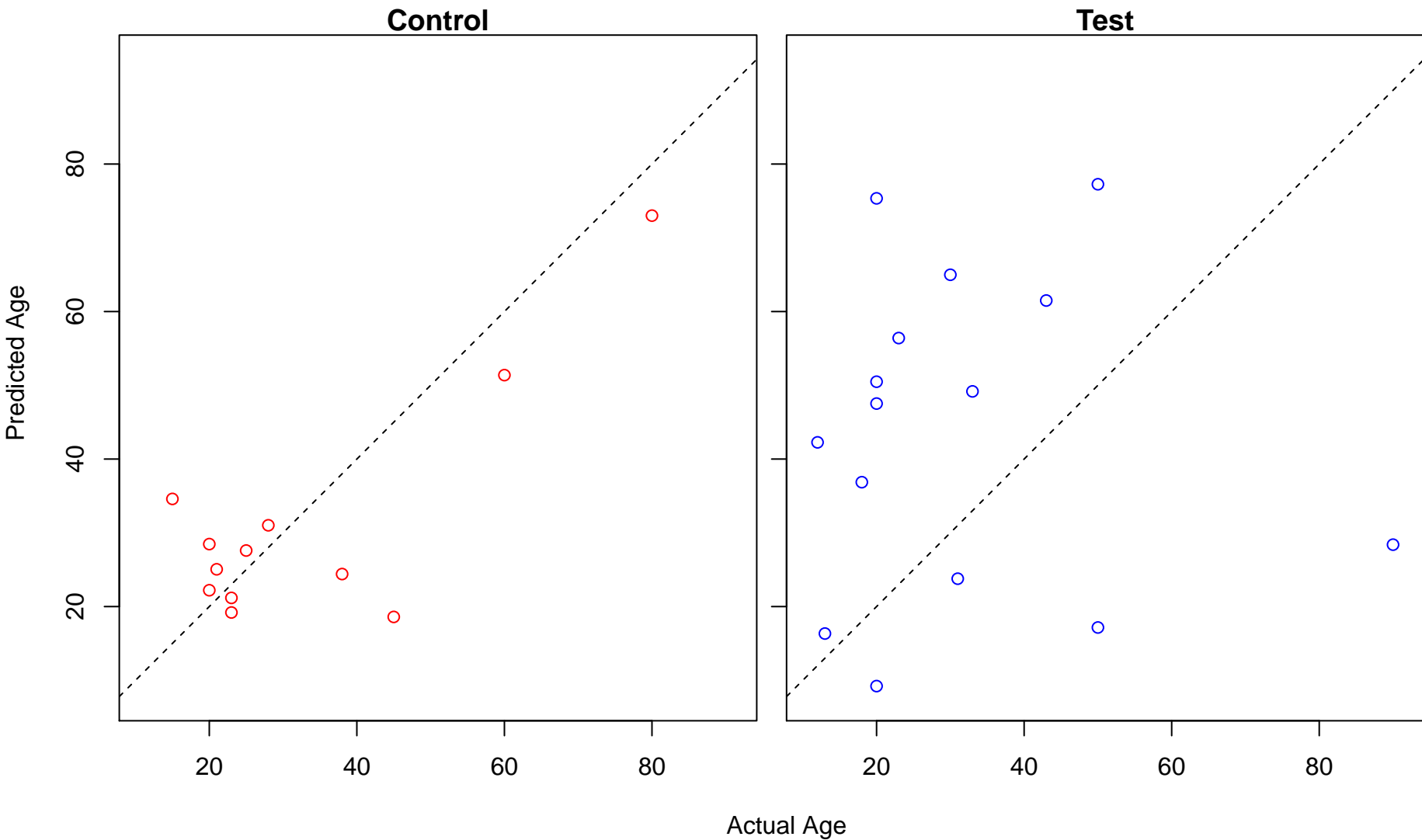
positive regulation of receptor biosynthetic process (Score: 3.230016)



centromere complex assembly (Score: 3.228669)

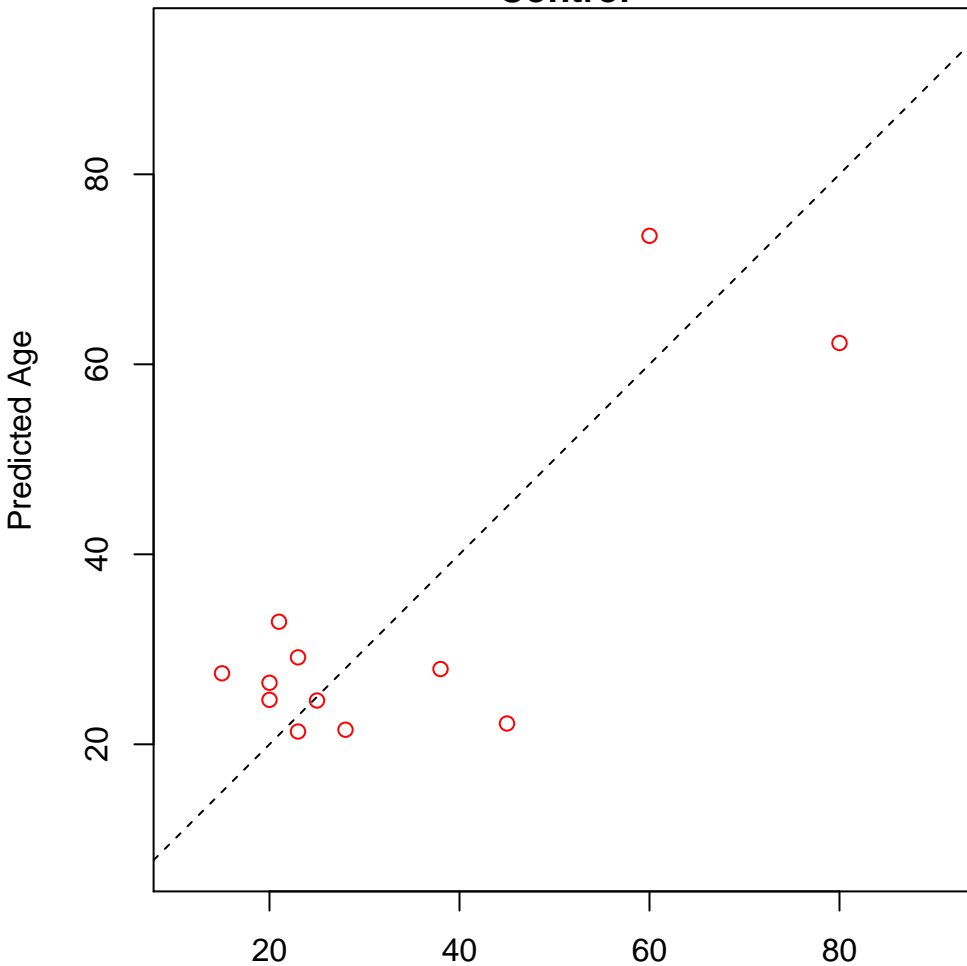


regulation of protein deubiquitination (Score: 3.227355)

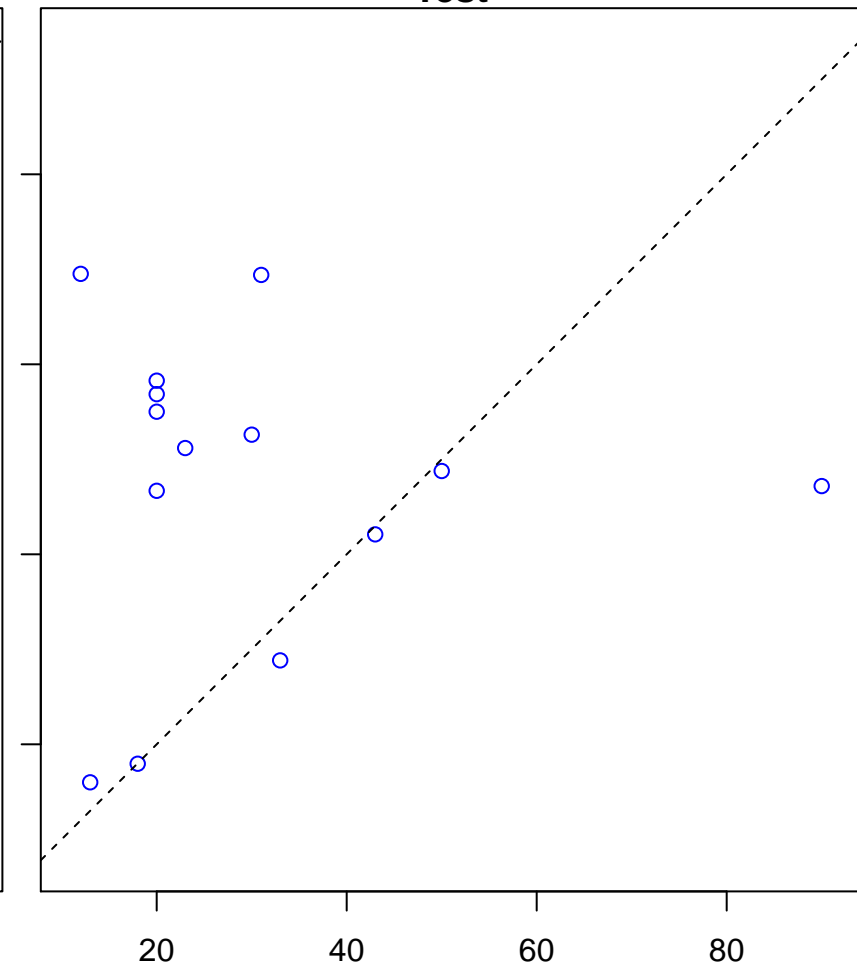


regulation of keratinocyte differentiation (Score: 3.224008)

Control

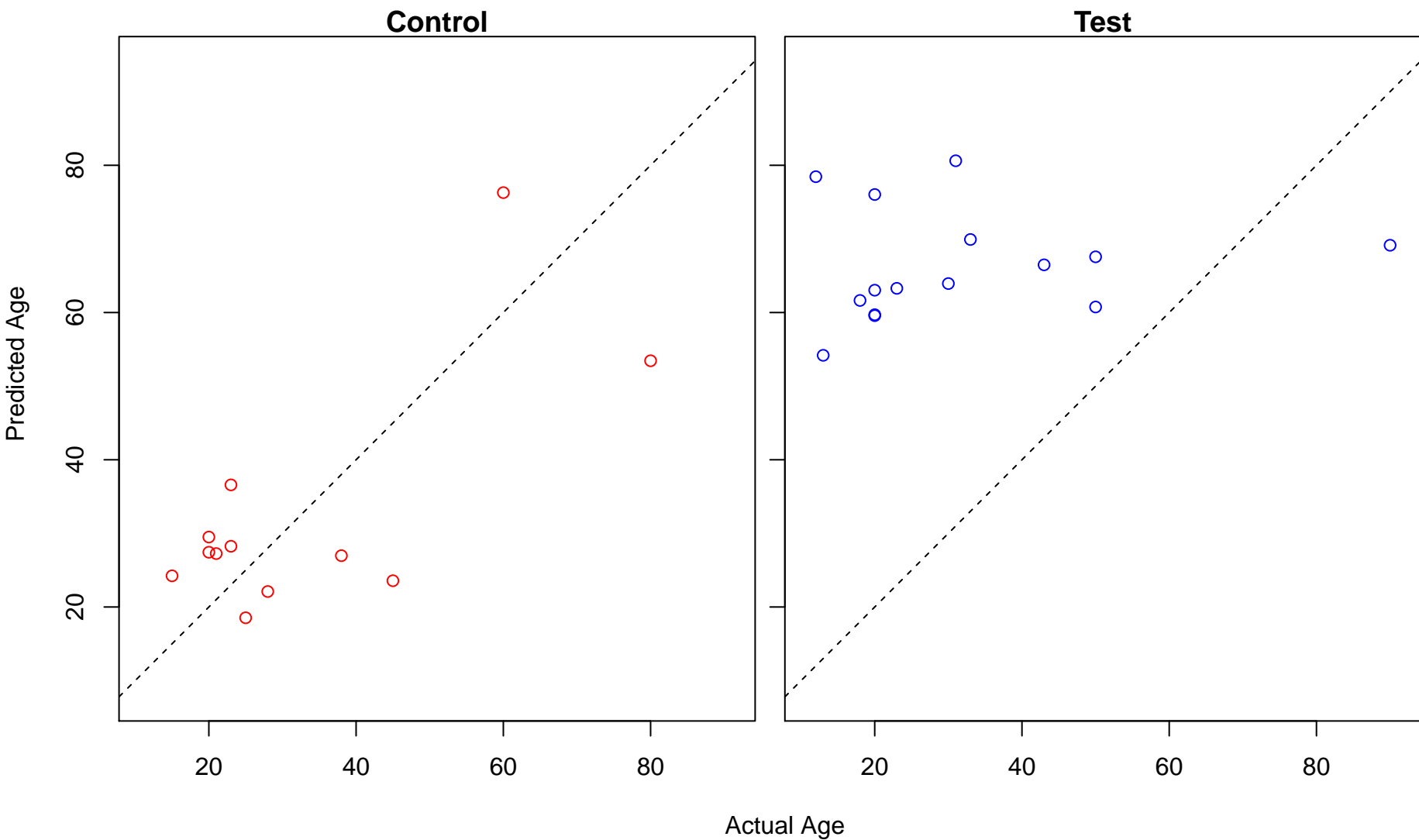


Test

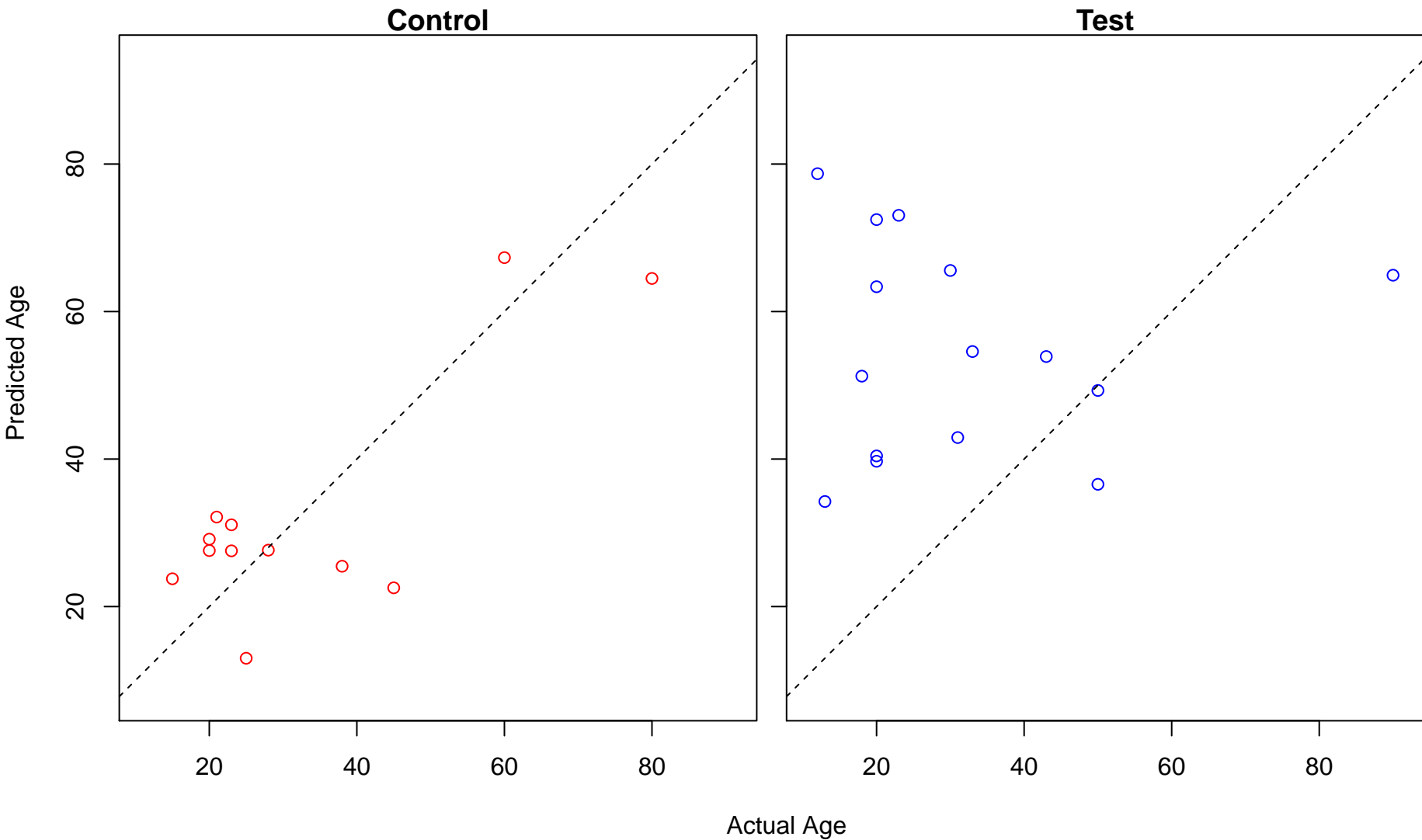


Actual Age

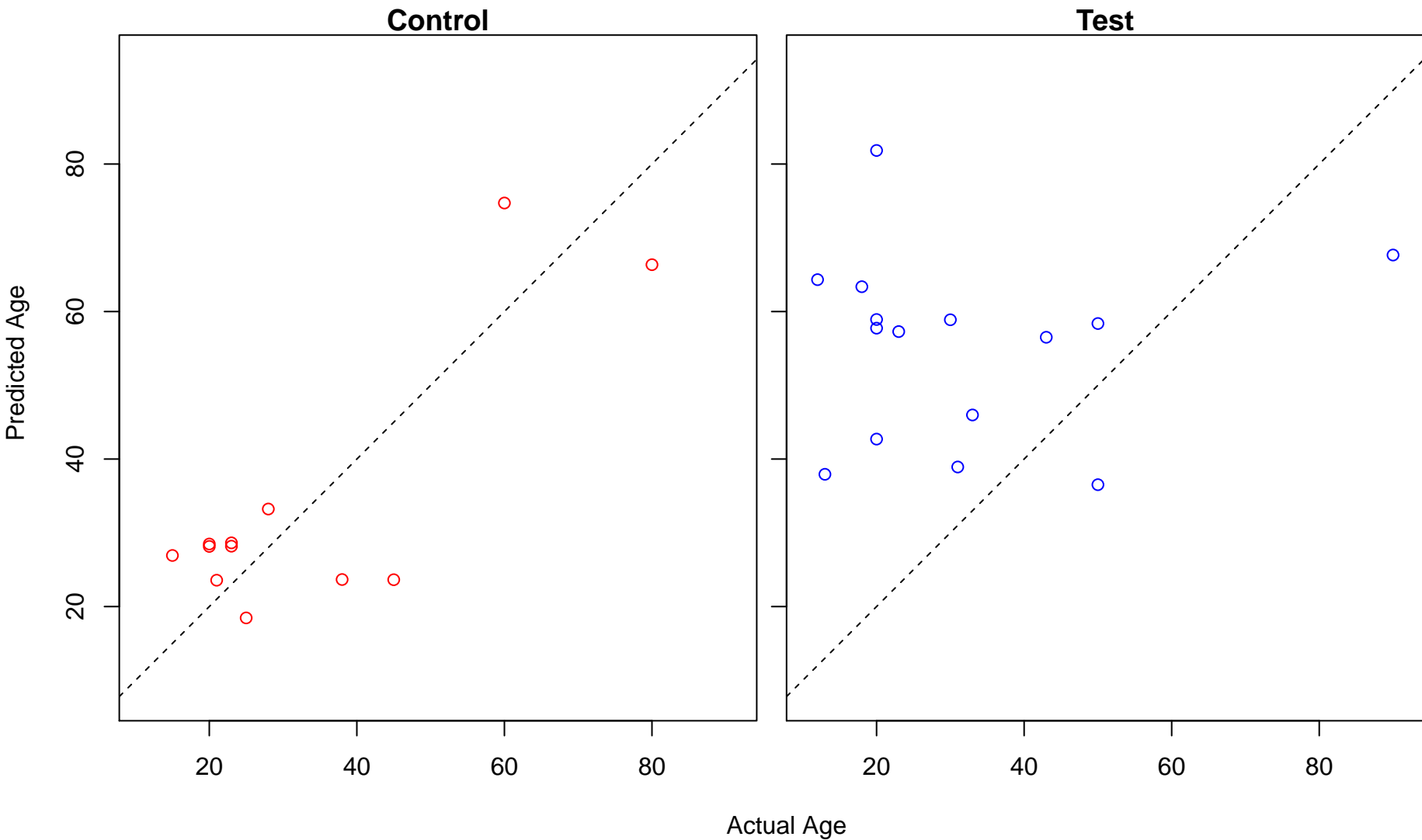
positive regulation of sequestering of triglyceride (Score: 3.222872)



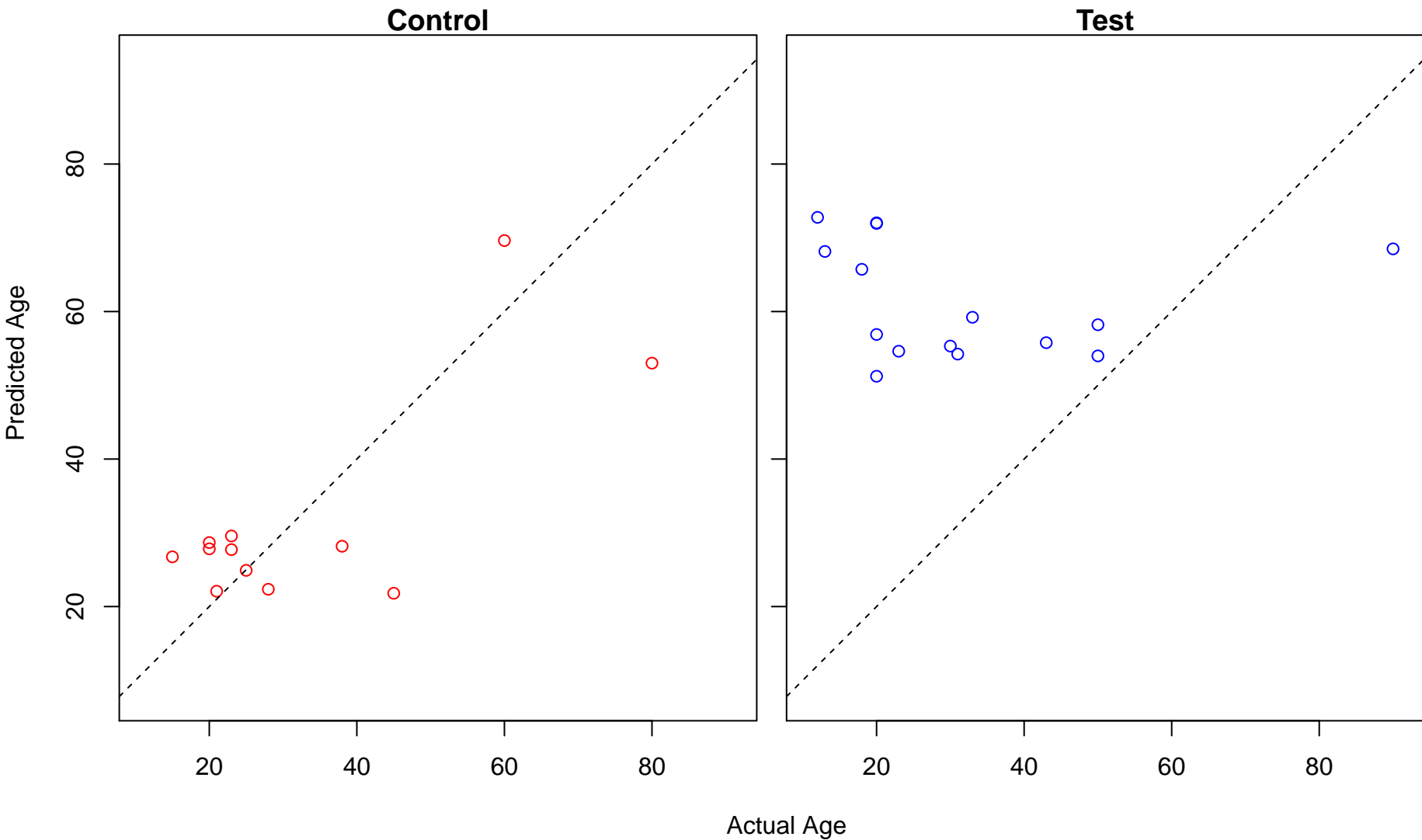
positive regulation of telomere capping (Score: 3.222362)



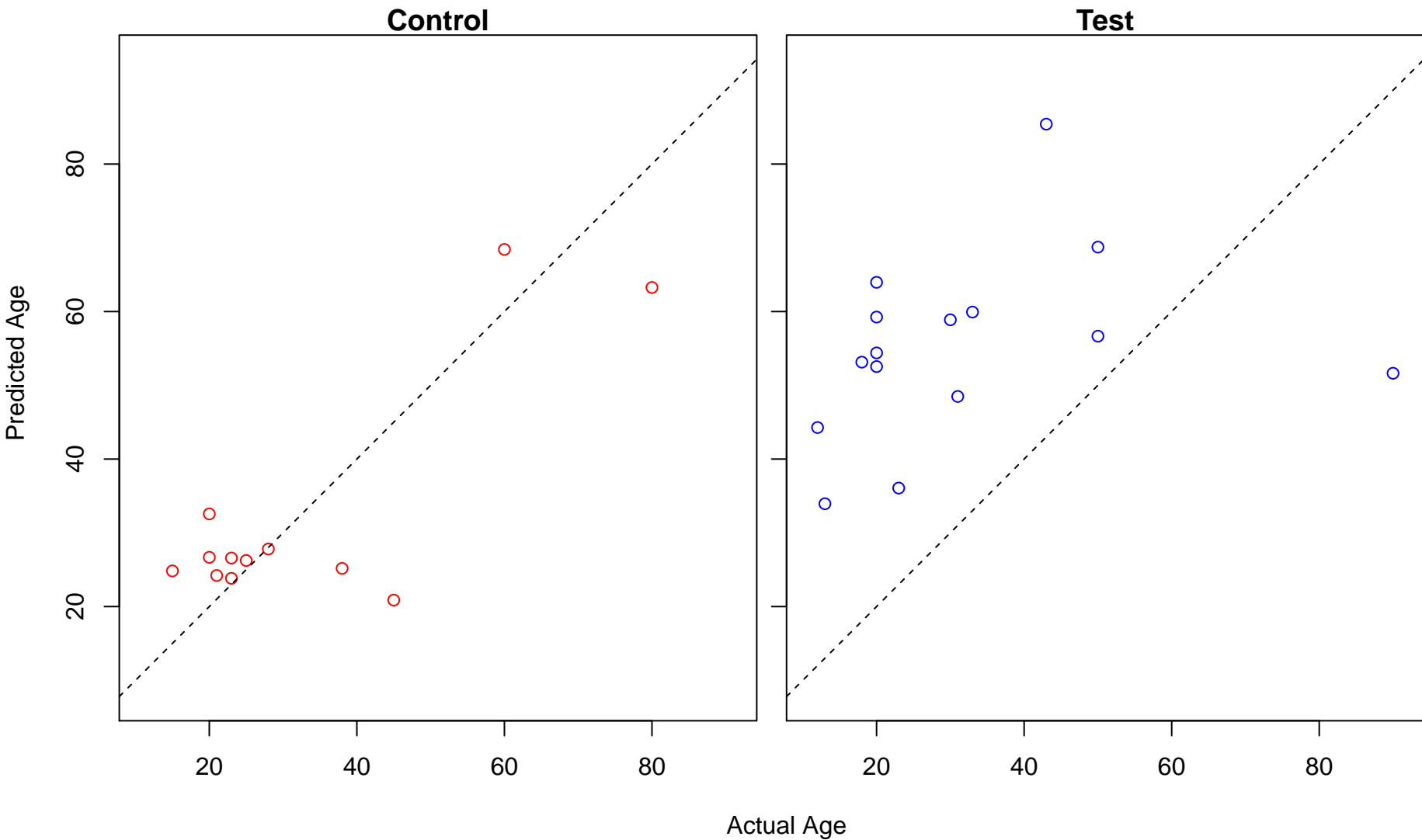
DNA-templated transcription, elongation (Score: 3.220815)



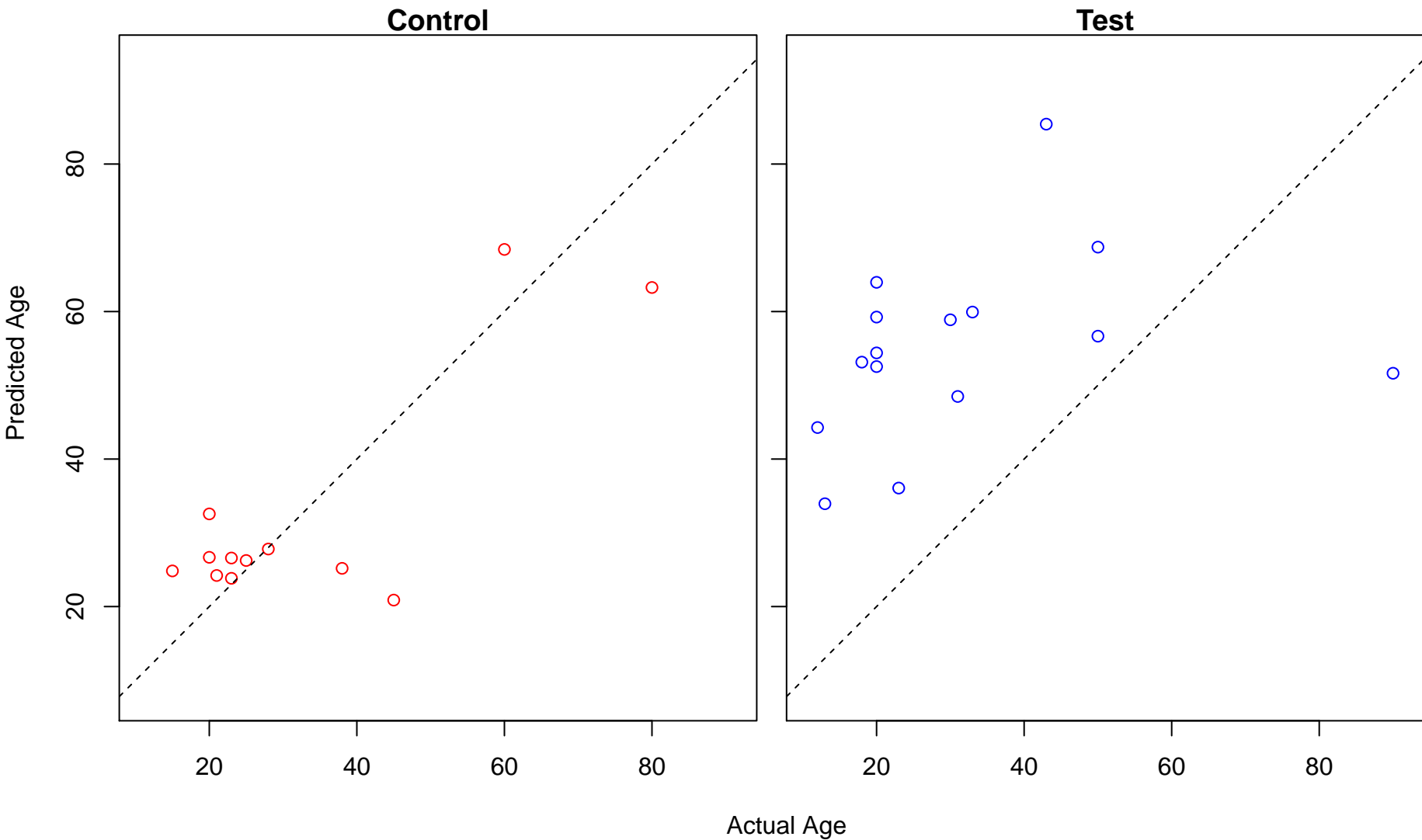
negative regulation of myeloid leukocyte differentiation (Score: 3.219876)



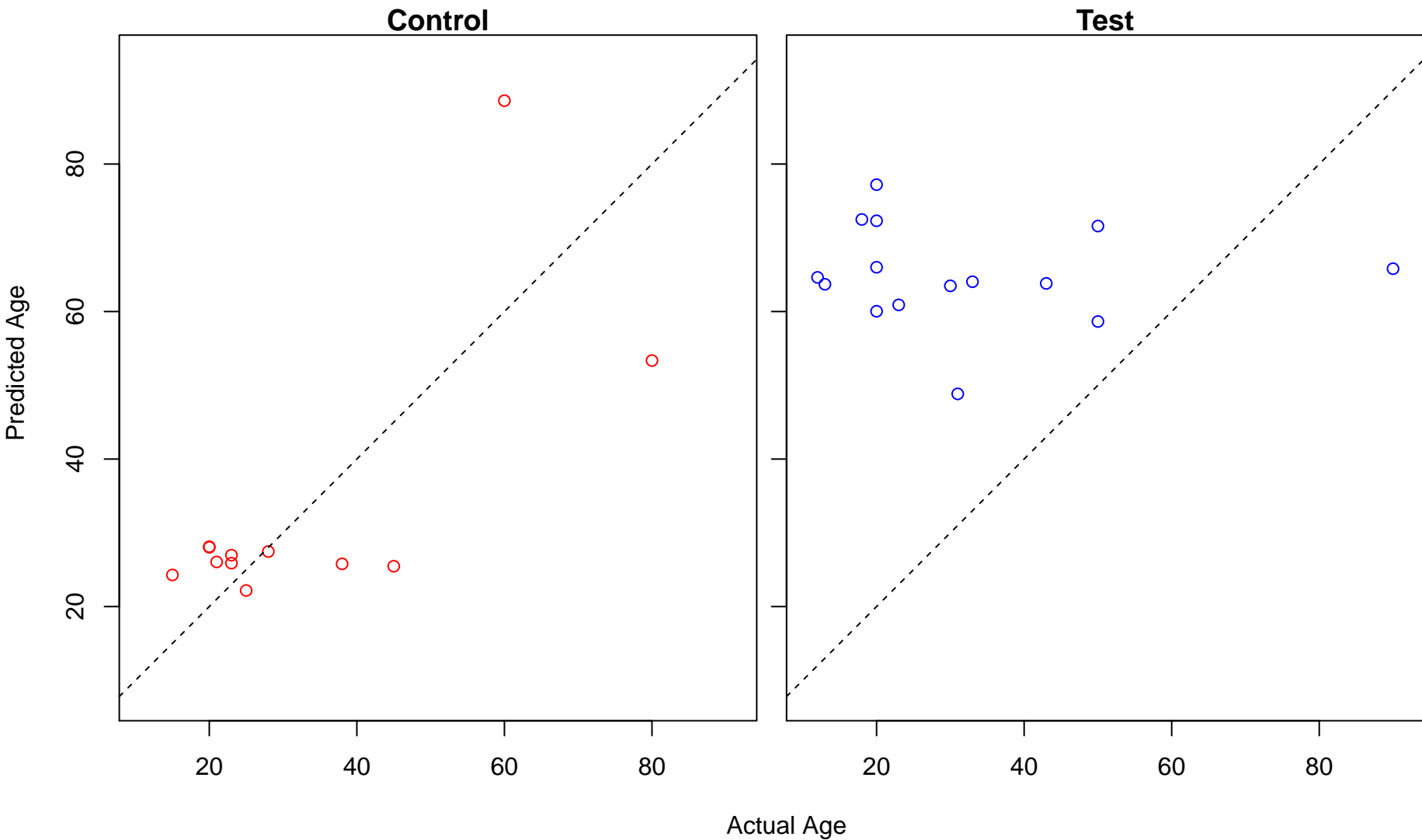
indole-containing compound biosynthetic process (Score: 3.215181)



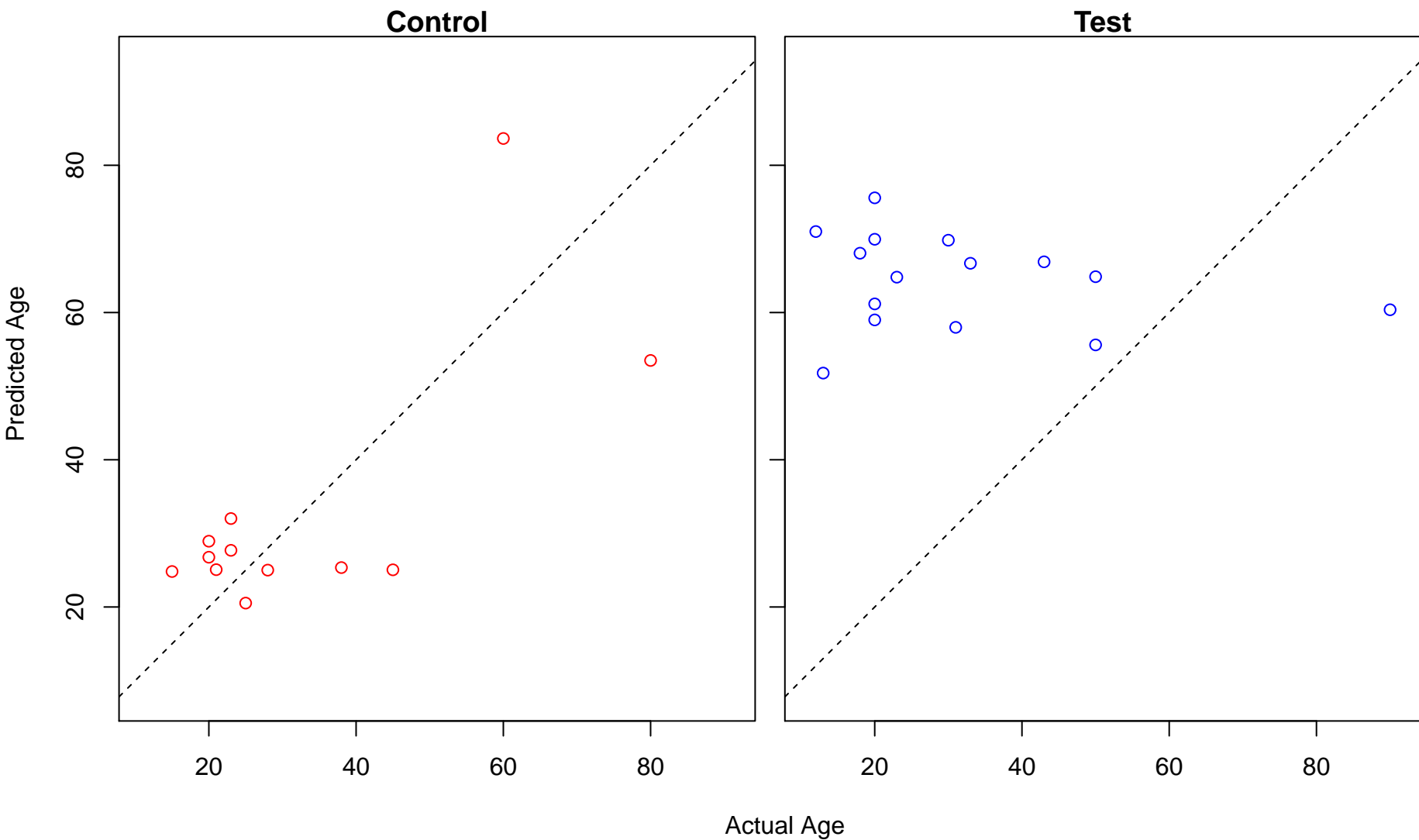
indolalkylamine biosynthetic process (Score: 3.215181)



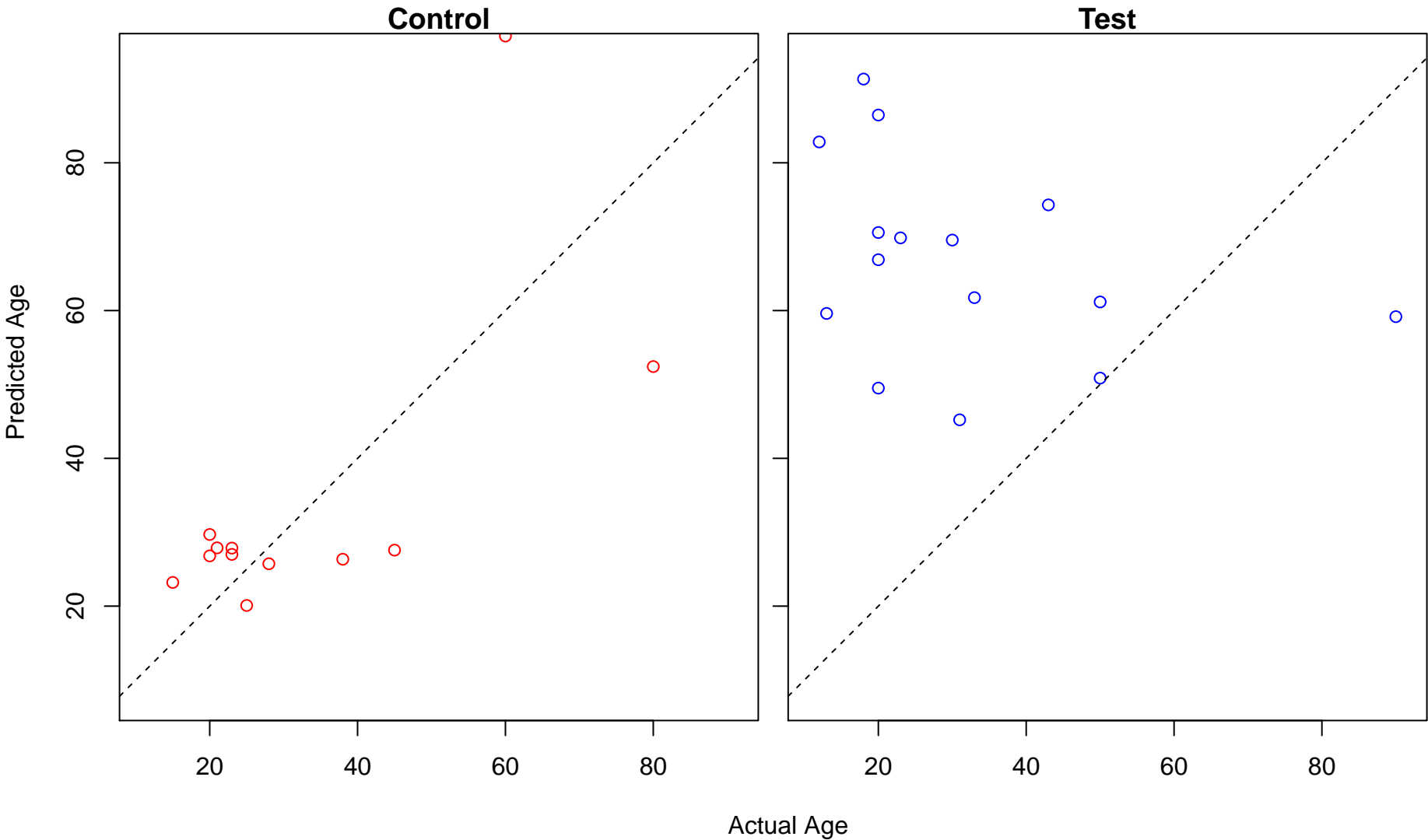
histone exchange (Score: 3.209657)



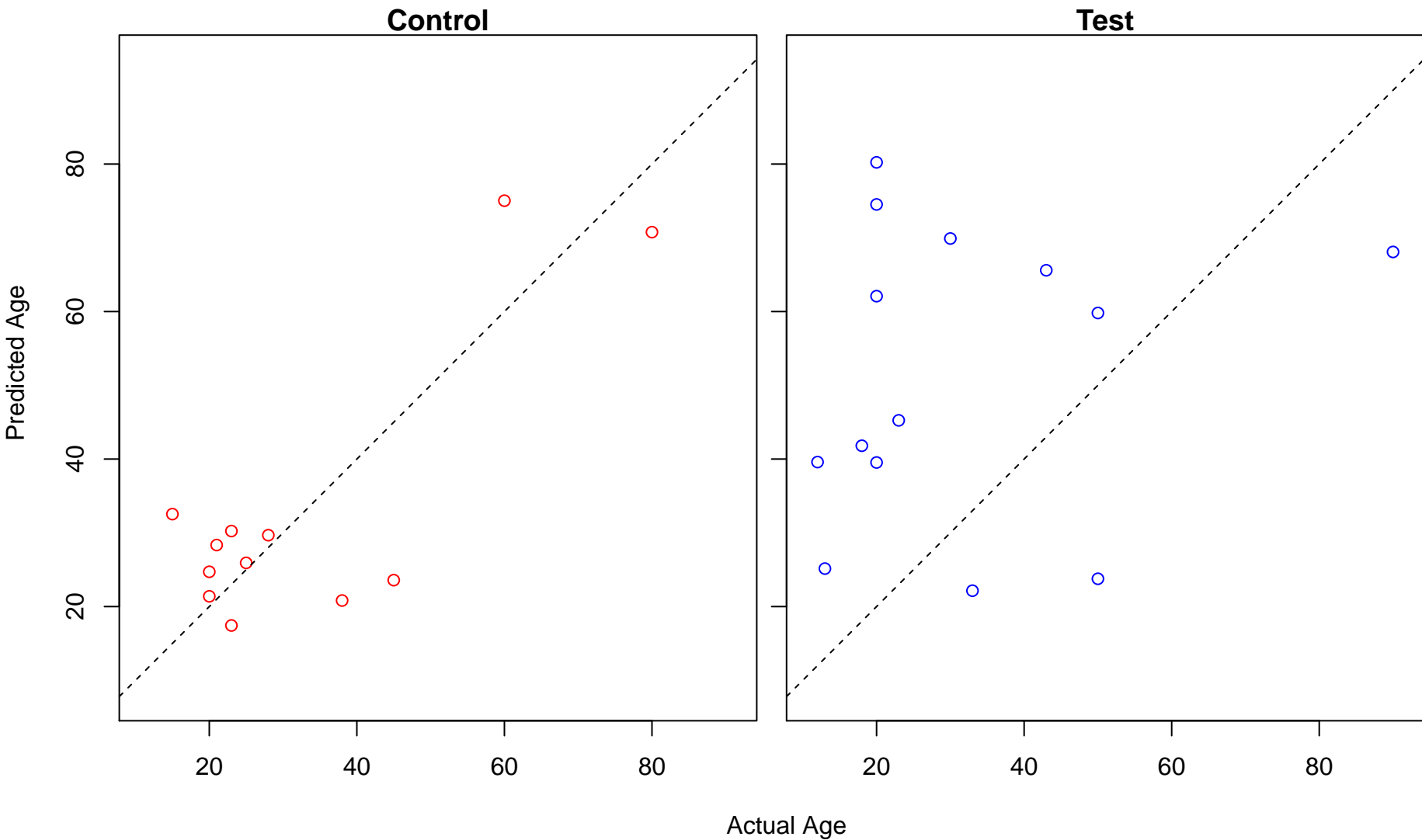
inositol phosphate-mediated signaling (Score: 3.208747)



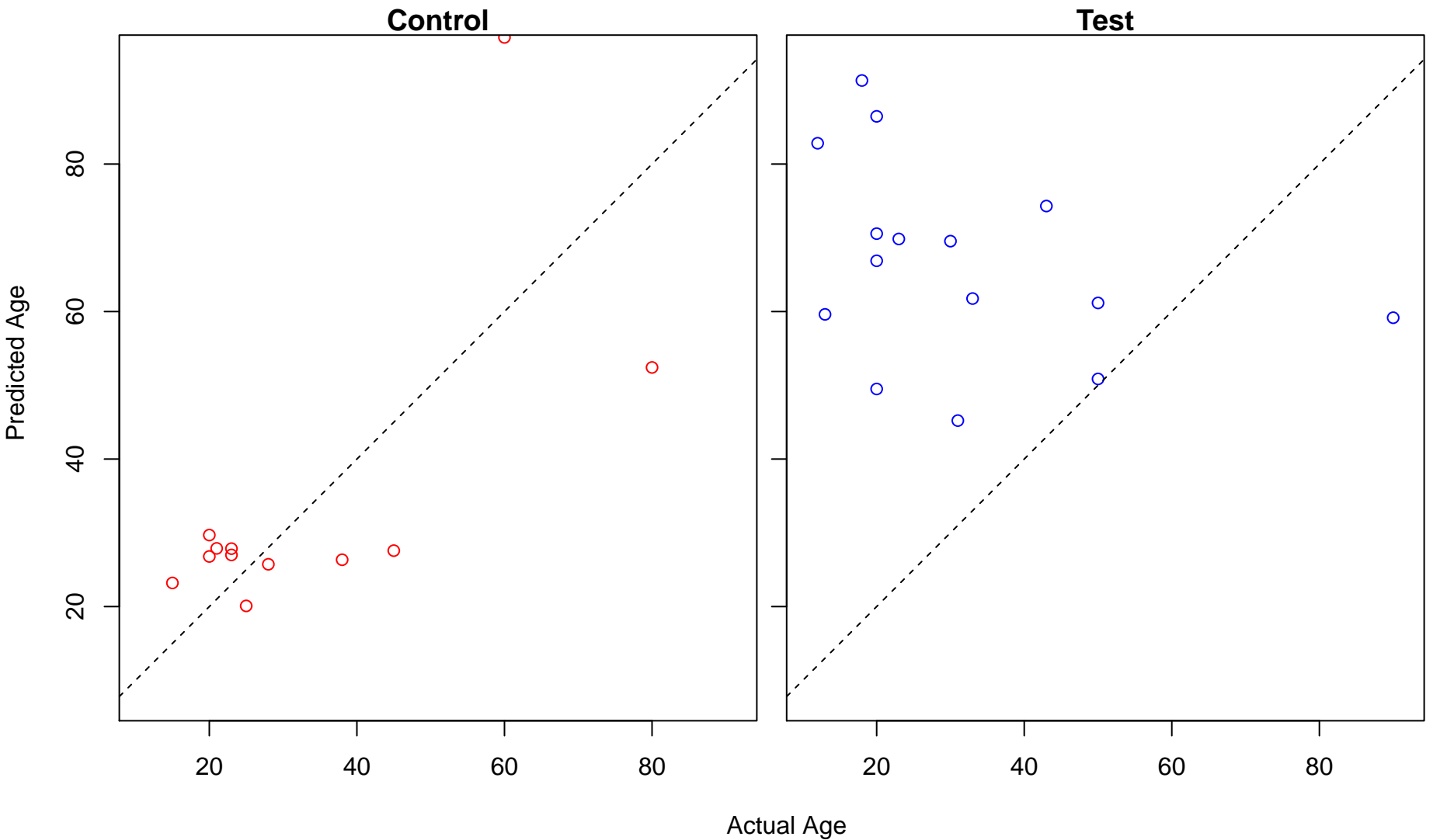
regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis (Score: 3.20)



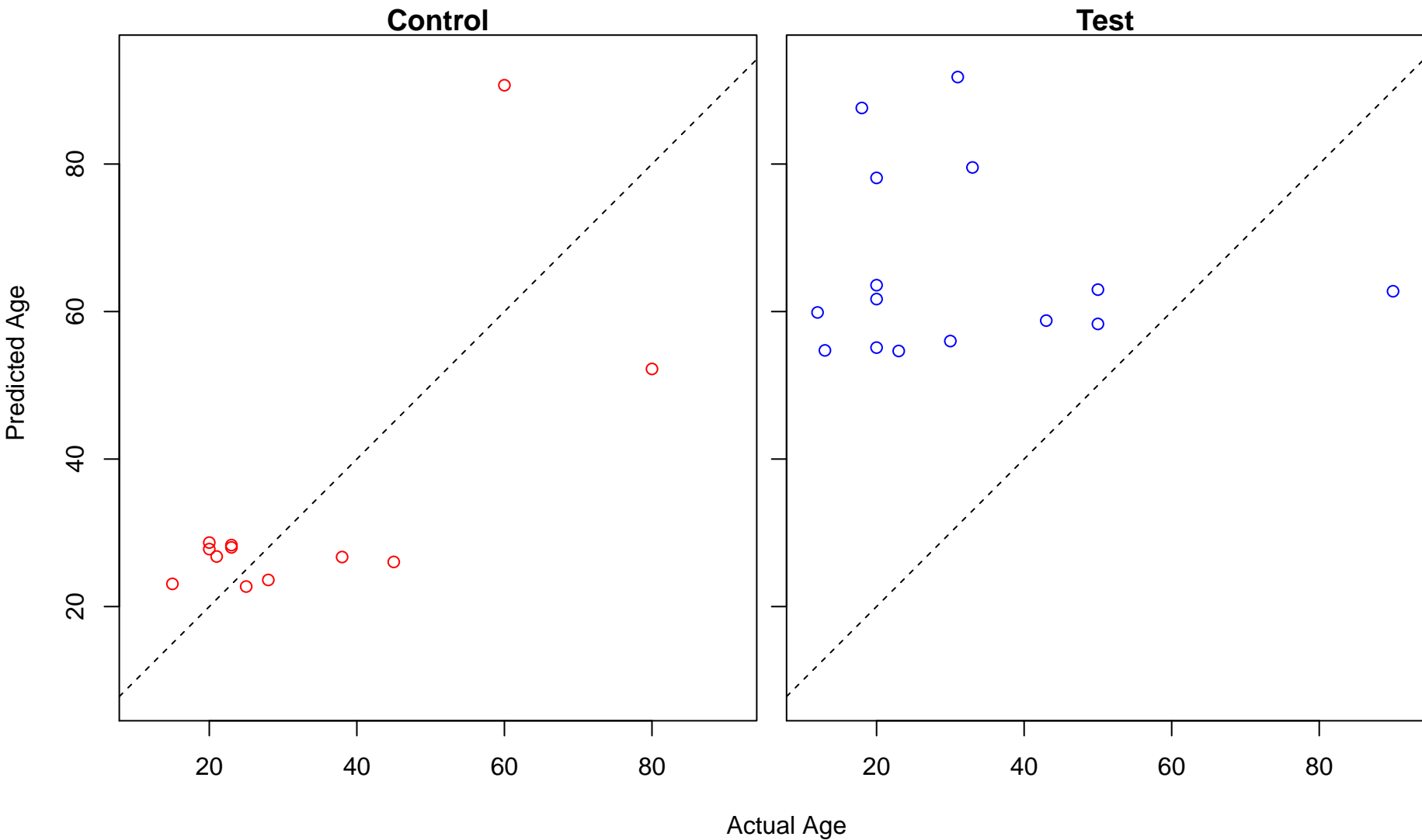
response to magnesium ion (Score: 3.205755)



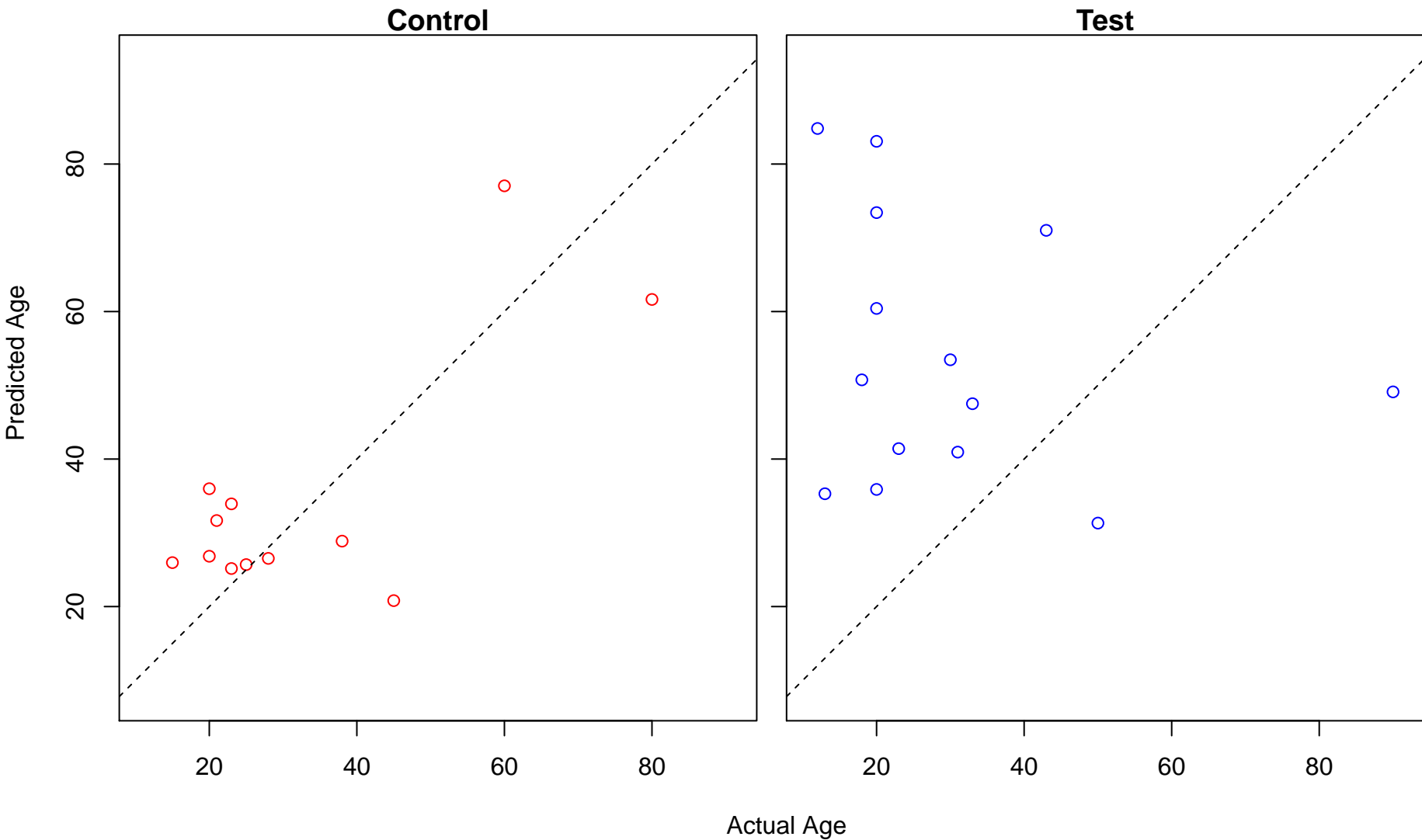
Negative regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis (Score: 10)



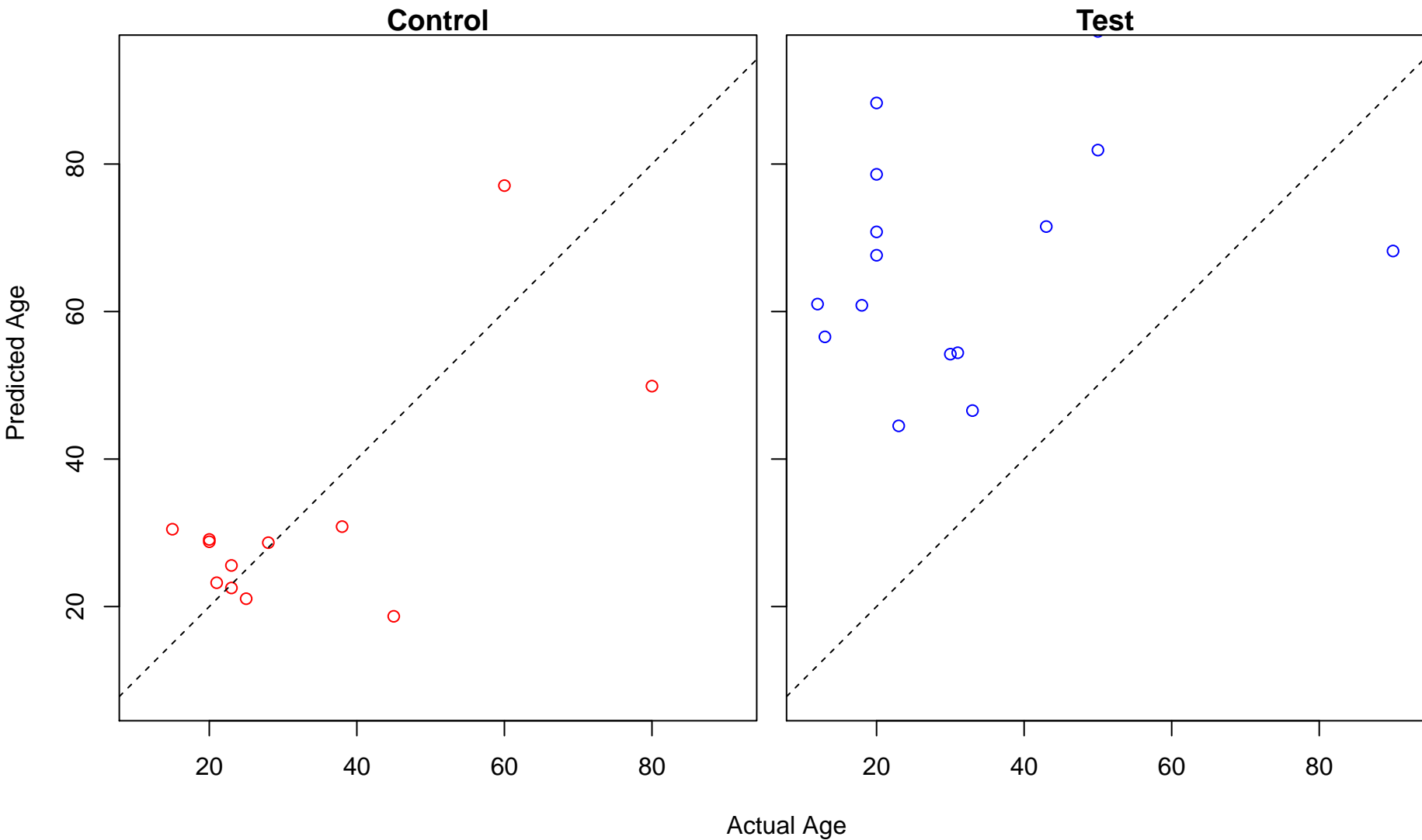
negative regulation of dendritic spine development (Score: 3.204023)



negative regulation of fatty acid metabolic process (Score: 3.203698)

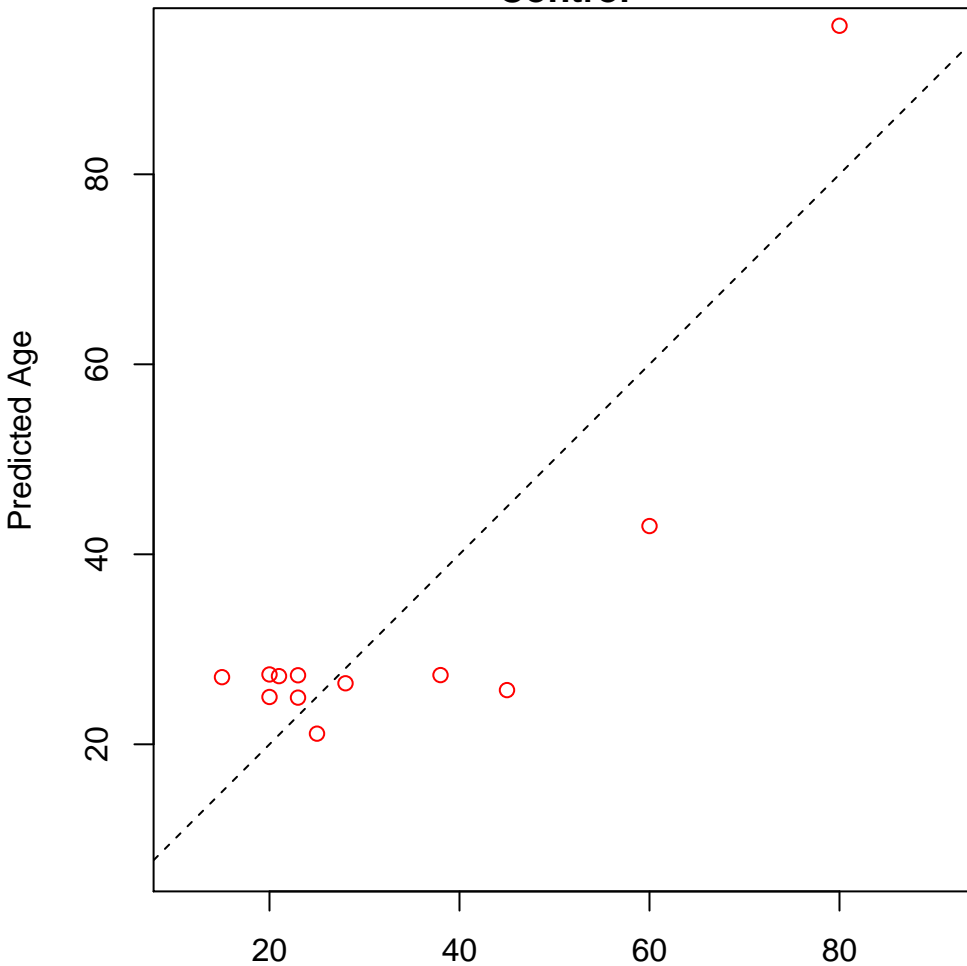


sterol transport (Score: 3.202448)

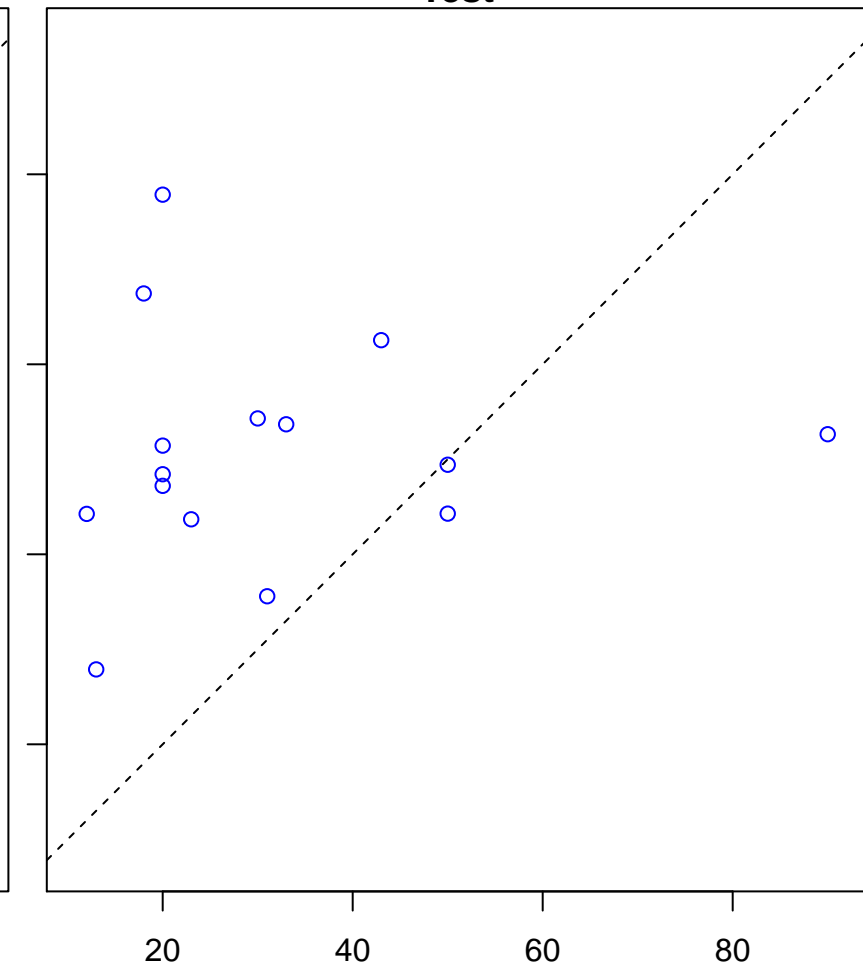


organelle transport along microtubule (Score: 3.201601)

Control

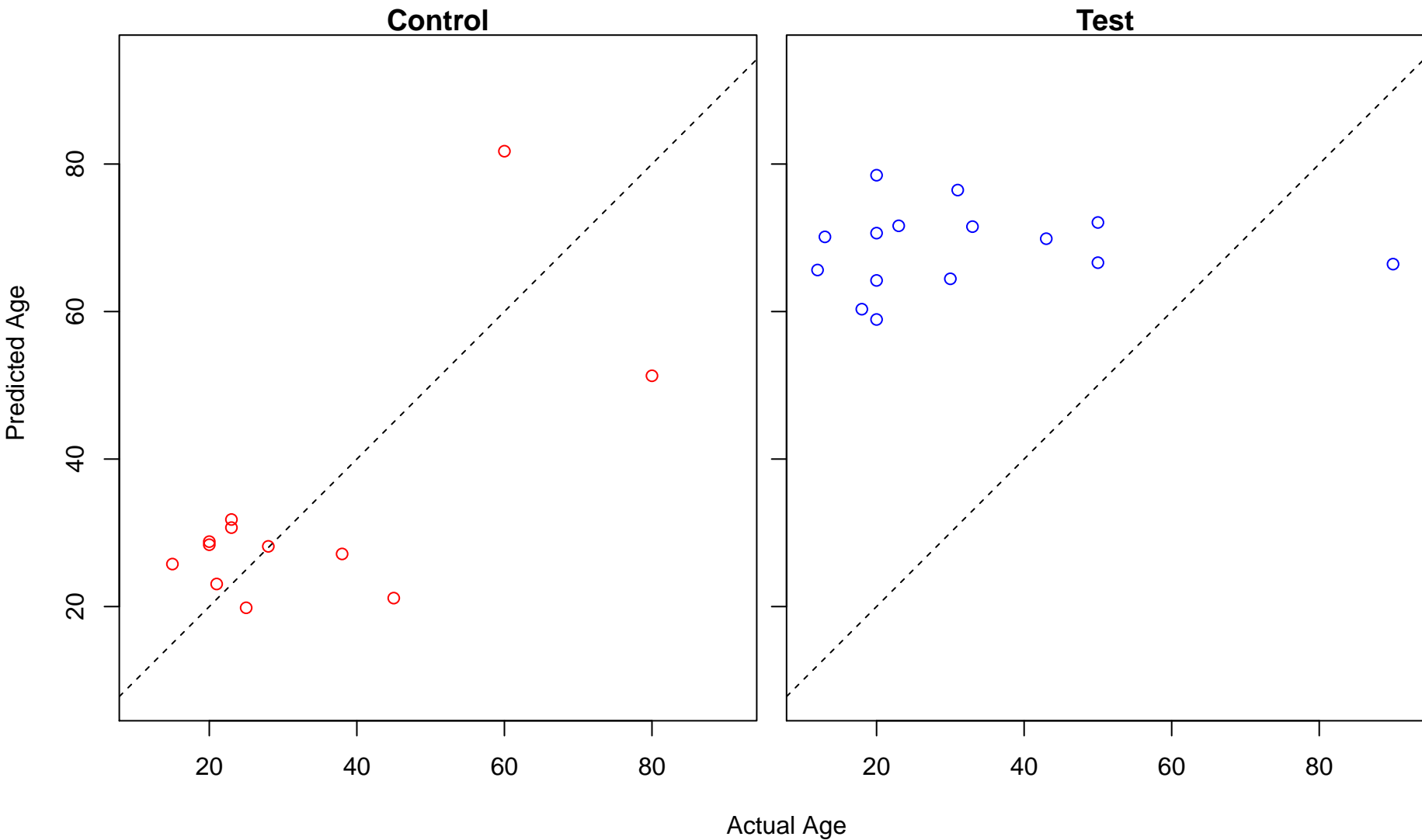


Test

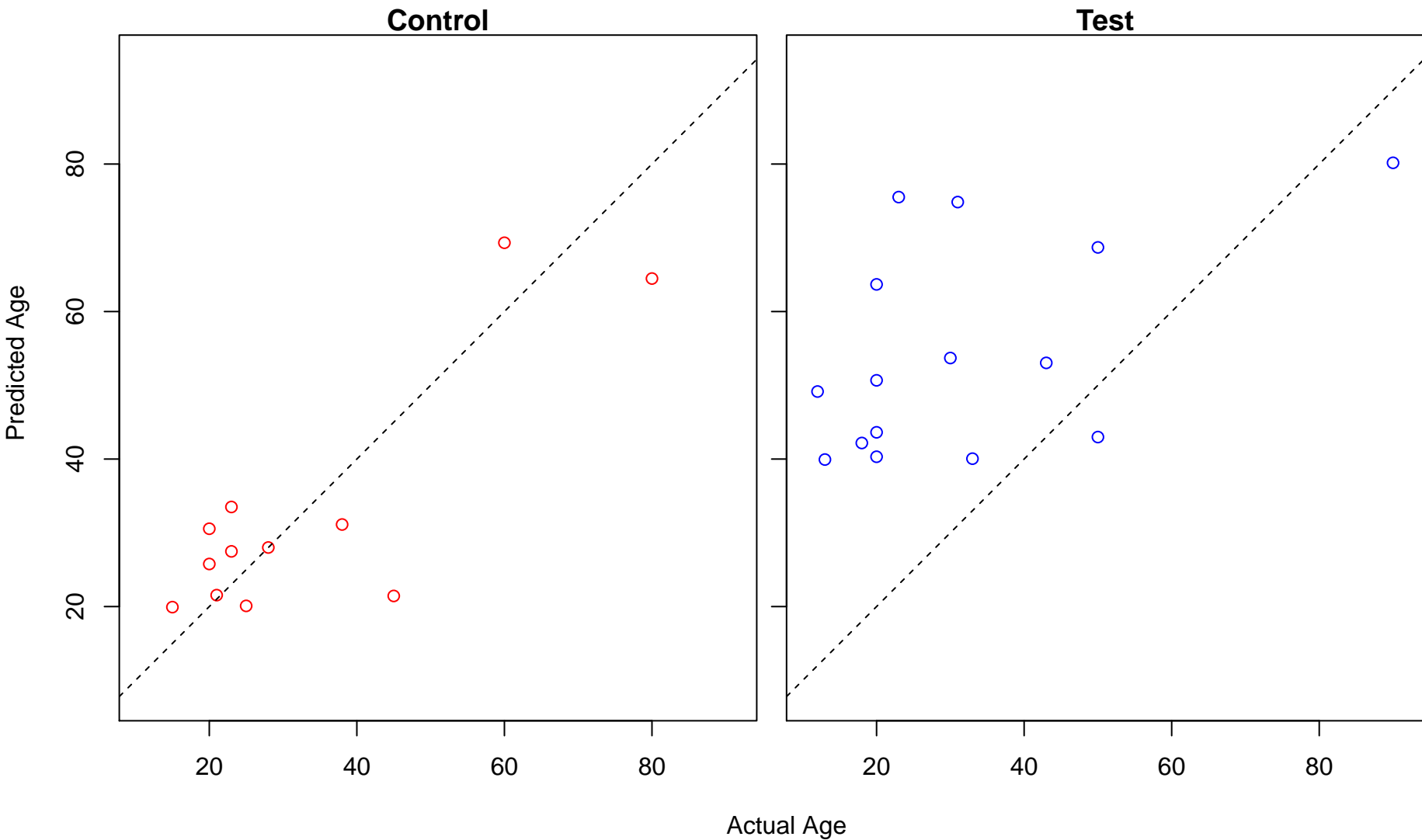


Actual Age

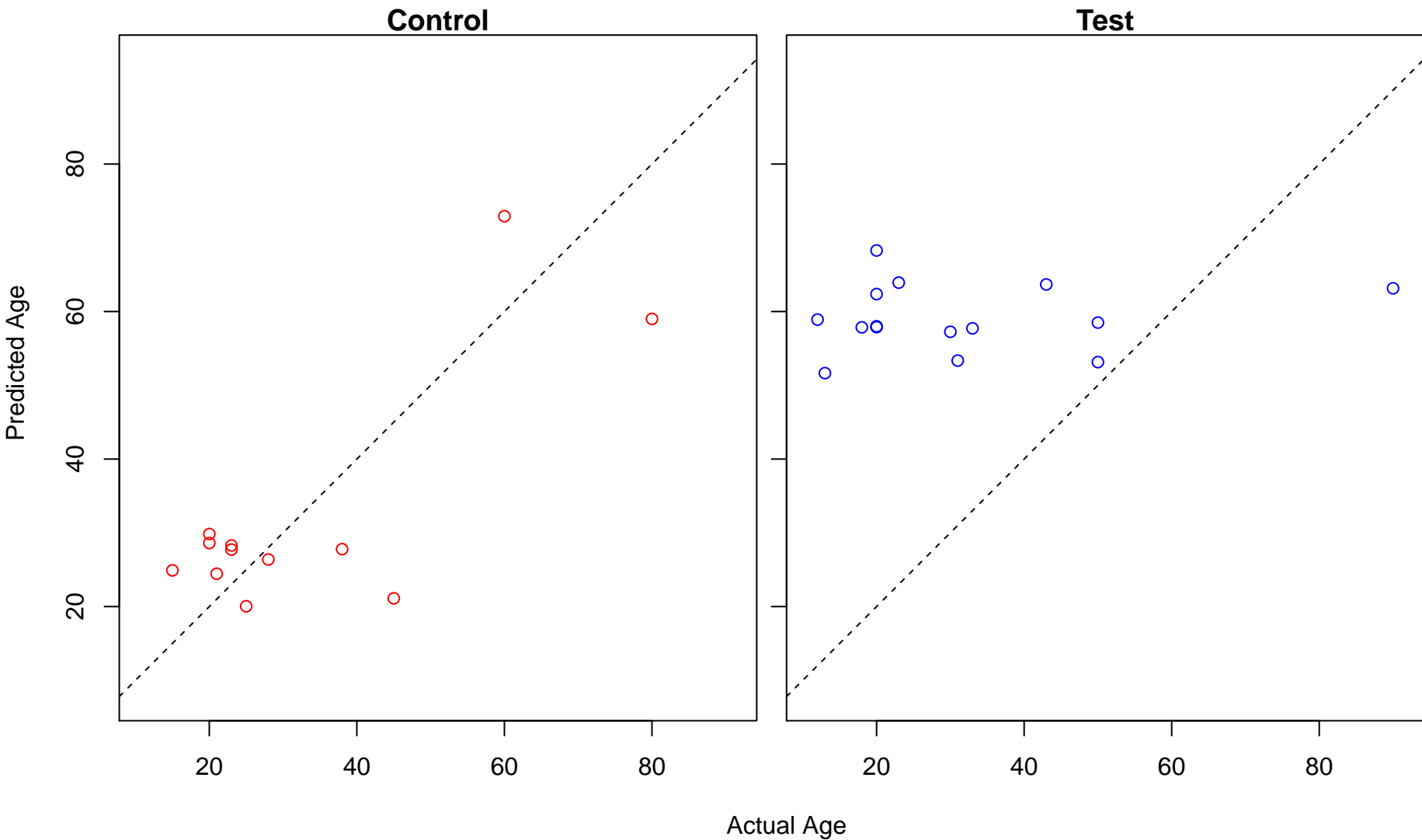
regulation of non-canoncal Wnt signaling pathway (Score: 3.200462)



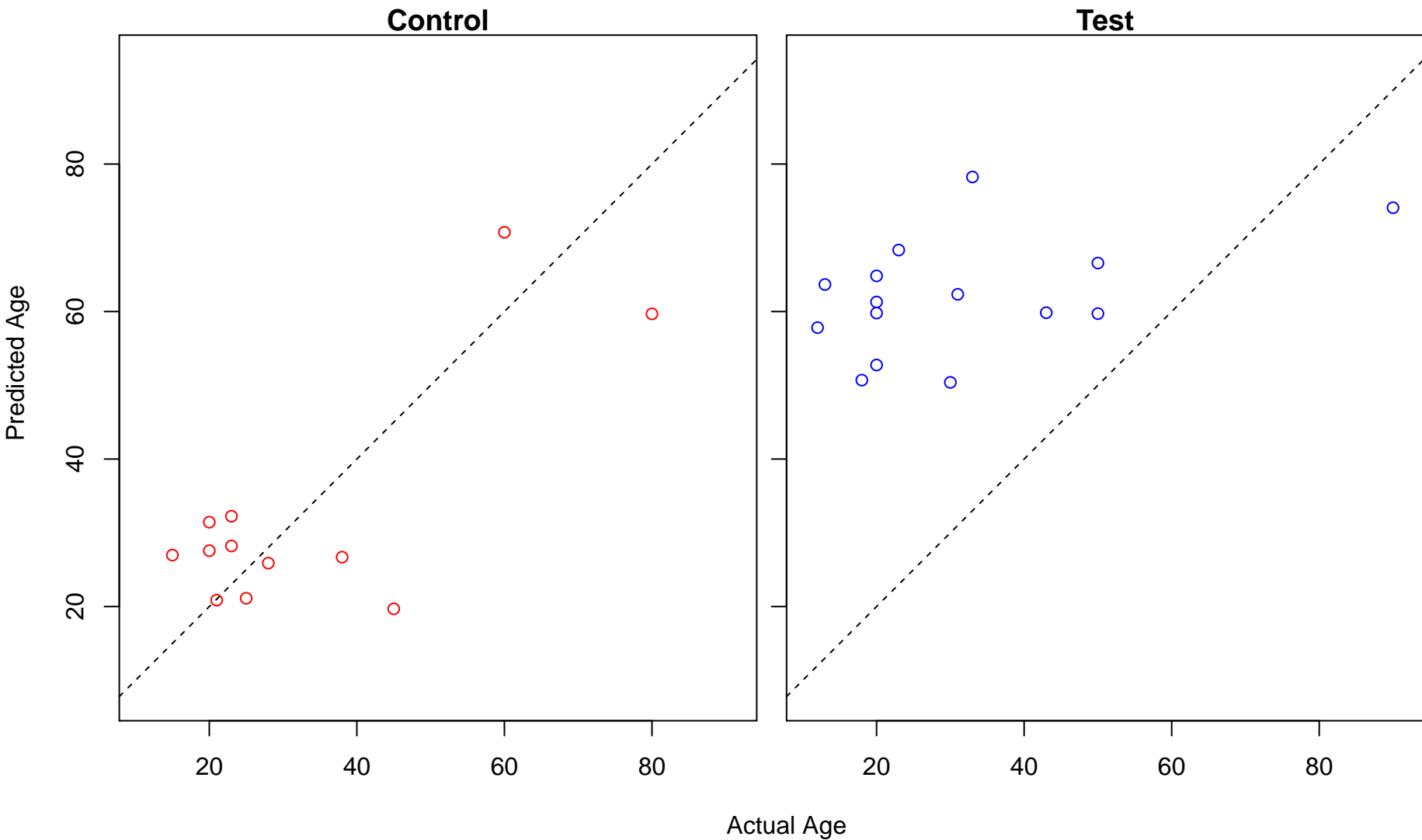
single strand break repair (Score: 3.199951)



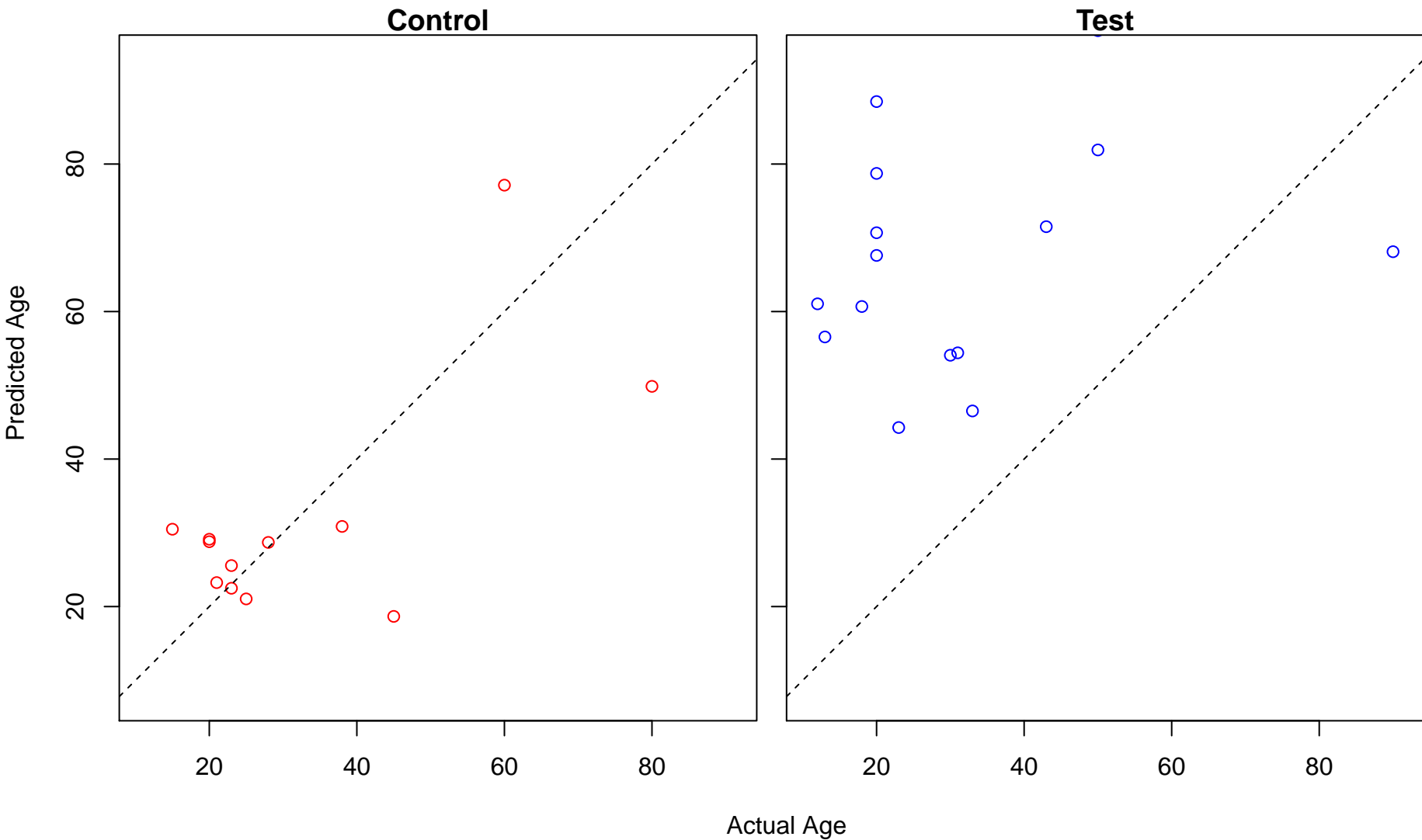
regulation of lipid transport (Score: 3.199835)



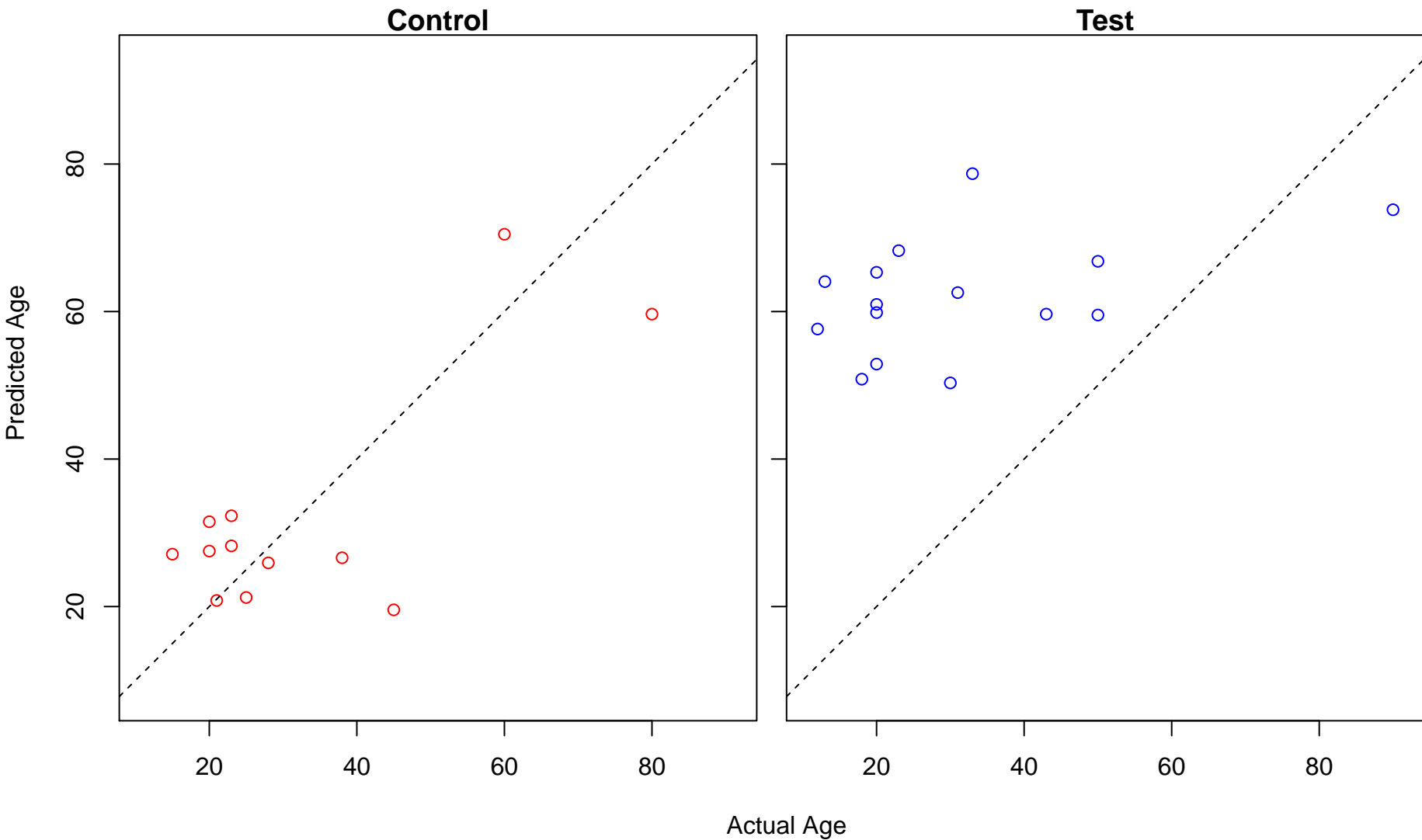
retina layer formation (Score: 3.197705)



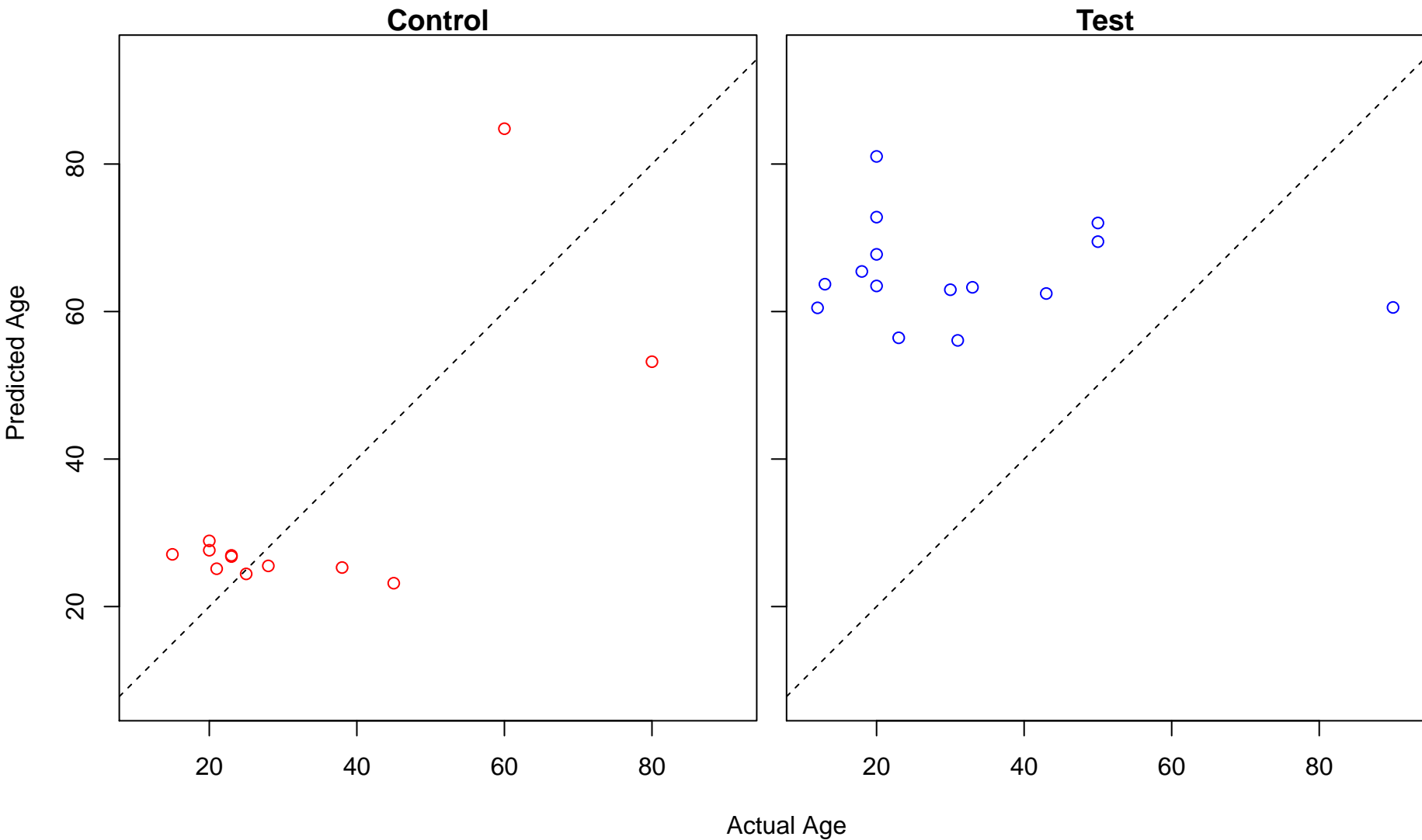
cholesterol transport (Score: 3.197019)



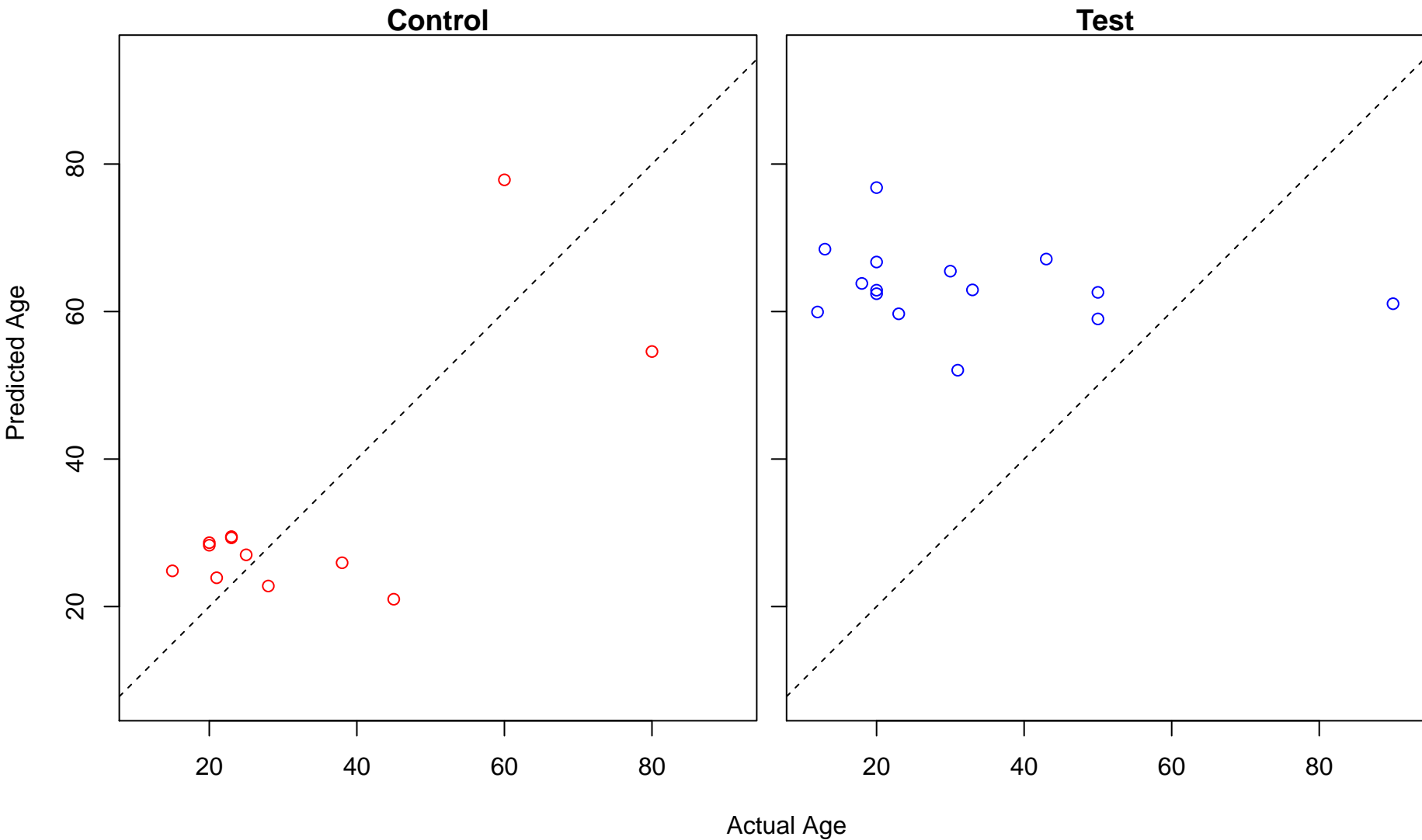
camera-type eye photoreceptor cell differentiation (Score: 3.196089)



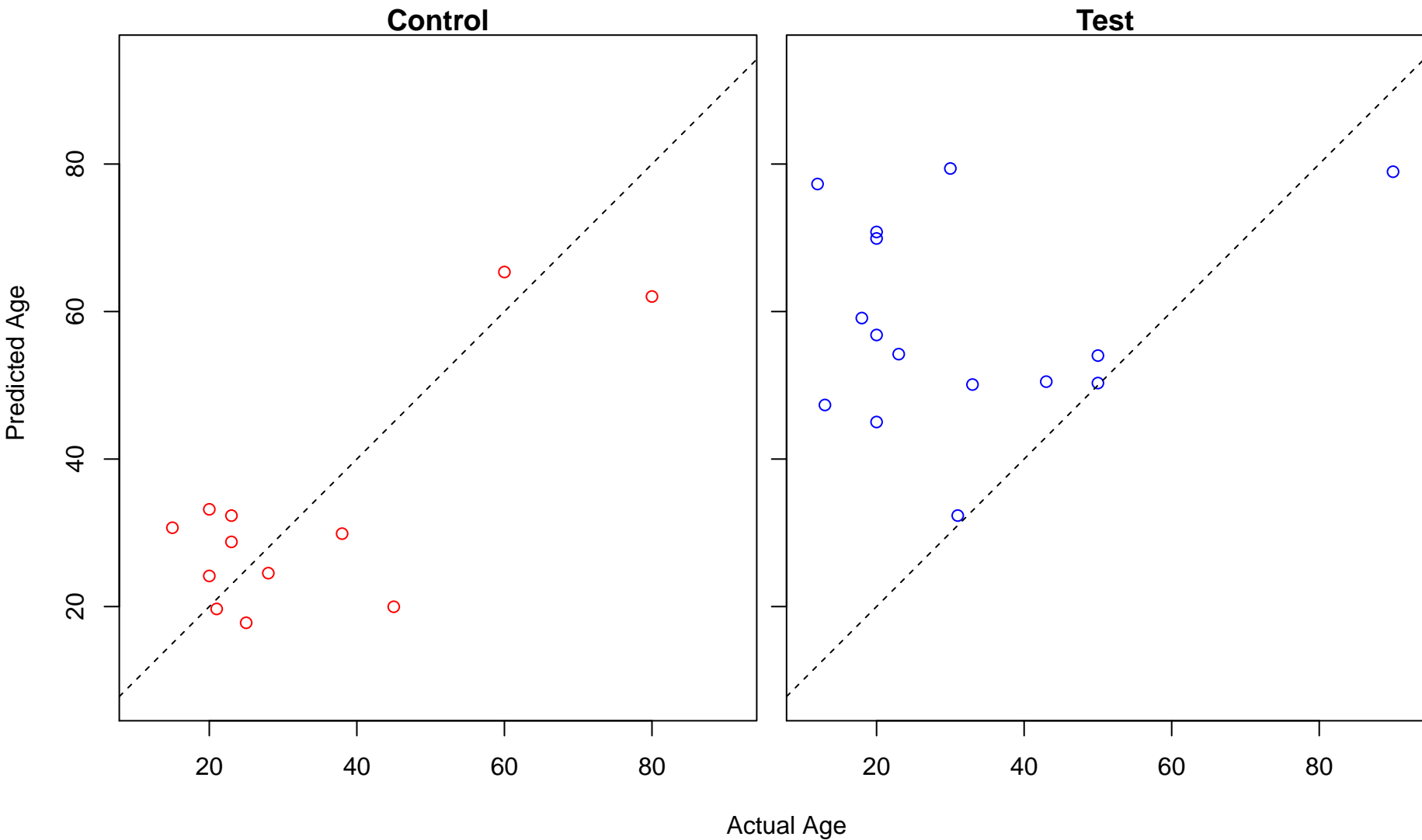
iron ion transport (Score: 3.194062)



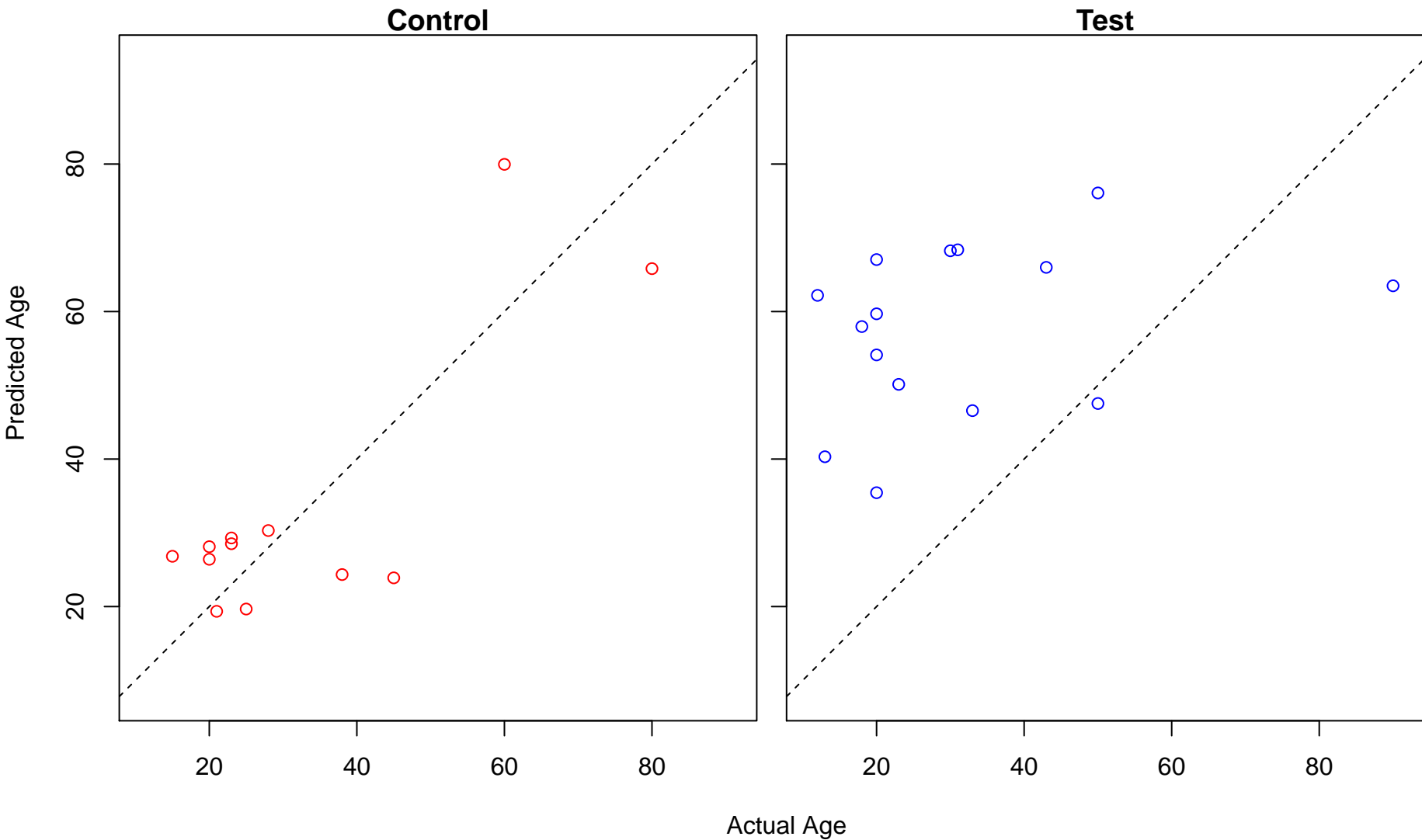
megakaryocyte differentiation (Score: 3.193440)



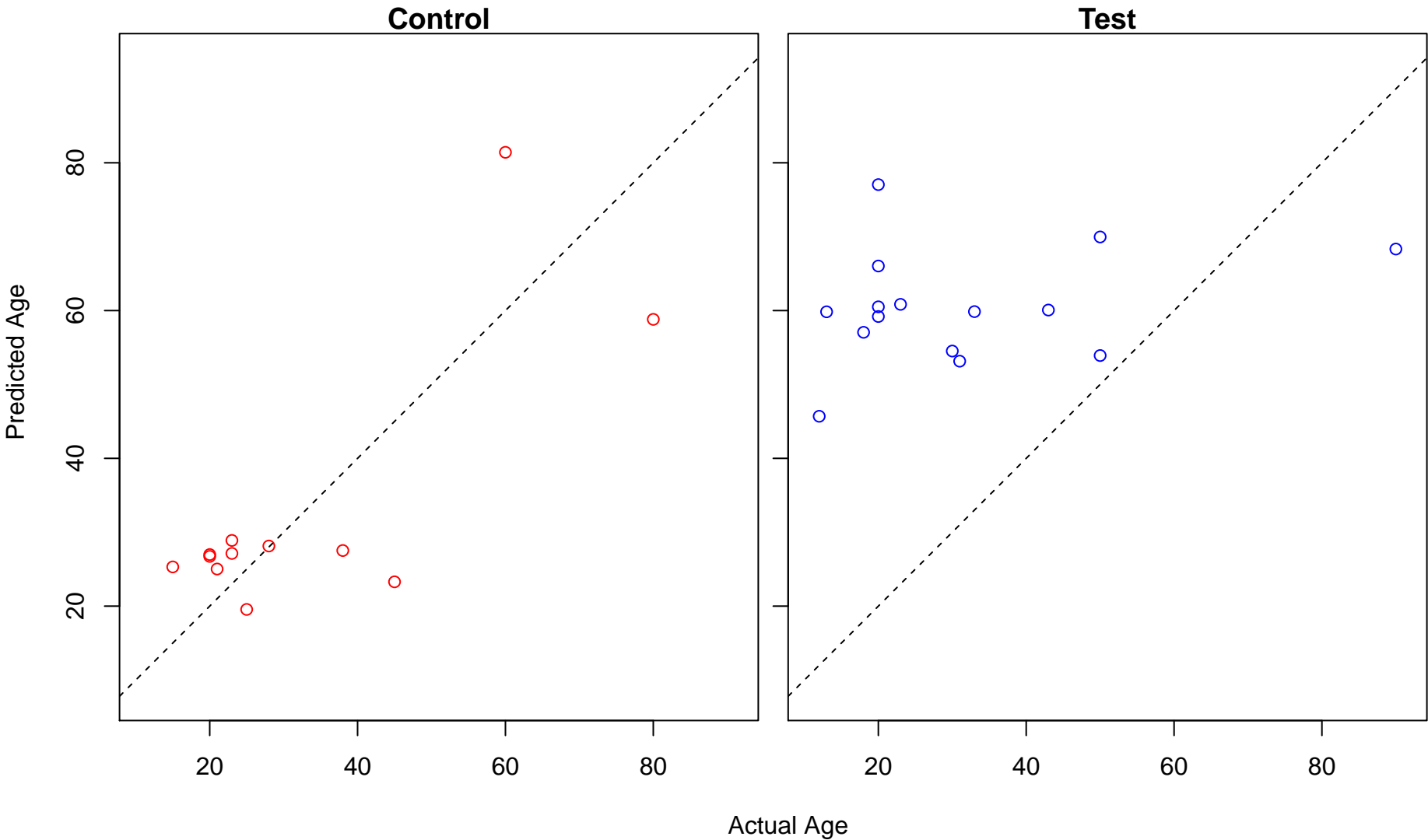
atrioventricular valve formation (Score: 3.188006)



response to ATP (Score: 3.187571)

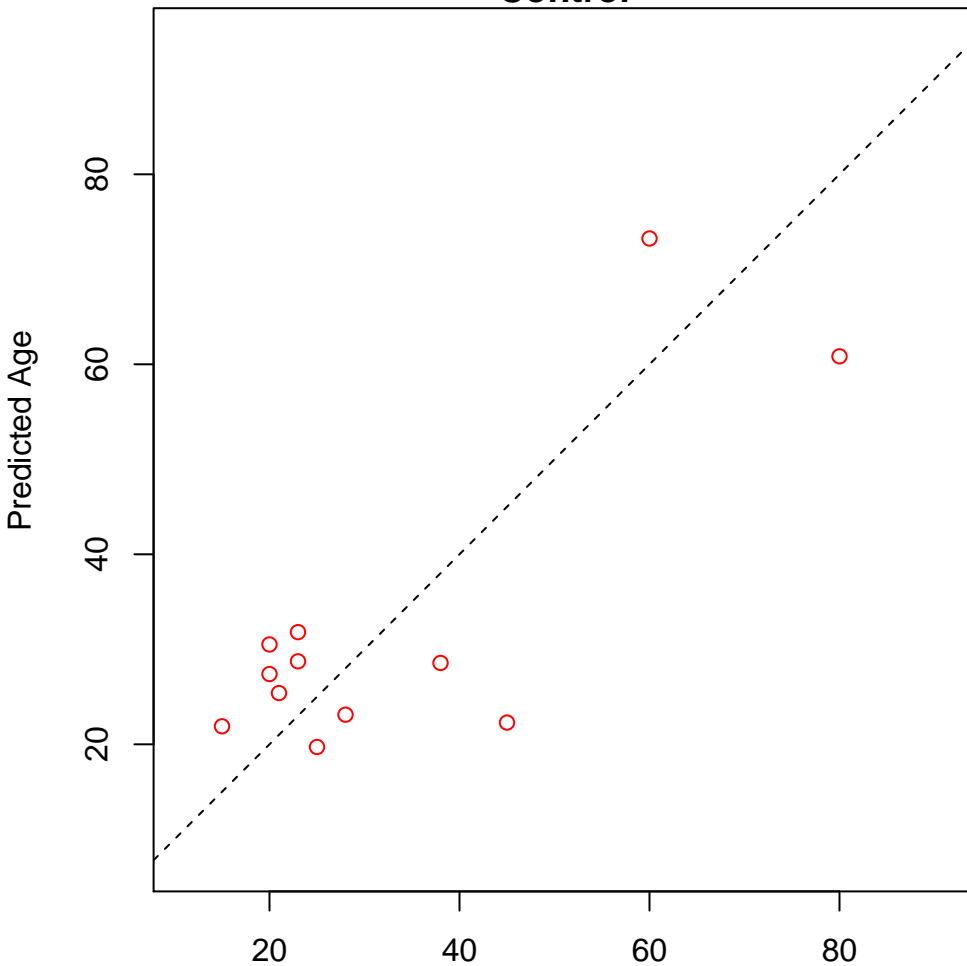


negative regulation of establishment of protein localization to plasma membrane (Score: 3.186905)

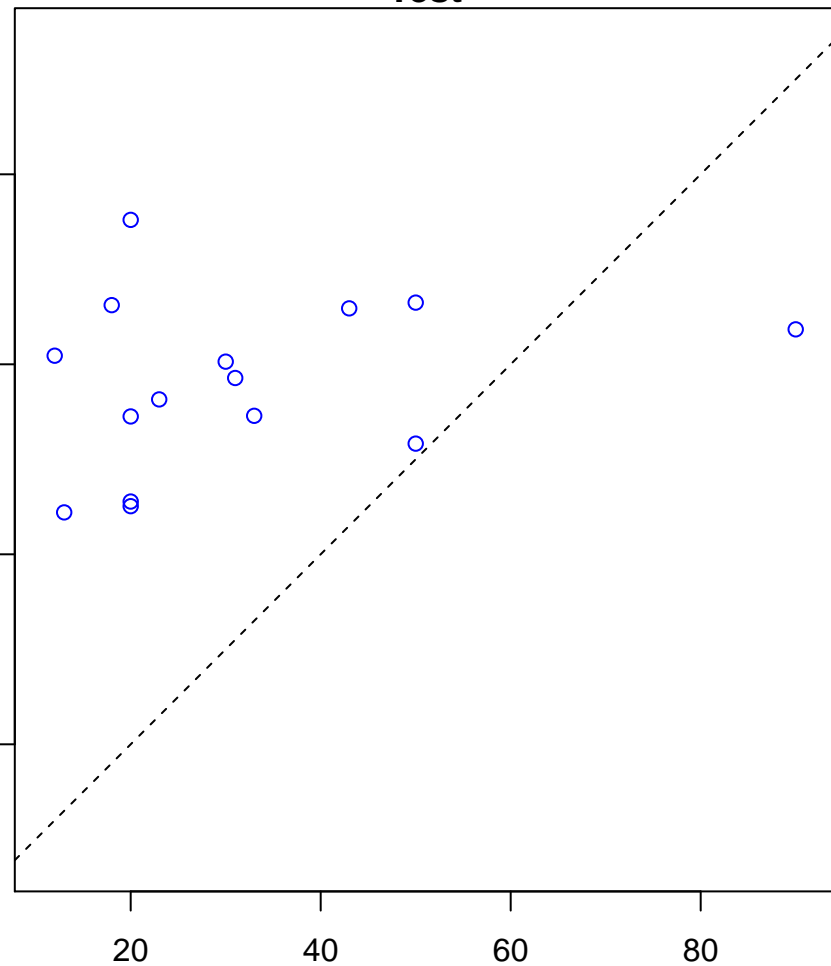


regulation of cholesterol homeostasis (Score: 3.176003)

Control

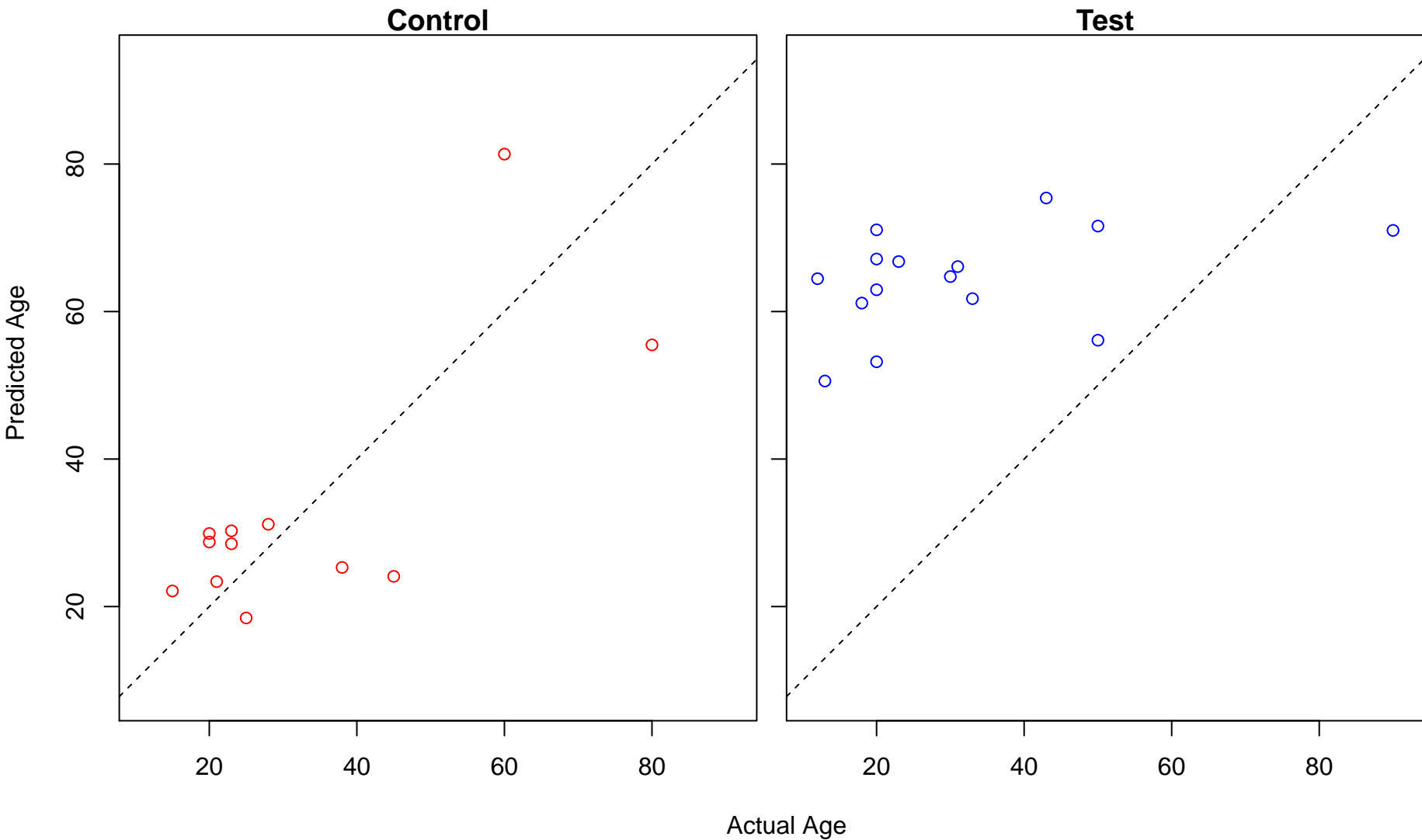


Test

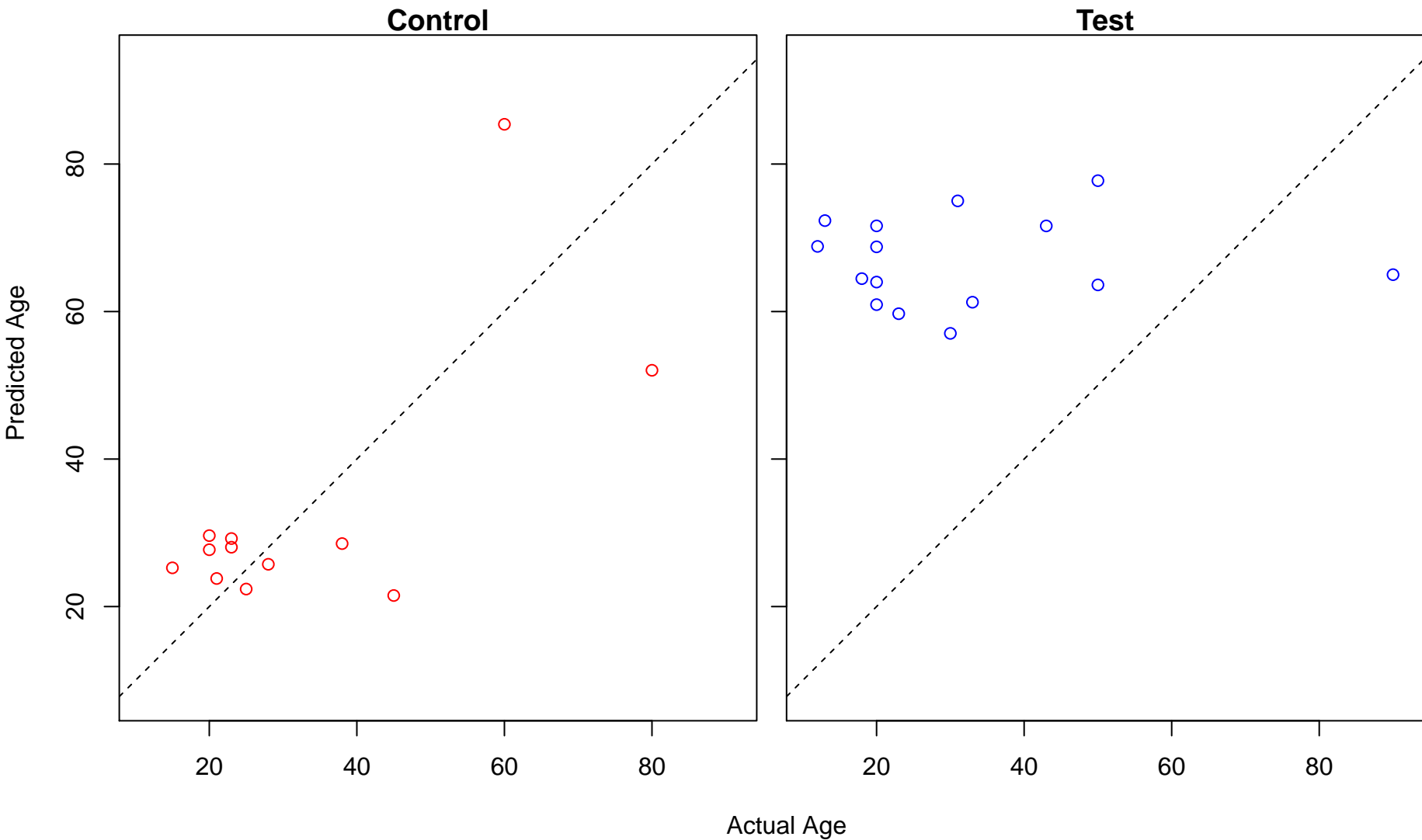


Actual Age

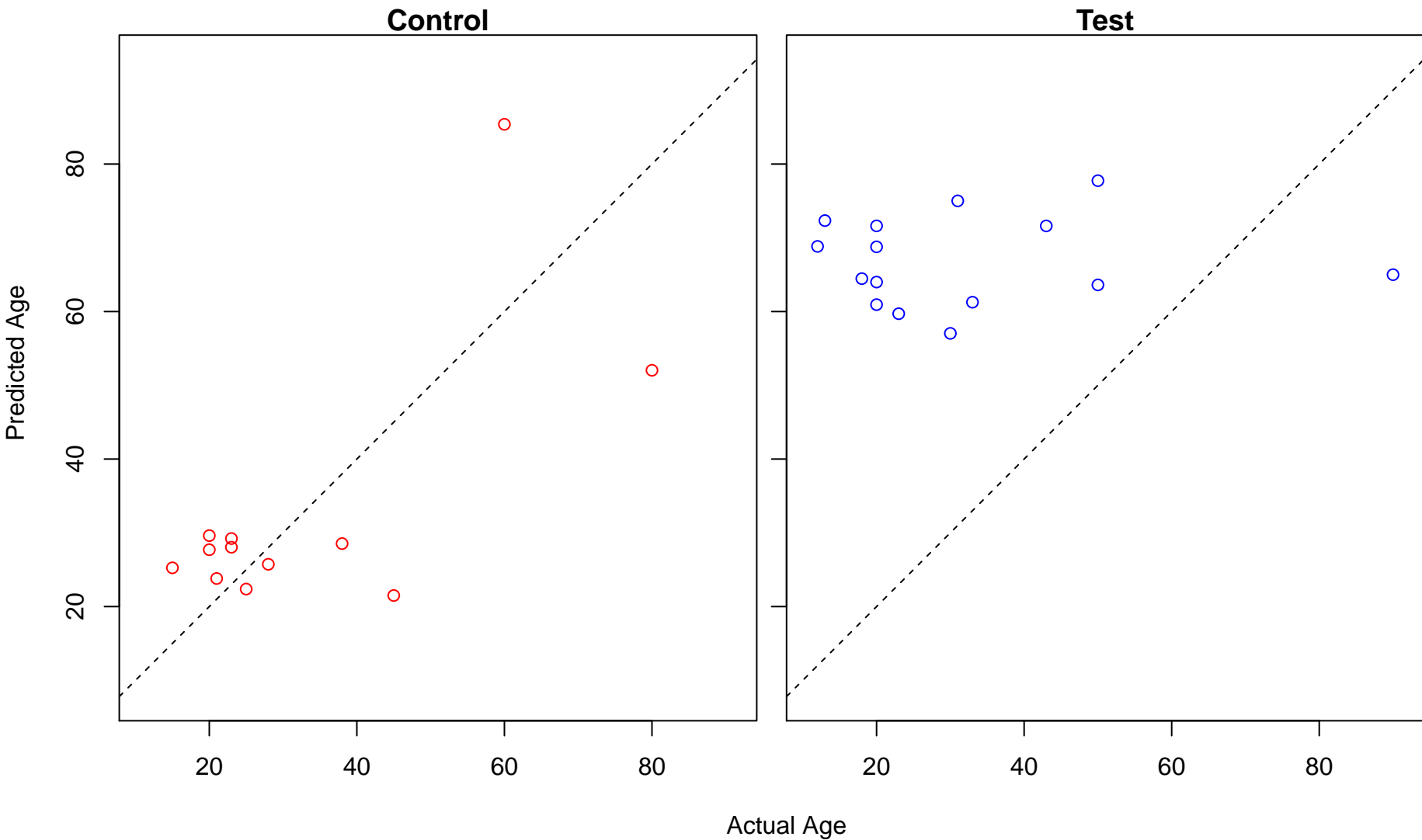
phosphatidylglycerol acyl-chain remodeling (Score: 3.173941)



