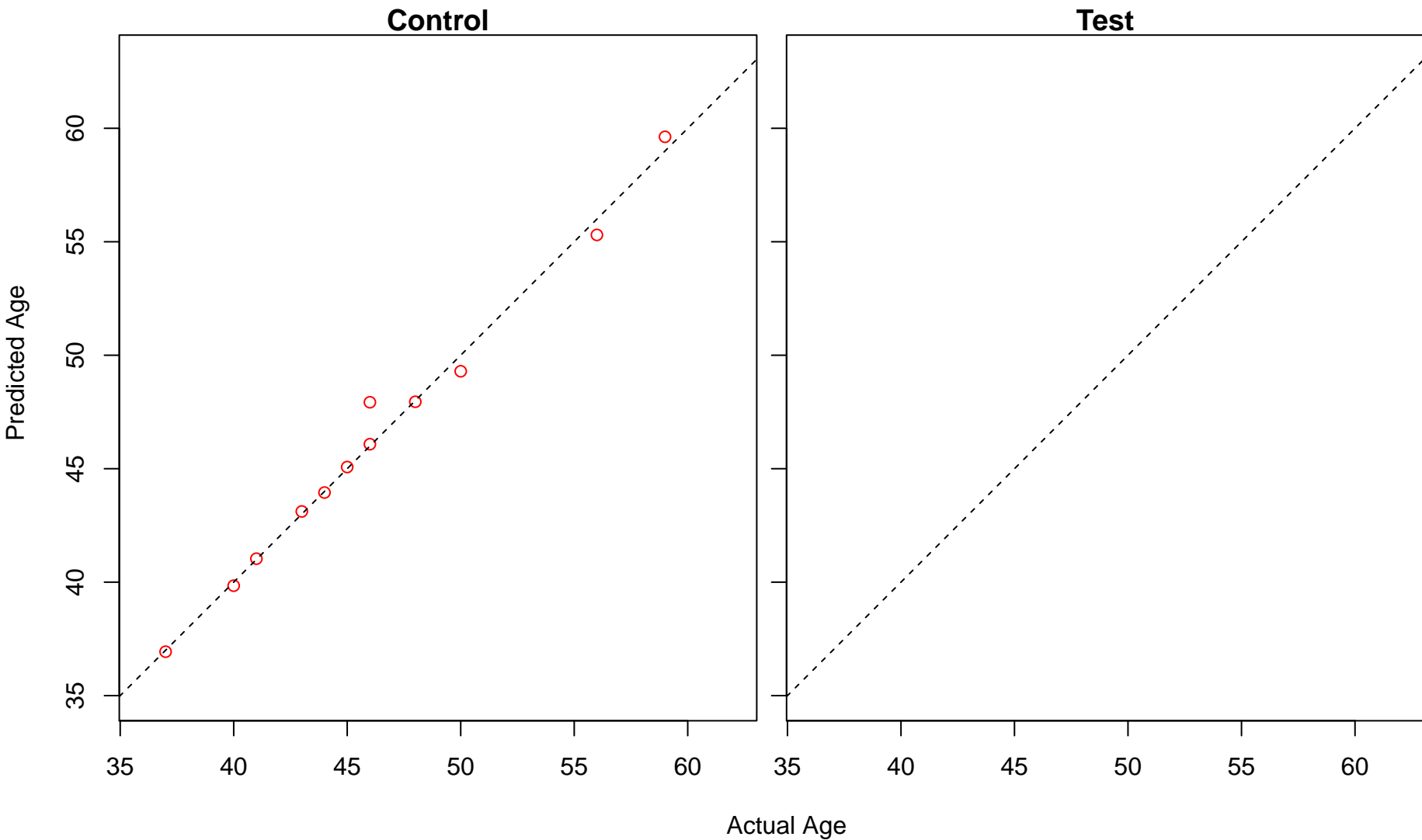
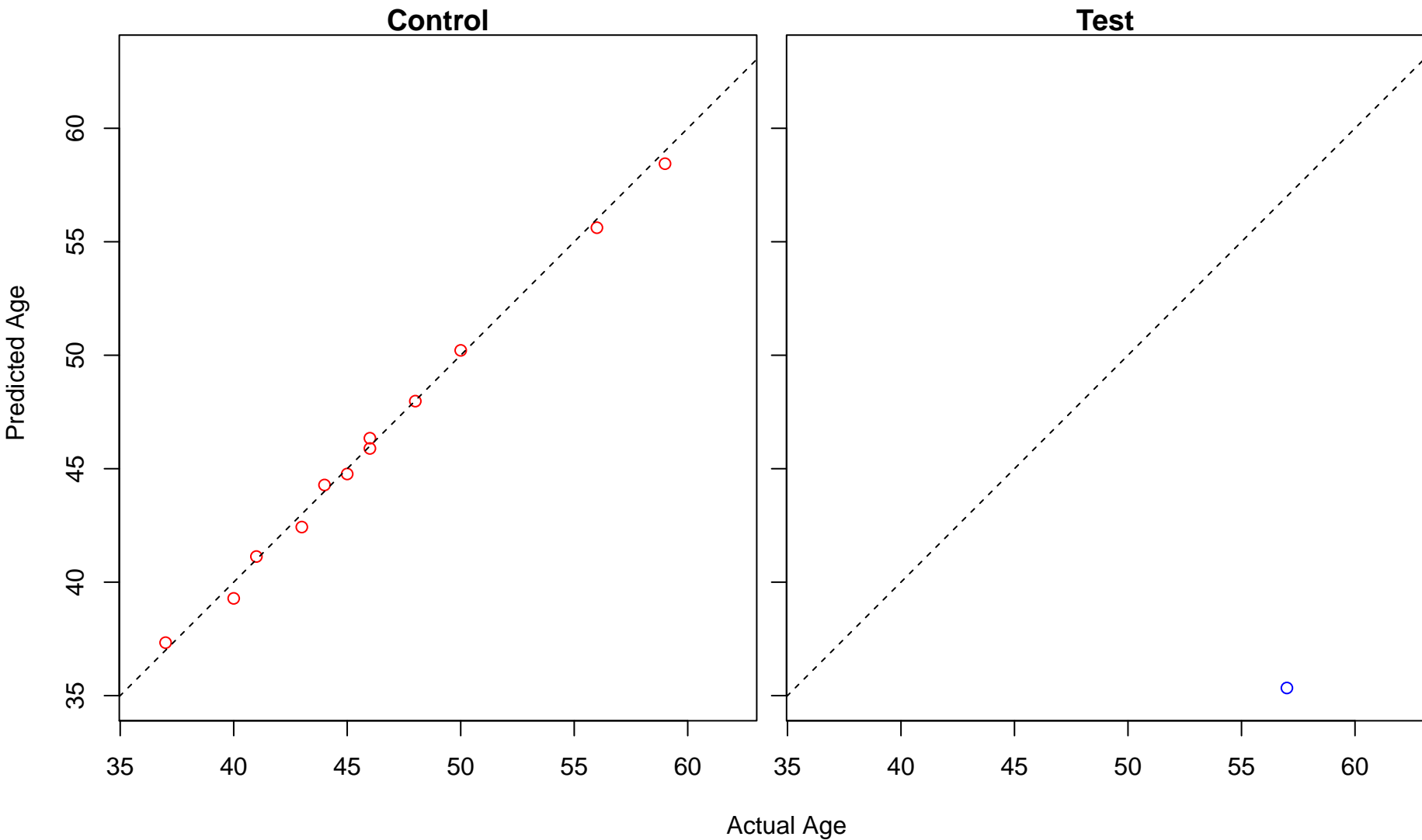


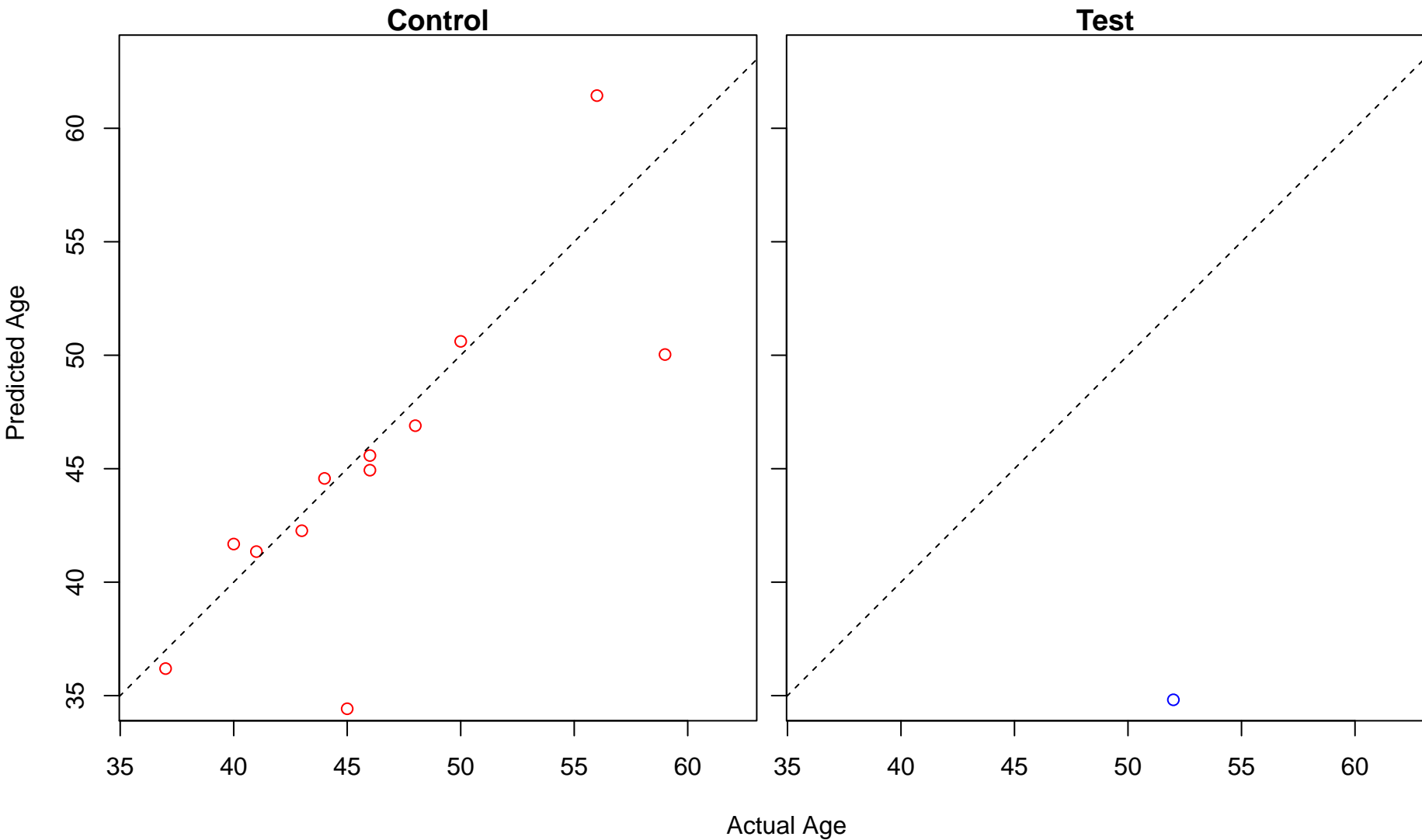
alanine transport (Score: 305.976955)



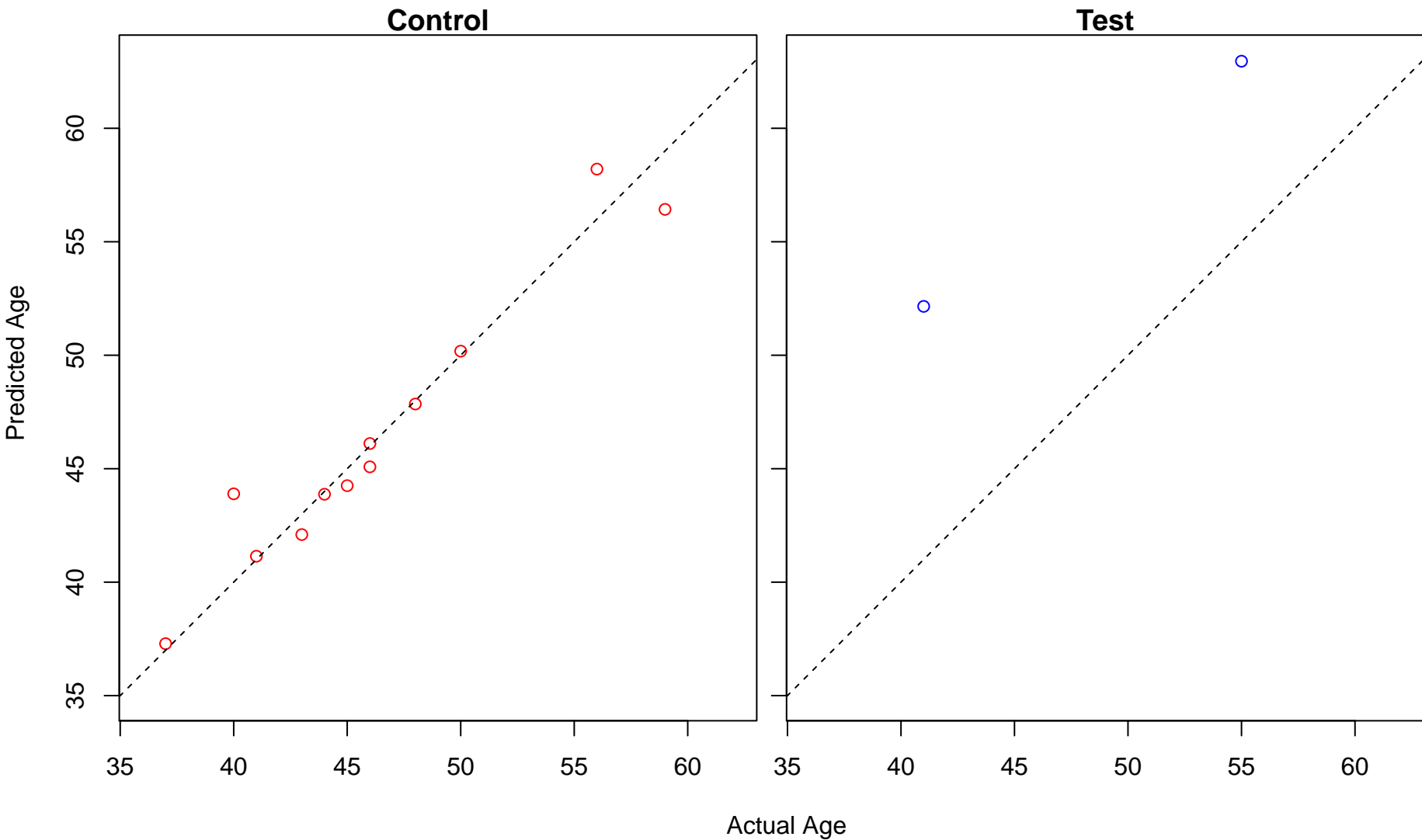
positive regulation of interferon-gamma secretion (Score: 272.446822)



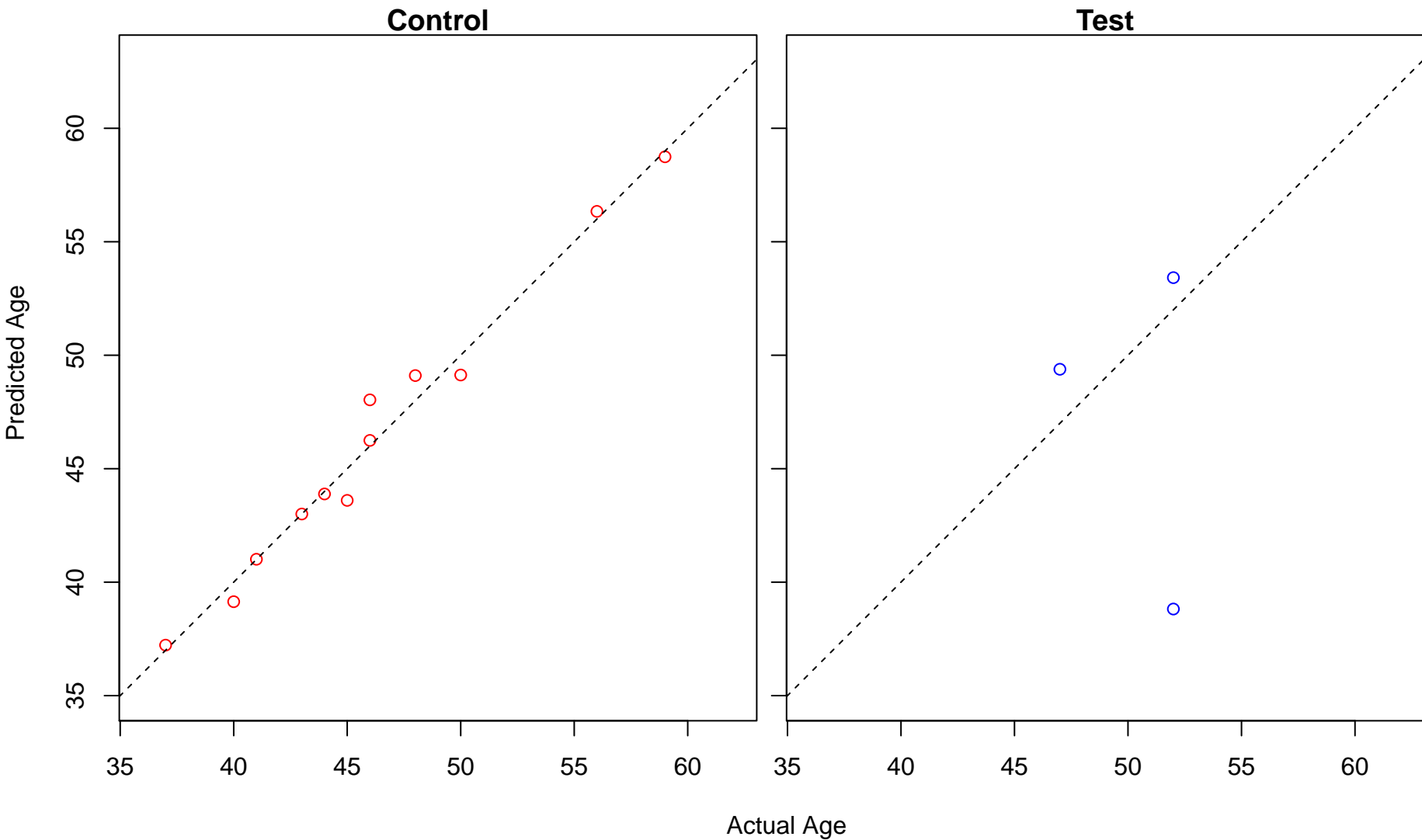
adult feeding behavior (Score: 221.132502)



positive regulation of phospholipid biosynthetic process (Score: 202.529932)

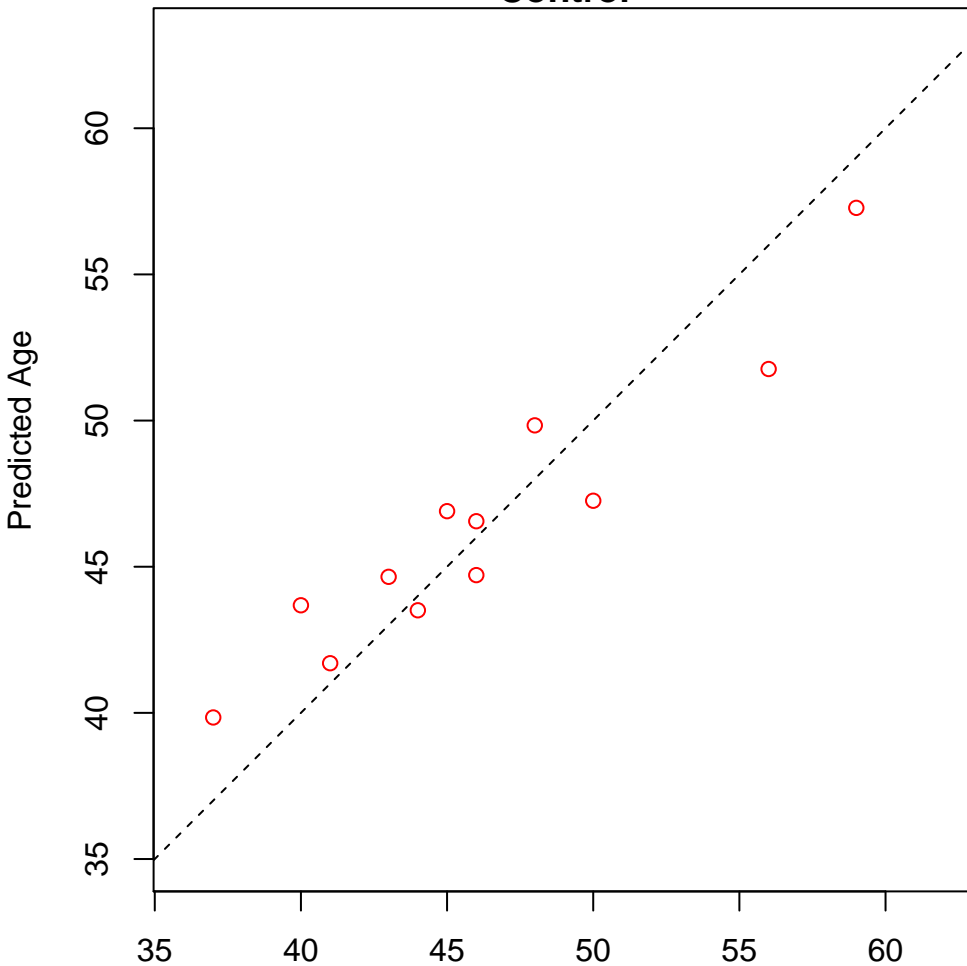


transcytosis (Score: 192.610731)

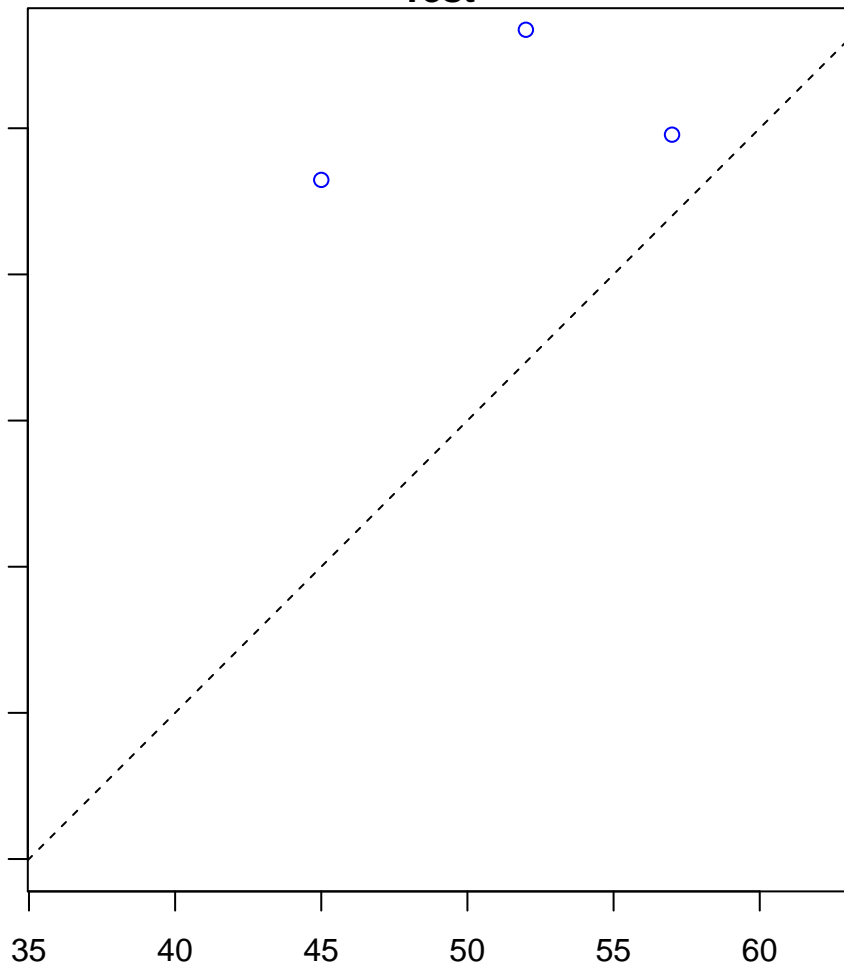


T-helper cell lineage commitment (Score: 183.348189)

Control



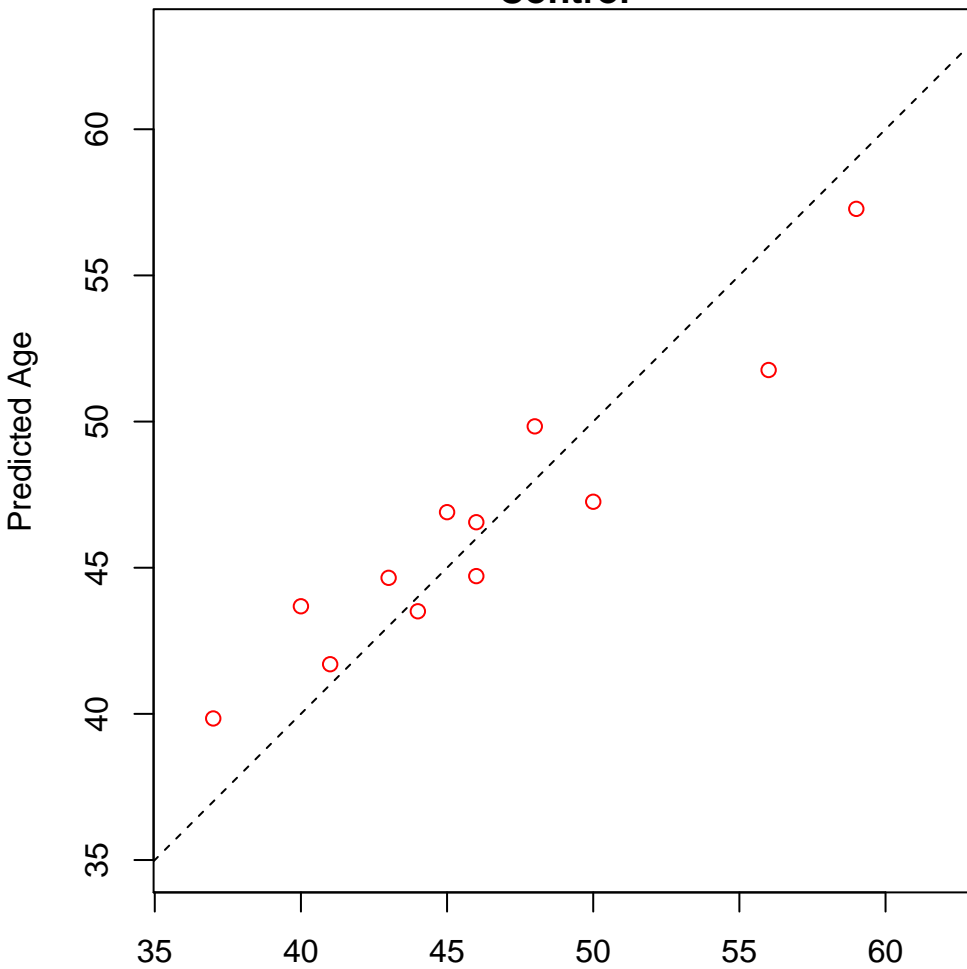
Test



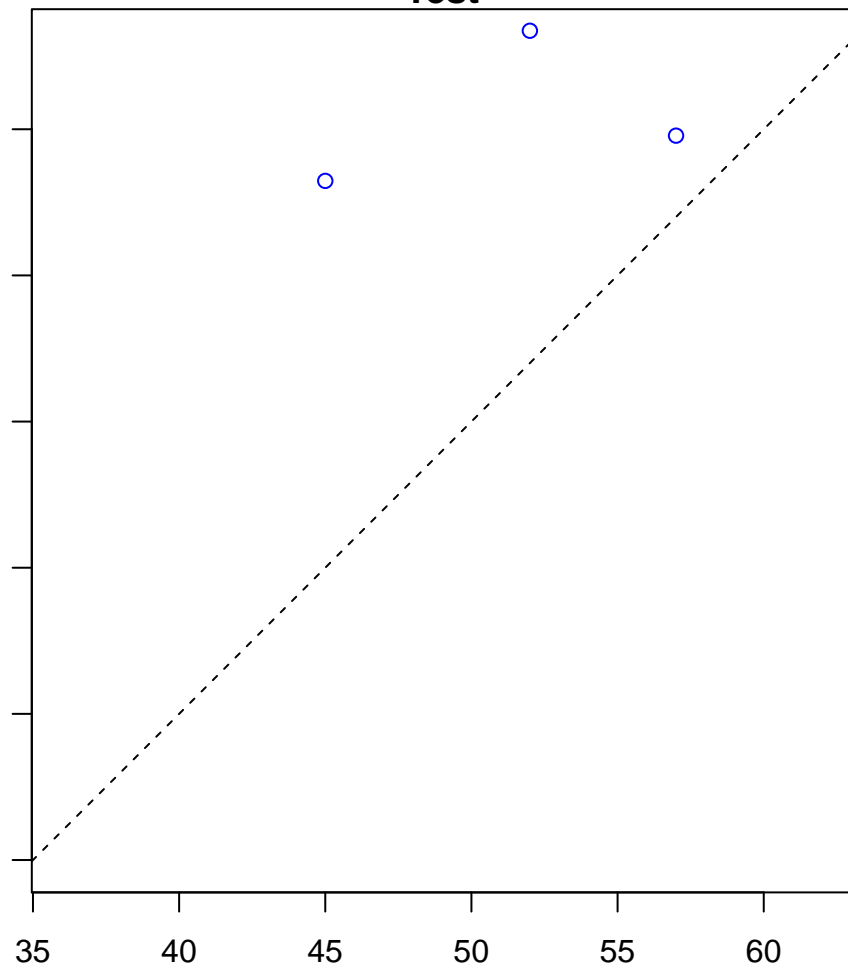
Actual Age

T-helper 17 cell lineage commitment (Score: 183.348189)

Control

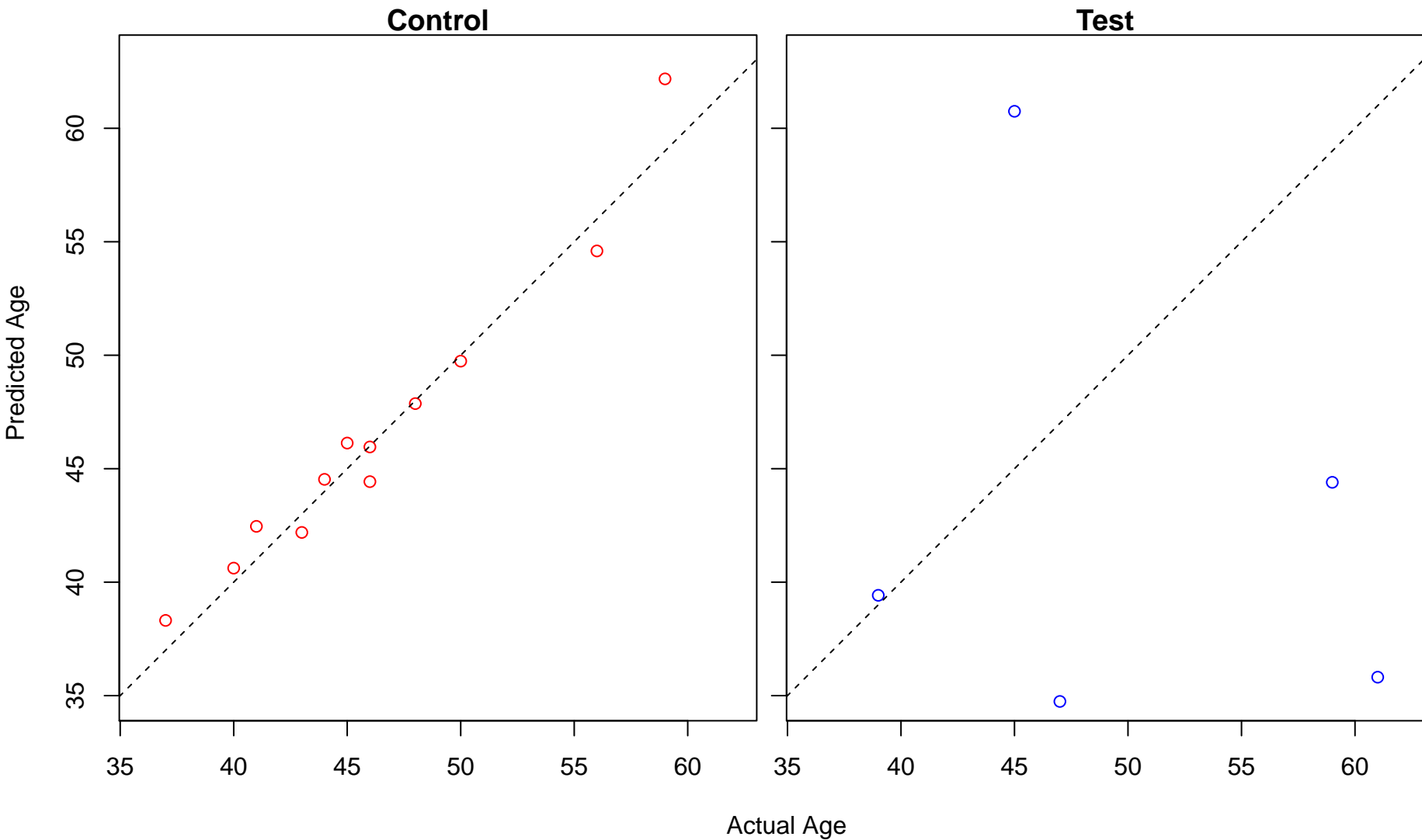


Test

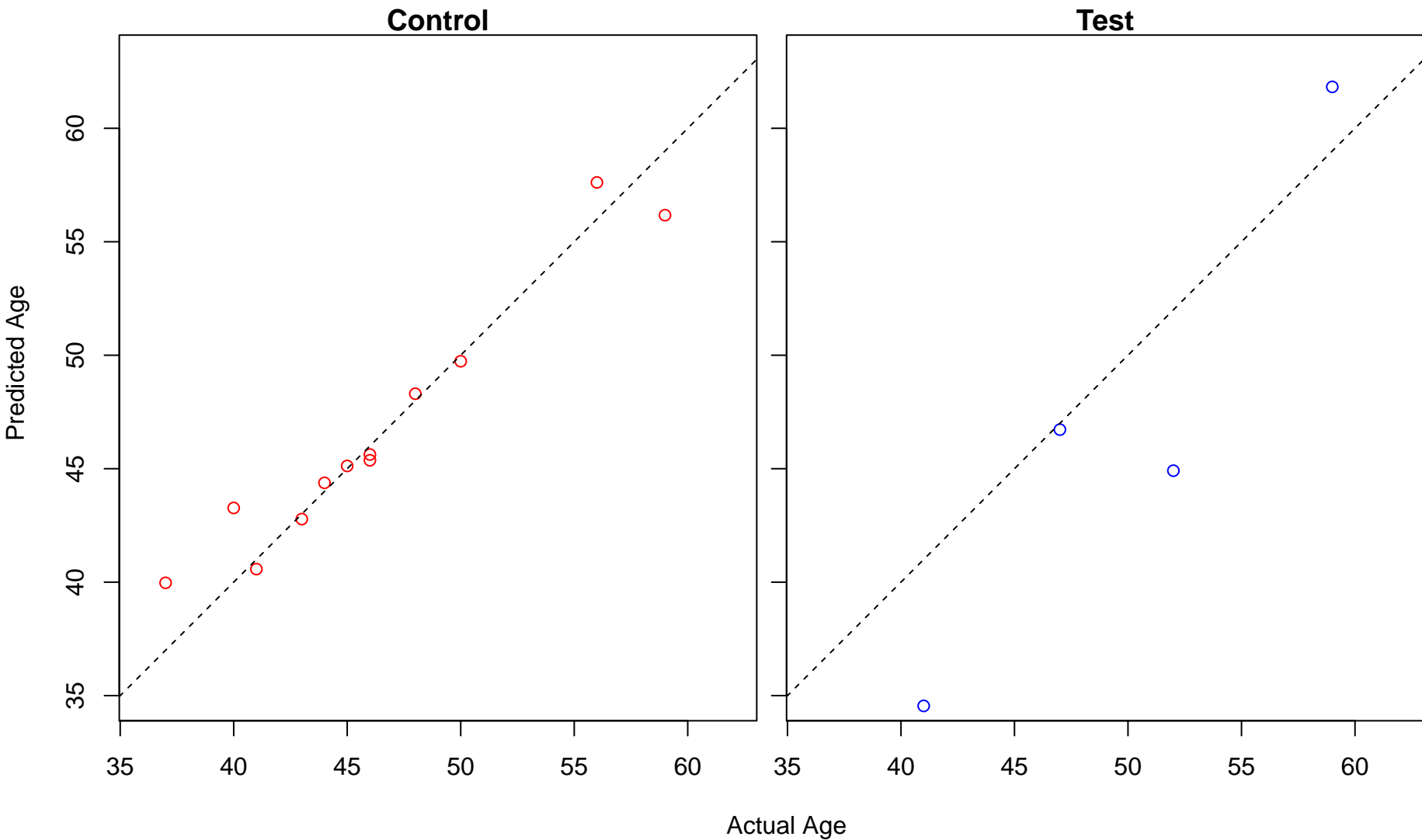


Actual Age

nephric duct development (Score: 175.893566)



vascular smooth muscle cell development (Score: 174.912874)

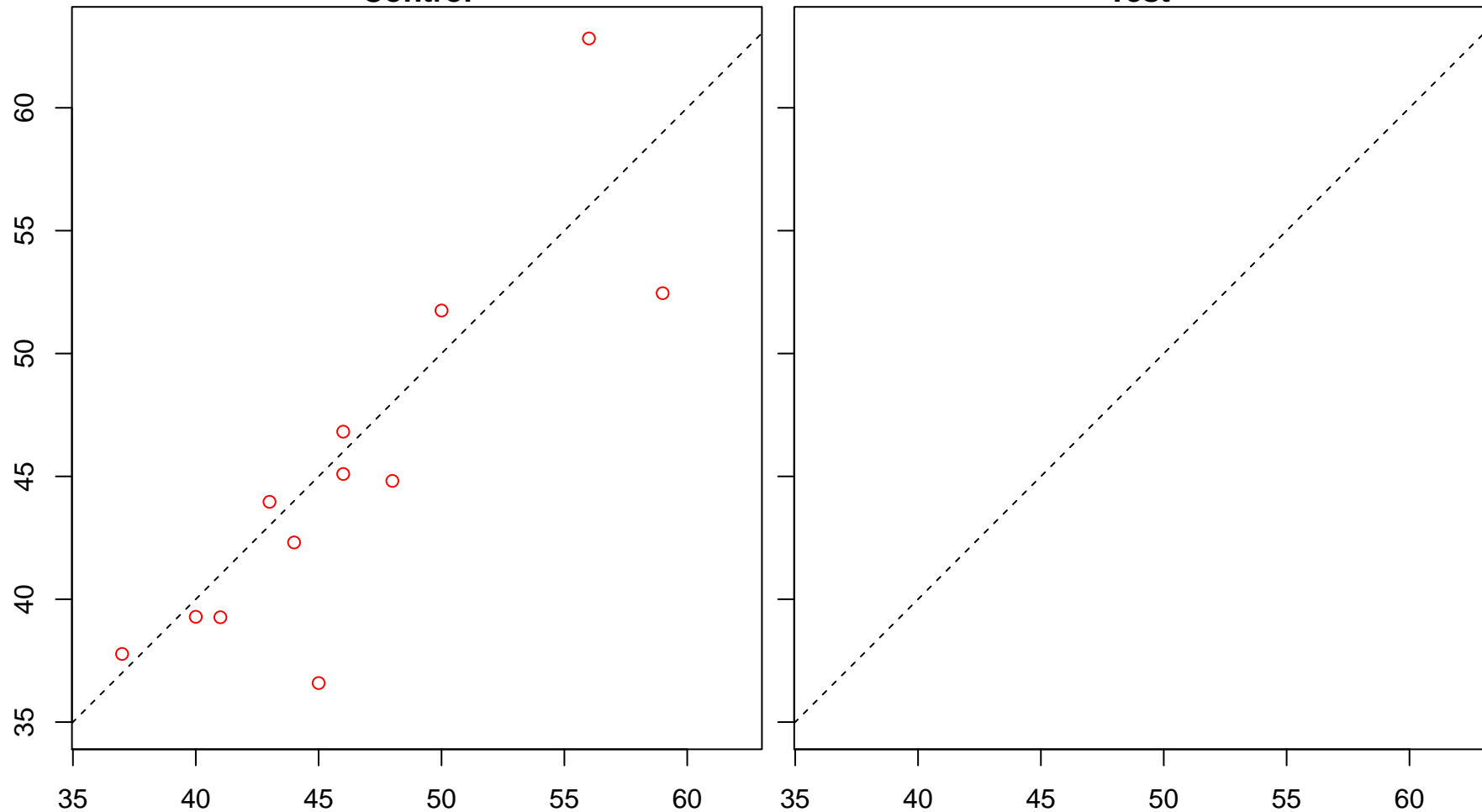


regulation of interleukin-13 secretion (Score: 152.246992)

Control

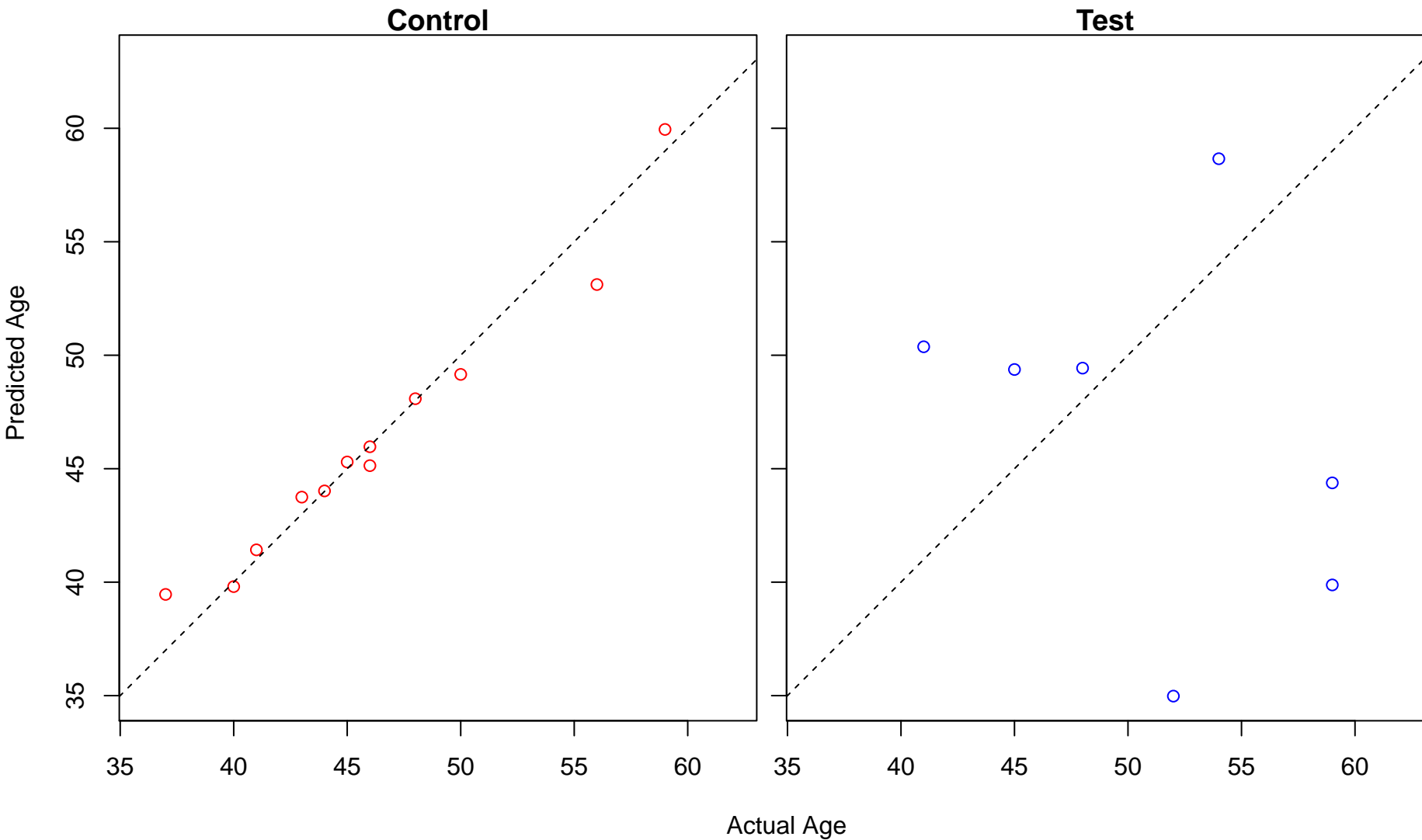
Test

Predicted Age

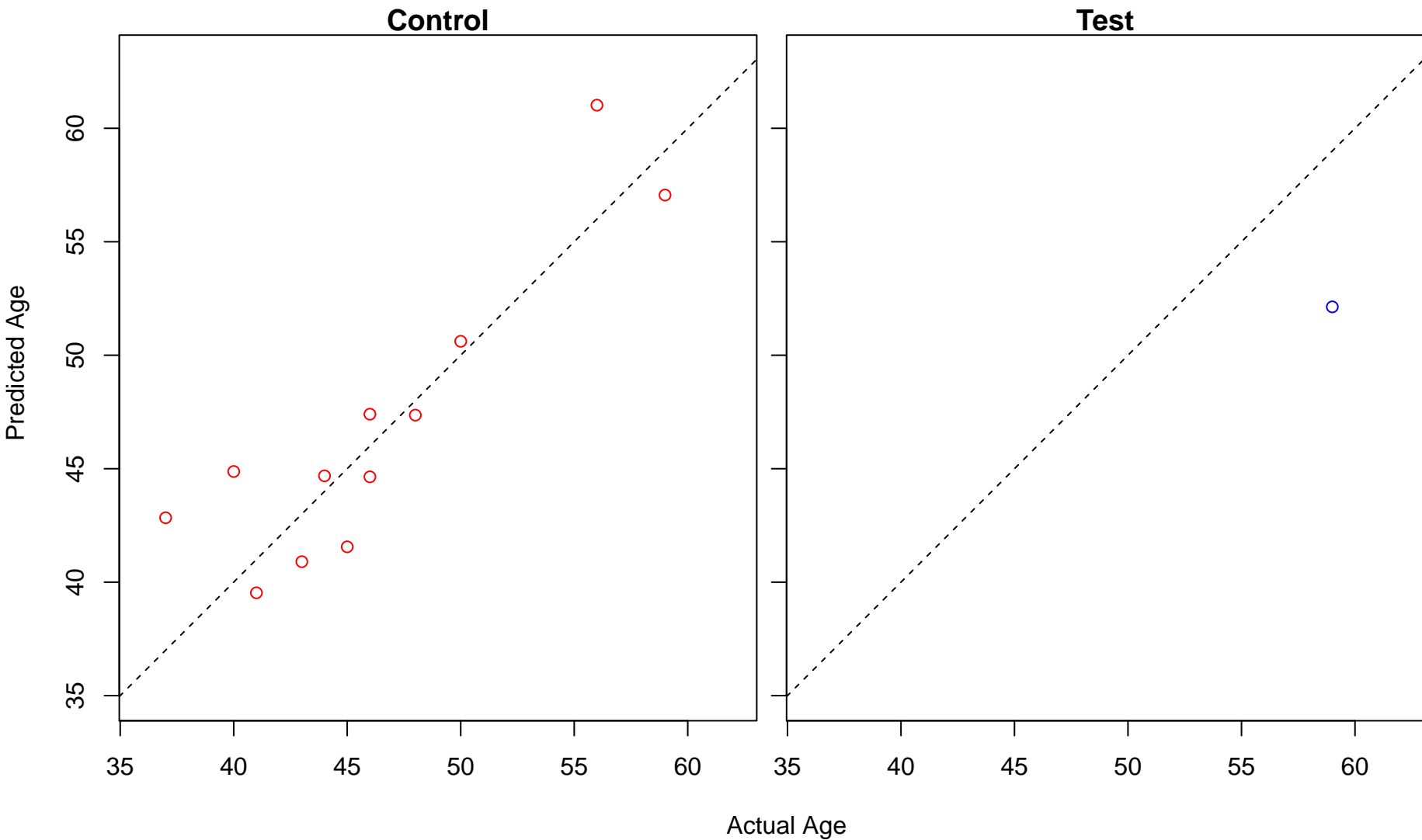


Actual Age

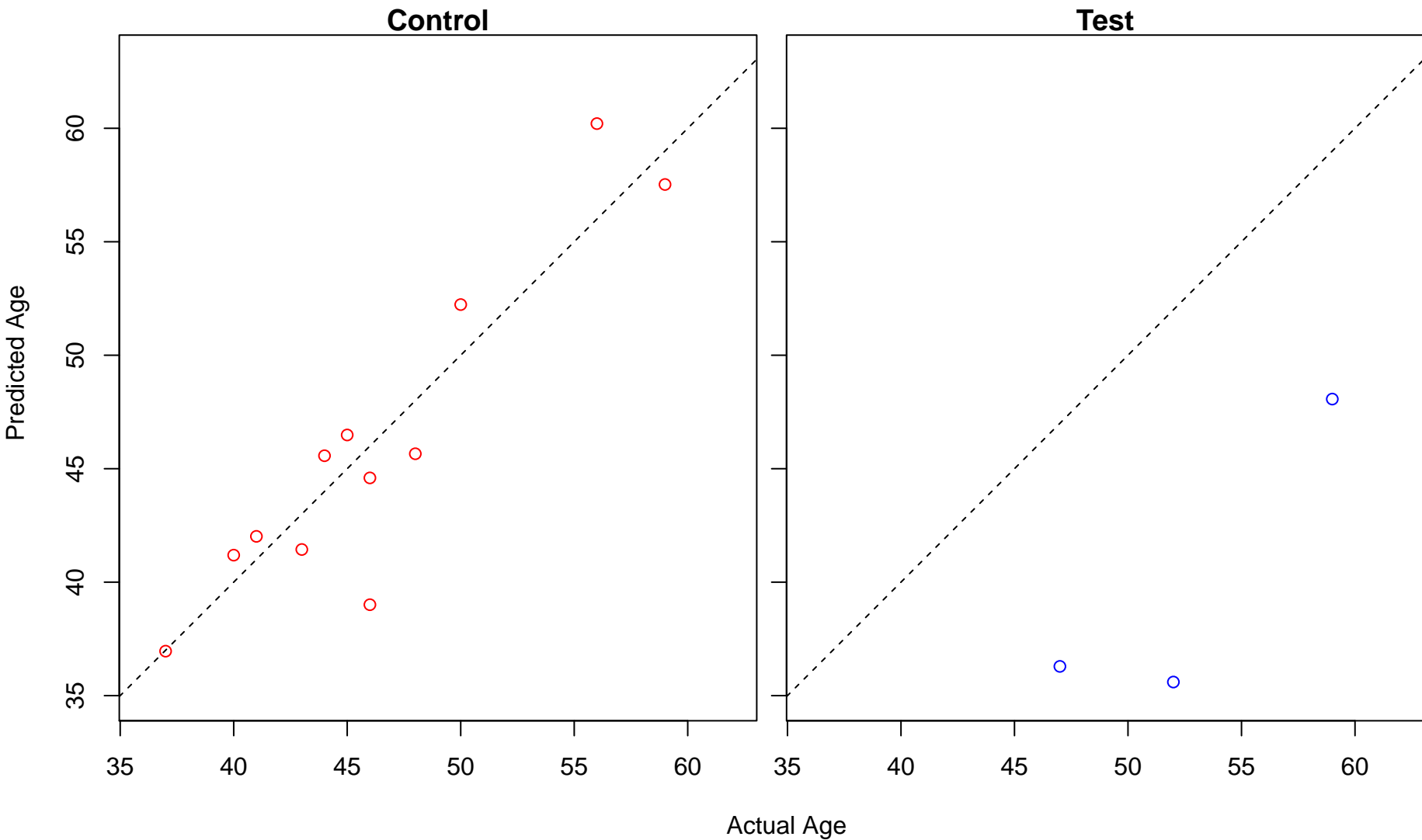
mRNA transcription from RNA polymerase II promoter (Score: 136.295375)



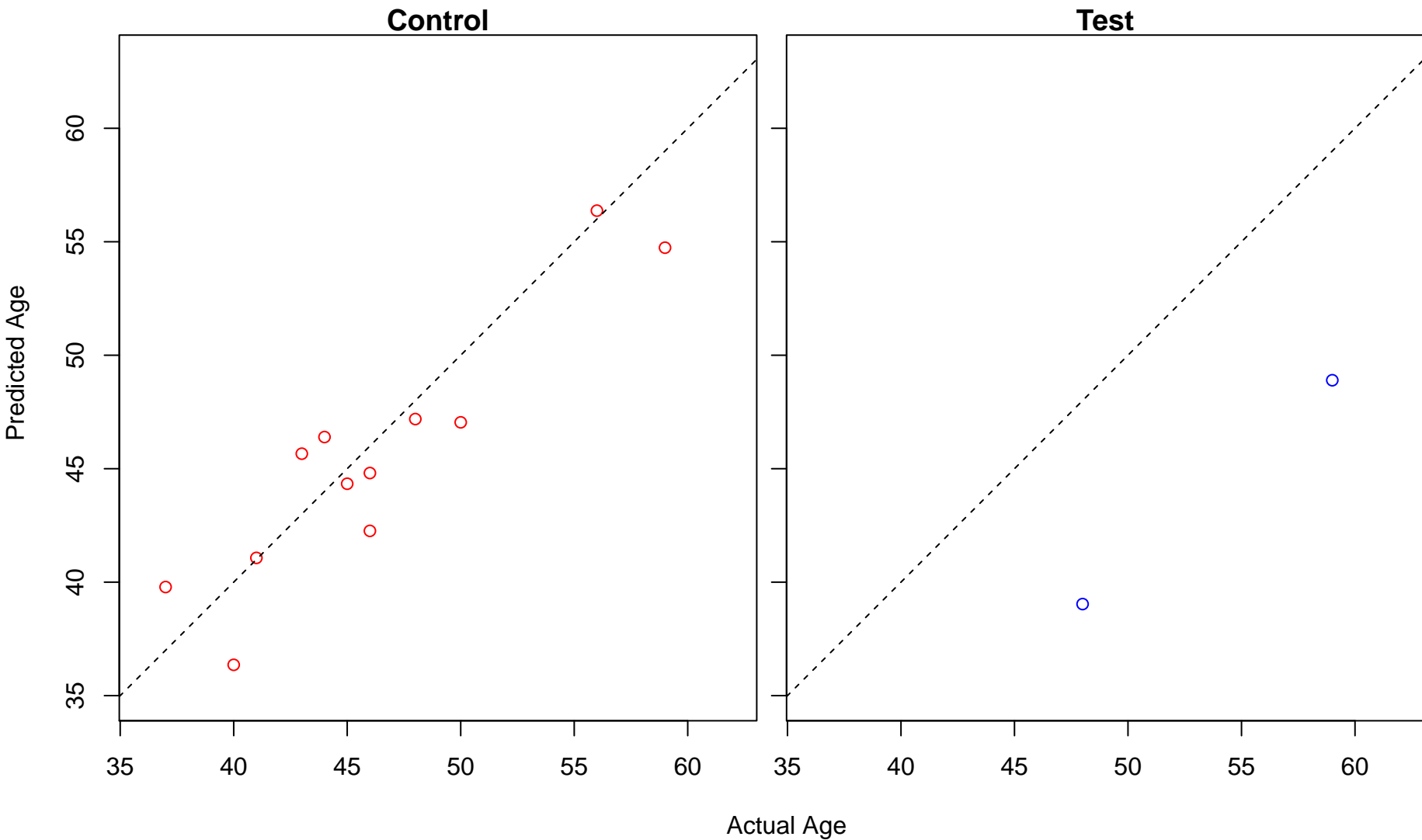
sperm chromatin condensation (Score: 132.503390)



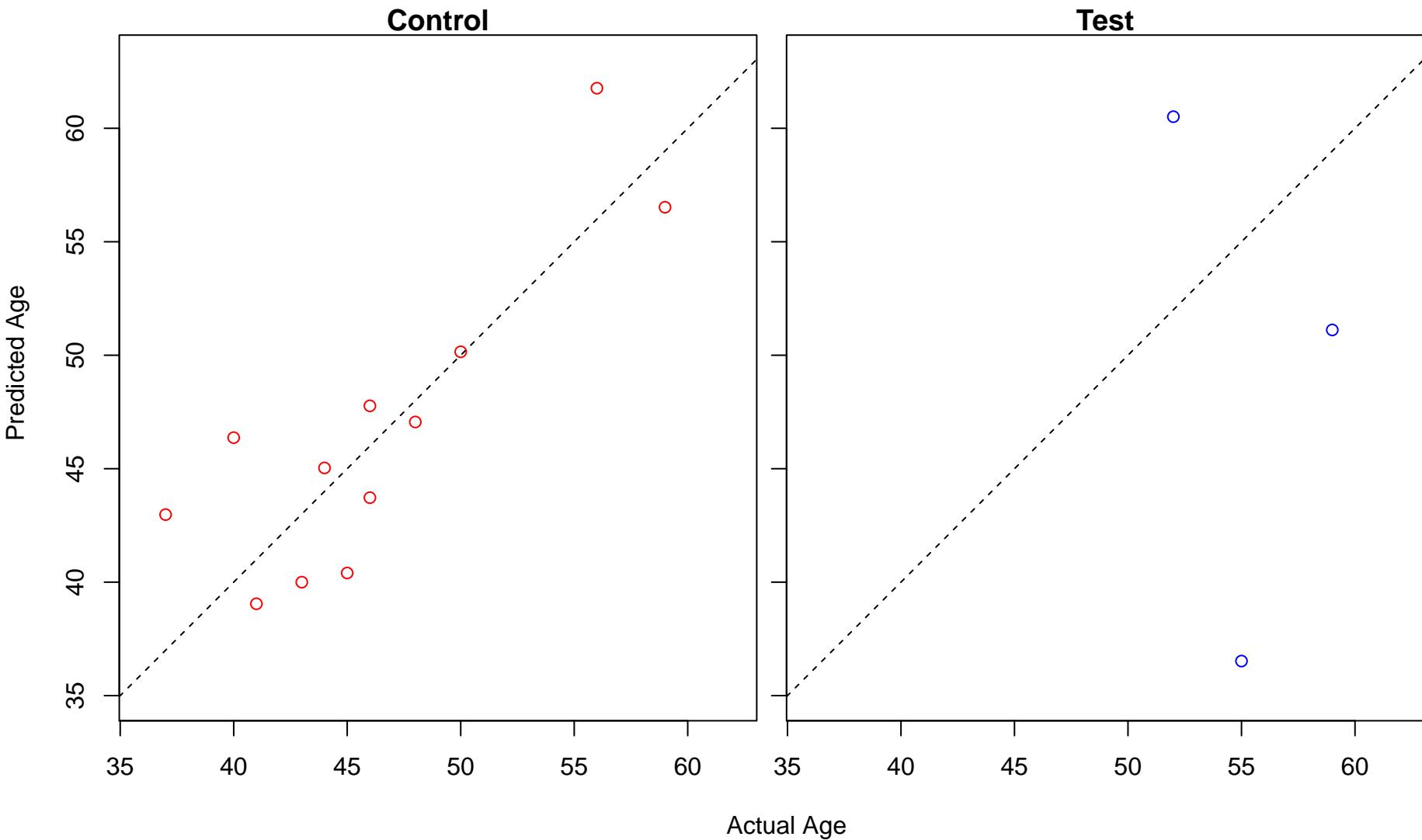
opioid receptor signaling pathway (Score: 128.398213)



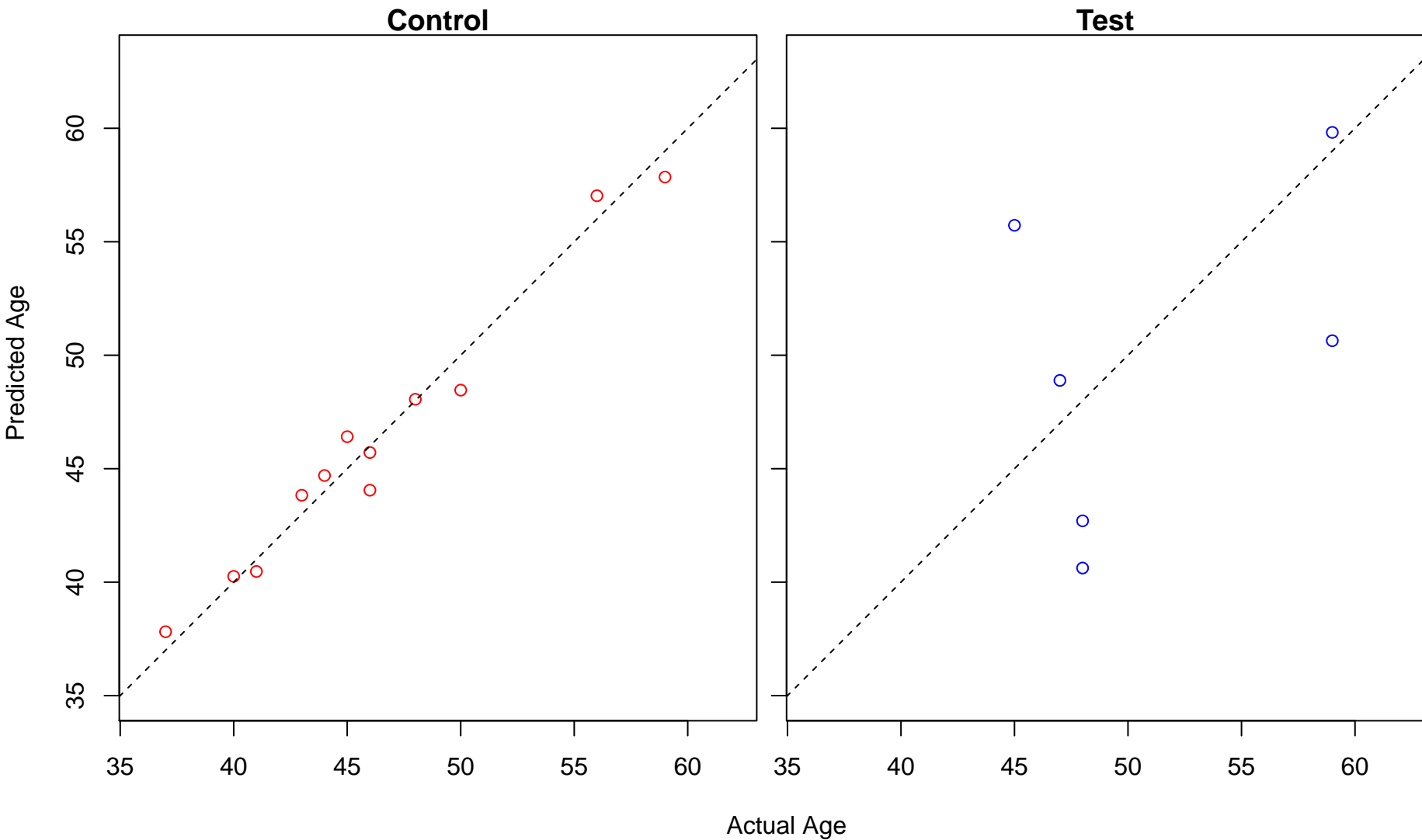
regulation of extracellular matrix organization (Score: 119.900646)



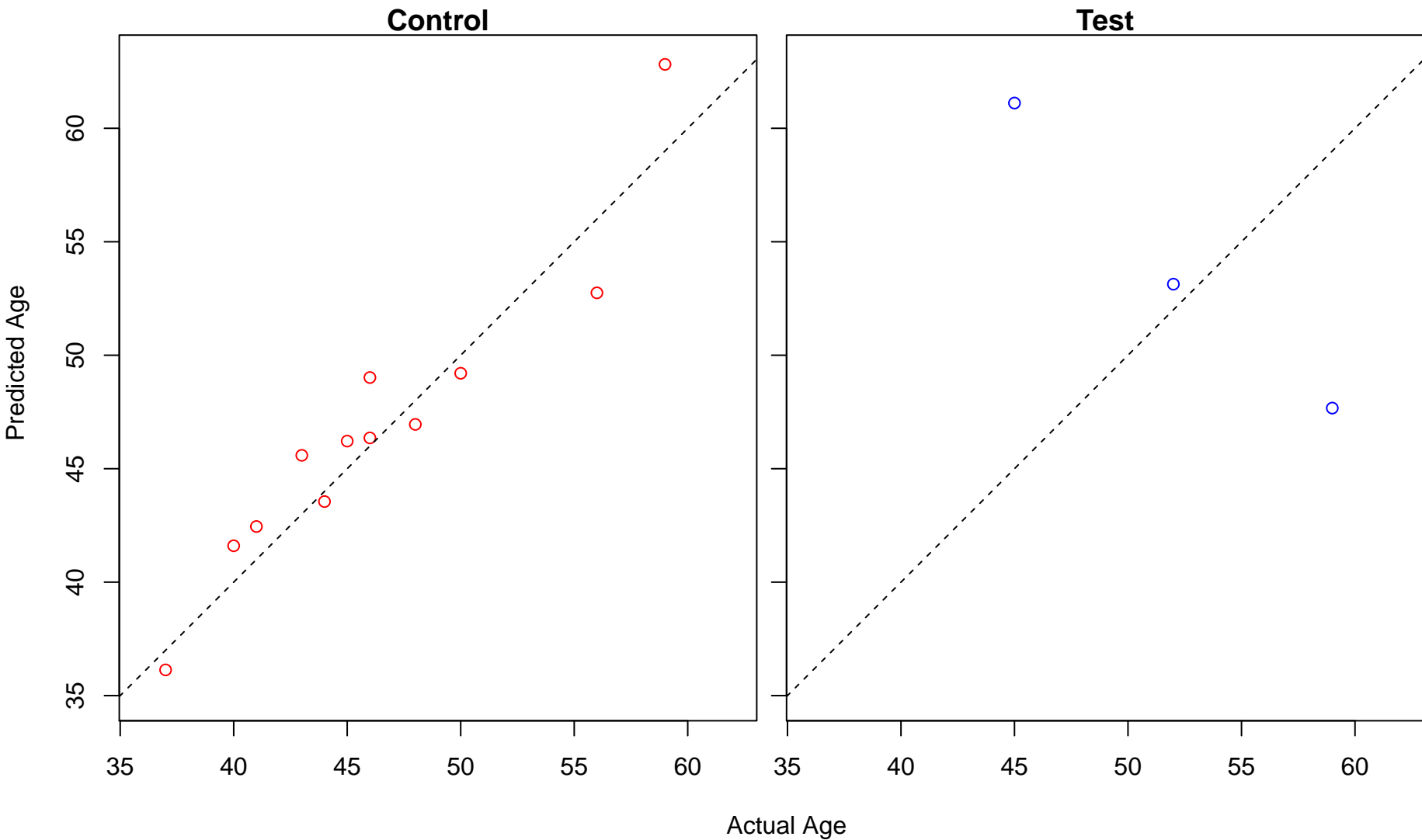
spermatid nucleus differentiation (Score: 113.008941)



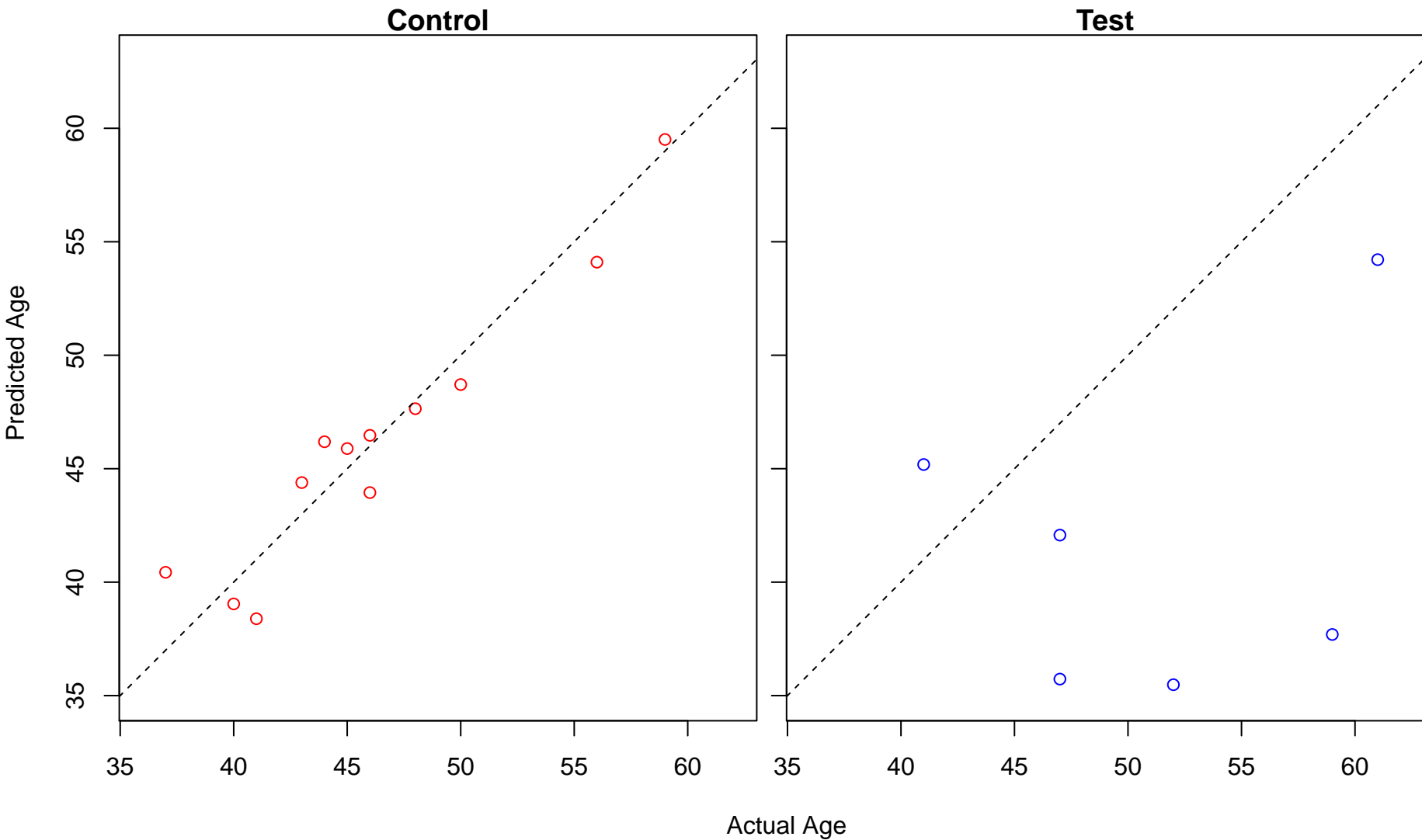
epithelial tube branching involved in lung morphogenesis (Score: 108.991053)



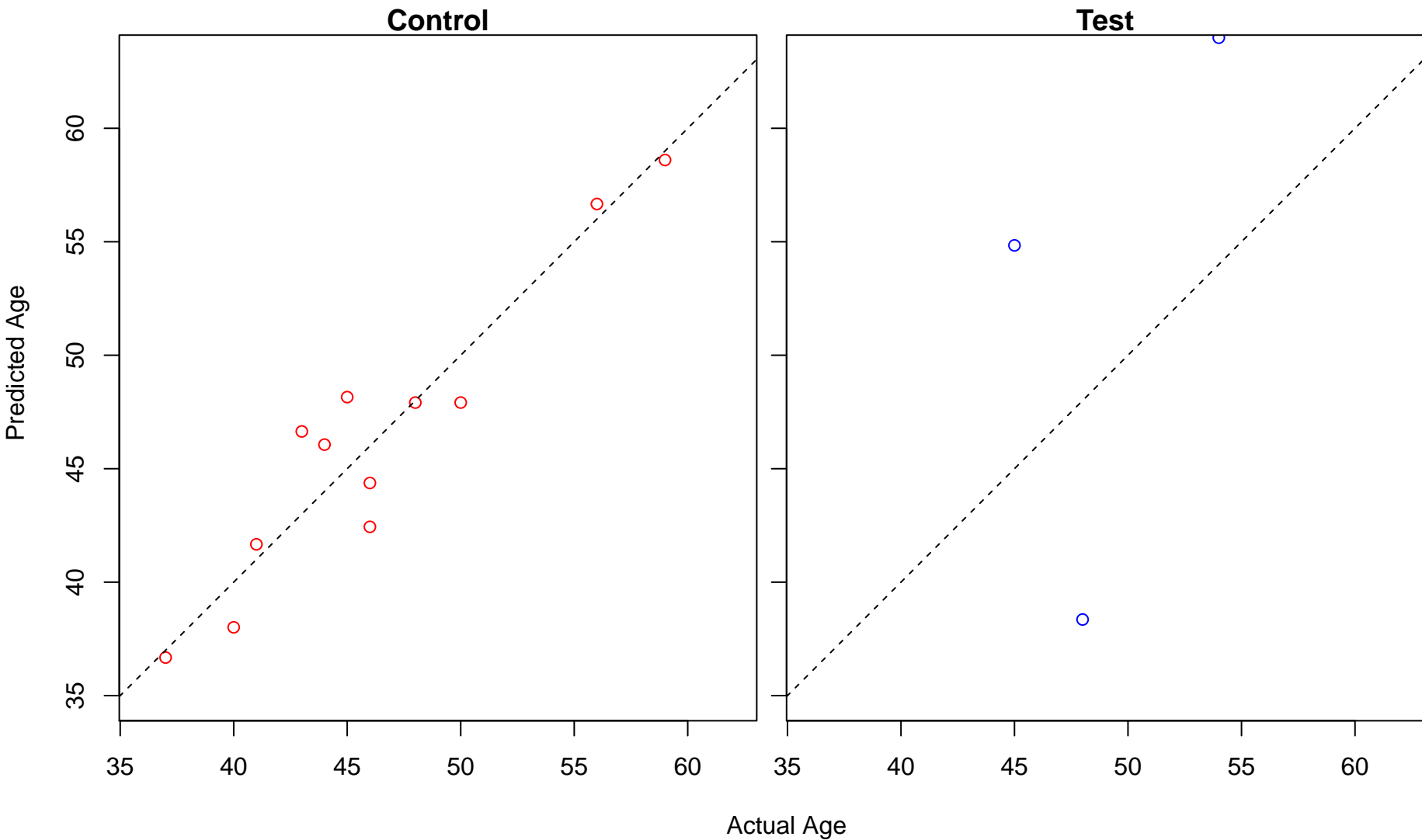
RNA surveillance (Score: 106.867972)



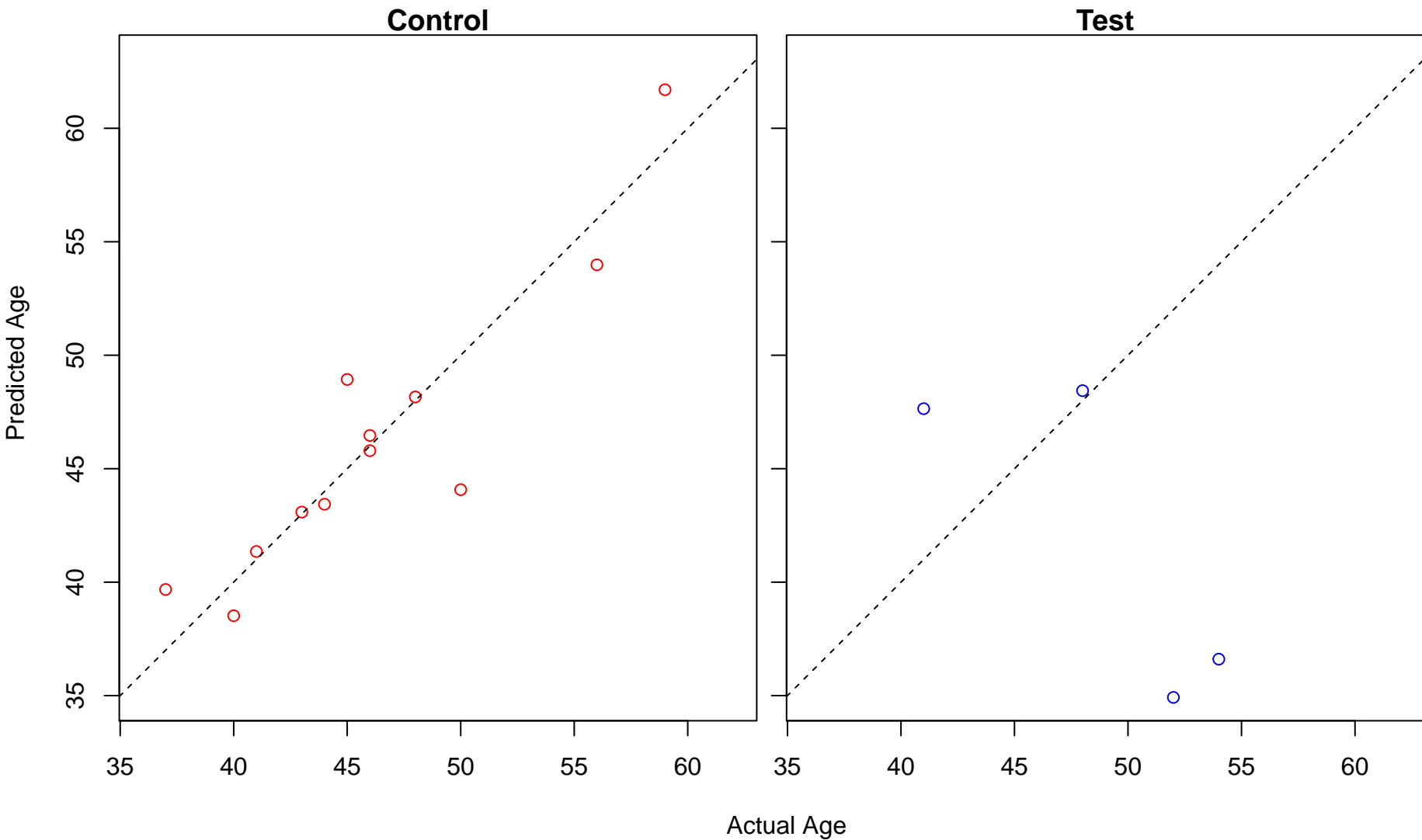
purine nucleobase transport (Score: 98.518341)



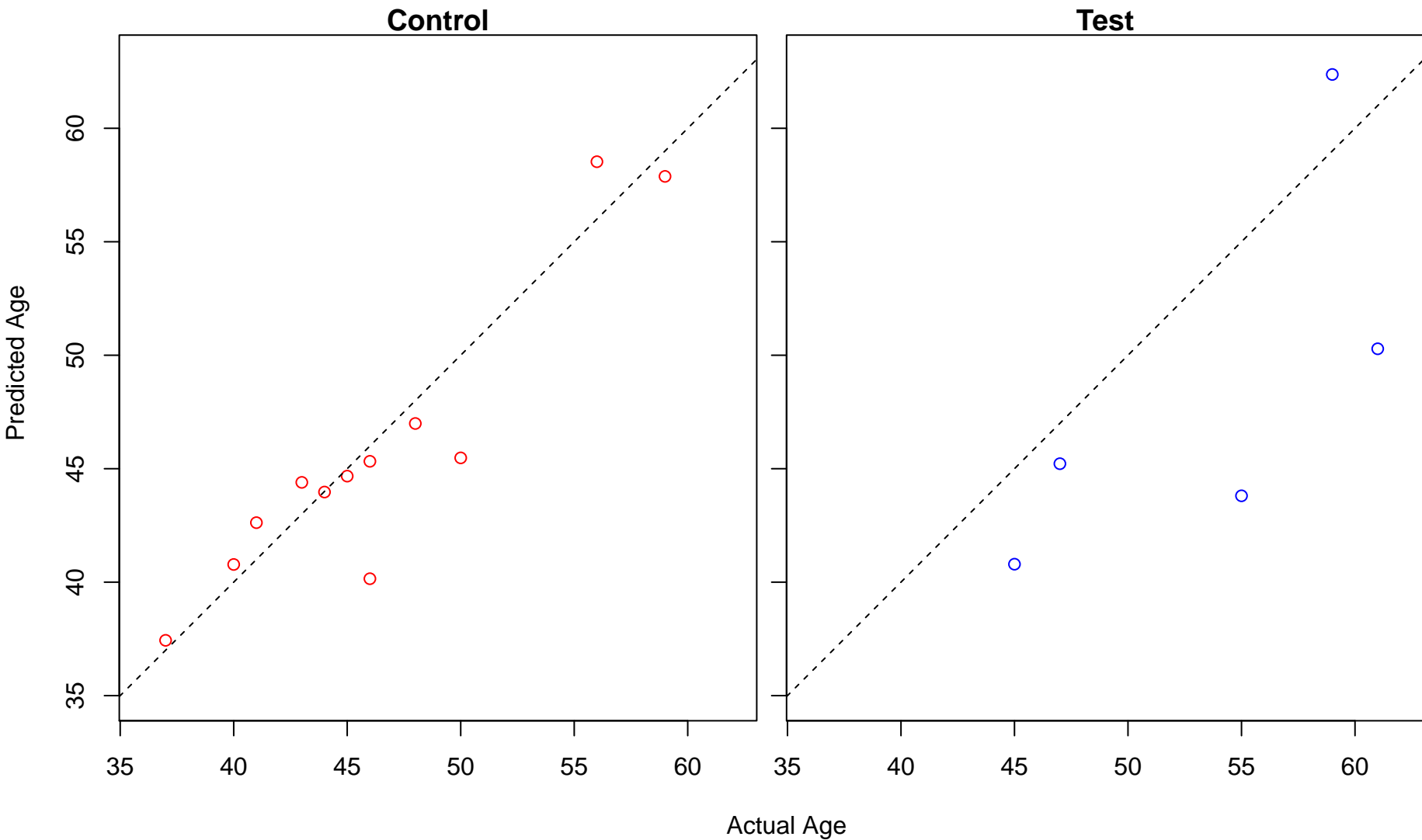
monocyte chemotaxis (Score: 96.364187)



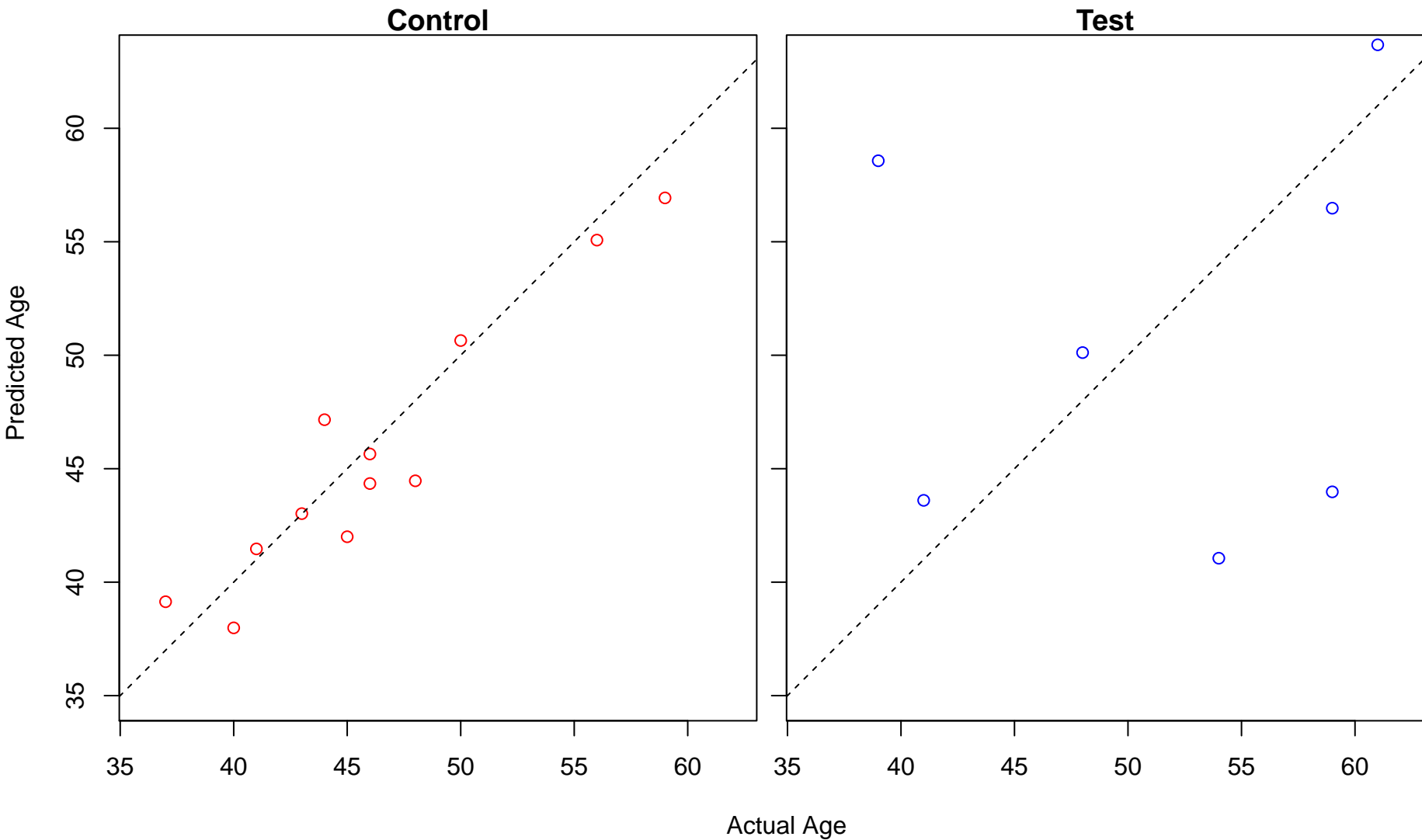
cell proliferation in forebrain (Score: 95.777066)



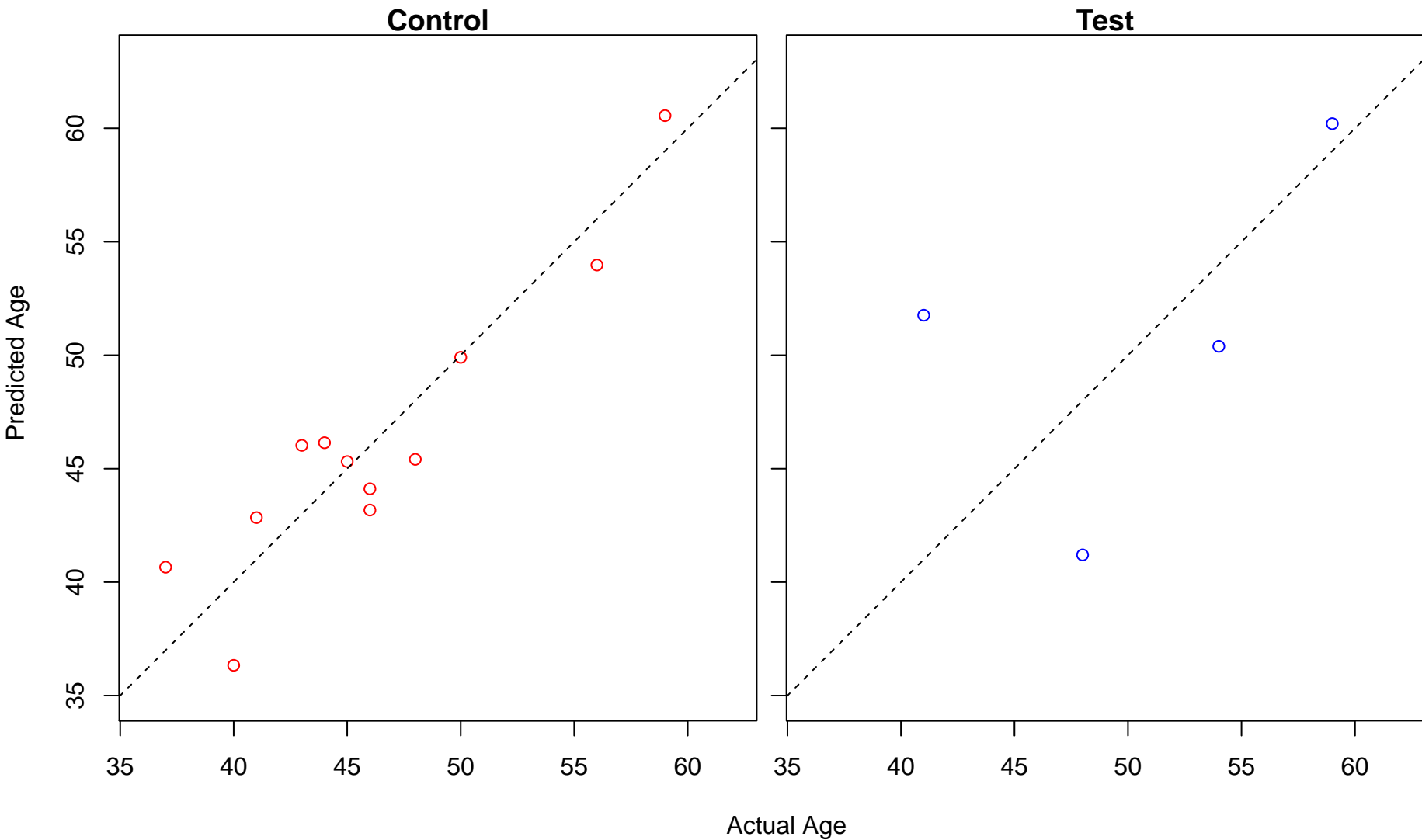
regulation of cell-cell adhesion mediated by cadherin (Score: 93.083841)



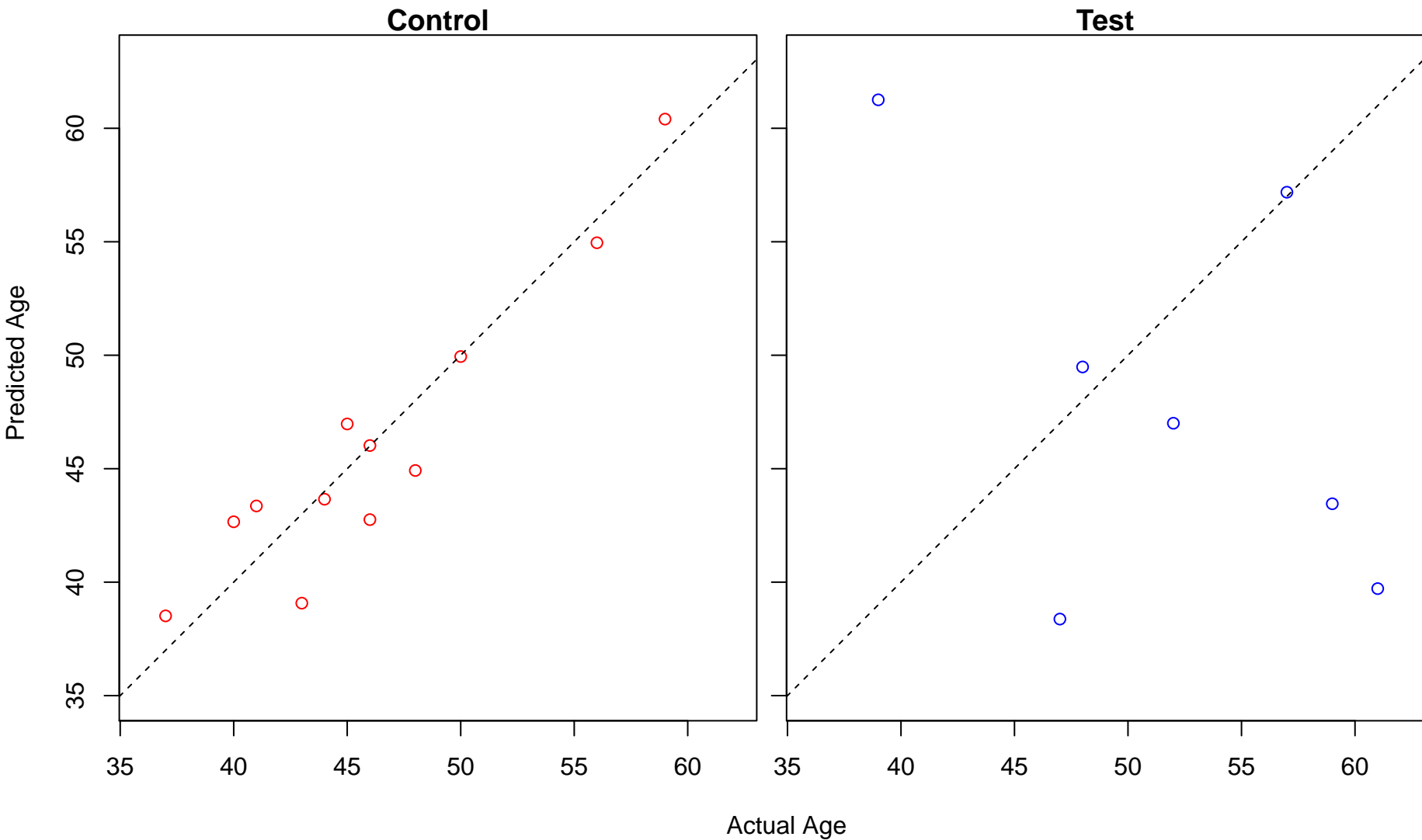
negative regulation of extracellular matrix organization (Score: 88.267779)



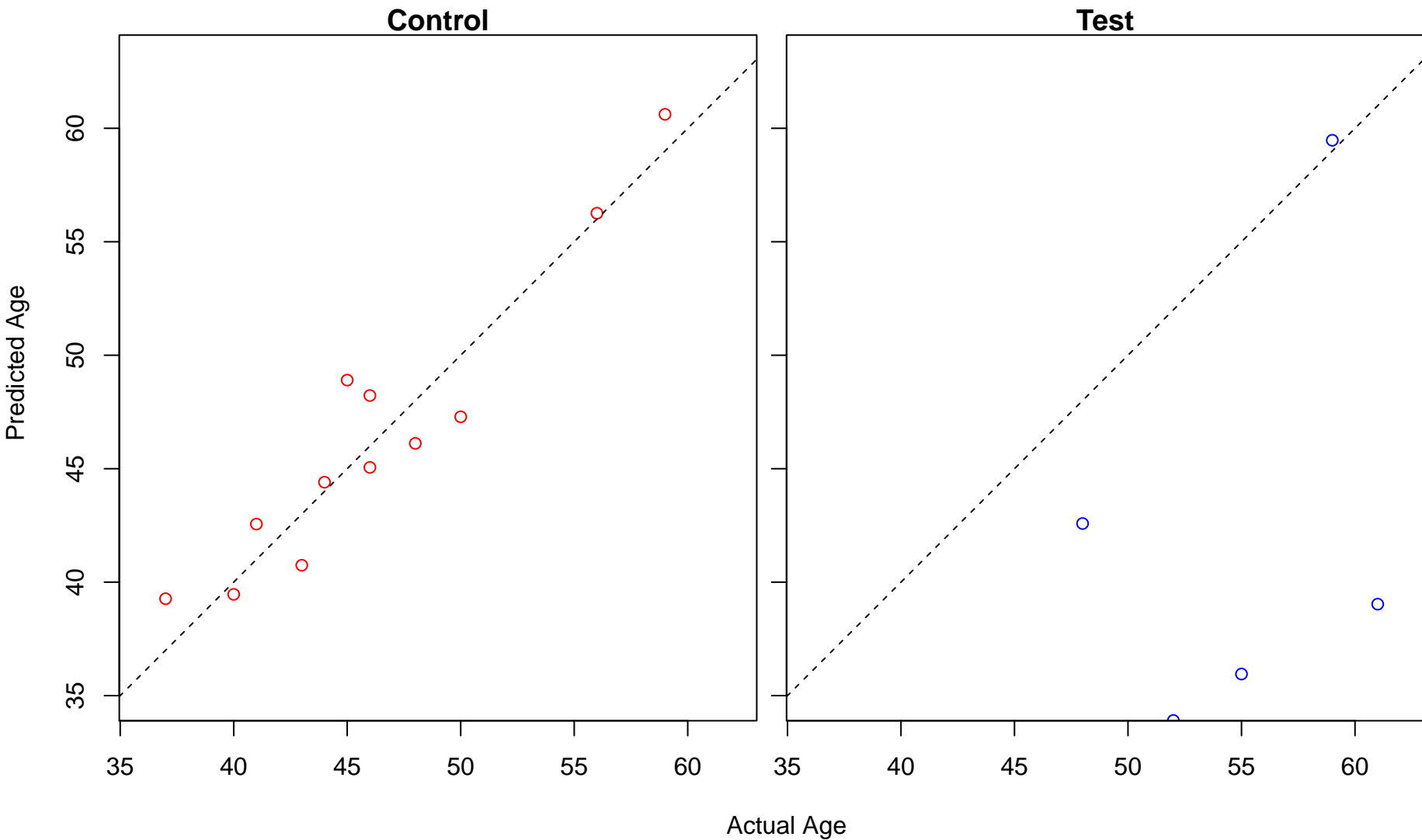
regulation of protein complex stability (Score: 86.932882)



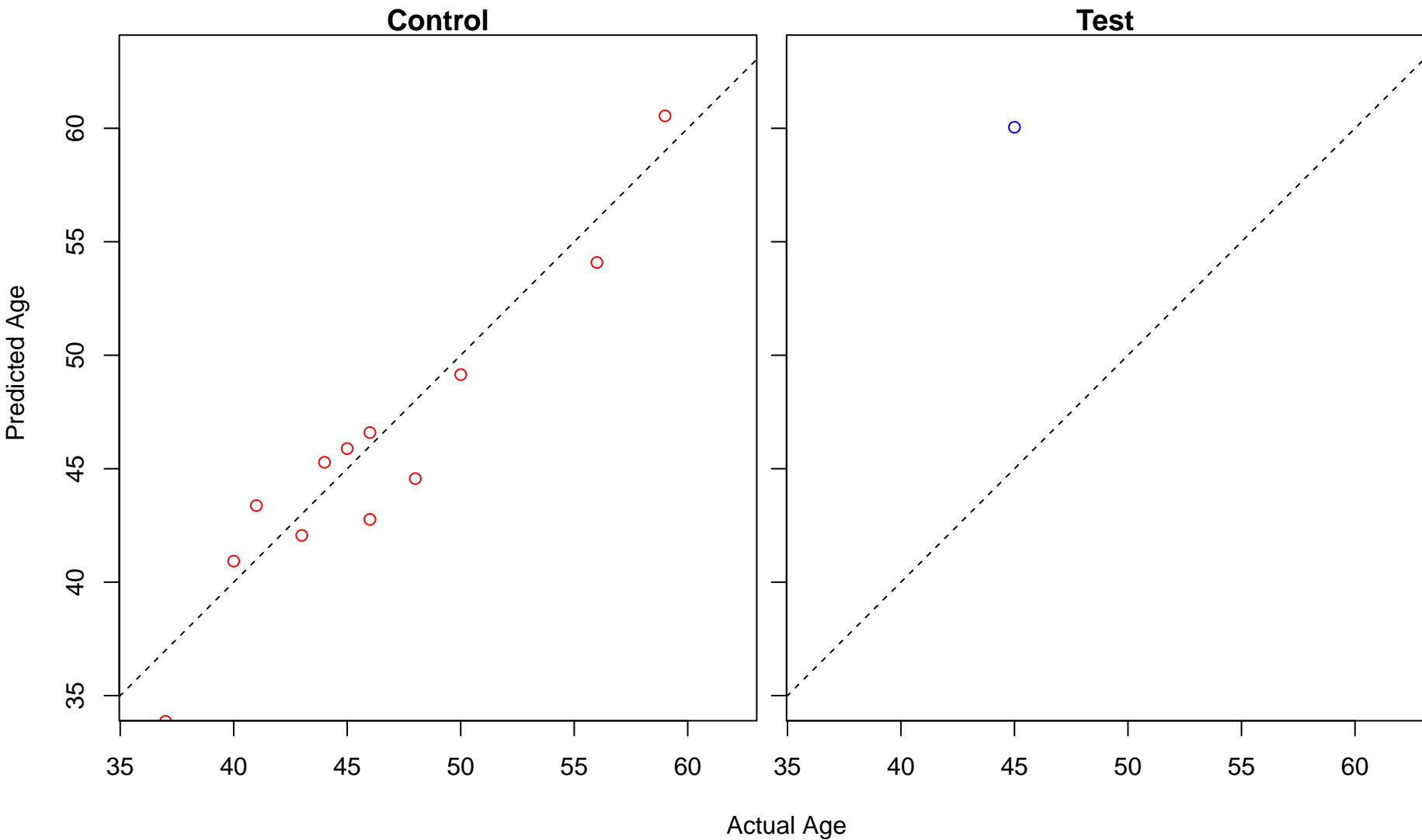
regulation of oligodendrocyte differentiation (Score: 86.698080)



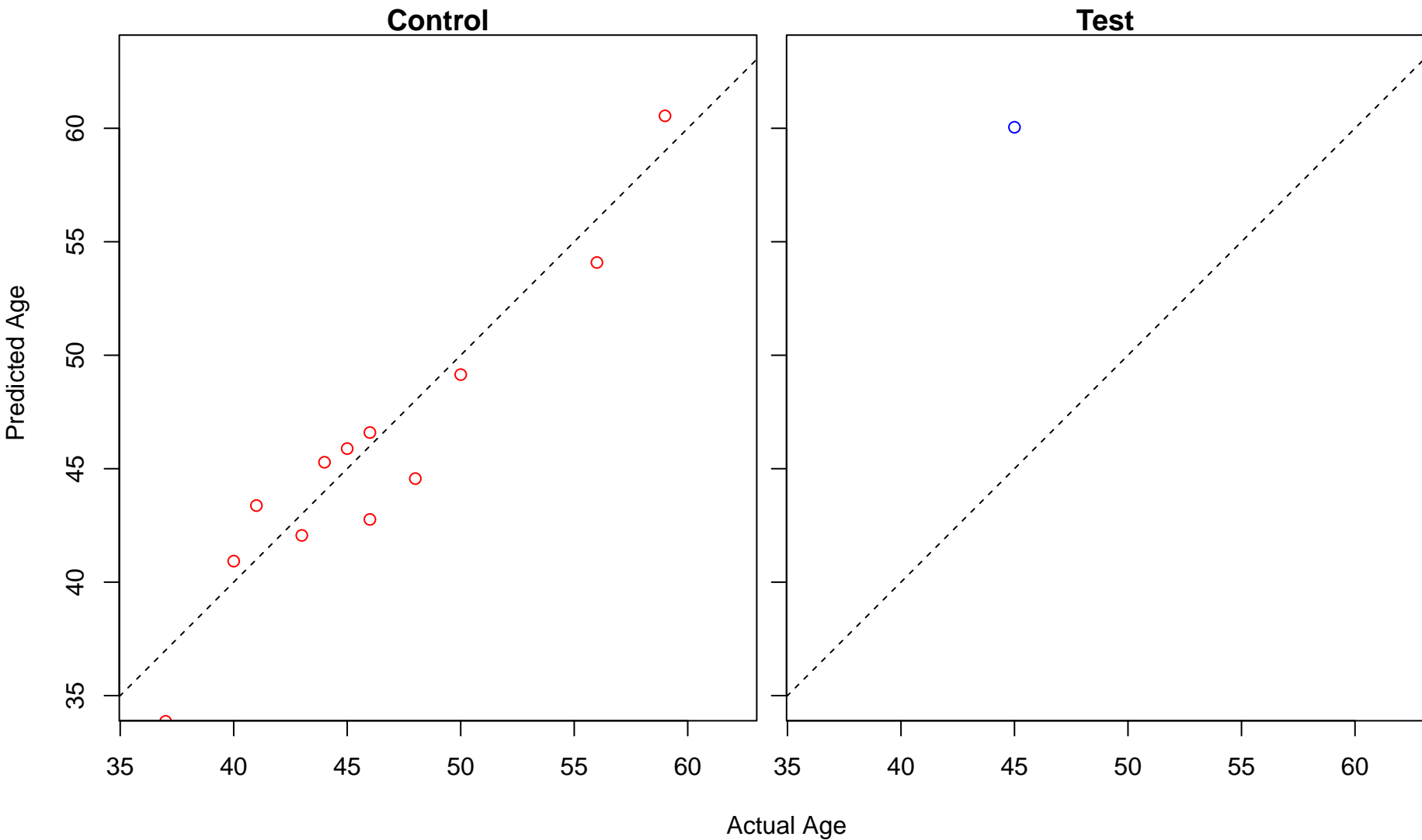
glutamine family amino acid metabolic process (Score: 83.558478)



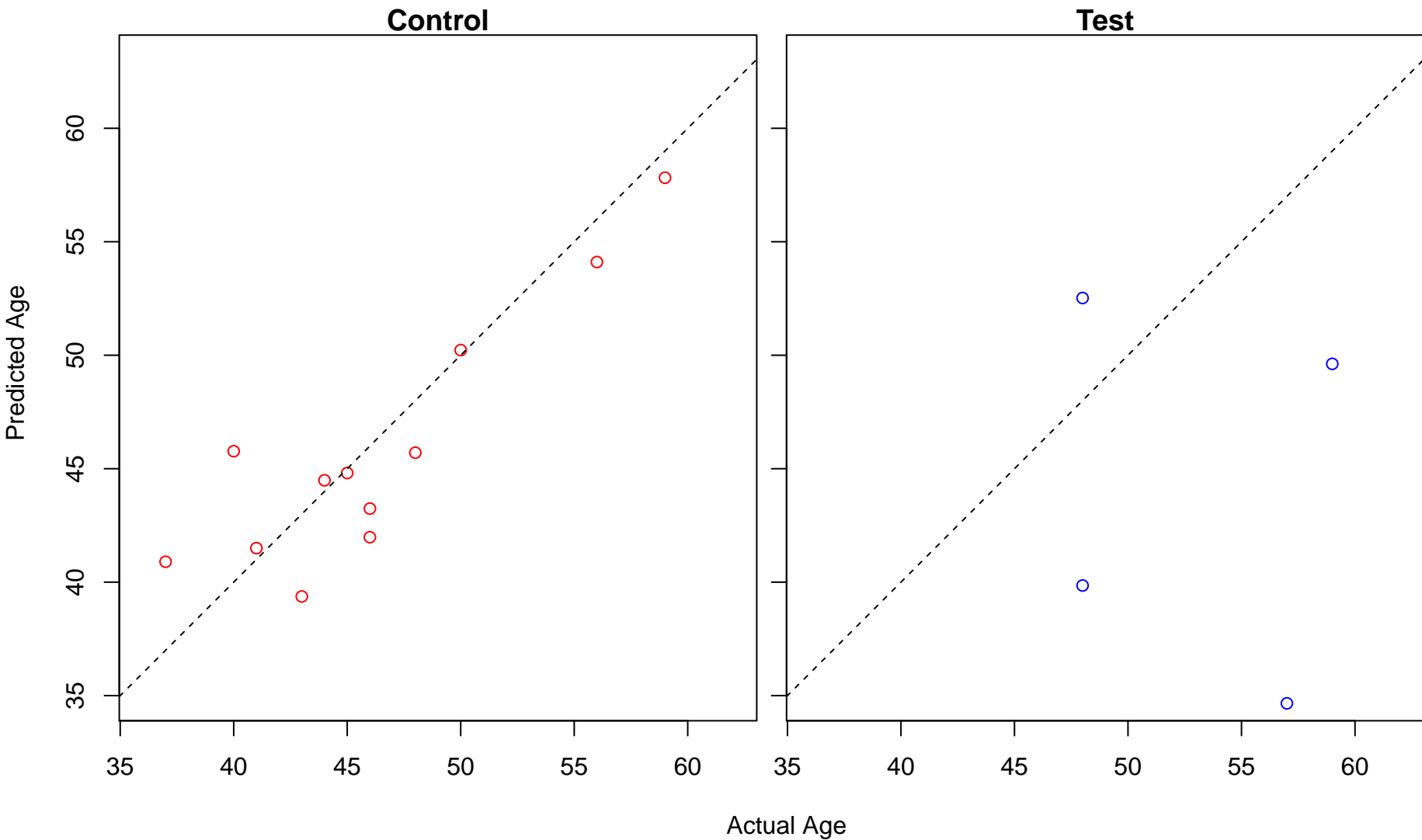
sulfide oxidation (Score: 83.121375)



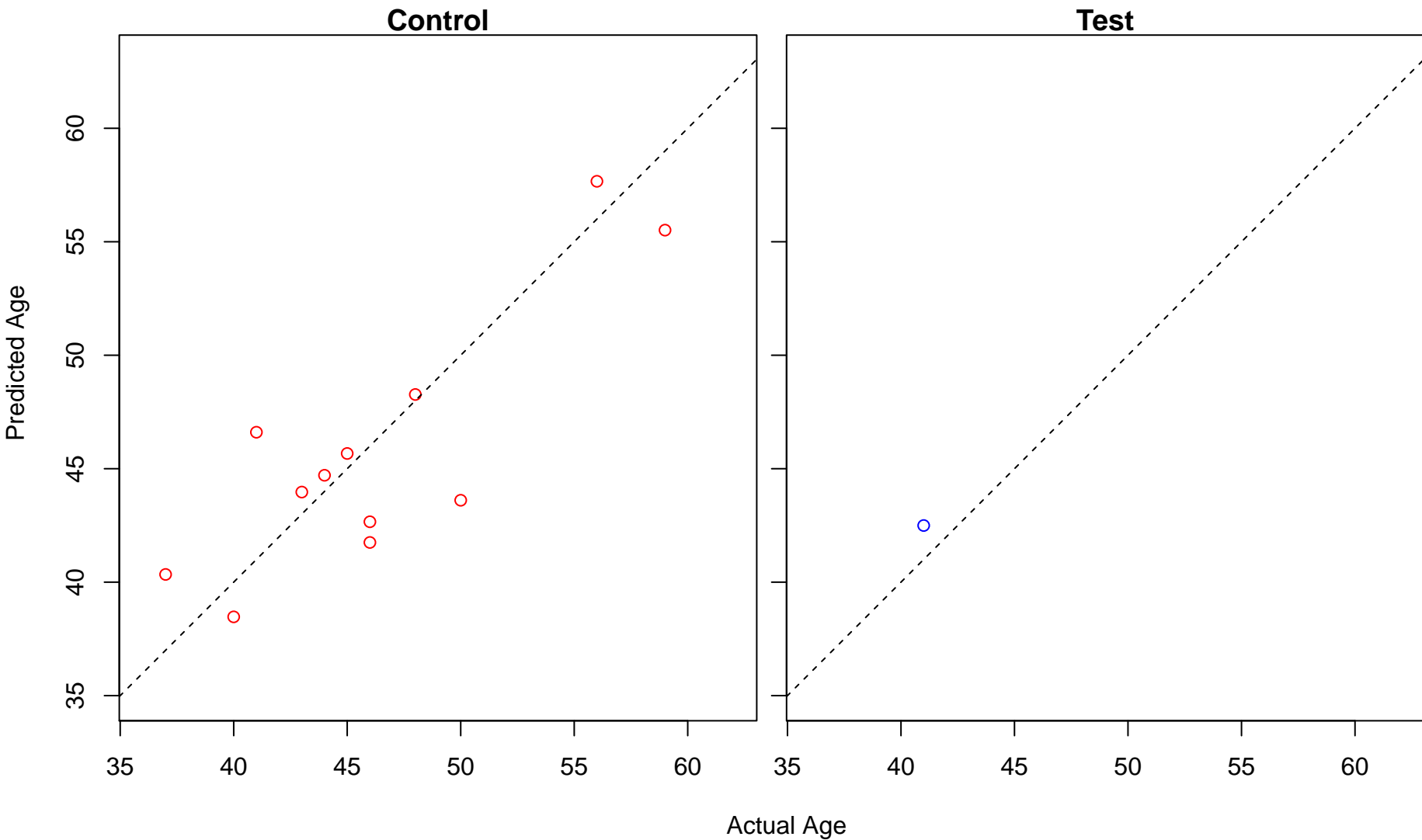
sulfide oxidation, using sulfide:quinone oxidoreductase (Score: 83.121375)



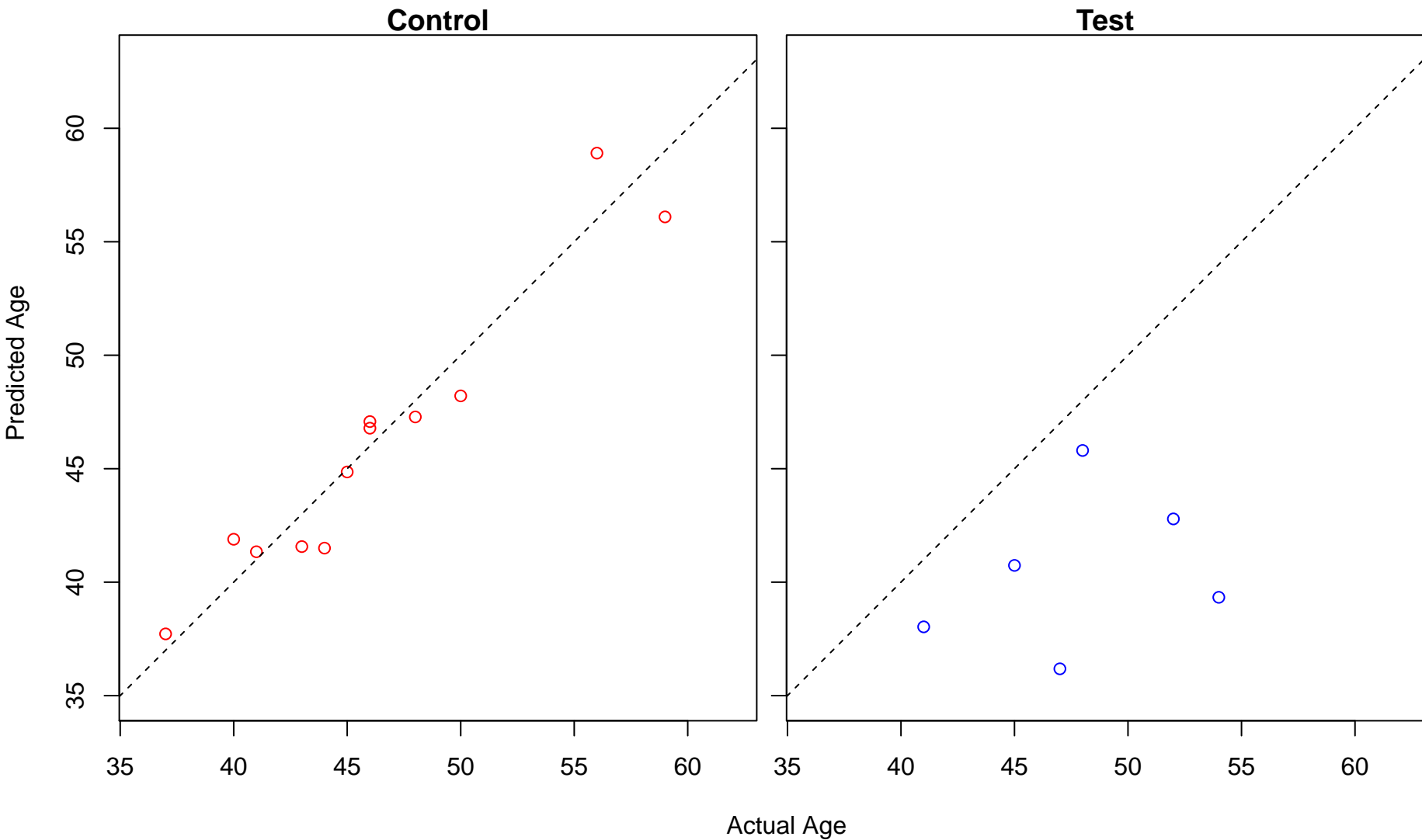
adrenal gland development (Score: 82.670390)



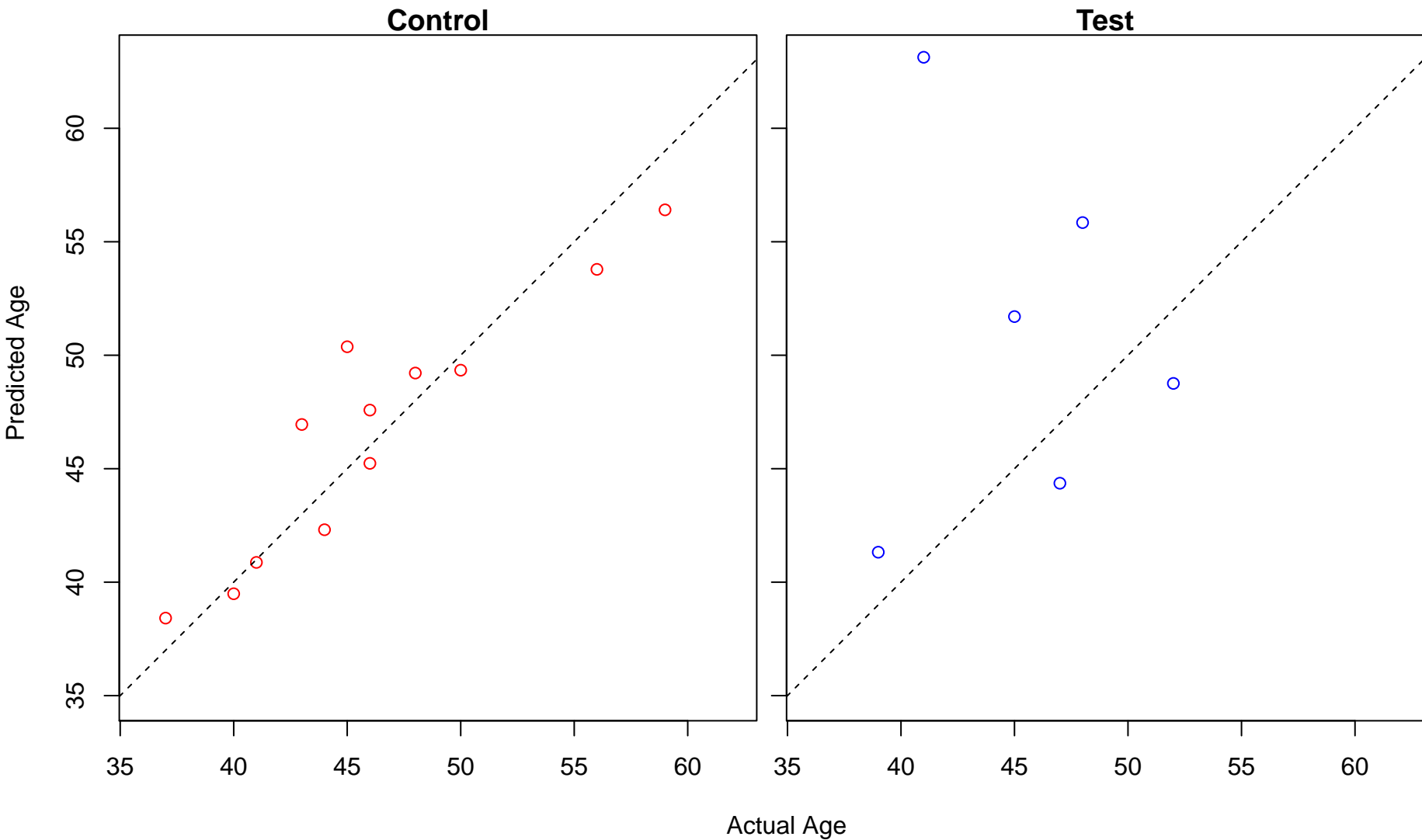
somatic stem cell division (Score: 80.101862)



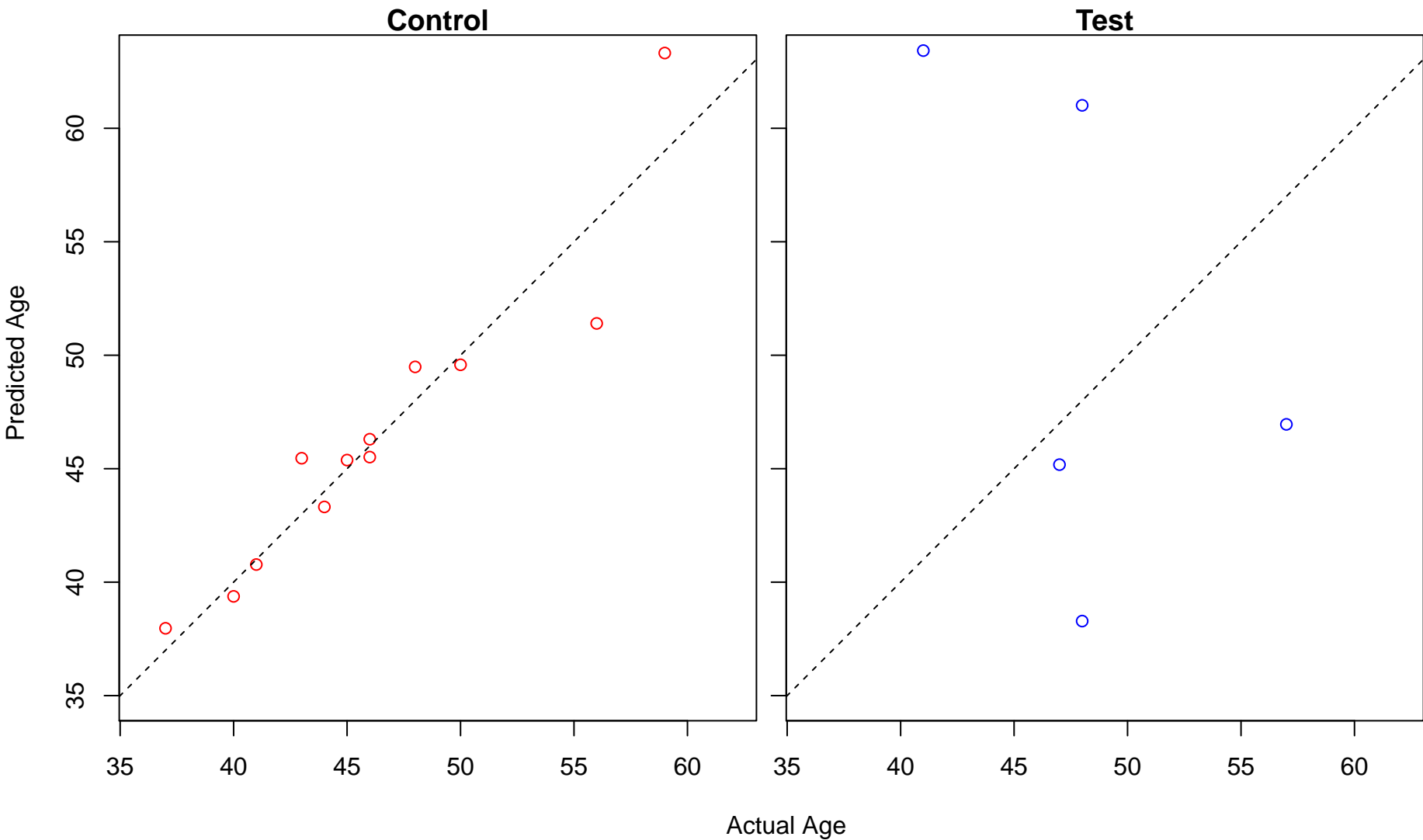
pyrimidine-containing compound transmembrane transport (Score: 79.557715)



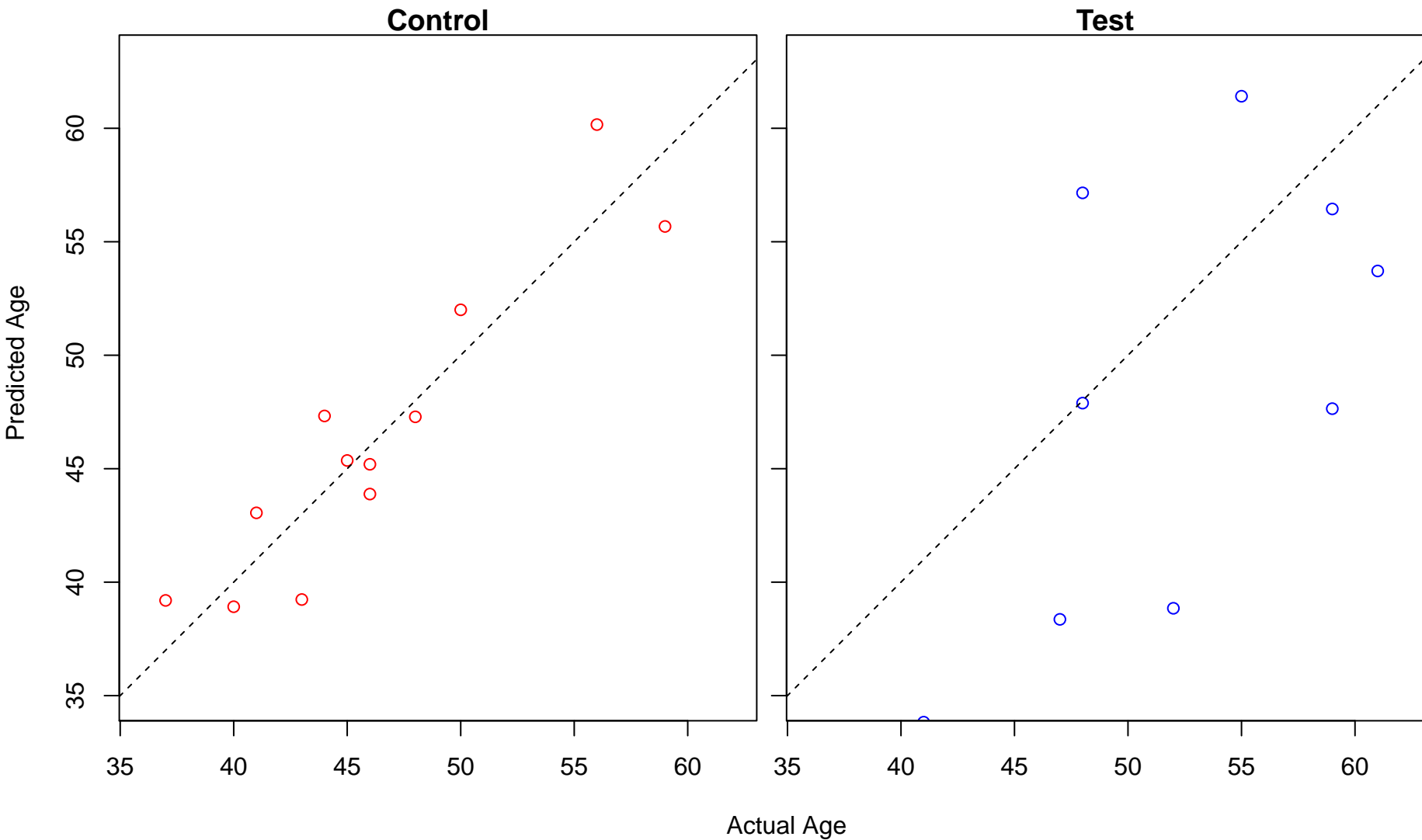
regulation of cardiac muscle cell membrane potential (Score: 79.467754)



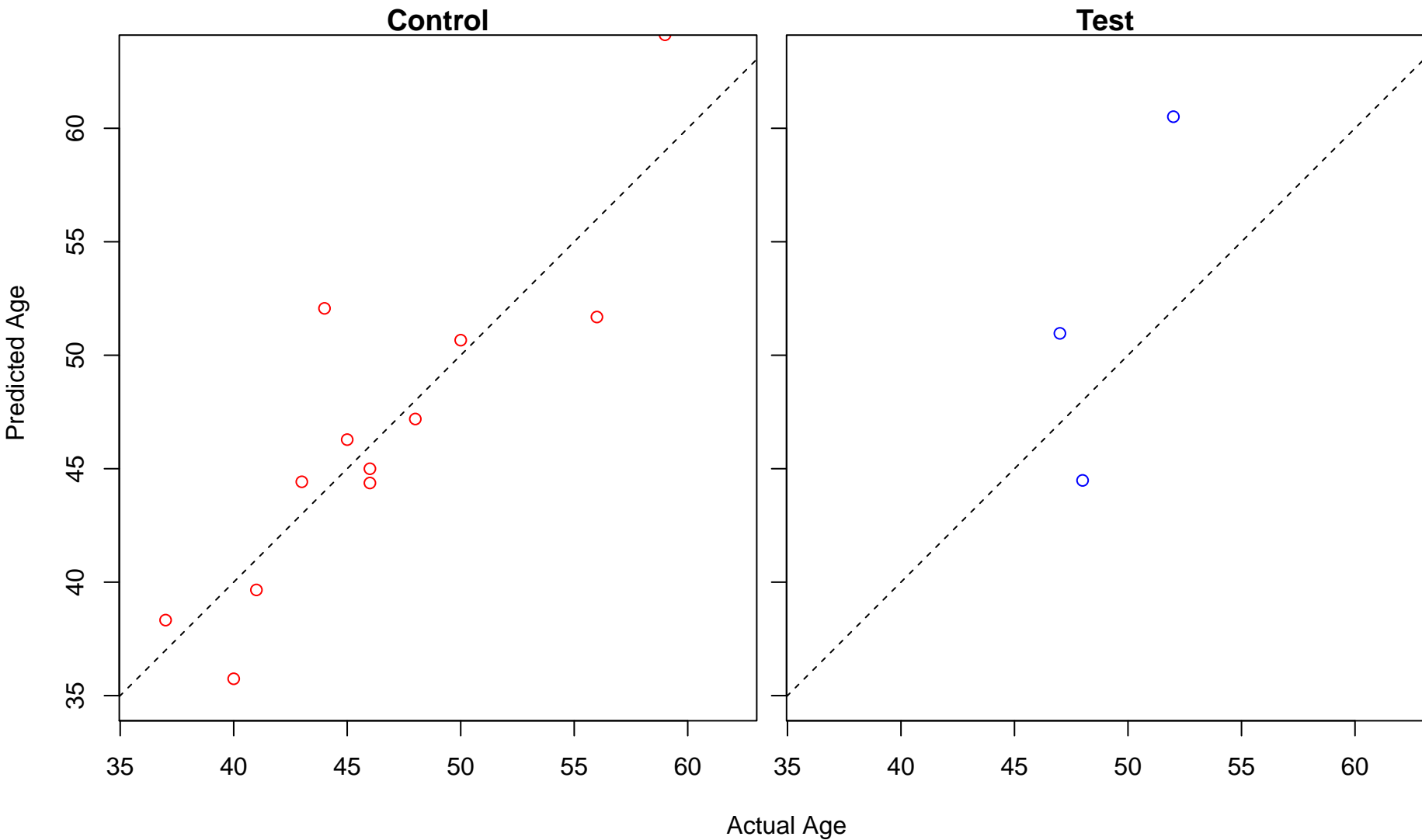
Regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (S



negative regulation of activin receptor signaling pathway (Score: 78.409938)

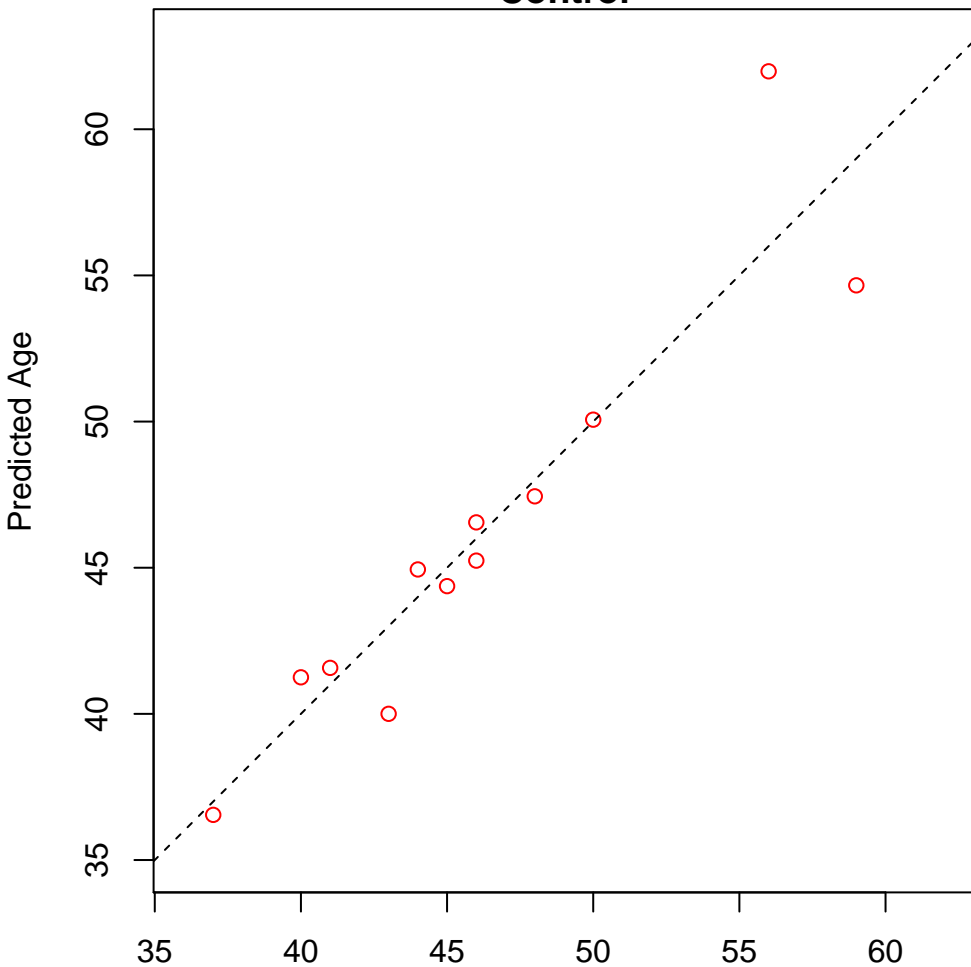


negative regulation of type 2 immune response (Score: 78.399573)

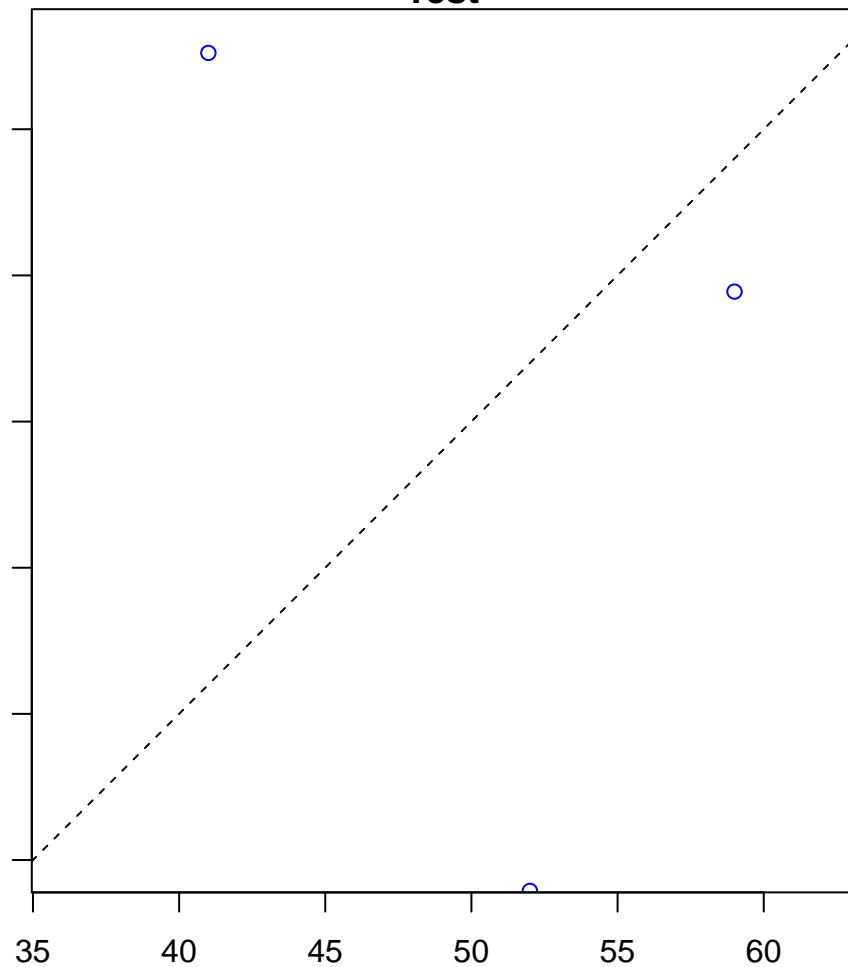


regulation of microvillus organization (Score: 77.182424)

Control

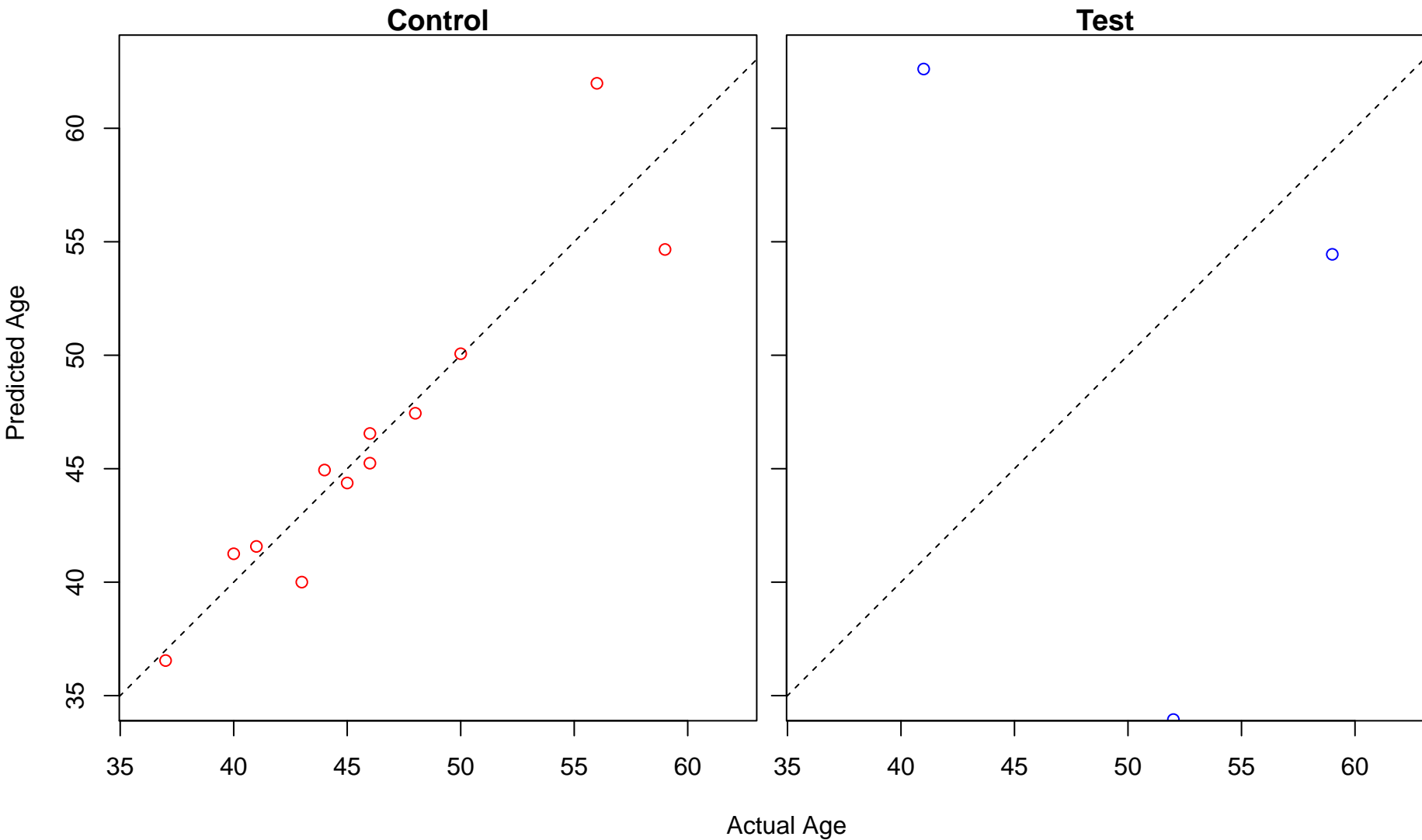


Test

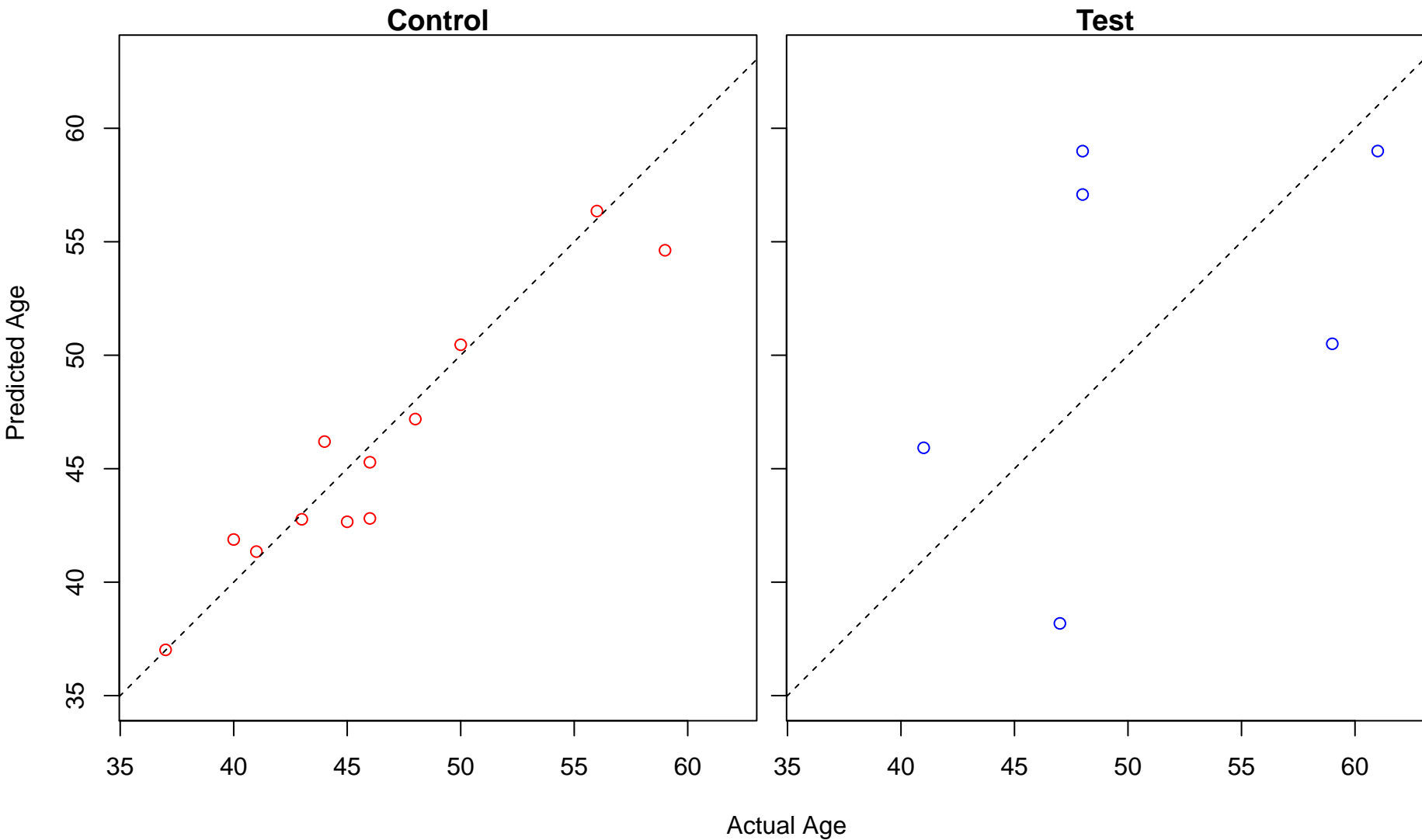


Actual Age

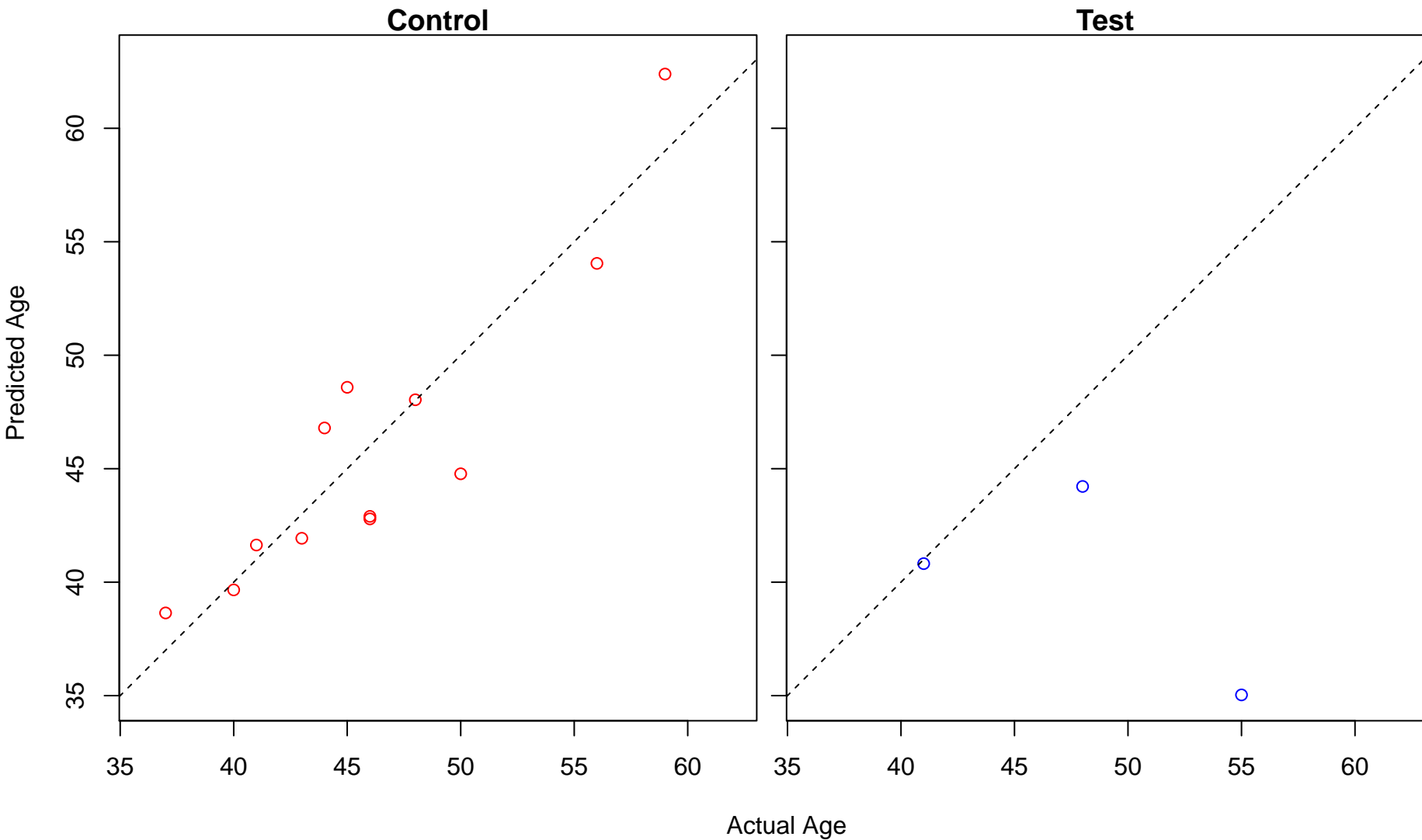
regulation of microvillus assembly (Score: 77.182424)



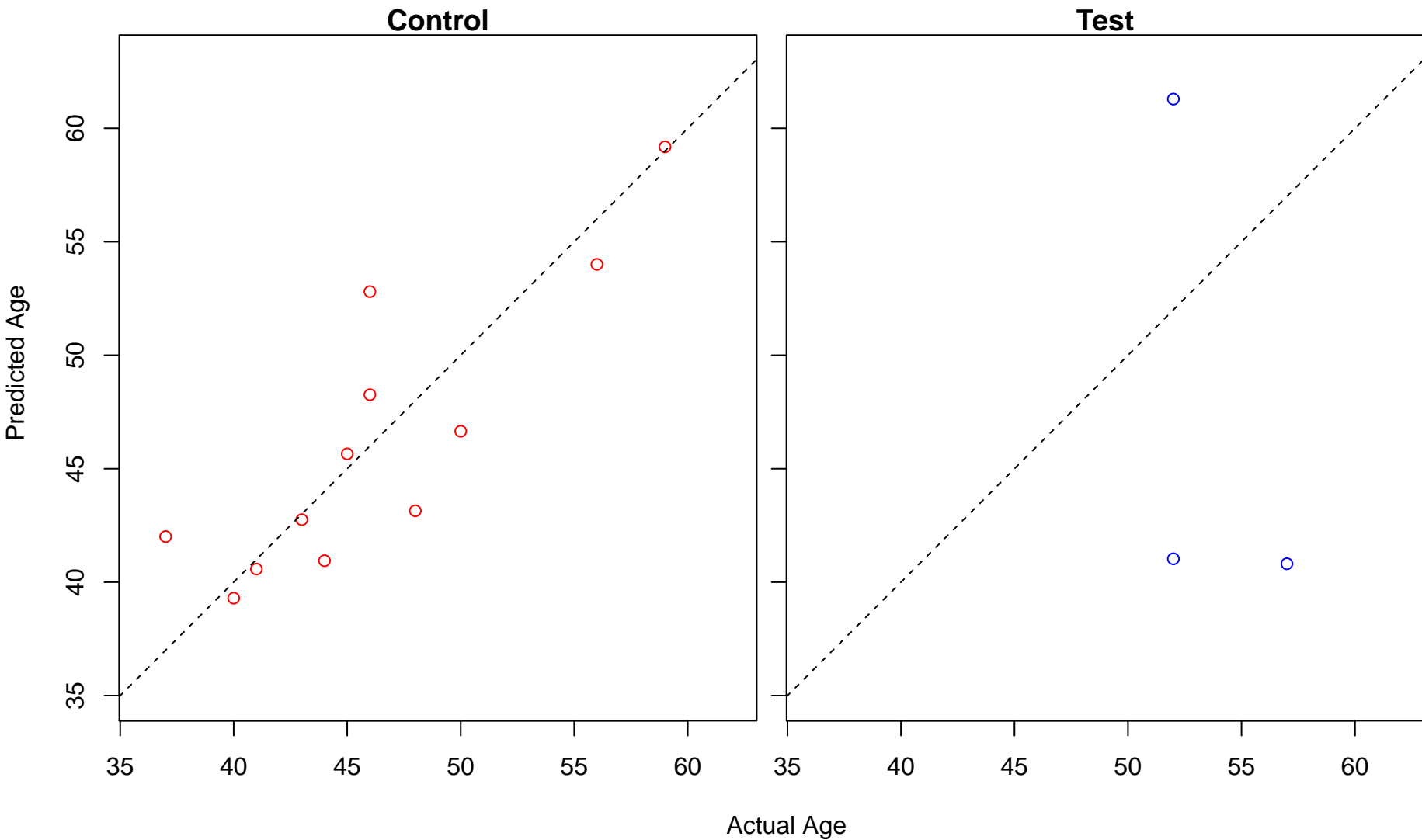
glutamine transport (Score: 76.017670)



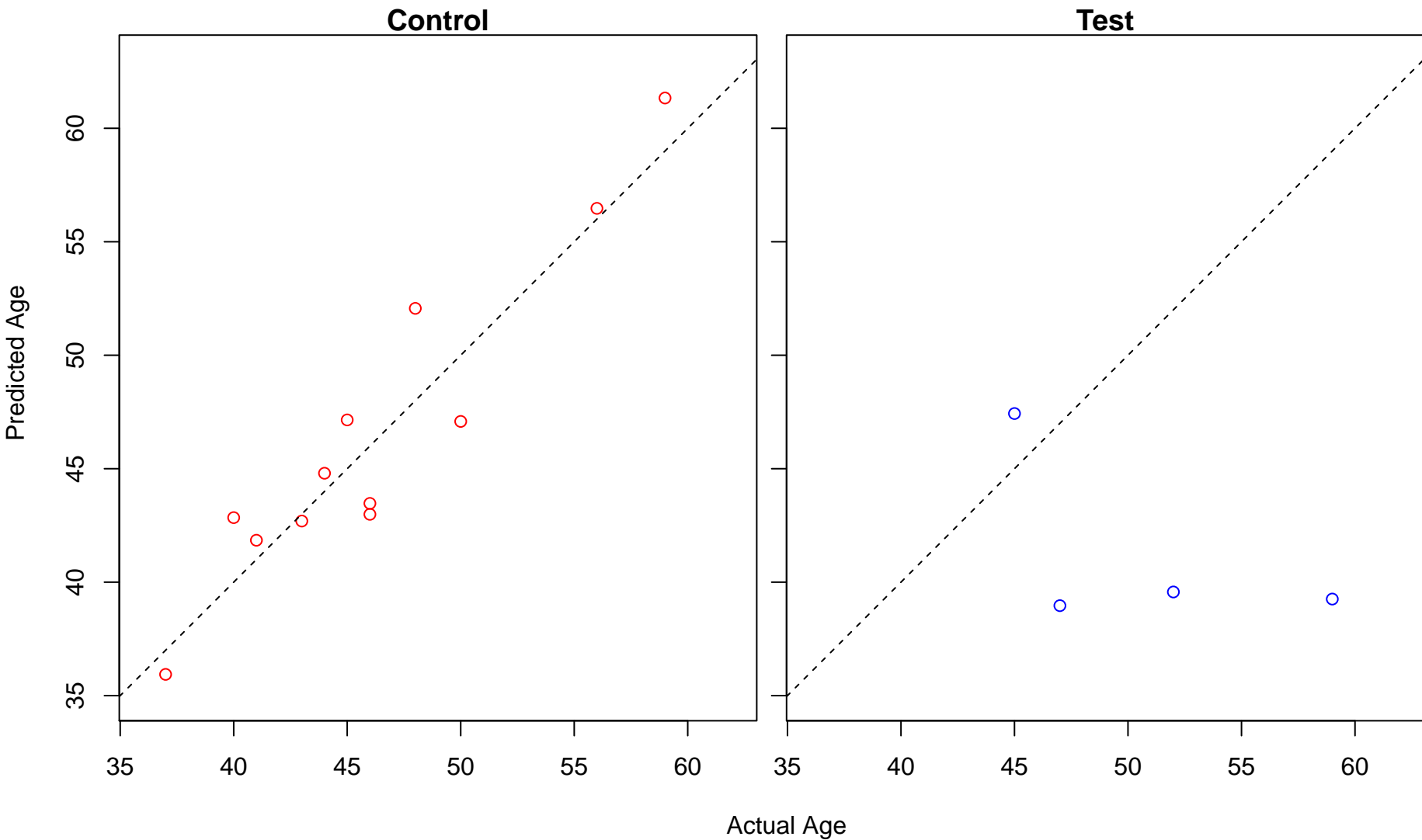
neuroblast proliferation (Score: 75.439543)



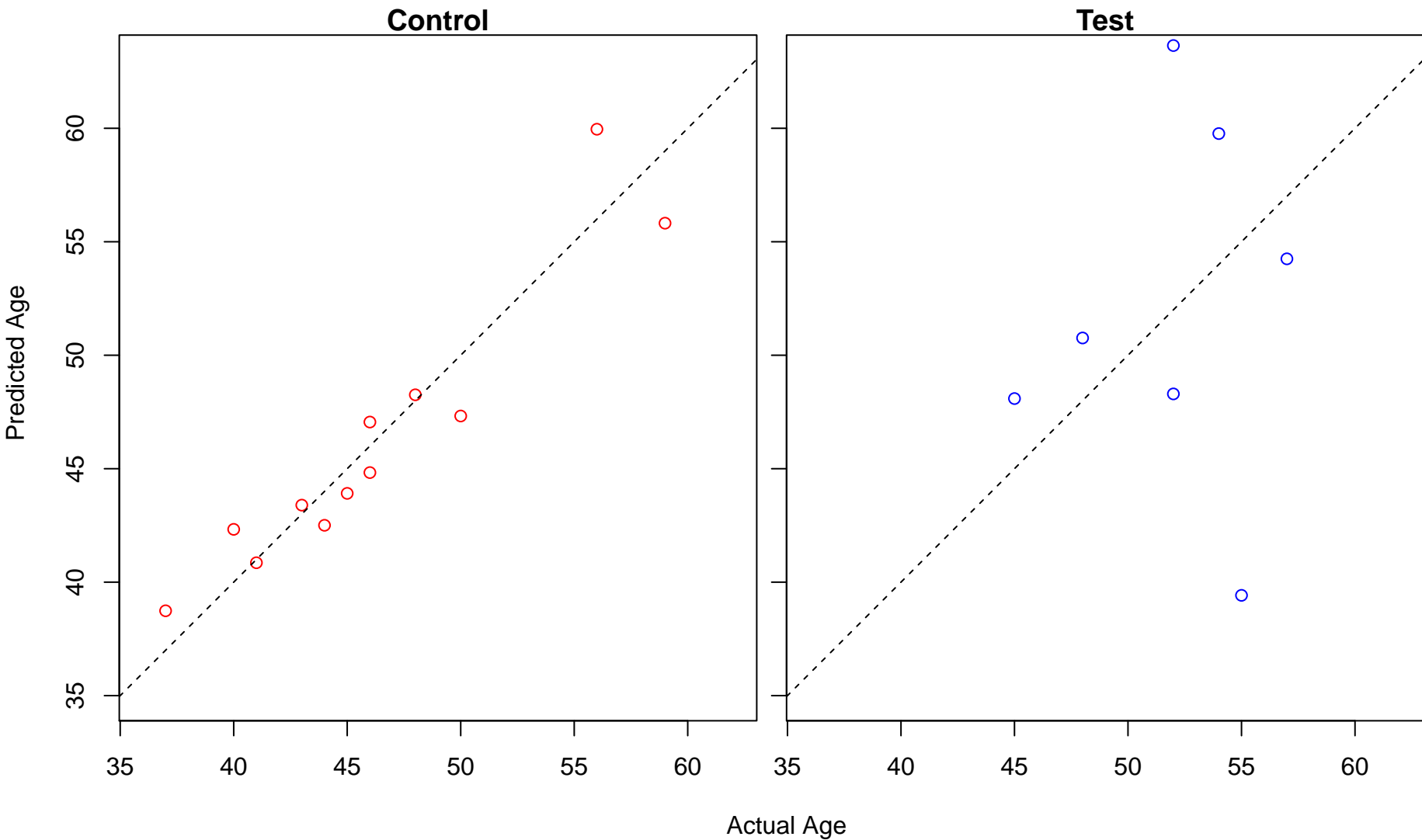
neutrophil homeostasis (Score: 74.653542)



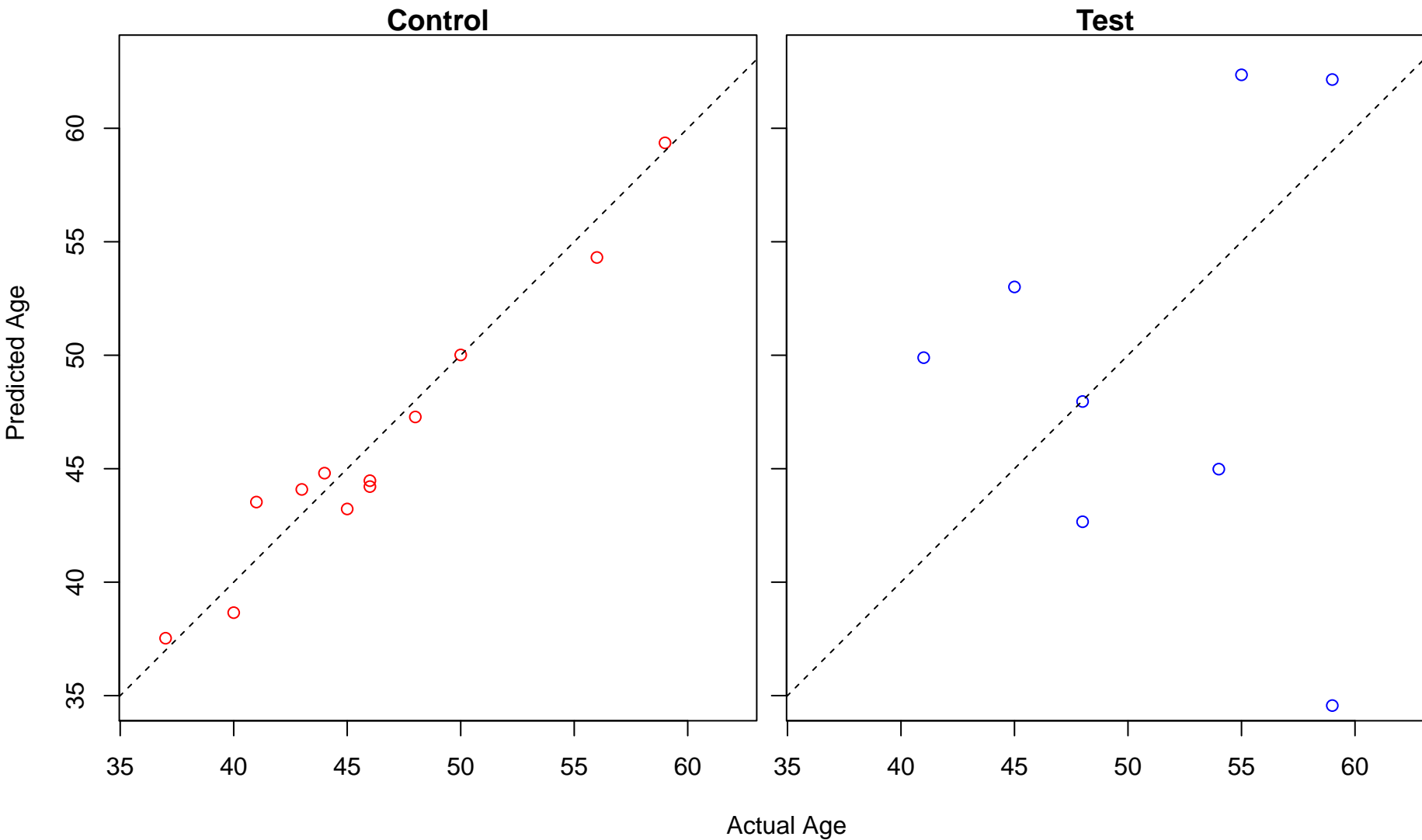
sequestering of metal ion (Score: 73.463055)



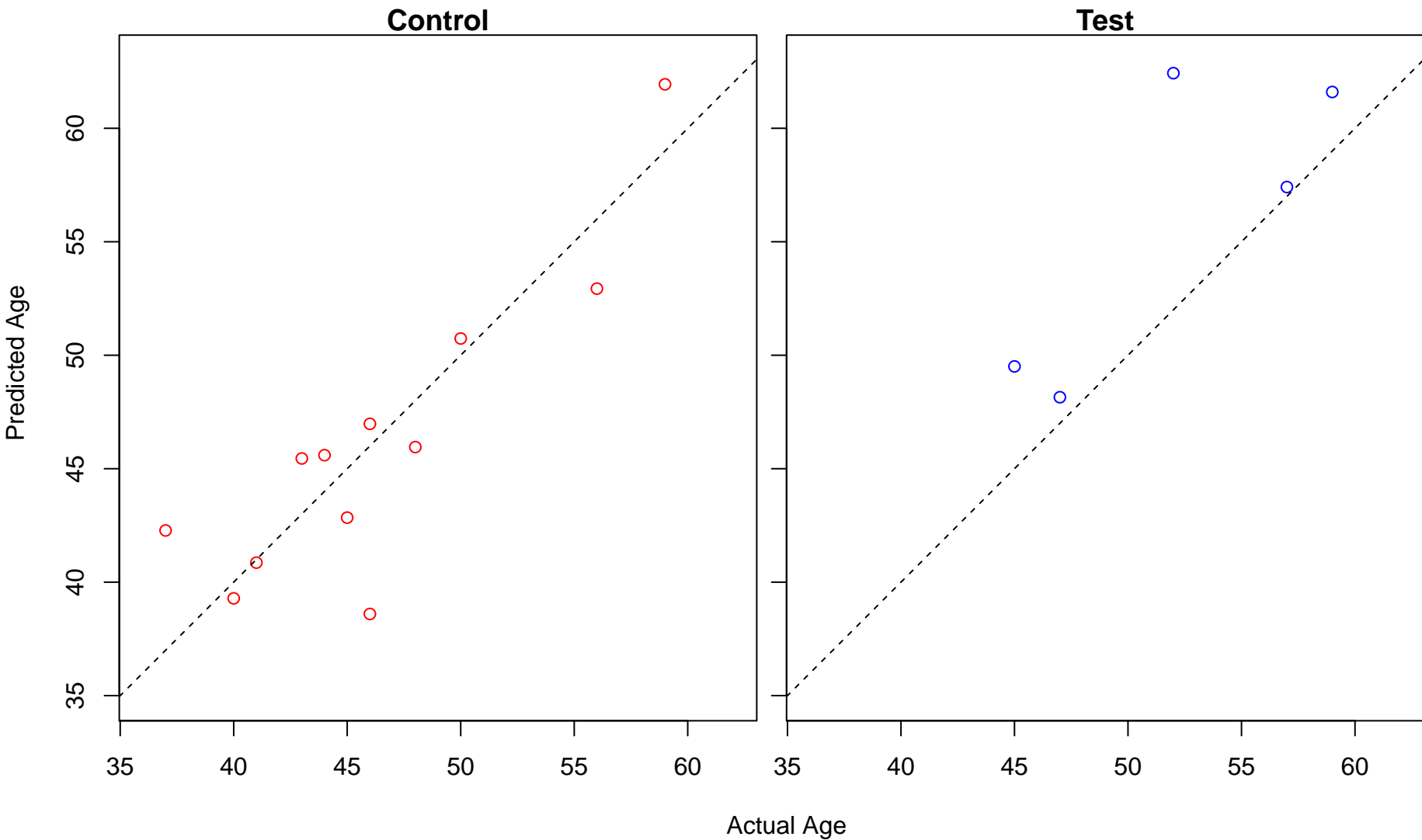
negative regulation of protein sumoylation (Score: 73.111073)



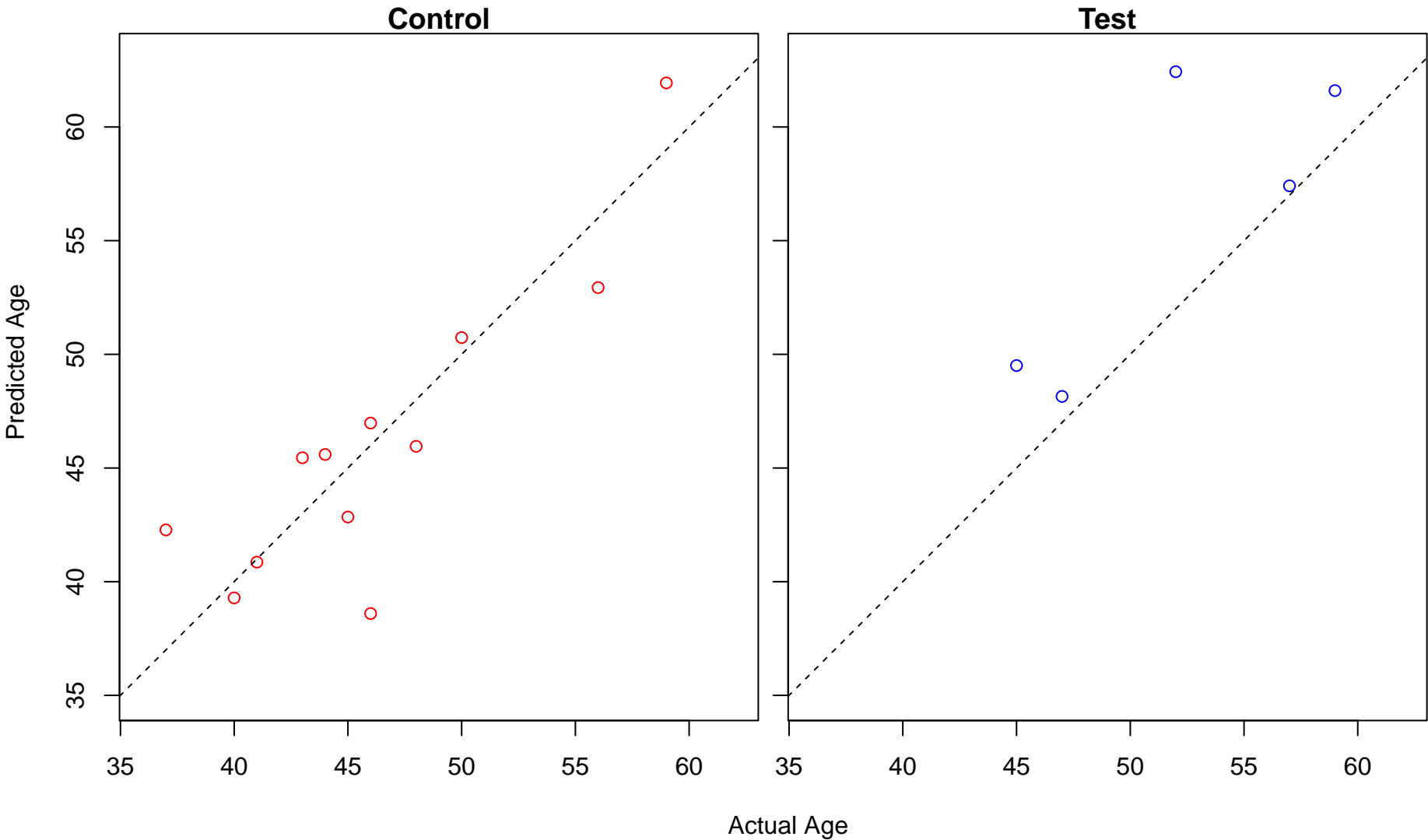
nucleobase-containing small molecule interconversion (Score: 71.325732)



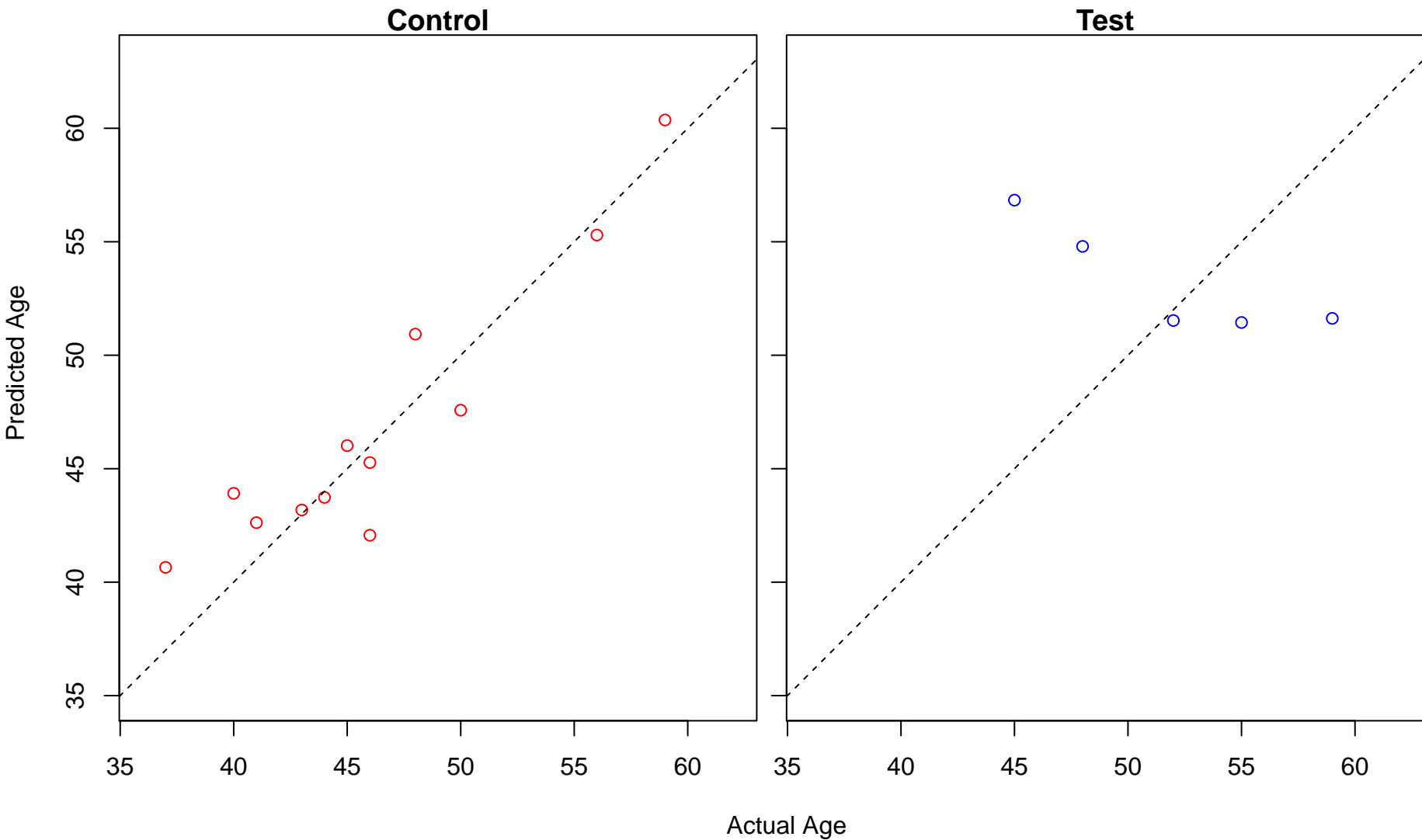
cardiac muscle cell–cardiac muscle cell adhesion (Score: 67.843427)



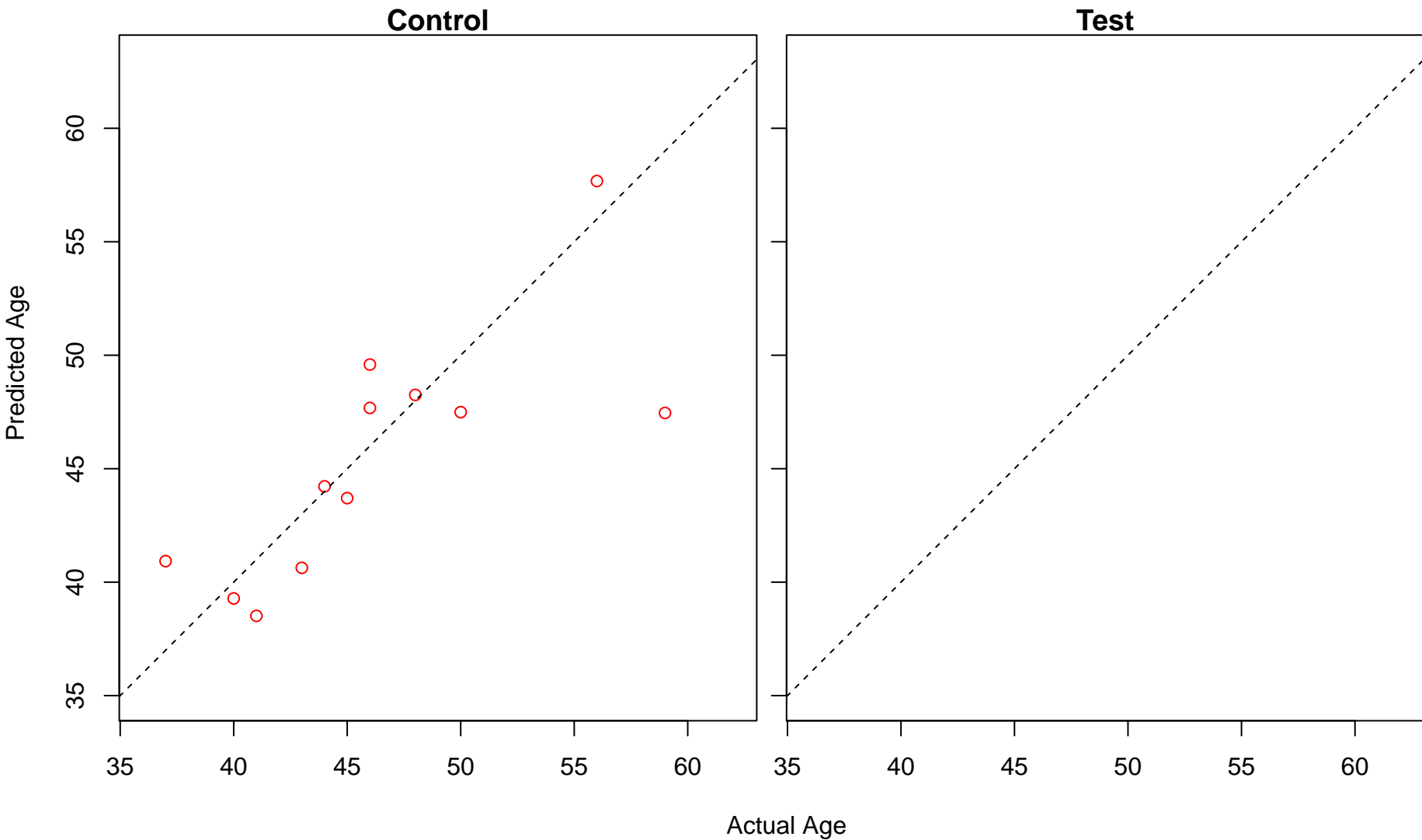
bundle of His cell–Purkinje myocyte adhesion involved in cell communication (Score: 67.843427)



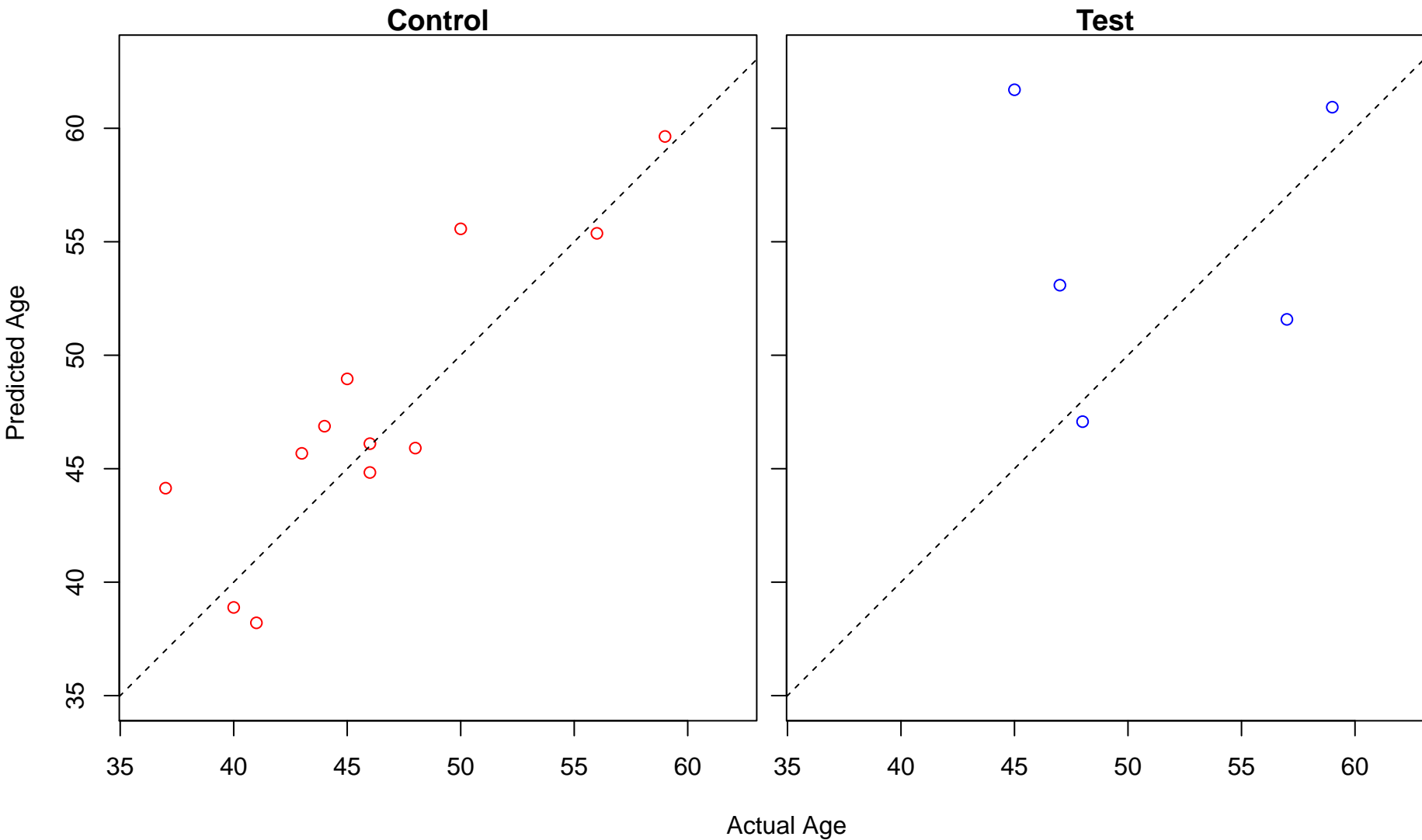
positive regulation of Rho protein signal transduction (Score: 62.166187)



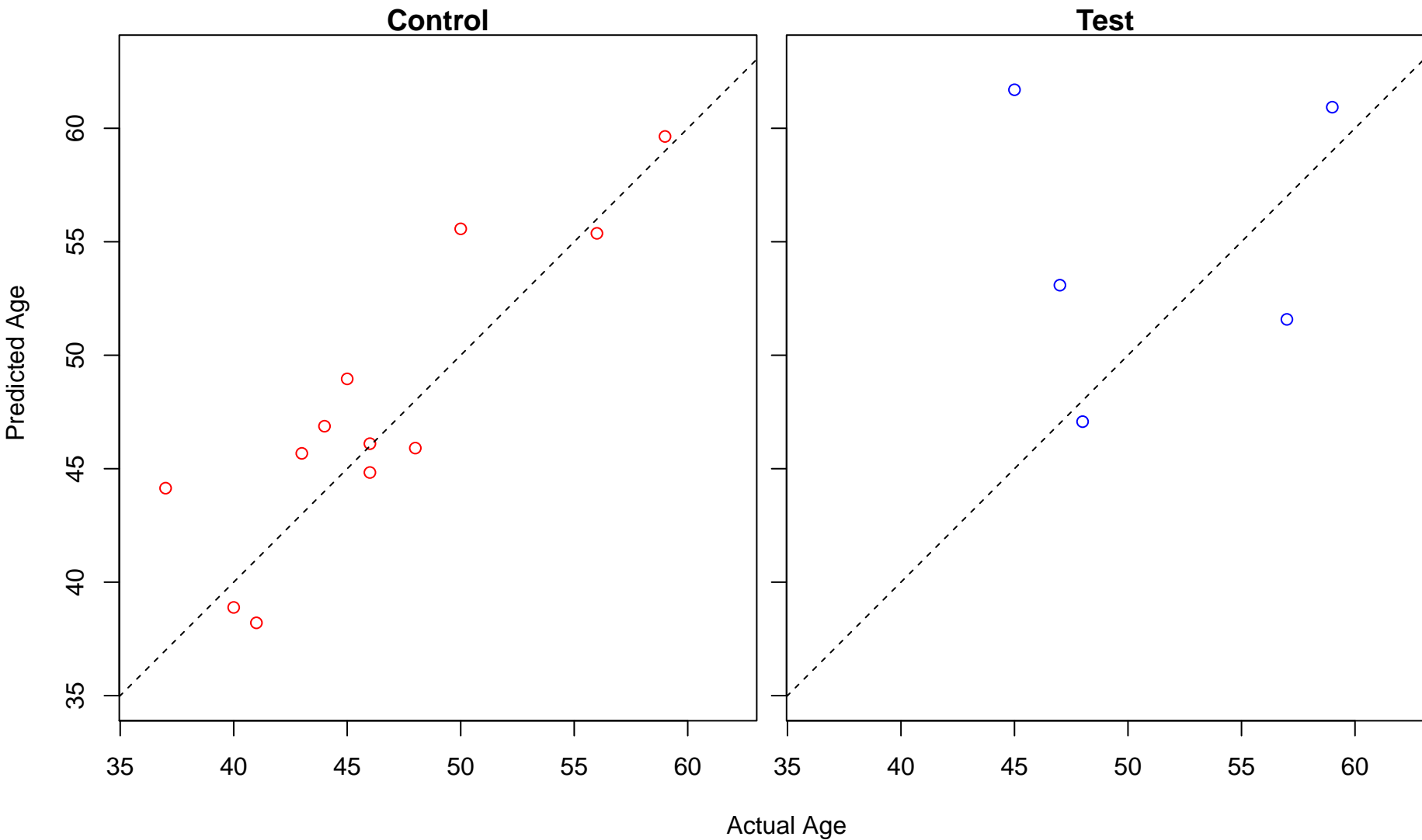
detection of chemical stimulus involved in sensory perception (Score: 61.484764)



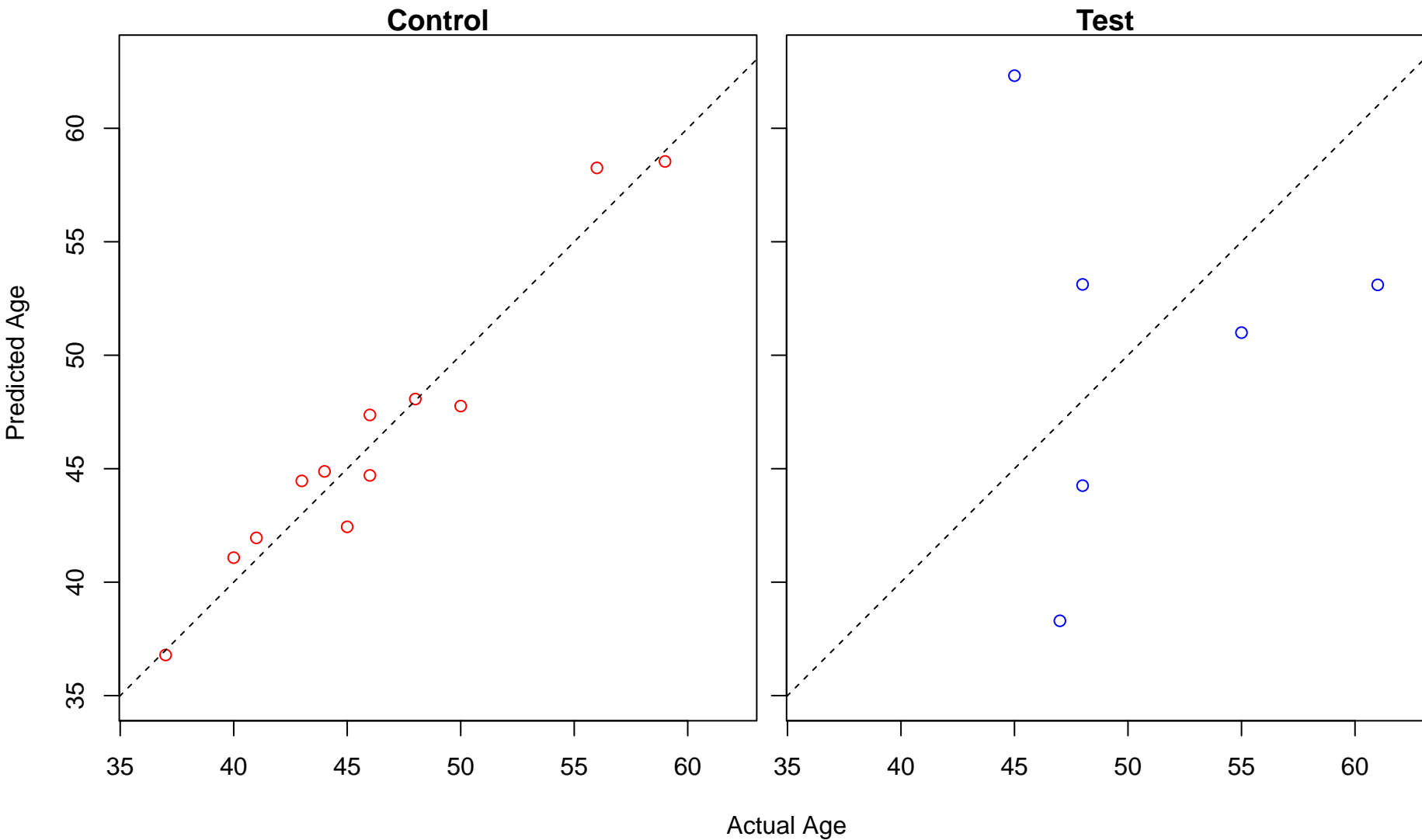
regulation of protein localization to early endosome (Score: 59.887041)



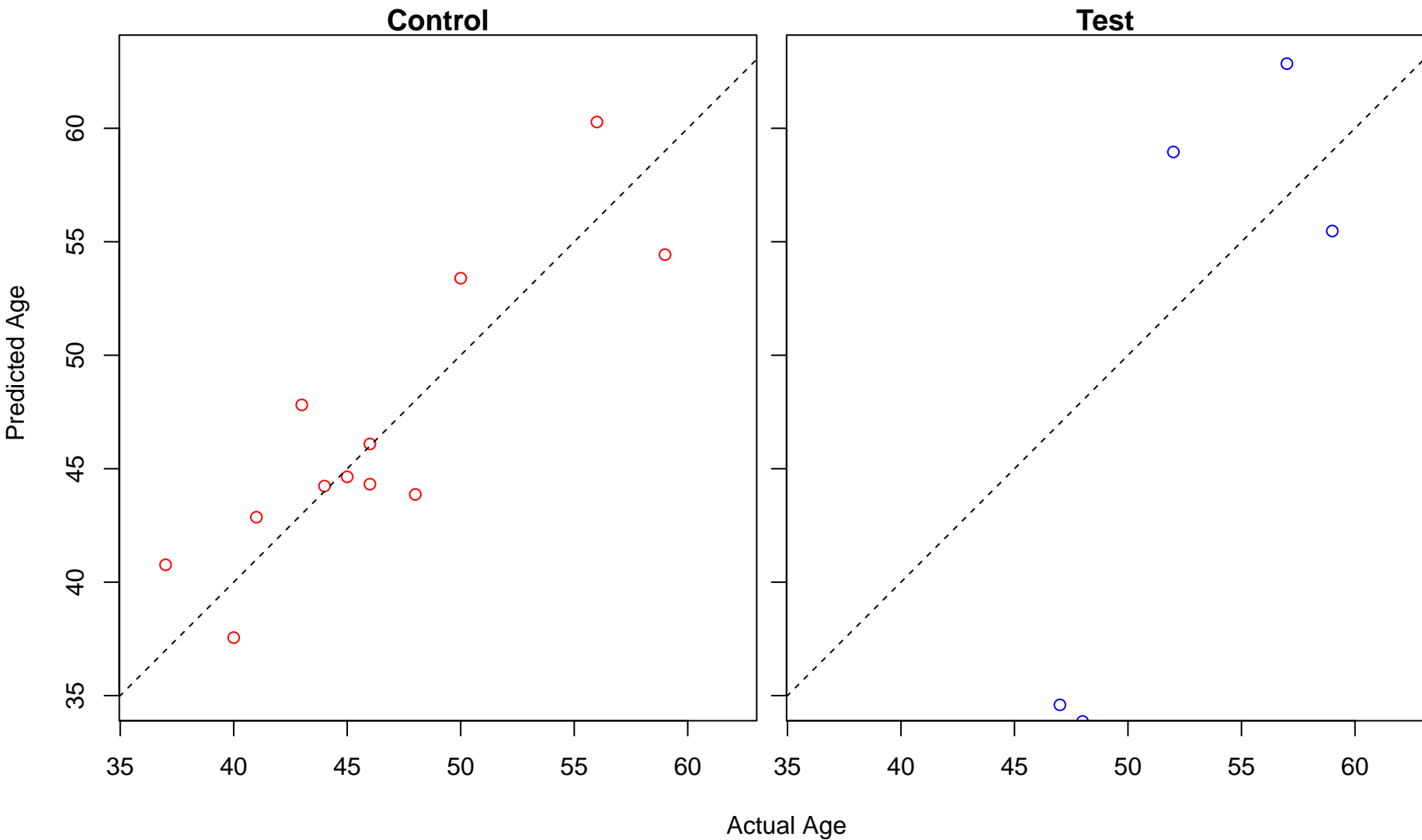
positive regulation of protein localization to early endosome (Score: 59.887041)



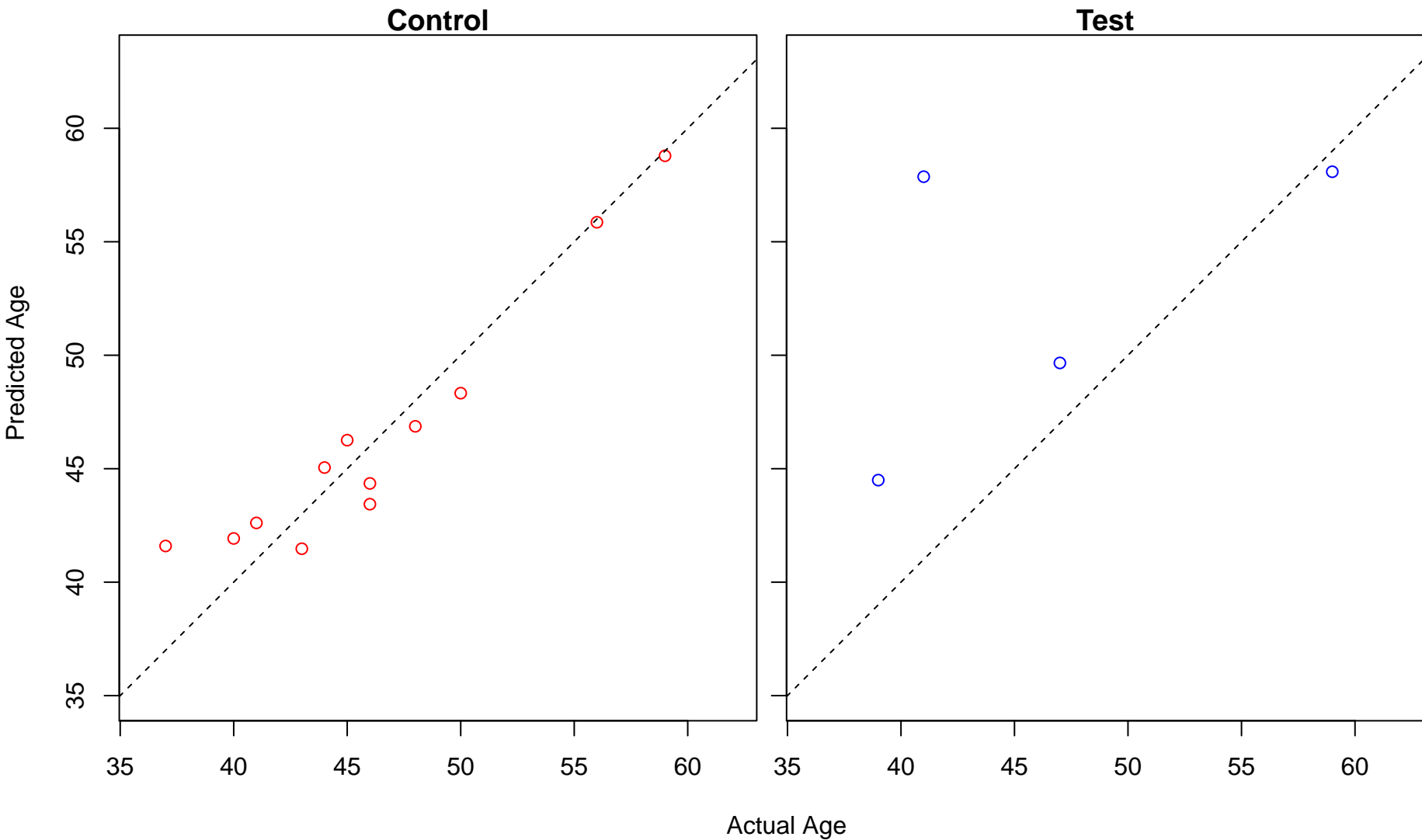
response to acid chemical (Score: 58.855894)



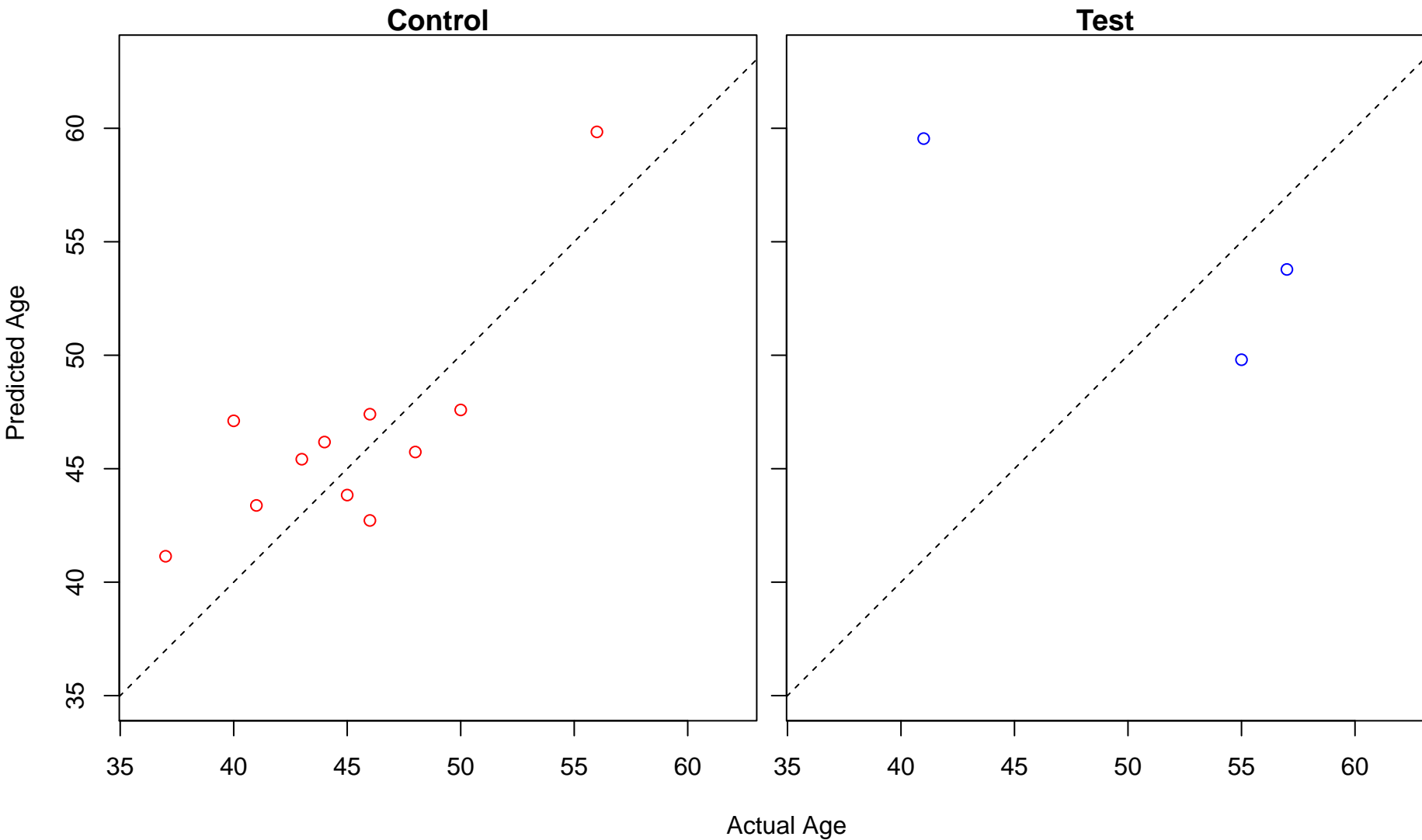
positive regulation of tolerance induction (Score: 57.992291)



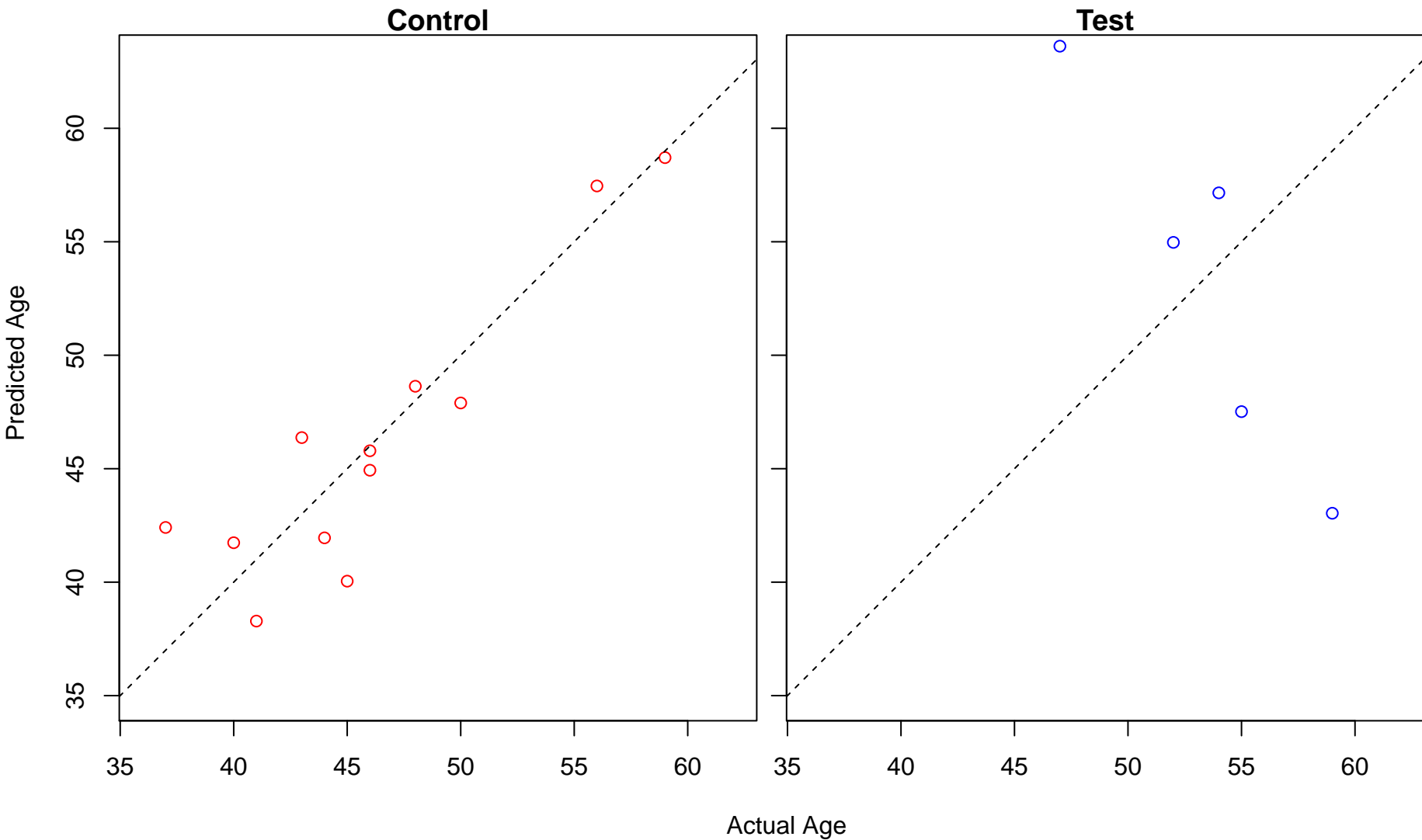
regulation of cardiac muscle contraction by calcium ion signaling (Score: 57.289658)



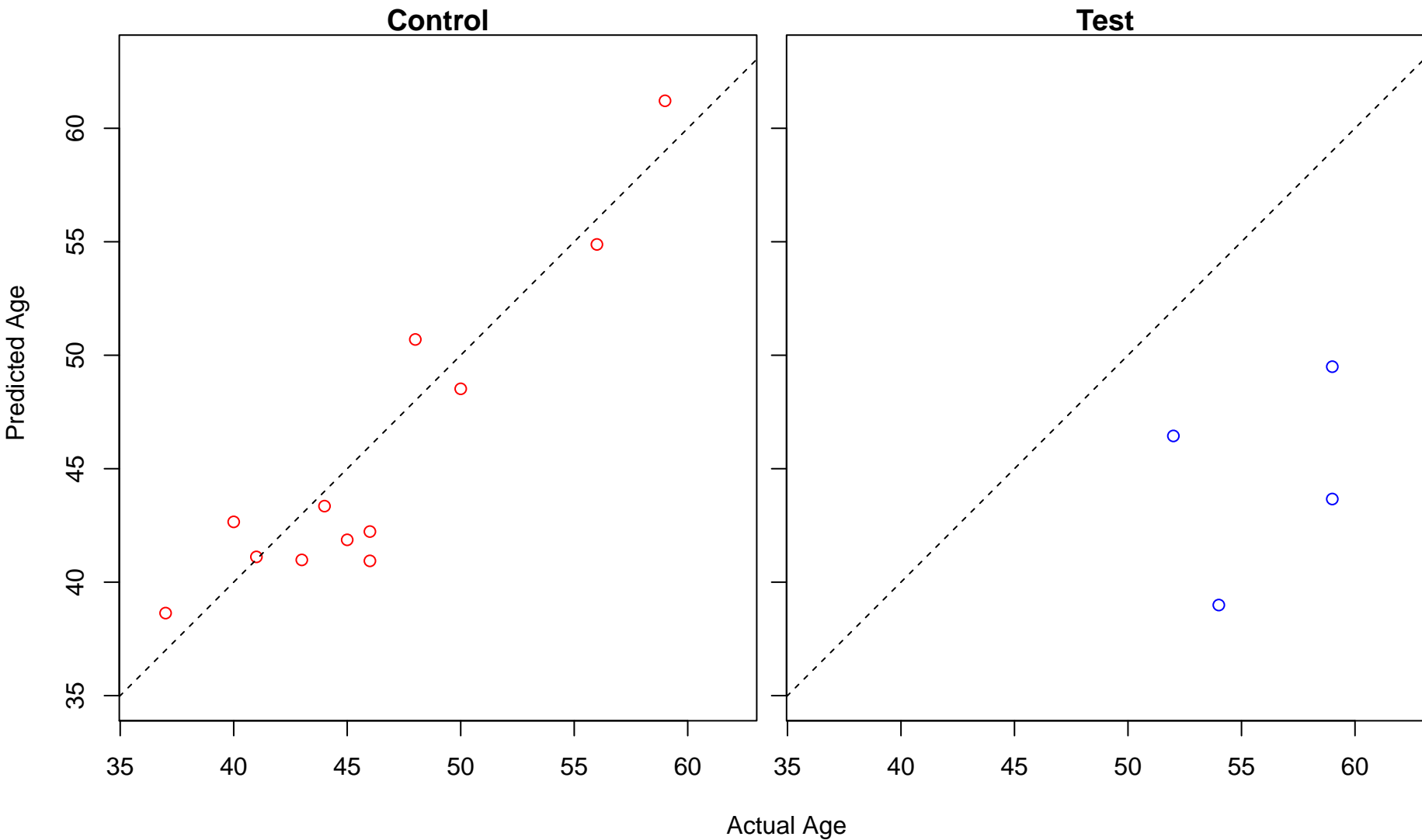
neuromuscular process controlling balance (Score: 57.243002)



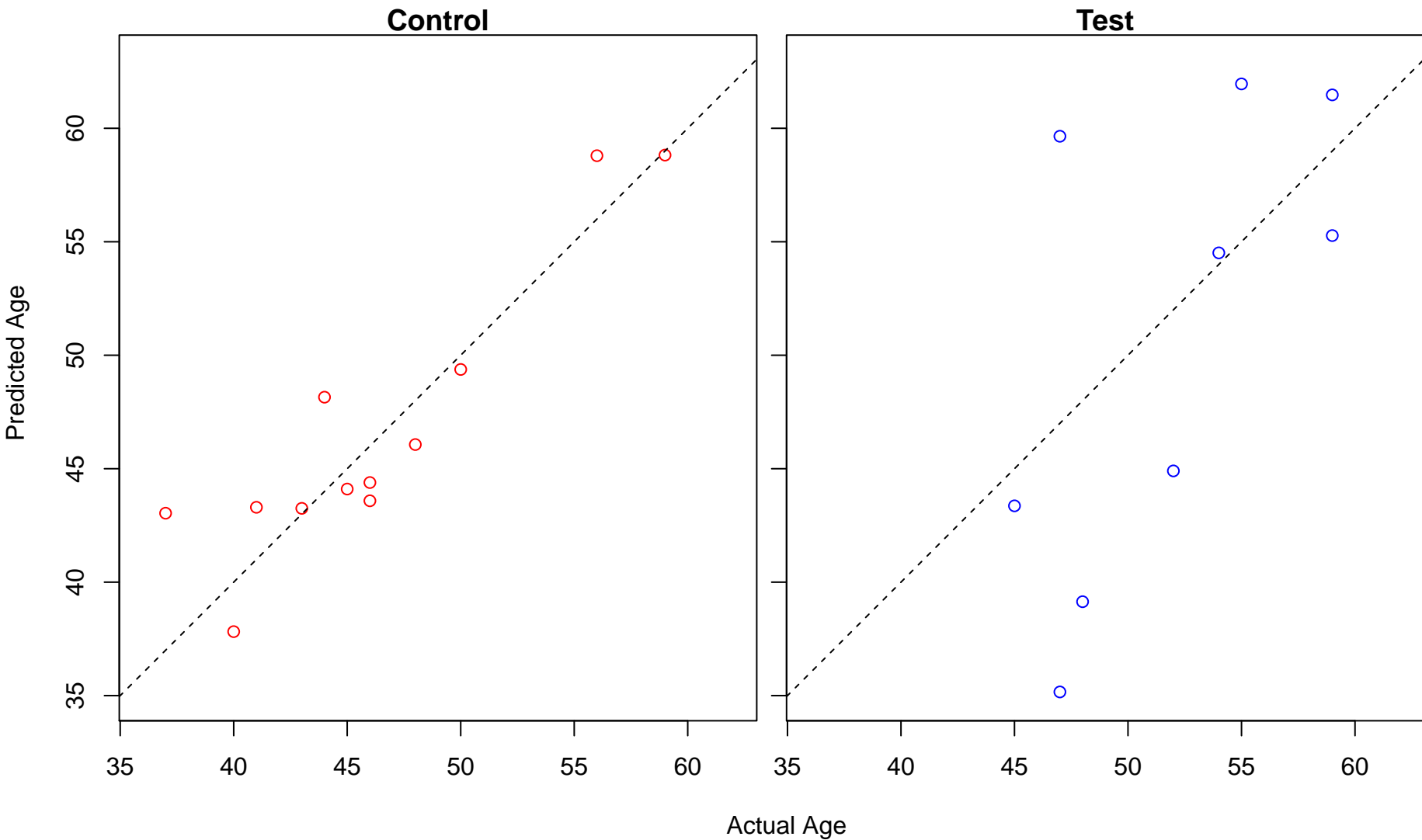
bicellular tight junction assembly (Score: 57.159975)



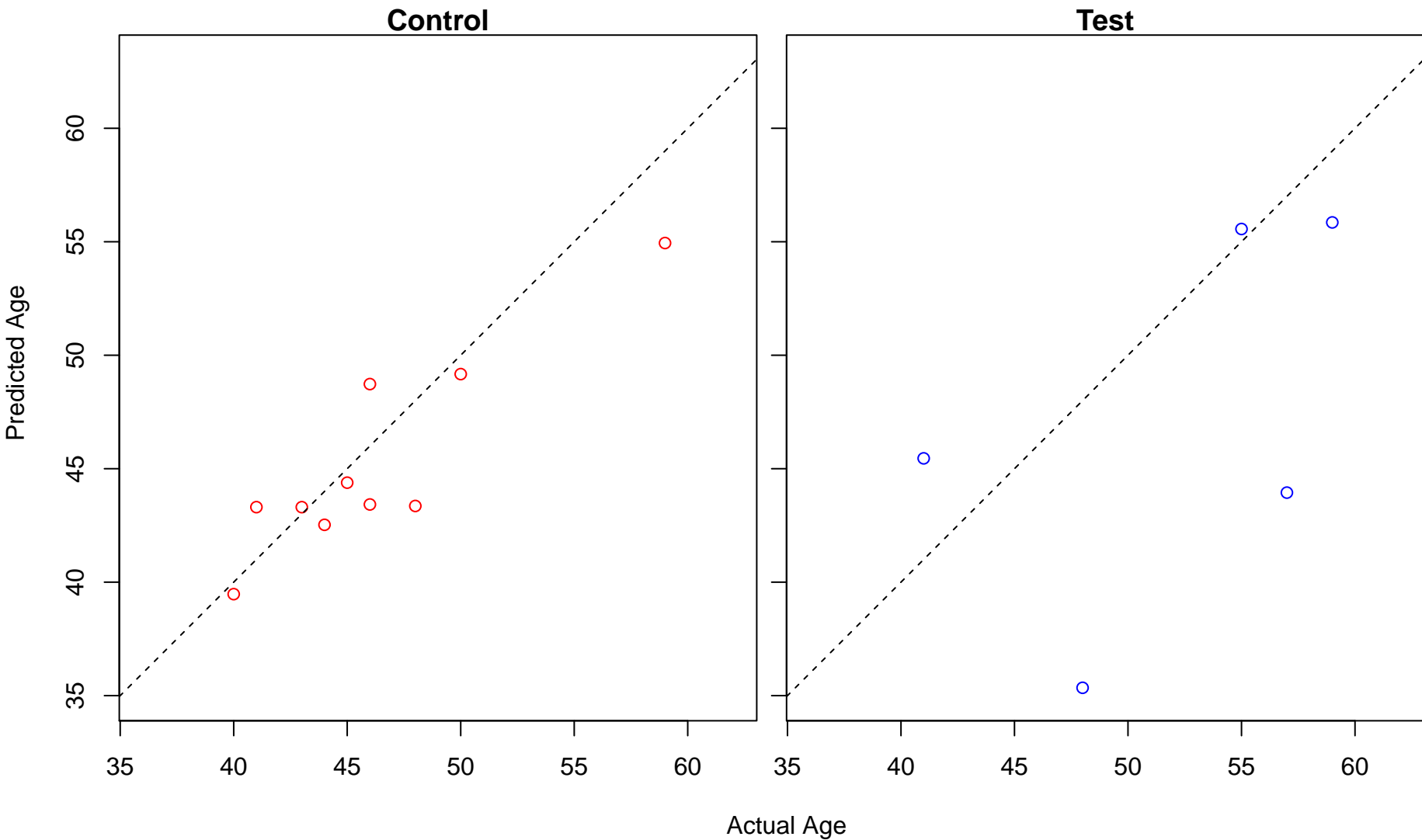
intestinal absorption (Score: 56.157571)



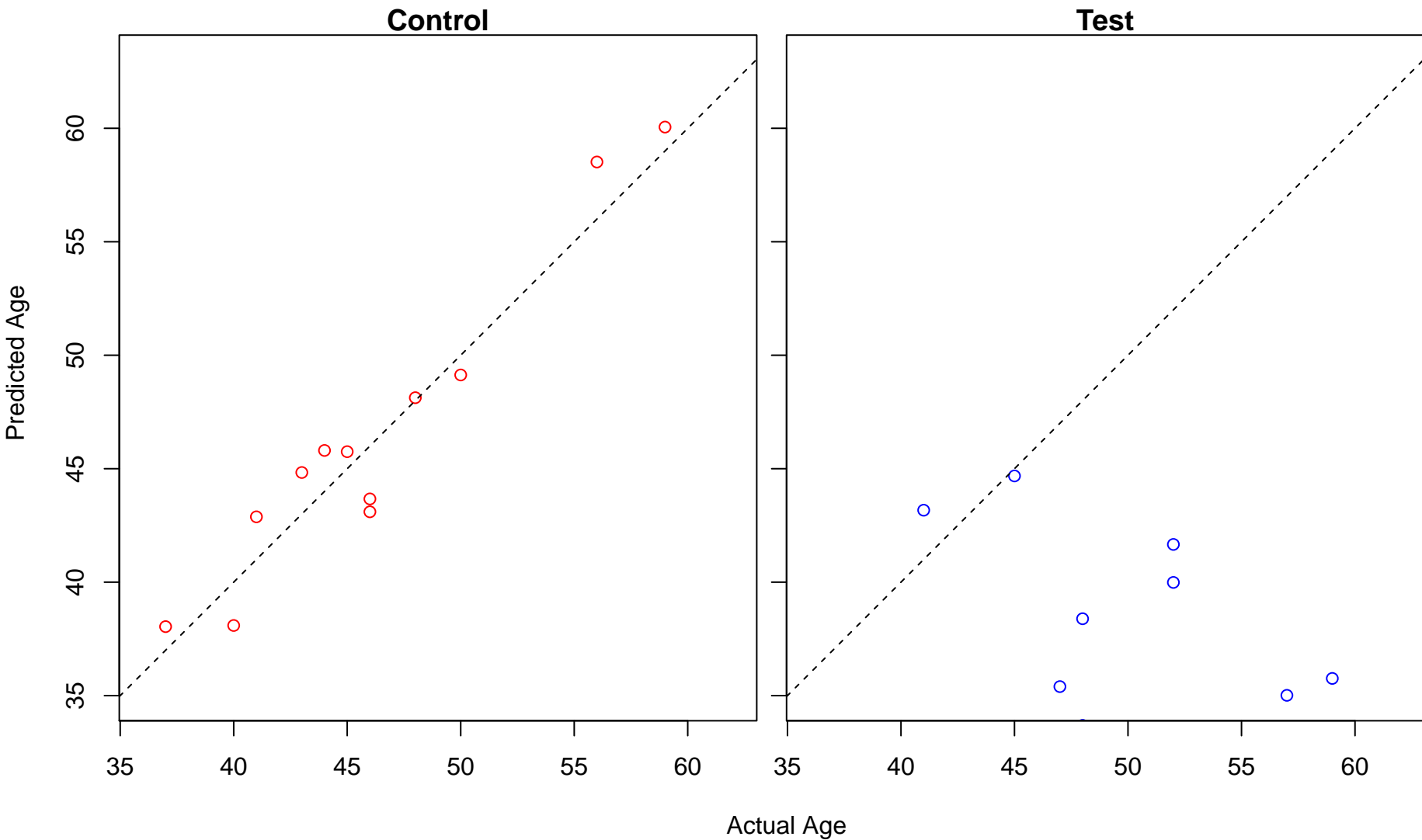
macropinocytosis (Score: 55.713761)



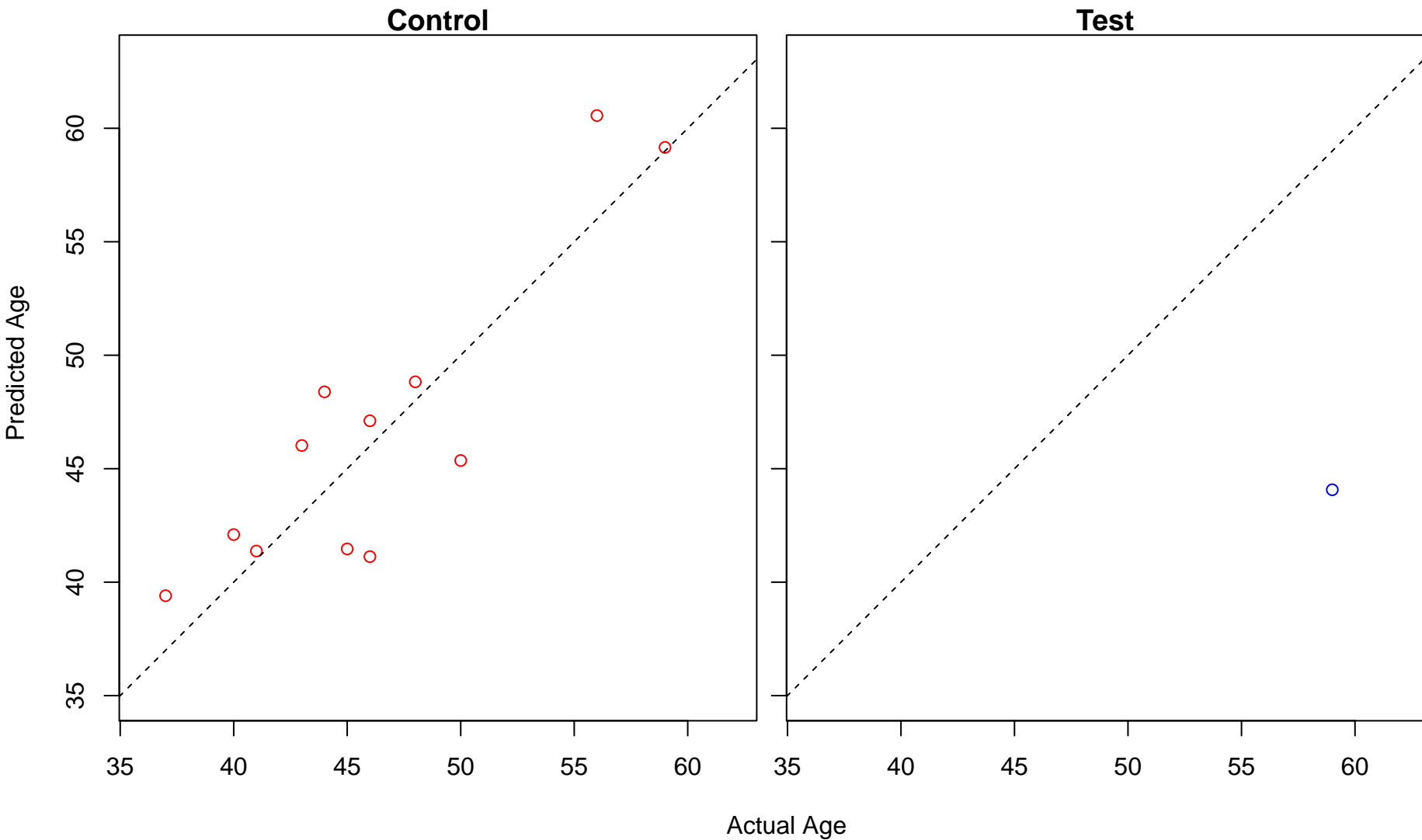
negative regulation of oligodendrocyte differentiation (Score: 55.578998)



negative regulation of antigen processing and presentation (Score: 55.434243)

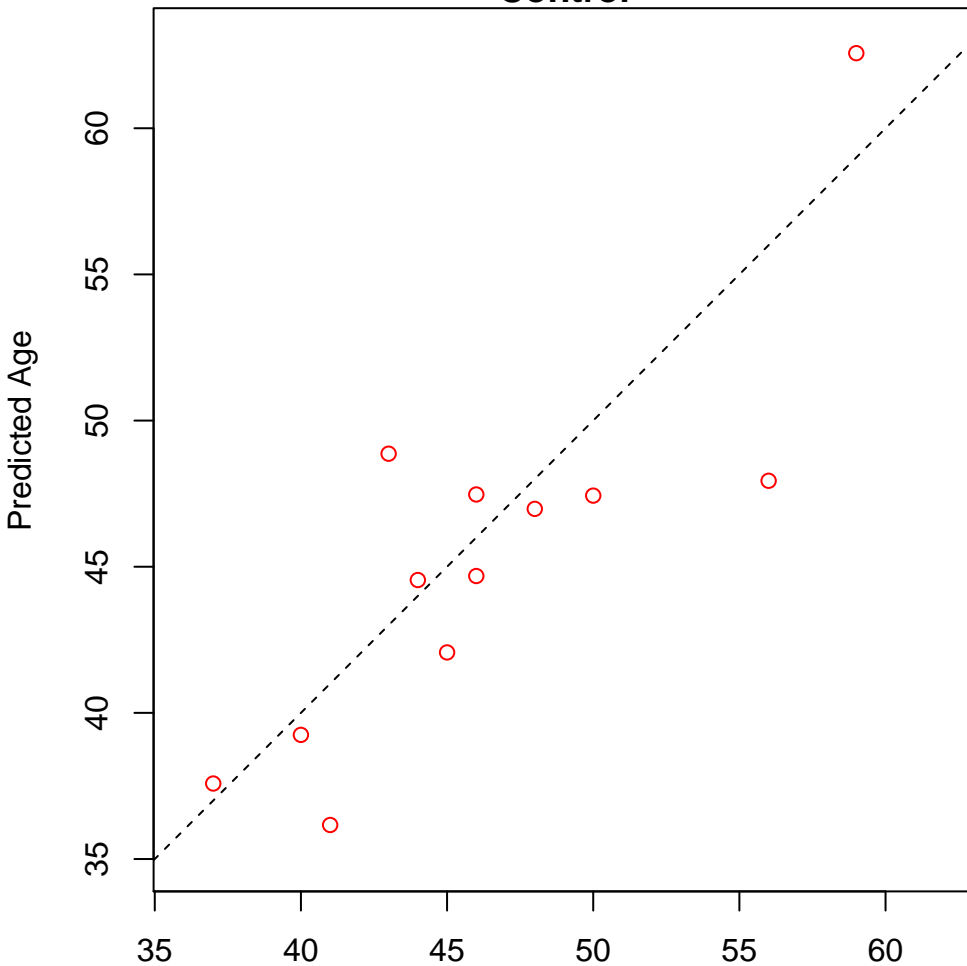


sequestering of actin monomers (Score: 55.258194)

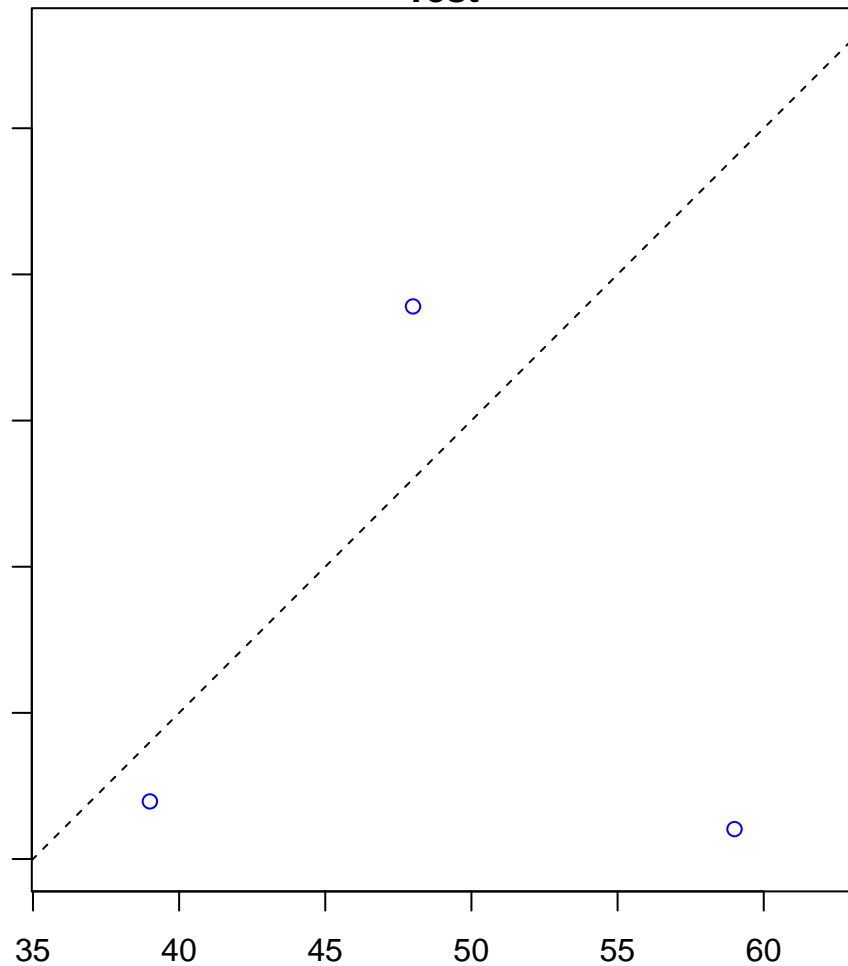


post-embryonic organ development (Score: 54.615133)

Control

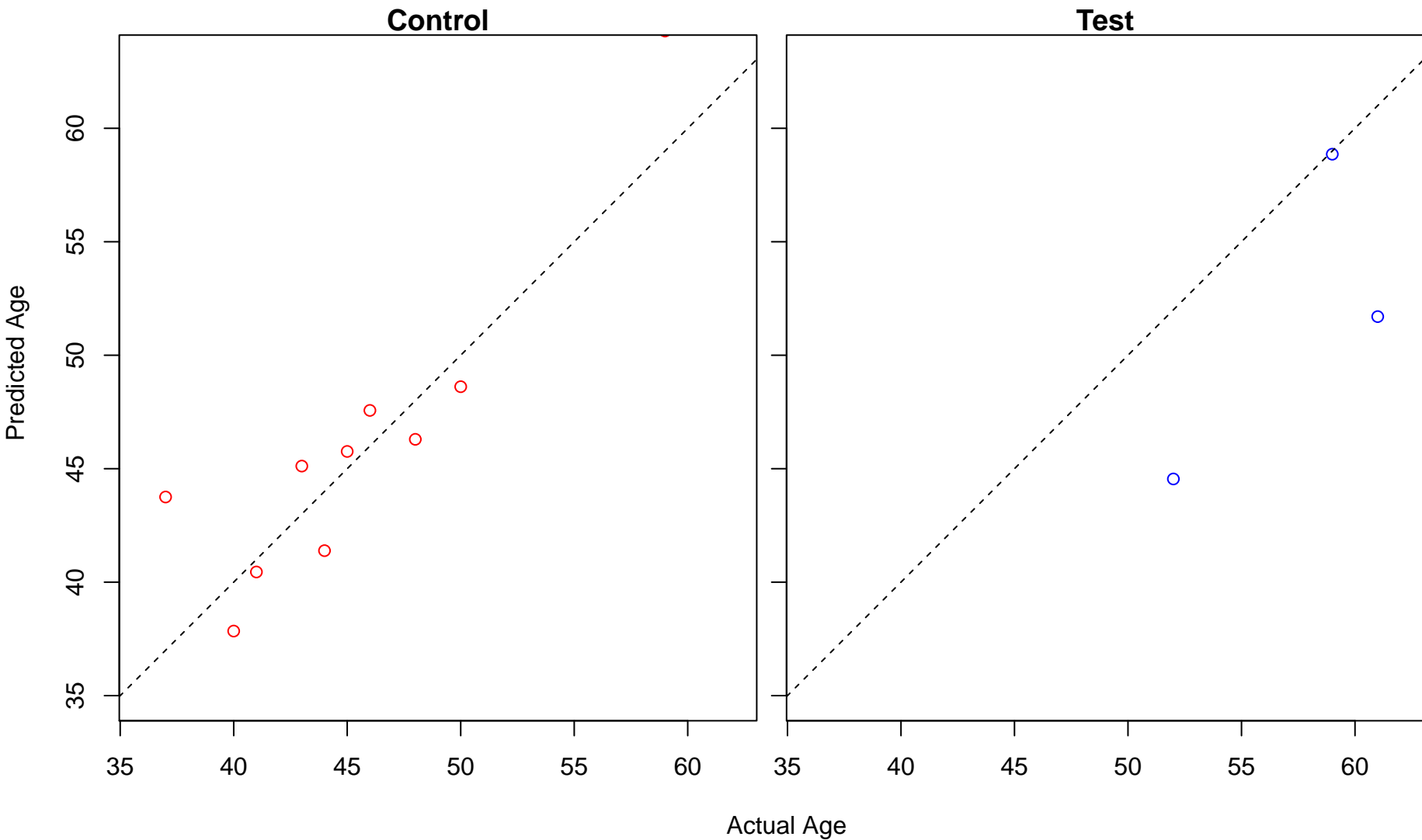


Test

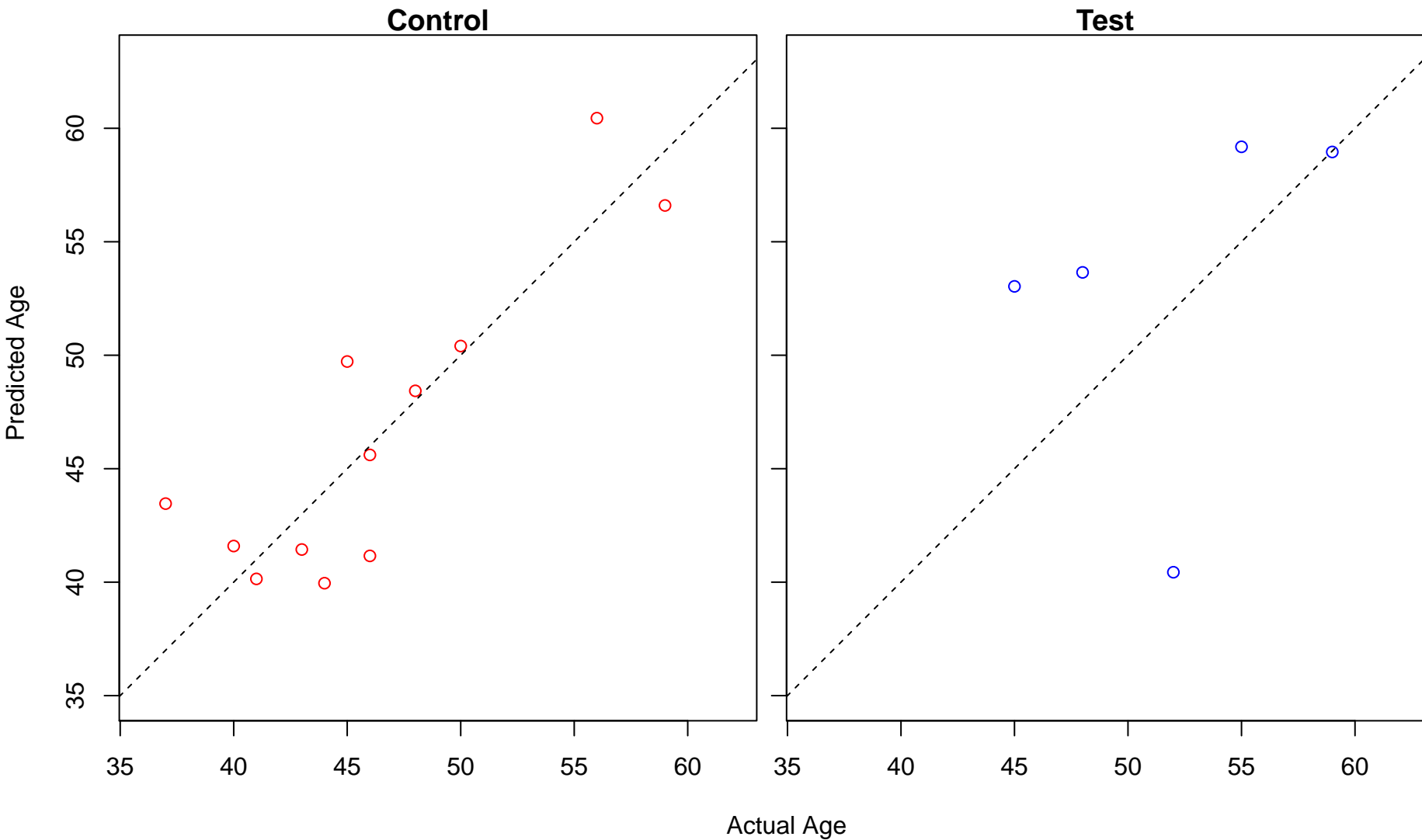


Actual Age

detection of chemical stimulus involved in sensory perception of smell (Score: 53.456969)

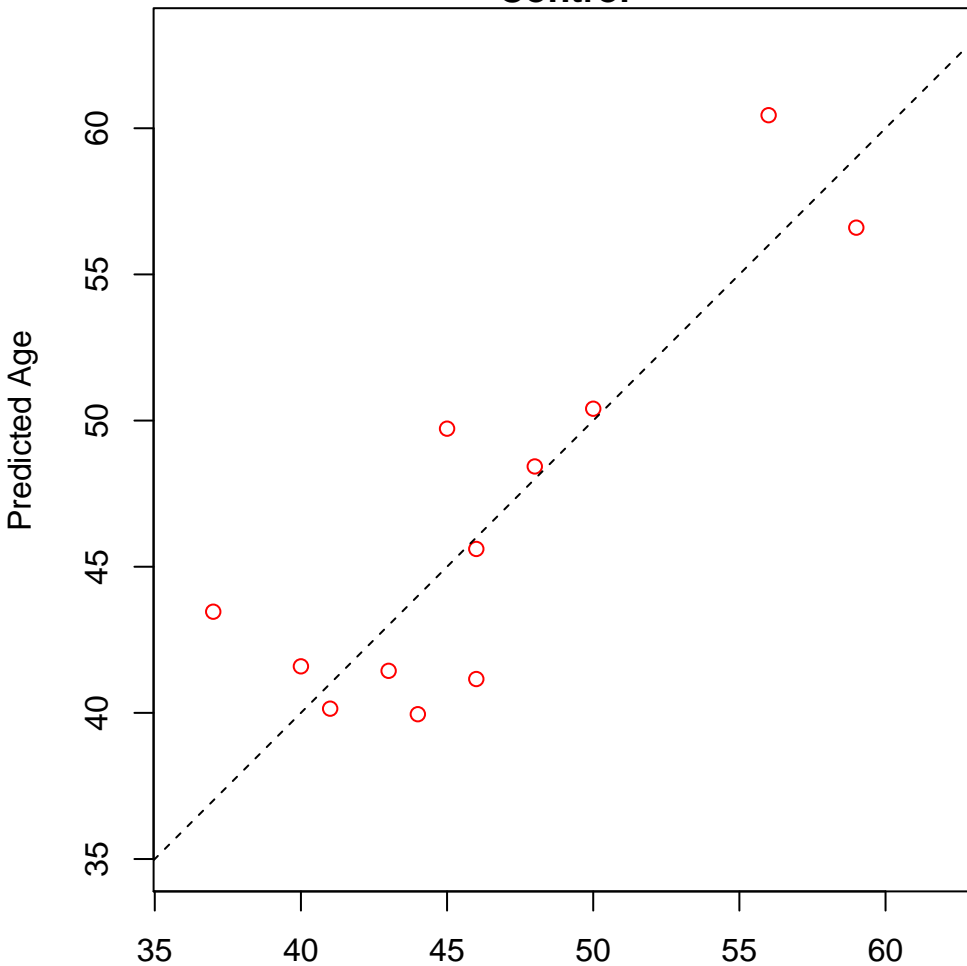


nucleotide-sugar transport (Score: 52.930769)

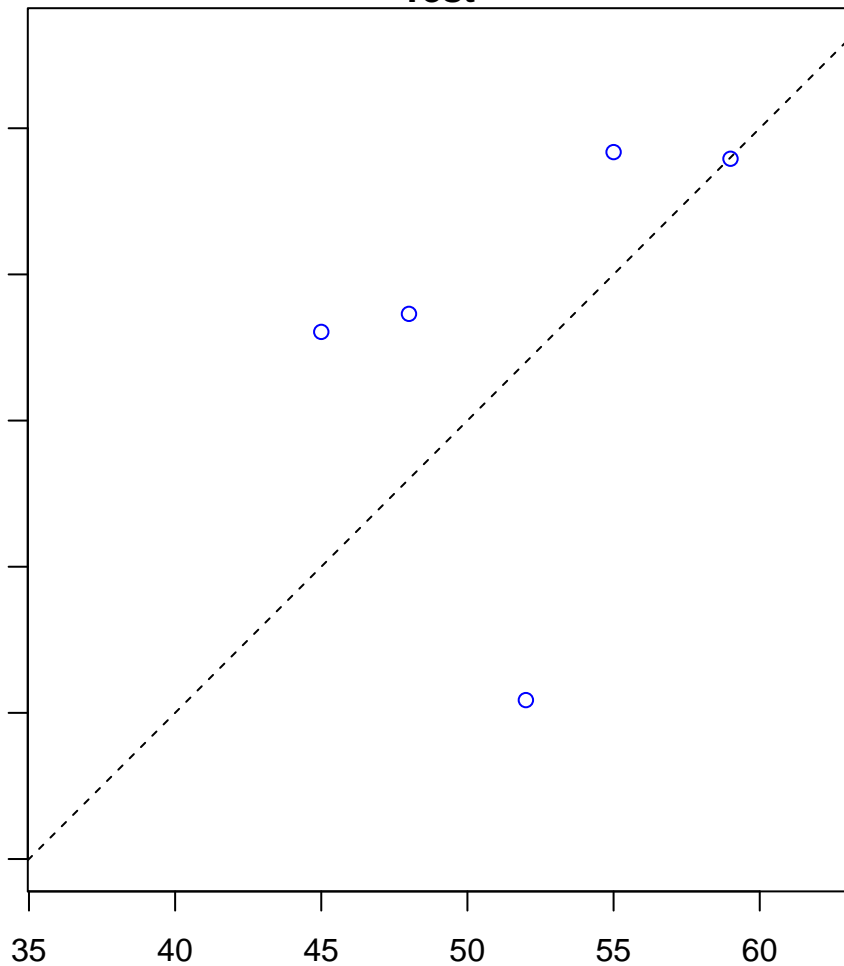


pyrimidine nucleotide–sugar transport (Score: 52.930769)

Control

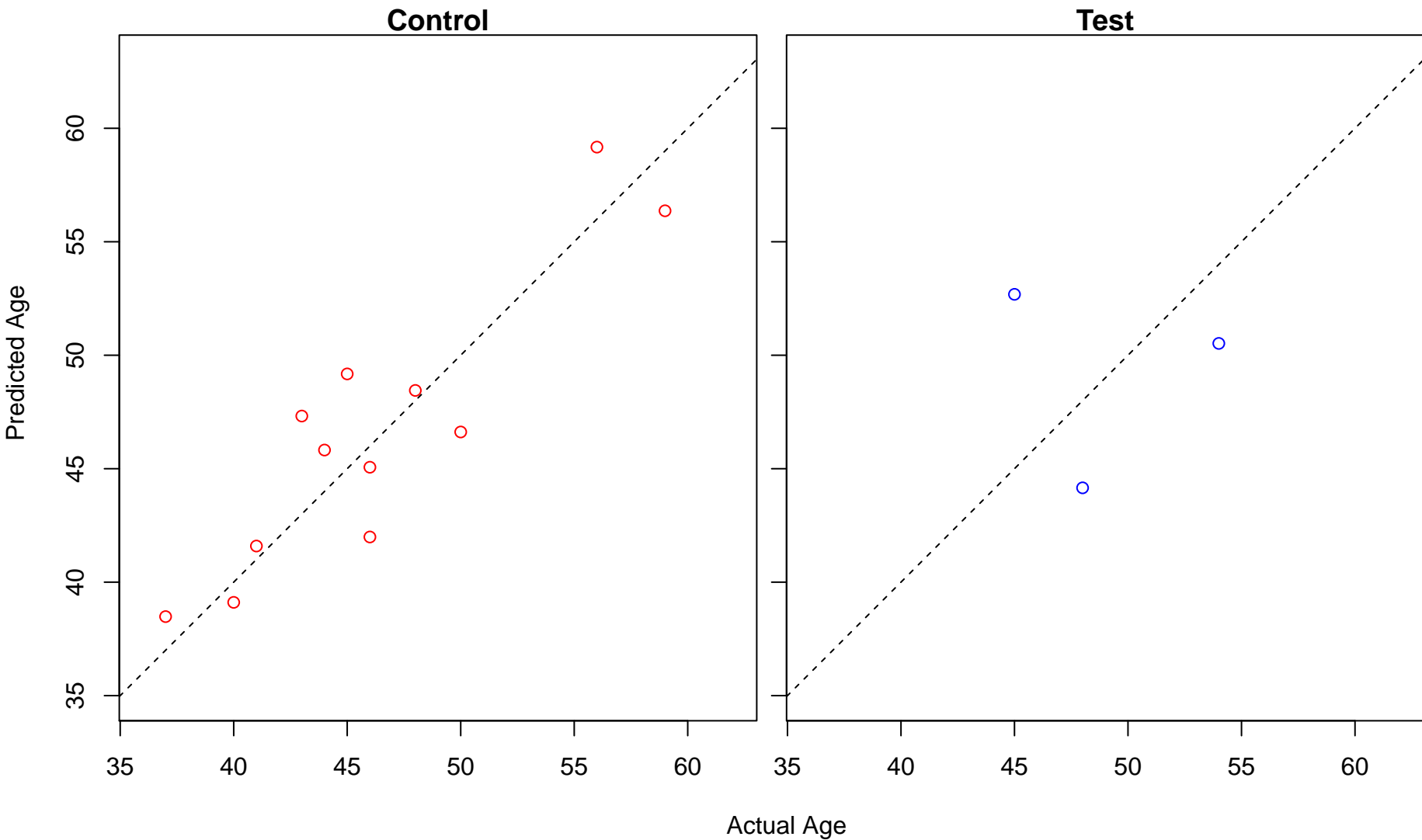


Test



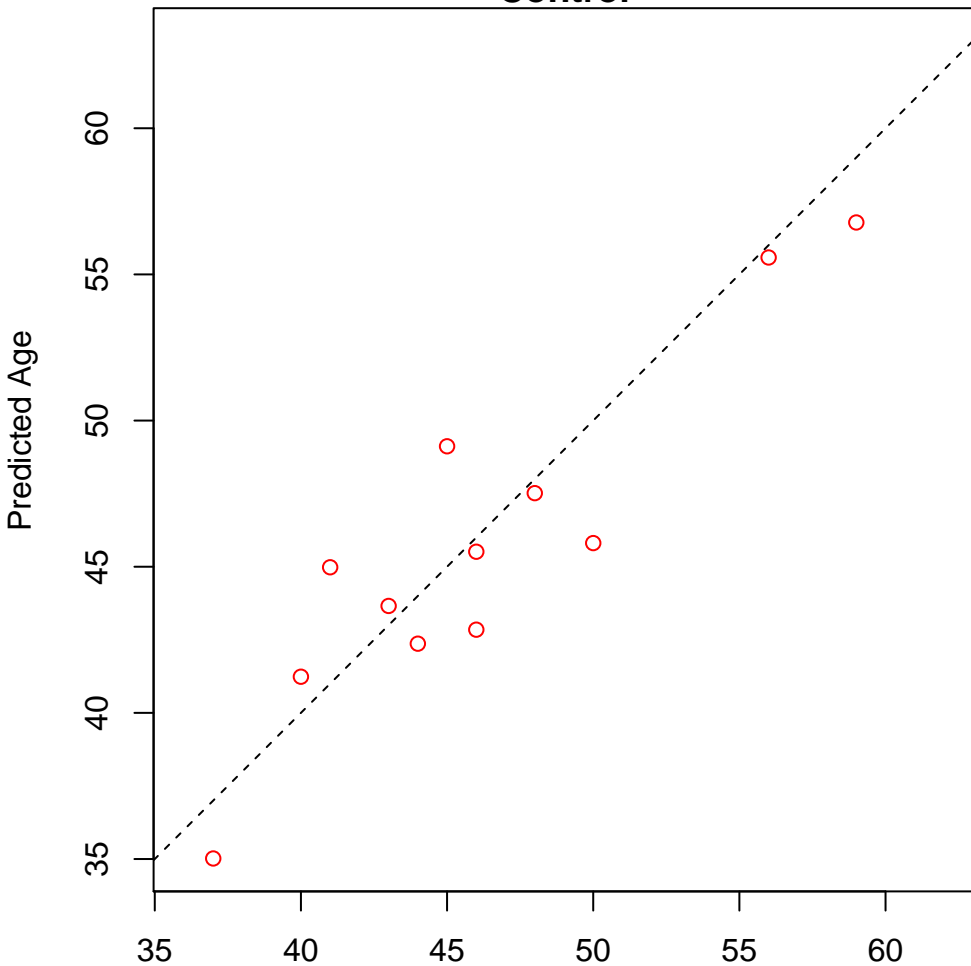
Actual Age

myeloid leukocyte migration (Score: 51.055351)

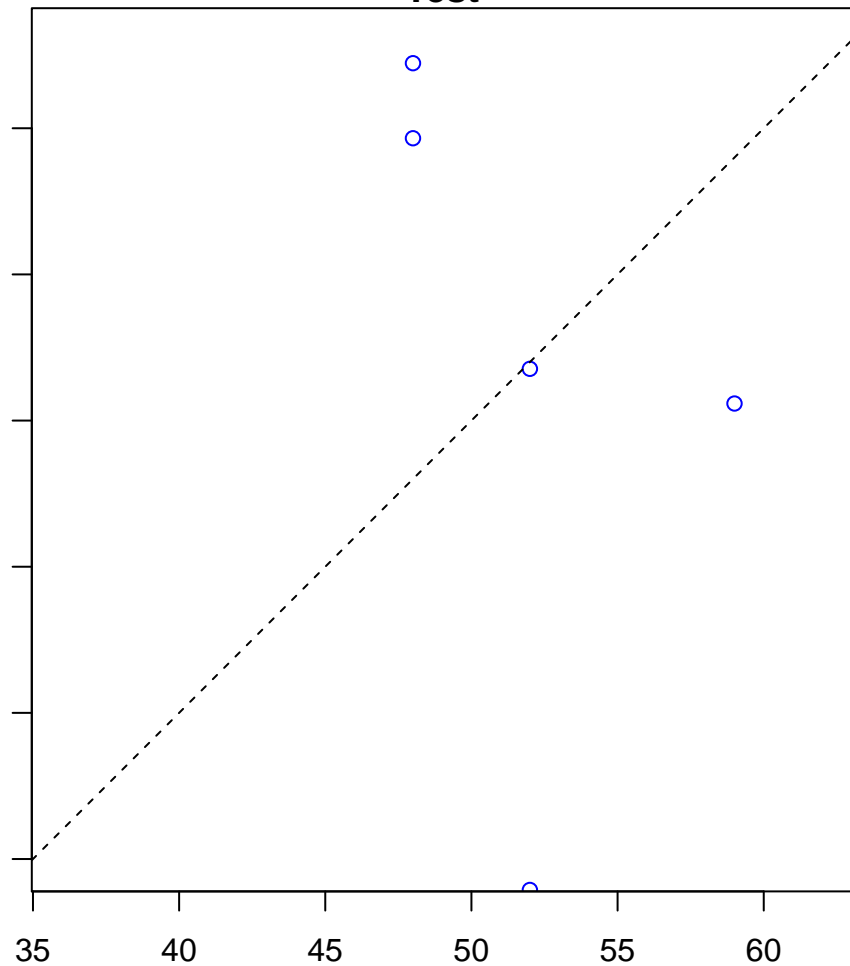


blood coagulation, intrinsic pathway (Score: 50.812167)

Control

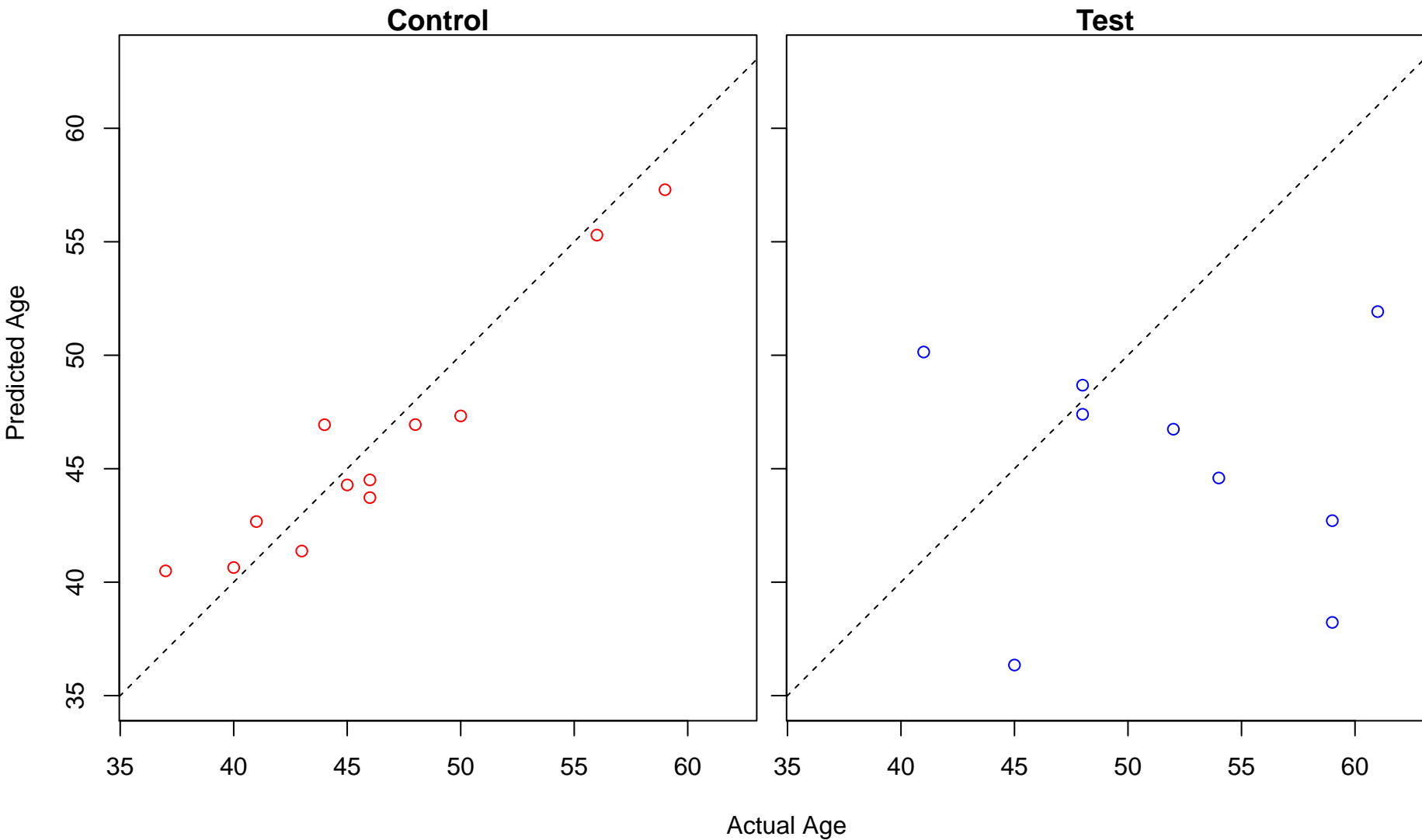


Test

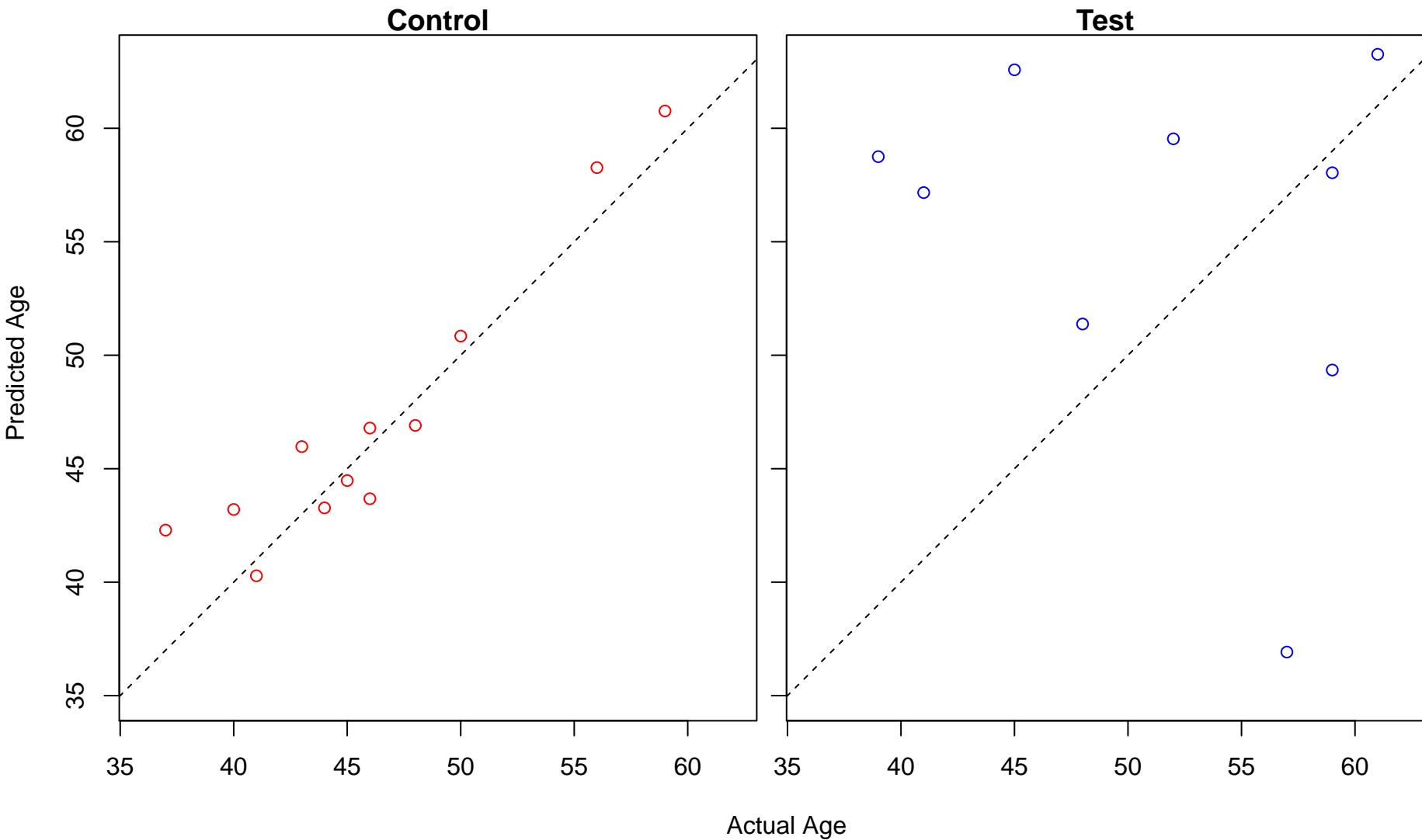


Actual Age

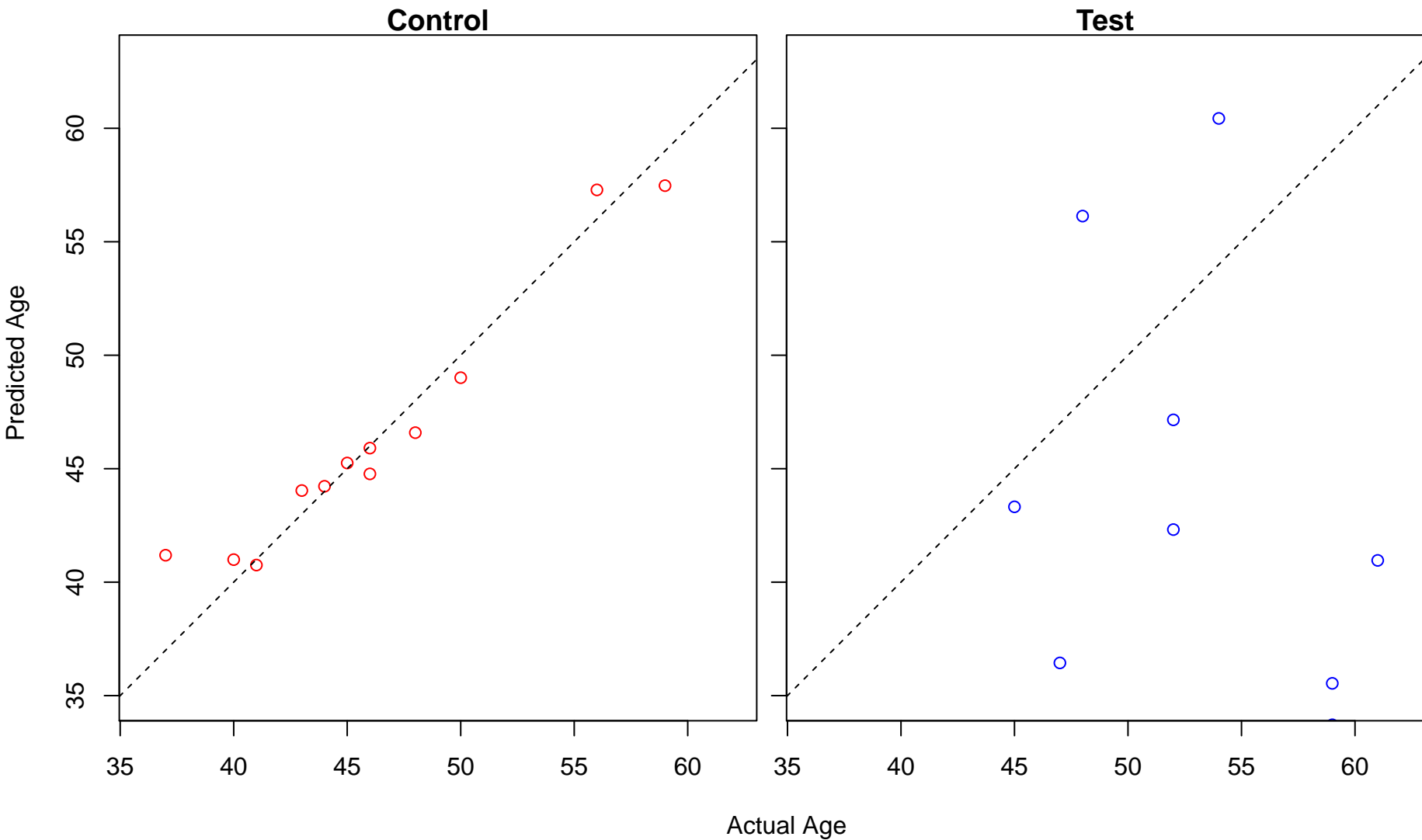
regulation of epithelial cell differentiation (Score: 49.843726)



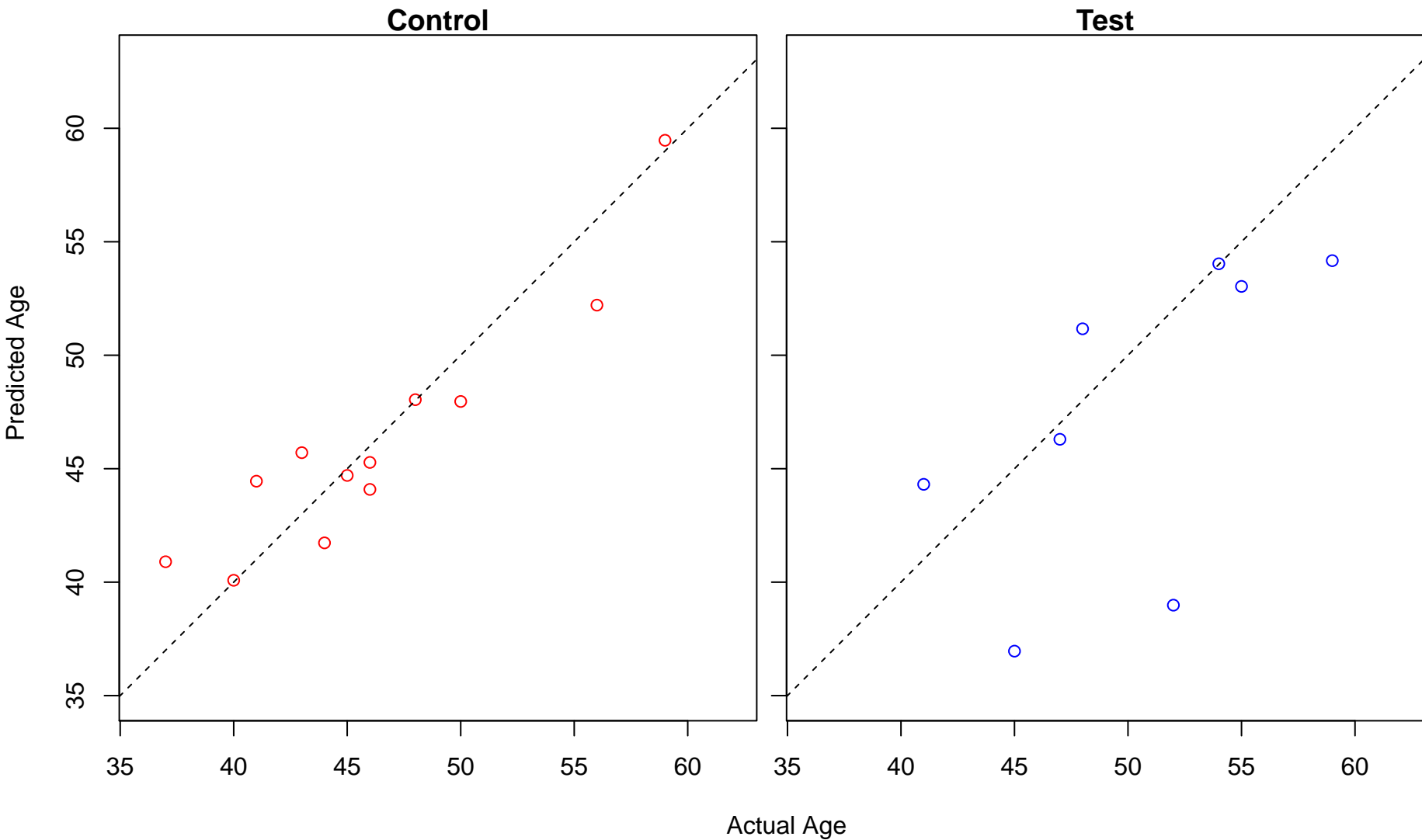
cytoplasmic mRNA processing body assembly (Score: 49.481210)



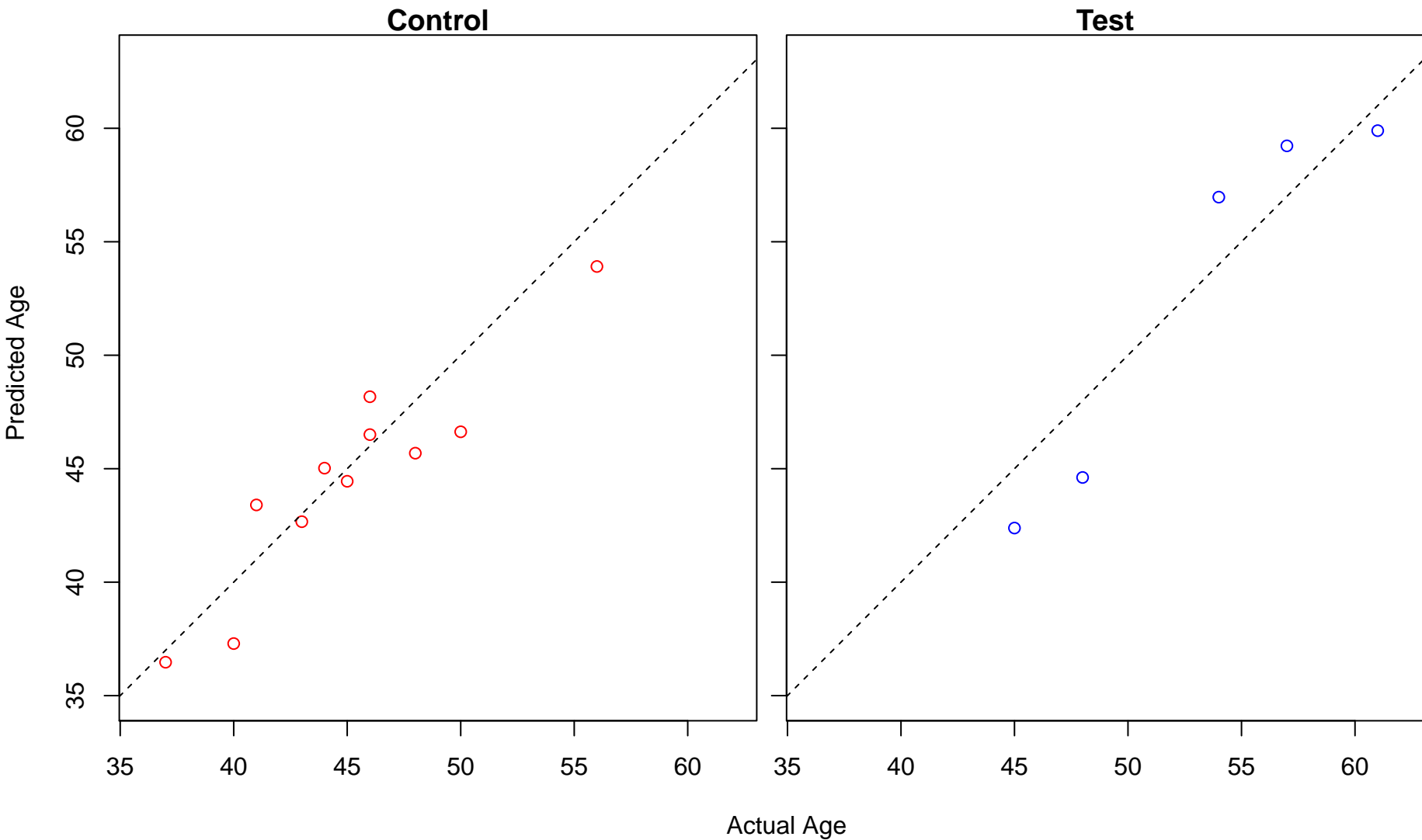
keratan sulfate biosynthetic process (Score: 49.466707)



regulation of actin cytoskeleton reorganization (Score: 49.220101)

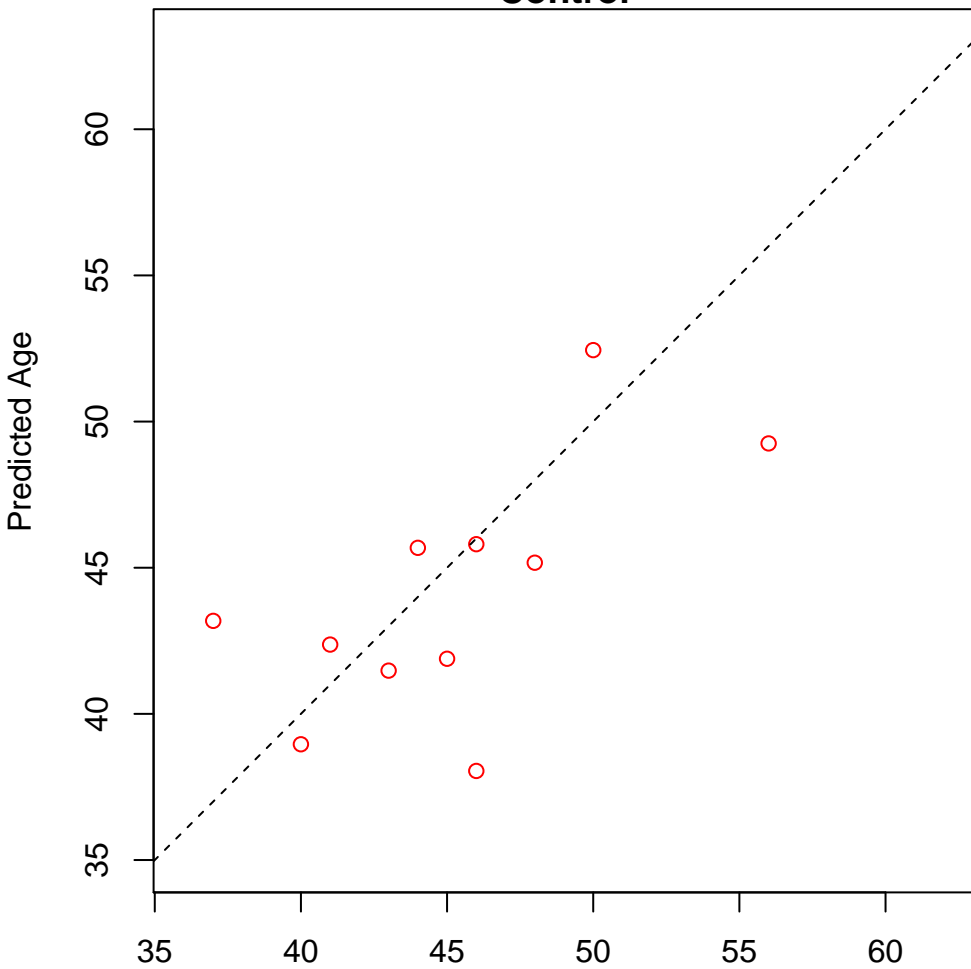


bone cell development (Score: 48.625024)

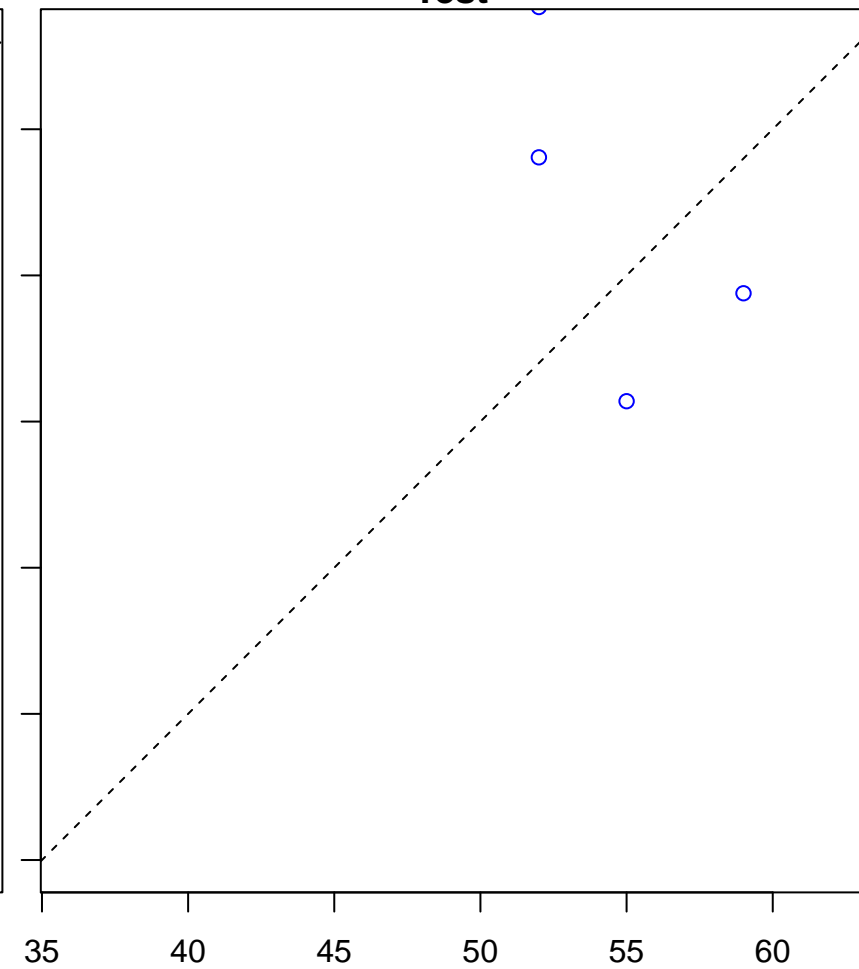


neuromuscular junction development (Score: 48.361382)

Control

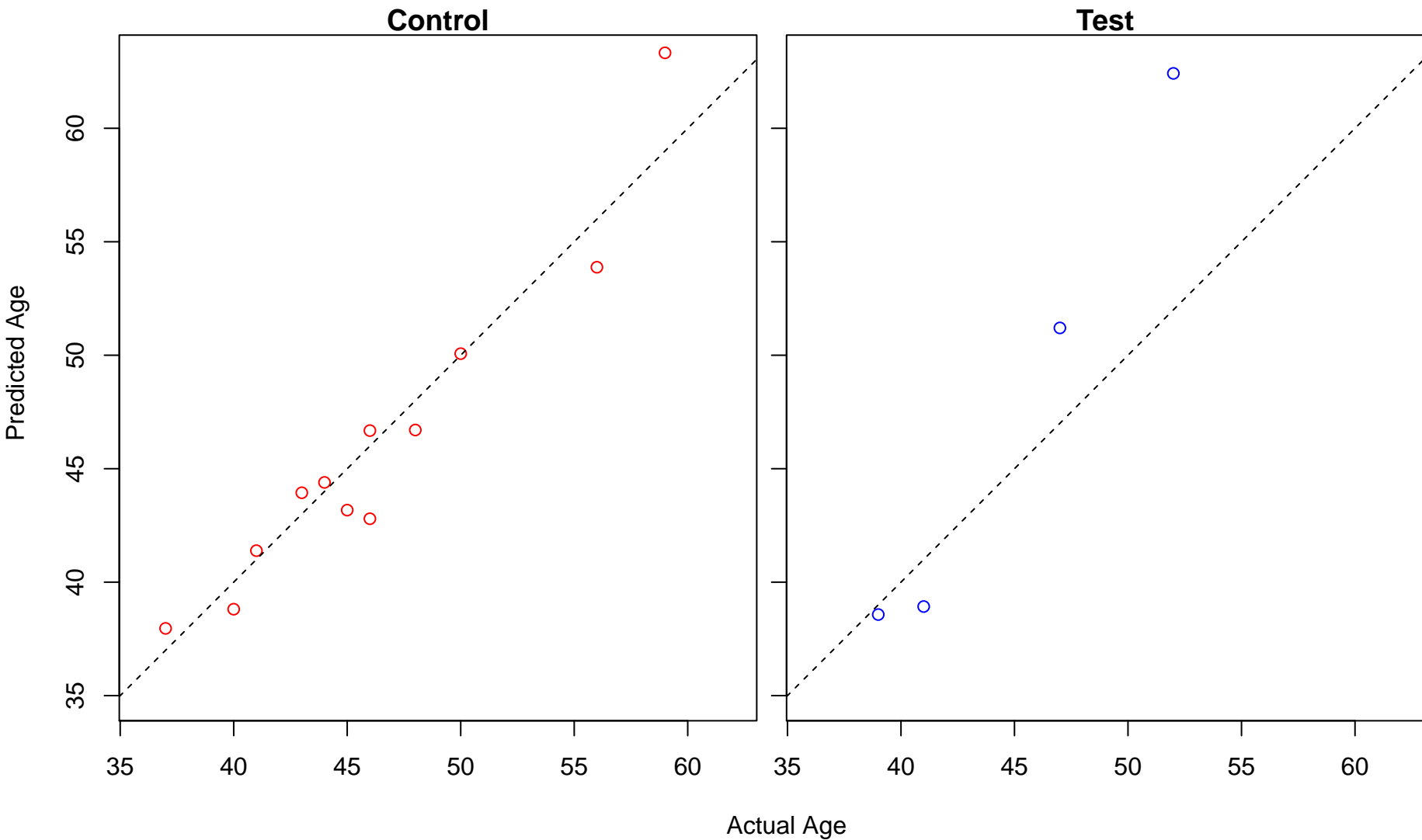


Test

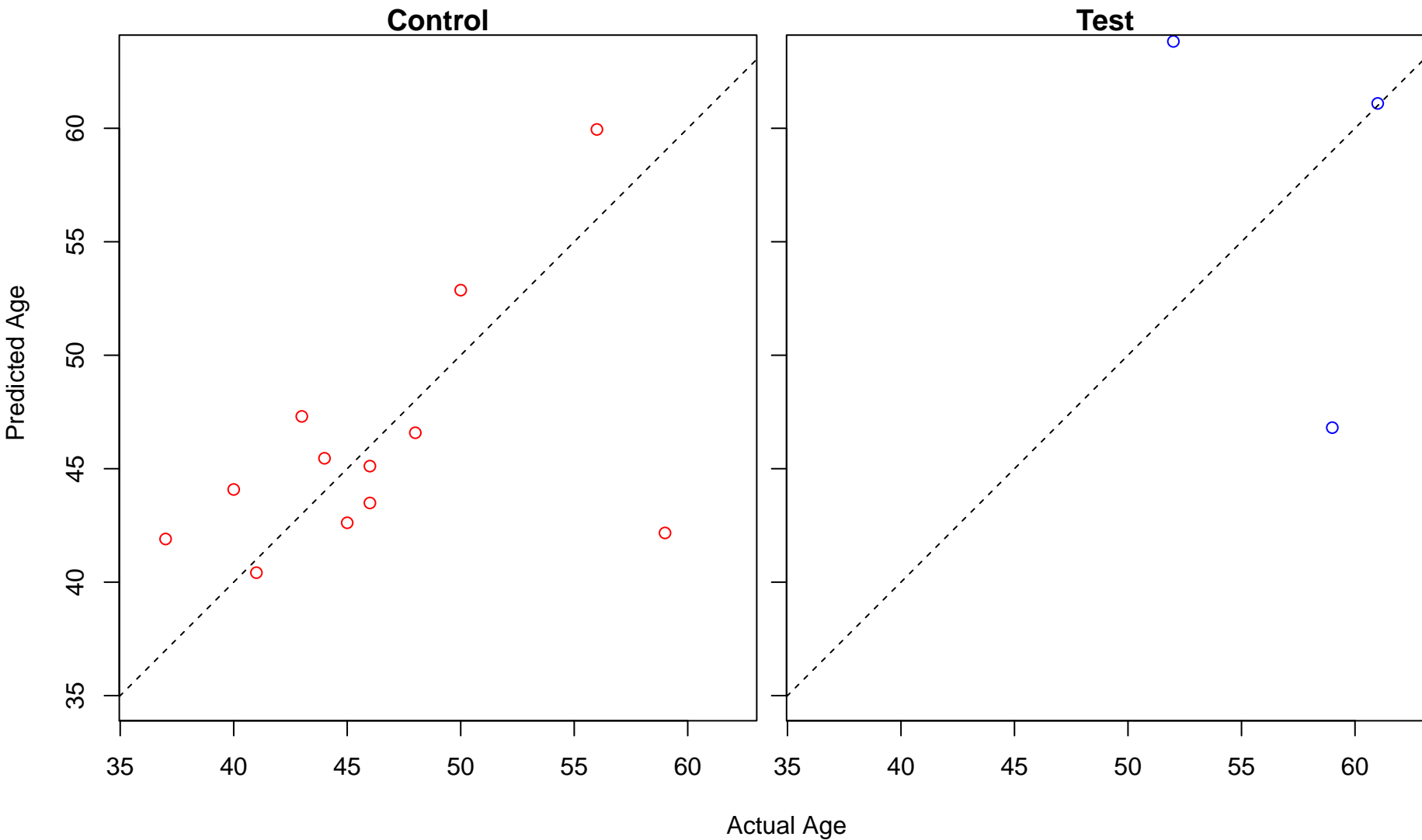


Actual Age

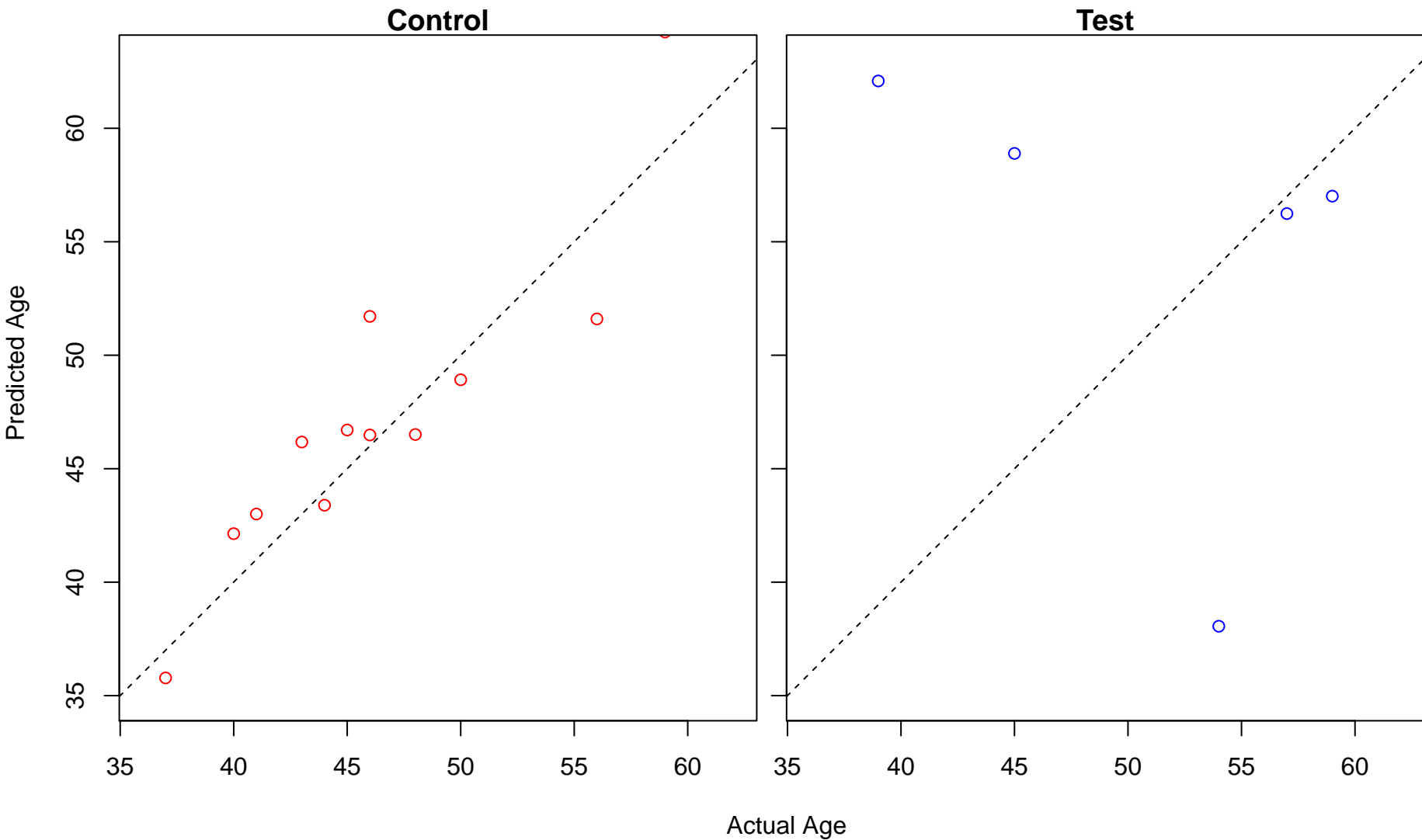
glutathione biosynthetic process (Score: 48.349637)



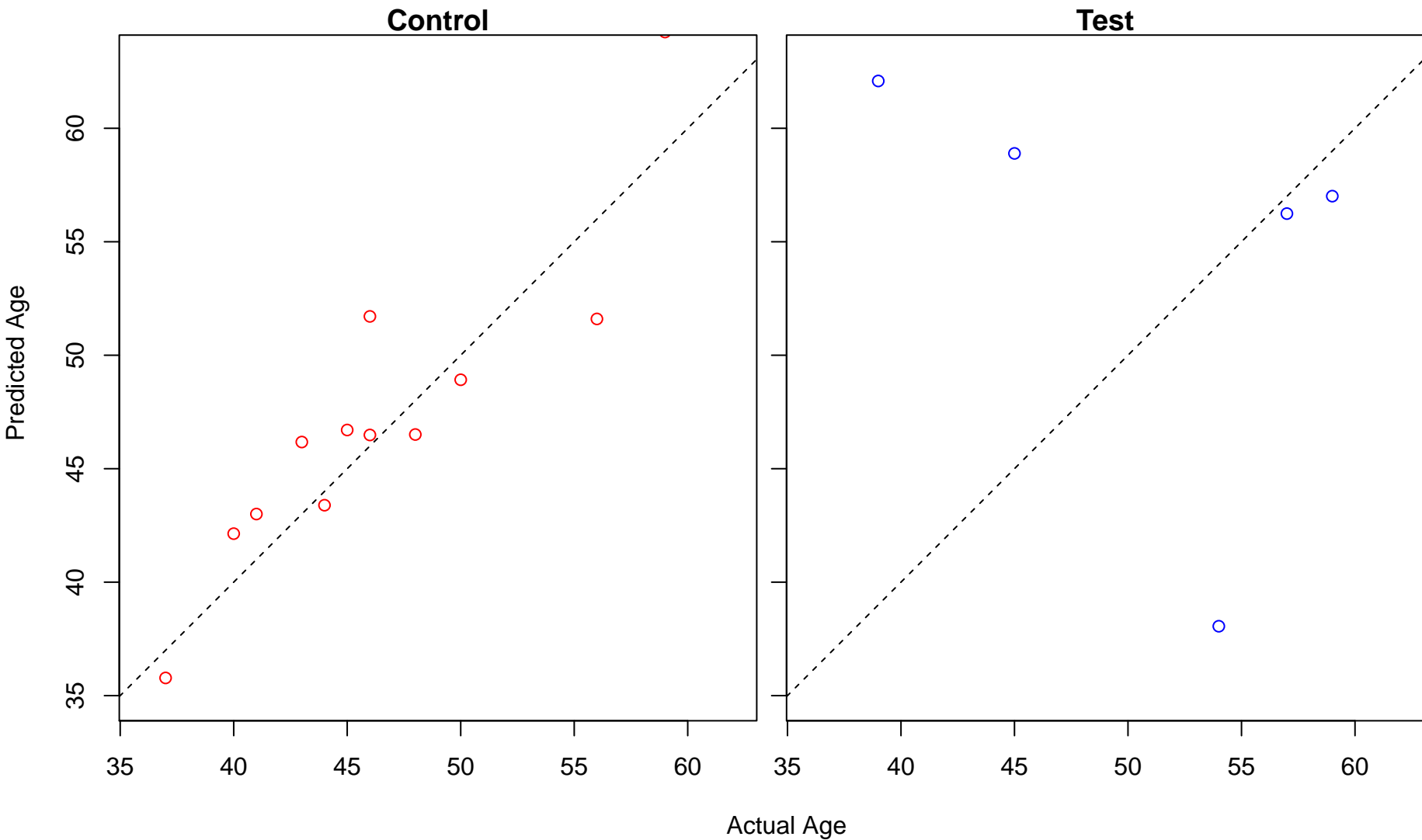
positive regulation of corticosteroid hormone secretion (Score: 47.493301)



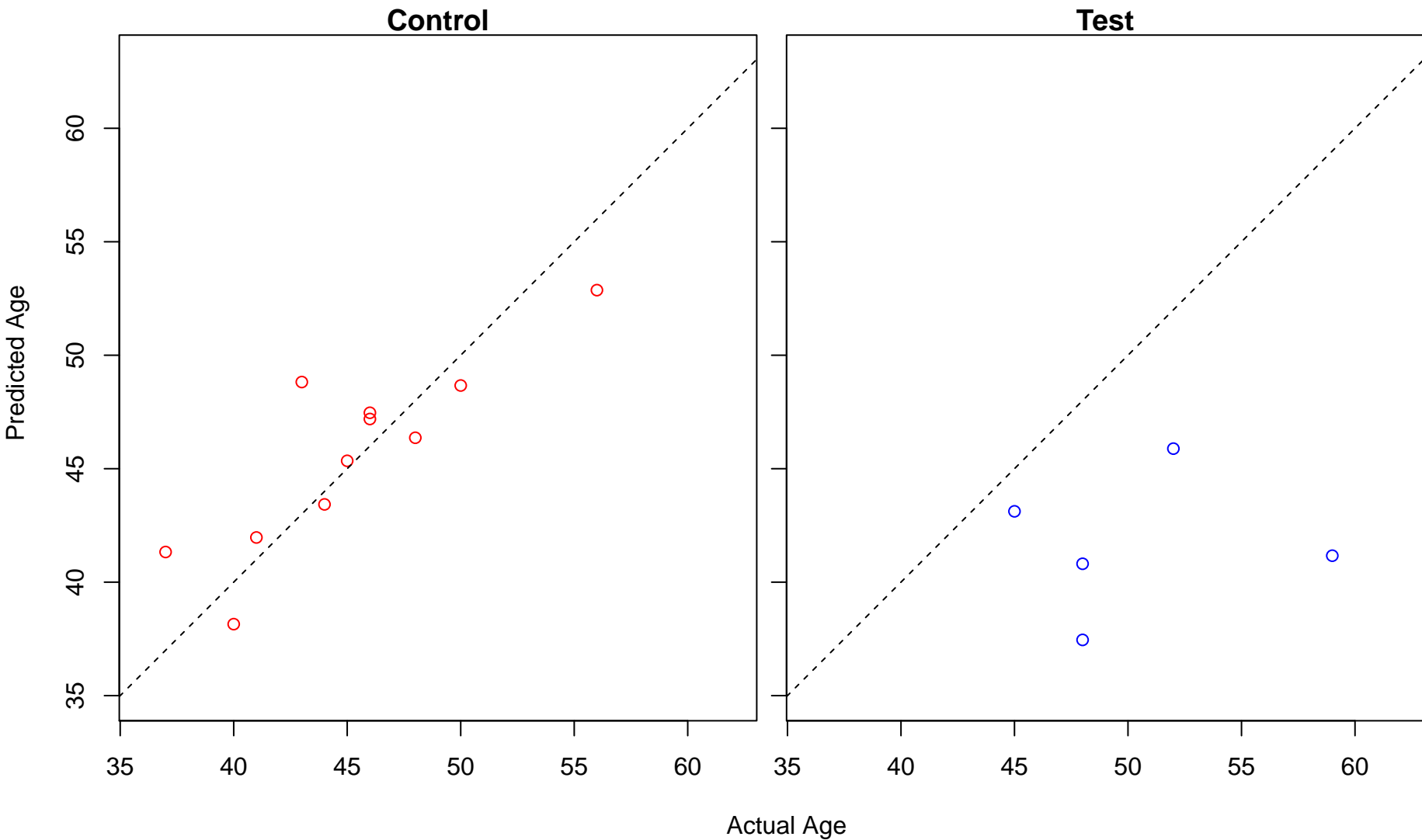
nuclear RNA surveillance (Score: 47.086353)



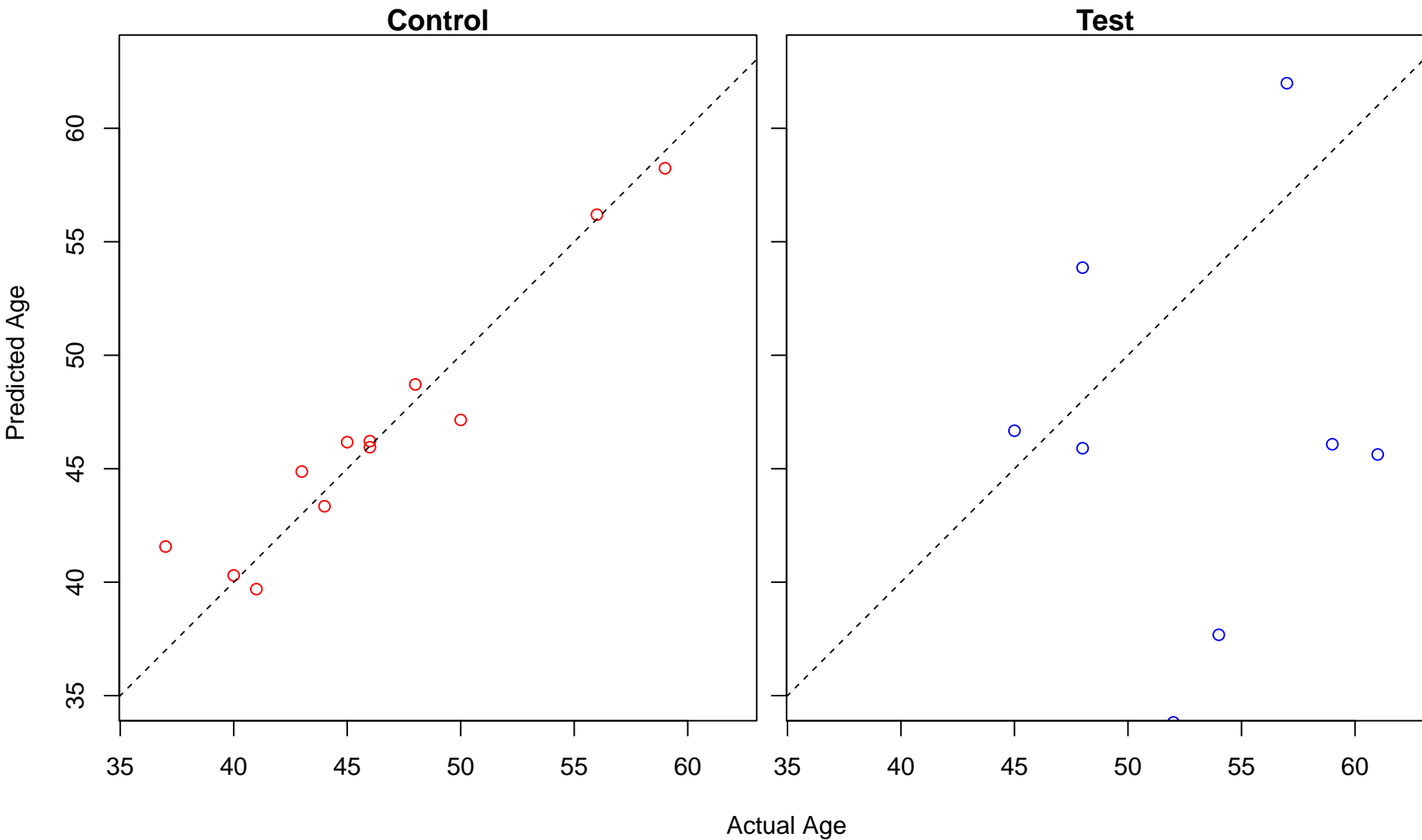
nuclear mRNA surveillance (Score: 47.086353)



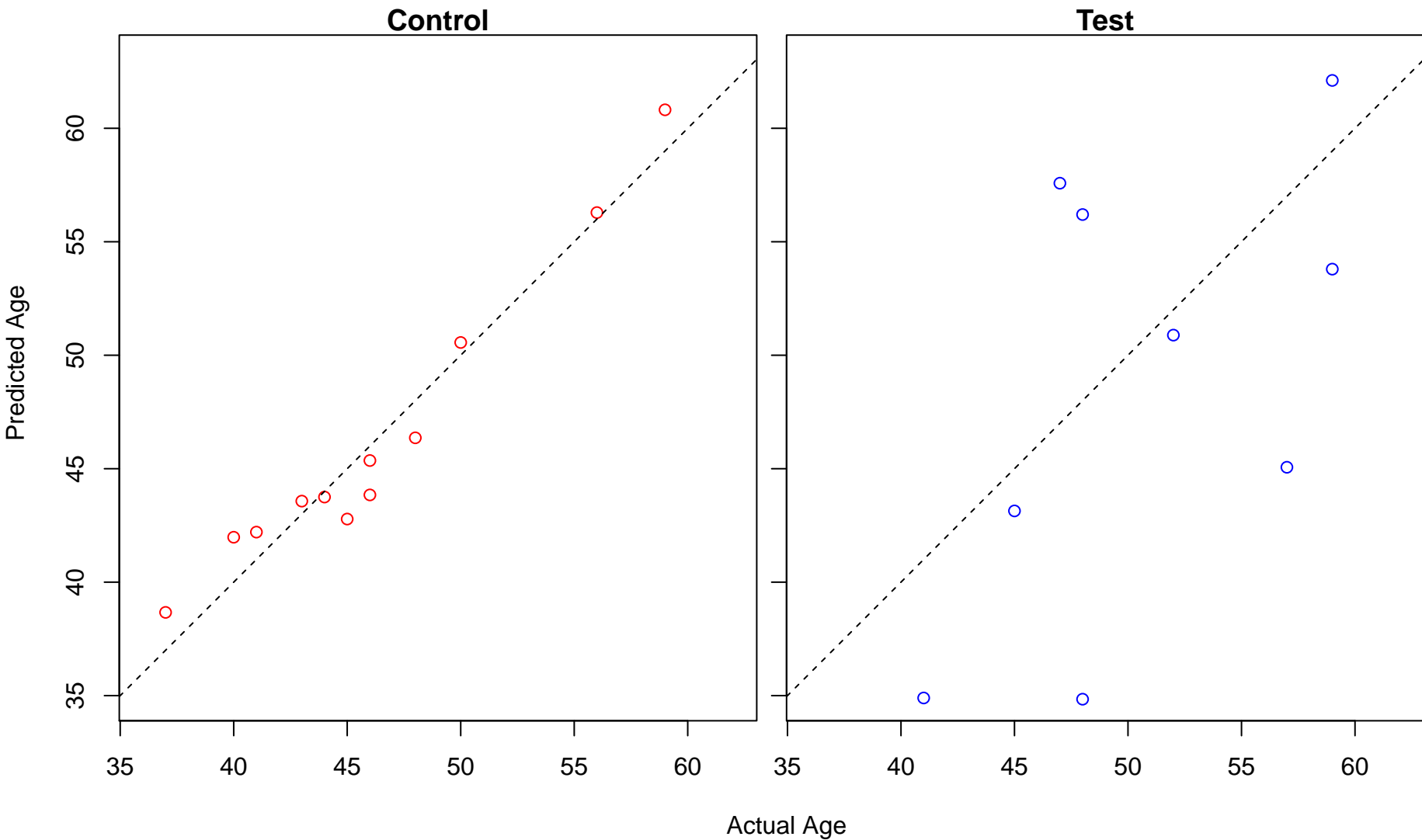
regulation of ventricular cardiac muscle cell action potential (Score: 46.945725)



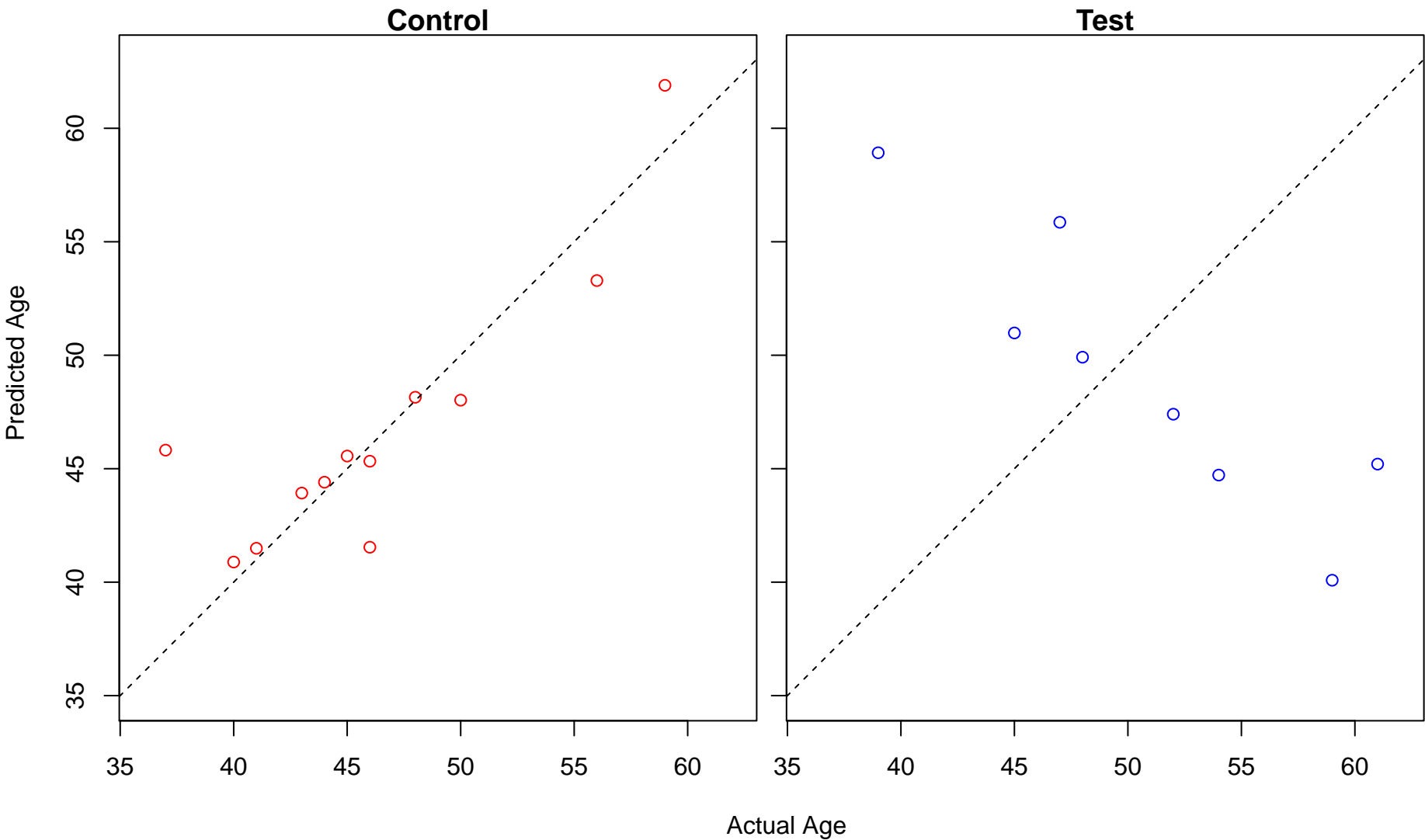
extrinsic apoptotic signaling pathway (Score: 46.697149)



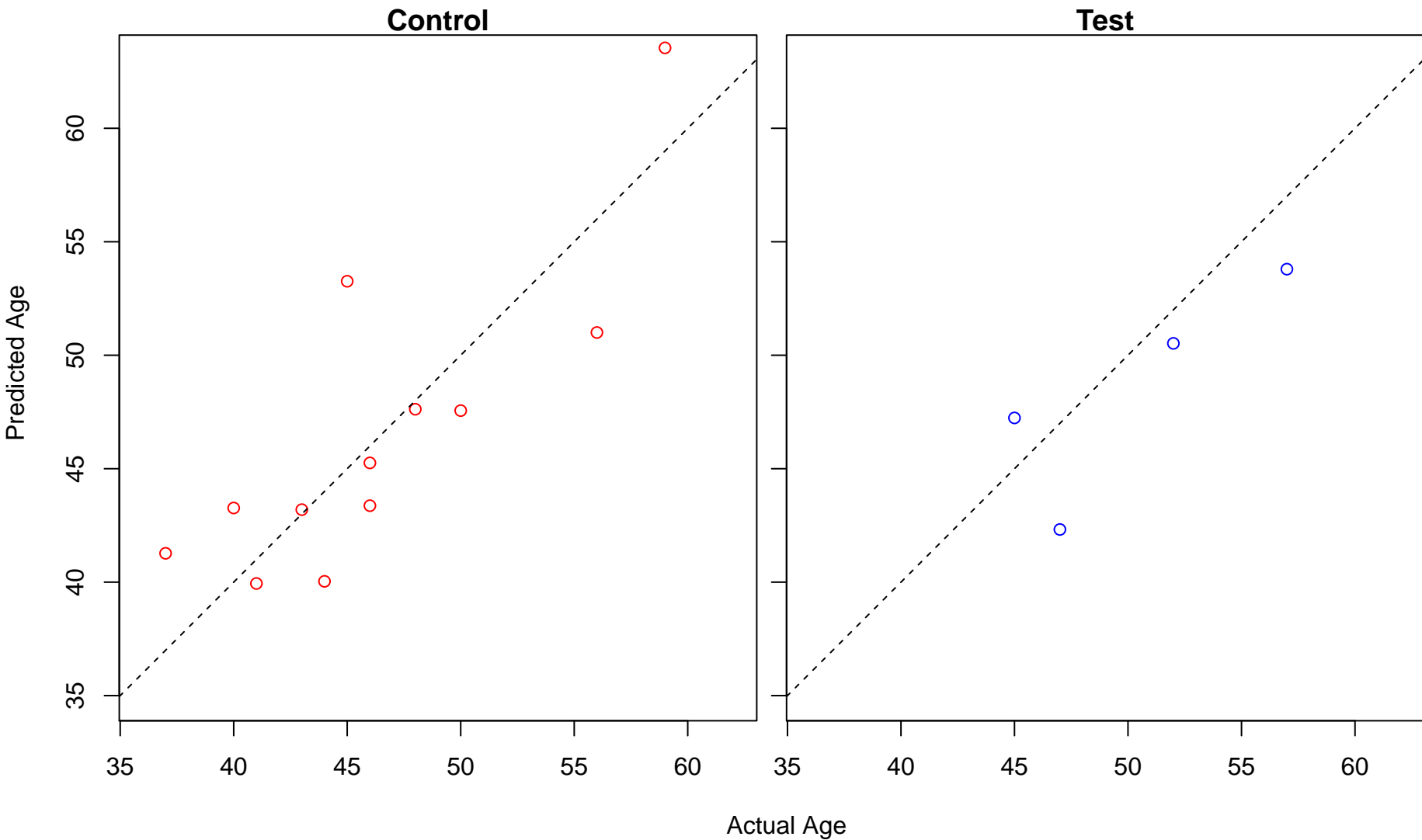
locomotor rhythm (Score: 46.585116)



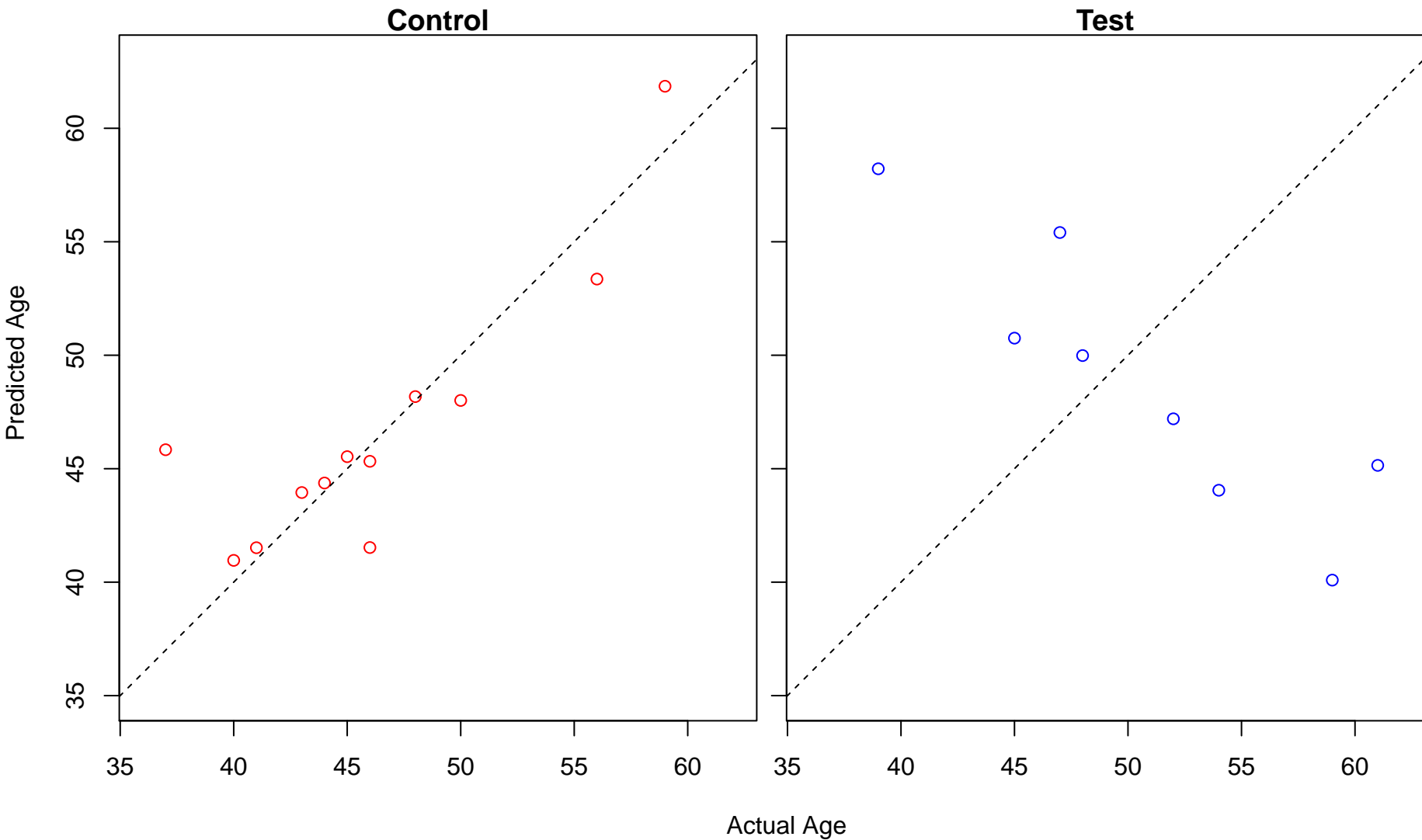
neutrophil migration (Score: 46.422458)



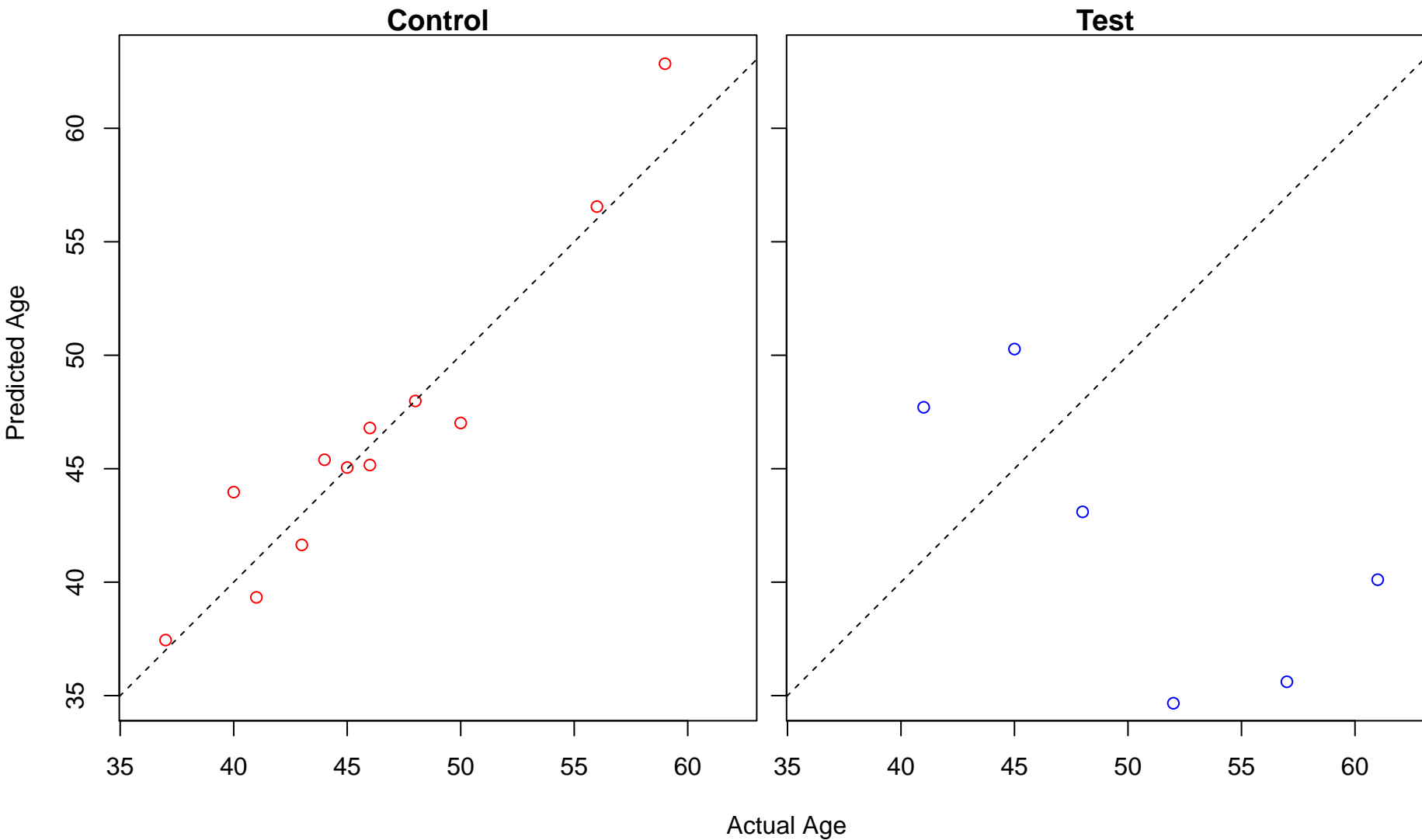
transmission of nerve impulse (Score: 46.079869)