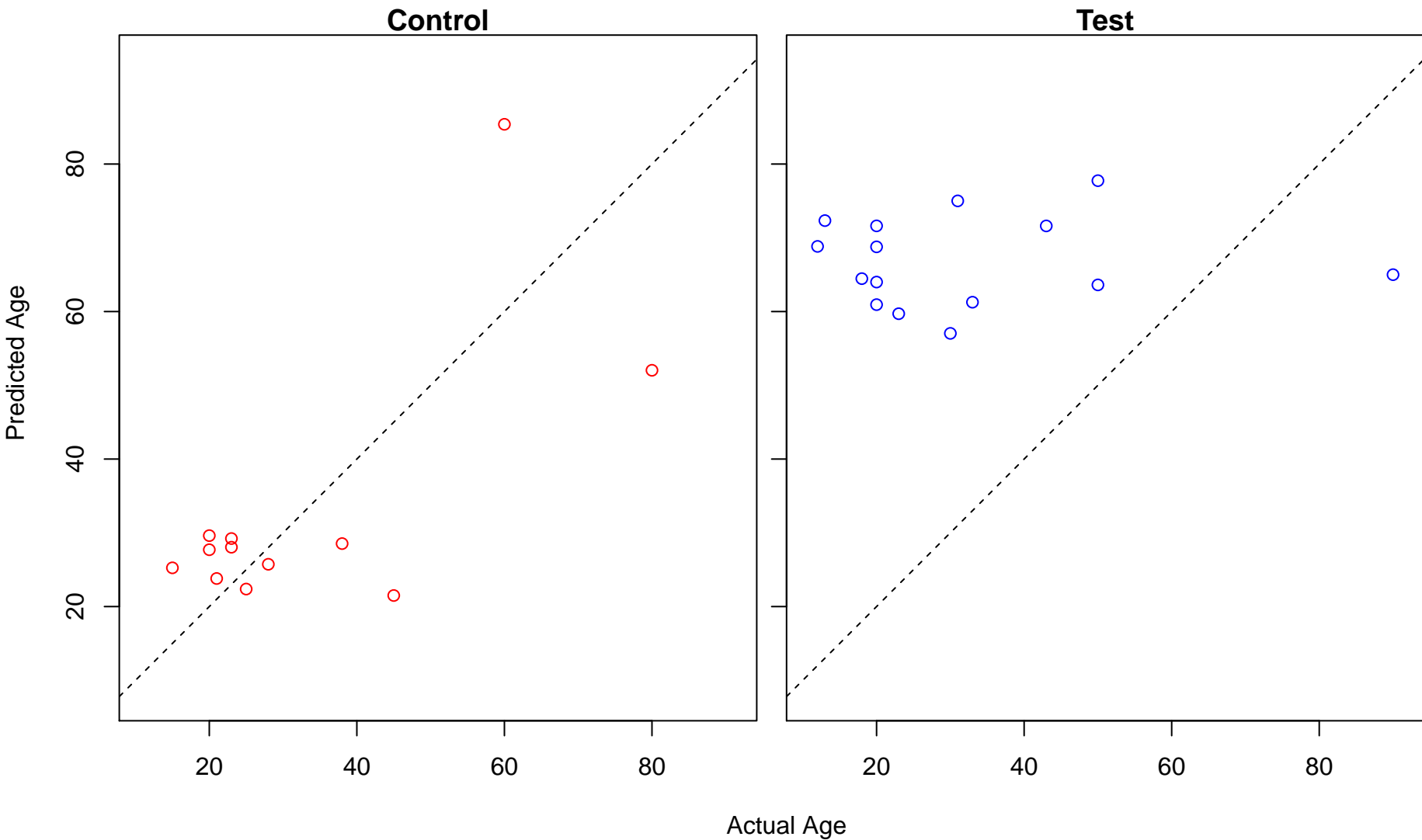
response to inactivity (Score: 3.173088)



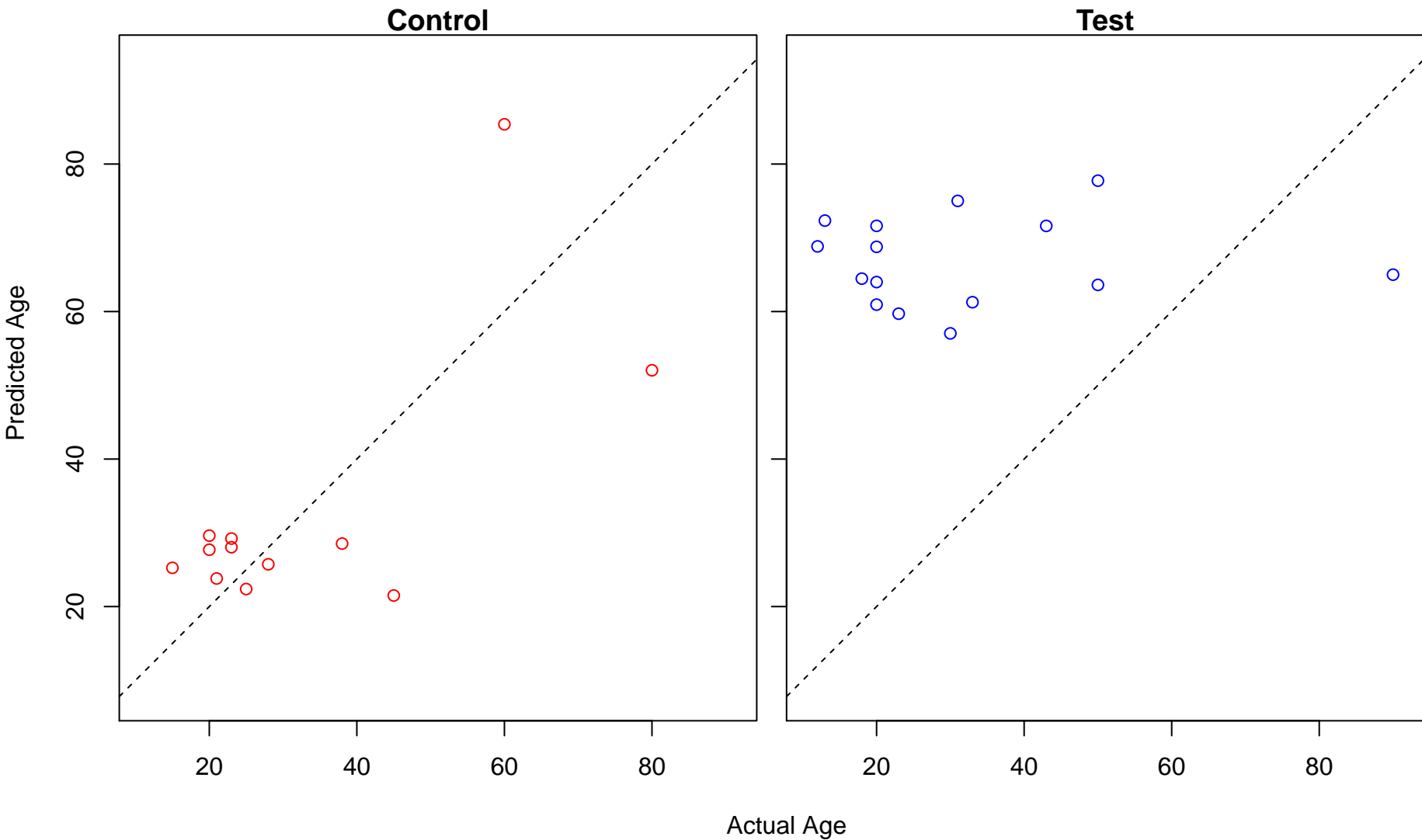
response to muscle inactivity (Score: 3.173088)



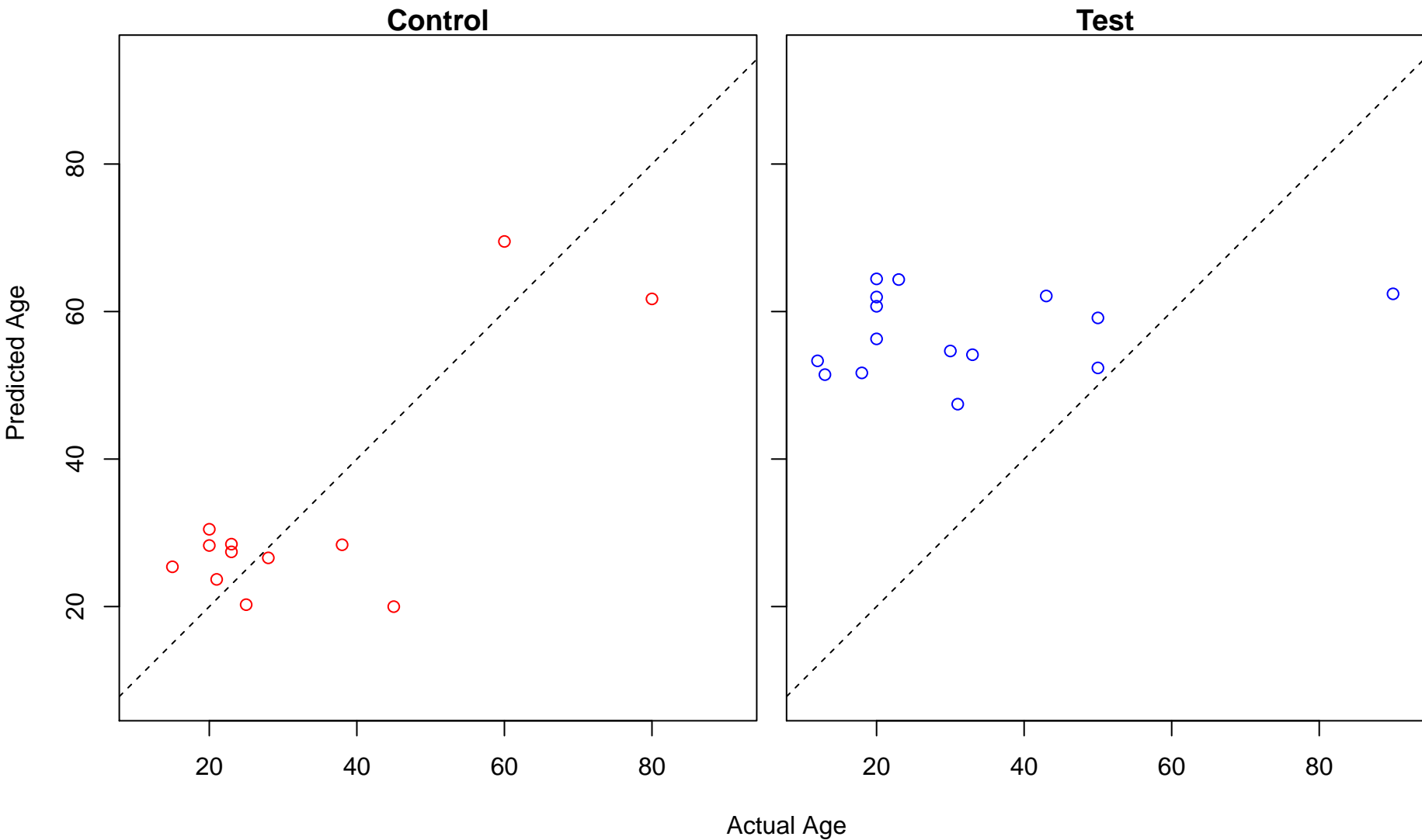
response to muscle inactivity involved in regulation of muscle adaptation (Score: 3.173088)



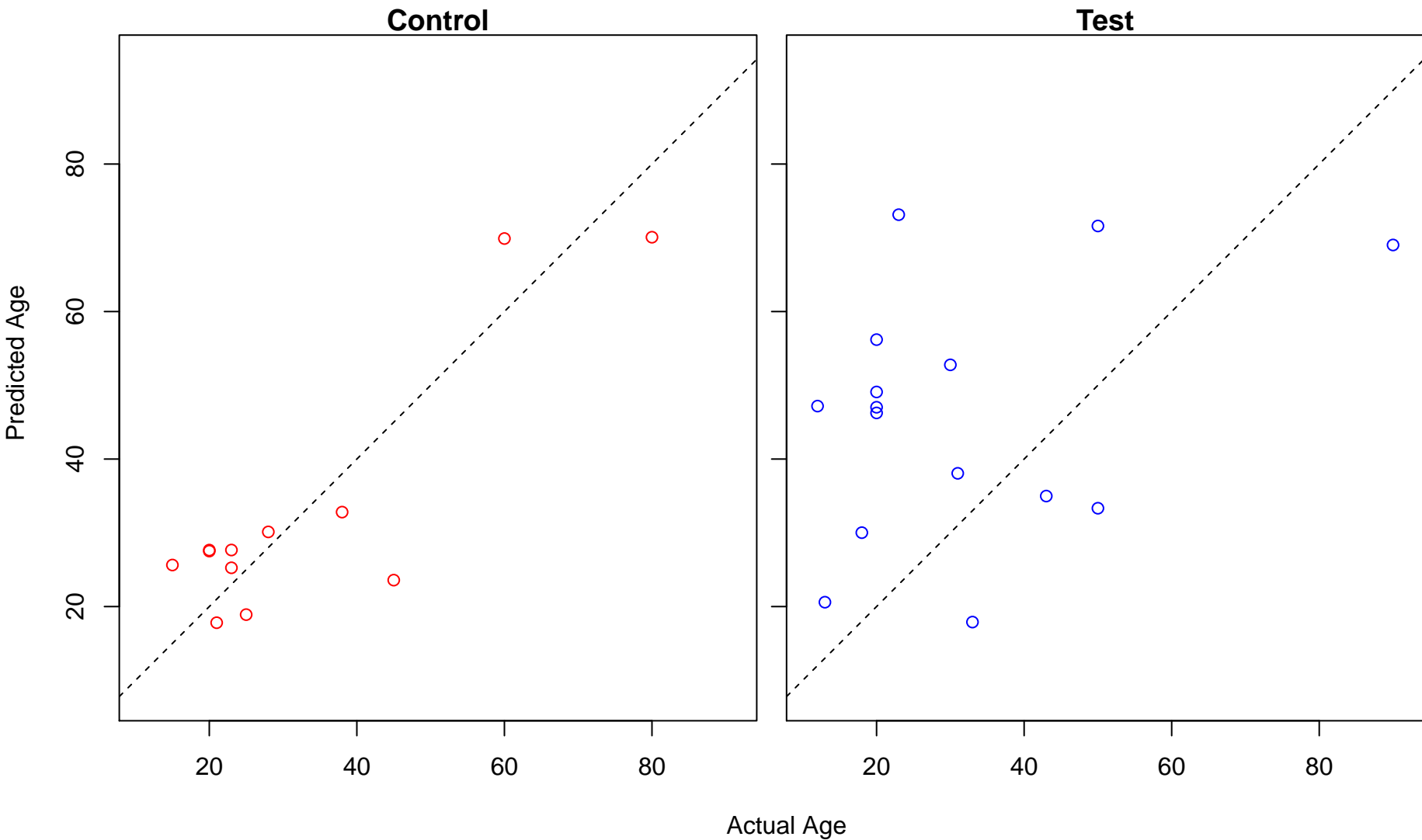
response to denervation involved in regulation of muscle adaptation (Score: 3.173088)



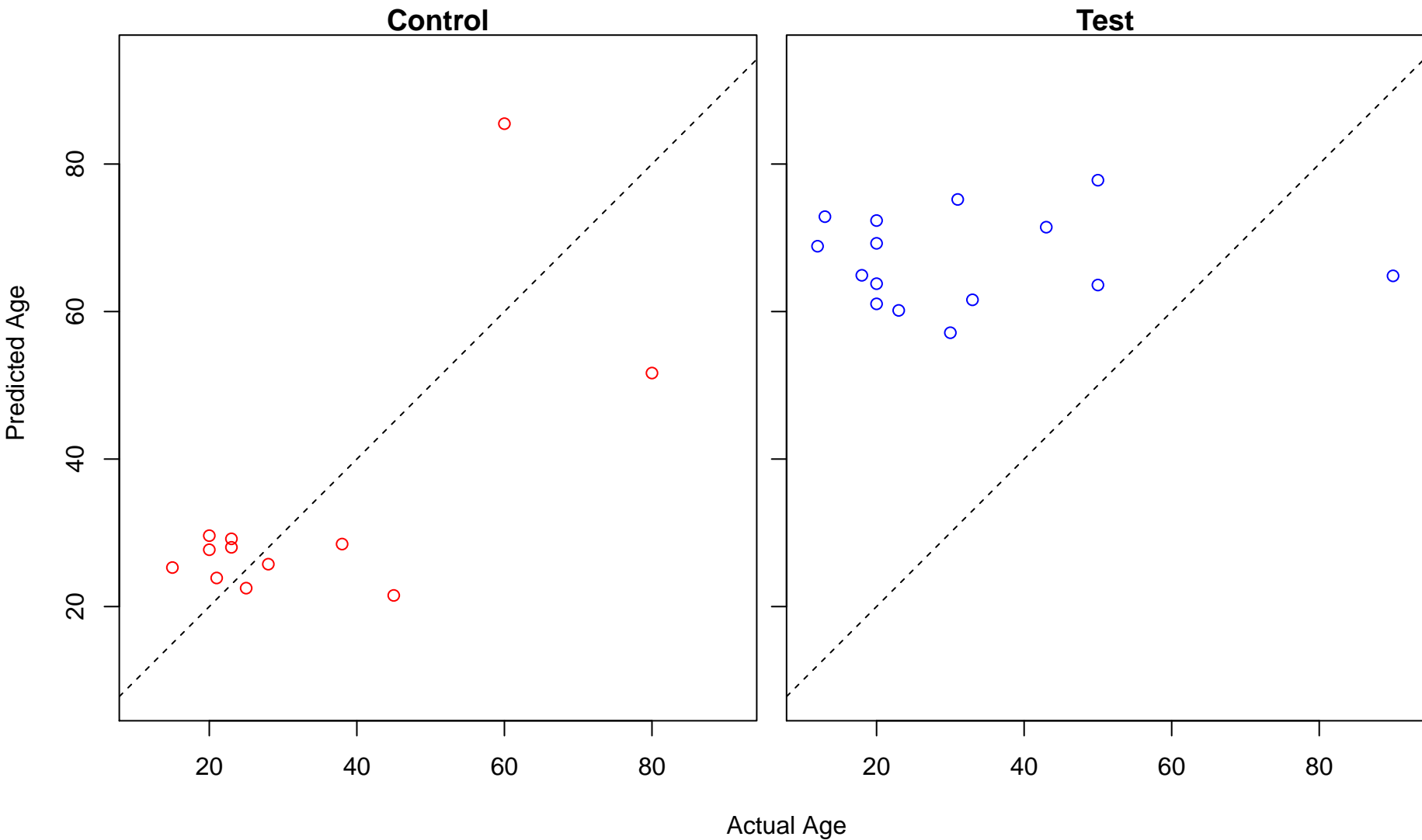
regulation of lipoprotein particle clearance (Score: 3.169714)



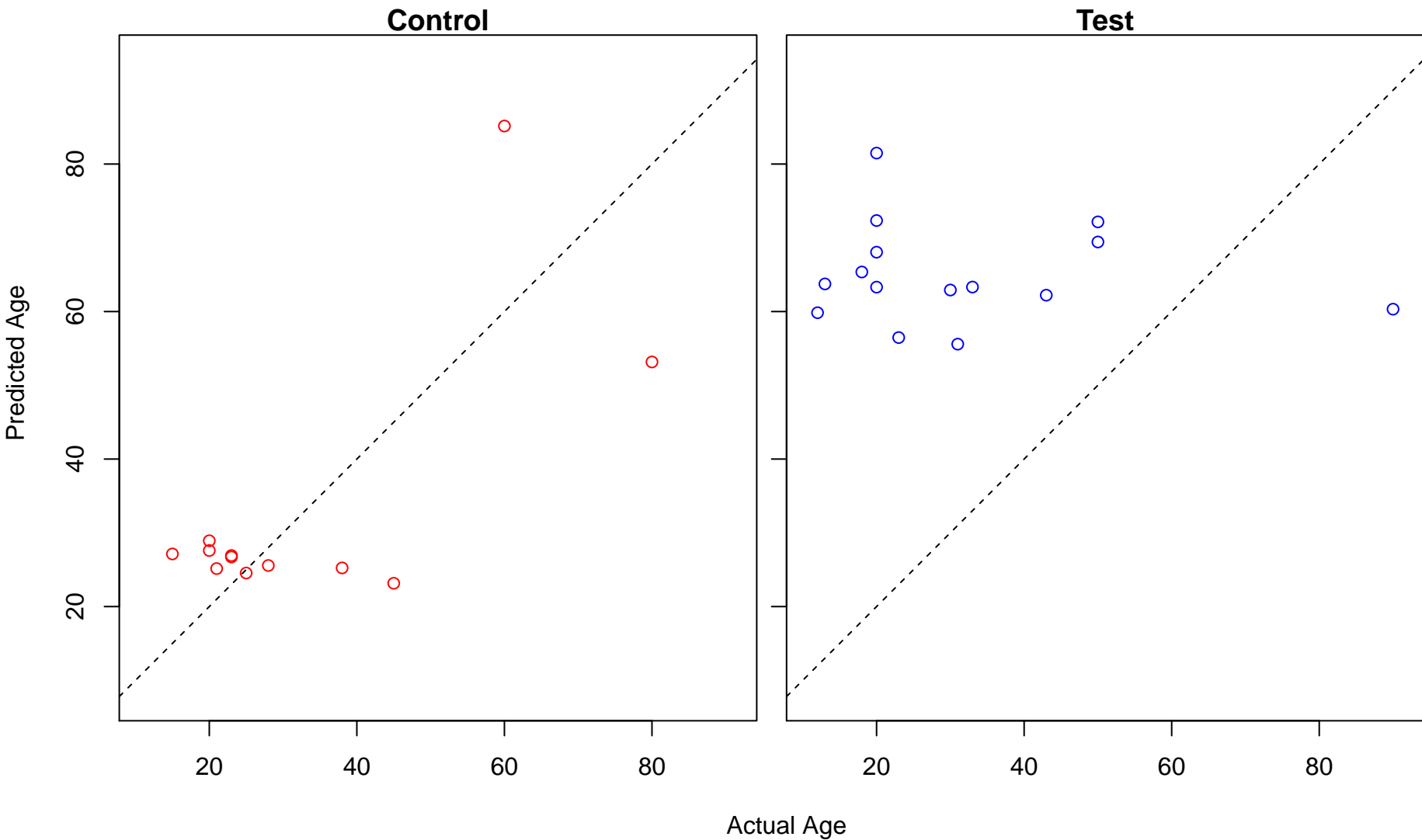
signal release (Score: 3.169578)



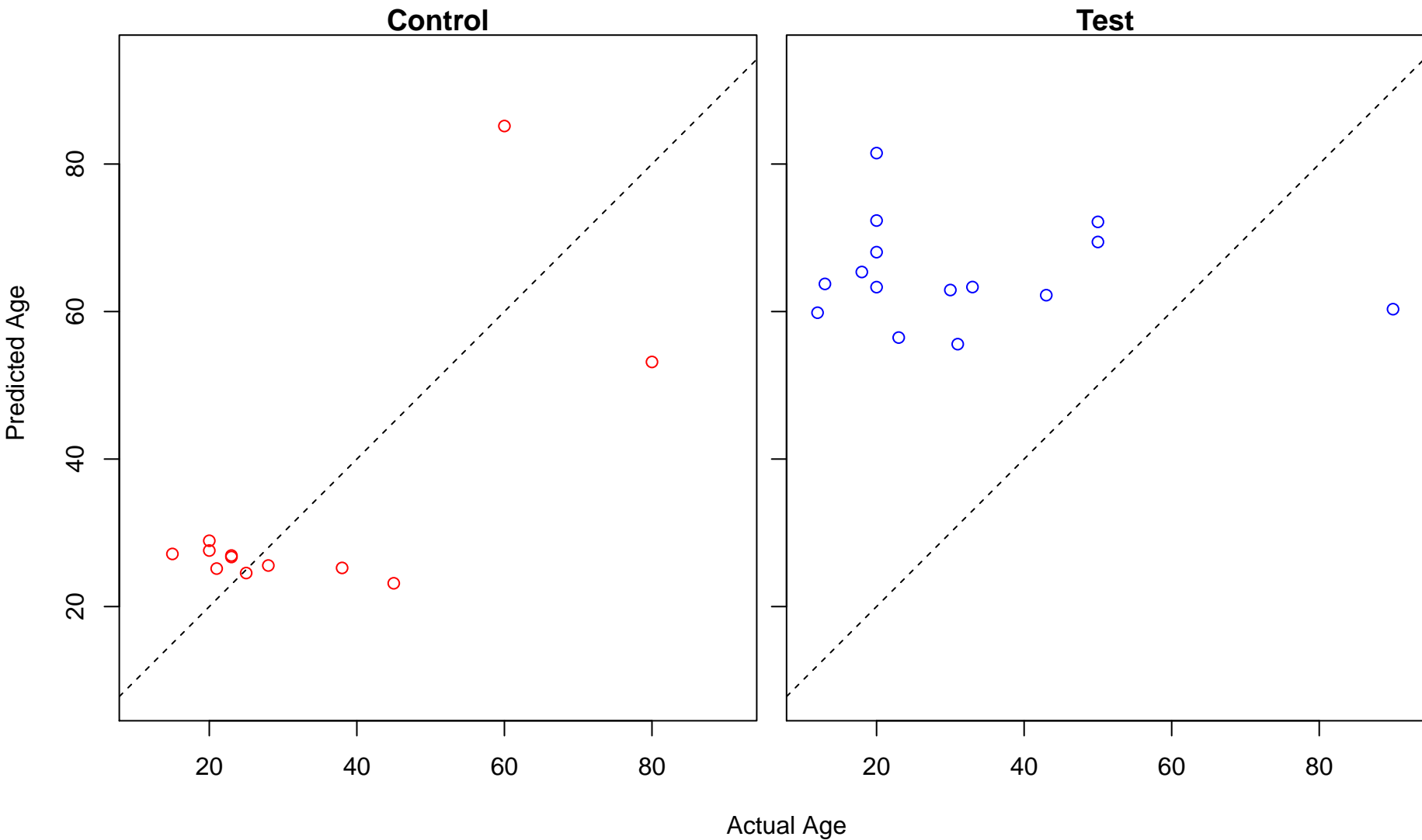
response to stimulus involved in regulation of muscle adaptation (Score: 3.168491)



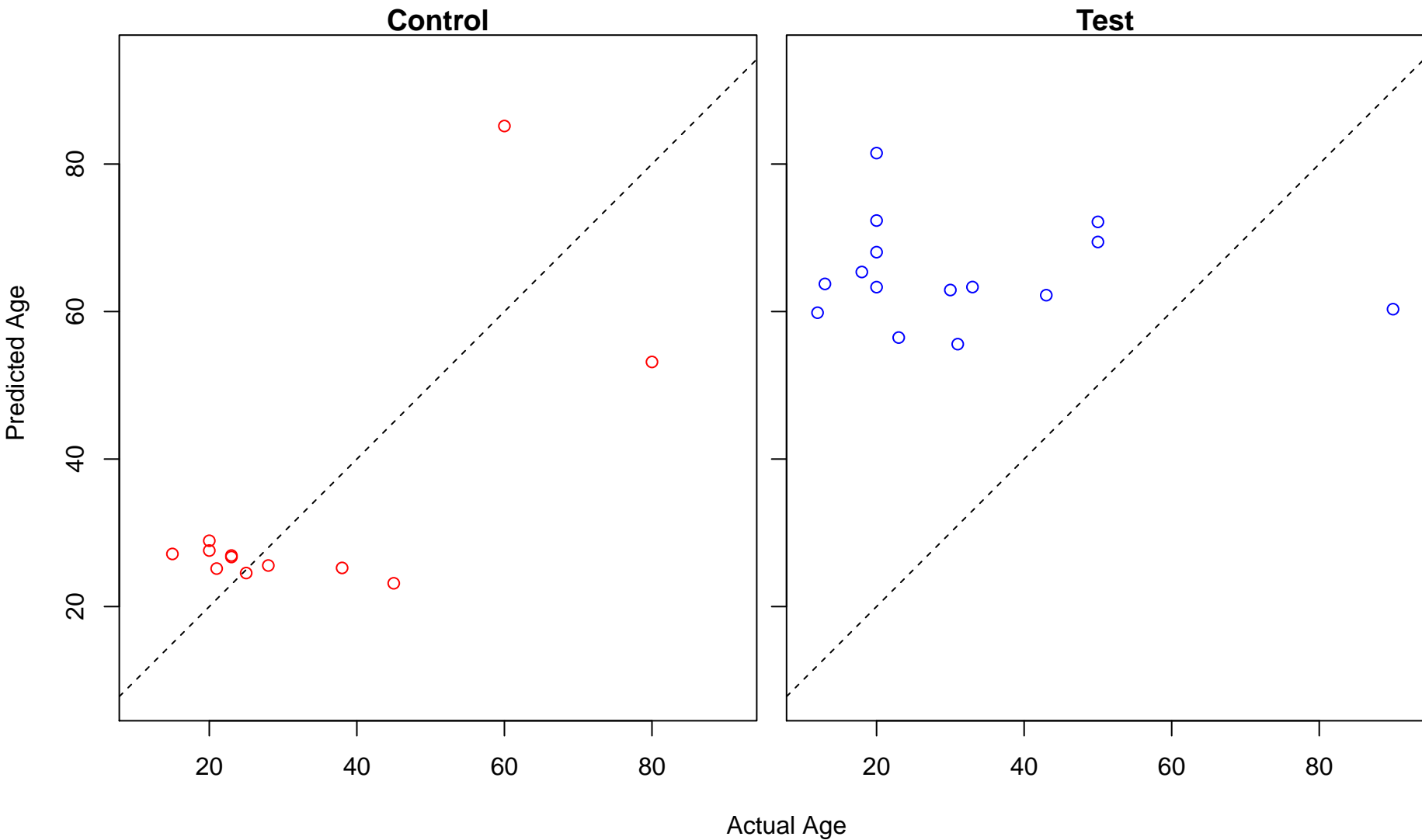
ferric iron transport (Score: 3.167962)



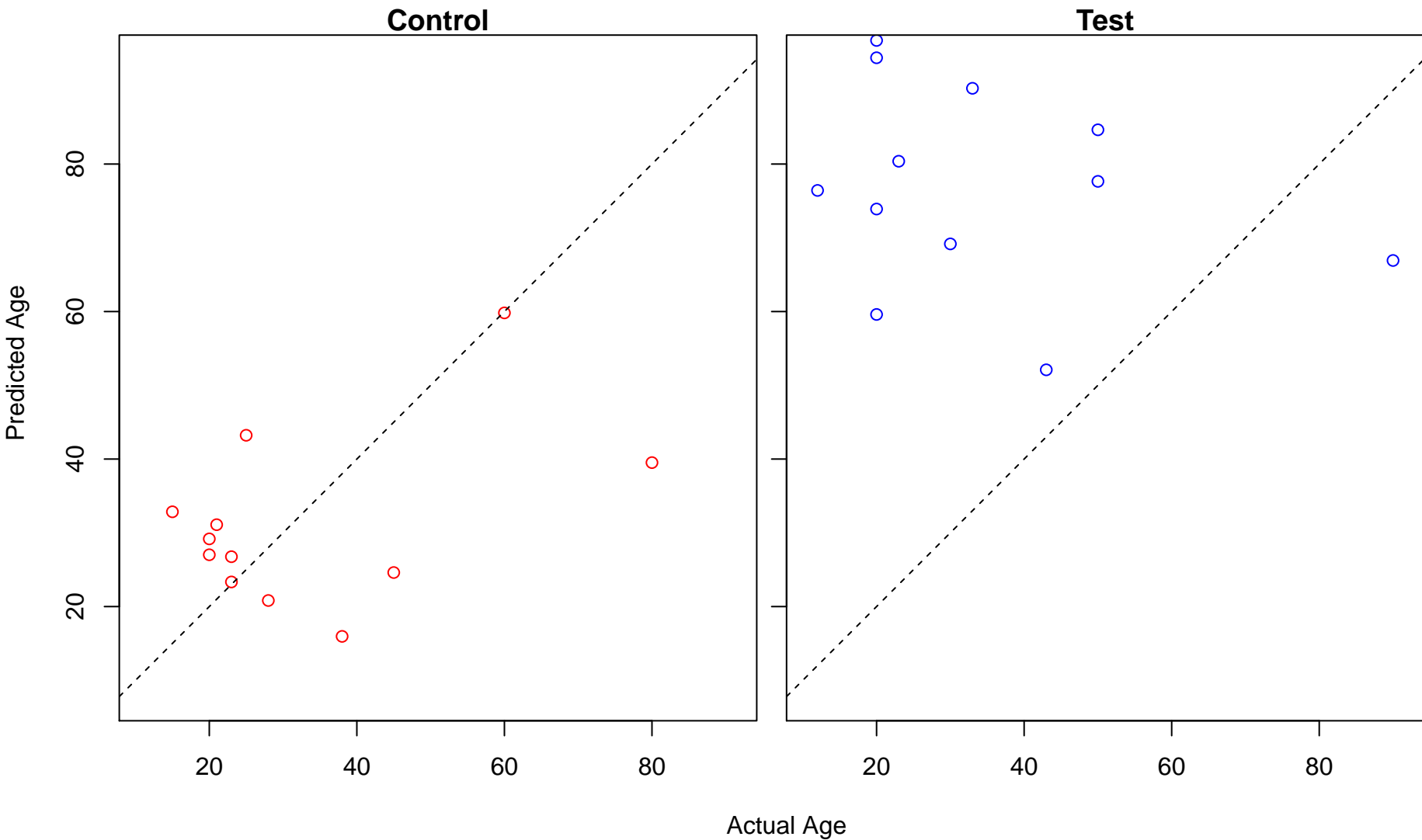
transferrin transport (Score: 3.167962)



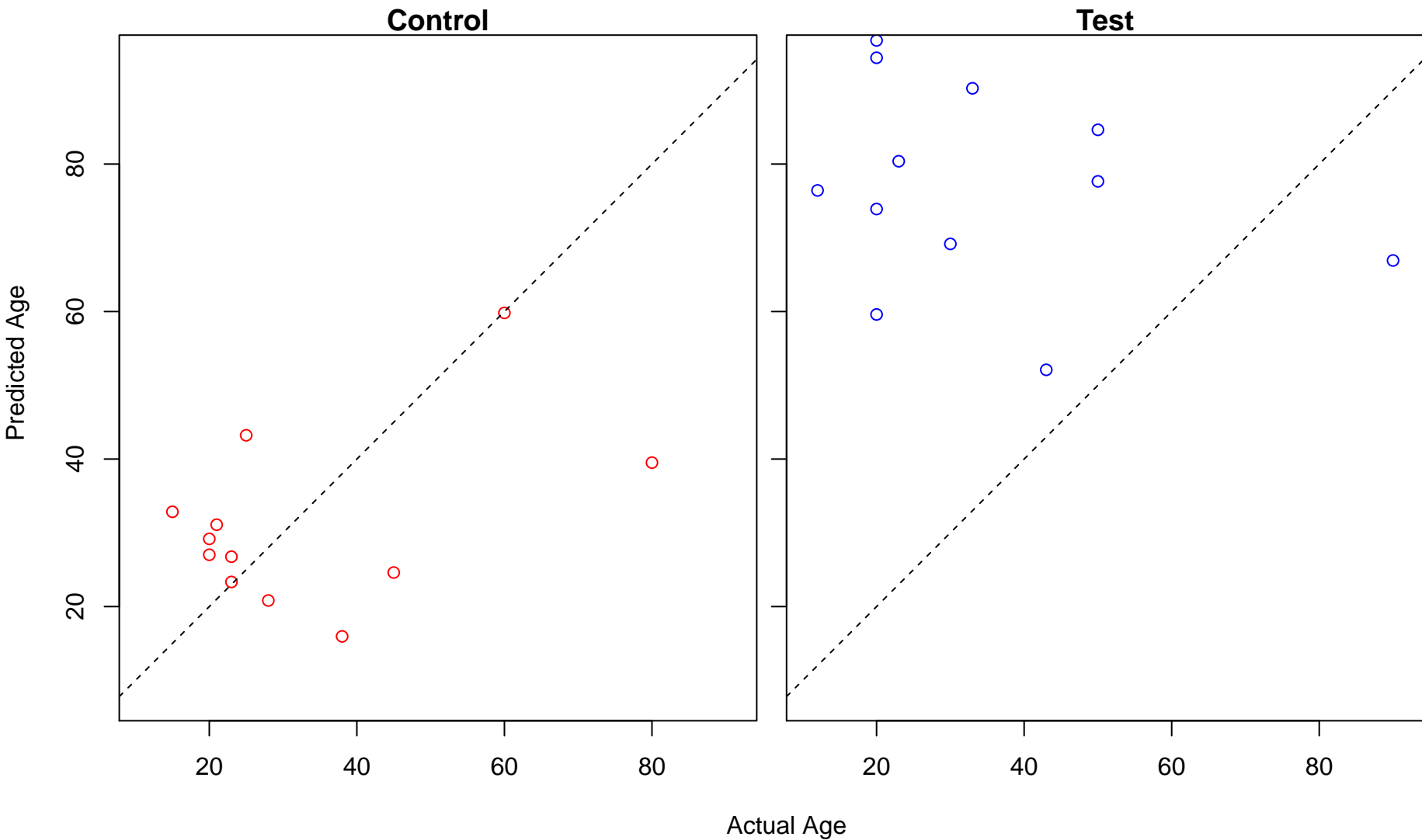
trivalent inorganic cation transport (Score: 3.167962)



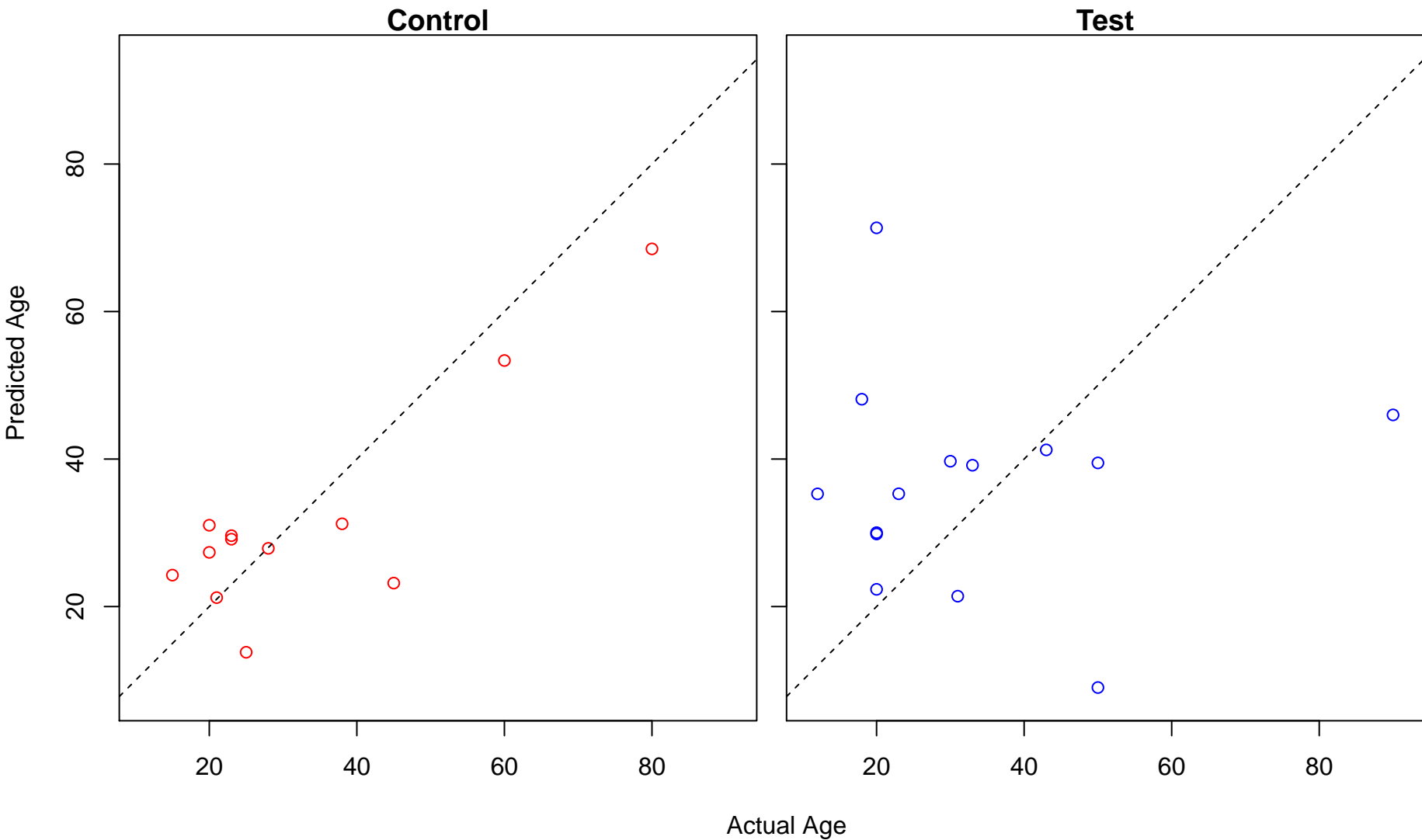
alpha-beta T cell lineage commitment (Score: 3.164199)



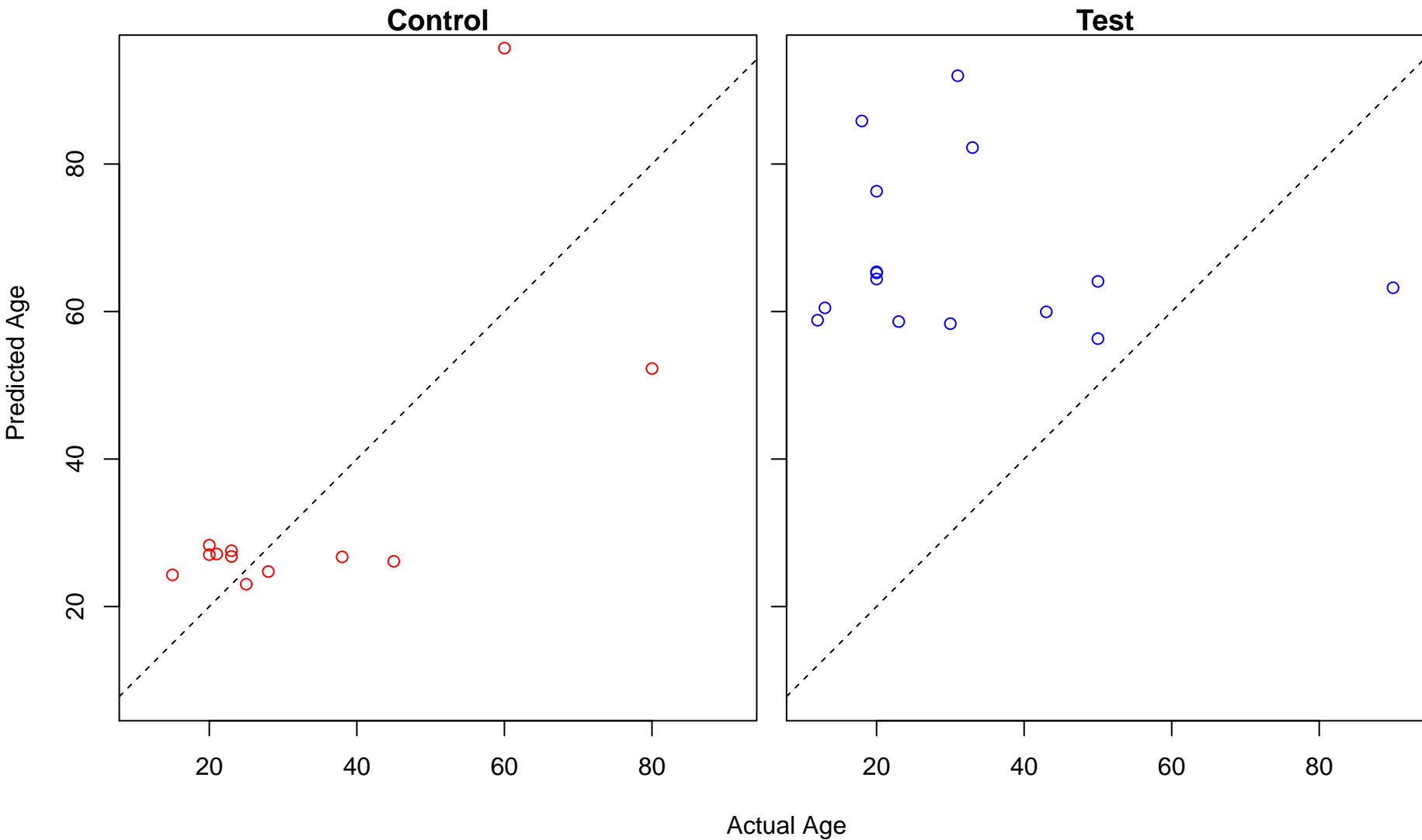
CD4-positive, alpha-beta T cell lineage commitment (Score: 3.164199)



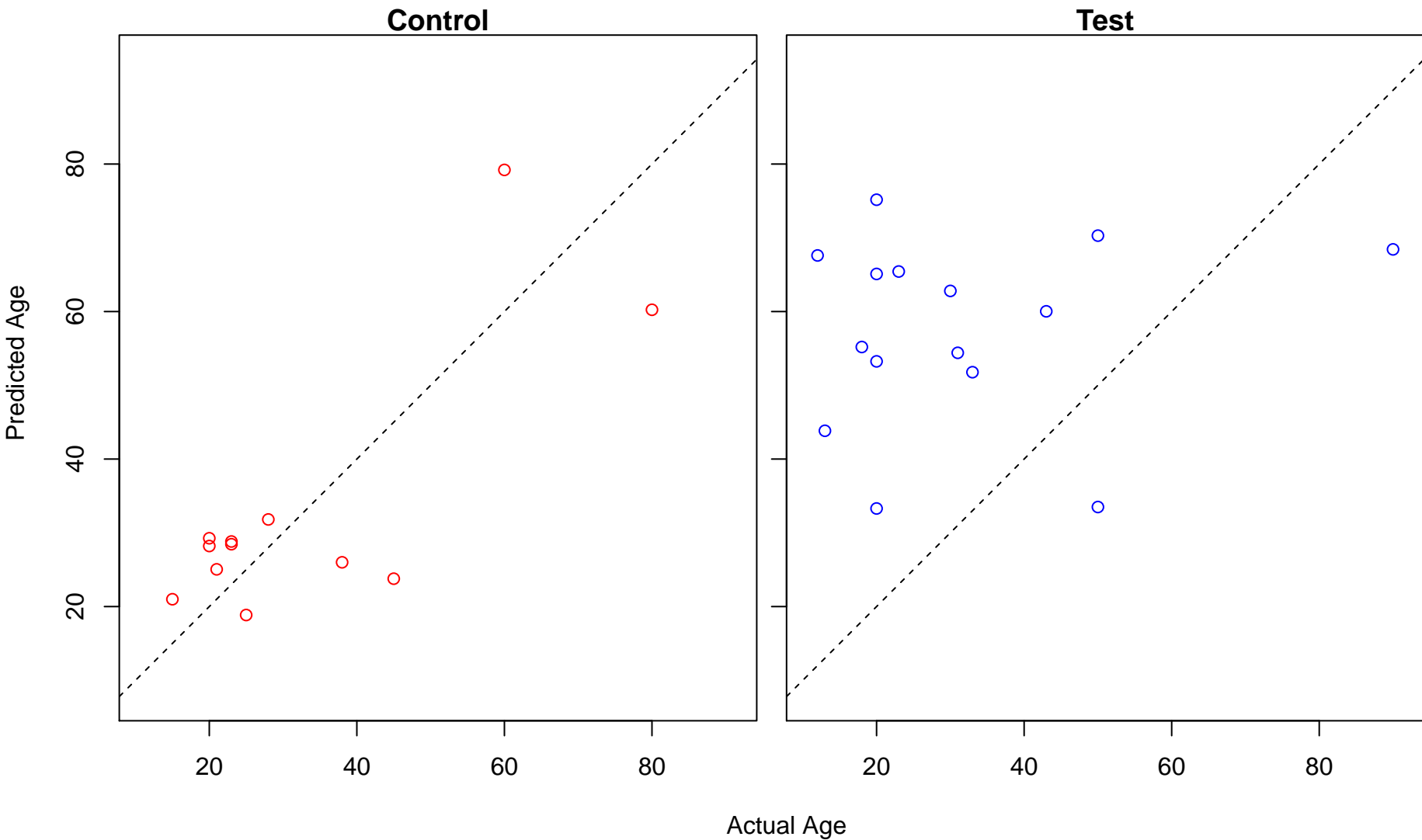
drug transport (Score: 3.162721)



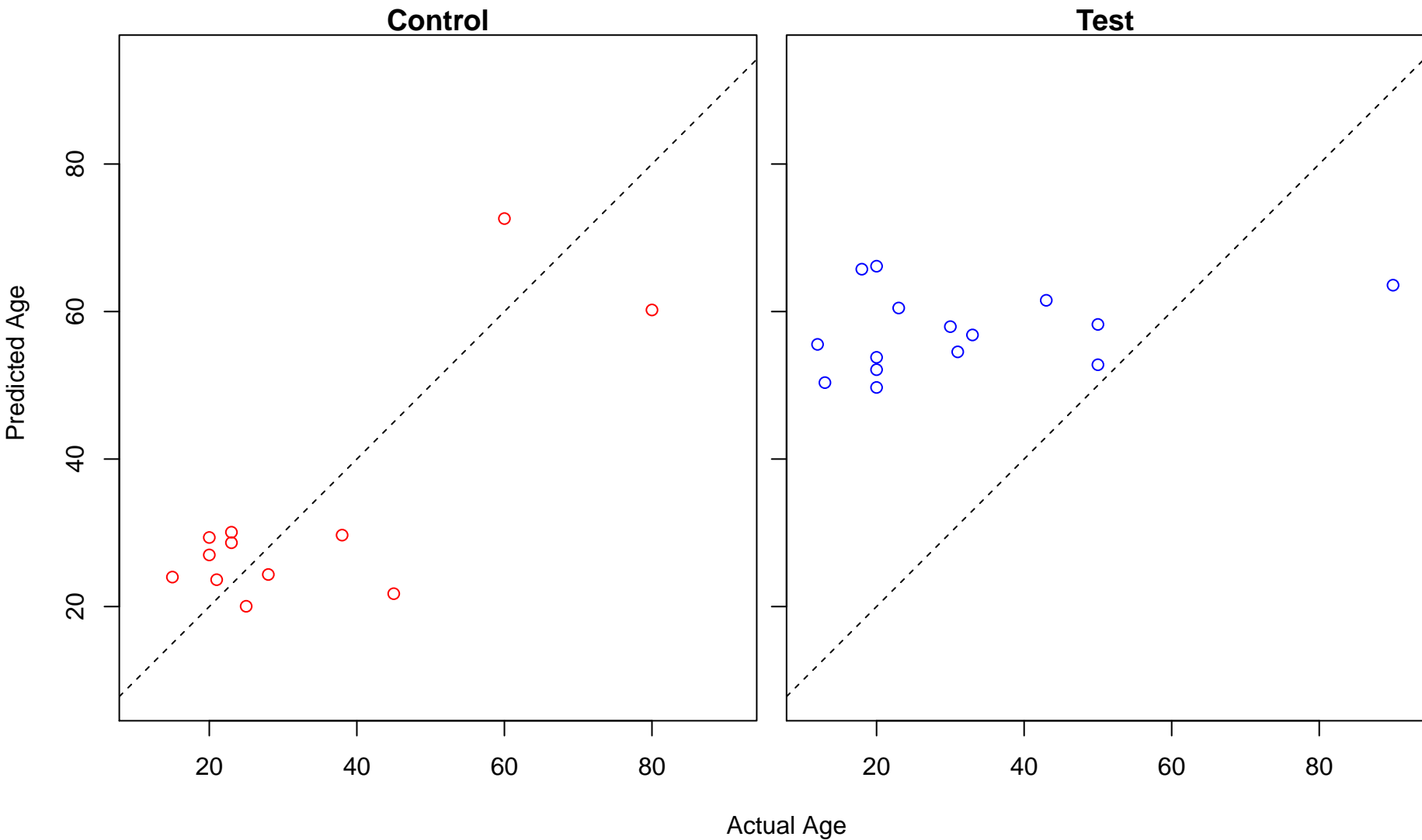
negative regulation of organ growth (Score: 3.162561)



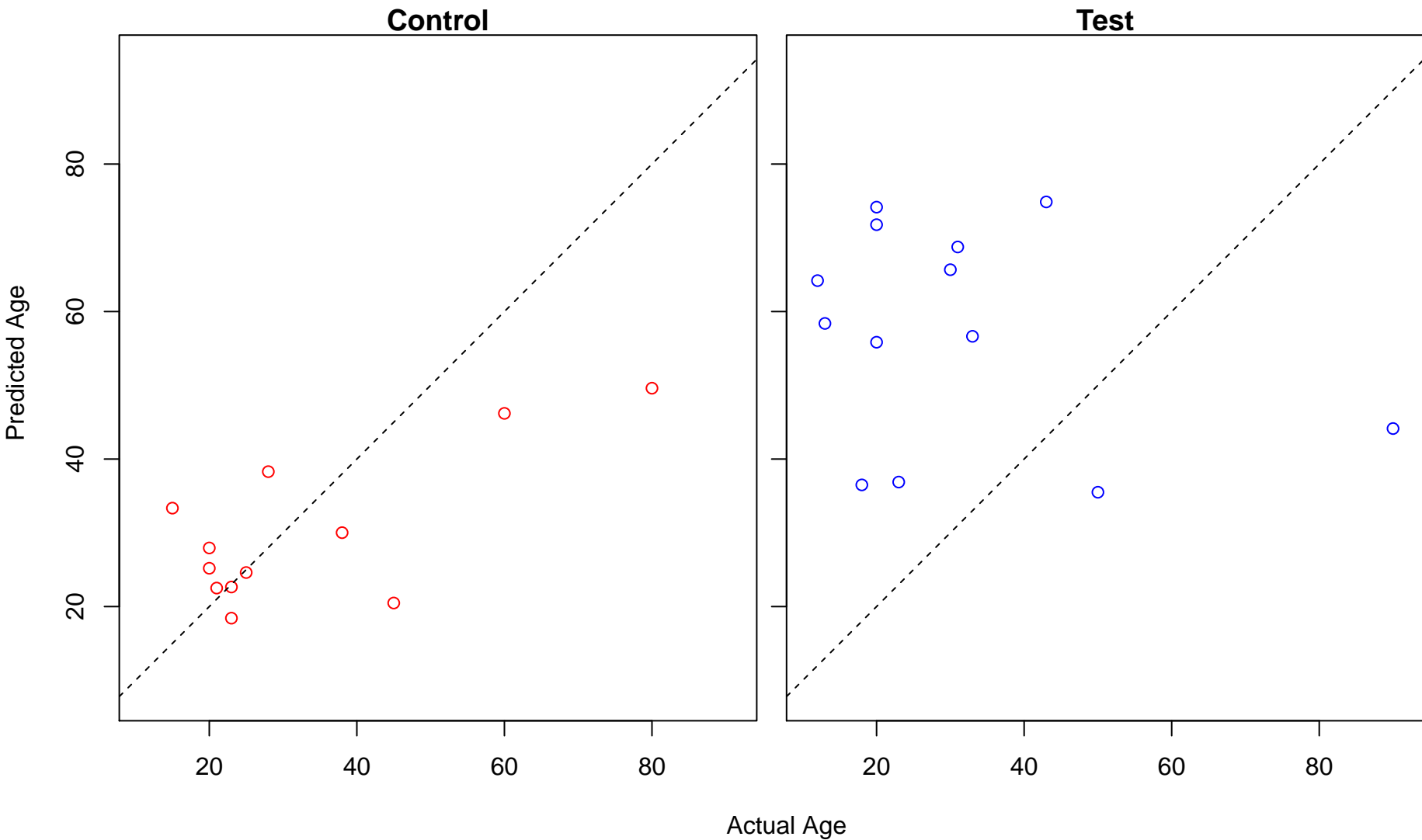
positive regulation of cell aging (Score: 3.162075)



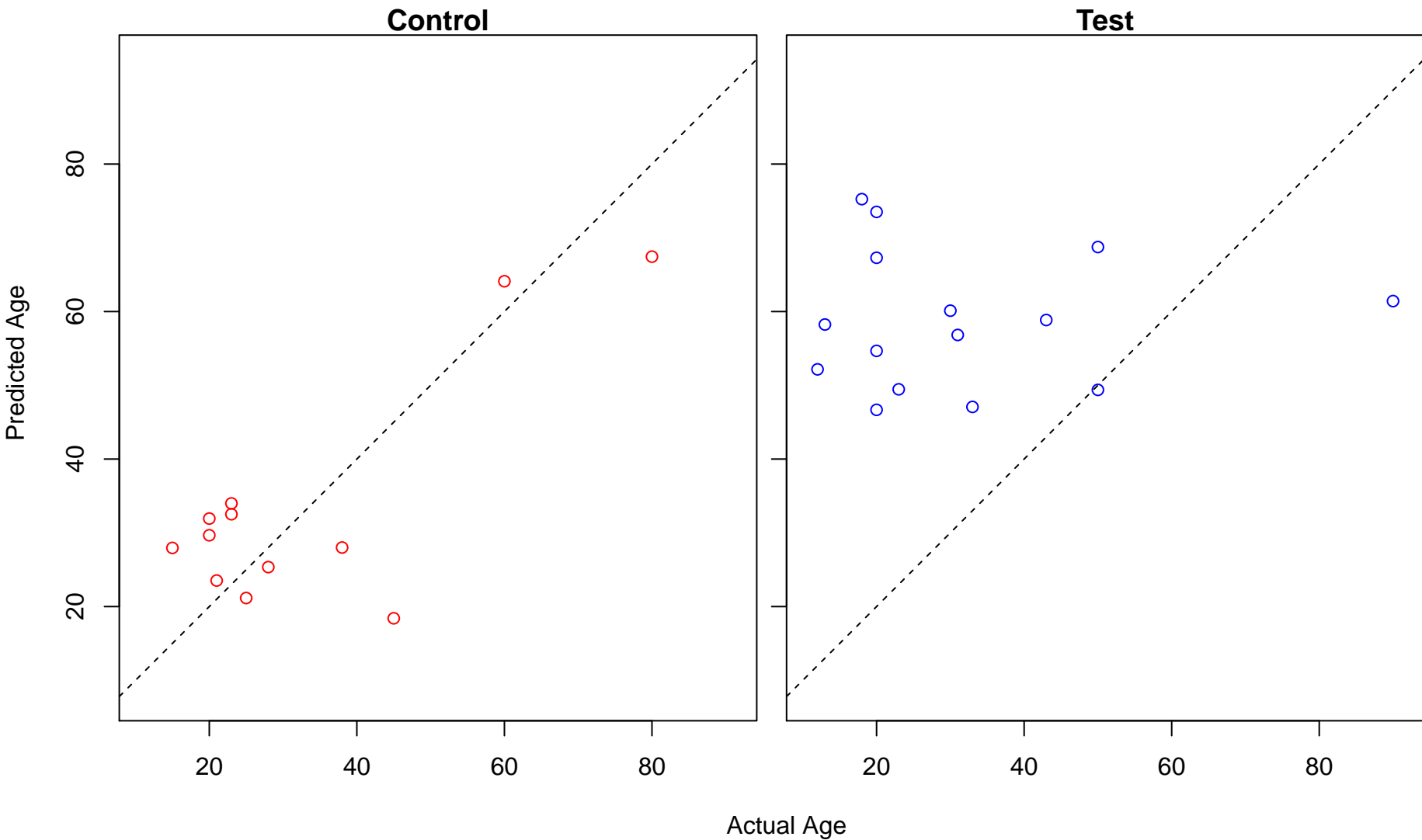
positive regulation of circadian rhythm (Score: 3.159826)



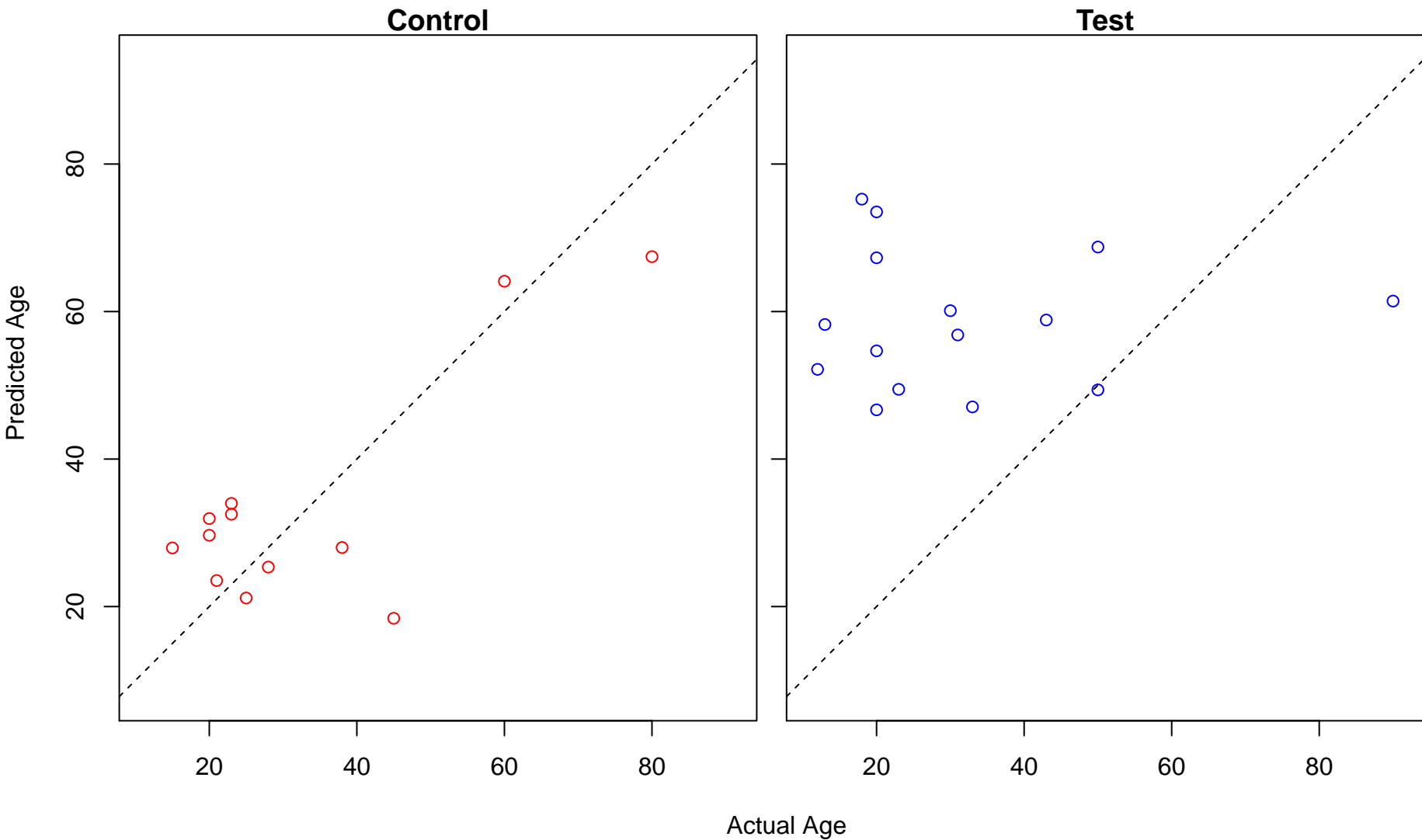
synaptic transmission, cholinergic (Score: 3.159537)



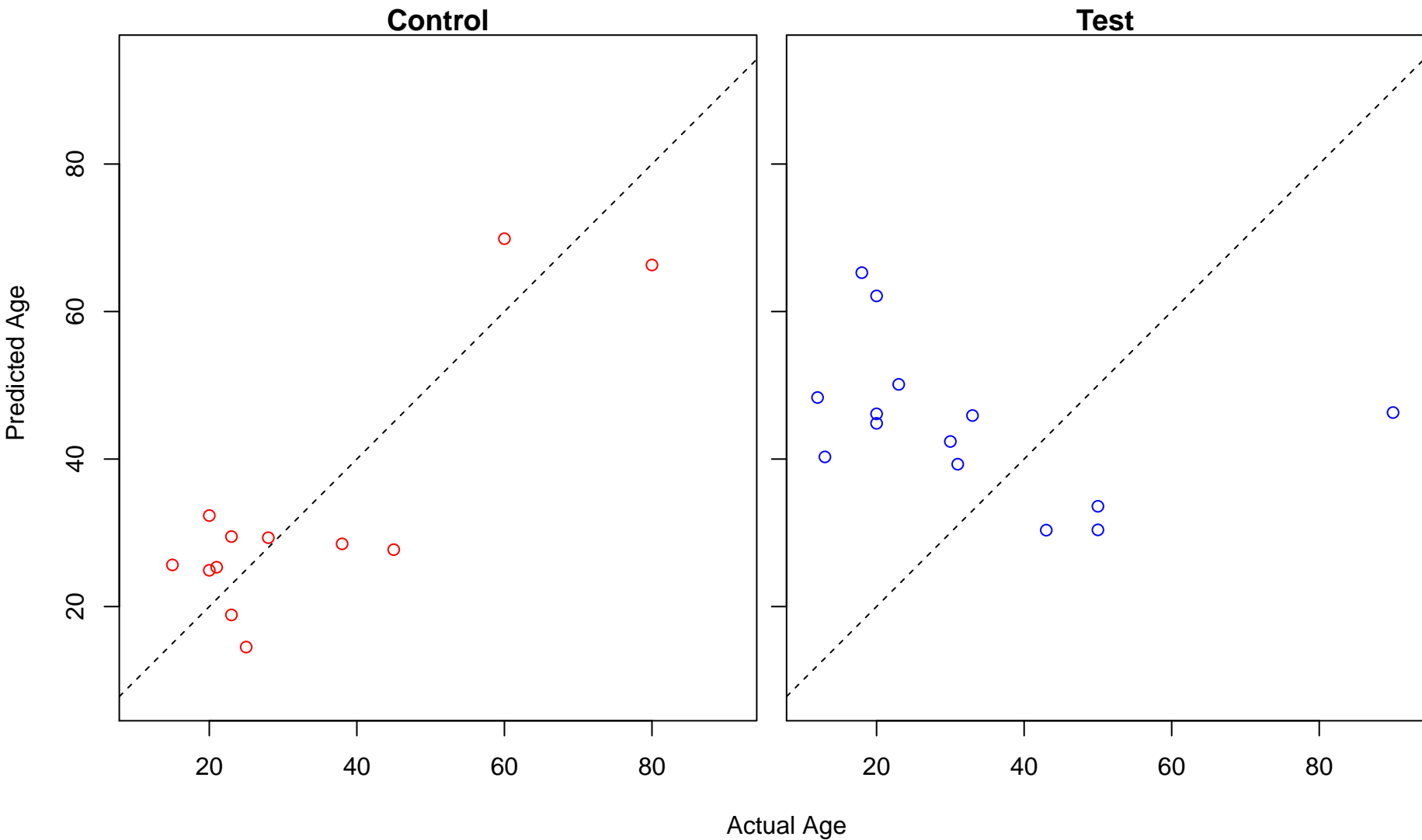
positive regulation of axon extension involved in axon guidance (Score: 3.159154)



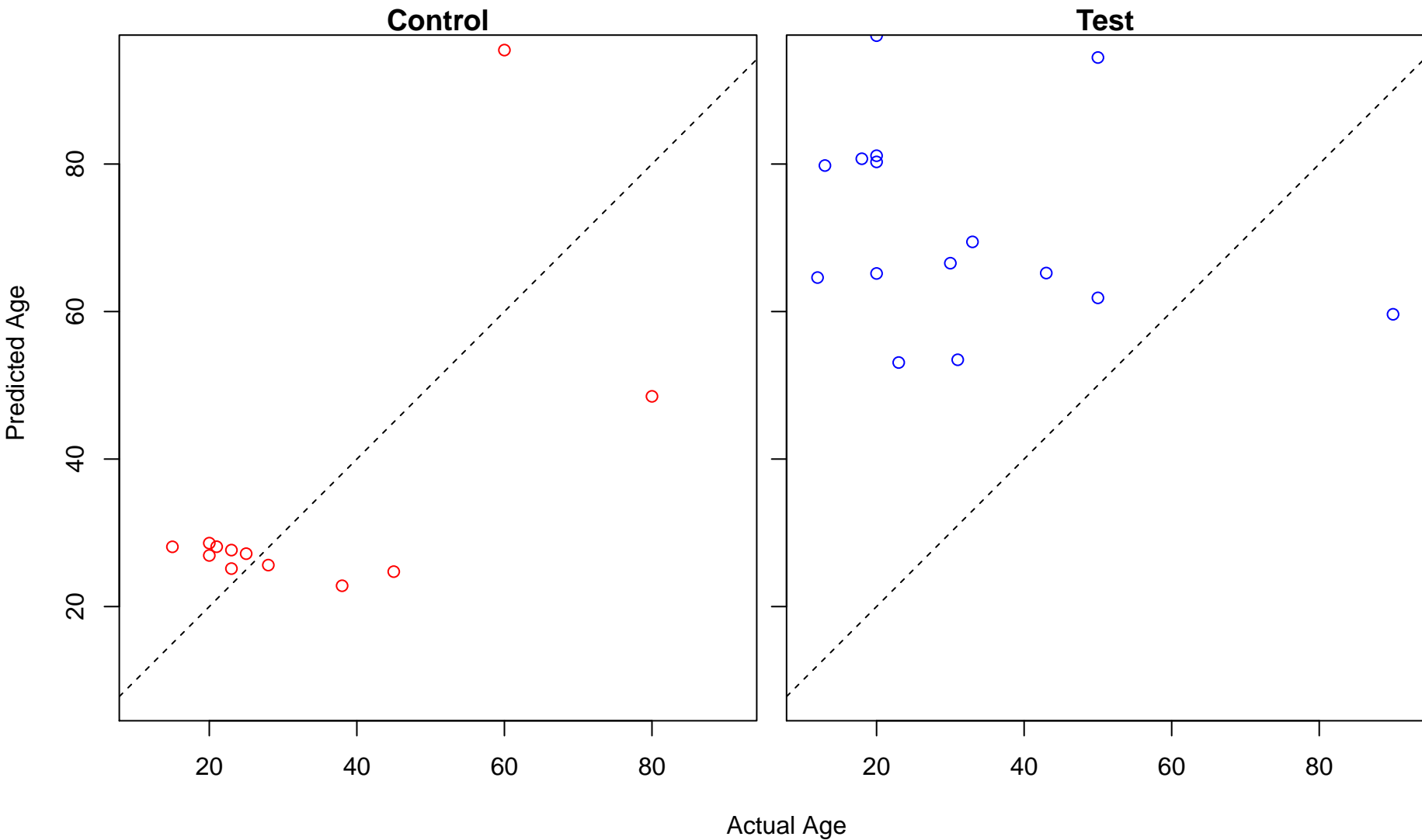
positive regulation of axon guidance (Score: 3.159154)



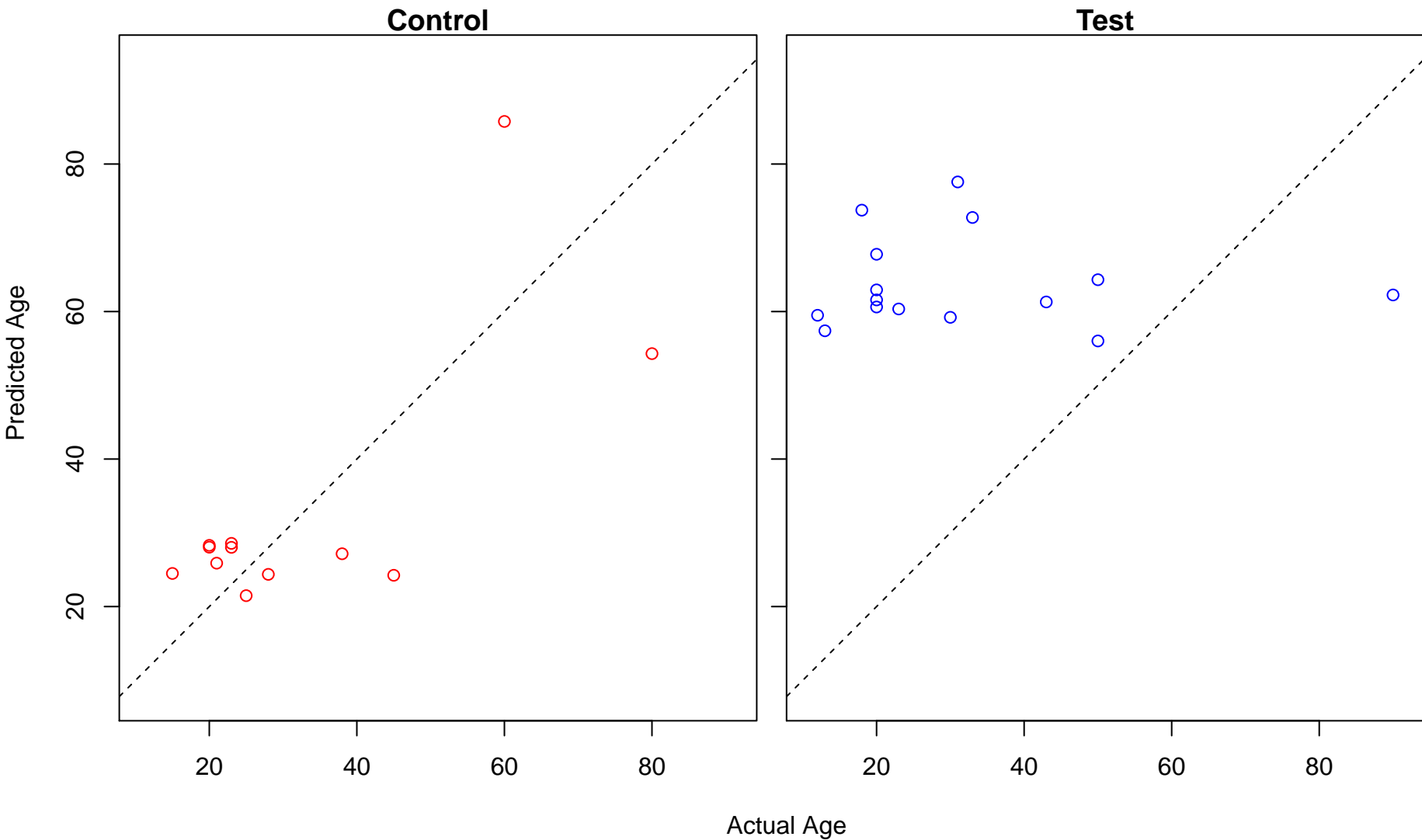
centriole replication (Score: 3.157401)



vacuolar acidification (Score: 3.155898)

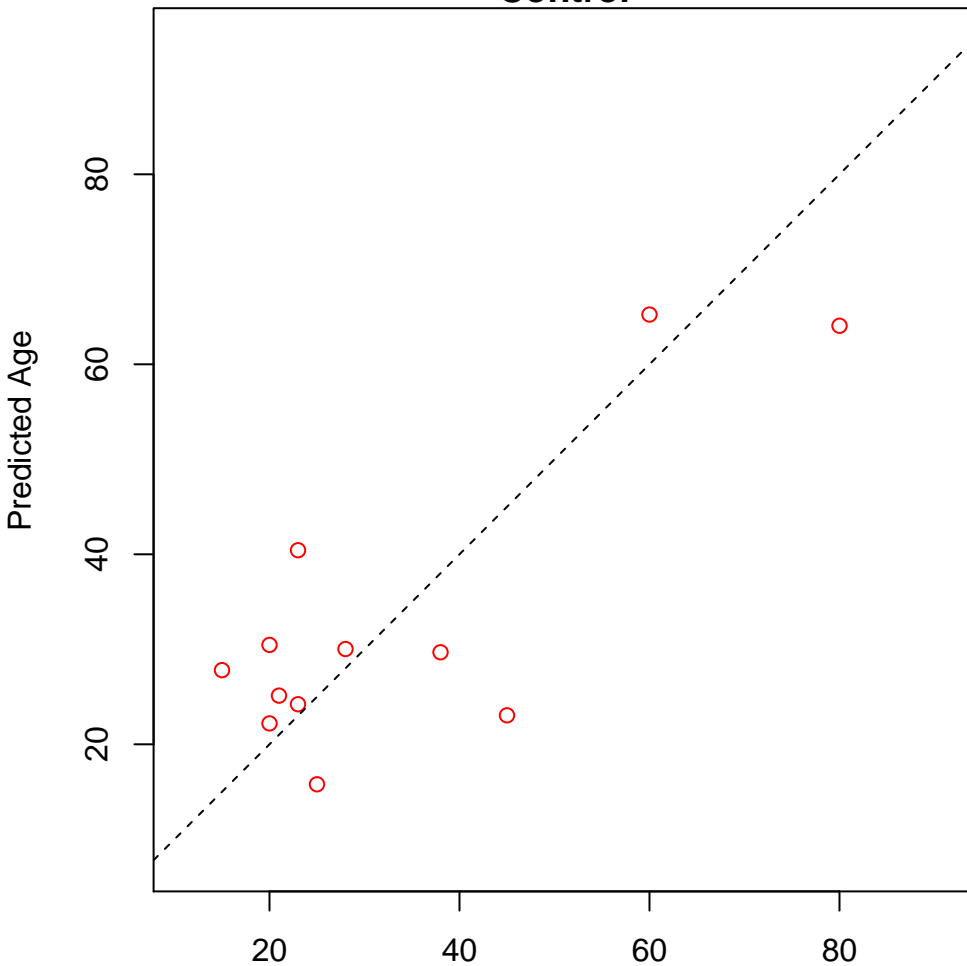


negative regulation of dendrite development (Score: 3.146059)

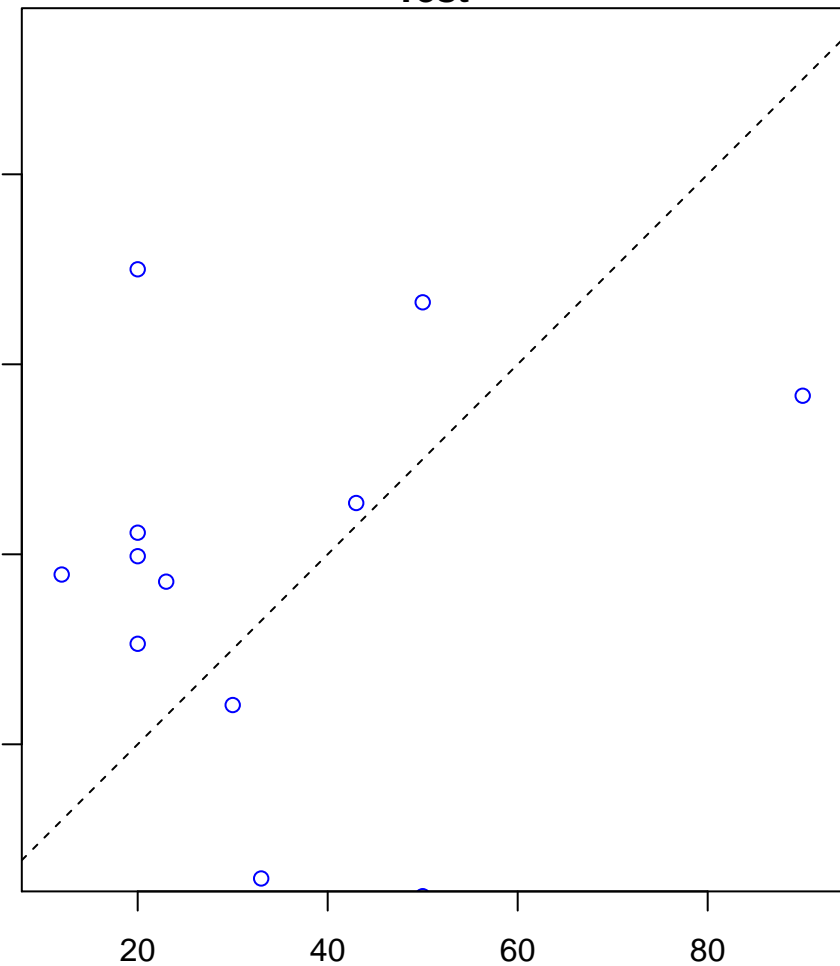


monovalent inorganic anion homeostasis (Score: 3.139387)

Control

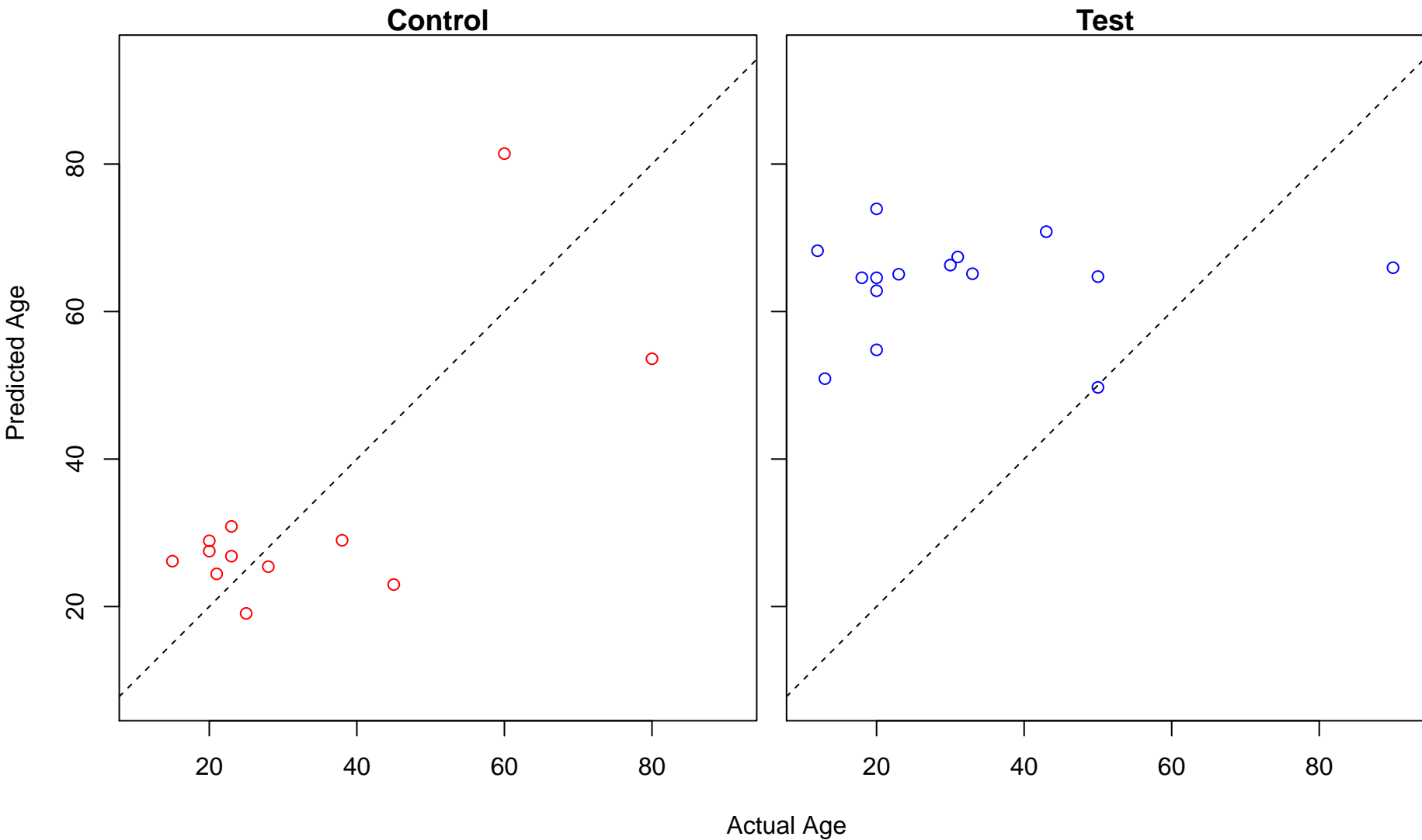


Test

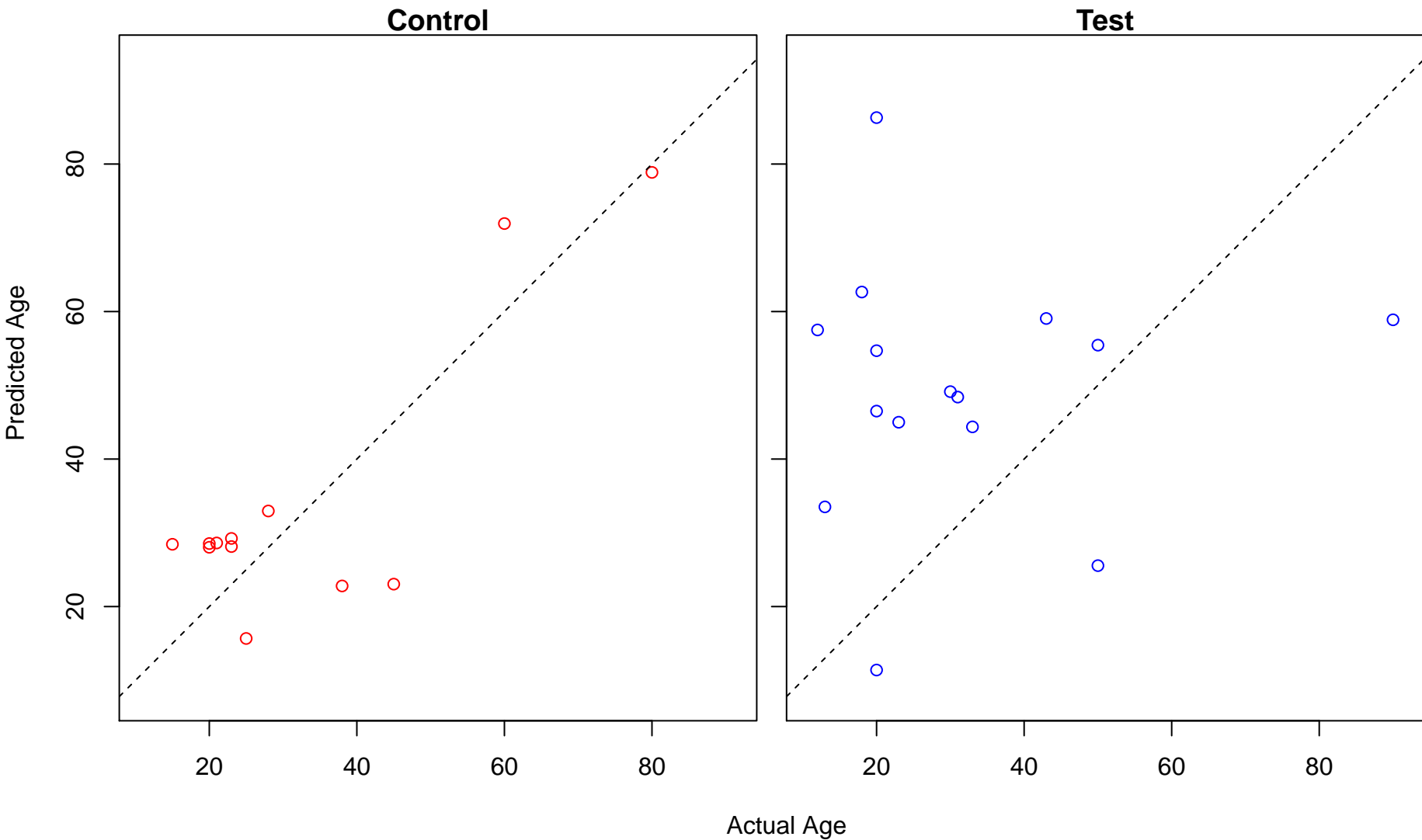


Actual Age

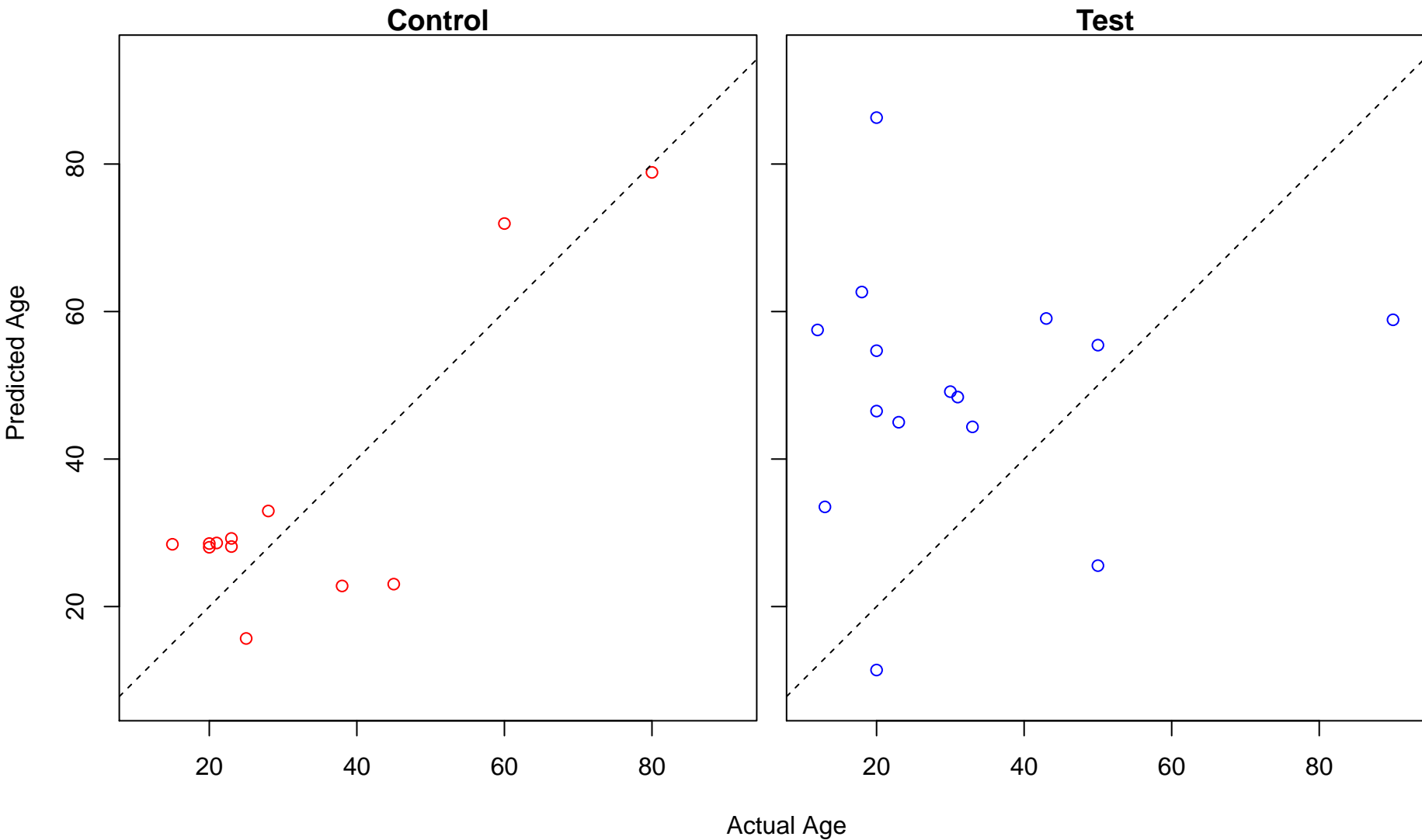
hindbrain morphogenesis (Score: 3.136788)



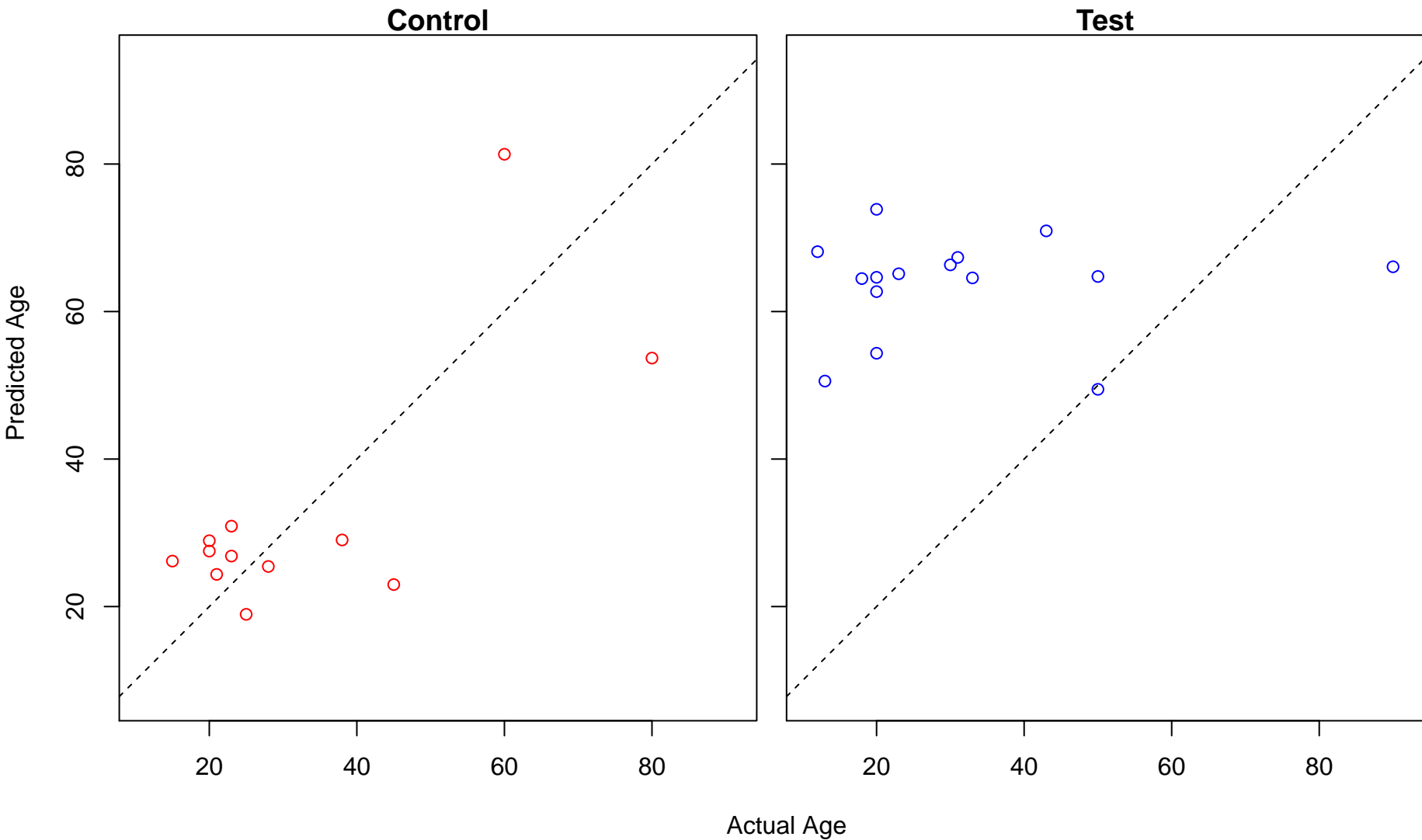
electron transport chain (Score: 3.136395)



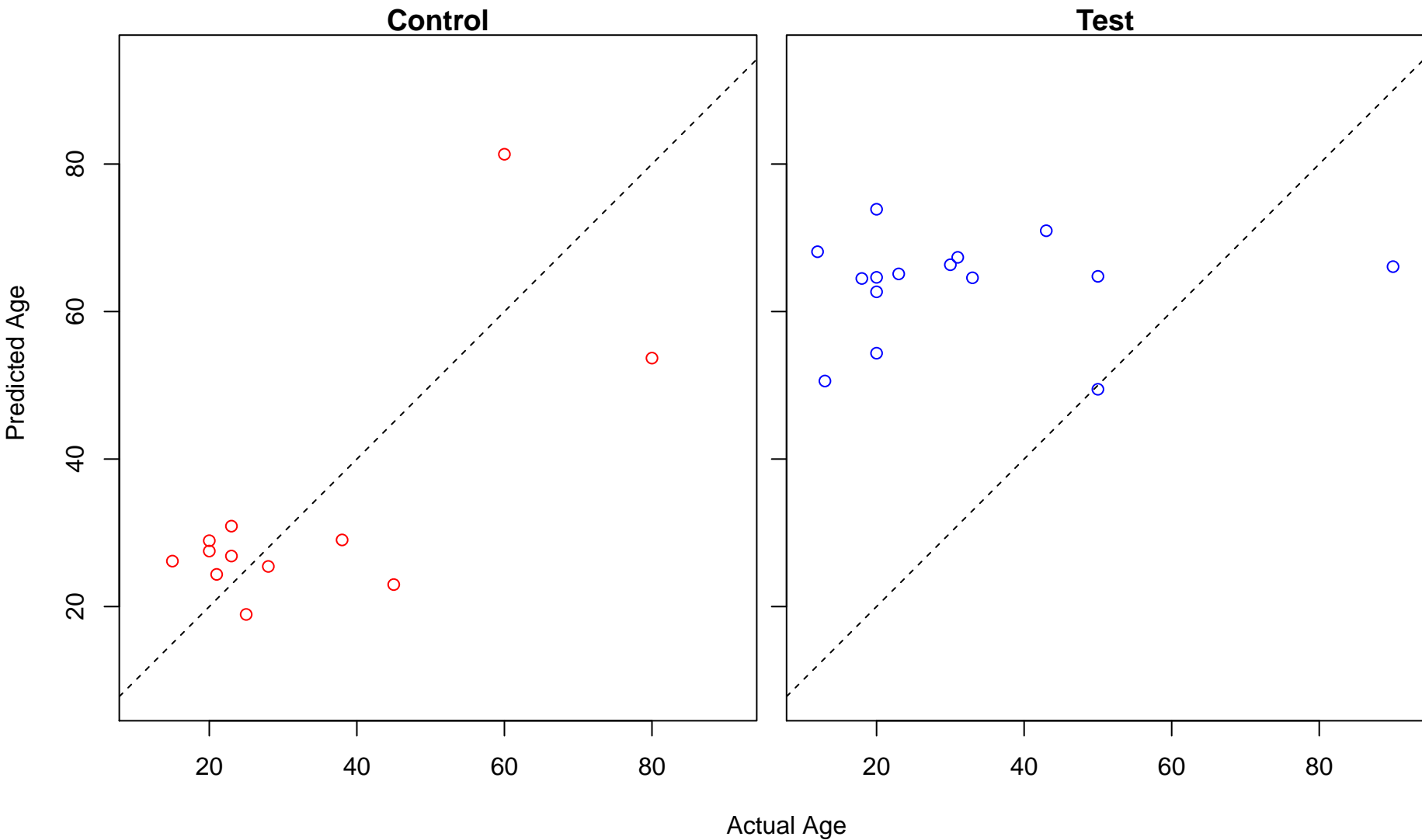
respiratory electron transport chain (Score: 3.136395)



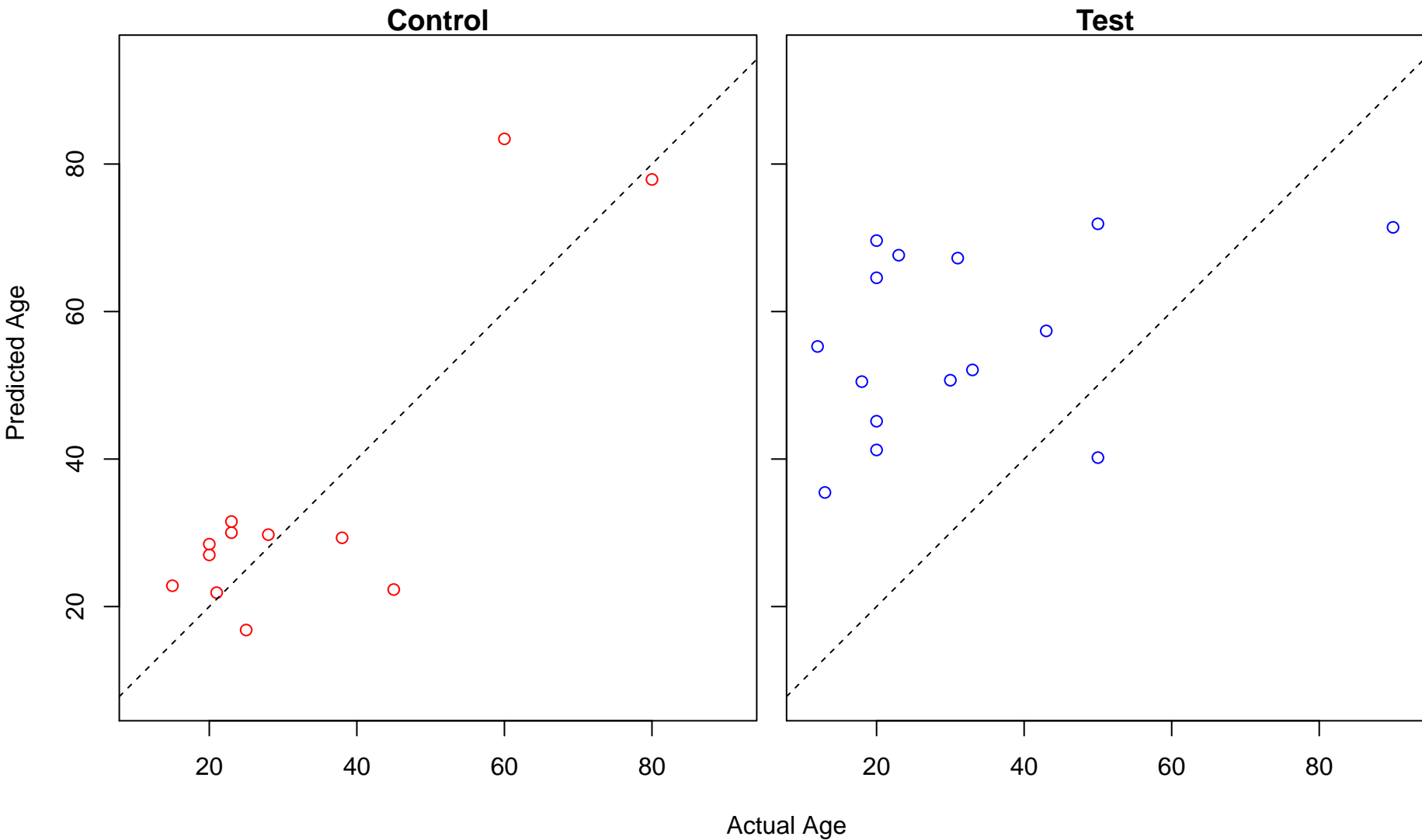
cerebellum morphogenesis (Score: 3.132920)



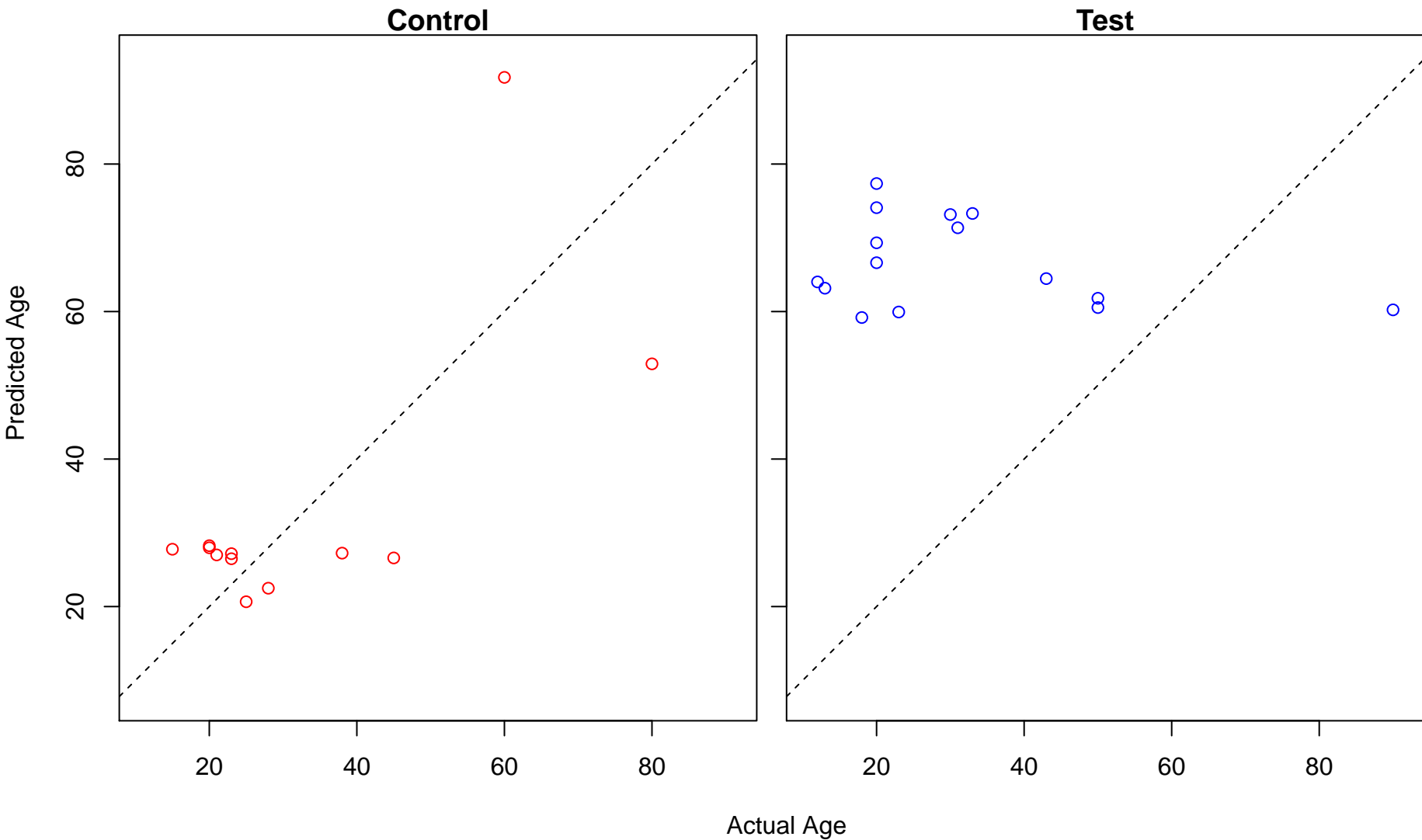
cerebellar cortex morphogenesis (Score: 3.132740)



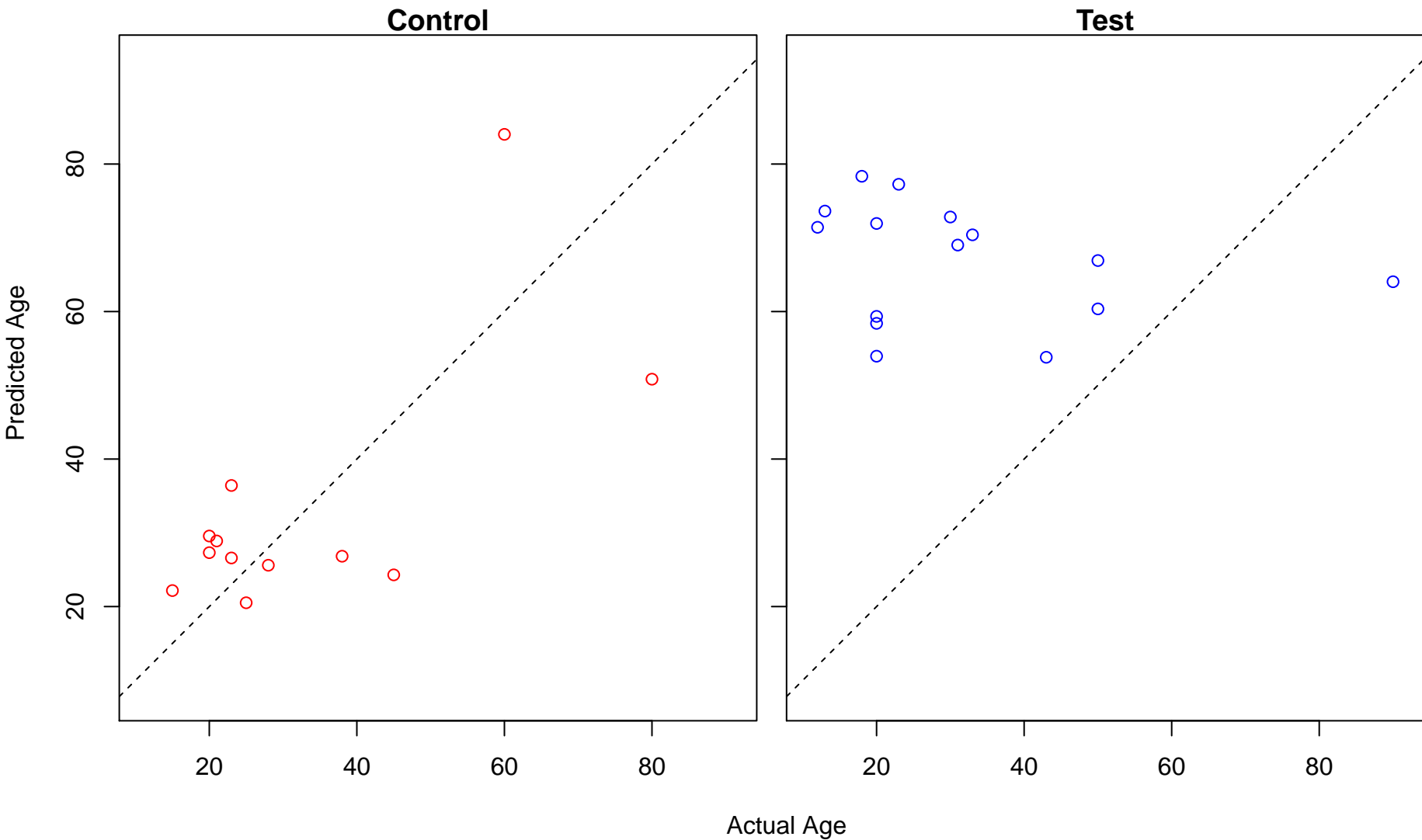
primary miRNA processing (Score: 3.126884)



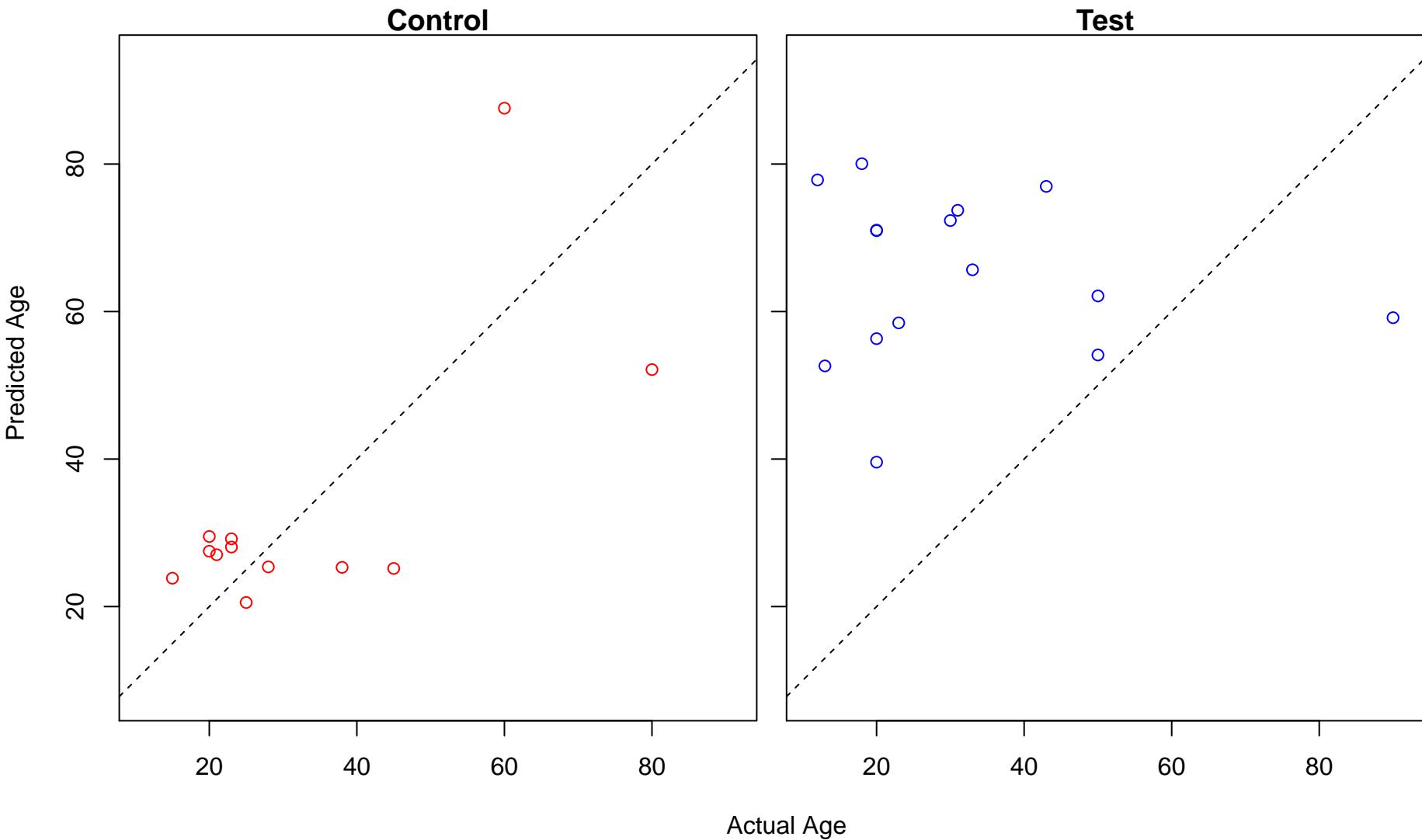
actin filament capping (Score: 3.122838)



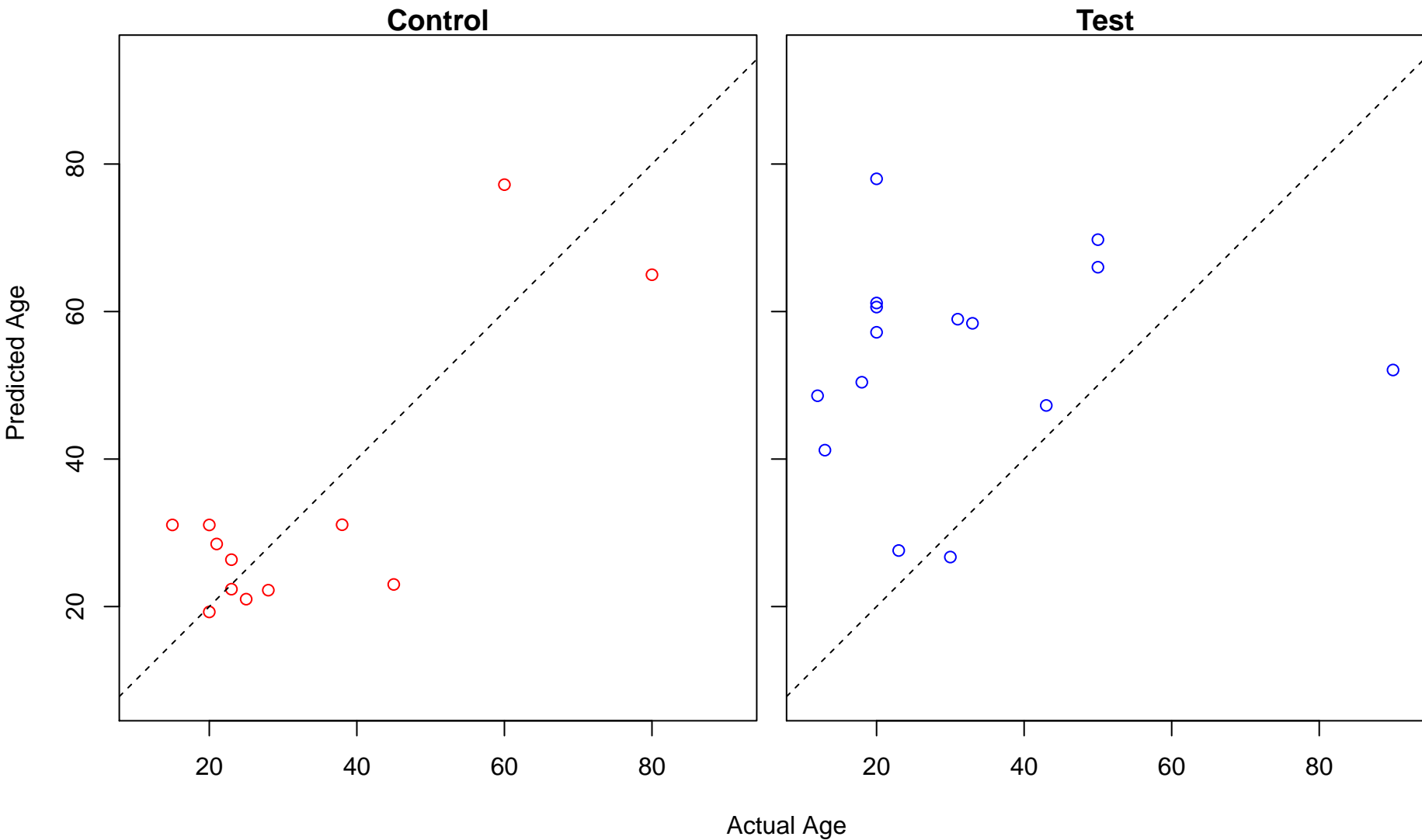
regulation of dendritic cell antigen processing and presentation (Score: 3.116374)



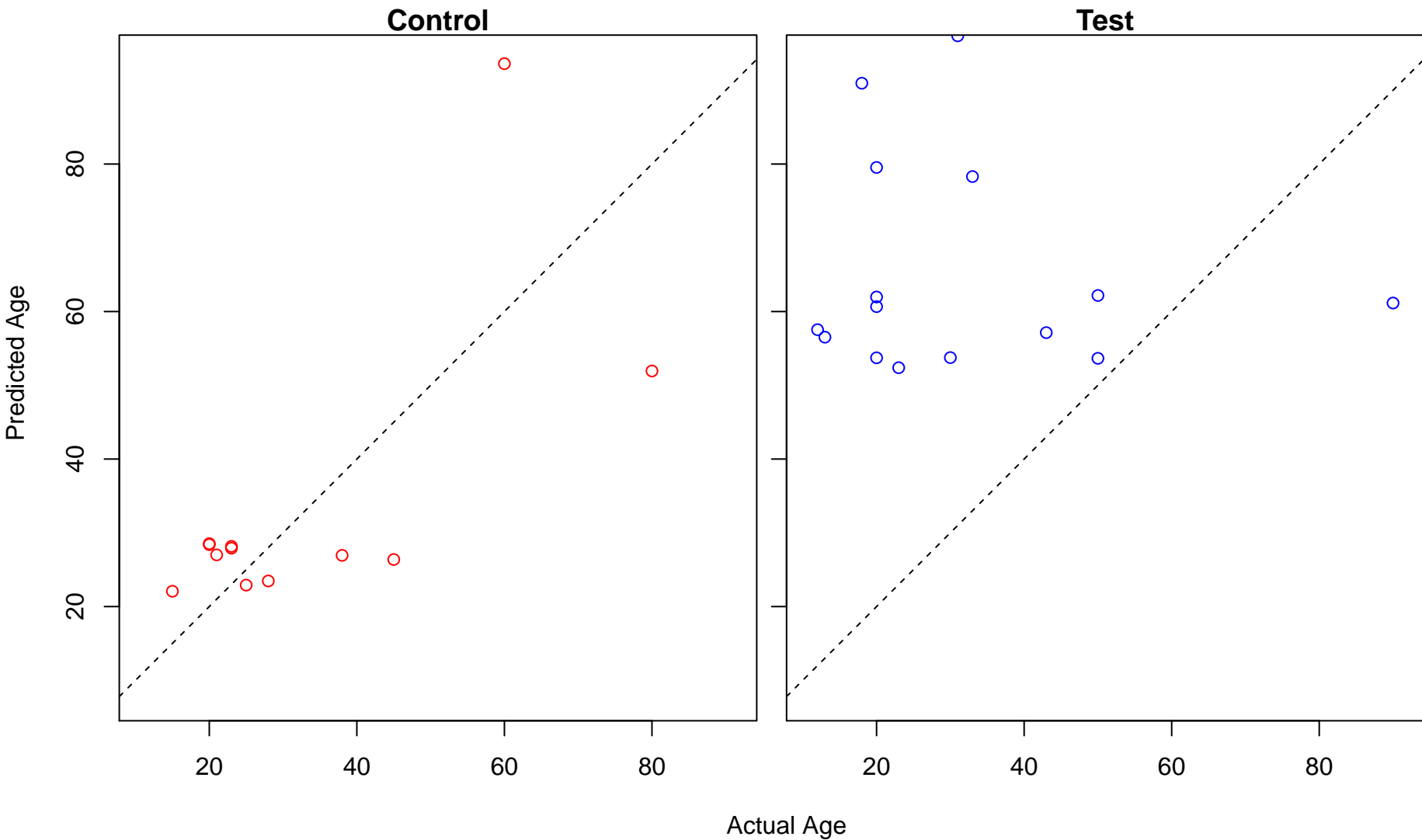
neutrophil mediated immunity (Score: 3.116076)



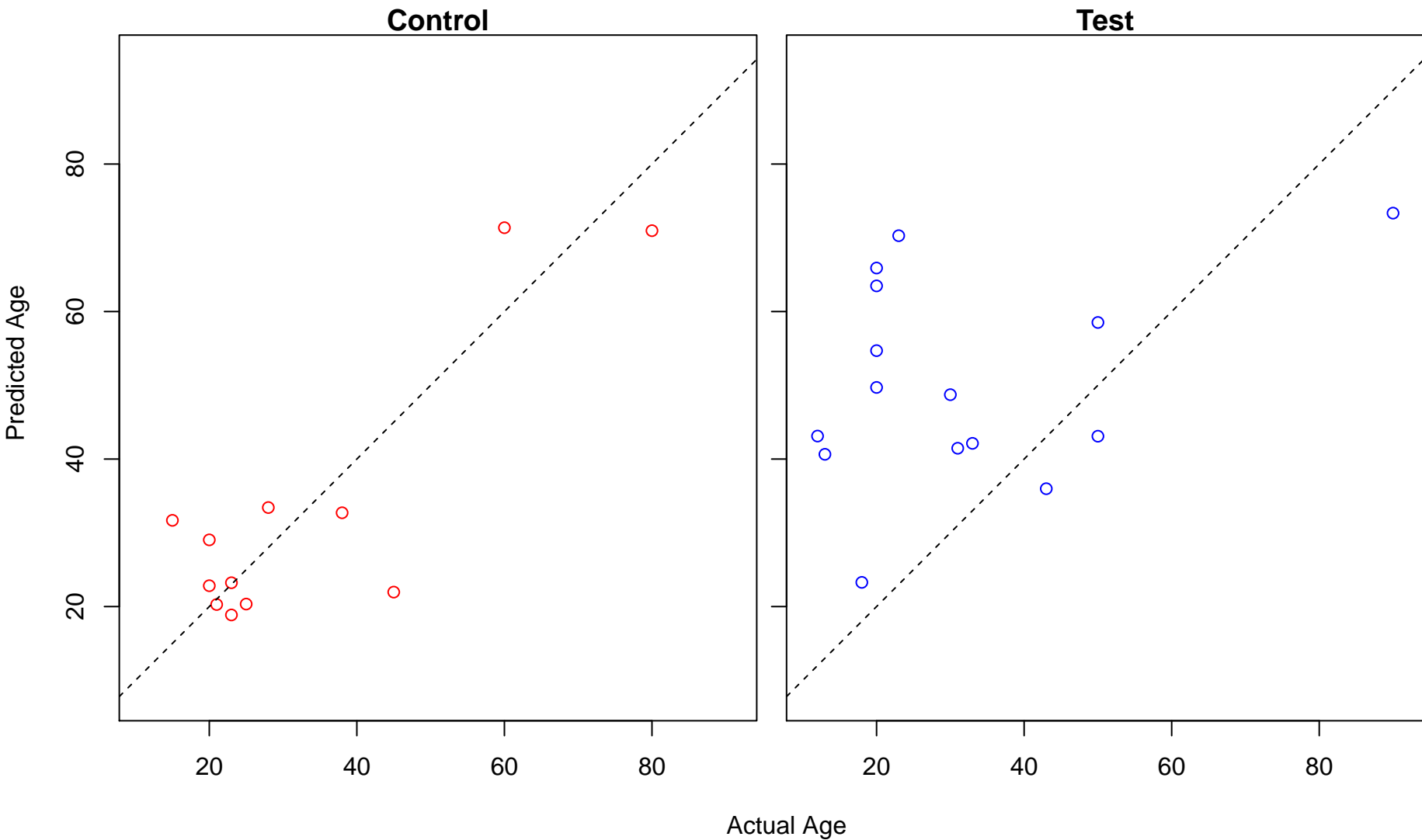
regulation of intracellular estrogen receptor signaling pathway (Score: 3.113284)



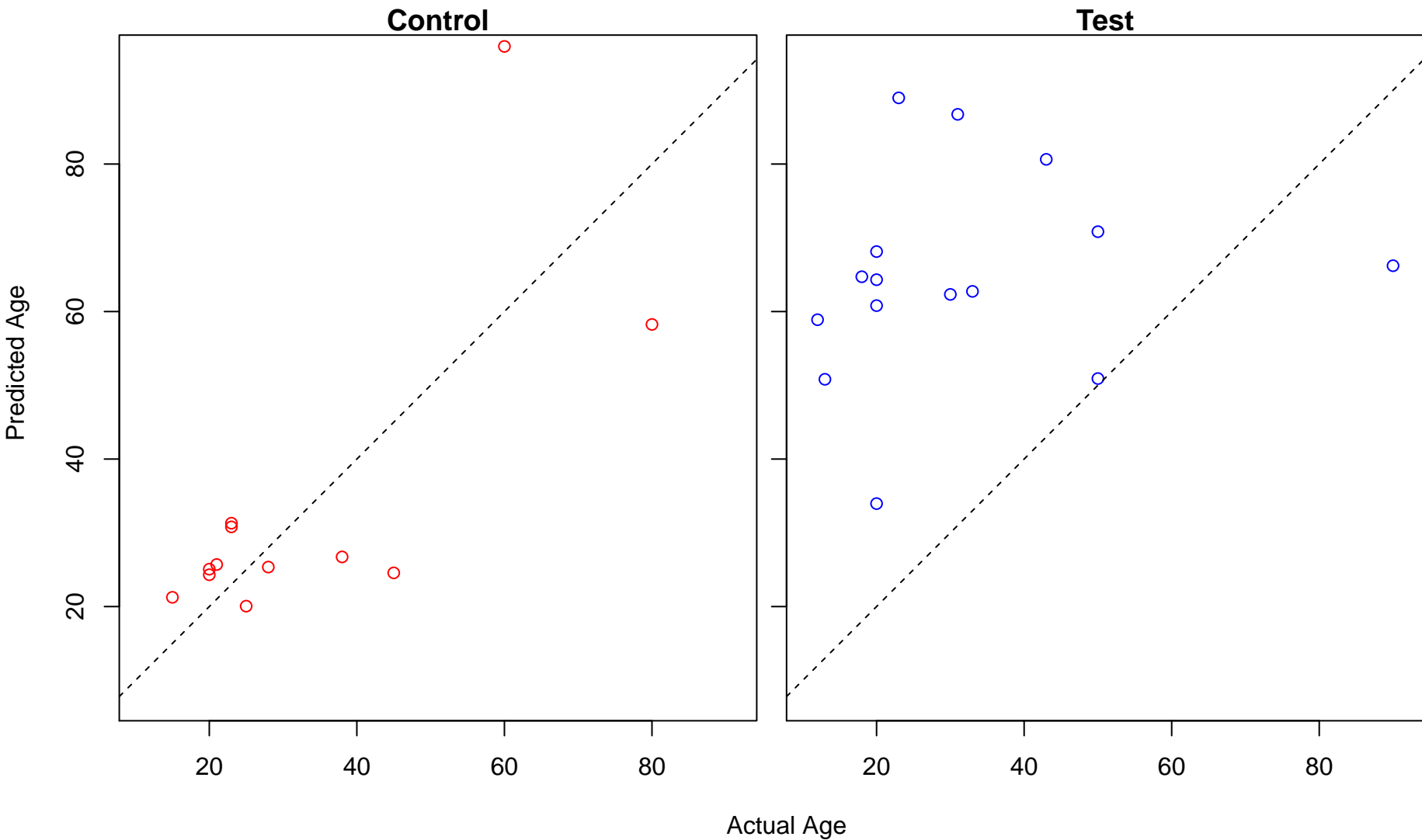
multicellular organismal response to stress (Score: 3.111068)



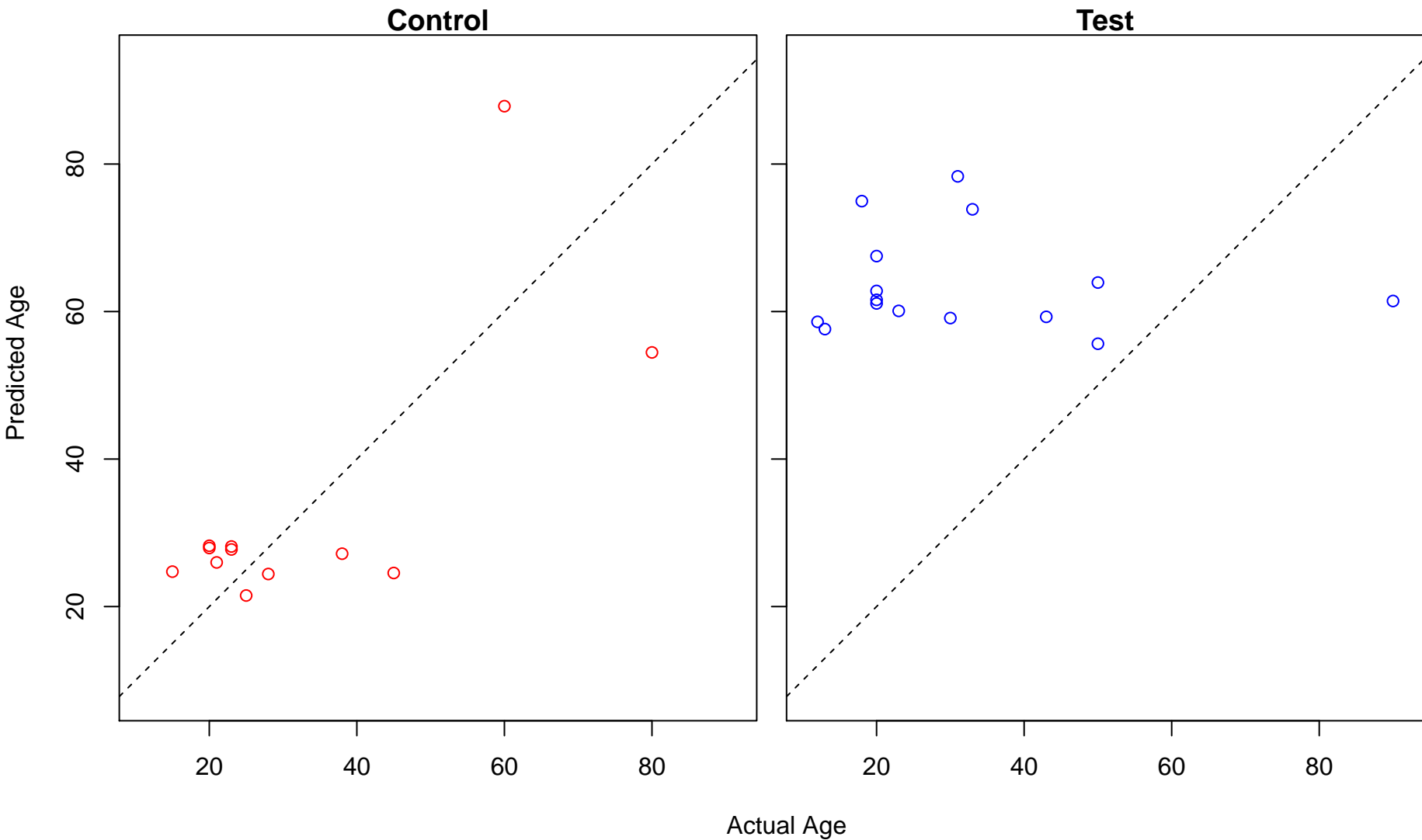
negative regulation of osteoblast differentiation (Score: 3.105590)



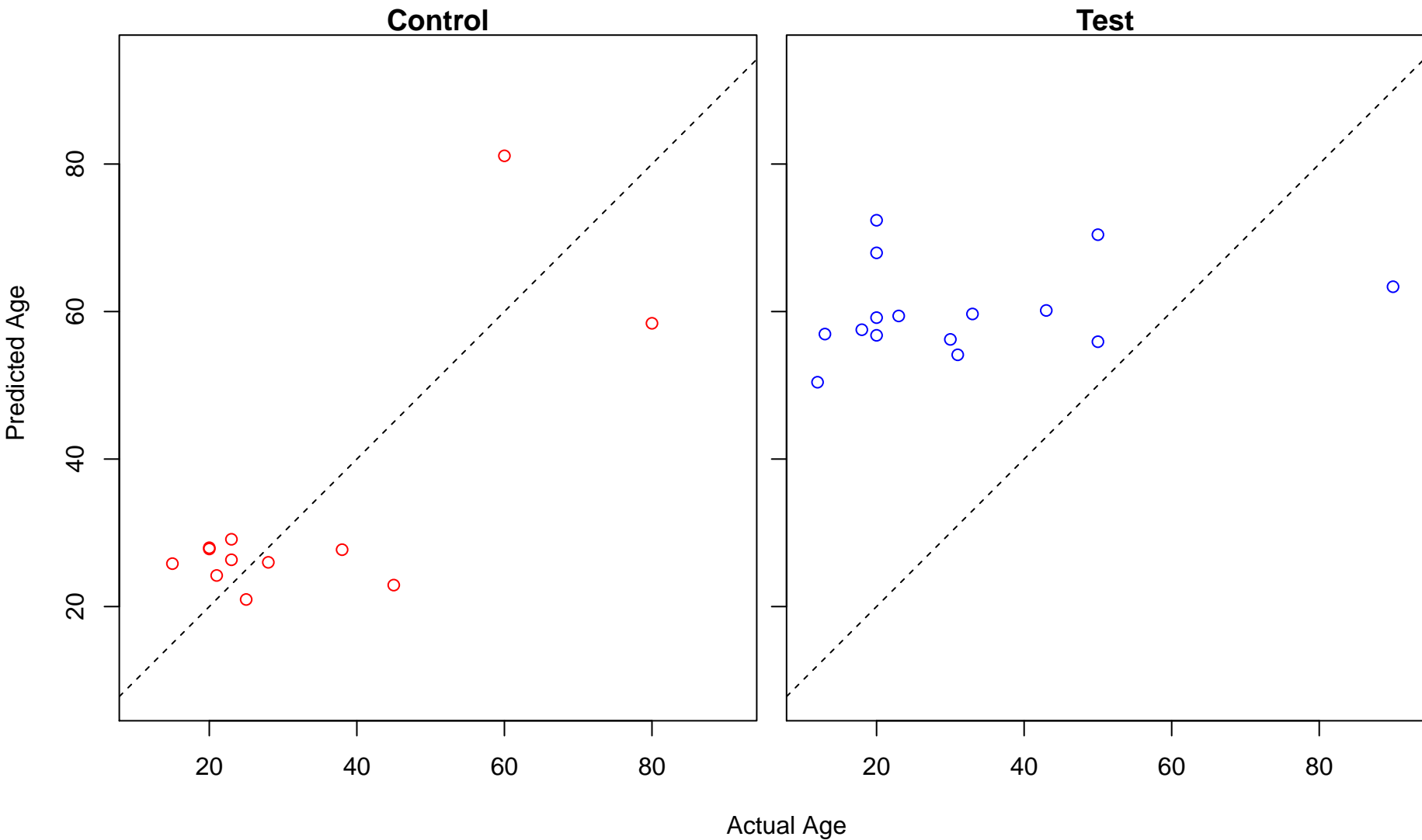
negative regulation of muscle tissue development (Score: 3.102058)



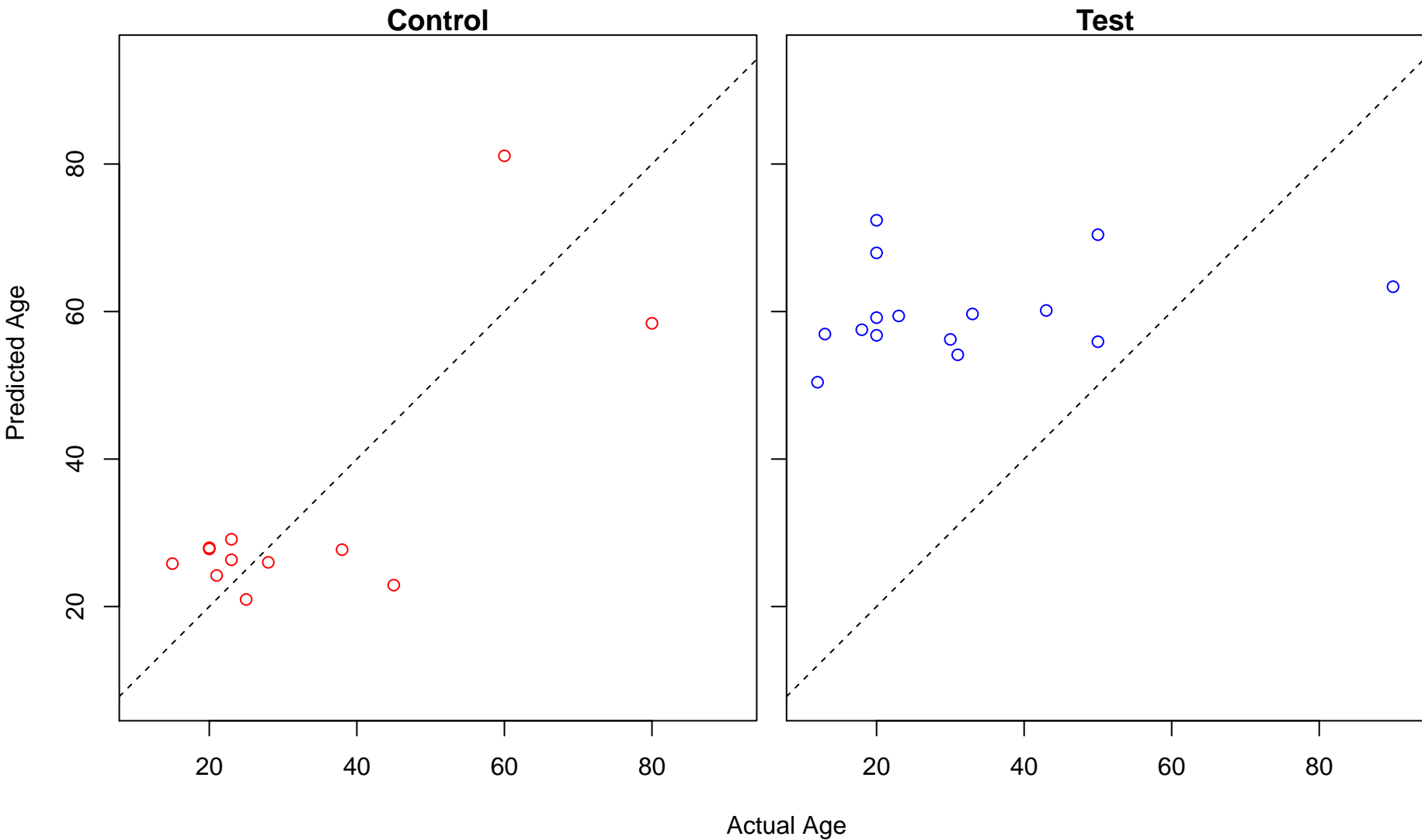
negative regulation of dendrite morphogenesis (Score: 3.099226)



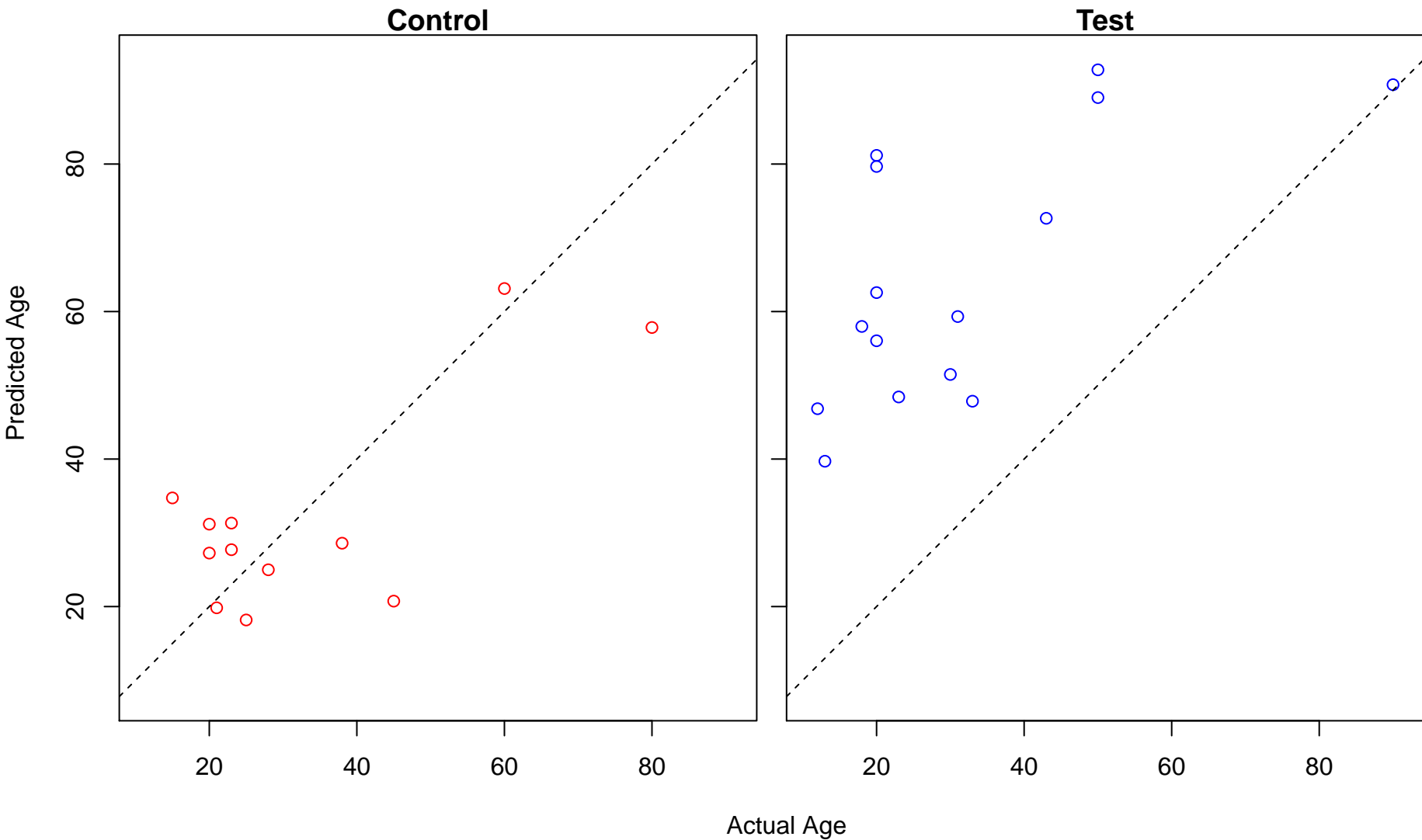
negative regulation of protein localization to plasma membrane (Score: 3.098249)



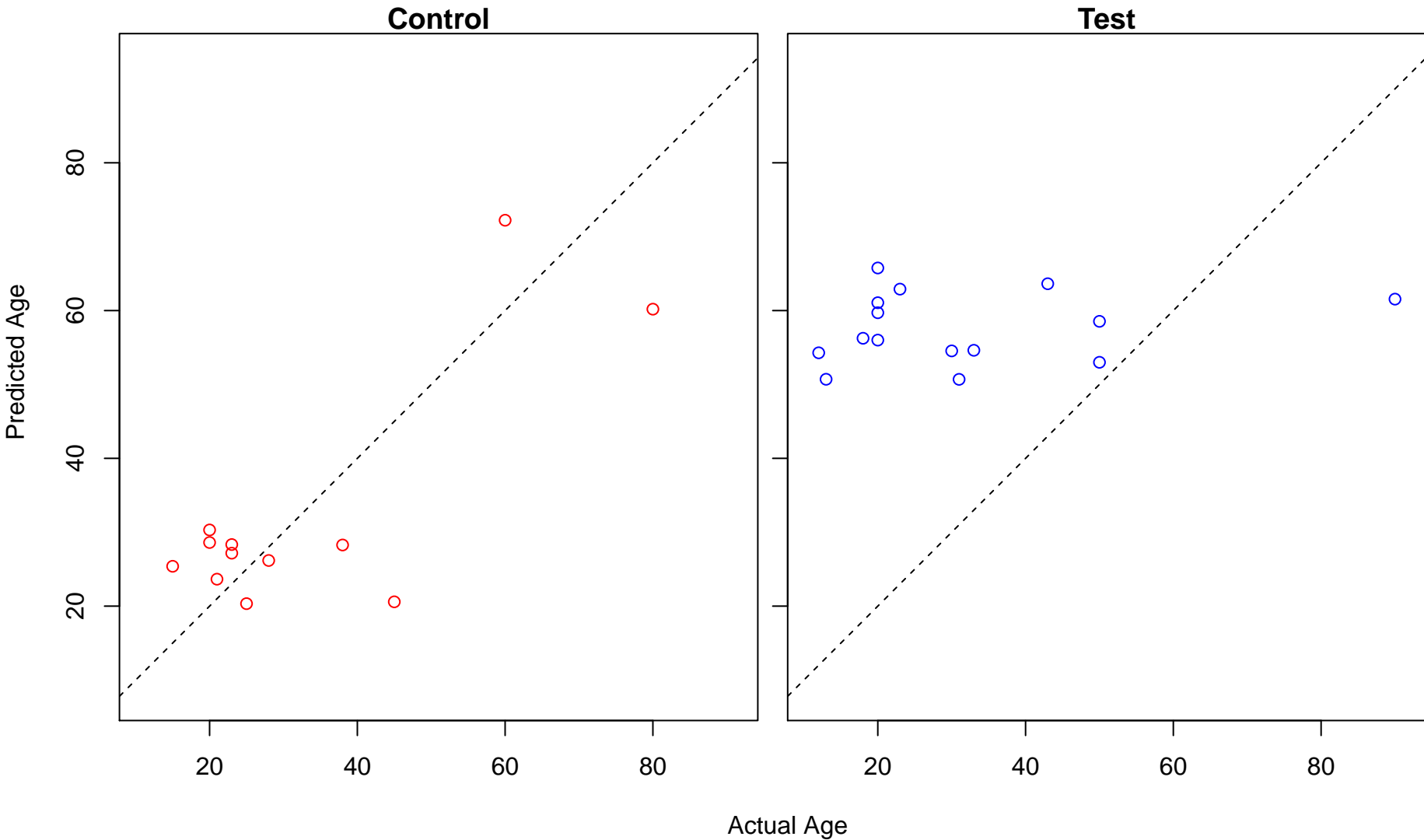
negative regulation of protein localization to cell periphery (Score: 3.098249)



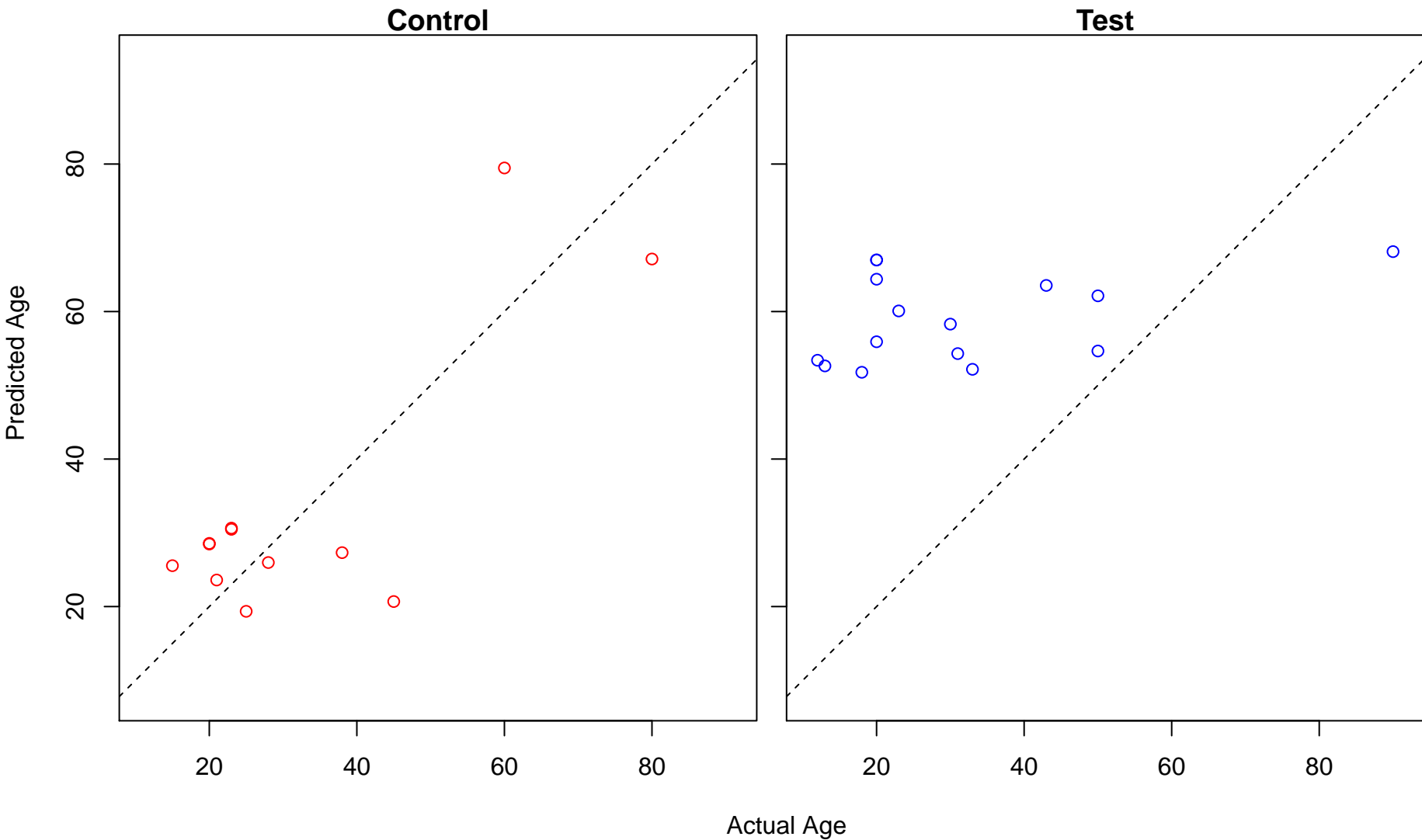
cell-substrate junction assembly (Score: 3.096024)



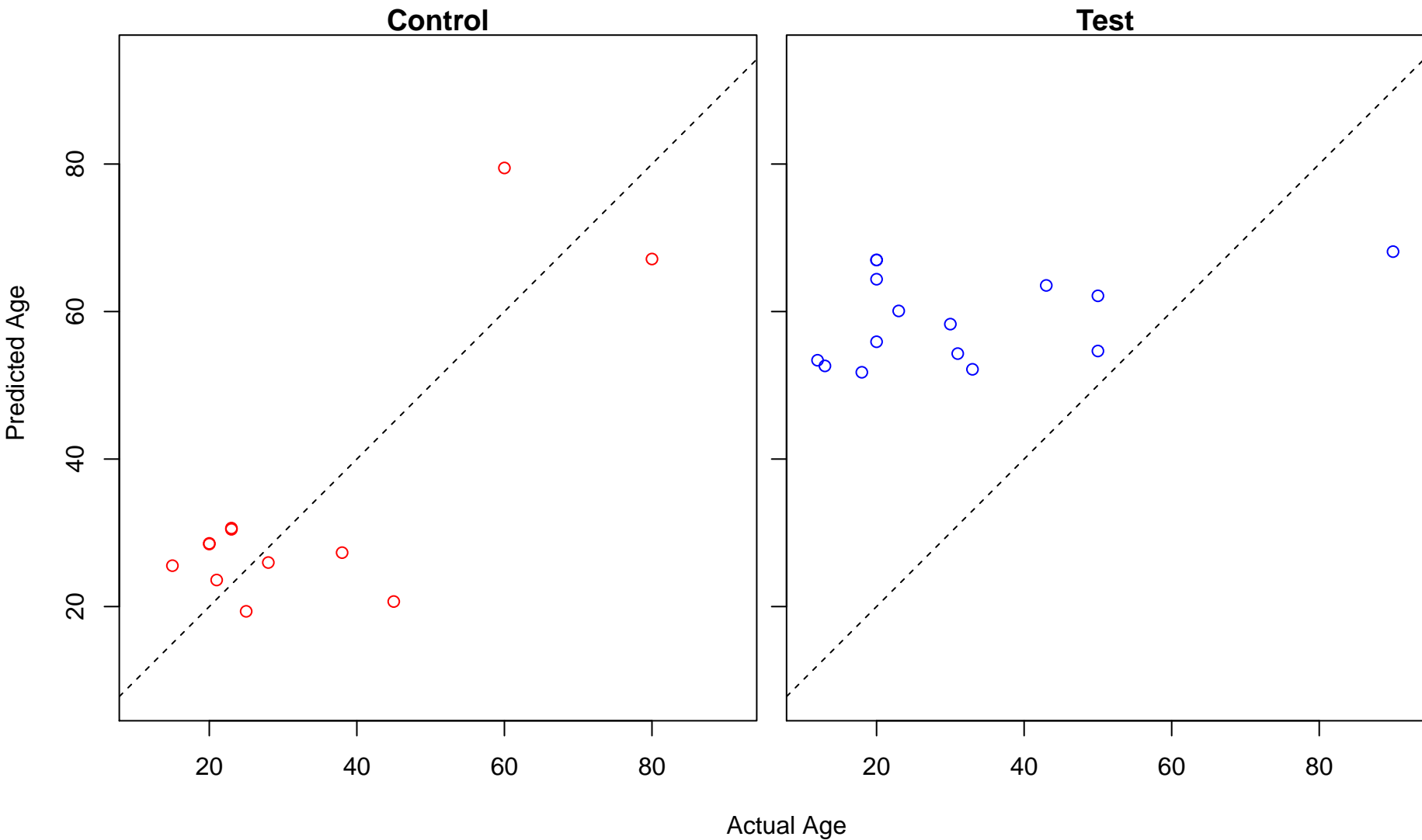
regulation of receptor biosynthetic process (Score: 3.091568)



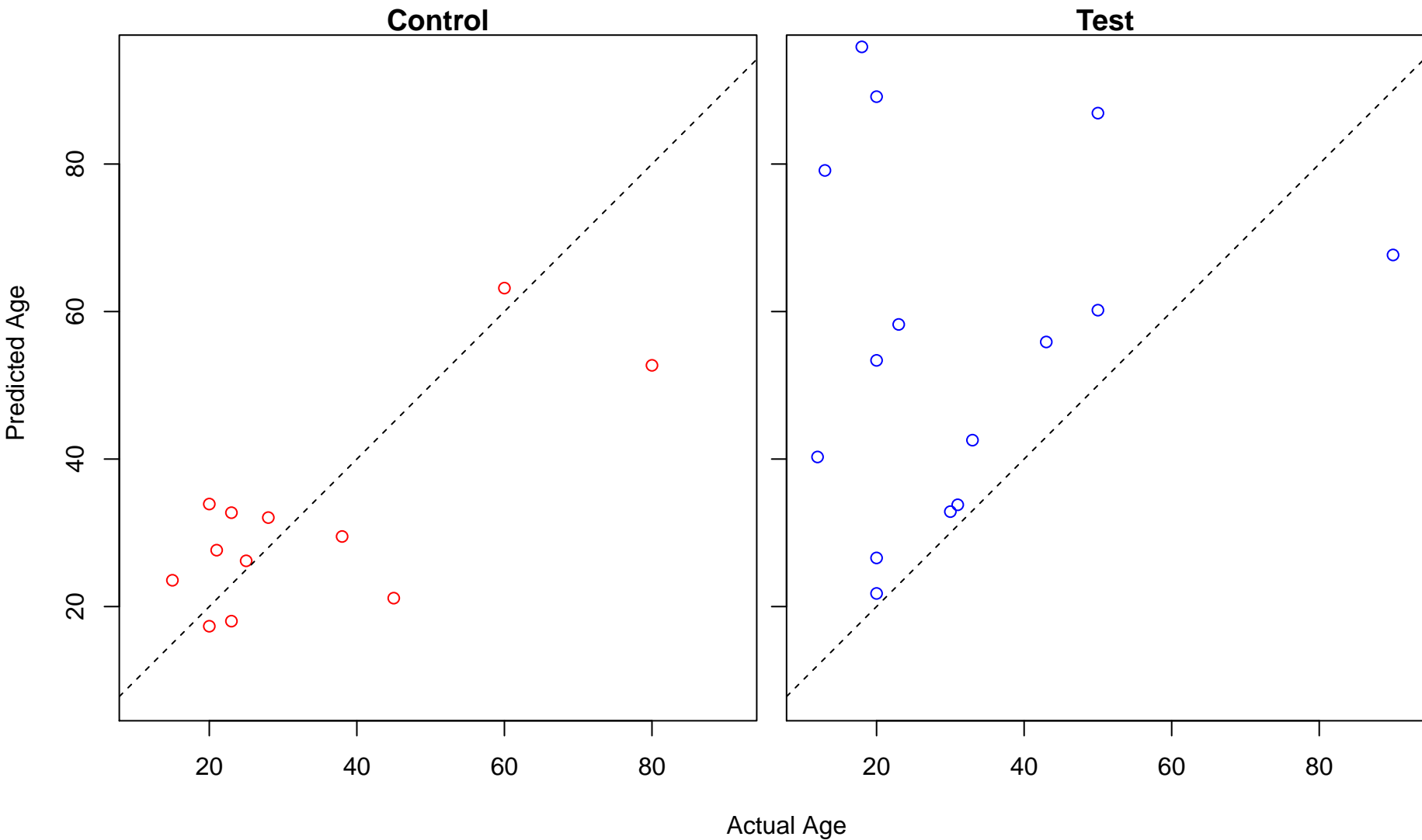
regulation of nucleoside metabolic process (Score: 3.089665)



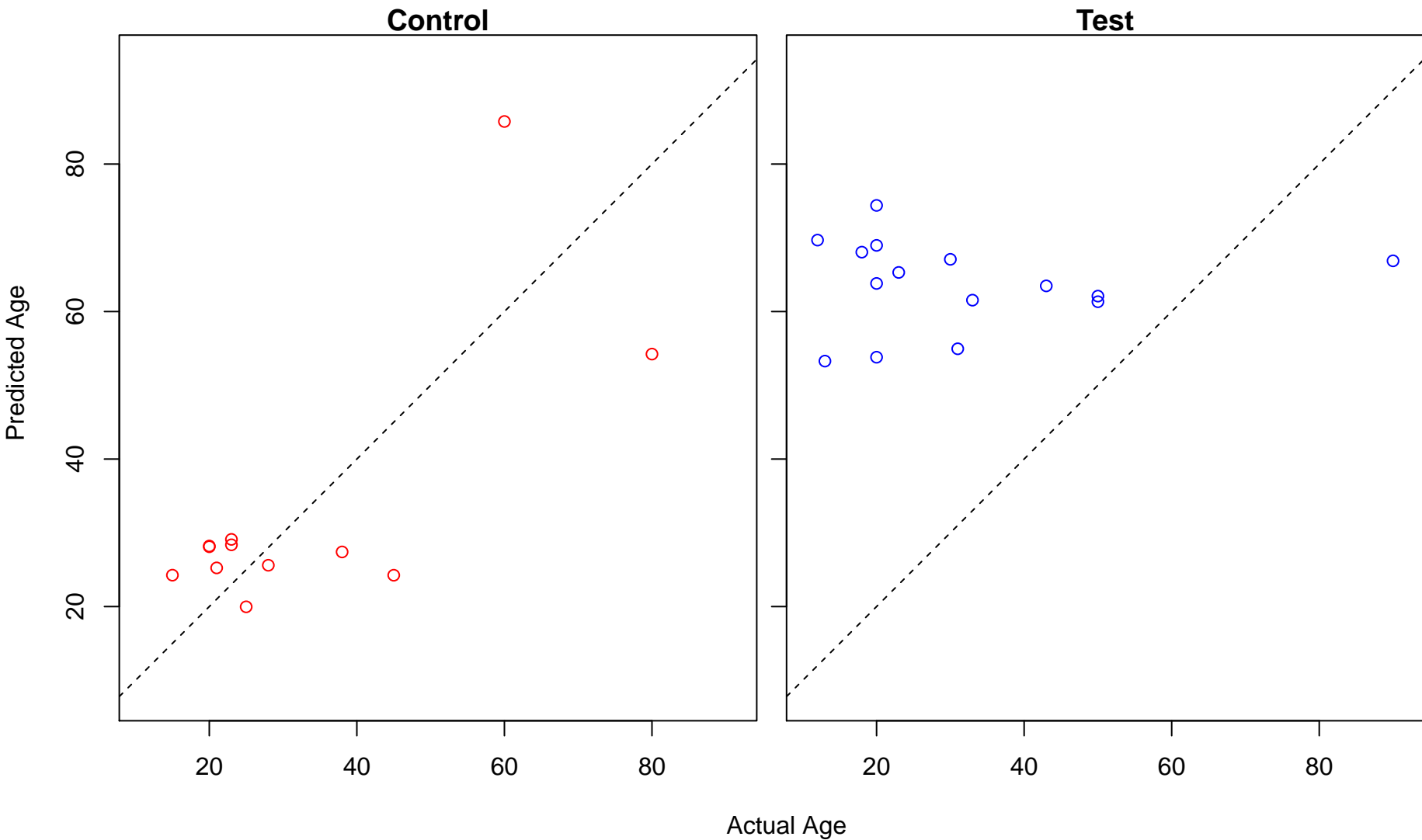
regulation of ATP metabolic process (Score: 3.089665)



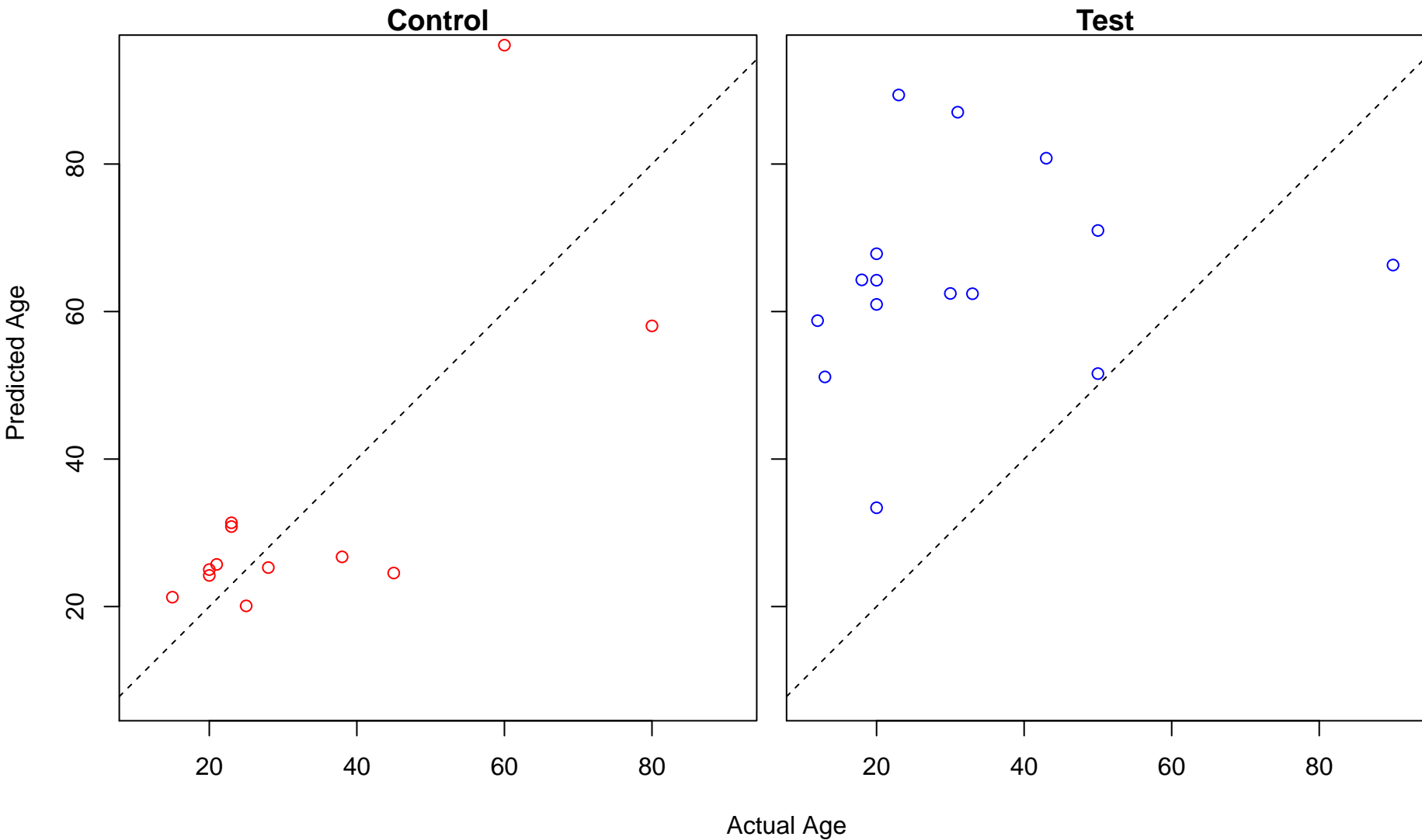
regulation of protein heterodimerization activity (Score: 3.088466)



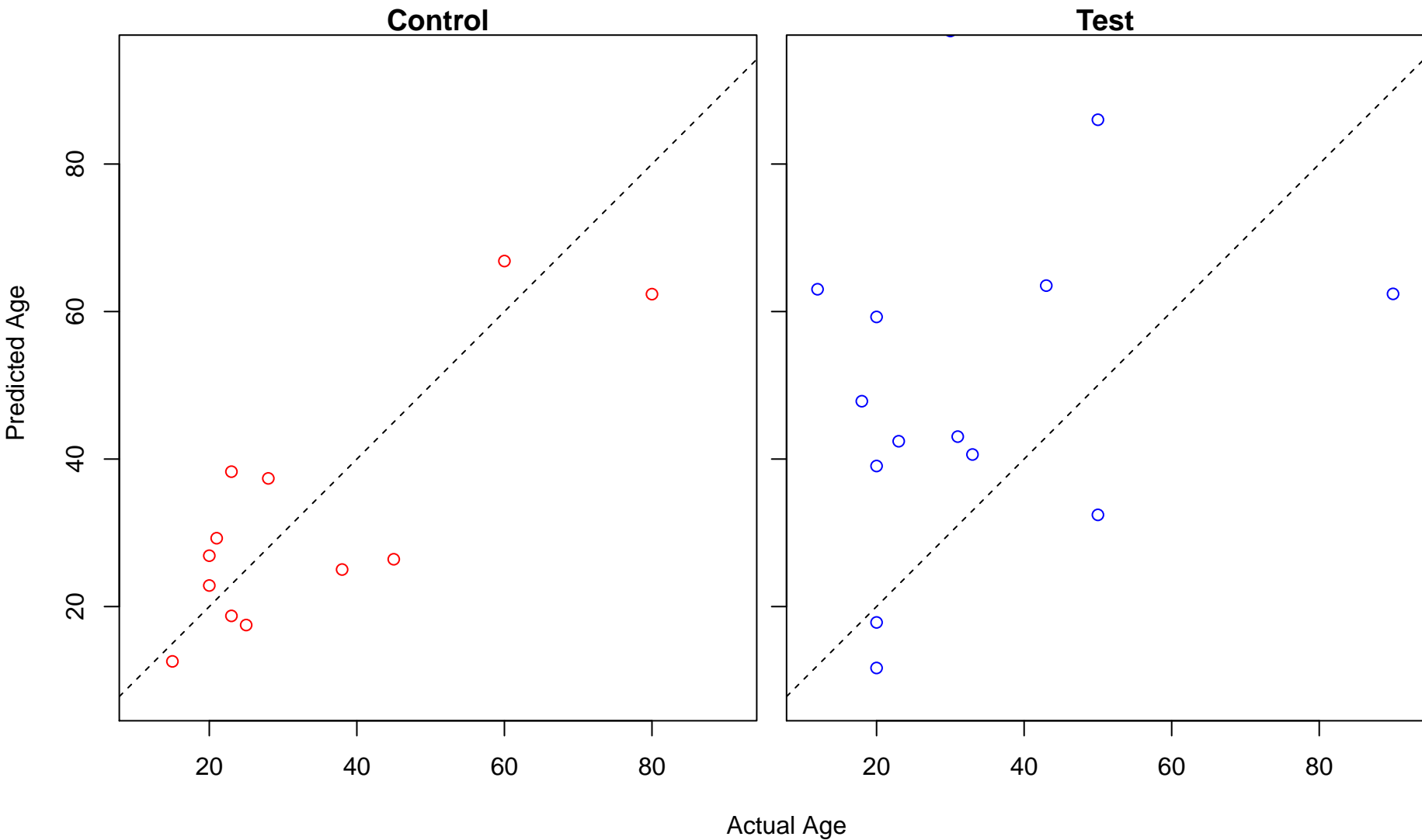
maturation of 5.8S rRNA (Score: 3.087832)



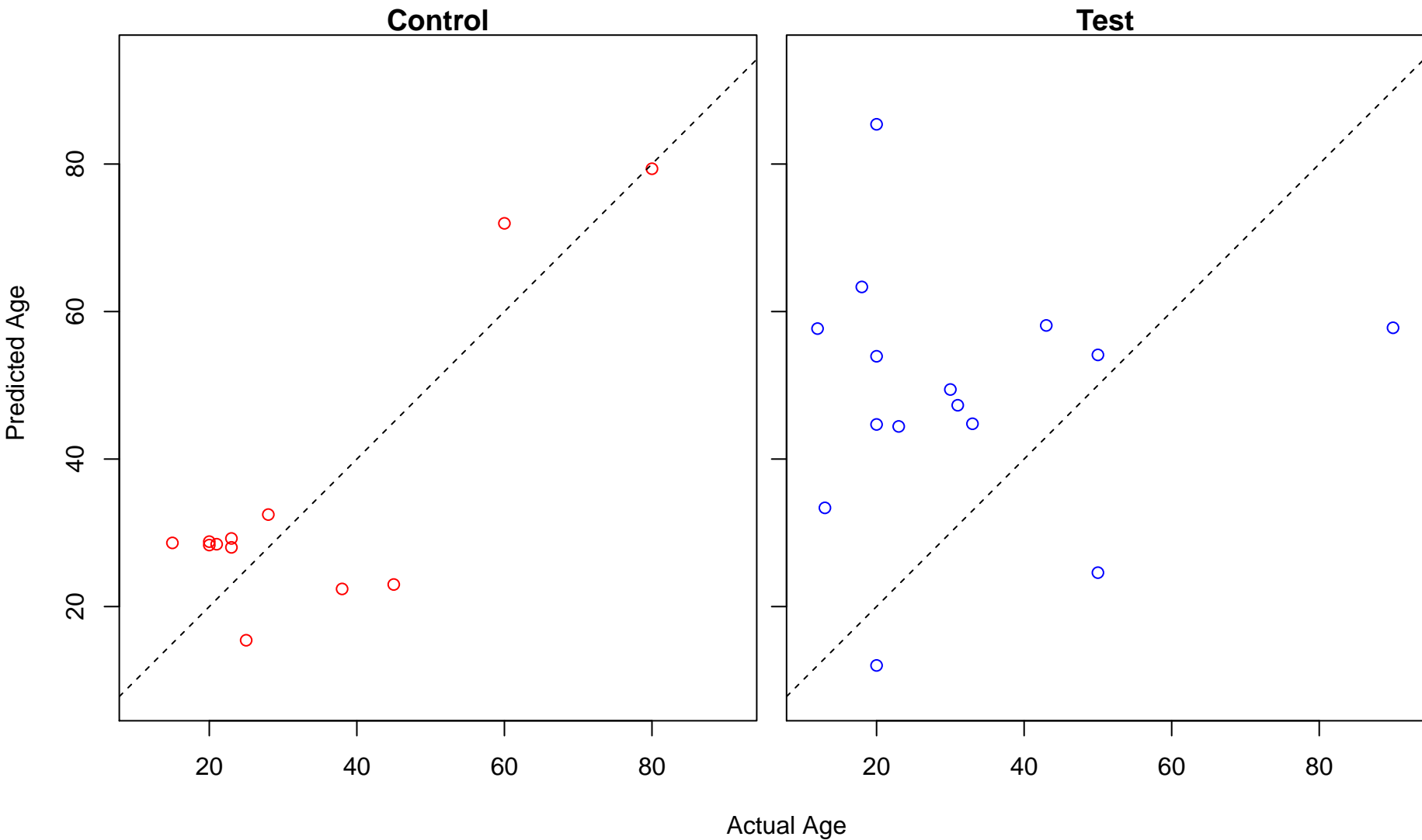
negative regulation of striated muscle tissue development (Score: 3.086010)



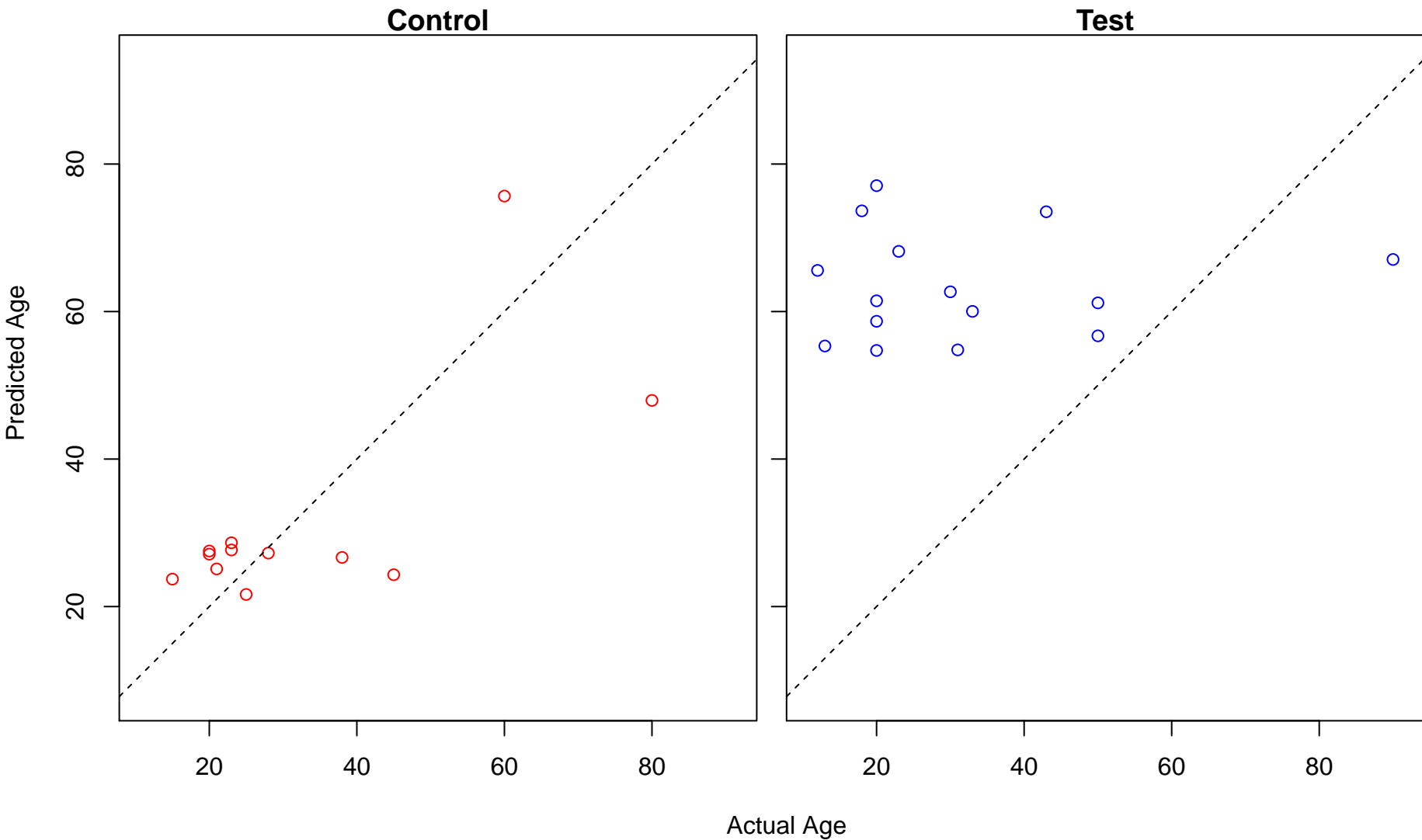
cell fate determination (Score: 3.081199)



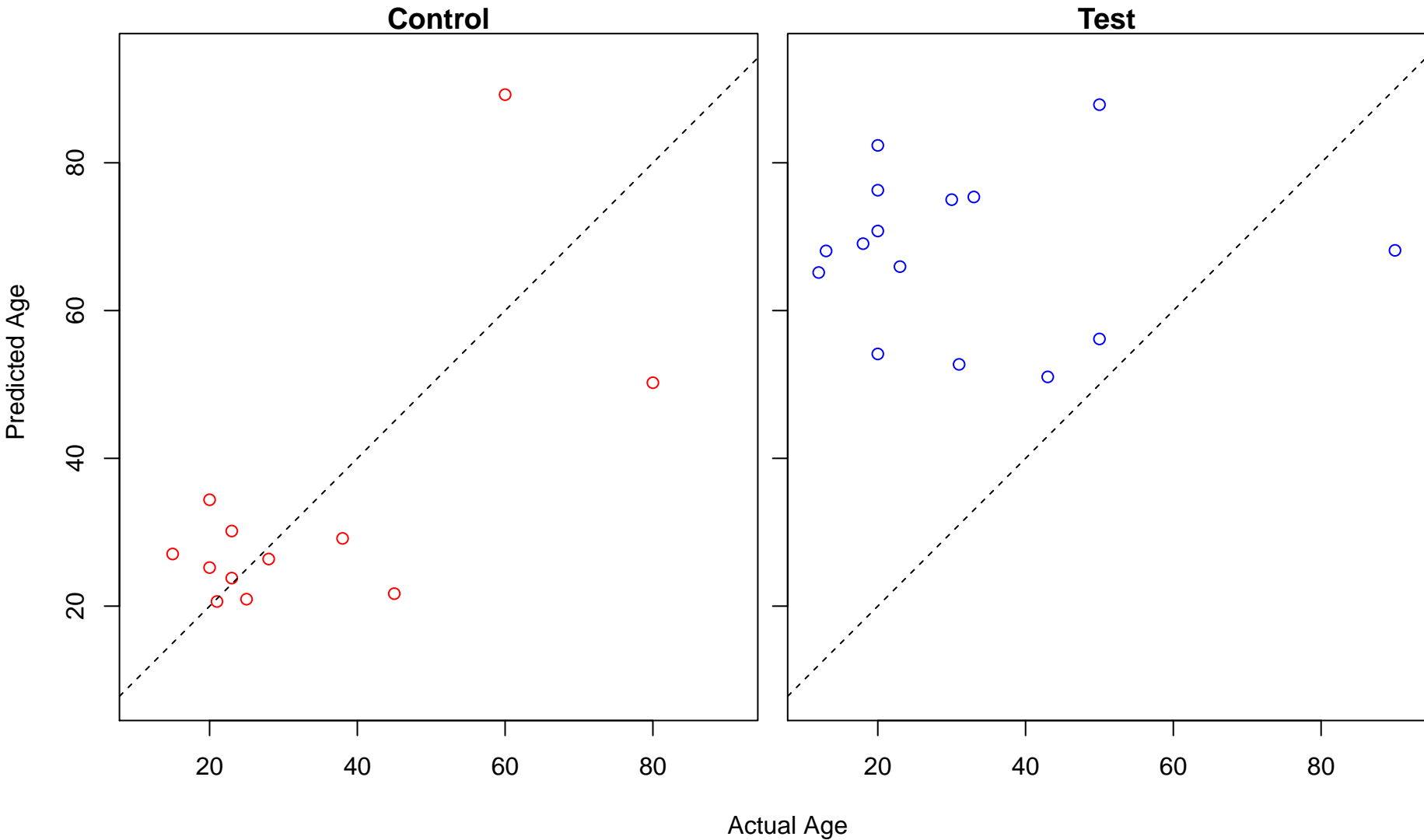
cellular respiration (Score: 3.075690)



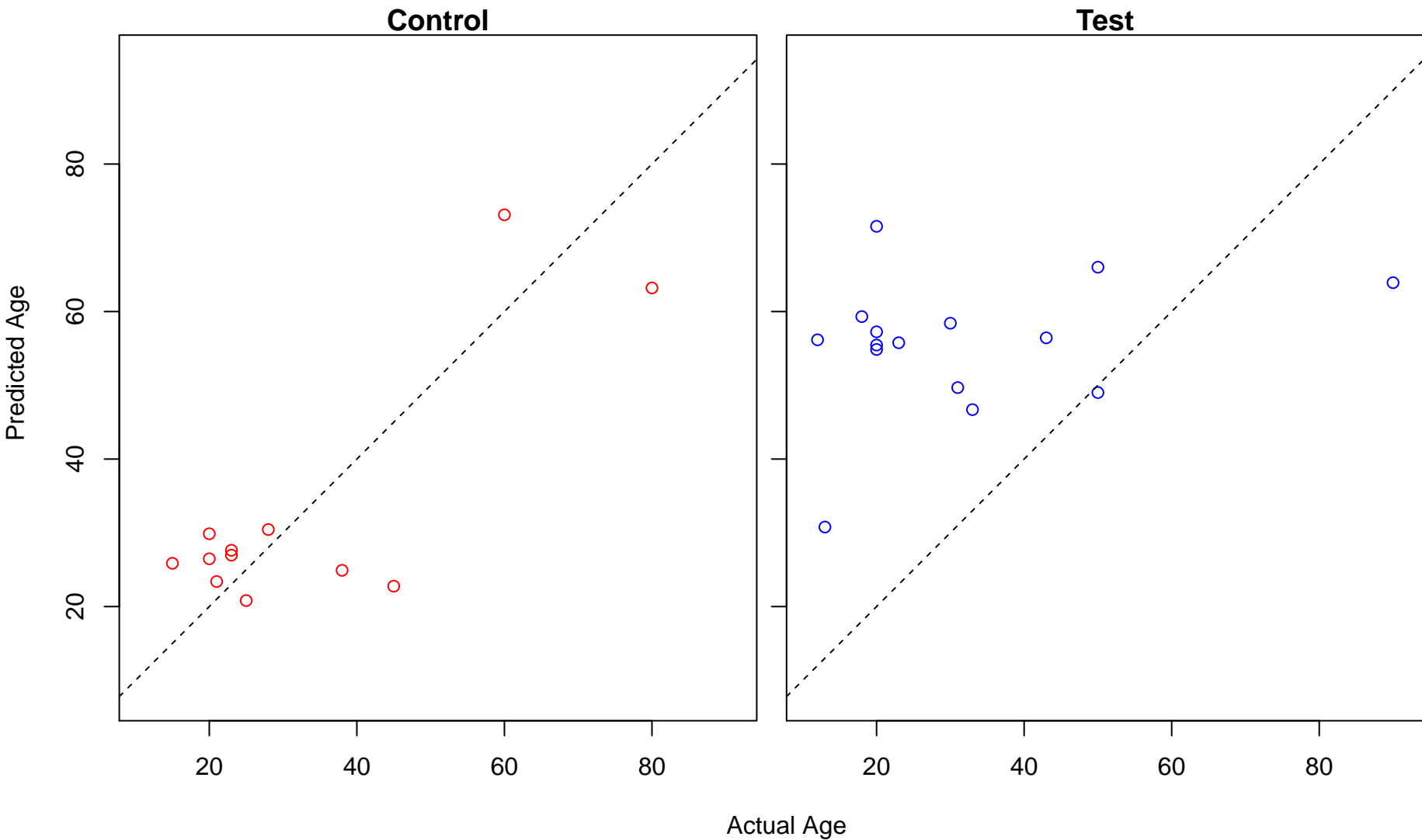
protein palmitoylation (Score: 3.073430)



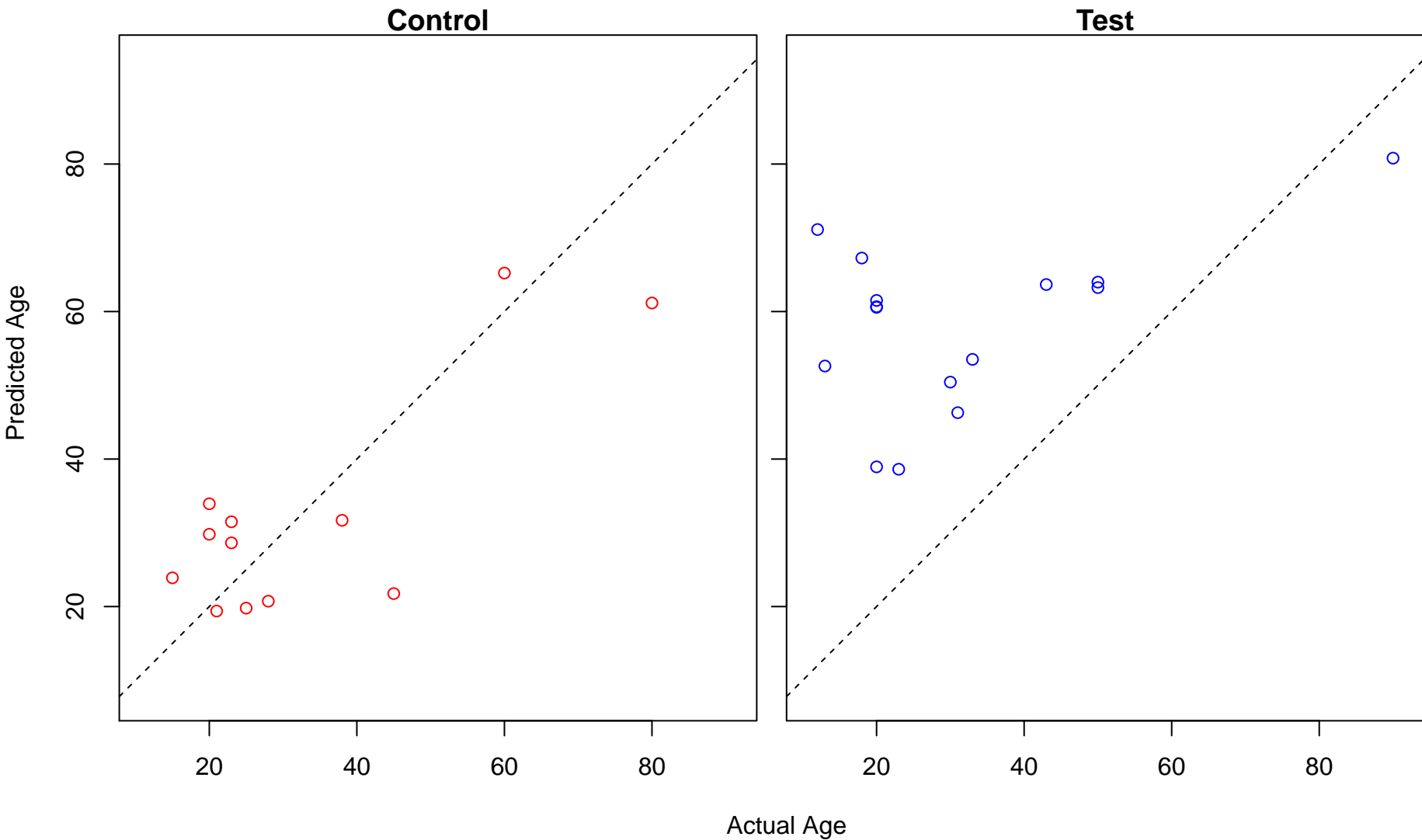
regulation of triglyceride metabolic process (Score: 3.073223)



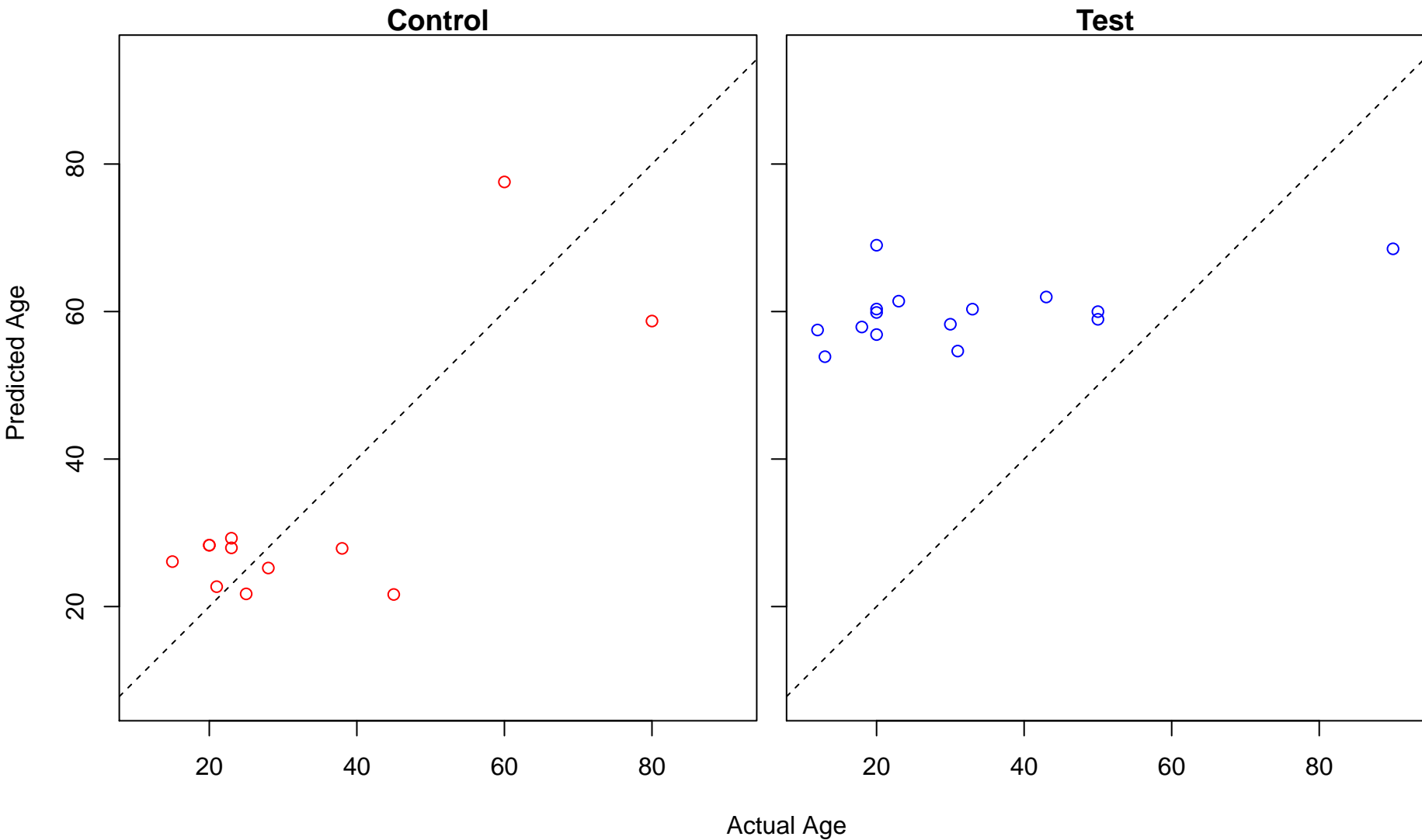
spindle assembly (Score: 3.071870)



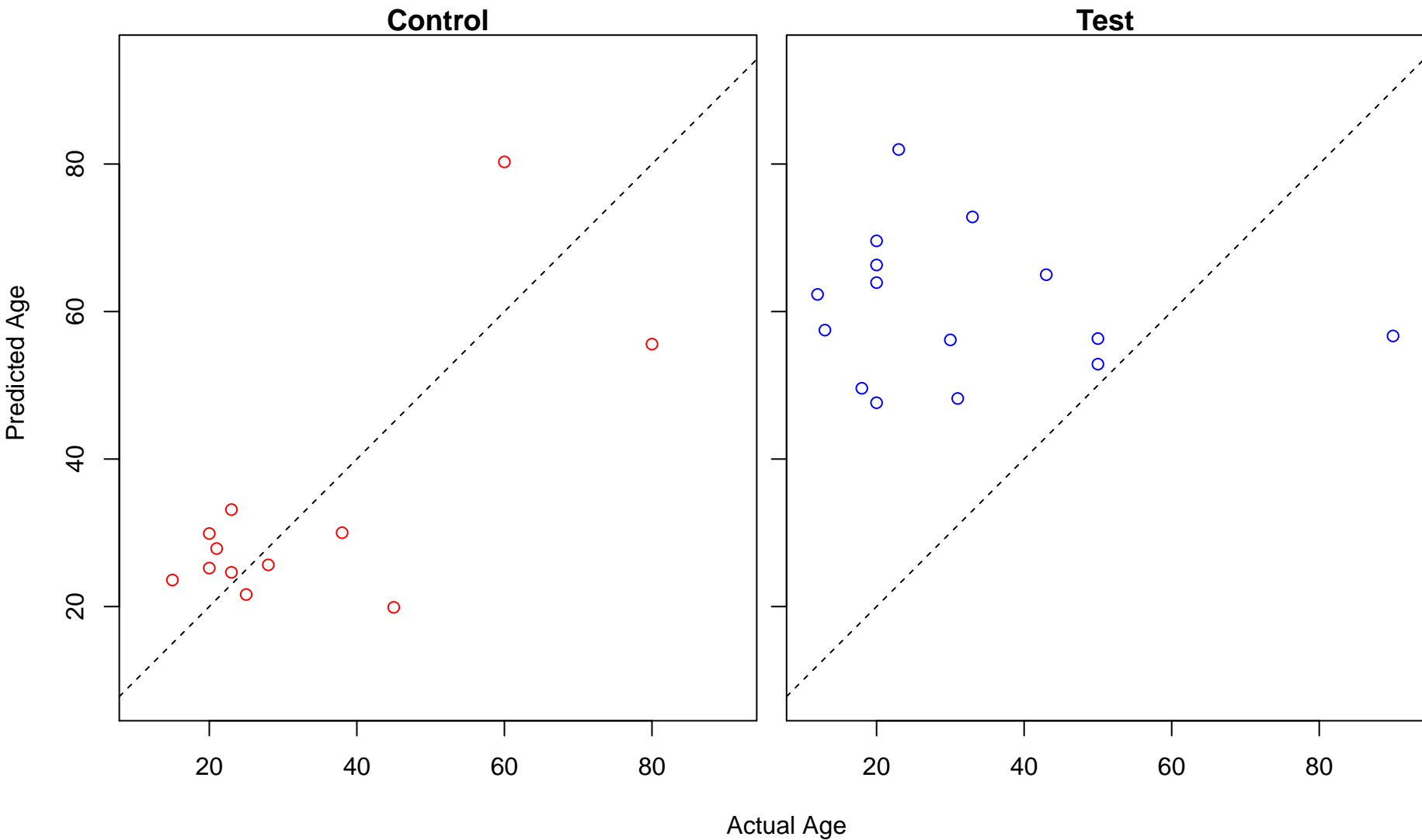
positive regulation of cardiac muscle cell differentiation (Score: 3.065254)



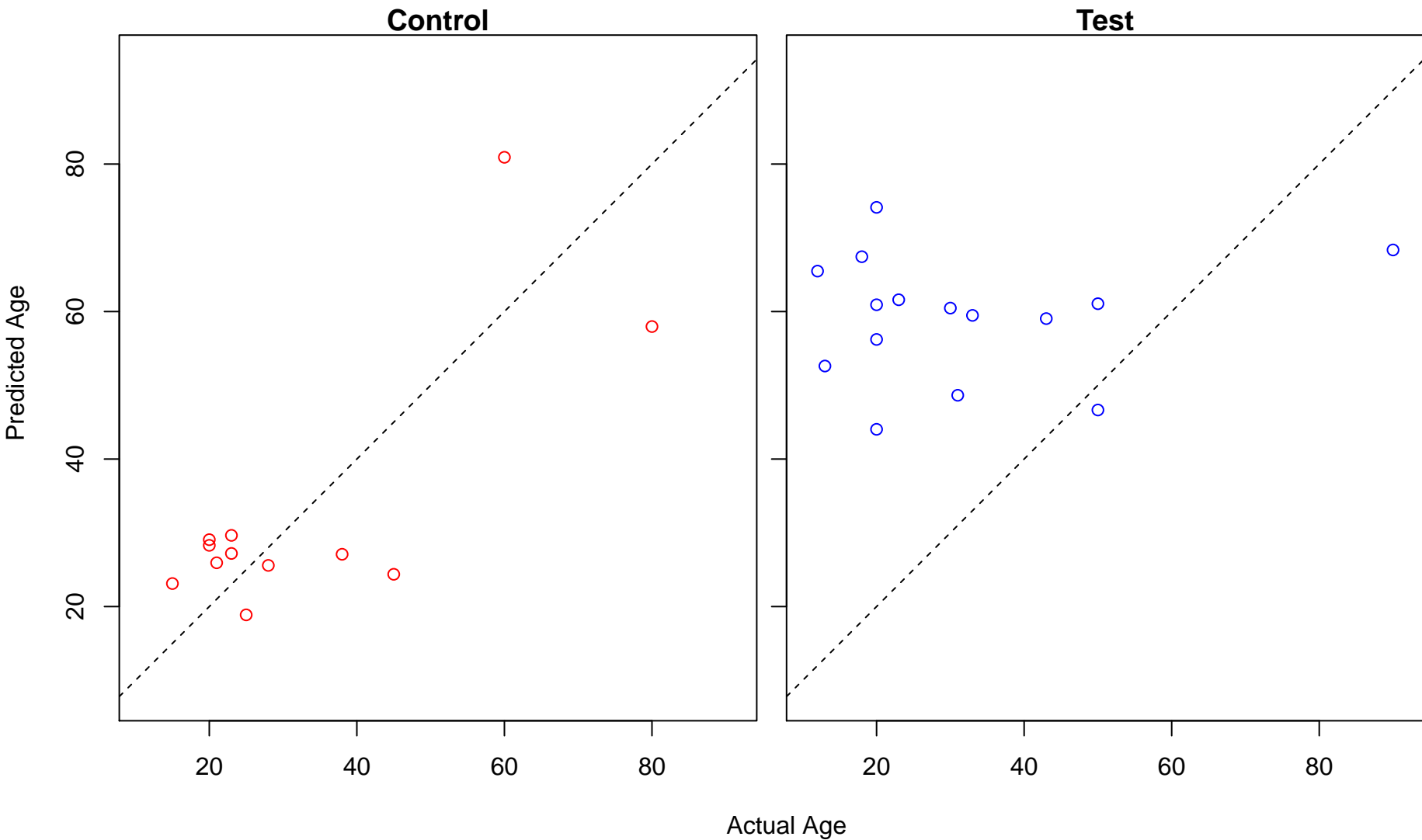
endosomal vesicle fusion (Score: 3.062623)



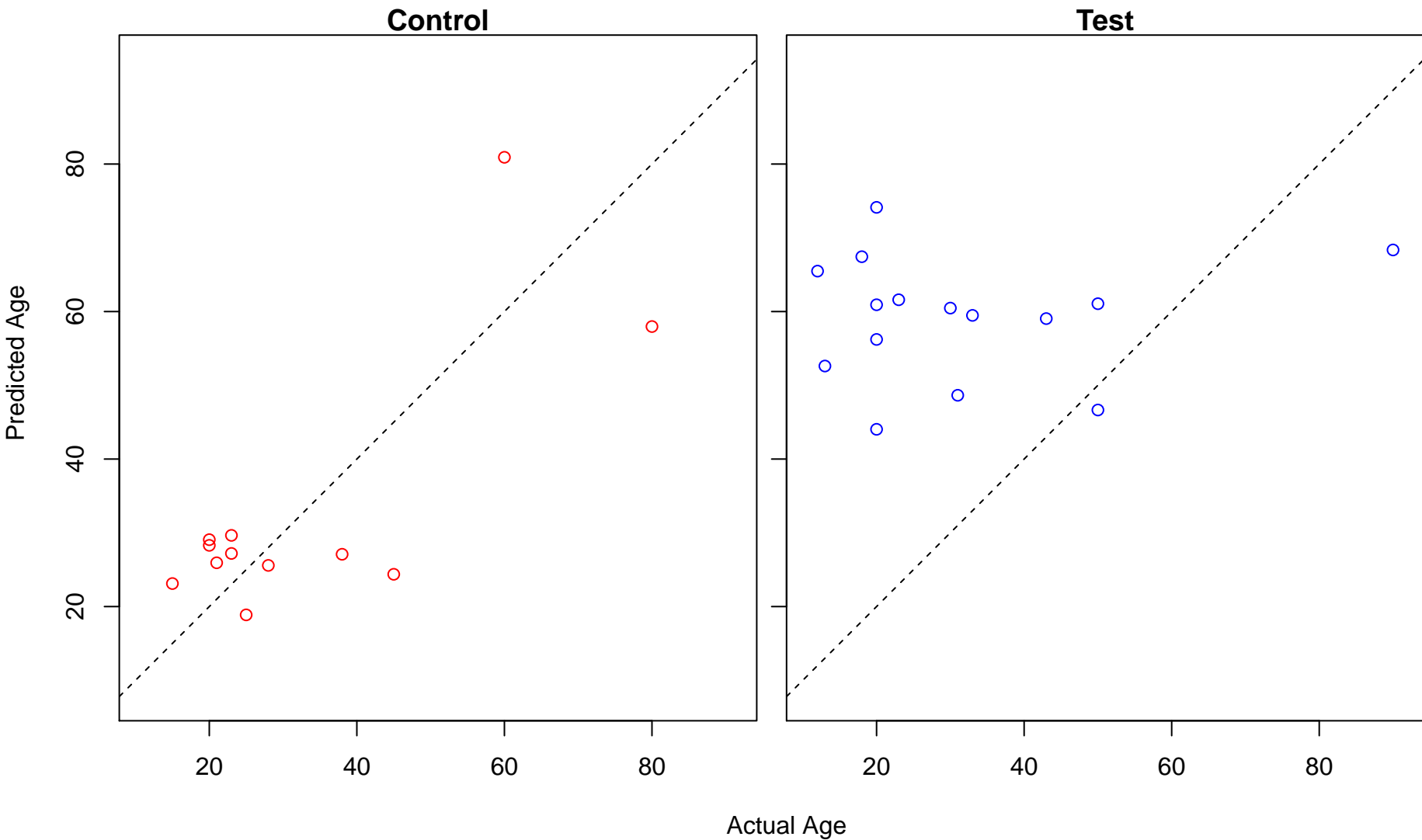
response to gonadotropin (Score: 3.059606)



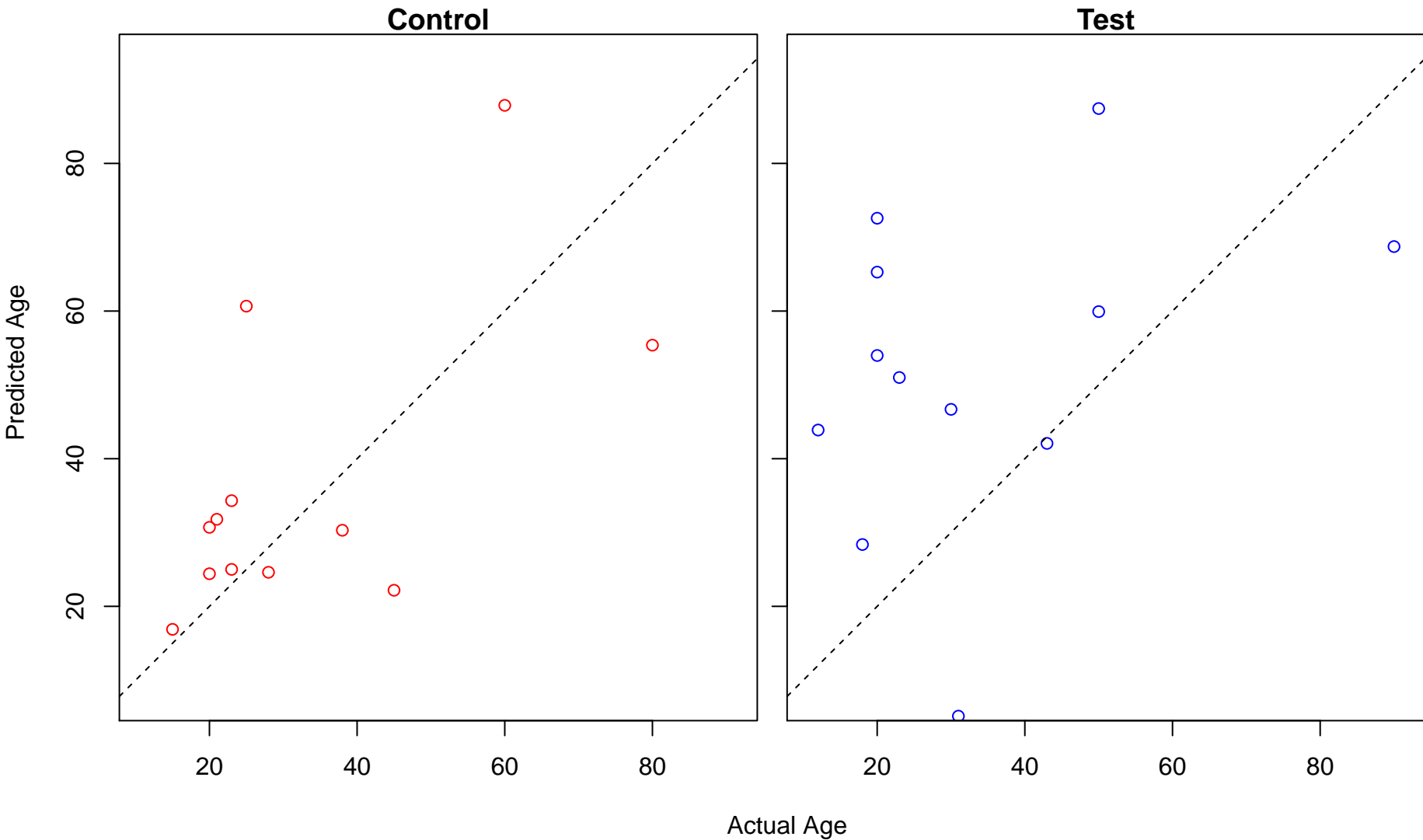
positive regulation of cardiac muscle hypertrophy (Score: 3.051462)



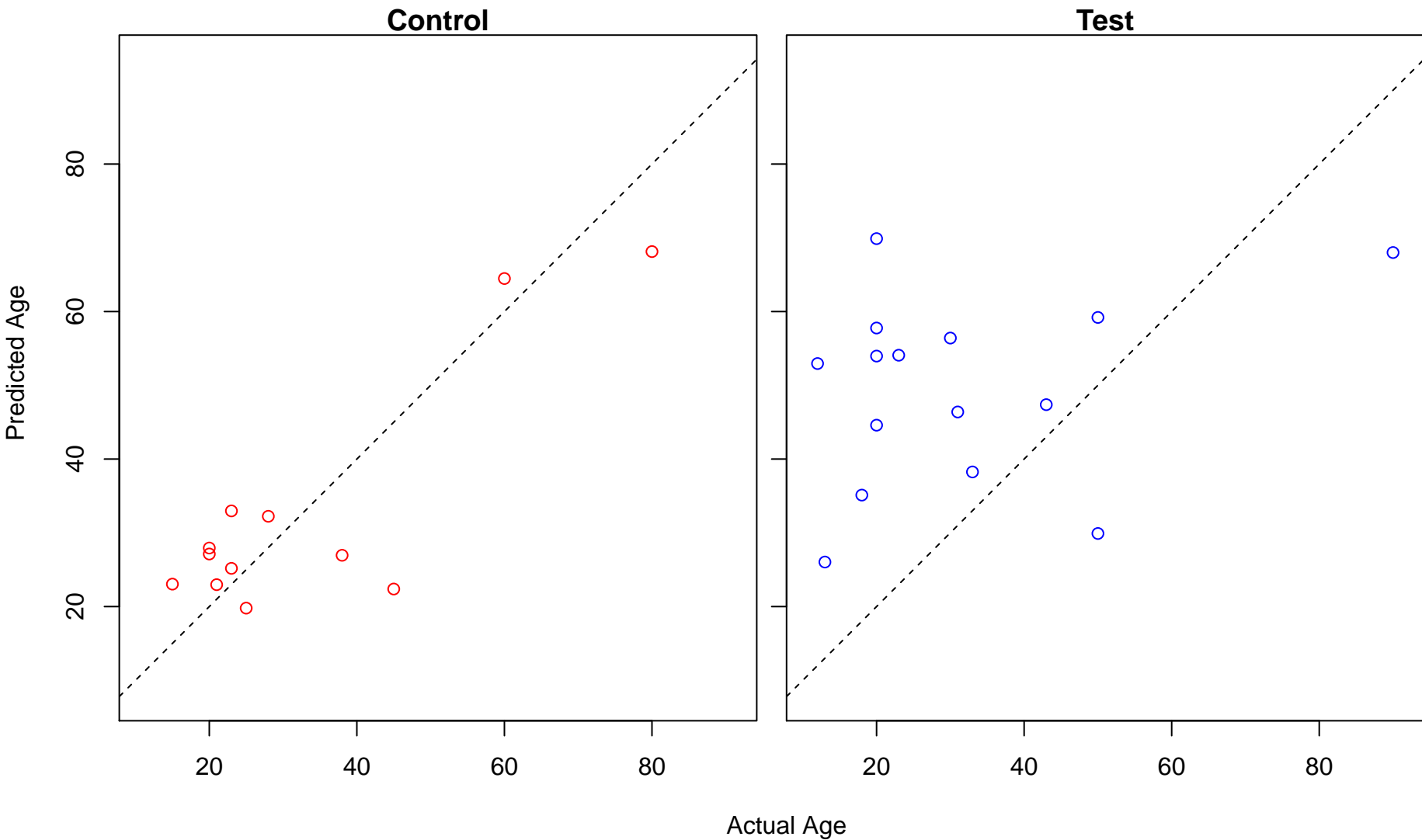
positive regulation of muscle hypertrophy (Score: 3.051462)



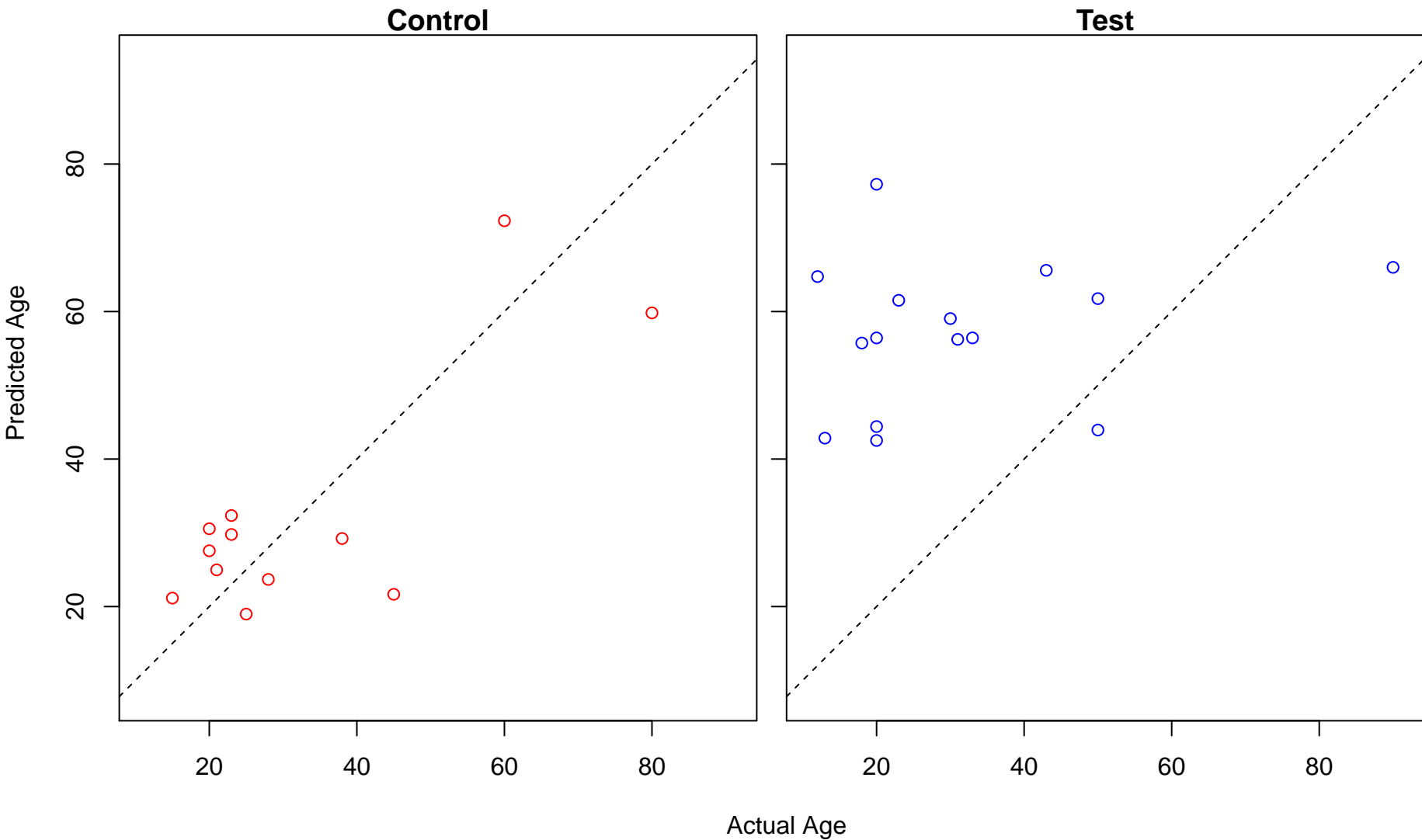
regulation of activation of JAK2 kinase activity (Score: 3.048602)



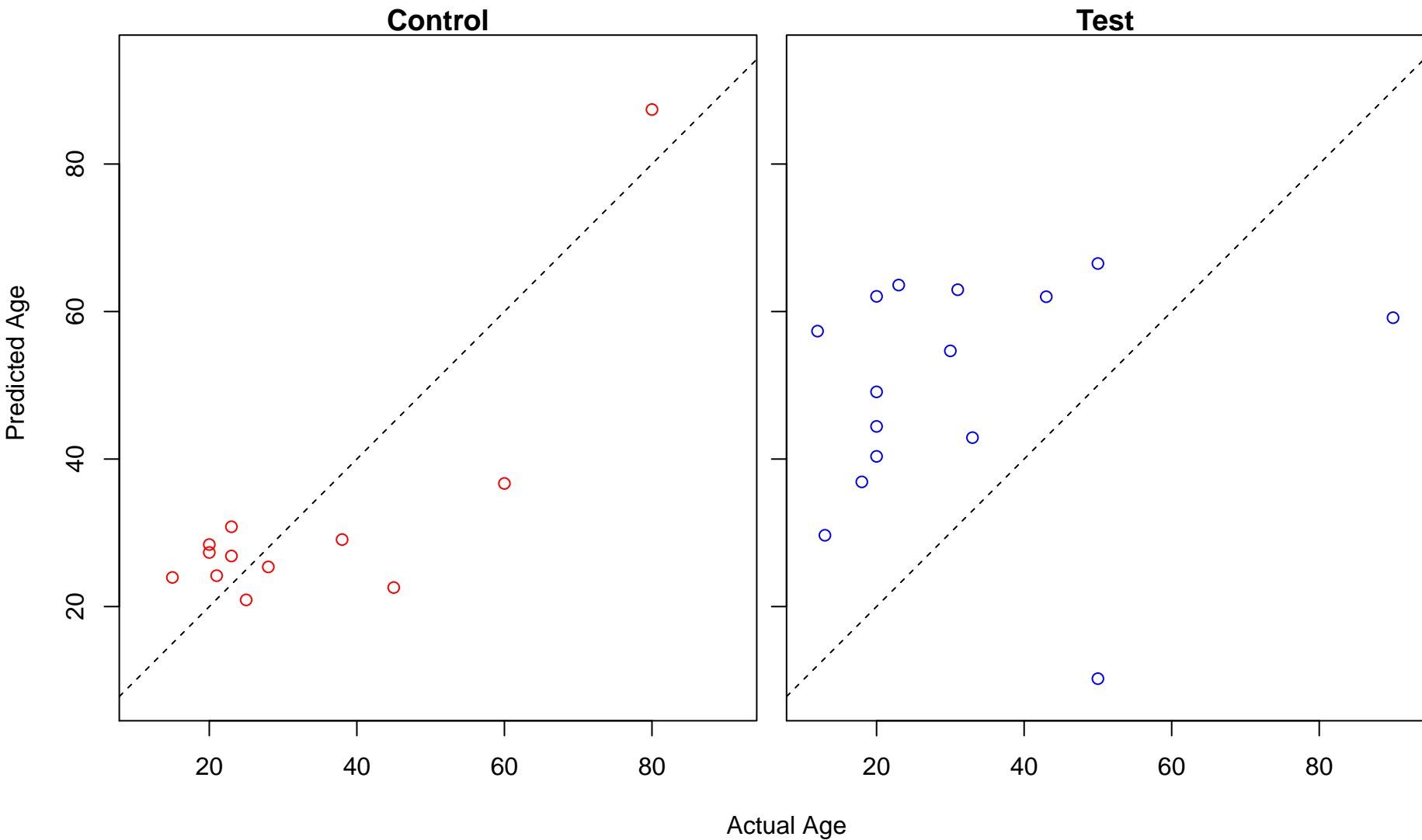
excretion (Score: 3.045714)



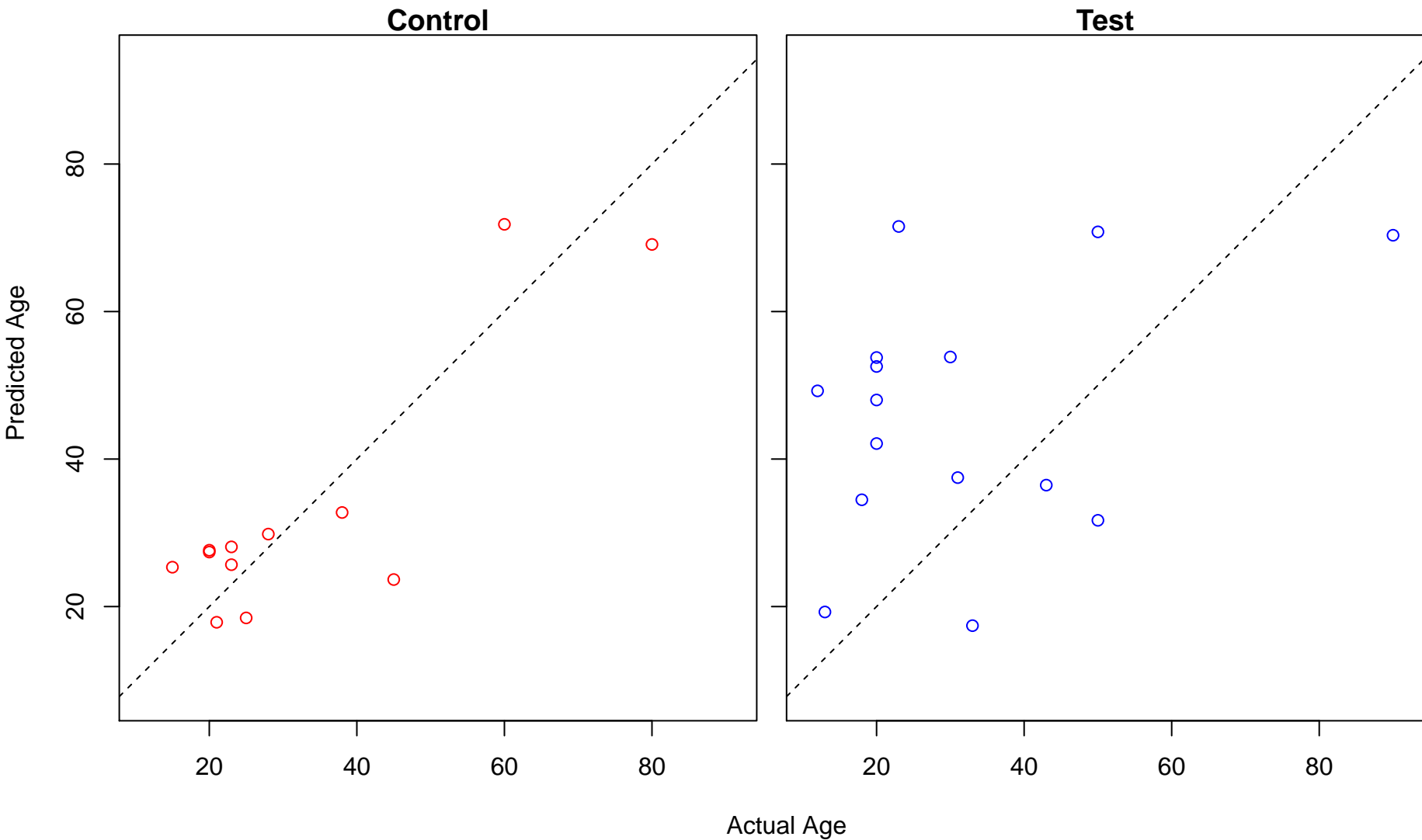
cellular response to sterol (Score: 3.036361)



carbohydrate transport (Score: 3.033750)

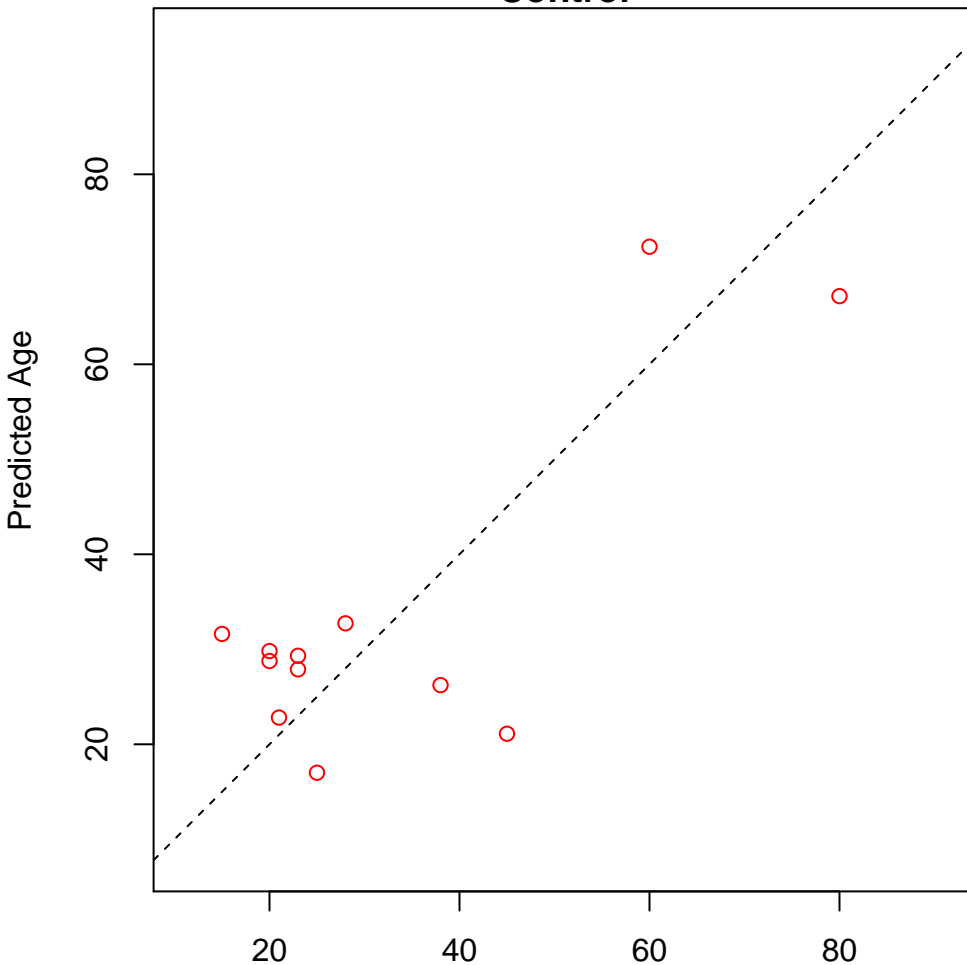


neurotransmitter secretion (Score: 3.026551)

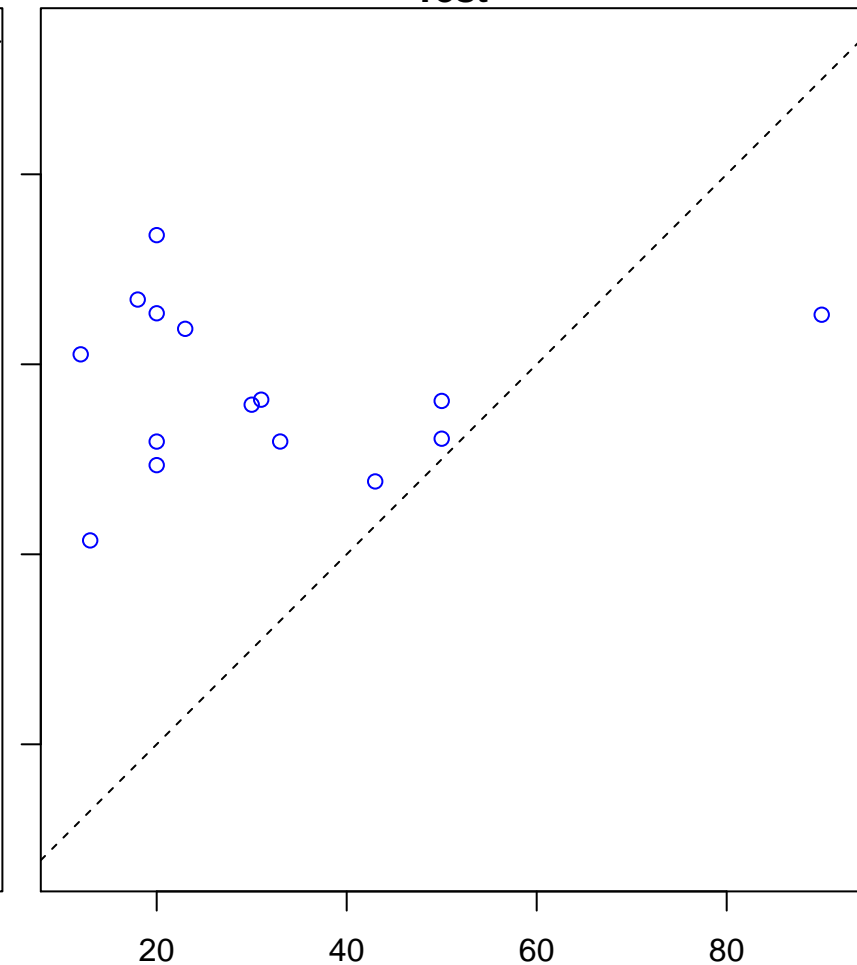


regulation of interferon-beta production (Score: 3.023372)

Control

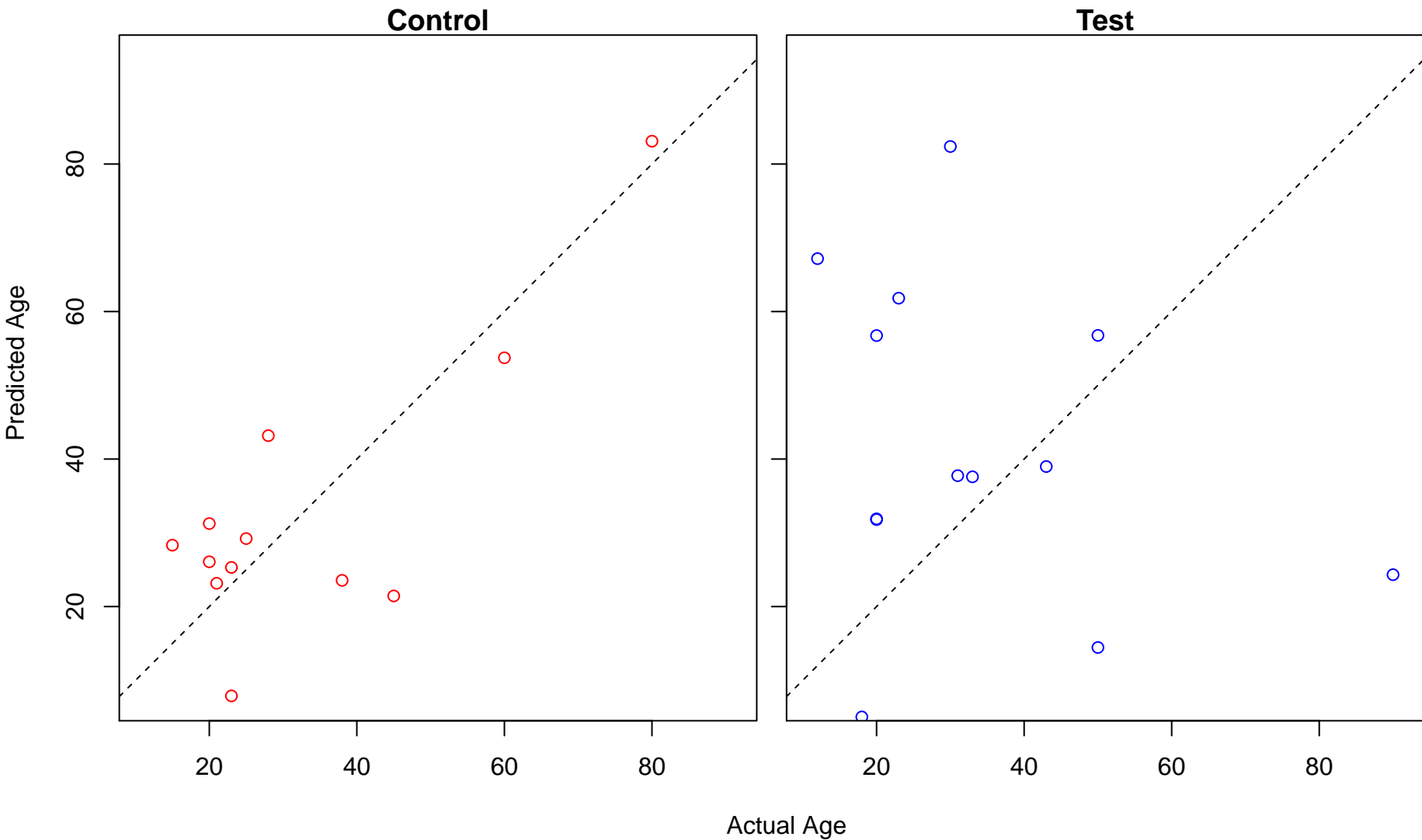


Test

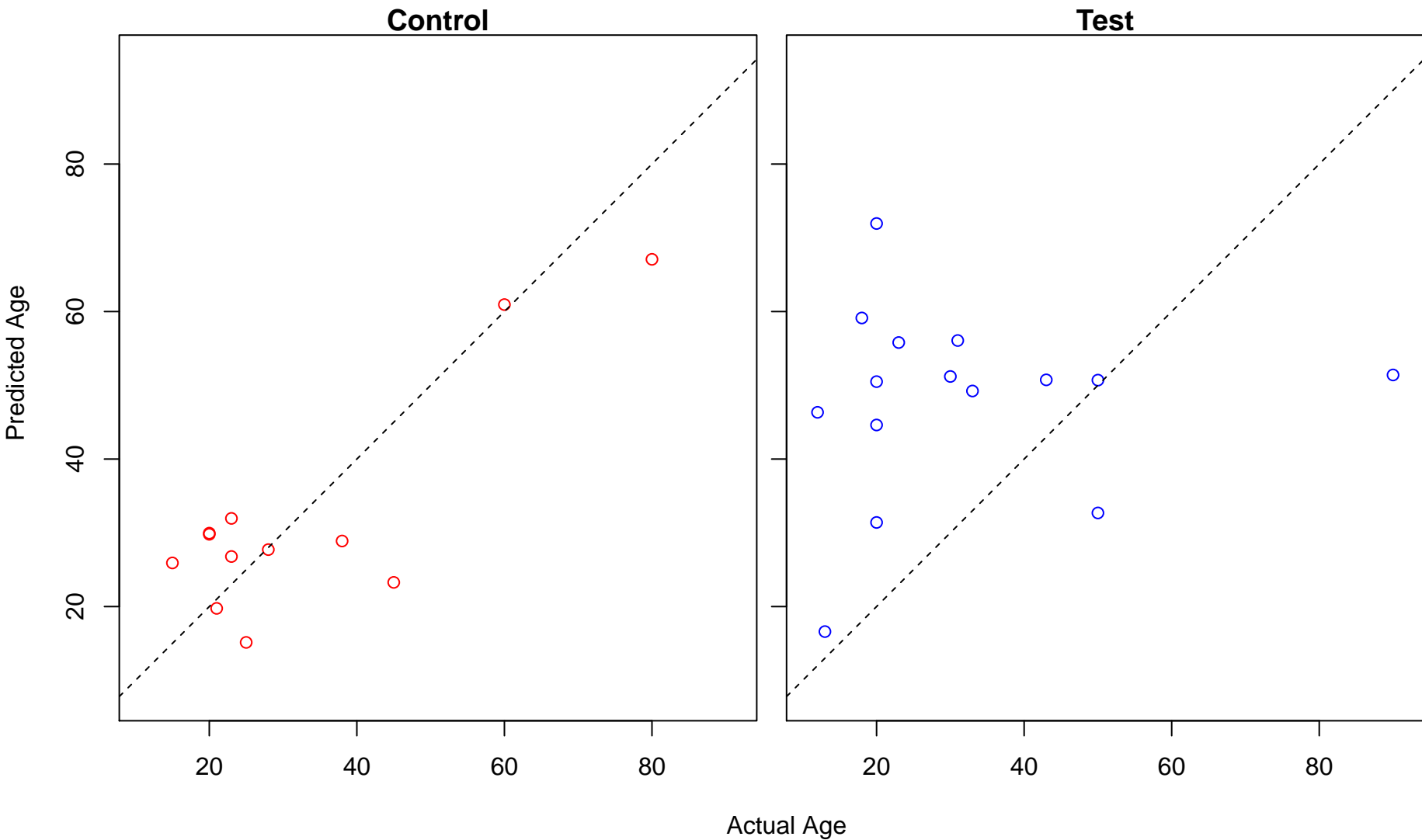


Actual Age

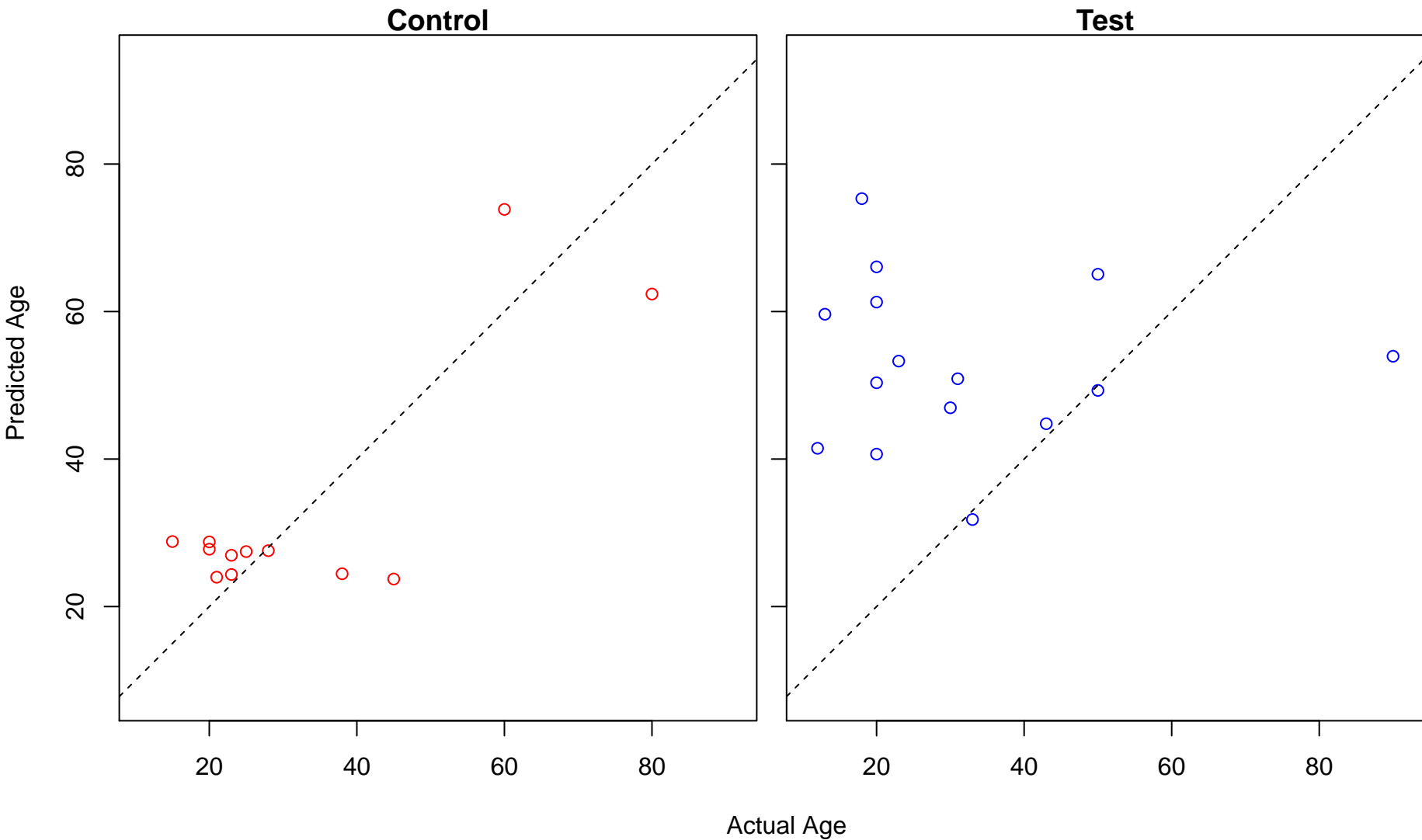
anatomical structure maturation (Score: 3.017825)



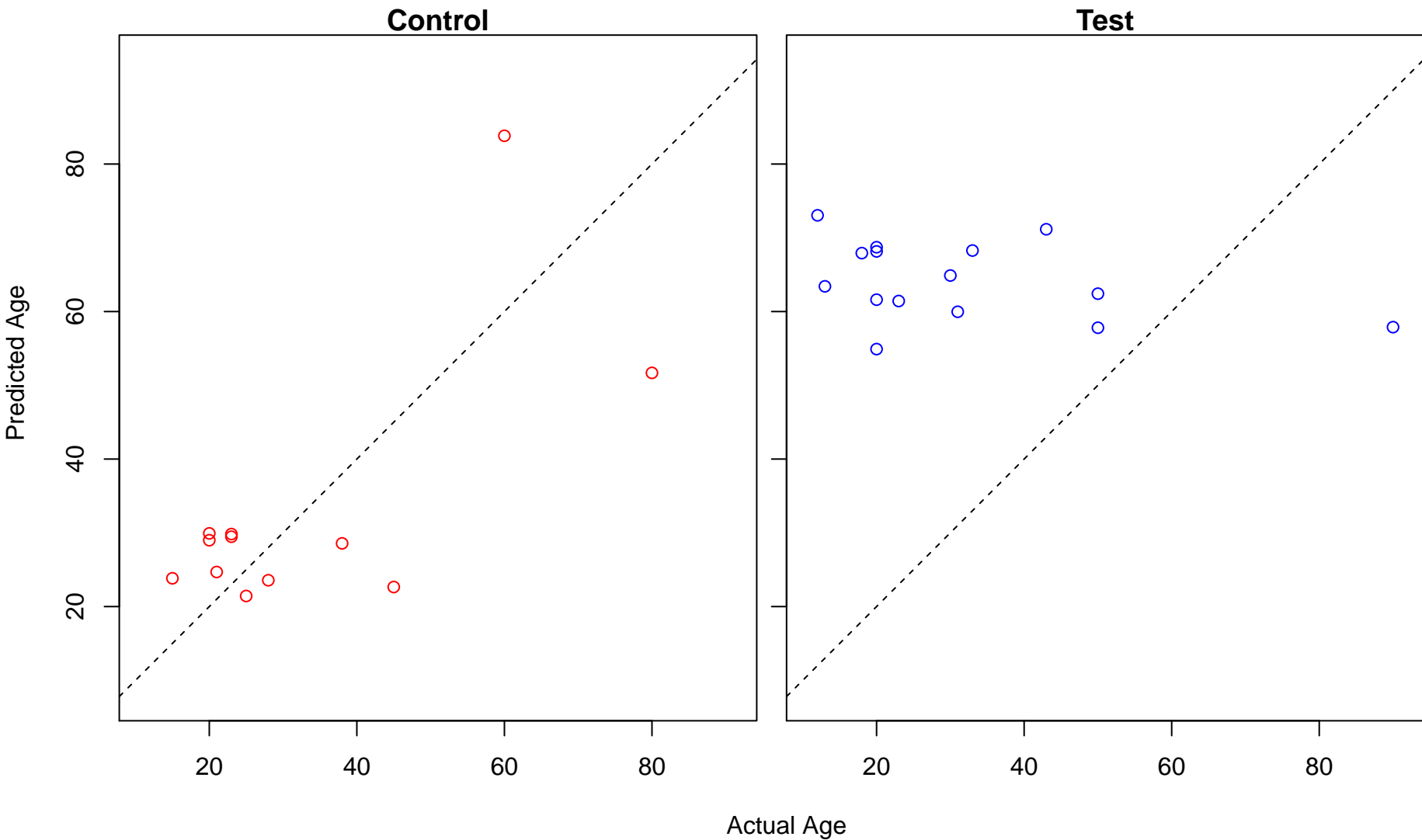
phospholipid transport (Score: 3.017792)



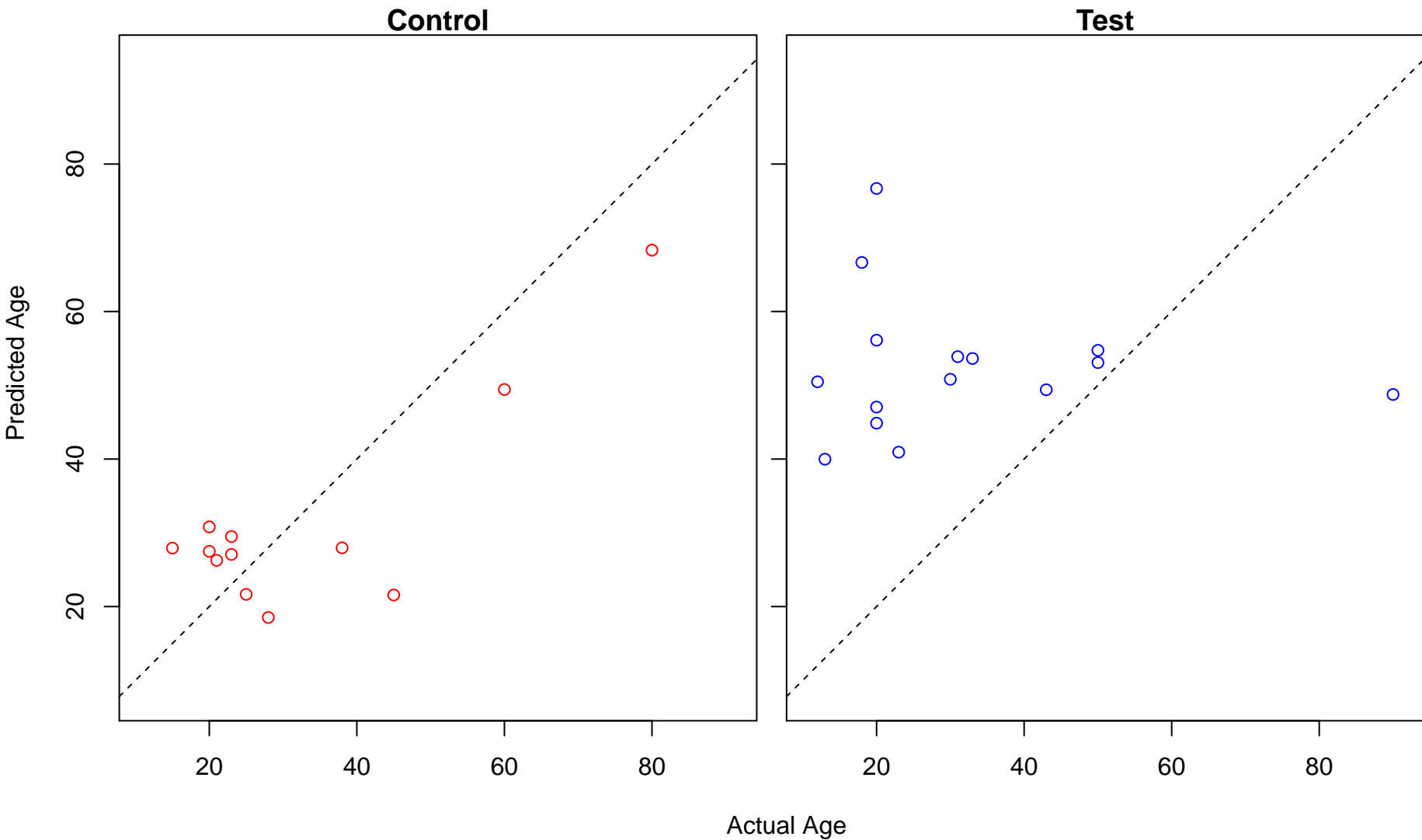
hexose biosynthetic process (Score: 3.015003)