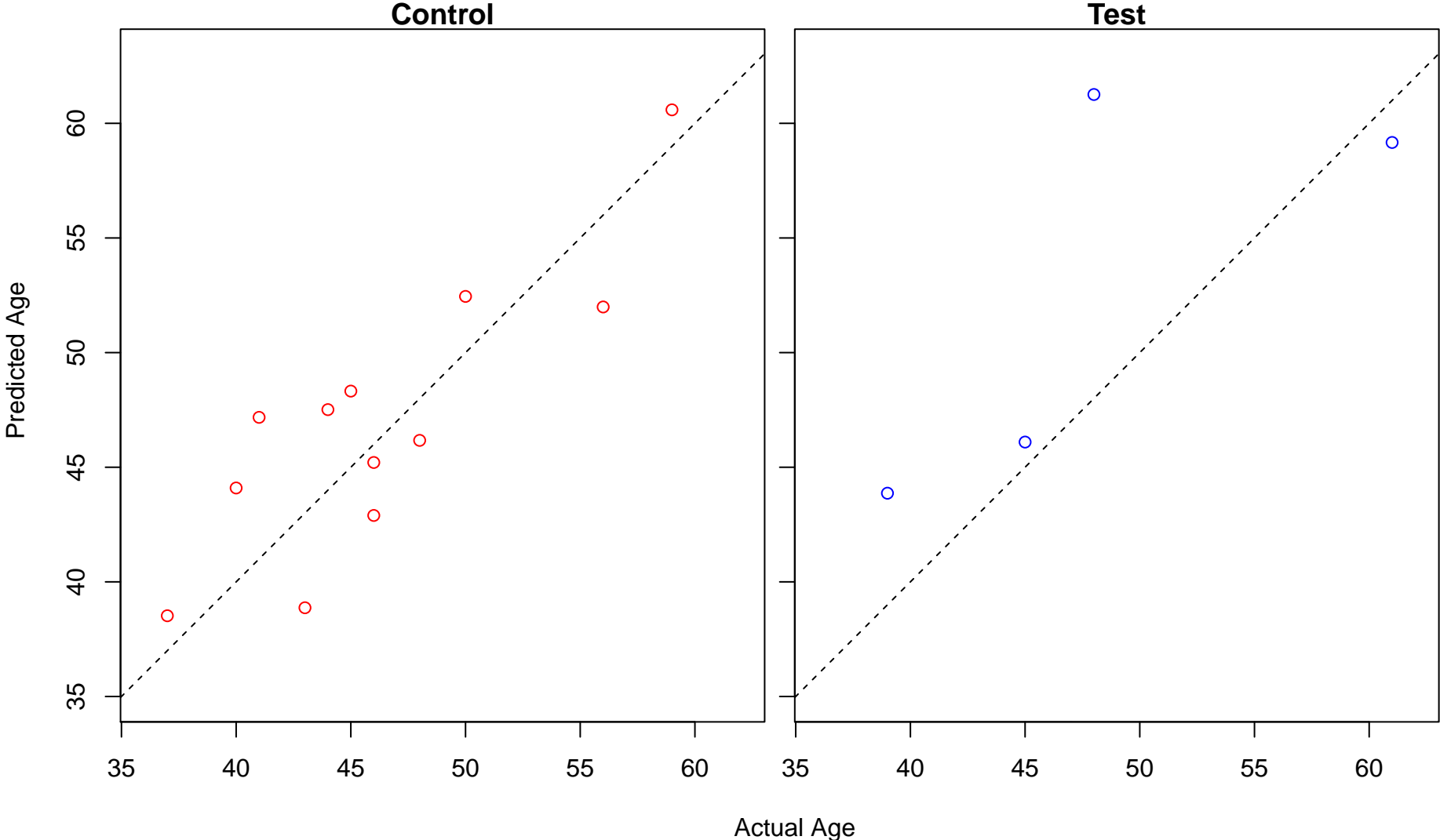
neutrophil chemotaxis (Score: 45.920130)



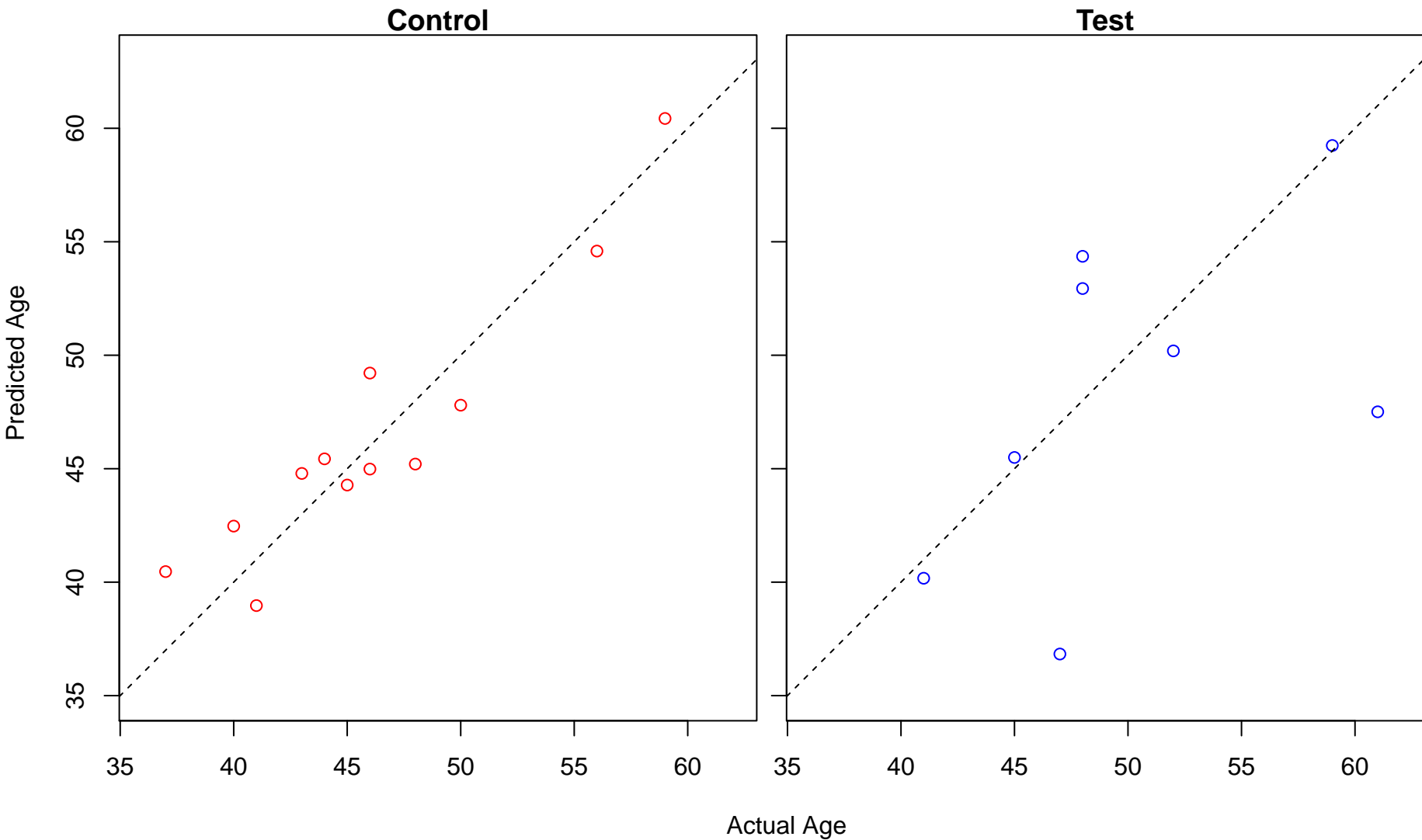
positive regulation of branching involved in ureteric bud morphogenesis (Score: 45.813930)



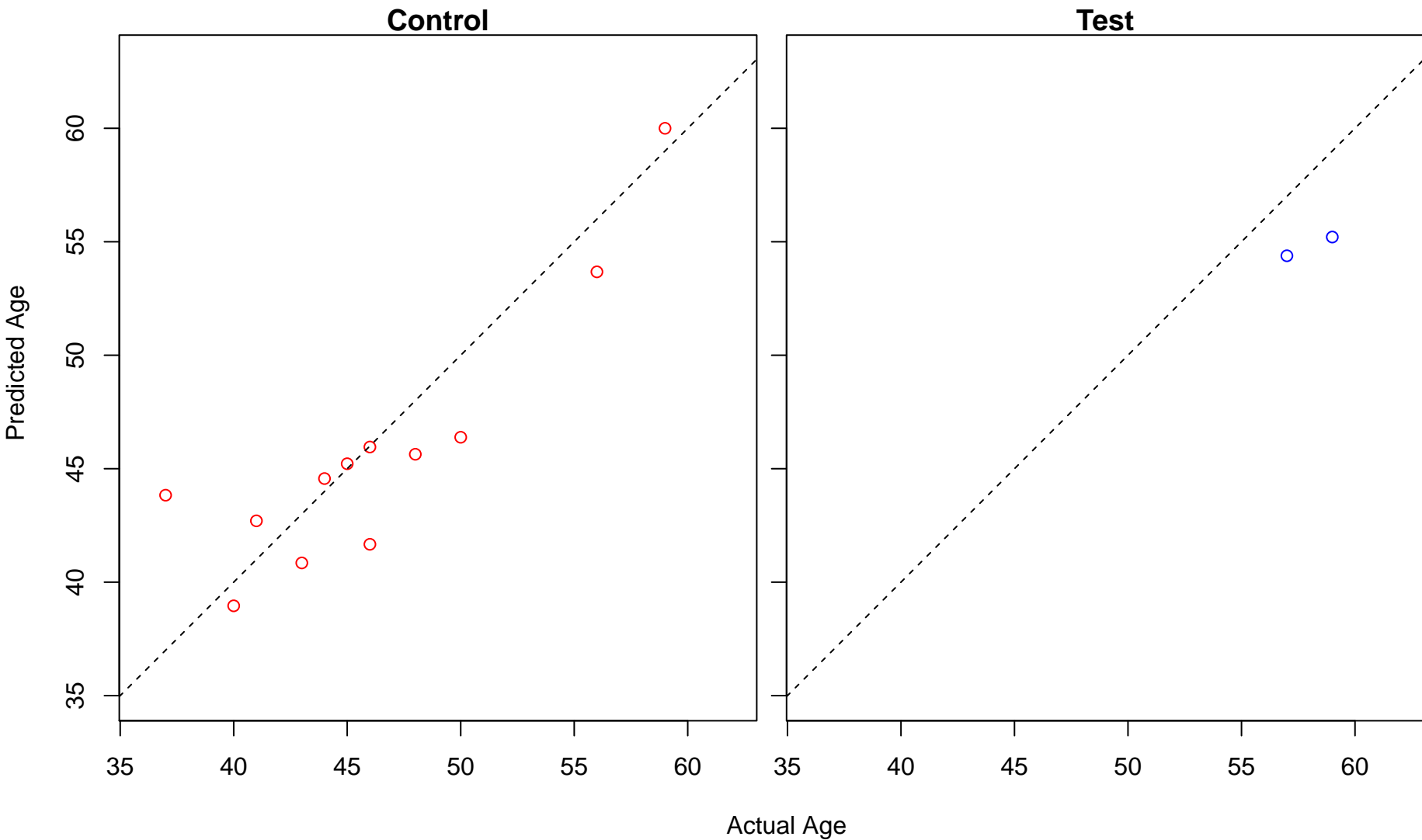
regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway (Score: 45.5373)



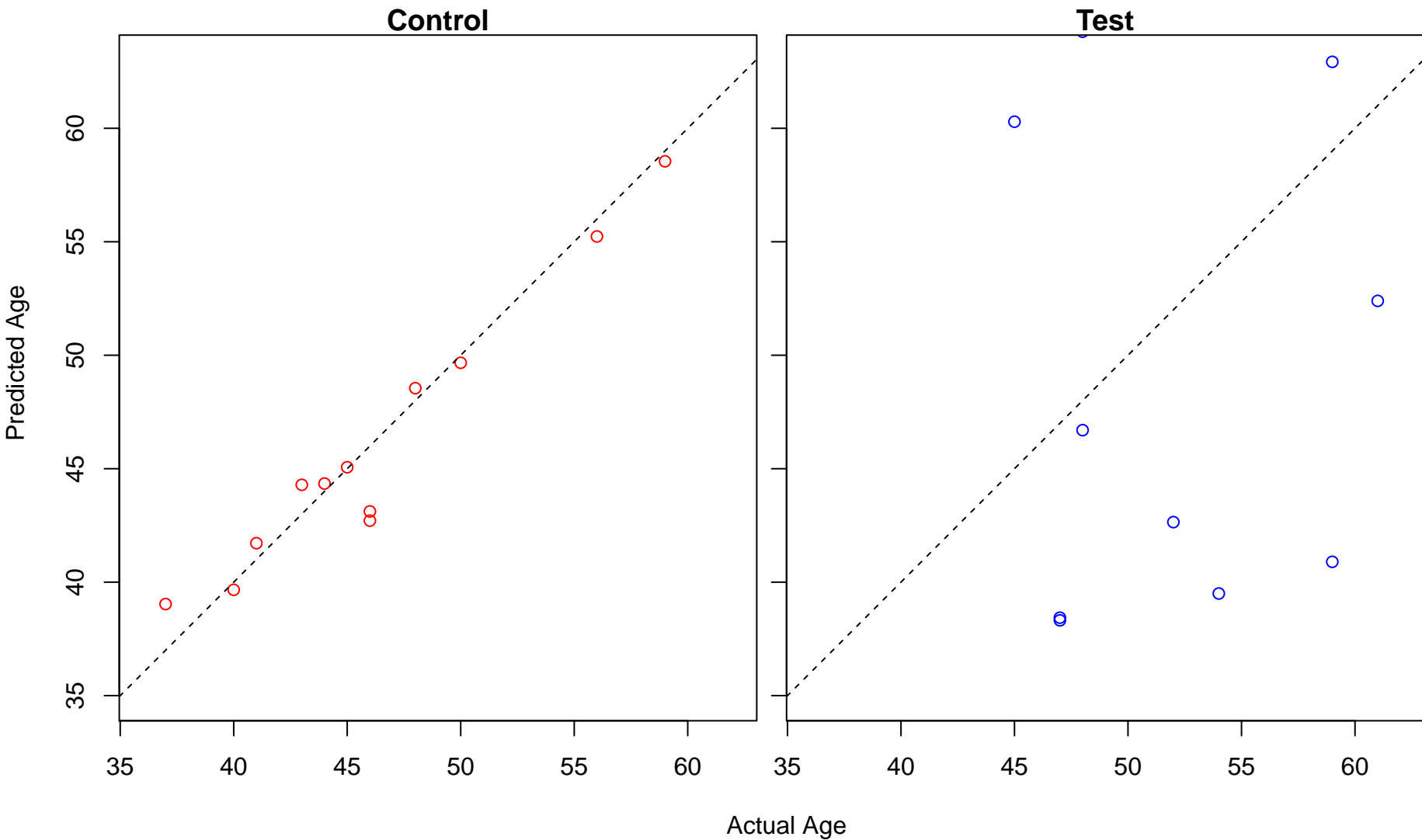
regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 45.2)



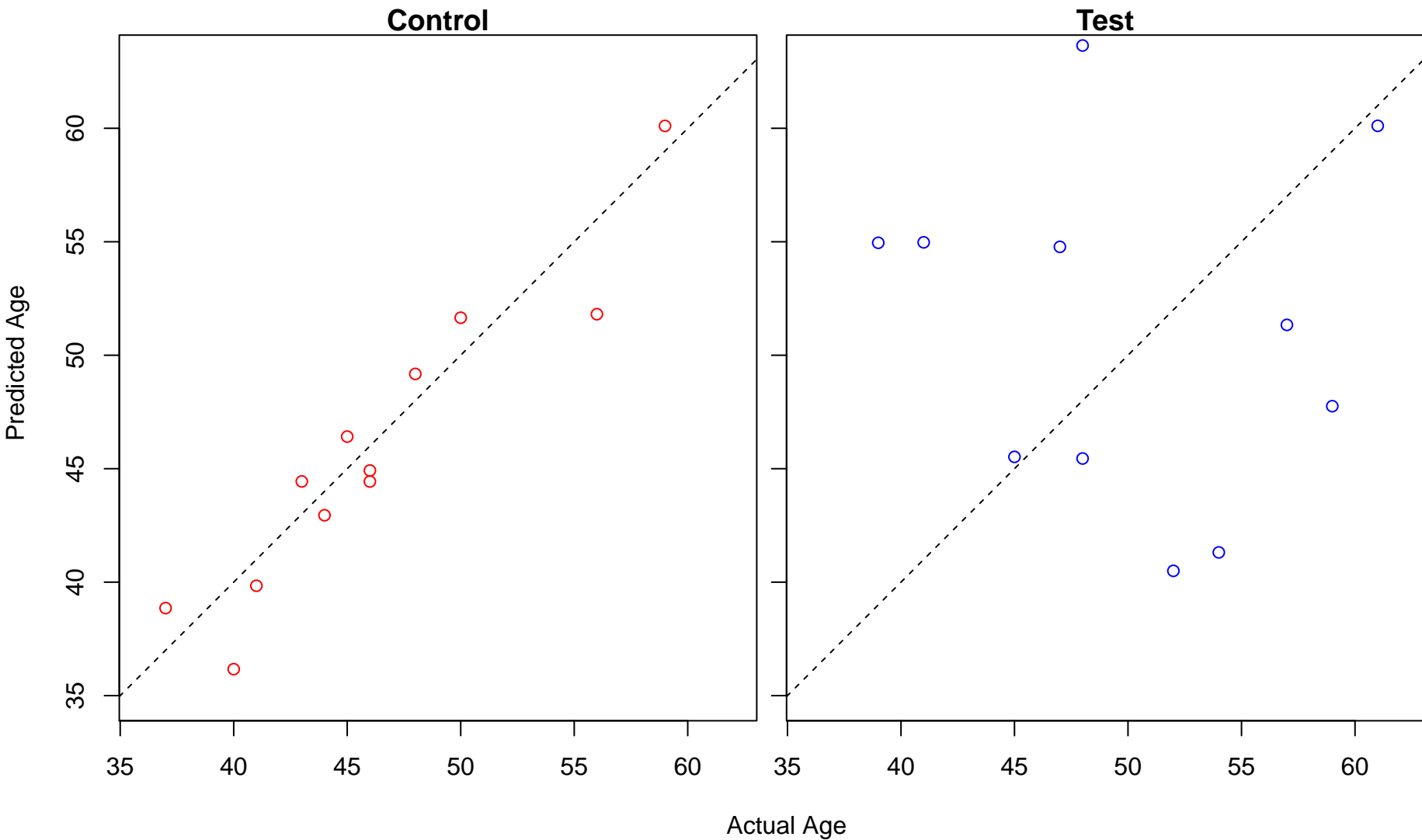
negative regulation of epithelial to mesenchymal transition (Score: 44.872726)



response to starvation (Score: 44.610196)

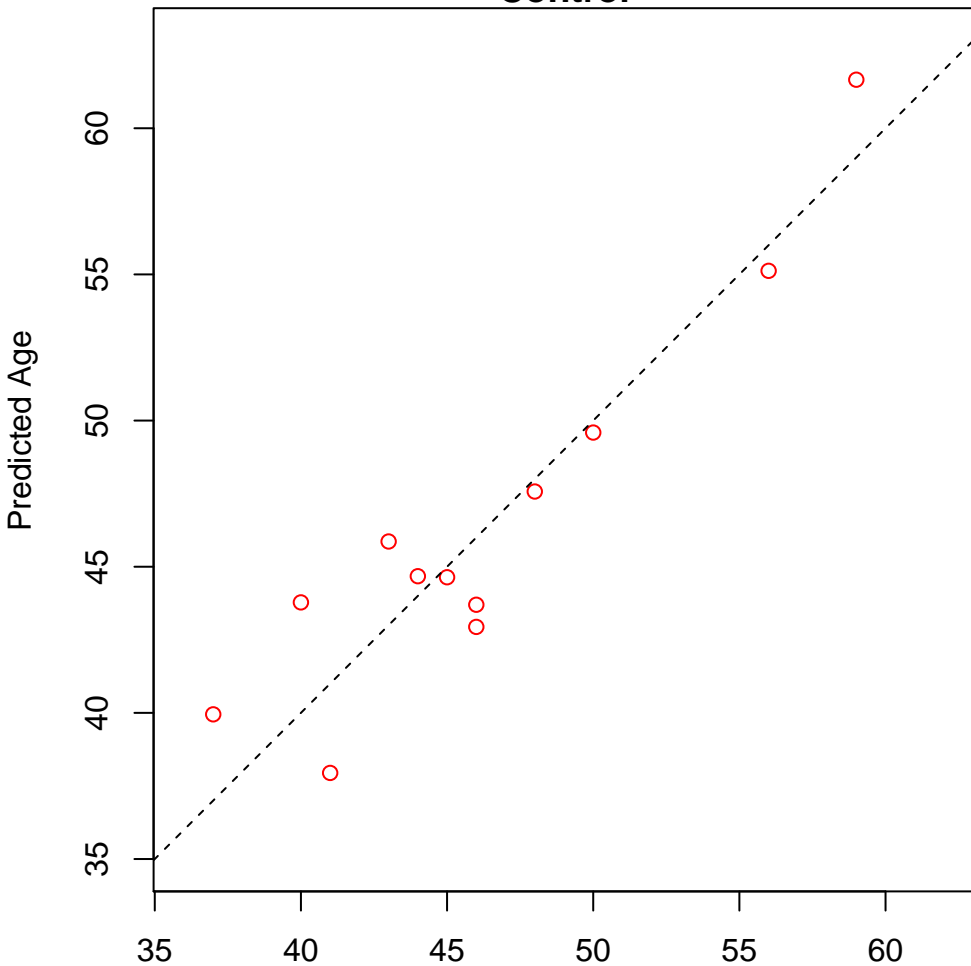


cellular response to heparin (Score: 44.425541)

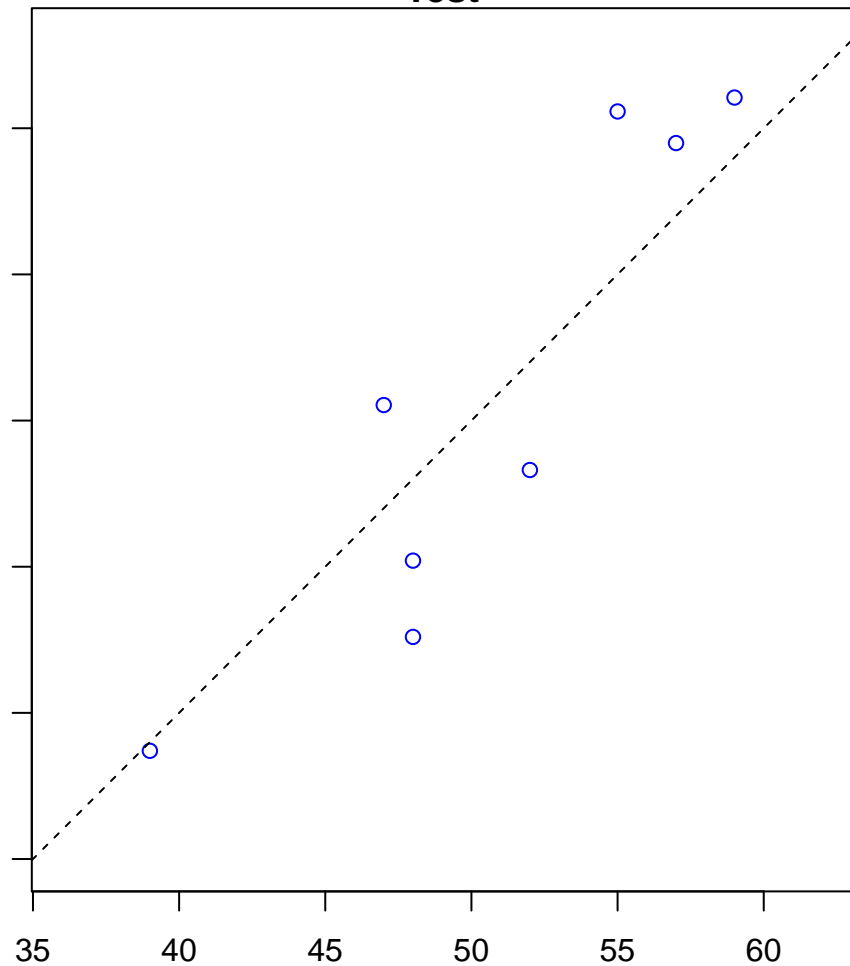


fat-soluble vitamin catabolic process (Score: 43.304509)

Control

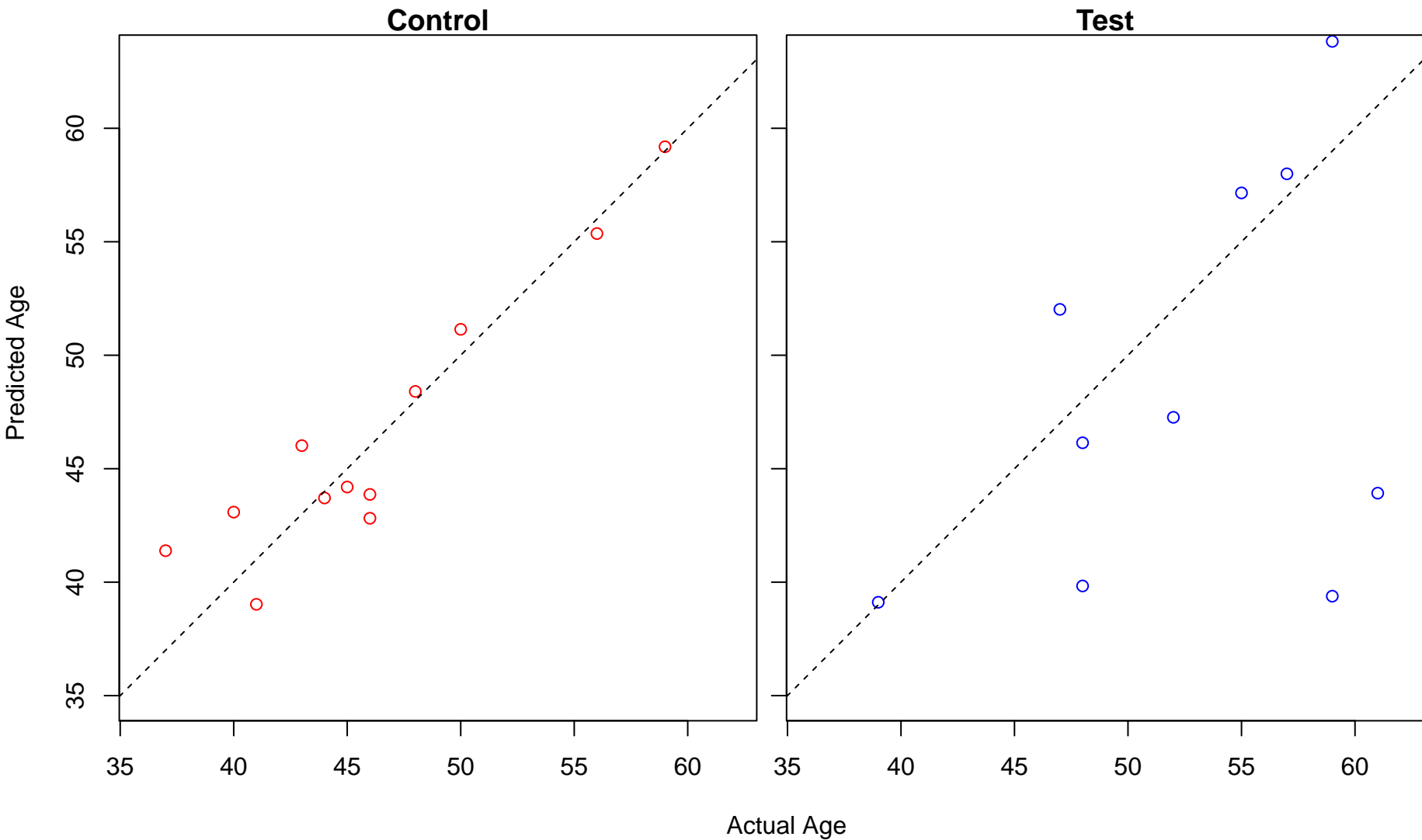


Test

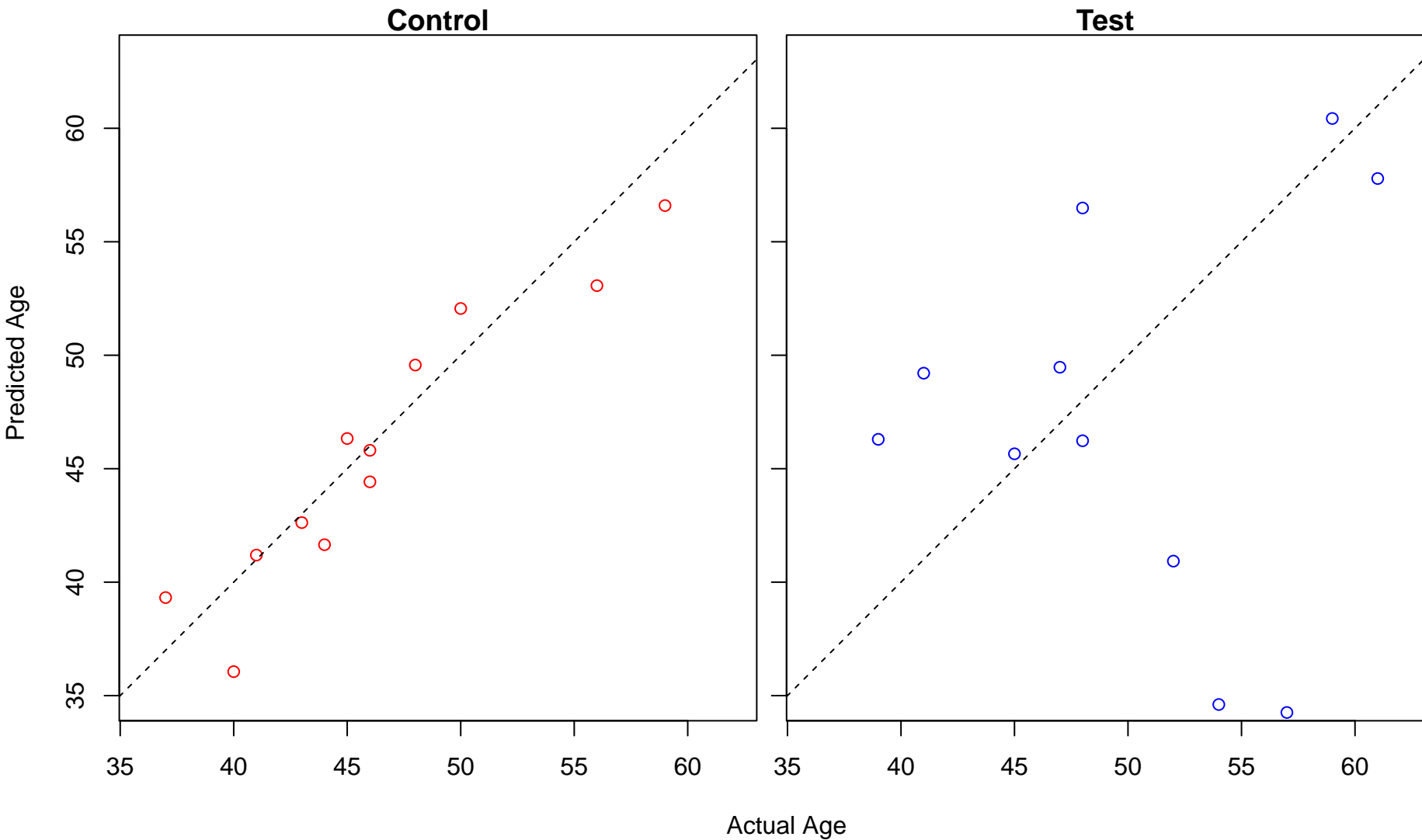


Actual Age

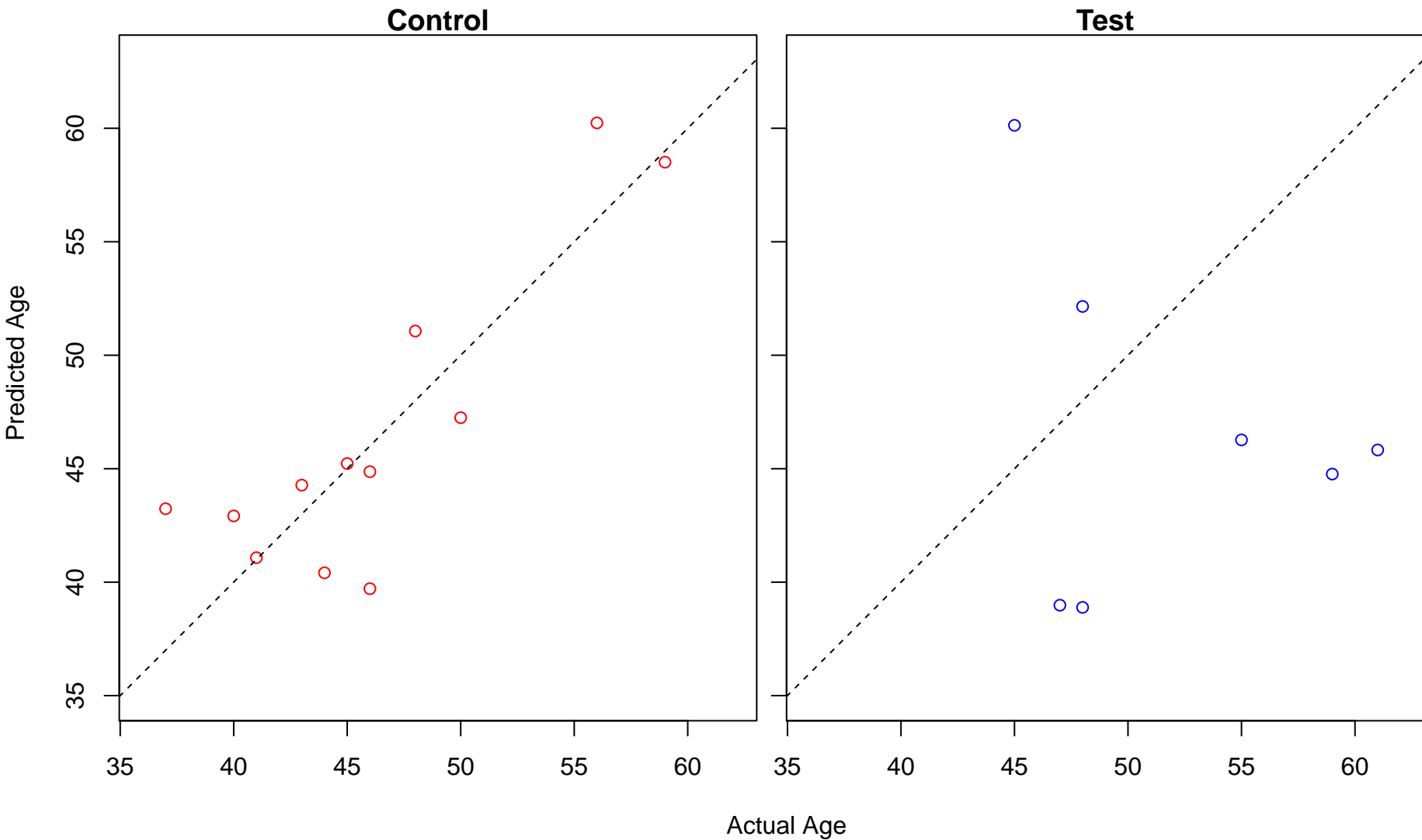
vitamin catabolic process (Score: 43.252422)



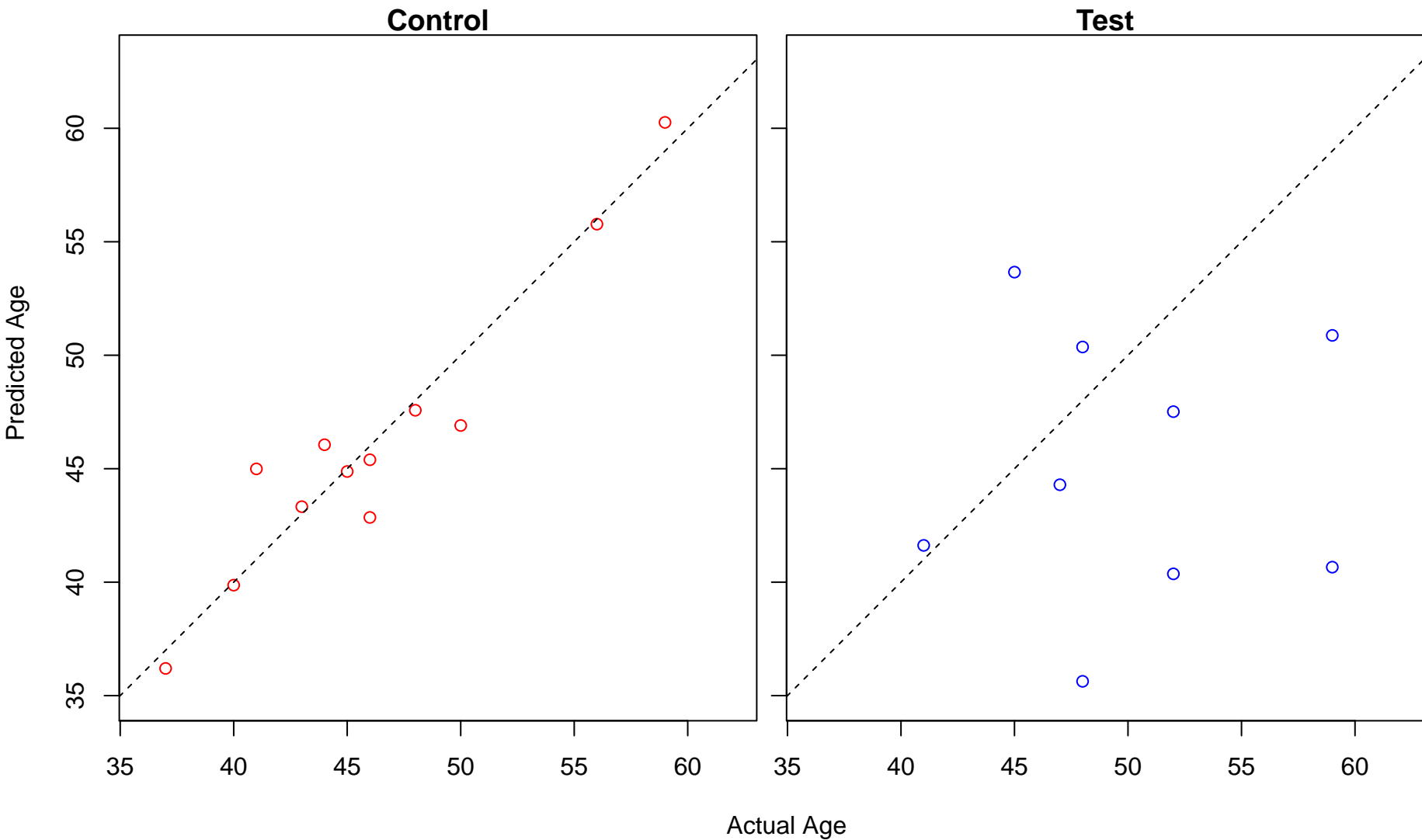
response to heparin (Score: 42.804823)



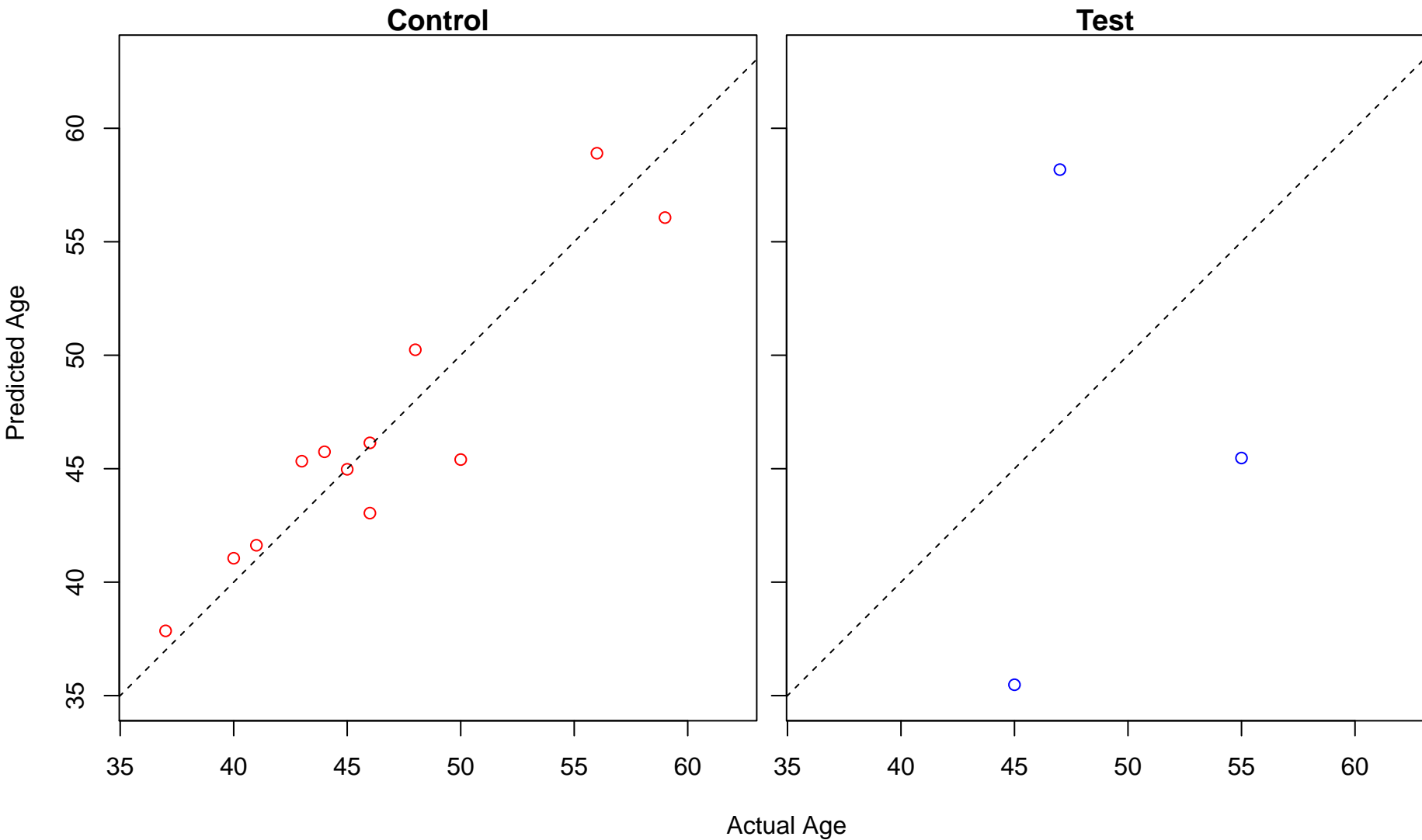
regulation of cellular respiration (Score: 42.498981)



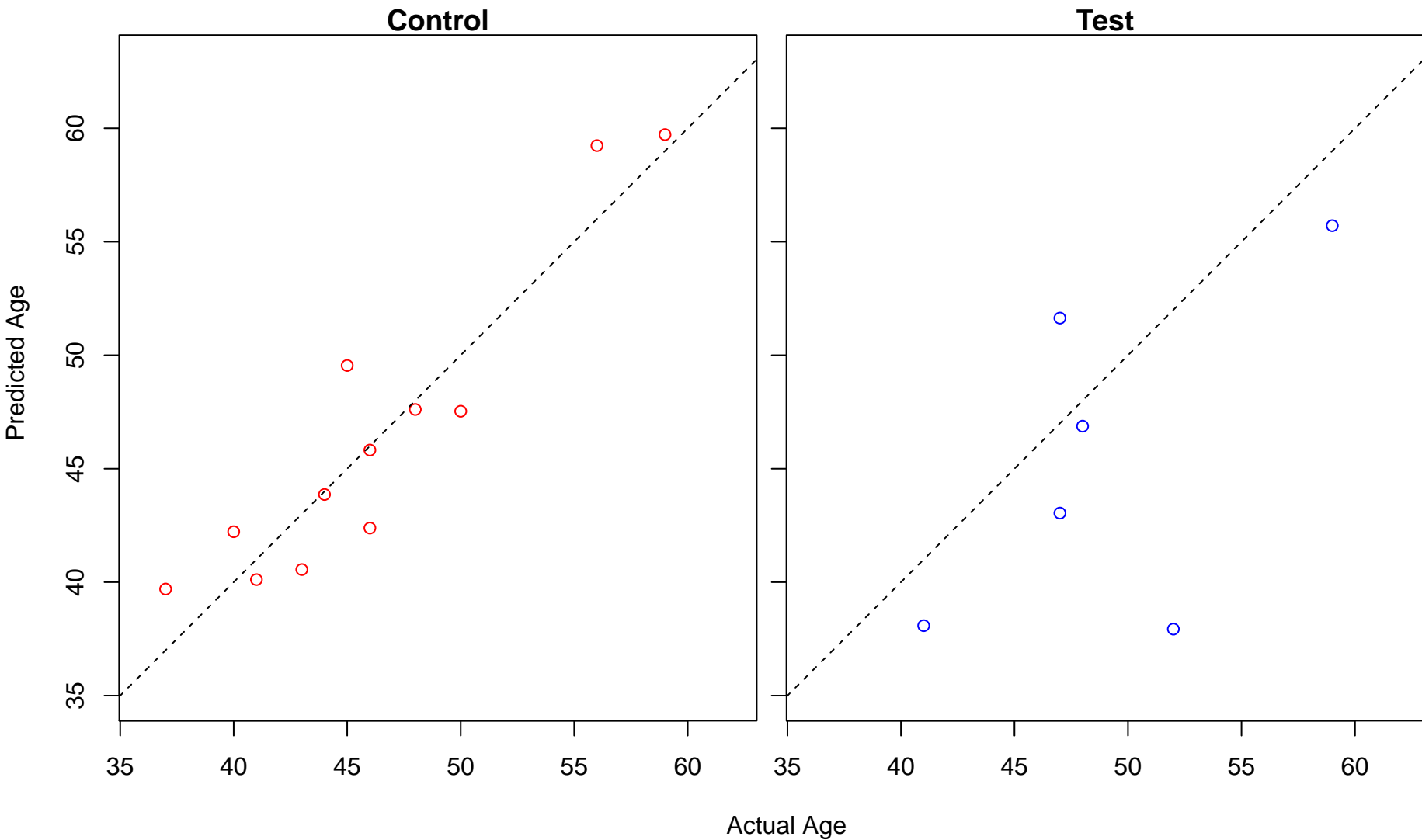
response to drug (Score: 42.377116)



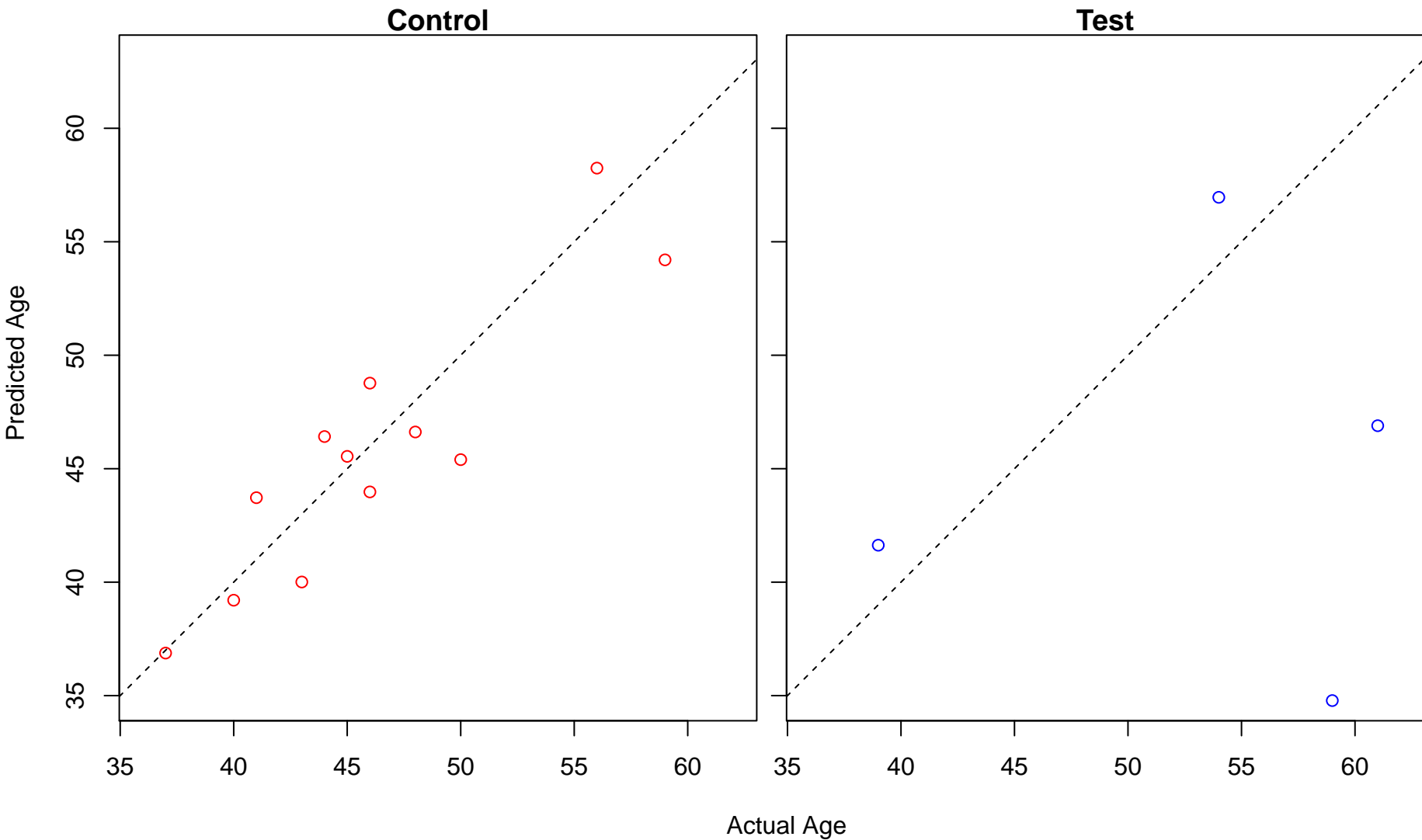
maturation of SSU-rRNA (Score: 42.120261)



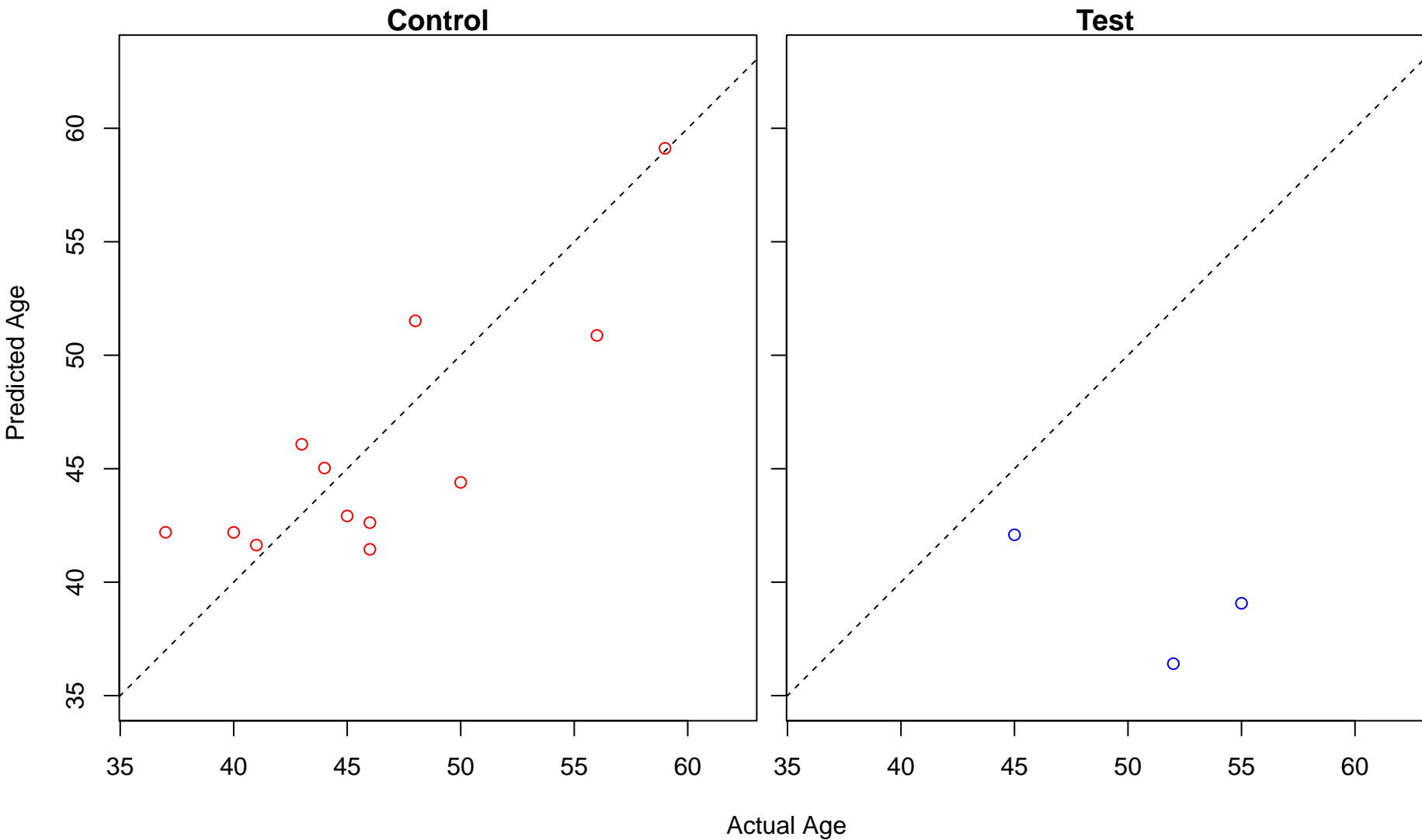
lung epithelium development (Score: 41.459469)



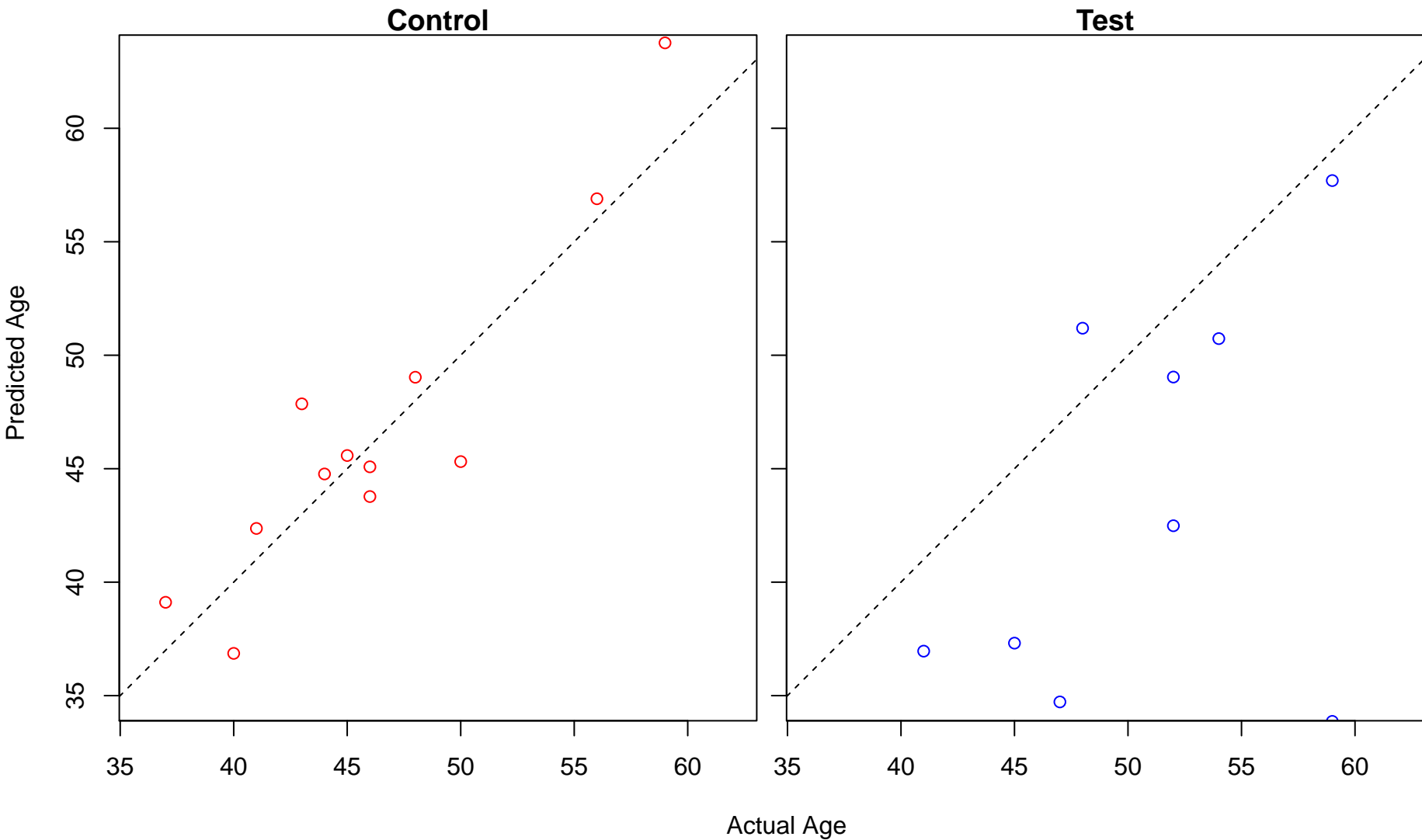
retina morphogenesis in camera-type eye (Score: 41.234722)



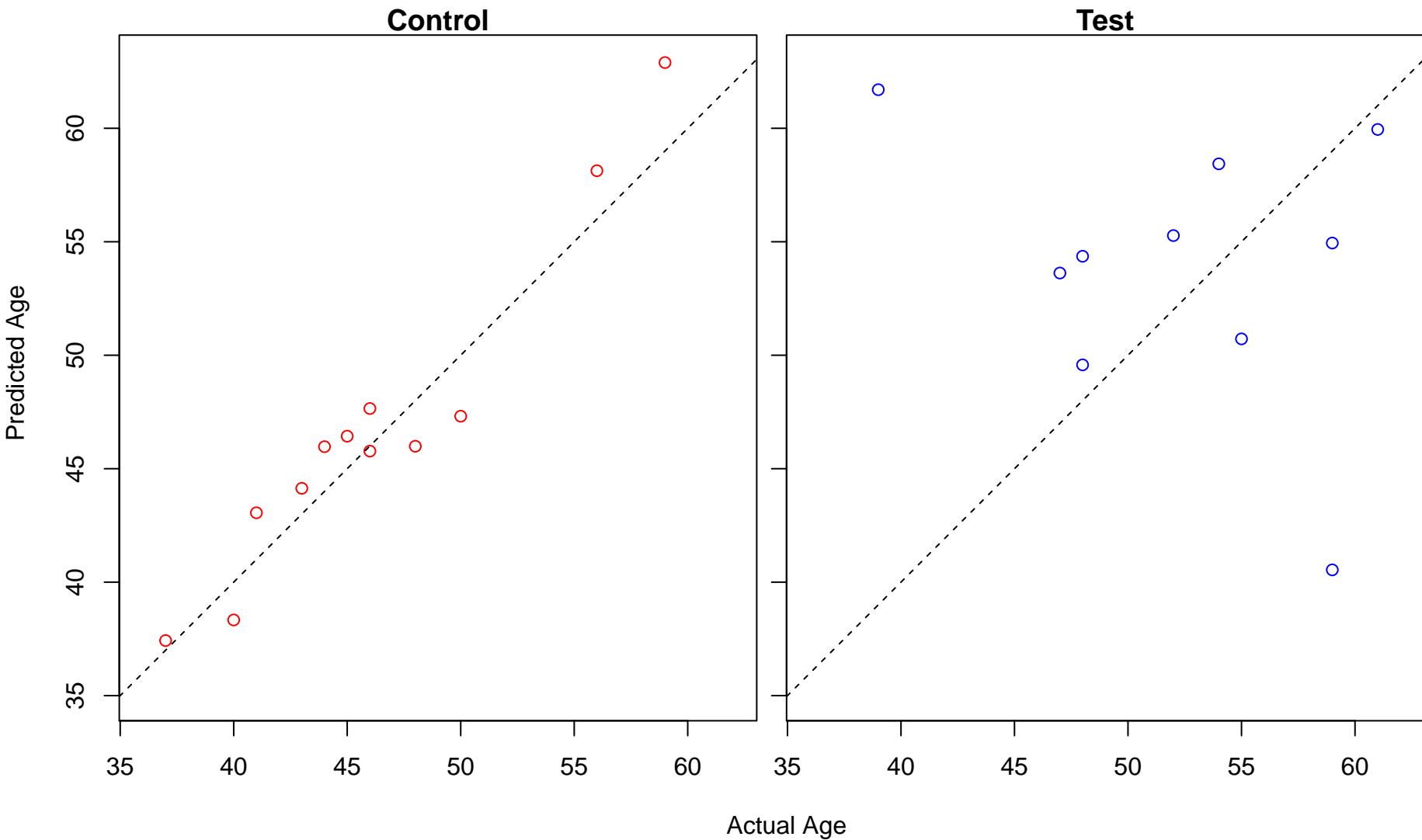
alpha-amino acid biosynthetic process (Score: 40.493031)



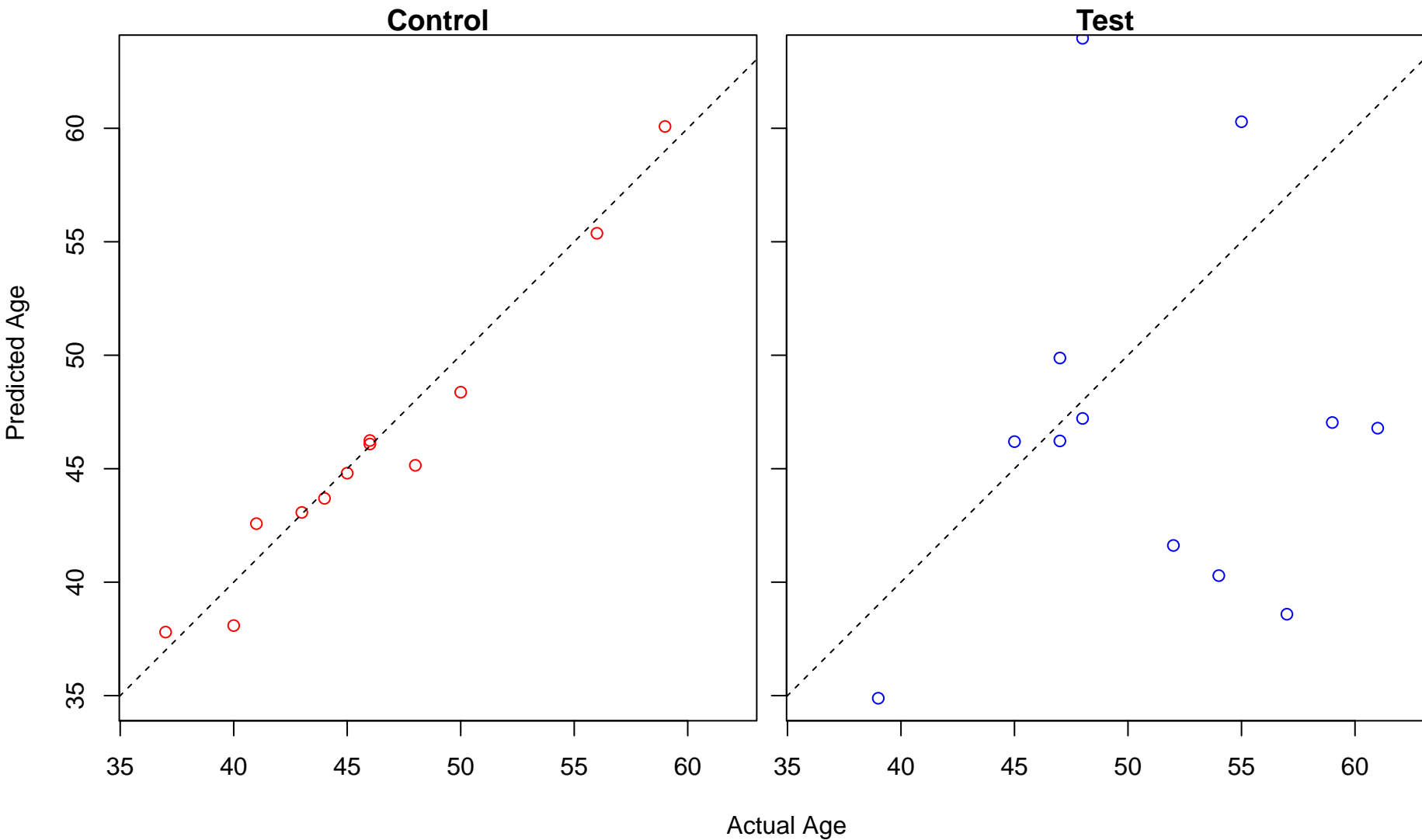
regulation of organ growth (Score: 40.484769)



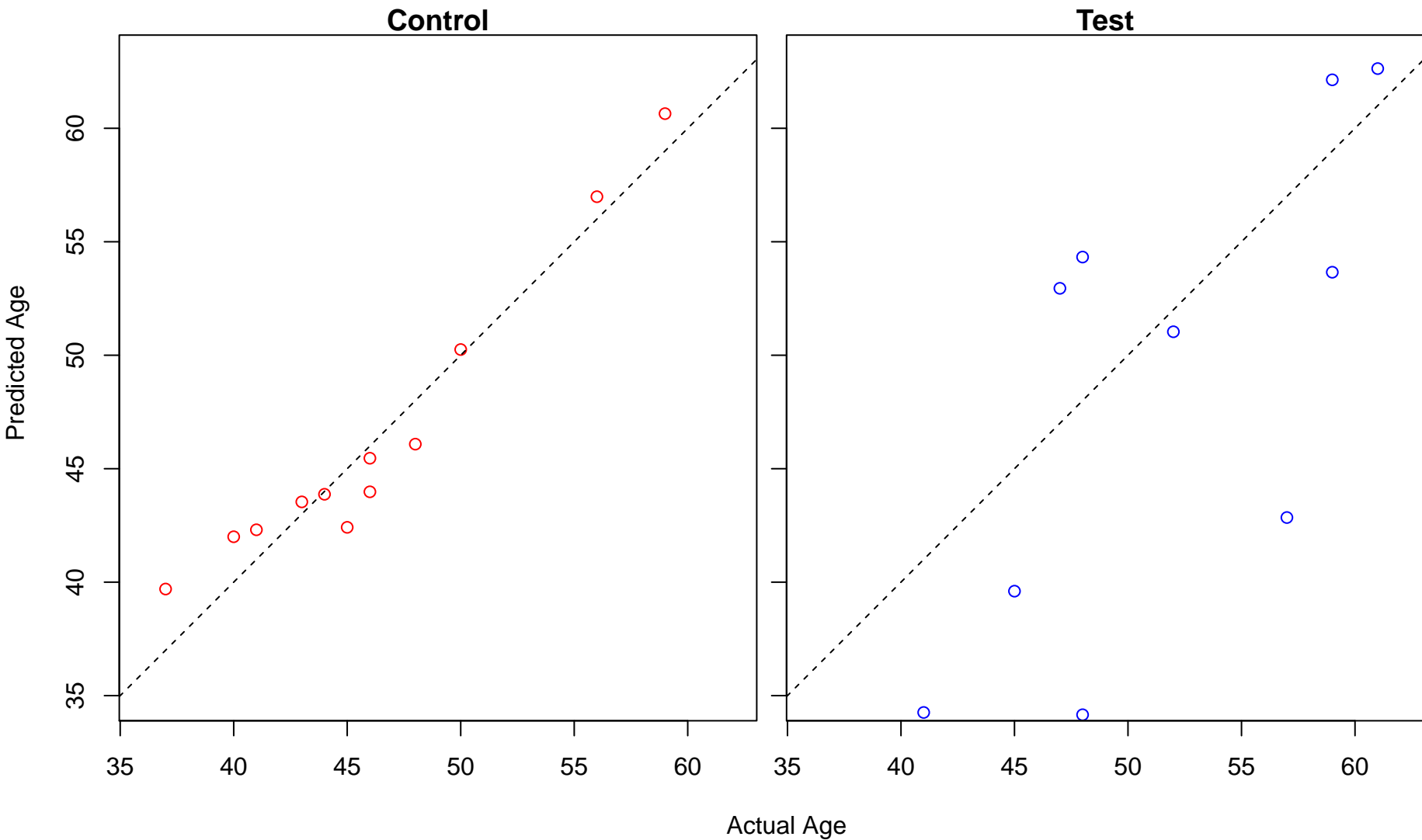
myeloid leukocyte differentiation (Score: 39.869127)



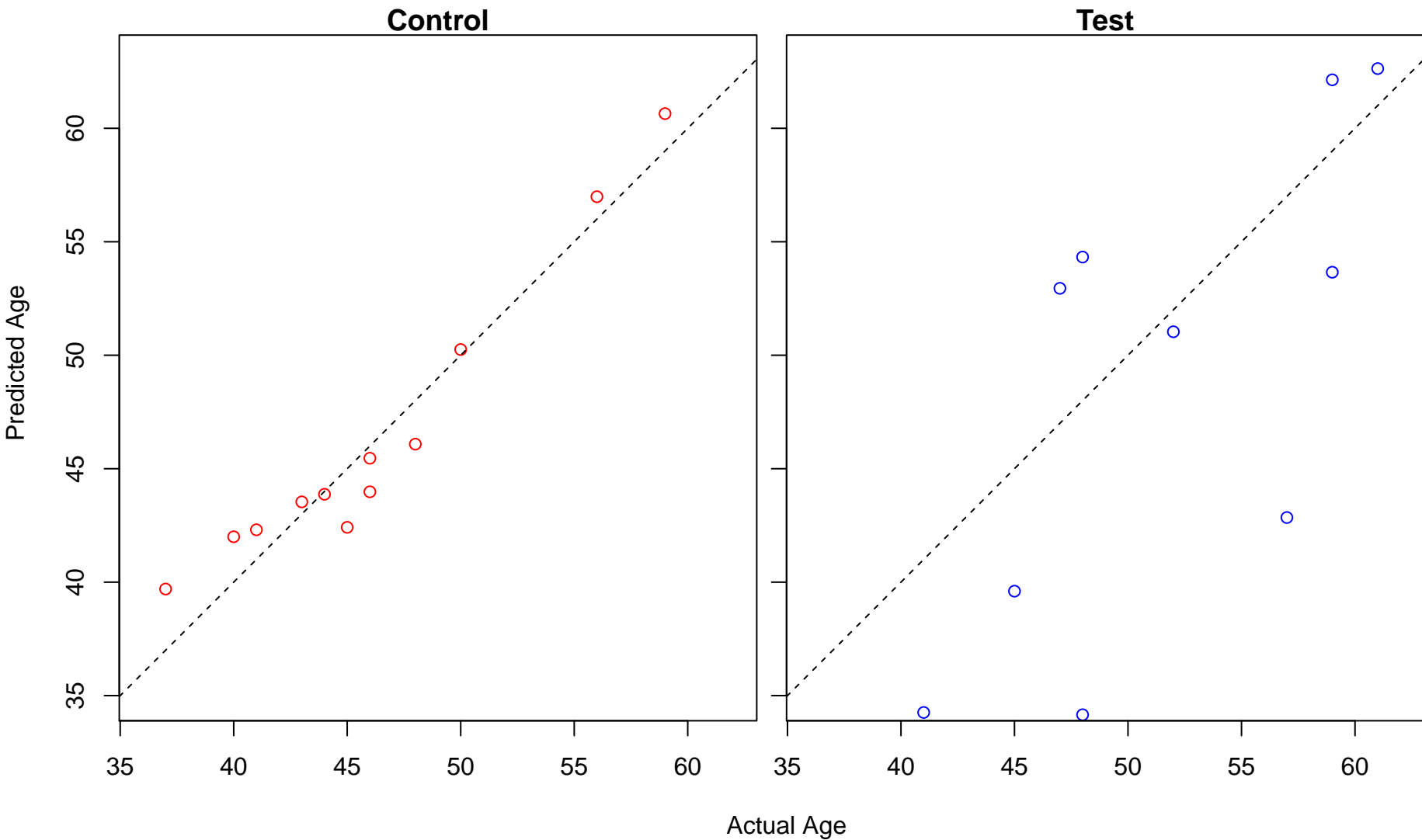
negative regulation of JUN kinase activity (Score: 38.890668)



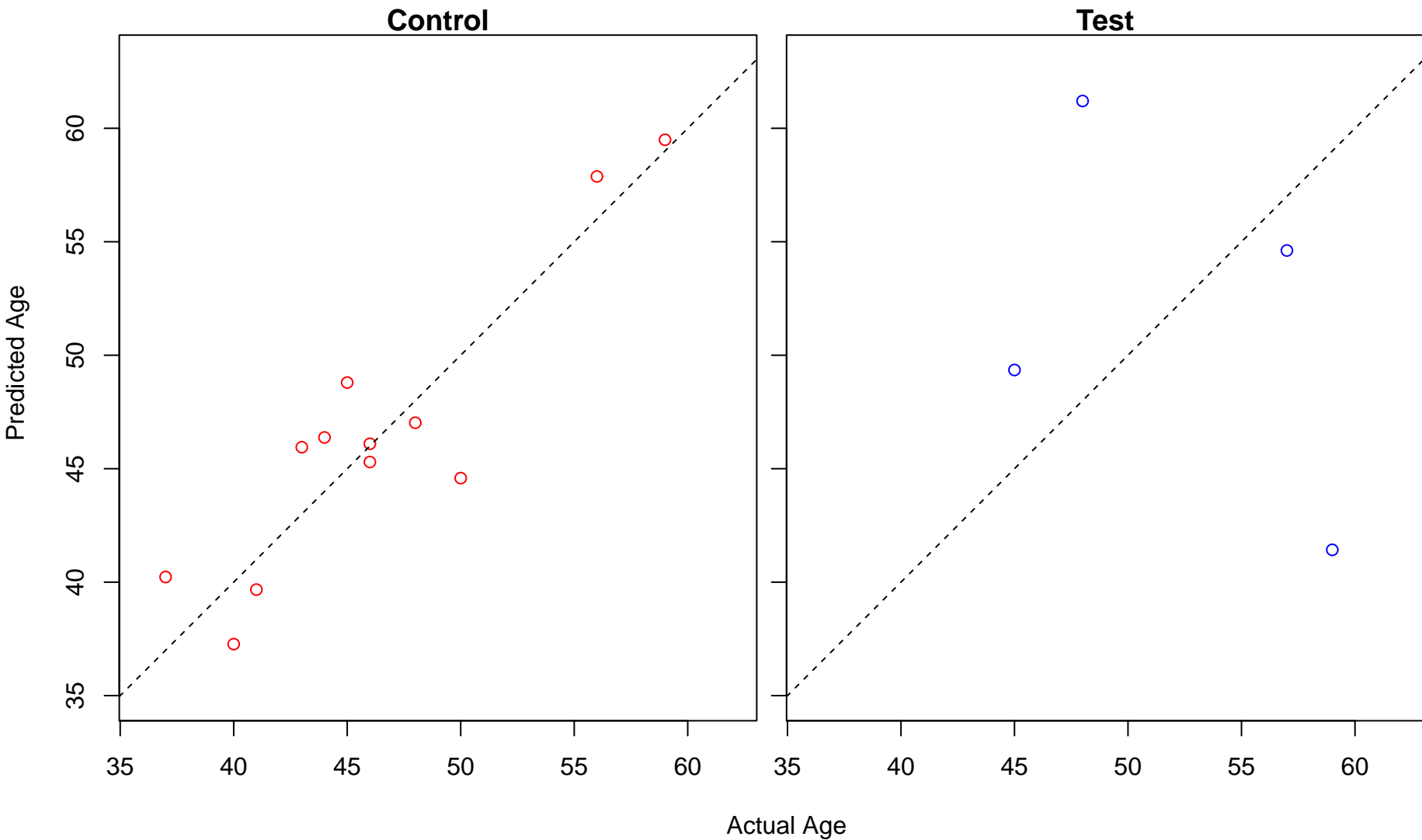
rhythmic behavior (Score: 38.120464)



circadian behavior (Score: 38.120464)



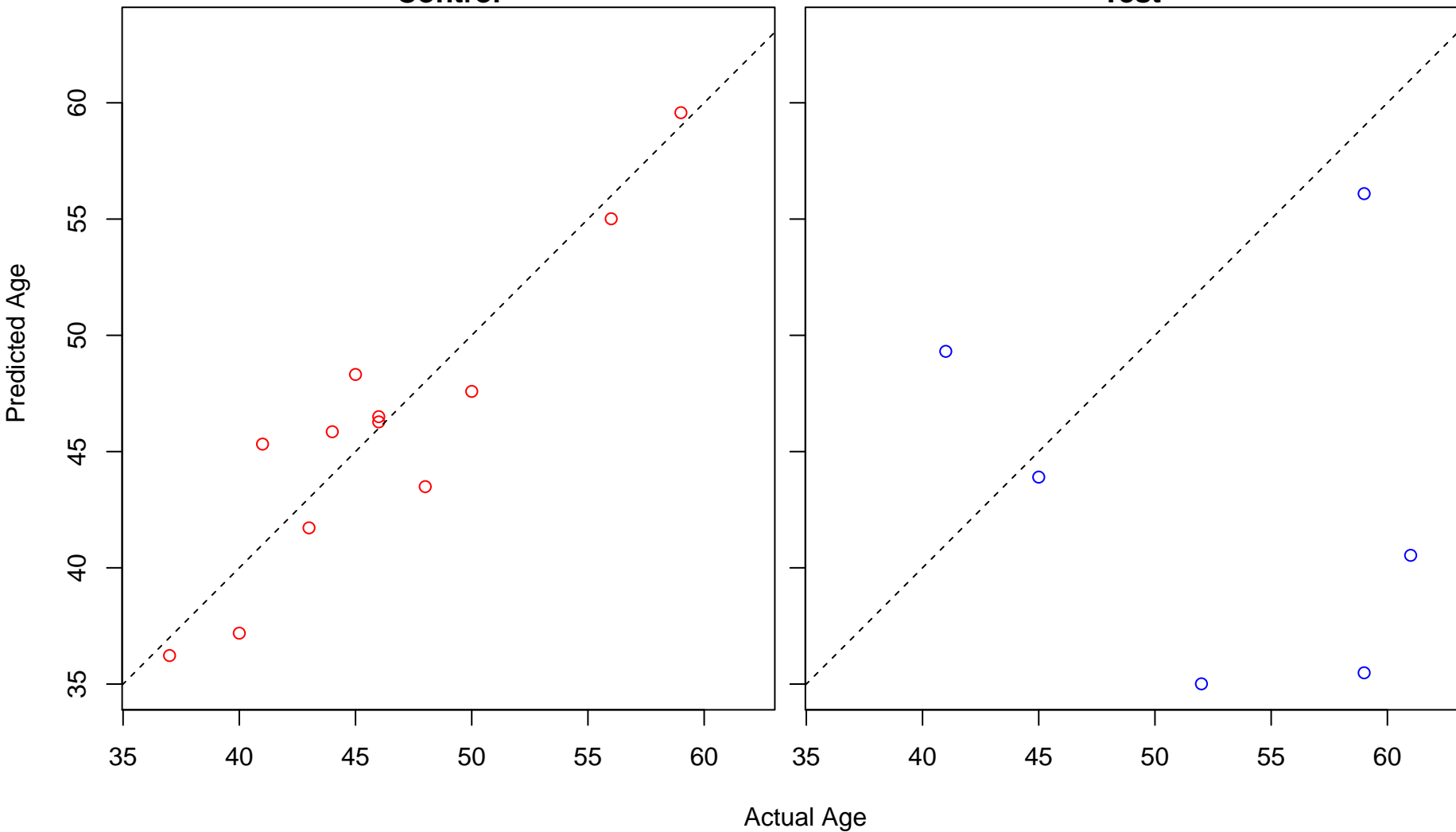
biomineral tissue development (Score: 38.061984)



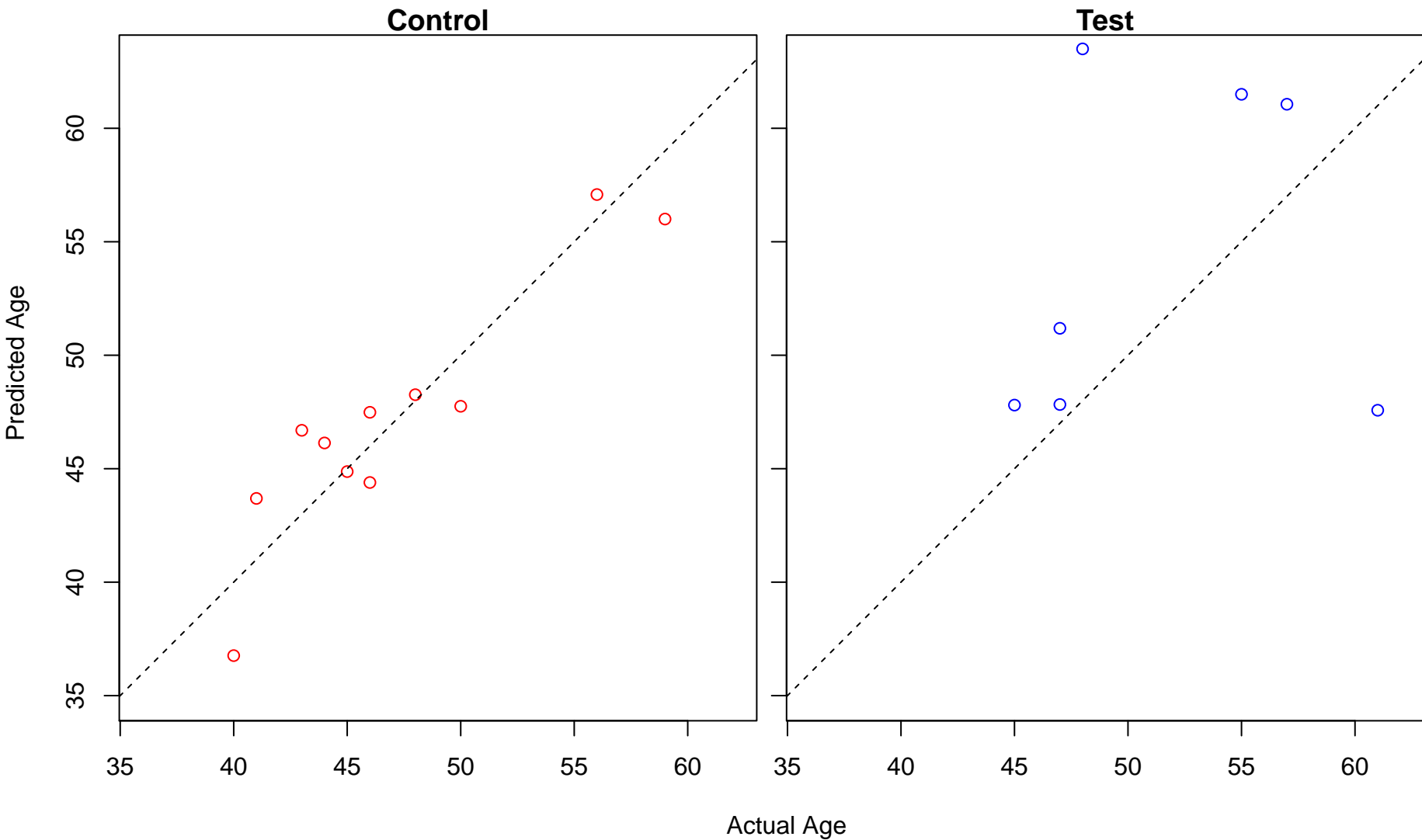
positive regulation of cholesterol efflux (Score: 37.863864)

Control

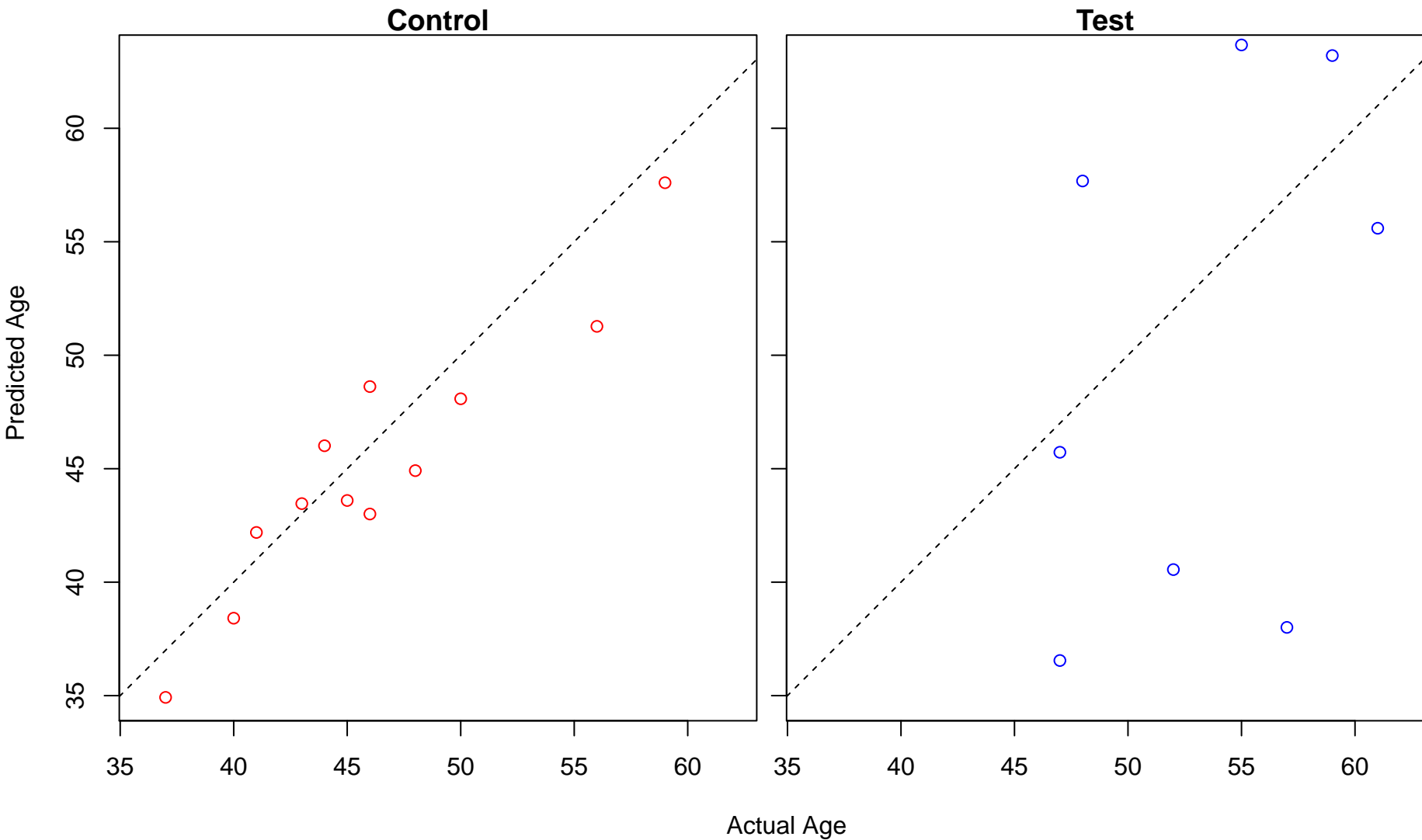
Test



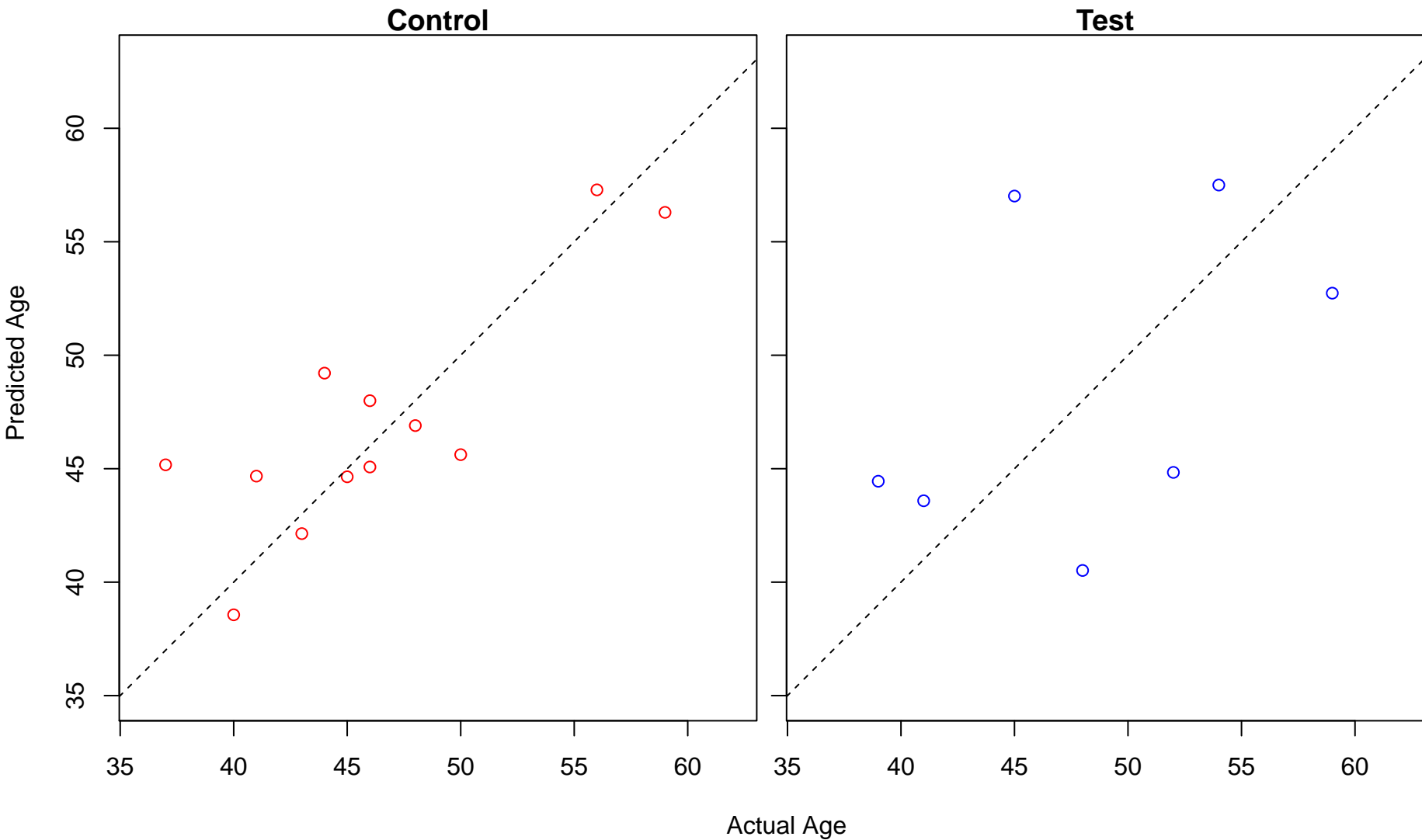
negative regulation of translational initiation in response to stress (Score: 37.811105)



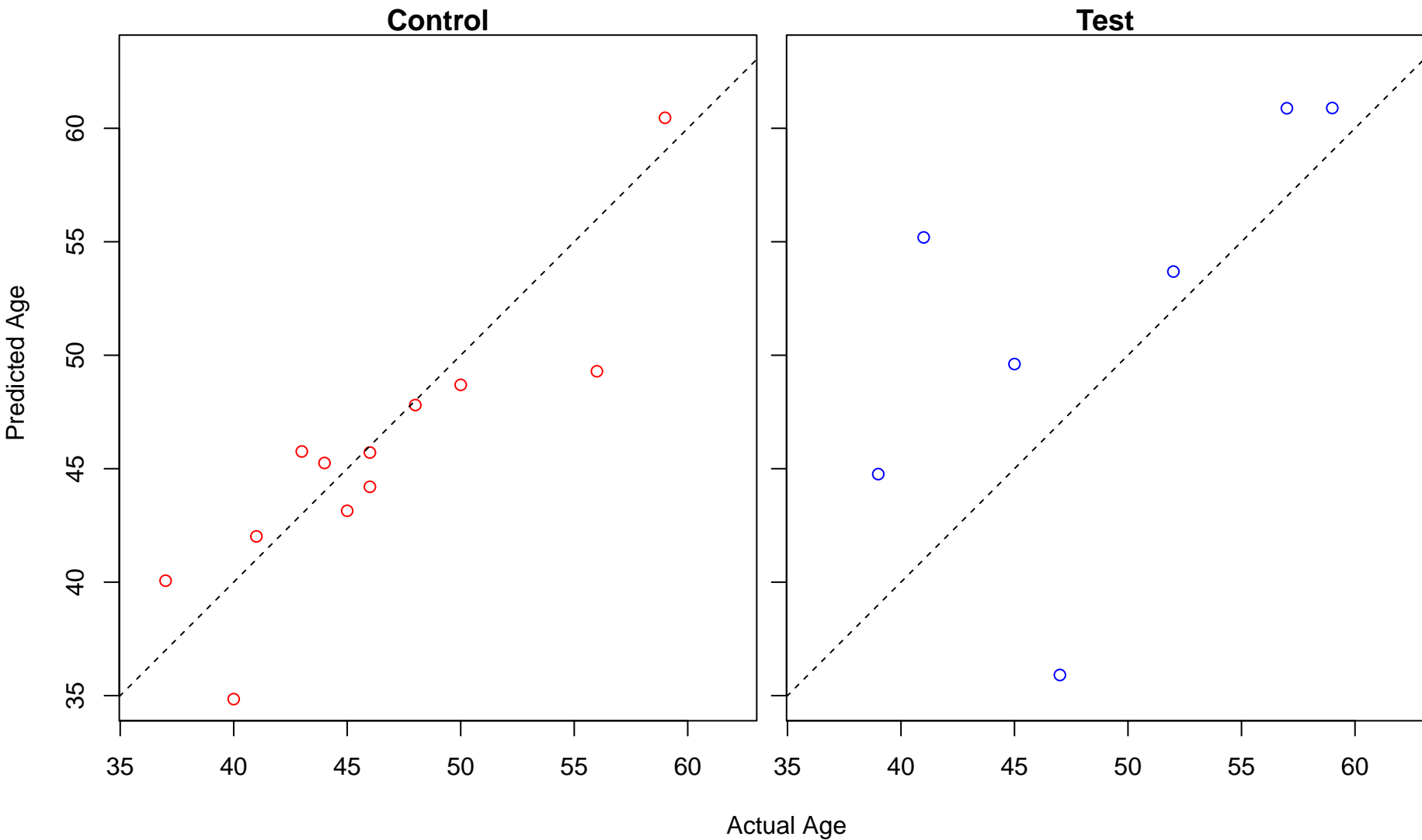
nonribosomal peptide biosynthetic process (Score: 37.747044)



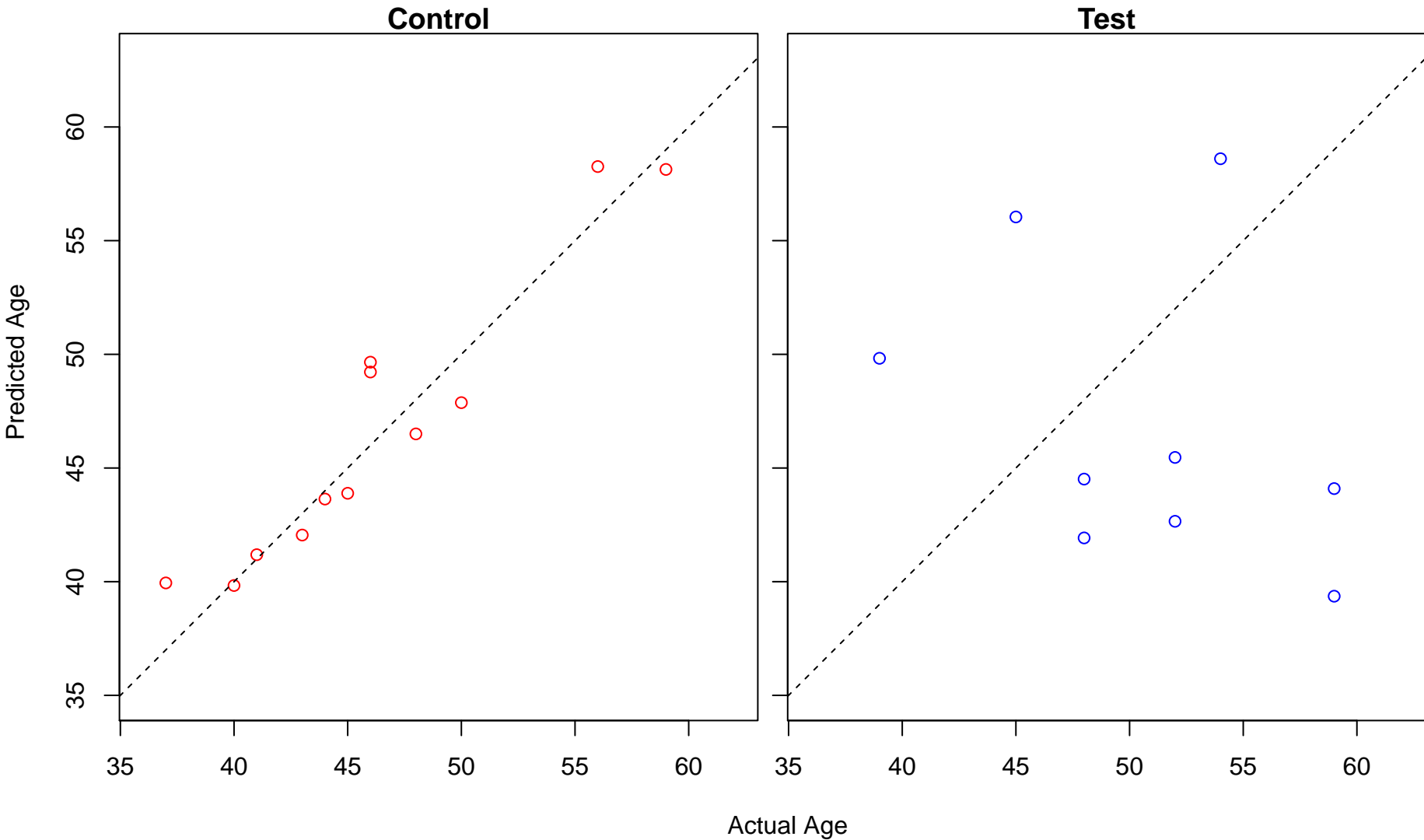
neutrophil activation (Score: 37.382206)



glomerulus morphogenesis (Score: 37.349014)

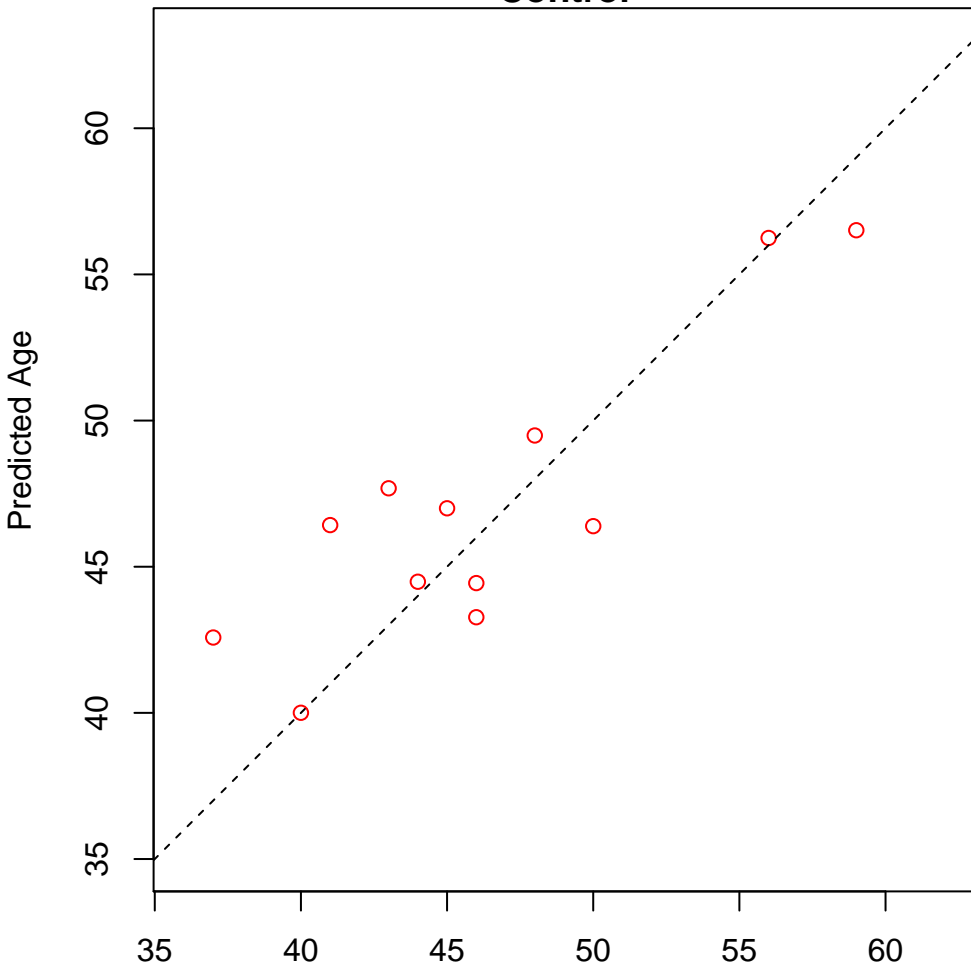


regulation of leukocyte apoptotic process (Score: 36.772946)

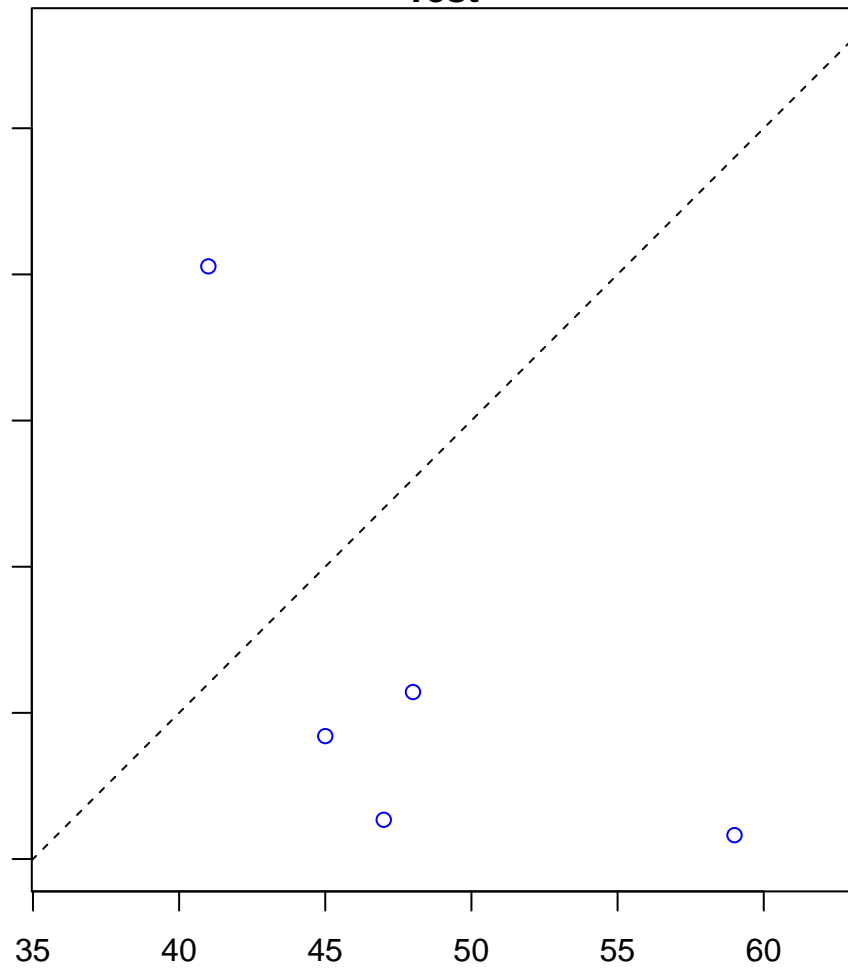


cellular response to misfolded protein (Score: 36.748631)

Control

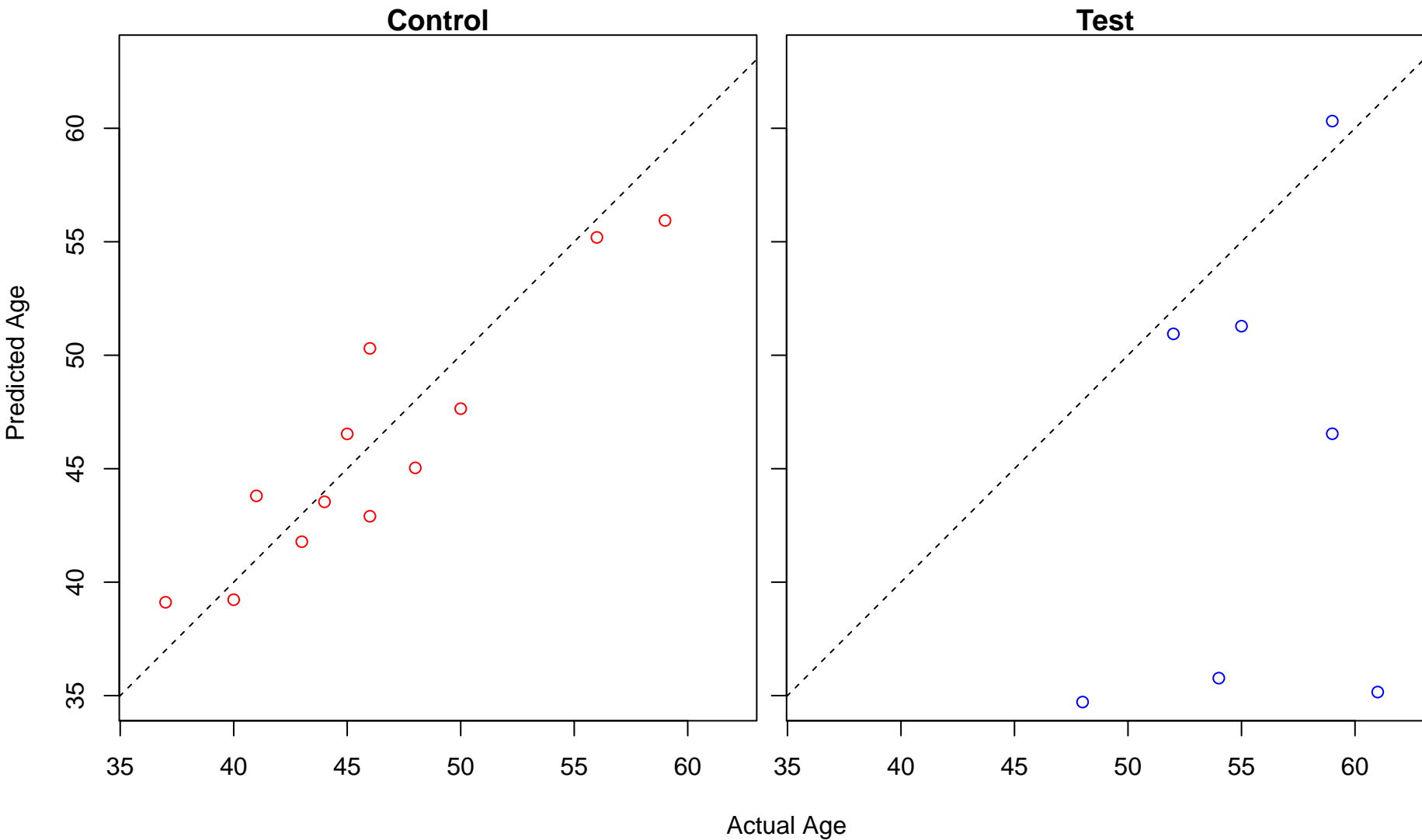


Test

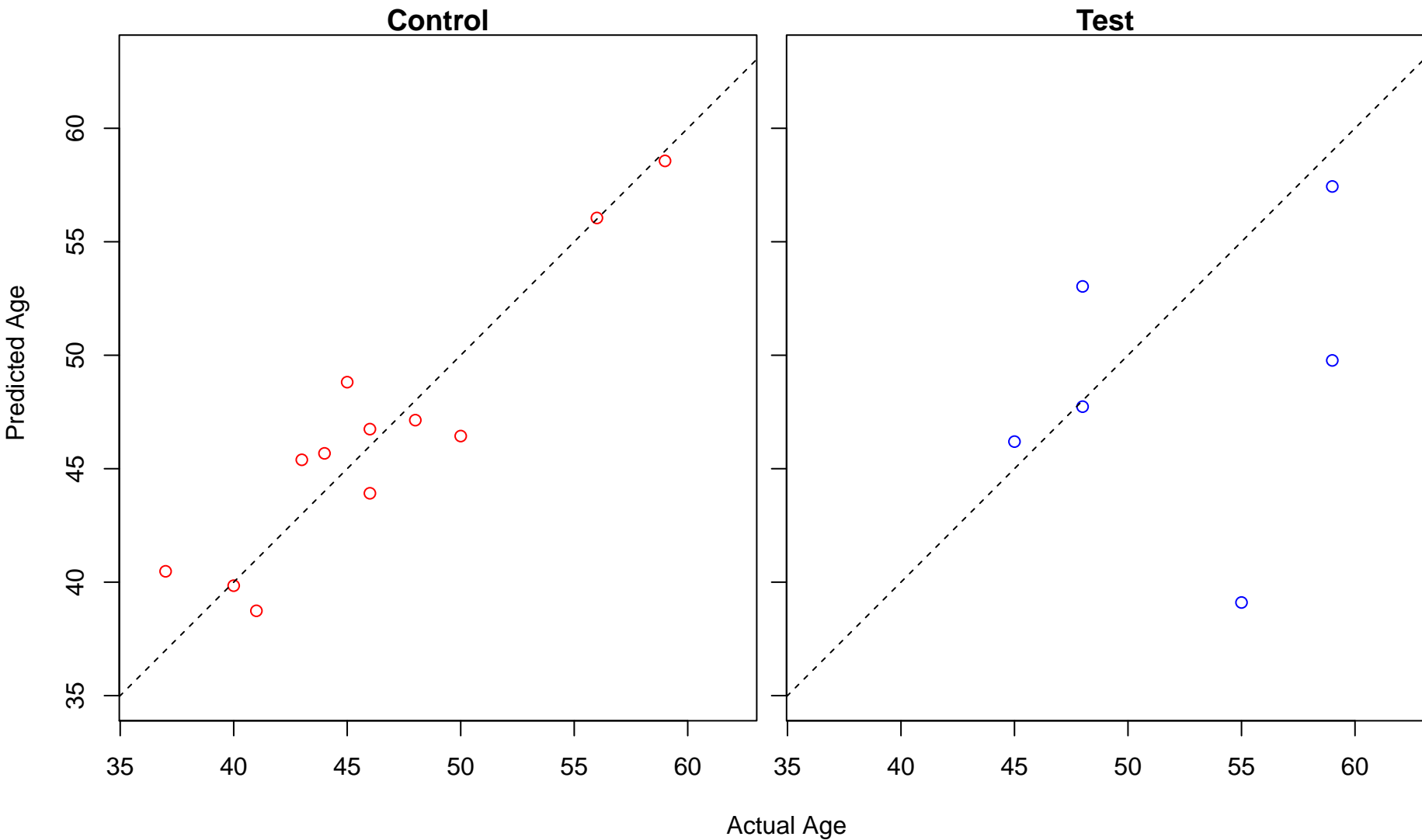


Actual Age

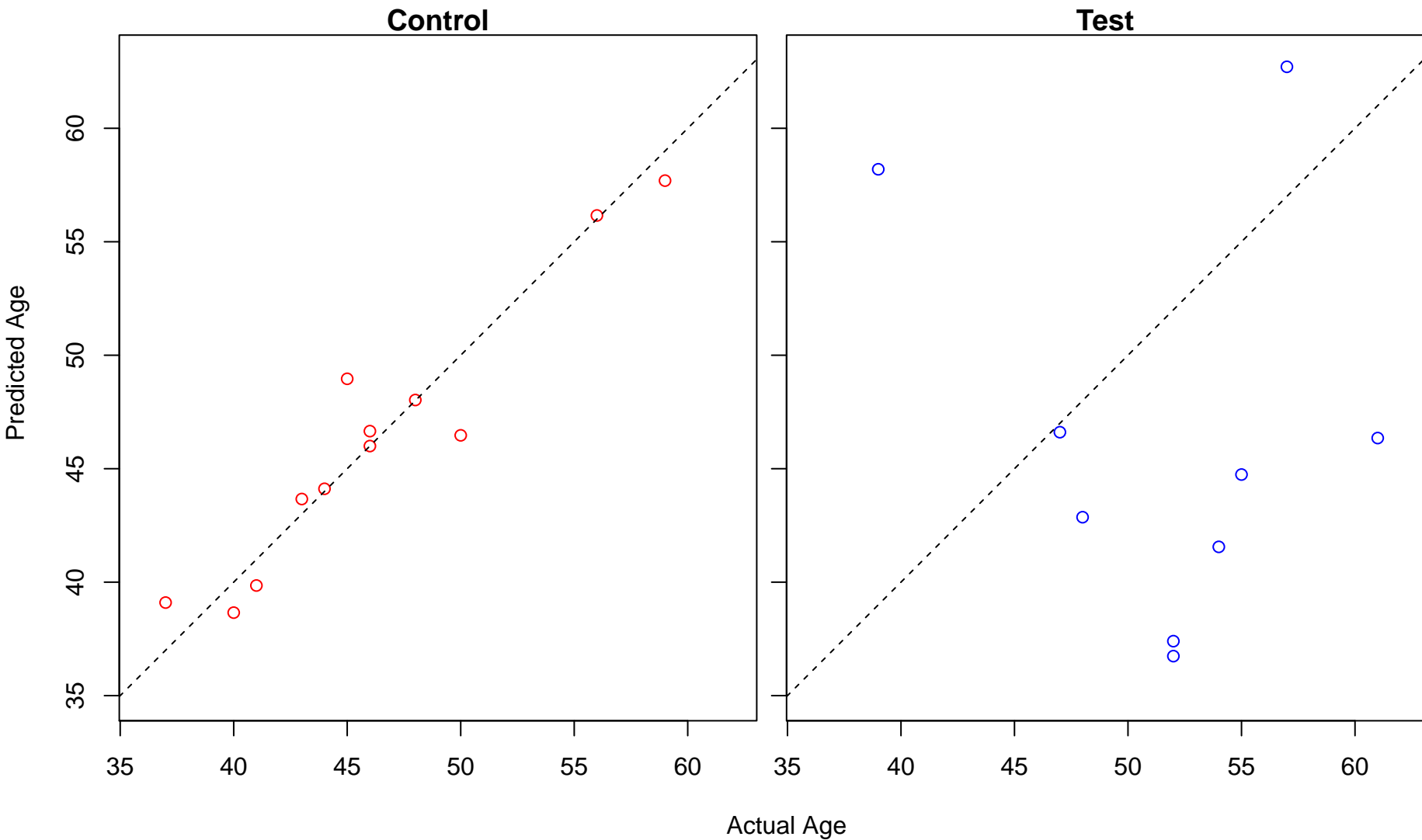
glutamate metabolic process (Score: 36.664605)



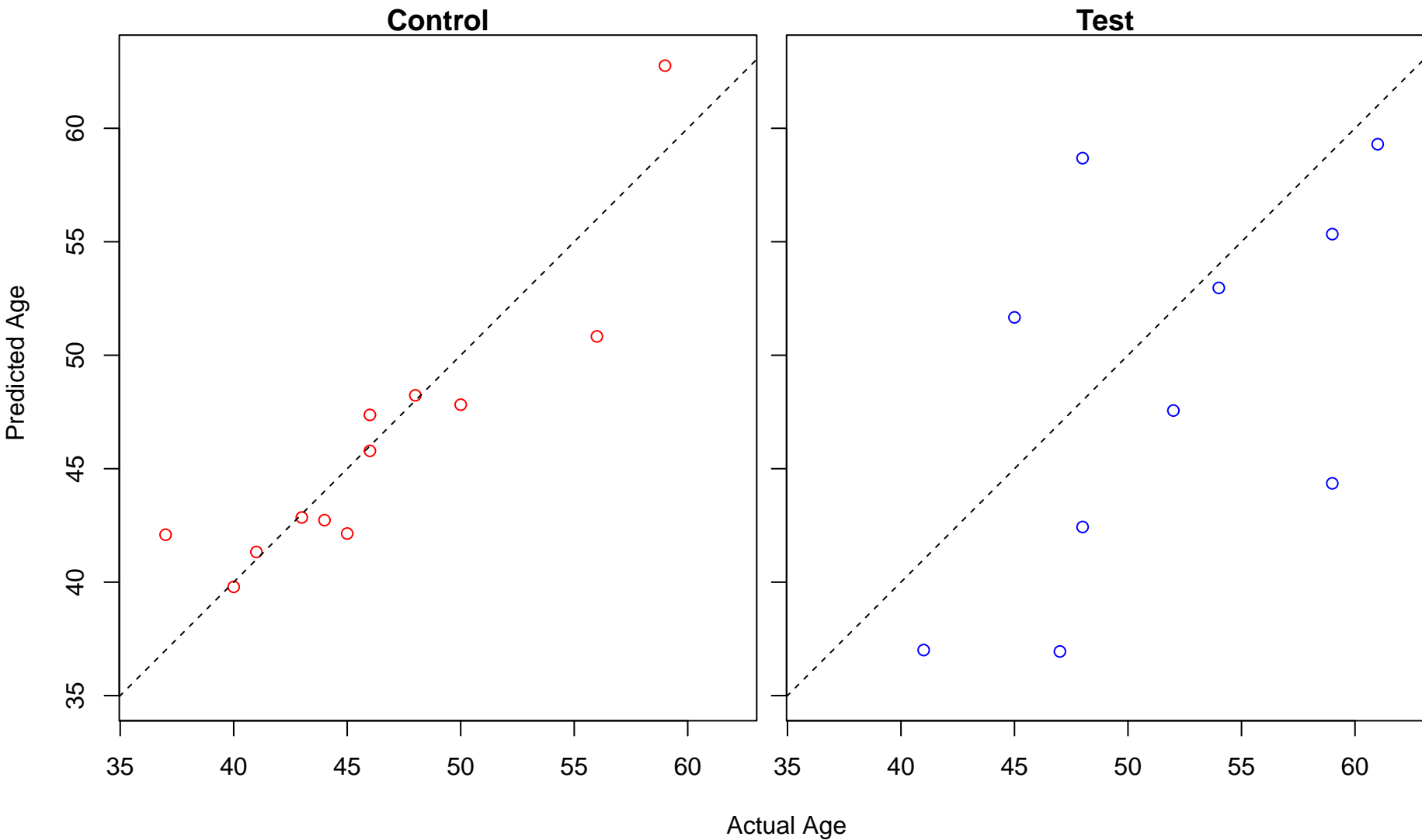
lung morphogenesis (Score: 36.658875)



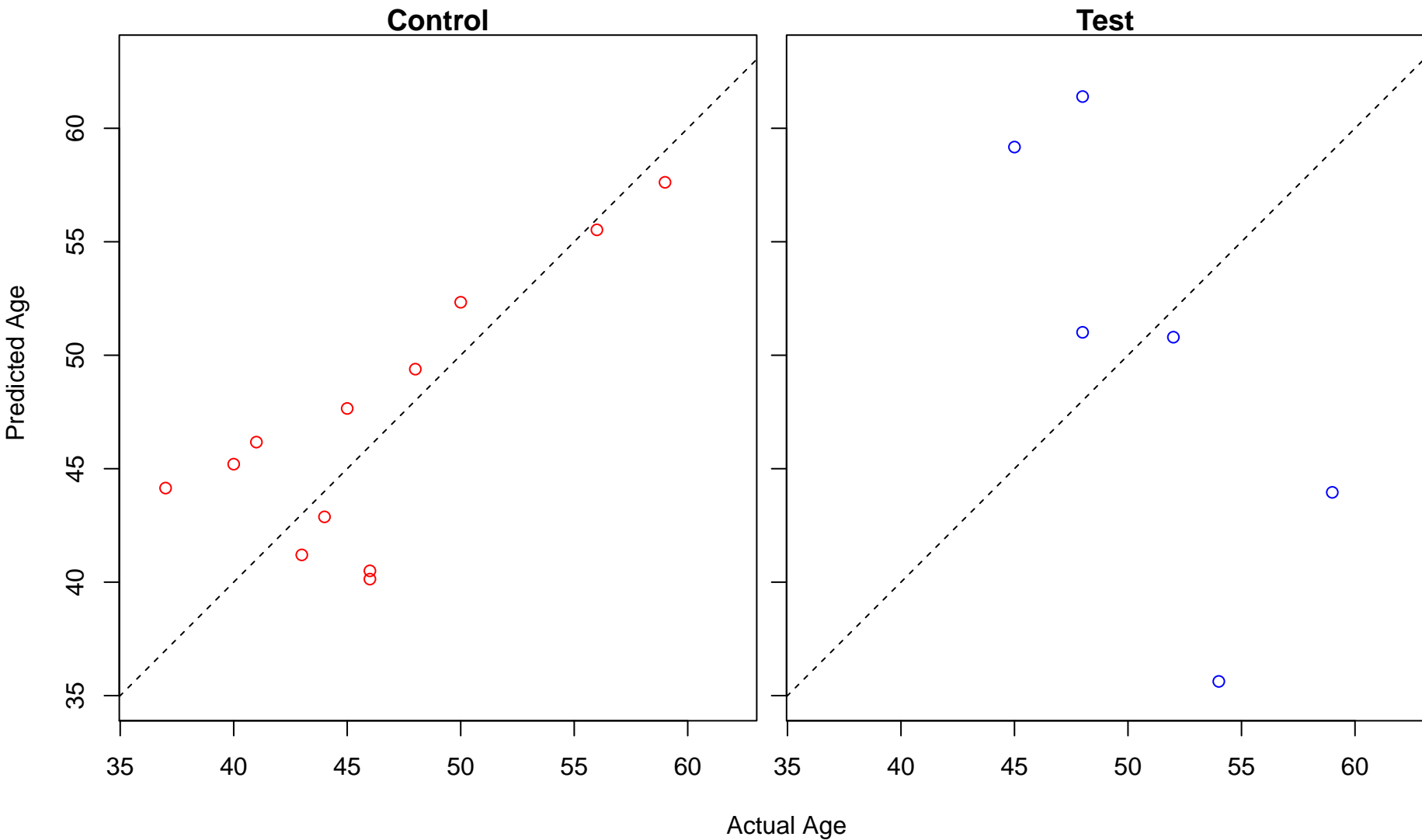
regulation of kidney development (Score: 36.441138)



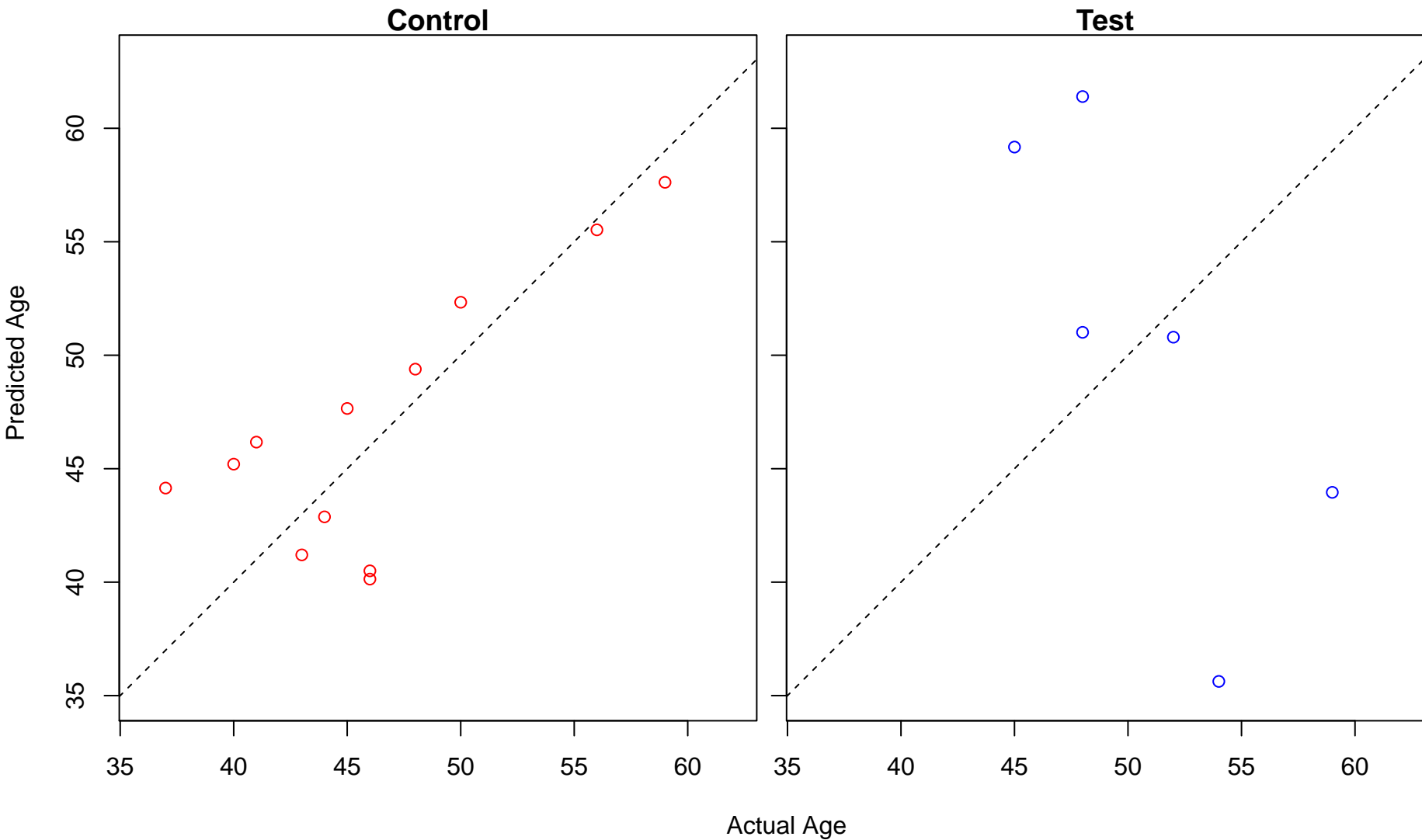
negative regulation of cell size (Score: 36.154068)



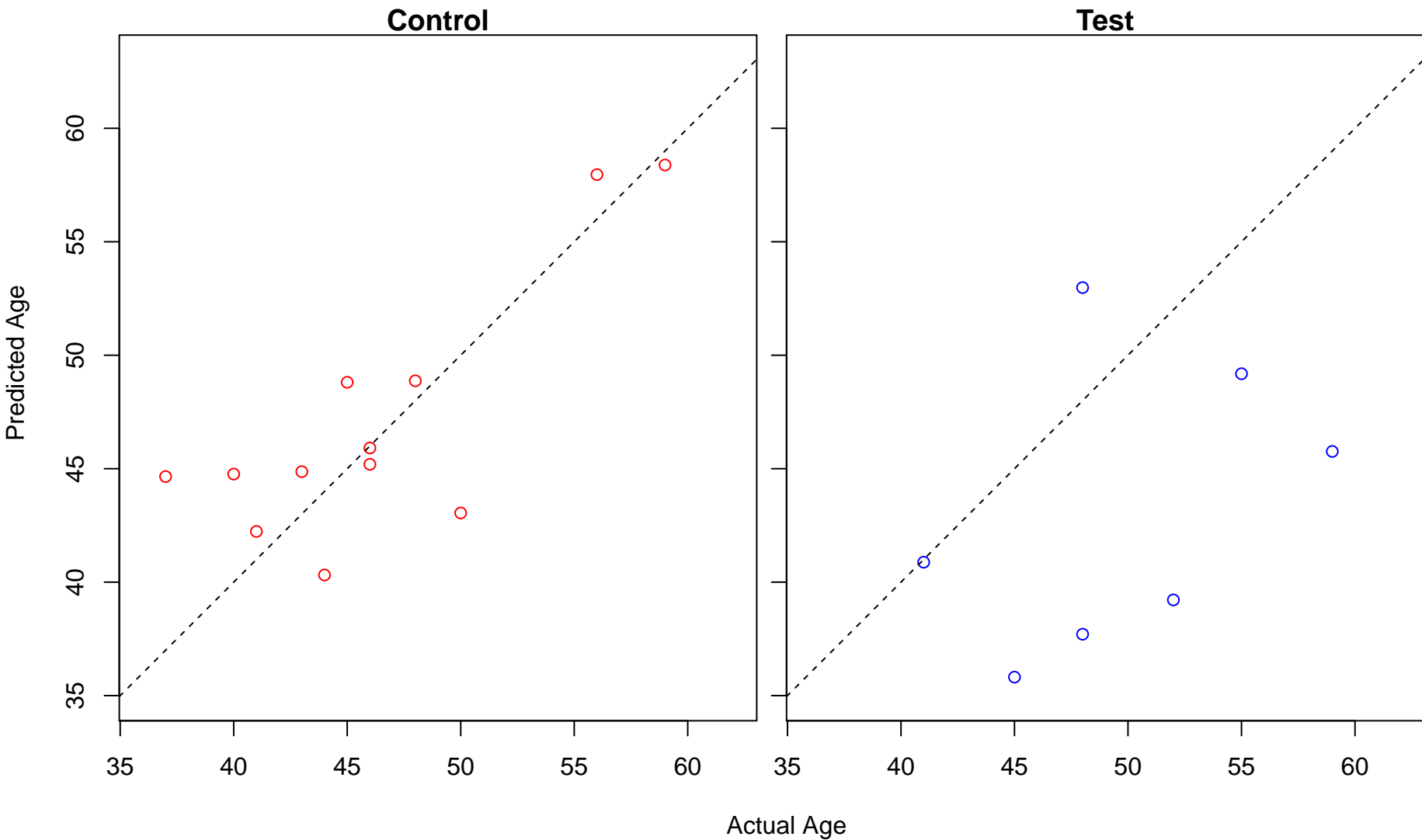
intracellular sterol transport (Score: 35.747604)



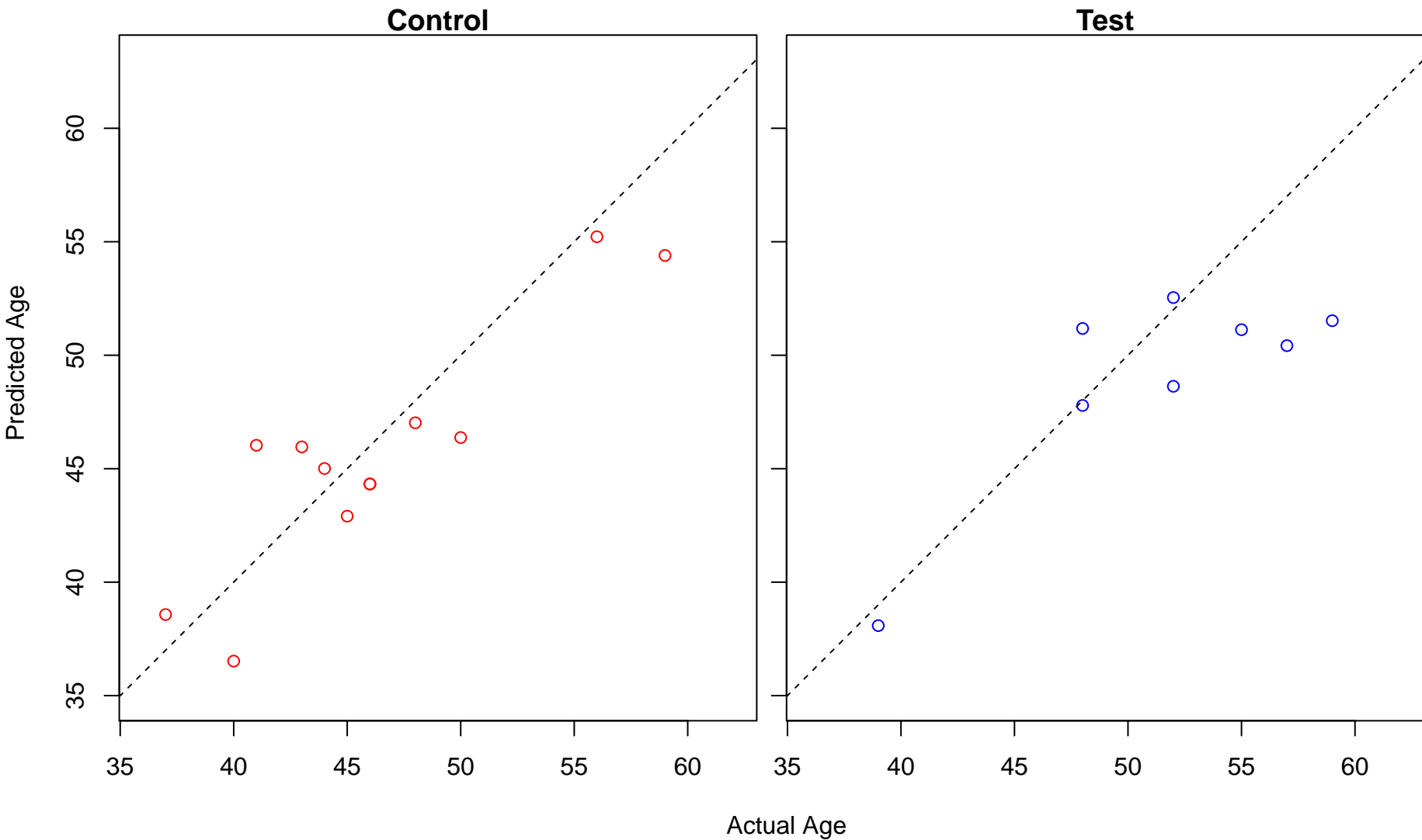
intracellular cholesterol transport (Score: 35.747604)



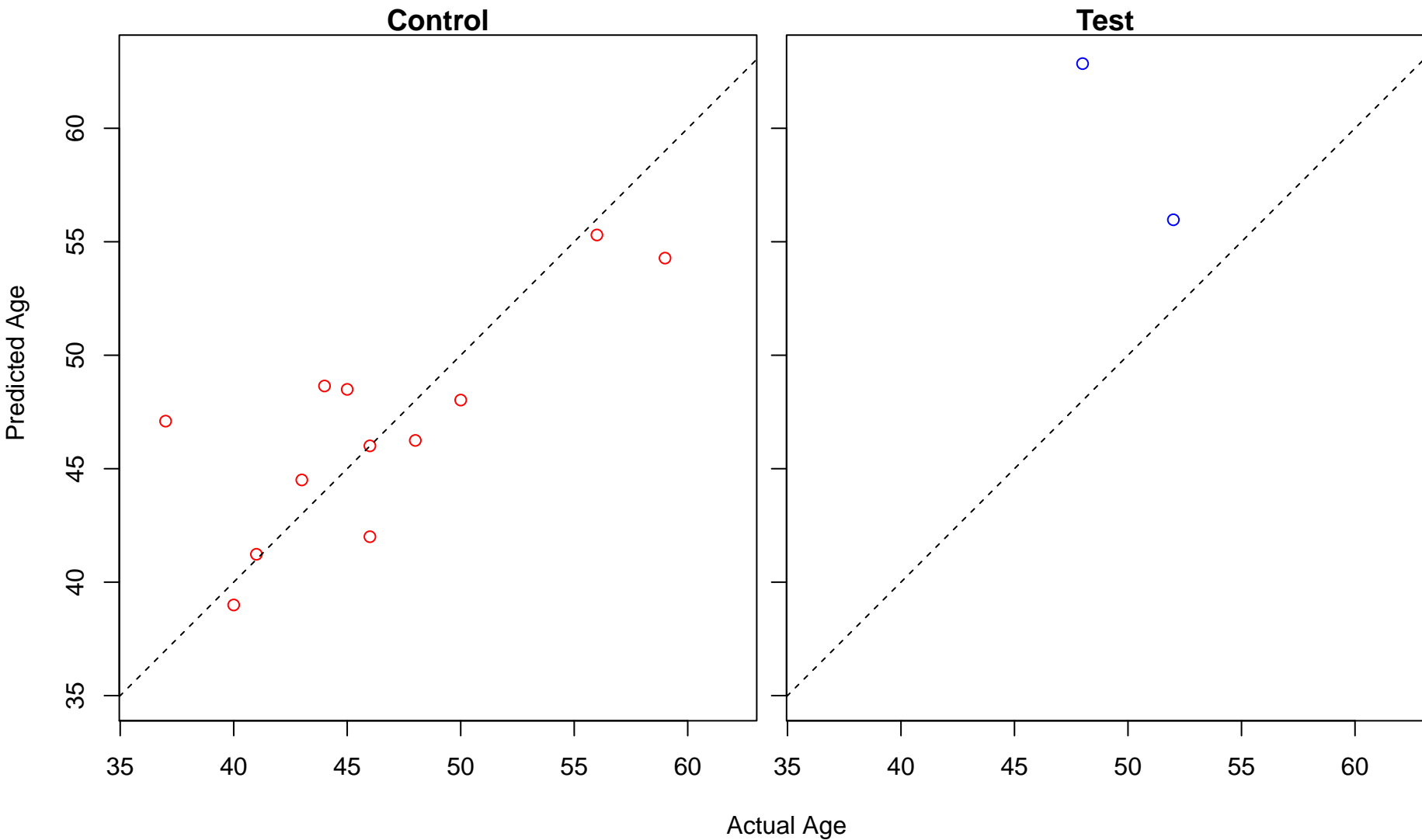
odontogenesis (Score: 35.361299)



regulation of store-operated calcium channel activity (Score: 34.899413)

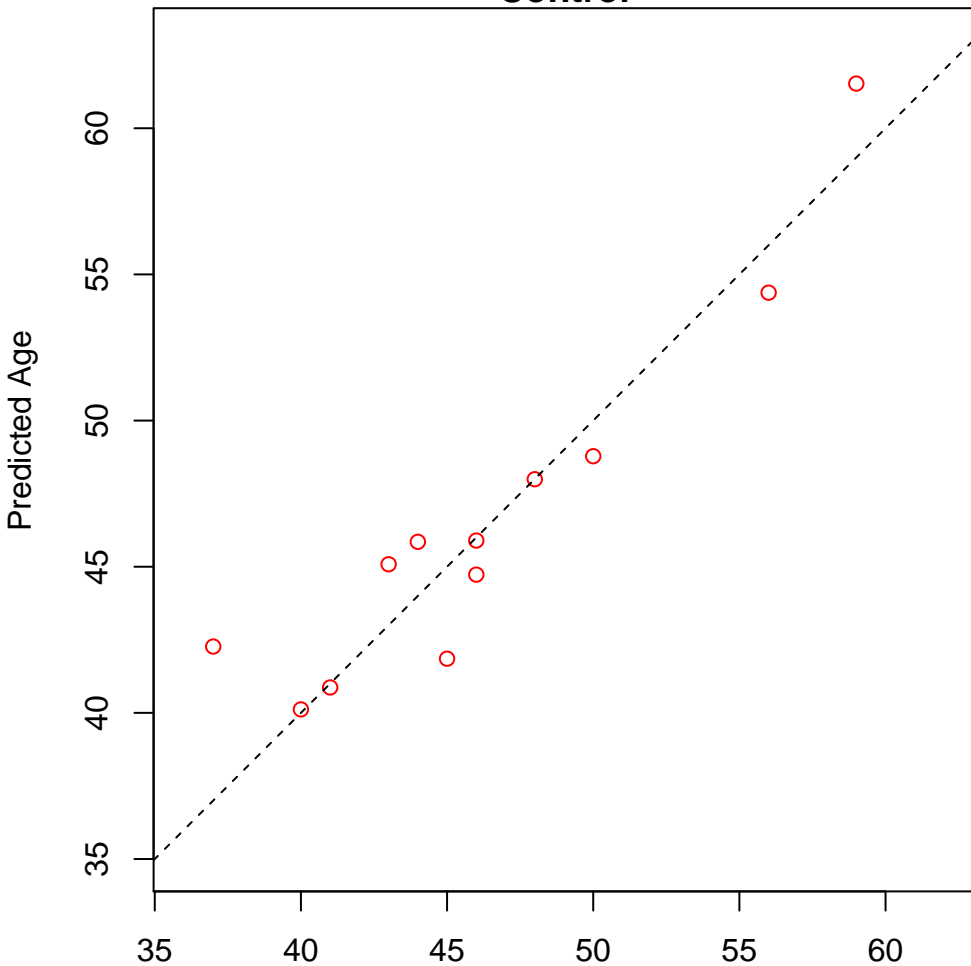


positive regulation of heterotypic cell-cell adhesion (Score: 34.831567)

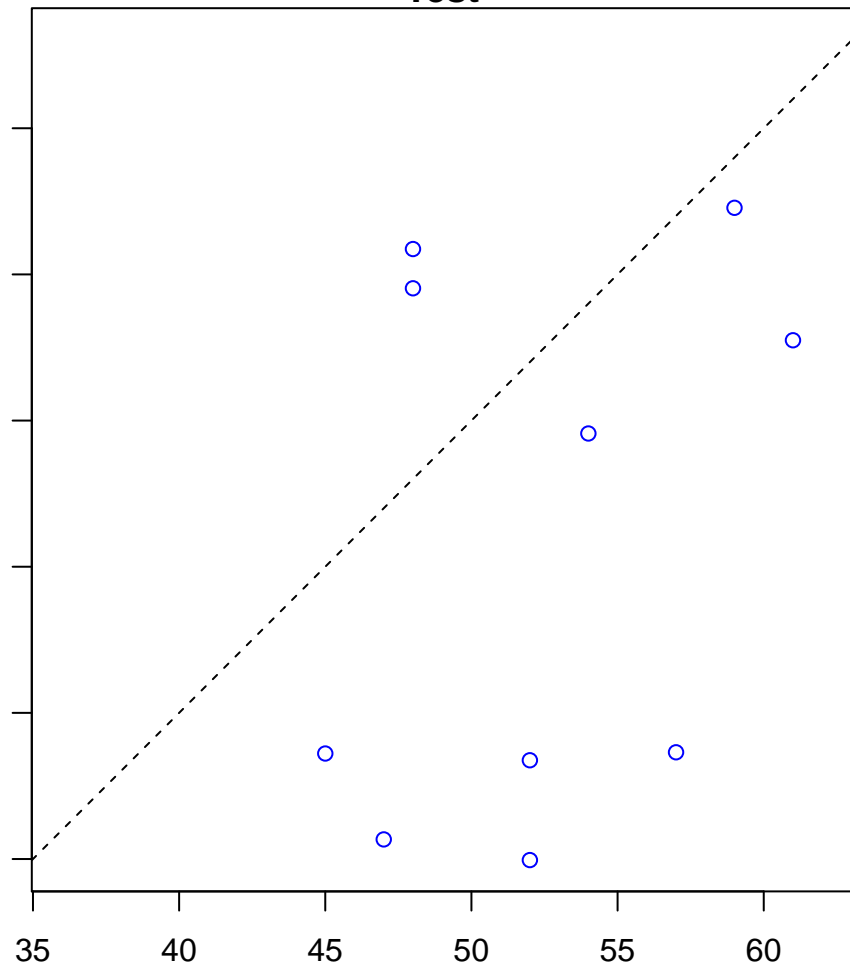


cardiac muscle cell action potential (Score: 34.758329)

Control

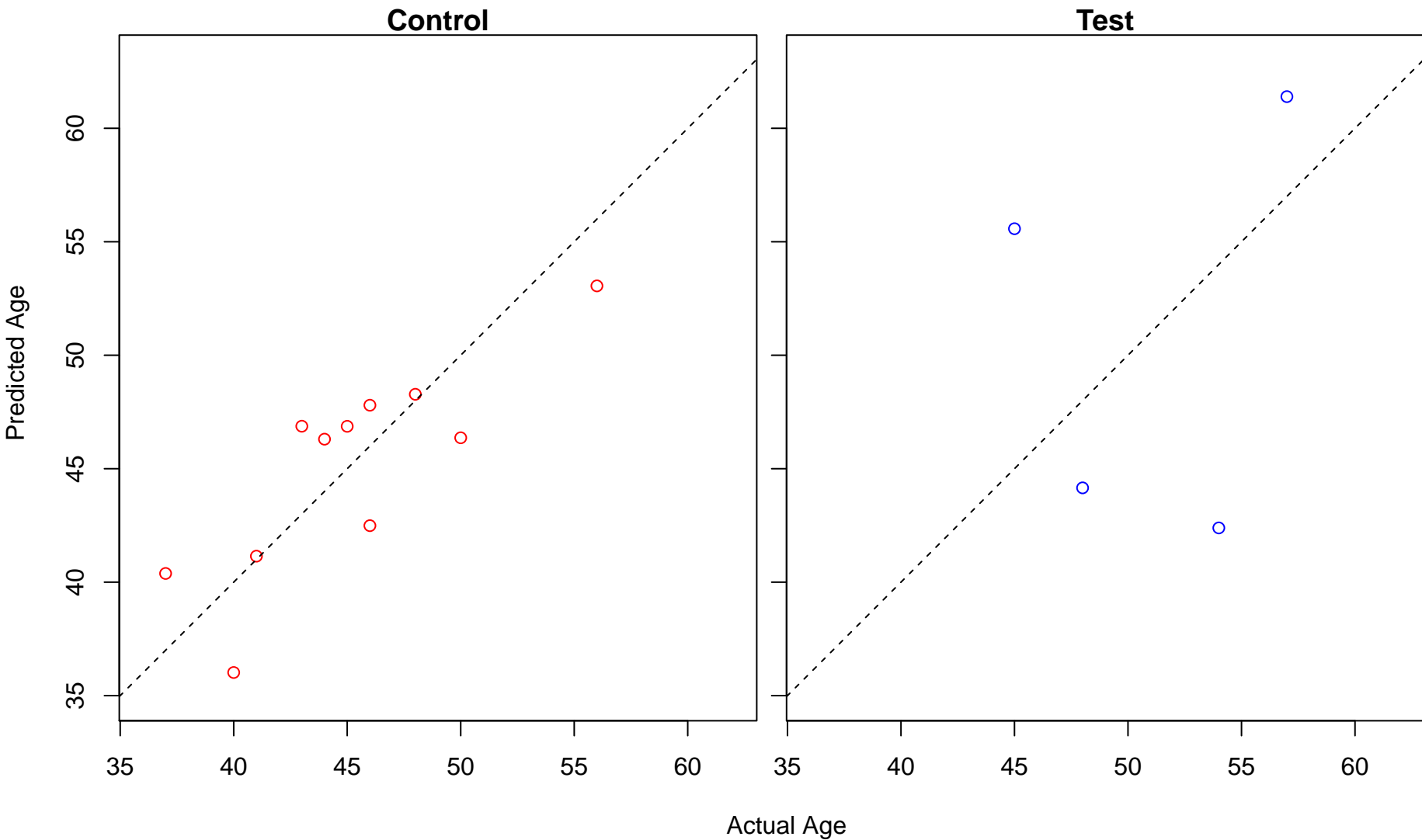


Test

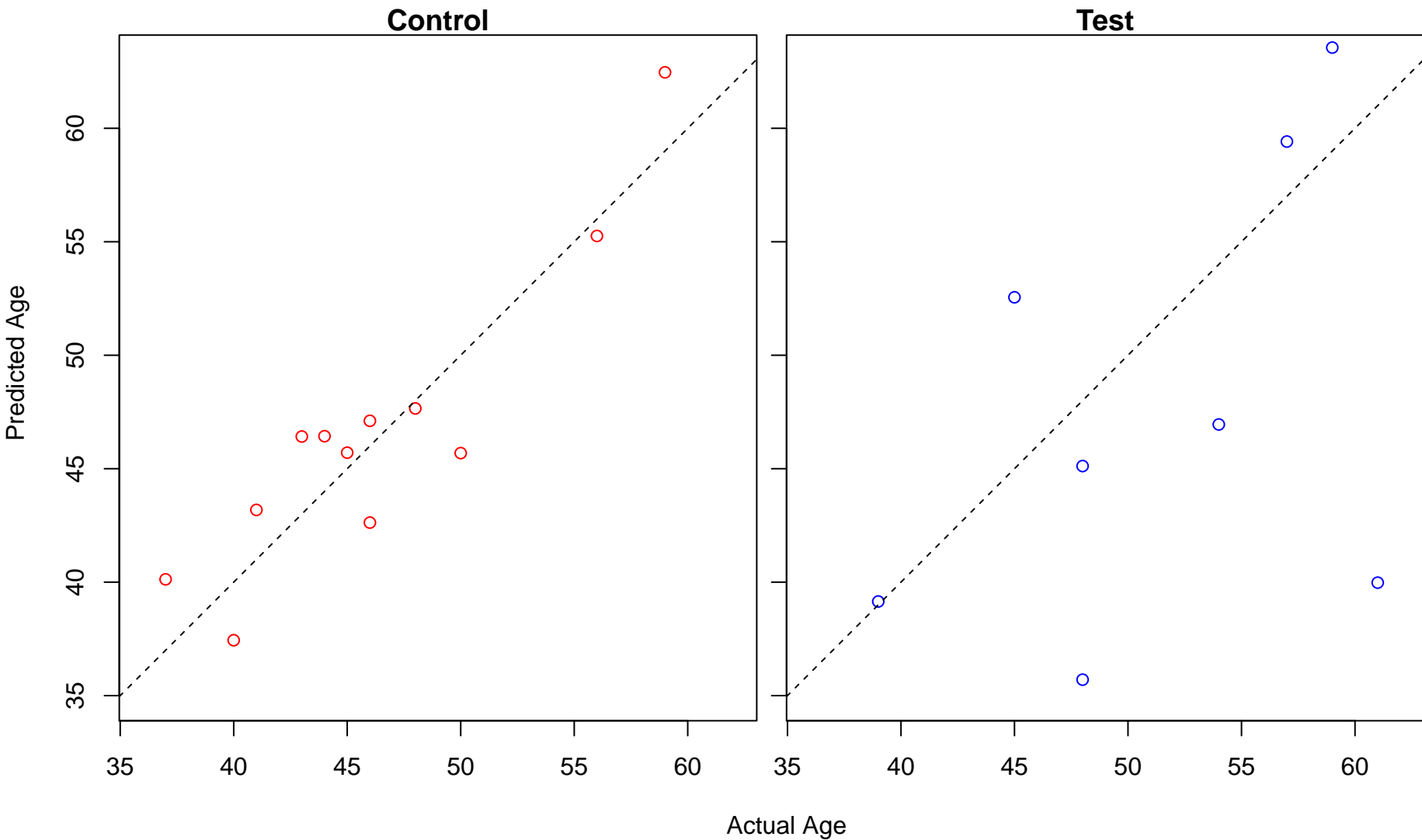


Actual Age

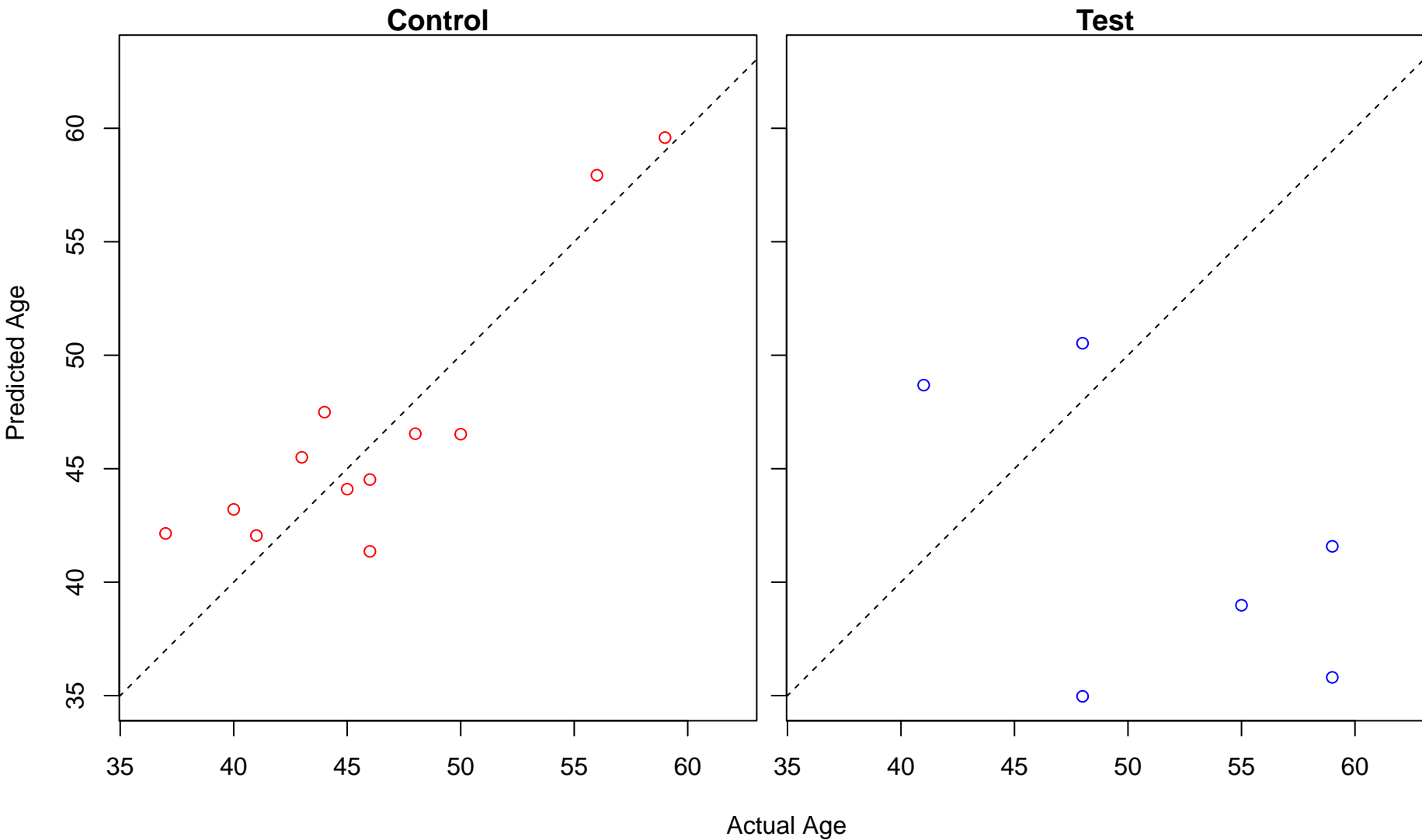
leukocyte chemotaxis (Score: 34.728107)



cell chemotaxis (Score: 34.715654)

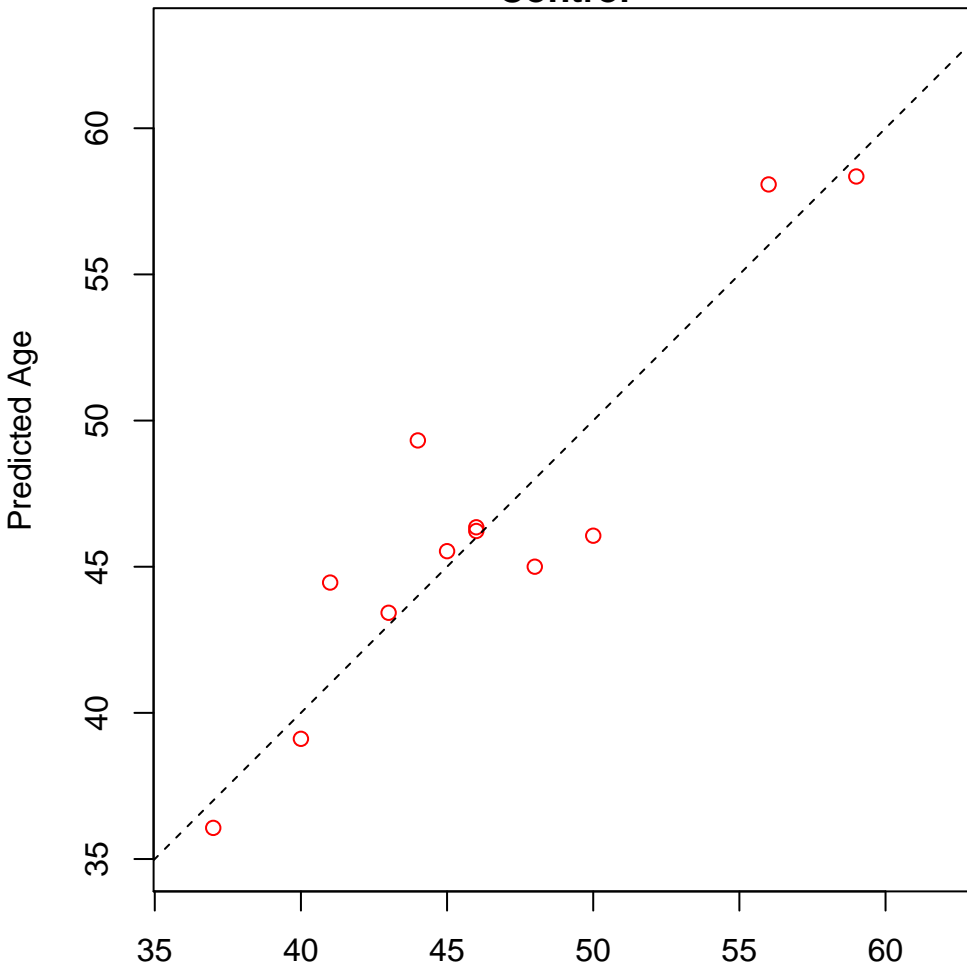


regulation of actin cytoskeleton organization (Score: 34.234304)

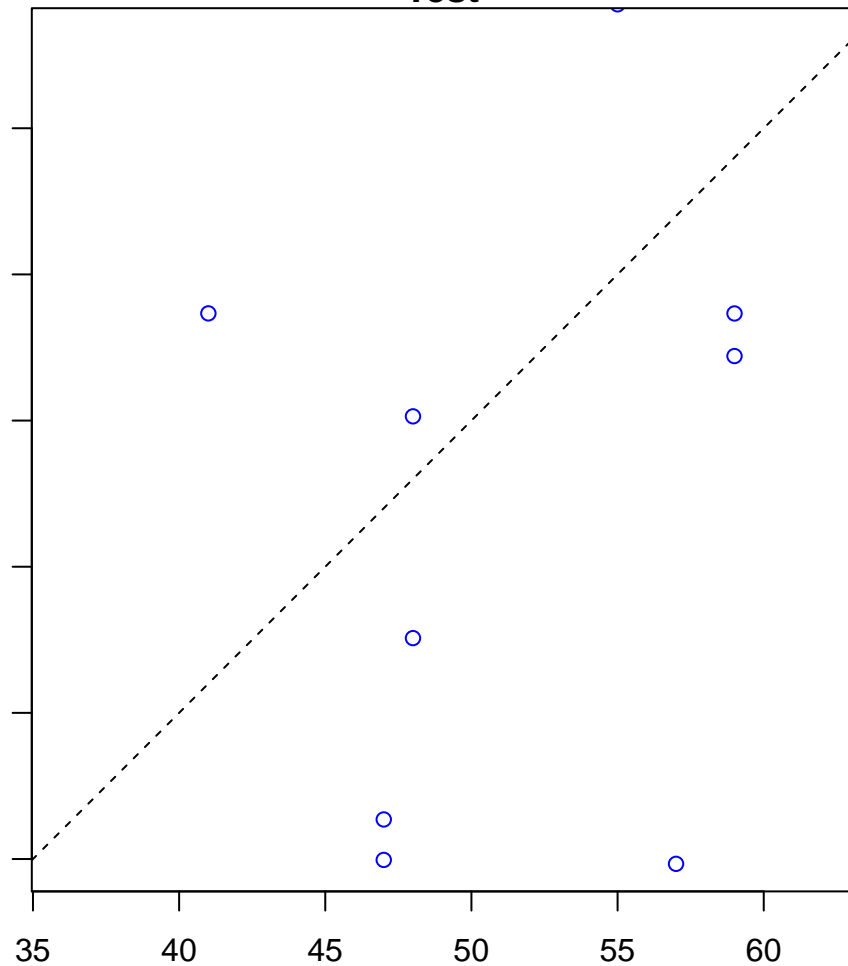


endochondral bone morphogenesis (Score: 34.220464)

Control

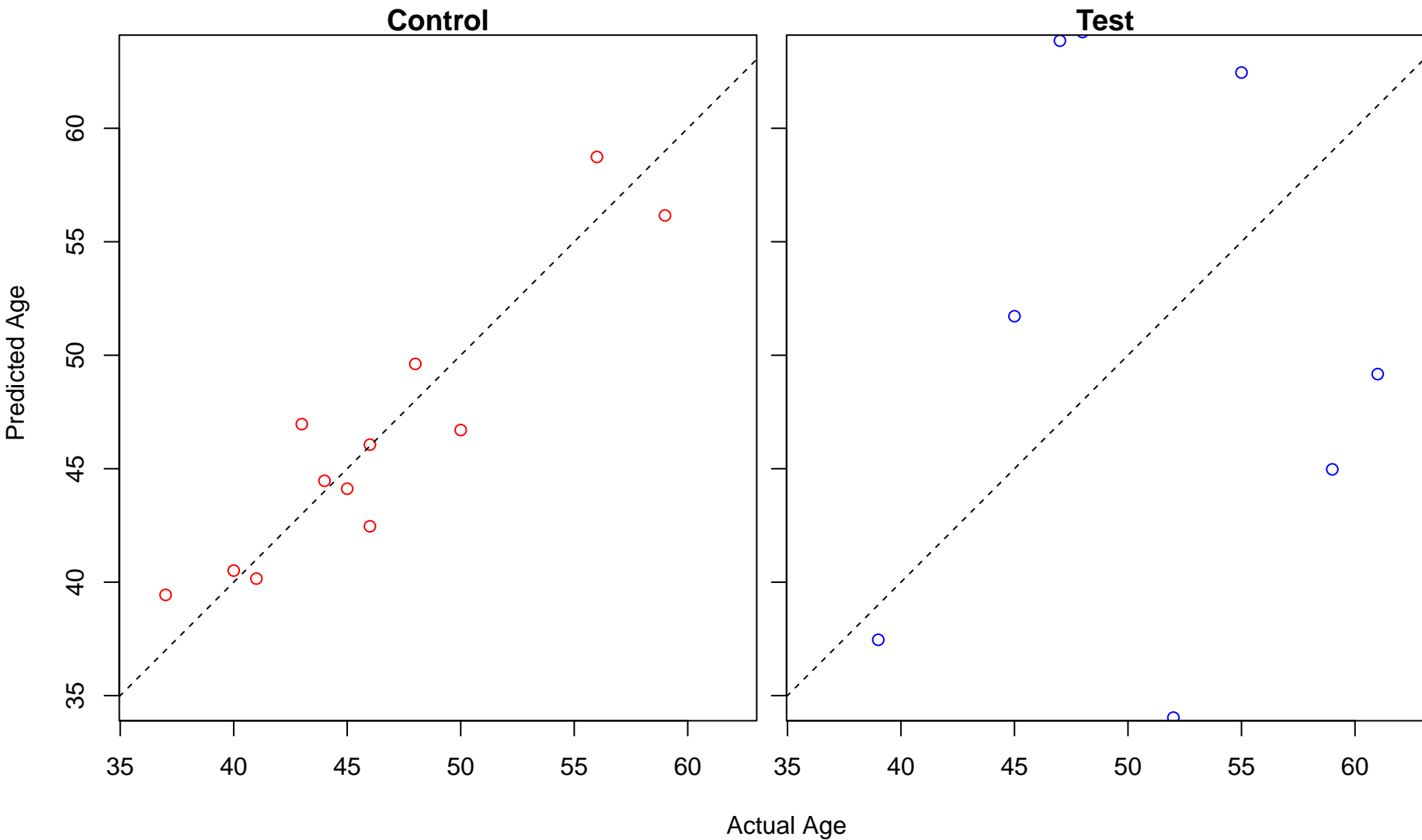


Test

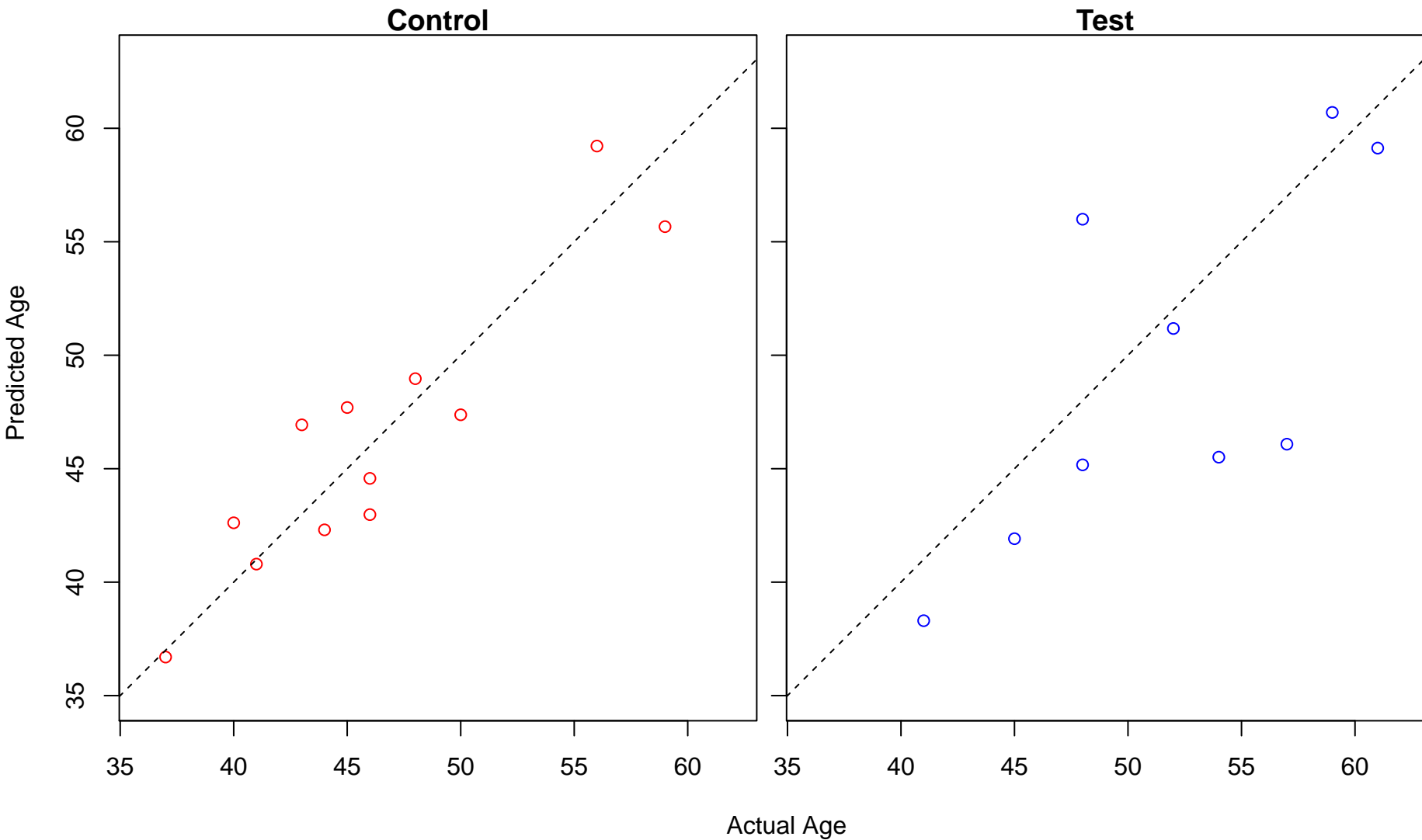


Actual Age

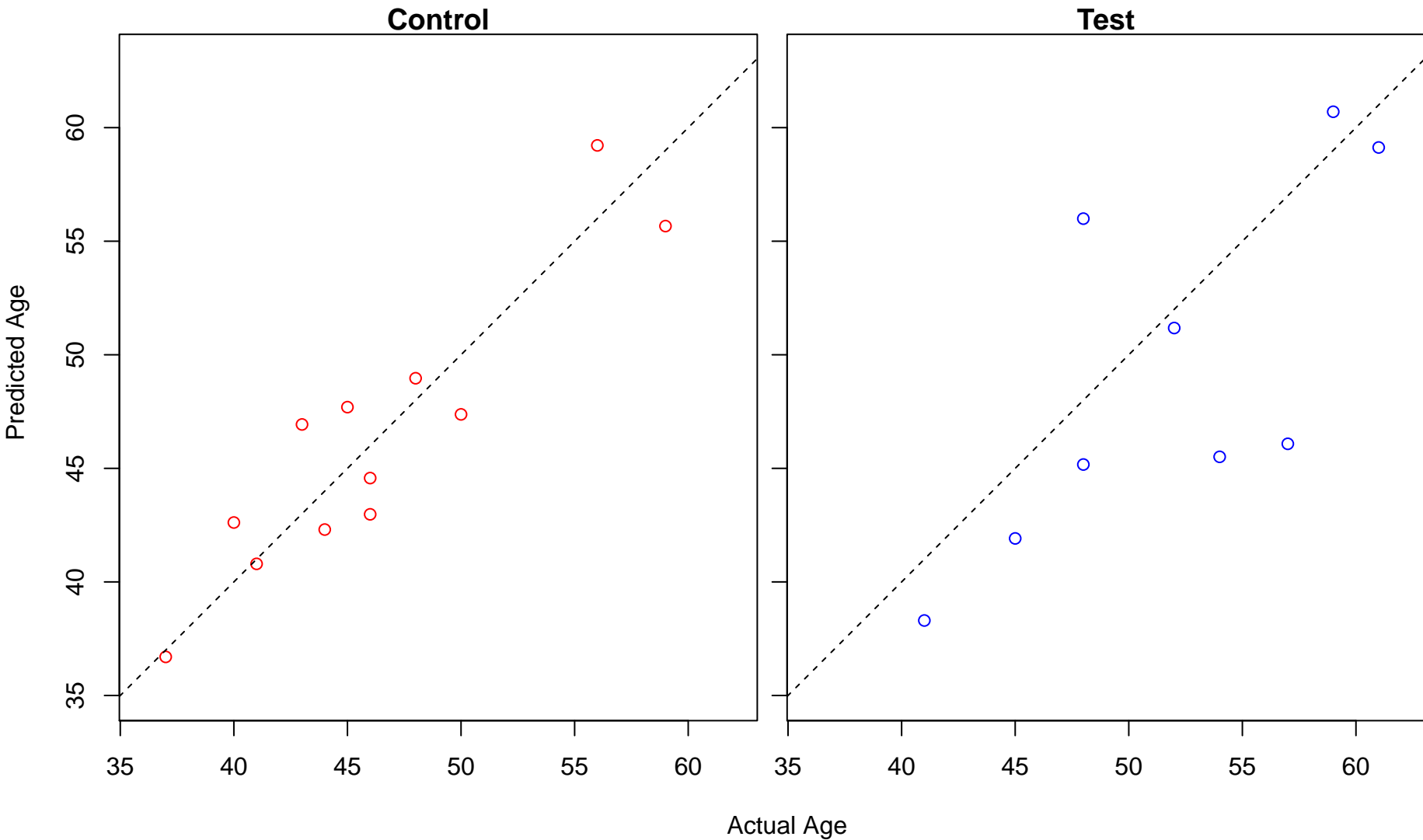
negative regulation of mRNA processing (Score: 34.057196)



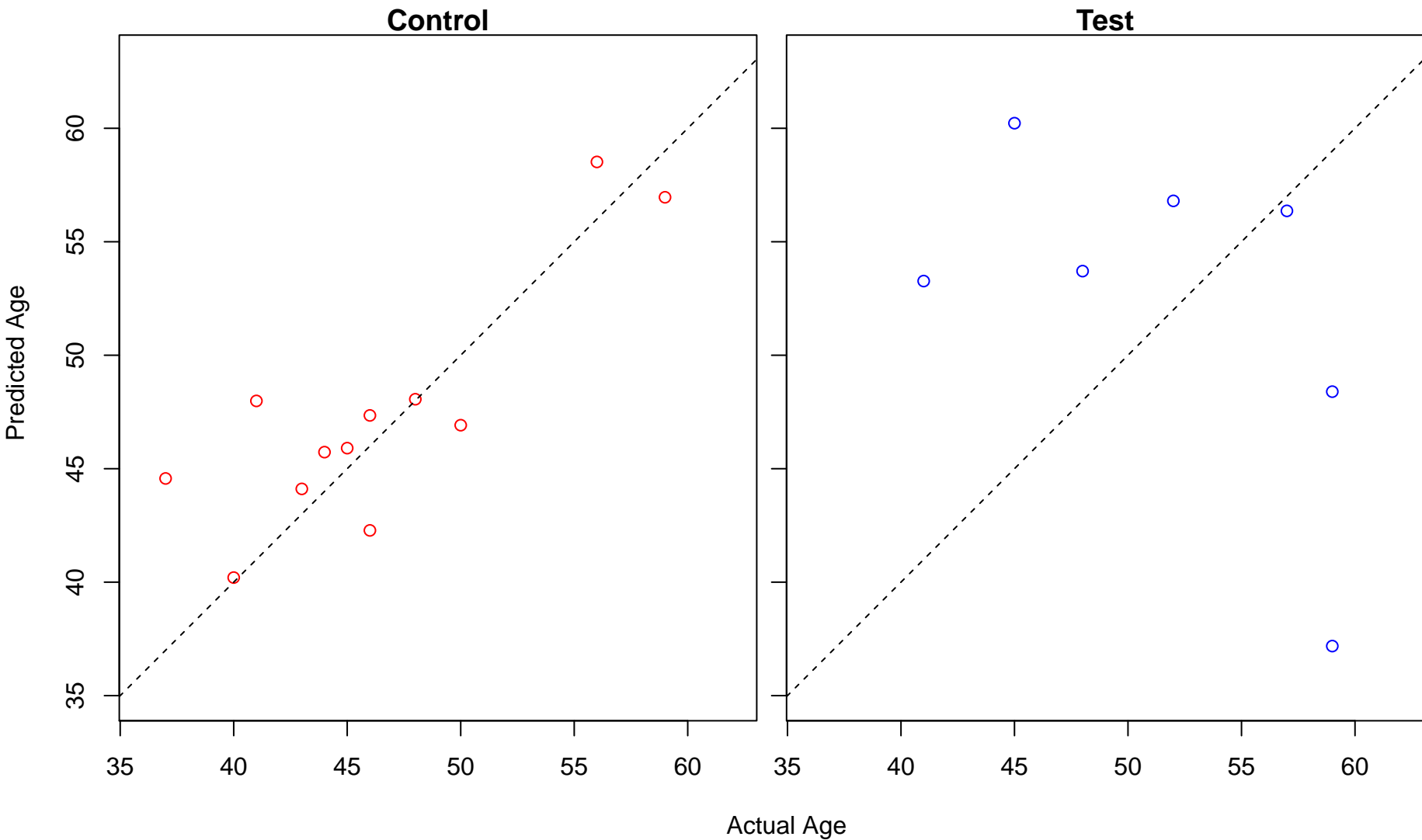
membrane repolarization during action potential (Score: 34.010565)



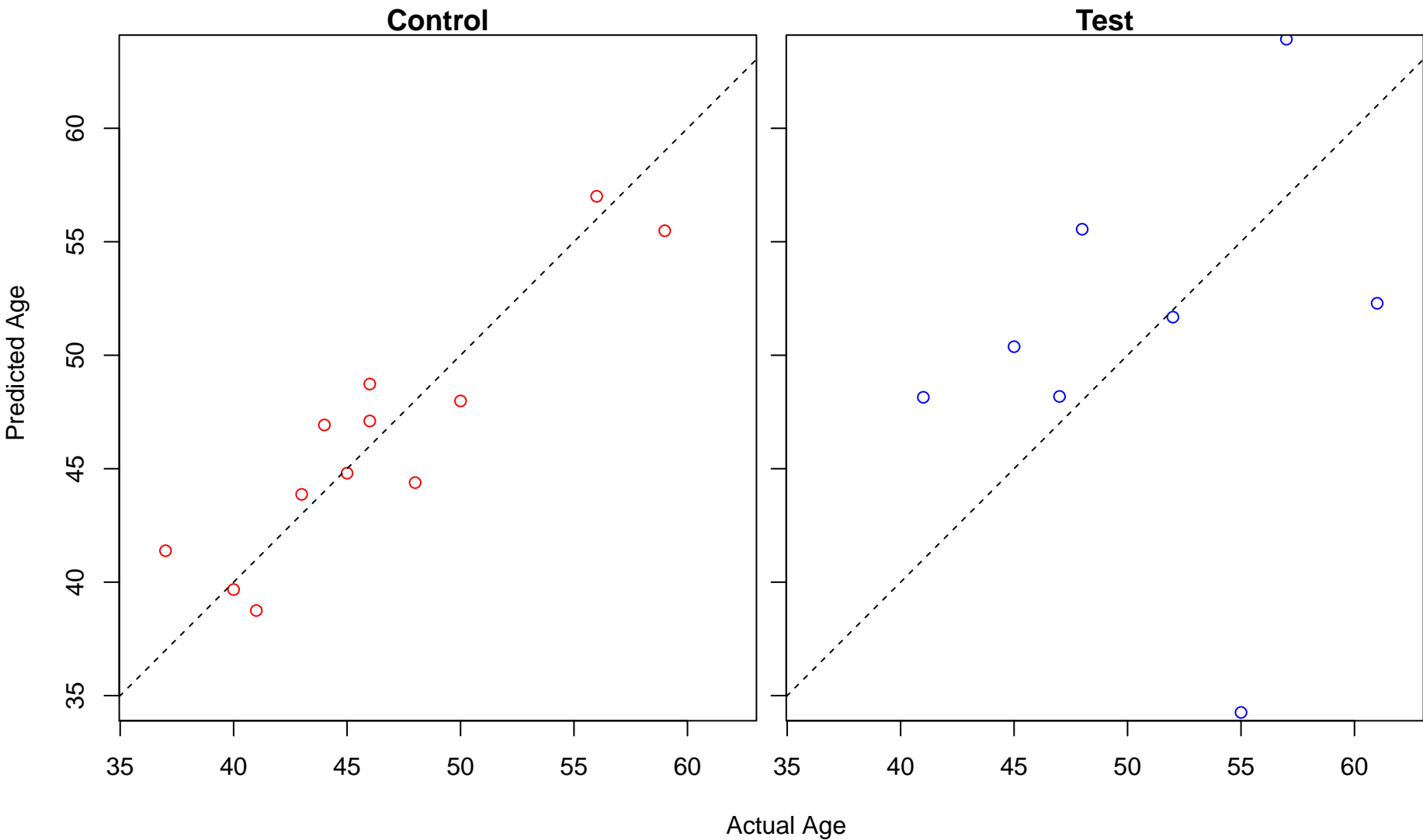
membrane repolarization during cardiac muscle cell action potential (Score: 34.010565)



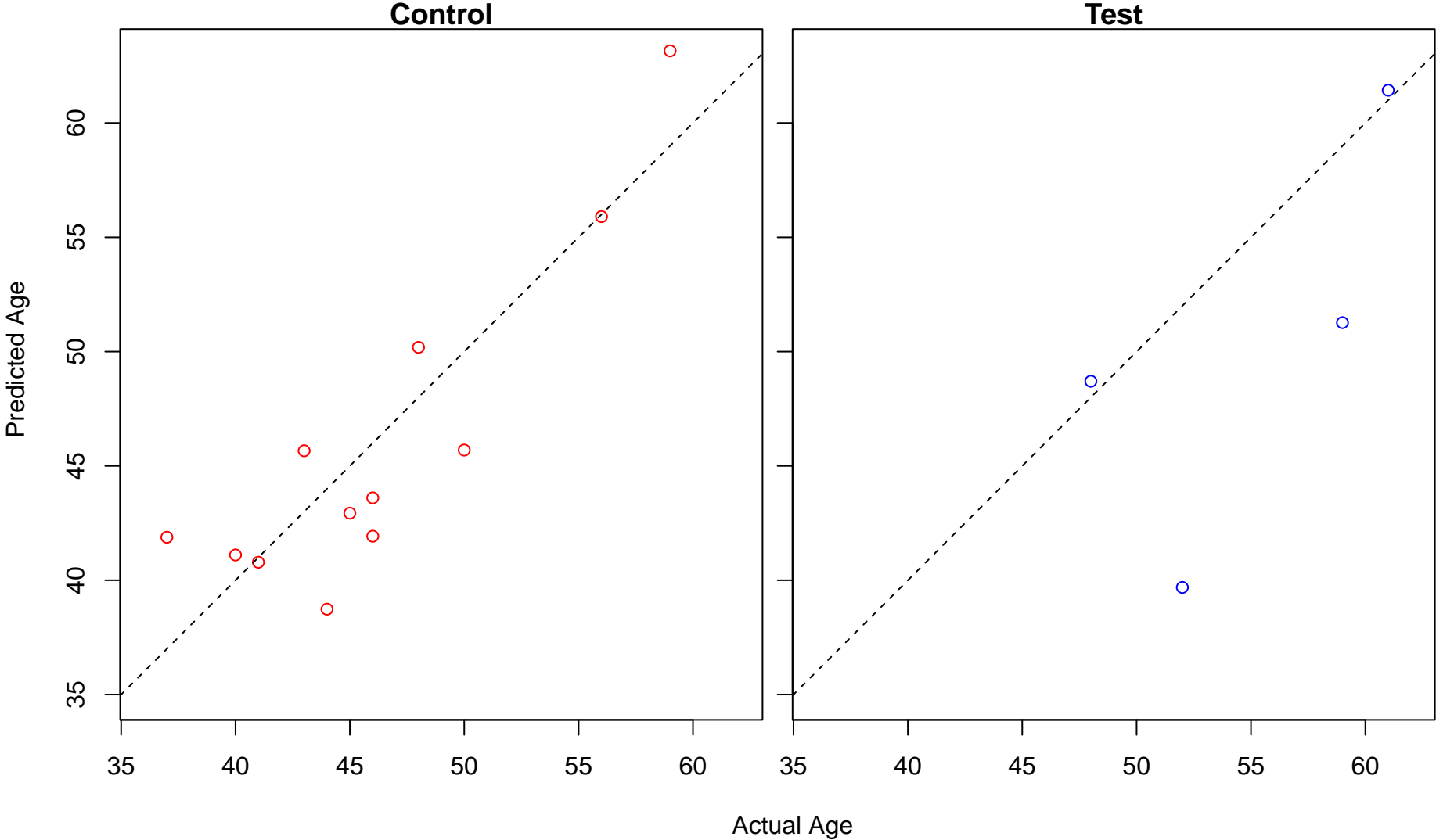
regulation of lymphocyte chemotaxis (Score: 33.672503)



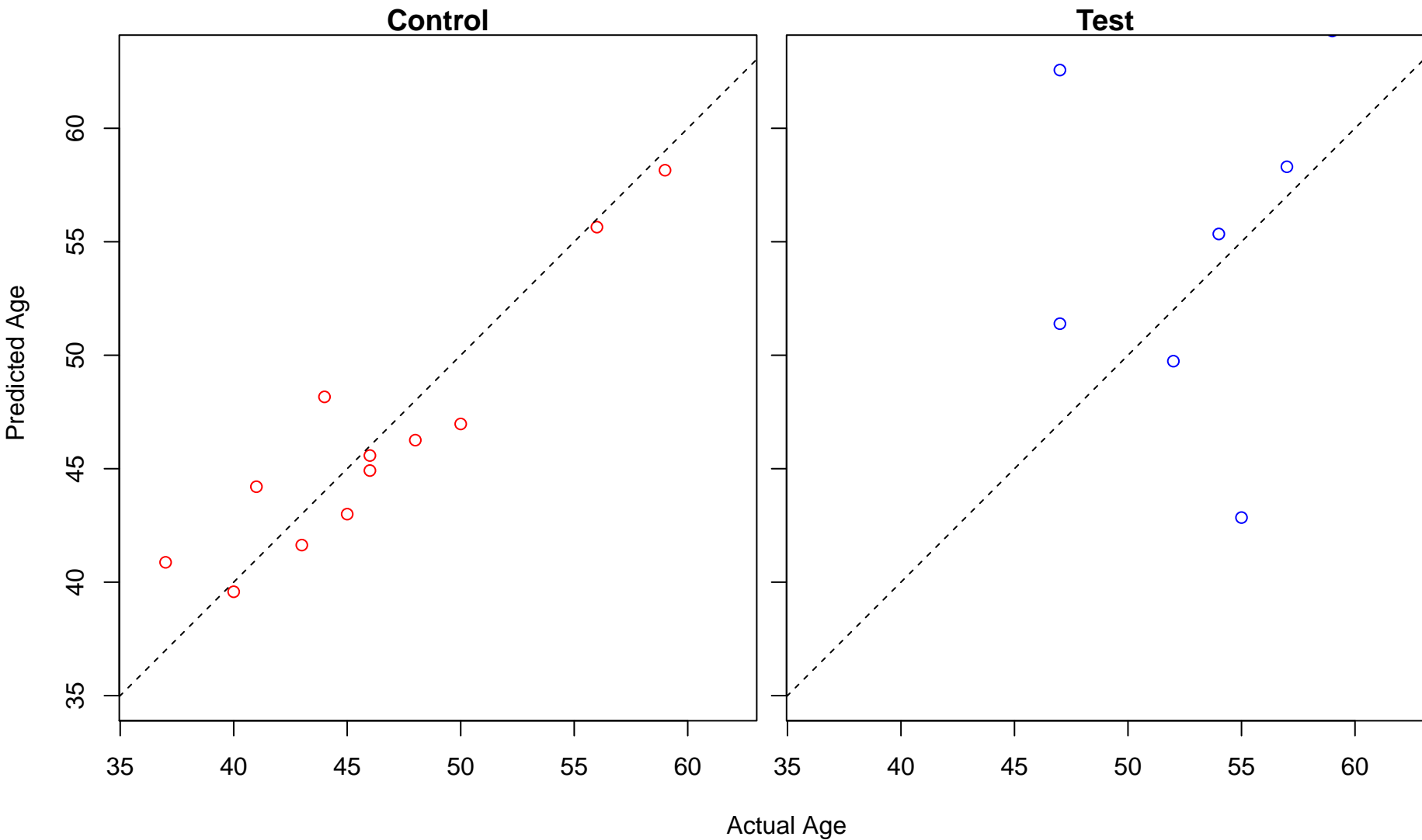
Positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 1)



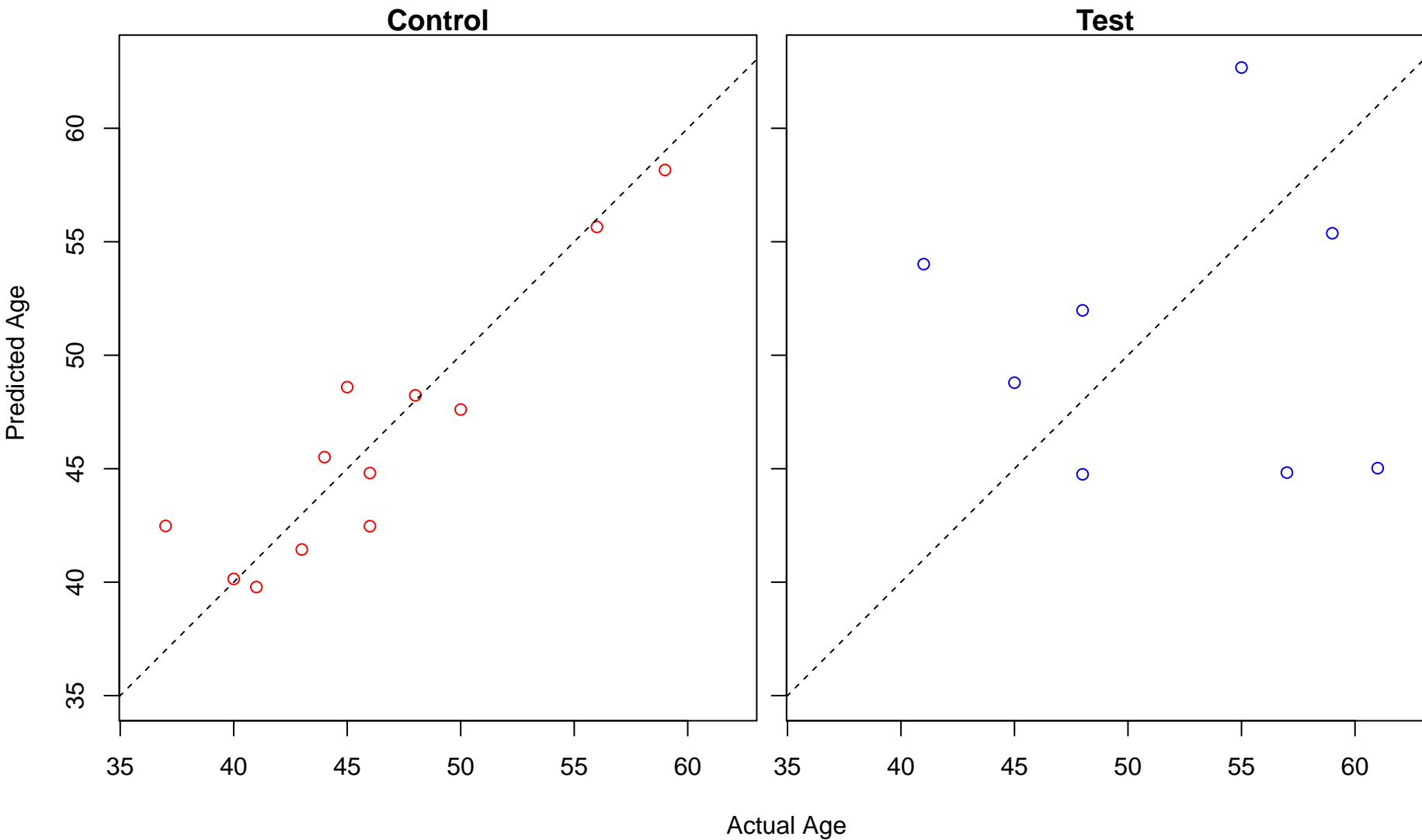
negative regulation of cellular carbohydrate metabolic process (Score: 33.607876)



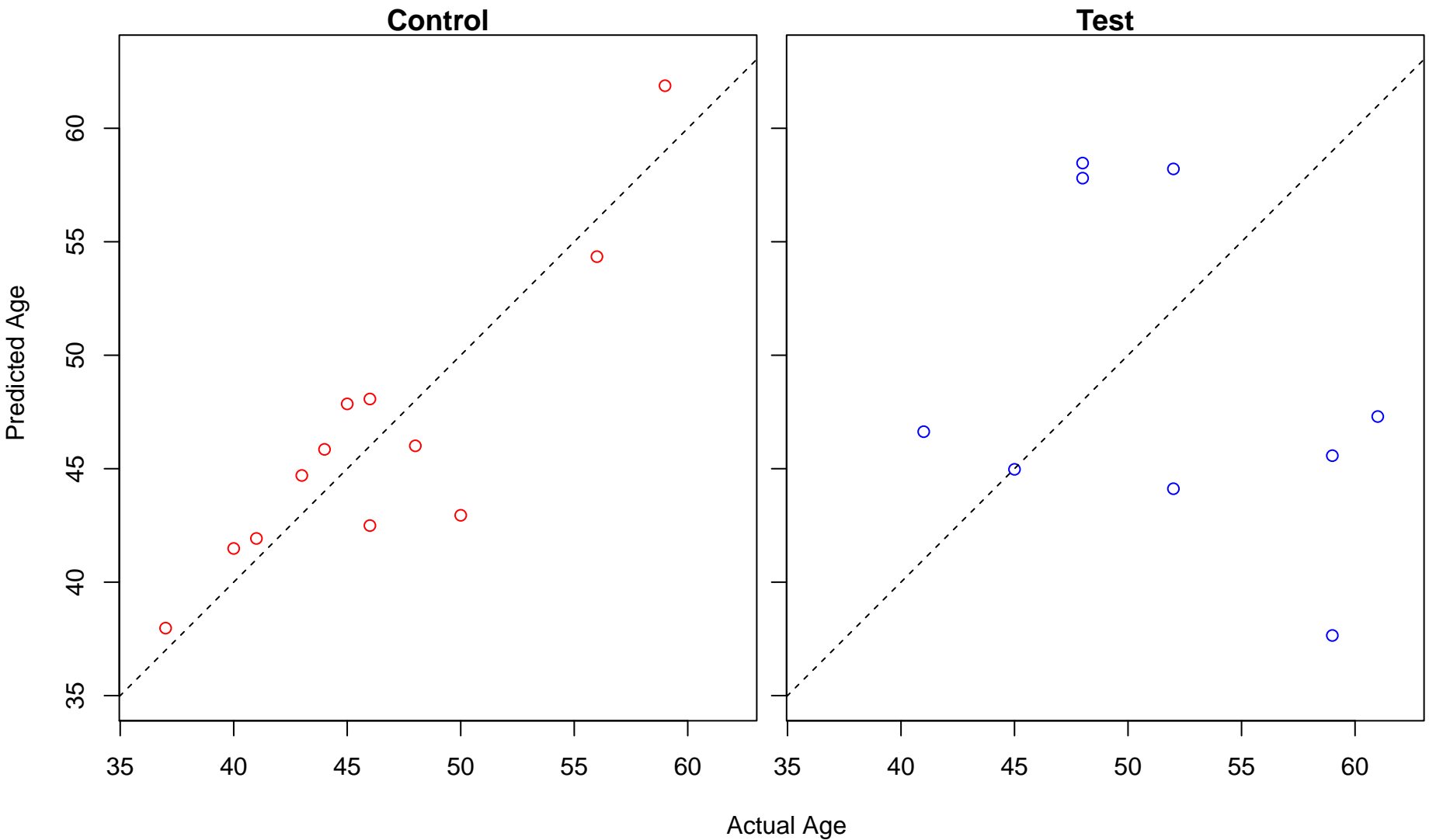
negative regulation of lymphocyte migration (Score: 33.559053)



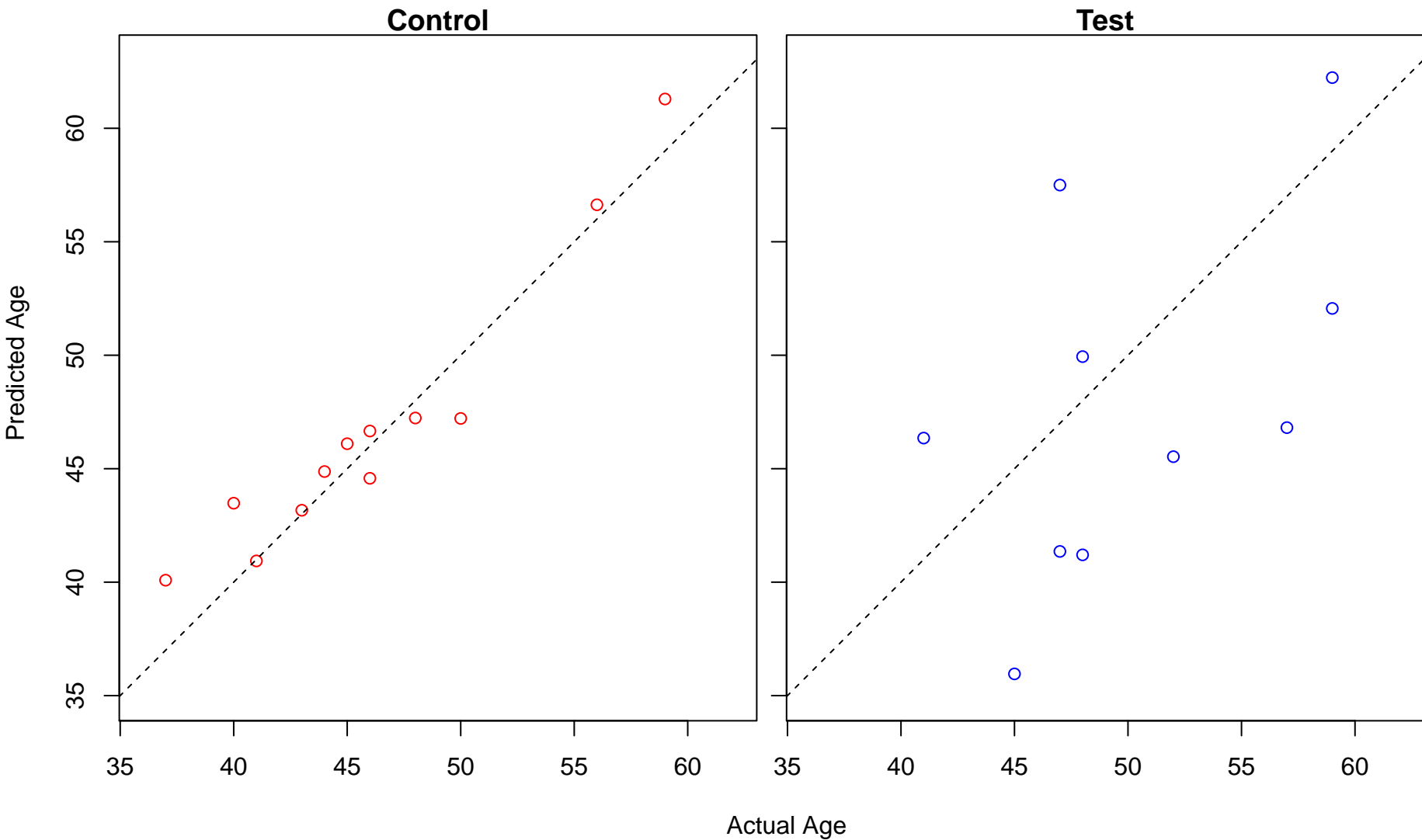
B cell activation involved in immune response (Score: 33.506820)



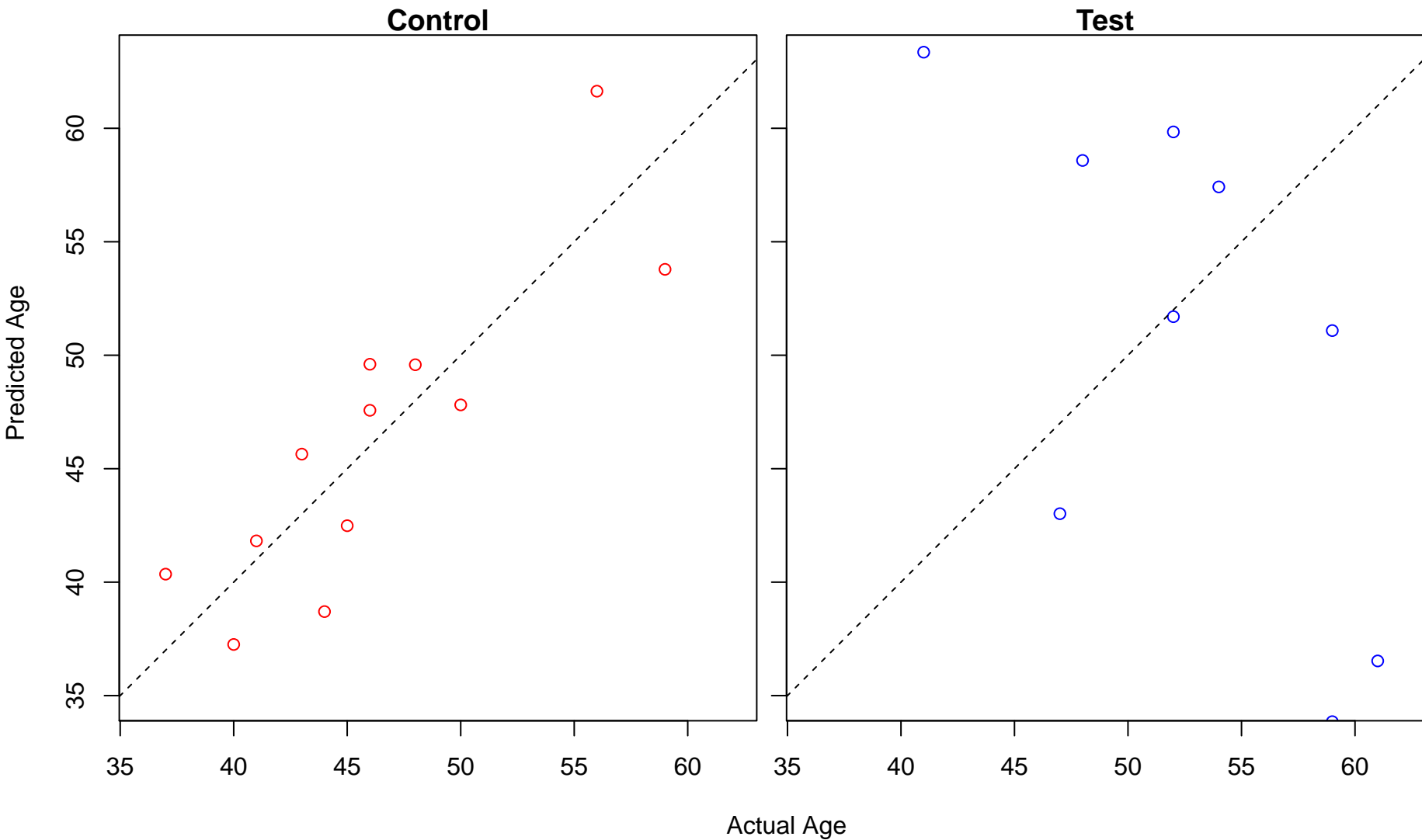
ve immune response based on somatic recombination of immune receptors built from immunoglobulin sup



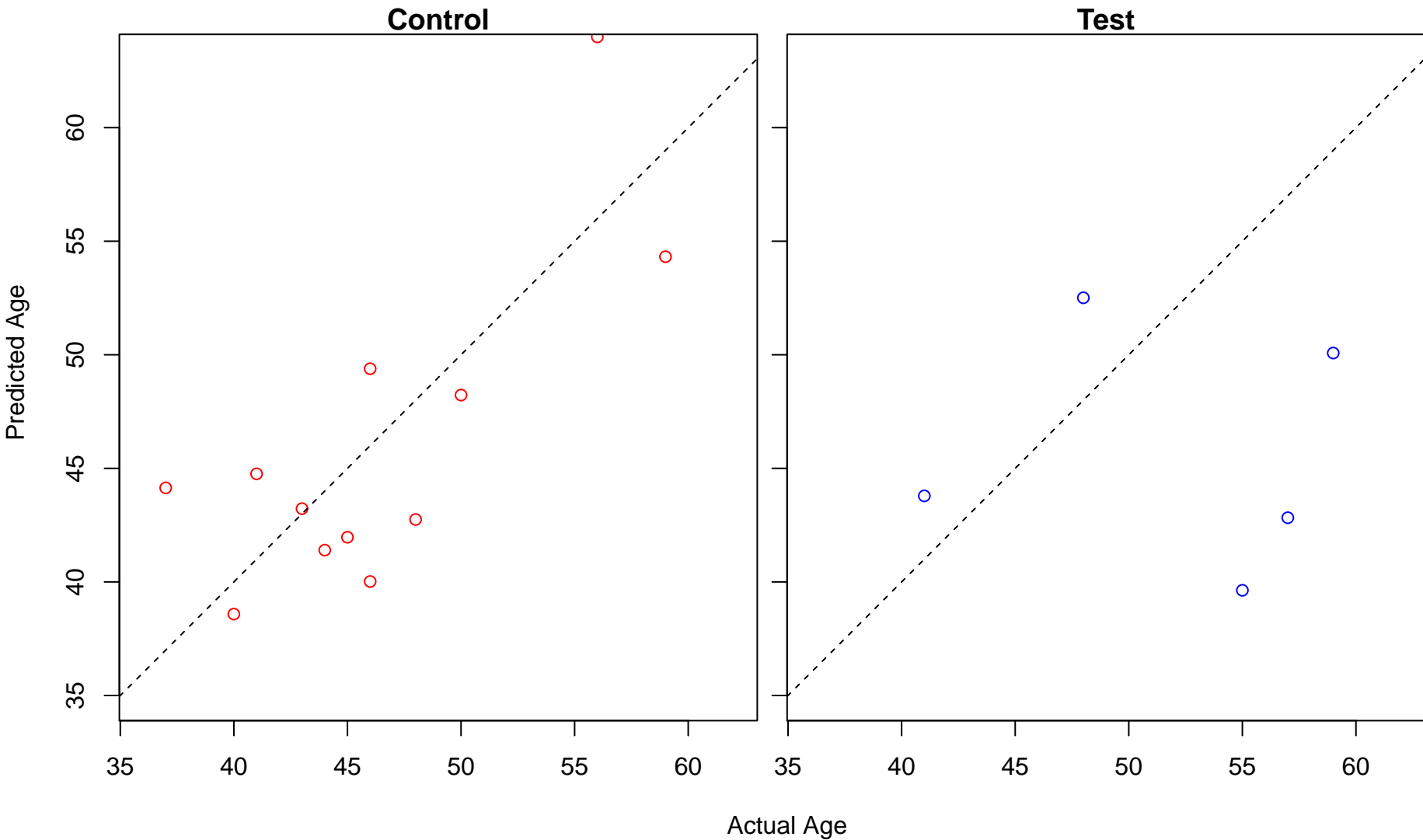
protein kinase B signaling (Score: 33.317064)



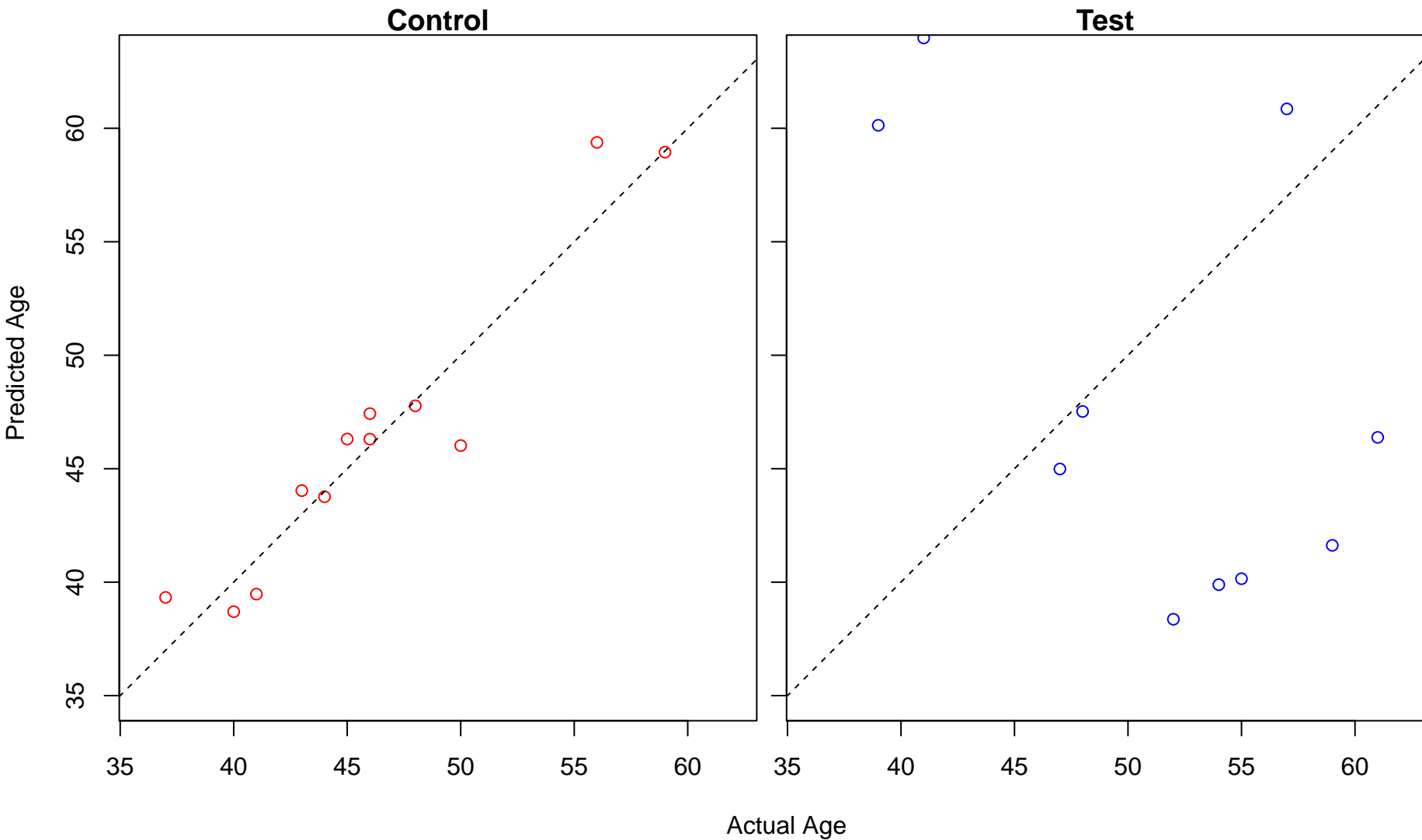
regulation of endosome size (Score: 32.965637)



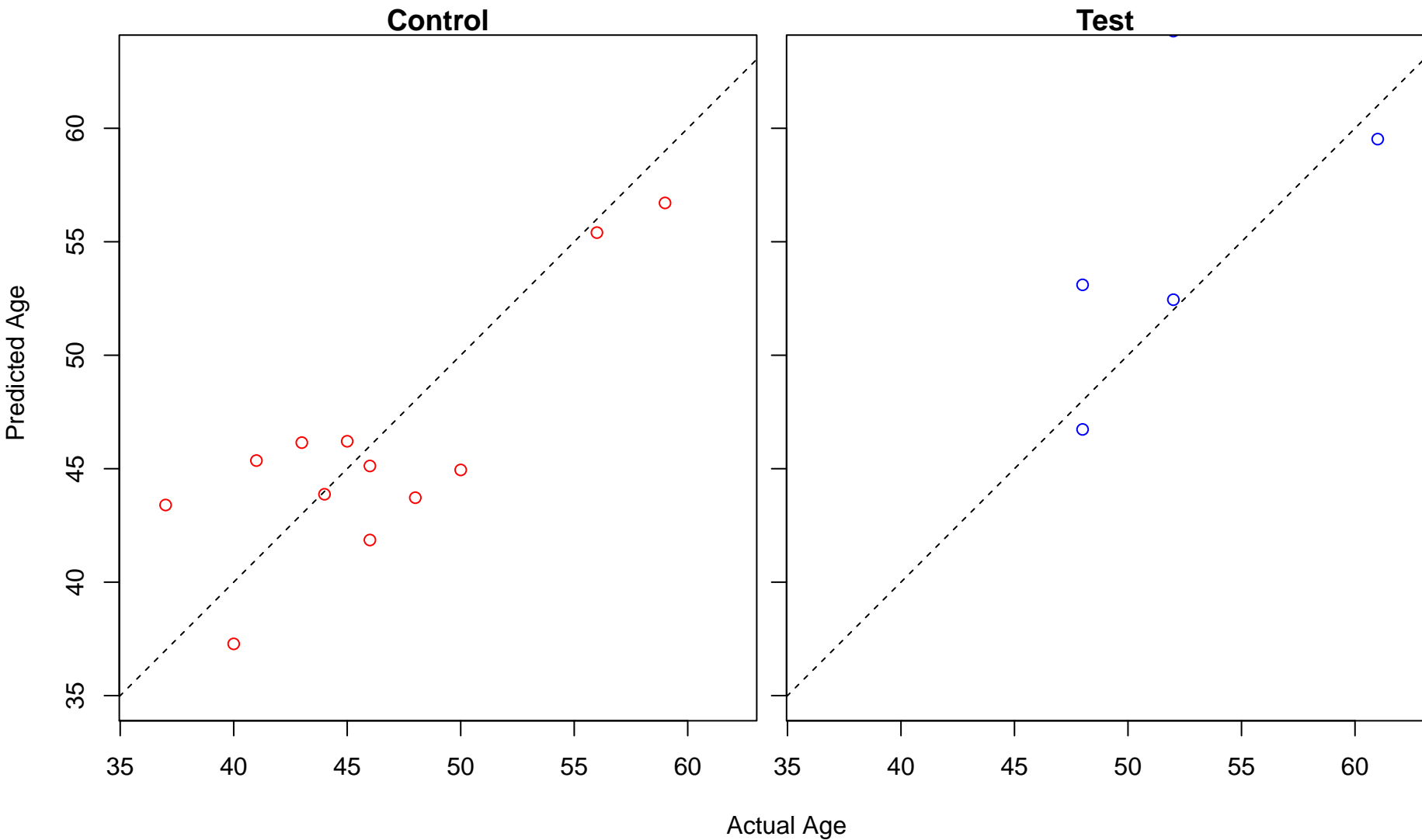
negative regulation of glial cell differentiation (Score: 32.607991)



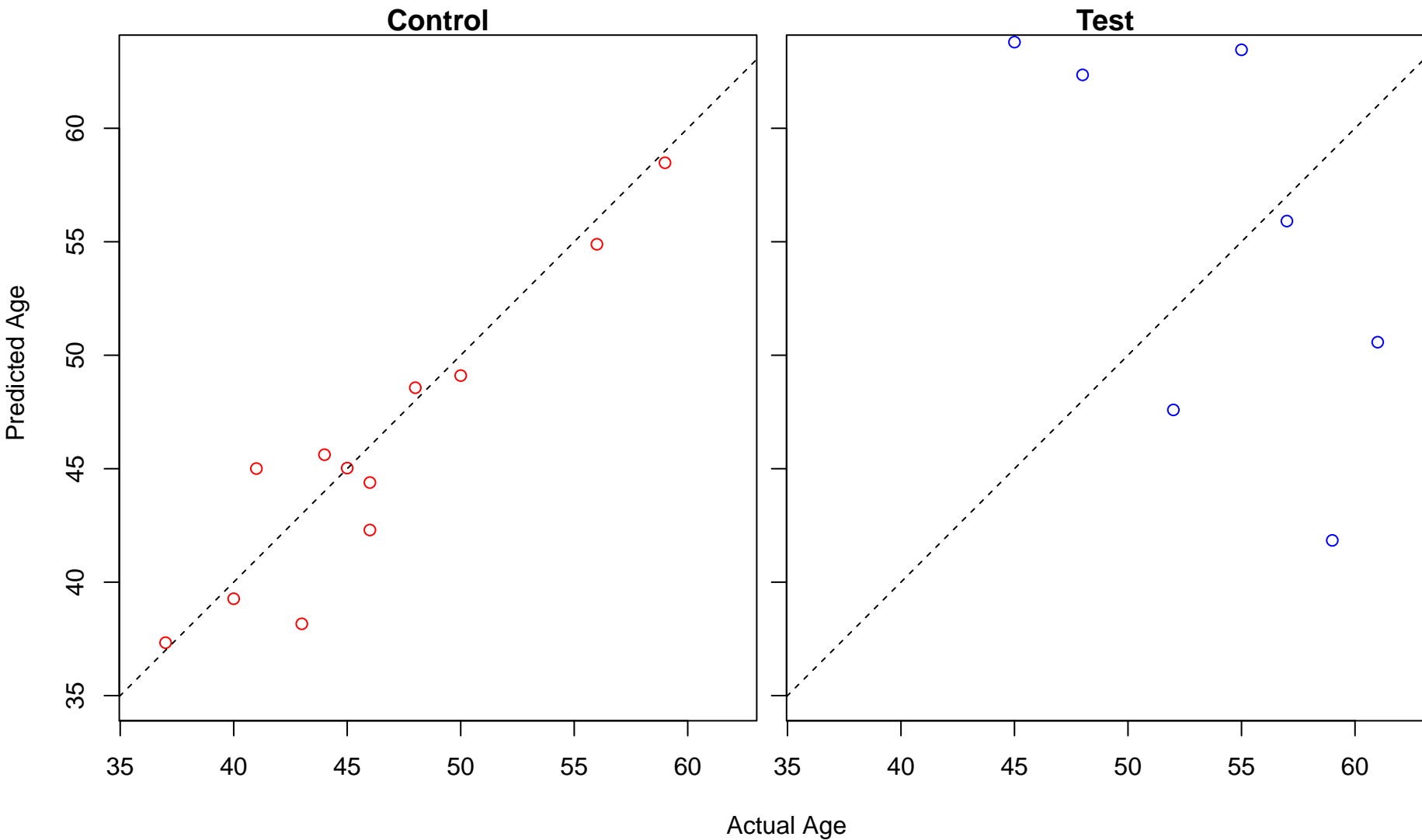
positive regulation of kidney development (Score: 32.190927)



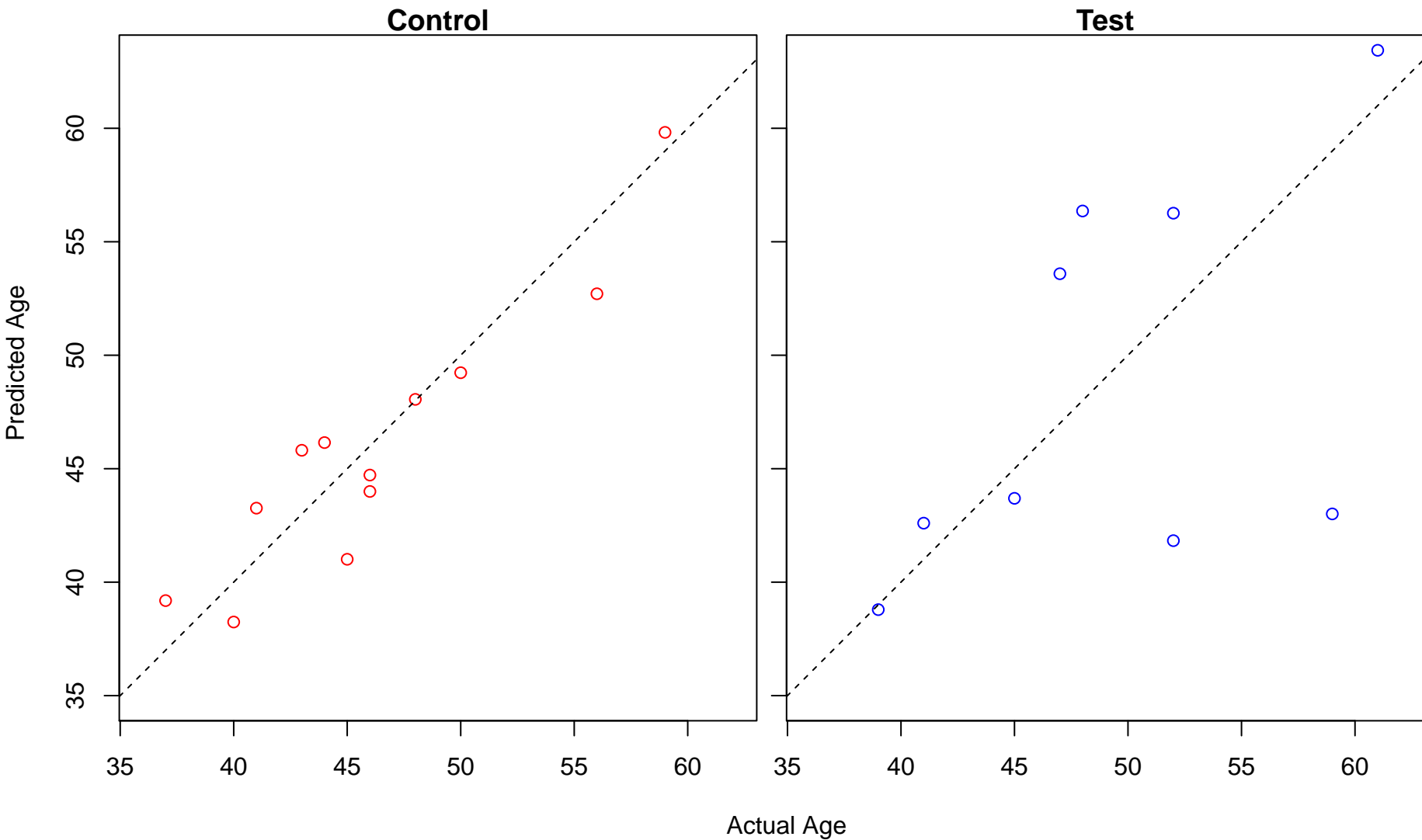
protein kinase C signaling (Score: 31.887639)



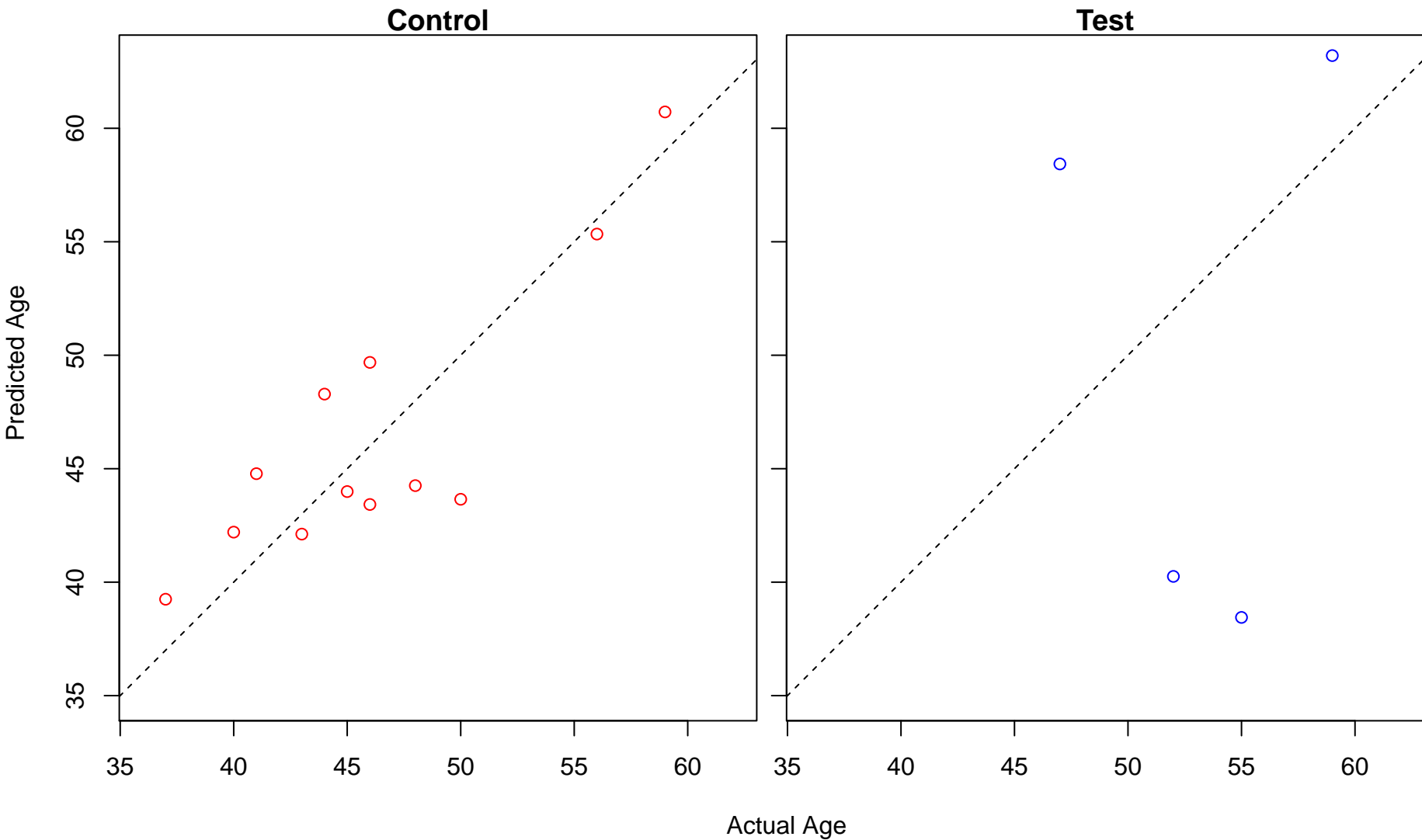
positive regulation of endothelial cell apoptotic process (Score: 31.864396)



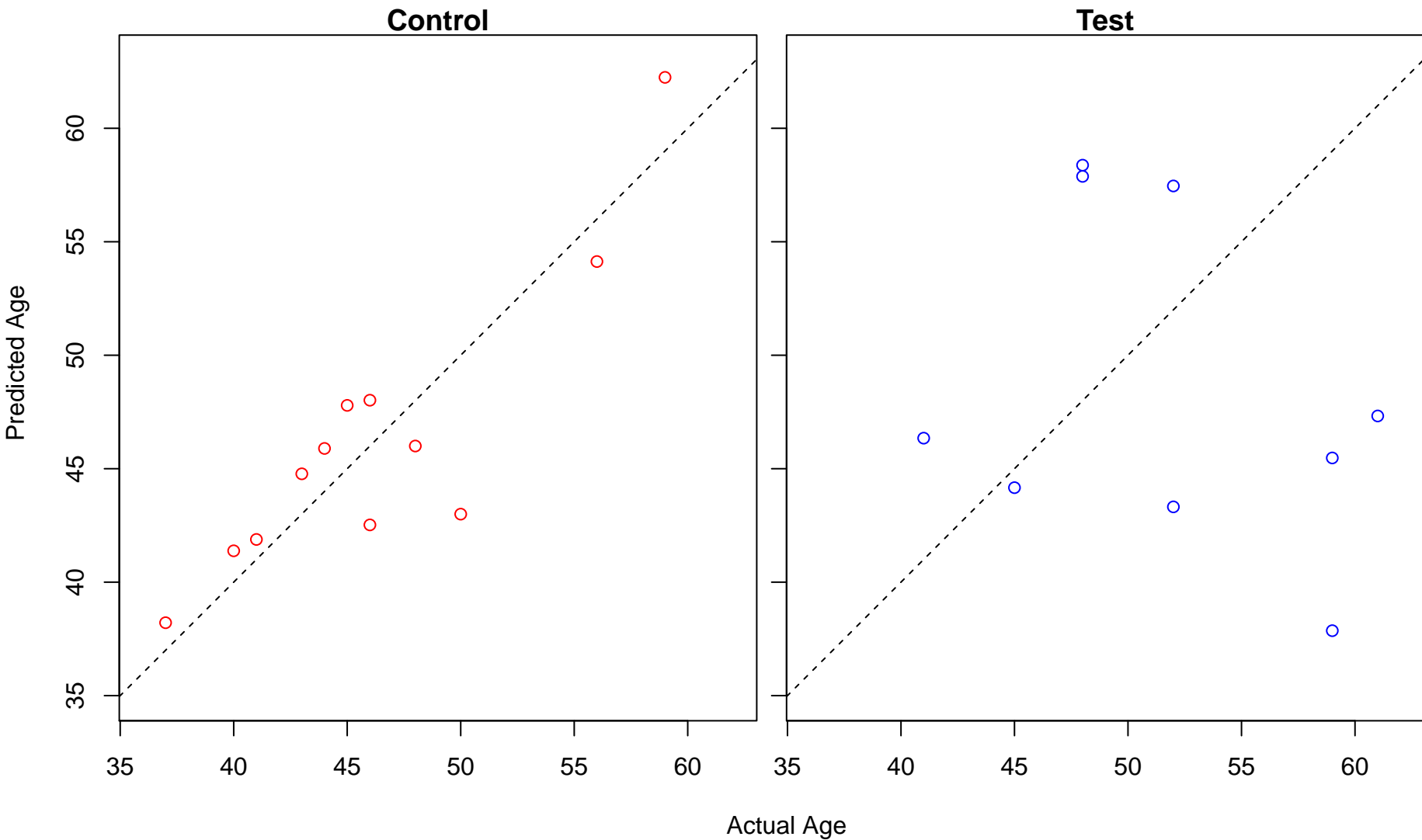
epithelial structure maintenance (Score: 31.817157)



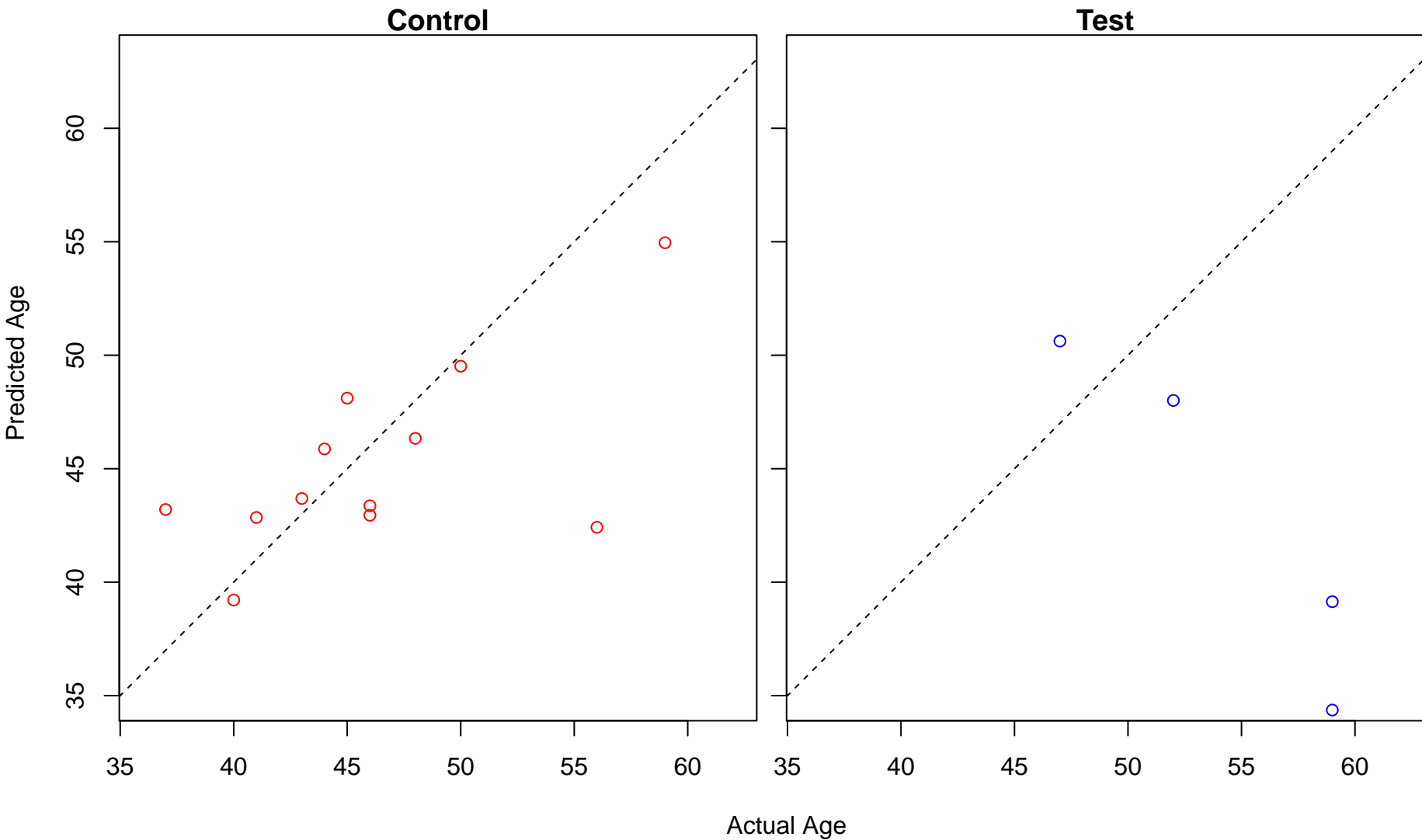
alpha-beta T cell differentiation (Score: 31.083841)



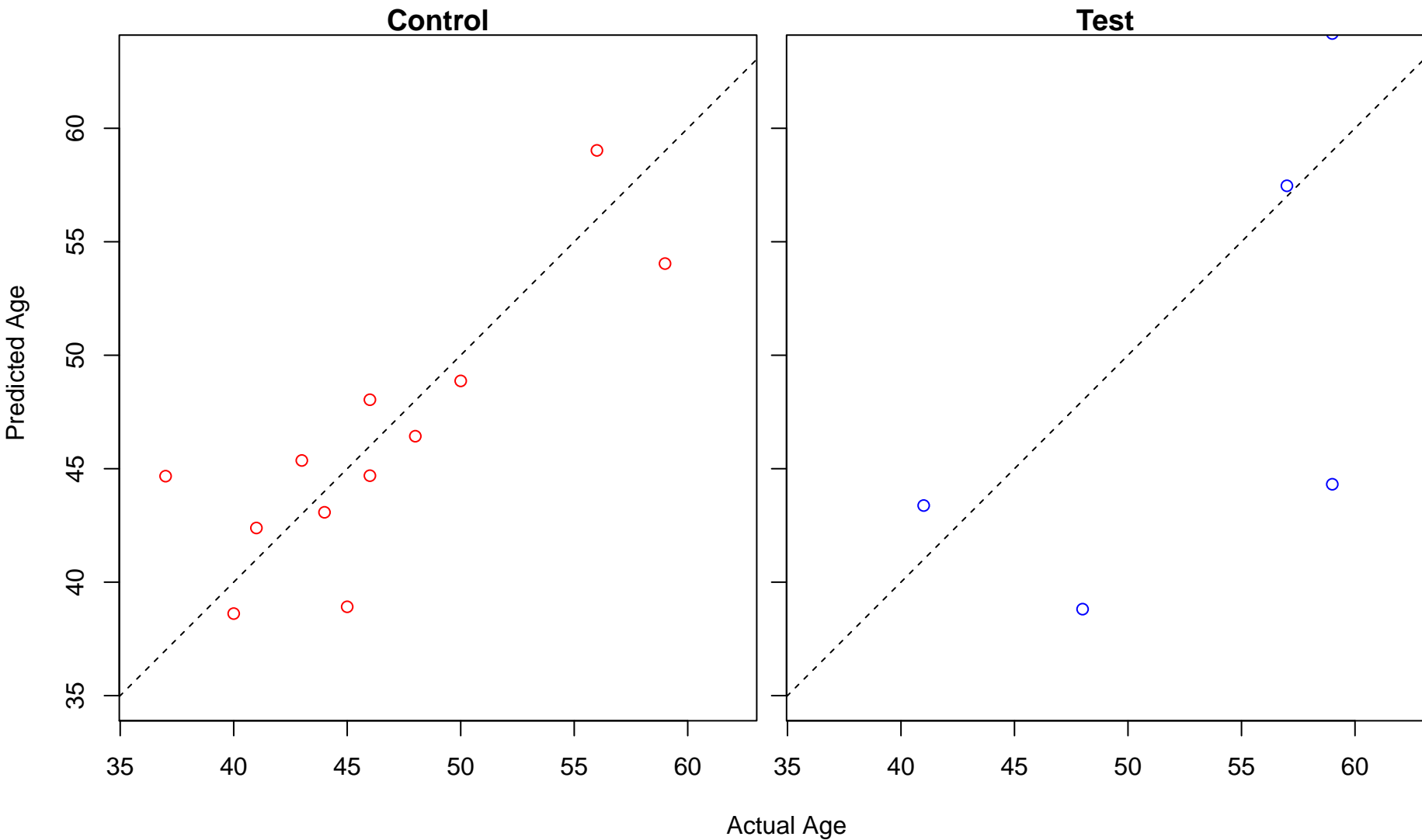
positive regulation of adaptive immune response (Score: 31.019663)



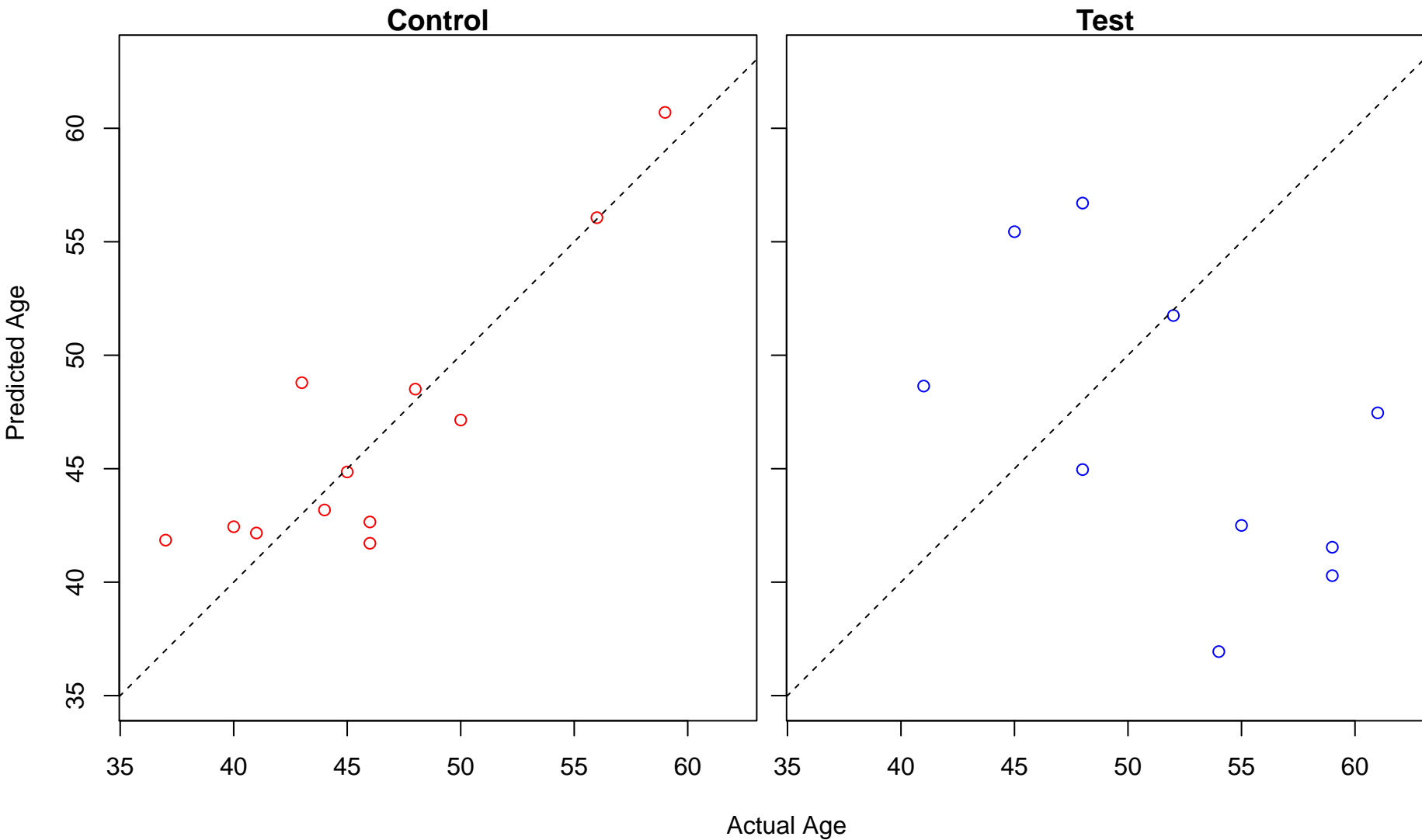
leukotriene biosynthetic process (Score: 30.852226)



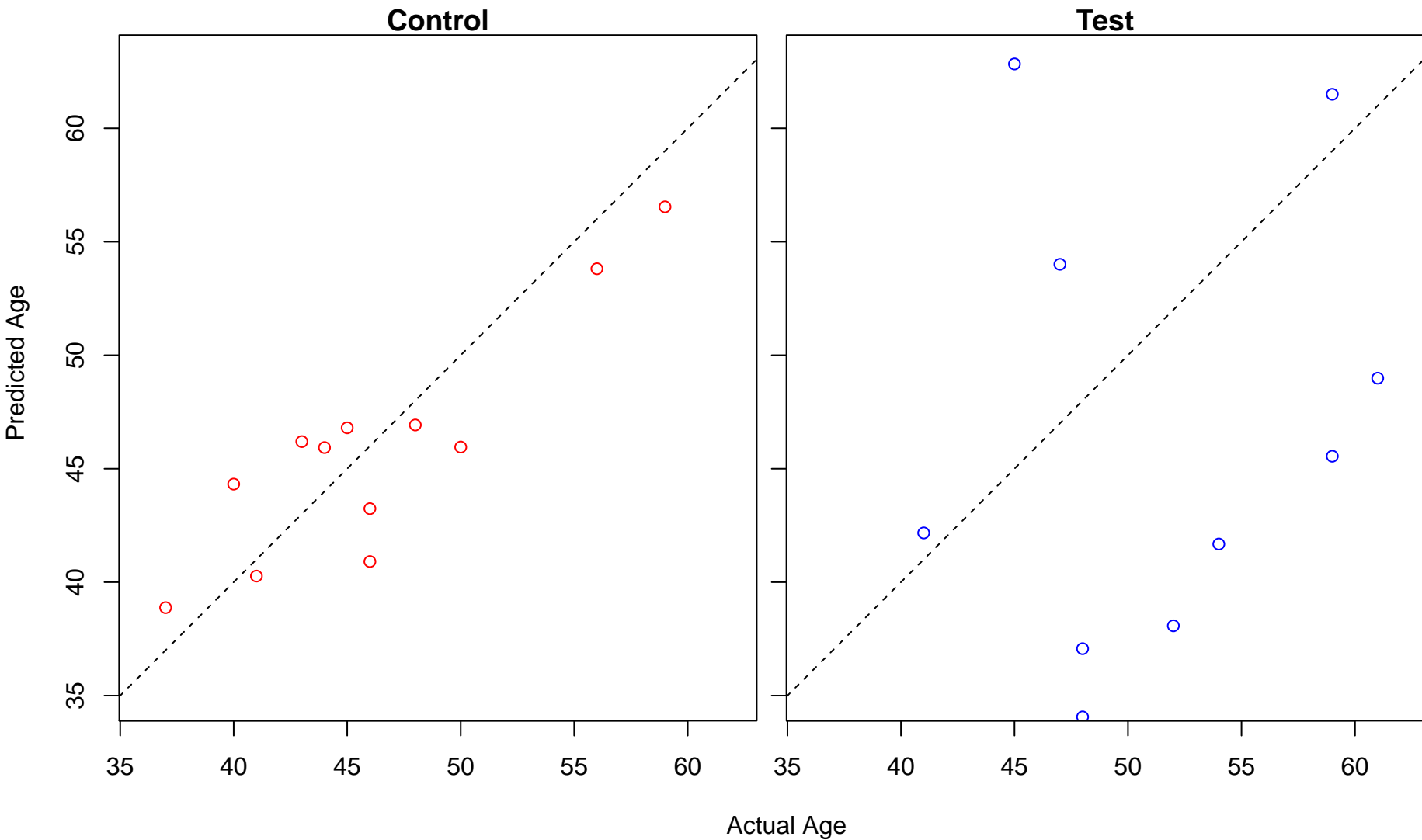
primary miRNA processing (Score: 30.836226)



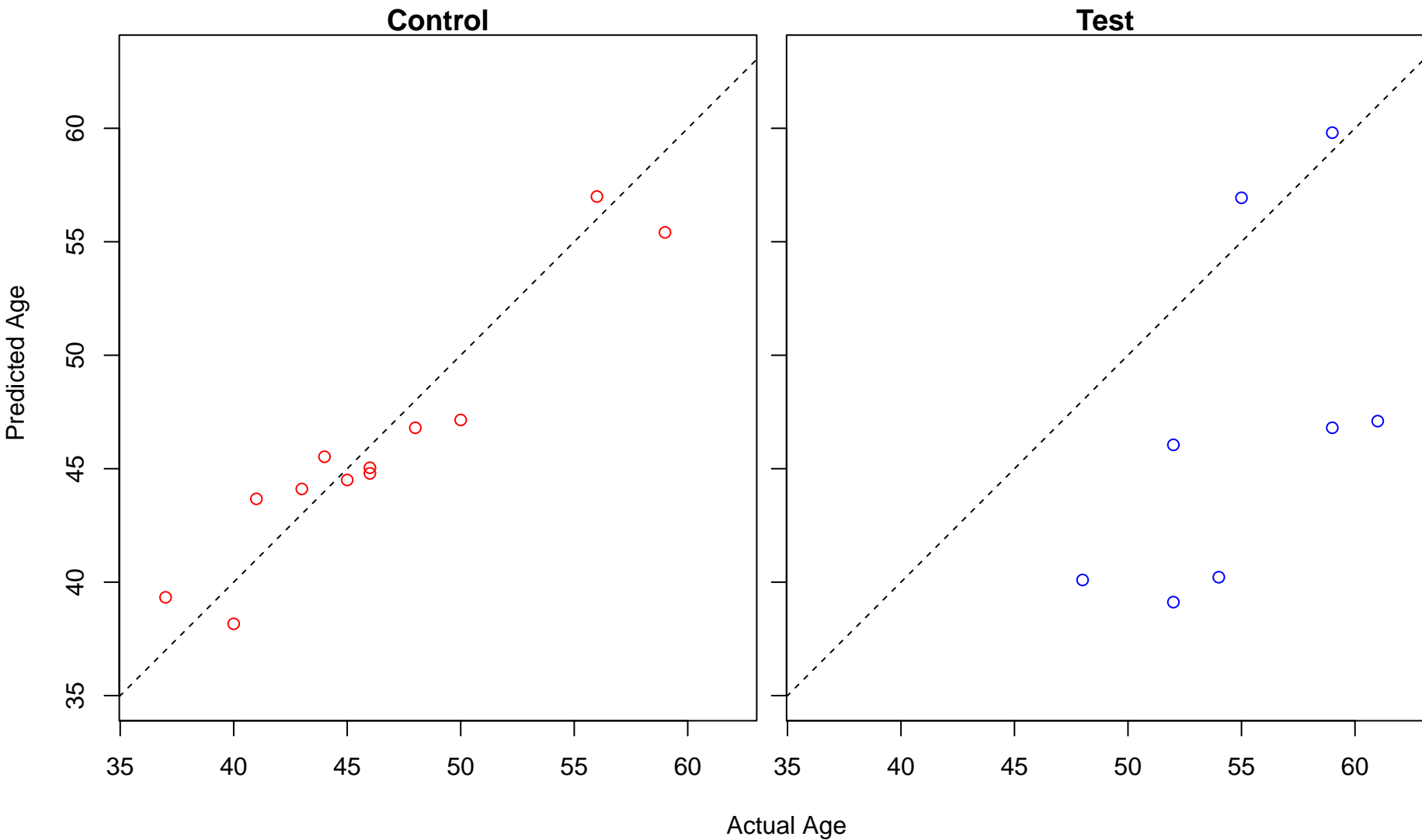
negative regulation of osteoblast differentiation (Score: 30.796925)



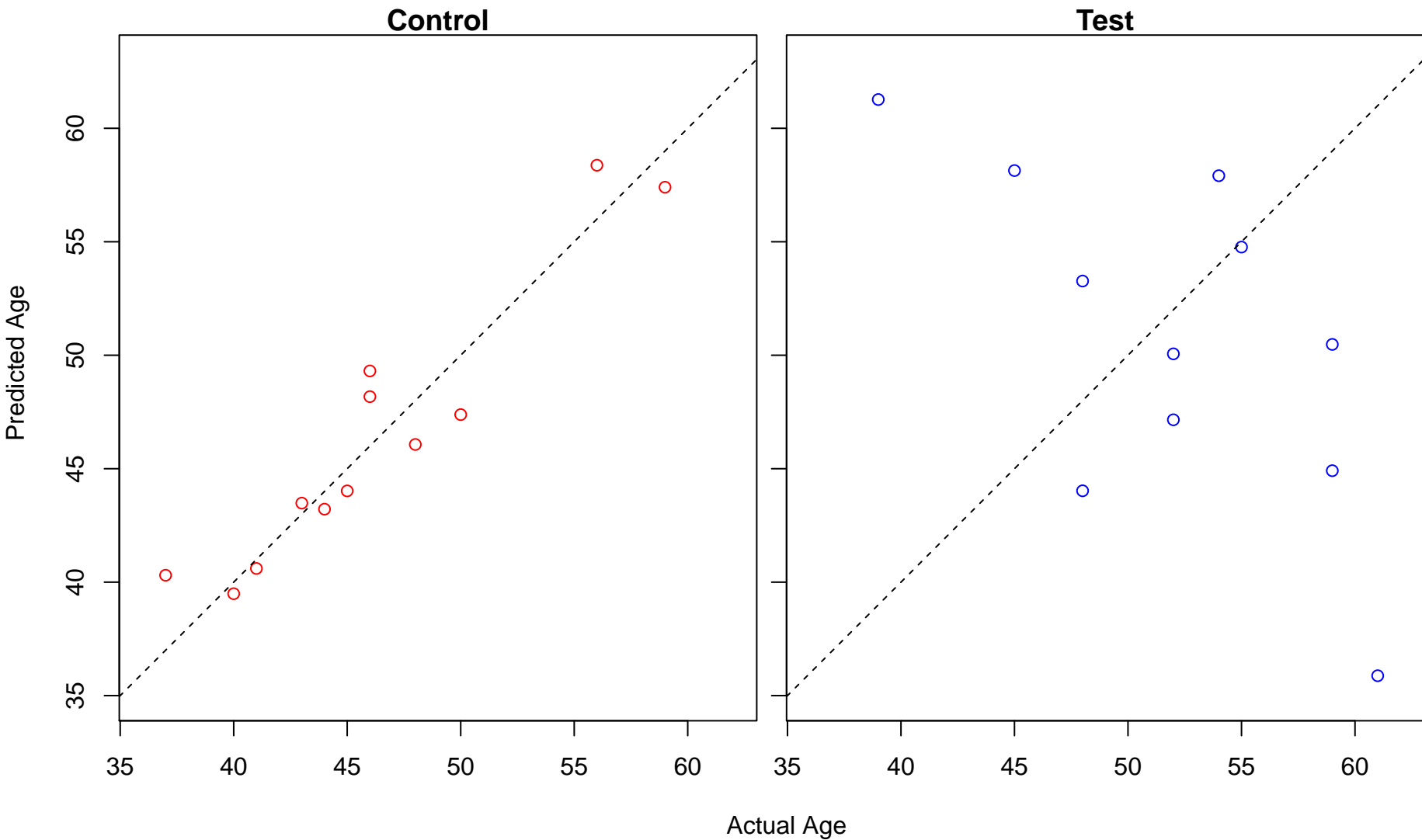
peptidyl-proline modification (Score: 30.672499)



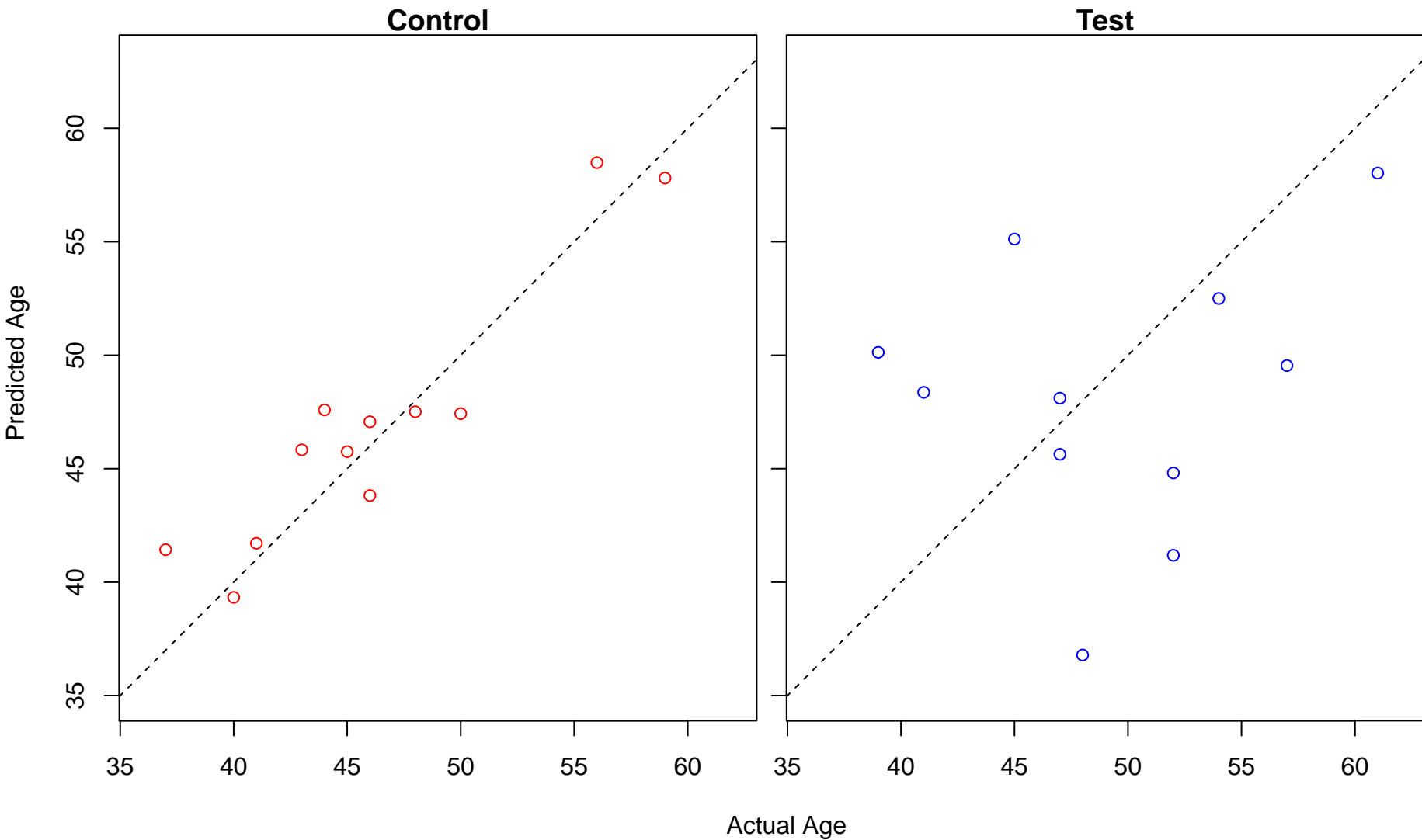
dicarboxylic acid metabolic process (Score: 30.557051)



regulation of lymphocyte apoptotic process (Score: 30.208879)

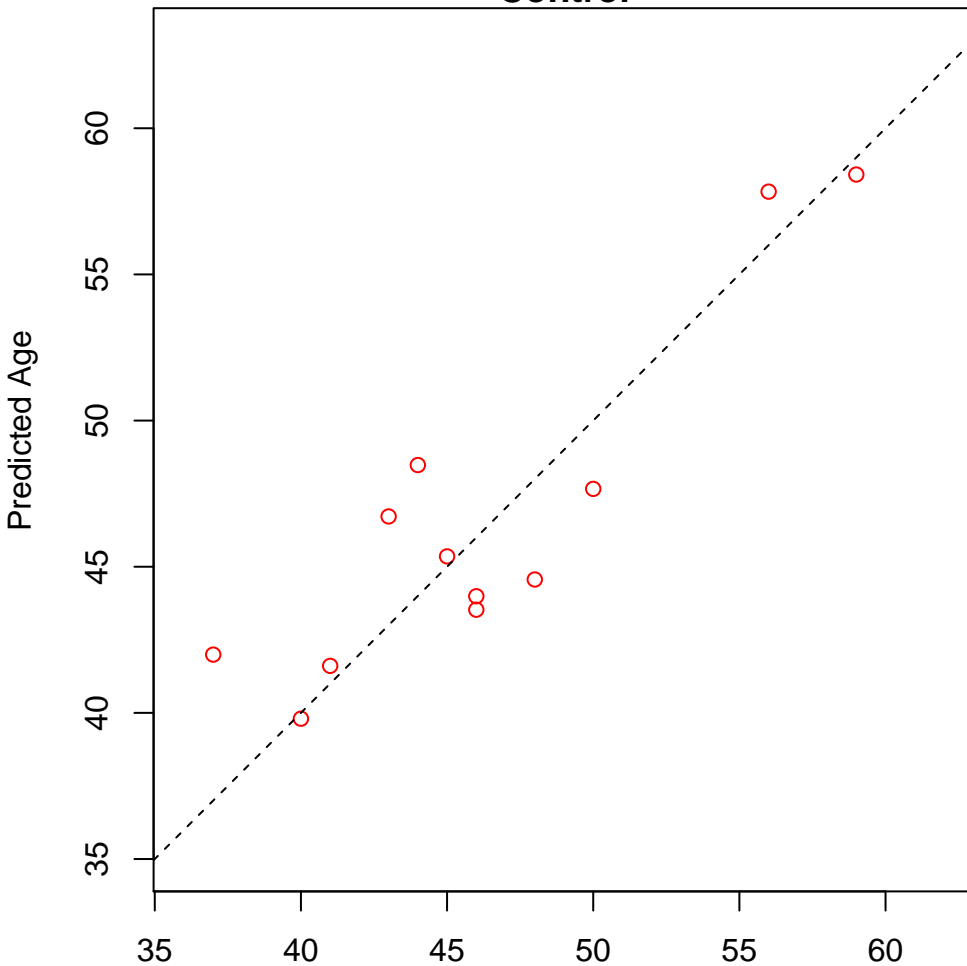


positive regulation of NF-kappaB import into nucleus (Score: 29.956649)

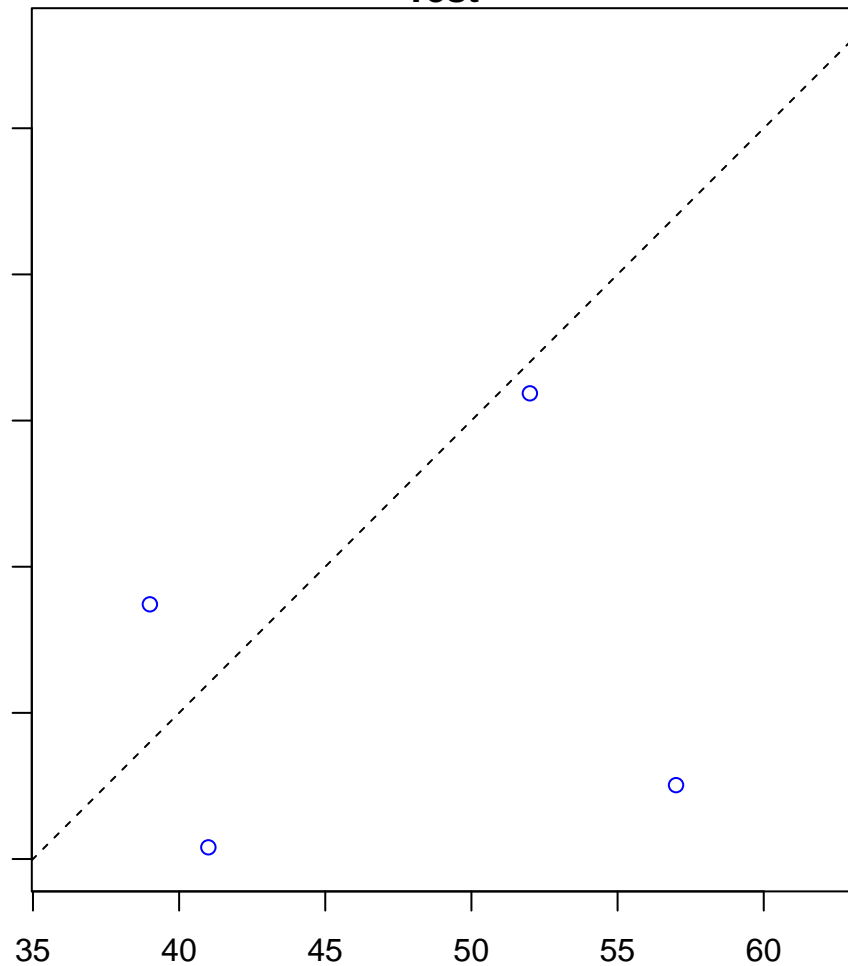


multivesicular body sorting pathway (Score: 29.733175)

Control

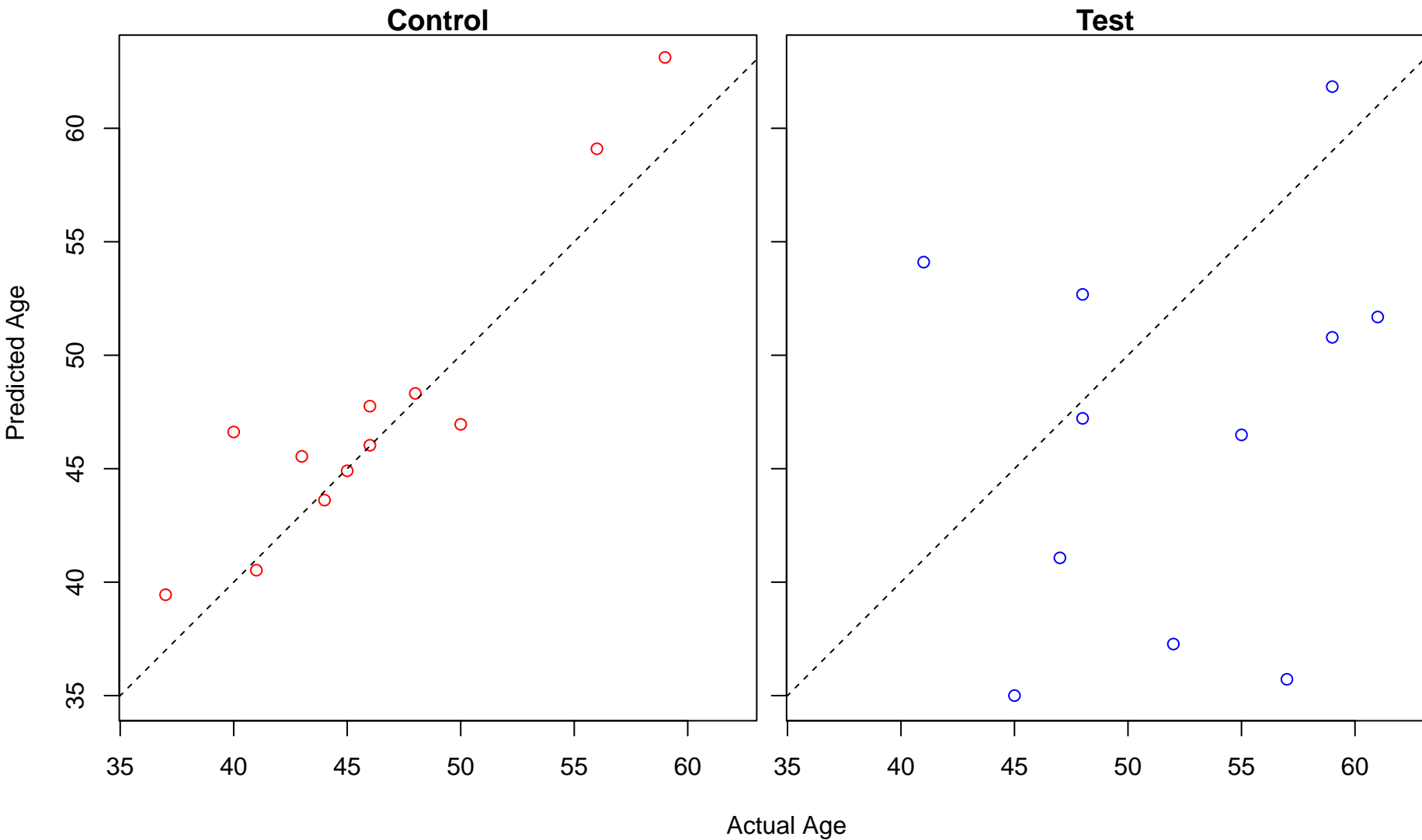


Test

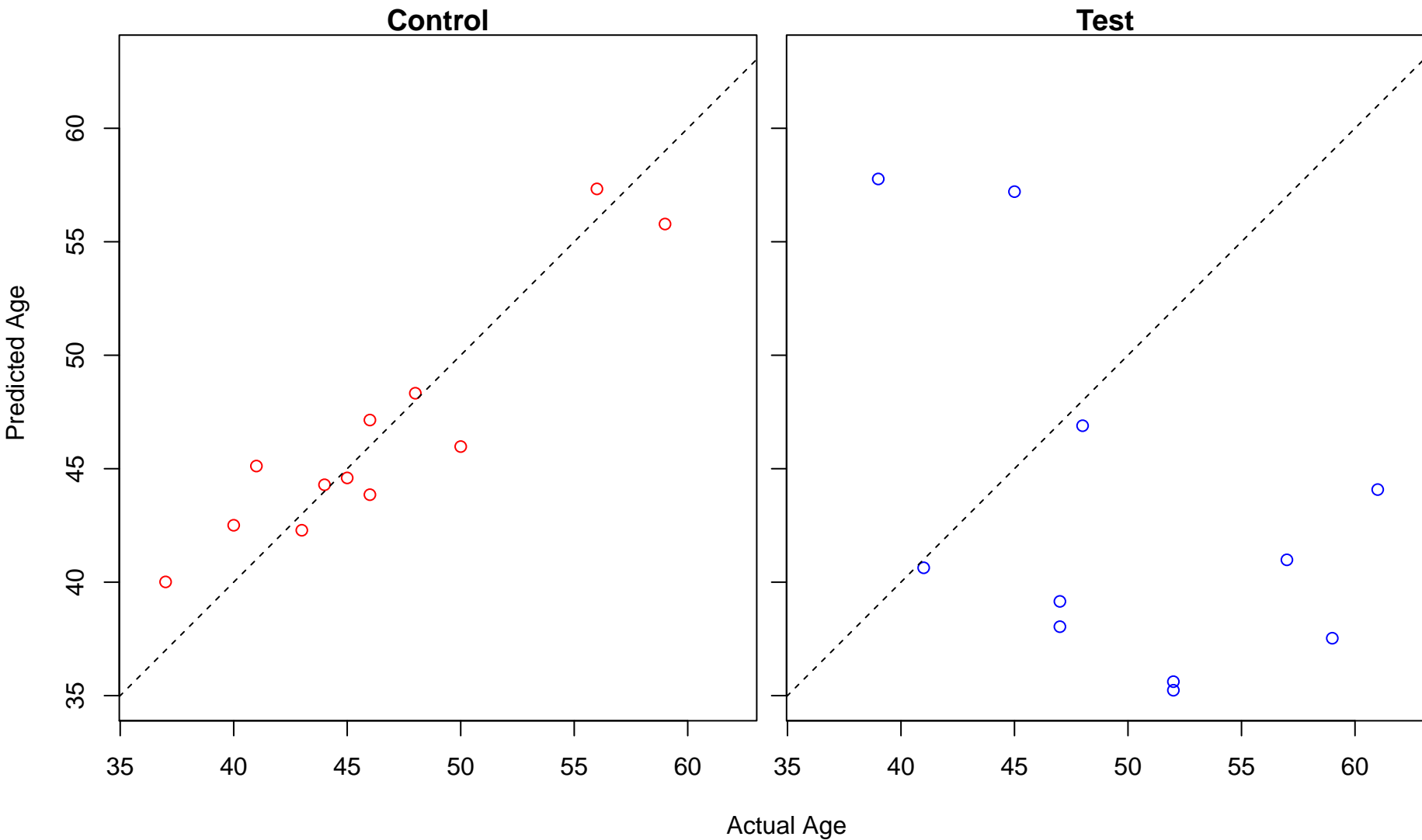


Actual Age

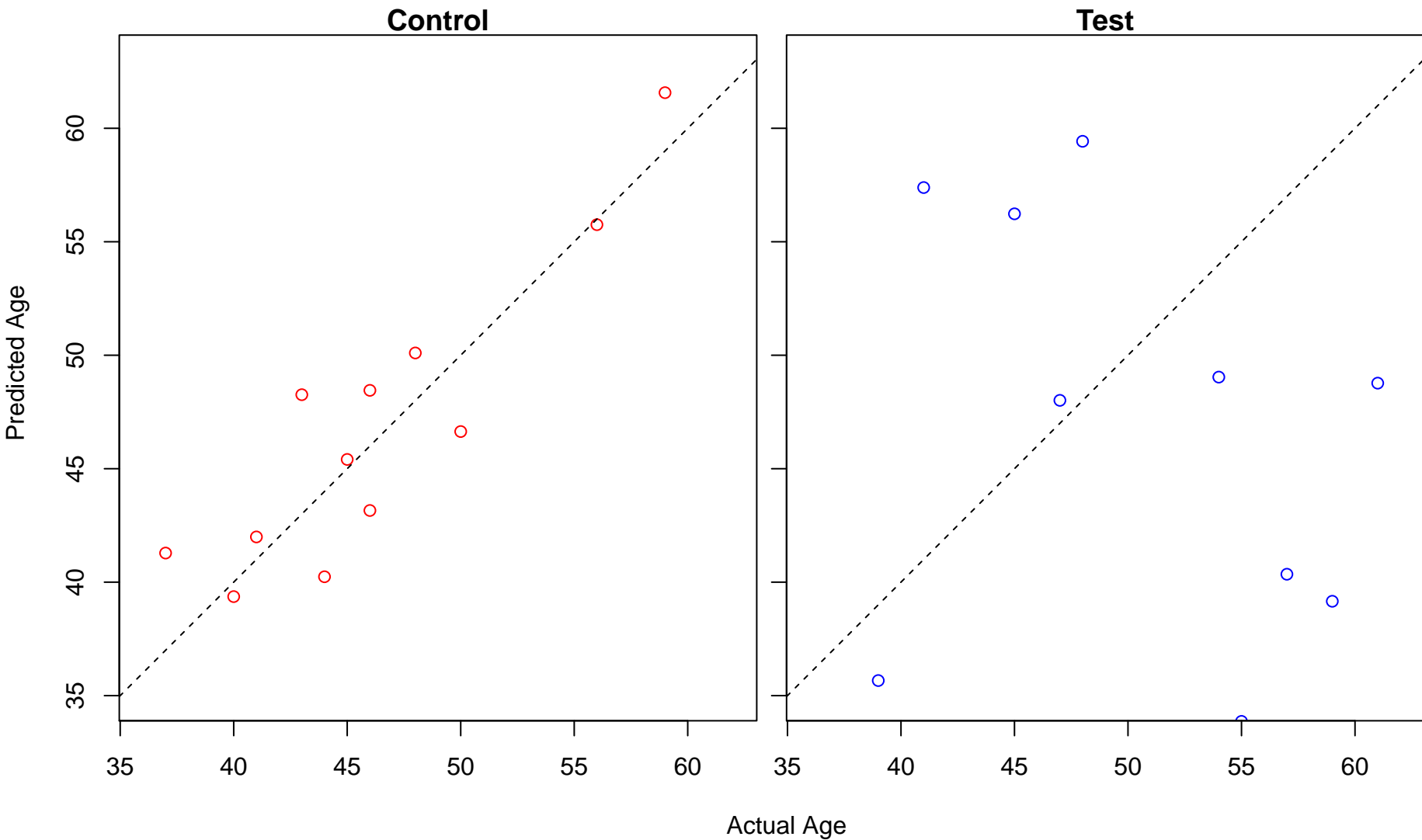
neuron apoptotic process (Score: 29.730240)



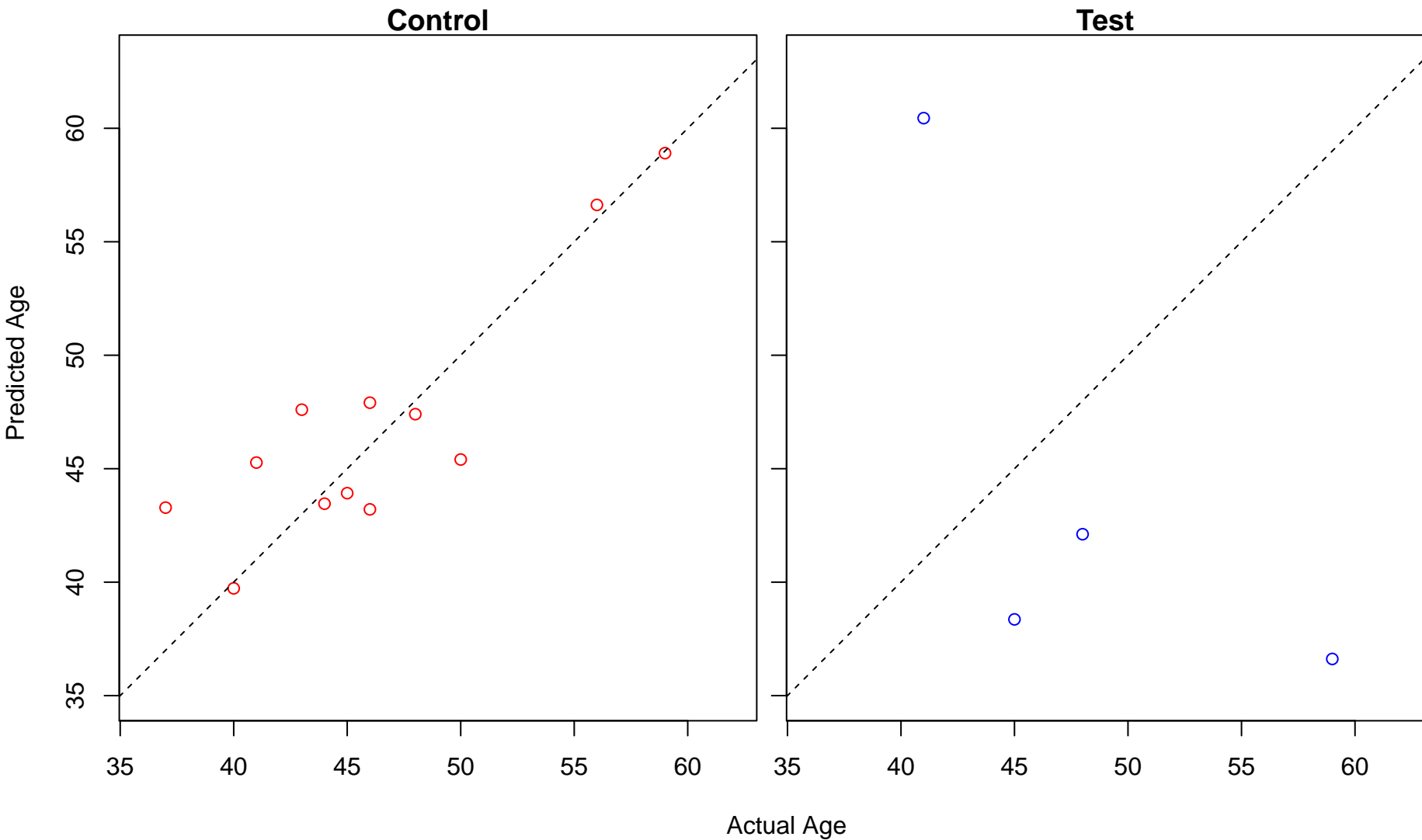
regulation of membrane protein ectodomain proteolysis (Score: 29.635179)



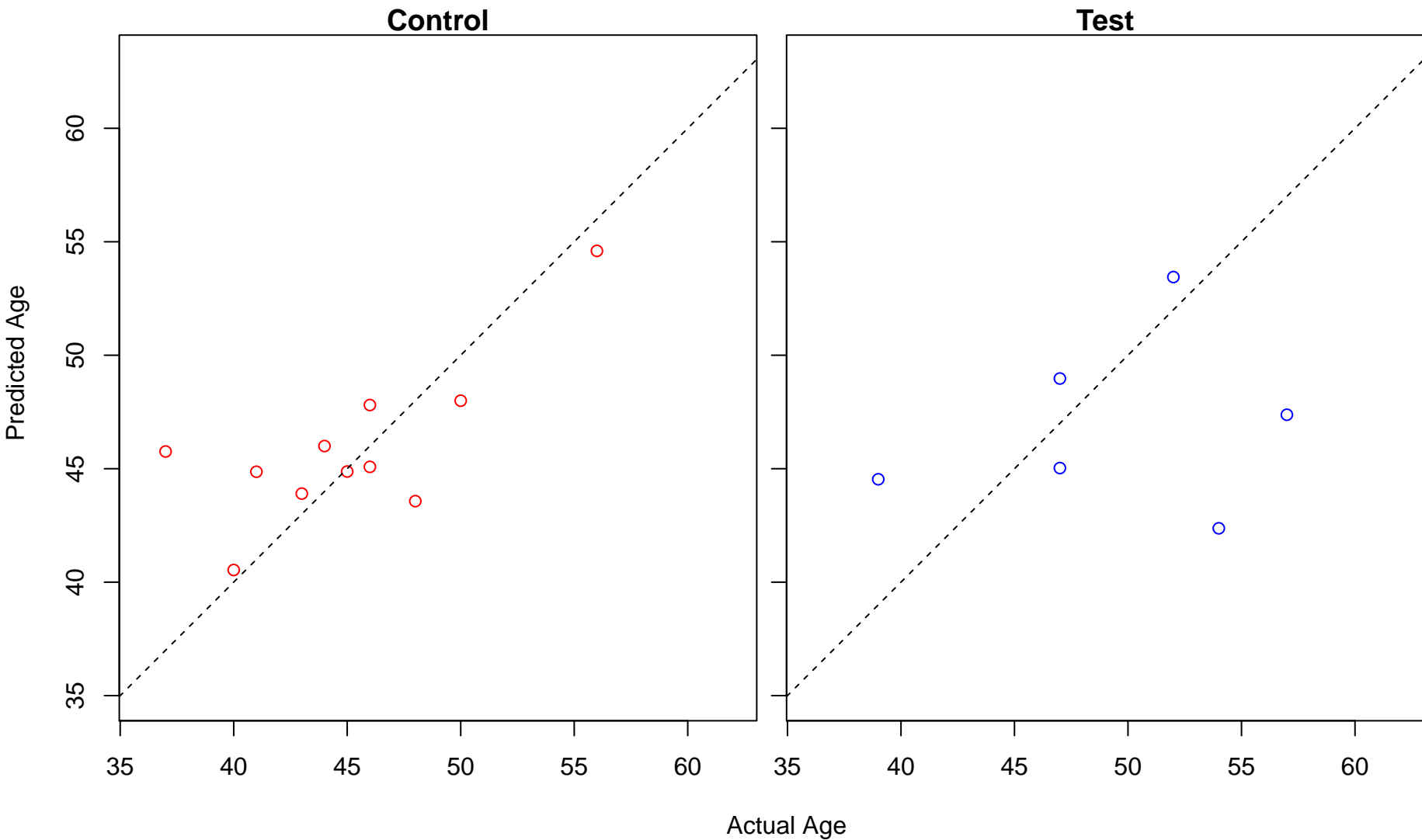
regulation of vasculogenesis (Score: 29.550653)



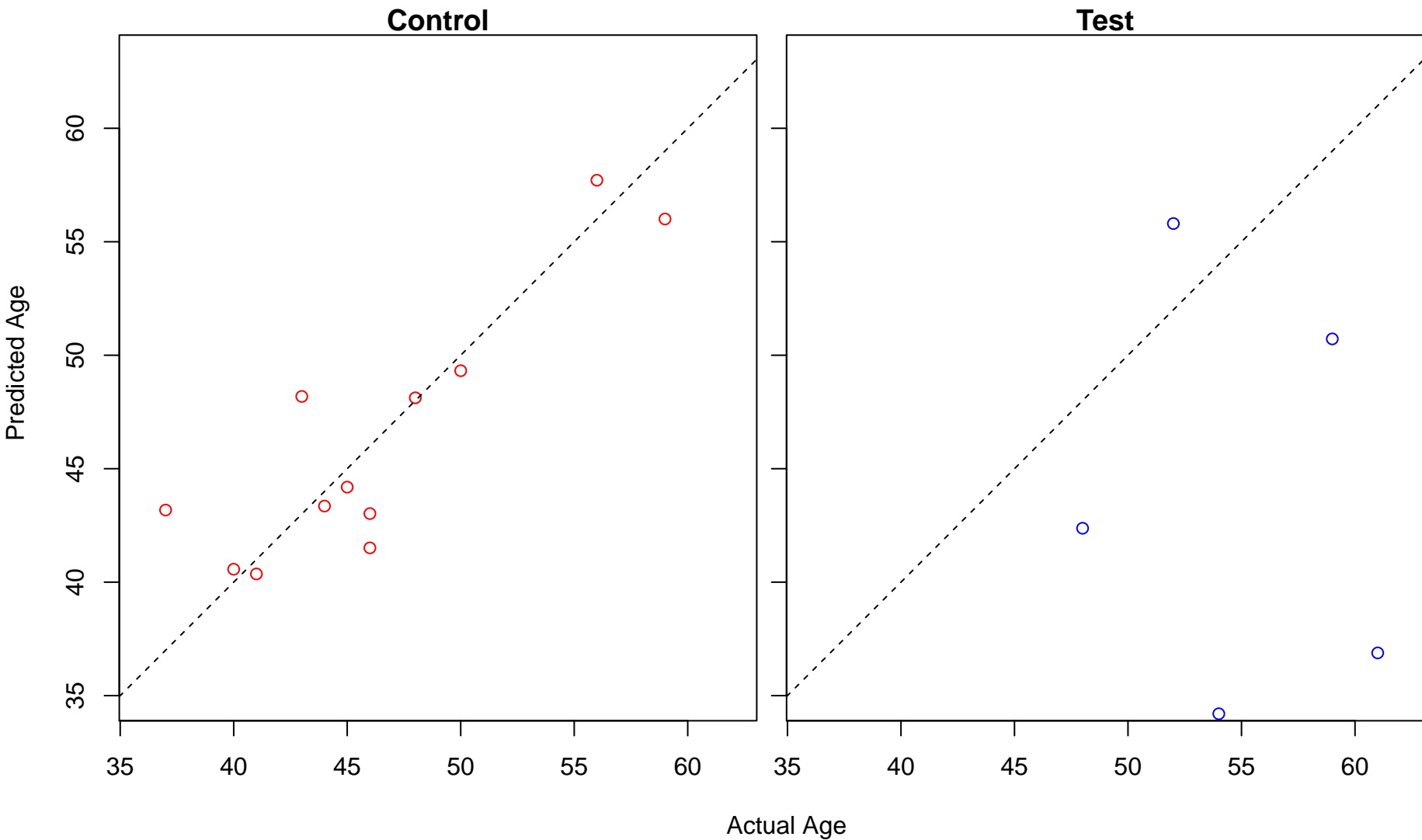
misfolded or incompletely synthesized protein catabolic process (Score: 29.526778)



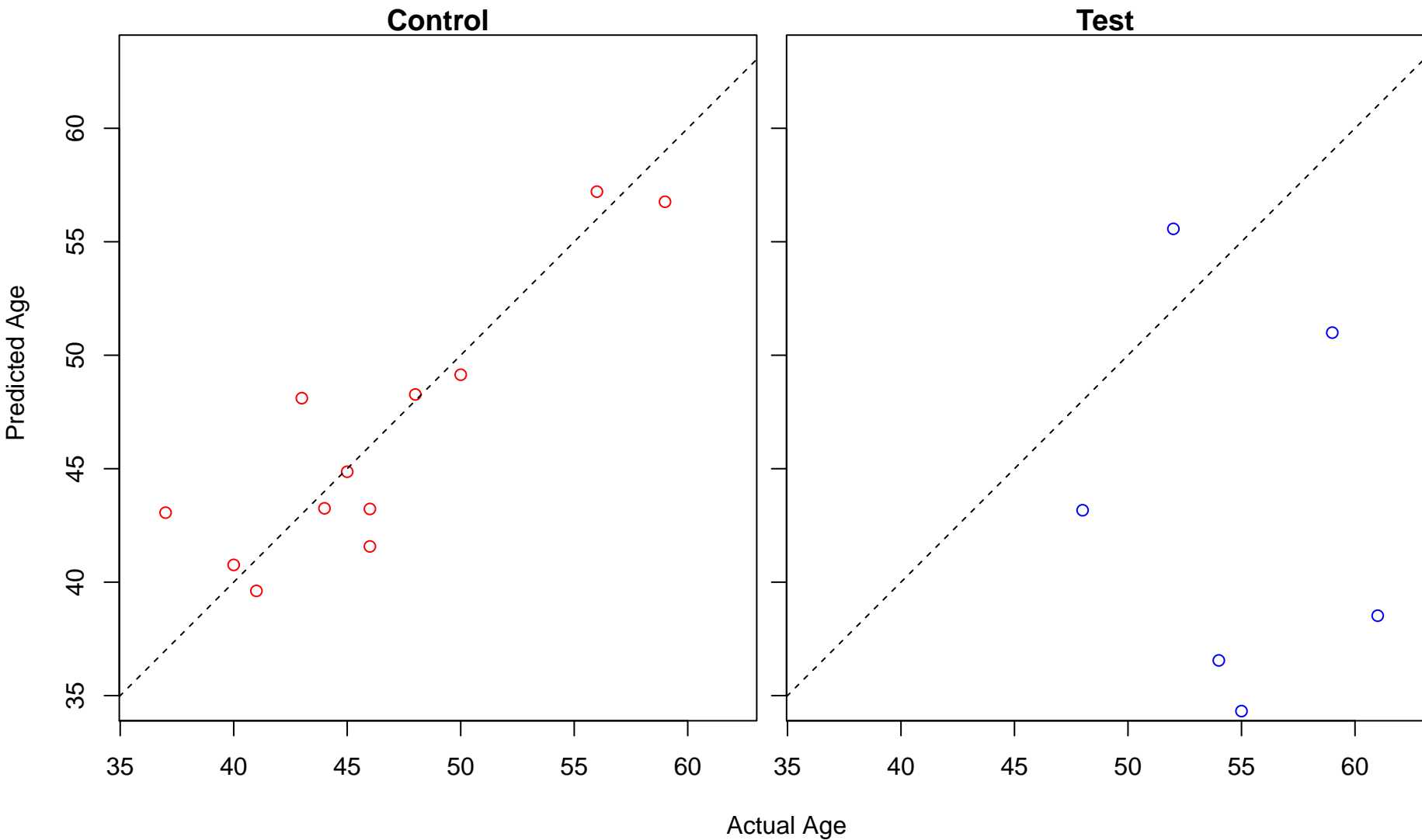
mitochondrial genome maintenance (Score: 29.448742)



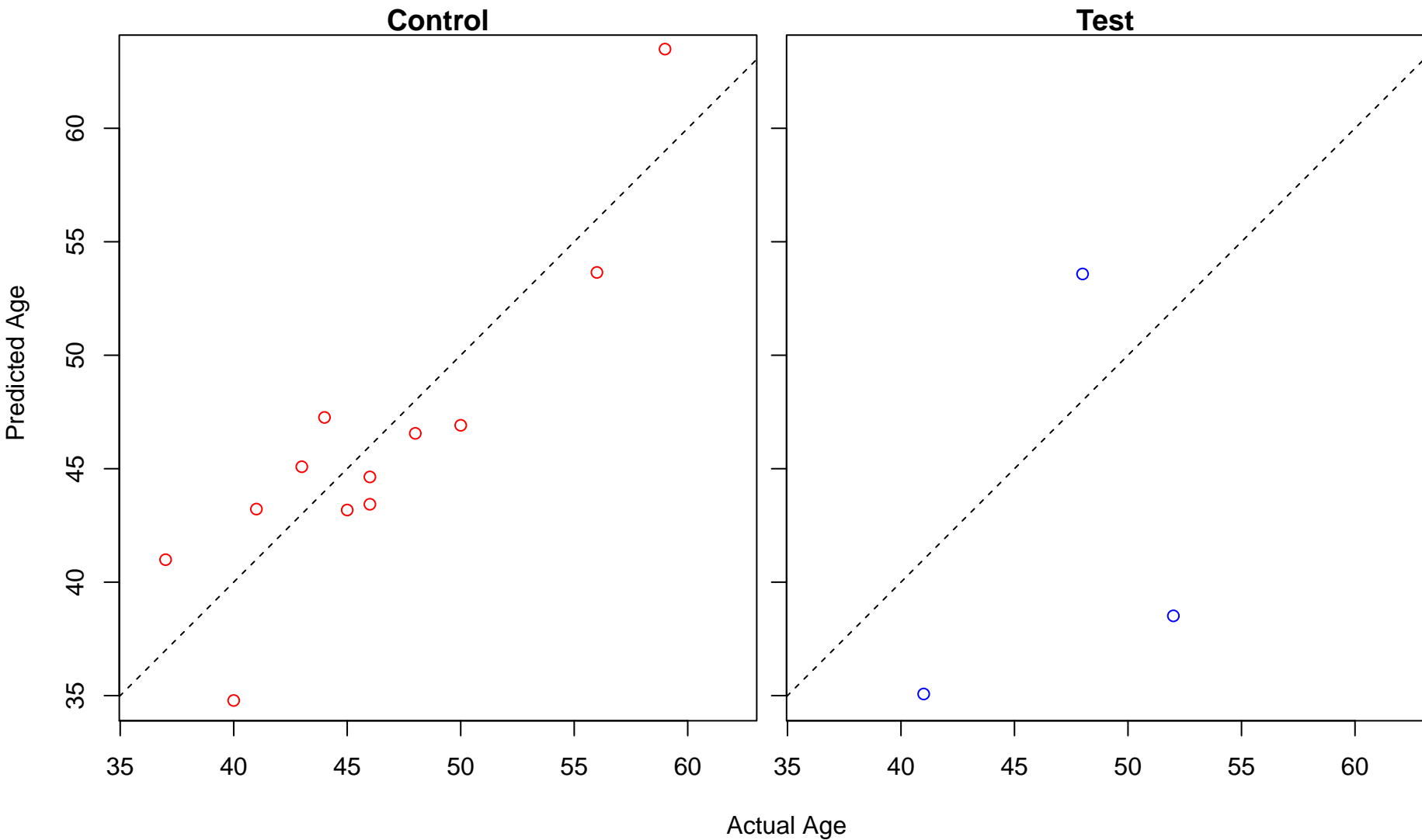
establishment of endothelial barrier (Score: 29.370629)



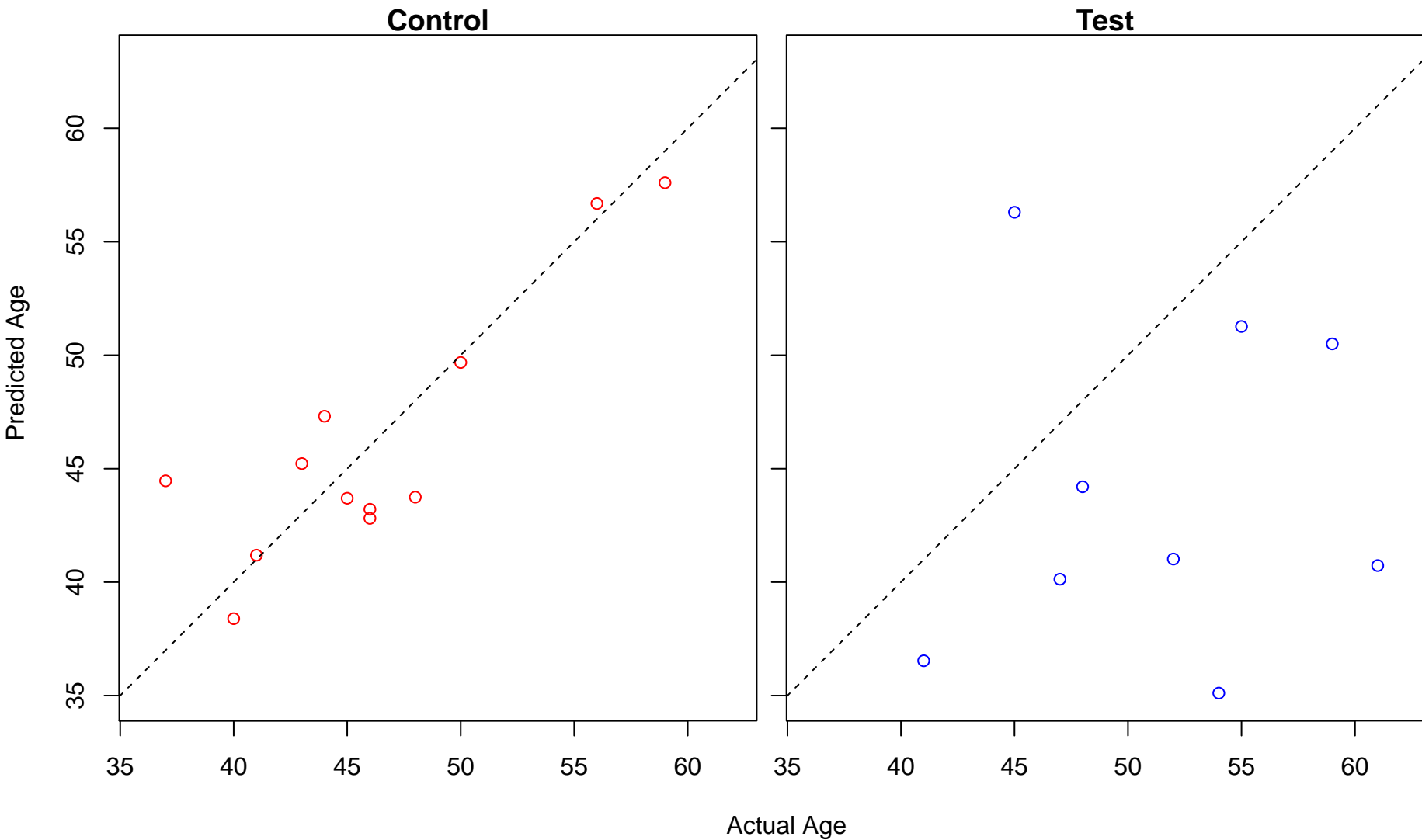
endothelial cell development (Score: 29.065384)



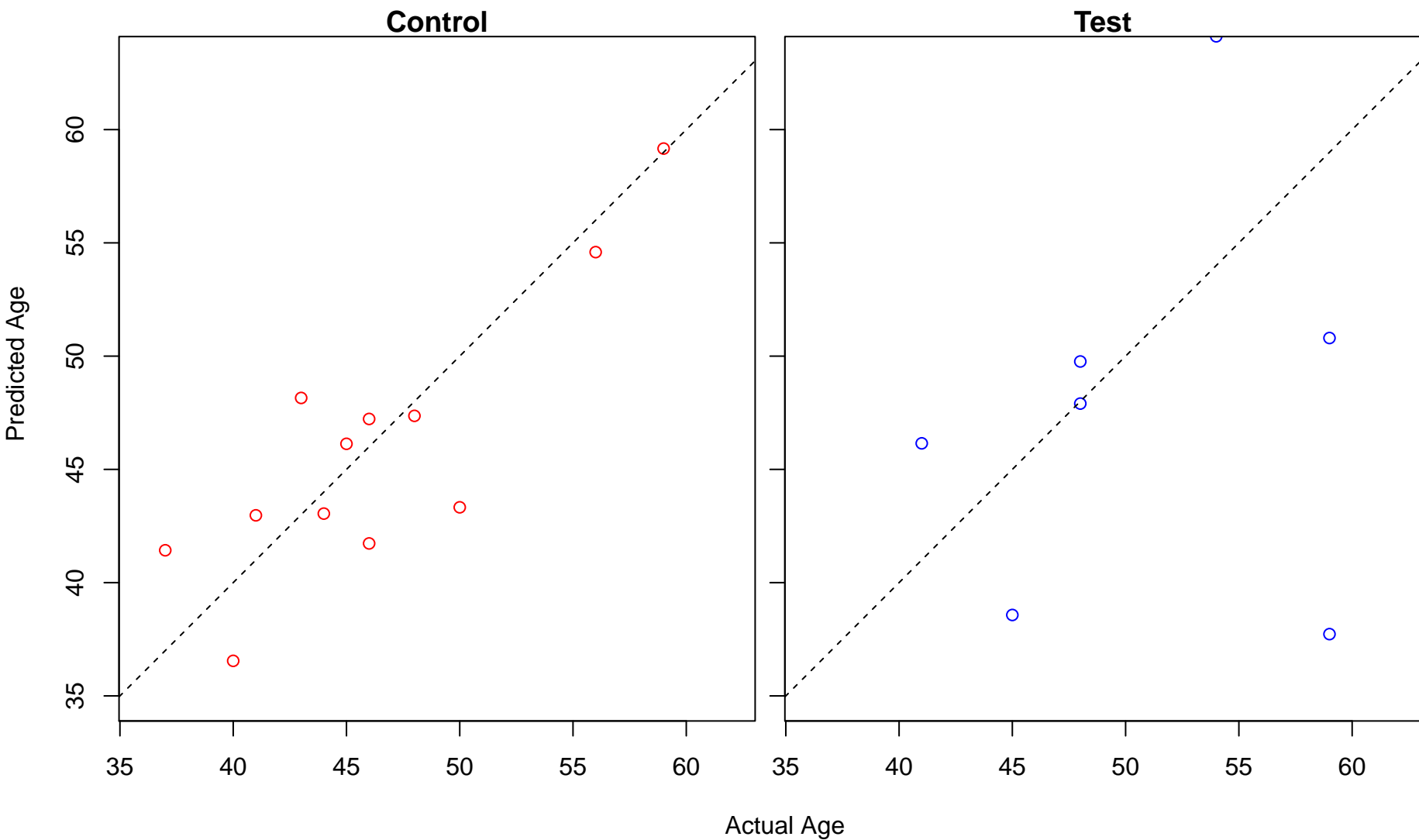
female gamete generation (Score: 29.032161)



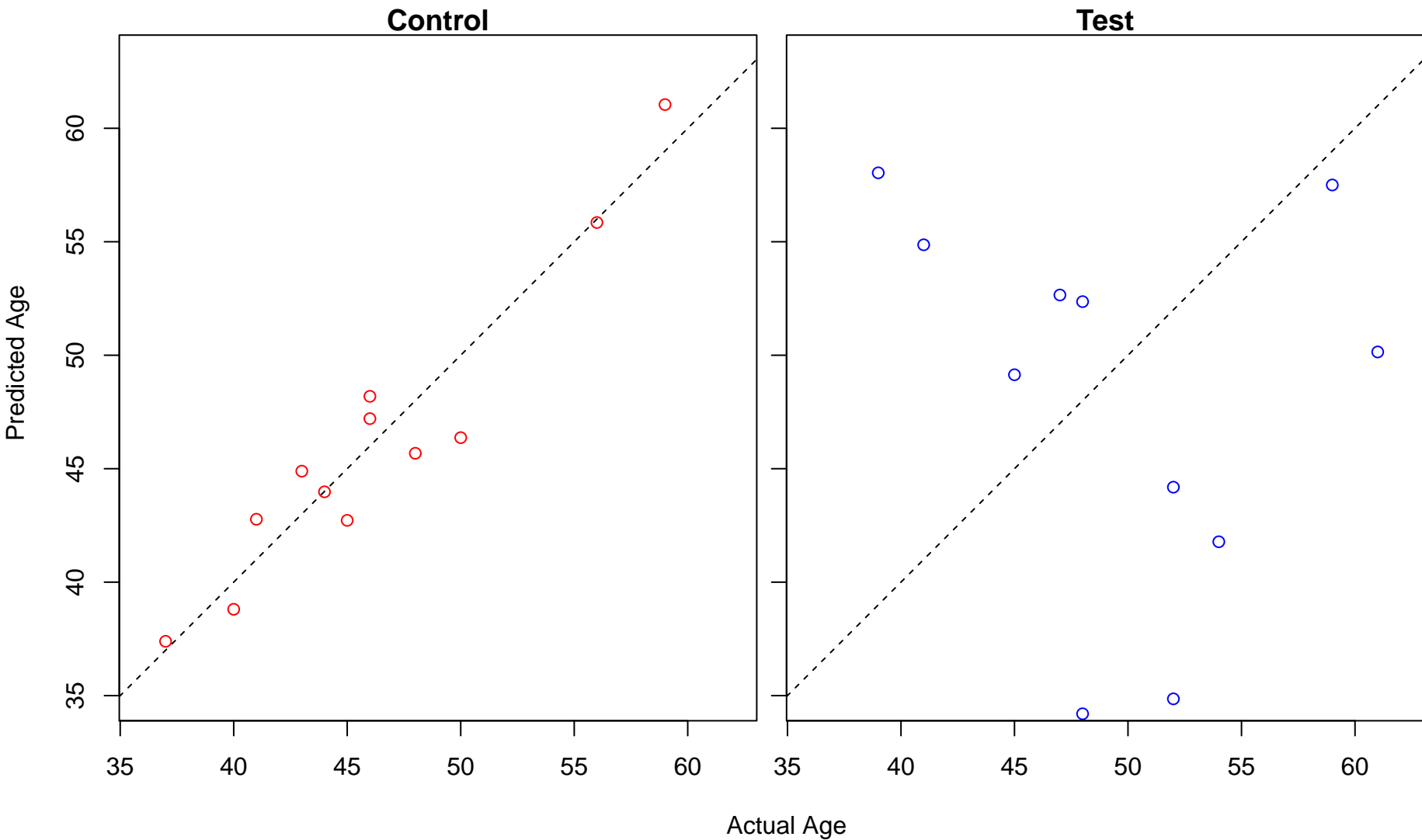
drug transport (Score: 29.000381)



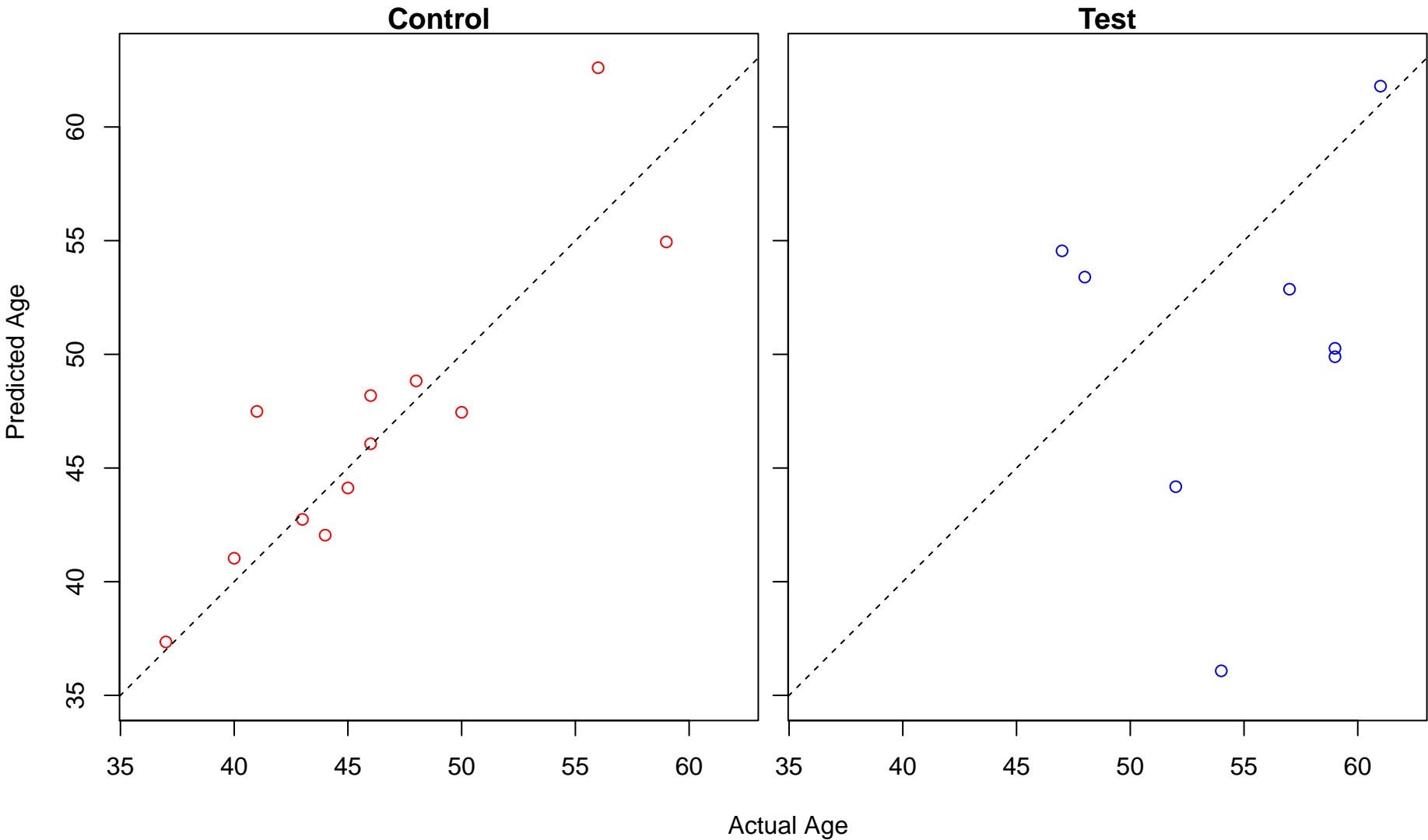
regulation of T cell cytokine production (Score: 28.756072)



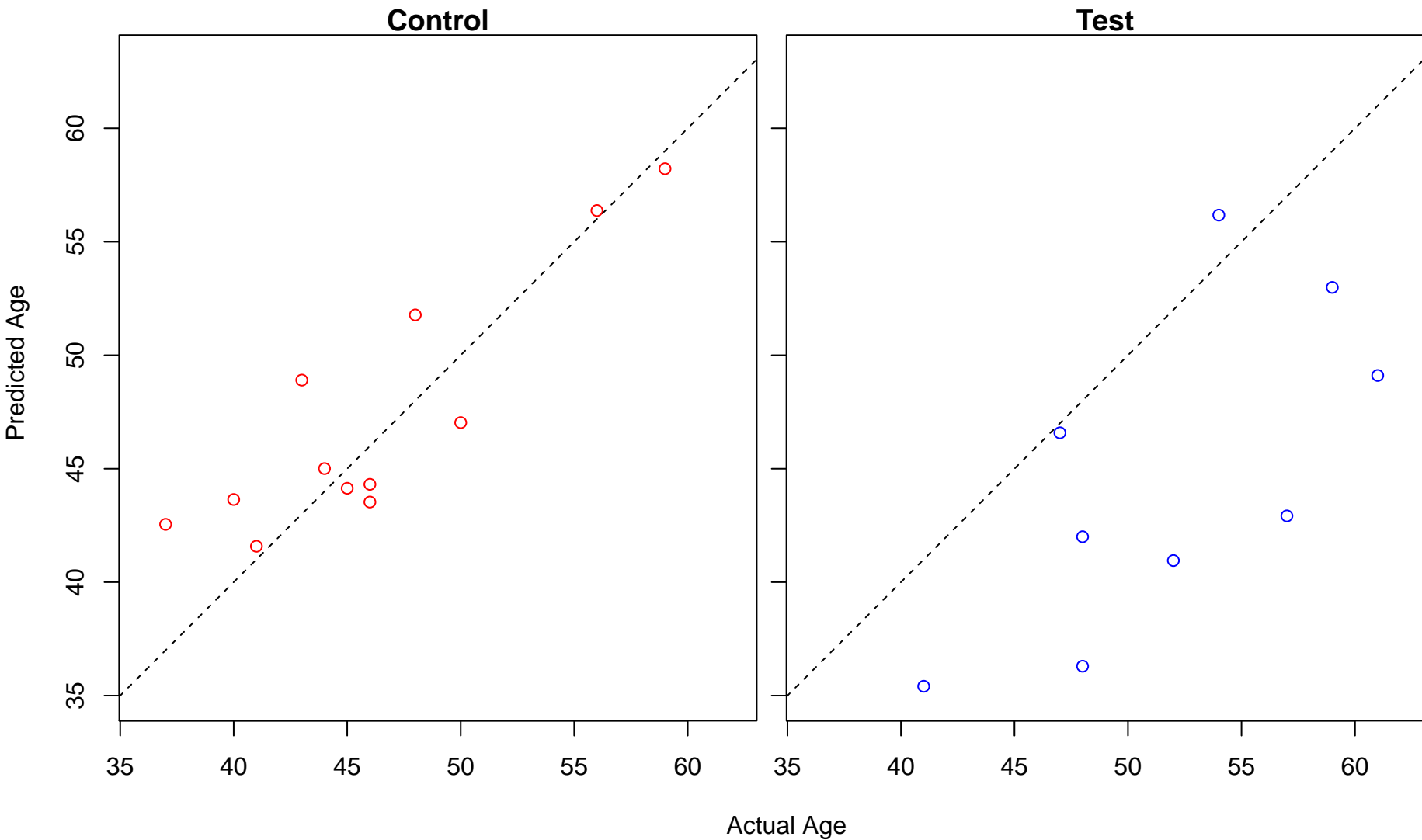
positive regulation of vasculature development (Score: 28.751834)



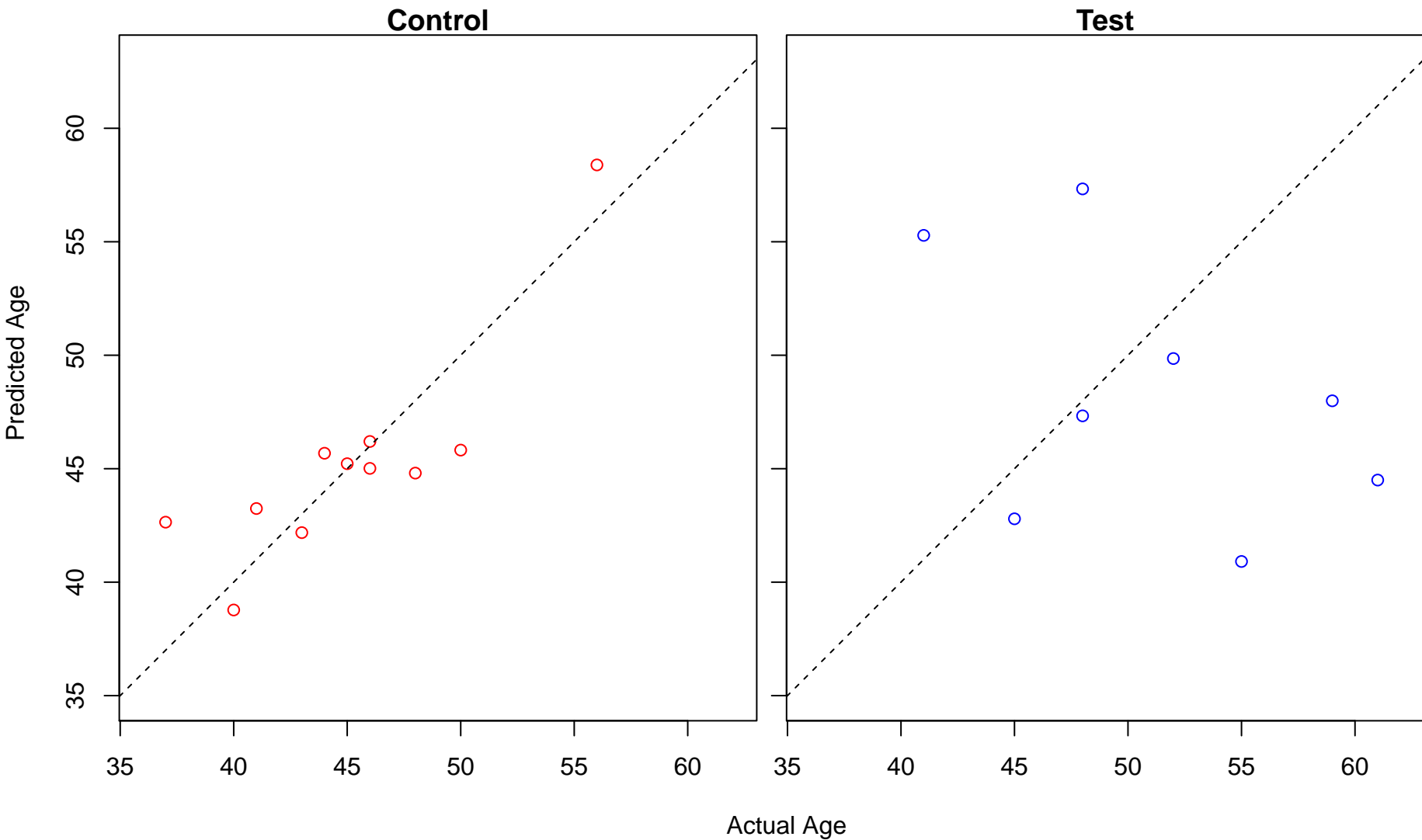
positive regulation of granulocyte macrophage colony-stimulating factor production (Score: 28.6667)



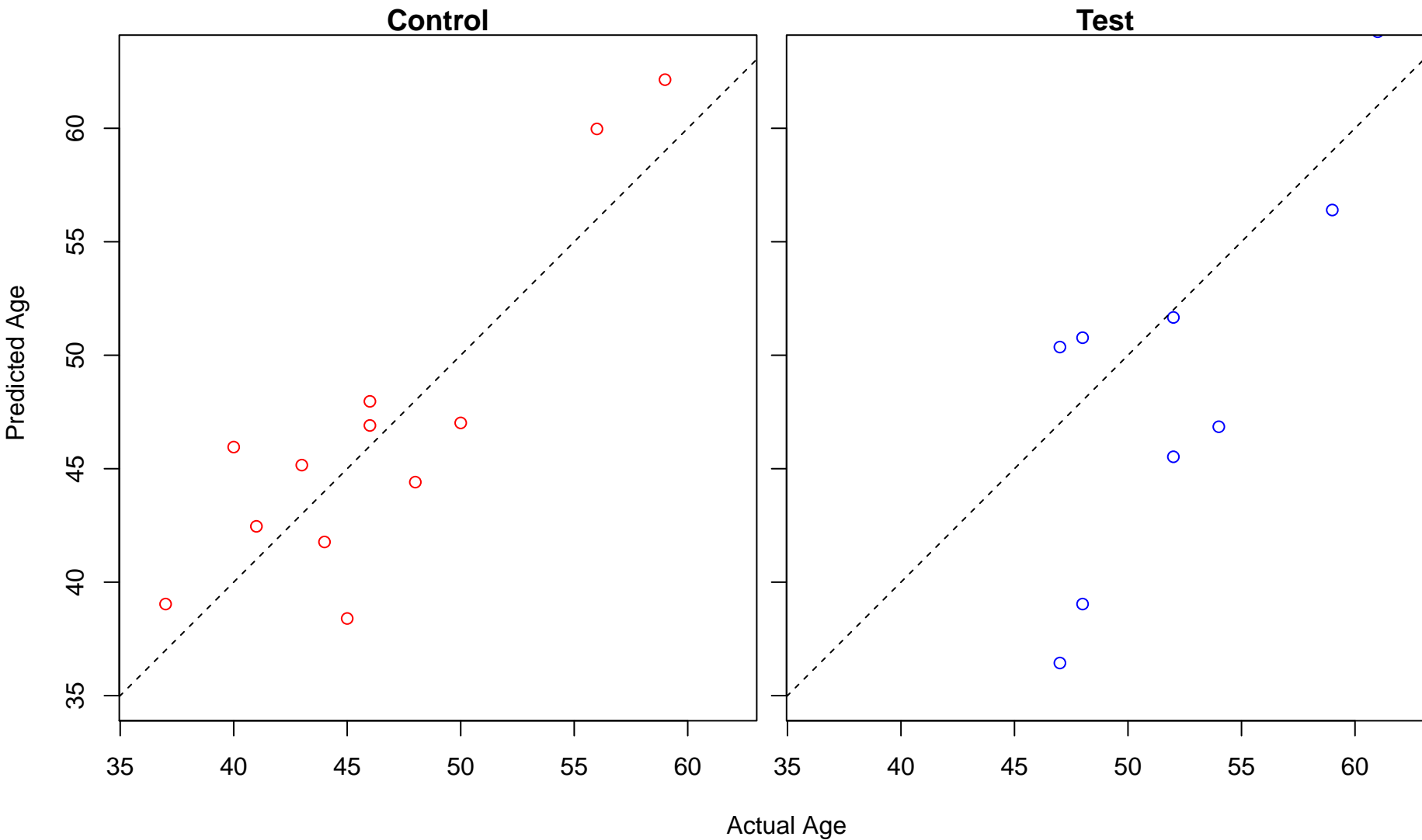
cardiac muscle cell action potential involved in contraction (Score: 28.299955)