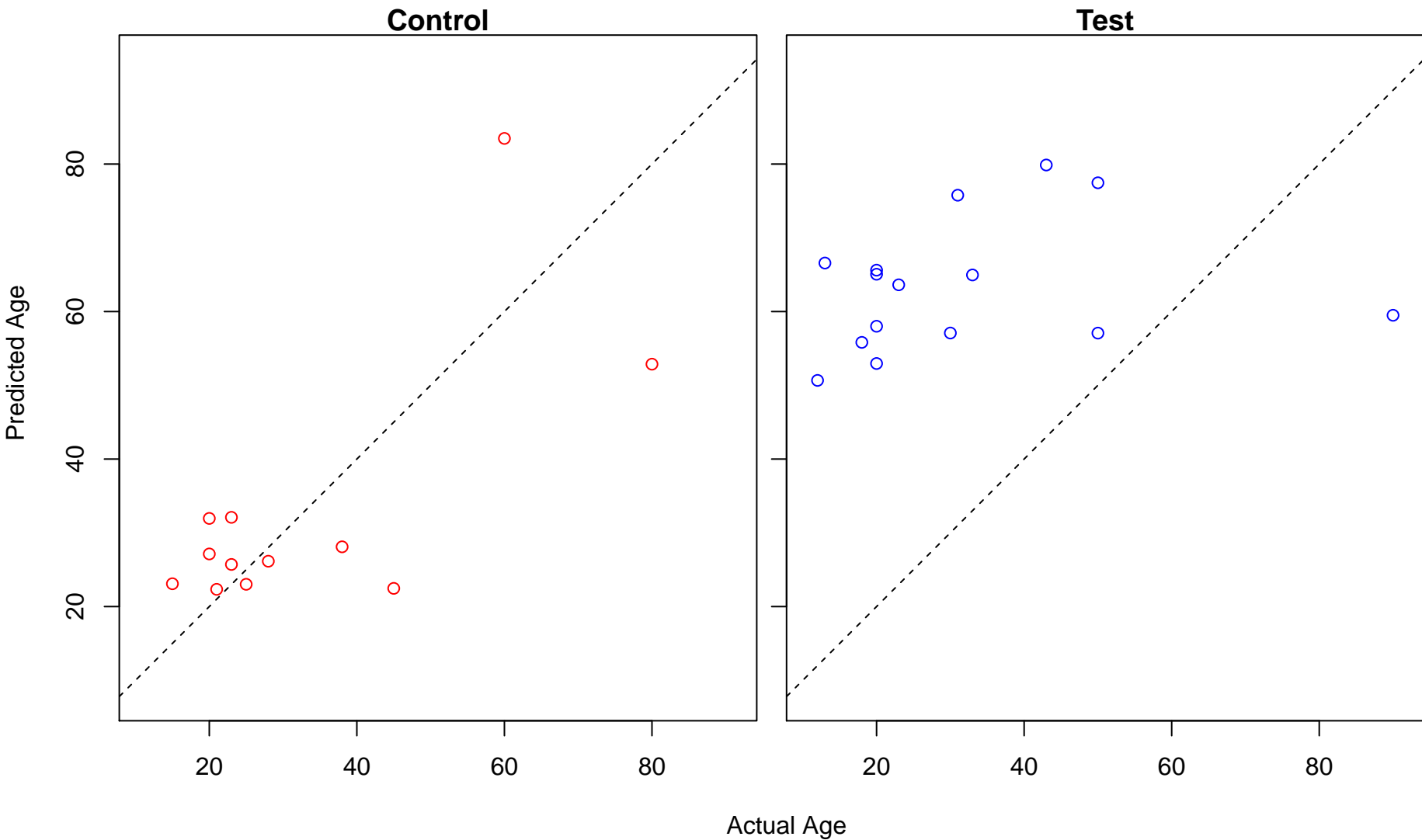
regulation of establishment of planar polarity (Score: 3.007538)



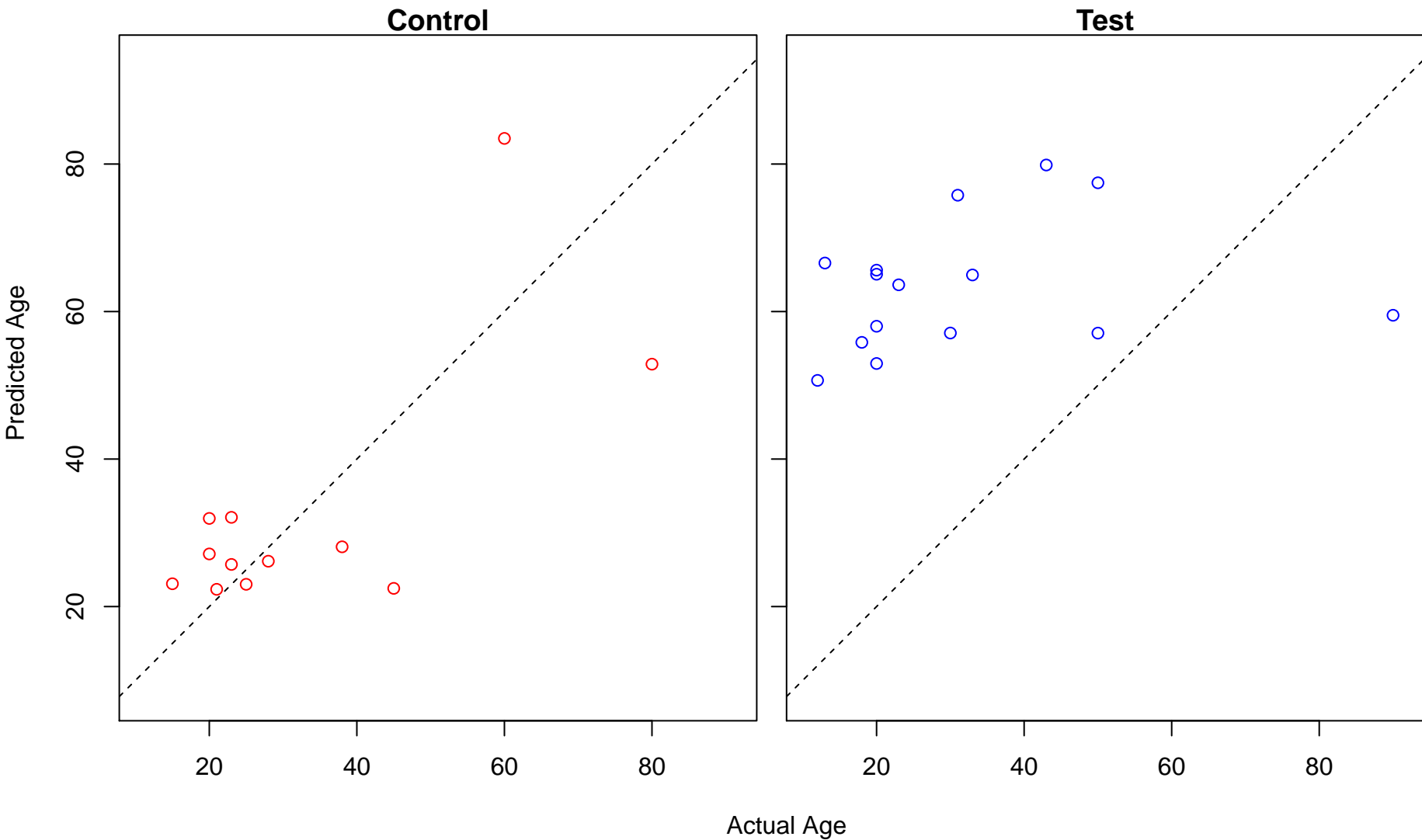
lipid localization (Score: 3.005685)



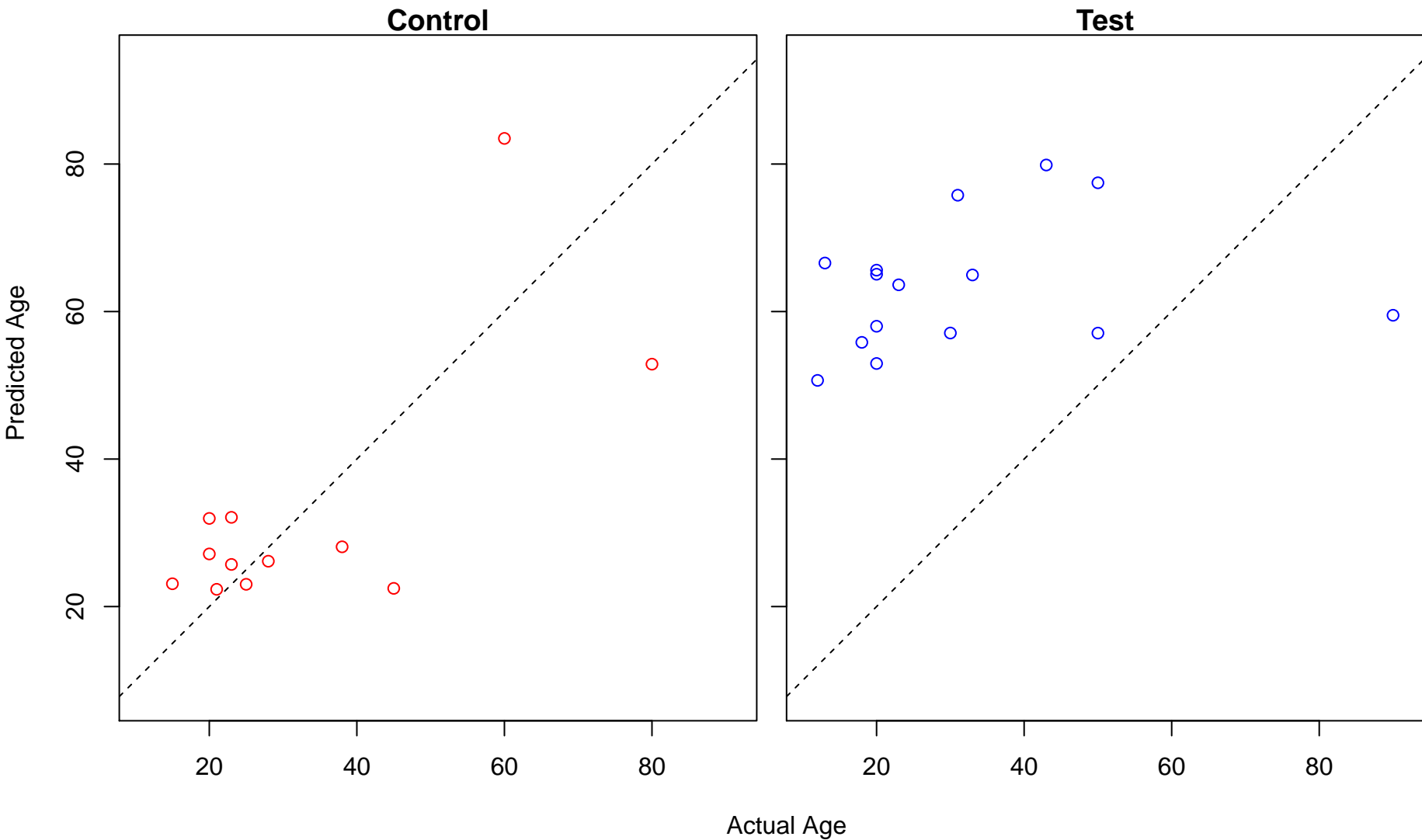
SA node cell action potential (Score: 2.991529)



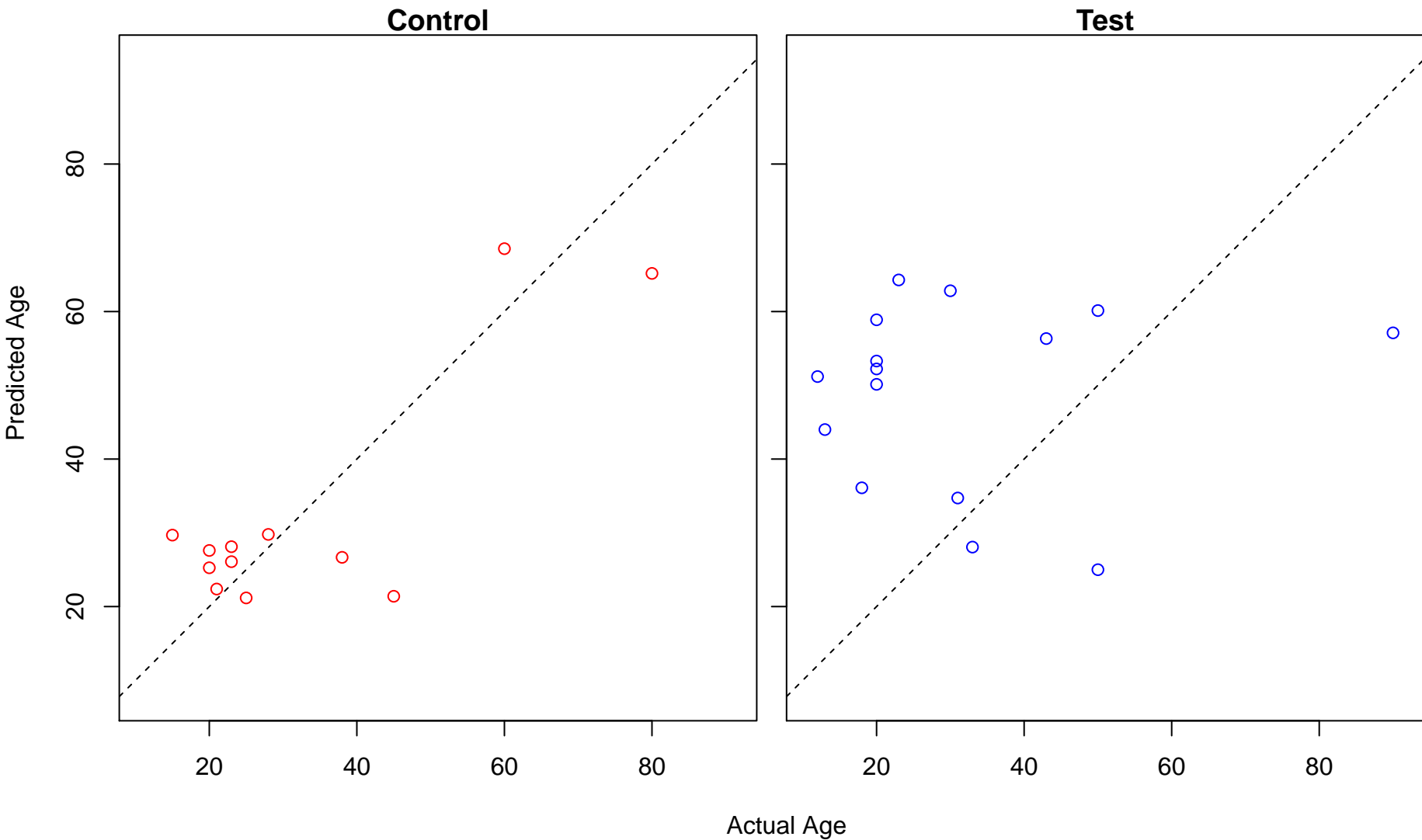
SA node cell to atrial cardiac muscle cell signalling (Score: 2.991529)



SA node cell to atrial cardiac muscle cell communication (Score: 2.991529)

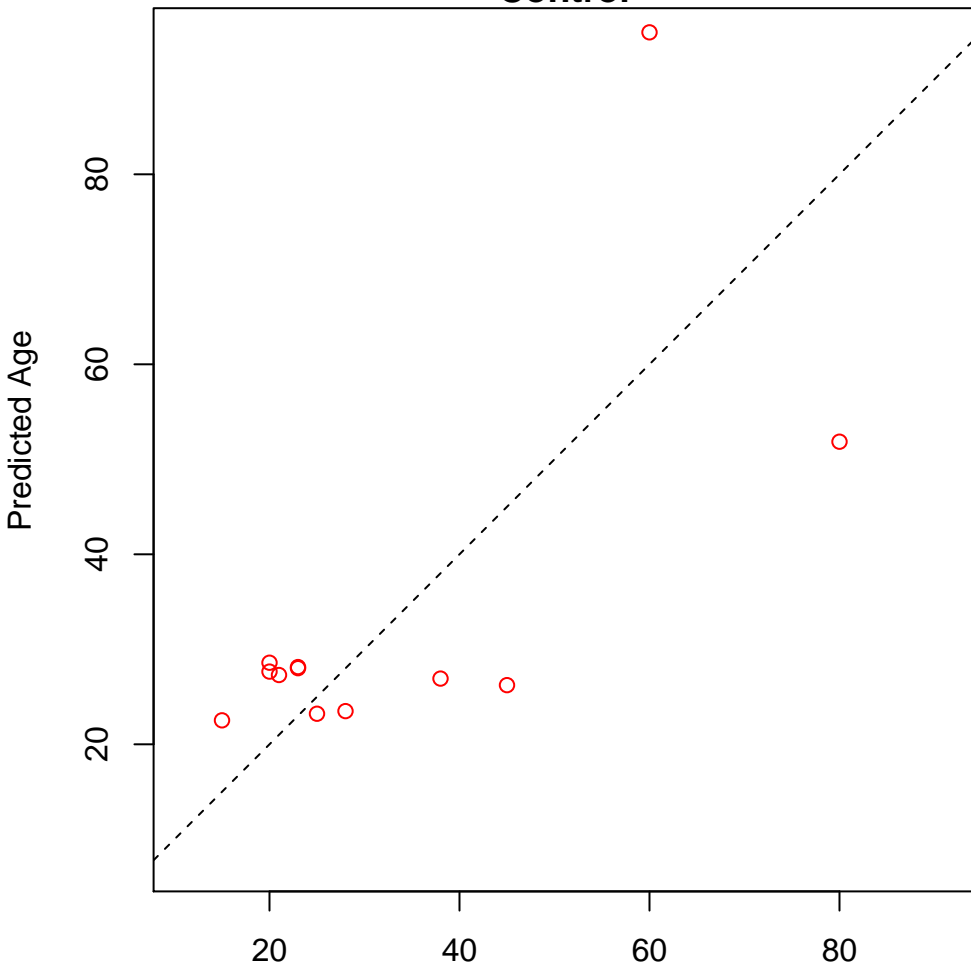


negative regulation of proteasomal protein catabolic process (Score: 2.988941)

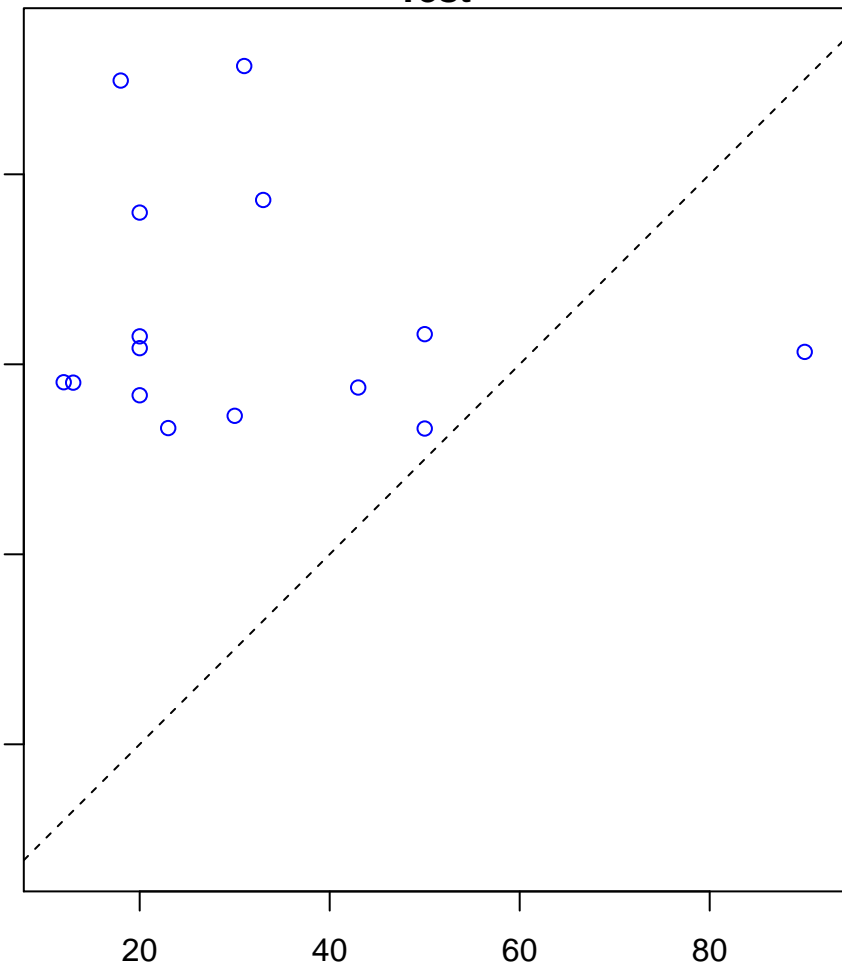


neuron-neuron synaptic transmission (Score: 2.979850)

Control

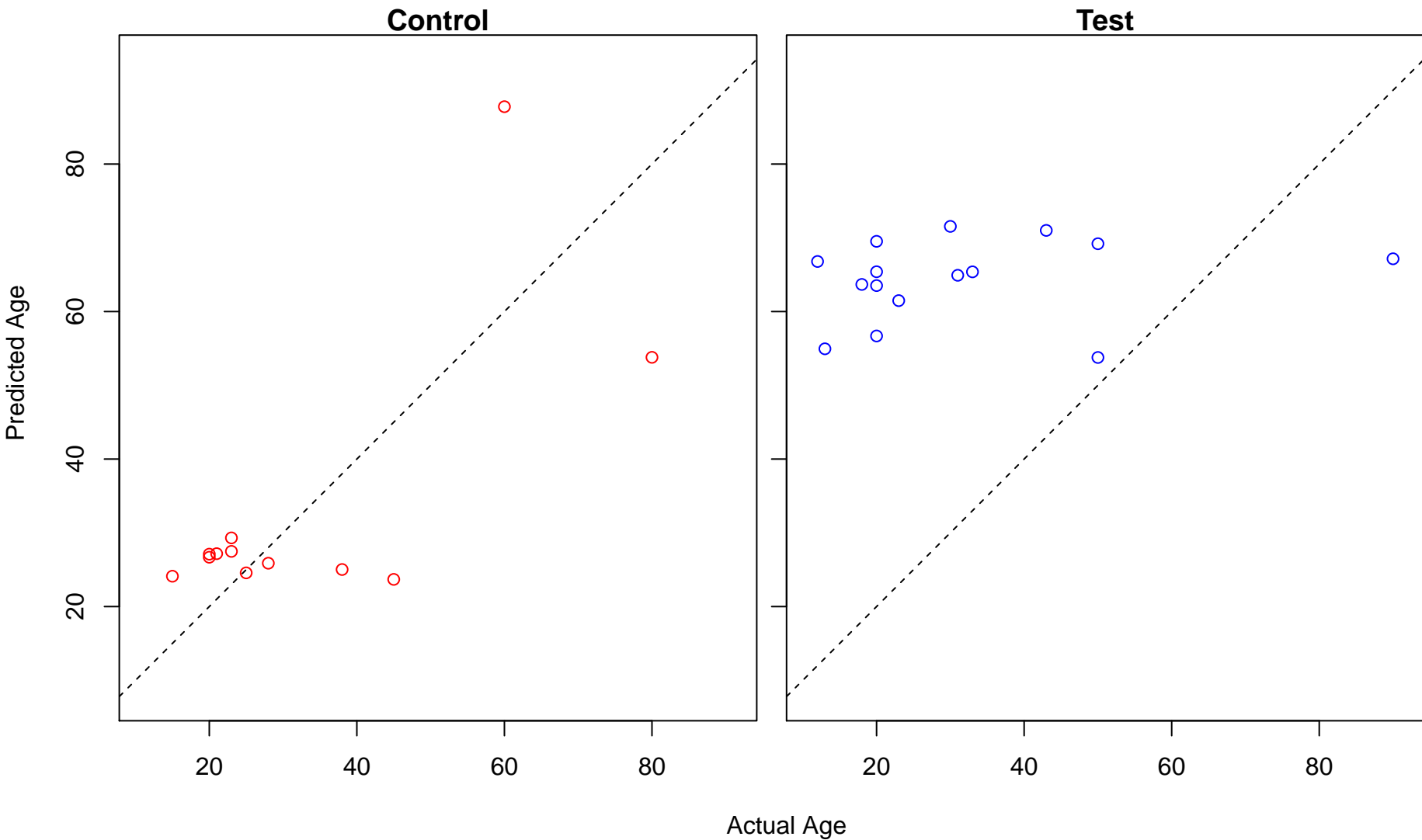


Test

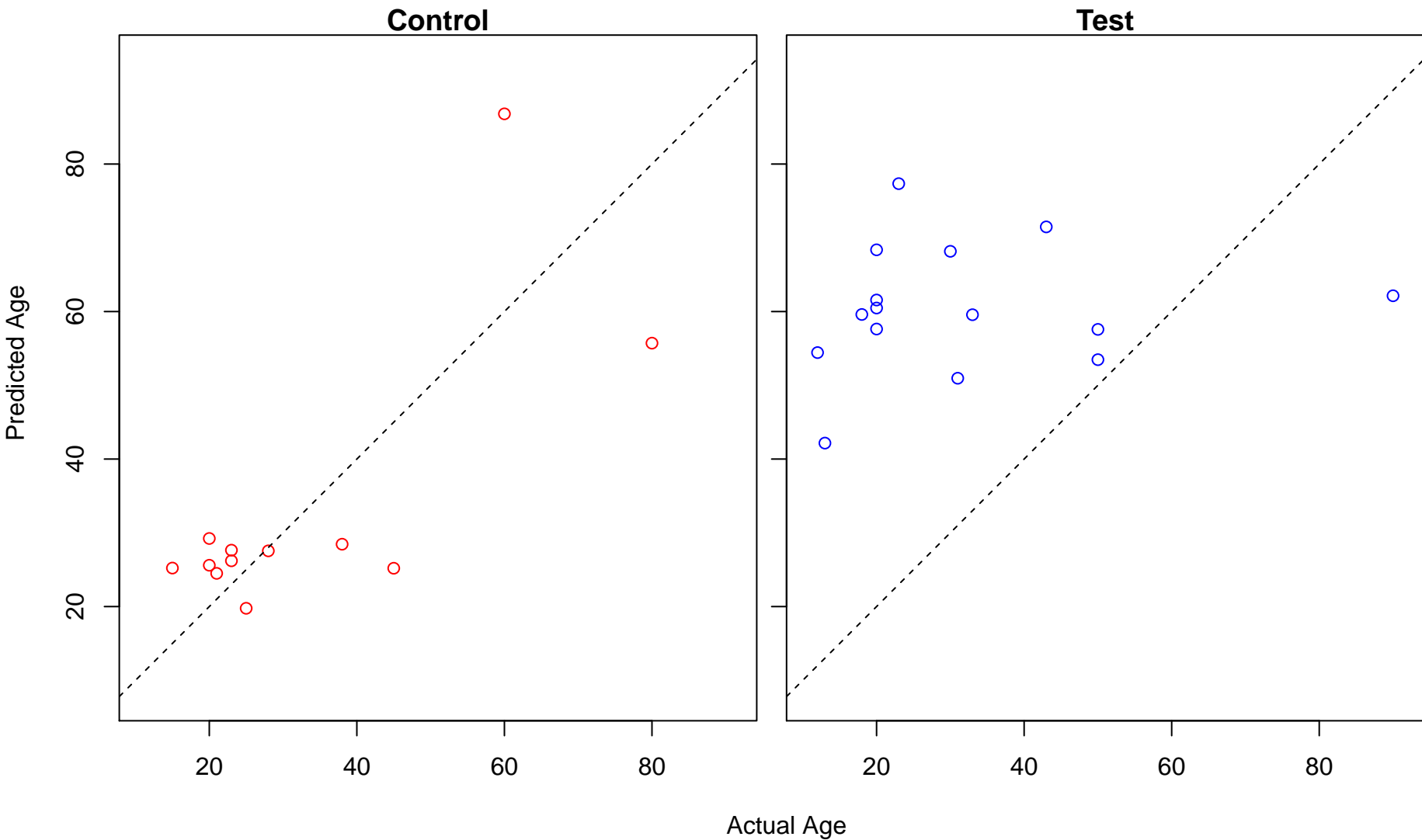


Actual Age

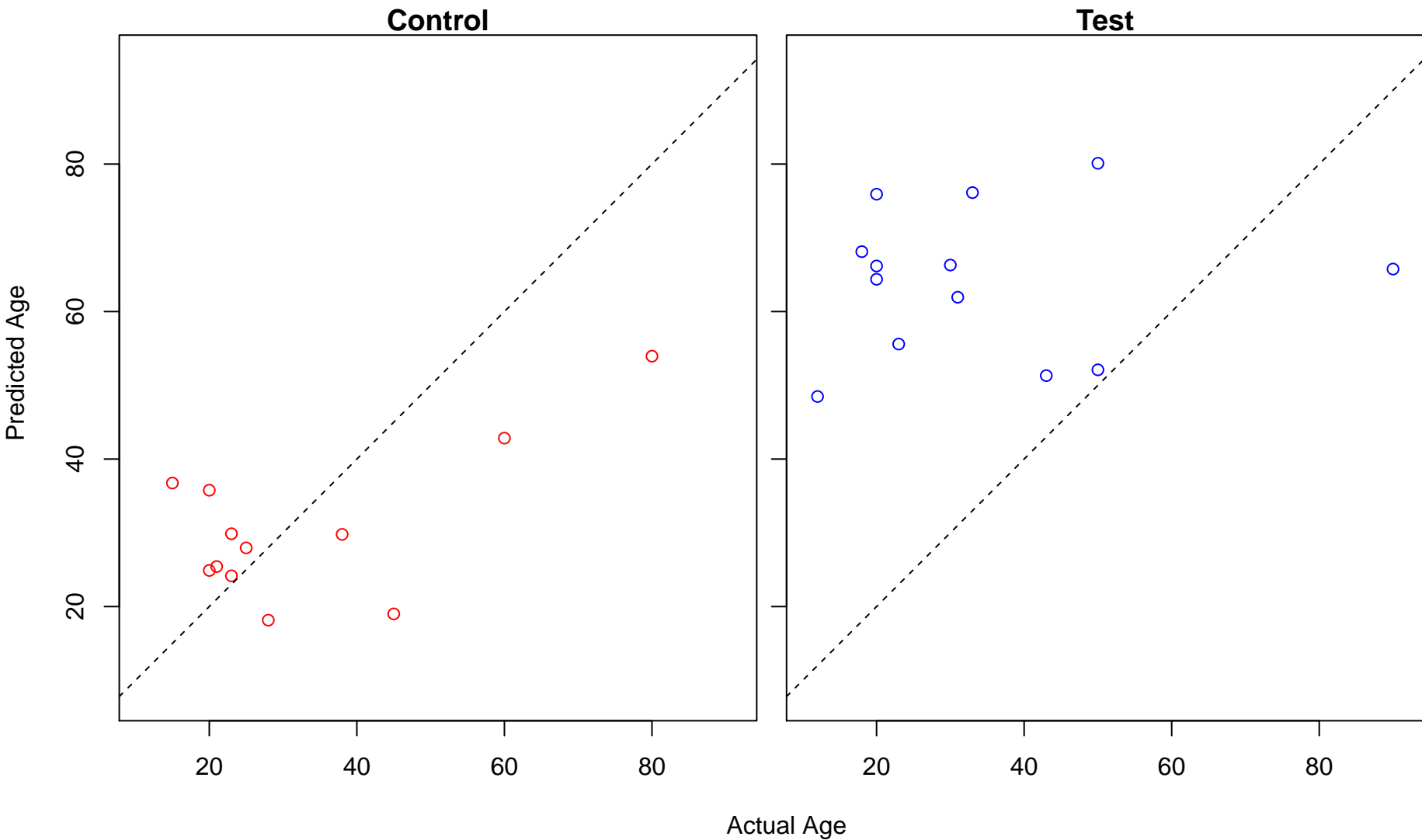
protein localization to cytoplasmic stress granule (Score: 2.976516)



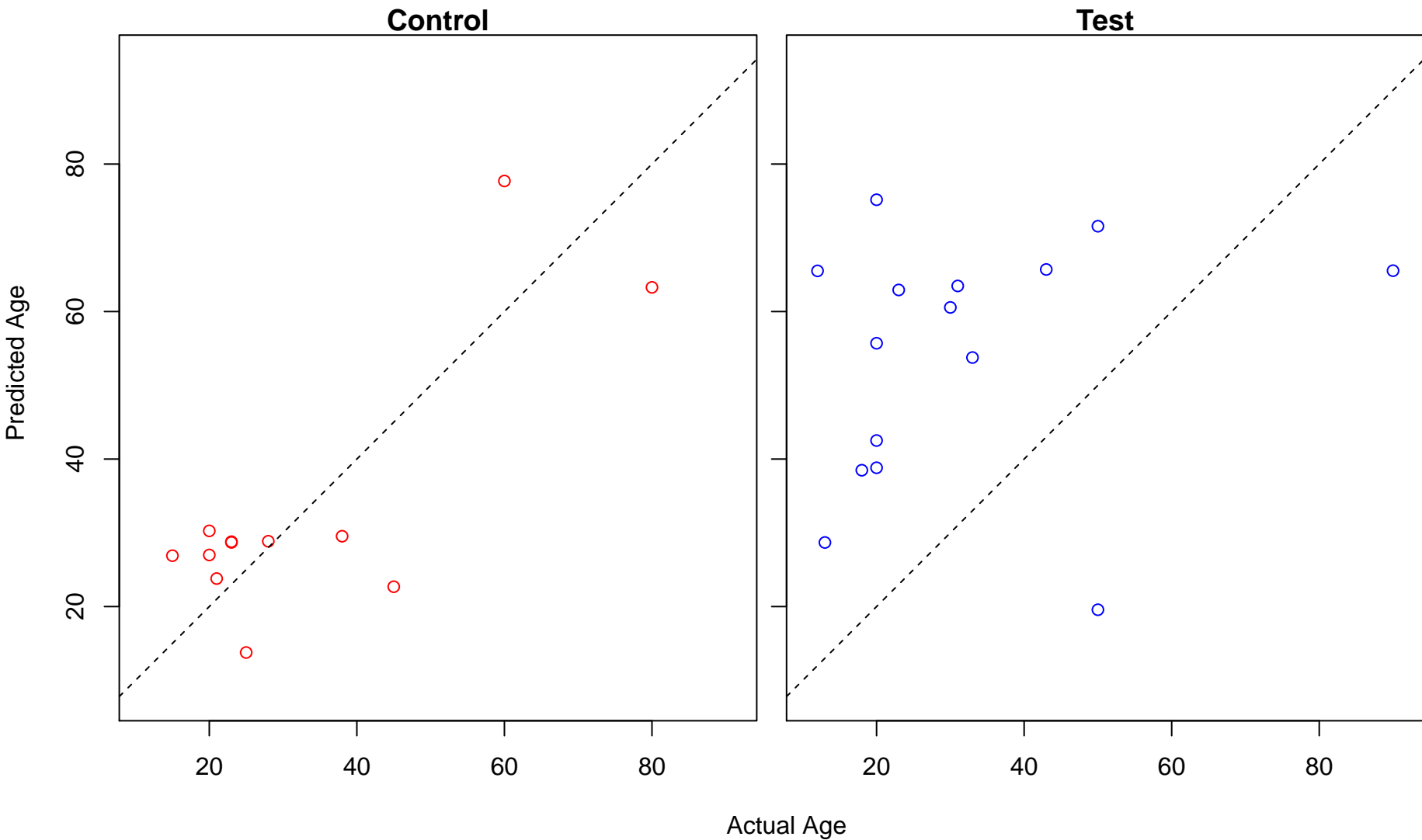
somite development (Score: 2.976376)



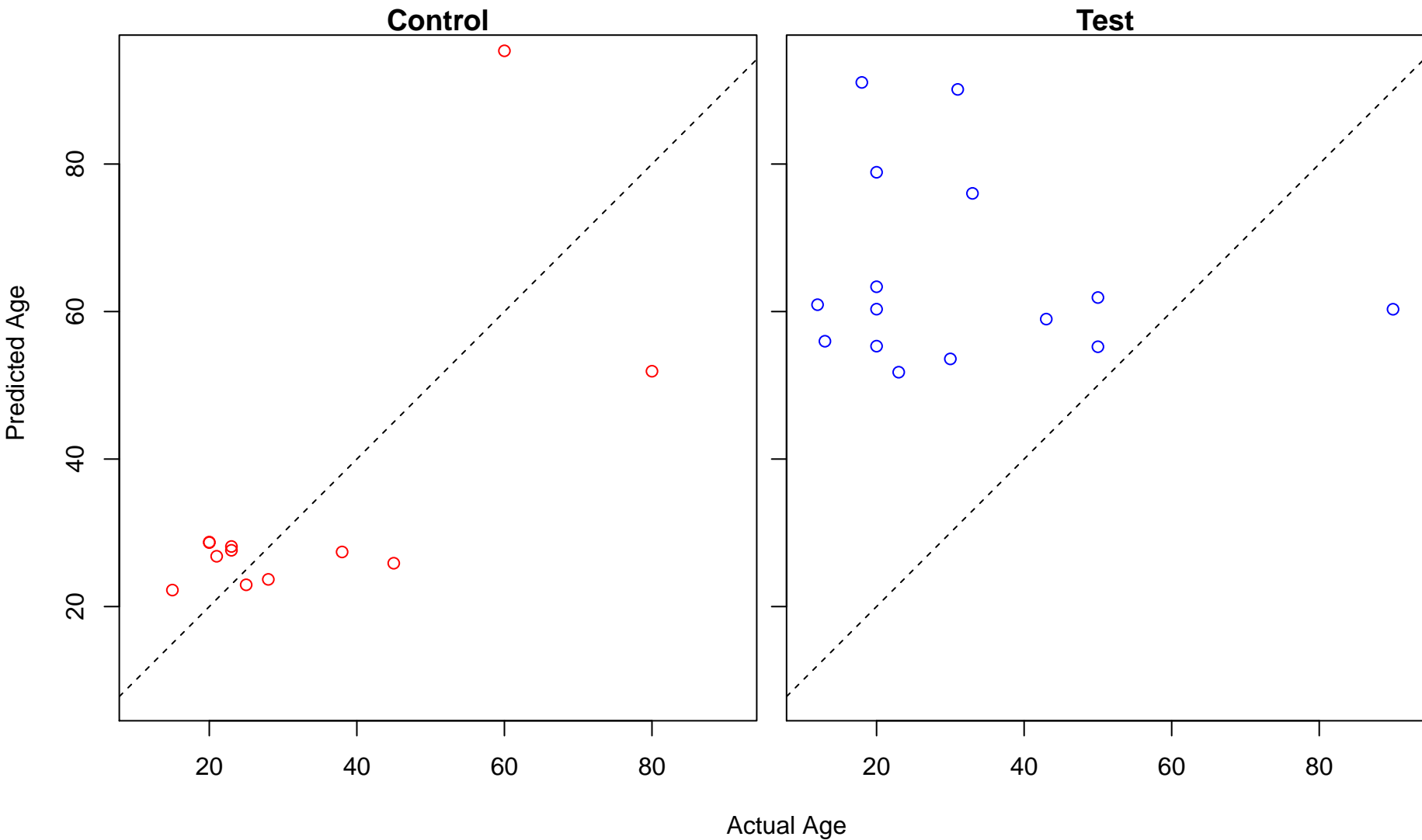
regulation of hair follicle development (Score: 2.975057)



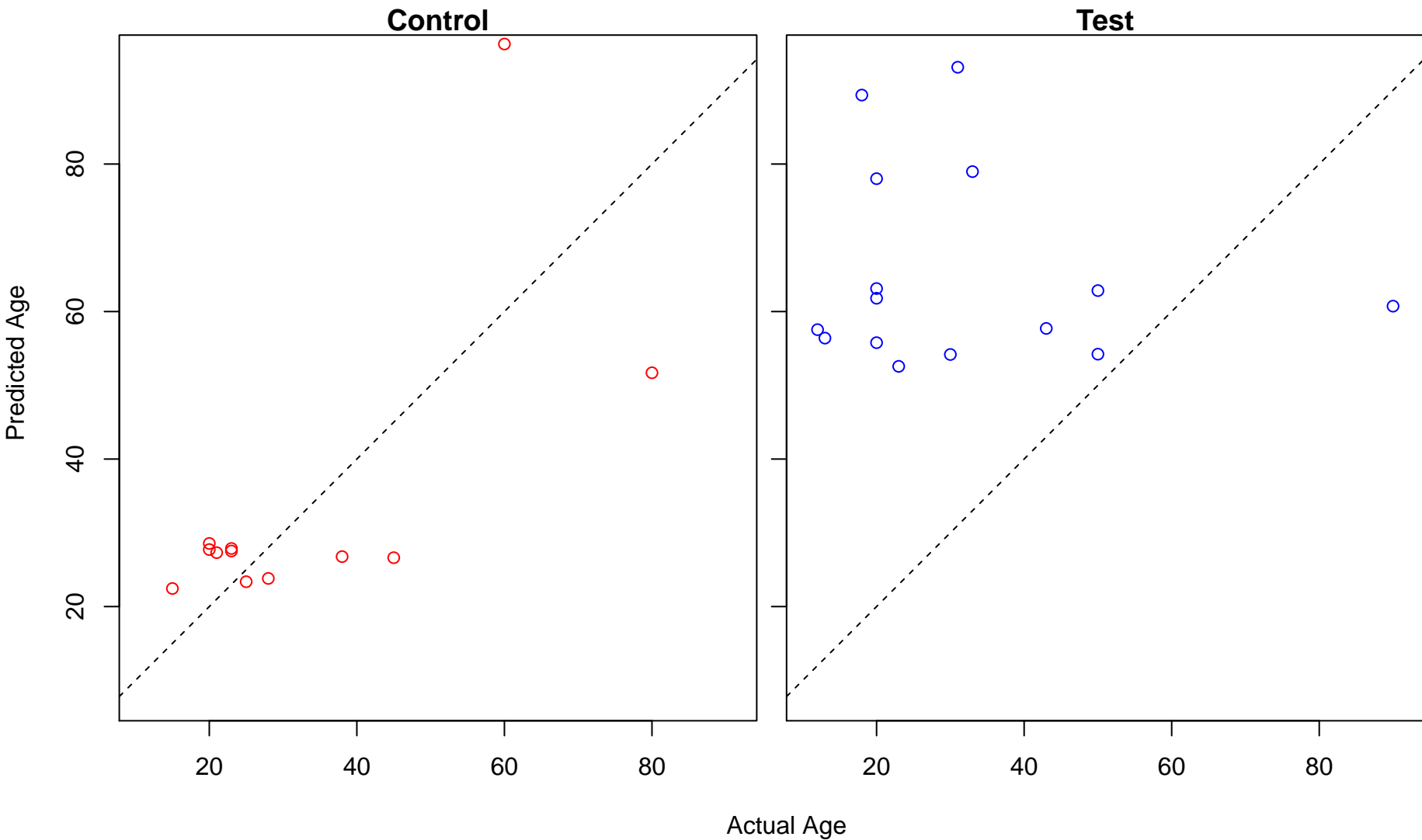
negative regulation of interleukin-12 production (Score: 2.972176)



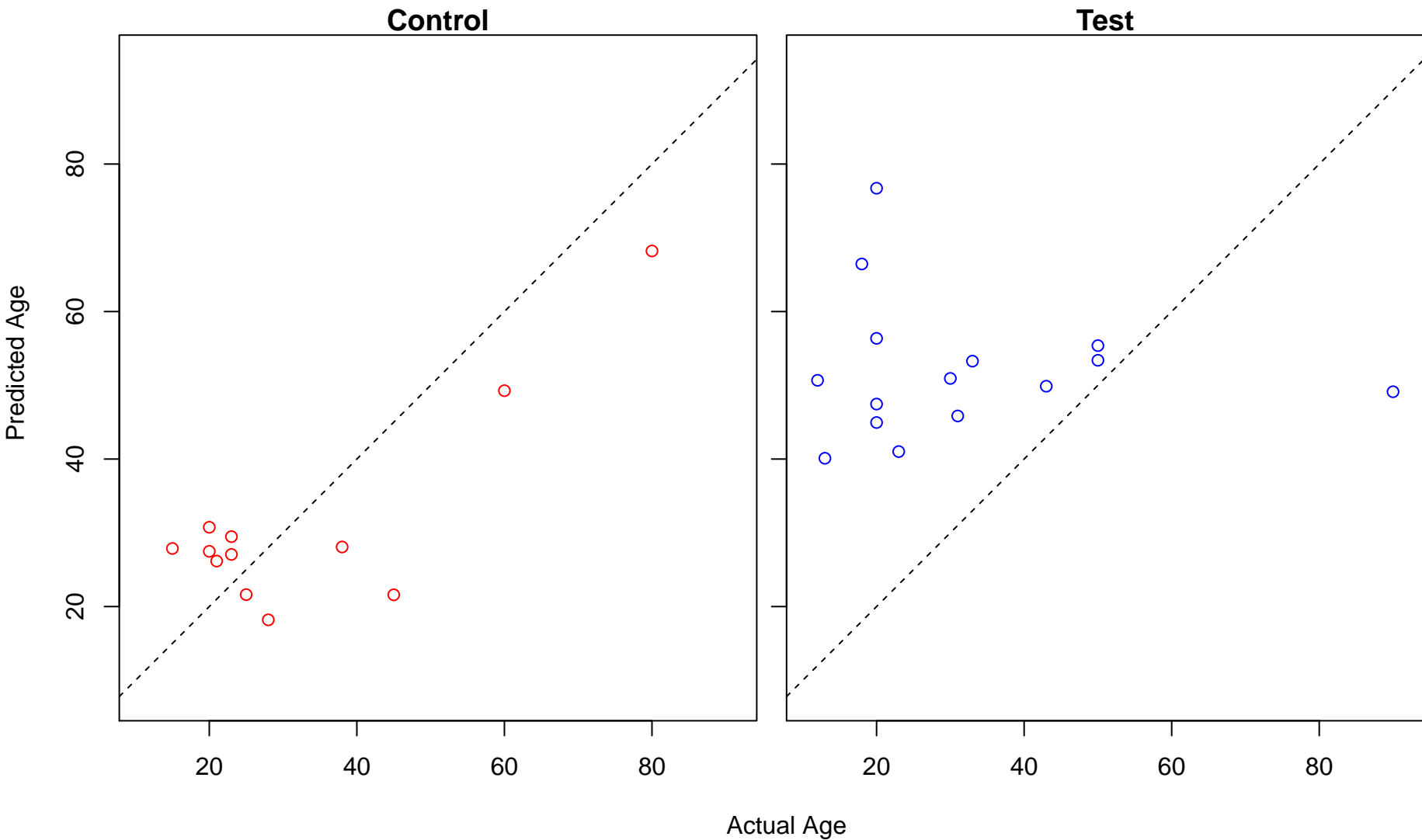
excitatory synapse assembly (Score: 2.967332)



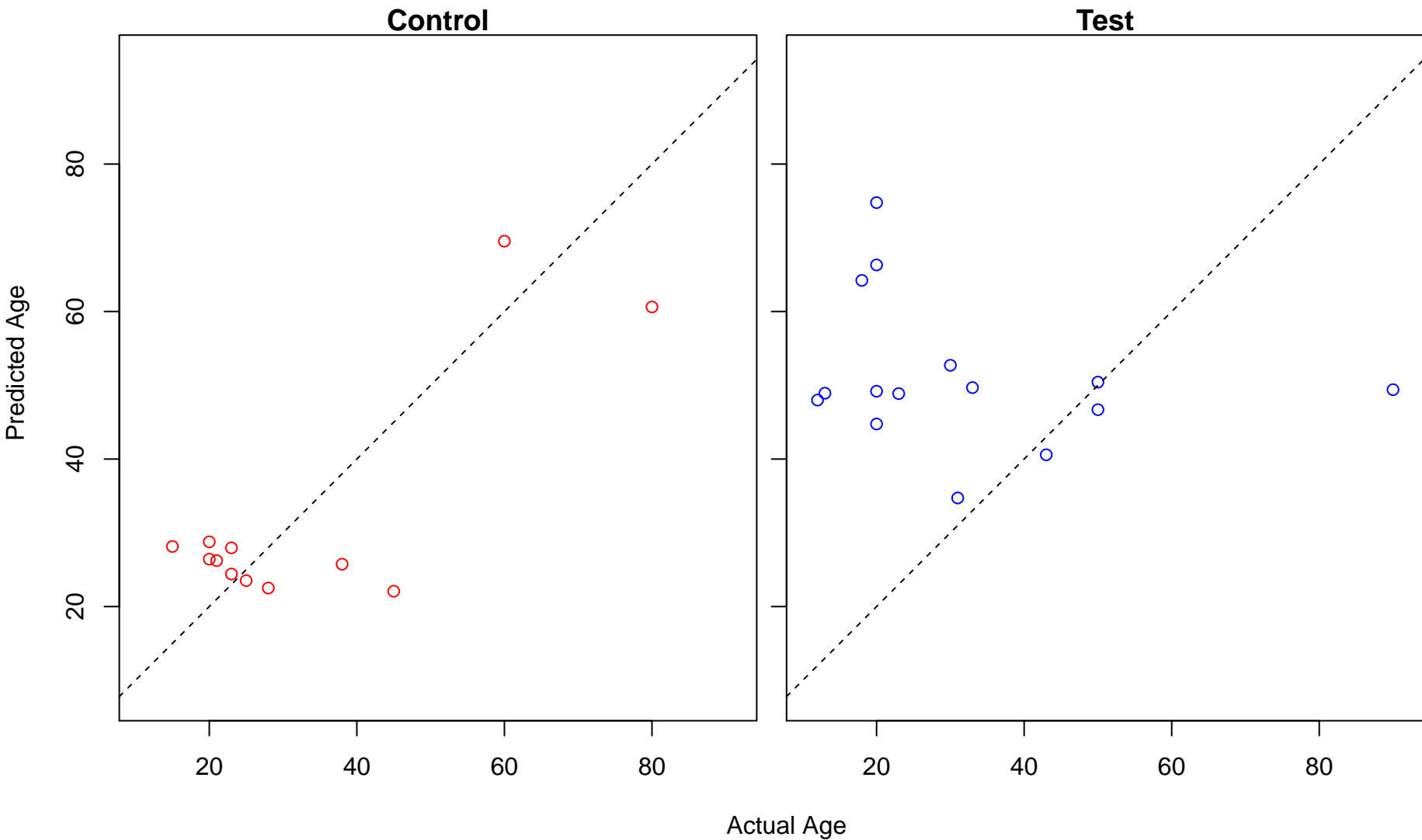
dendritic spine morphogenesis (Score: 2.957968)



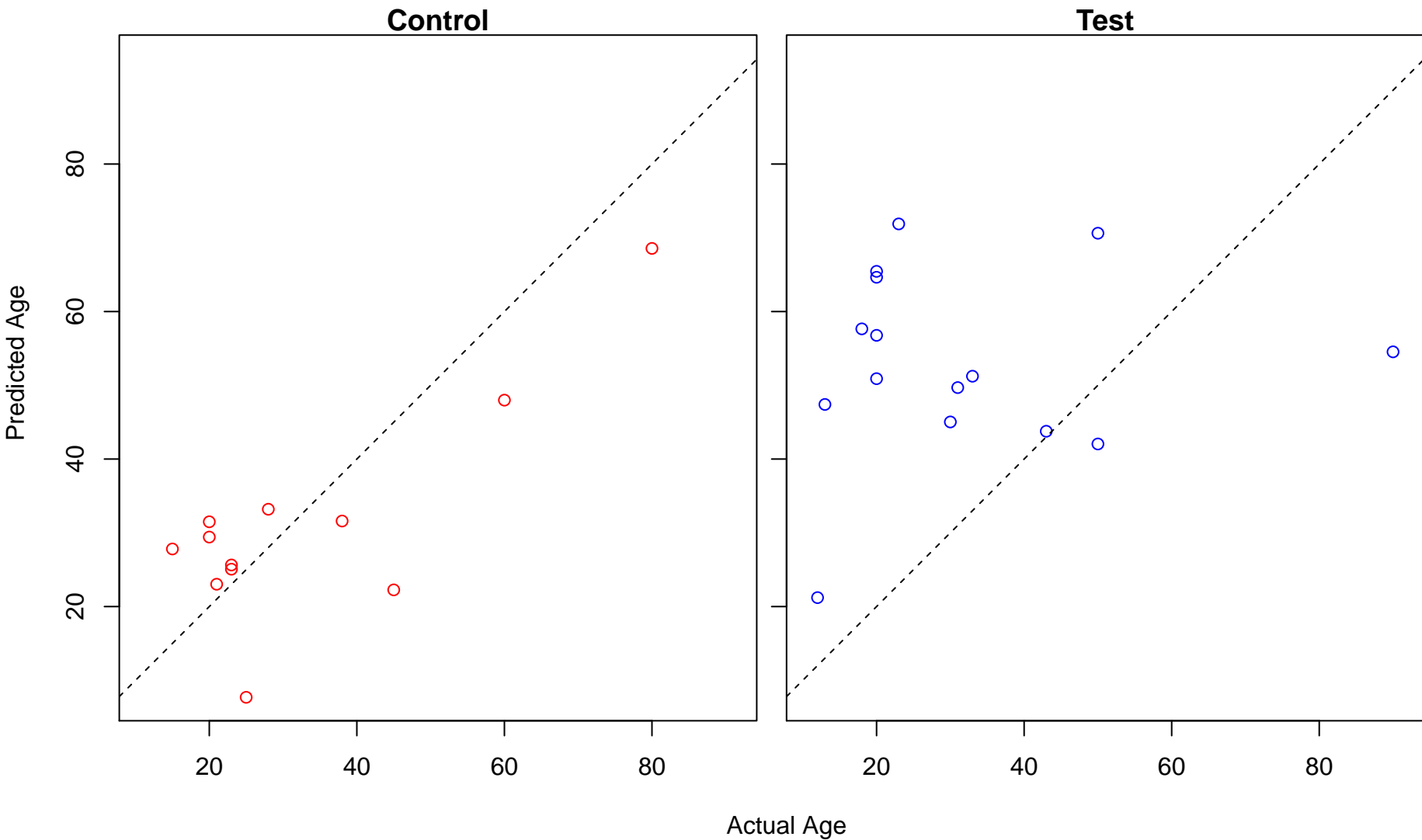
lipid transport (Score: 2.957470)



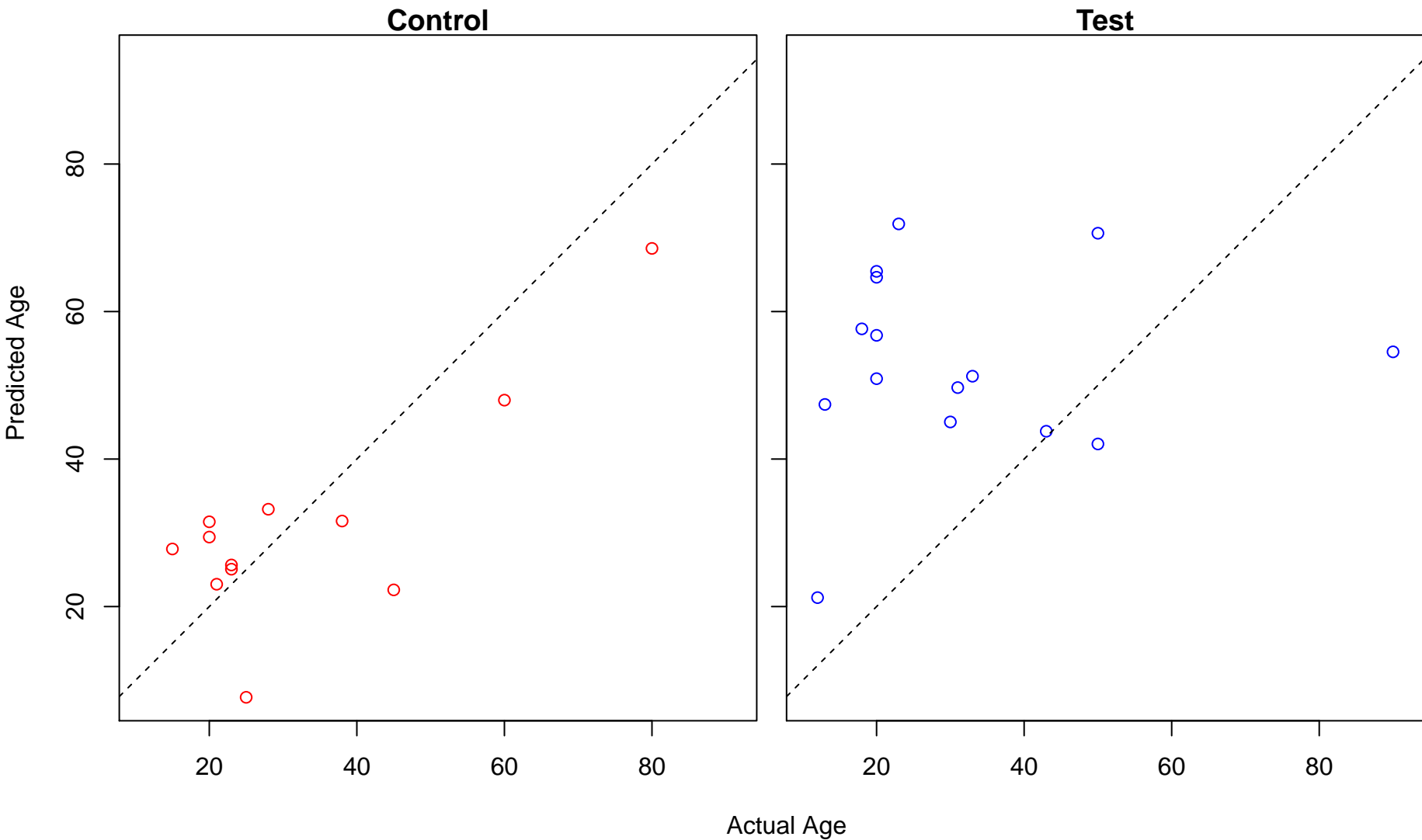
plasma membrane organization (Score: 2.956110)



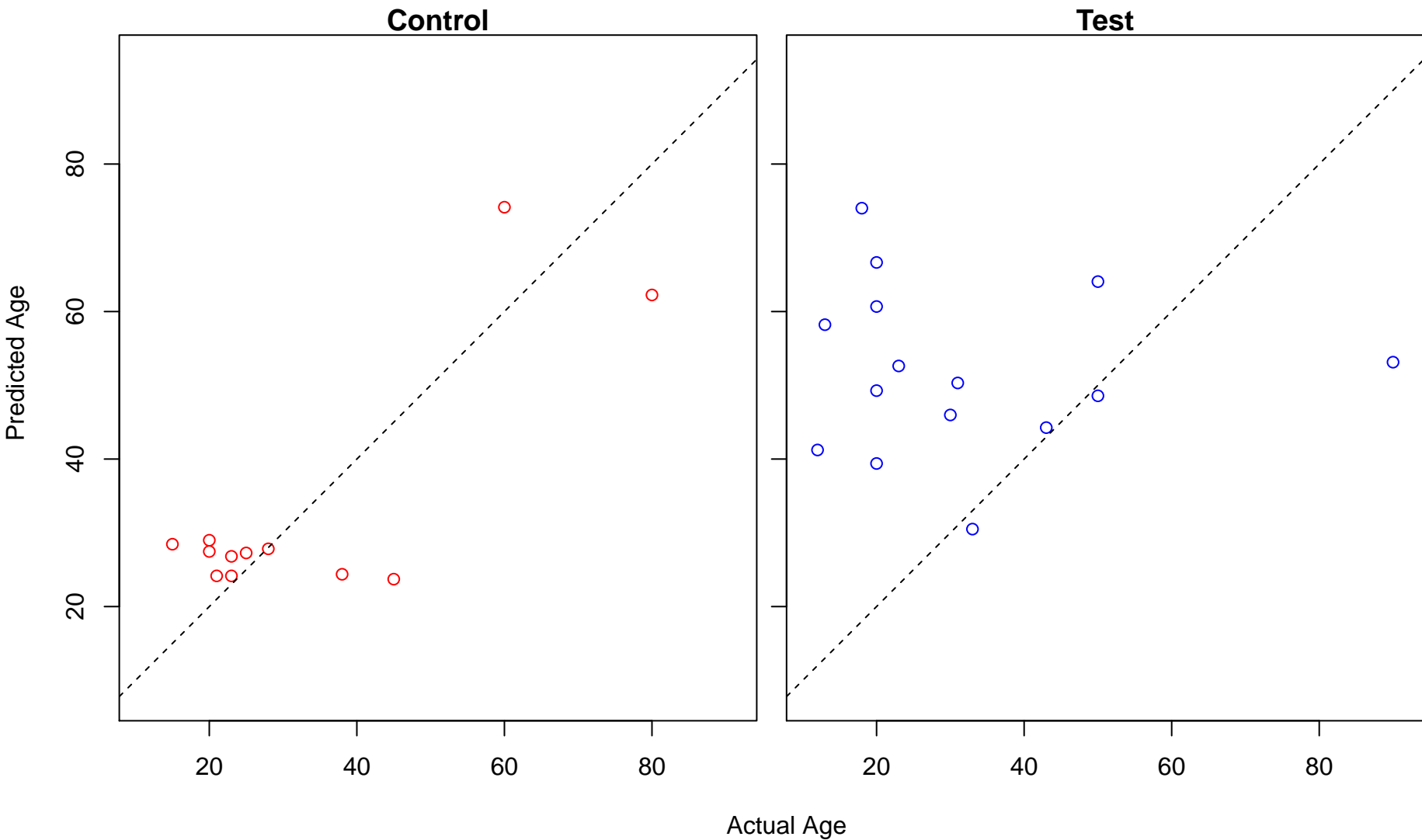
protein demethylation (Score: 2.955903)



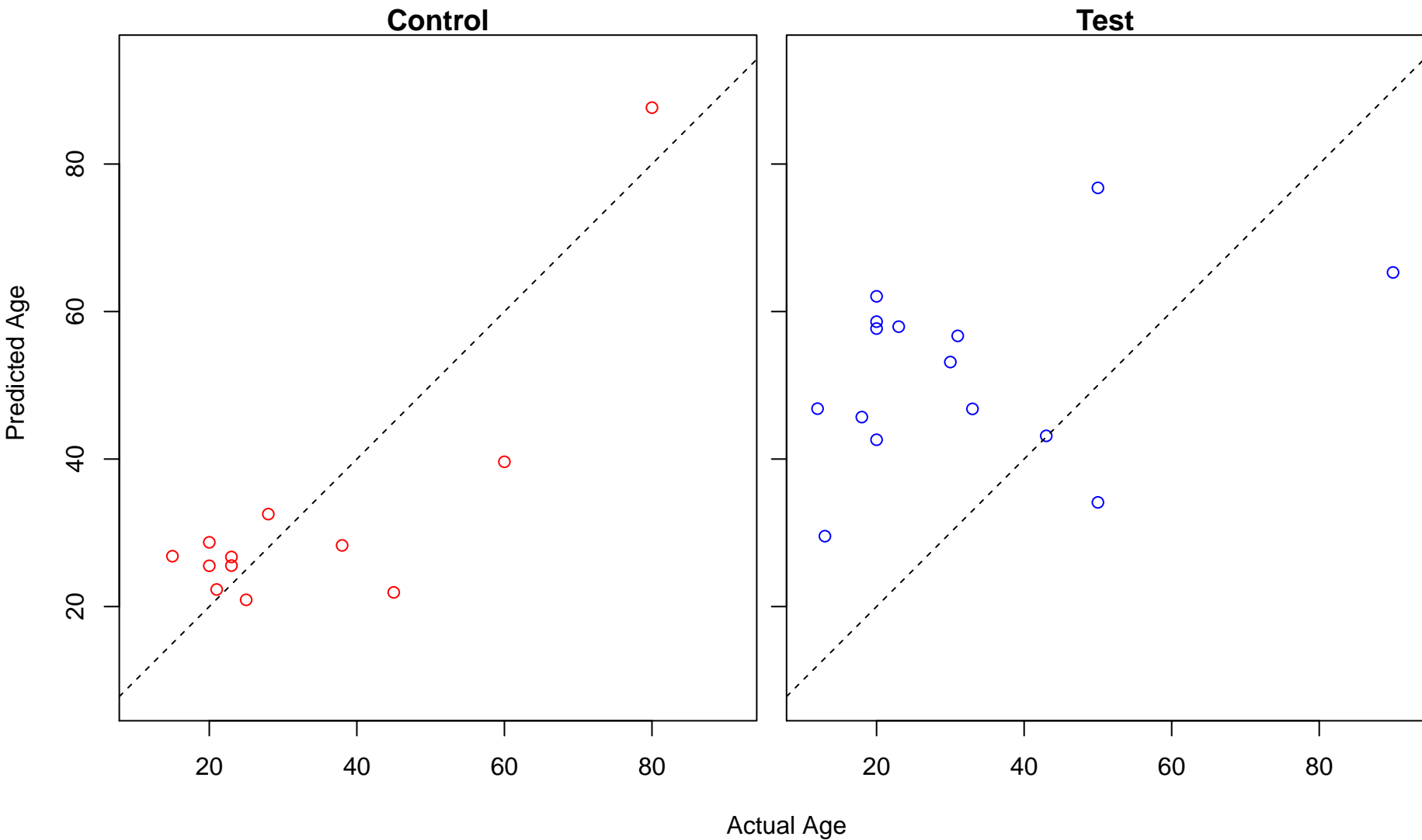
protein dealkylation (Score: 2.955903)



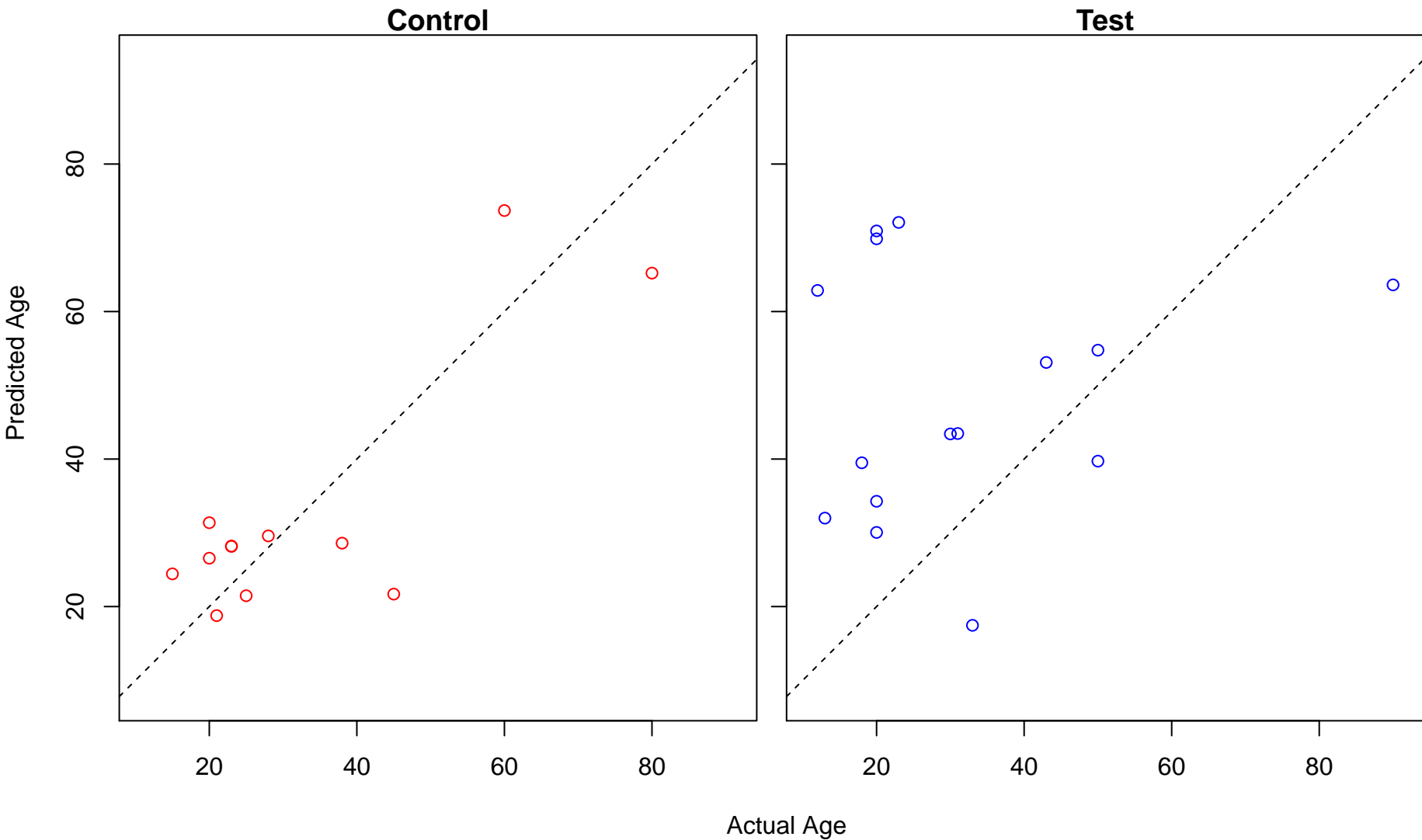
gluconeogenesis (Score: 2.954141)



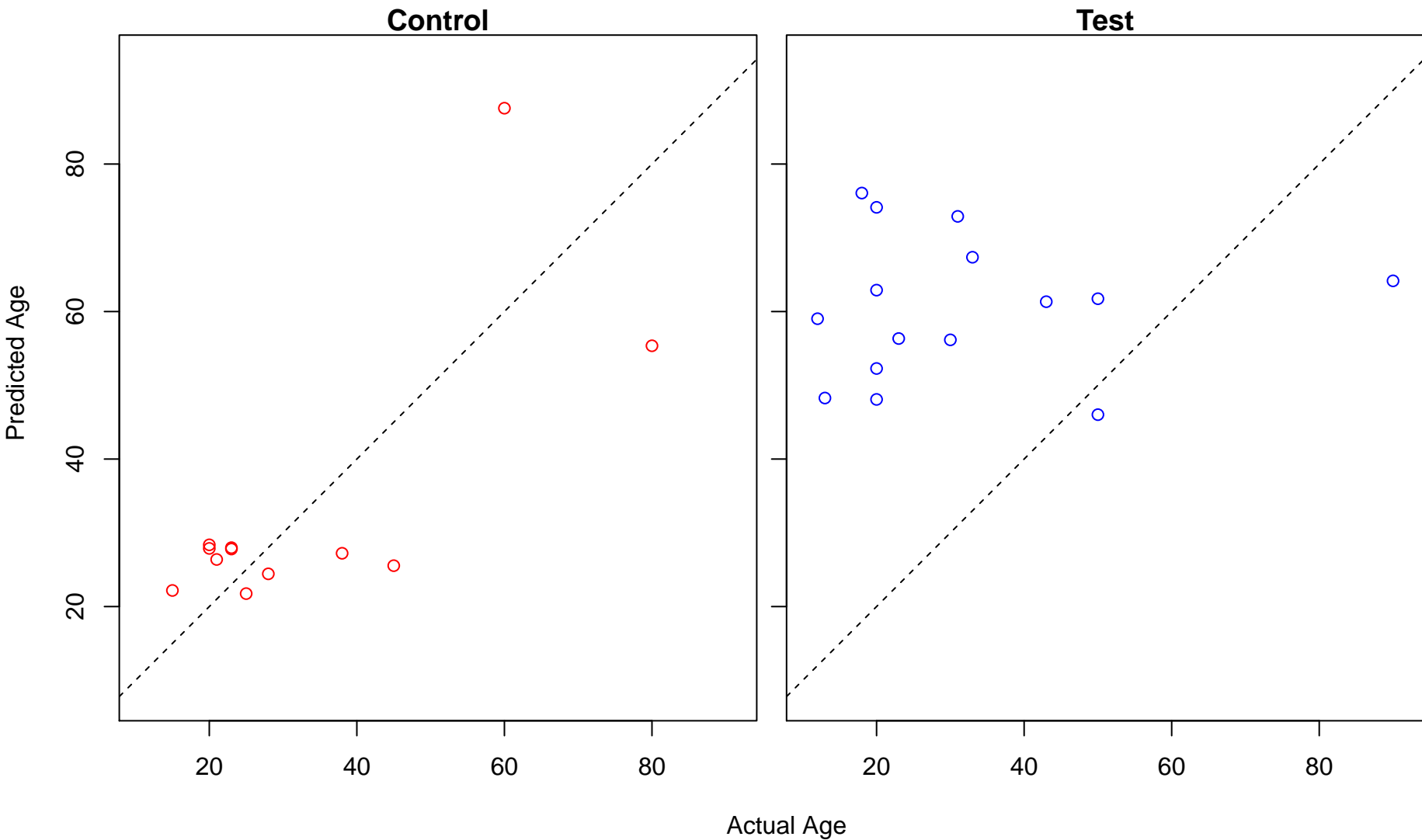
regulation of cytoplasmic translation (Score: 2.952124)



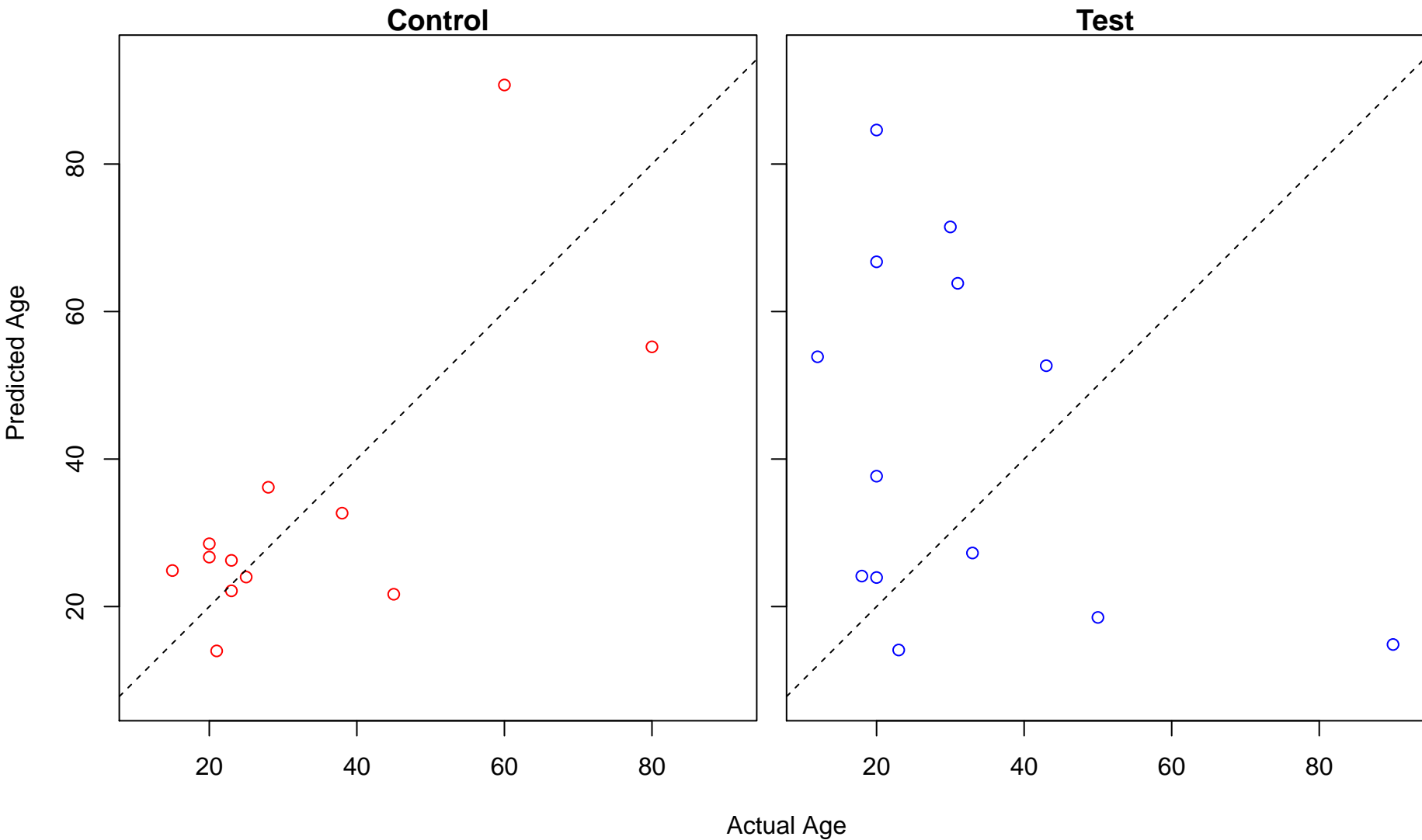
mitochondrial RNA processing (Score: 2.951667)



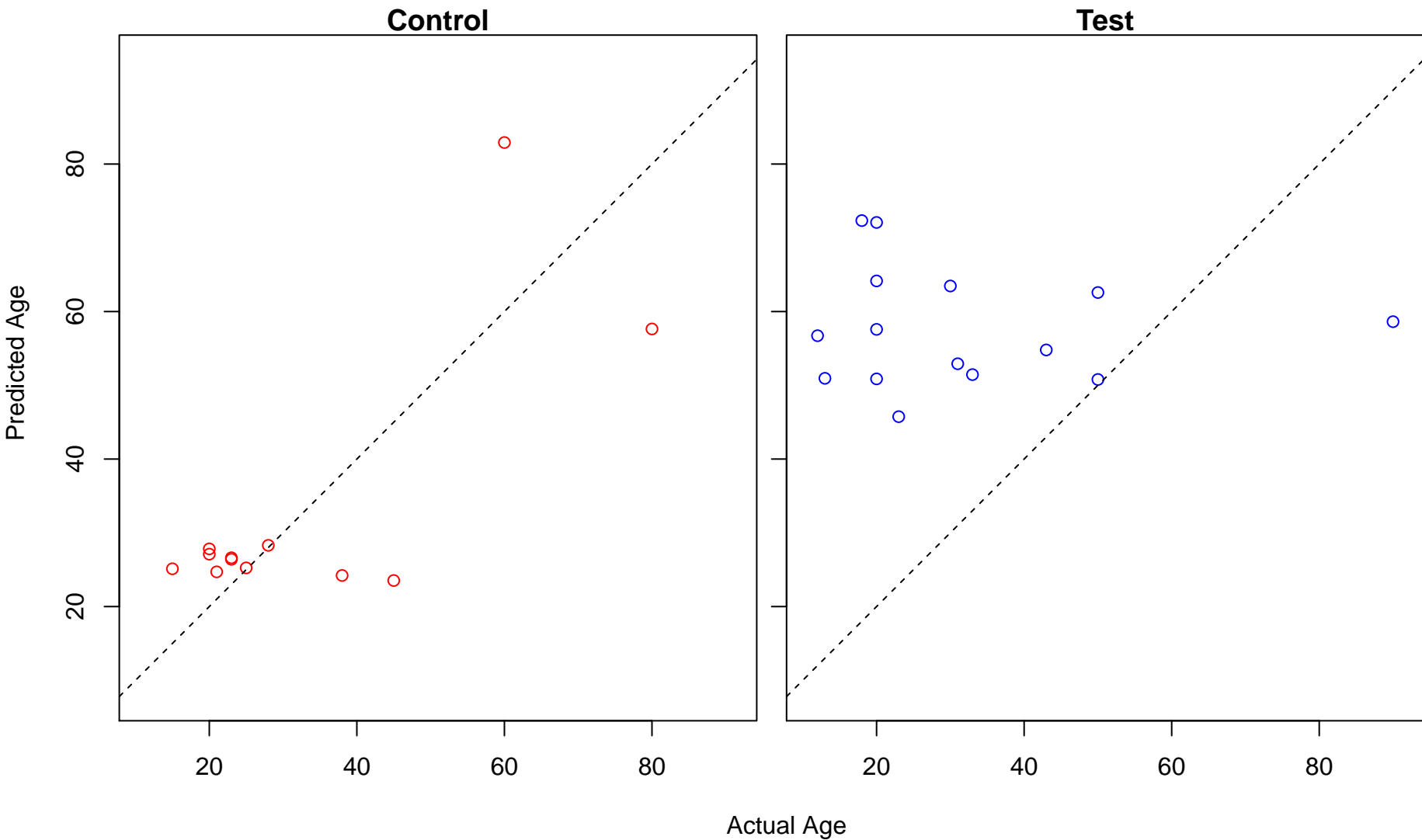
negative regulation of cell size (Score: 2.949519)



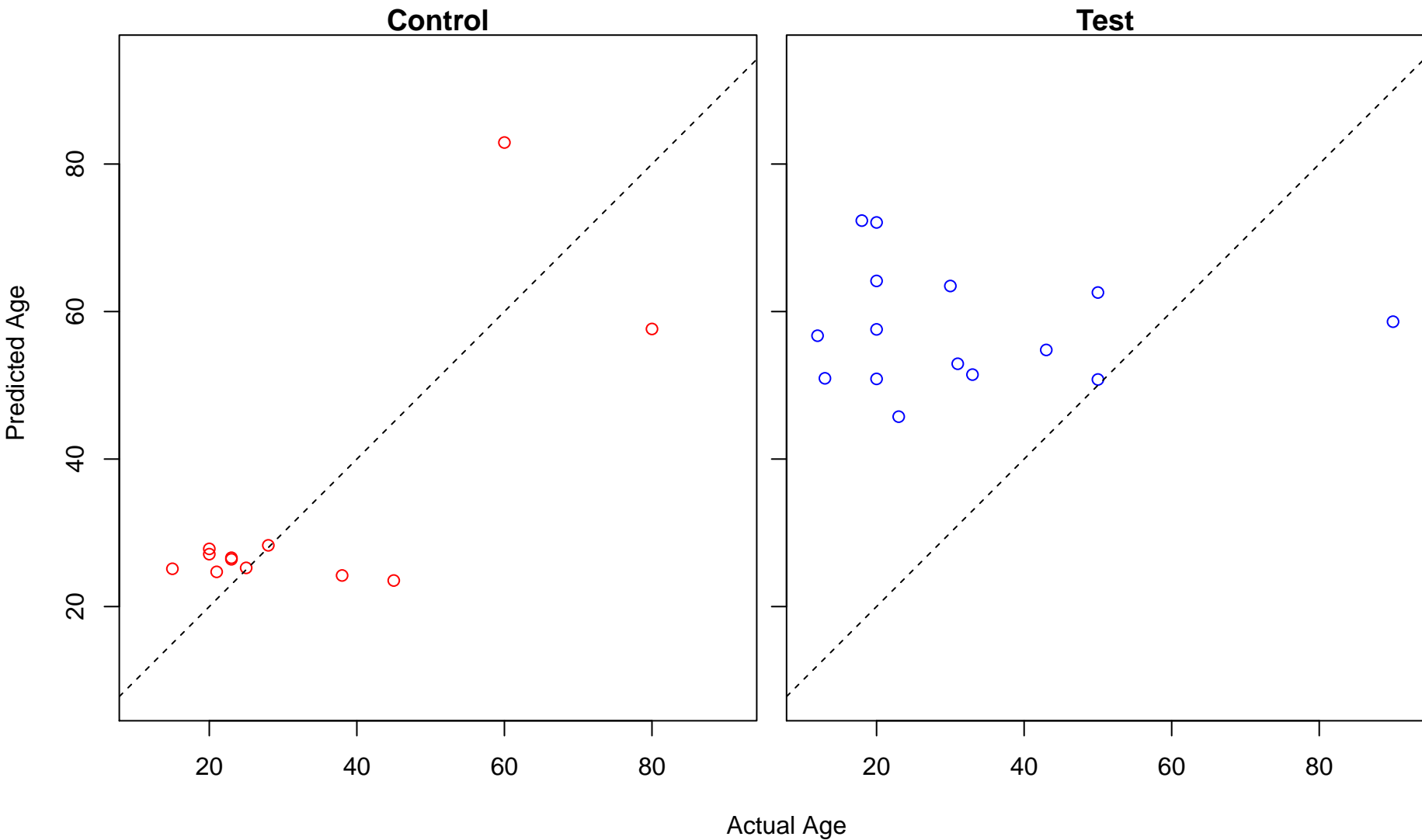
leukocyte activation involved in immune response (Score: 2.946285)



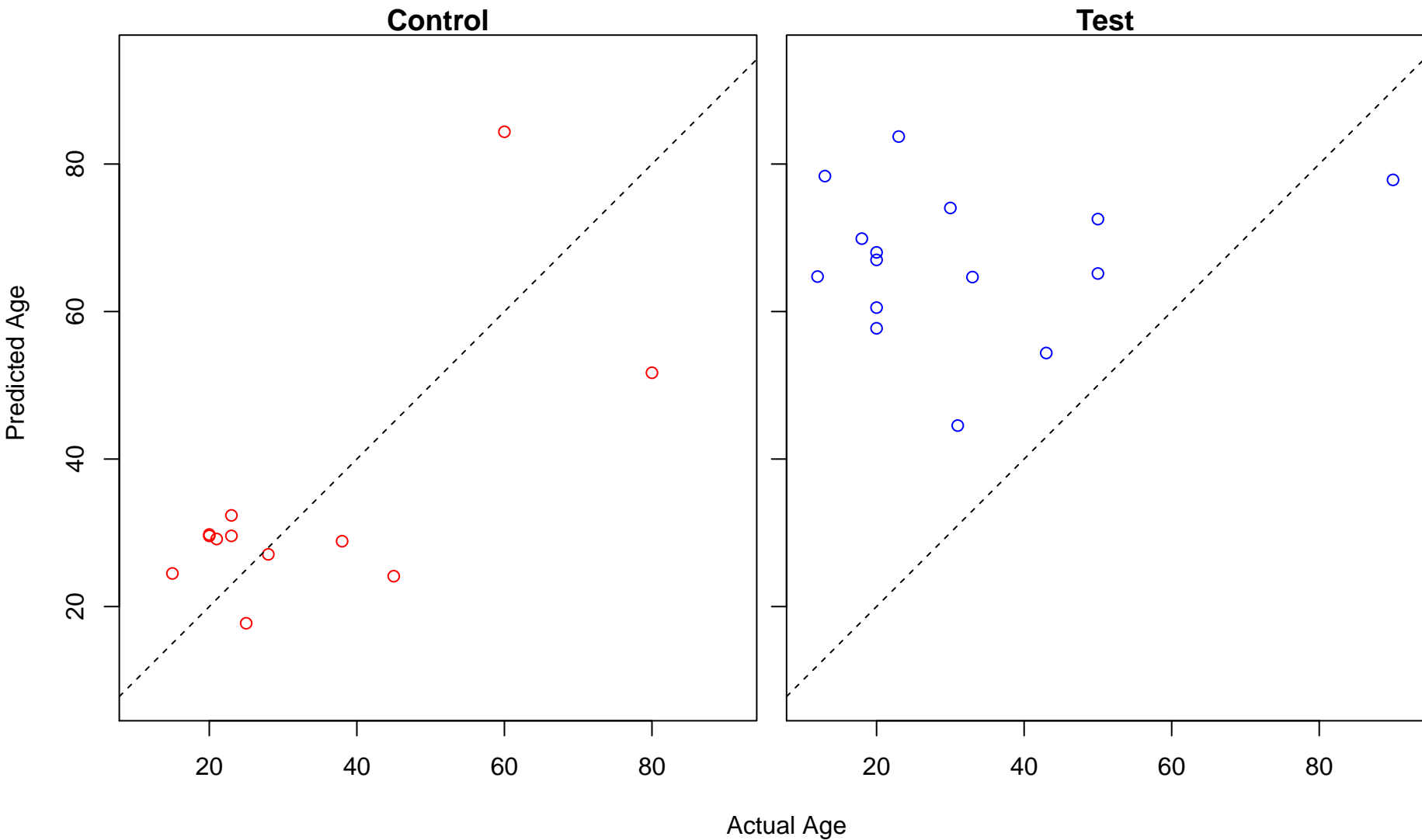
lysine metabolic process (Score: 2.943606)



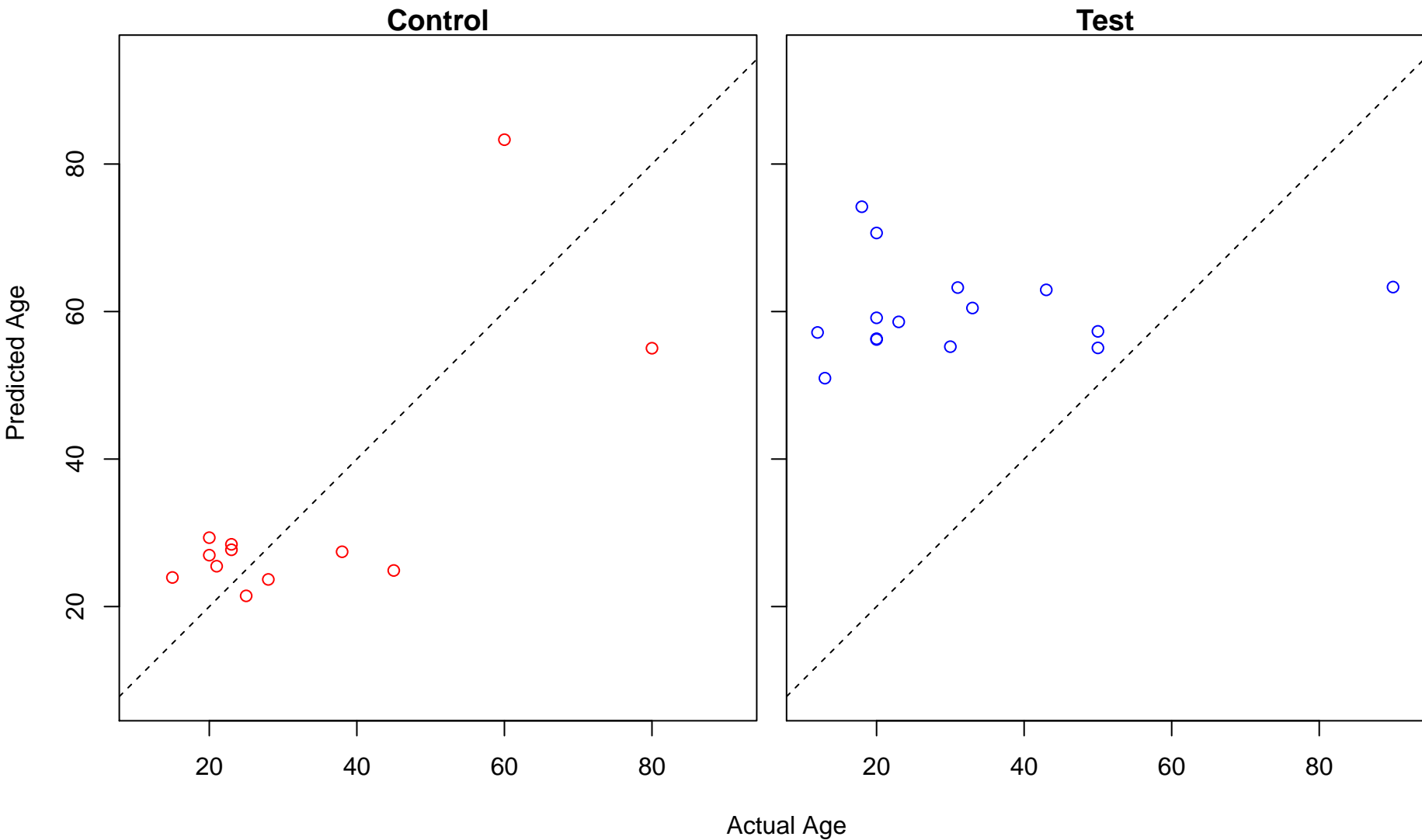
lysine catabolic process (Score: 2.943606)



positive regulation of antigen processing and presentation (Score: 2.941094)

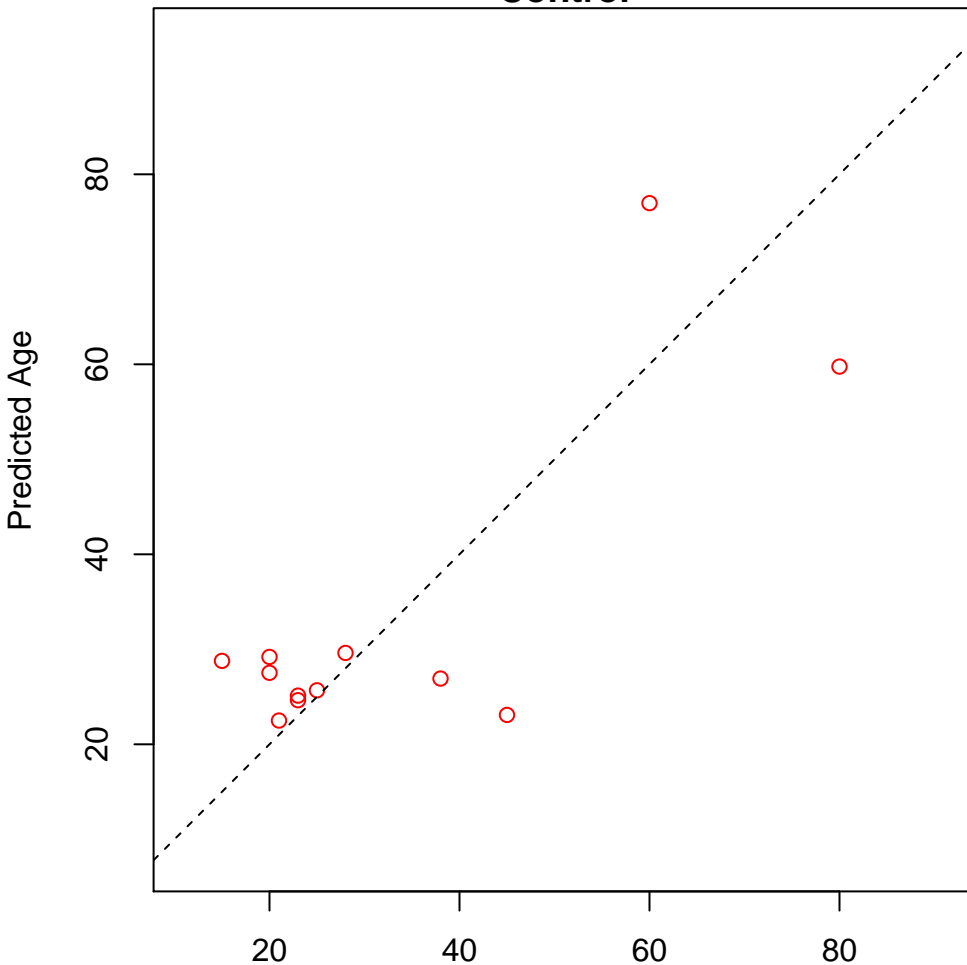


phospholipid dephosphorylation (Score: 2.933321)

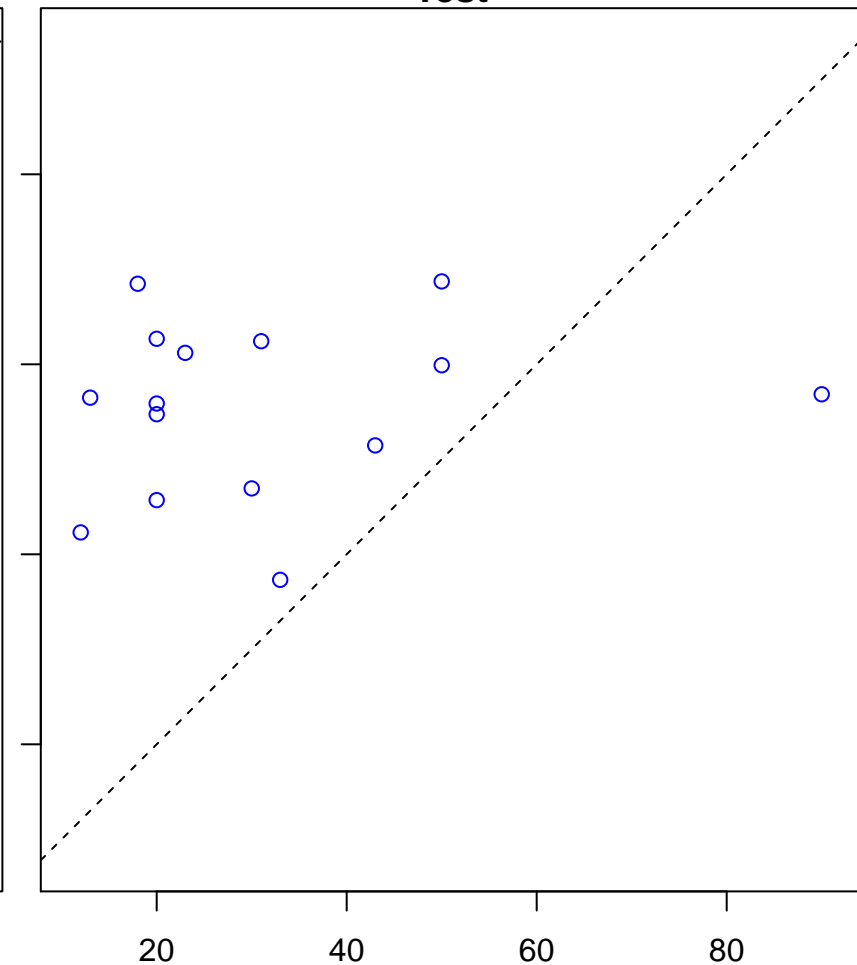


nucleoside diphosphate phosphorylation (Score: 2.930958)

Control

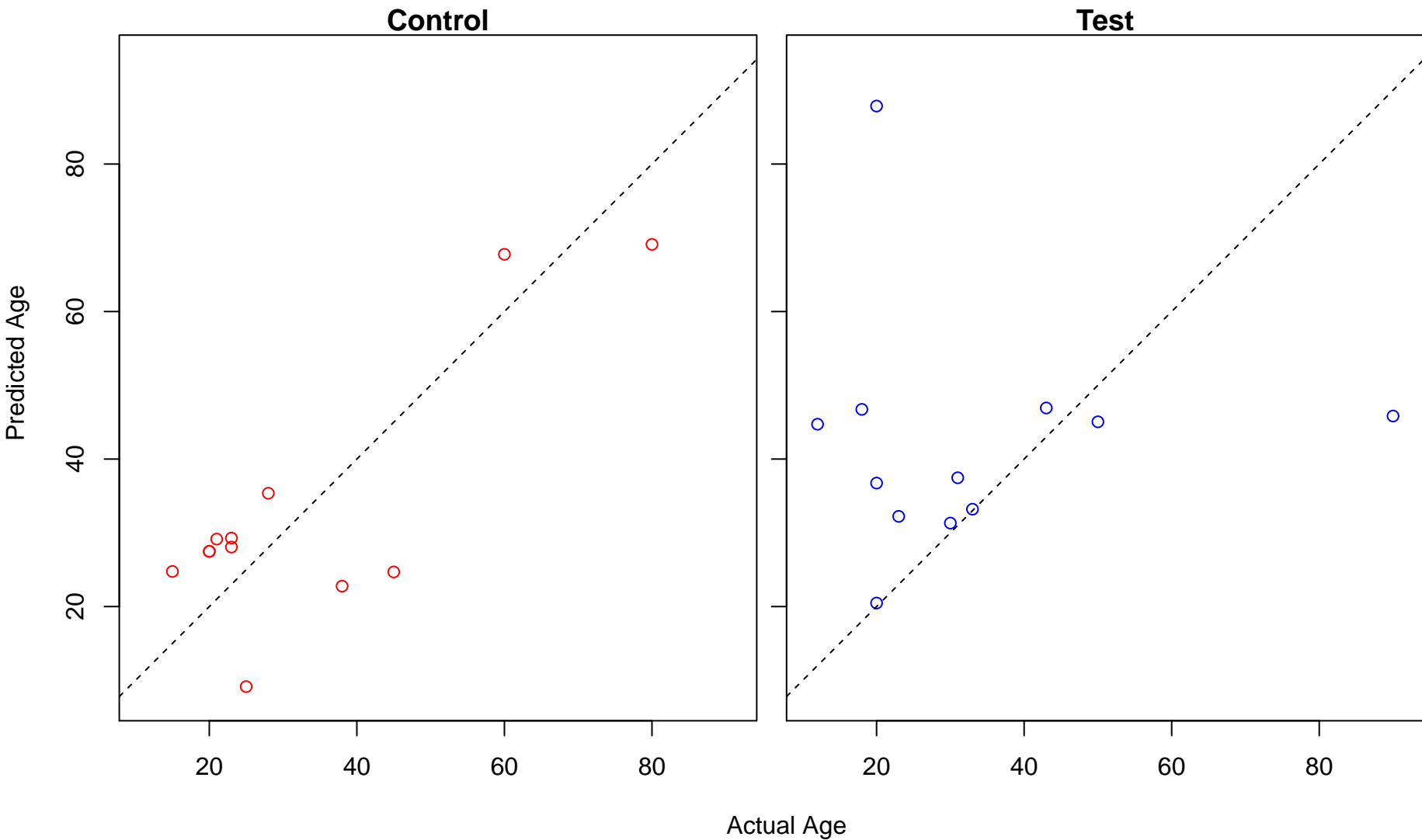


Test

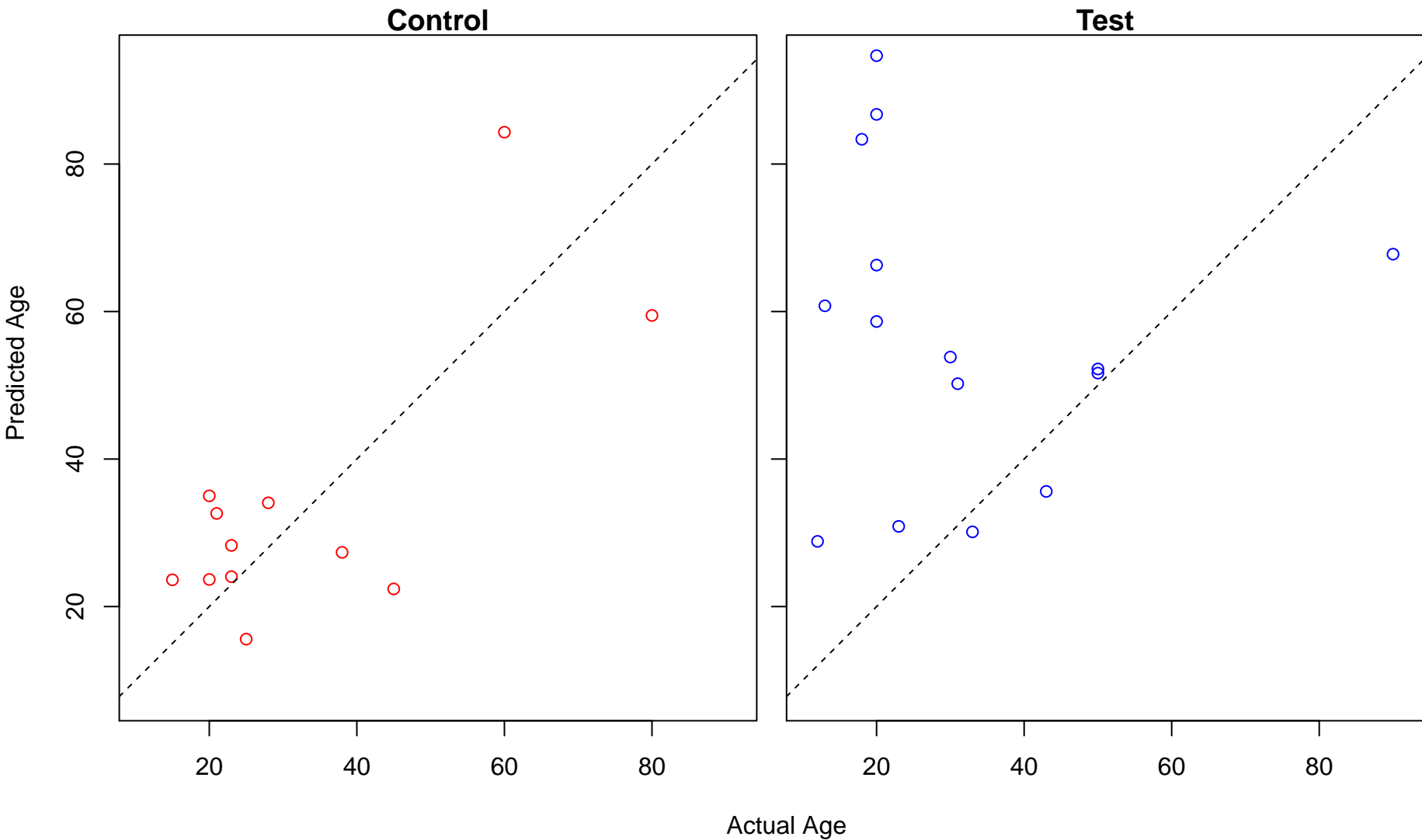


Actual Age

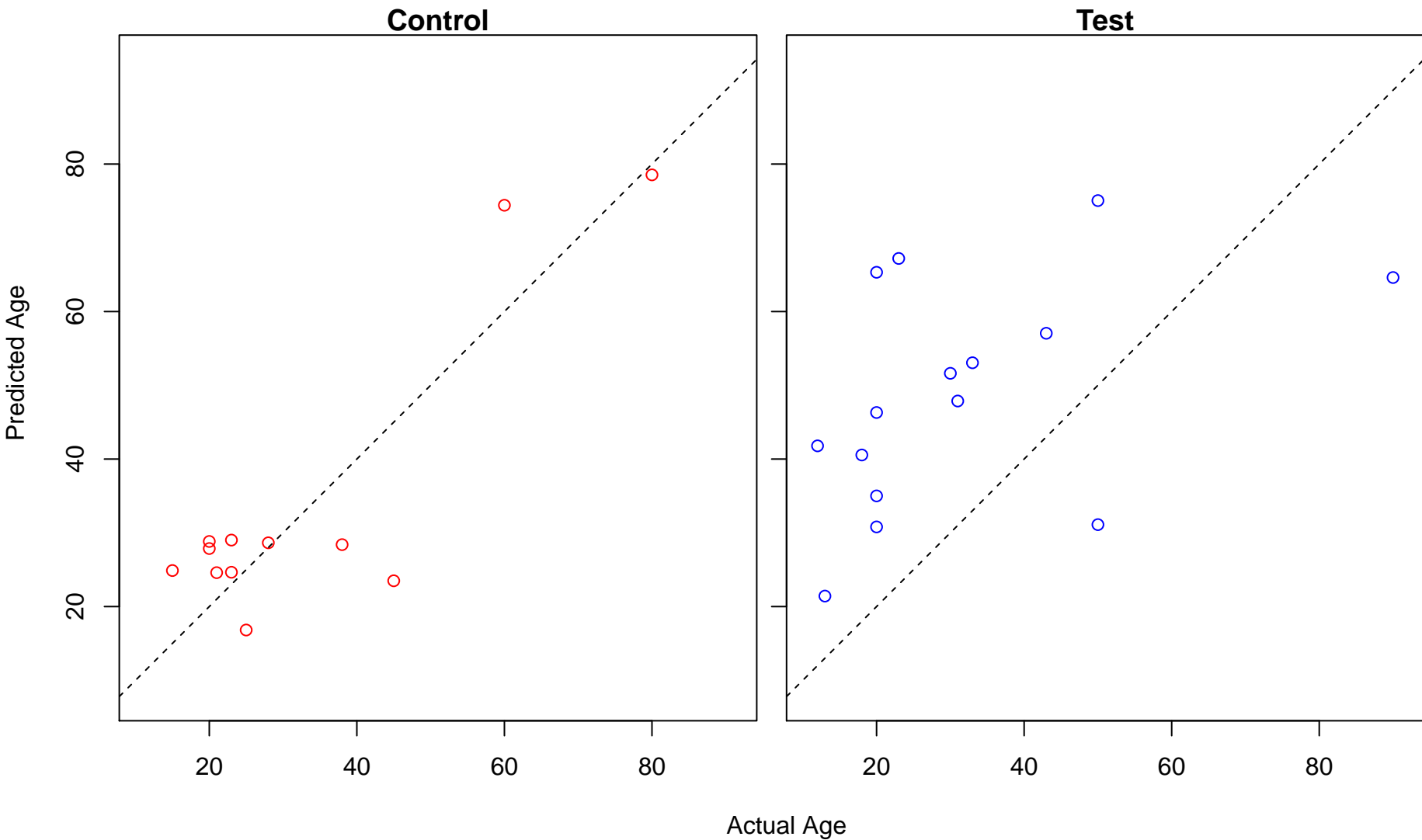
smooth muscle contraction (Score: 2.930014)



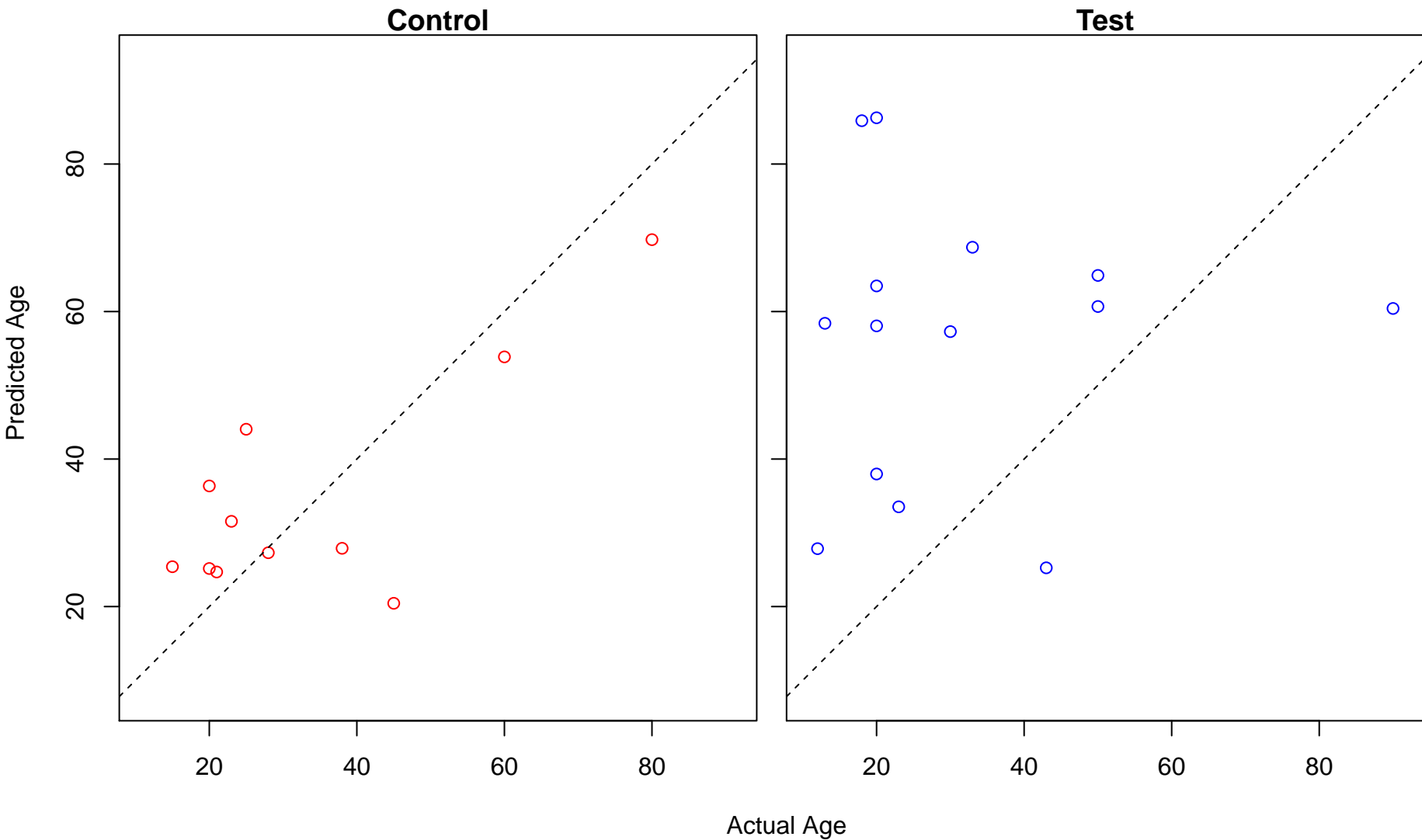
UV protection (Score: 2.928850)



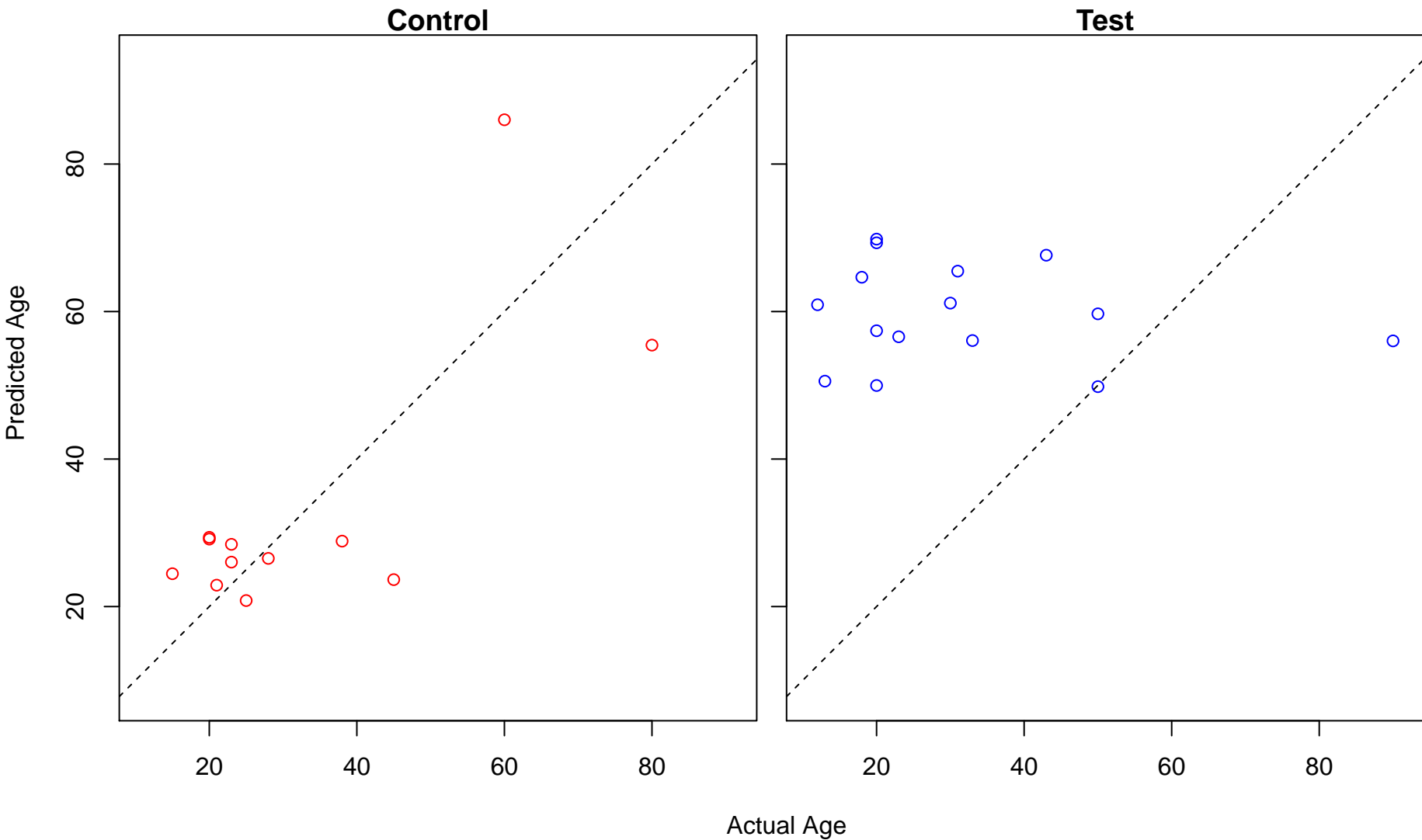
vesicle transport along microtubule (Score: 2.925713)



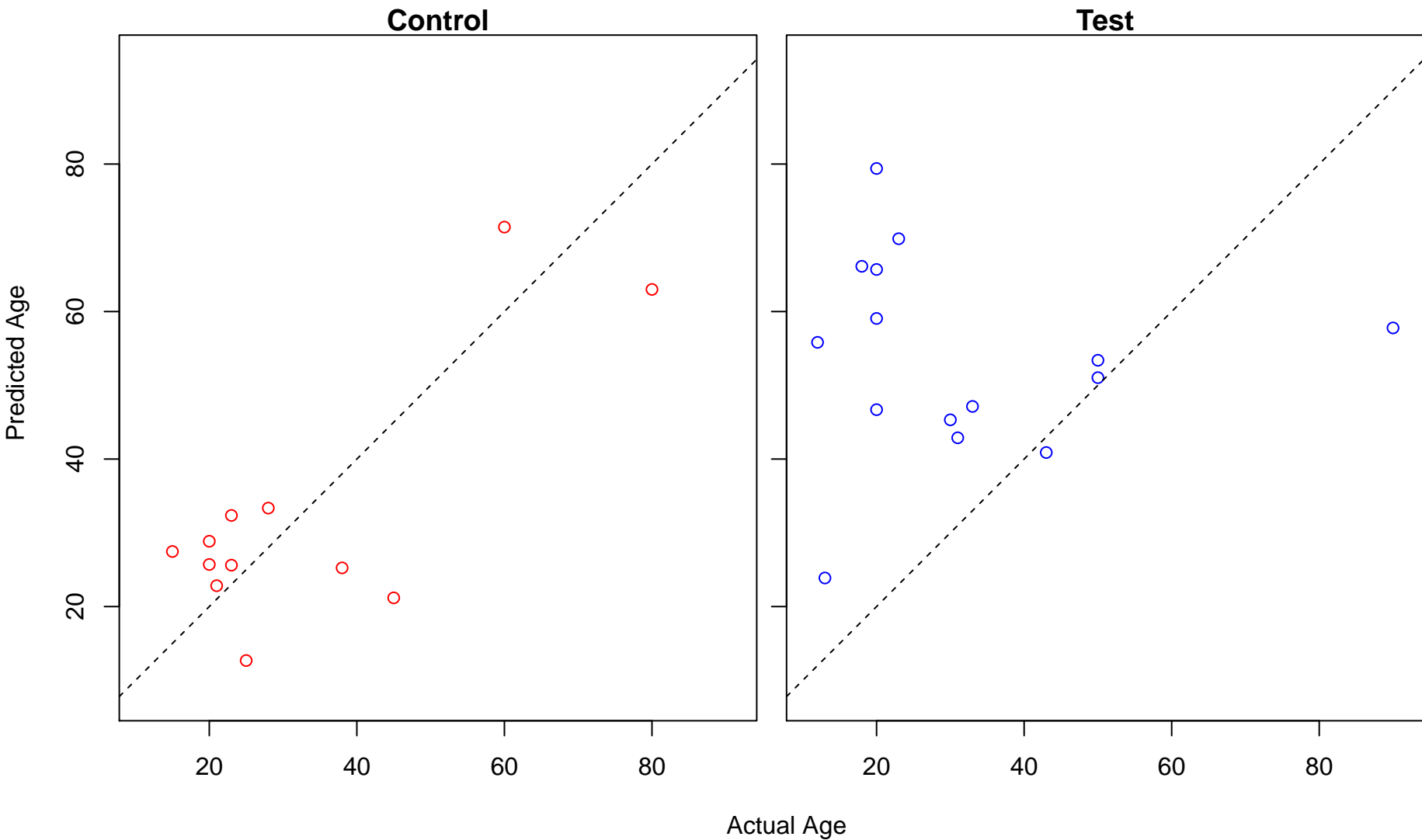
regulation of protein kinase C signaling (Score: 2.924813)



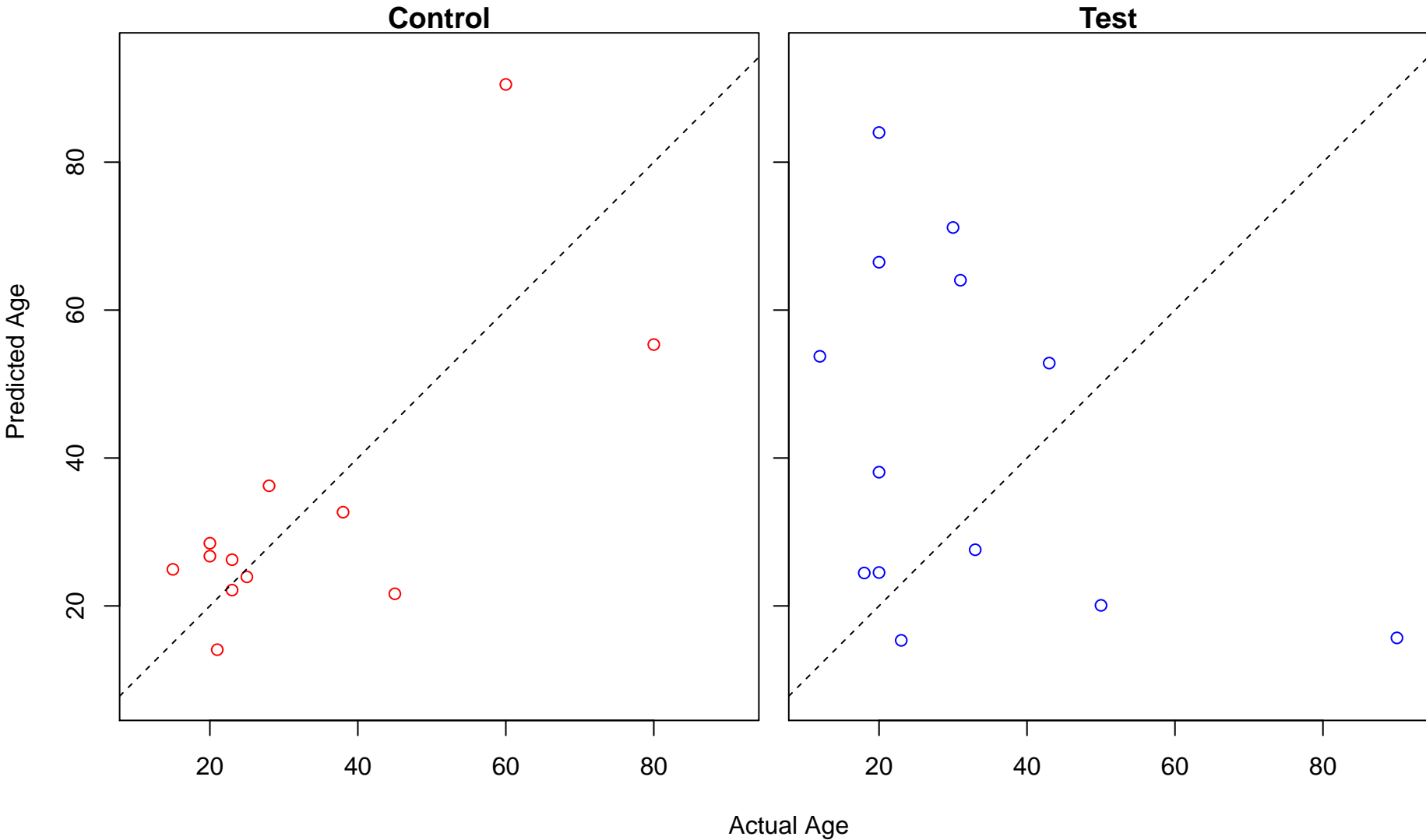
positive regulation of response to biotic stimulus (Score: 2.911020)



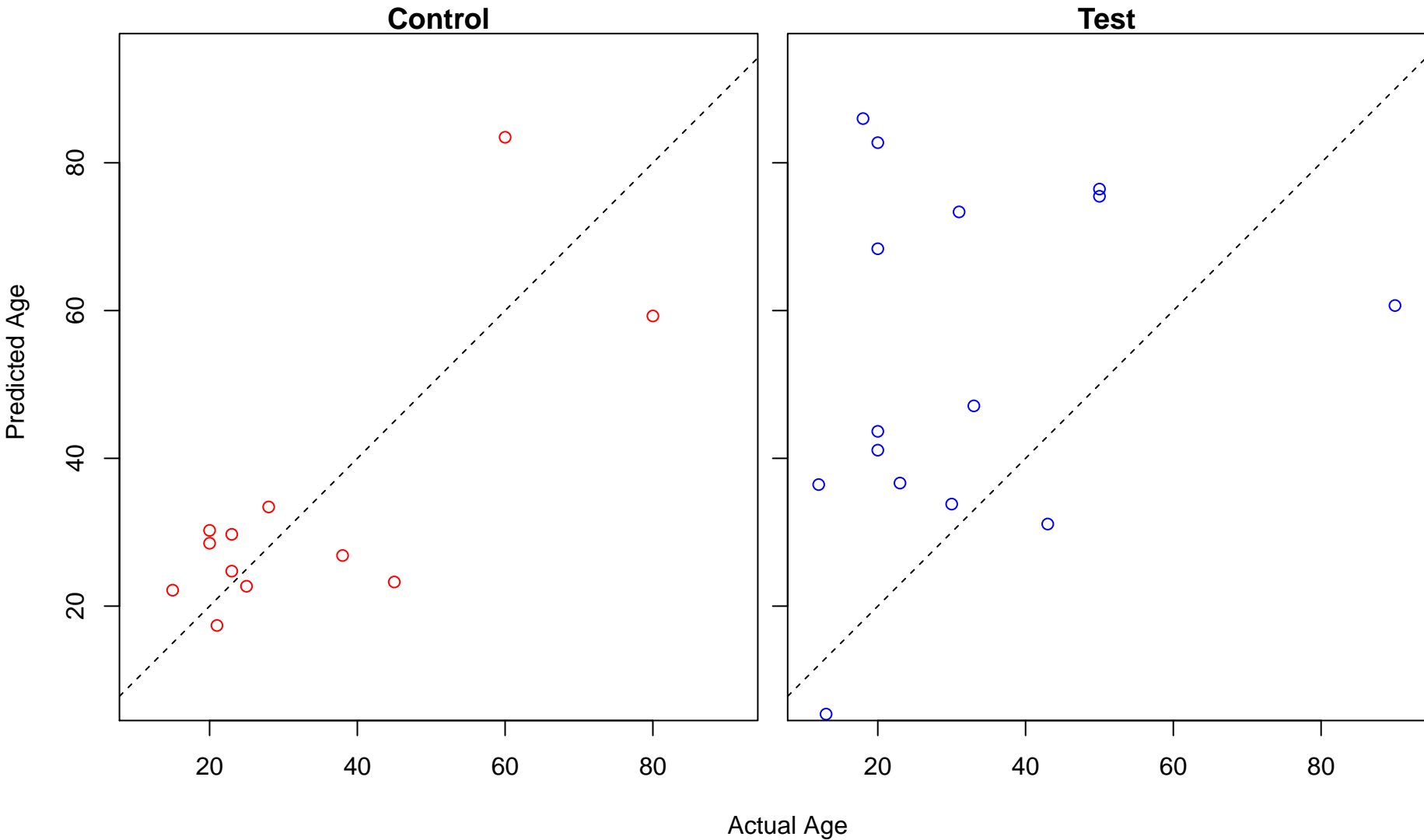
ribonucleoprotein complex assembly (Score: 2.908265)



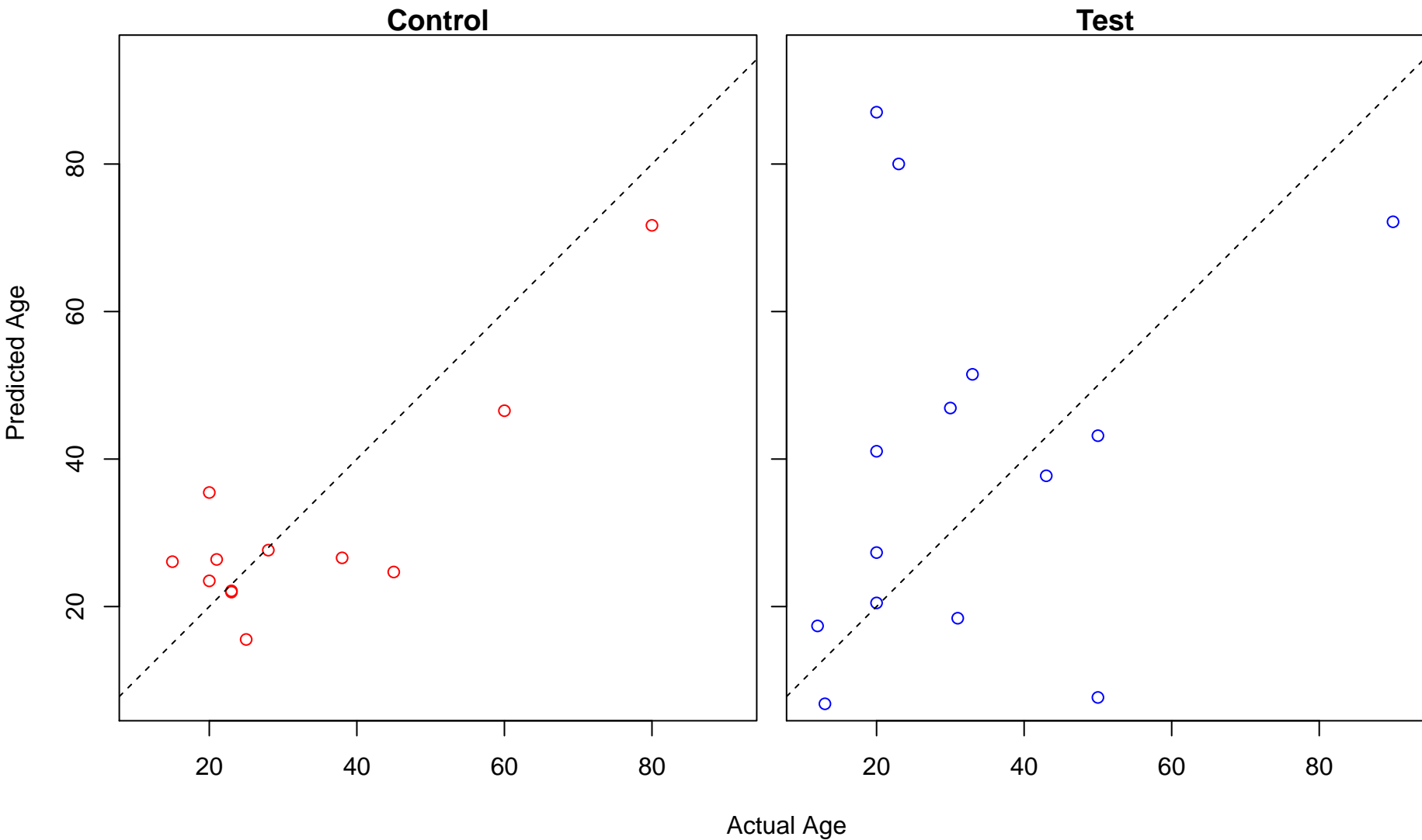
cell activation involved in immune response (Score: 2.904874)



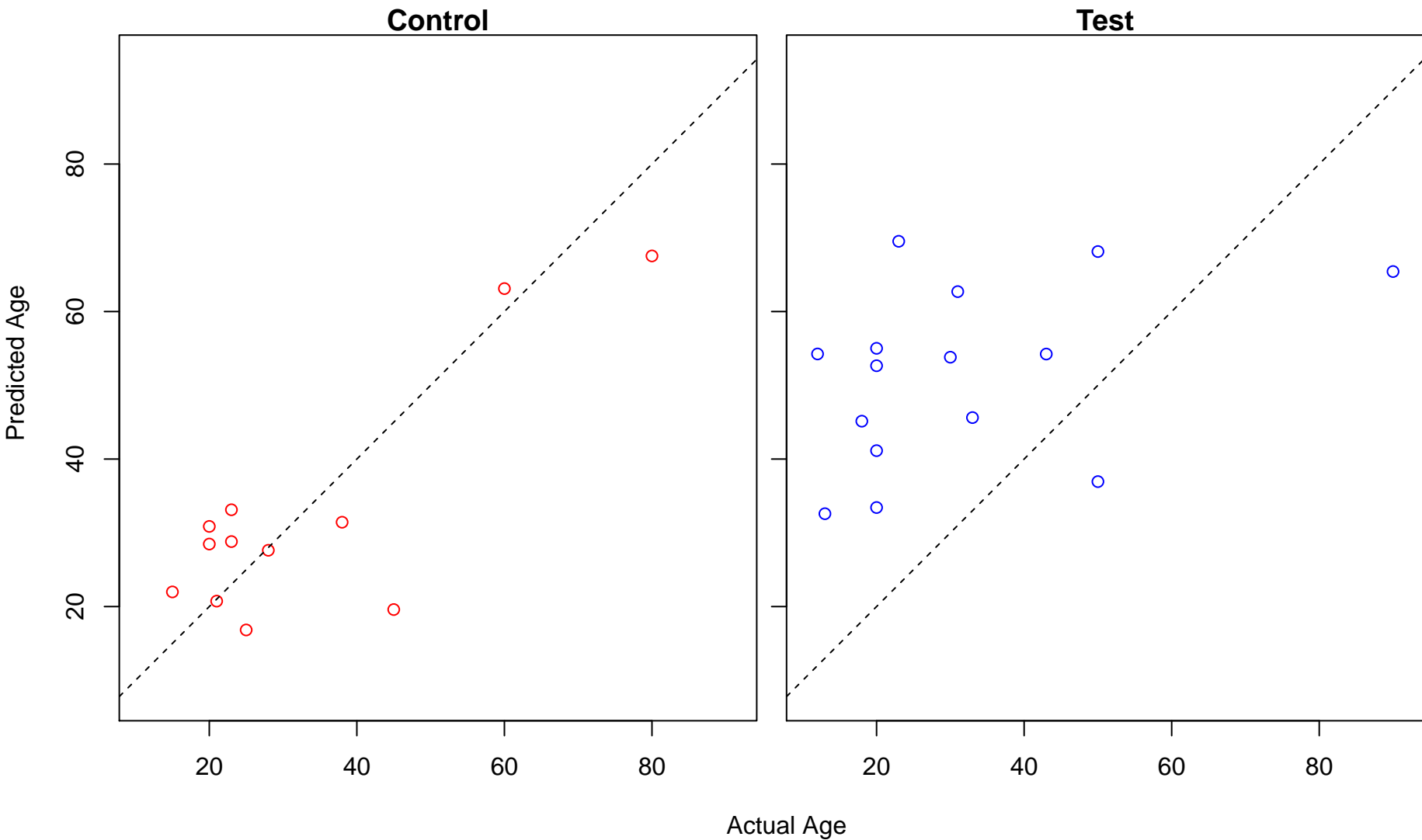
alternative mRNA splicing, via spliceosome (Score: 2.902494)



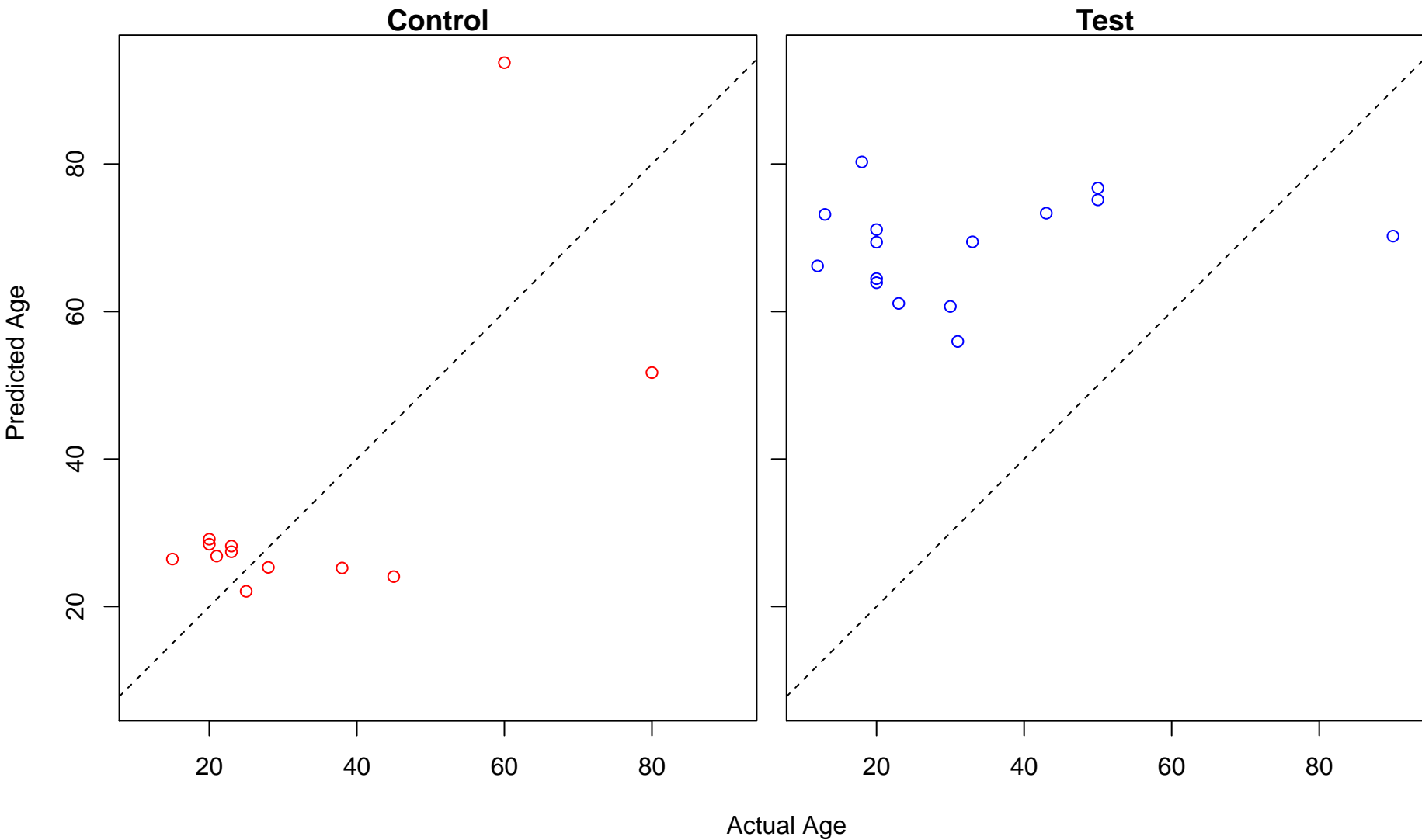
kidney morphogenesis (Score: 2.899045)



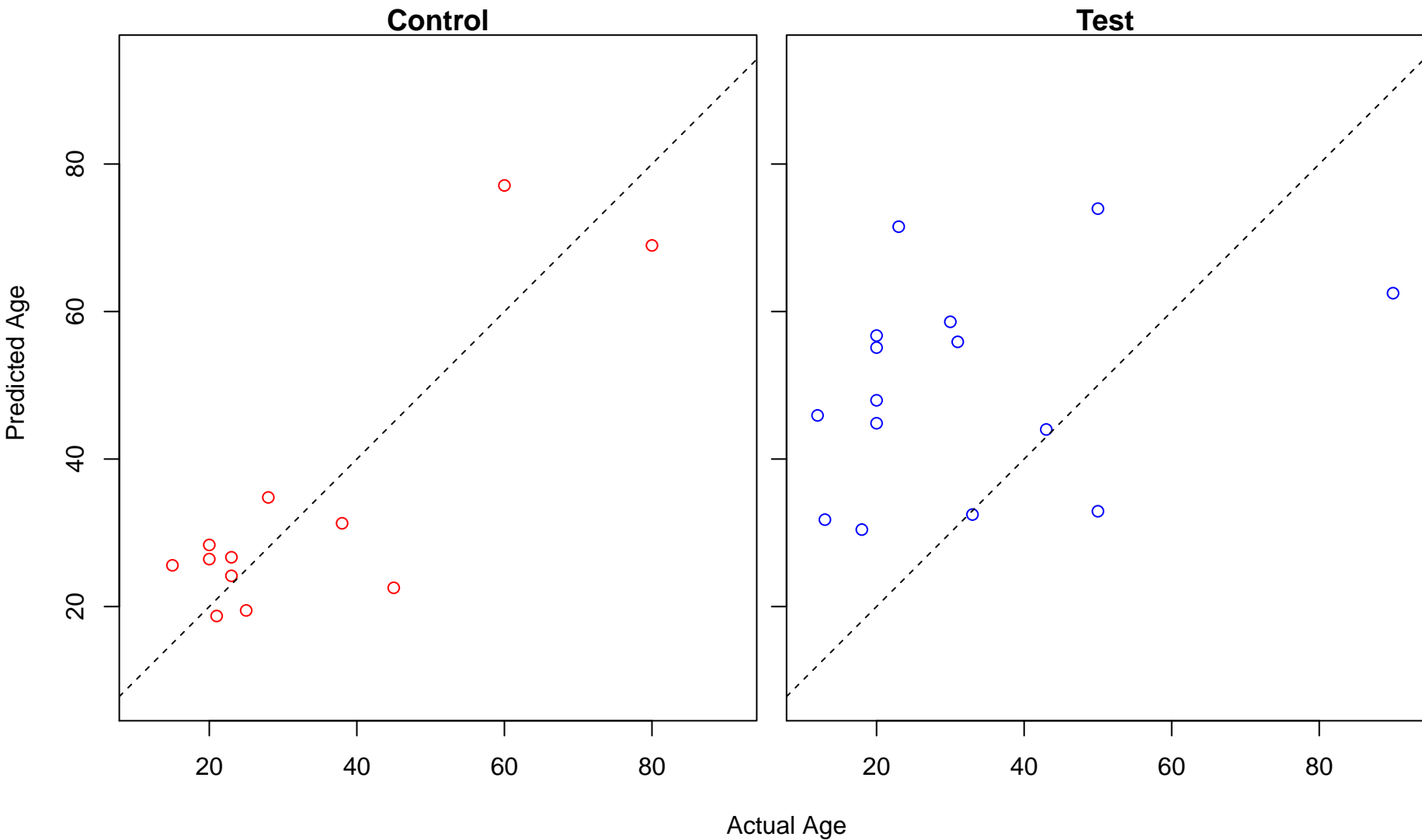
regulation of memory T cell differentiation (Score: 2.896437)



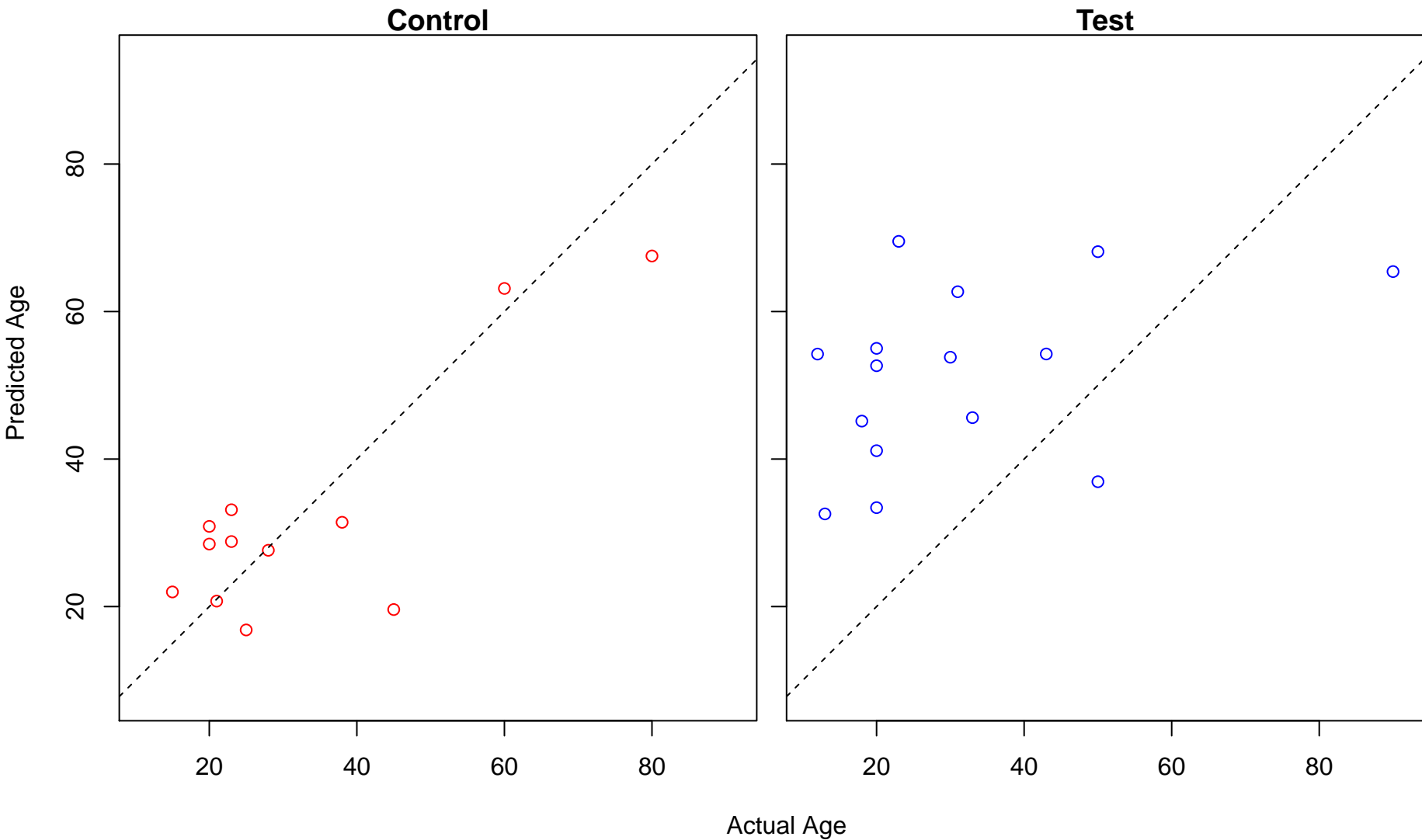
positive regulation of DNA binding (Score: 2.896183)



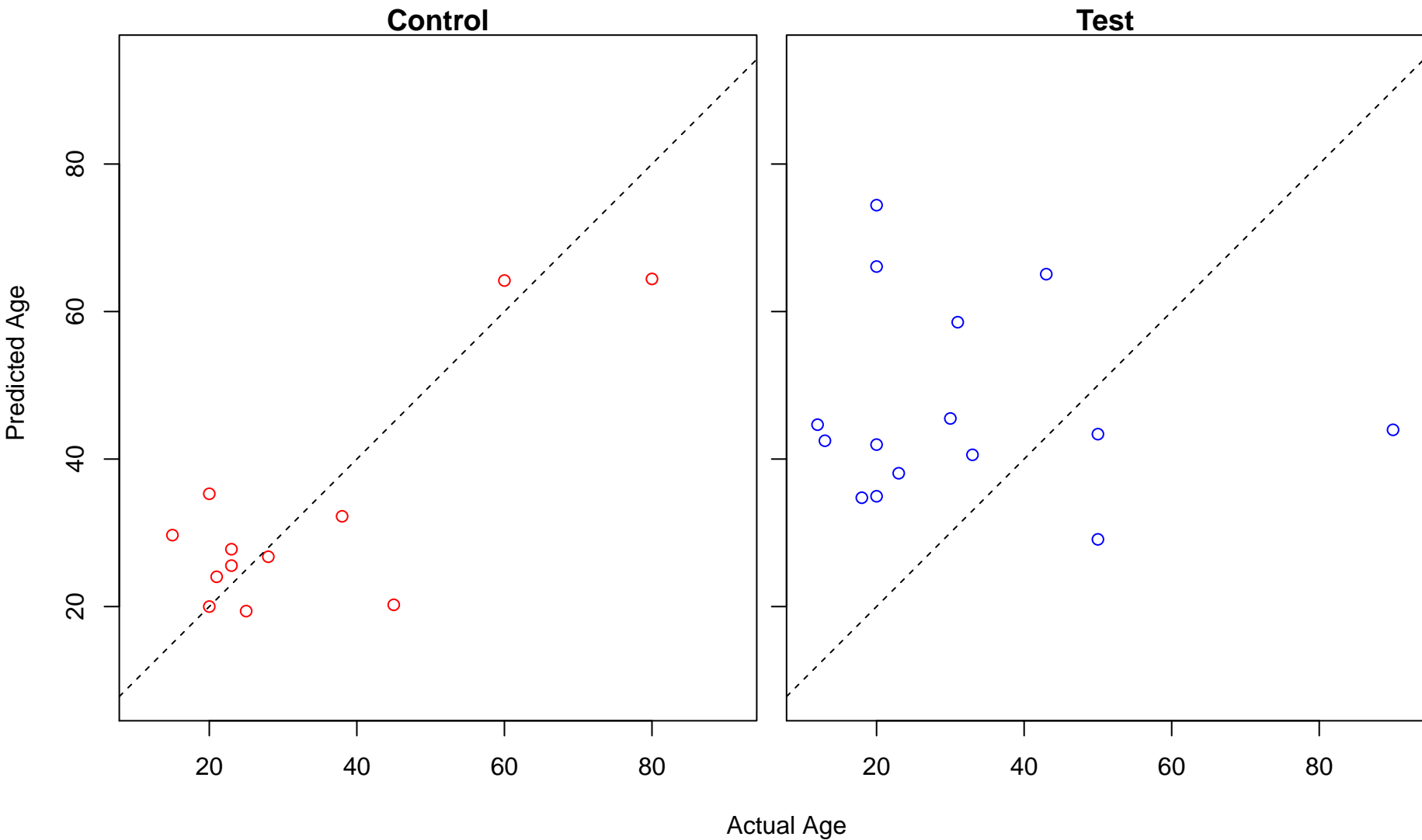
regulation of extracellular matrix organization (Score: 2.895148)



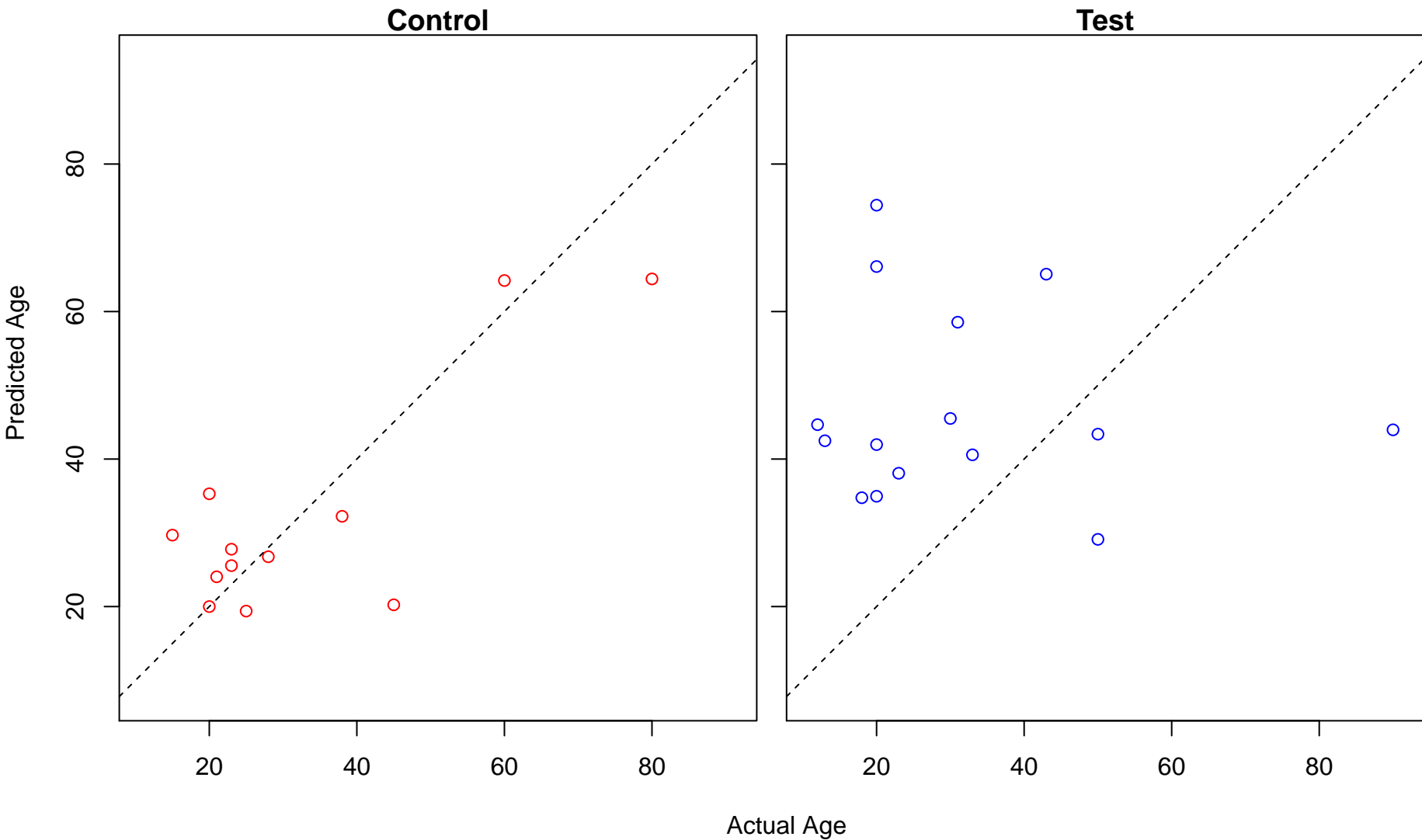
positive regulation of memory T cell differentiation (Score: 2.894783)



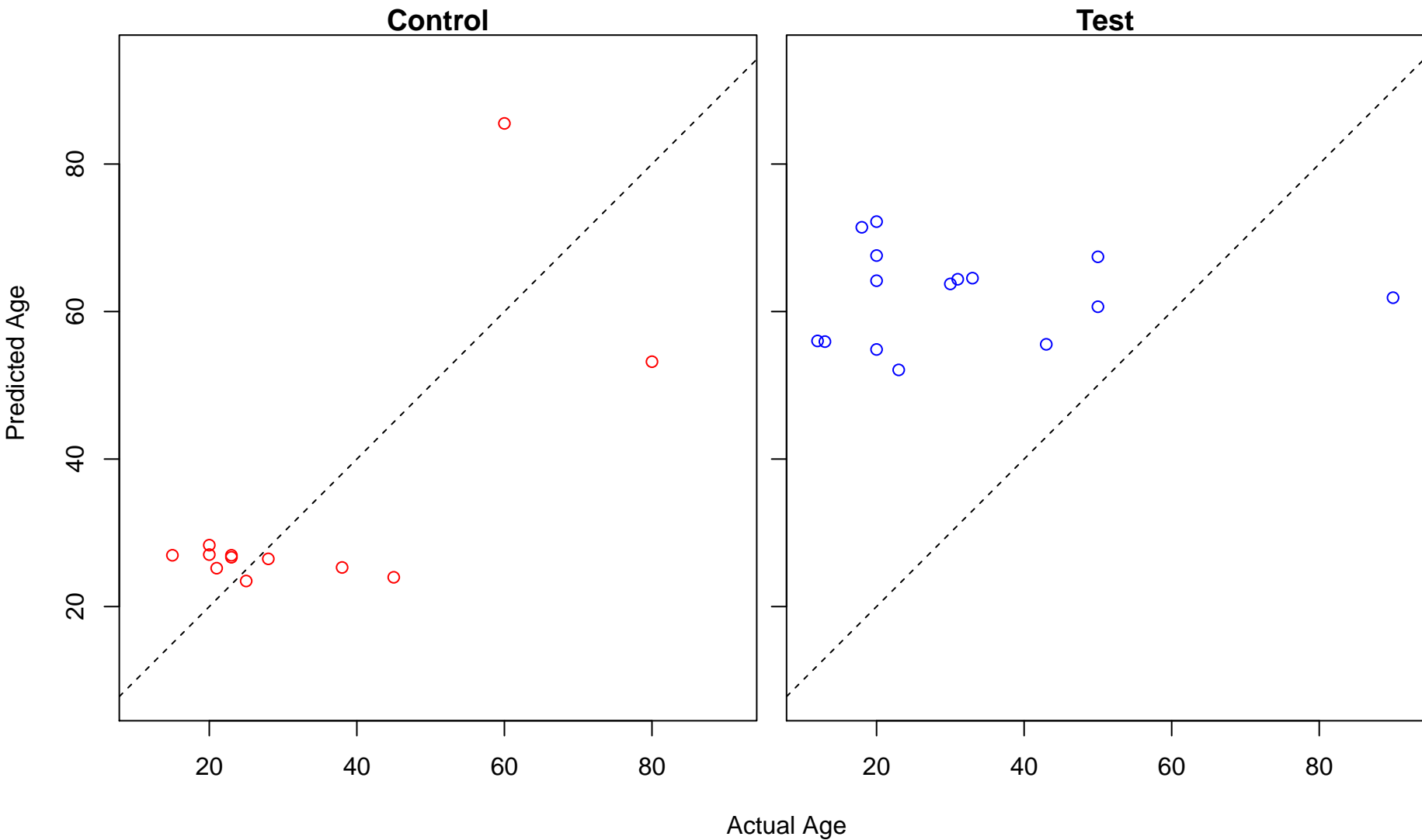
AV node cell action potential (Score: 2.891855)



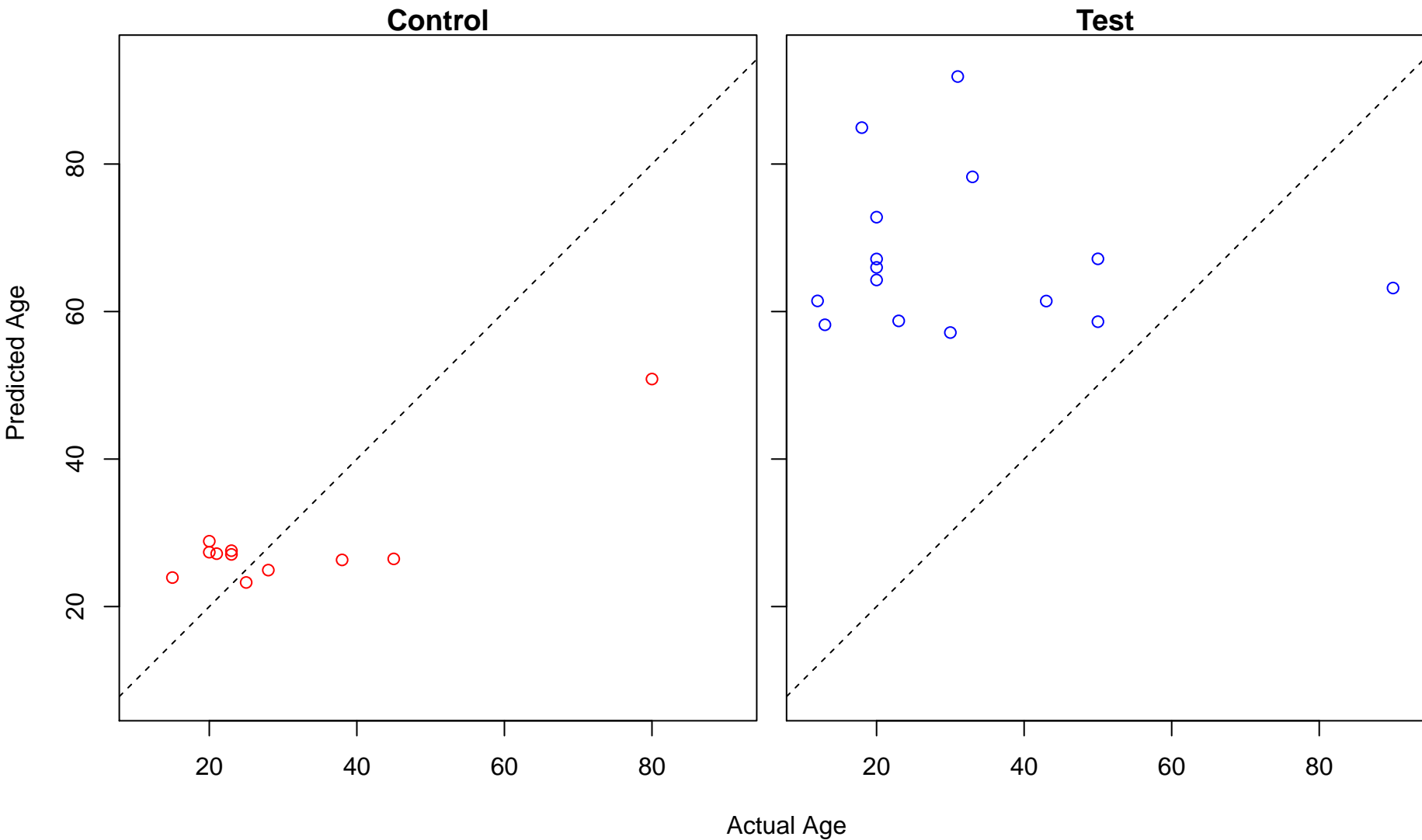
AV node cell to bundle of His cell signaling (Score: 2.891855)



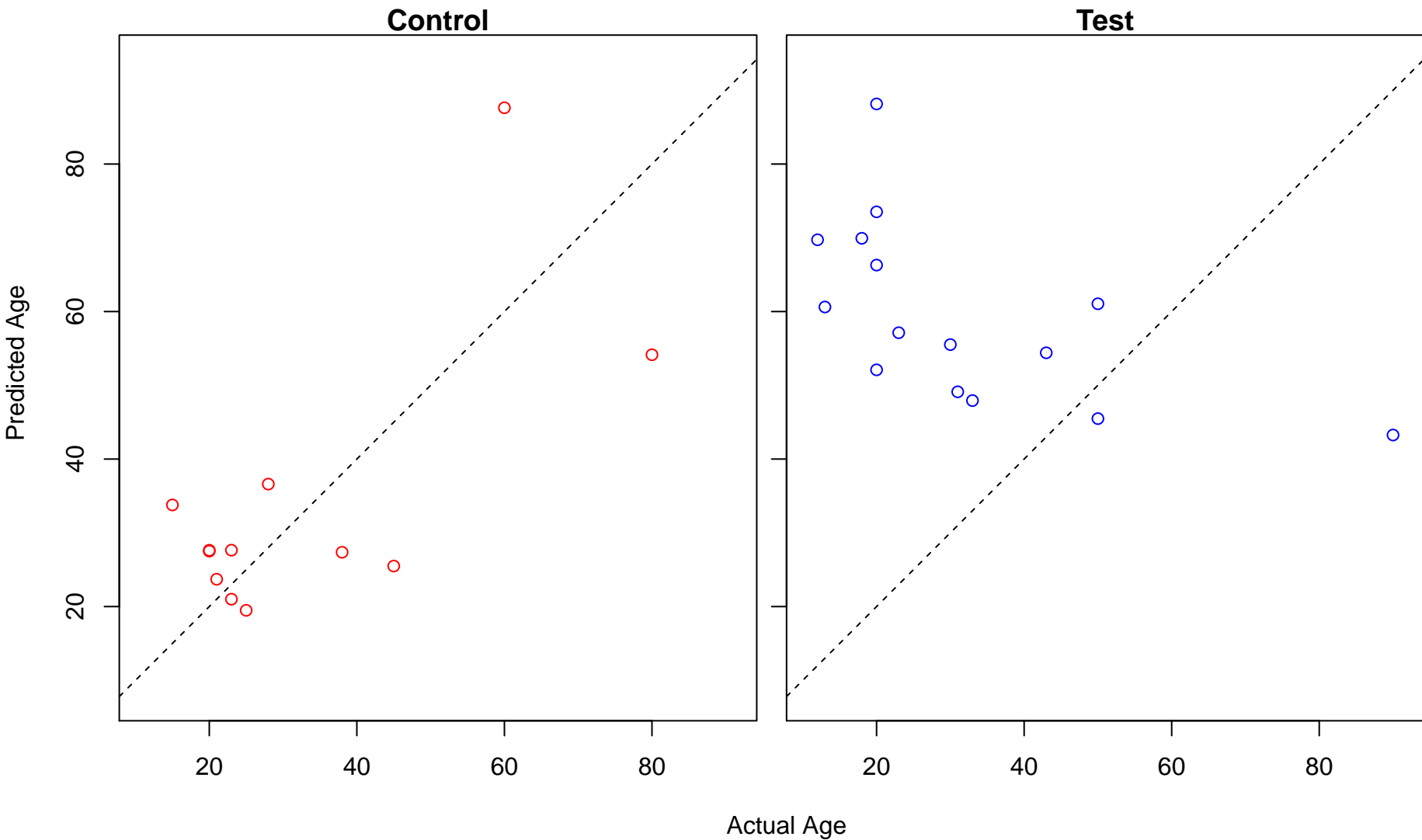
positive regulation of organelle assembly (Score: 2.887379)



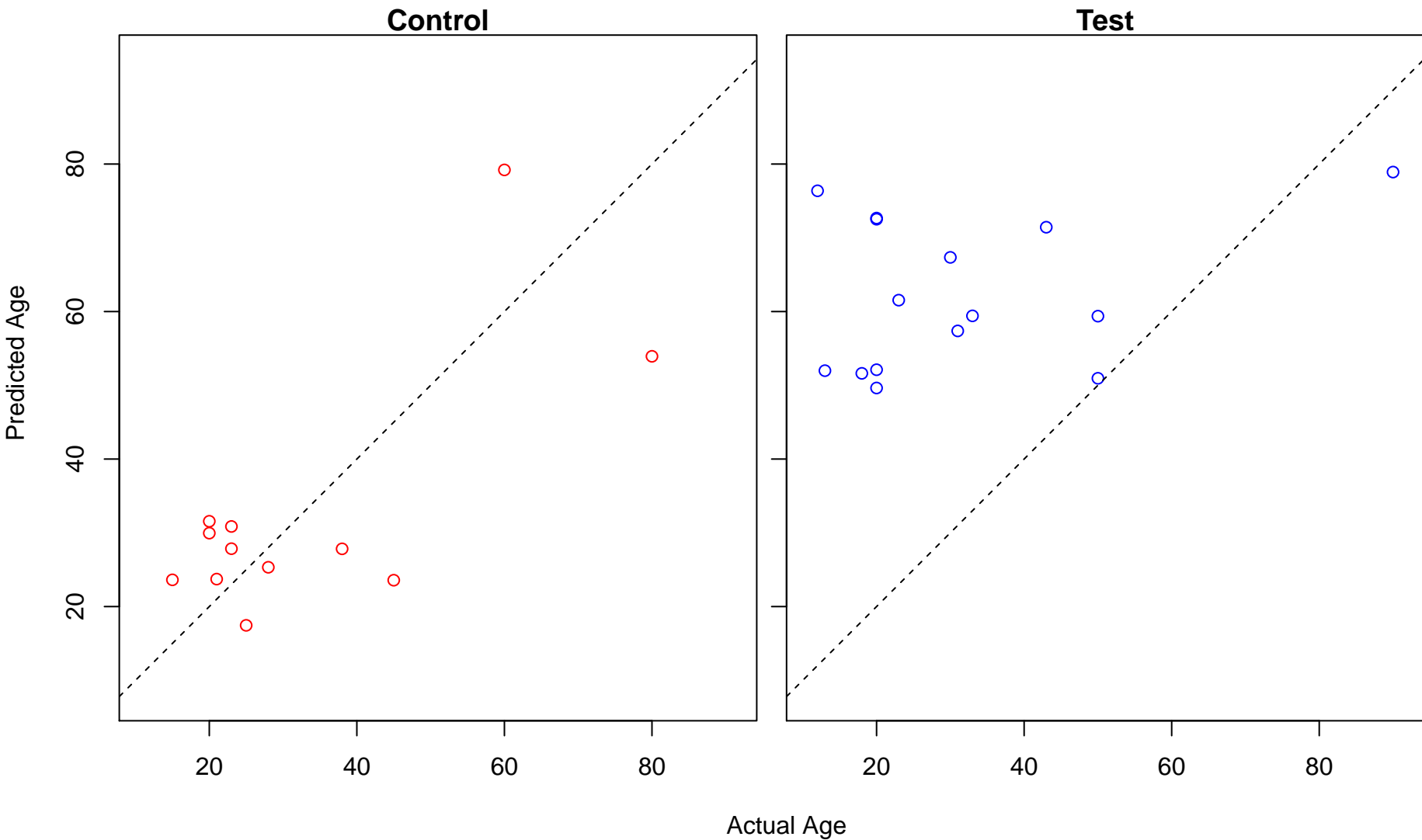
positive regulation of excitatory postsynaptic potential (Score: 2.875474)



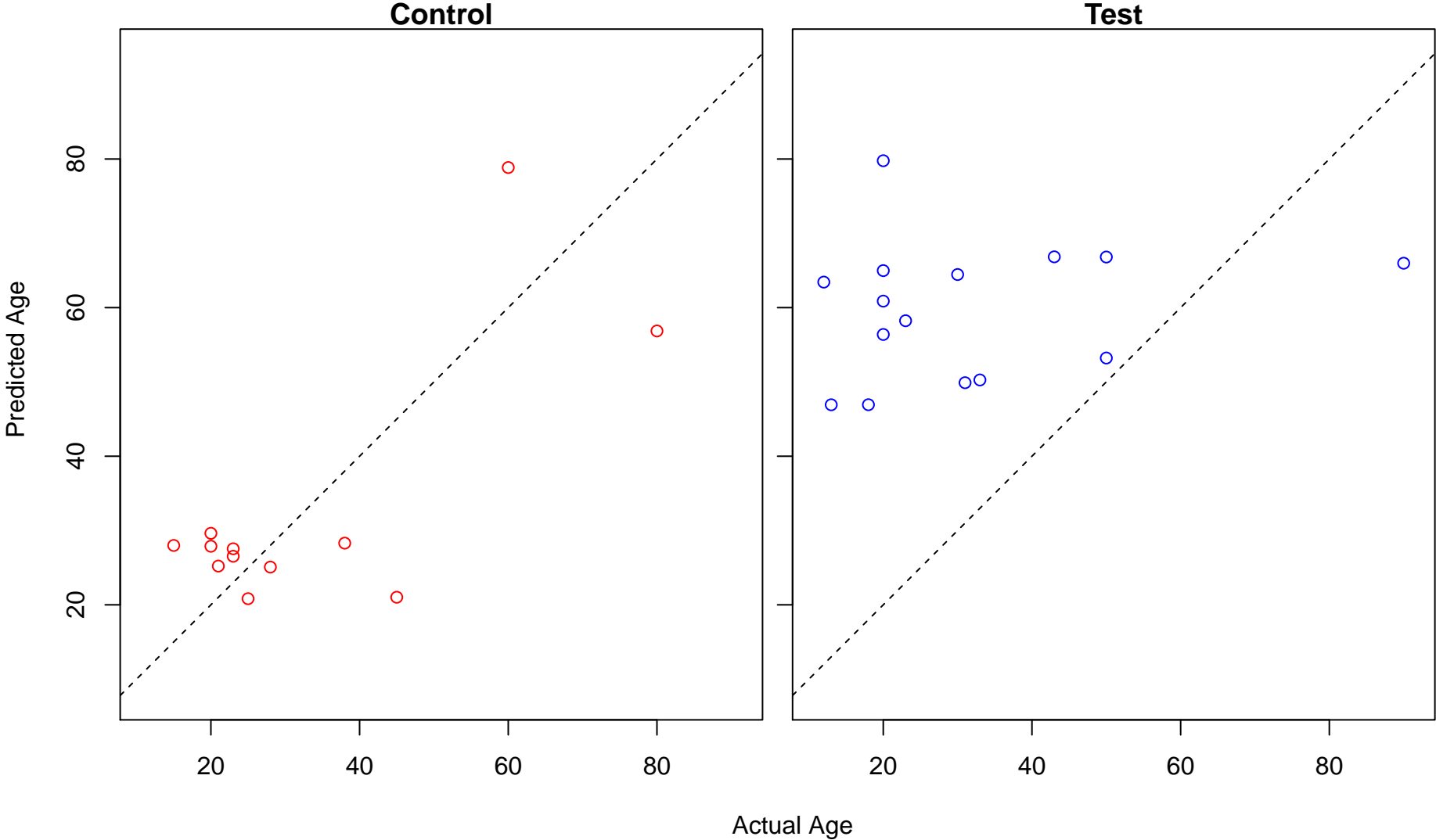
inner mitochondrial membrane organization (Score: 2.875306)



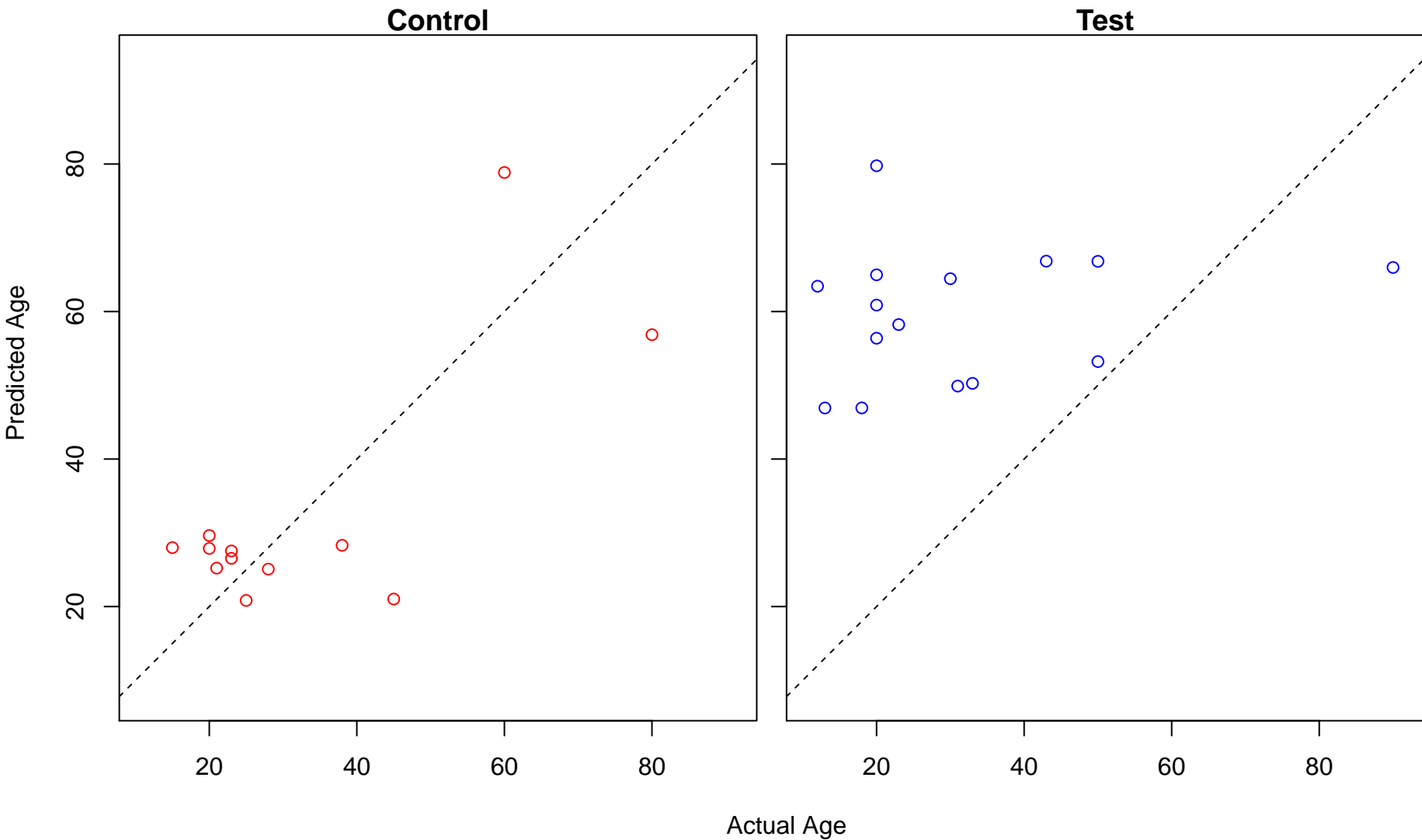
regulation of energy homeostasis (Score: 2.870727)



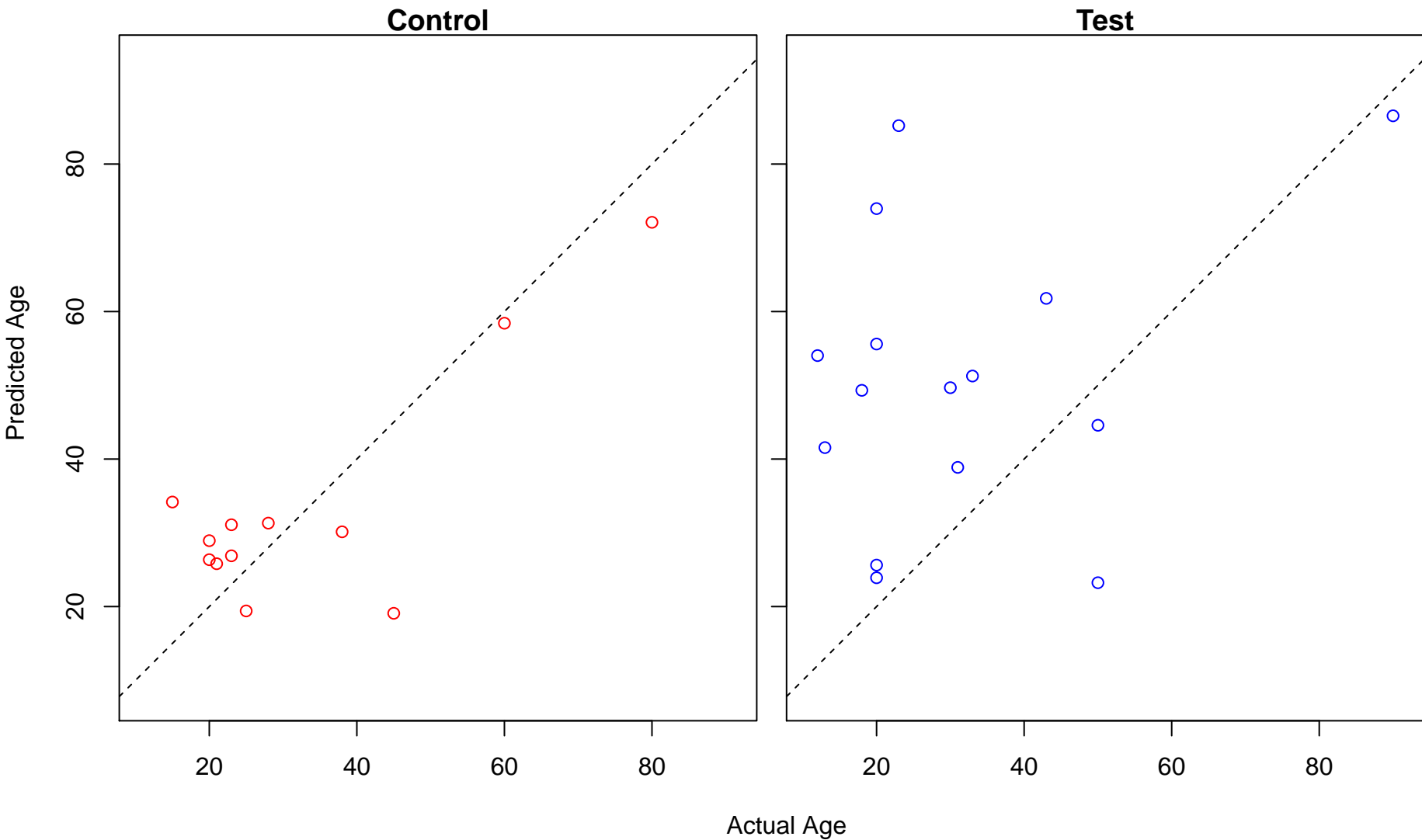
purine ribonucleoside bisphosphate metabolic process (Score: 2.868997)



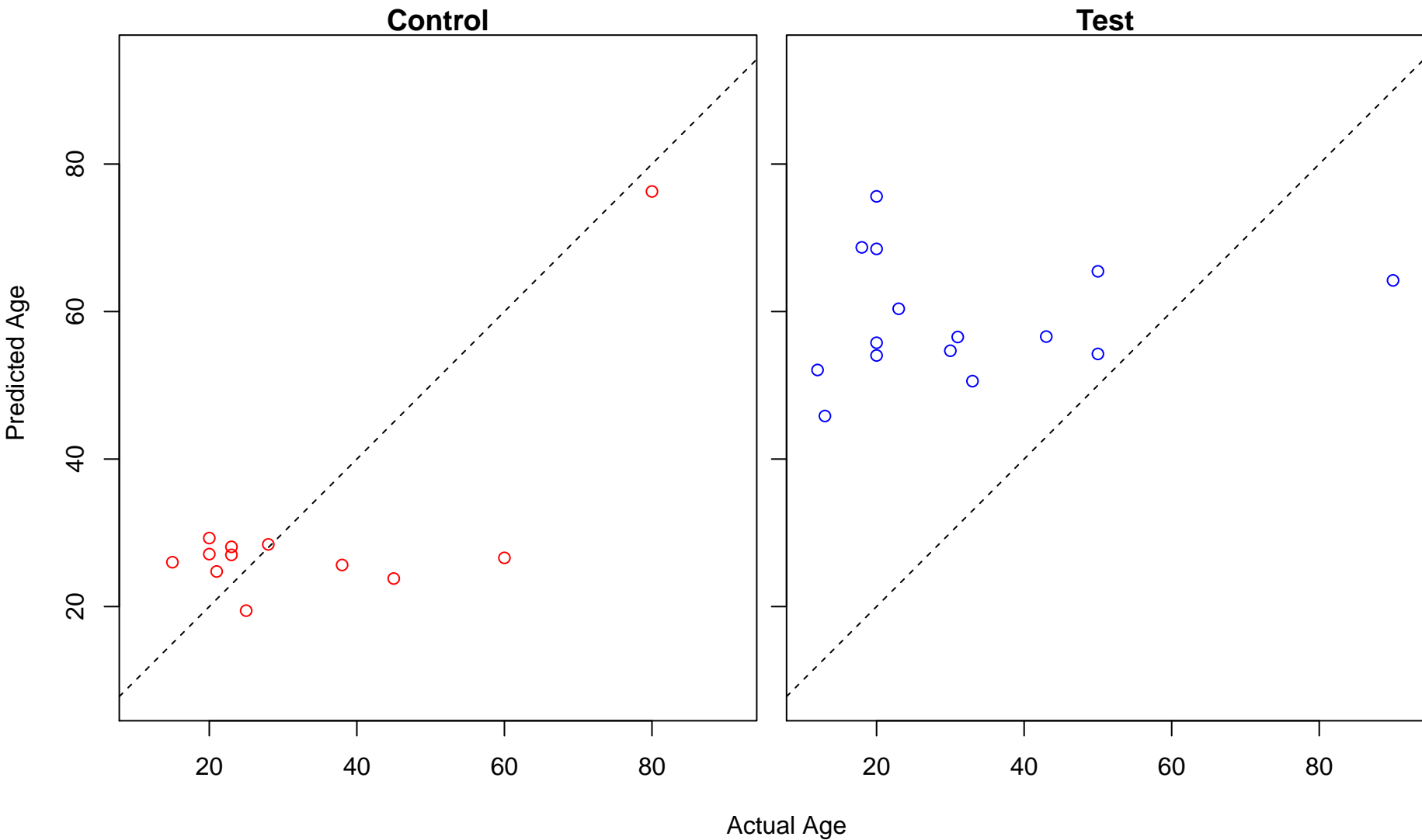
3'-phosphoadenosine 5'-phosphosulfate metabolic process (Score: 2.868997)



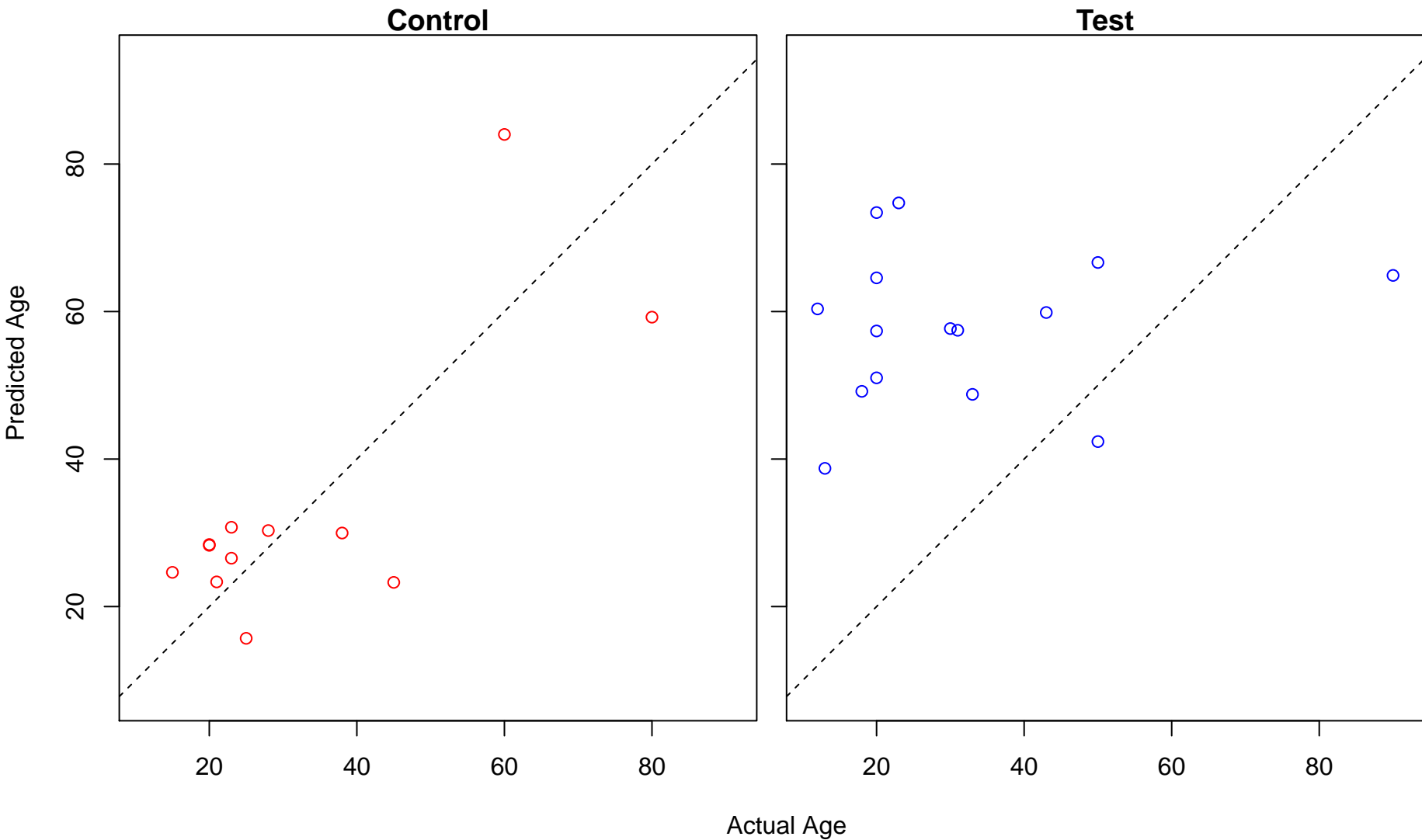
negative regulation of activin receptor signaling pathway (Score: 2.868272)



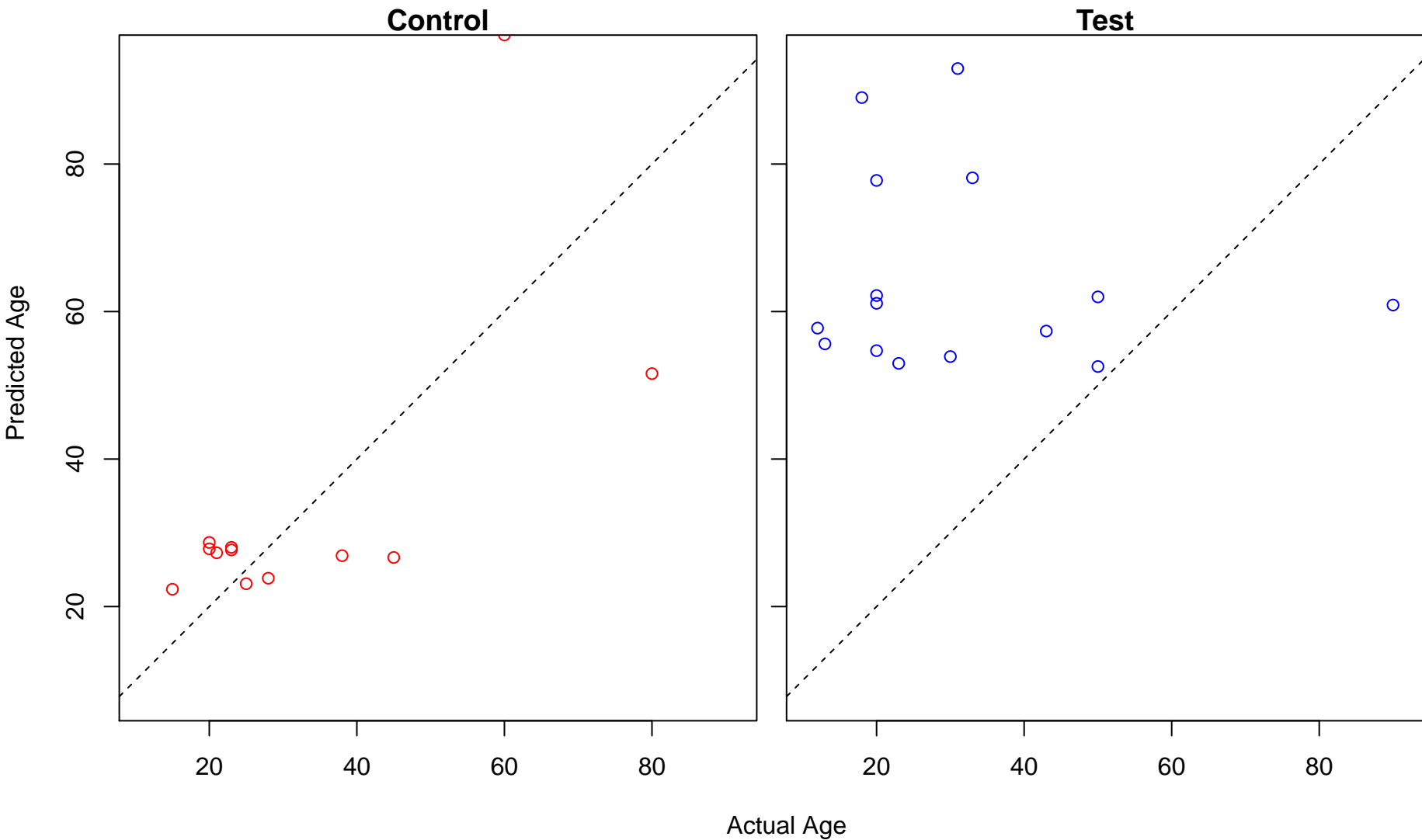
regulation of cell size (Score: 2.857356)



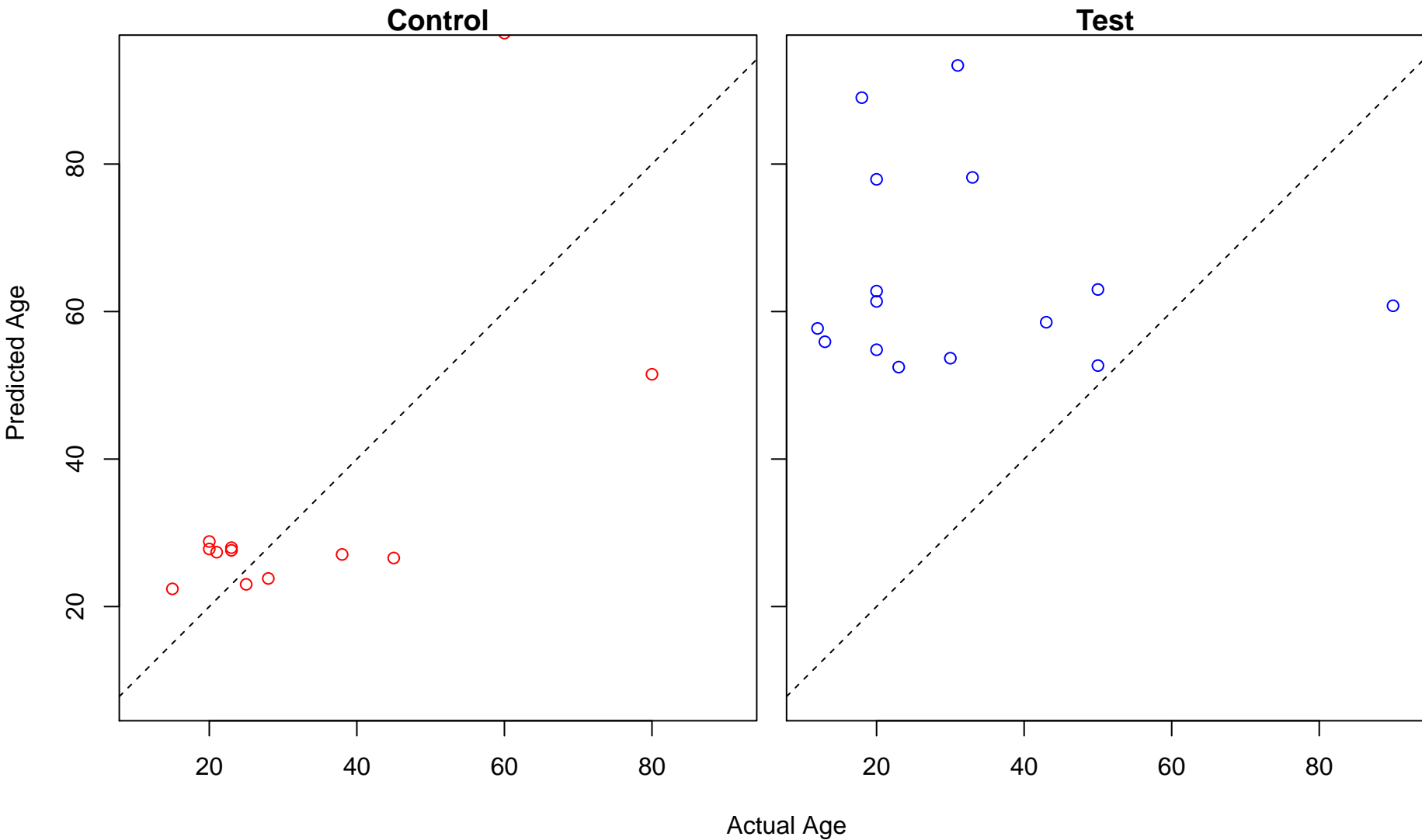
telencephalon development (Score: 2.851562)



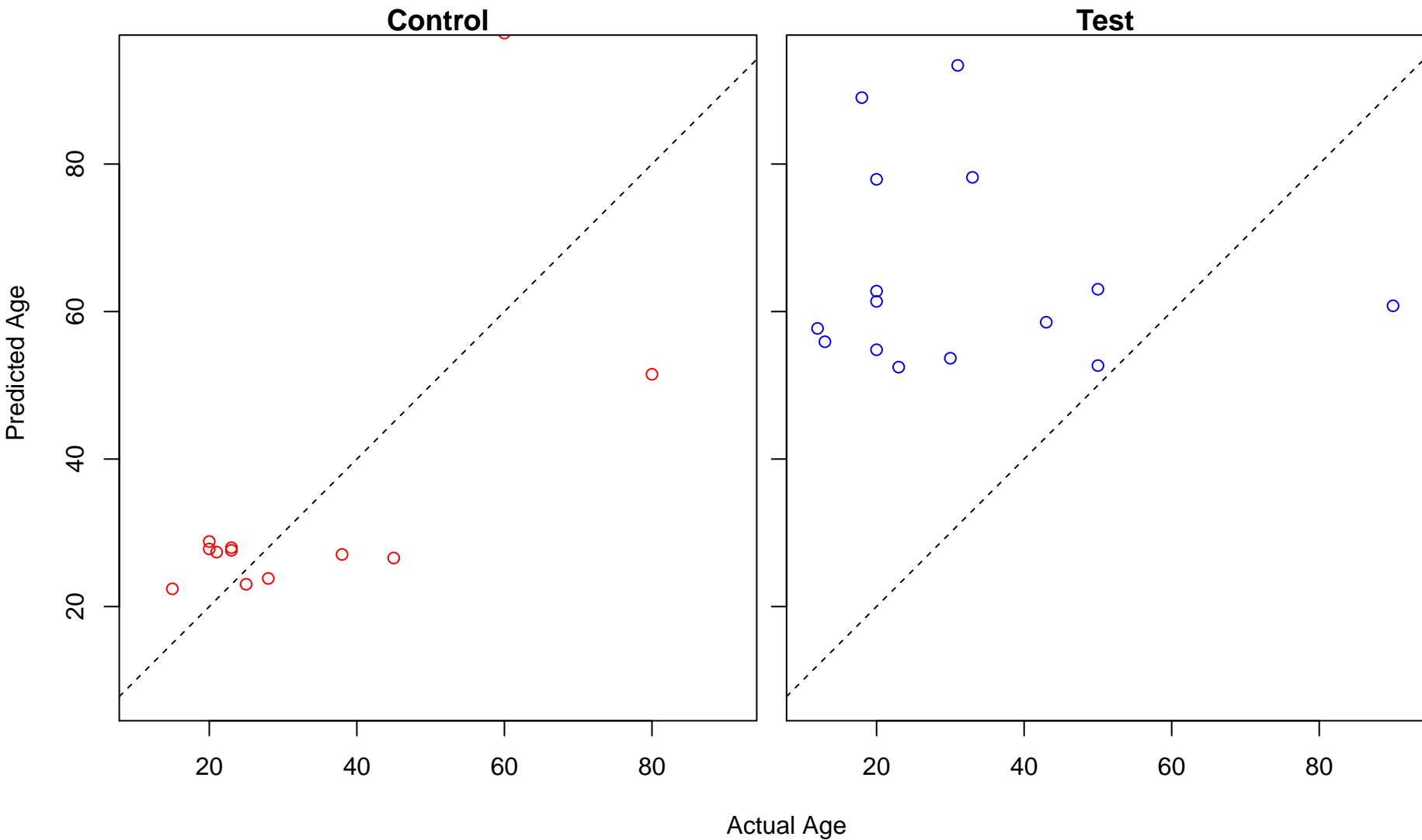
startle response (Score: 2.846075)



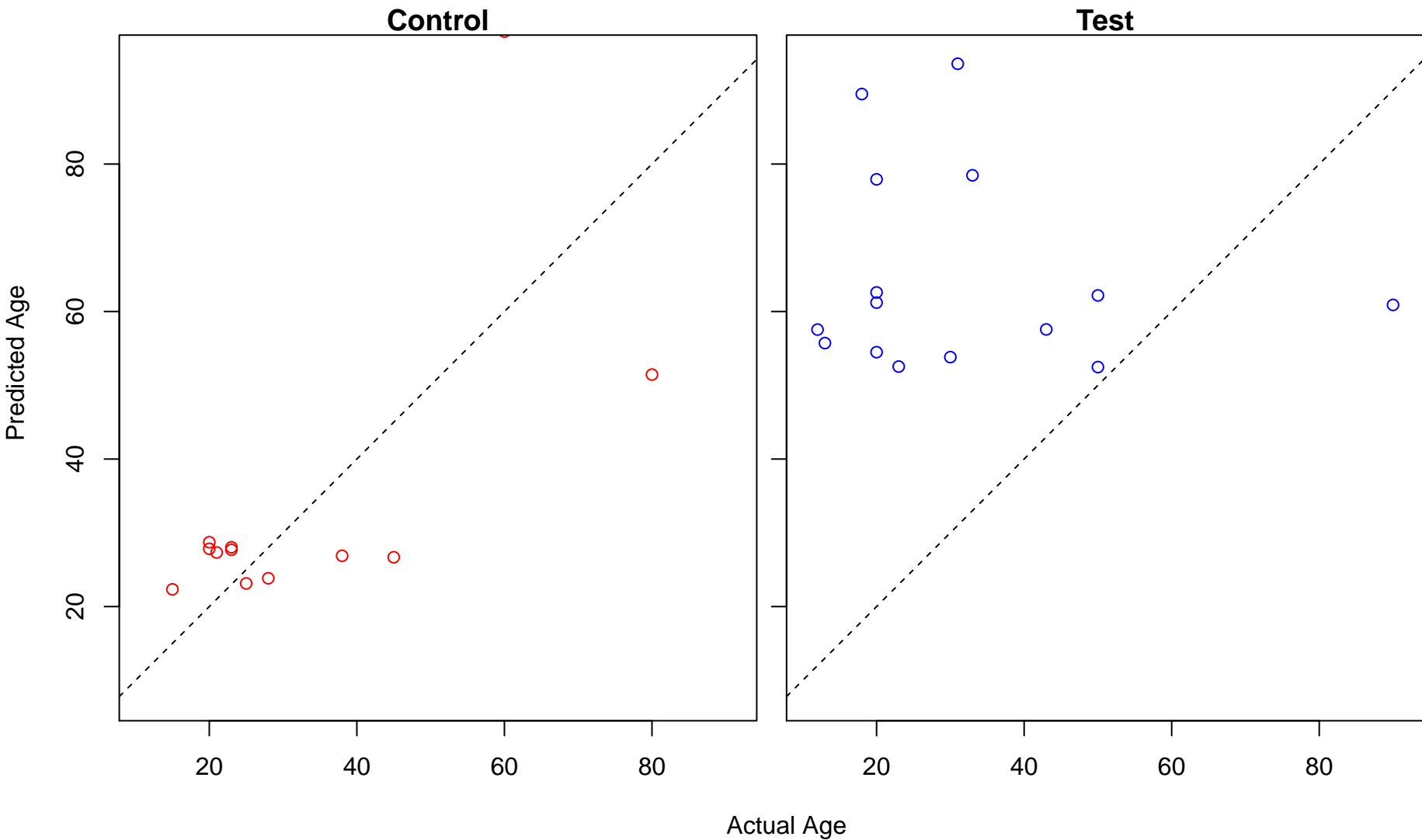
presynaptic membrane organization (Score: 2.845815)



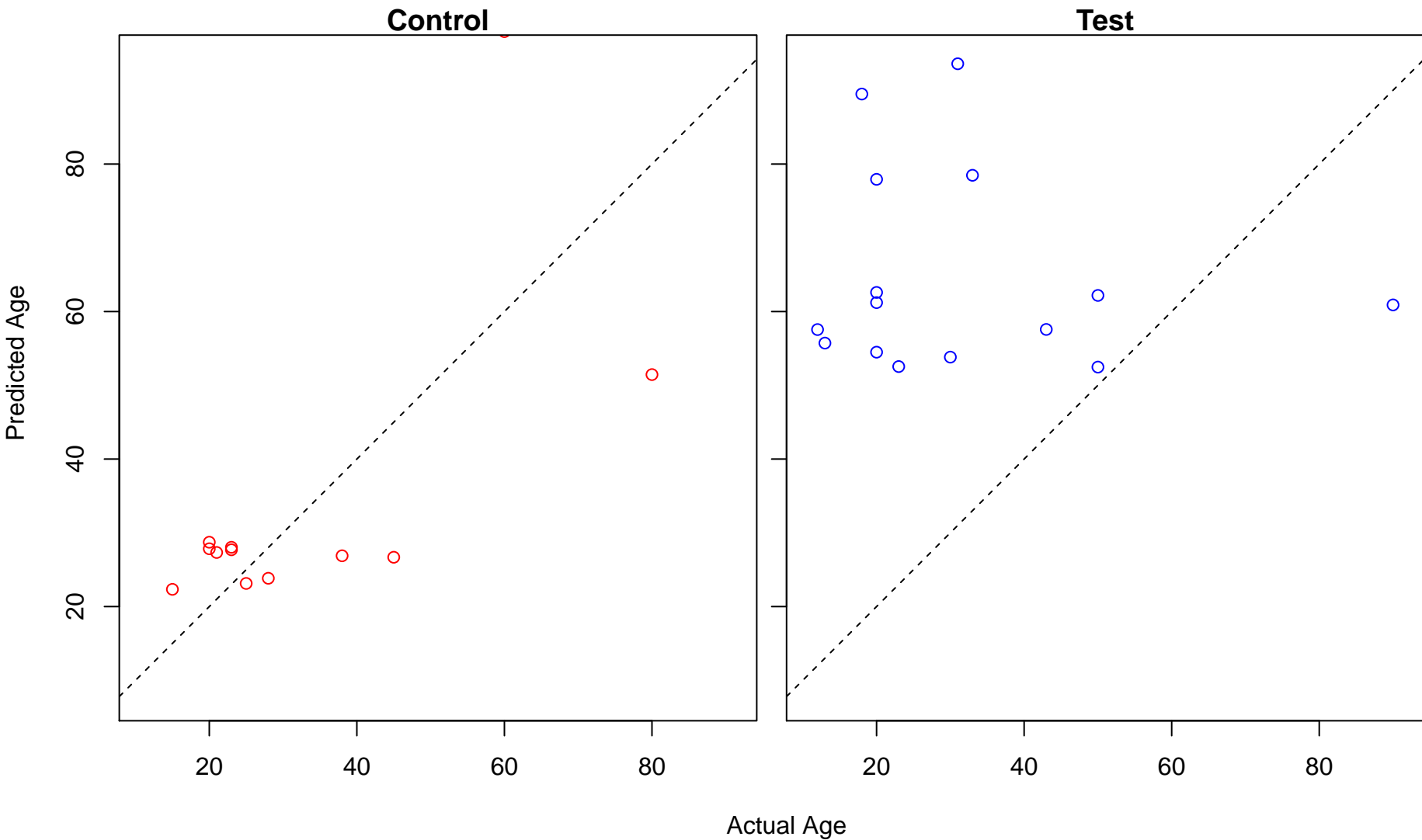
presynaptic membrane assembly (Score: 2.845507)



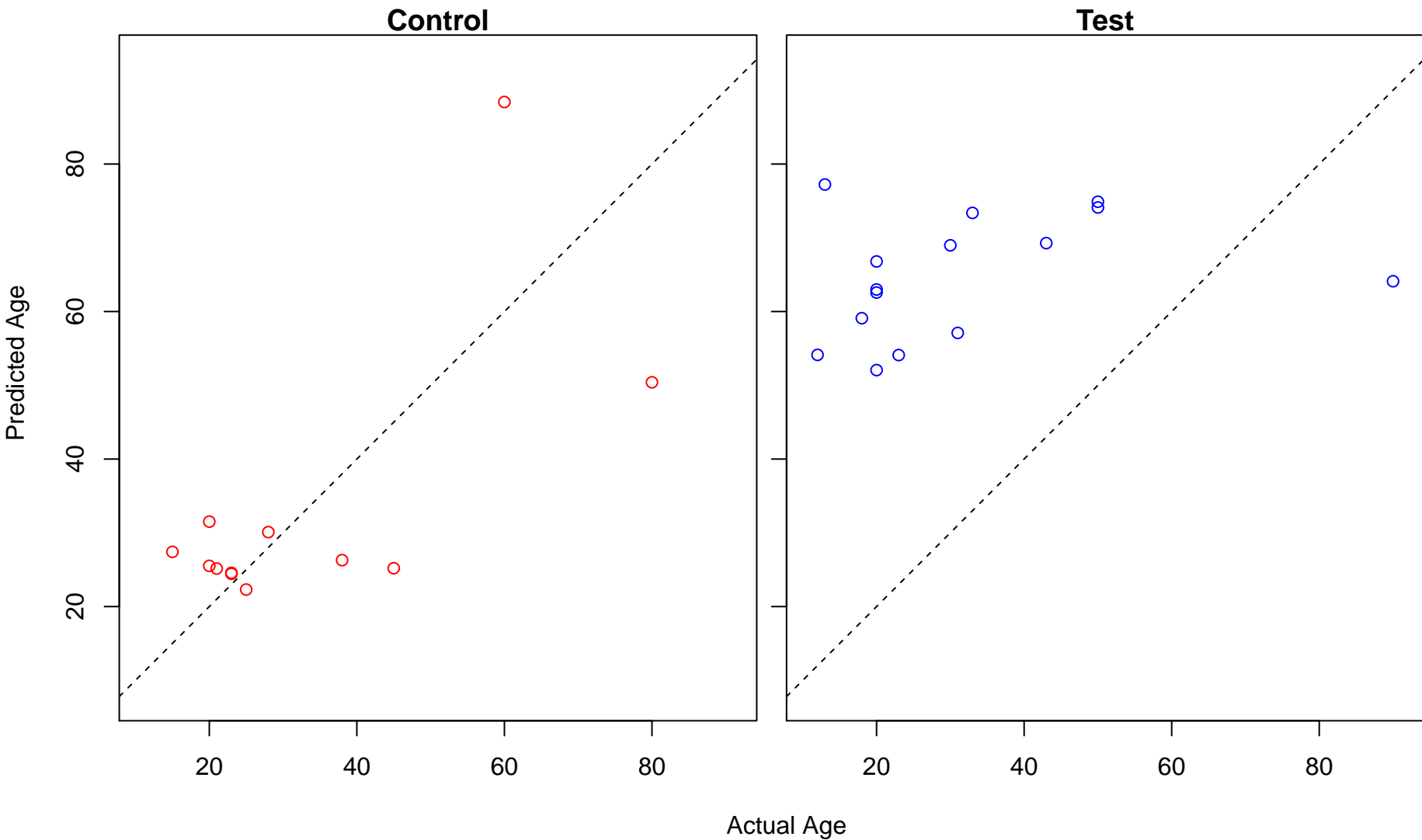
postsynaptic density organization (Score: 2.833721)



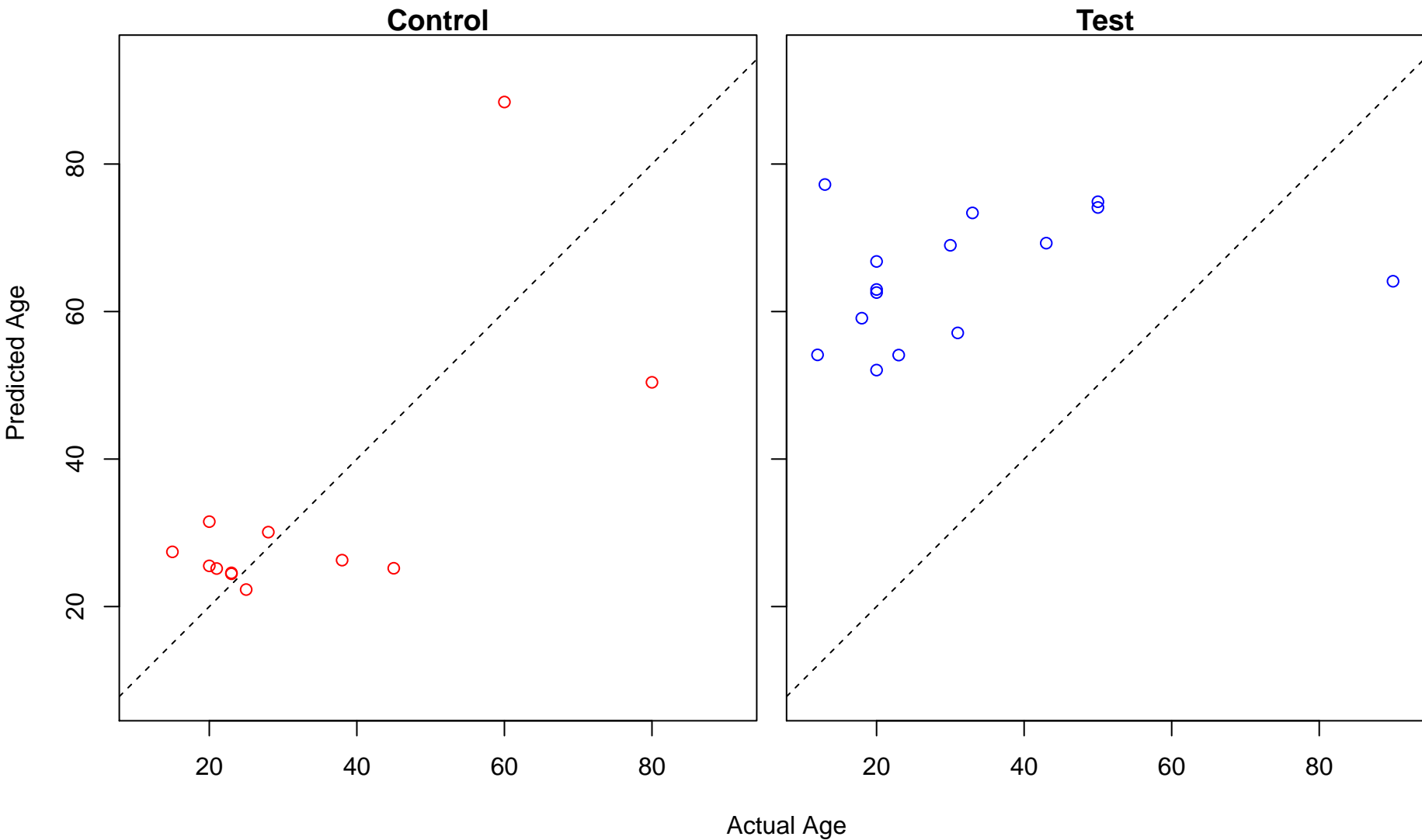
postsynaptic density assembly (Score: 2.833721)



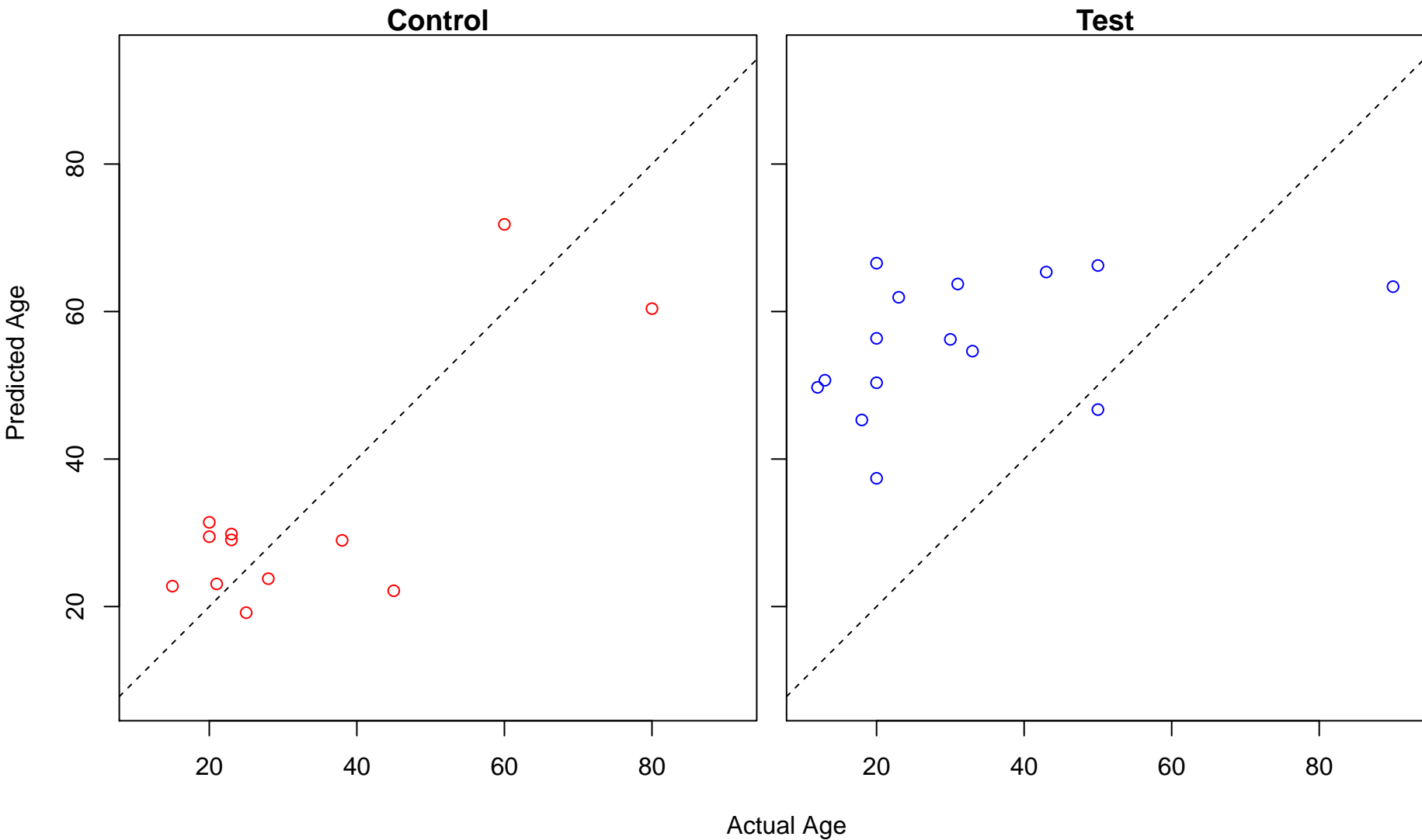
phosphatidylinositol-mediated signaling (Score: 2.833668)



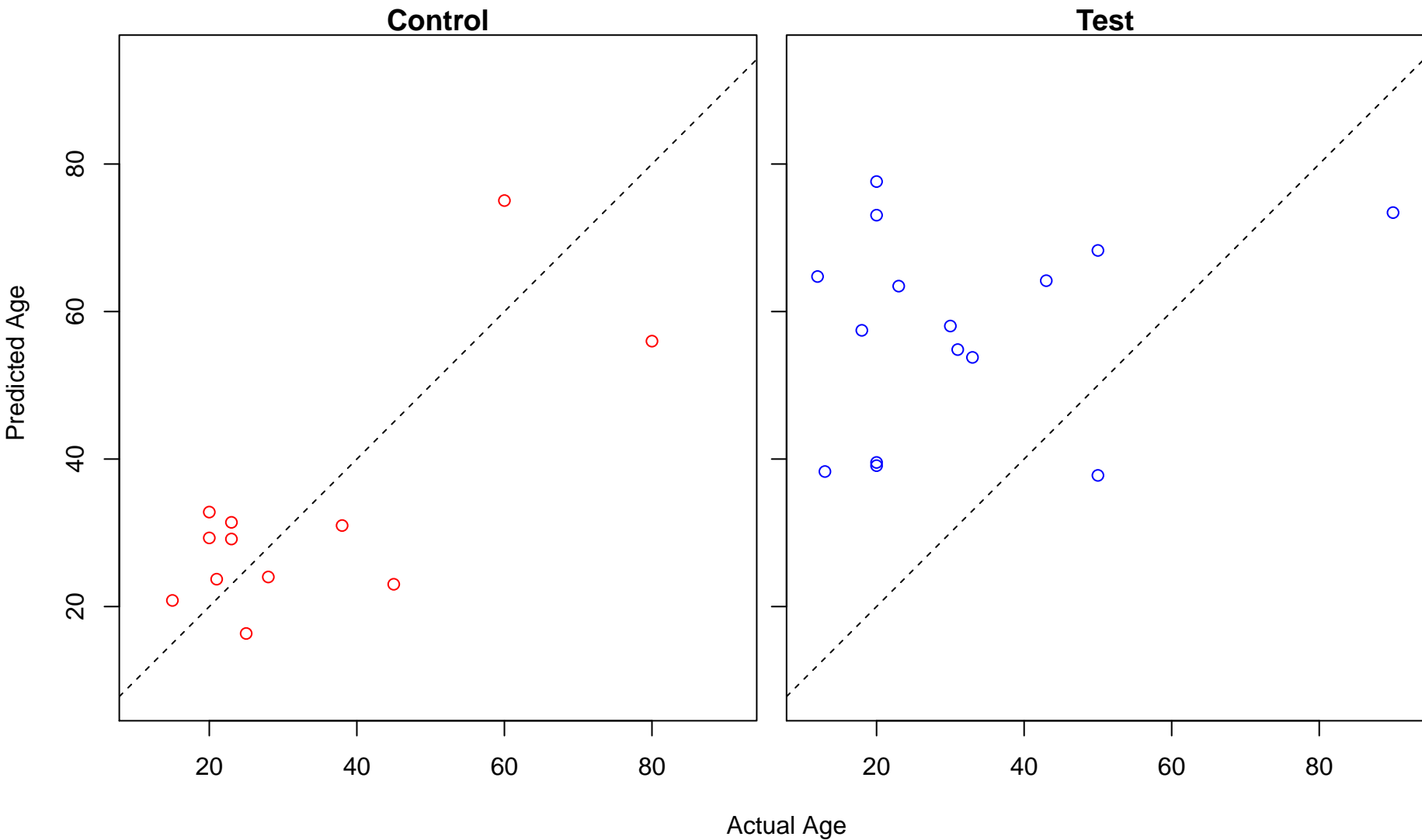
inositol lipid-mediated signaling (Score: 2.833668)



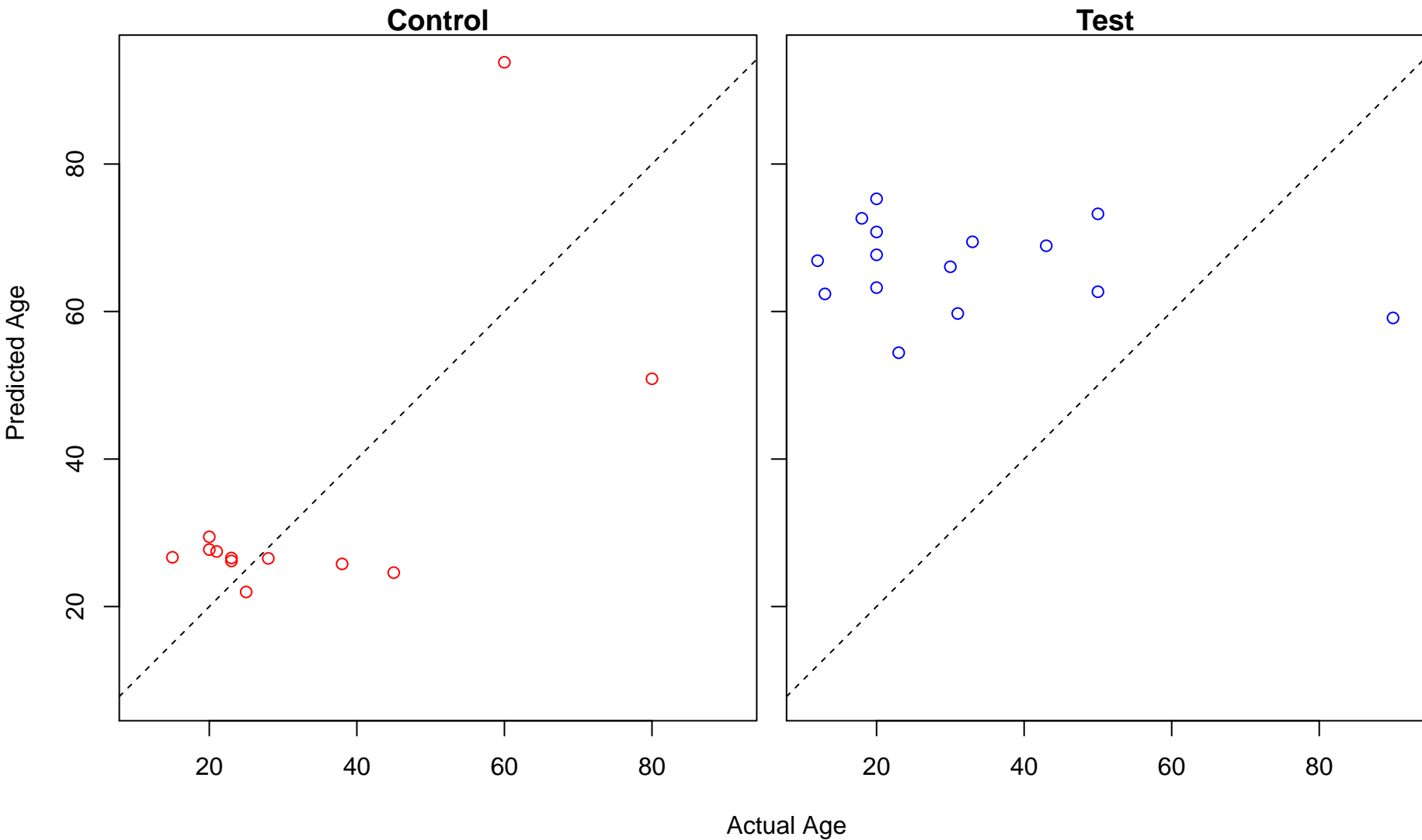
positive regulation of axon extension (Score: 2.827799)



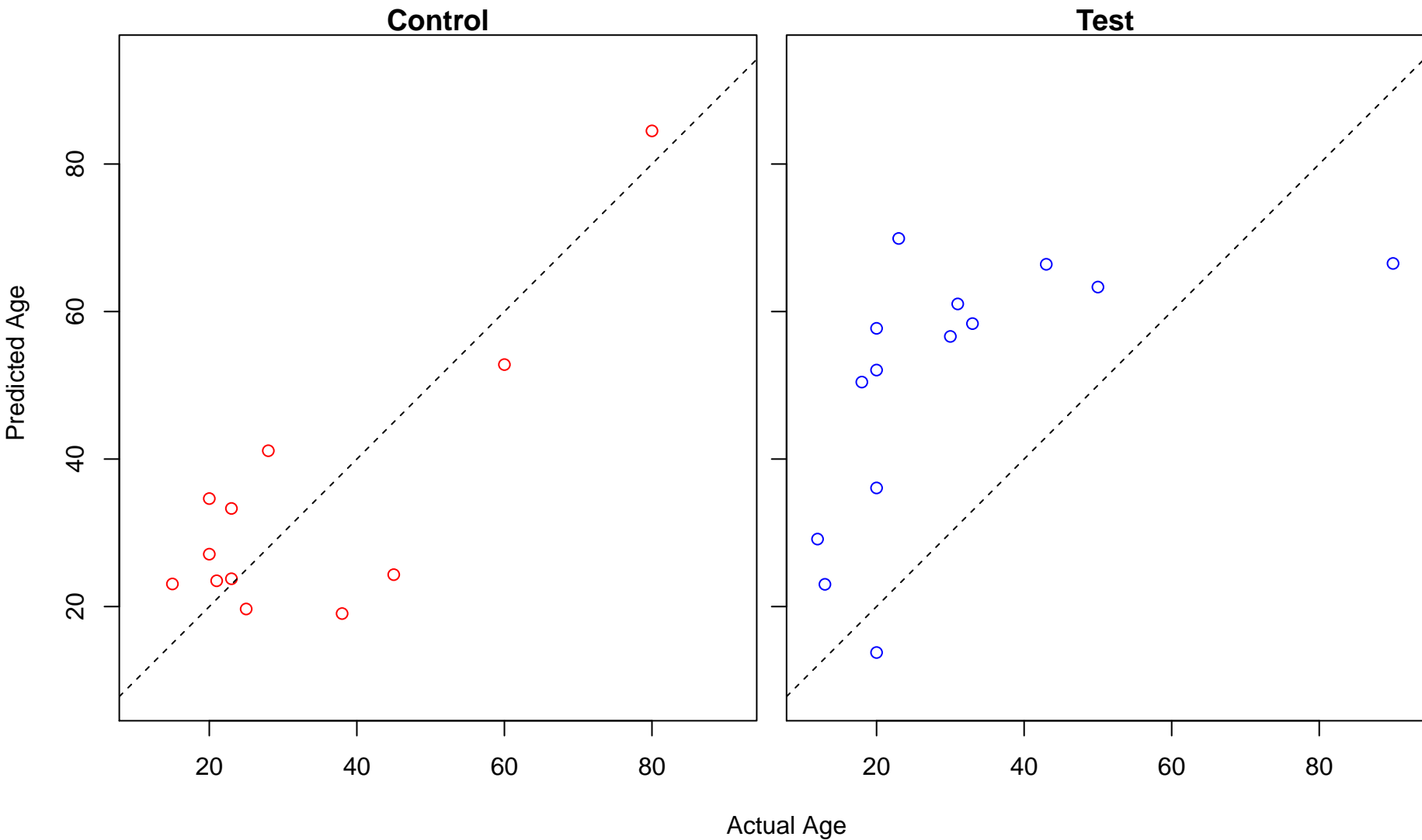
regulation of tyrosine phosphorylation of Stat1 protein (Score: 2.827720)



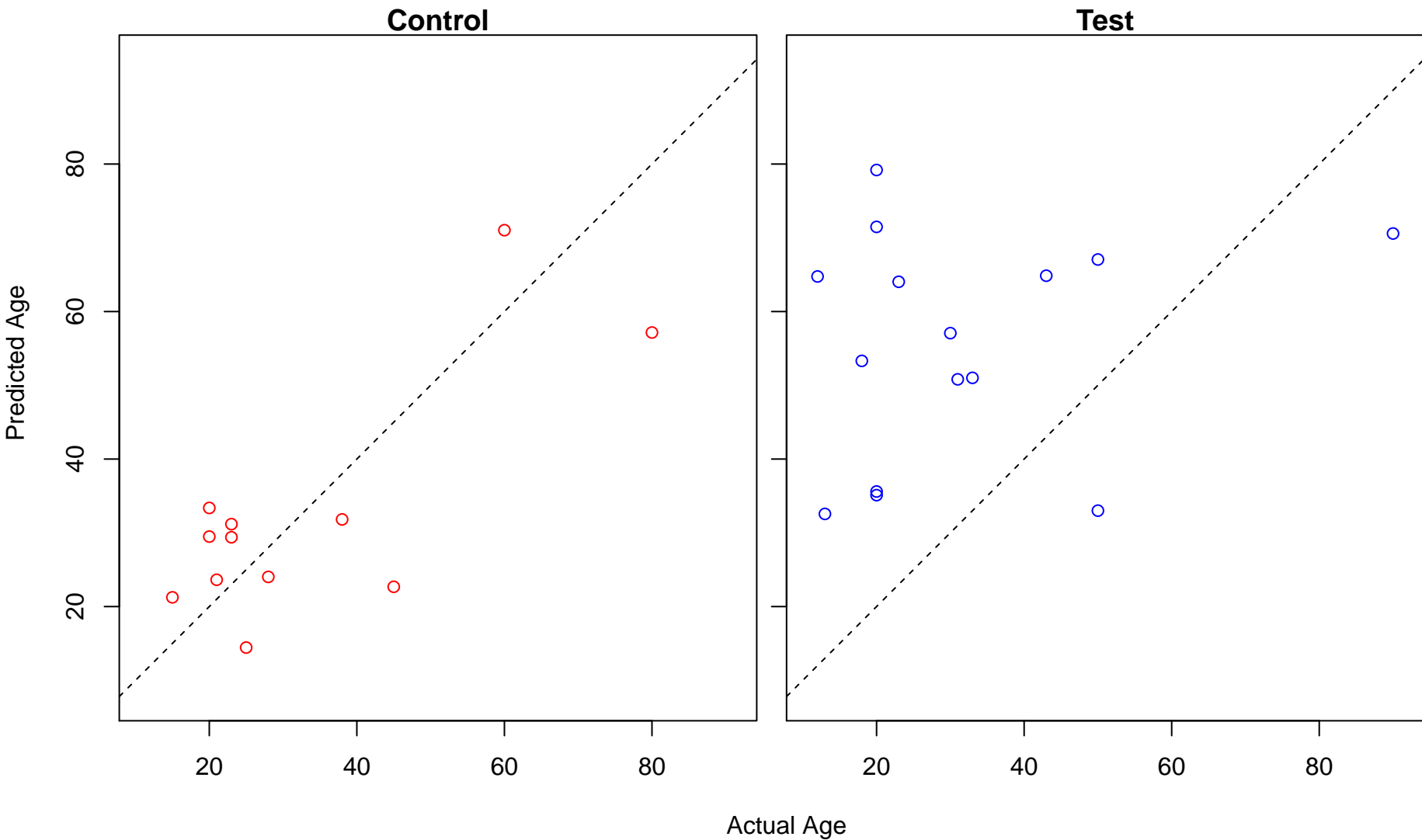
cell recognition (Score: 2.815088)



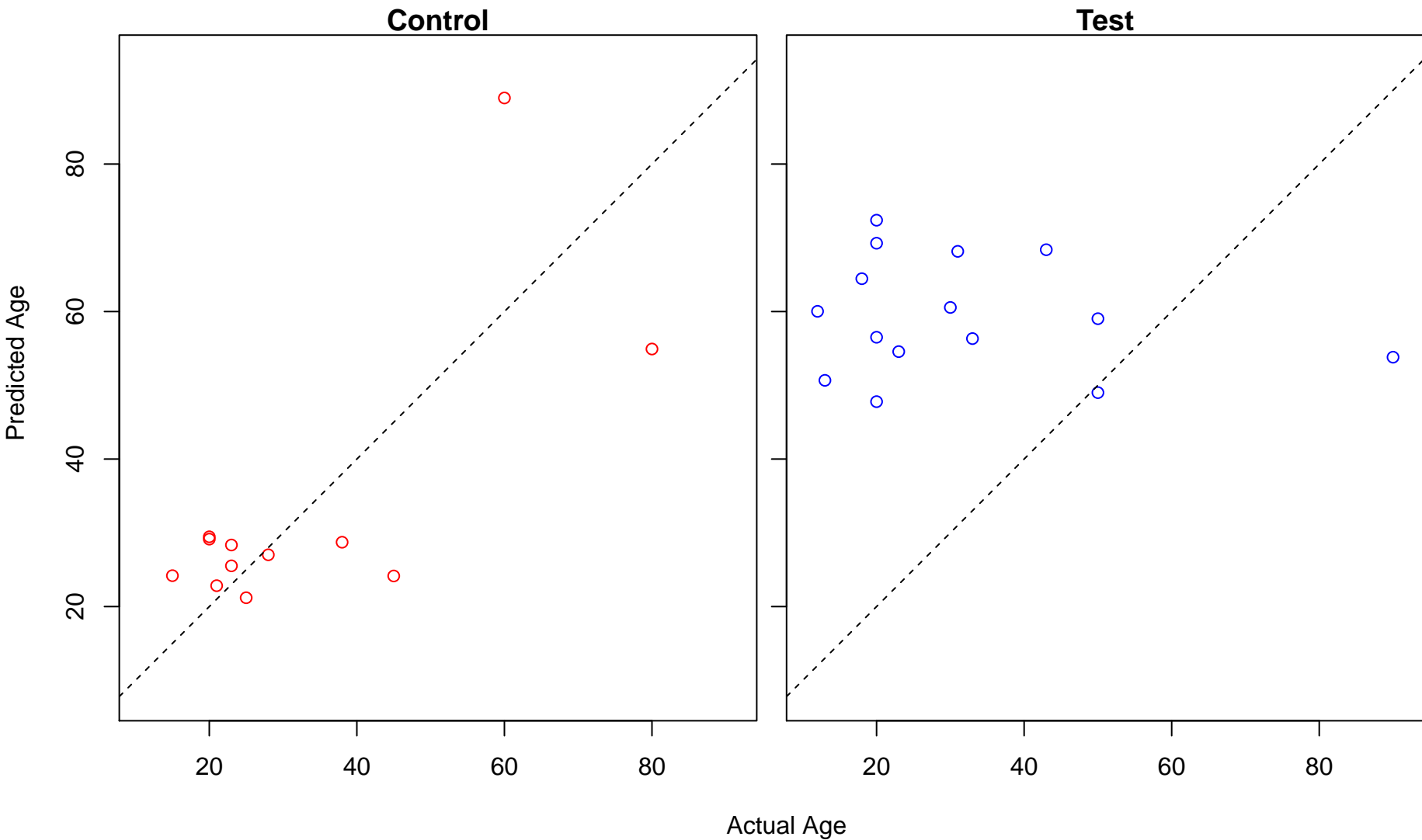
cerebellar cortex development (Score: 2.814176)



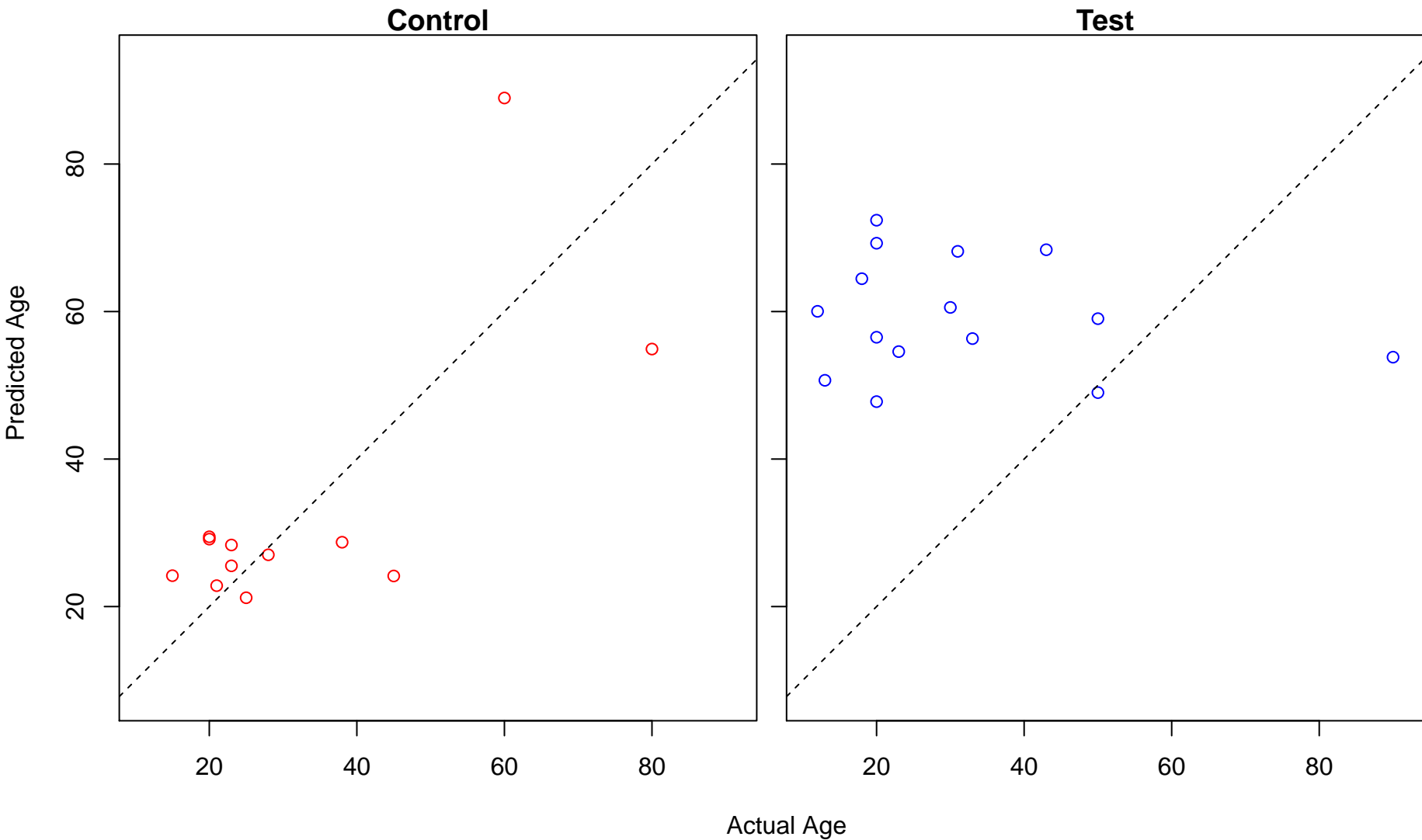
oncostatin-M-mediated signaling pathway (Score: 2.813749)



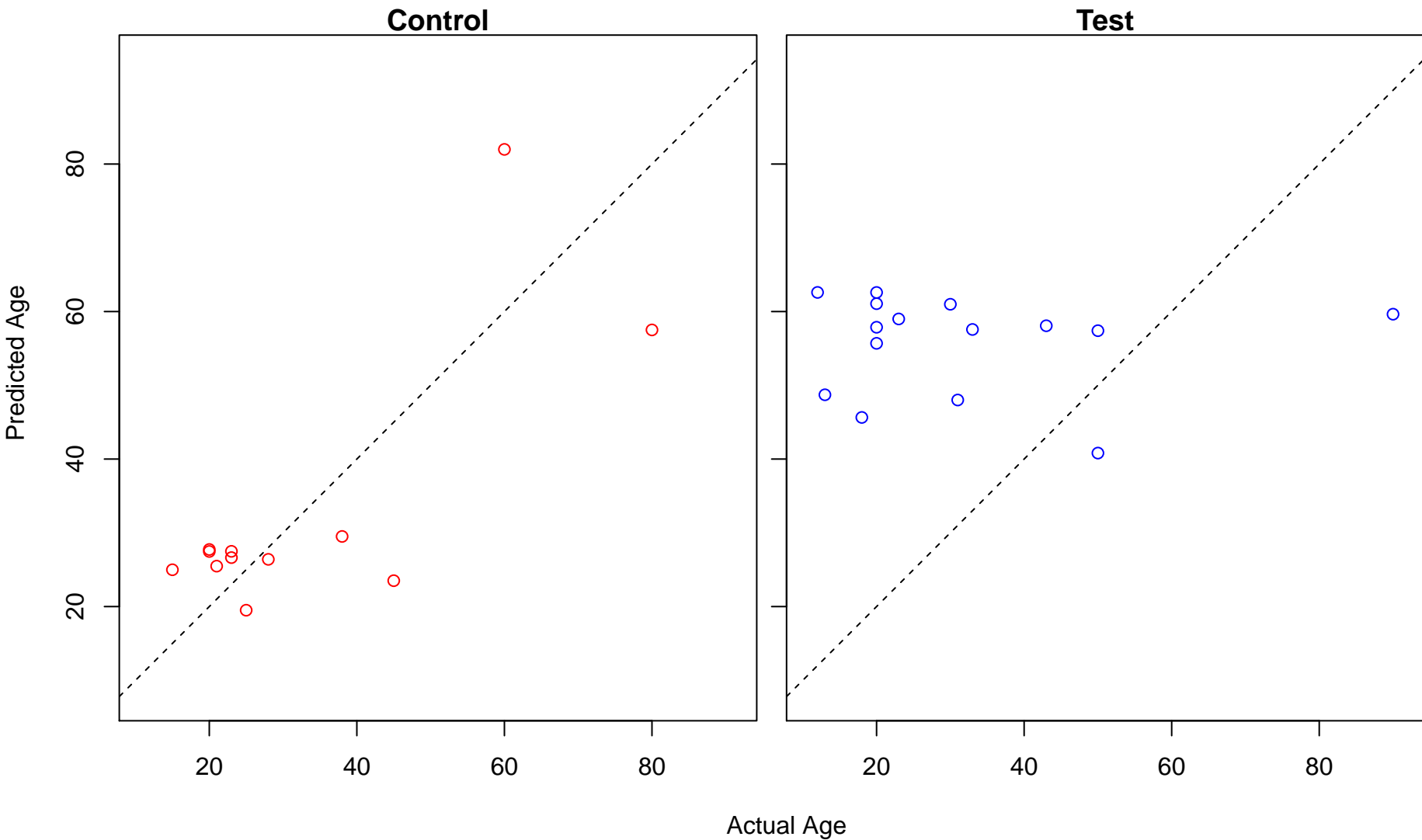
positive regulation of interferon- α production (Score: 2.812660)



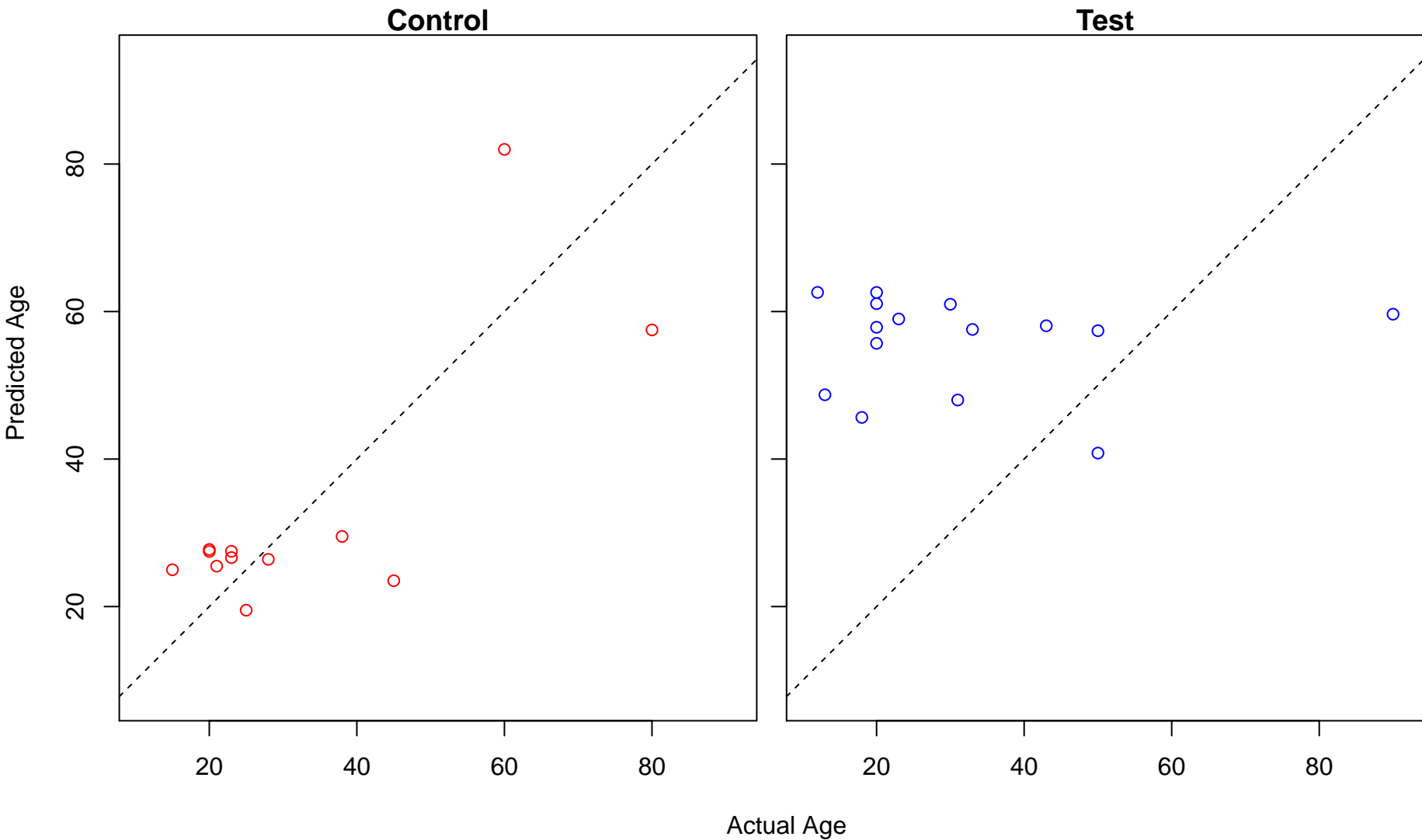
regulation of interferon- α production (Score: 2.812561)



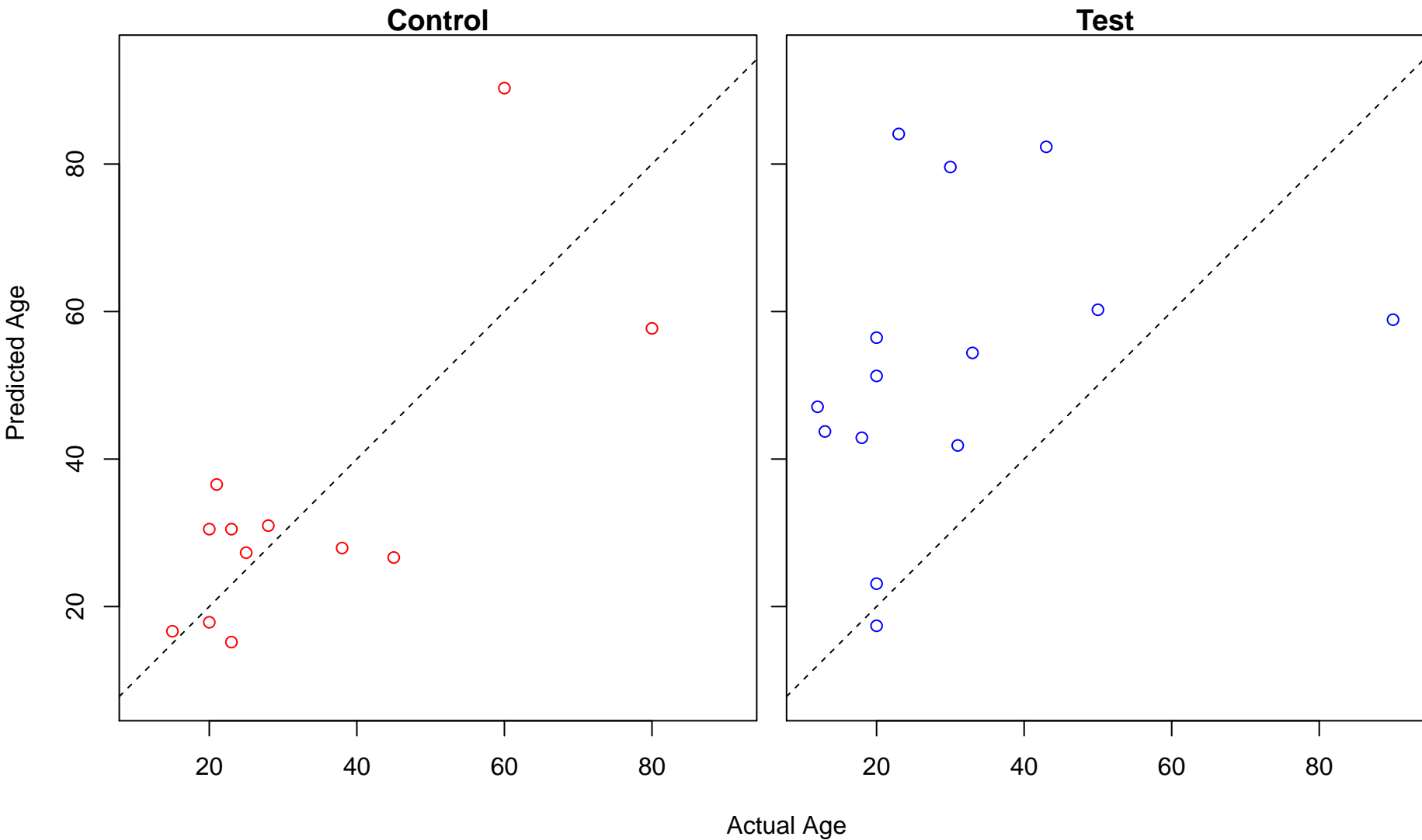
DNA replication-dependent nucleosome assembly (Score: 2.805783)