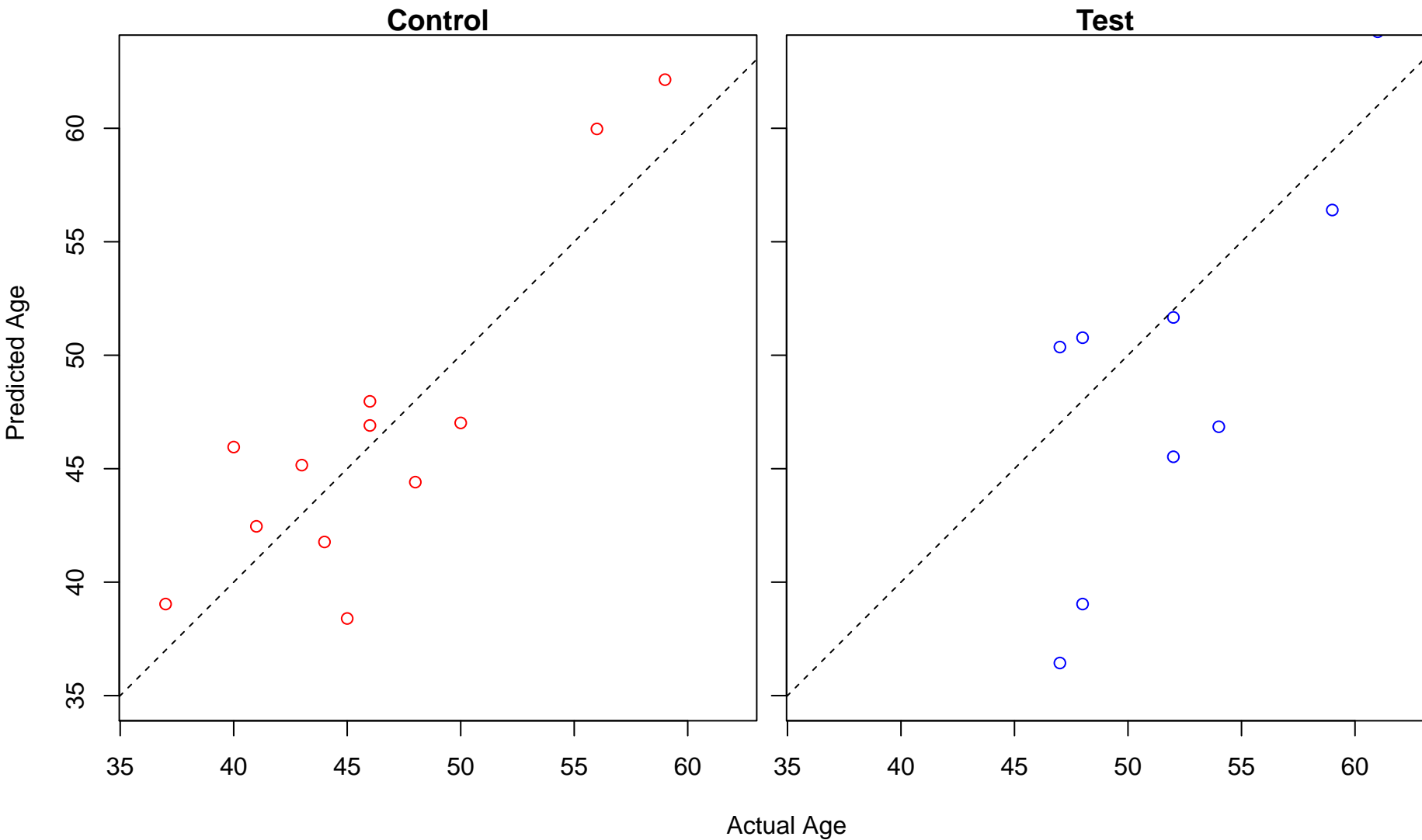
histone phosphorylation (Score: 28.079699)



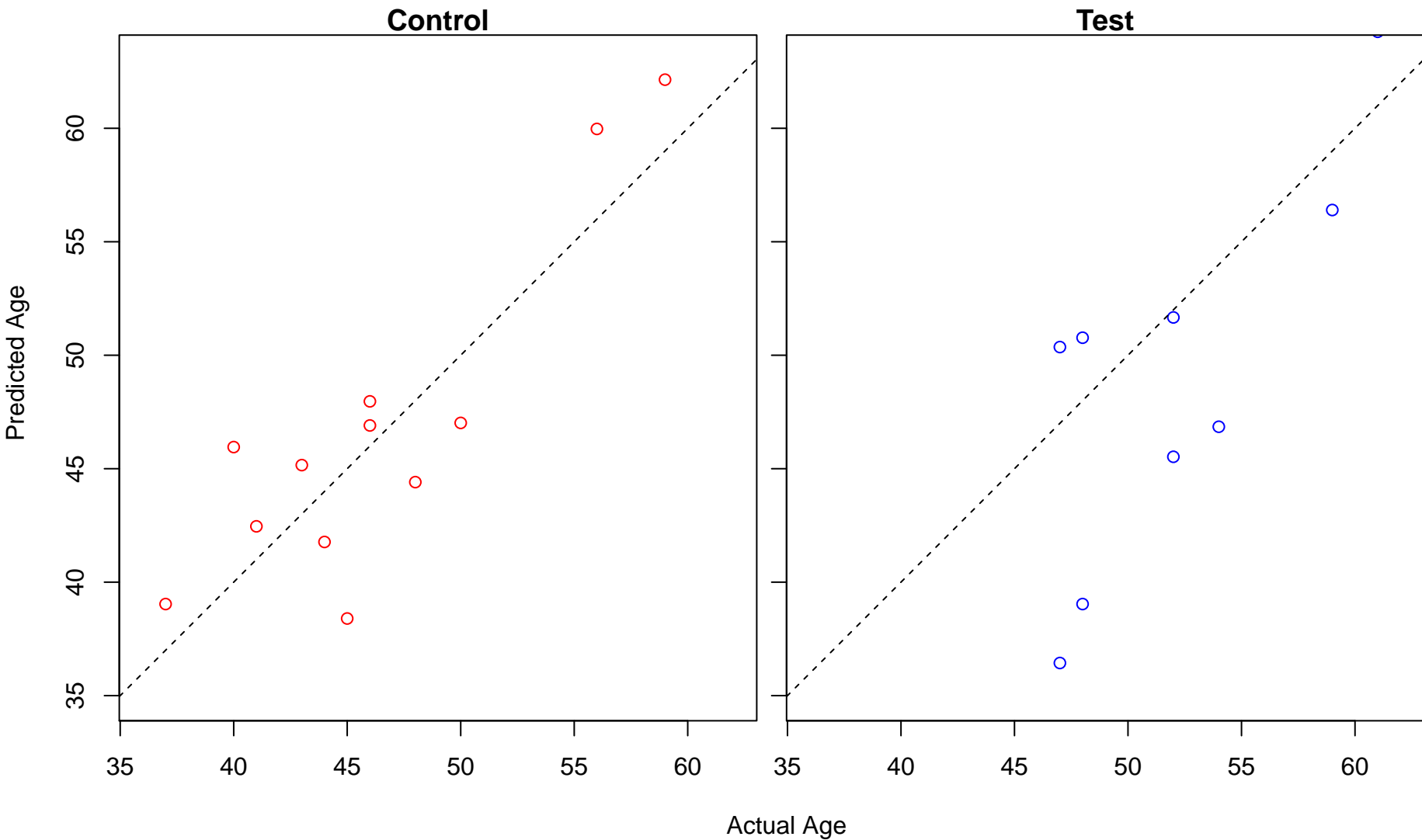
positive regulation of mitotic metaphase/anaphase transition (Score: 28.040842)



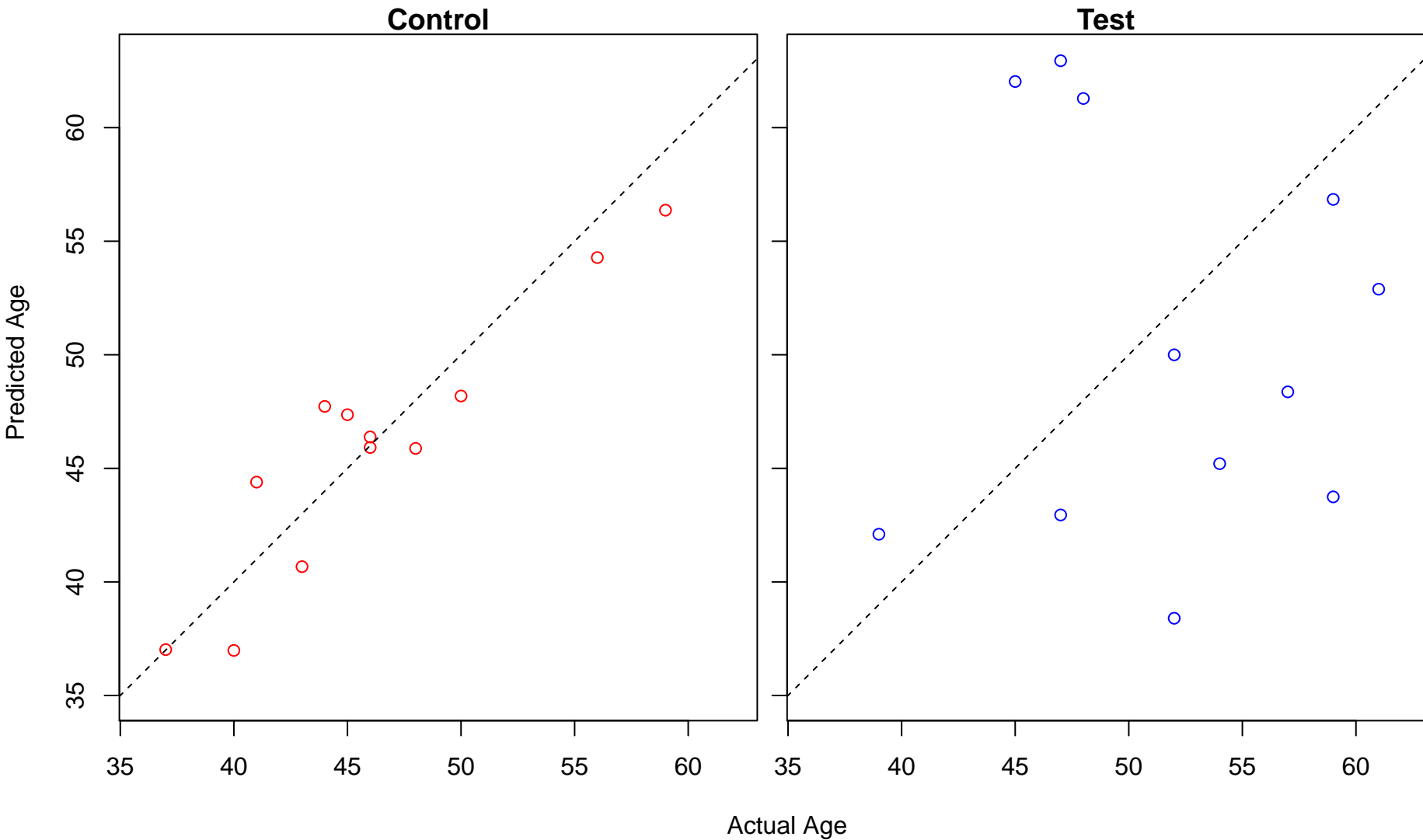
positive regulation of mitotic sister chromatid separation (Score: 28.040842)



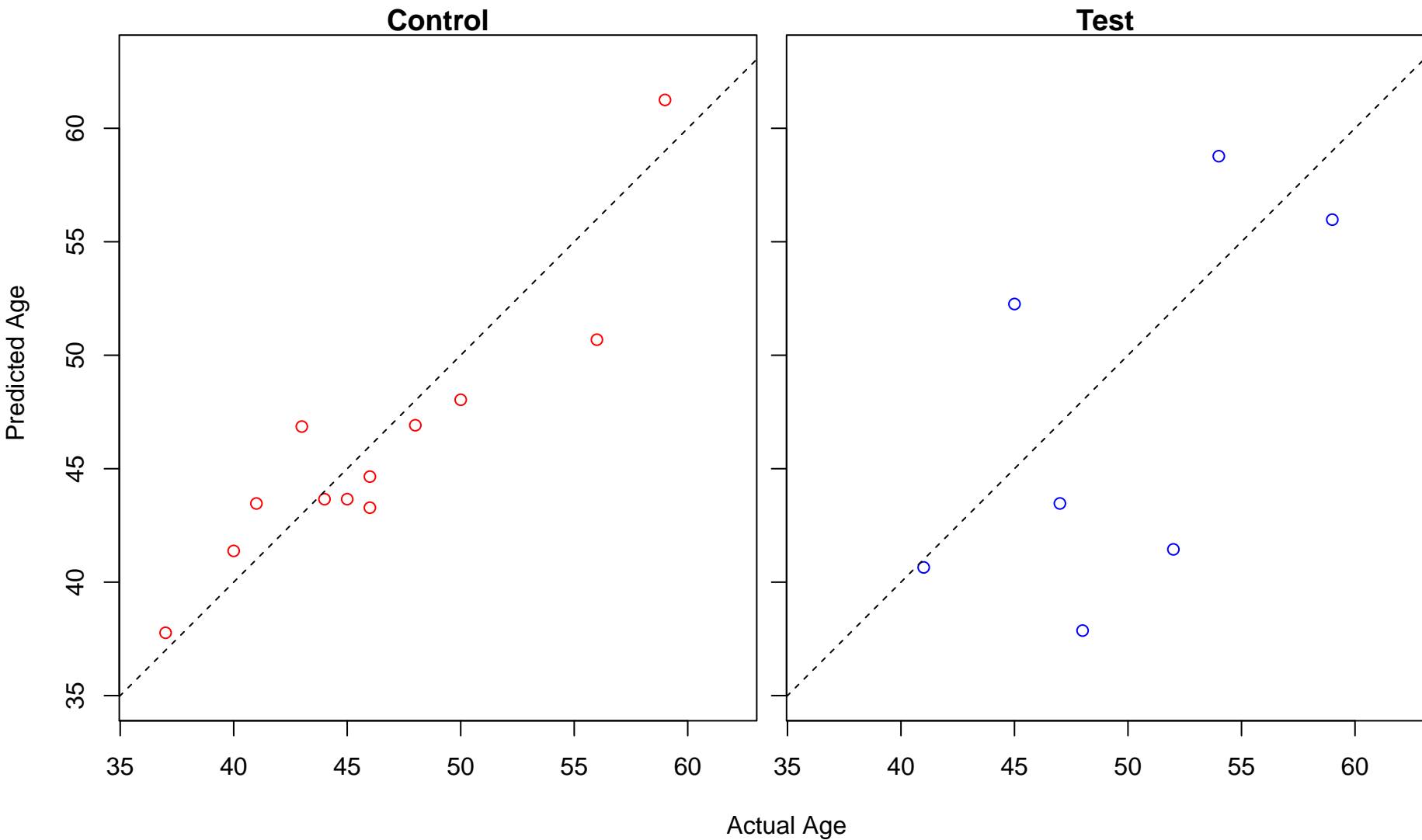
positive regulation of metaphase/anaphase transition of cell cycle (Score: 28.040842)



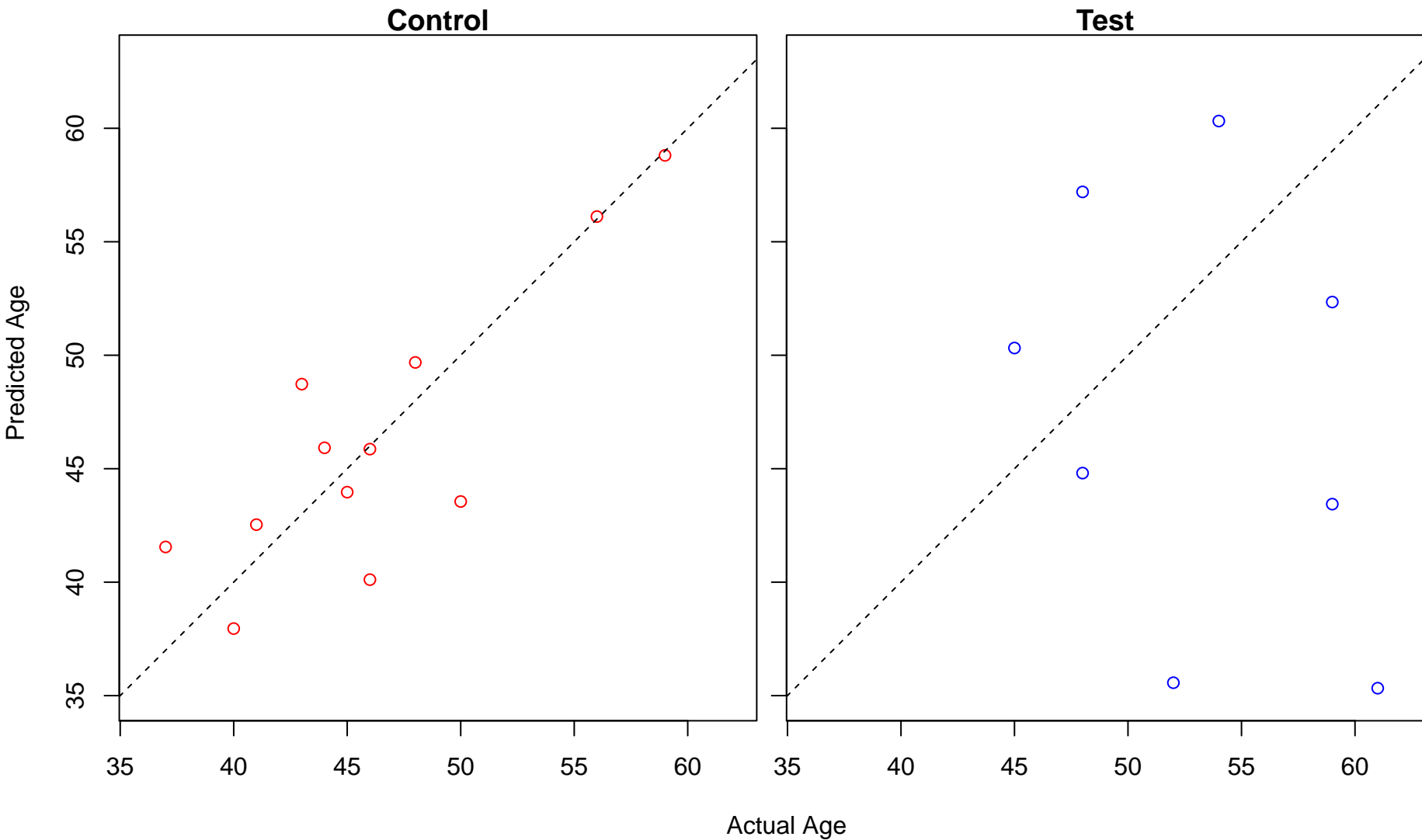
pyrimidine ribonucleoside catabolic process (Score: 27.822454)



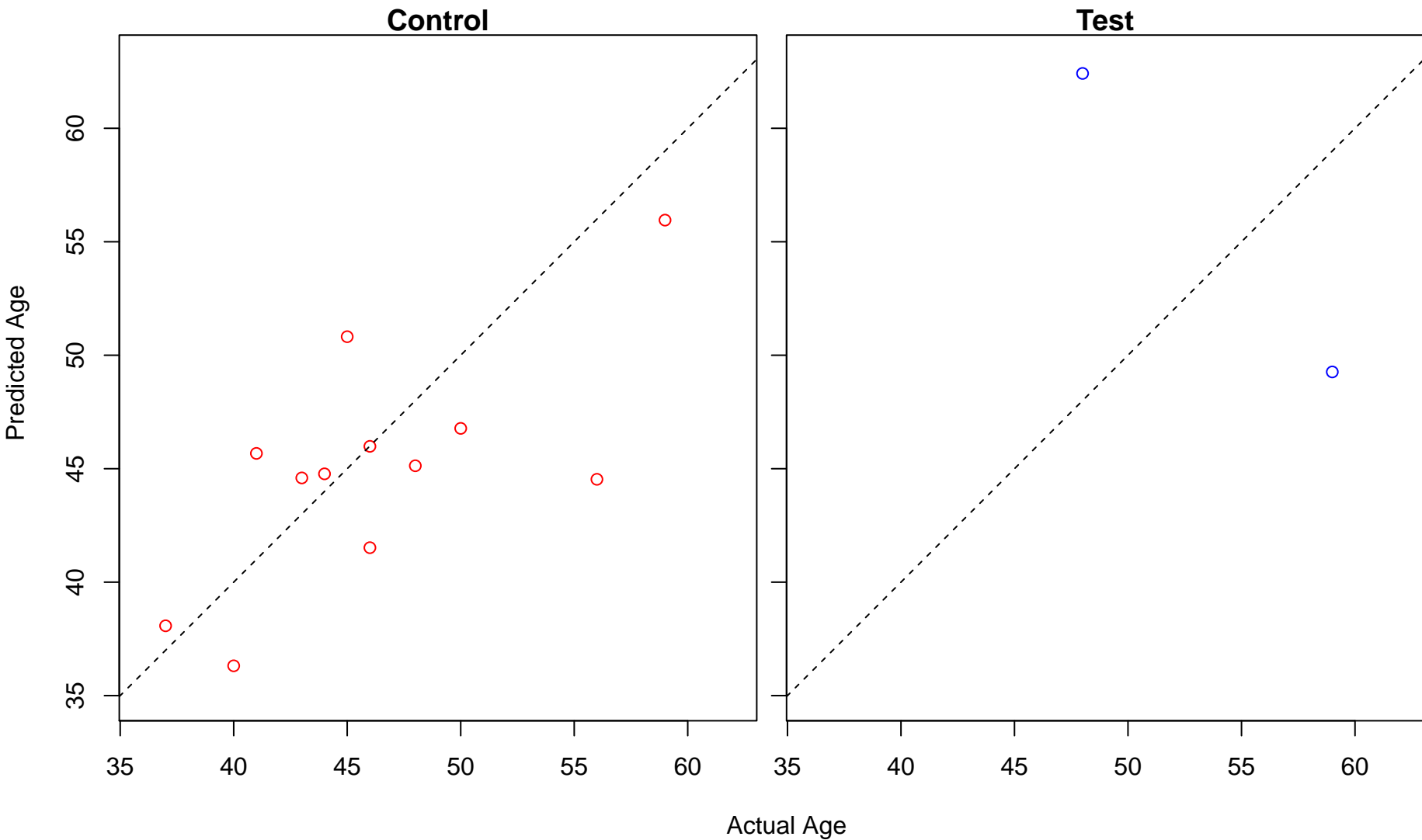
positive regulation of actin cytoskeleton reorganization (Score: 27.774650)



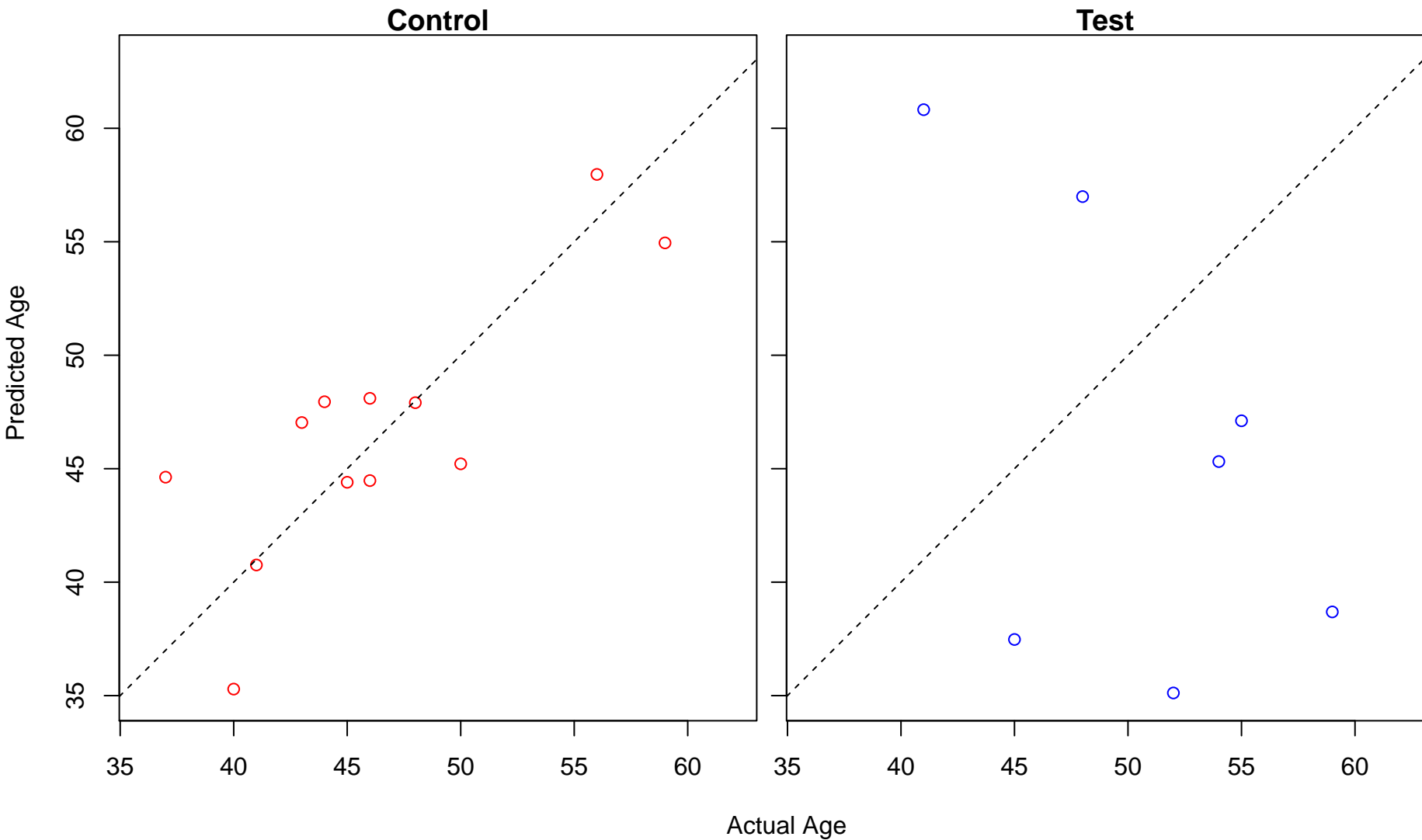
histone ubiquitination (Score: 27.726408)



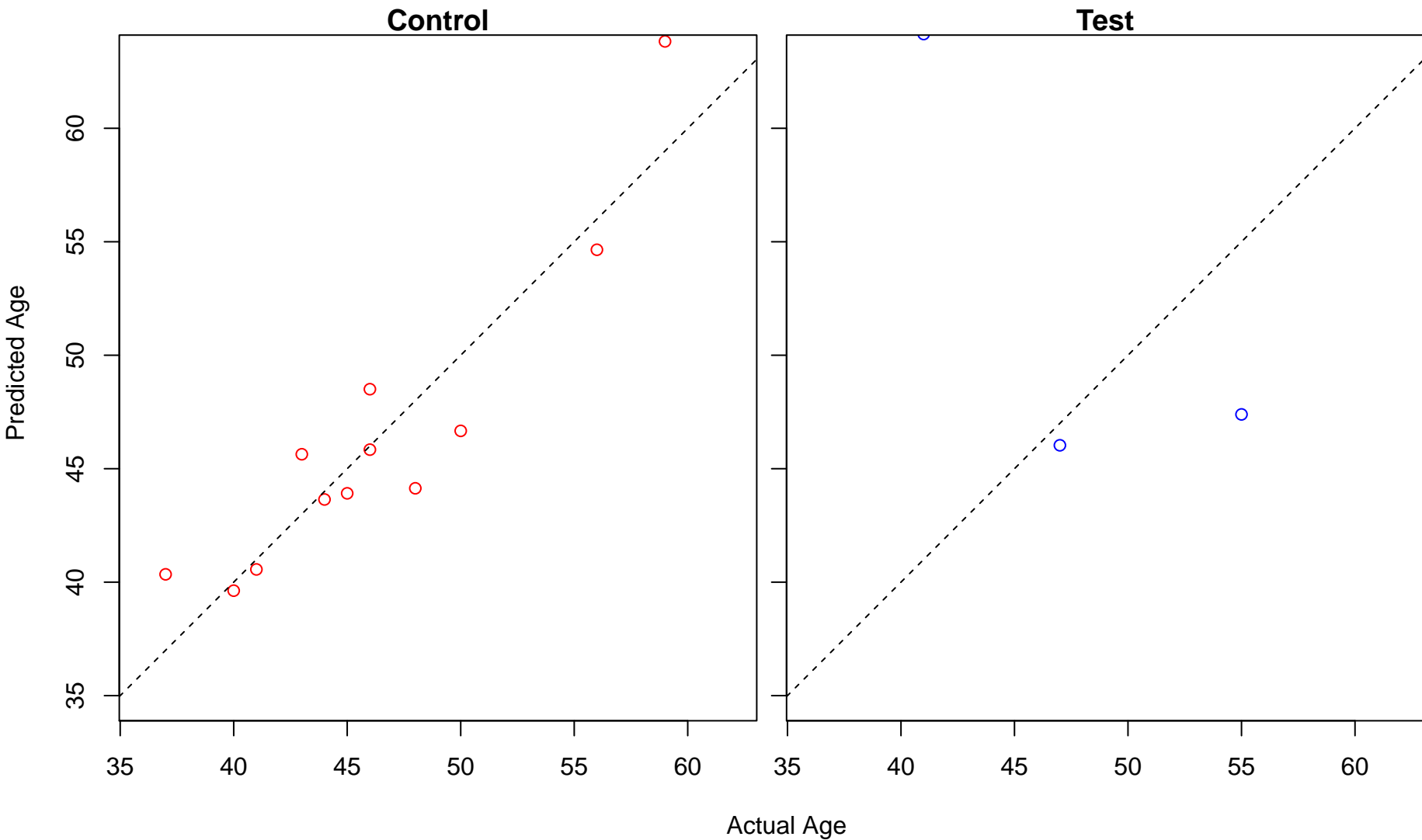
interleukin-4-mediated signaling pathway (Score: 27.686569)



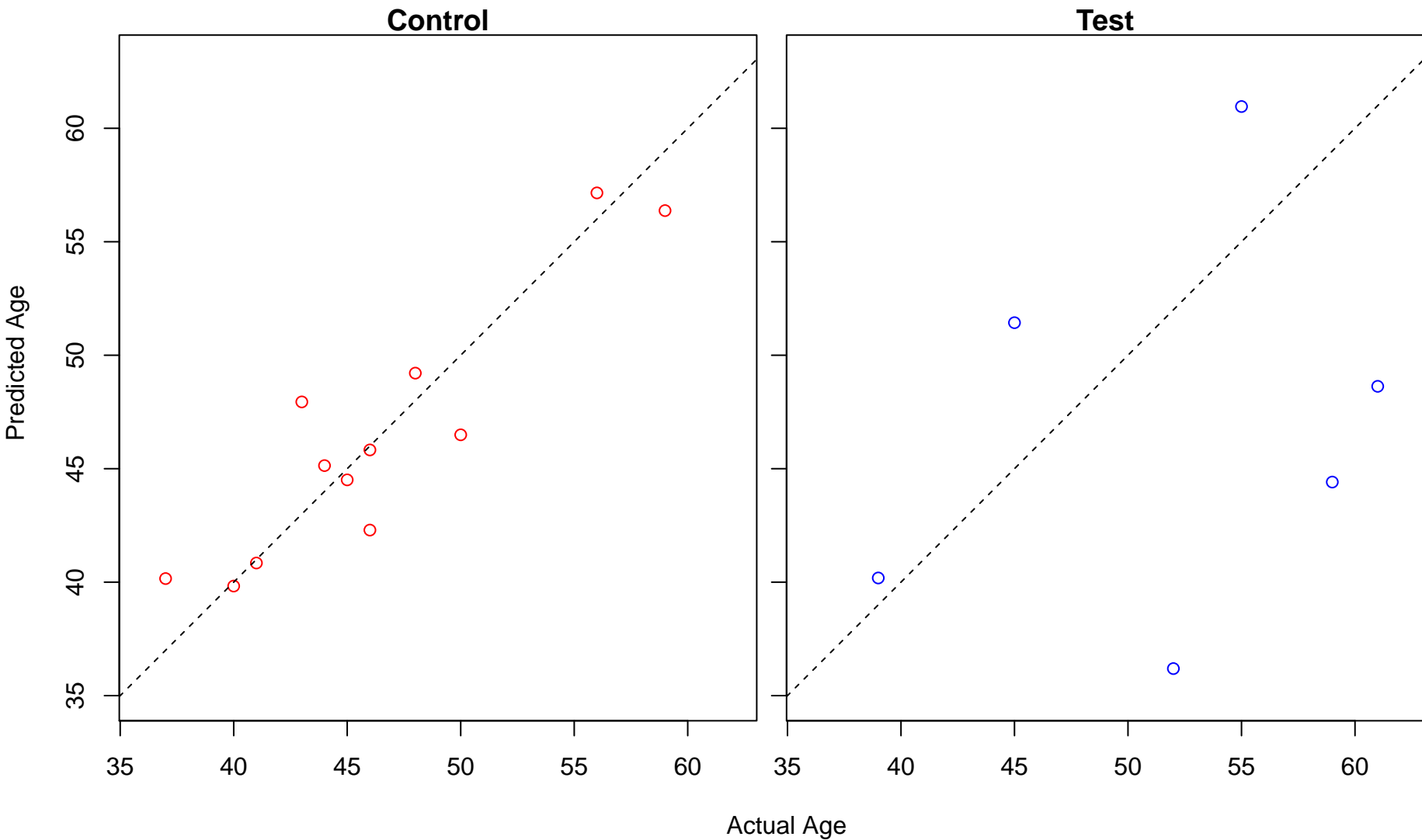
mesenchyme morphogenesis (Score: 27.646864)



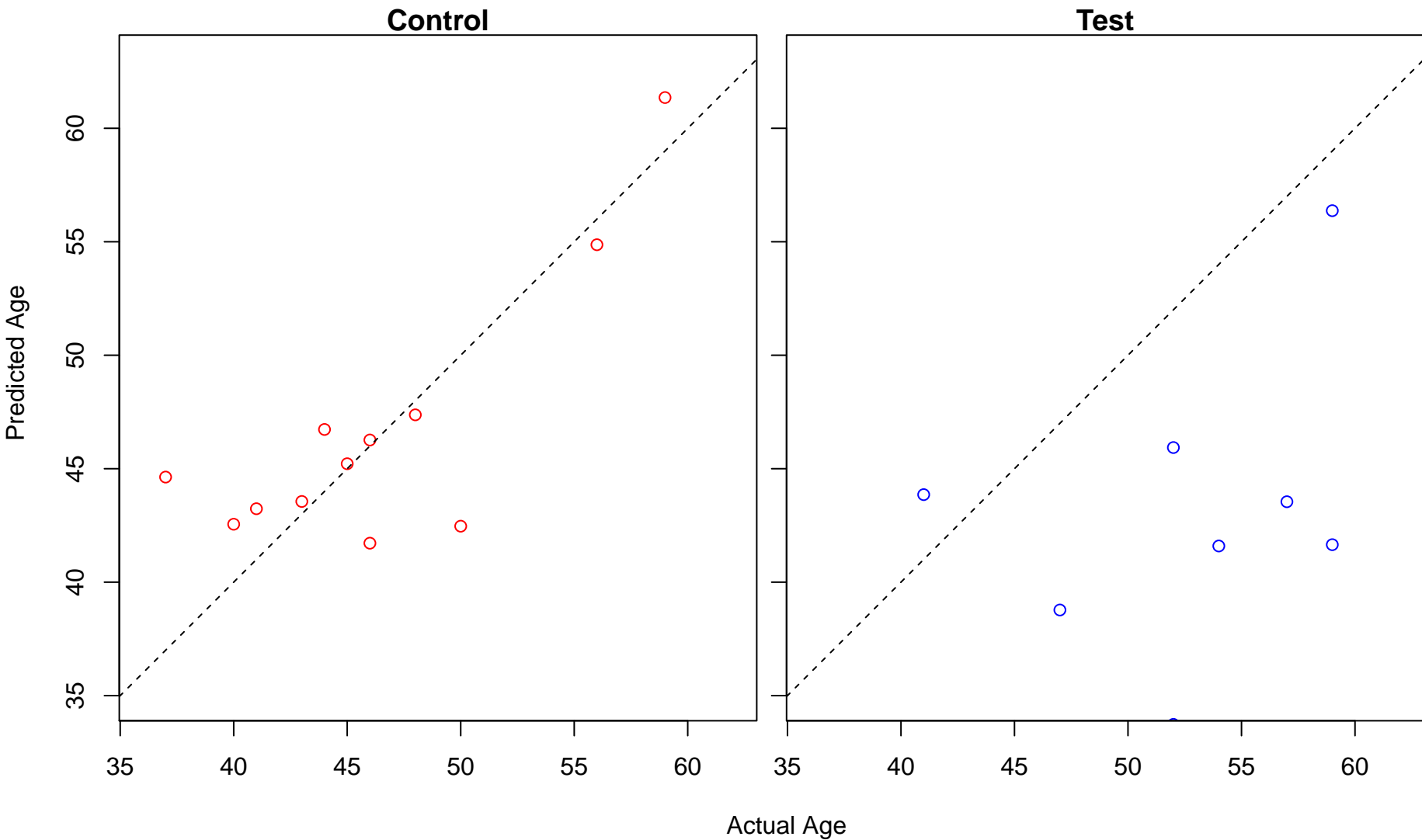
regulation of T-helper 2 cell differentiation (Score: 27.630123)



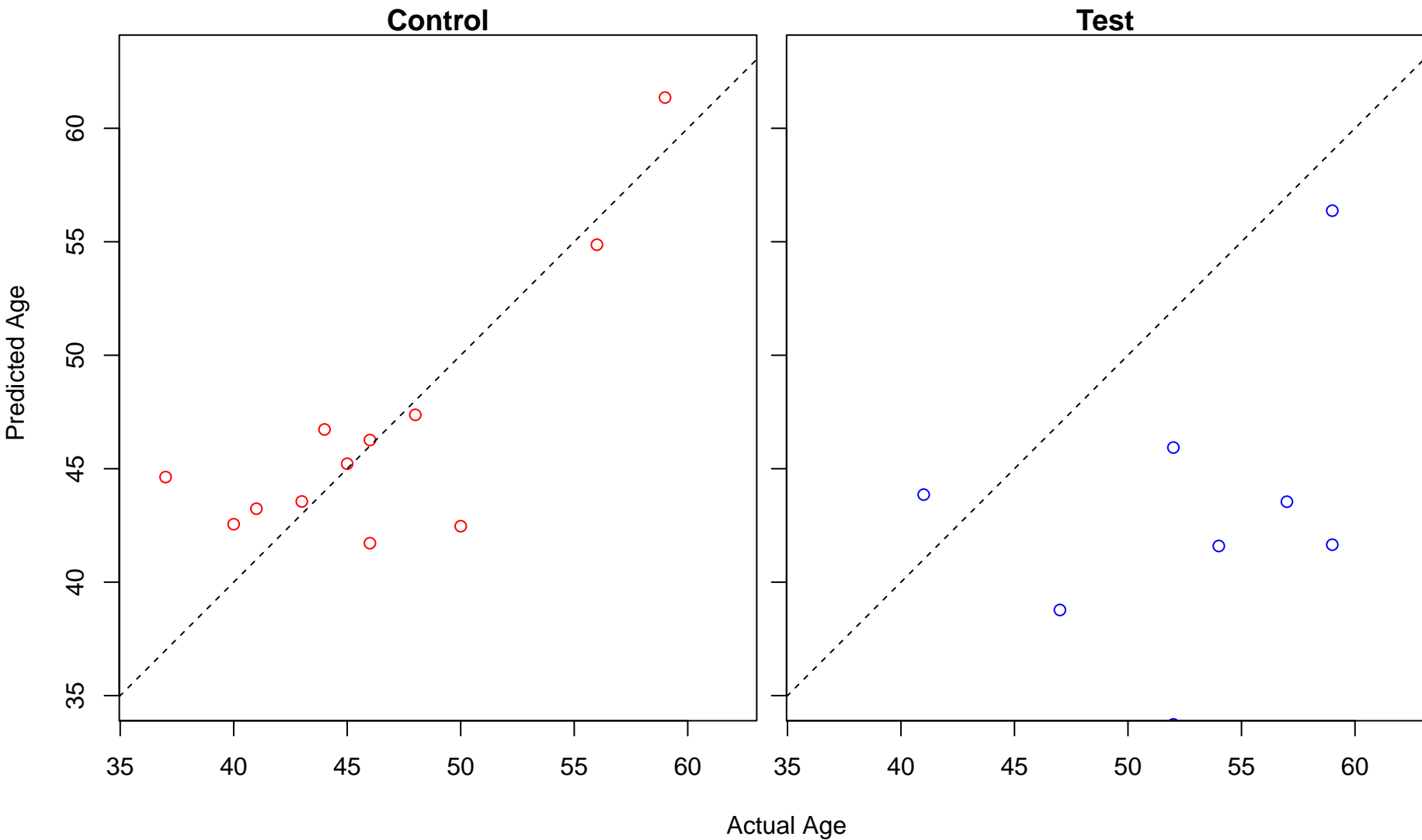
negative regulation of mRNA metabolic process (Score: 27.617367)



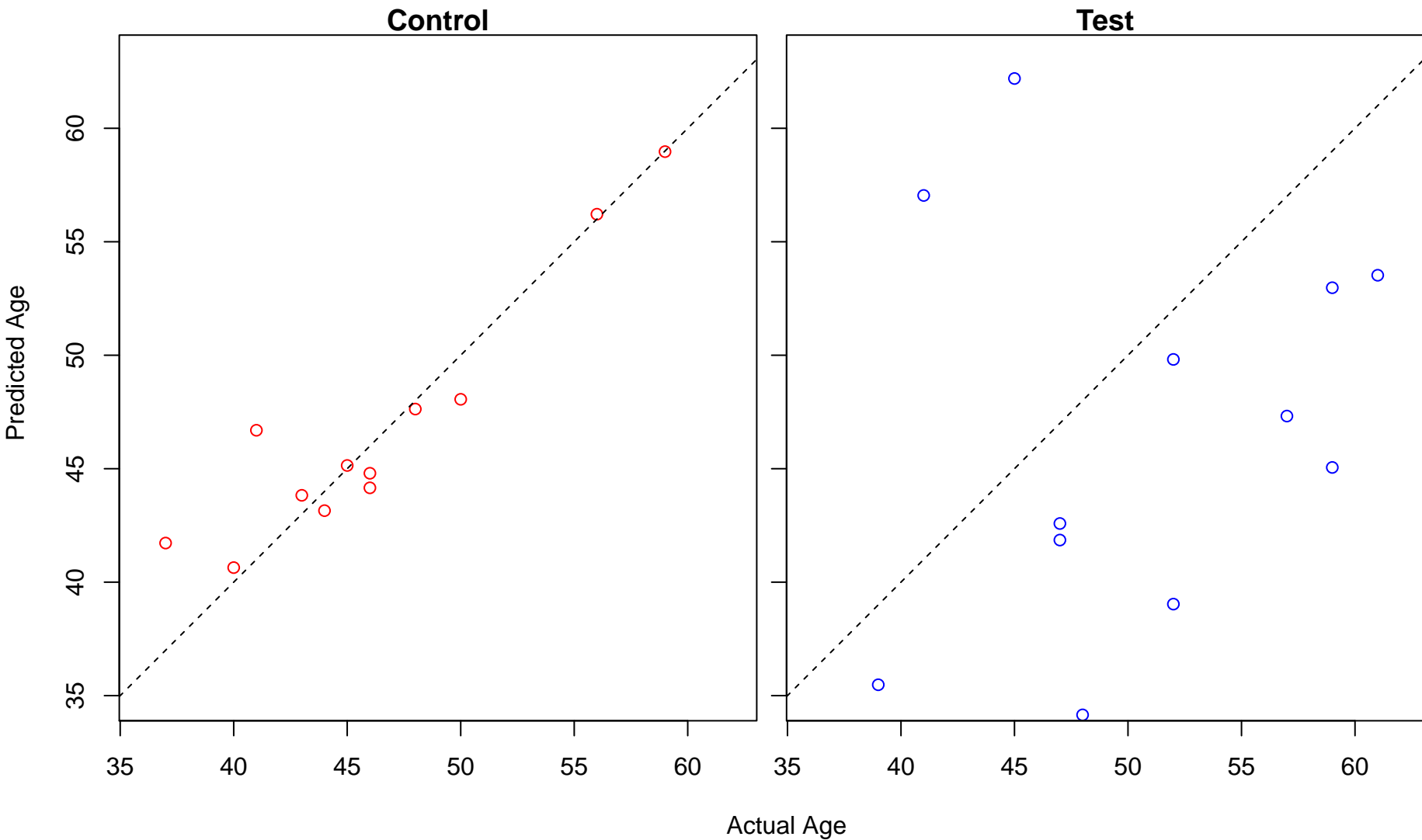
neuronal stem cell division (Score: 27.606054)



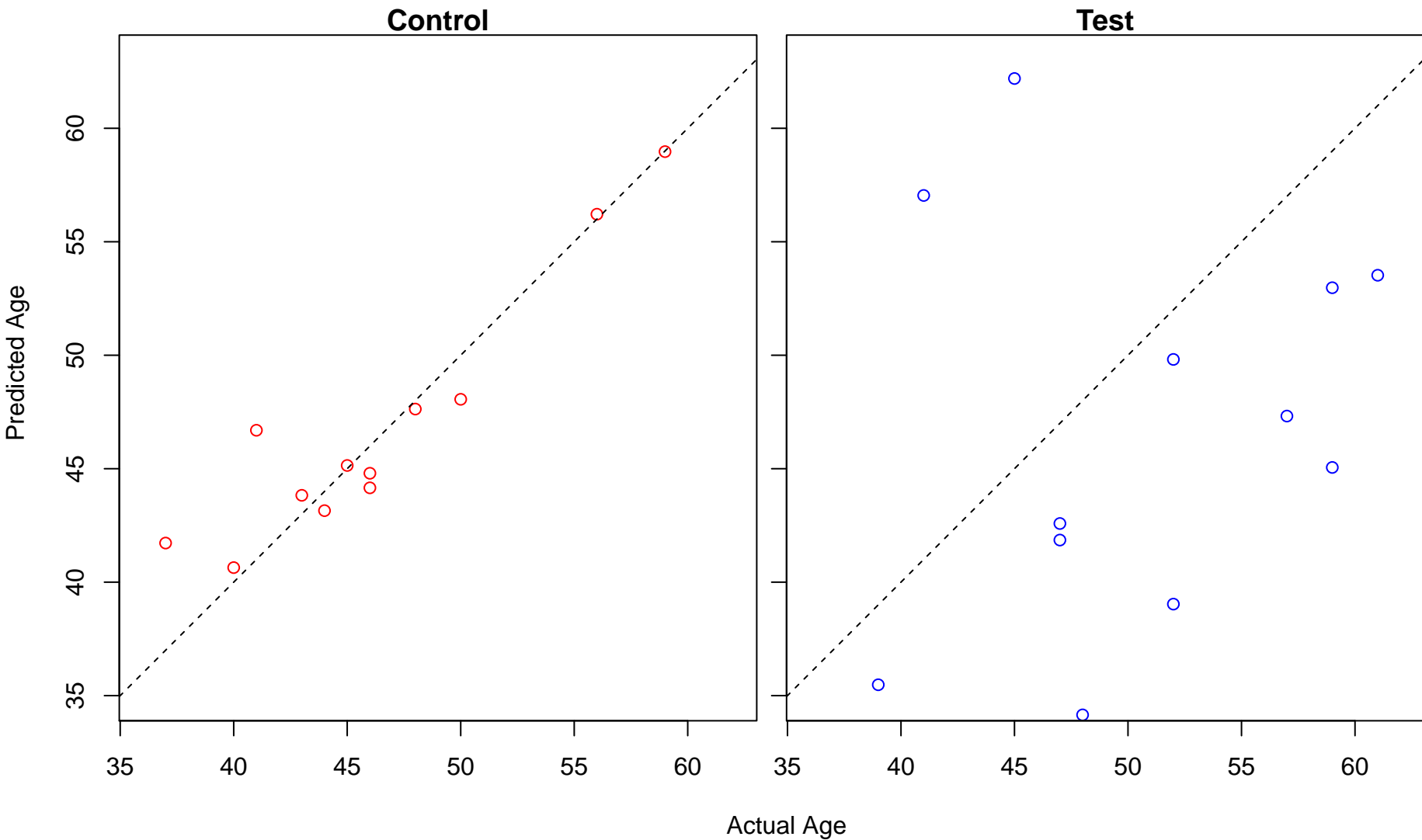
neuroblast division (Score: 27.606054)



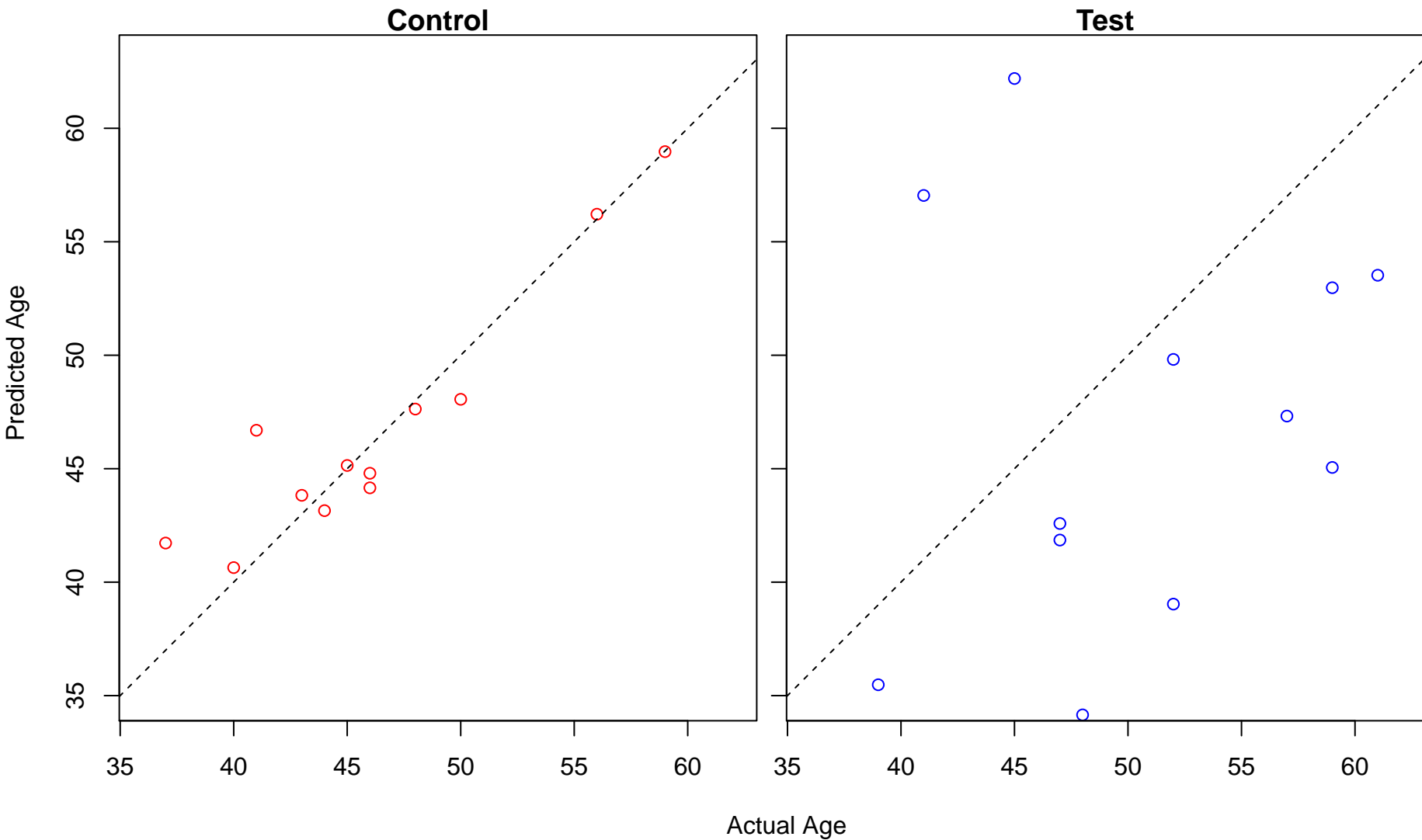
release of sequestered calcium ion into cytosol (Score: 27.580673)



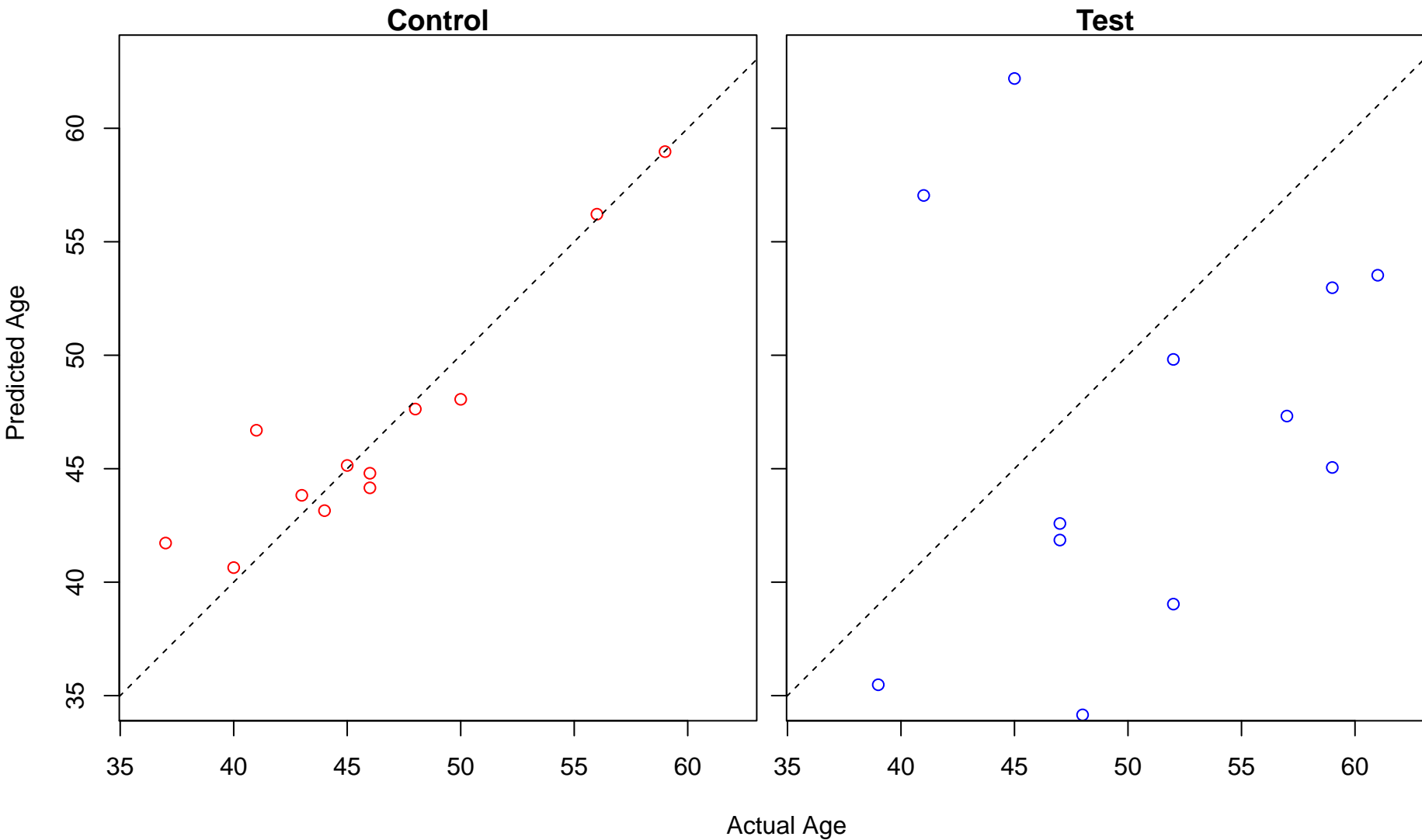
negative regulation of sequestering of calcium ion (Score: 27.580673)



calcium ion transmembrane import into cytosol (Score: 27.580673)

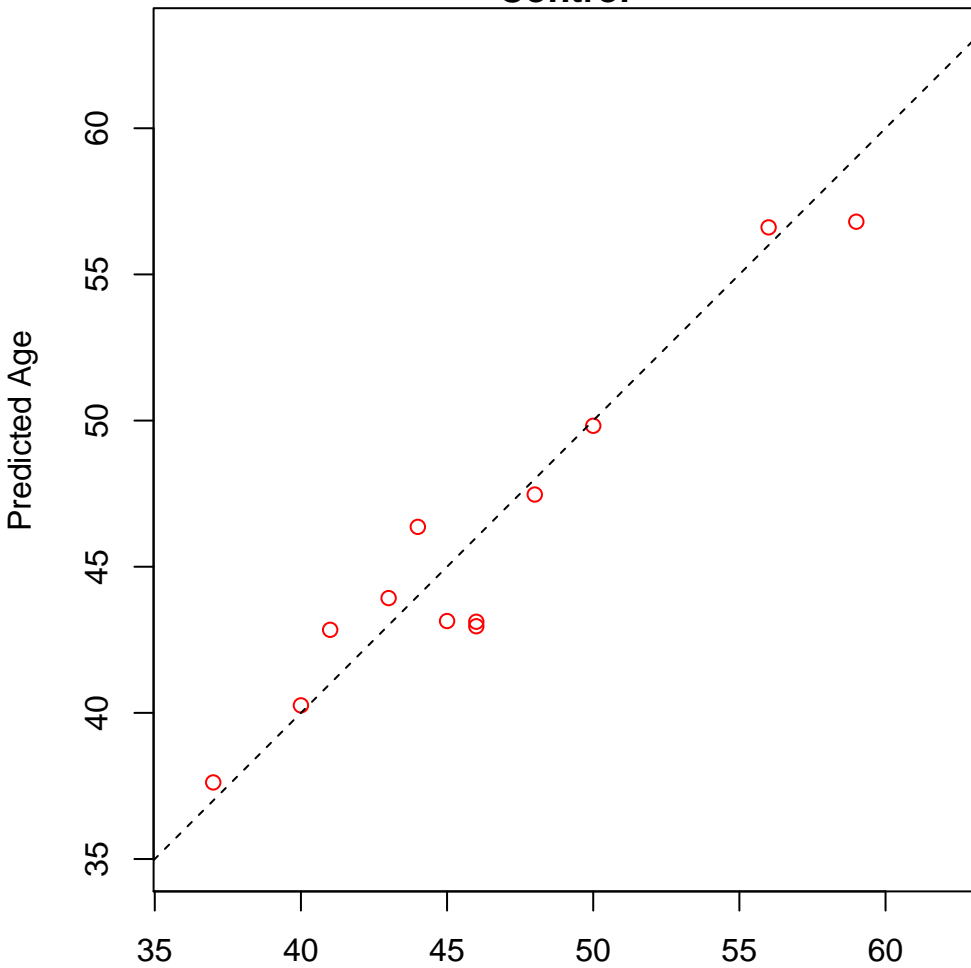


calcium ion import into cytosol (Score: 27.580673)

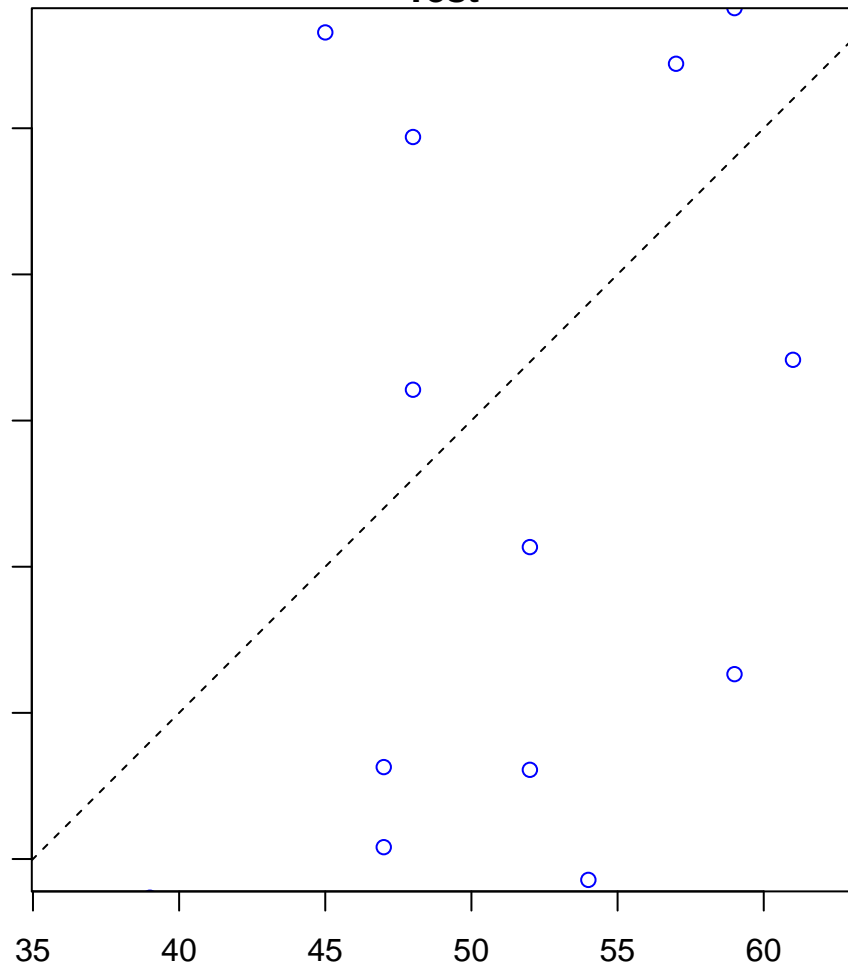


cellular response to external stimulus (Score: 27.554095)

Control

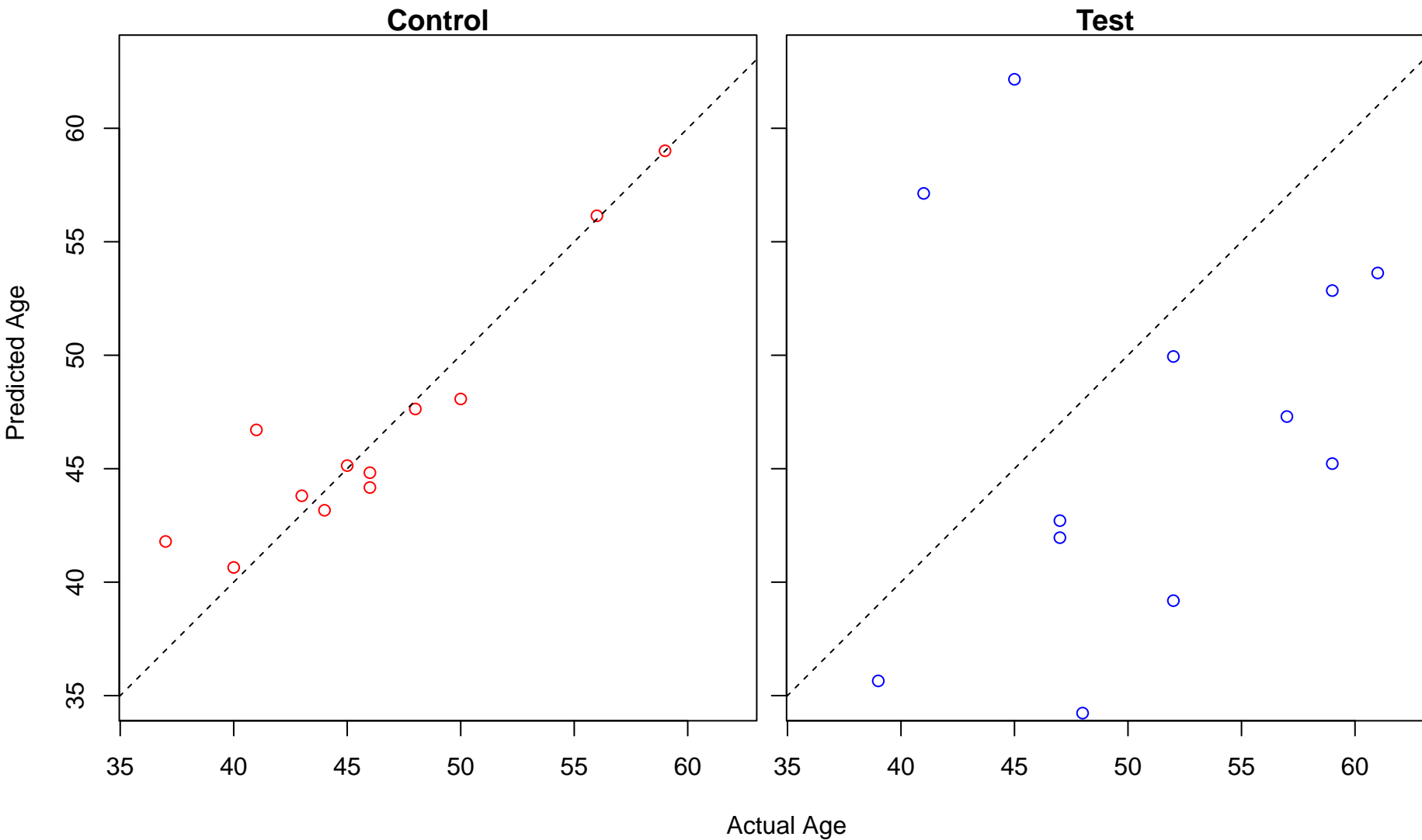


Test

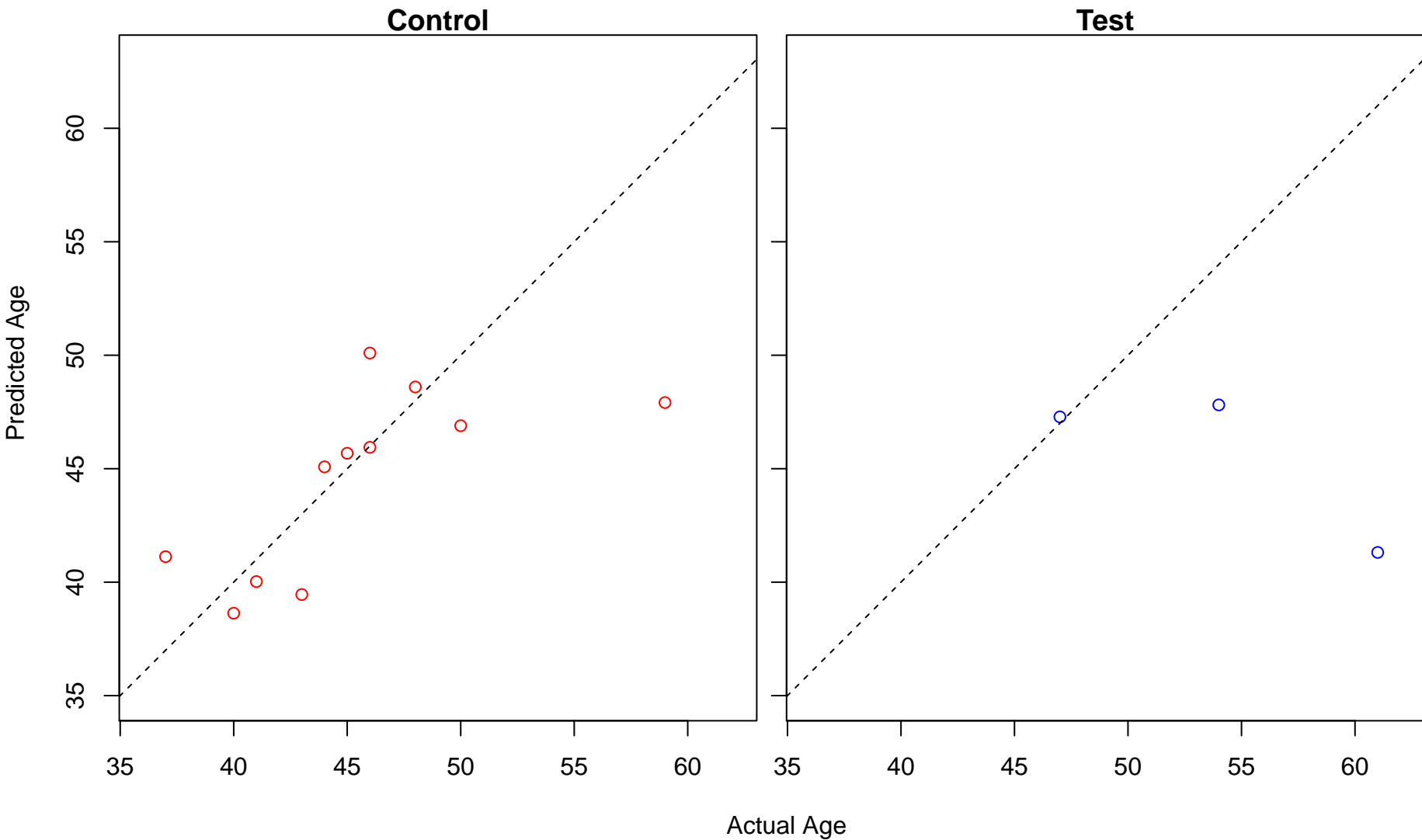


Actual Age

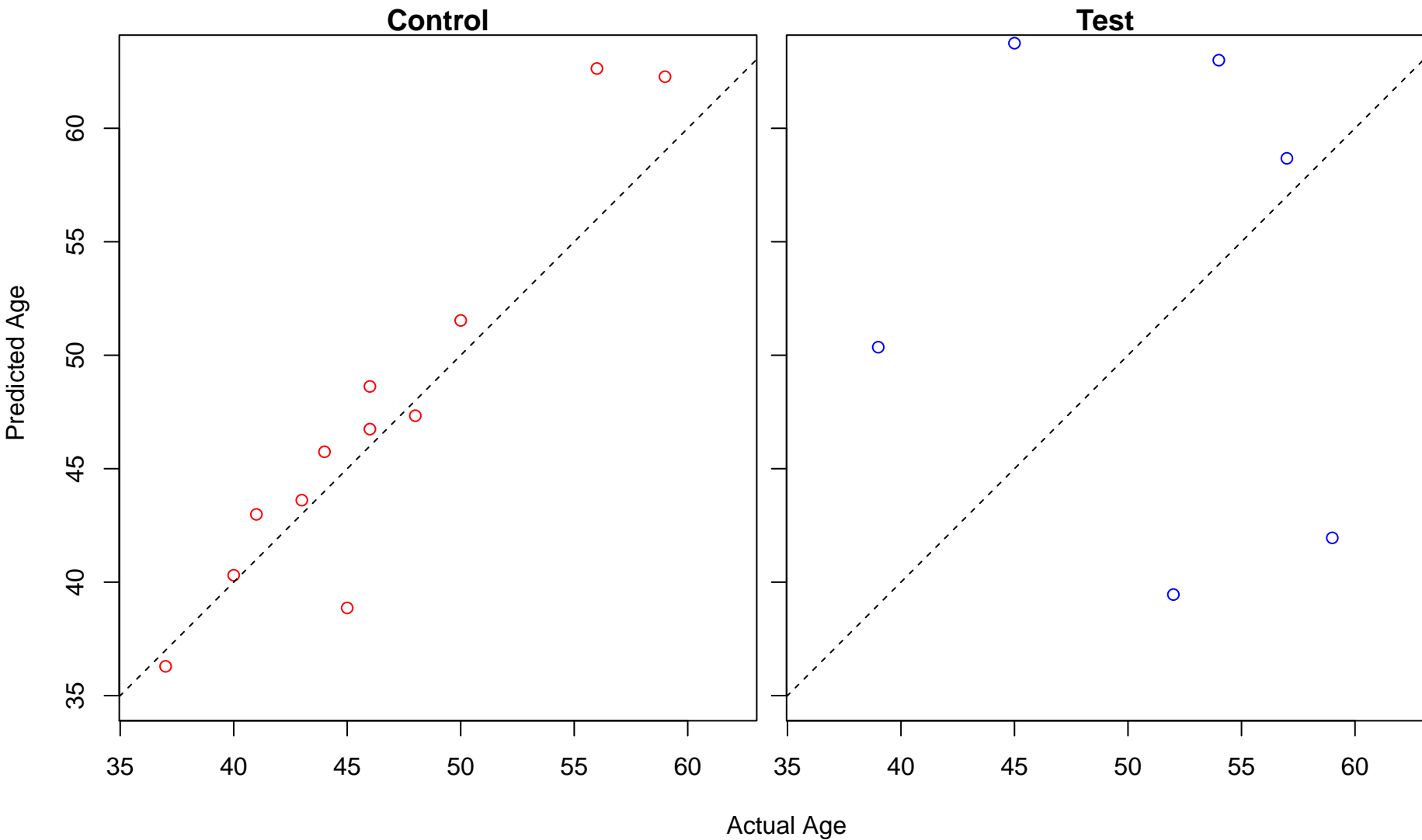
calcium ion transport into cytosol (Score: 27.456417)



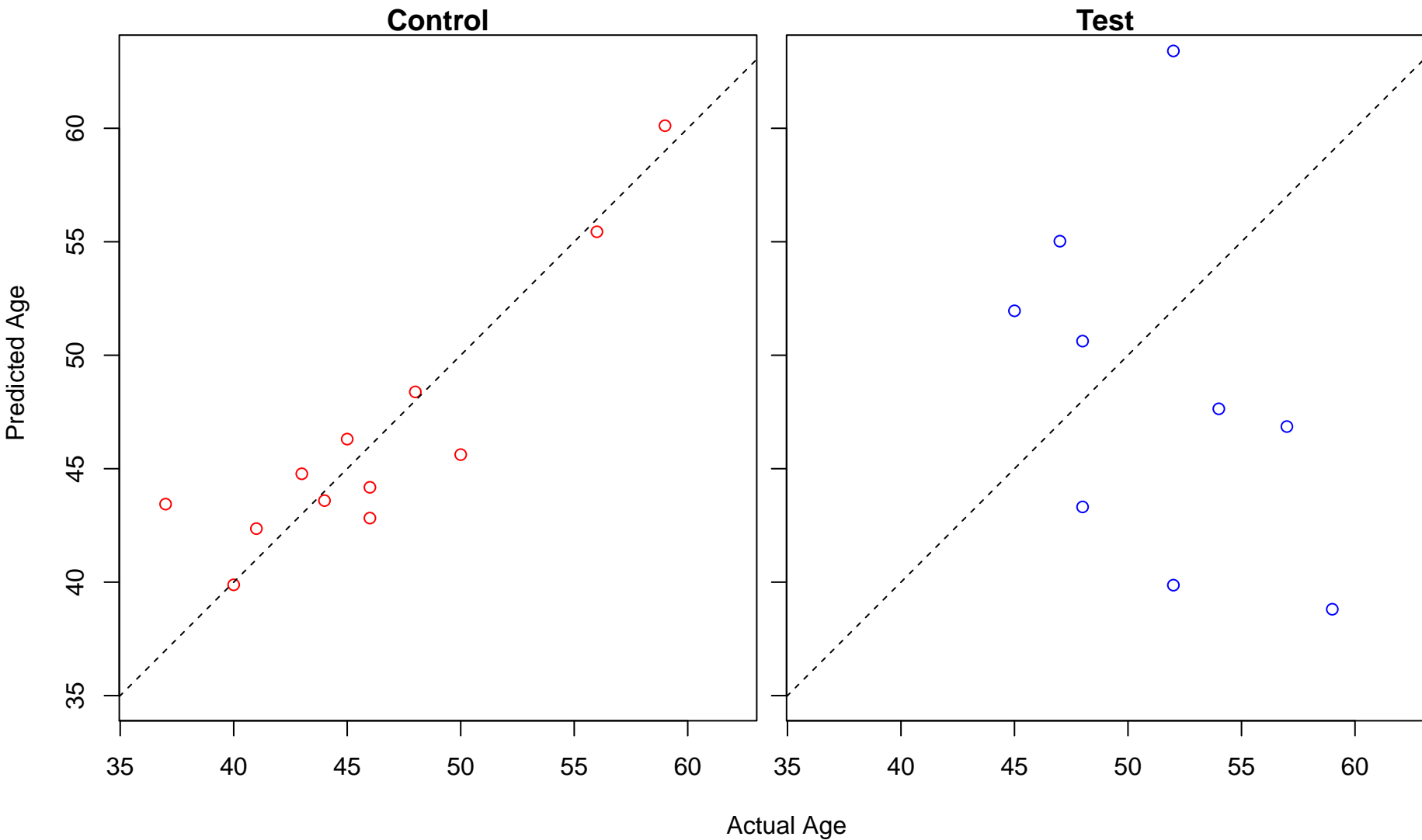
detection of chemical stimulus involved in sensory perception of bitter taste (Score: 27.415417)



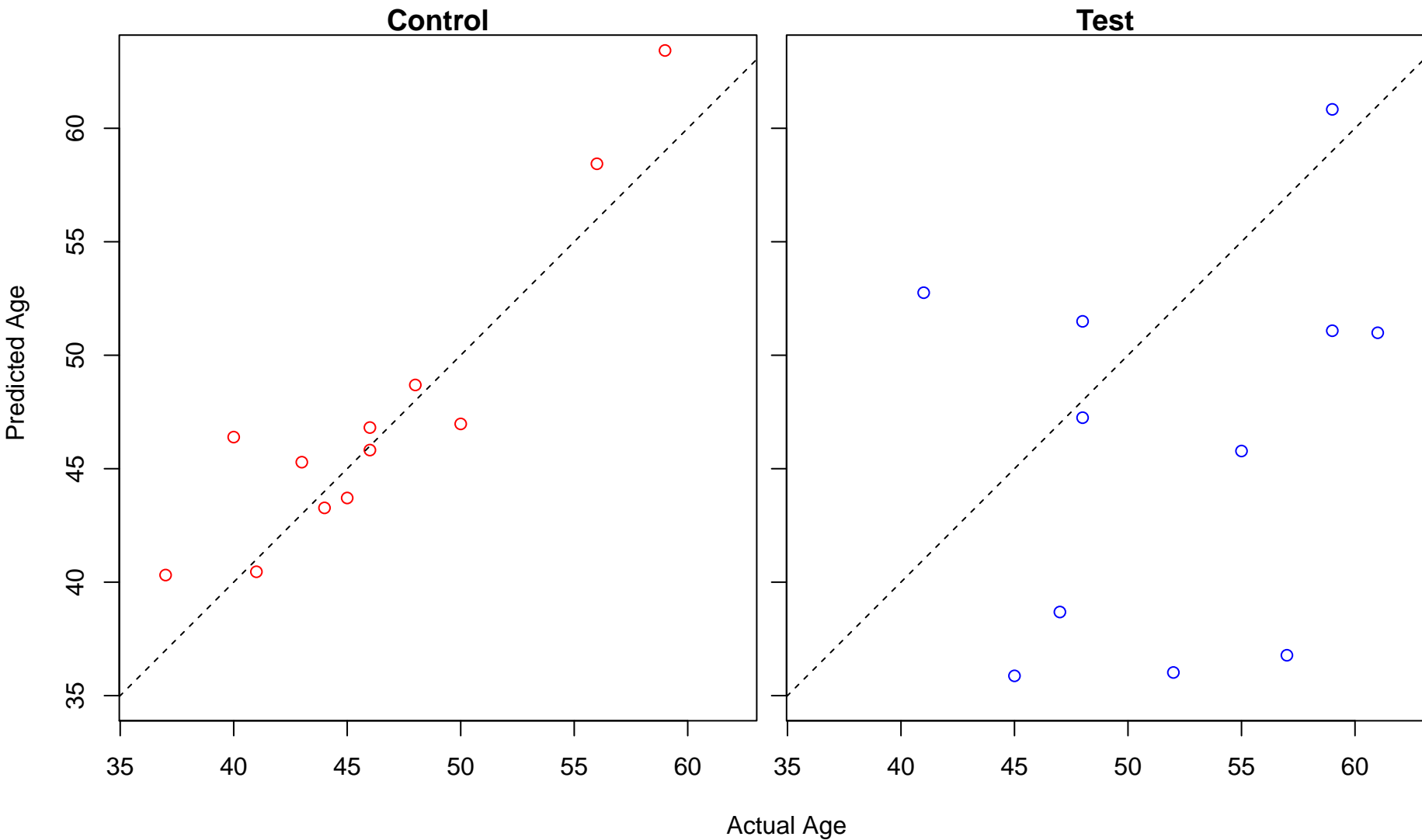
definitive hemopoiesis (Score: 27.356230)



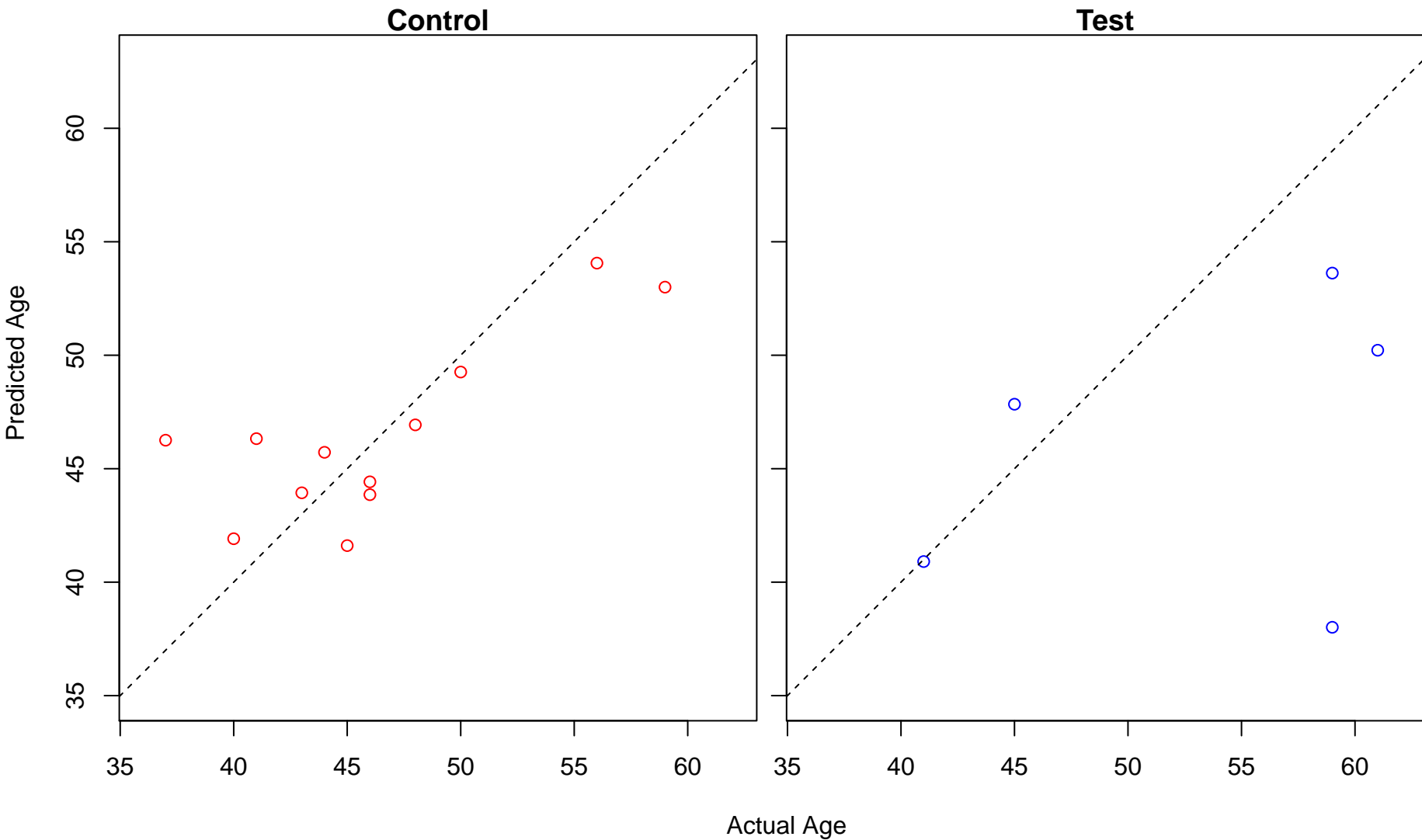
protein deubiquitination (Score: 27.284941)



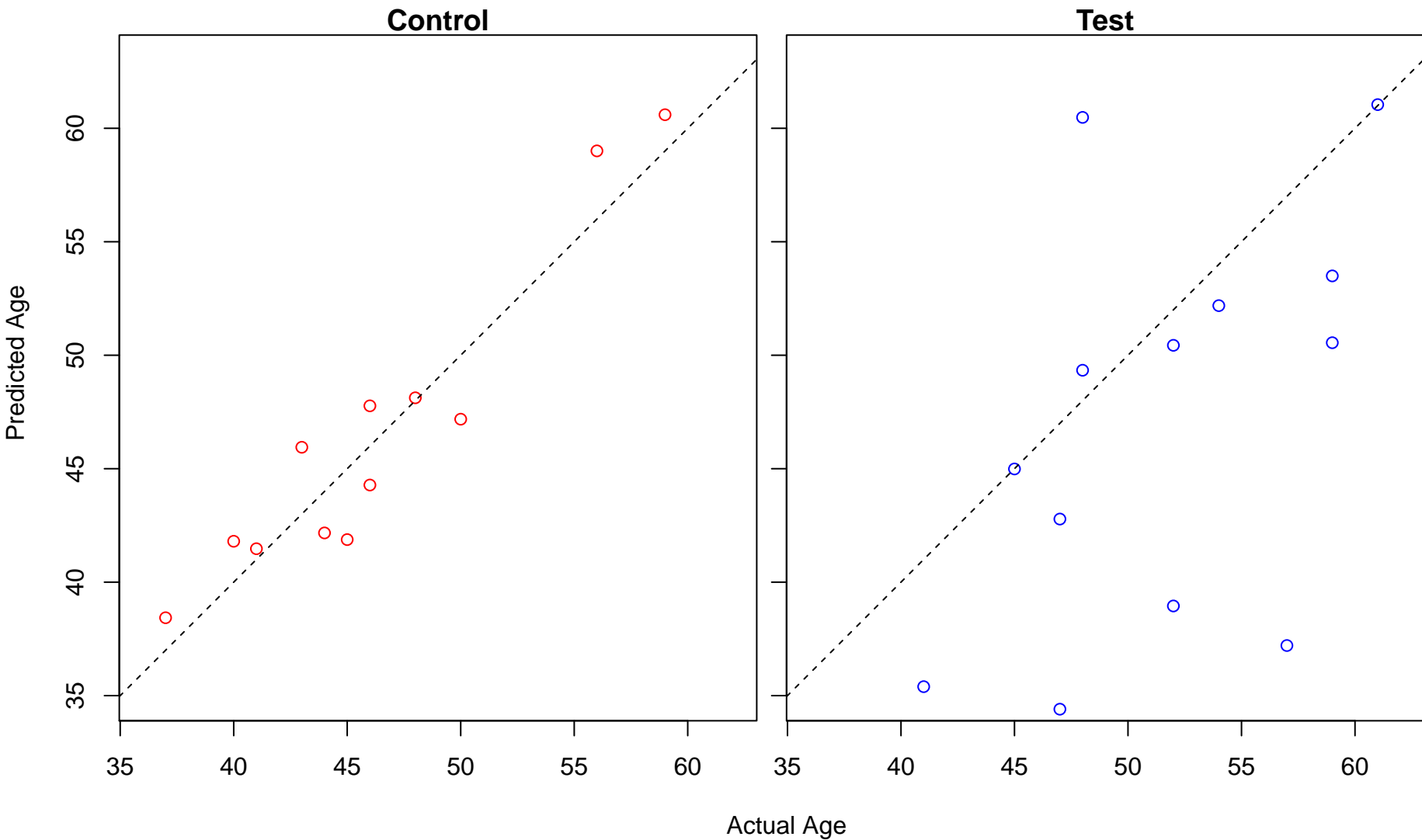
neuron death (Score: 27.065675)



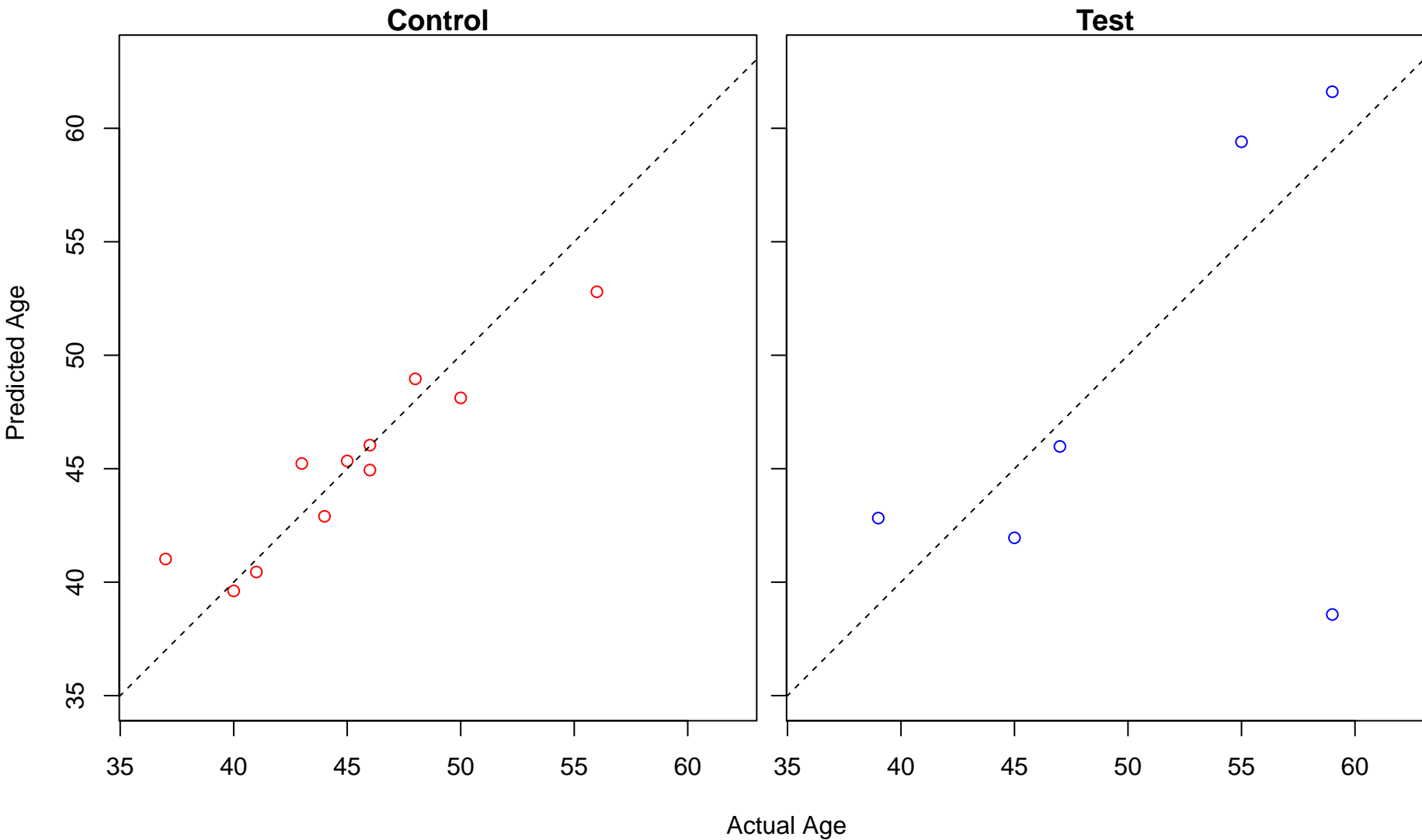
hyaluronan catabolic process (Score: 27.001044)



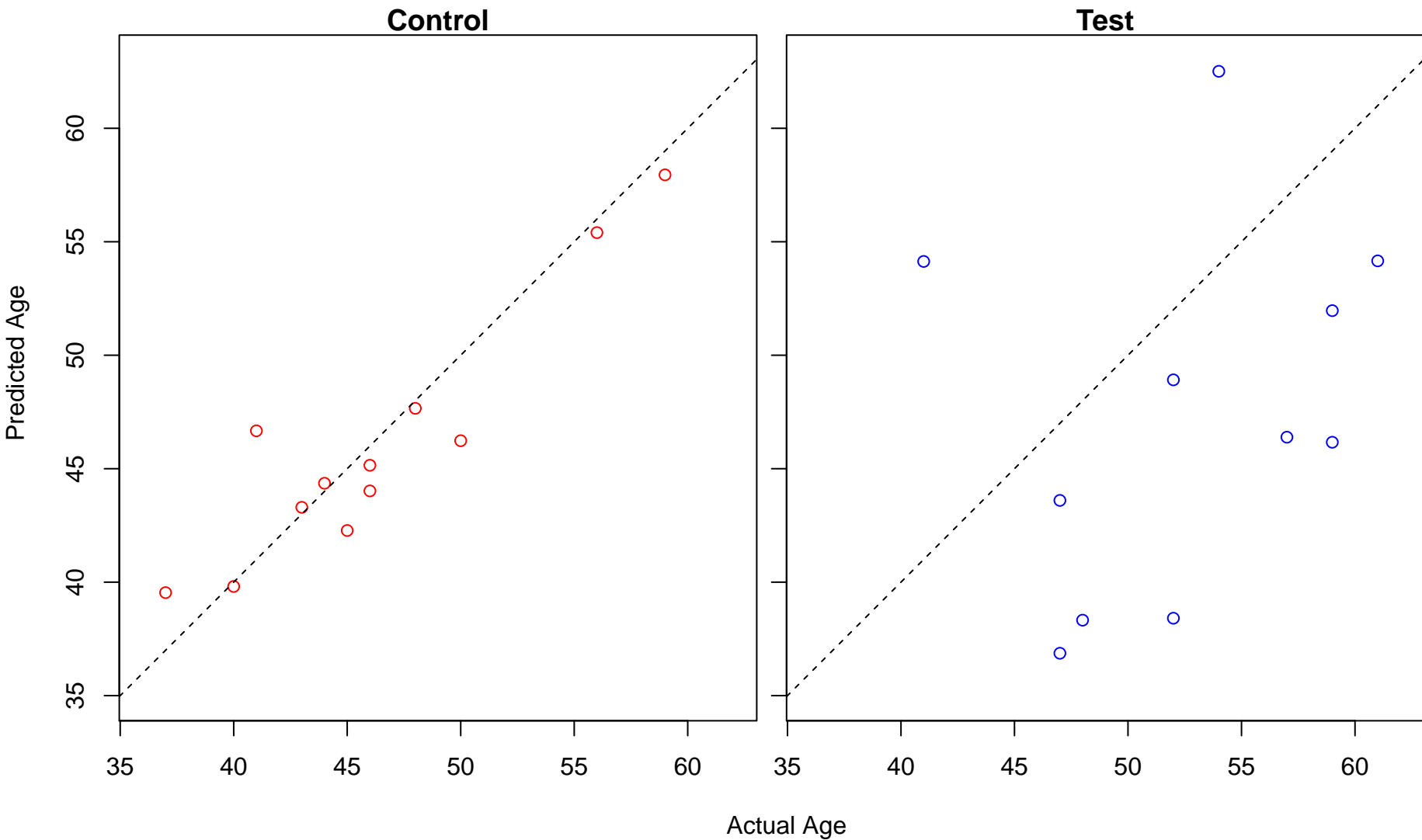
dendritic spine organization (Score: 26.918226)



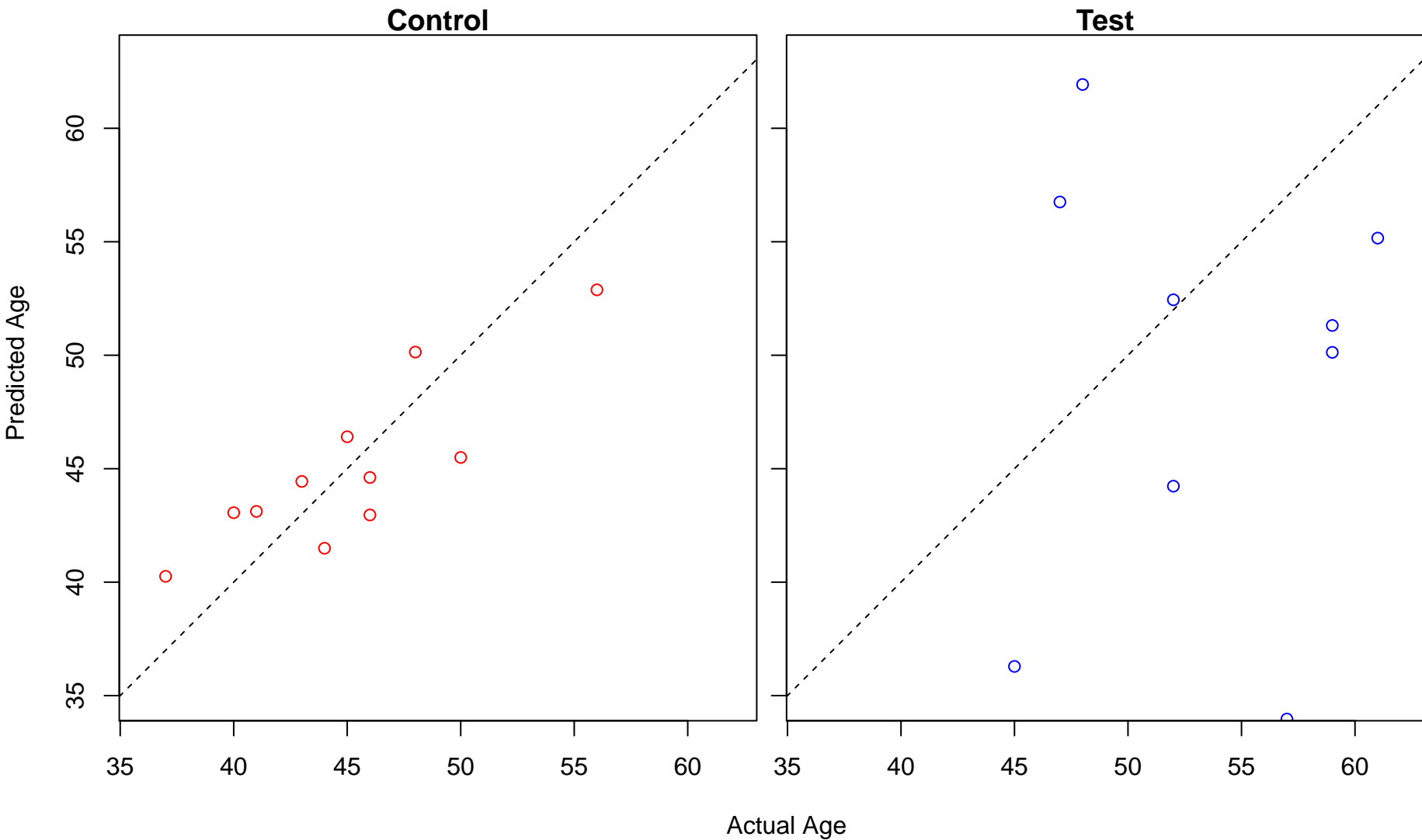
cytoskeletal anchoring at nuclear membrane (Score: 26.837858)



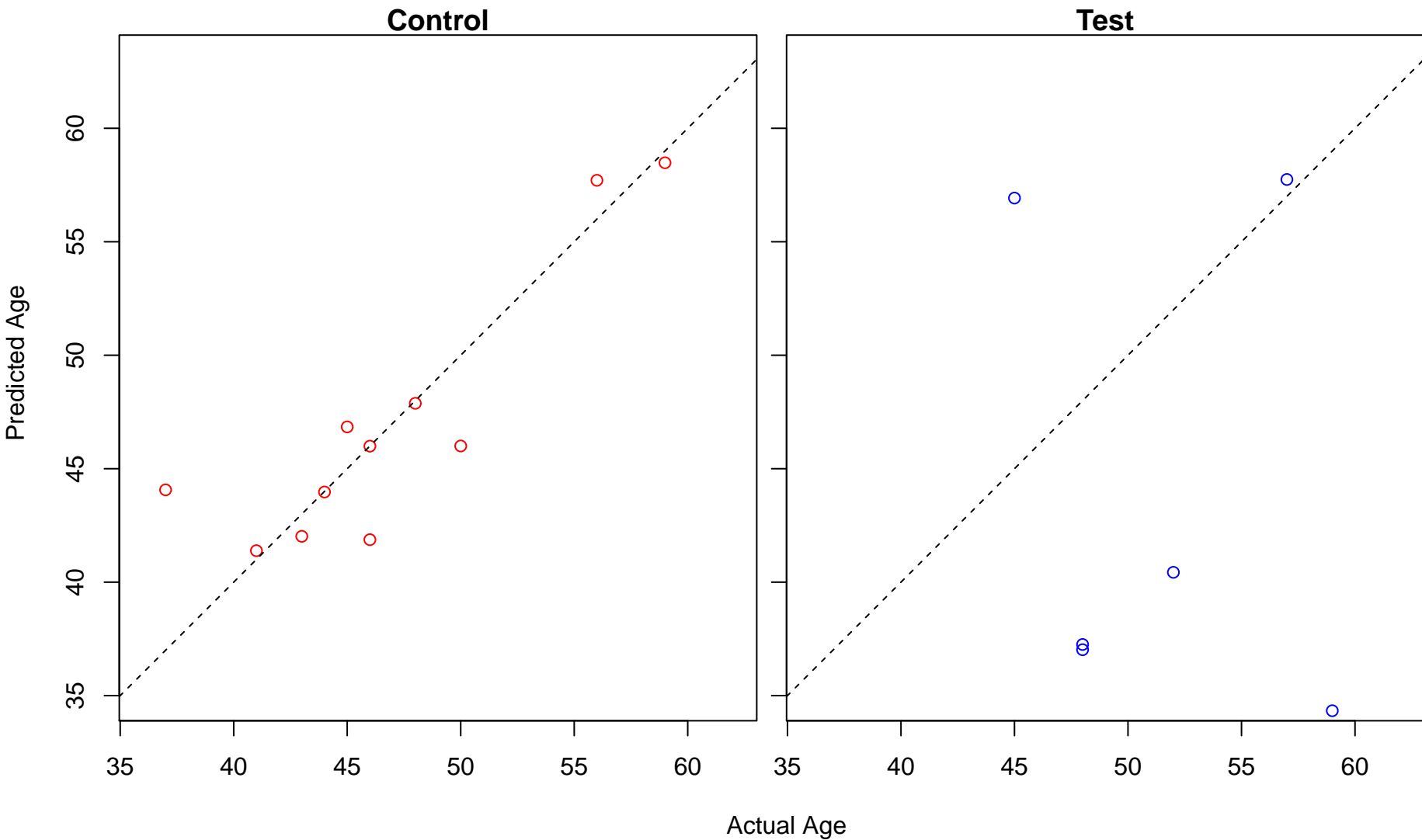
cytosolic calcium ion transport (Score: 26.682629)



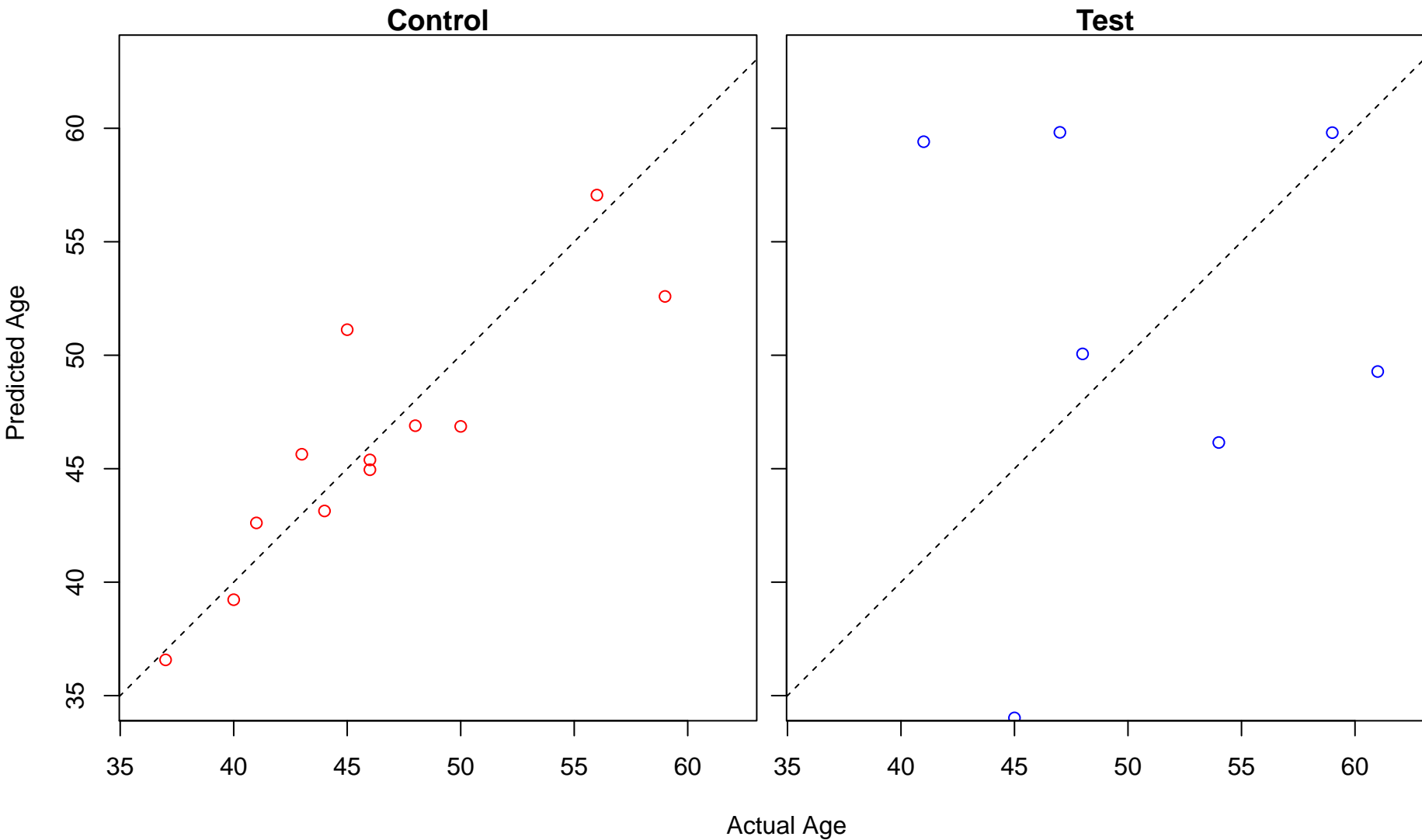
negative regulation of dendrite morphogenesis (Score: 26.617675)



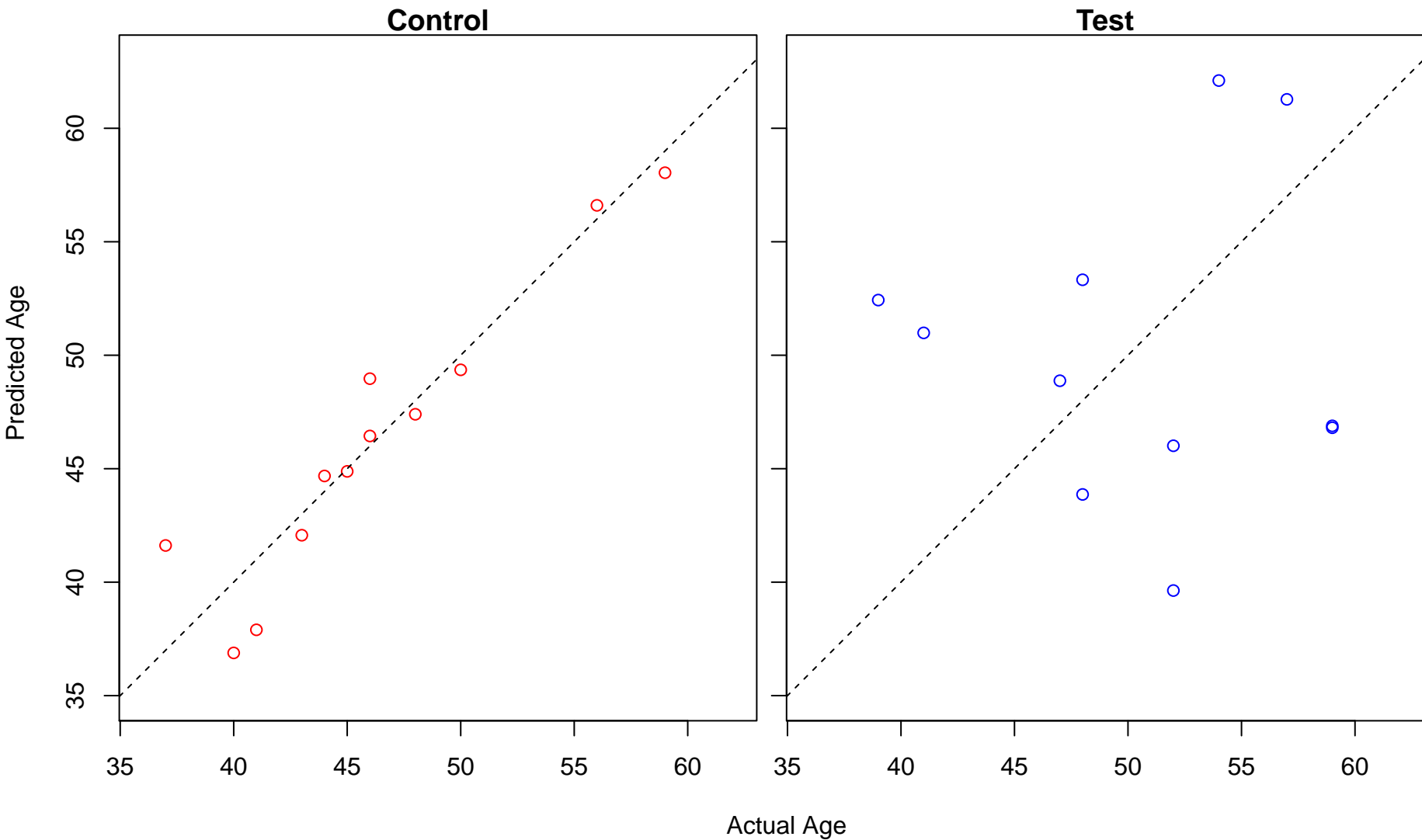
macrophage chemotaxis (Score: 26.456137)



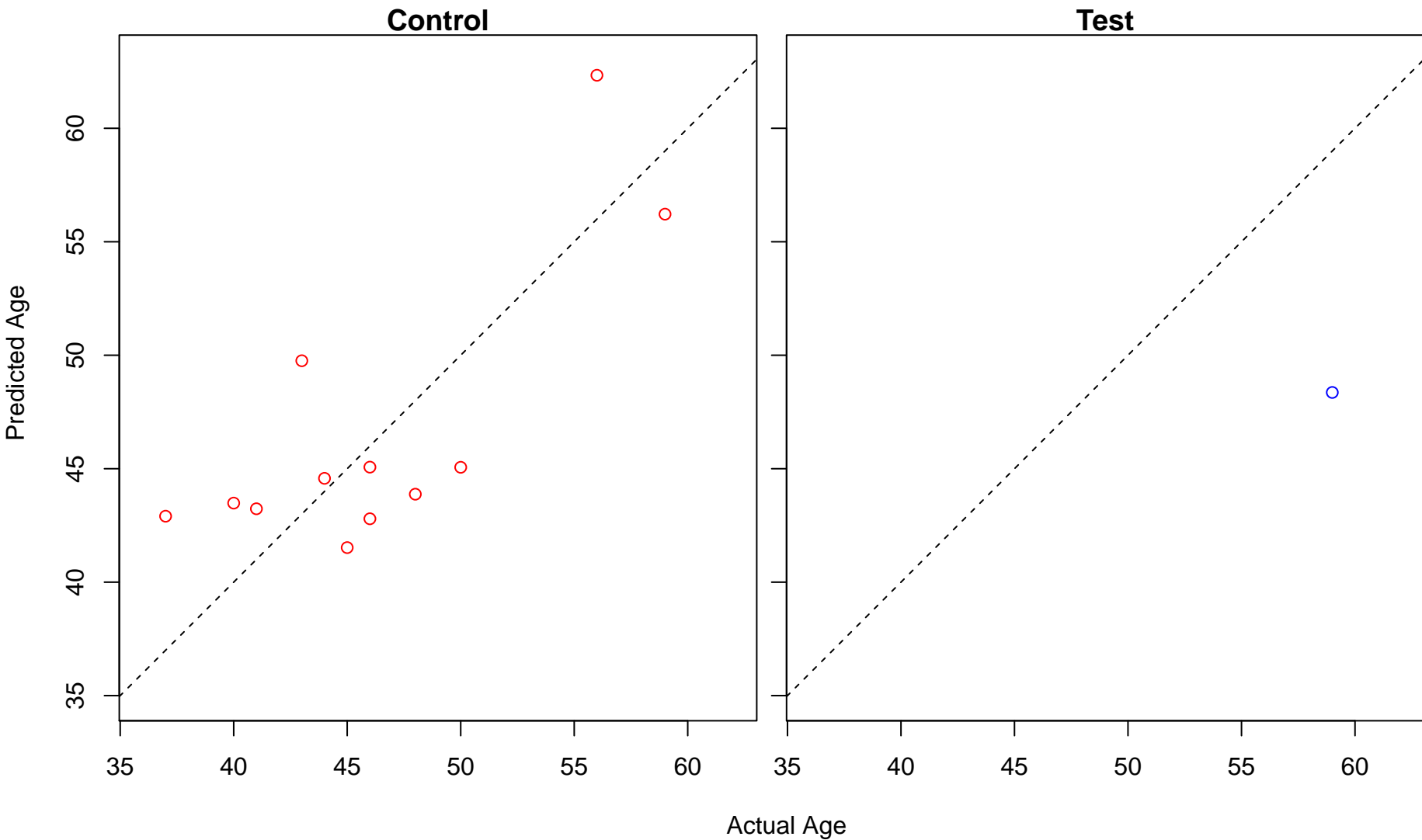
positive regulation of oxidative stress-induced cell death (Score: 26.451923)



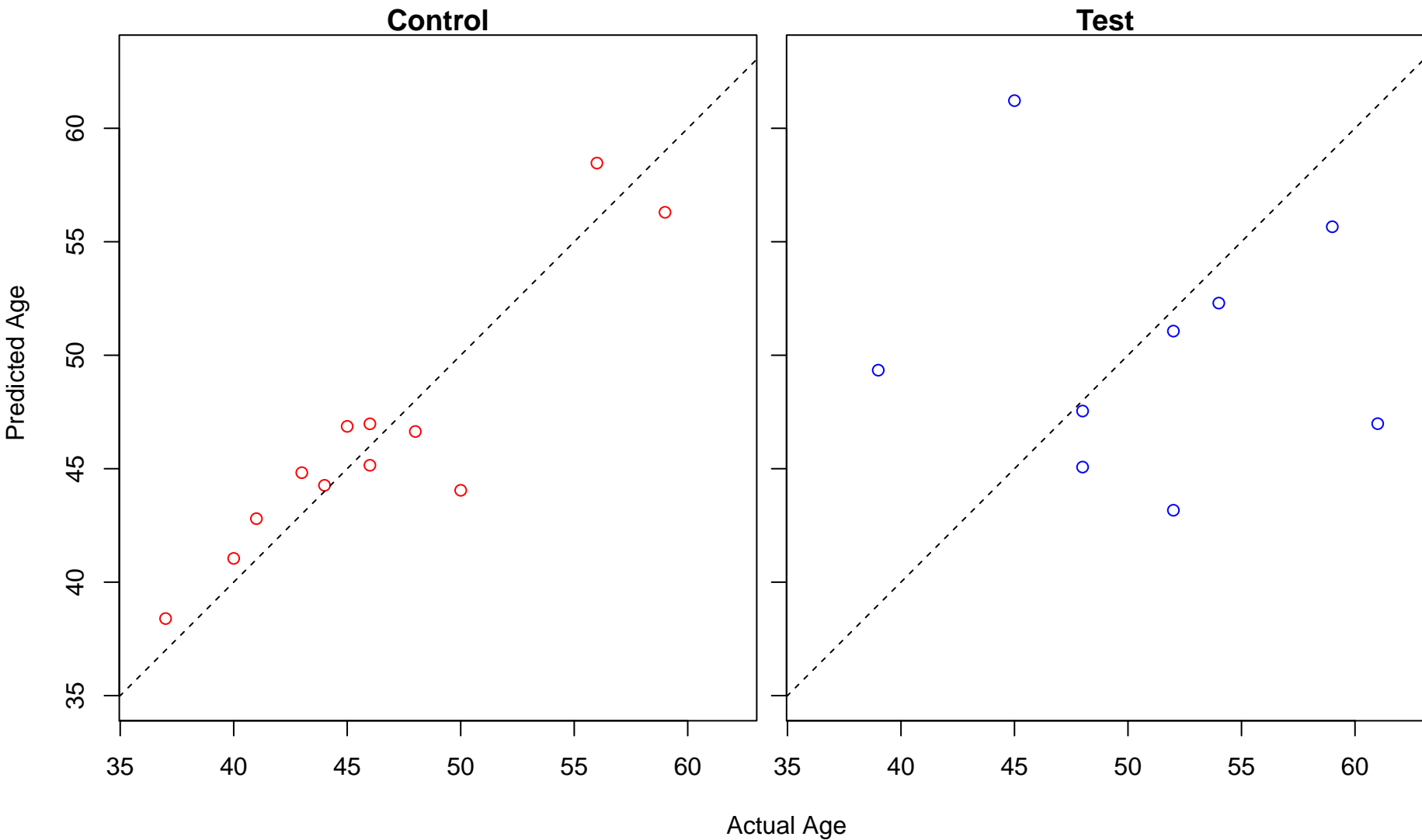
regulation of T cell apoptotic process (Score: 26.247995)



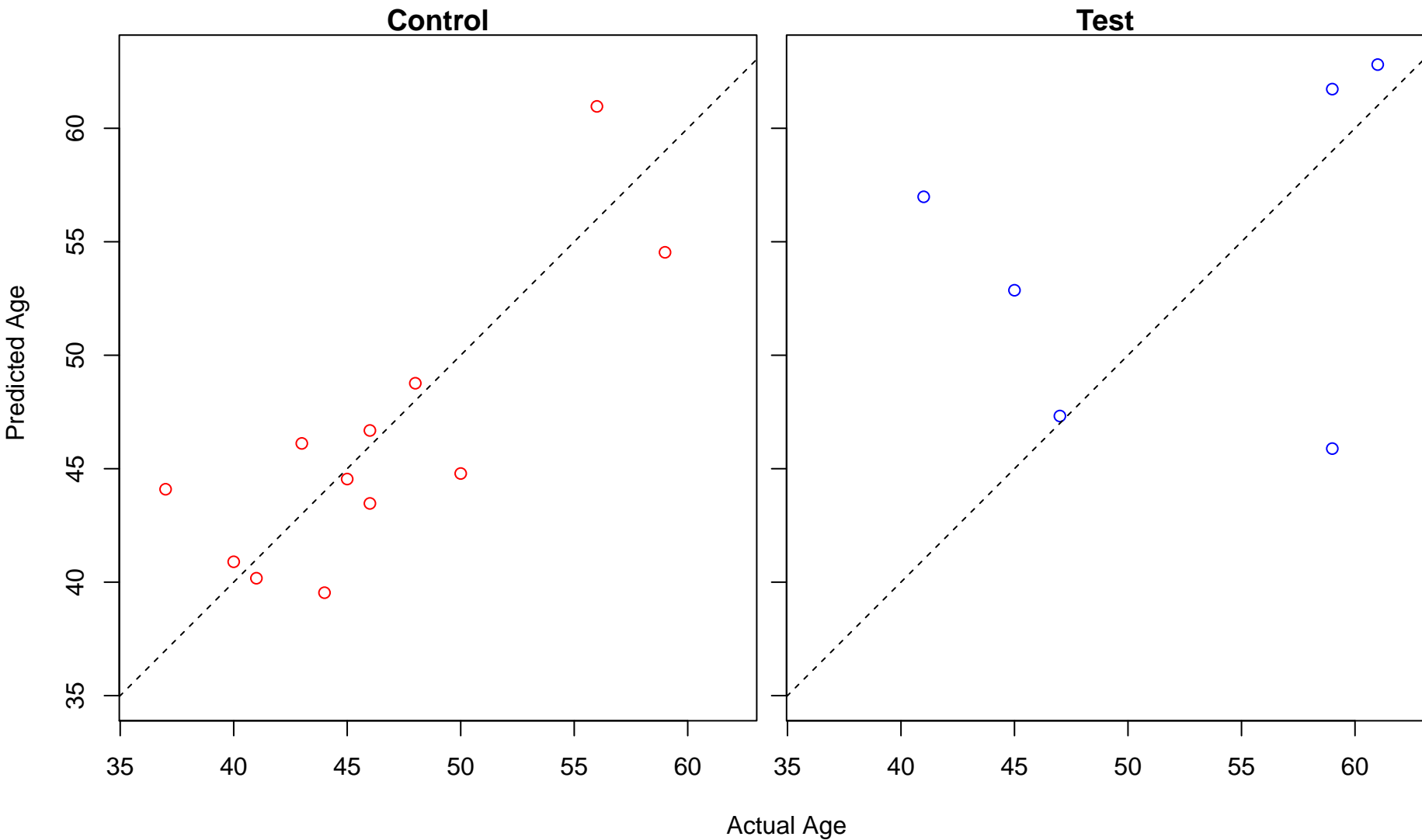
enteric nervous system development (Score: 26.023711)



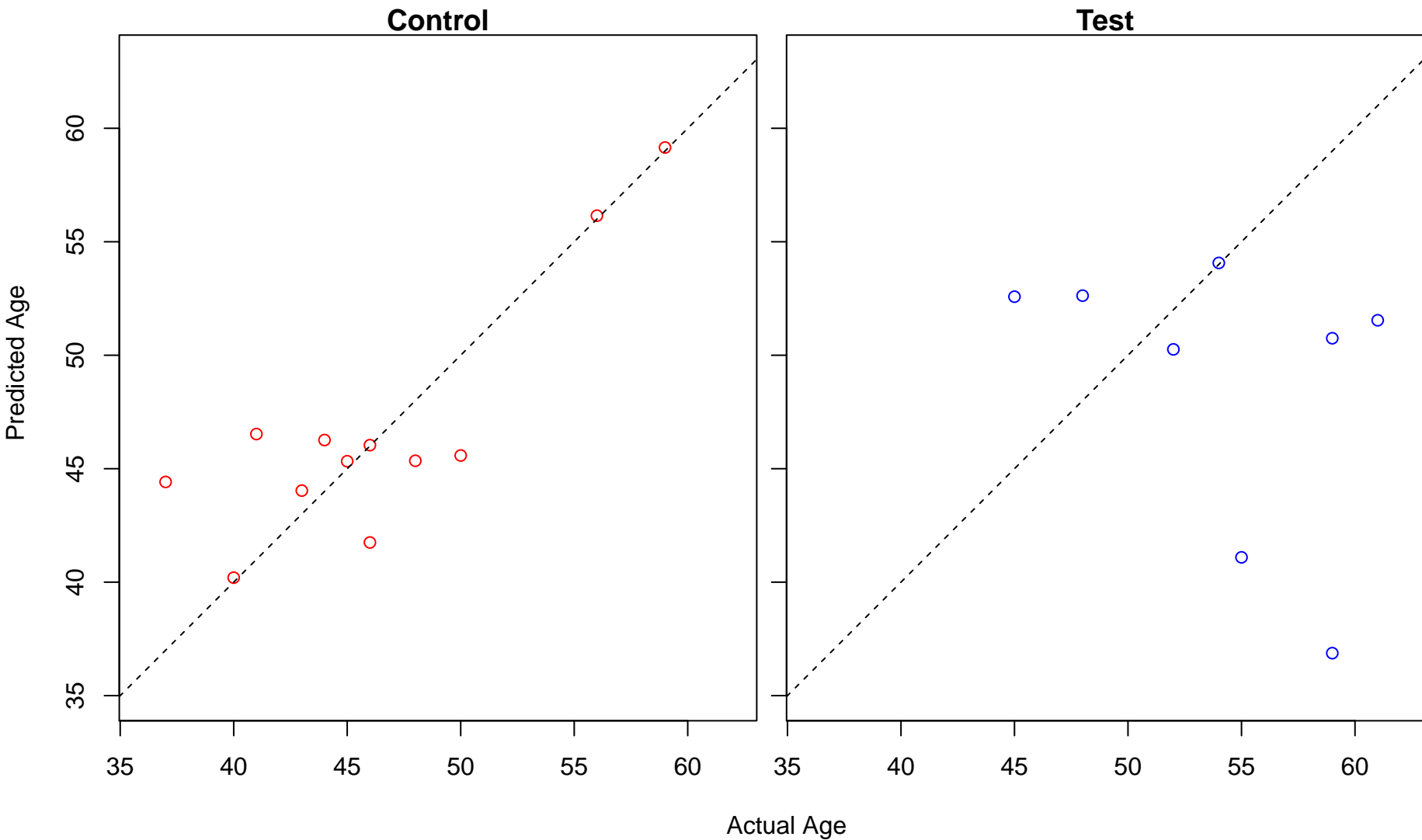
negative regulation of immune response (Score: 25.932438)



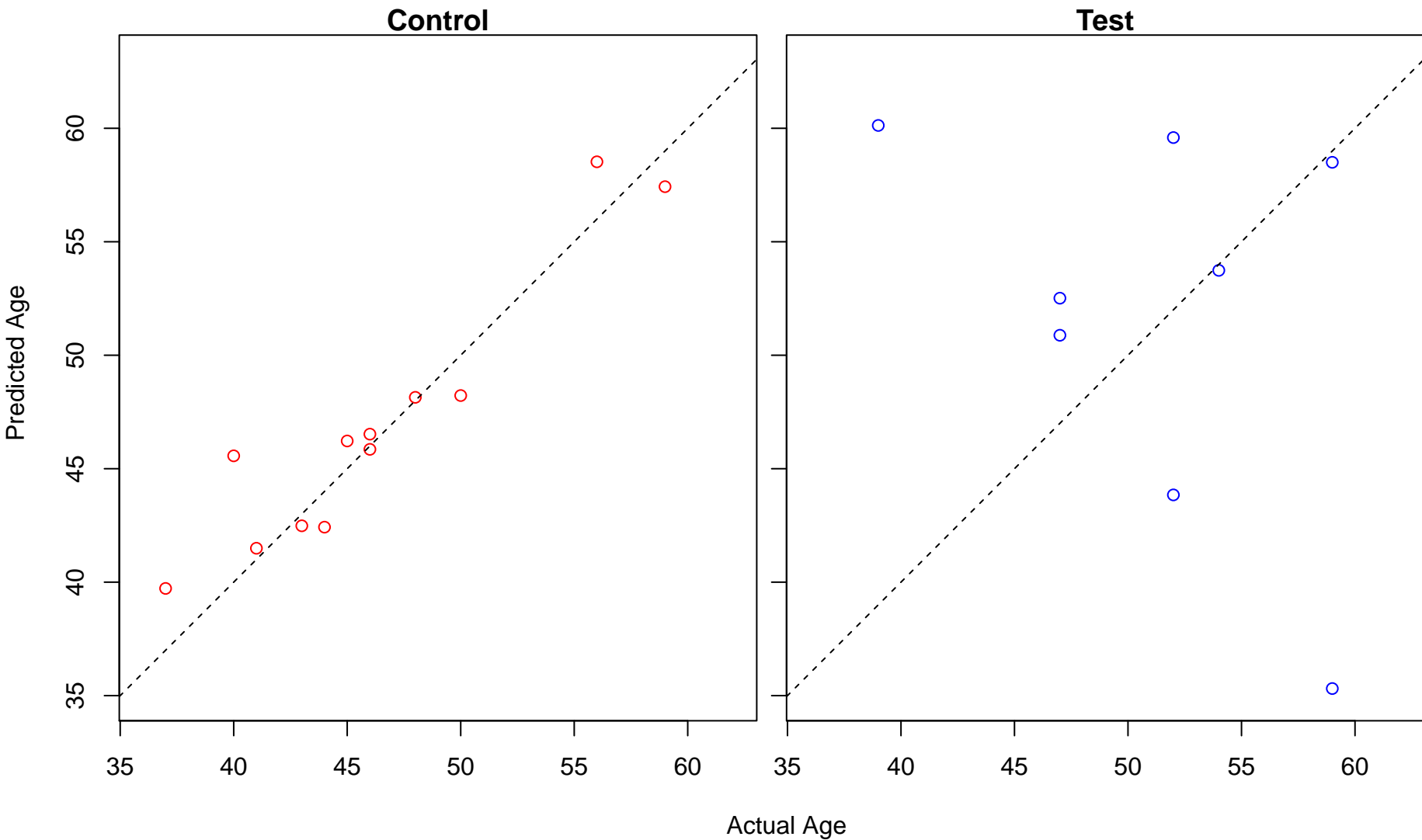
negative regulation of insulin receptor signaling pathway (Score: 25.927778)



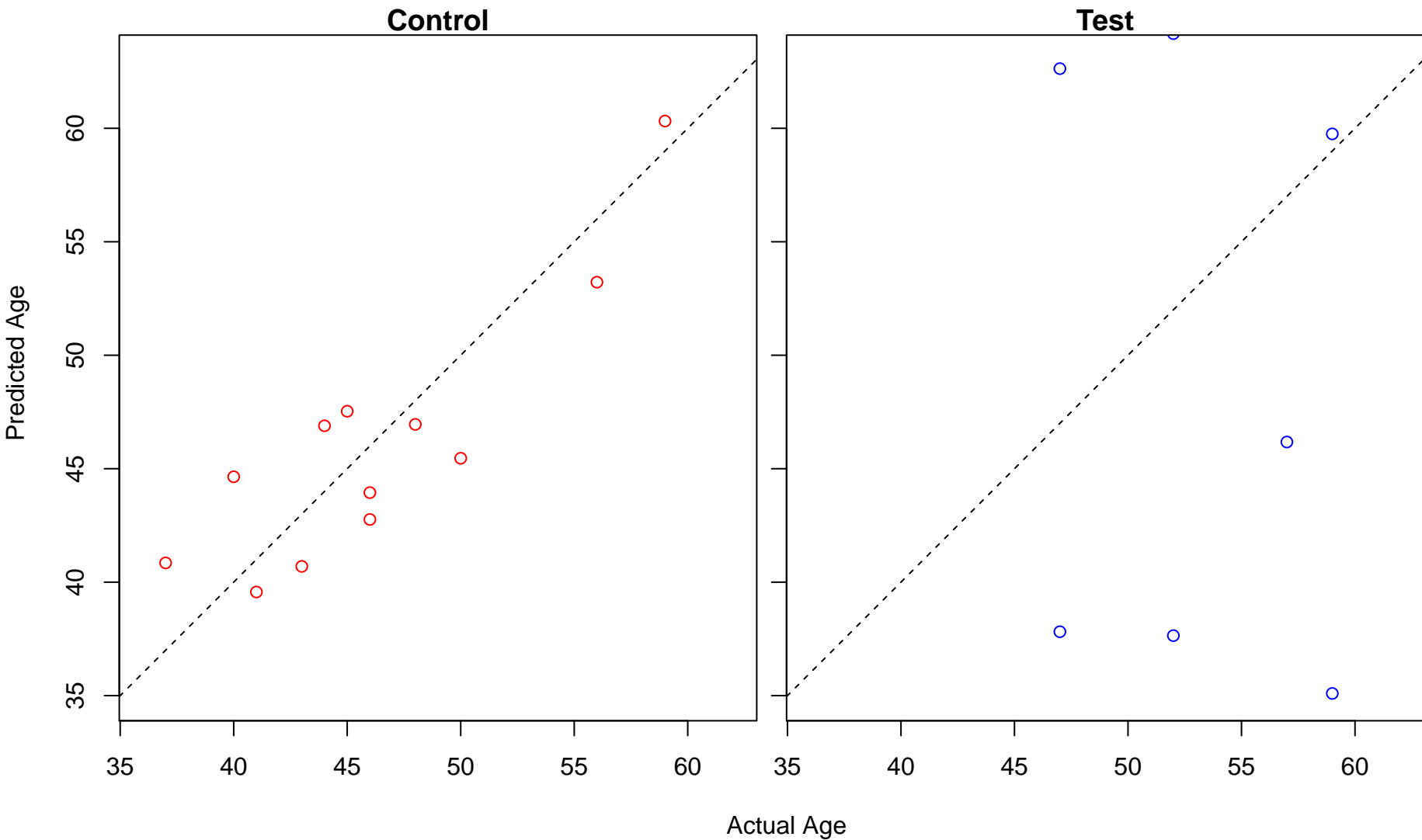
regulation of toll-like receptor signaling pathway (Score: 25.797382)



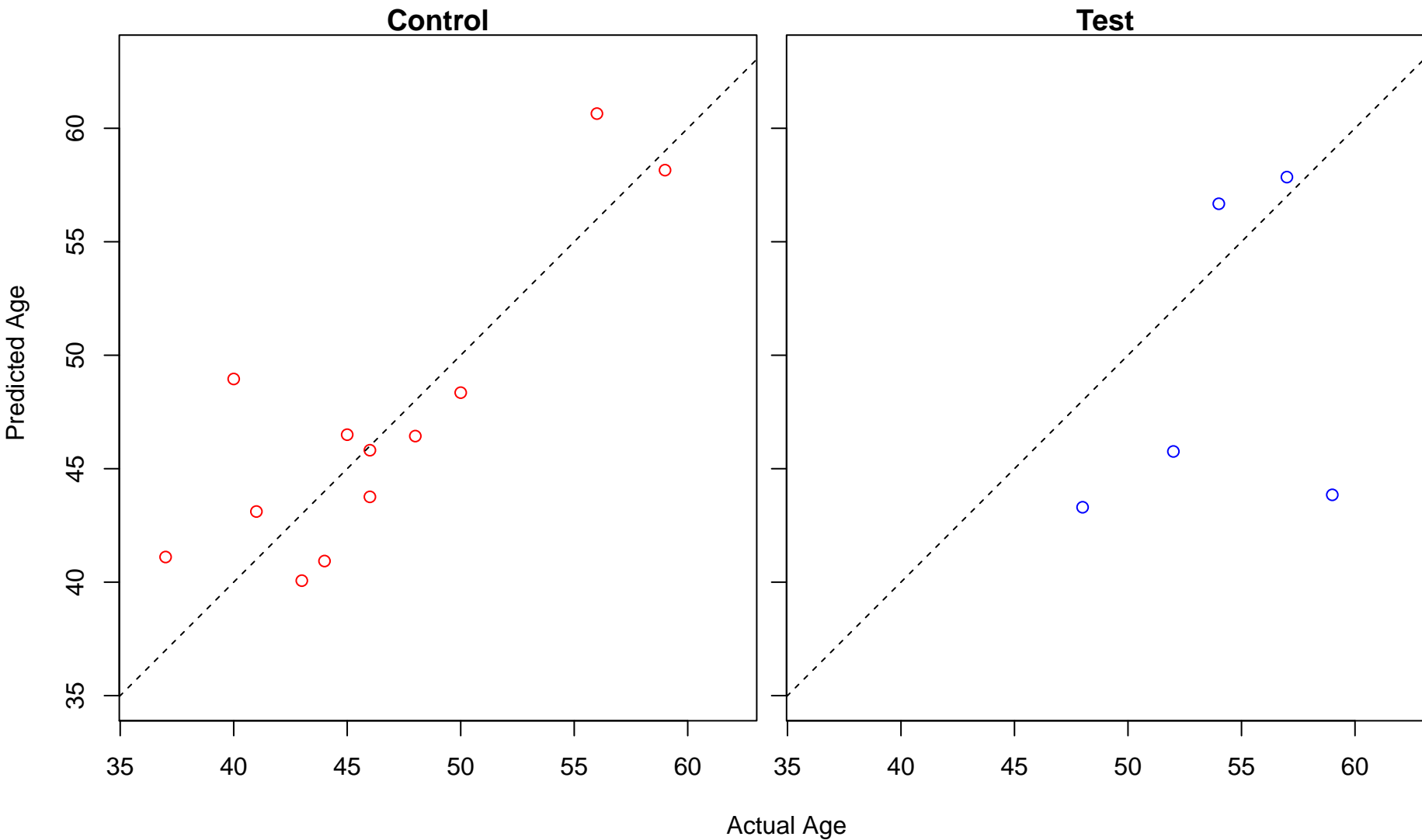
cytokine production involved in immune response (Score: 25.779193)



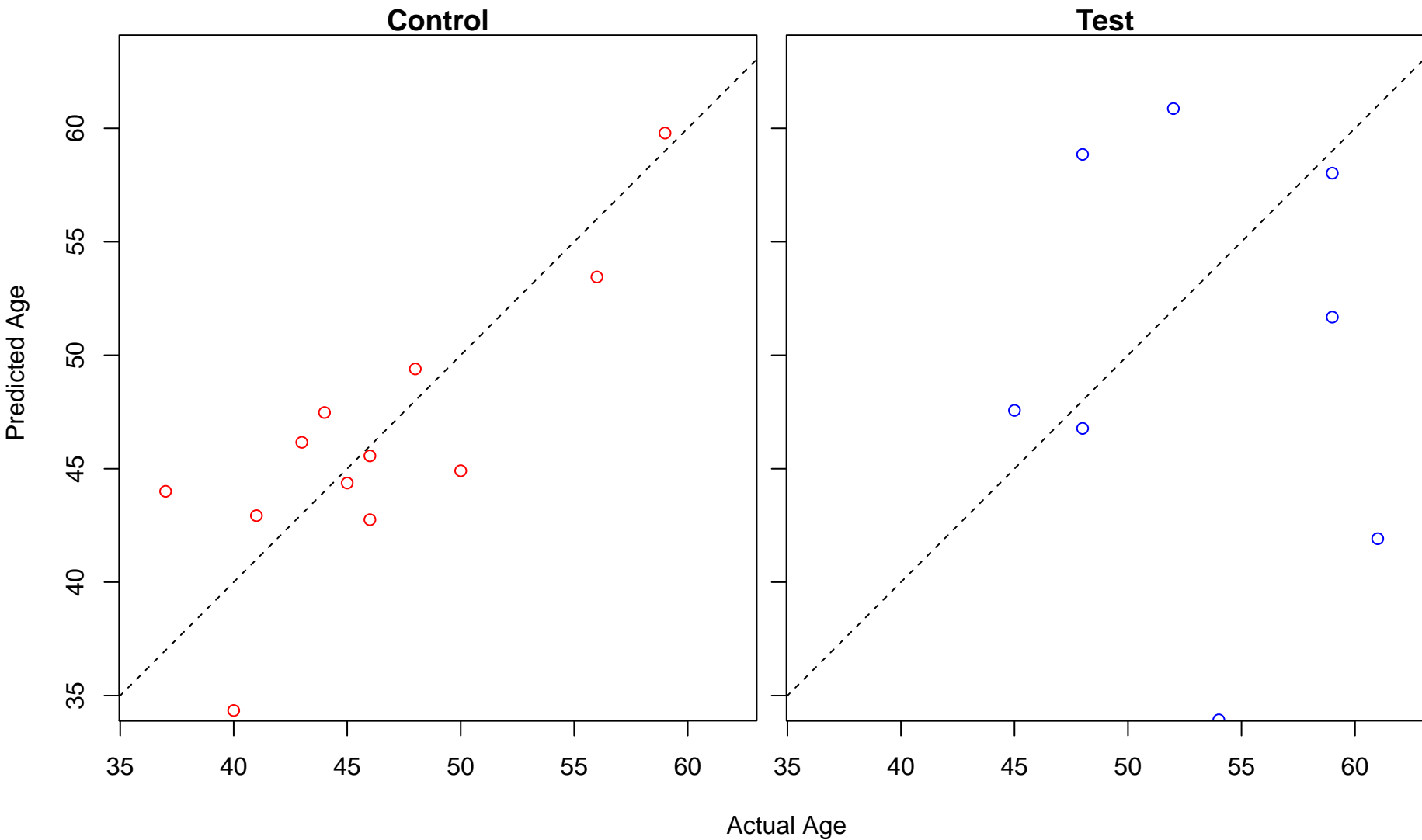
negative regulation of Rho protein signal transduction (Score: 25.615548)



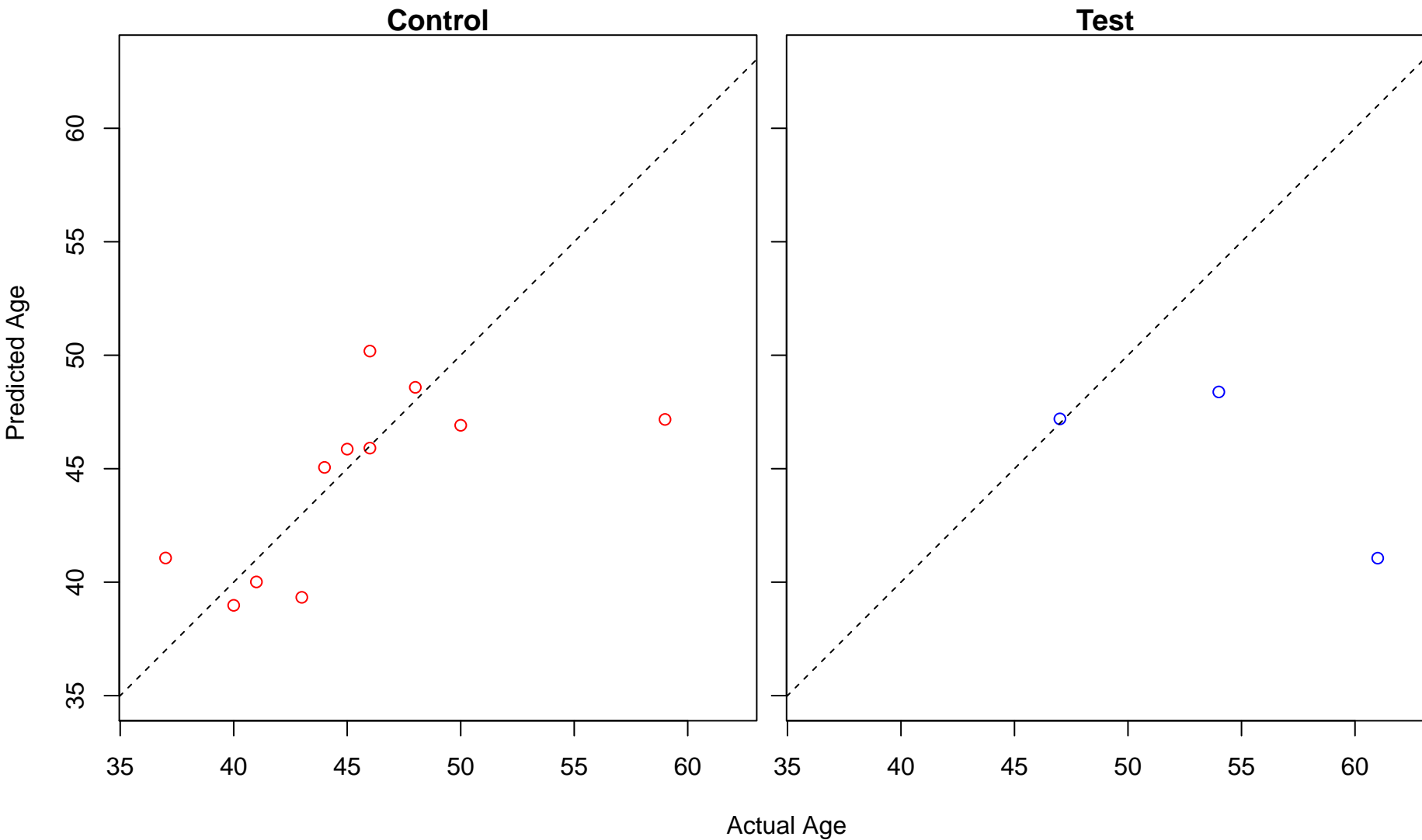
valine metabolic process (Score: 25.569326)



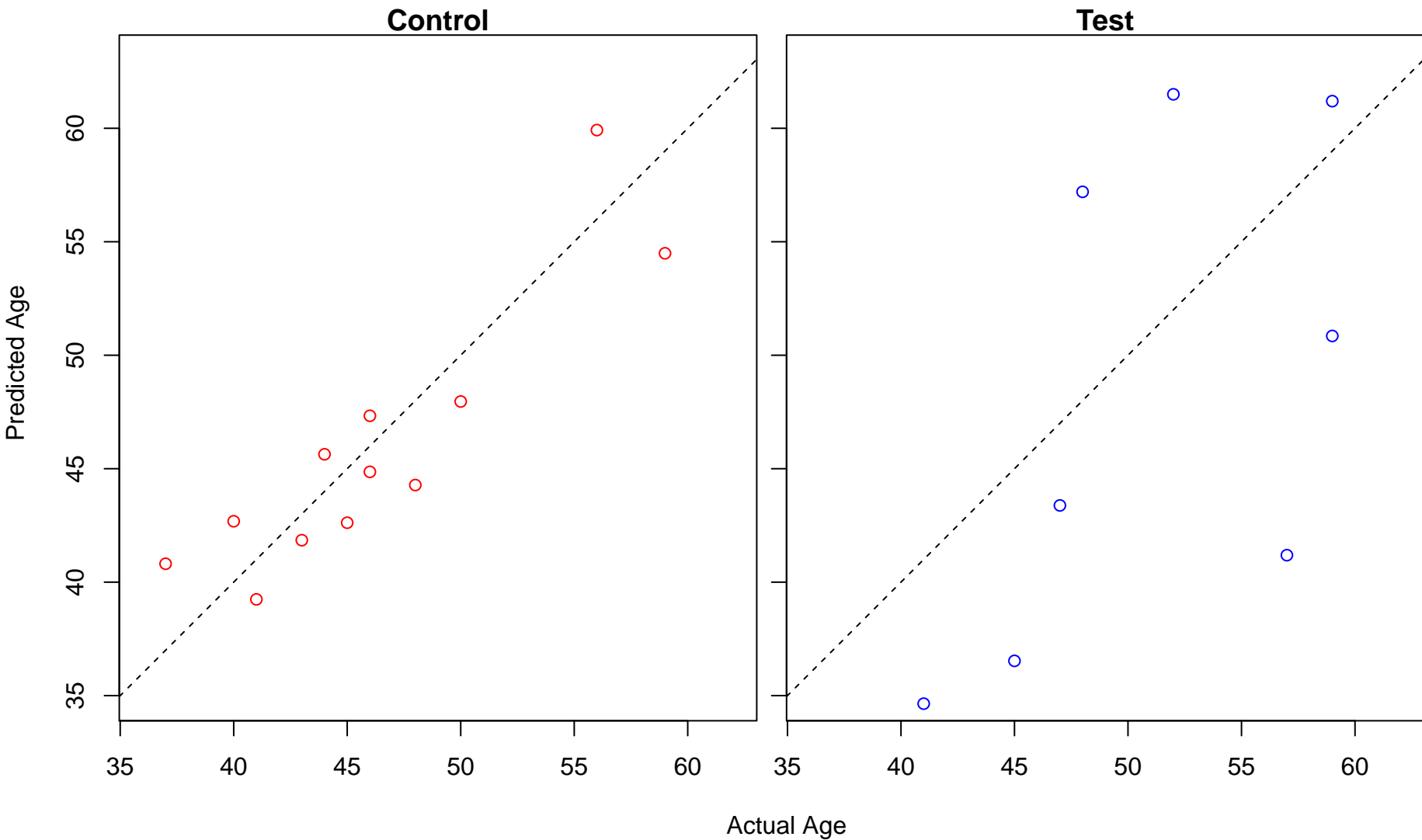
positive regulation of response to wounding (Score: 25.565226)



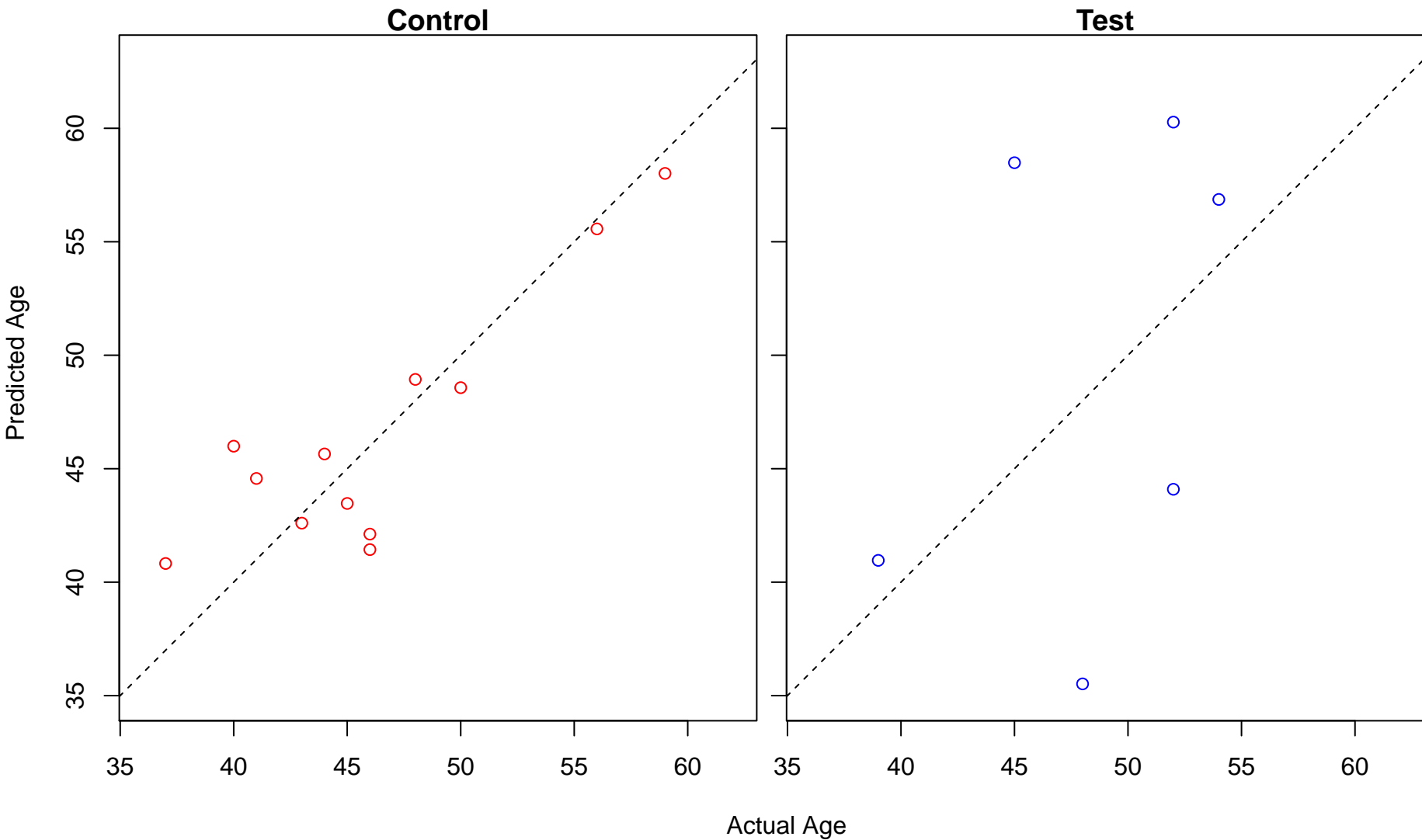
sensory perception of bitter taste (Score: 25.551622)



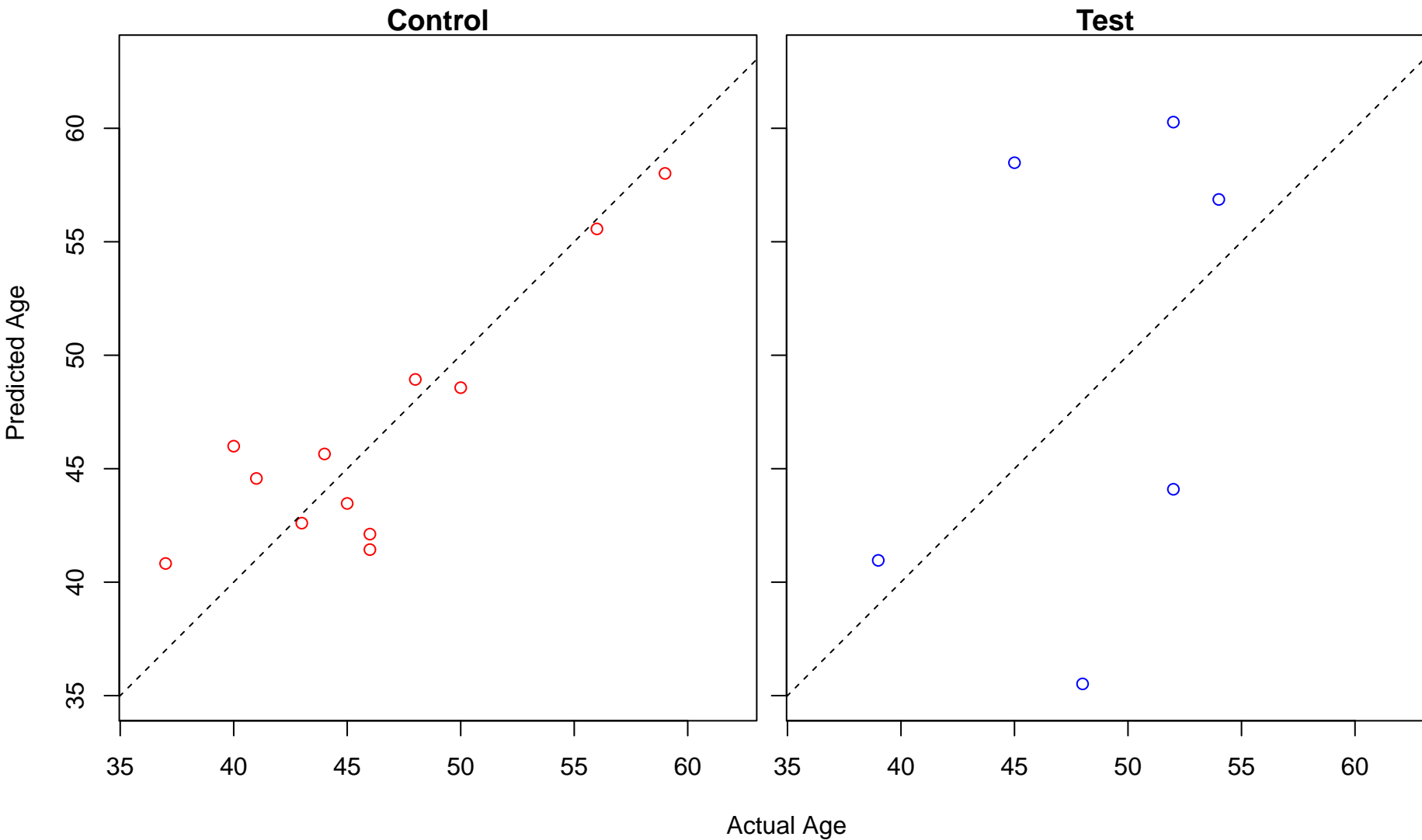
negative regulation of phosphatidylinositol 3-kinase signaling (Score: 25.524286)



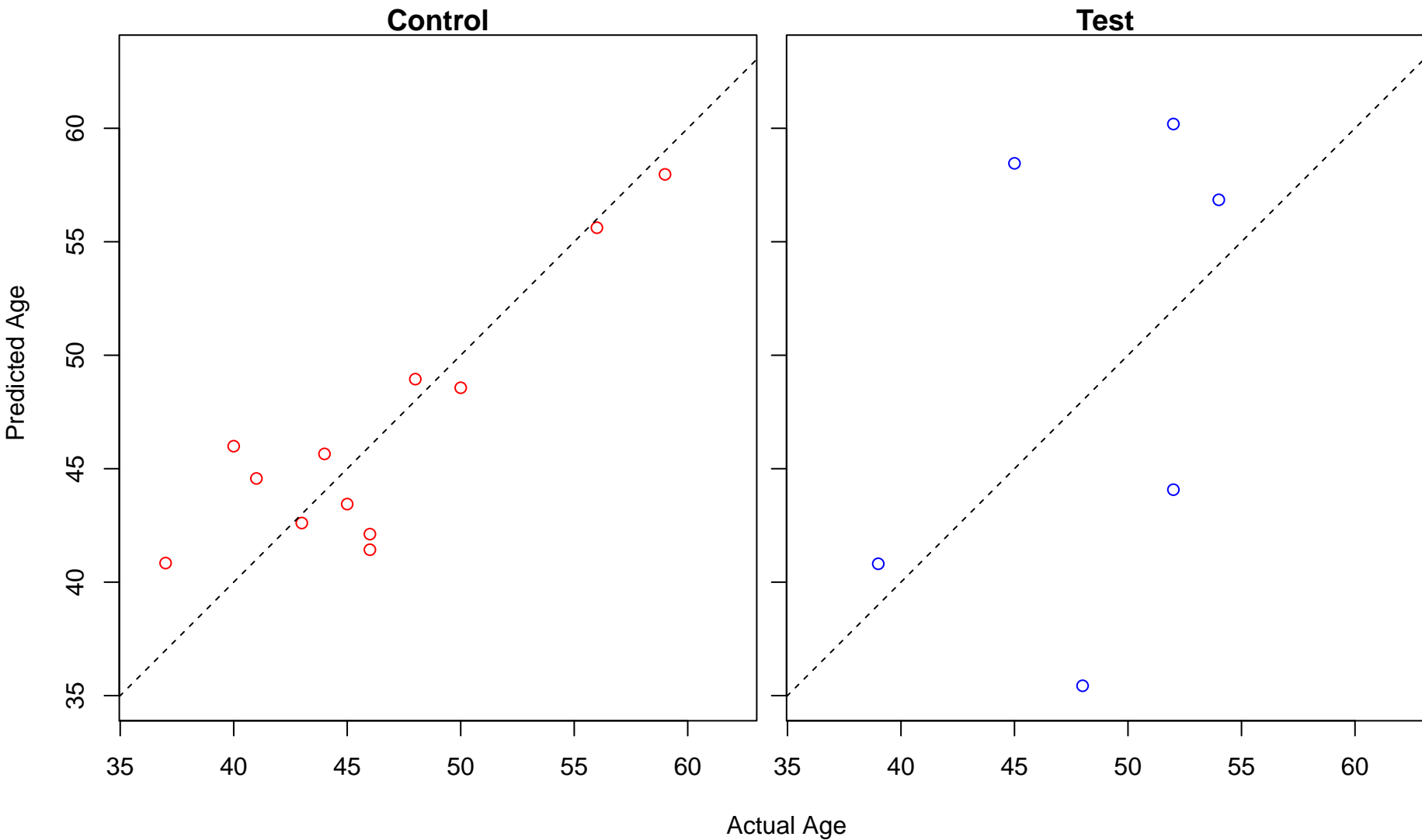
male gonad development (Score: 25.523132)



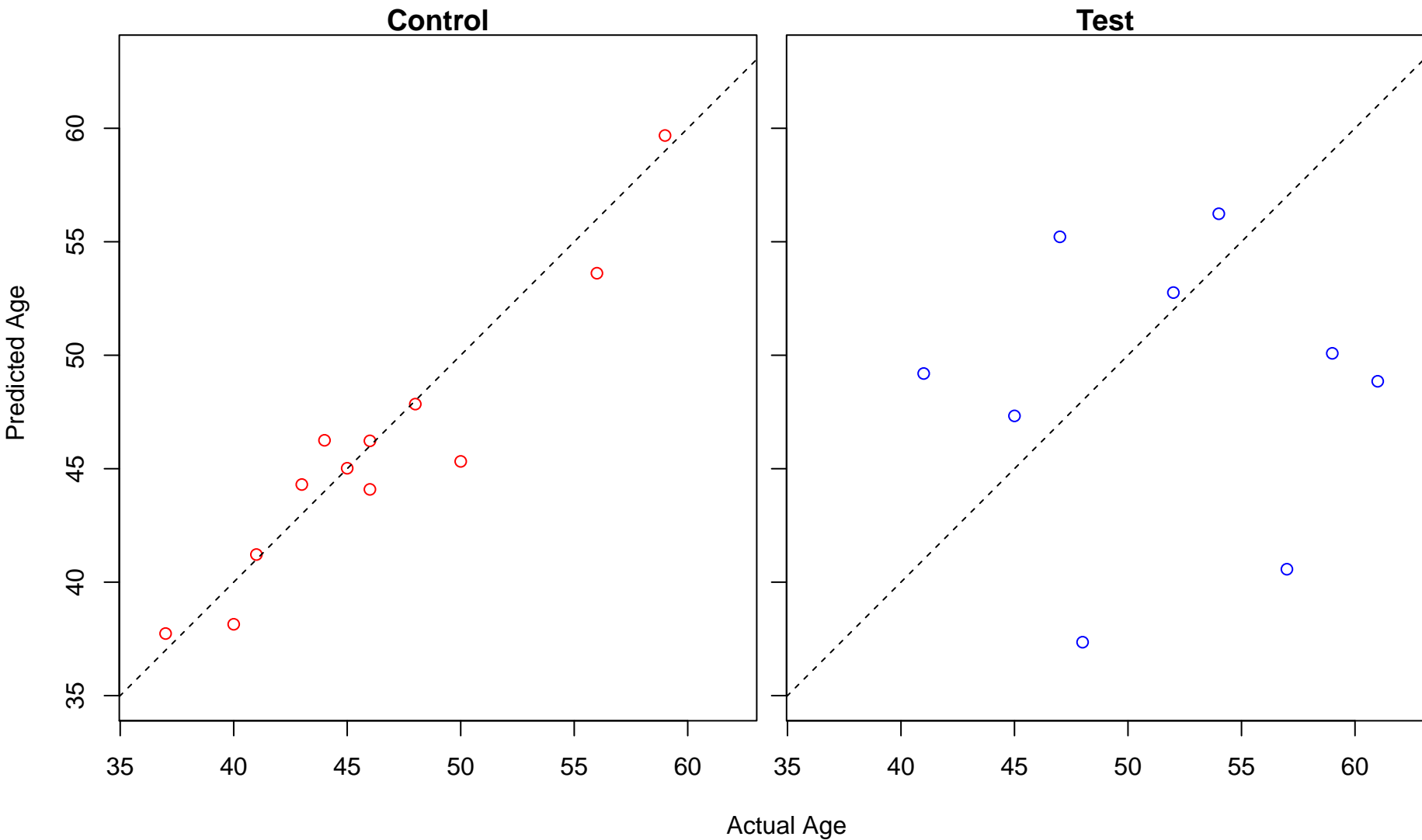
development of primary male sexual characteristics (Score: 25.523132)



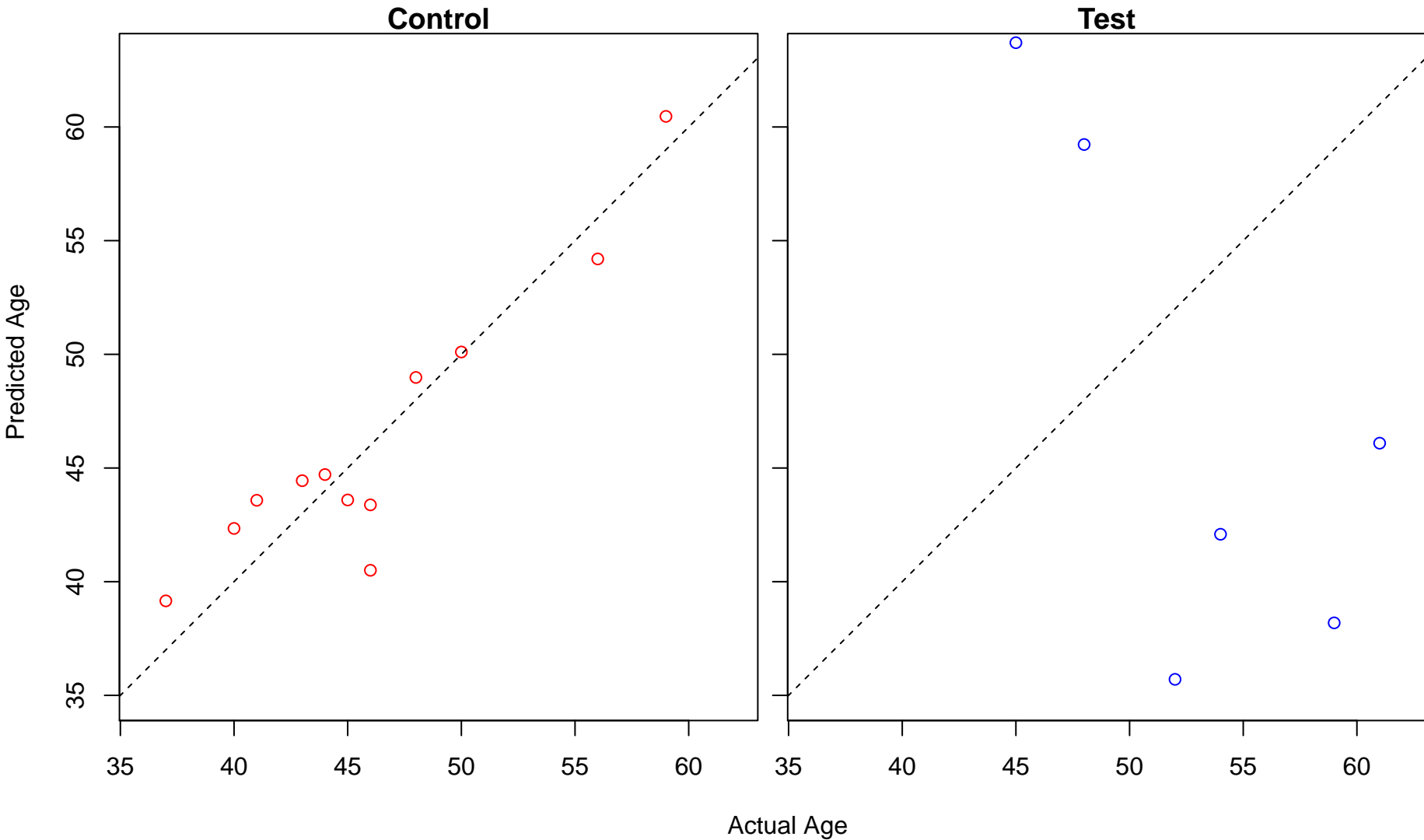
male sex differentiation (Score: 25.371884)



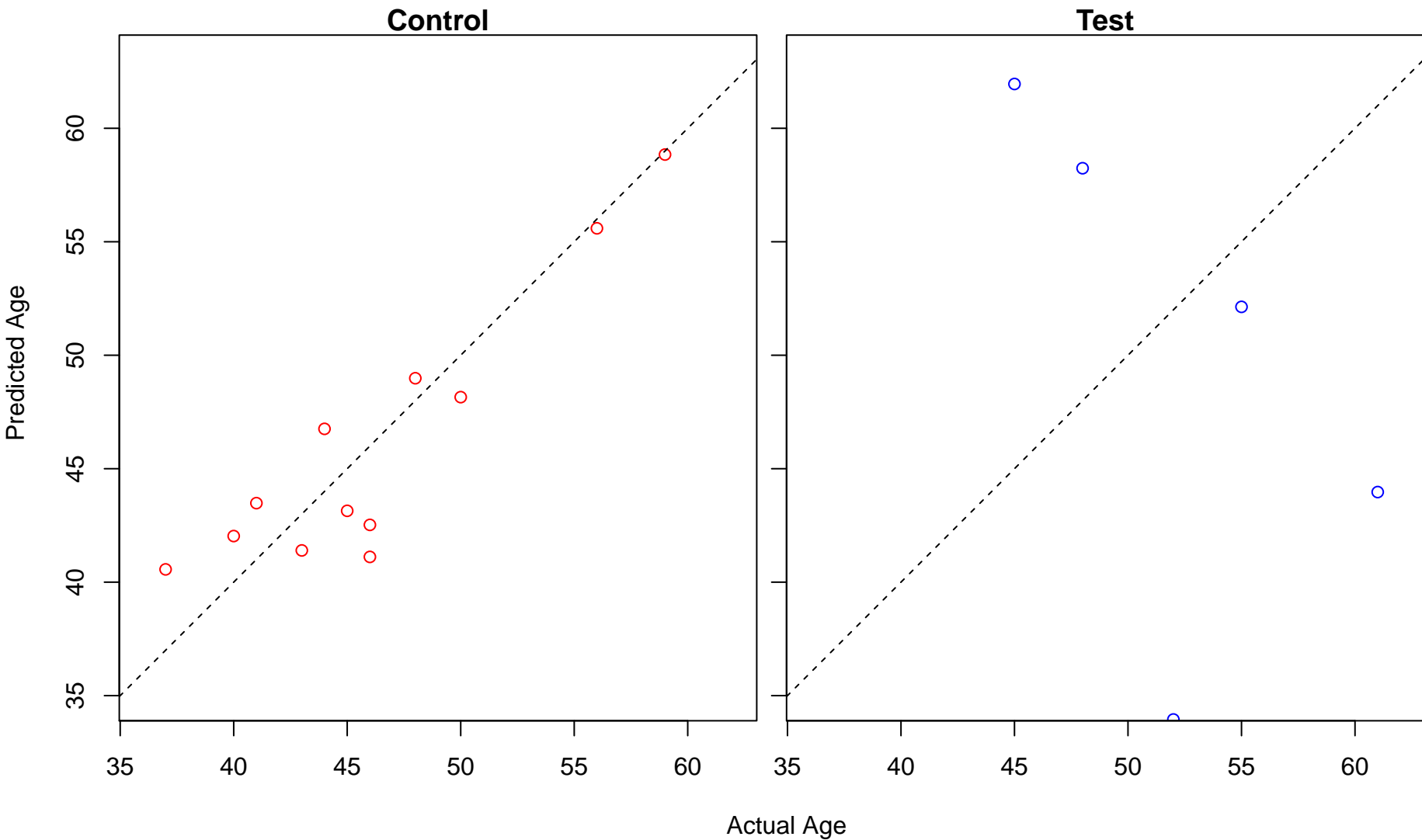
limbic system development (Score: 25.322708)



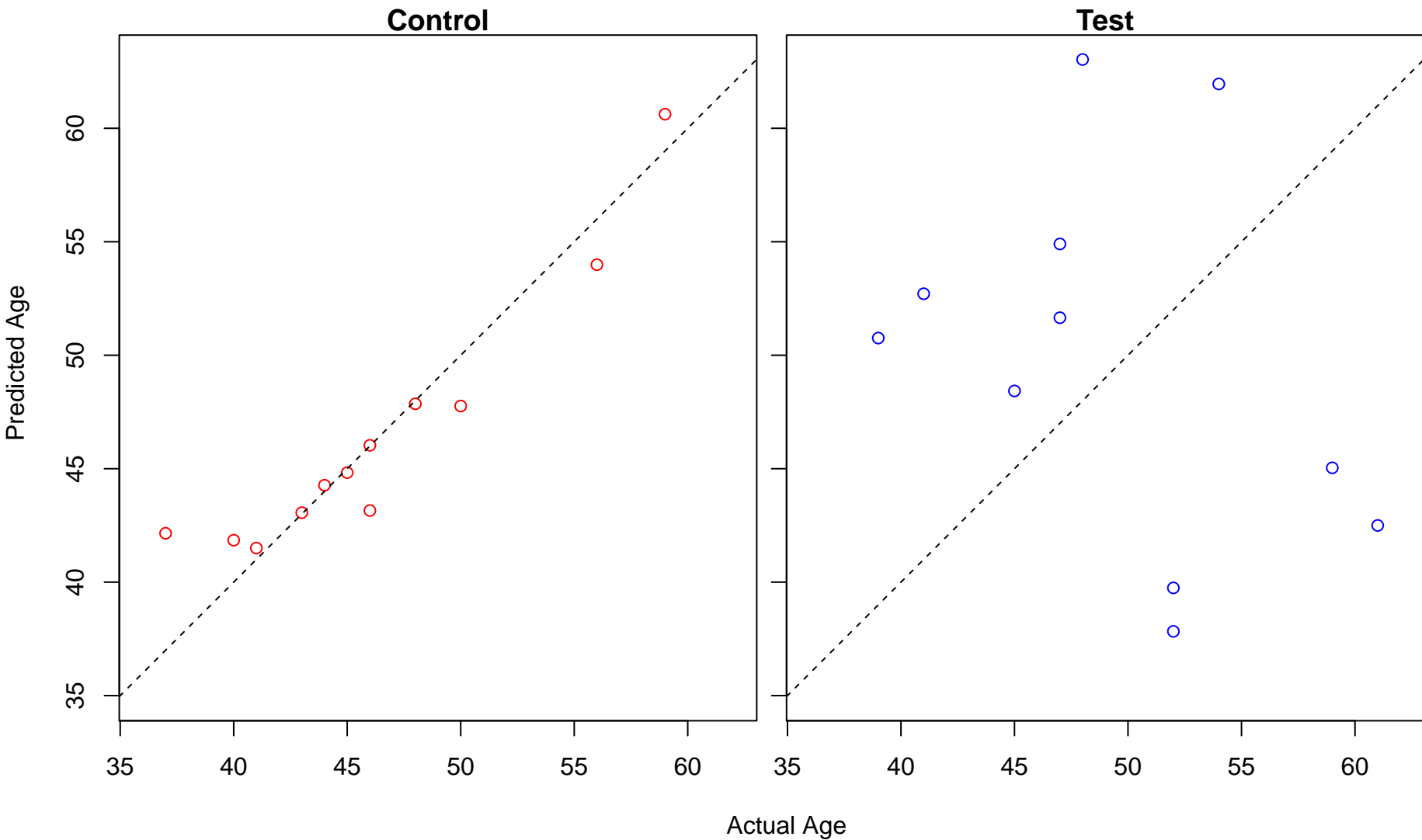
regulation of endothelial cell apoptotic process (Score: 25.200495)



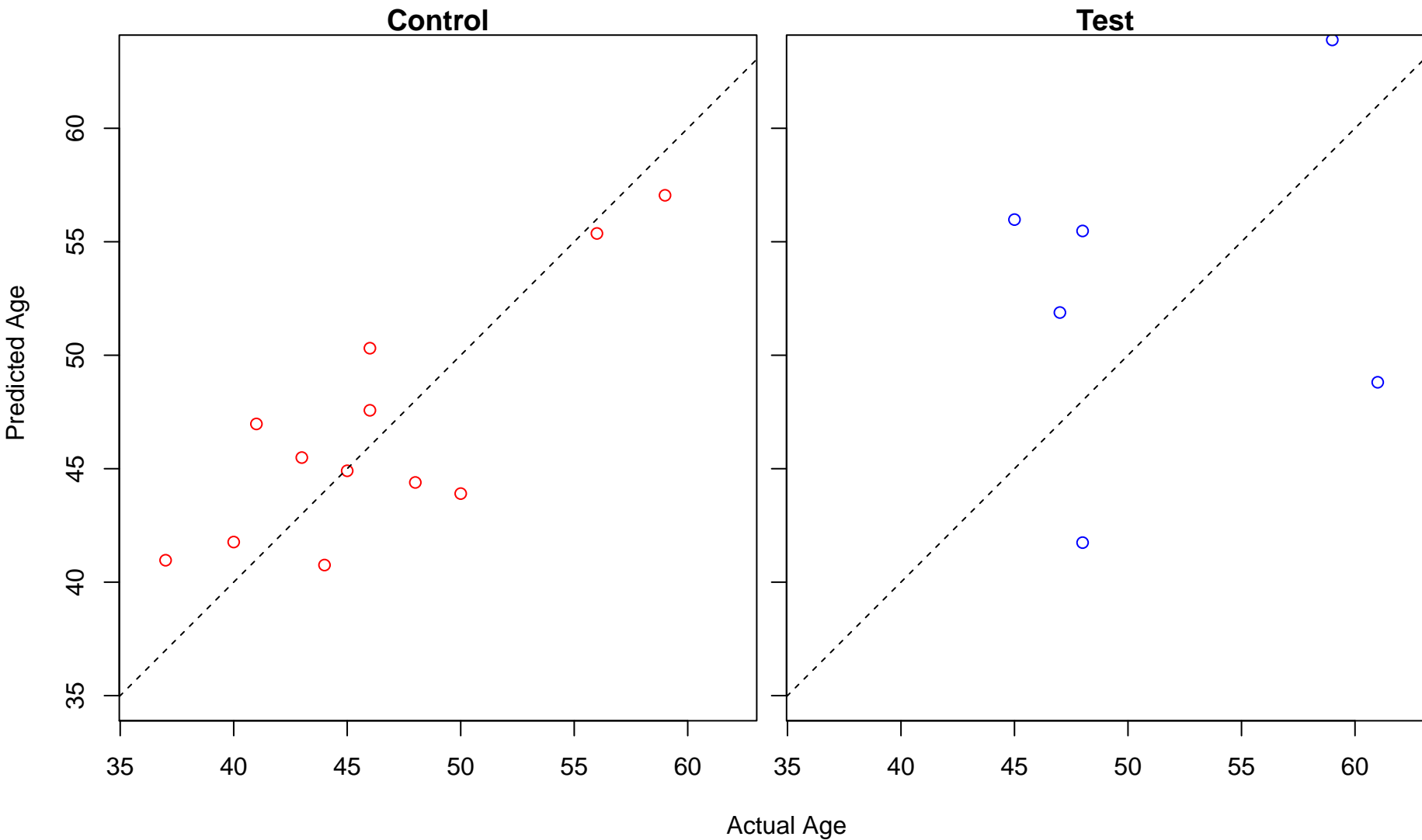
response to steroid hormone (Score: 25.094632)



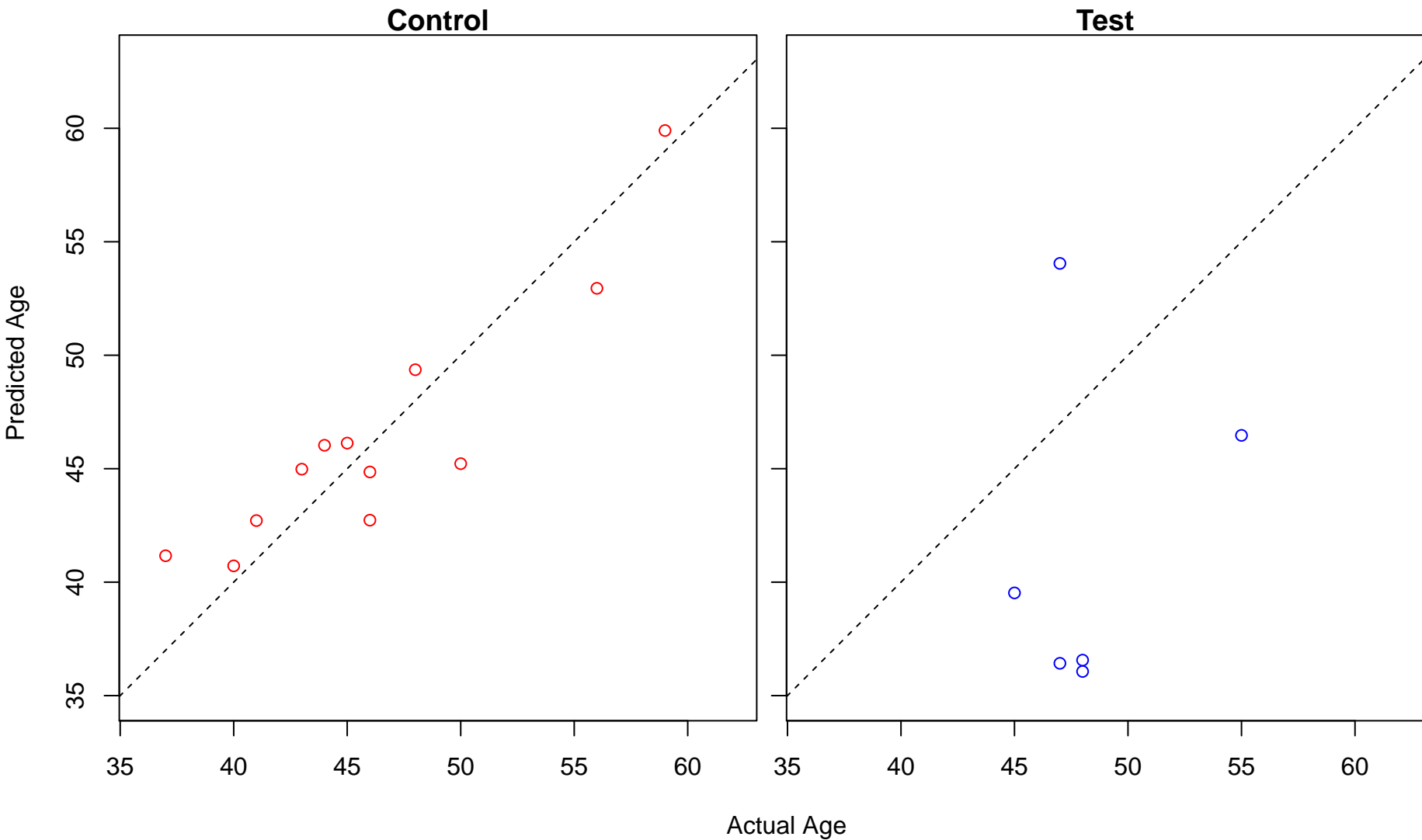
calcium ion homeostasis (Score: 25.052192)



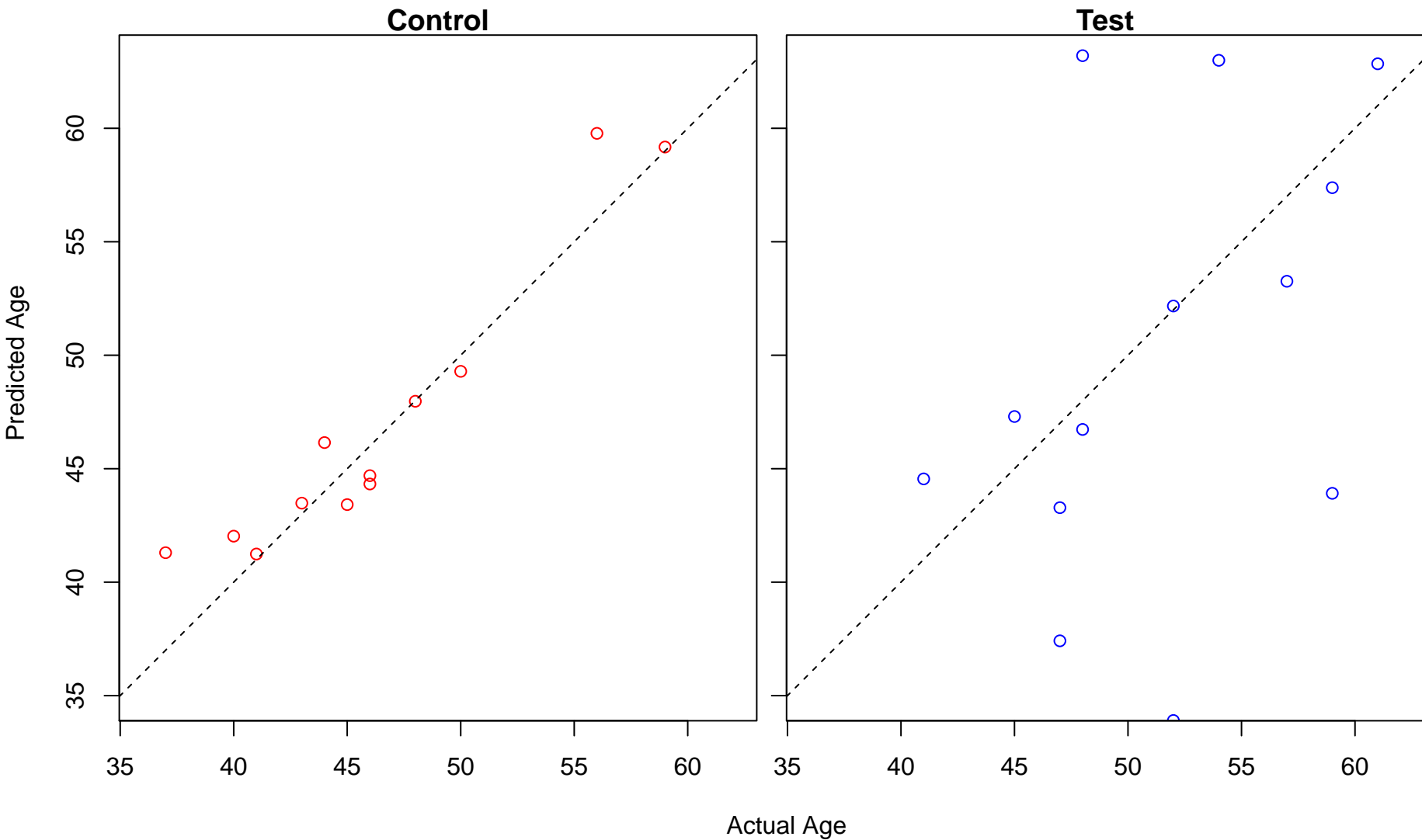
neurotransmitter uptake (Score: 25.028415)



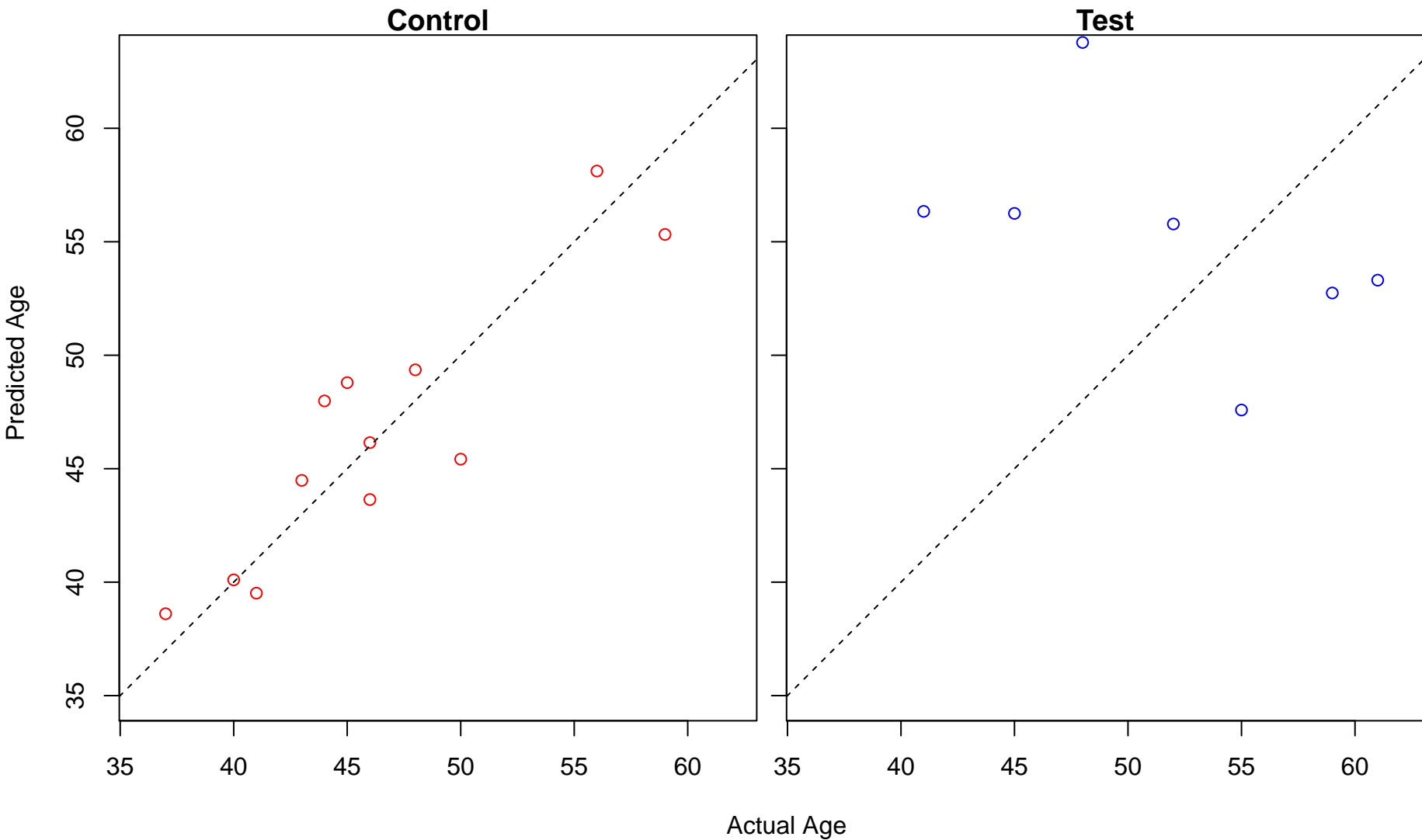
ribosome assembly (Score: 25.025379)



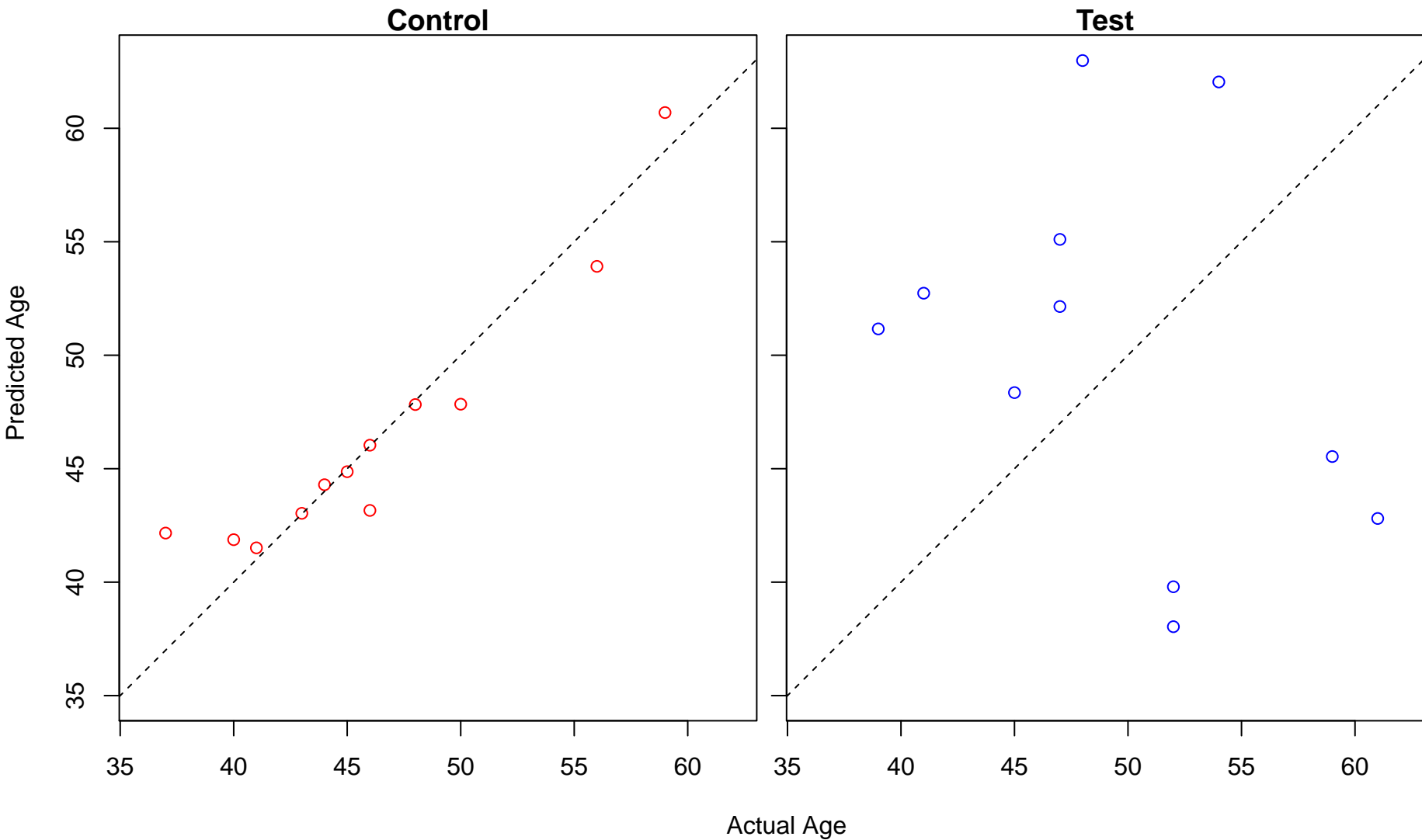
phospholipid dephosphorylation (Score: 24.969280)



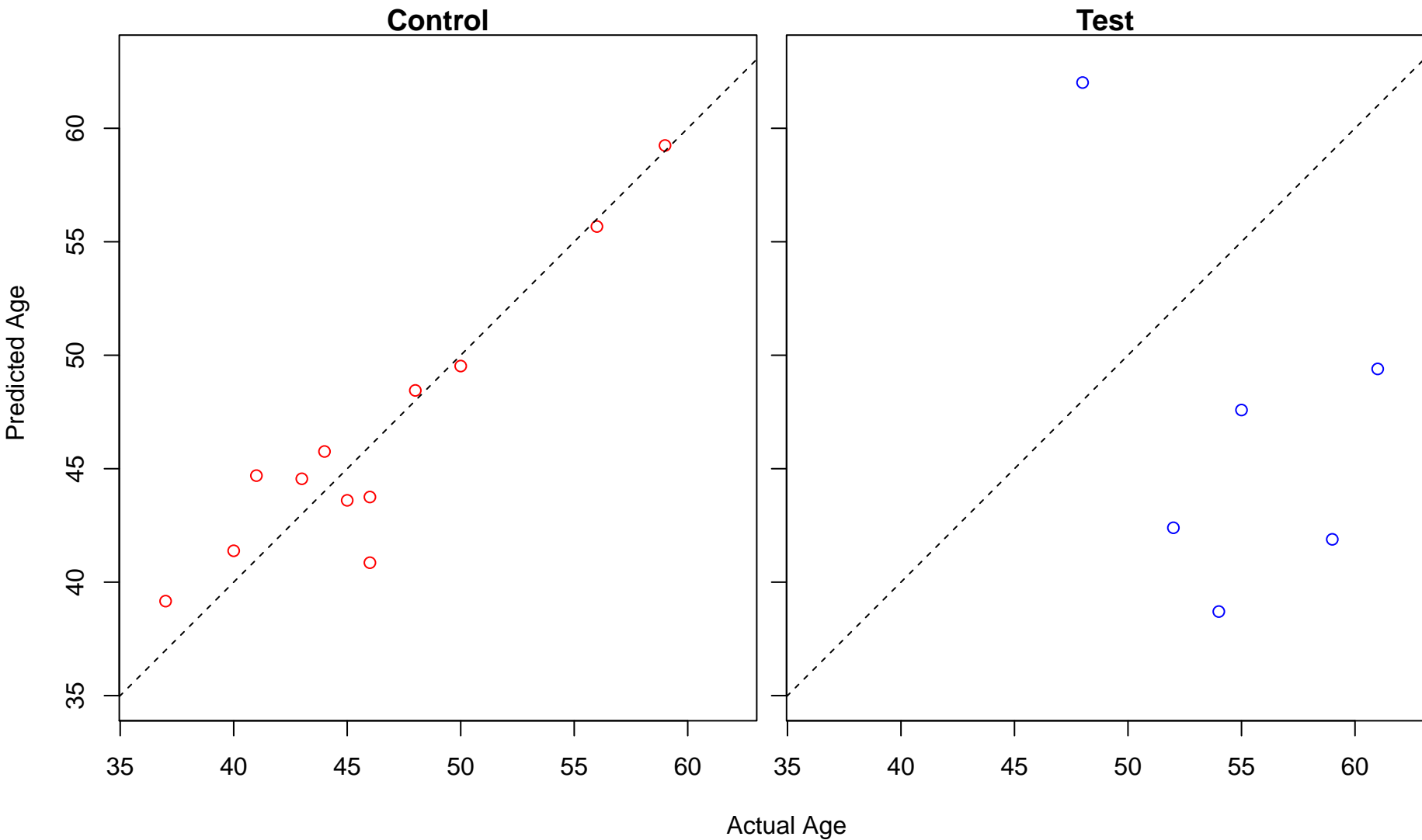
negative regulation of cell migration involved in sprouting angiogenesis (Score: 24.950006)



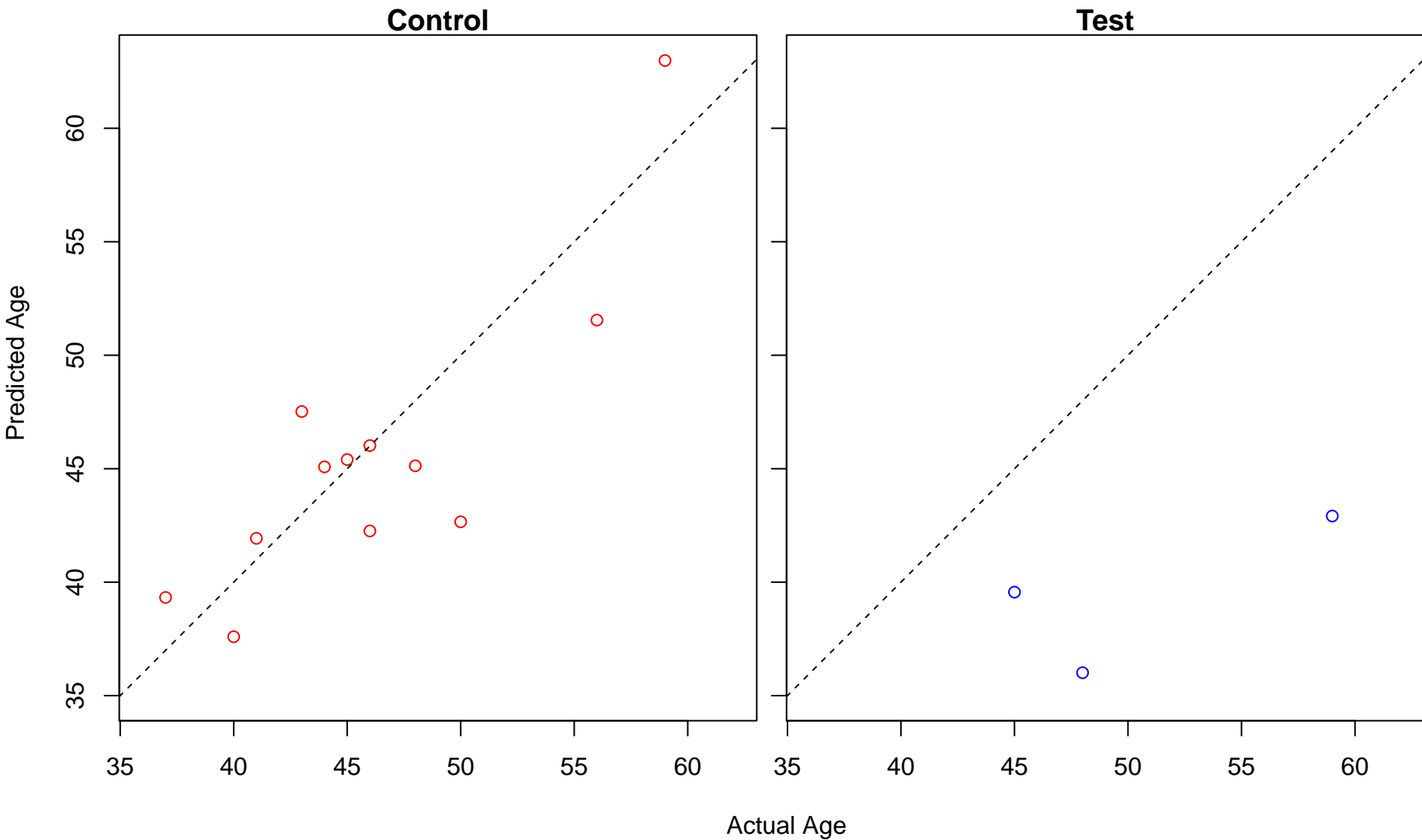
cellular calcium ion homeostasis (Score: 24.926289)



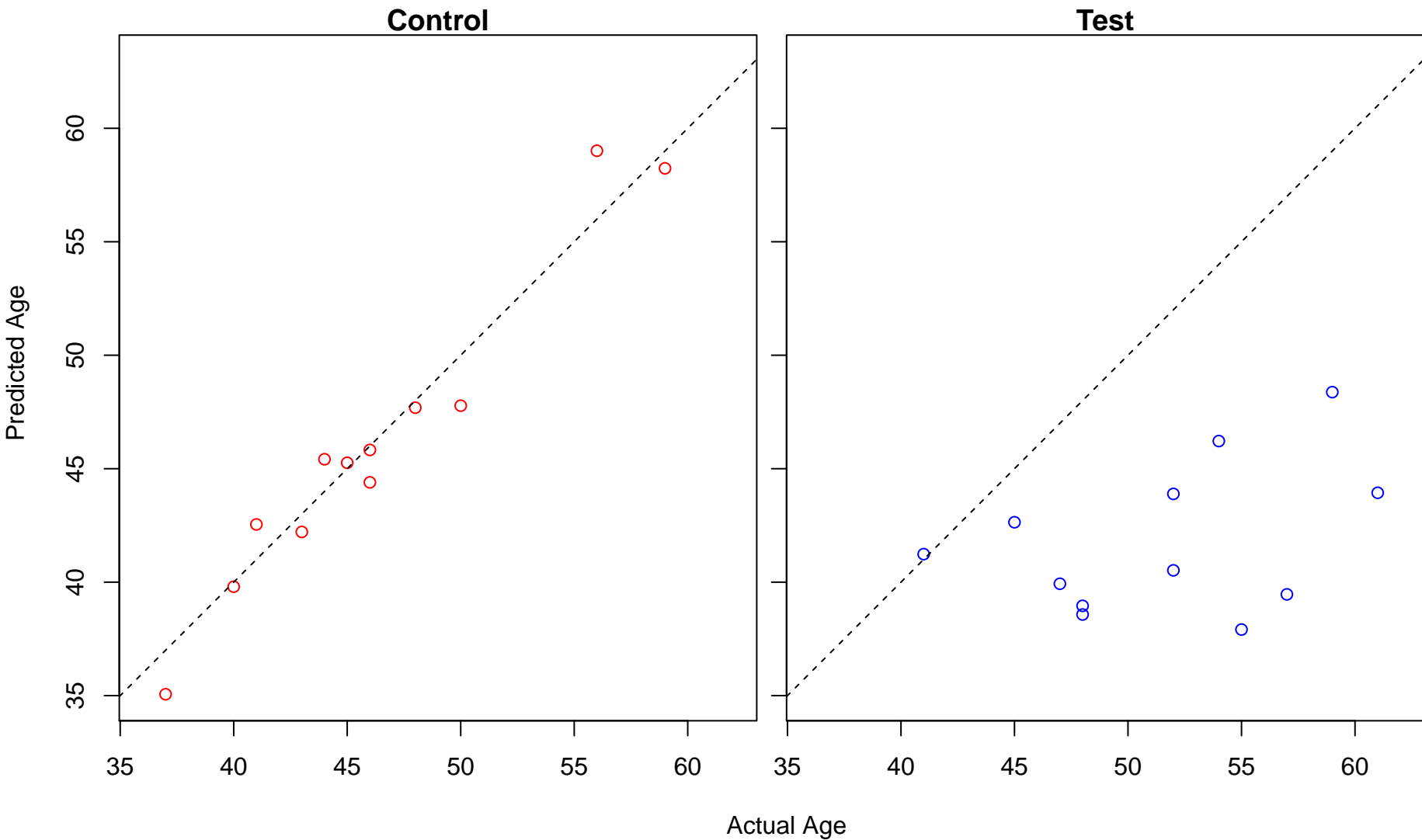
regulation of hormone metabolic process (Score: 24.917543)



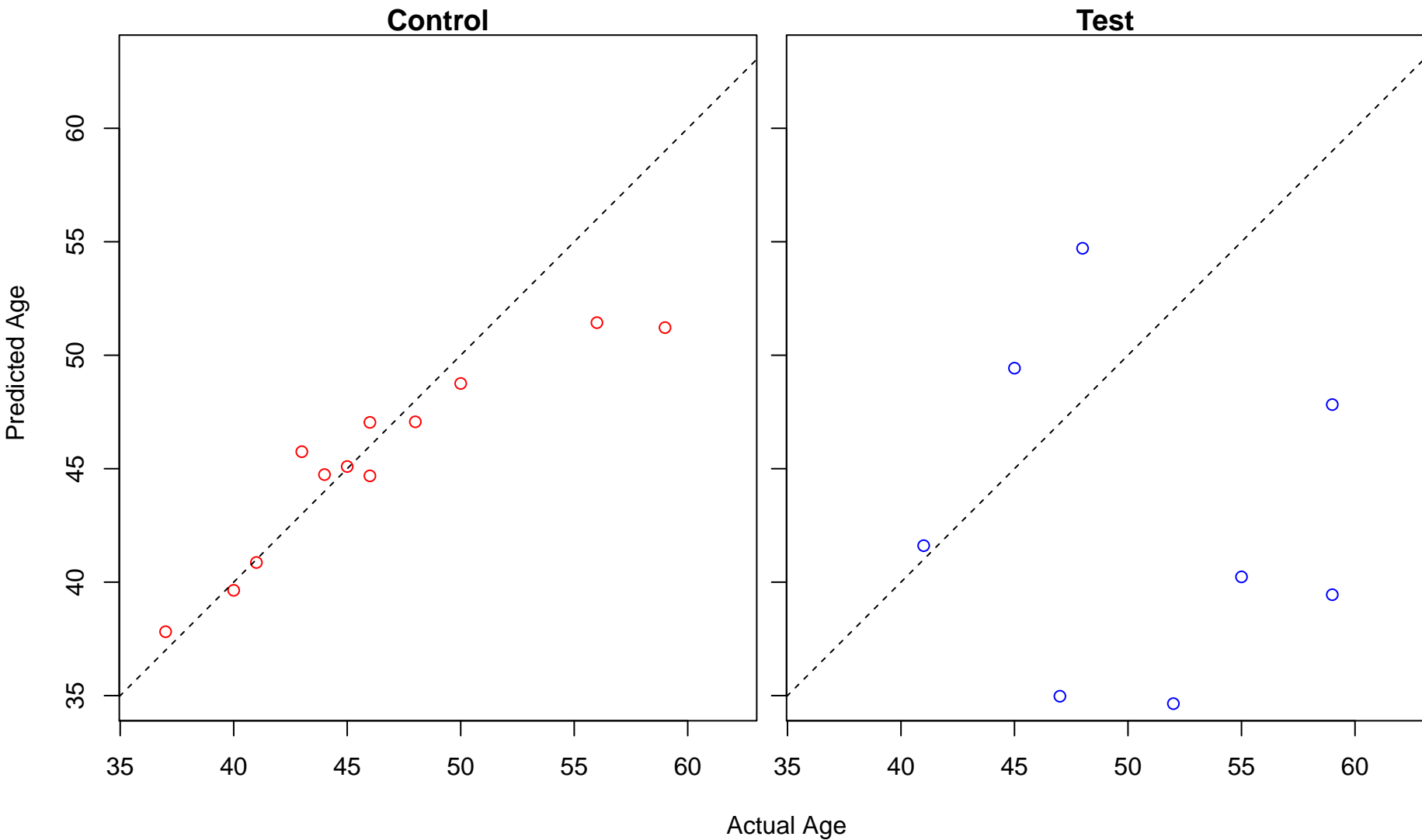
positive regulation of protein glycosylation (Score: 24.905197)



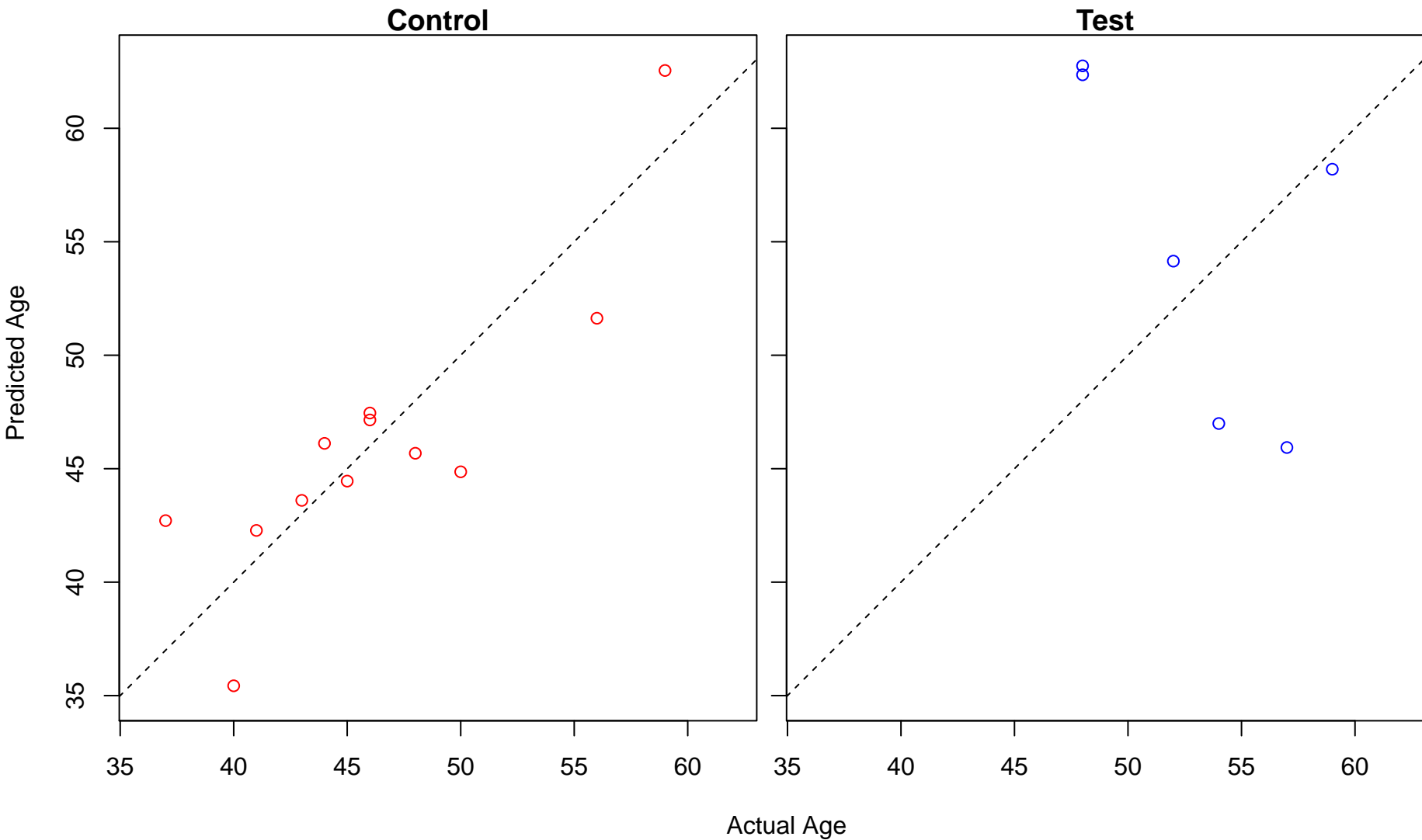
negative regulation of kidney development (Score: 24.892350)



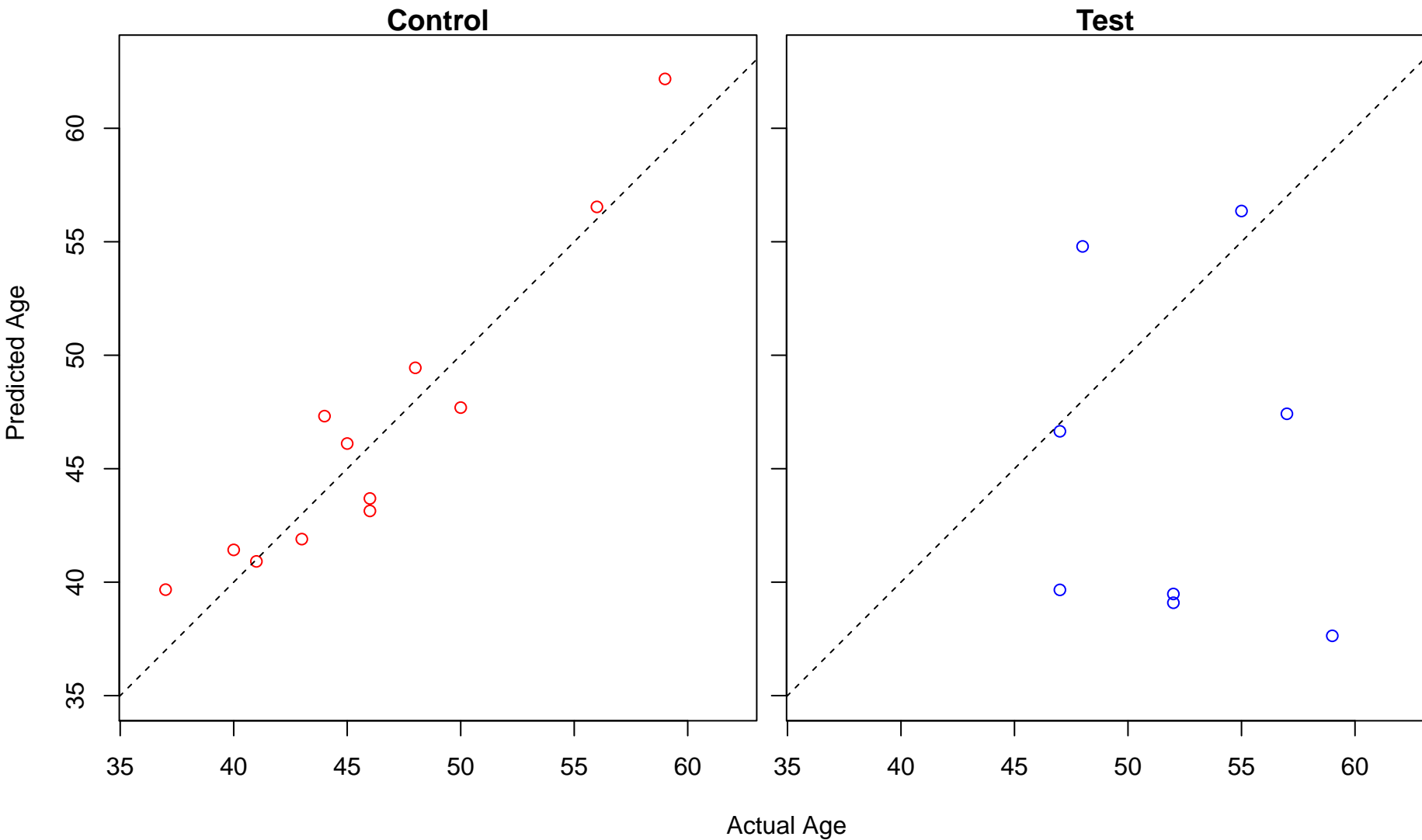
leukocyte apoptotic process (Score: 24.890283)



regulation of response to reactive oxygen species (Score: 24.861451)

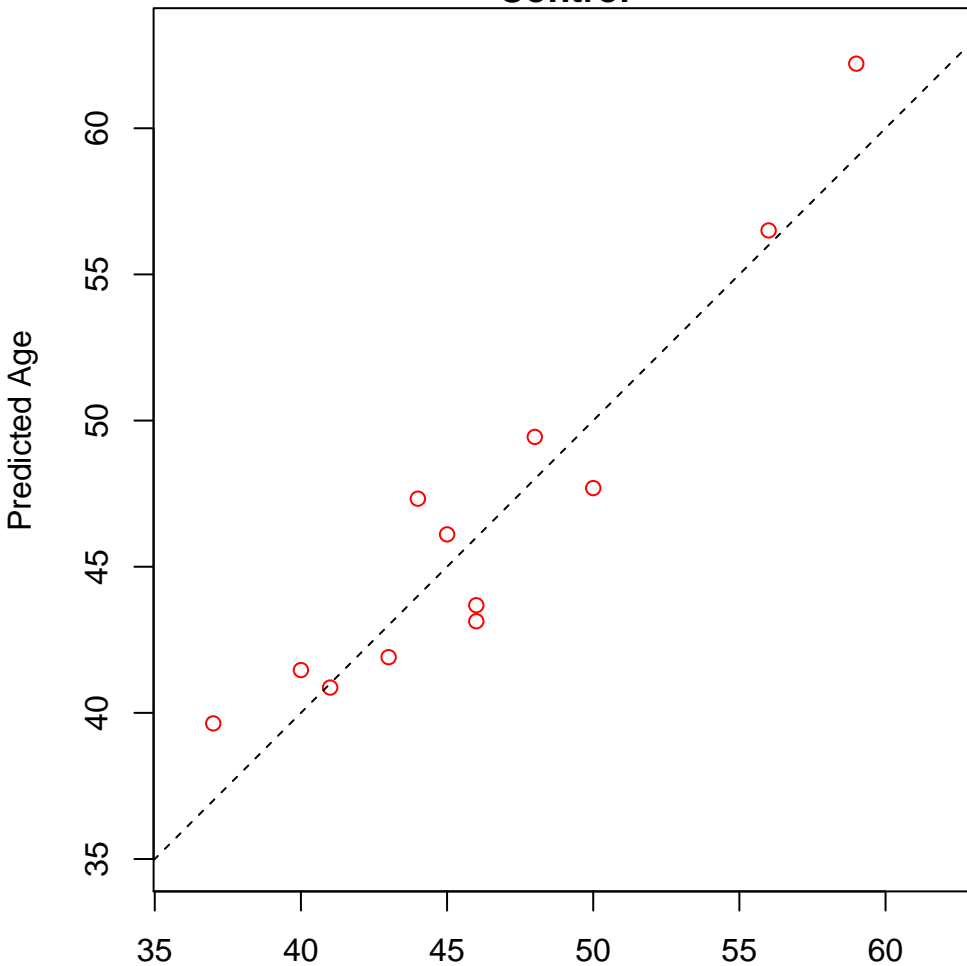


response to cadmium ion (Score: 24.823362)

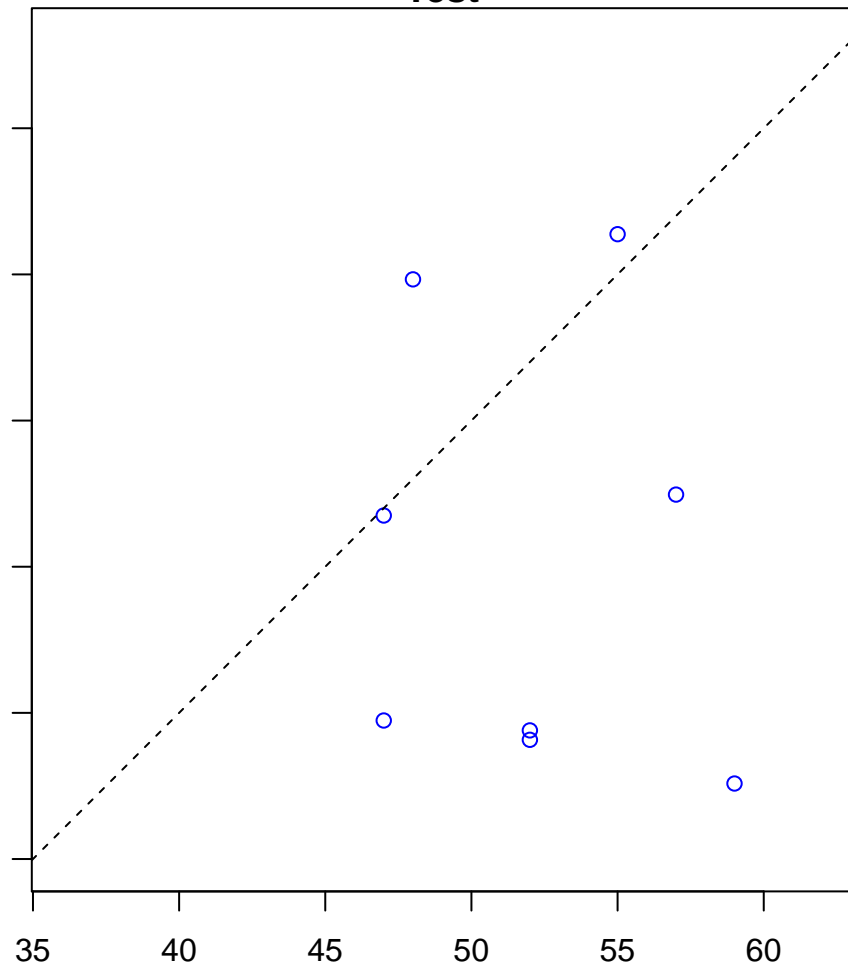


cellular response to cadmium ion (Score: 24.722679)

Control



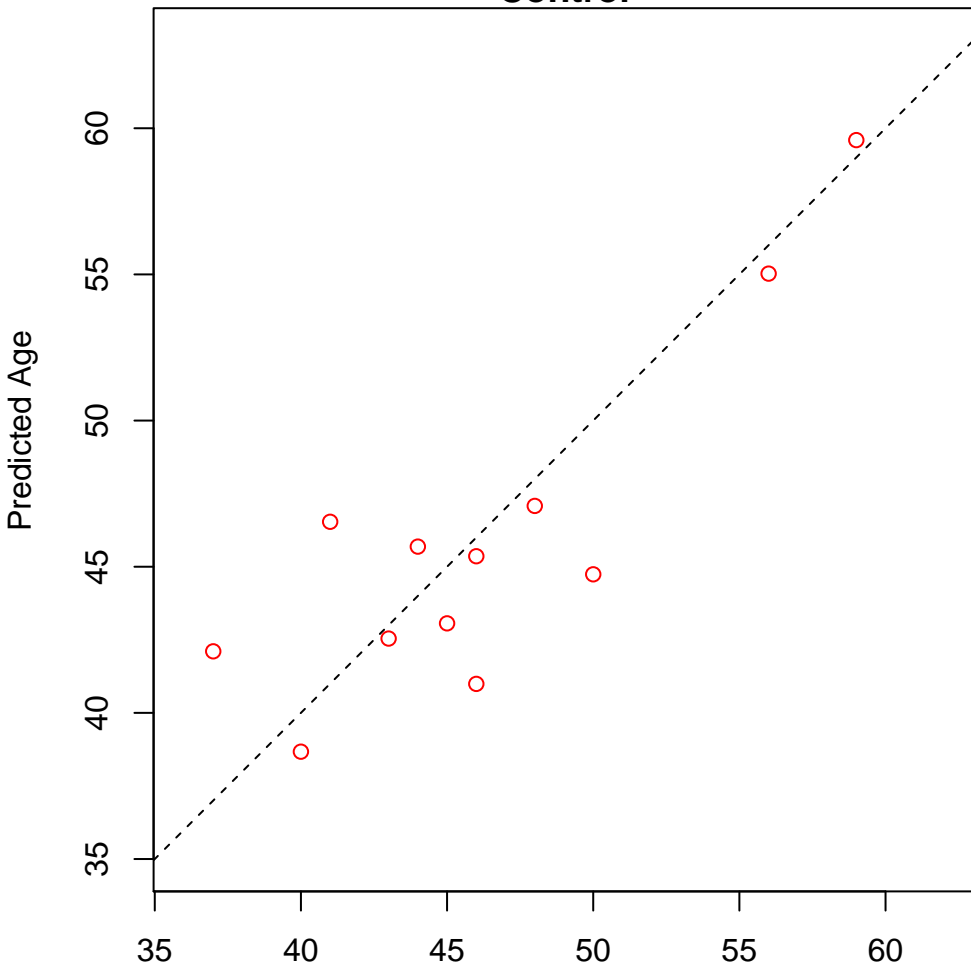
Test



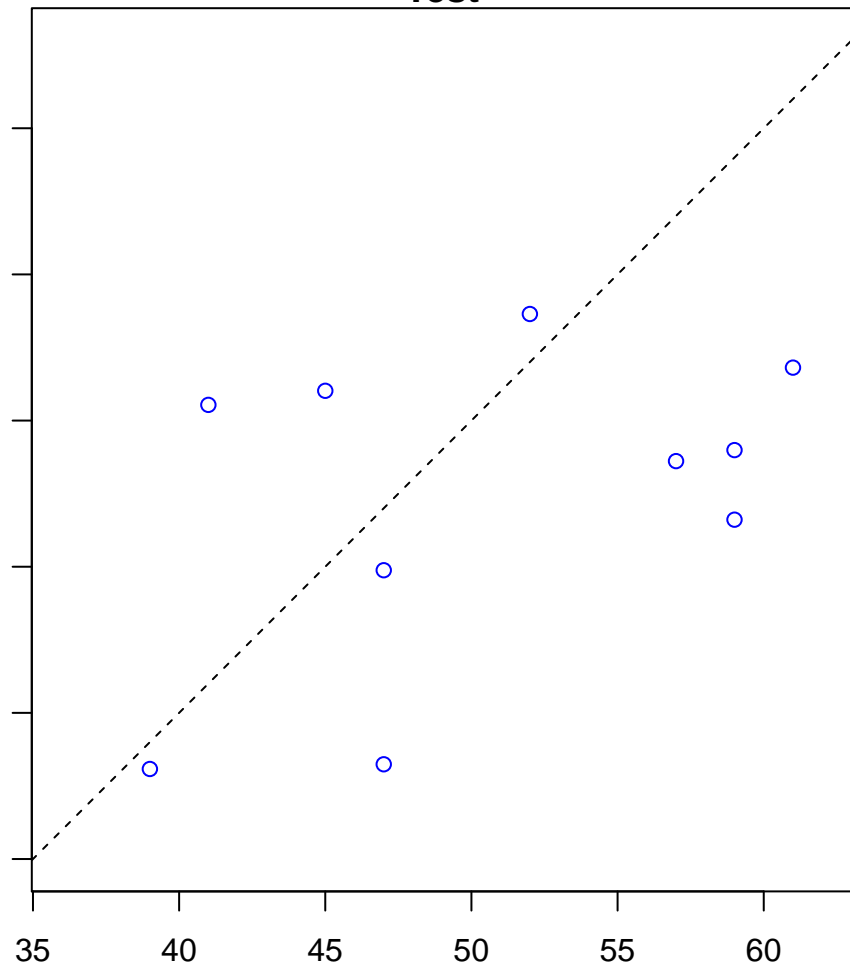
Actual Age

calcium ion transmembrane transport (Score: 24.618577)

Control

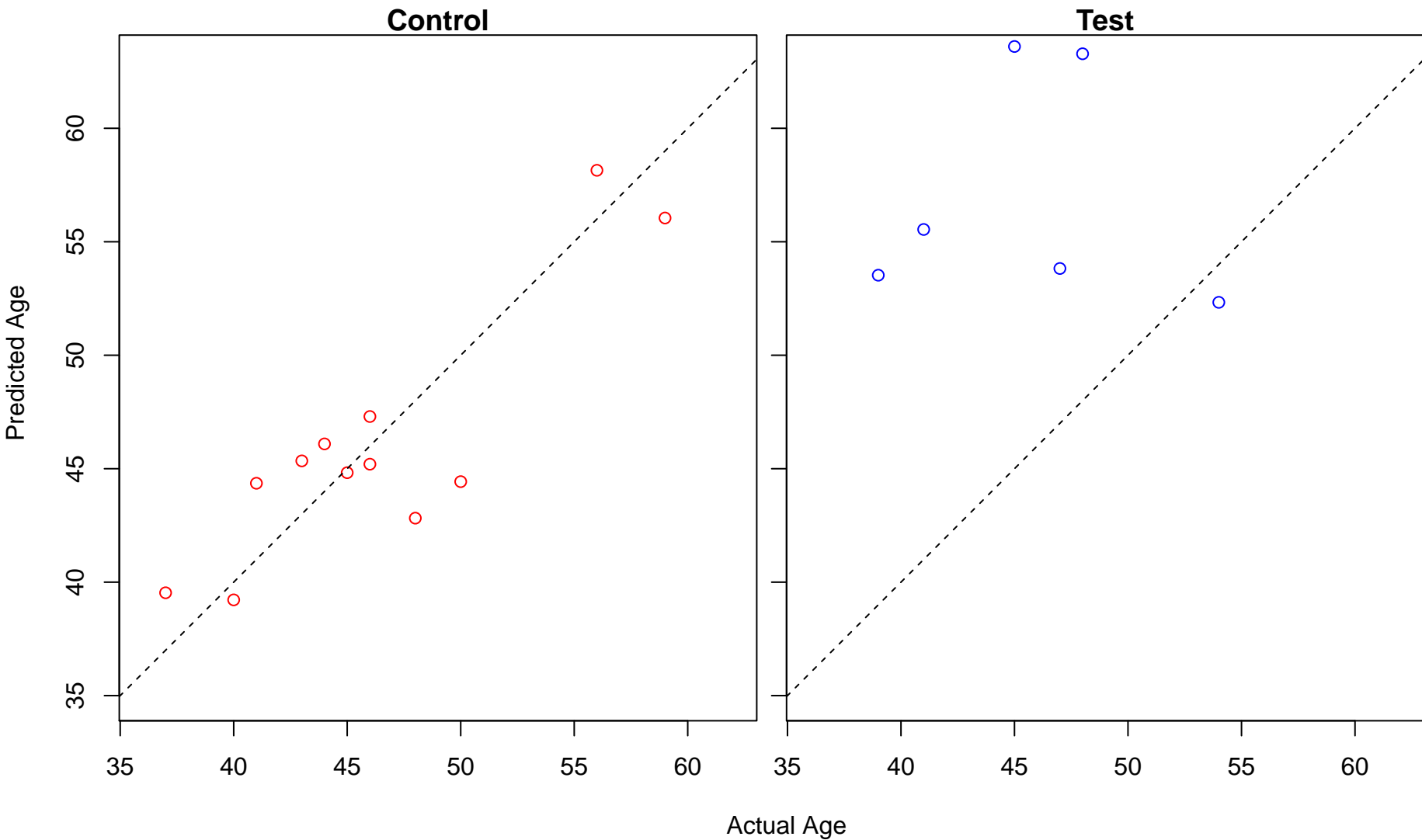


Test

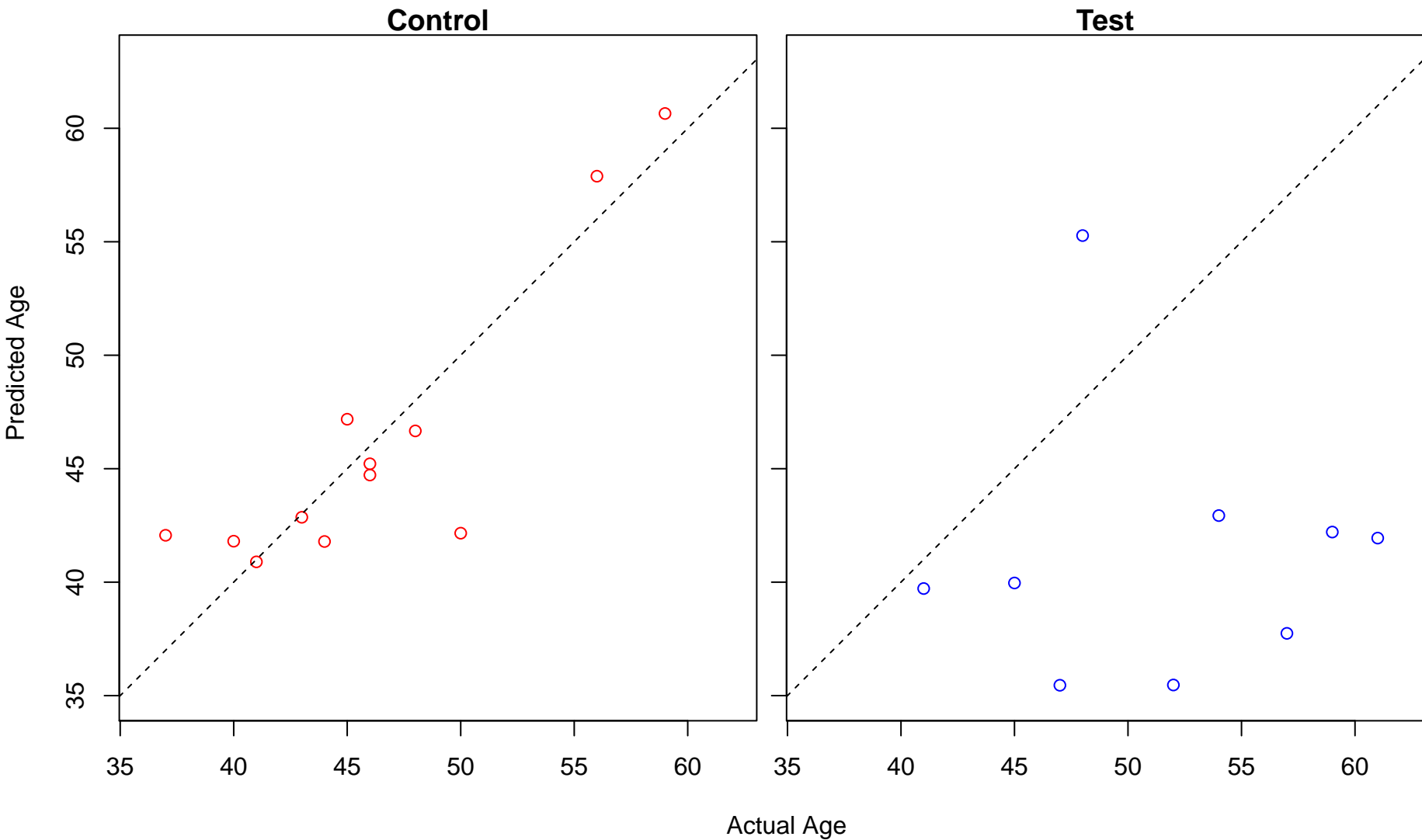


Actual Age

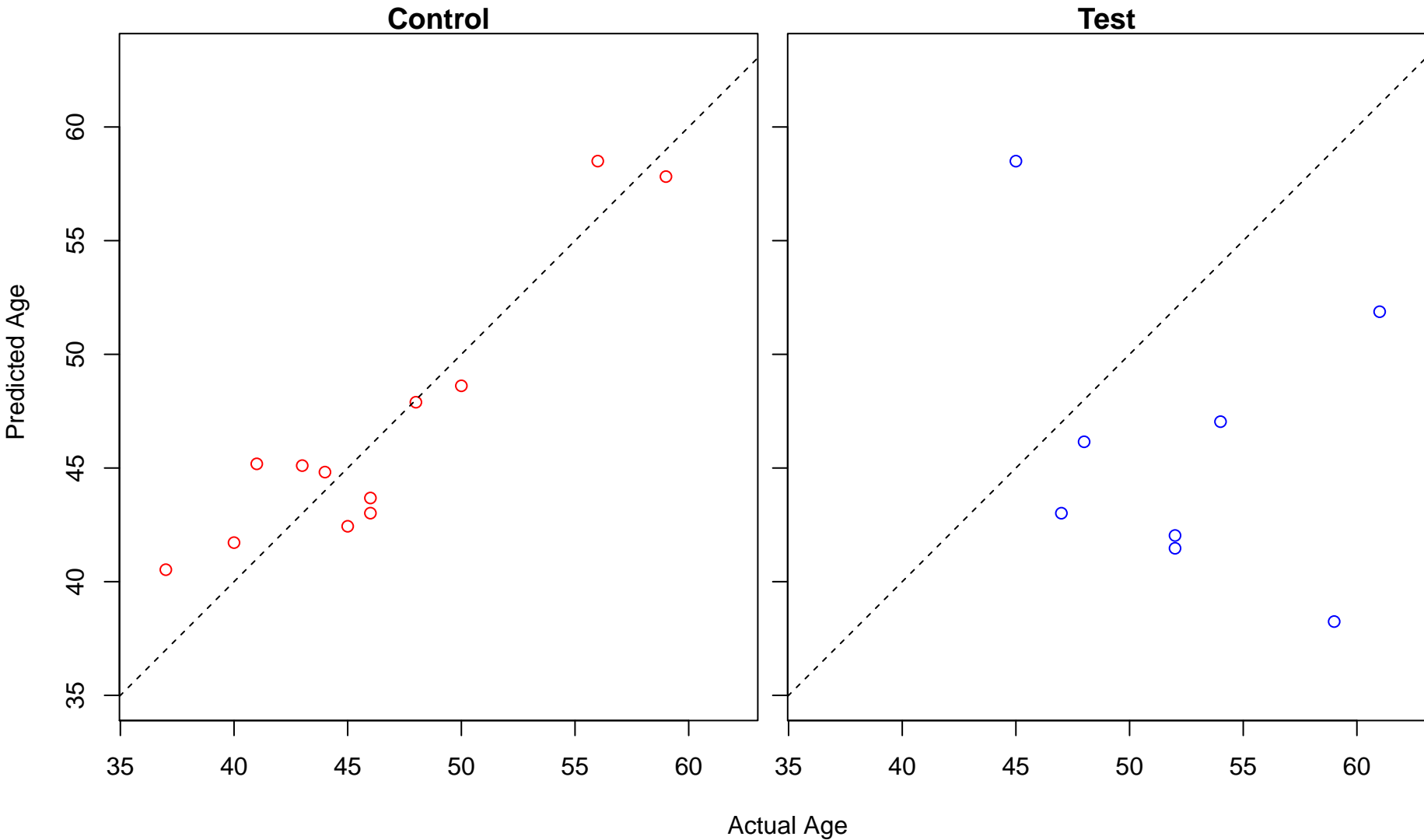
CD4-positive, alpha-beta T cell activation (Score: 24.556446)



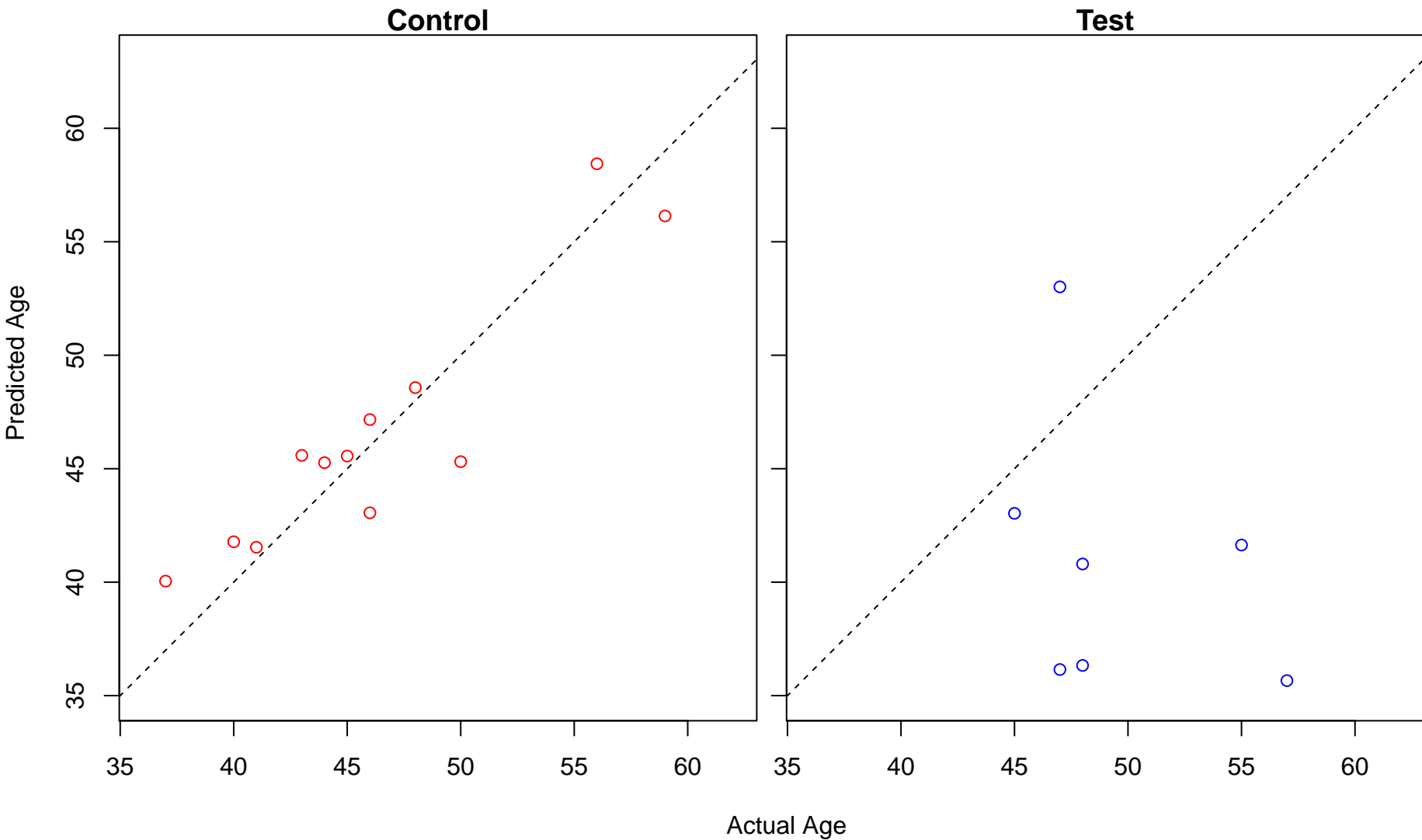
developmental growth involved in morphogenesis (Score: 24.390325)



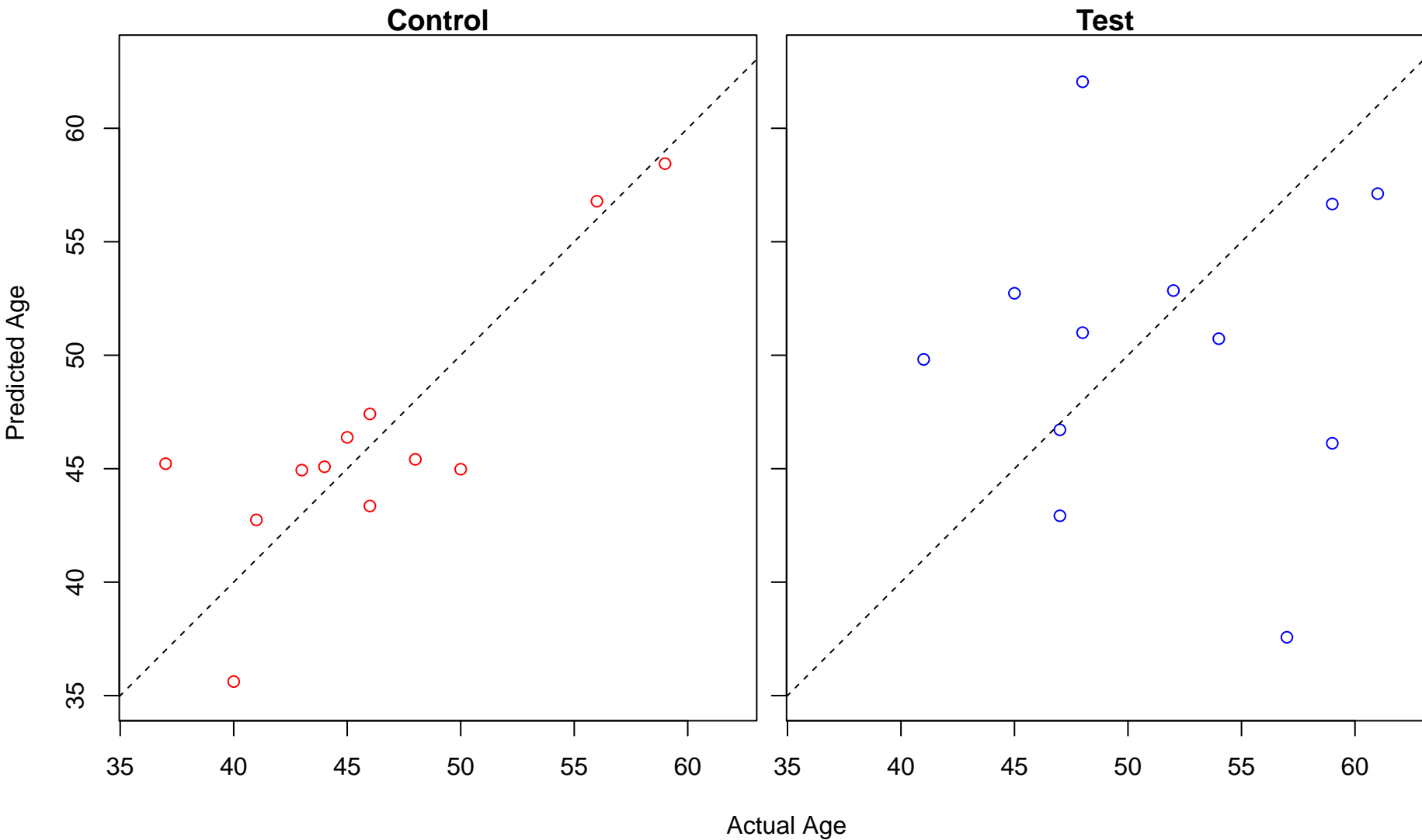
regulation of alcohol biosynthetic process (Score: 24.354947)



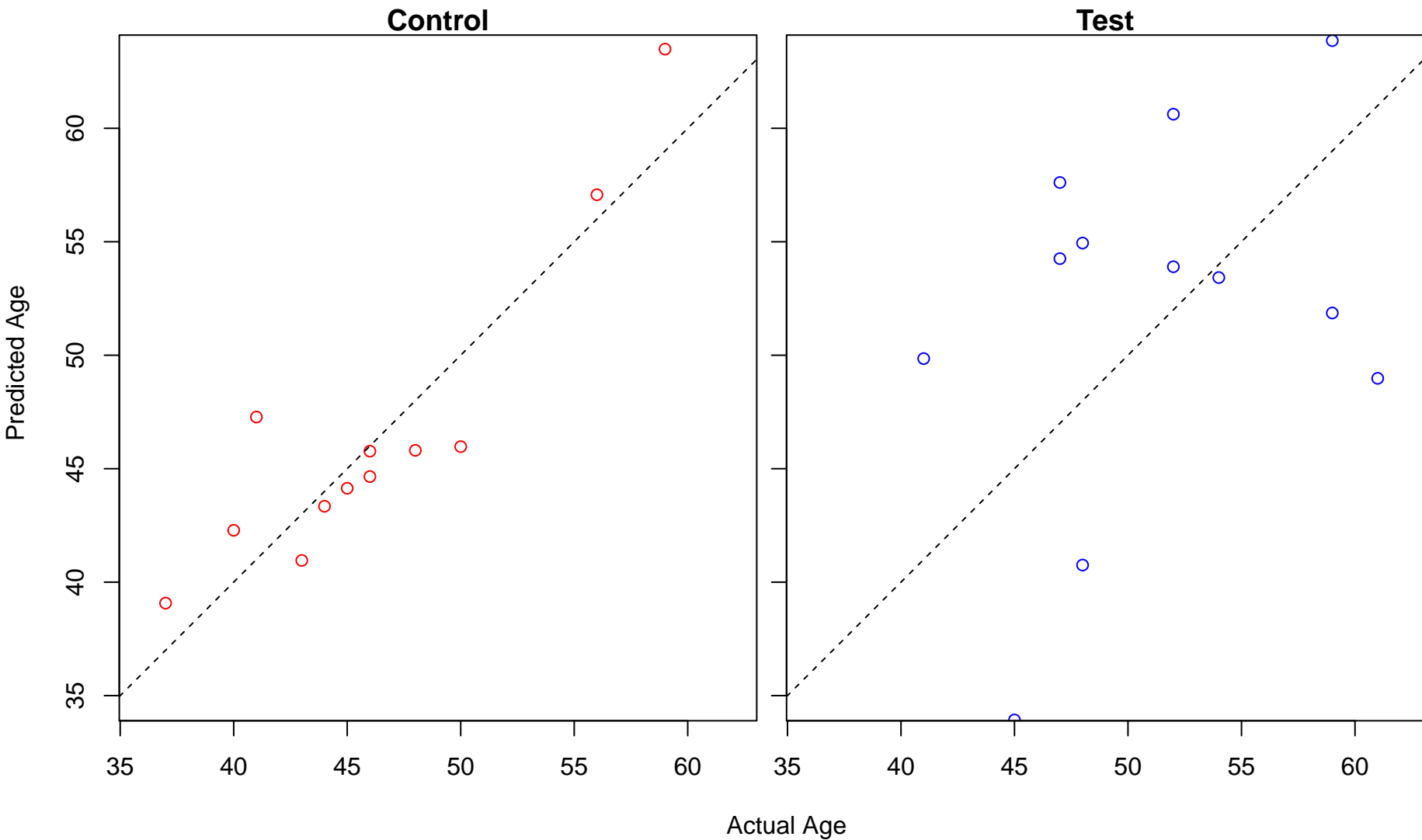
erythrocyte differentiation (Score: 24.326285)



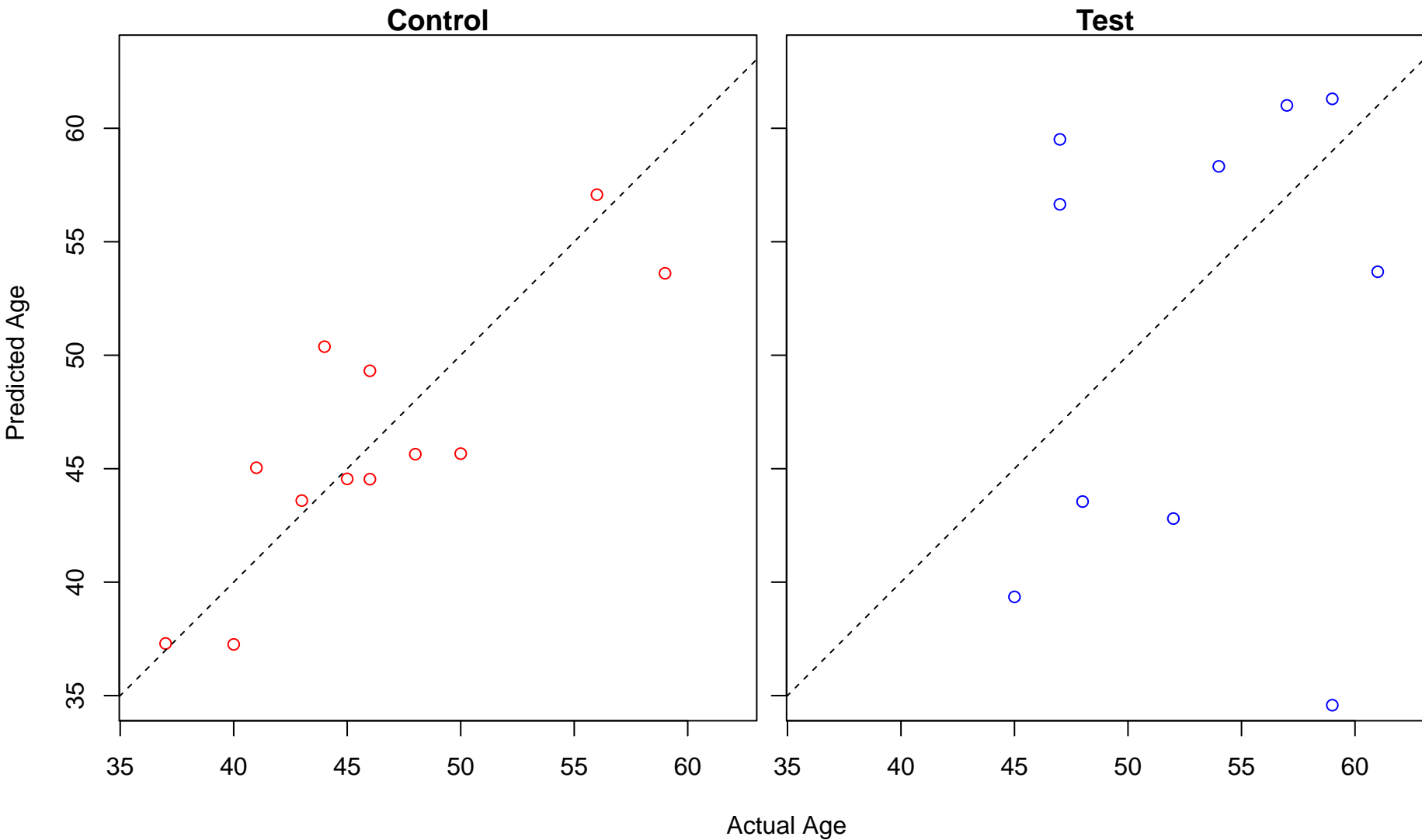
maintenance of protein location (Score: 24.156779)



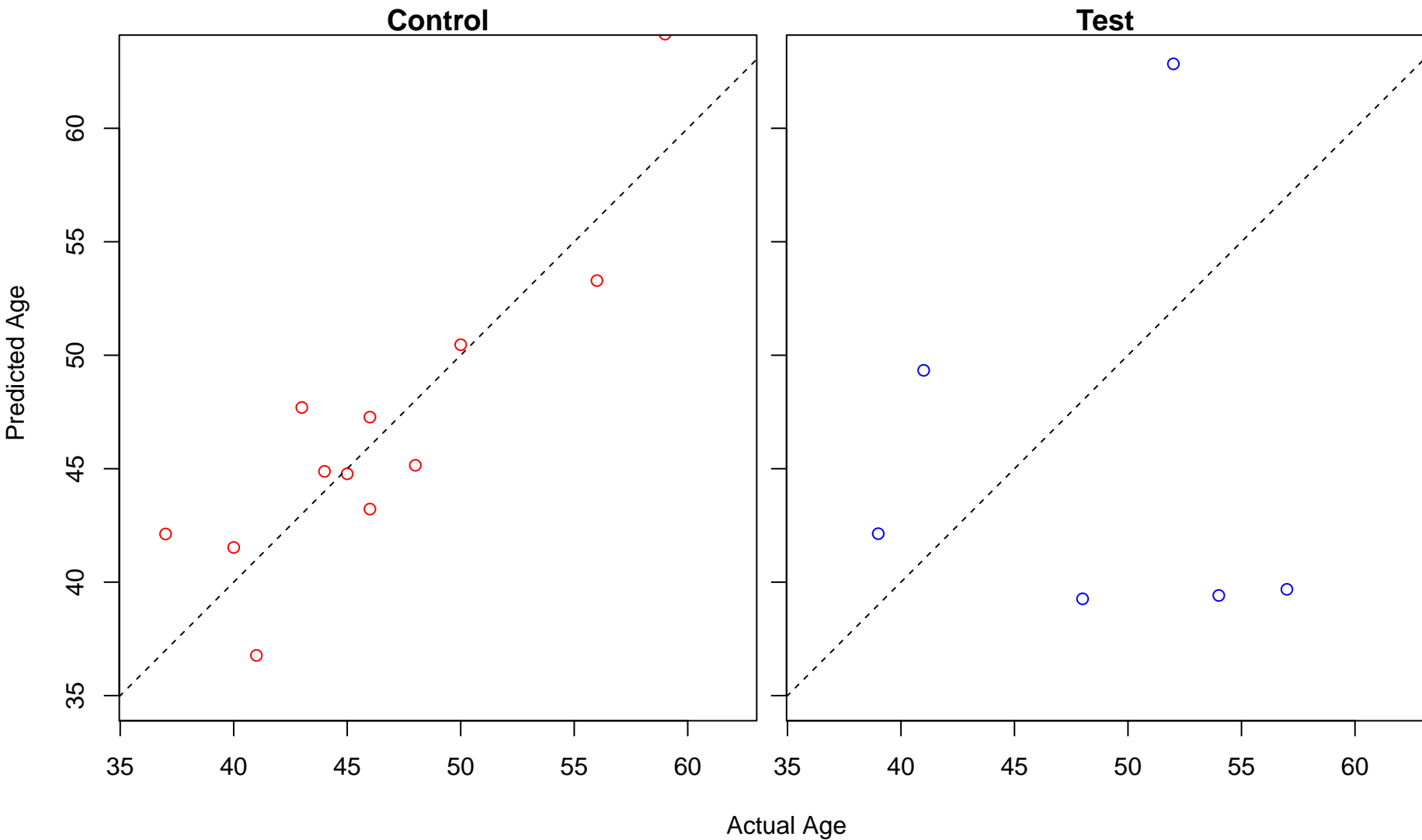
I-kappaB phosphorylation (Score: 24.151331)



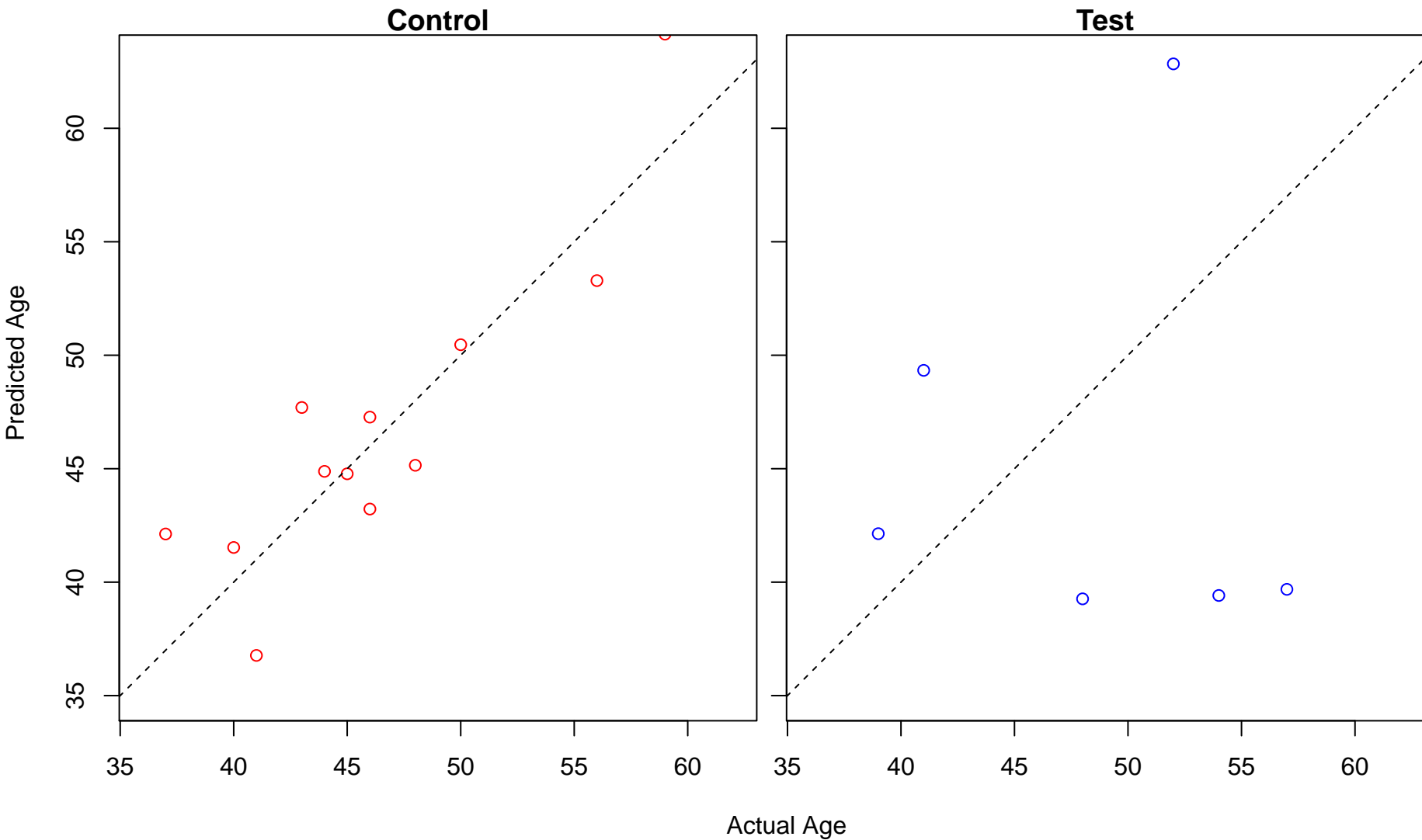
regulation of platelet activation (Score: 24.148873)



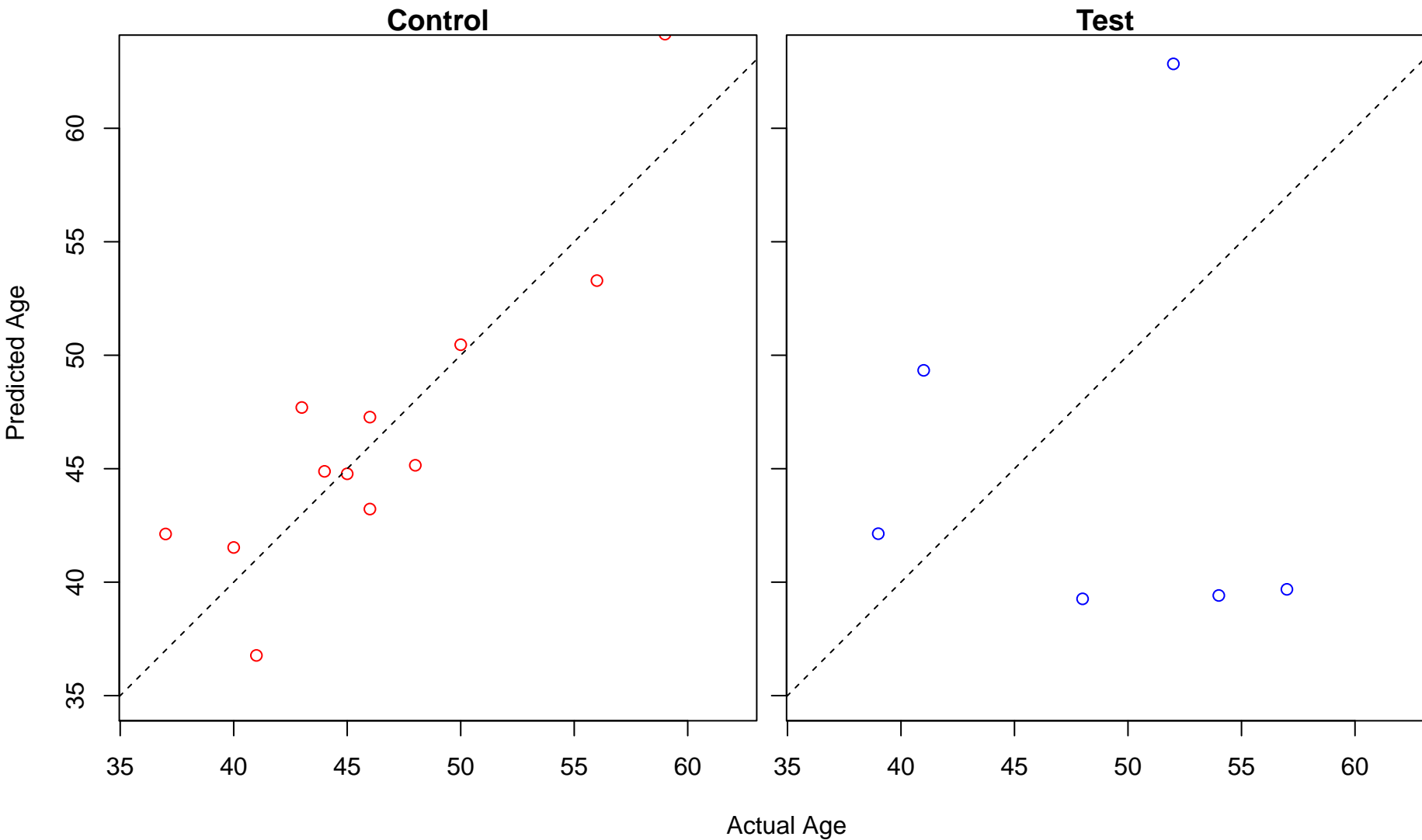
nucleoside bisphosphate biosynthetic process (Score: 24.144176)



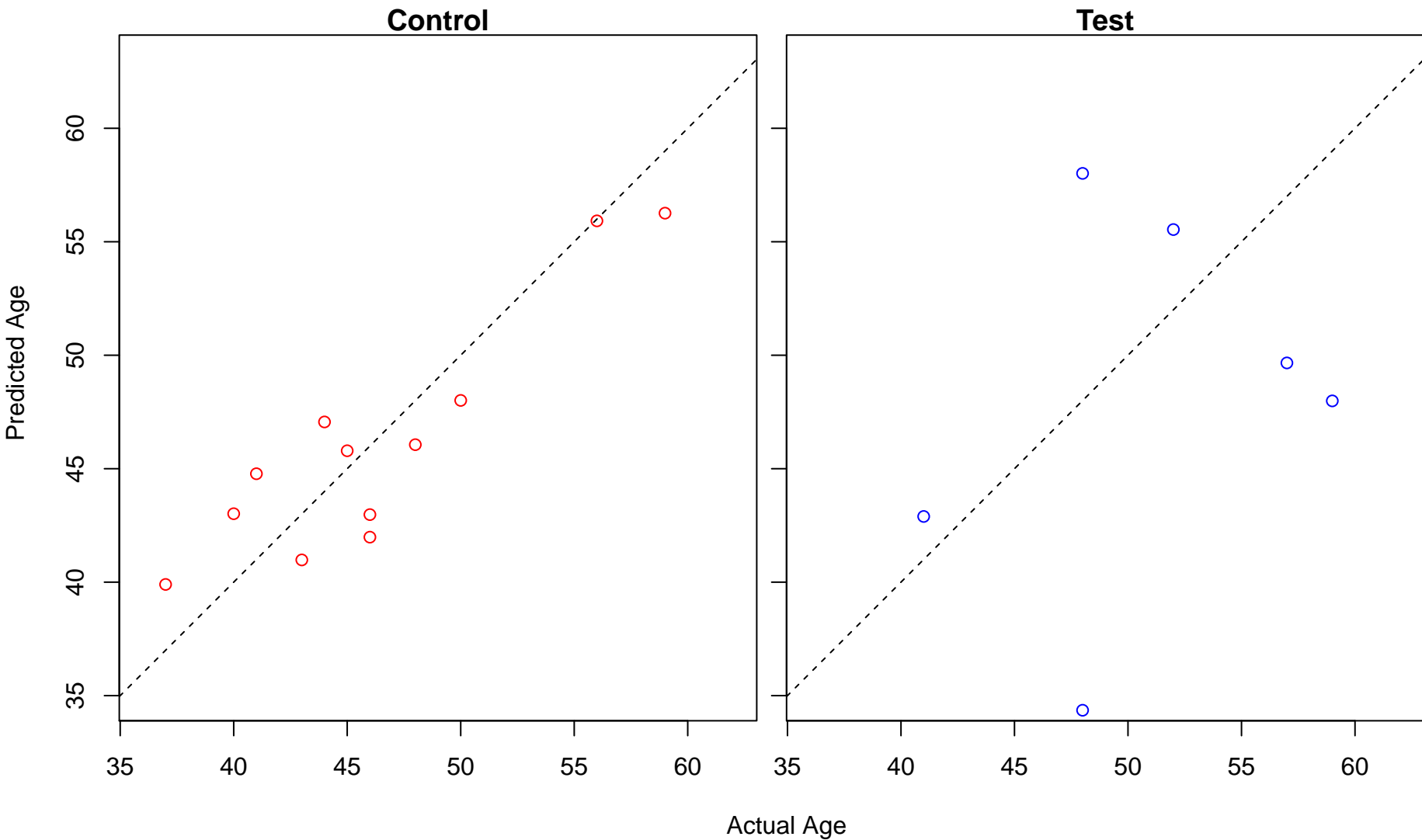
ribonucleoside biphosphate biosynthetic process (Score: 24.144176)



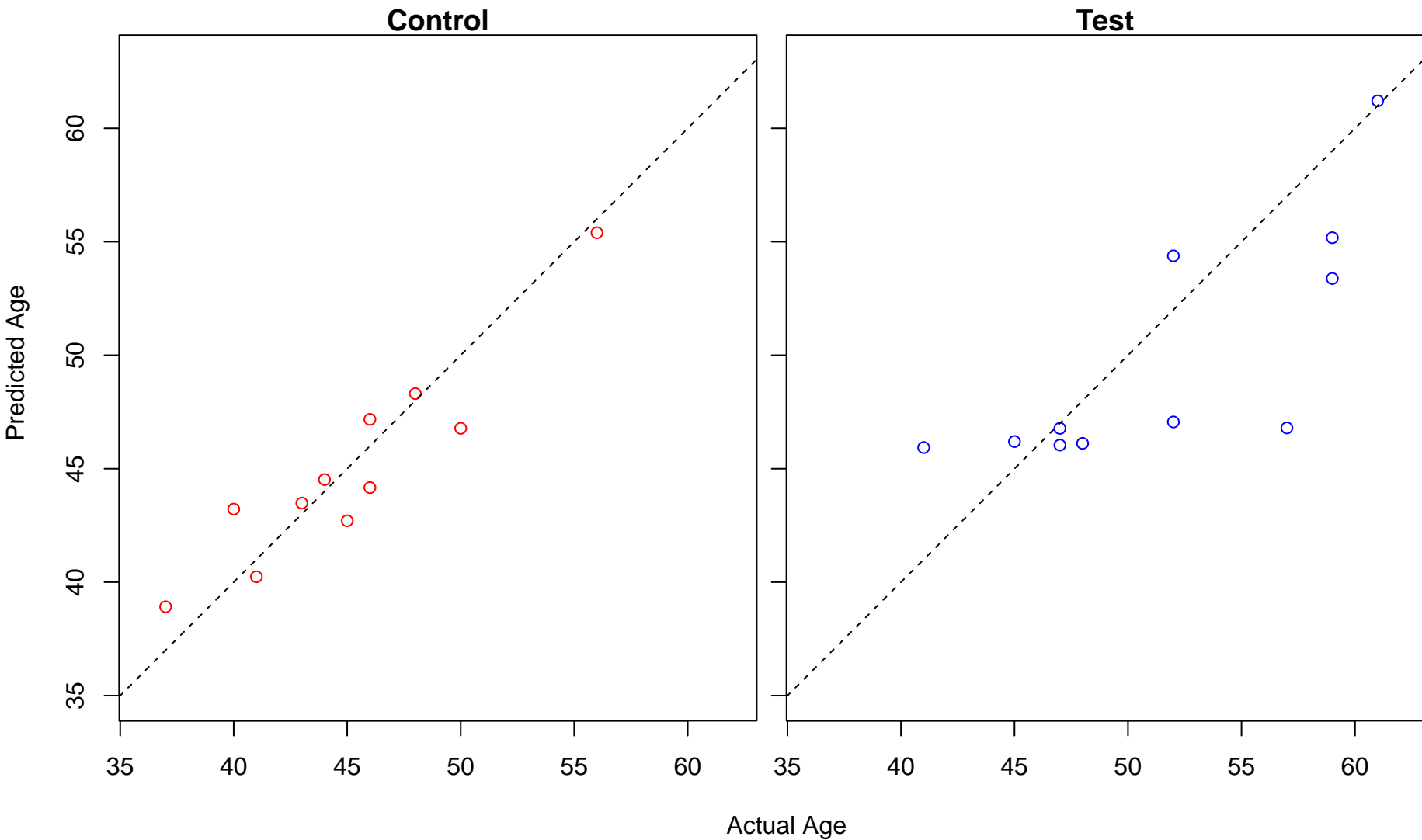
purine nucleoside bisphosphate biosynthetic process (Score: 24.144176)



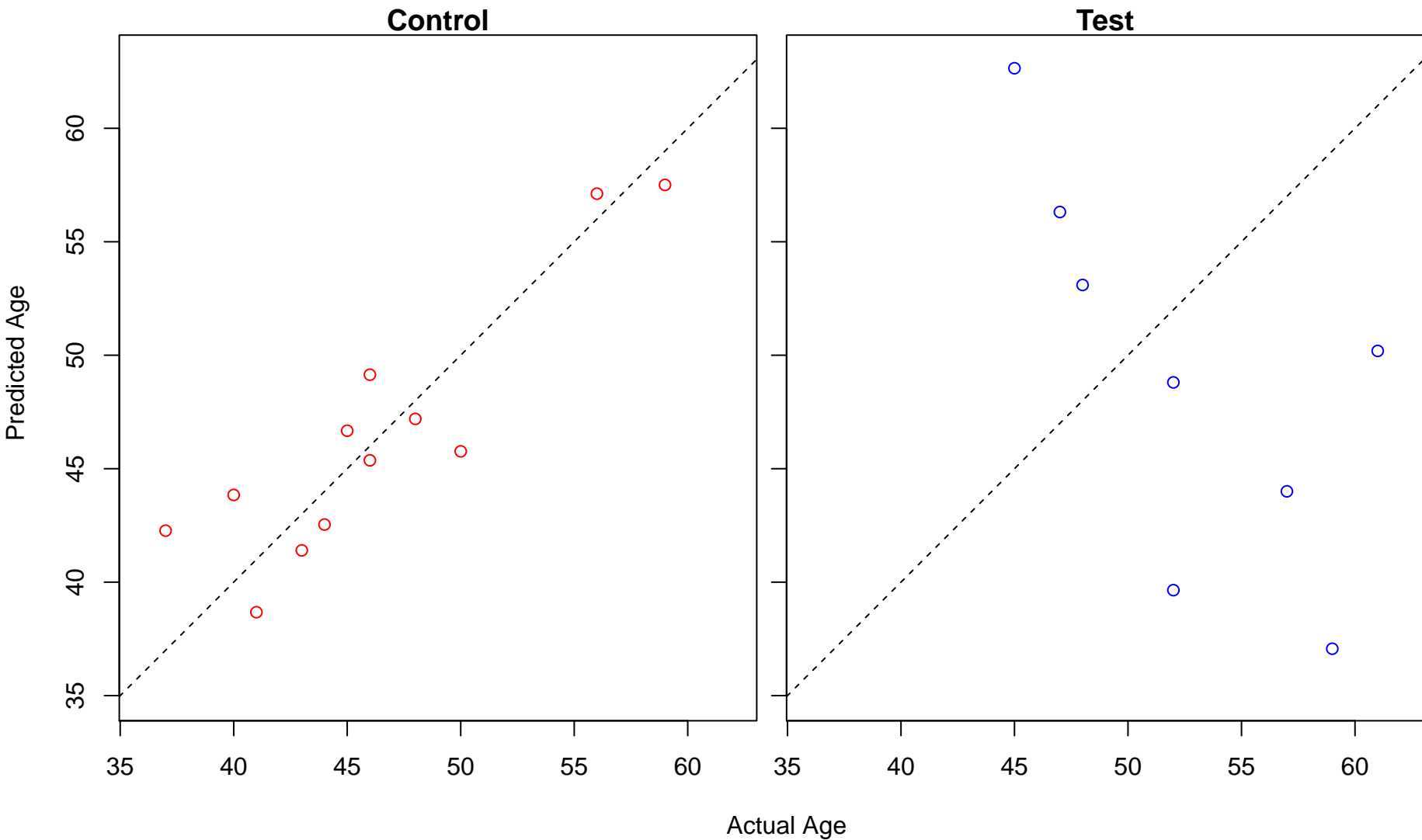
muscle cell fate commitment (Score: 24.034638)



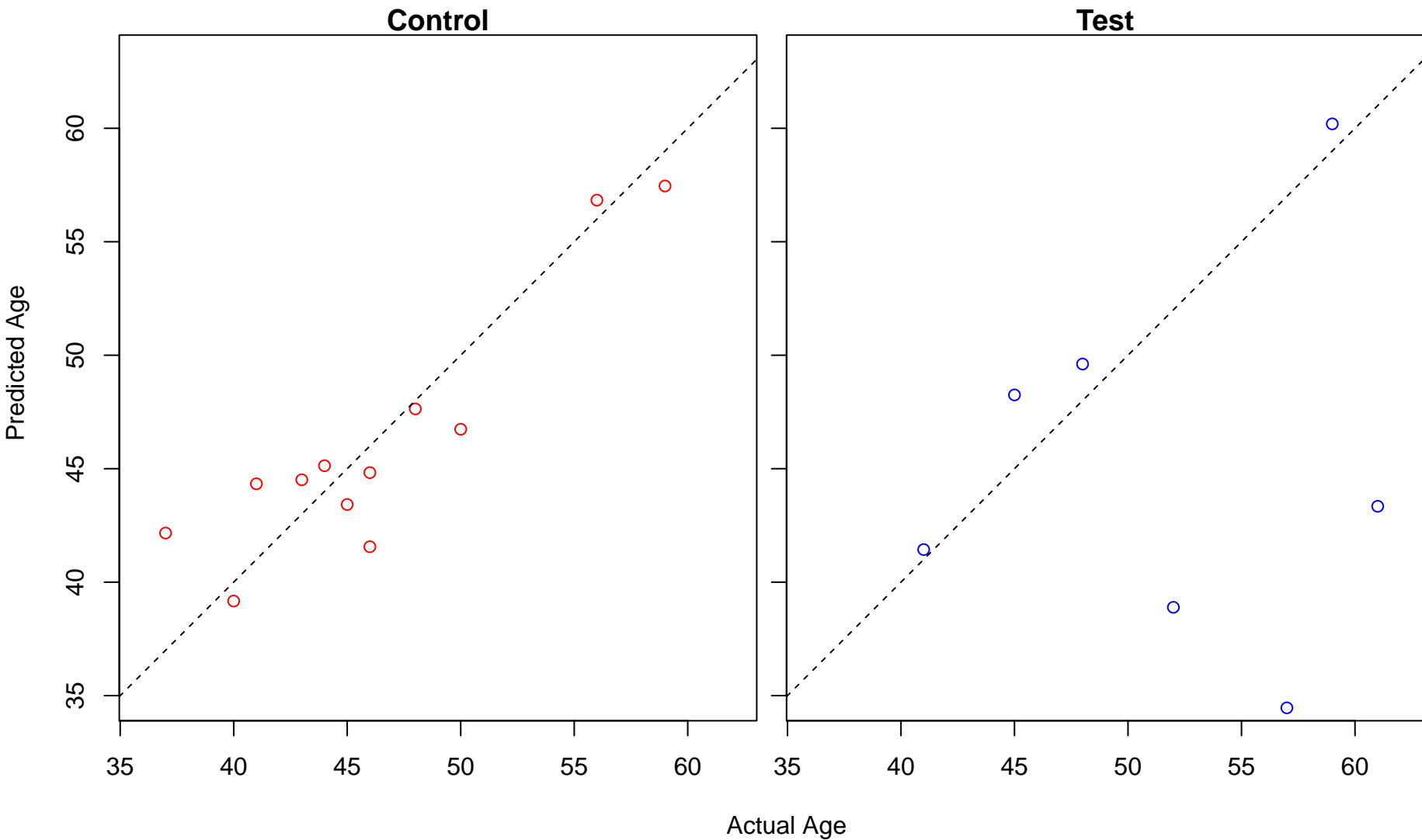
modulation of excitatory postsynaptic potential (Score: 23.984464)



regulation of CD4-positive, alpha-beta T cell activation (Score: 23.973565)

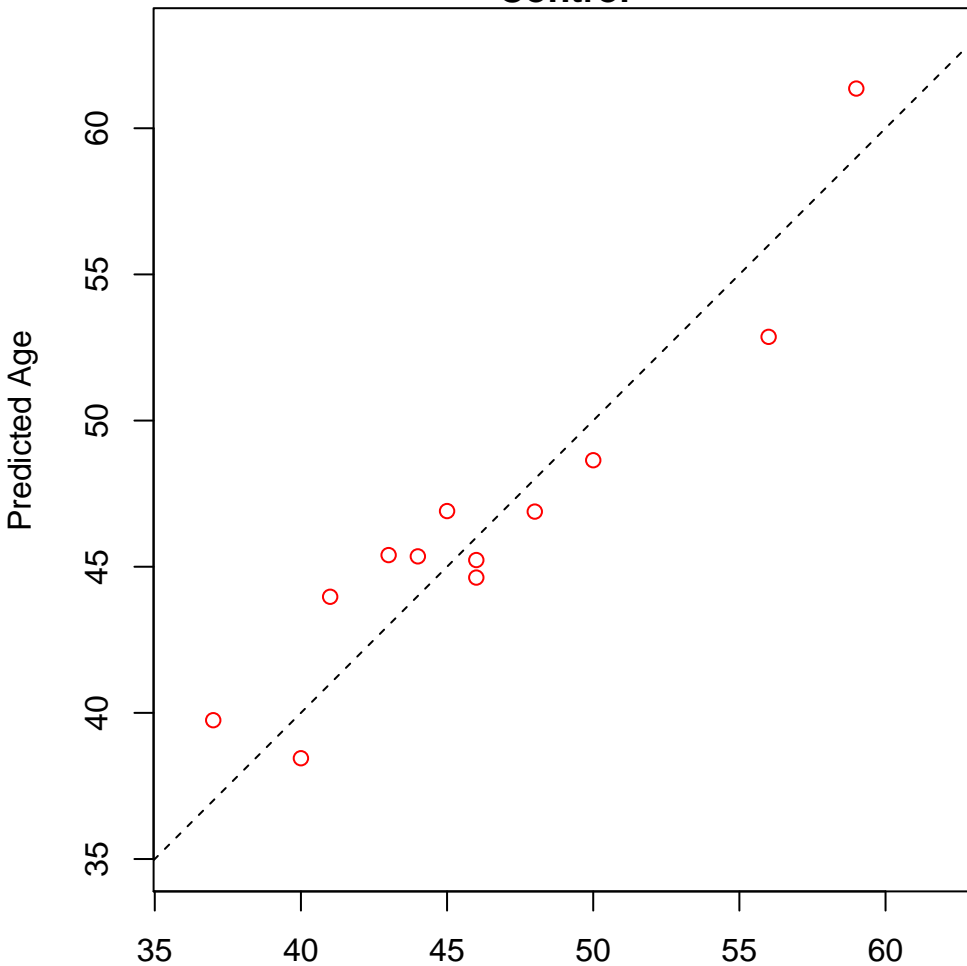


negative regulation of DNA metabolic process (Score: 23.929346)

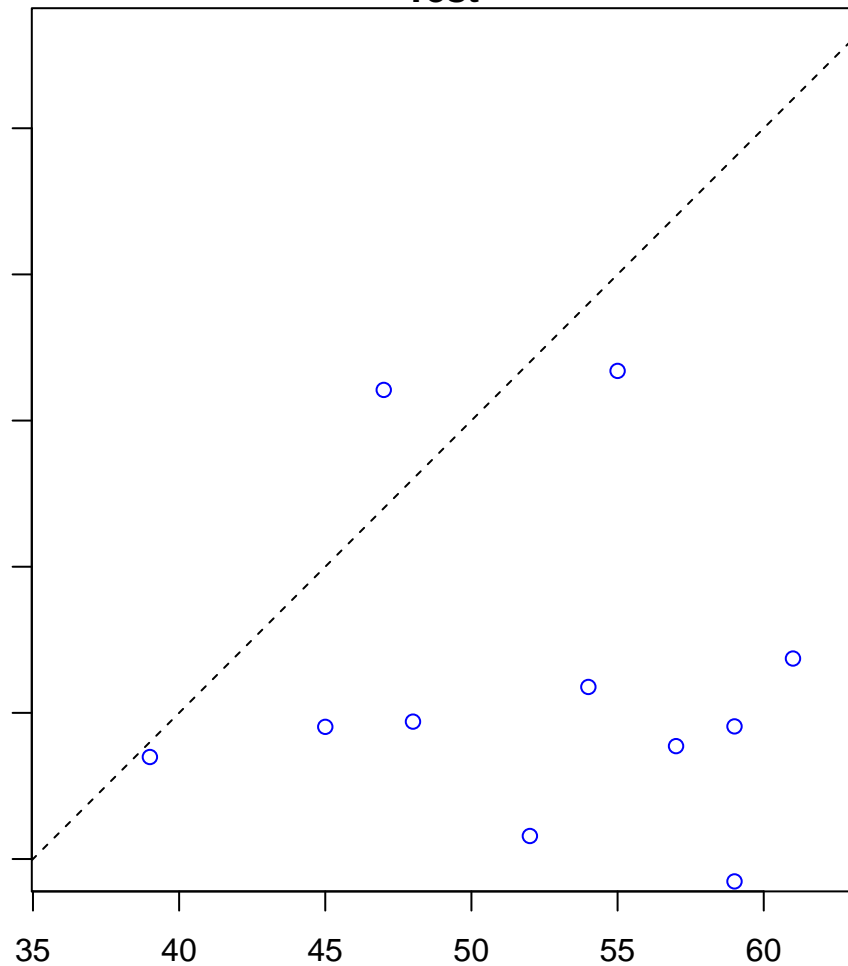


forebrain neuron differentiation (Score: 23.910690)

Control

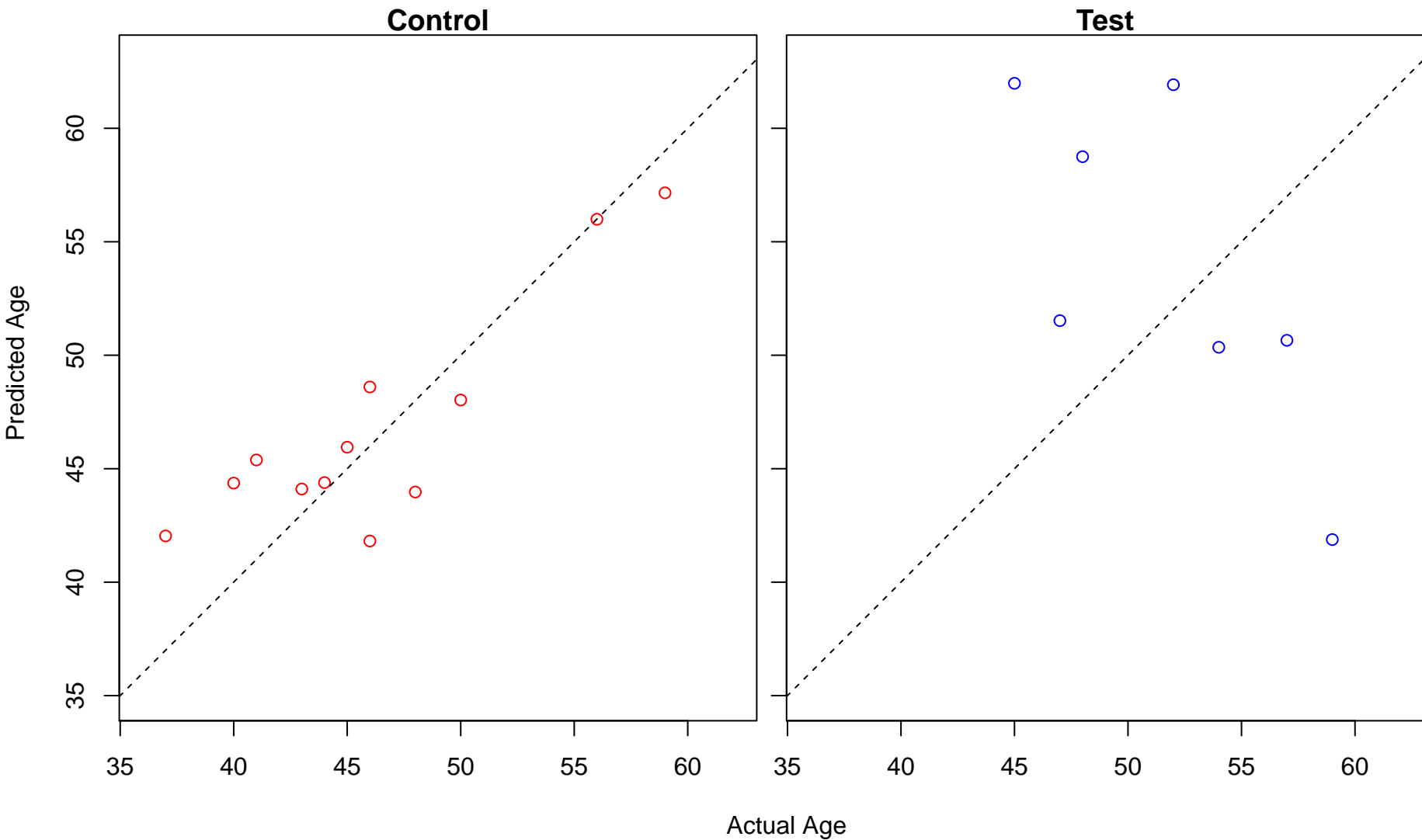


Test

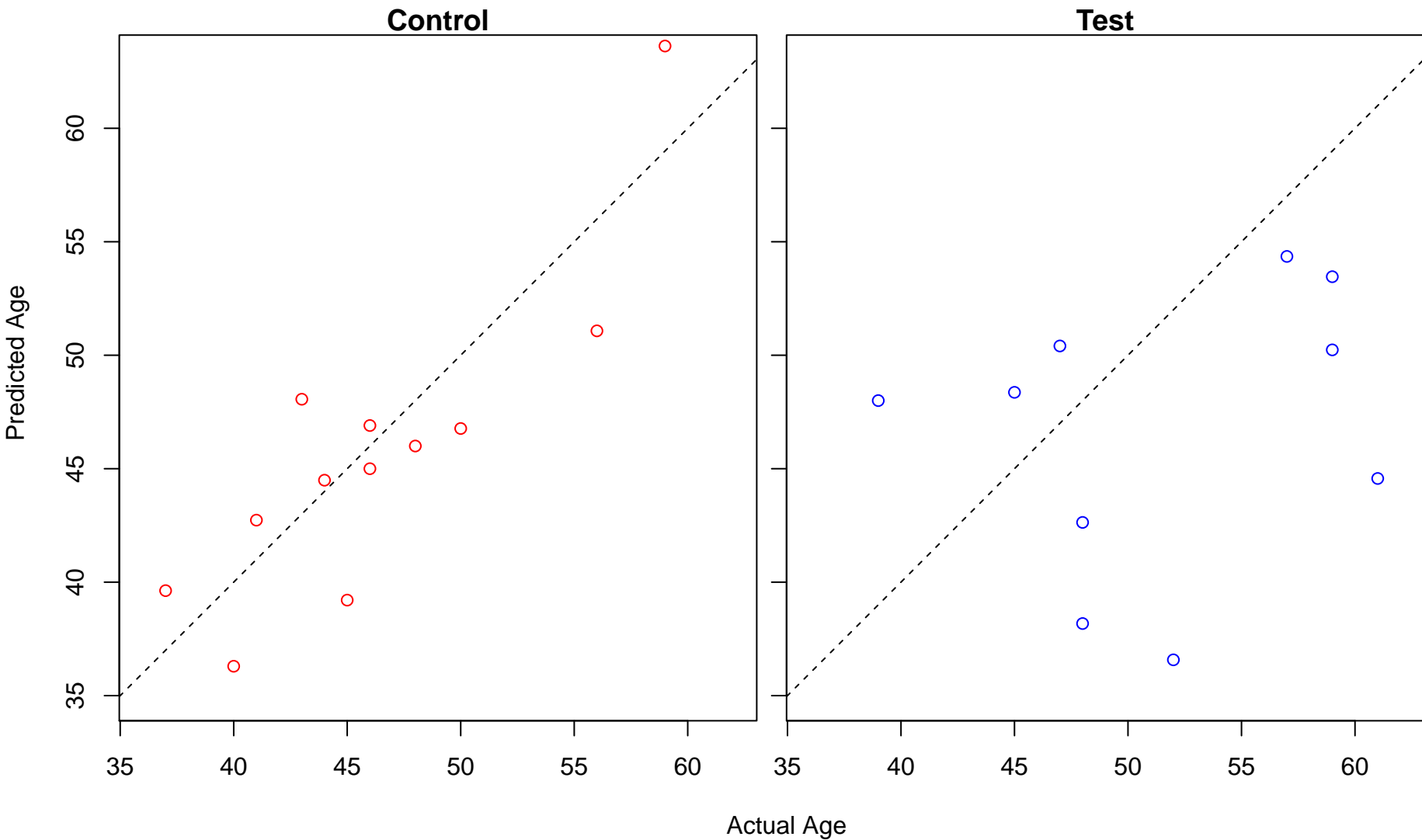


Actual Age

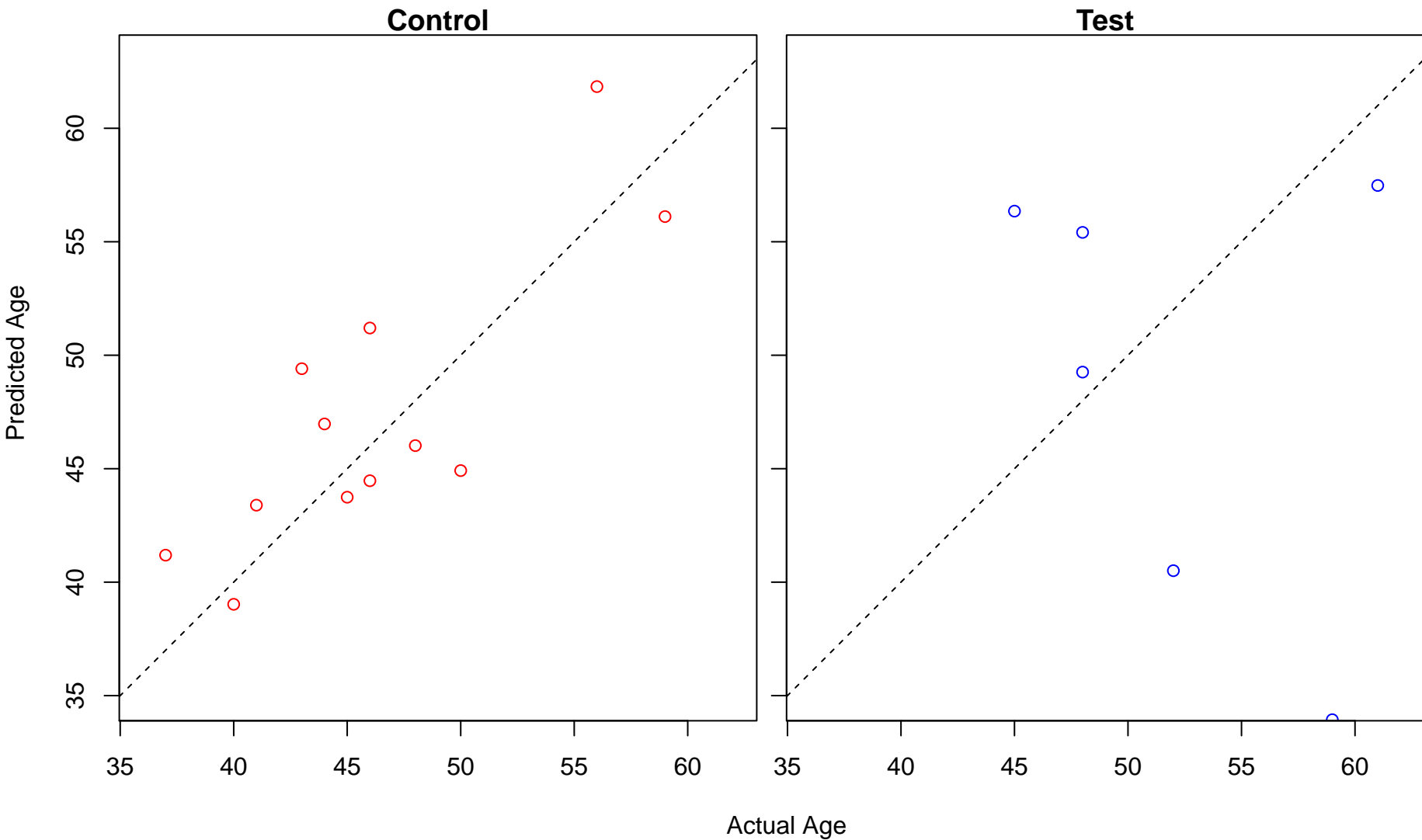
sarcoplasmic reticulum calcium ion transport (Score: 23.877365)



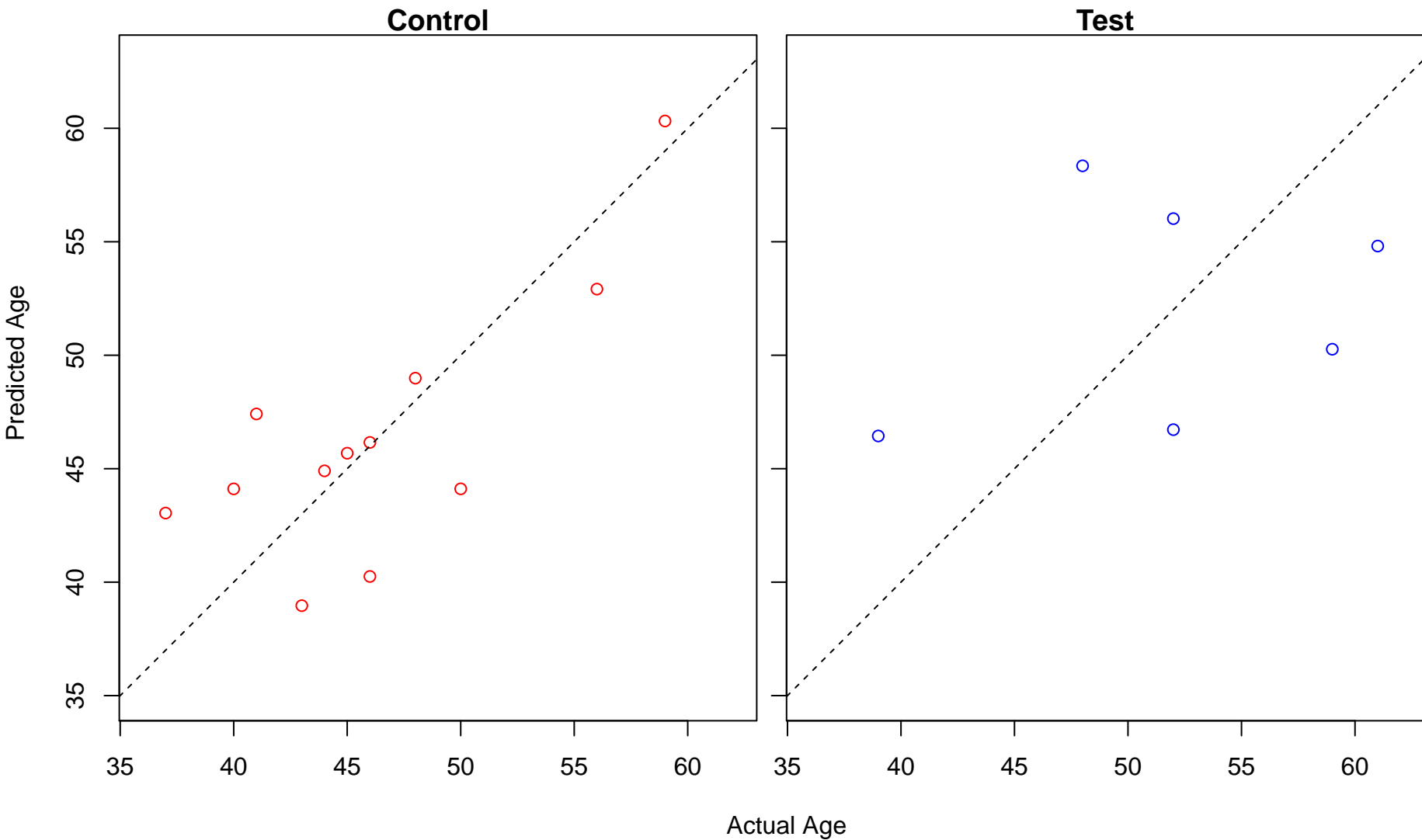
positive regulation of epidermal cell differentiation (Score: 23.846797)



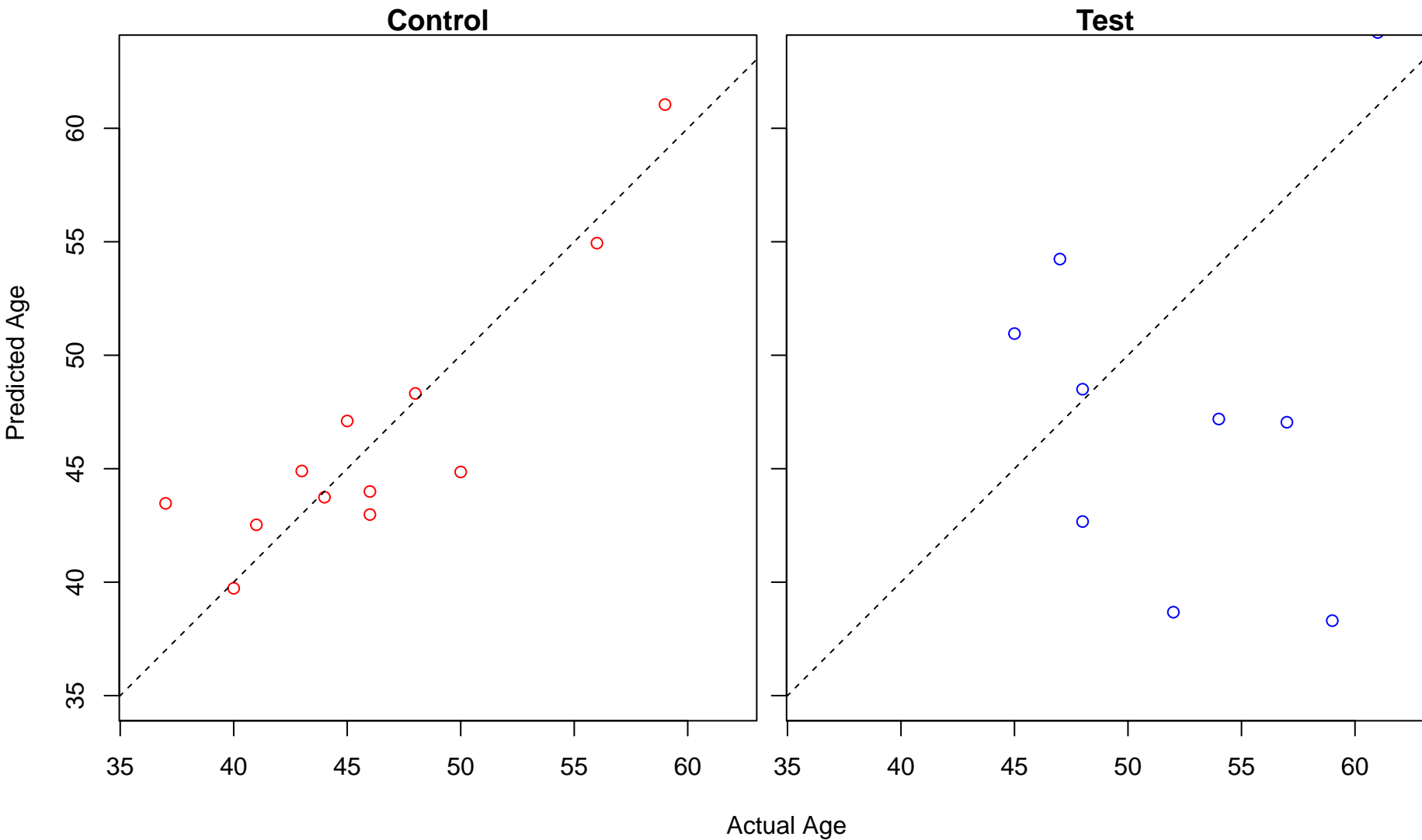
positive regulation of receptor-mediated endocytosis (Score: 23.761175)



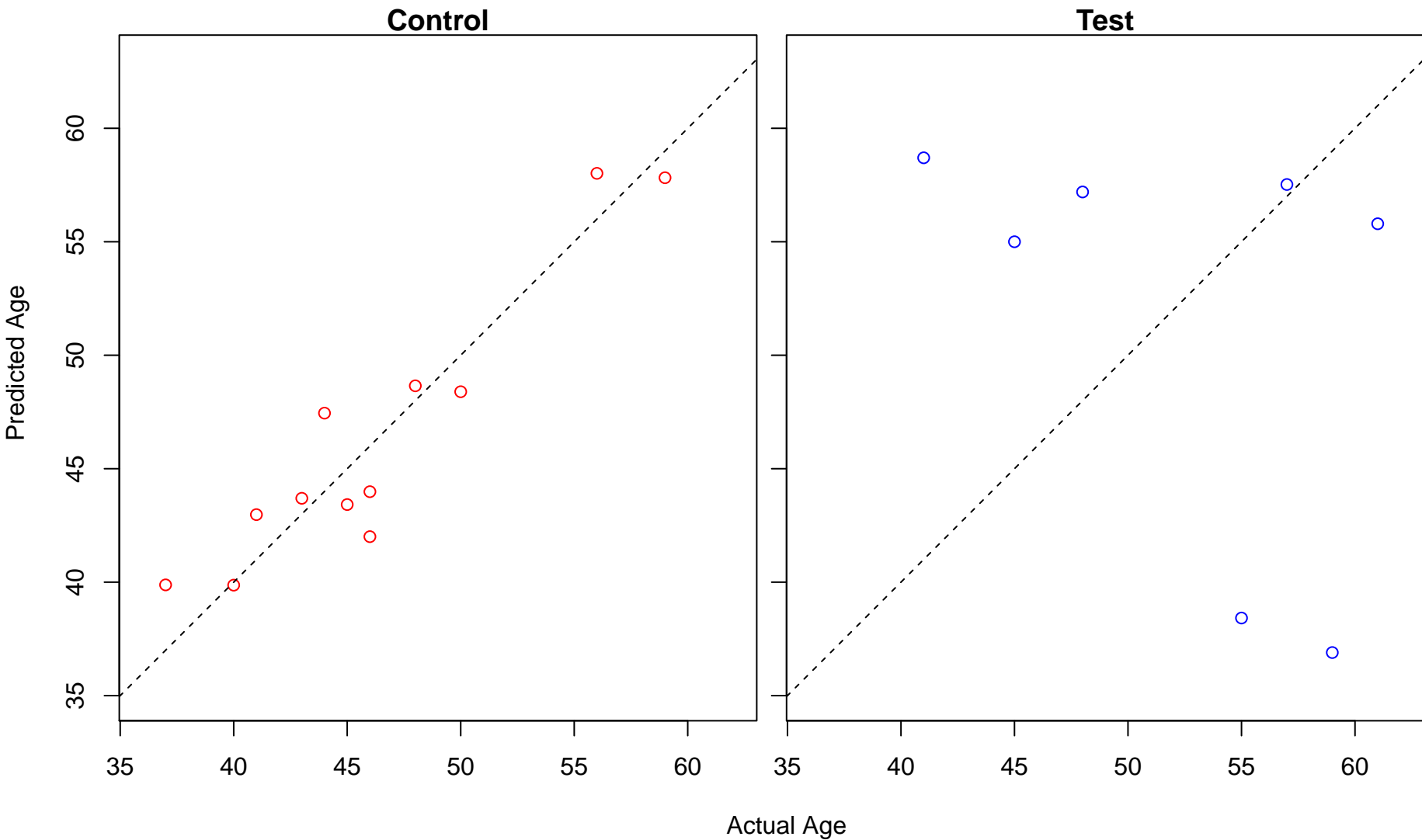
linoleic acid metabolic process (Score: 23.671083)



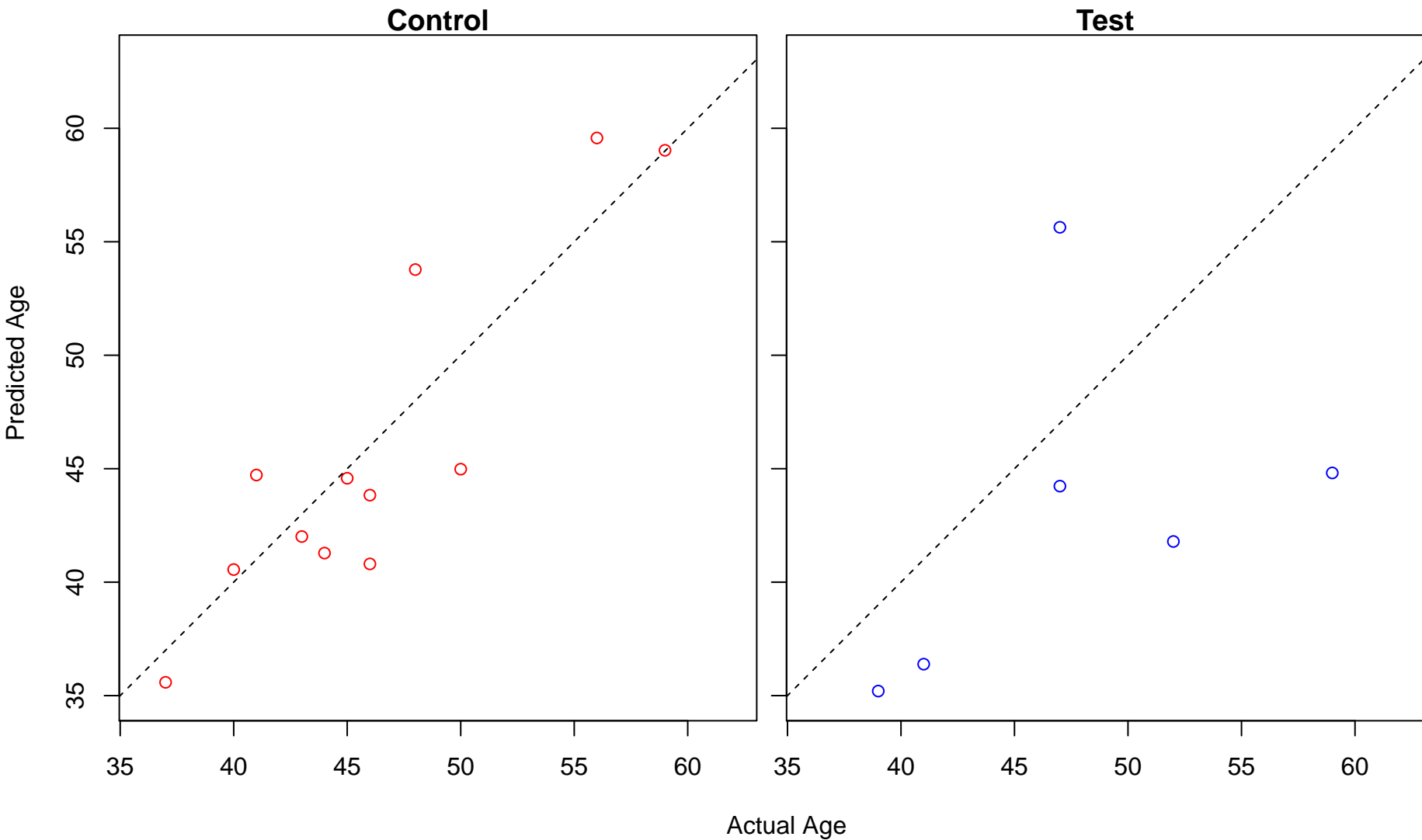
protein modification by small protein removal (Score: 23.634816)



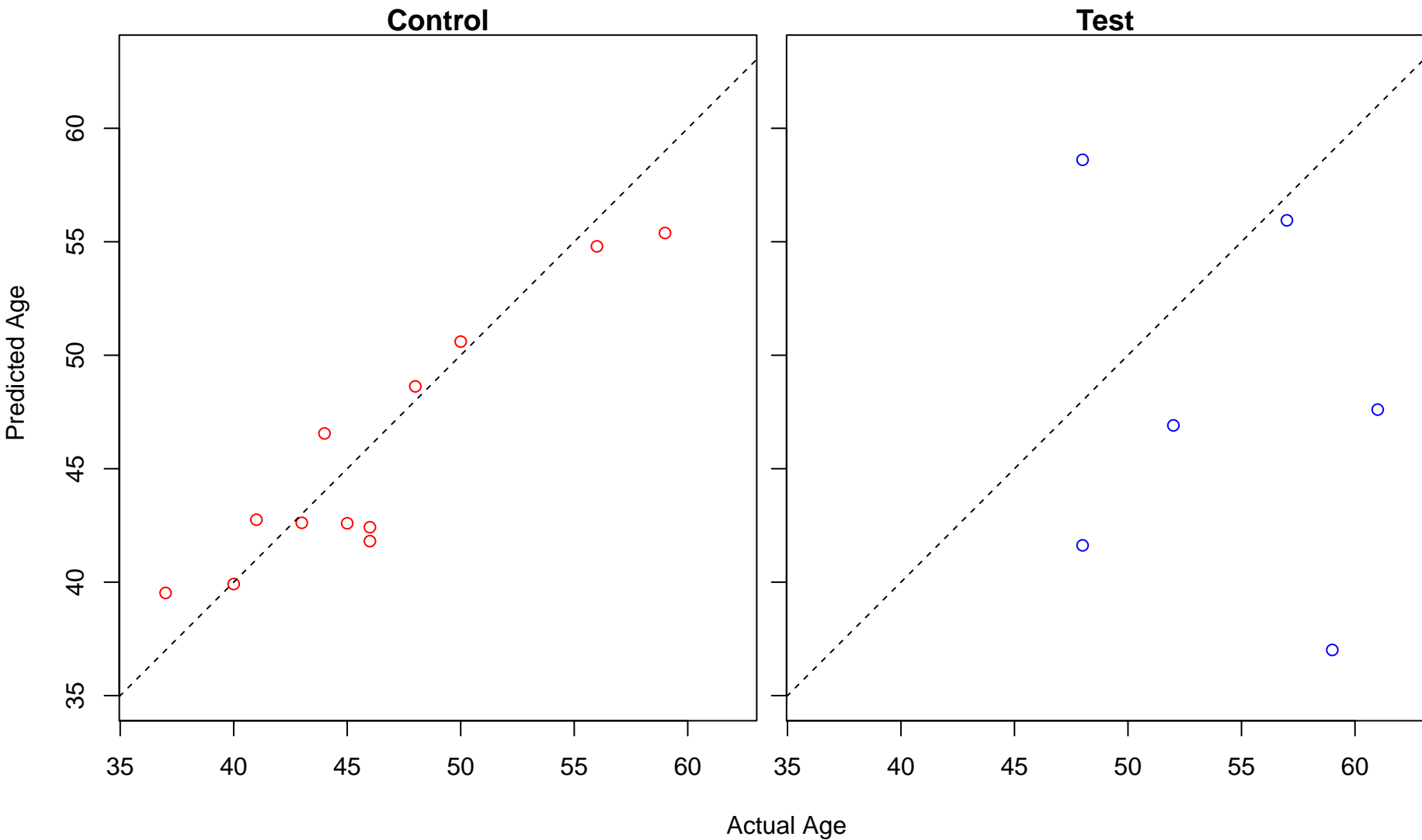
multicellular organismal macromolecule metabolic process (Score: 23.533565)