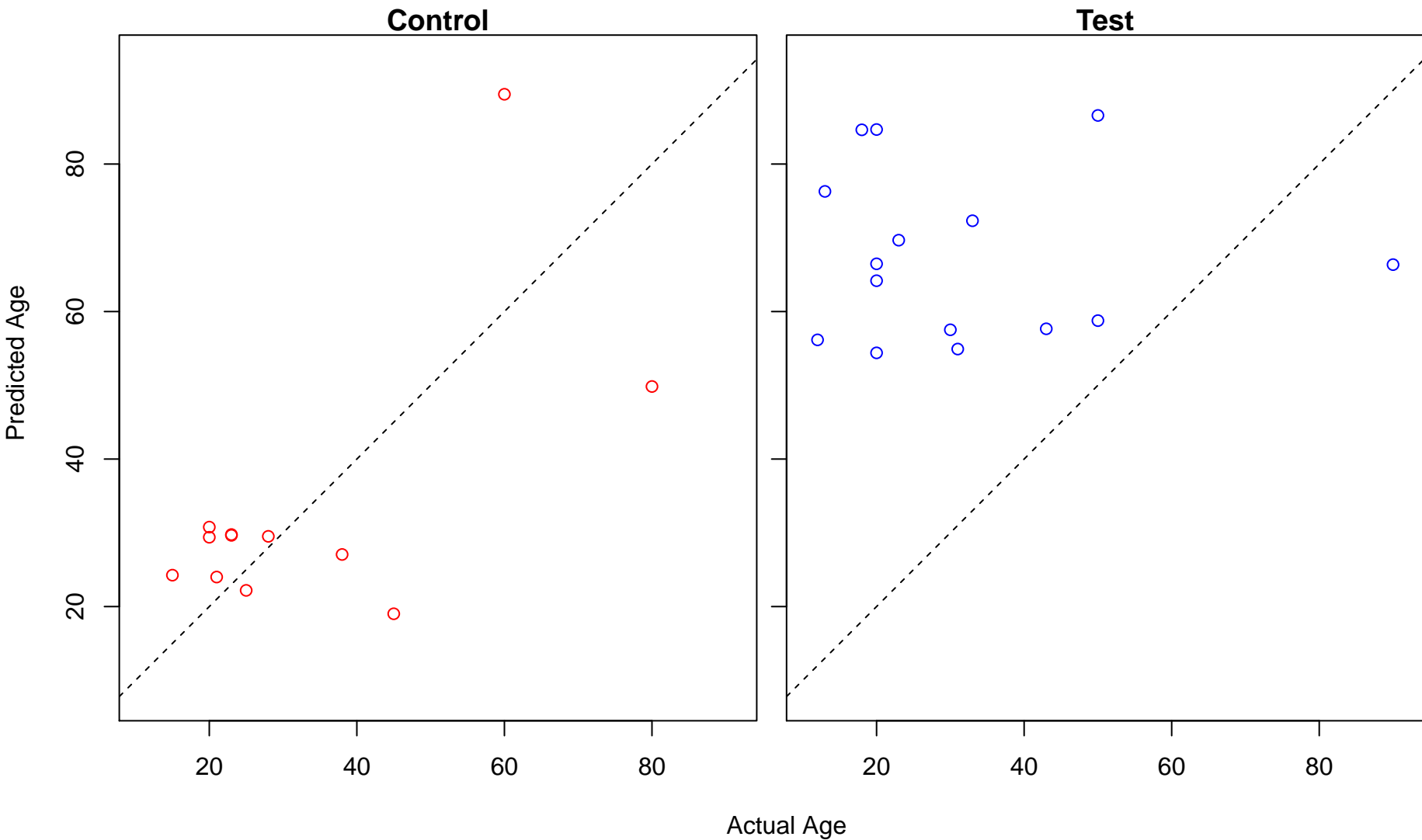
DNA replication-dependent nucleosome organization (Score: 2.805783)



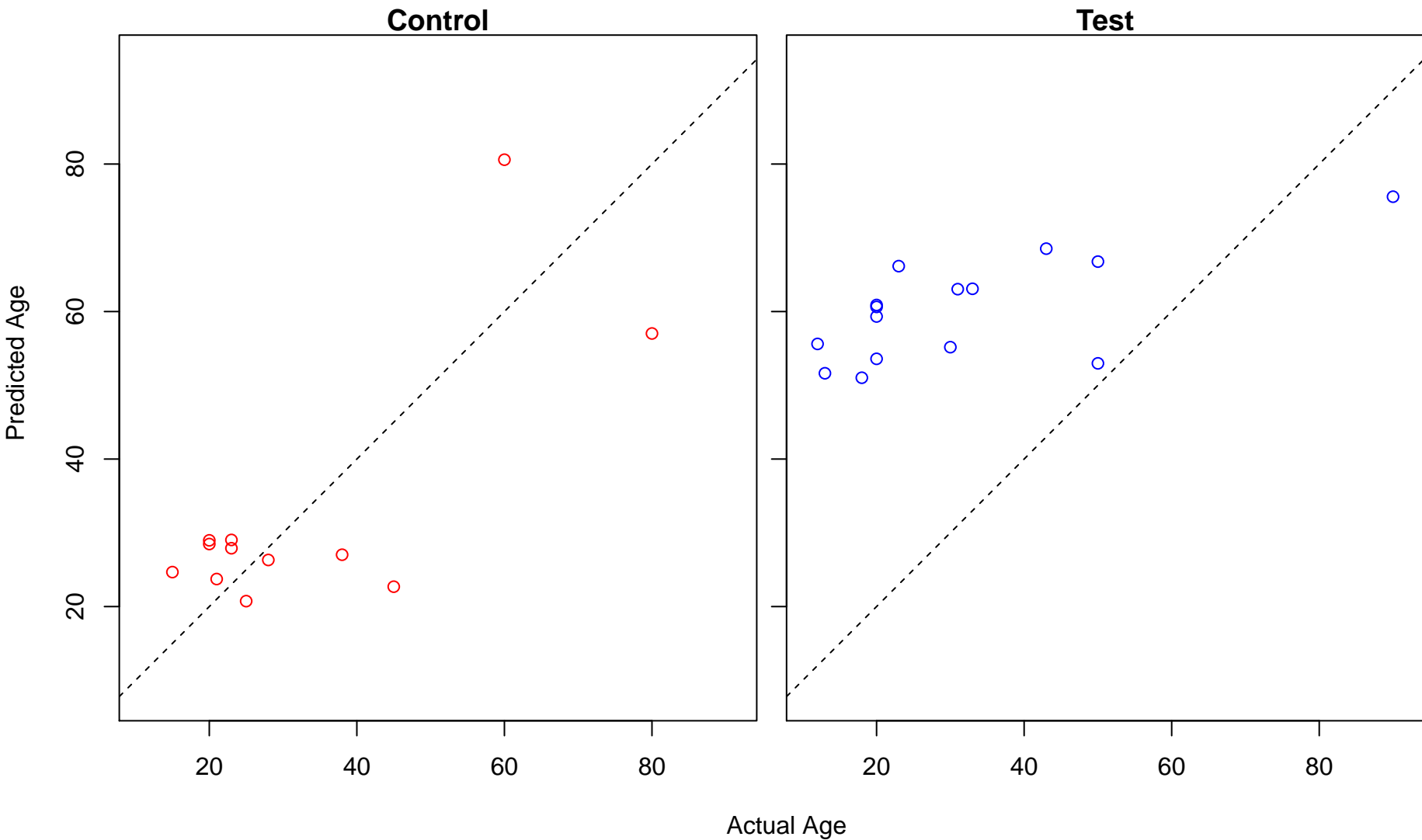
response to muramyl dipeptide (Score: 2.798835)



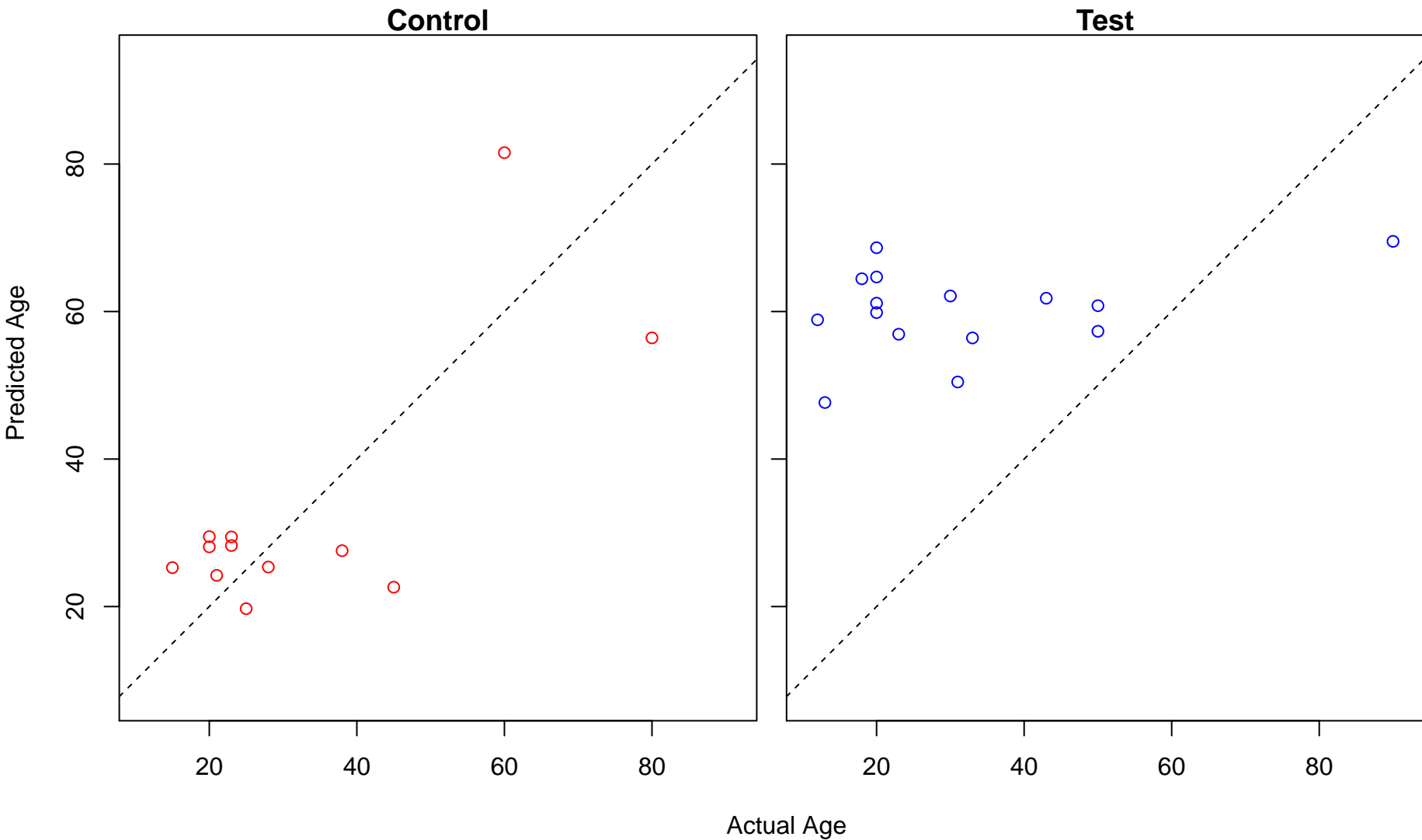
negative regulation of substrate adhesion-dependent cell spreading (Score: 2.788925)



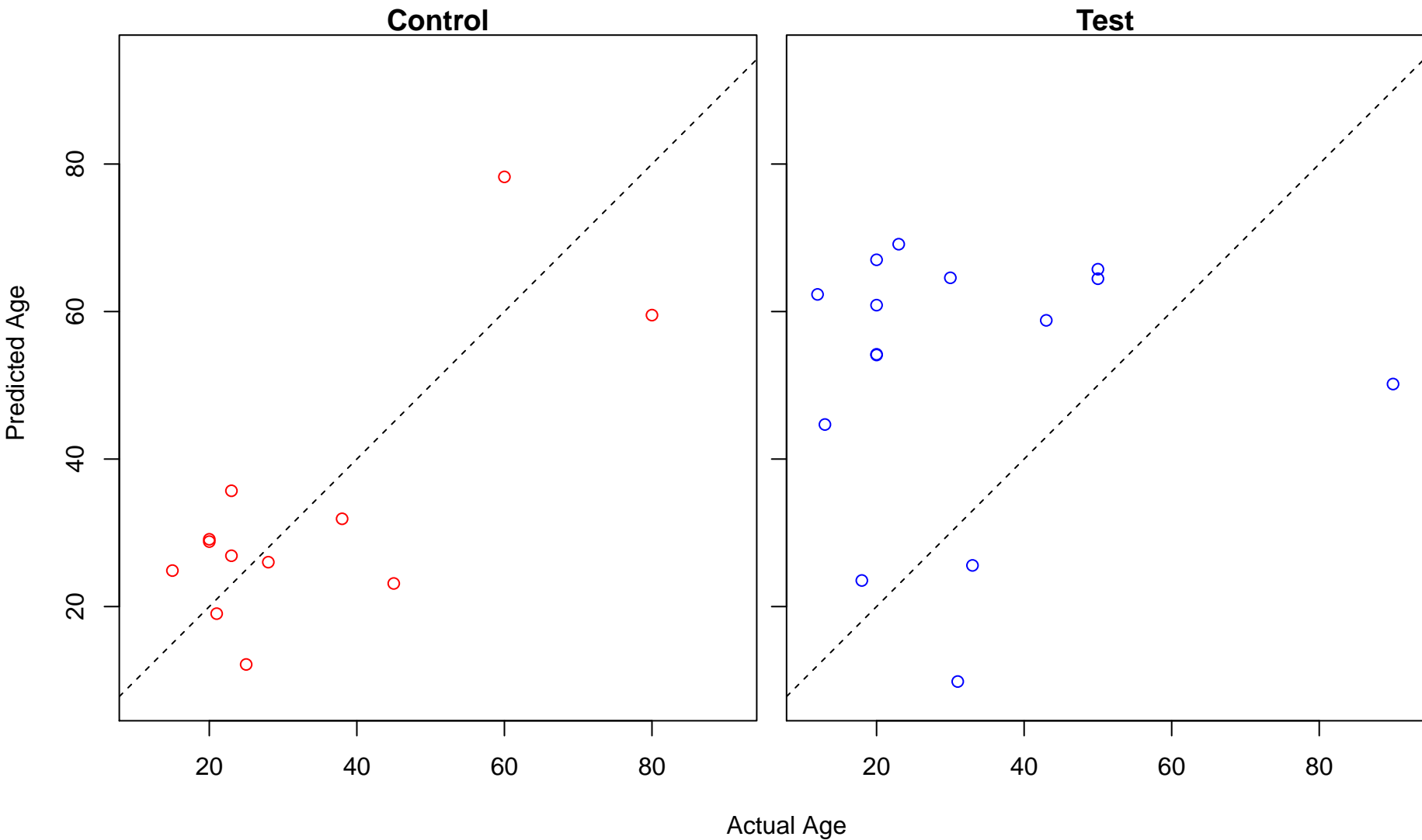
snRNA processing (Score: 2.784480)



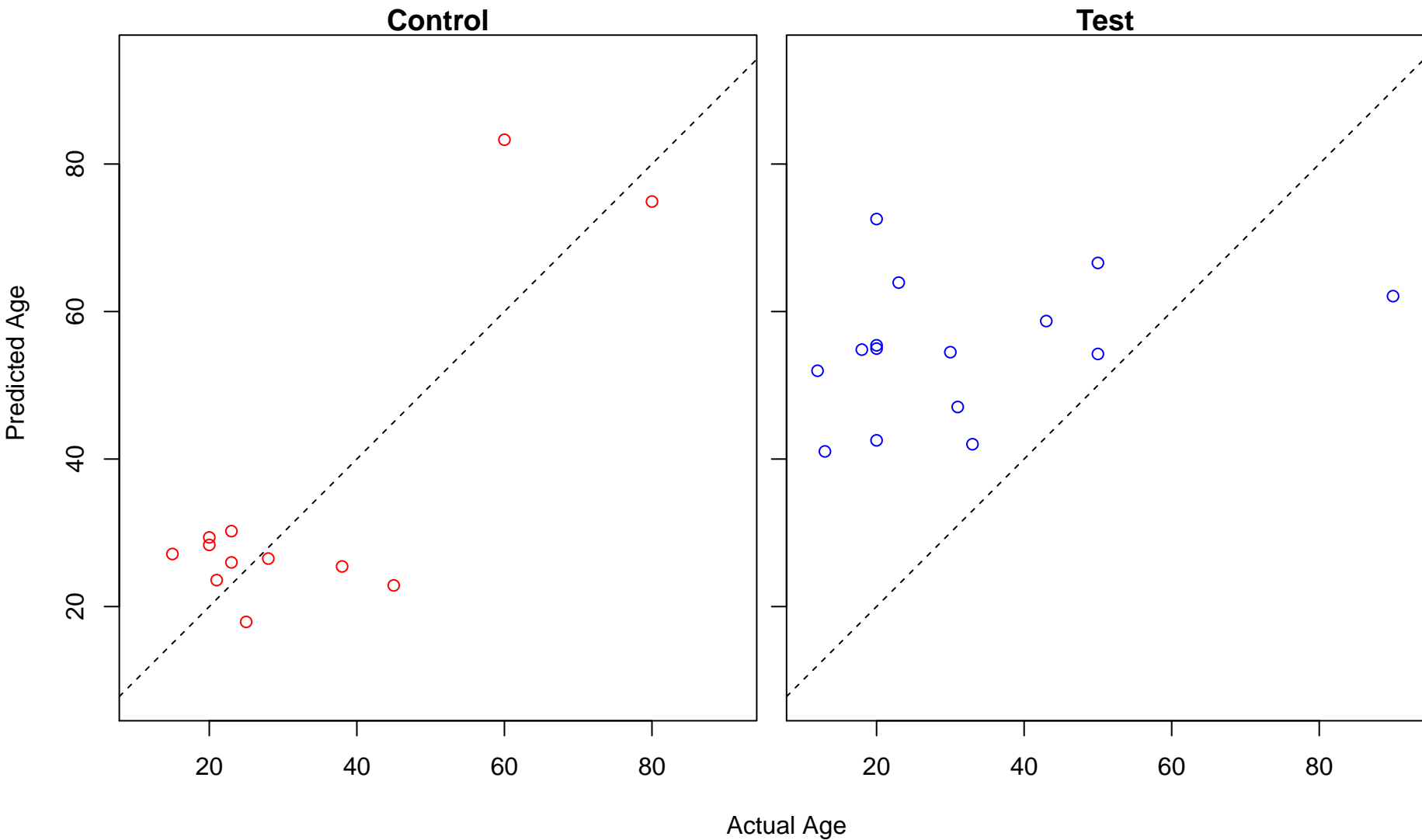
homophilic cell adhesion via plasma membrane adhesion molecules (Score: 2.784274)



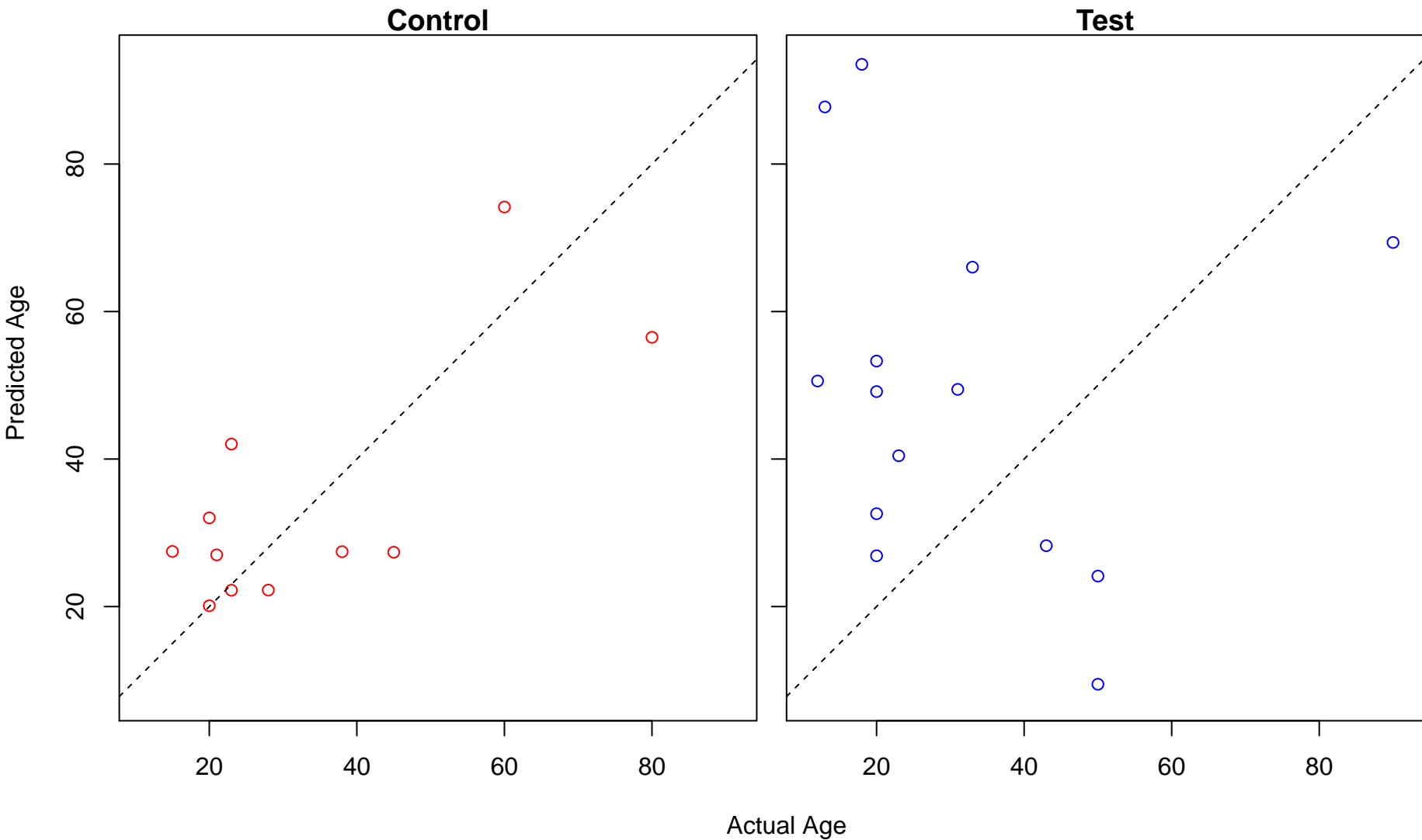
memory (Score: 2.784050)



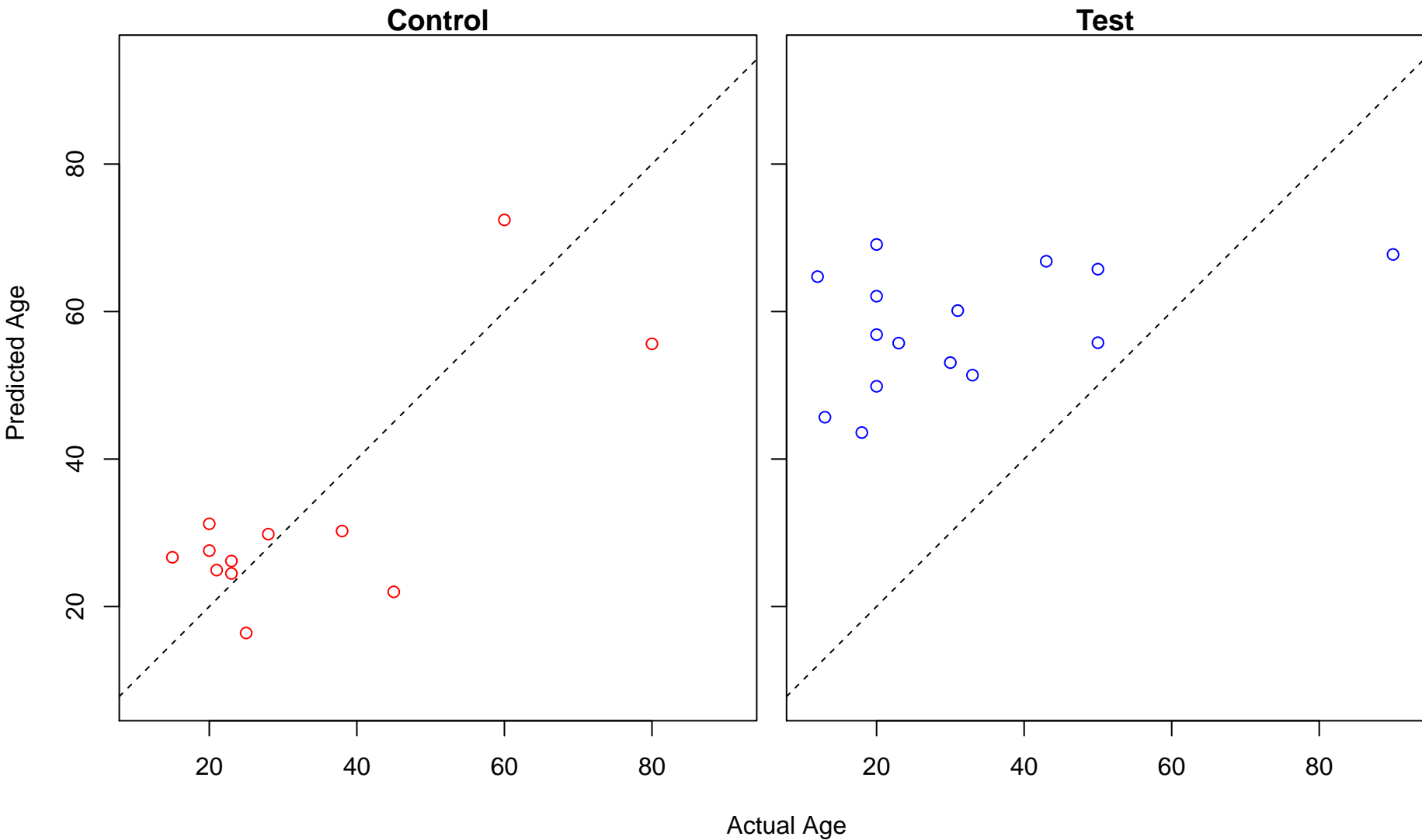
actin filament organization (Score: 2.781537)



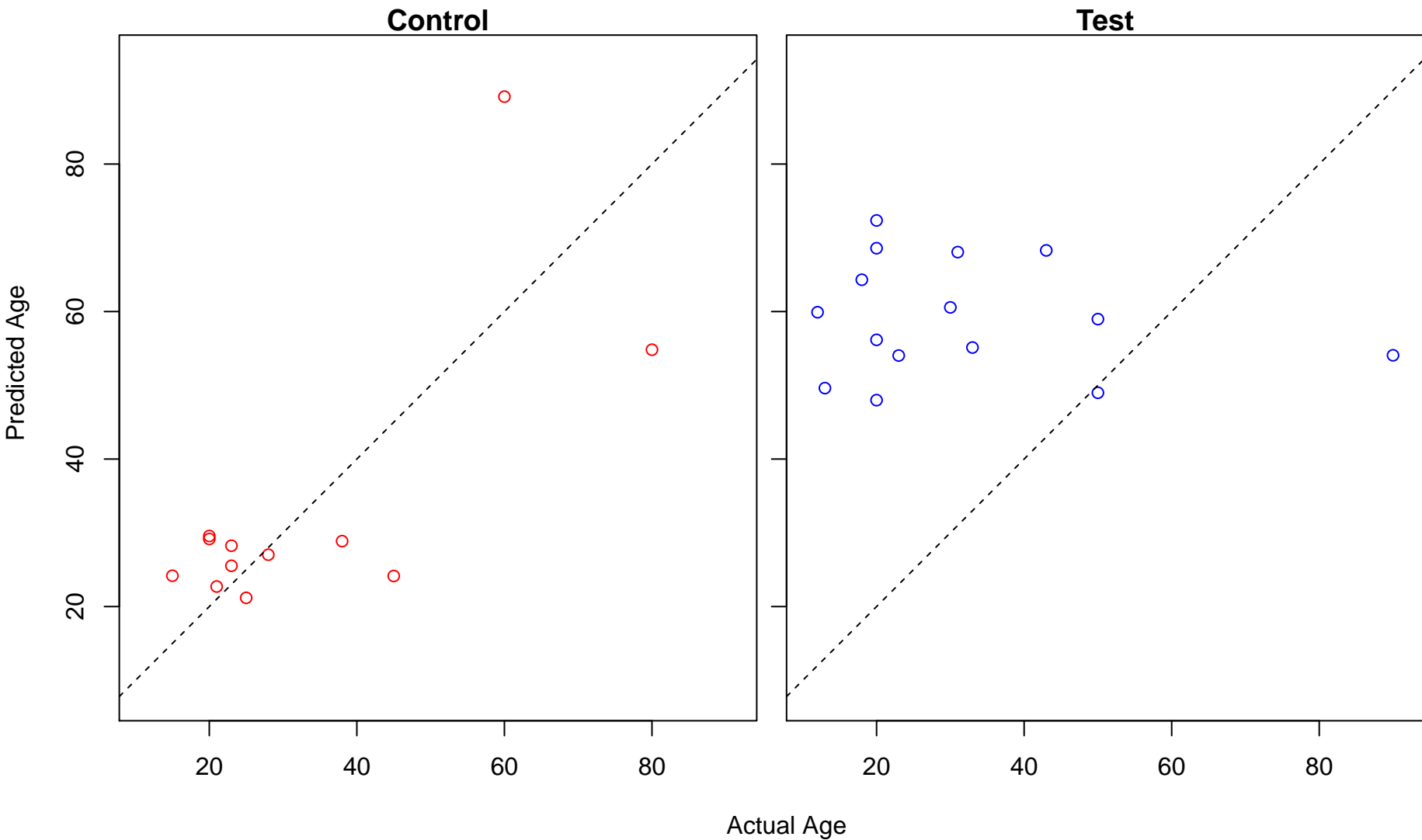
regulation of glomerulus development (Score: 2.777190)



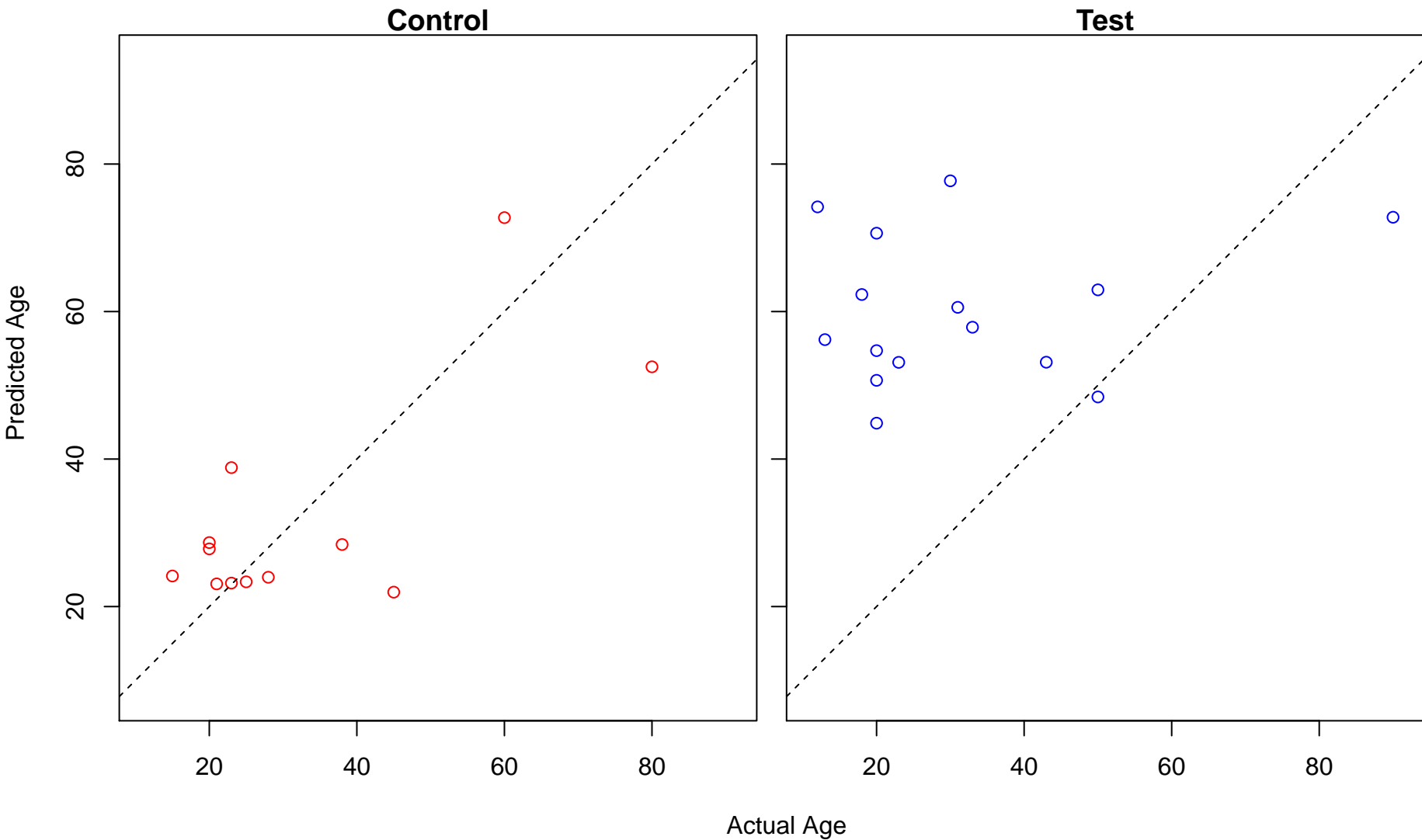
negative regulation of vascular endothelial growth factor receptor signaling pathway (Score: 2.7749)



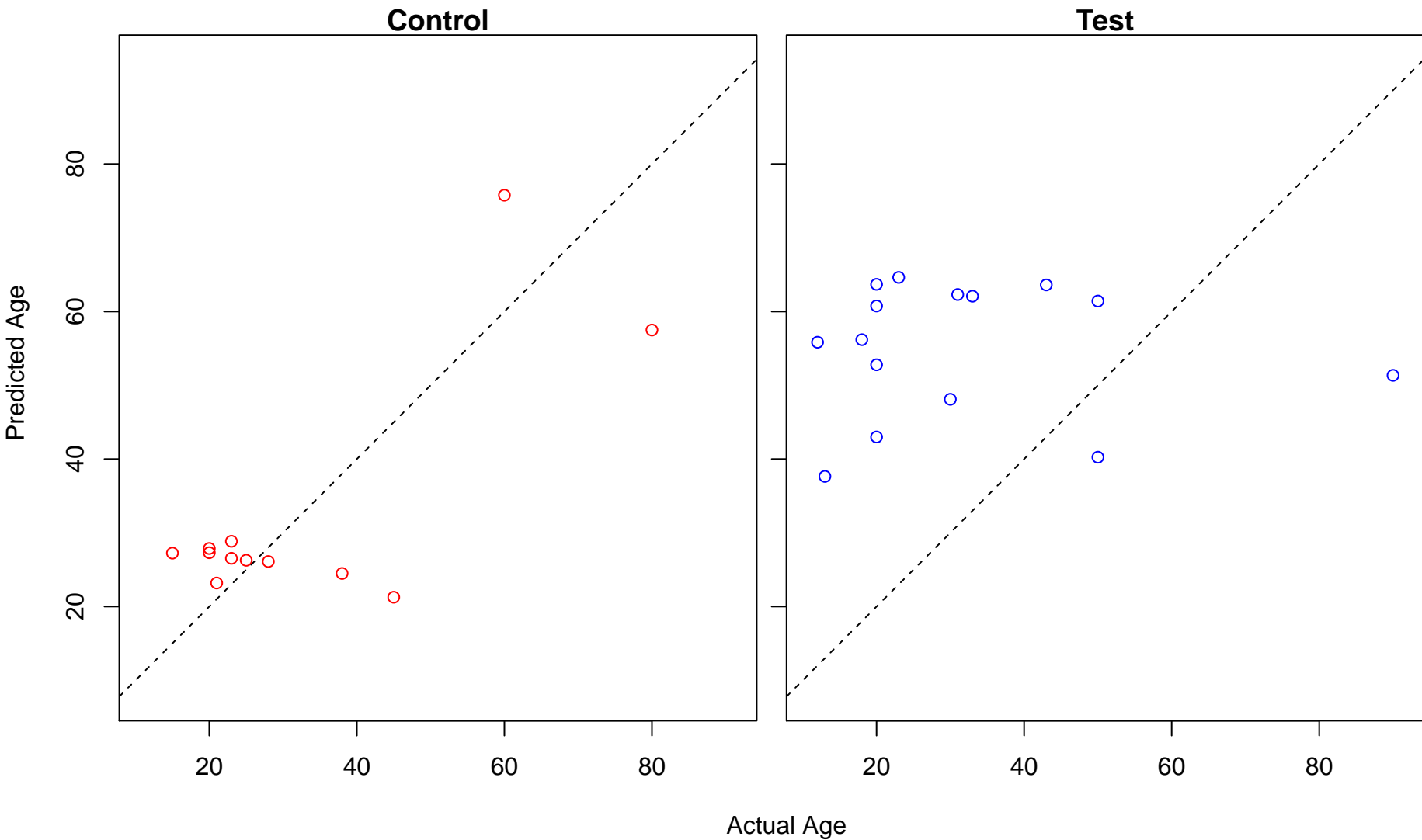
B cell activation involved in immune response (Score: 2.770540)



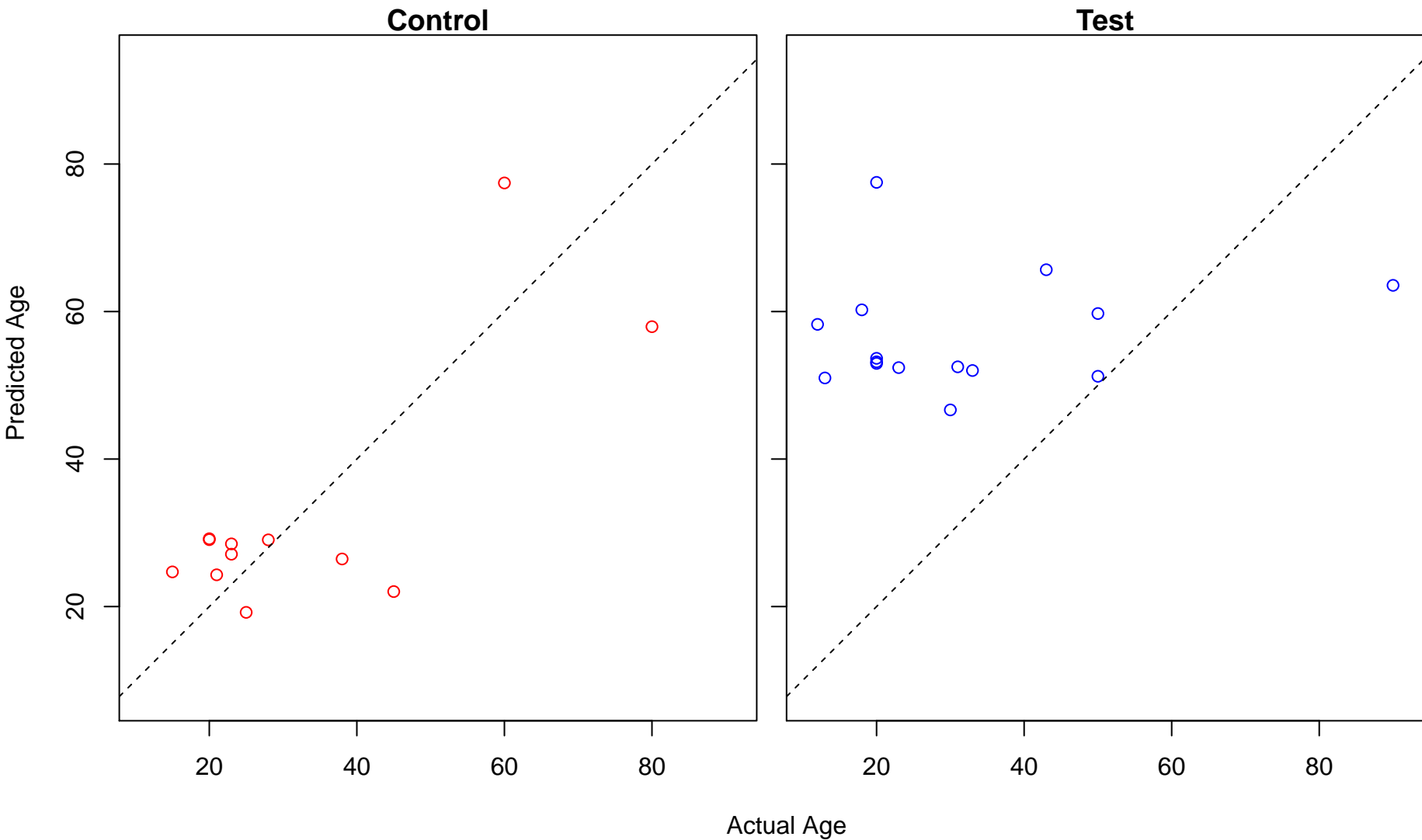
SMAD protein signal transduction (Score: 2.749389)



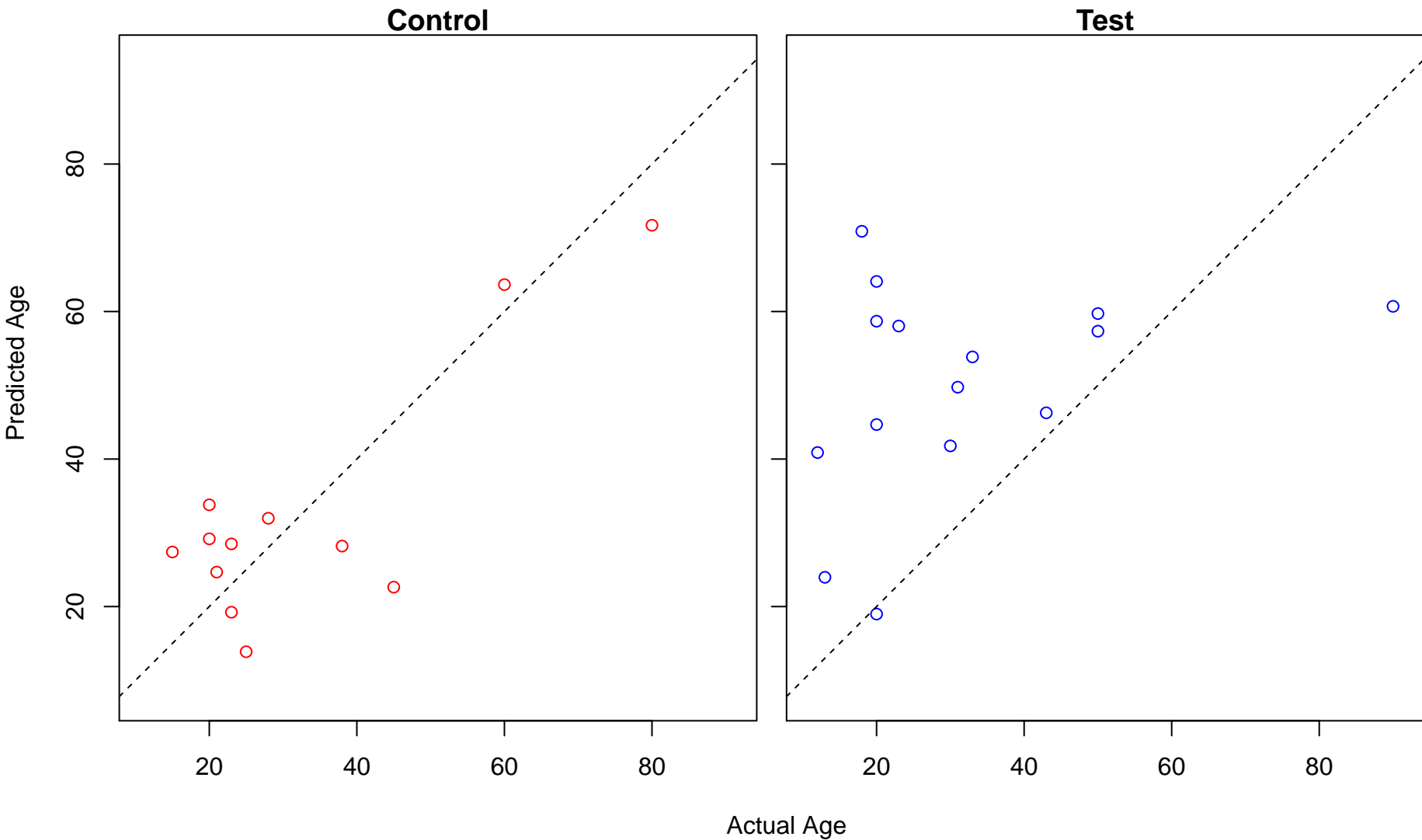
replicative senescence (Score: 2.745206)



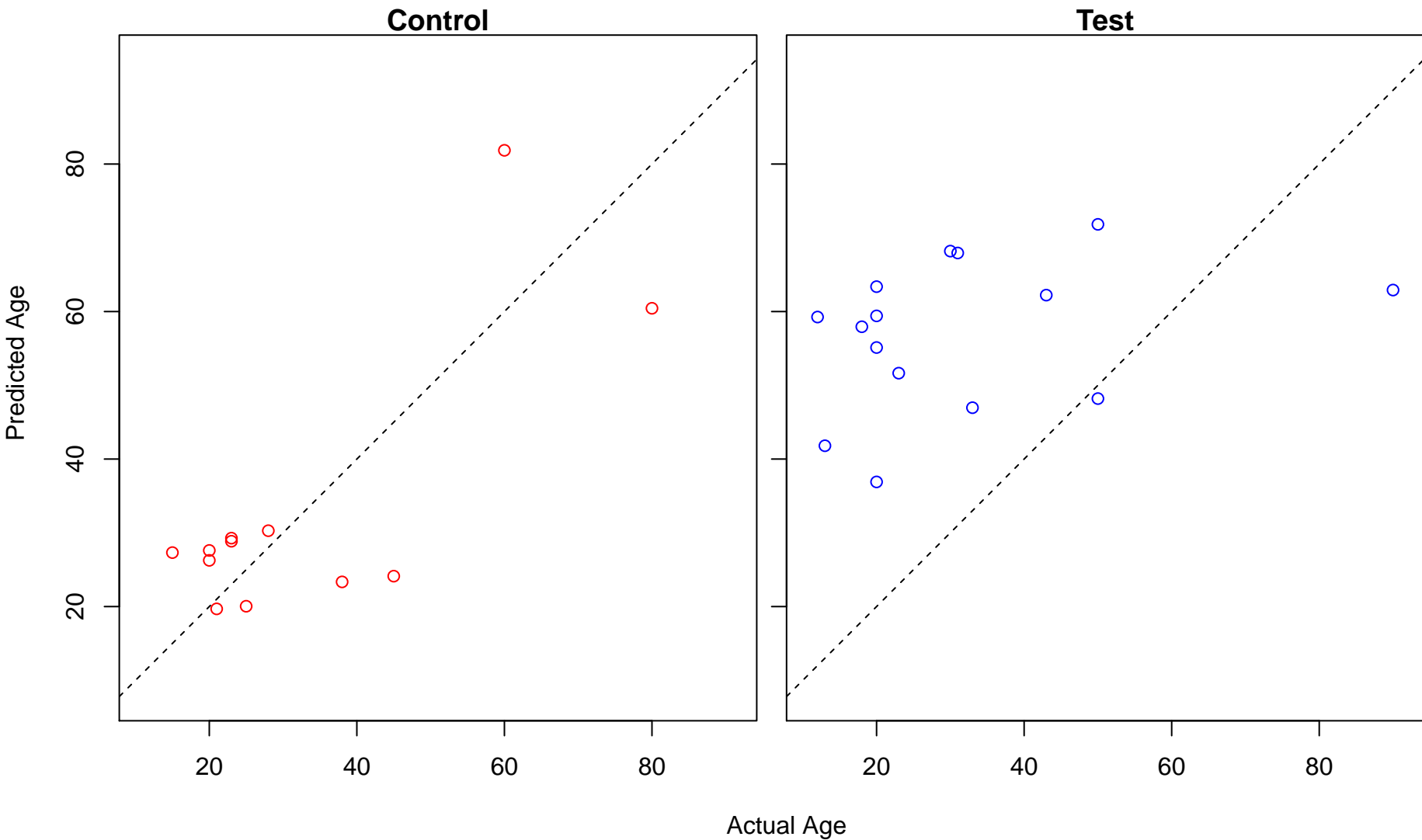
mannosylation (Score: 2.742937)



negative regulation of response to endoplasmic reticulum stress (Score: 2.739502)

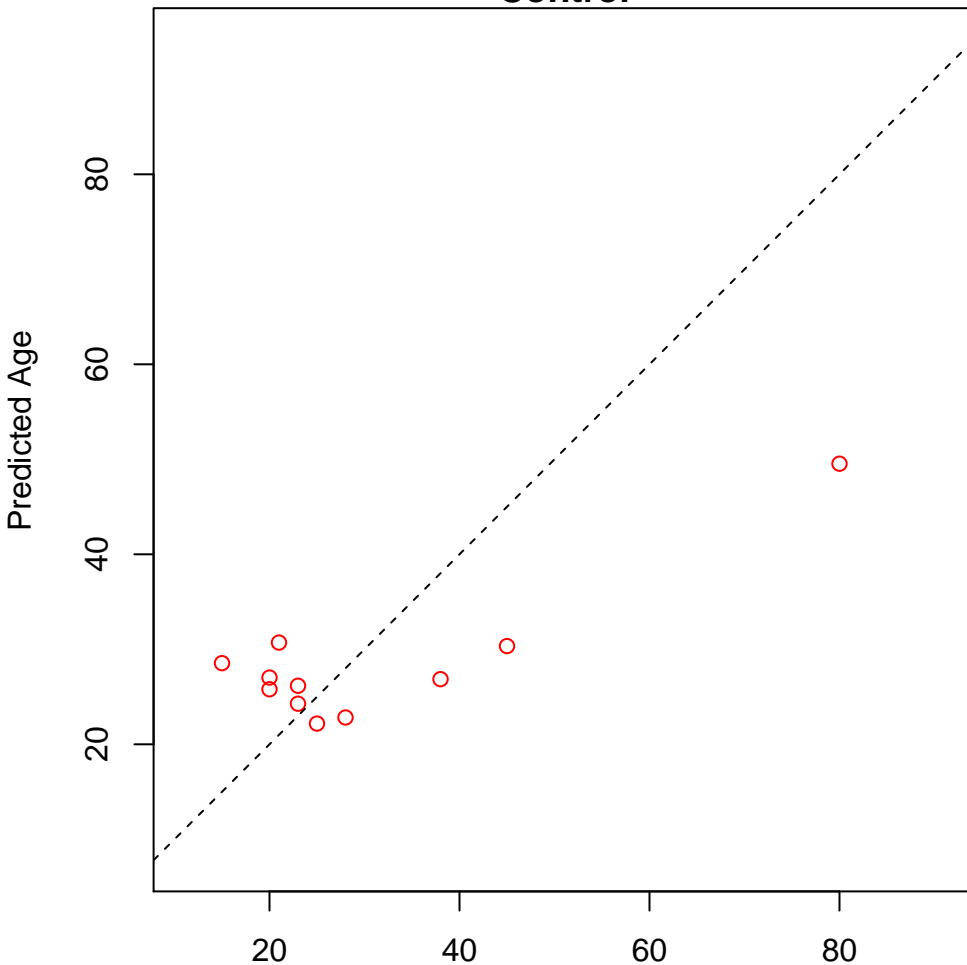


cellular response to ATP (Score: 2.732580)

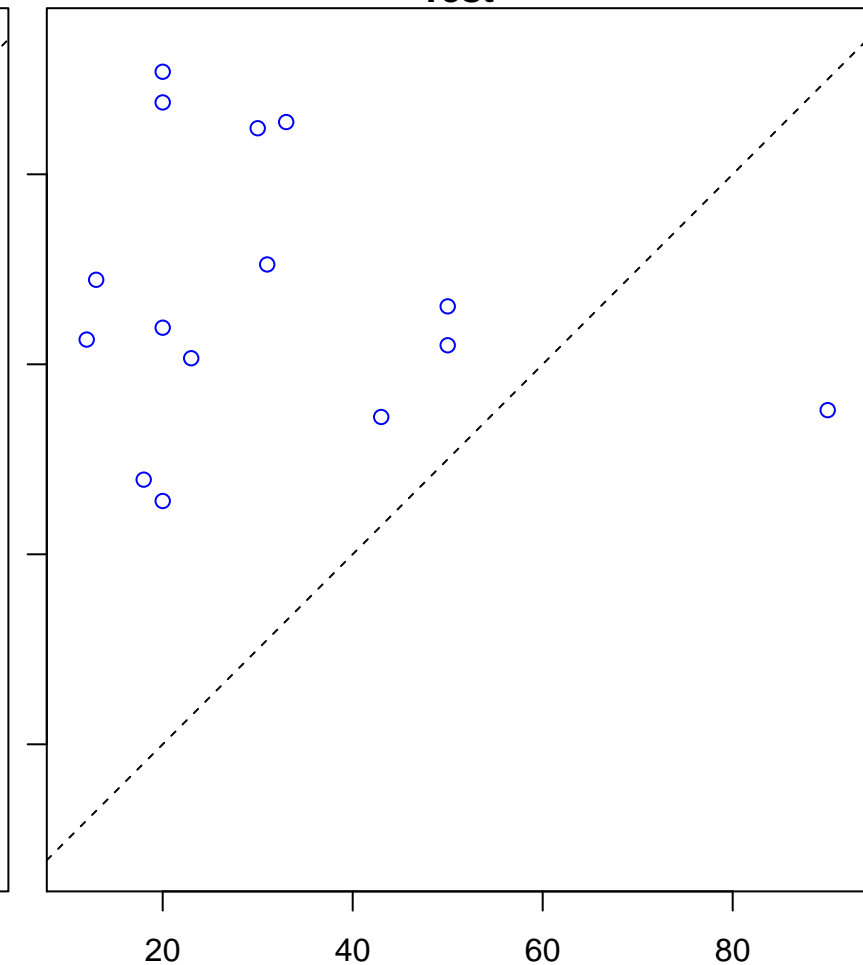


positive regulation of protein maturation (Score: 2.732290)

Control

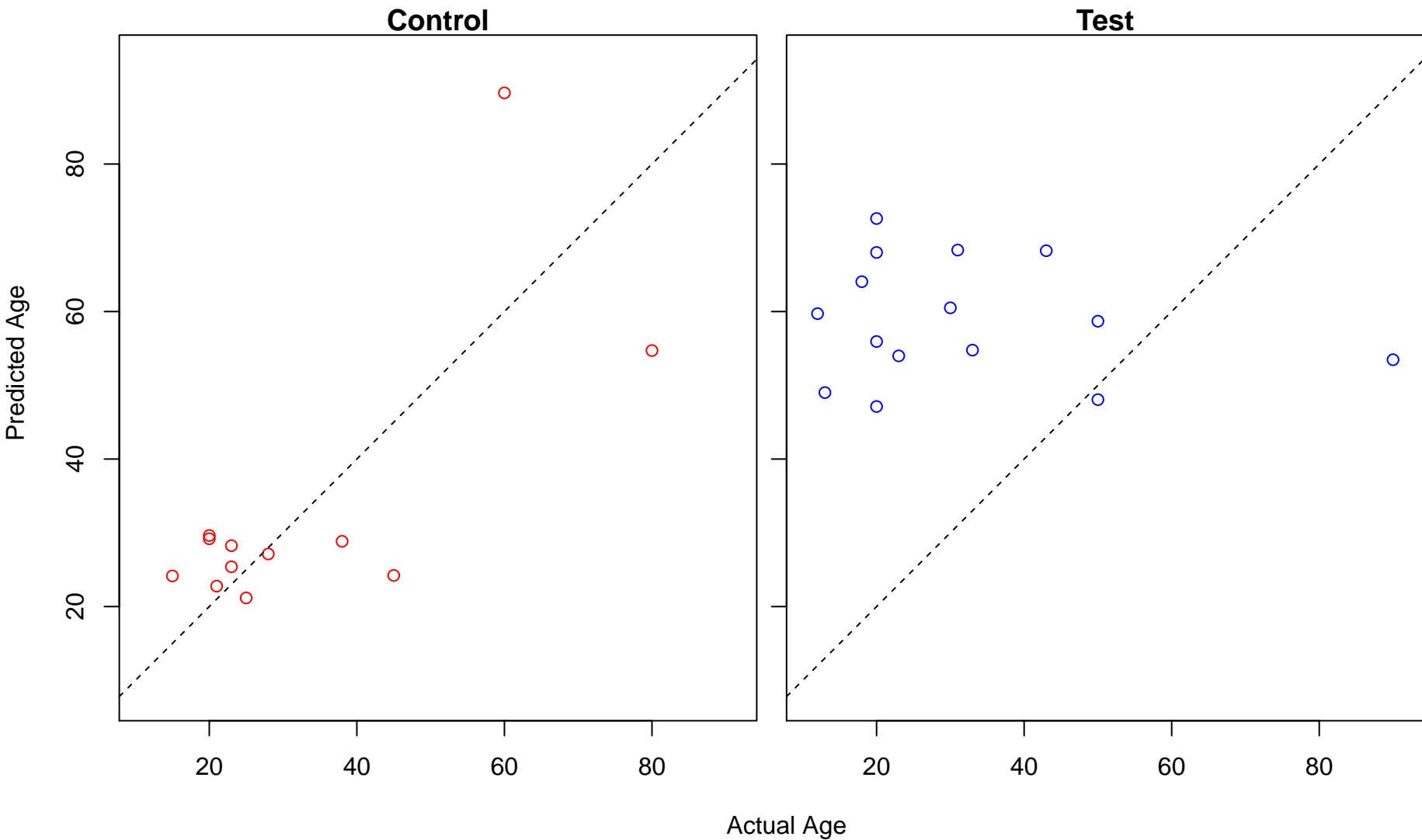


Test

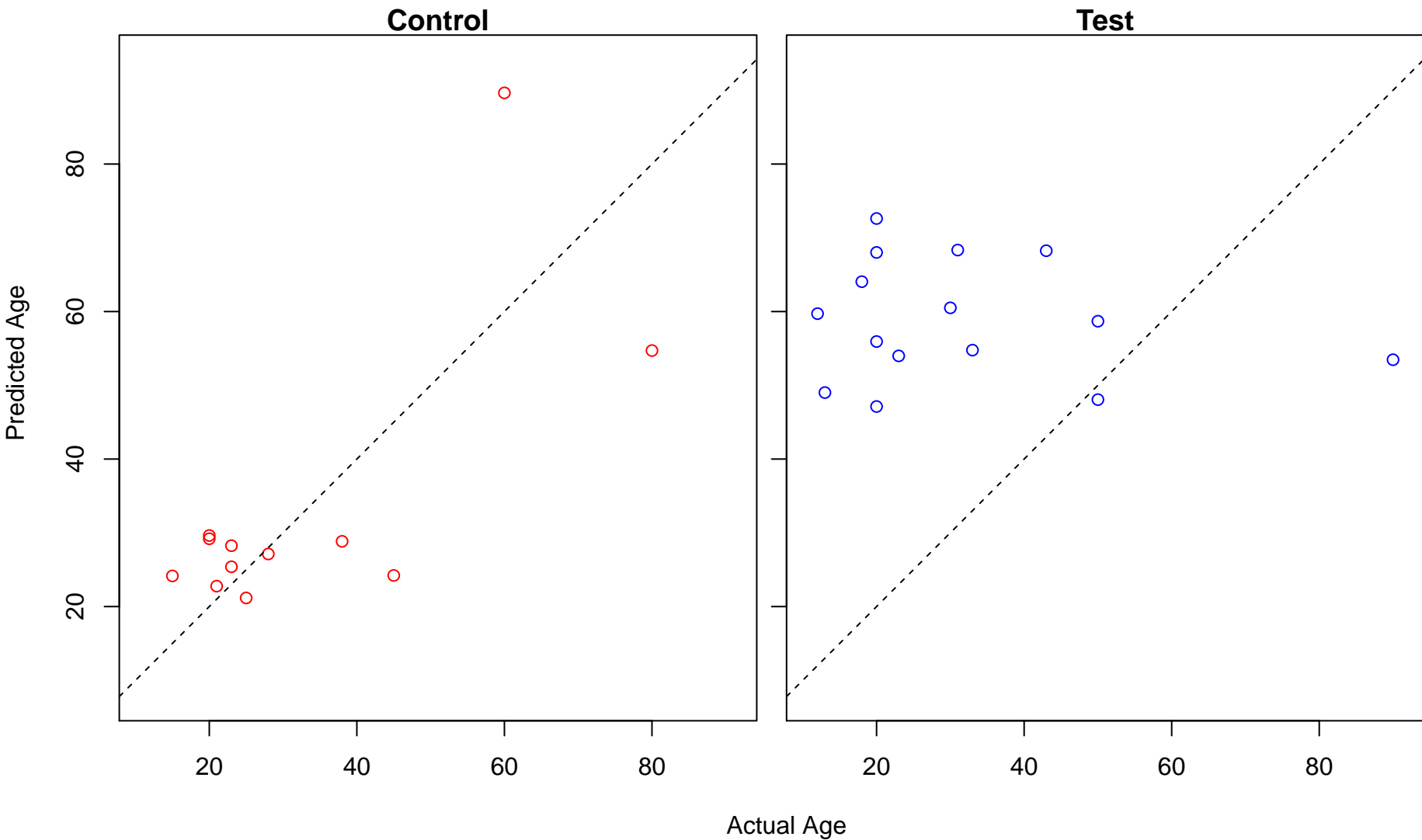


Actual Age

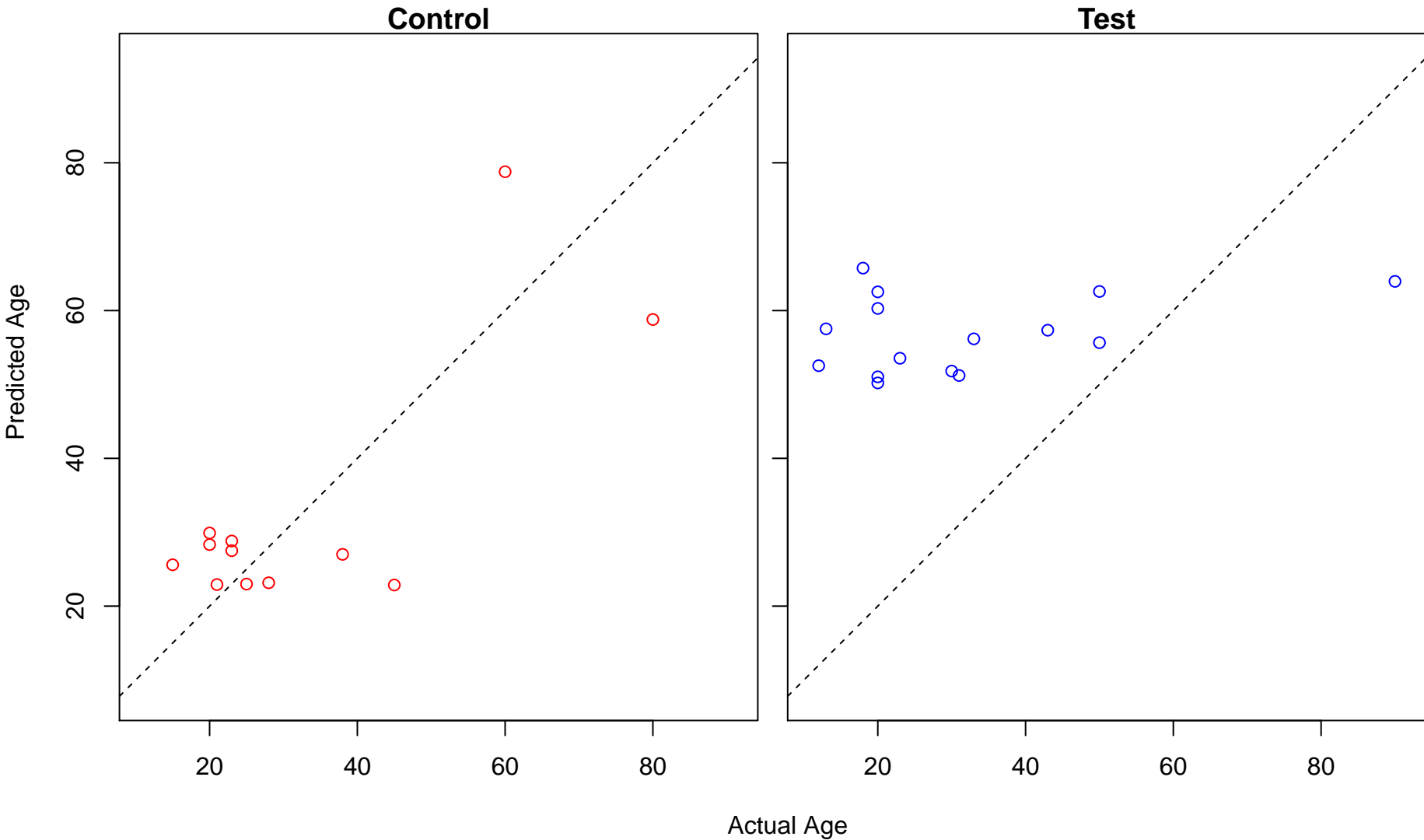
positive regulation of response to tumor cell (Score: 2.731669)



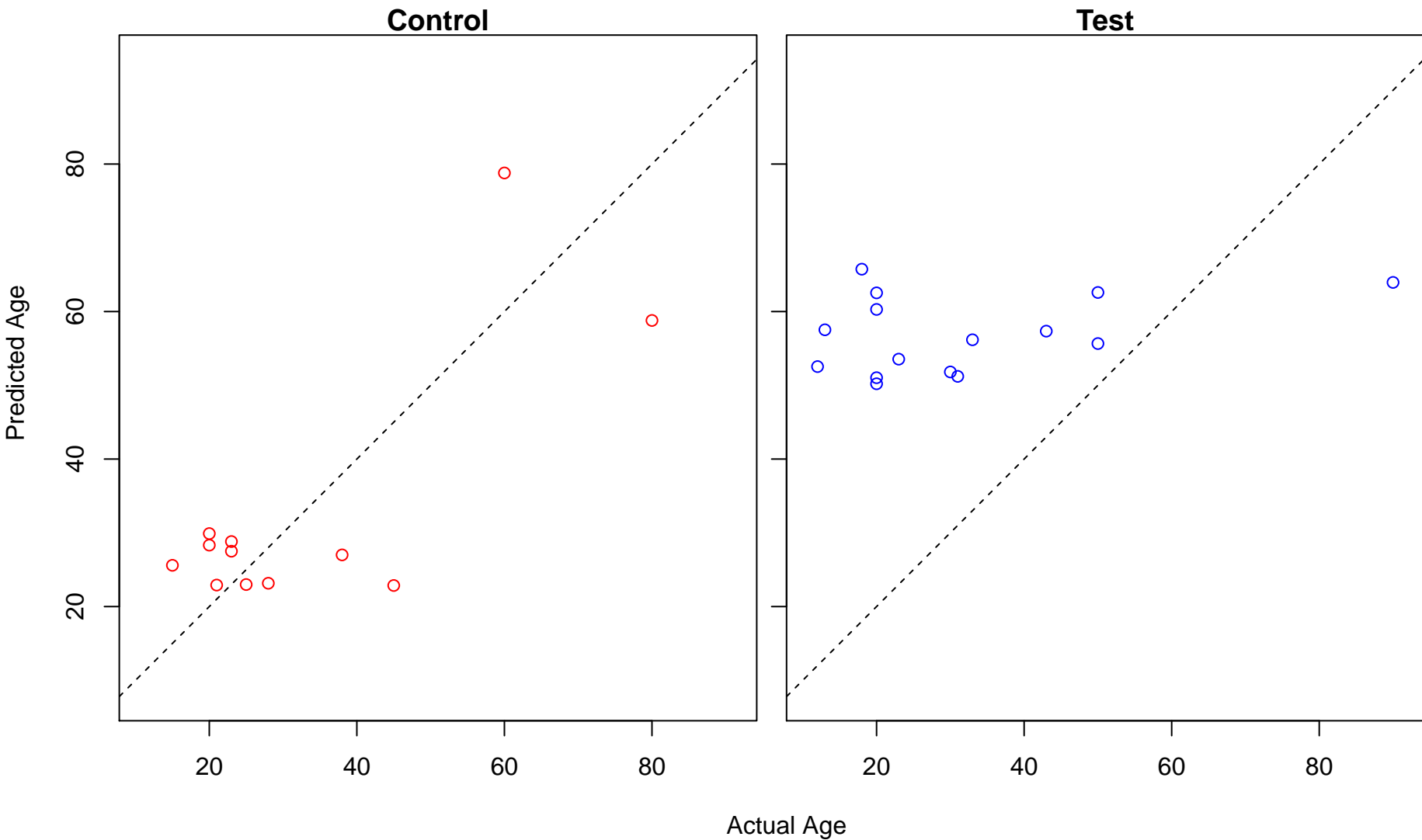
positive regulation of immune response to tumor cell (Score: 2.731669)



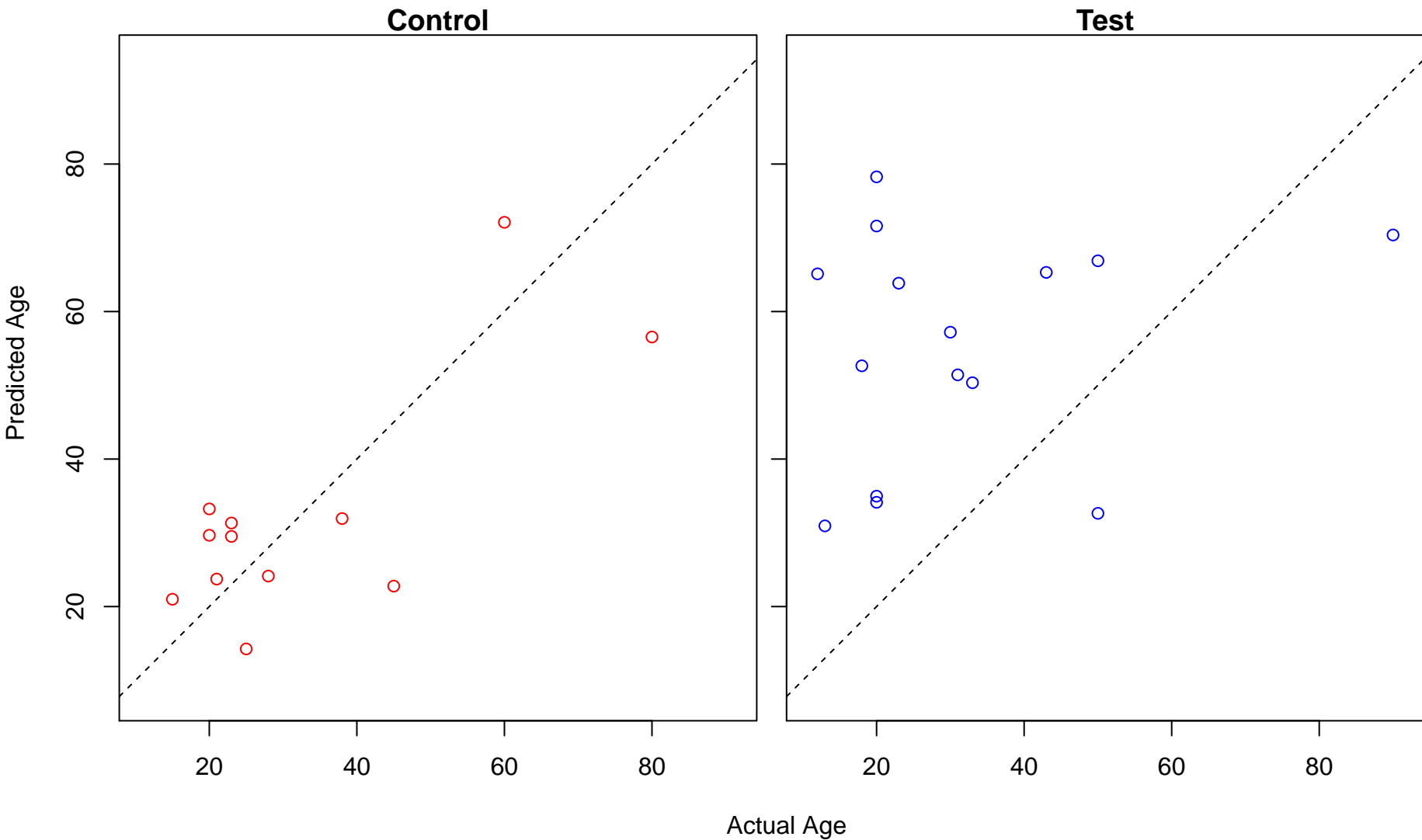
peripheral nervous system neuron differentiation (Score: 2.729477)



peripheral nervous system neuron development (Score: 2.729477)

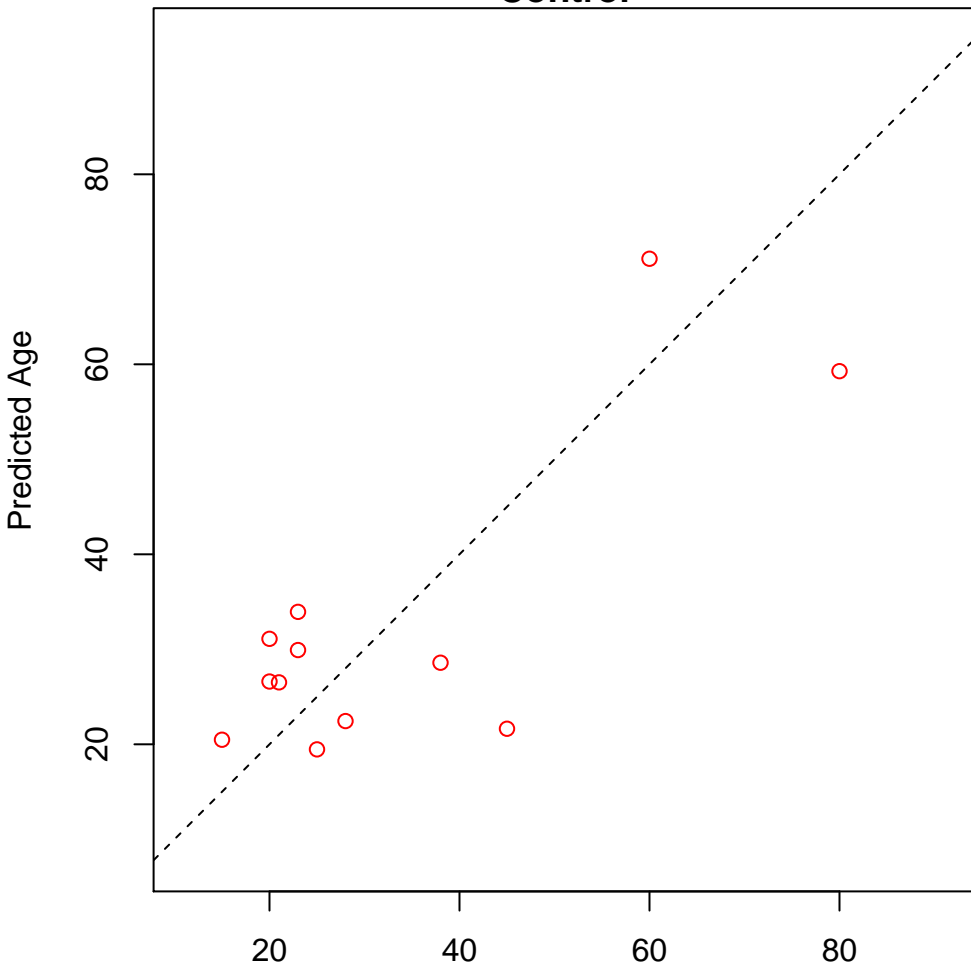


ciliary neurotrophic factor-mediated signaling pathway (Score: 2.725139)

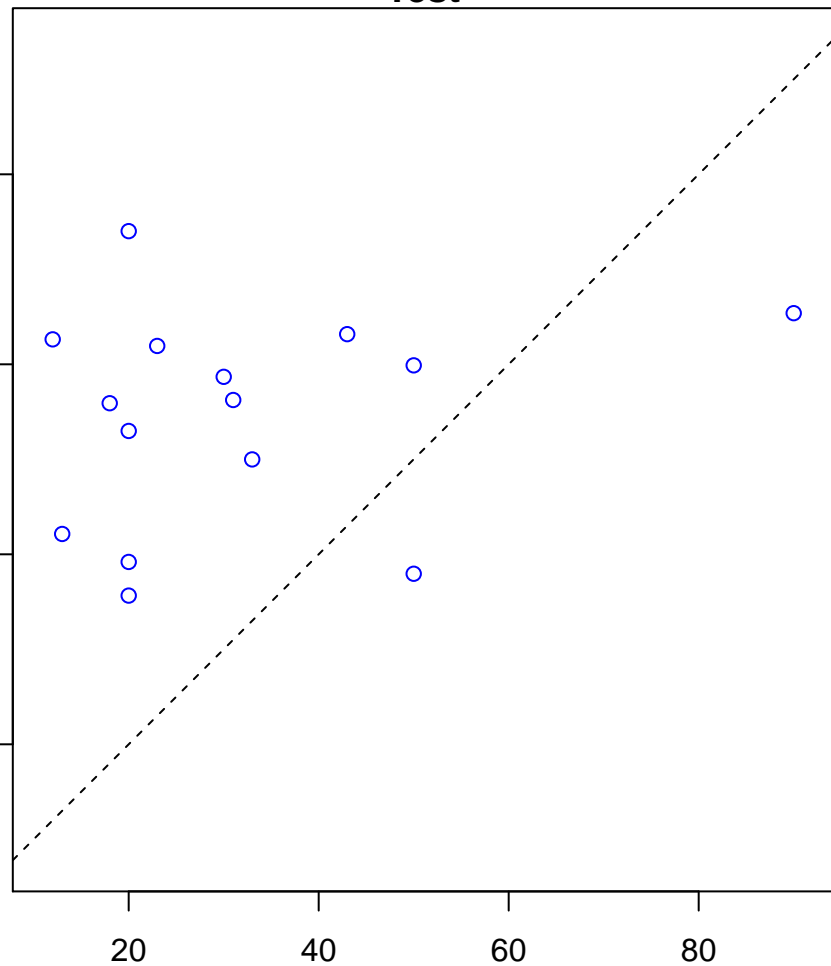


T-helper 17 type immune response (Score: 2.709178)

Control

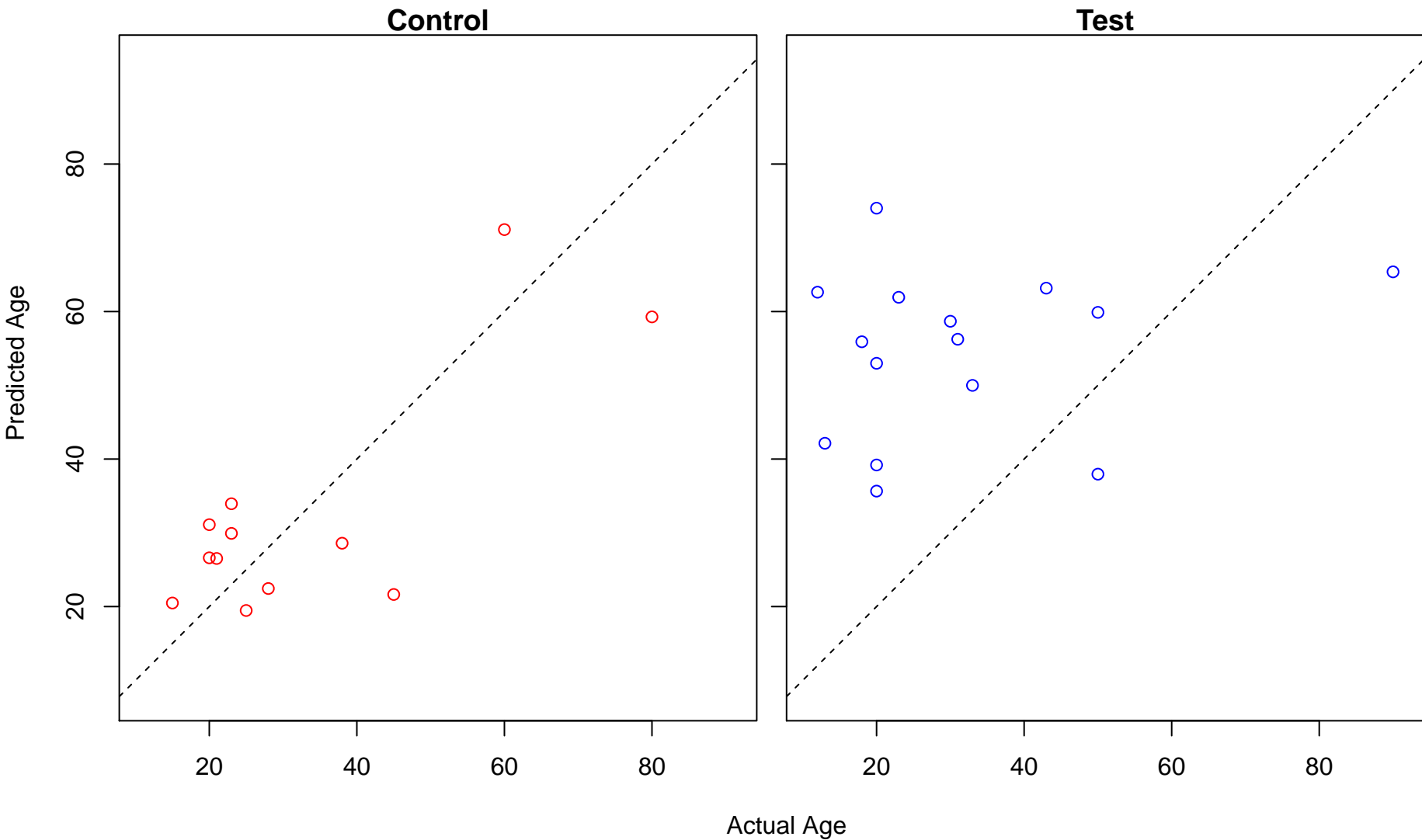


Test

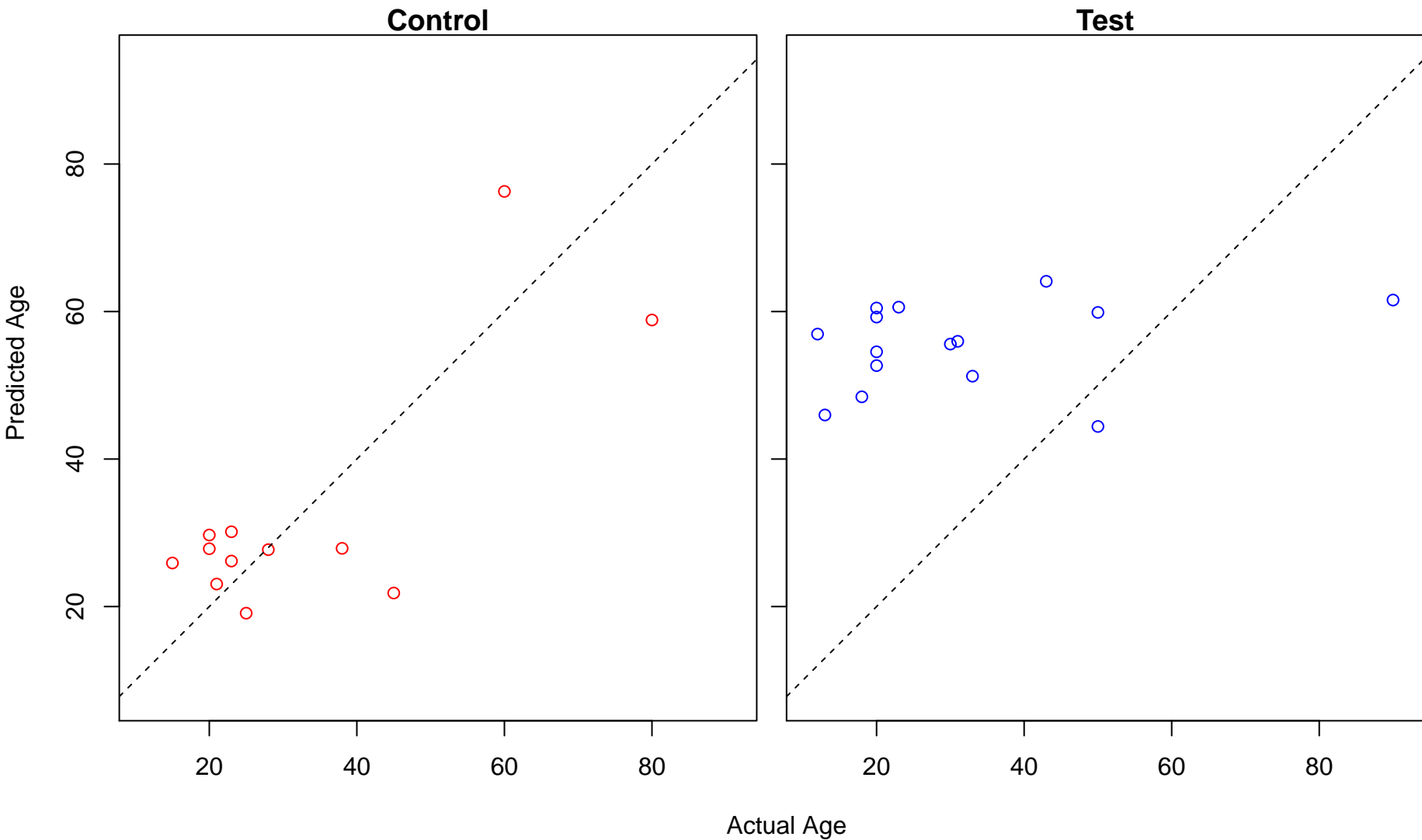


Actual Age

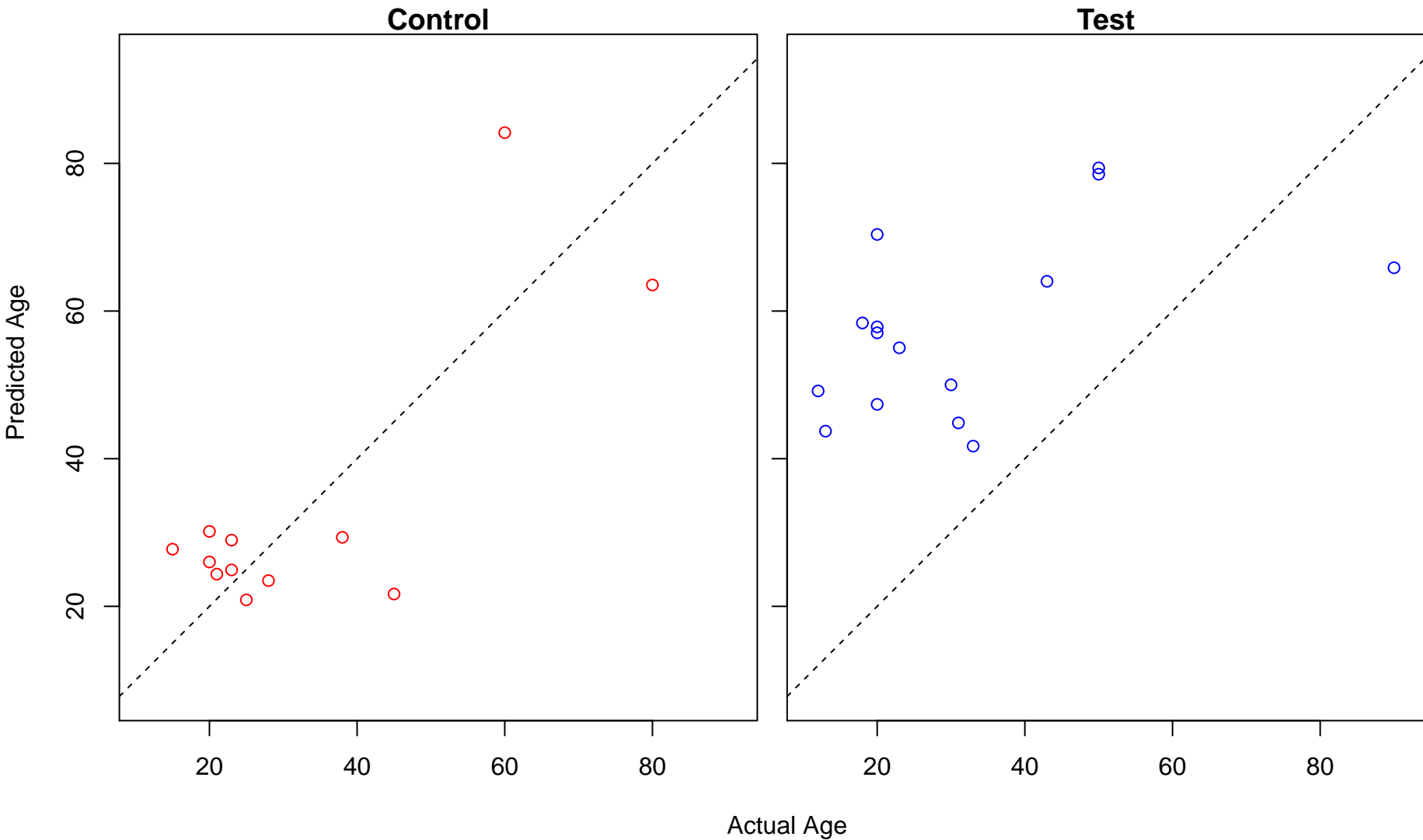
T-helper 17 cell differentiation (Score: 2.709178)



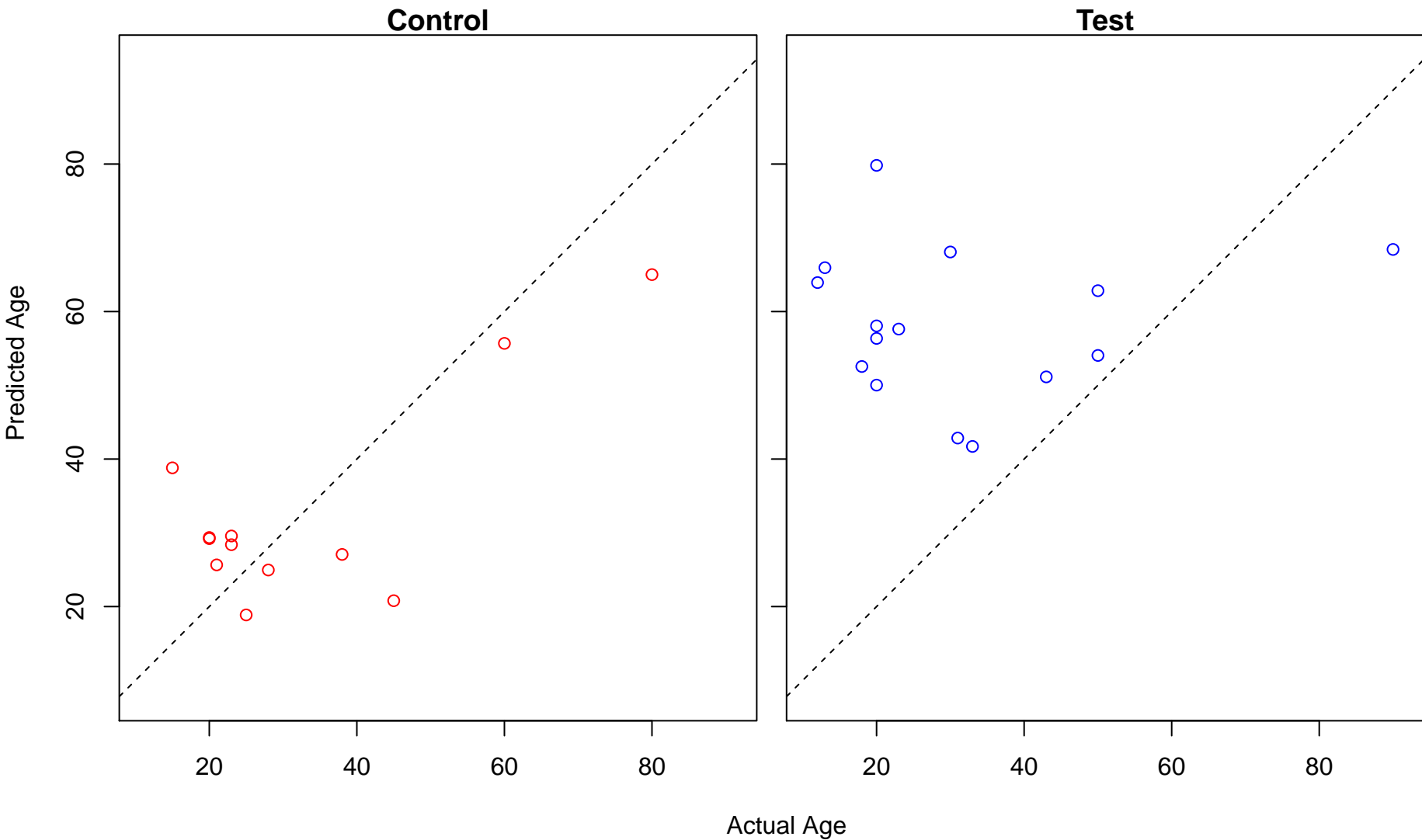
response to gamma radiation (Score: 2.703054)



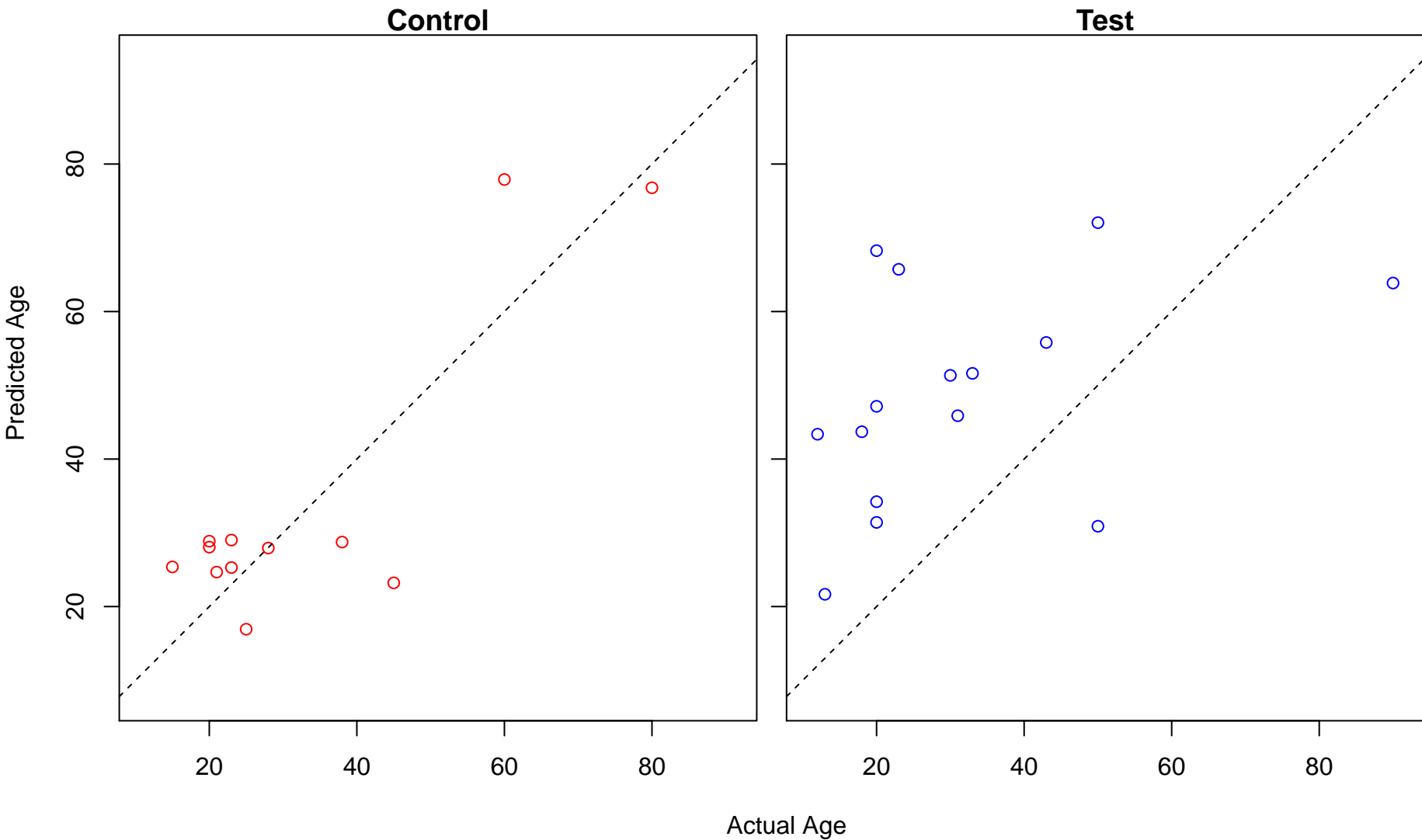
somatic recombination of immunoglobulin gene segments (Score: 2.697601)



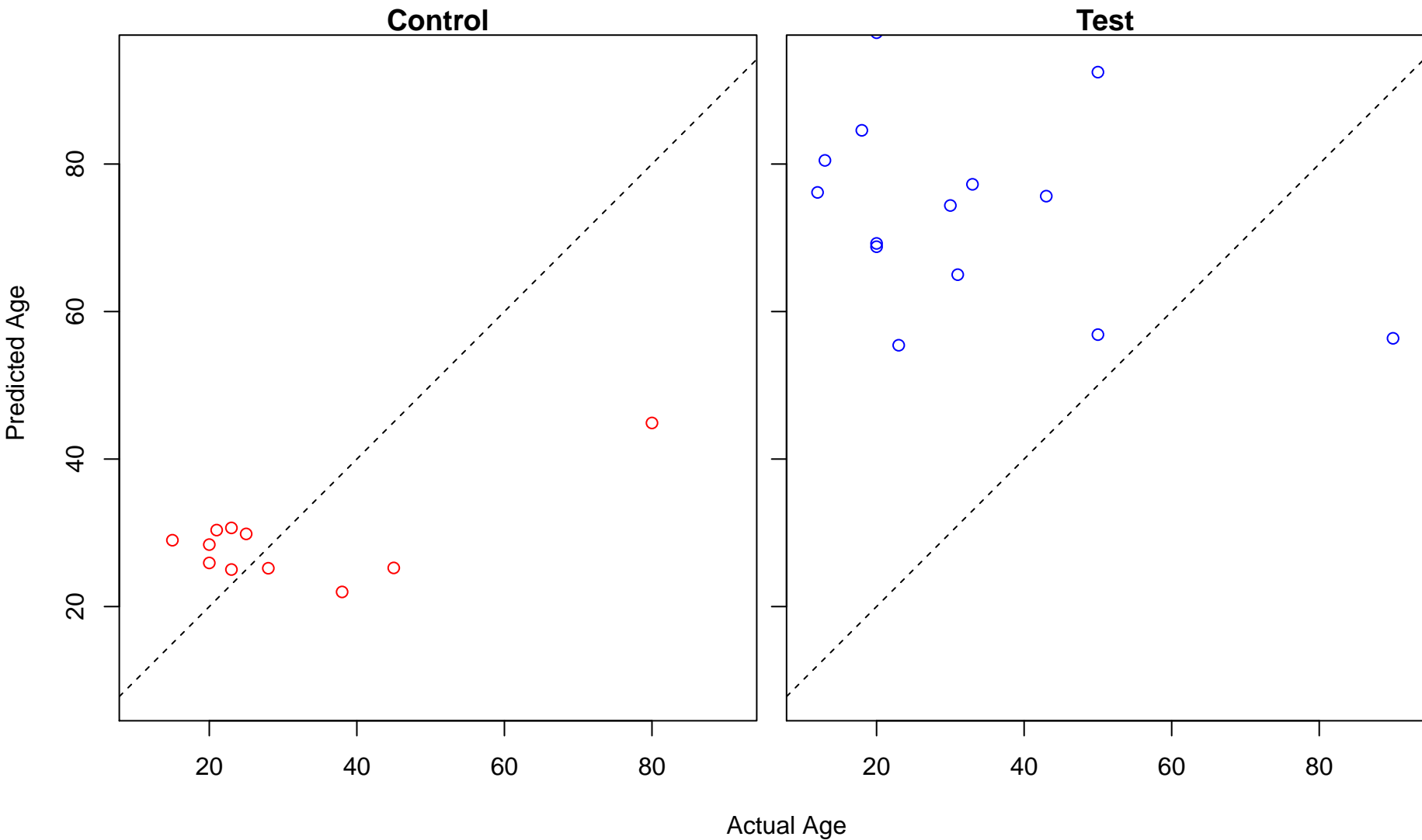
muscle cell fate commitment (Score: 2.695502)



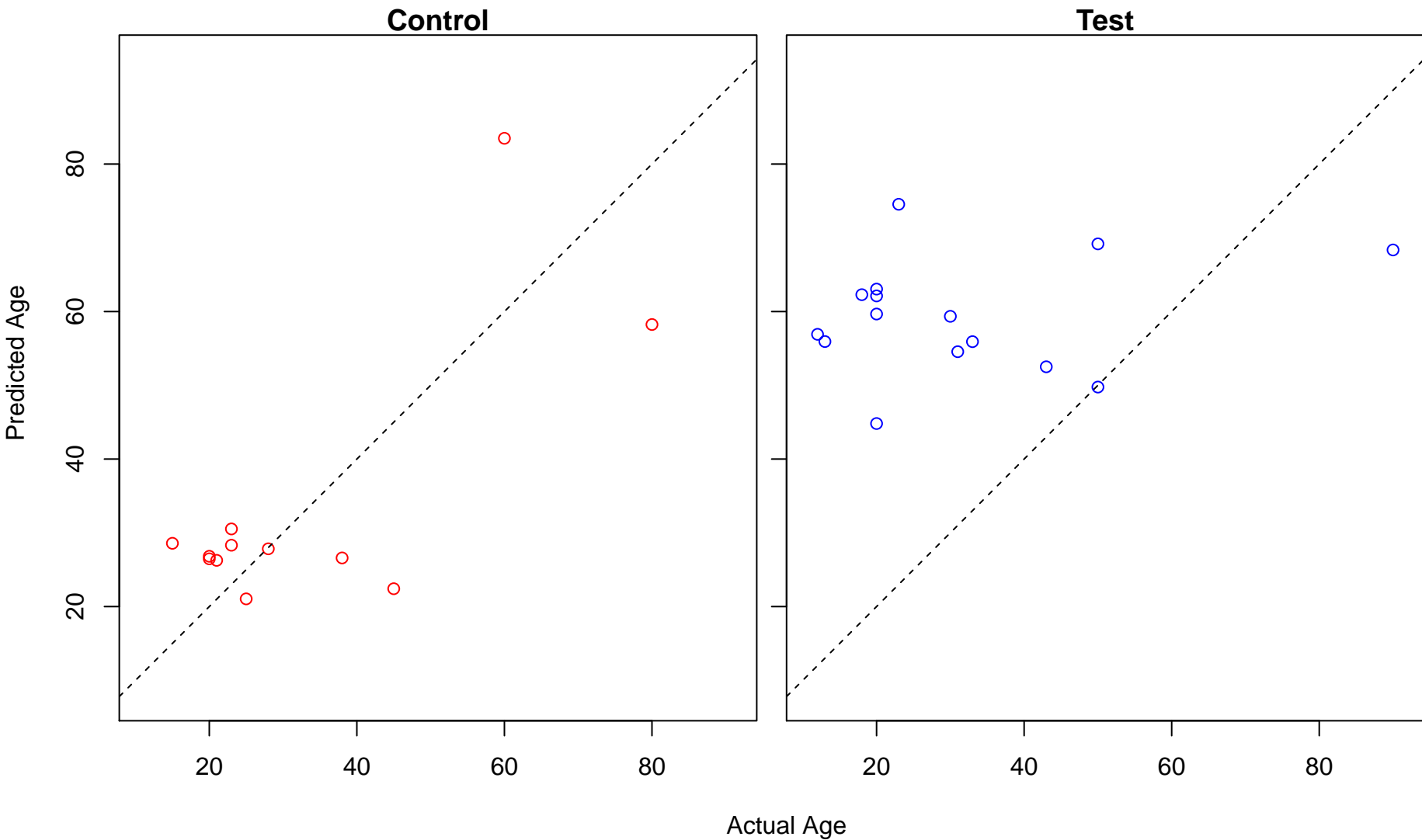
vesicle cytoskeletal trafficking (Score: 2.694484)



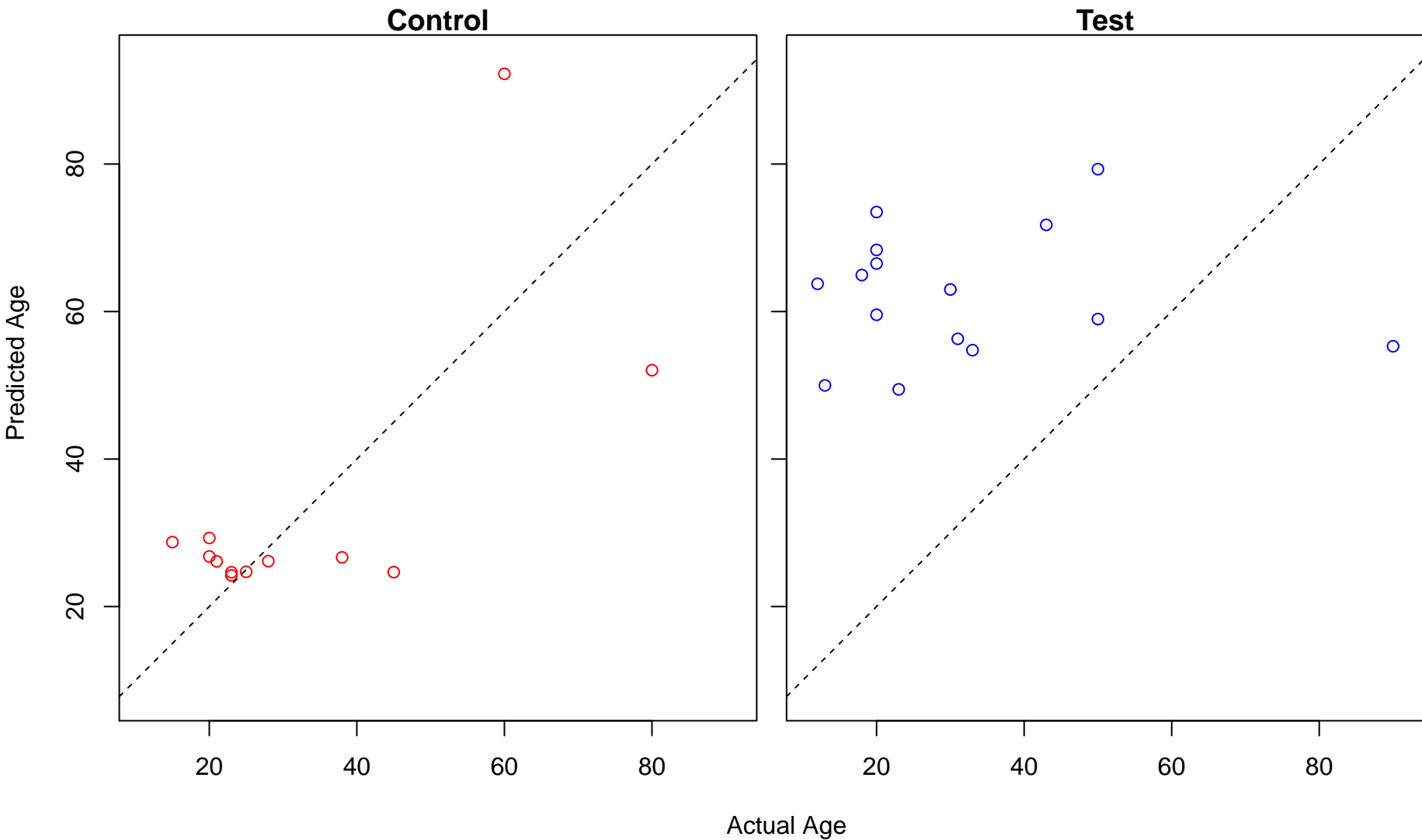
macromolecule depalmitoylation (Score: 2.693480)



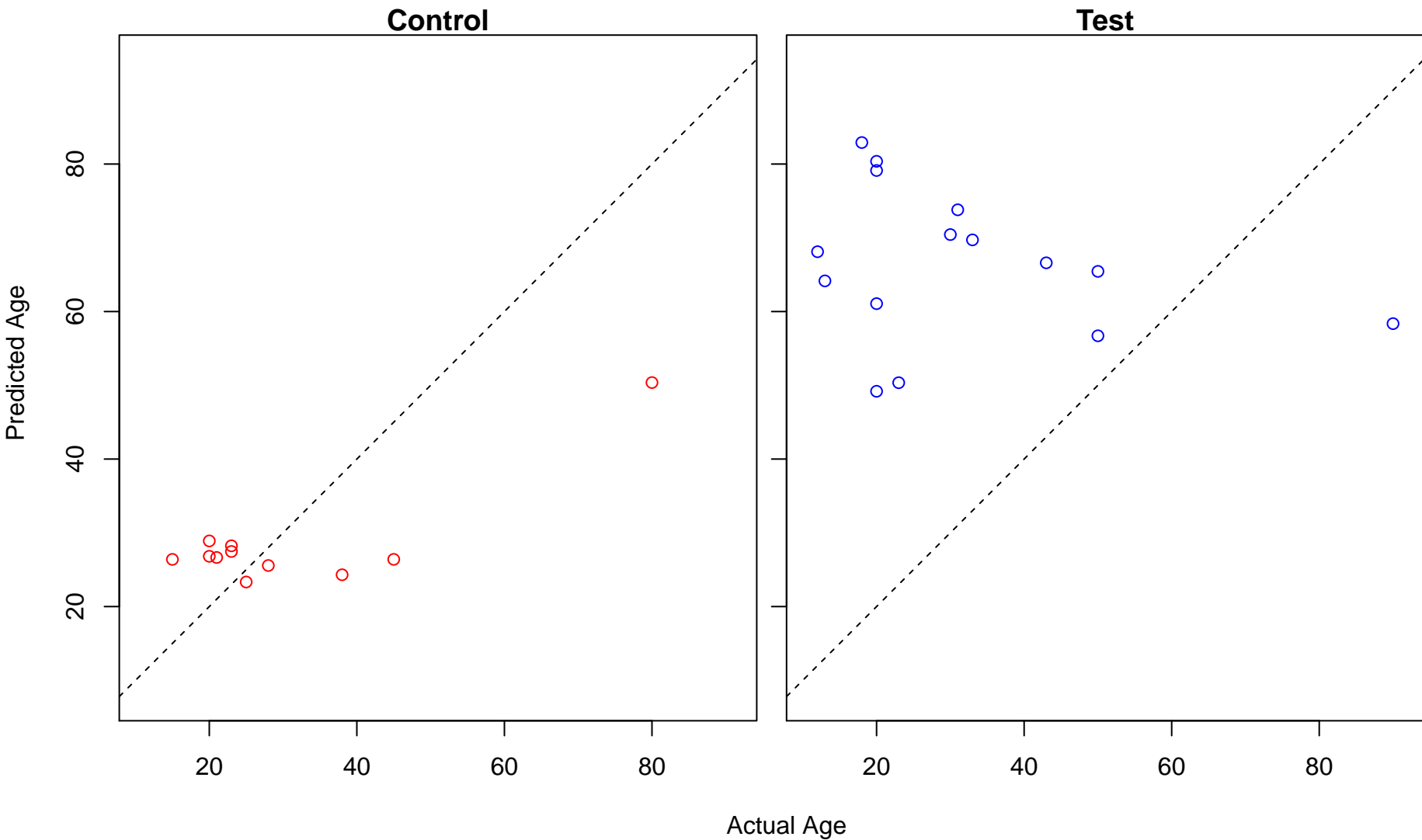
mitochondrial fusion (Score: 2.690108)



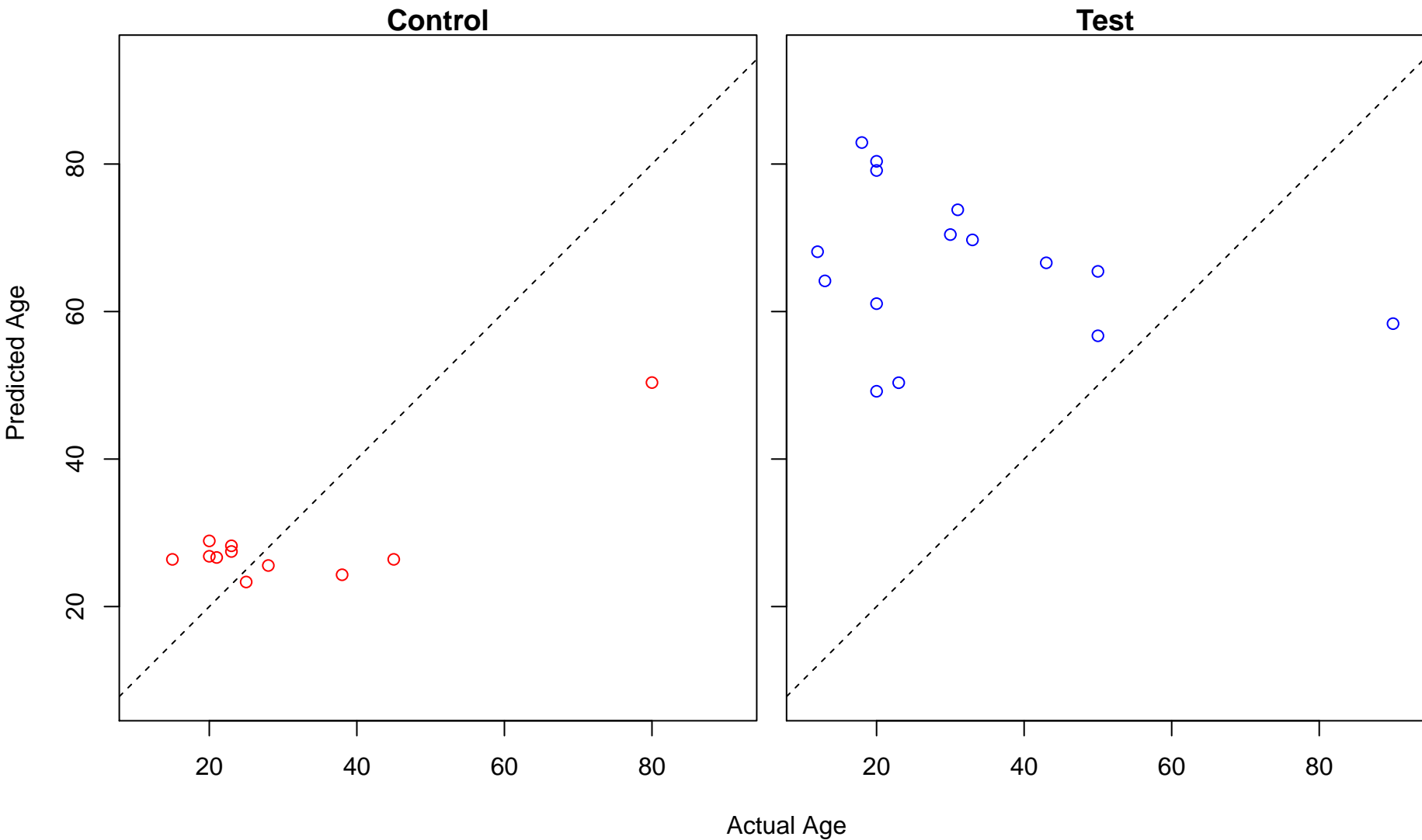
cofactor catabolic process (Score: 2.684995)



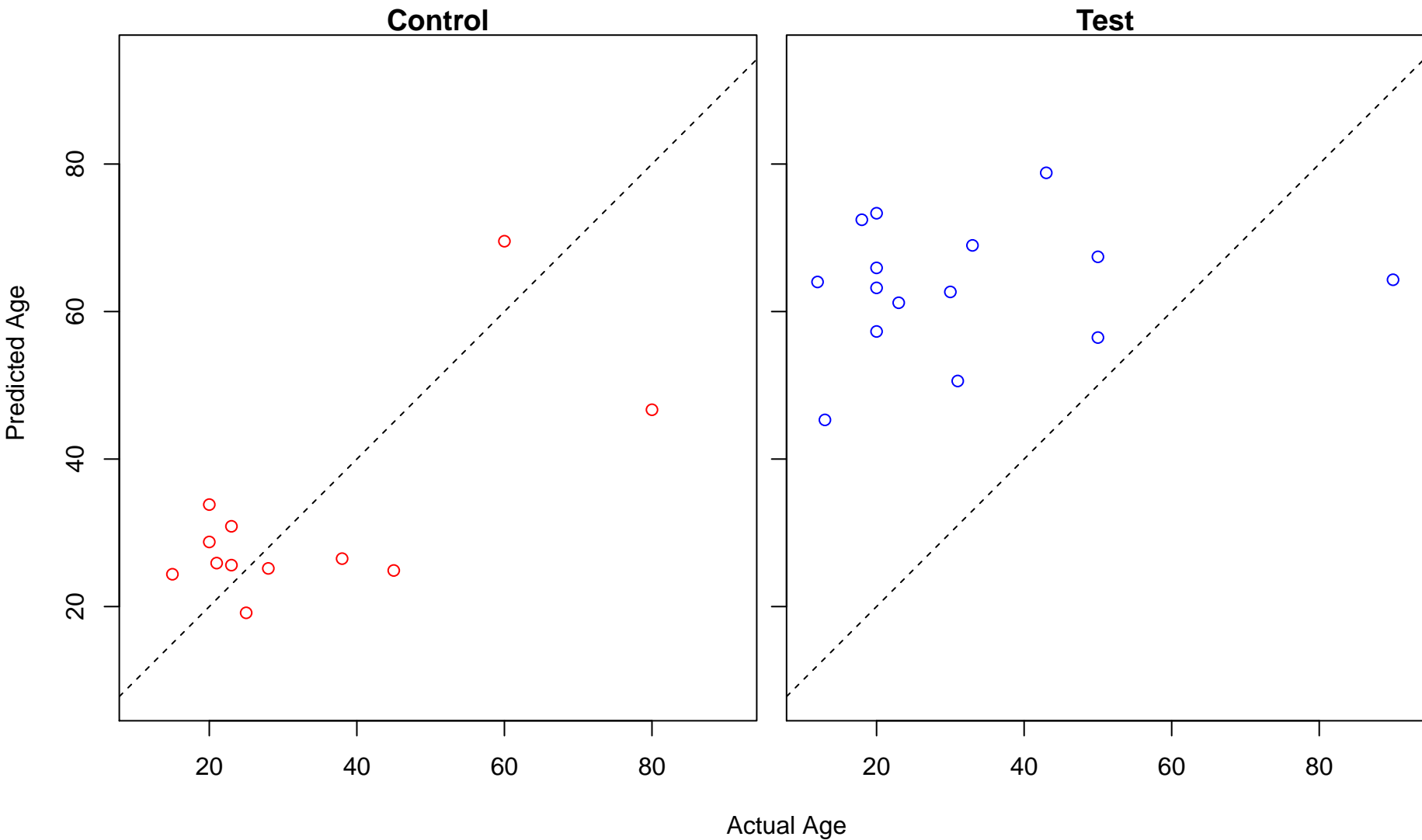
mast cell activation involved in immune response (Score: 2.684654)



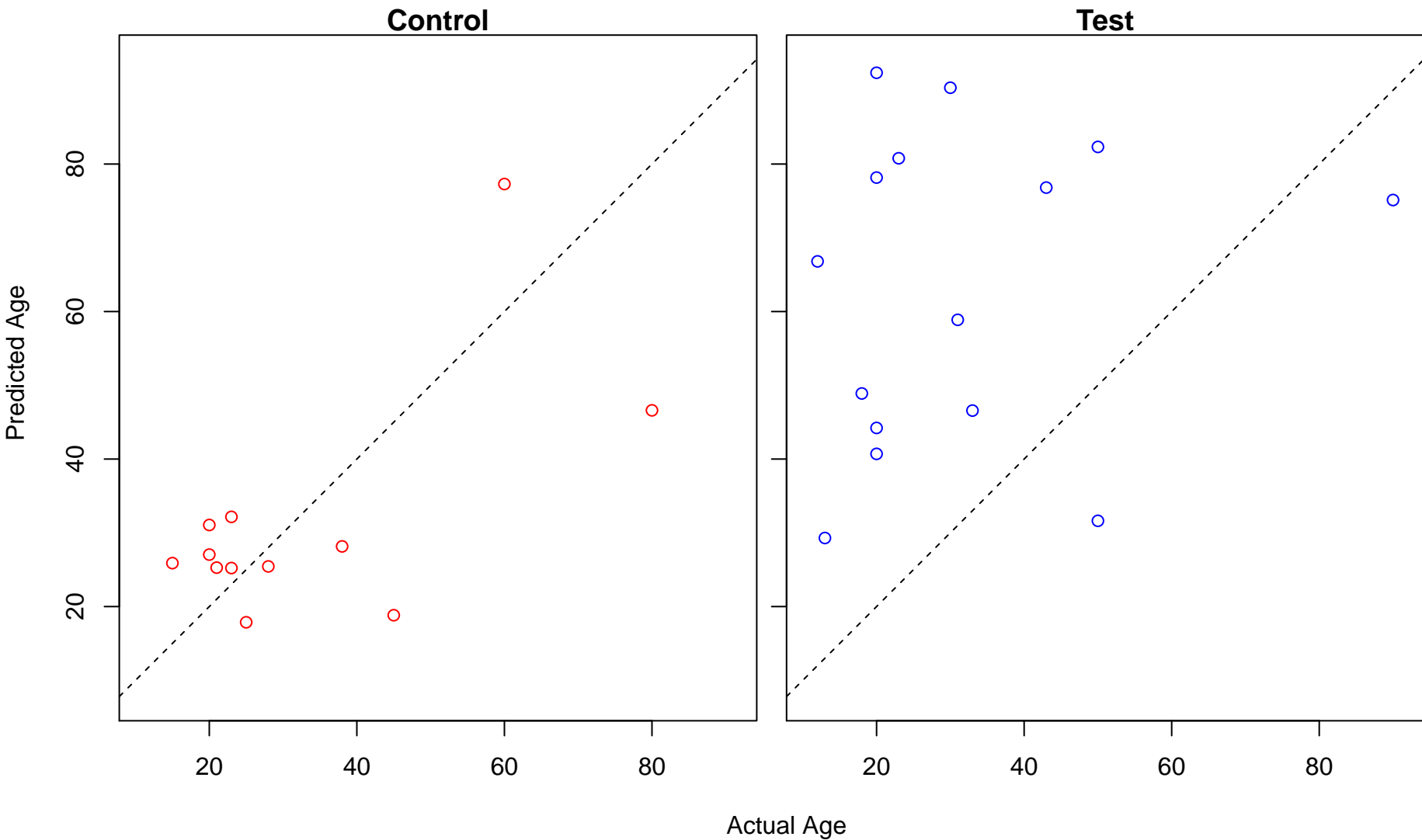
mast cell degranulation (Score: 2.684654)



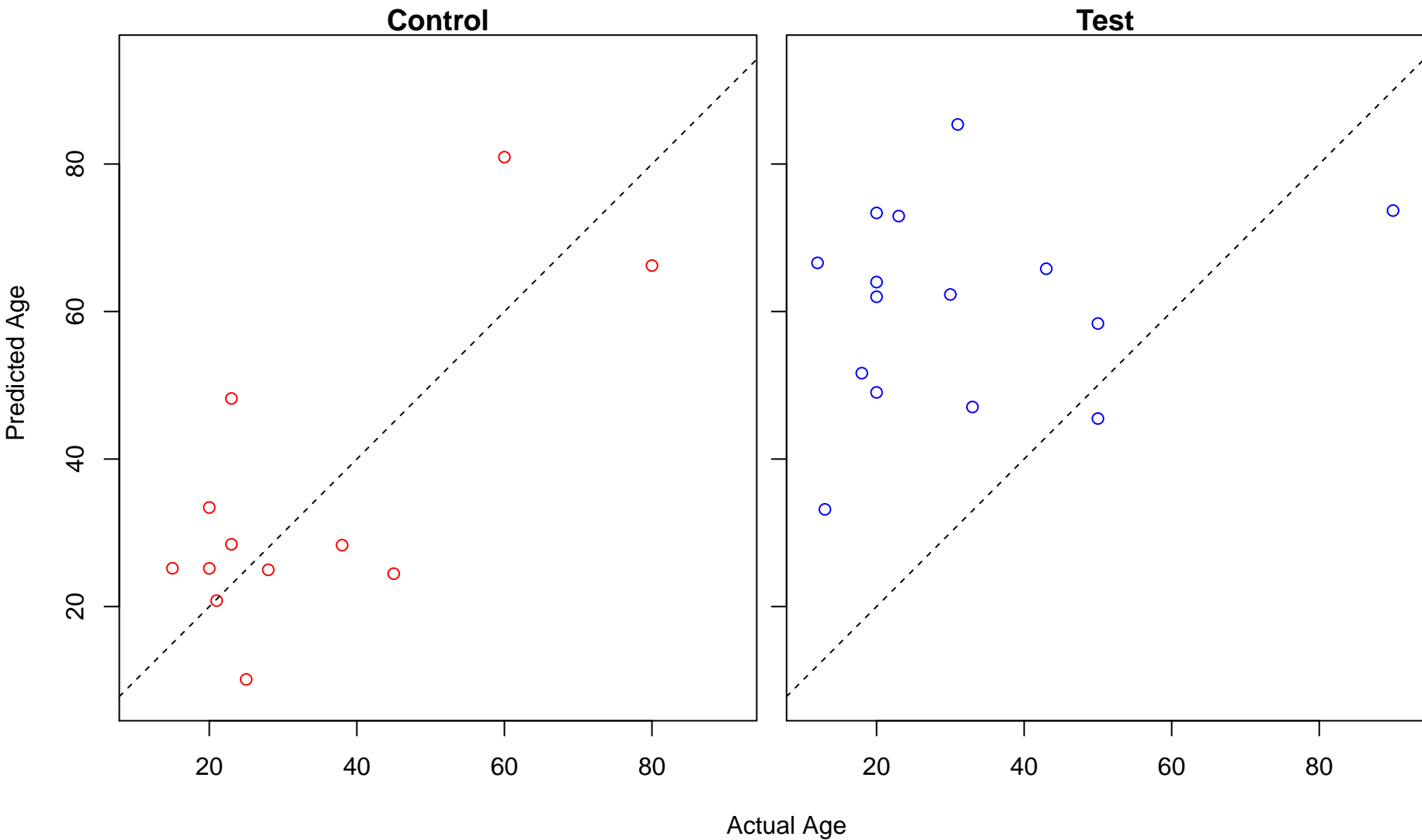
negative regulation of lipid transport (Score: 2.683254)



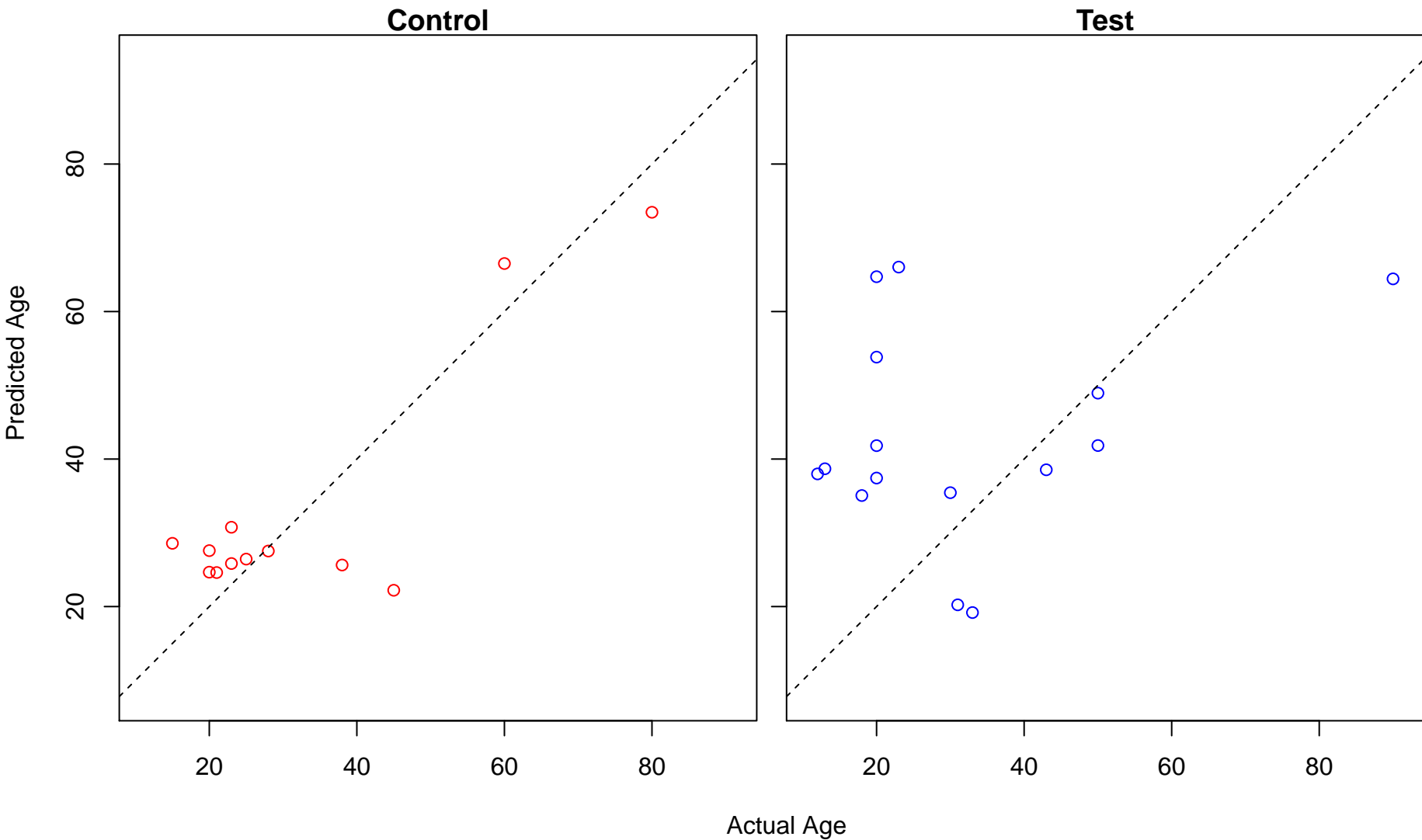
positive regulation of amine transport (Score: 2.671834)



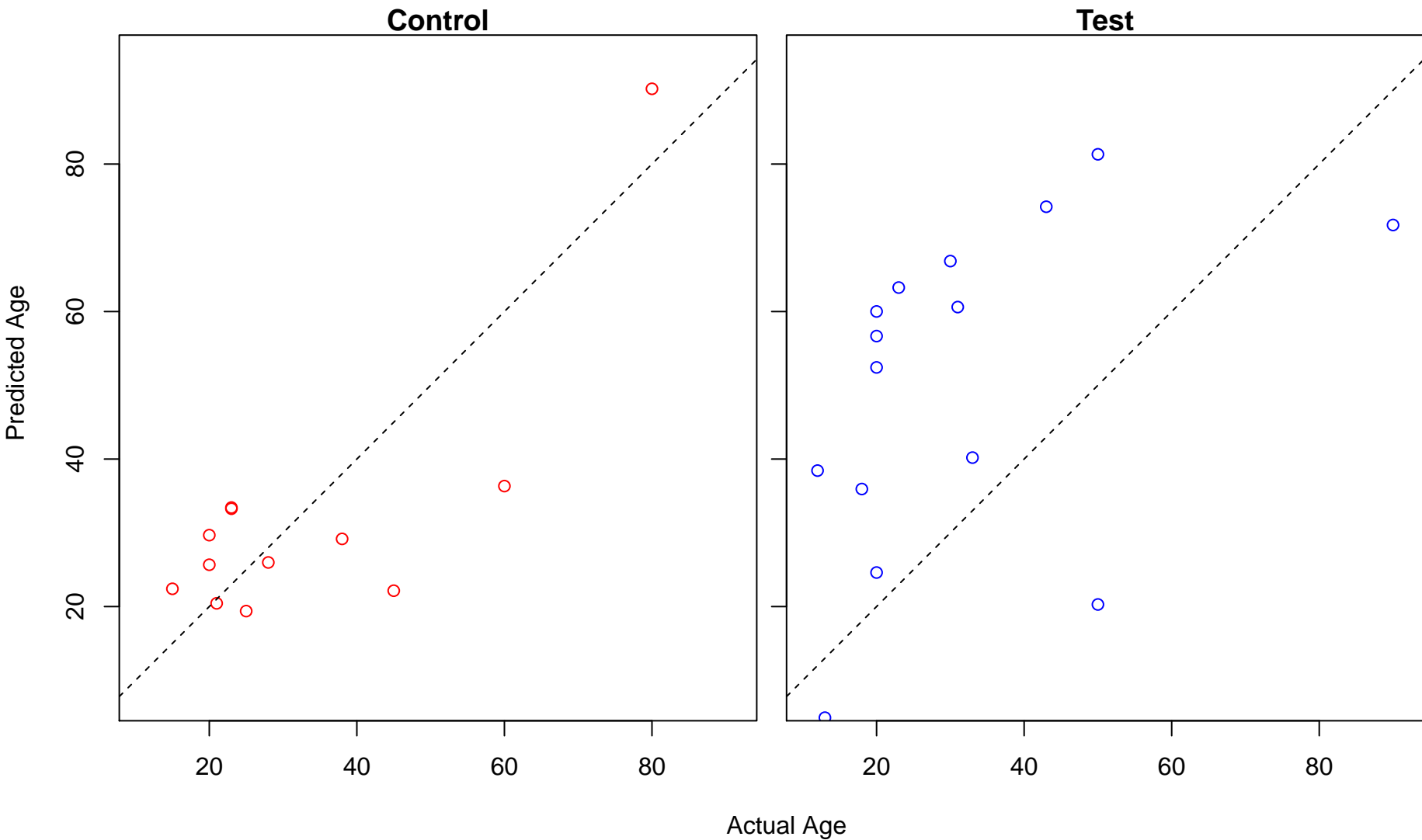
production of molecular mediator of immune response (Score: 2.656776)



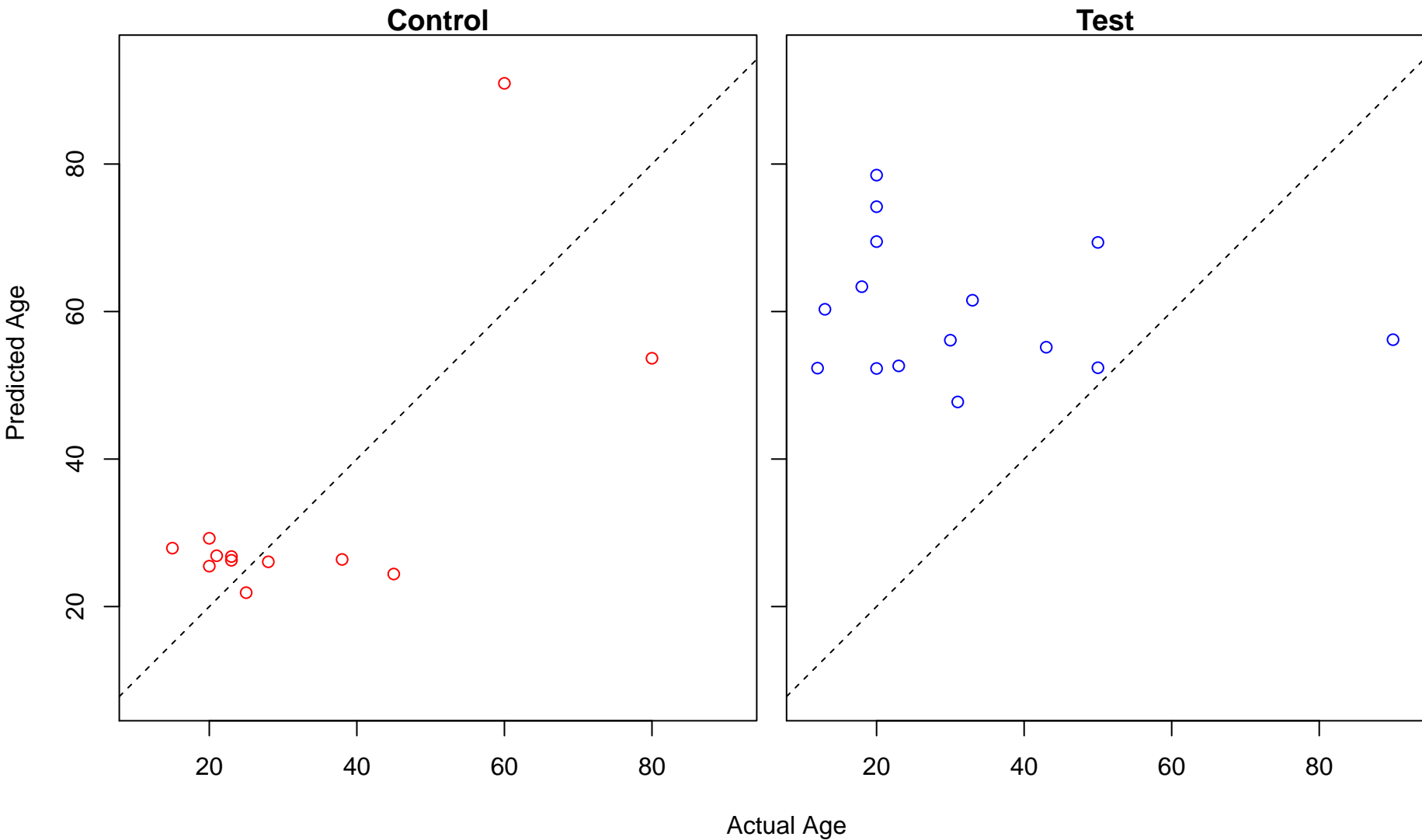
RNA methylation (Score: 2.652404)



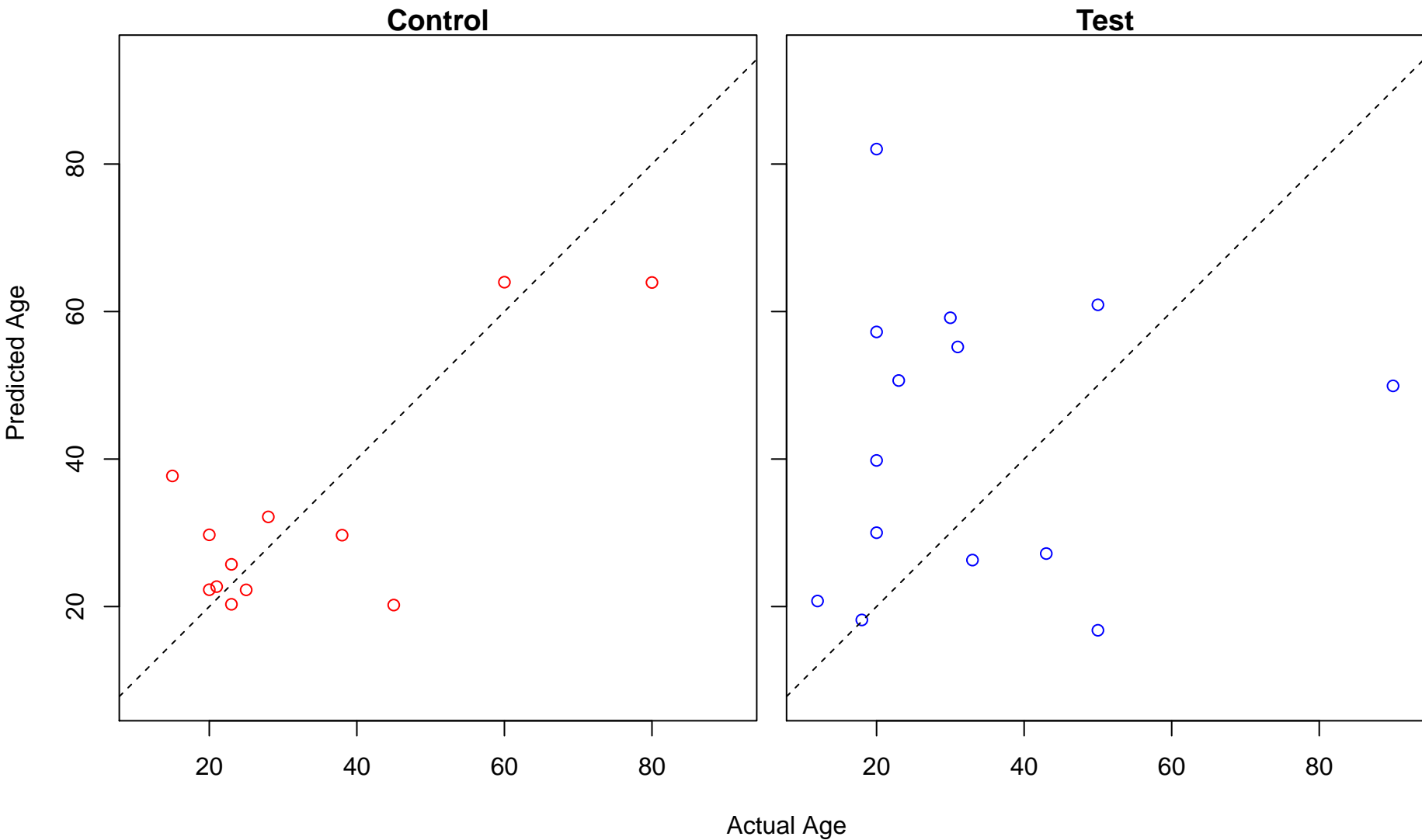
response to osmotic stress (Score: 2.643697)



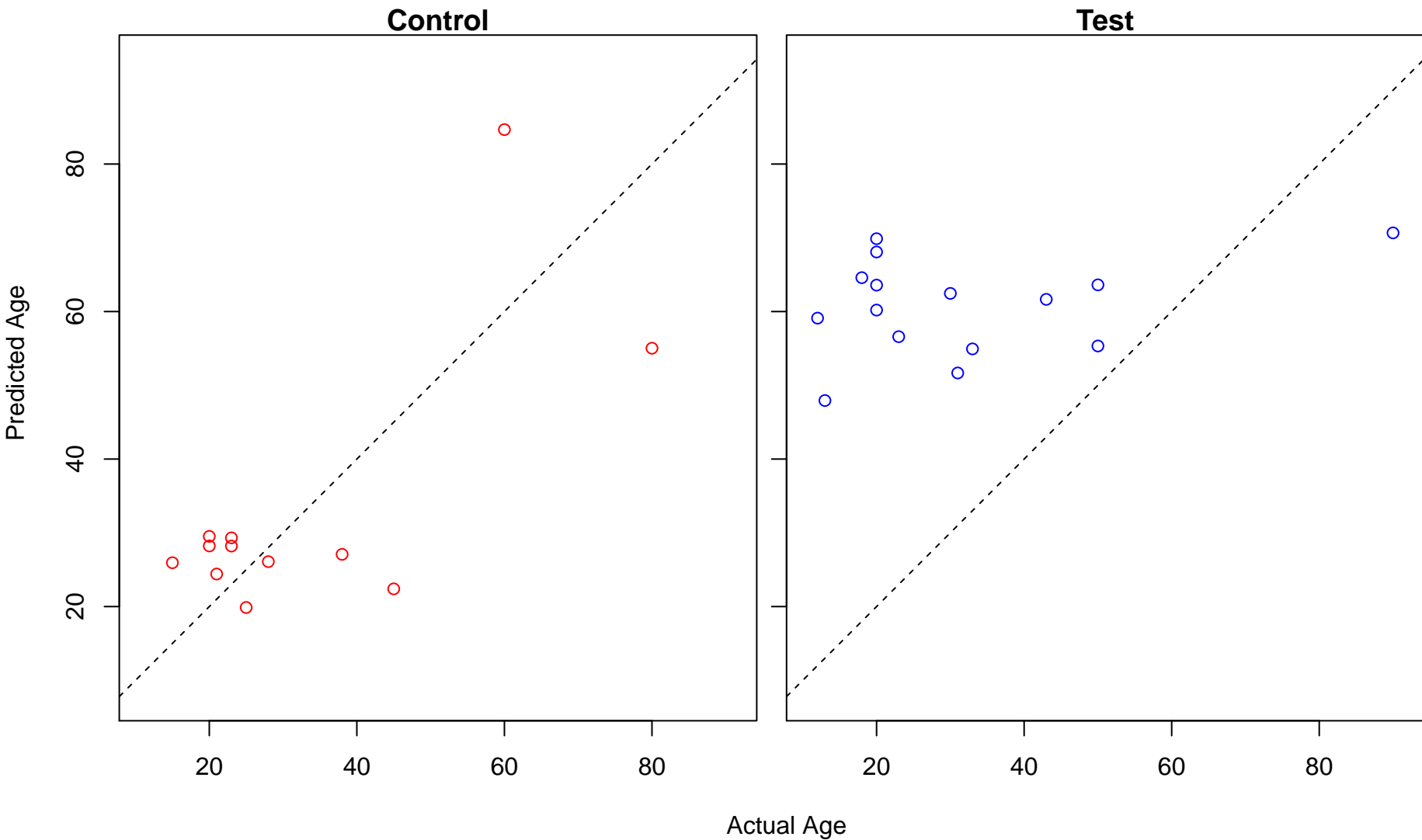
regulation of bile acid metabolic process (Score: 2.641503)



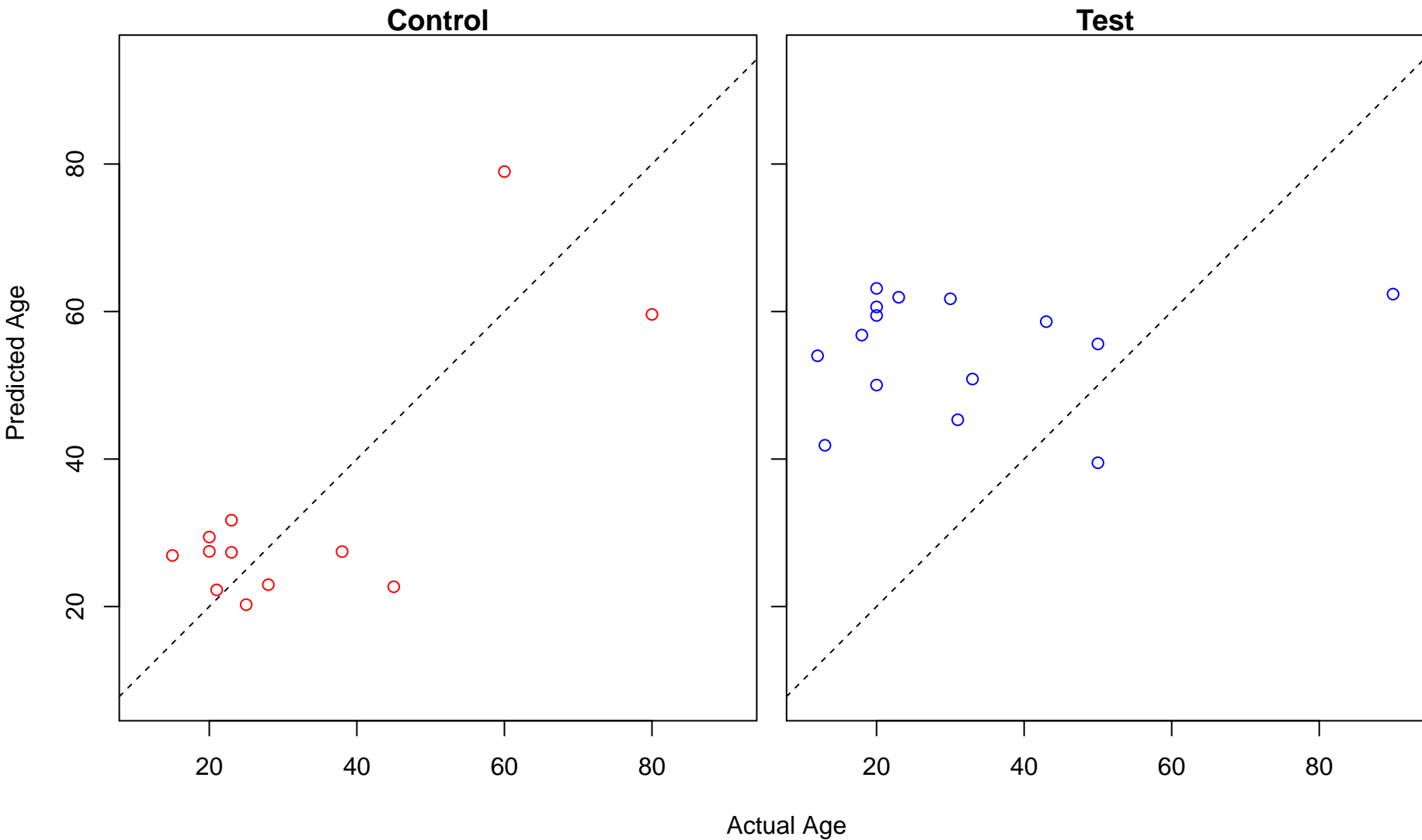
negative regulation of hippo signaling (Score: 2.638995)



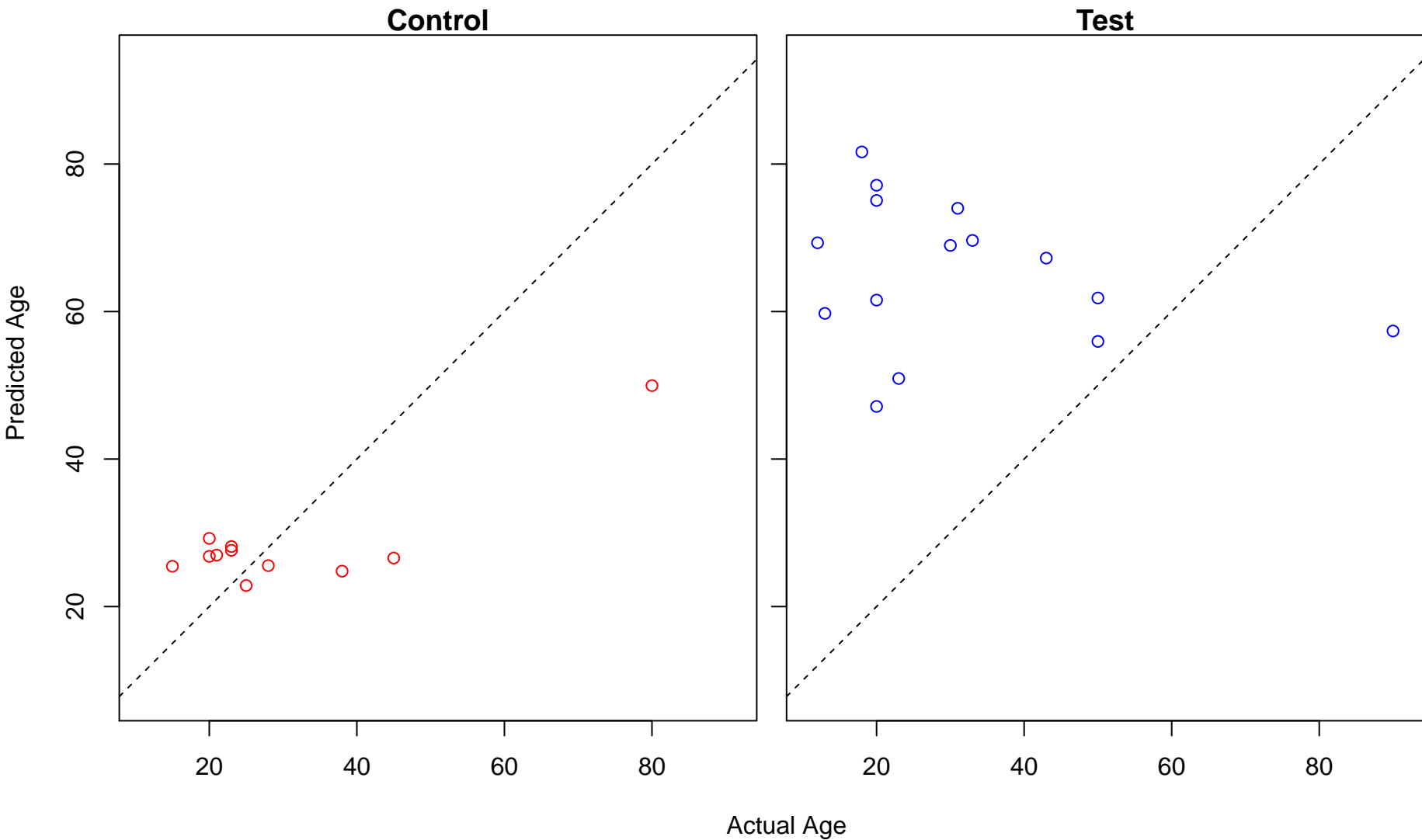
regulation of long-term neuronal synaptic plasticity (Score: 2.627978)



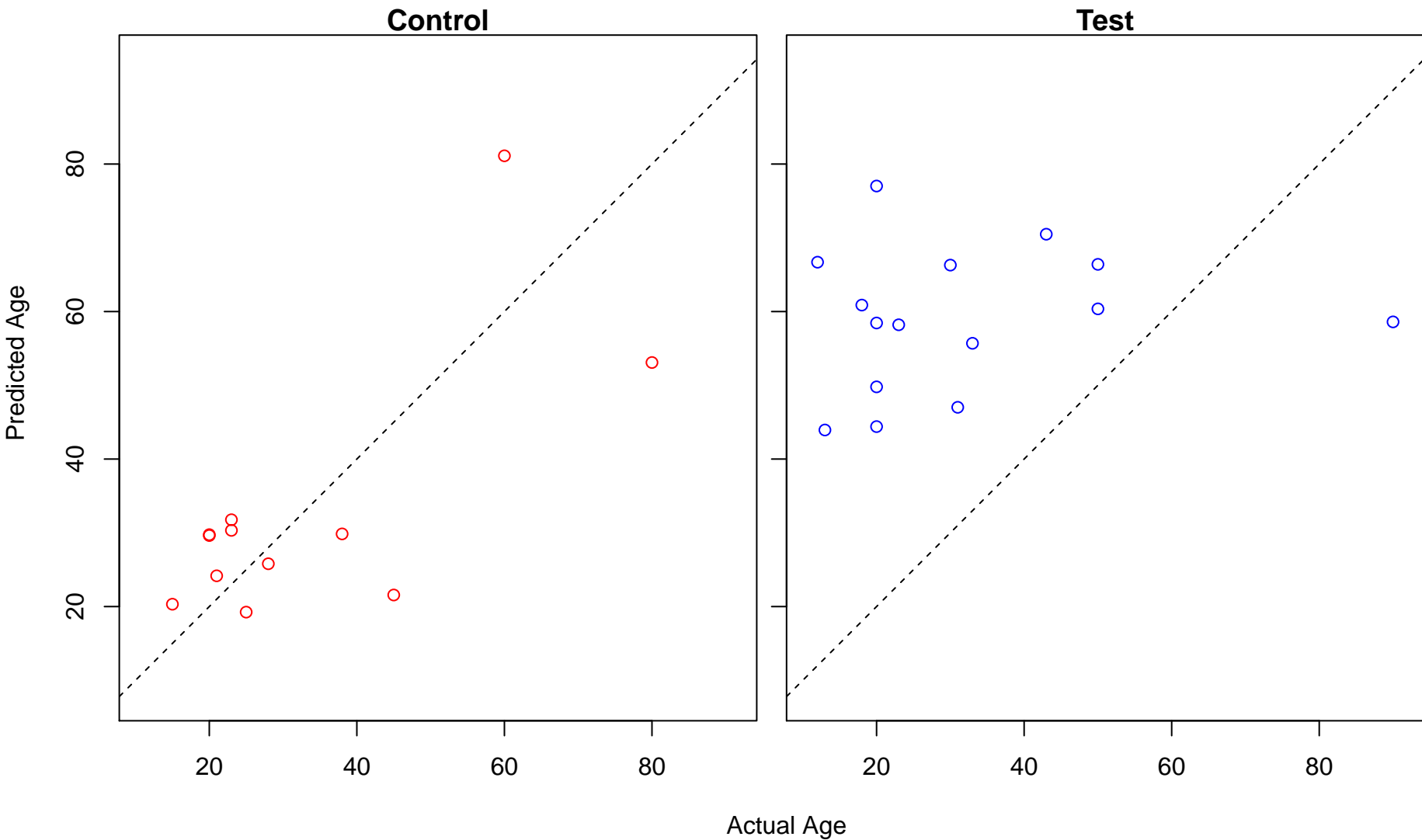
regulation of dendrite morphogenesis (Score: 2.627200)



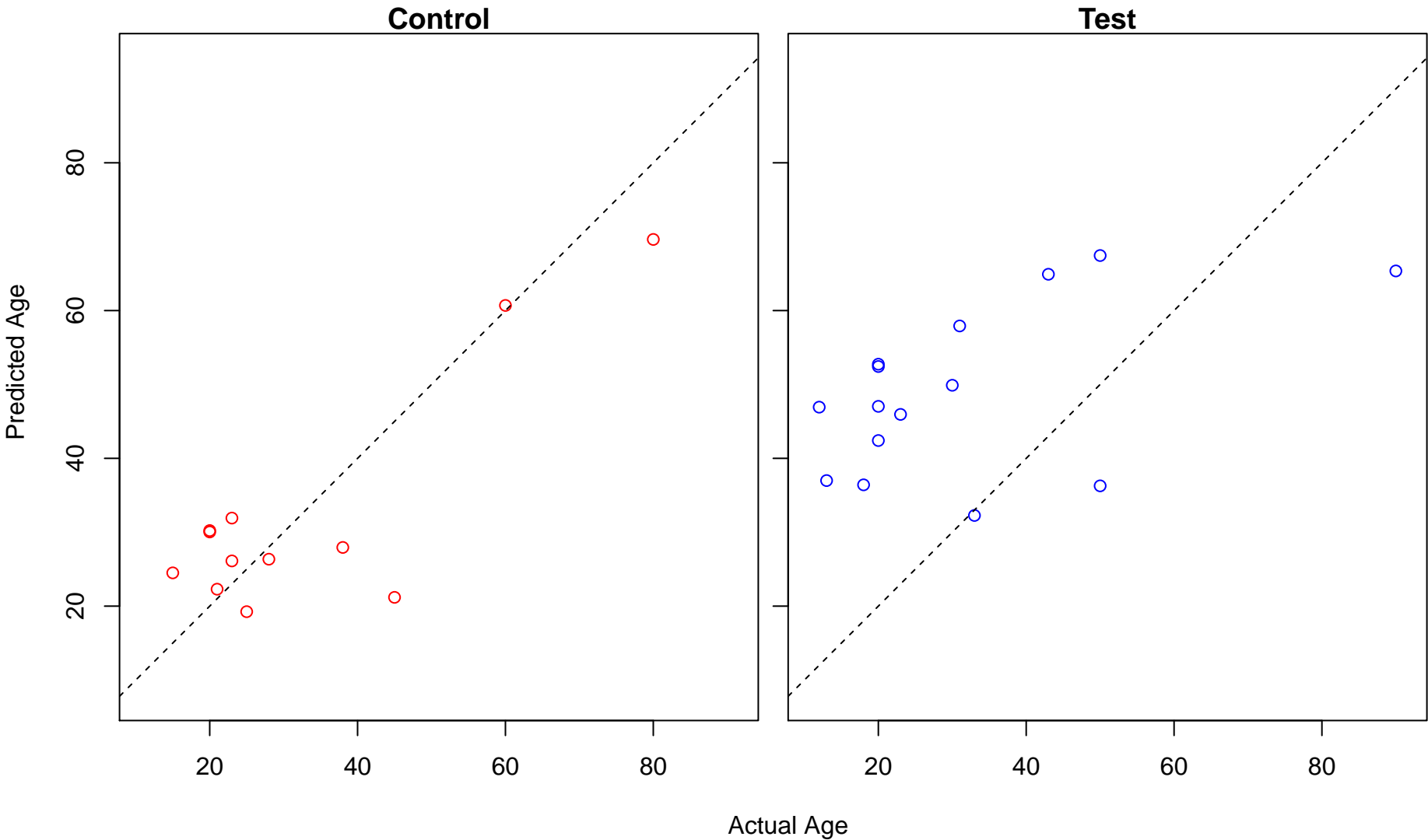
myeloid cell activation involved in immune response (Score: 2.621174)



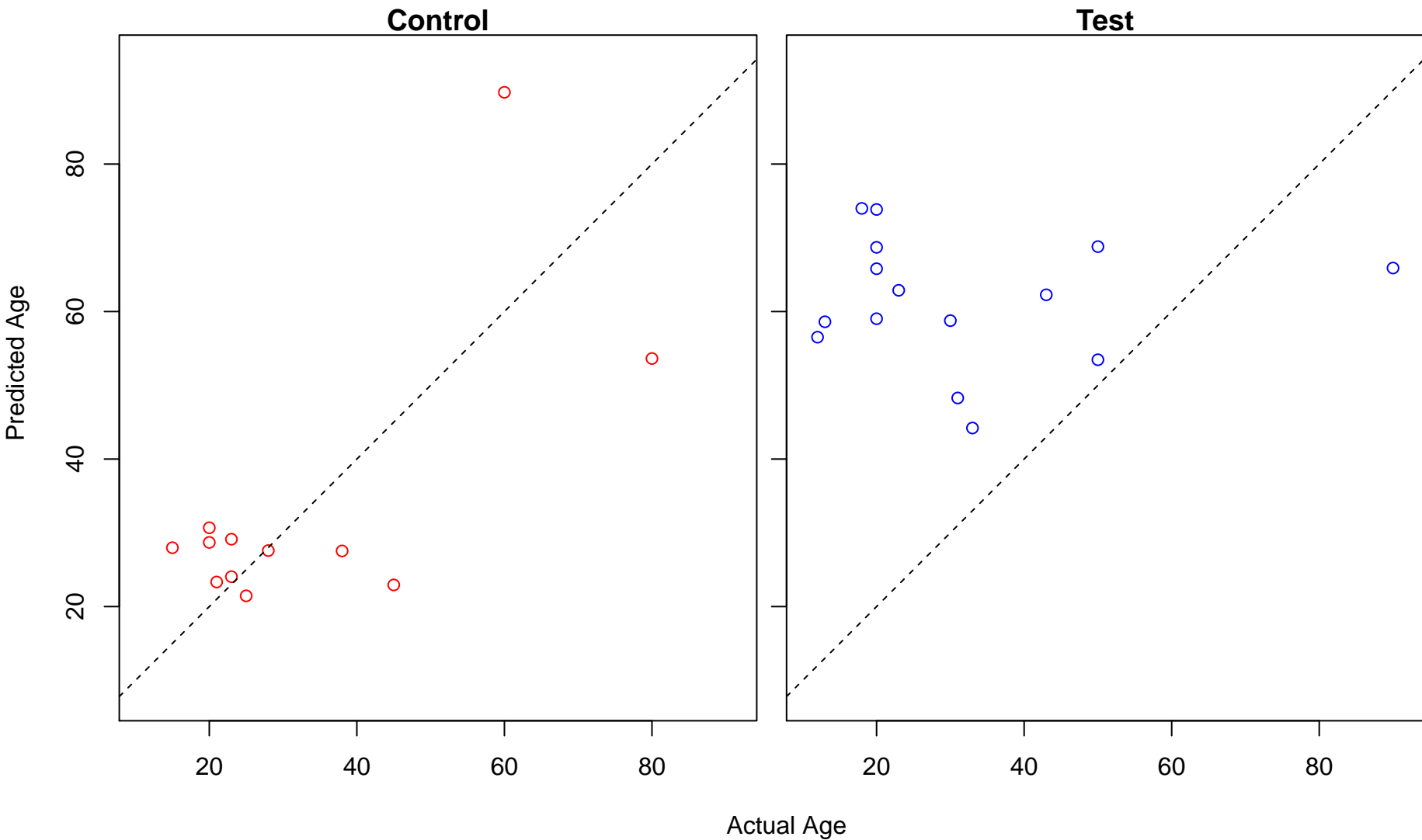
lymphangiogenesis (Score: 2.616760)



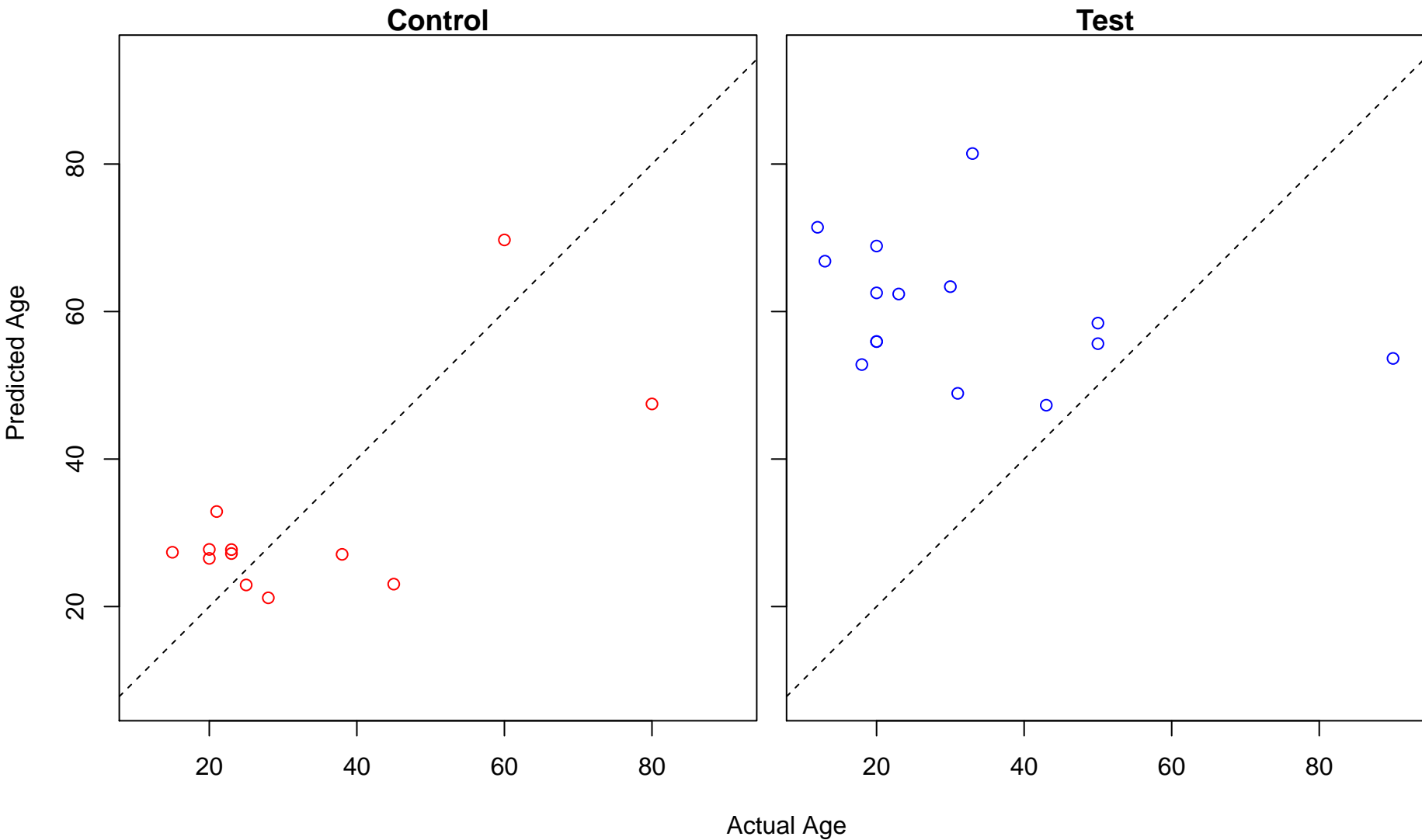
protein kinase C-activating G-protein coupled receptor signaling pathway (Score: 2.614786)



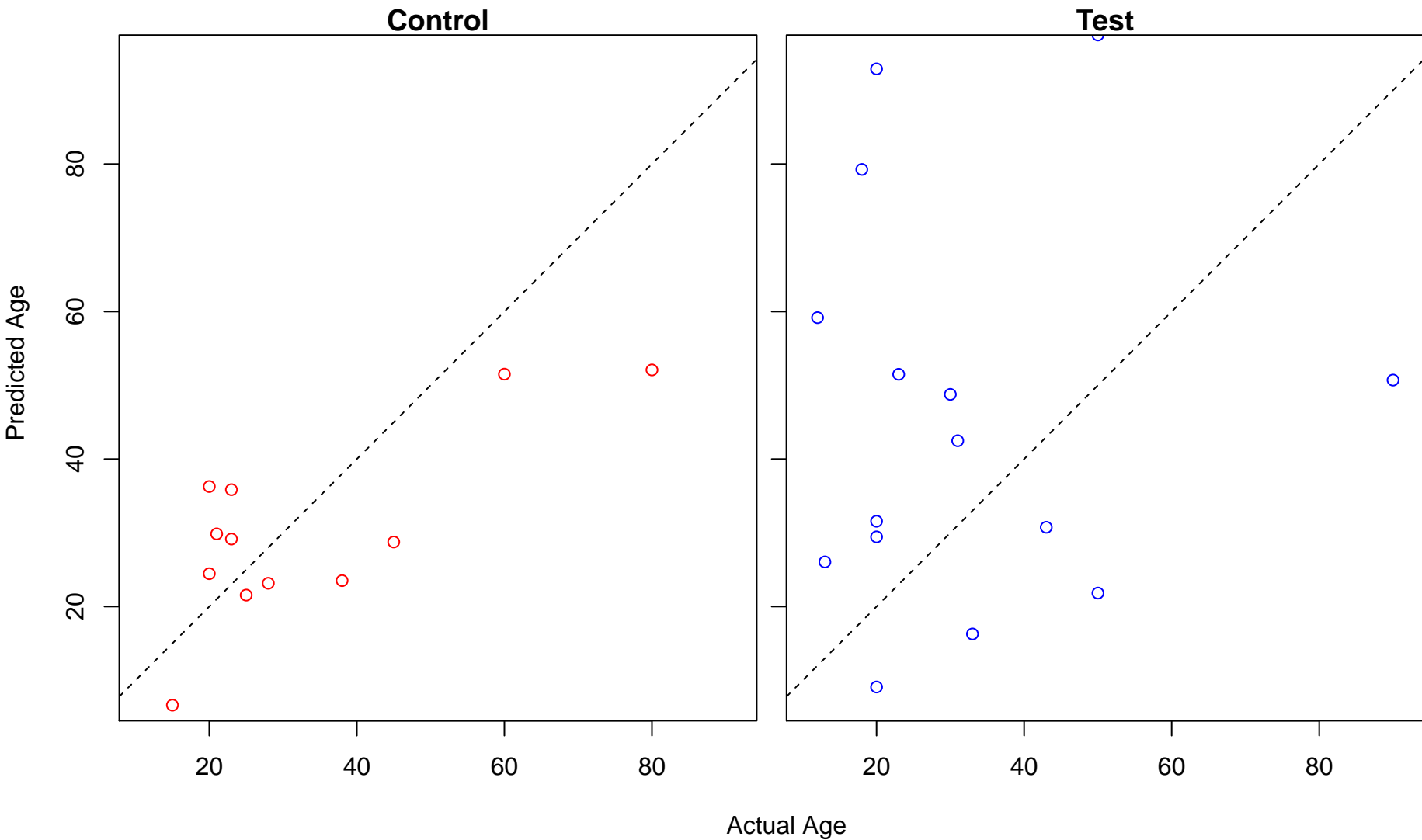
endoderm development (Score: 2.614005)



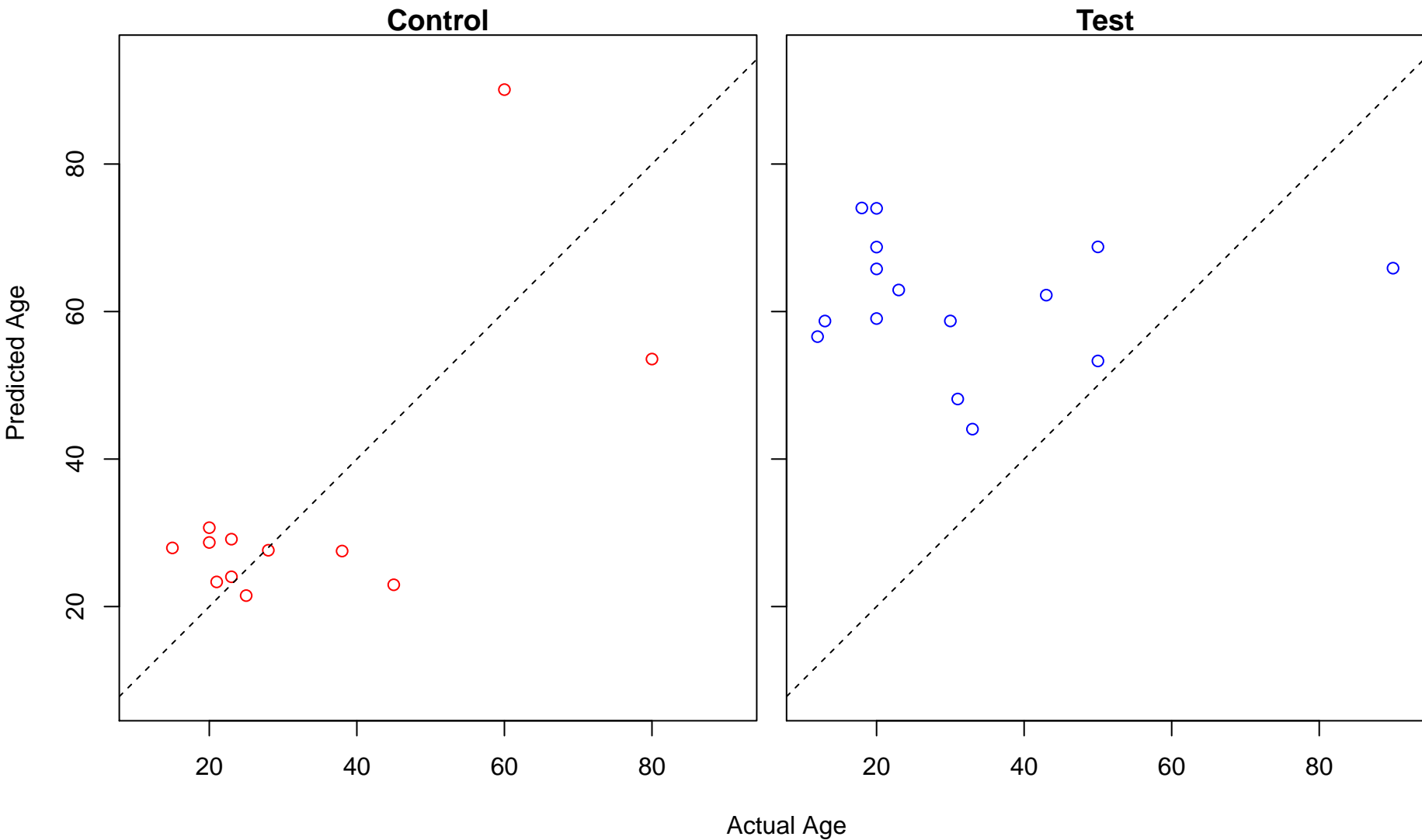
cGMP metabolic process (Score: 2.611059)



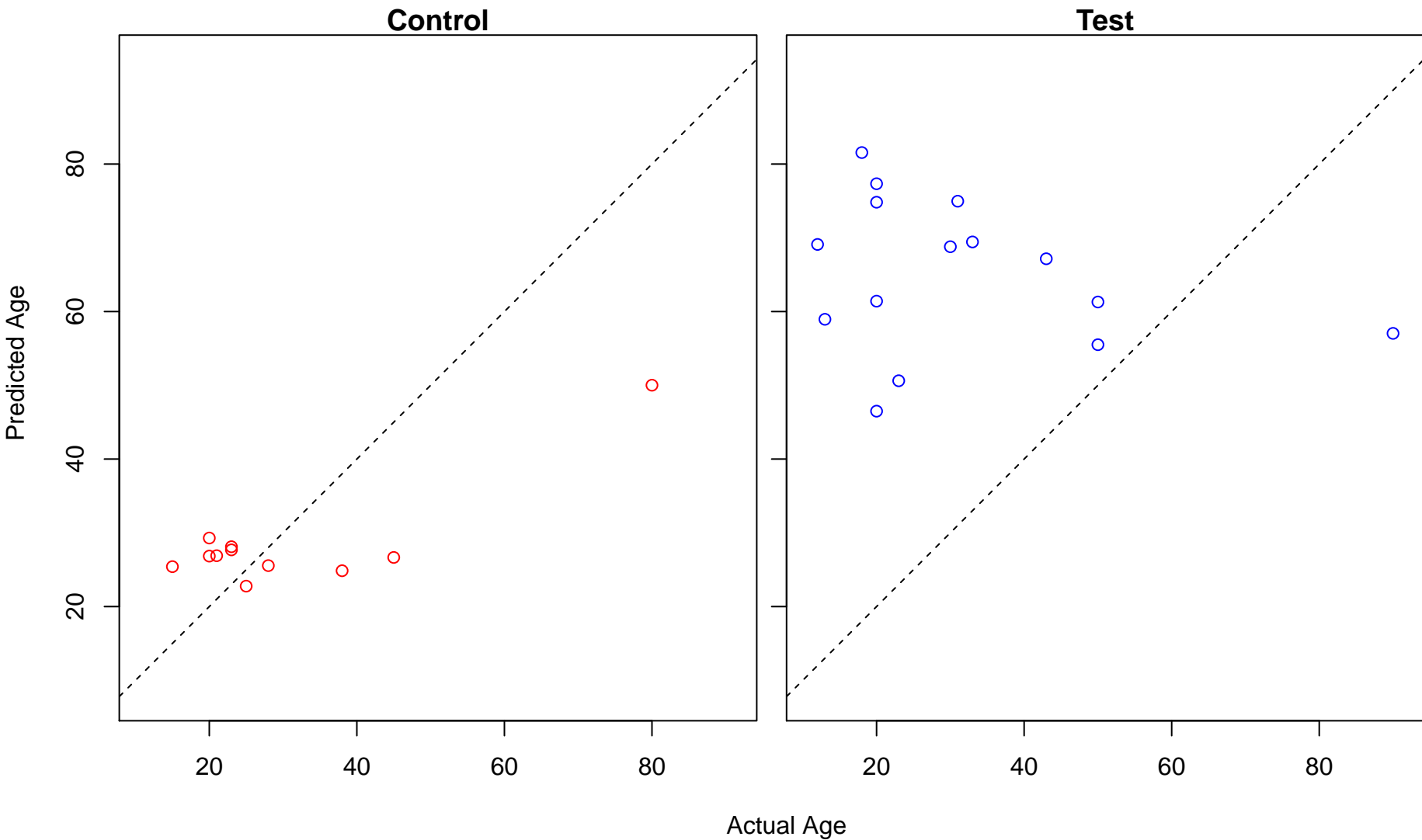
cholesterol efflux (Score: 2.602590)



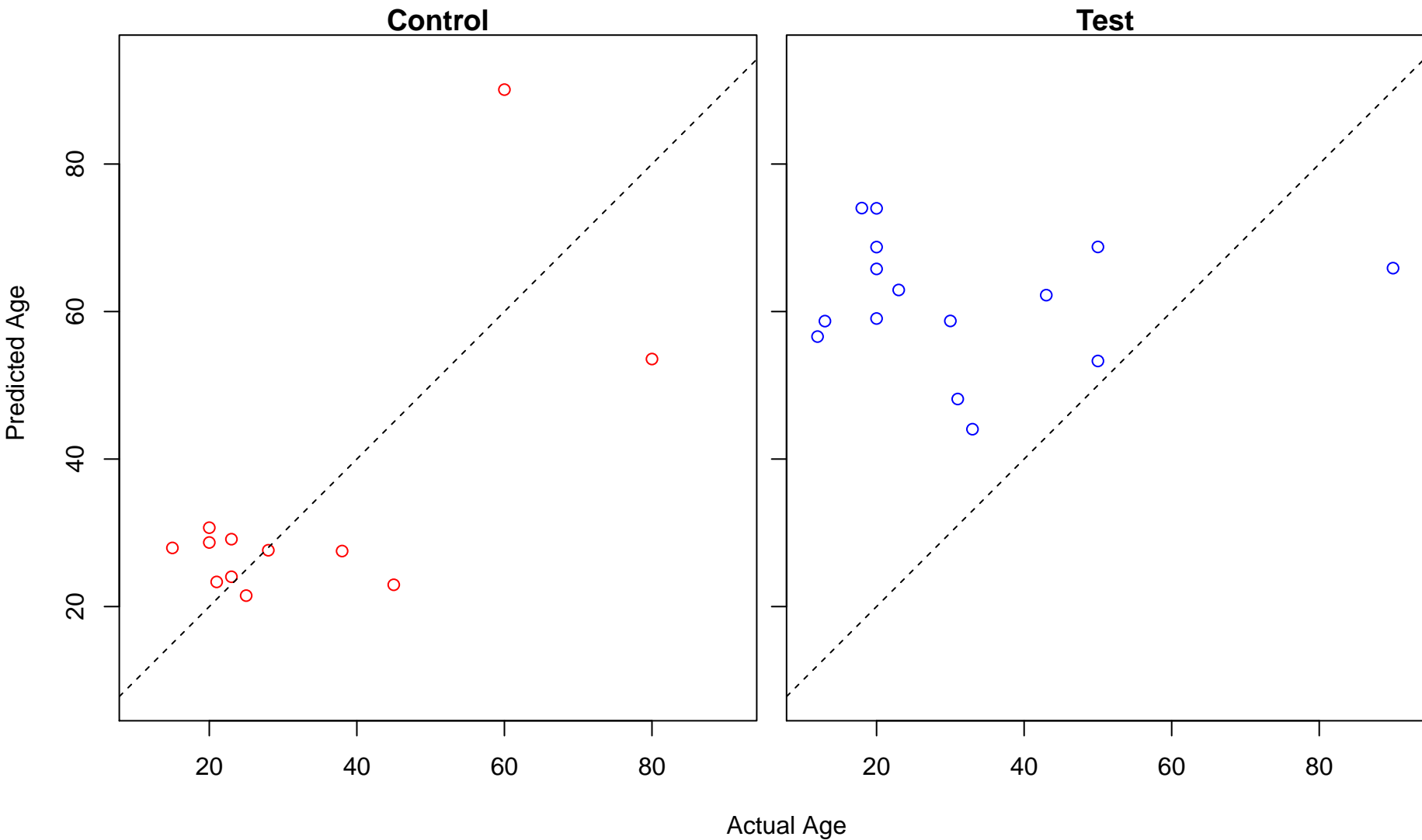
endoderm formation (Score: 2.600671)



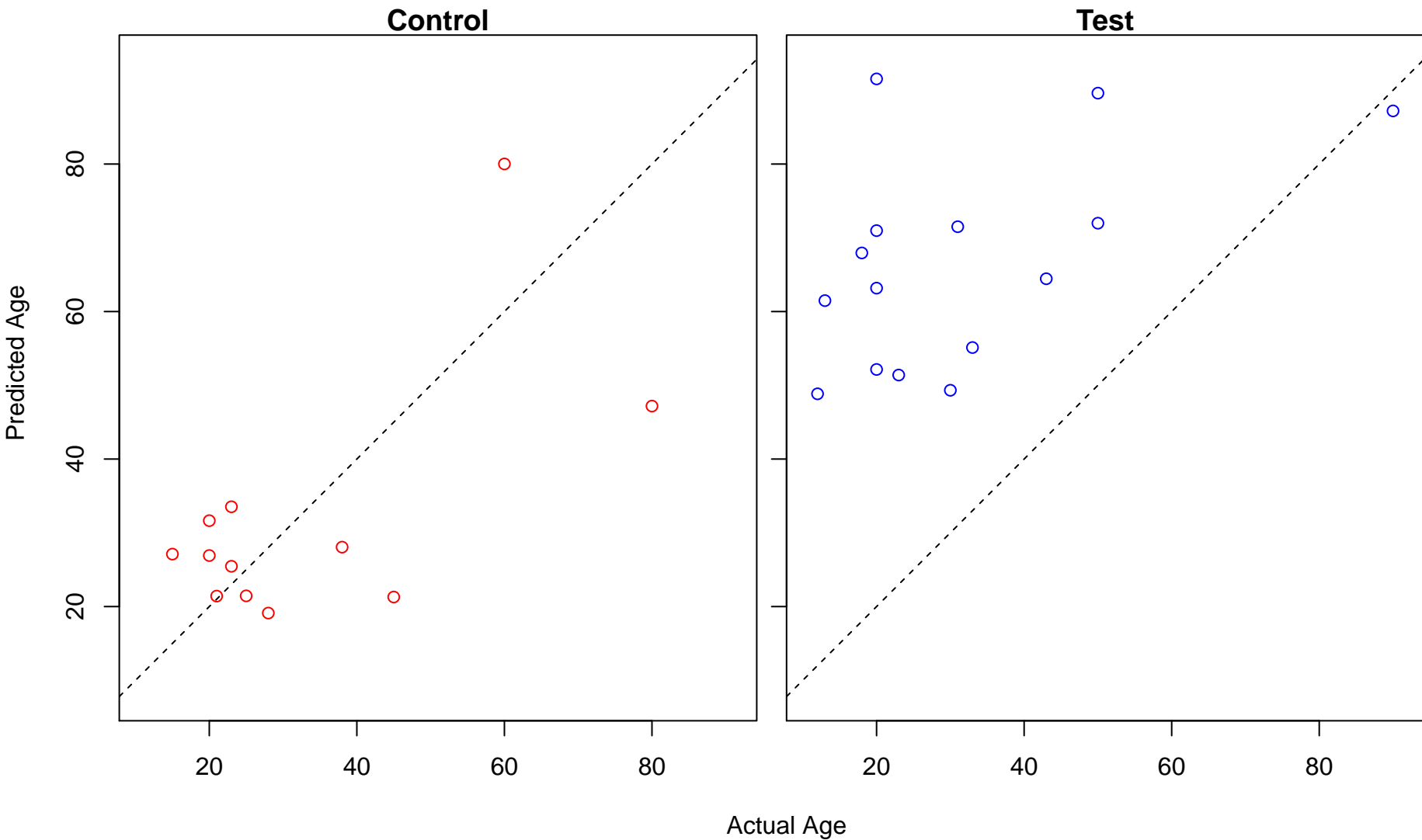
leukocyte degranulation (Score: 2.600587)



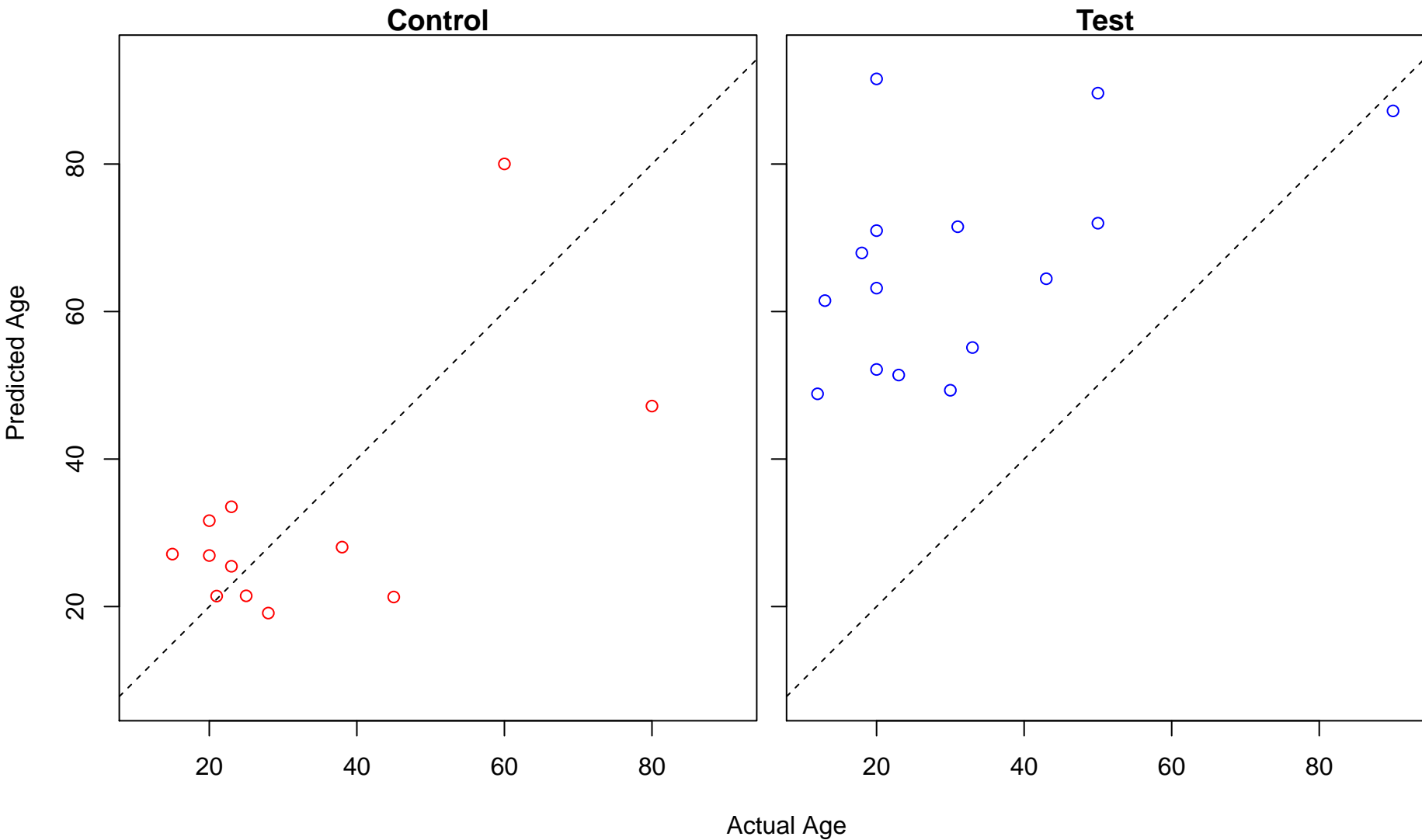
endodermal cell differentiation (Score: 2.600540)



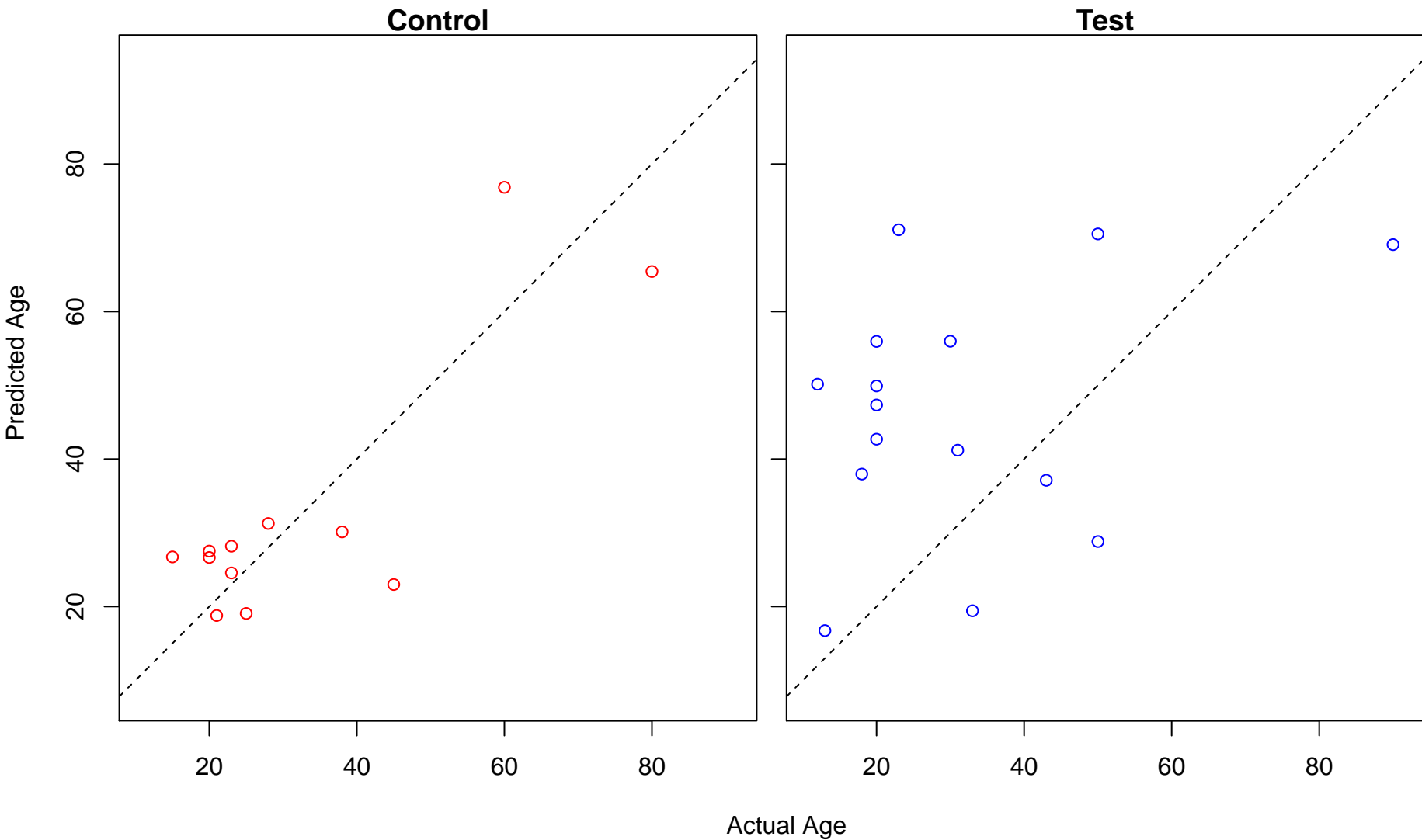
cell-substrate adherens junction assembly (Score: 2.600360)



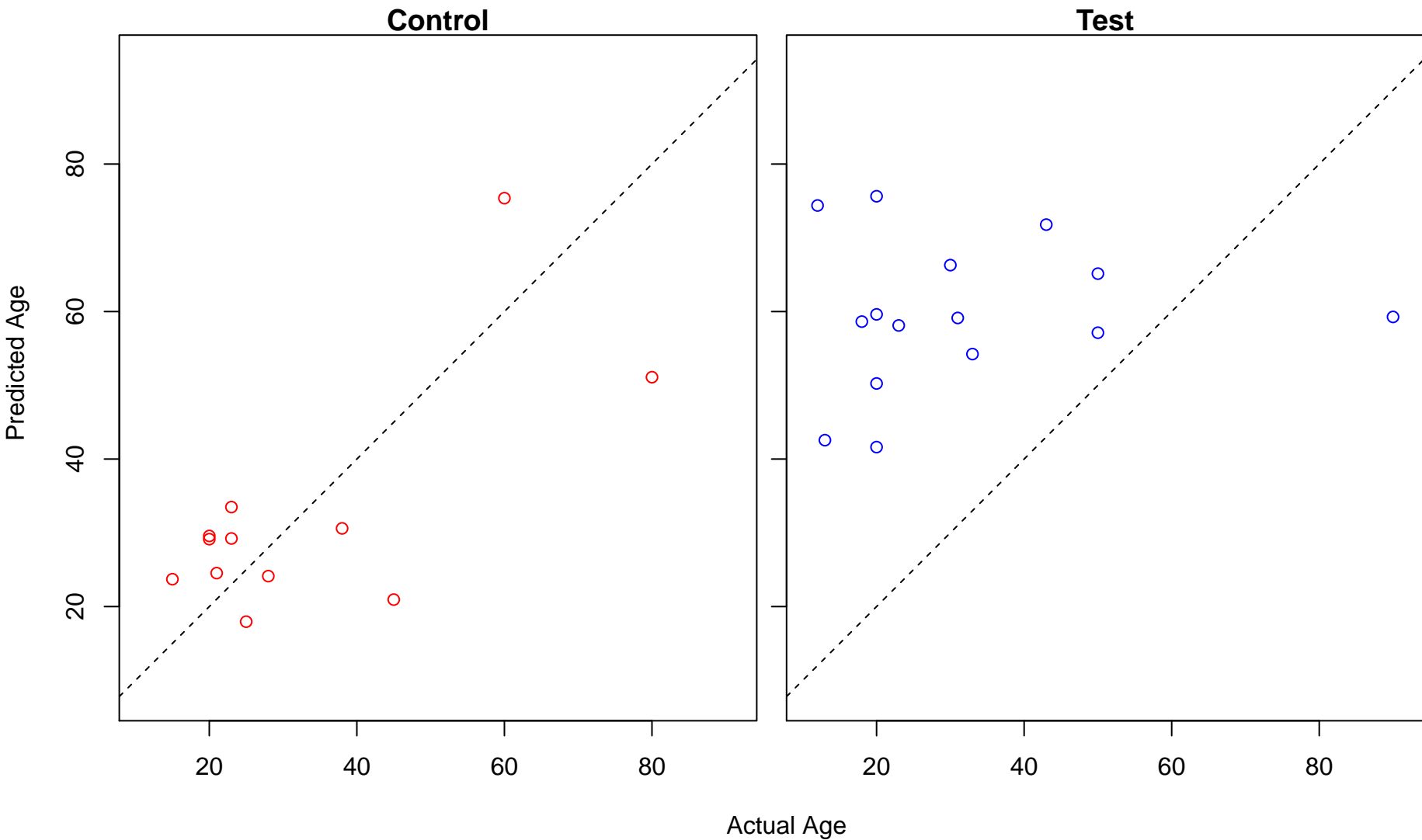
focal adhesion assembly (Score: 2.600360)



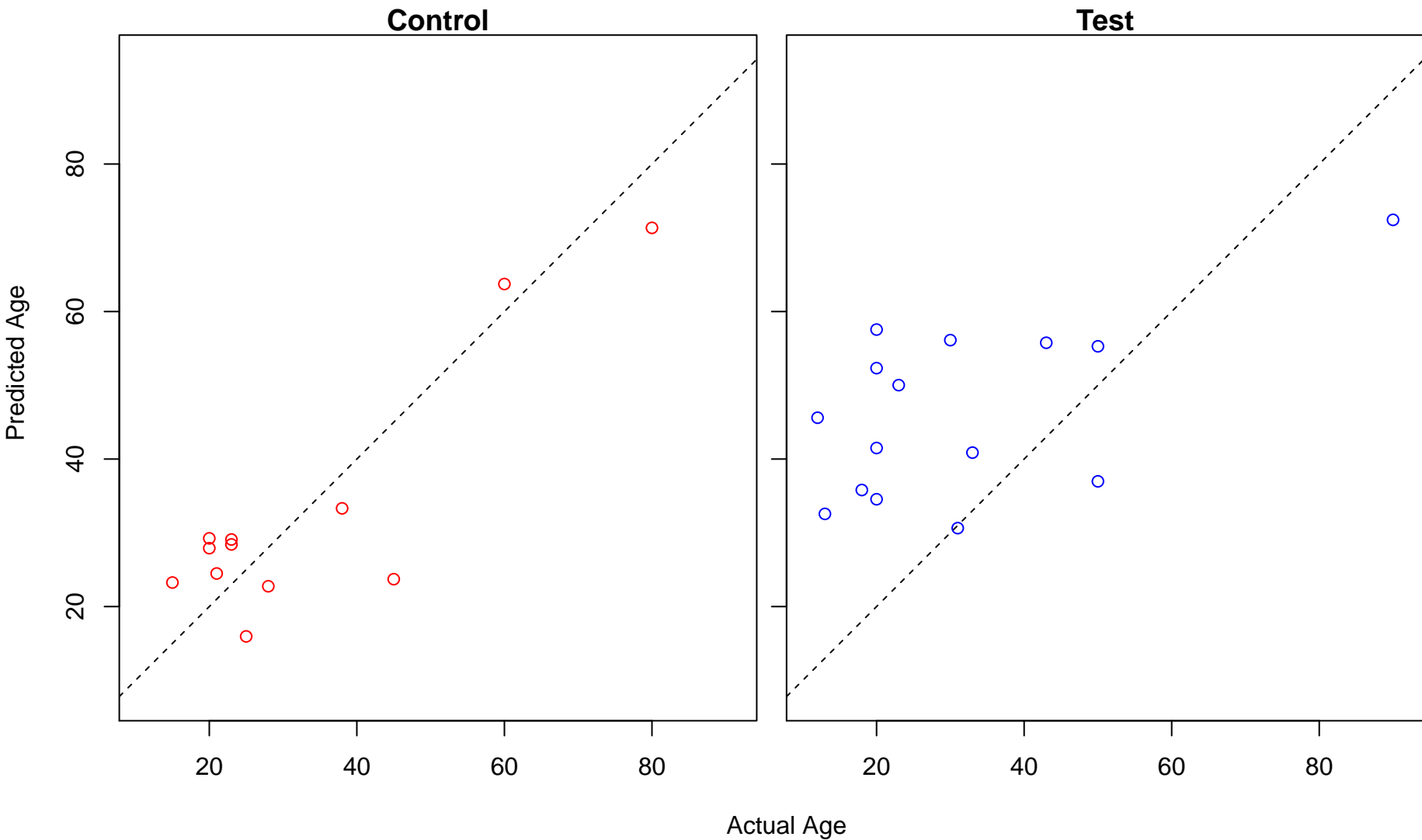
protein localization to vacuole (Score: 2.587422)



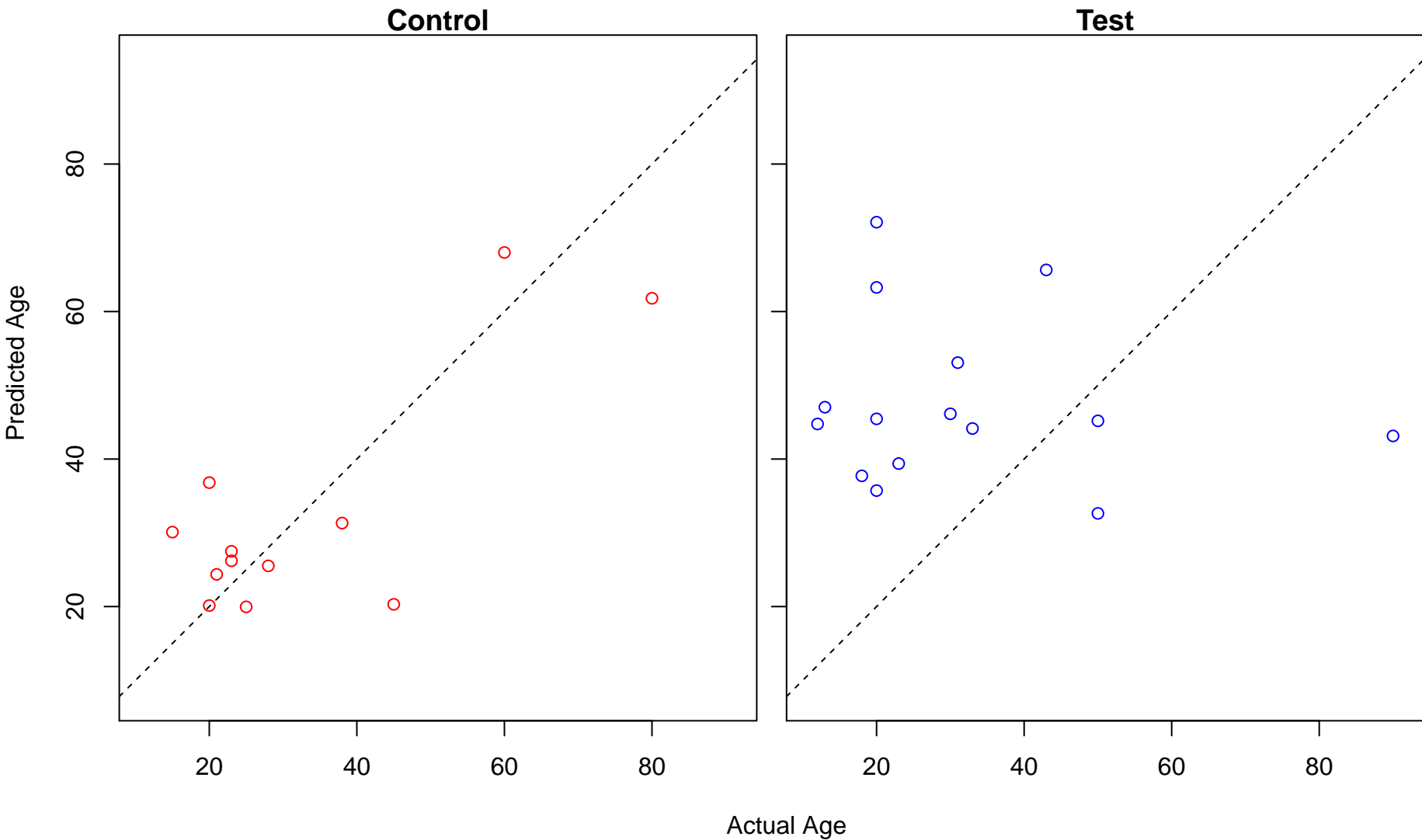
blood vessel remodeling (Score: 2.577849)



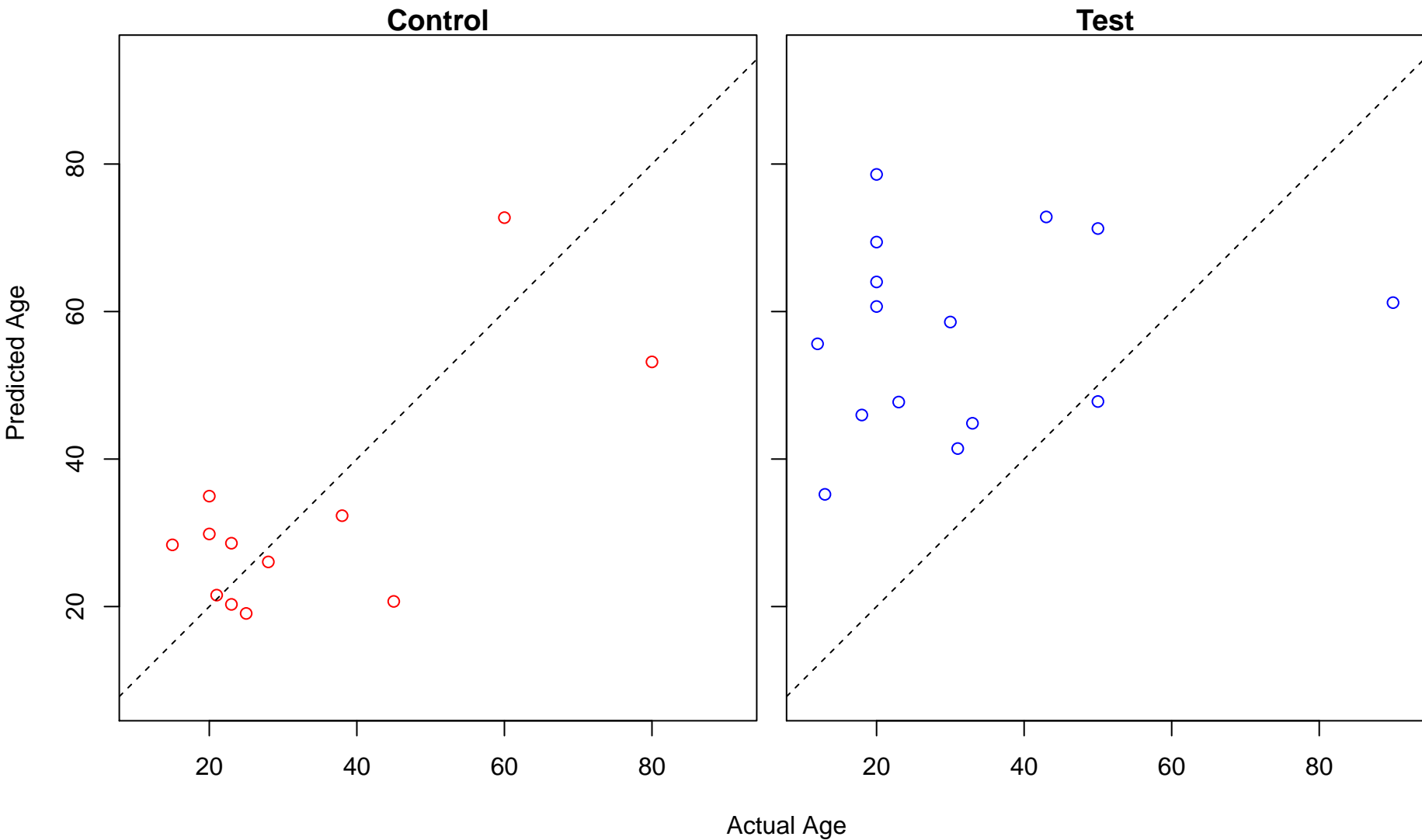
basic amino acid transport (Score: 2.563793)



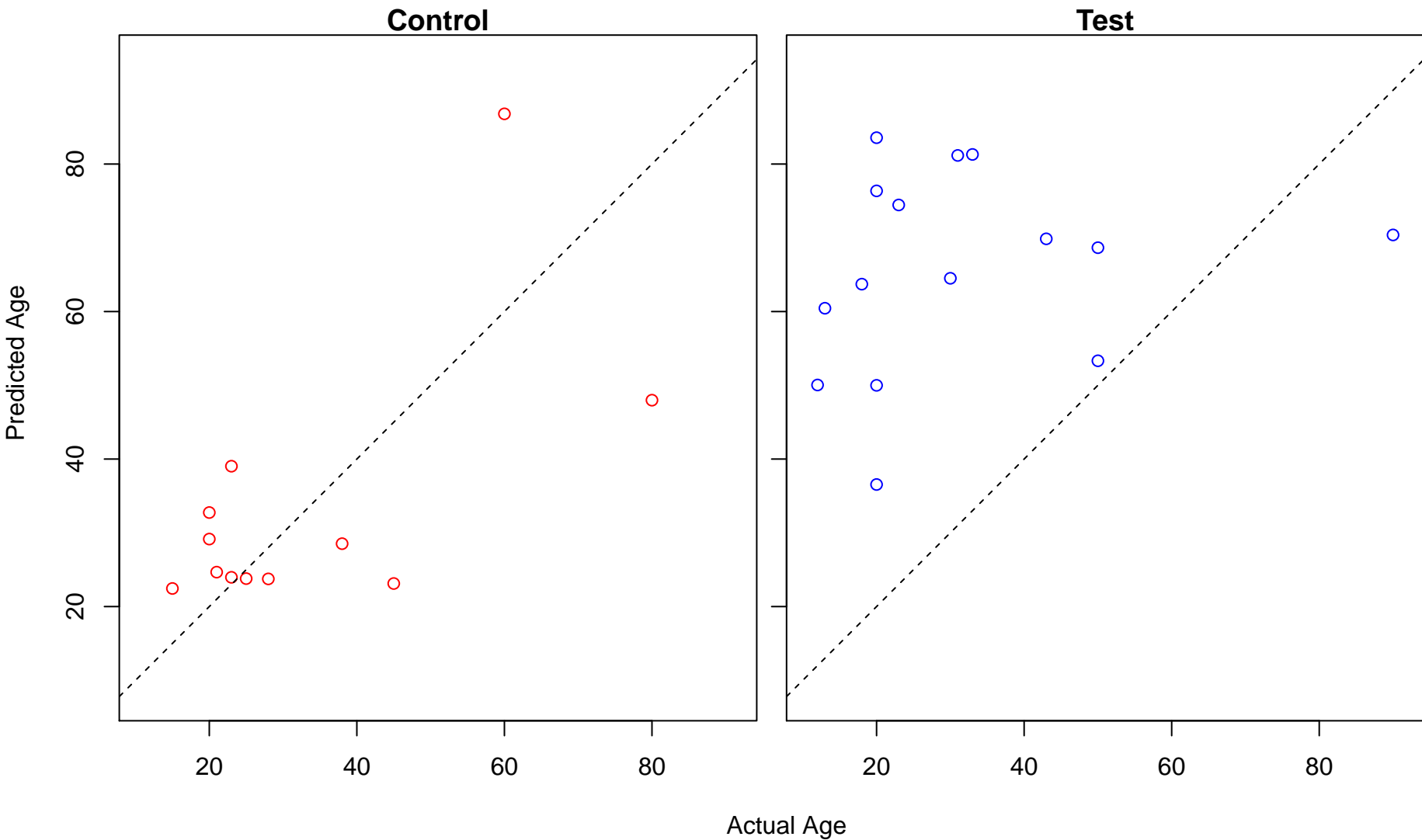
membrane depolarization during cardiac muscle cell action potential (Score: 2.552278)



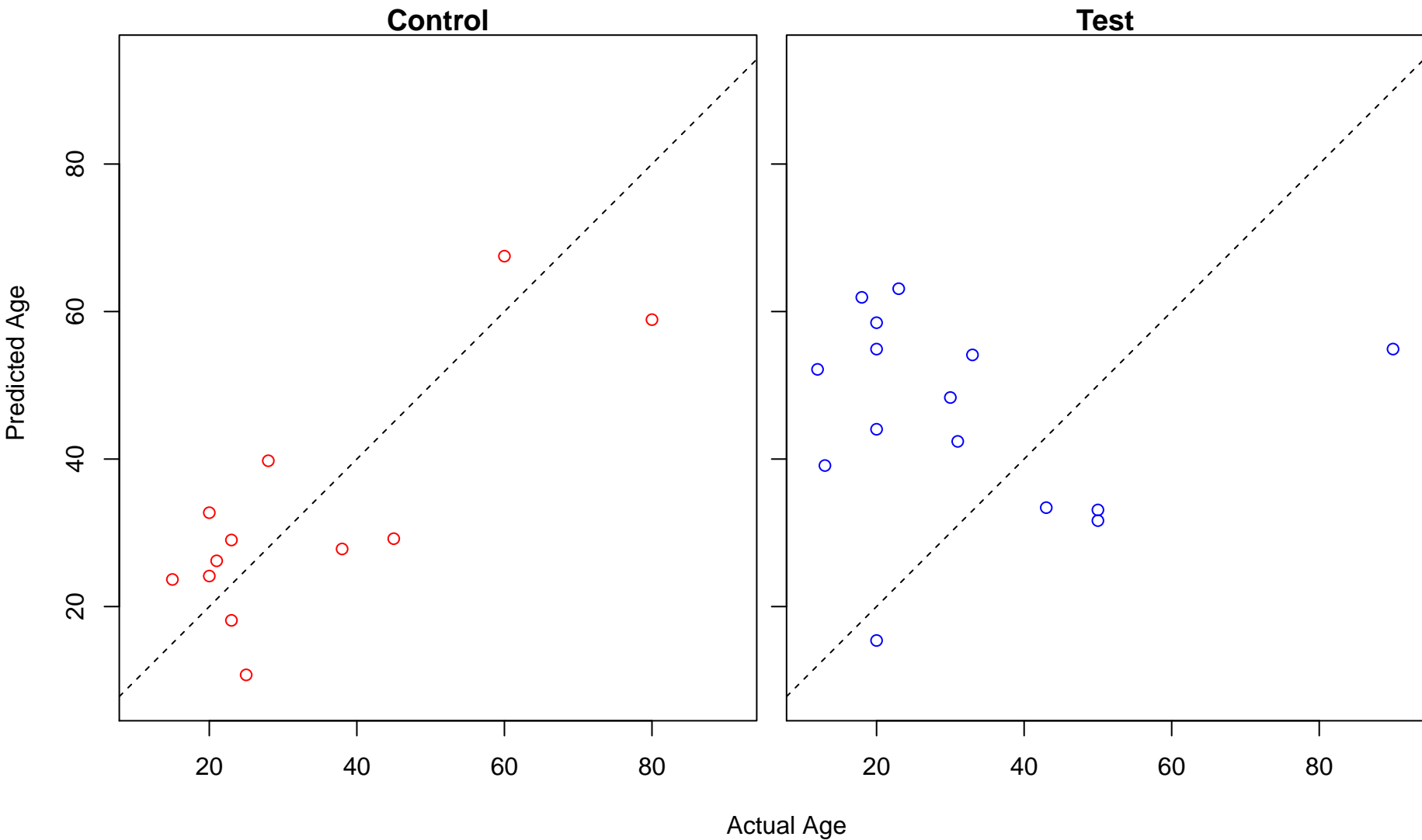
organic anion transport (Score: 2.546520)



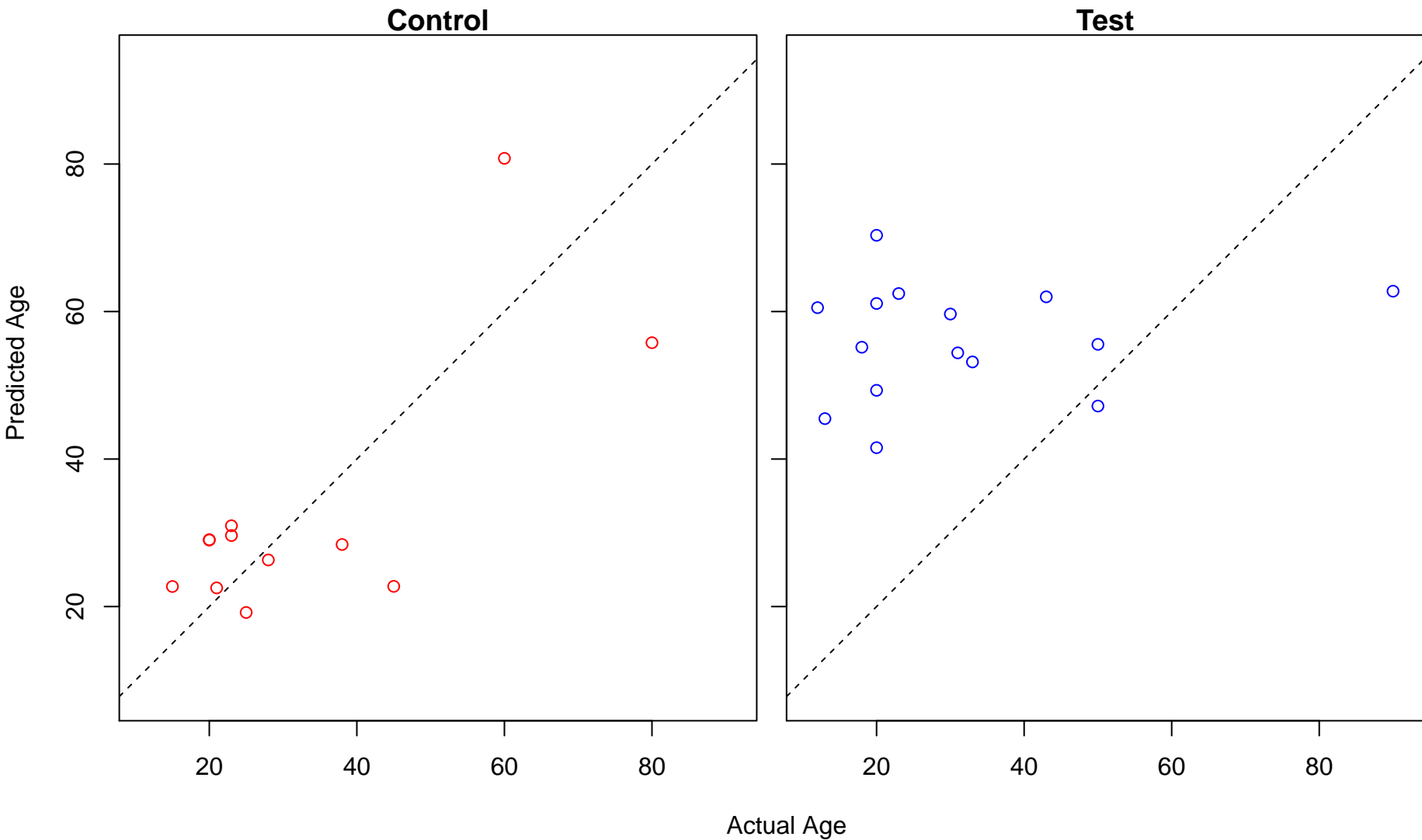
drug catabolic process (Score: 2.542764)



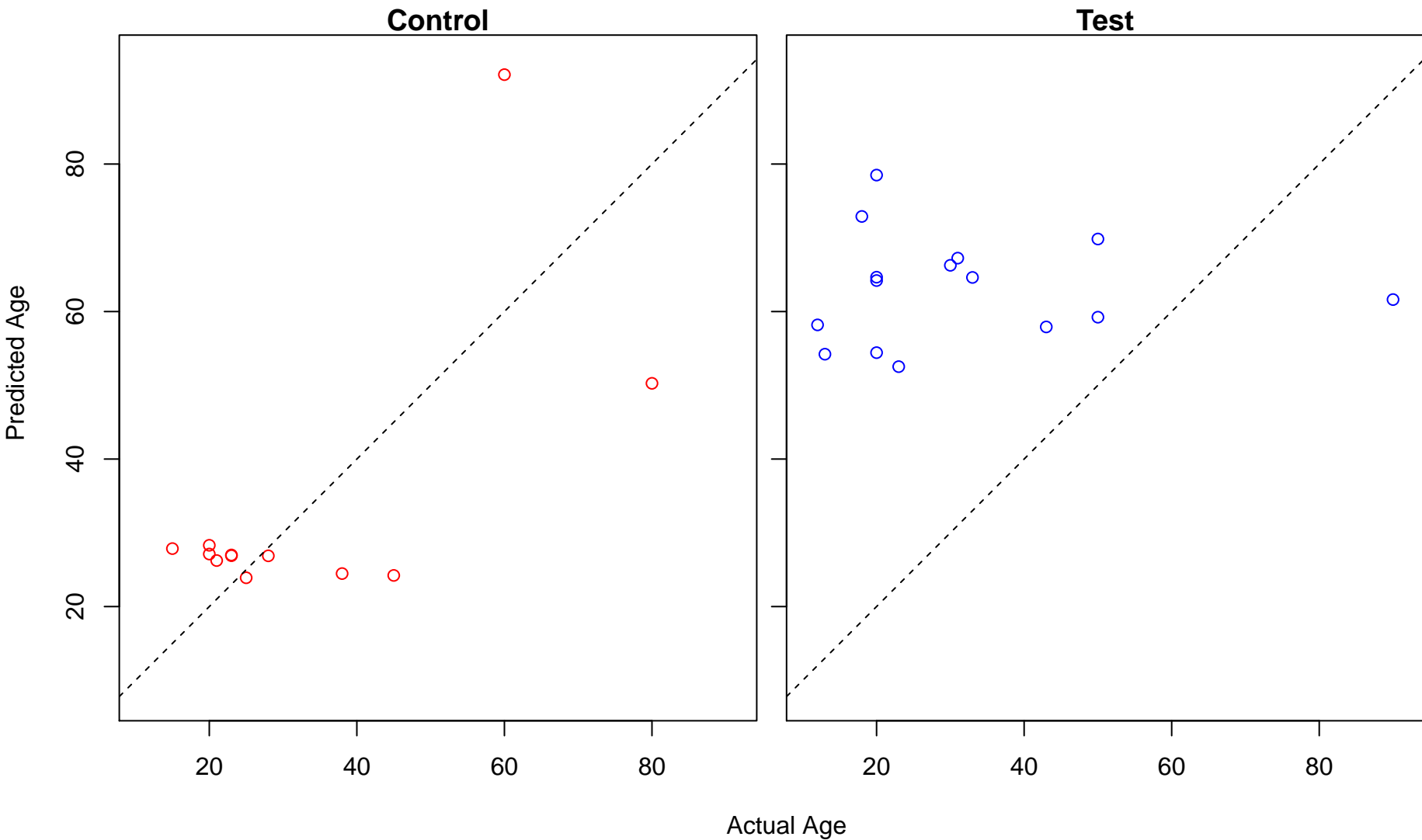
centriole assembly (Score: 2.542514)



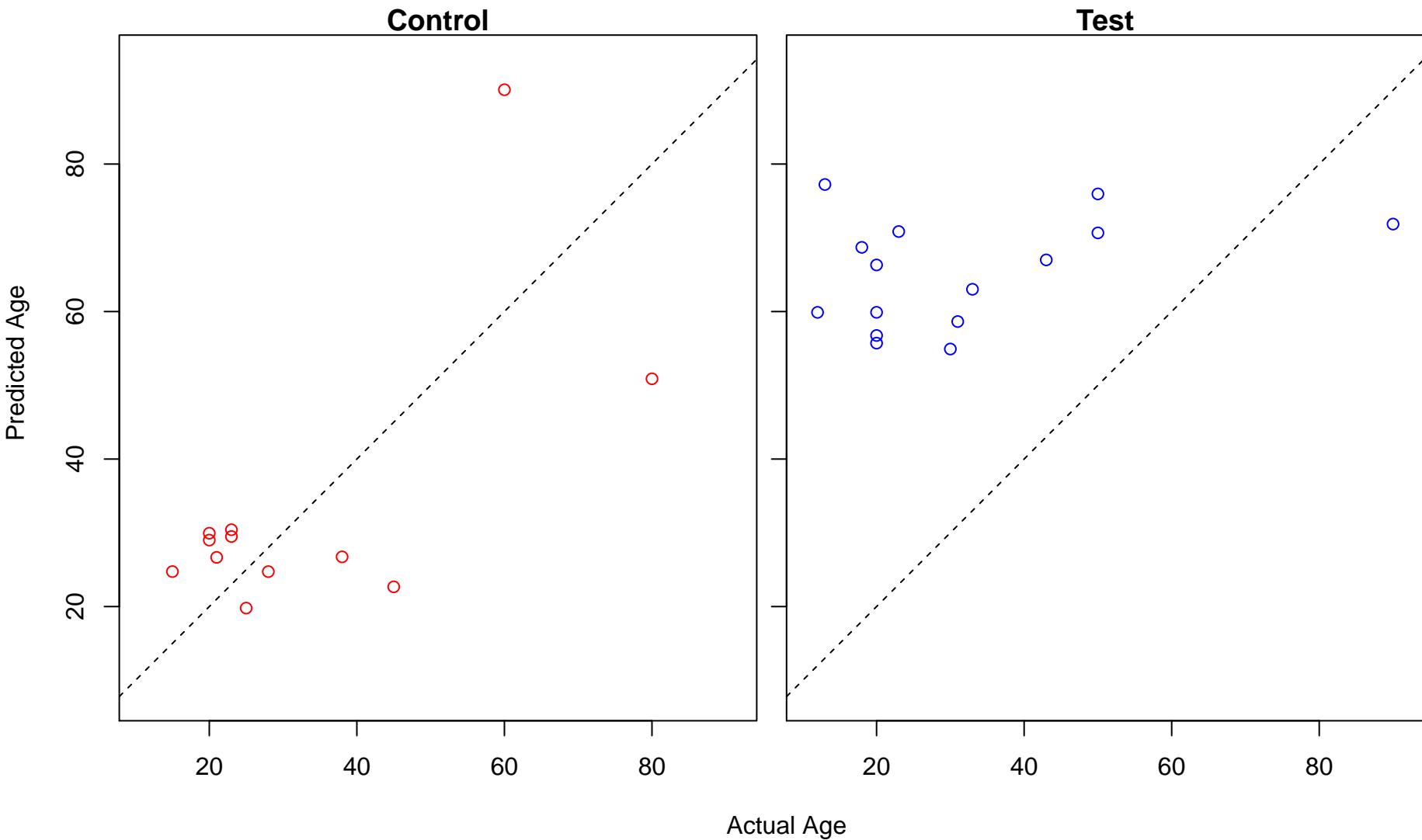
mRNA cis splicing, via spliceosome (Score: 2.534728)



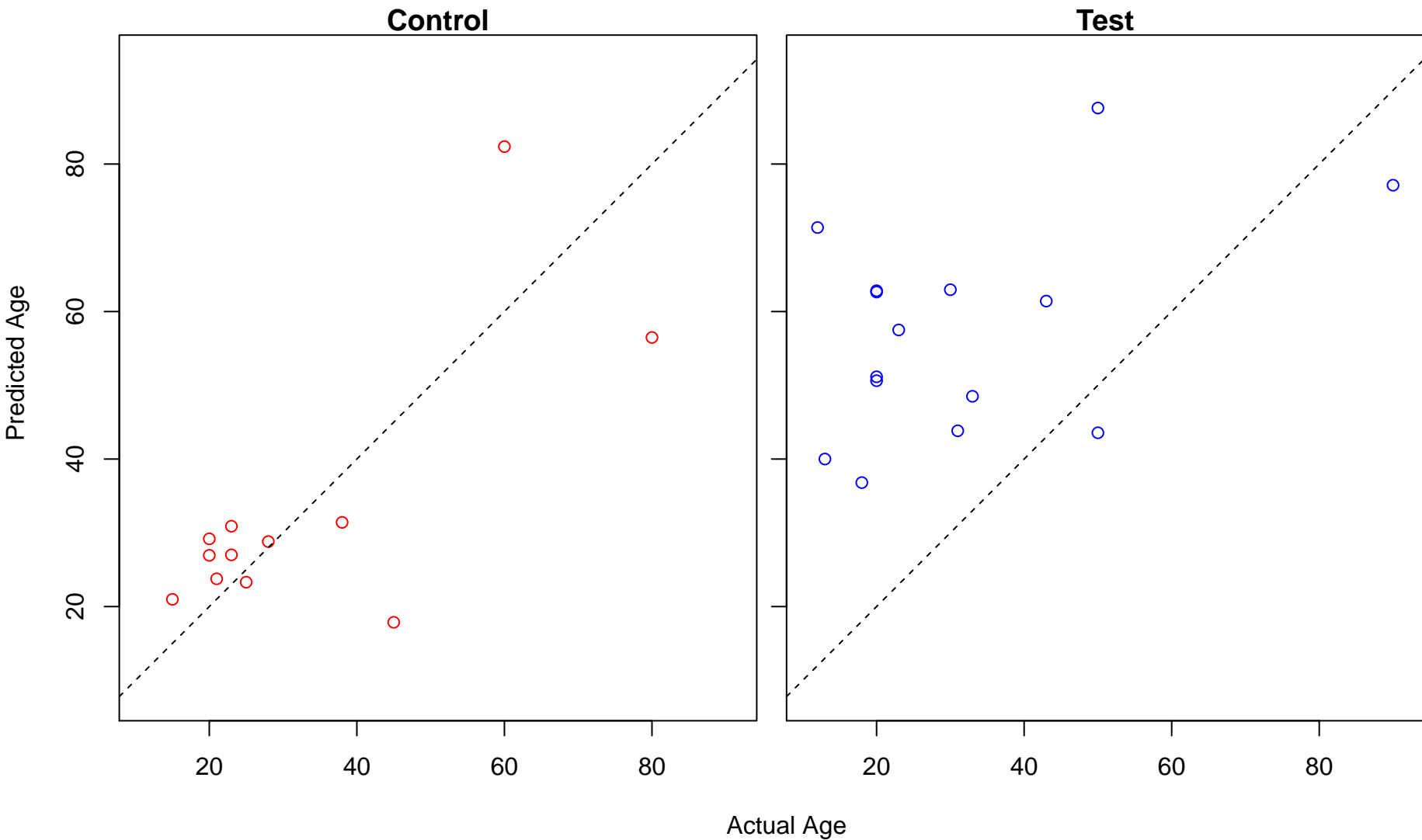
regulation of exosomal secretion (Score: 2.525647)



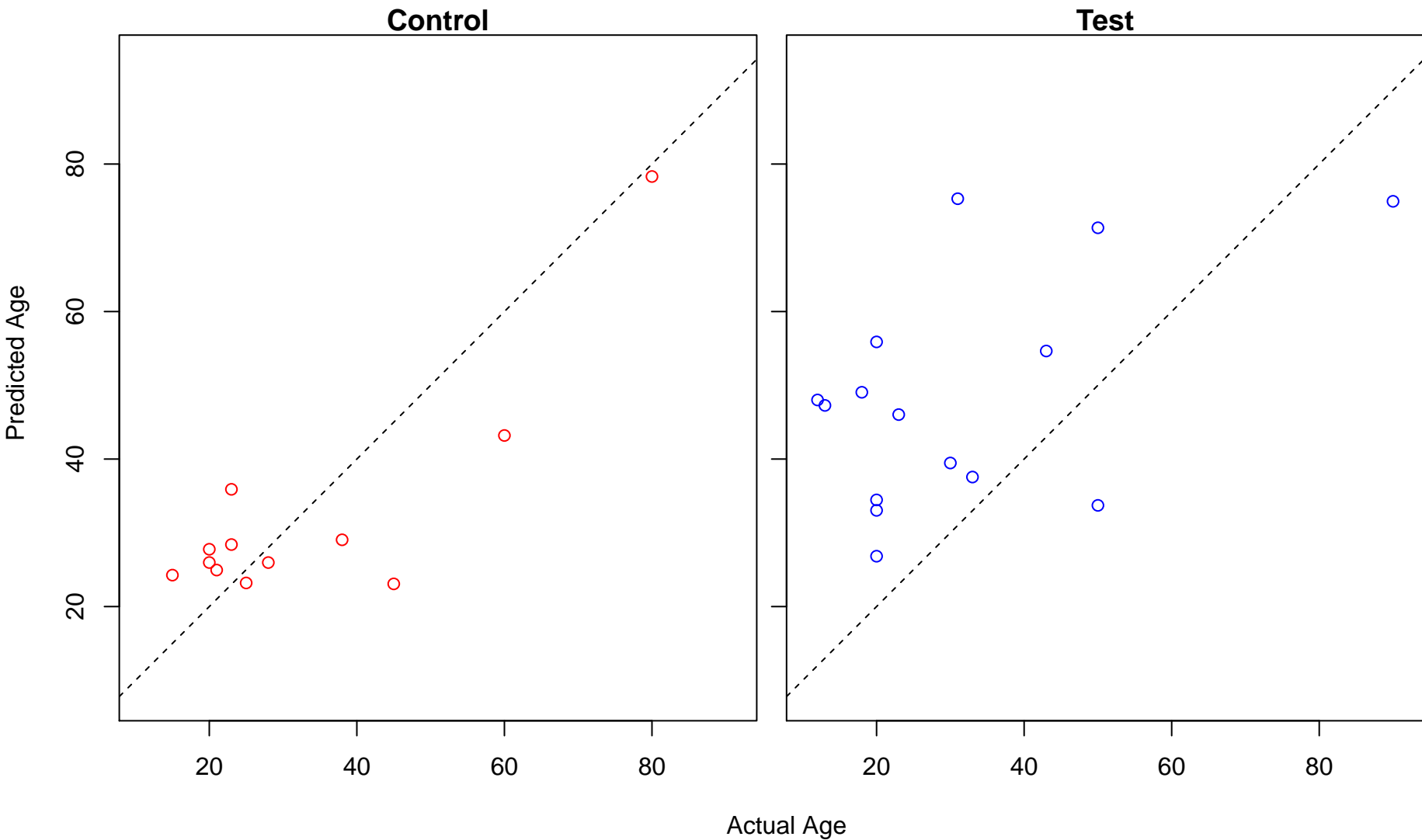
positive regulation of interleukin-1 production (Score: 2.523777)



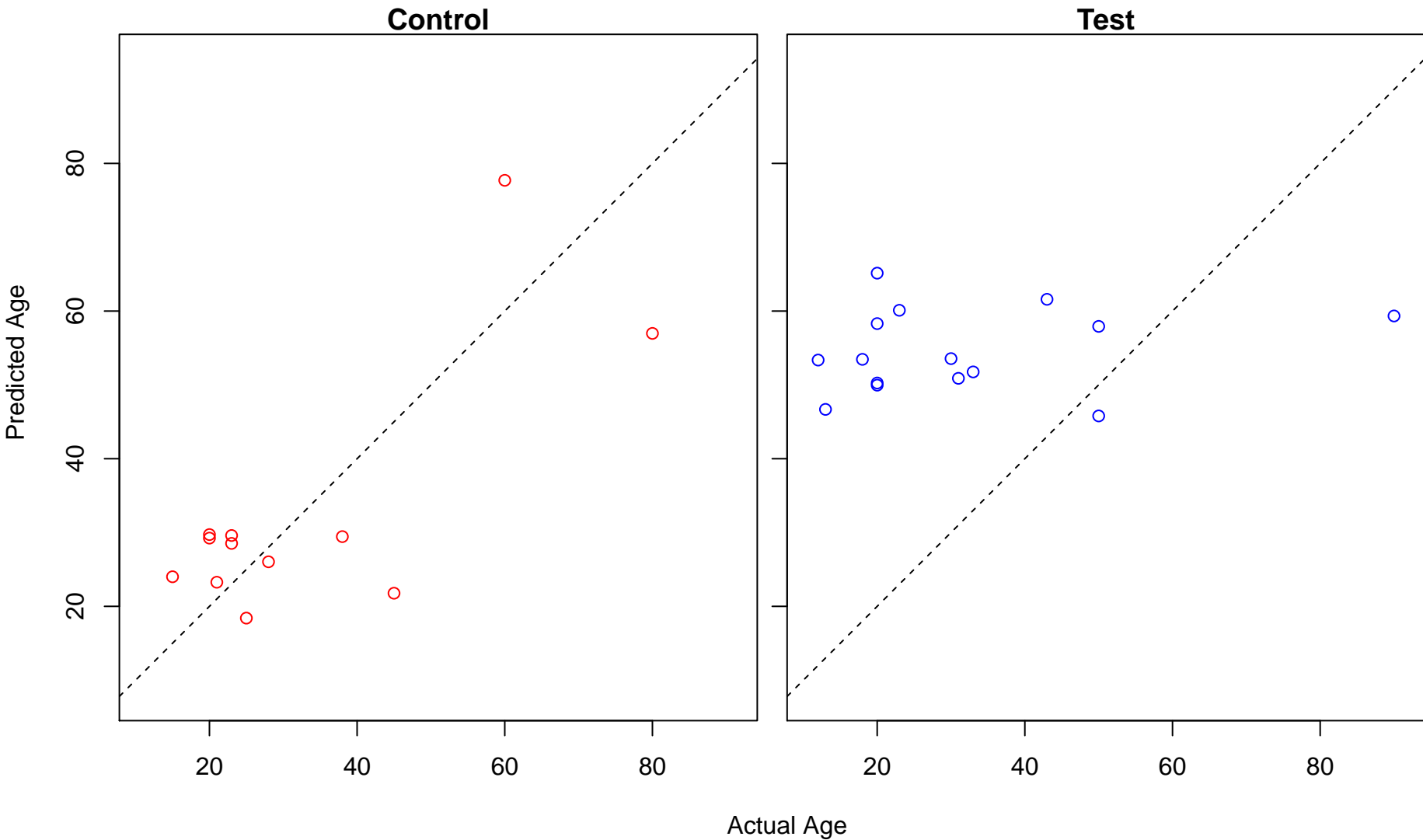
regulation of urine volume (Score: 2.510865)



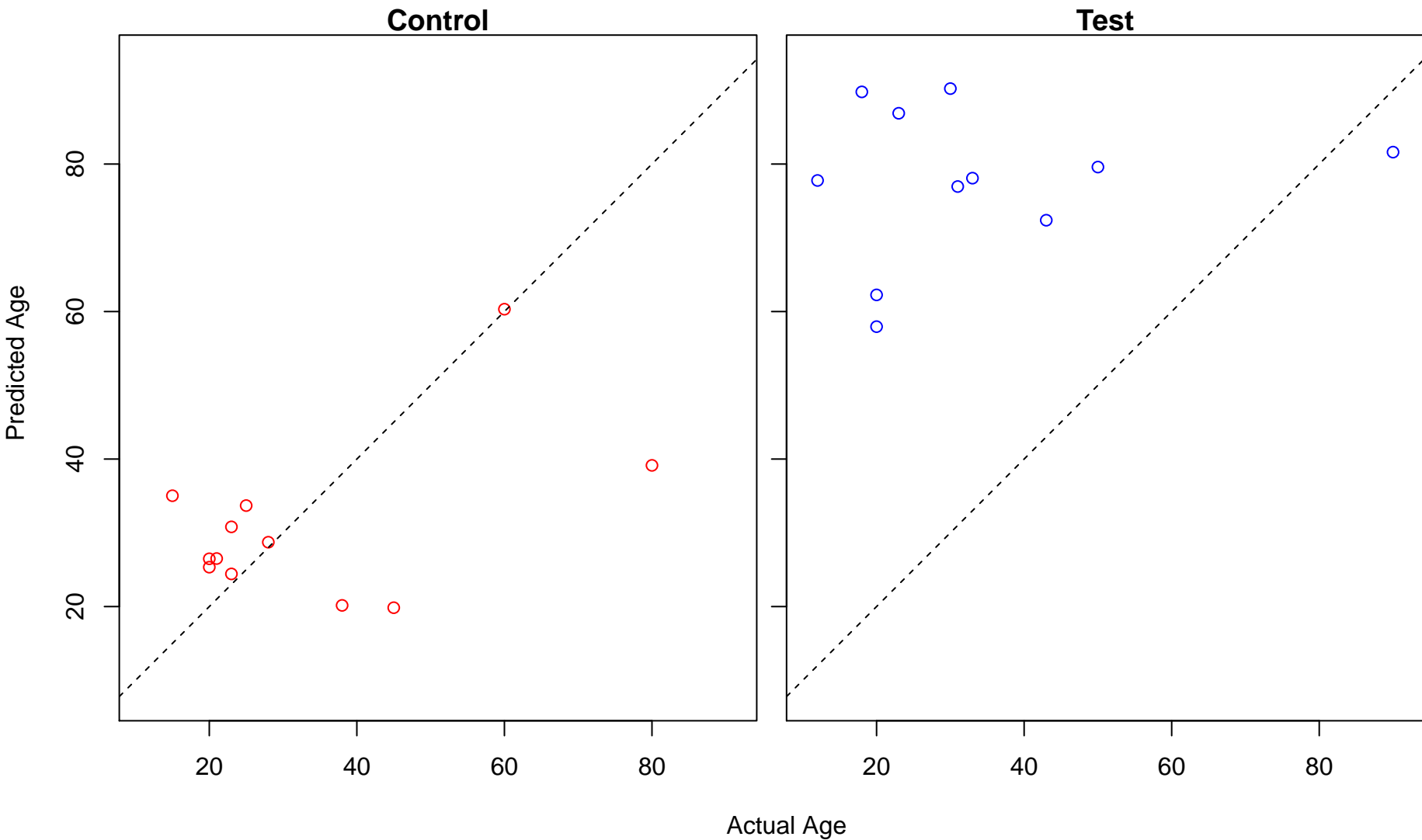
myoblast fusion (Score: 2.500751)



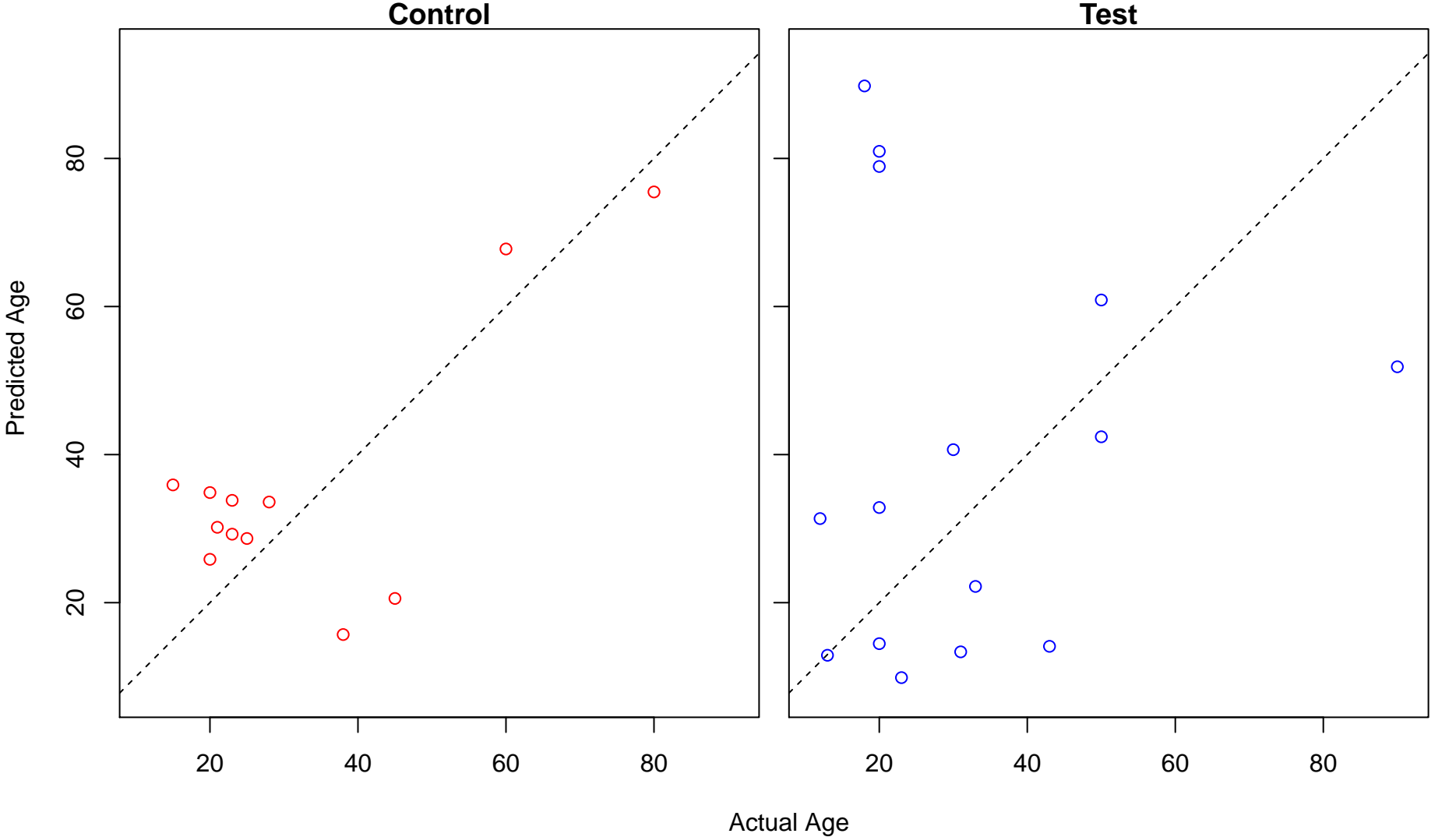
cellular response to gamma radiation (Score: 2.489523)