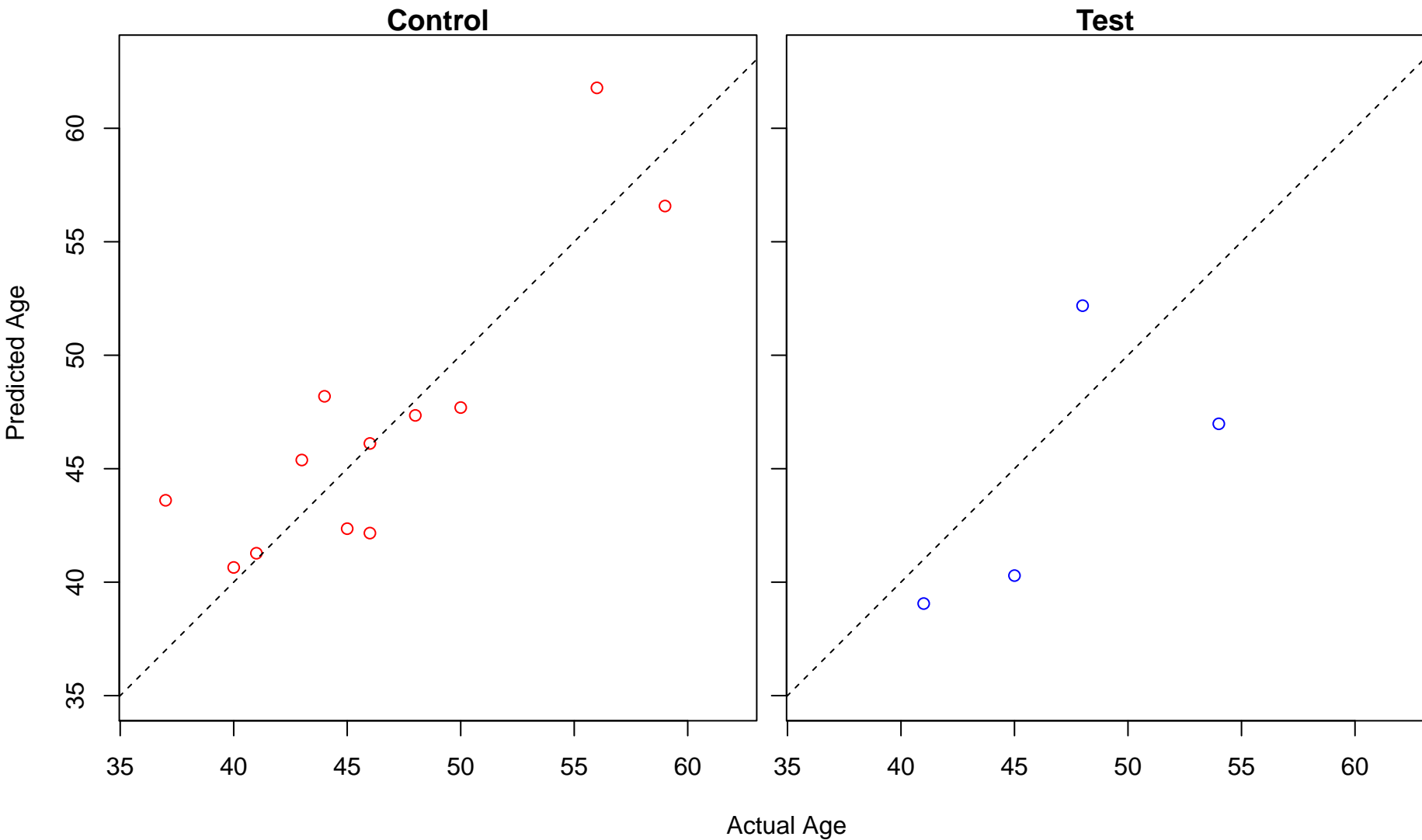
G-protein coupled glutamate receptor signaling pathway (Score: 23.379098)



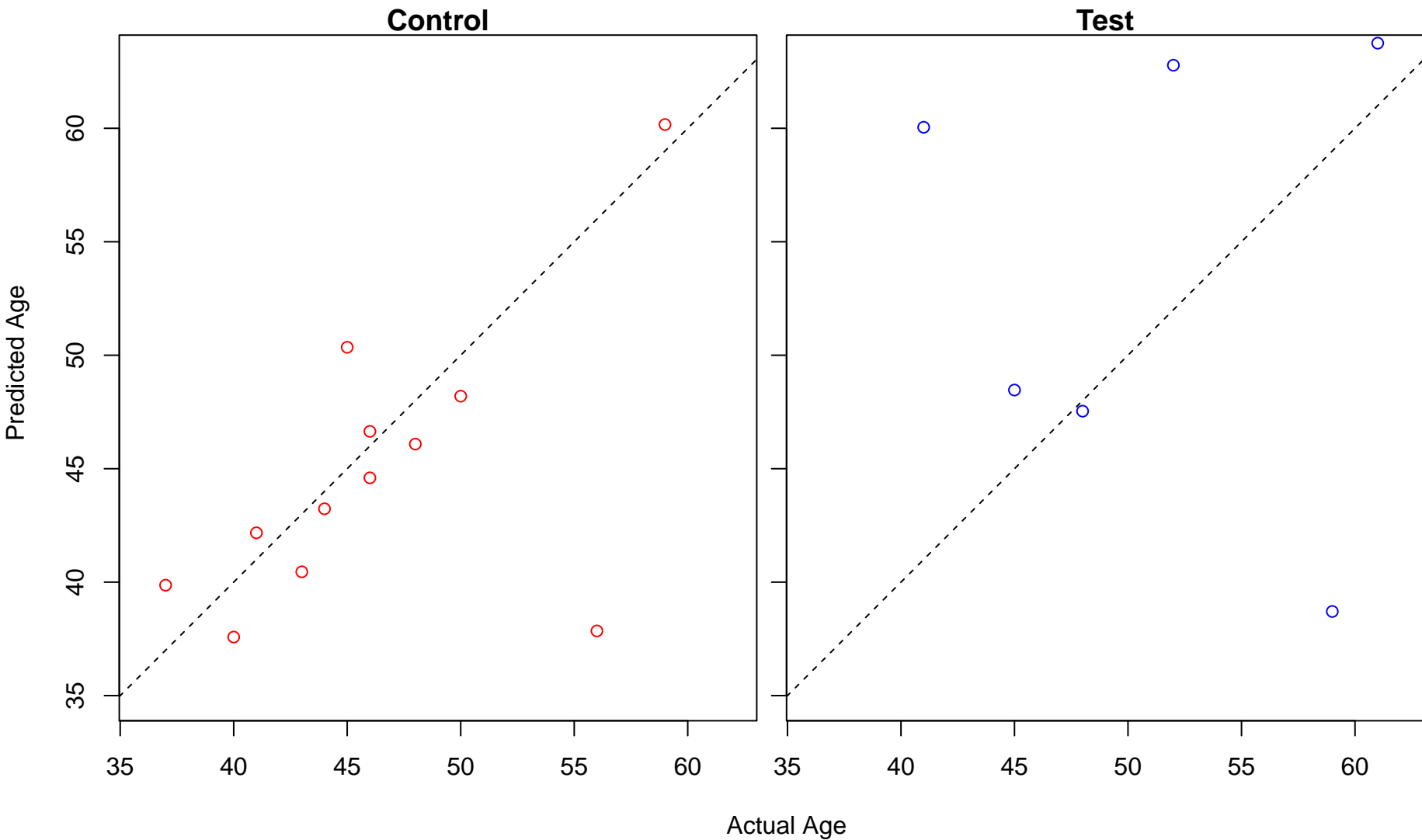
response to nutrient levels (Score: 23.344231)



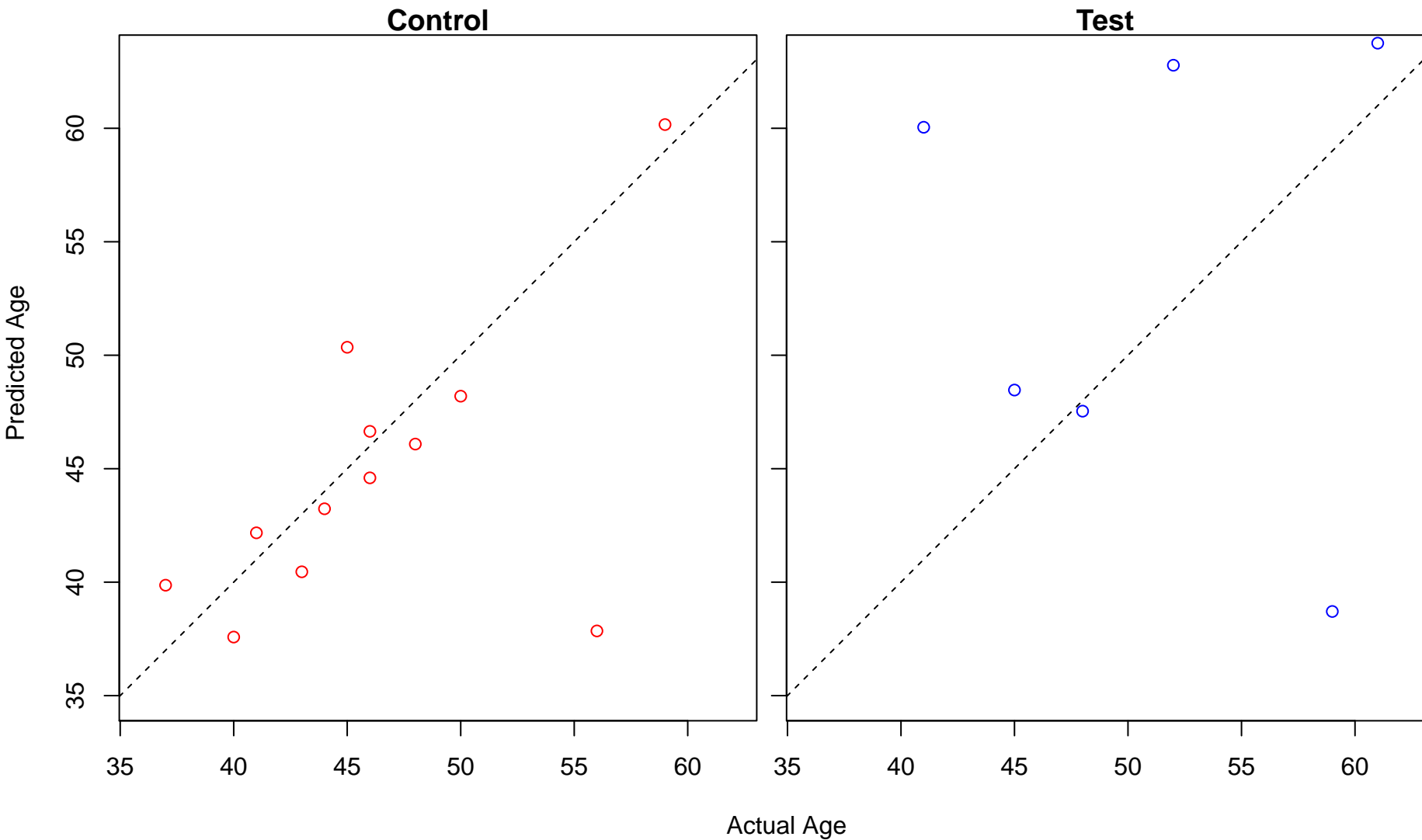
response to pH (Score: 23.175981)



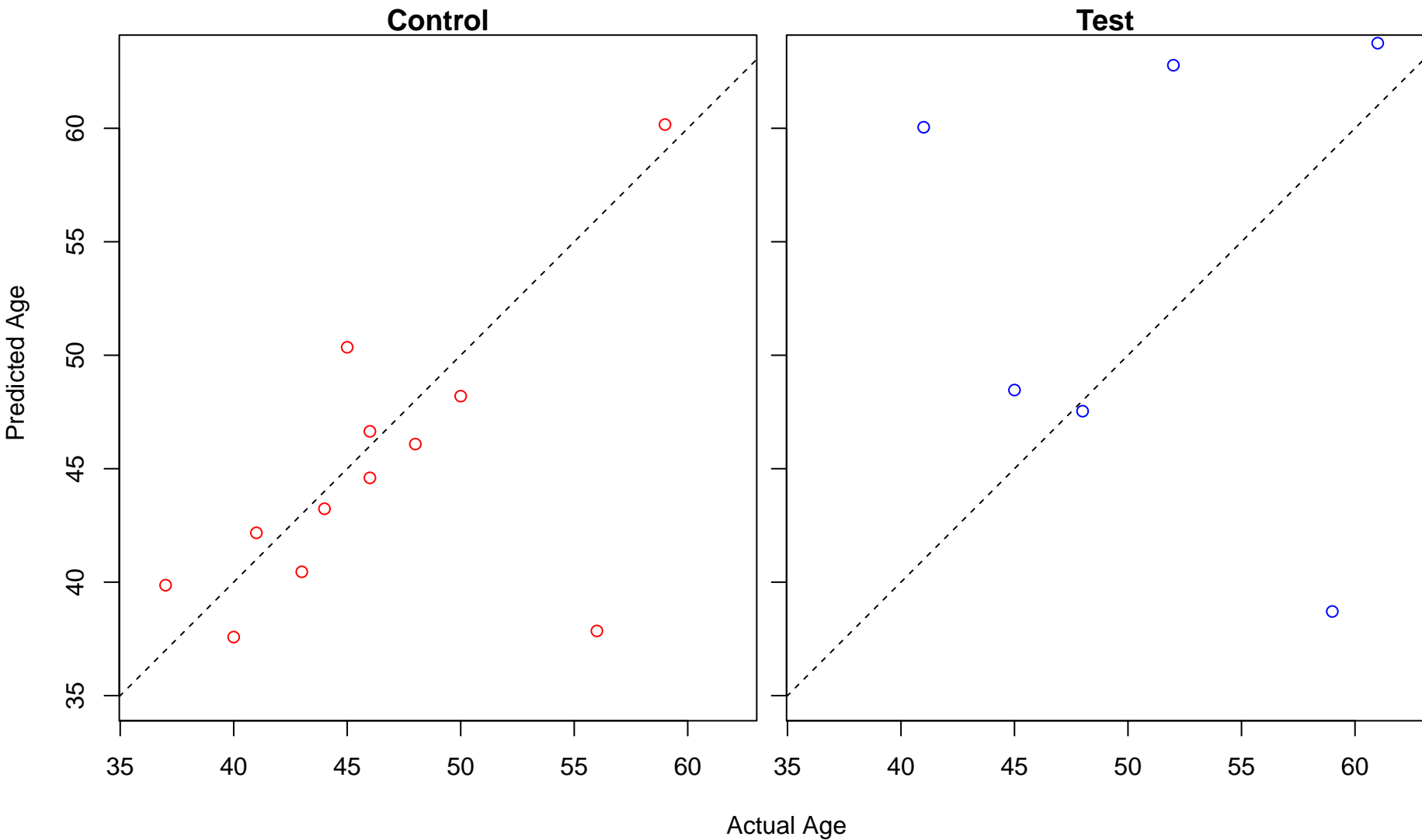
cytidine catabolic process (Score: 23.047816)



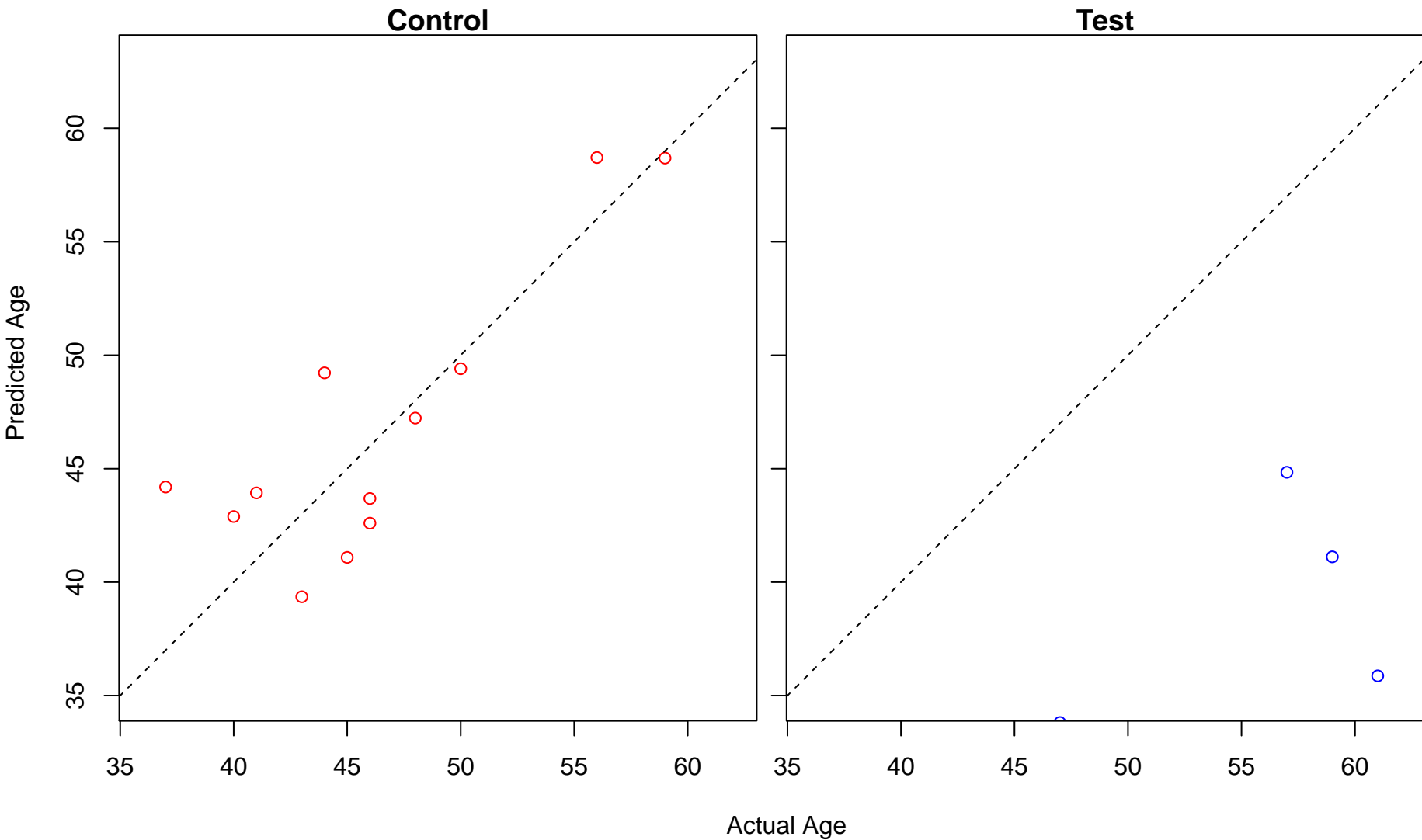
cytidine deamination (Score: 23.047816)



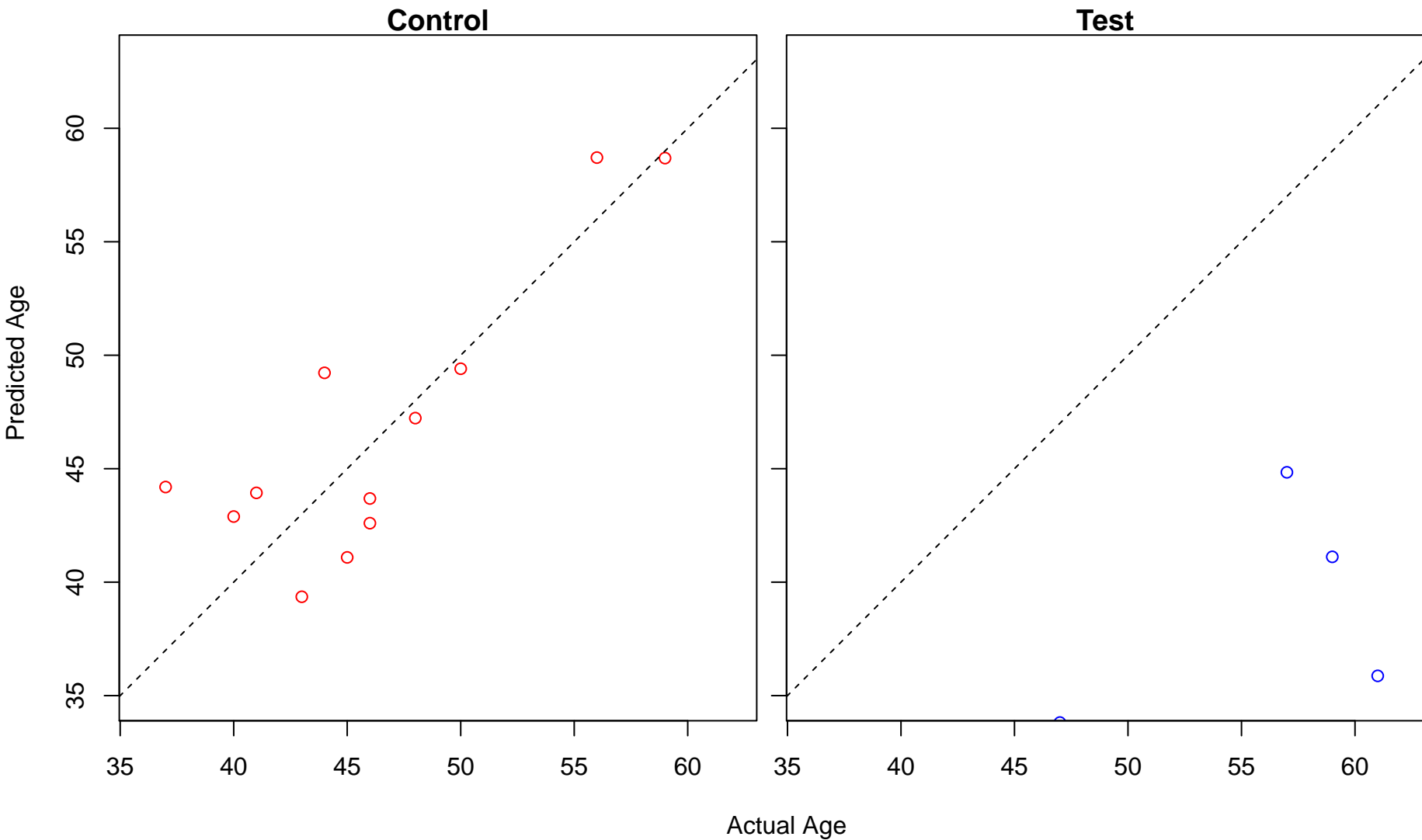
cytidine metabolic process (Score: 23.047816)



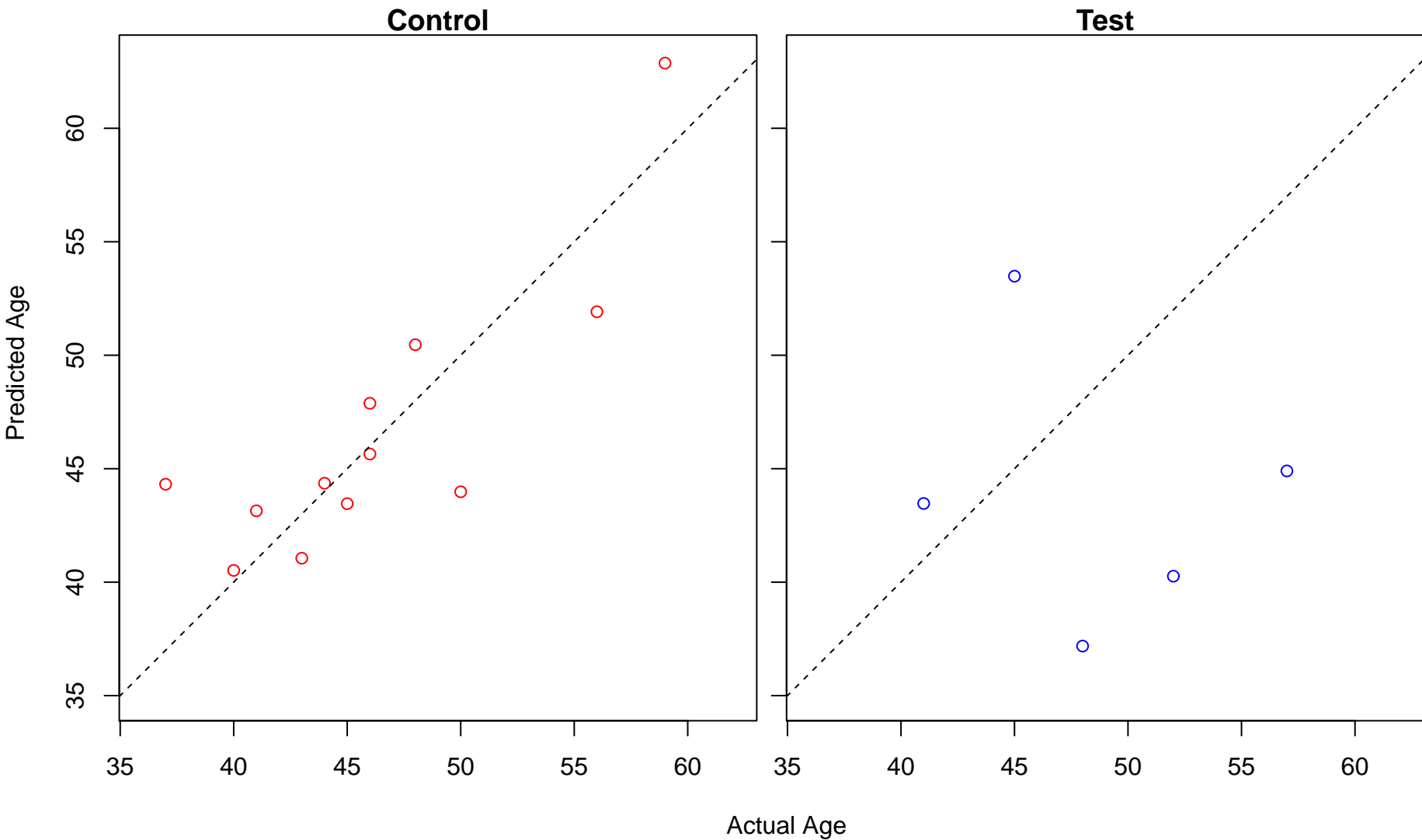
plus-end-directed vesicle transport along microtubule (Score: 23.029180)



plus-end-directed organelle transport along microtubule (Score: 23.029180)

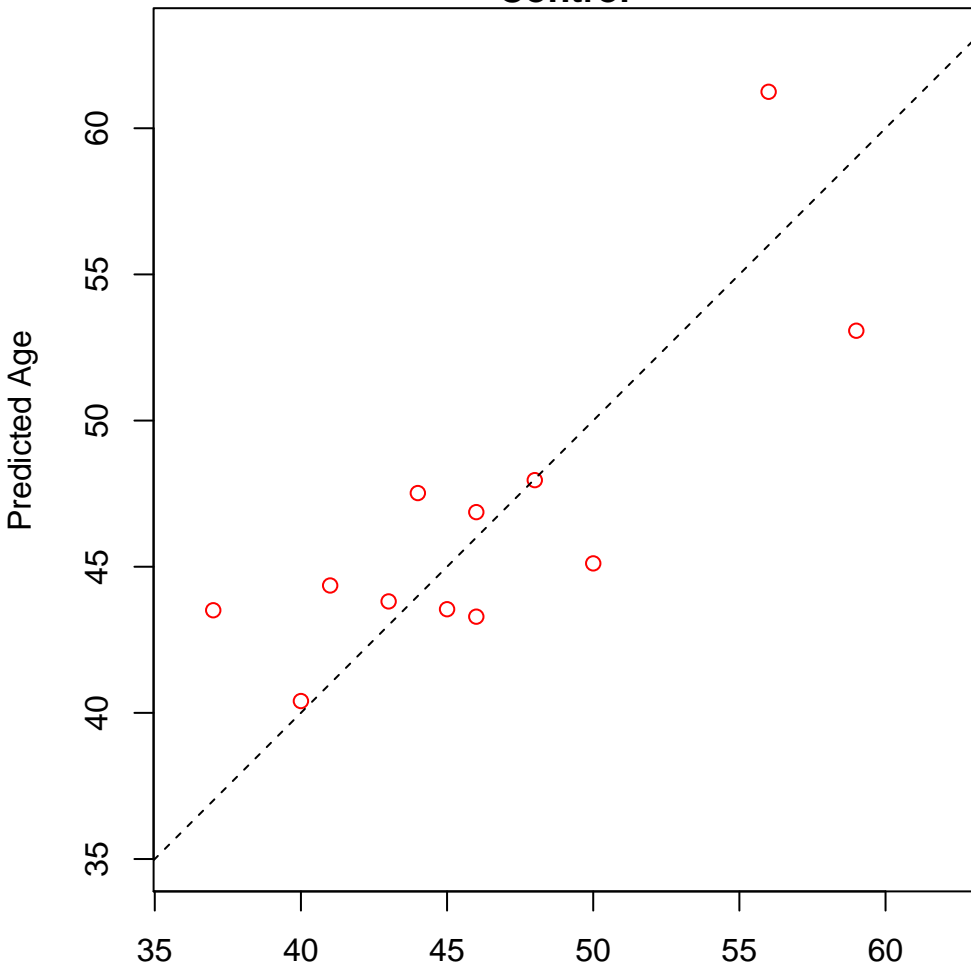


mitotic G2/M transition checkpoint (Score: 23.005291)

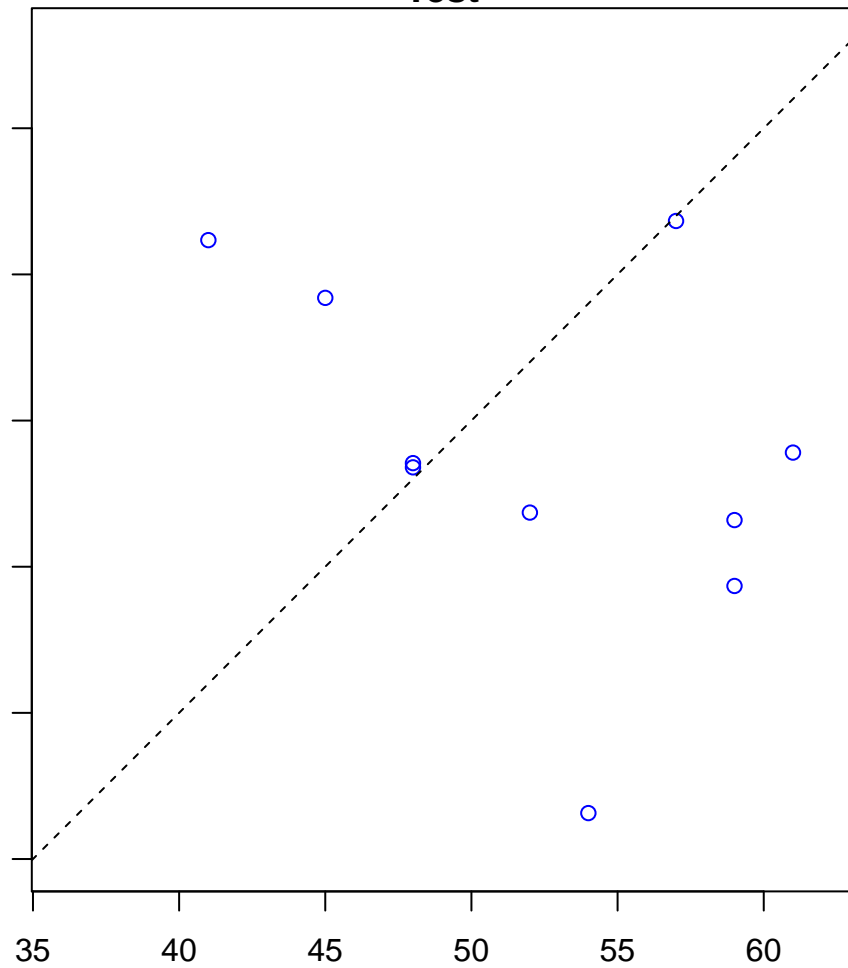


response to mechanical stimulus (Score: 22.954830)

Control

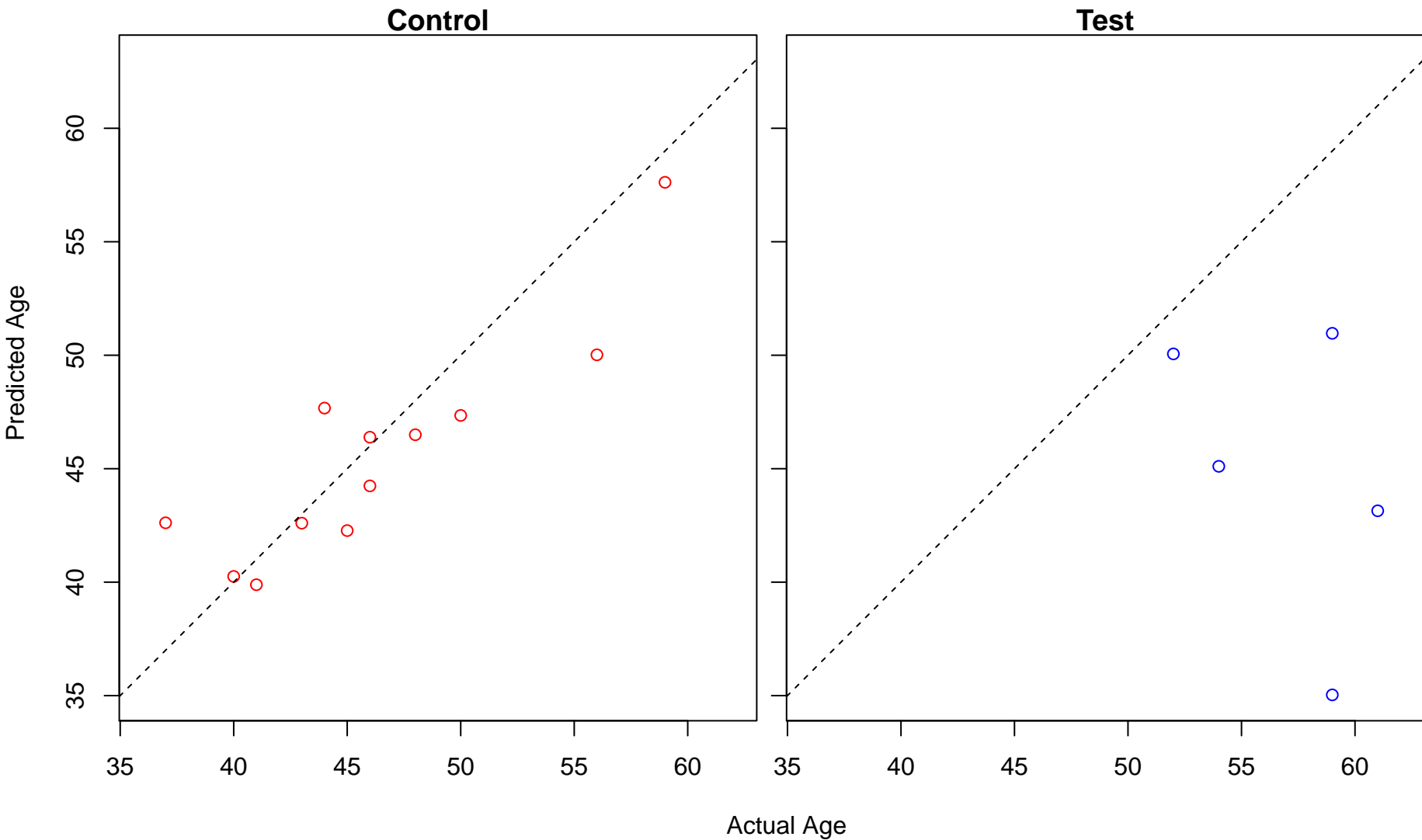


Test

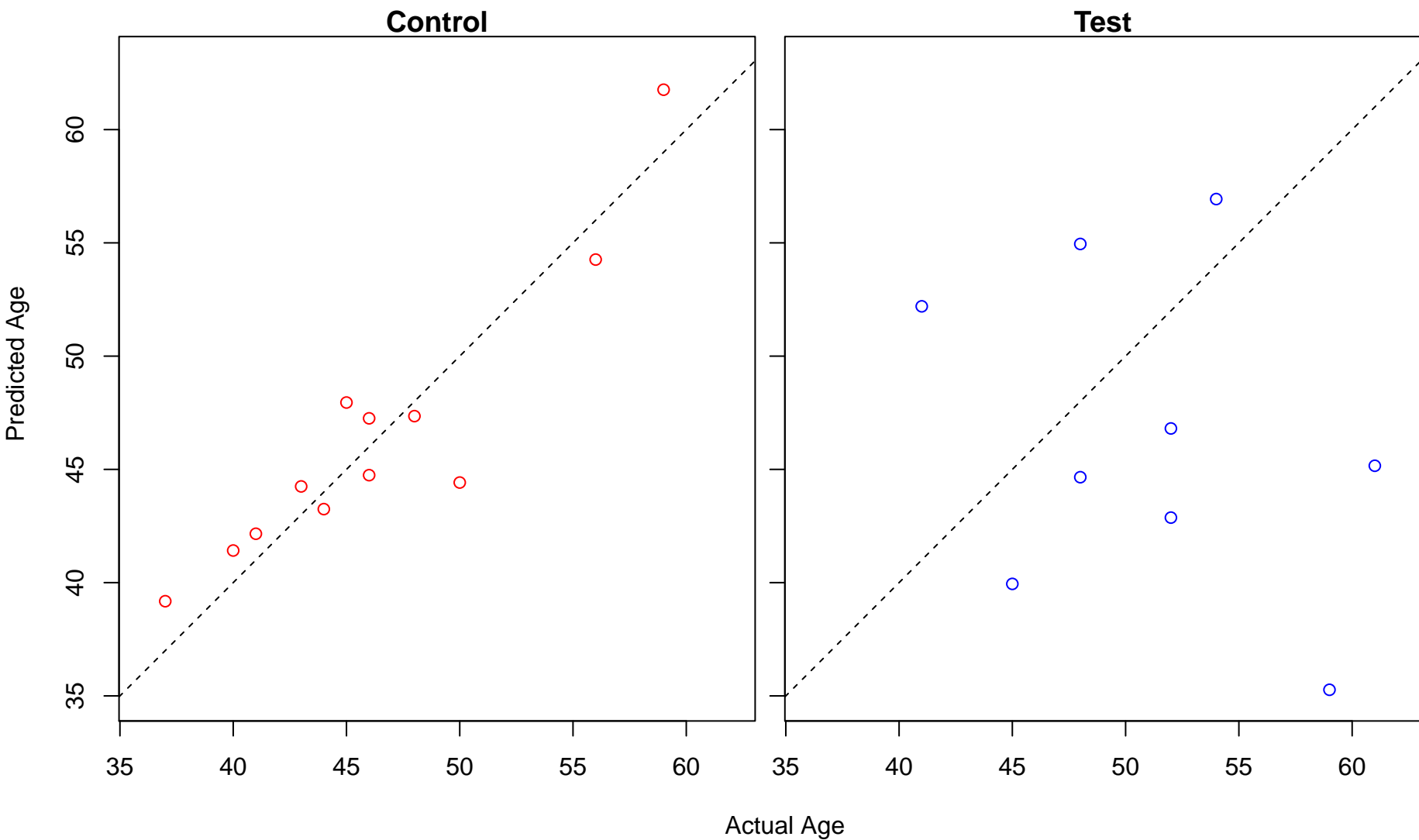


Actual Age

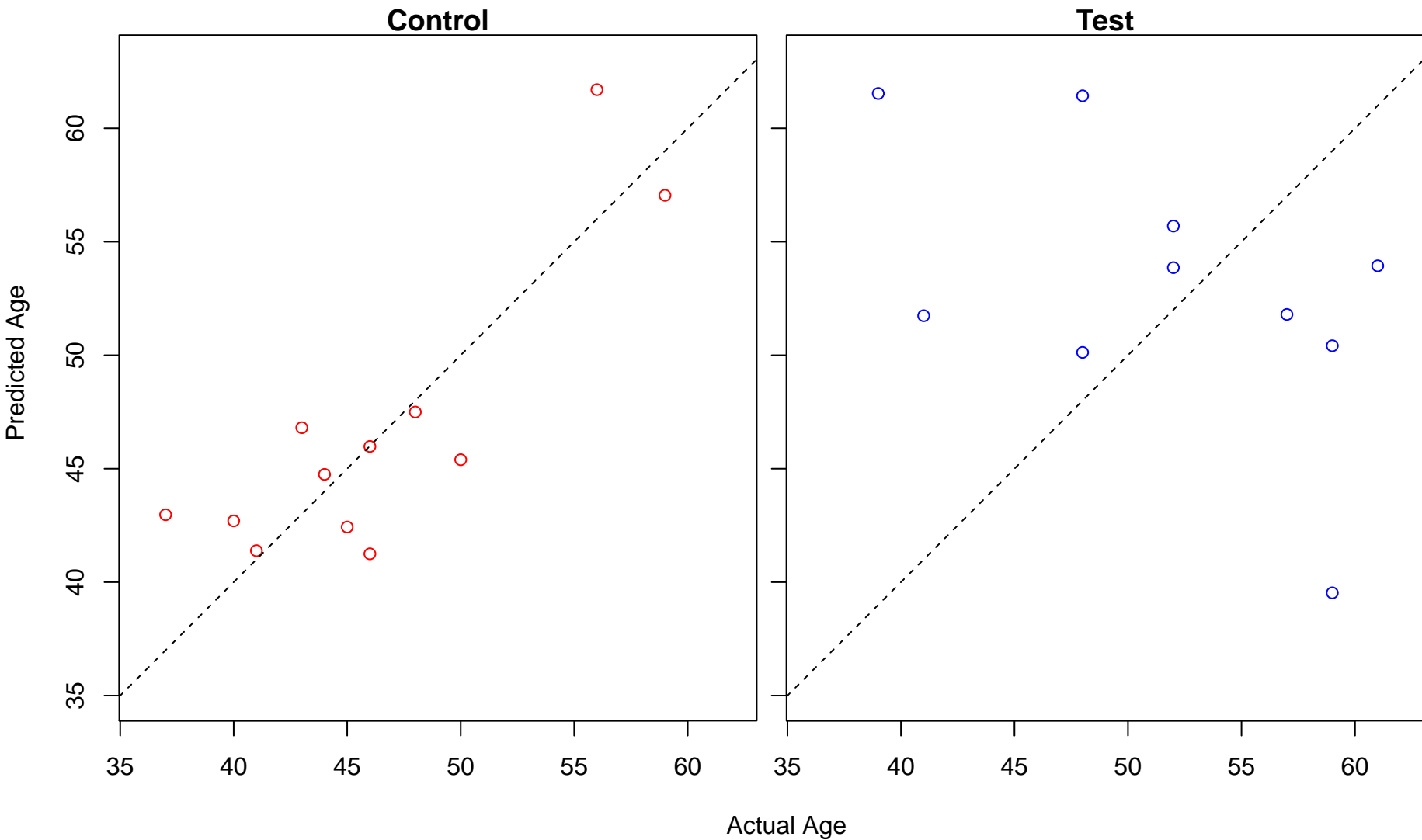
vitamin transport (Score: 22.947597)



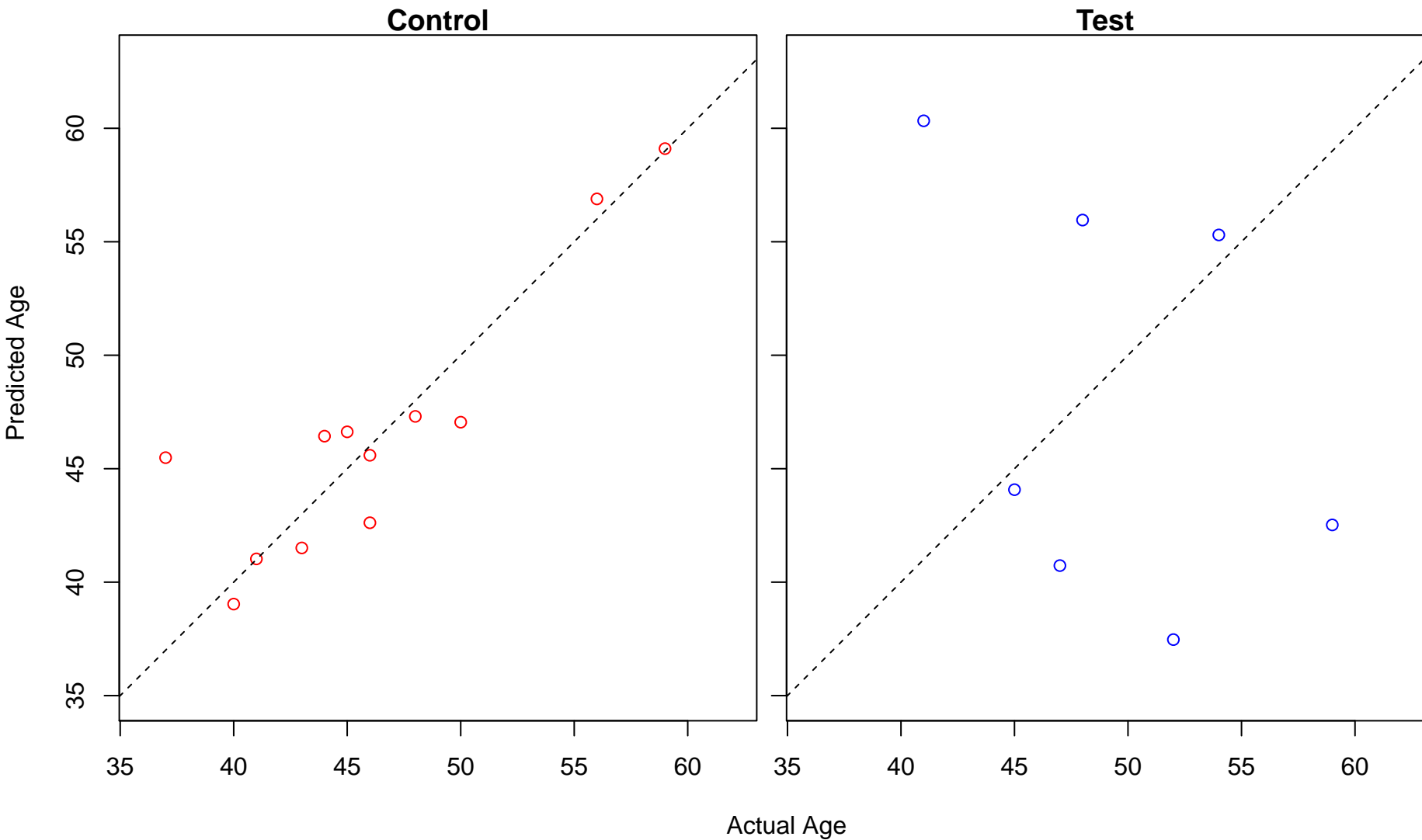
positive regulation of T cell proliferation (Score: 22.908015)



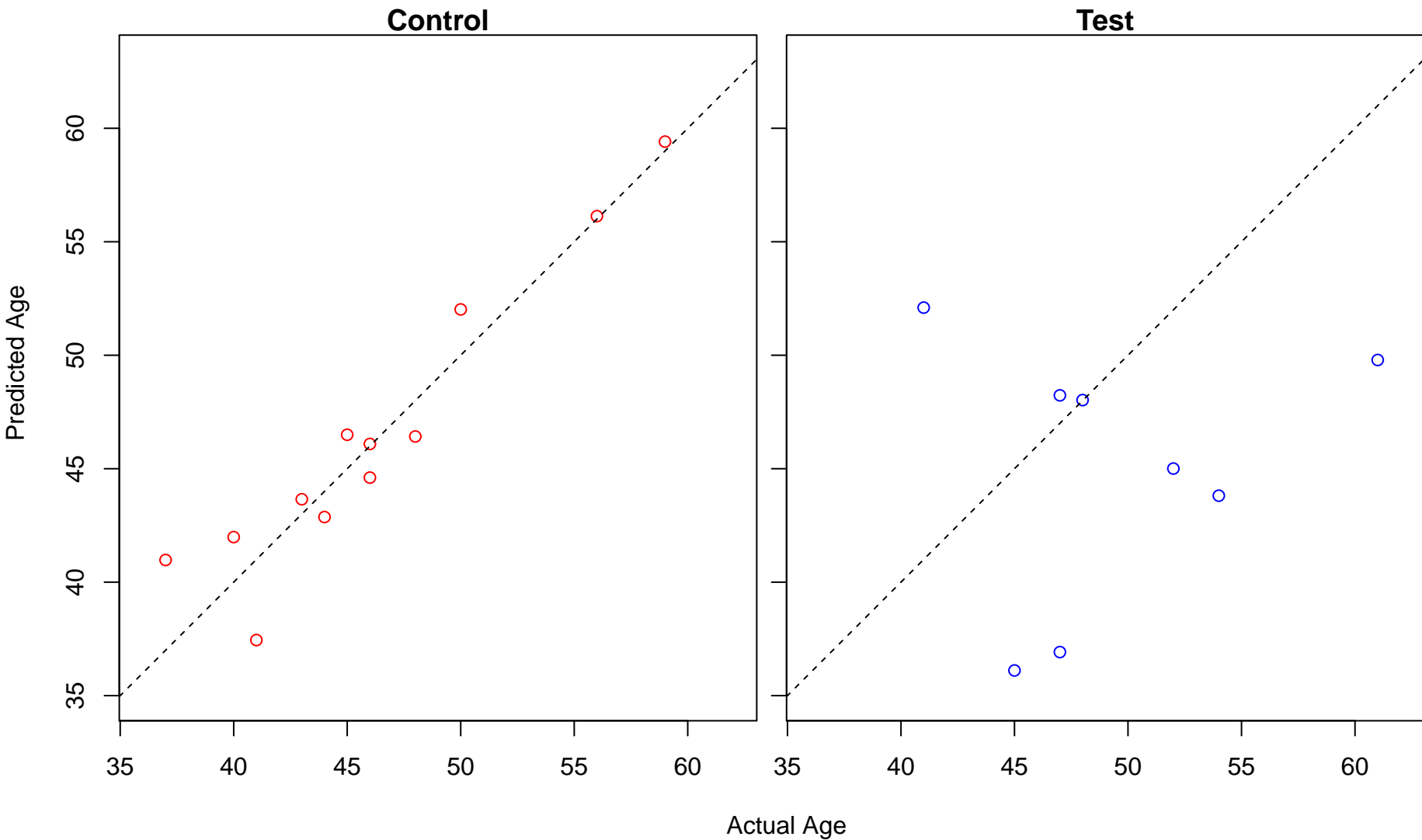
protein K48-linked ubiquitination (Score: 22.782245)



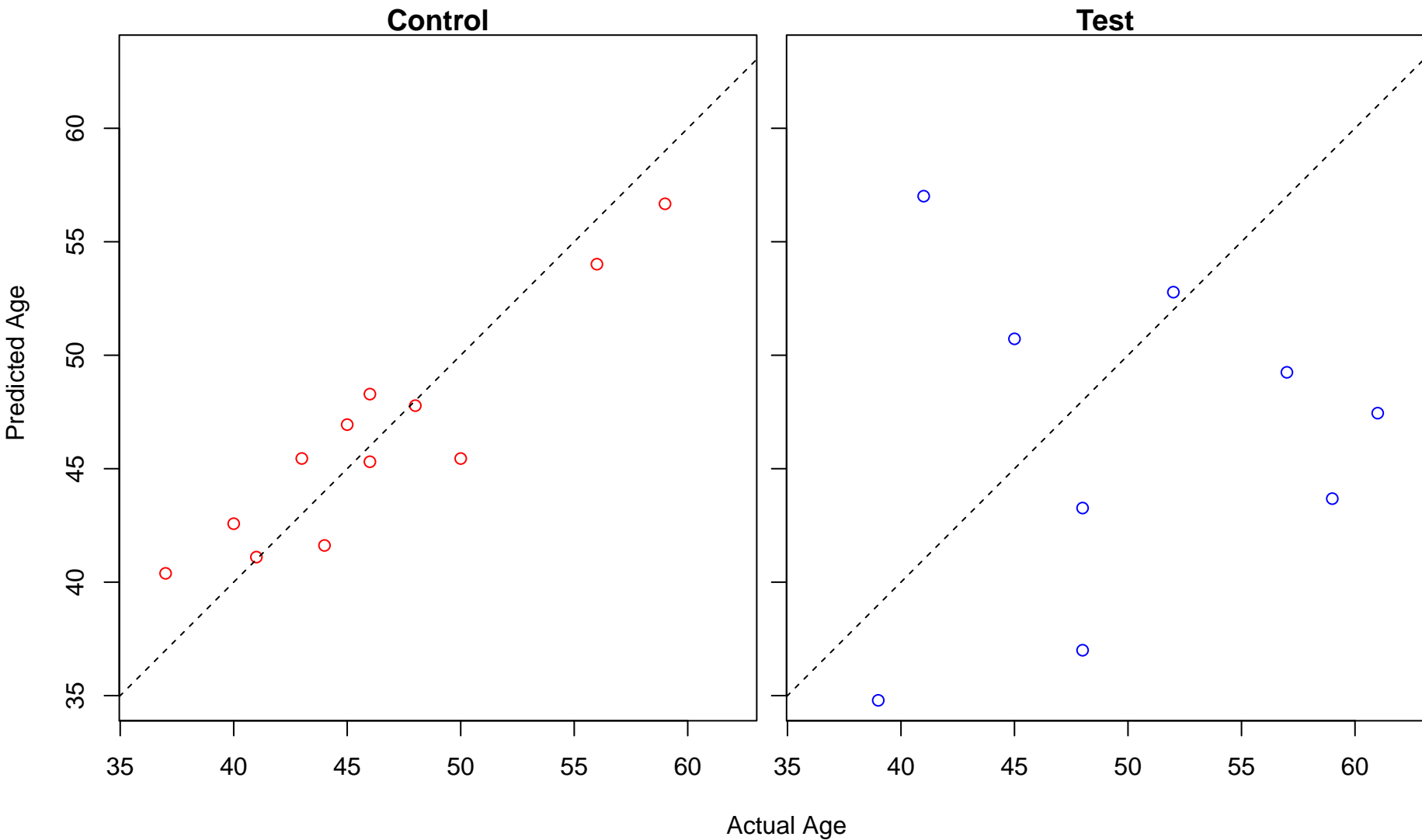
regulation of cardiac muscle contraction (Score: 22.773866)



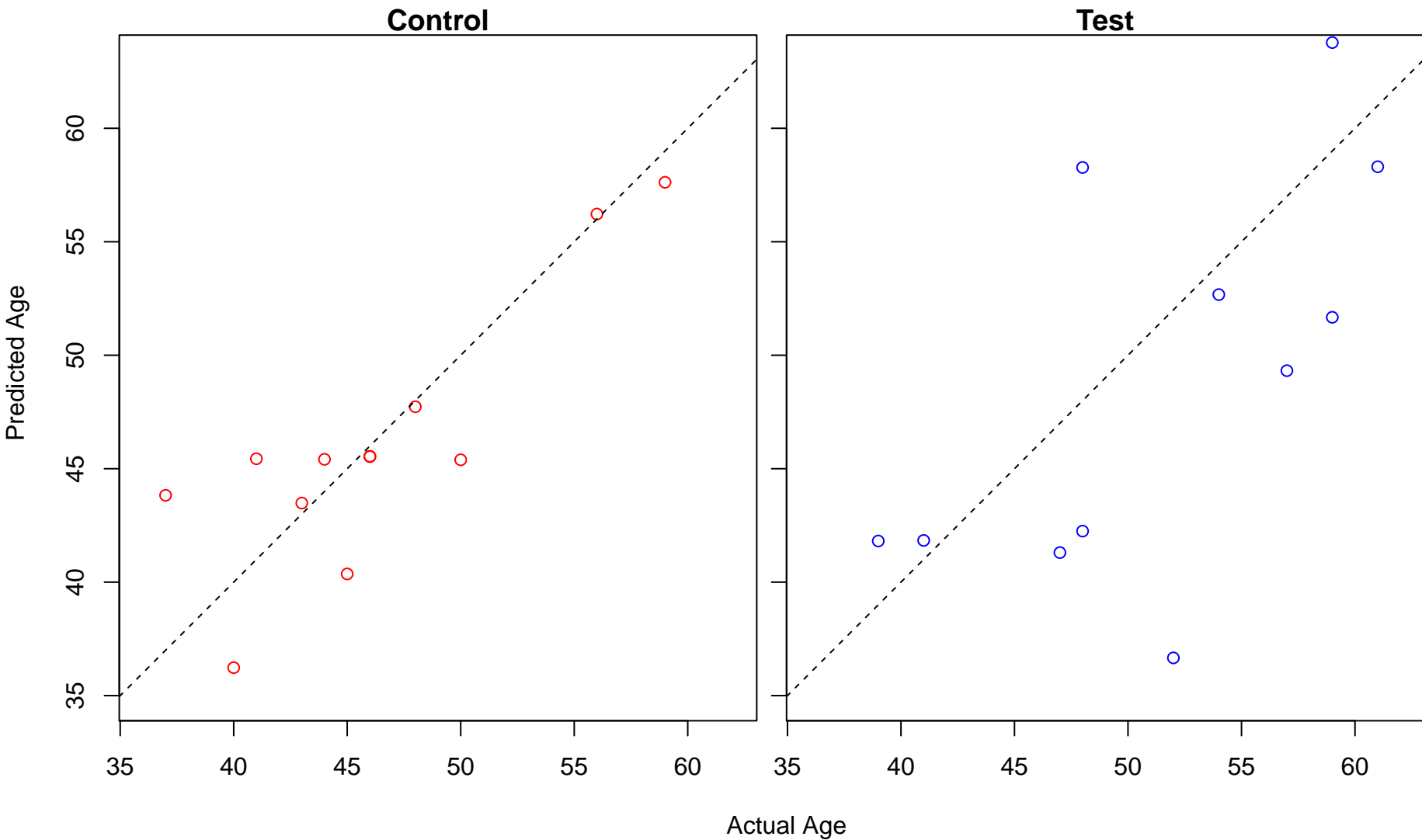
positive regulation of focal adhesion assembly (Score: 22.716183)



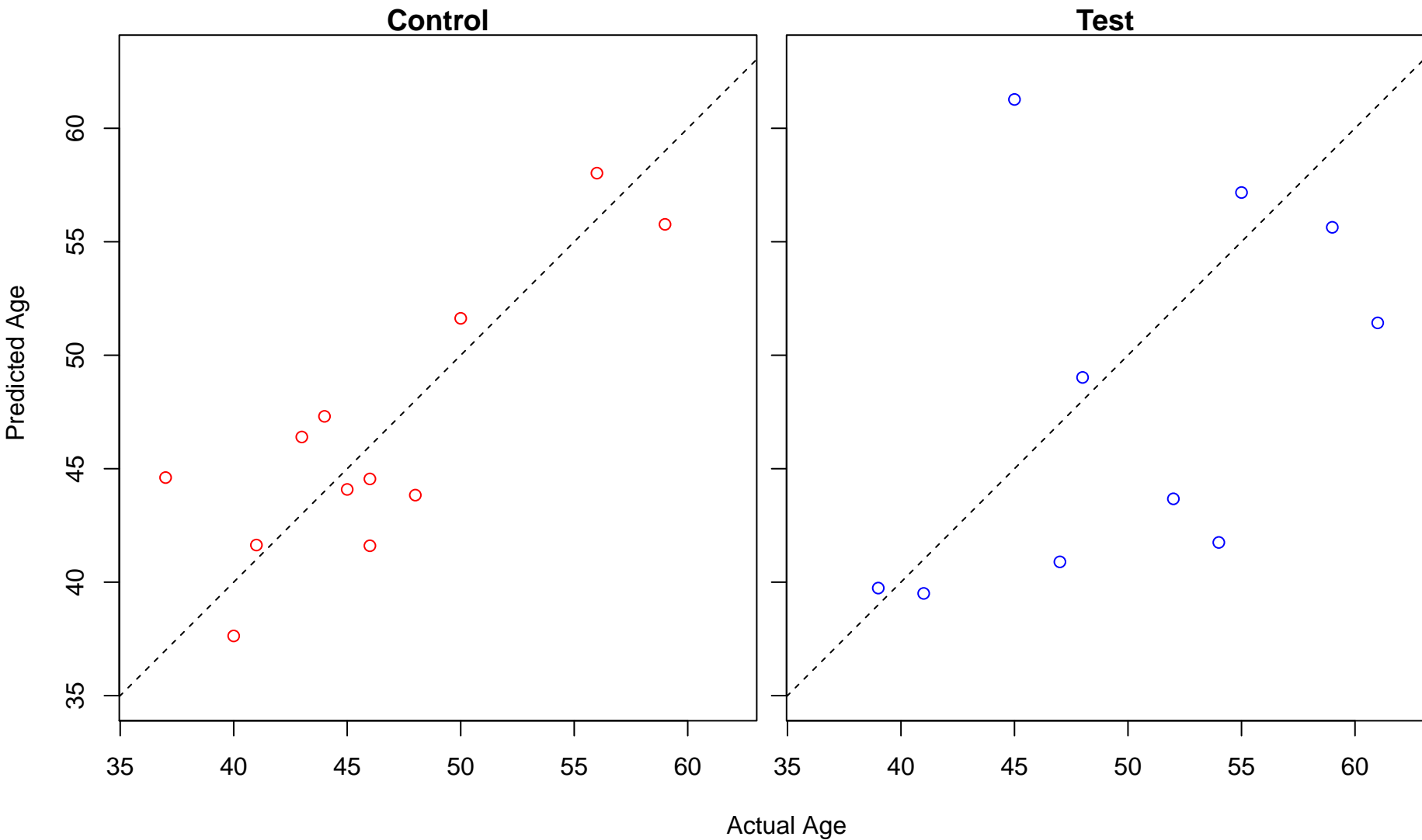
induction of positive chemotaxis (Score: 22.685124)



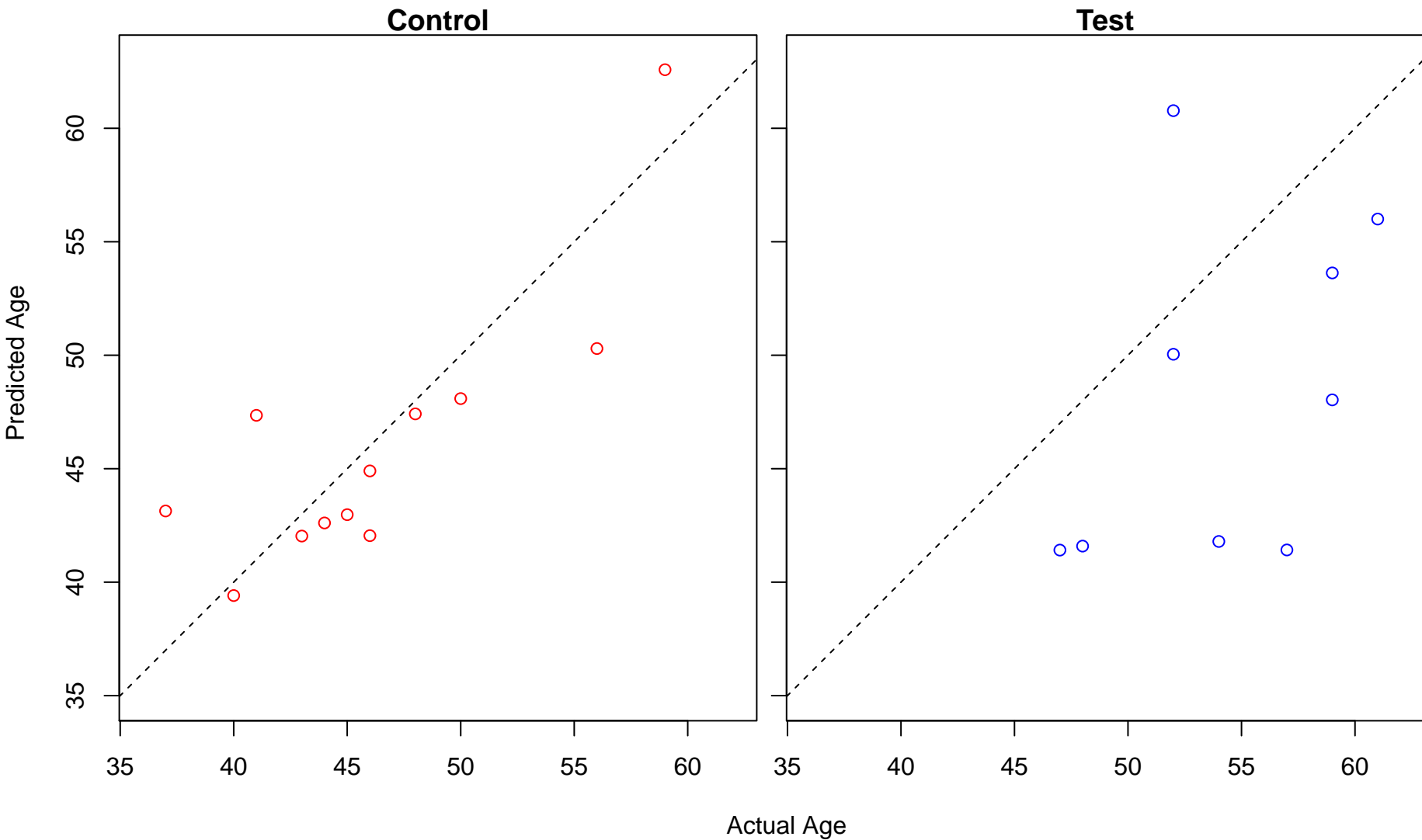
negative regulation of macrophage derived foam cell differentiation (Score: 22.628207)



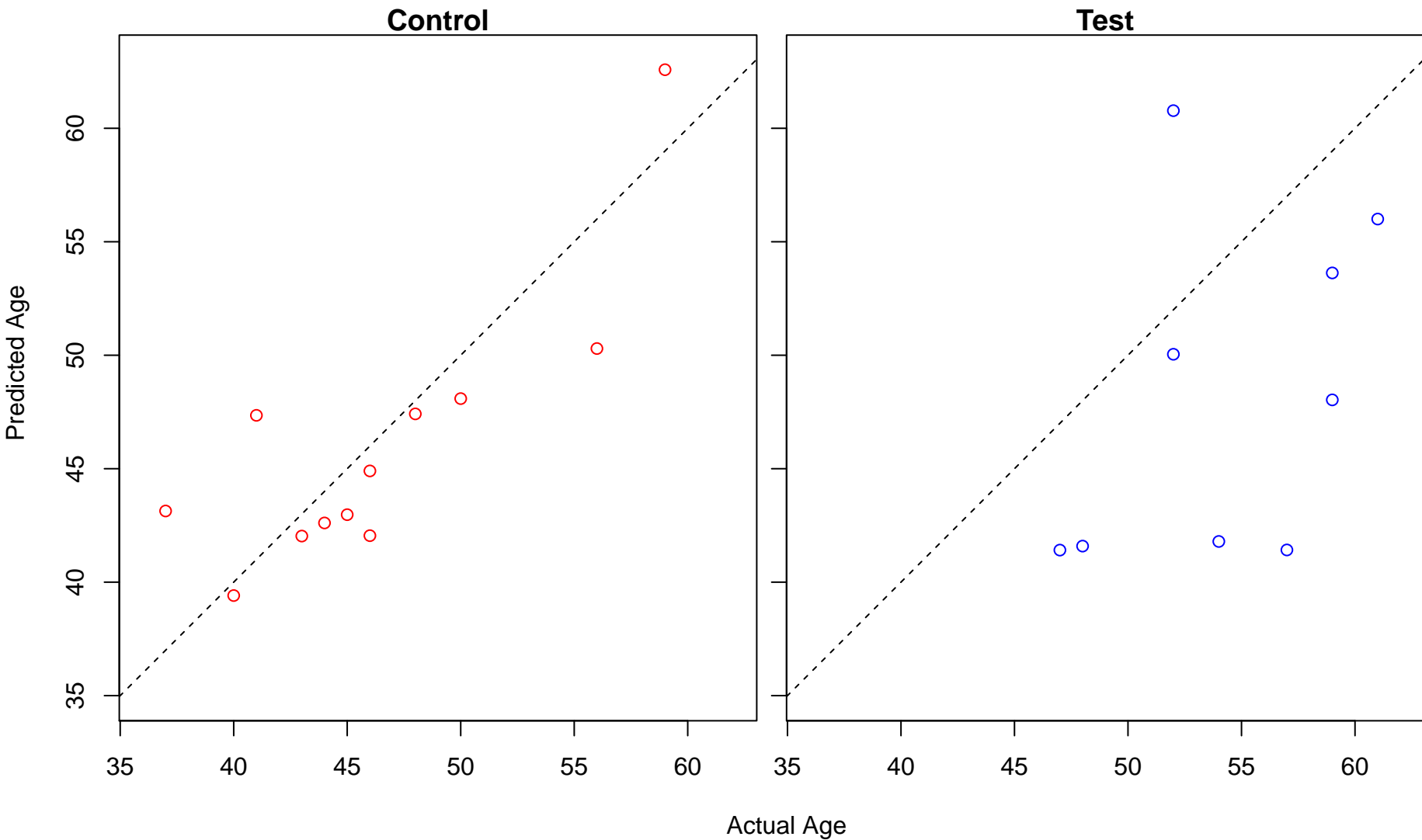
drug transmembrane transport (Score: 22.579200)



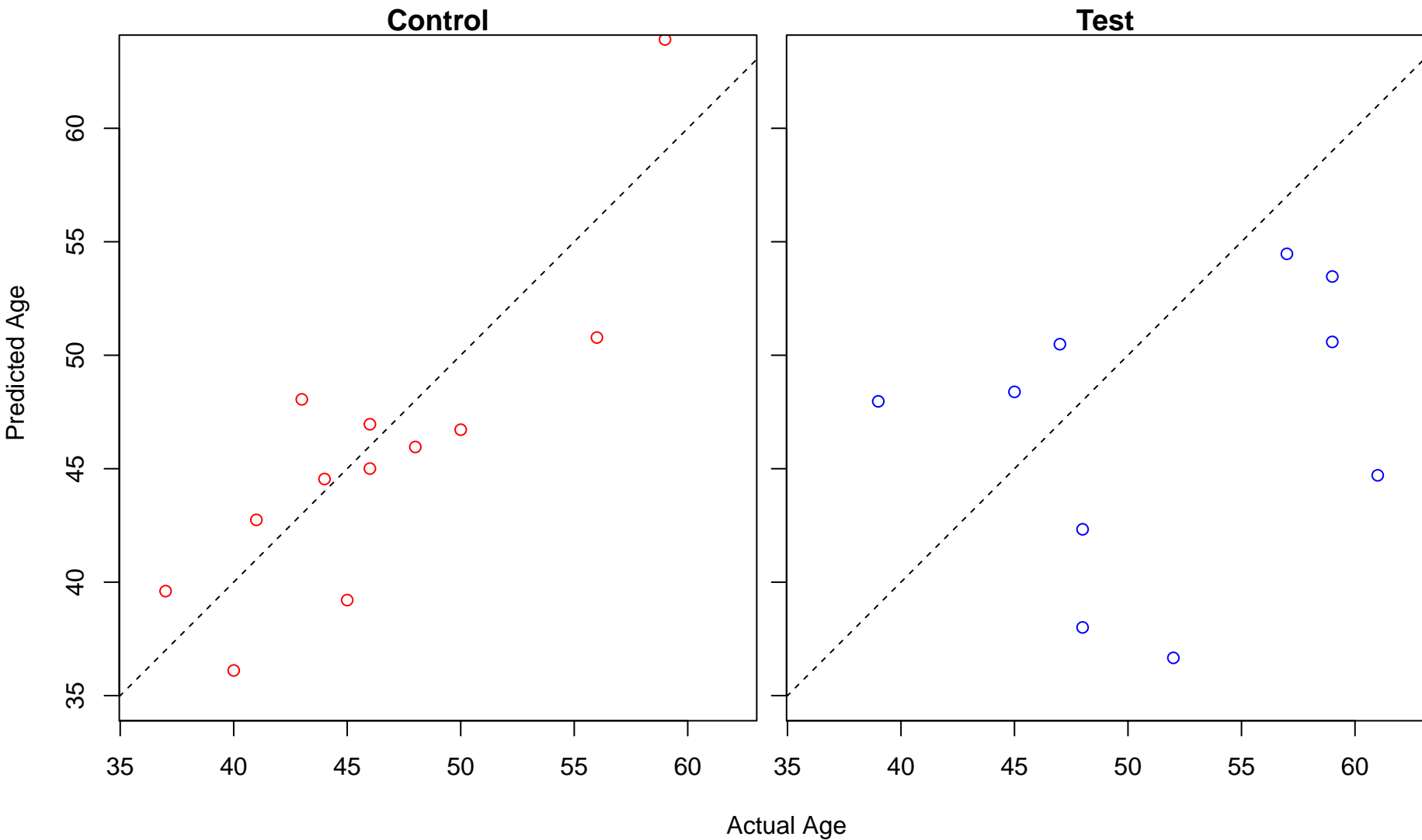
L-glutamate transport (Score: 22.550311)



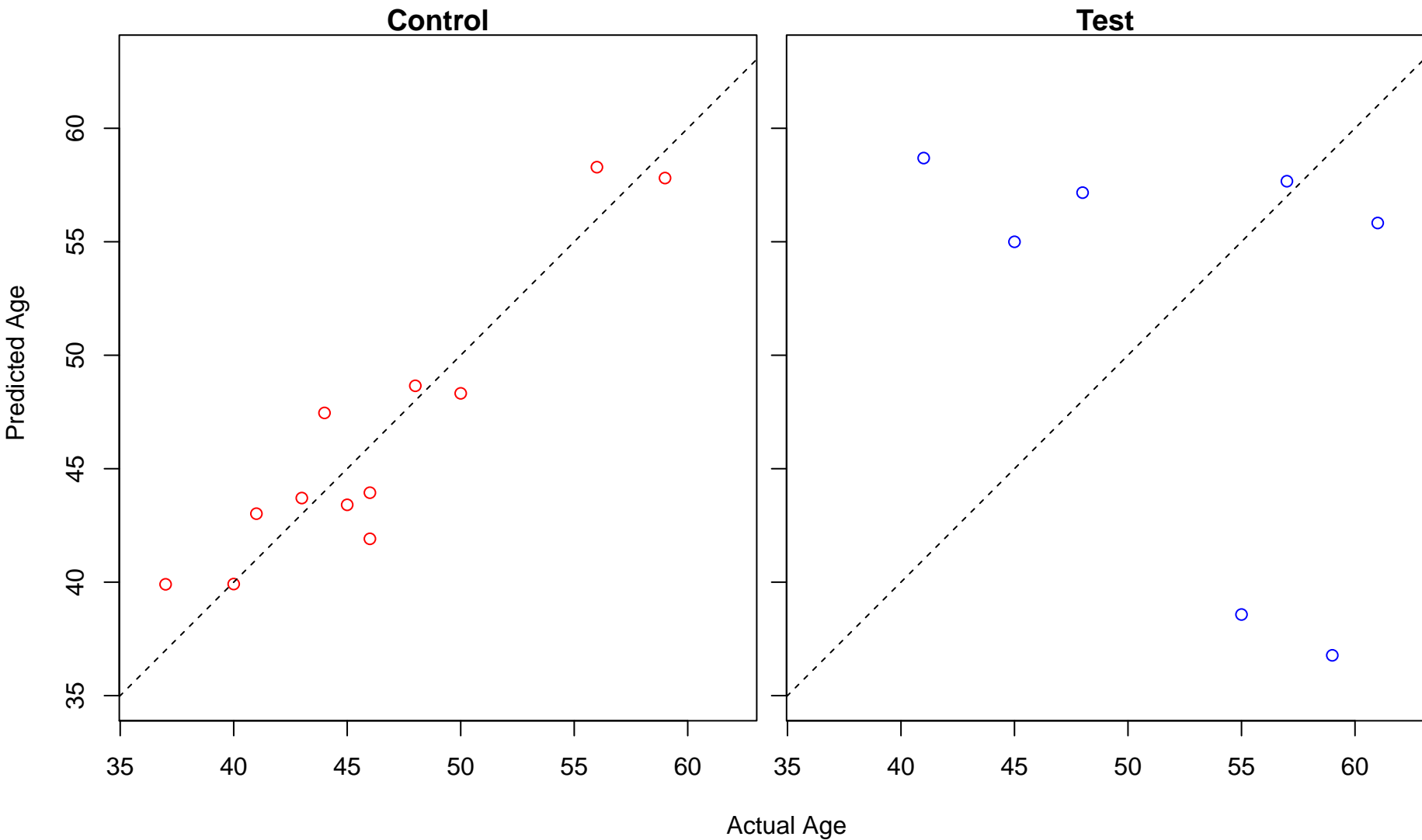
acidic amino acid transport (Score: 22.550311)



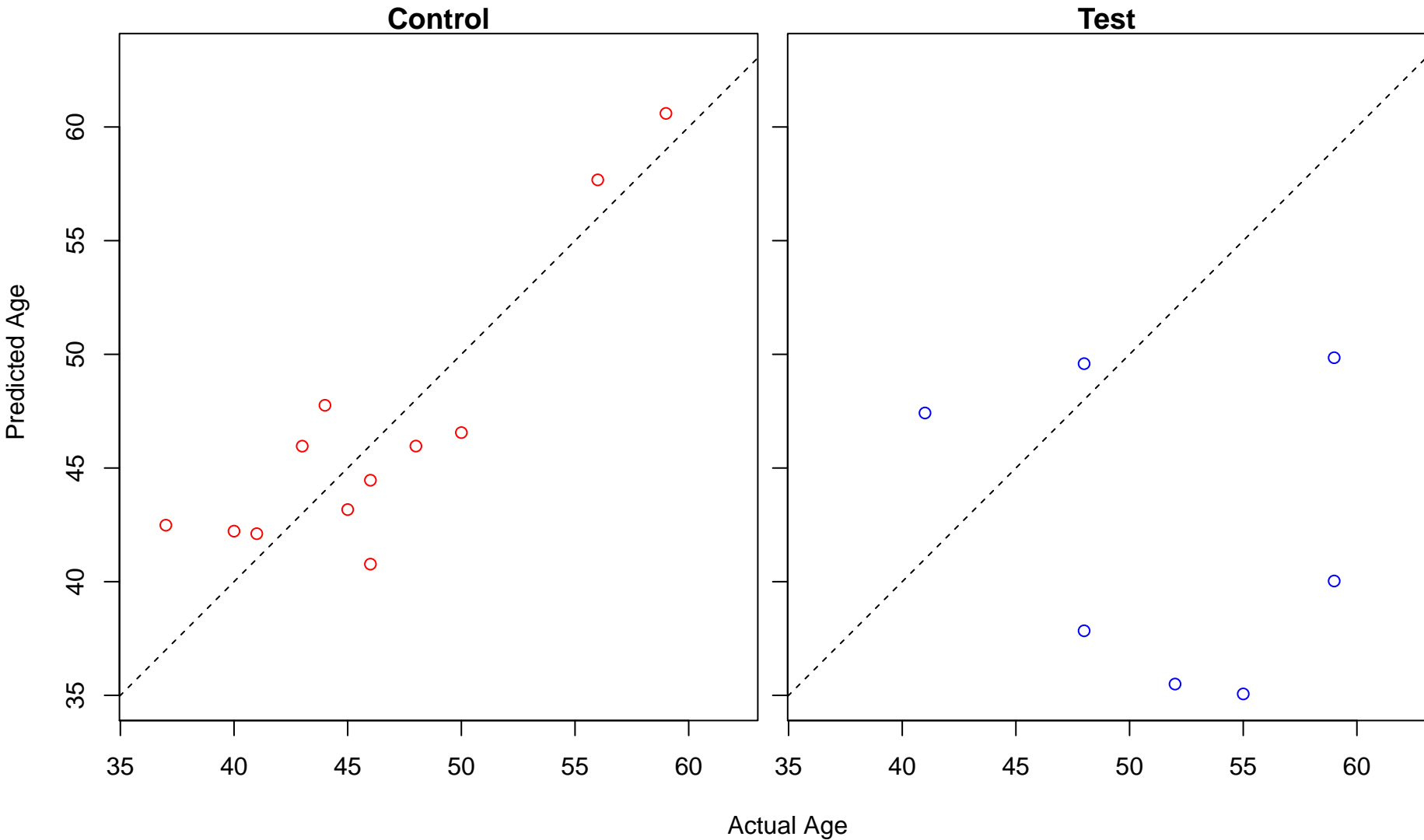
positive regulation of epidermis development (Score: 22.473024)



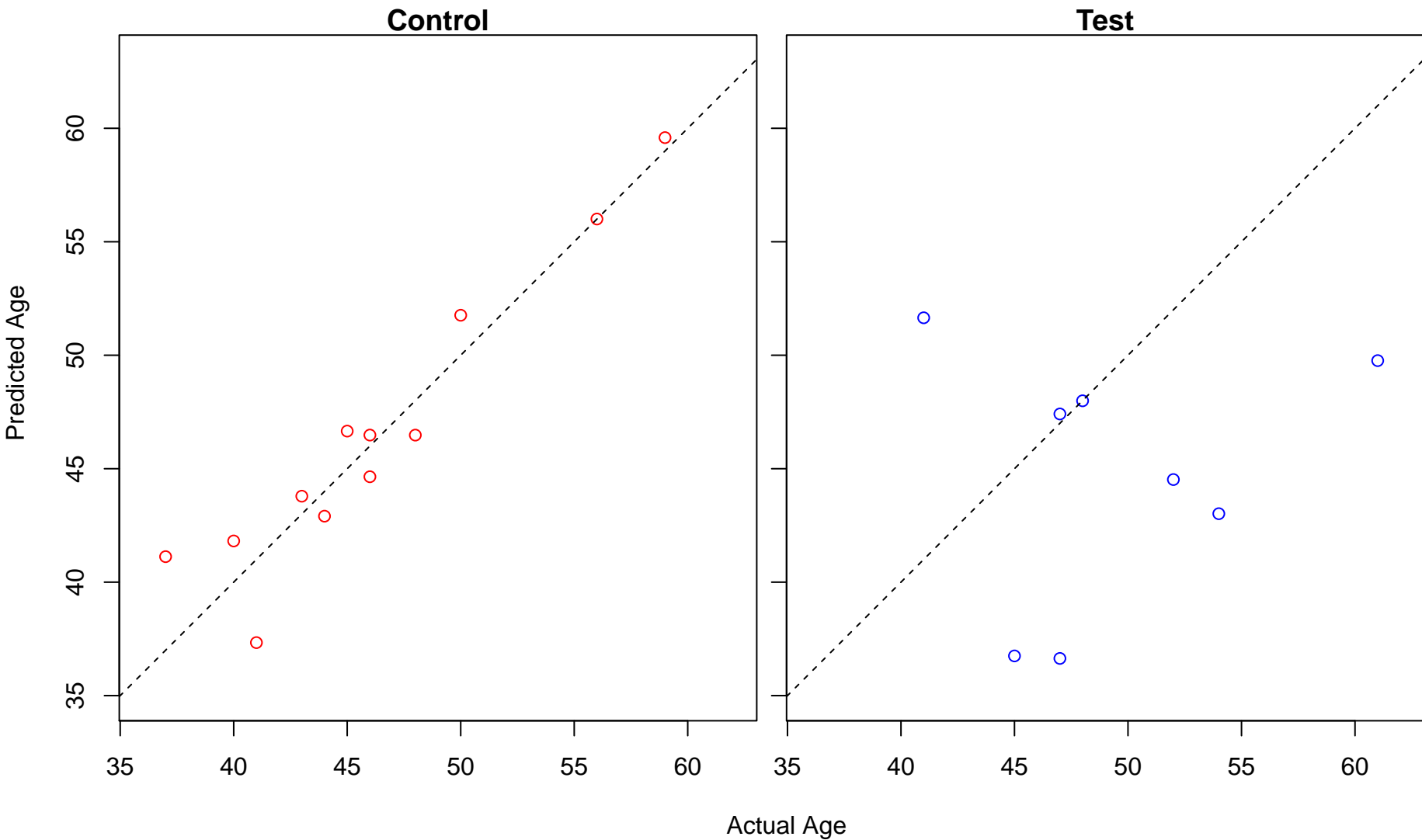
multicellular organismal metabolic process (Score: 22.370009)



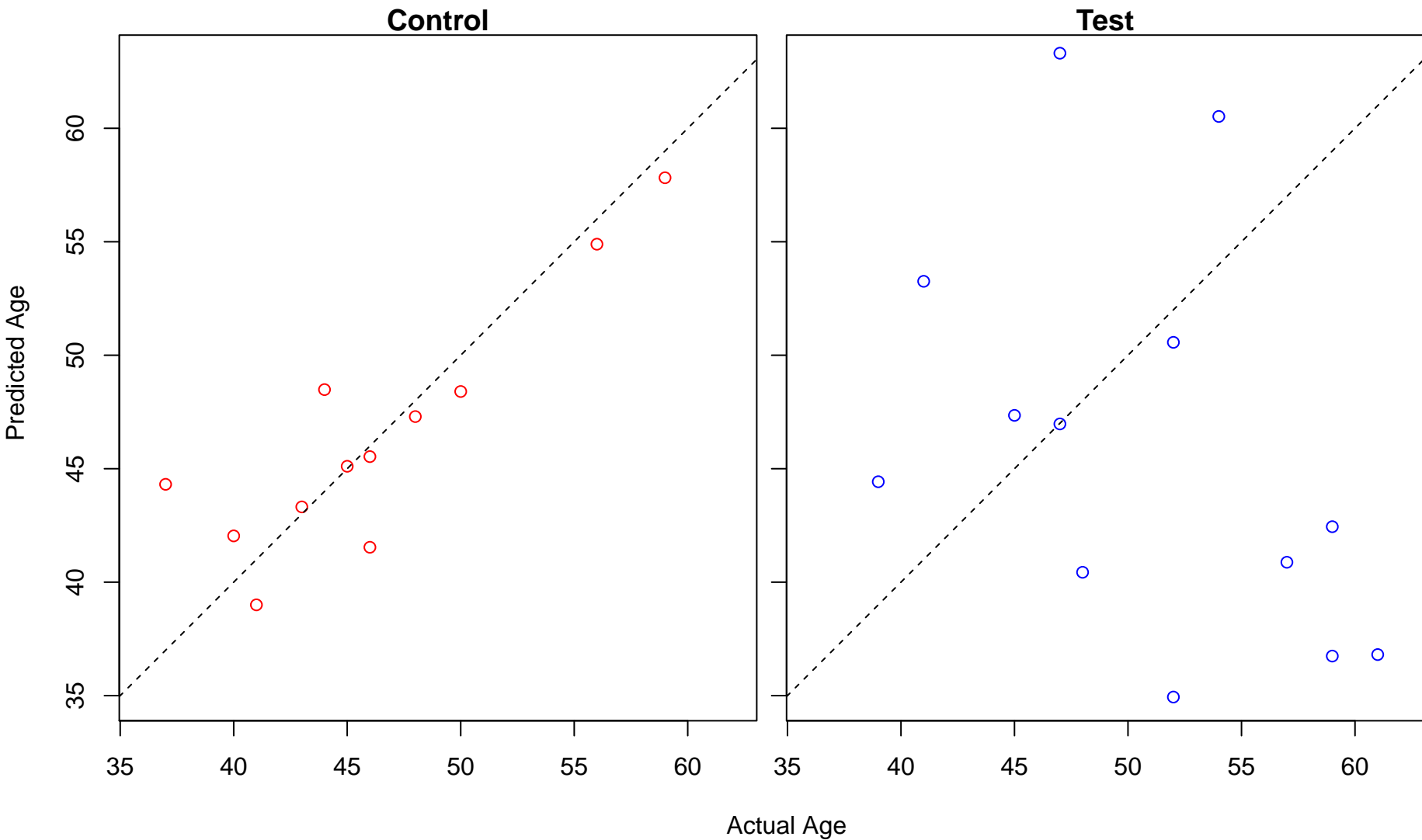
regulation of actin filament-based process (Score: 22.291045)



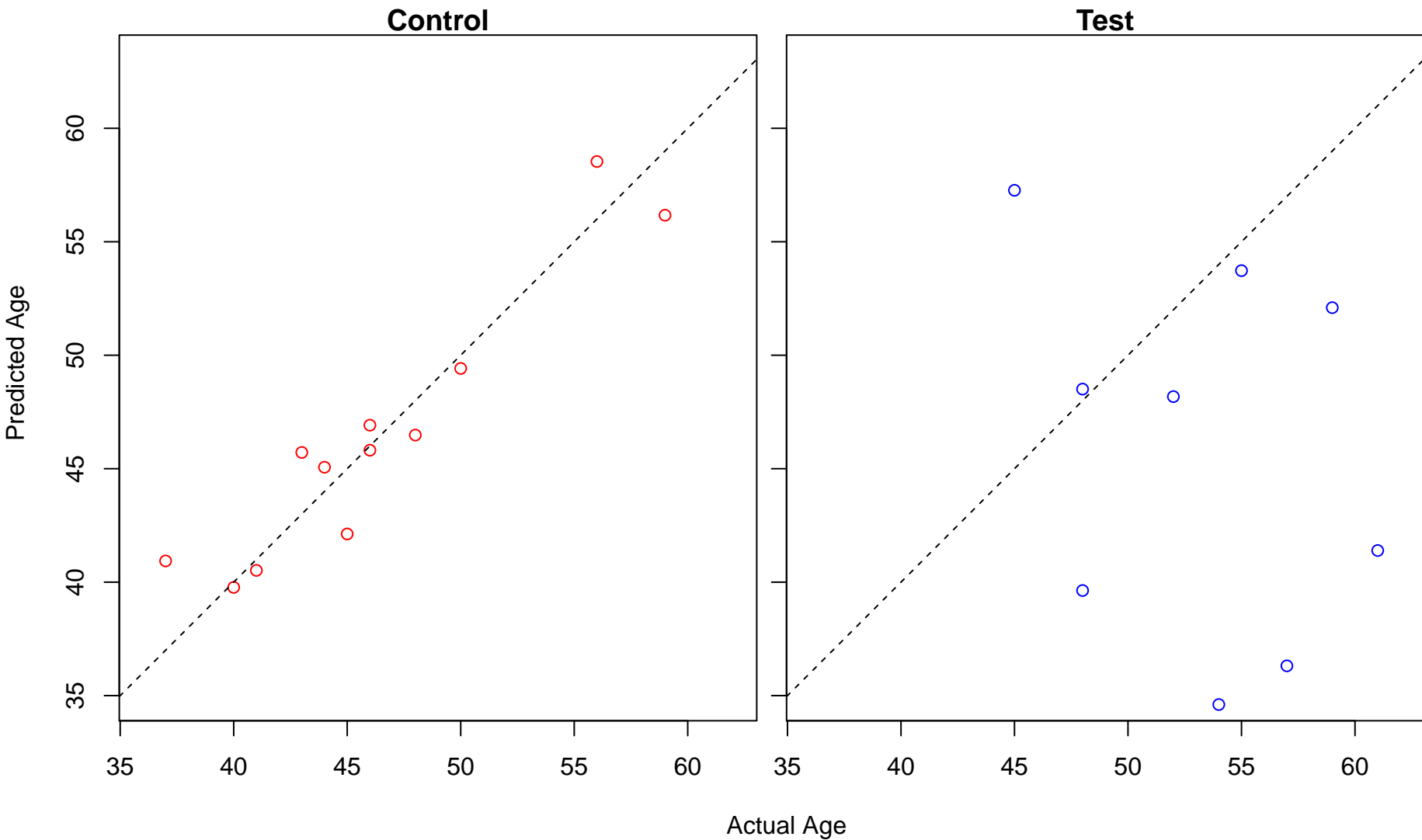
positive regulation of adherens junction organization (Score: 22.238533)



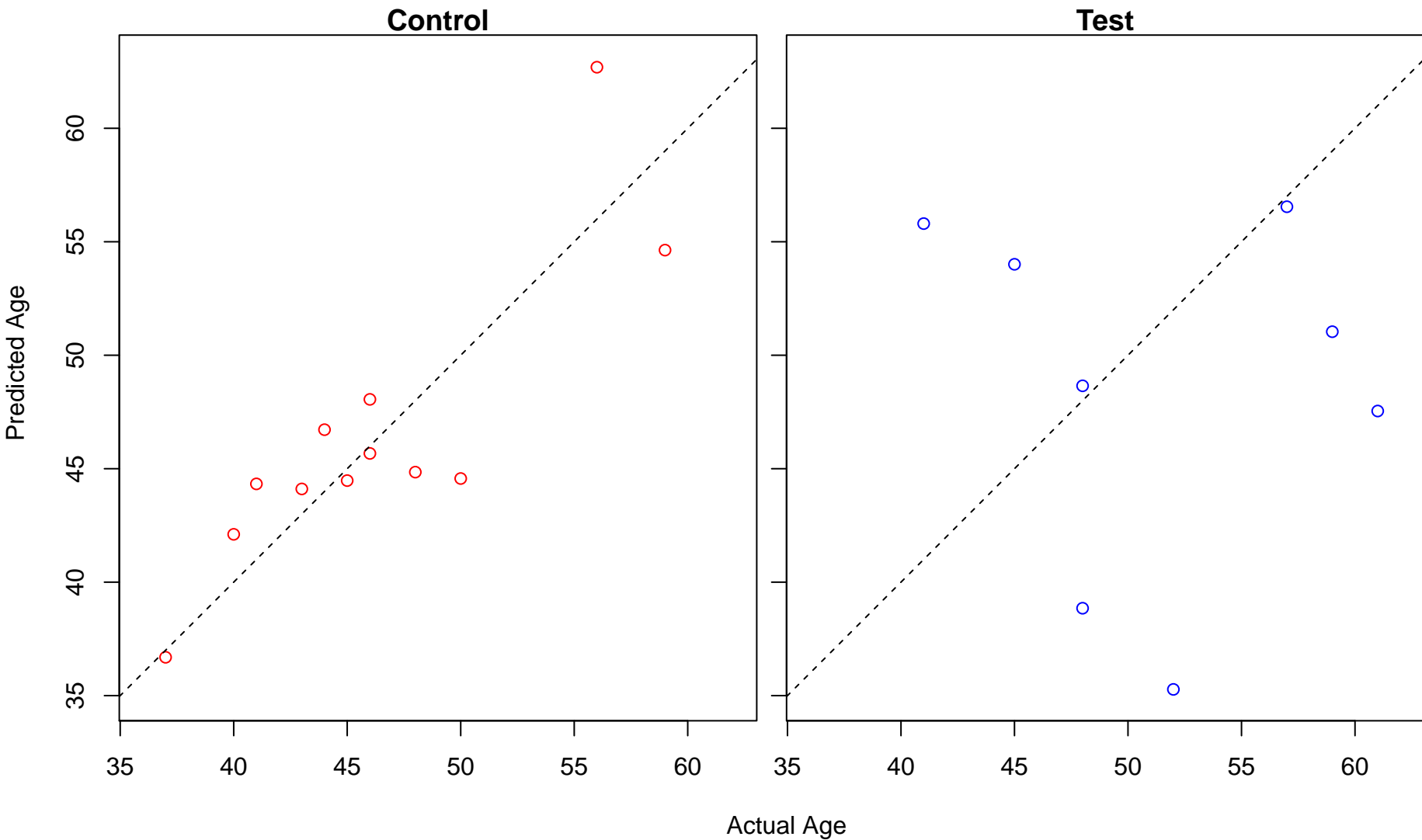
water-soluble vitamin metabolic process (Score: 22.237772)



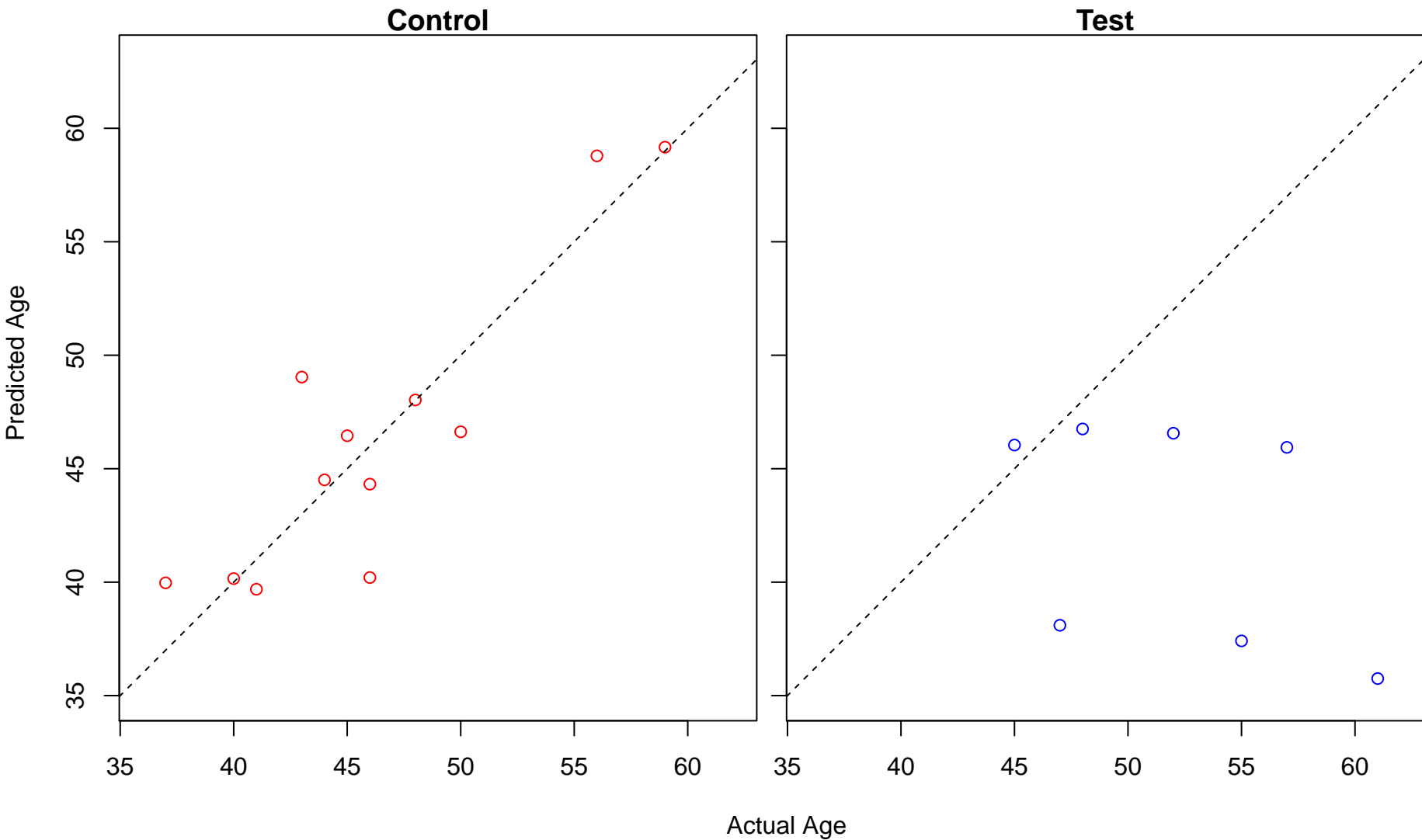
camera-type eye development (Score: 22.163513)



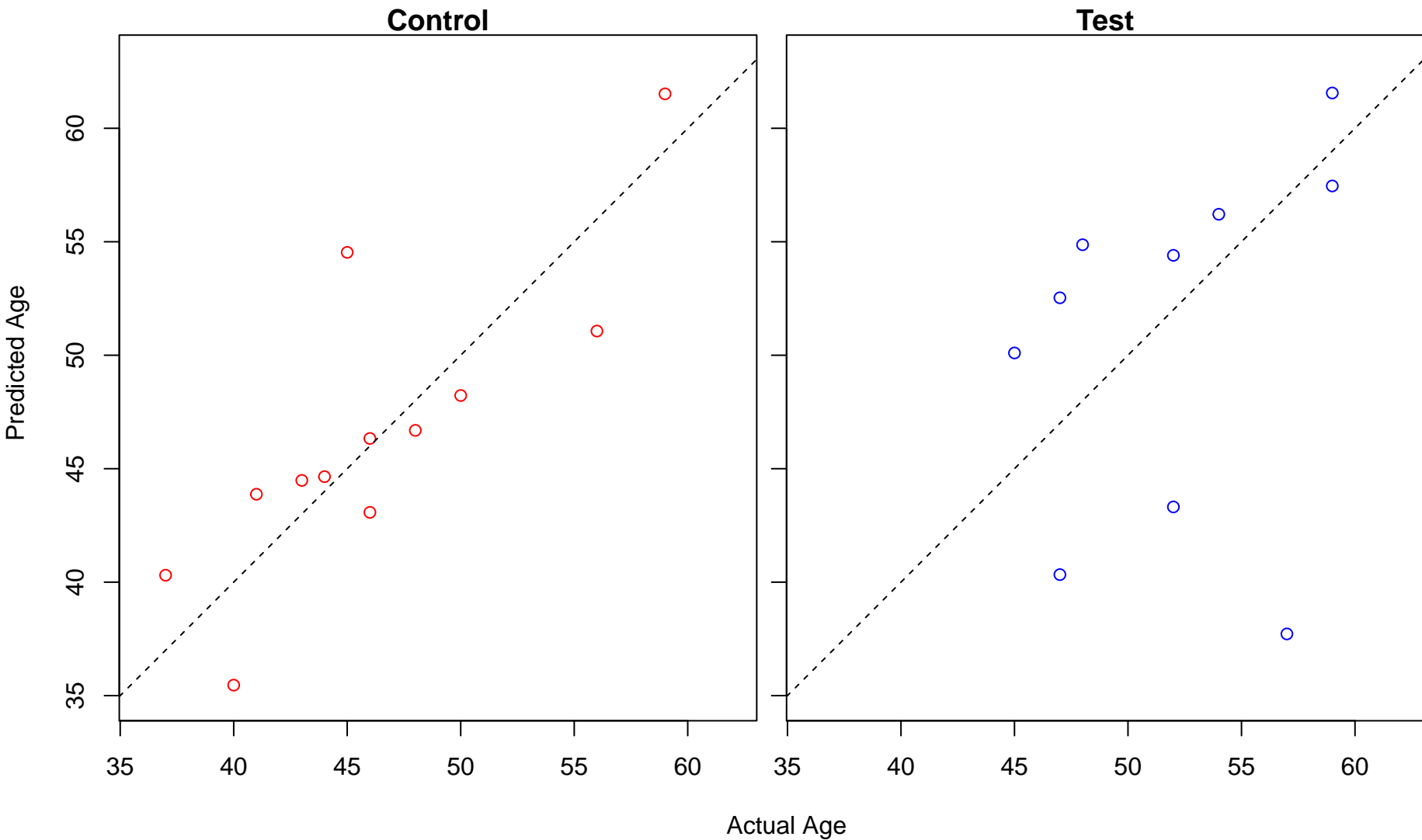
positive regulation of angiogenesis (Score: 22.145761)



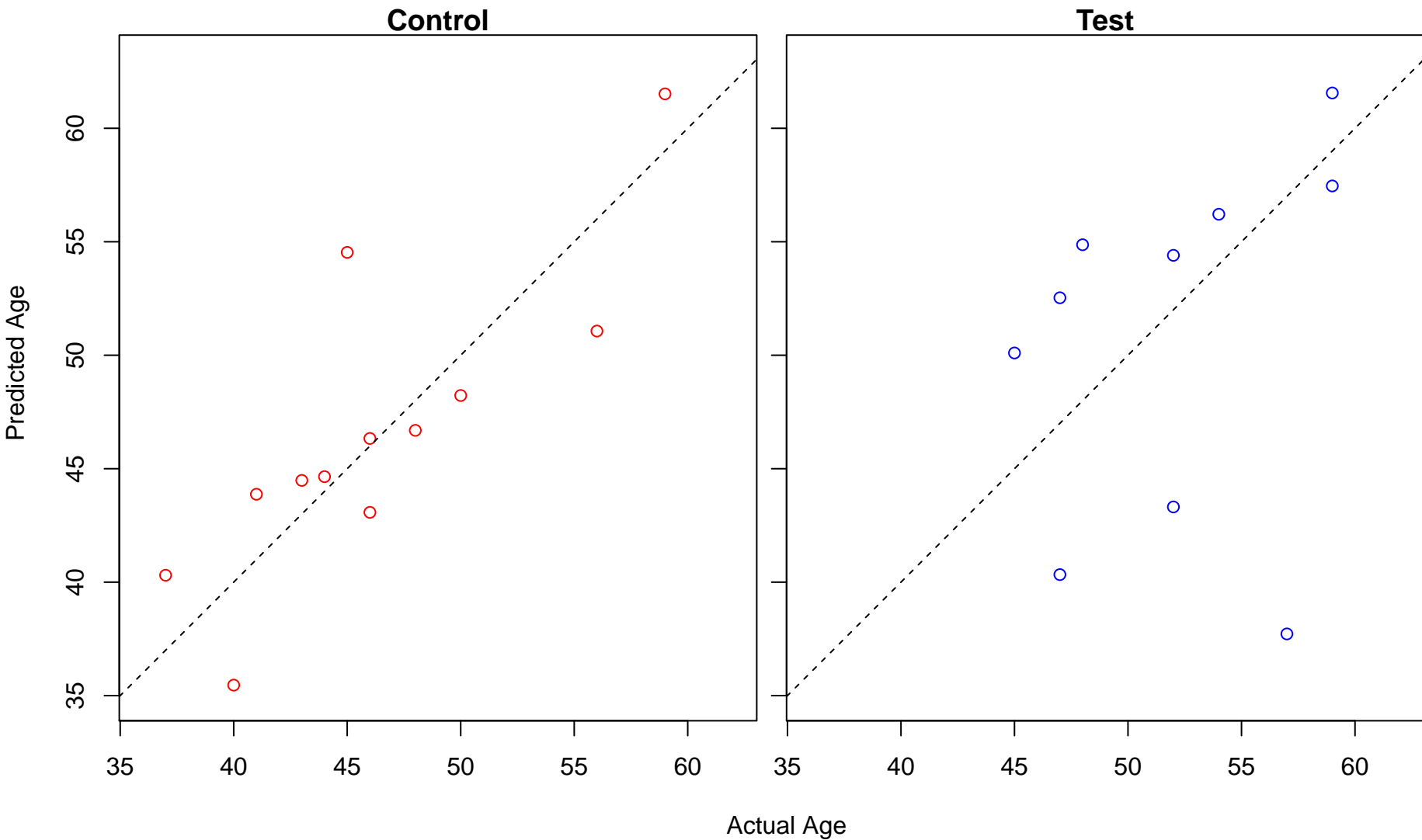
negative regulation of calcium-mediated signaling (Score: 22.020853)



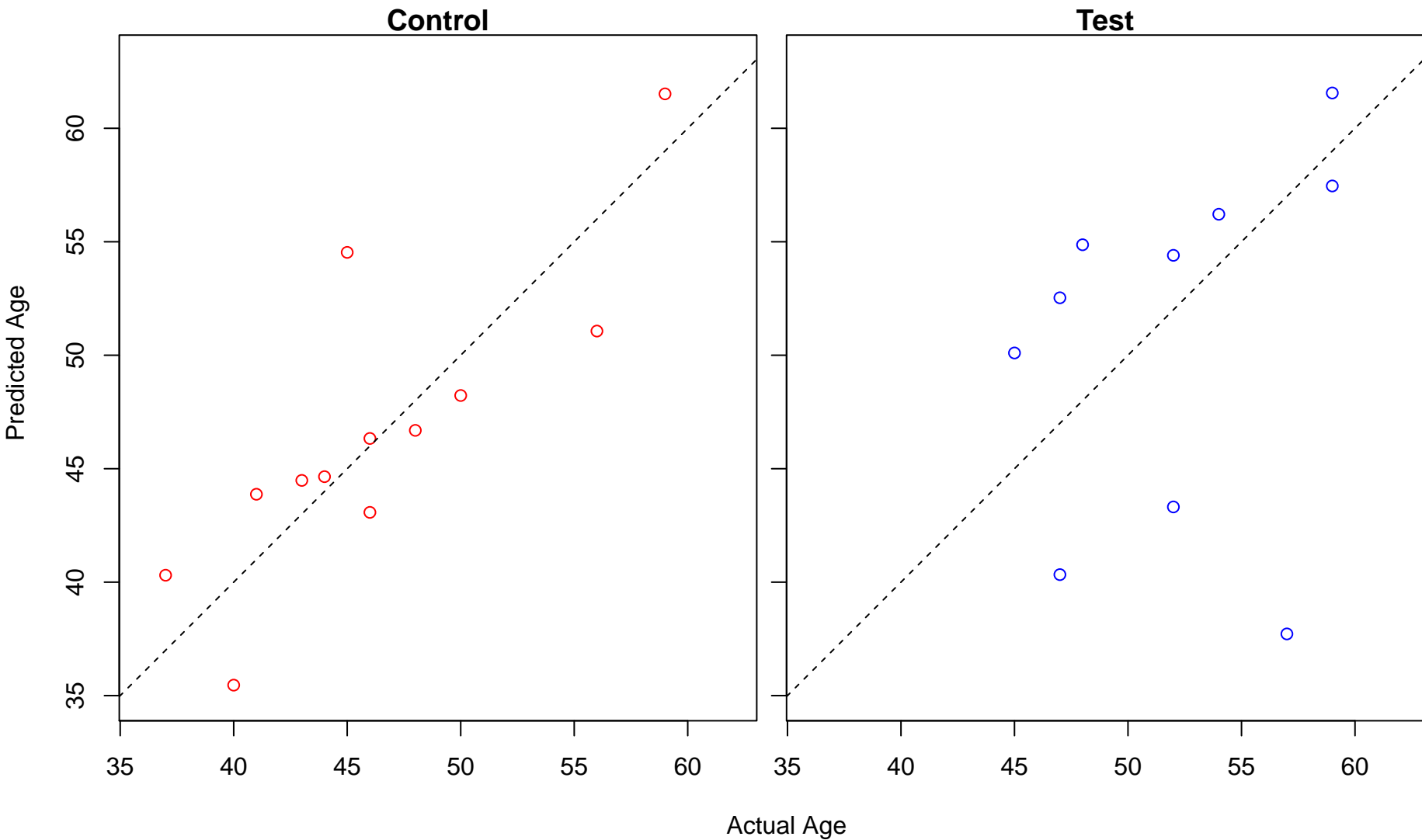
positive regulation of blood coagulation (Score: 22.001325)



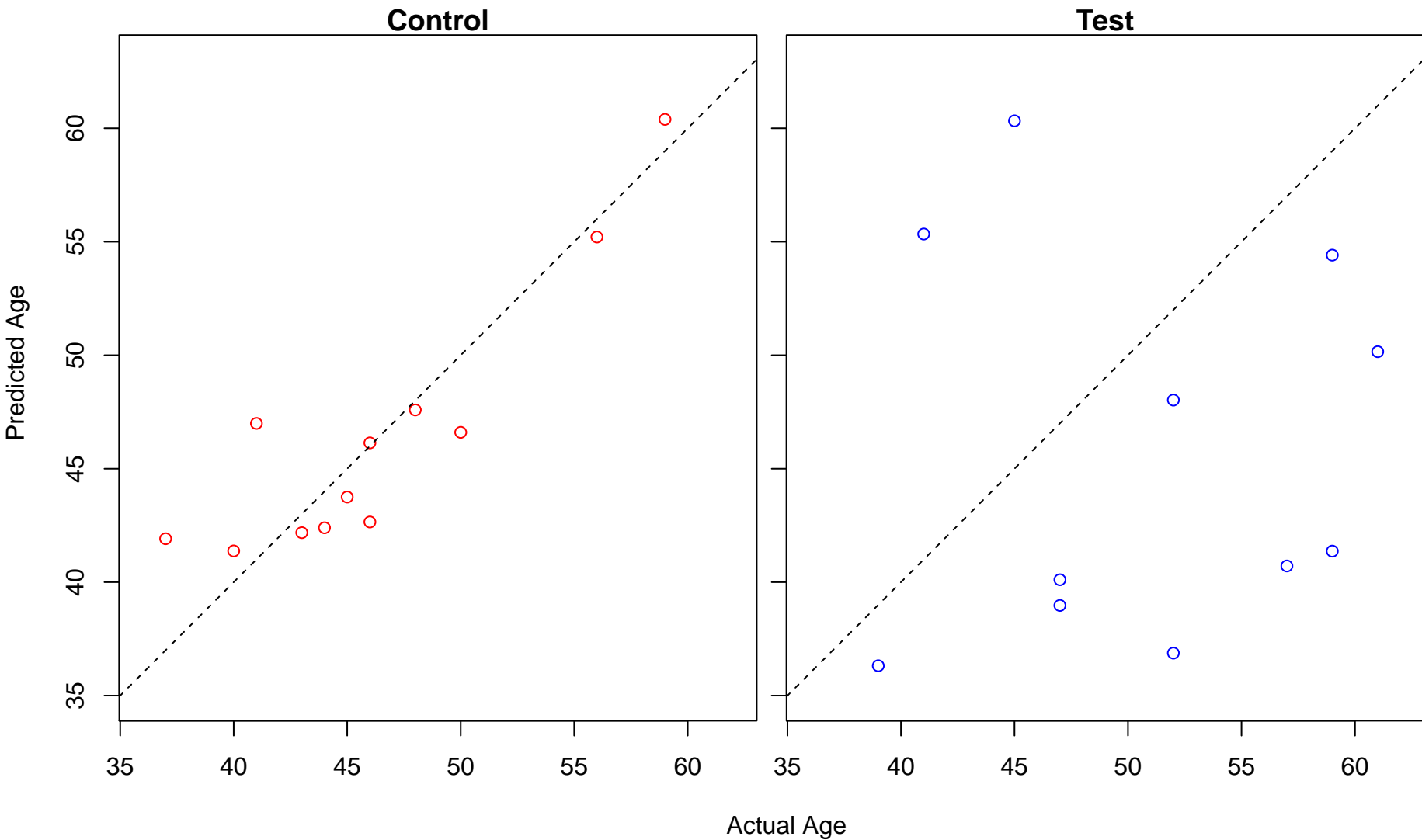
positive regulation of coagulation (Score: 22.001325)



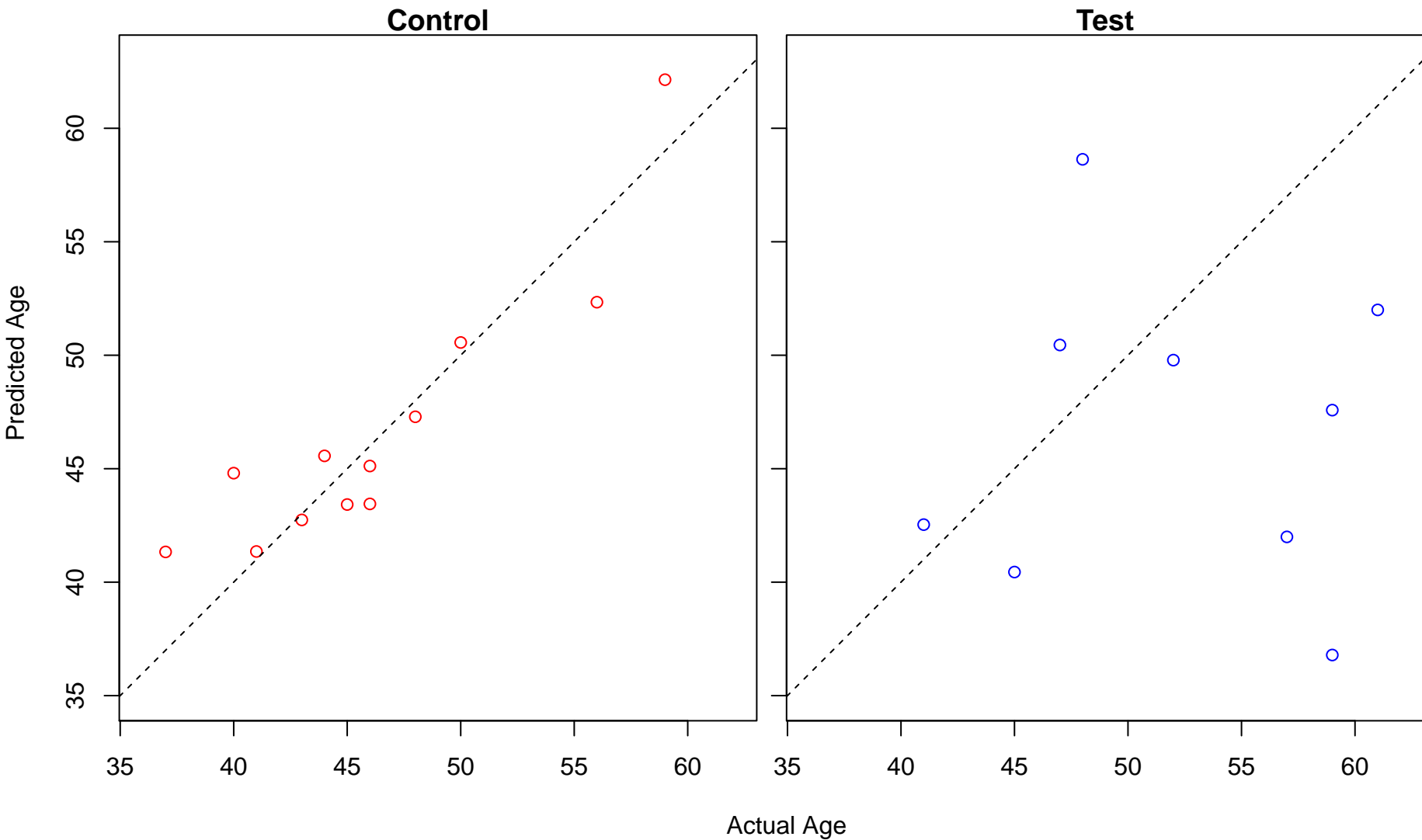
positive regulation of hemostasis (Score: 22.001325)



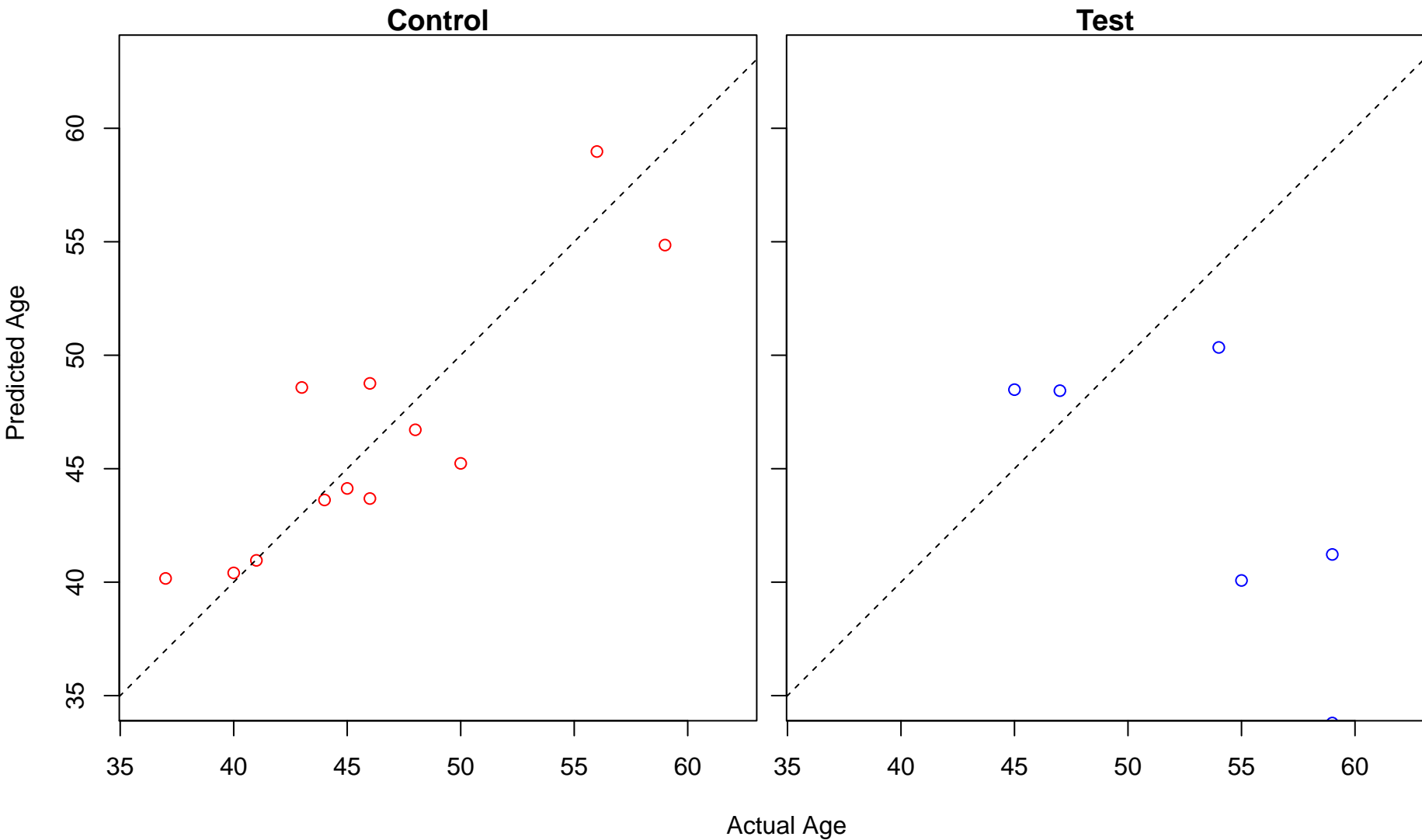
calcium ion import (Score: 21.912126)



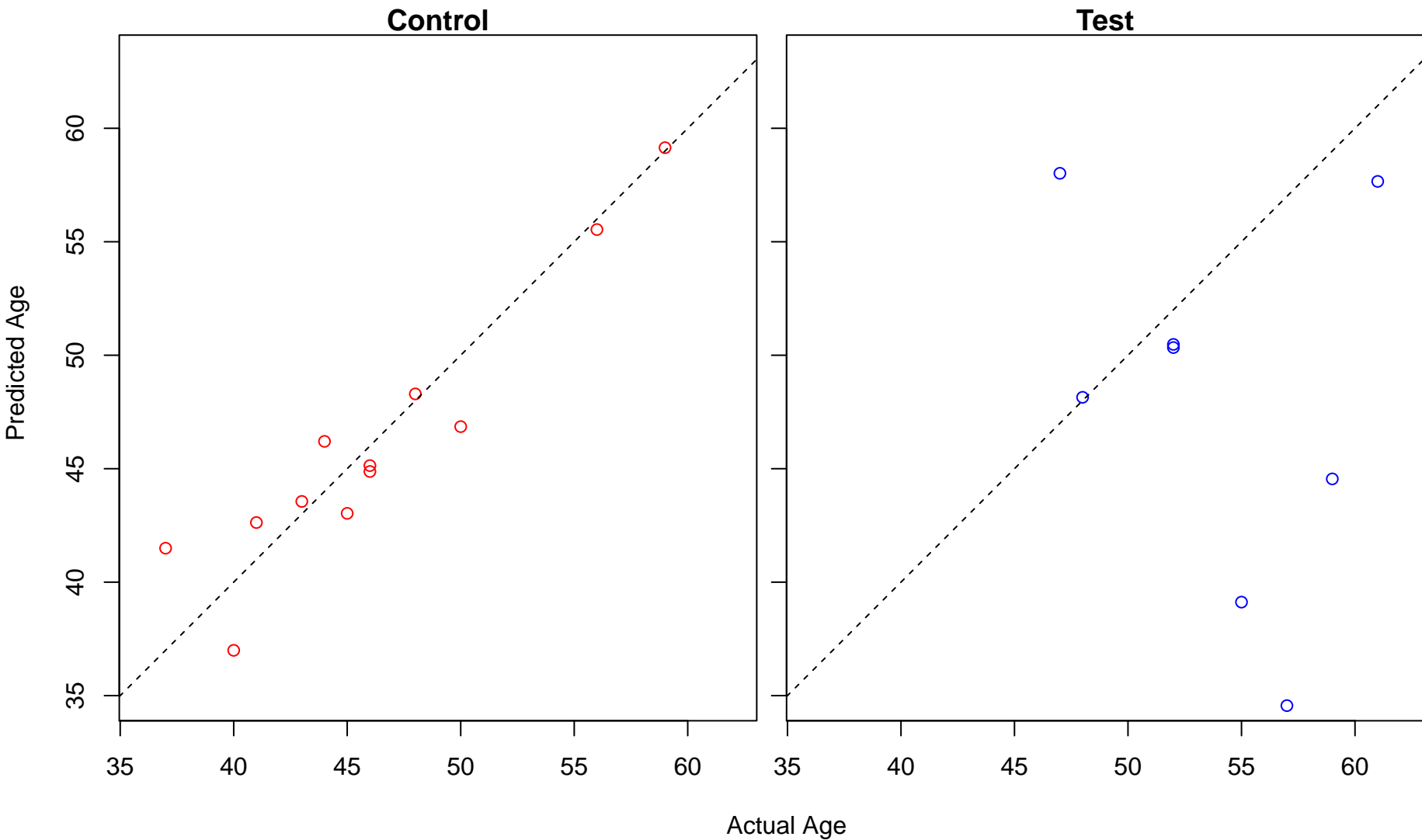
central nervous system neuron axonogenesis (Score: 21.76350)



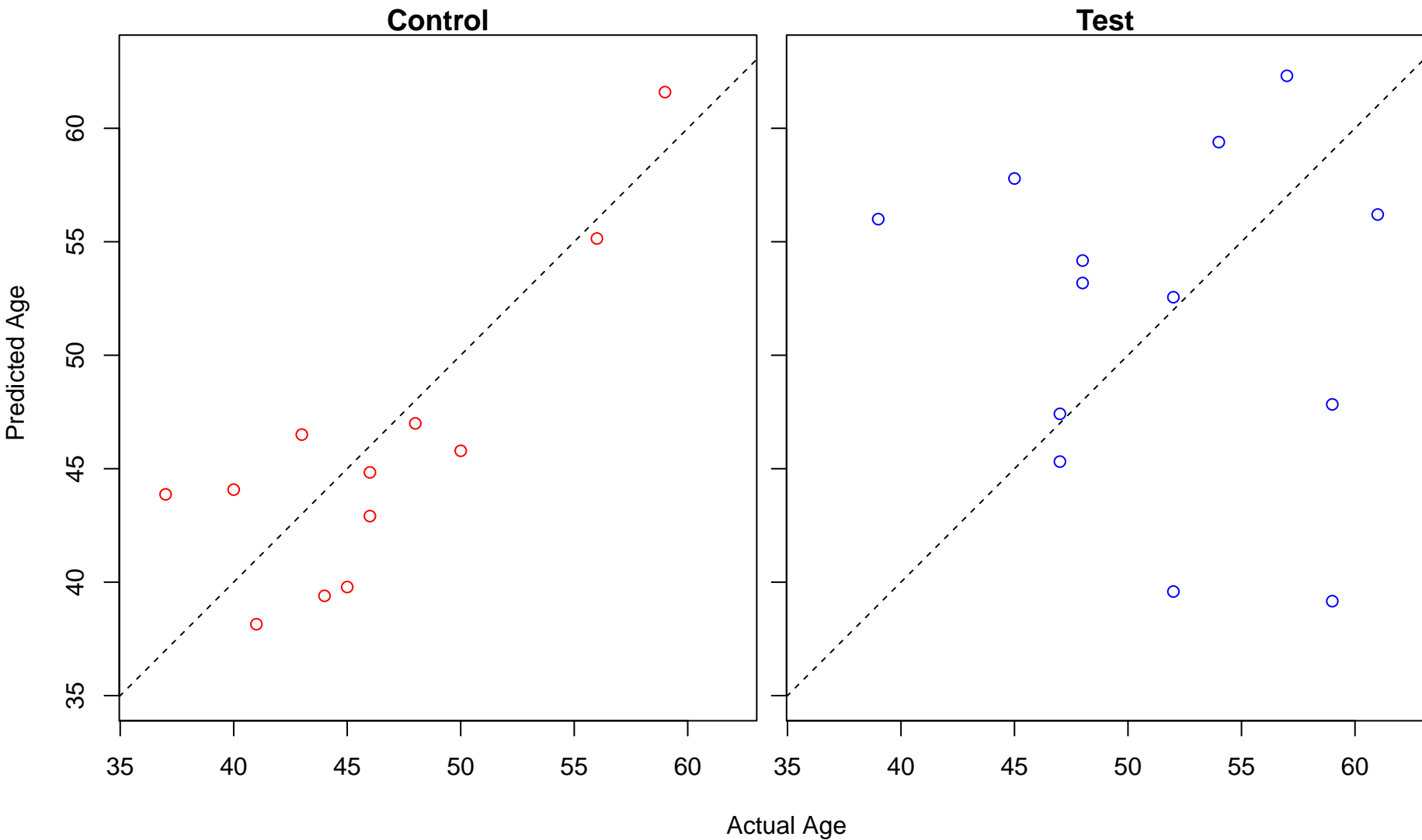
positive regulation of histone modification (Score: 21.729729)



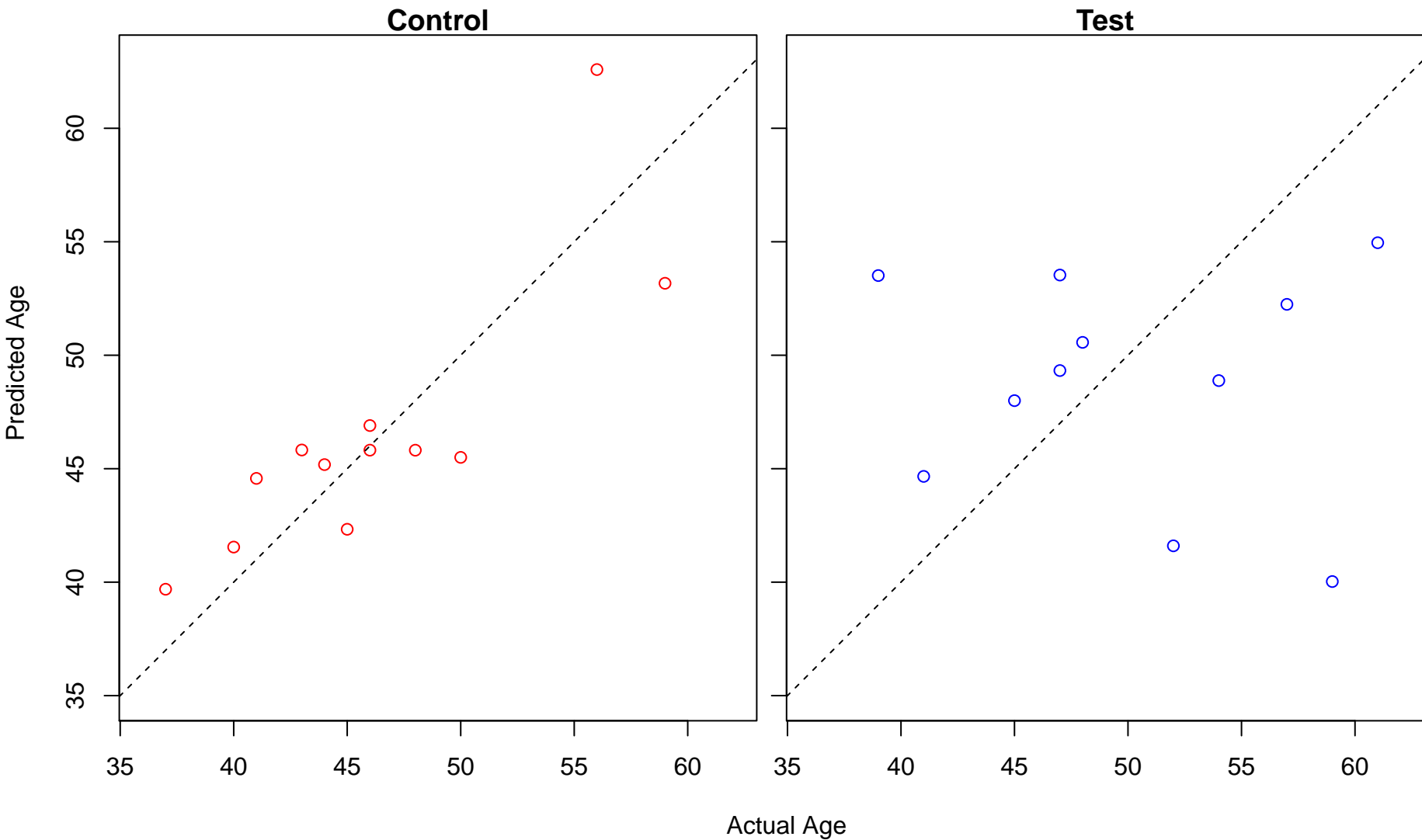
membrane invagination (Score: 21.626504)



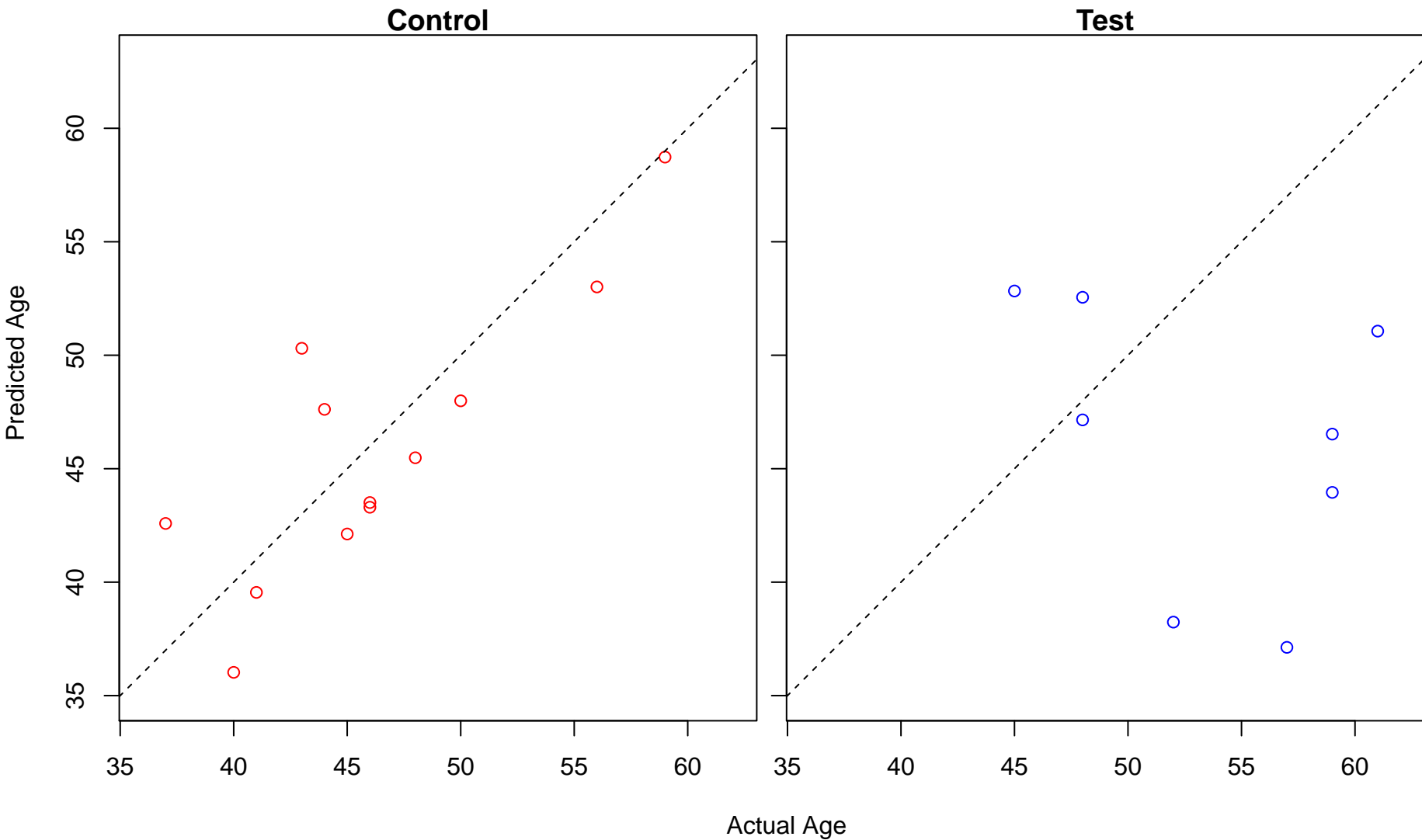
regulation of organic acid transport (Score: 21.620877)



nitric oxide mediated signal transduction (Score: 21.595215)

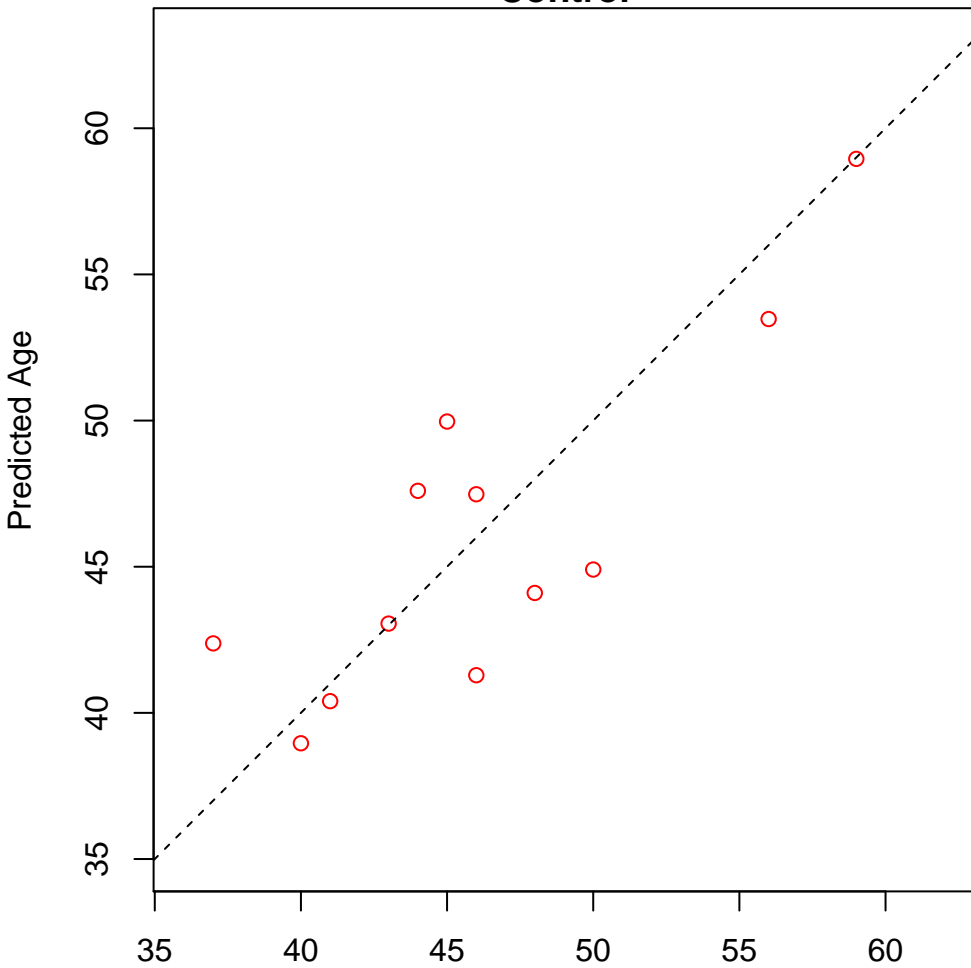


regulation of histone acetylation (Score: 21.577802)

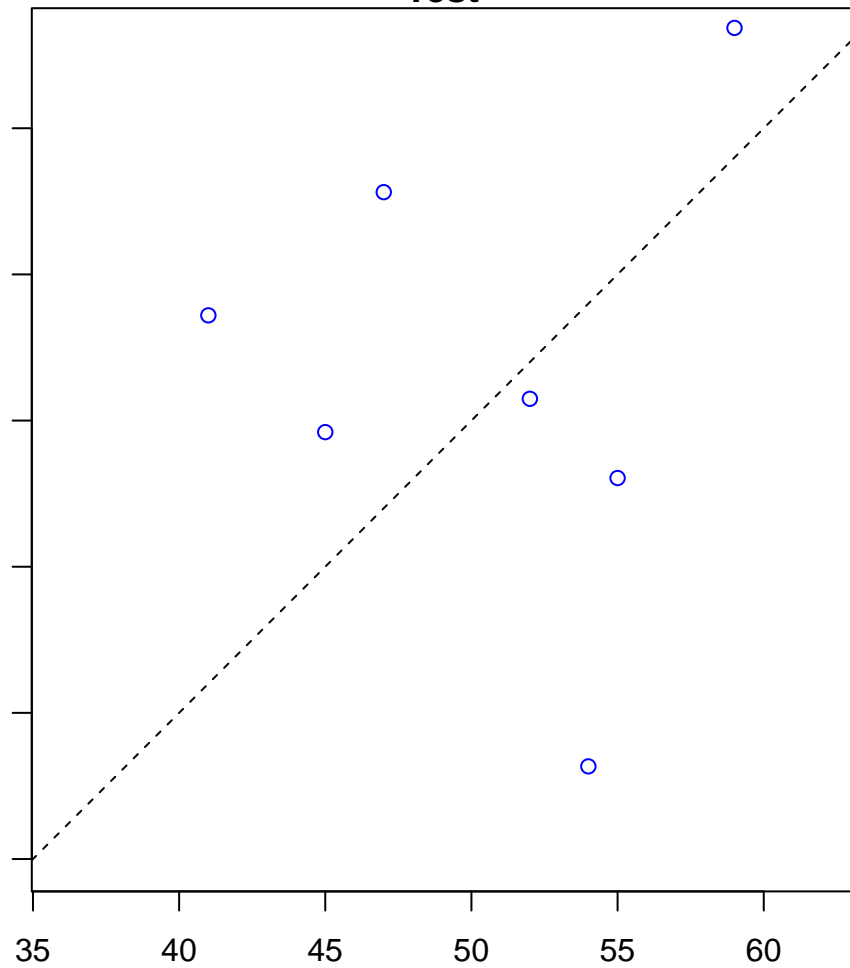


mitotic nuclear envelope reassembly (Score: 21.498085)

Control

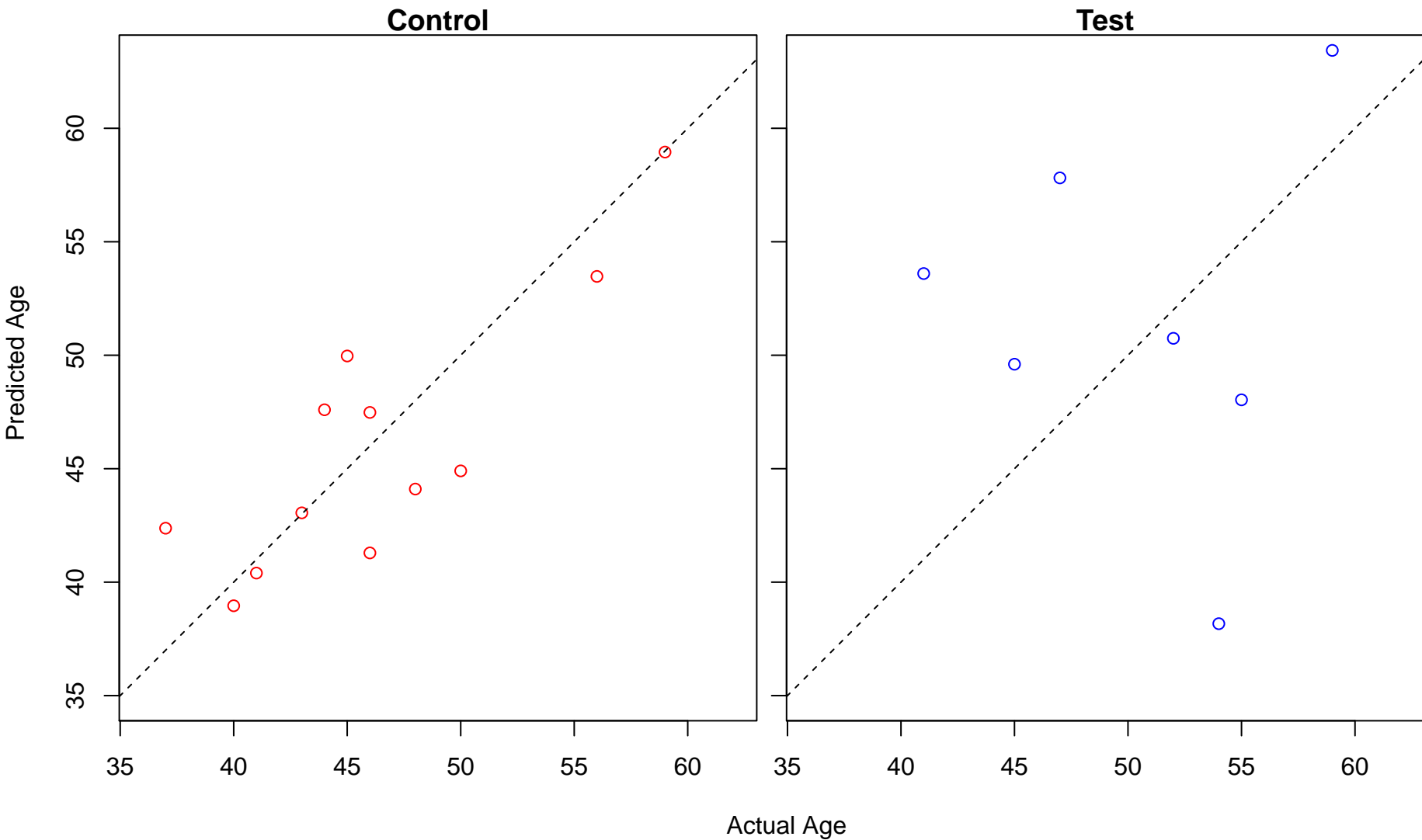


Test

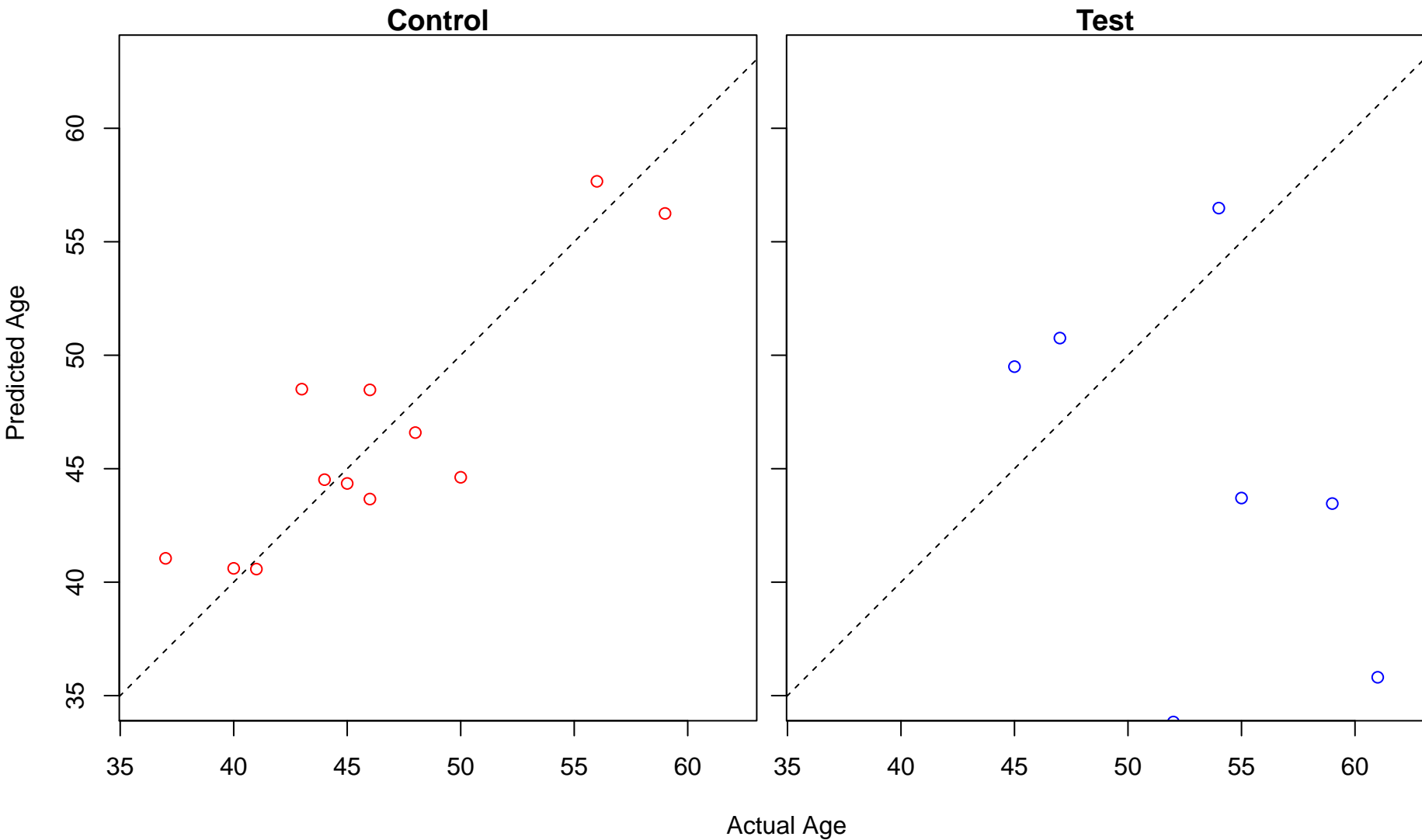


Actual Age

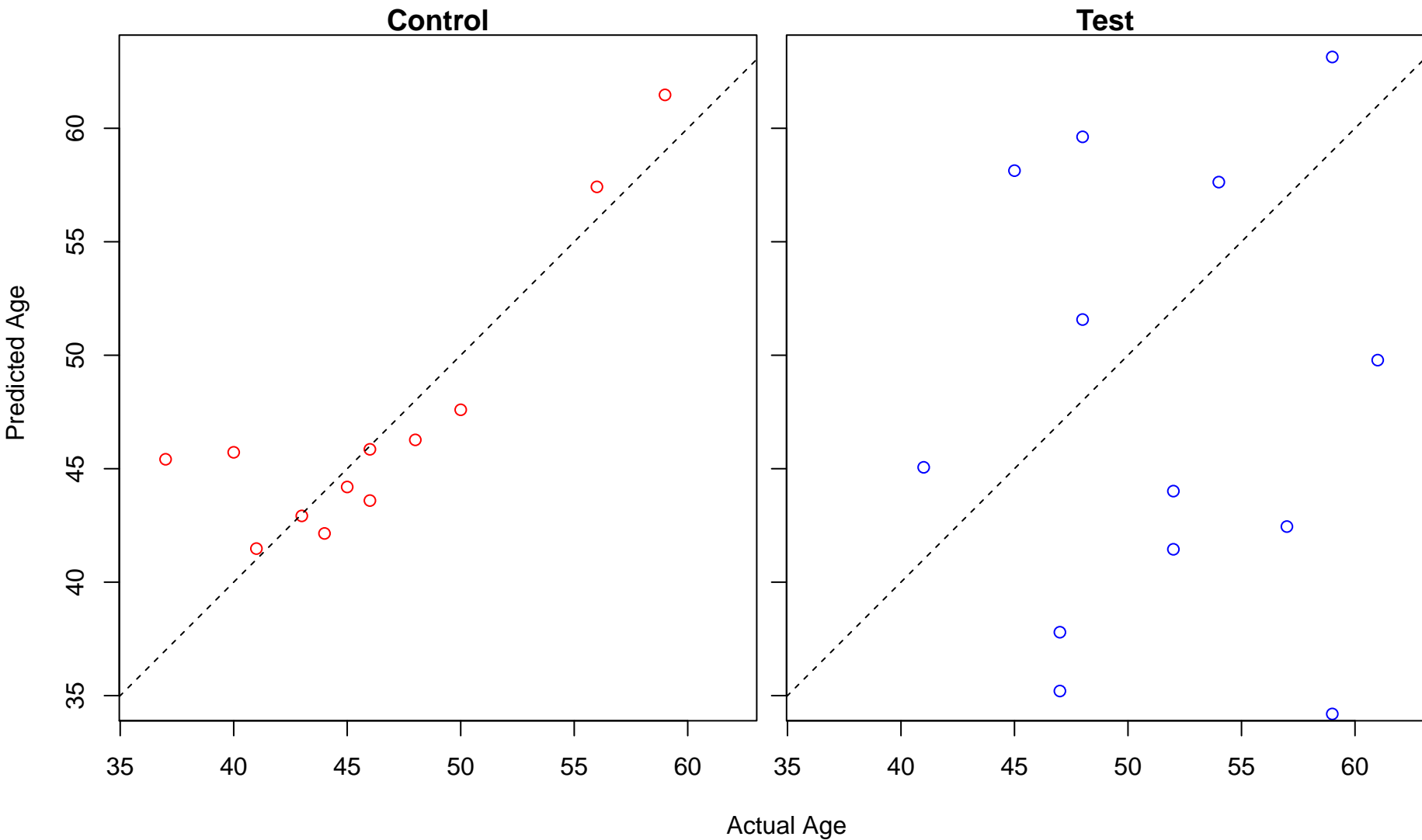
nuclear envelope reassembly (Score: 21.498085)



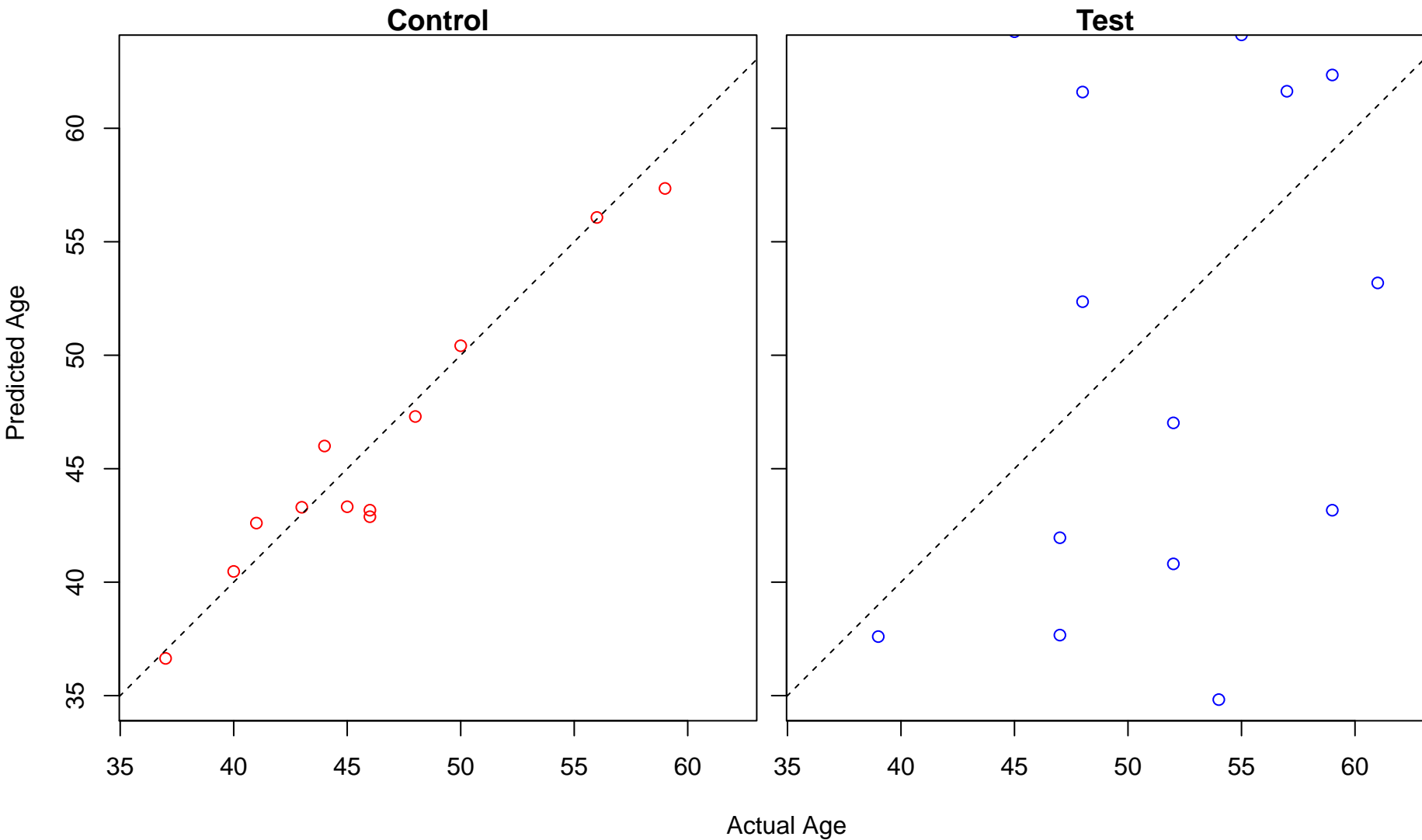
positive regulation of chromatin modification (Score: 21.400697)



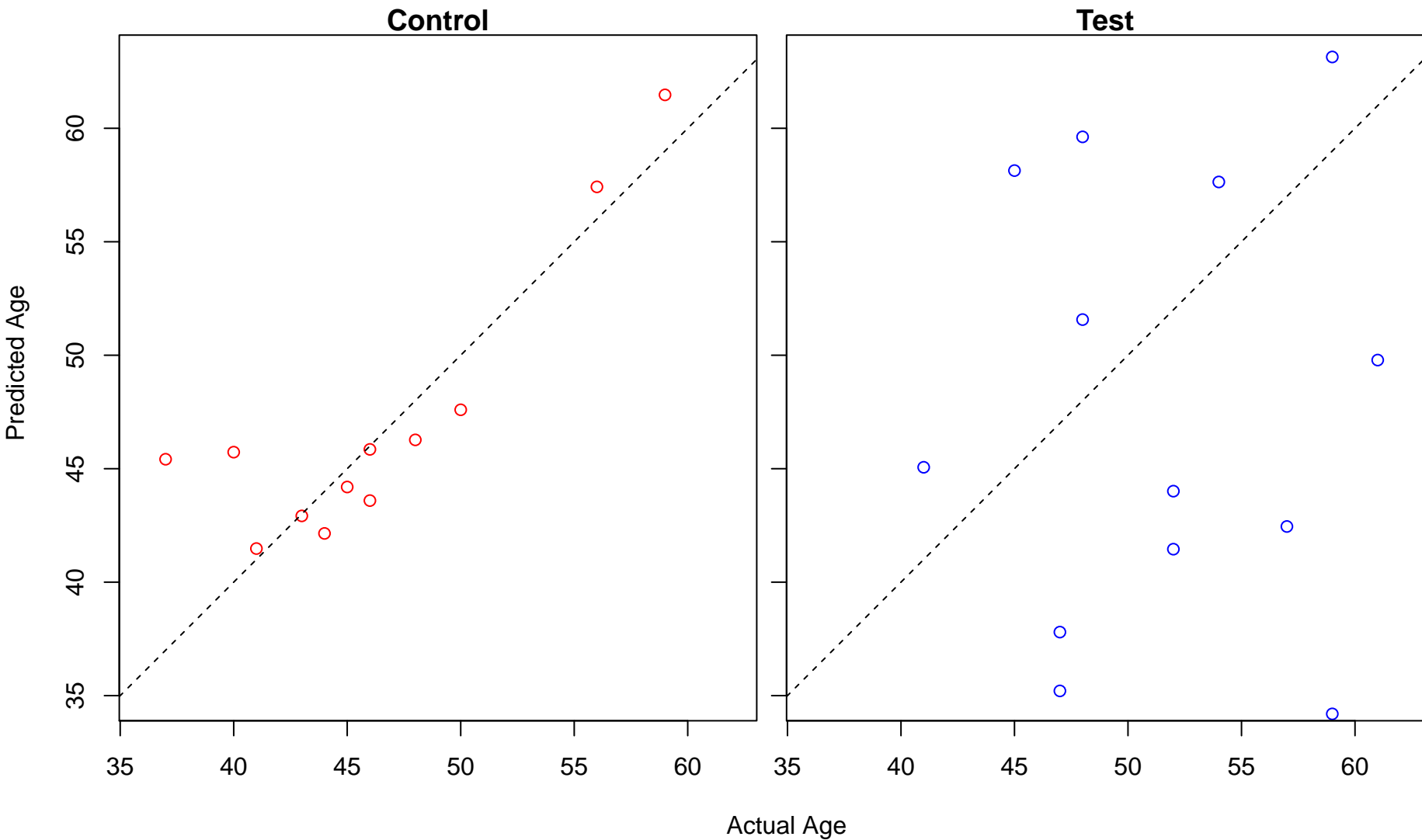
glycosaminoglycan biosynthetic process (Score: 21.384157)



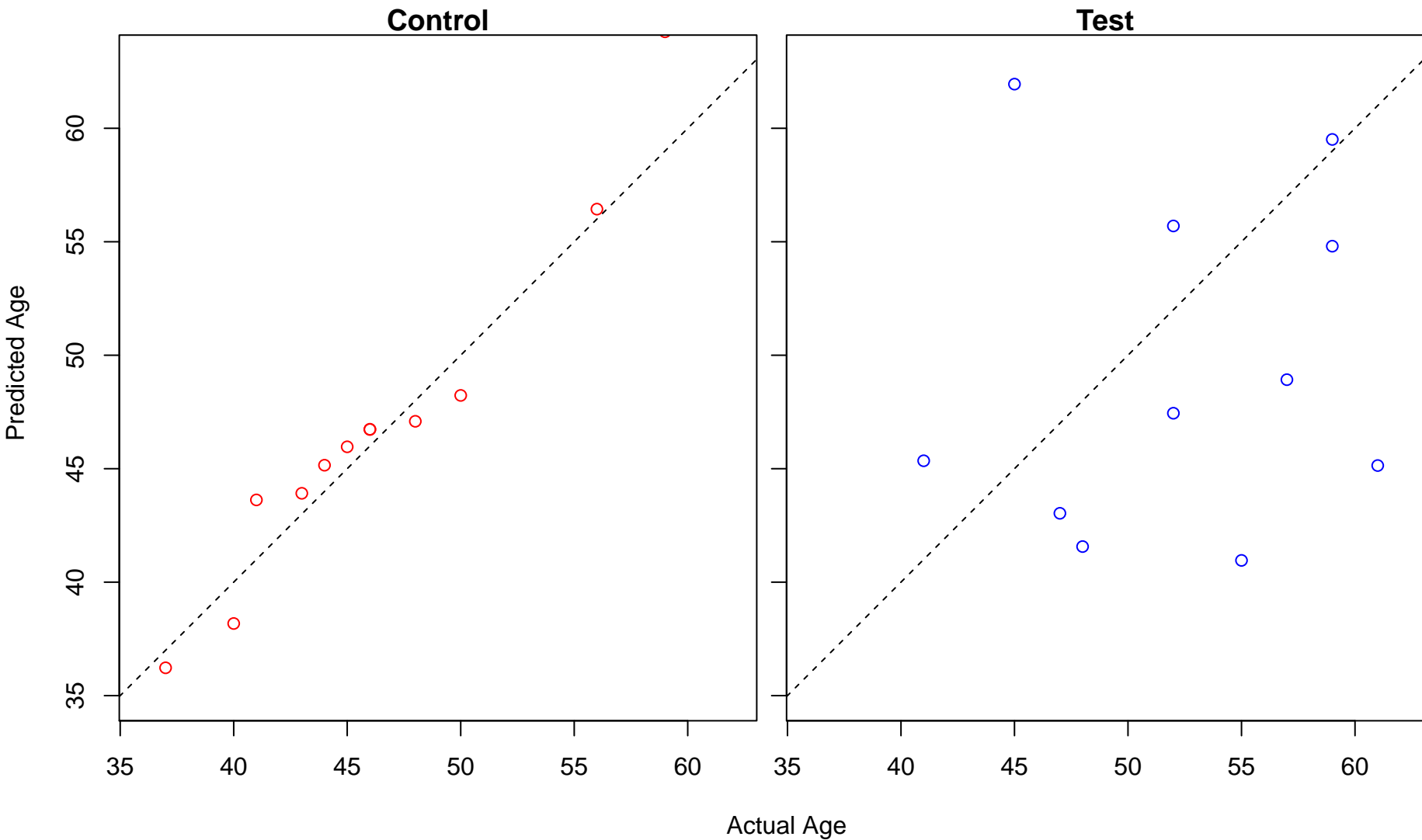
cellular response to extracellular stimulus (Score: 21.358726)



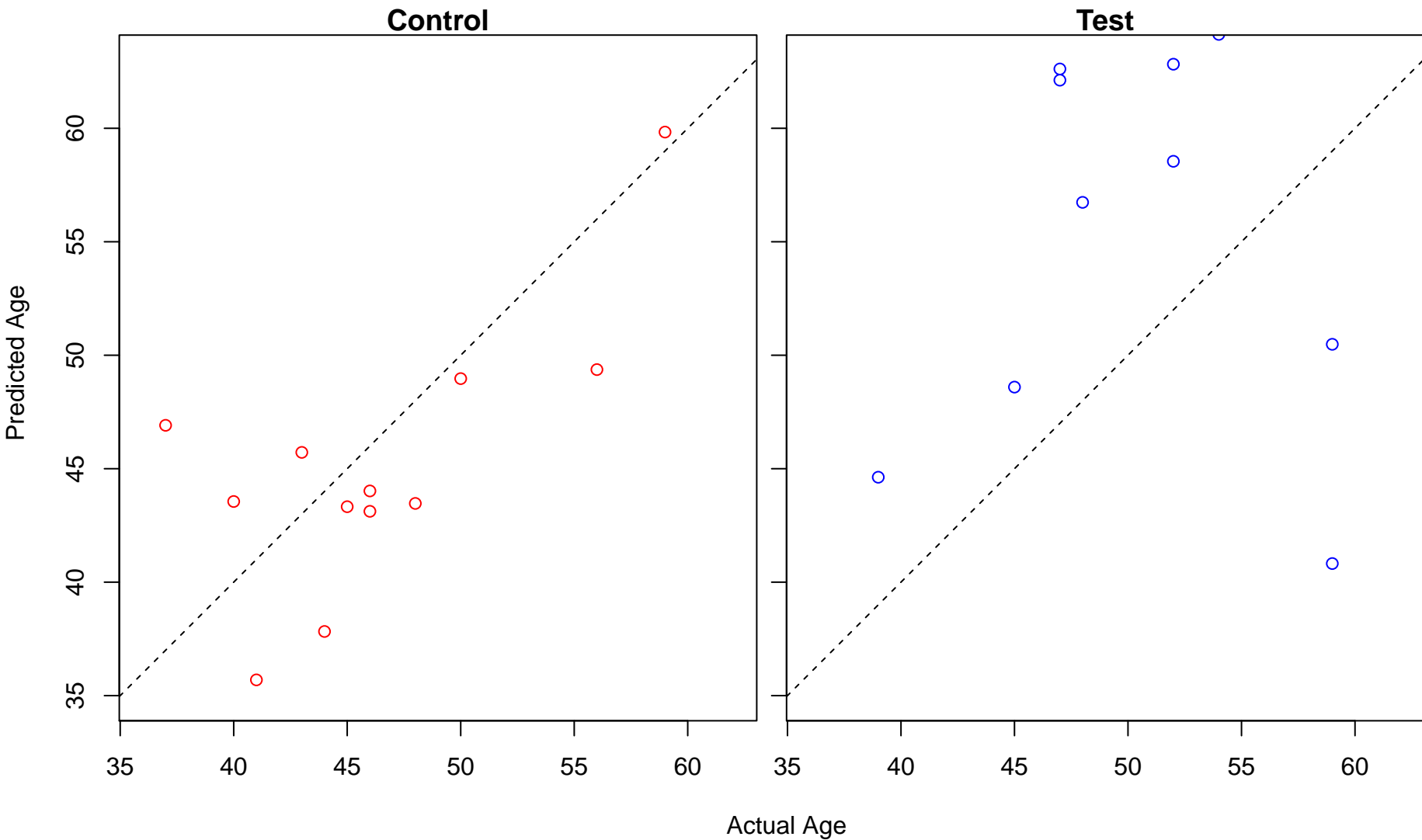
aminoglycan biosynthetic process (Score: 21.357720)



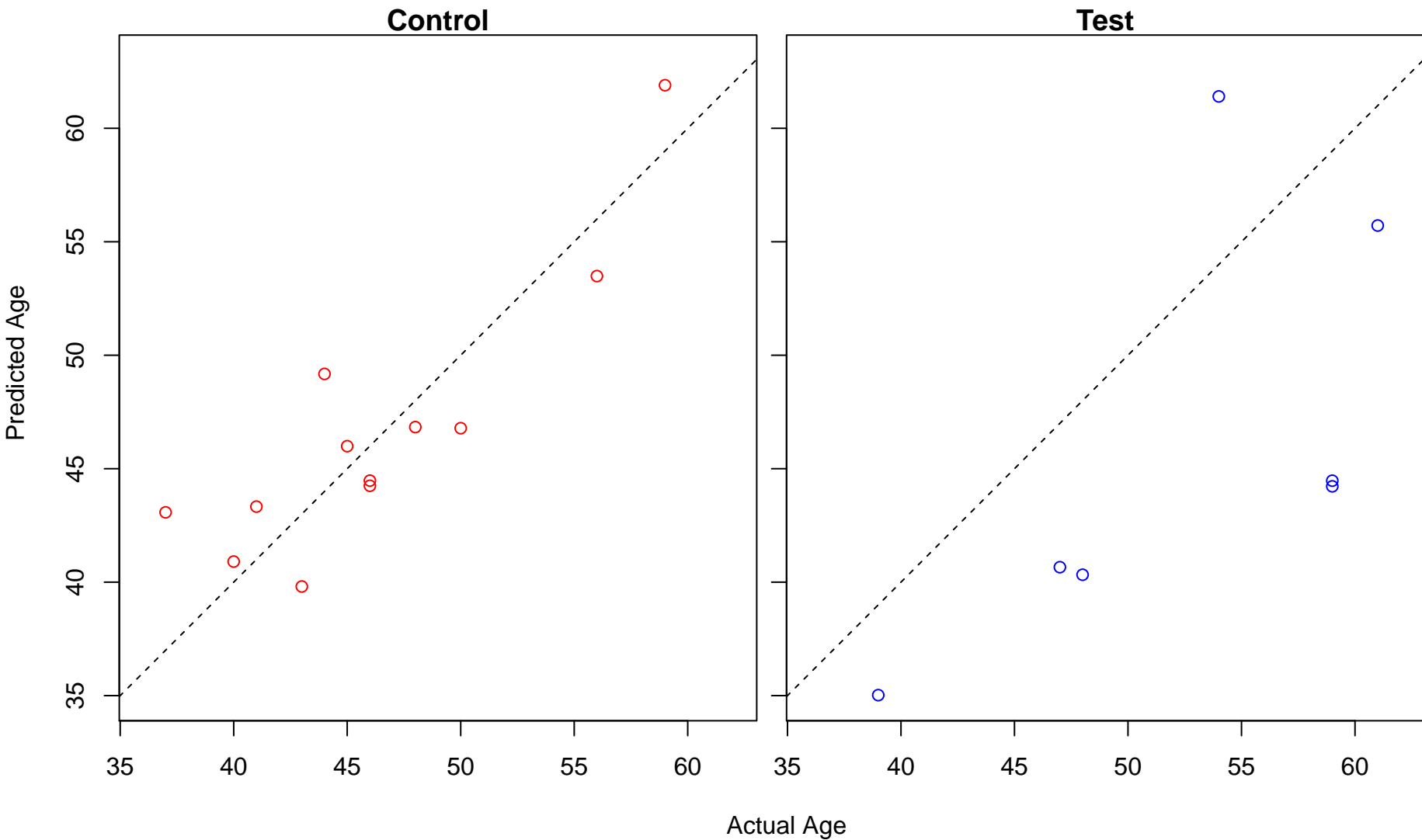
kidney mesenchyme development (Score: 21.355067)



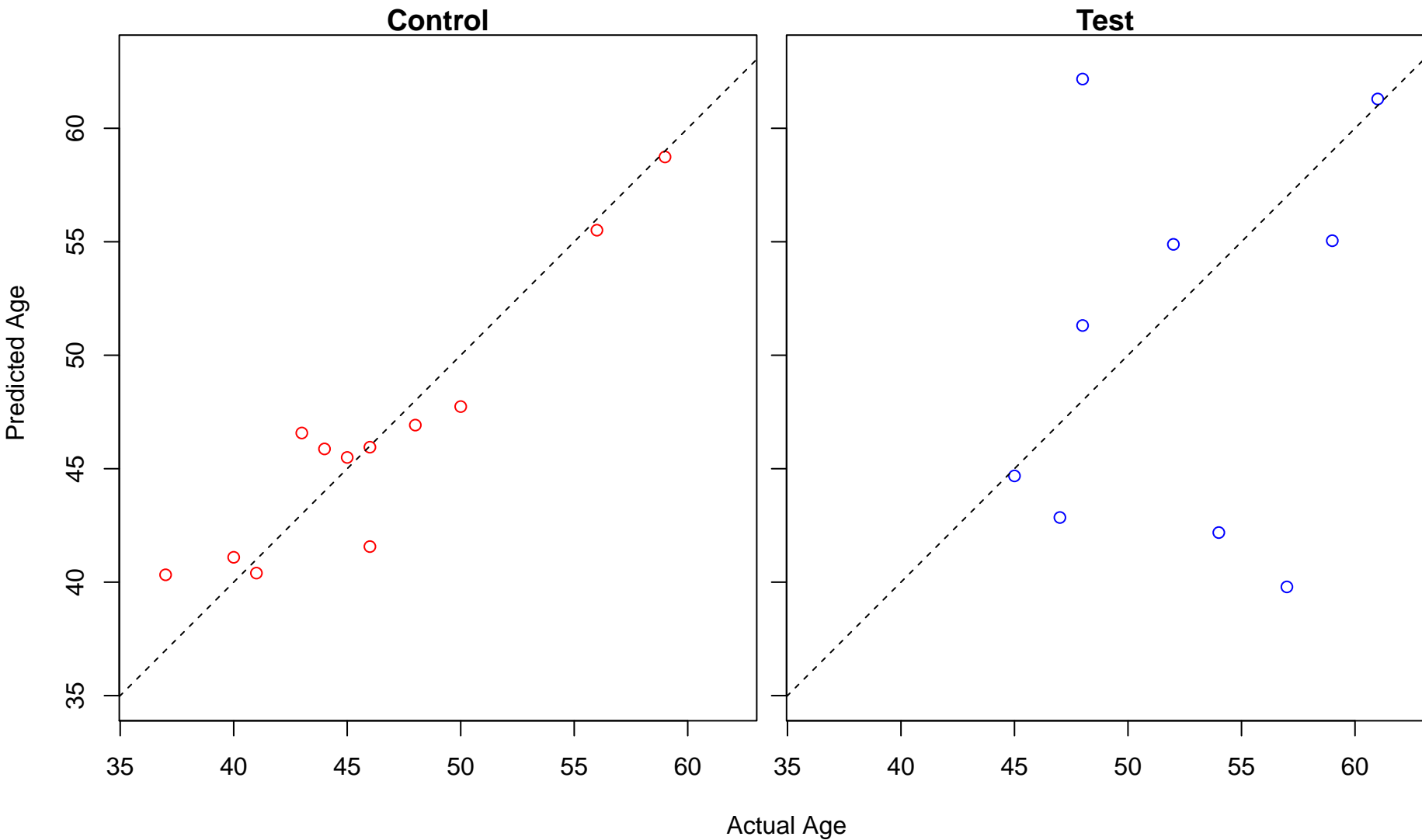
regulation of fatty acid transport (Score: 21.345758)



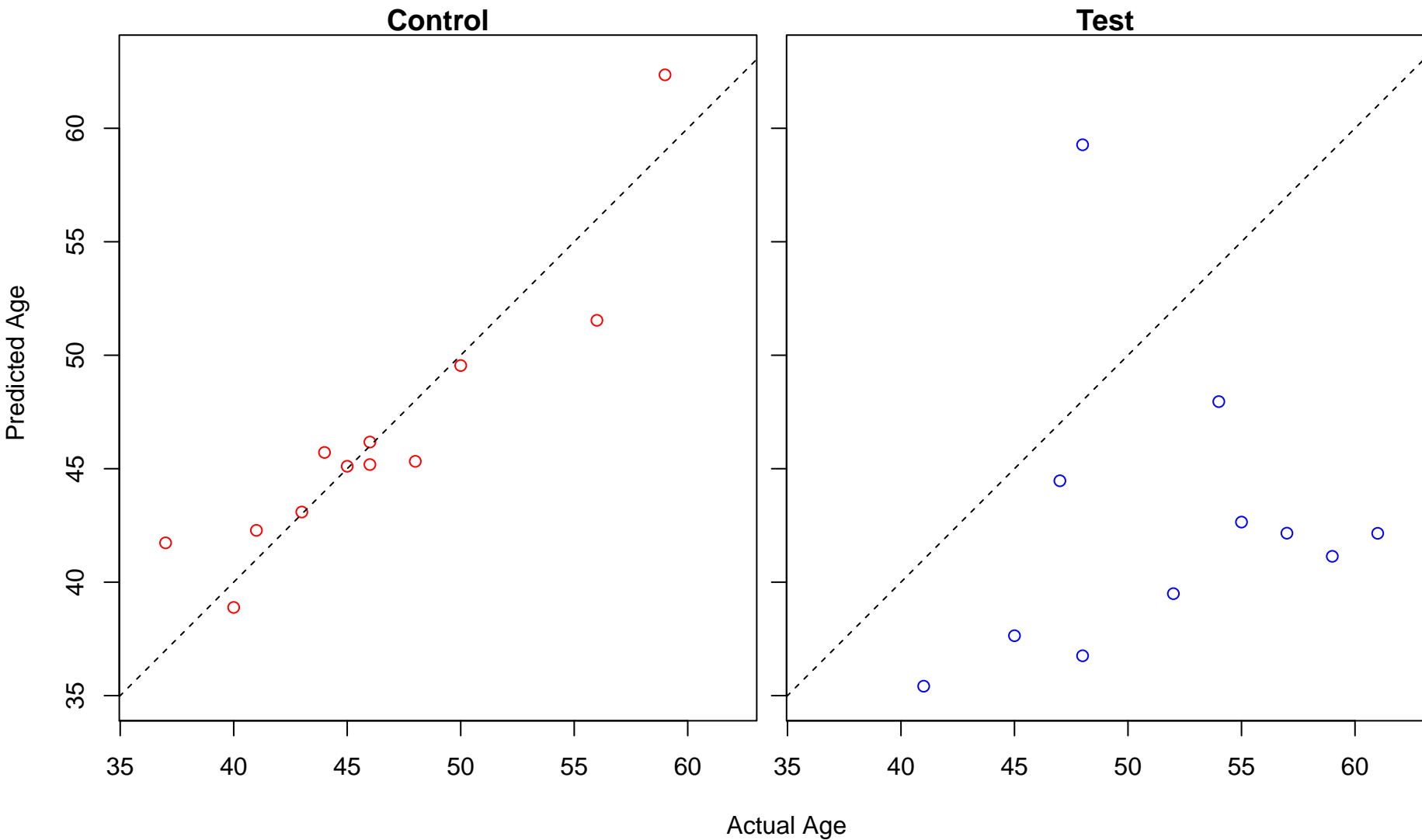
neural retina development (Score: 21.119633)



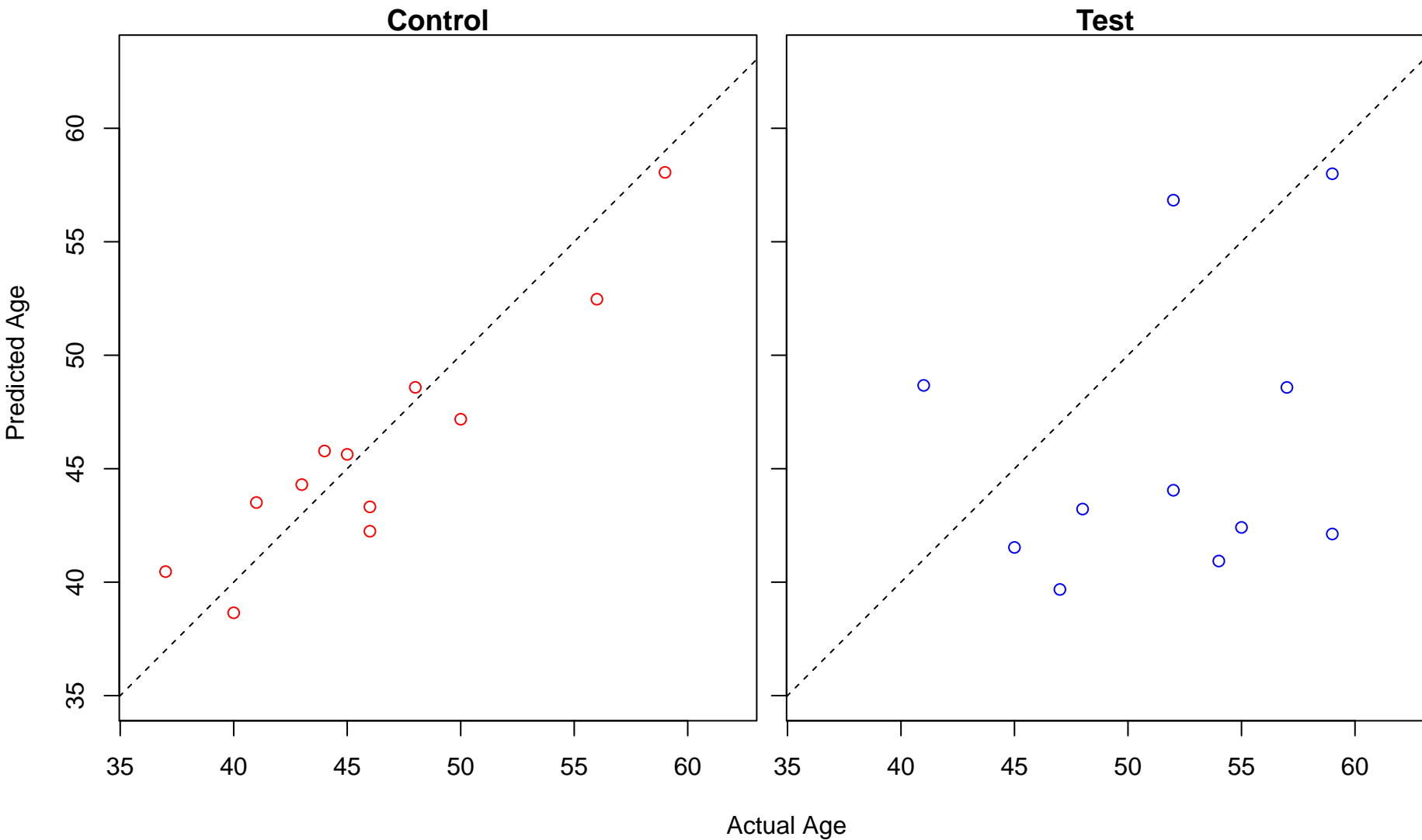
negative regulation of ERK1 and ERK2 cascade (Score: 21.079398)



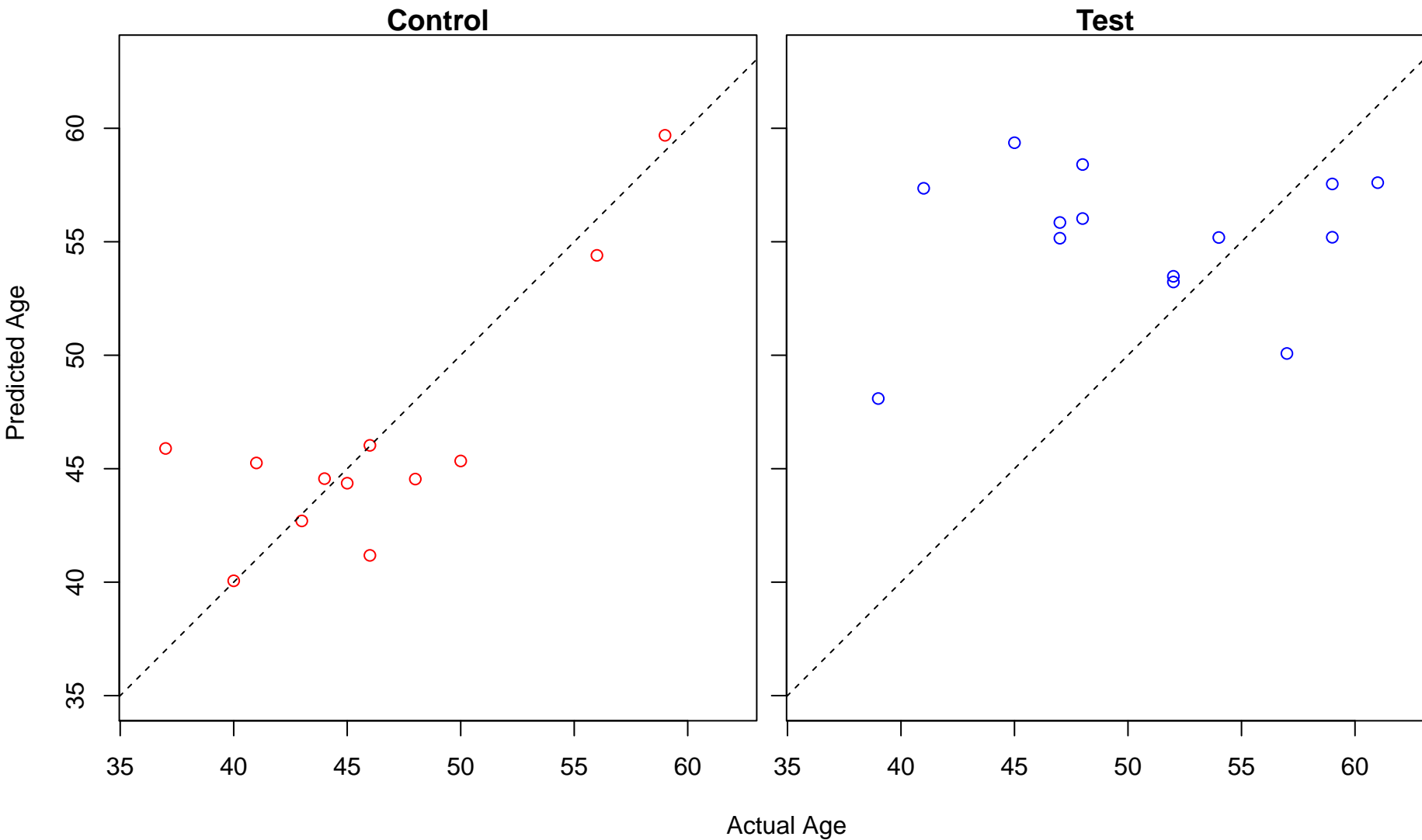
central nervous system neuron development (Score: 20.973504)



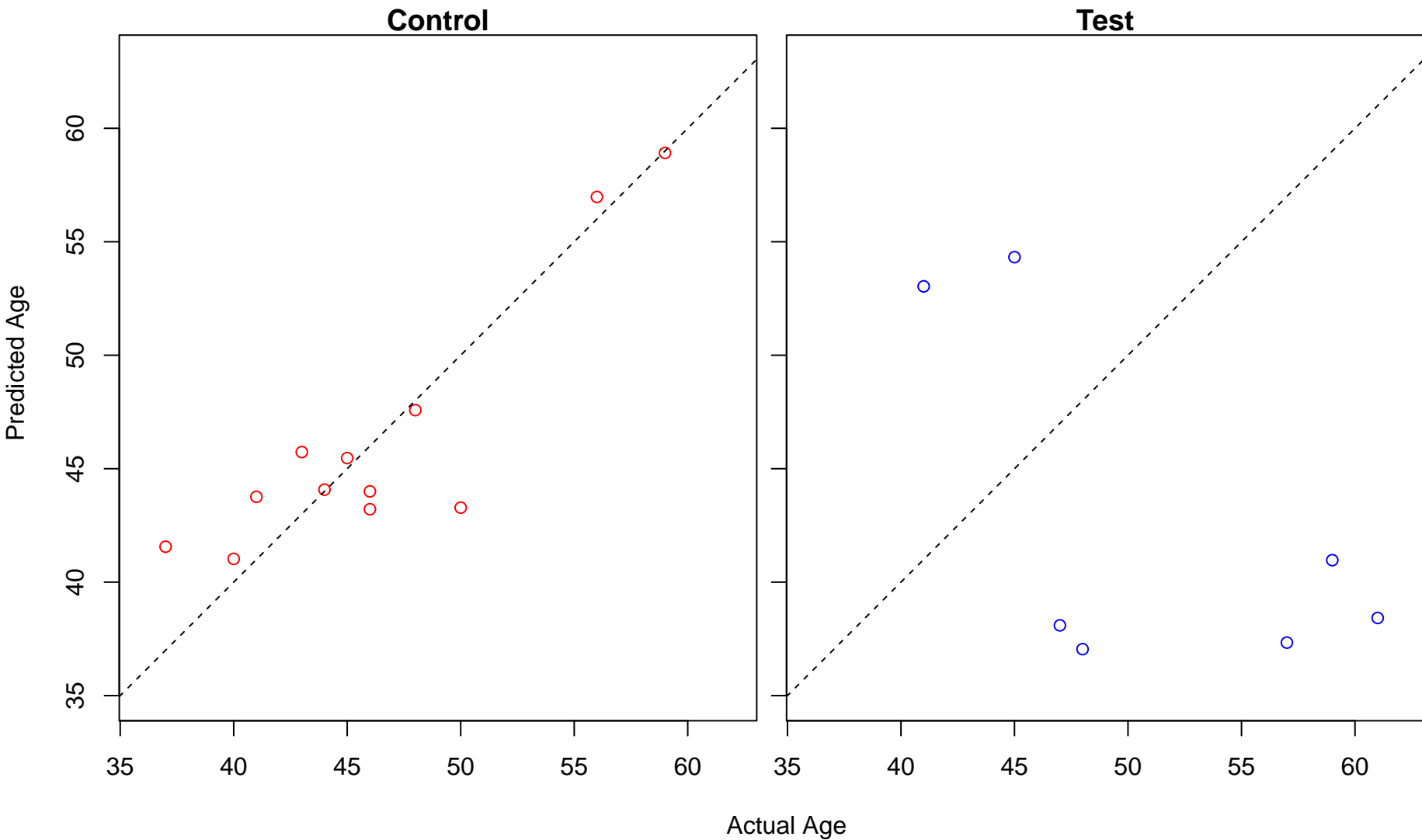
stem cell proliferation (Score: 20.970872)



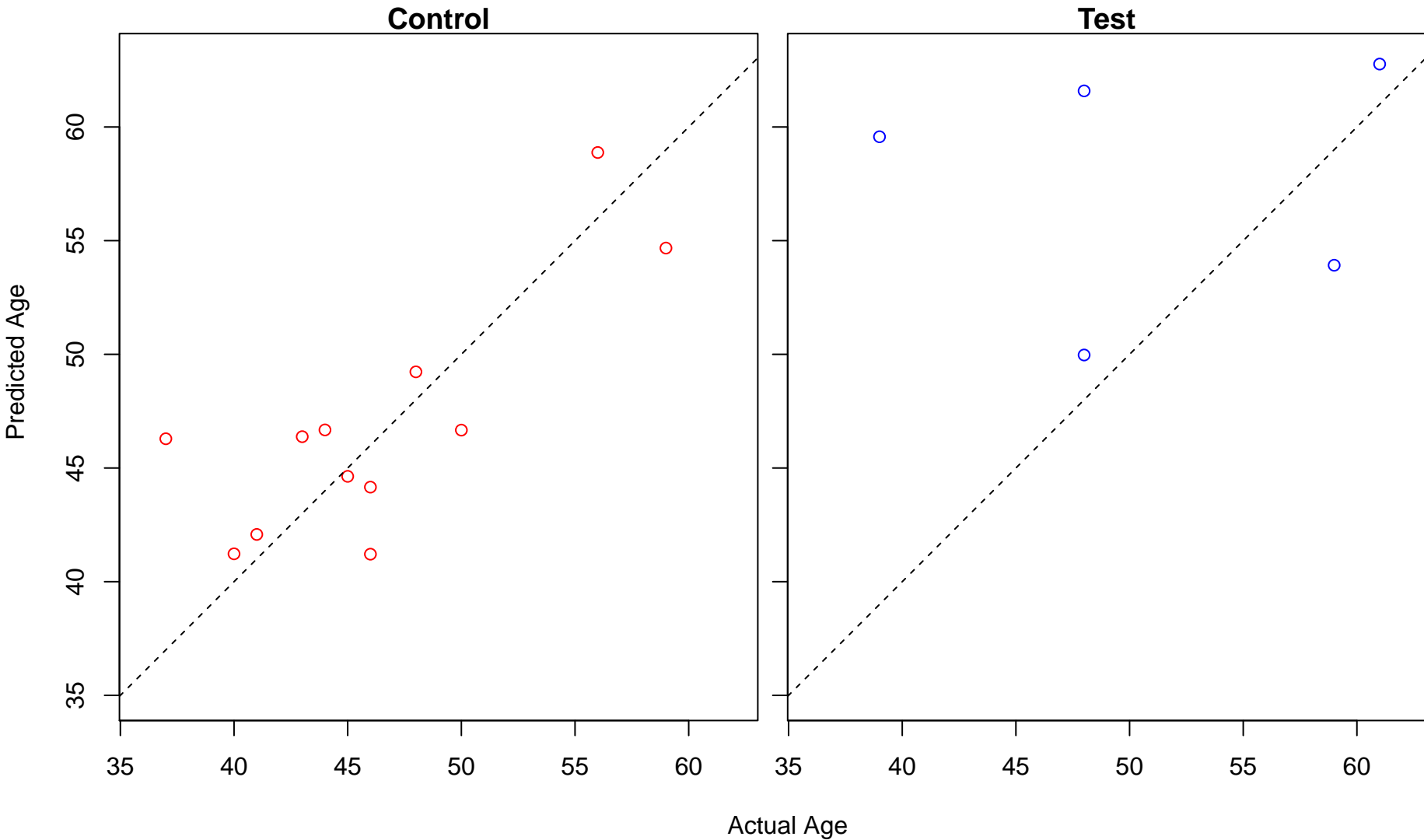
thrombin receptor signaling pathway (Score: 20.765307)



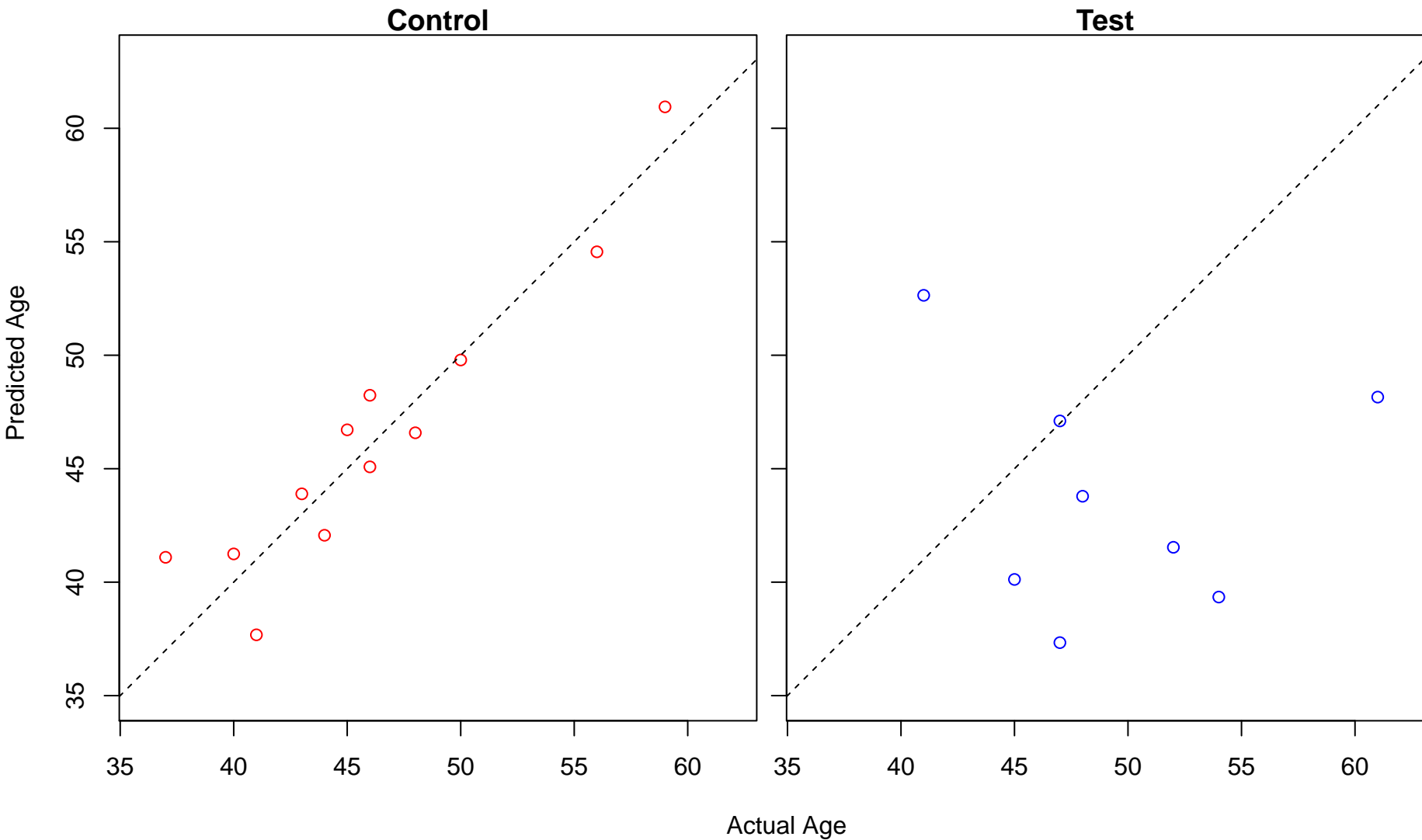
cell-matrix adhesion (Score: 20.627542)



presynaptic process involved in synaptic transmission (Score: 20.621860)

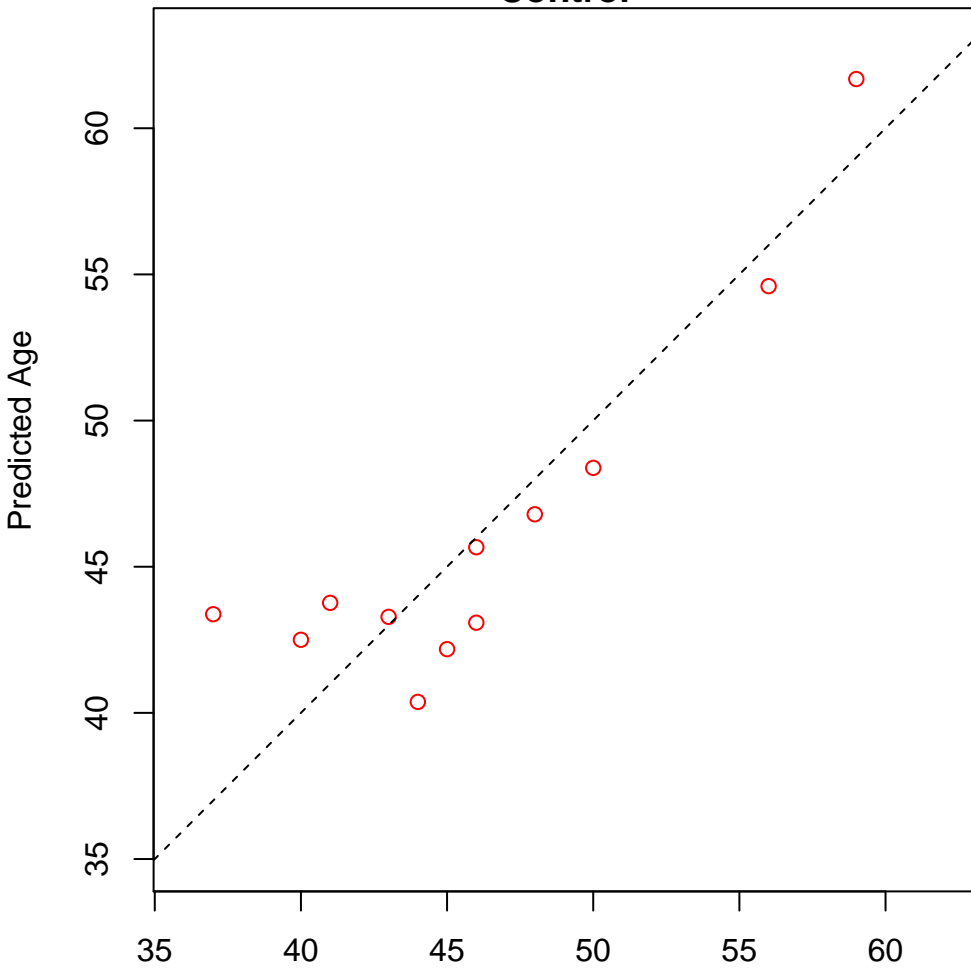


positive regulation of cell junction assembly (Score: 20.532413)

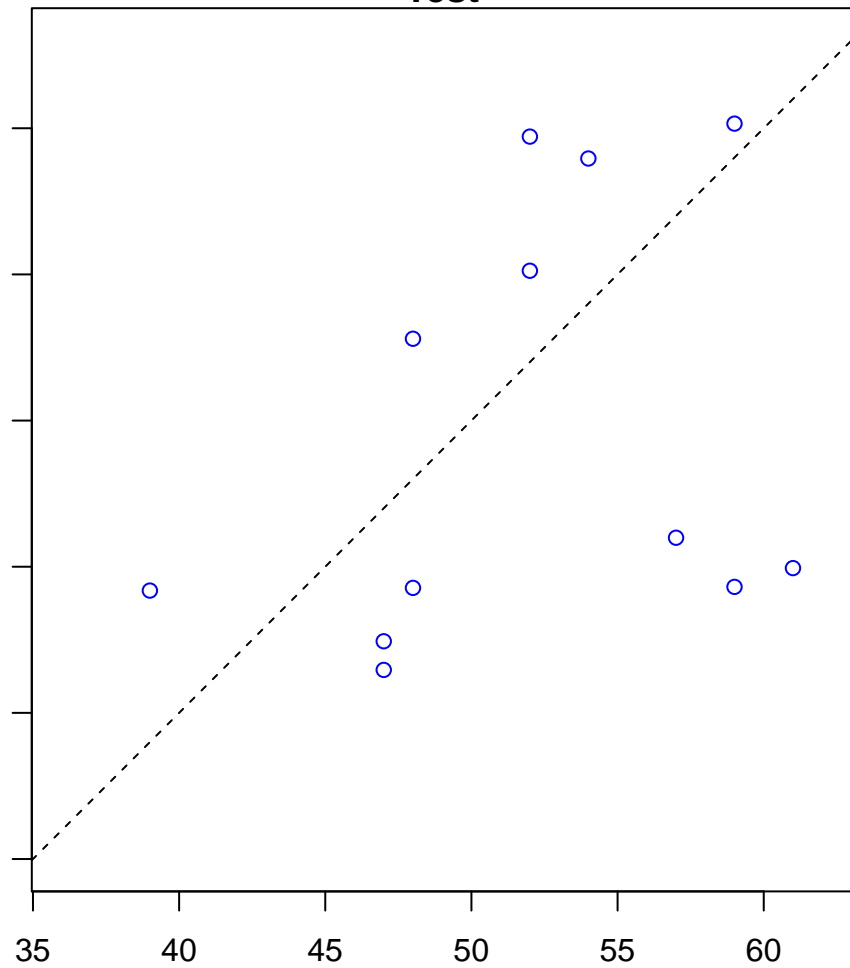


organic acid transmembrane transport (Score: 20.492221)

Control

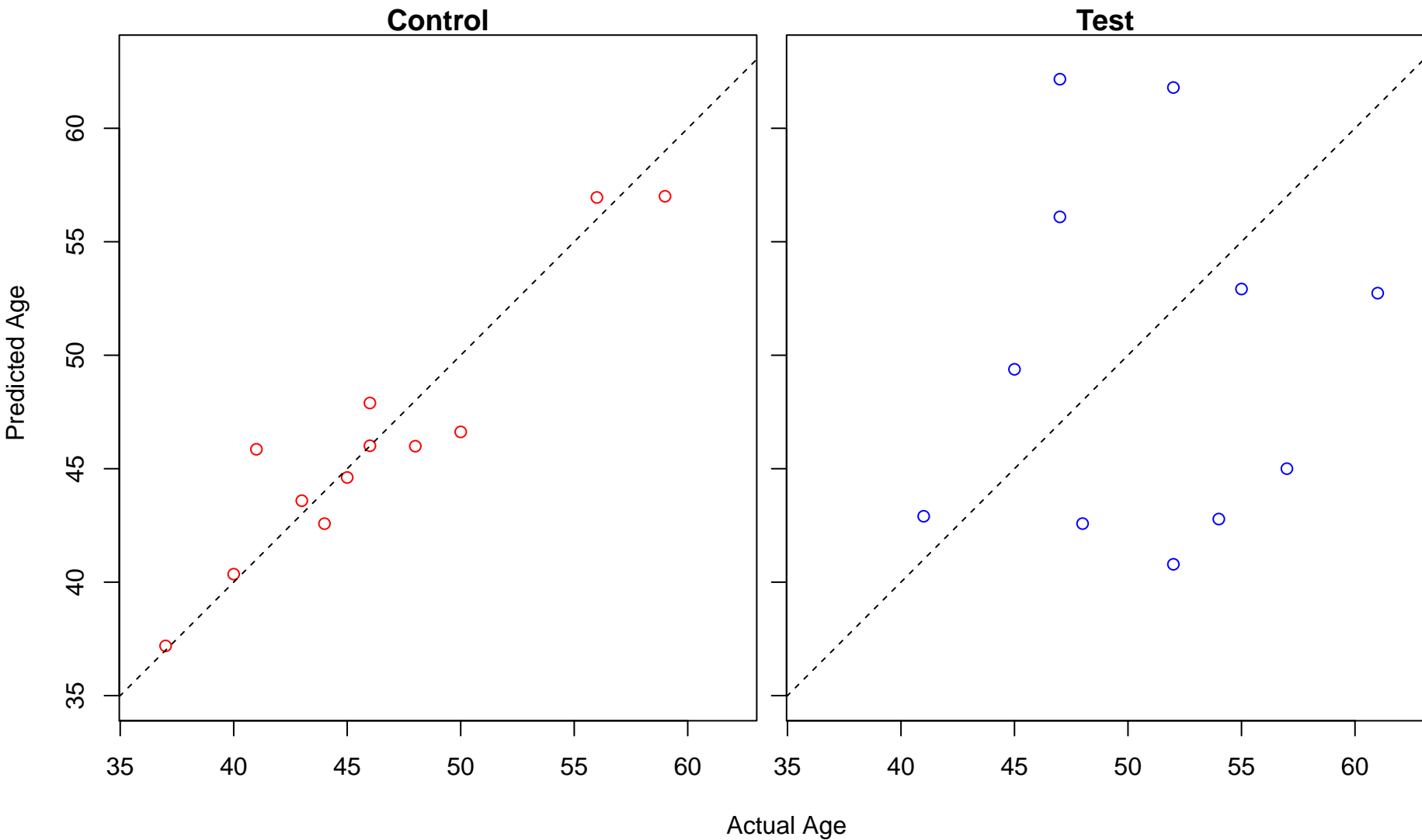


Test

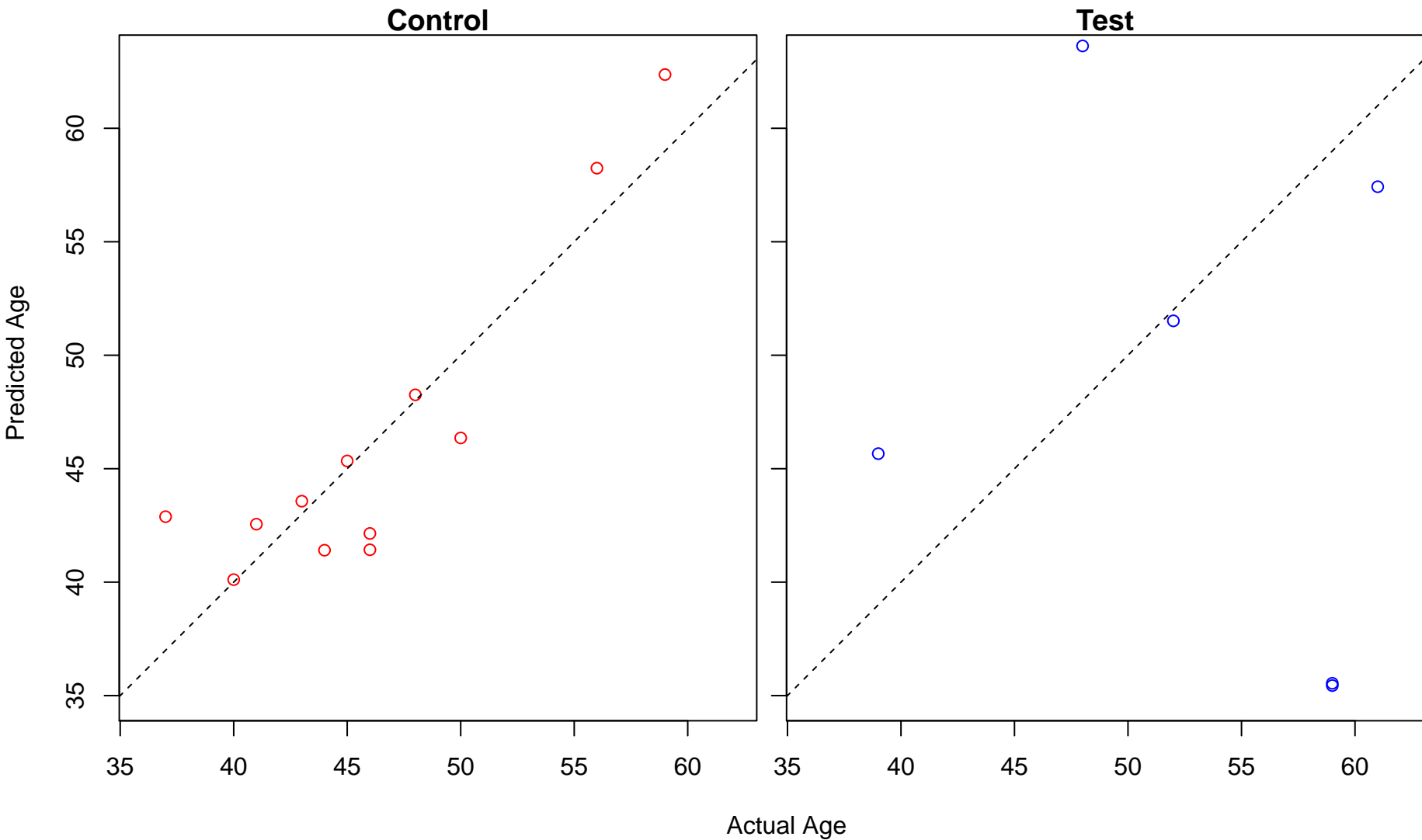


Actual Age

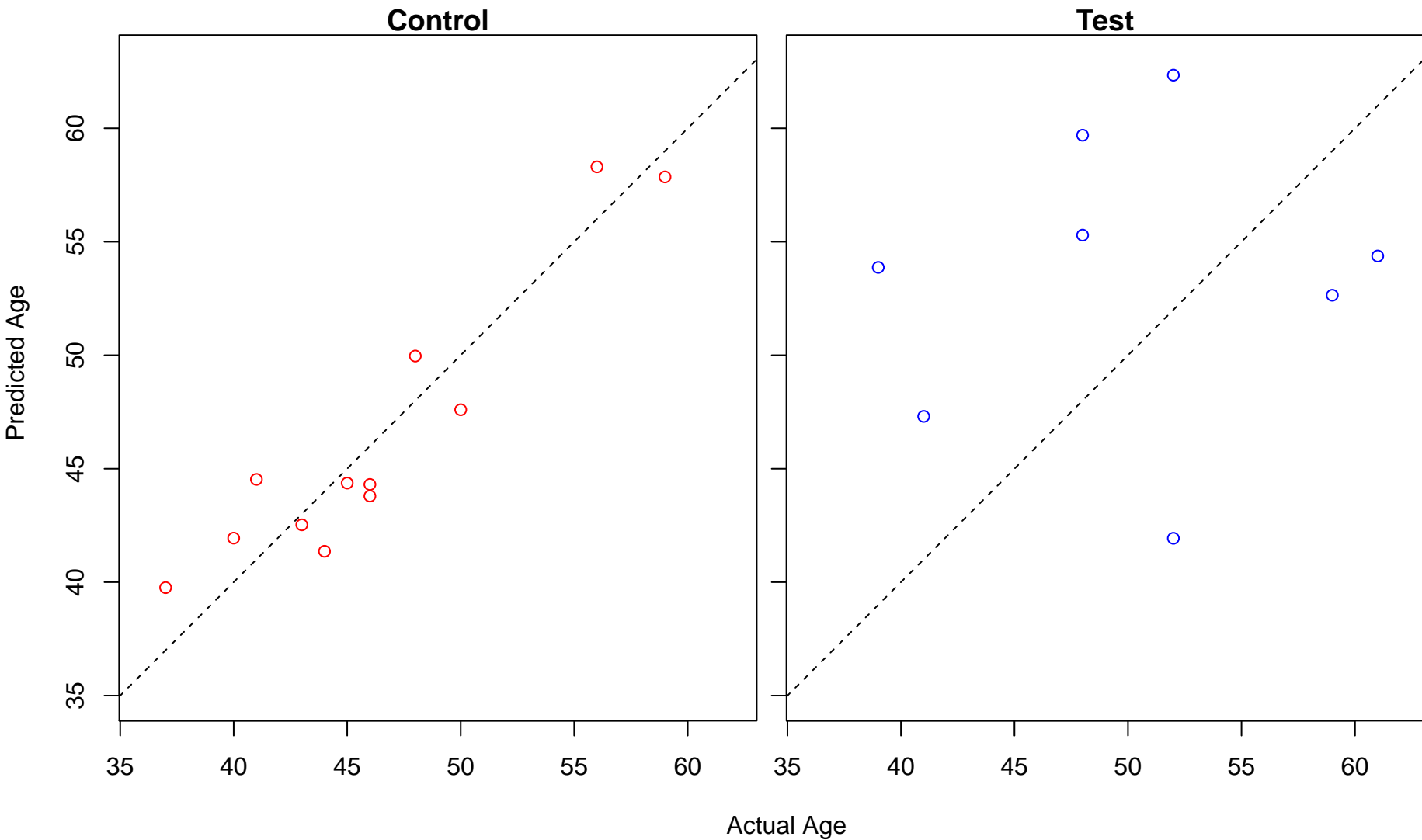
high-density lipoprotein particle assembly (Score: 20.475184)



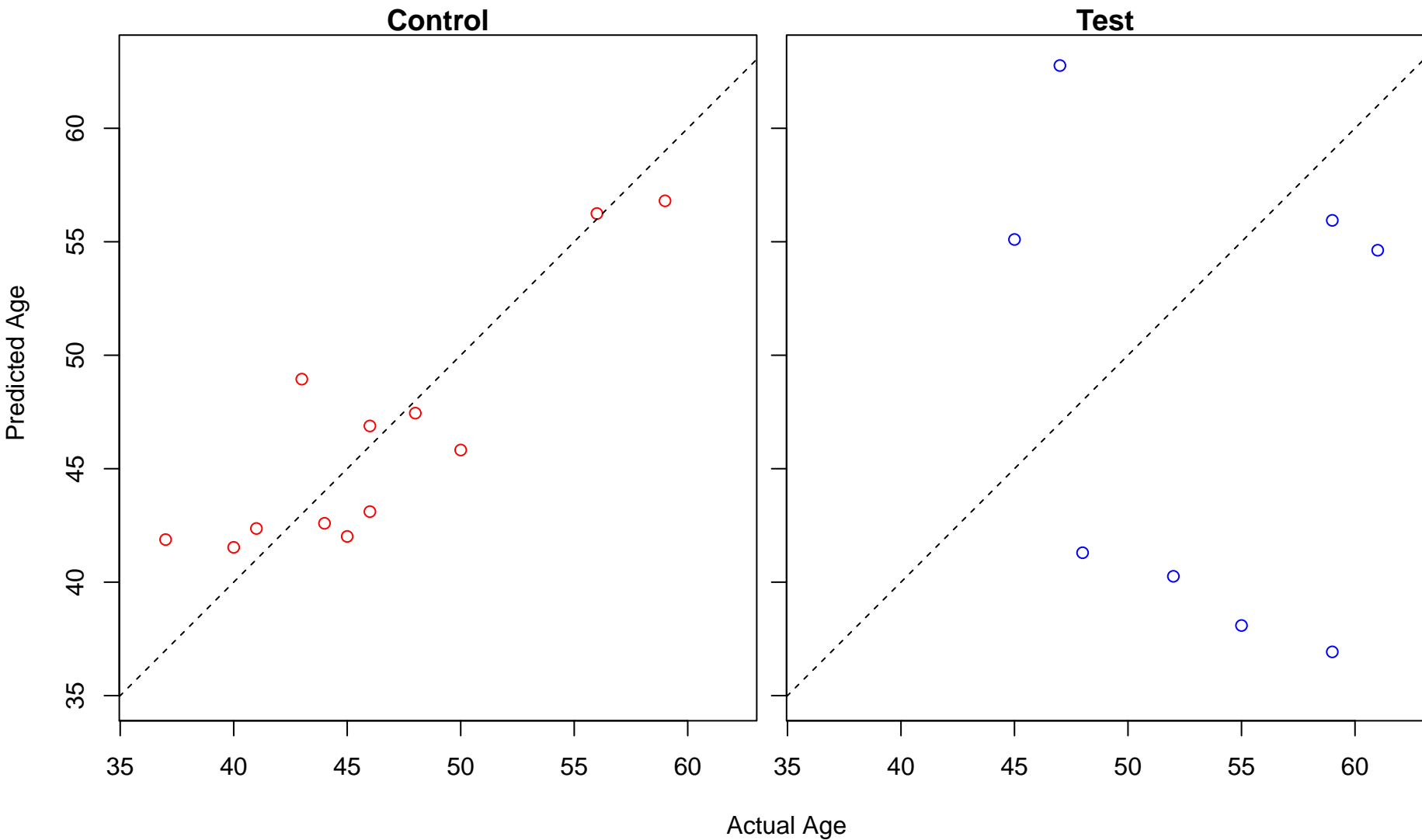
regulation of cardiac muscle cell action potential (Score: 20.470680)



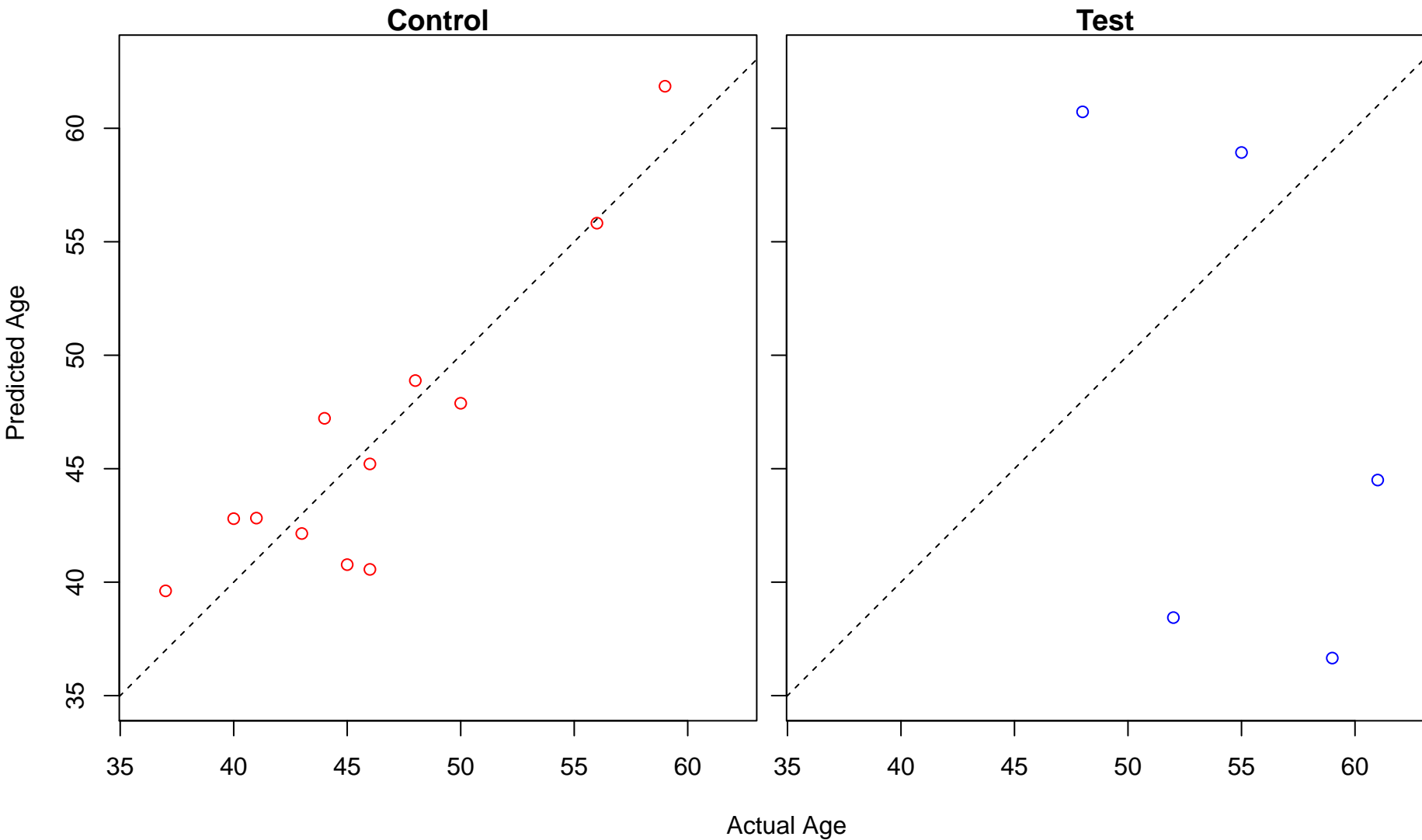
folic acid metabolic process (Score: 20.449564)



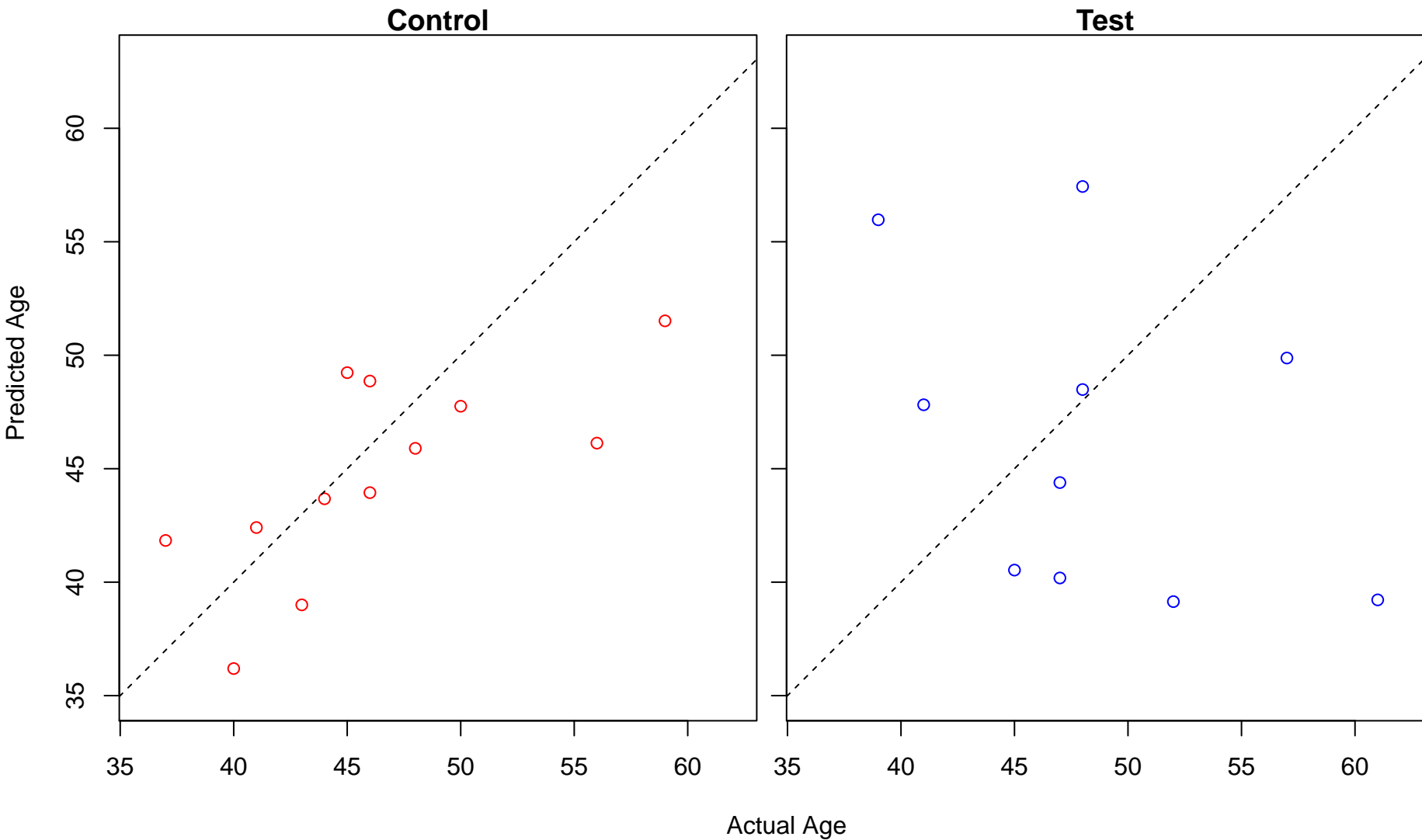
angiogenesis (Score: 20.376834)



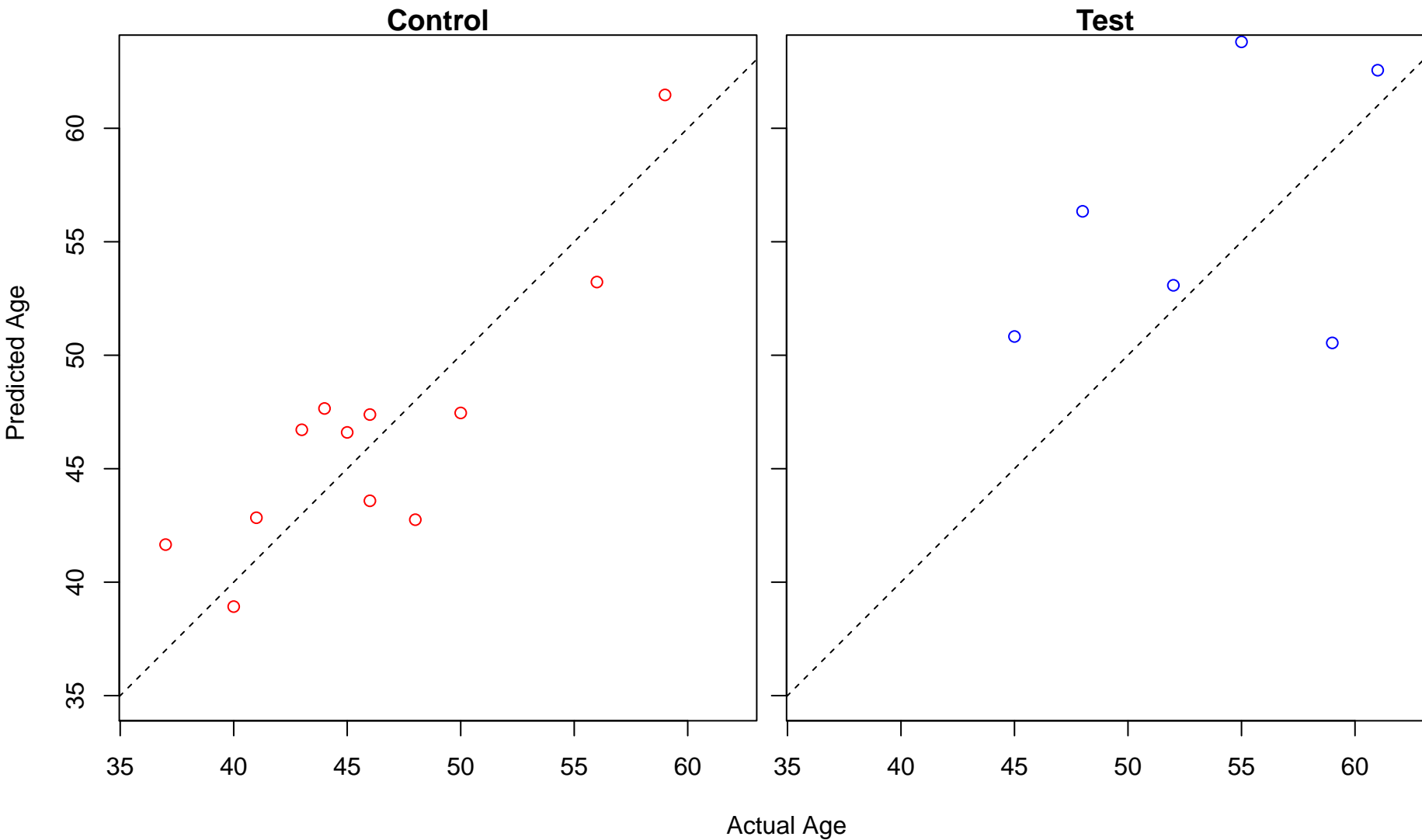
response to nutrient (Score: 20.216987)



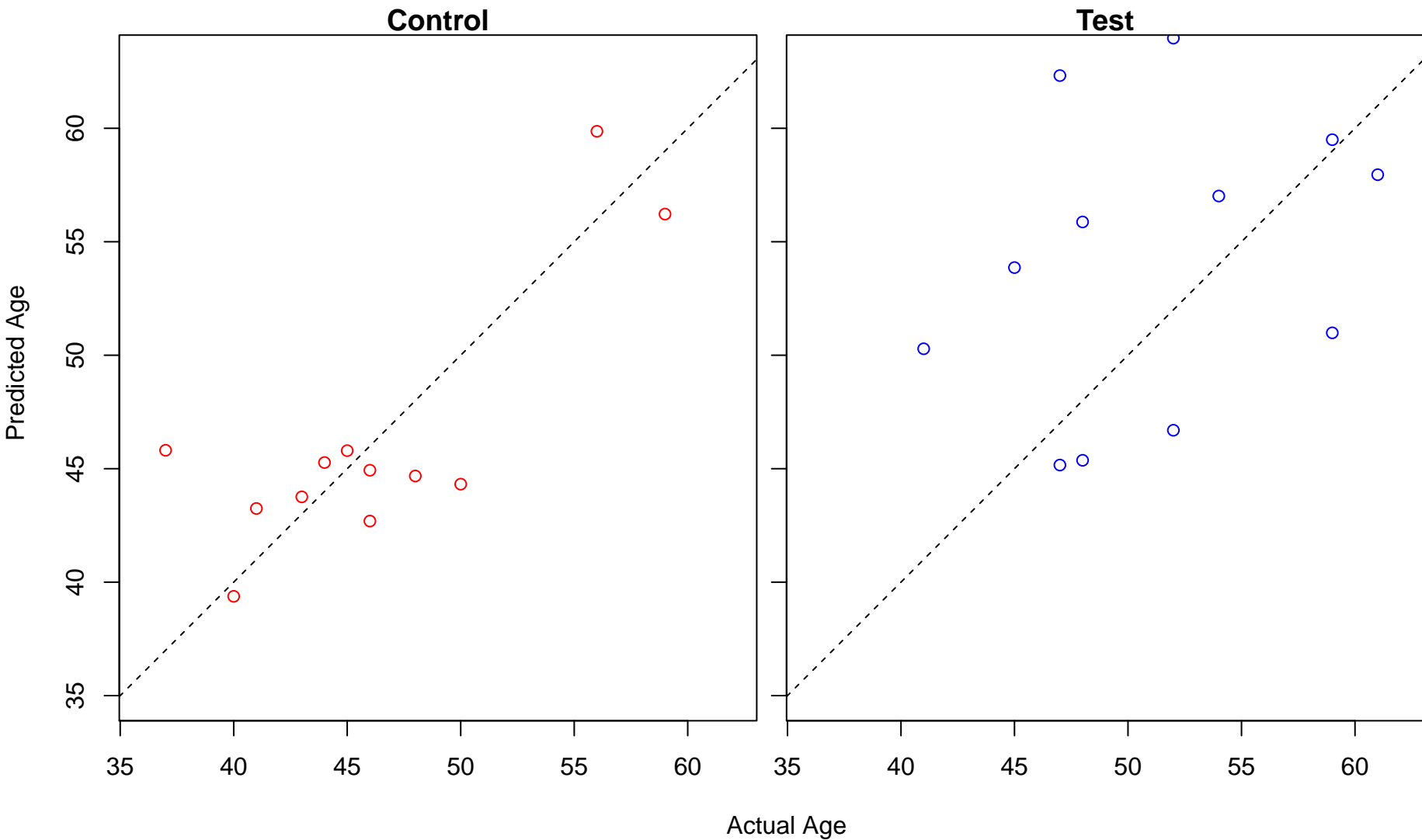
DNA cytosine deamination (Score: 20.212477)



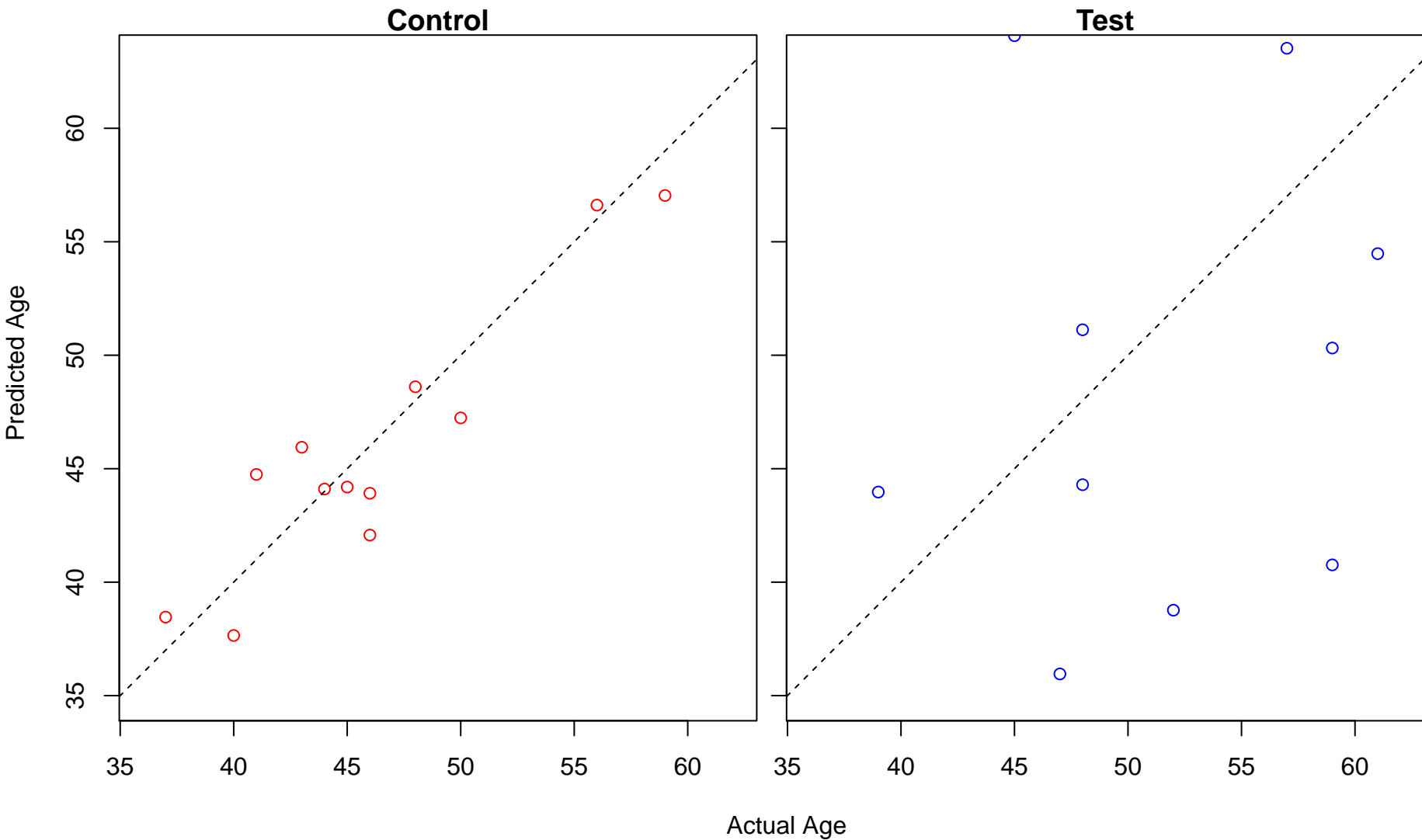
angiotensin maturation (Score: 20.208545)



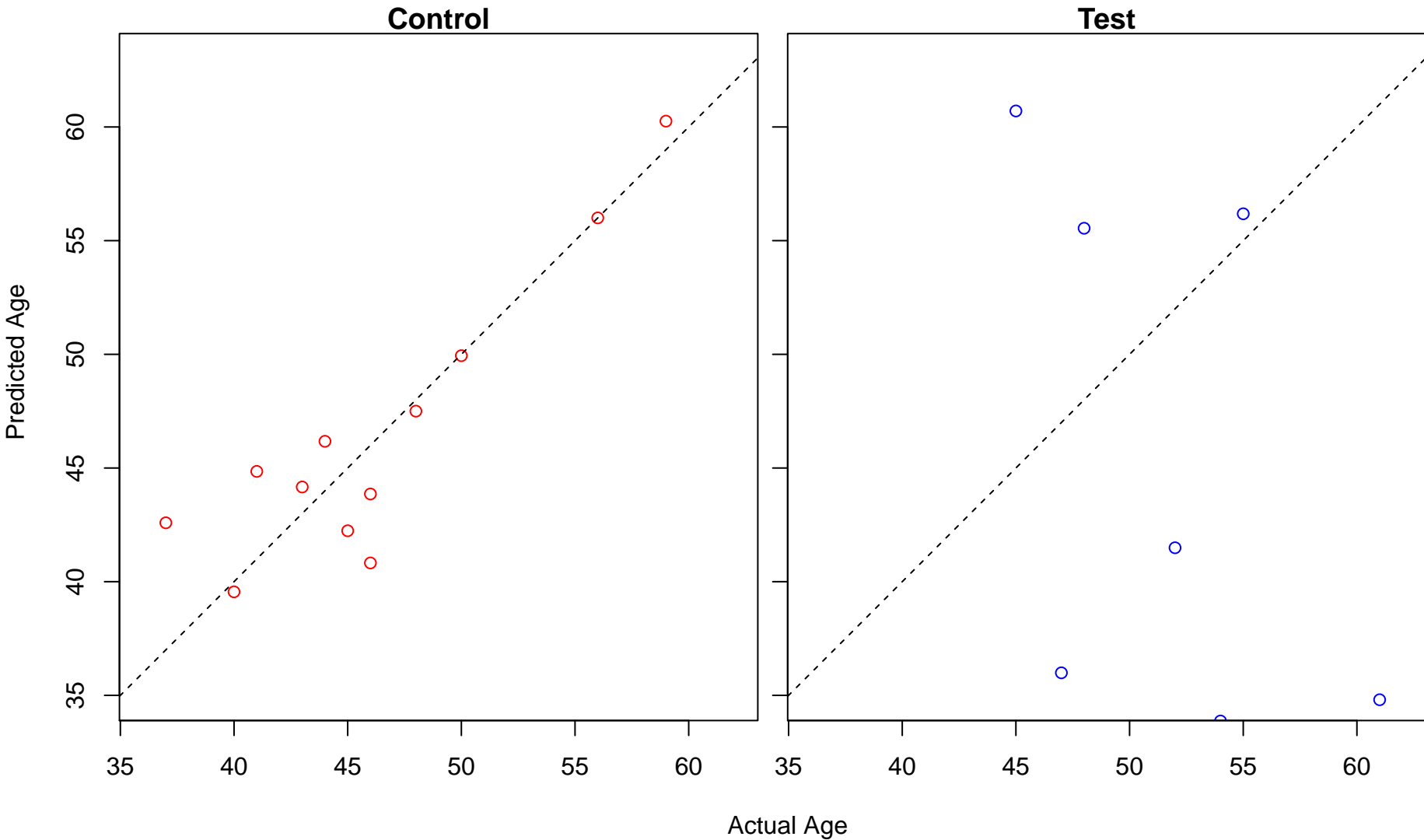
positive regulation of cellular extravasation (Score: 20.203536)



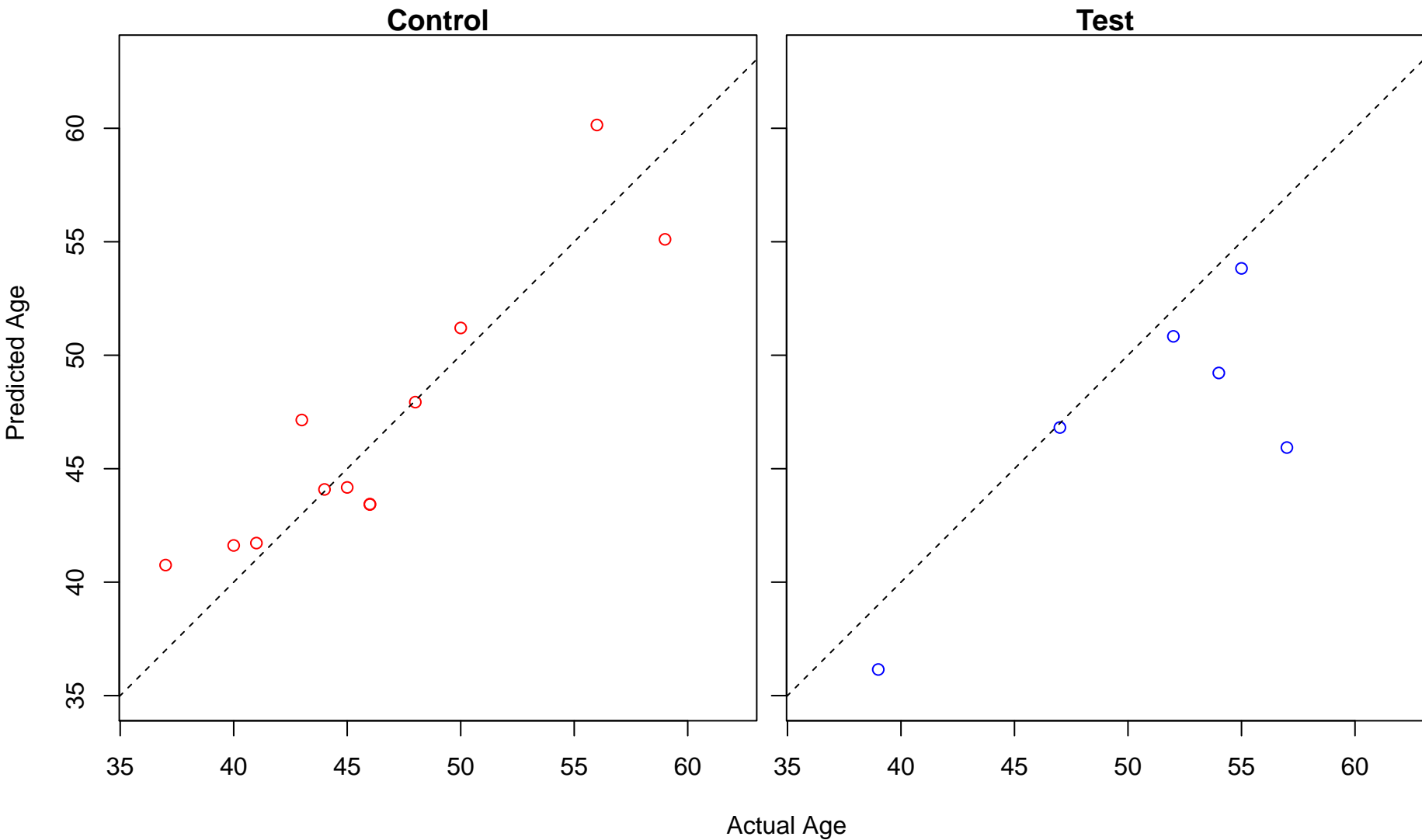
cellular response to reactive oxygen species (Score: 20.195953)



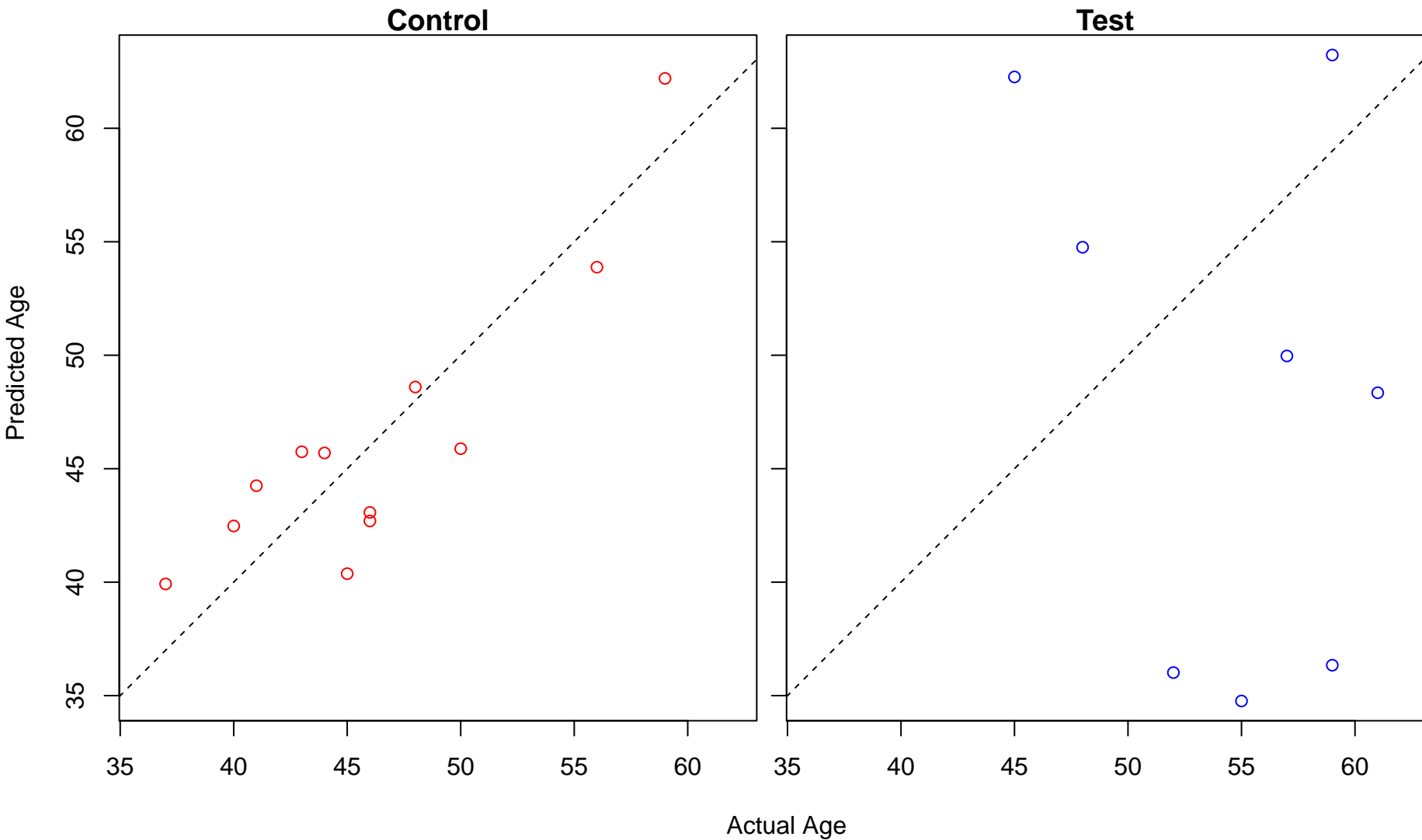
regulation of ketone biosynthetic process (Score: 20.178618)



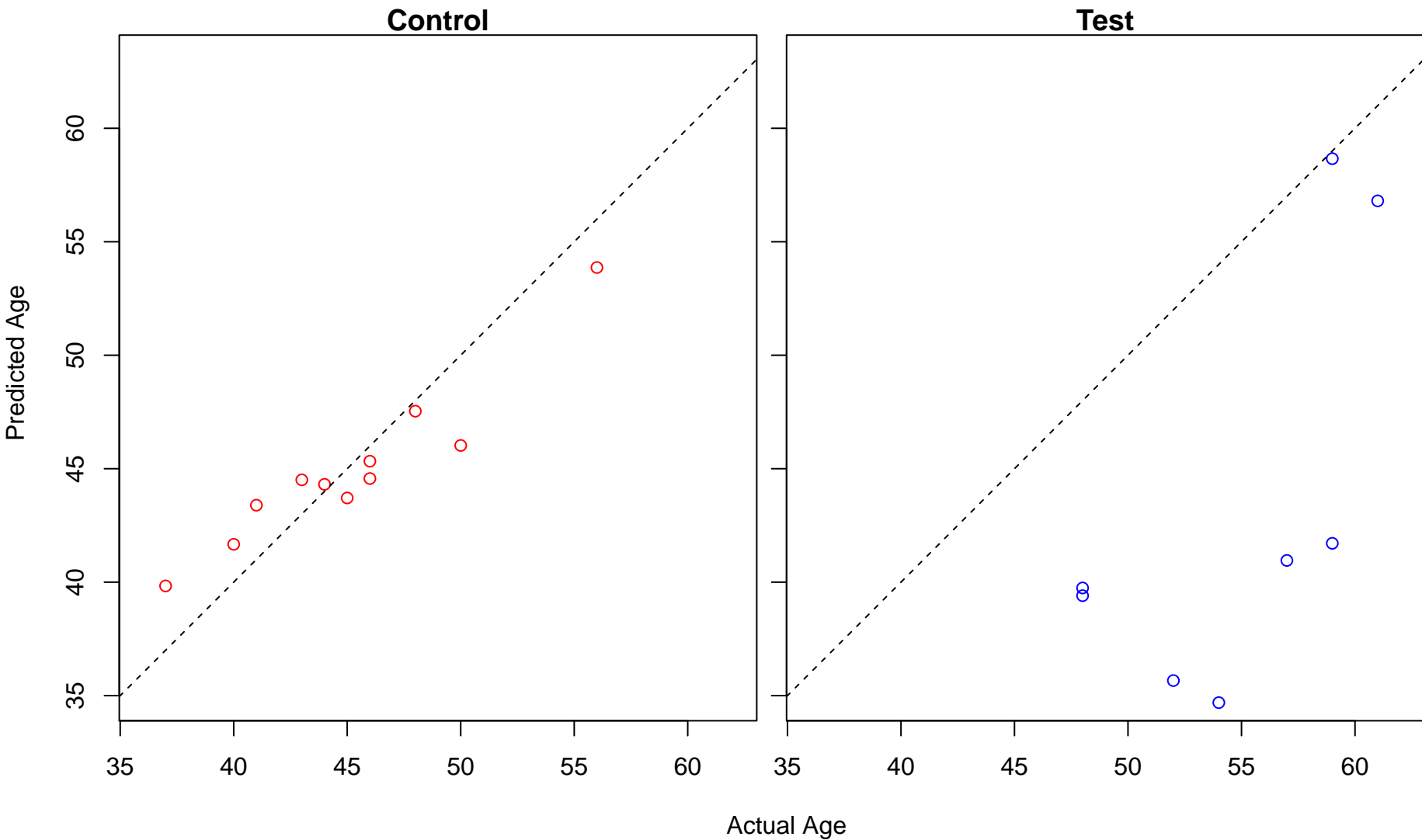
diencephalon development (Score: 20.141534)



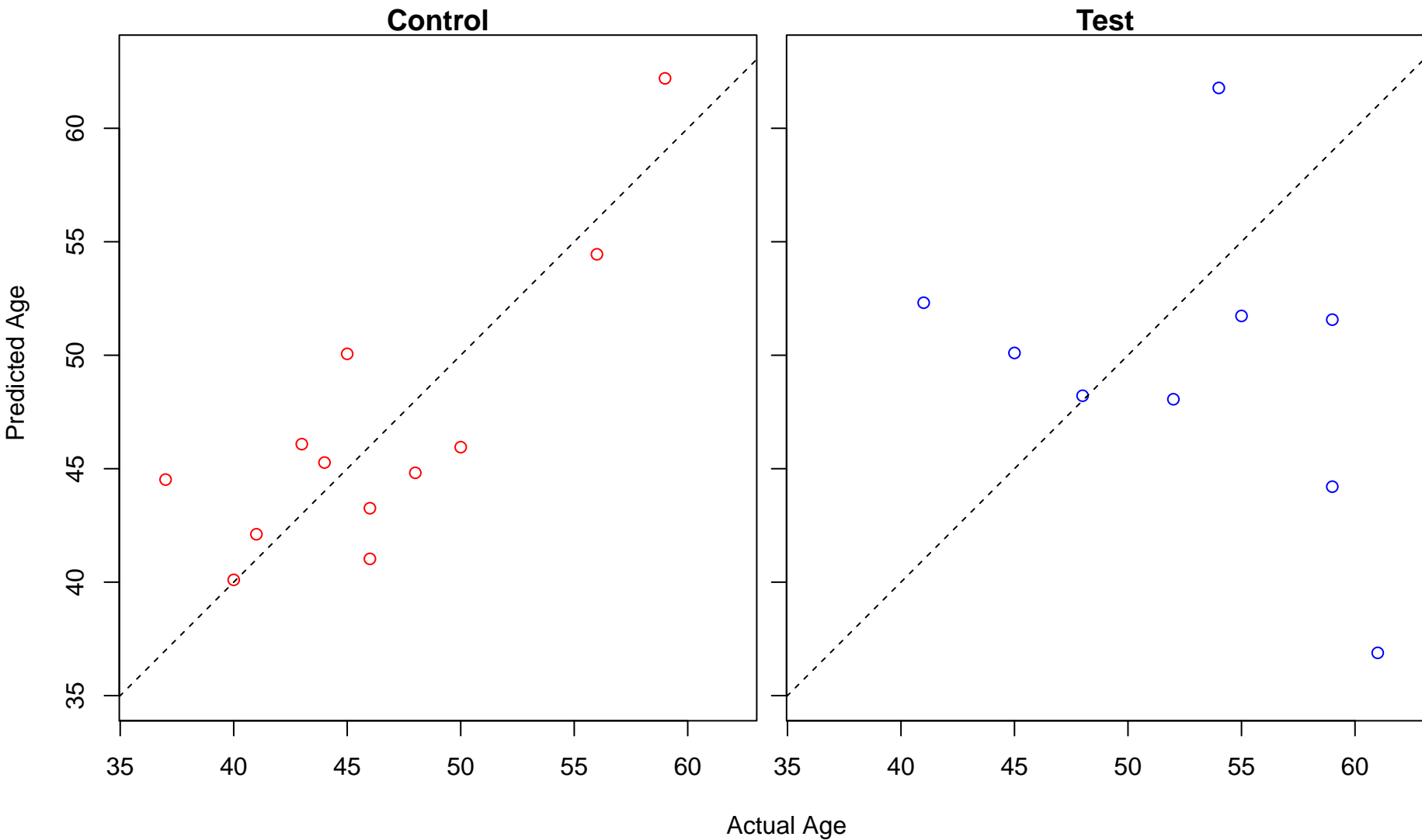
response to lipid (Score: 20.089651)



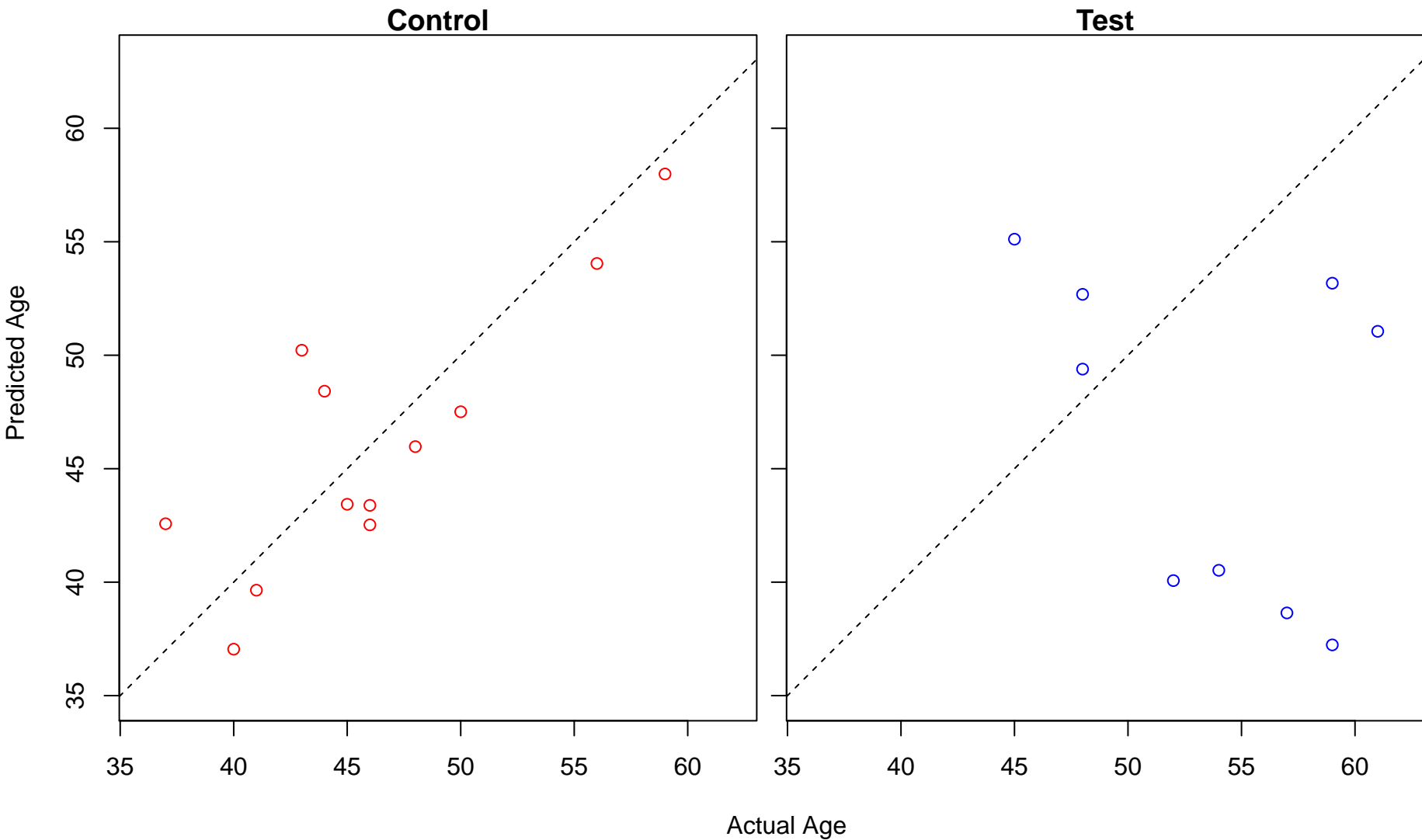
positive regulation of chromosome segregation (Score: 19.996902)



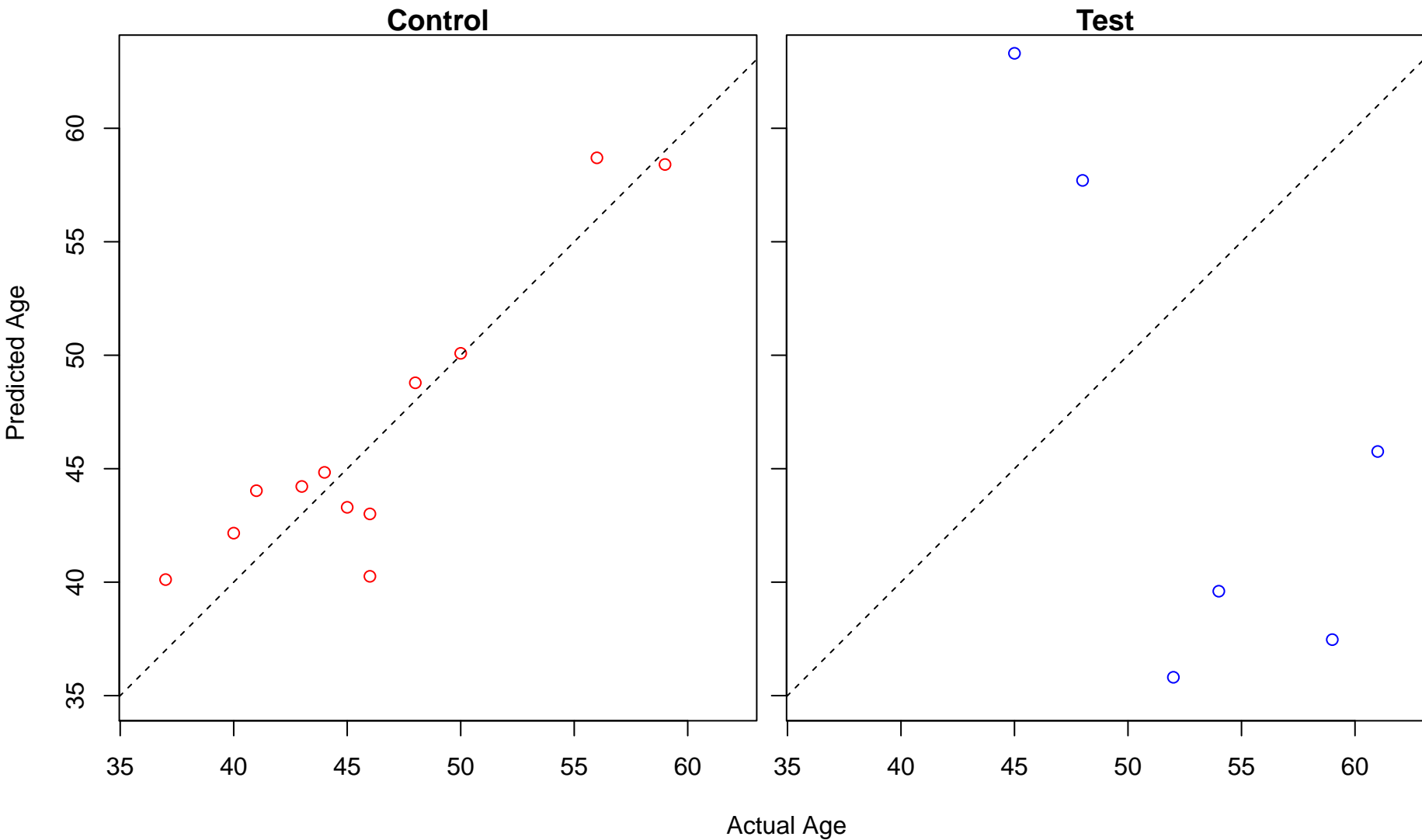
regulation of hippo signaling (Score: 19.985793)



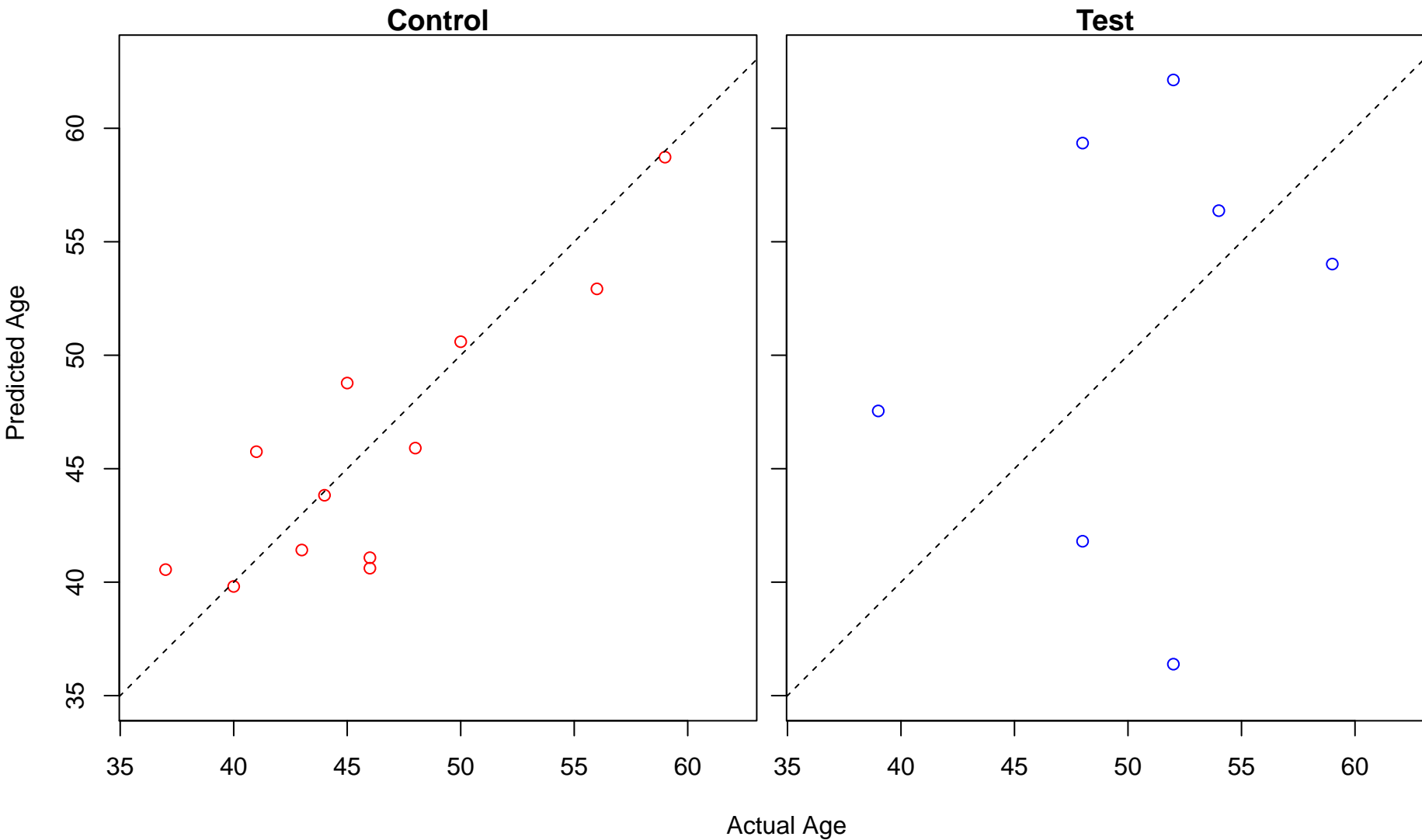
regulation of peptidyl-lysine acetylation (Score: 19.985187)



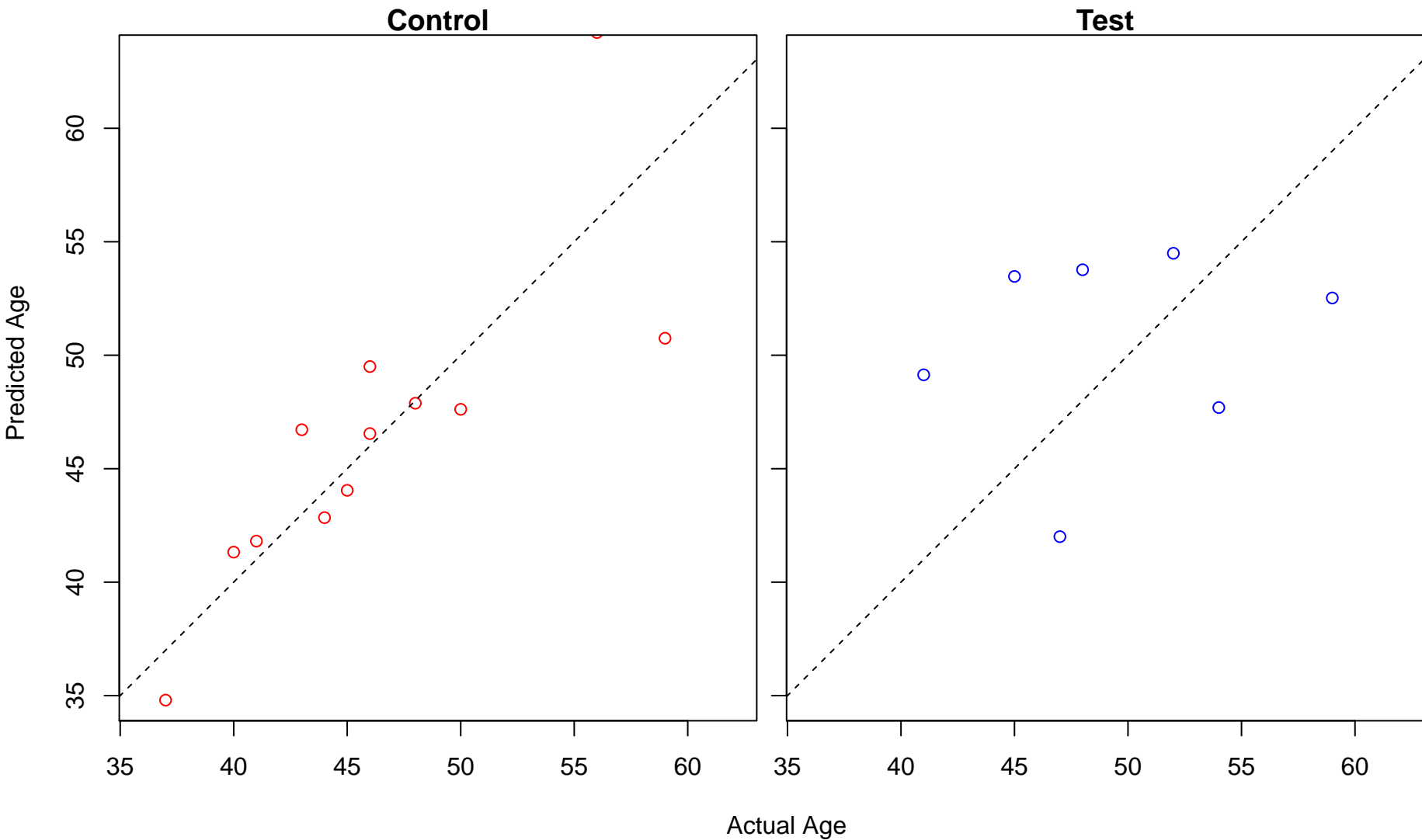
regulation of epithelial cell apoptotic process (Score: 19.871120)



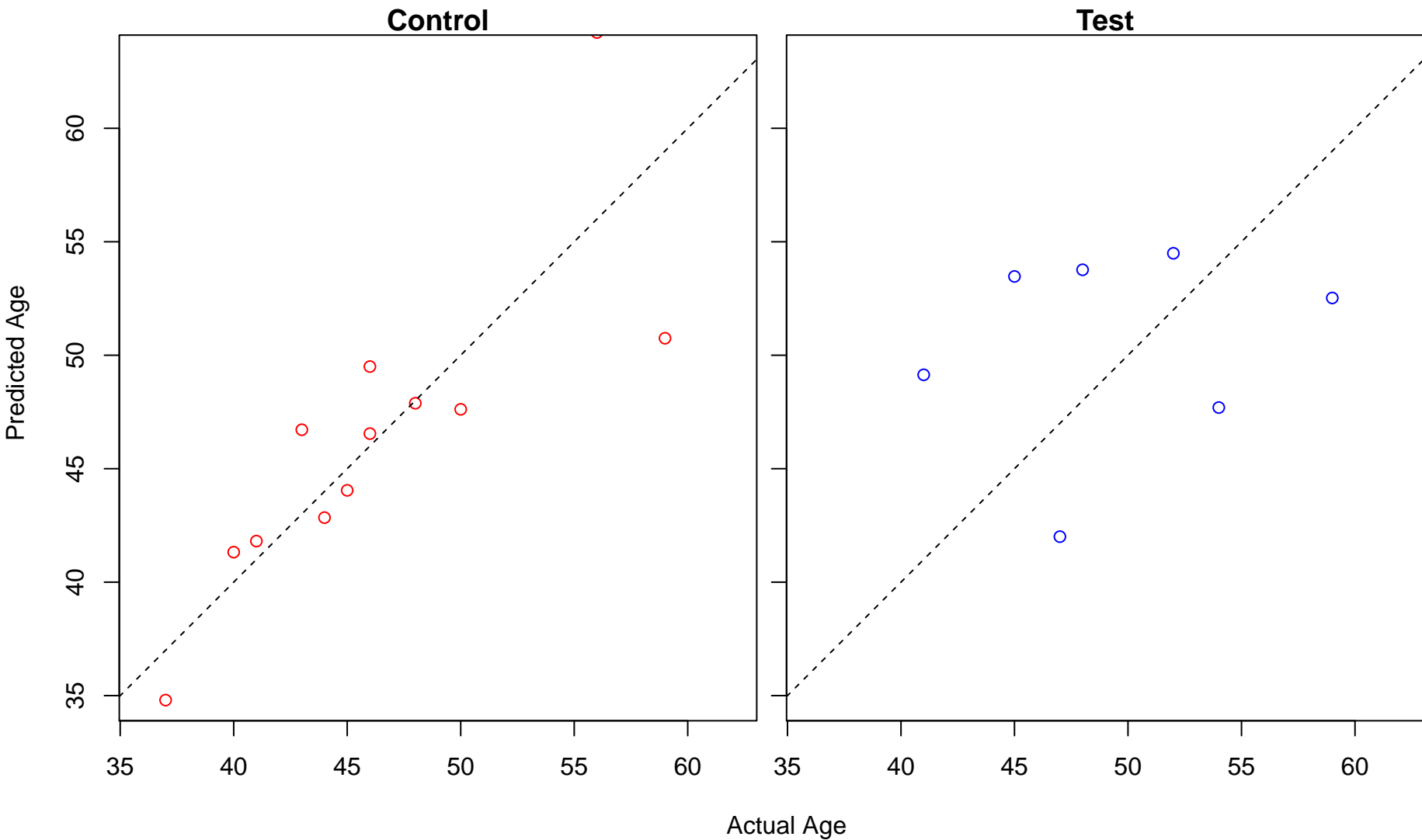
regulation of cell communication by electrical coupling (Score: 19.826986)



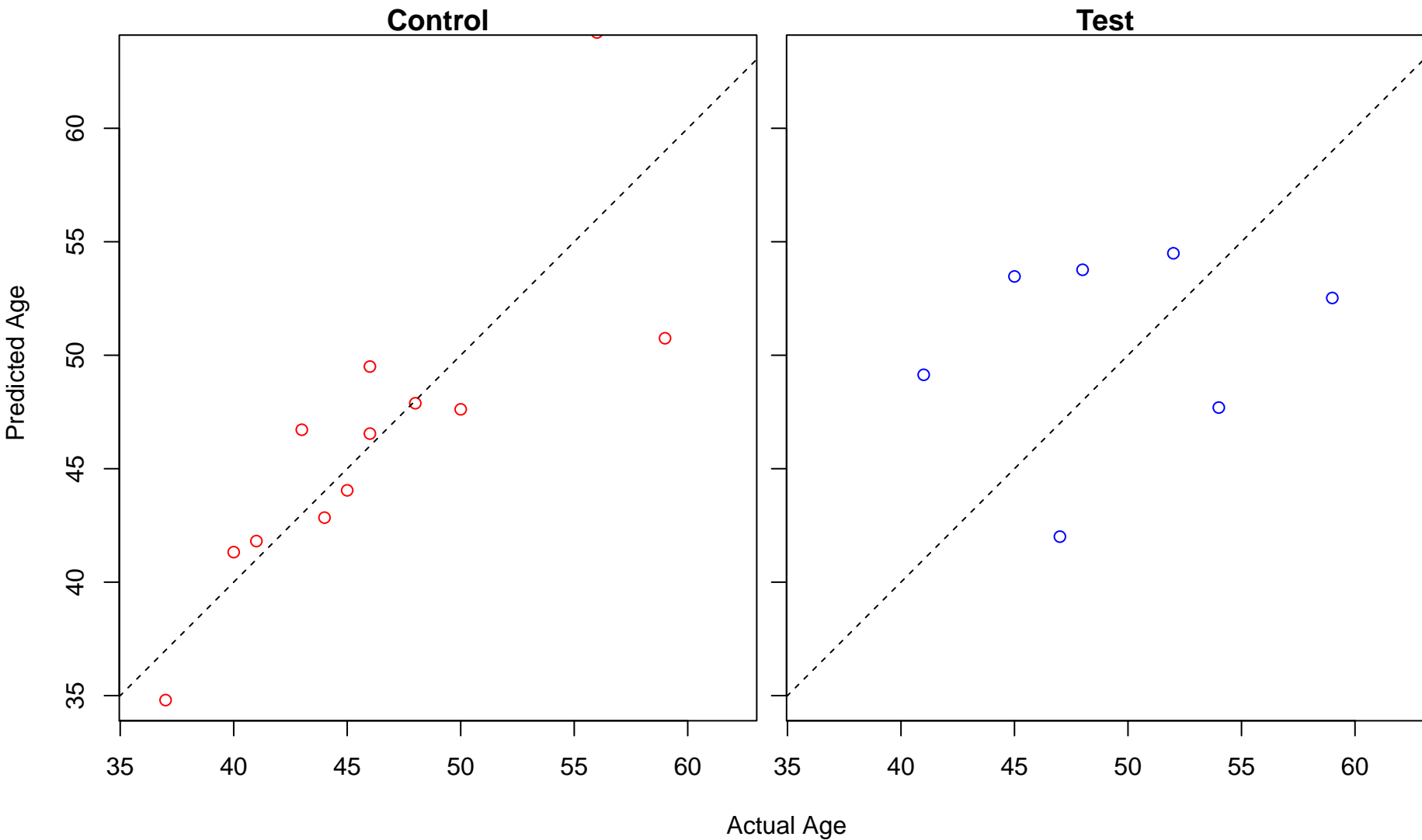
glucuronate catabolic process (Score: 19.800941)



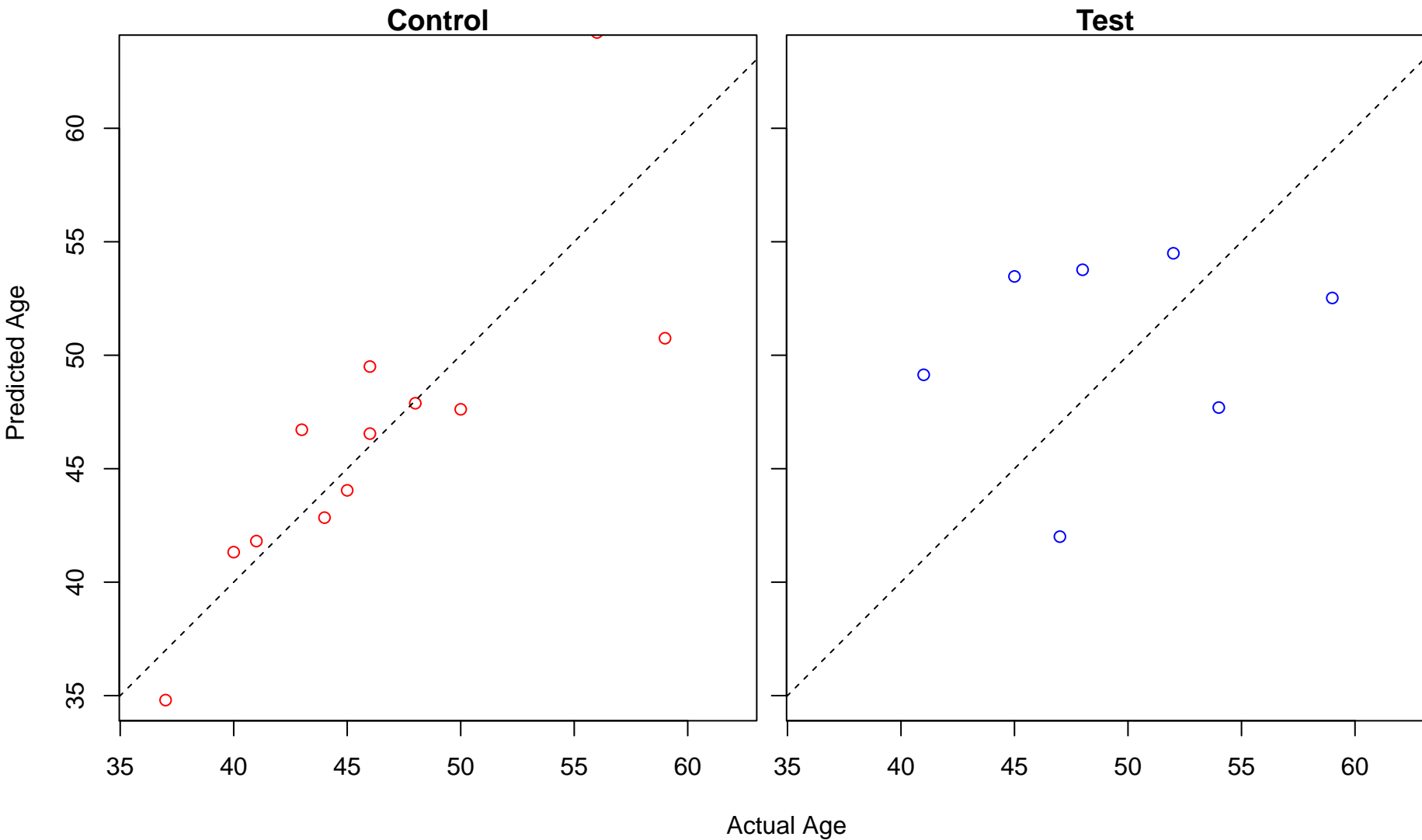
glucuronate catabolic process to xylulose 5-phosphate (Score: 19.800941)



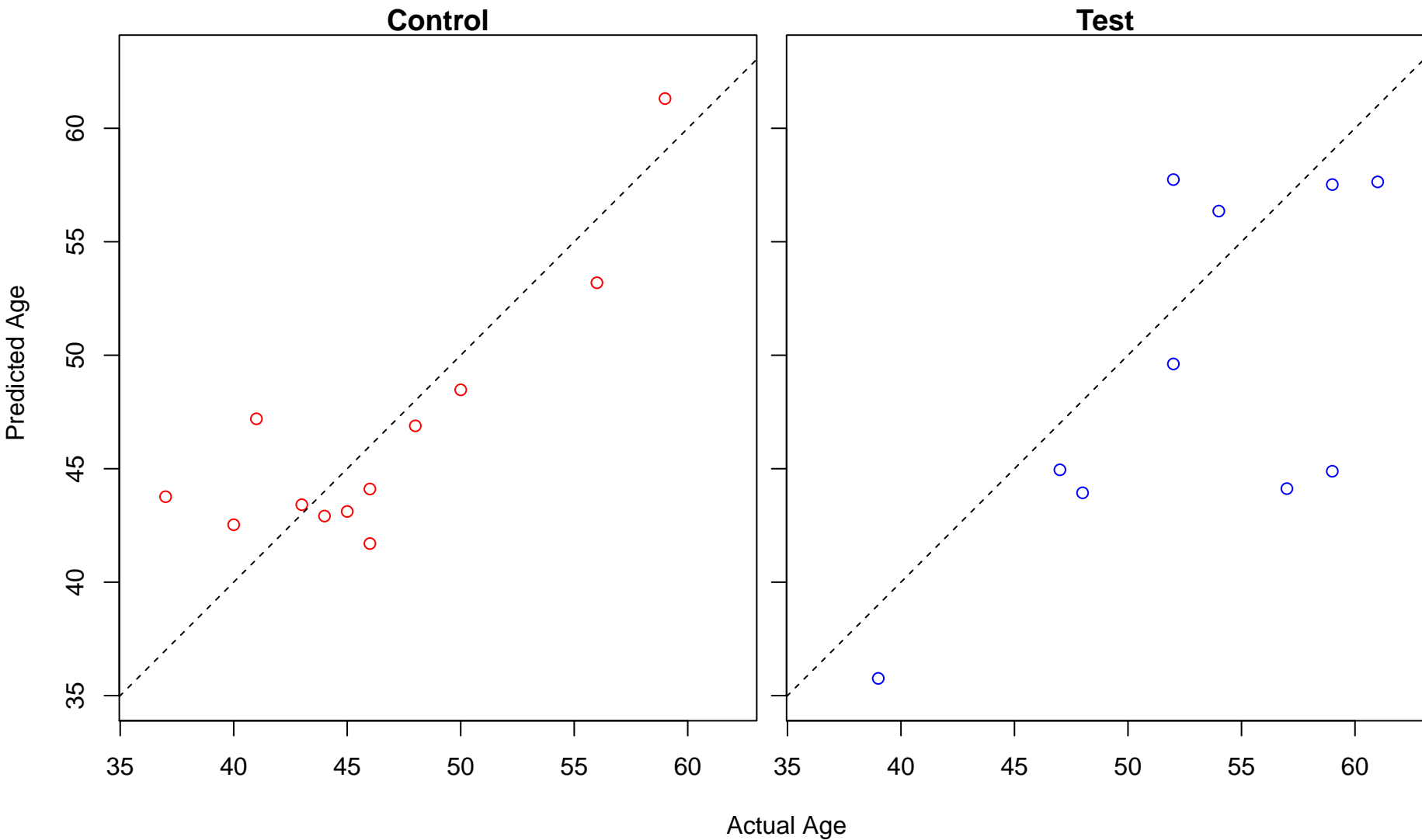
xylulose 5-phosphate metabolic process (Score: 19.800941)



xylulose 5-phosphate biosynthetic process (Score: 19.800941)

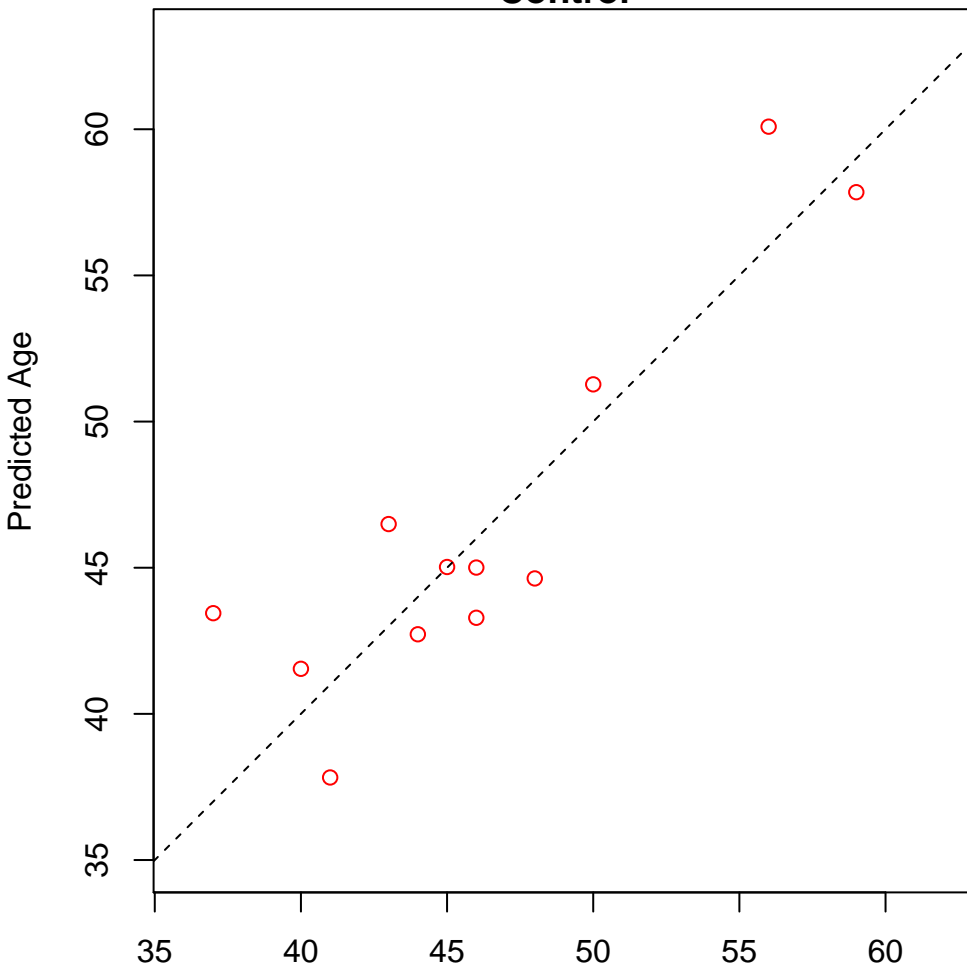


L-amino acid transport (Score: 19.685284)

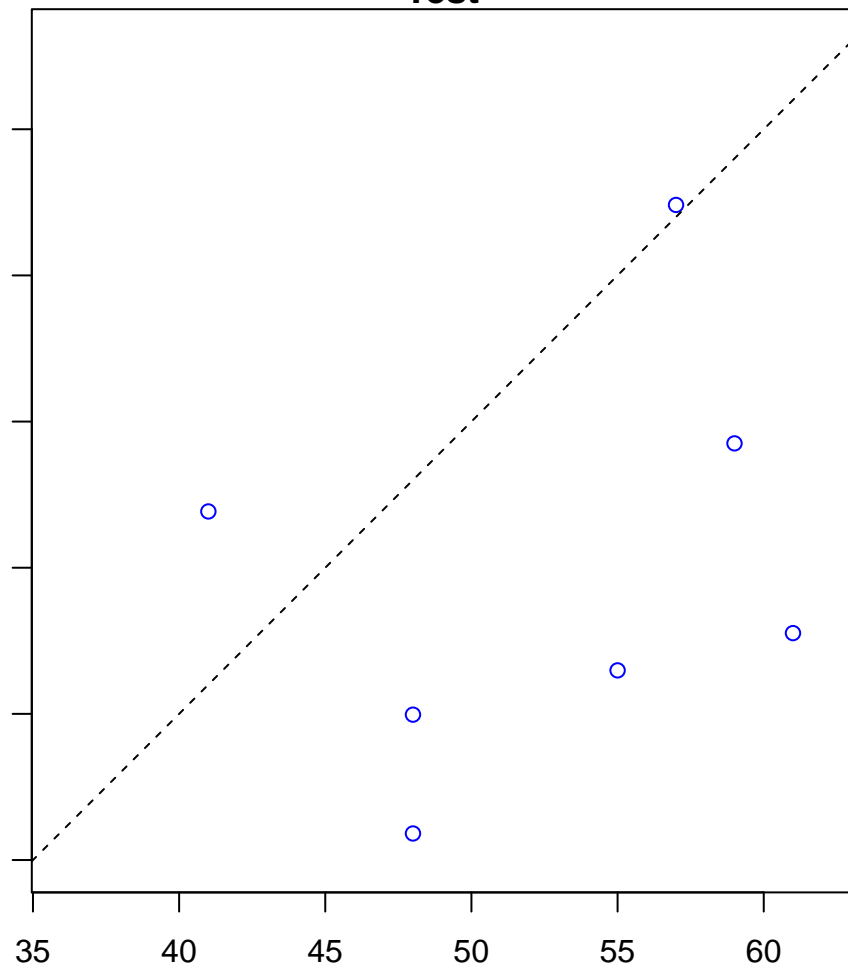


protein import into peroxisome matrix (Score: 19.625240)

Control

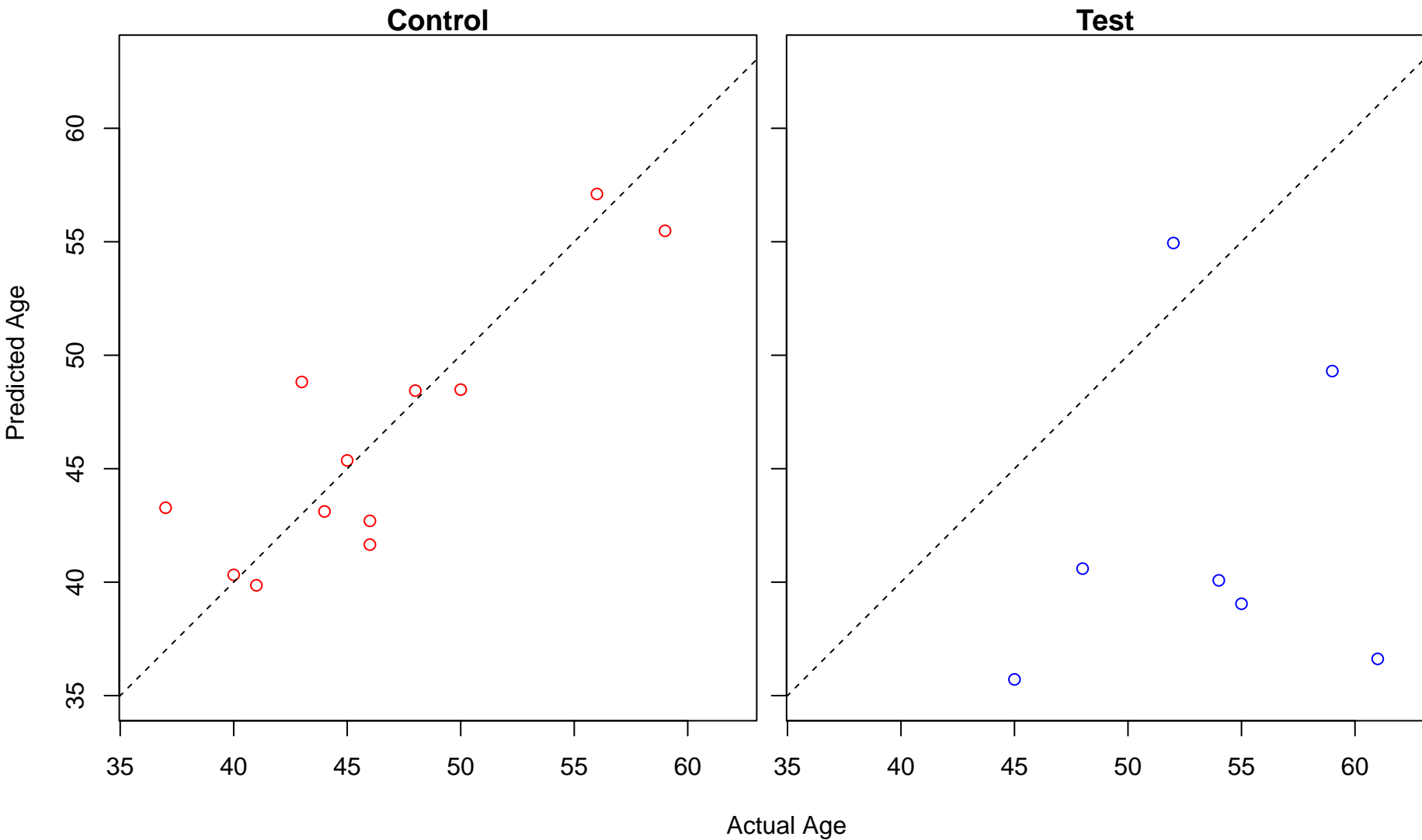


Test

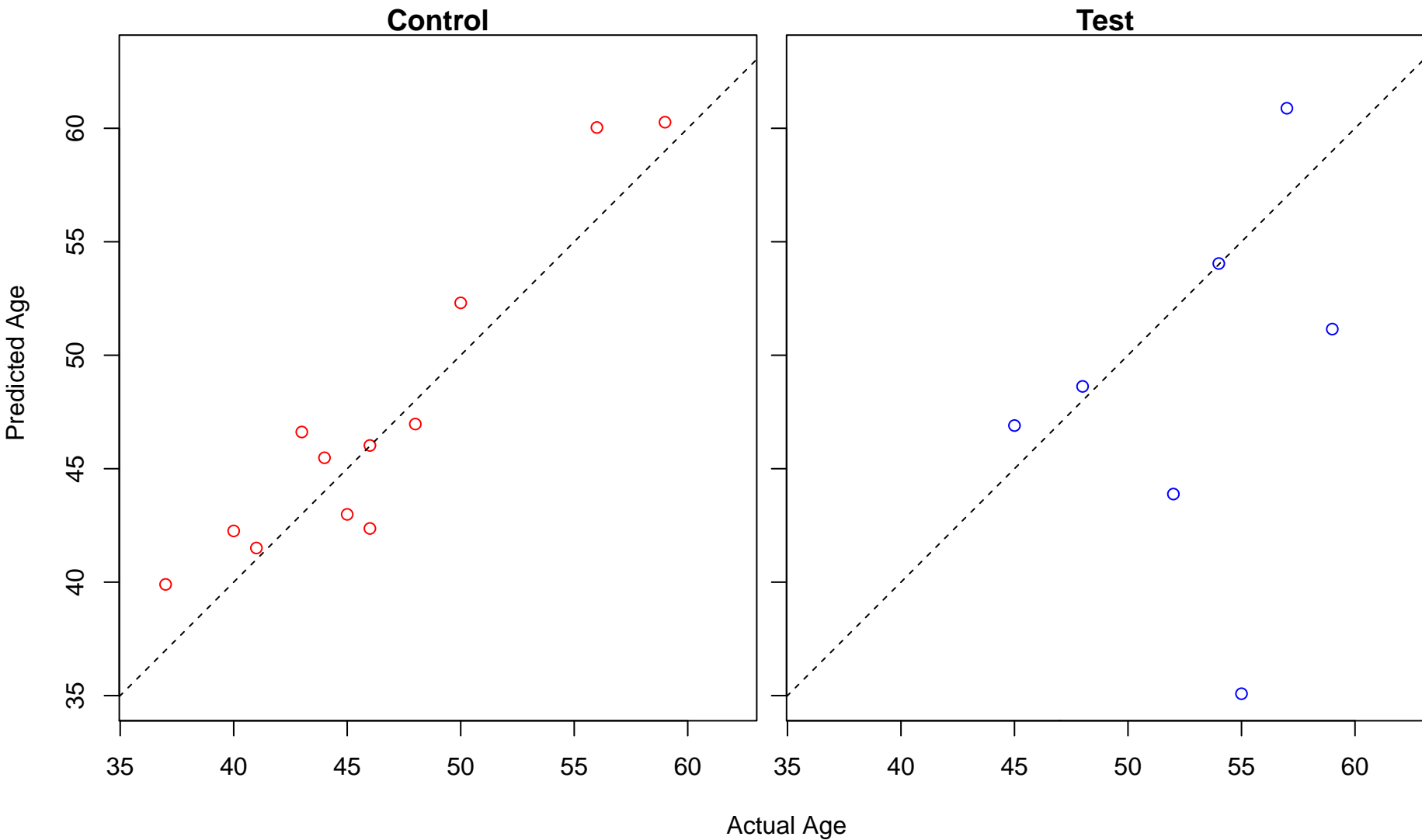


Actual Age

endothelial cell differentiation (Score: 19.559129)

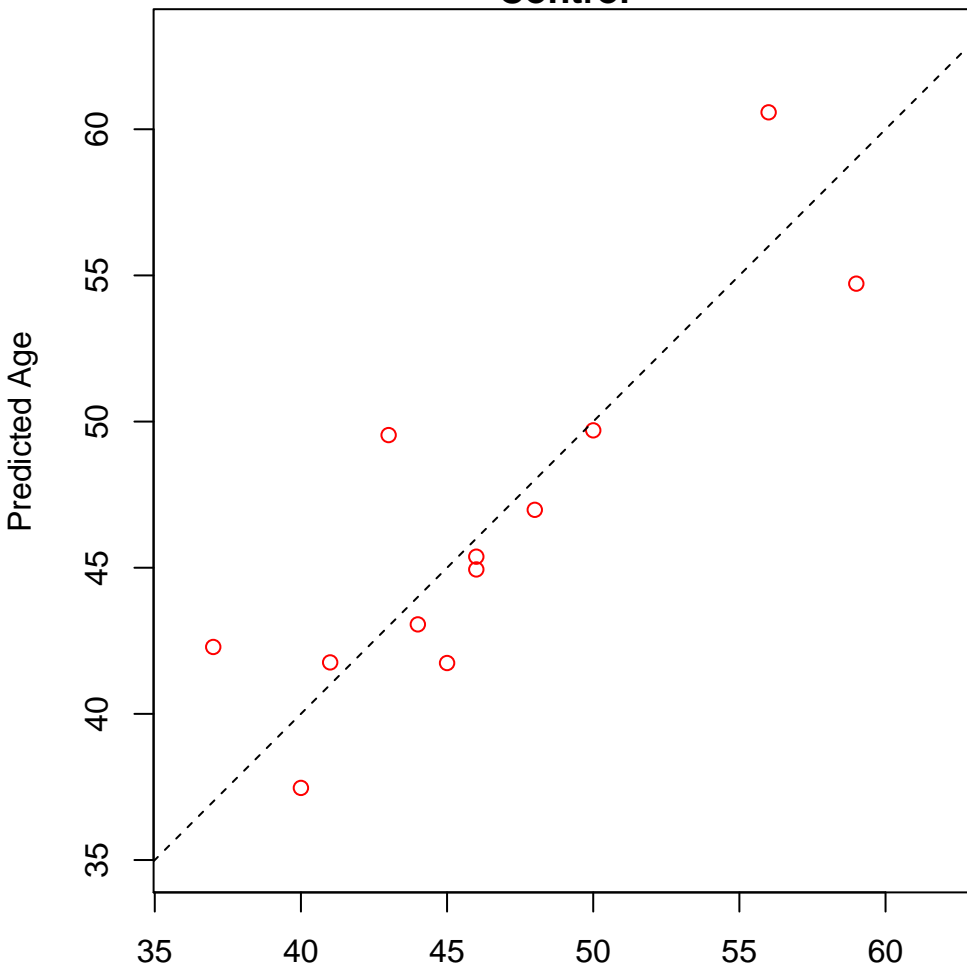


positive regulation of early endosome to late endosome transport (Score: 19.507147)

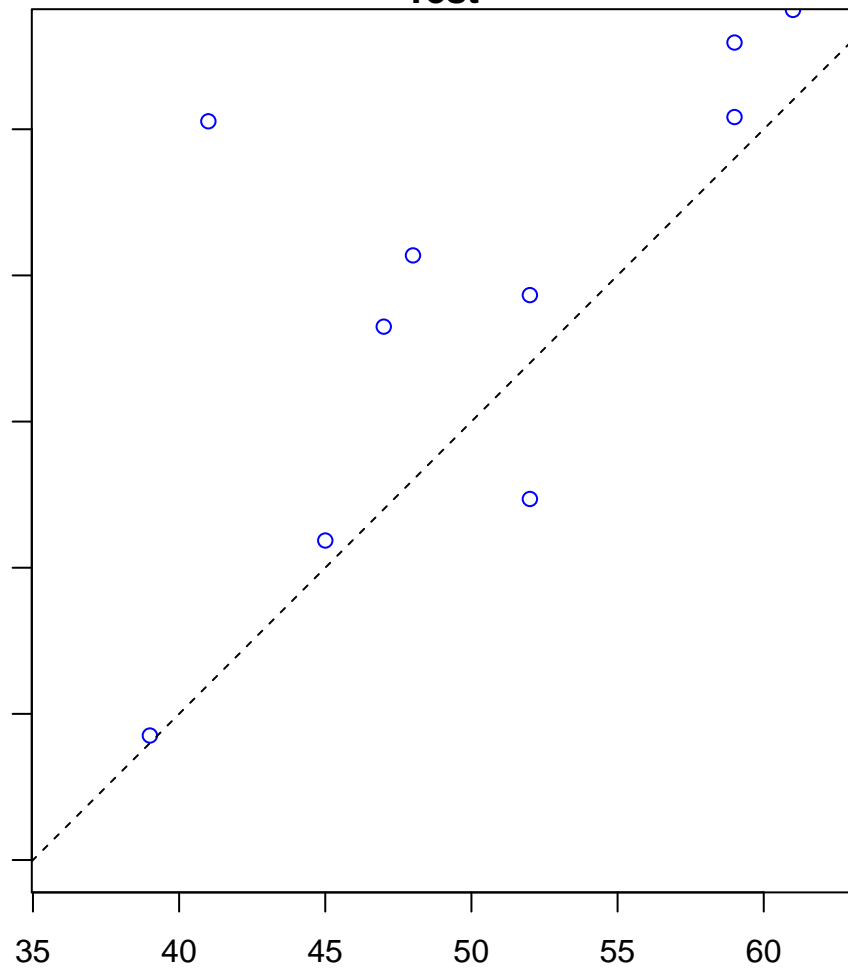


positive regulation of myoblast fusion (Score: 19.35219)

Control



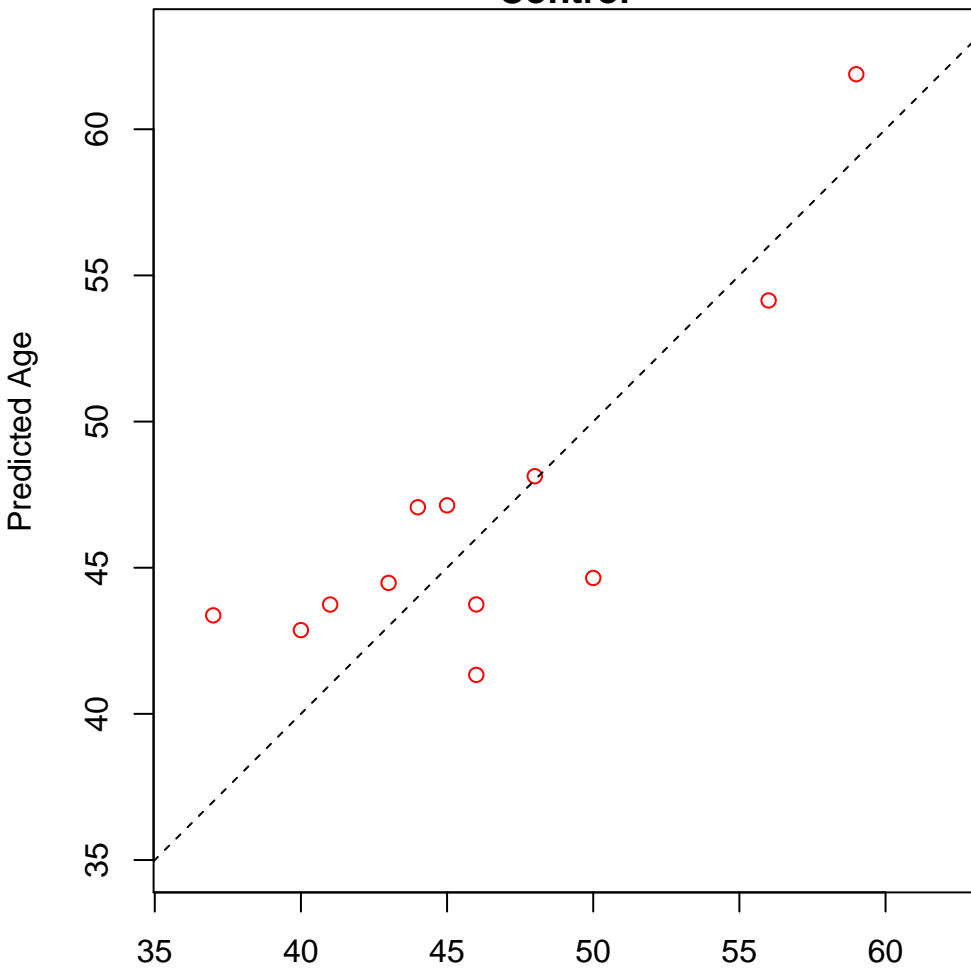
Test



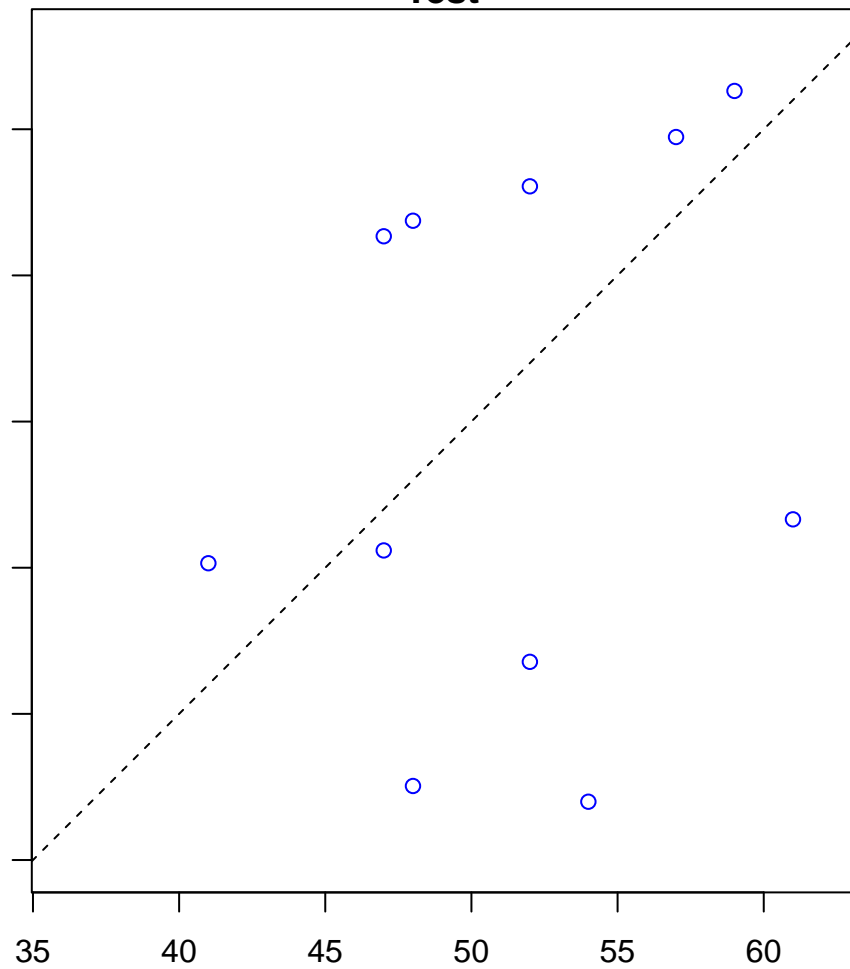
Actual Age

positive regulation of mitotic cell cycle (Score: 19.329538)

Control



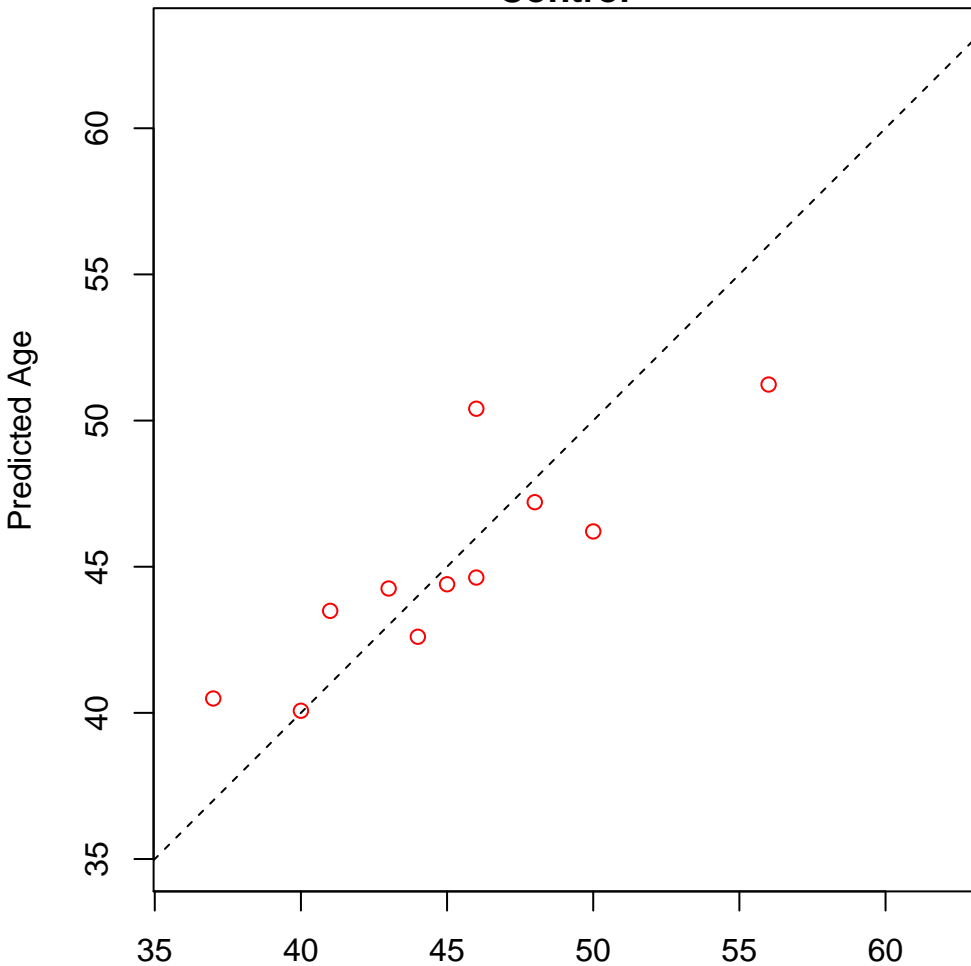
Test



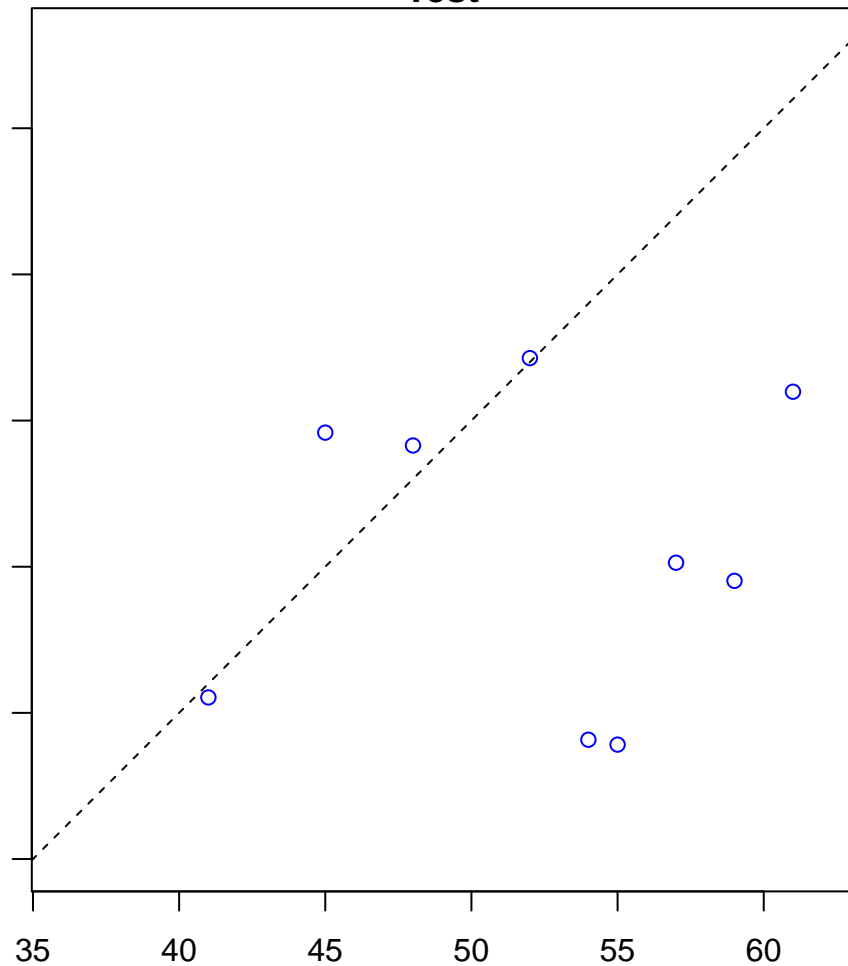
Actual Age

glomerular mesangium development (Score: 19.326899)