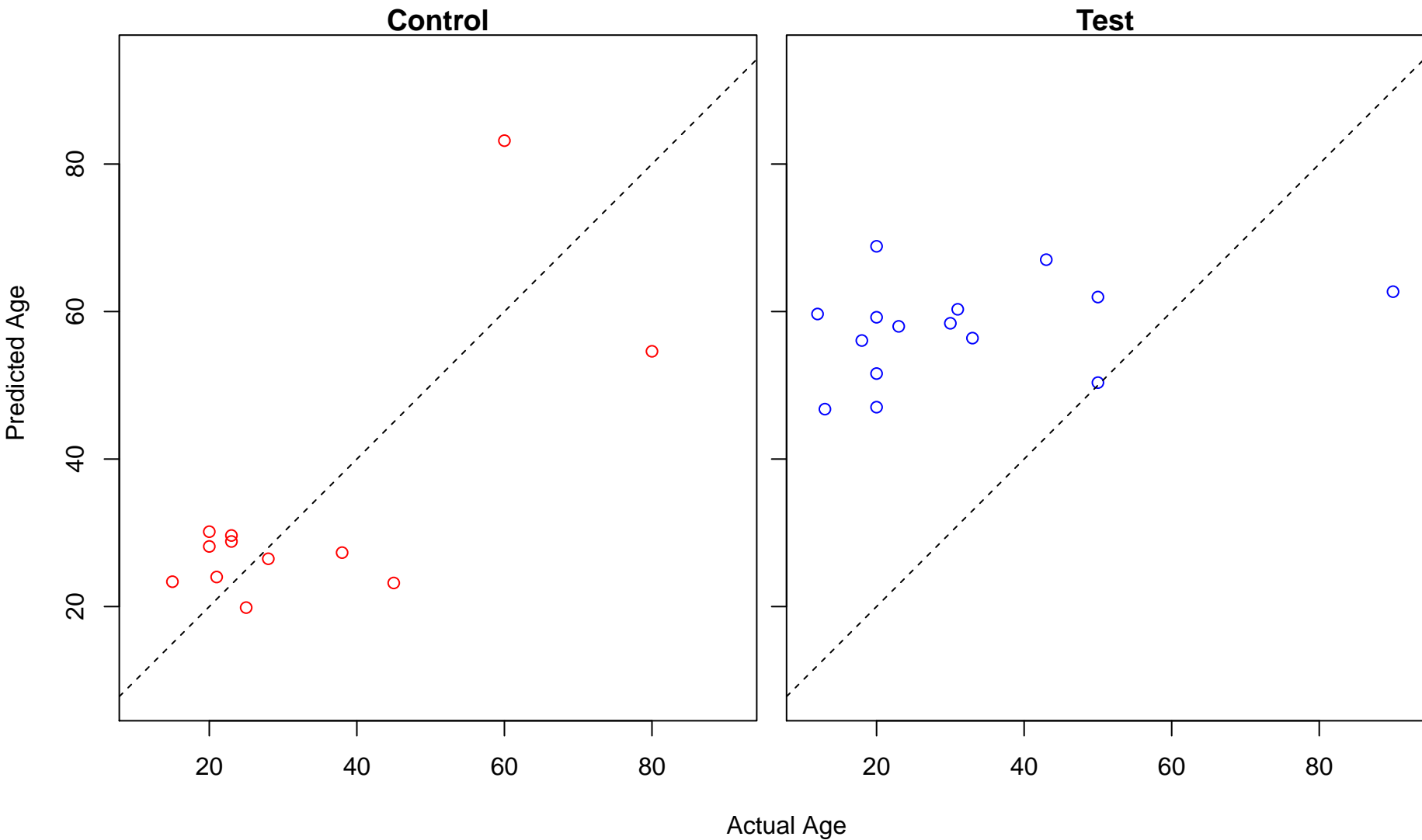
negative regulation of T cell cytokine production (Score: 2.484991)



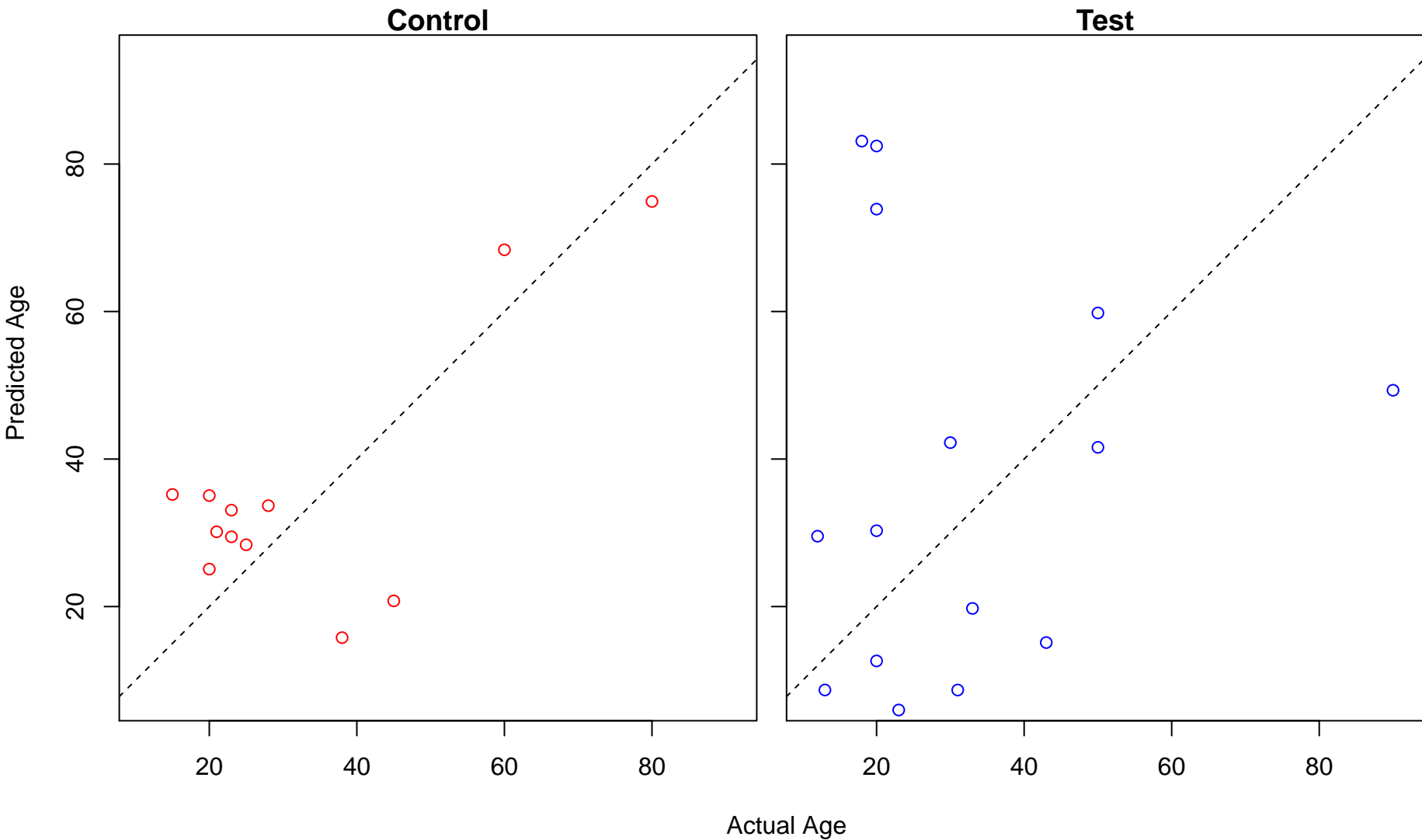
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 2.48)



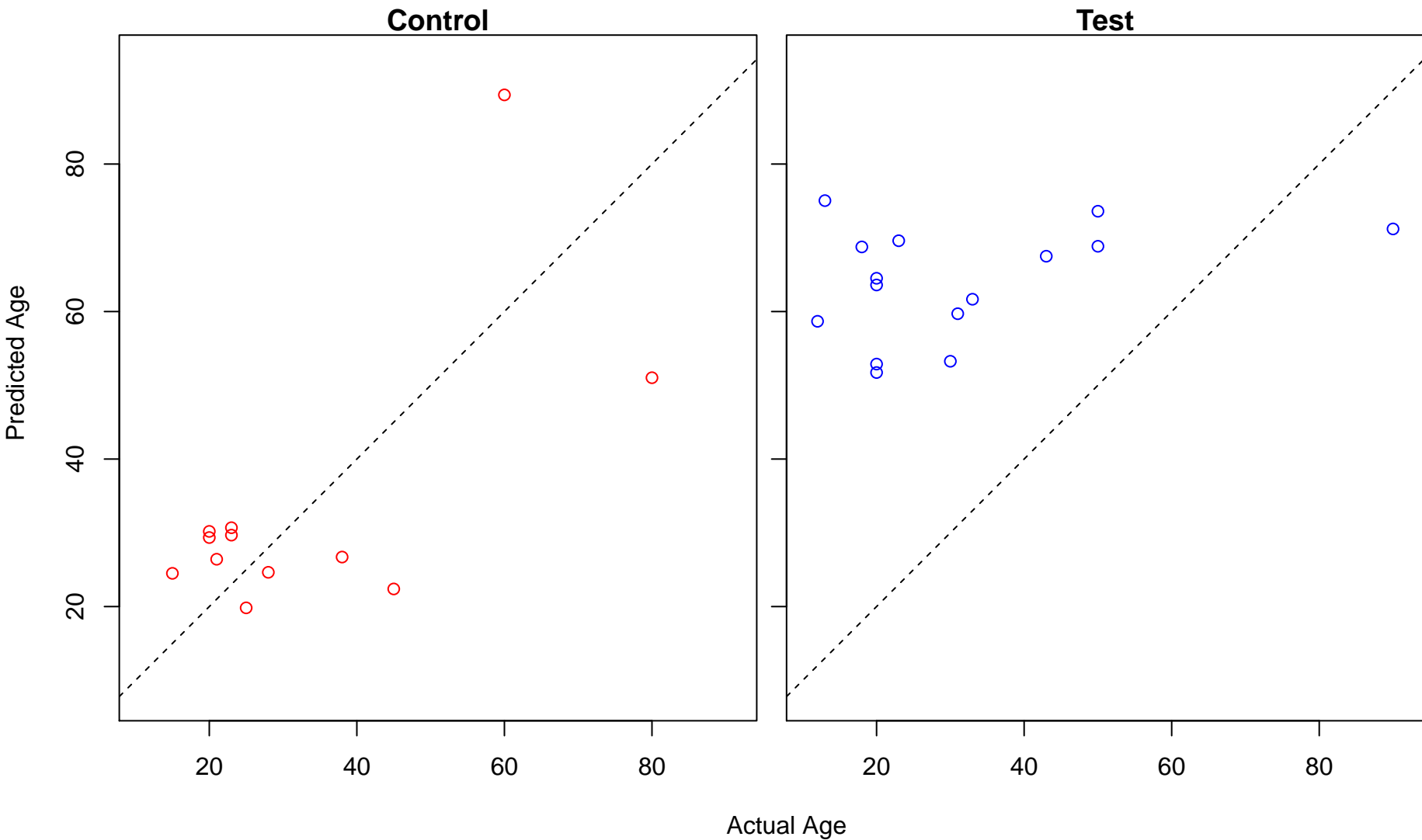
DNA-dependent DNA replication maintenance of fidelity (Score: 2.477538)



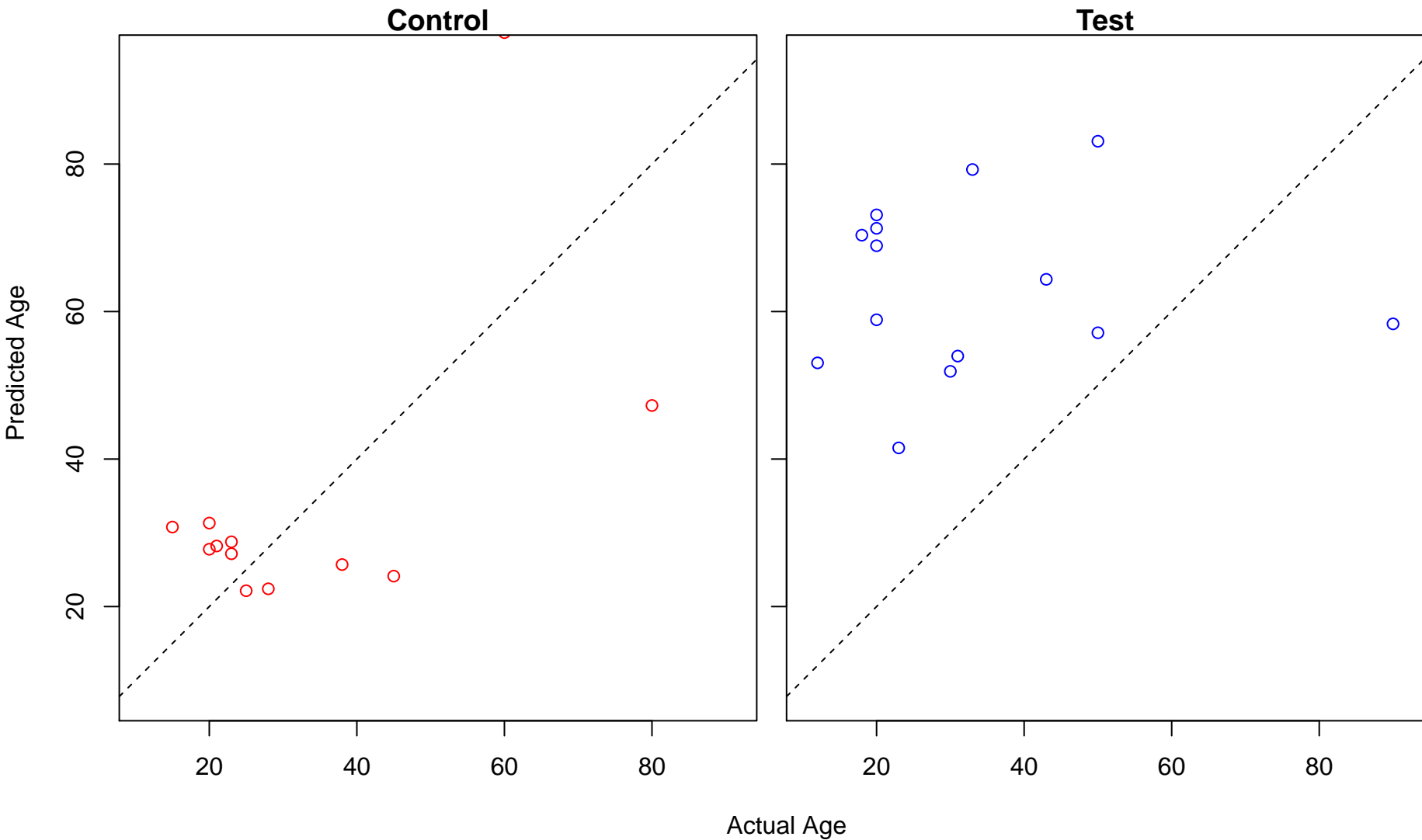
negative regulation of cysteine-type endopeptidase activity (Score: 2.464775)



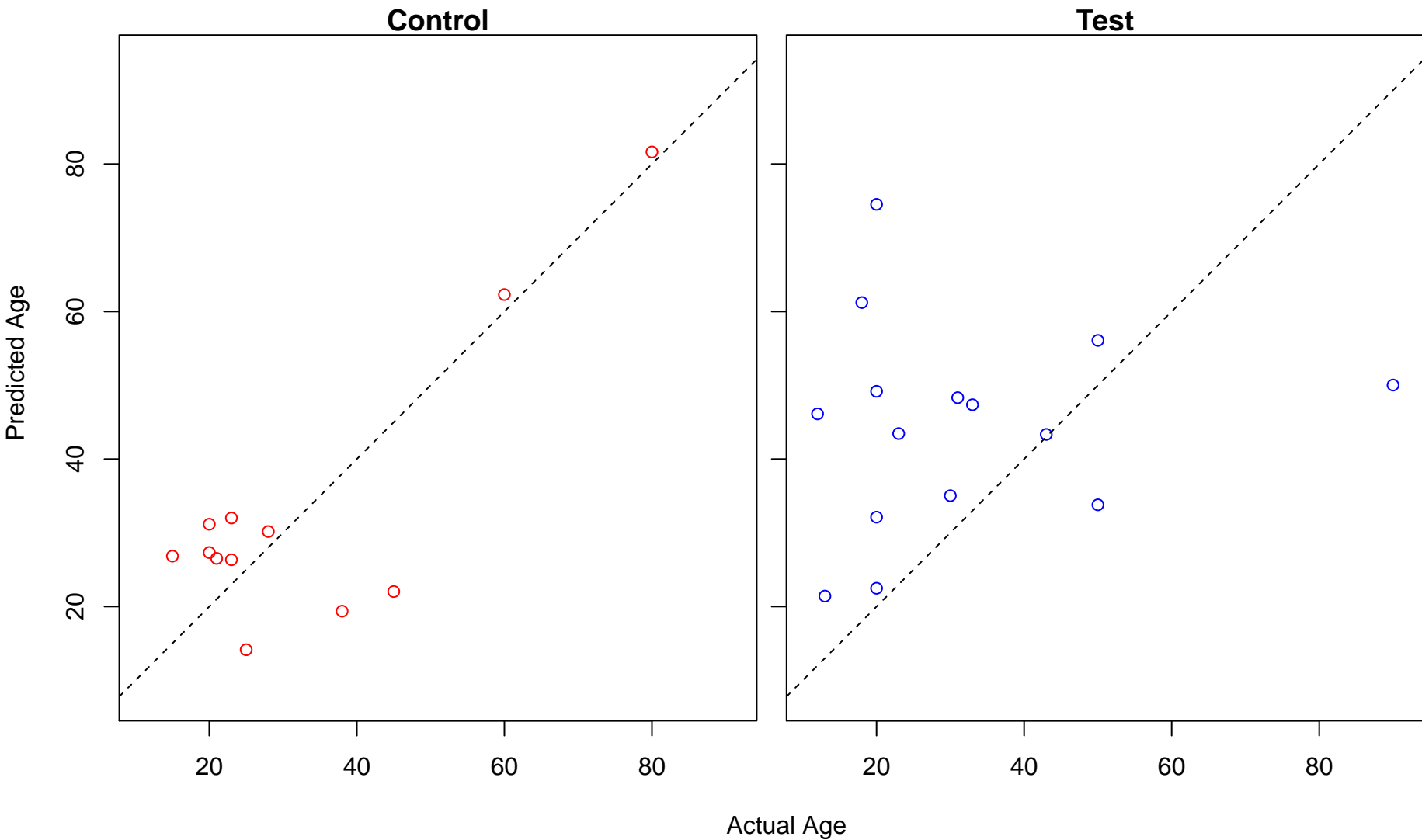
dendritic cell migration (Score: 2.437276)



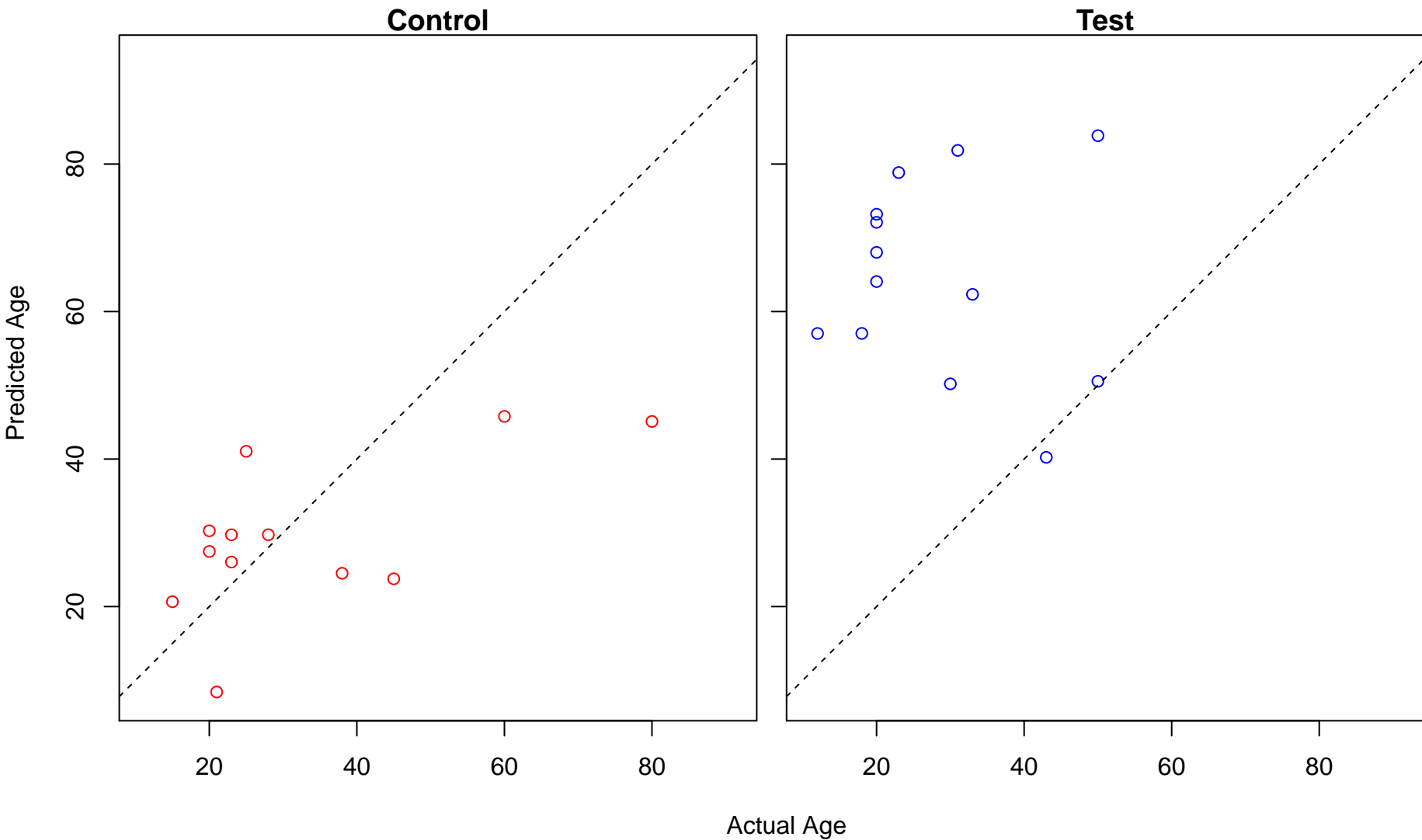
regulation of short-term neuronal synaptic plasticity (Score: 2.434789)



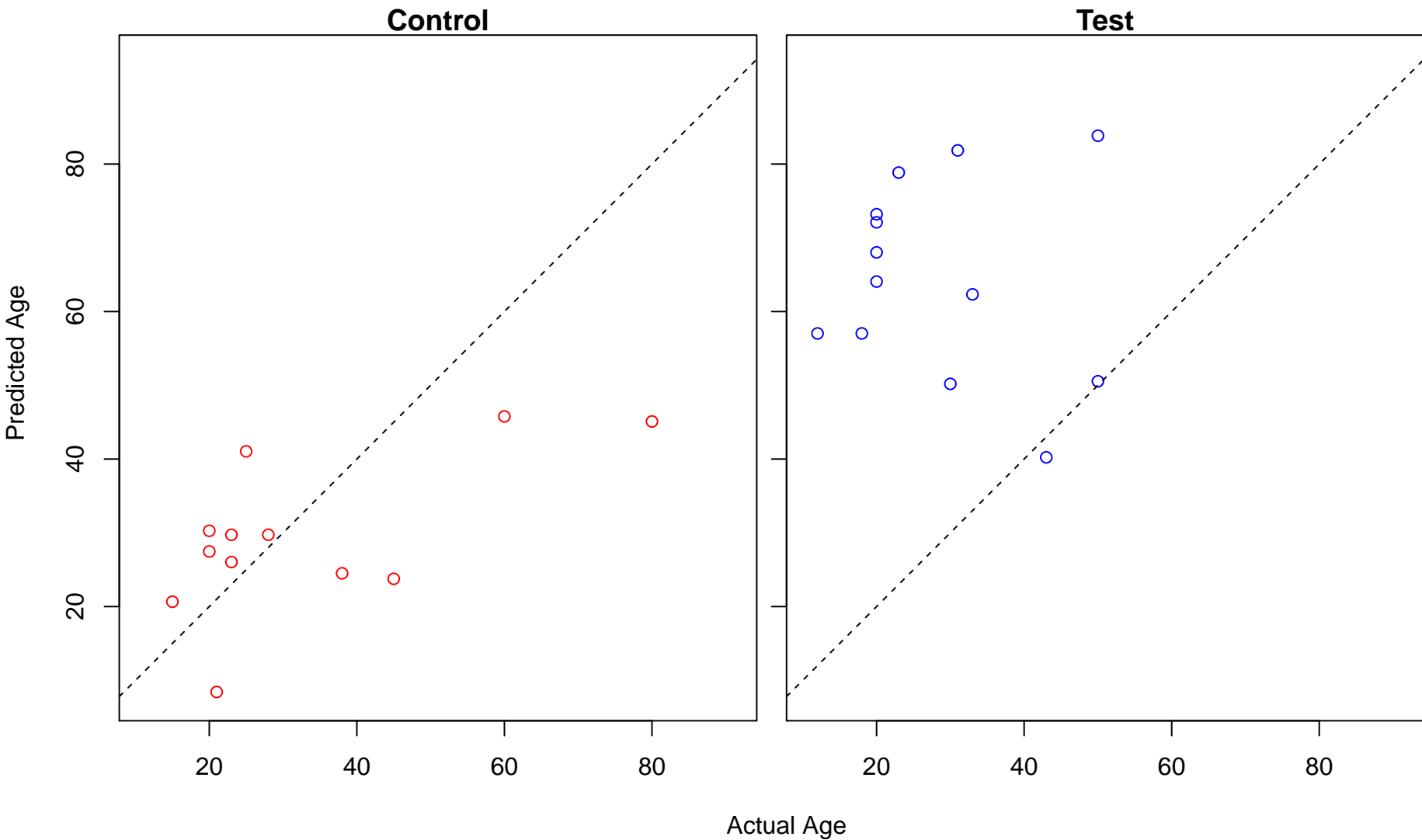
ncRNA metabolic process (Score: 2.431147)



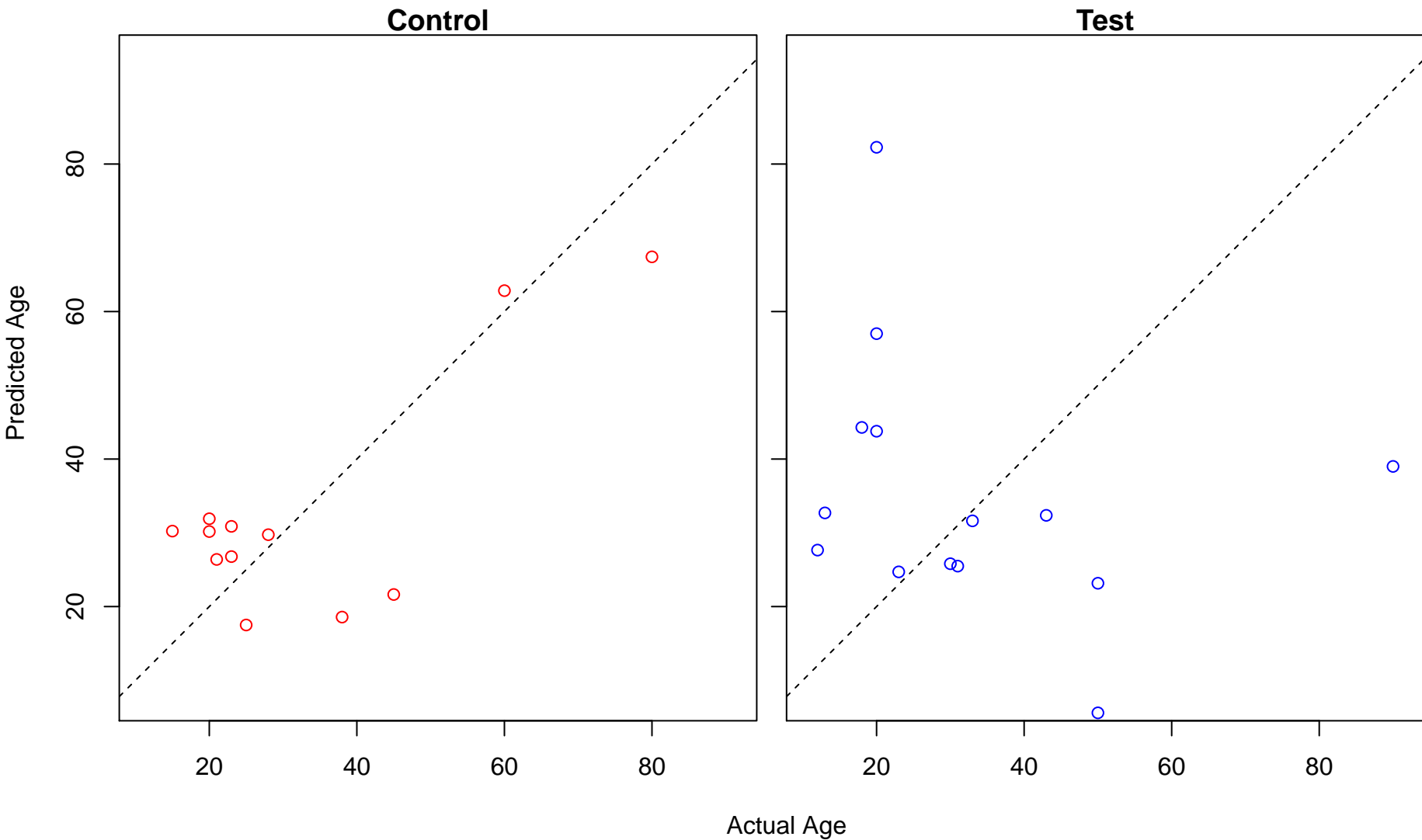
regulation of antimicrobial humoral response (Score: 2.428020)



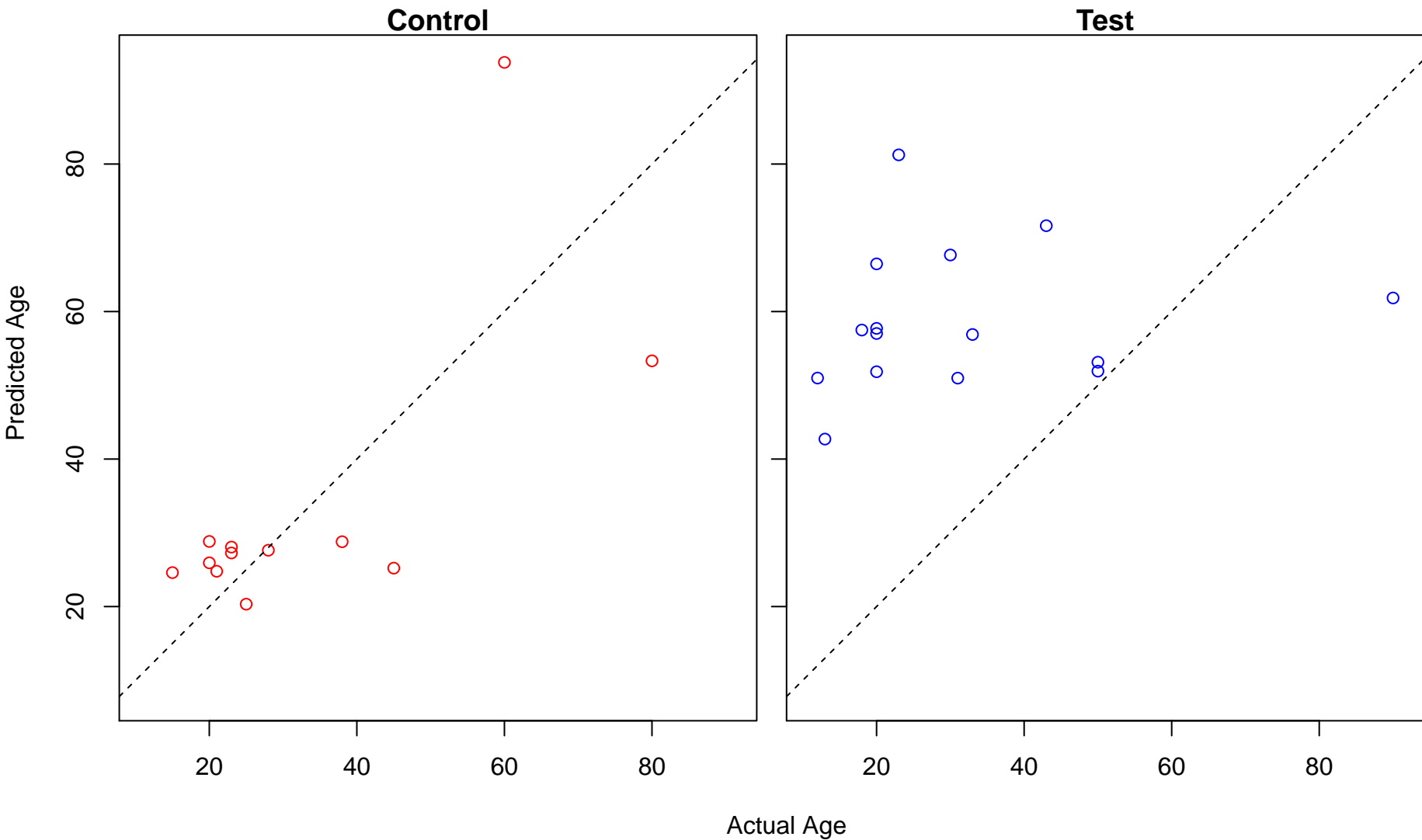
positive regulation of antimicrobial humoral response (Score: 2.428020)



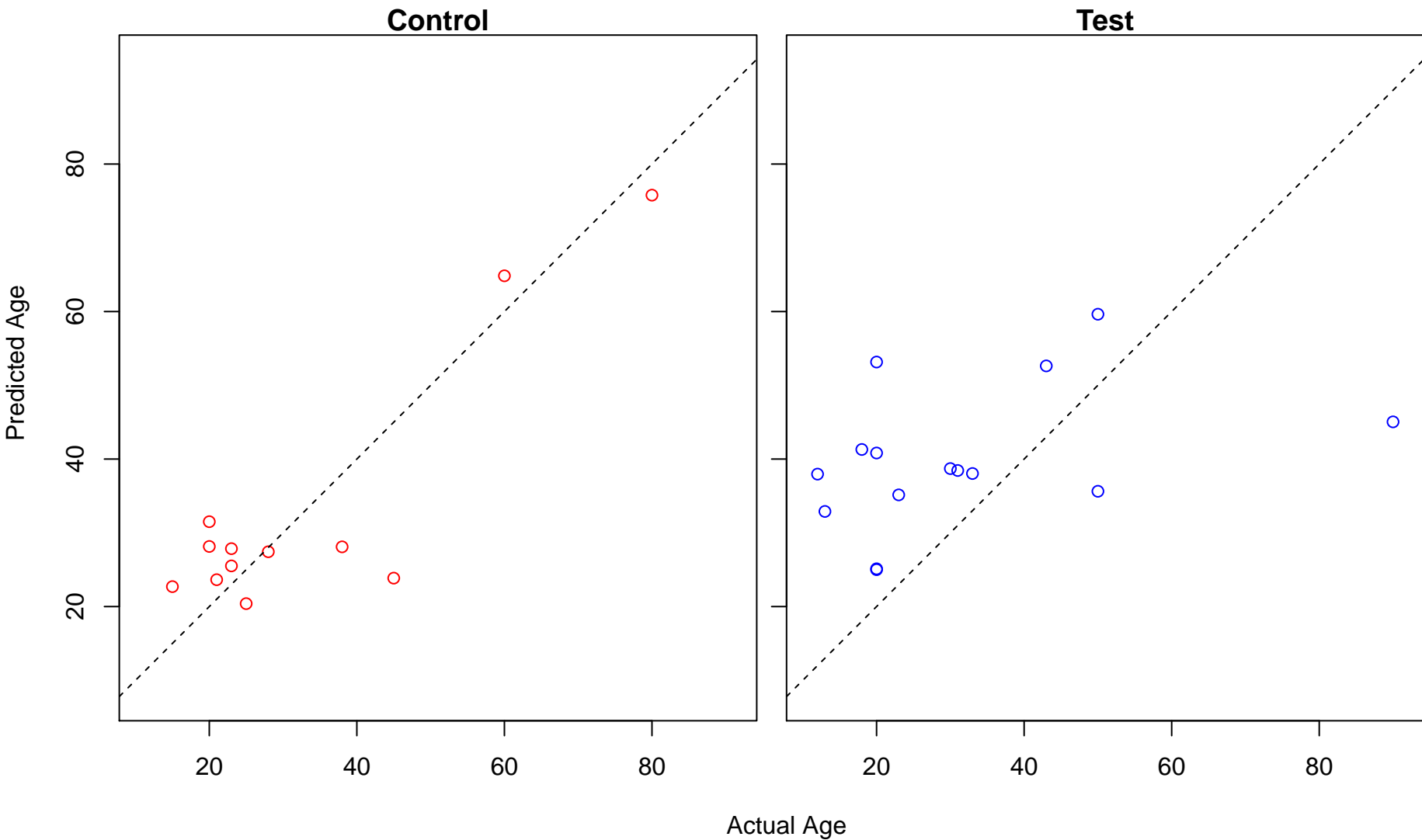
aspartate family amino acid catabolic process (Score: 2.408914)



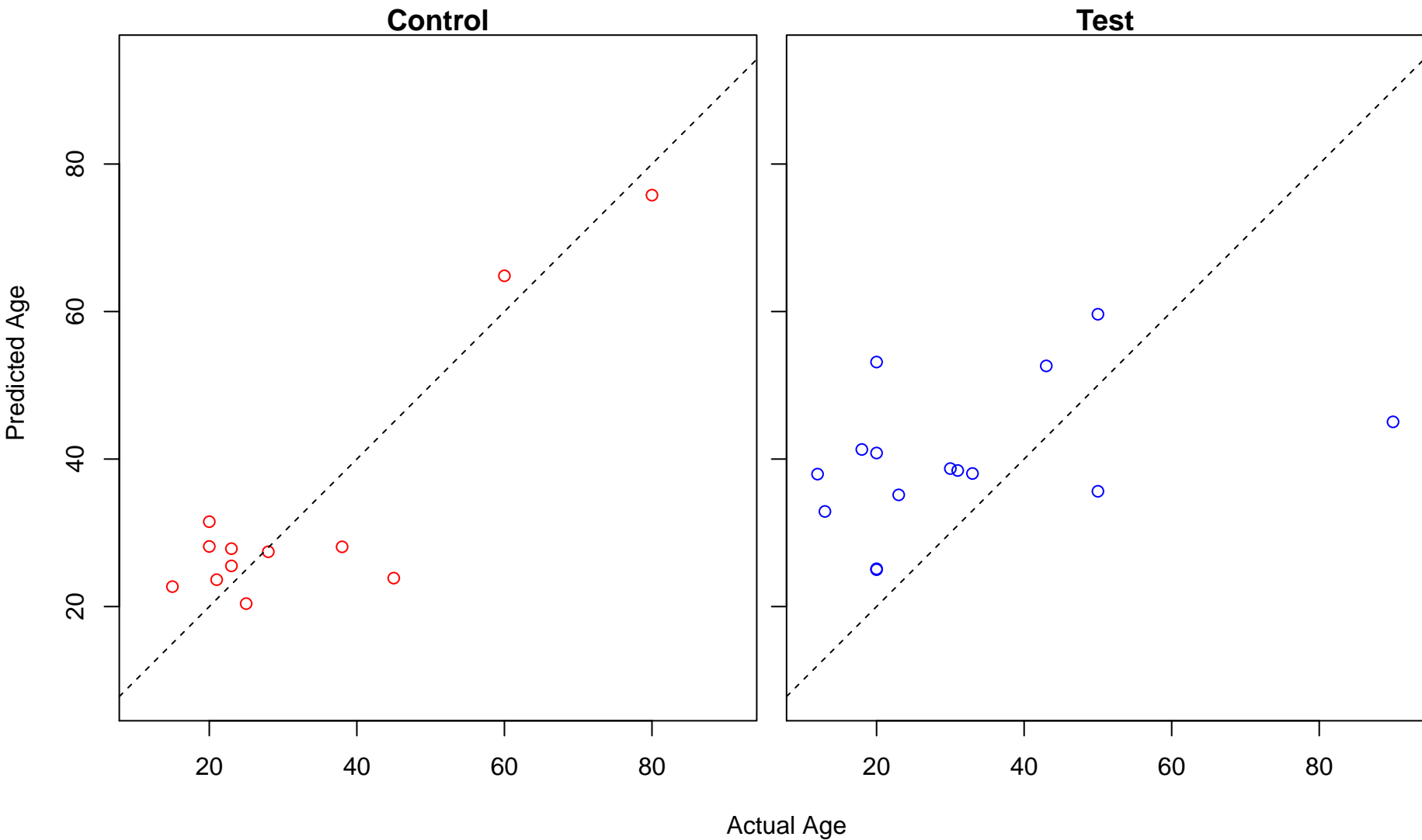
negative regulation of muscle organ development (Score: 2.407516)



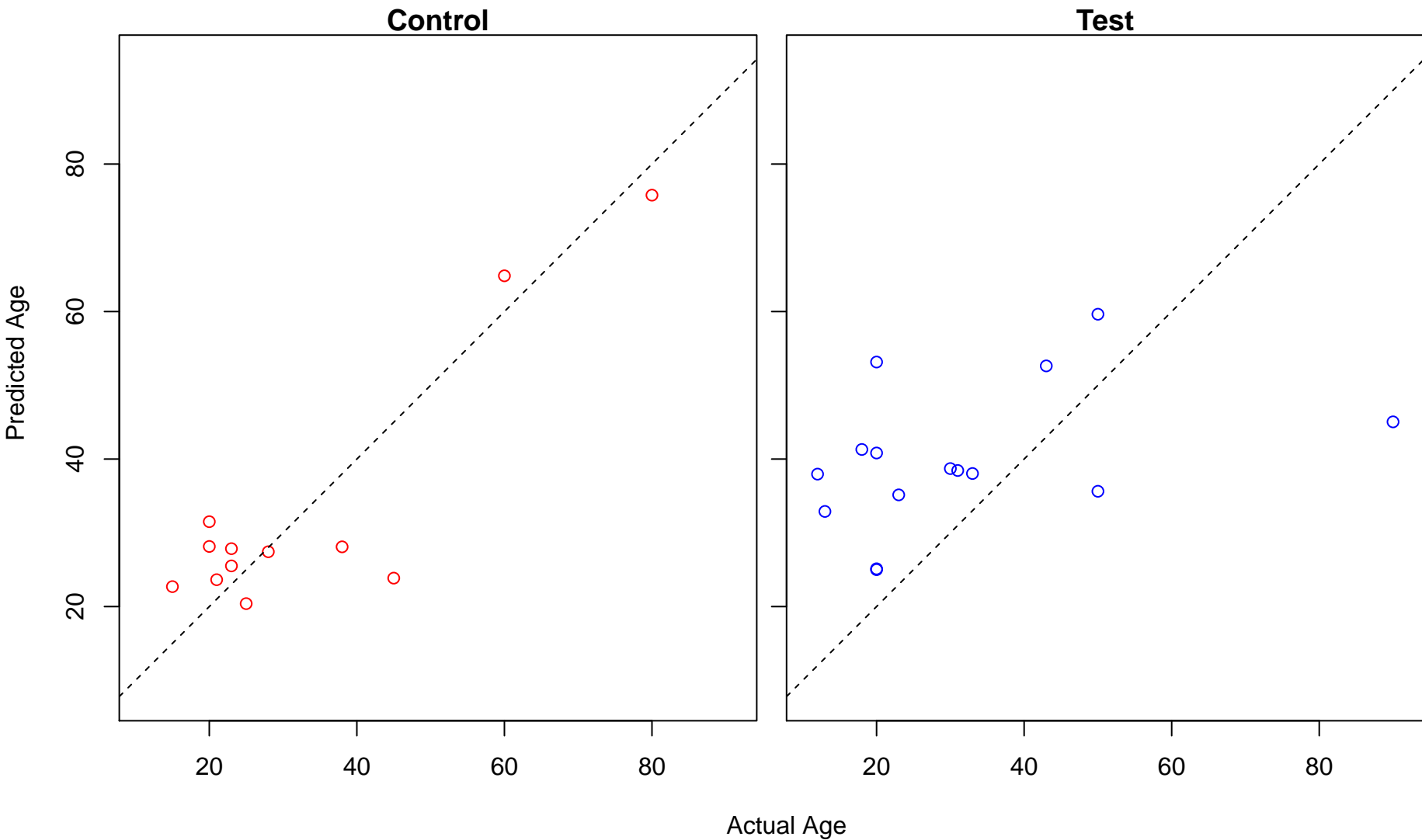
respiratory chain complex III assembly (Score: 2.395416)



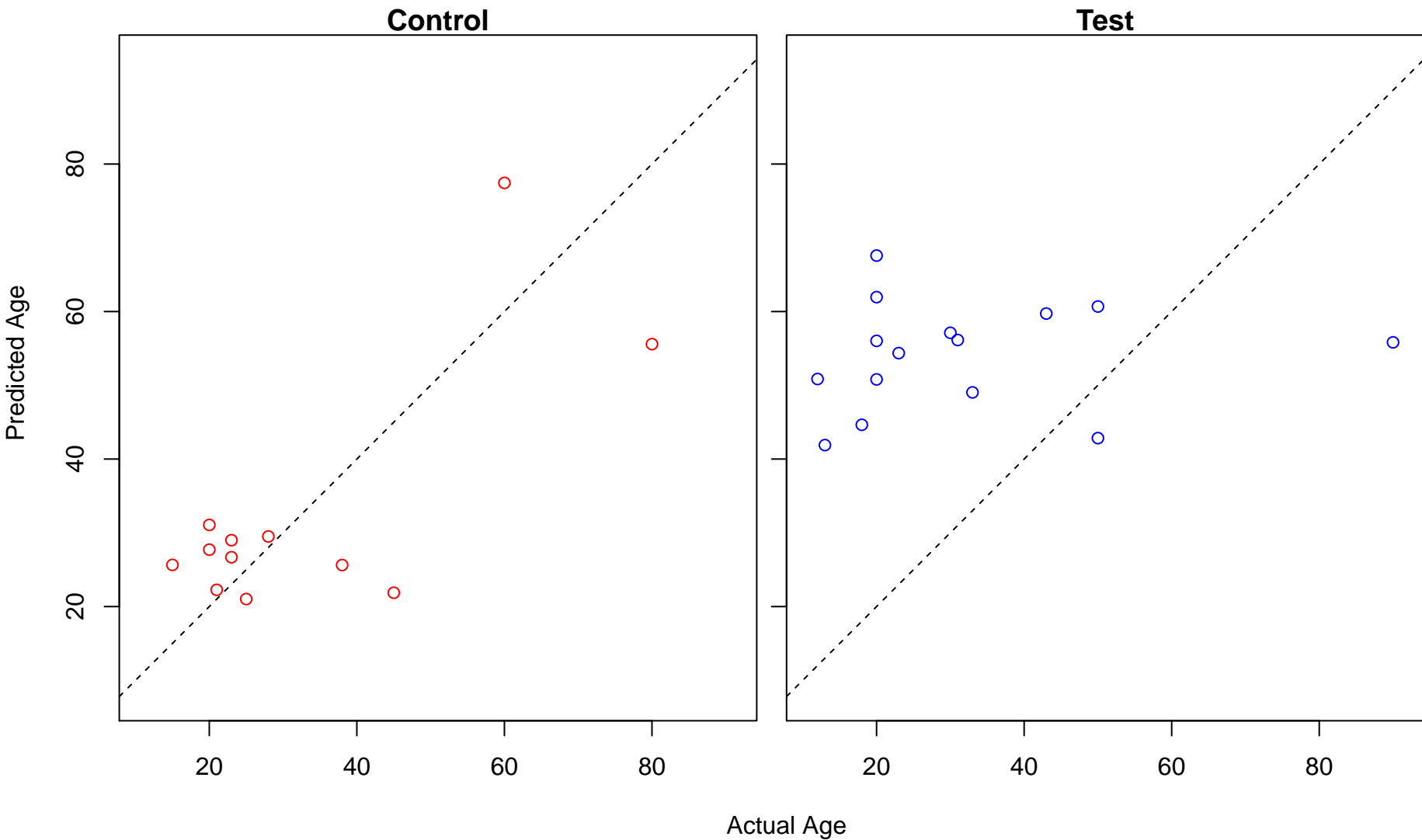
mitochondrial respiratory chain complex III assembly (Score: 2.395416)



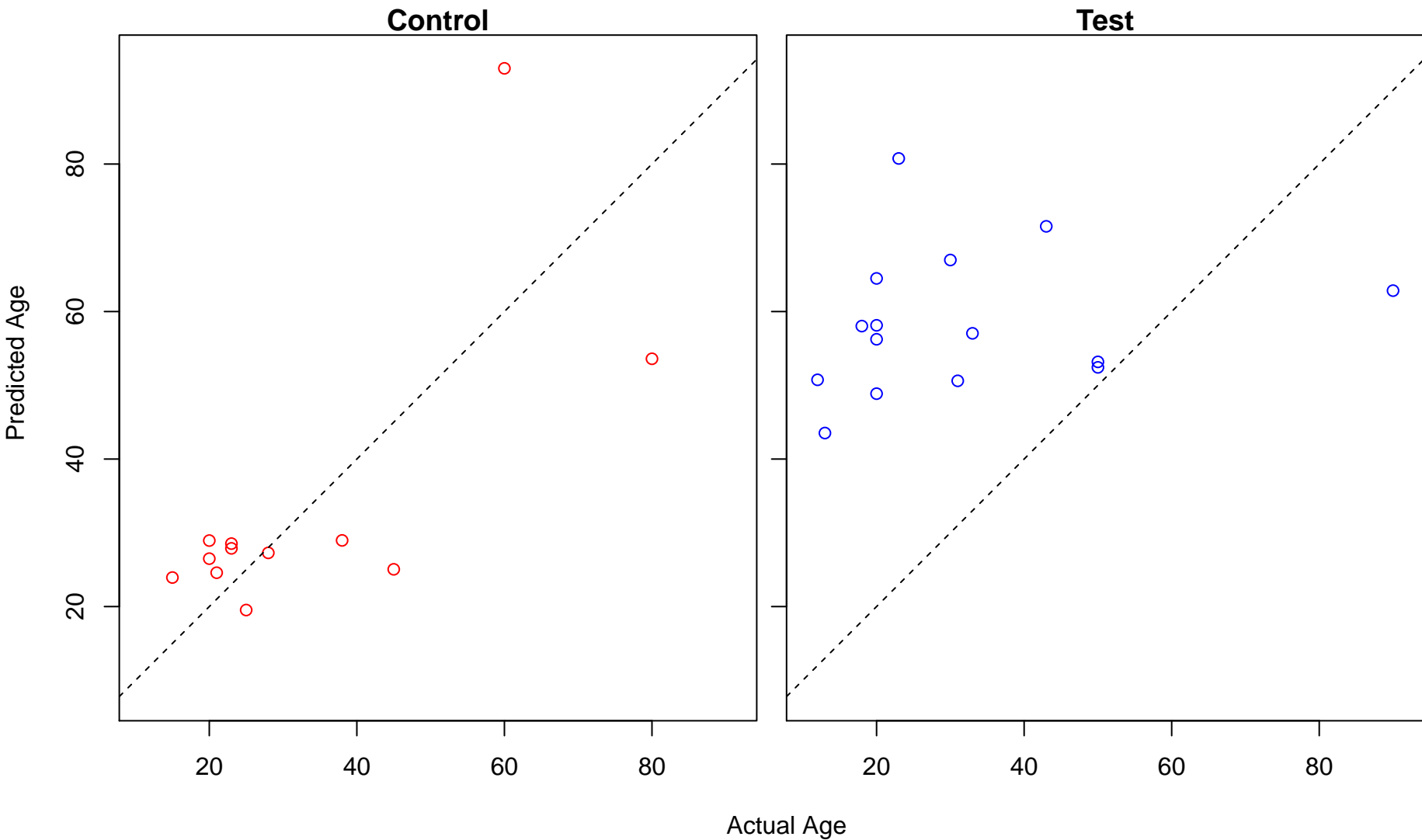
mitochondrial respiratory chain complex III biogenesis (Score: 2.395416)



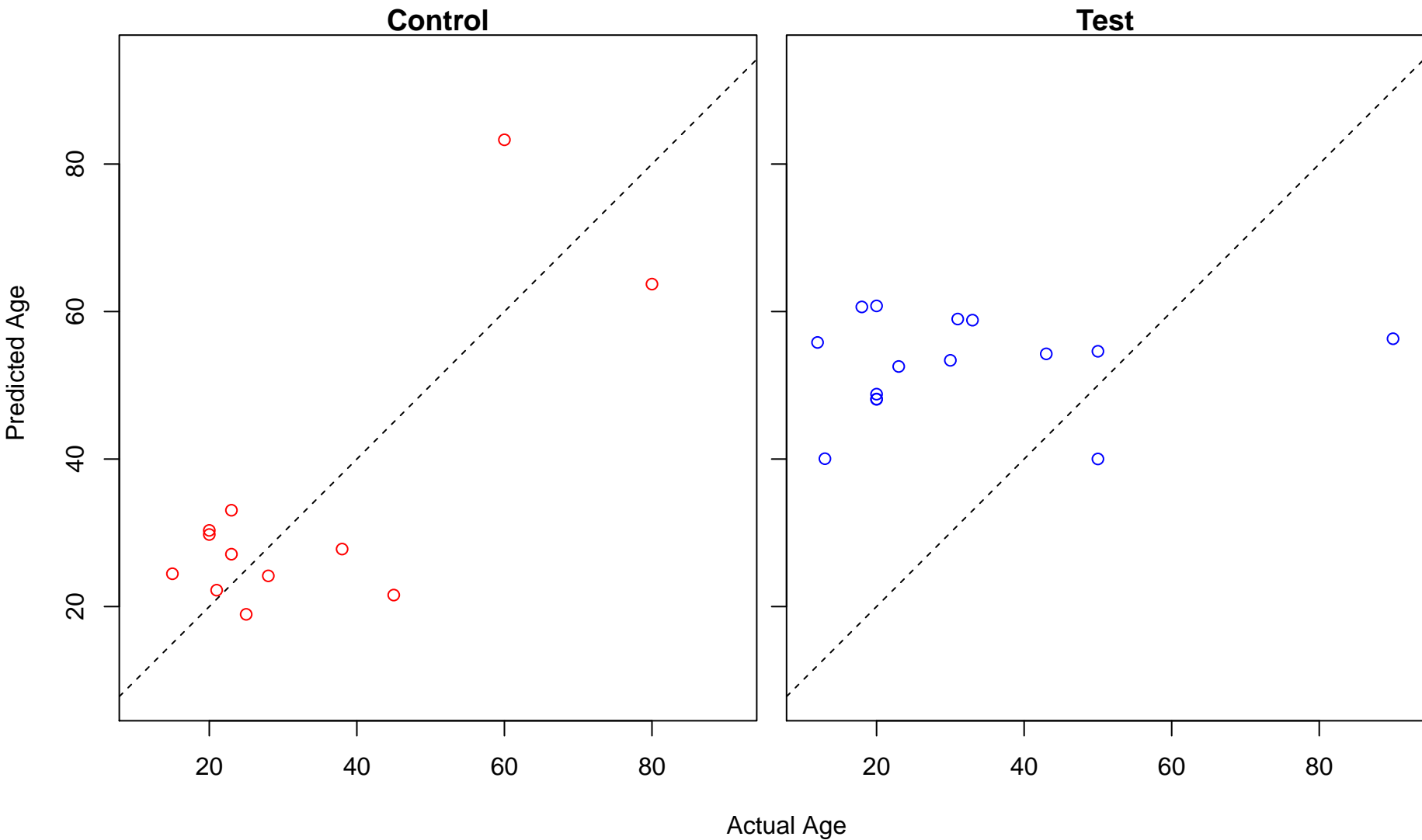
protein localization to cilium (Score: 2.392604)



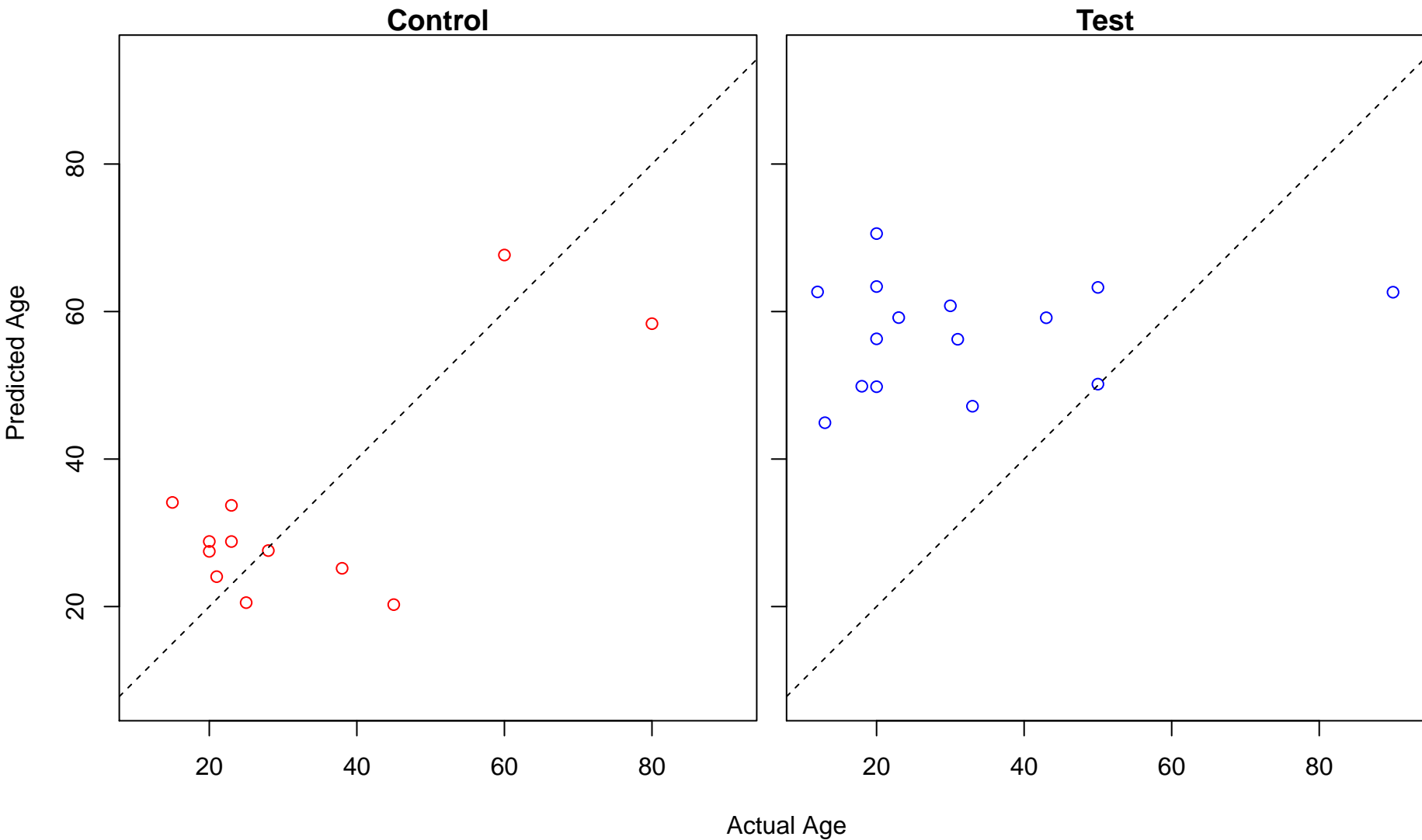
nose development (Score: 2.383474)



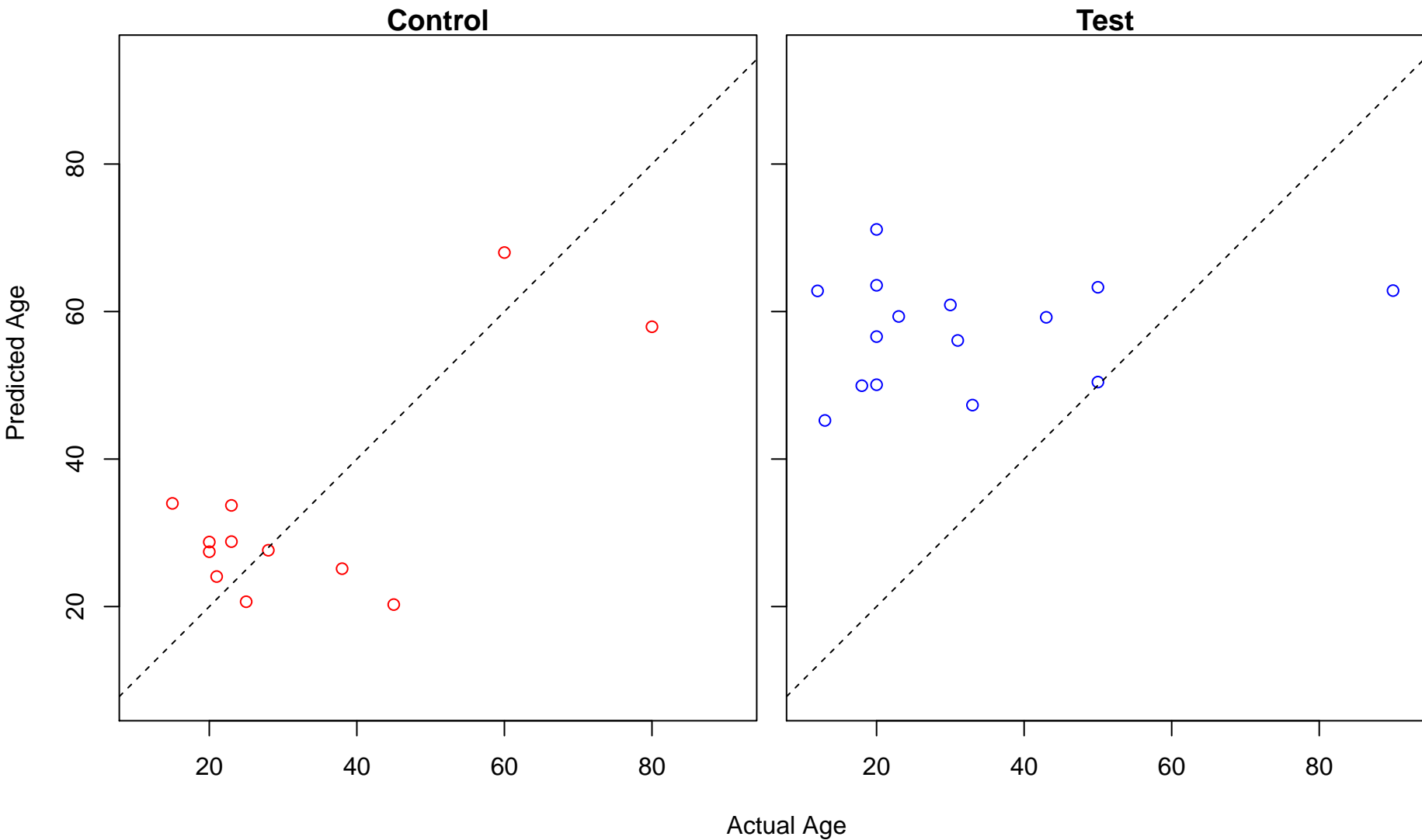
DNA damage induced protein phosphorylation (Score: 2.378239)



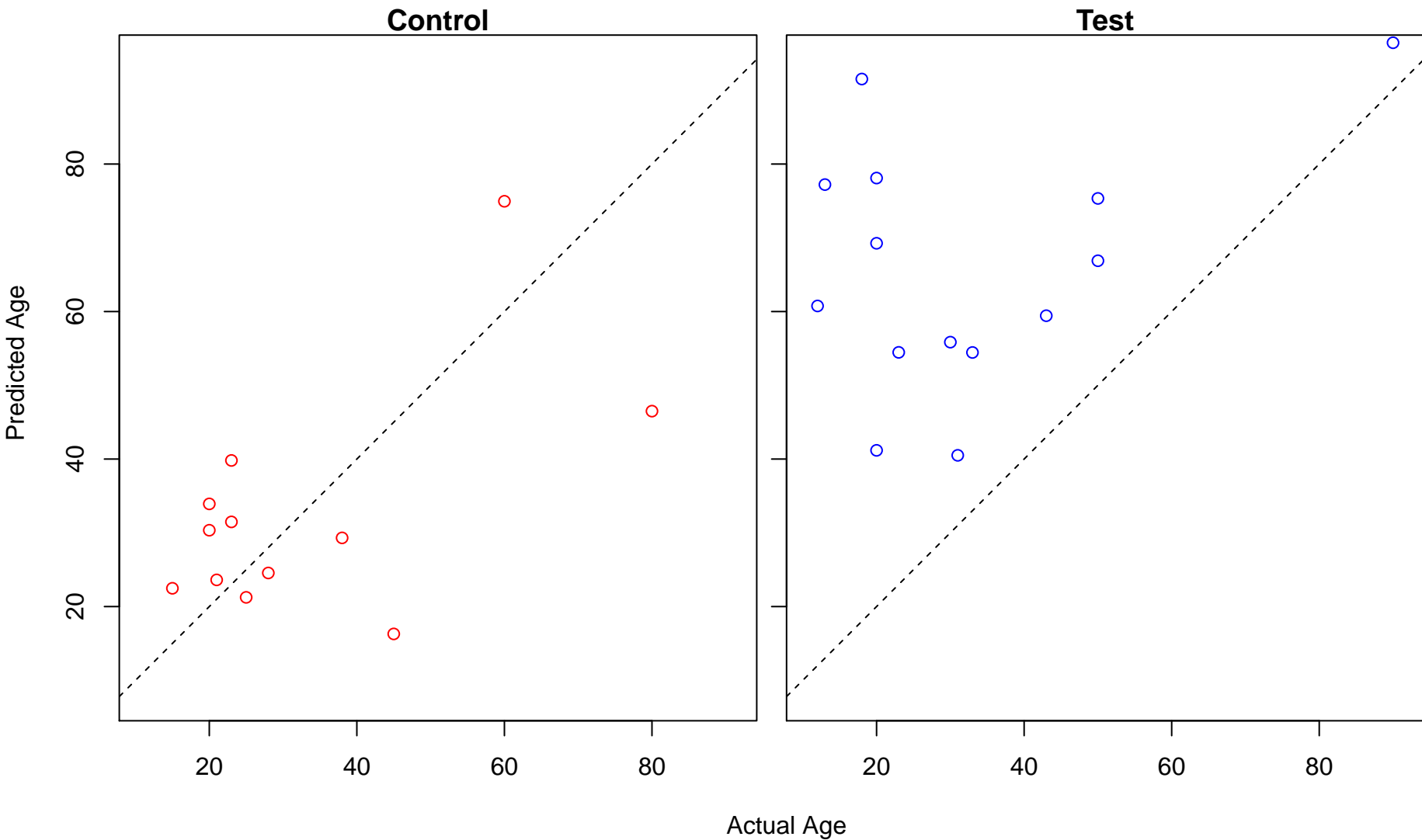
iron ion homeostasis (Score: 2.375086)



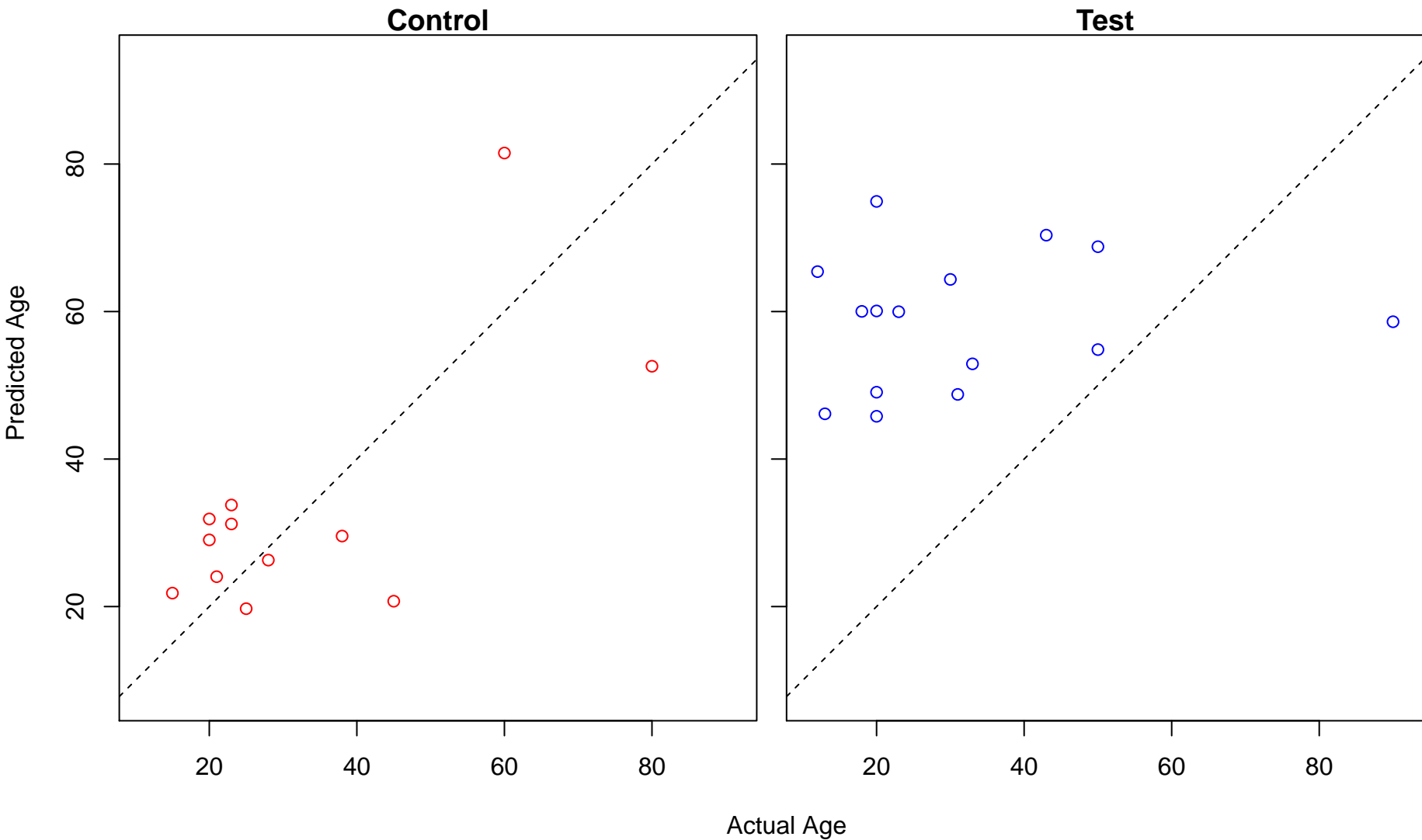
cellular iron ion homeostasis (Score: 2.374882)



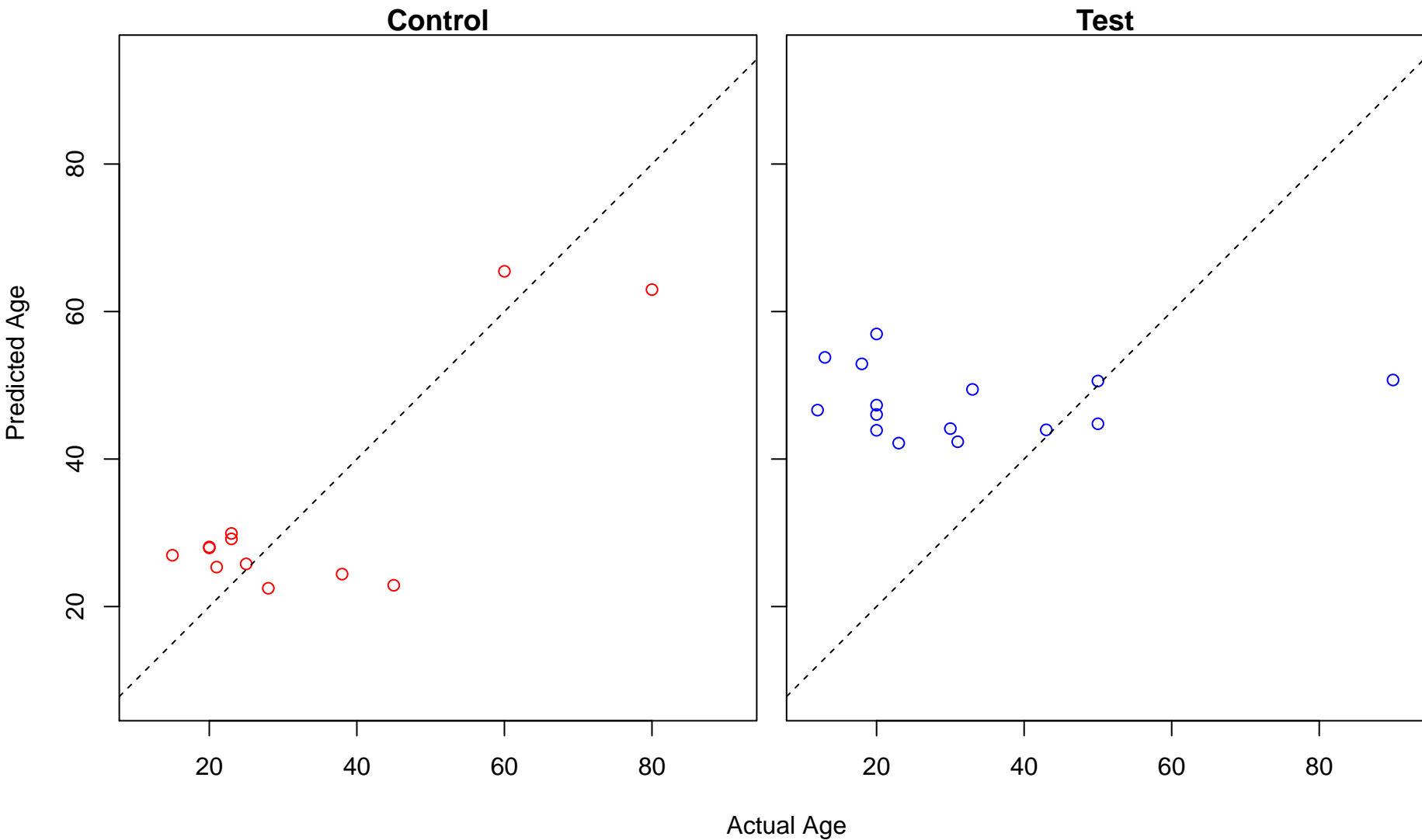
endochondral bone growth (Score: 2.361841)



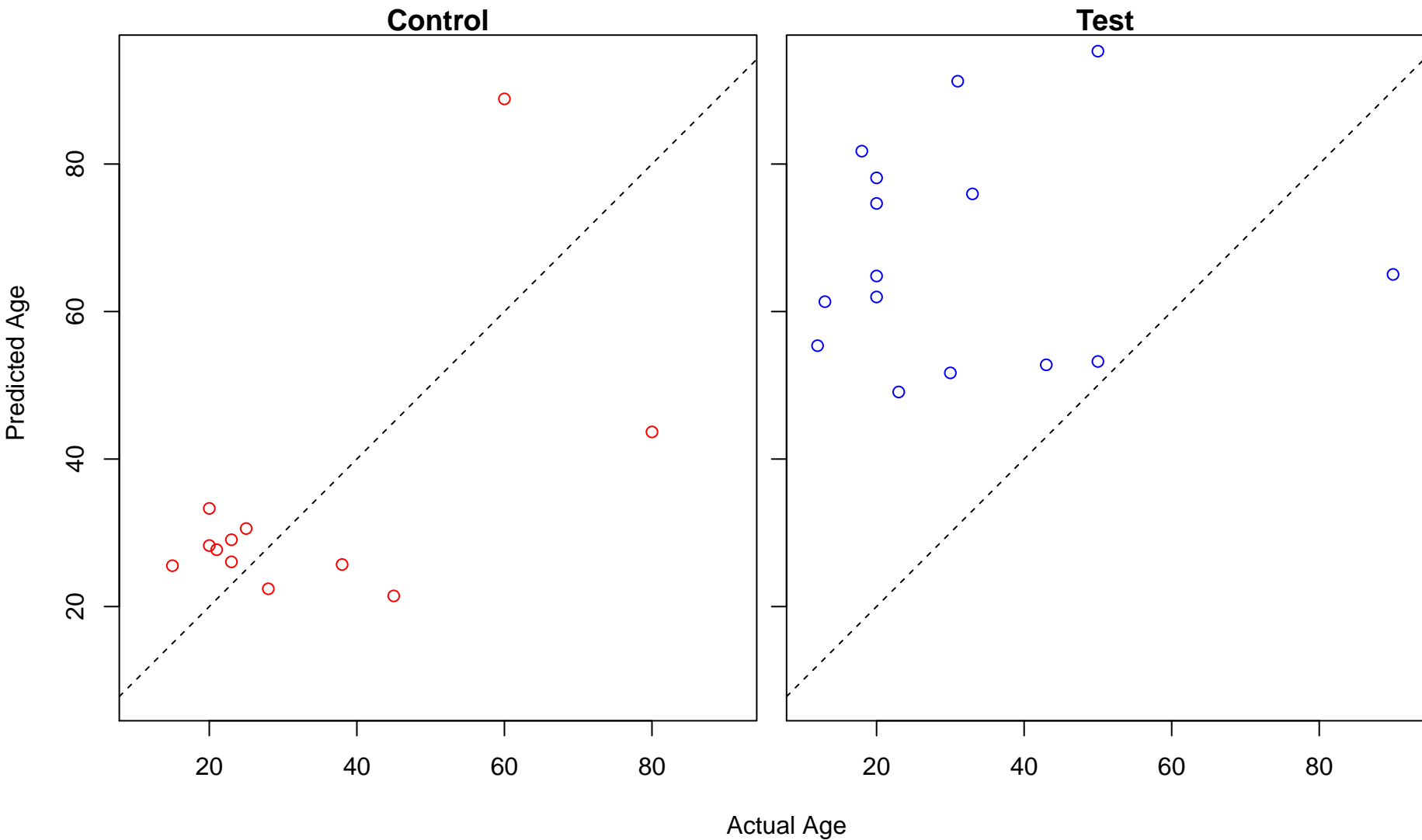
lymph vessel morphogenesis (Score: 2.357862)



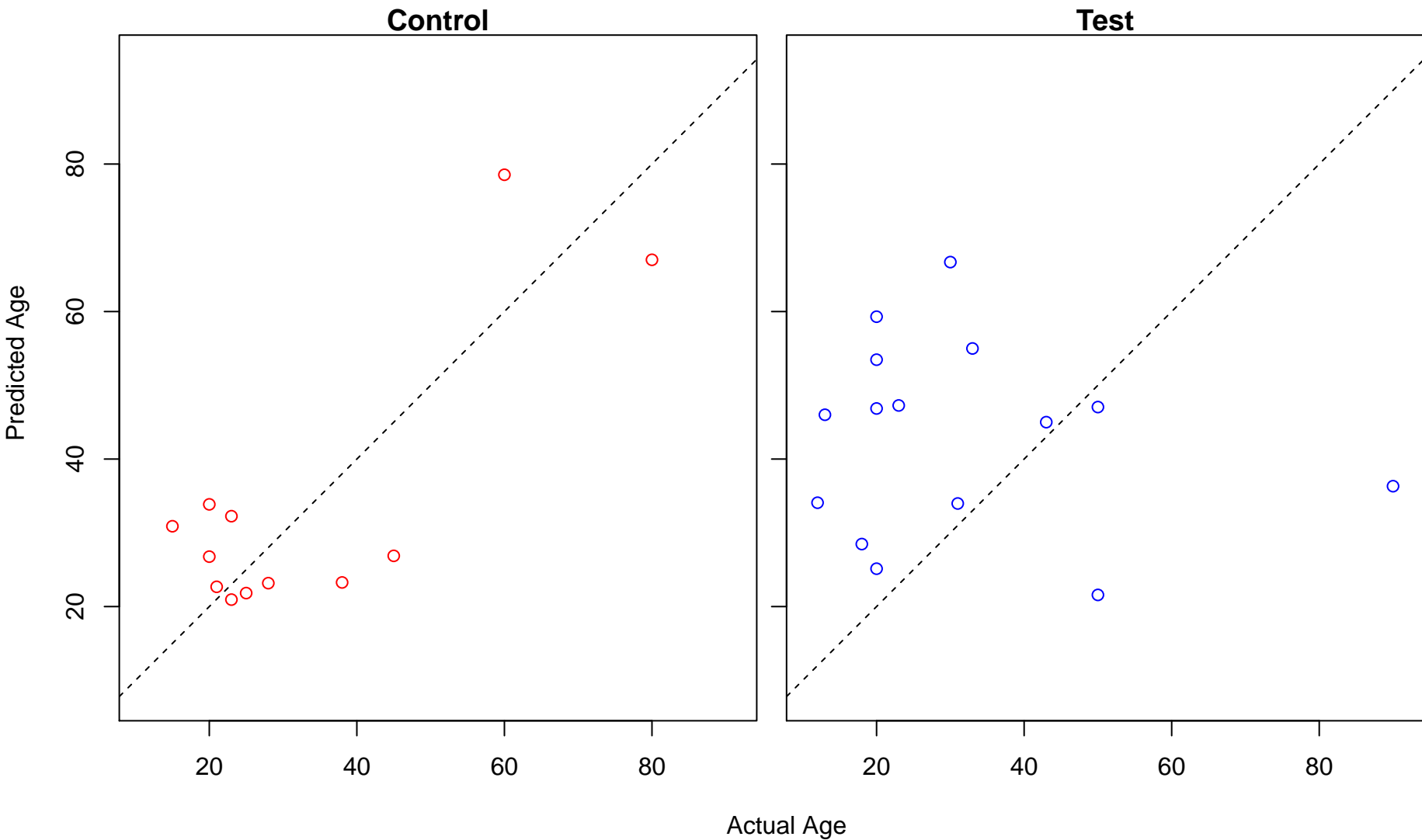
negative regulation of granulocyte differentiation (Score: 2.340385)



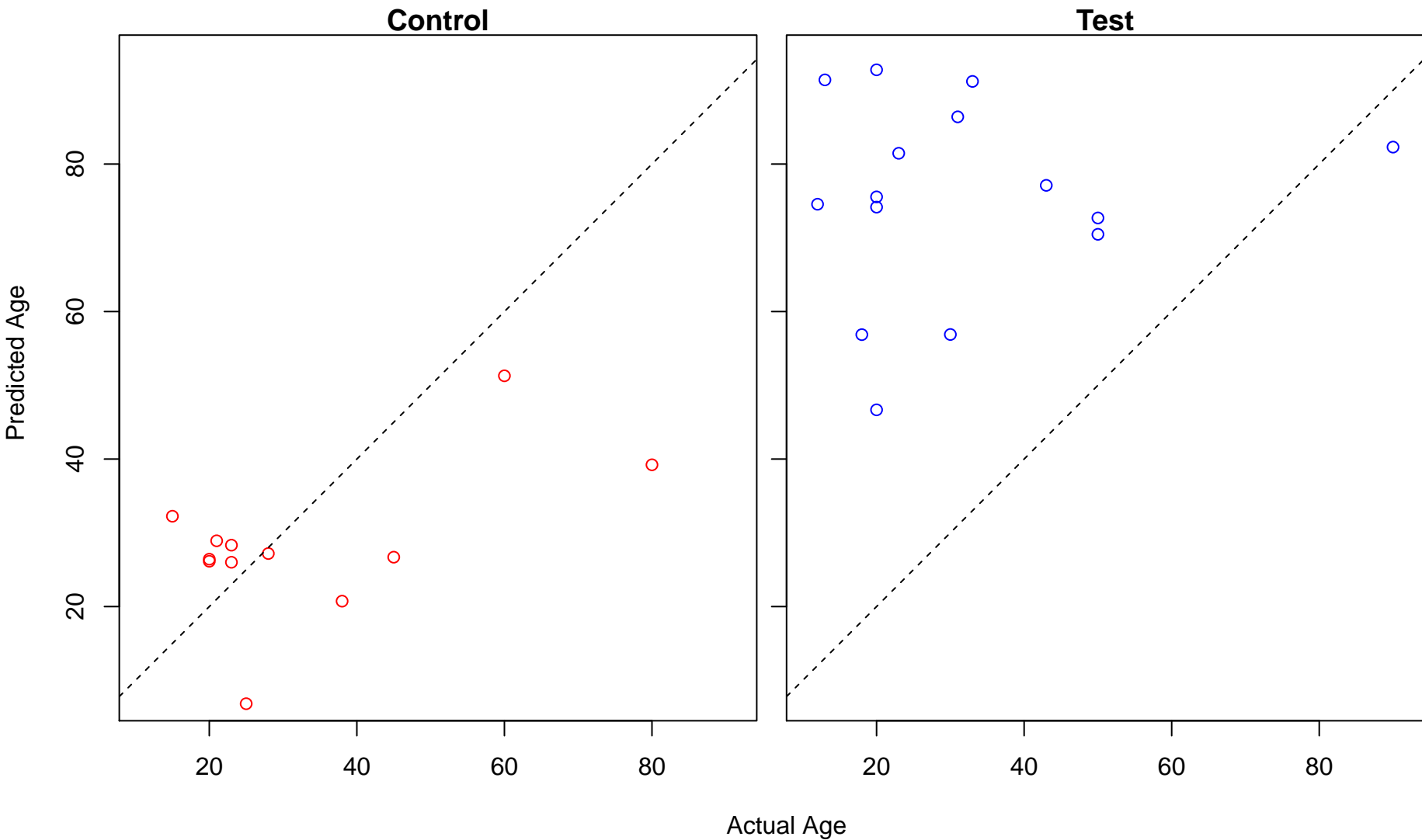
activation of transmembrane receptor protein tyrosine kinase activity (Score: 2.335661)



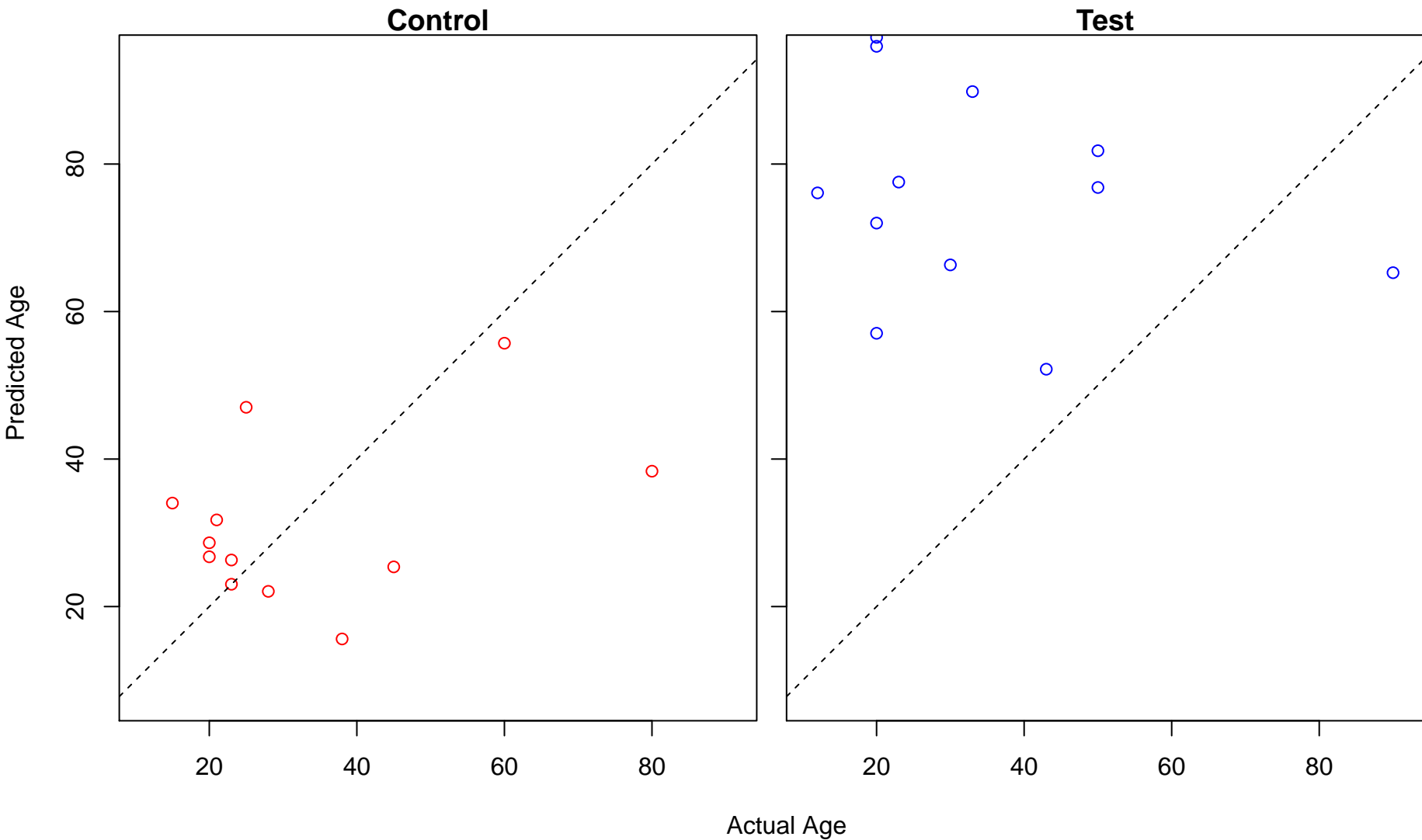
negative regulation of triglyceride metabolic process (Score: 2.306980)



receptor guanylyl cyclase signaling pathway (Score: 2.302157)

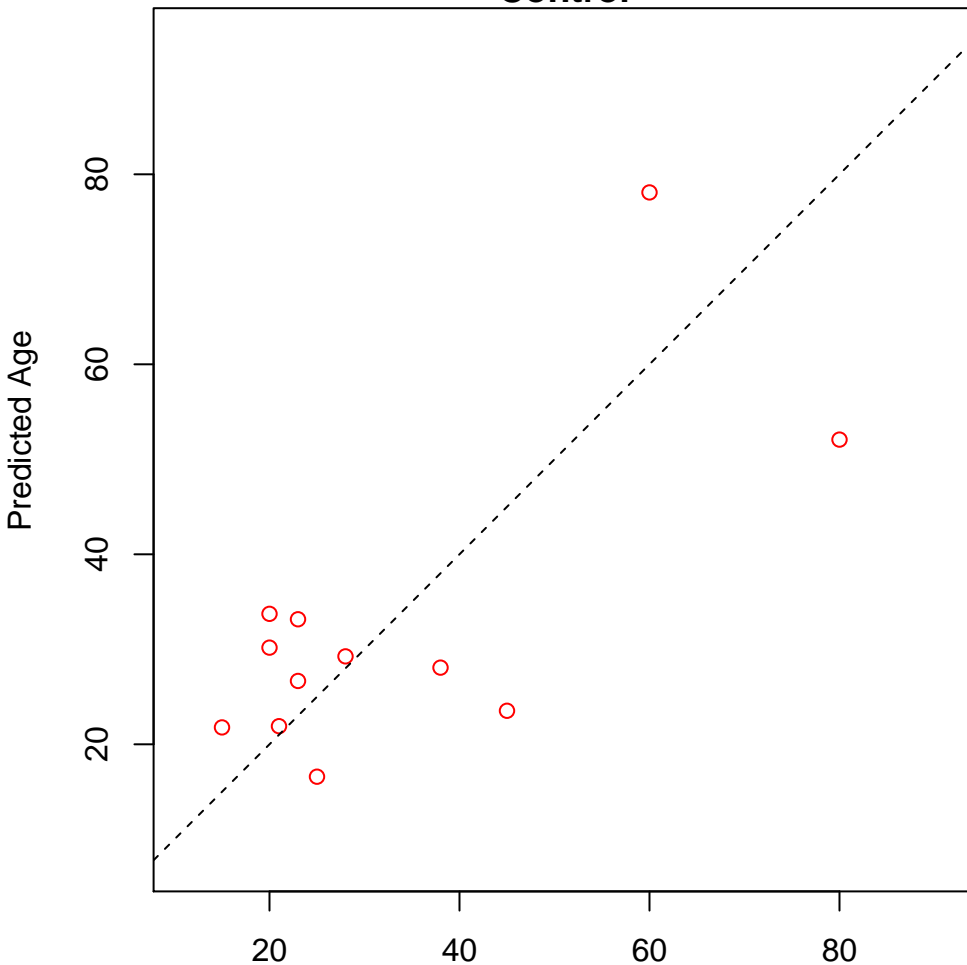


T-helper cell lineage commitment (Score: 2.280420)

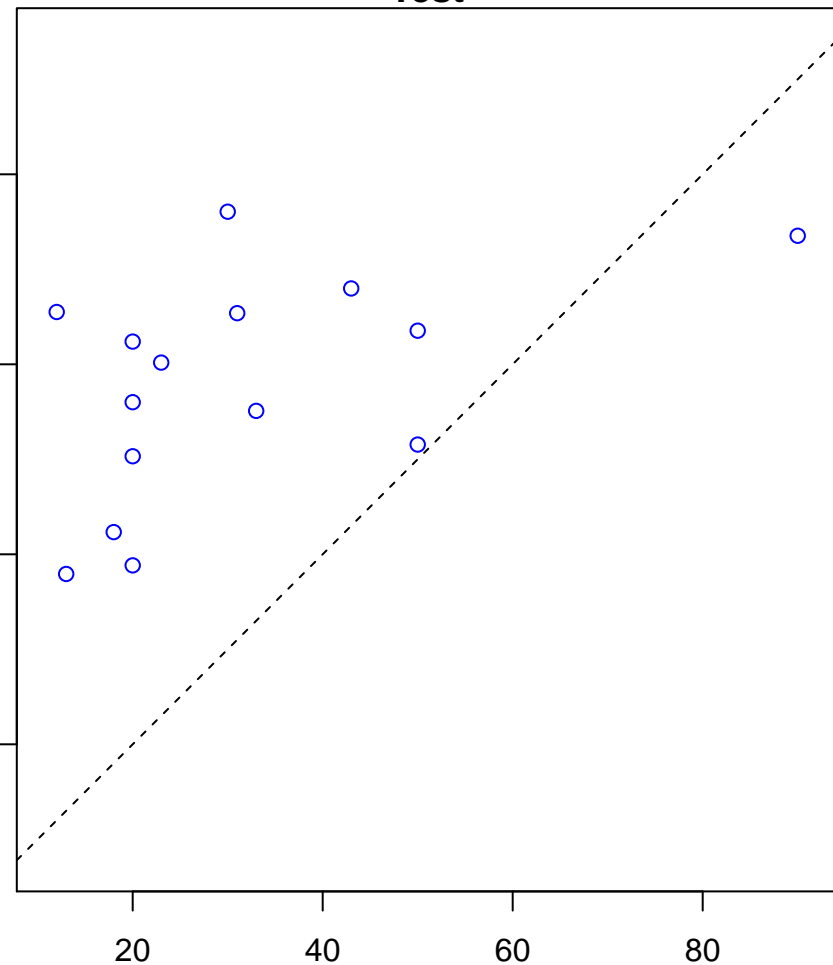


eye photoreceptor cell development (Score: 2.250057)

Control

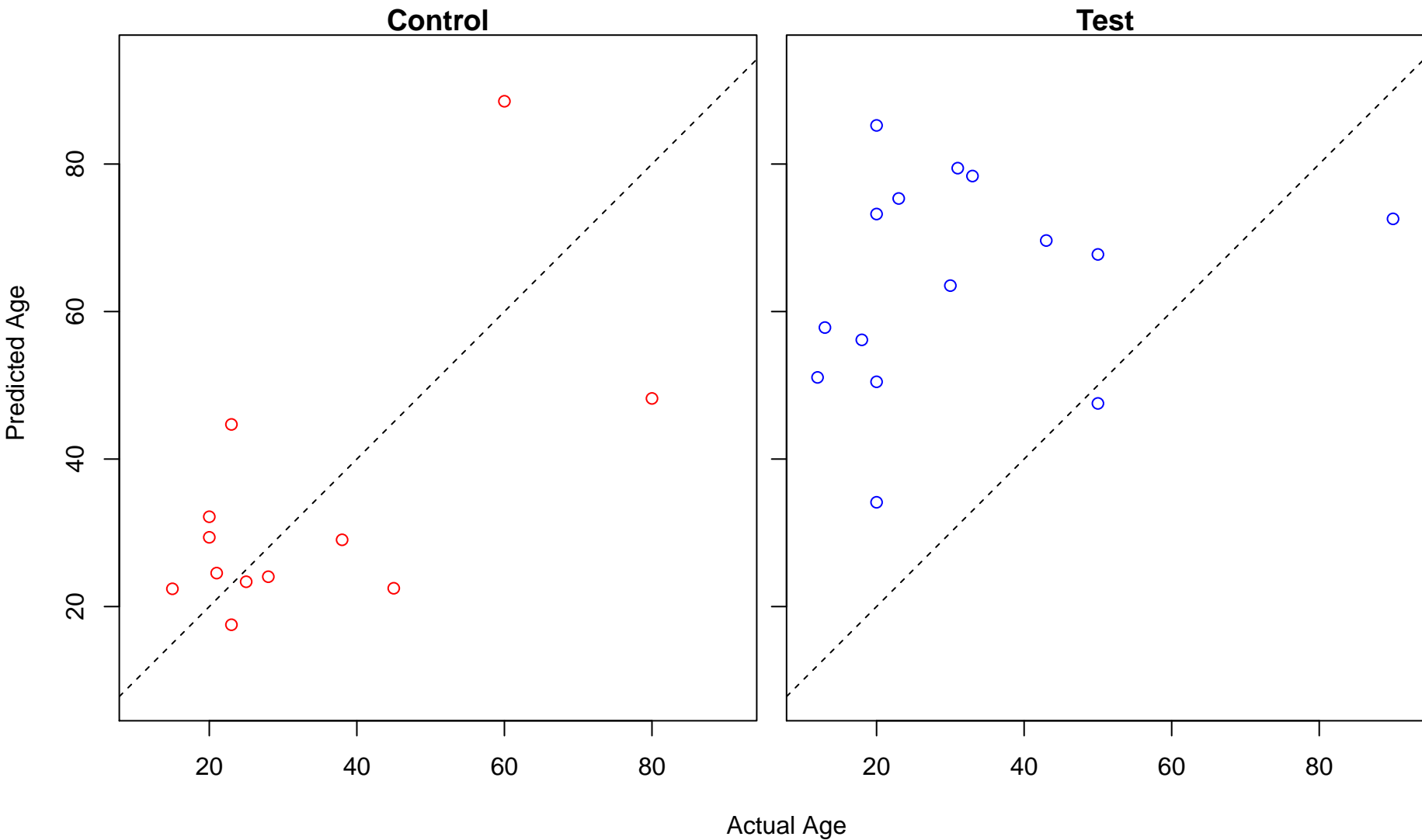


Test

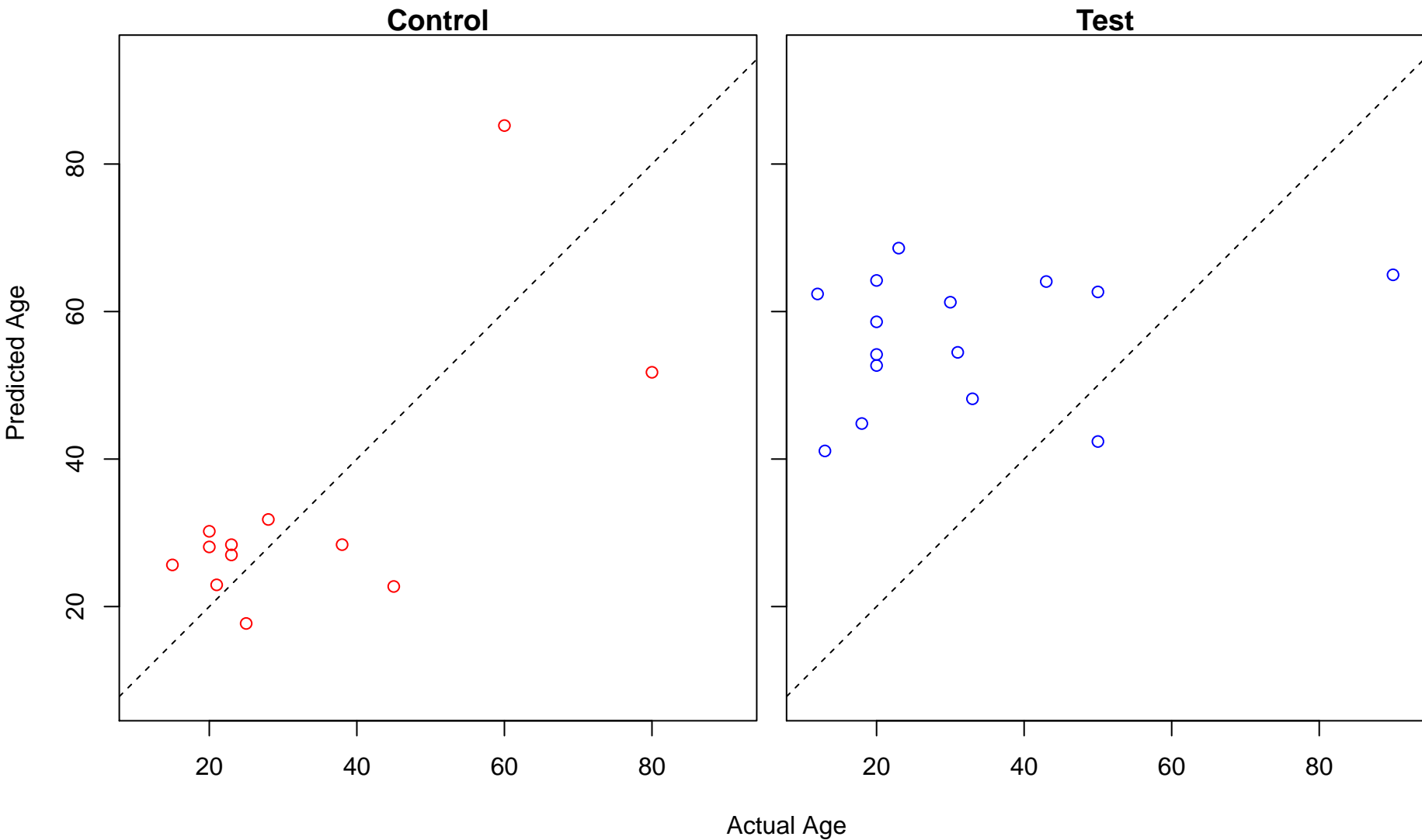


Actual Age

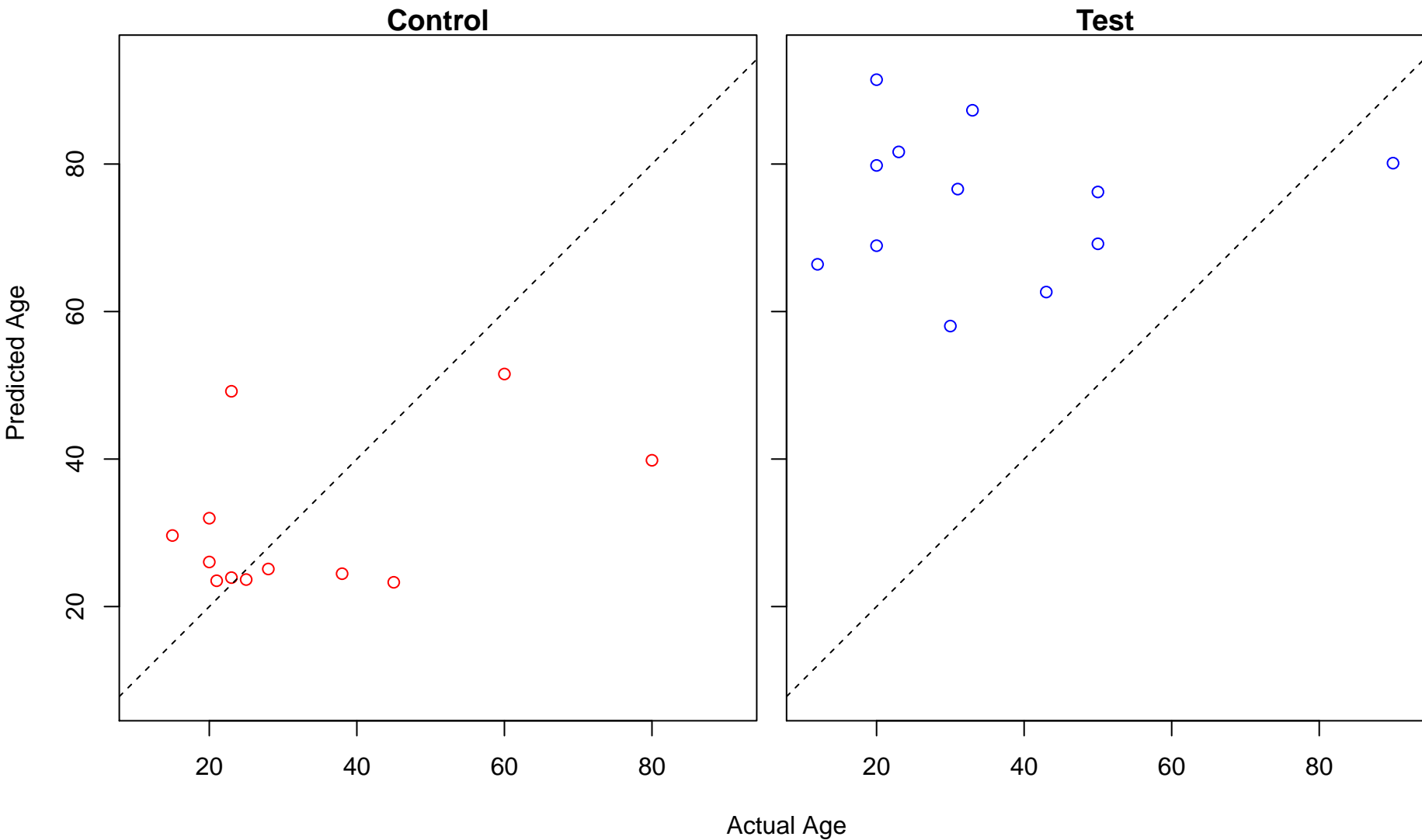
exogenous drug catabolic process (Score: 2.242417)



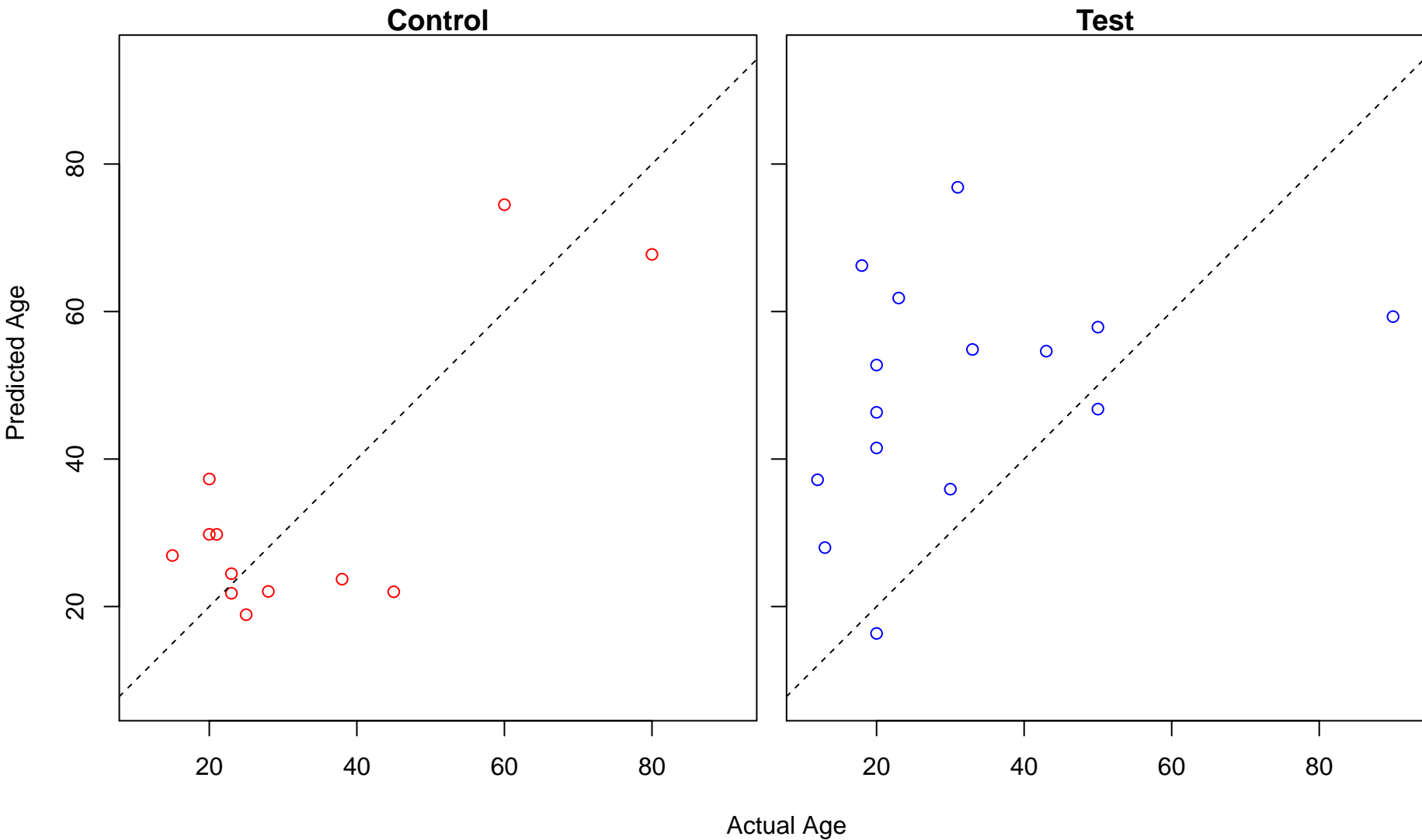
regulation of response to food (Score: 2.187085)



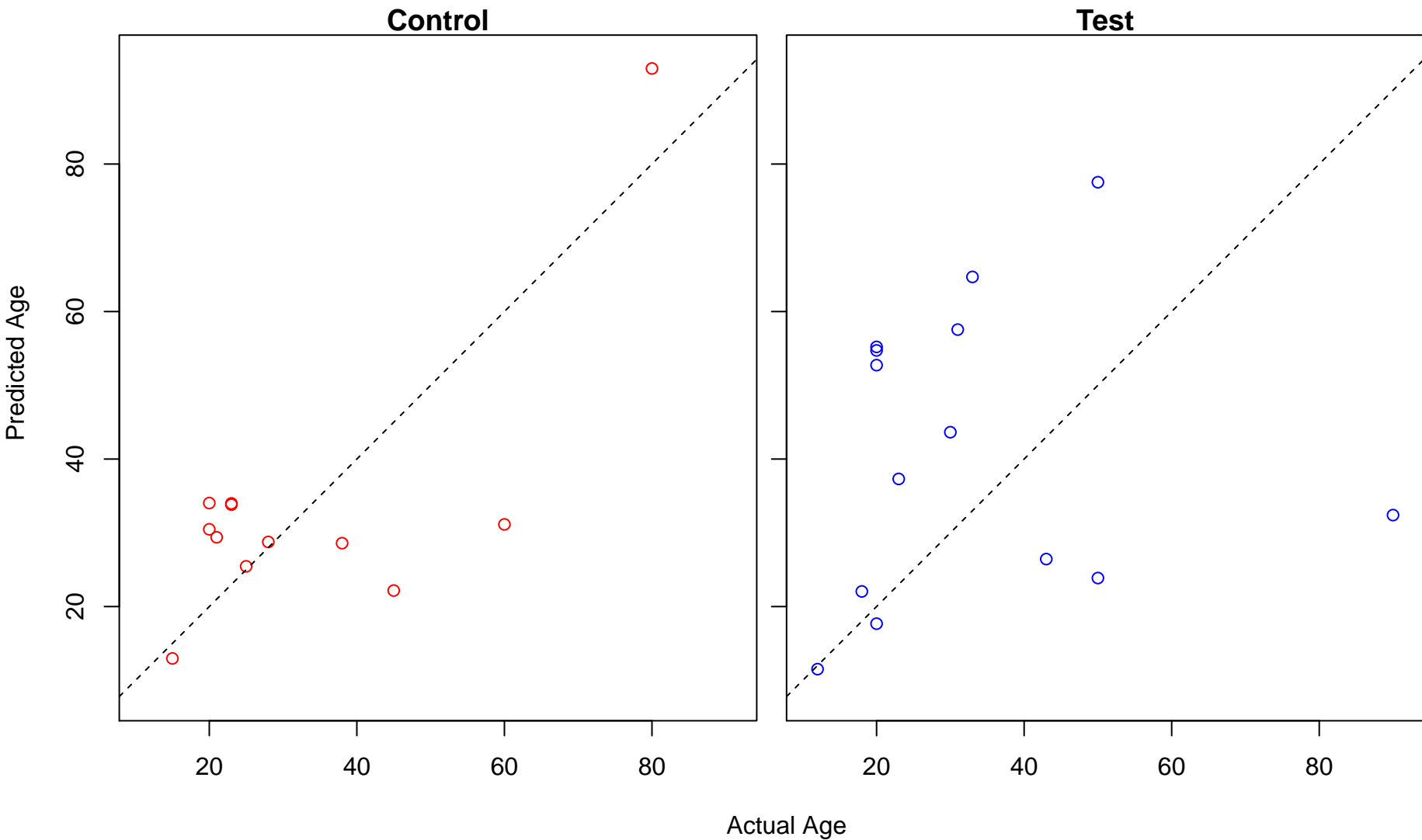
complement activation, classical pathway (Score: 2.186716)



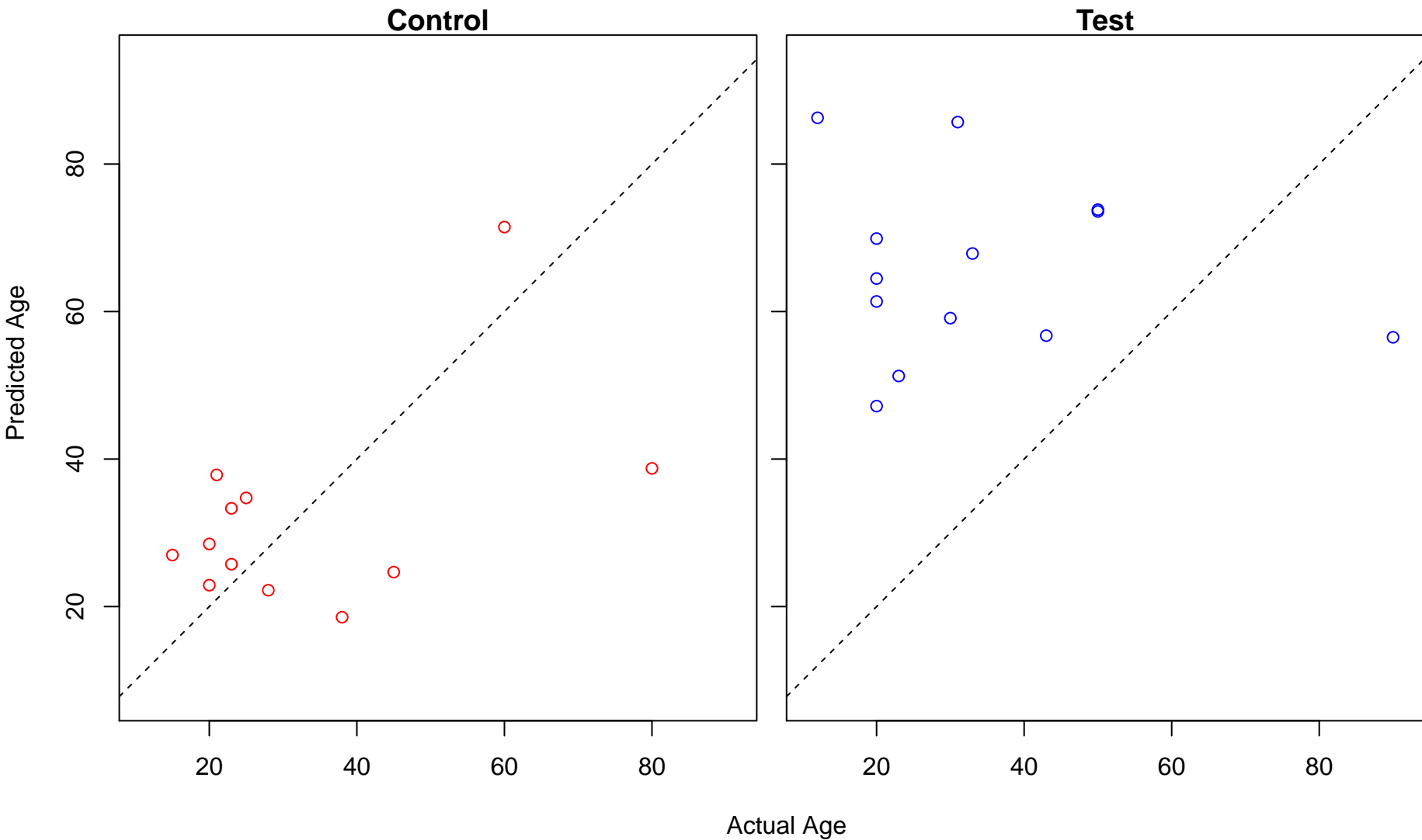
intermediate filament organization (Score: 2.150013)



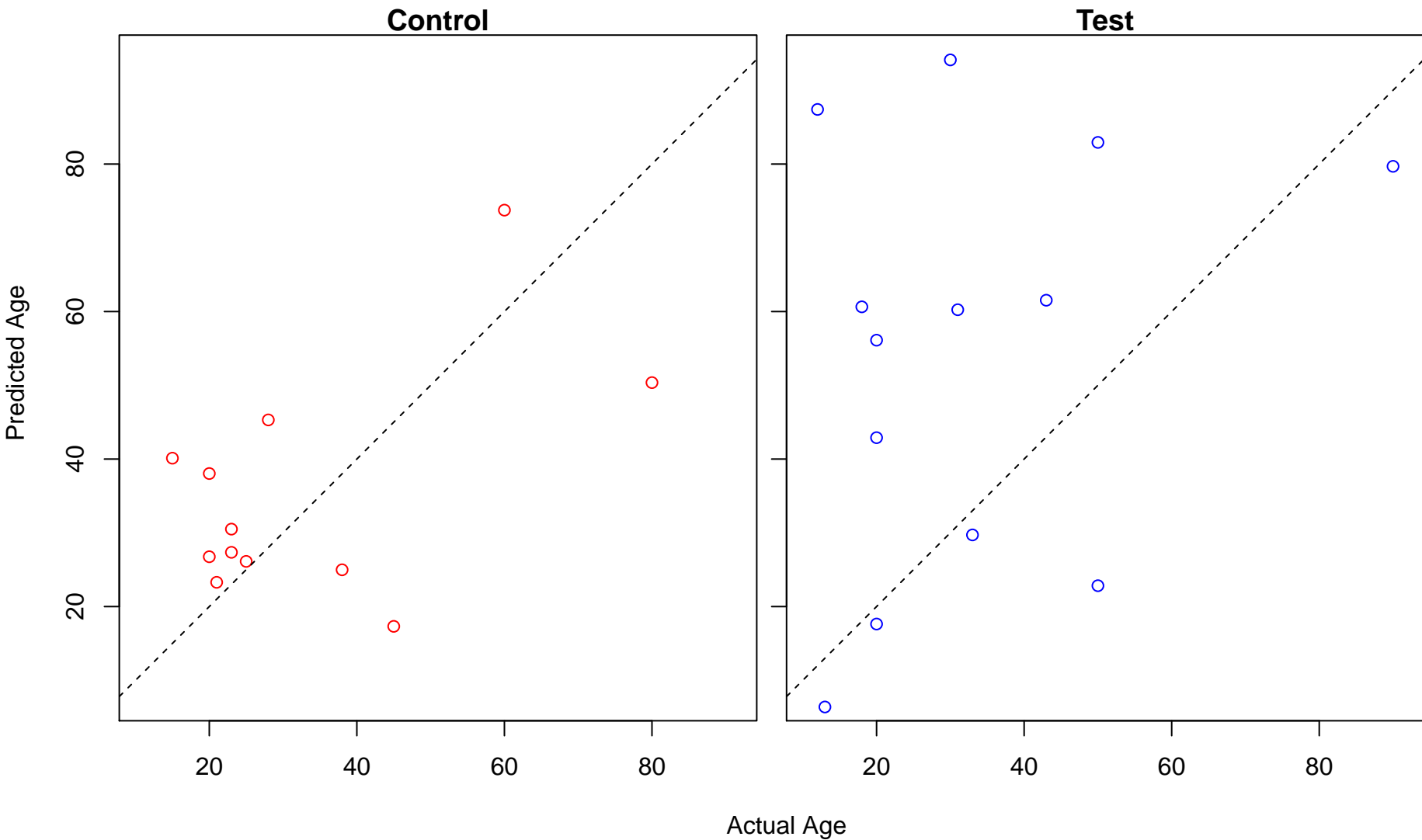
transcription, RNA-templated (Score: 2.081496)



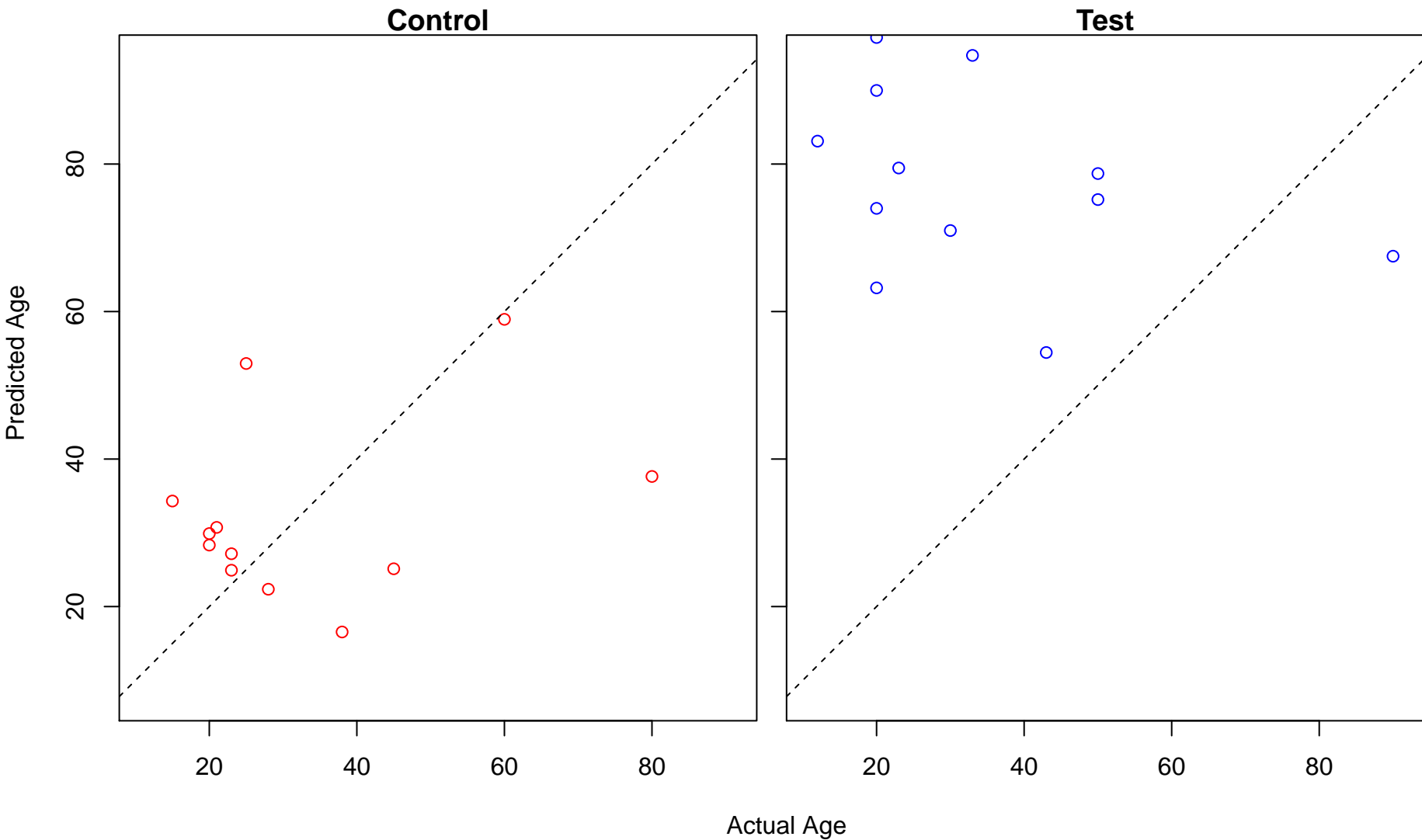
monoamine transport (Score: 2.021692)



regulation of amine transport (Score: 2.015622)



positive T cell selection (Score: 1.798487)



neuronal ion channel clustering (Score: 1.735409)