Control

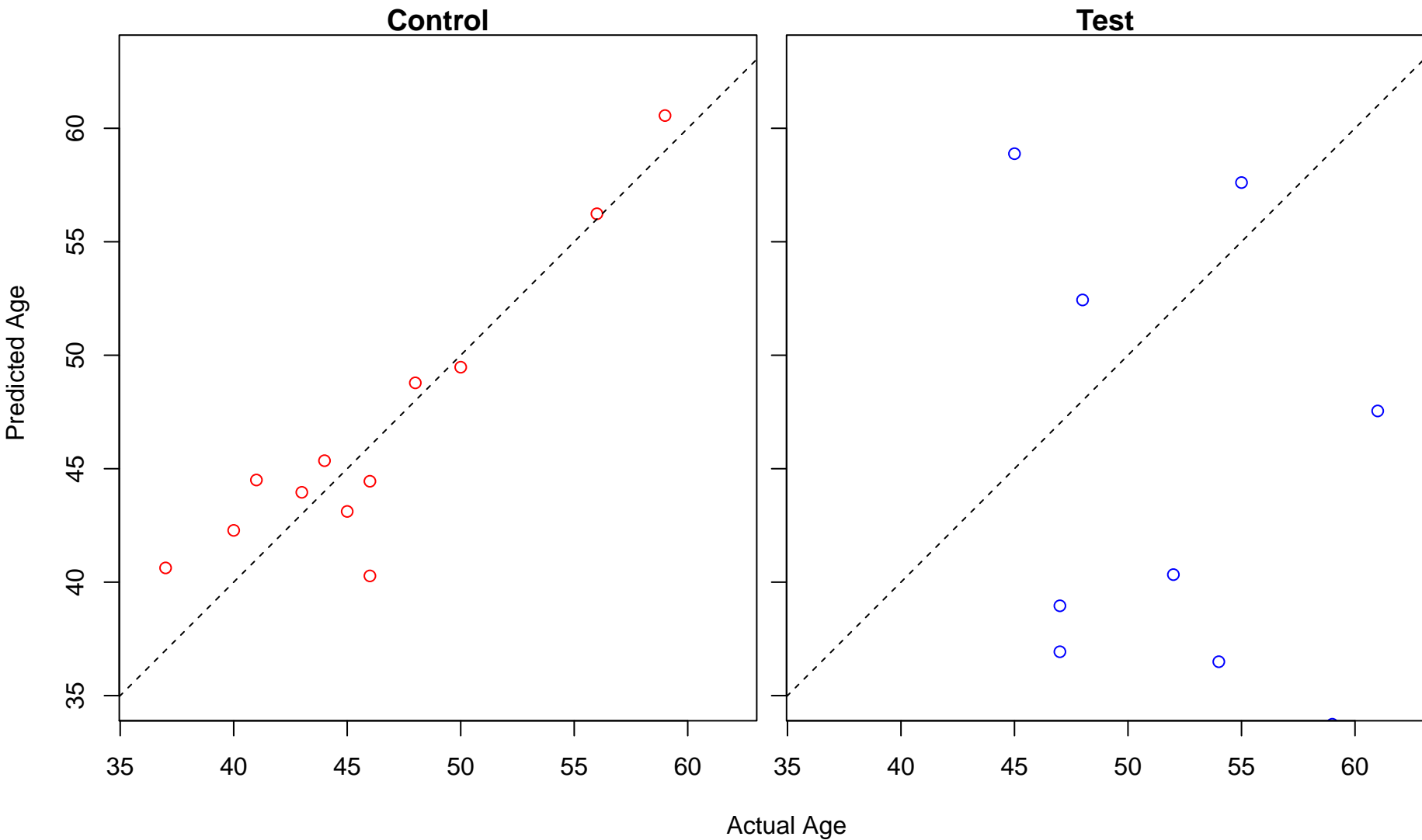


Test

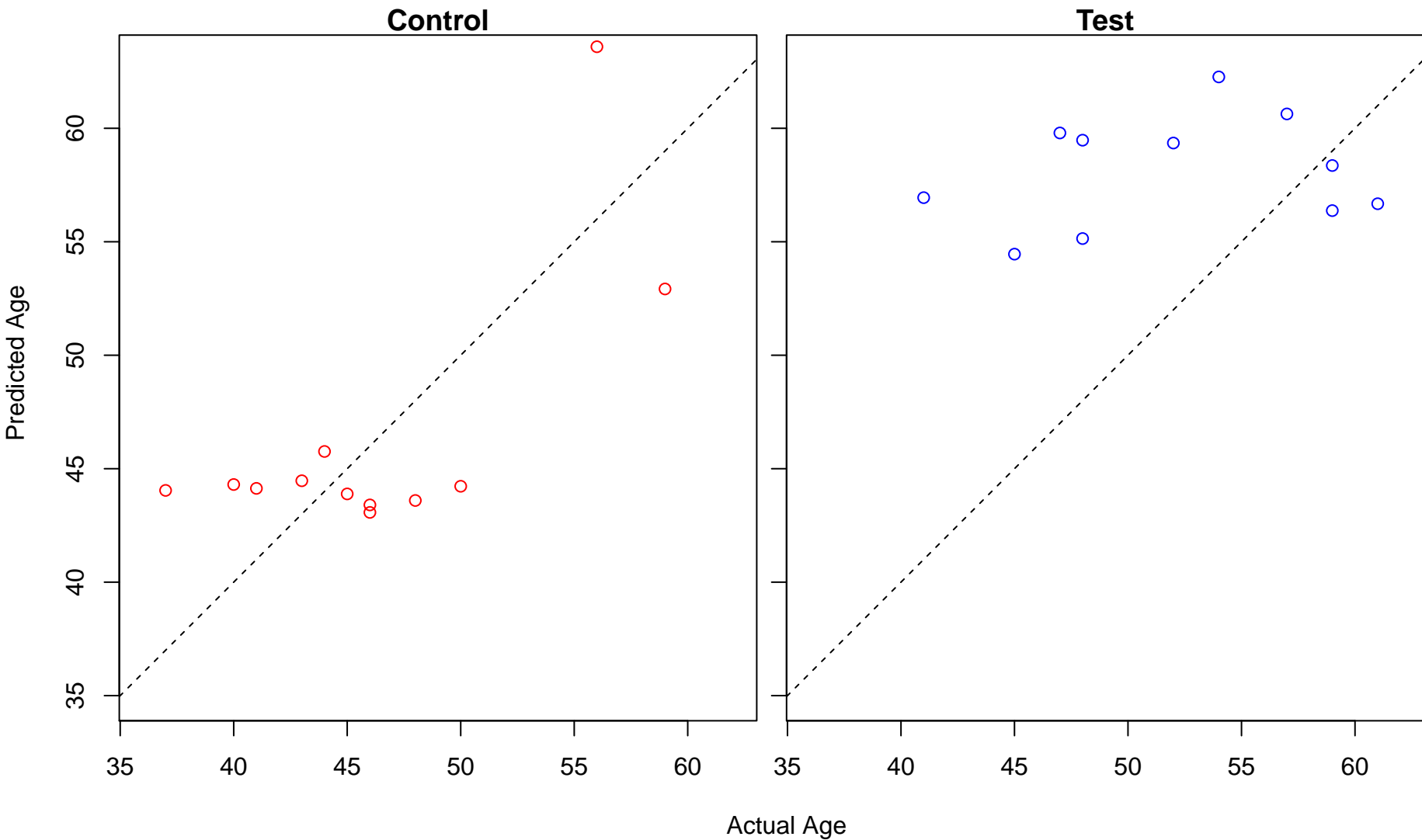


Actual Age

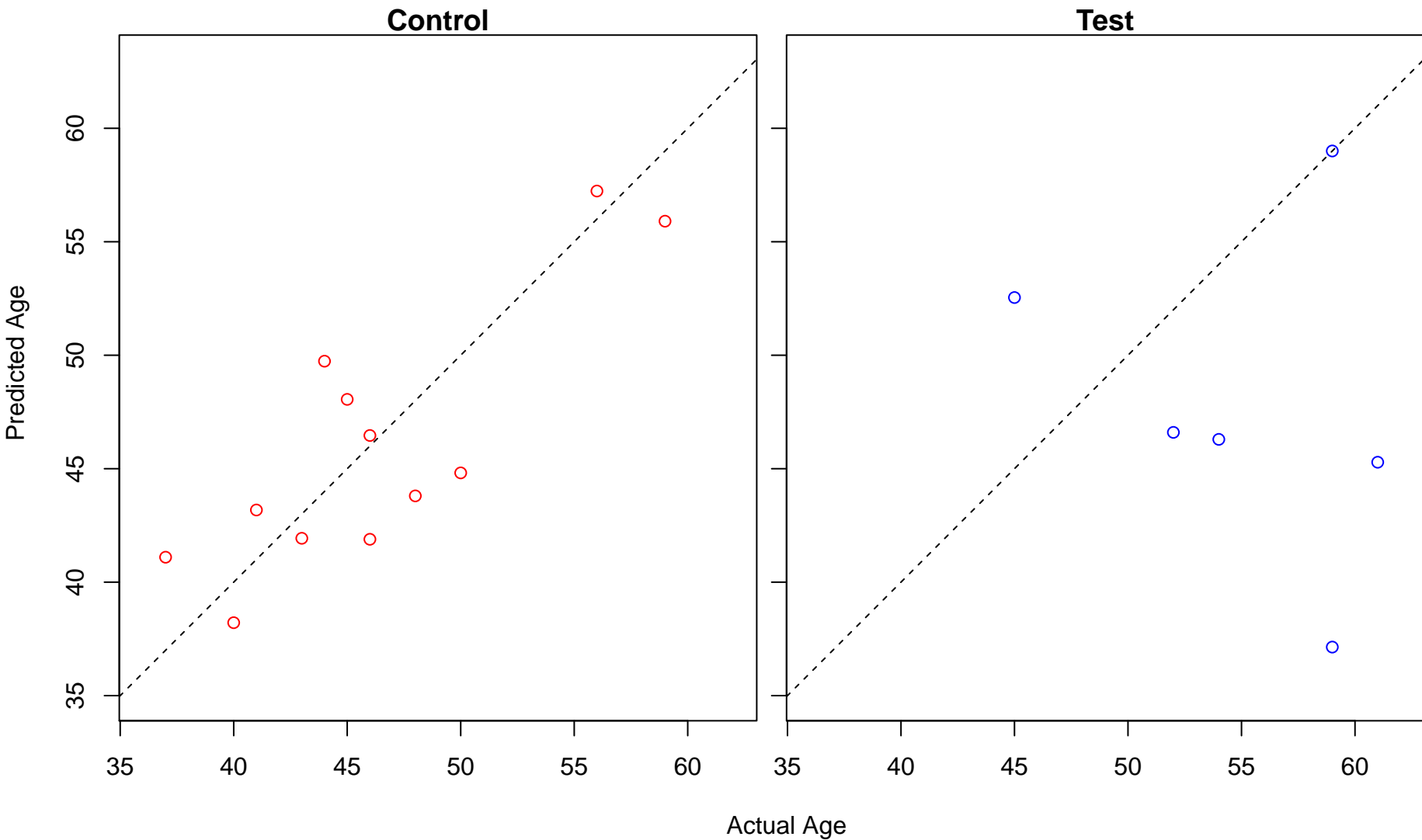
negative regulation of hormone metabolic process (Score: 19.265578)



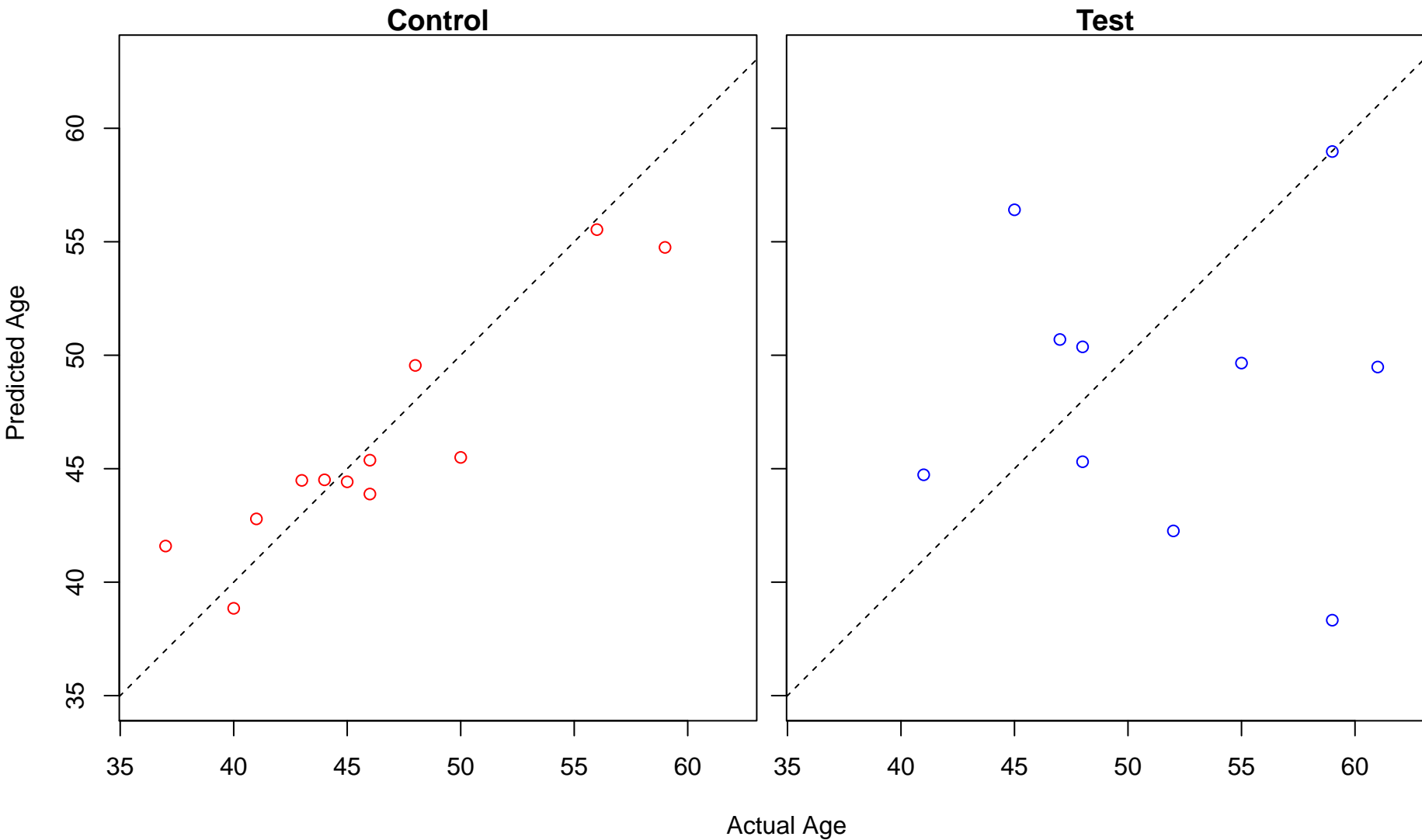
regulation of calcidiol 1-monooxygenase activity (Score: 19.205867)



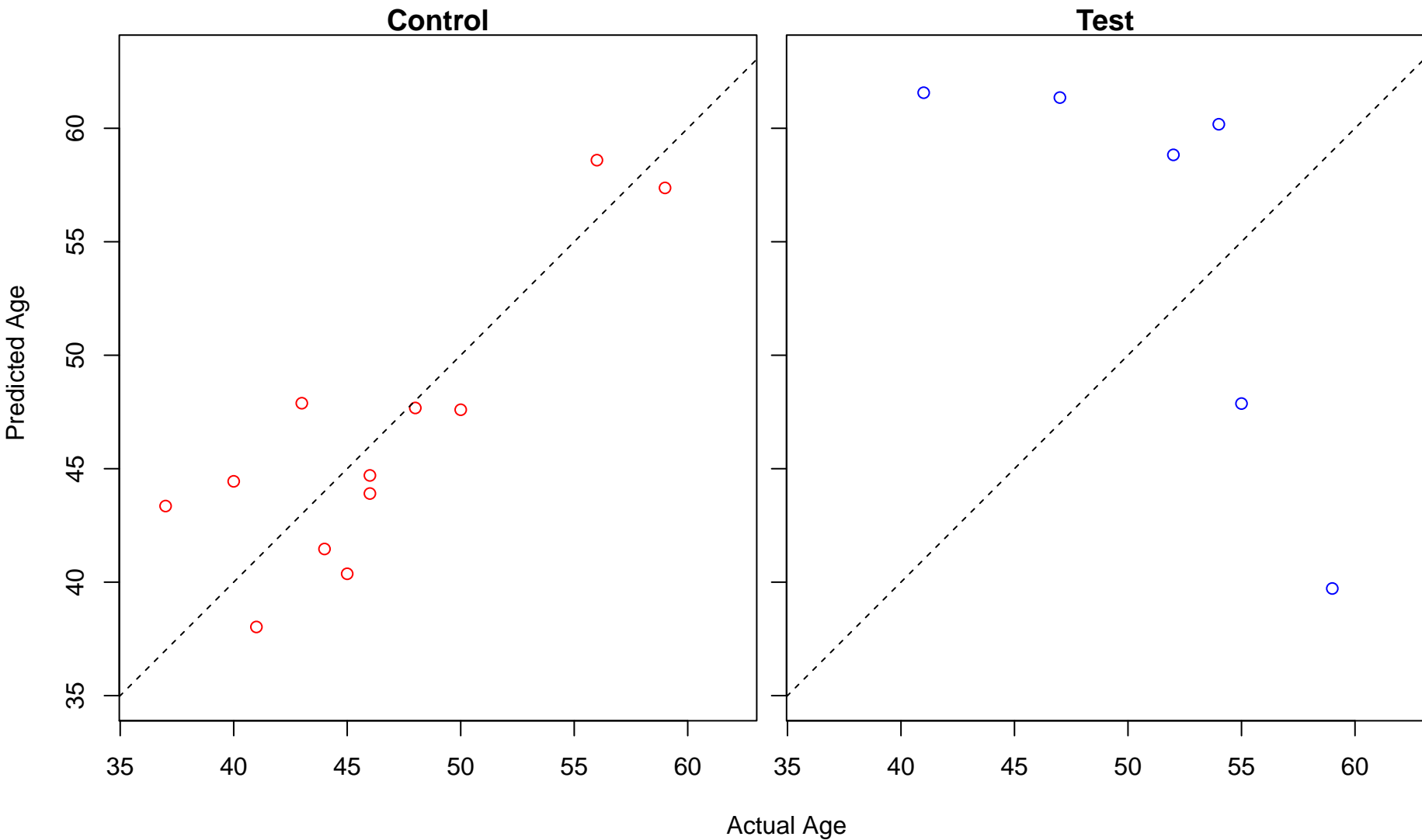
positive regulation of toll-like receptor 4 signaling pathway (Score: 19.138270)



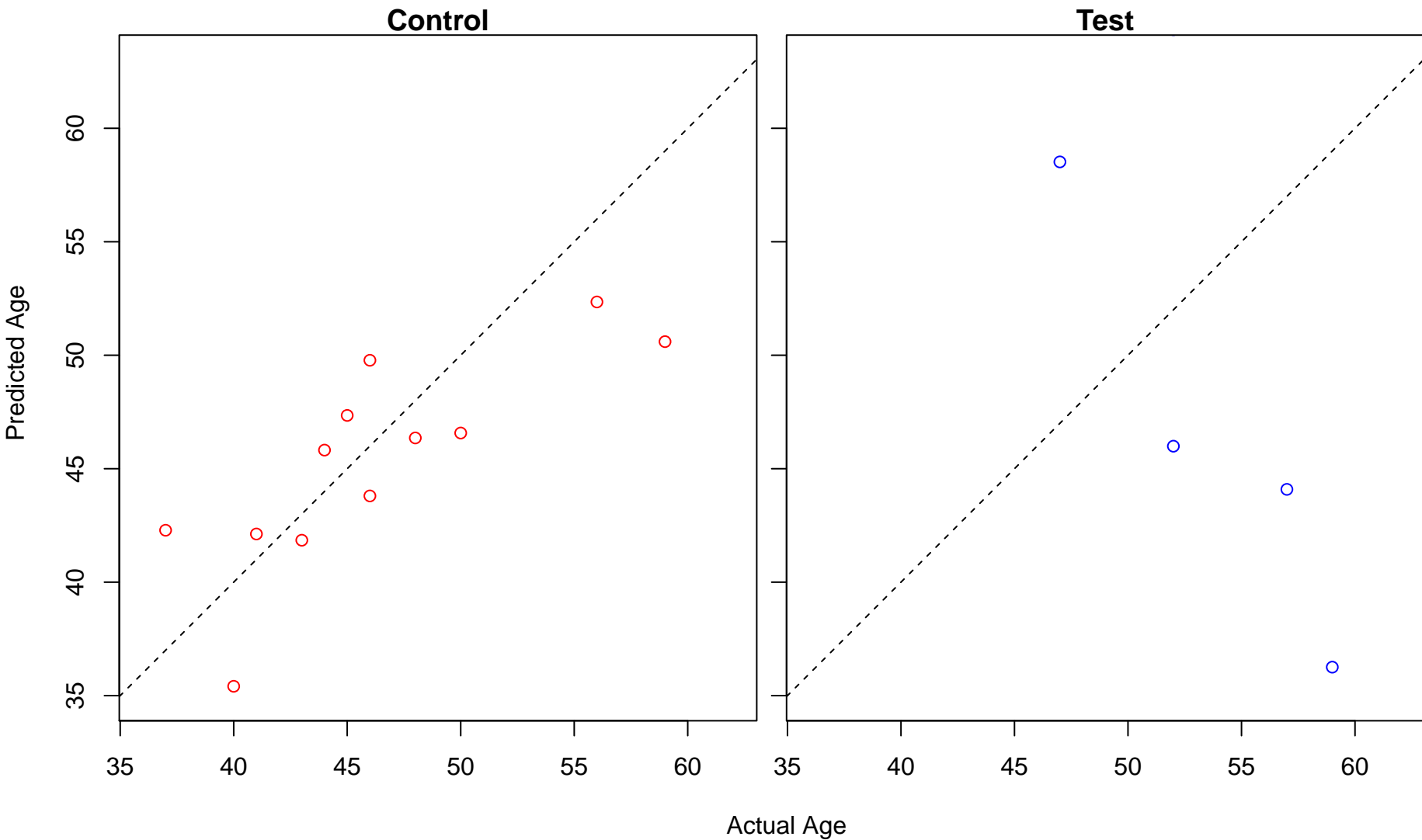
regulation of translational initiation (Score: 19.123420)



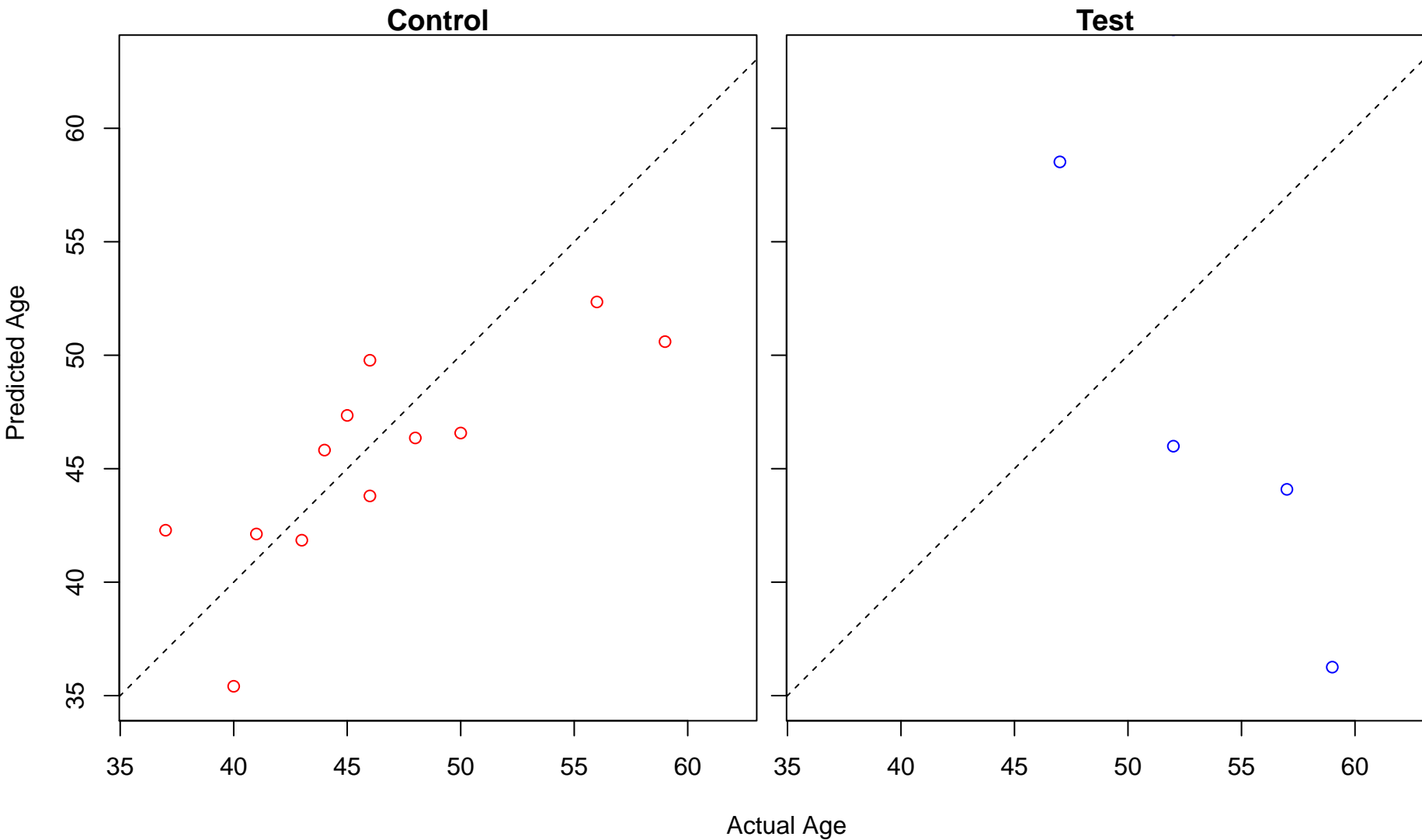
apical junction assembly (Score: 18.979619)



regulation of transposition (Score: 18.822655)

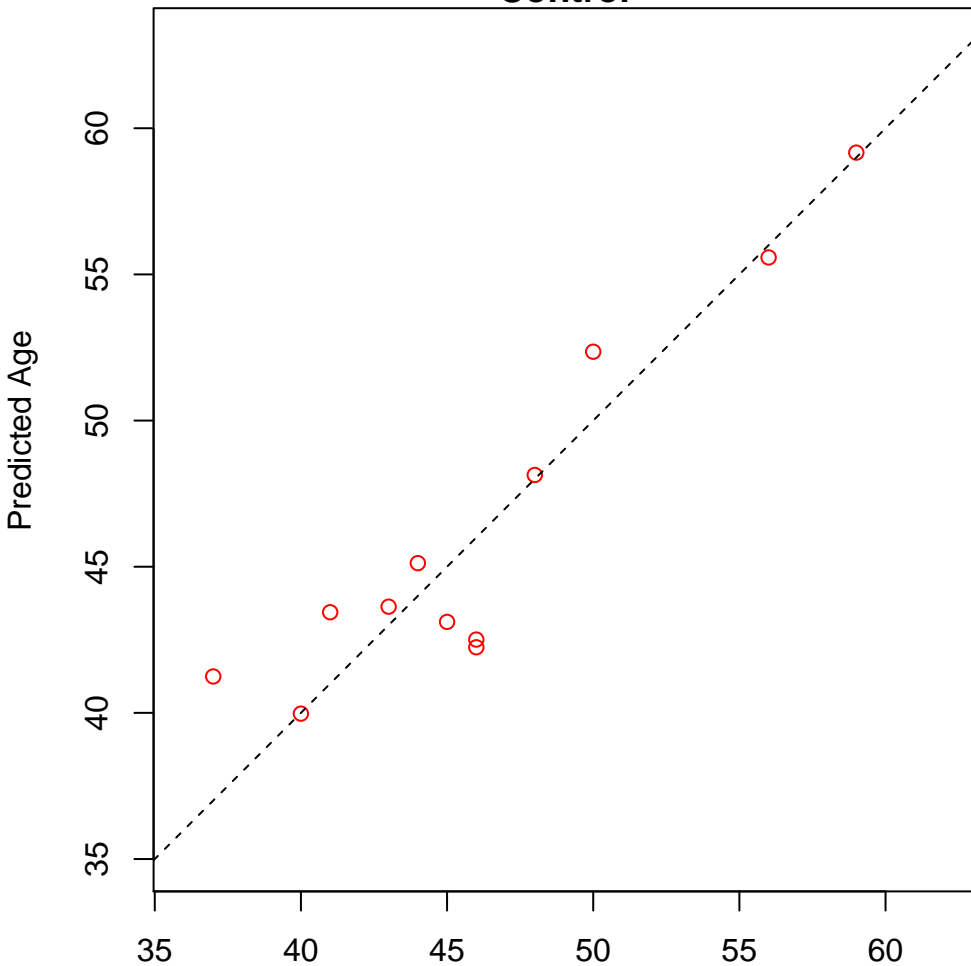


negative regulation of transposition (Score: 18.822655)

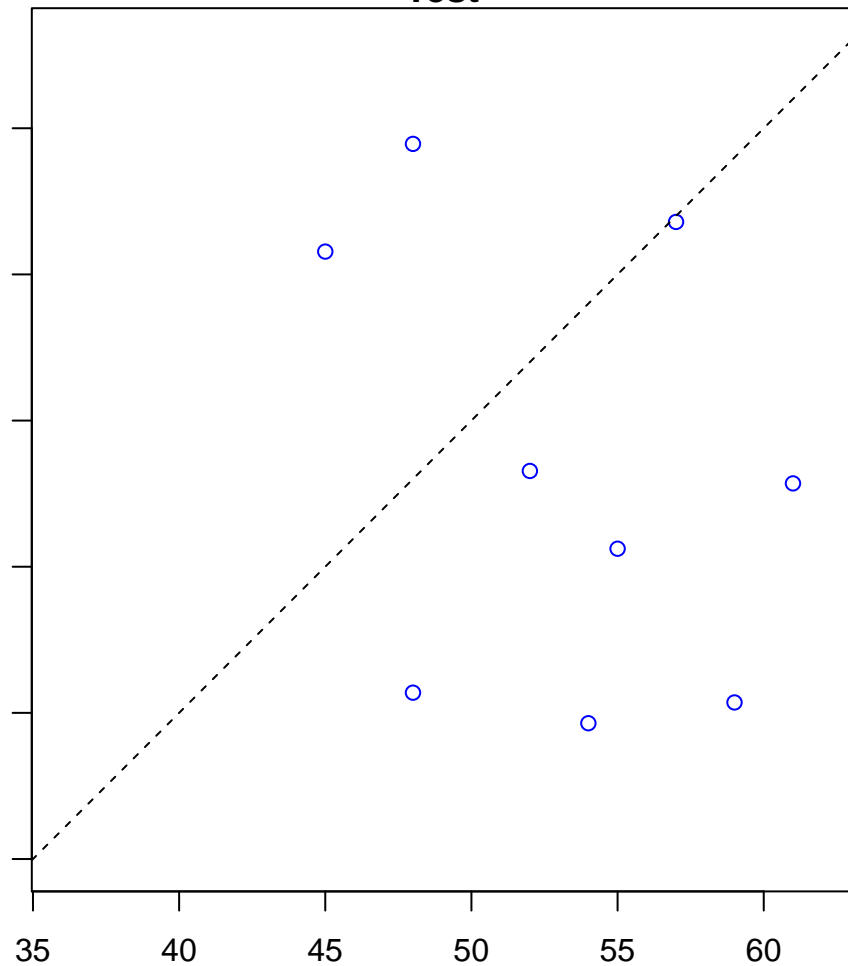


cellular response to nutrient levels (Score: 18.658239)

Control

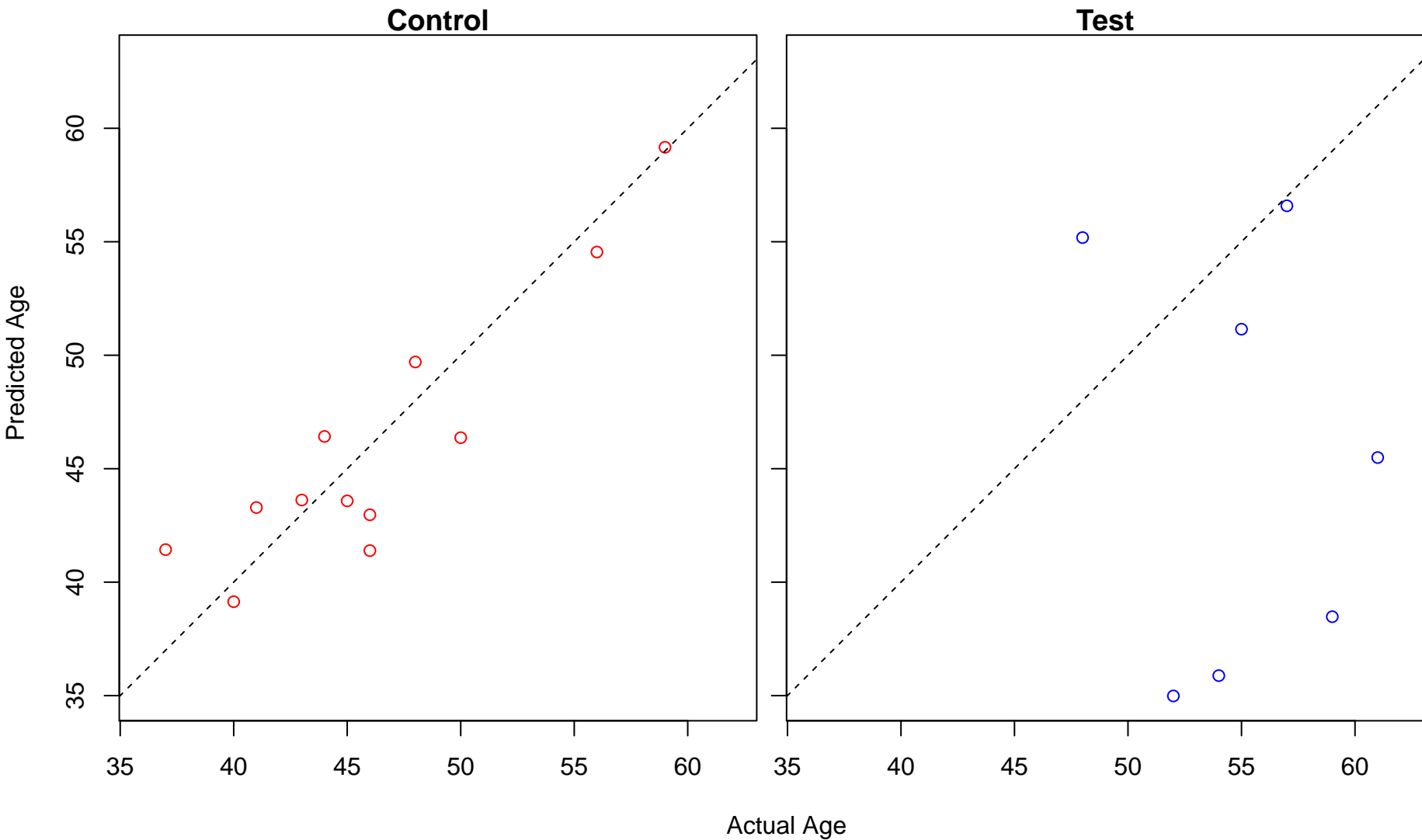


Test

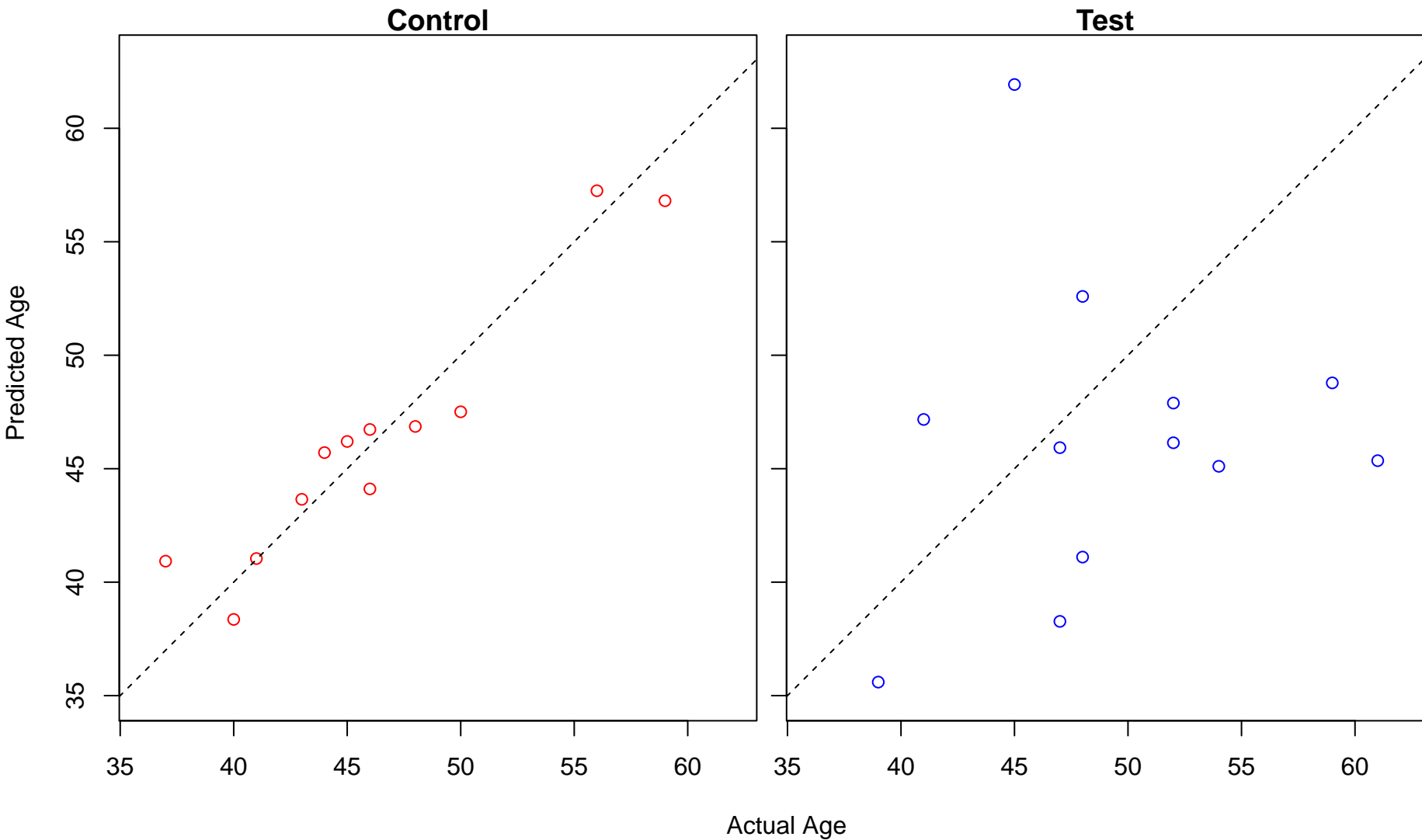


Actual Age

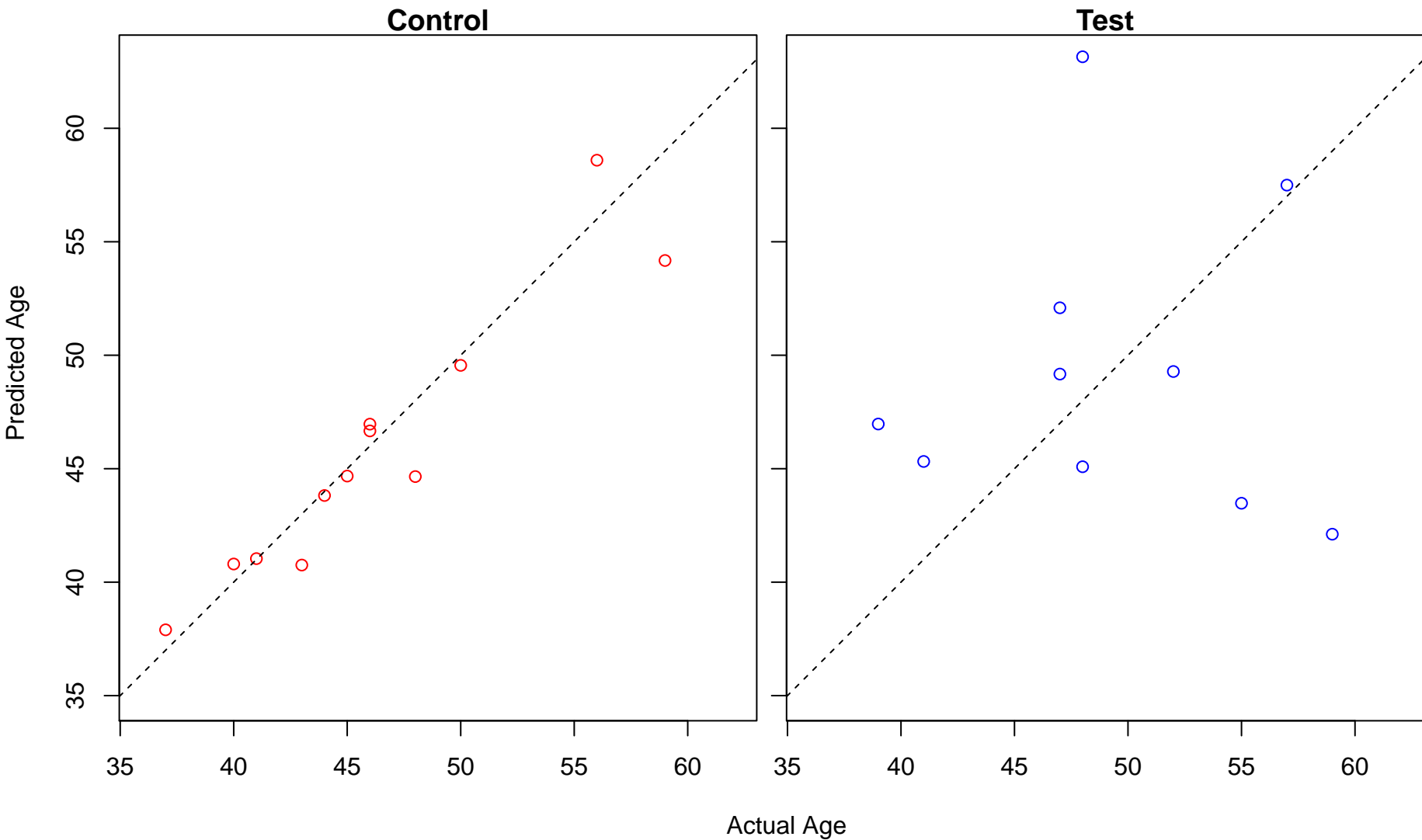
small molecule catabolic process (Score: 18.646540)



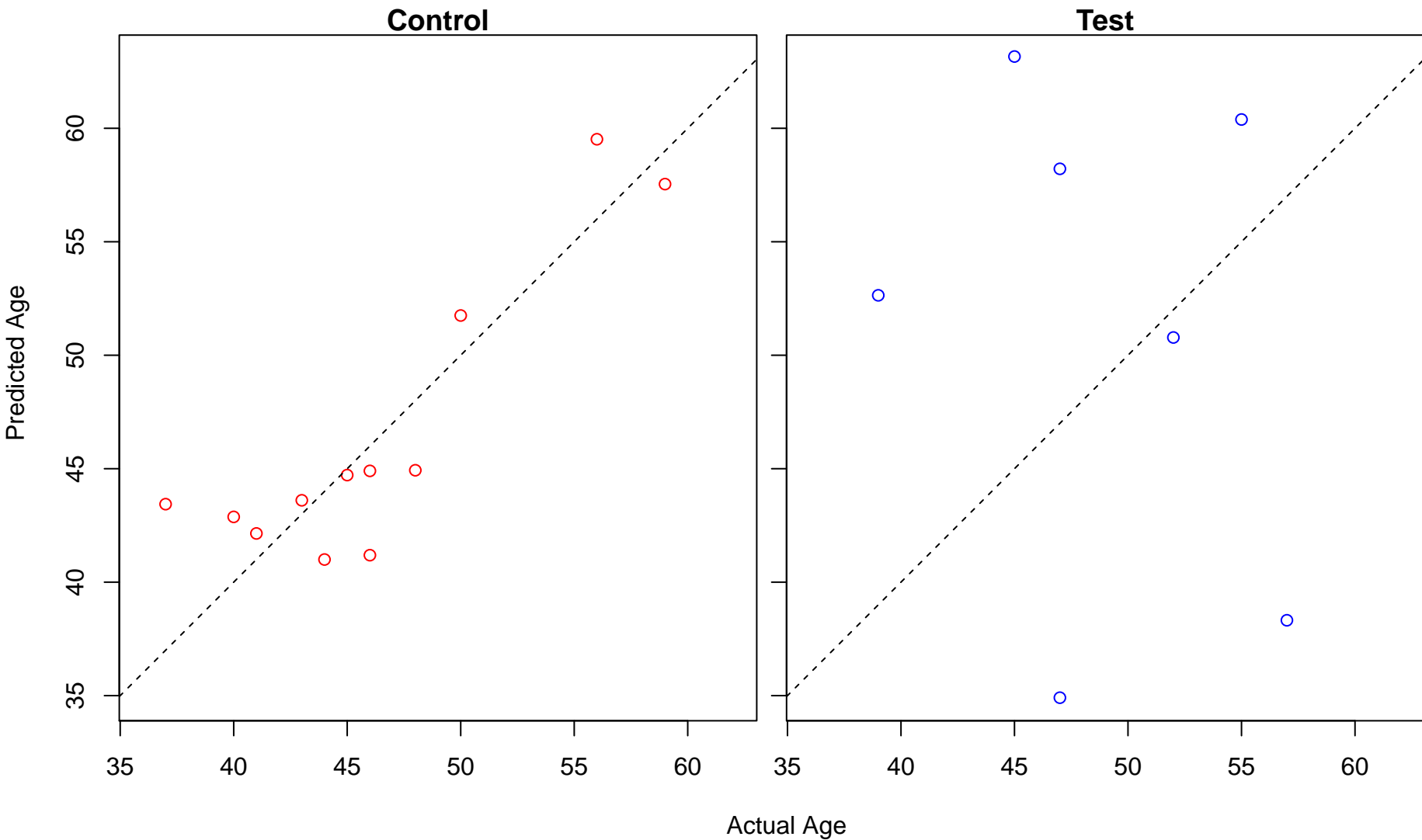
activation of cysteine-type endopeptidase activity (Score: 18.644866)



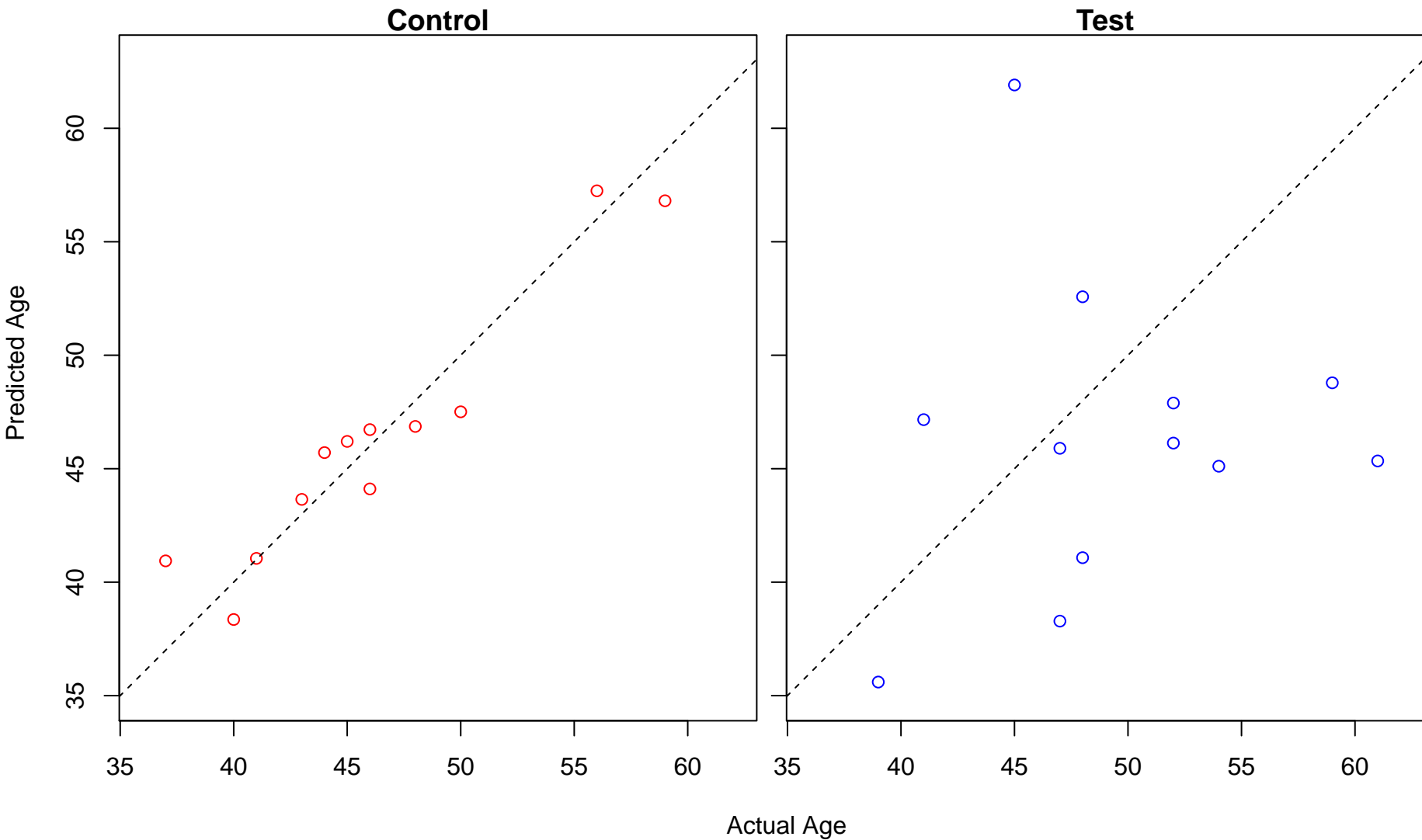
midbrain dopaminergic neuron differentiation (Score: 18.631666)



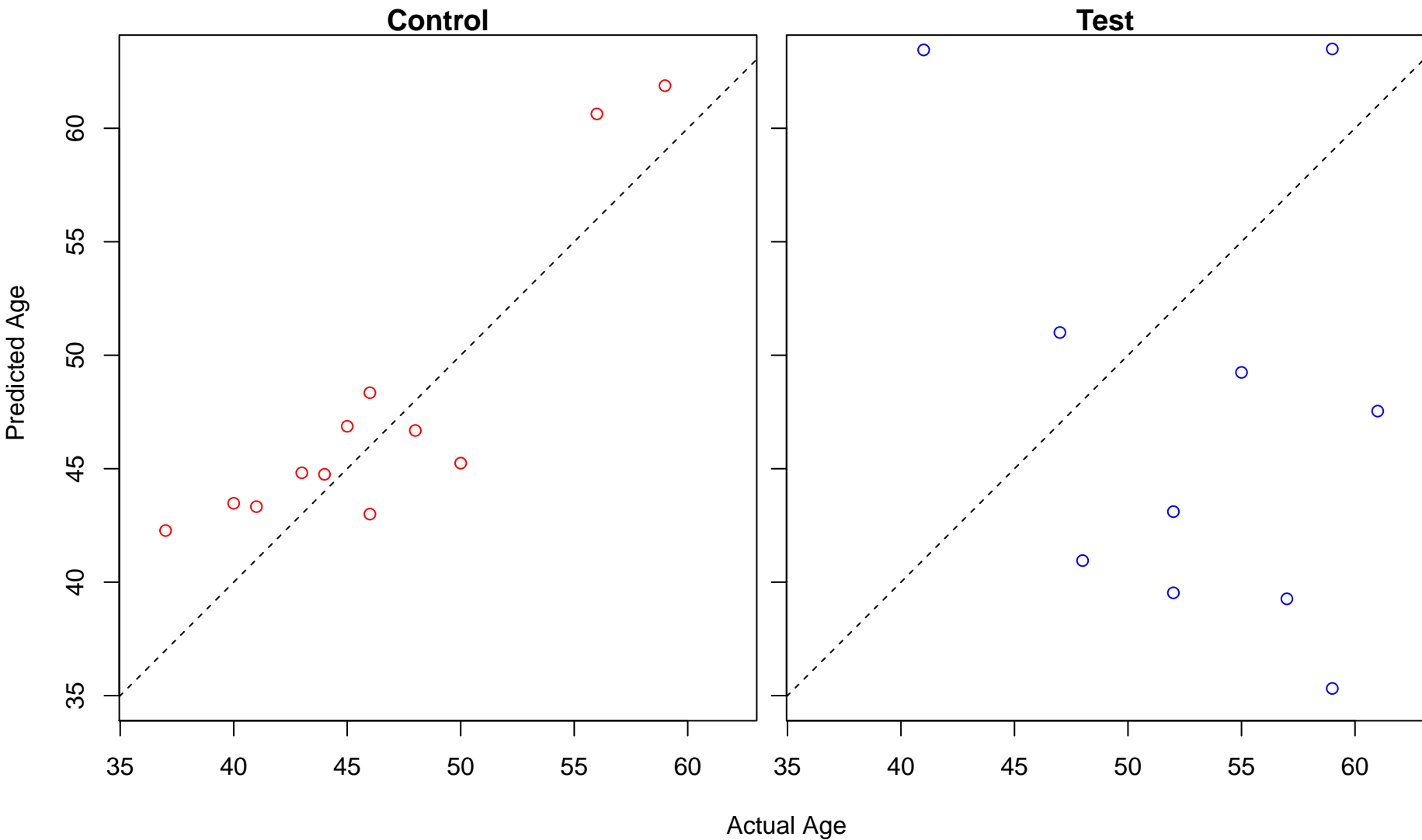
pituitary gland development (Score: 18.591694)



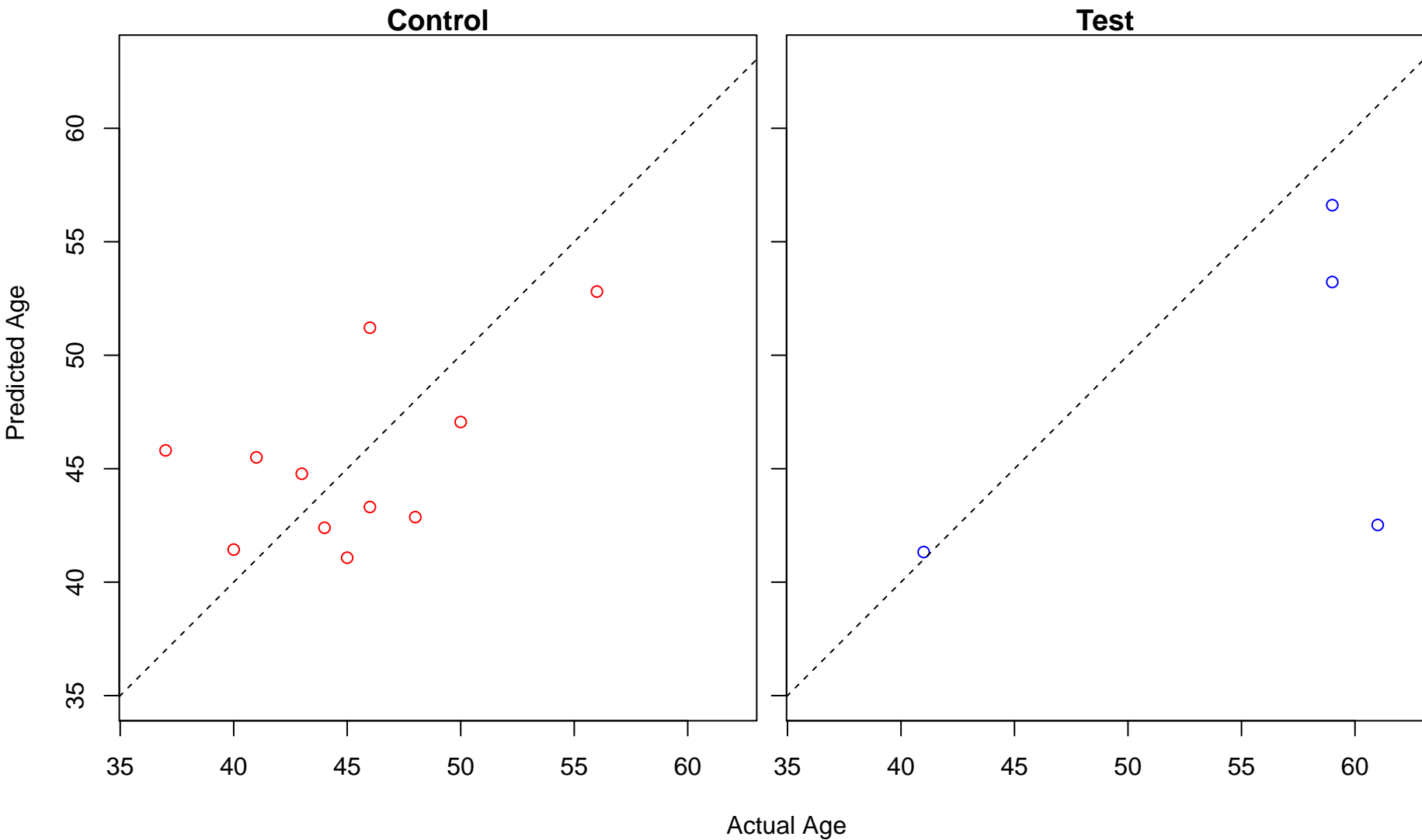
zymogen activation (Score: 18.571036)



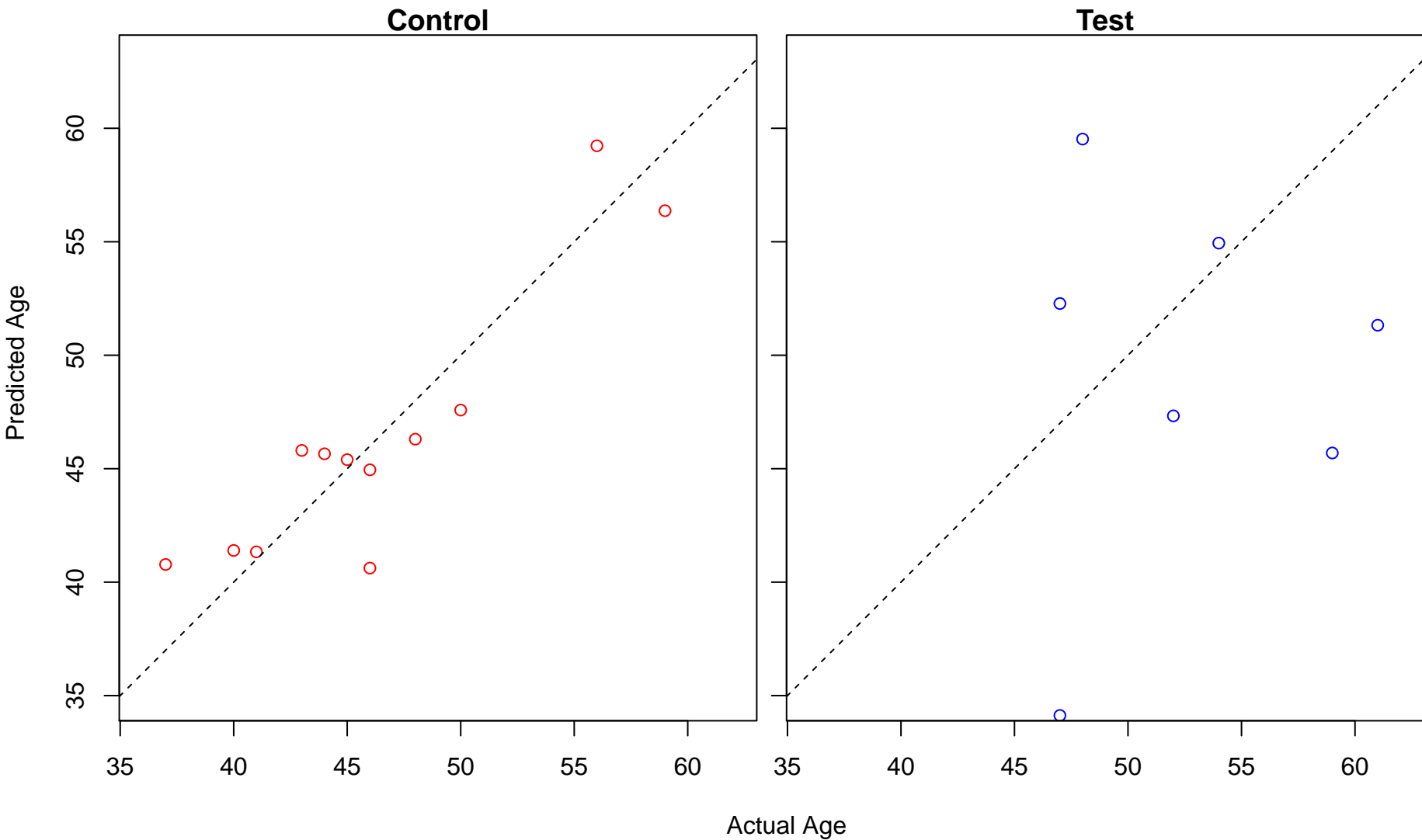
response to transforming growth factor beta (Score: 18.496779)



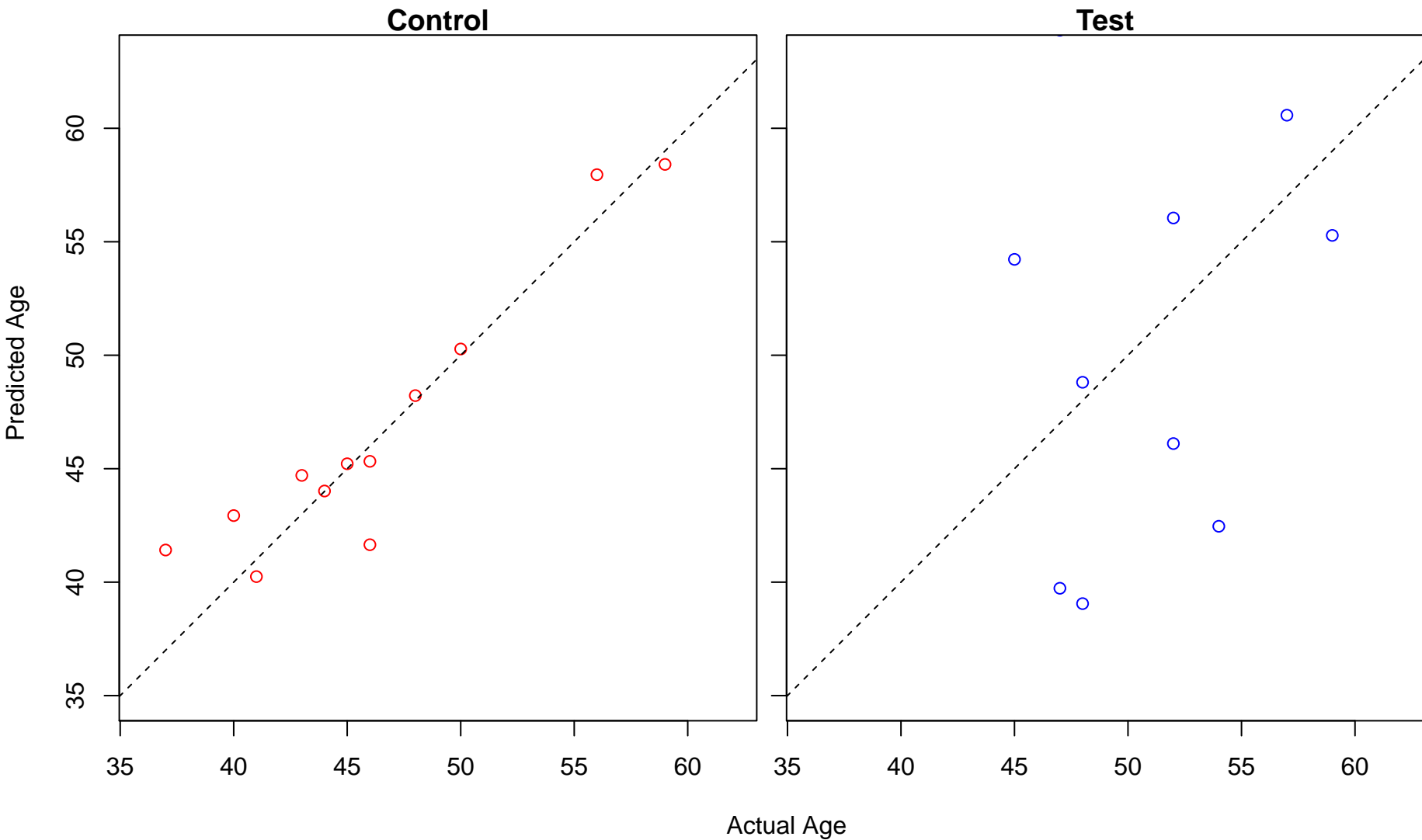
positive regulation of the force of heart contraction (Score: 18.495062)



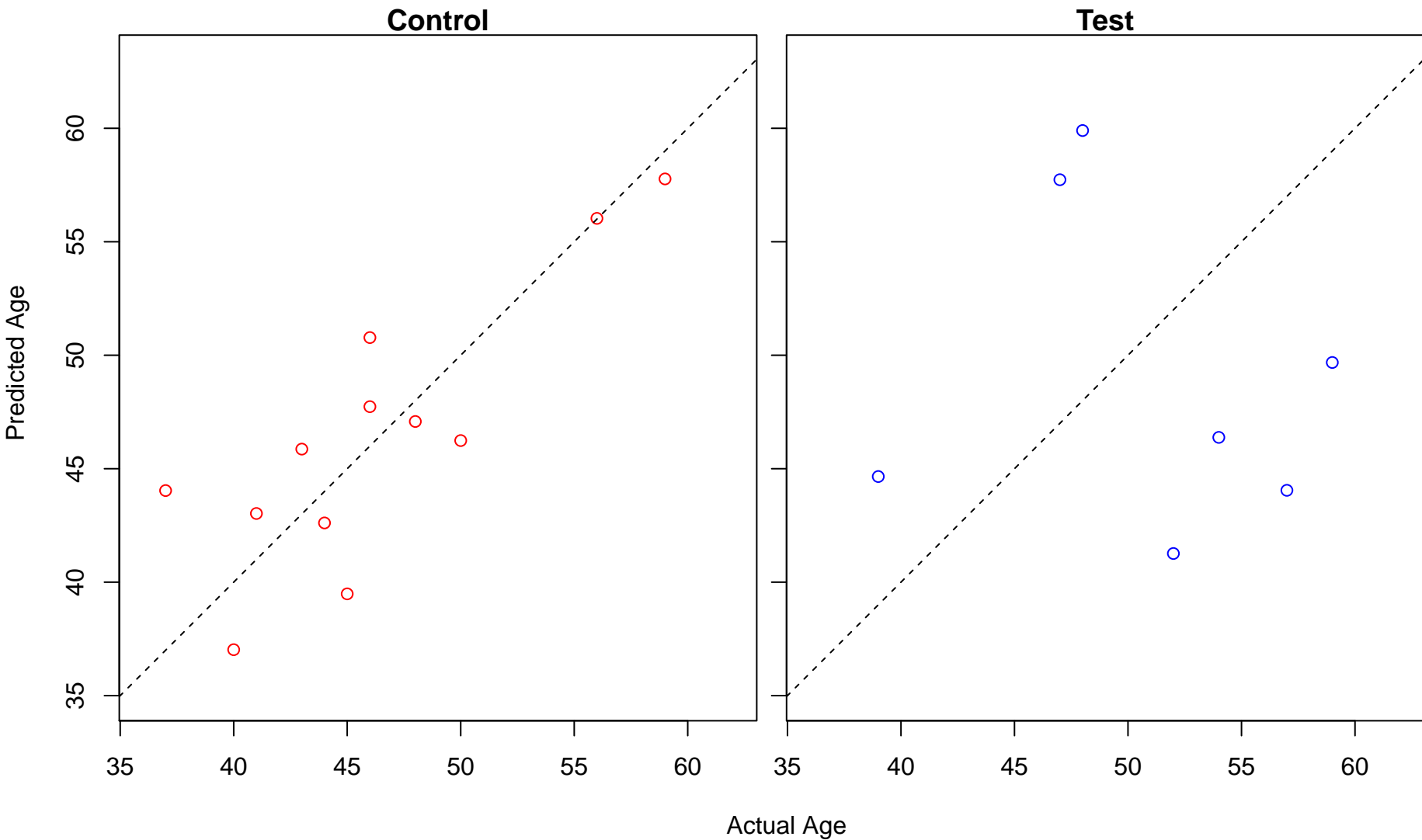
regulation of hormone biosynthetic process (Score: 18.465586)



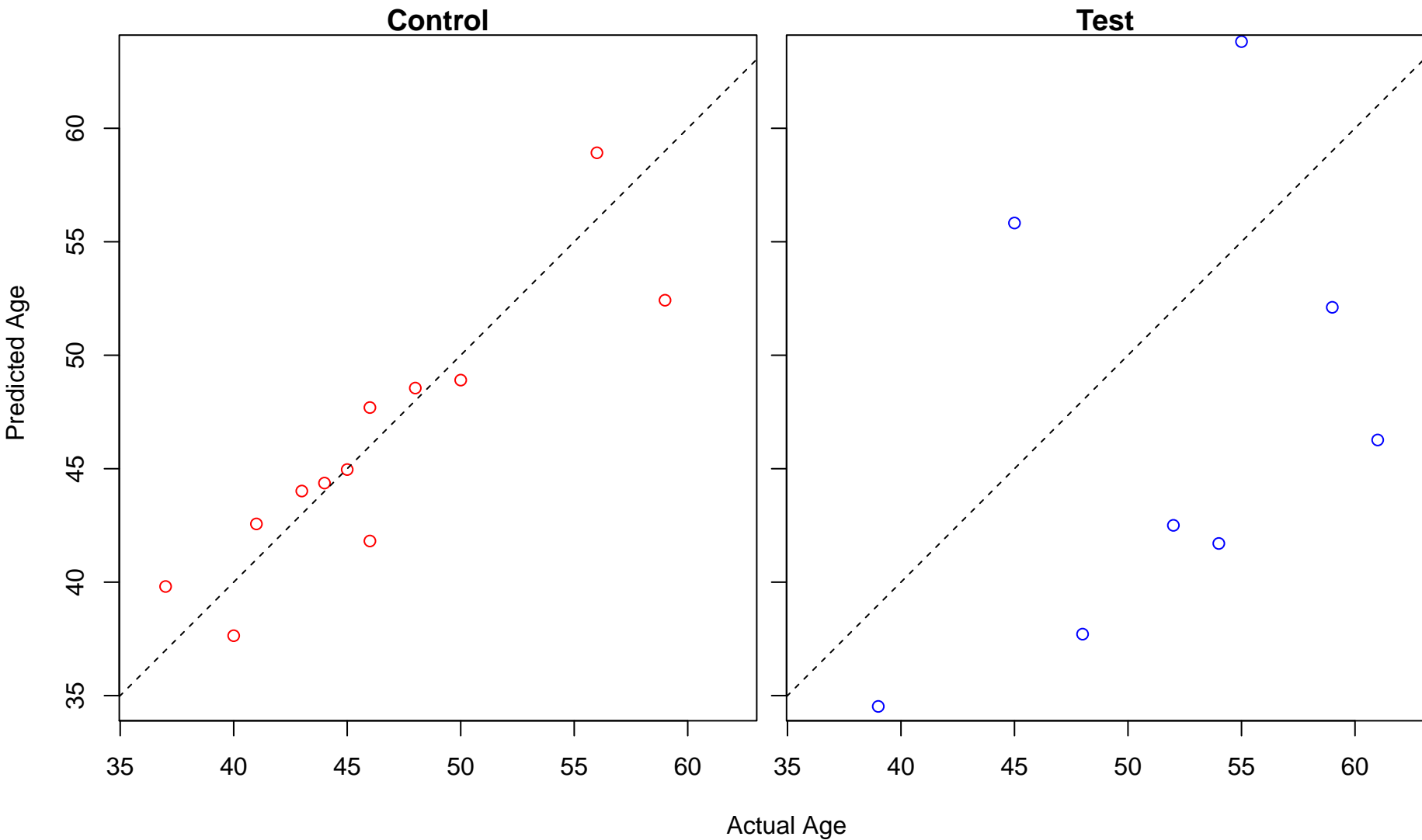
negative regulation of T cell receptor signaling pathway (Score: 18.421242)



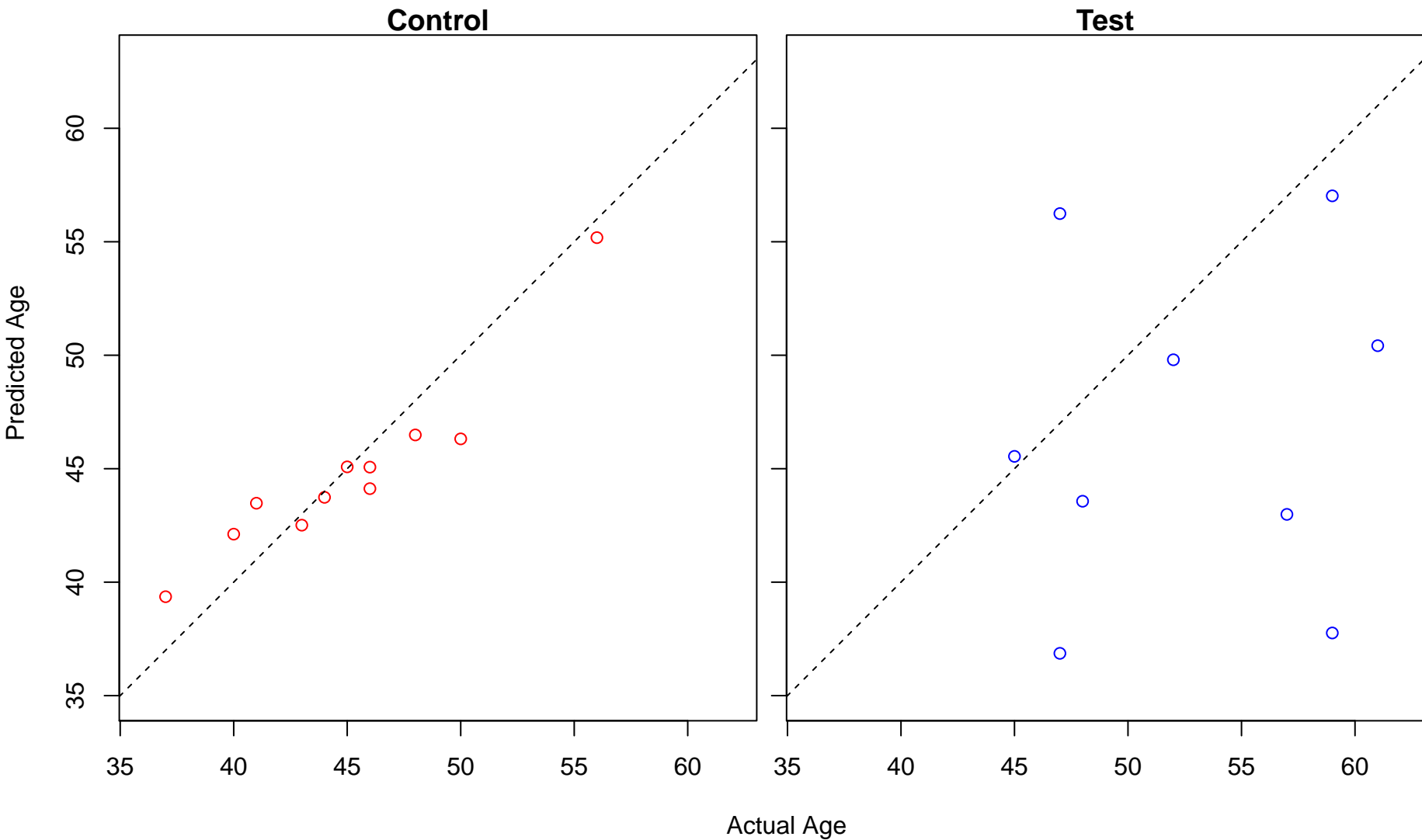
negative regulation of hydrogen peroxide-induced cell death (Score: 18.365526)



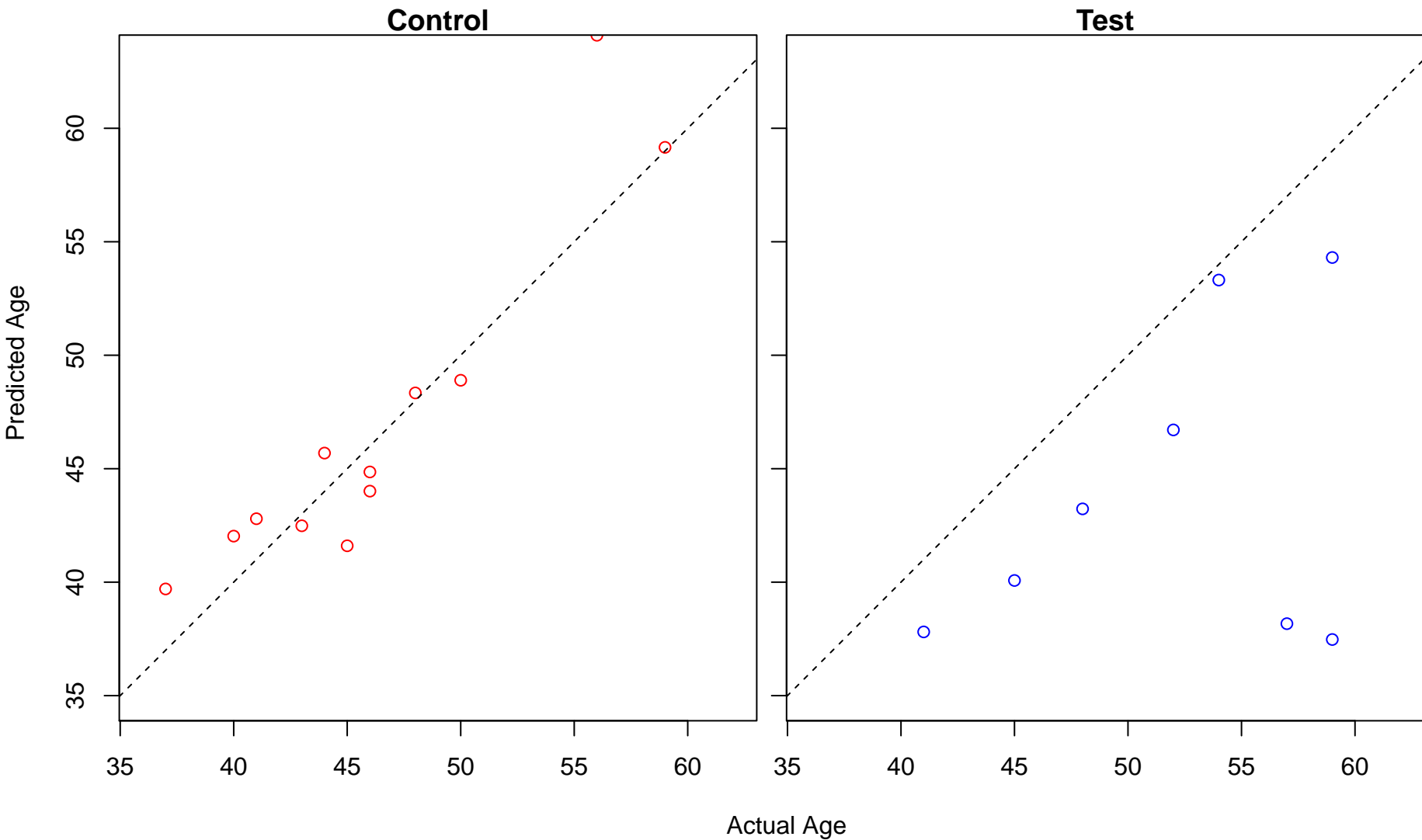
negative regulation of endoplasmic reticulum unfolded protein response (Score: 18.353131)



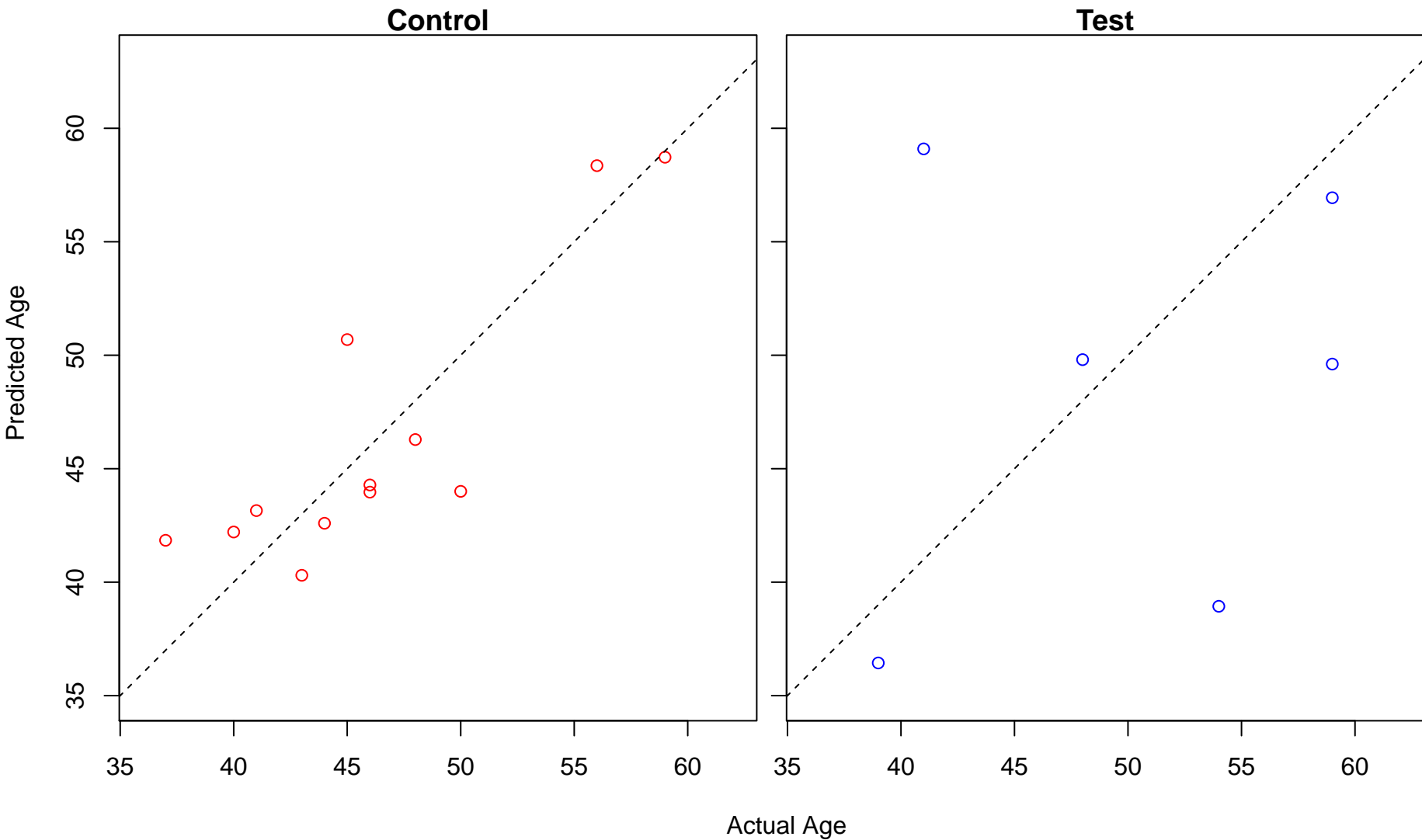
brain morphogenesis (Score: 18.352131)



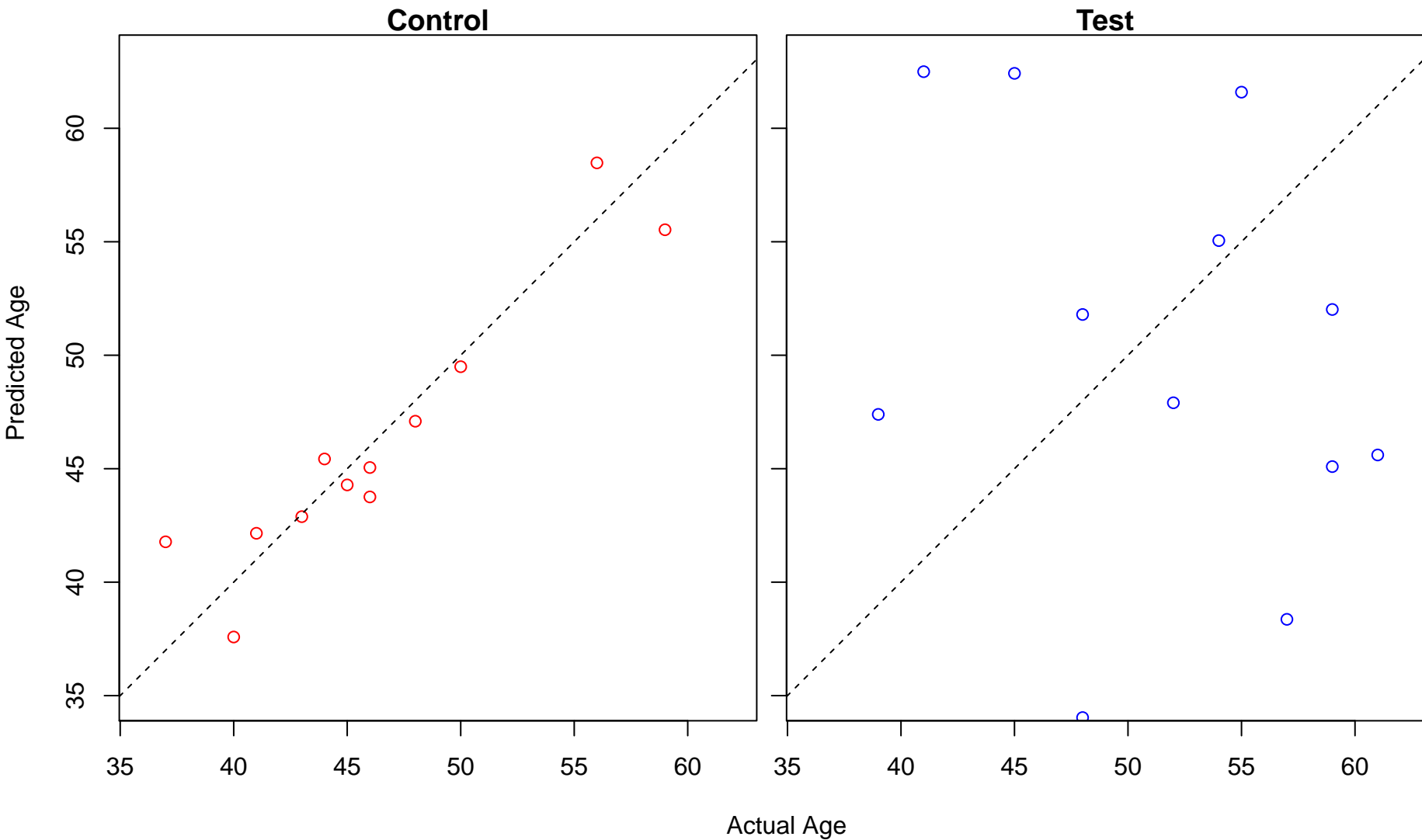
detection of chemical stimulus (Score: 18.351051)



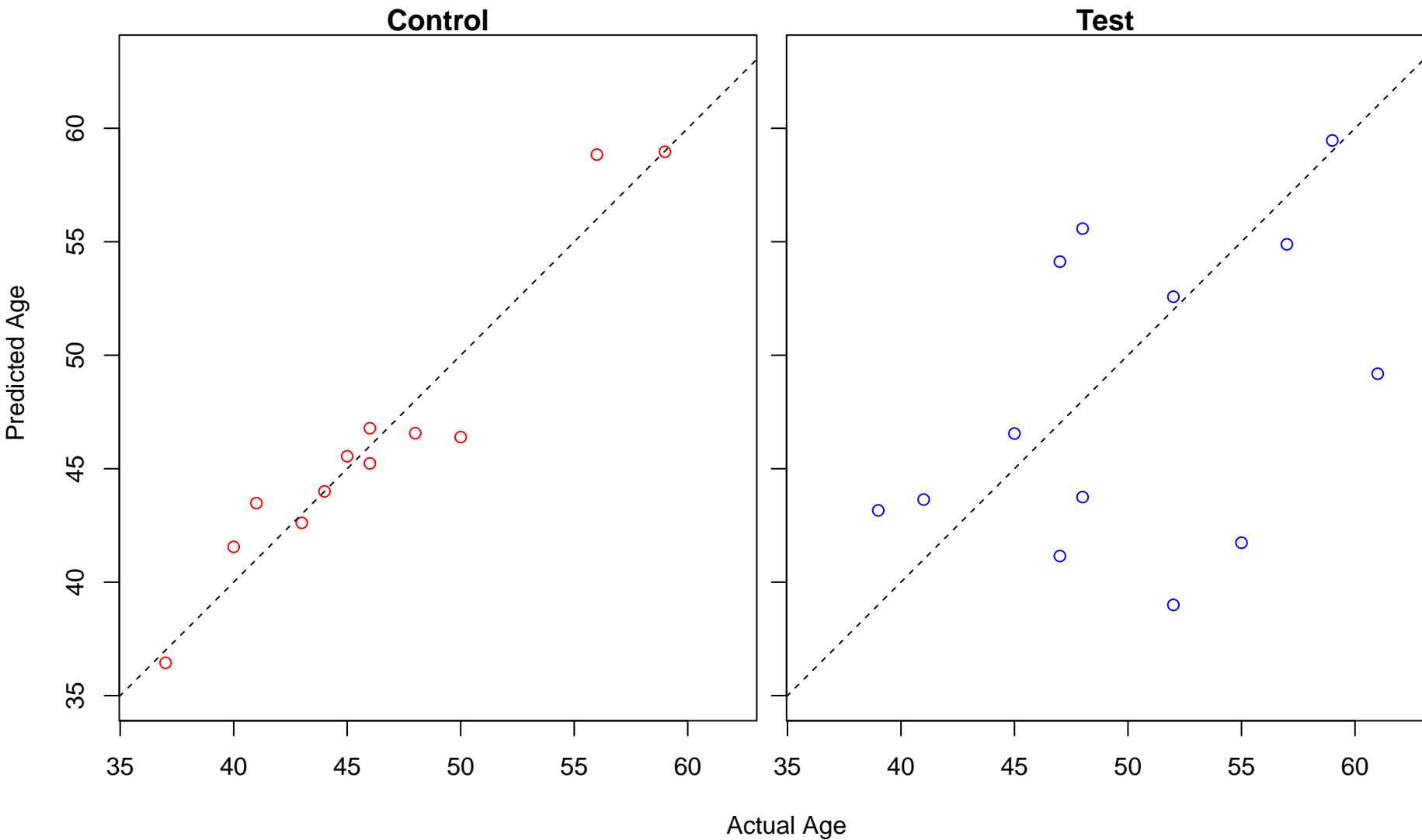
regulation of myelination (Score: 18.288275)



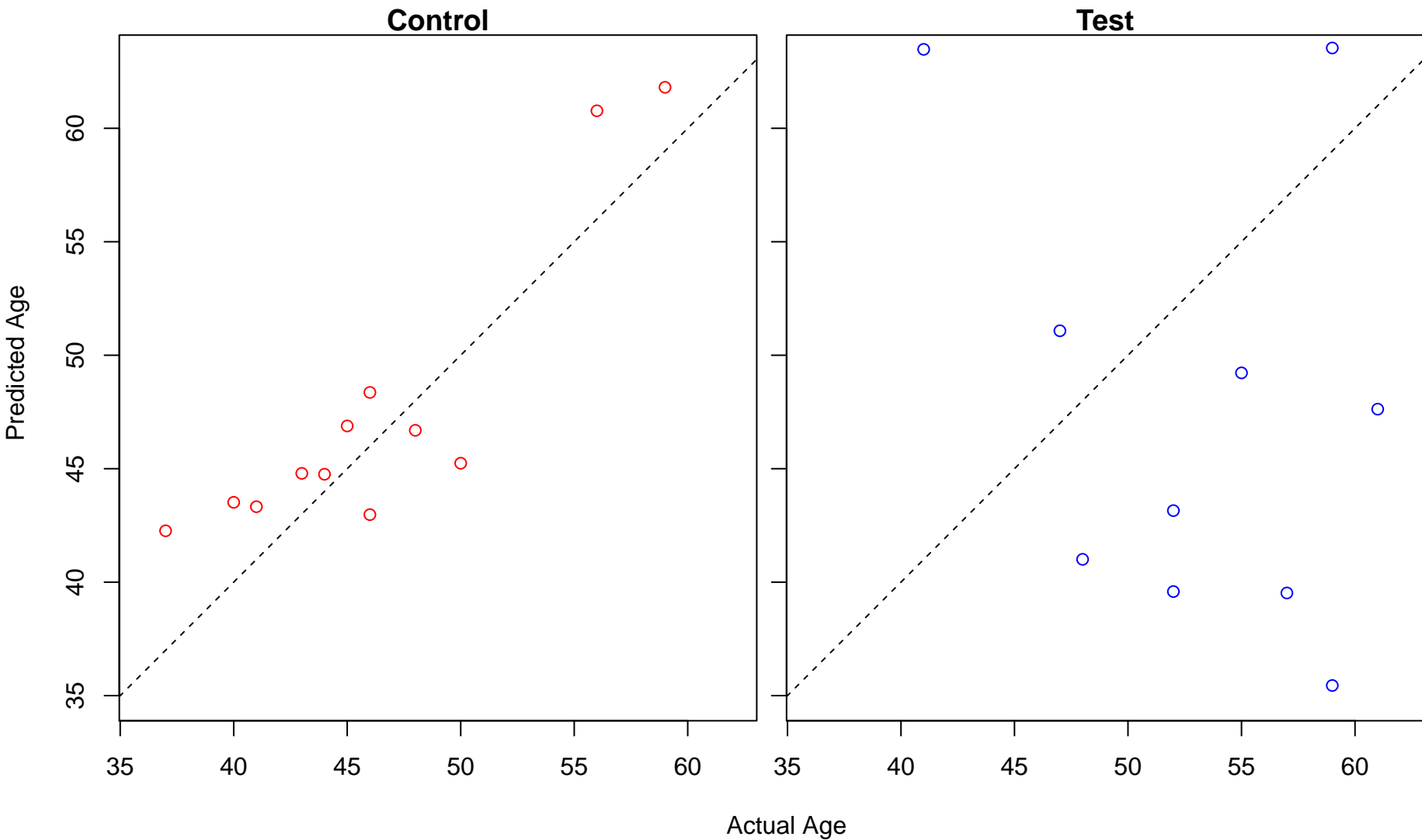
response to copper ion (Score: 18.272334)



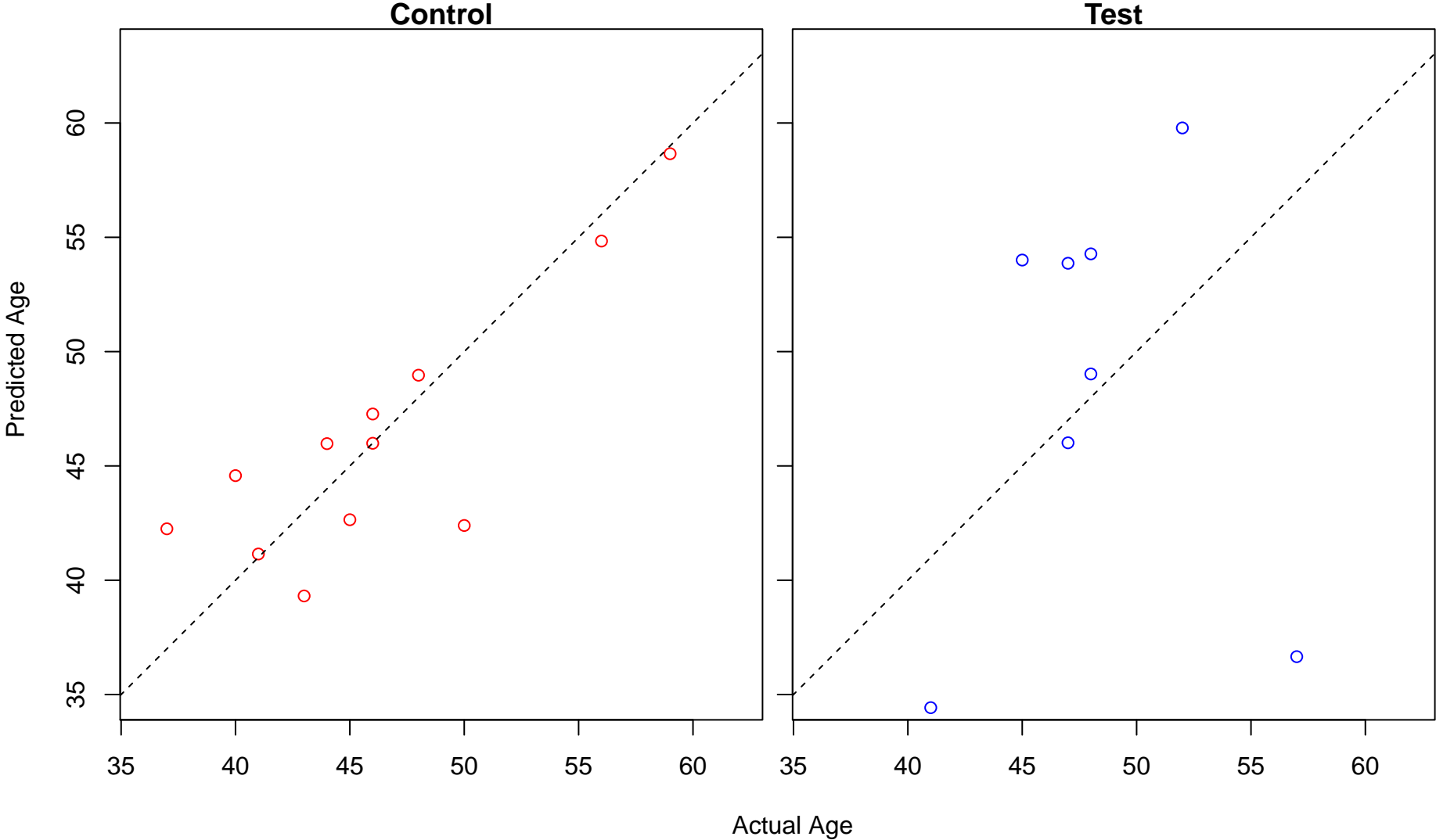
Wnt signaling pathway (Score: 18.252321)



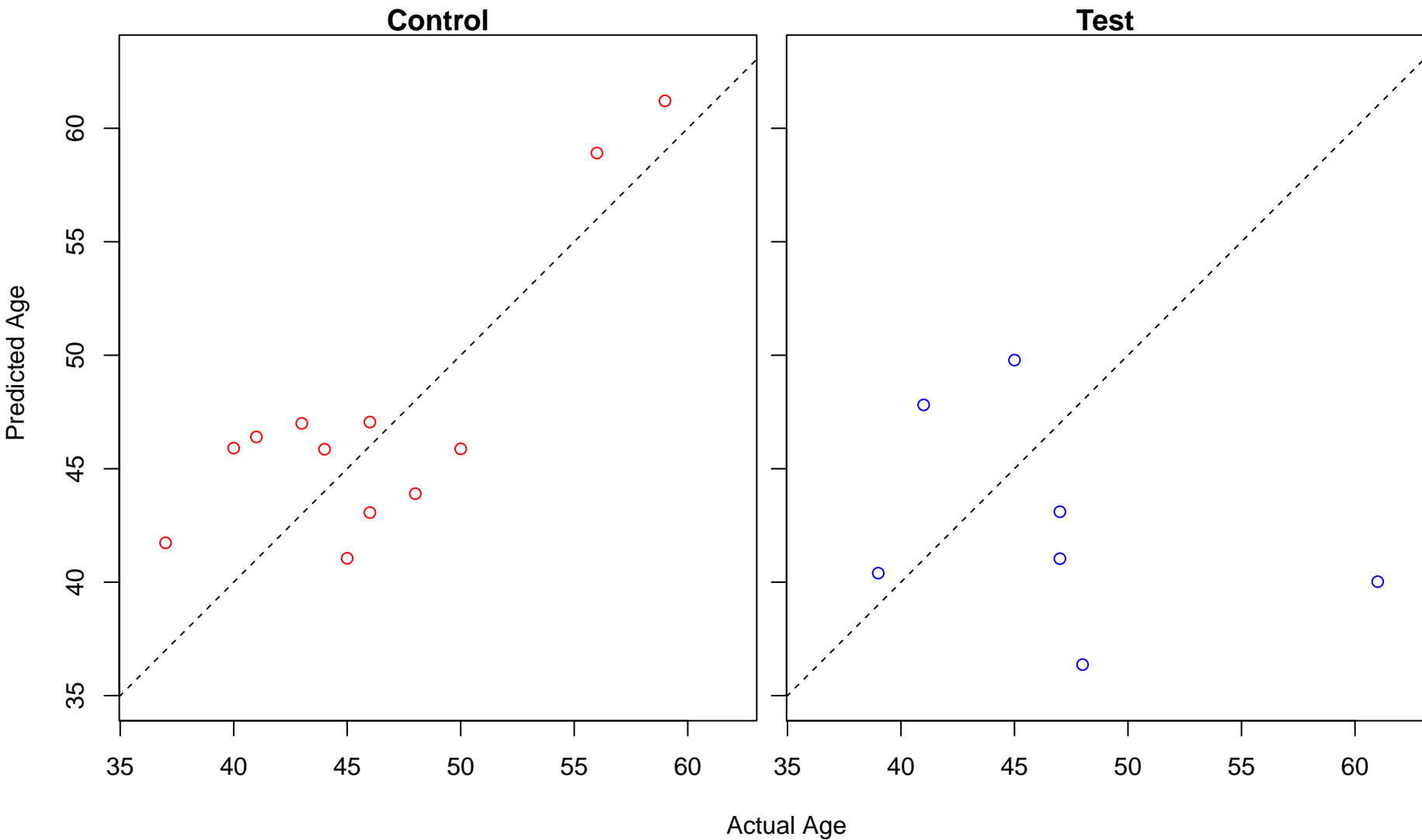
cellular response to transforming growth factor beta stimulus (Score: 18.234374)



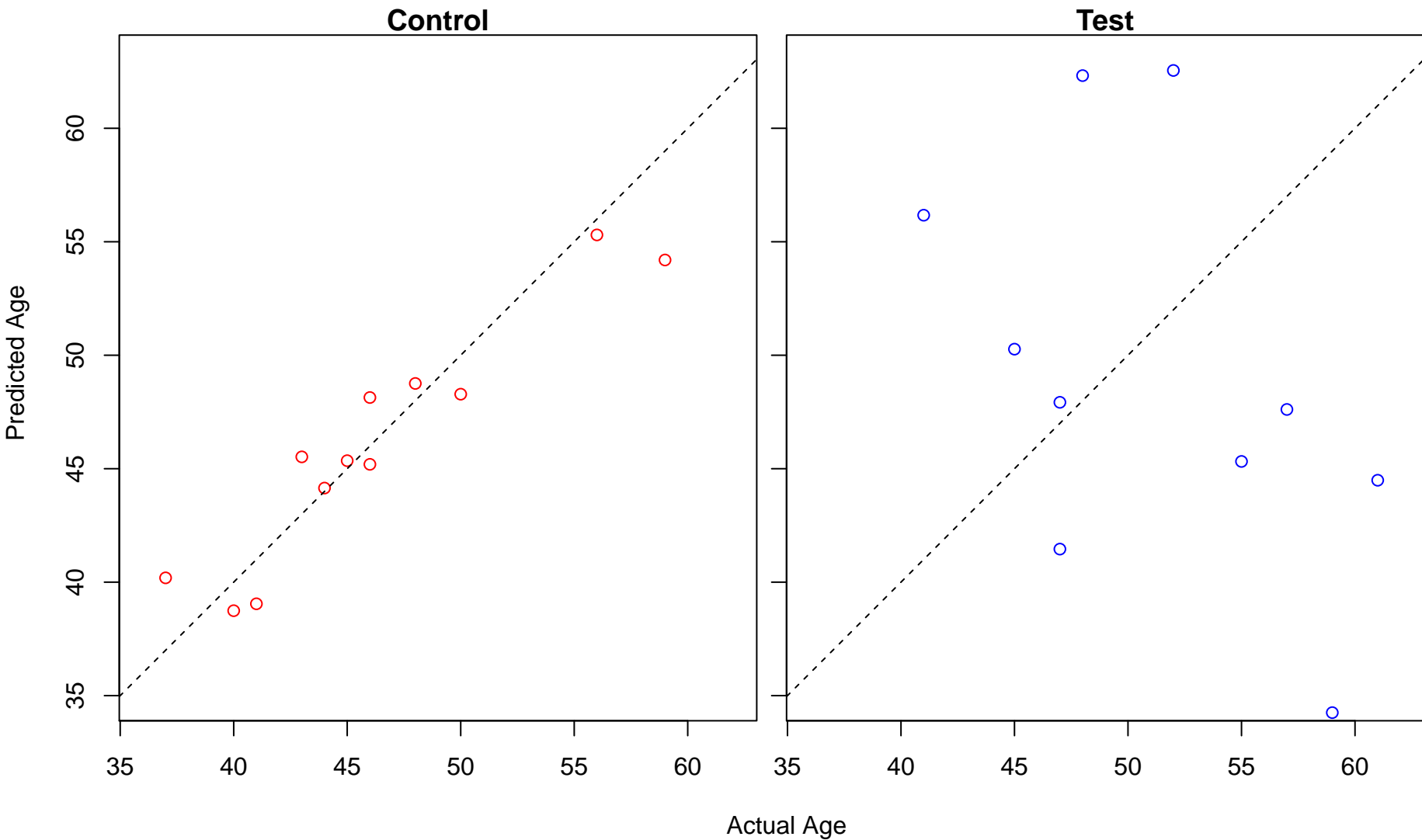
antigen processing and presentation of endogenous peptide antigen via MHC class I (Score: 18.2032)



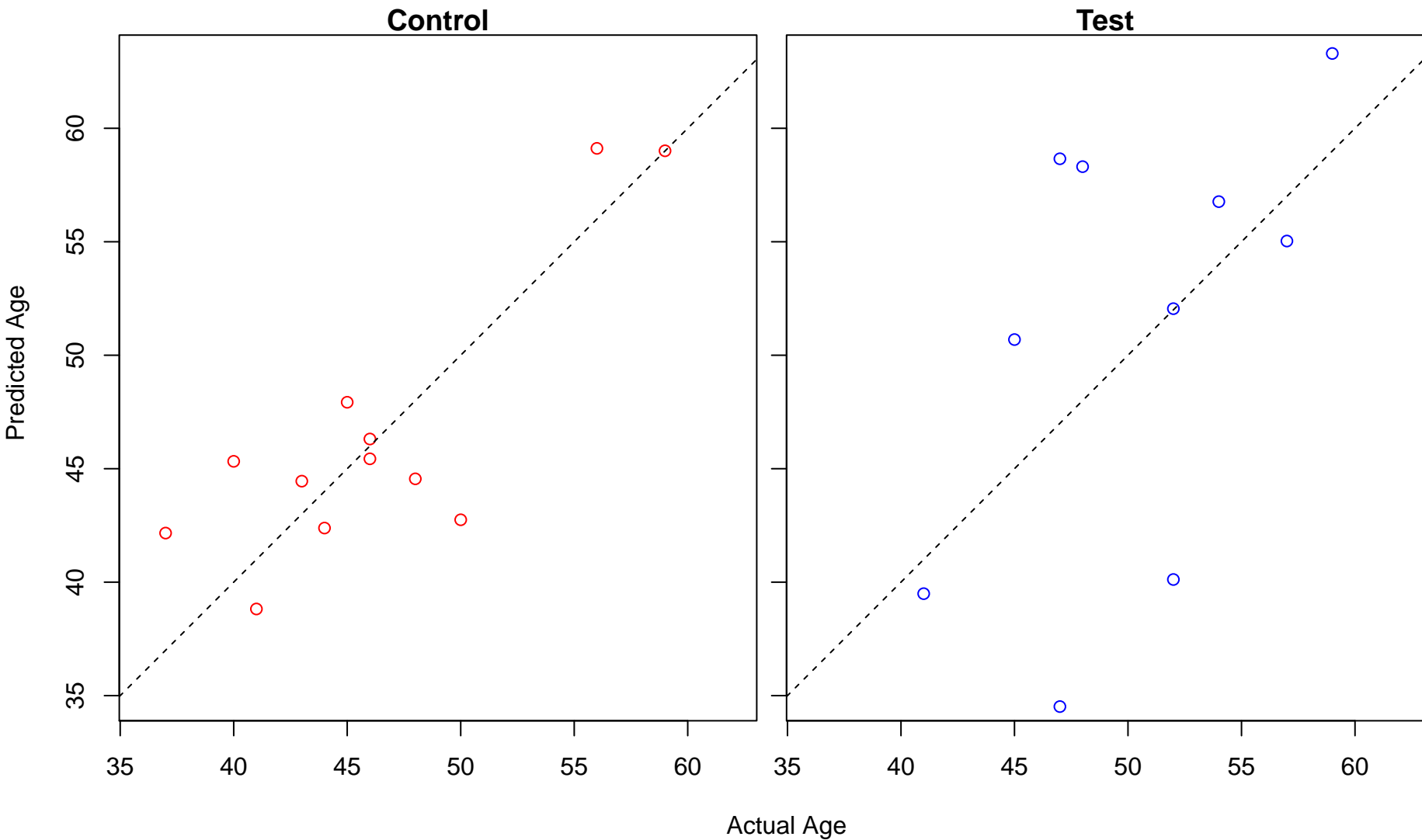
regulation of podosome assembly (Score: 18.154886)



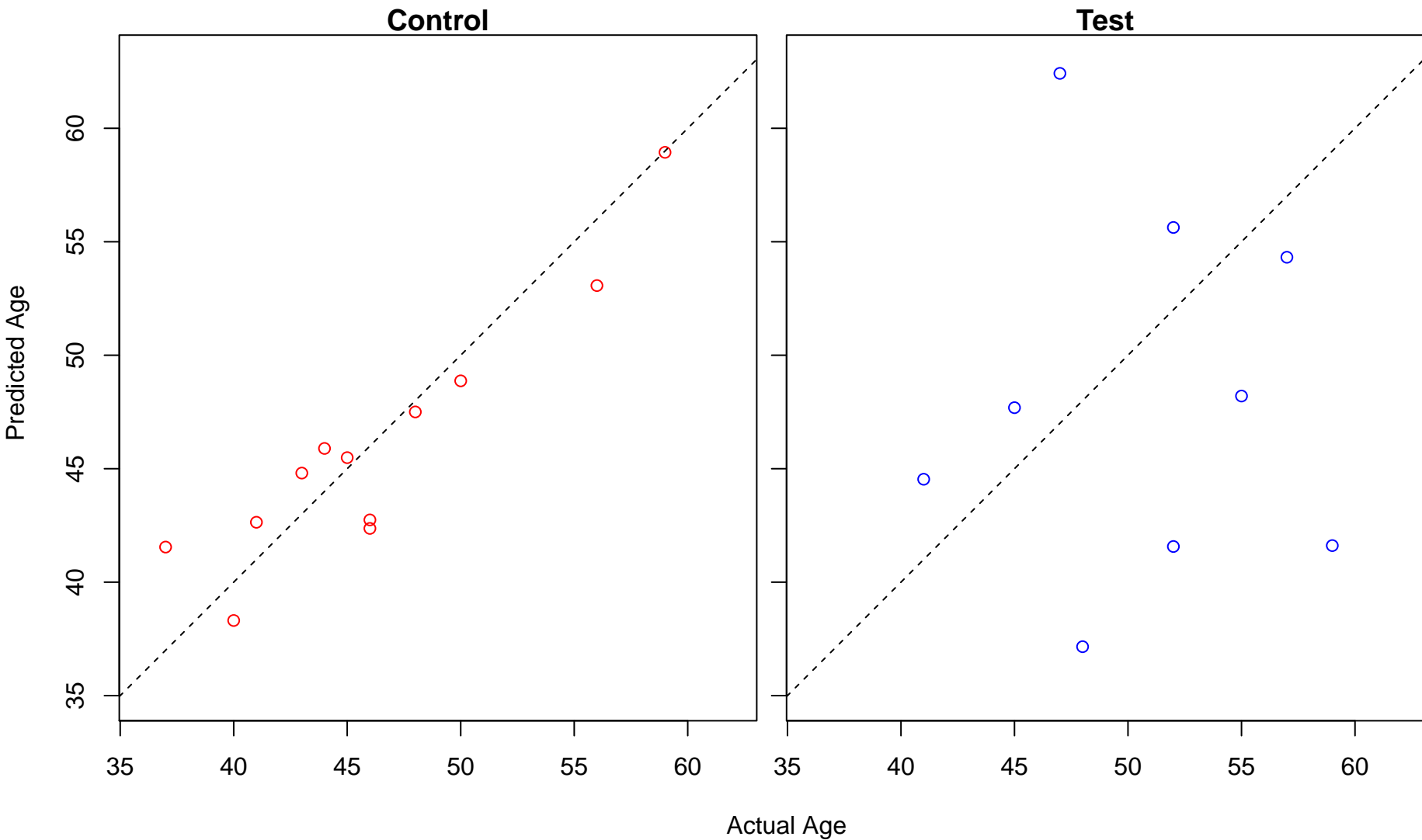
negative regulation of translation in response to stress (Score: 18.065983)



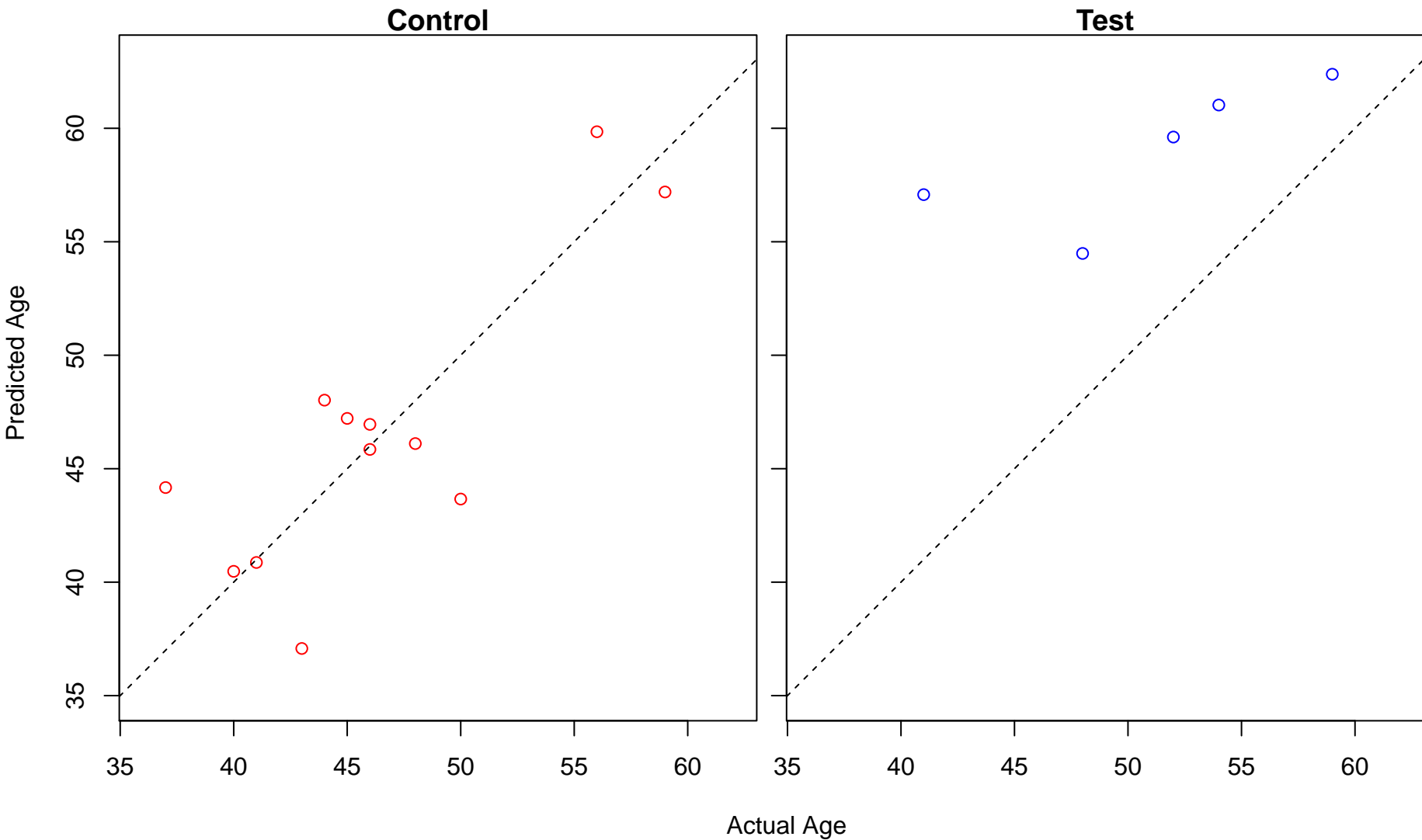
response to glucocorticoid (Score: 18.052659)



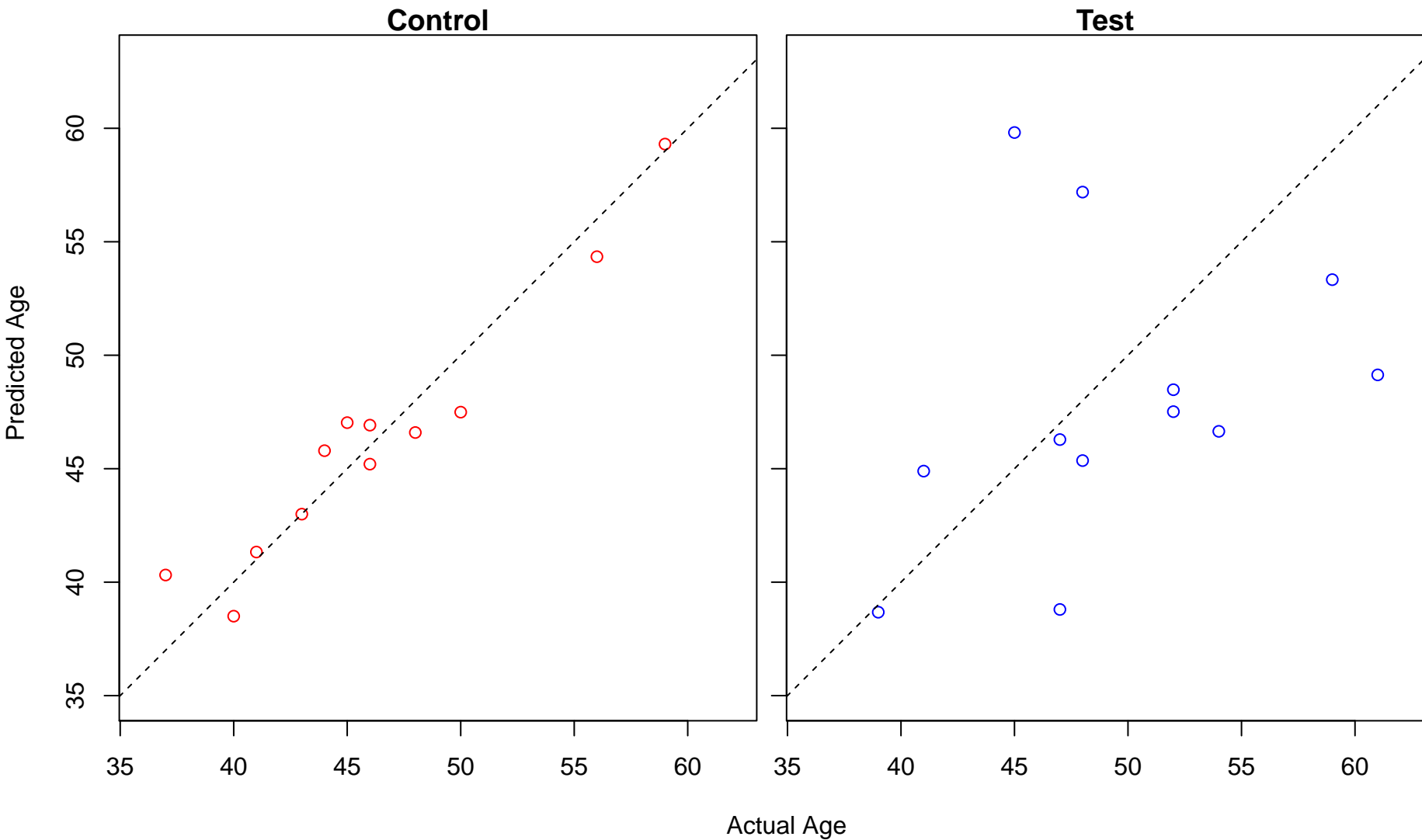
regulation of antigen processing and presentation of peptide antigen (Score: 18.034241)



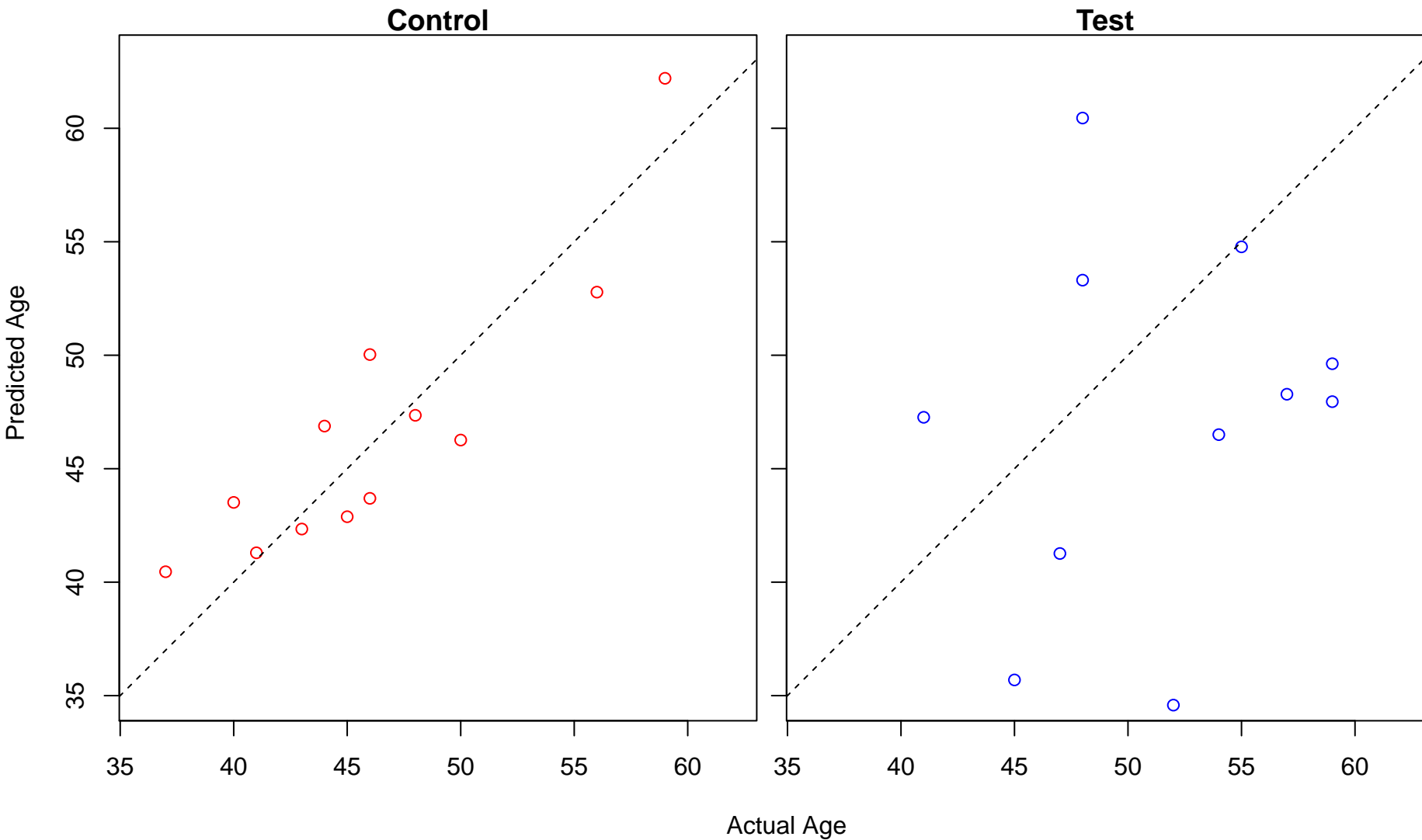
gamma-aminobutyric acid signaling pathway (Score: 17.992319)



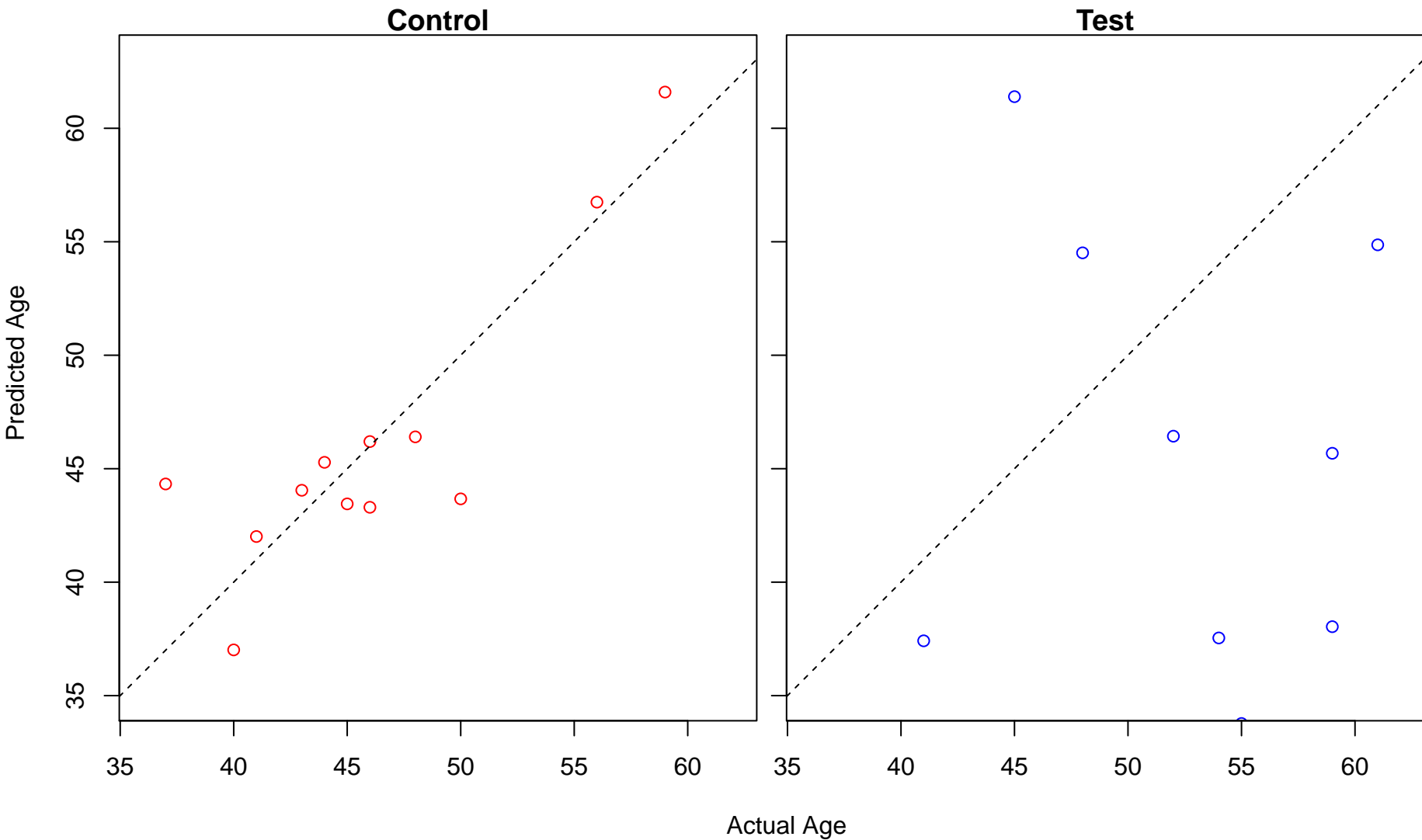
activation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 17.968028)



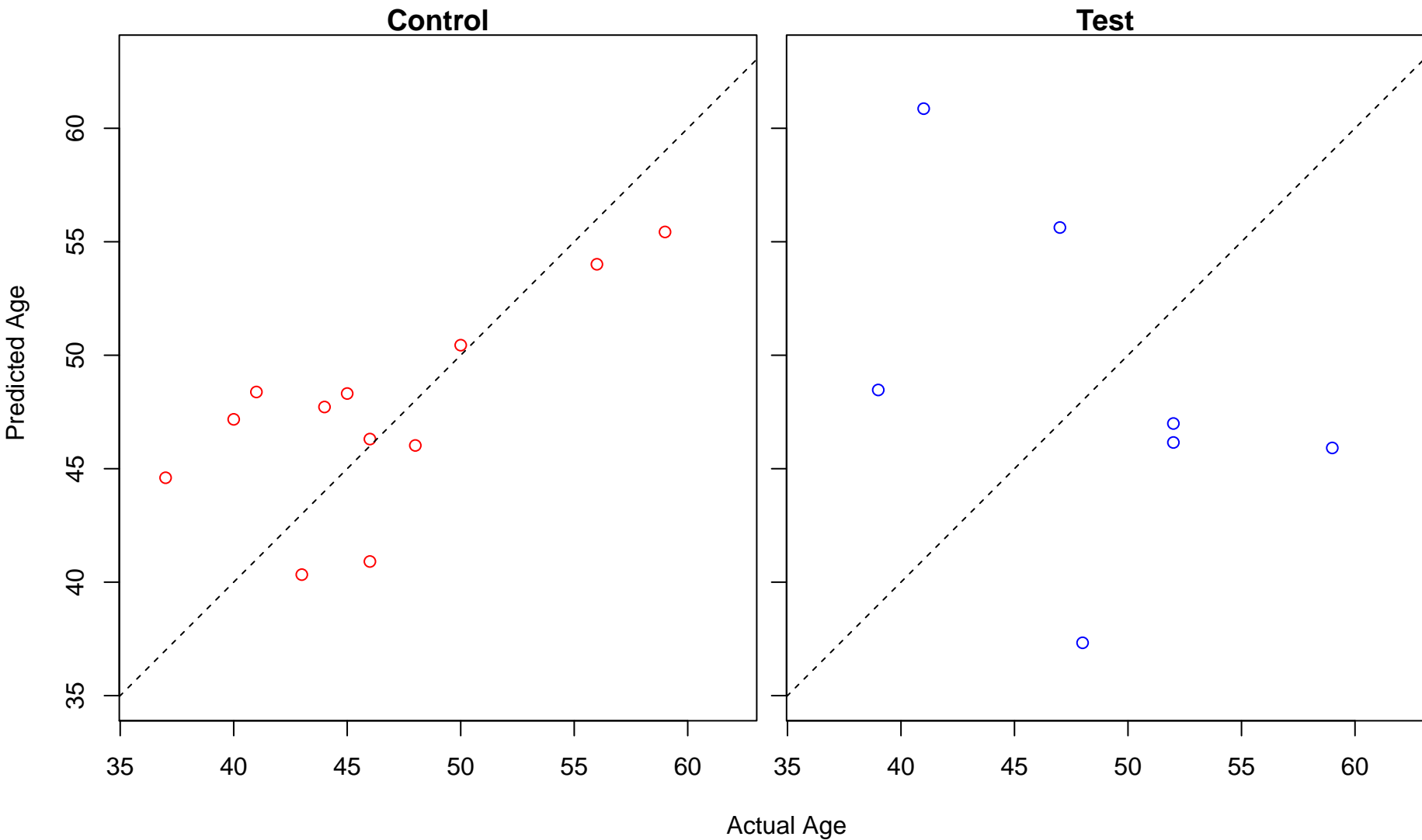
learning or memory (Score: 17.917397)



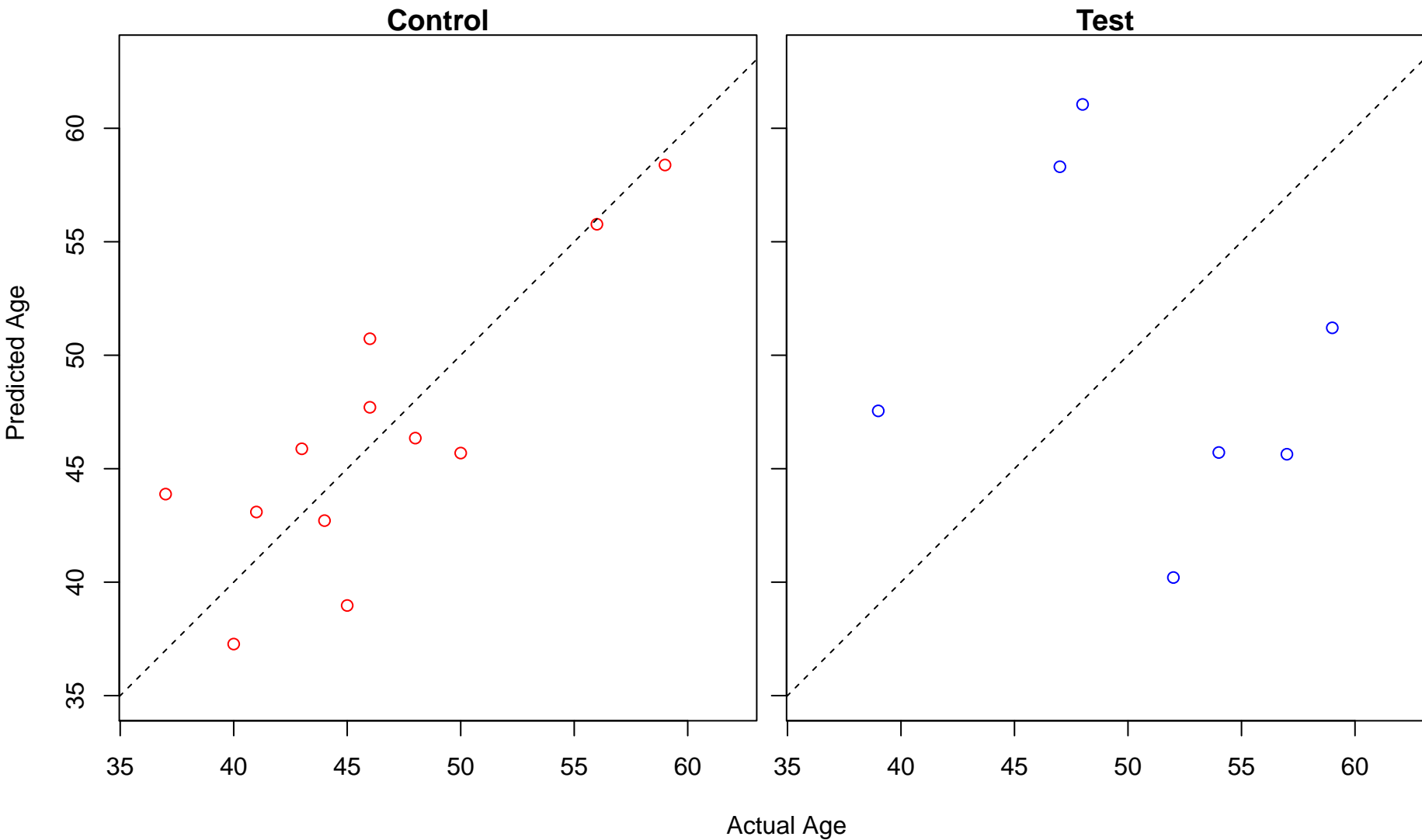
multicellular organismal reproductive process (Score: 17.909363)



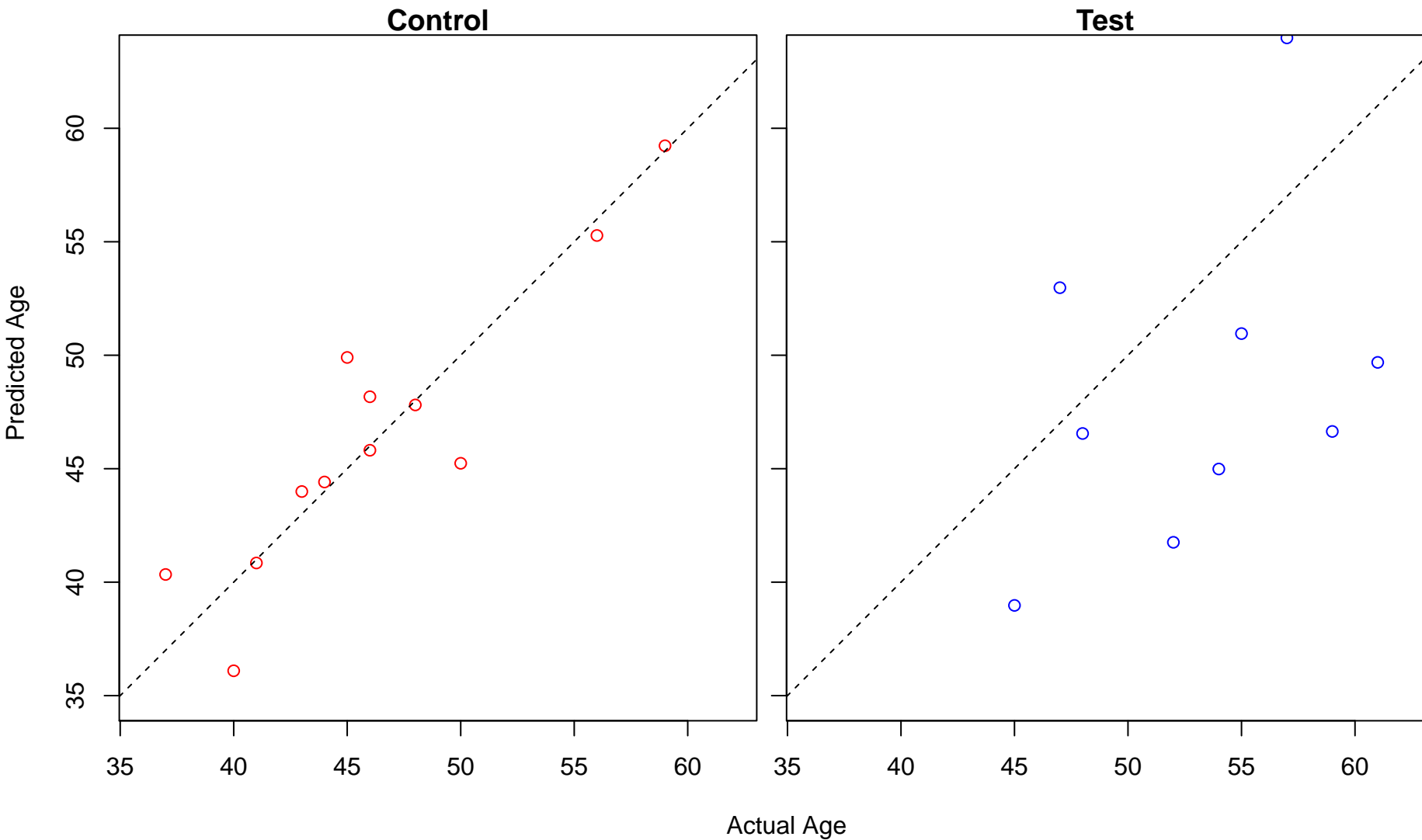
hyaluronan metabolic process (Score: 17.844345)



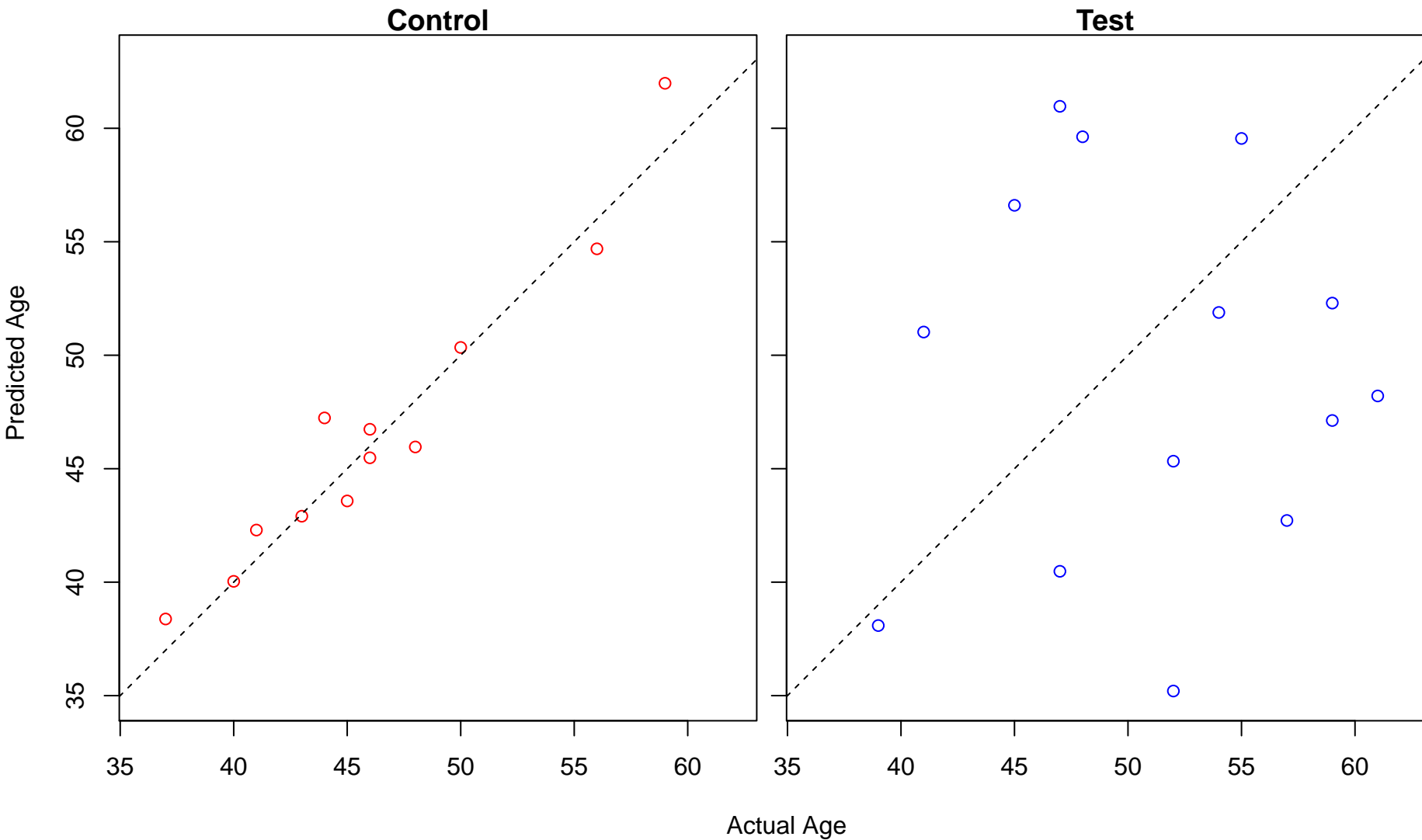
negative regulation of response to reactive oxygen species (Score: 17.801031)



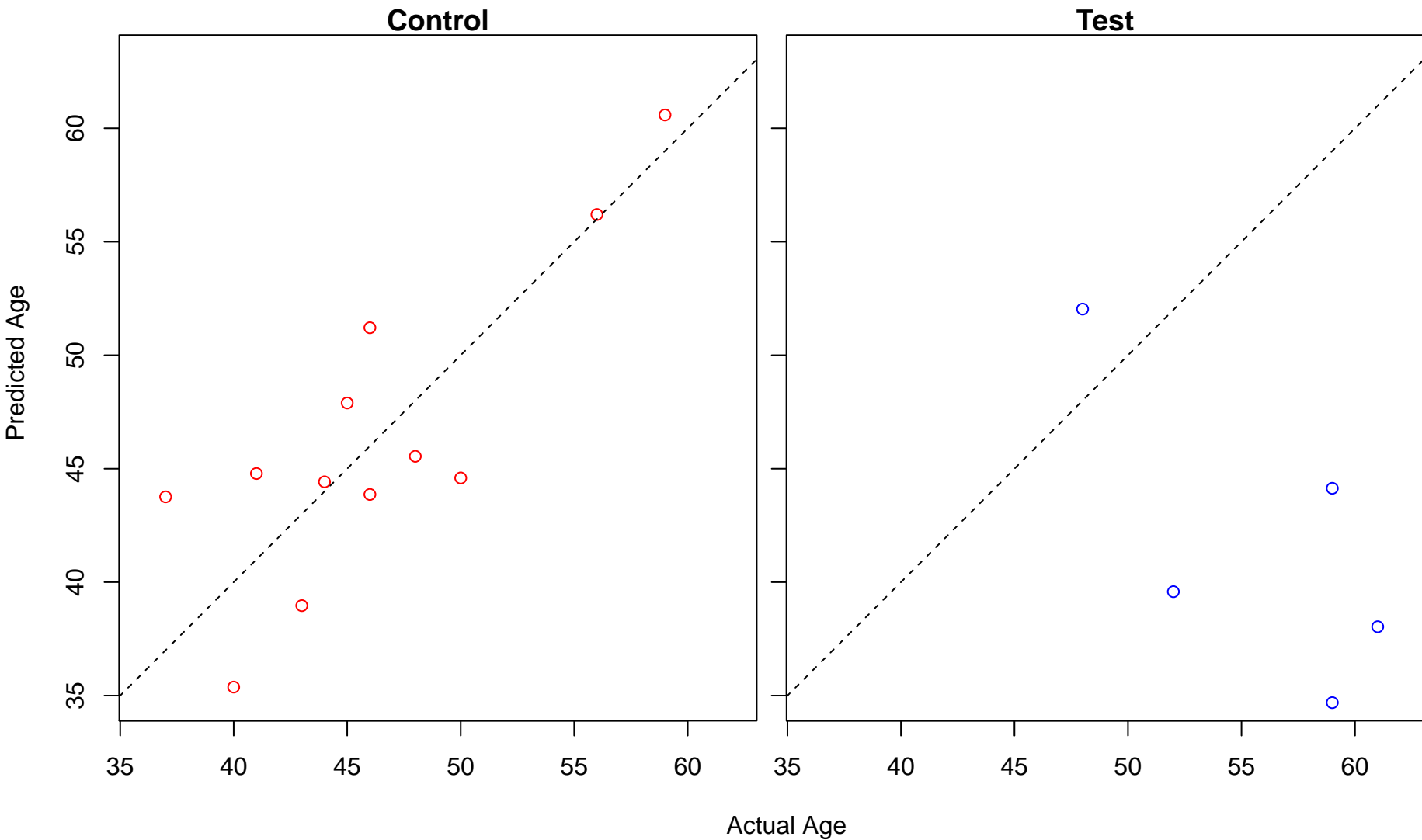
nephron development (Score: 17.758587)



negative regulation of peptidyl-serine phosphorylation (Score: 17.686271)

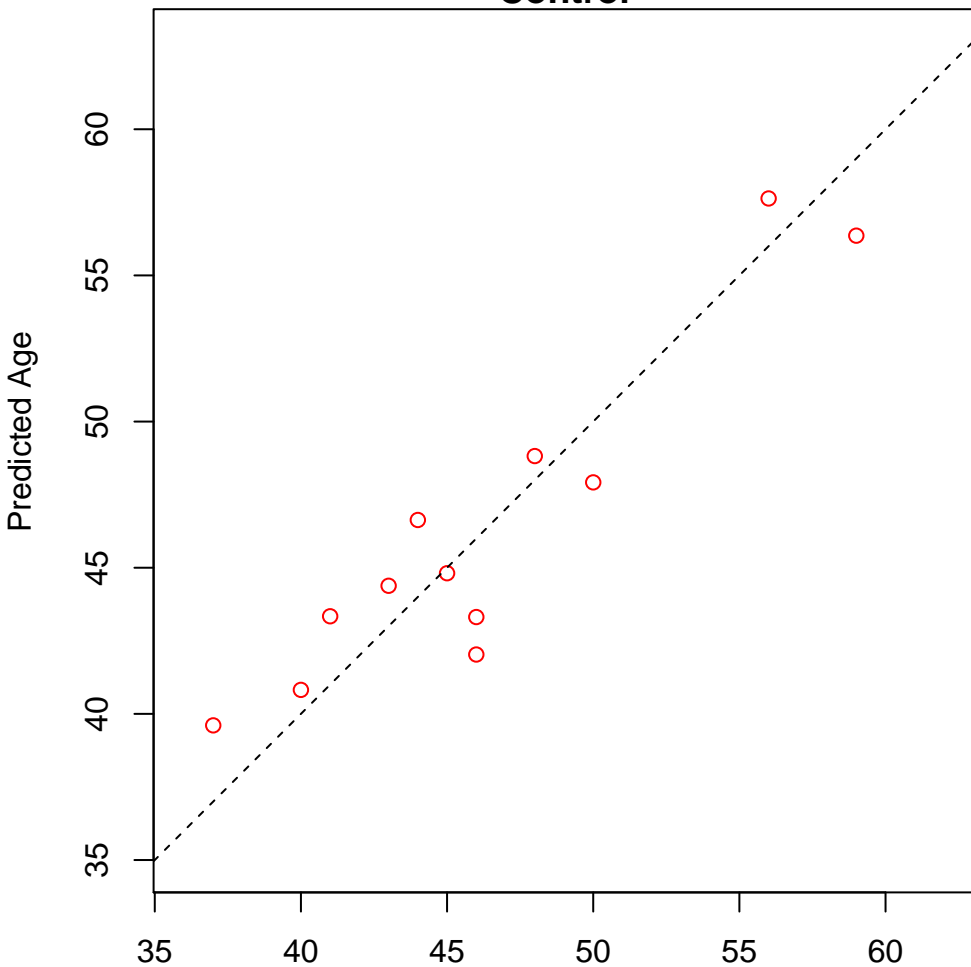


positive regulation of calcineurin–NFAT signaling cascade (Score: 17.665998)

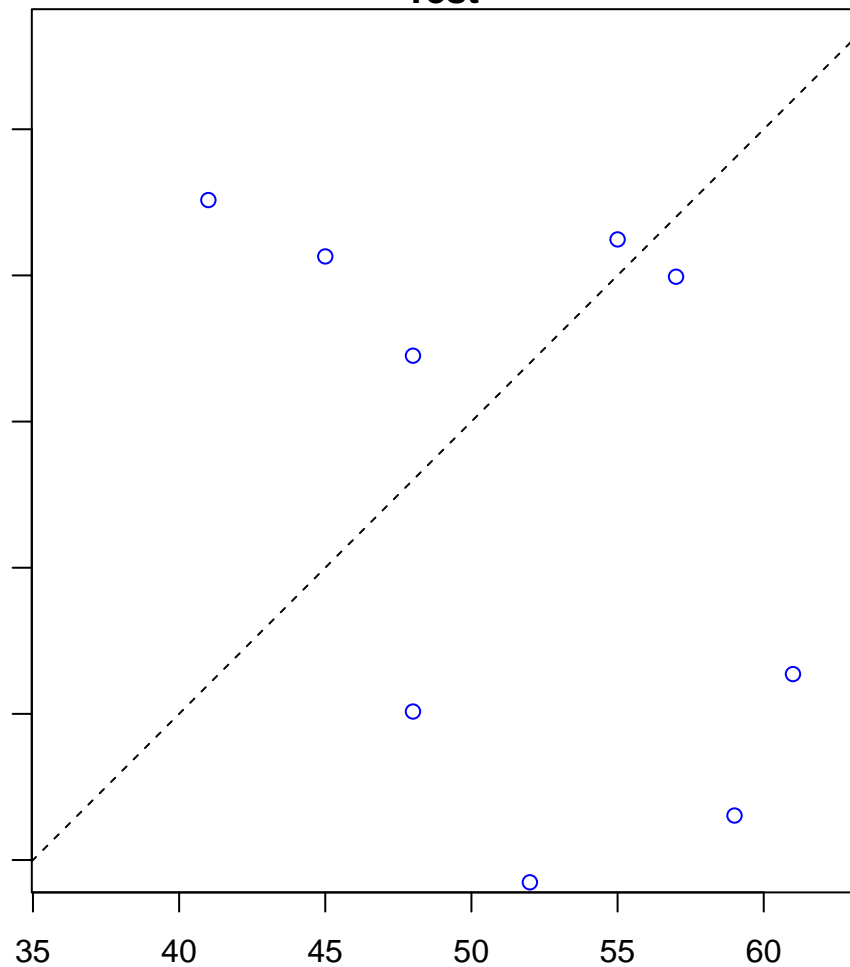


response to extracellular stimulus (Score: 17.660060)

Control



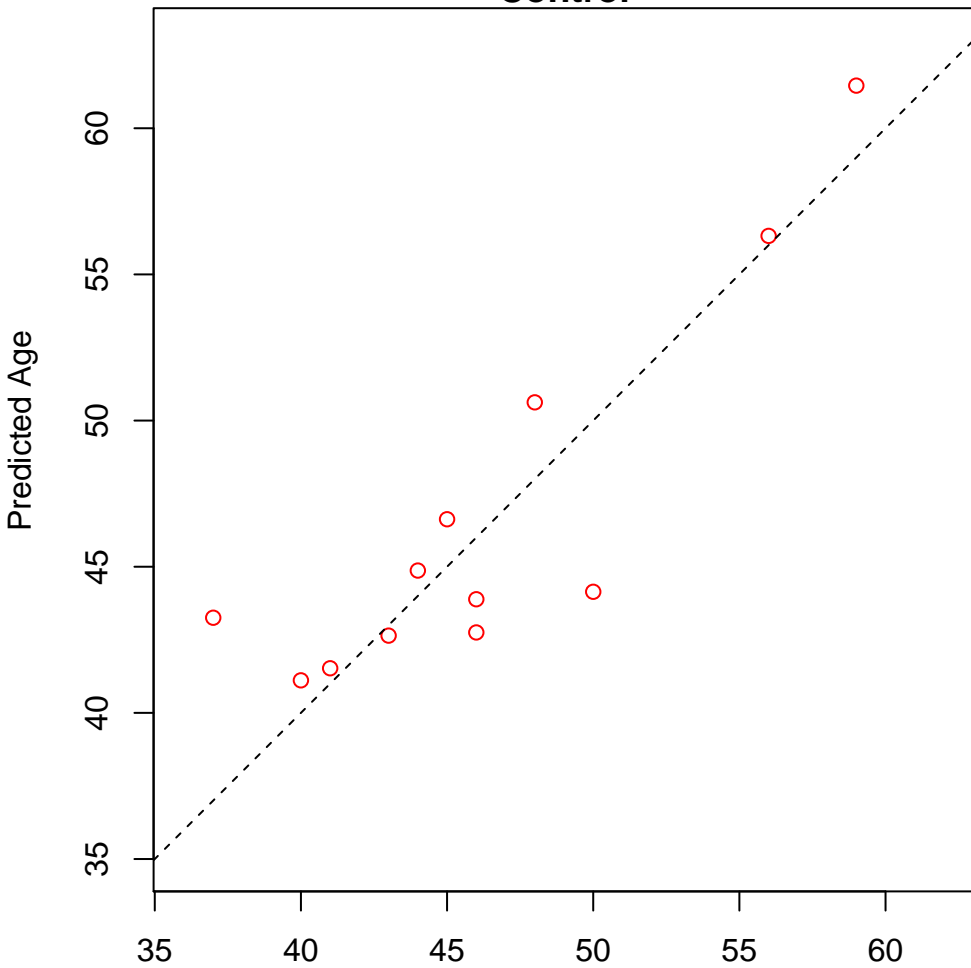
Test



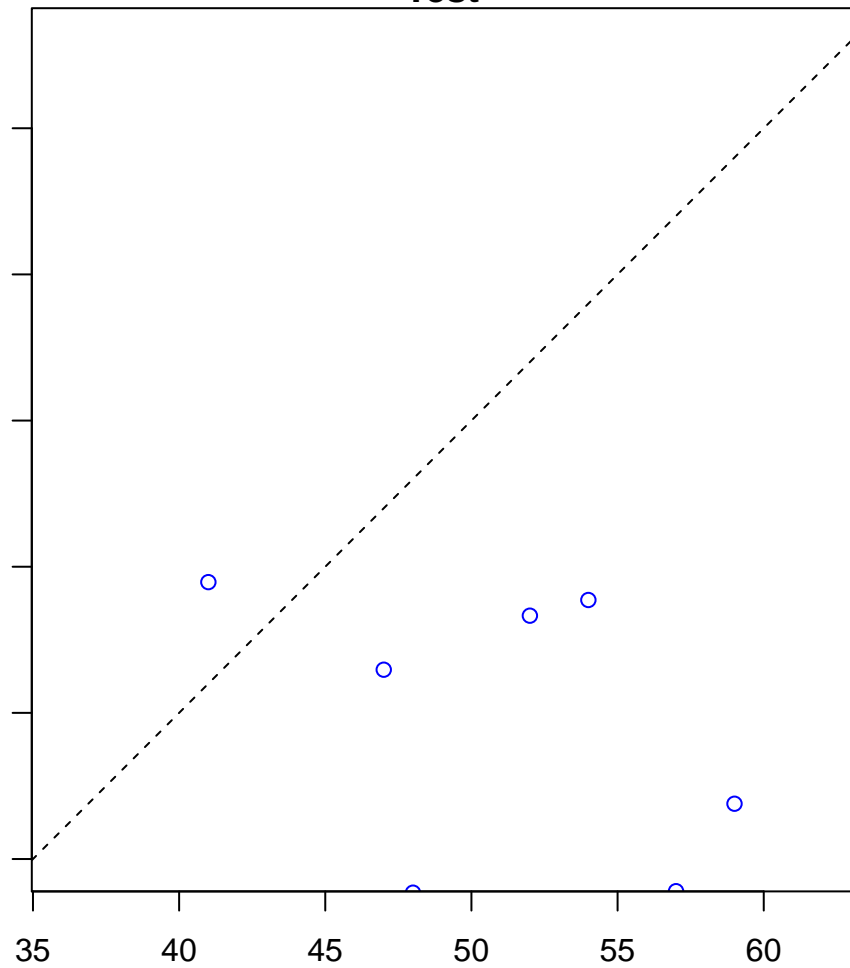
Actual Age

histone mRNA catabolic process (Score: 17.656836)

Control

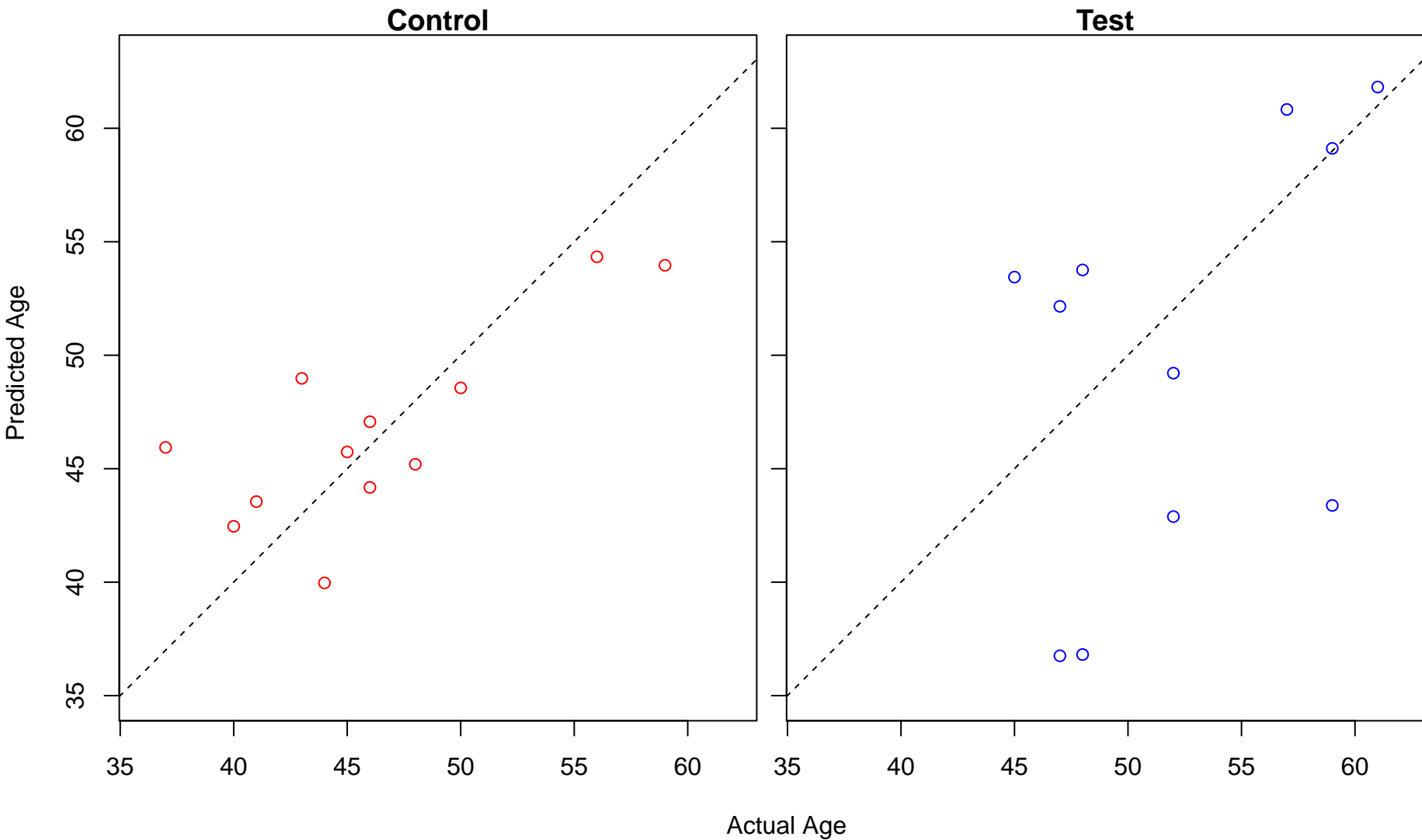


Test



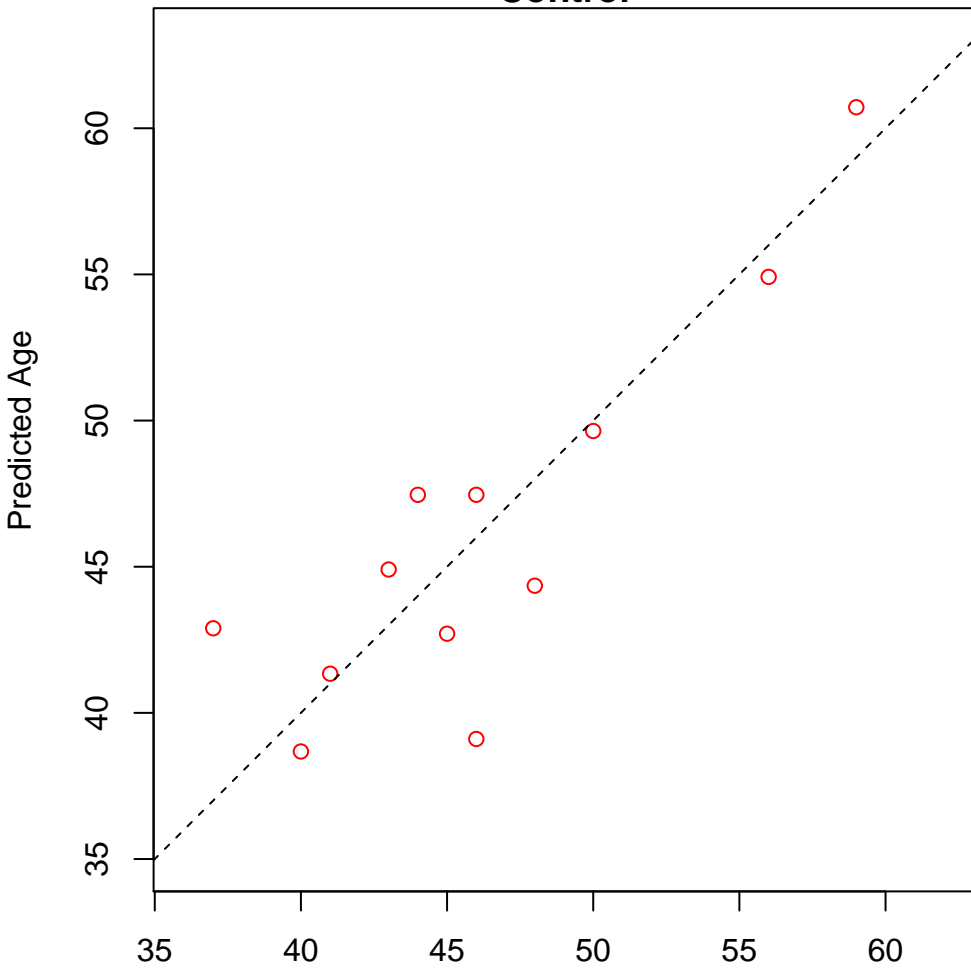
Actual Age

regulation of cytokine biosynthetic process (Score: 17.627436)

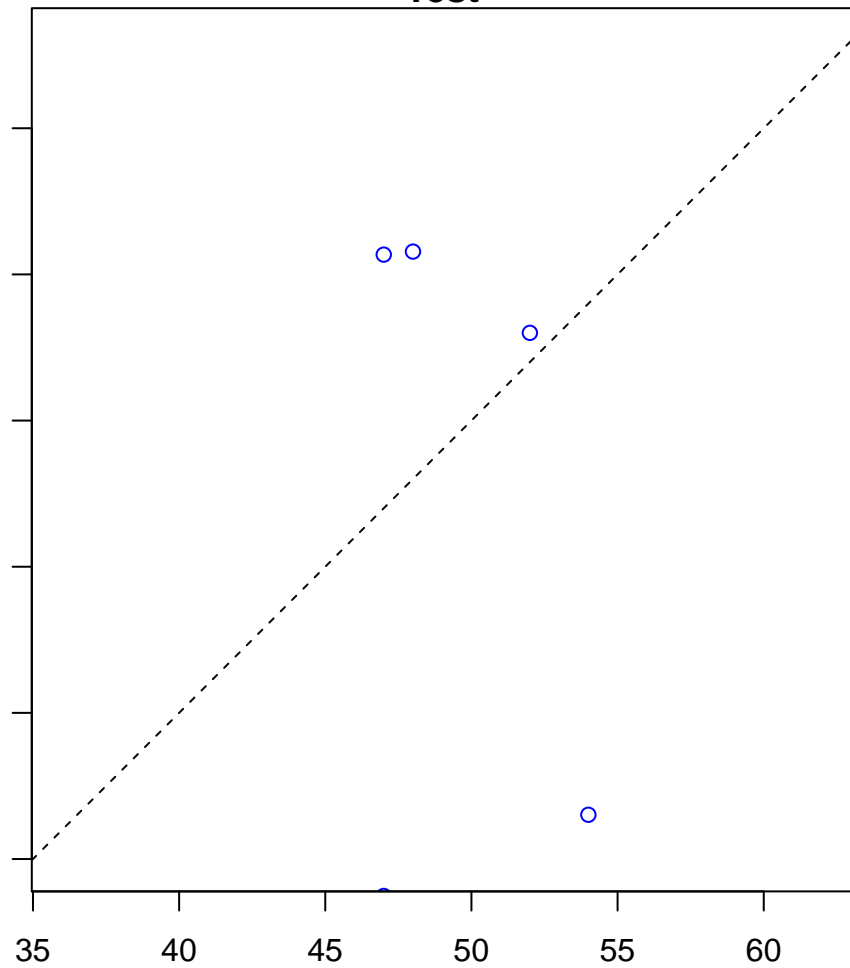


regulation of trophoblast cell migration (Score: 17.609542)

Control

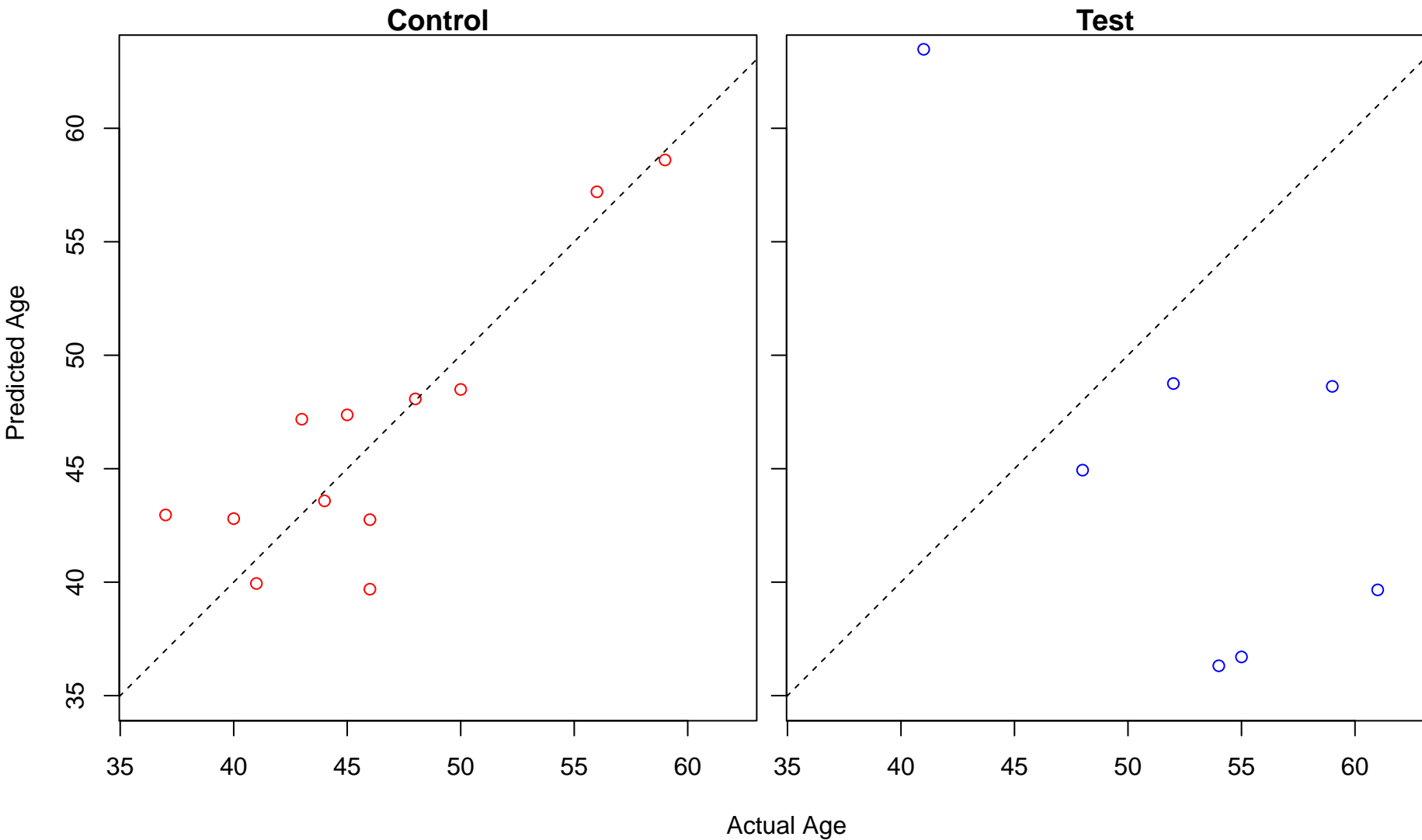


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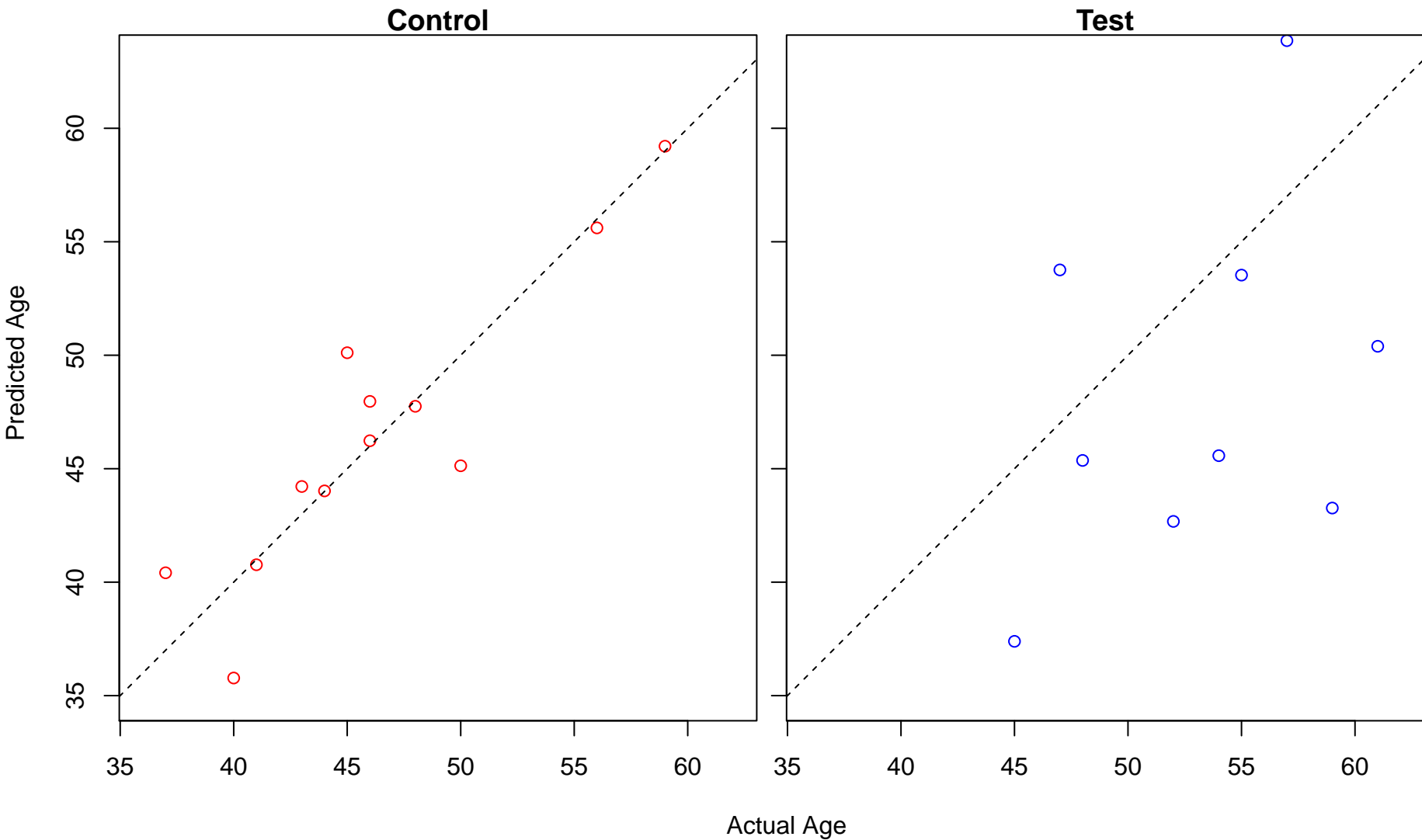


Actual Age

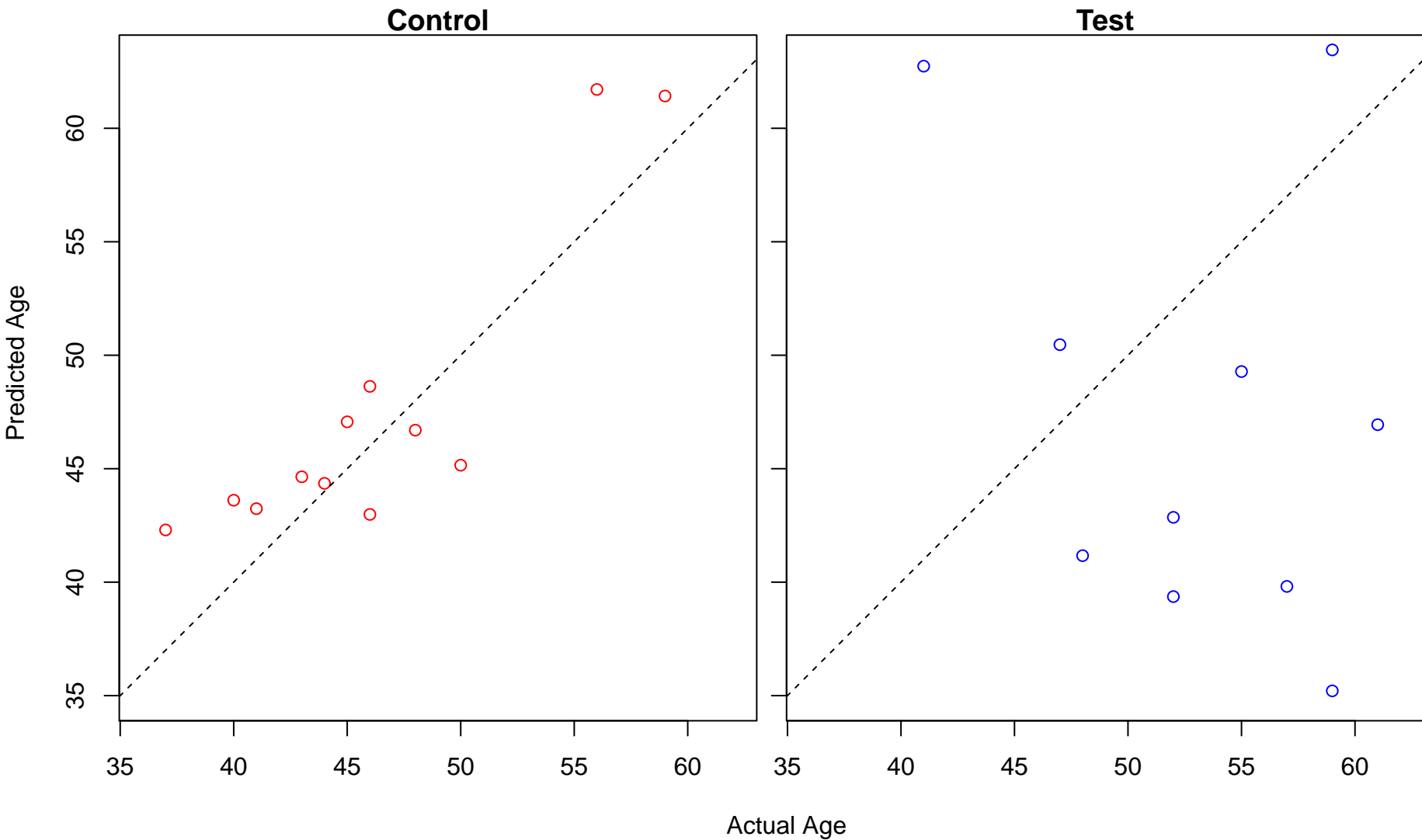
epithelial cell development (Score: 17.580807)



glomerulus development (Score: 17.489627)

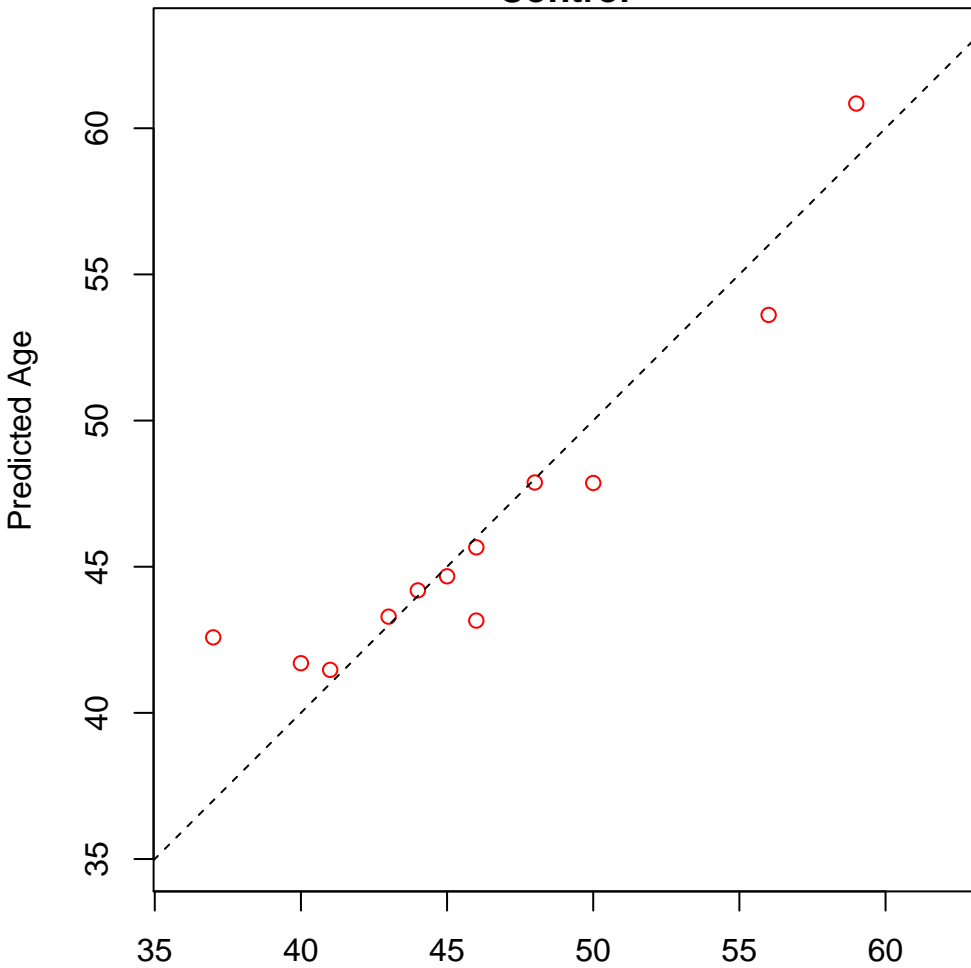


transforming growth factor beta receptor signaling pathway (Score: 17.472518)

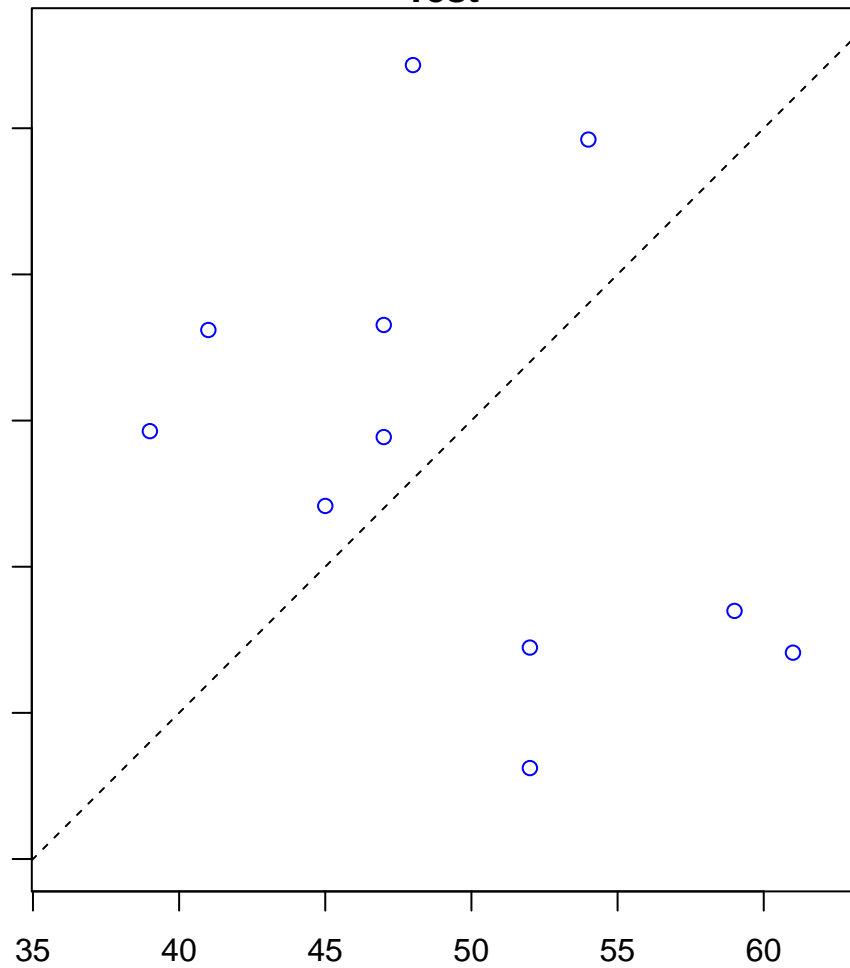


divalent inorganic cation homeostasis (Score: 17.470337)

Control

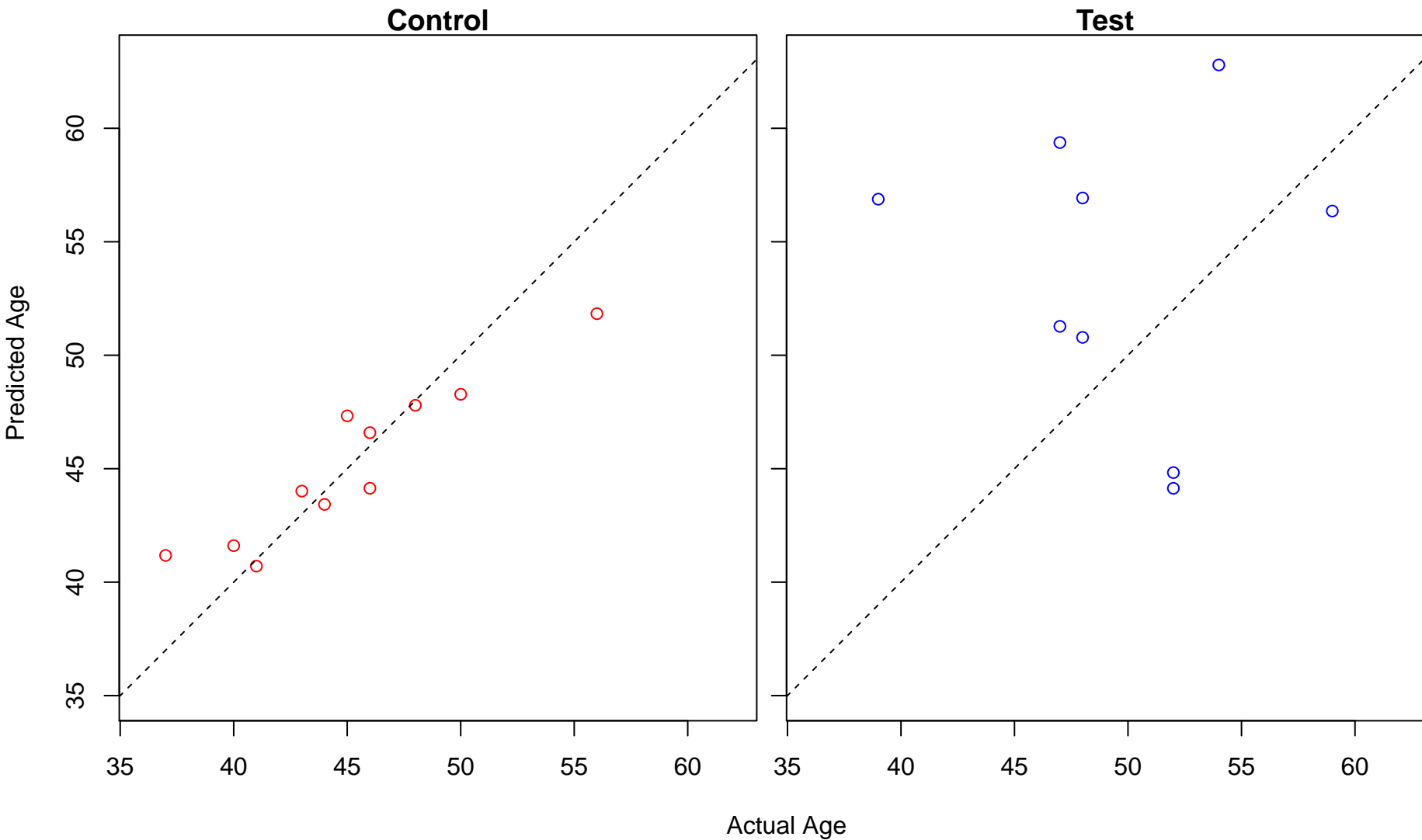


Test

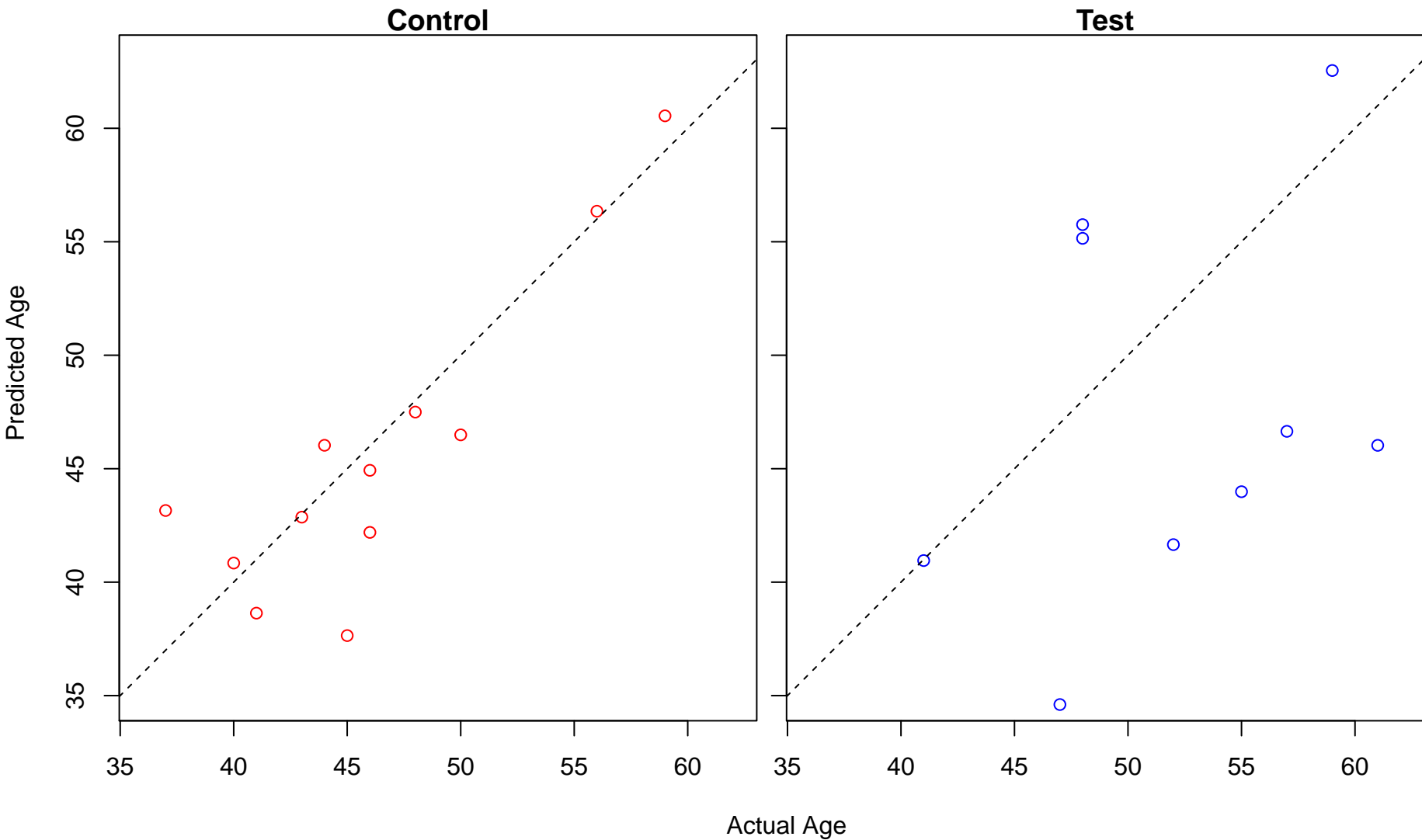


Actual Age

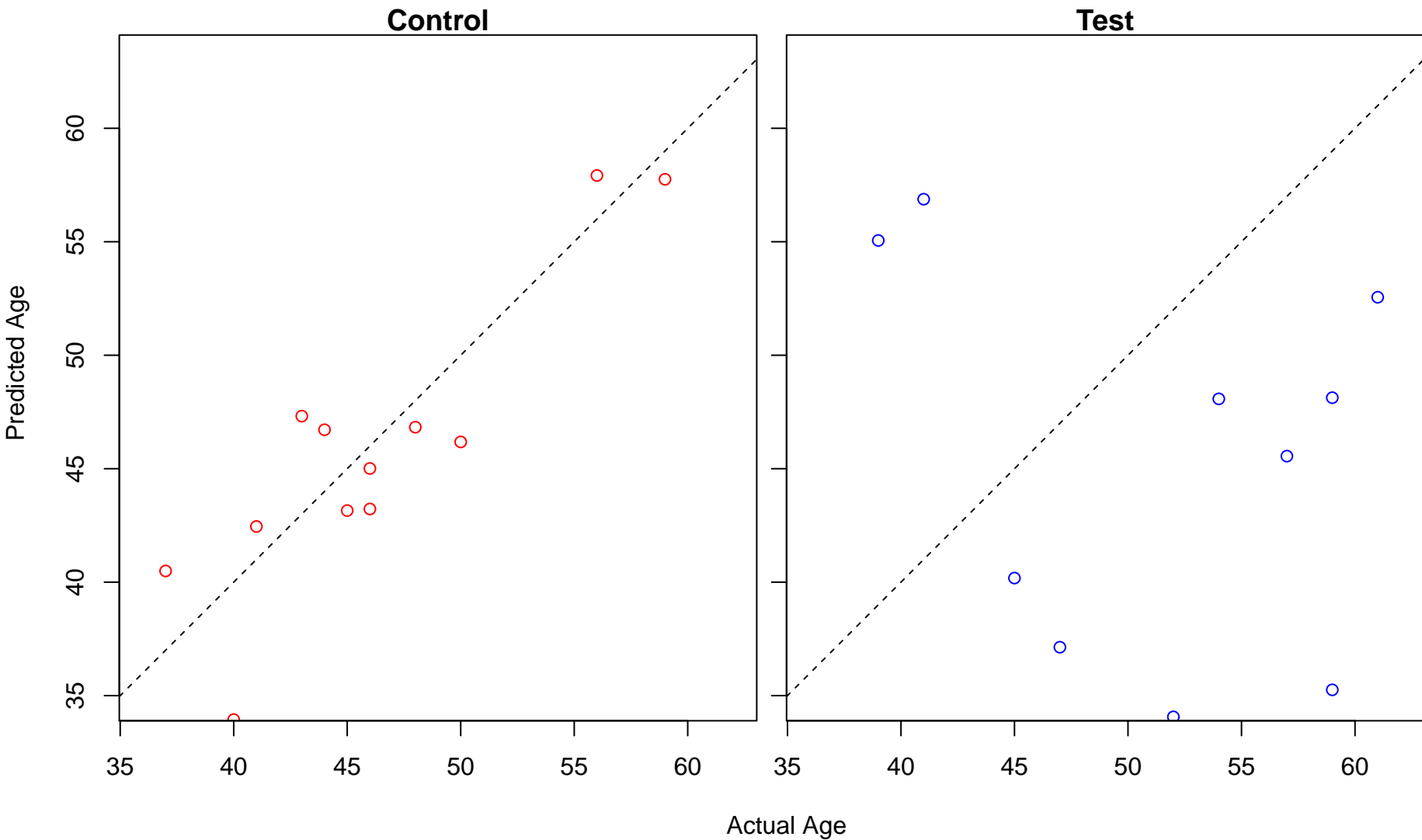
regulation of extrinsic apoptotic signaling pathway (Score: 17.452349)



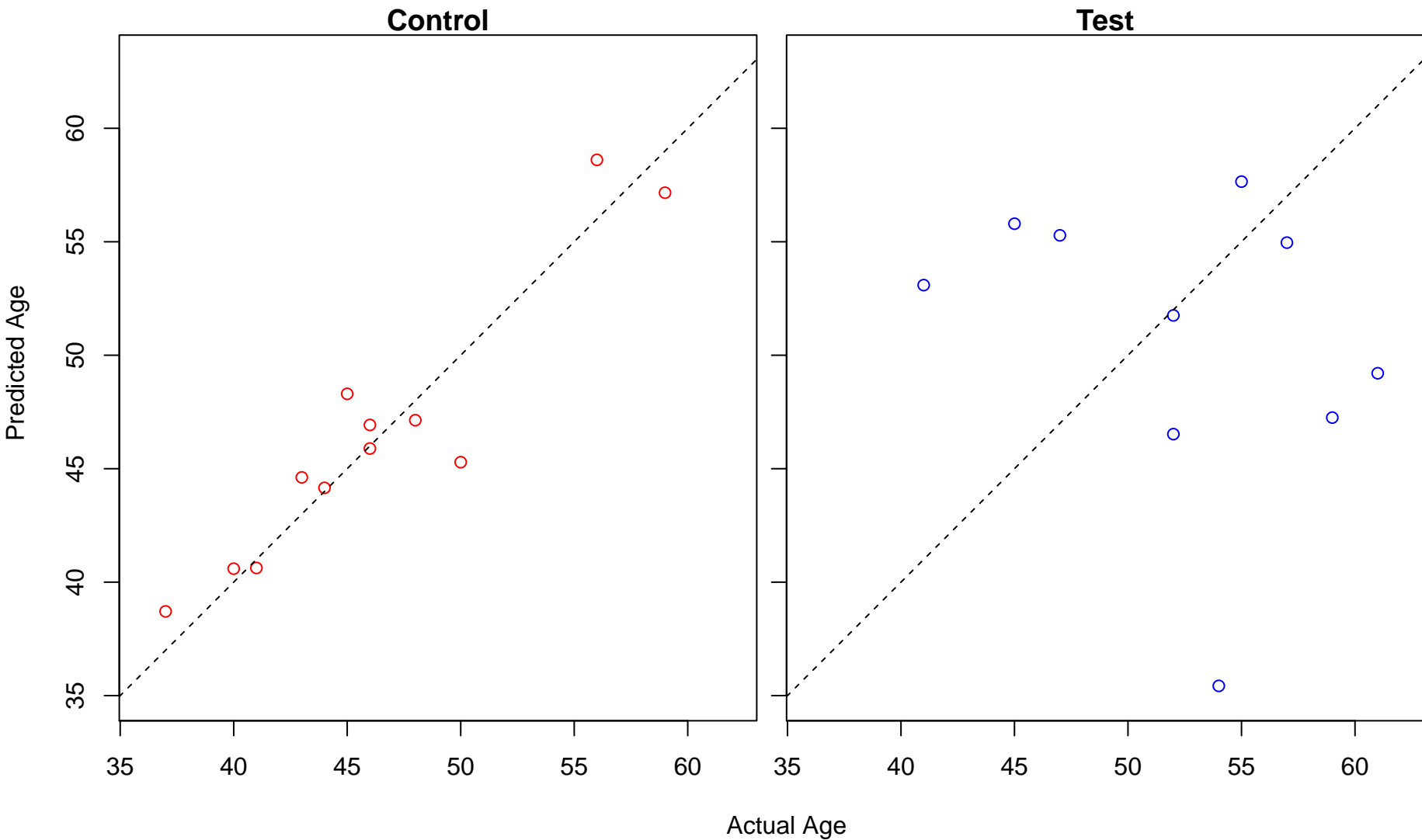
negative chemotaxis (Score: 17.289659)



negative regulation of NF-kappaB transcription factor activity (Score: 17.285115)

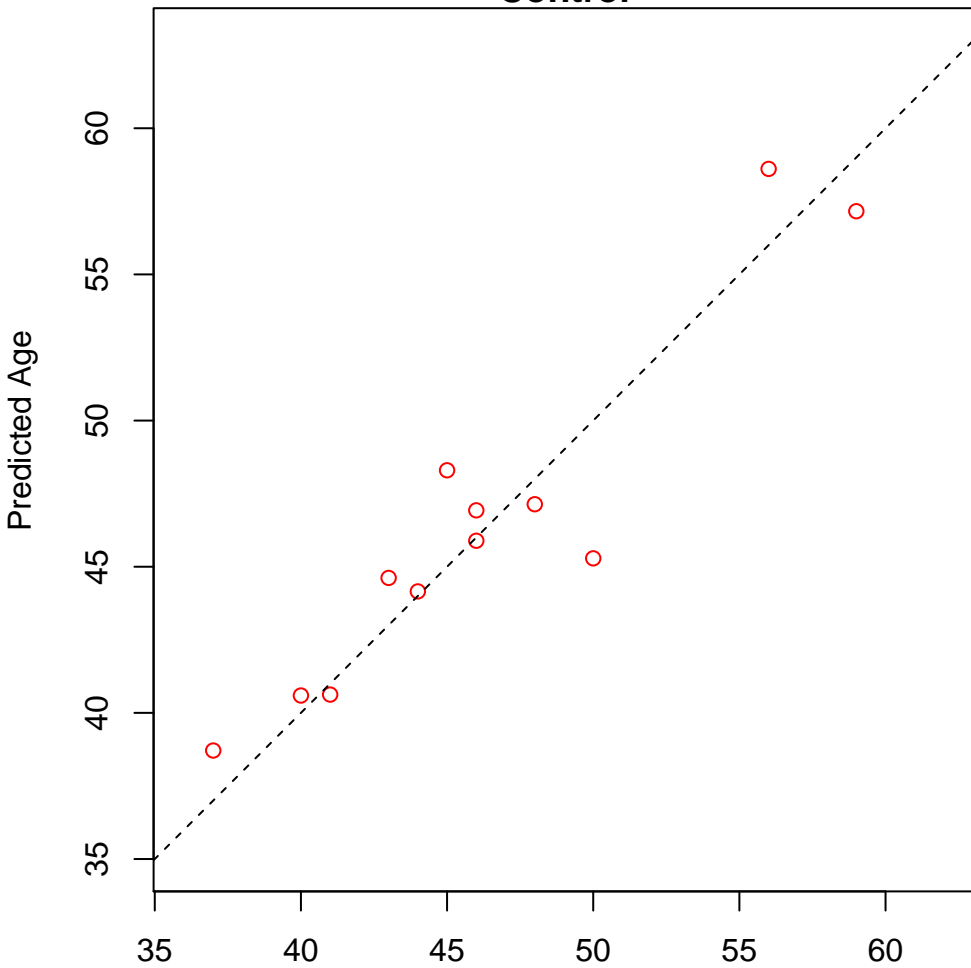


type I interferon signaling pathway (Score: 17.262169)

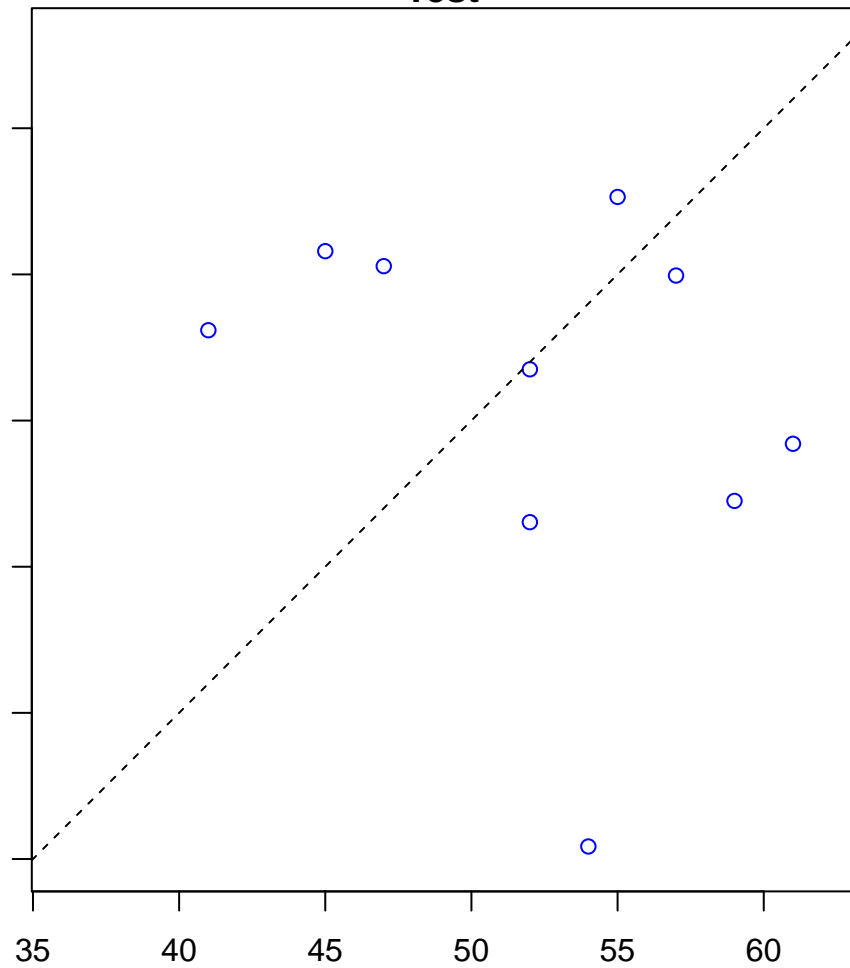


cellular response to type I interferon (Score: 17.262169)

Control

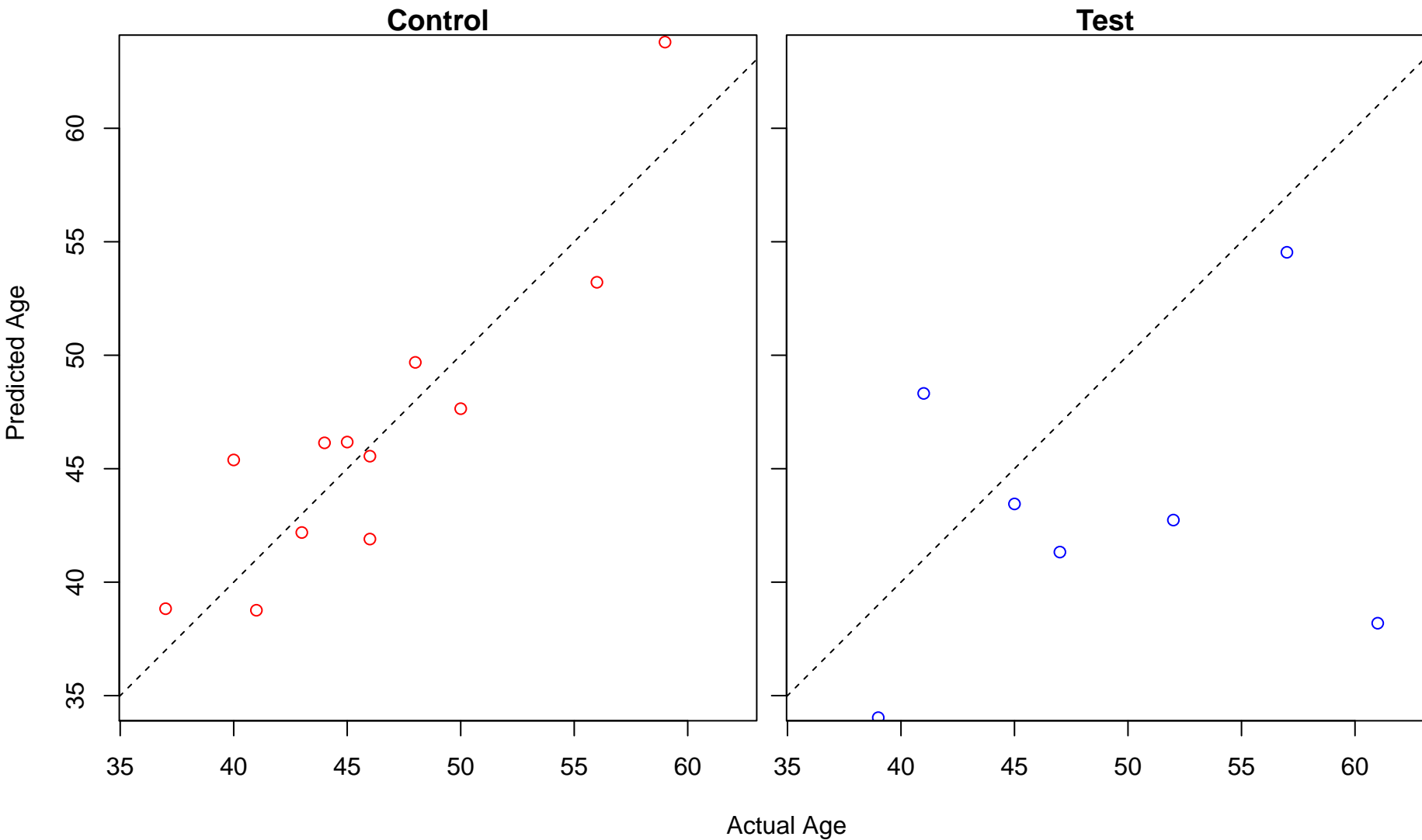


Test

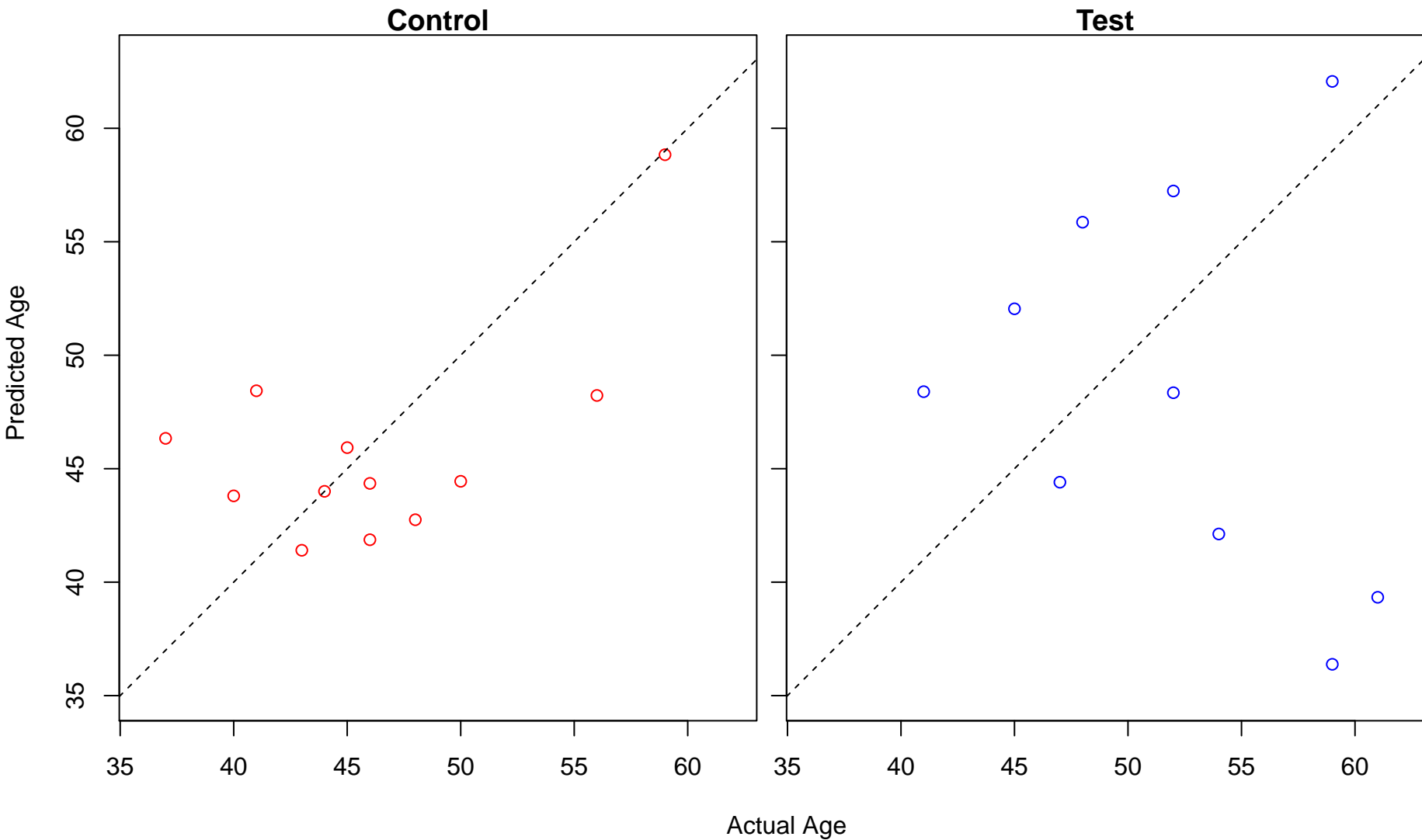


Actual Age

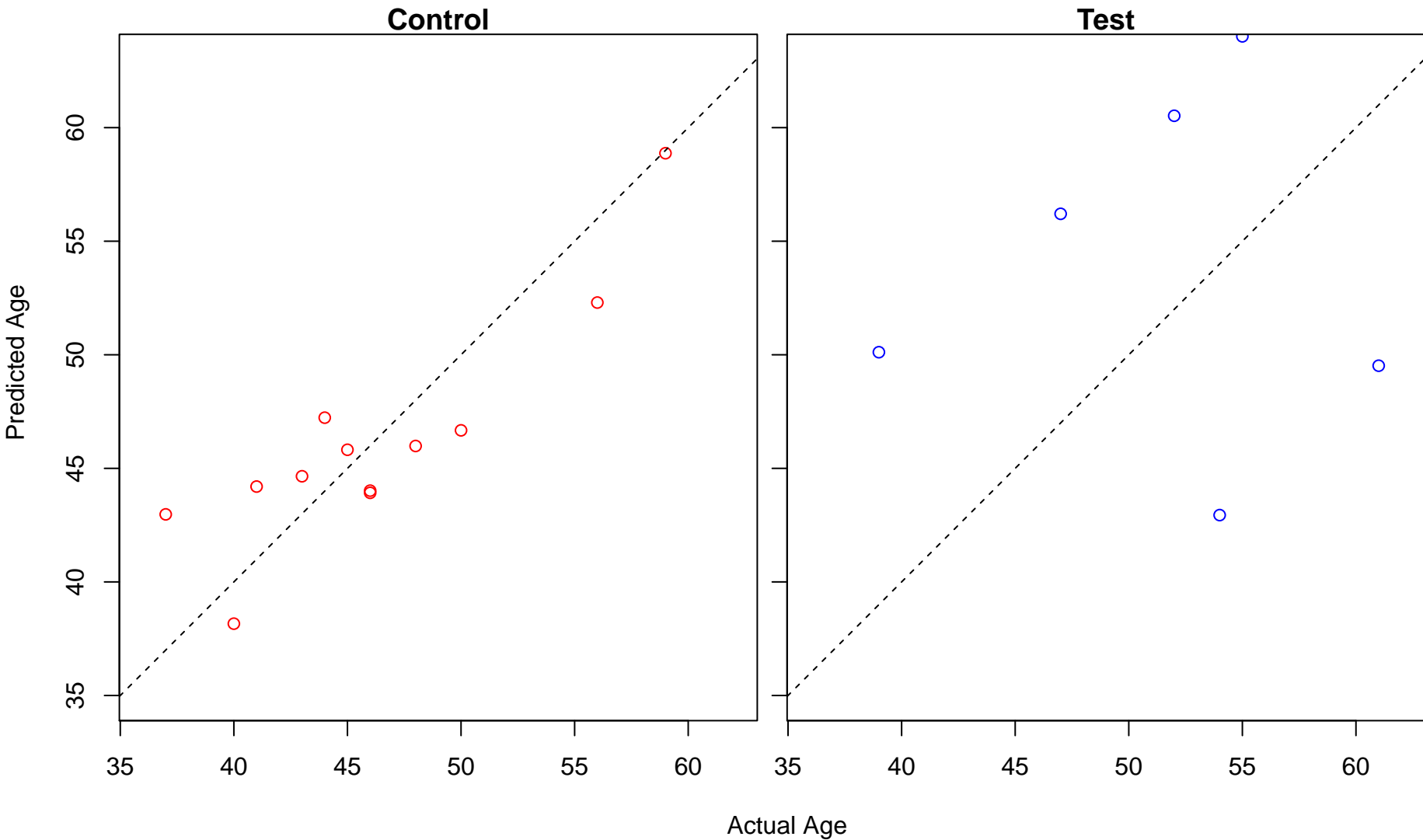
regulation of branching involved in ureteric bud morphogenesis (Score: 17.253517)



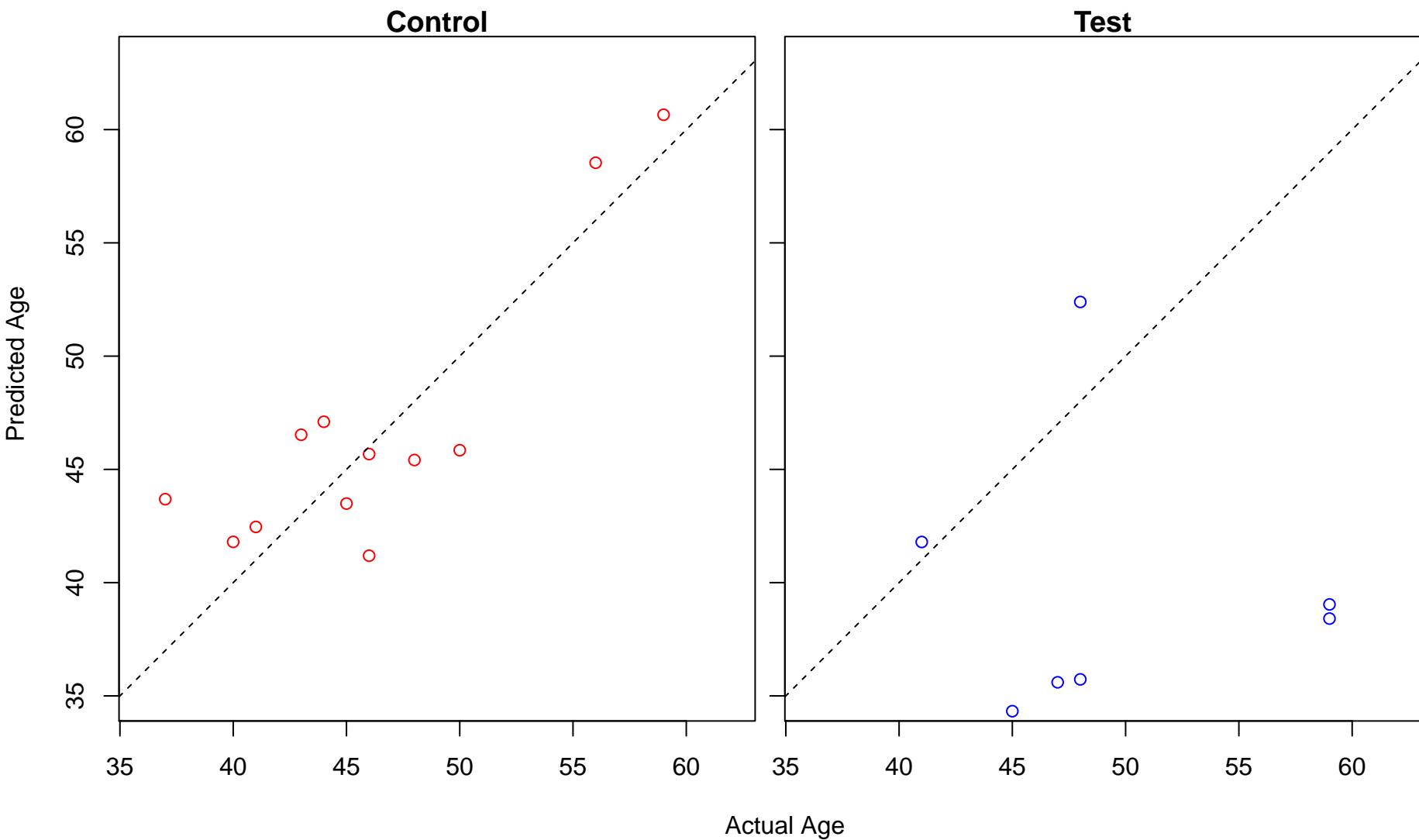
leukocyte migration involved in inflammatory response (Score: 17.194198)



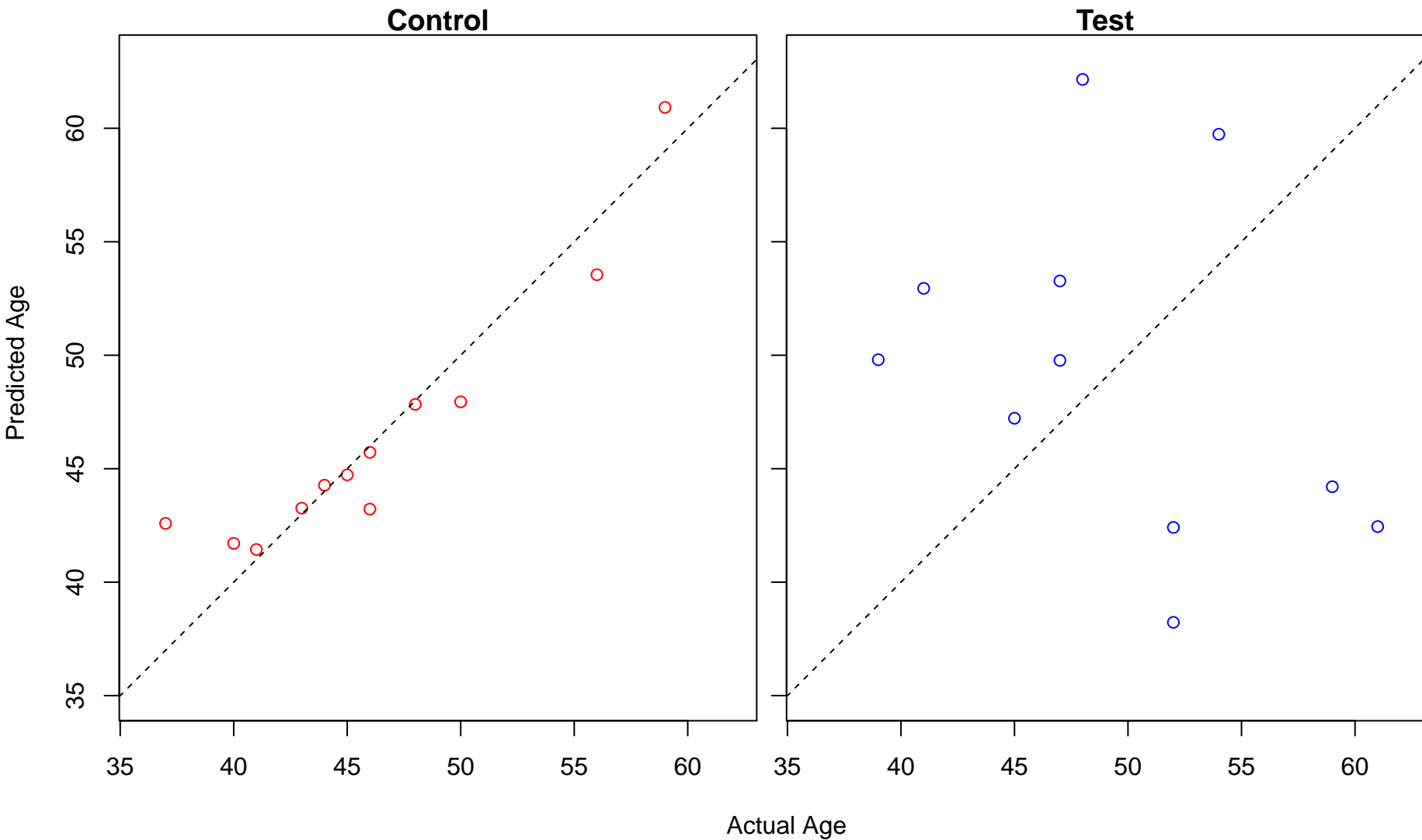
regulation of nephron tubule epithelial cell differentiation (Score: 17.171719)



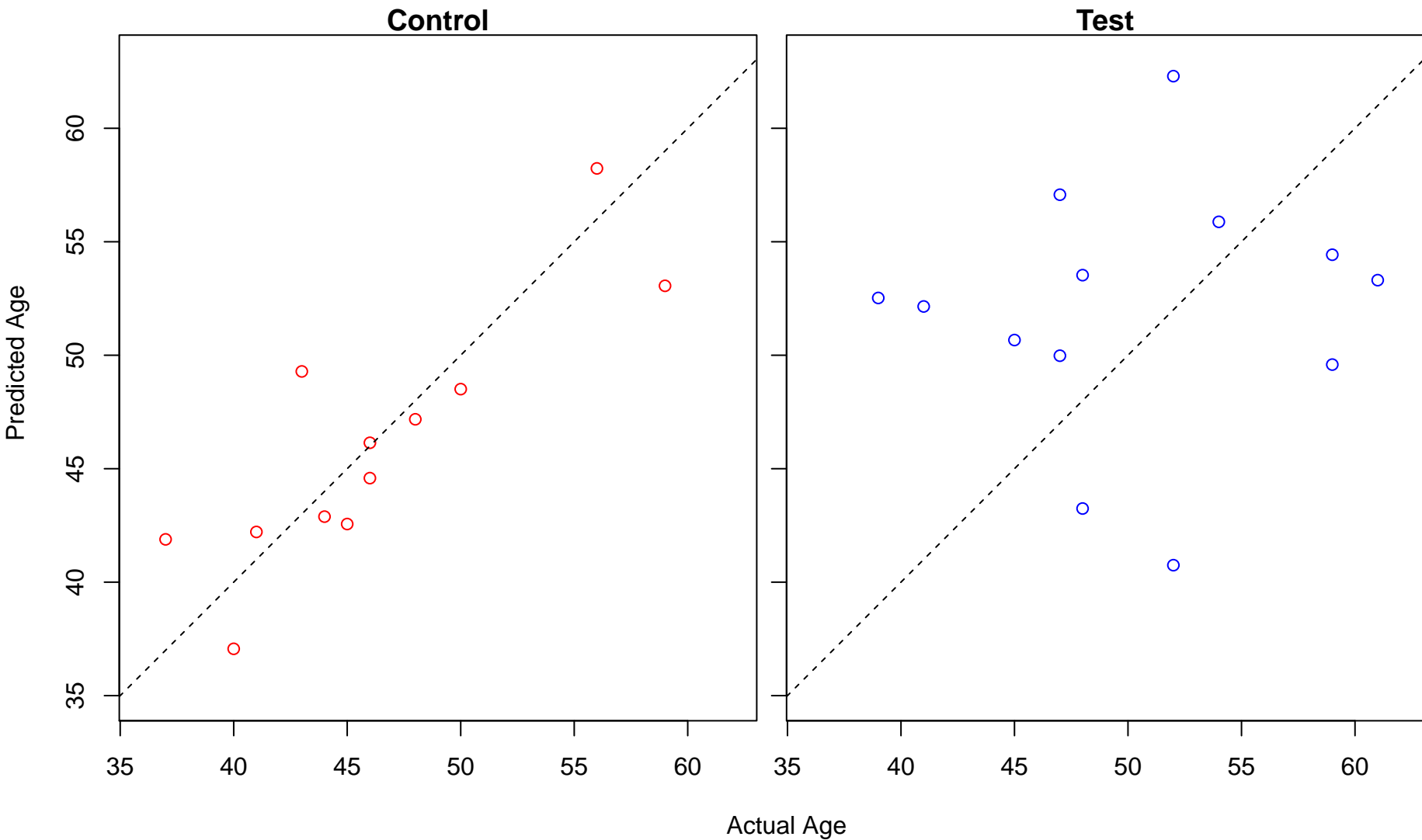
regulation of cytoskeleton organization (Score: 17.119422)



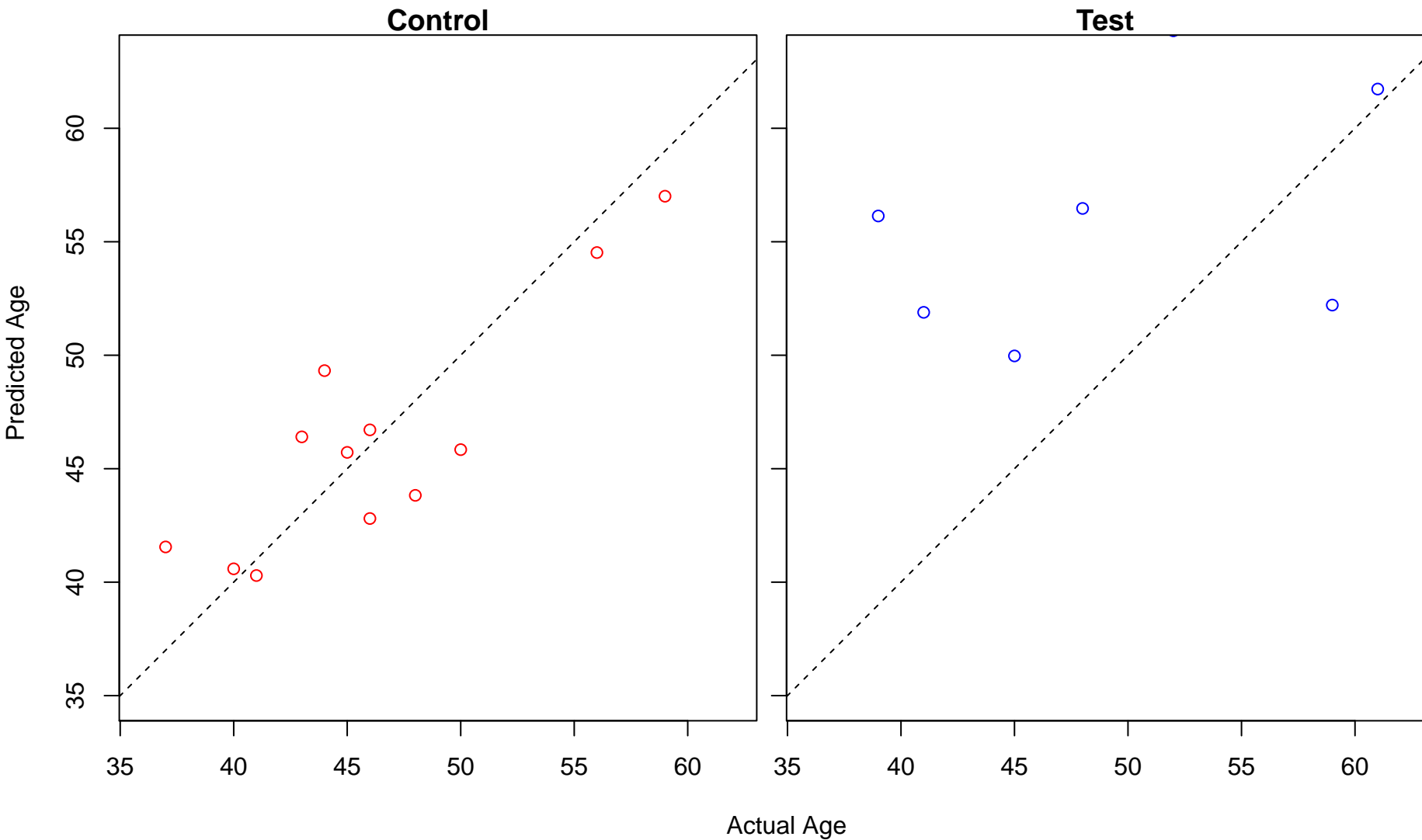
cellular divalent inorganic cation homeostasis (Score: 17.095728)



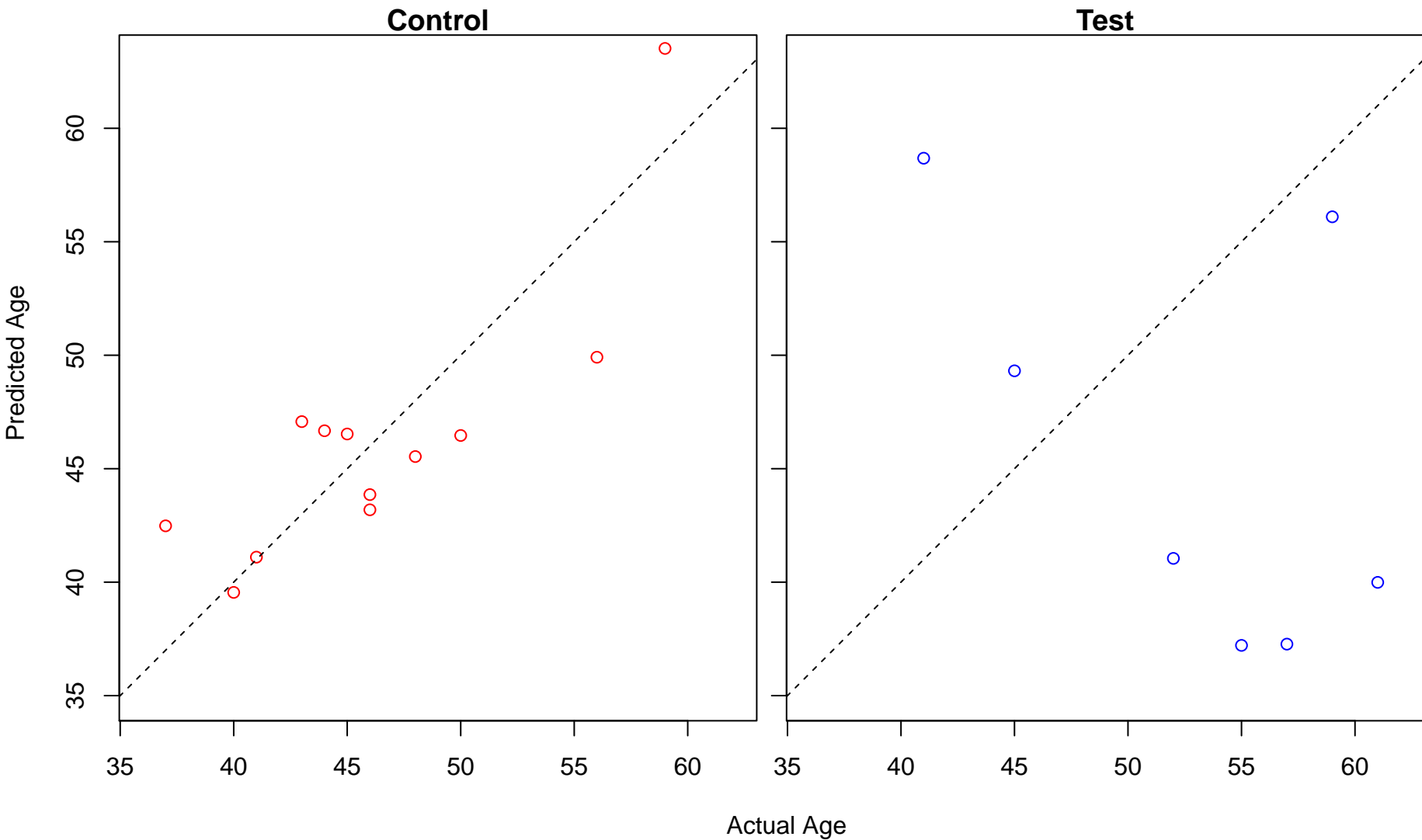
regulation of cholesterol efflux (Score: 17.076106)



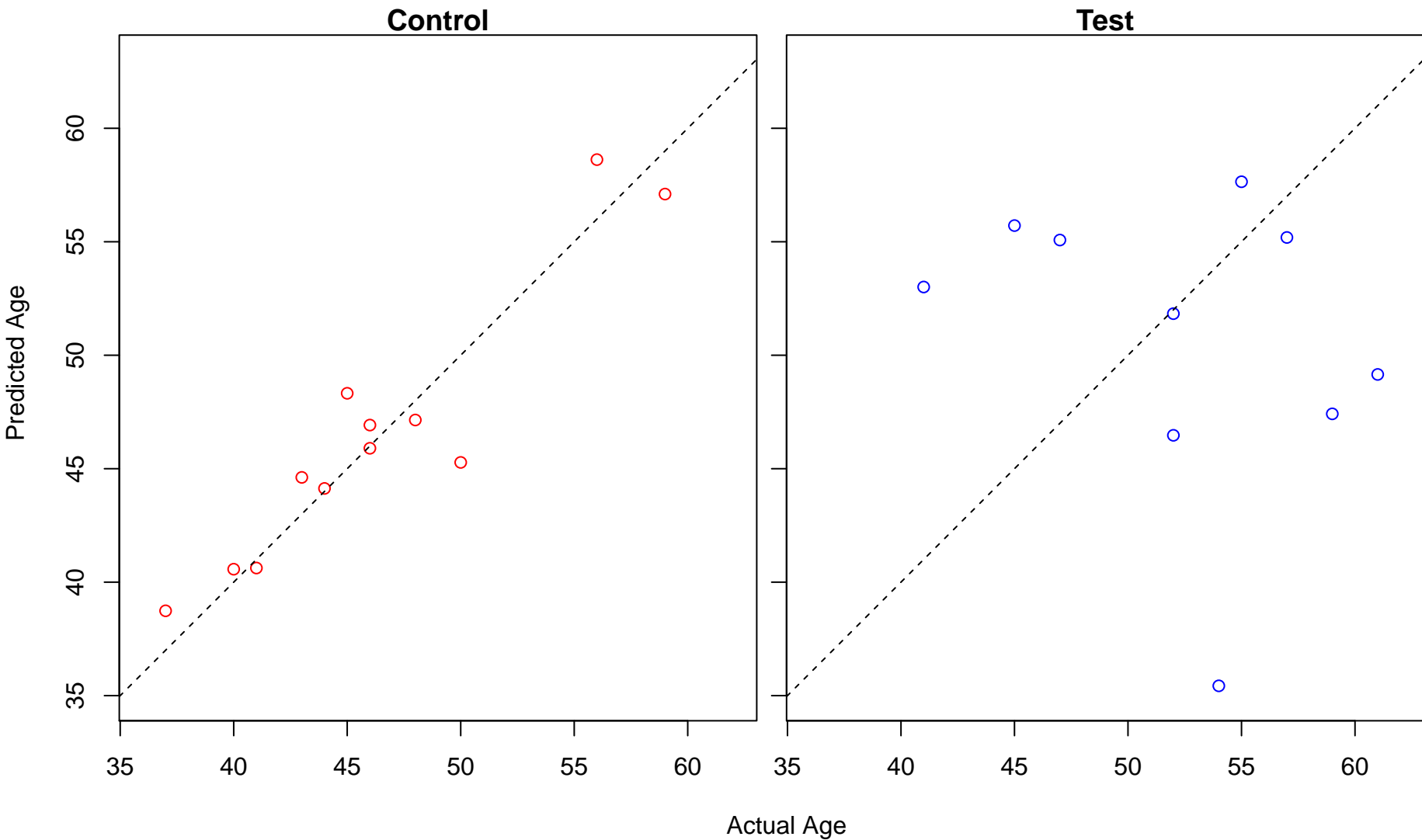
positive regulation of interleukin-4 production (Score: 16.982312)



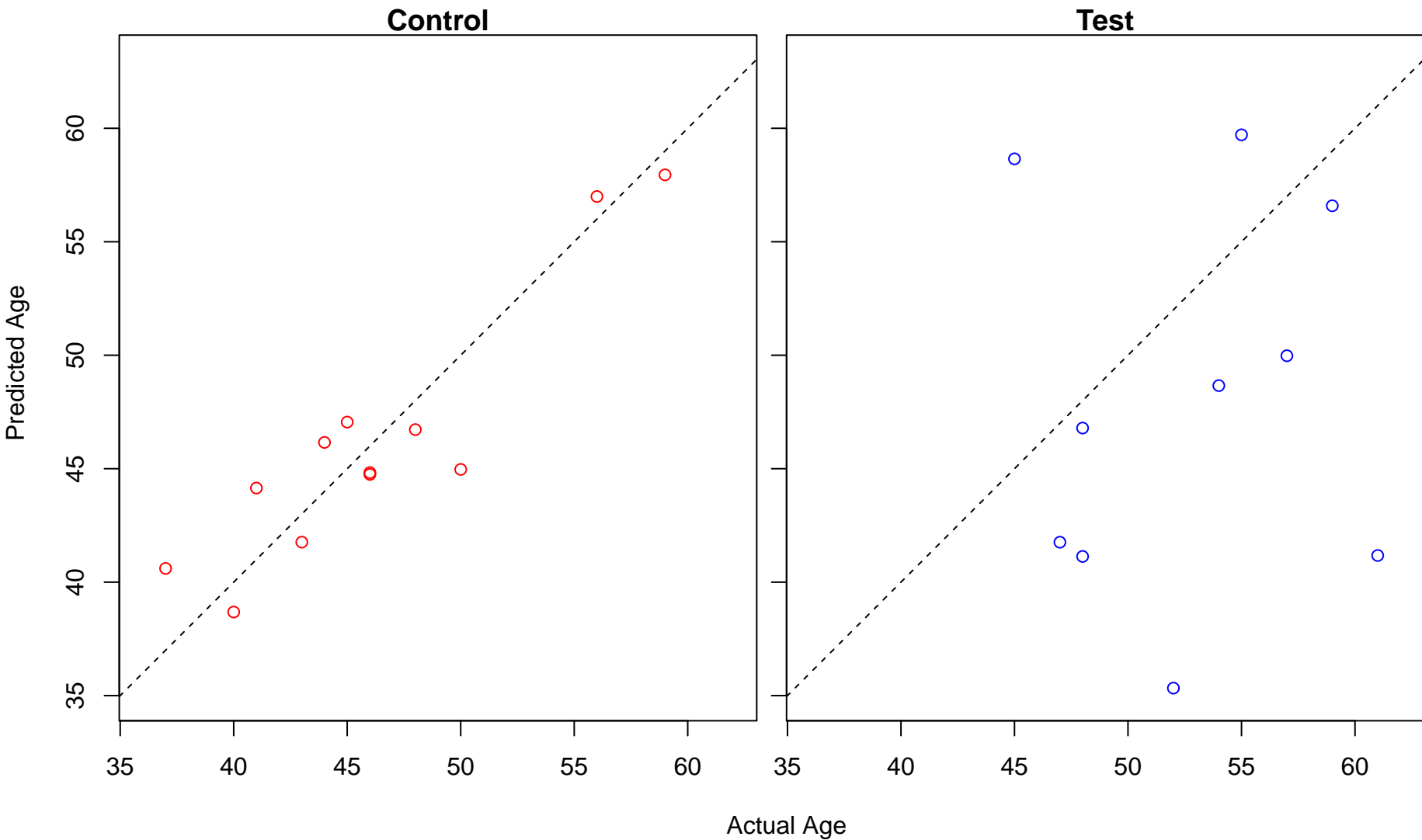
regulation of protein acetylation (Score: 16.972899)



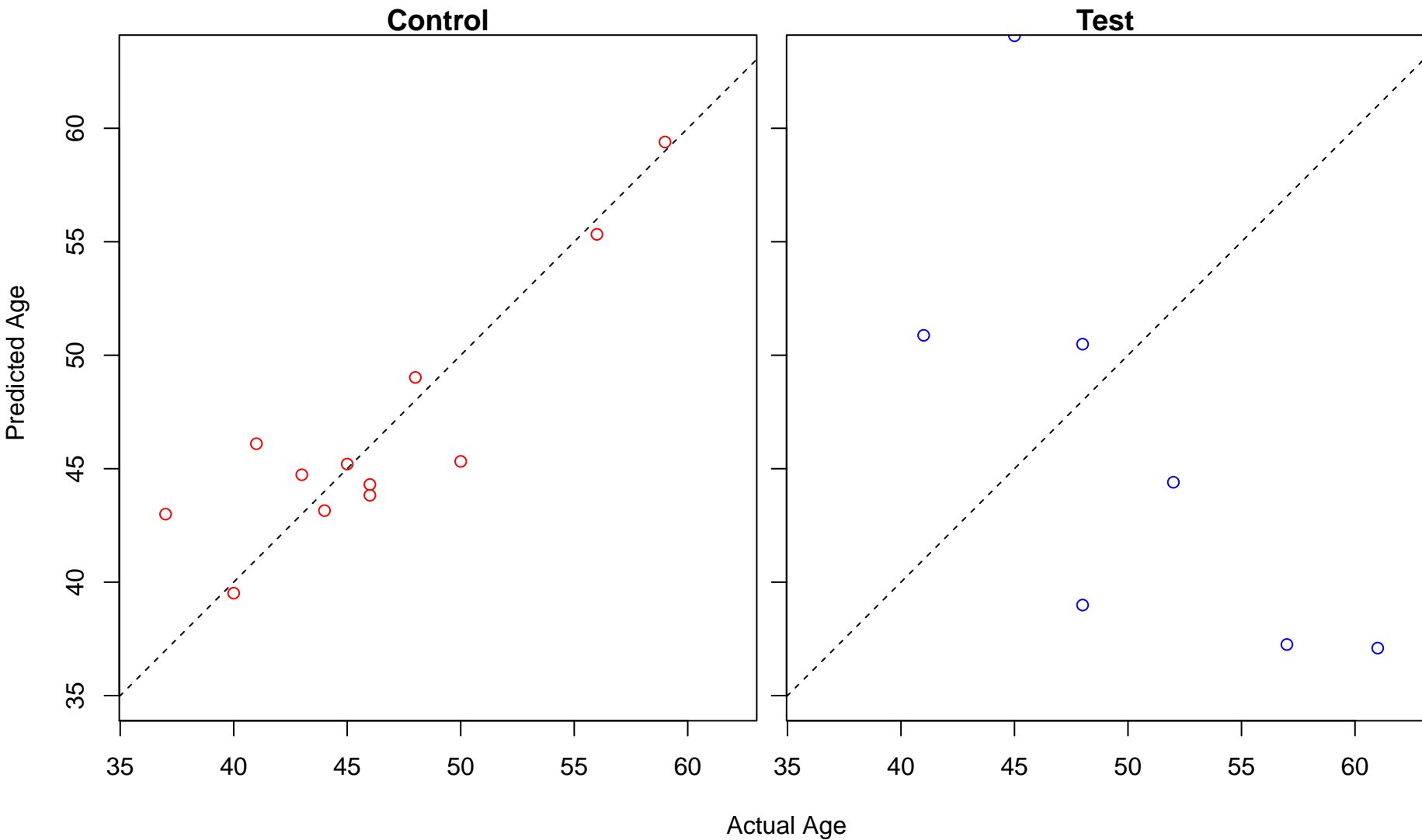
response to type I interferon (Score: 16.950565)



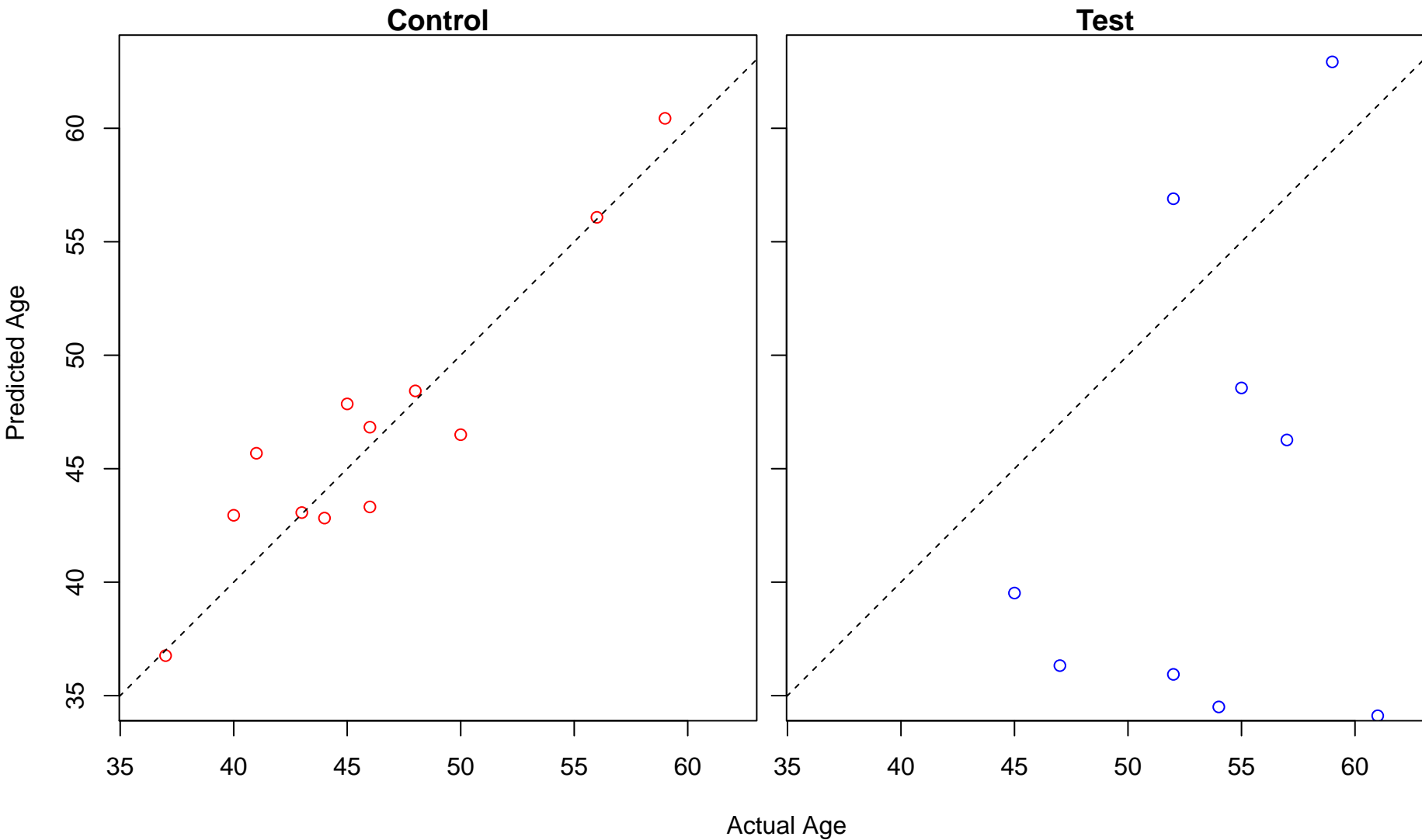
anion transmembrane transport (Score: 16.949186)



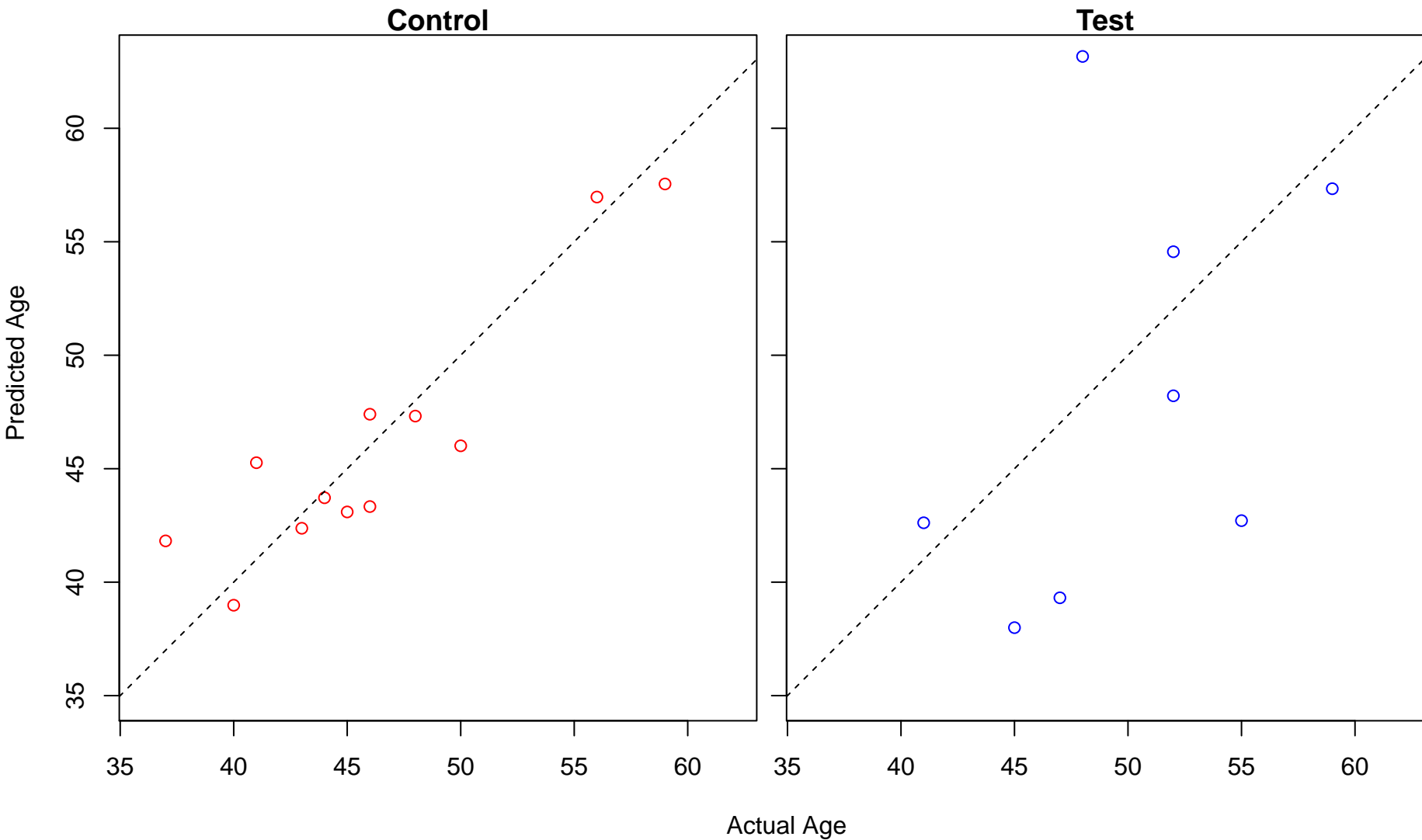
negative regulation of G2/M transition of mitotic cell cycle (Score: 16.829126)



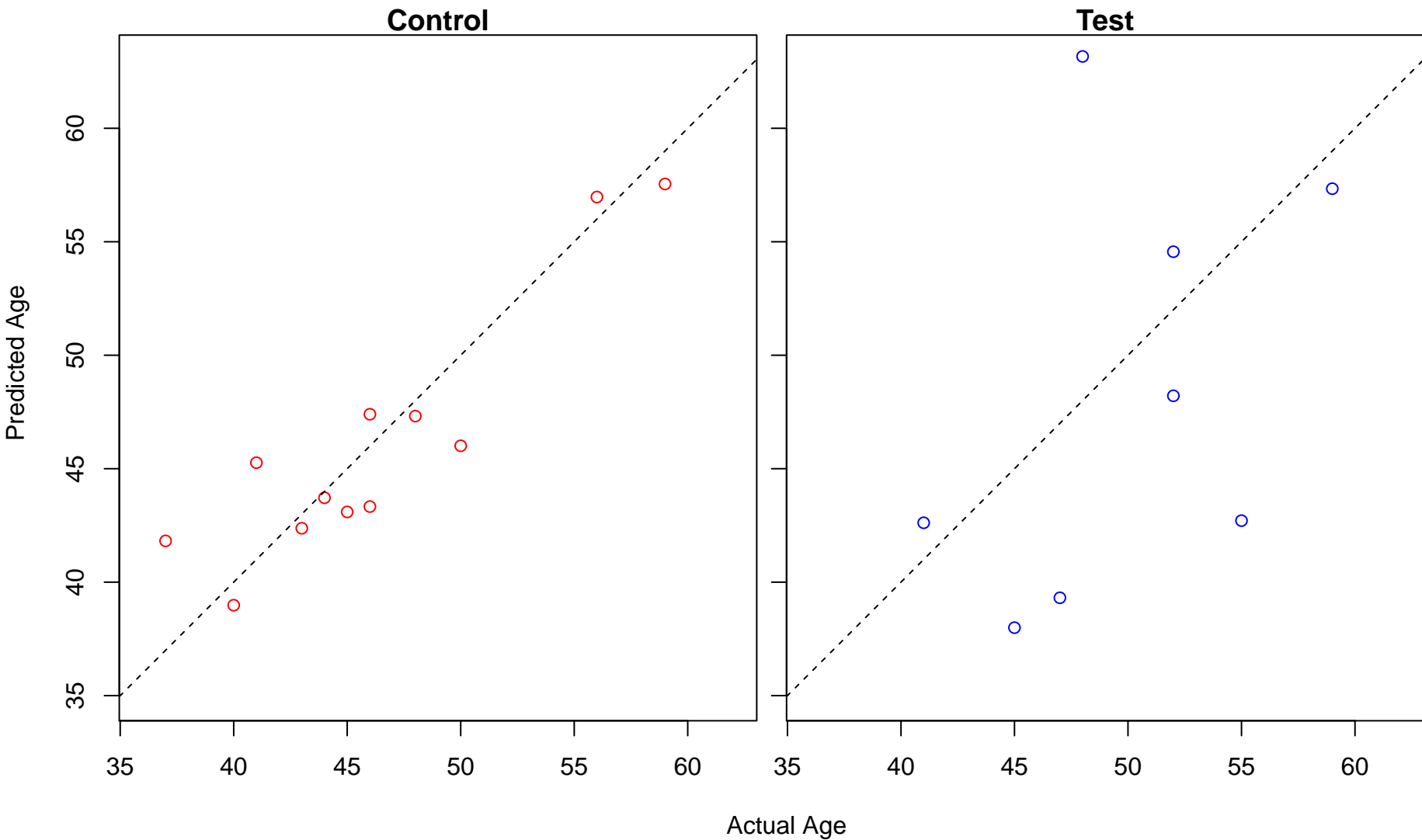
regulation of Rho protein signal transduction (Score: 16.807759)



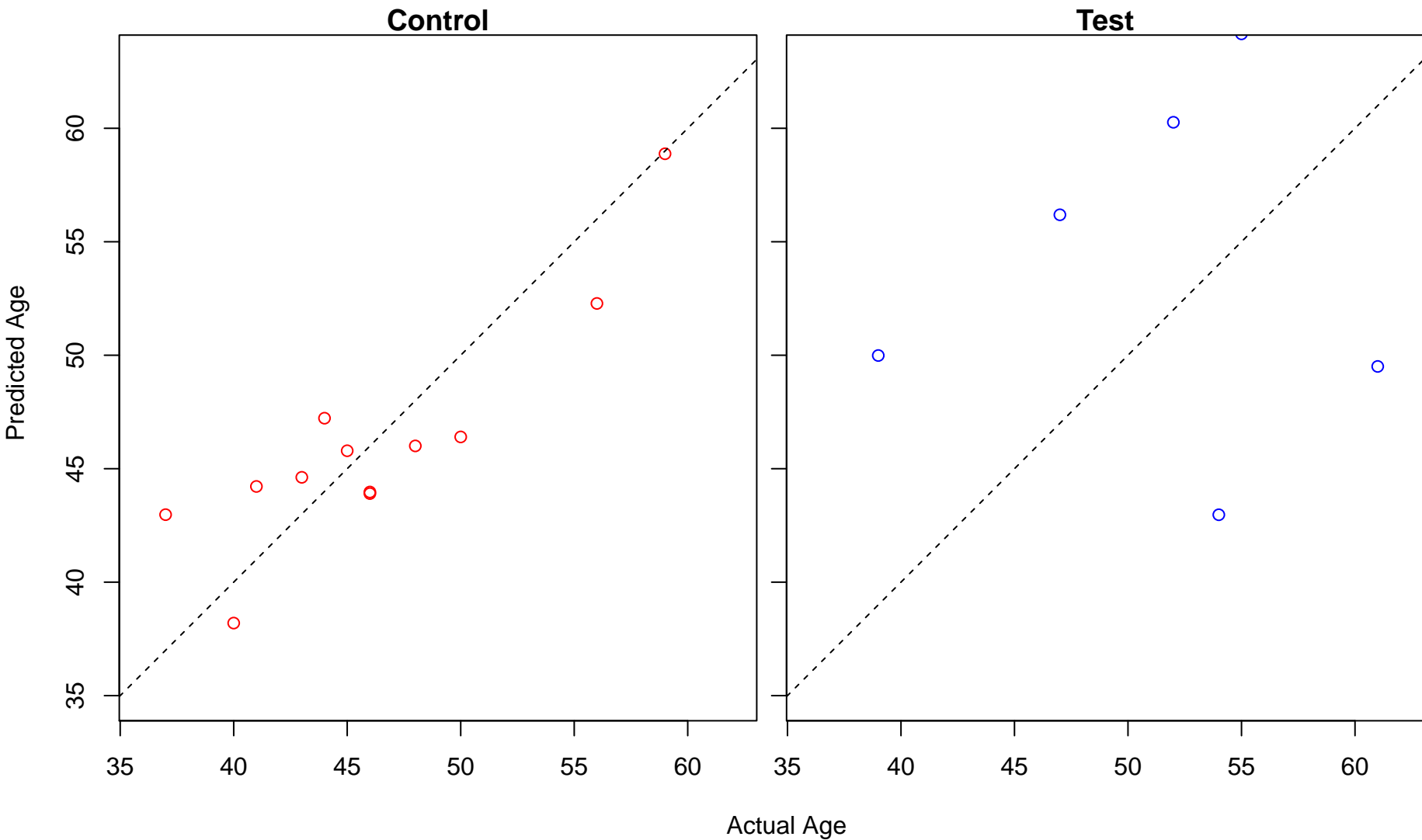
acylglycerol homeostasis (Score: 16.77554)



triglyceride homeostasis (Score: 16.775554)

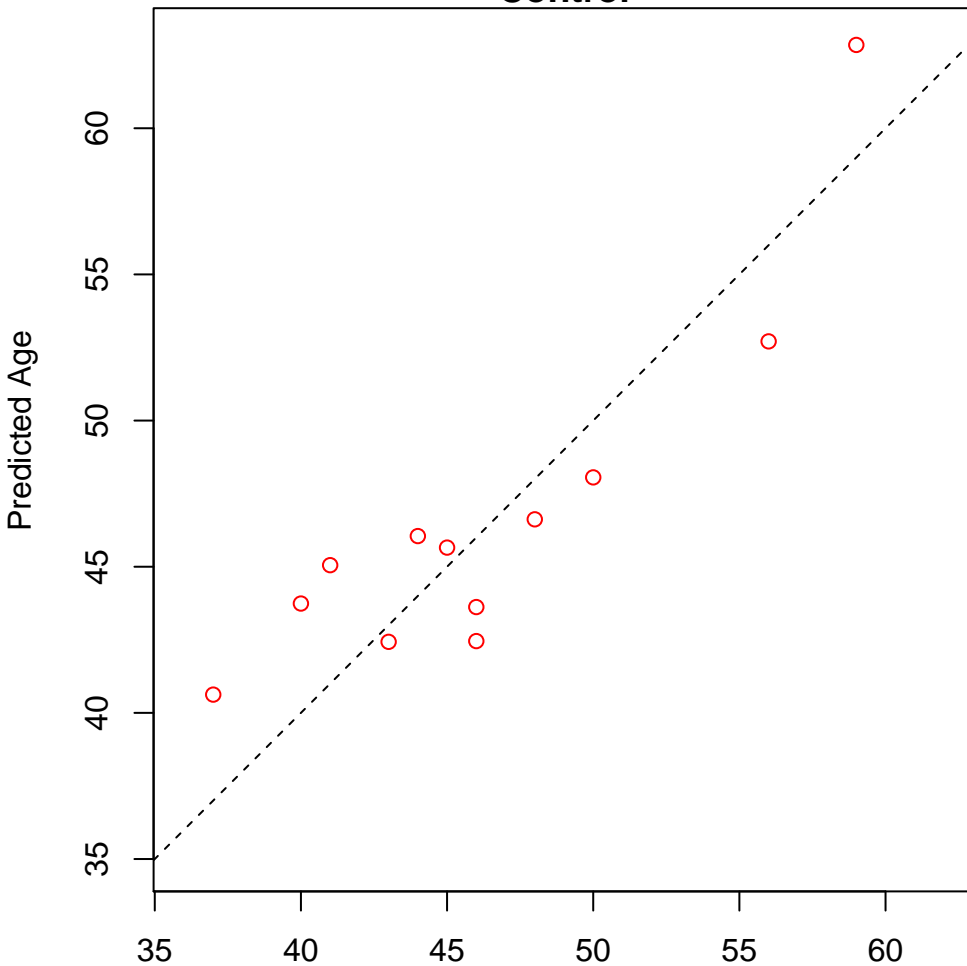


regulation of epithelial cell differentiation involved in kidney development (Score: 16.711152)

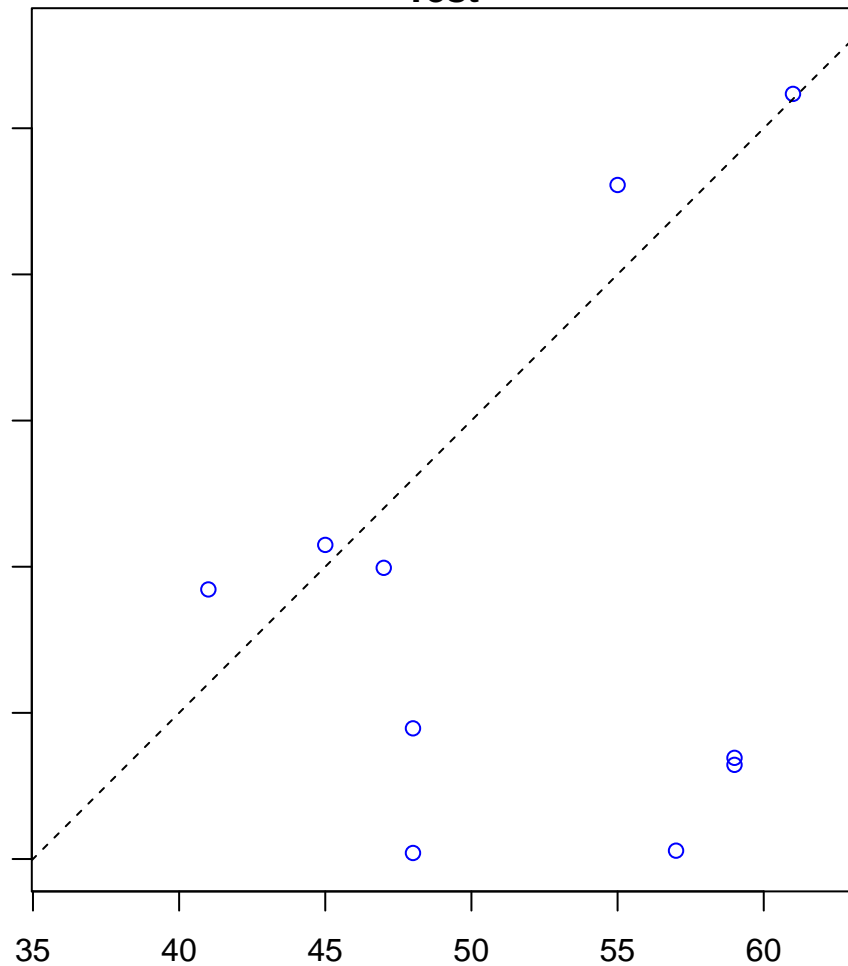


hormone-mediated signaling pathway (Score: 16.686070)

Control

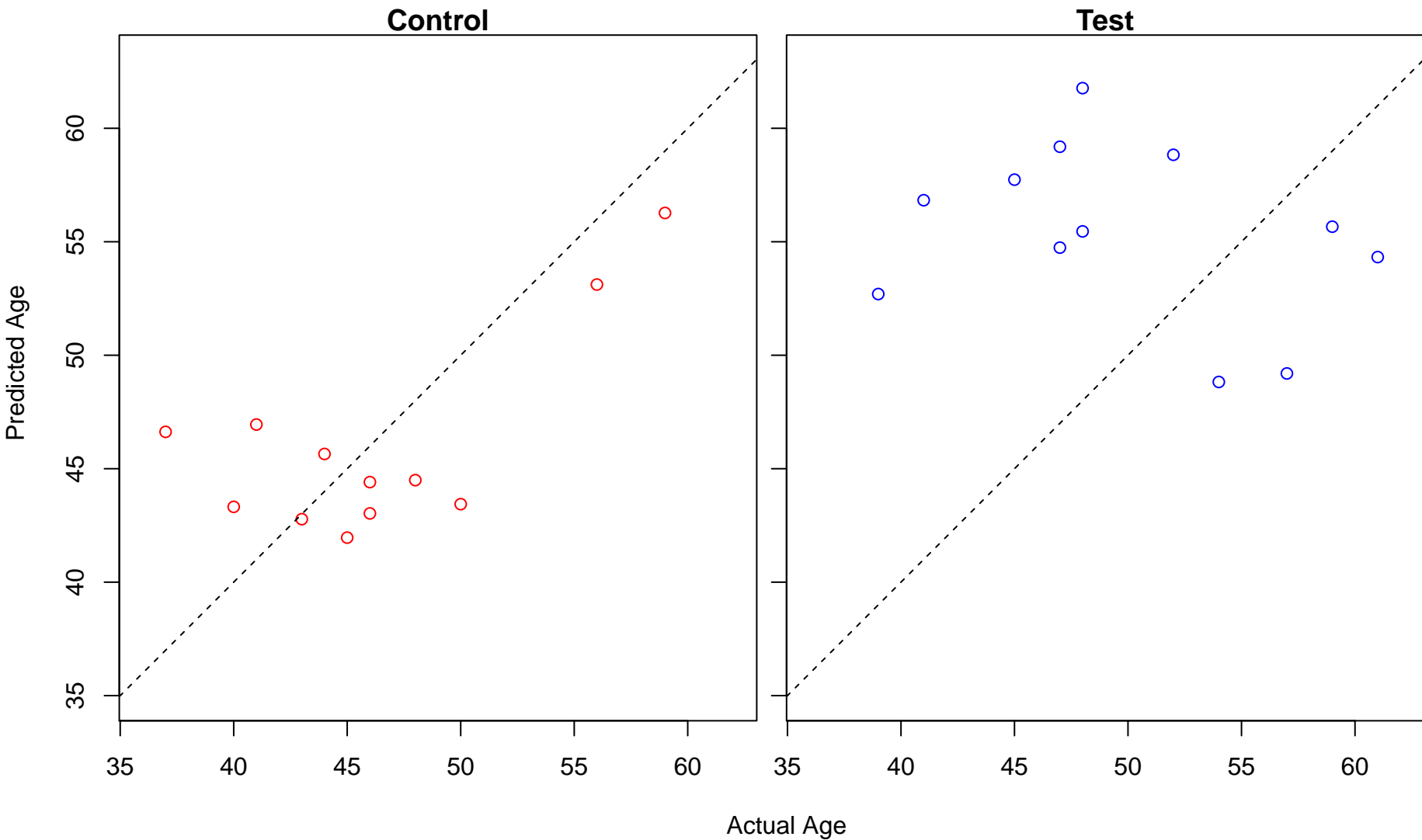


Test

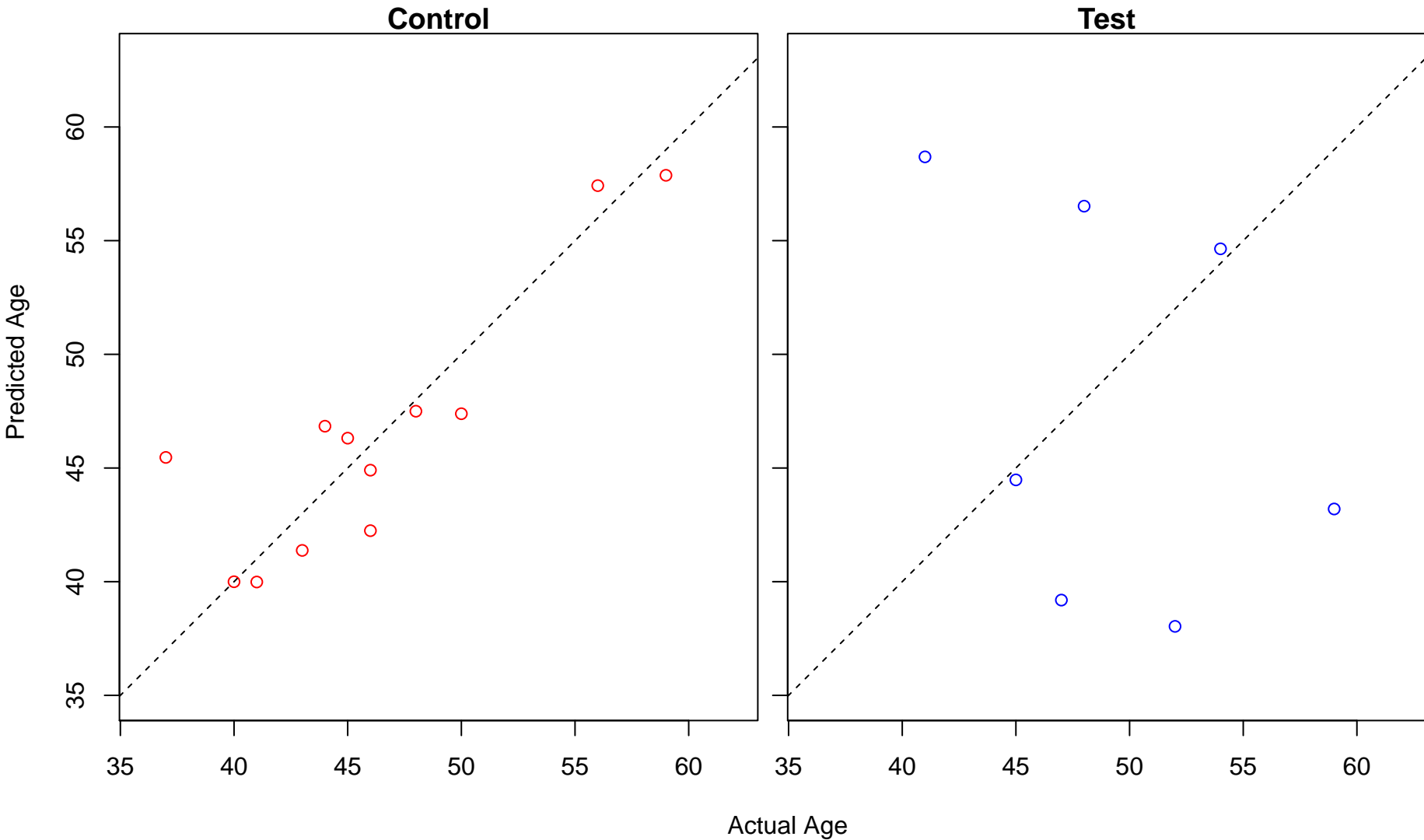


Actual Age

alkaloid metabolic process (Score: 16.66058)

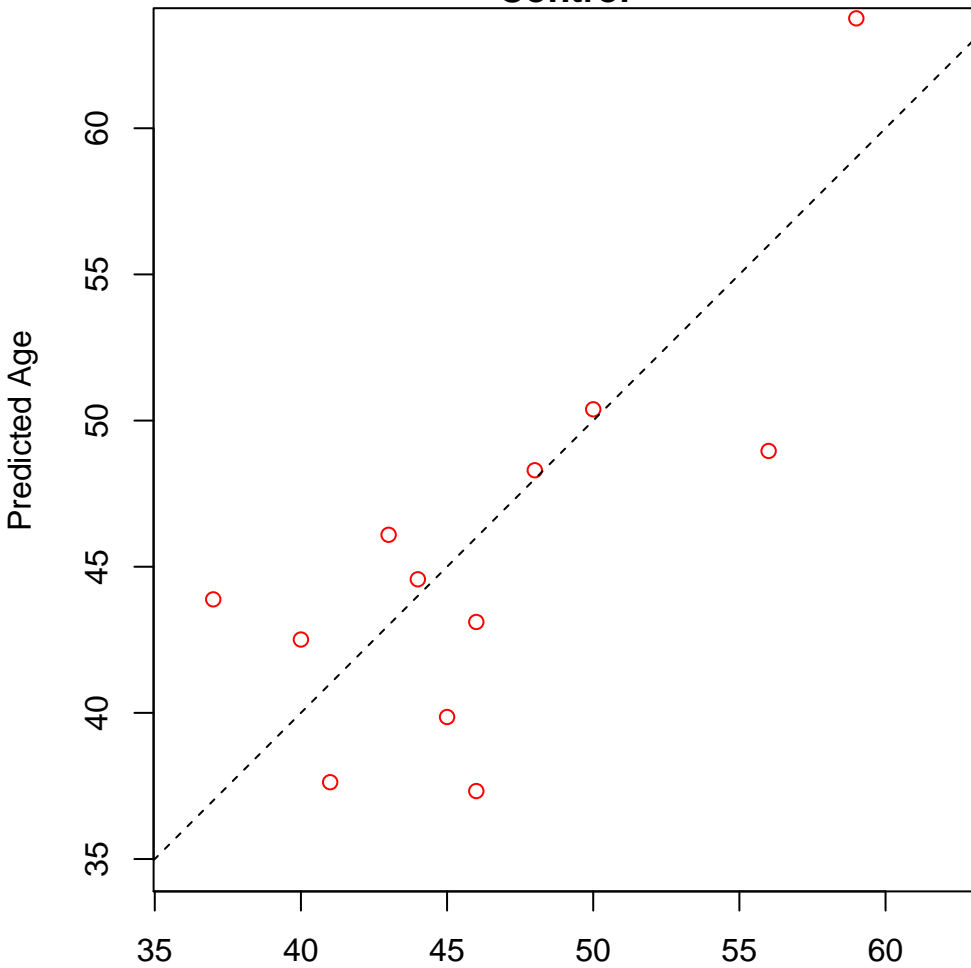


regulation of striated muscle contraction (Score: 16.601156)

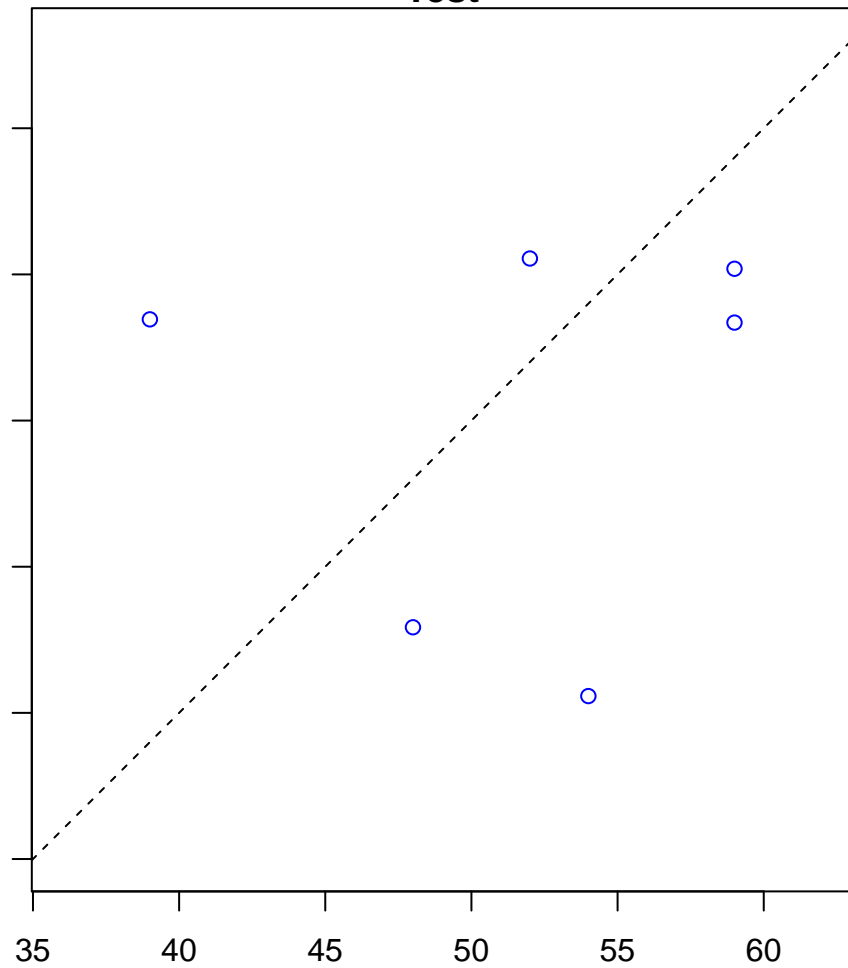


apoptotic chromosome condensation (Score: 16.519361)

Control

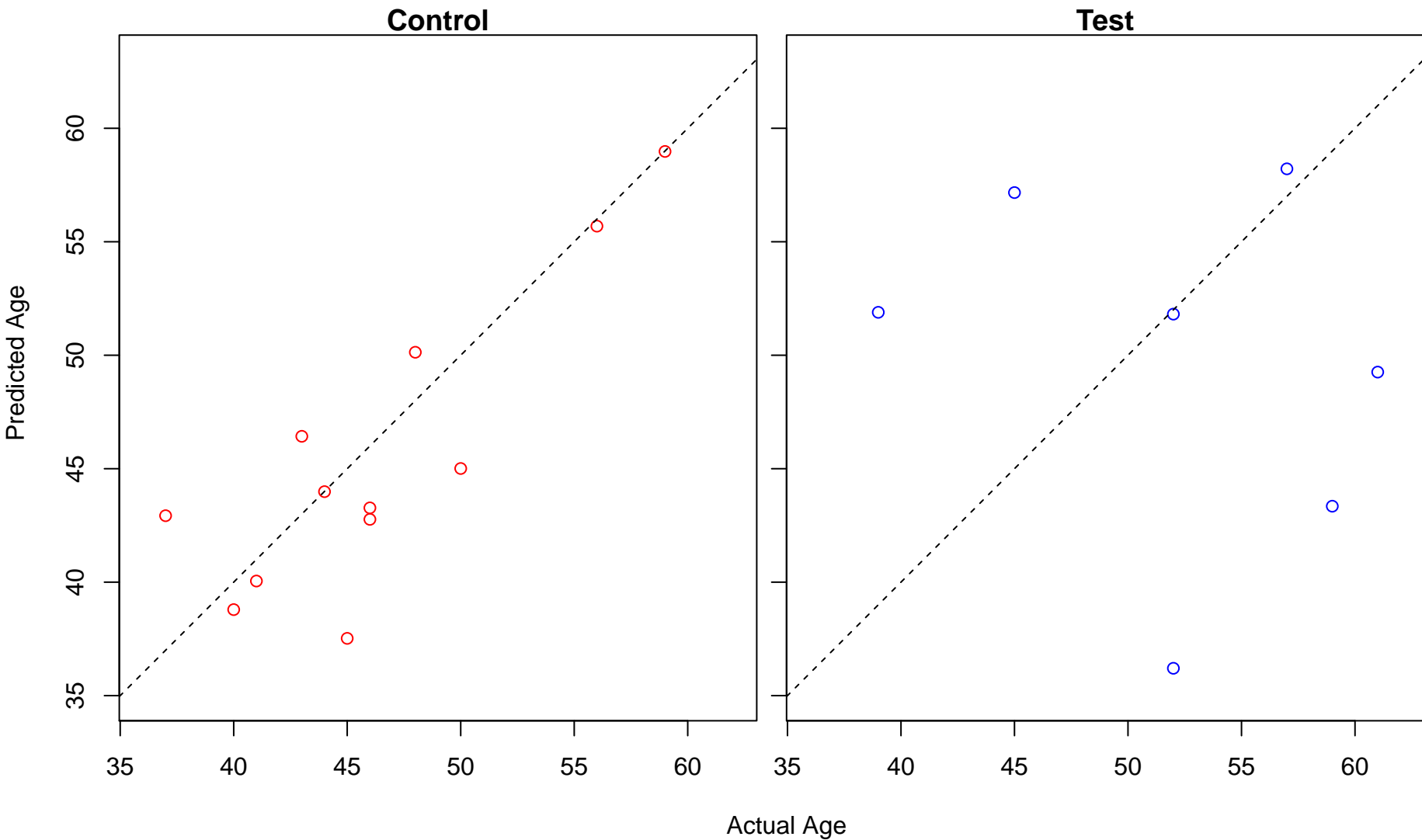


Test

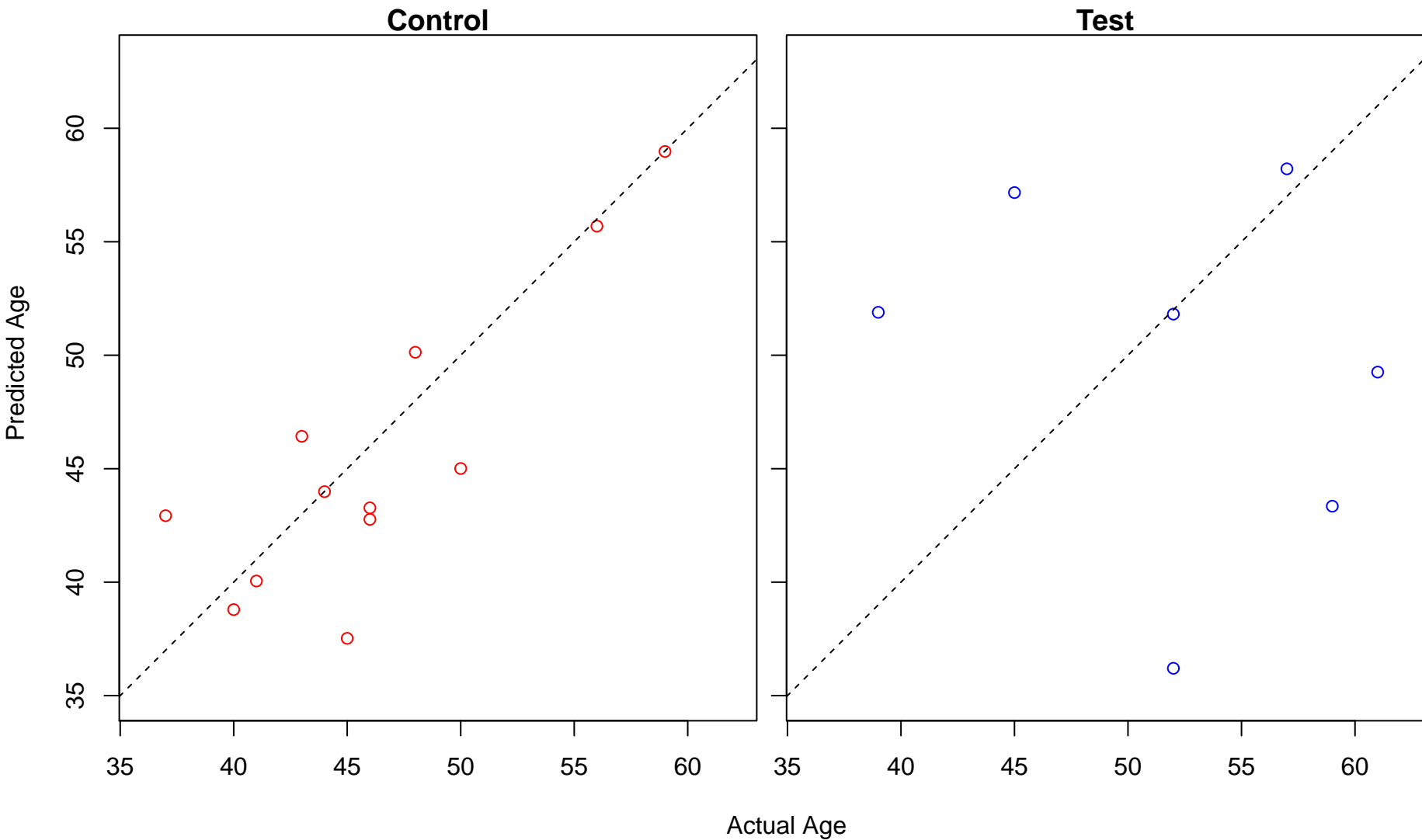


Actual Age

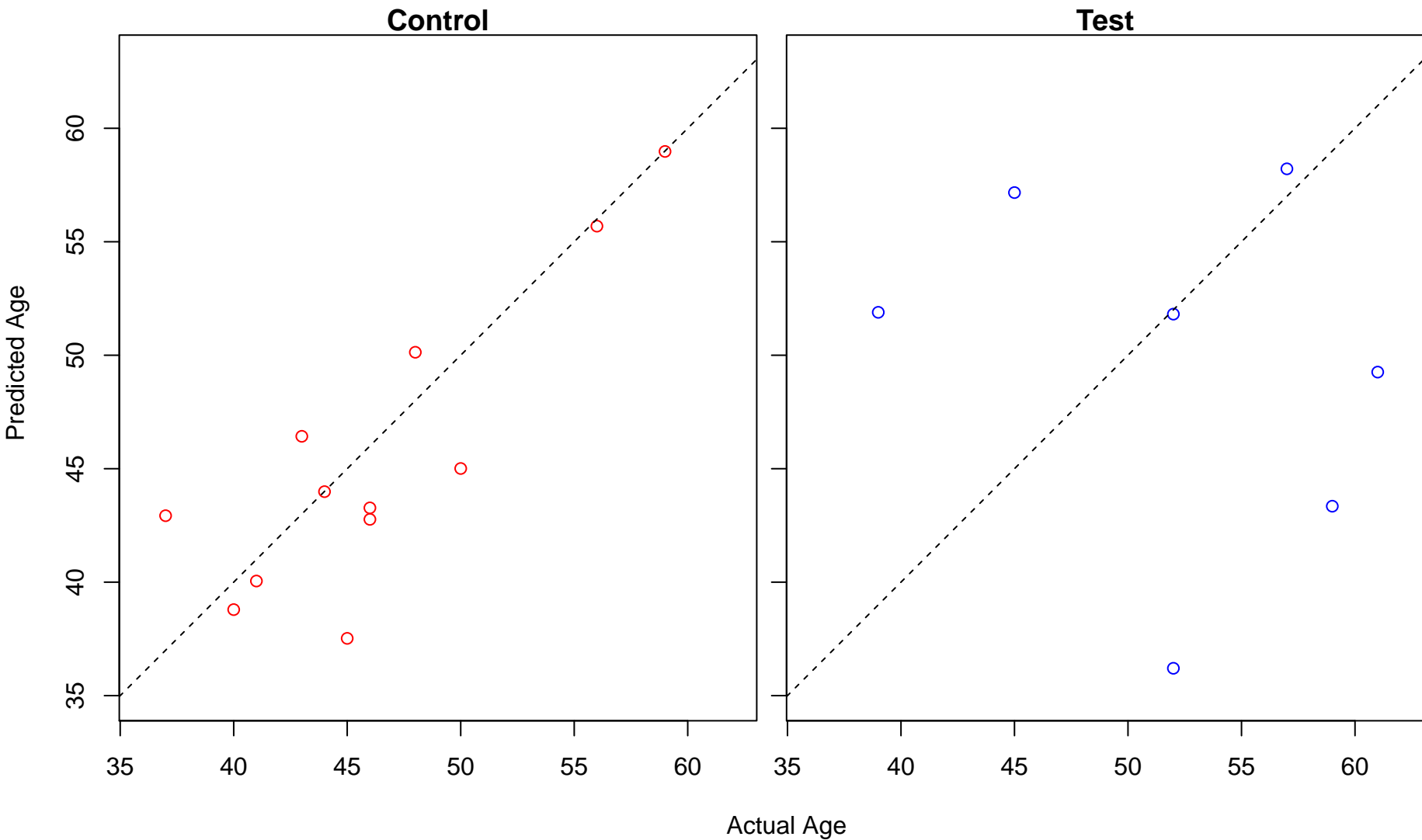
neural tube closure (Score: 16.500581)



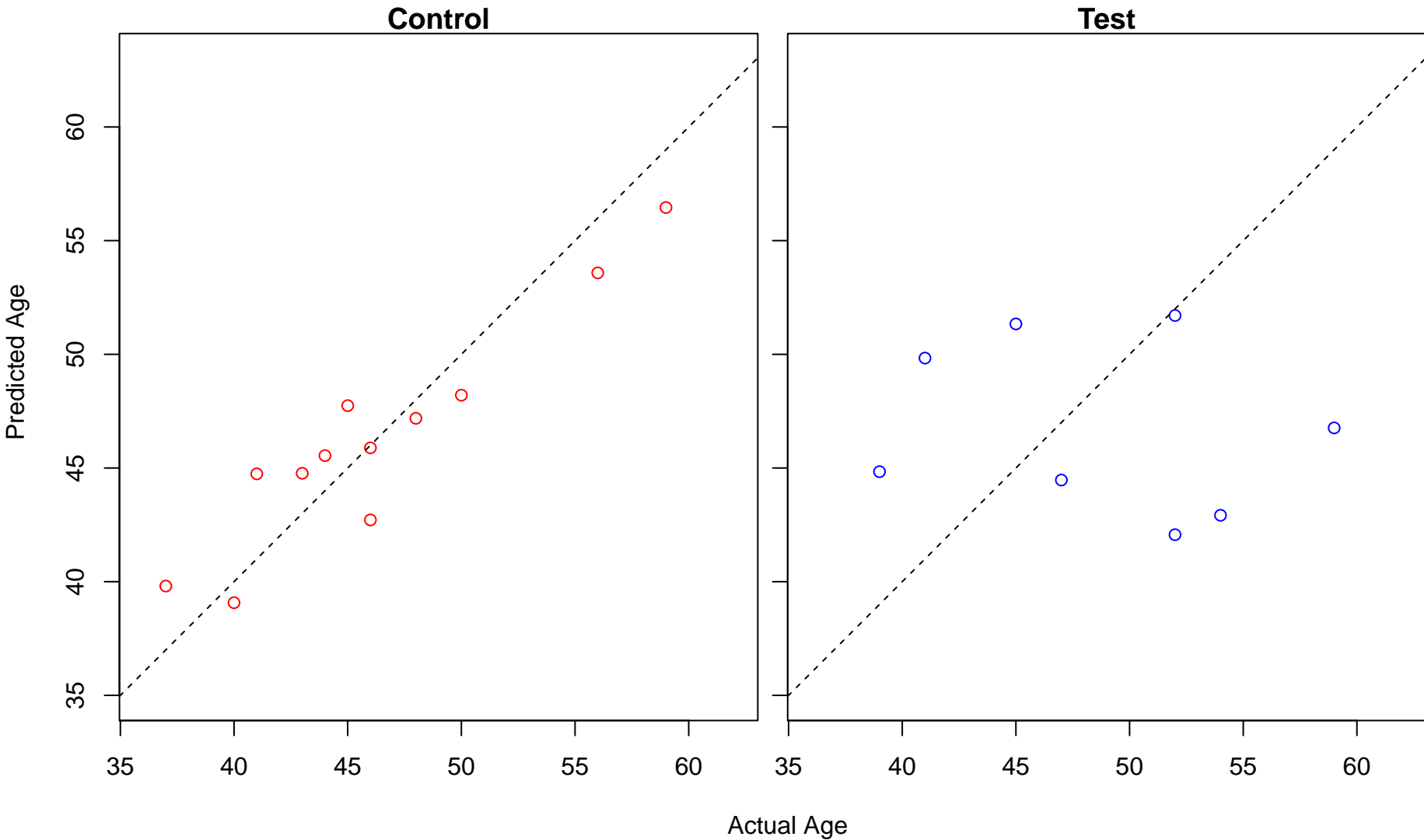
primary neural tube formation (Score: 16.500581)



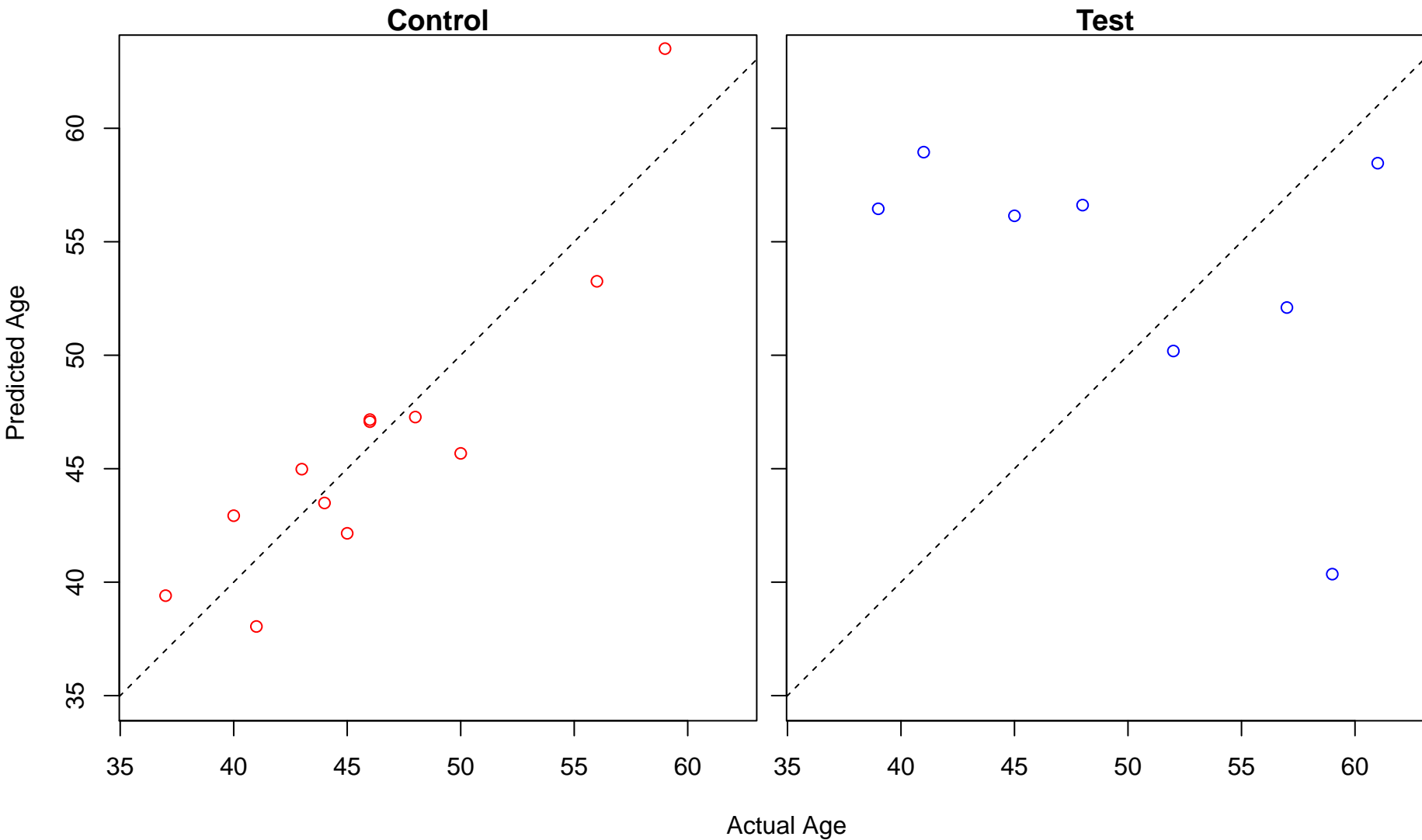
tube closure (Score: 16.500581)



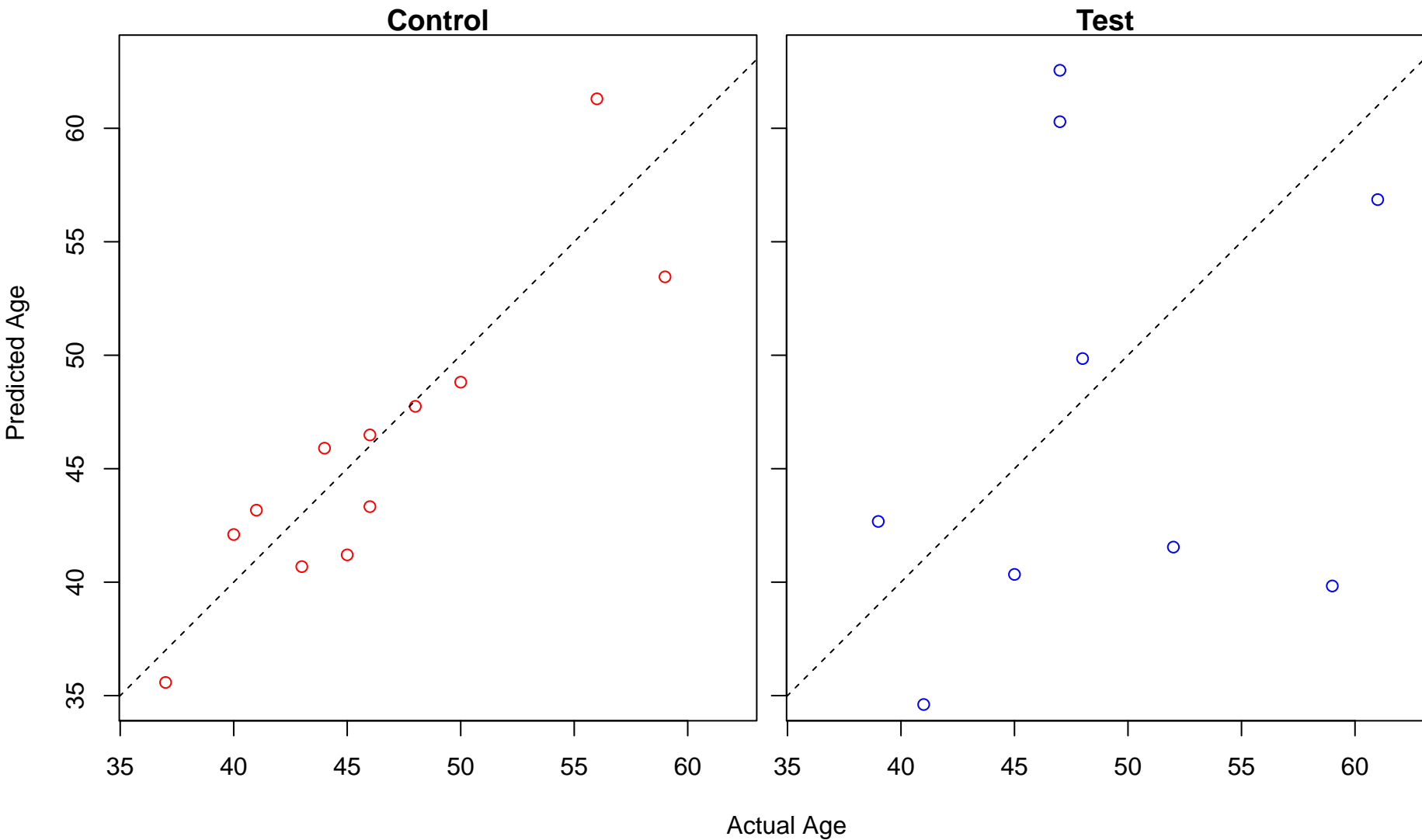
maintenance of gastrointestinal epithelium (Score: 16.363371)



negative regulation of mRNA 3'-end processing (Score: 16.279807)

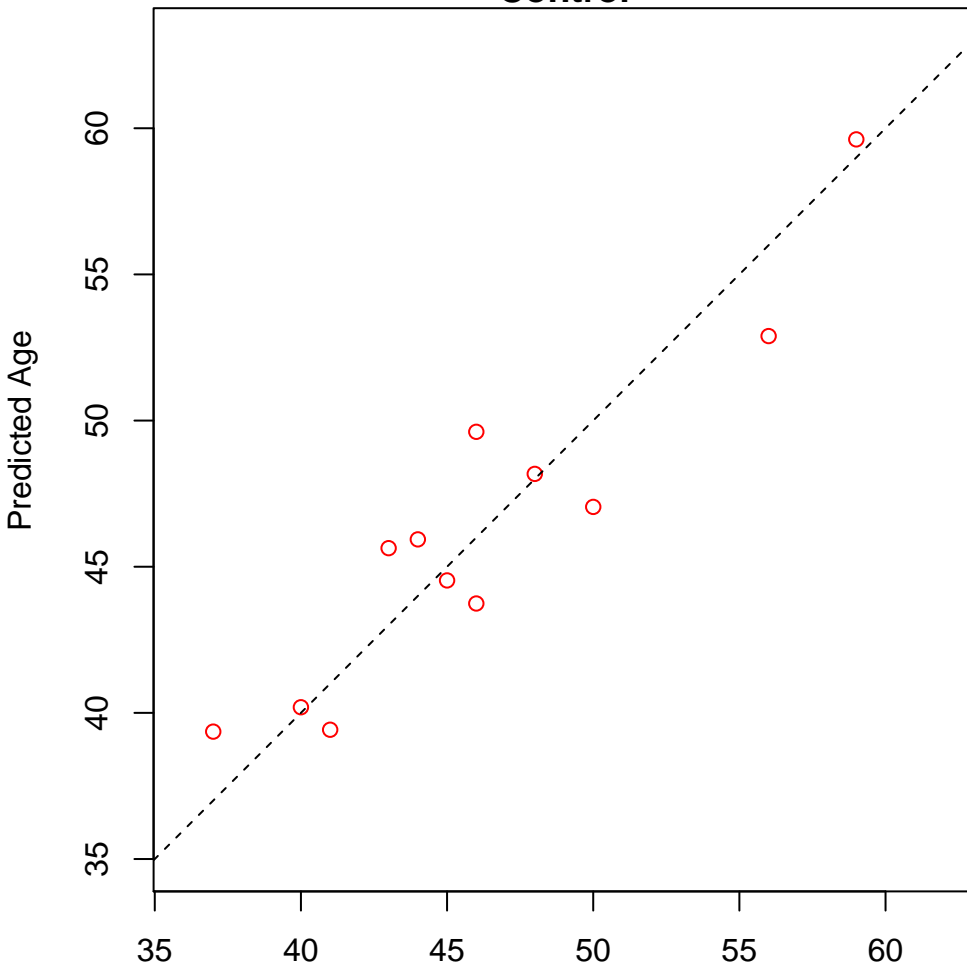


cellular response to ATP (Score: 16.279592)

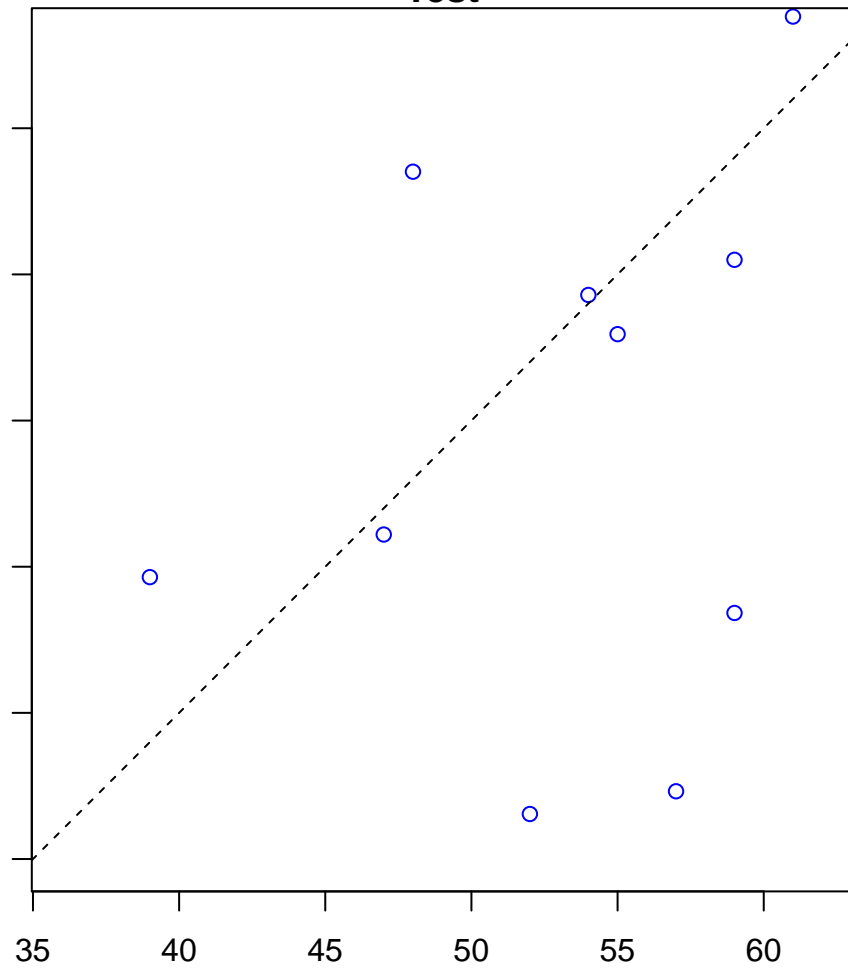


photoreceptor cell differentiation (Score: 16.227269)

Control

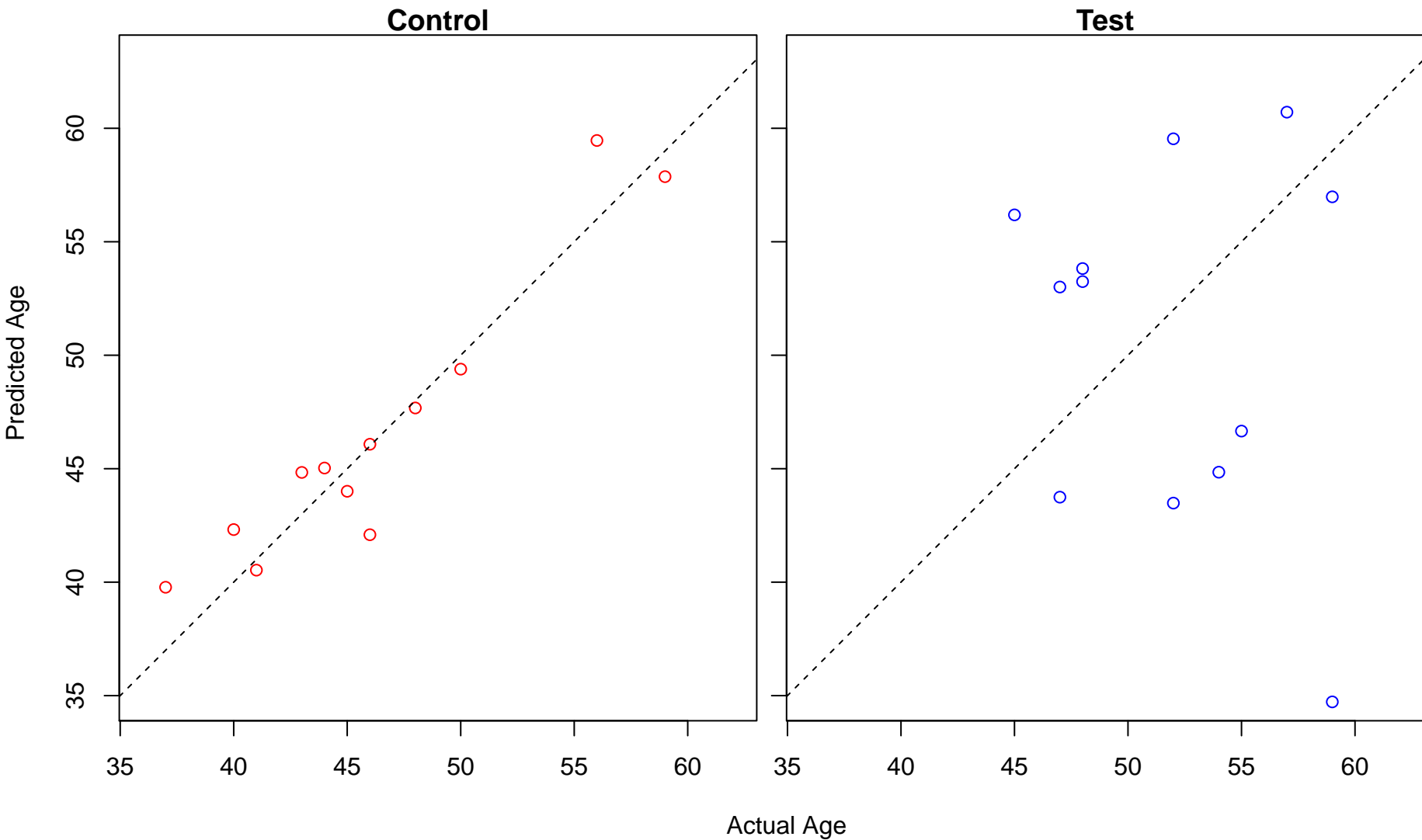


Test

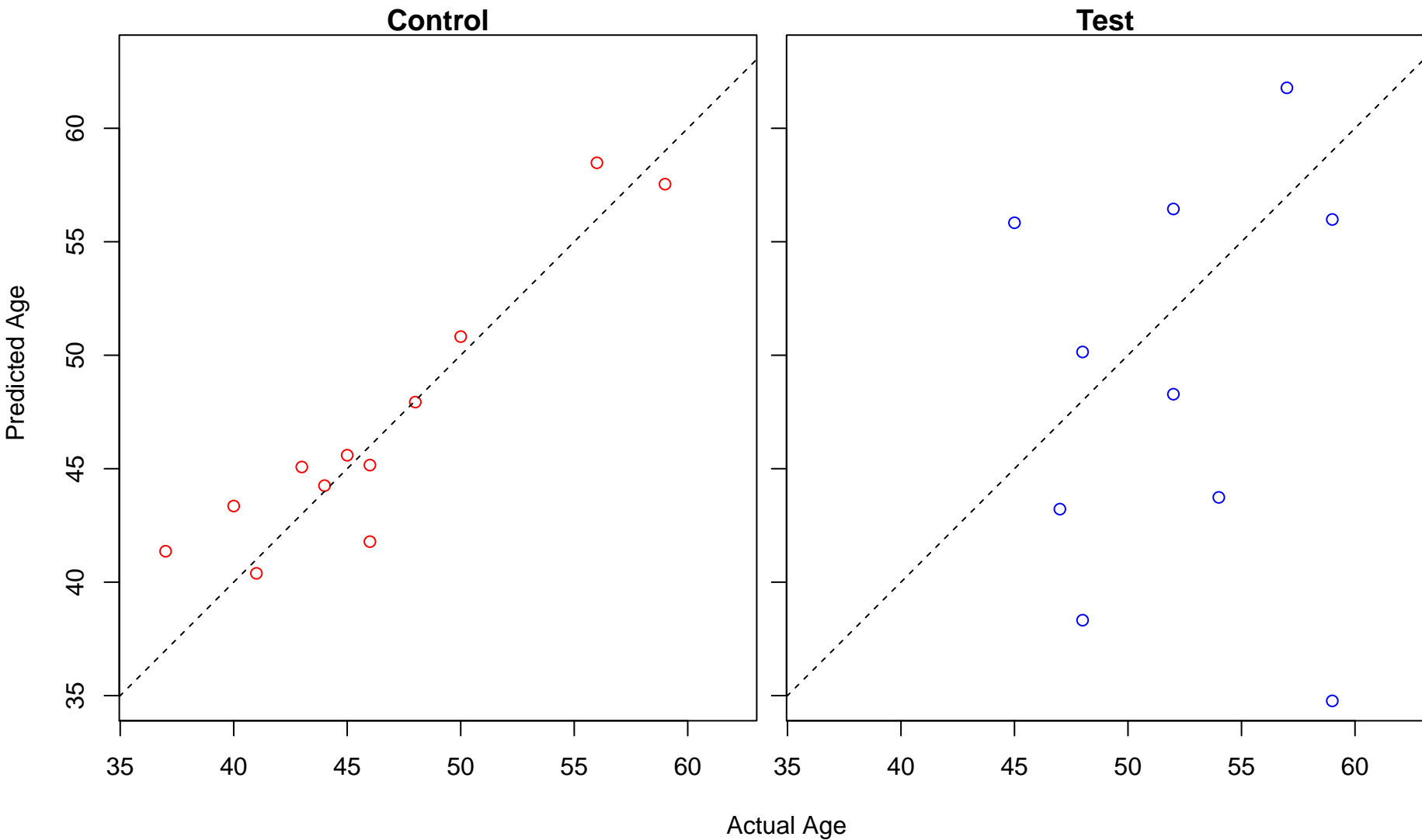


Actual Age

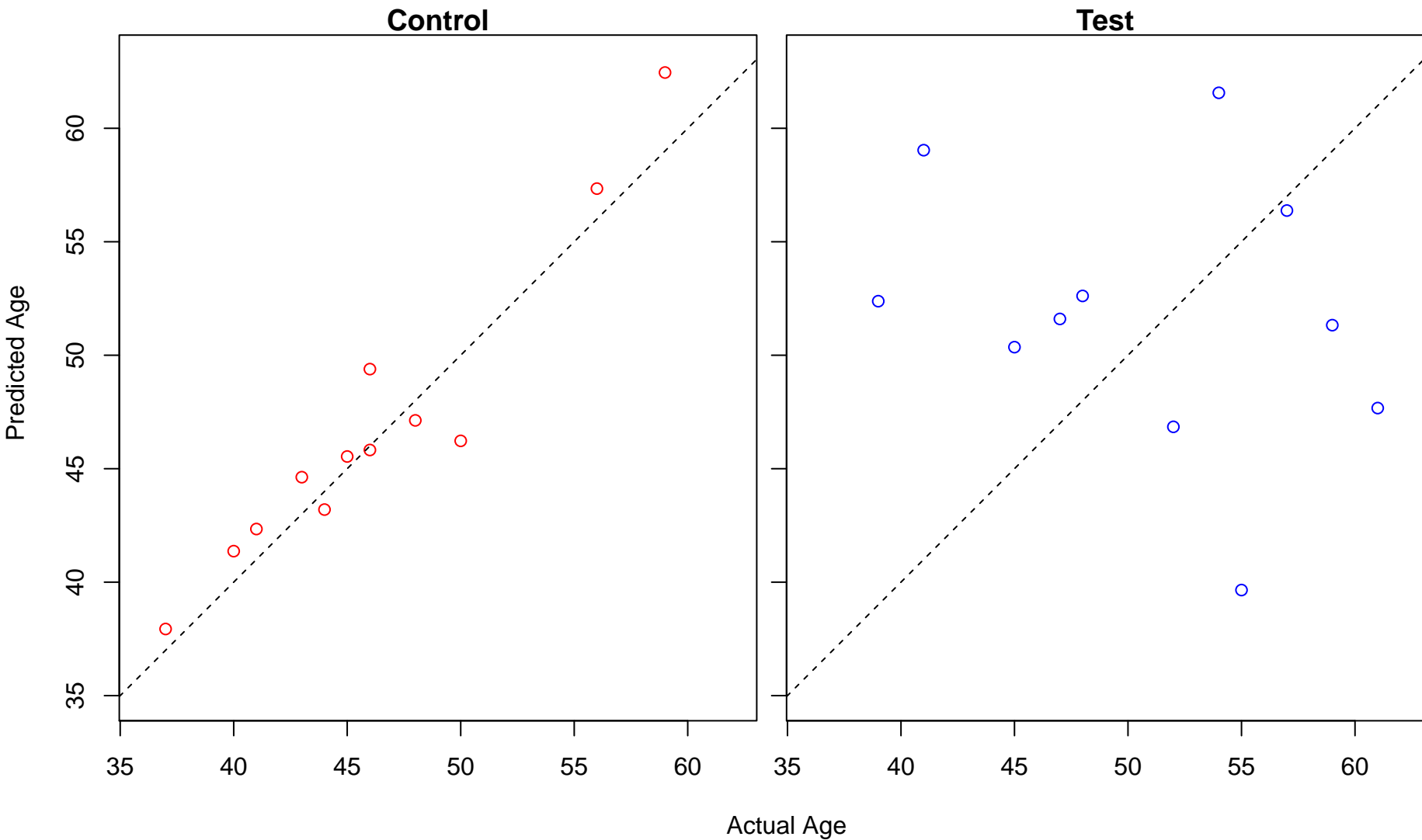
regulation of T cell receptor signaling pathway (Score: 16.223115)



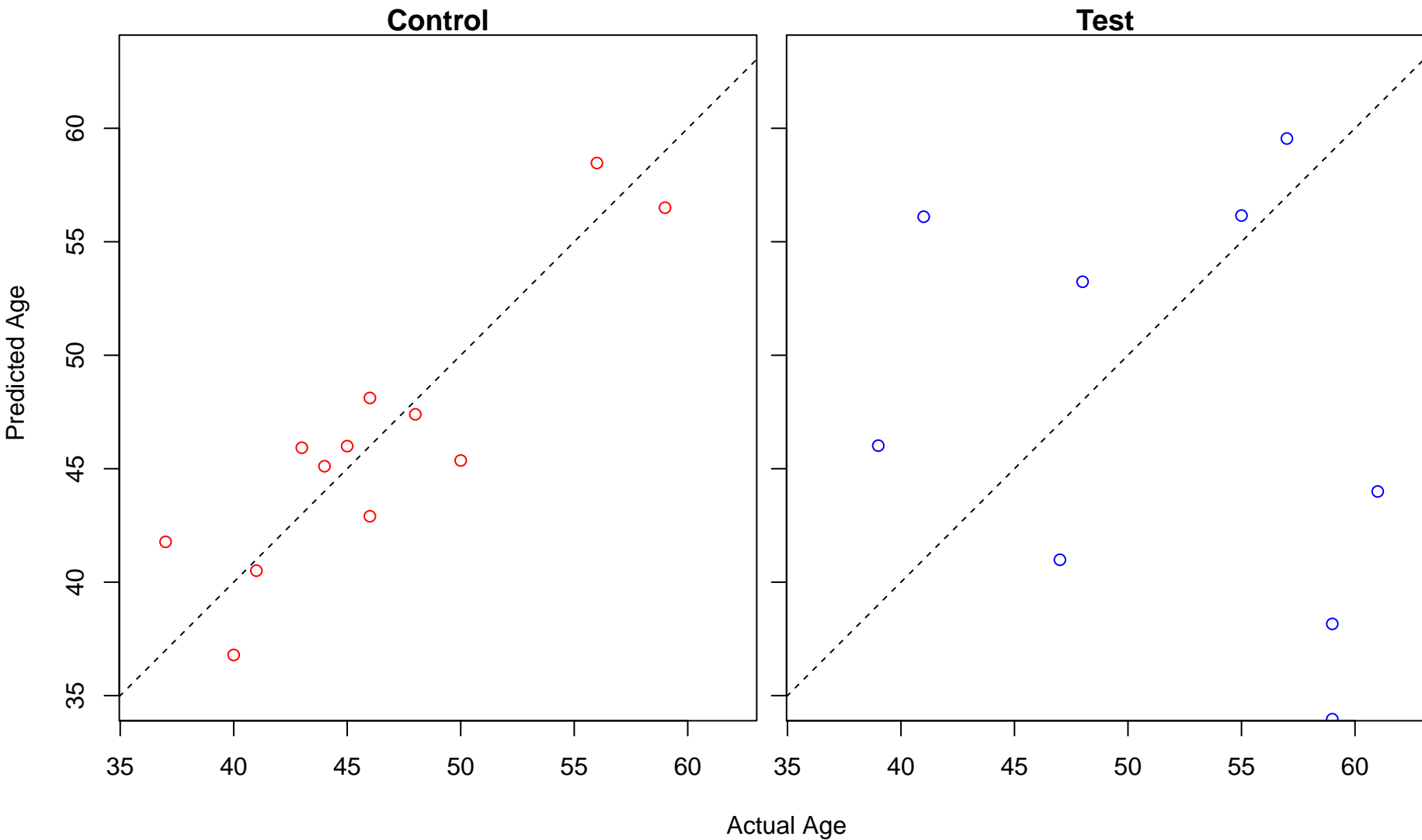
negative regulation of antigen receptor-mediated signaling pathway (Score: 16.223110)



mammary gland development (Score: 16.193227)

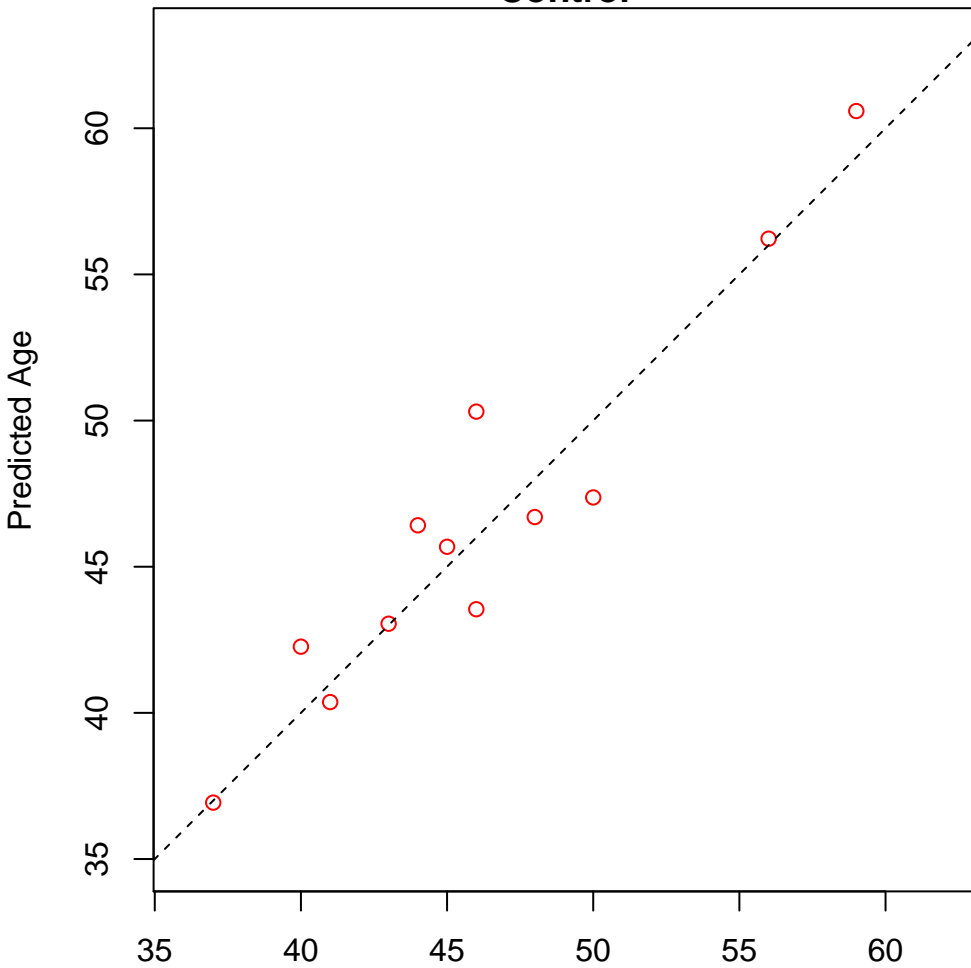


positive regulation of peptidyl-tyrosine phosphorylation (Score: 16.189752)

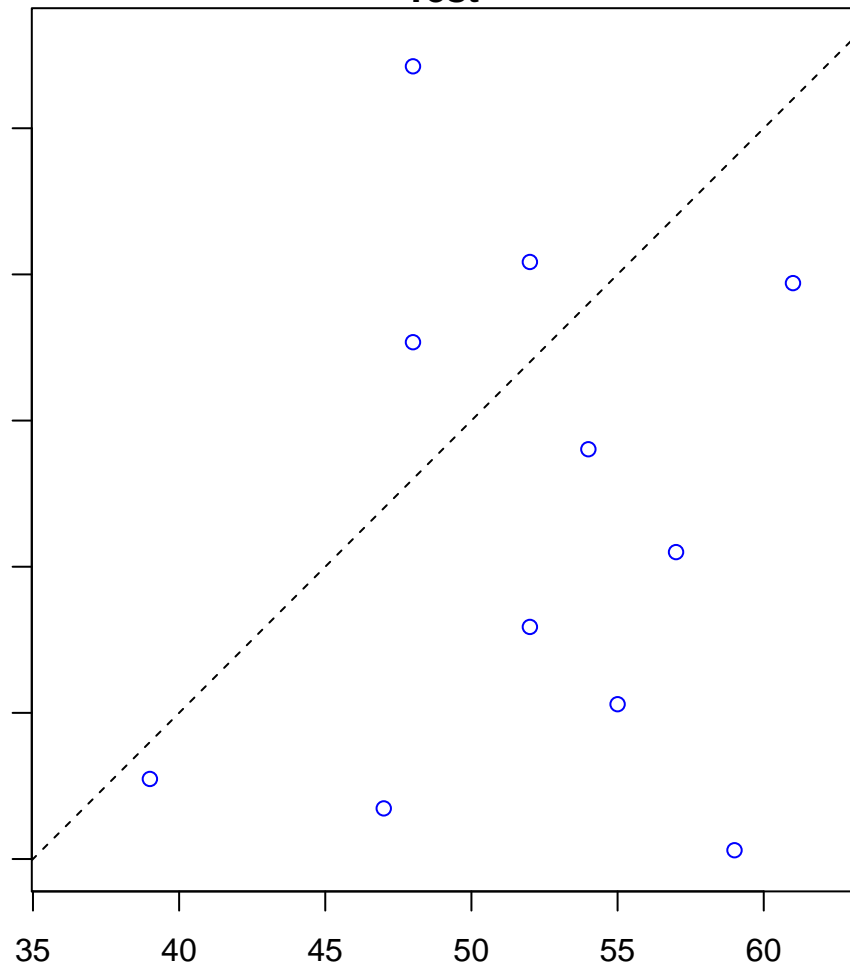


camera-type eye morphogenesis (Score: 16.159004)

Control

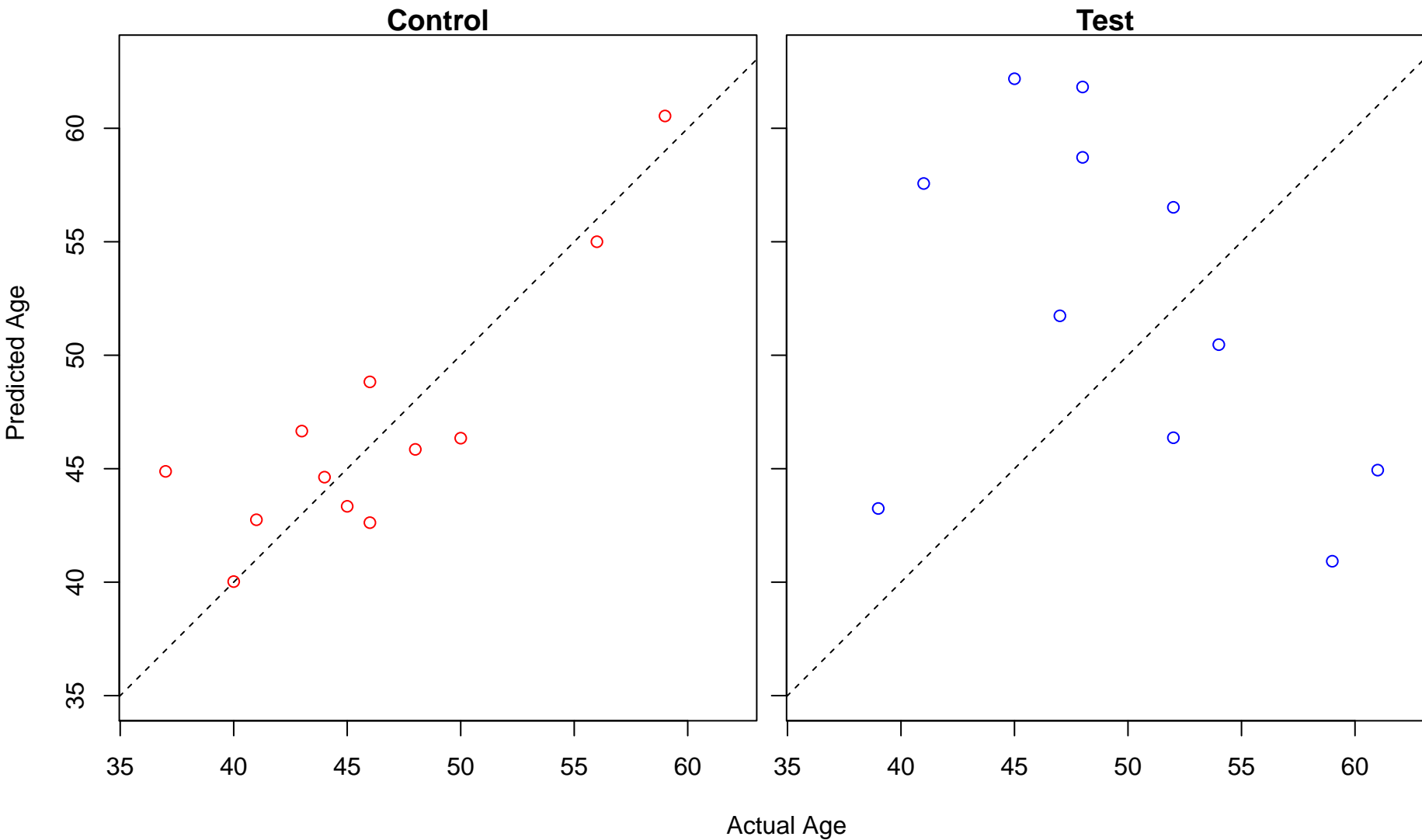


Test

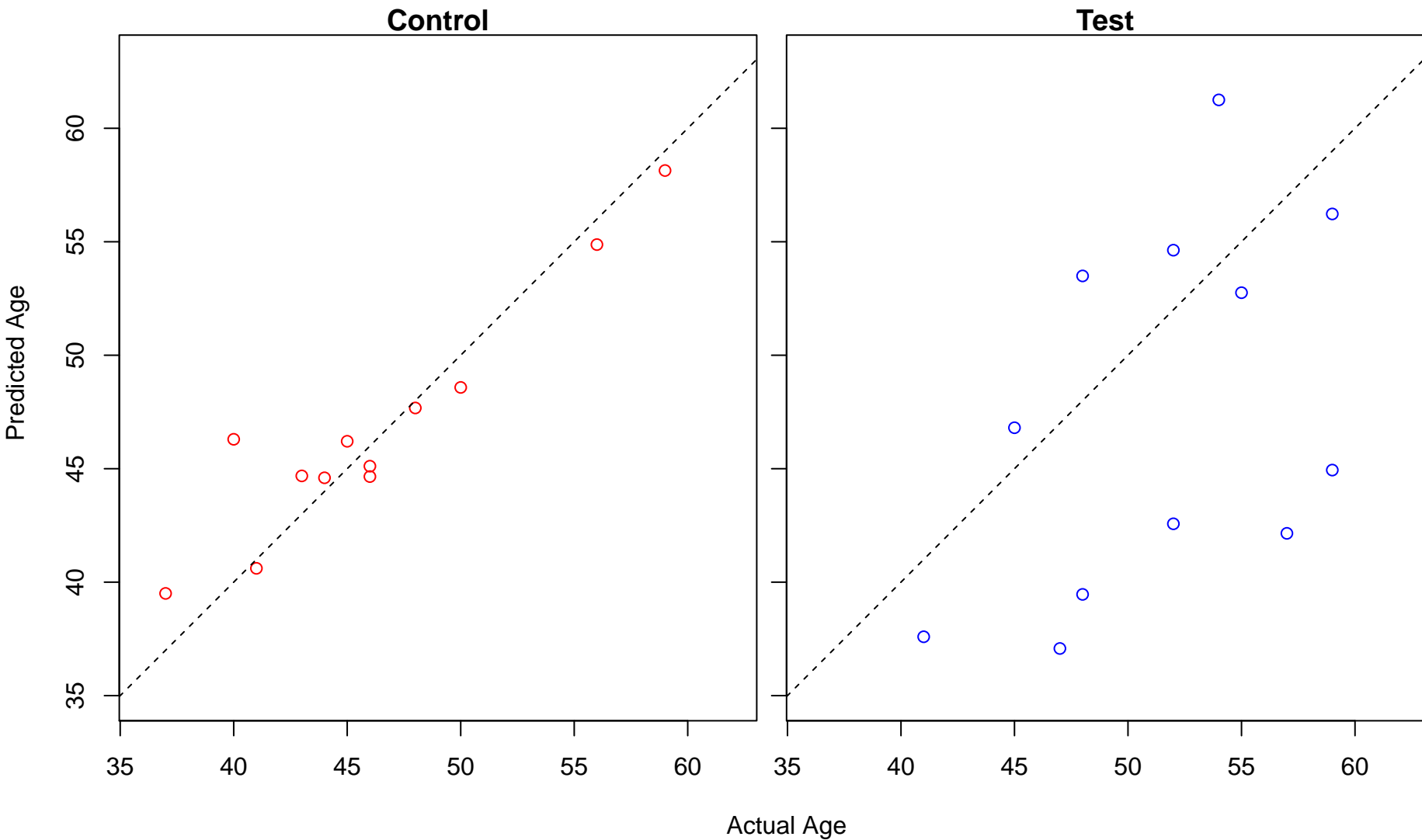


Actual Age

regulation of pathway-restricted SMAD protein phosphorylation (Score: 16.118637)

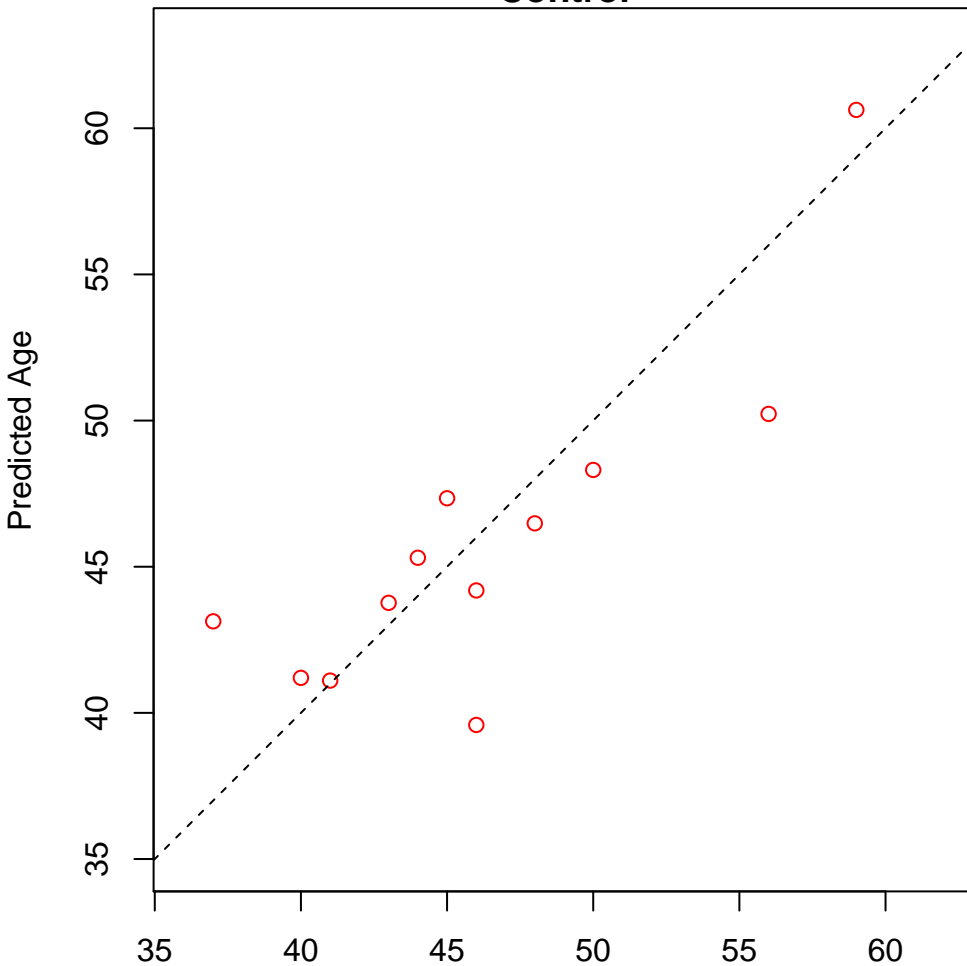


salivary gland morphogenesis (Score: 16.094124)

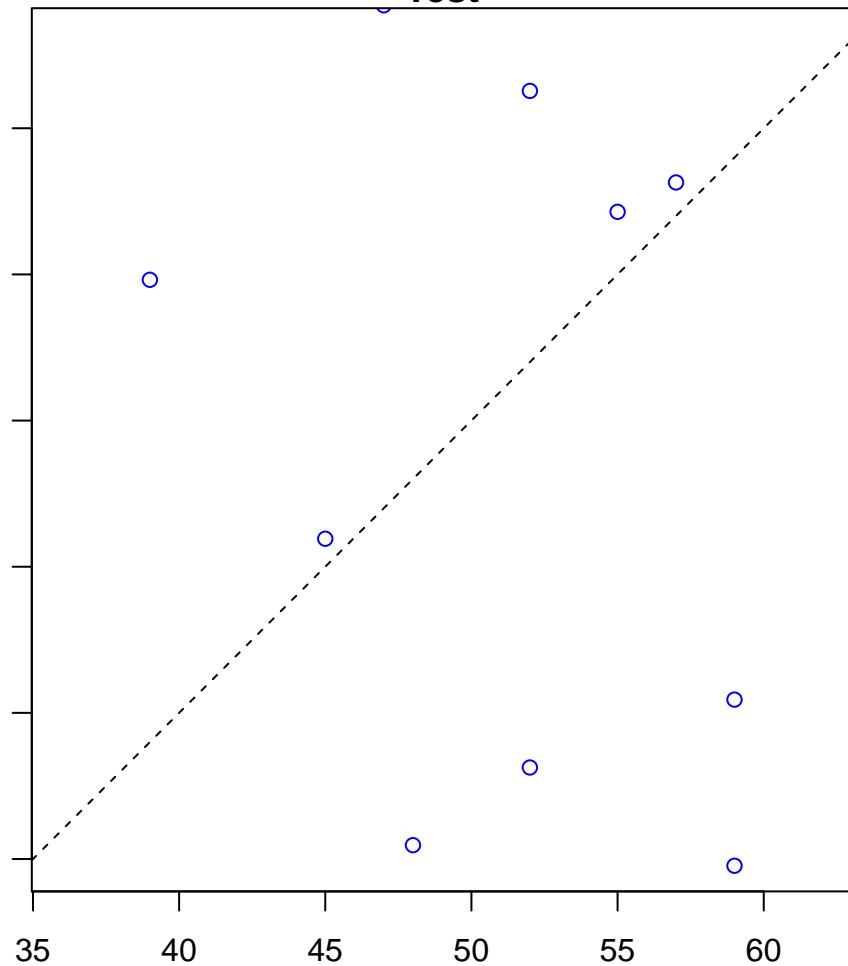


L-ascorbic acid metabolic process (Score: 16.081244)

Control

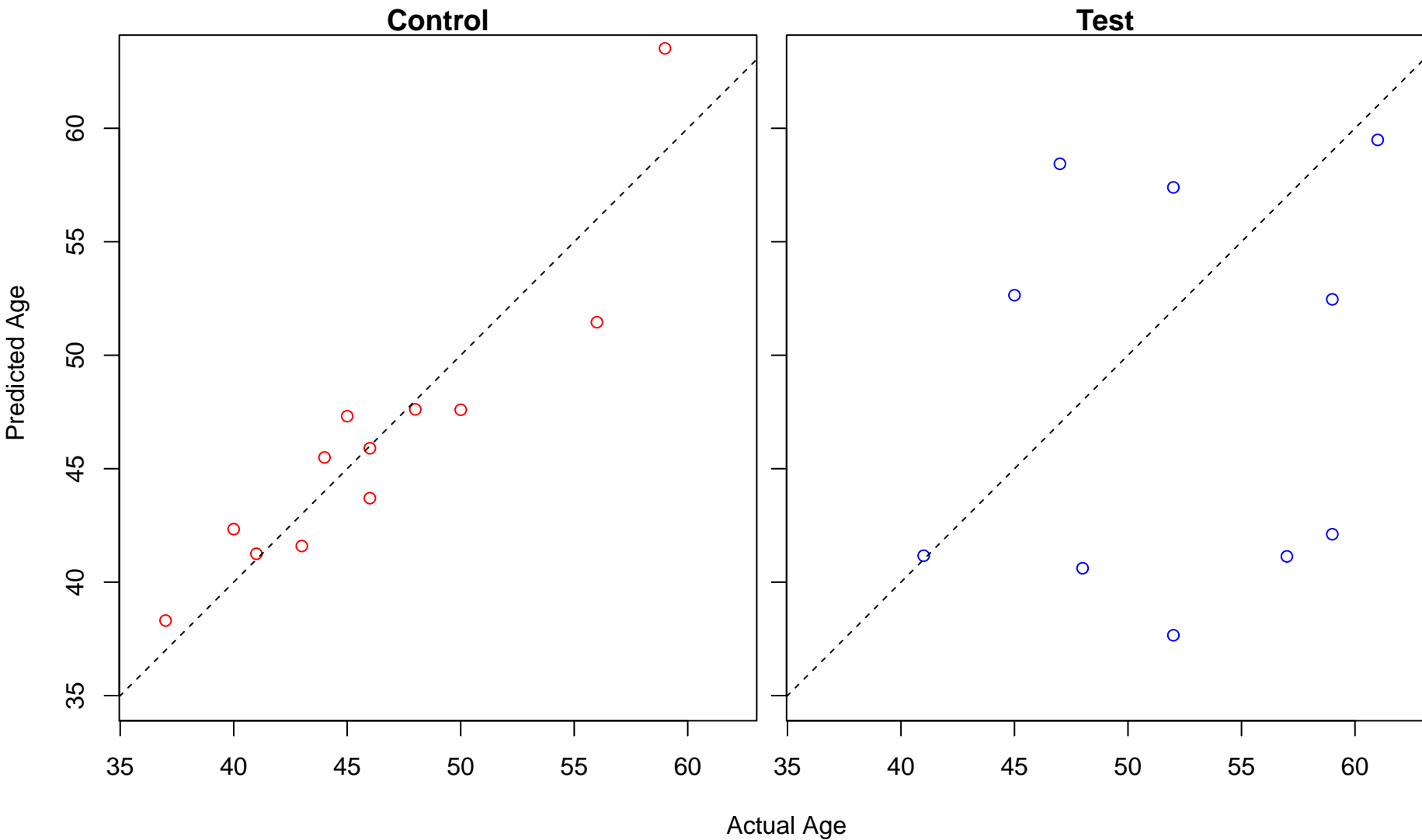


Test

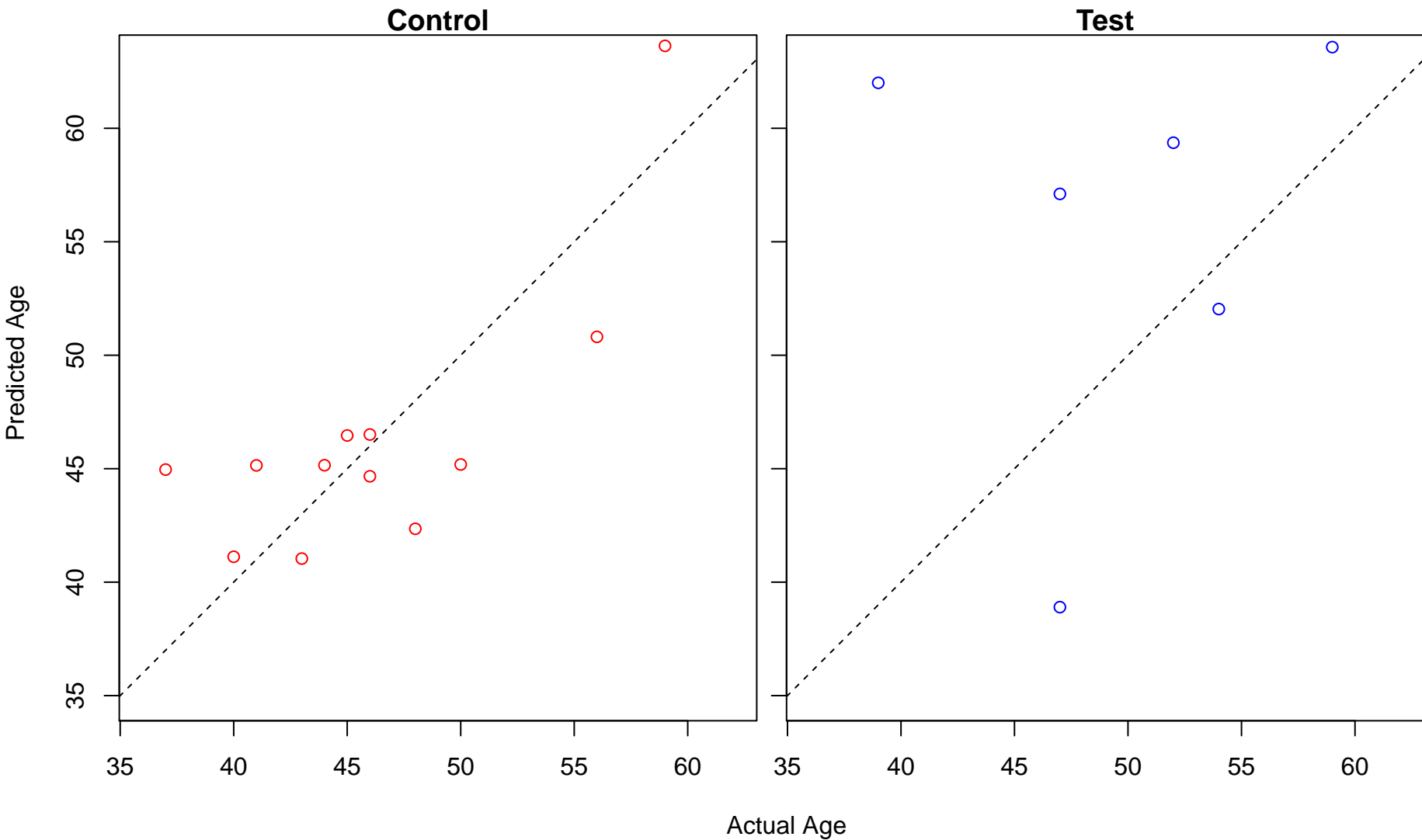


Actual Age

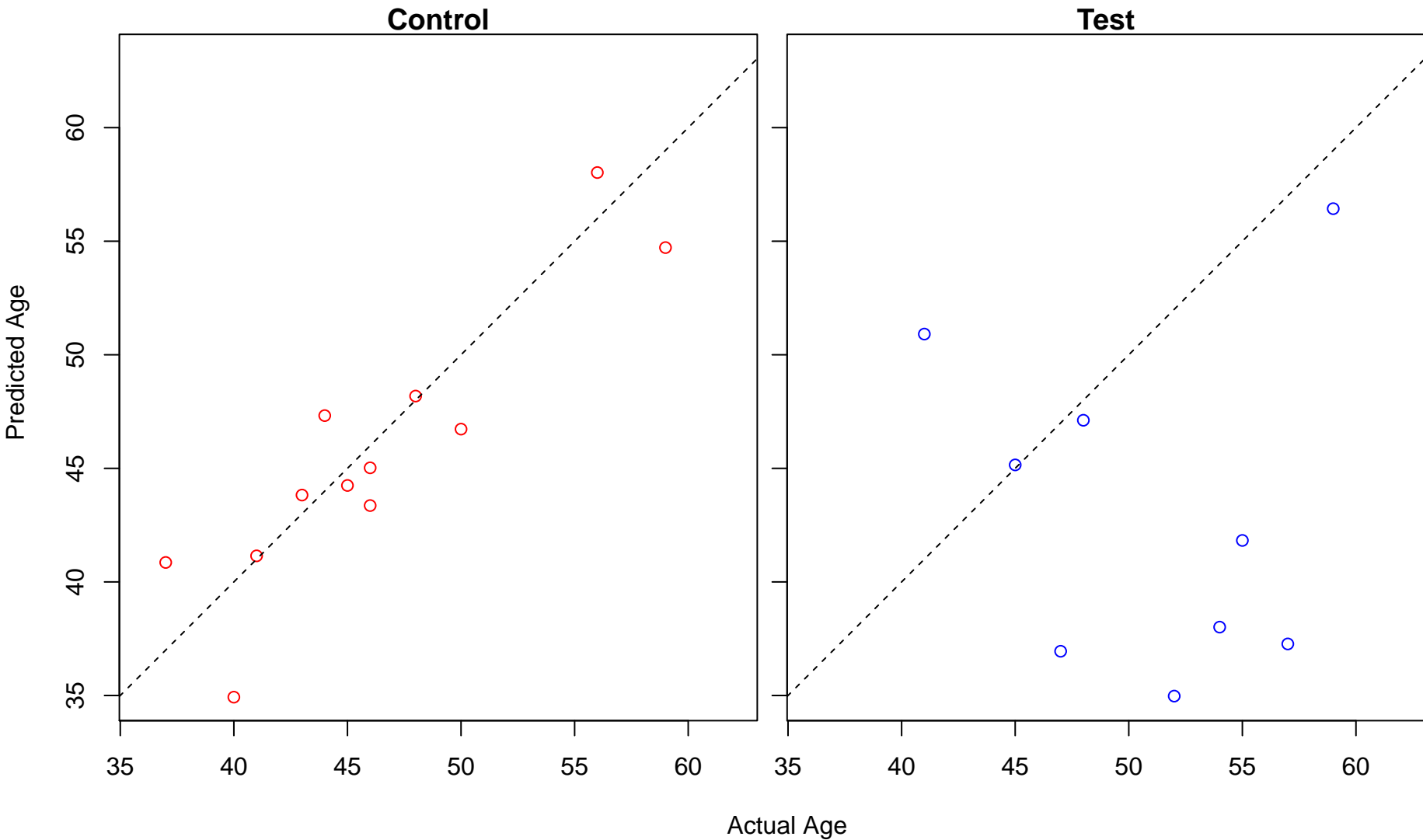
hippocampus development (Score: 15.955830)



regulation of glial cell differentiation (Score: 15.874397)

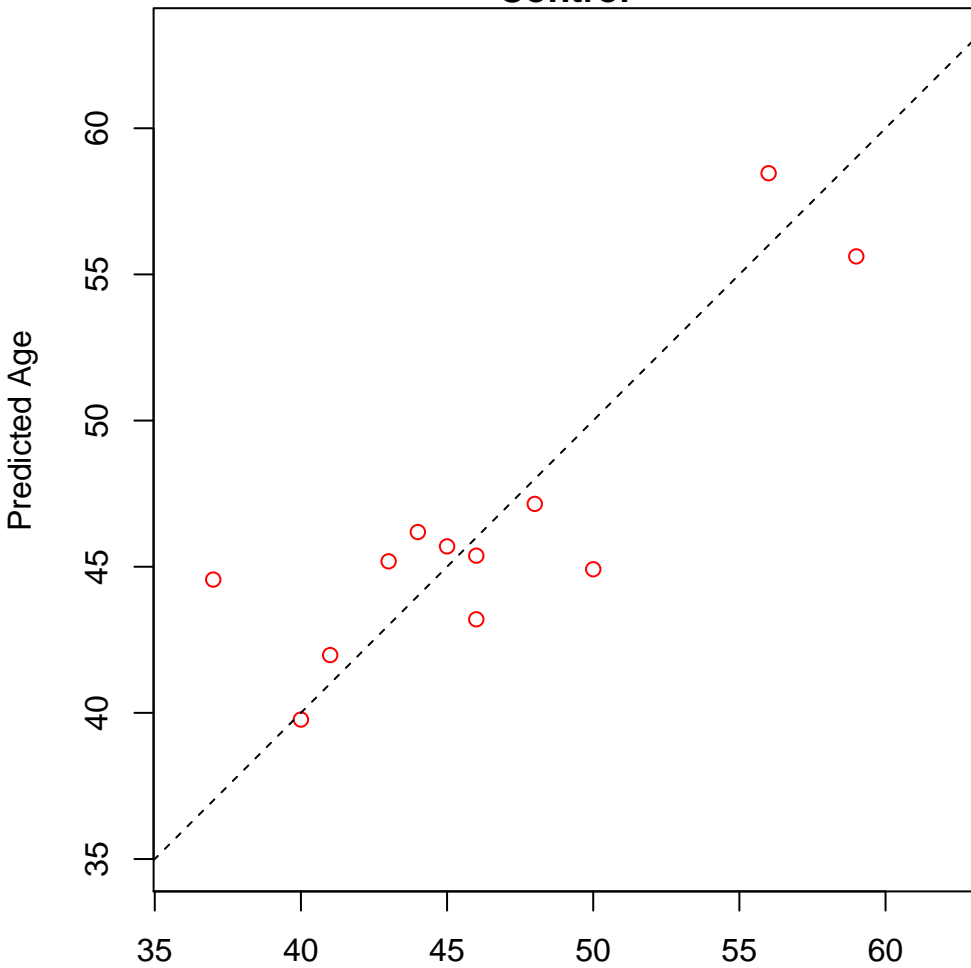


positive regulation of phosphatidylinositol 3-kinase signaling (Score: 15.854141)

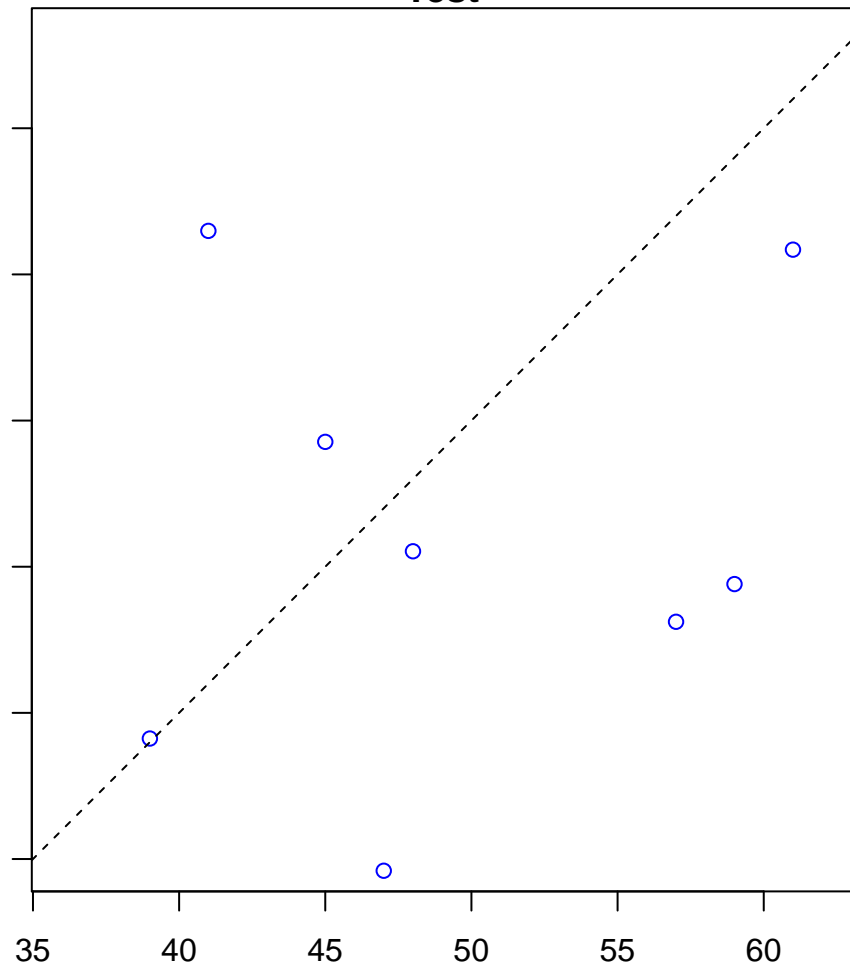


regulation of neuron apoptotic process (Score: 15.842274)

Control

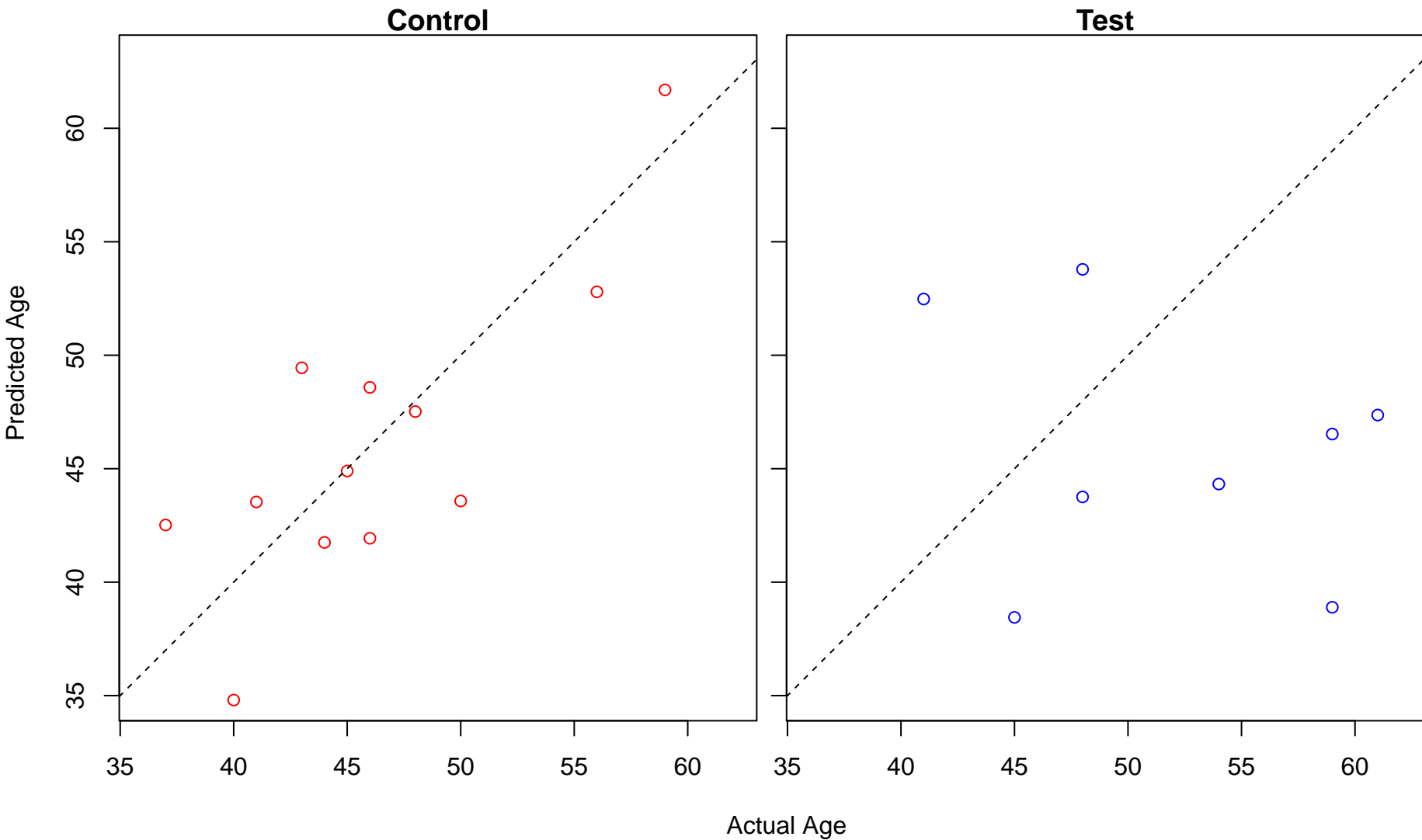


Test

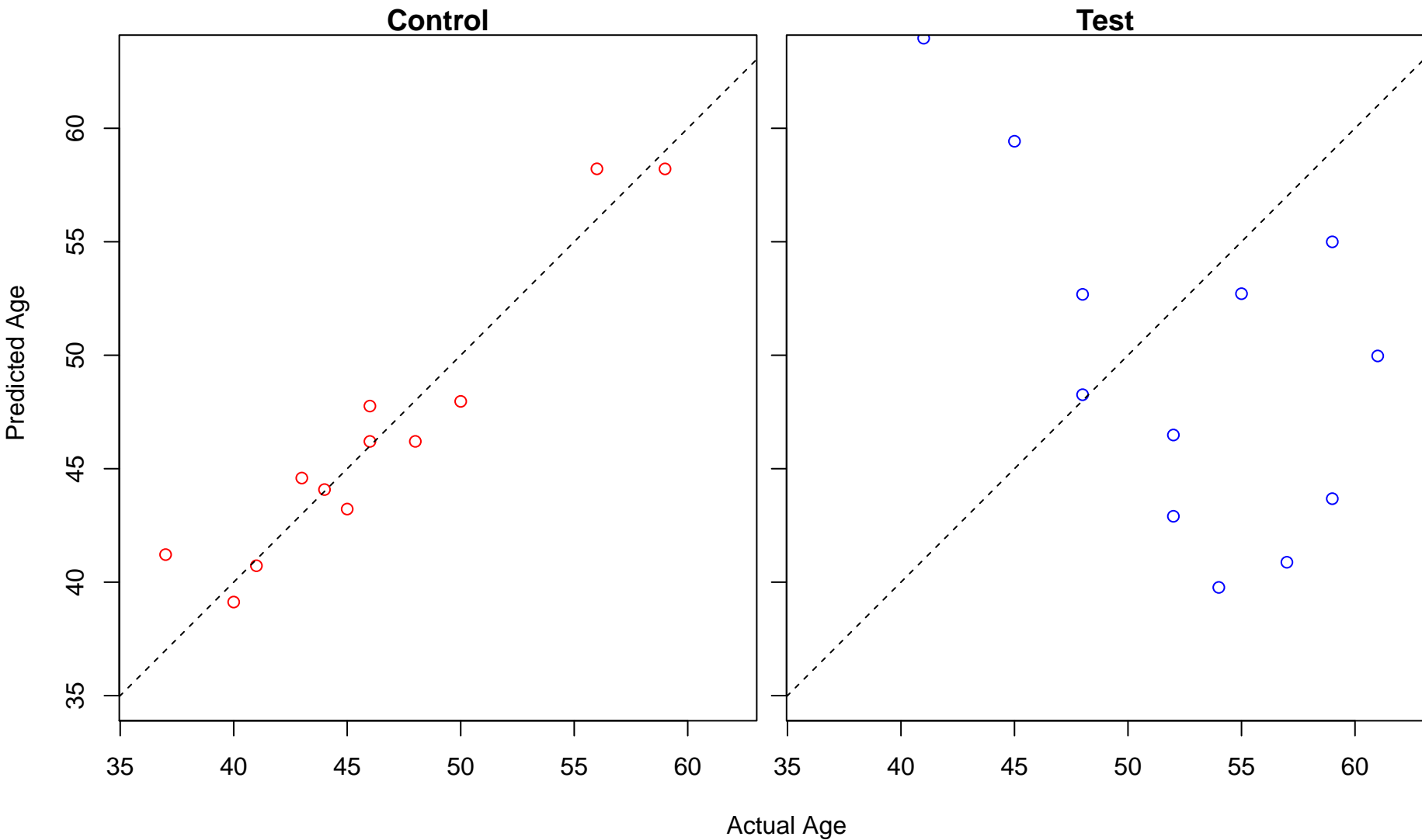


Actual Age

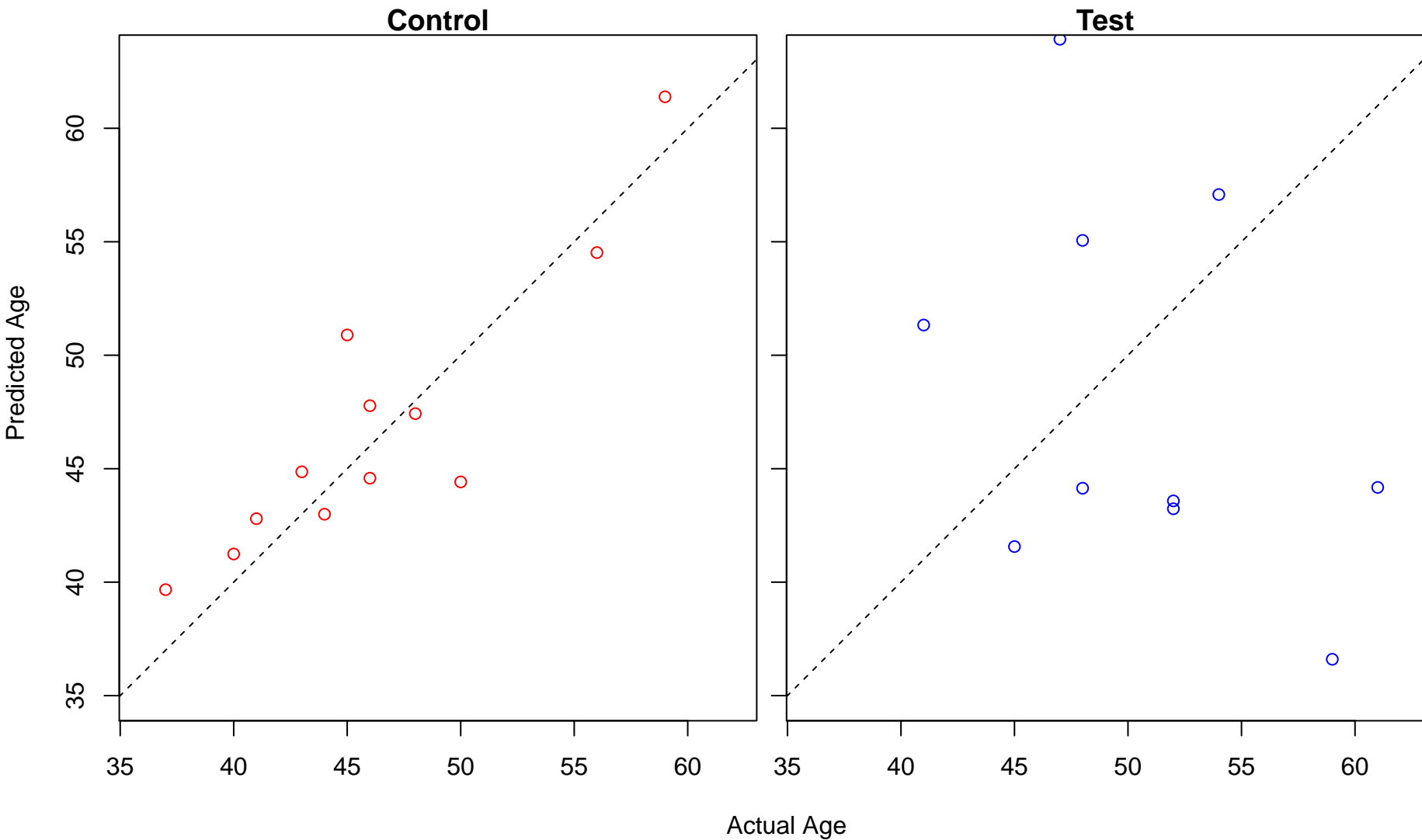
positive regulation of T cell cytokine production (Score: 15.796011)



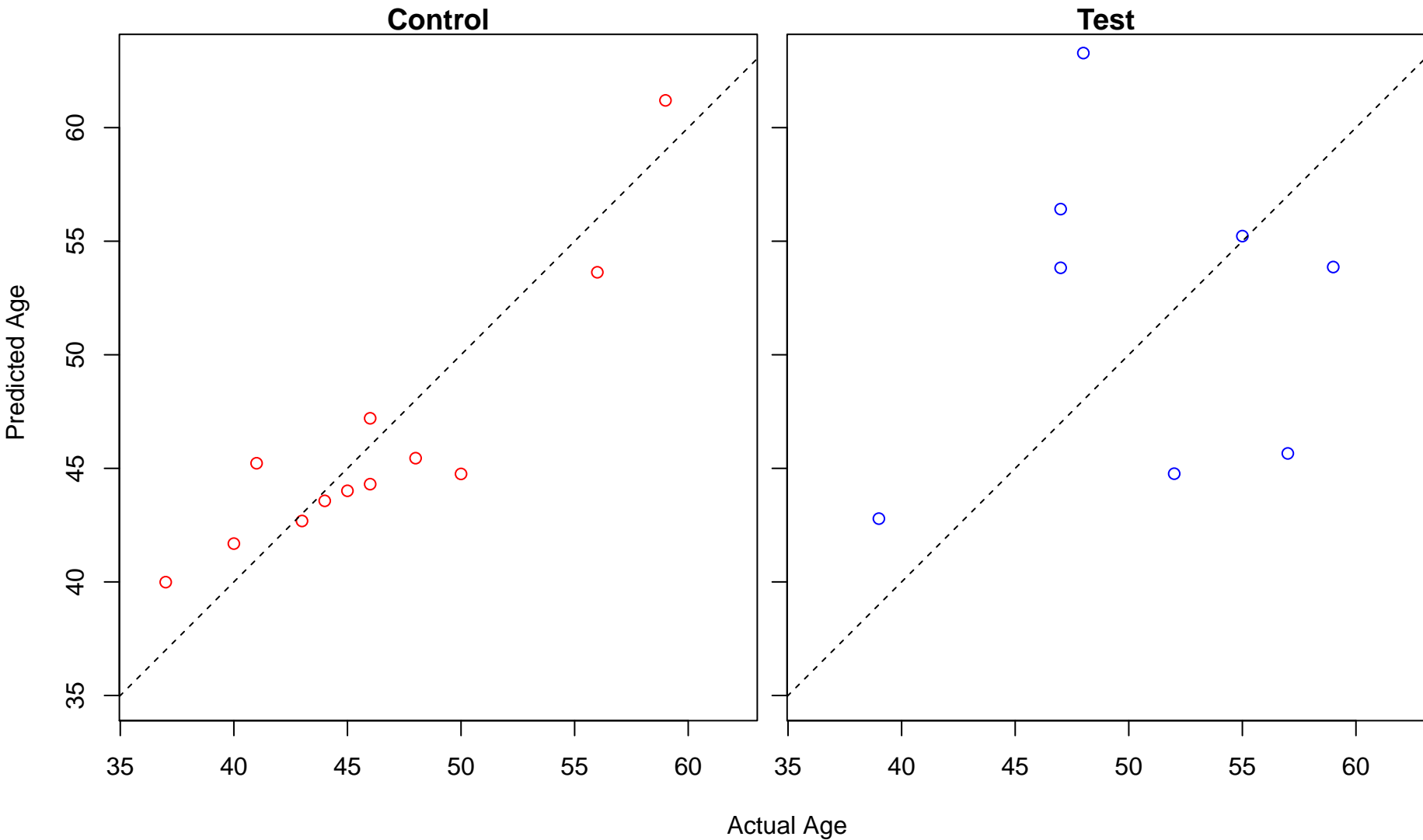
eye development (Score: 15.794334)



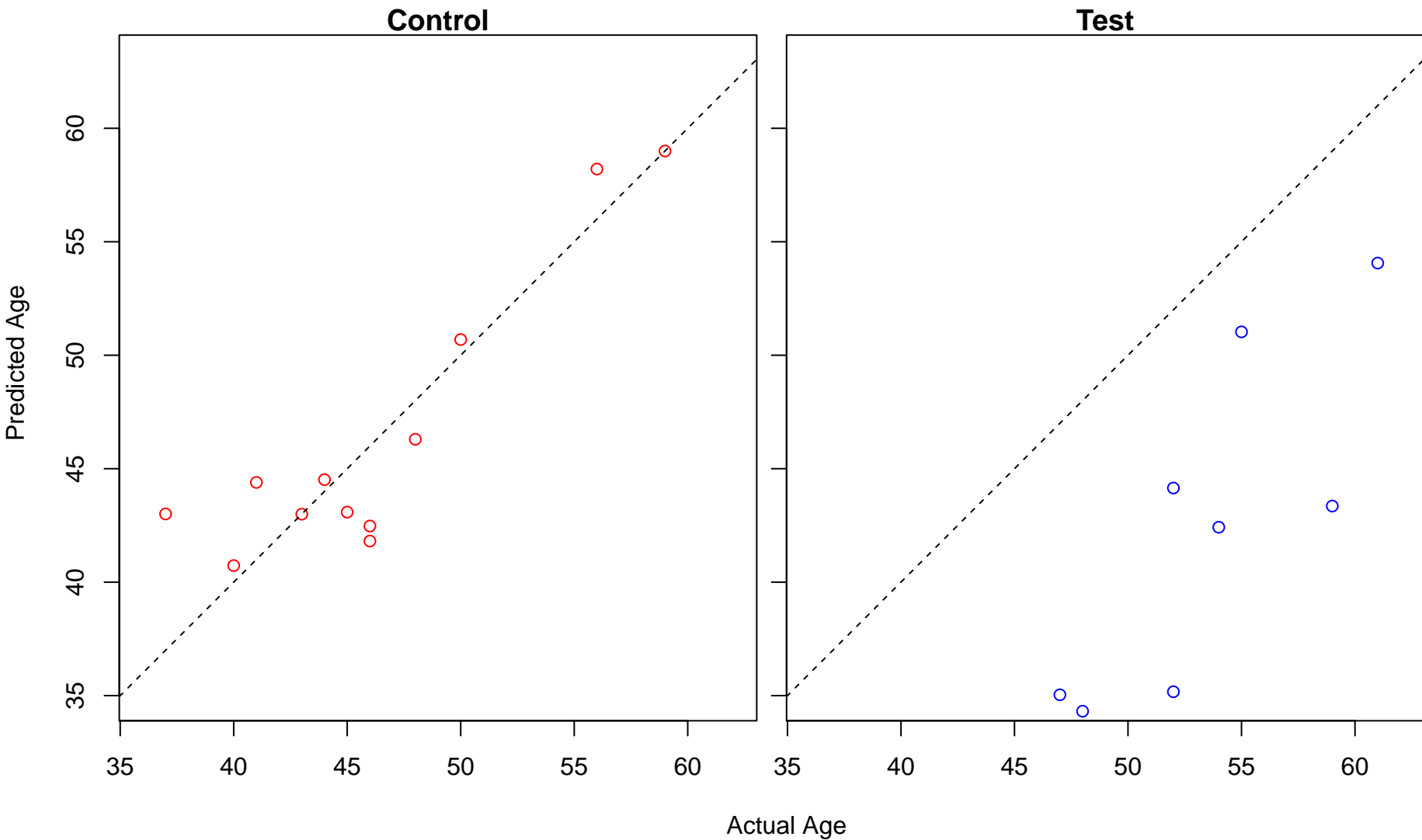
positive regulation of leukocyte proliferation (Score: 15.770477)



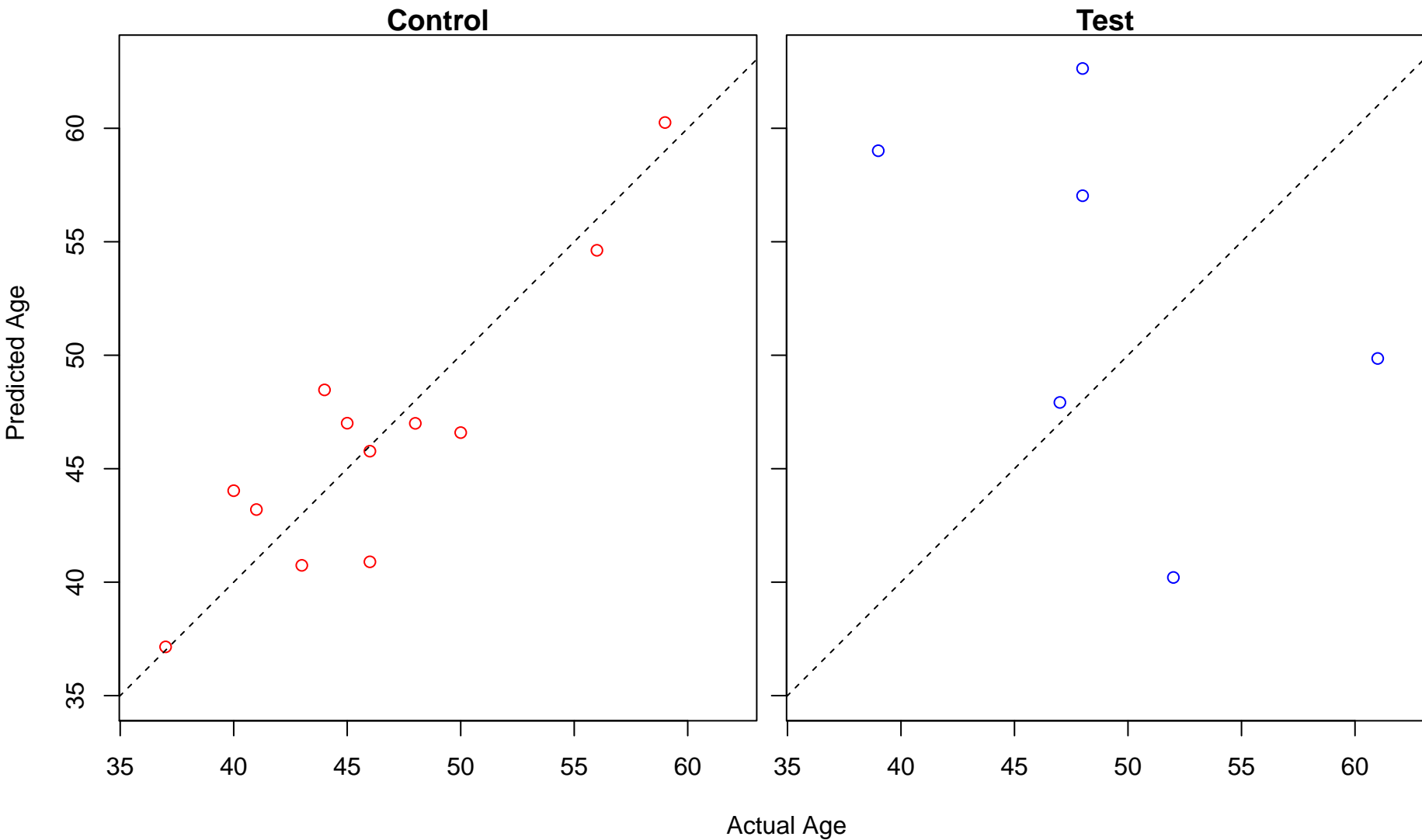
negative regulation of JNK cascade (Score: 15.738500)



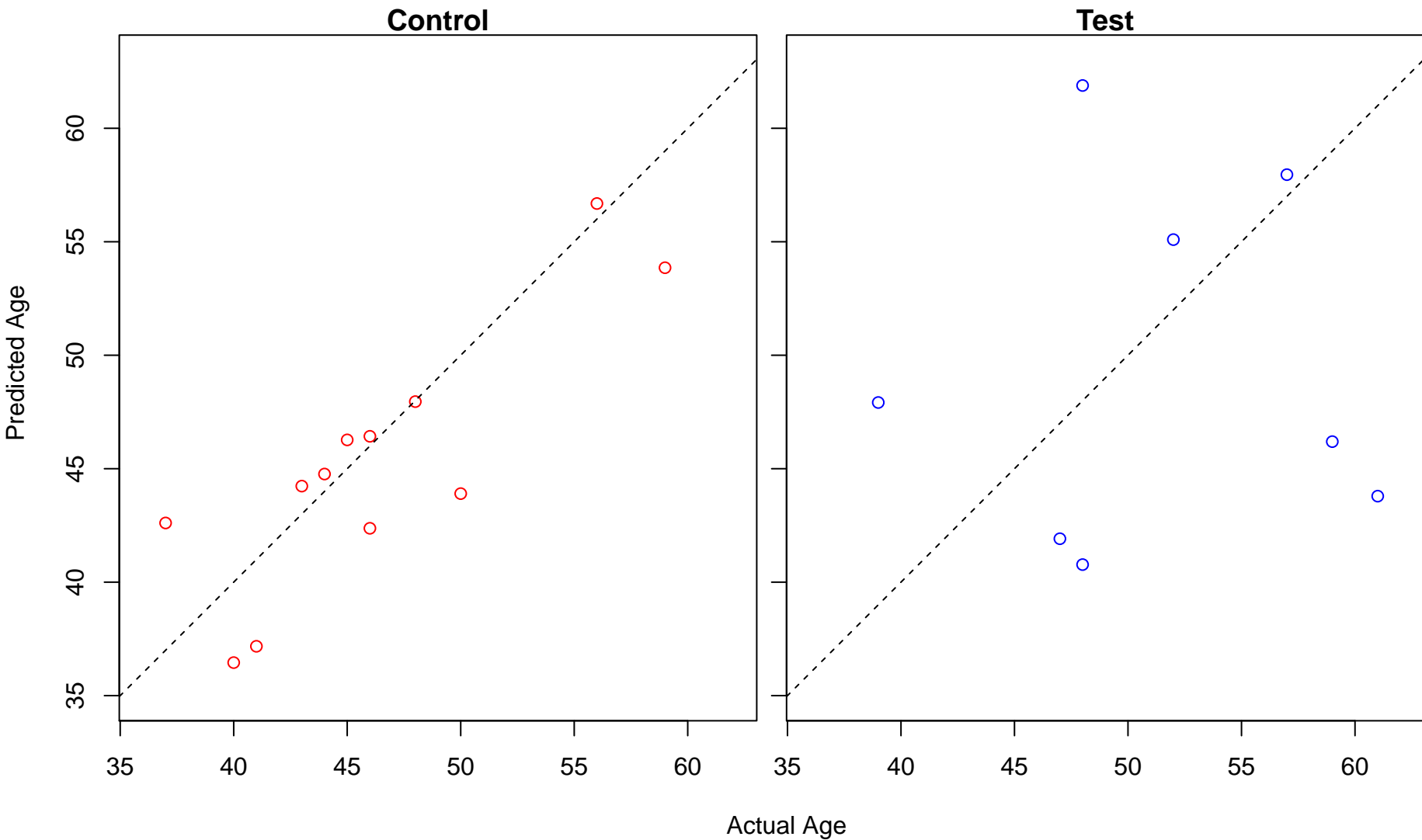
regulation of retinoic acid receptor signaling pathway (Score: 15.693797)



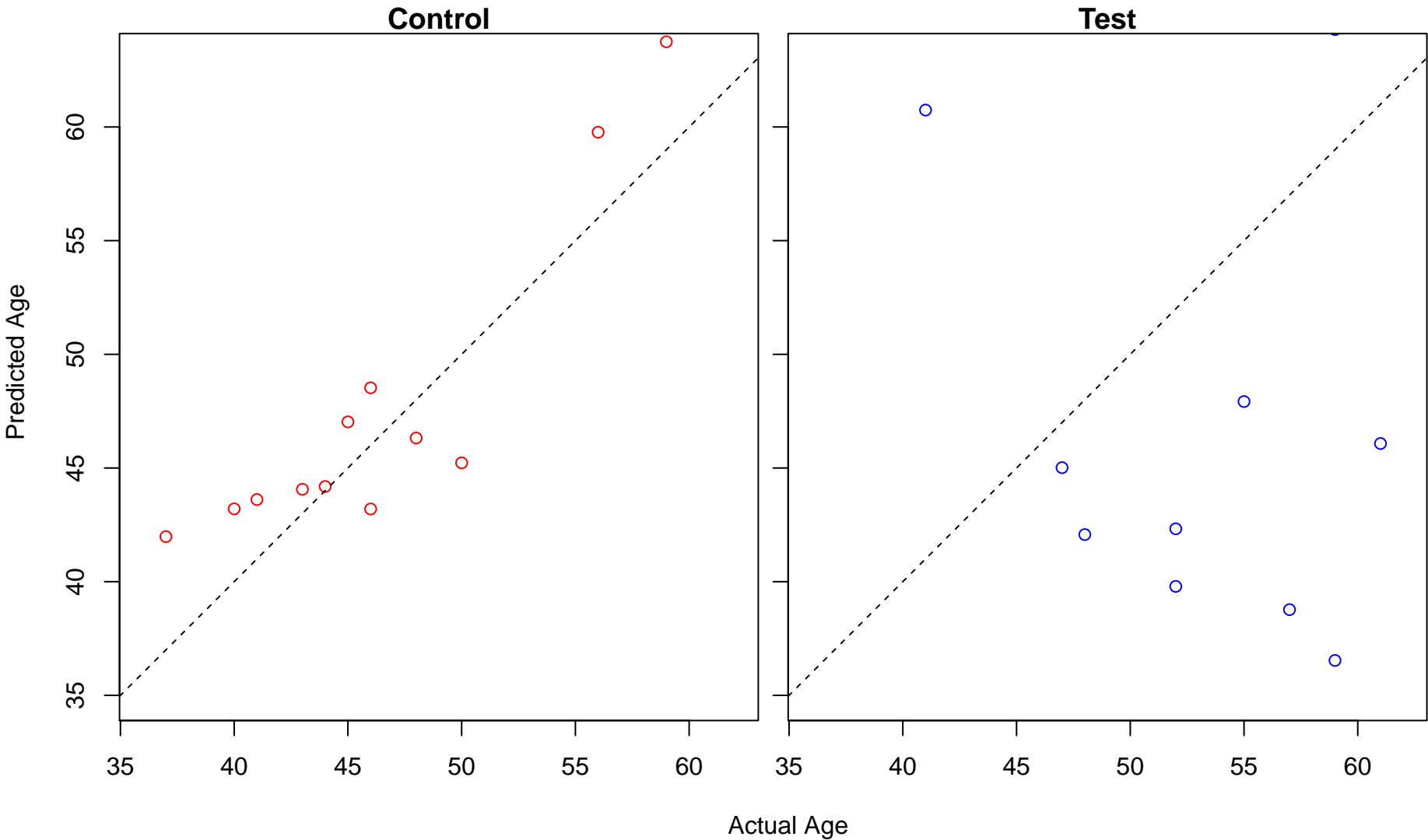
protein localization to cytoplasmic stress granule (Score: 15.691274)



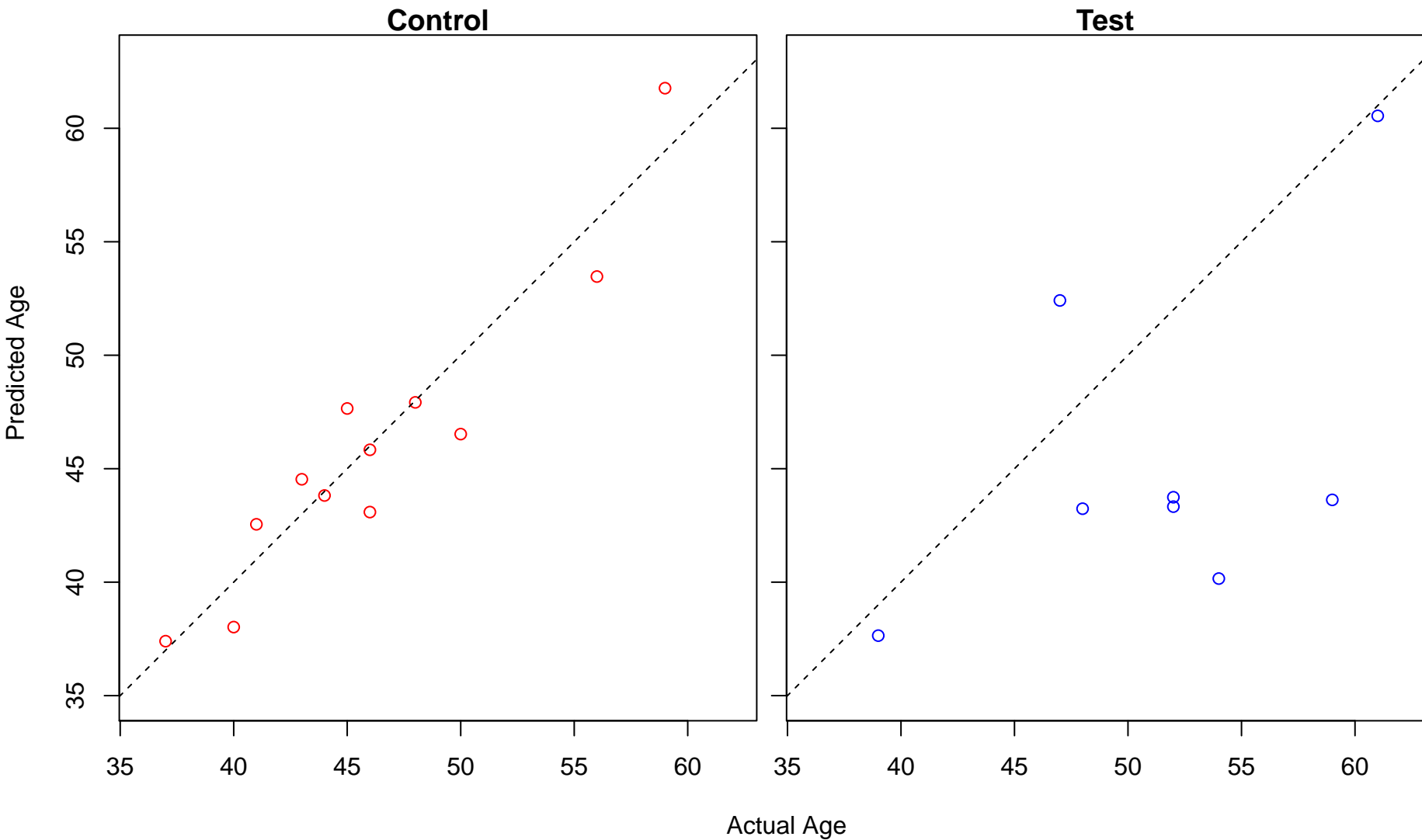
regulation of smooth muscle cell differentiation (Score: 15.665965)



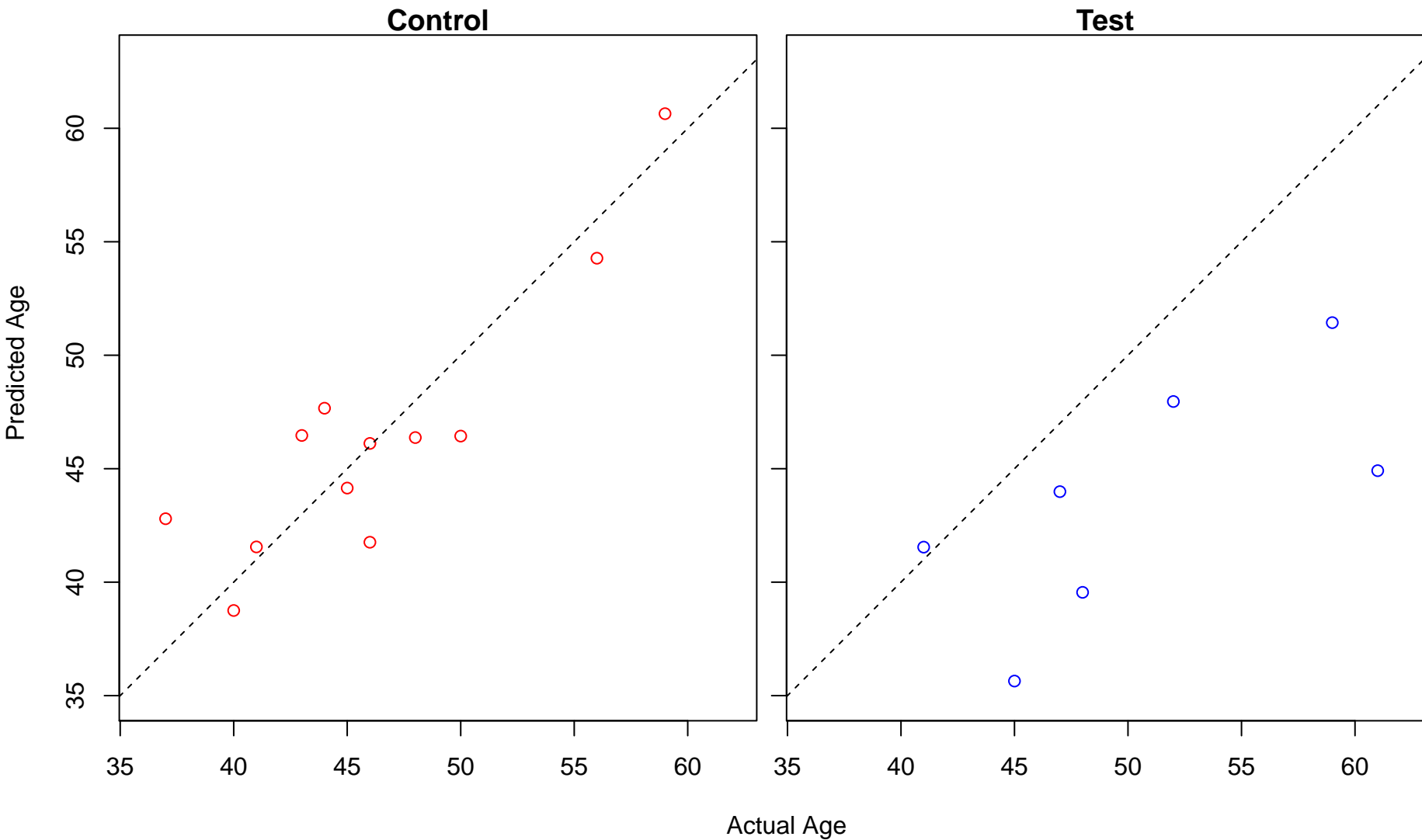
transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 15.654237)



cellular response to corticosteroid stimulus (Score: 15.635674)

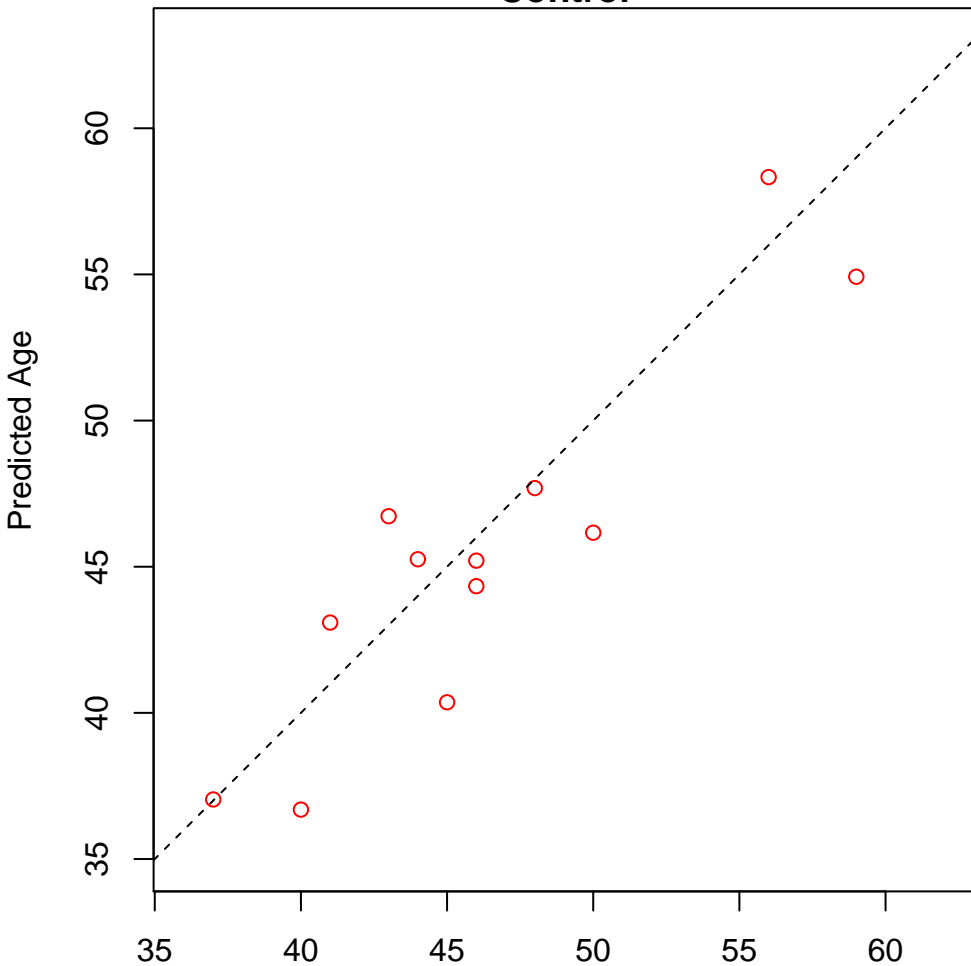


histone H2A acetylation (Score: 15.622180)

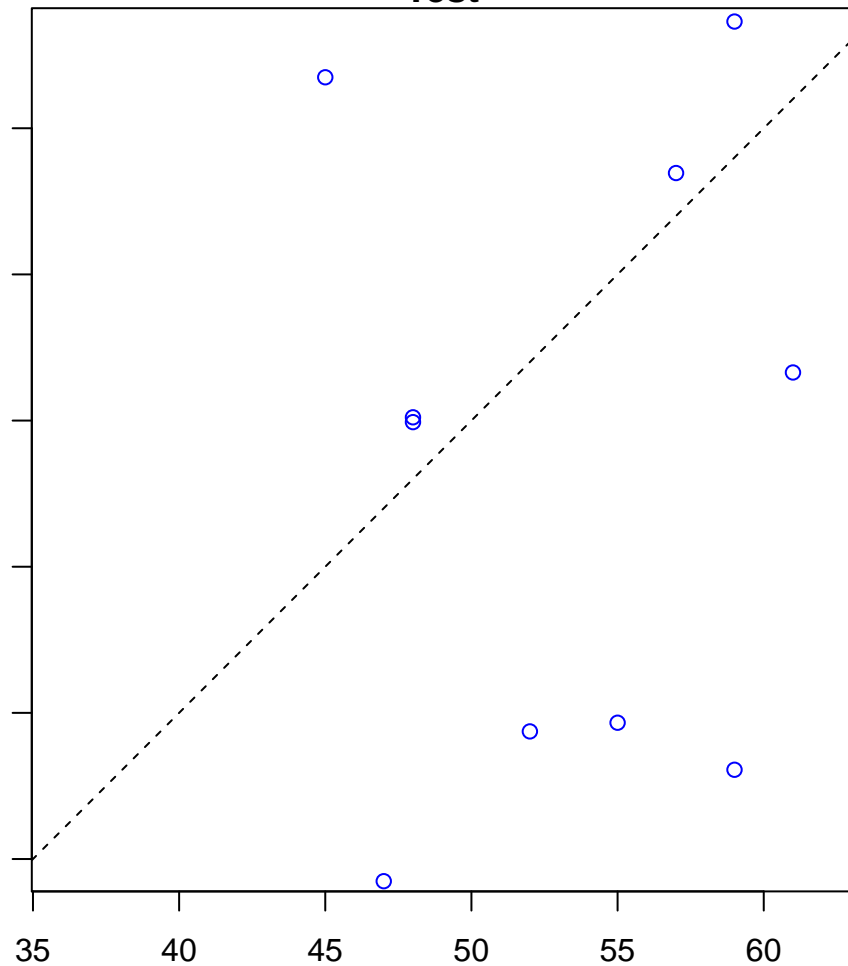


response to organic cyclic compound (Score: 15.606063)

Control



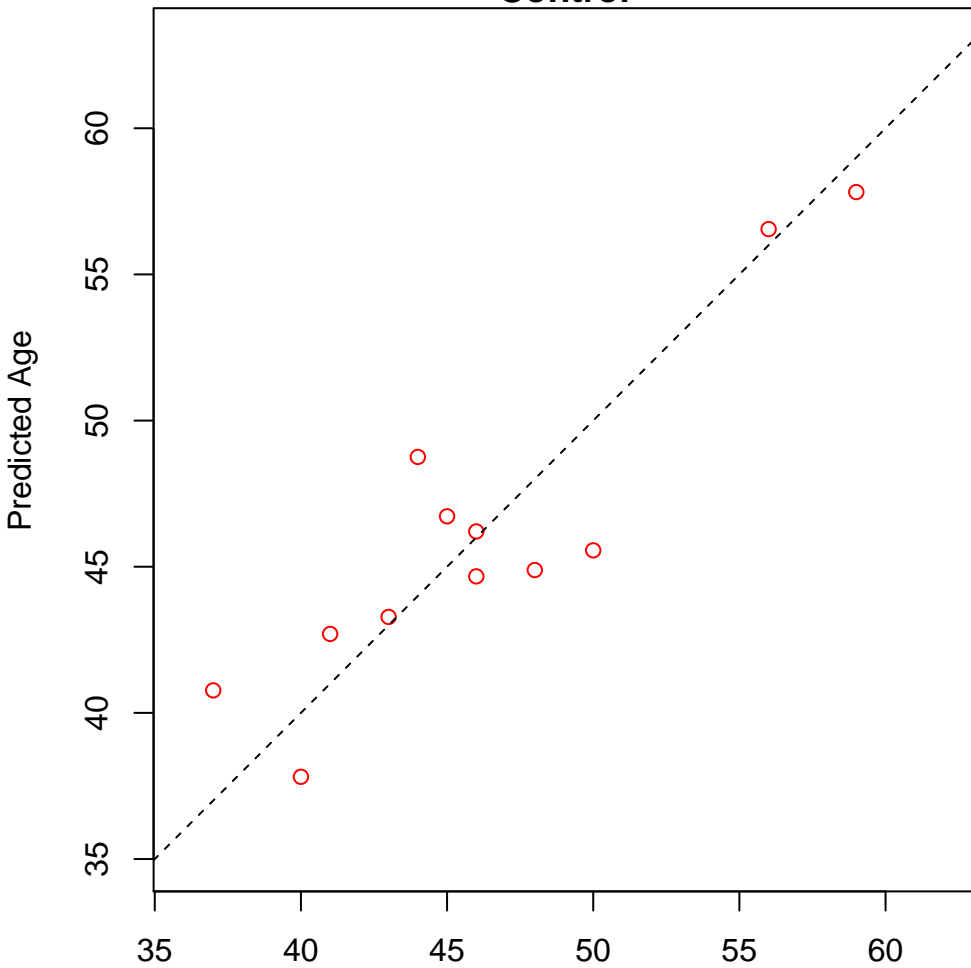
Test



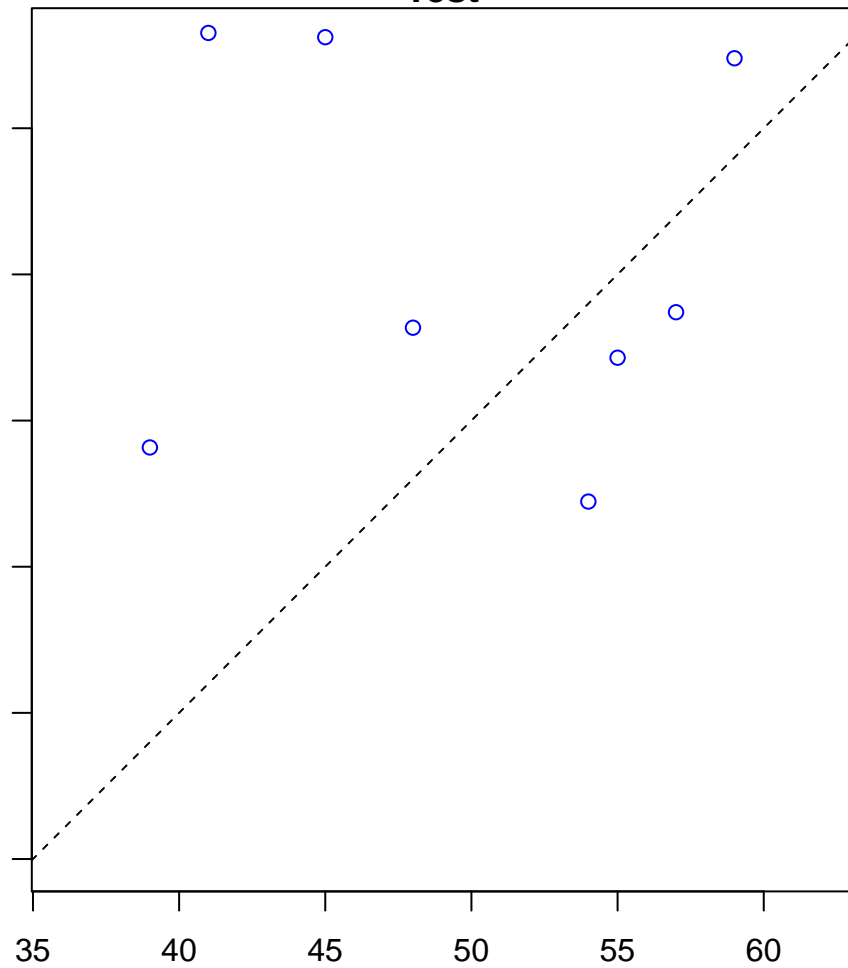
Actual Age

positive regulation of urine volume (Score: 15.597389)

Control

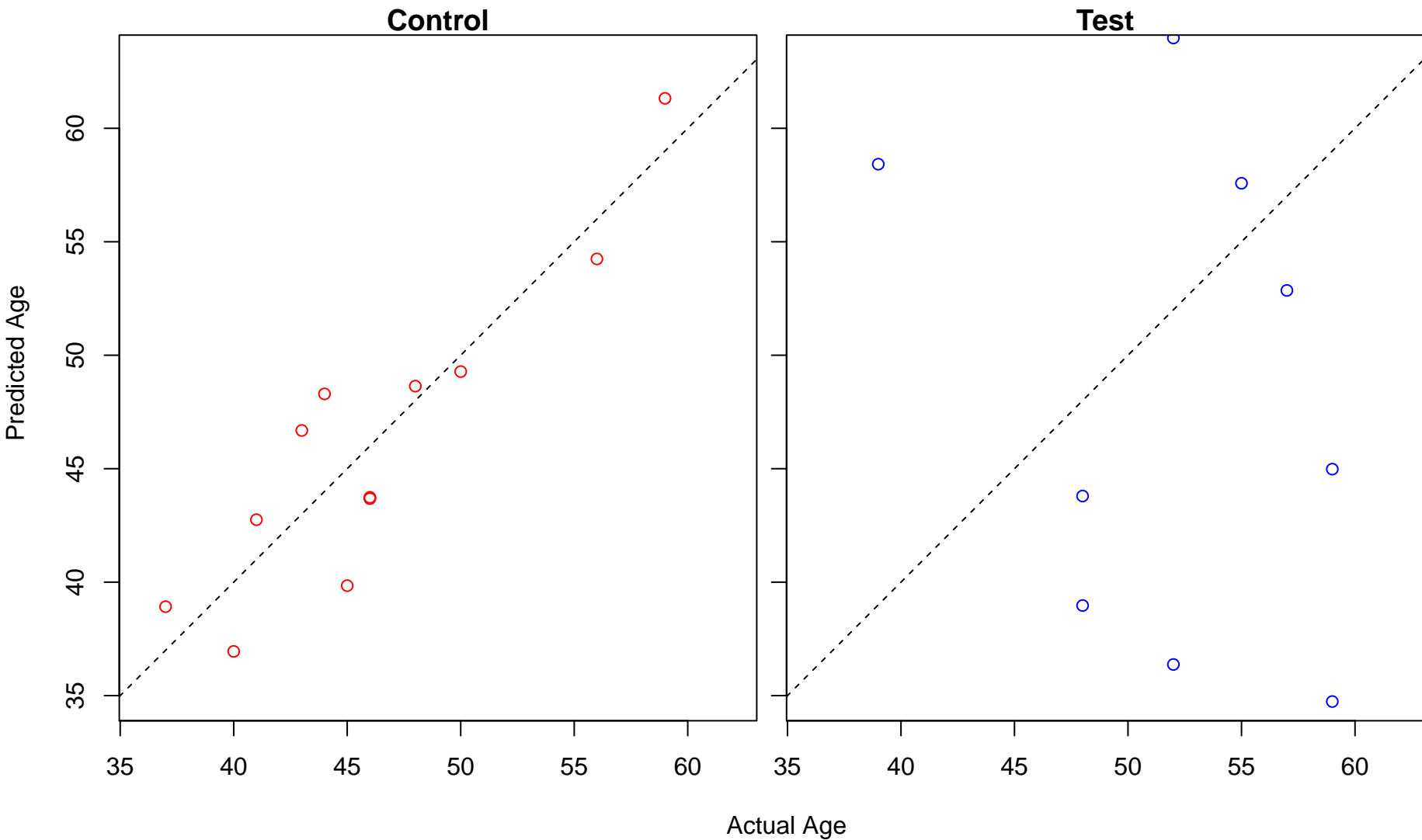


Test

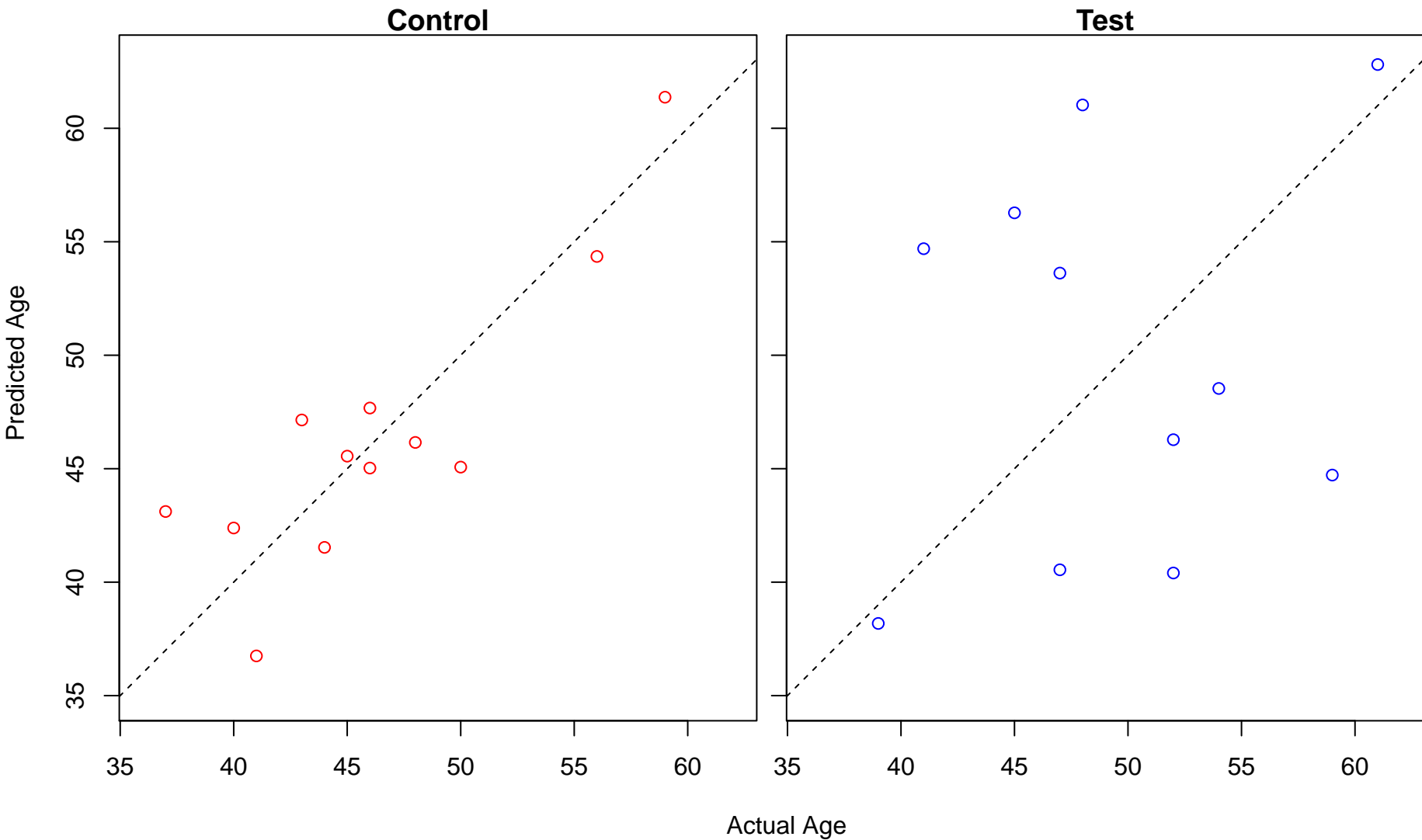


Actual Age

cardiolipin biosynthetic process (Score: 15.585864)

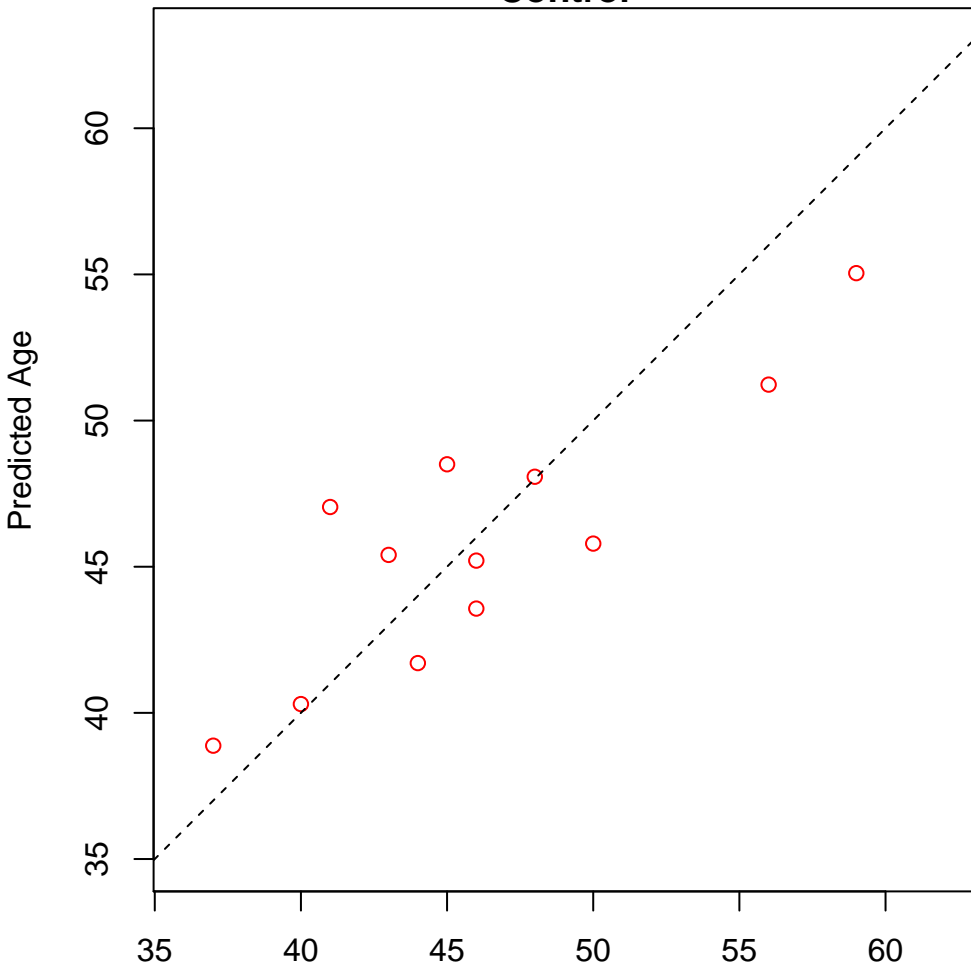


negative regulation of response to biotic stimulus (Score: 15.580398)

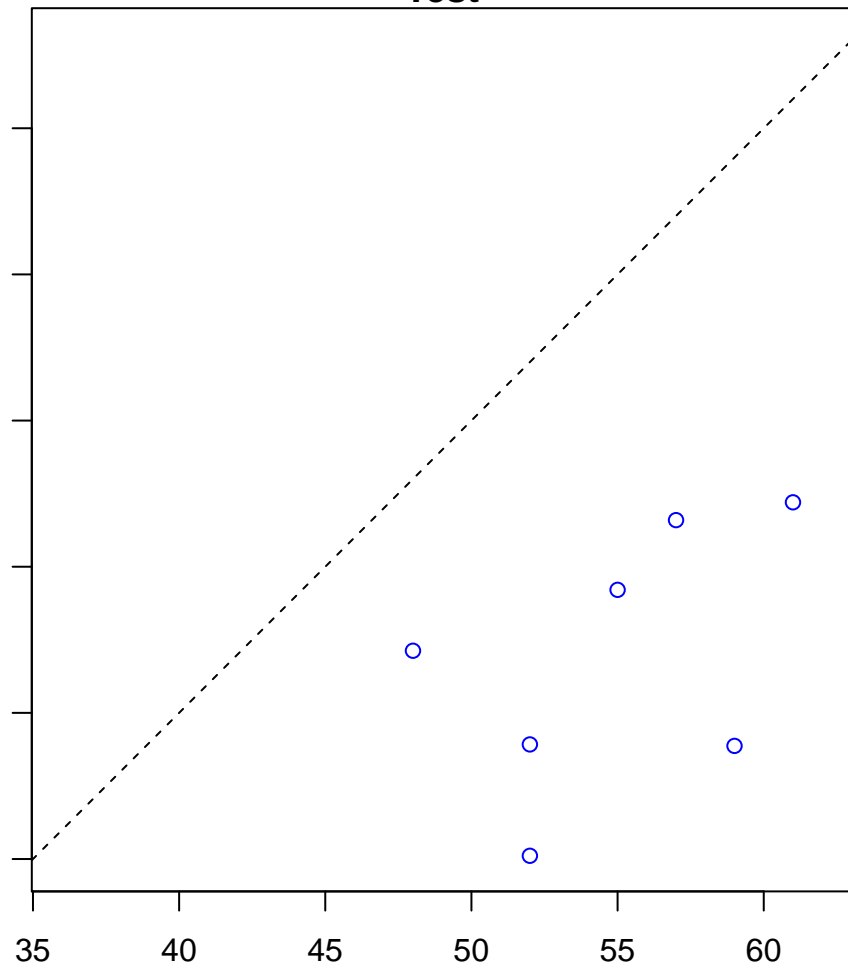


blood coagulation, fibrin clot formation (Score: 15.538426)

Control

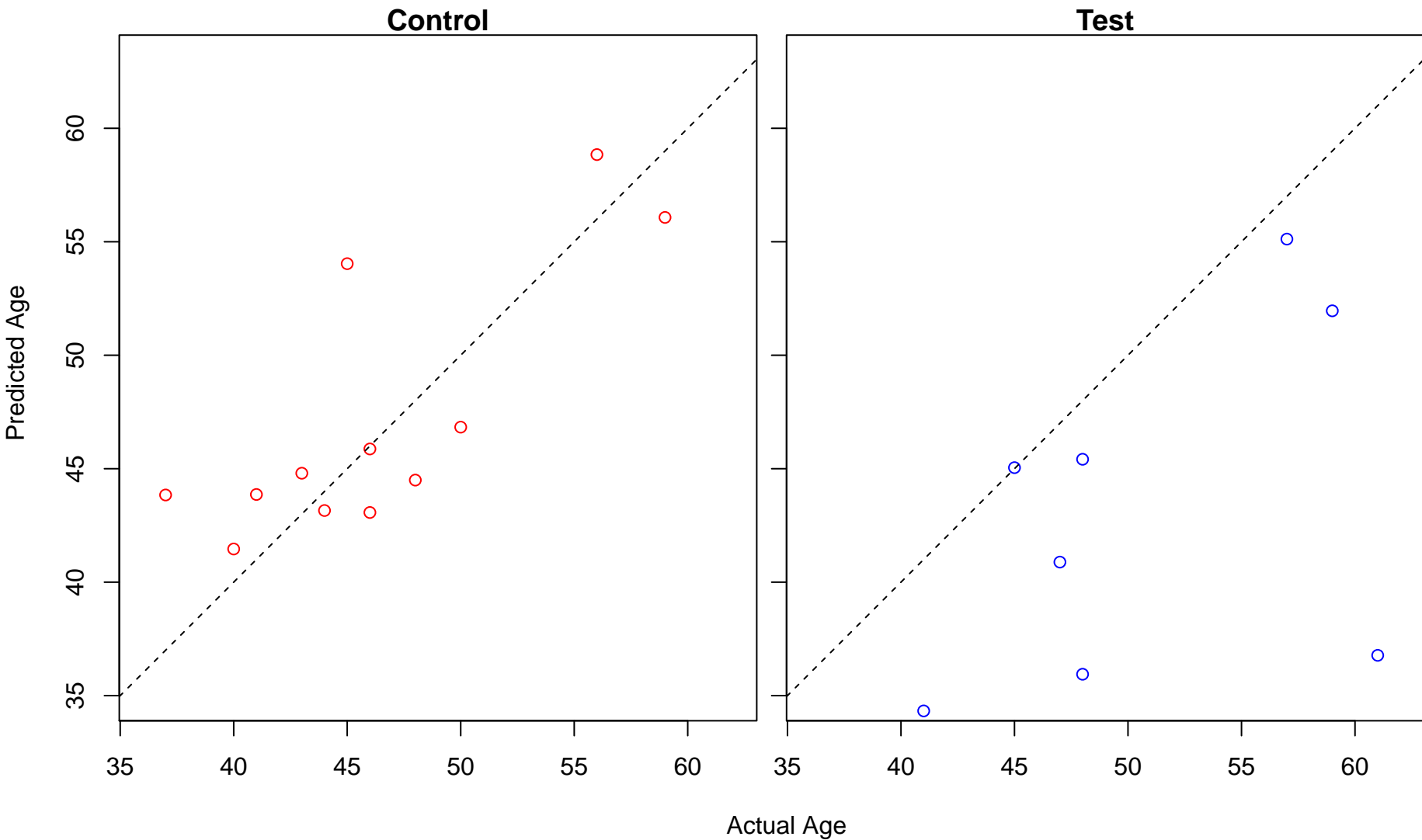


Test

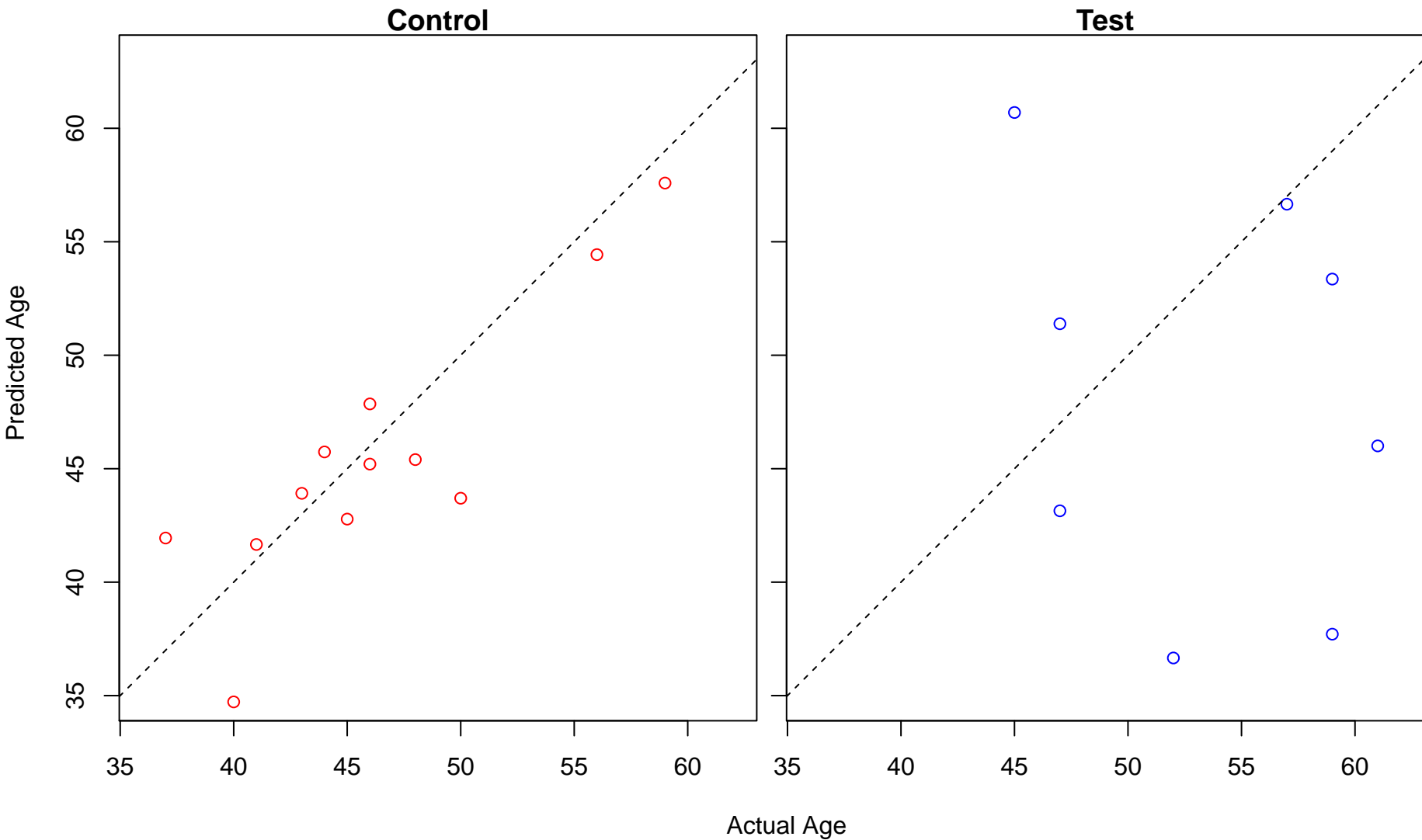


Actual Age

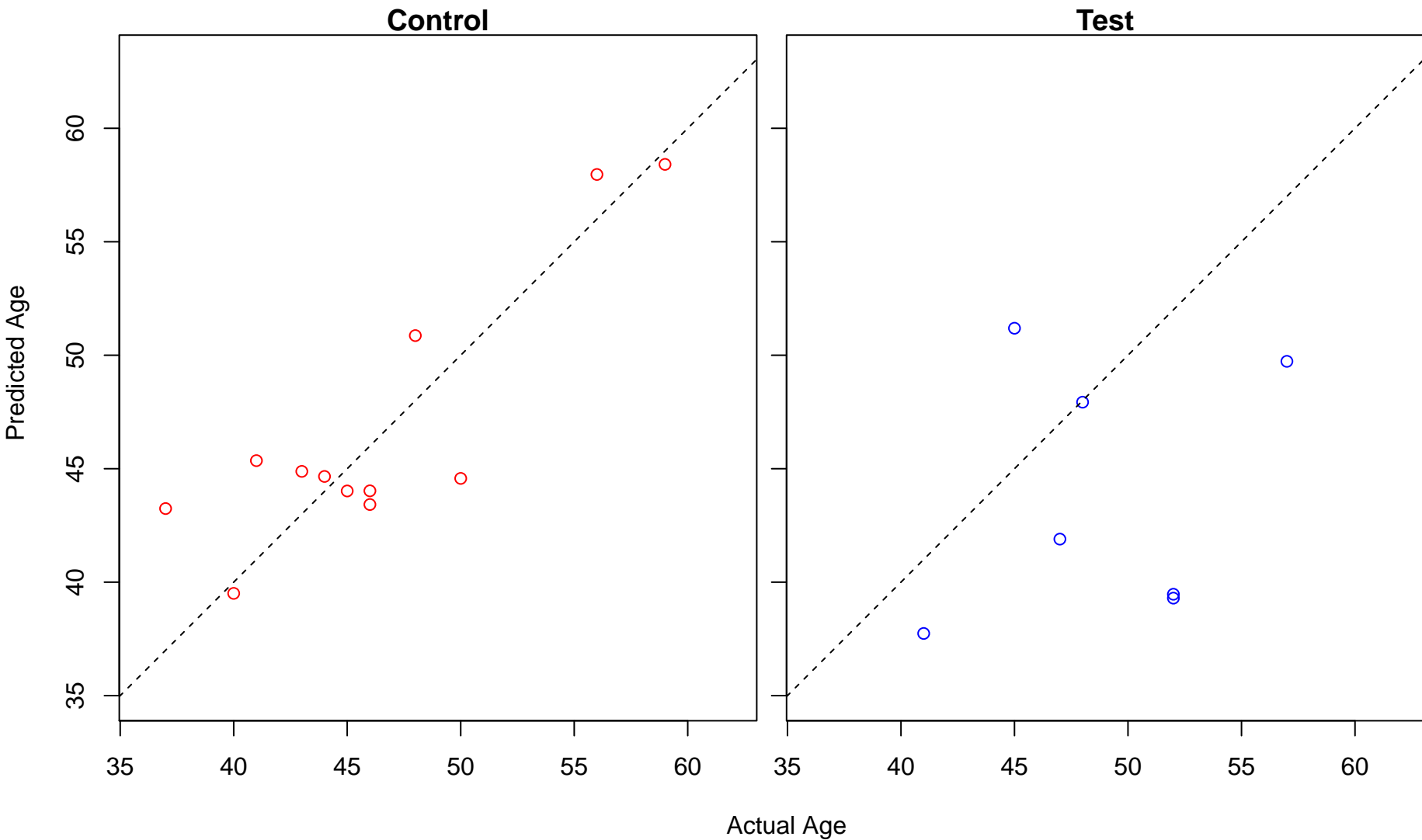
negative regulation of autophagy (Score: 15.518269)



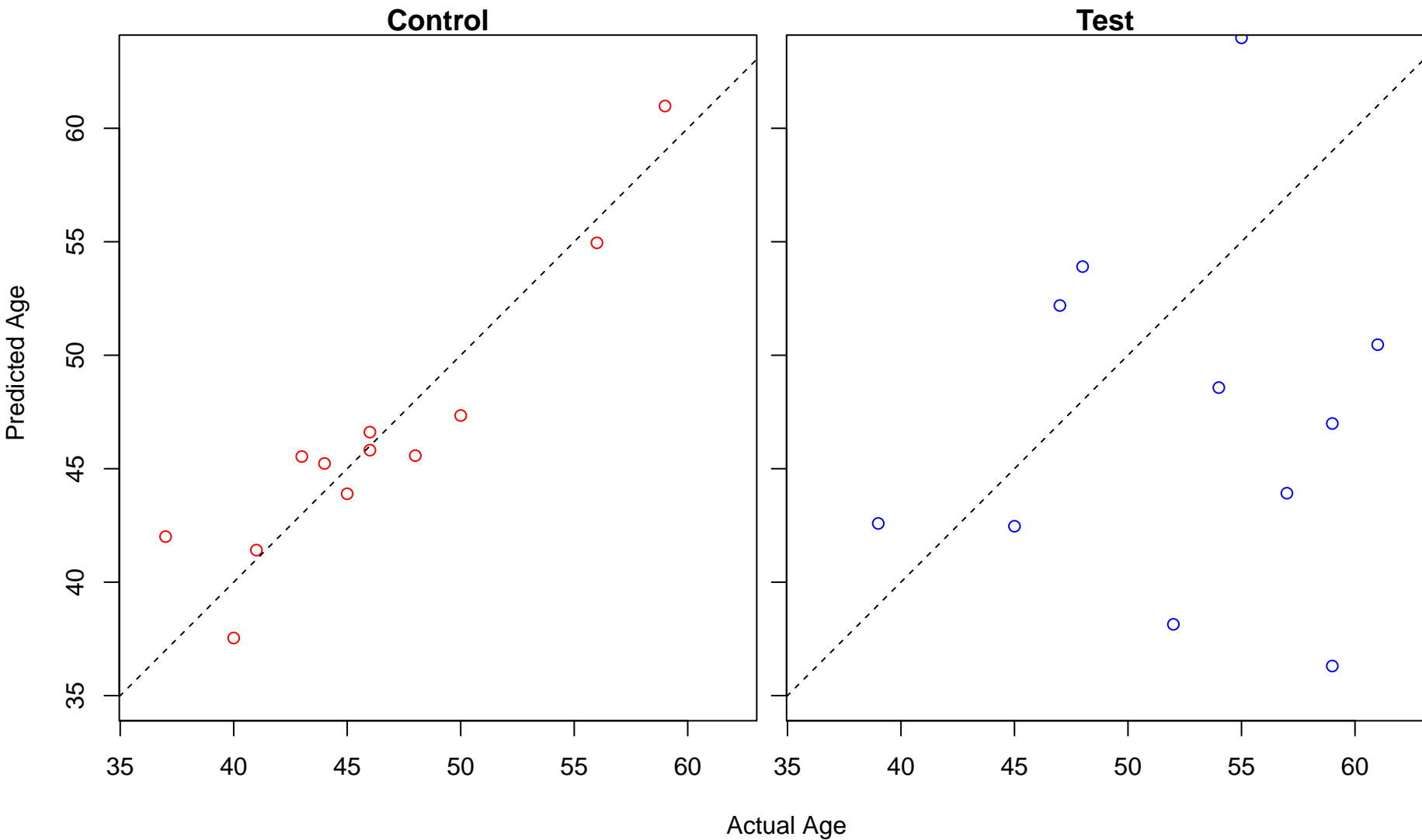
heart looping (Score: 15.496732)



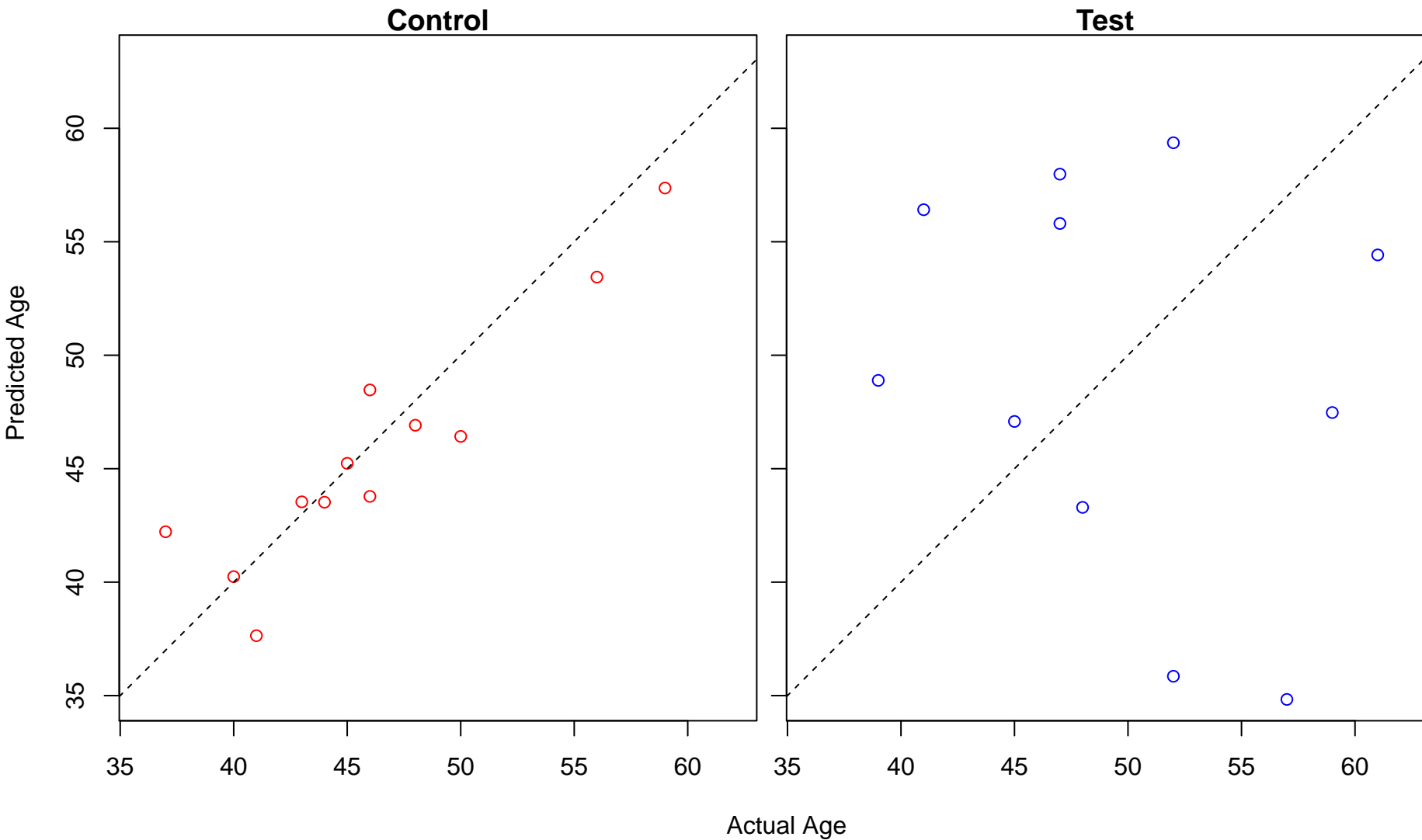
negative regulation of cell cycle G2/M phase transition (Score: 15.459060)



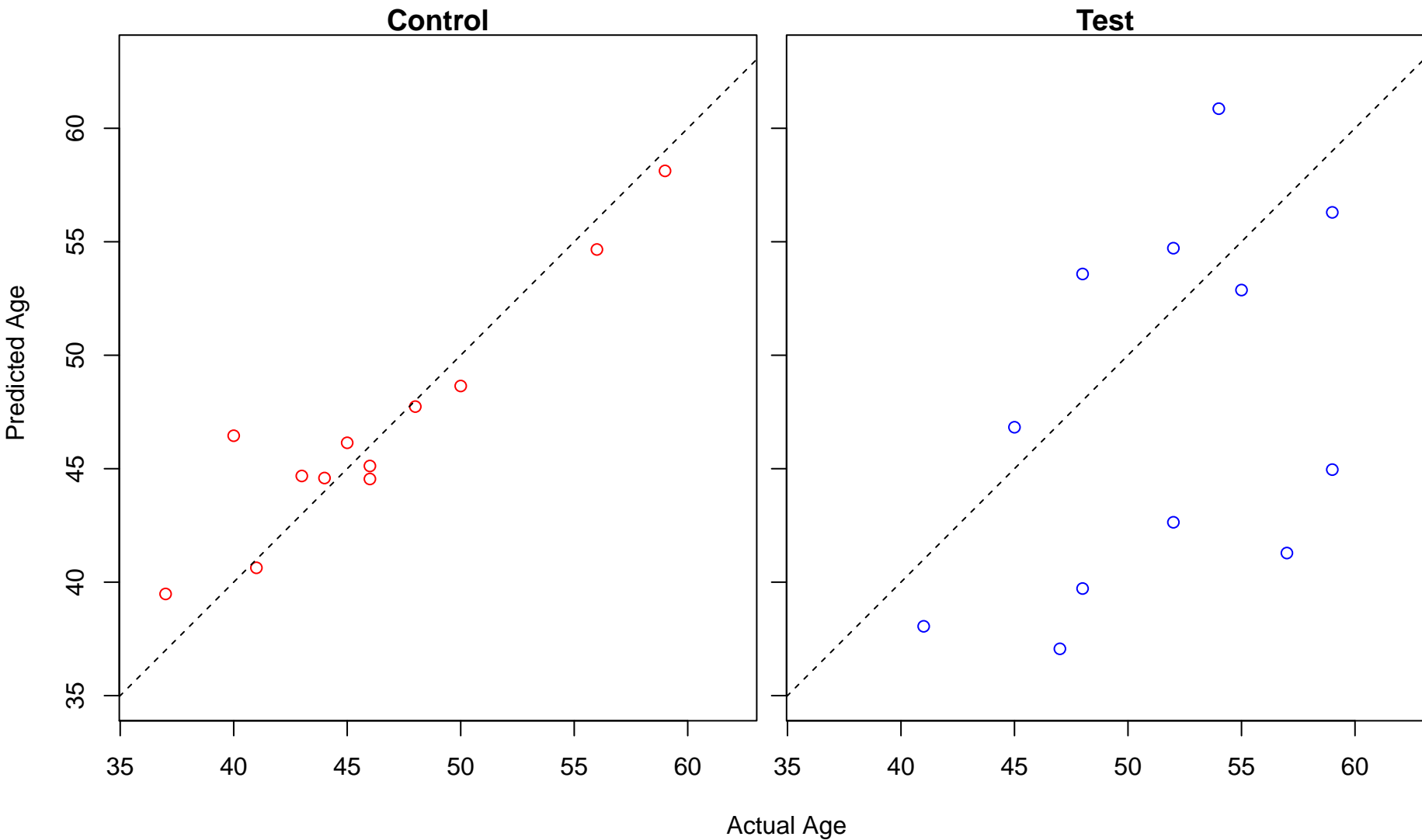
forebrain neuron development (Score: 15.434567)



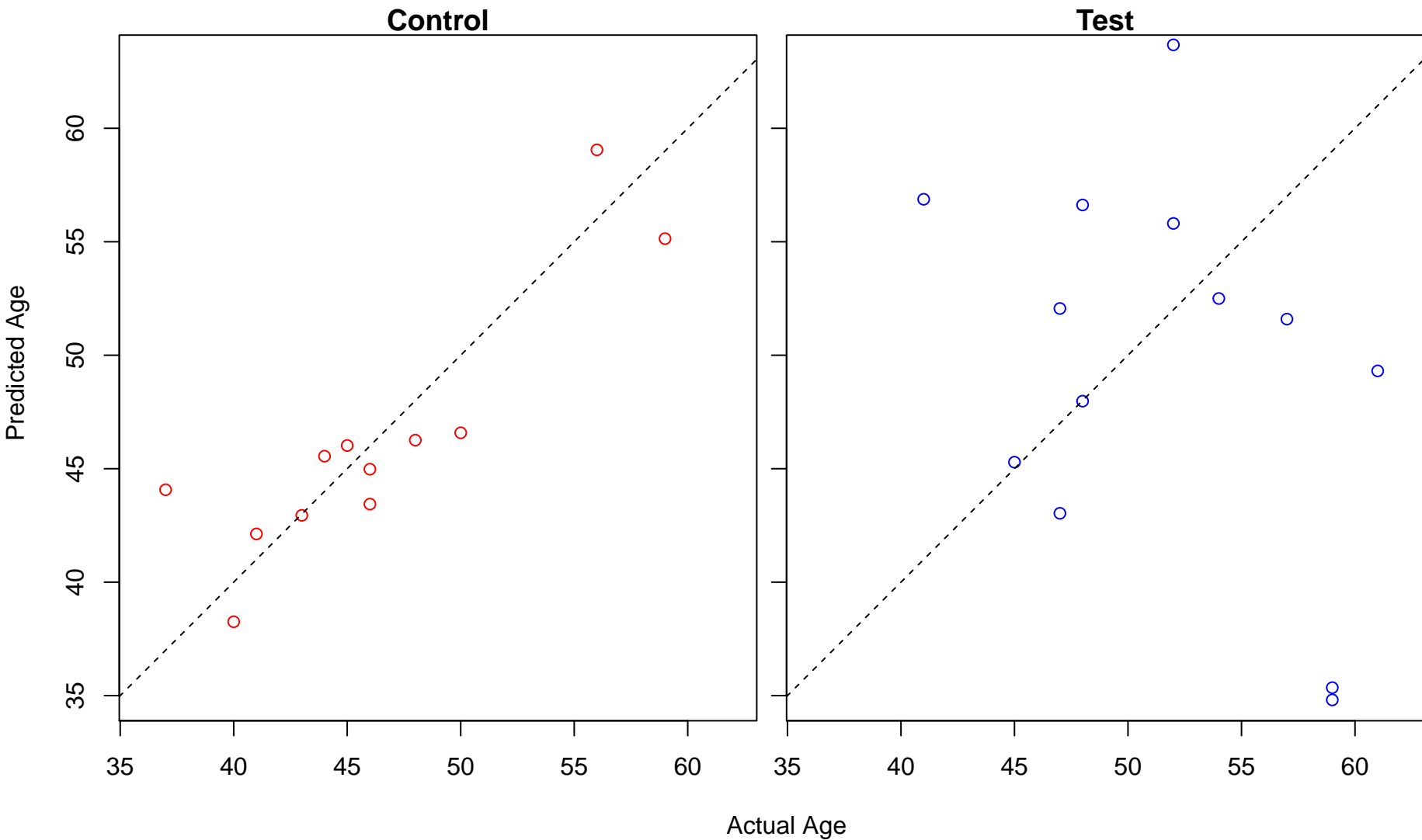
positive regulation of sodium ion transmembrane transport (Score: 15.377737)



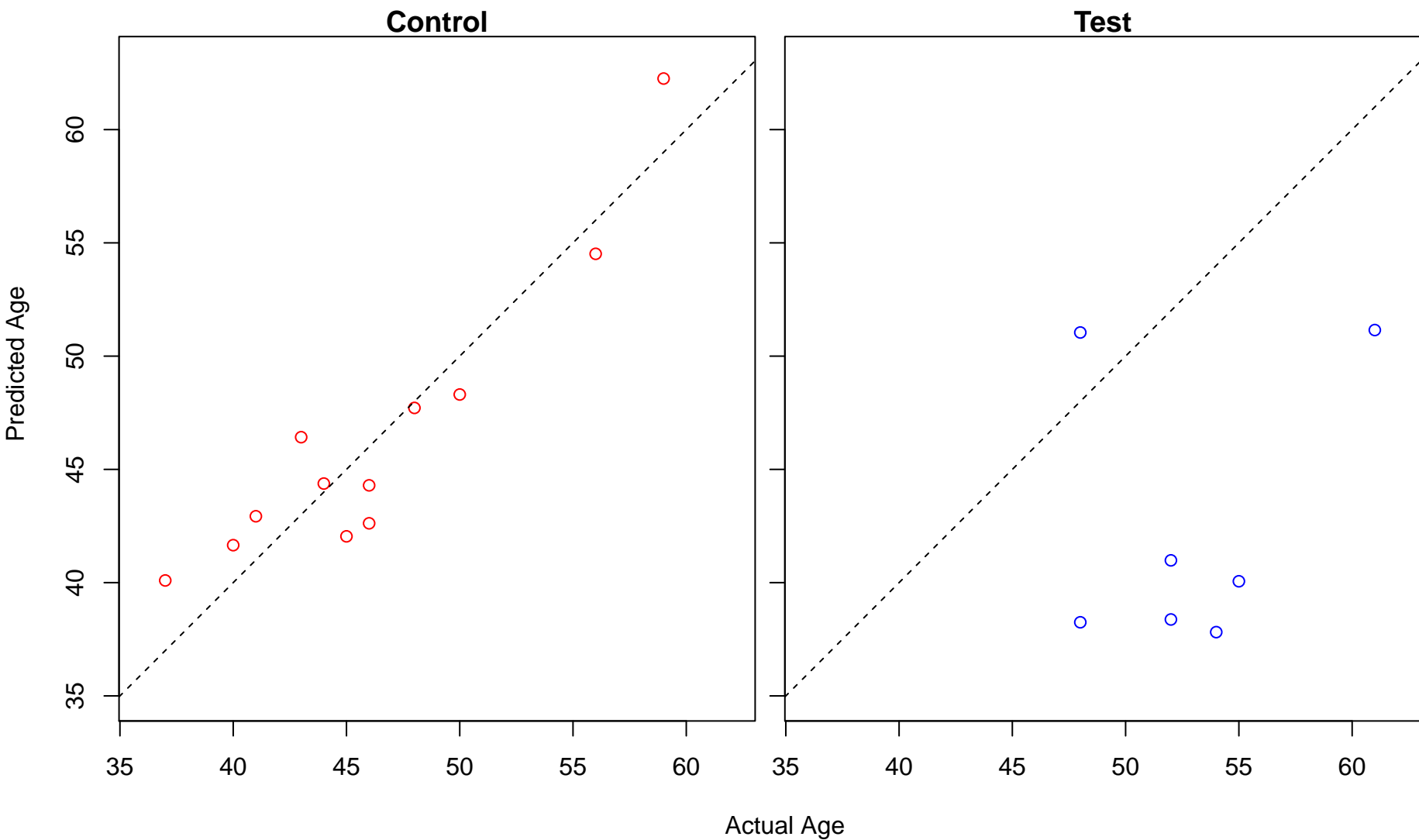
salivary gland development (Score: 15.370083)



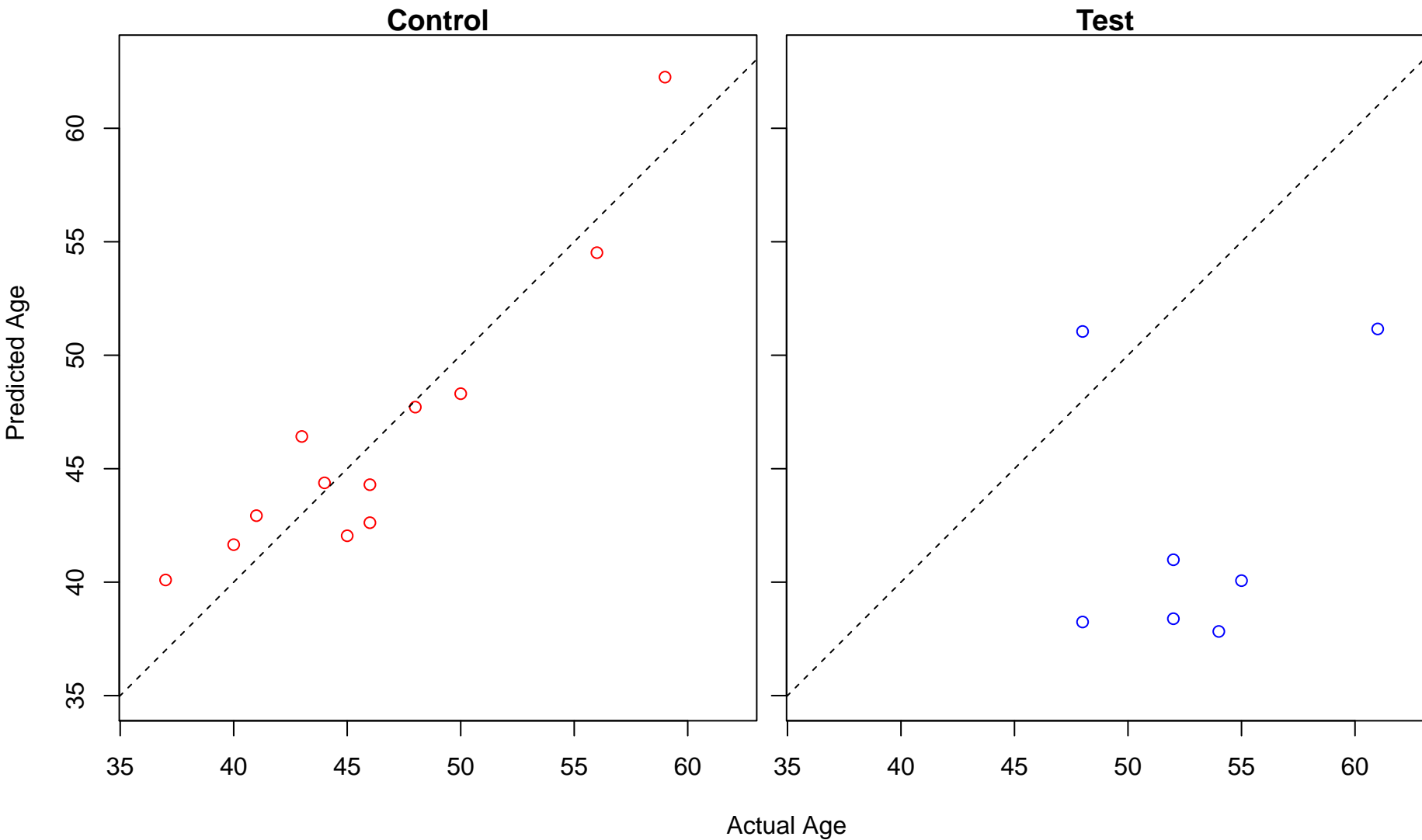
double-strand break repair via synthesis-dependent strand annealing (Score: 15.361086)



gonad development (Score: 15.348741)

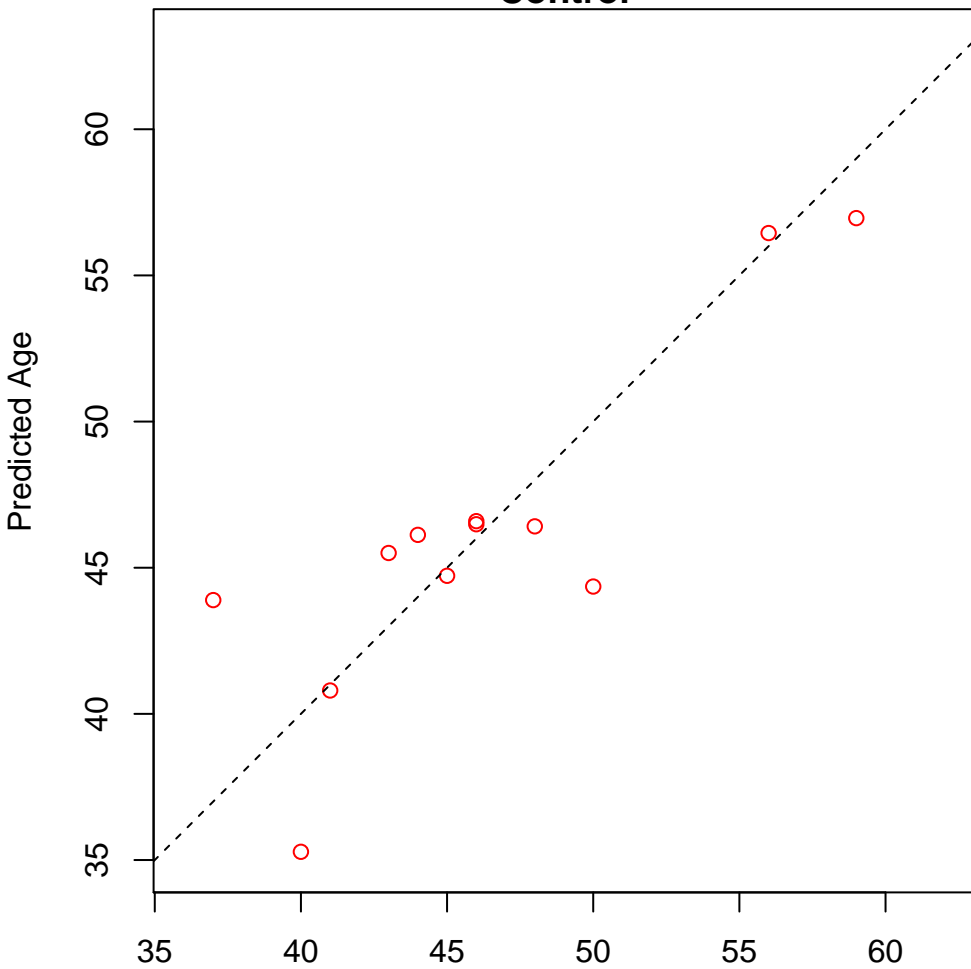


development of primary sexual characteristics (Score: 15.345930)

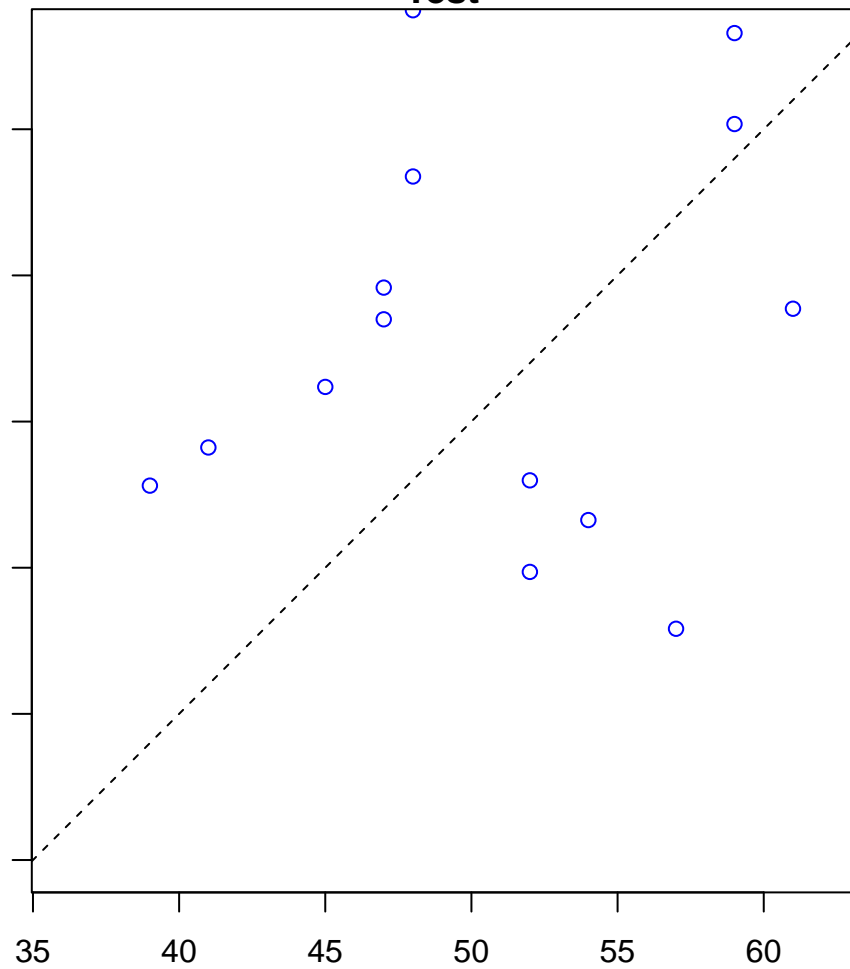


cytoplasmic sequestering of protein (Score: 15.315462)

Control

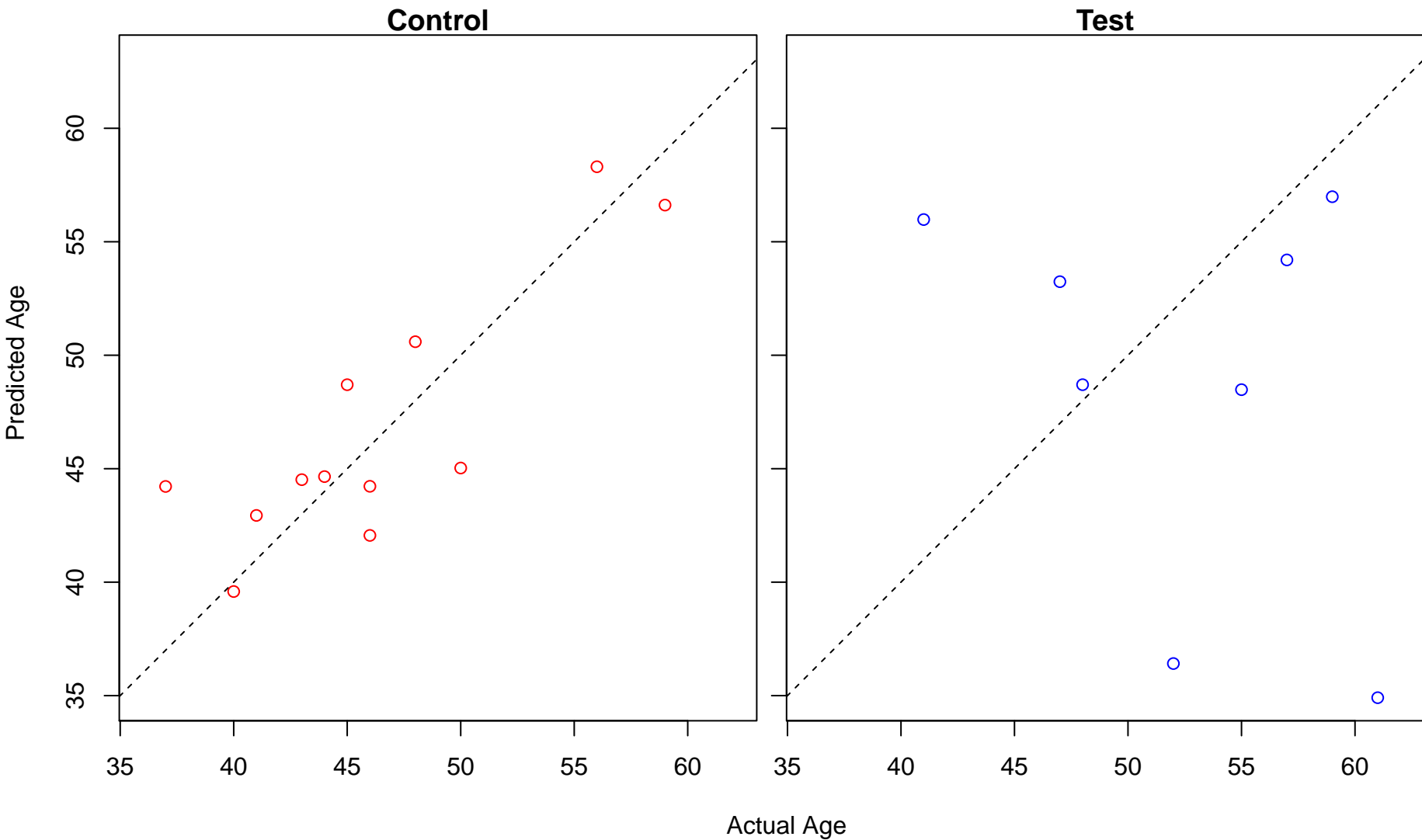


Test

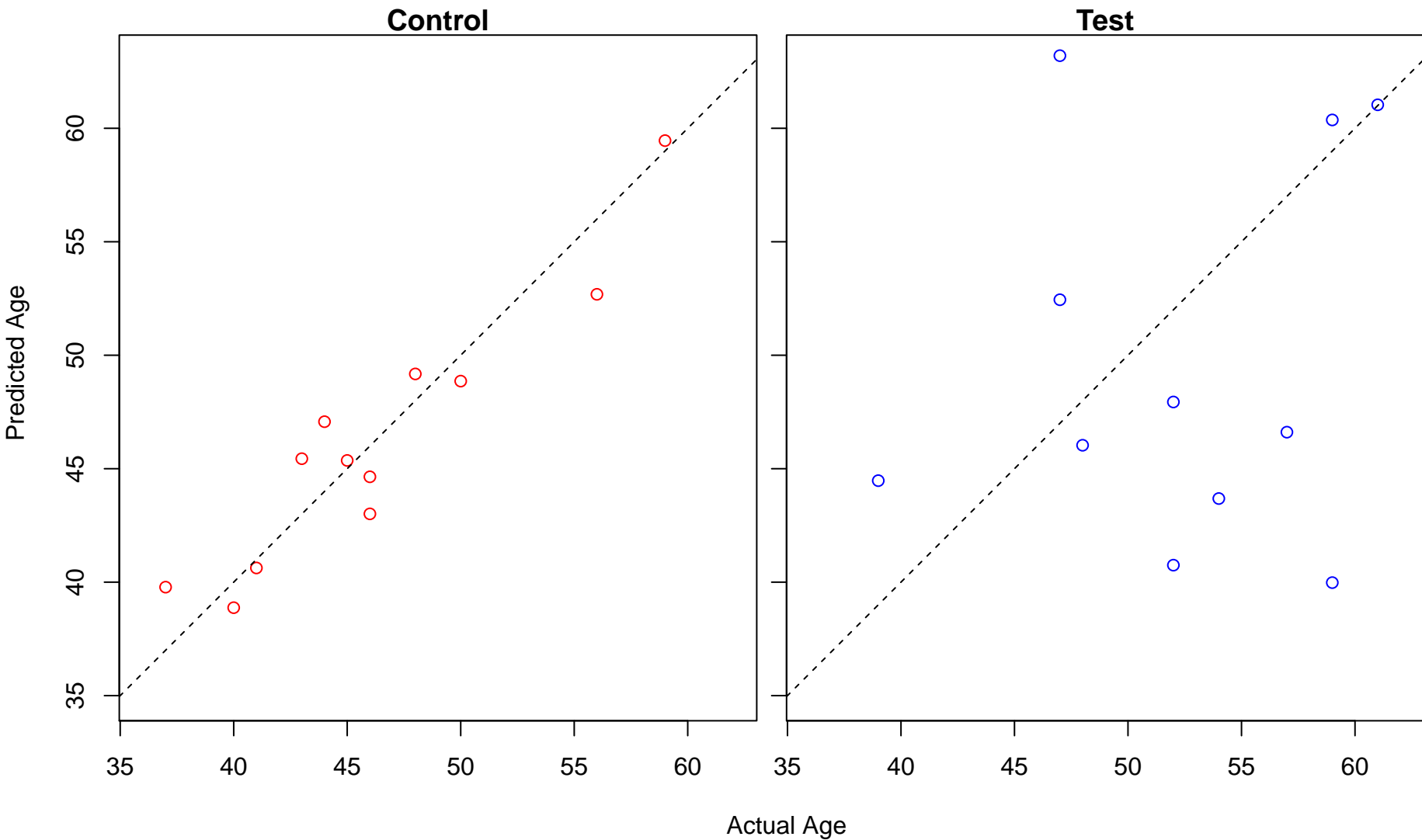


Actual Age

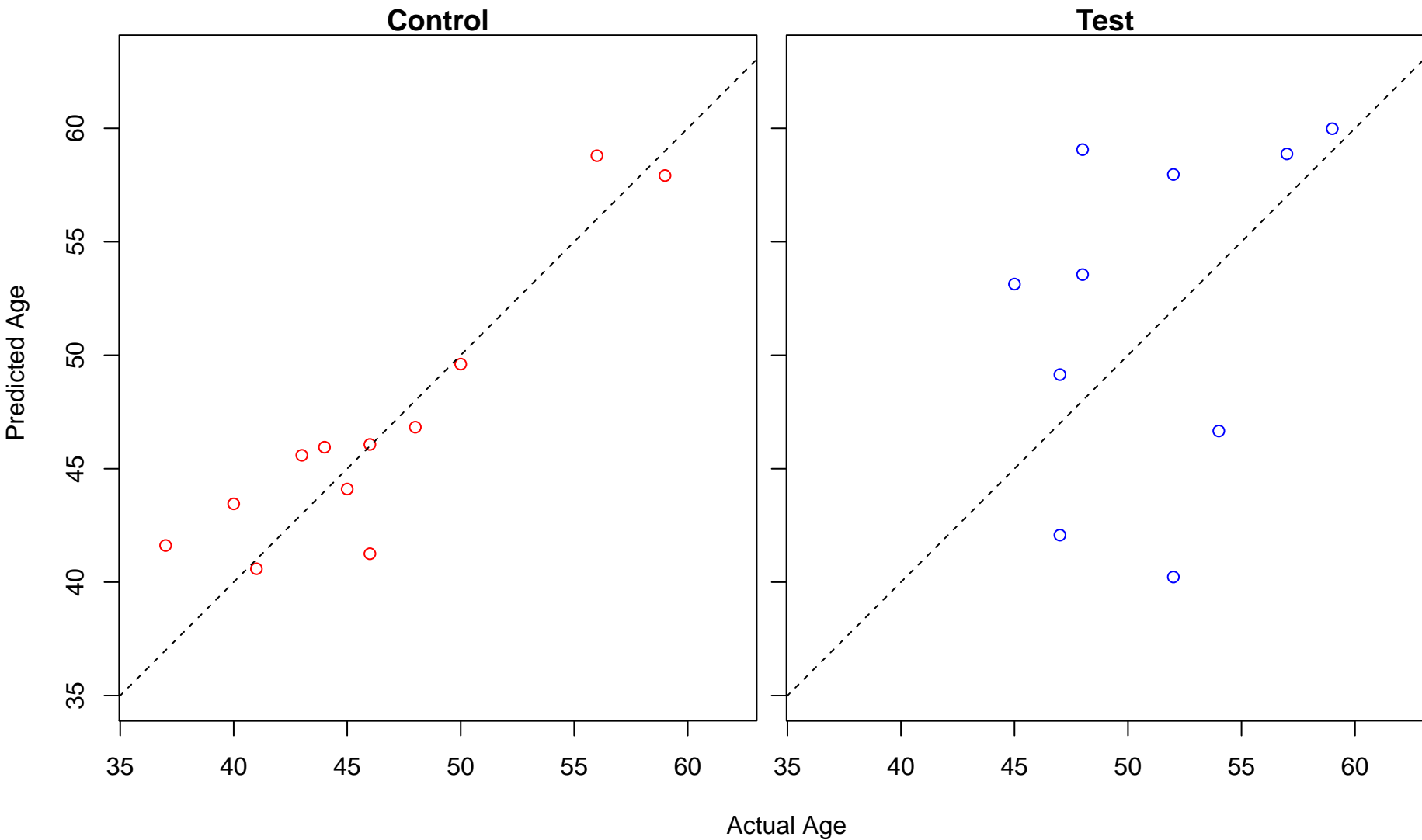
cardiac chamber morphogenesis (Score: 15.314933)



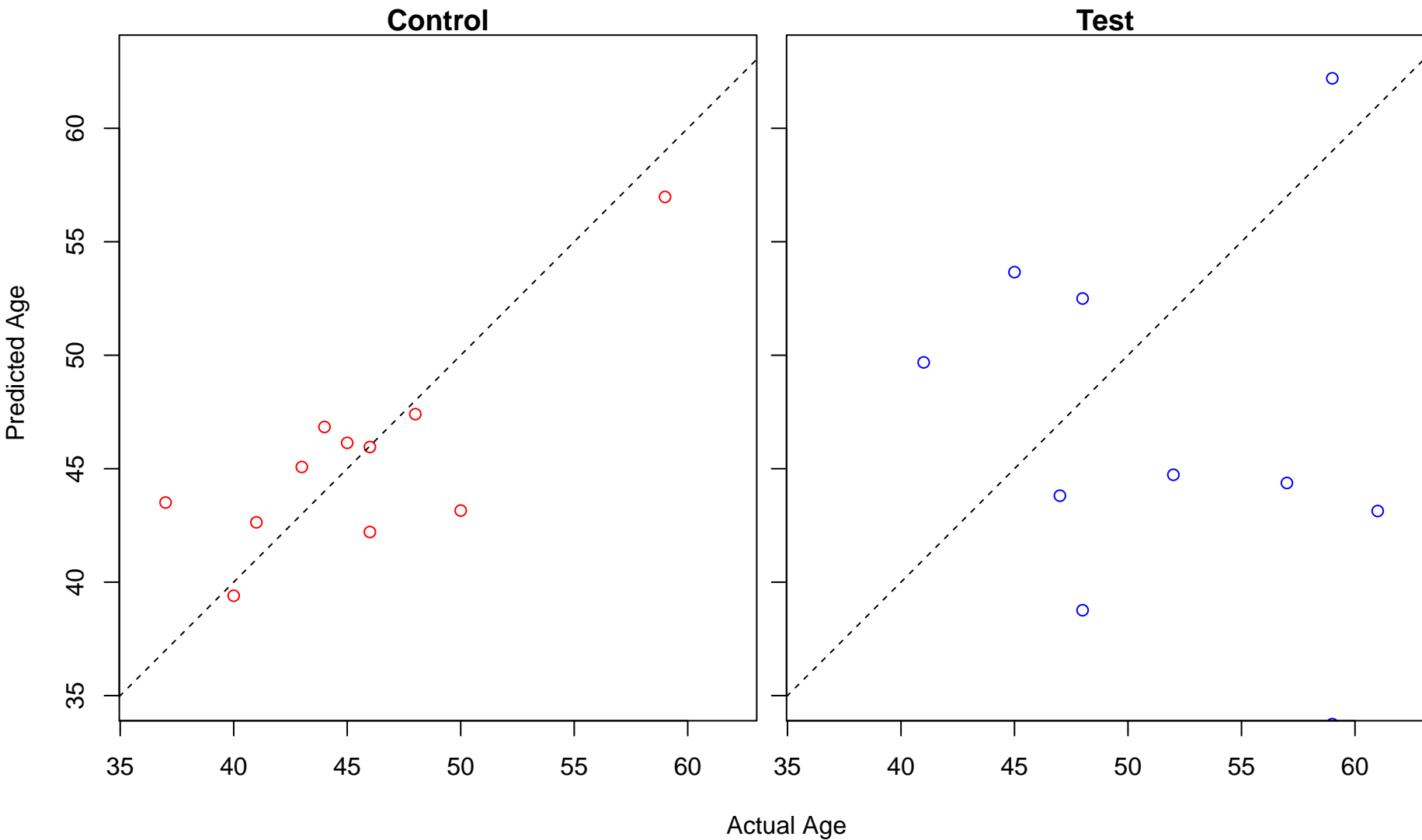
negative regulation of response to endoplasmic reticulum stress (Score: 15.311299)



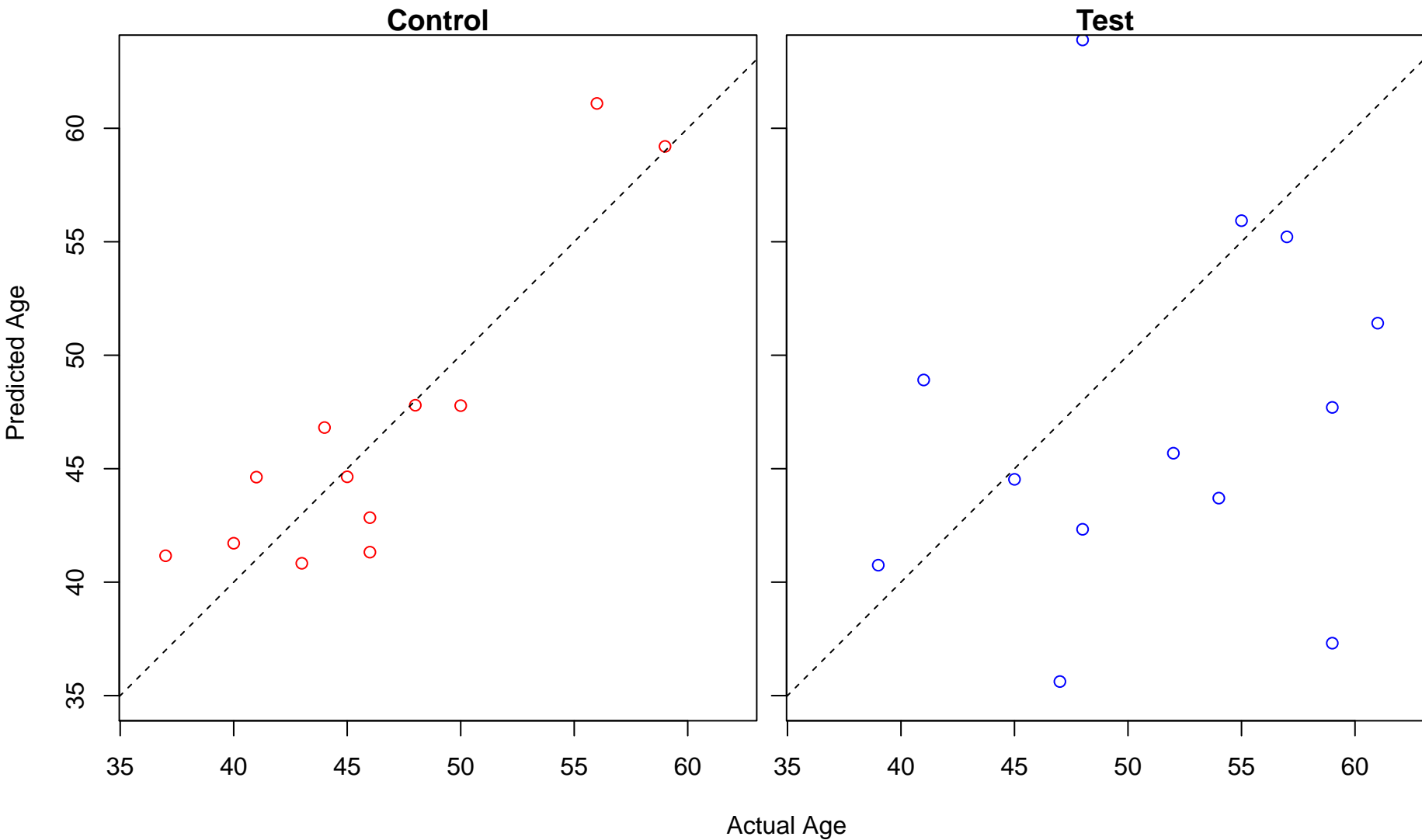
regulation of antigen receptor-mediated signaling pathway (Score: 15.246375)



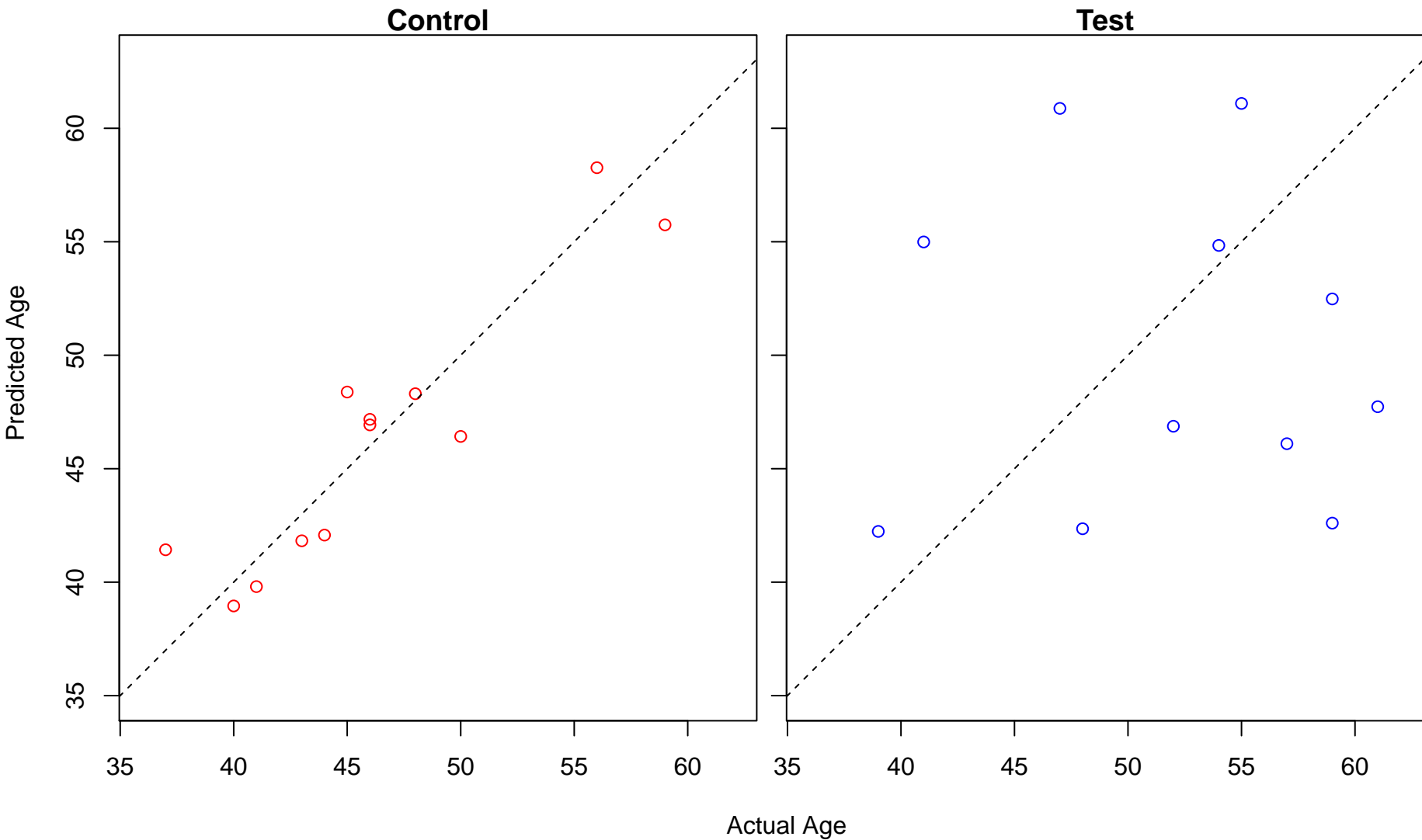
circadian regulation of gene expression (Score: 15.22696)



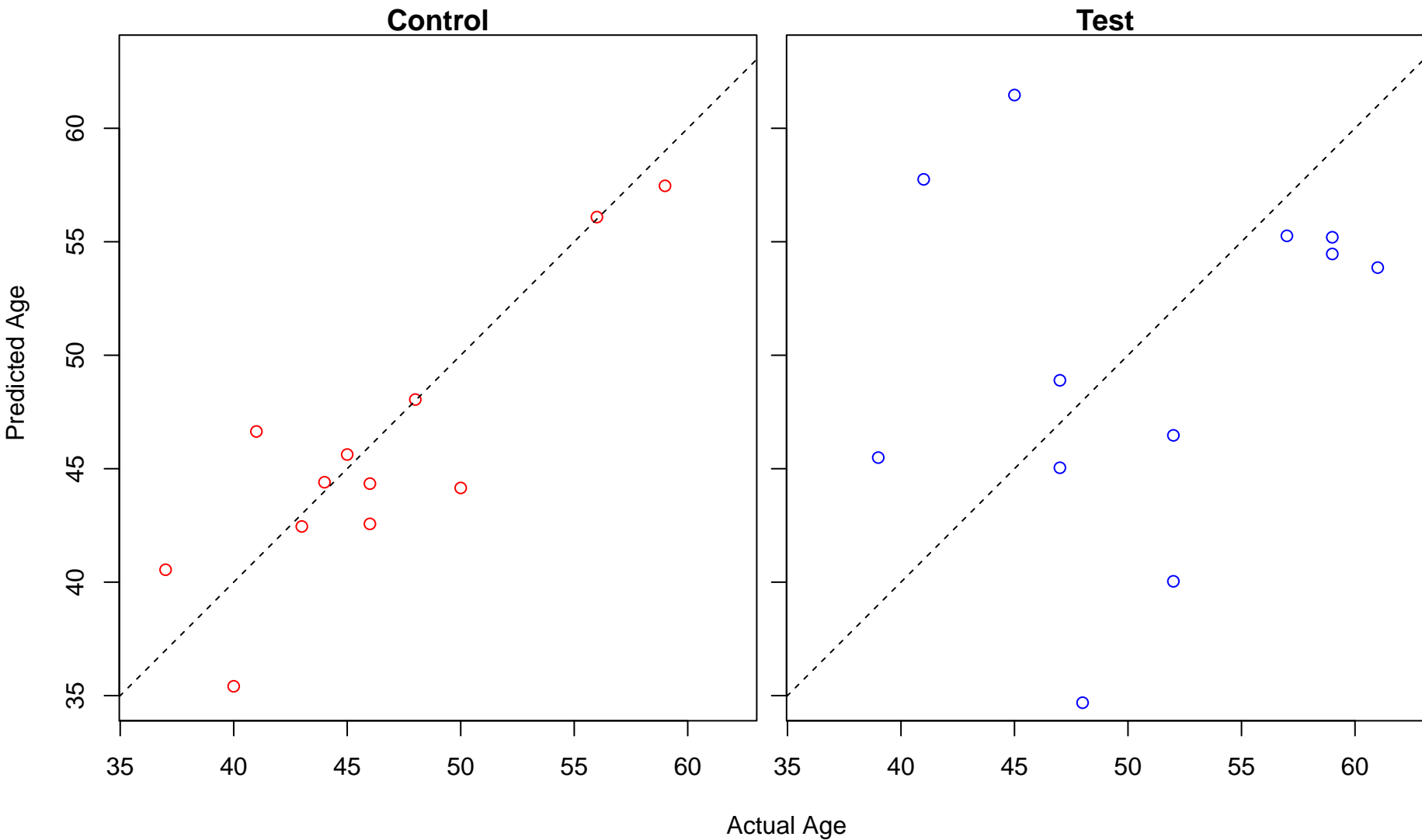
response to calcium ion (Score: 15.208835)



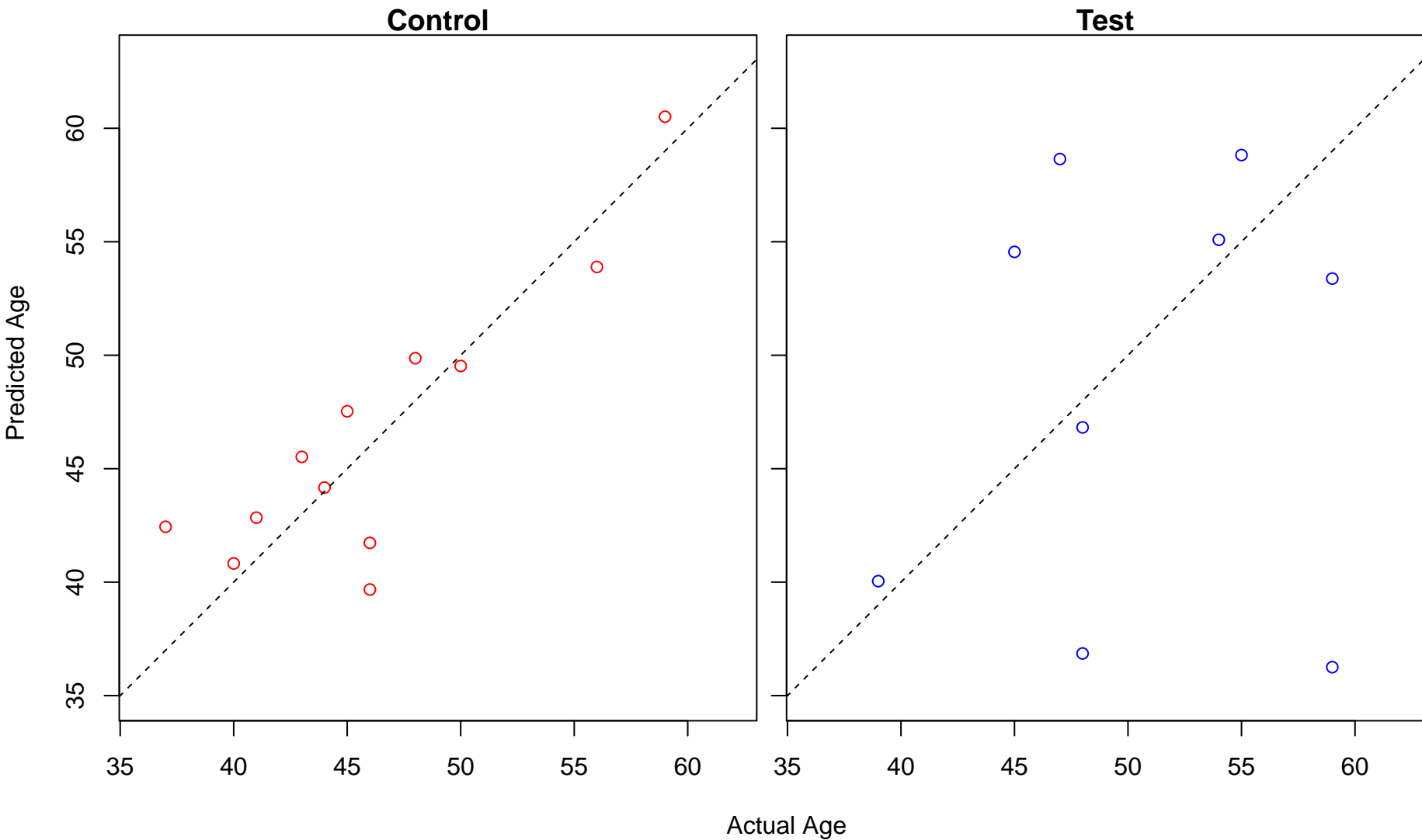
heart trabecula formation (Score: 15.200421)



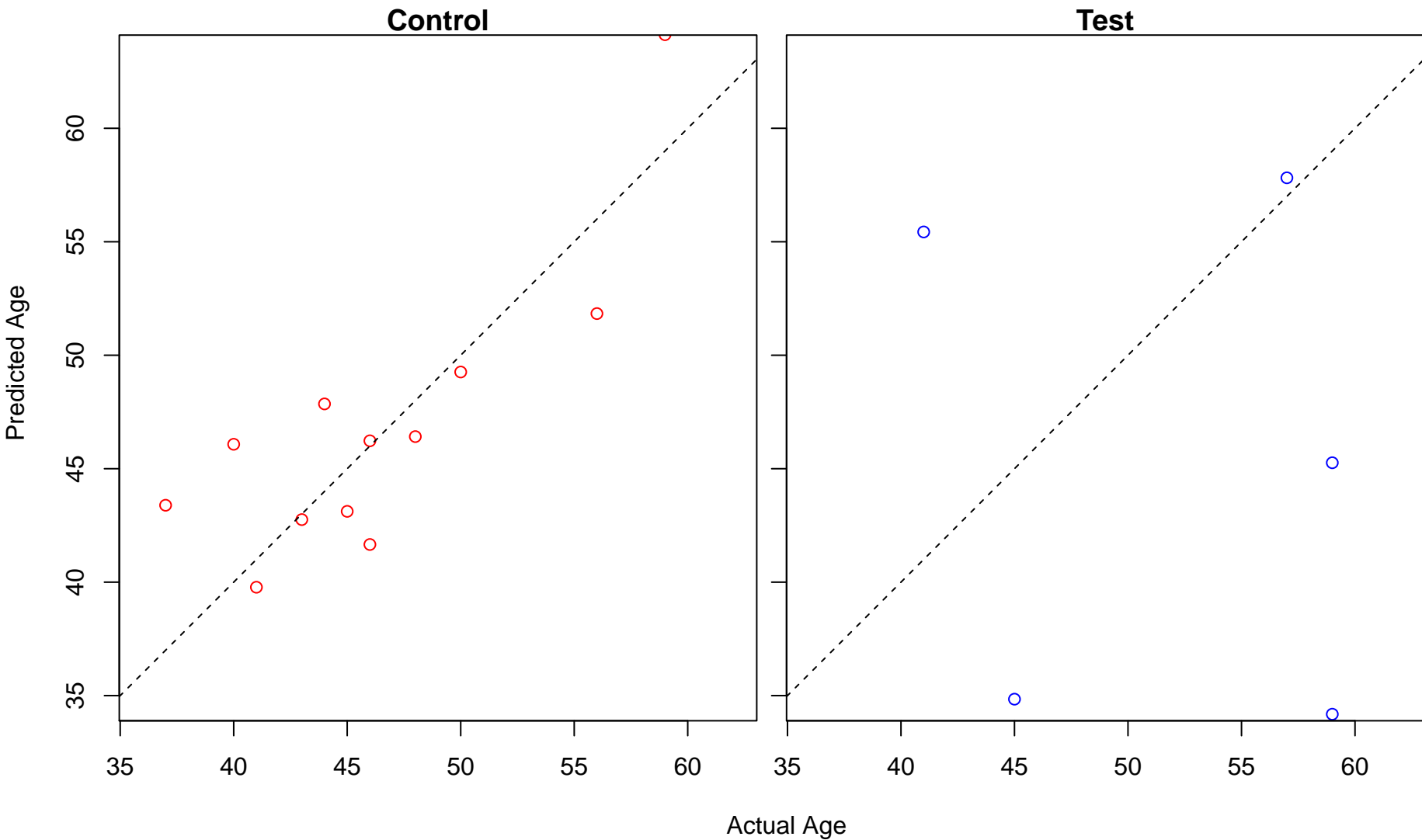
calcium ion transport (Score: 15.184862)



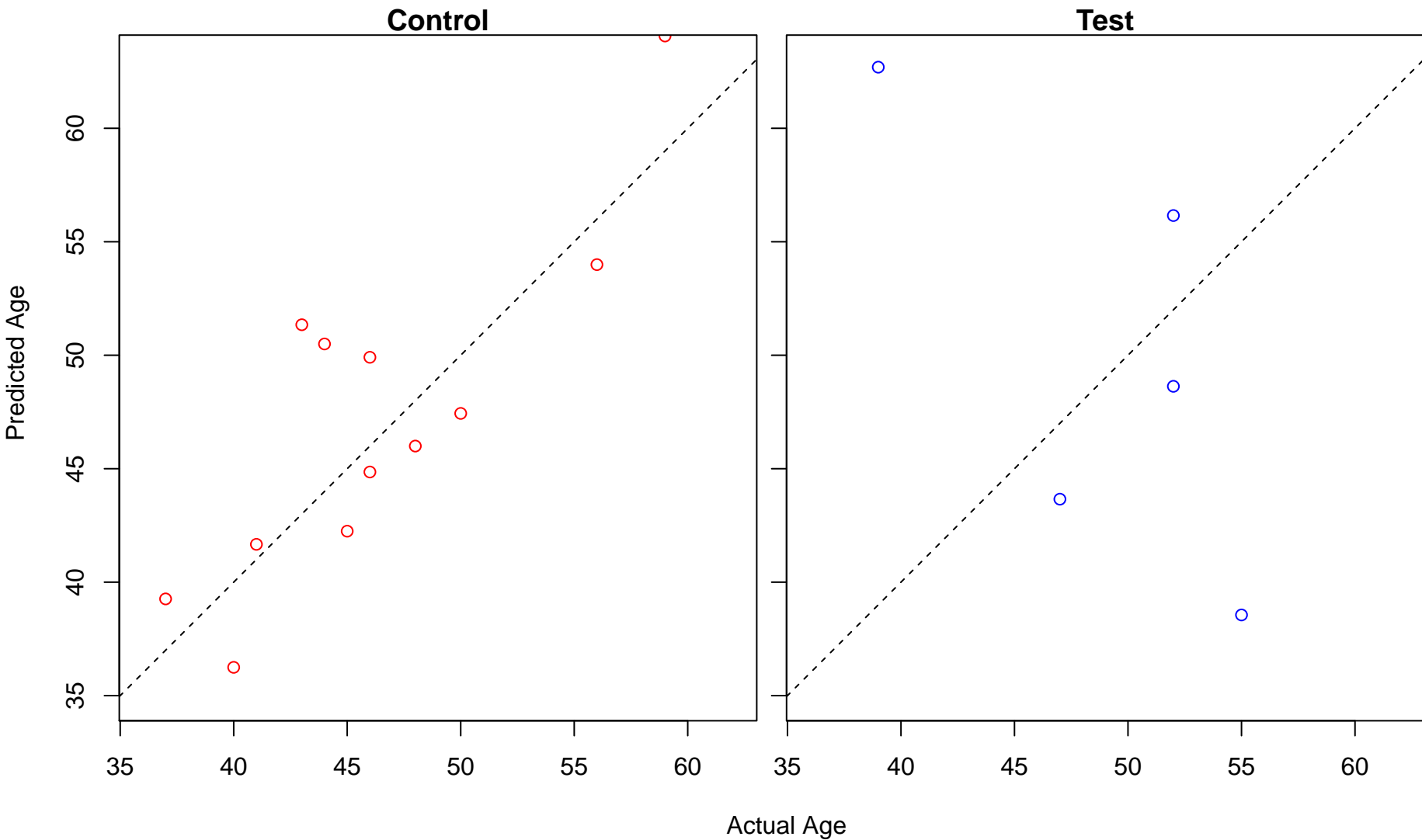
heme biosynthetic process (Score: 15.096230)



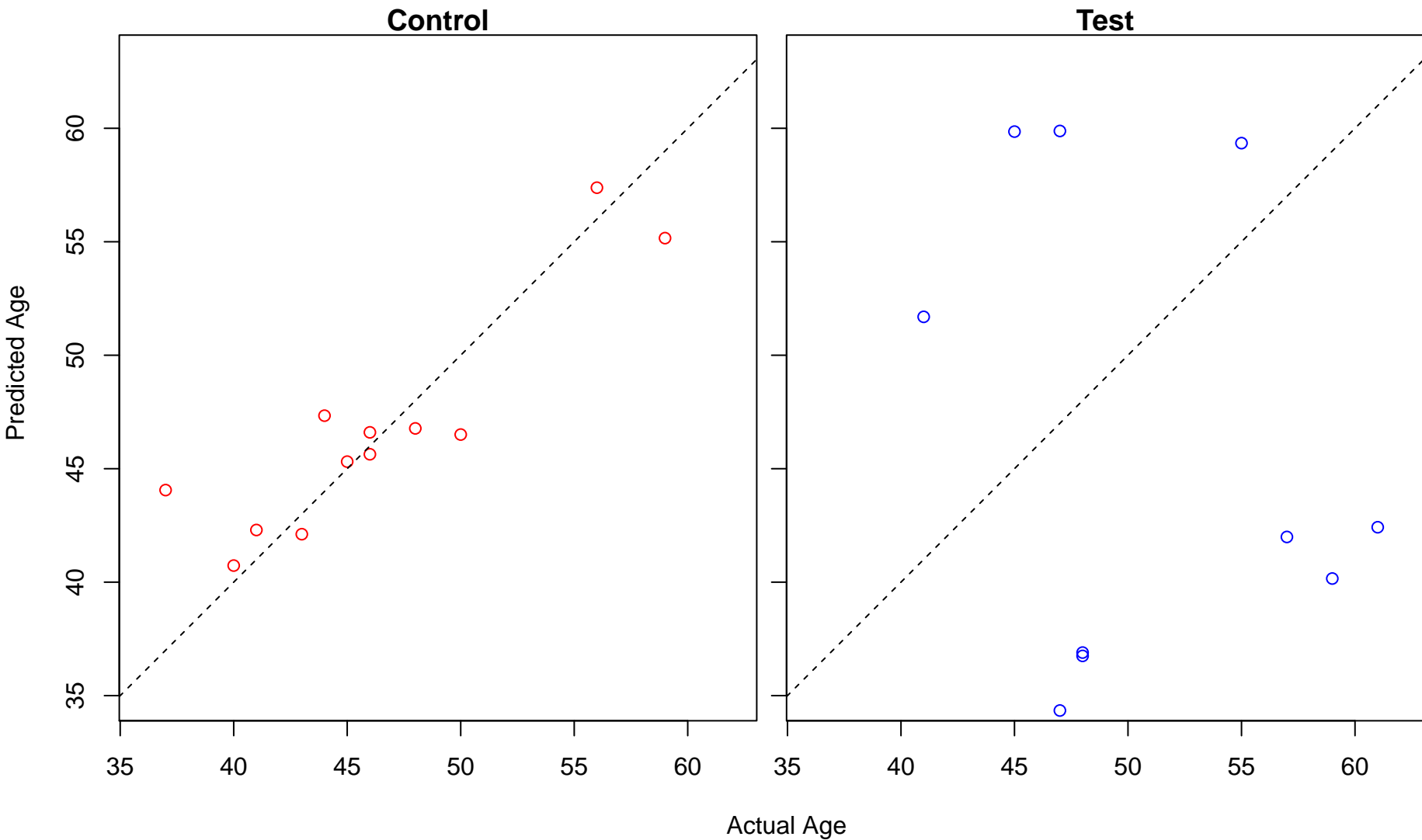
response to acidic pH (Score: 15.017032)



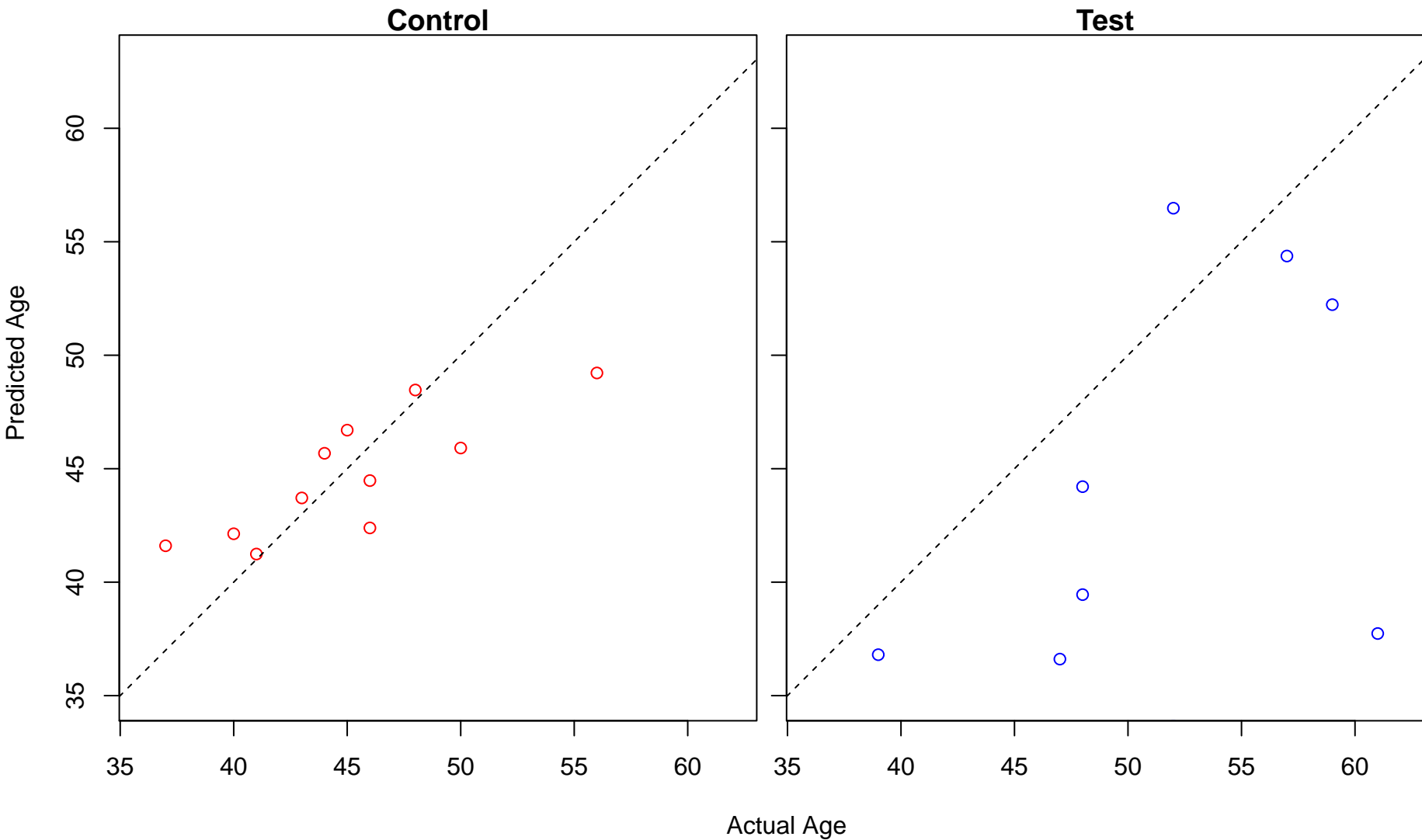
pharyngeal system development (Score: 15.003849)



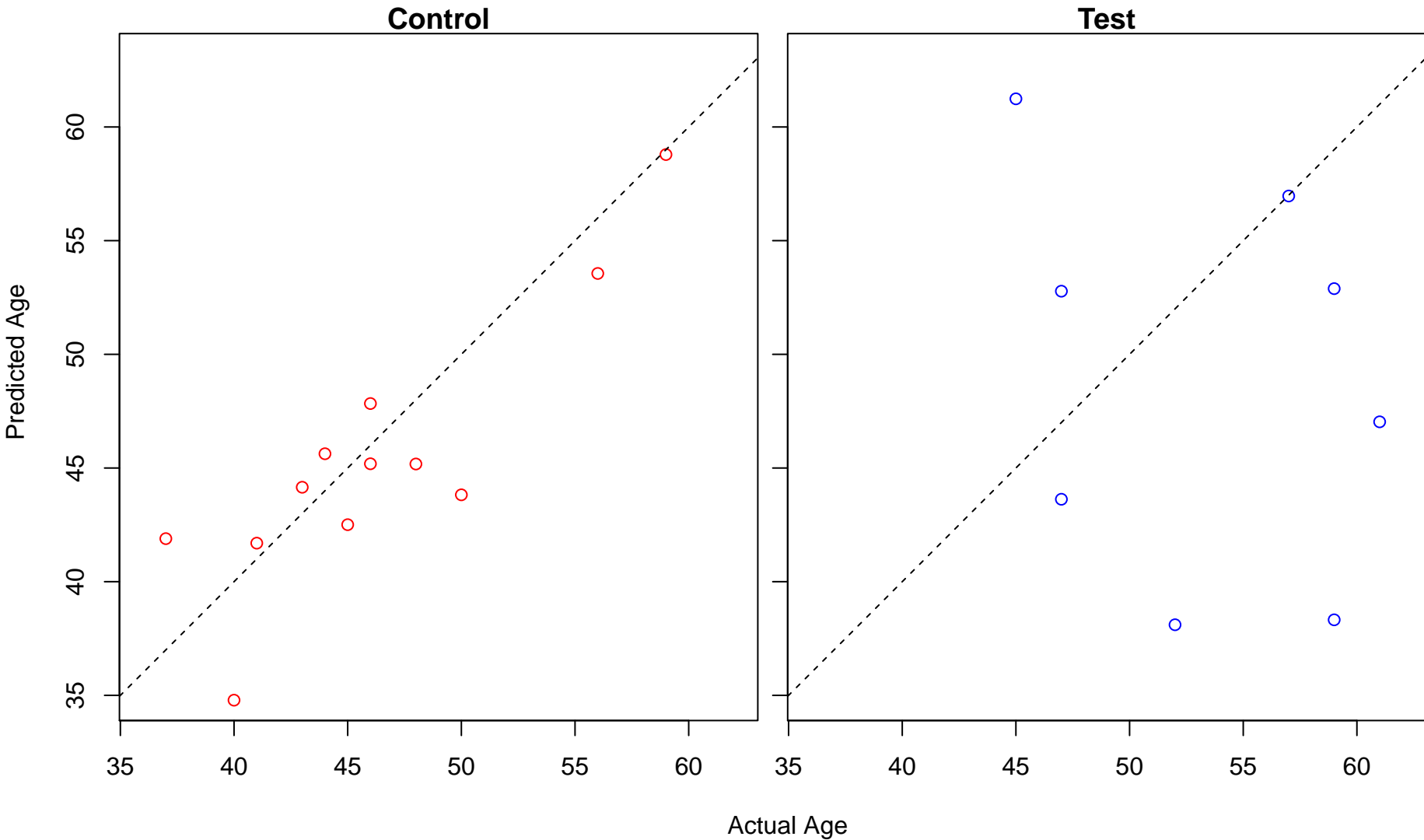
pyrimidine nucleoside catabolic process (Score: 14.957736)



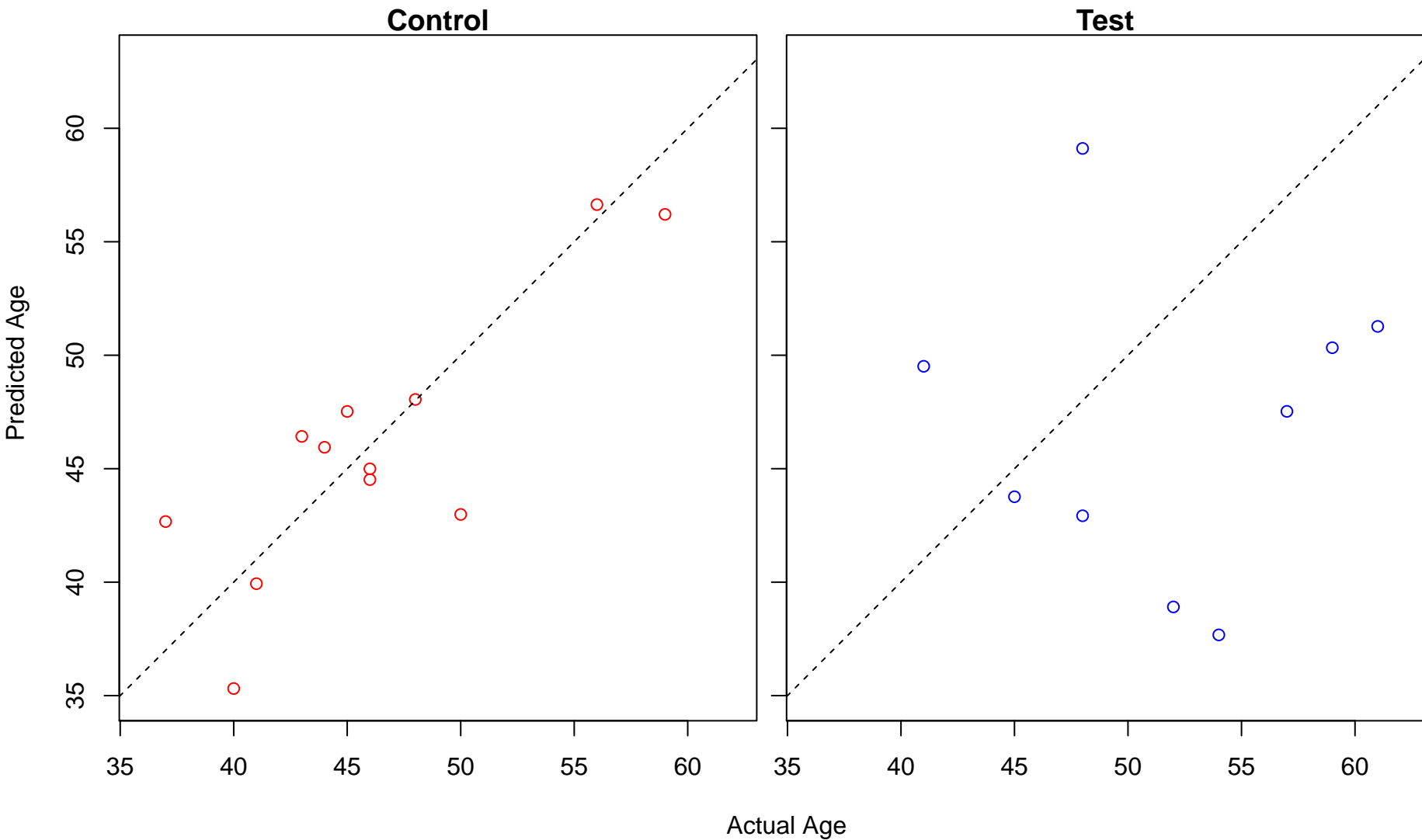
chromosome segregation (Score: 14.932682)



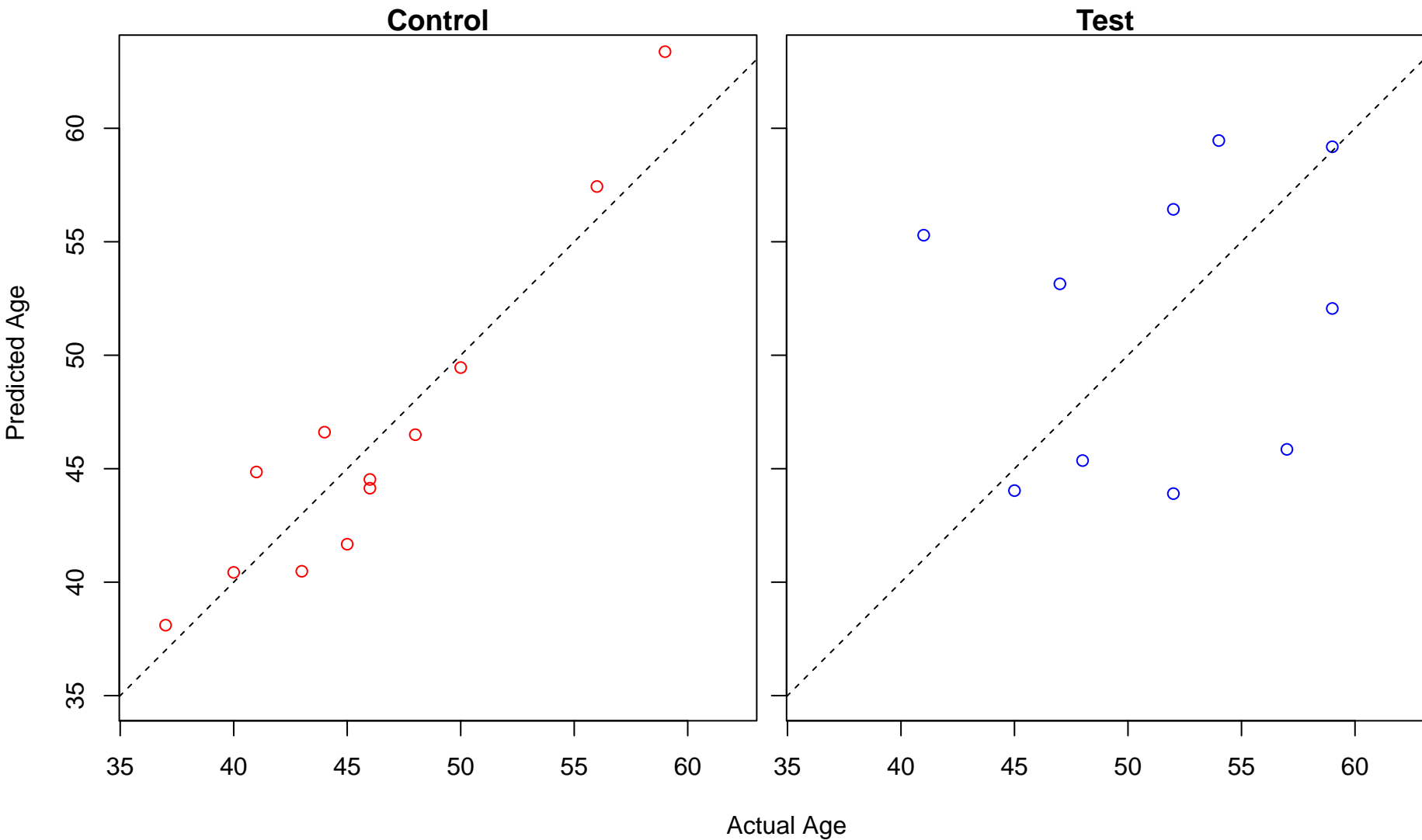
determination of heart left/right asymmetry (Score: 14.903496)



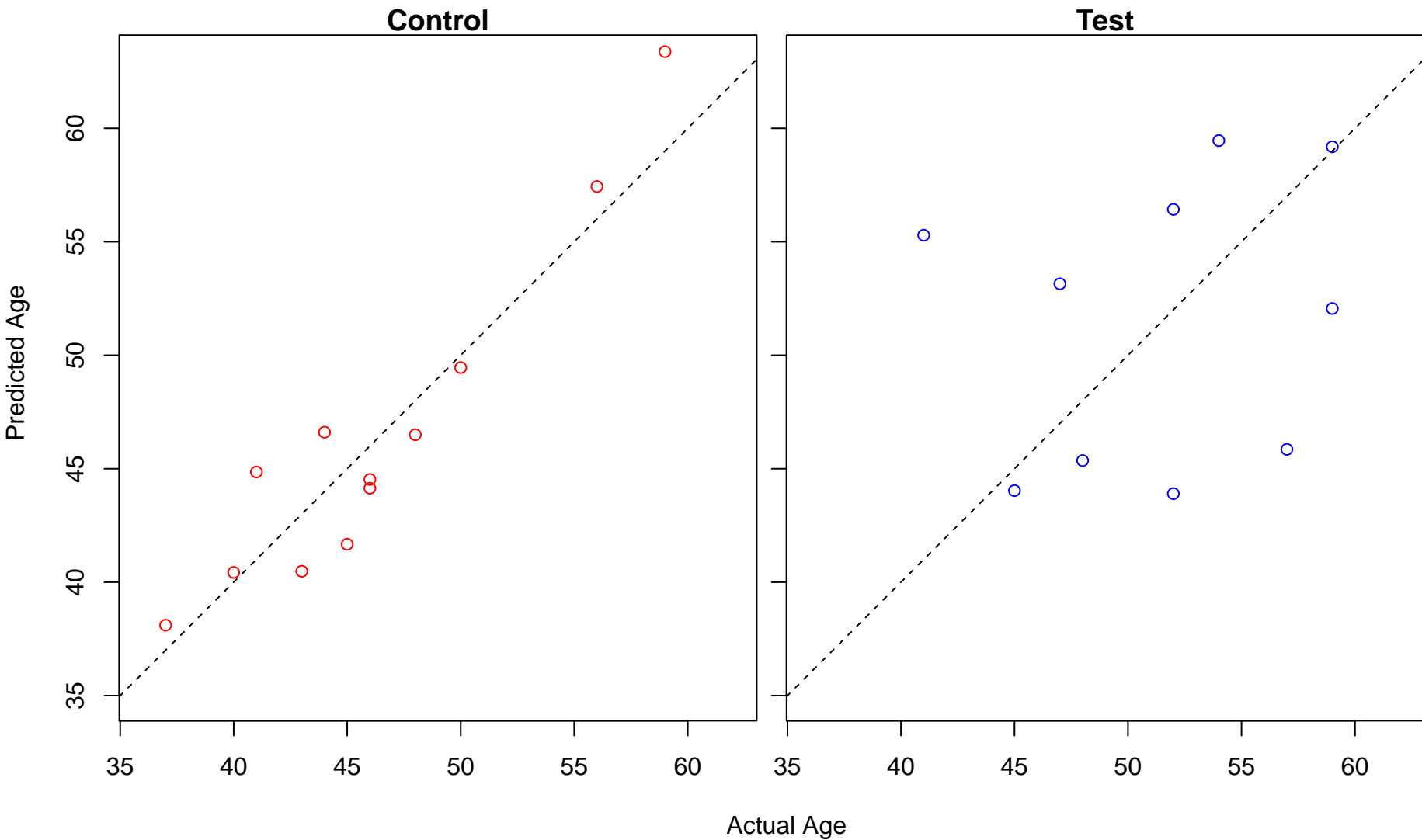
atrial septum development (Score: 14.886091)



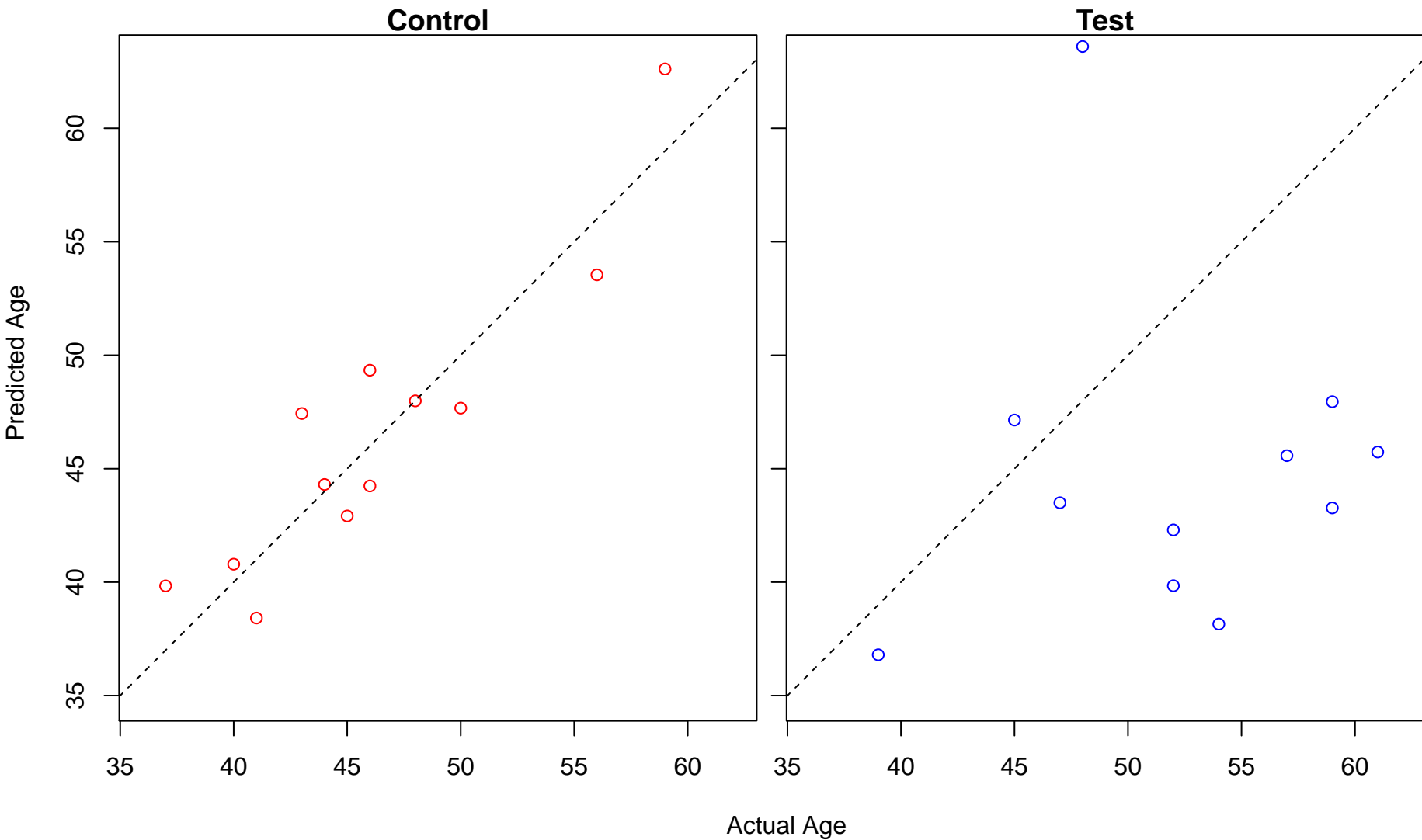
subpallium development (Score: 14.871027)



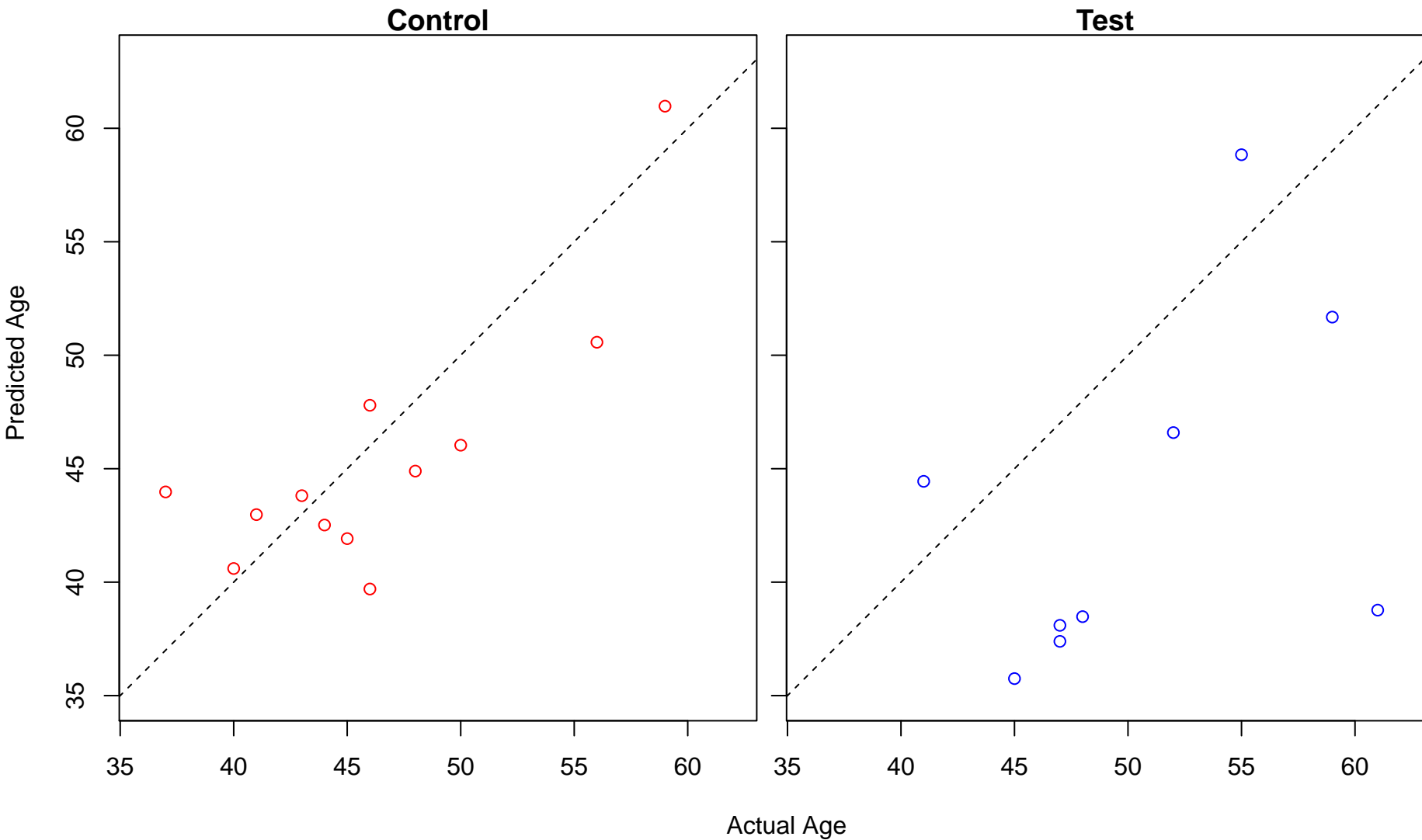
striatum development (Score: 14.871027)



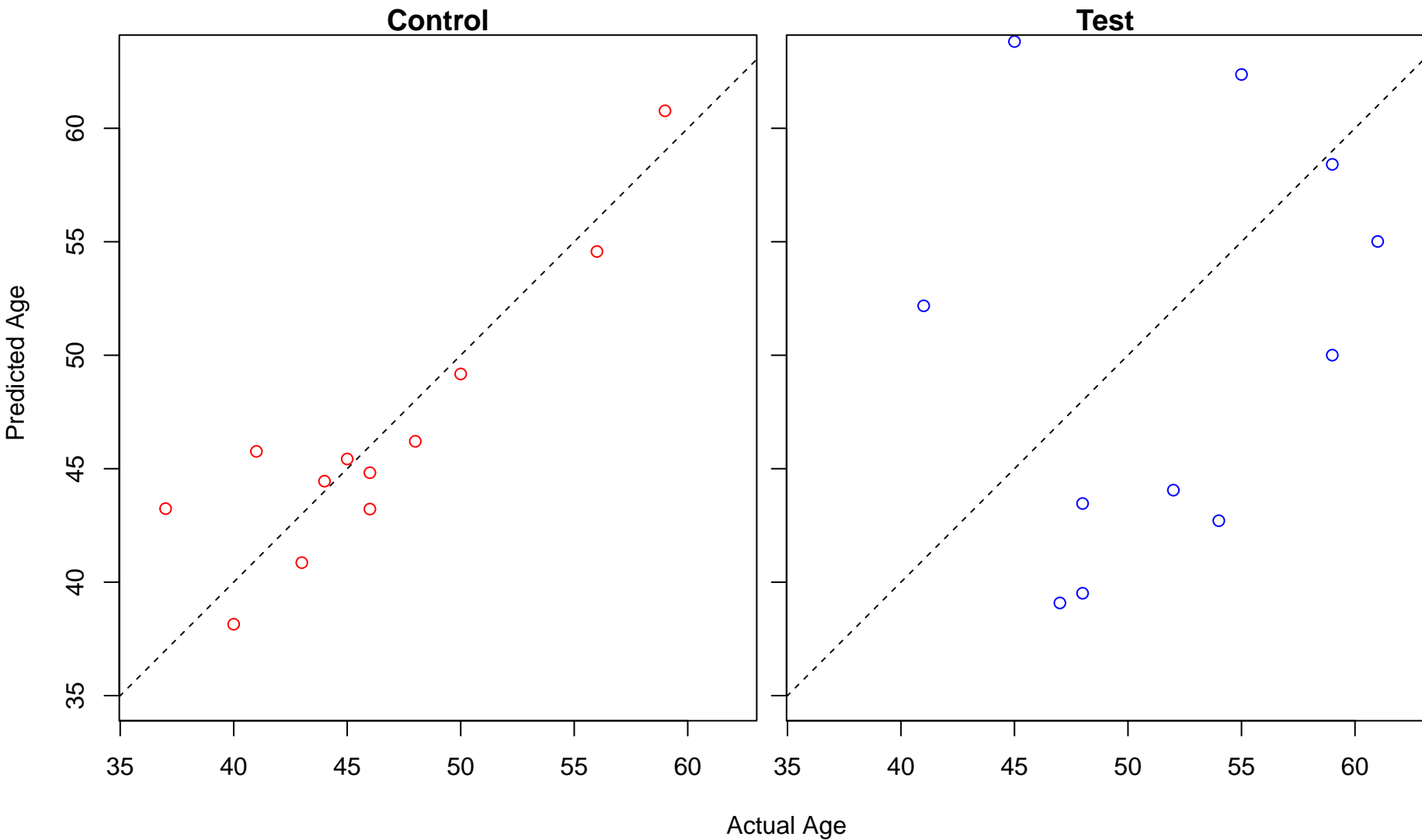
regulation of p38MAPK cascade (Score: 14.862862)



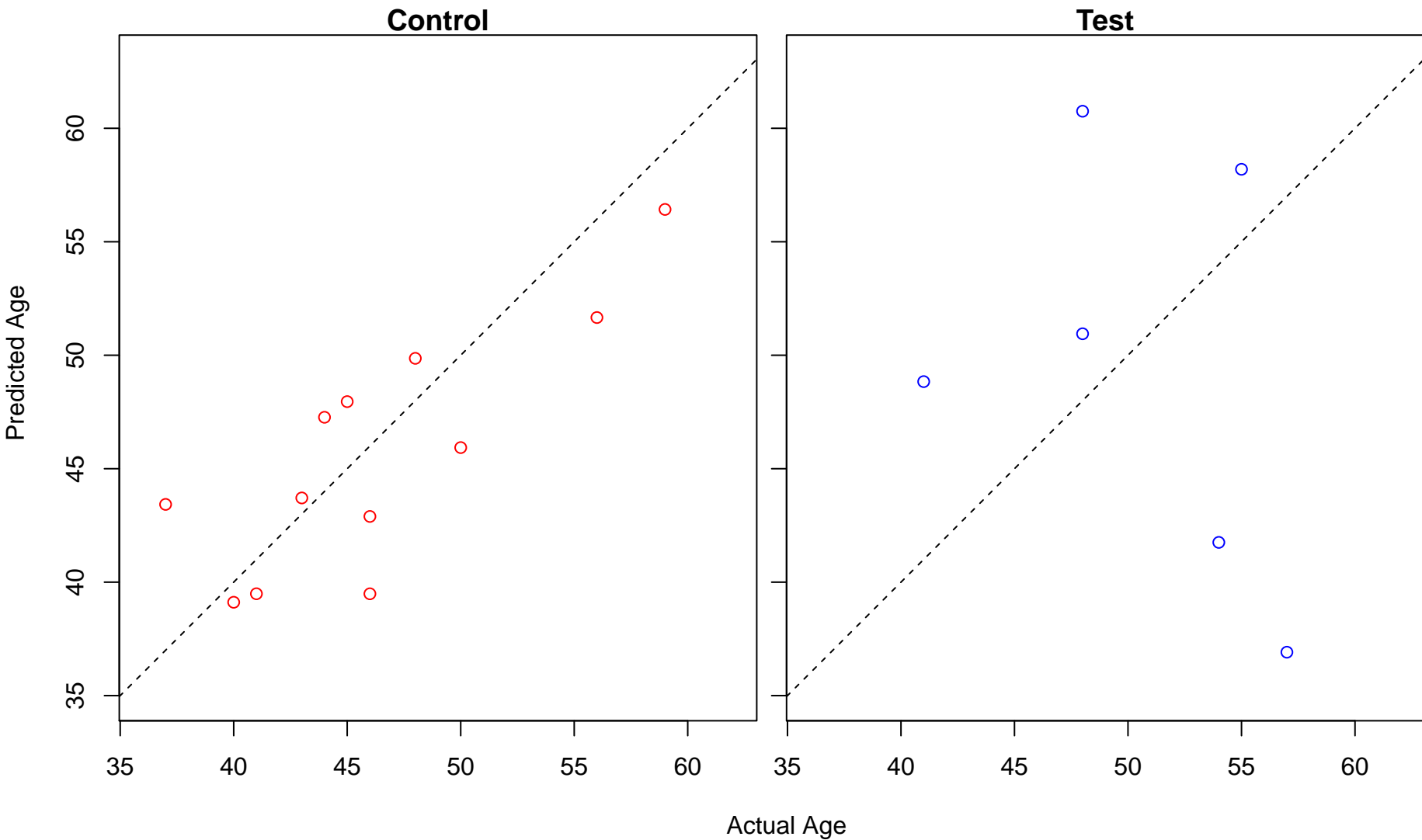
cellular defense response (Score: 14.856454)



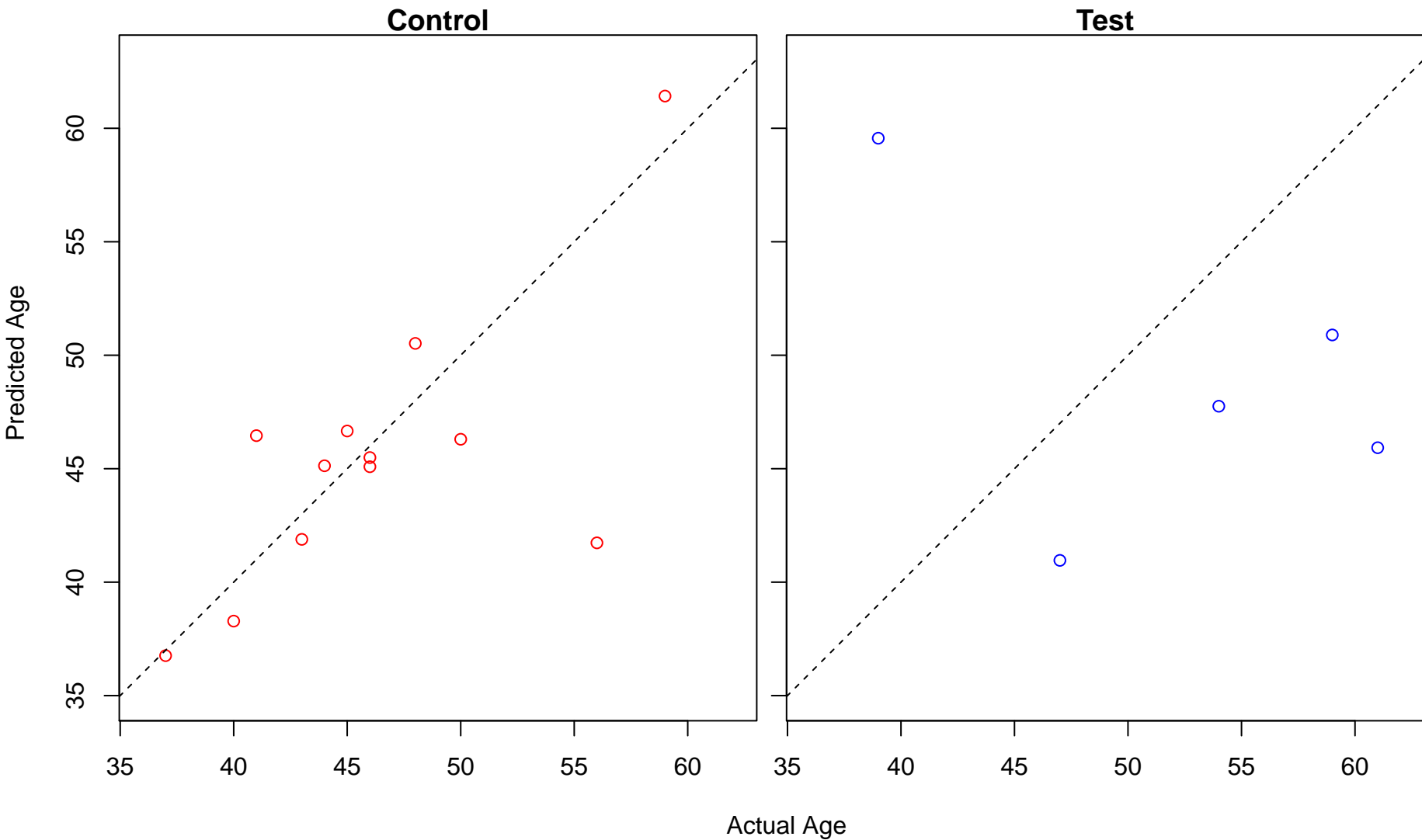
osteoblast differentiation (Score: 14.782941)



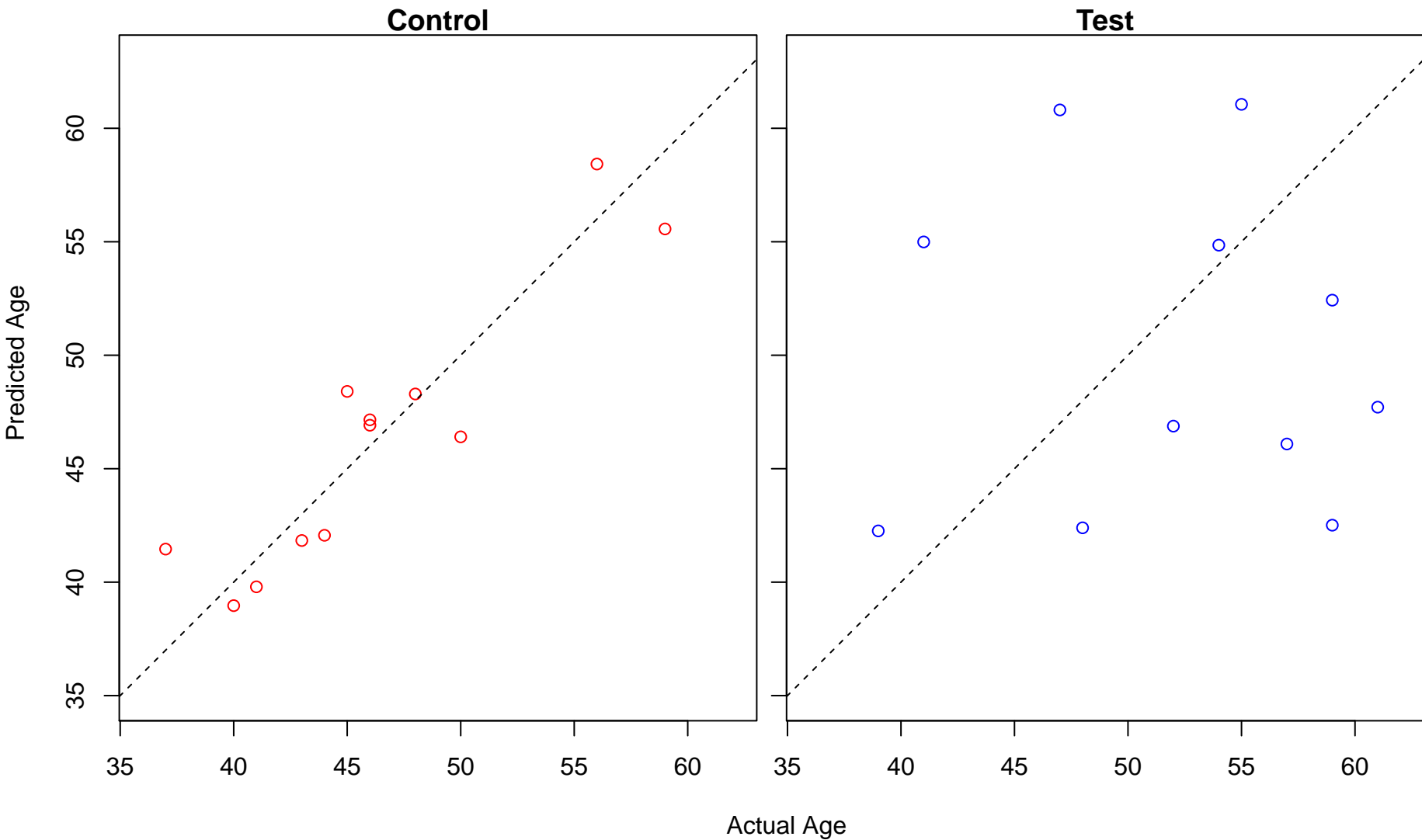
viral release from host cell (Score: 14.780217)



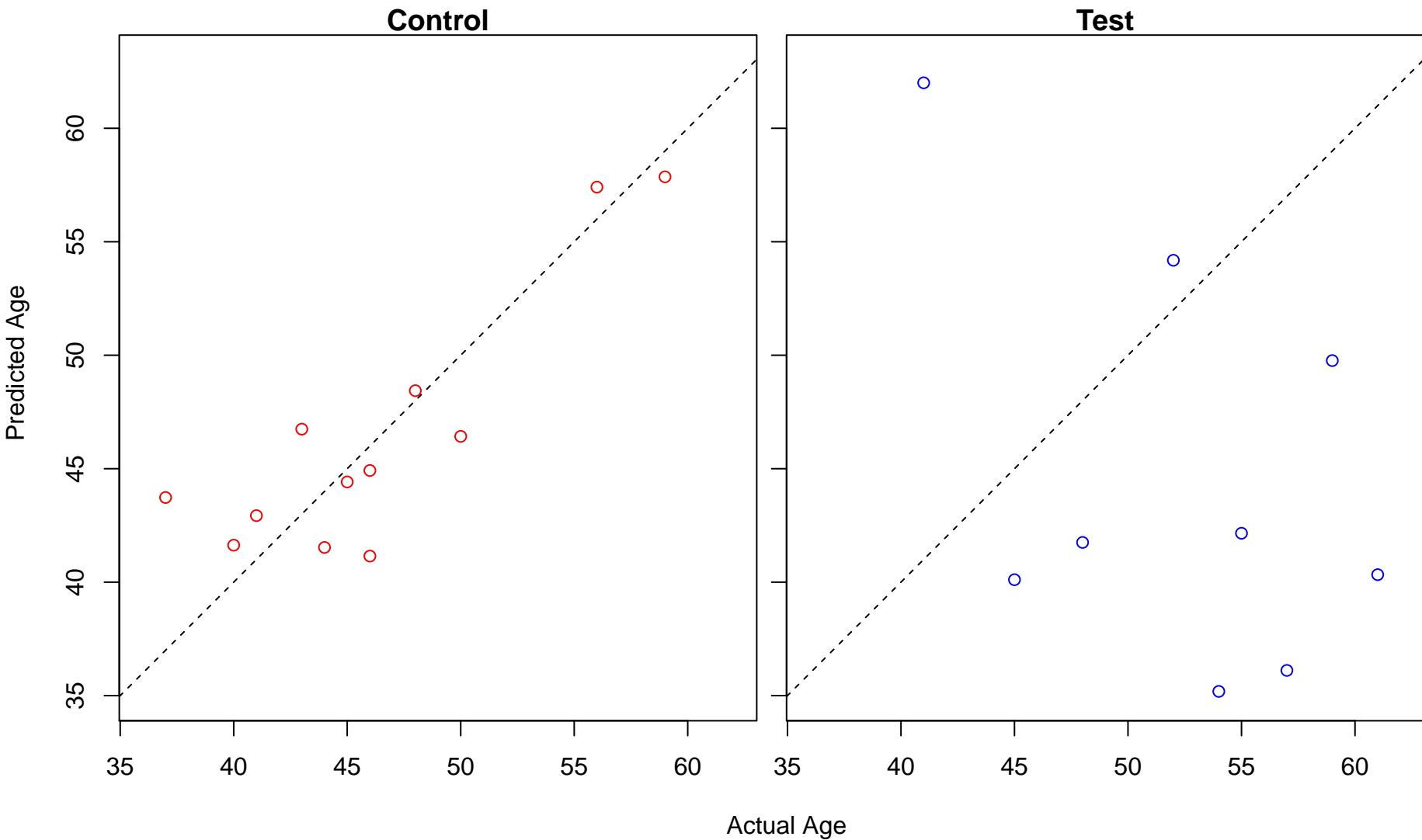
dopamine biosynthetic process (Score: 14.761021)

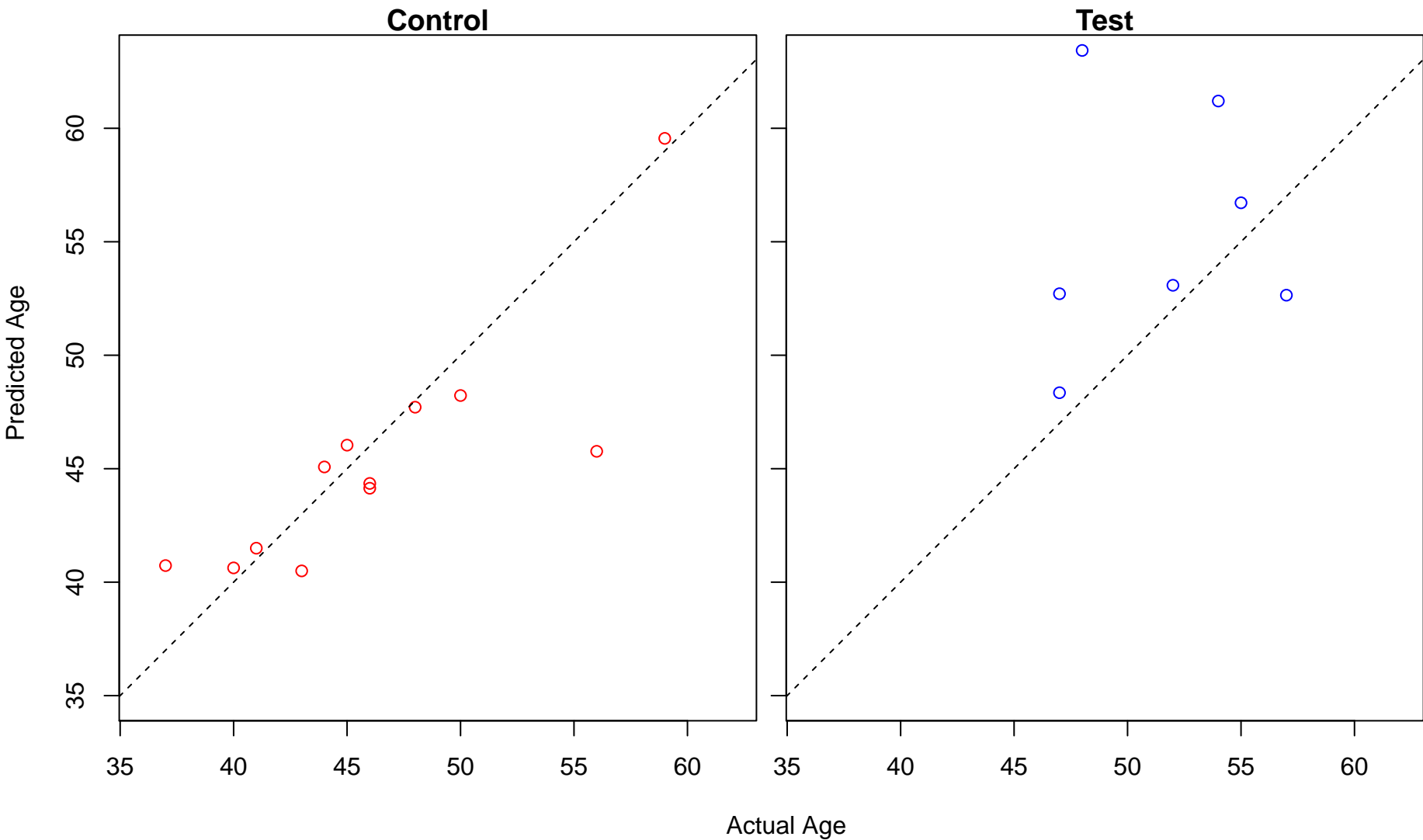


trabecula formation (Score: 14.735106)

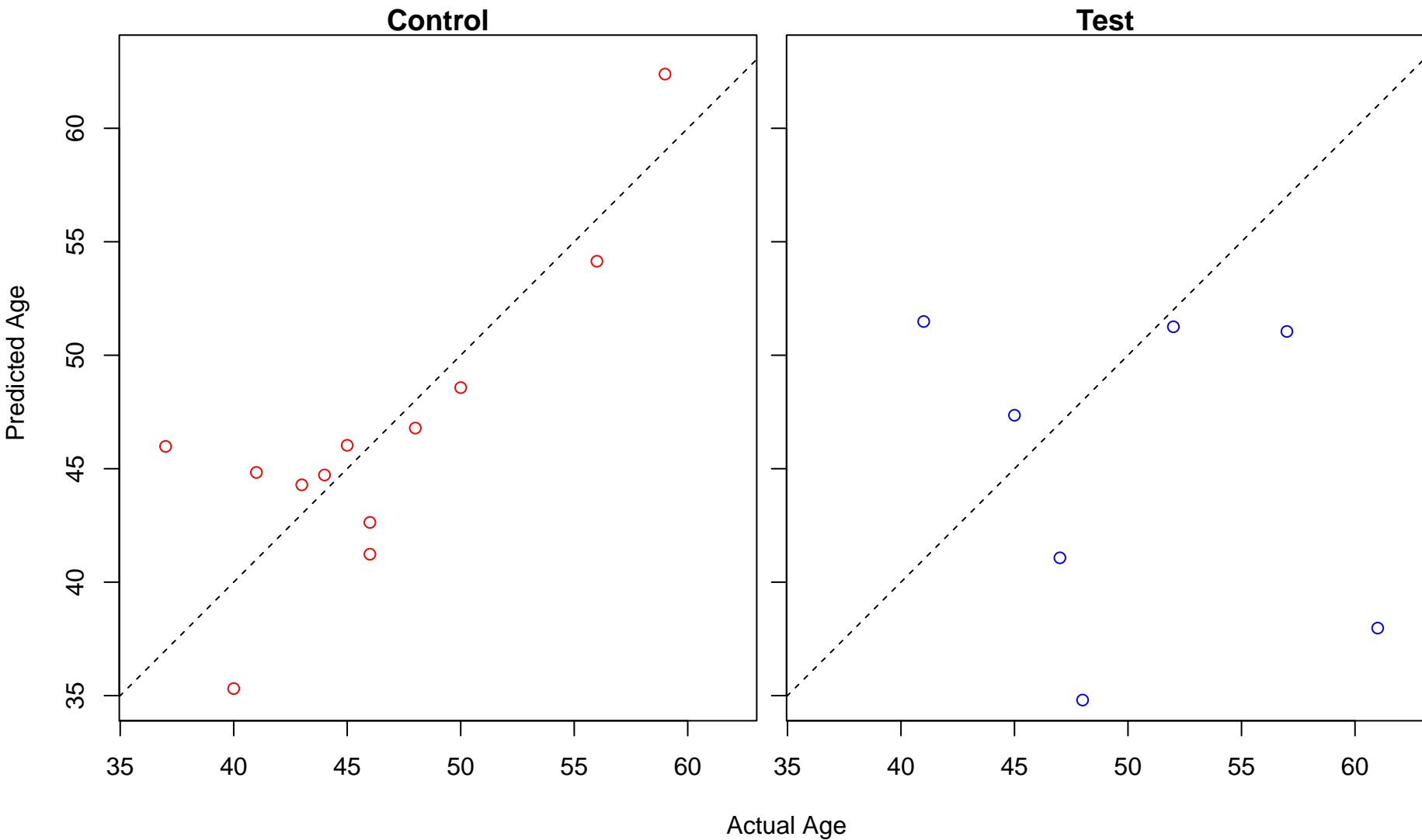


endothelium development (Score: 14.703888)

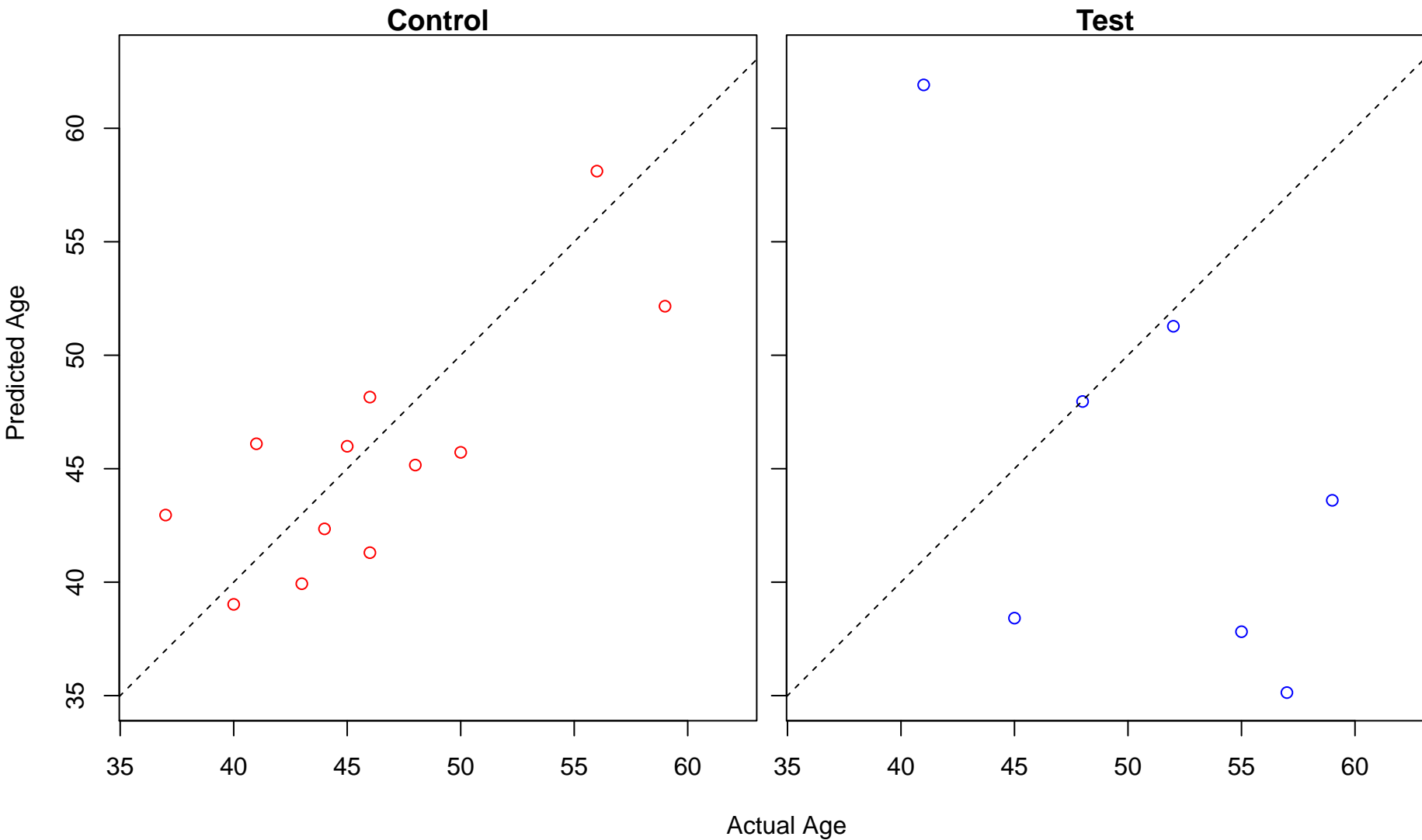




regulation of antigen processing and presentation (Score: 14.594154)

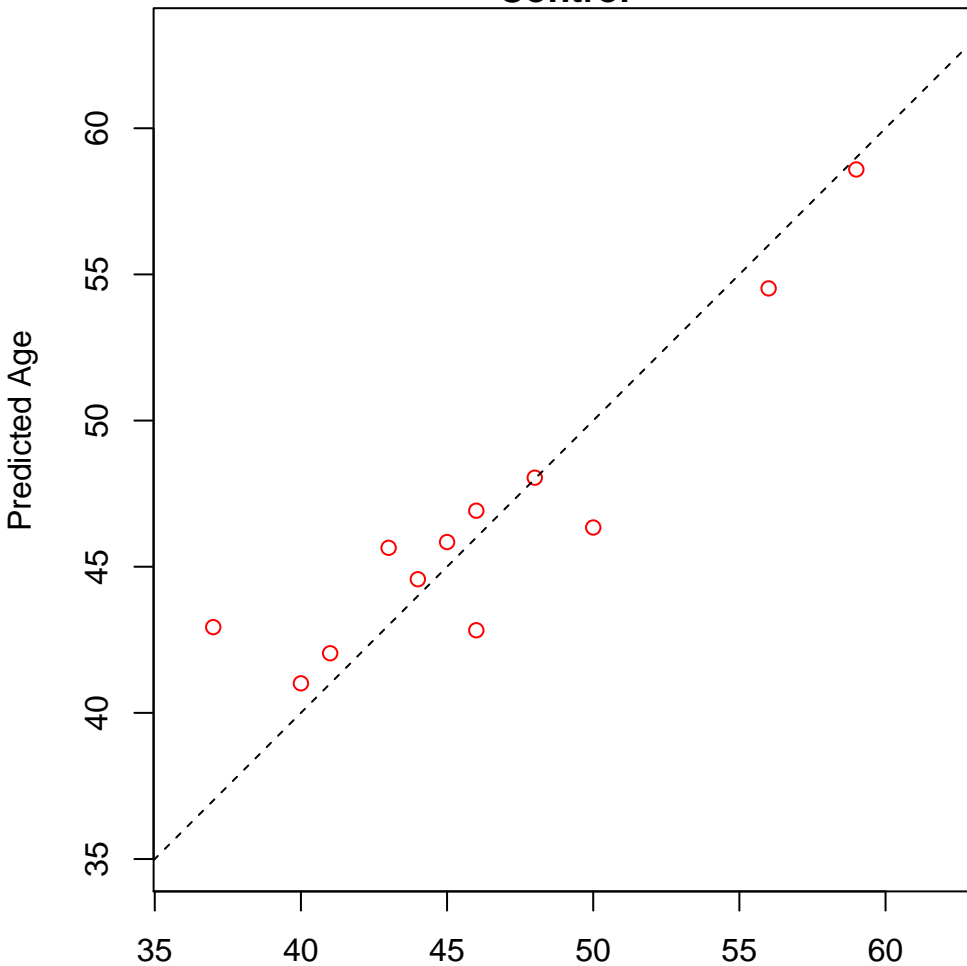


regulation of regulatory T cell differentiation (Score: 14.565902)

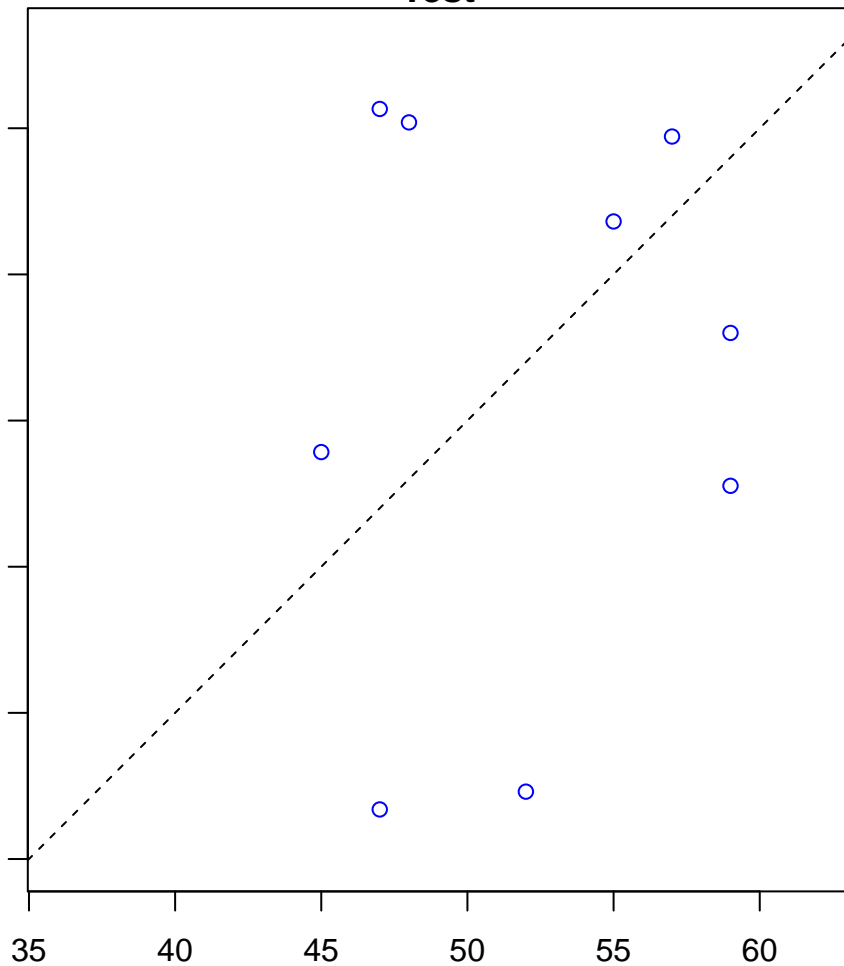


anterior/posterior pattern specification (Score: 14.532890)

Control

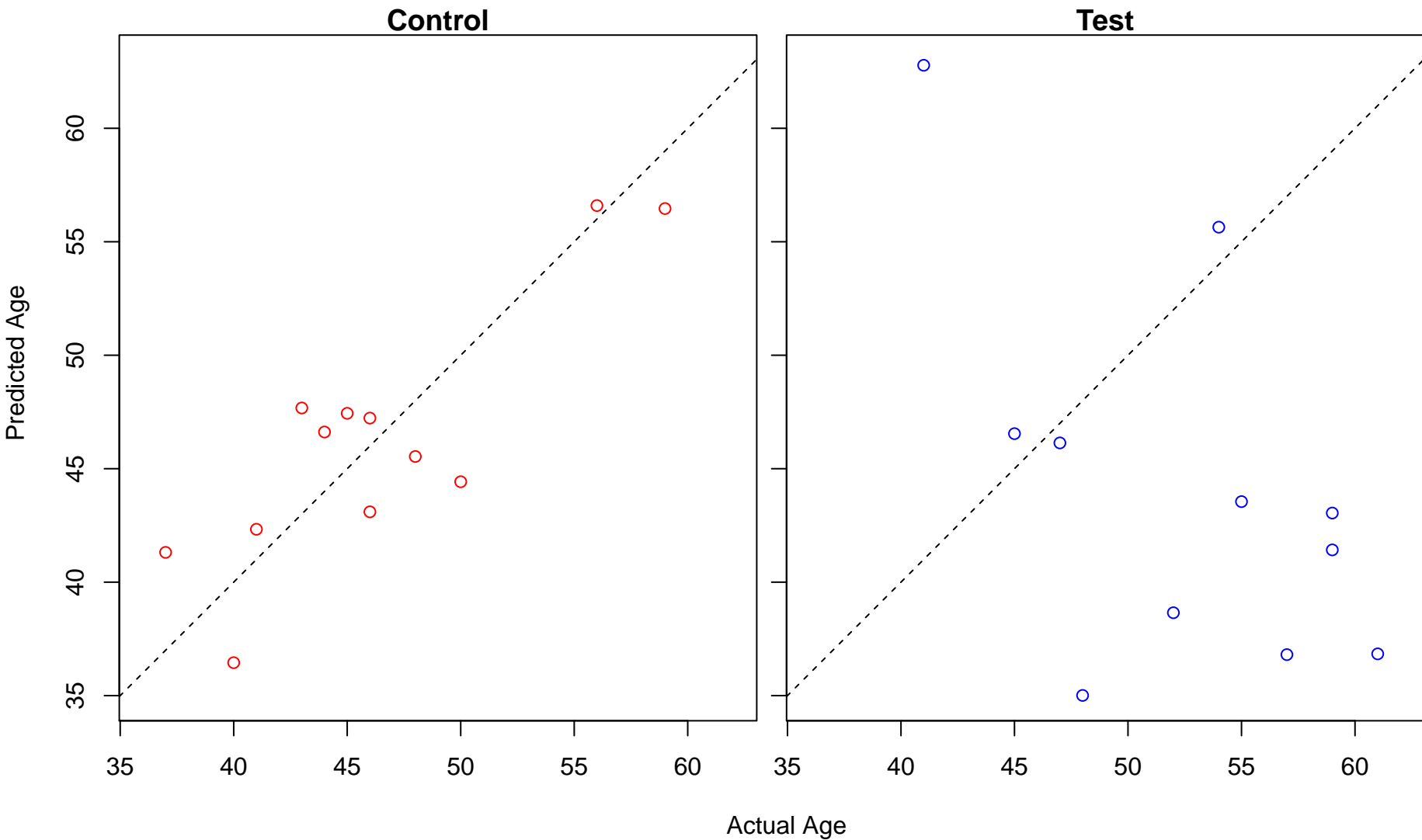


Test

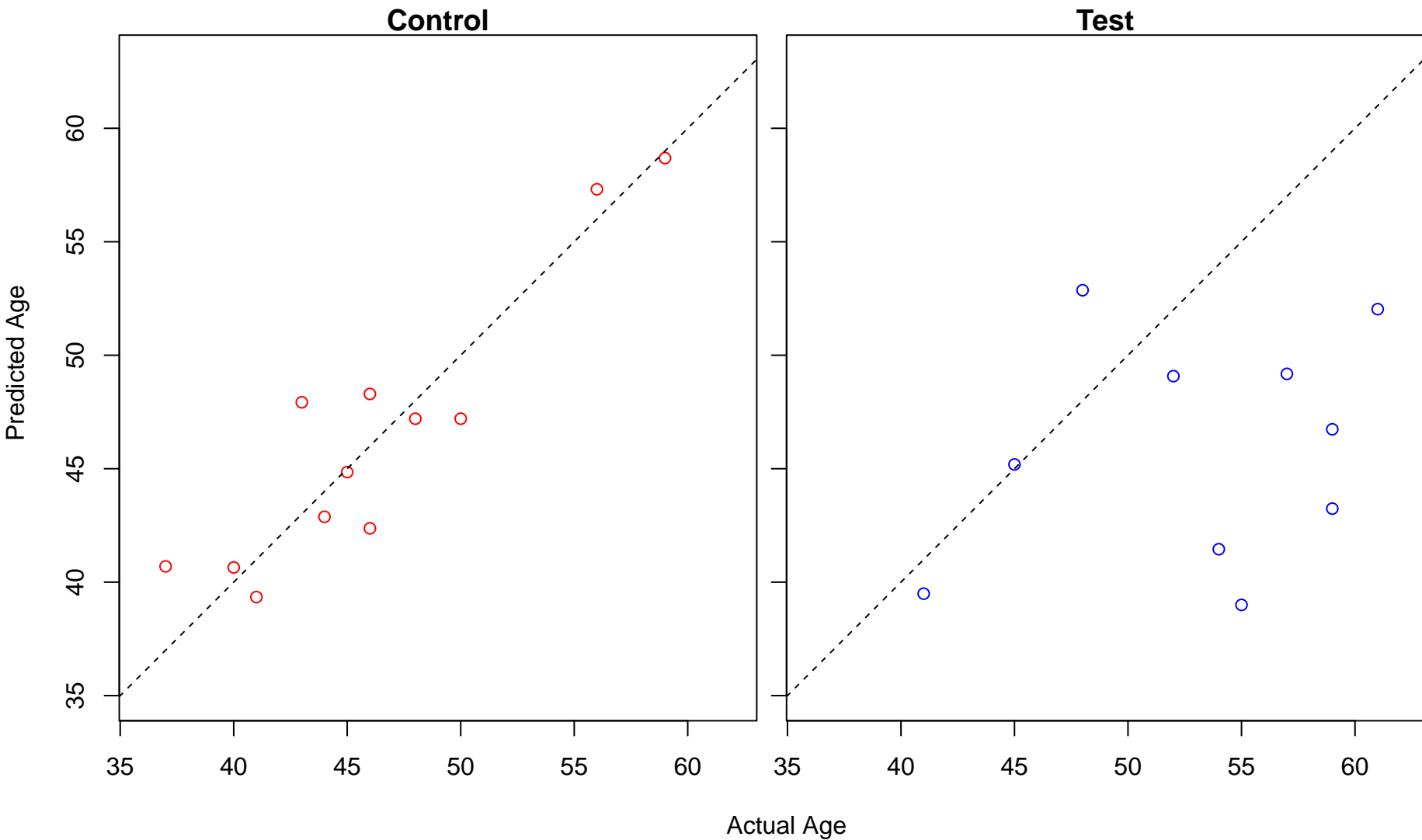


Actual Age

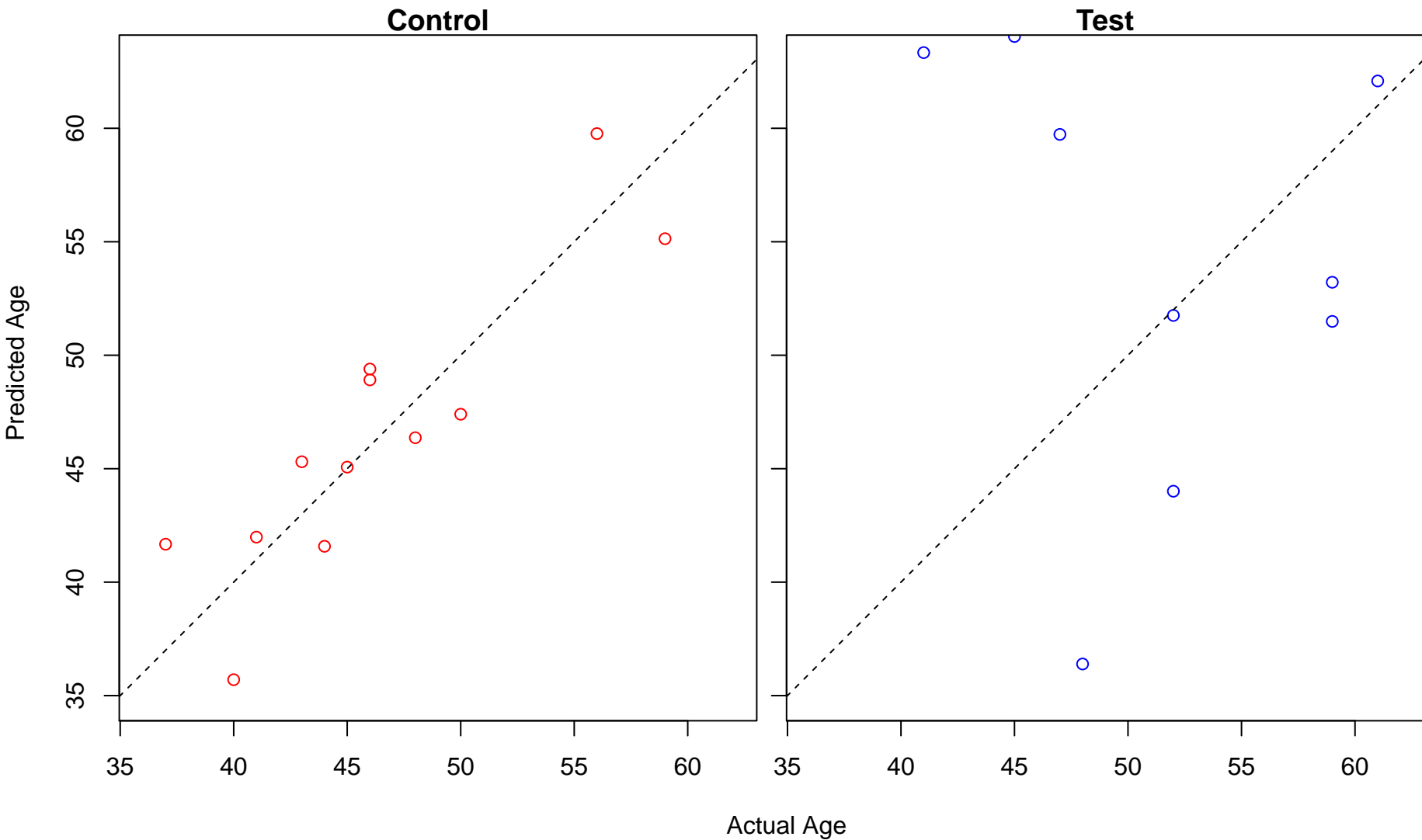
positive regulation of chromosome organization (Score: 14.532412)



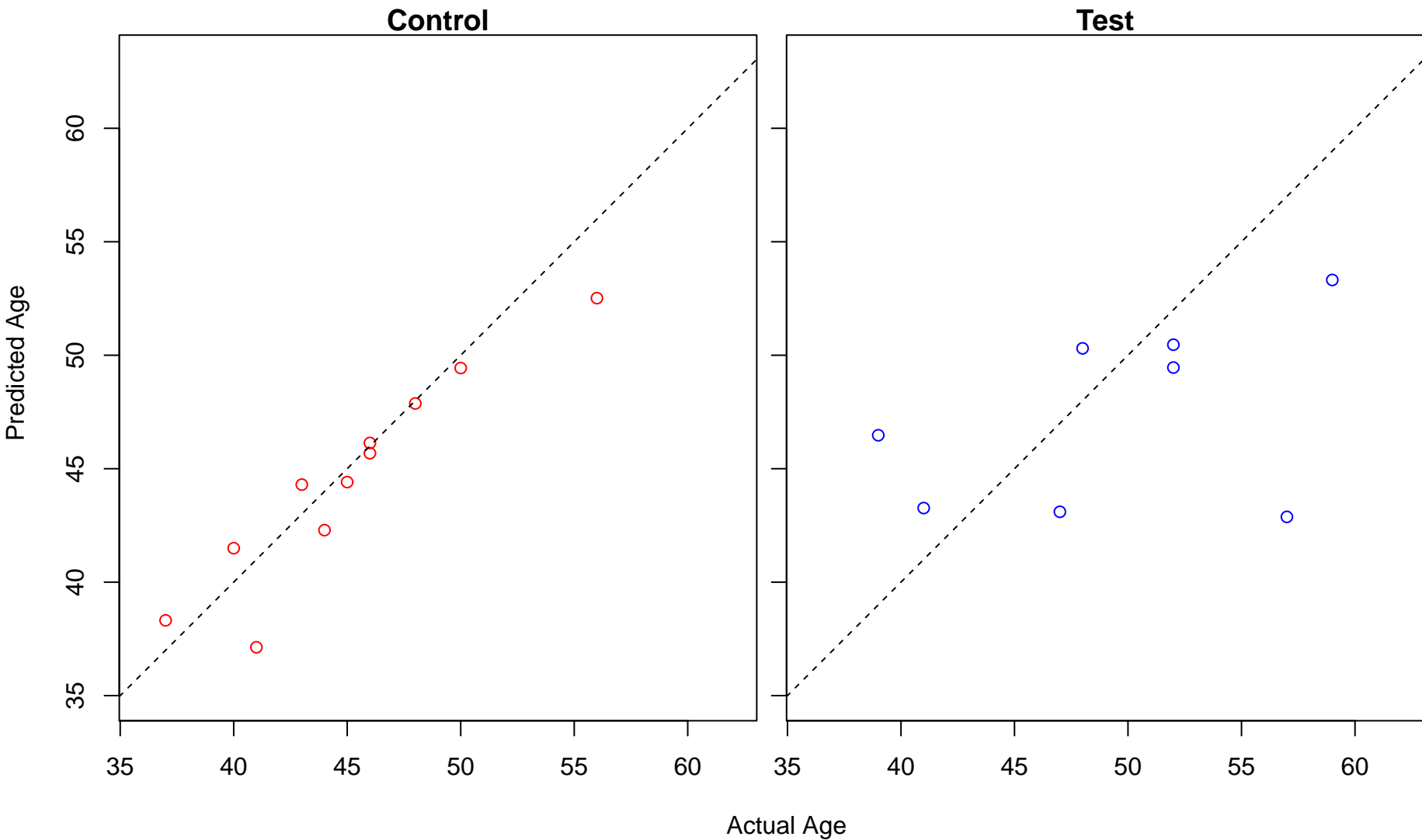
developmental maturation (Score: 14.518740)



cardiac epithelial to mesenchymal transition (Score: 14.505565)

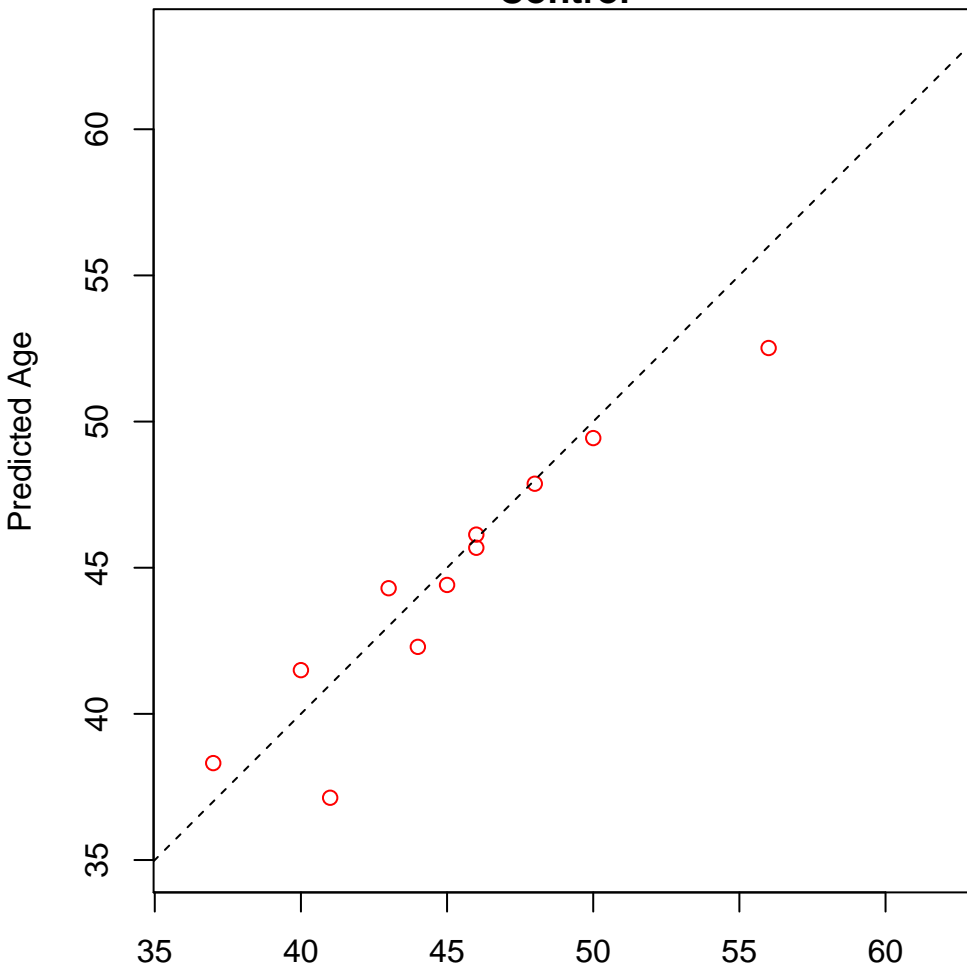


phosphorylated carbohydrate dephosphorylation (Score: 14.497725)

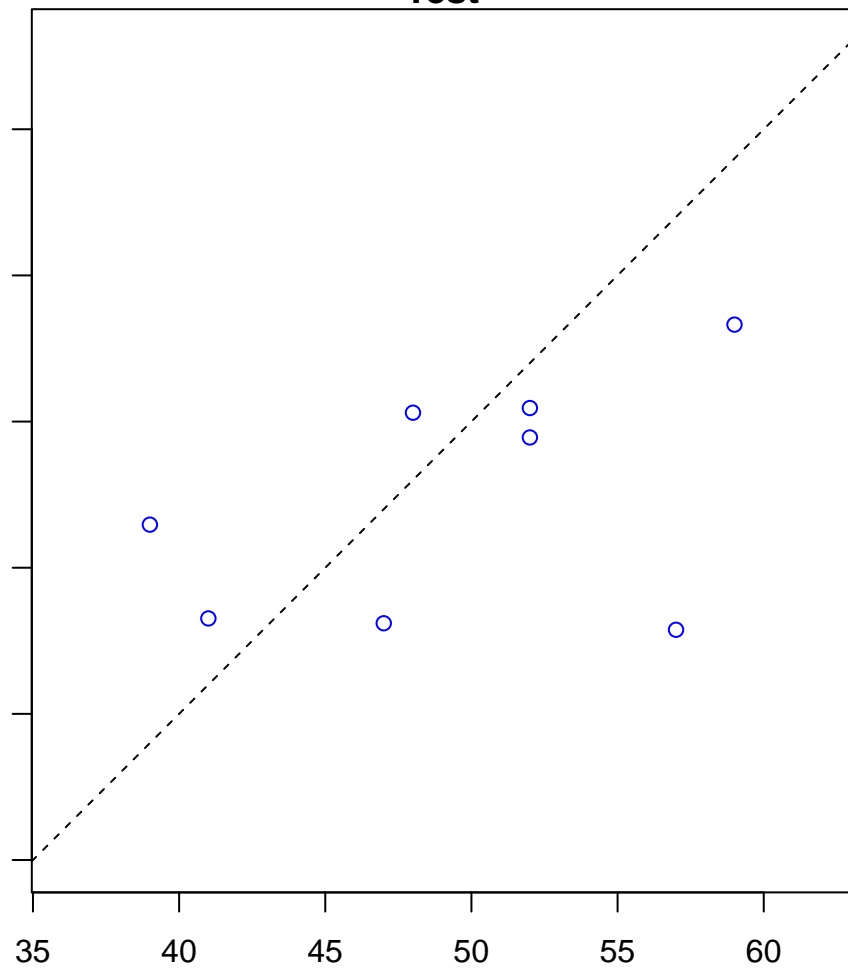


inositol phosphate dephosphorylation (Score: 14.497725)

Control

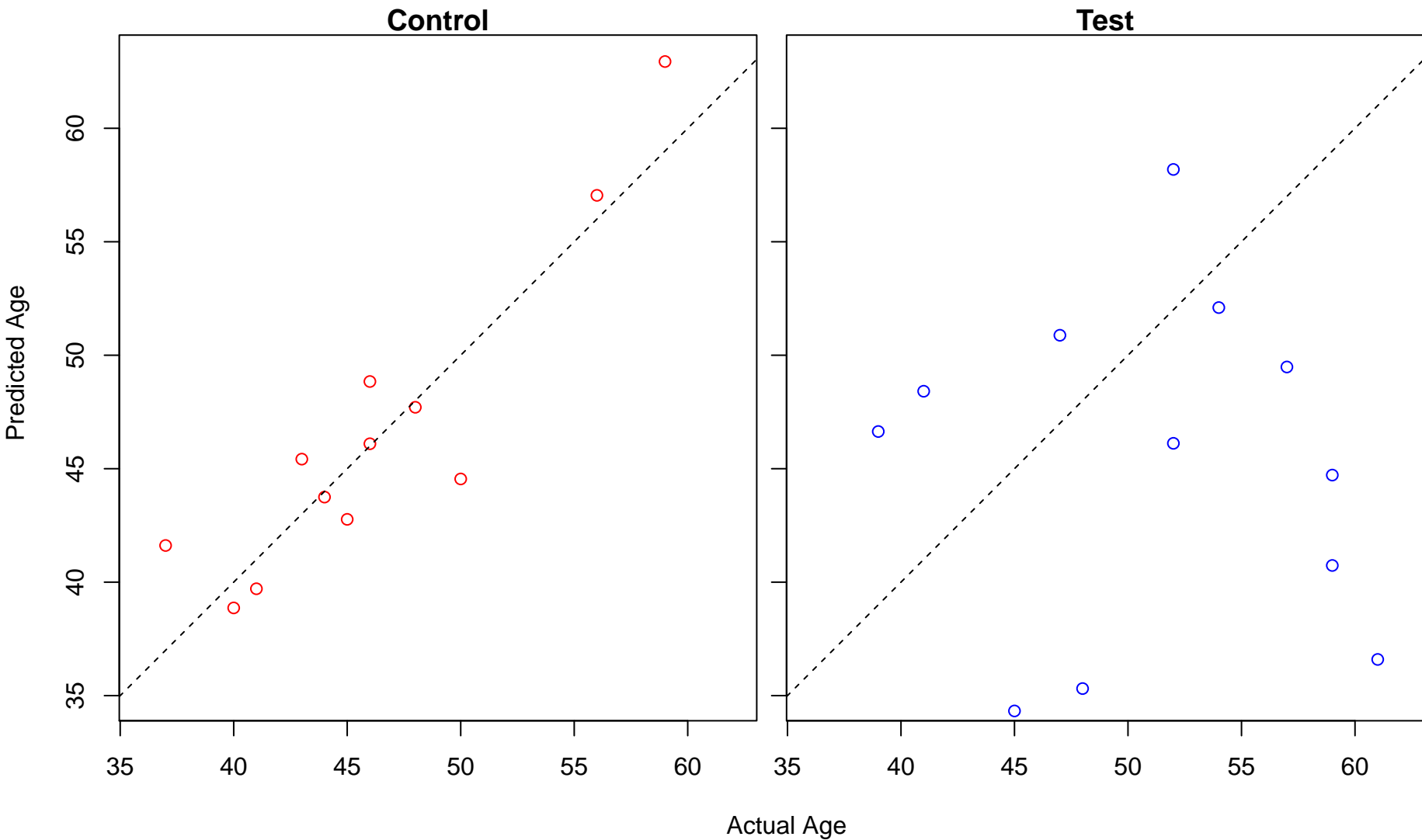


Test

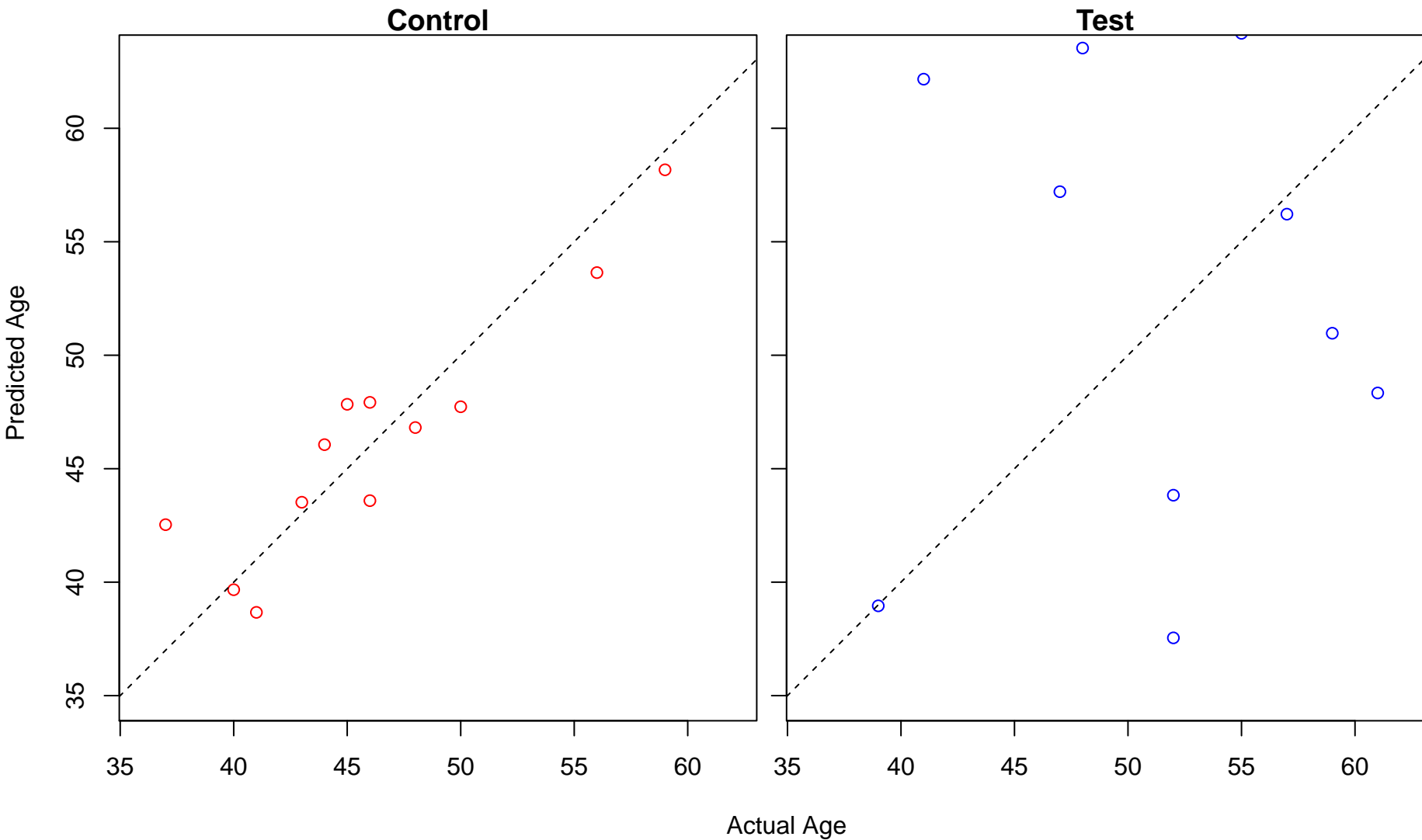


Actual Age

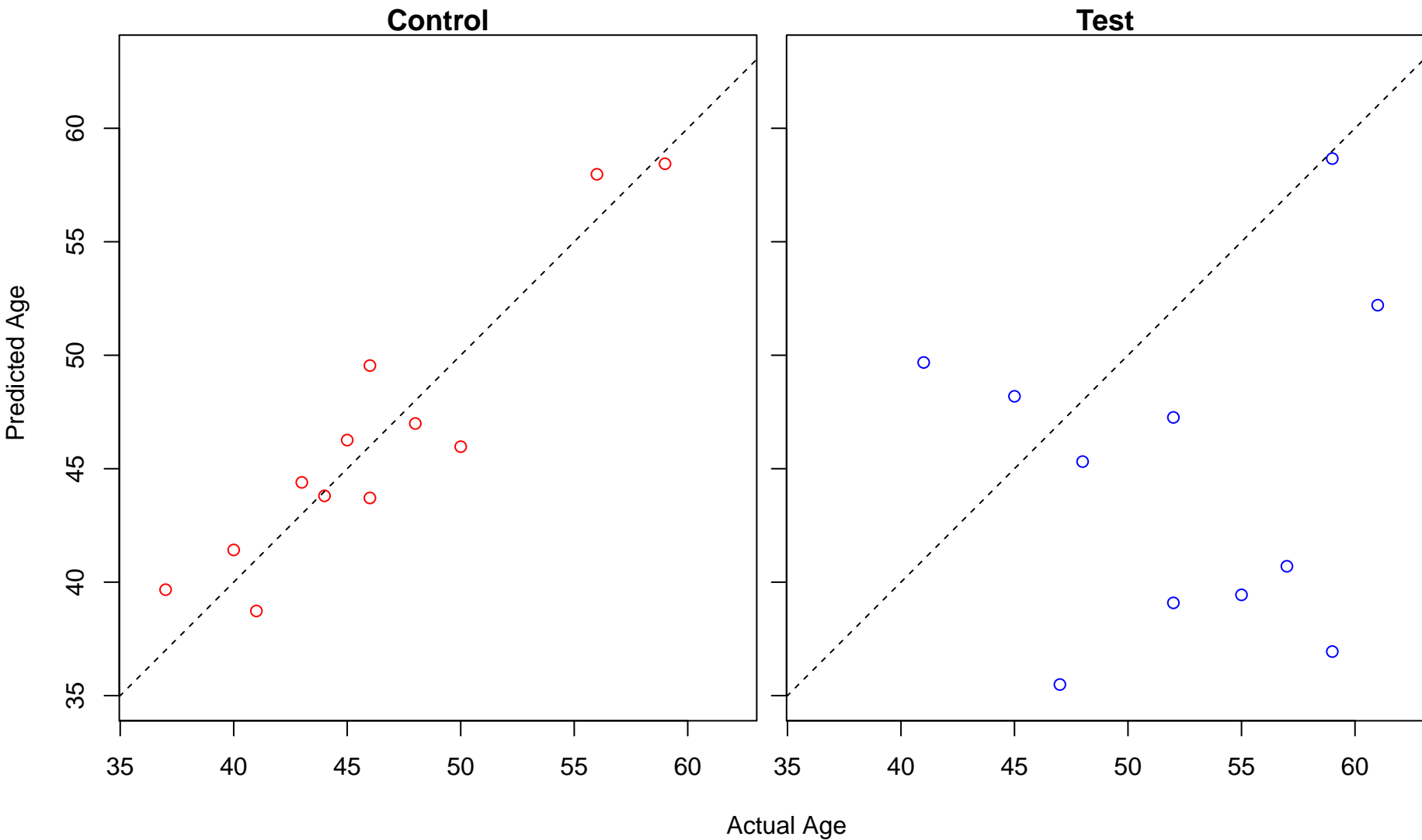
endothelial cell chemotaxis (Score: 14.438184)



heart morphogenesis (Score: 14.430684)

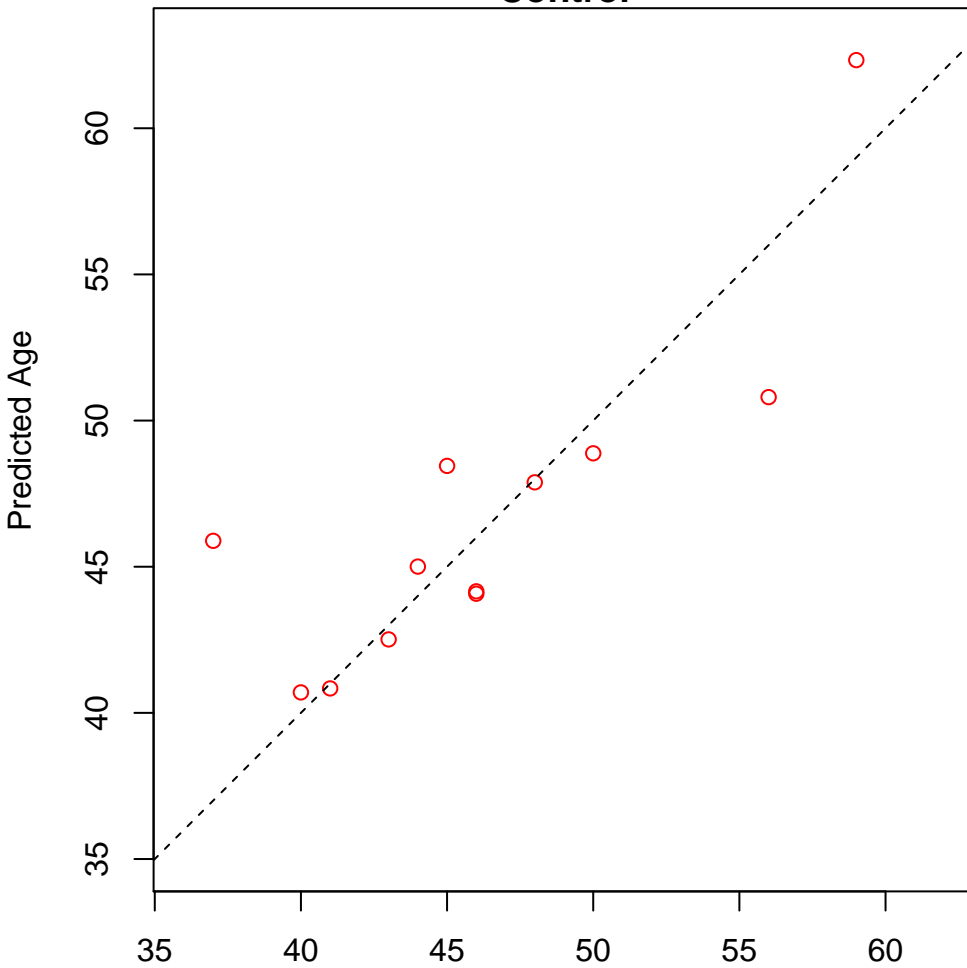


cell maturation (Score: 14.421220)

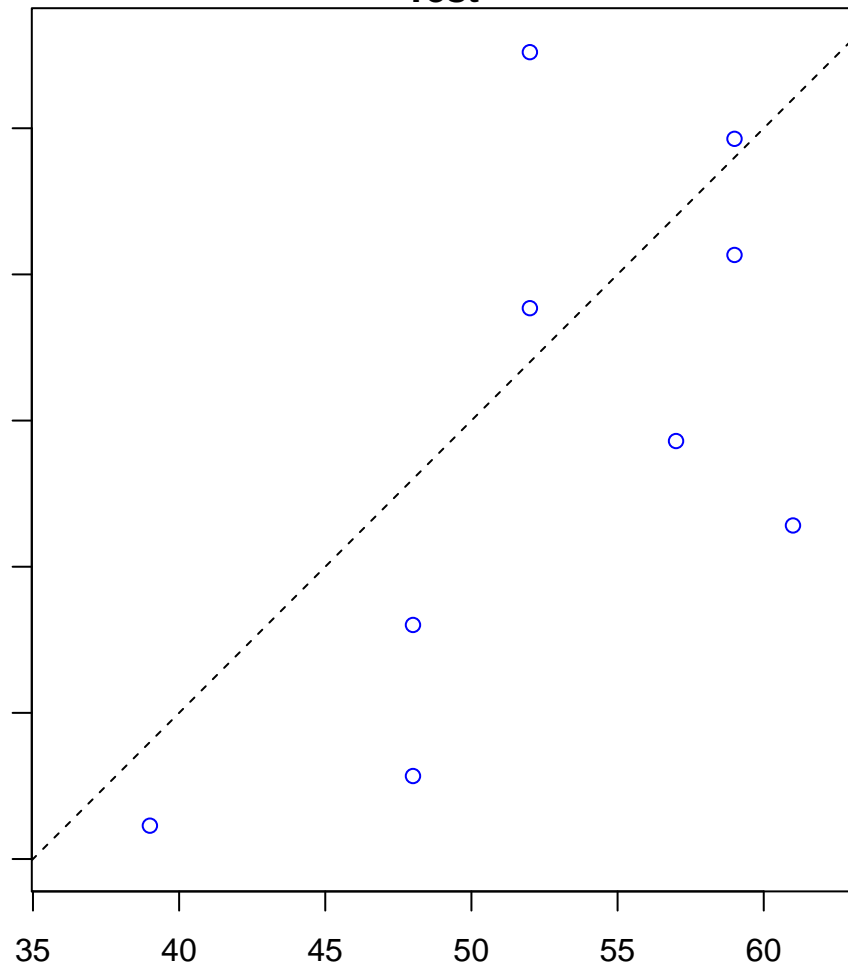


regulation of cholesterol homeostasis (Score: 14.416838)

Control

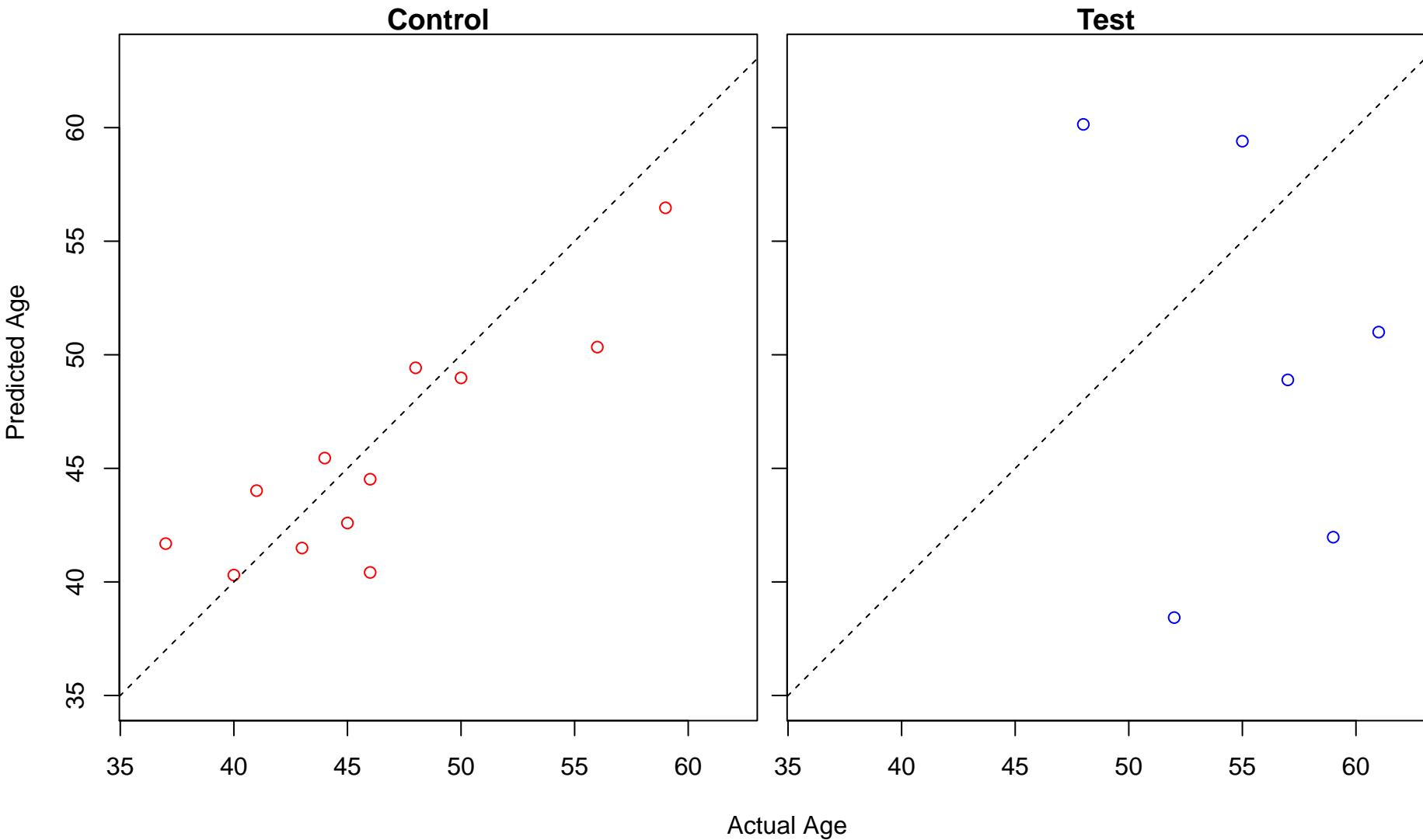


Test

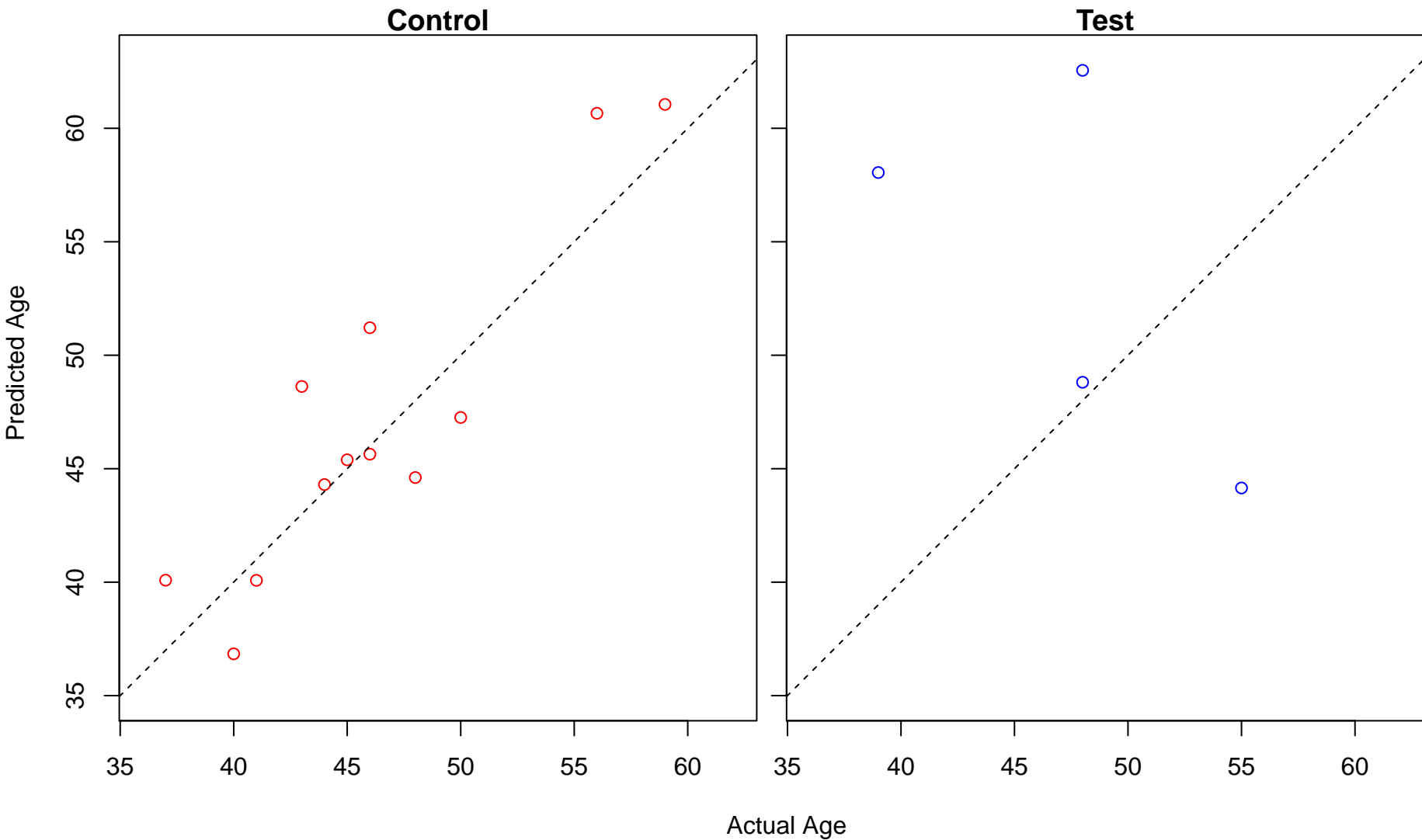


Actual Age

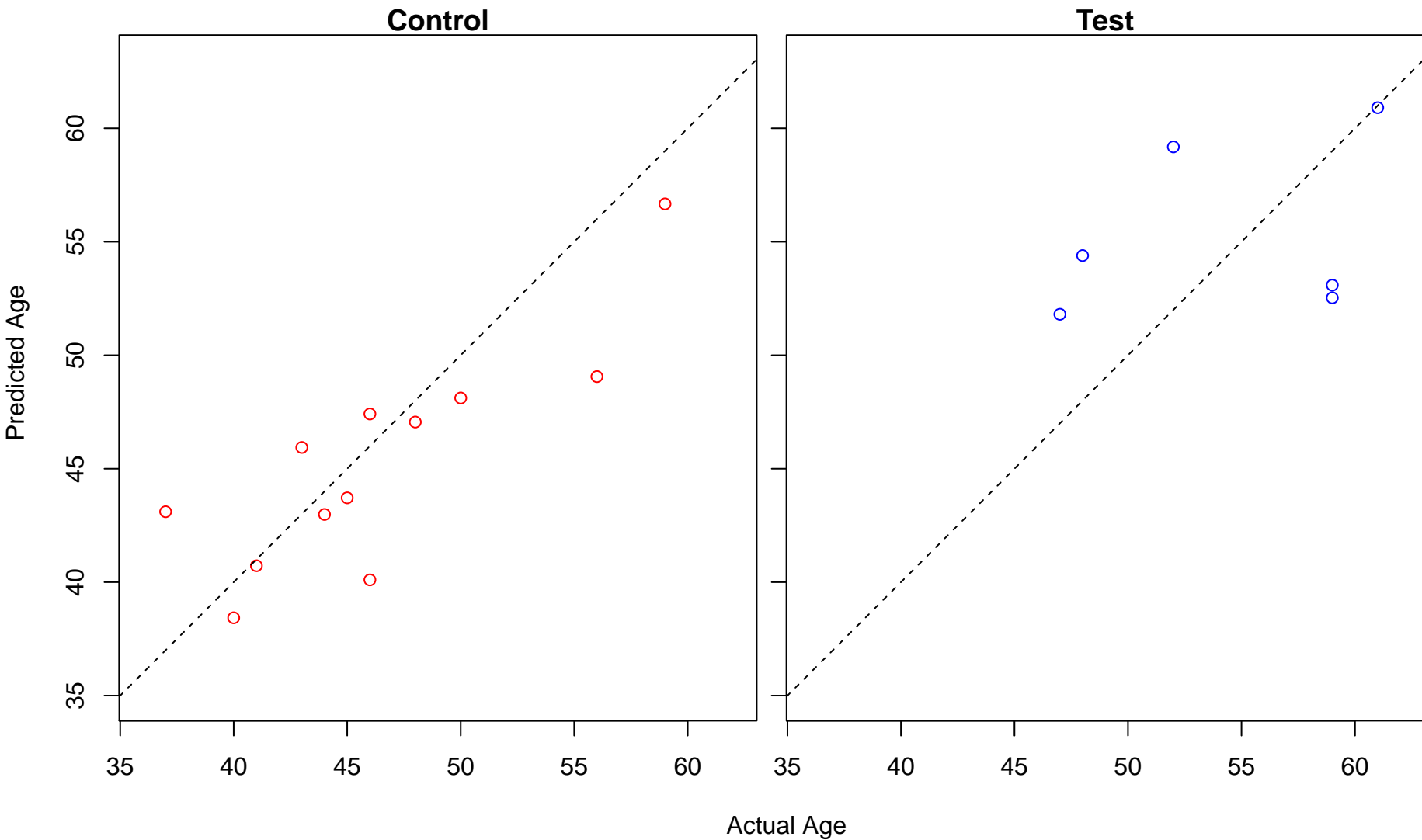
primary alcohol metabolic process (Score: 14.345488)



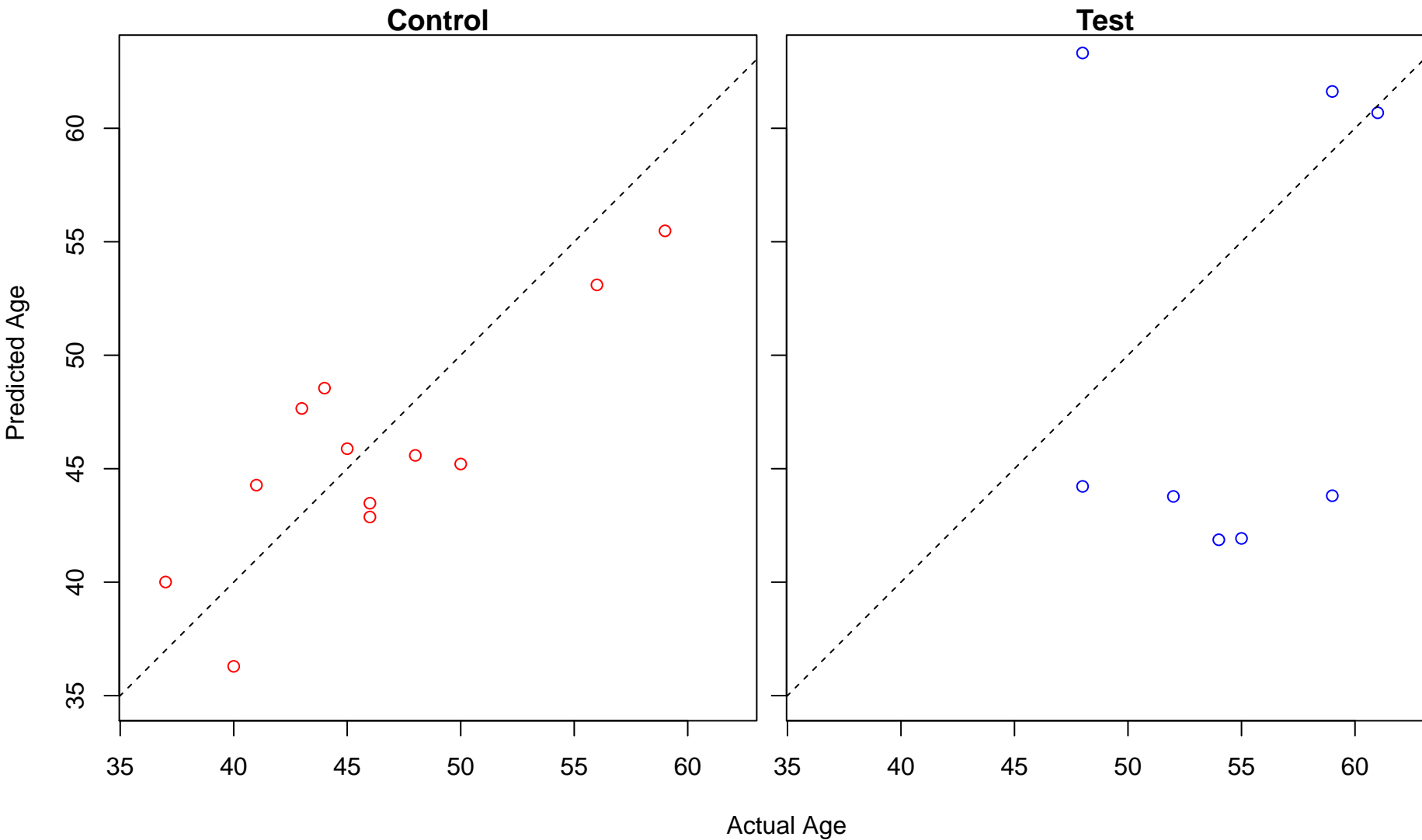
regulation of type 2 immune response (Score: 14.278792)



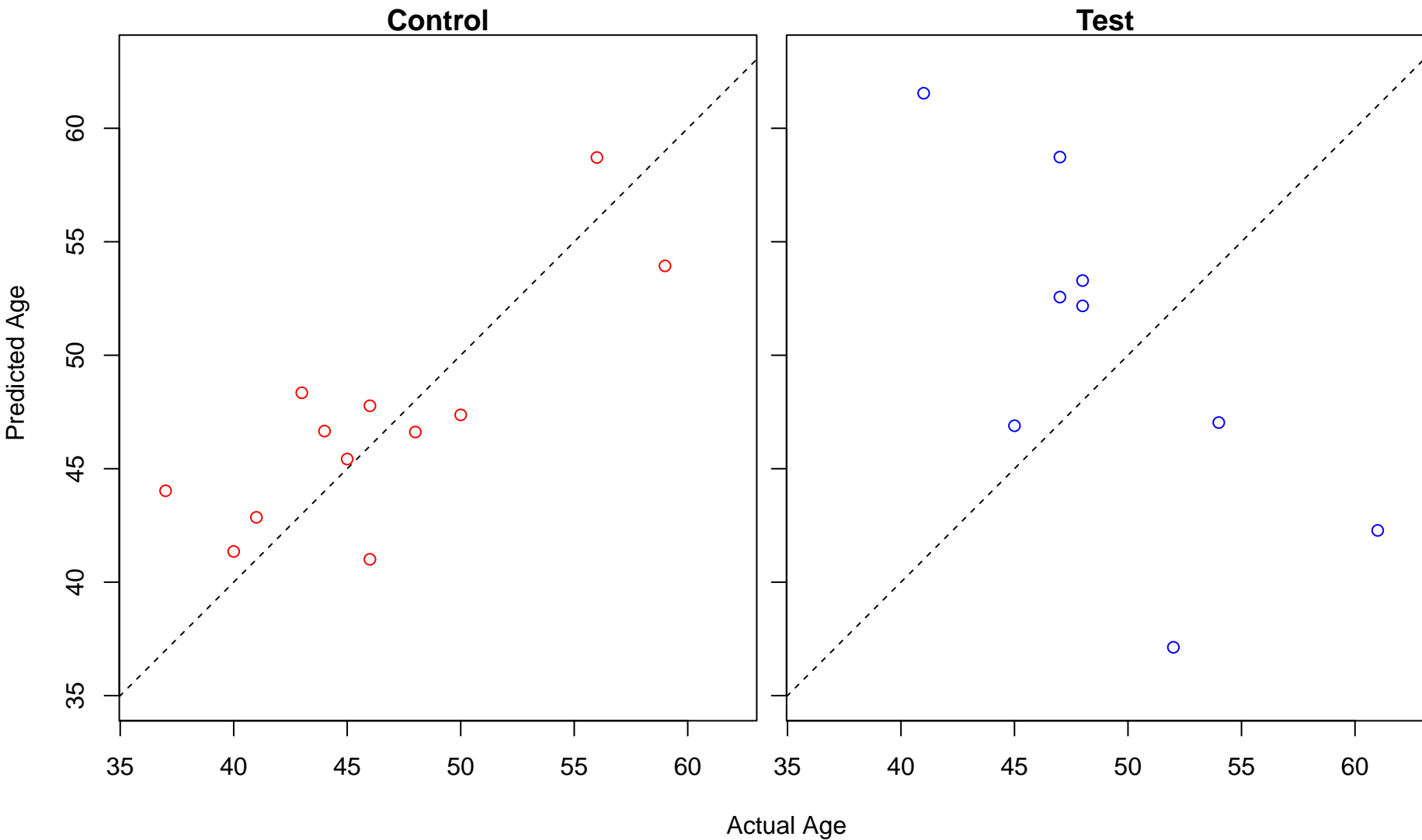
negative regulation of transcription regulatory region DNA binding (Score: 14.257920)



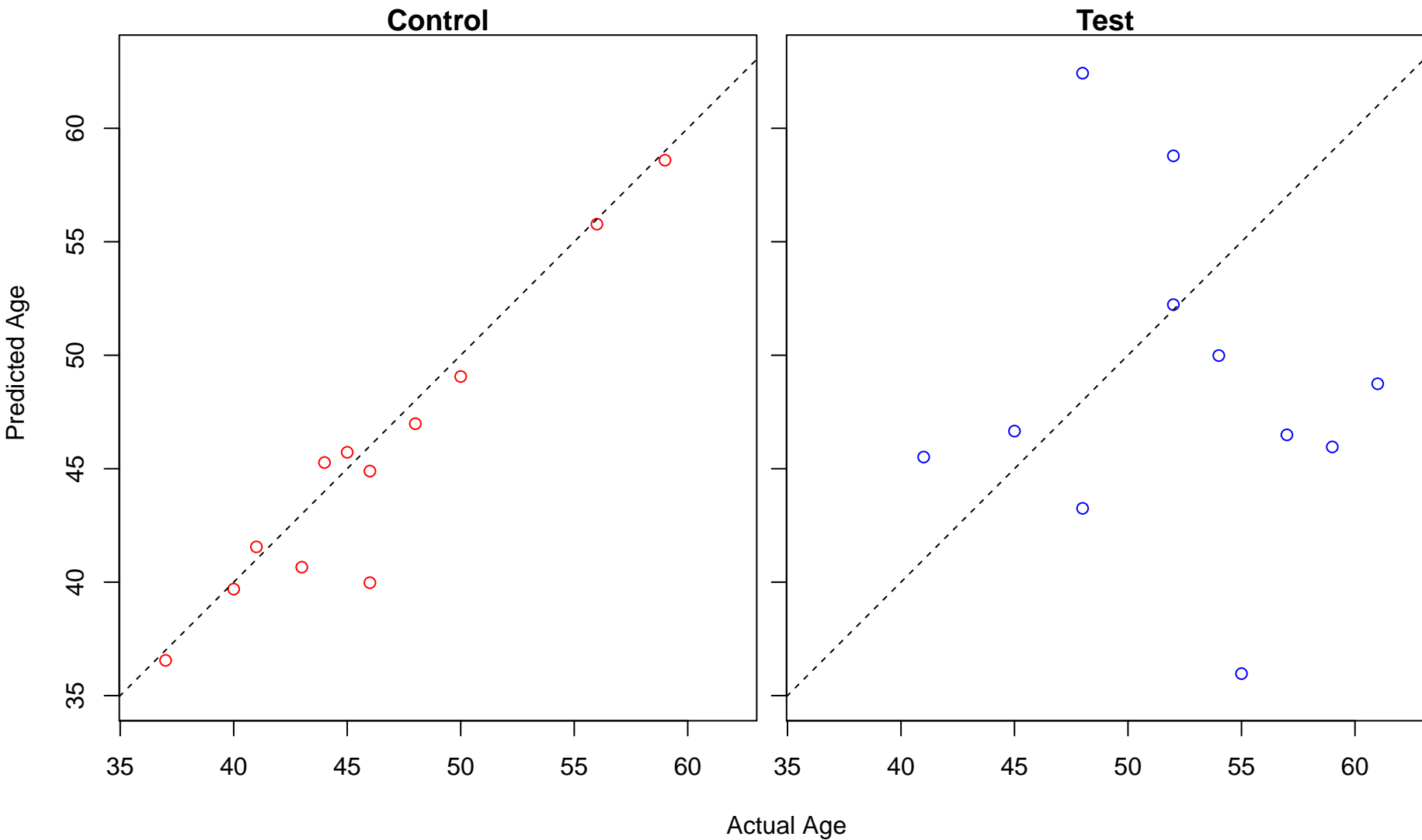
regulation of tumor necrosis factor-mediated signaling pathway (Score: 14.254704)



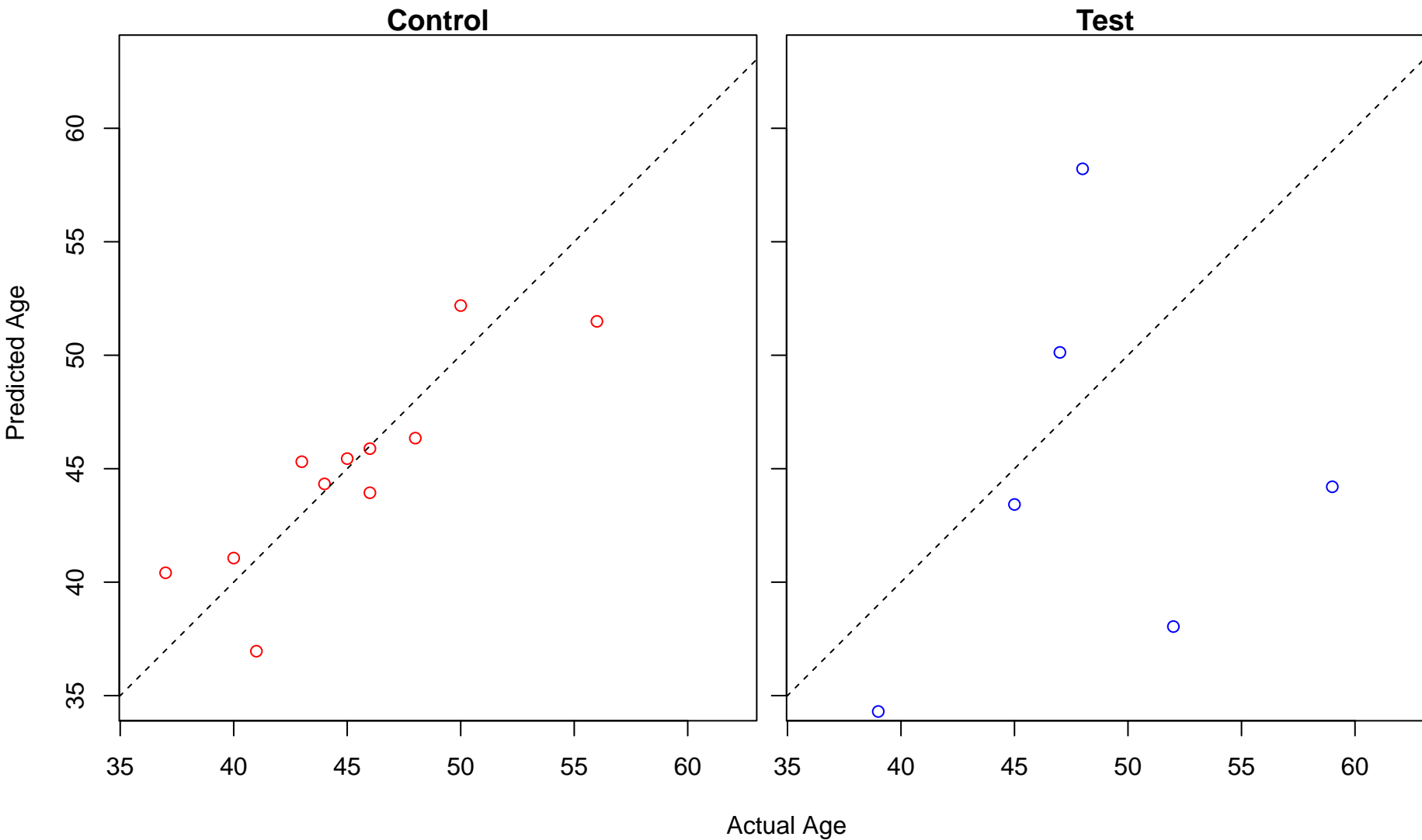
regulation of systemic arterial blood pressure (Score: 14.251615)



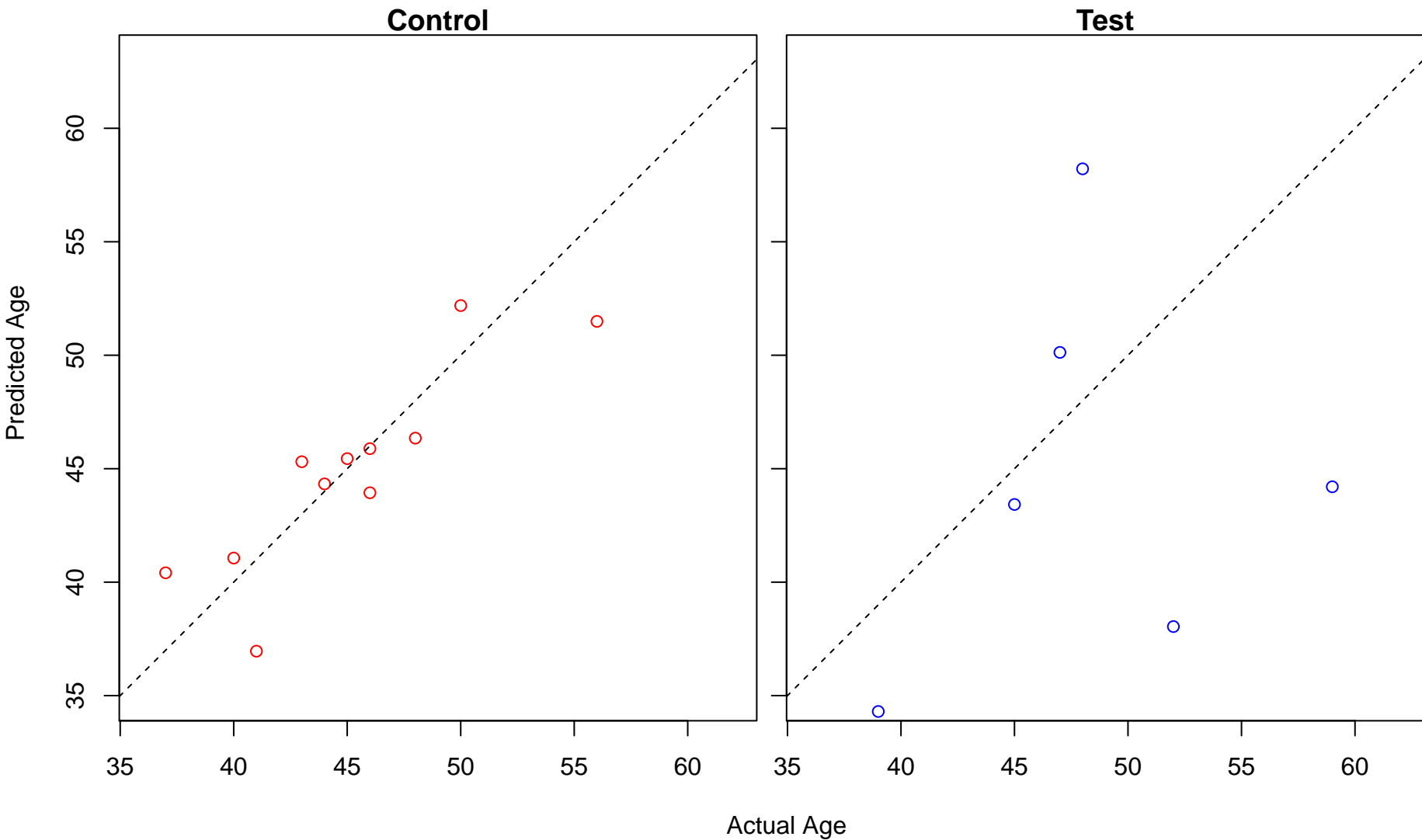
negative regulation of epithelial cell differentiation (Score: 14.248958)



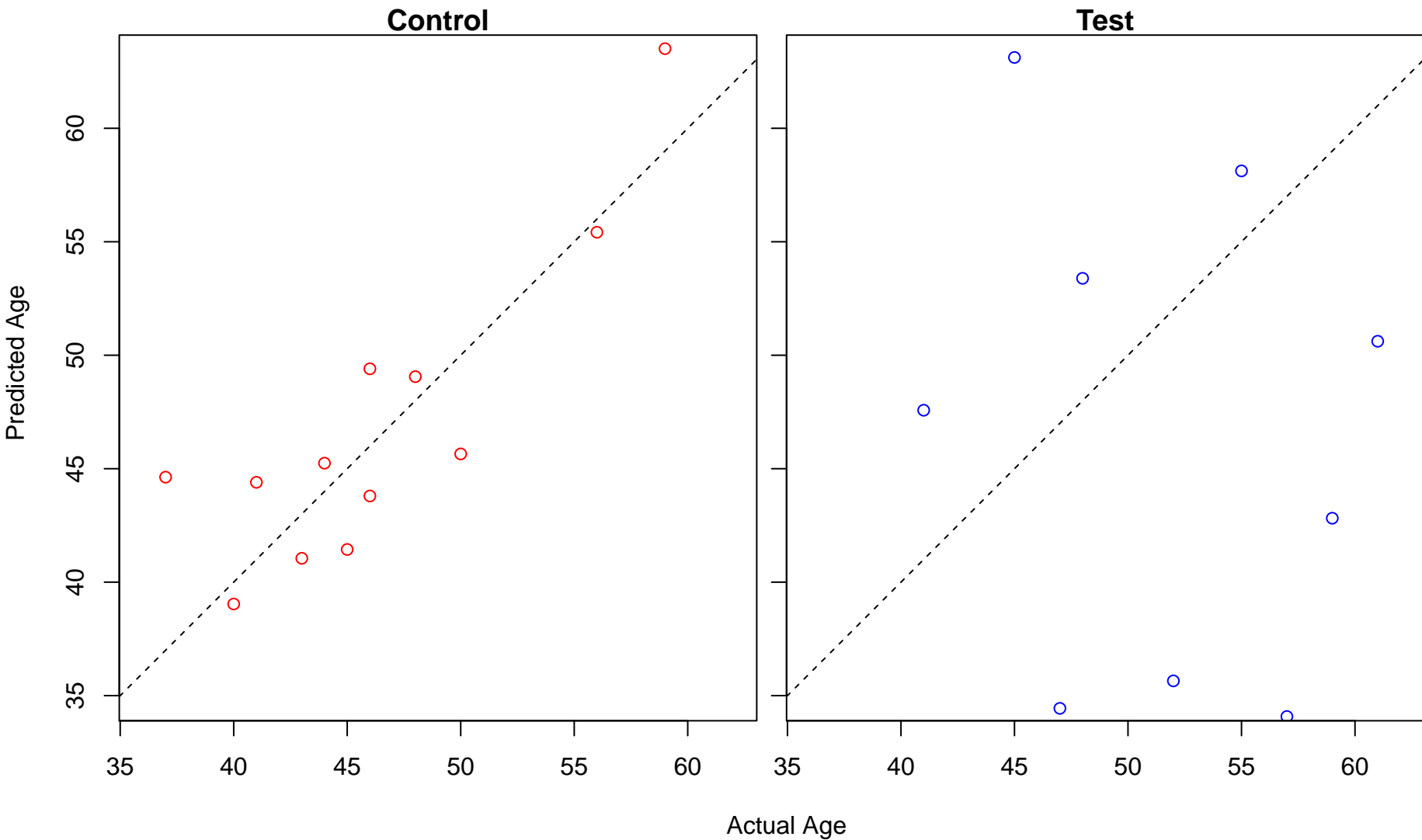
sphingosine-1-phosphate signaling pathway (Score: 14.210839)



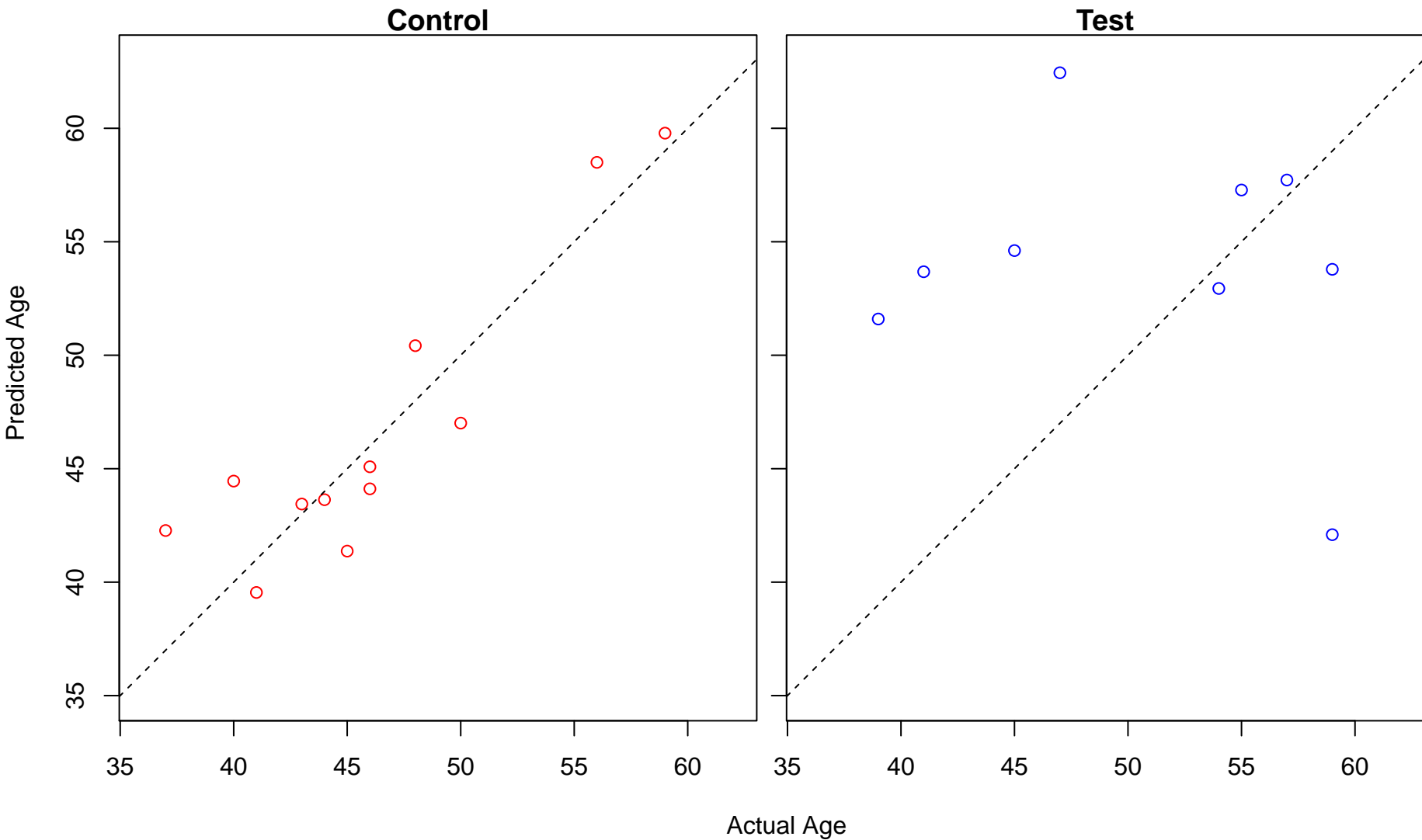
sphingolipid mediated signaling pathway (Score: 14.210839)



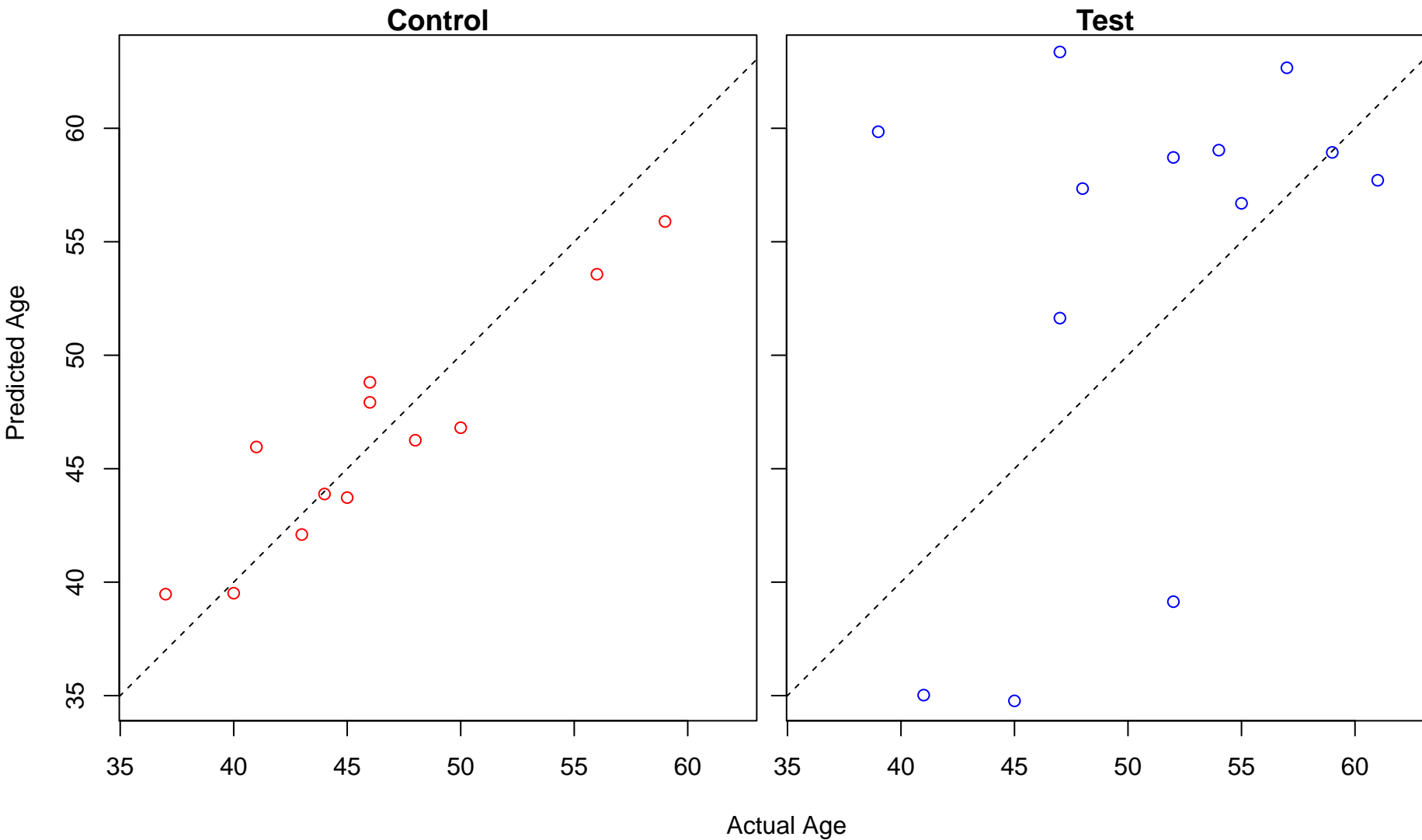
nerve development (Score: 14.174336)



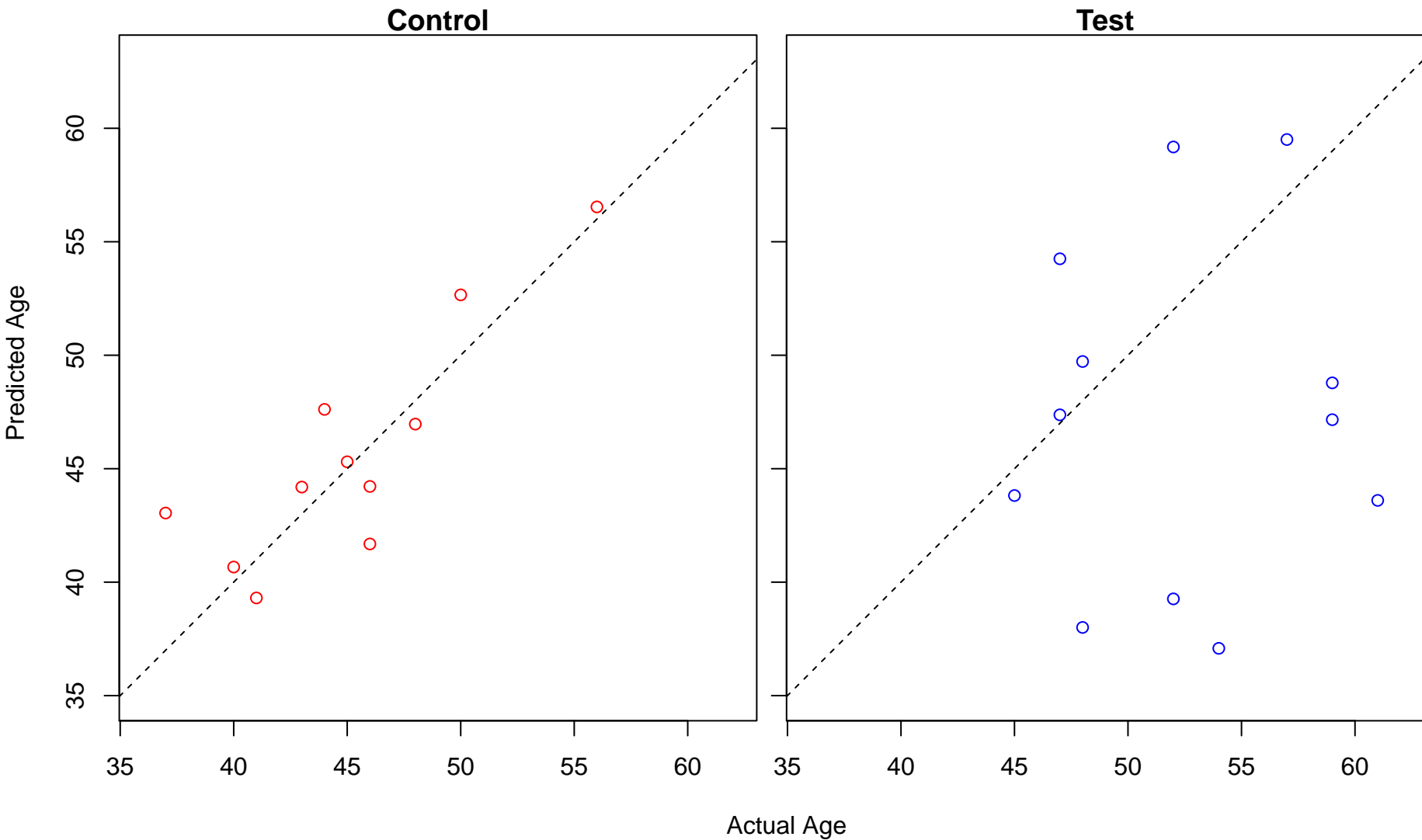
signal peptide processing (Score: 14.159838)



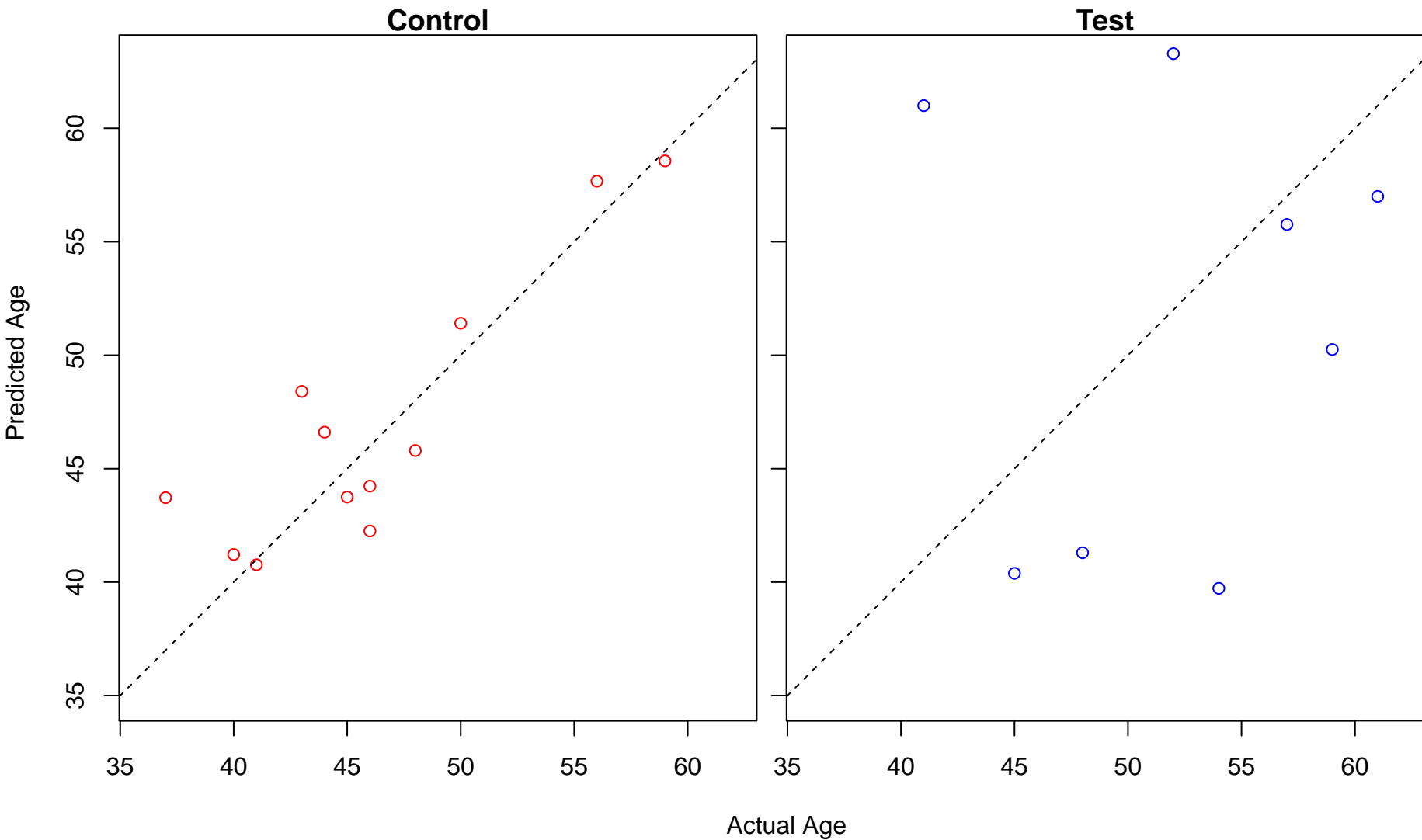
positive regulation of cholesterol esterification (Score: 14.147285)



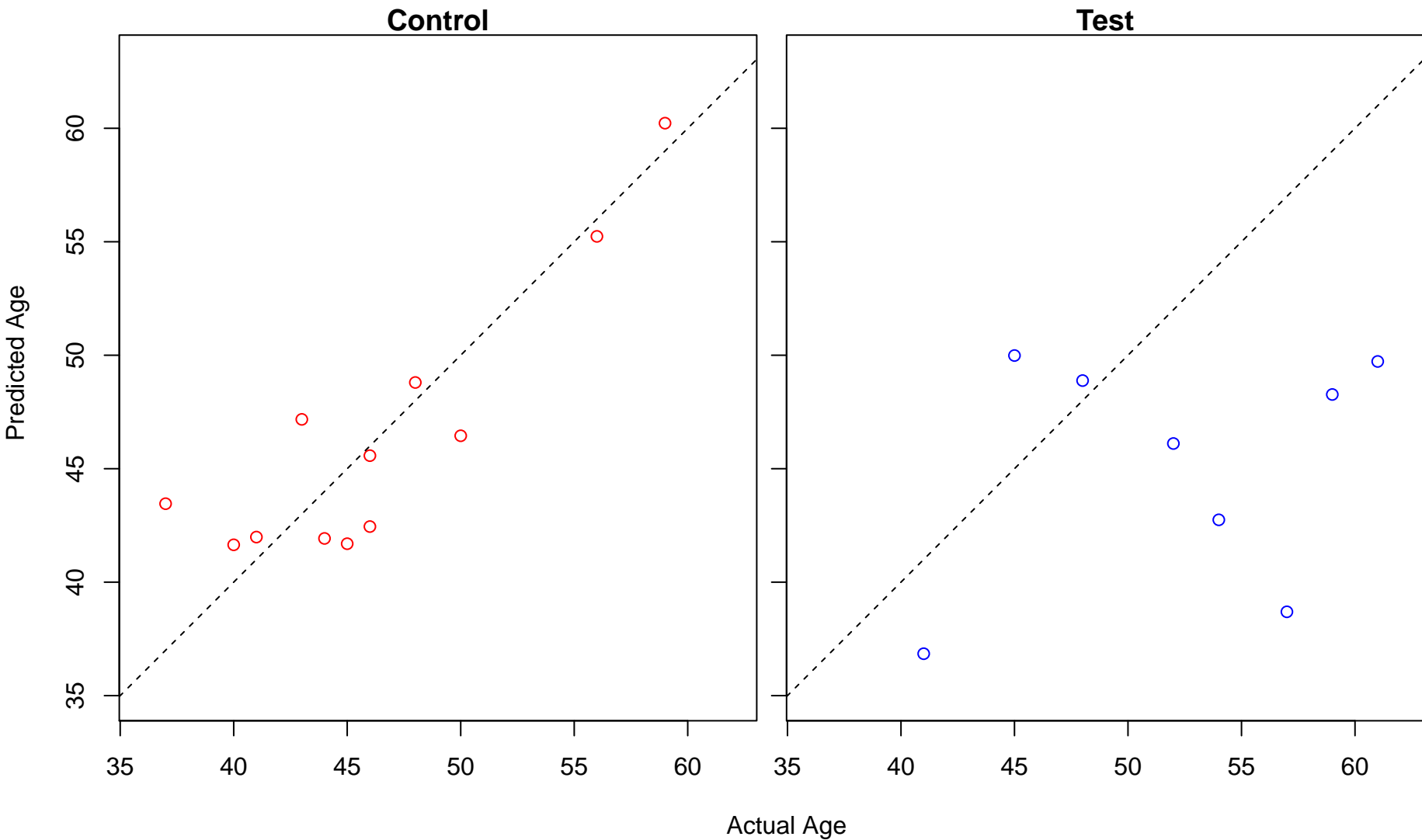
negative regulation of cyclic nucleotide biosynthetic process (Score: 14.142211)



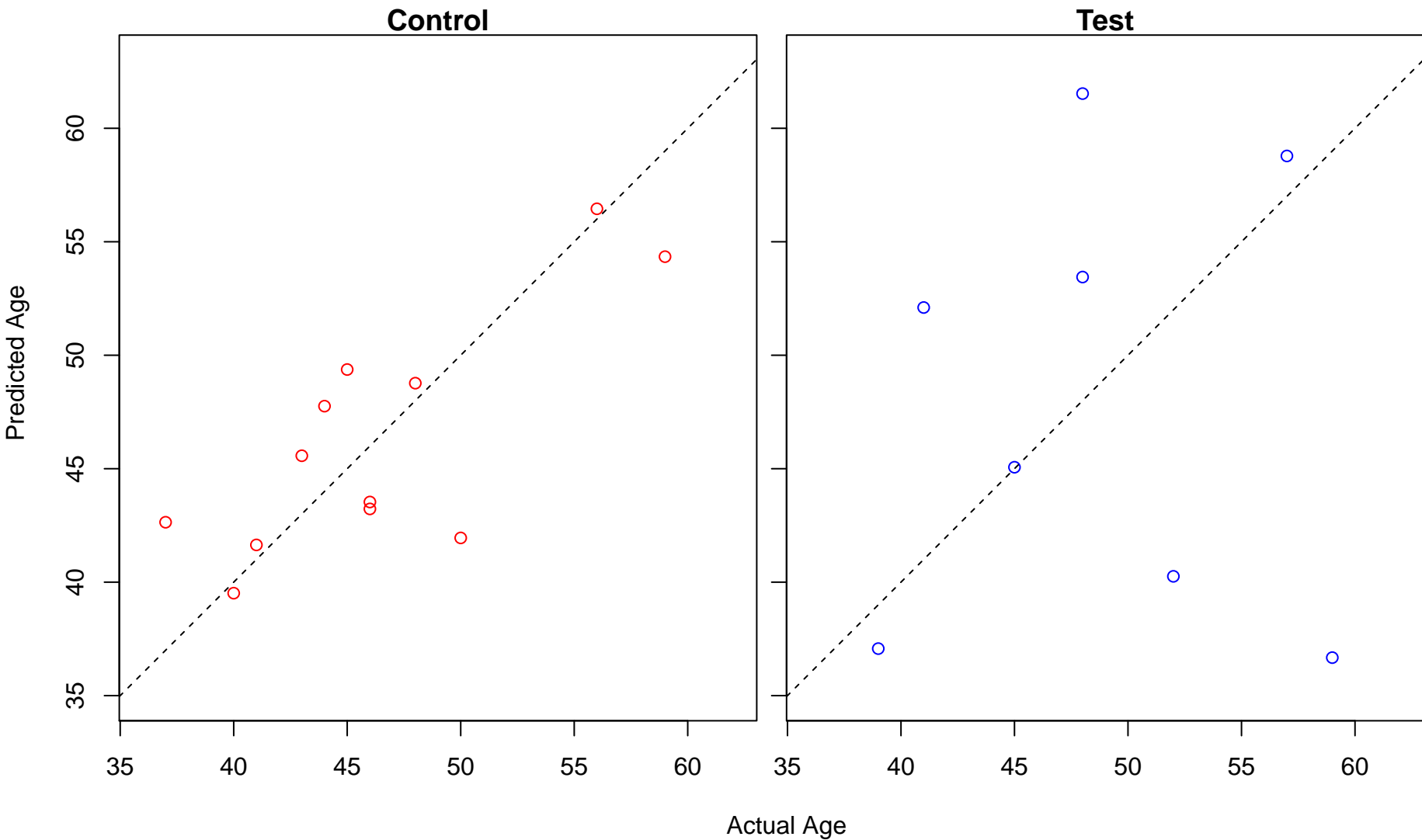
regulation of early endosome to late endosome transport (Score: 14.096231)



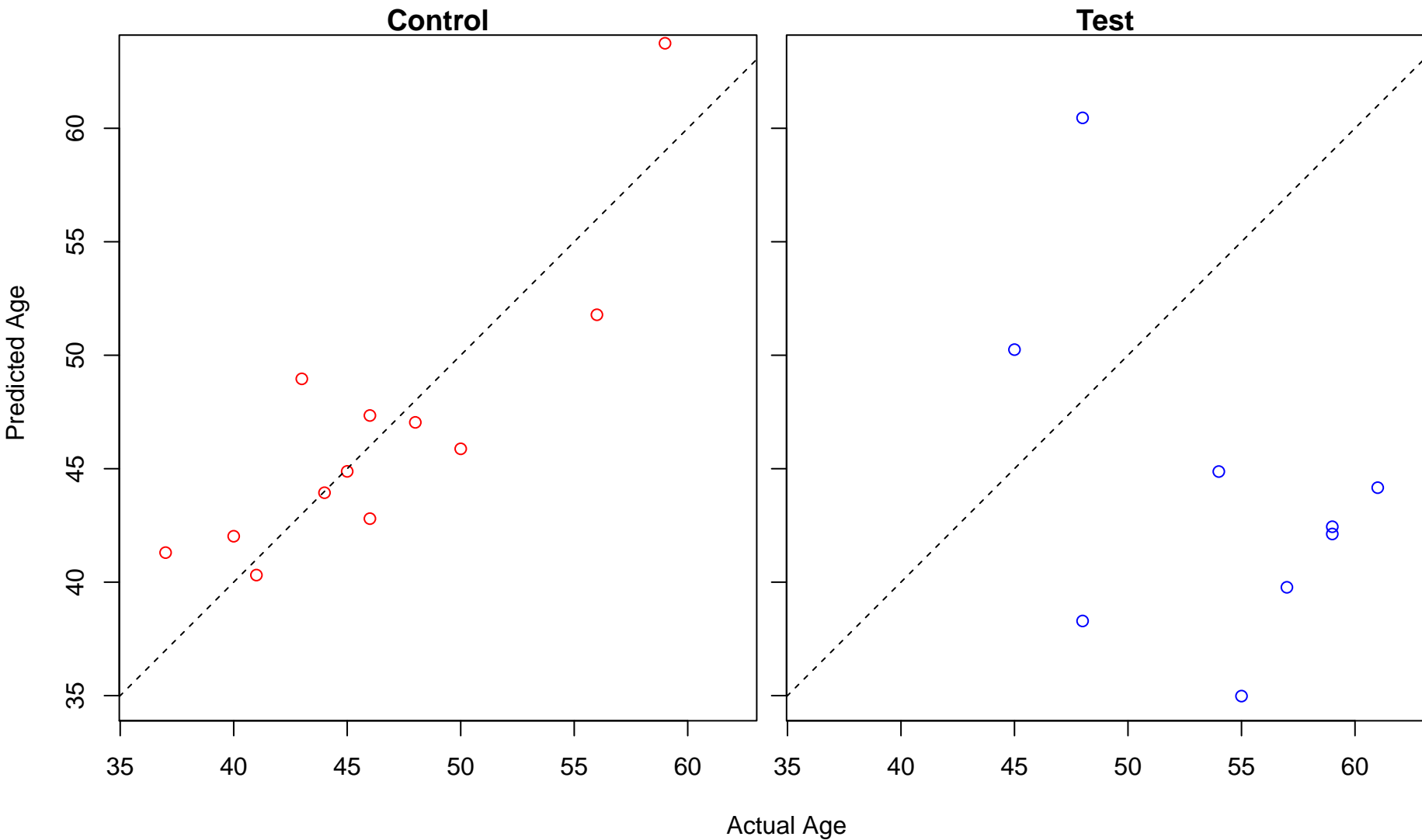
negative regulation of proteolysis (Score: 14.094440)



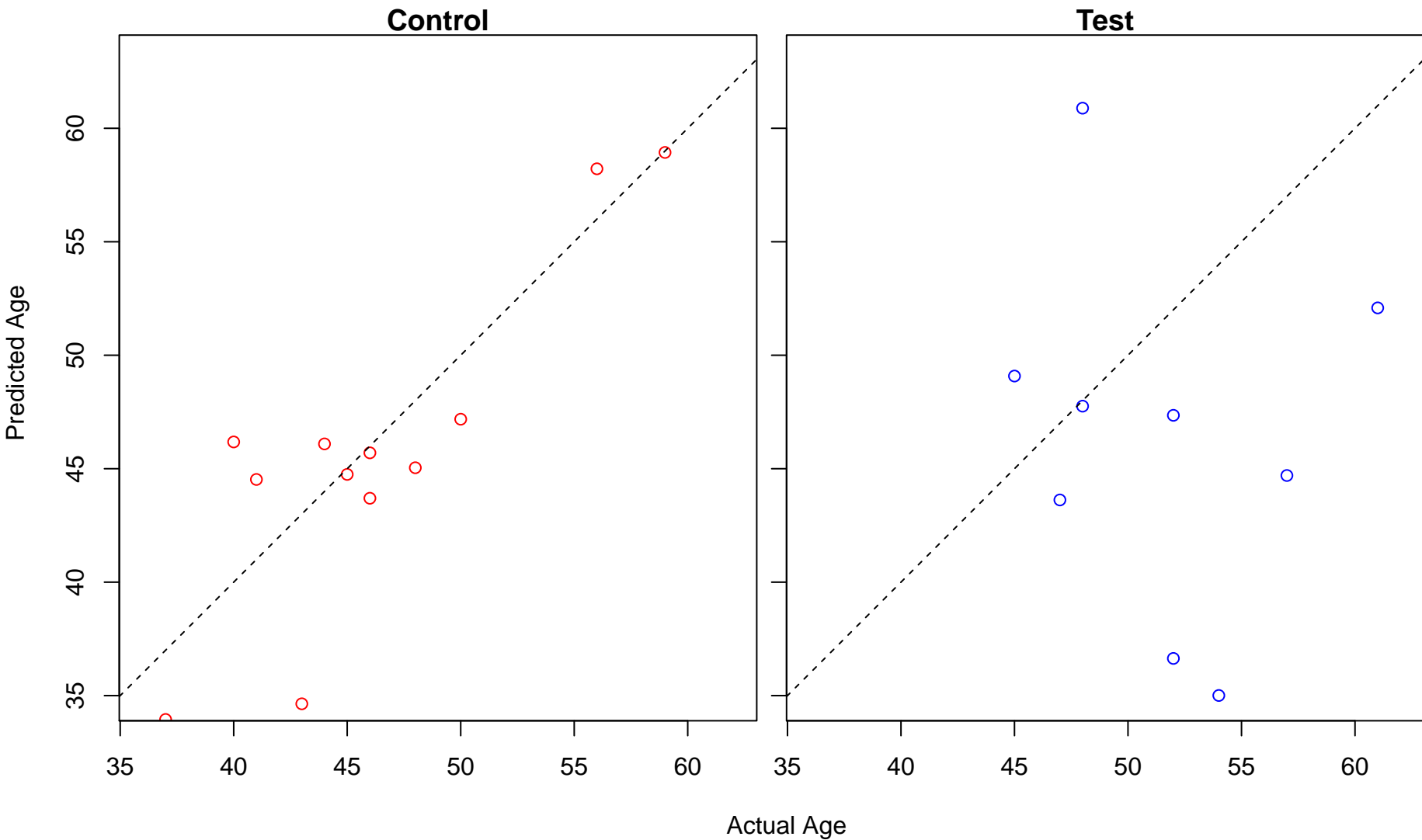
acid secretion (Score: 14.054480)



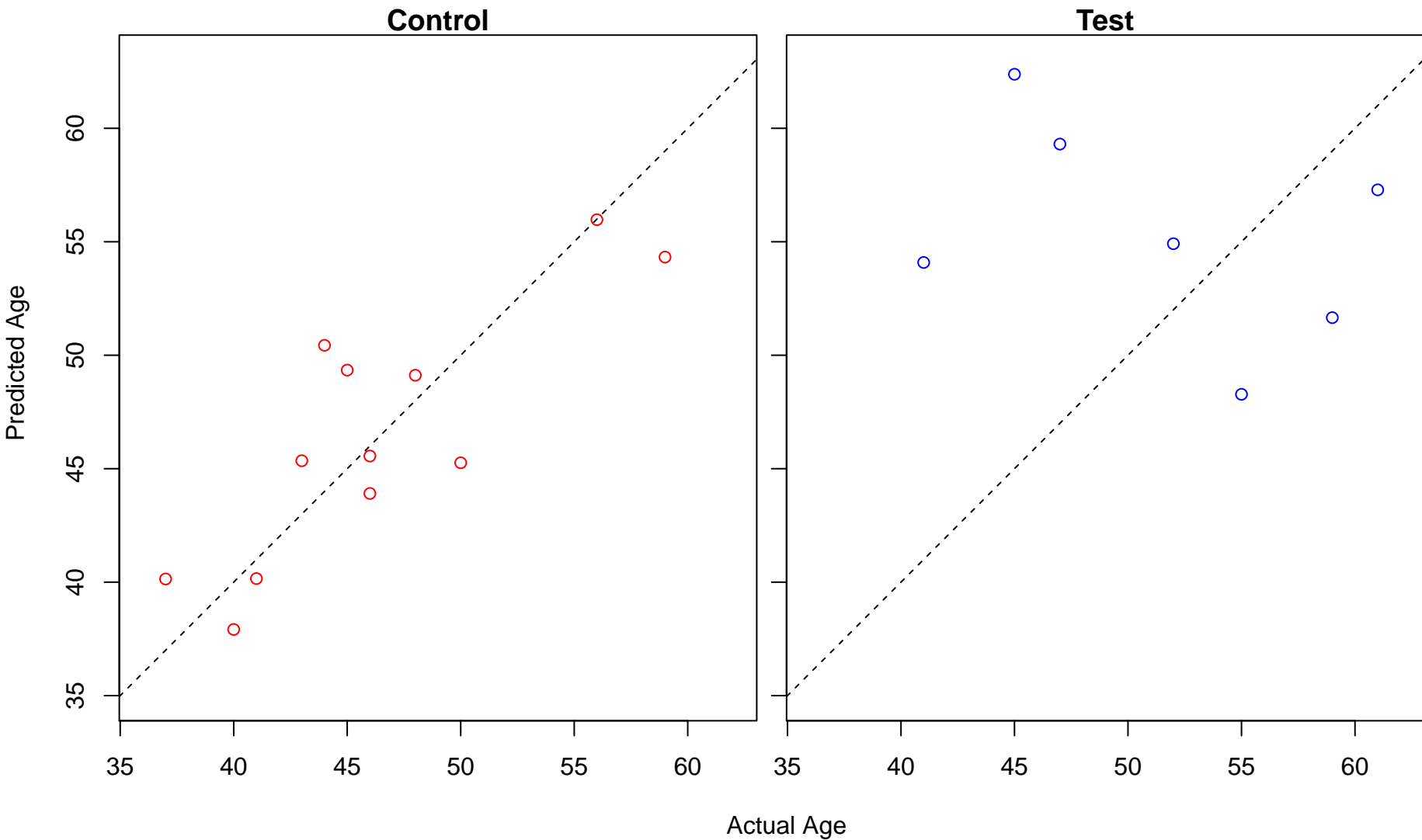
regulation of histone modification (Score: 14.054059)



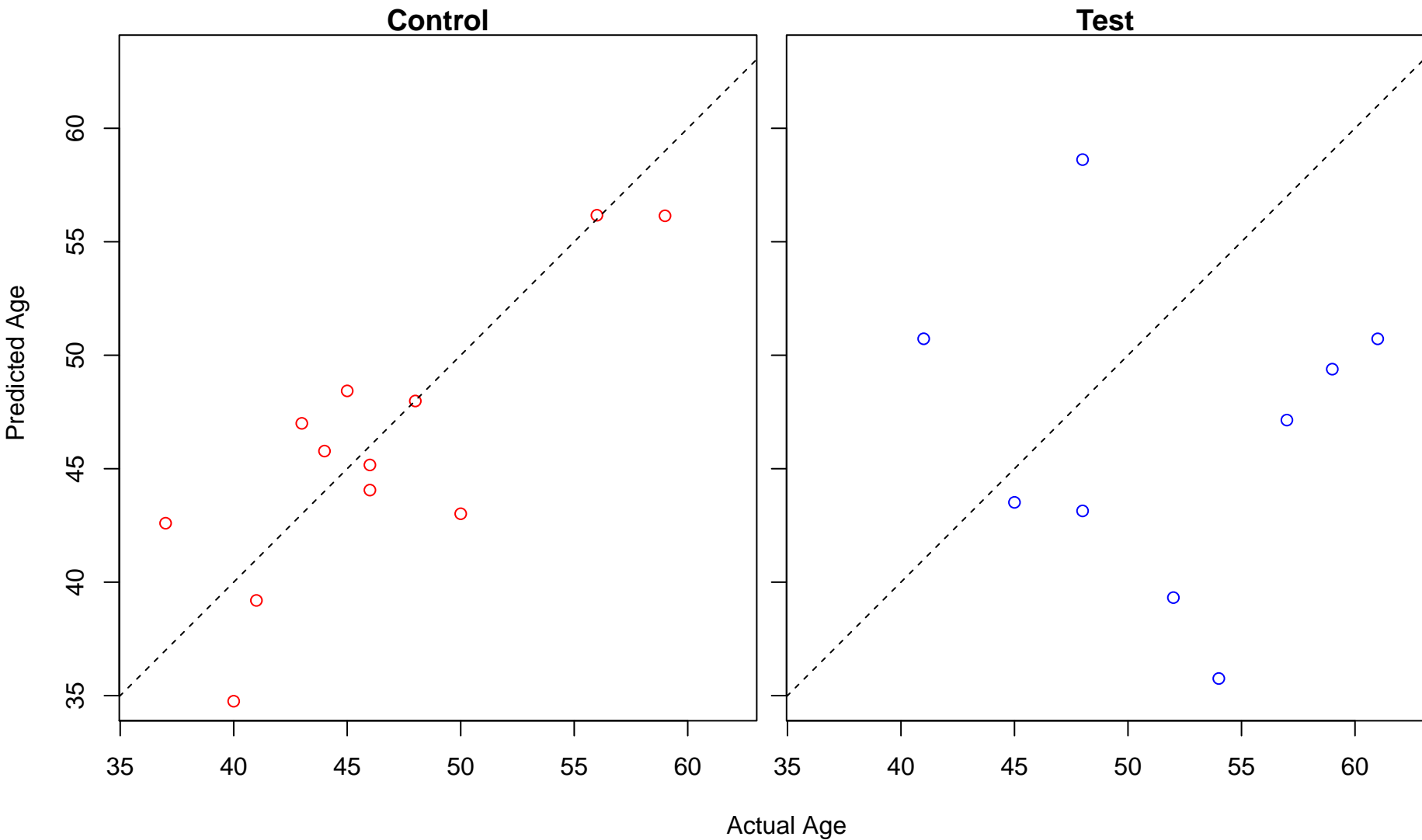
positive regulation of myeloid leukocyte mediated immunity (Score: 14.040012)



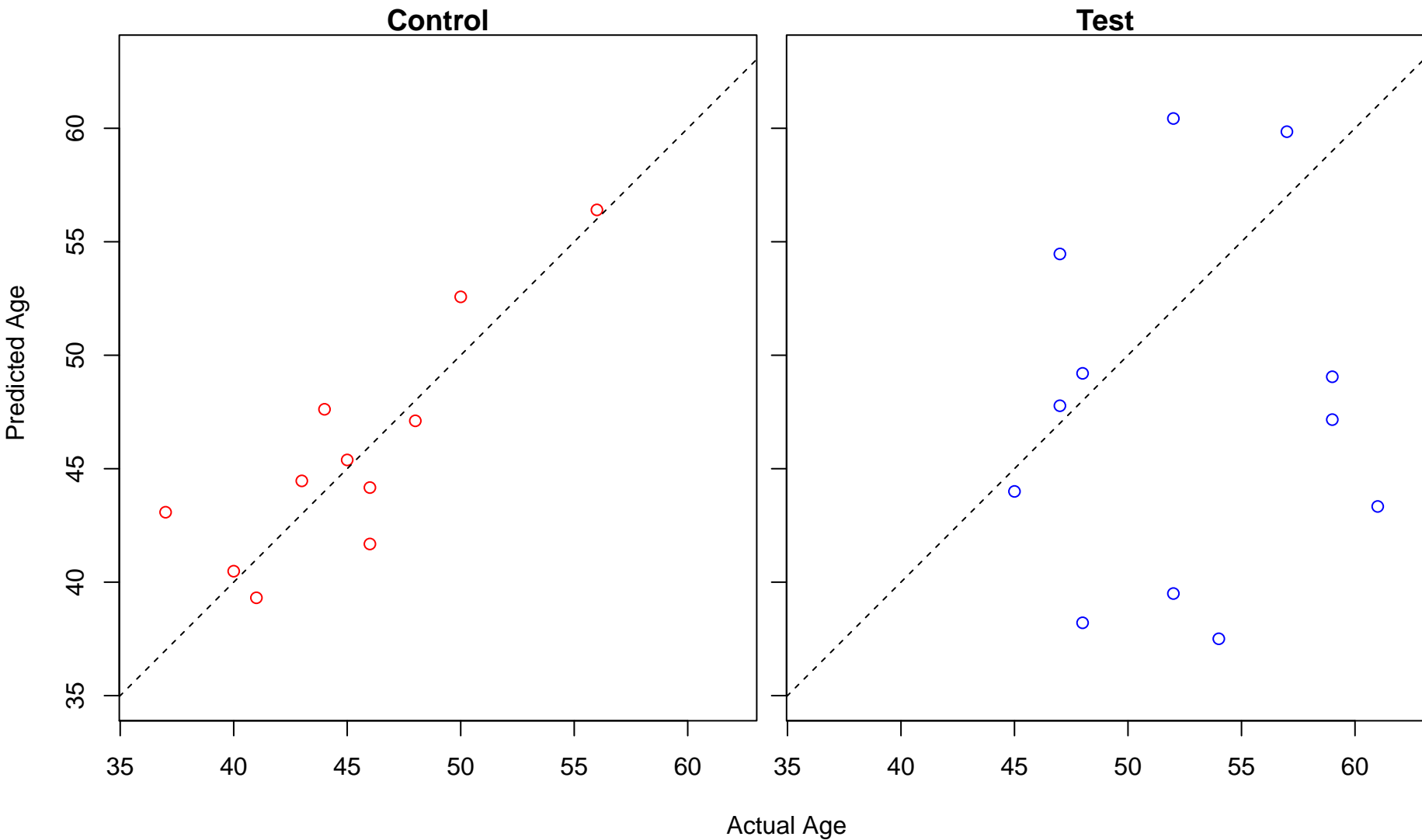
negative regulation of sprouting angiogenesis (Score: 14.024539)



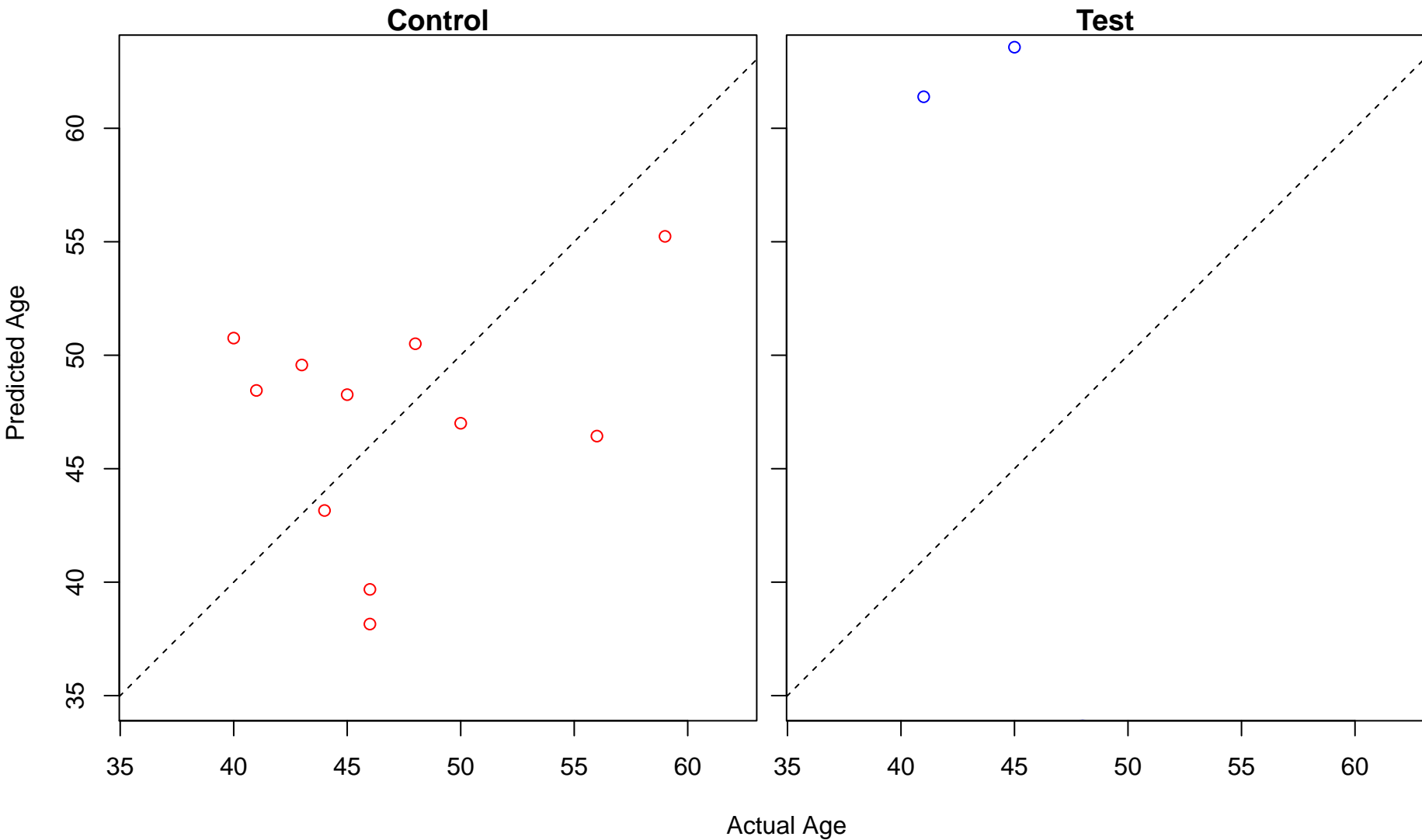
cardiac atrium development (Score: 14.023374)



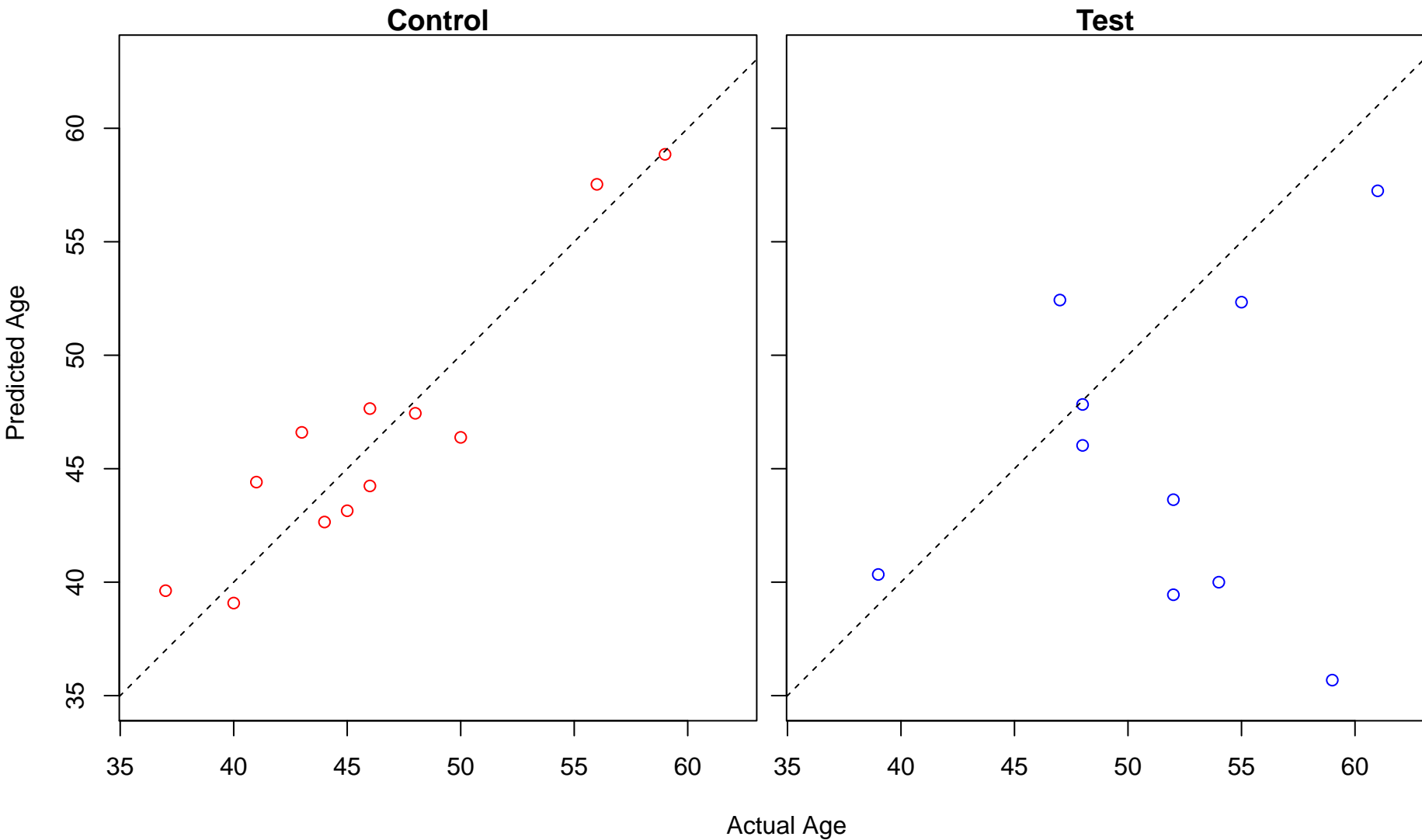
negative regulation of cAMP biosynthetic process (Score: 14.006144)



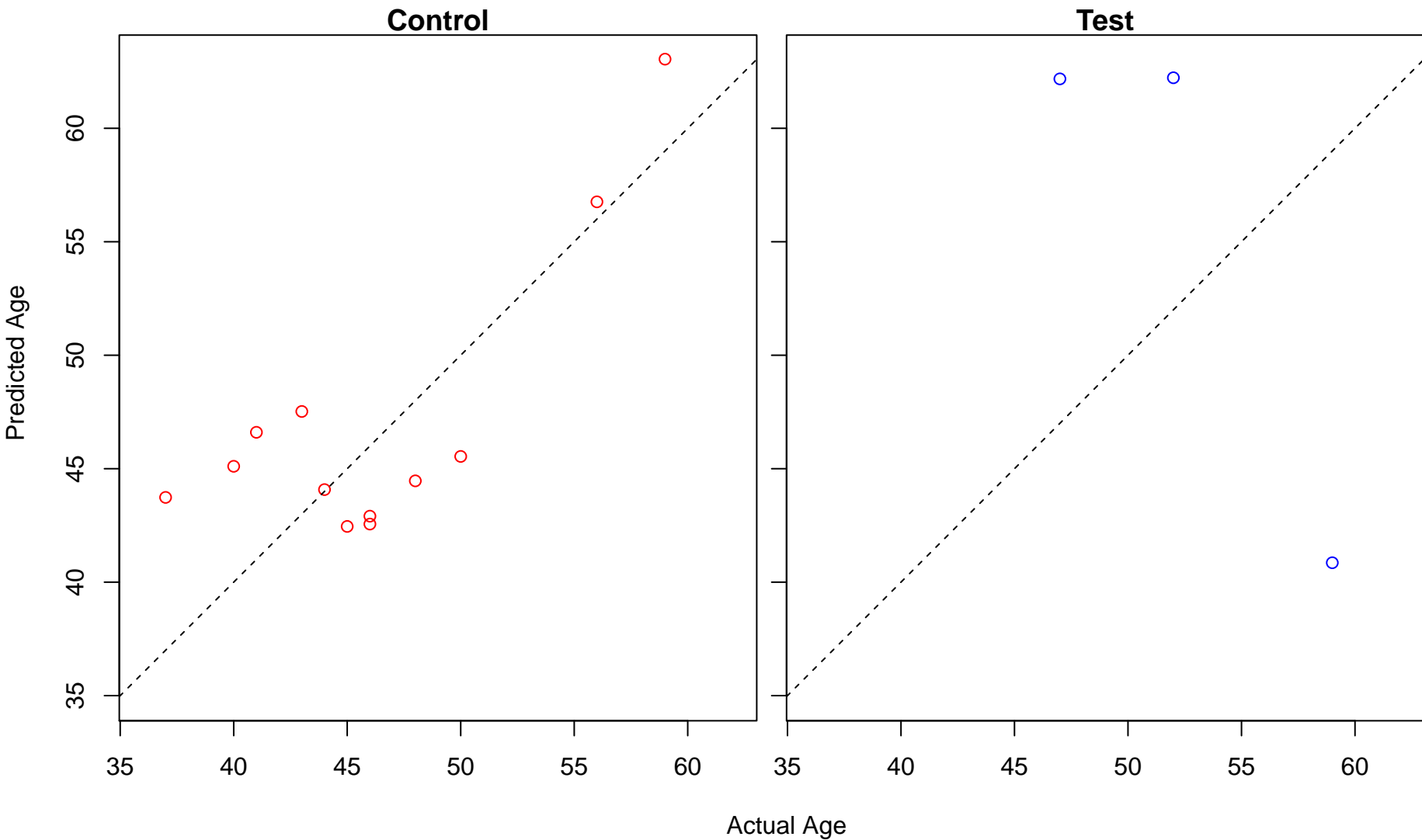
positive regulation of apoptotic cell clearance (Score: 14.002686)



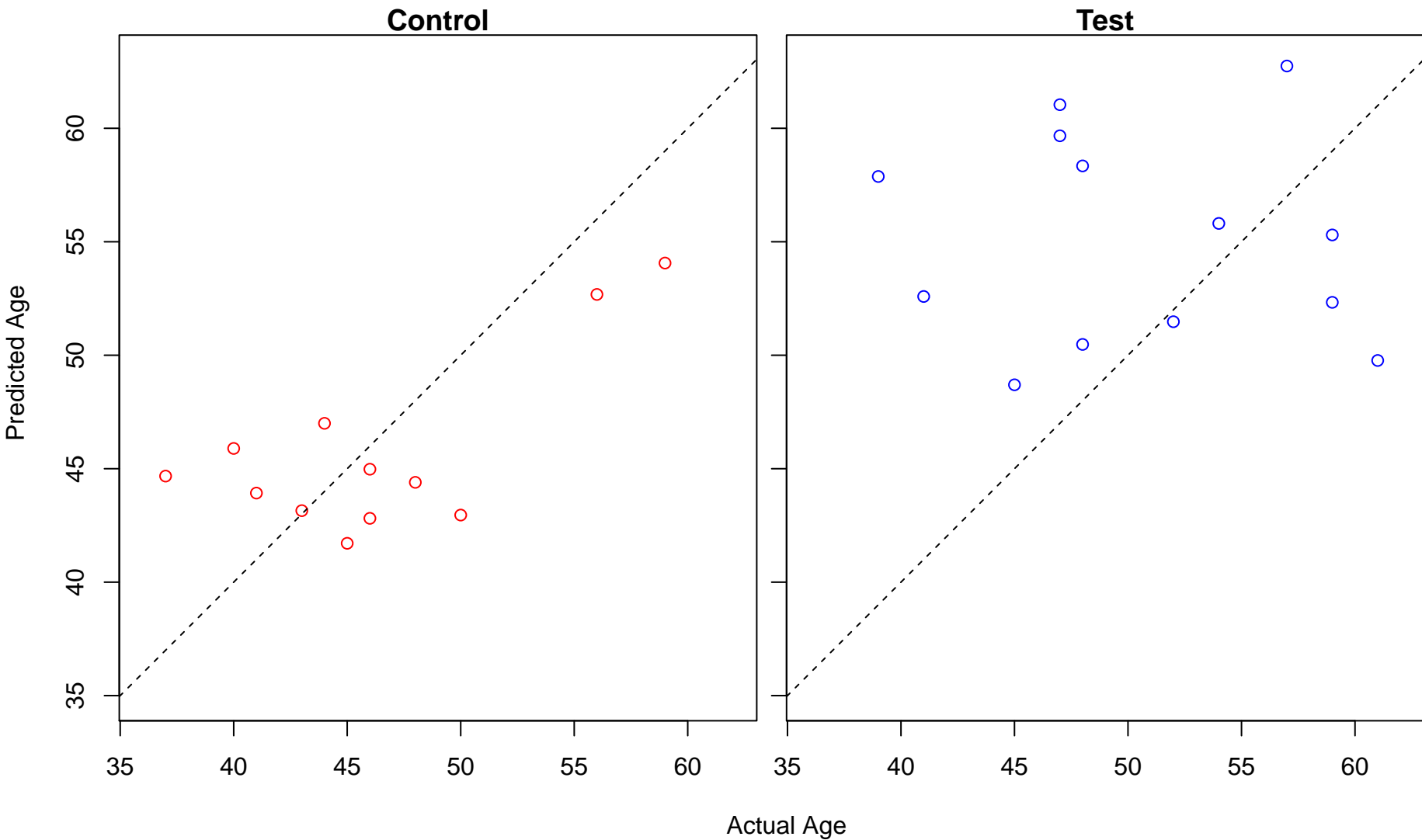
cellular response to acid chemical (Score: 13.993912)



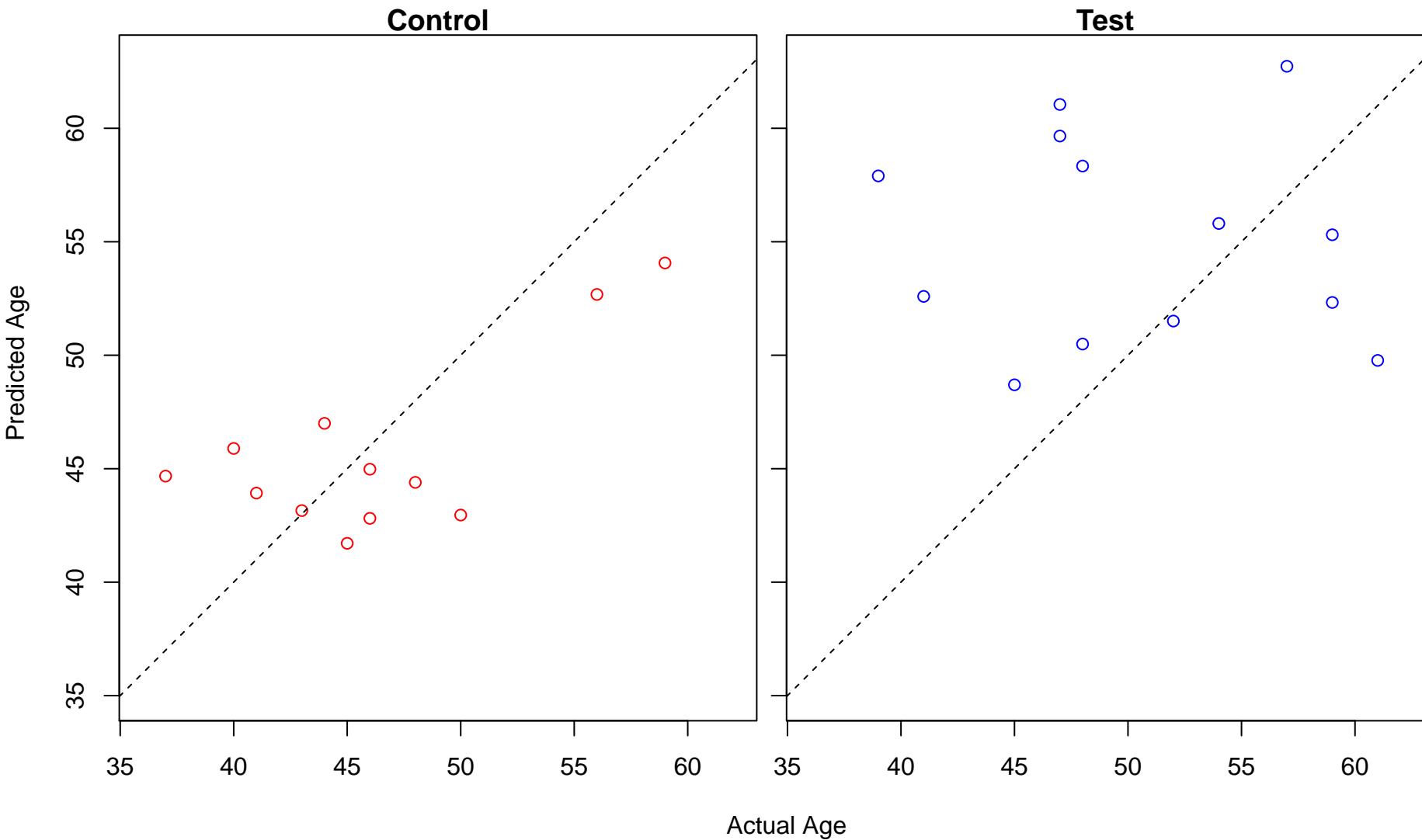
optic cup morphogenesis involved in camera-type eye development (Score: 13.990130)



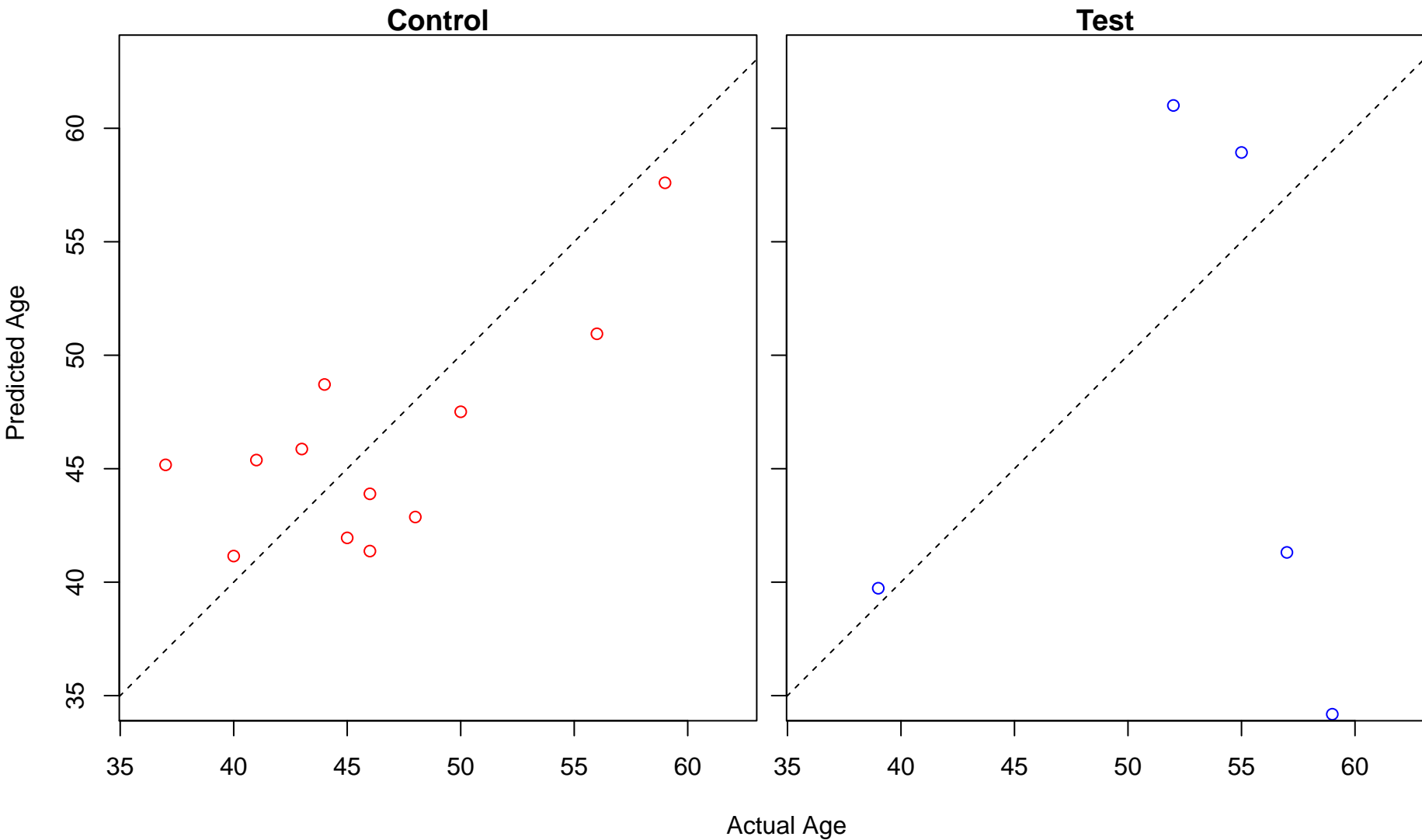
positive regulation of cardiac muscle contraction (Score: 13.958429)



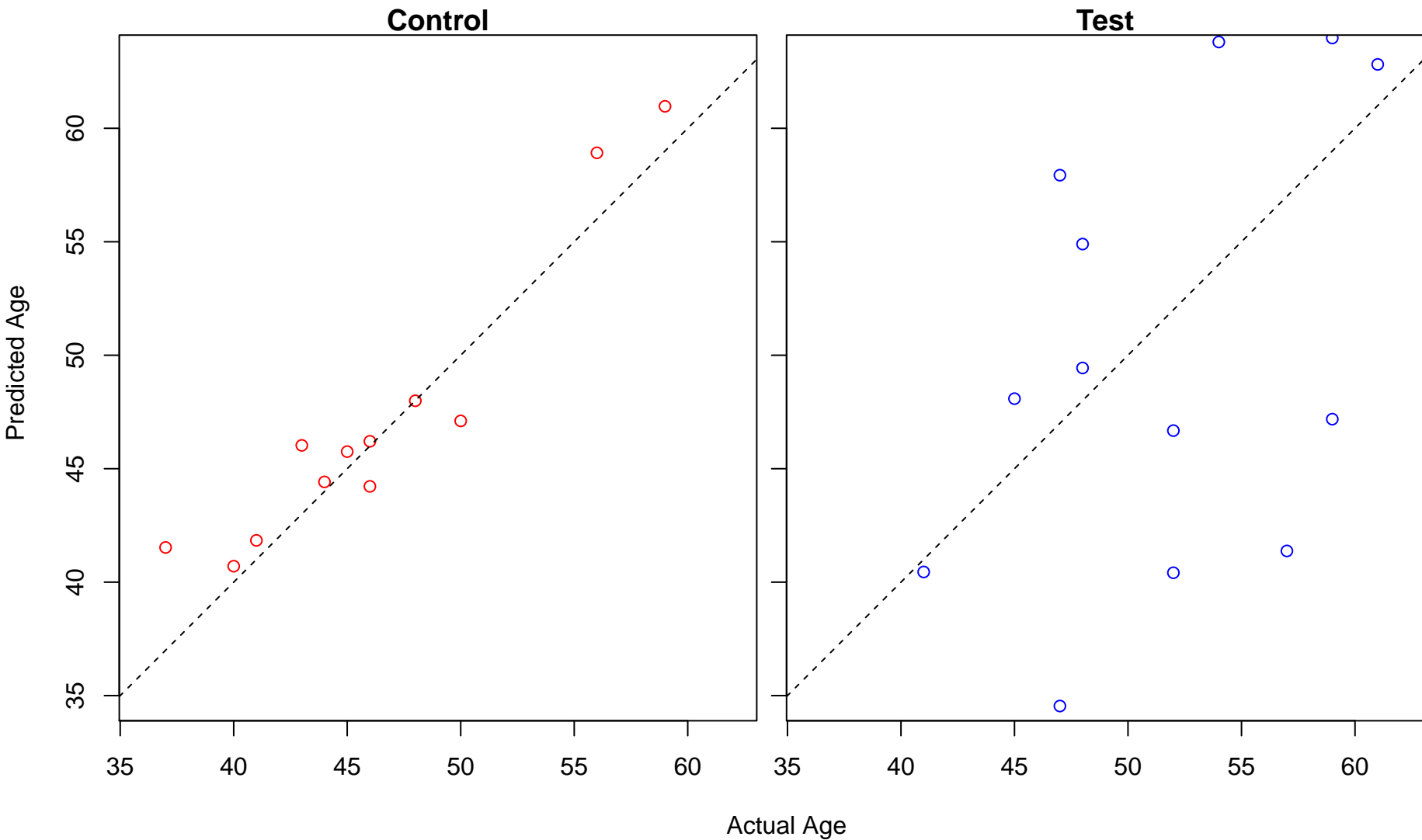
positive regulation of striated muscle contraction (Score: 13.953440)



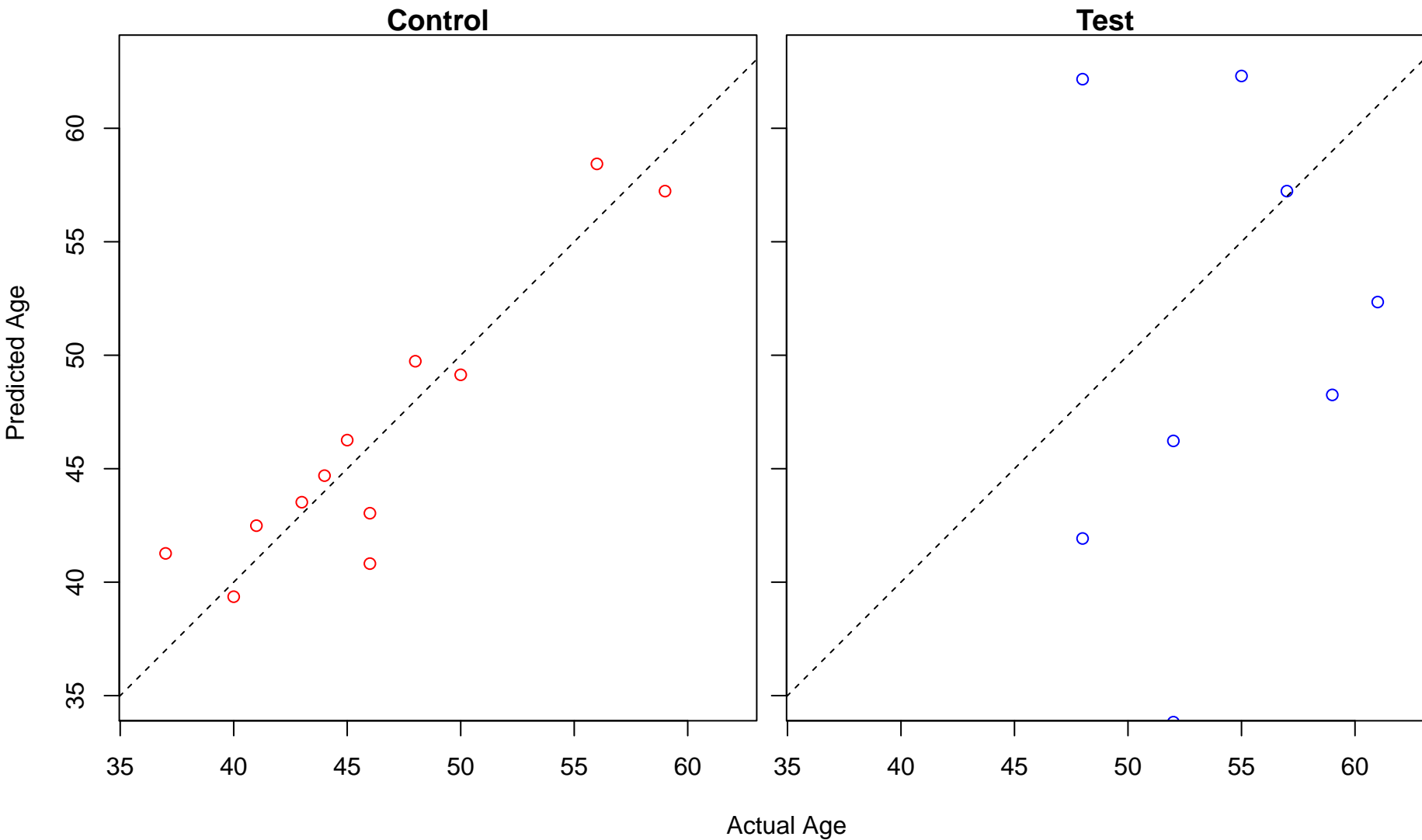
retina vasculature development in camera-type eye (Score: 13.952438)



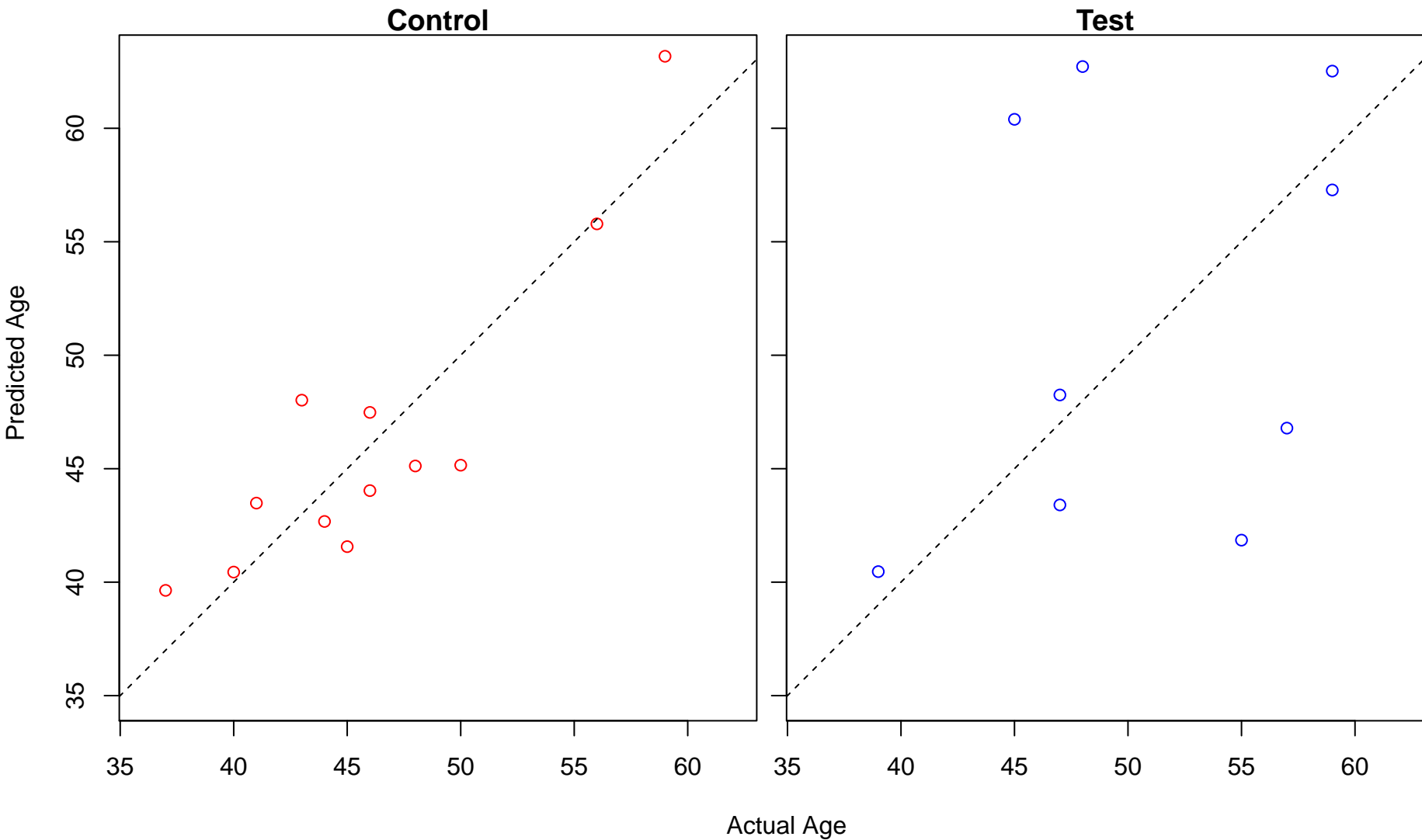
negative regulation of cell junction assembly (Score: 13.935768)



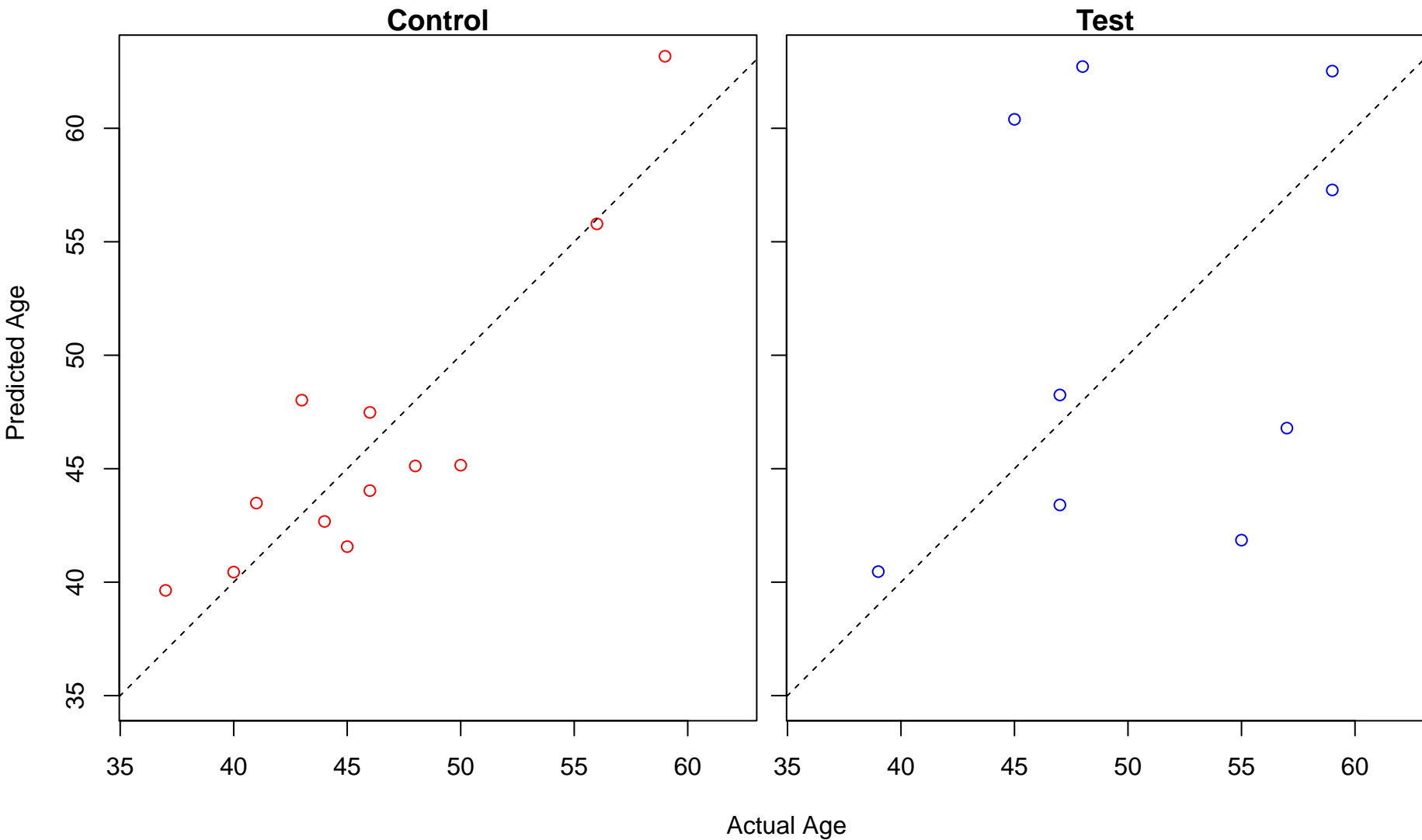
organic hydroxy compound biosynthetic process (Score: 13.932442)



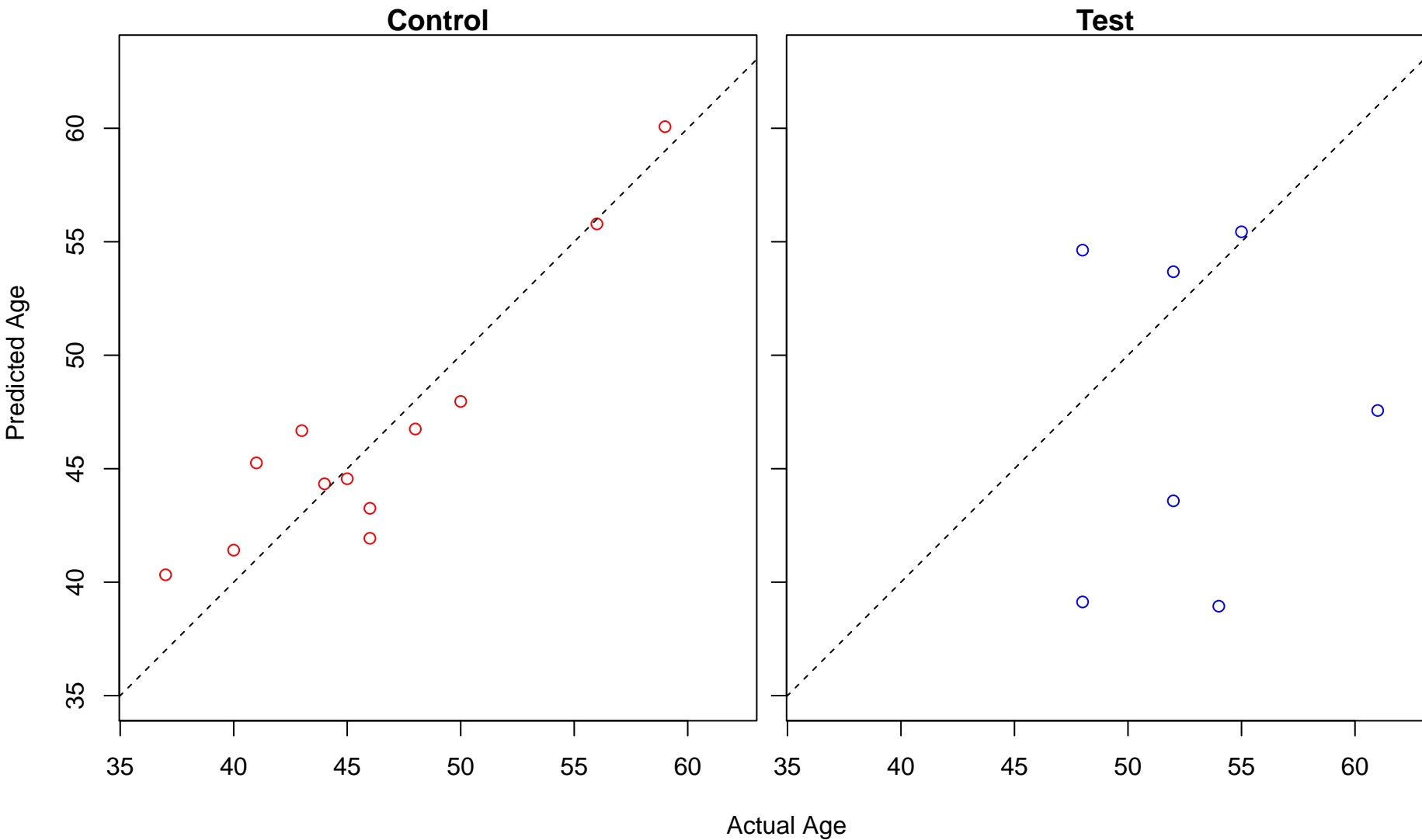
negative regulation of stress-activated MAPK cascade (Score: 13.929681)



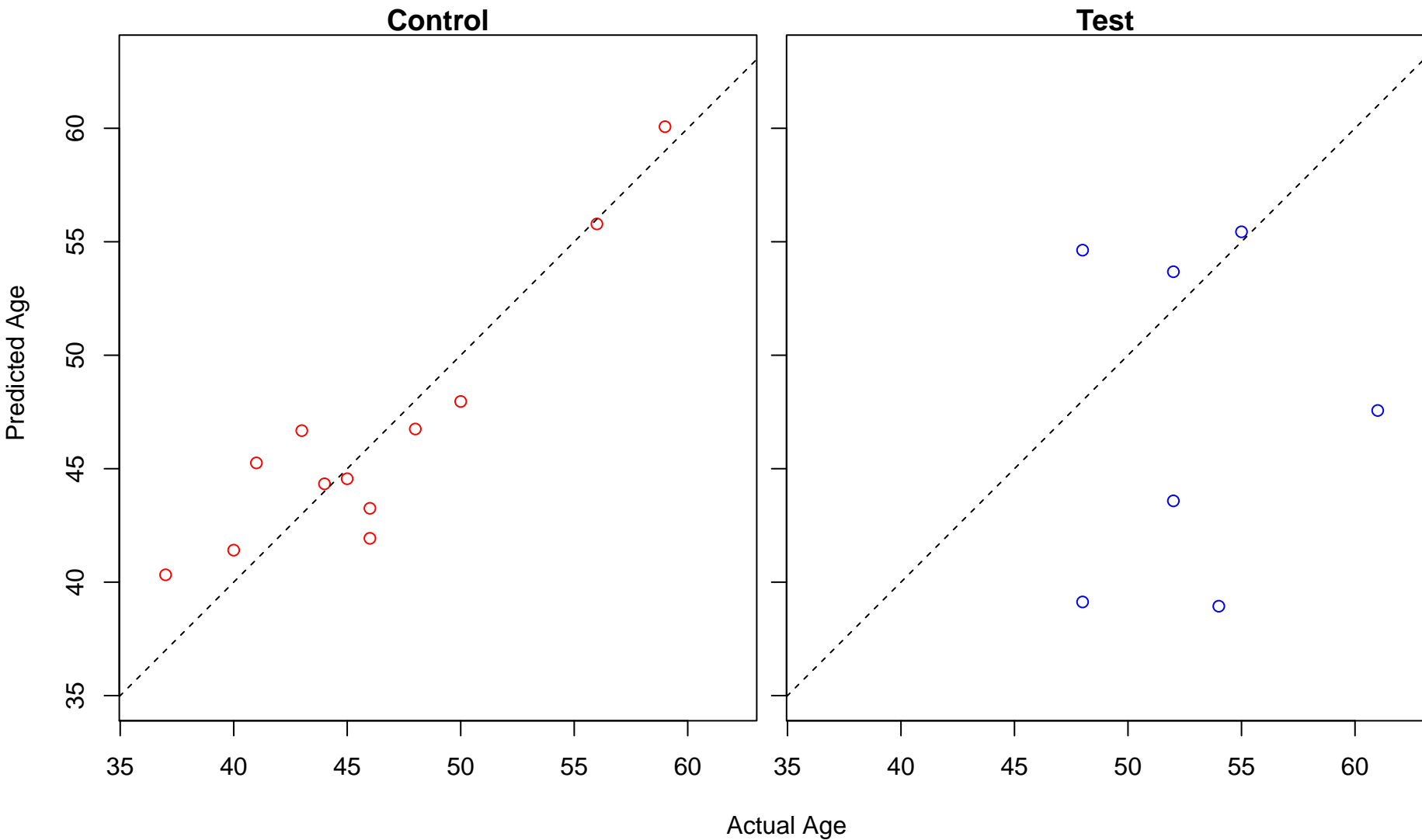
negative regulation of stress-activated protein kinase signaling cascade (Score: 13.929681)



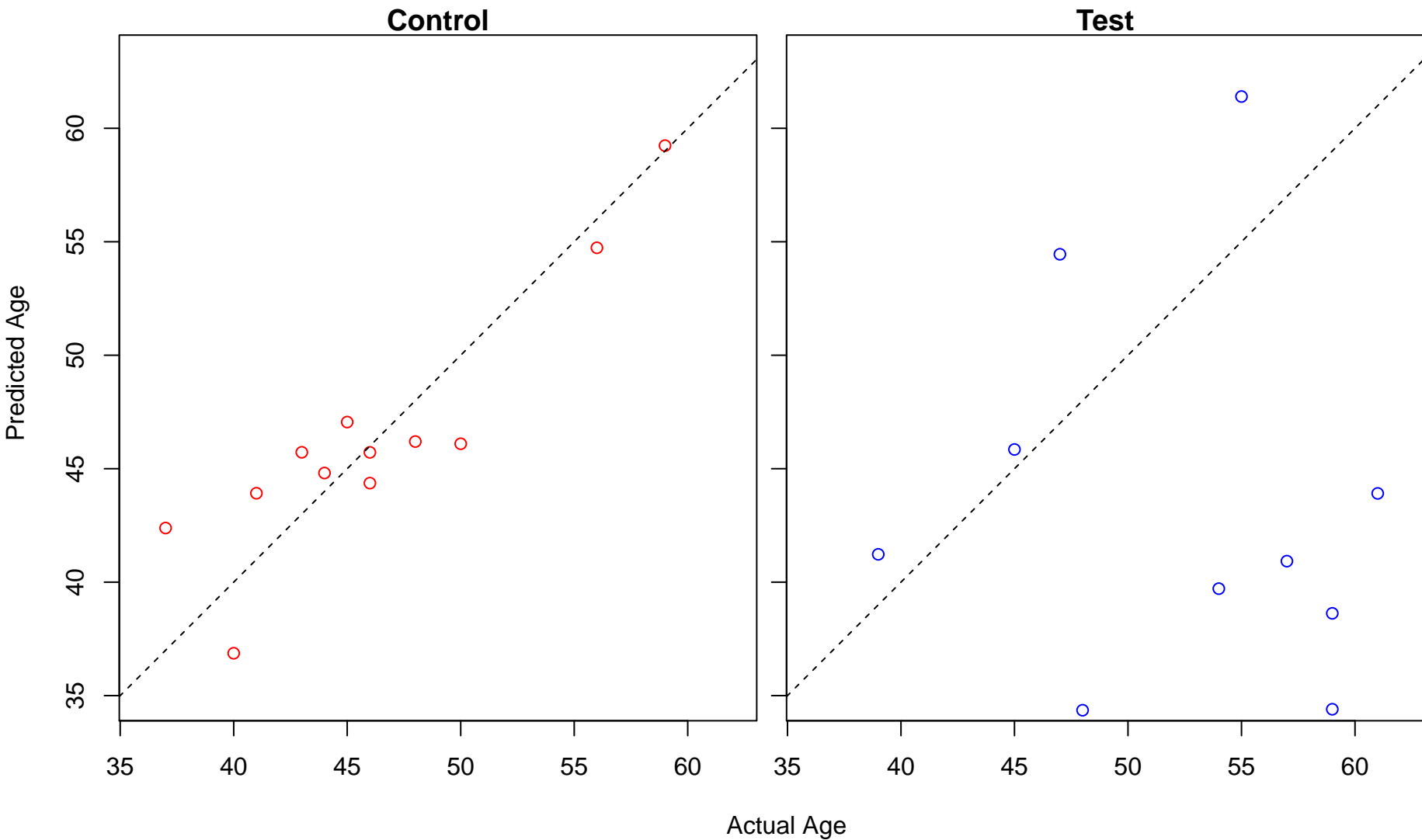
reproductive structure development (Score: 13.905387)



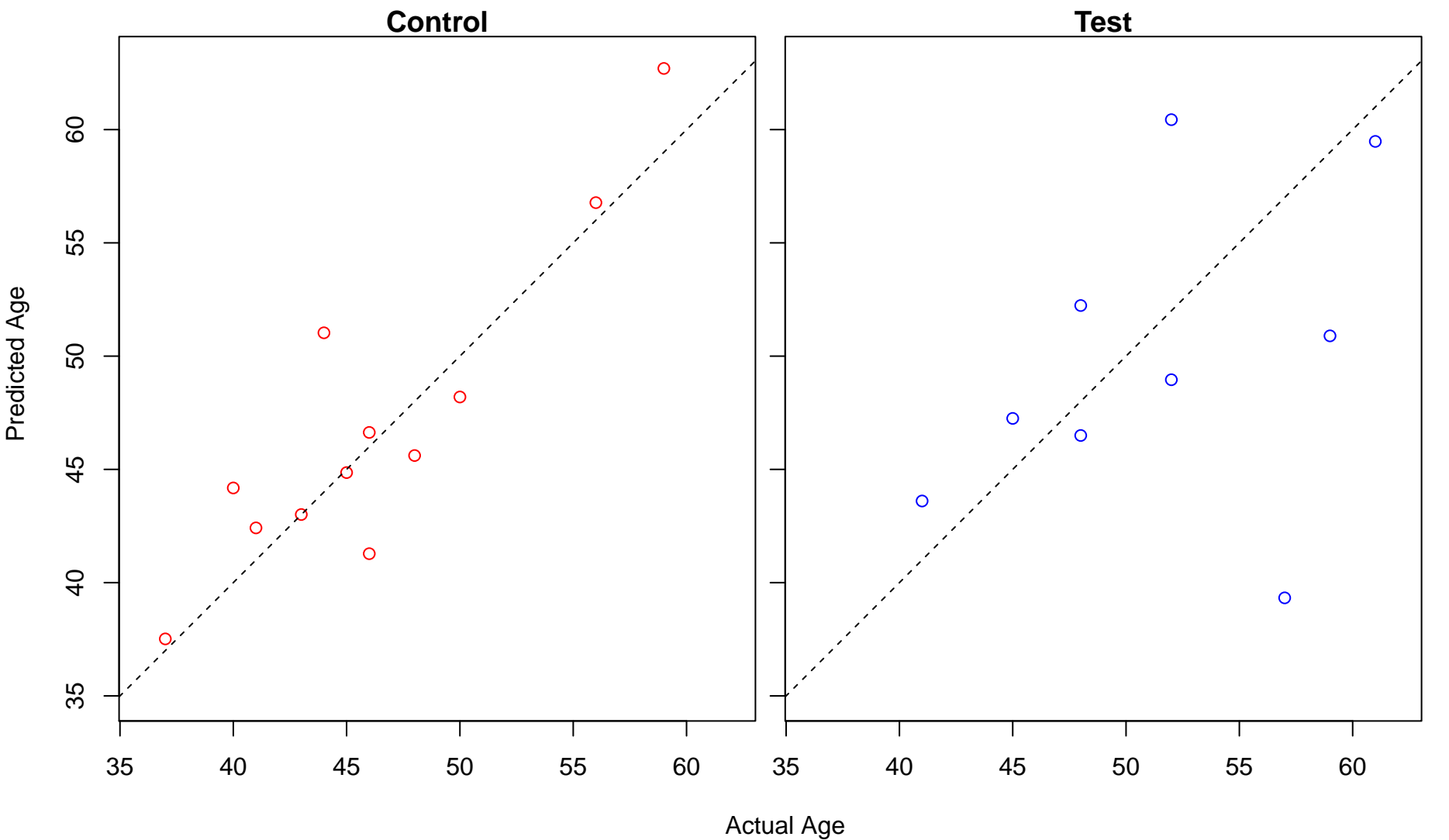
reproductive system development (Score: 13.905387)



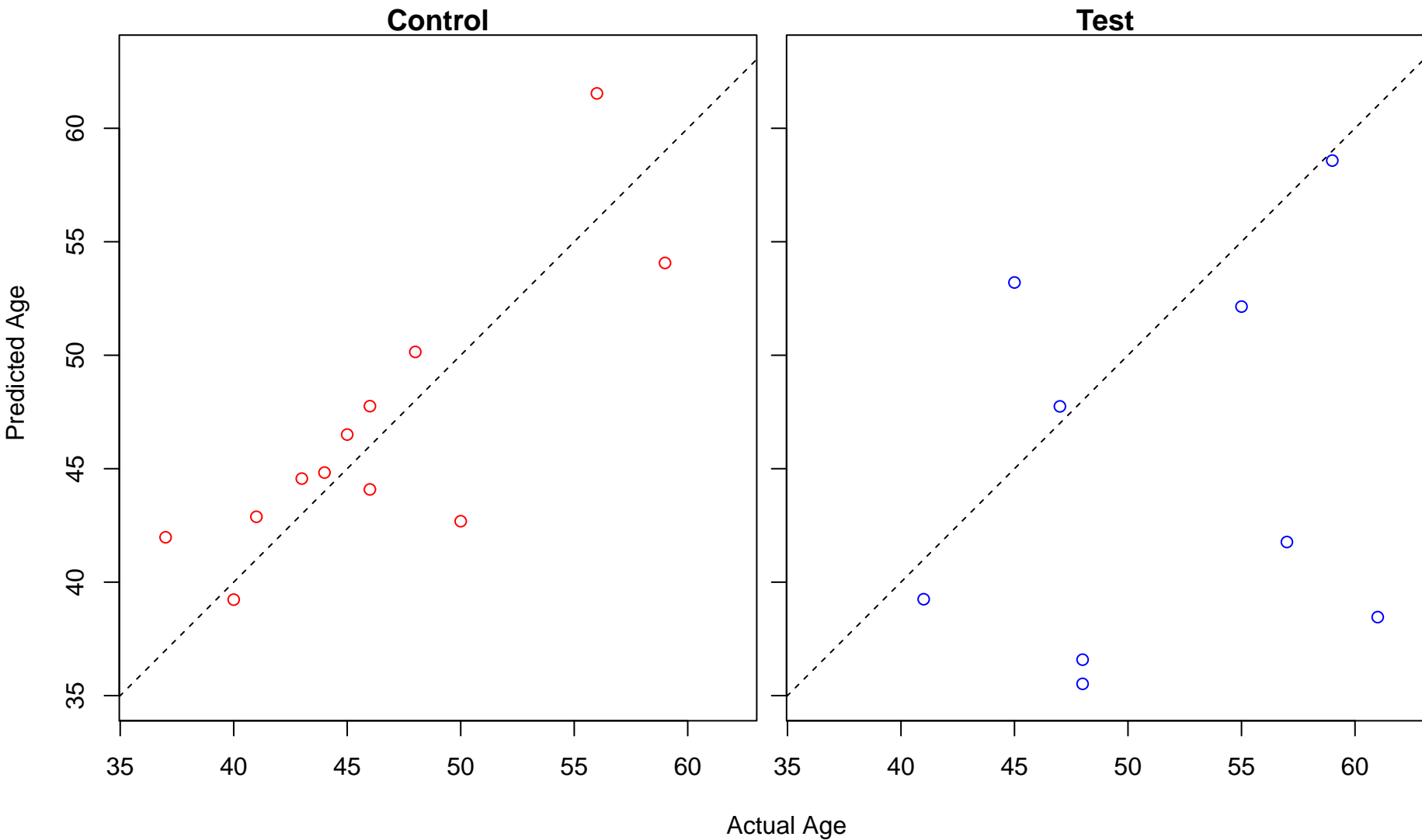
forebrain generation of neurons (Score: 13.886303)



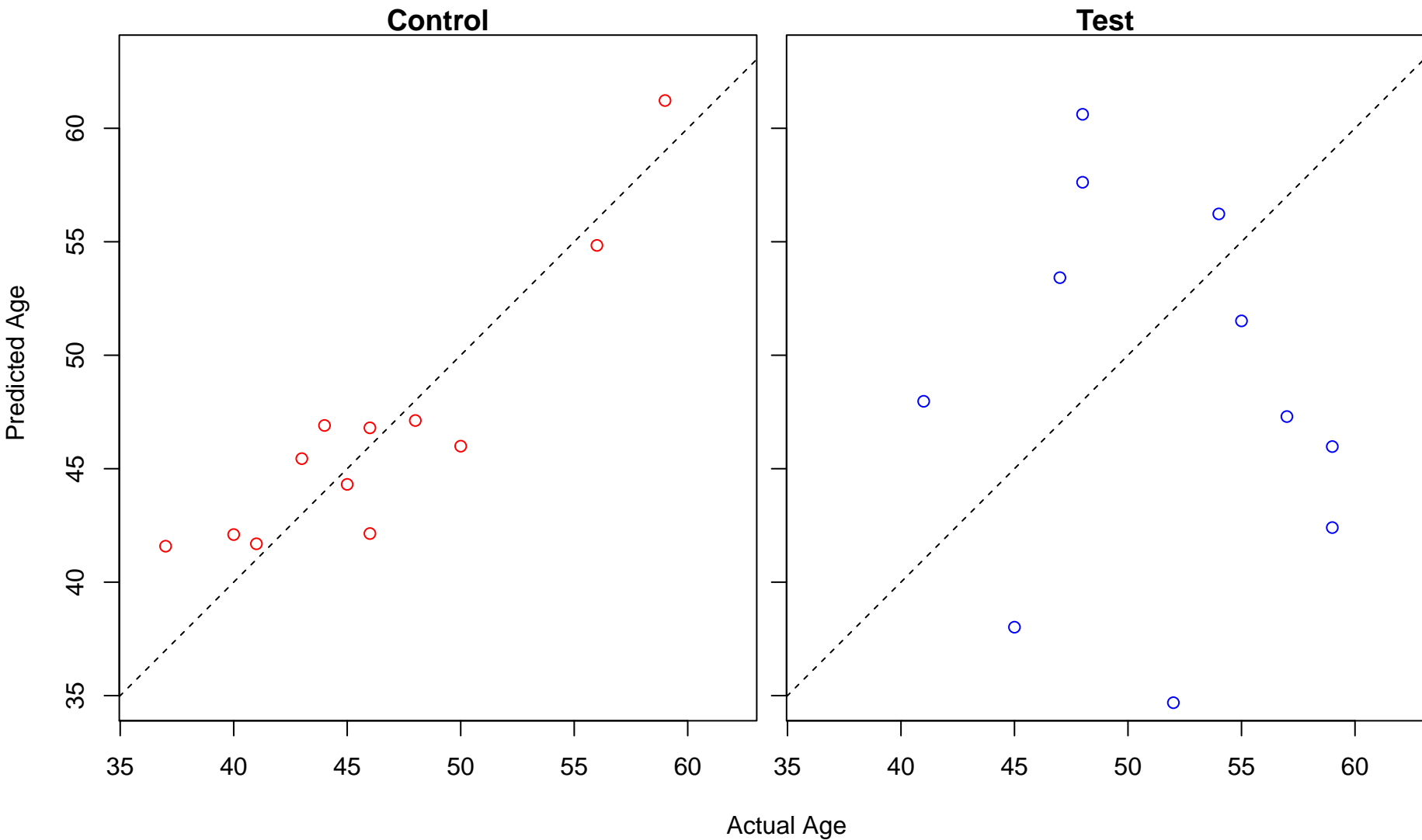
of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell cycle



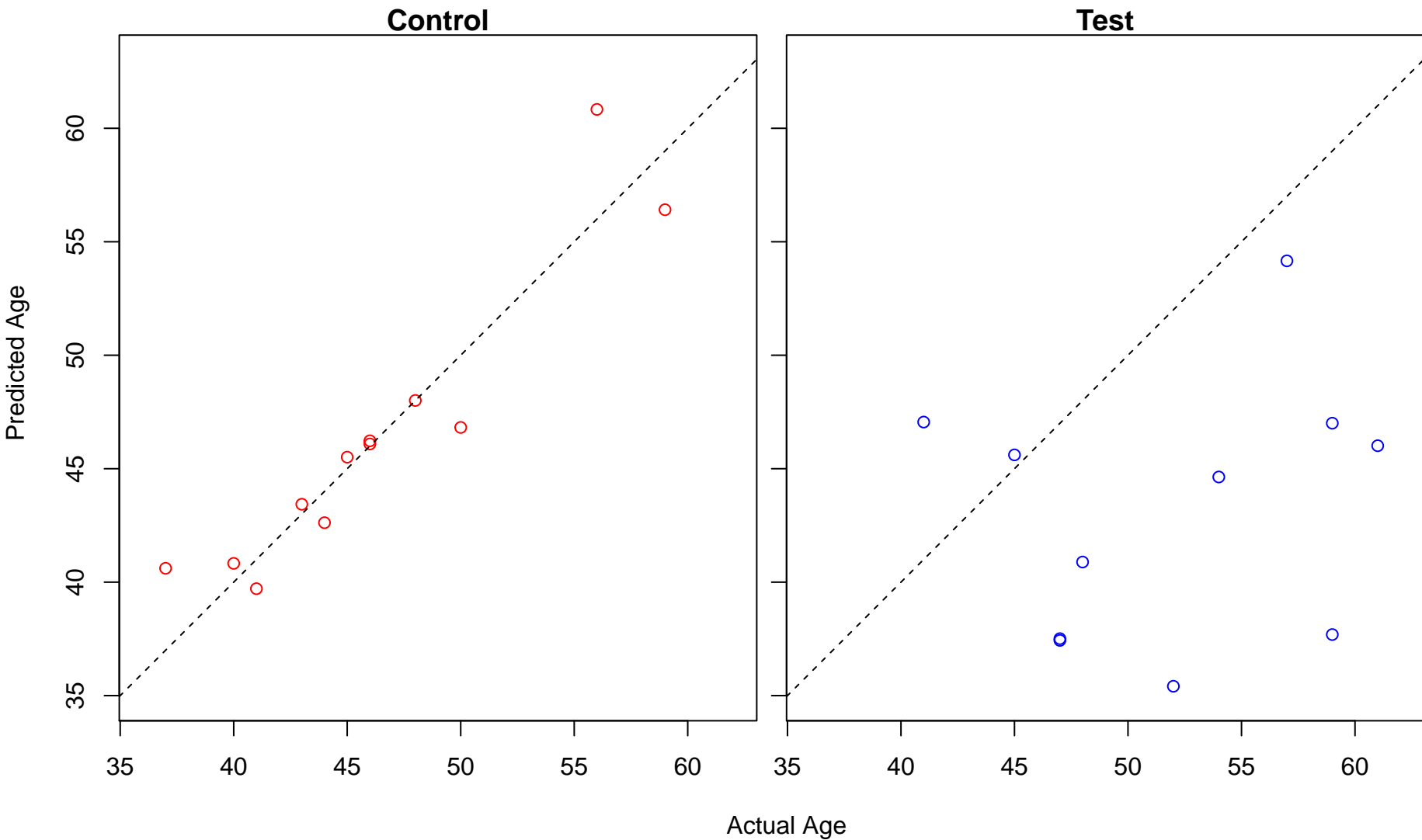
female pregnancy (Score: 13.788811)



single-organism behavior (Score: 13.766740)

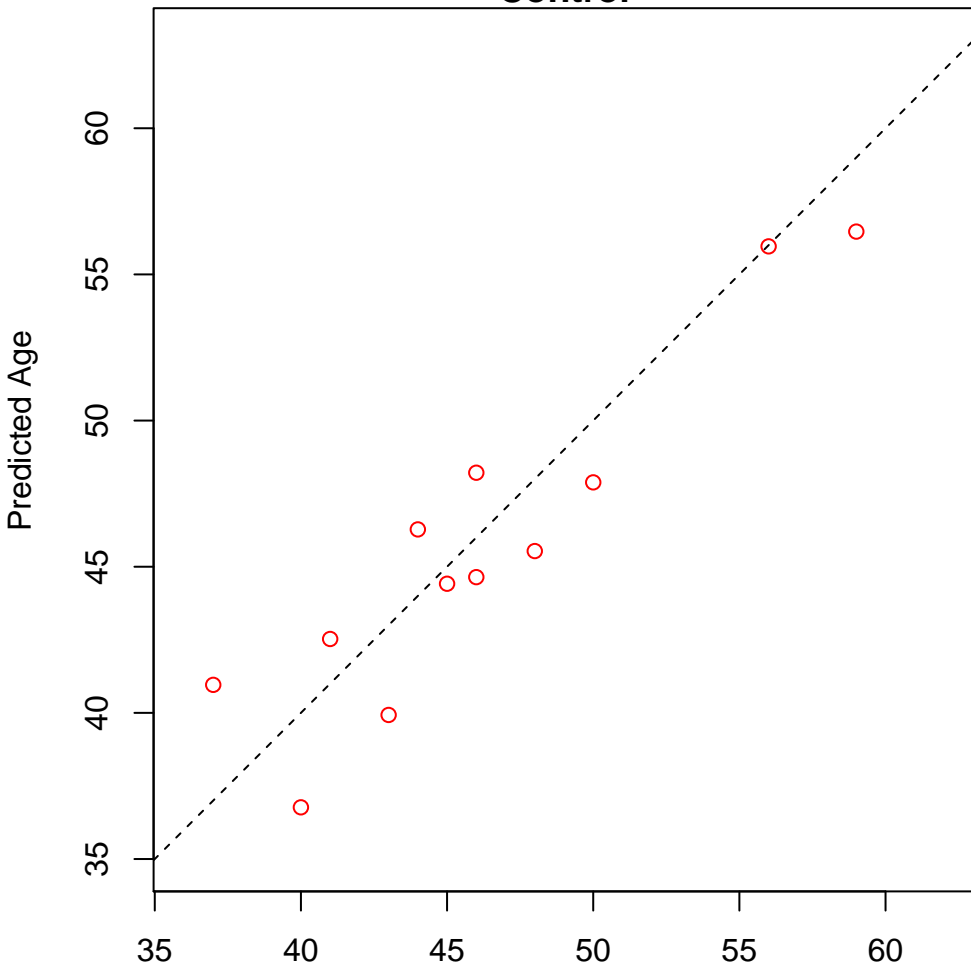


regulation of protein maturation (Score: 13.740523)

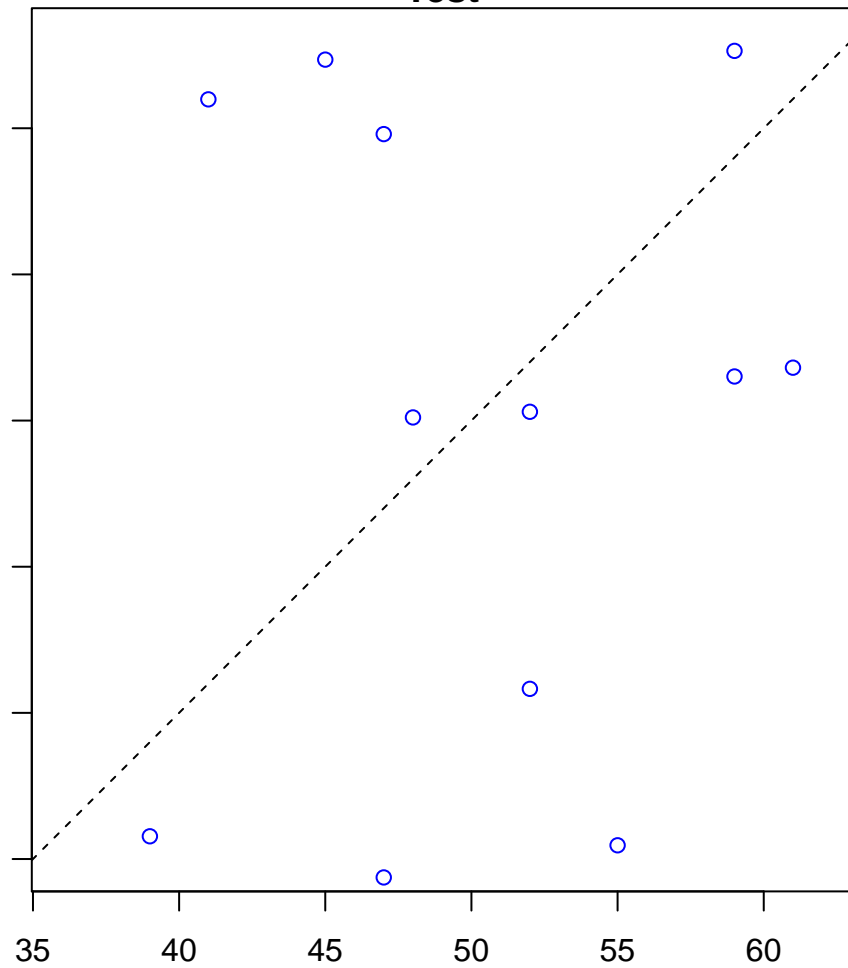


response to muramyl dipeptide (Score: 13.724948)

Control

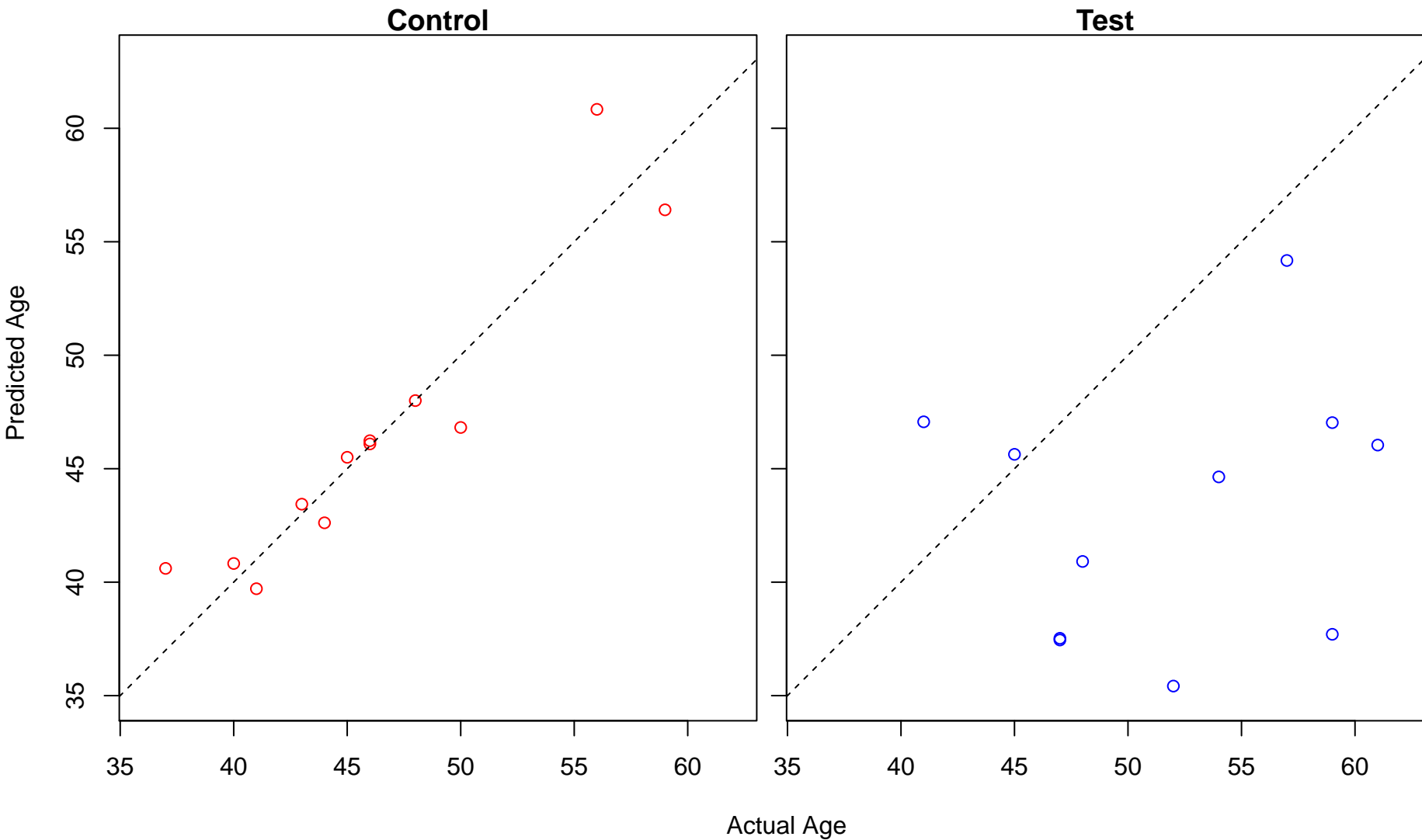


Test

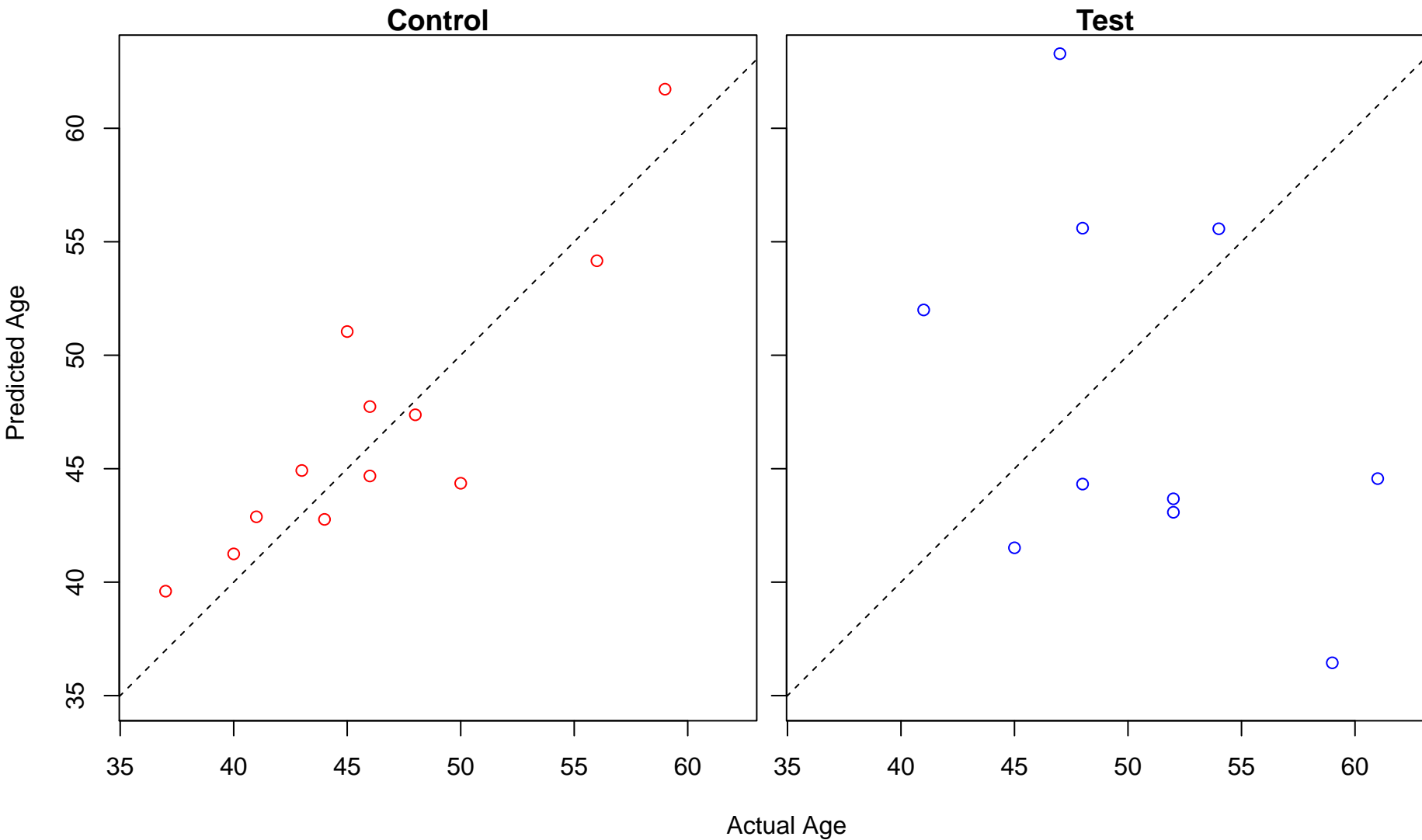


Actual Age

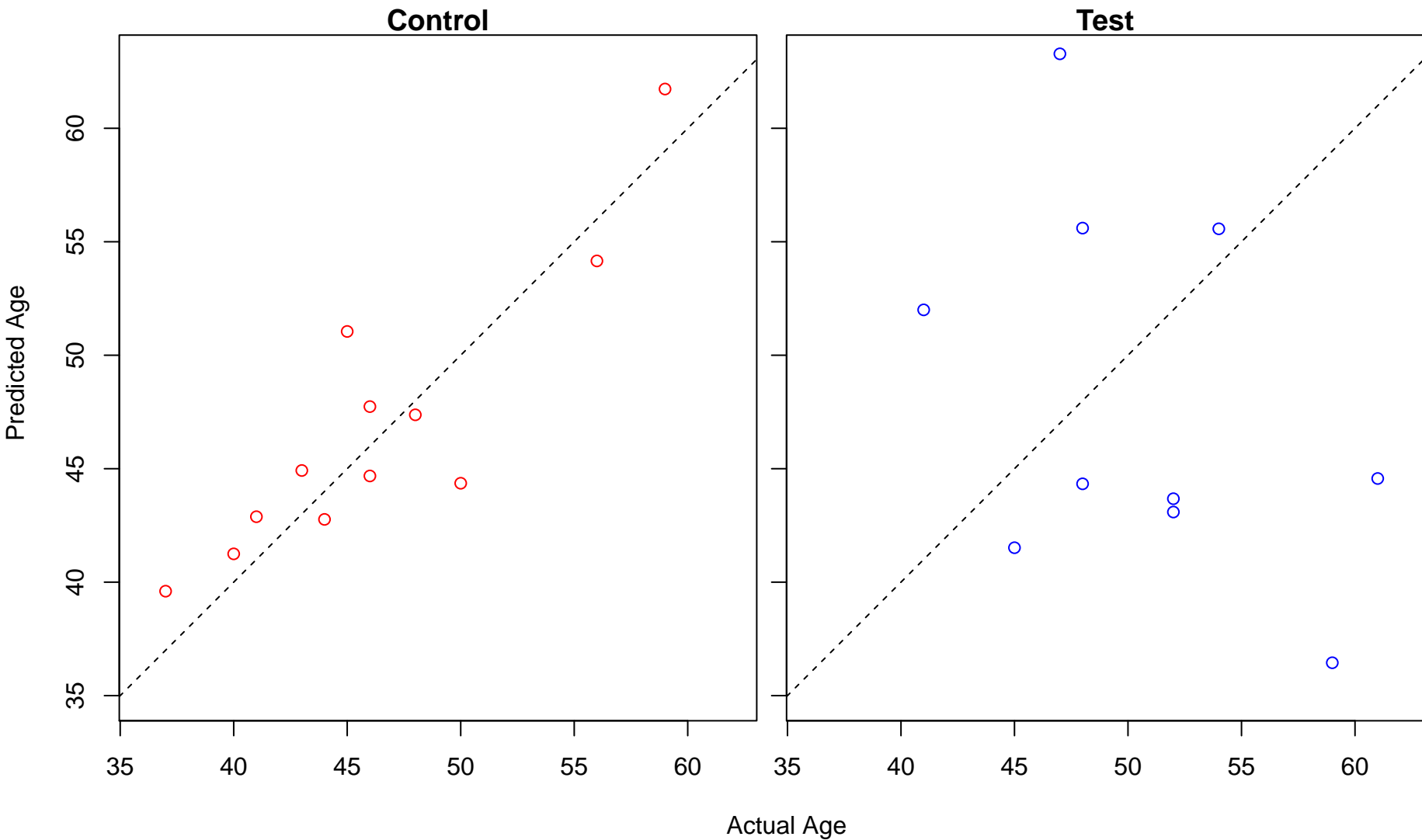
regulation of protein processing (Score: 13.692664)



positive regulation of lymphocyte proliferation (Score: 13.688644)

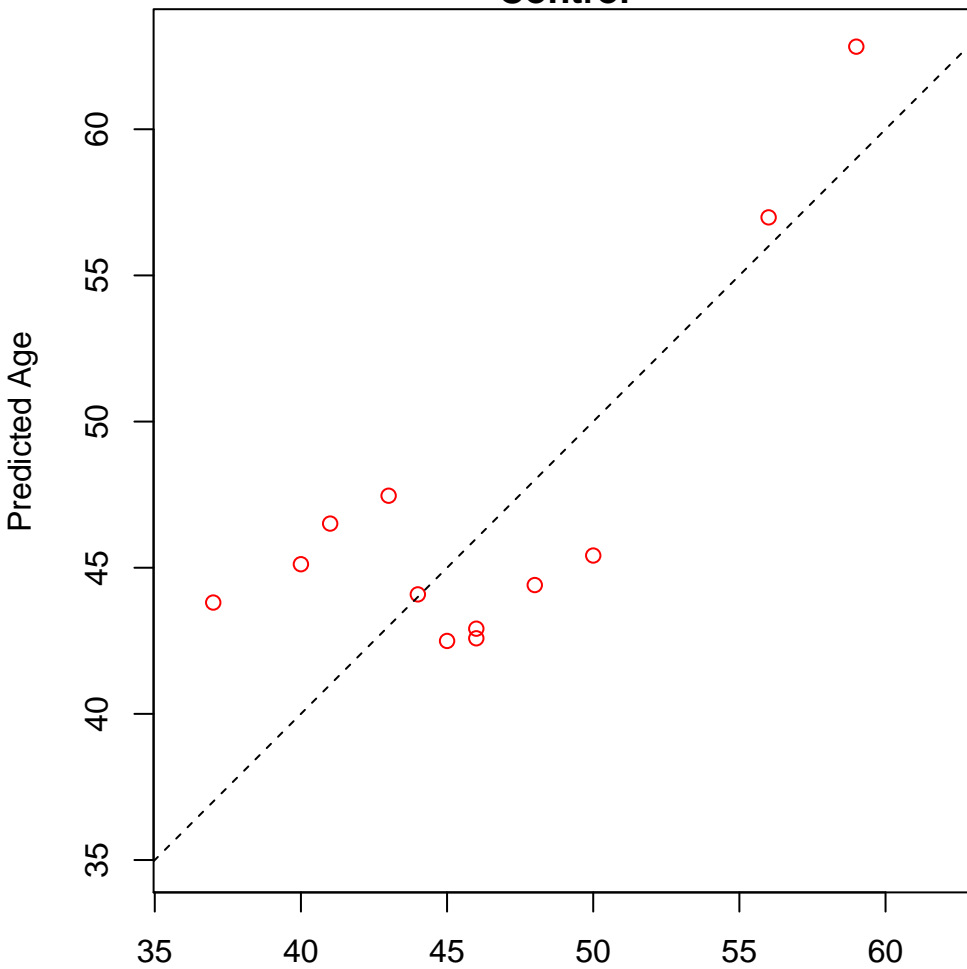


positive regulation of mononuclear cell proliferation (Score: 13.669295)

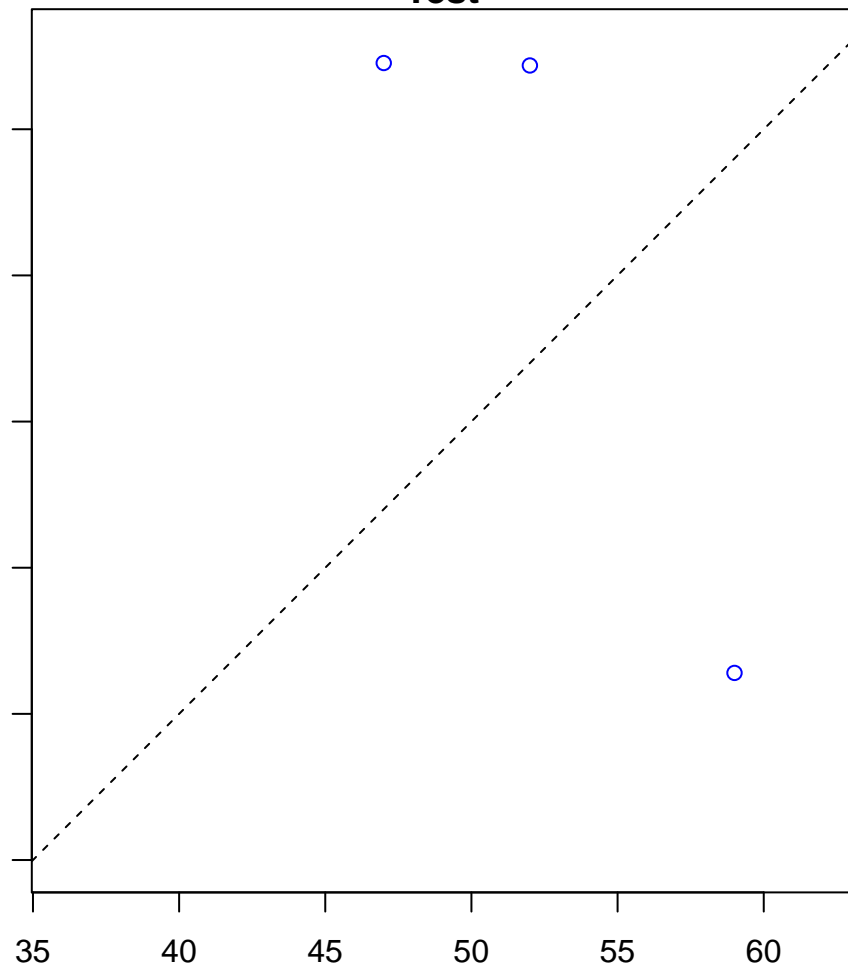


embryonic camera-type eye formation (Score: 13.642513)

Control

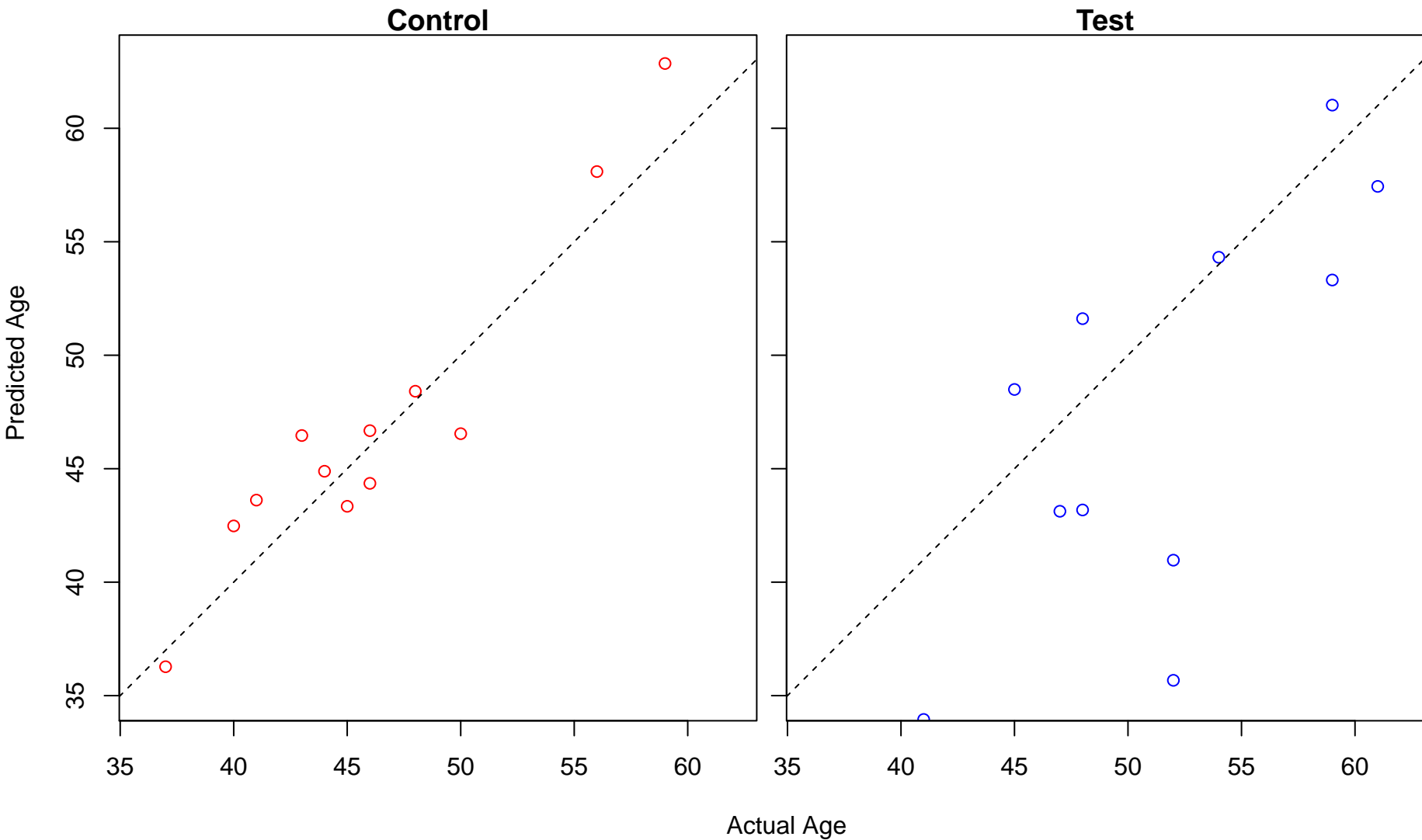


Test

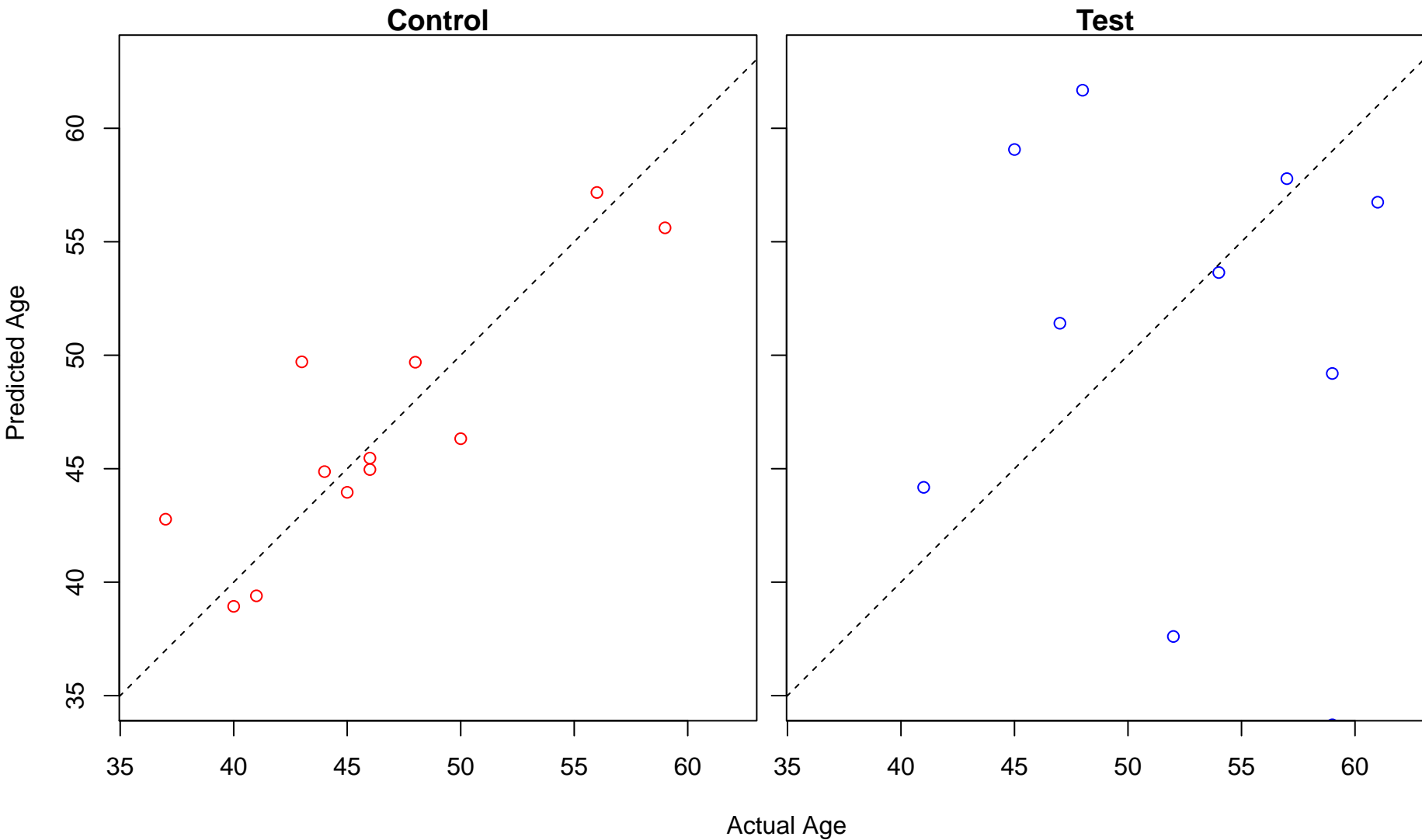


Actual Age

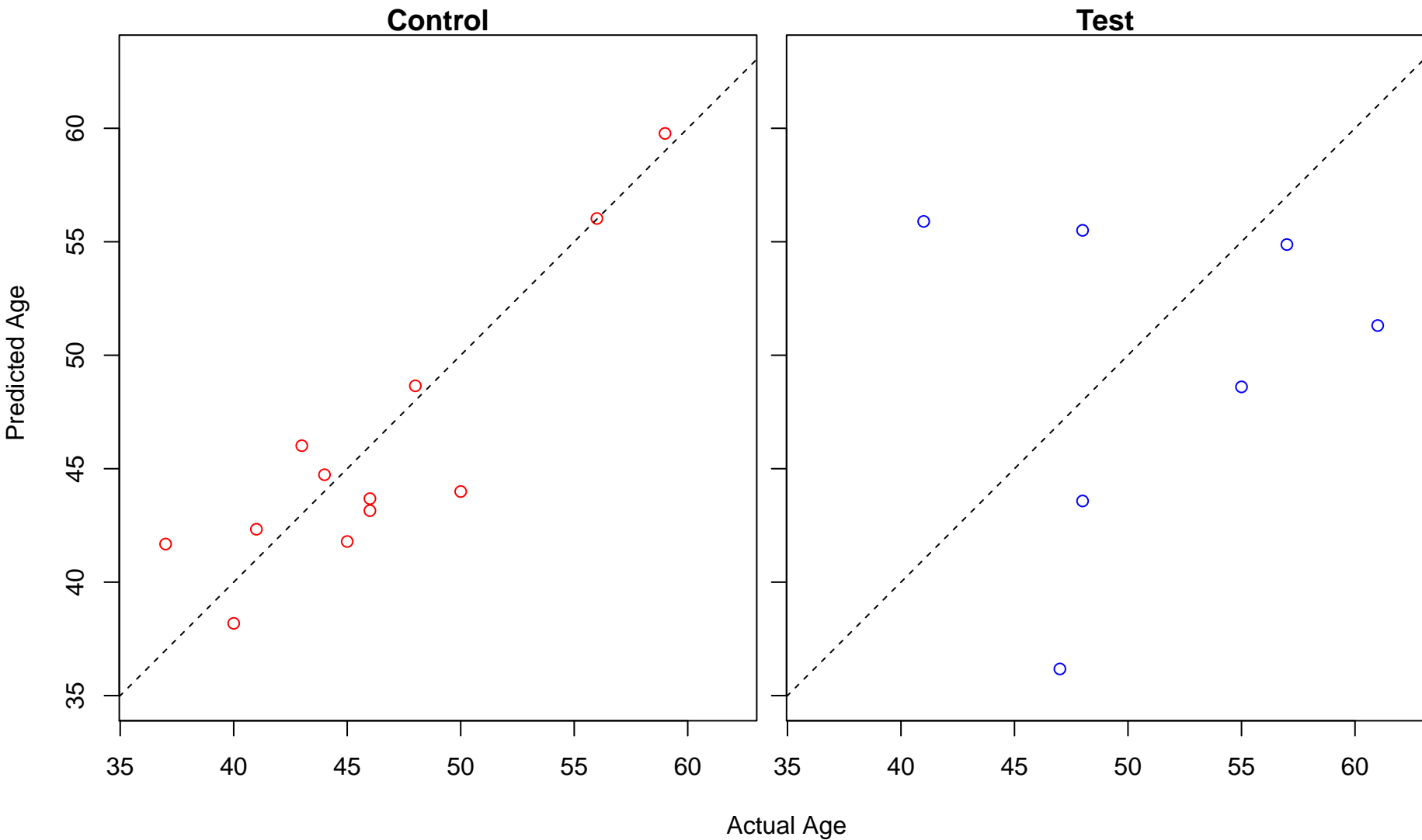
negative regulation of focal adhesion assembly (Score: 13.594967)



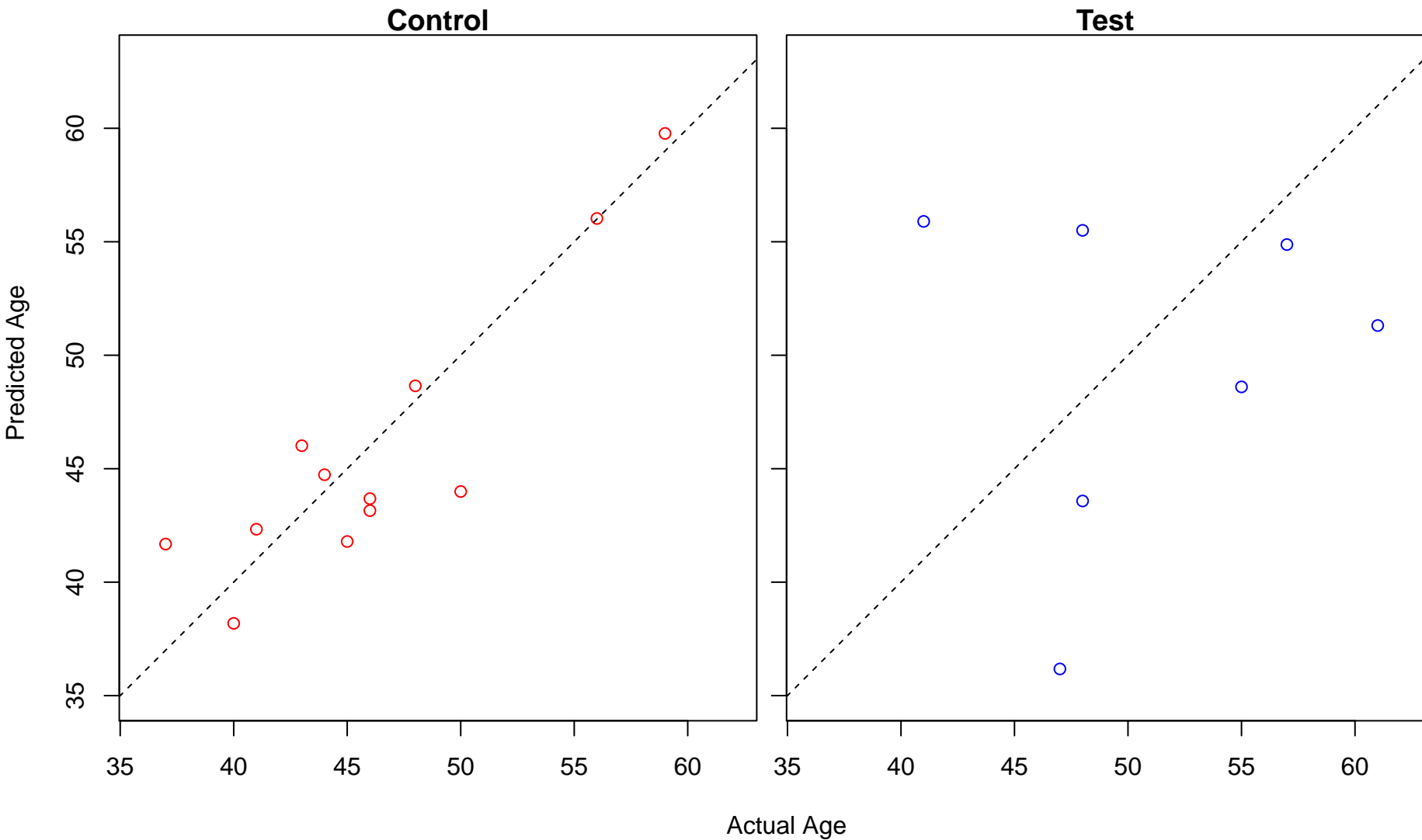
pteridine-containing compound metabolic process (Score: 13.548761)



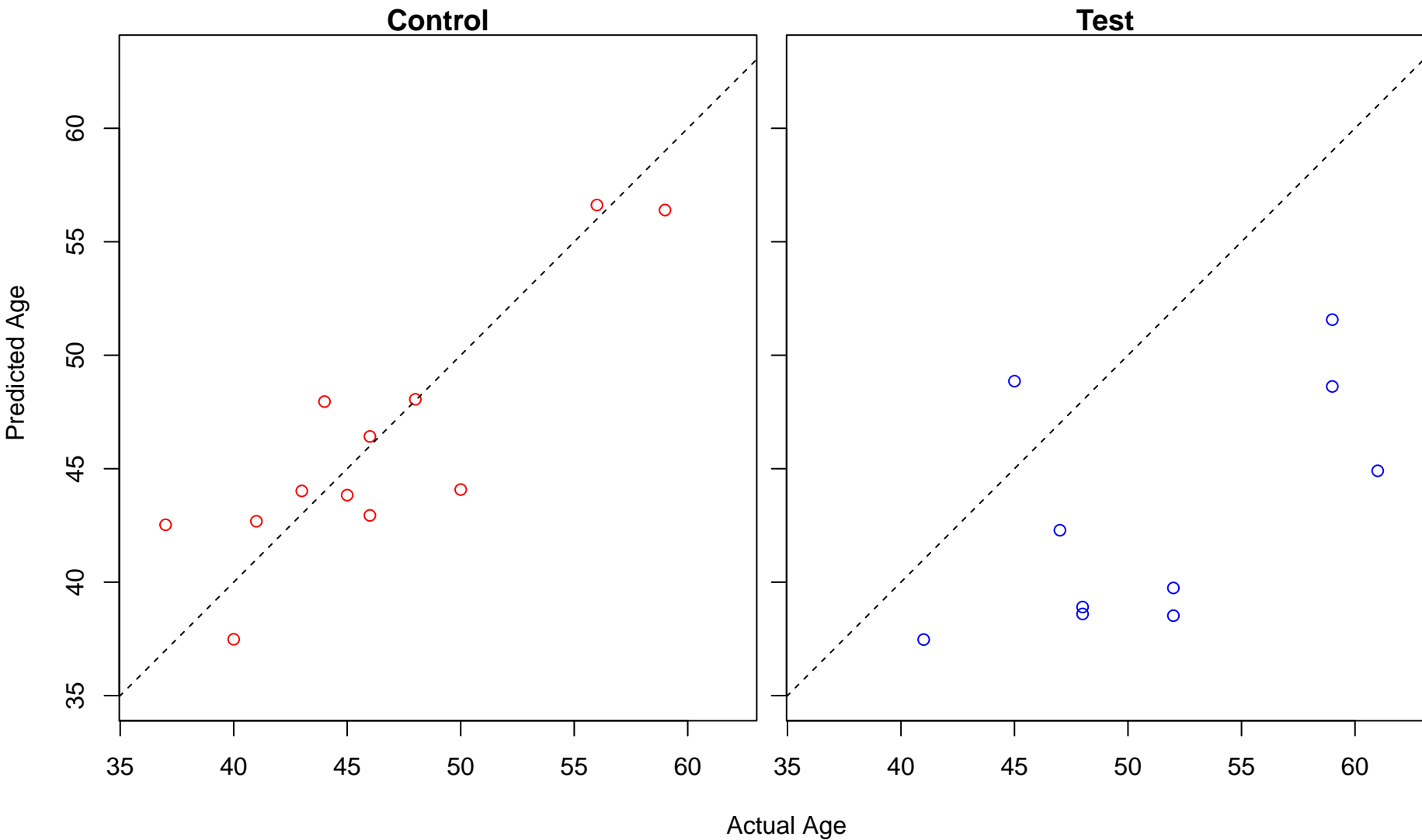
reproduction (Score: 13.535100)



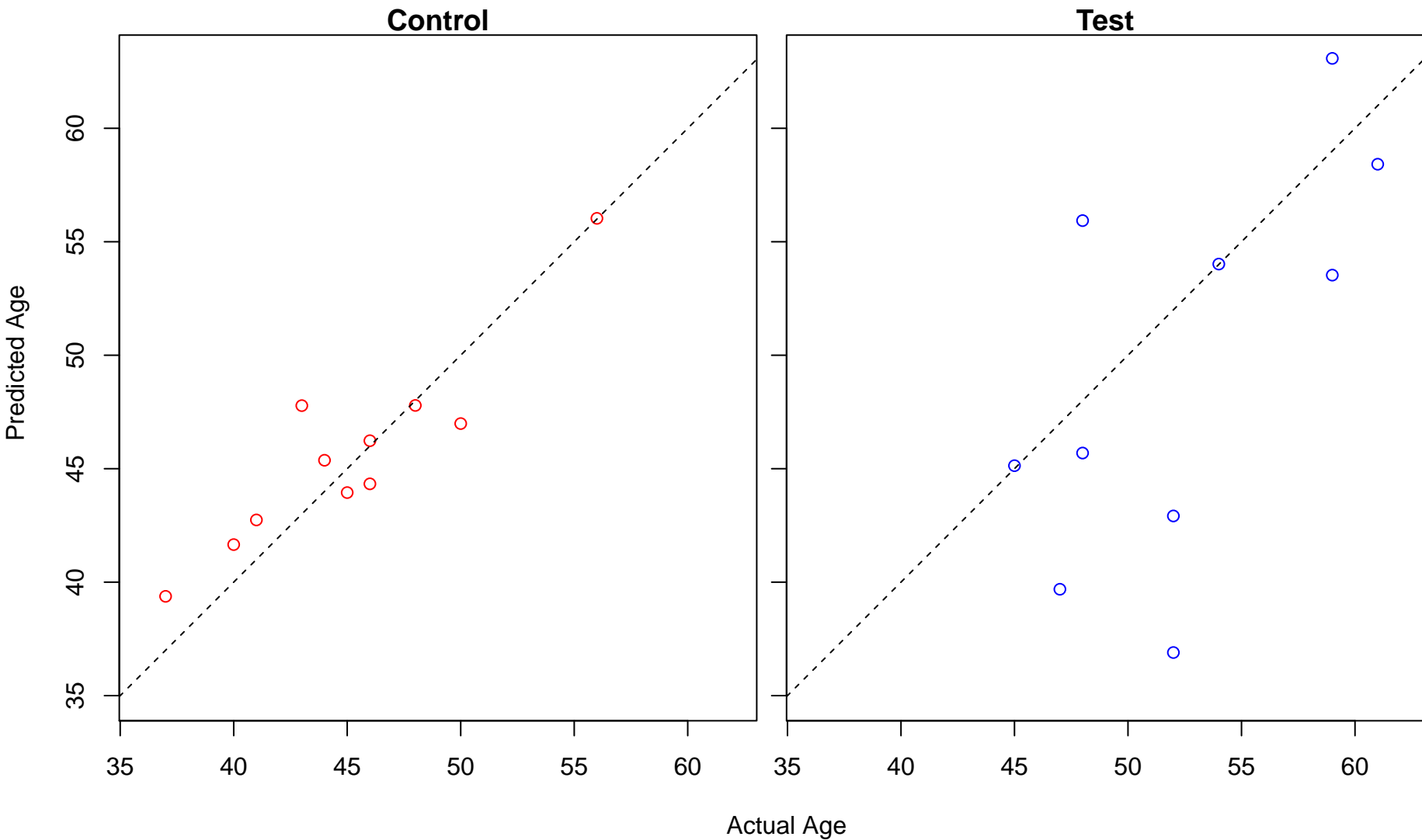
reproductive process (Score: 13.535033)



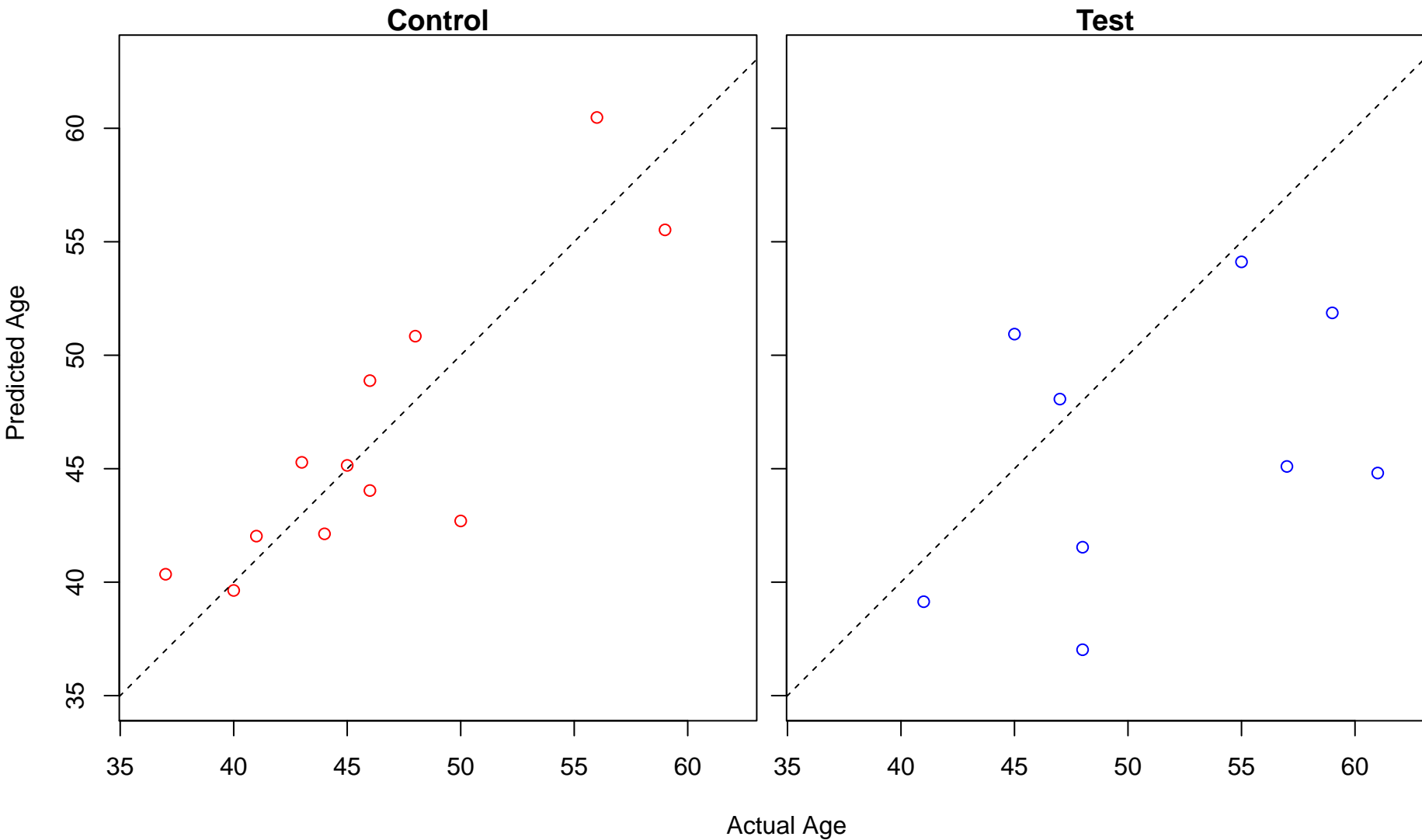
regulation of symbiosis, encompassing mutualism through parasitism (Score: 13.521212)



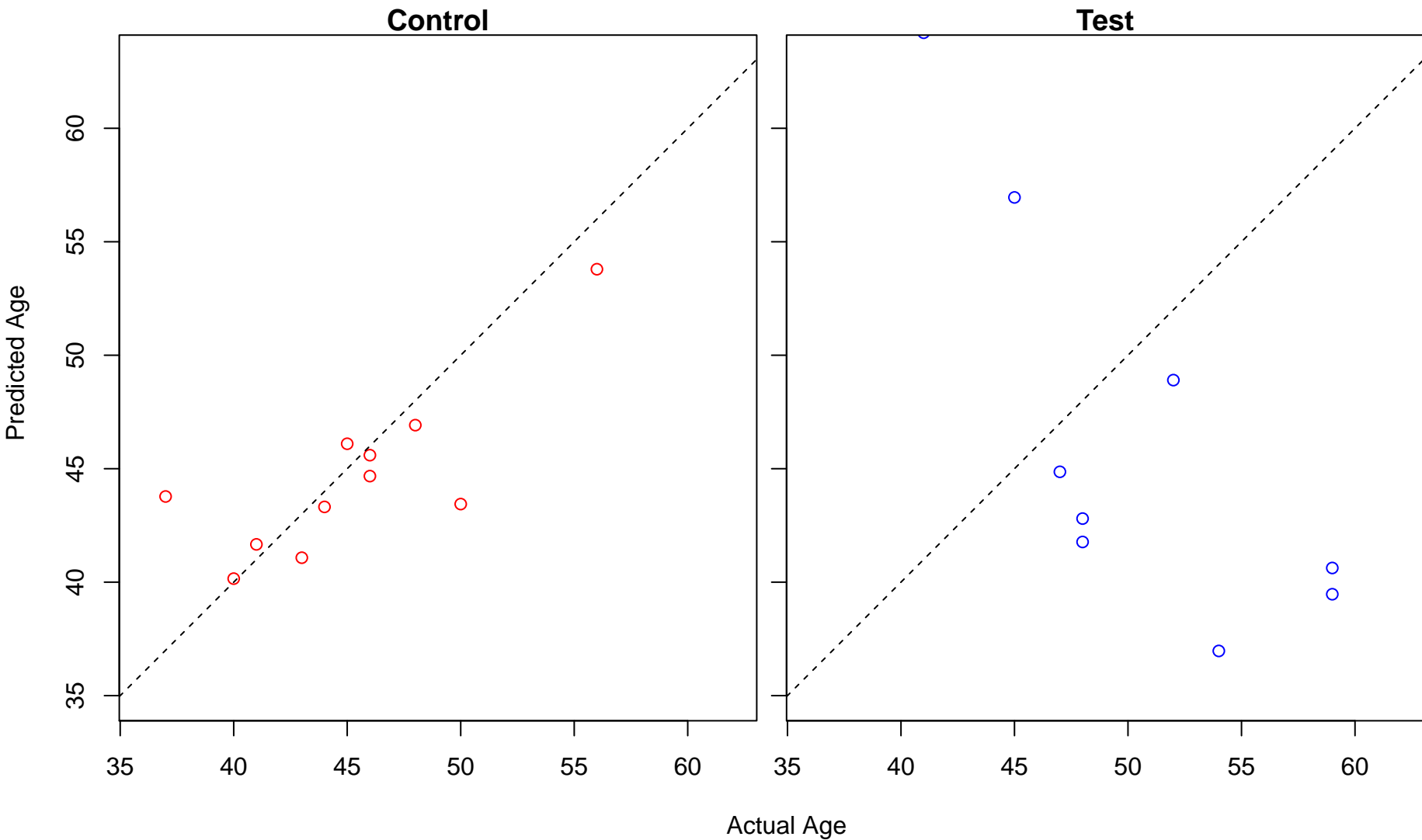
negative regulation of cell-matrix adhesion (Score: 13.485651)



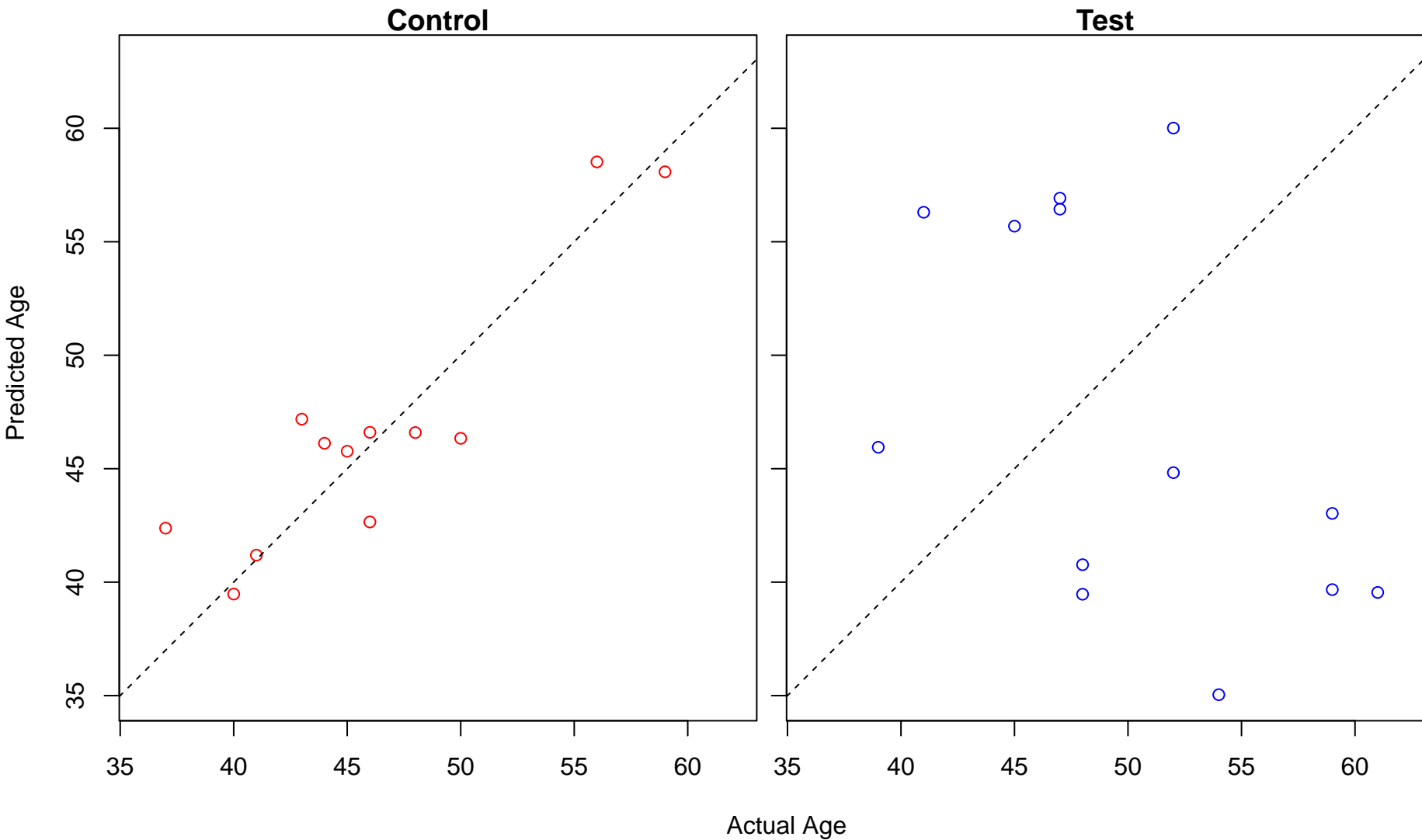
multi-multicellular organism process (Score: 13.466836)



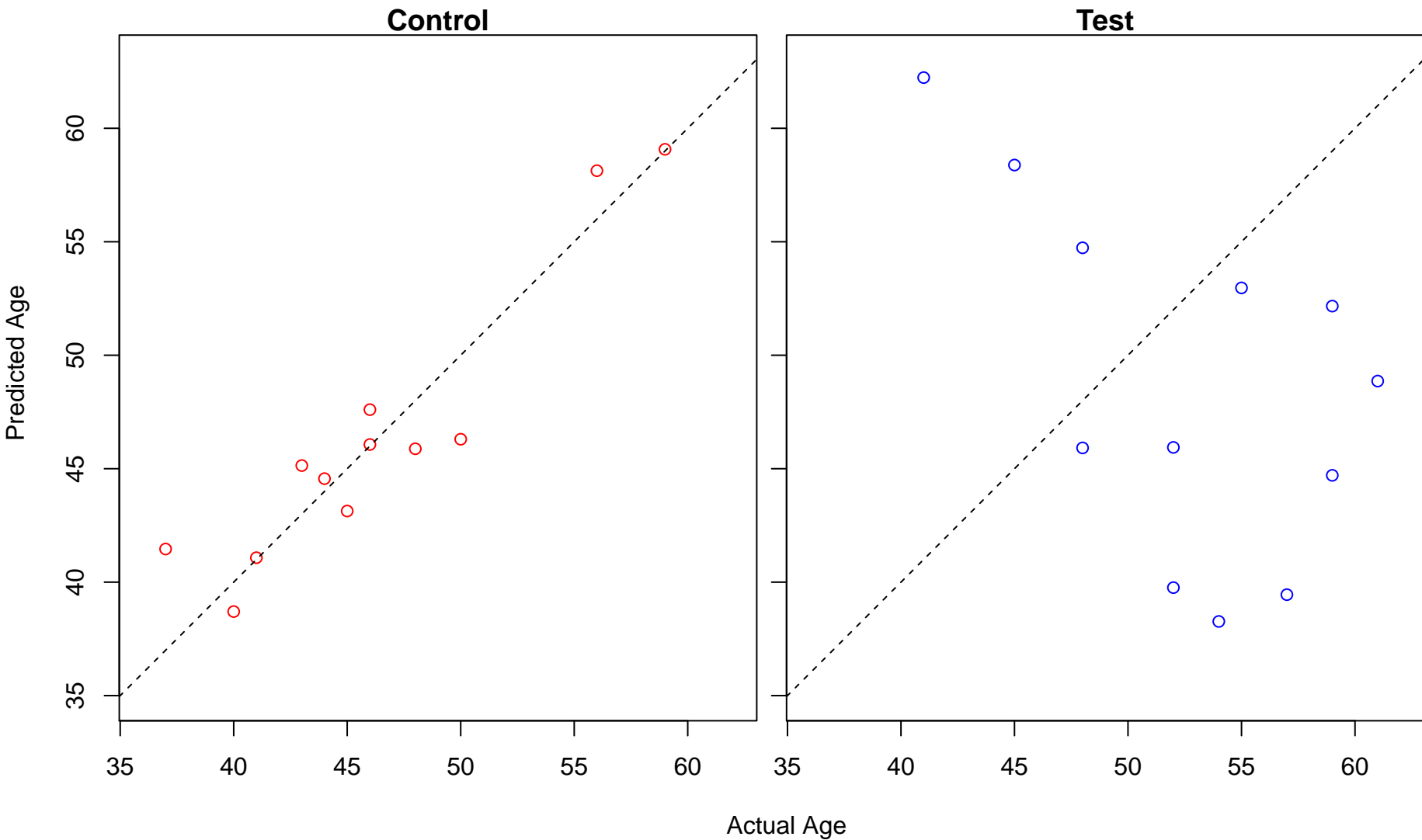
mitochondrial translational initiation (Score: 13.464639)



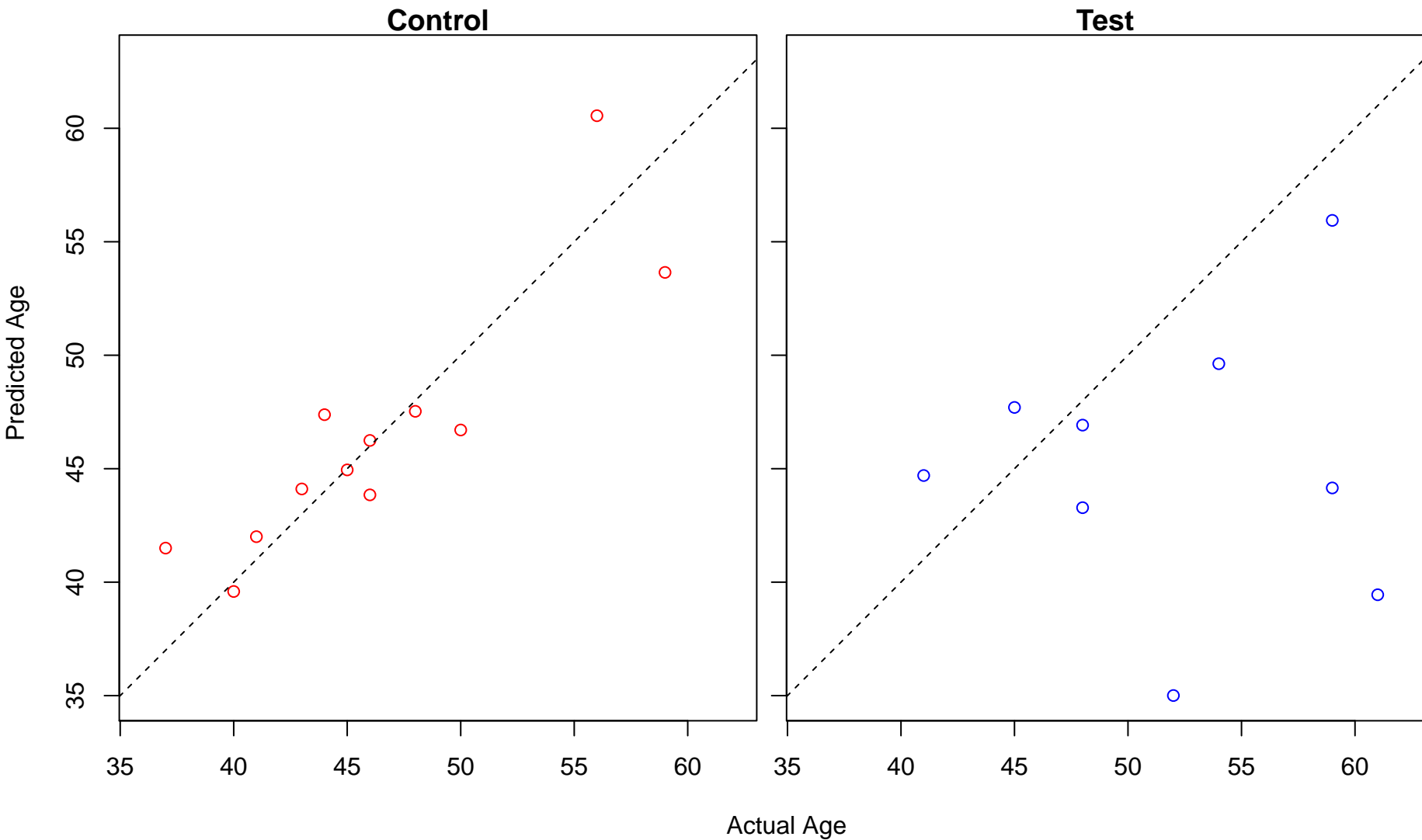
protein maturation (Score: 13.429802)



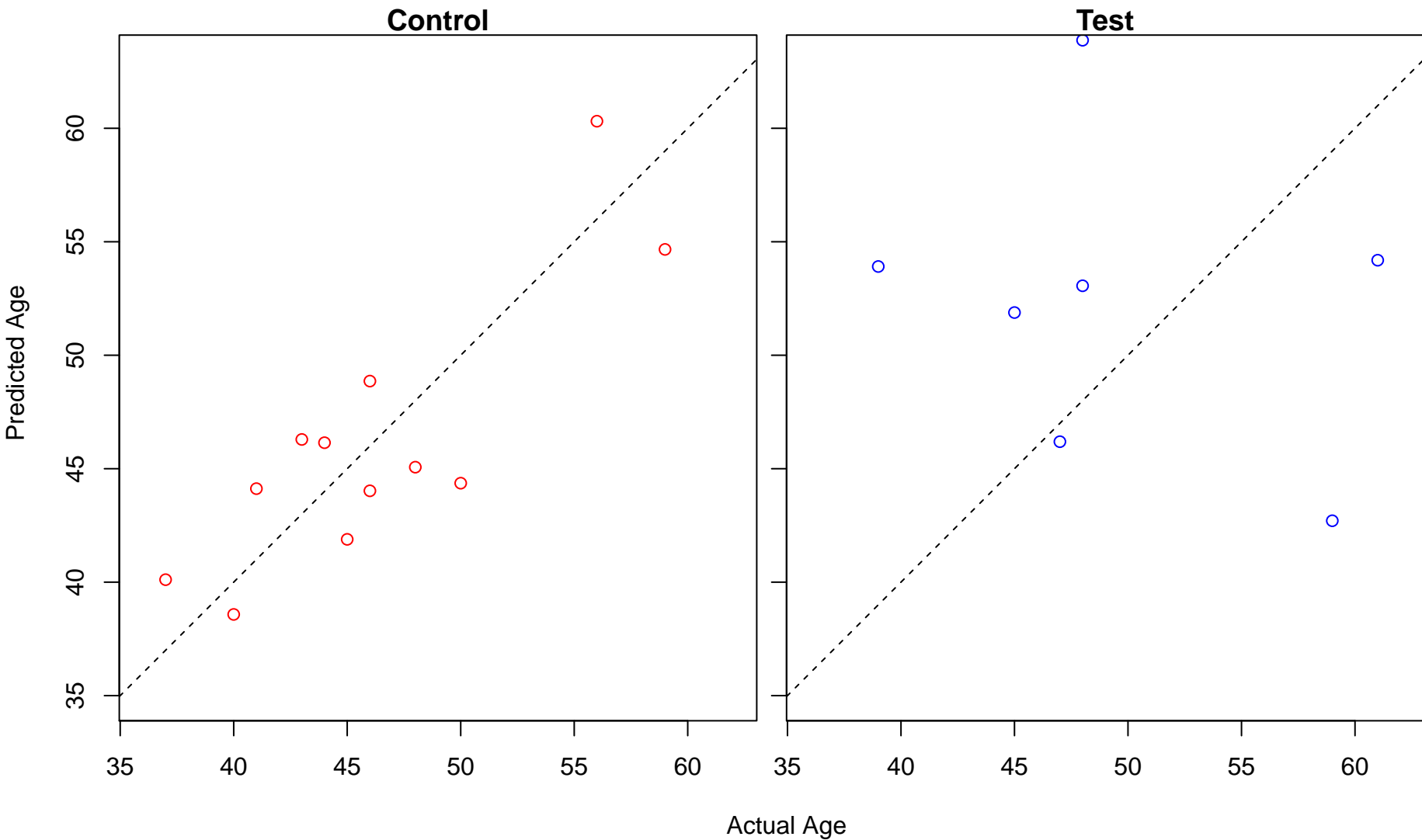
sensory organ development (Score: 13.356669)



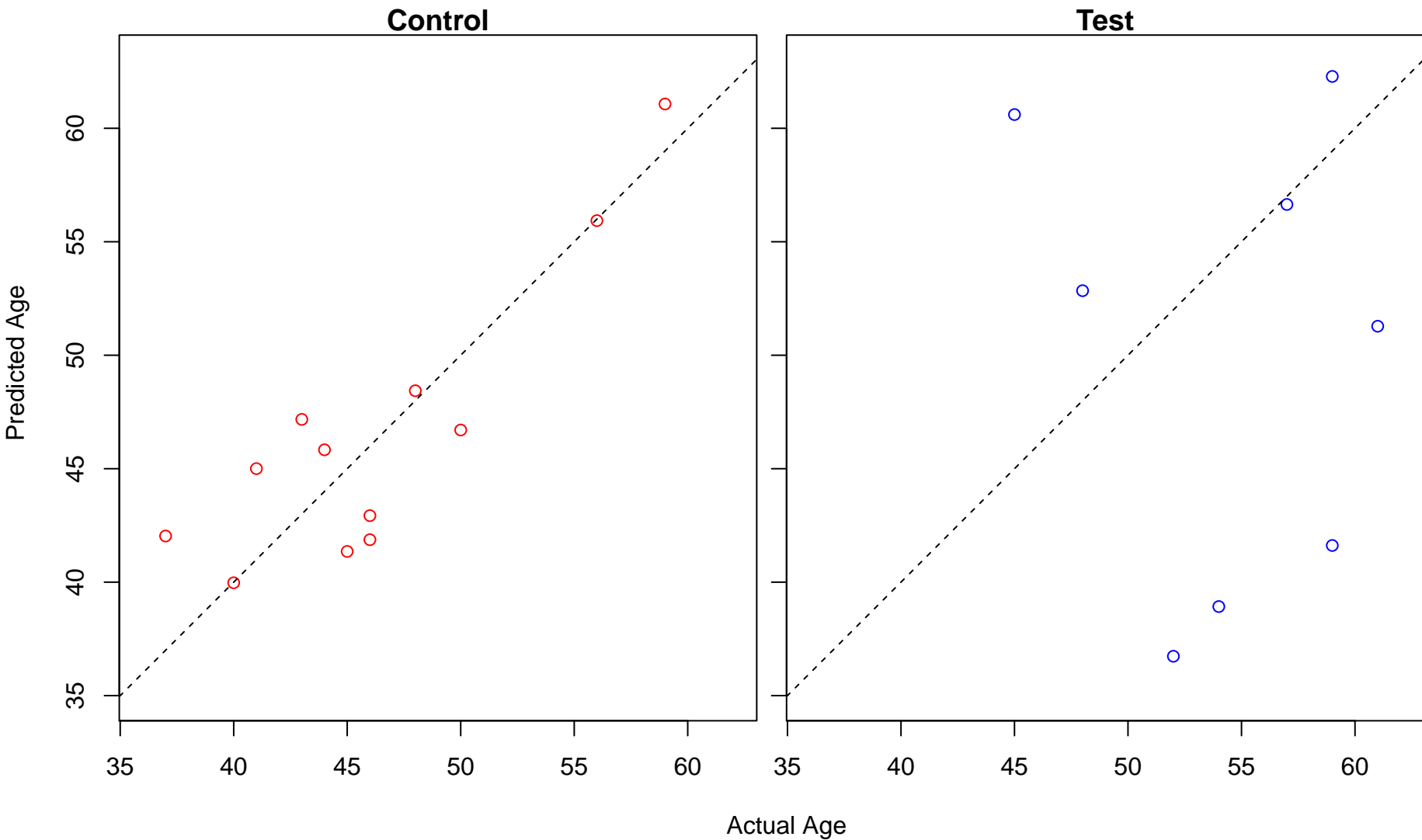
neurological system process (Score: 13.351443)



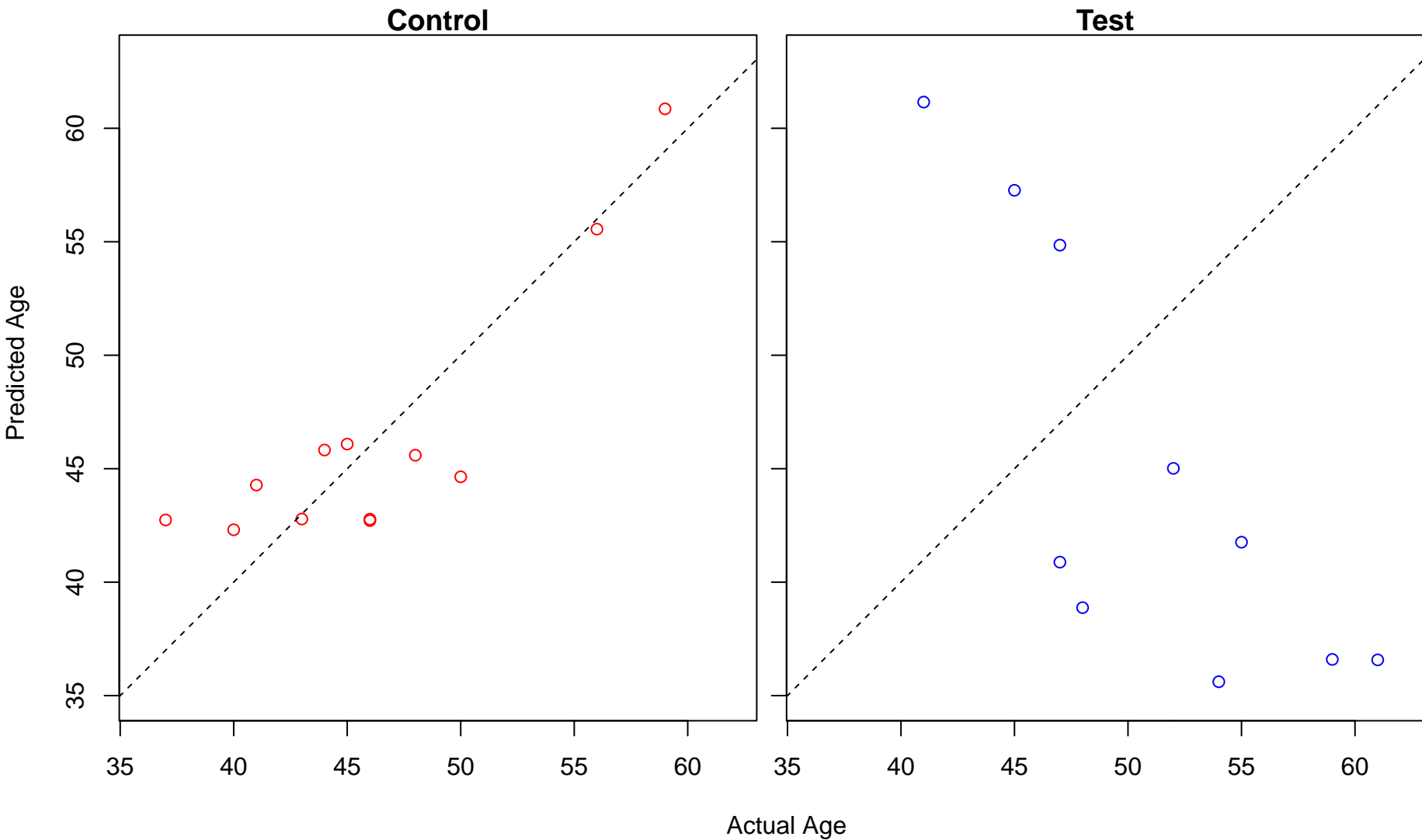
positive regulation of cytokine secretion (Score: 13.349286)



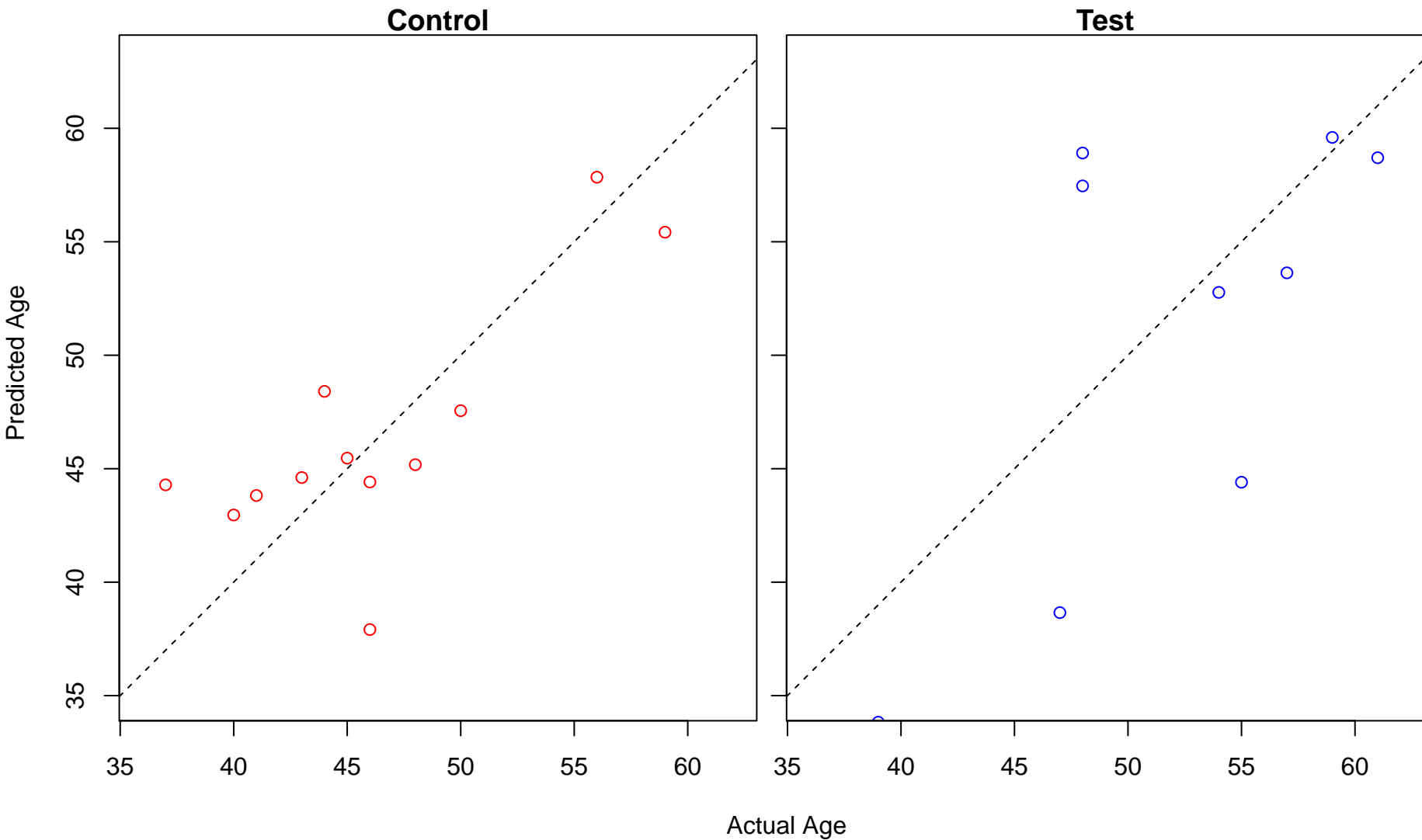
cellular response to lipid (Score: 13.333401)



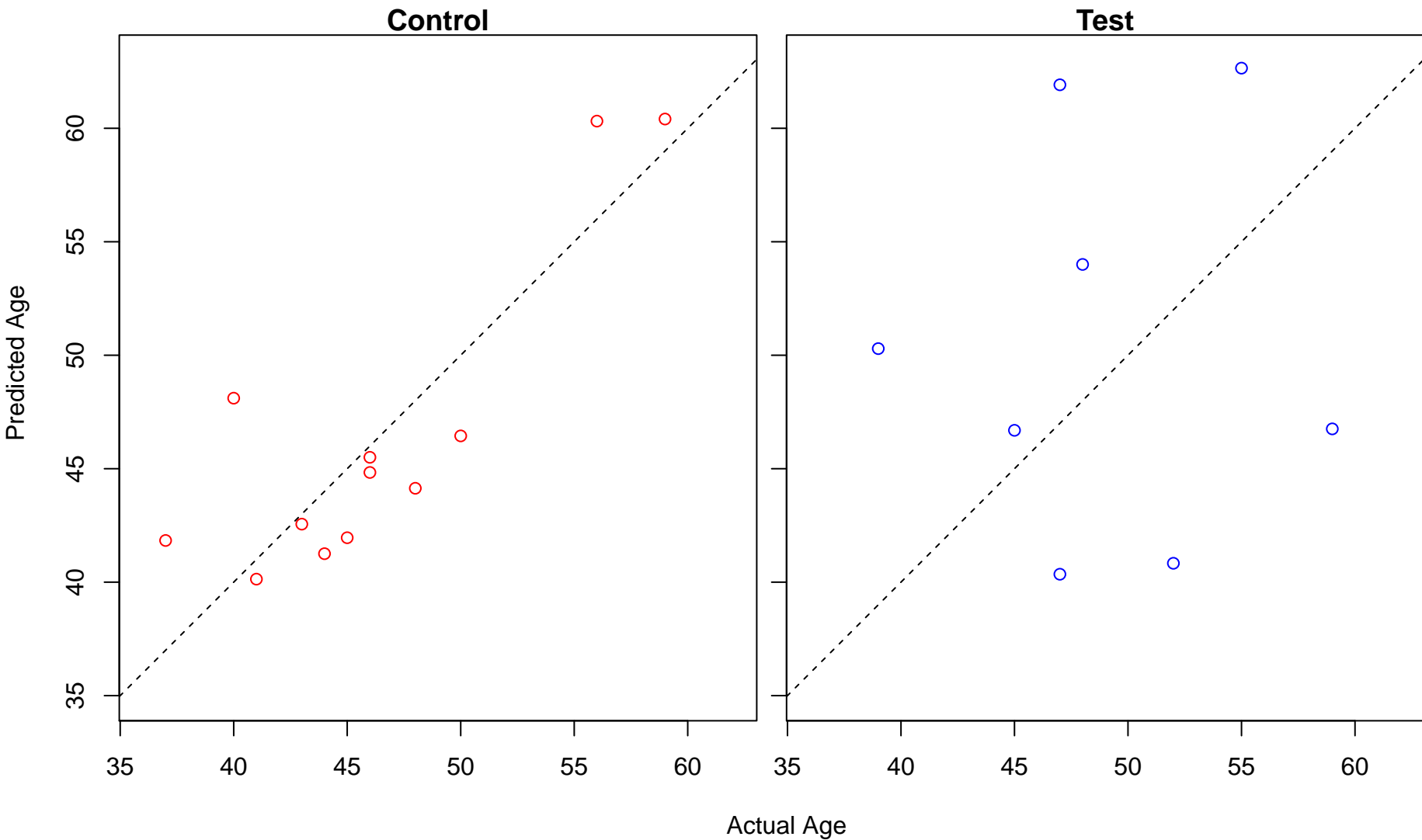
regulation of JNK cascade (Score: 13.313185)



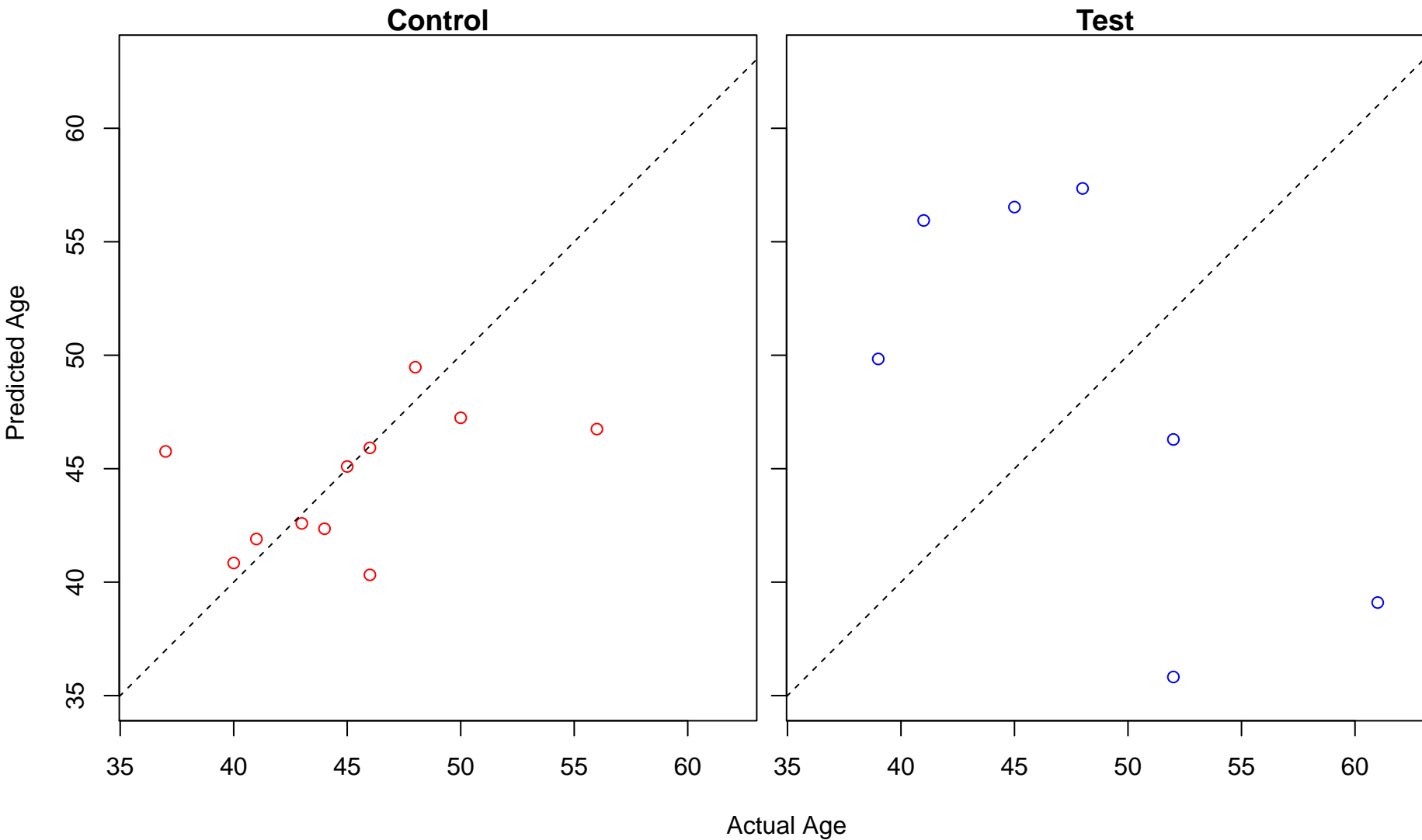
purine deoxyribonucleotide metabolic process (Score: 13.240167)



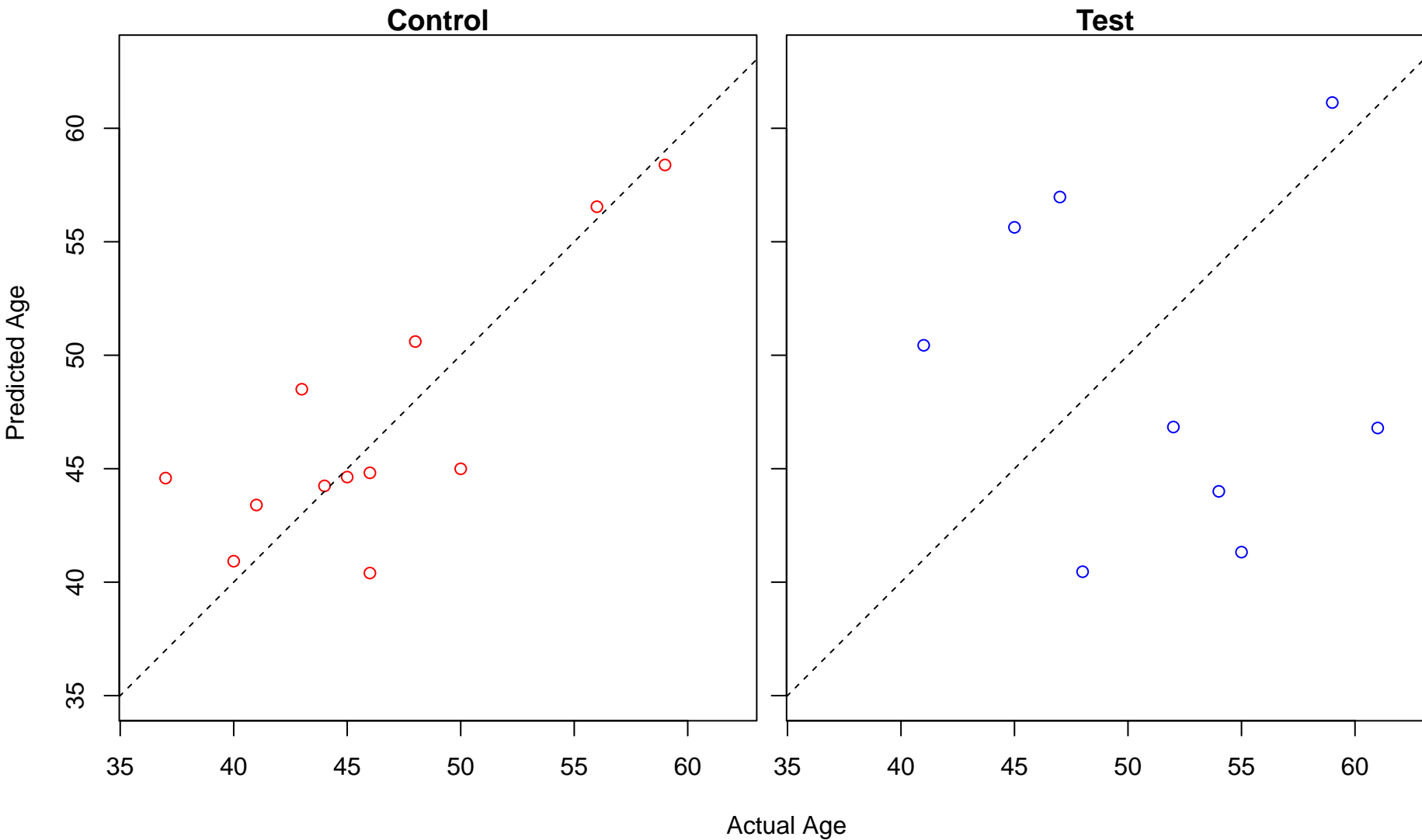
negative regulation of hydrogen peroxide-mediated programmed cell death (Score: 13.133805)



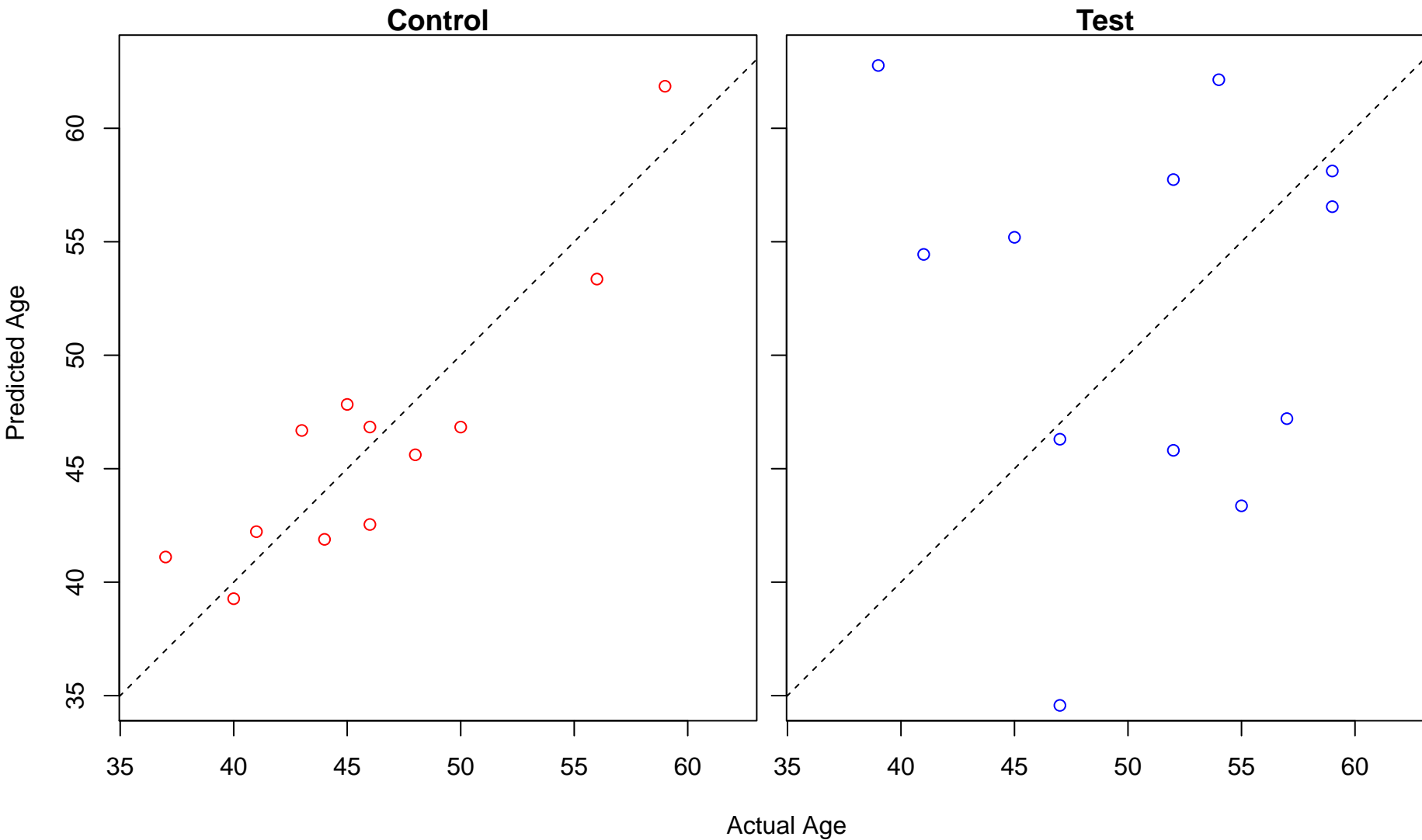
very long-chain fatty acid biosynthetic process (Score: 13.123048)



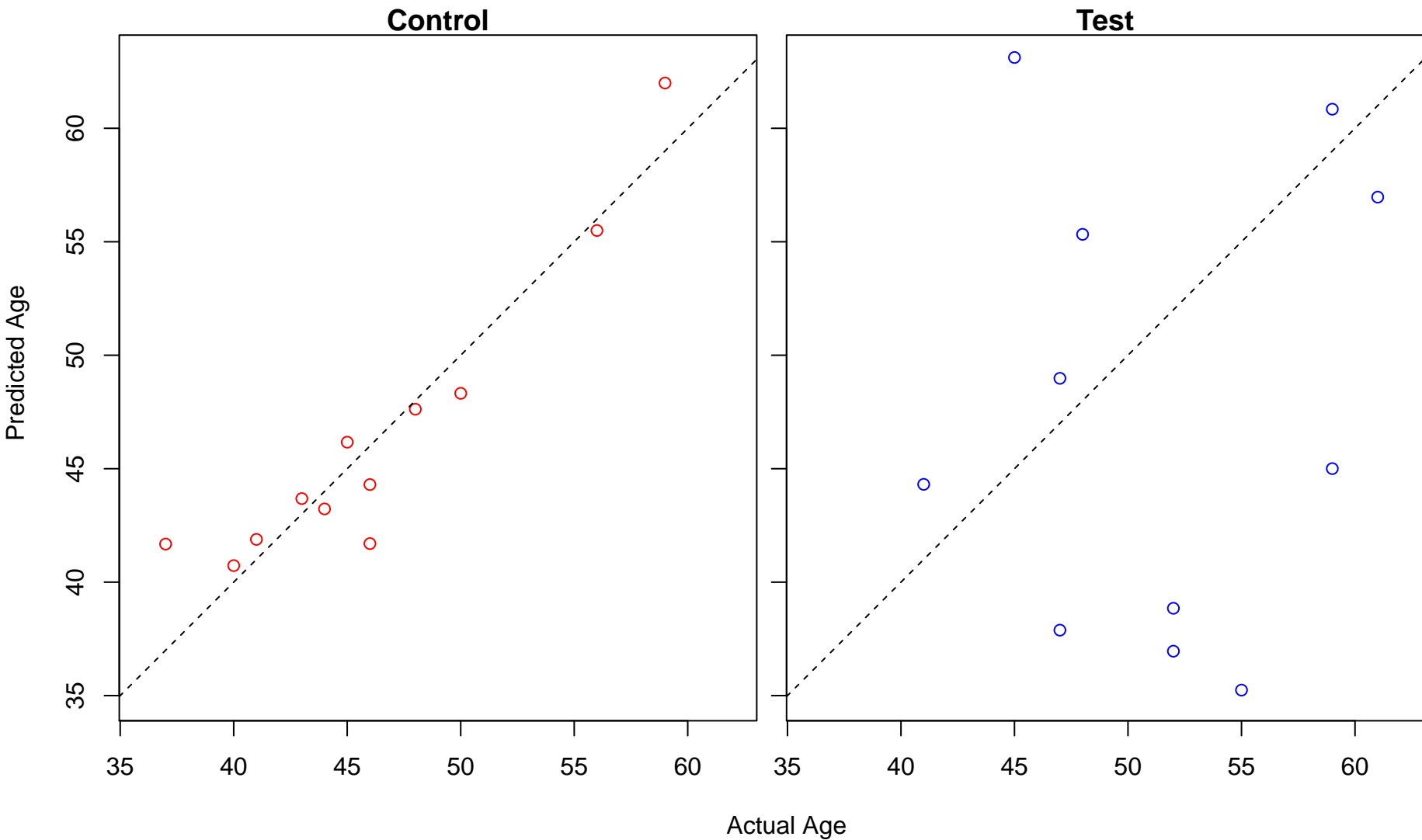
regulation of protein binding (Score: 13.079755)



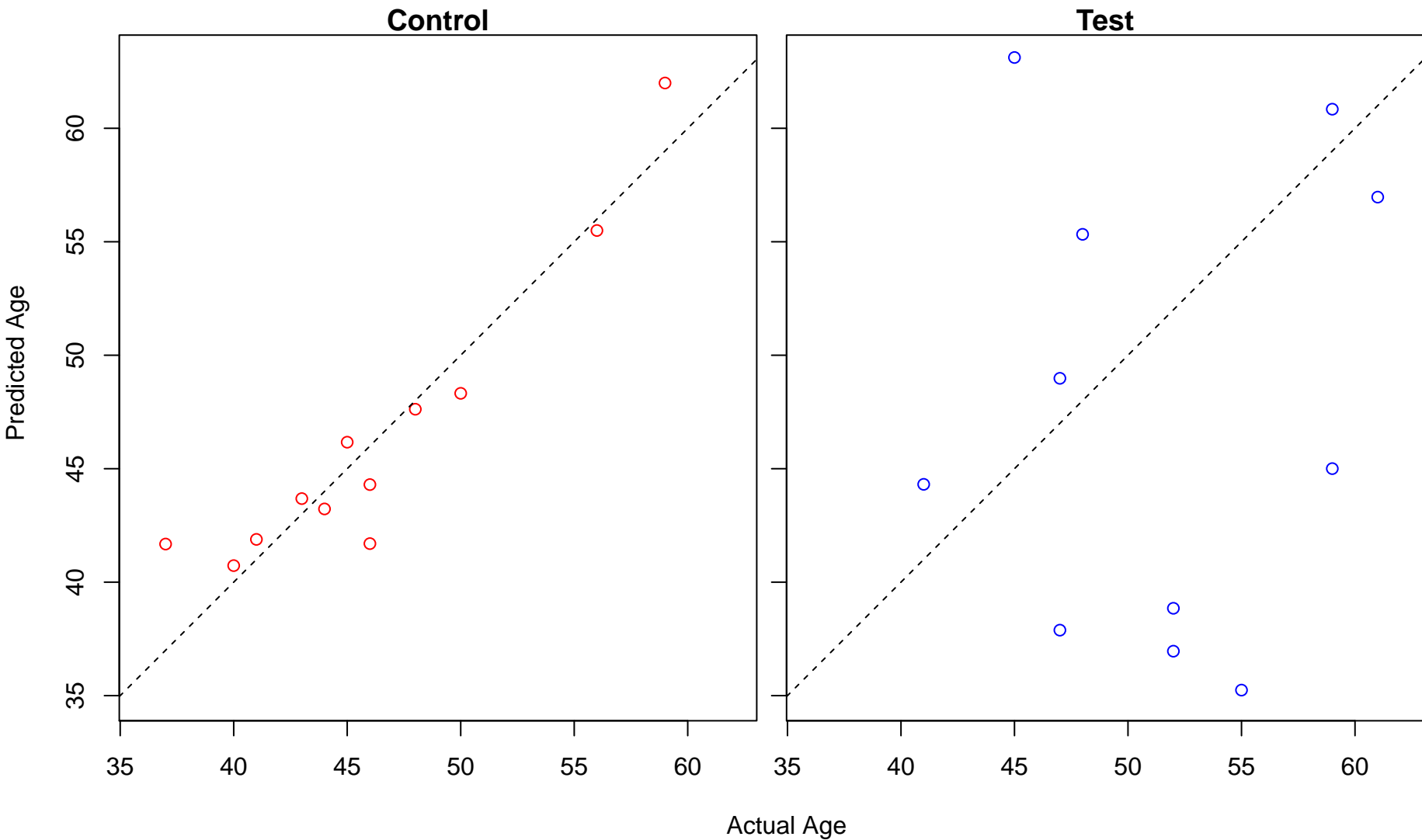
cell fate commitment involved in formation of primary germ layer (Score: 13.066004)



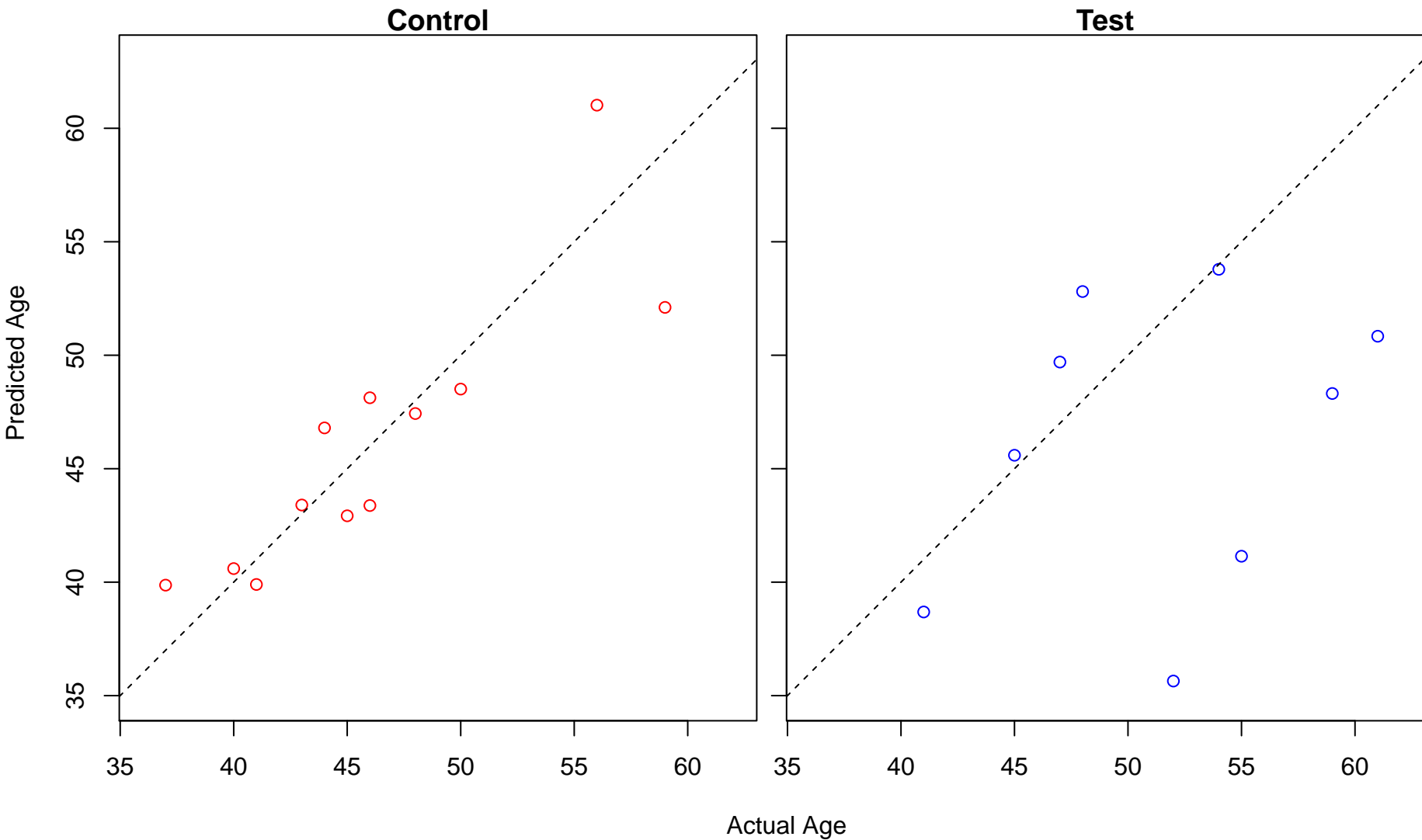
dolichol-linked oligosaccharide biosynthetic process (Score: 13.064173)



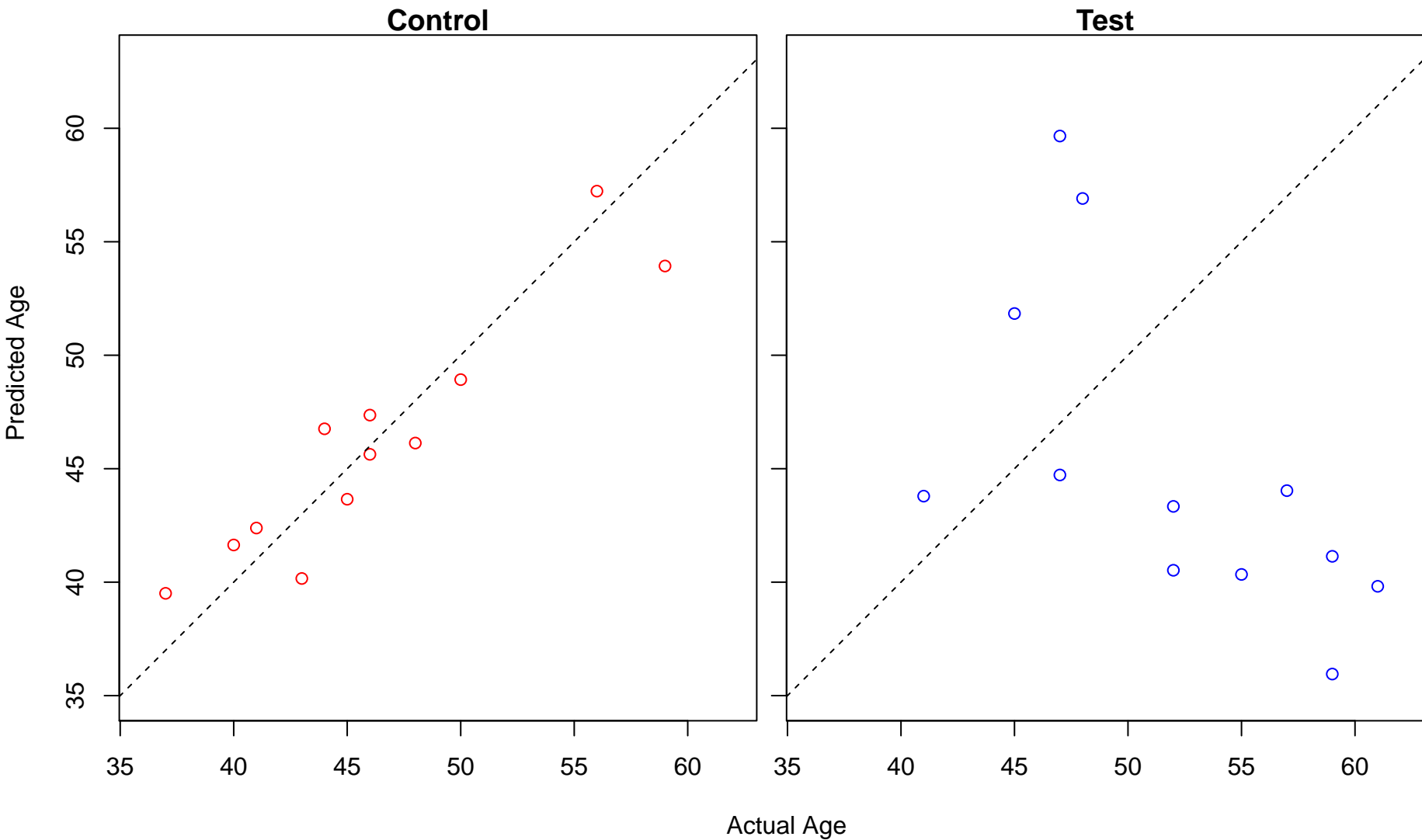
oligosaccharide–lipid intermediate biosynthetic process (Score: 13.064173)



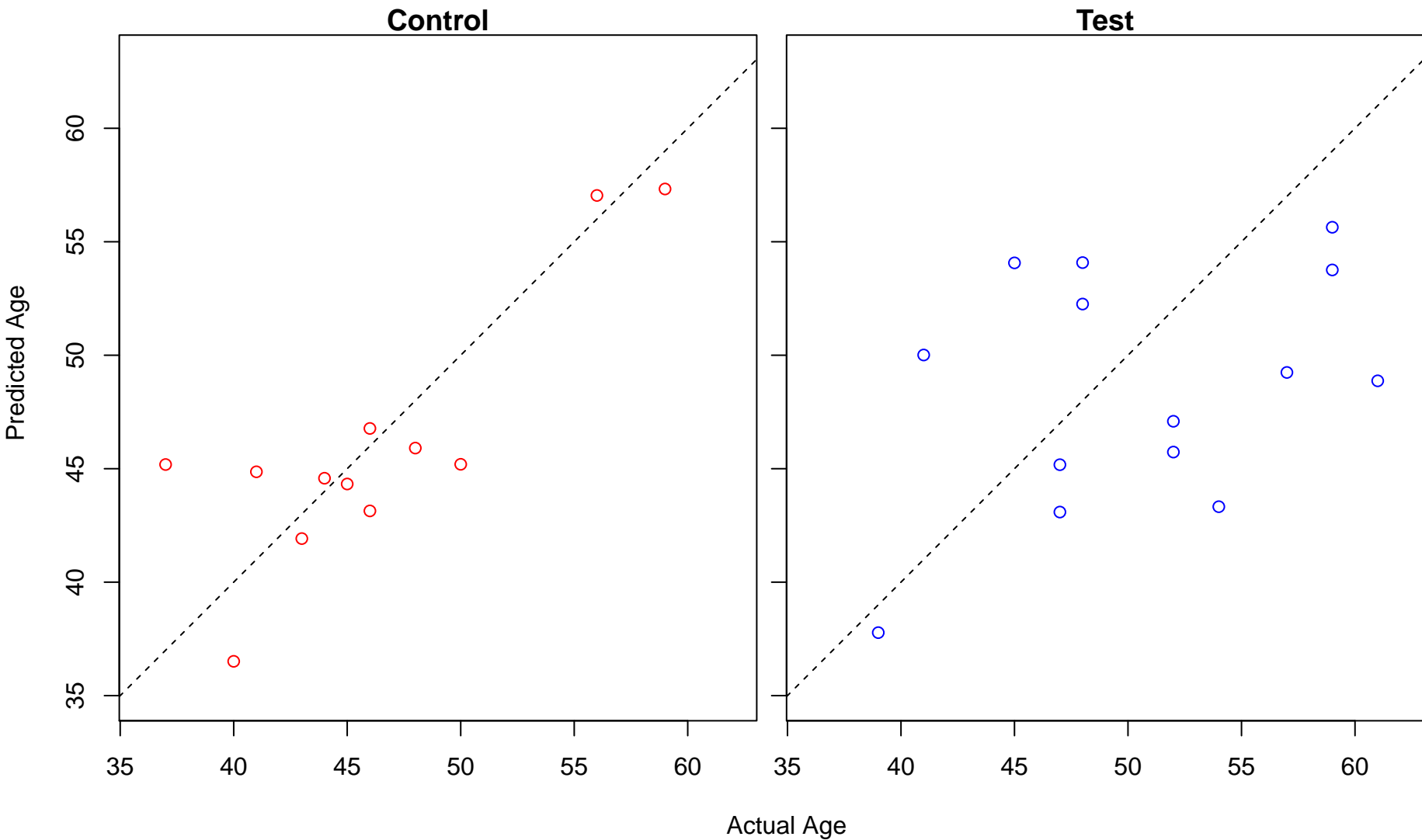
ribosomal large subunit biogenesis (Score: 13.006023)



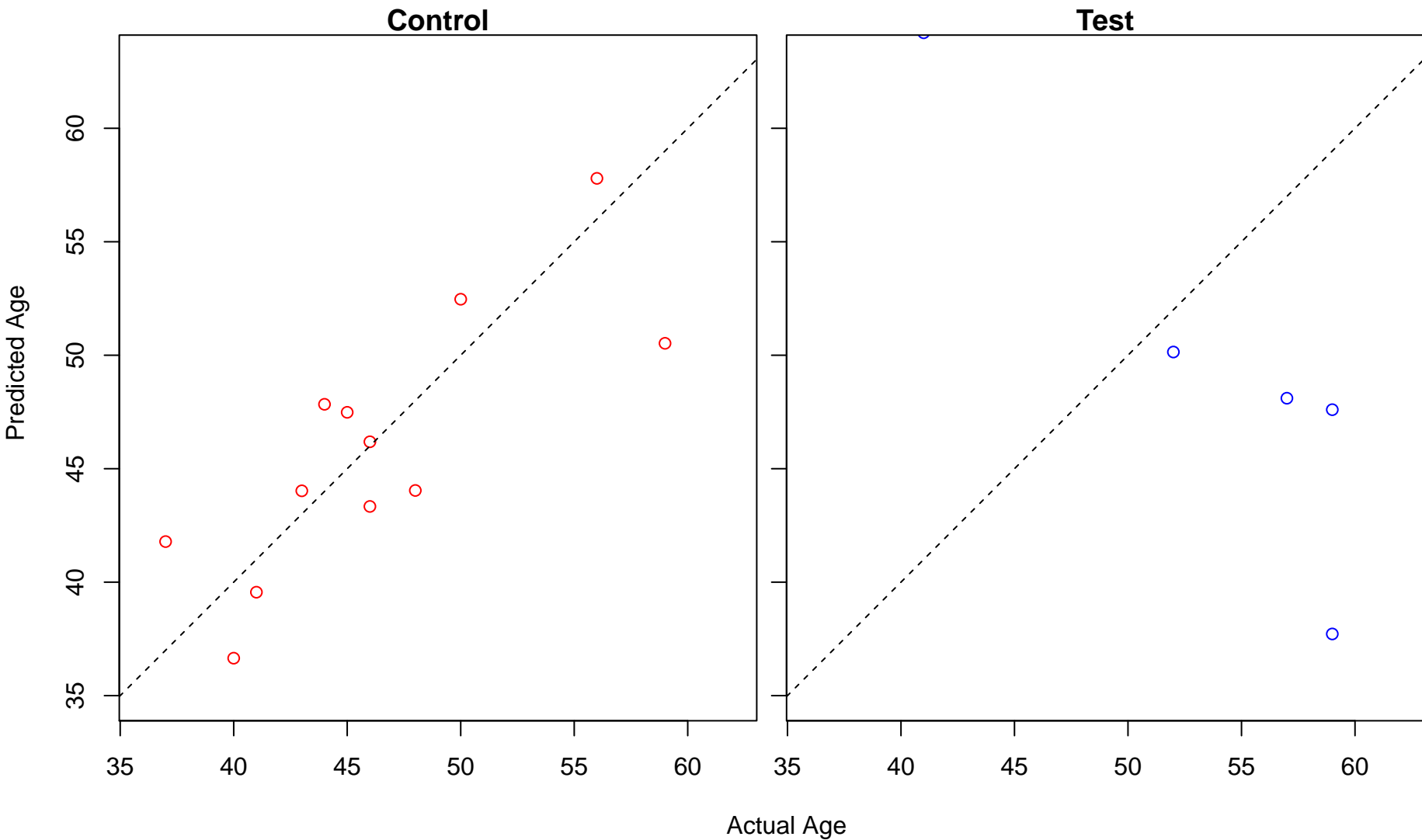
pyrimidine ribonucleoside metabolic process (Score: 12.973152)



negative regulation of transcription factor import into nucleus (Score: 12.968363)

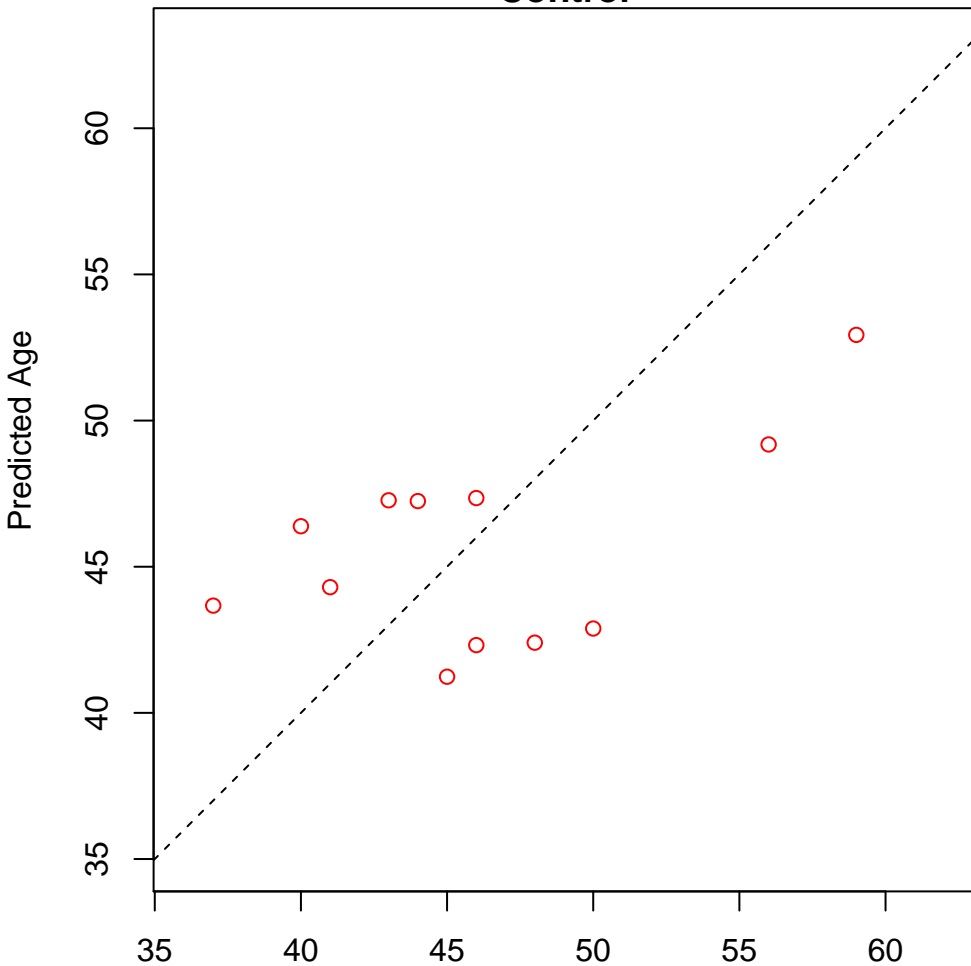


vitamin transmembrane transport (Score: 12.913801)

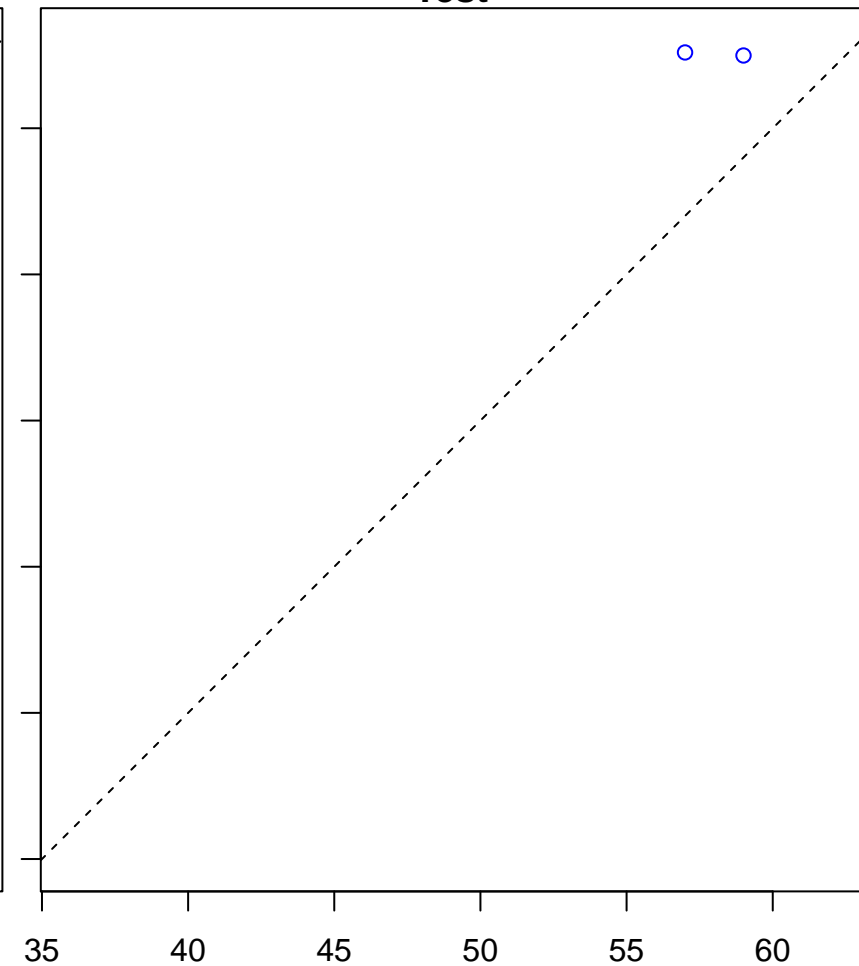


sensory perception of sweet taste (Score: 12.913015)

Control

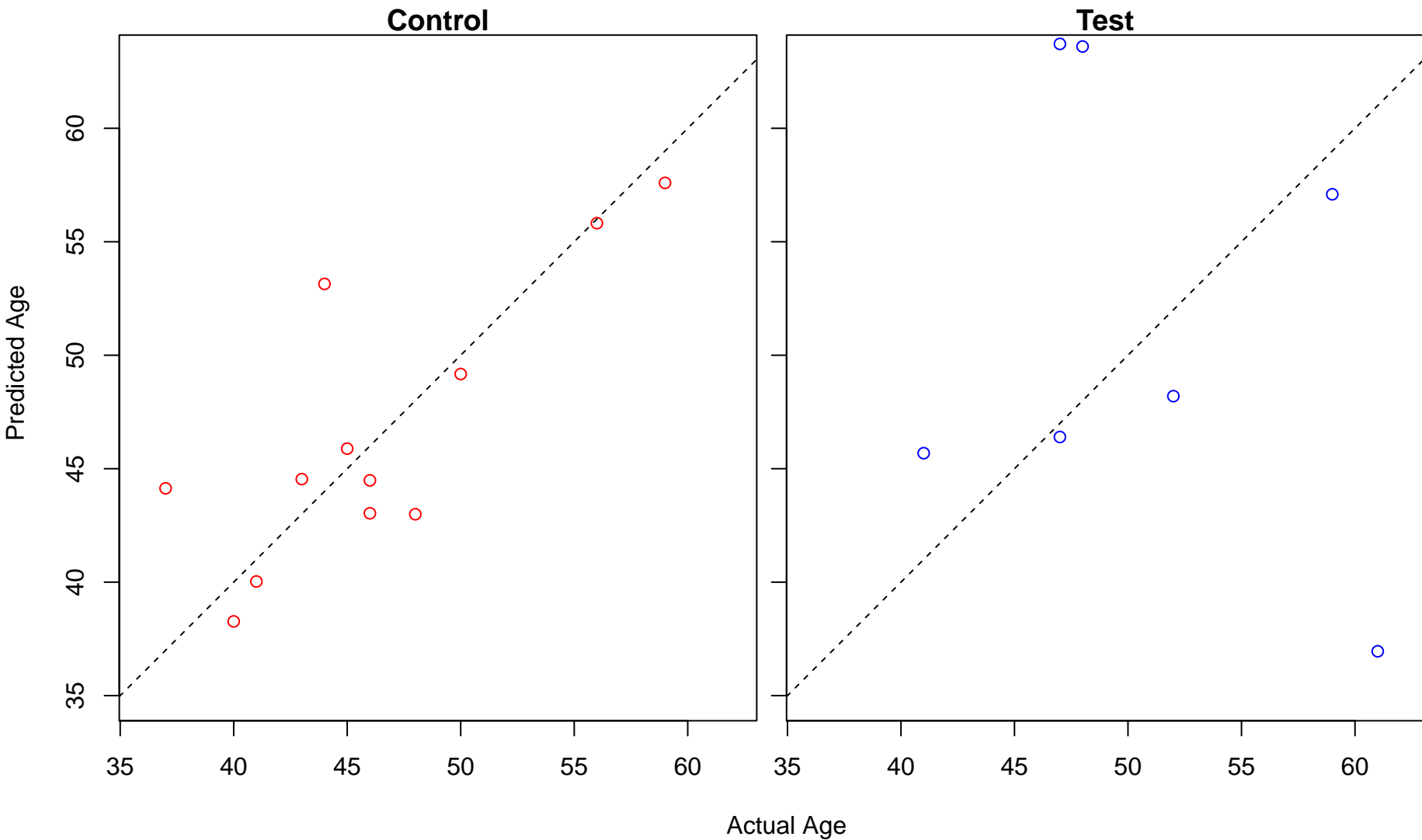


Test

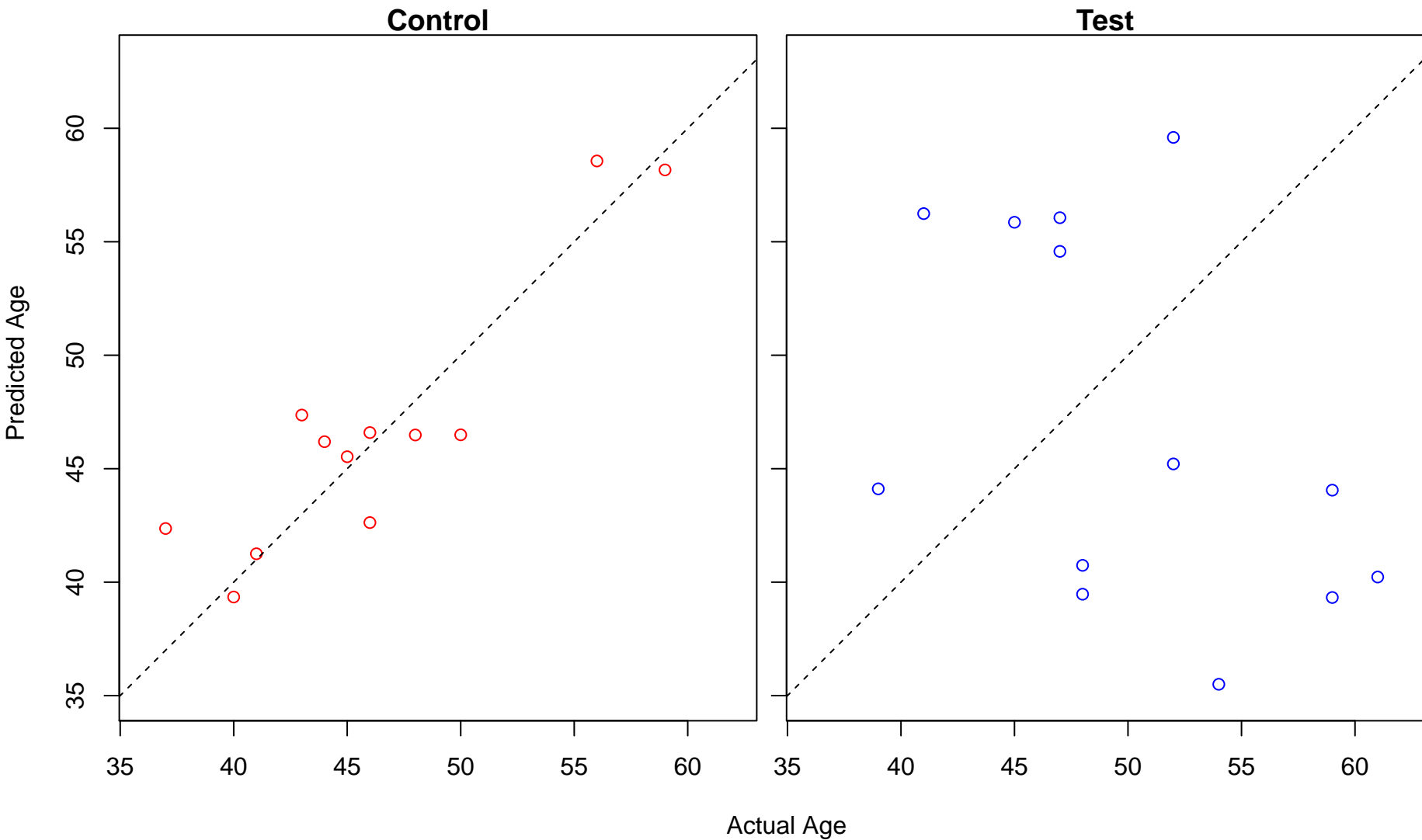


Actual Age

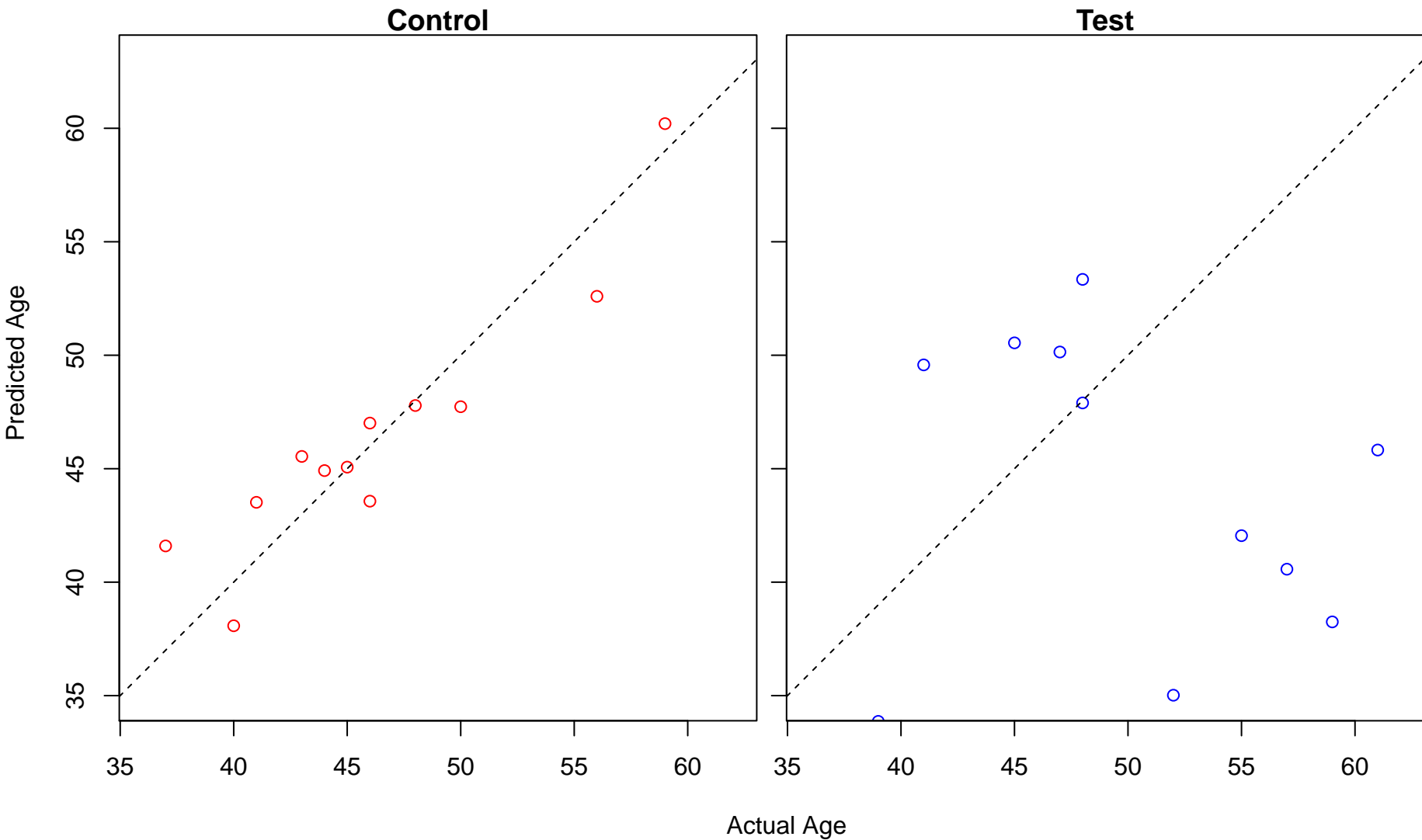
maintenance of protein localization in endoplasmic reticulum (Score: 12.900128)



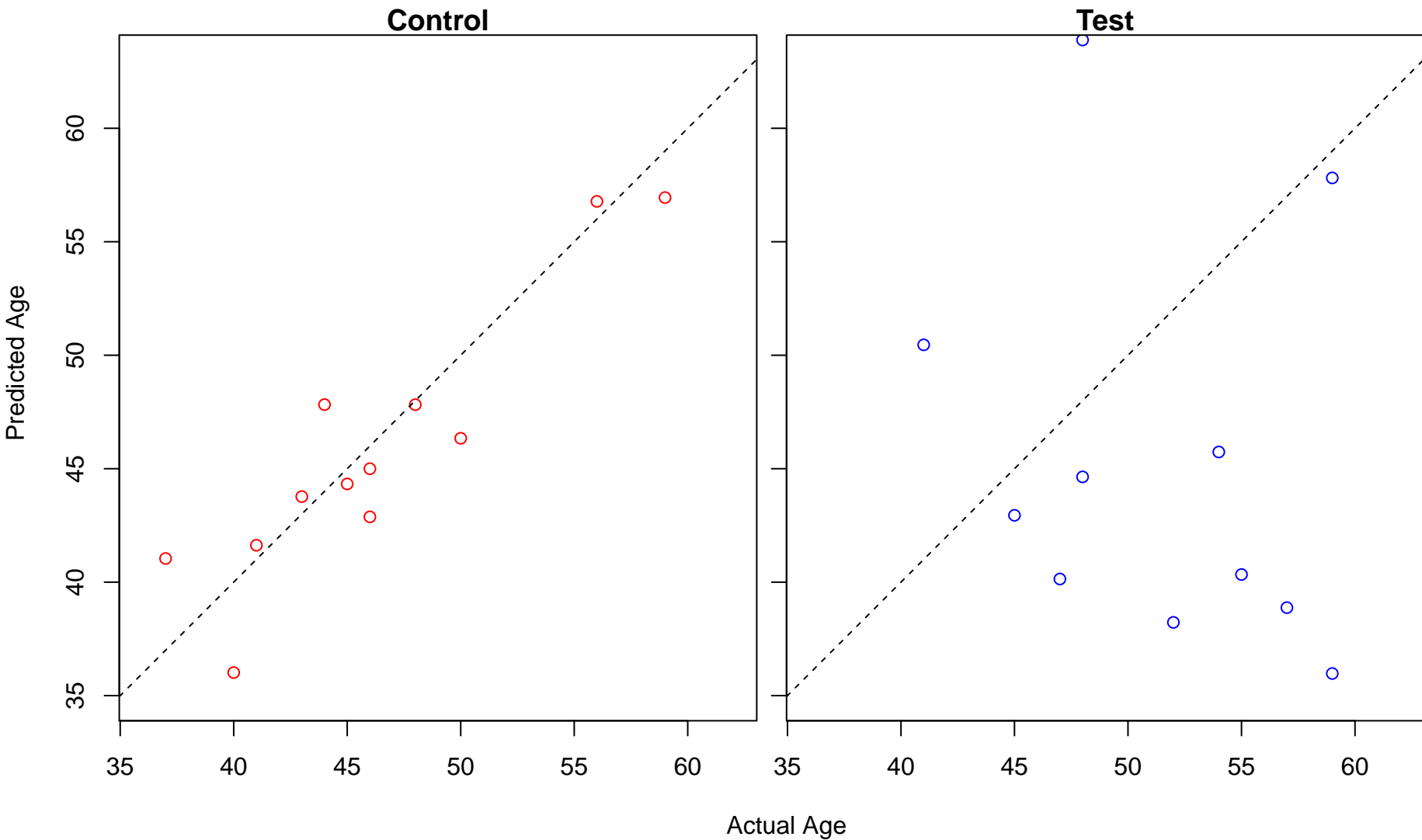
protein processing (Score: 12.864776)



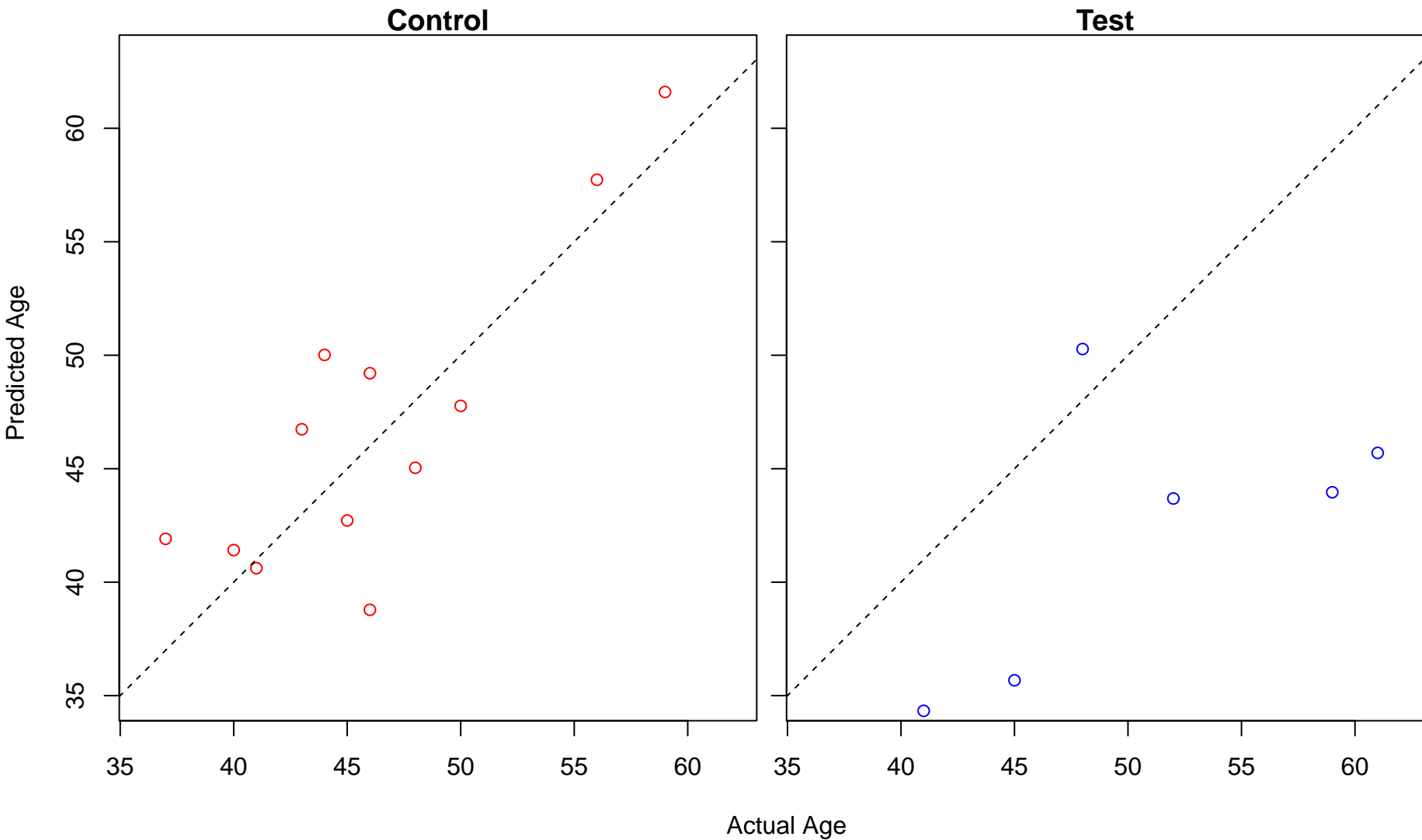
regulation of endothelial cell proliferation (Score: 12.849179)



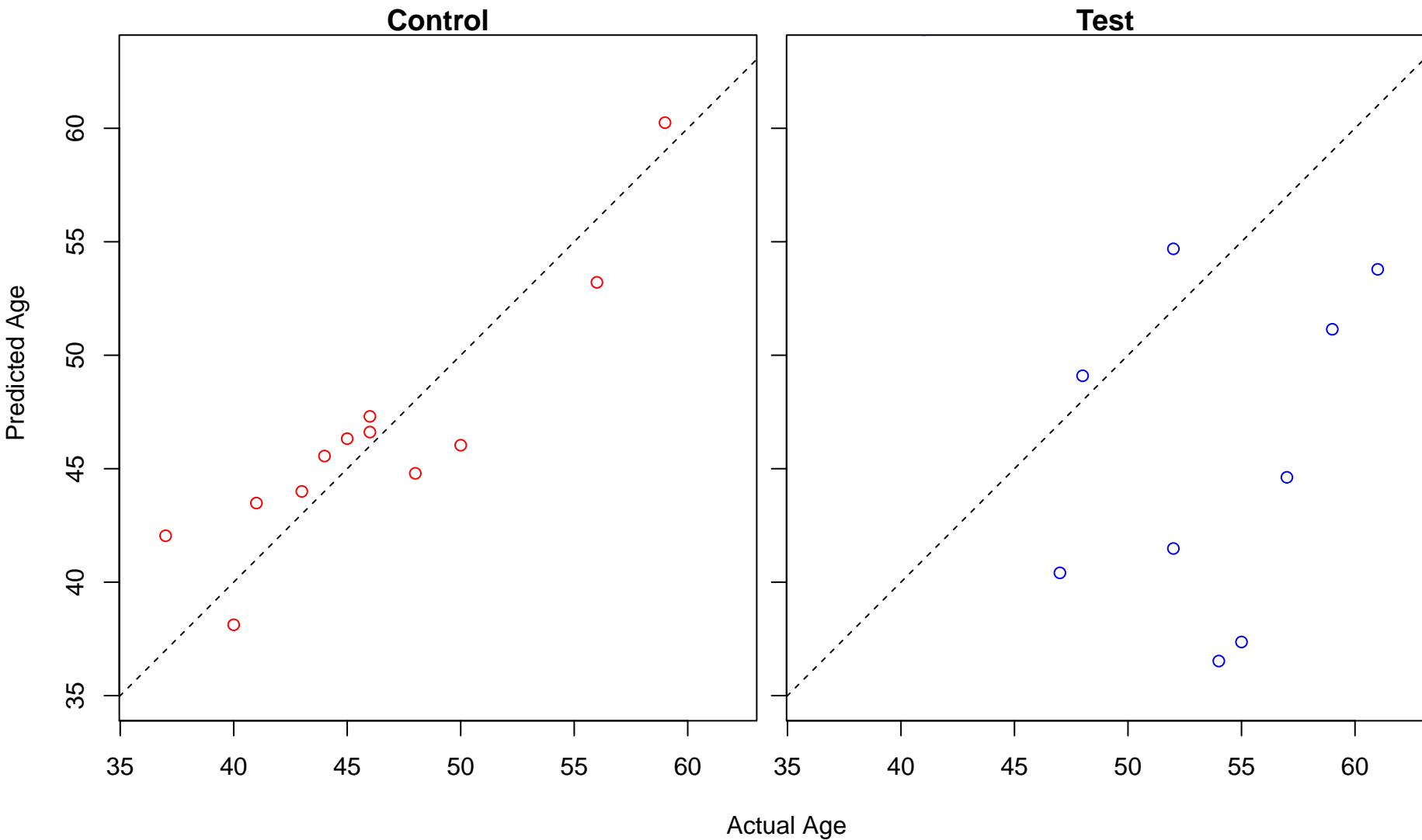
regulation of phosphatidylinositol 3-kinase signaling (Score: 12.837239)



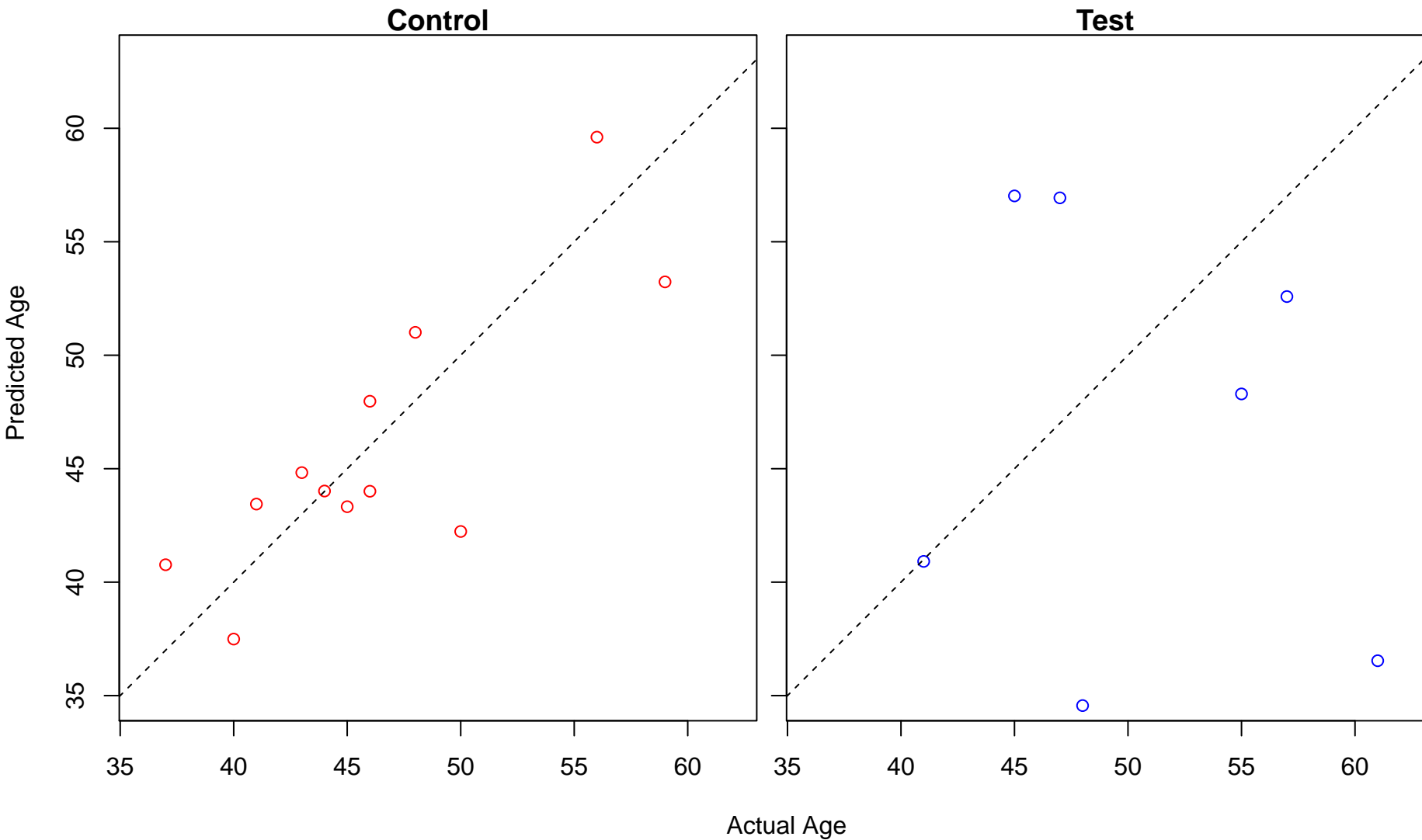
skeletal muscle tissue development (Score: 12.804839)



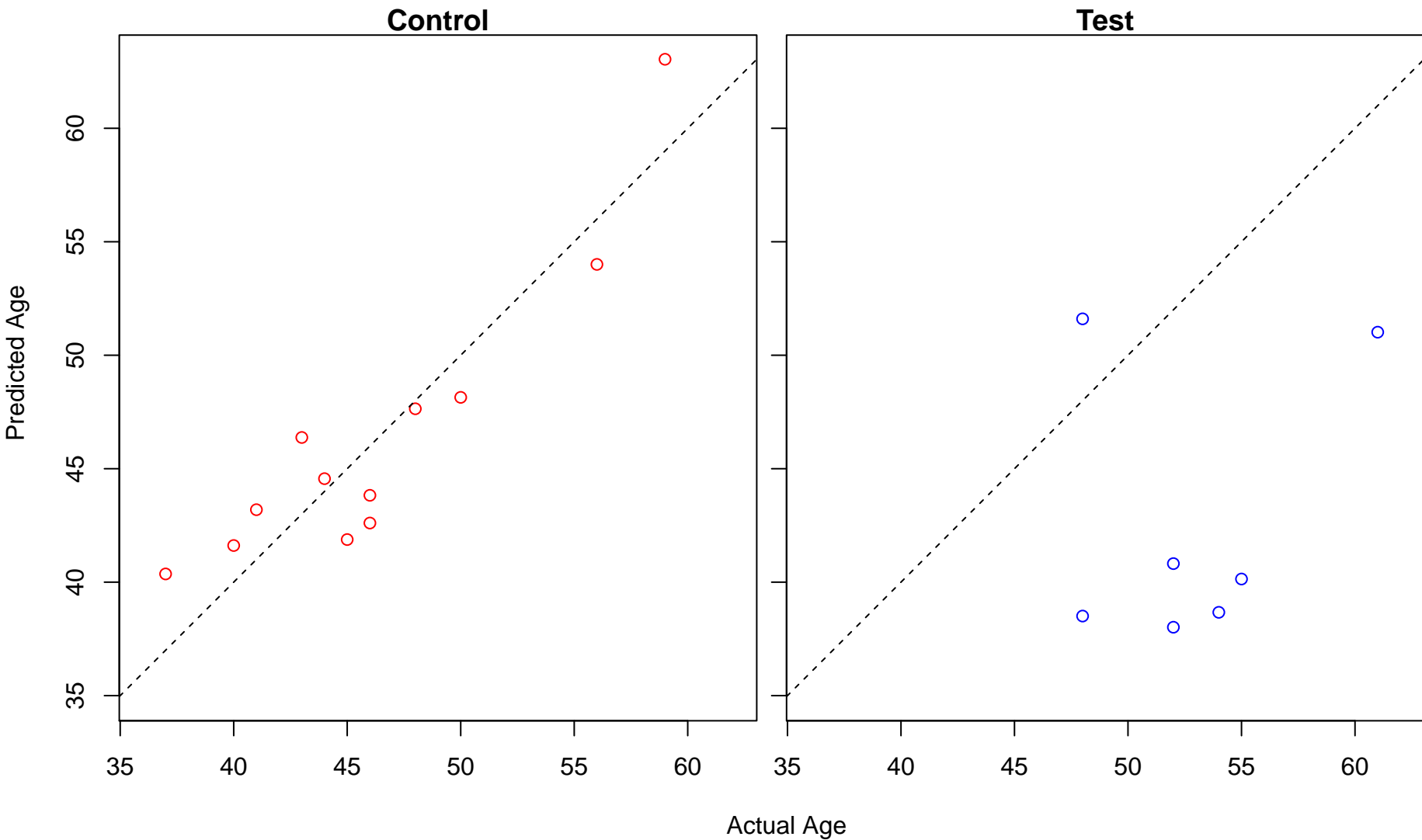
vascular process in circulatory system (Score: 12.764886)



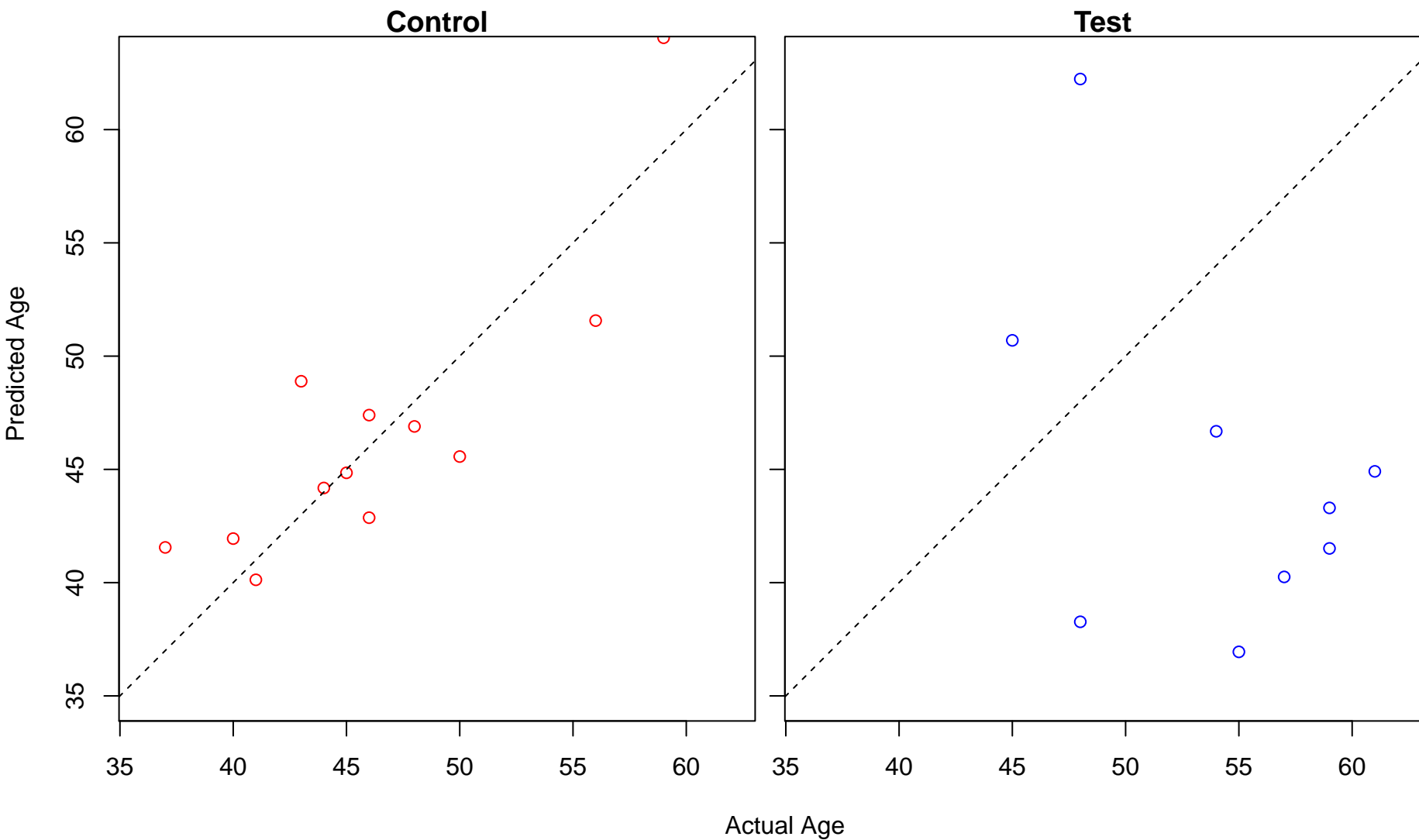
embryo implantation (Score: 12.691642)



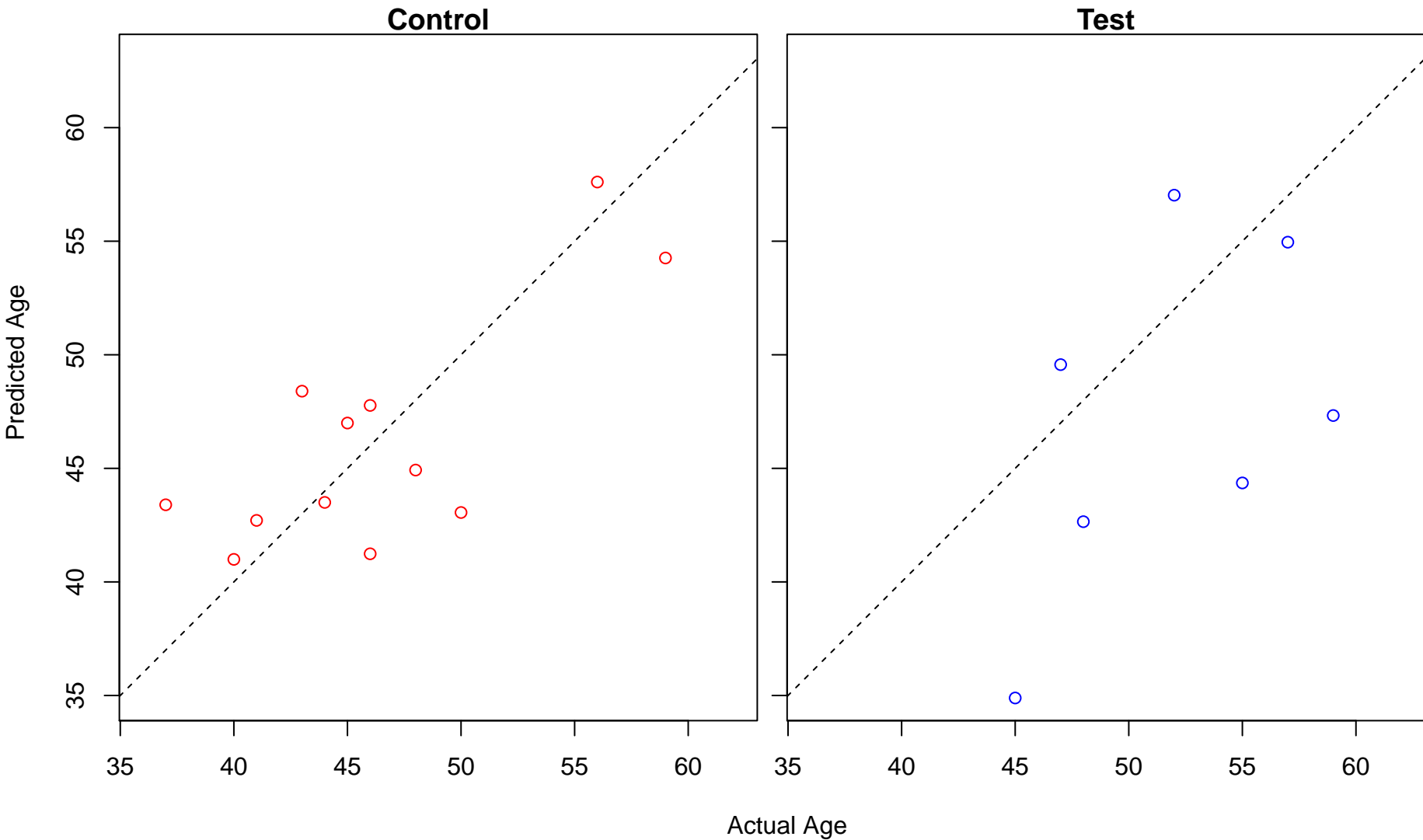
sex differentiation (Score: 12.659034)



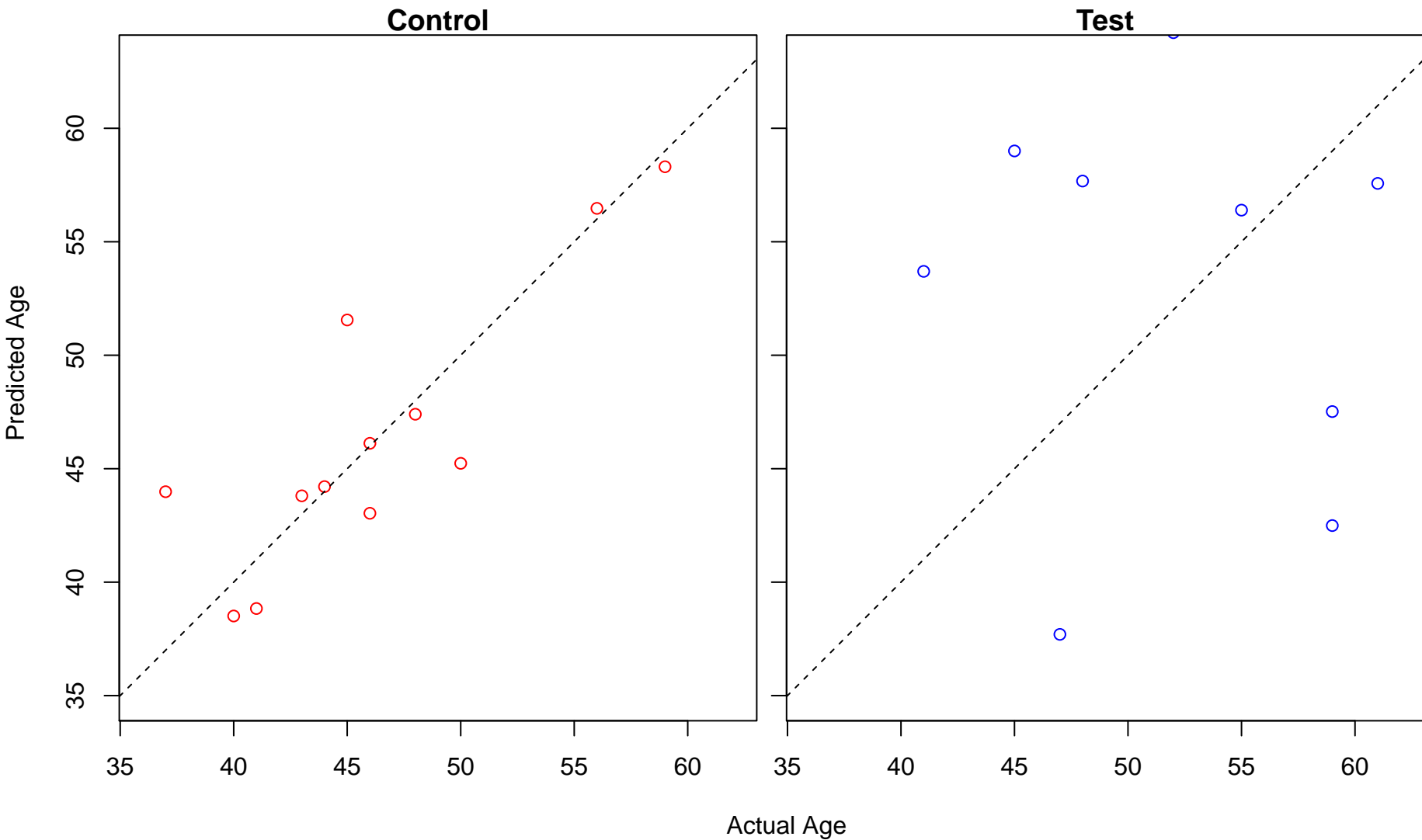
regulation of chromatin modification (Score: 12.638537)



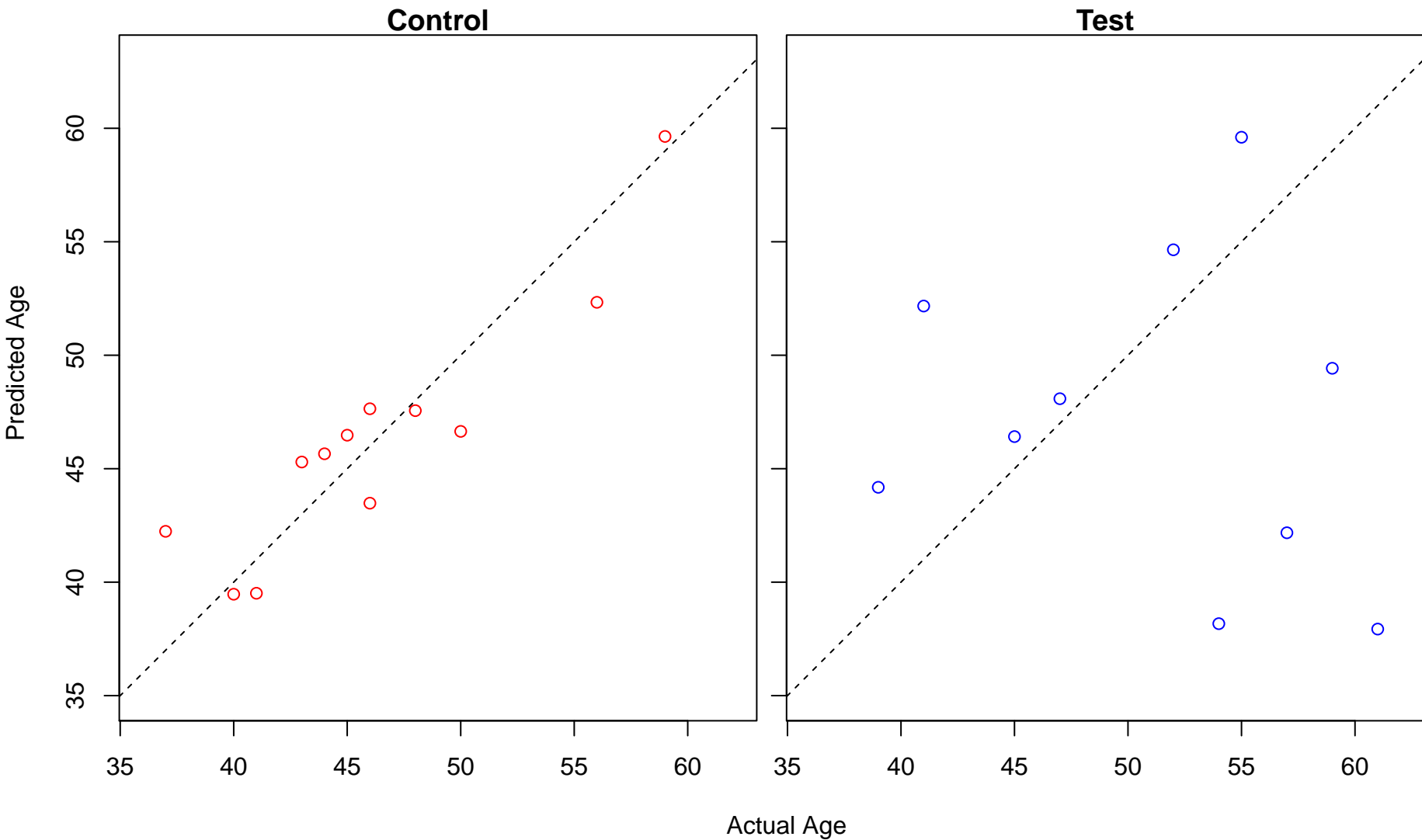
positive regulation of T cell differentiation (Score: 12.616704)



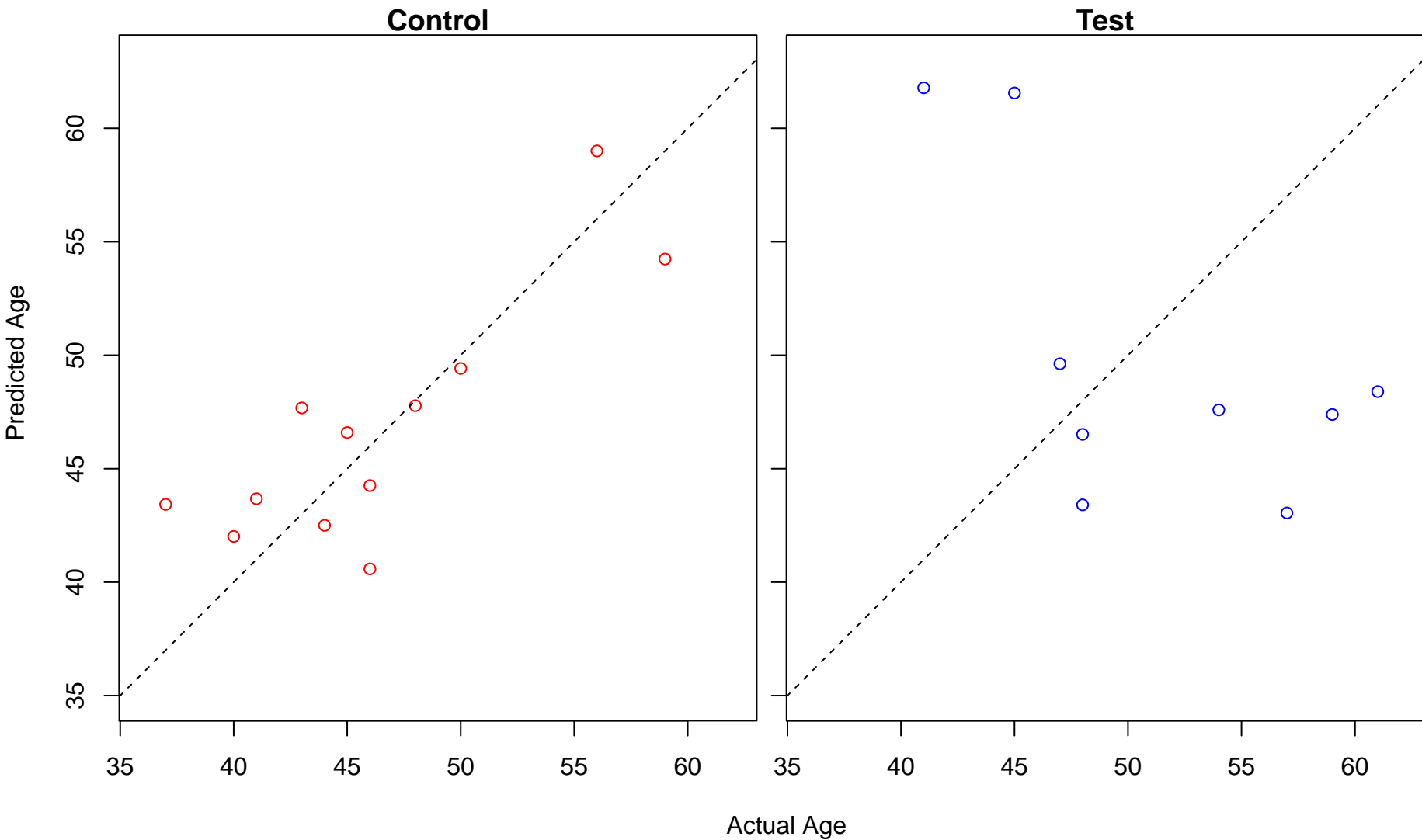
maintenance of protein localization in organelle (Score: 12.594641)



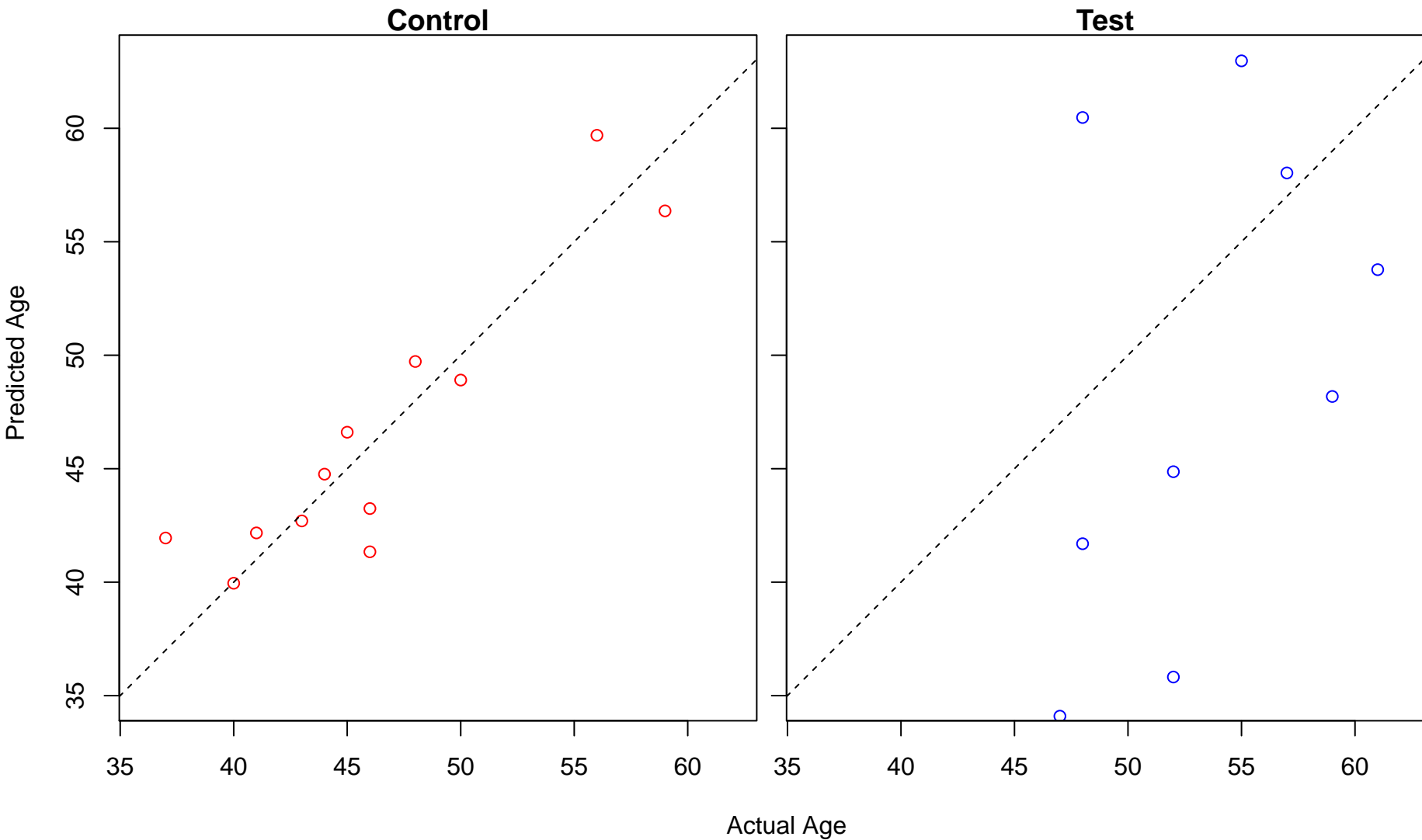
pattern specification process (Score: 12.583084)



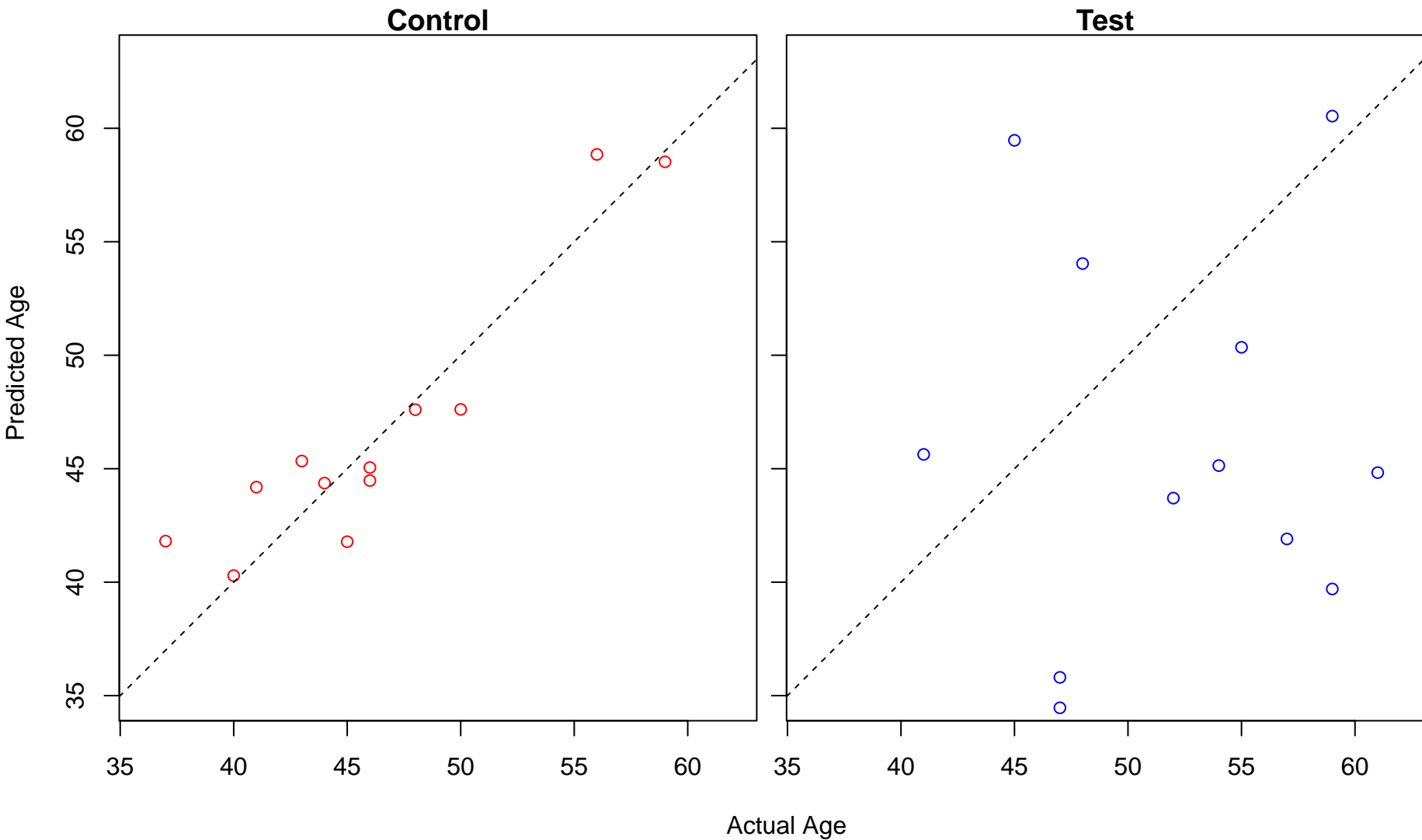
ER-associated misfolded protein catabolic process (Score: 12.558503)



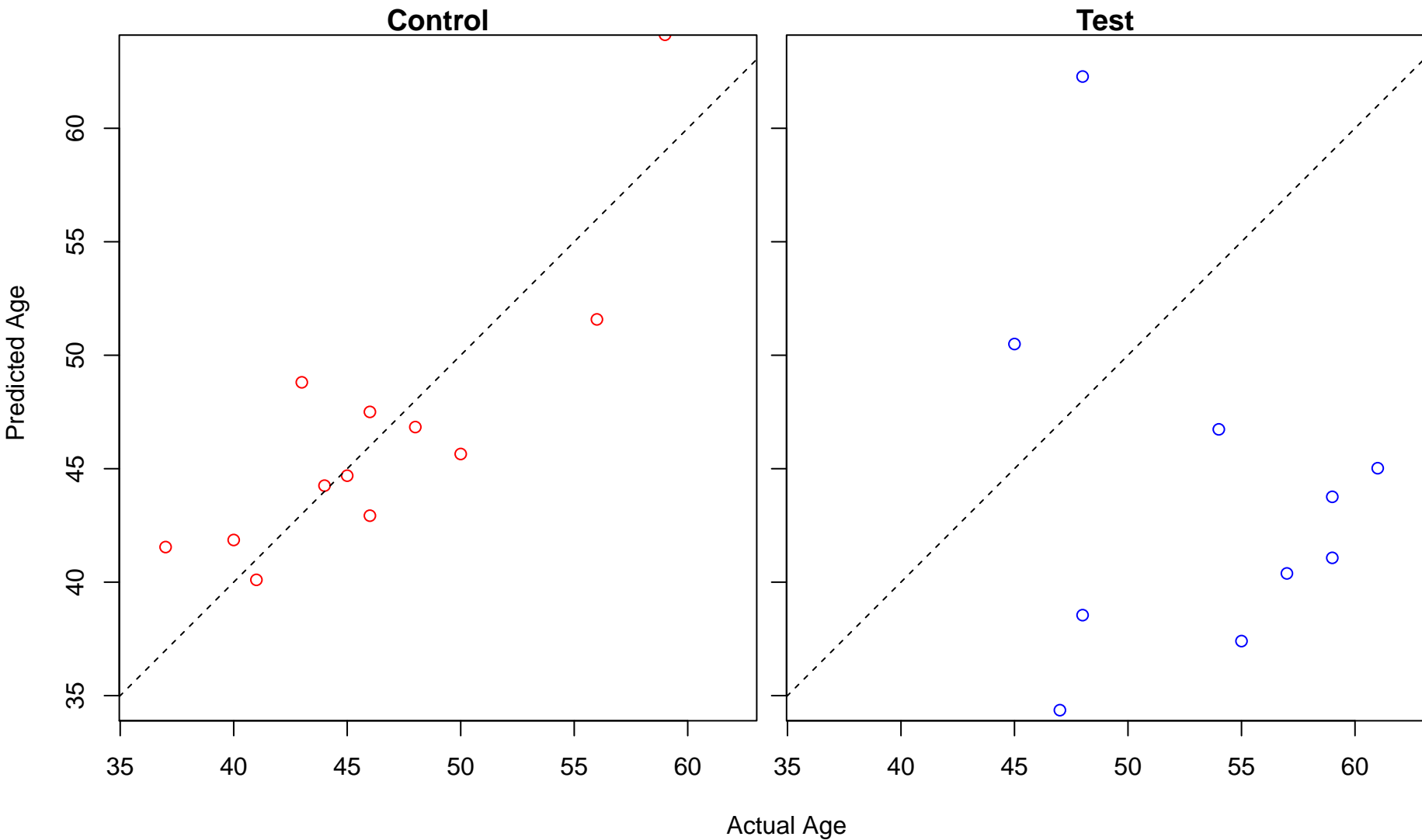
alcohol biosynthetic process (Score: 12.532441)



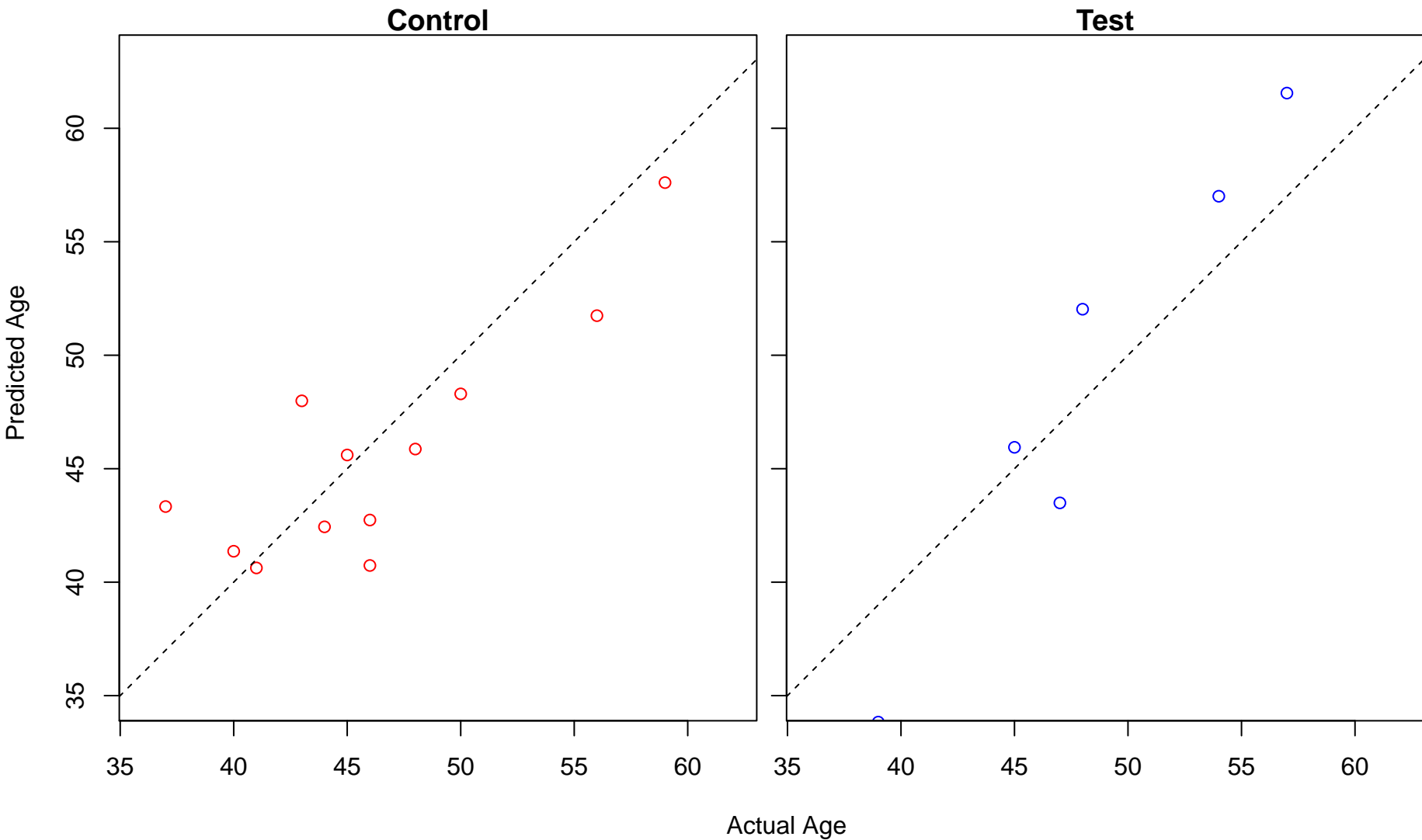
palate development (Score: 12.521190)



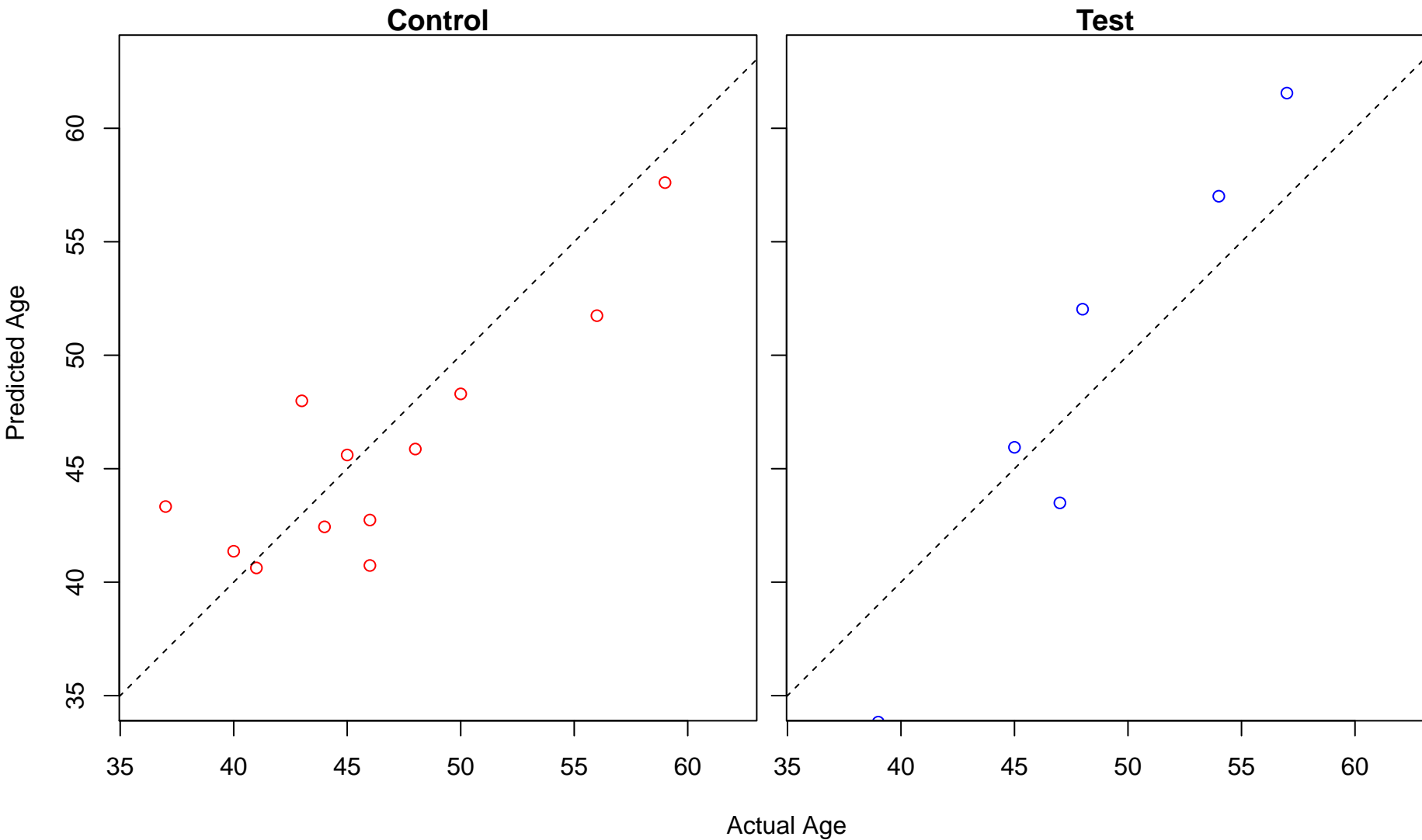
regulation of chromatin organization (Score: 12.499626)



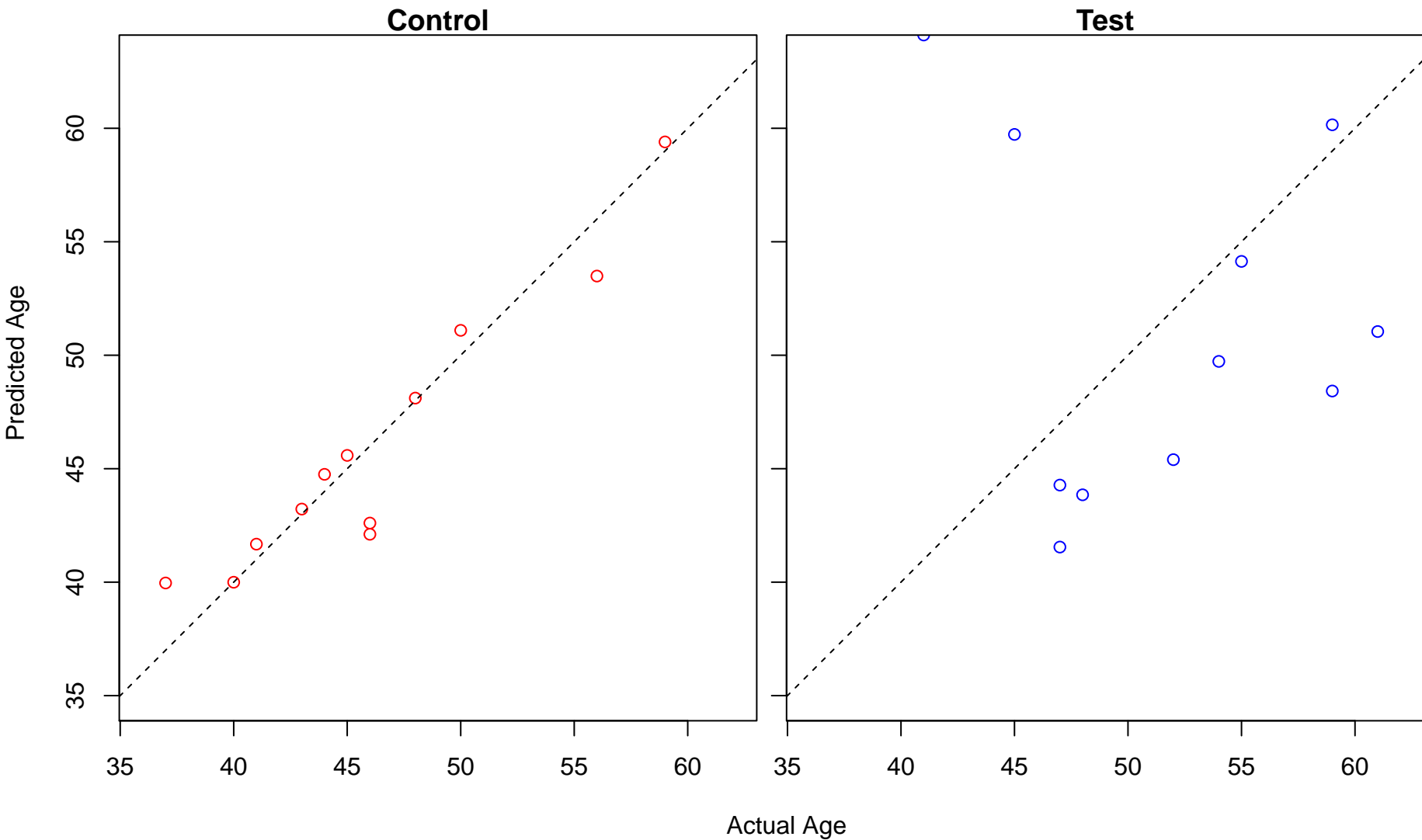
microvillus assembly (Score: 12.496678)



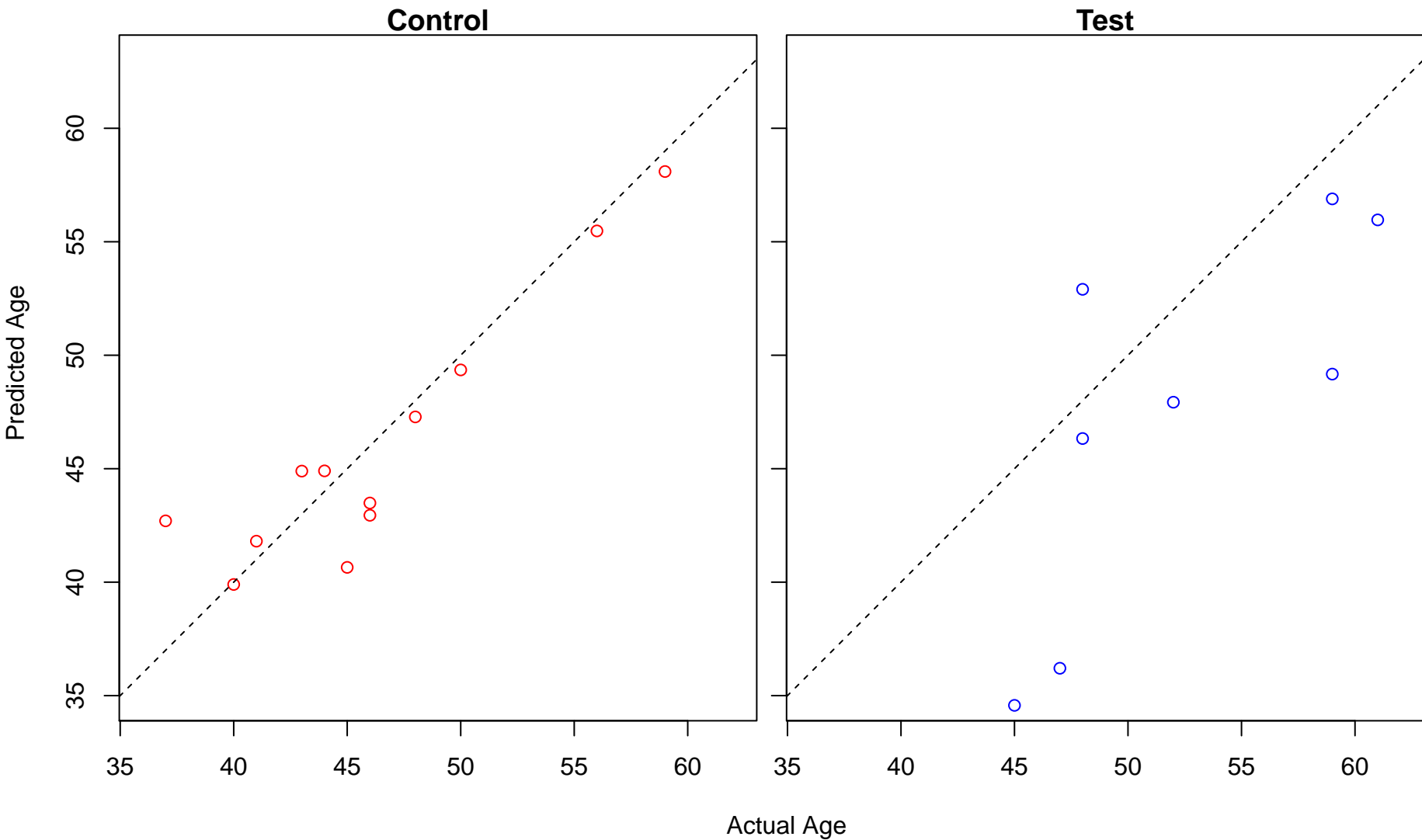
microvillus organization (Score: 12.496678)



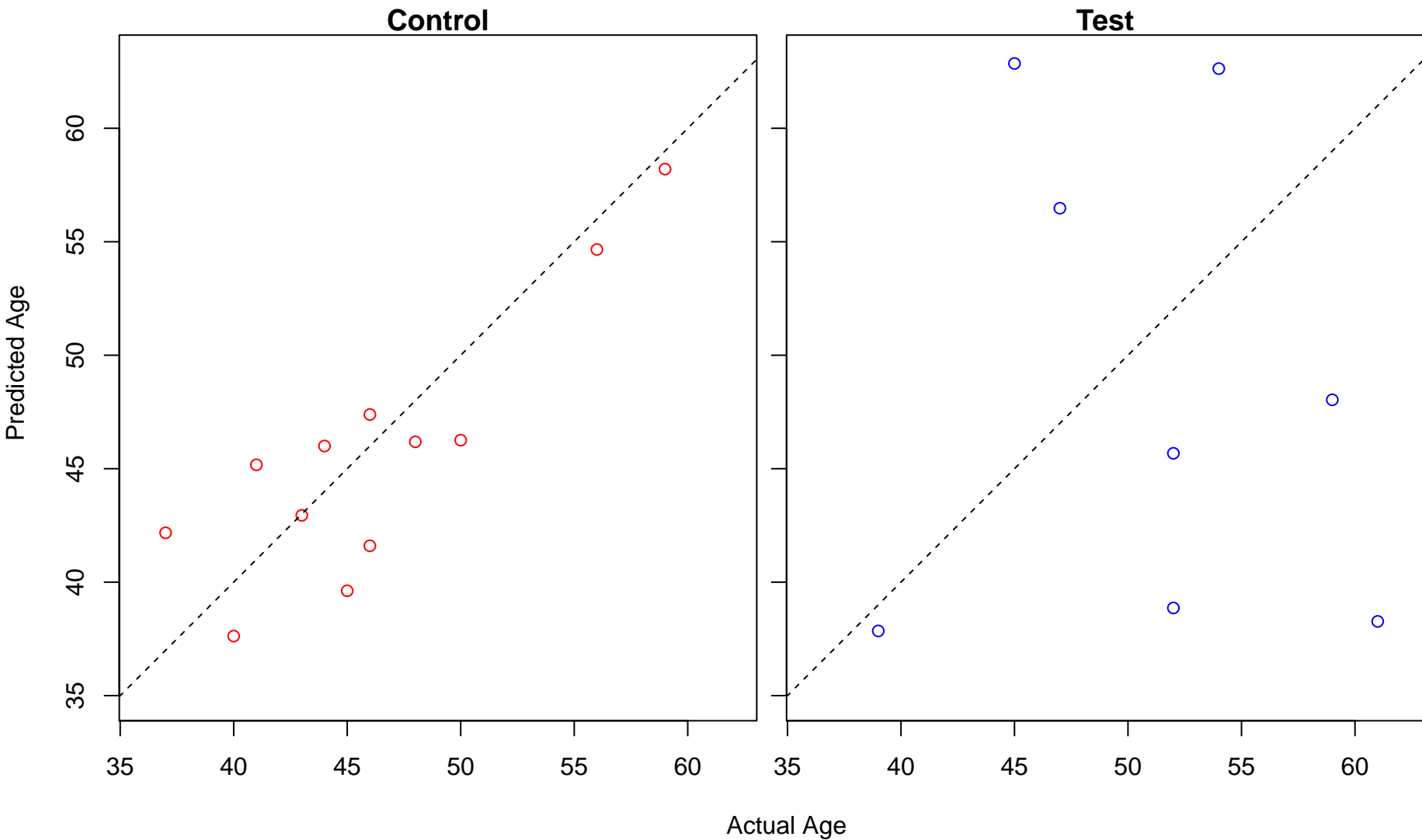
cellular response to starvation (Score: 12.453740)



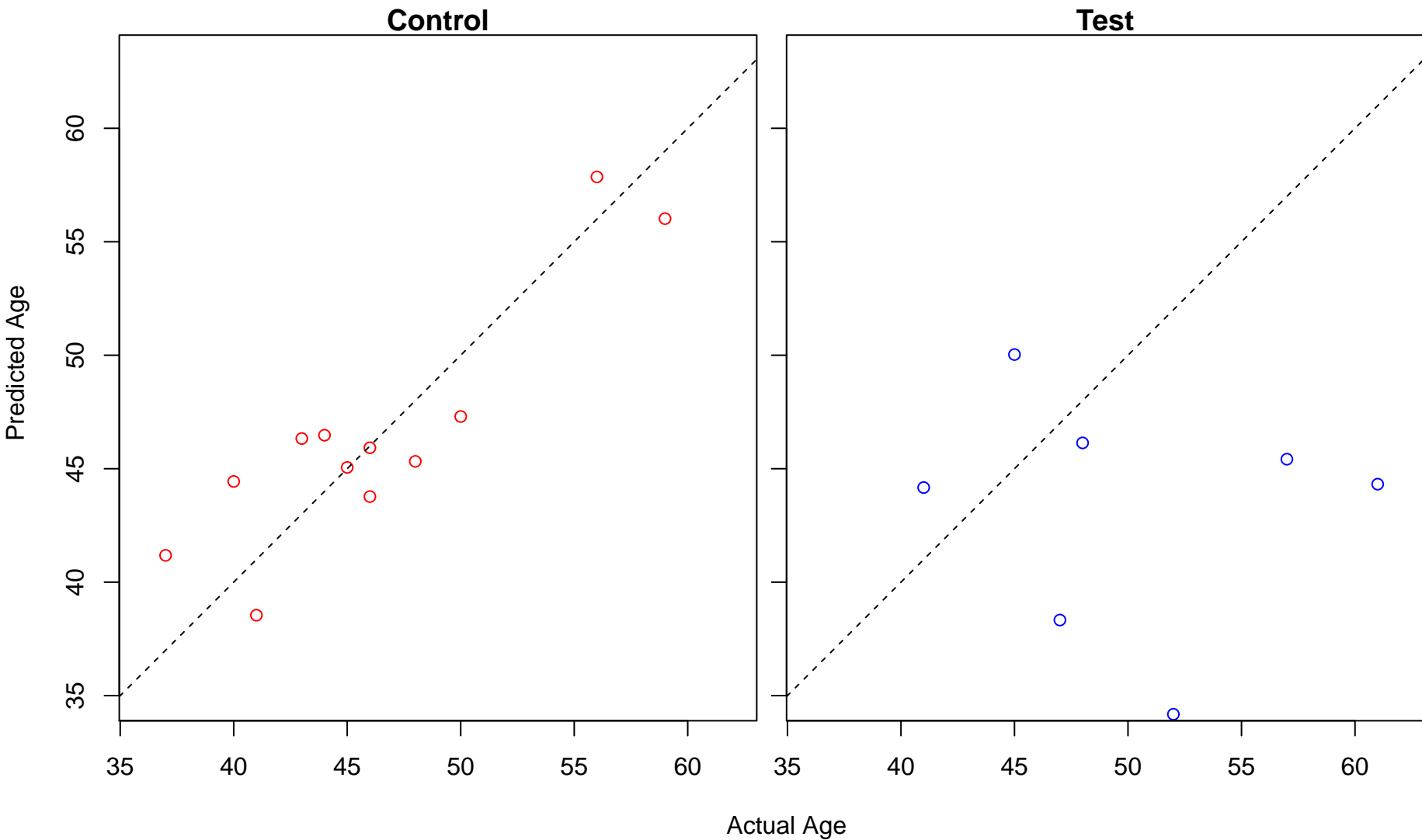
positive regulation of epithelial cell differentiation (Score: 12.397245)



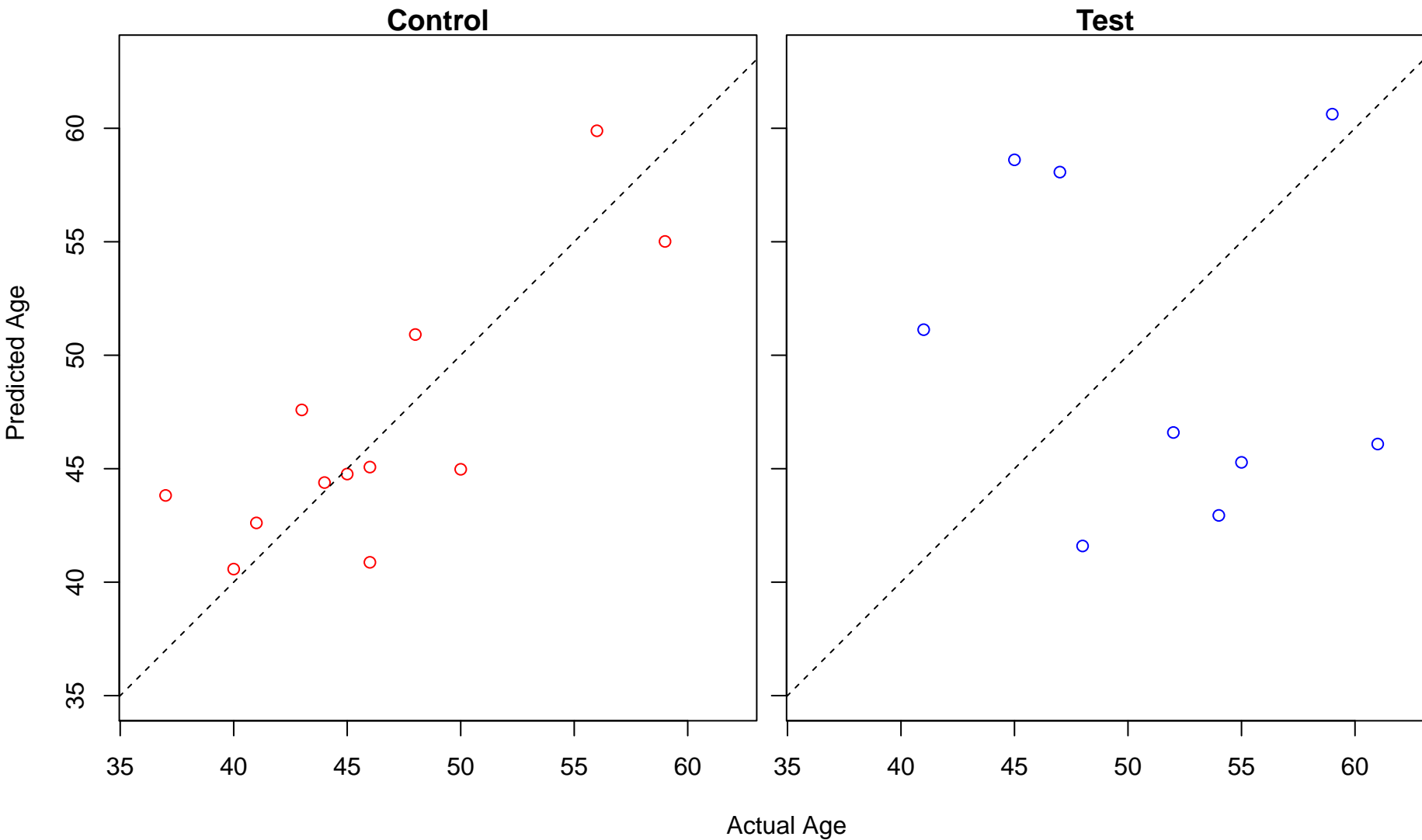
demethylation (Score: 12.360928)



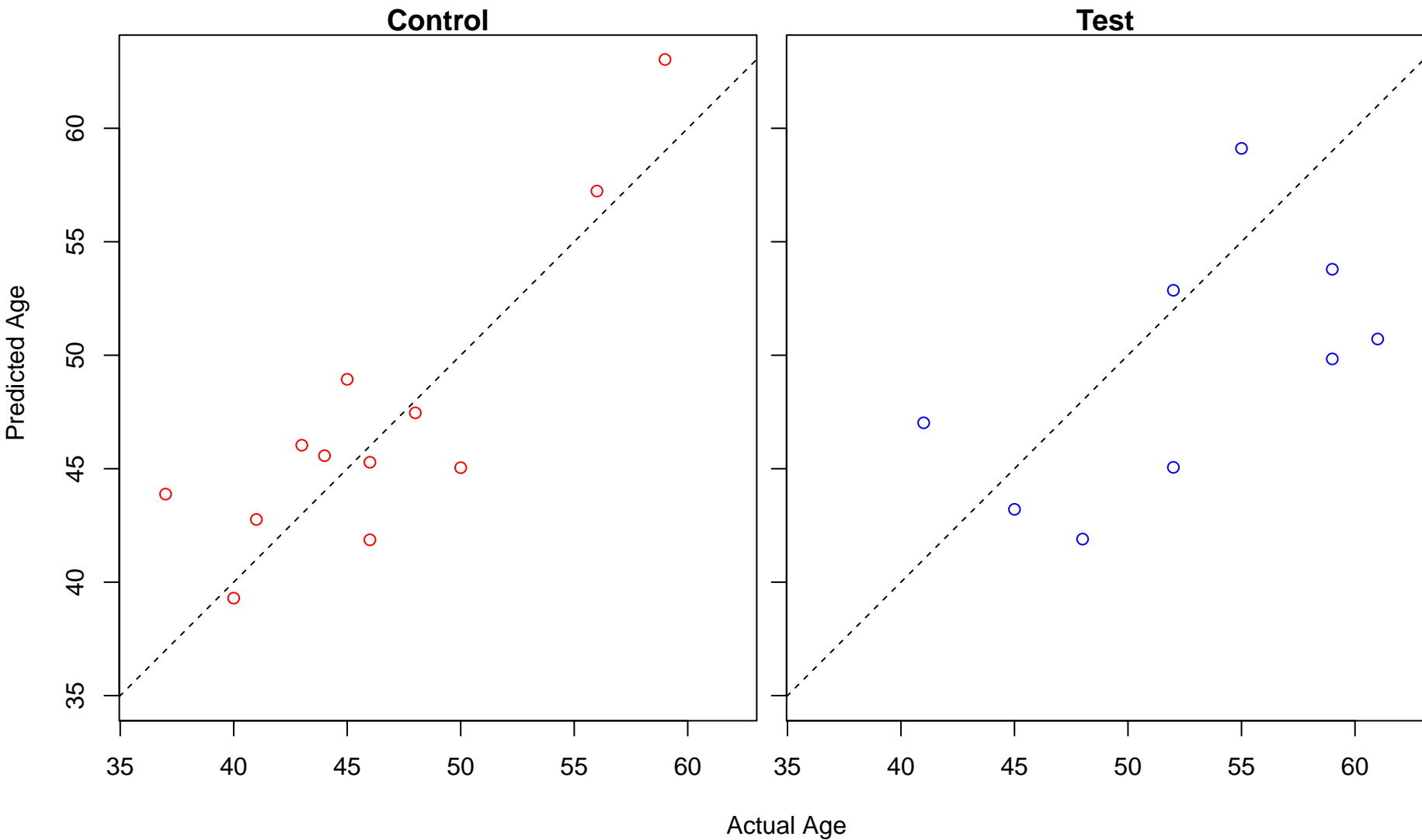
morphogenesis of a branching epithelium (Score: 12.342179)



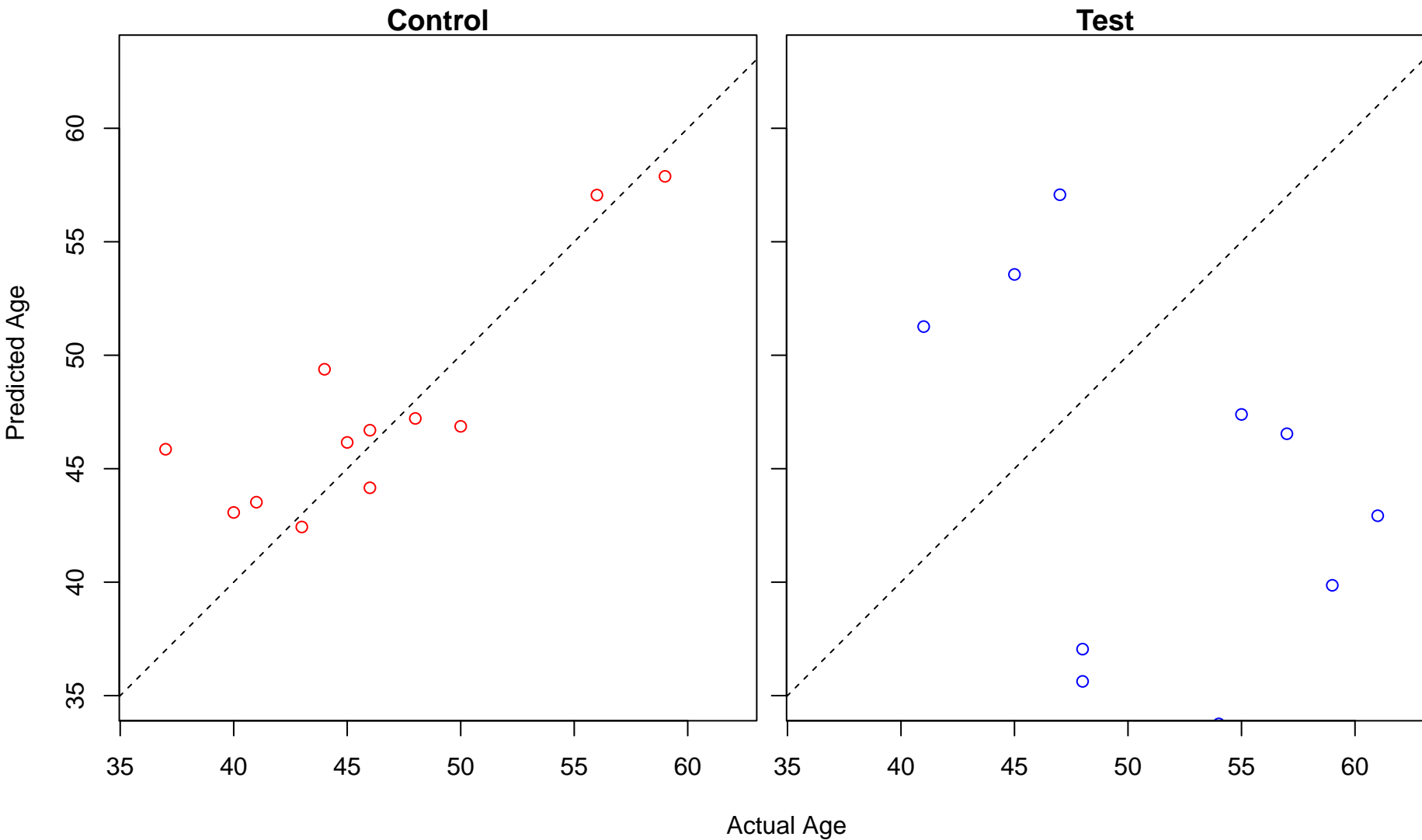
negative regulation of binding (Score: 12.273893)



regulation of phosphoprotein phosphatase activity (Score: 12.242602)

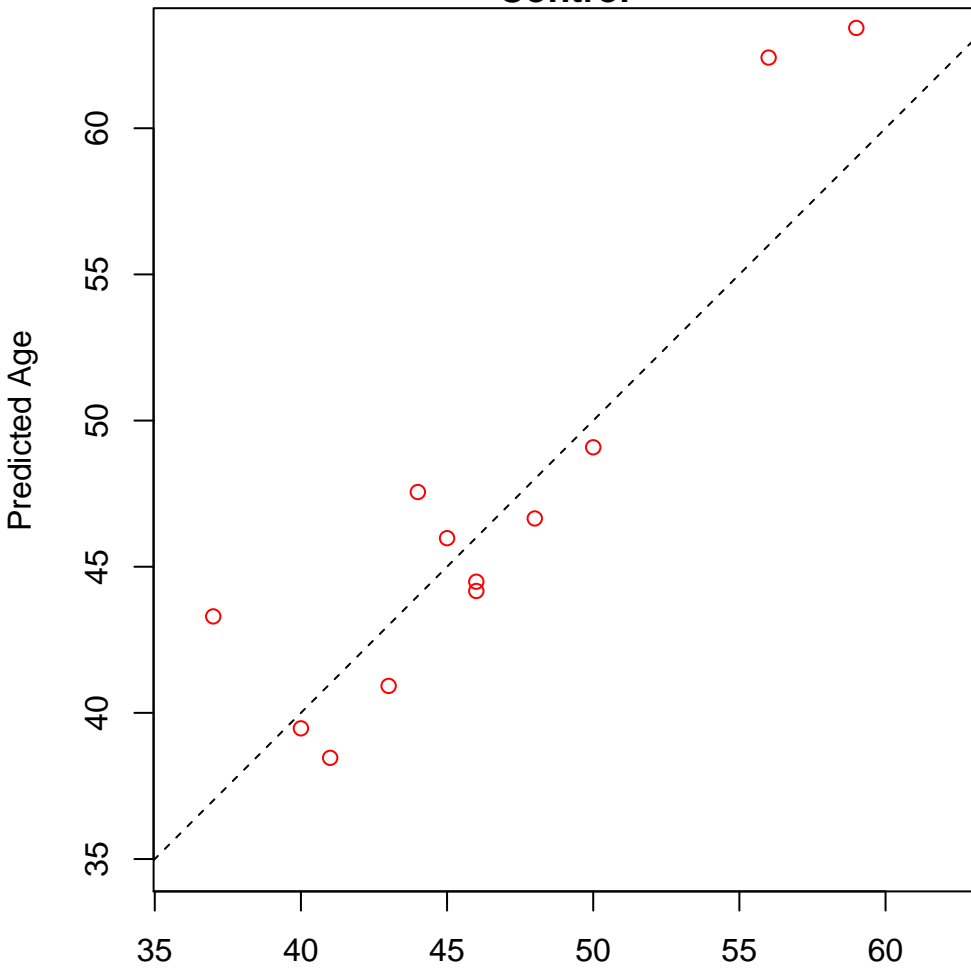


pyrimidine-containing compound catabolic process (Score: 12.214098)

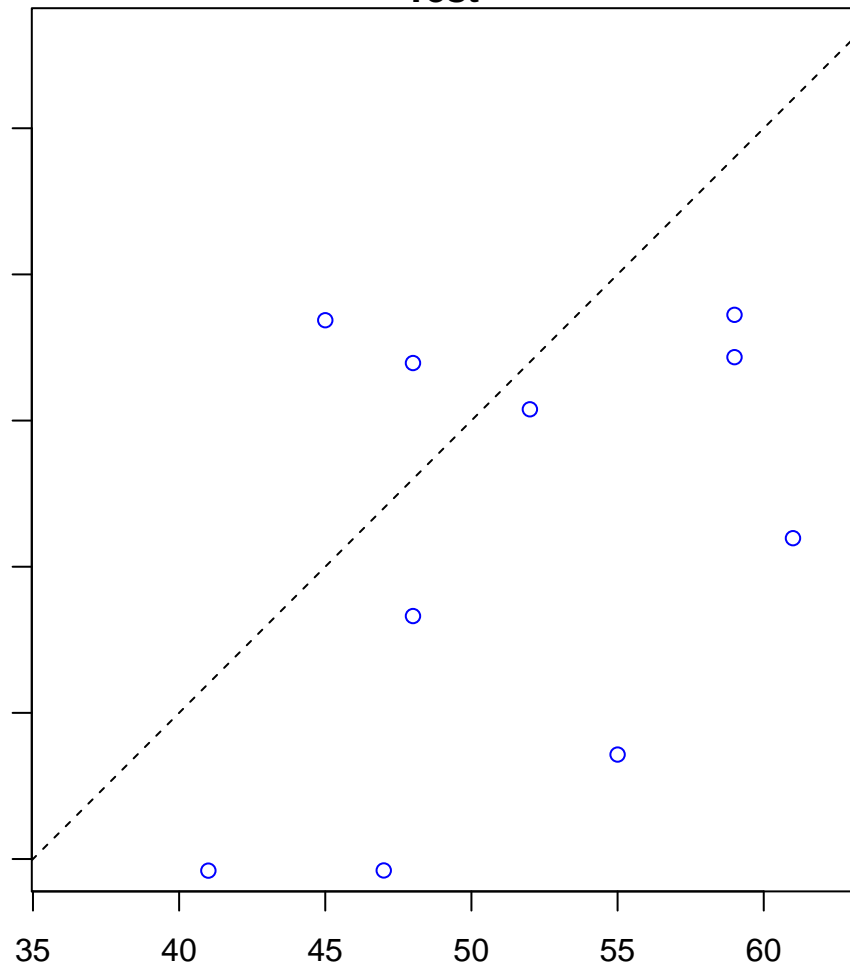


regulation of interleukin-5 production (Score: 12.178664)

Control

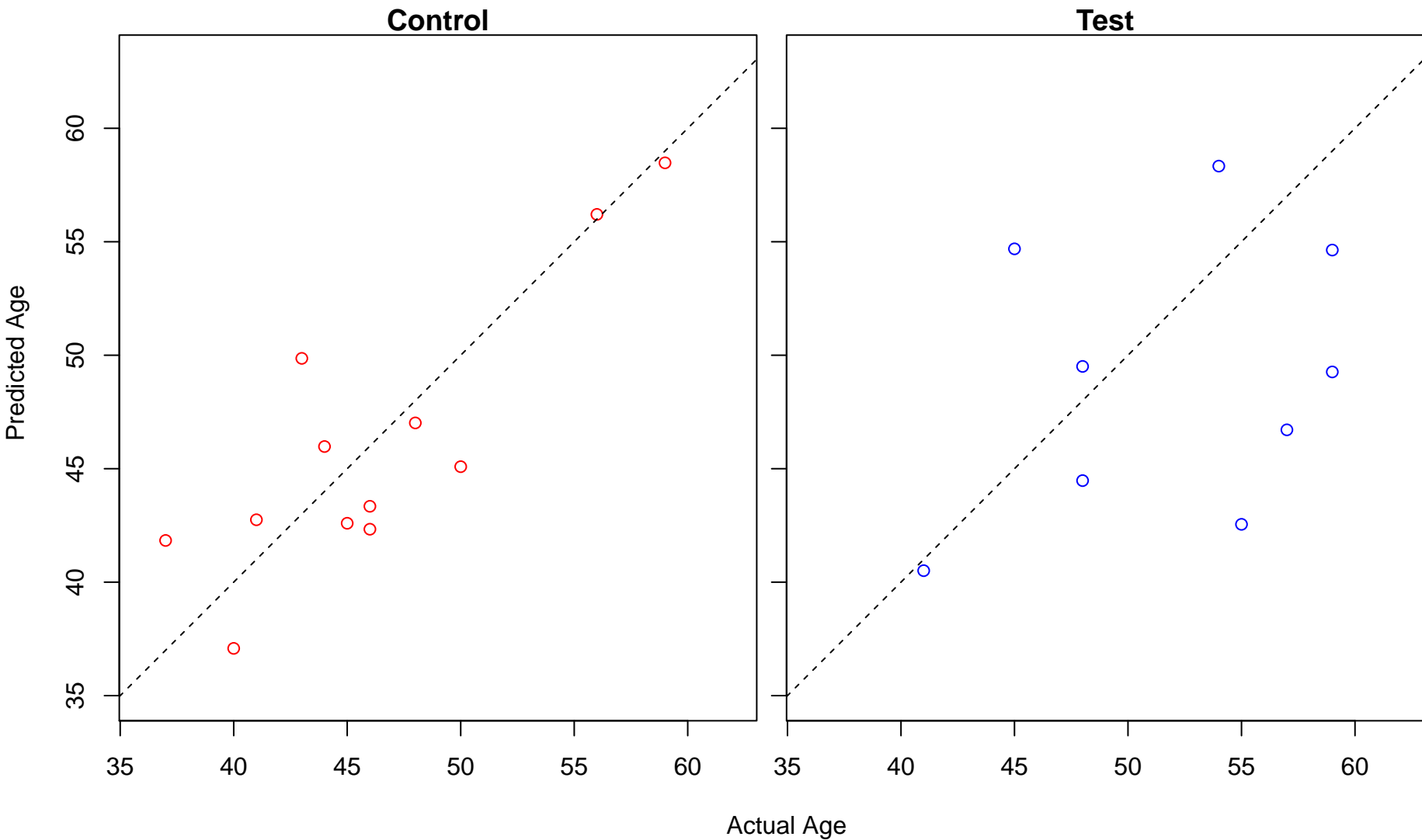


Test

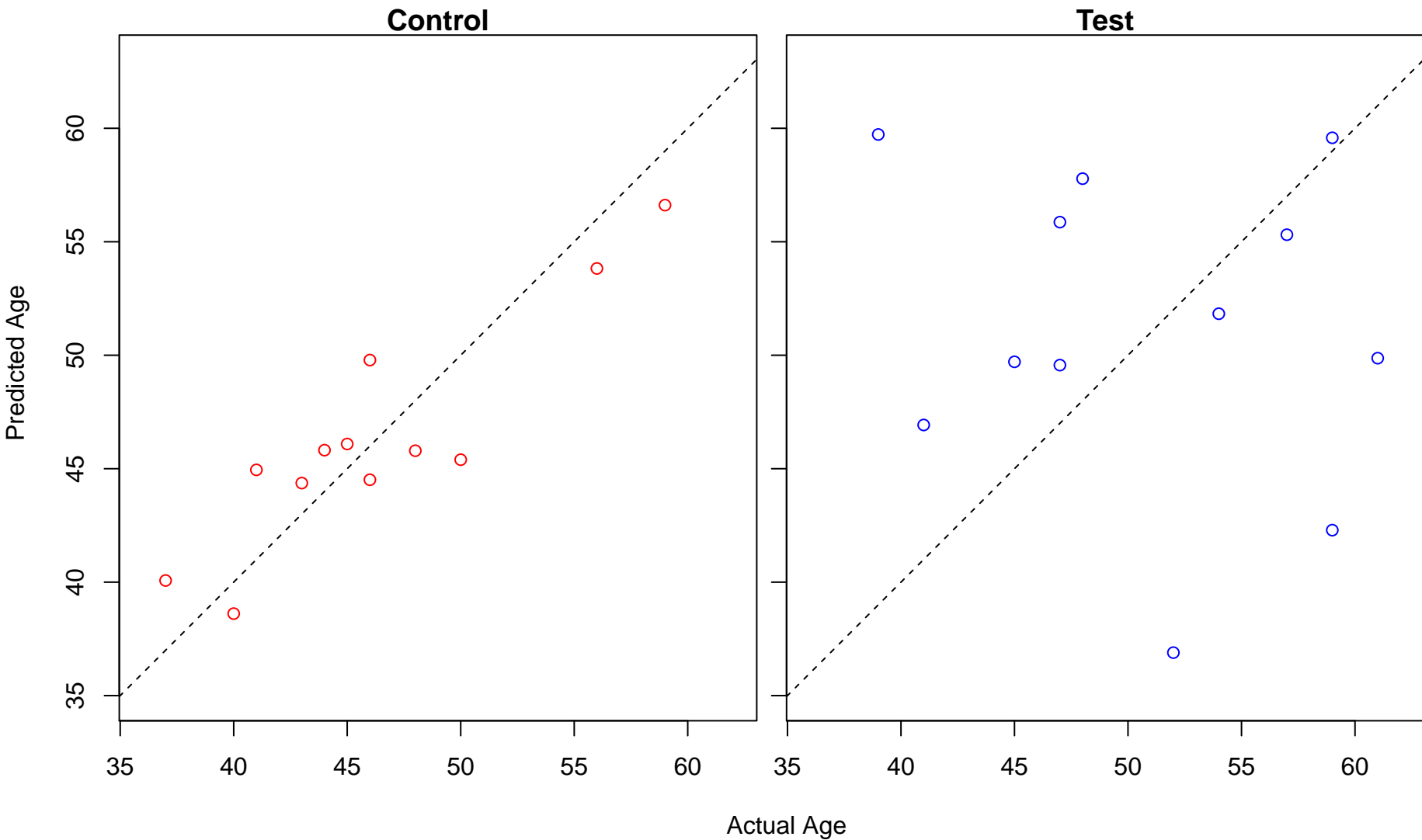


Actual Age

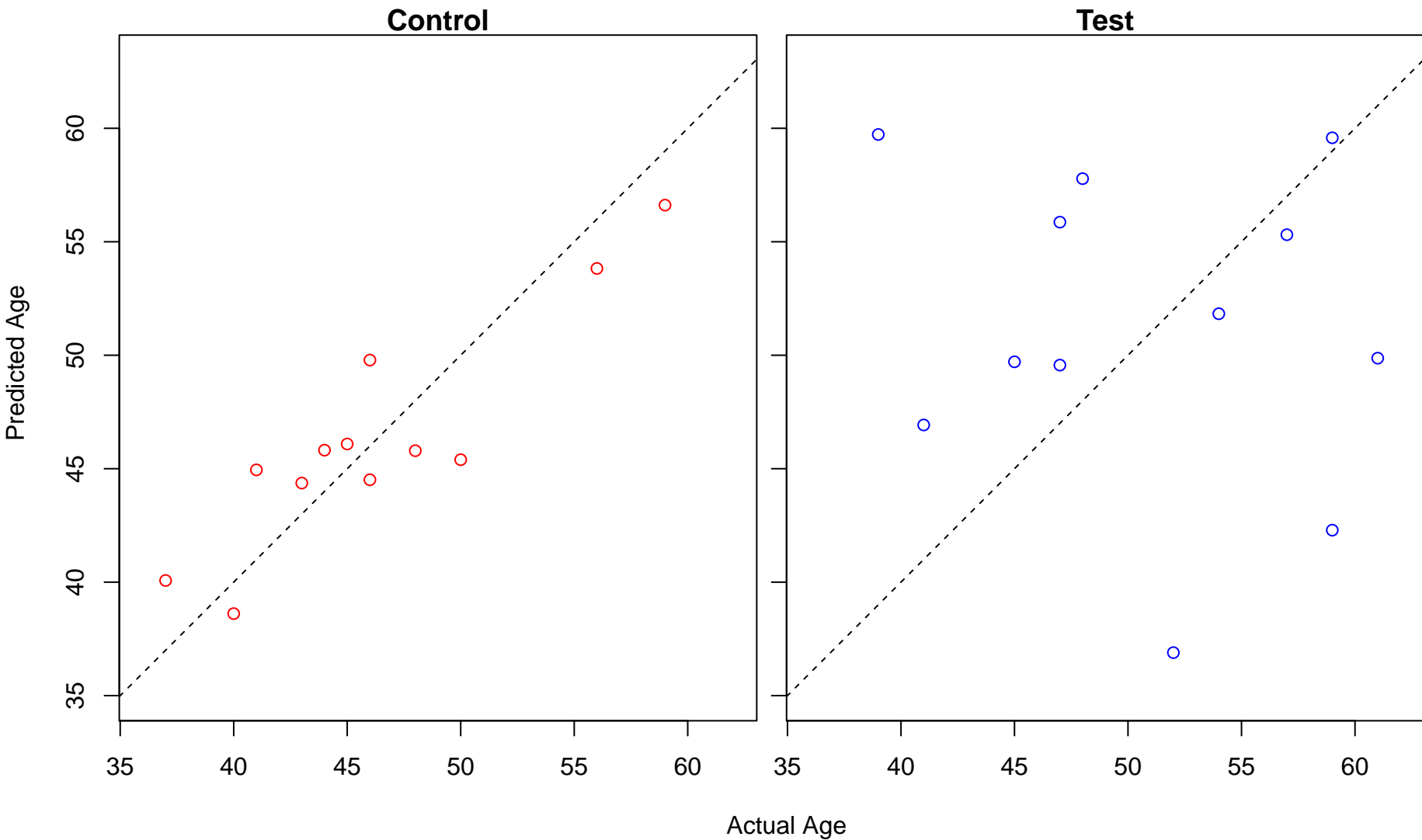
chromatin modification (Score: 12.149360)



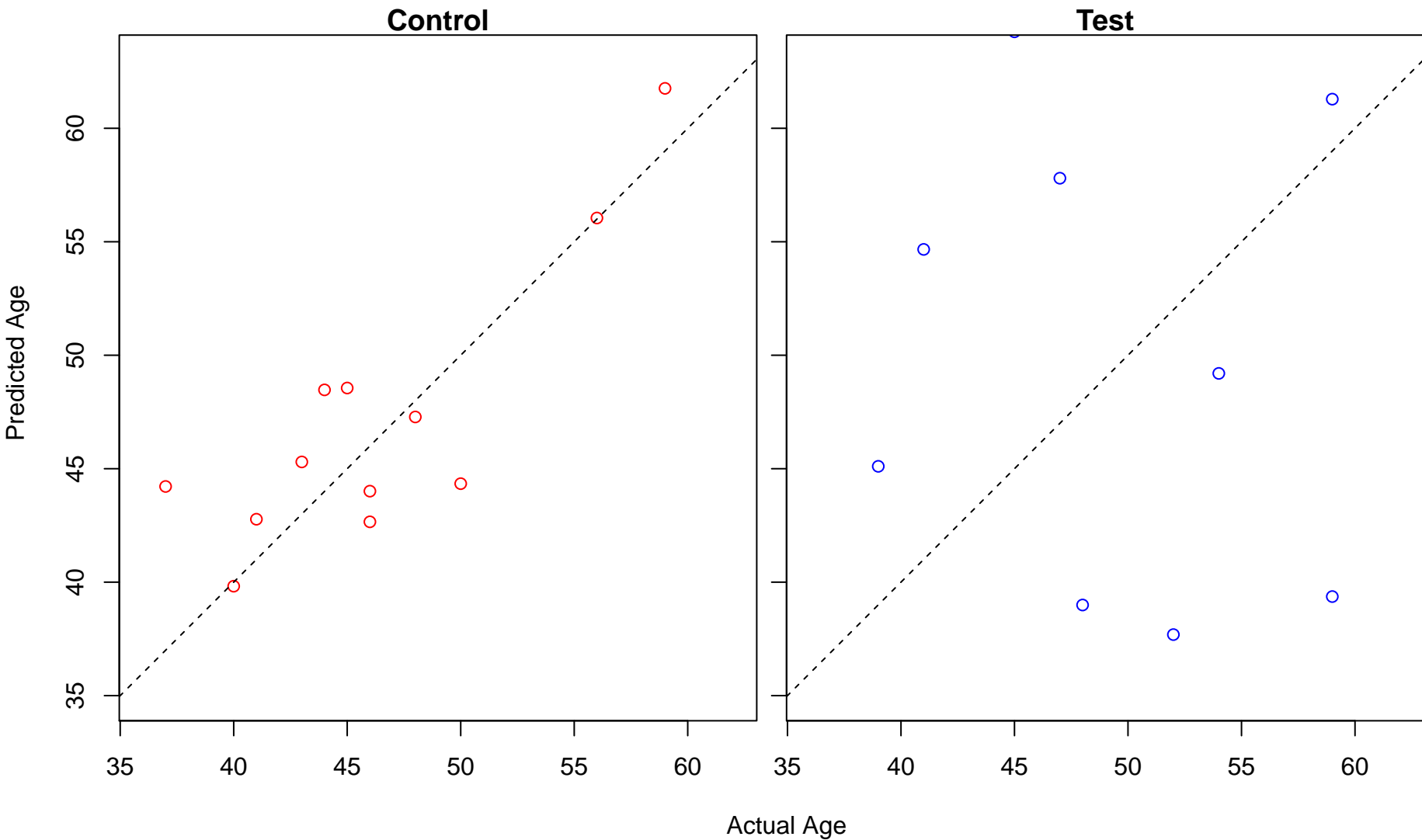
negative regulation of blood coagulation (Score: 12.131014)



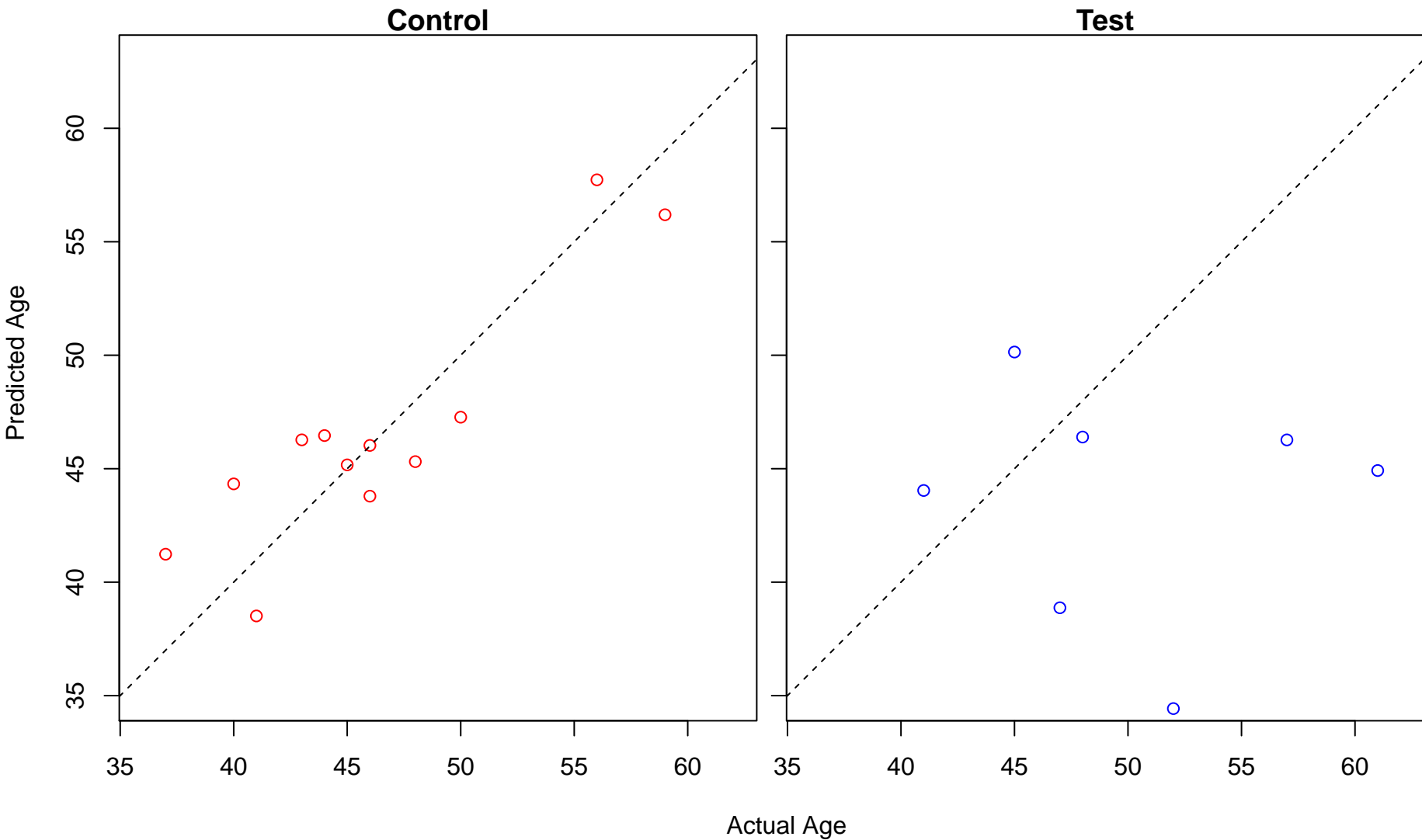
negative regulation of hemostasis (Score: 12.131014)



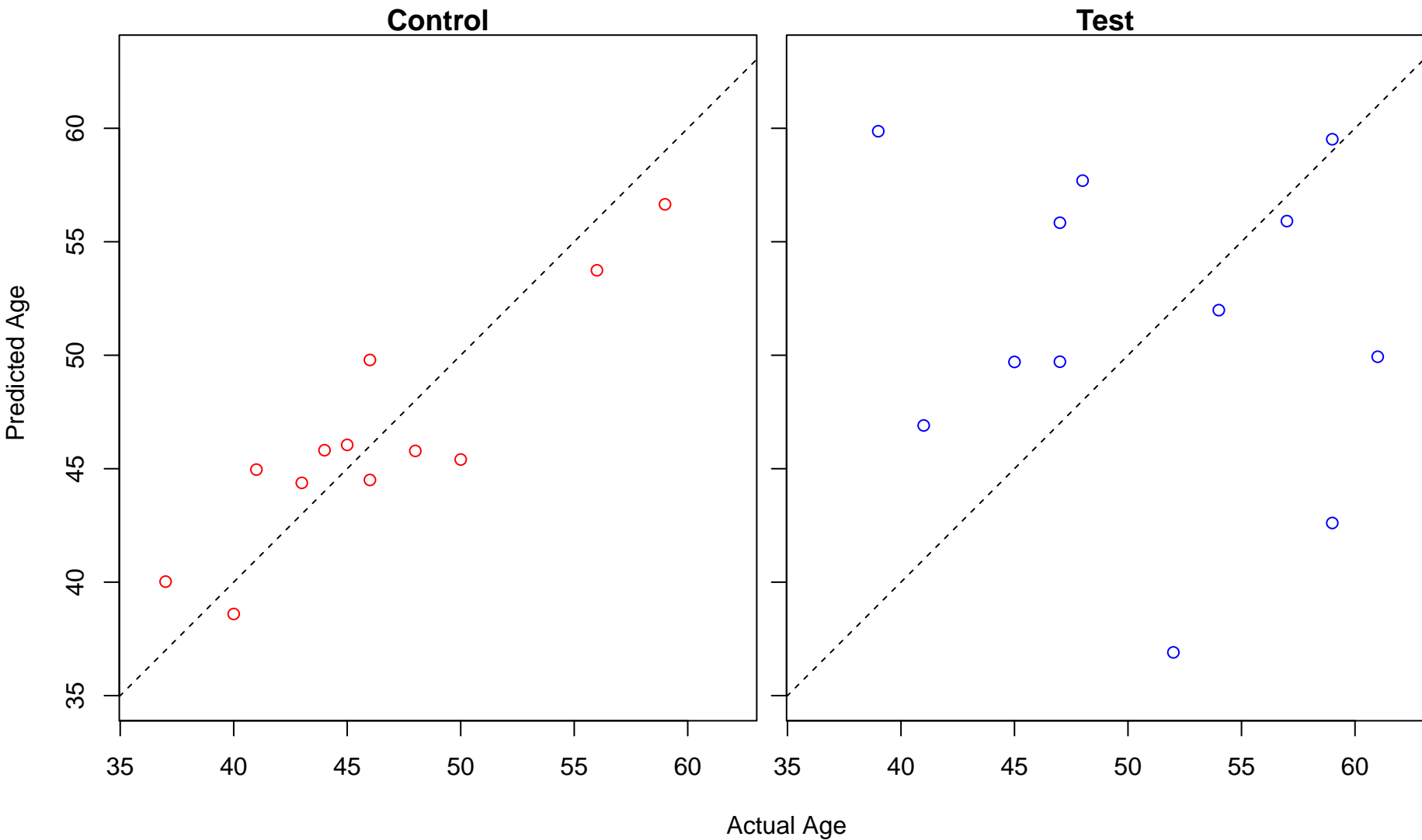
positive regulation of JNK cascade (Score: 12.079136)



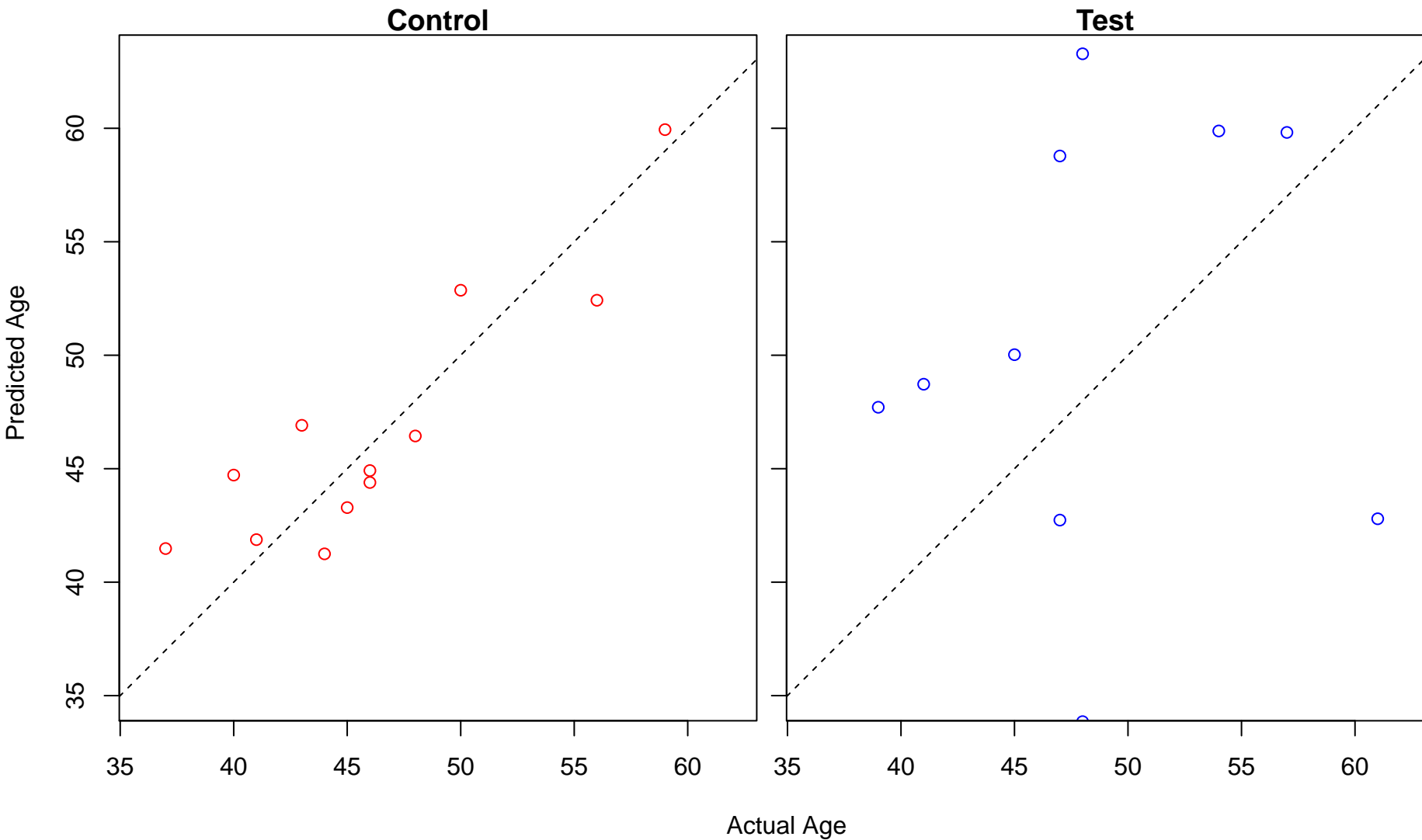
morphogenesis of a branching structure (Score: 12.072459)



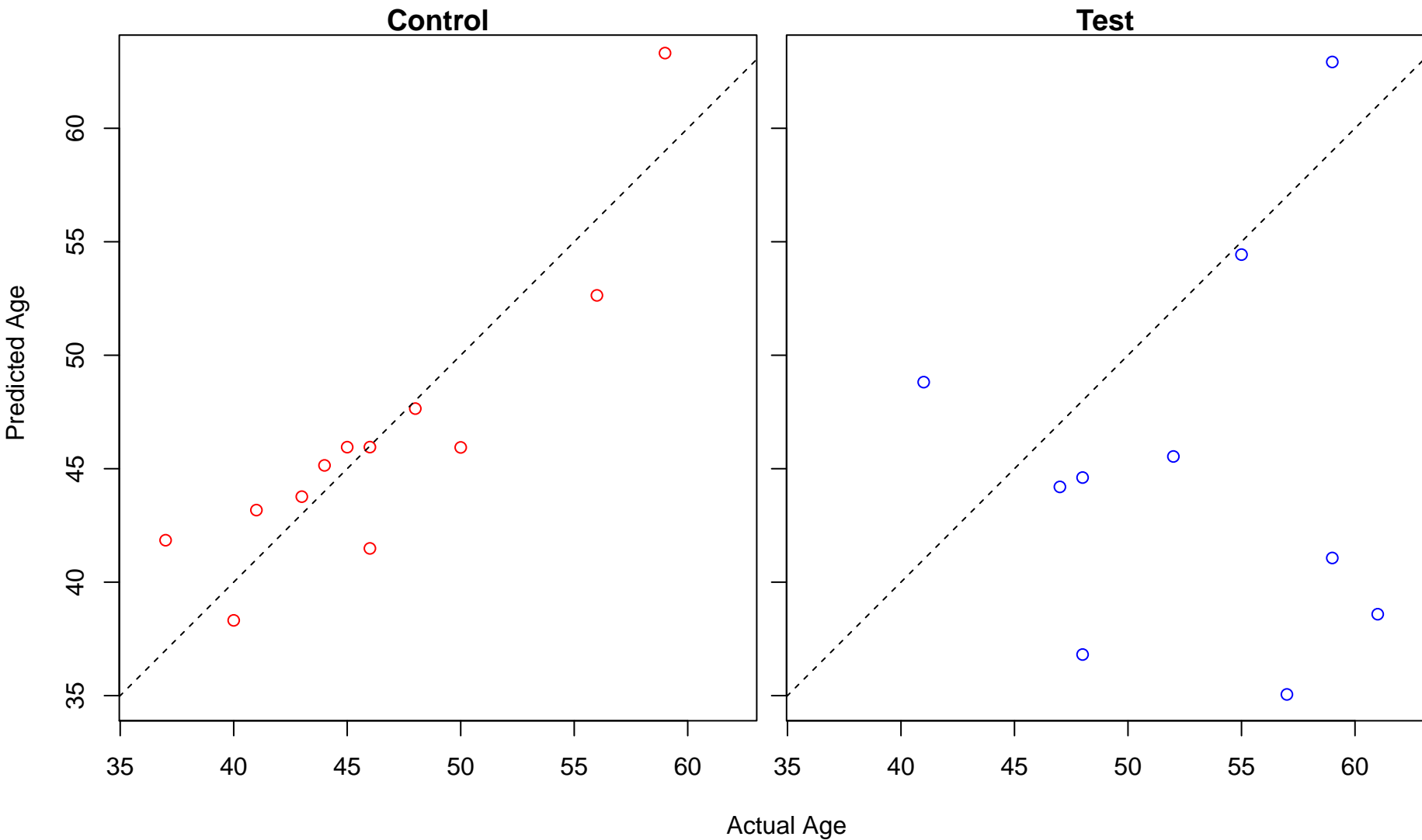
negative regulation of coagulation (Score: 12.059164)



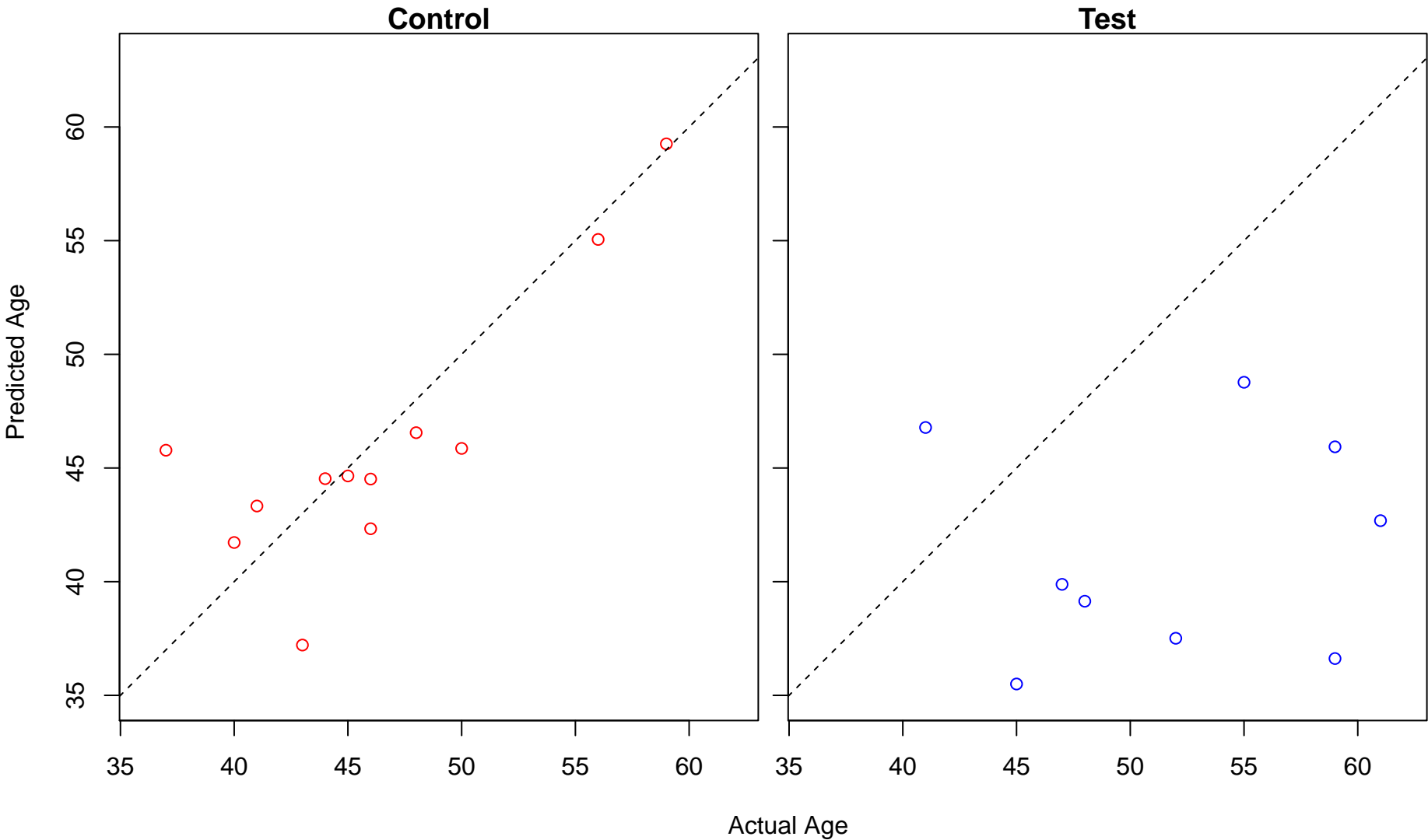
regulation of protein kinase C signaling (Score: 12.053062)



adenine transport (Score: 12.040660)

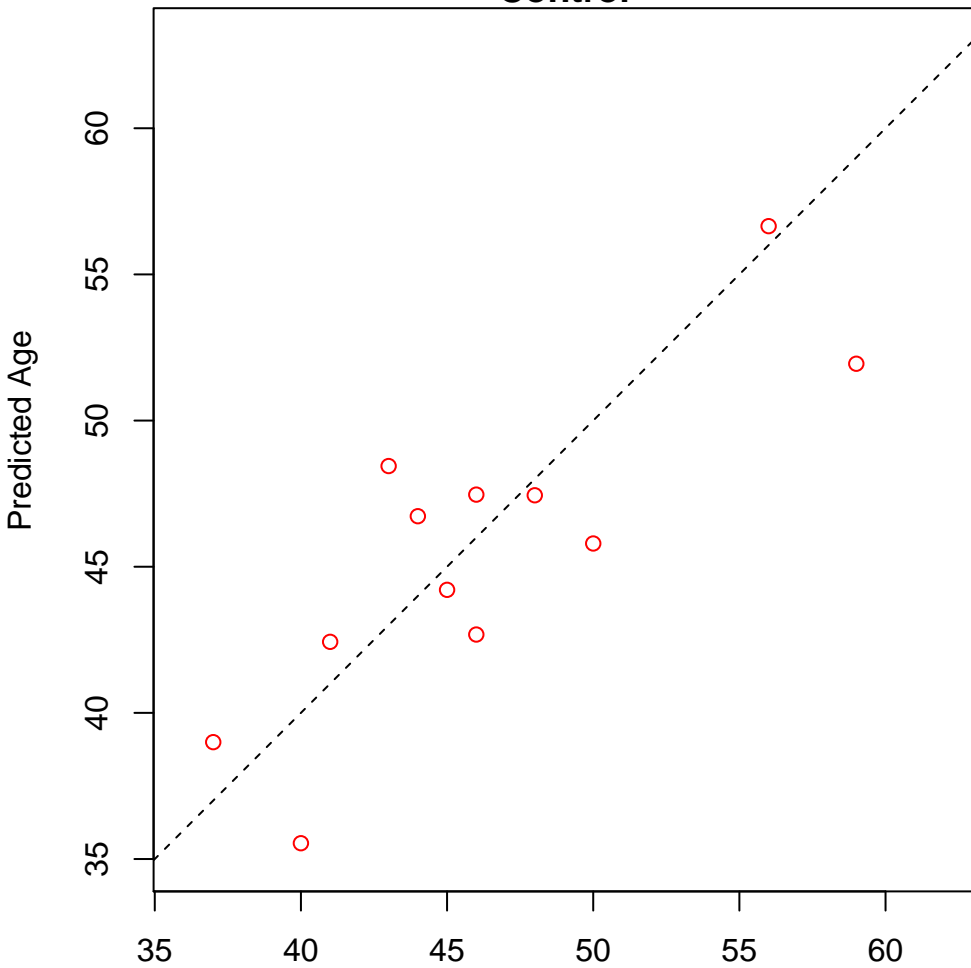


establishment of endothelial intestinal barrier (Score: 12.006920)

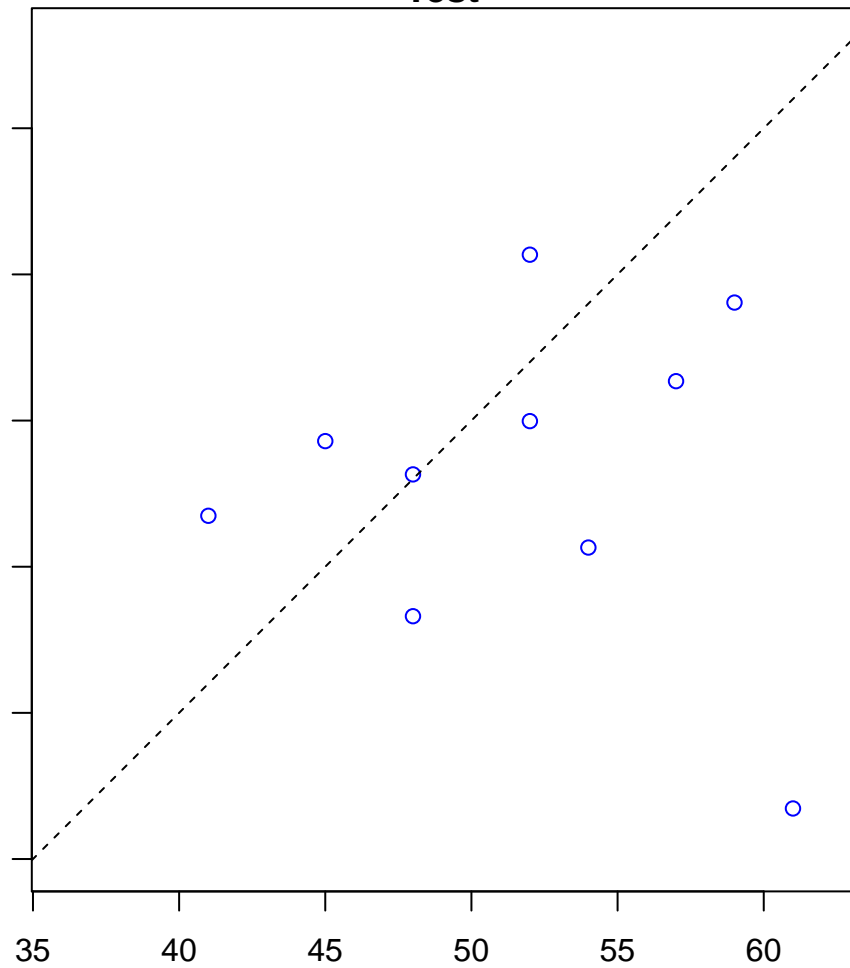


cardiac endothelial cell differentiation (Score: 11.926079)

Control

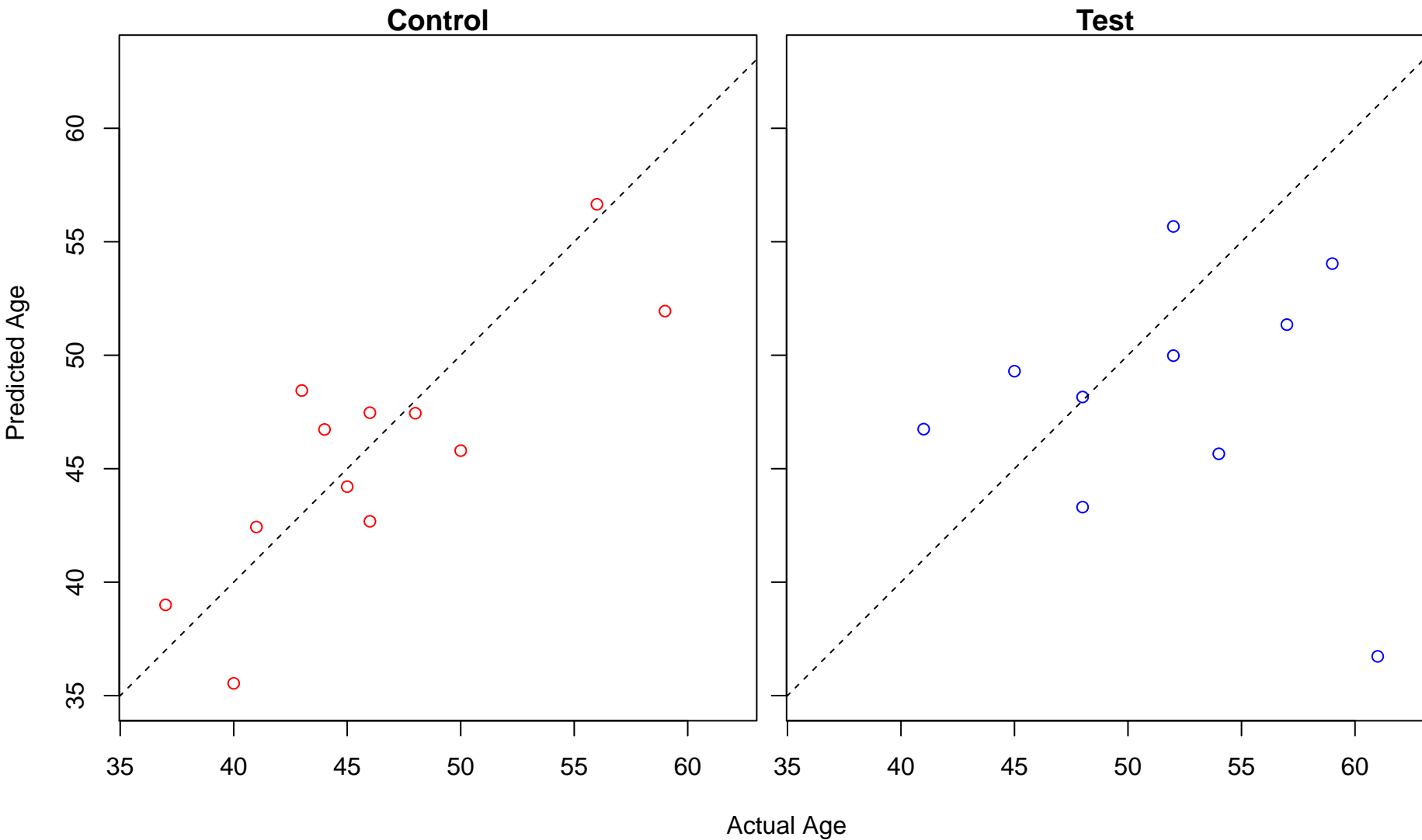


Test

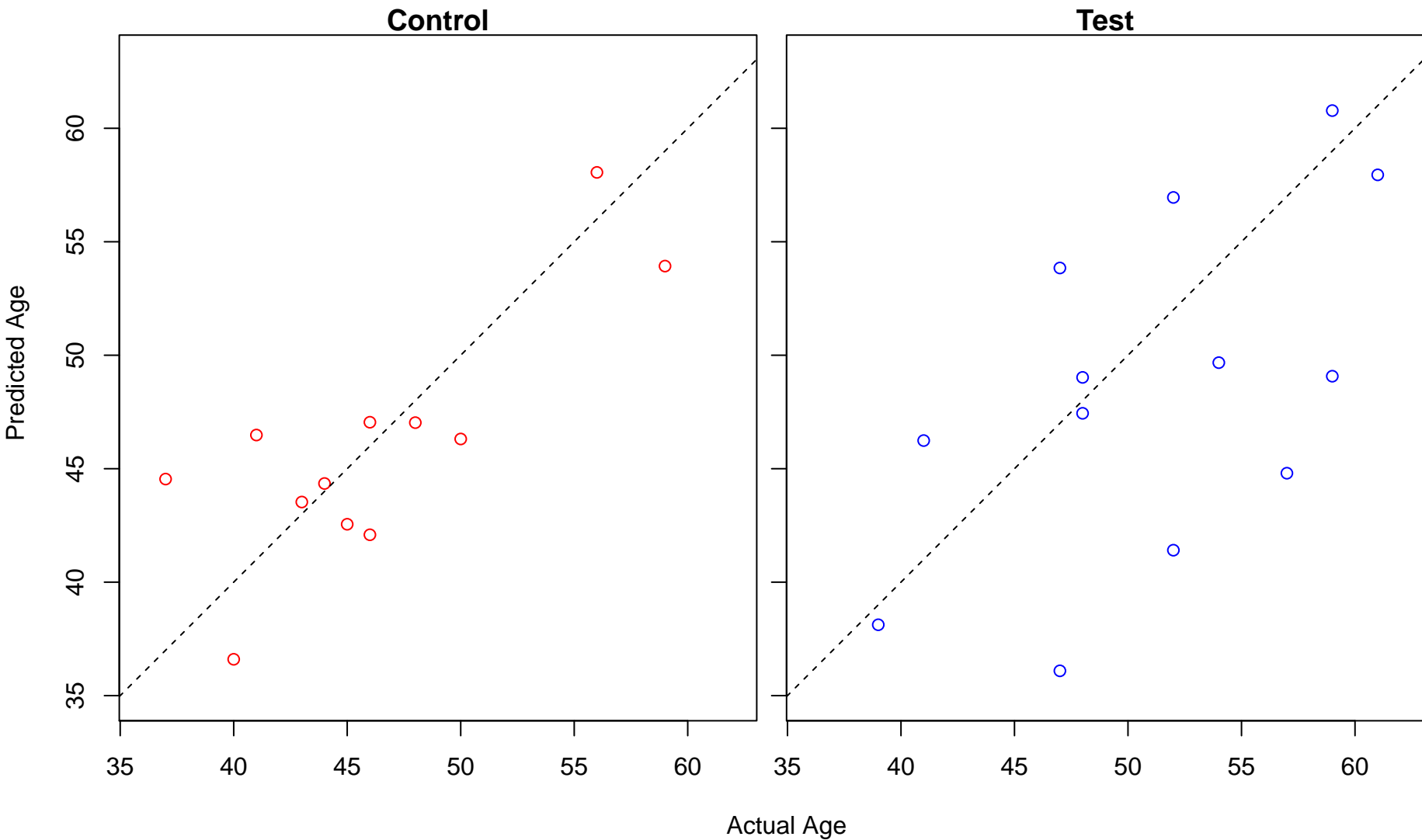


Actual Age

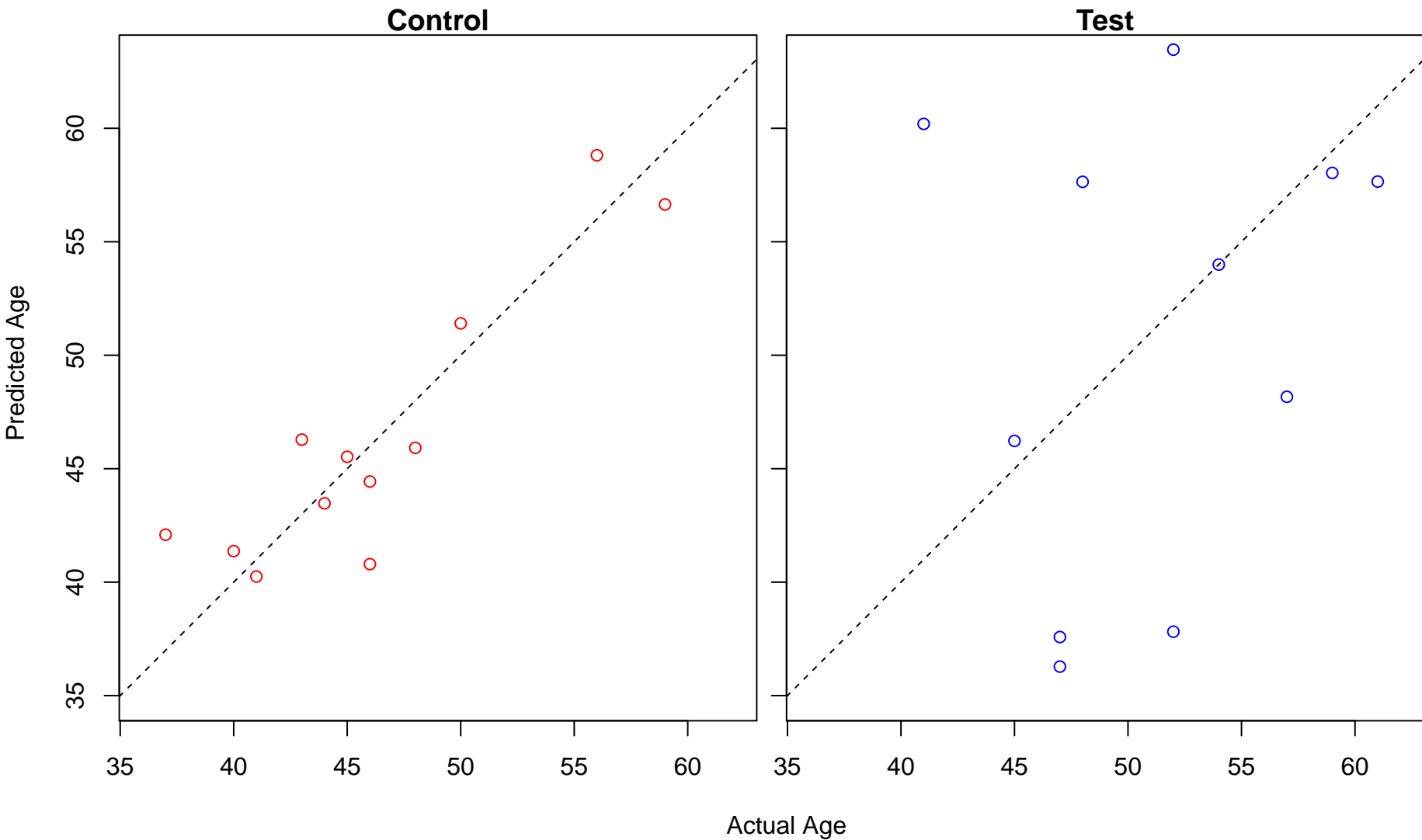
endocardial cell differentiation (Score: 11.926079)



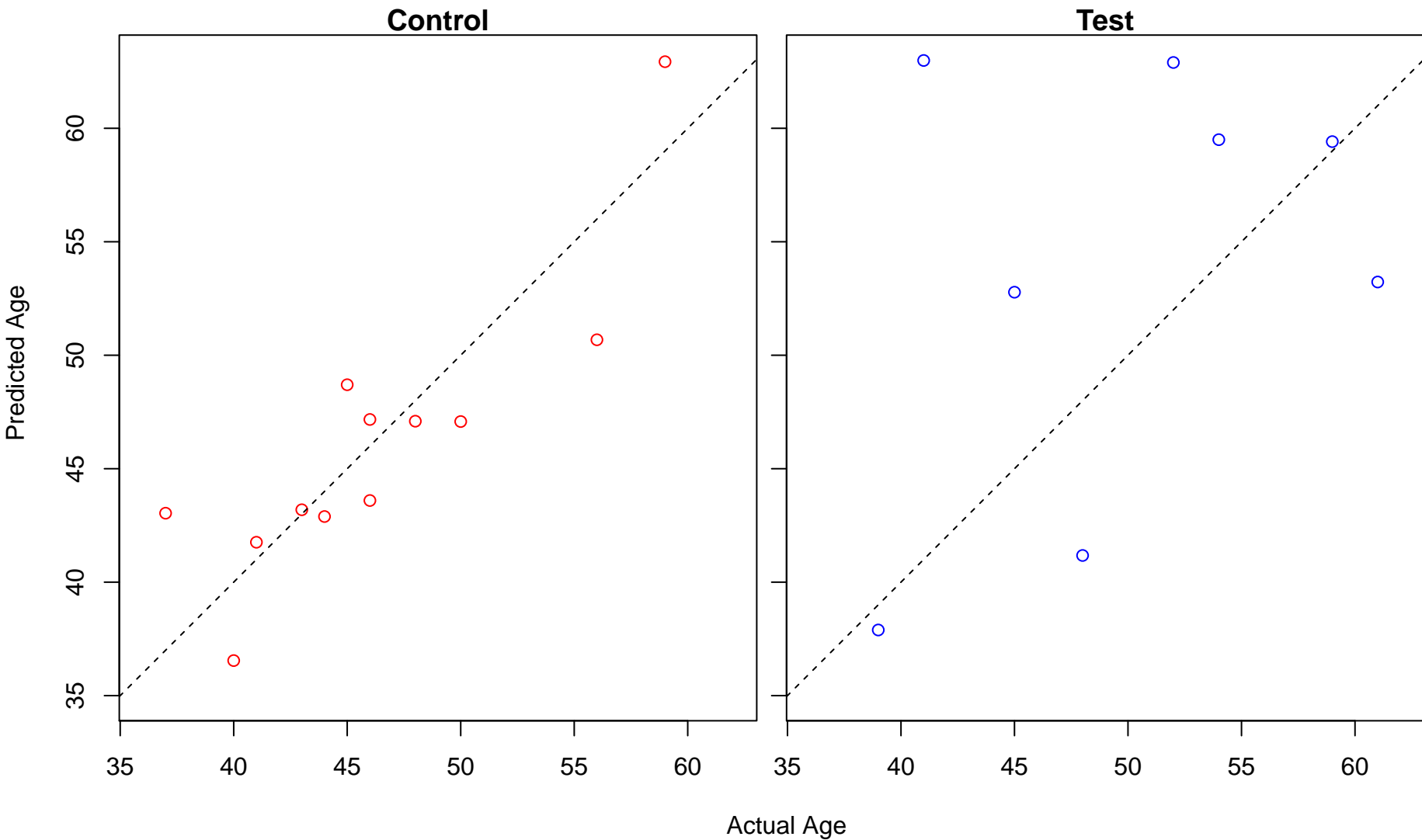
regulation of macrophage derived foam cell differentiation (Score: 11.923438)



negative regulation of interleukin-2 production (Score: 11.848713)

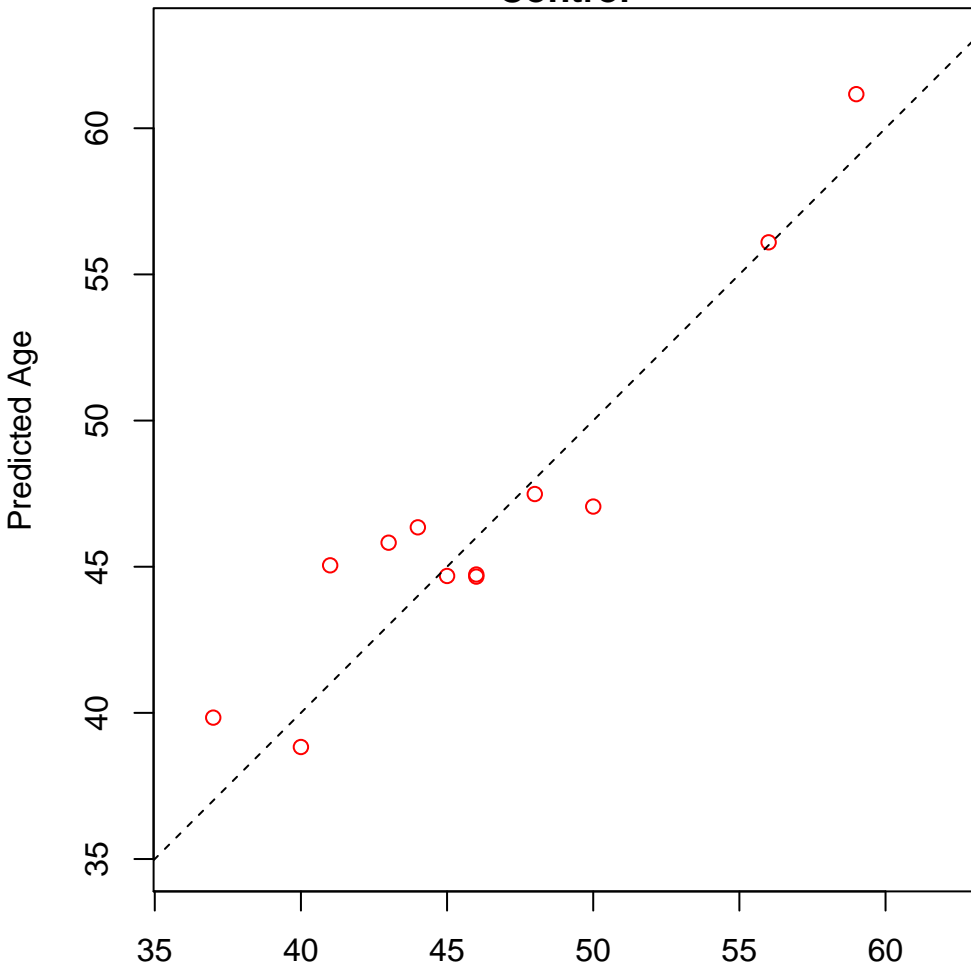


endocrine process (Score: 11.773046)

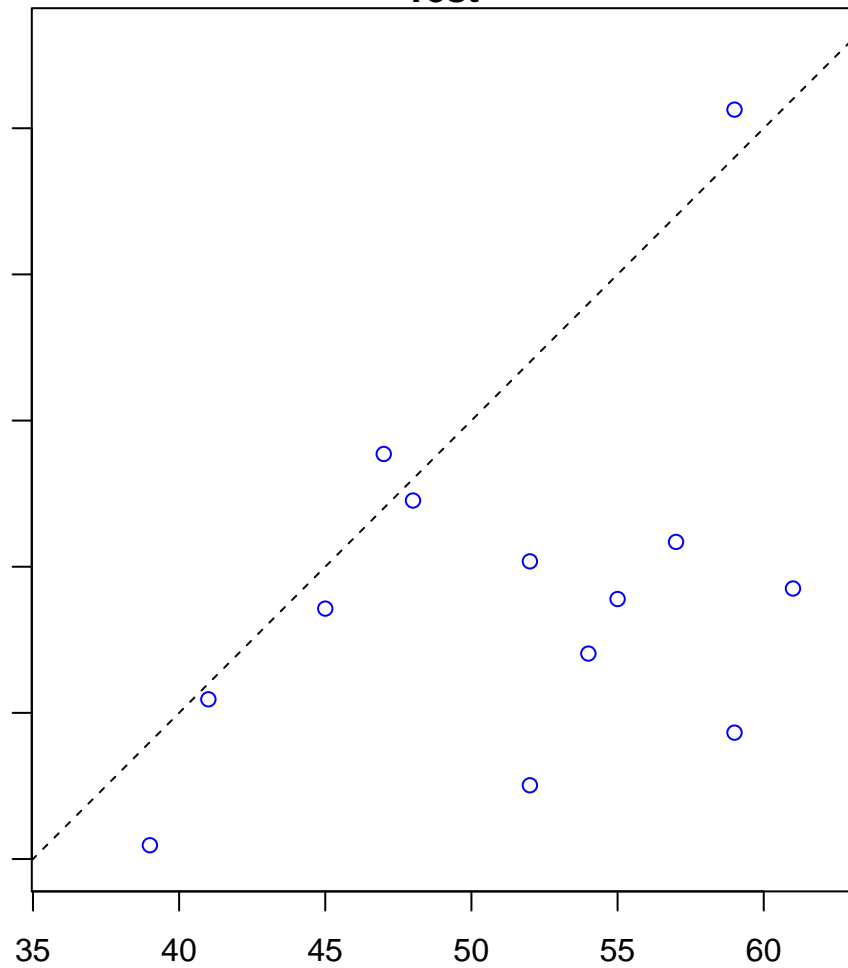


cyclic-nucleotide-mediated signaling (Score: 11.754927)

Control

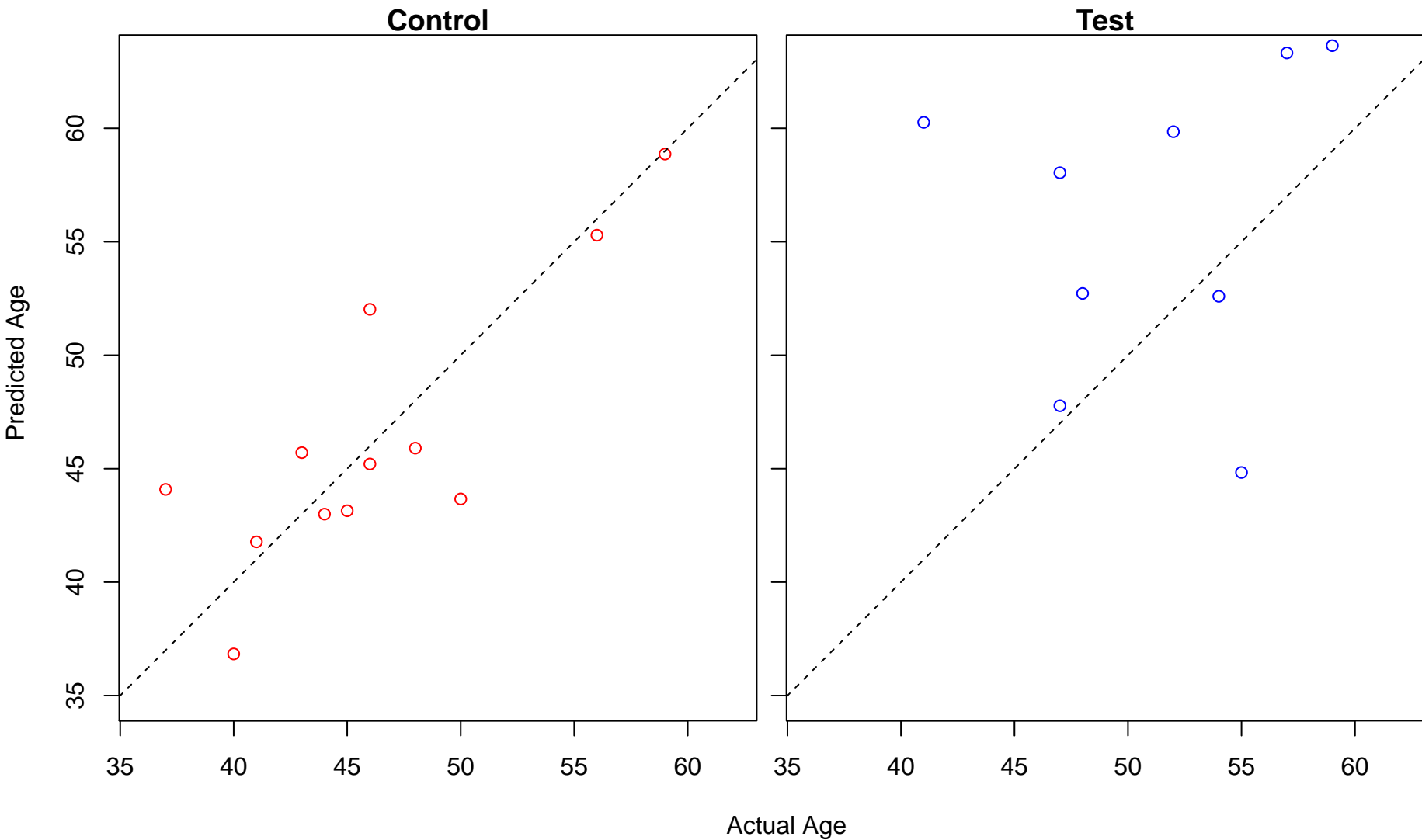


Test

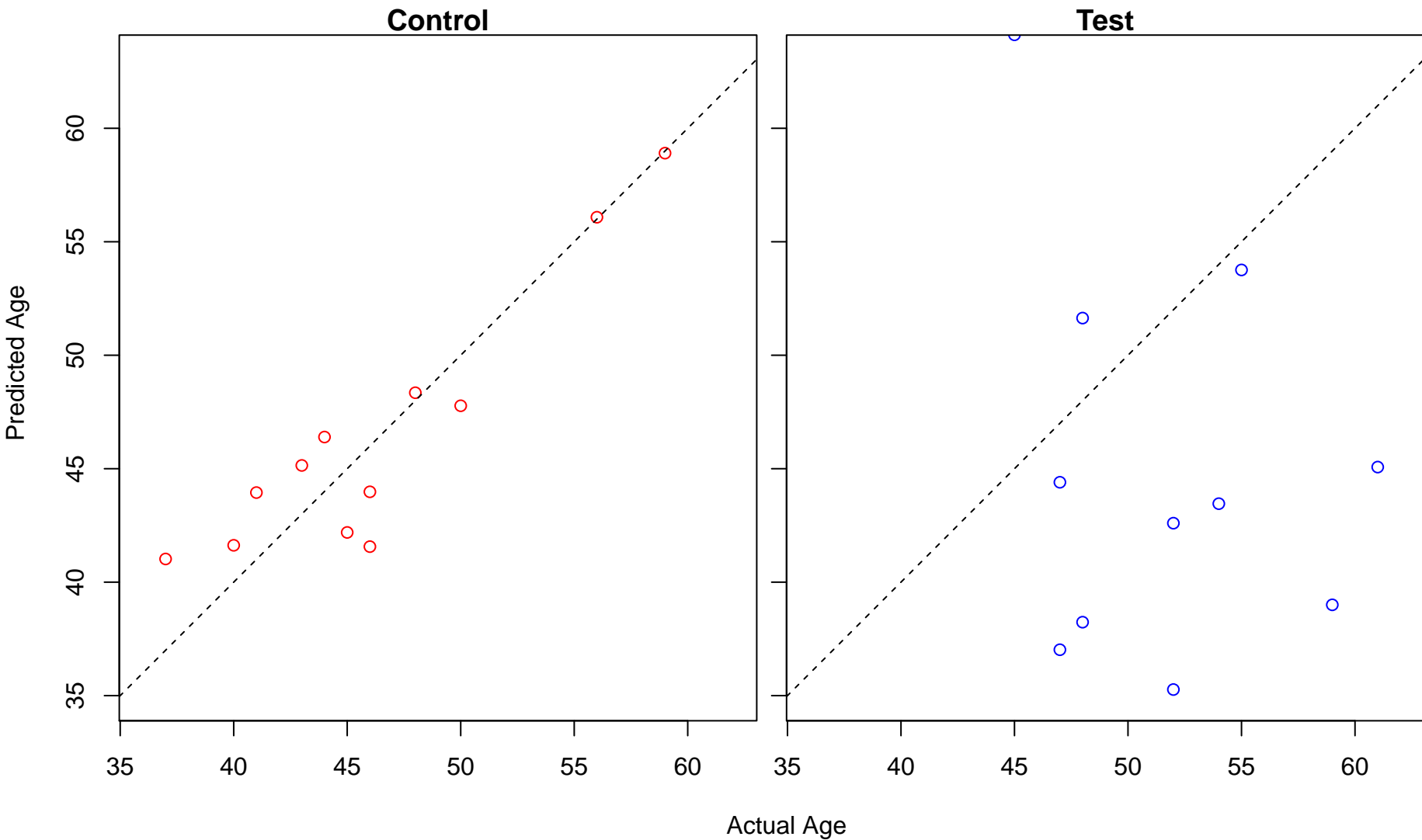


Actual Age

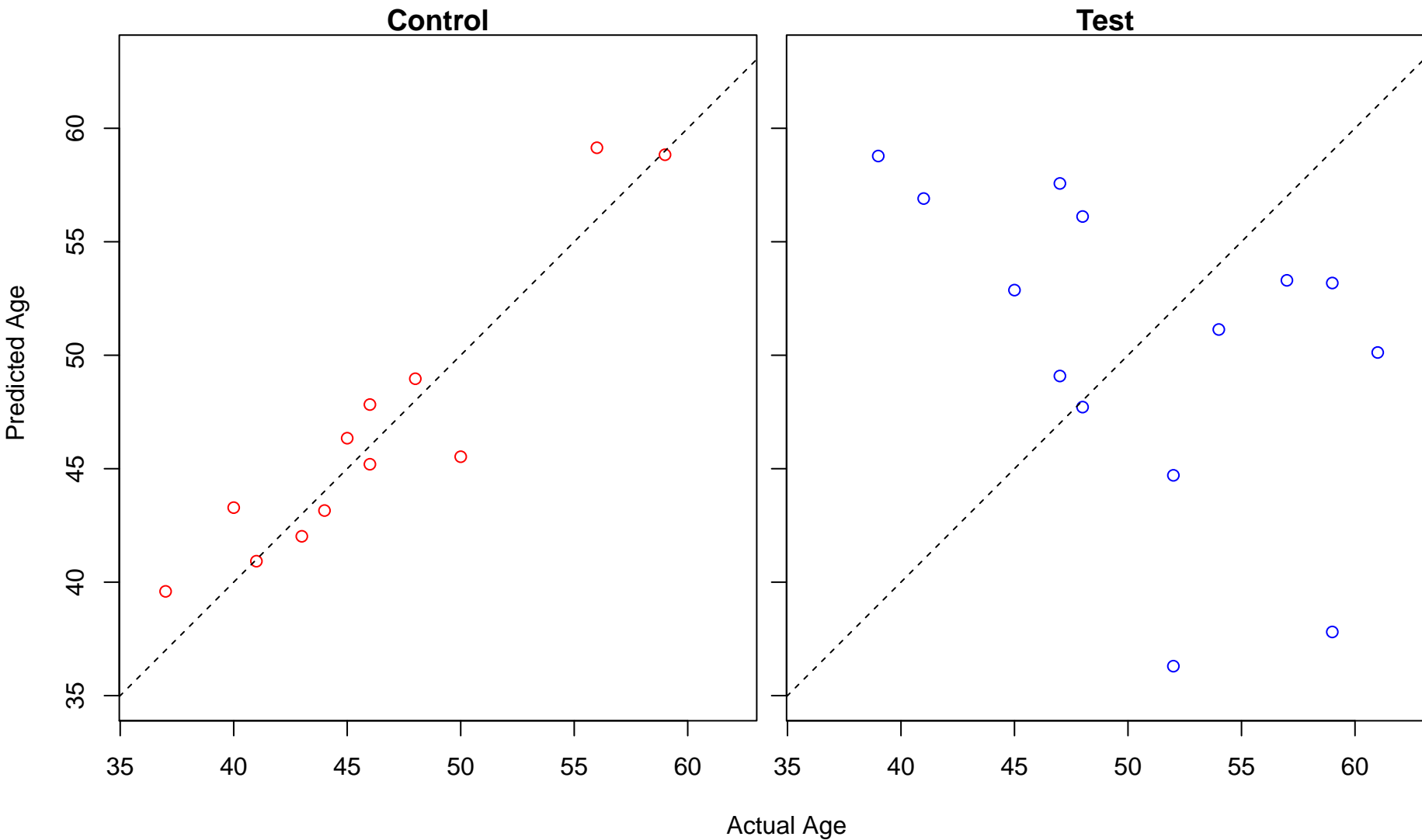
negative regulation of CREB transcription factor activity (Score: 11.734363)



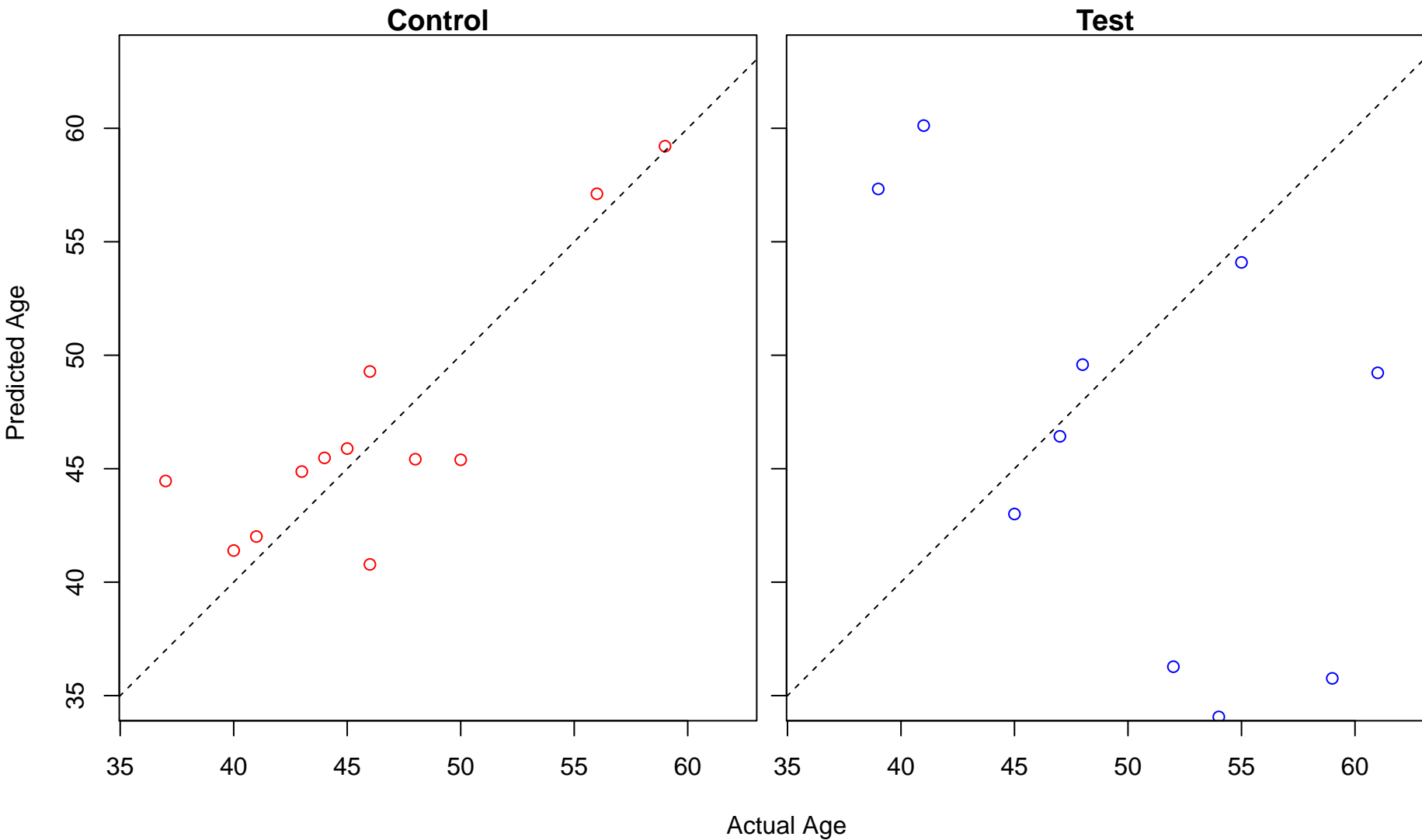
protein localization to nucleus (Score: 11.729569)



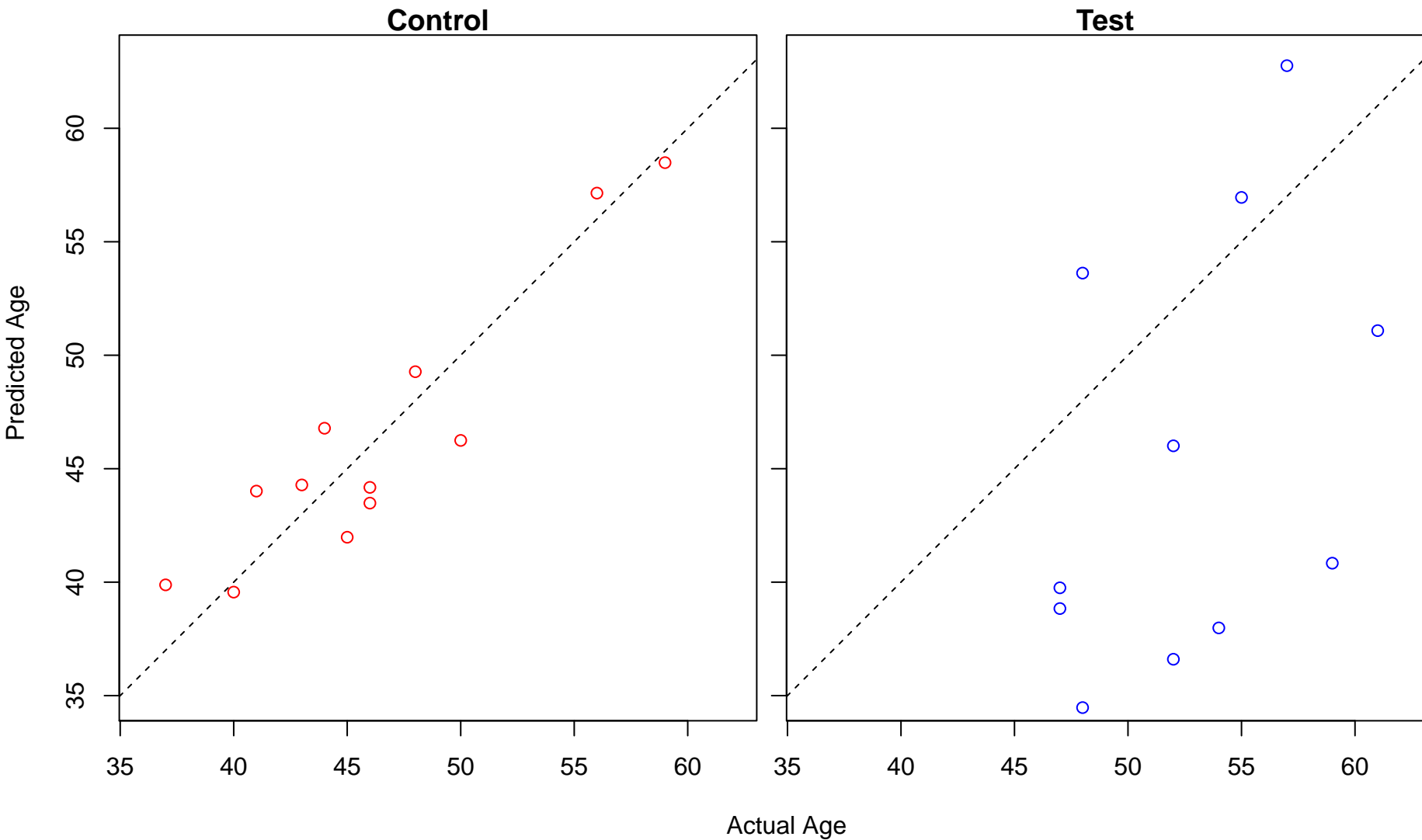
regulation of alpha-beta T cell activation (Score: 11.715793)



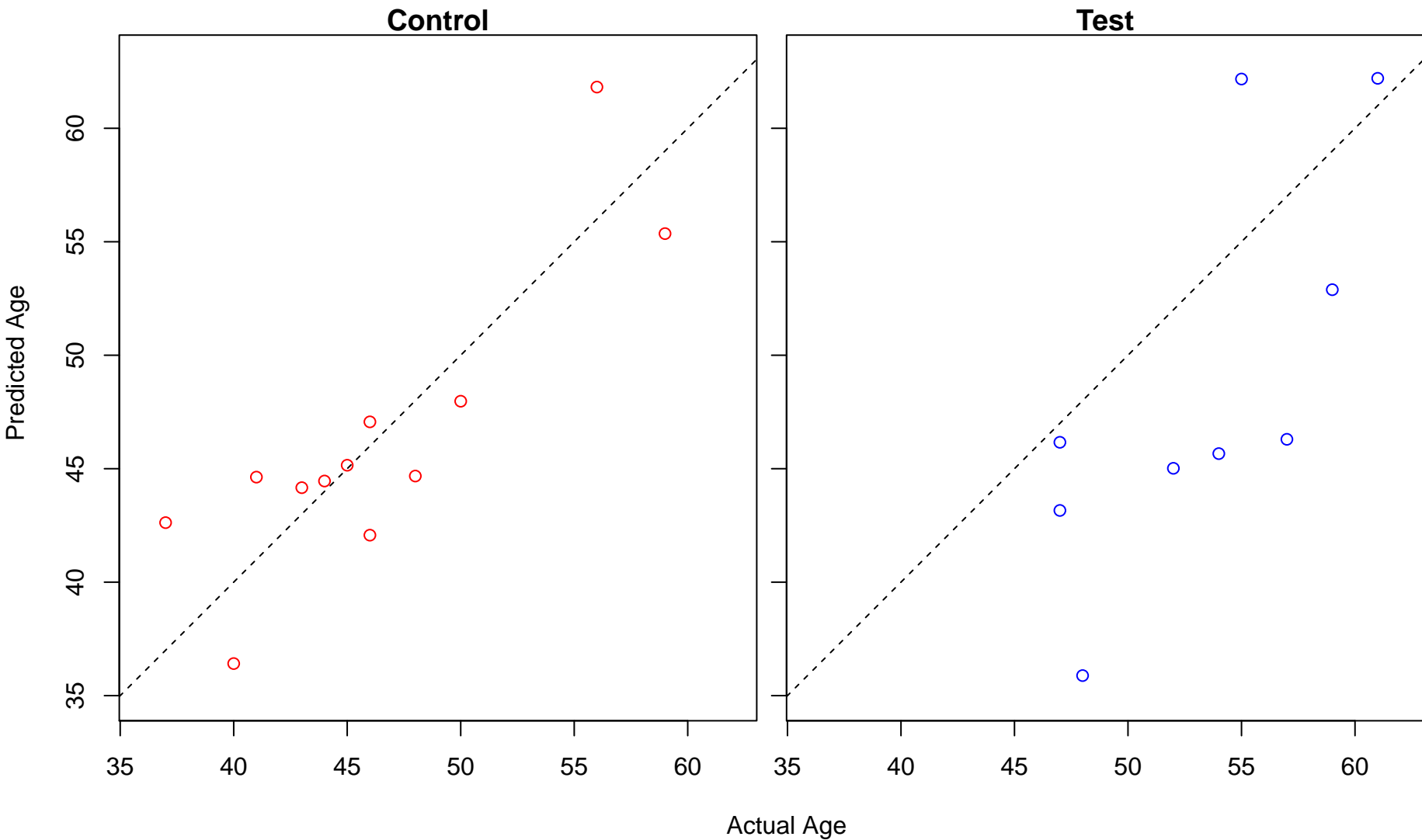
regulation of organ formation (Score: 11.709359)



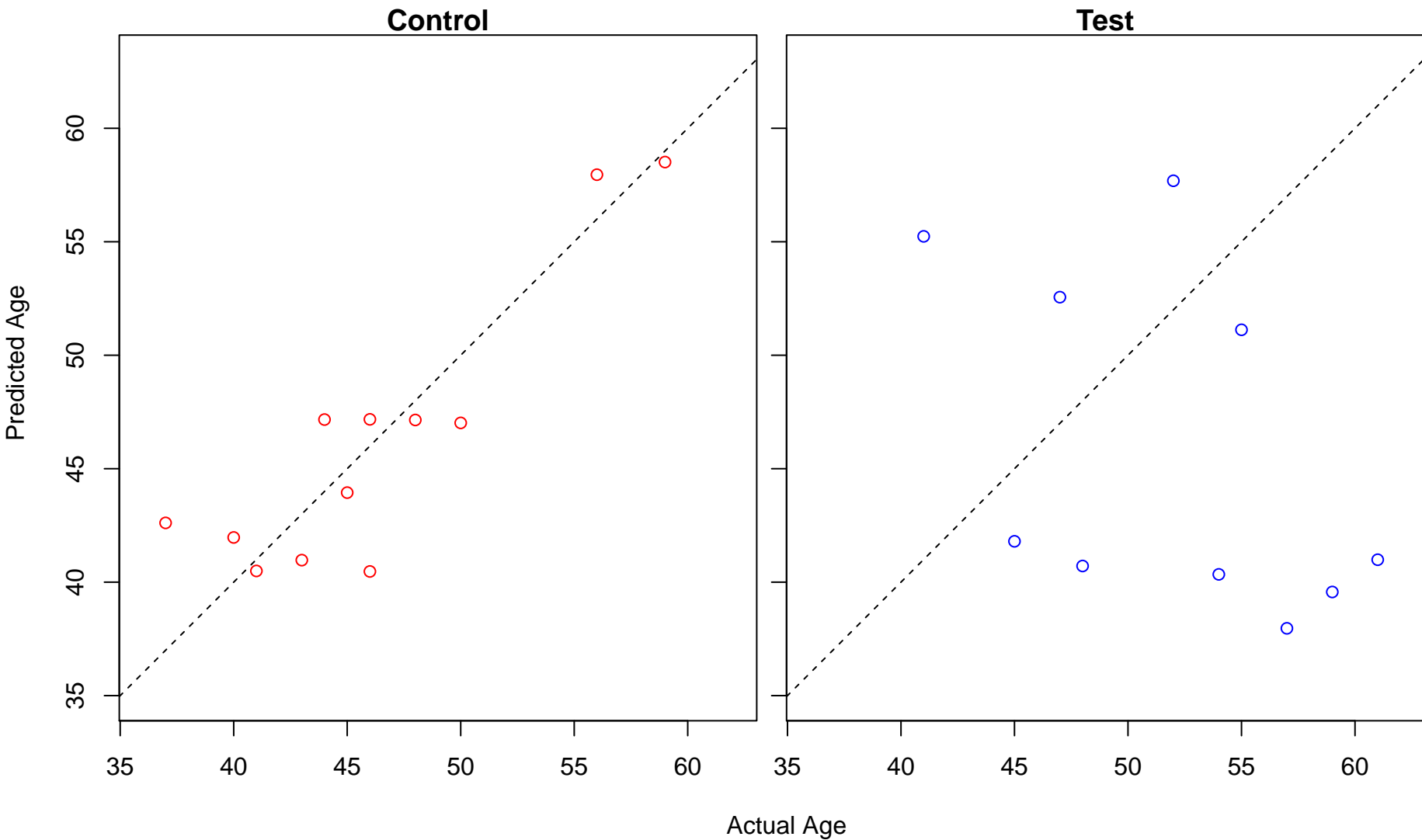
regulation of lipid biosynthetic process (Score: 11.682267)



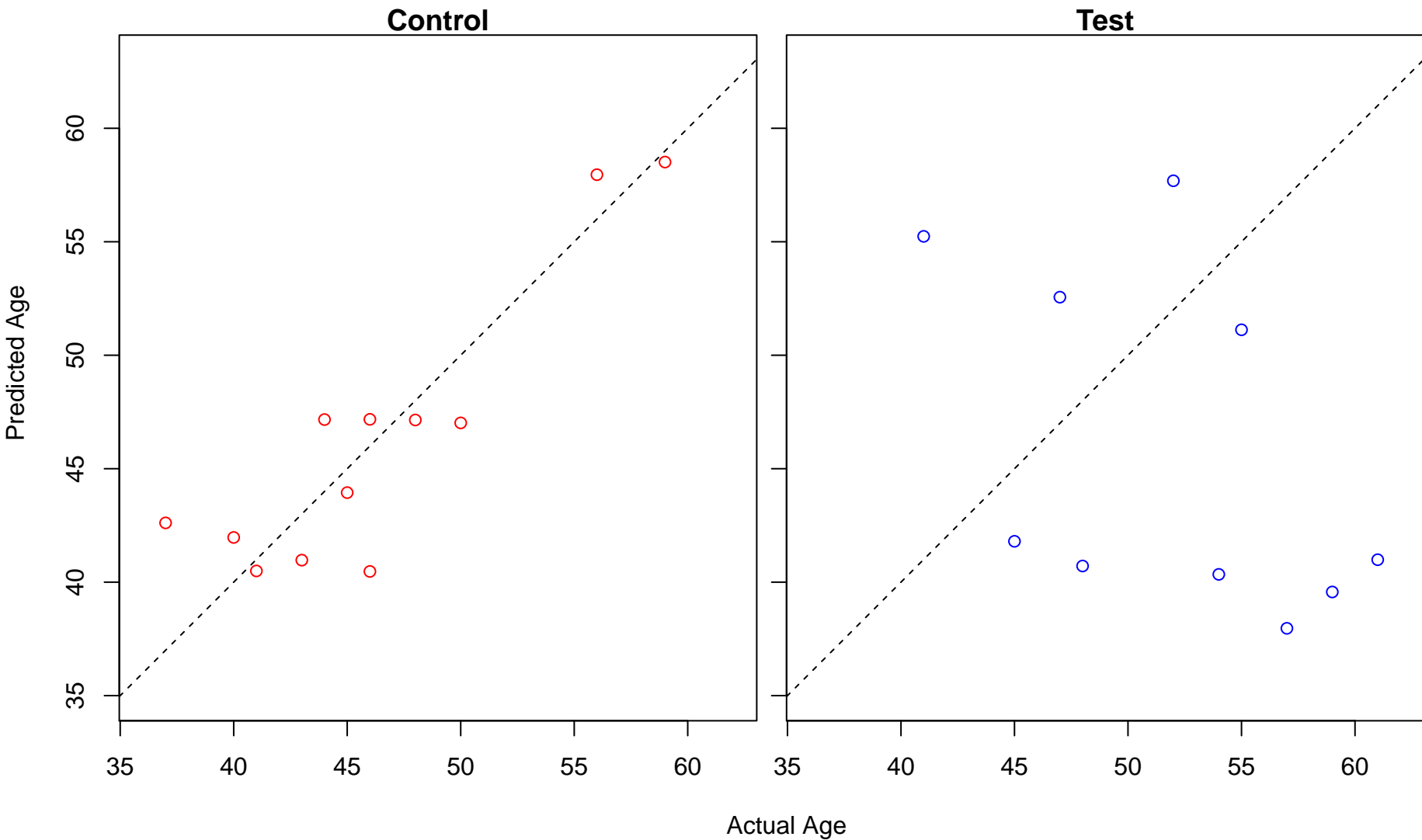
cellular modified amino acid biosynthetic process (Score: 11.674302)



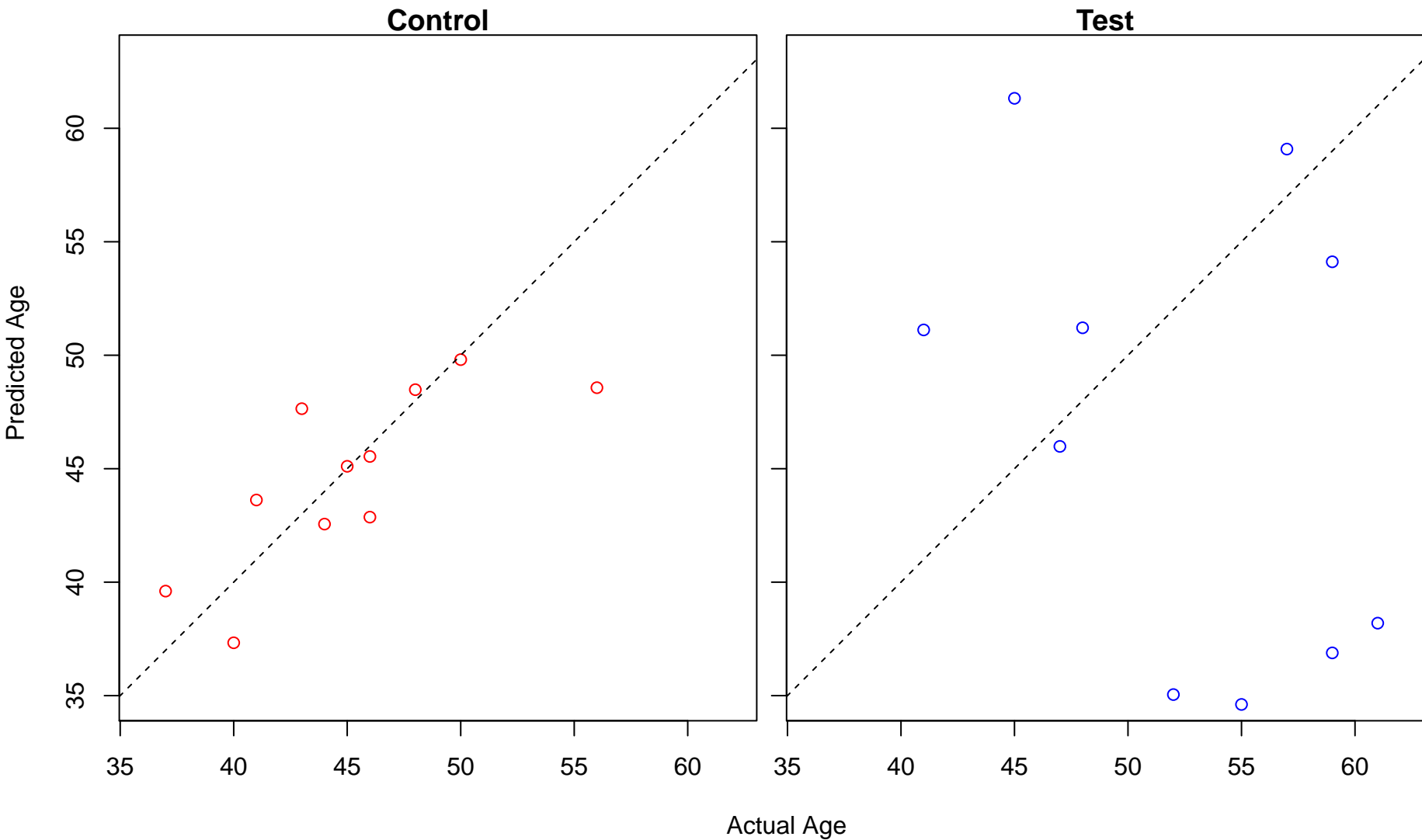
phosphate ion transport (Score: 11.665061)



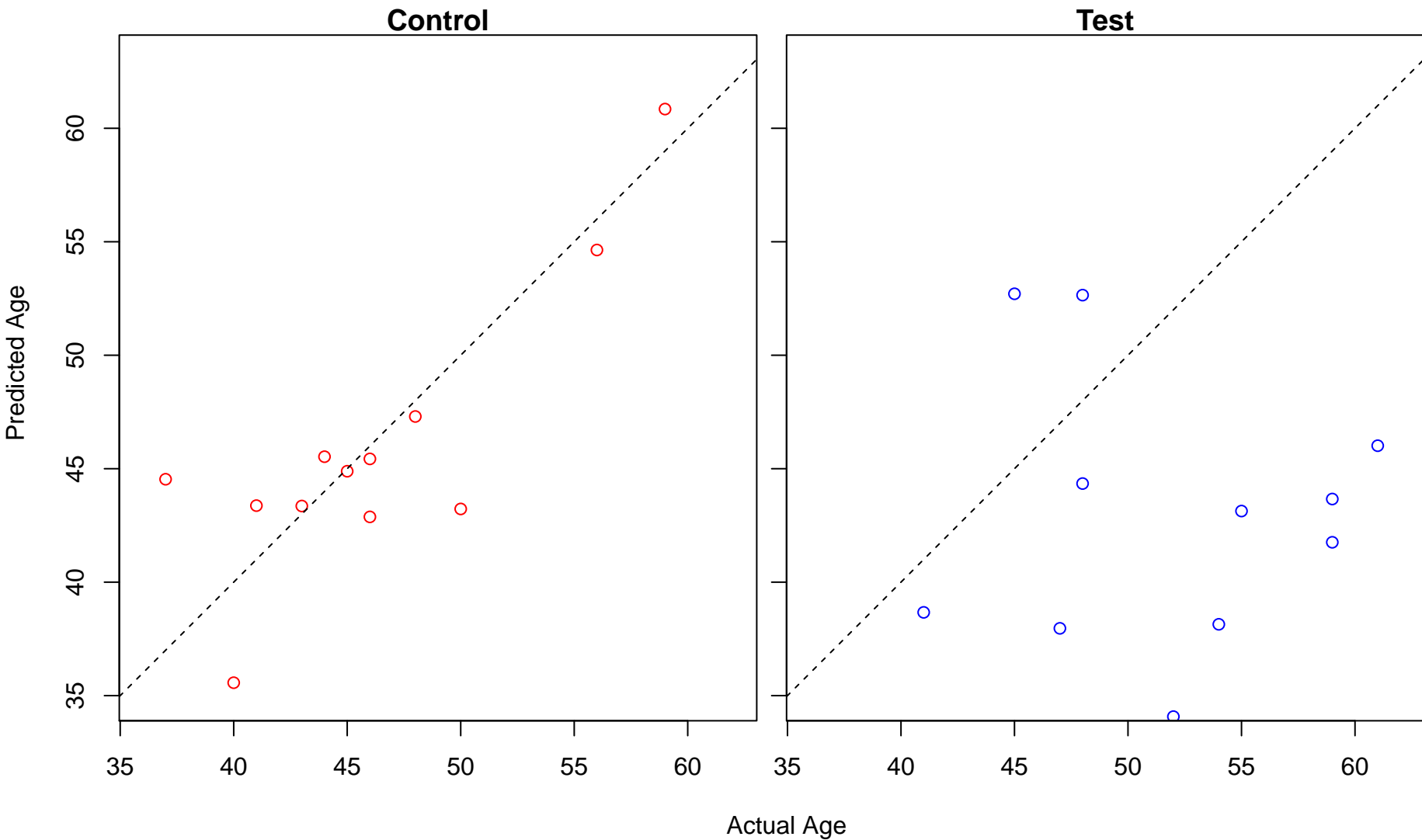
phosphate ion transmembrane transport (Score: 11.665061)



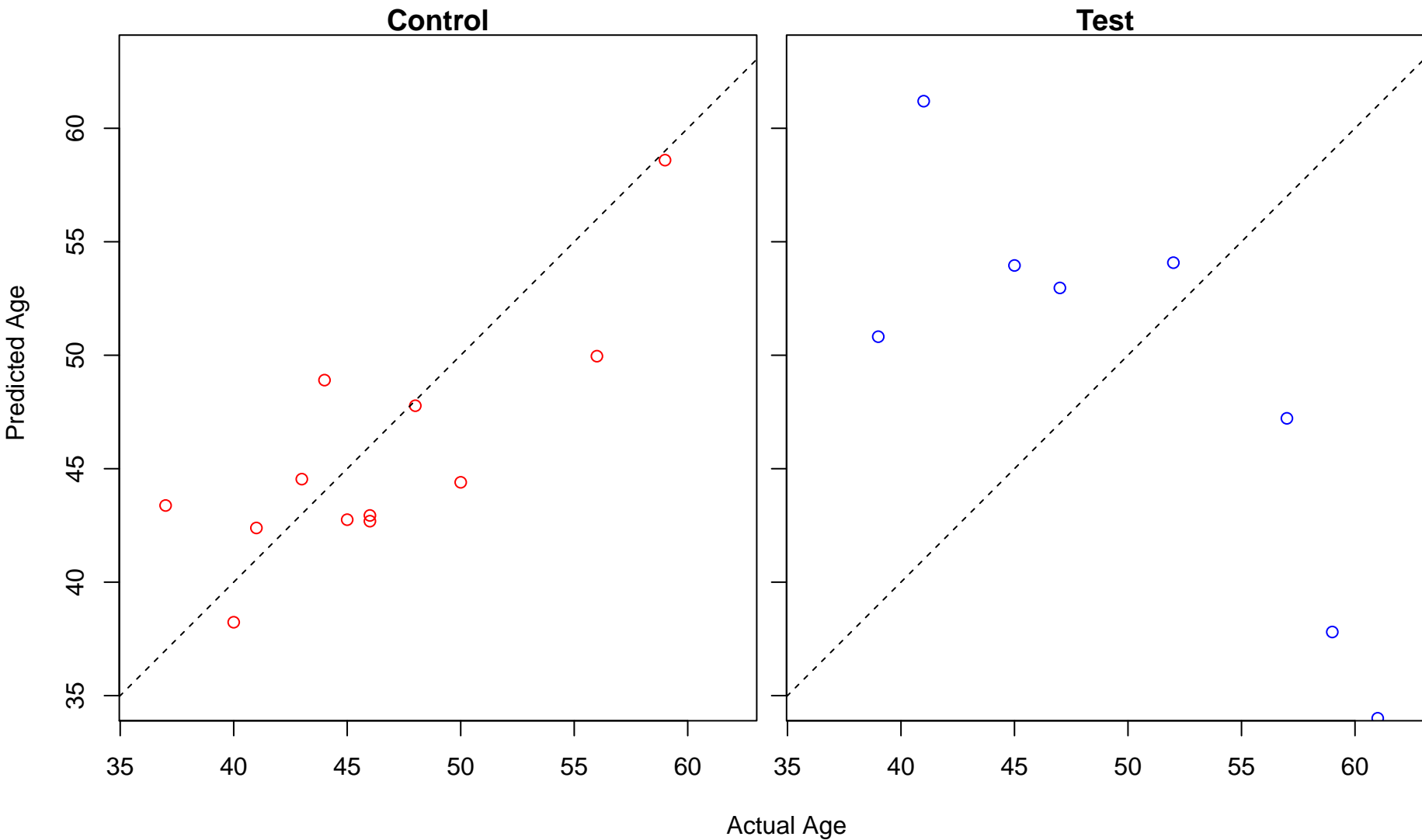
cAMP-mediated signaling (Score: 11.657167)



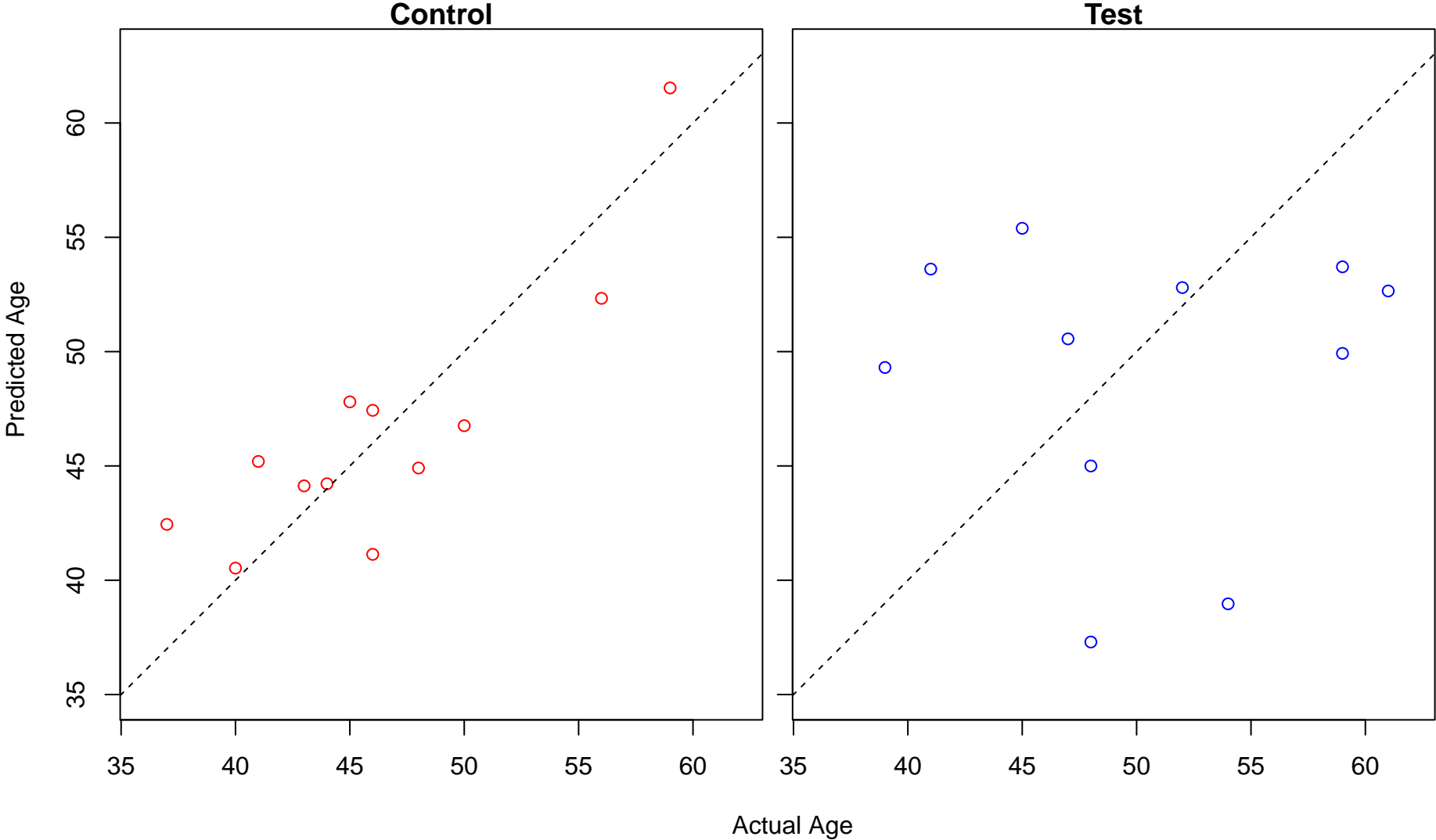
multi-organism reproductive process (Score: 11.562168)



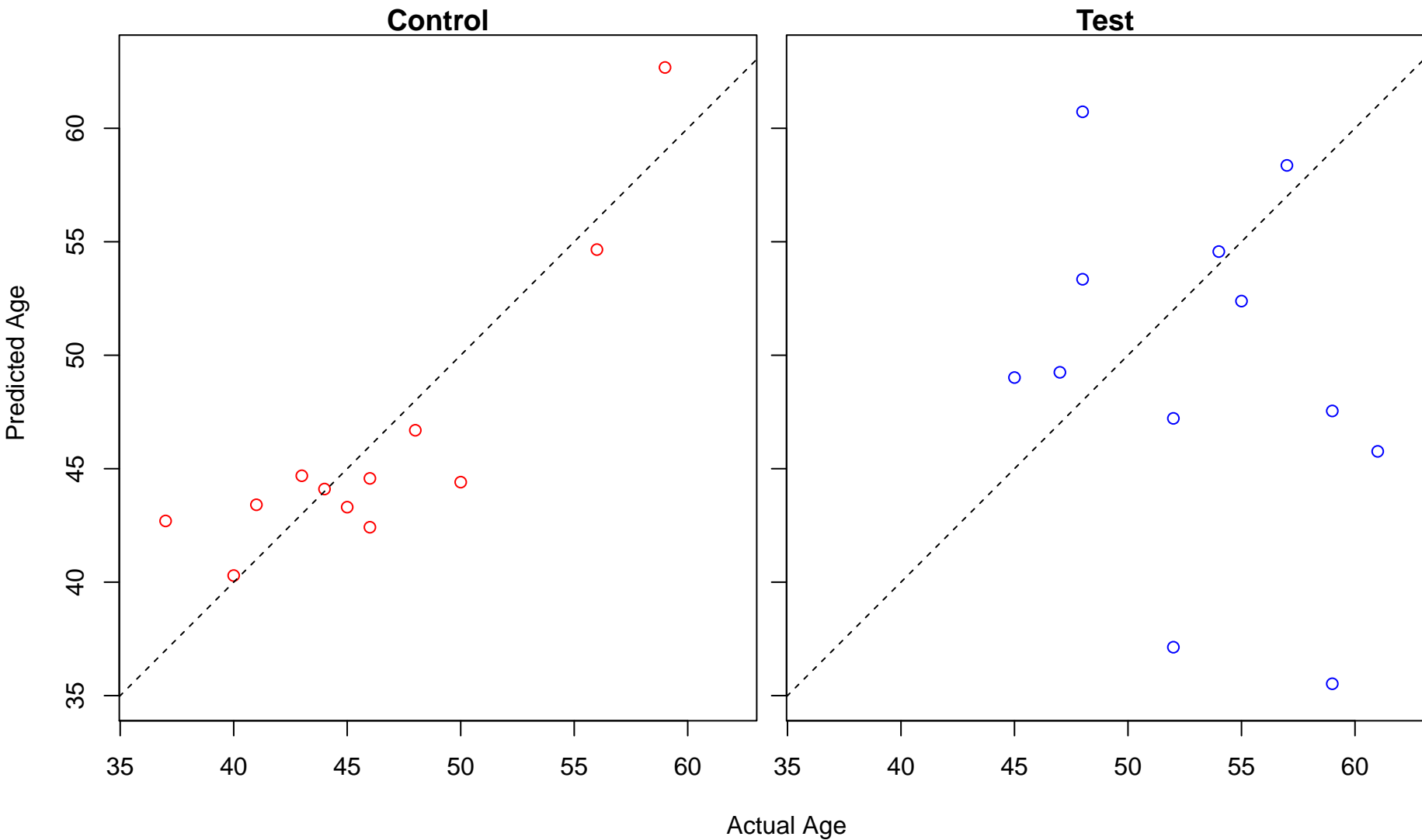
determination of left/right symmetry (Score: 11.561893)



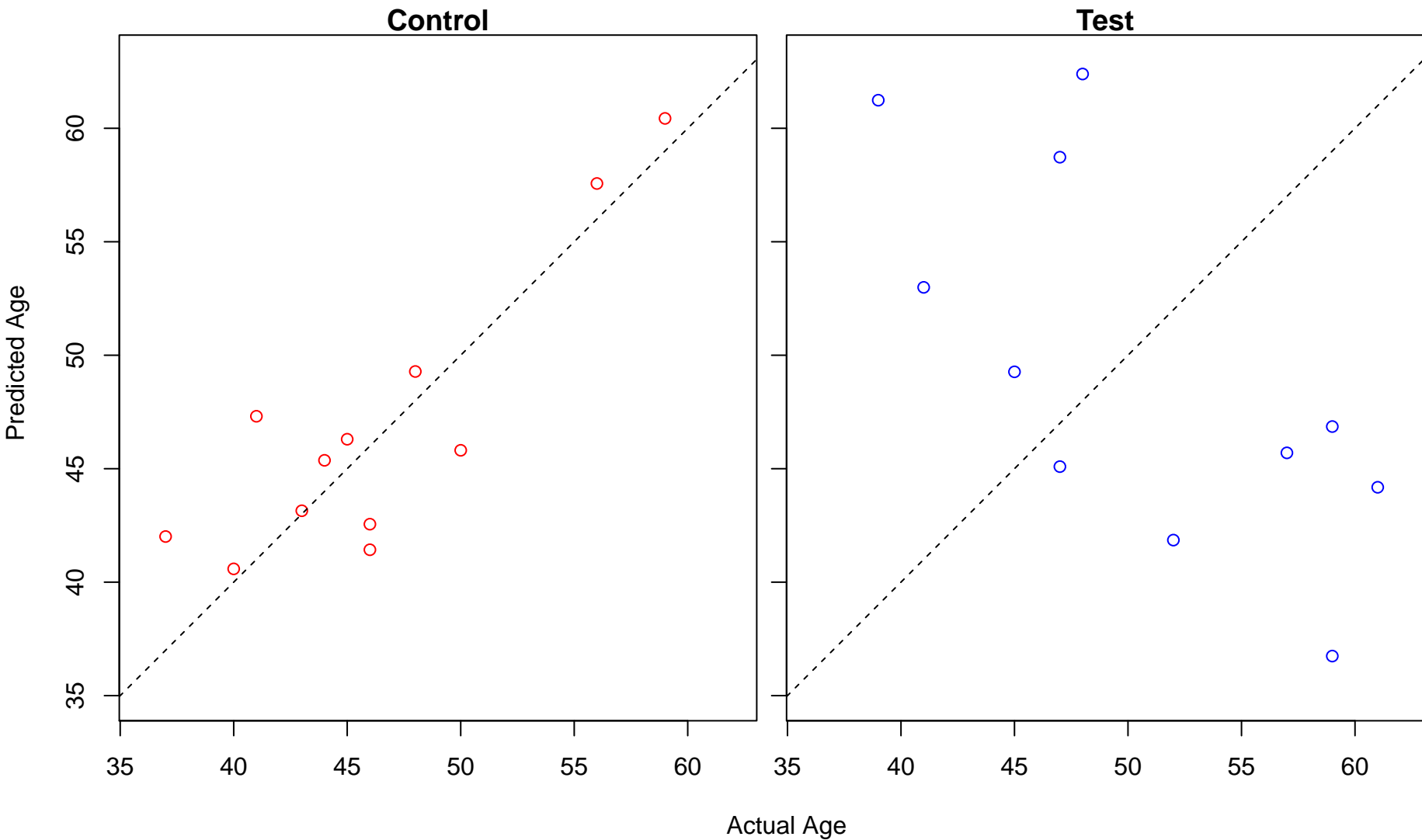
positive regulation of insulin secretion involved in cellular response to glucose stimulus (Score: 11.53)



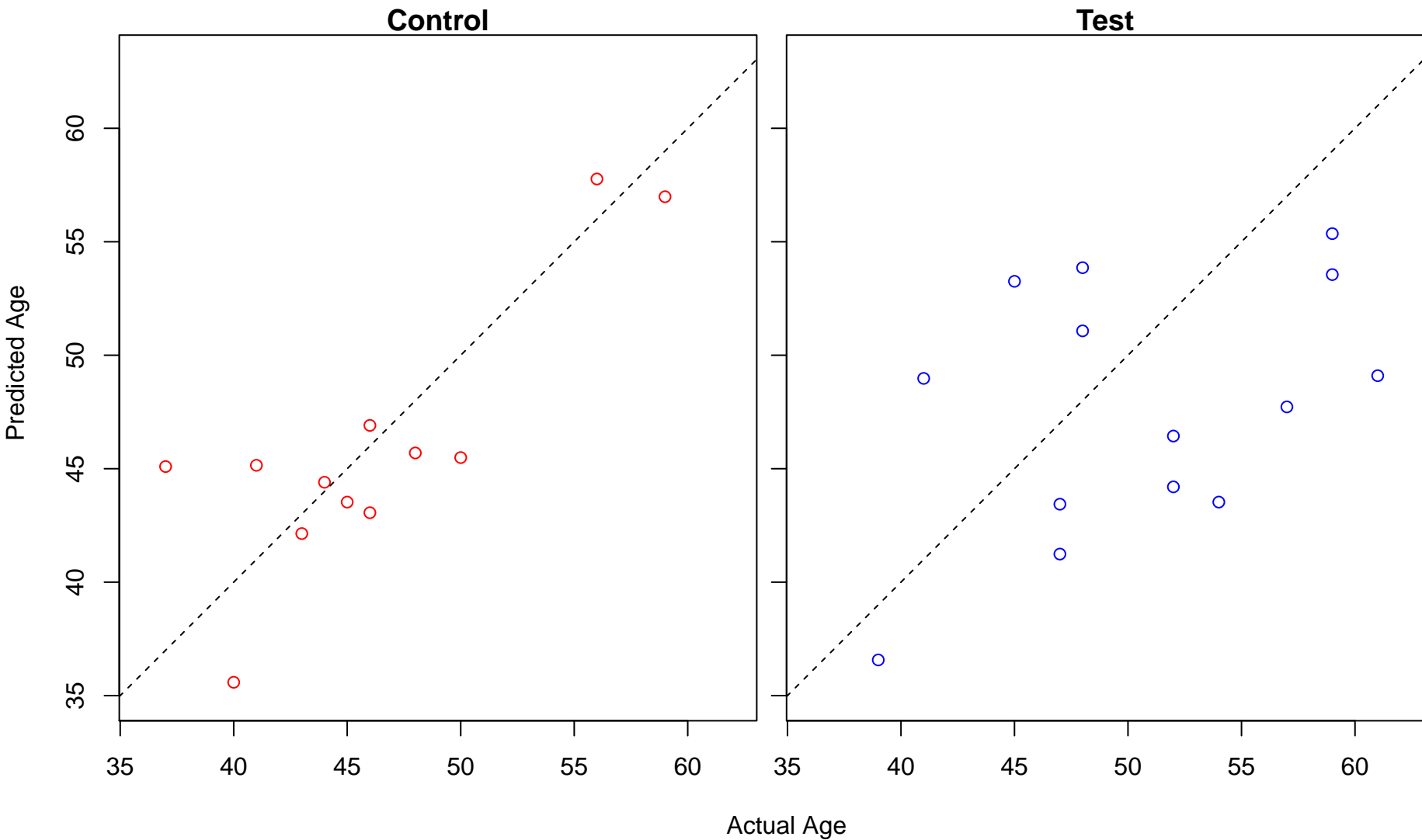
regulation of gene expression, epigenetic (Score: 11.516728)



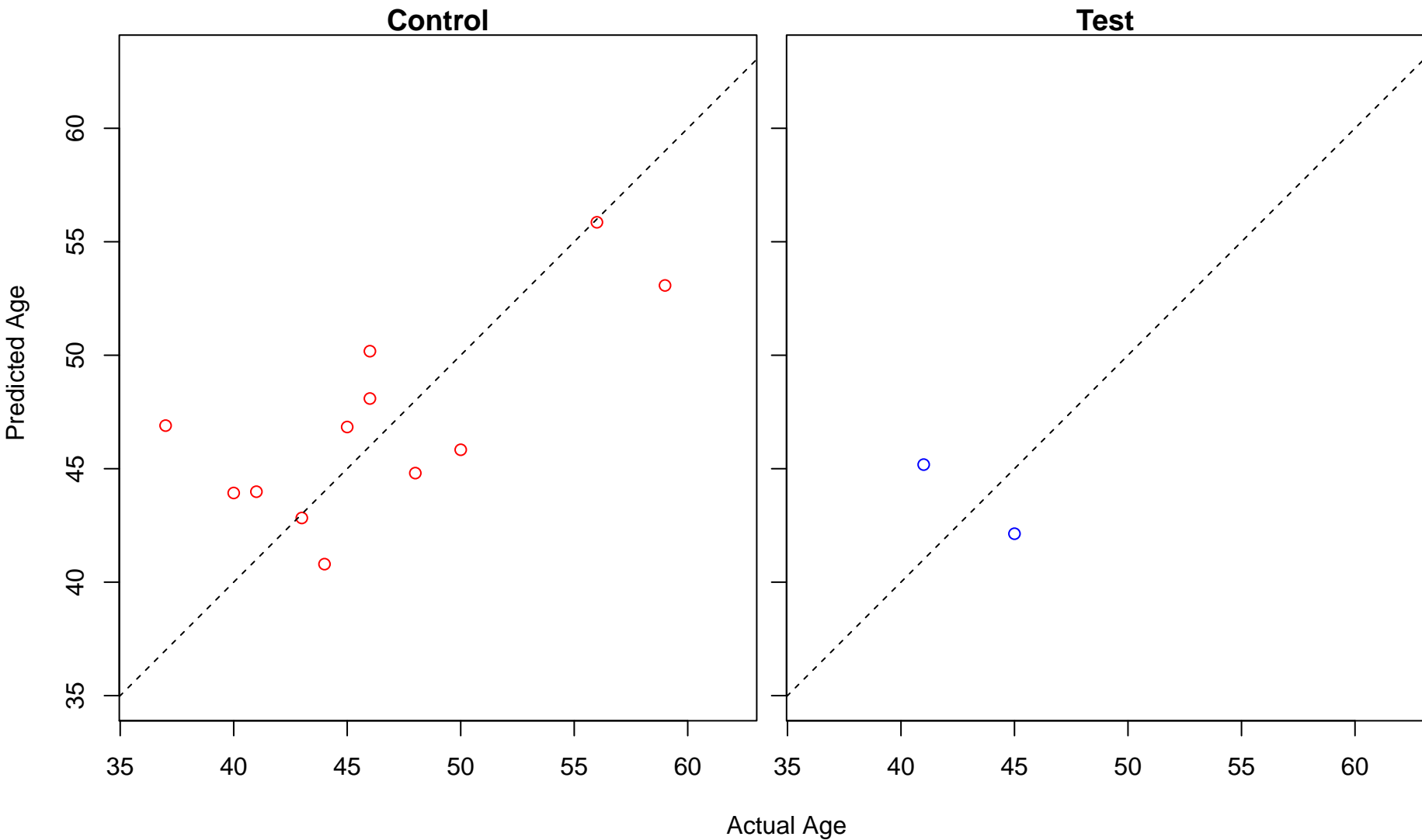
regulation of sequestering of calcium ion (Score: 11.473861)



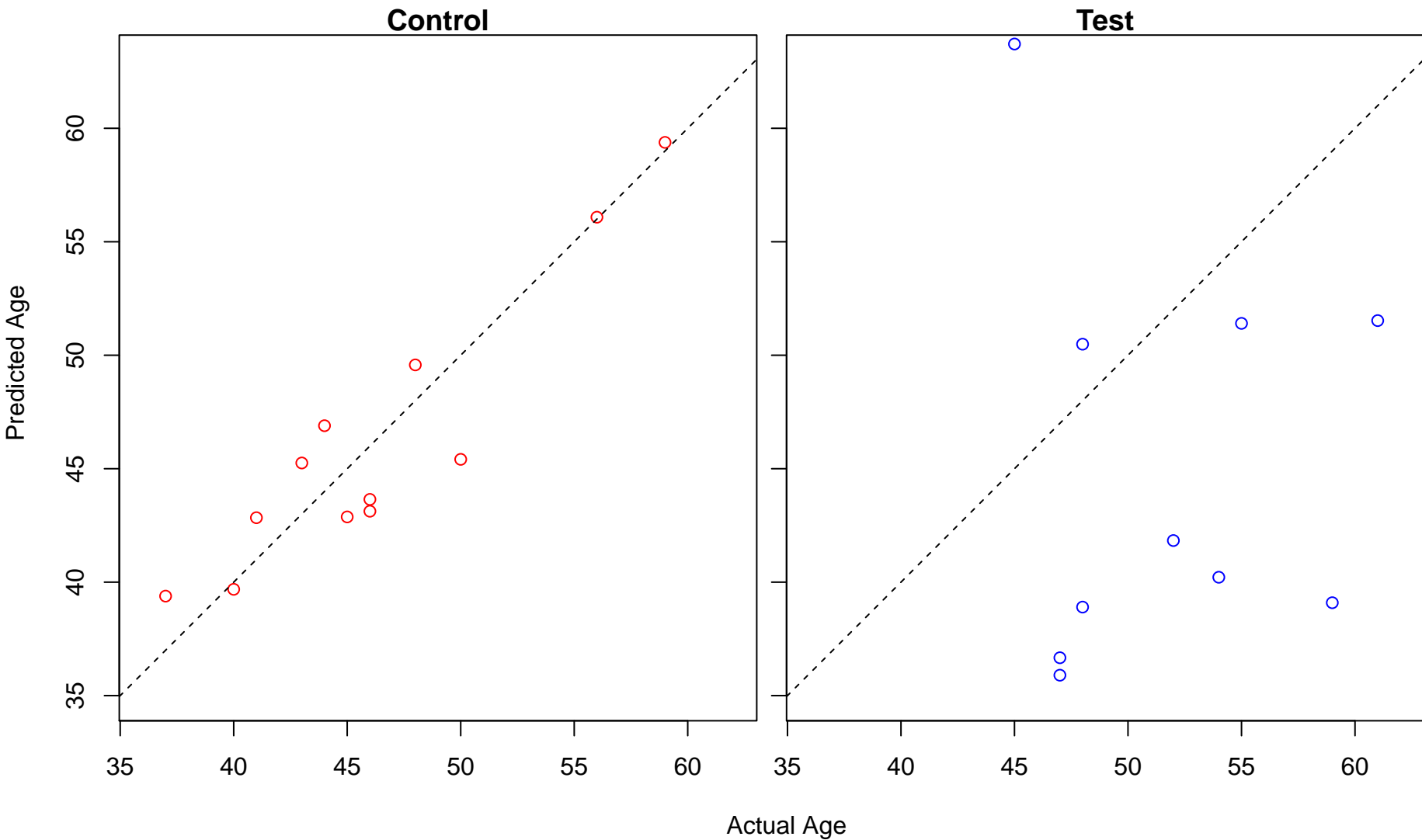
negative regulation of NF-kappaB import into nucleus (Score: 11.399809)



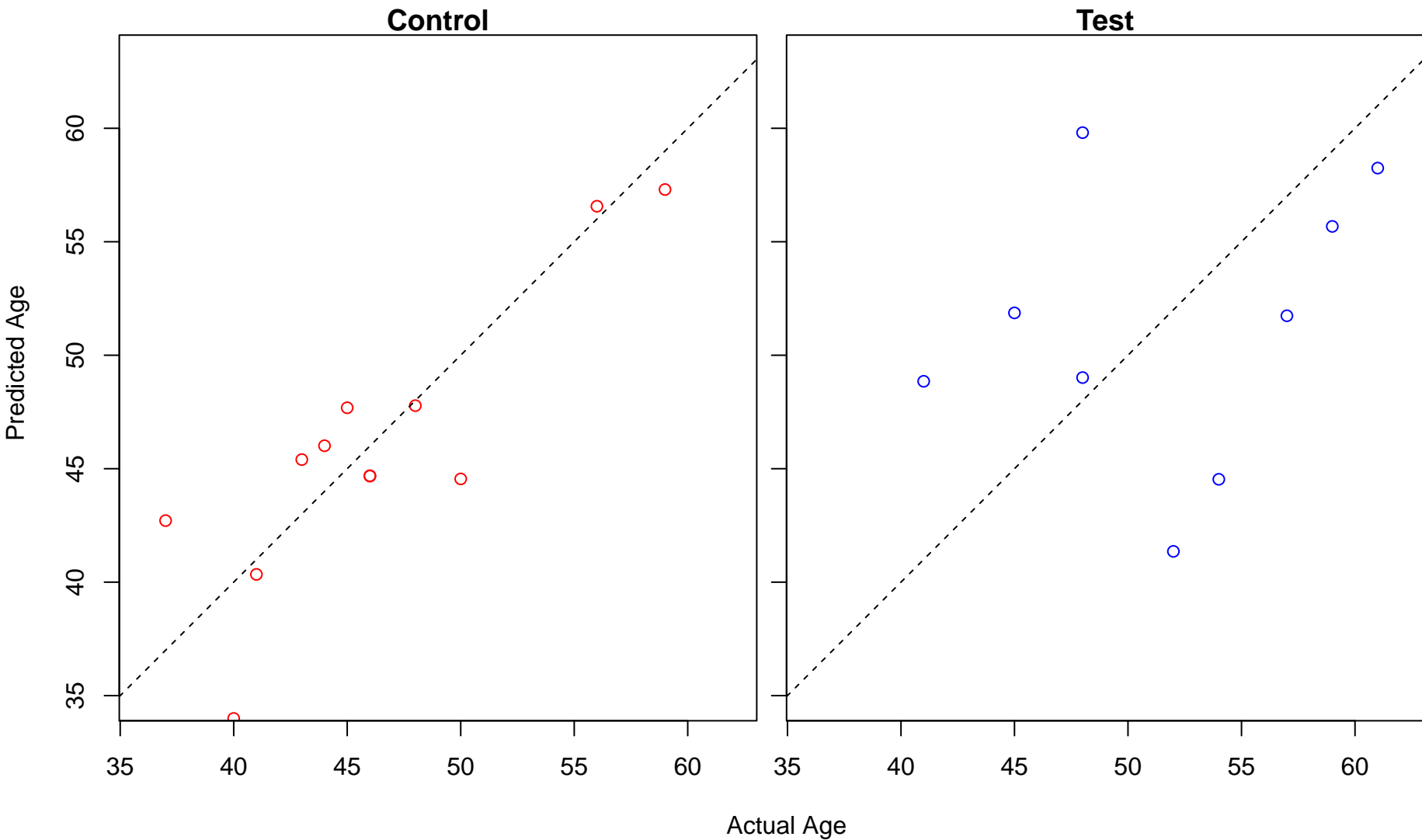
phagocytosis, recognition (Score: 11.397680)



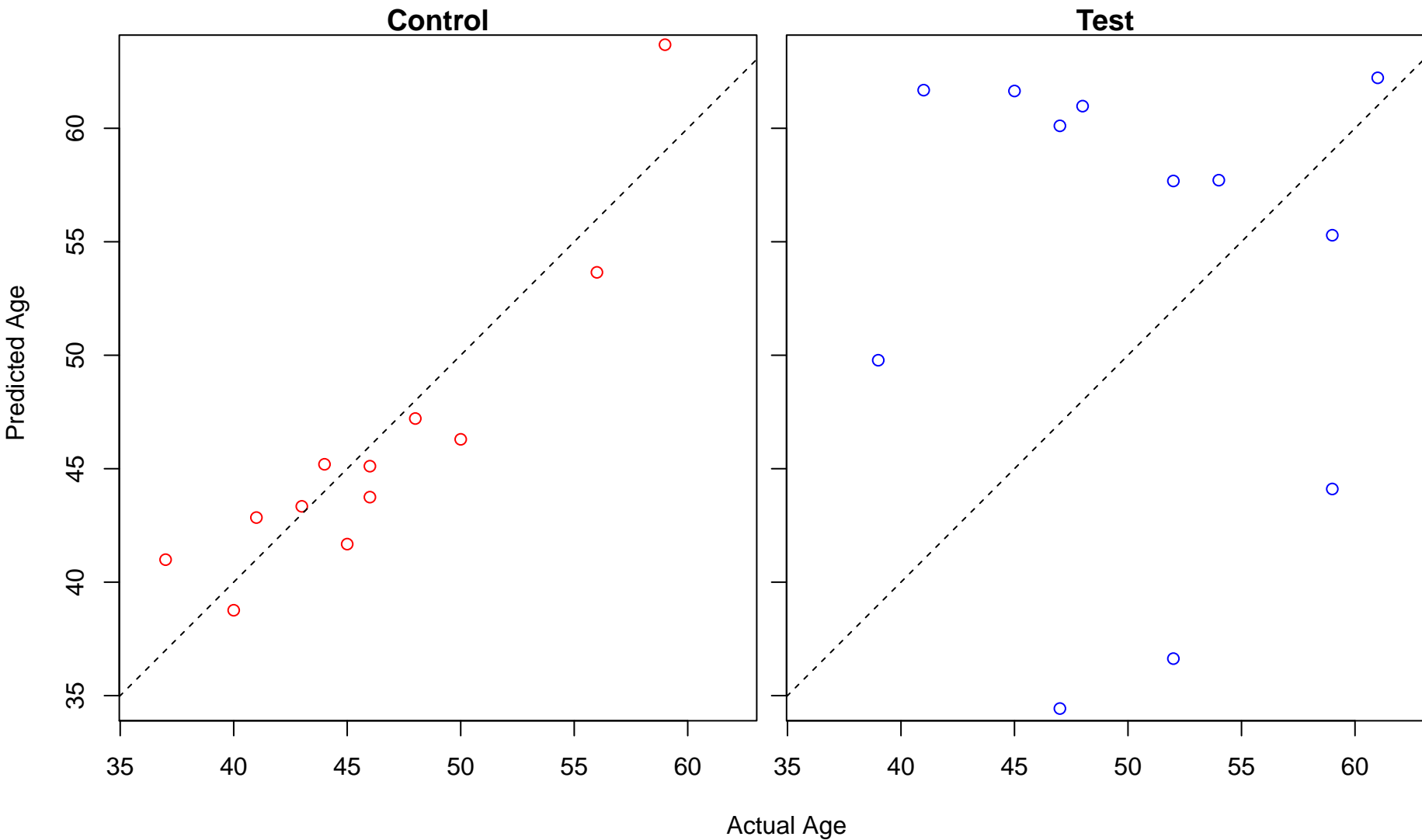
regulation of lipid metabolic process (Score: 11.379000)



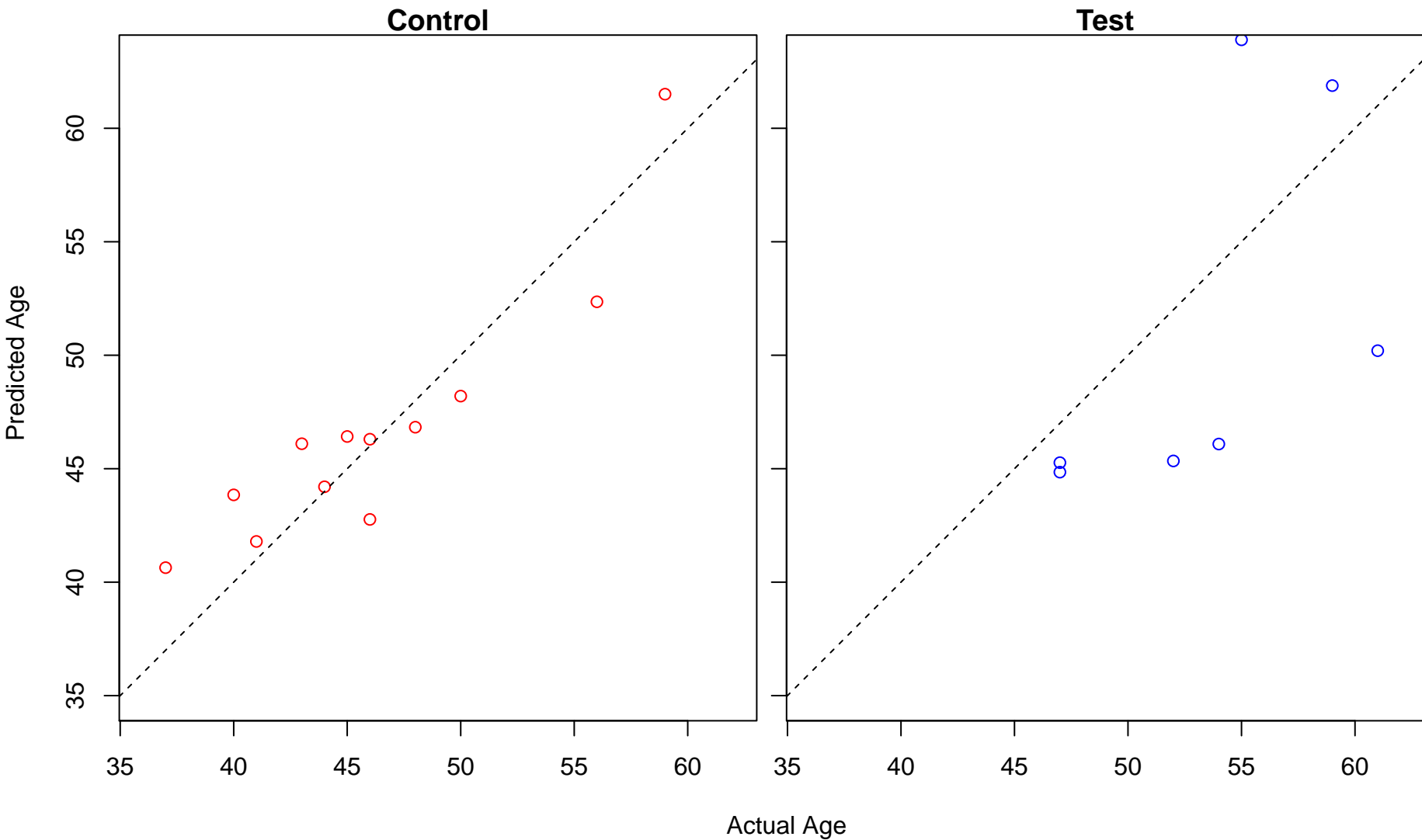
cardiac atrium morphogenesis (Score: 11.374502)



regulation of autophagosome assembly (Score: 11.350647)

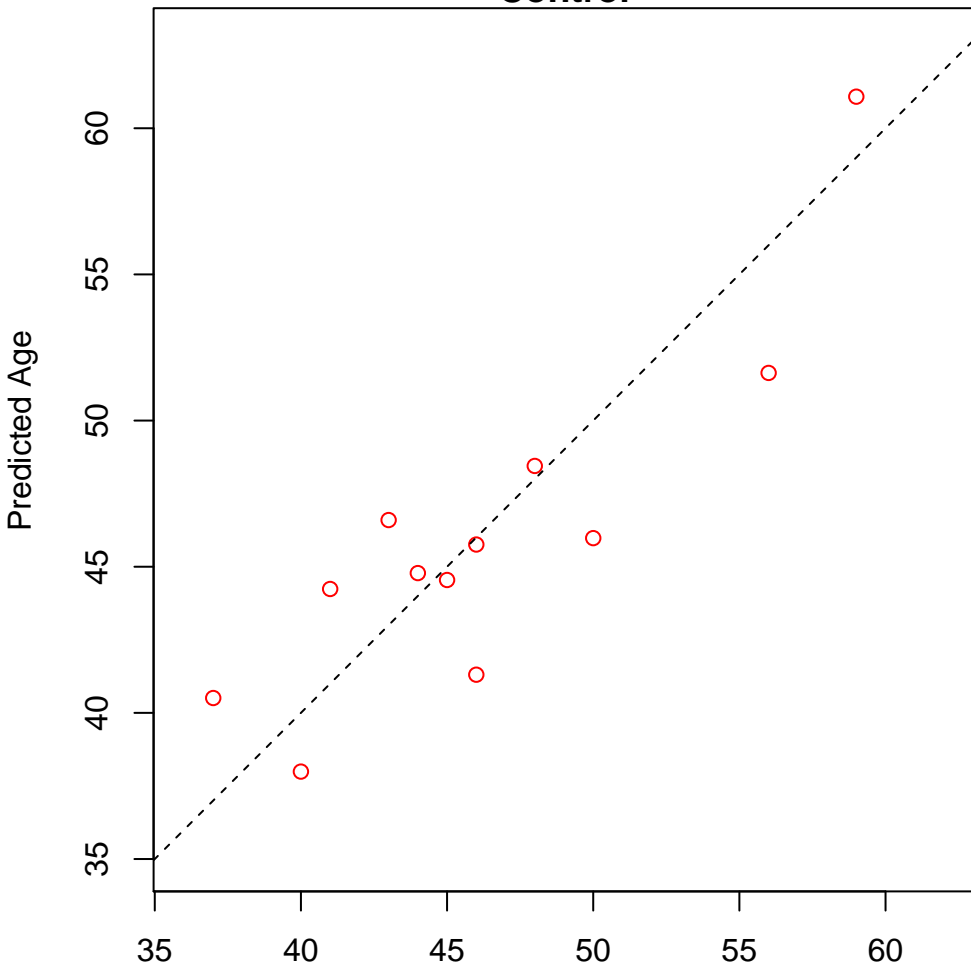


positive regulation of wound healing (Score: 11.335802)

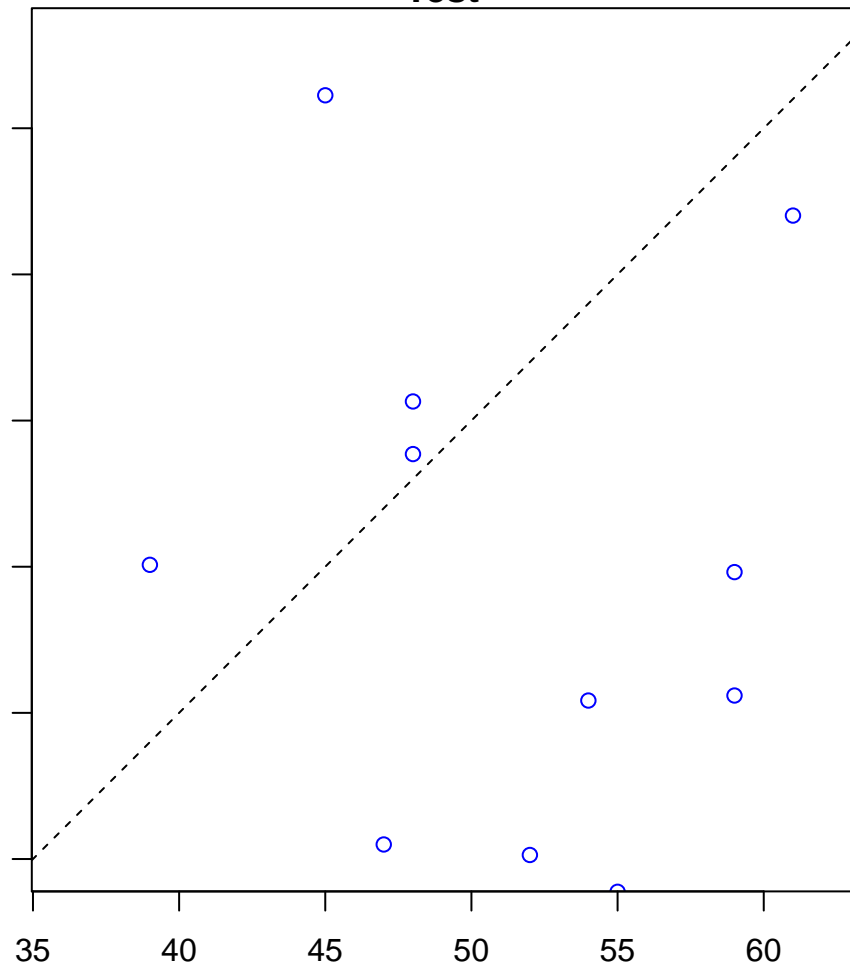


cellular response to oxidative stress (Score: 11.322586)

Control

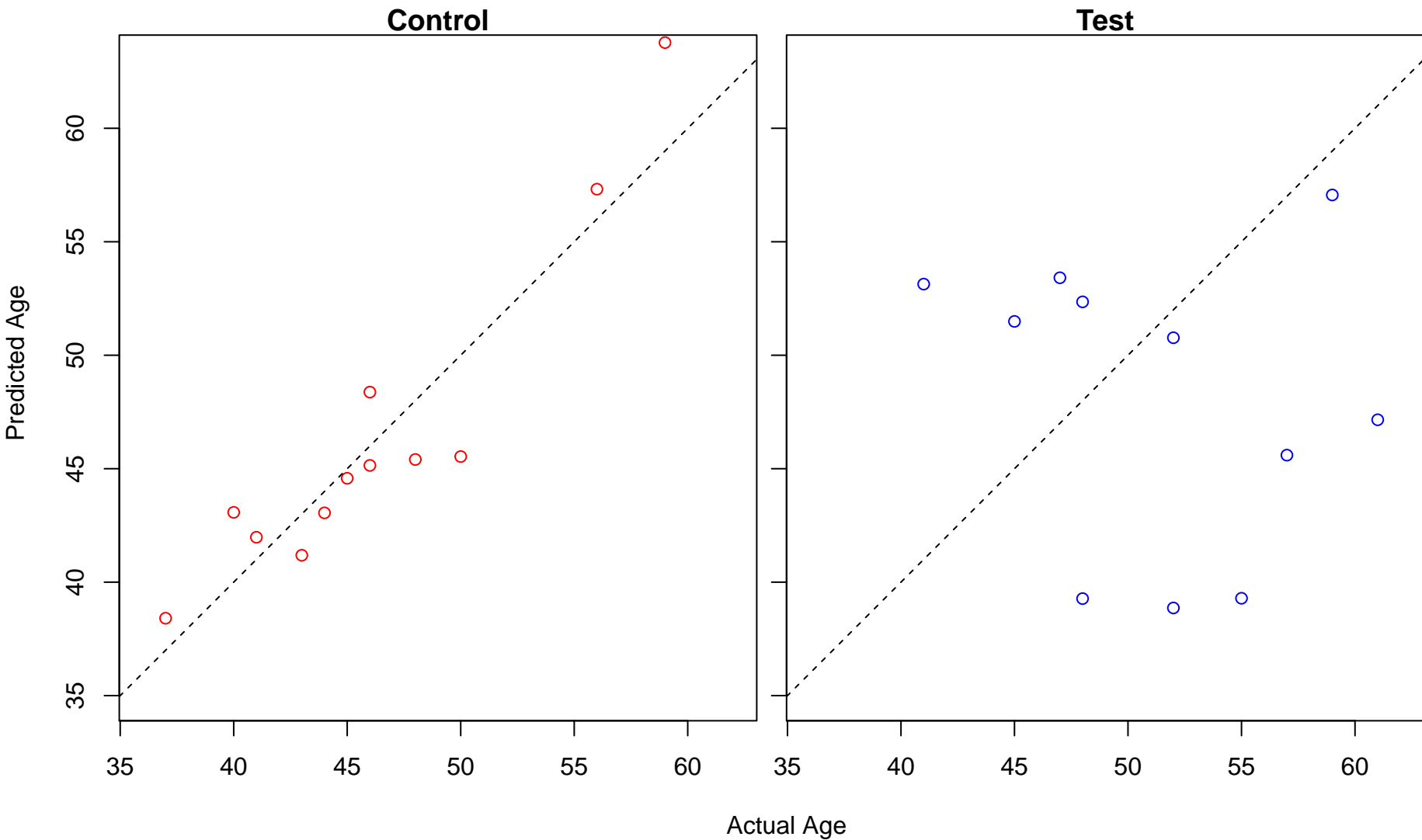


Test



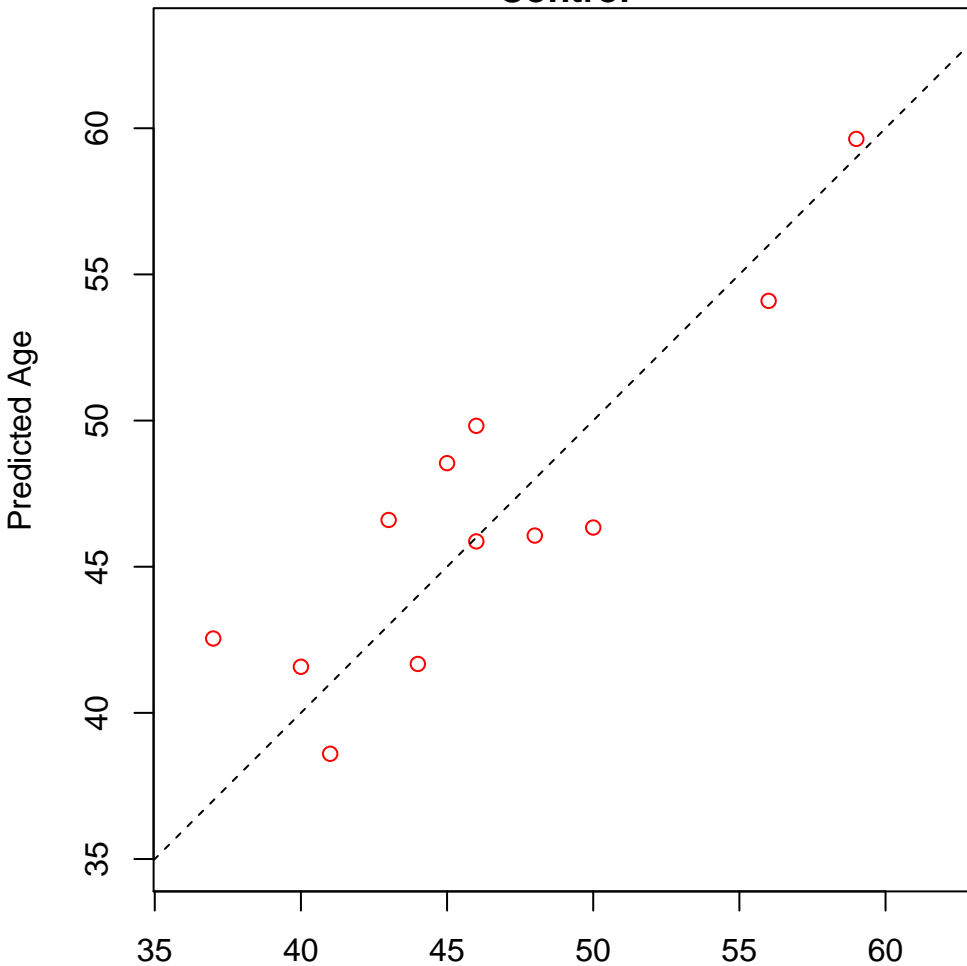
Actual Age

canonical Wnt signaling pathway (Score: 11.274619)

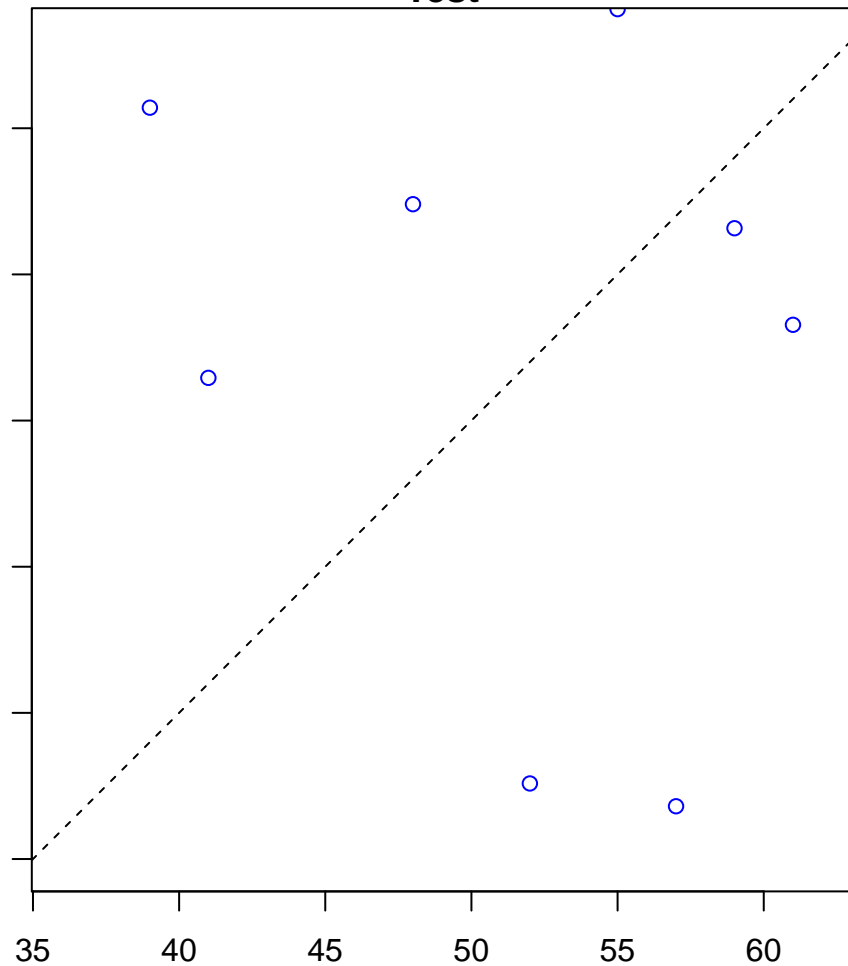


heart trabecula morphogenesis (Score: 11.261034)

Control

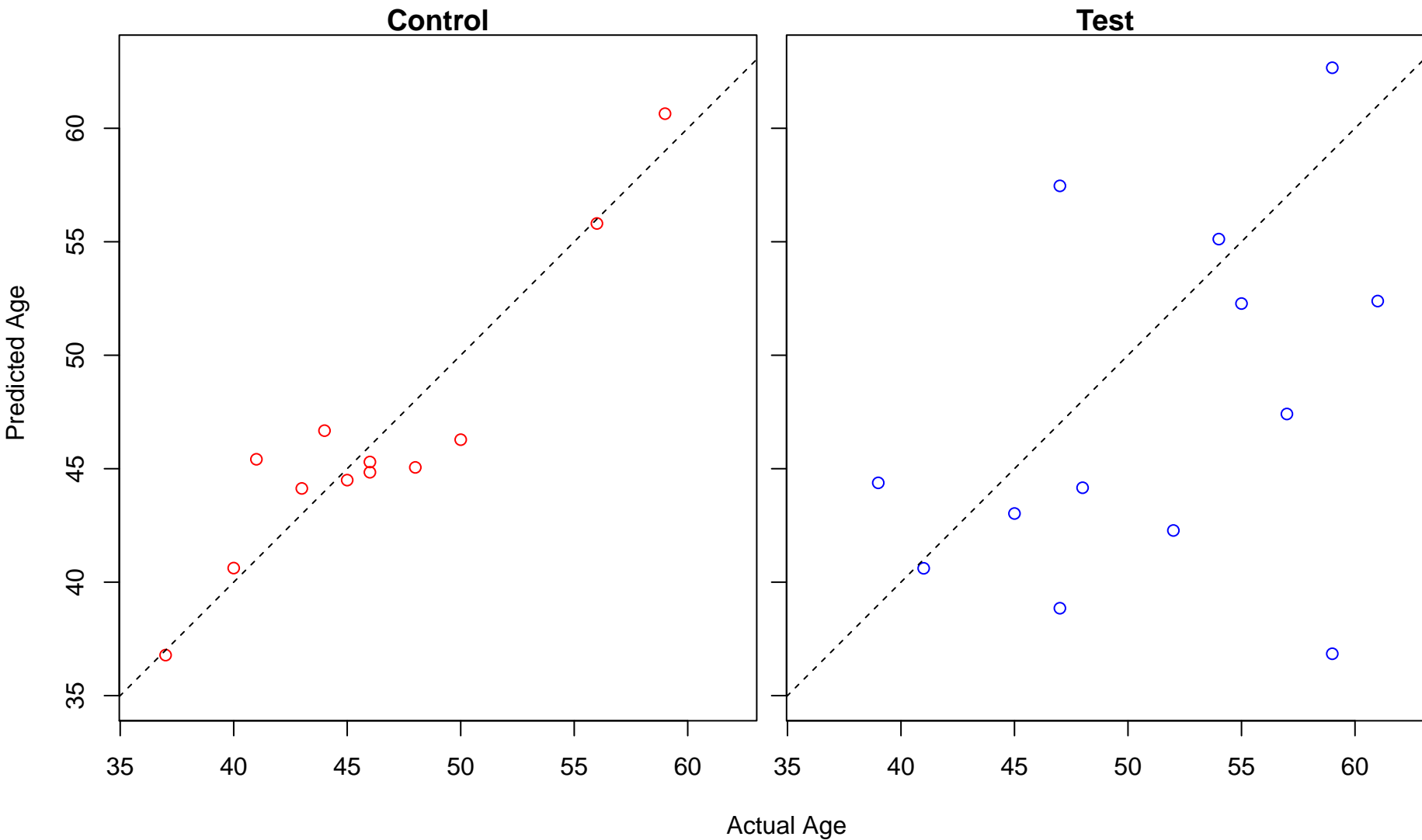


Test

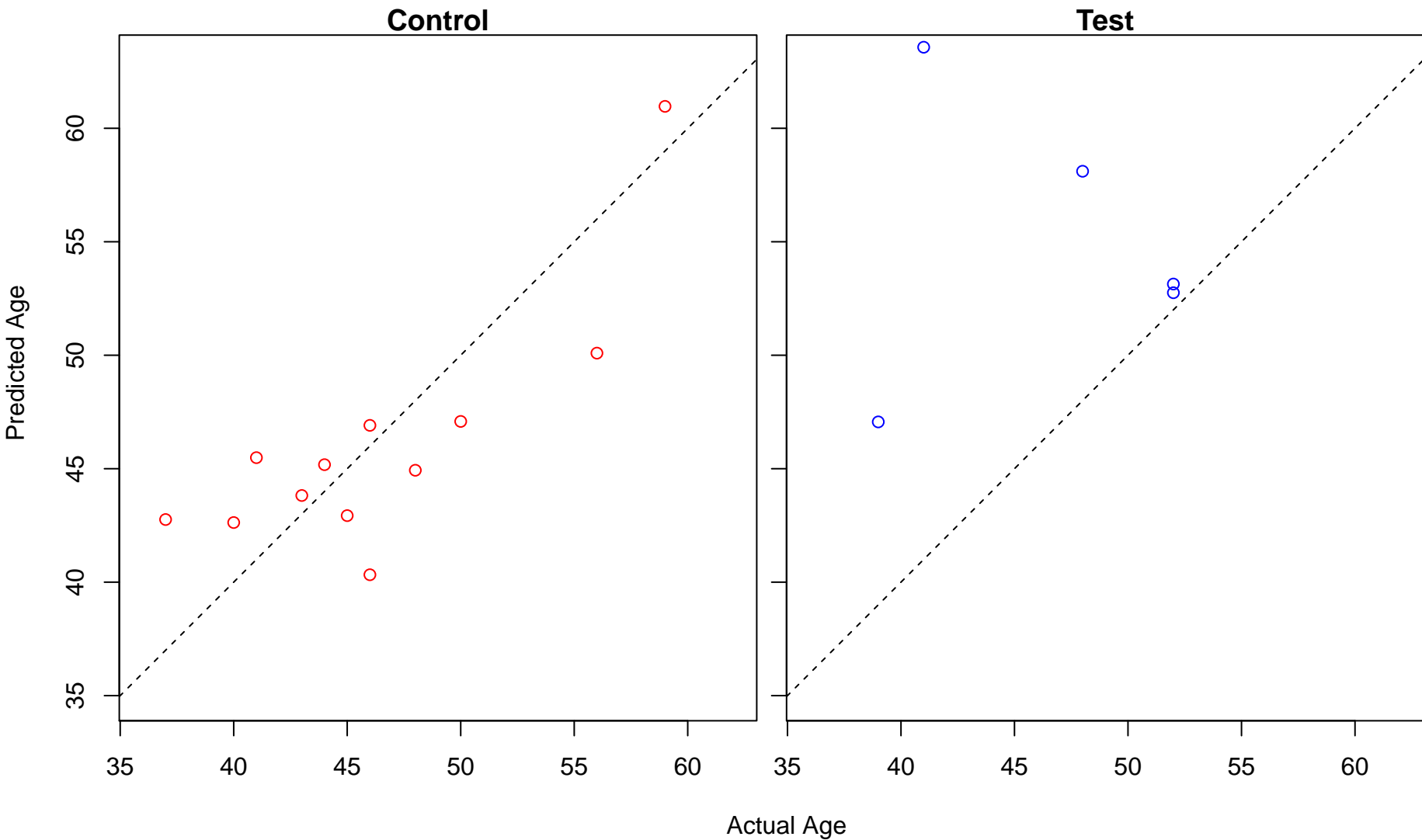


Actual Age

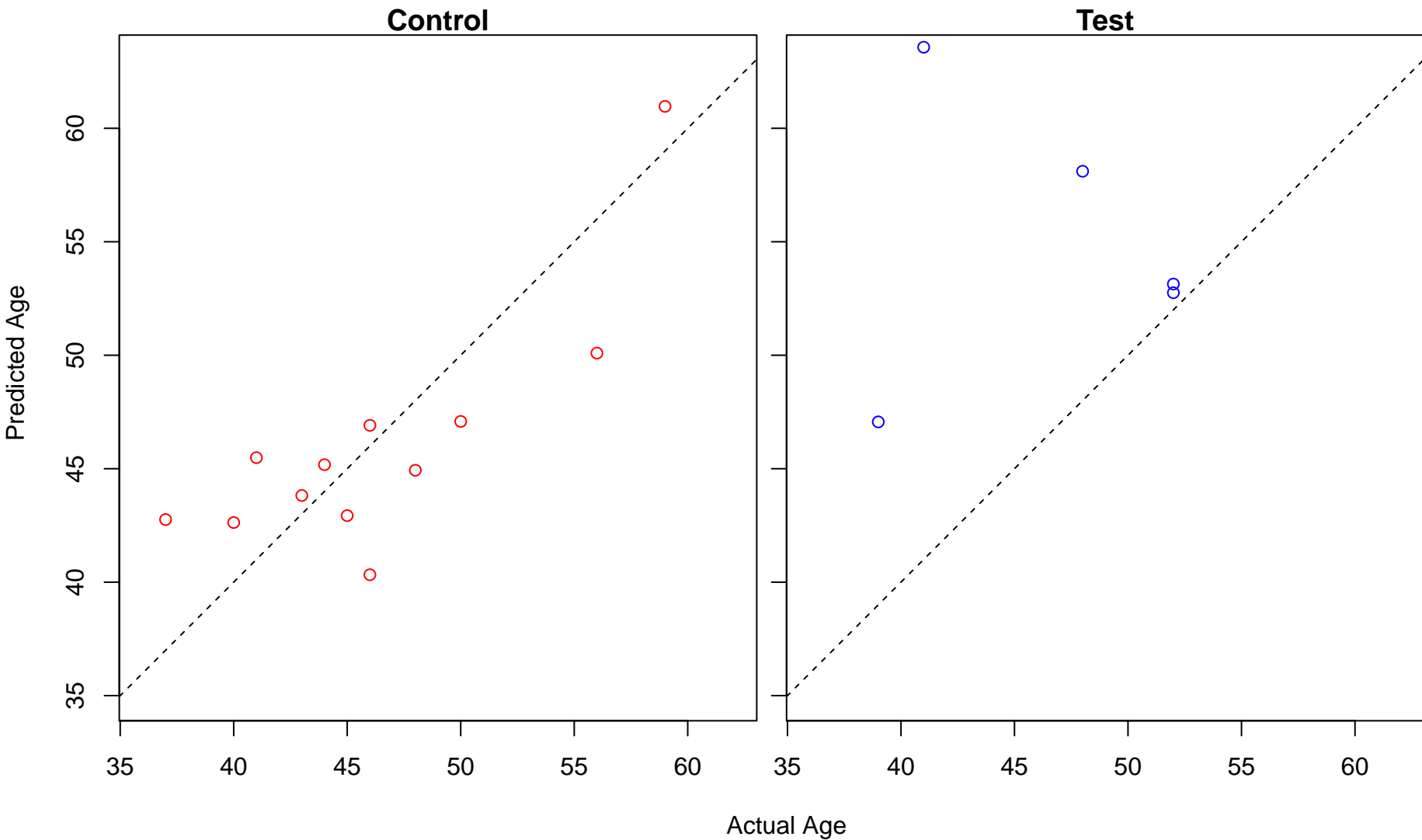
negative regulation of dendrite development (Score: 11.260180)



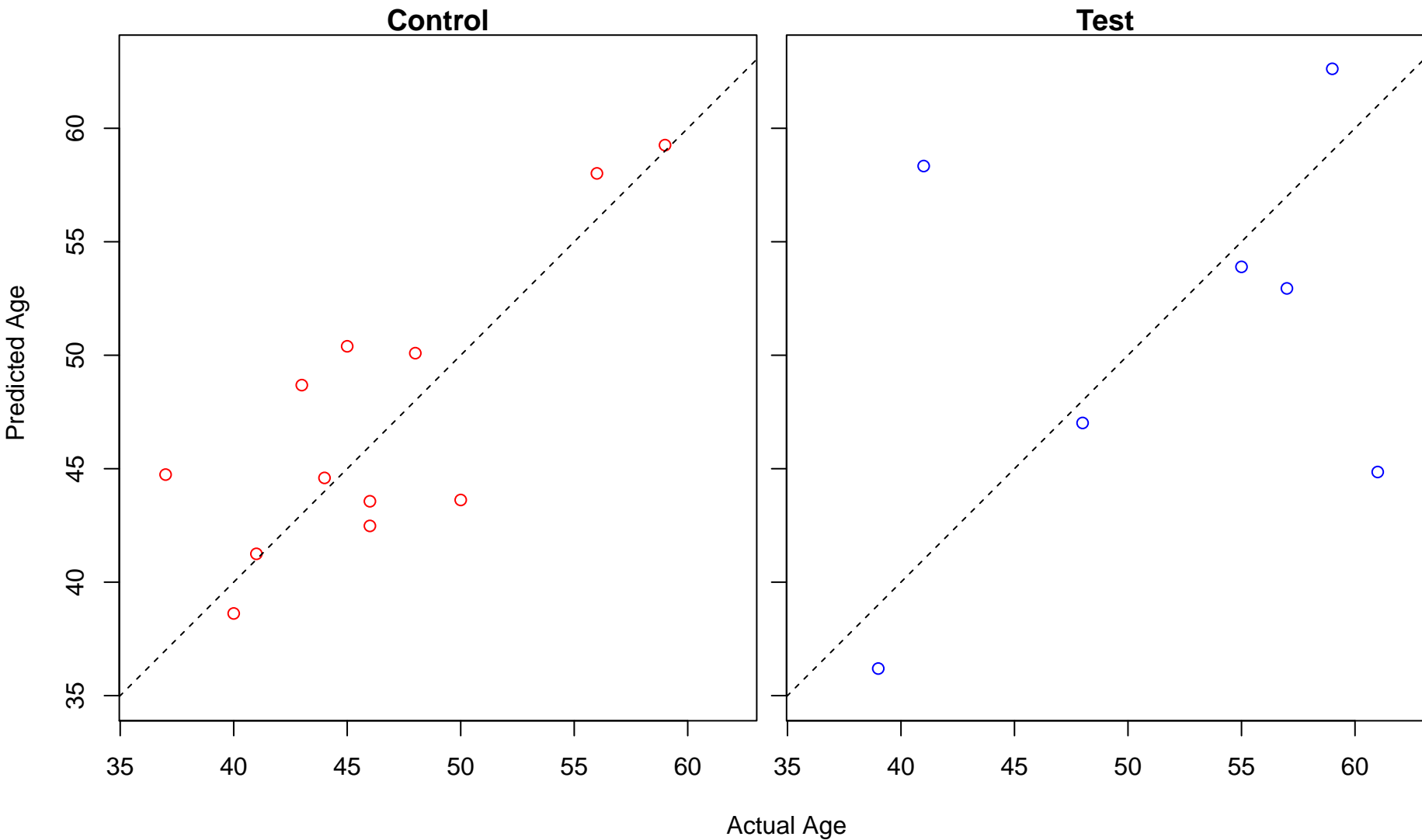
arginine metabolic process (Score: 11.255288)



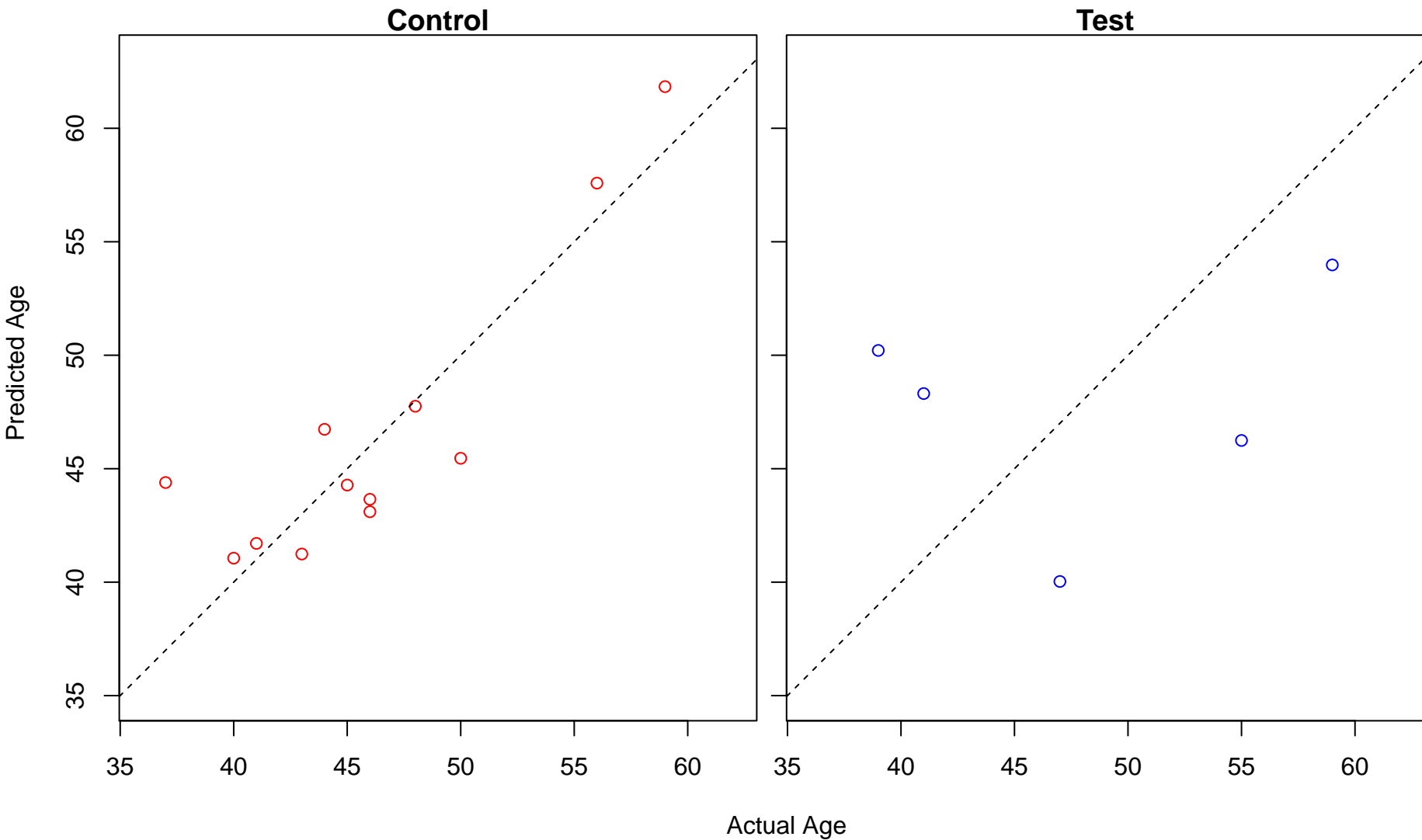
arginine catabolic process (Score: 11.255288)



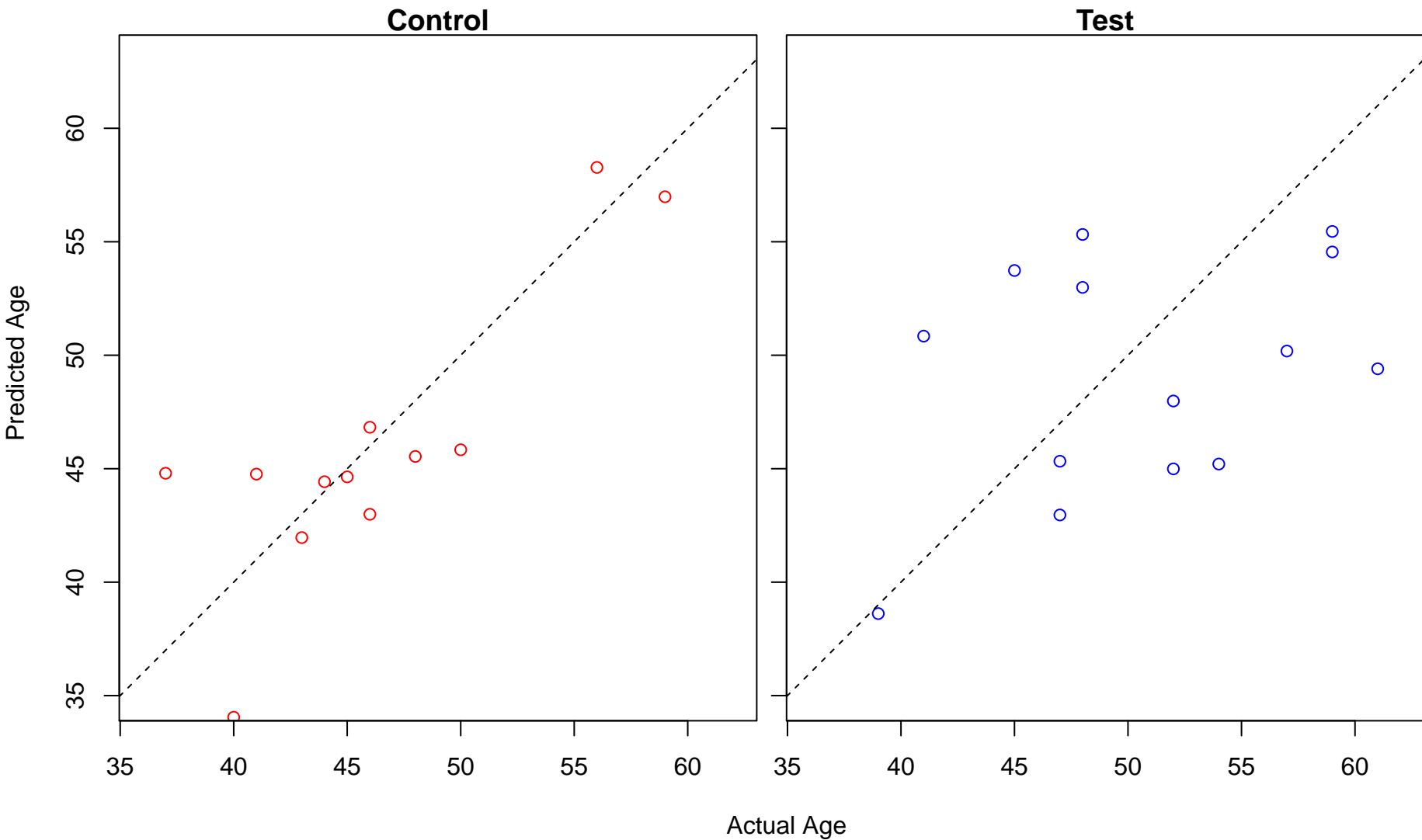
cardiac ventricle development (Score: 11.243562)



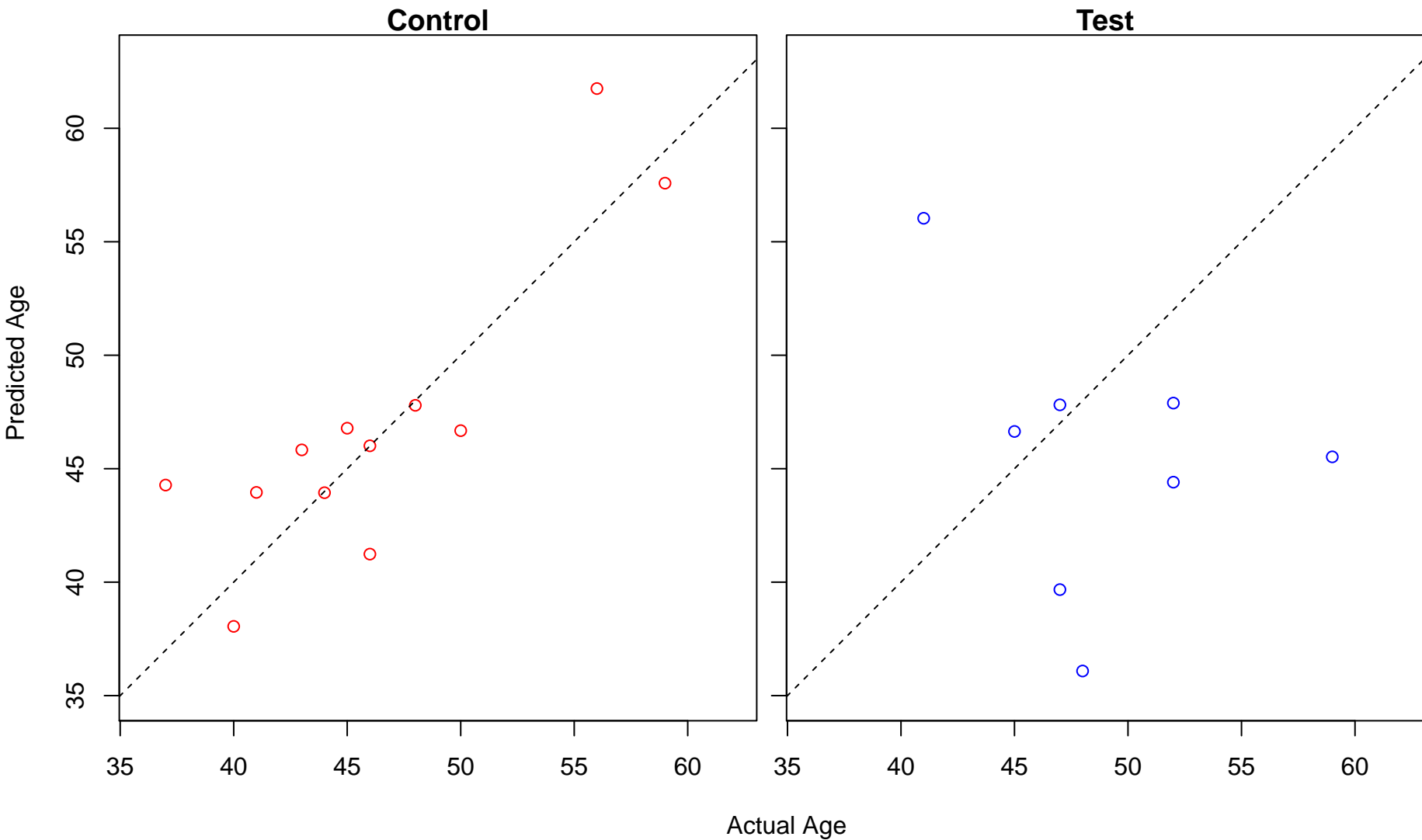
regulation of blood circulation (Score: 11.229234)



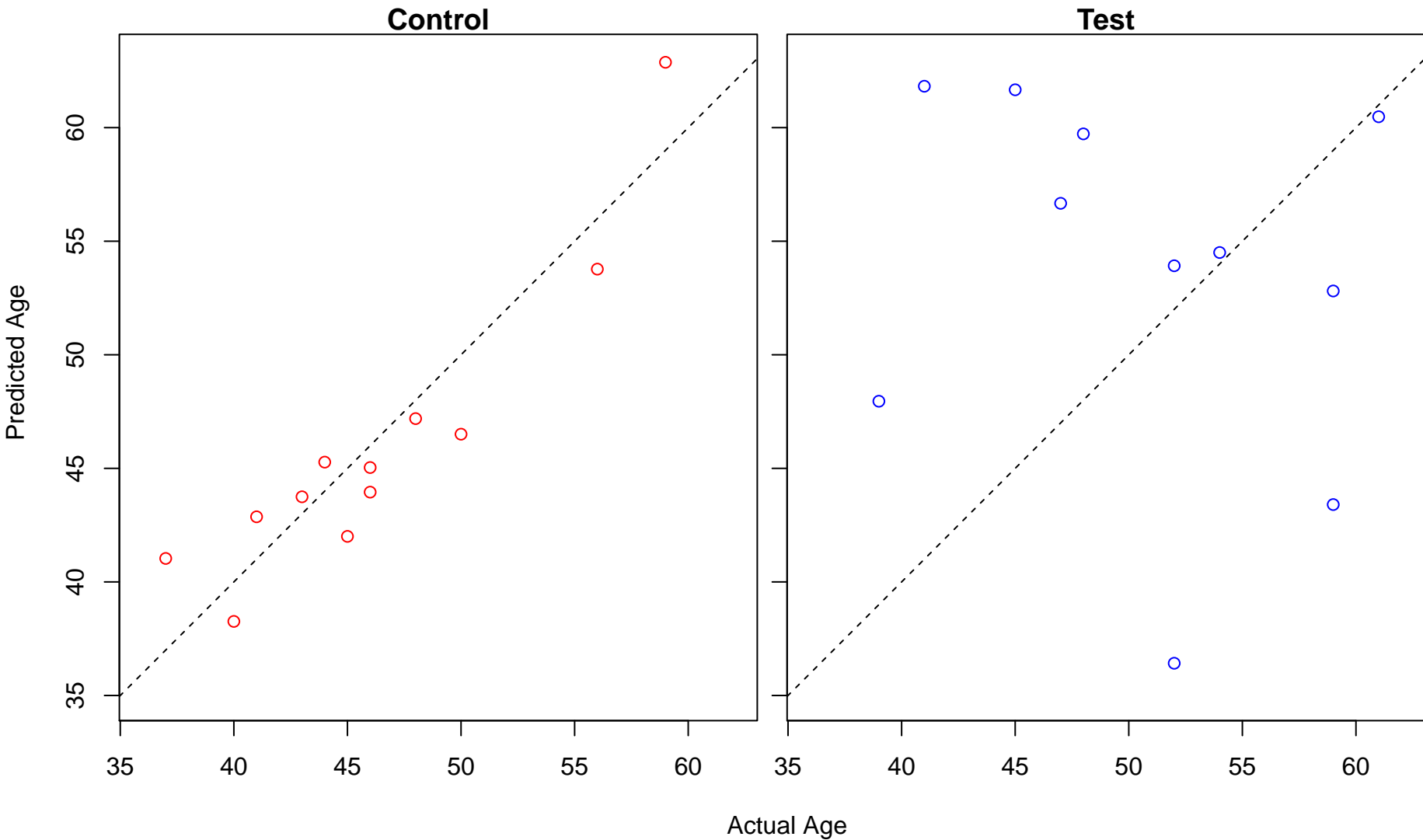
cytoplasmic sequestering of transcription factor (Score: 11.209090)



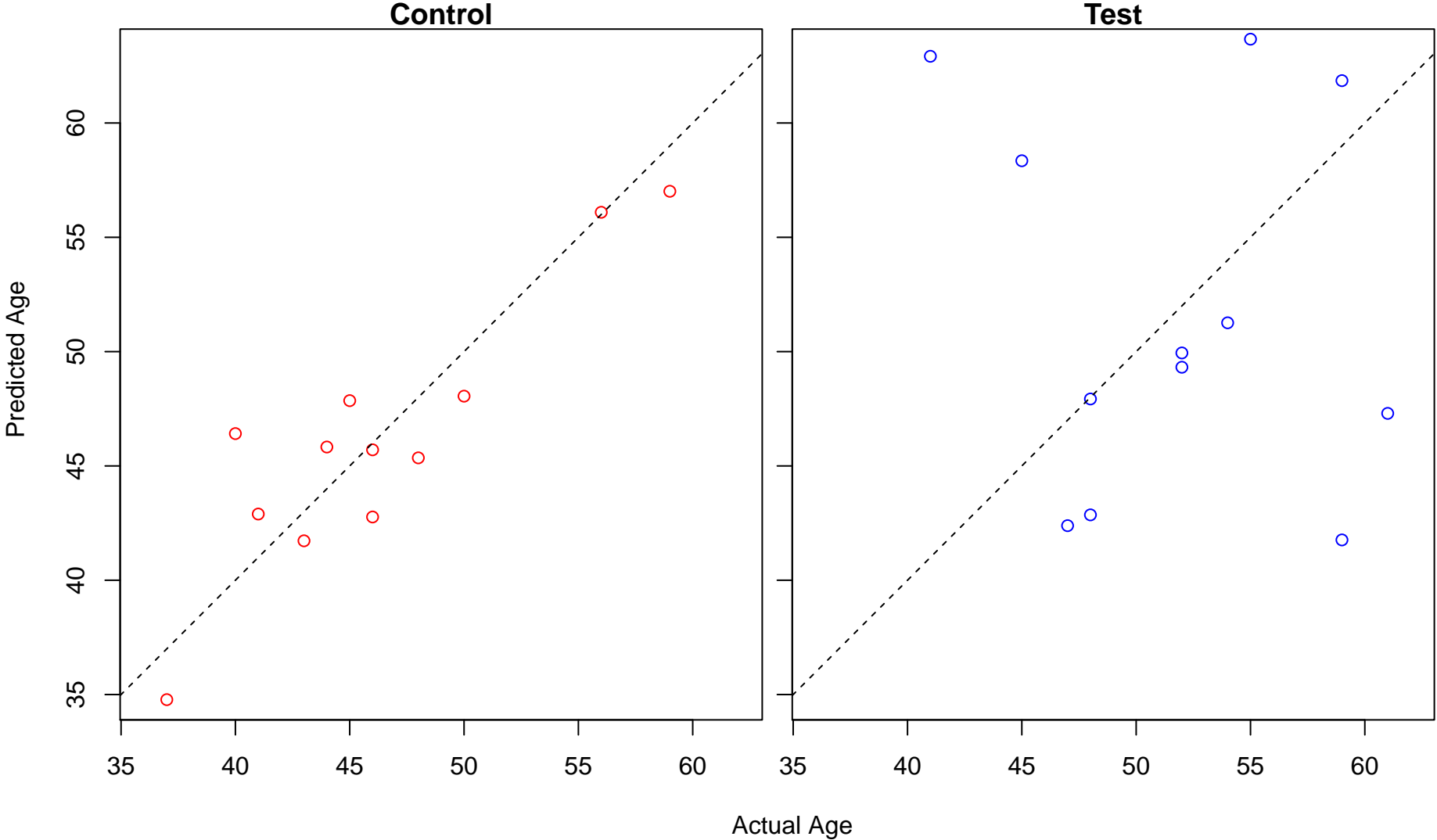
positive regulation of protein localization to chromosome, telomeric region (Score: 11.184768)



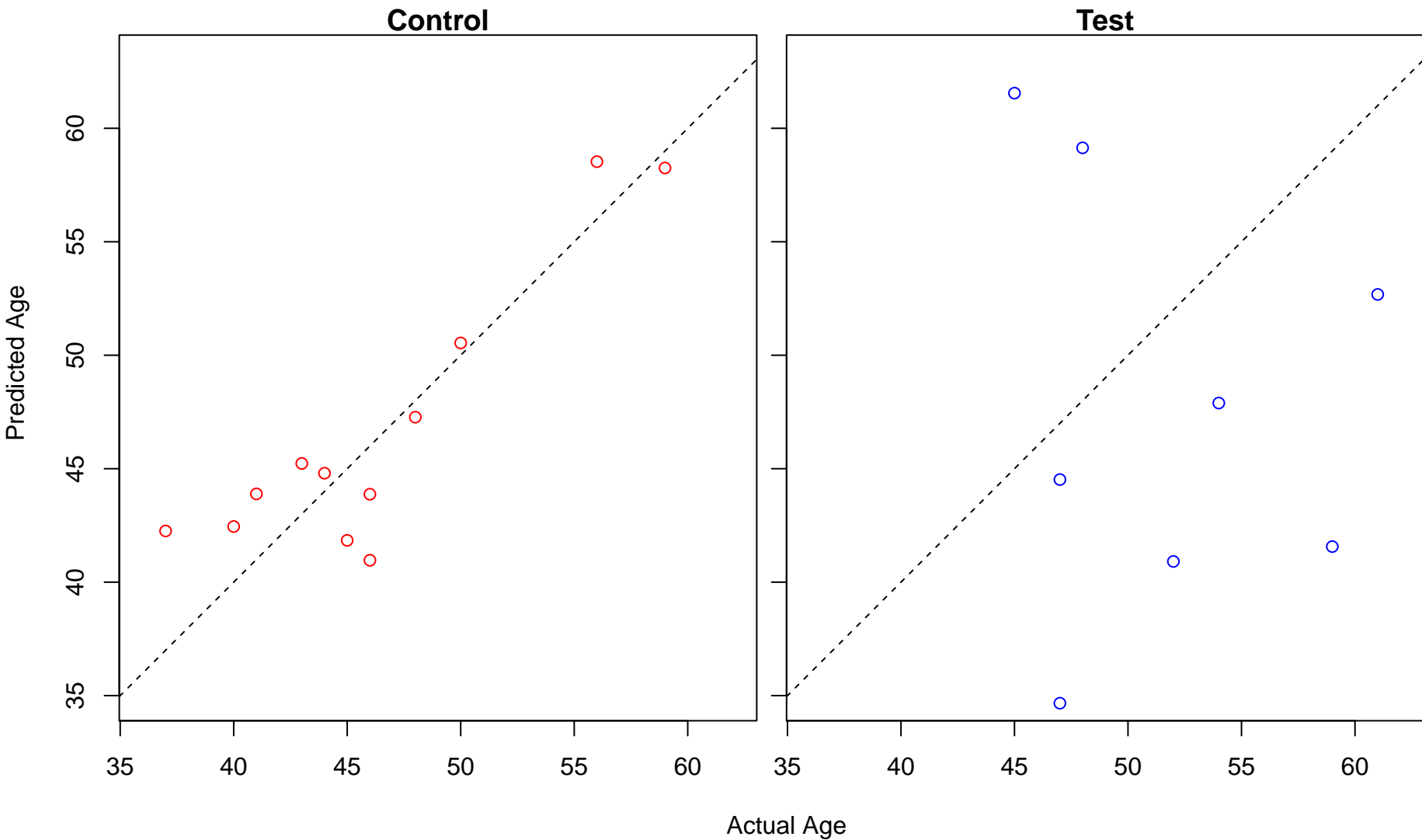
regulation of vacuole organization (Score: 11.177914)



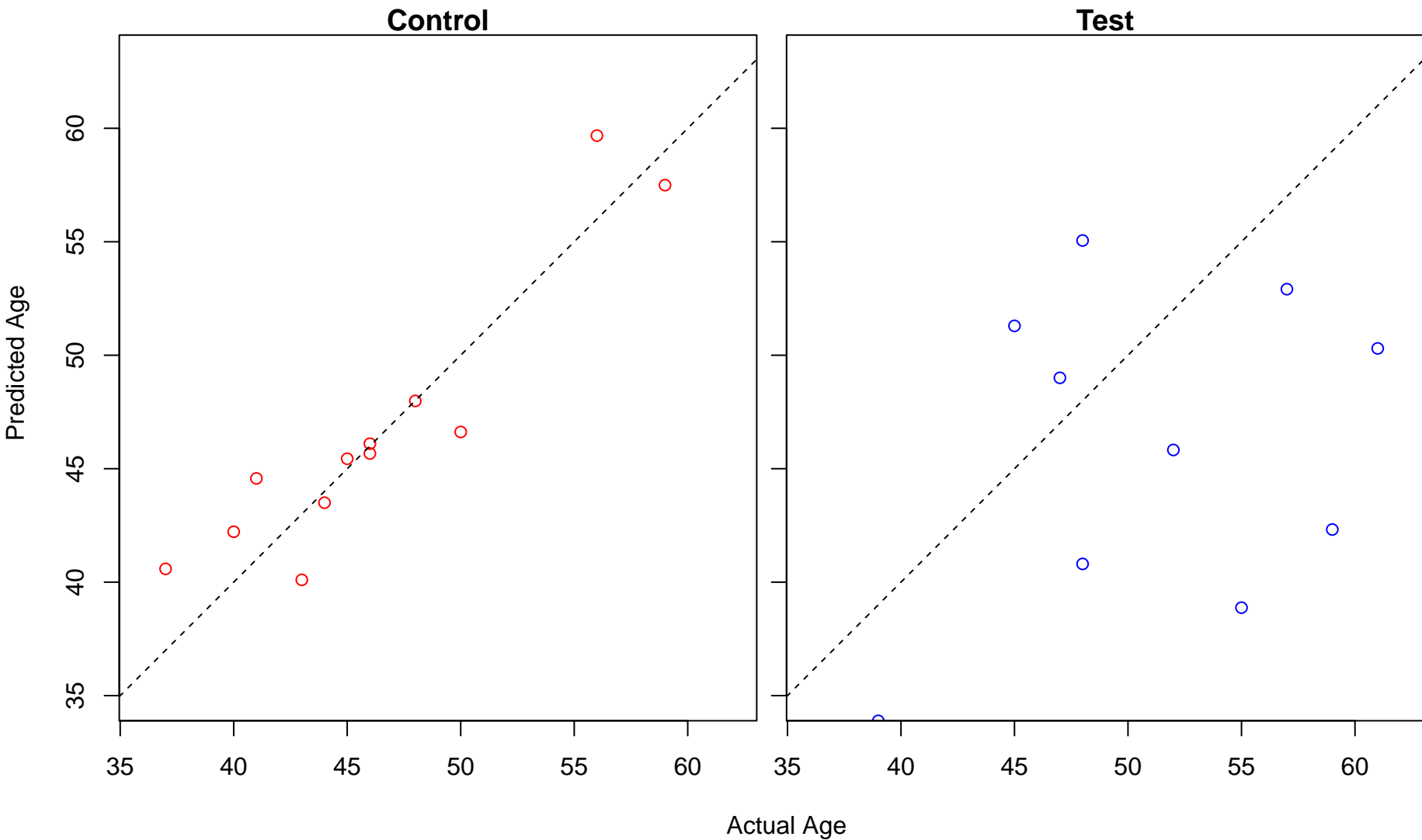
negative regulation of transcription from RNA polymerase II promoter in response to stress (Score: 11.1)



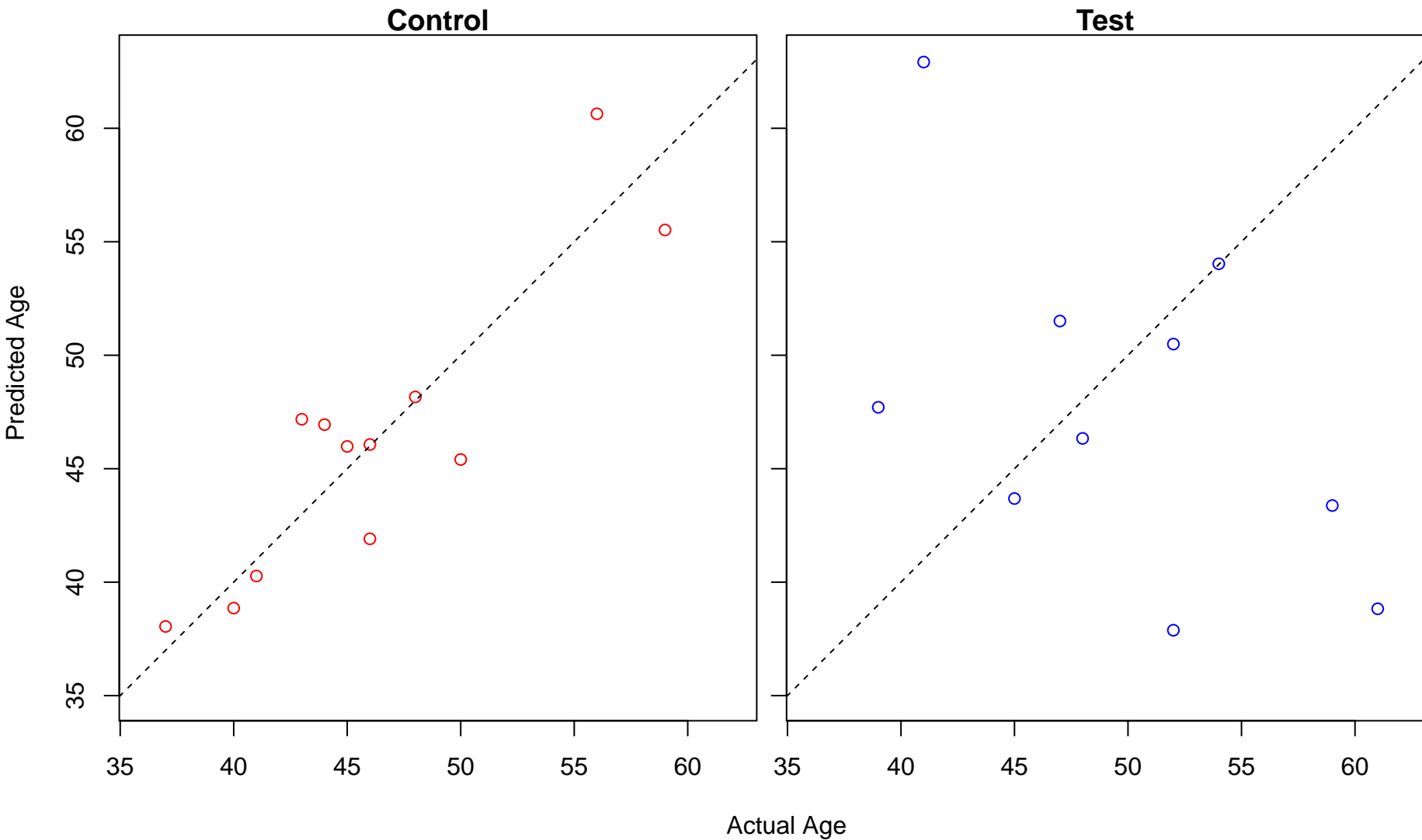
response to corticosteroid (Score: 11.138067)



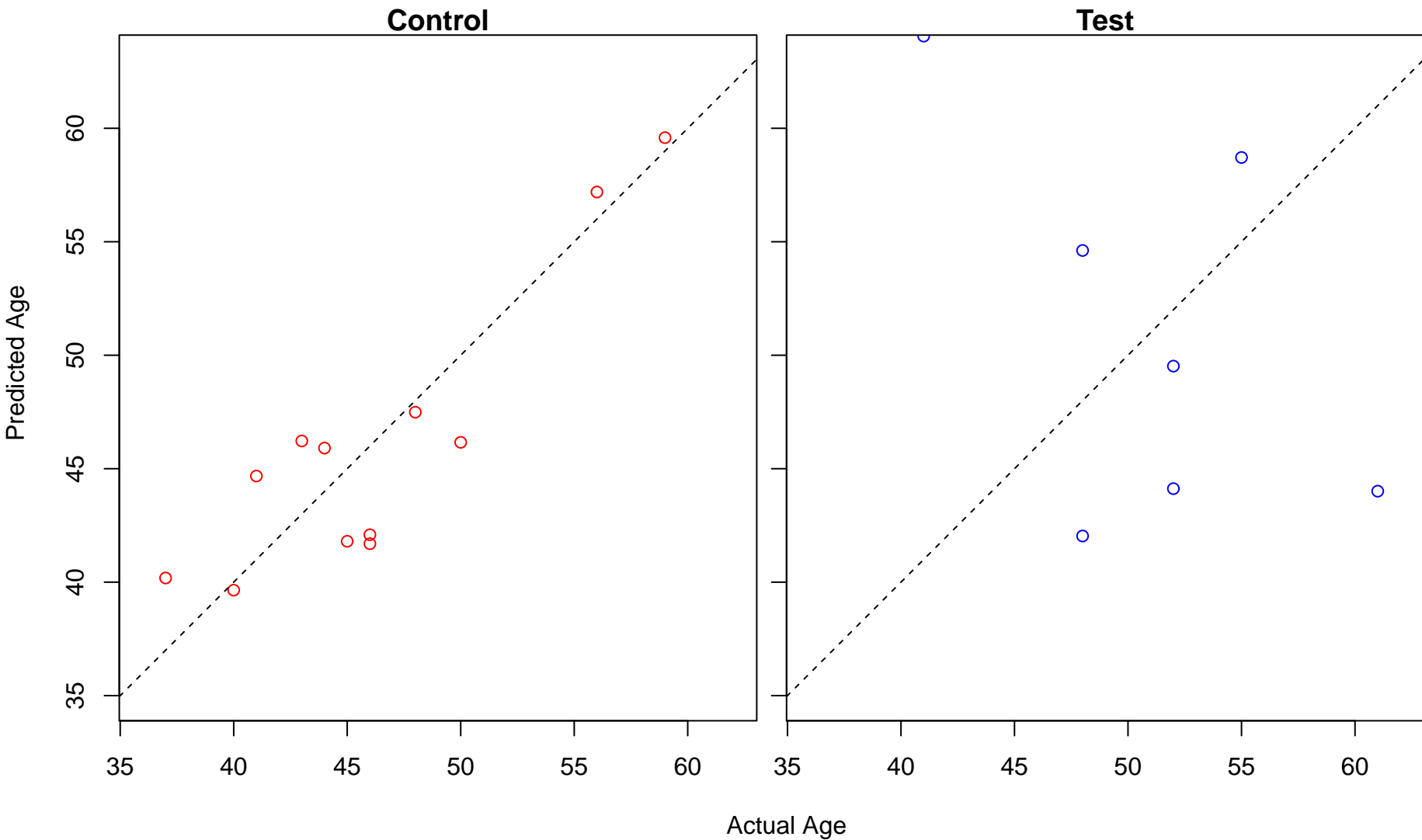
ribonucleoside catabolic process (Score: 11.086295)



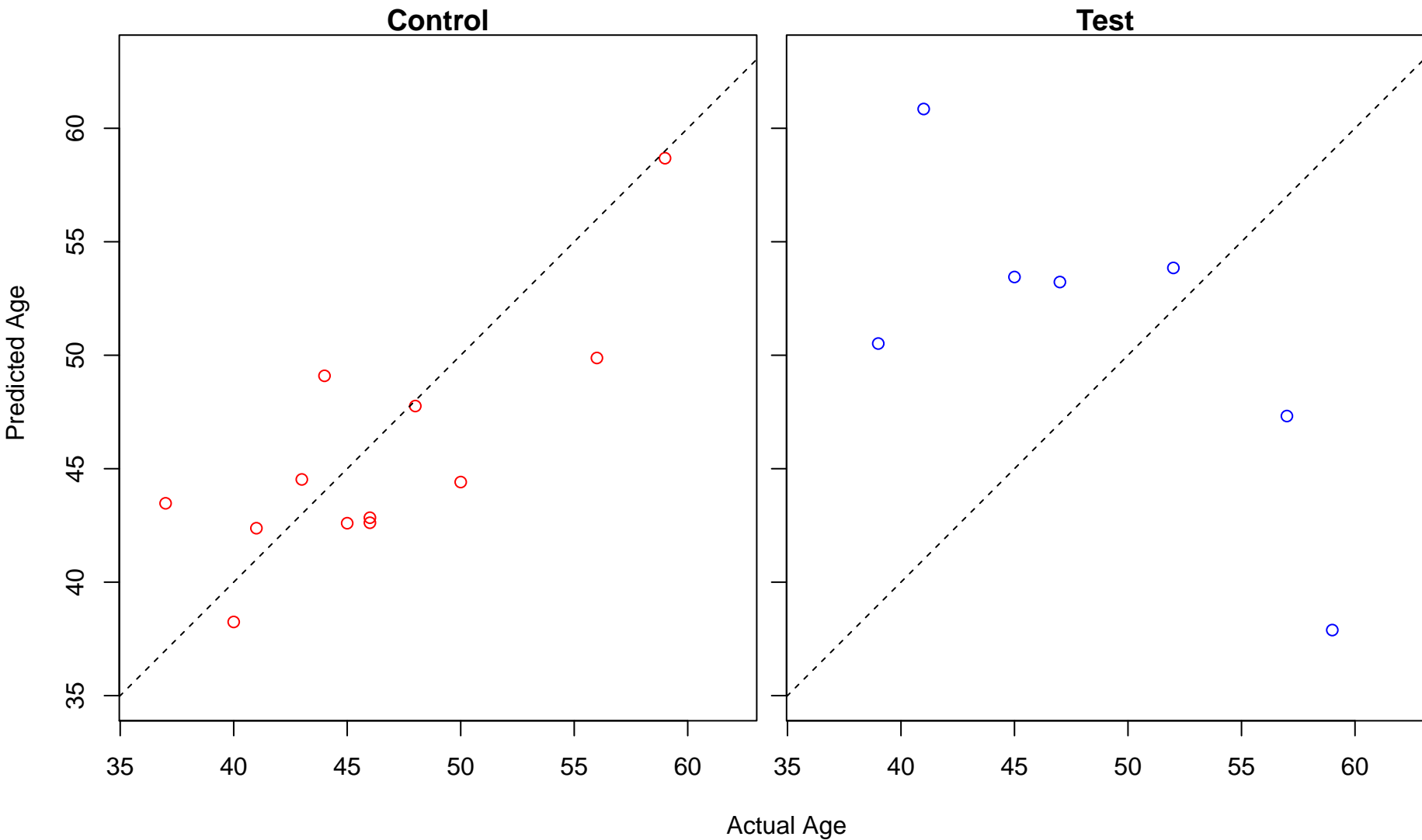
mucosal immune response (Score: 11.077382)



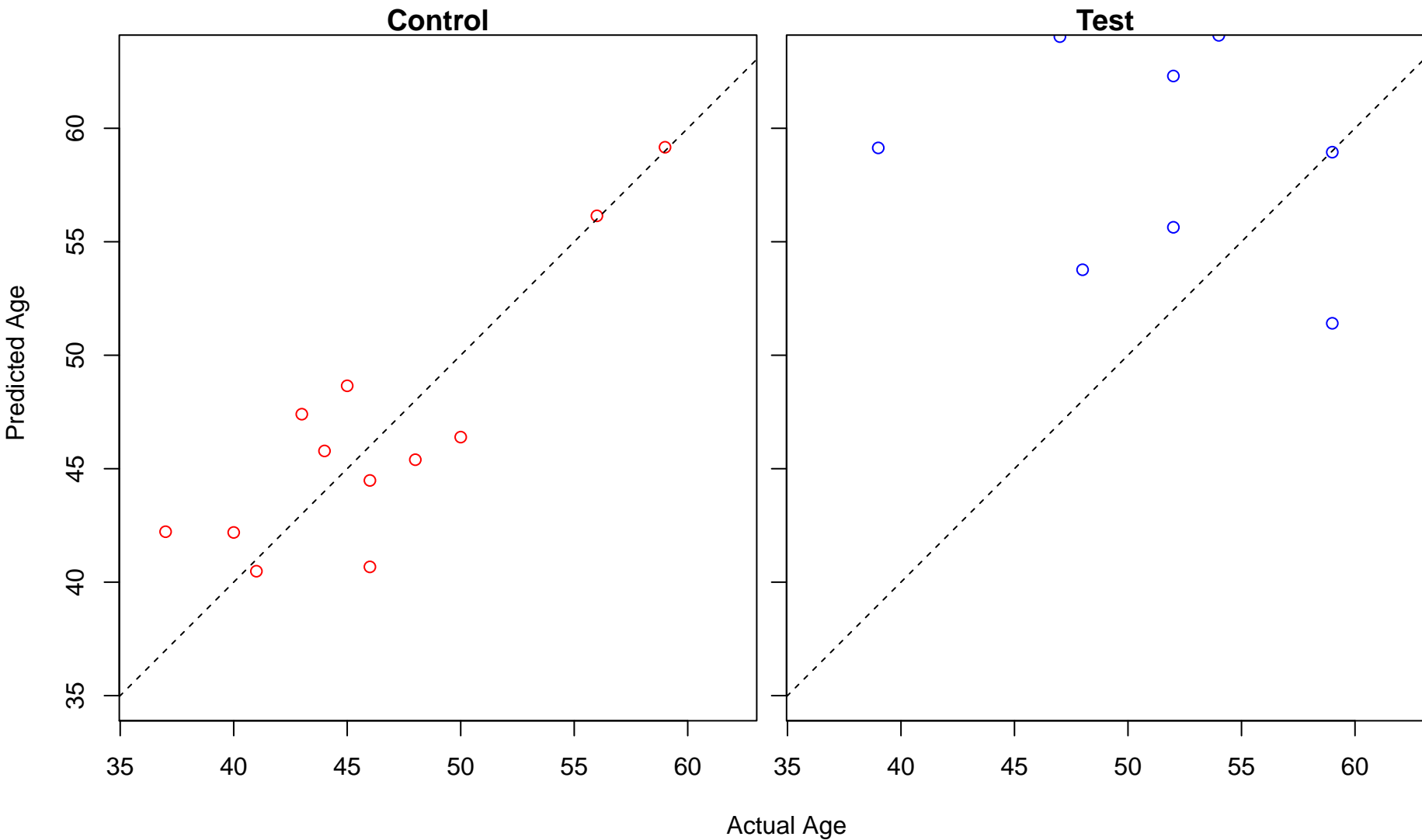
developmental process involved in reproduction (Score: 11.073515)



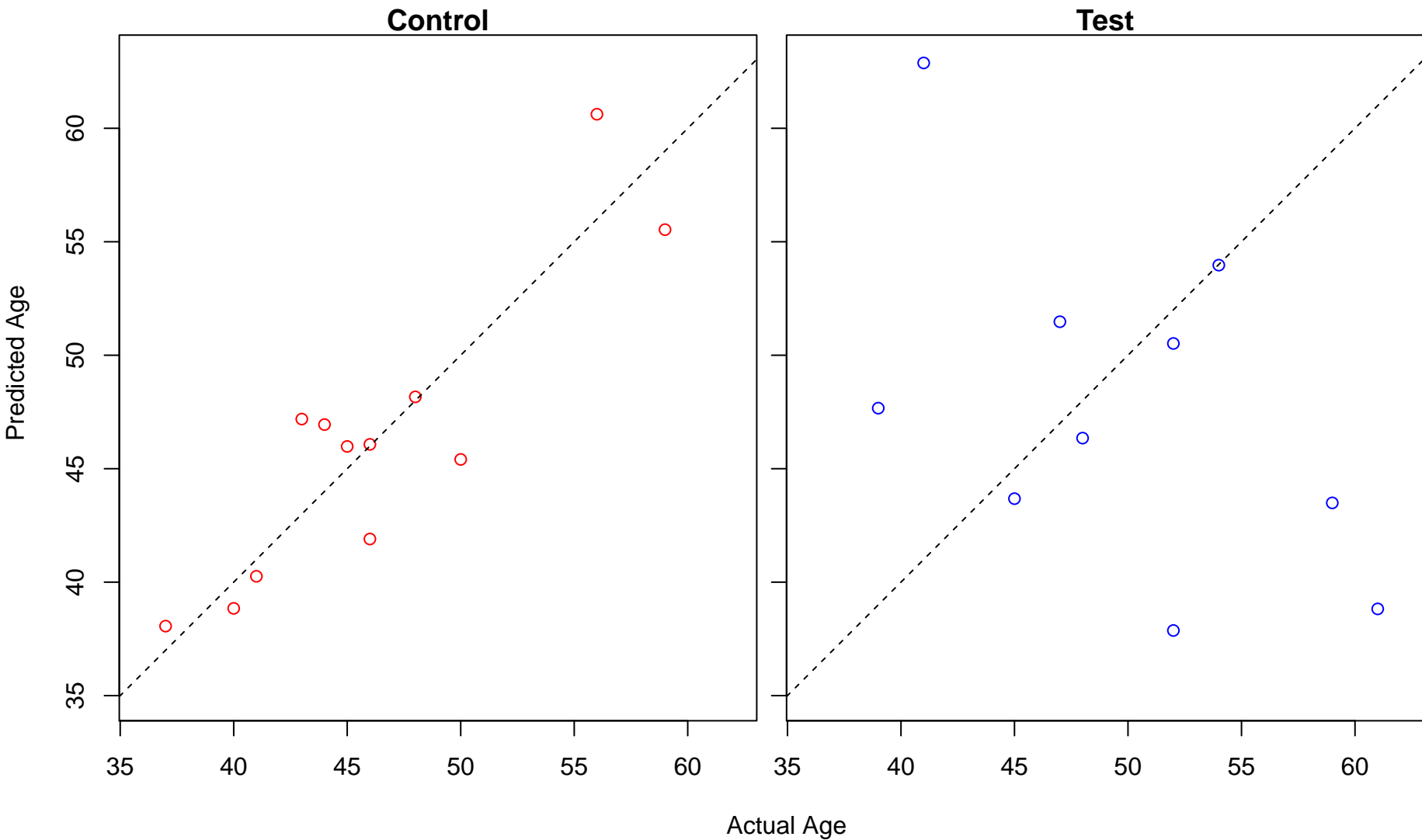
determination of bilateral symmetry (Score: 11.063465)



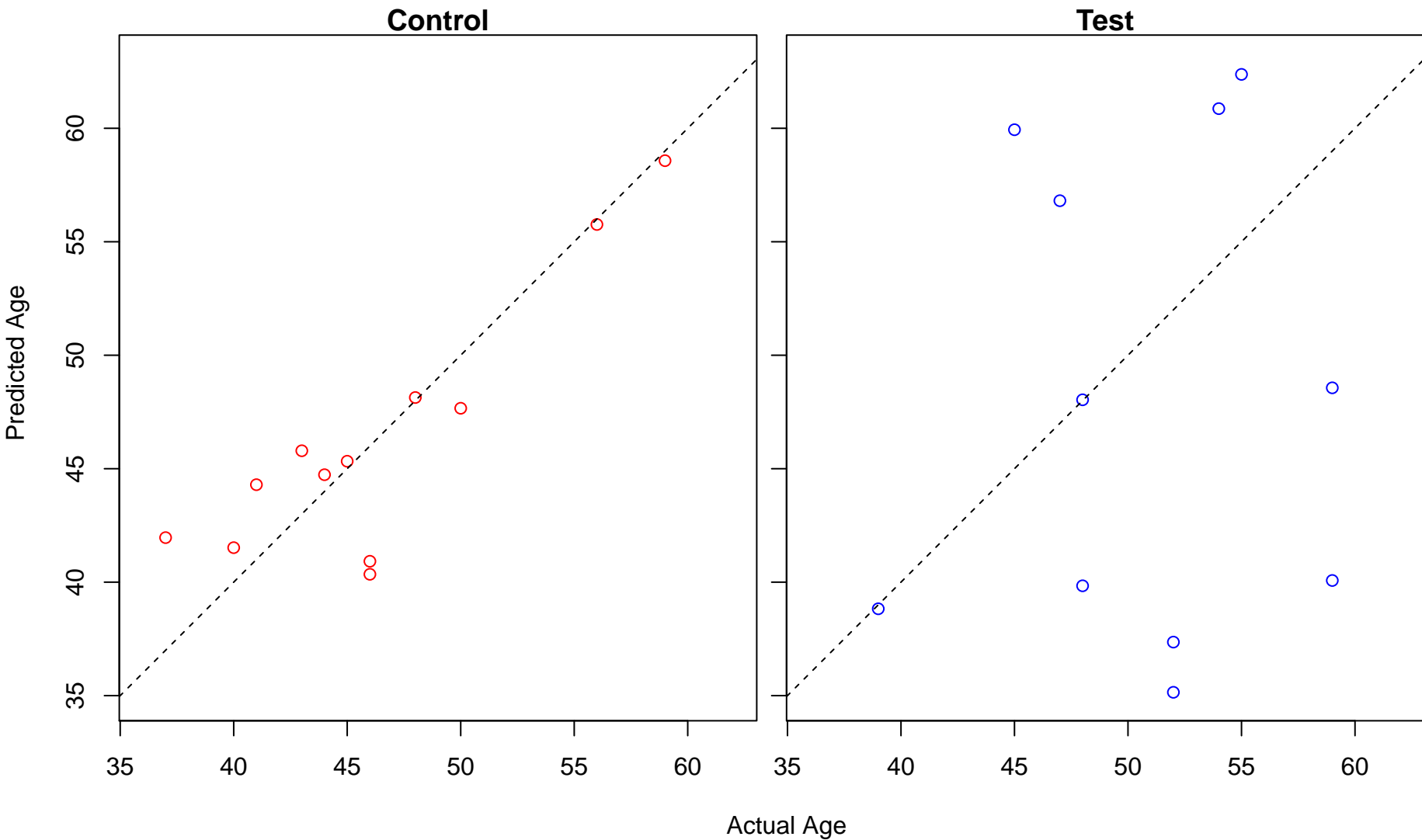
bone maturation (Score: 11.053102)



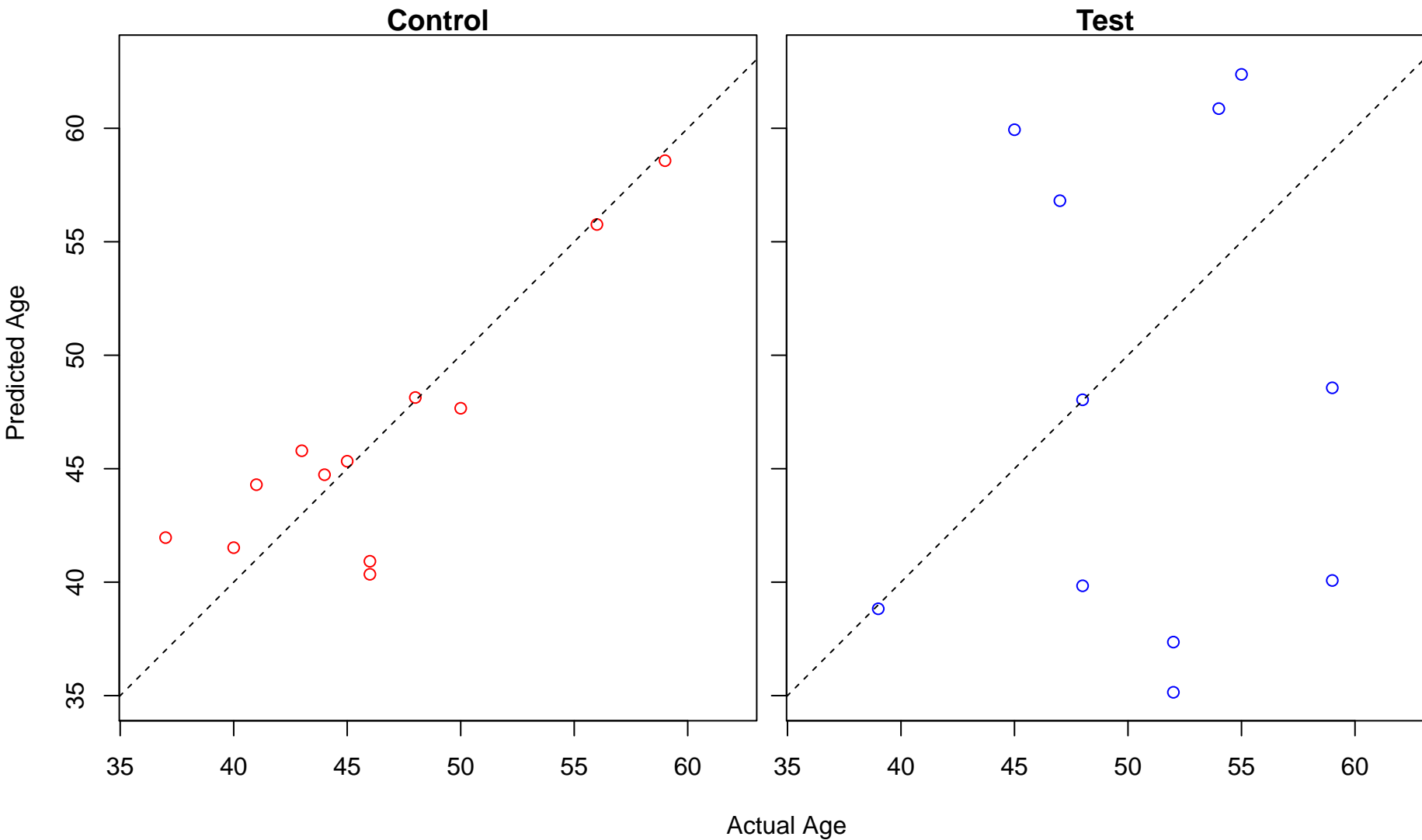
organ or tissue specific immune response (Score: 11.044679)



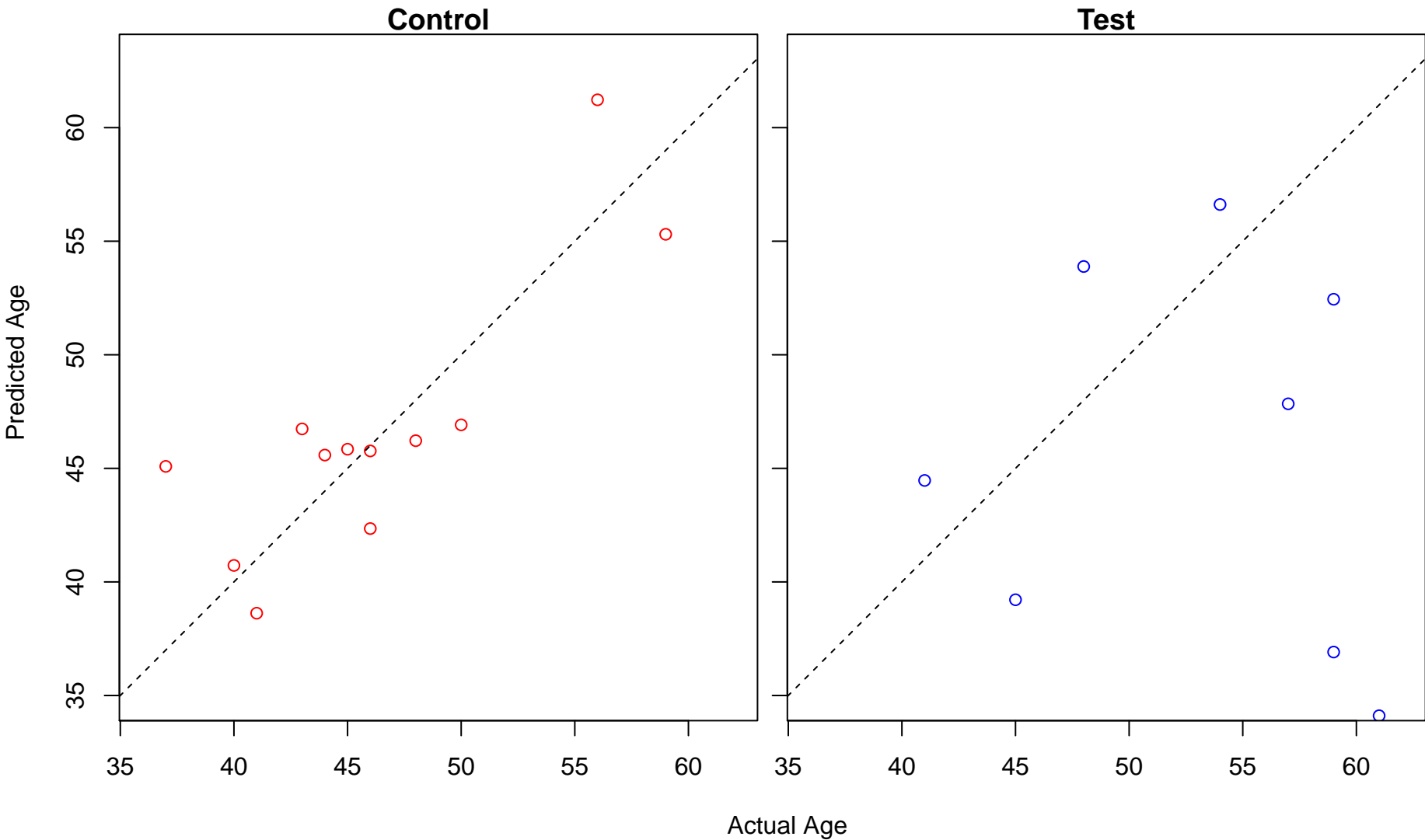
porphyrin-containing compound biosynthetic process (Score: 11.043242)



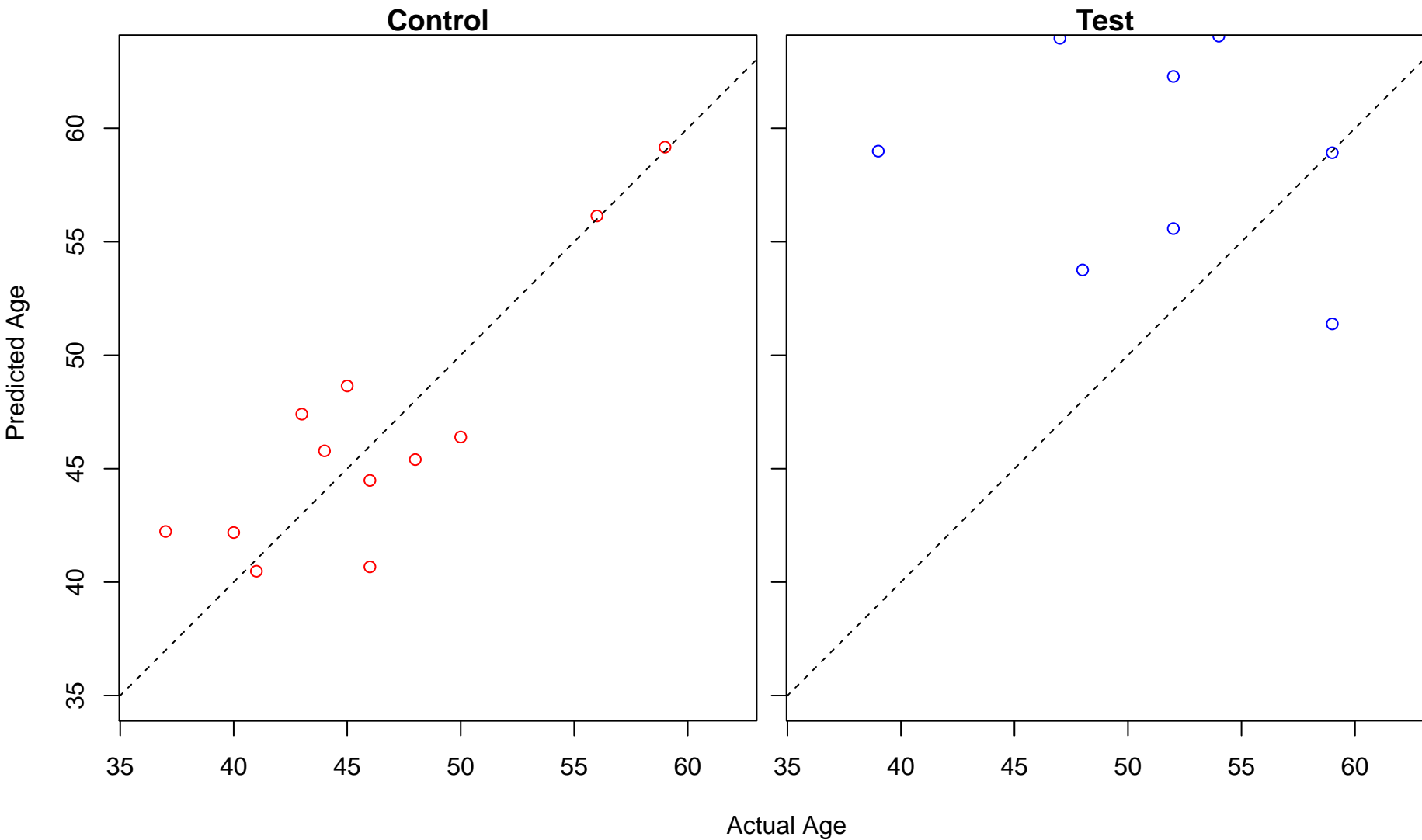
tetrapyrrole biosynthetic process (Score: 11.043242)



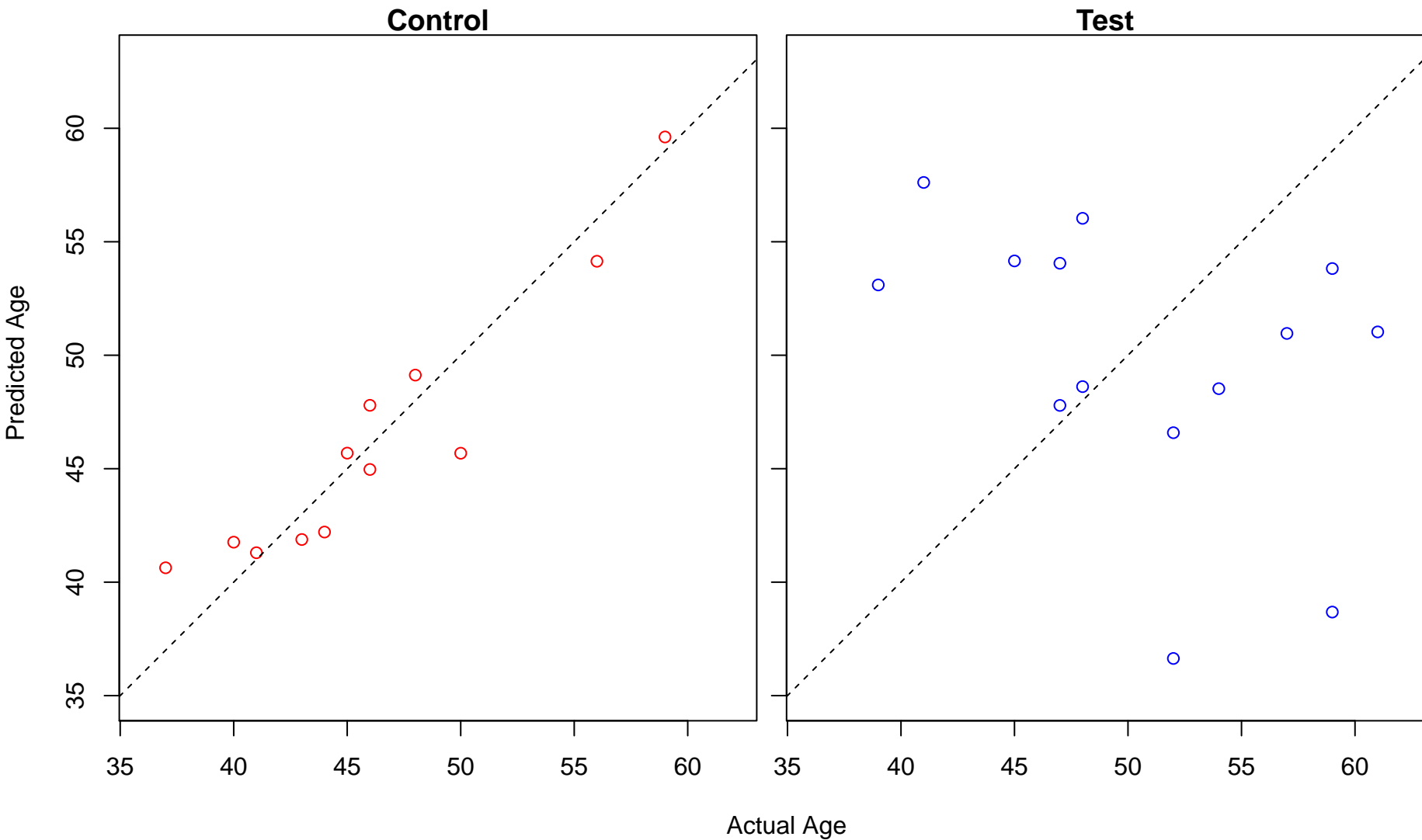
anatomical structure homeostasis (Score: 11.035624)



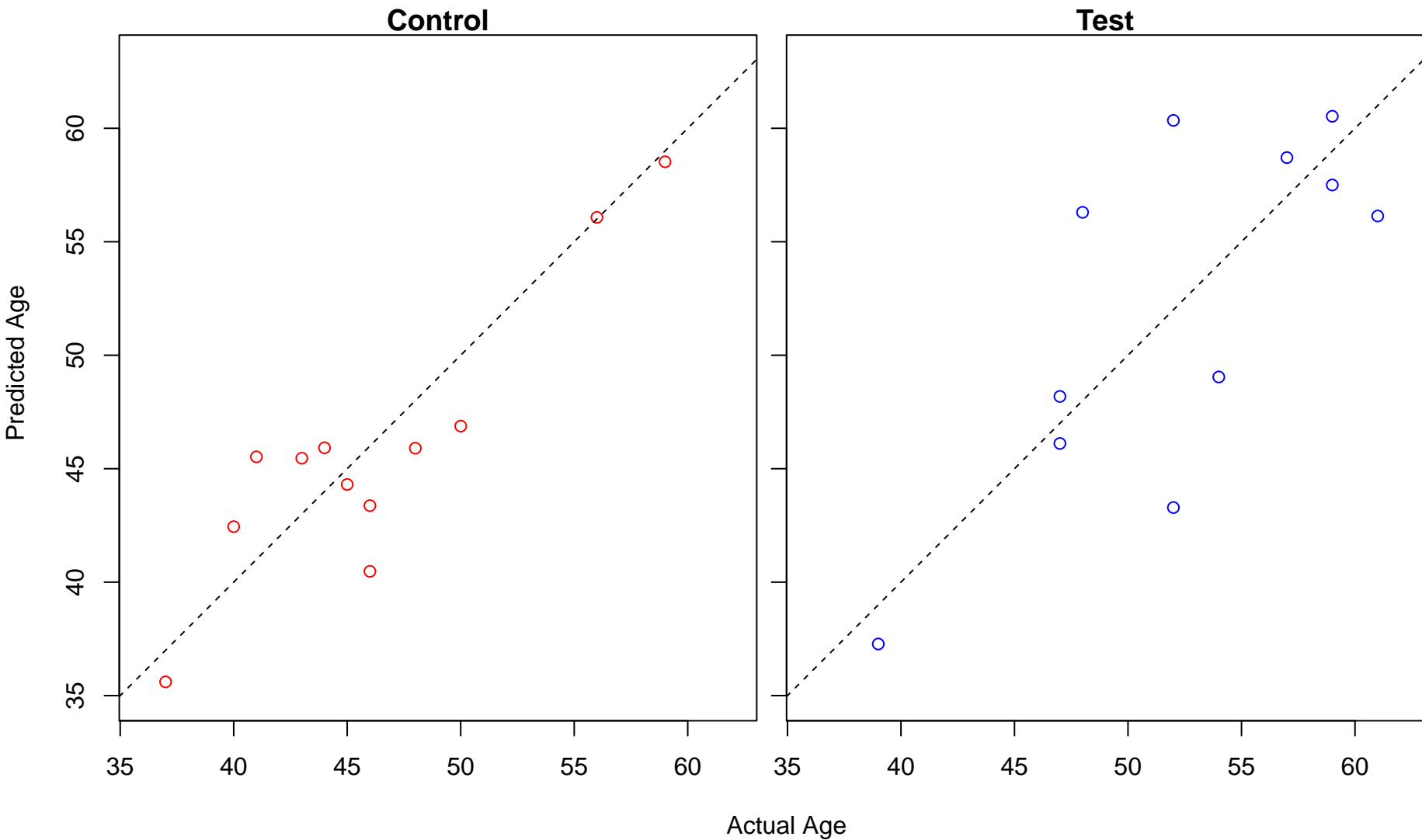
organ maturation (Score: 11.022407)



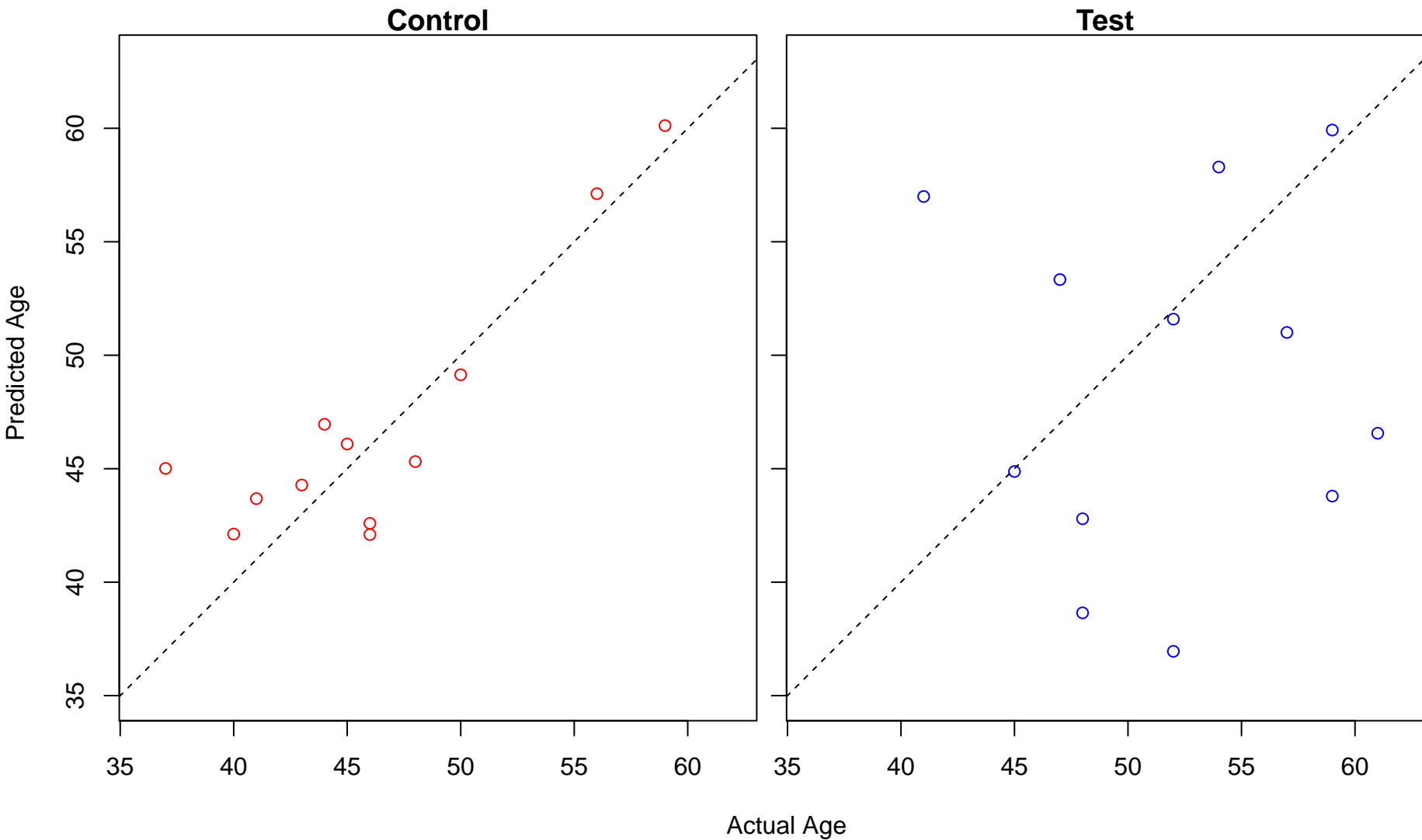
positive regulation of alpha-beta T cell activation (Score: 11.014957)



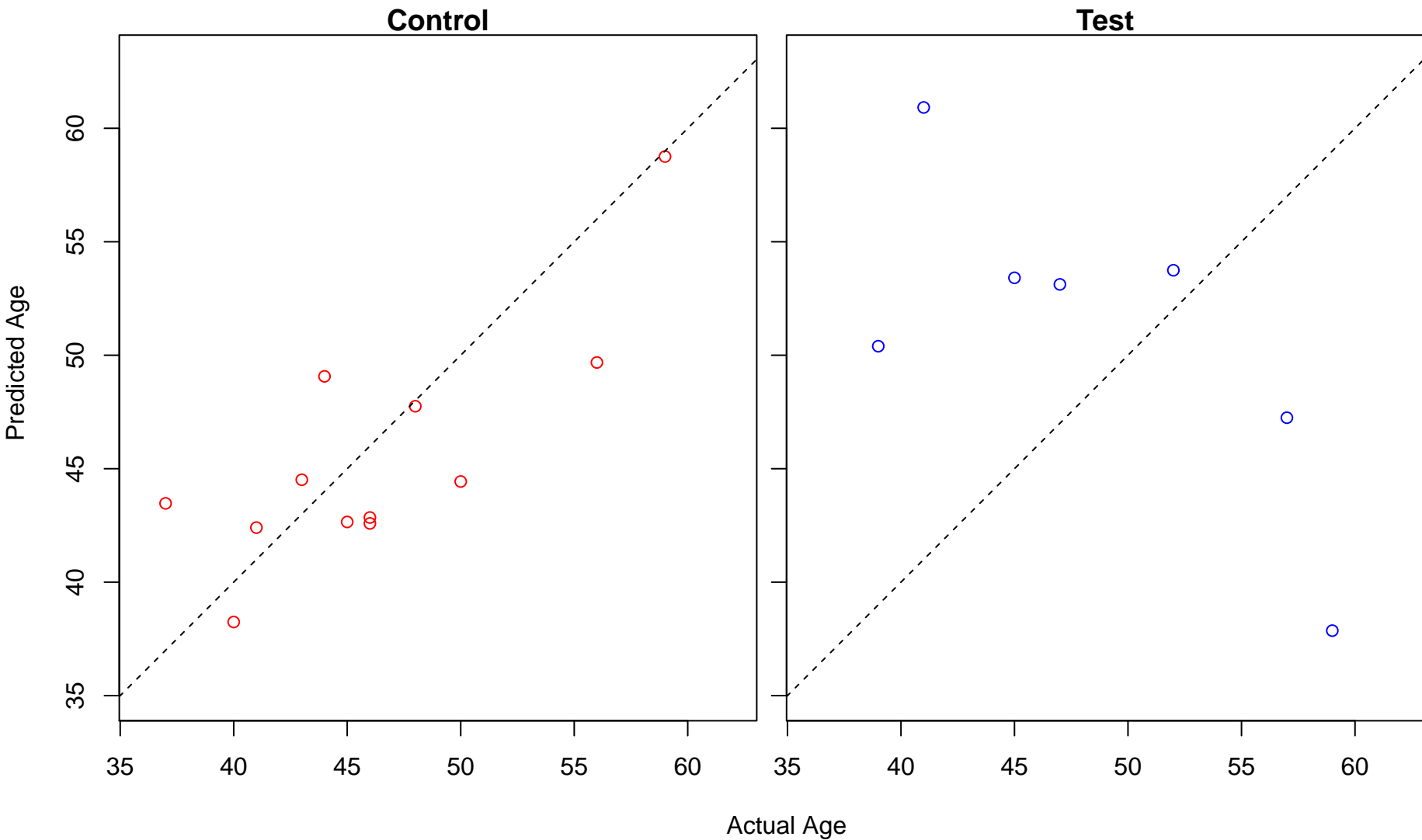
reactive oxygen species biosynthetic process (Score: 10.979642)



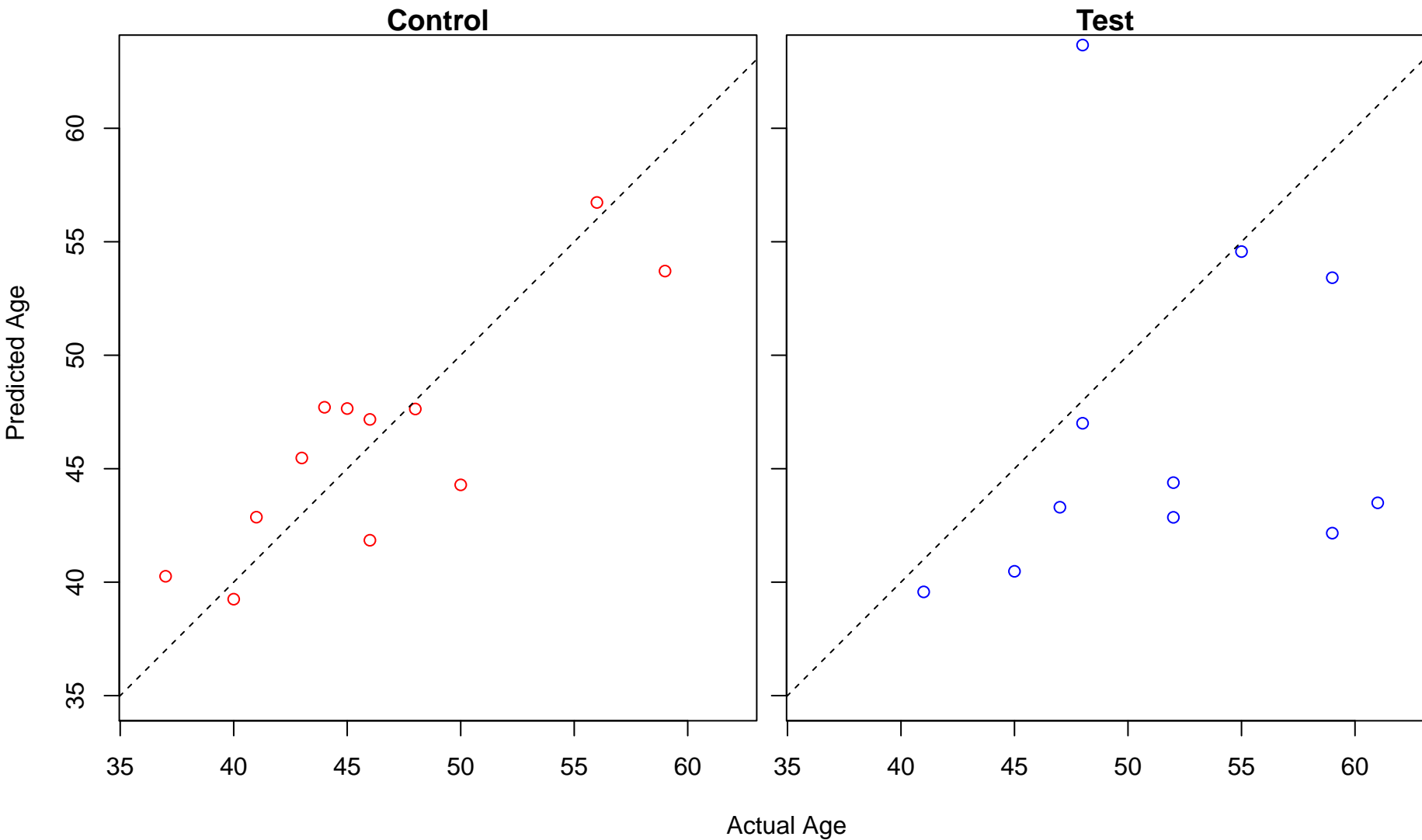
histone deubiquitination (Score: 10.929888)



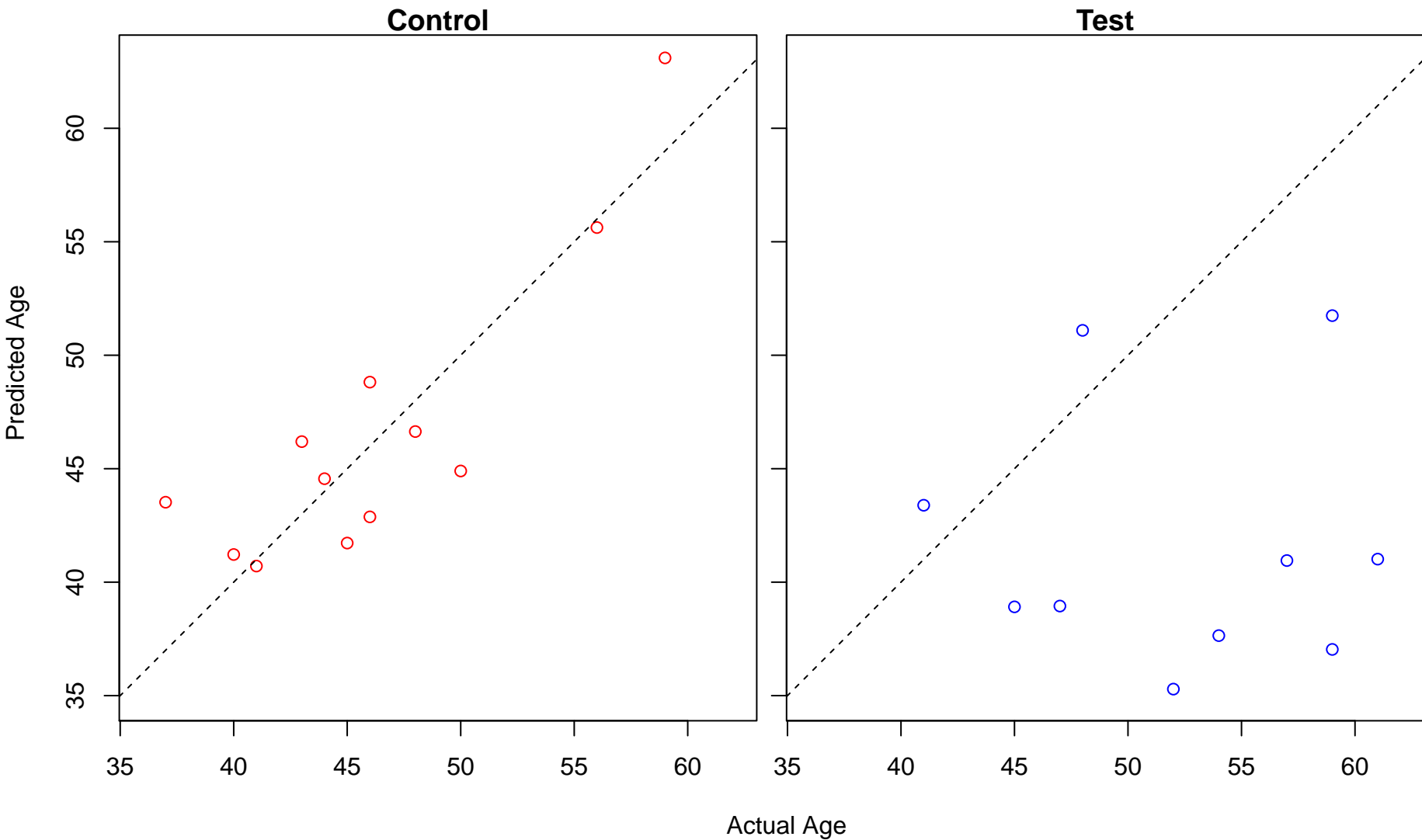
specification of symmetry (Score: 10.904944)



nucleus organization (Score: 10.877852)

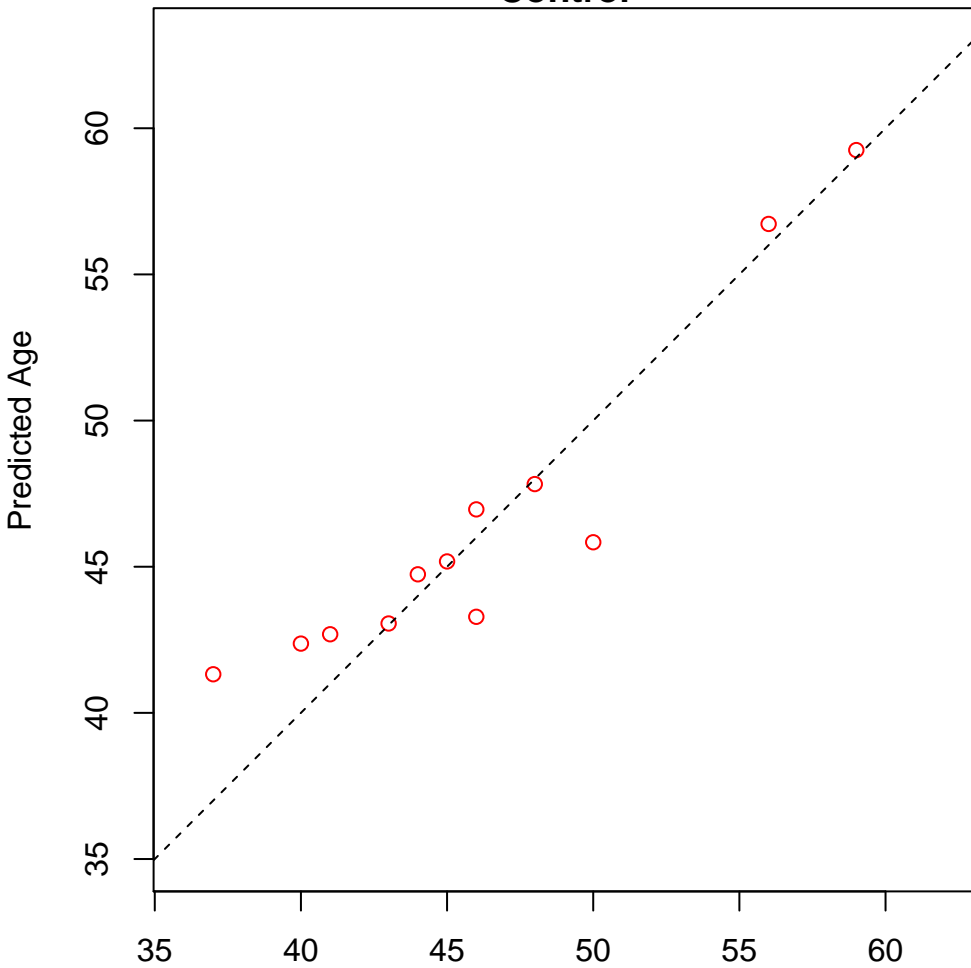


positive regulation of neurogenesis (Score: 10.848990)

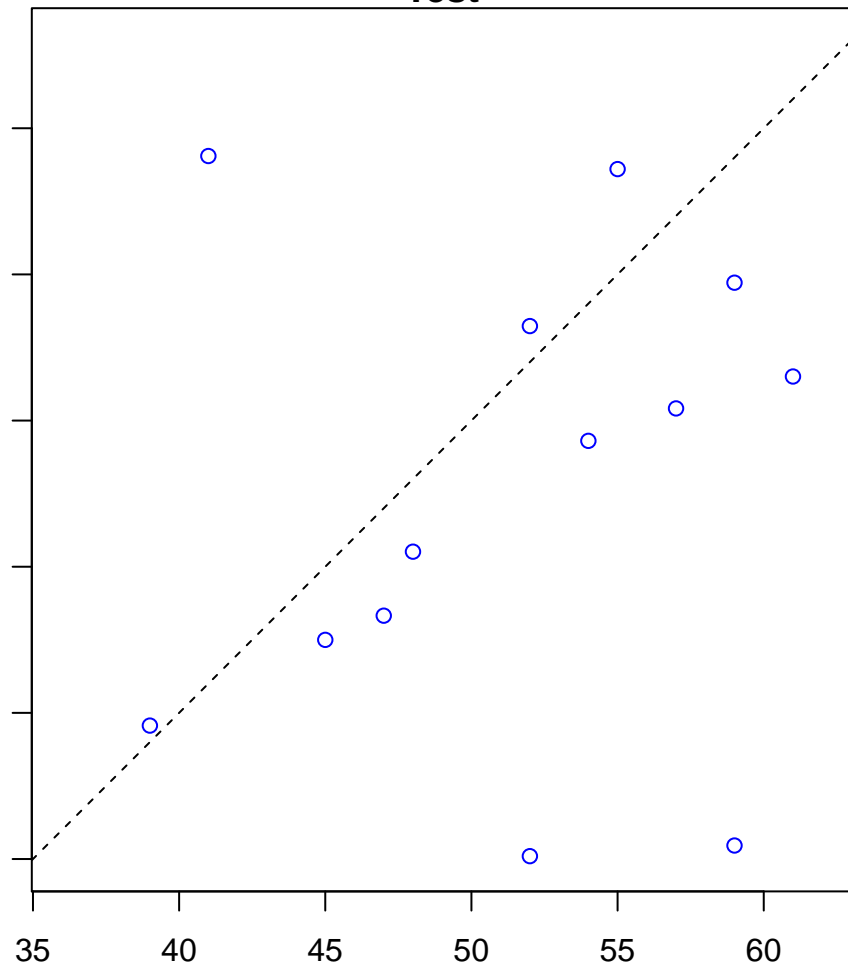


response to unfolded protein (Score: 10.847727)

Control

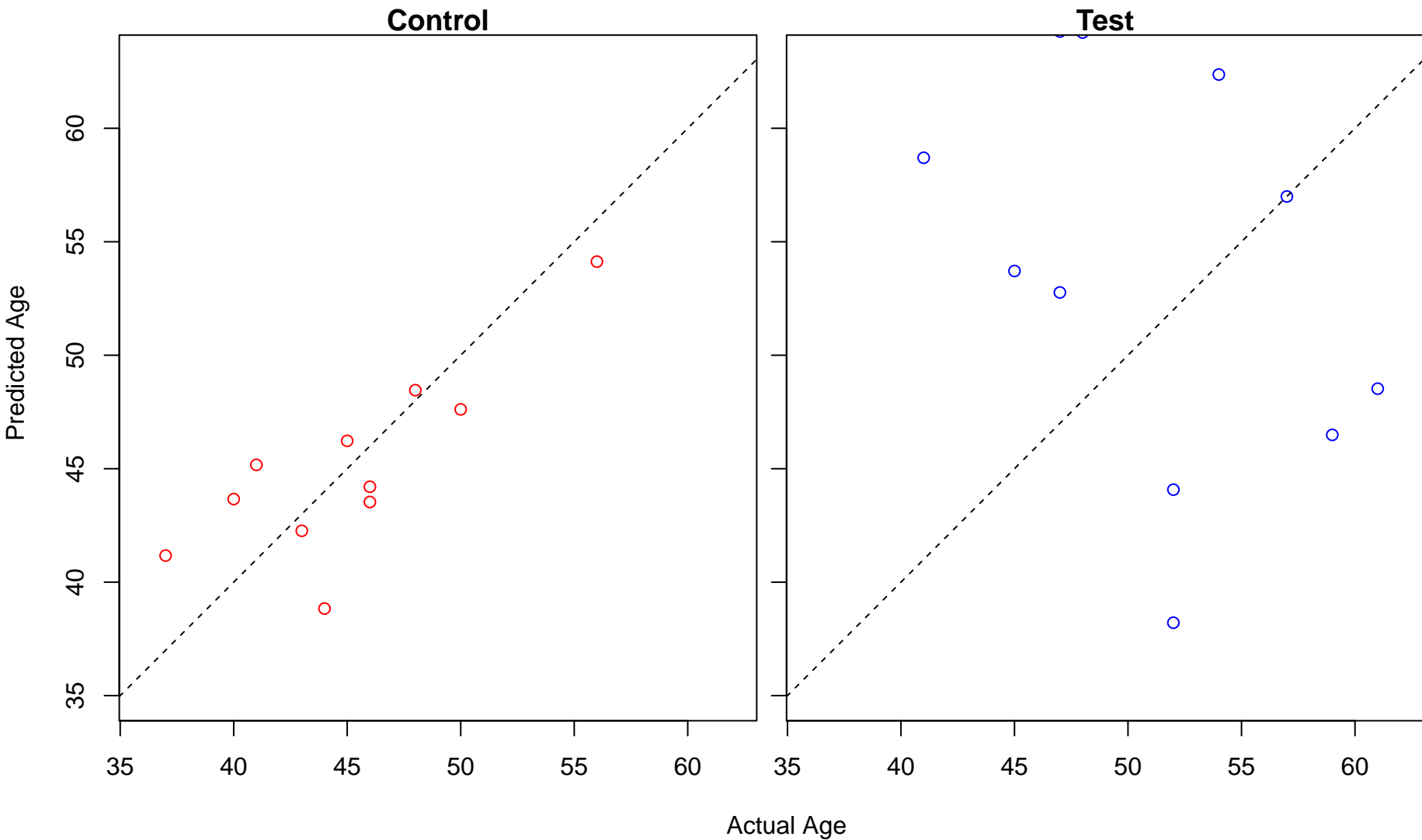


Test

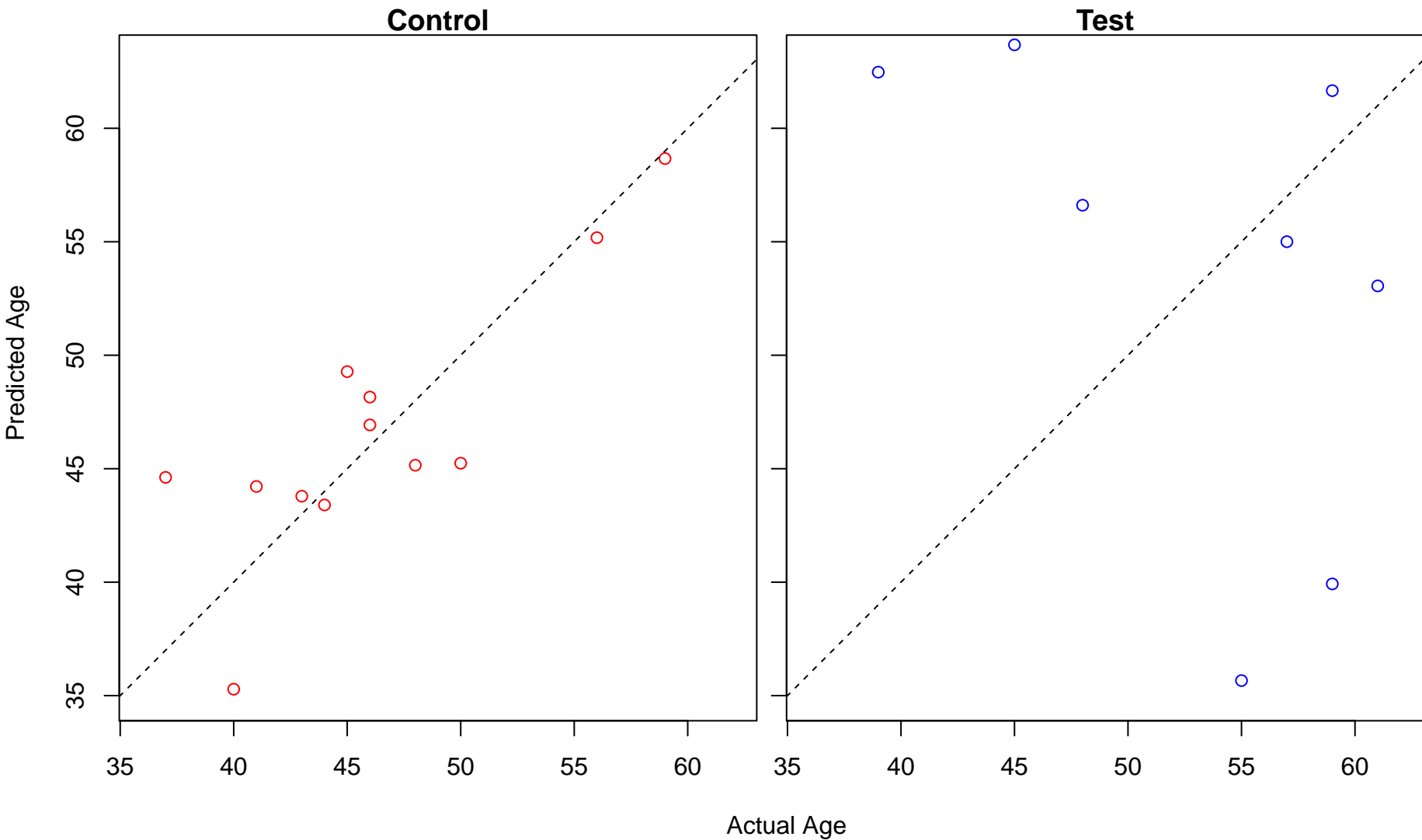


Actual Age

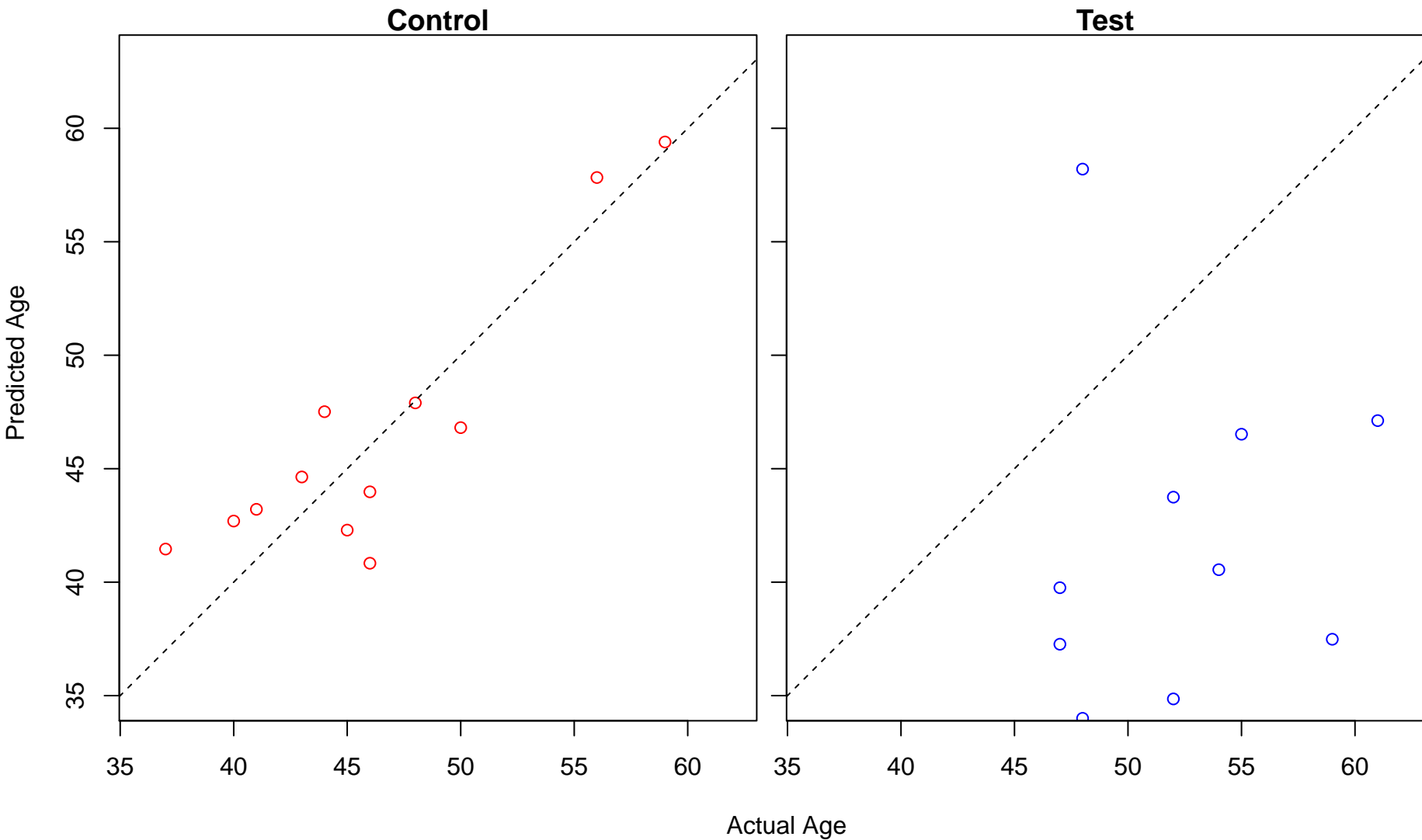
regulation of cytosolic calcium ion concentration (Score: 10.810247)



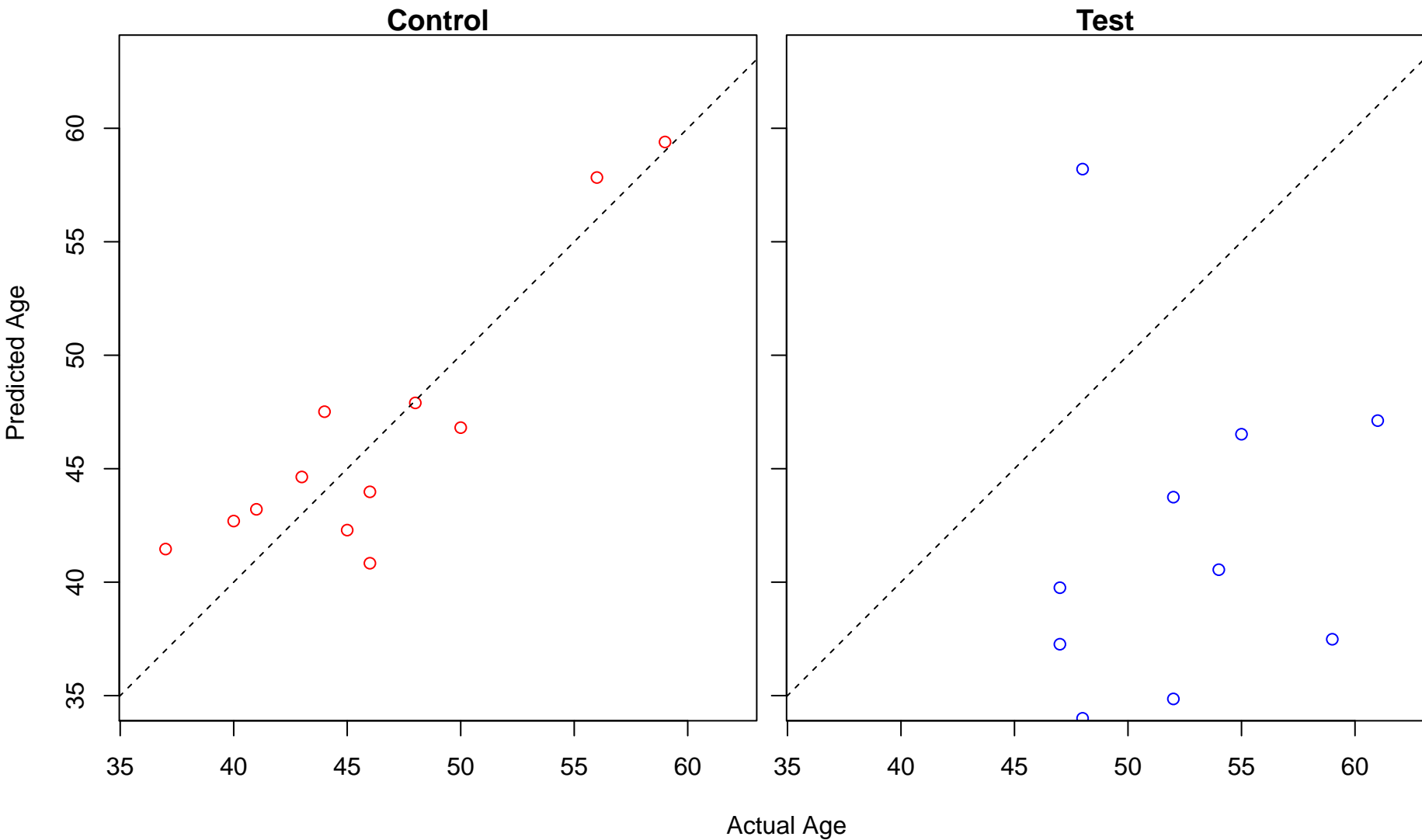
regulation of metalloenzyme activity (Score: 10.772180)



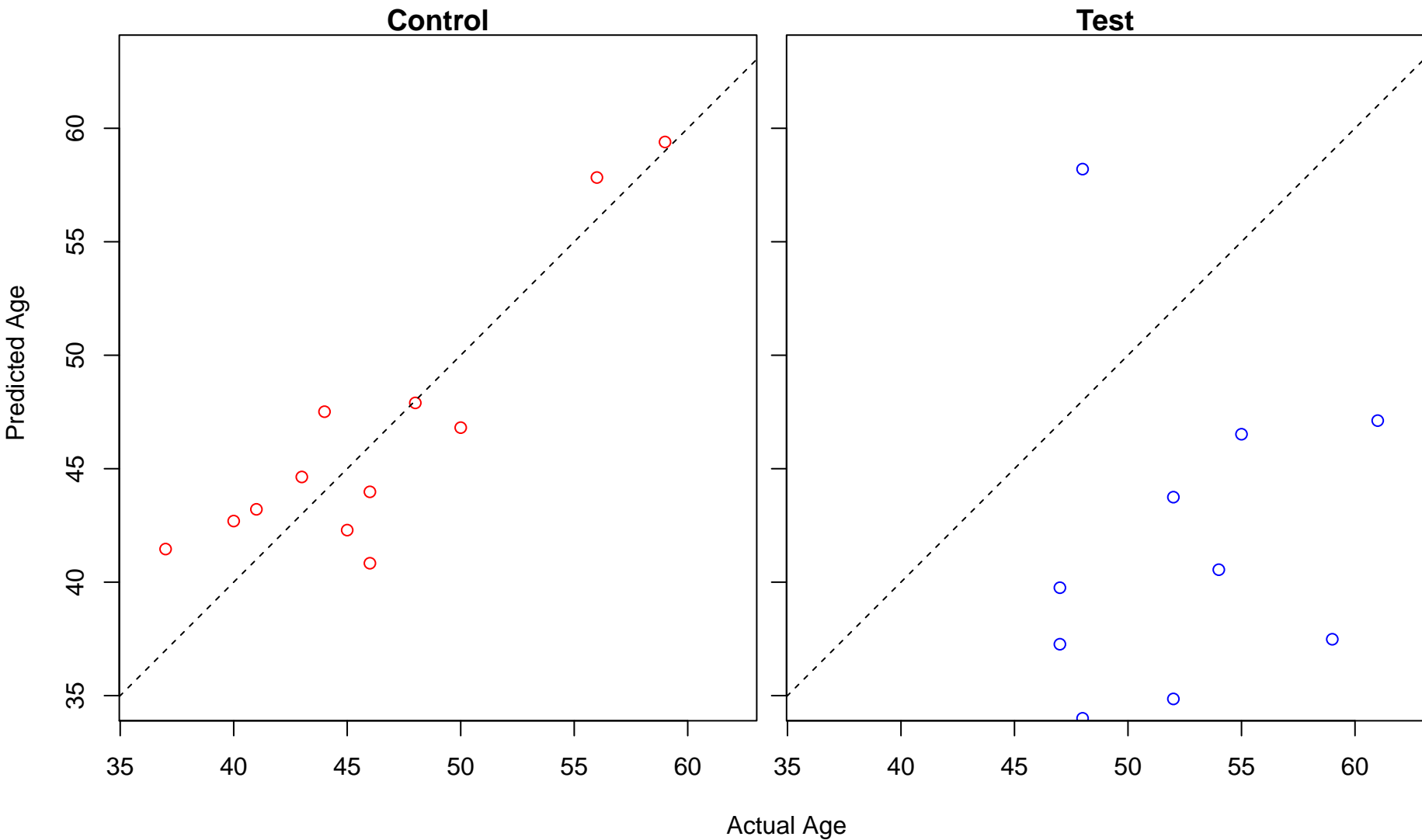
protein import into nucleus (Score: 10.771476)



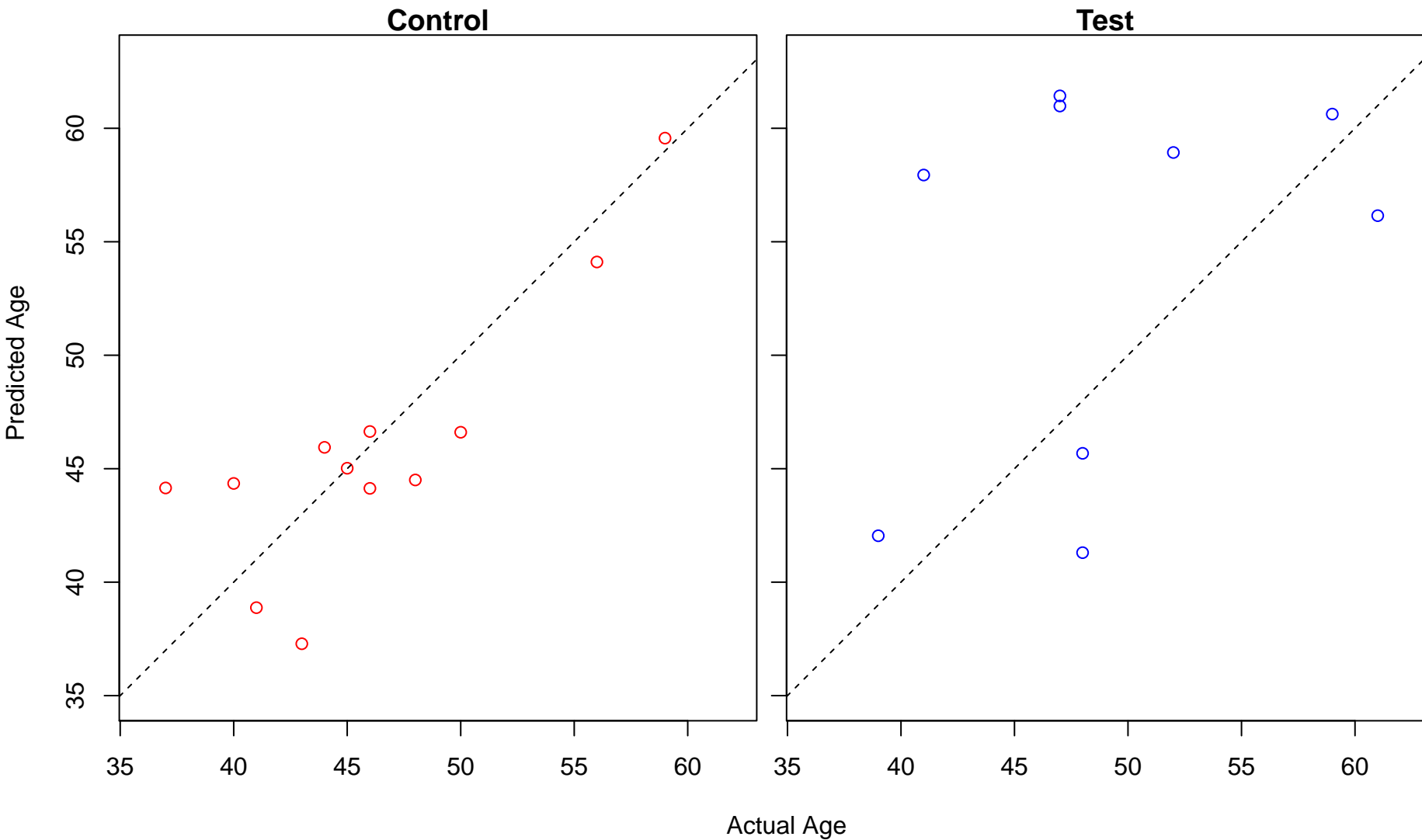
protein targeting to nucleus (Score: 10.771476)



single-organism nuclear import (Score: 10.771476)

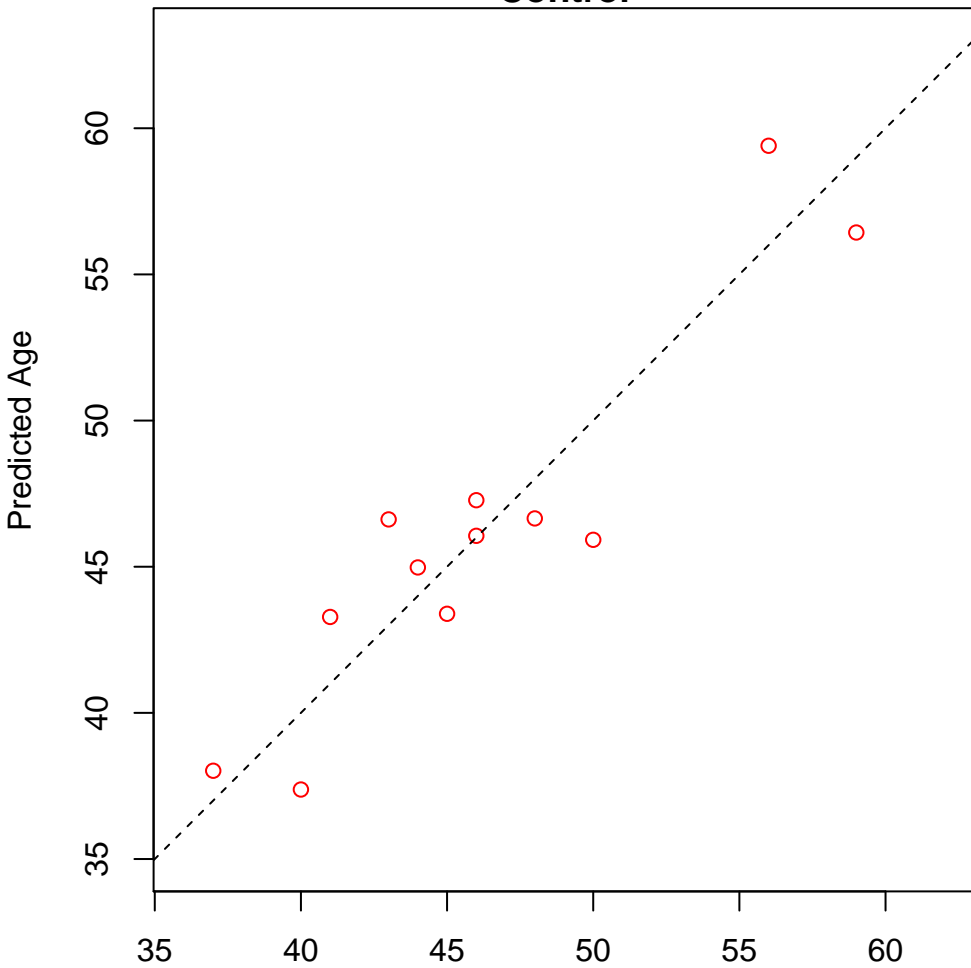


cardiac ventricle formation (Score: 10.757168)

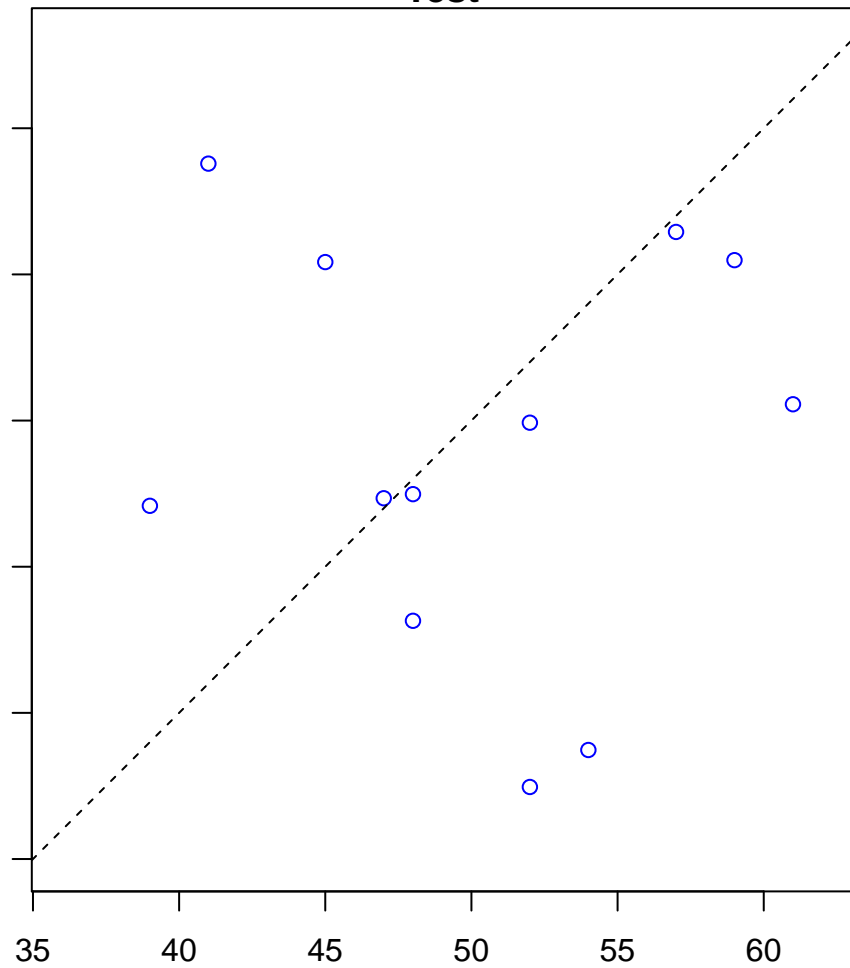


regulation of vasculature development (Score: 10.724733)

Control

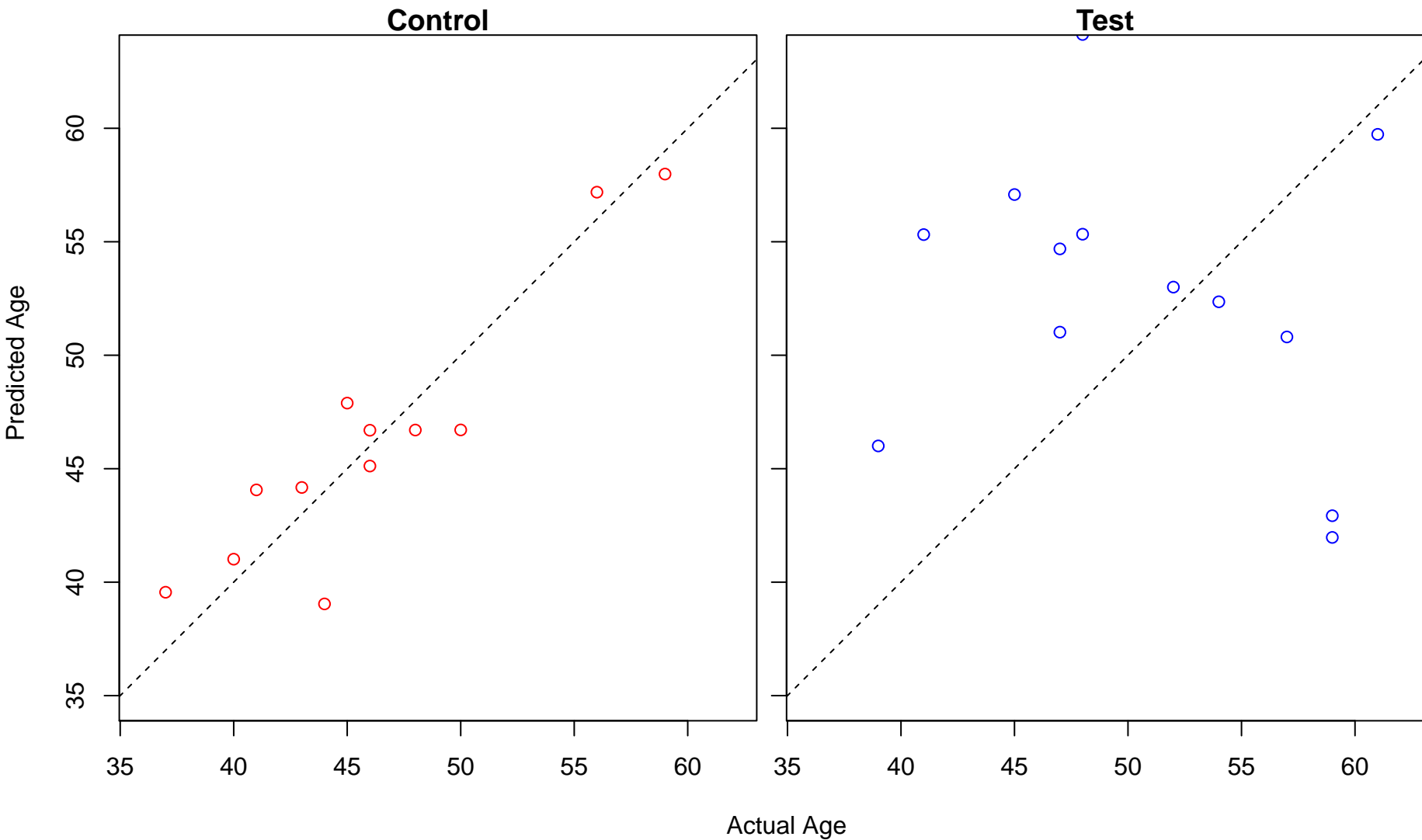


Test

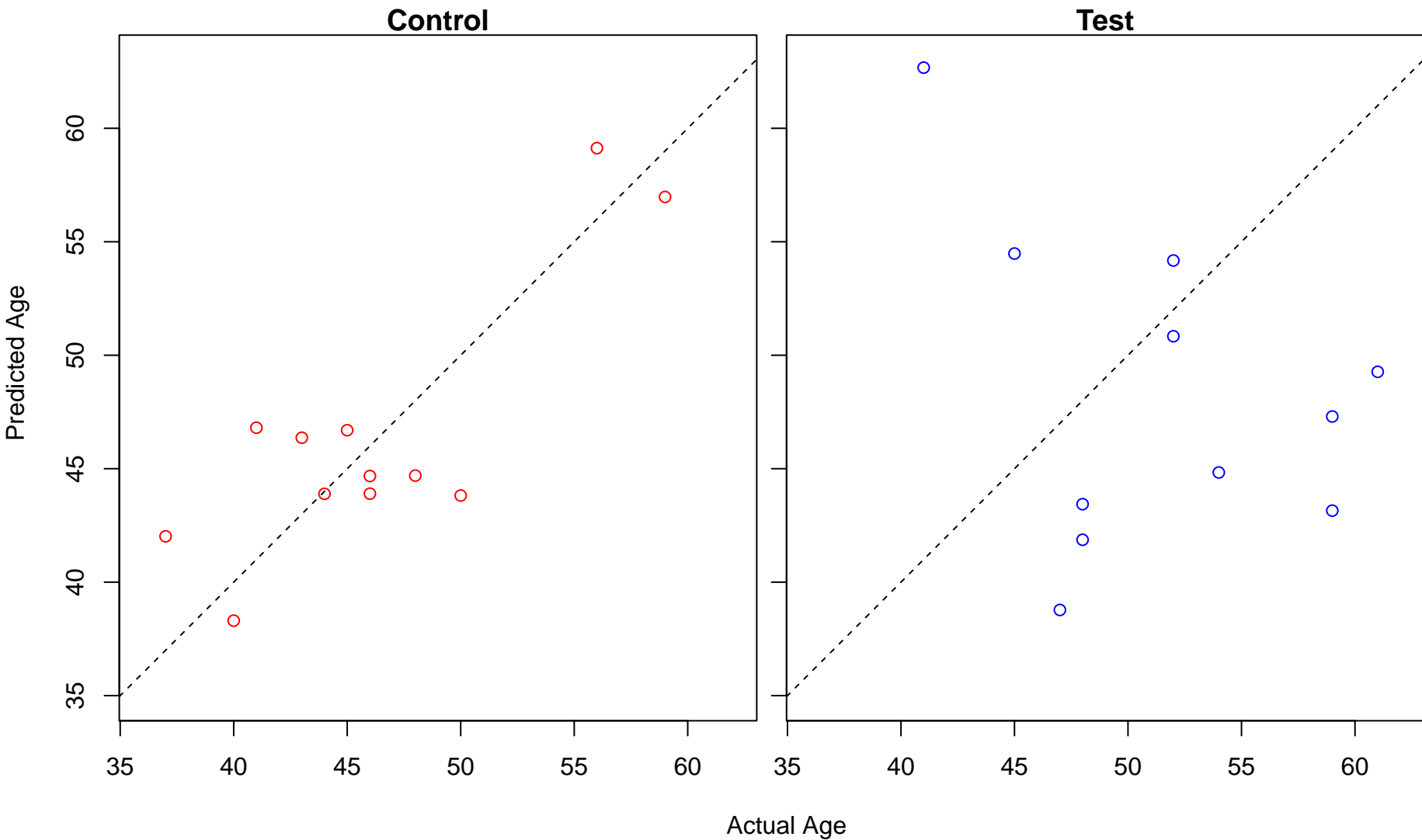


Actual Age

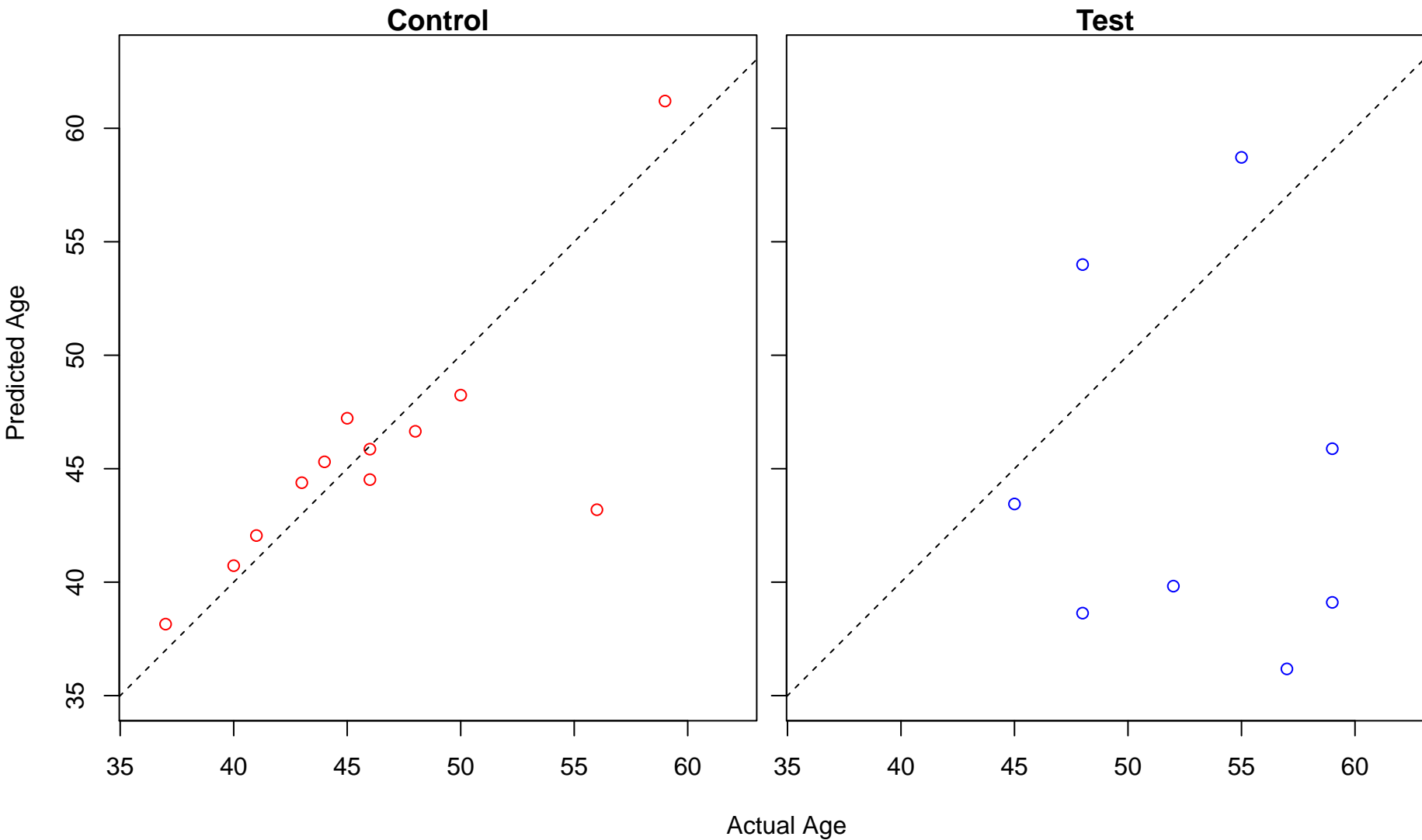
T cell mediated immunity (Score: 10.708883)



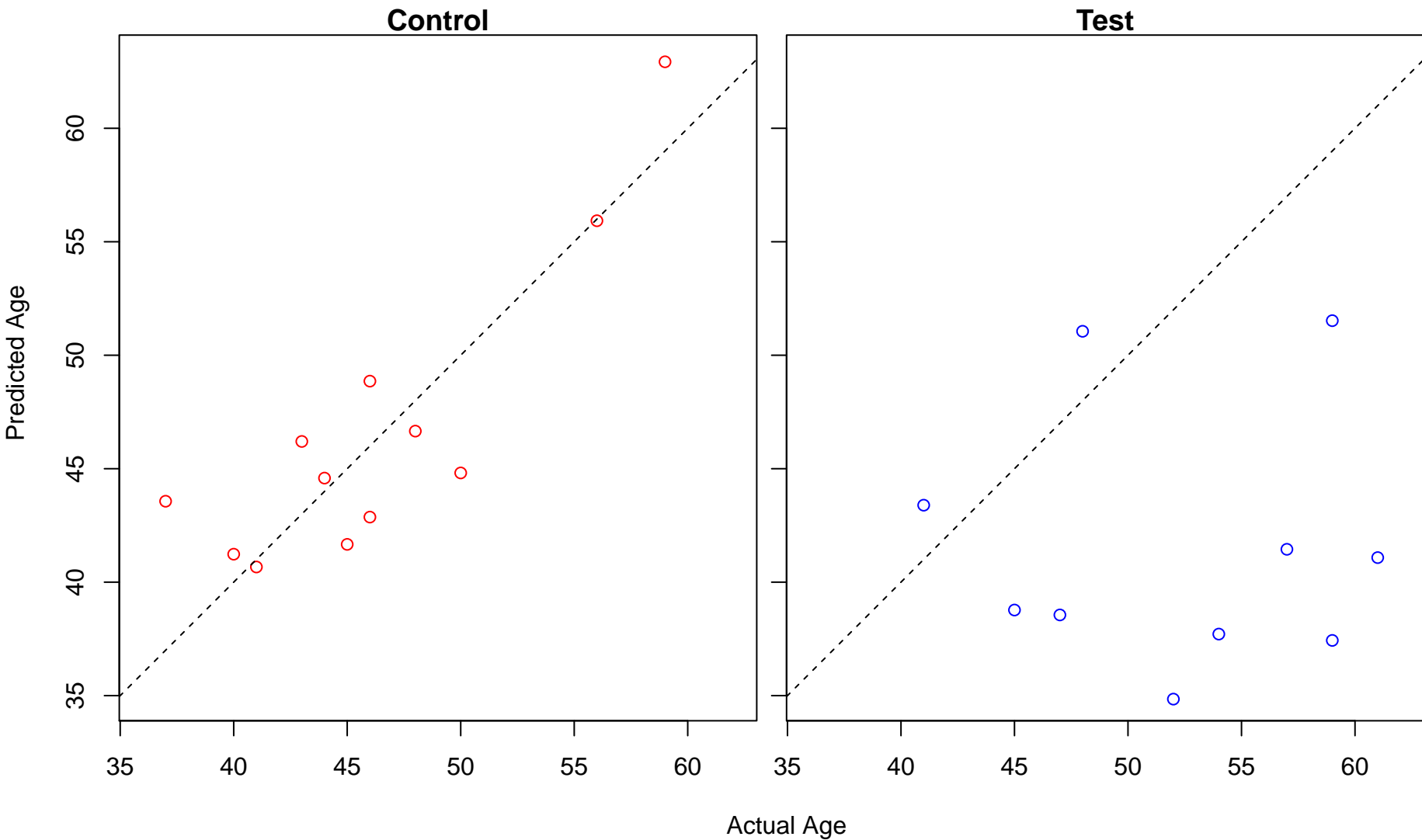
lipoxygenase pathway (Score: 10.699409)



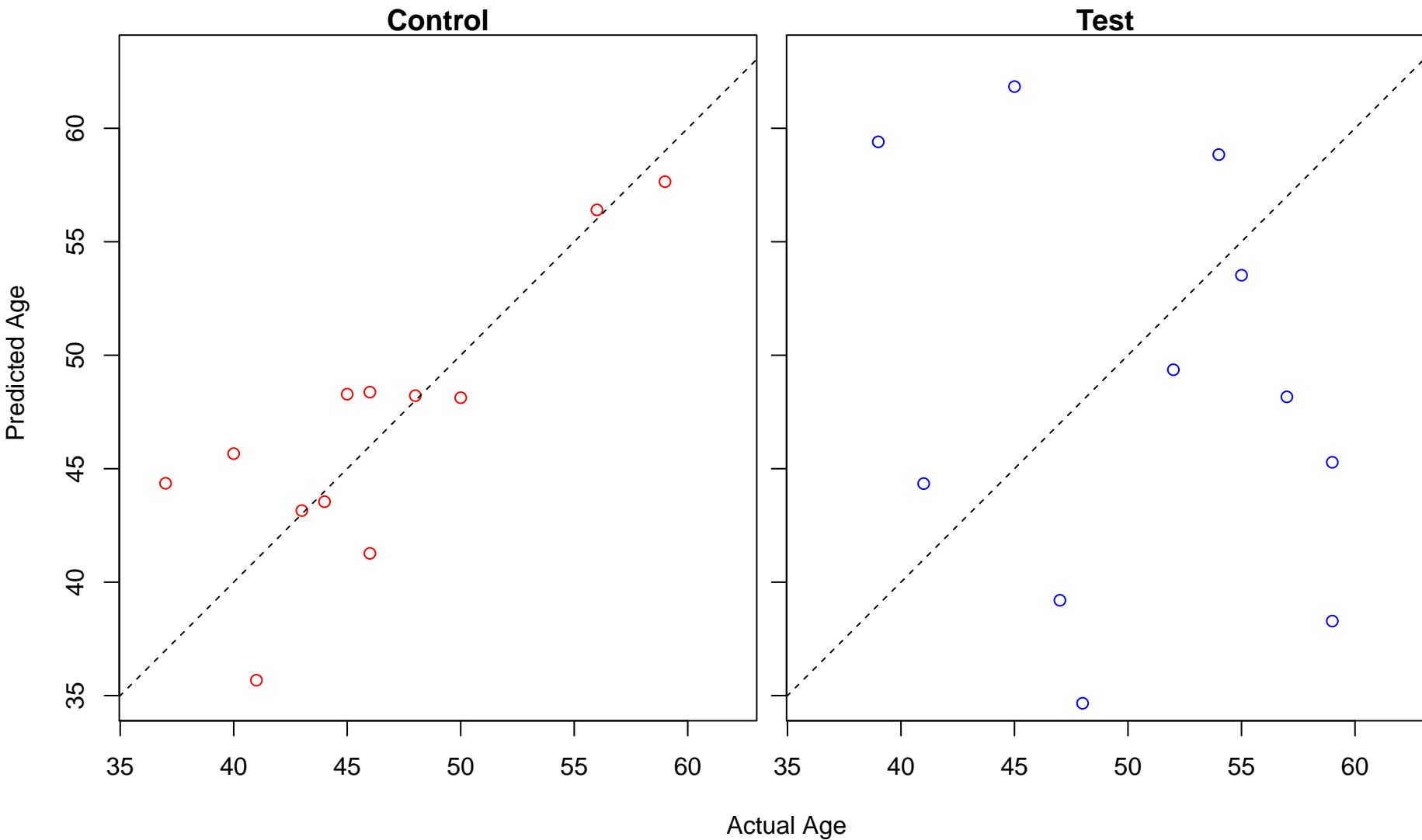
lymphocyte apoptotic process (Score: 10.680237)



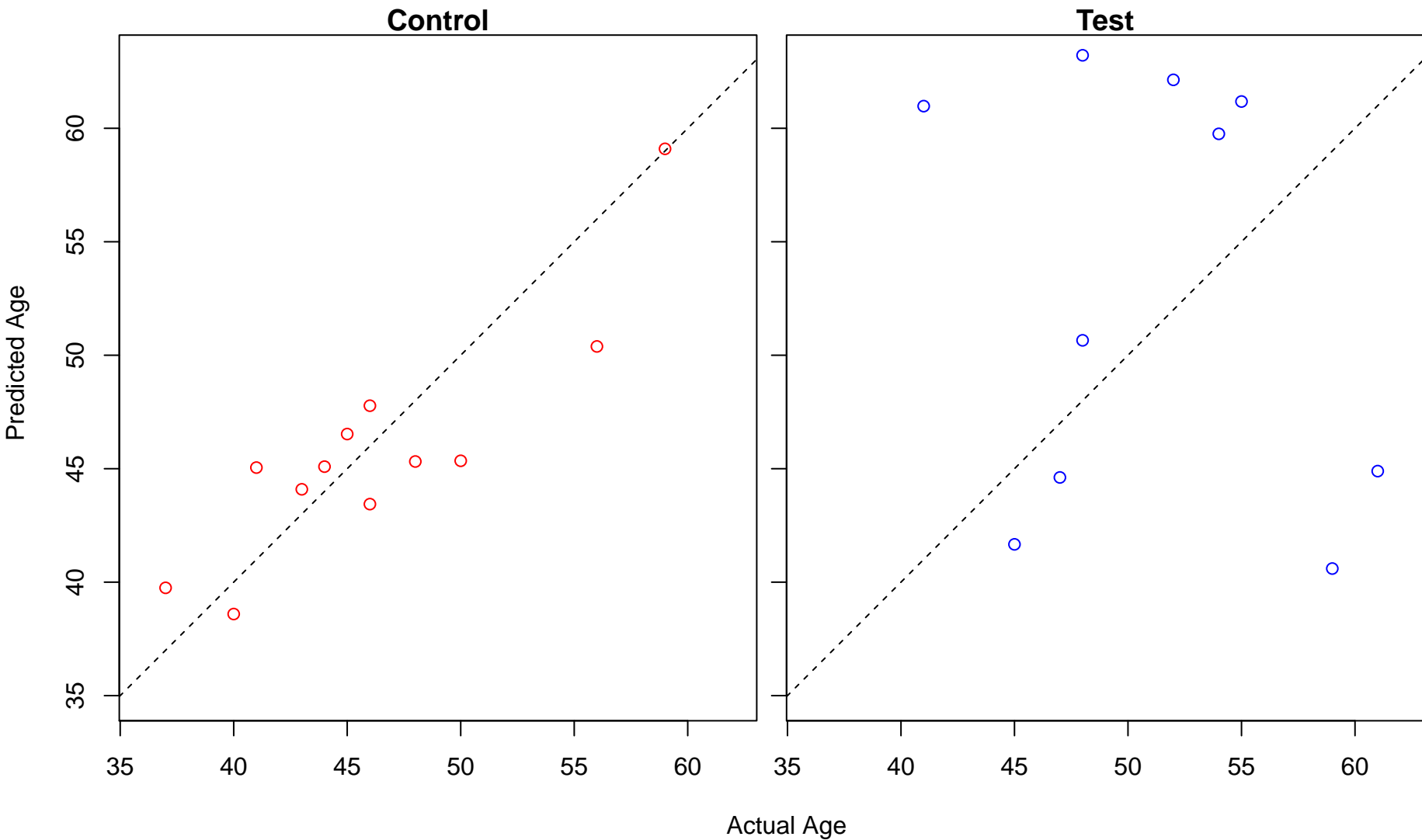
positive regulation of nervous system development (Score: 10.660549)



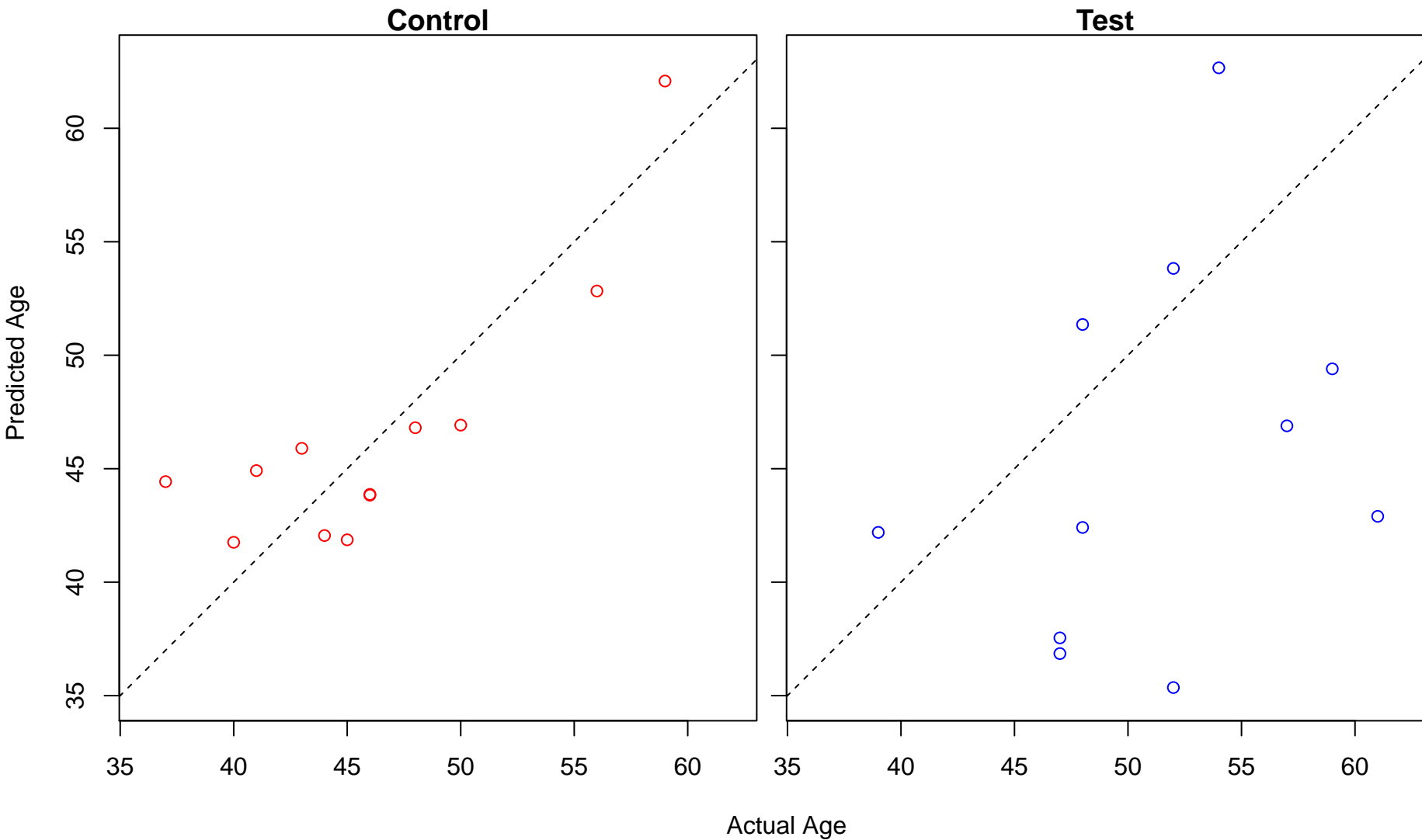
regulation of T cell chemotaxis (Score: 10.618234)



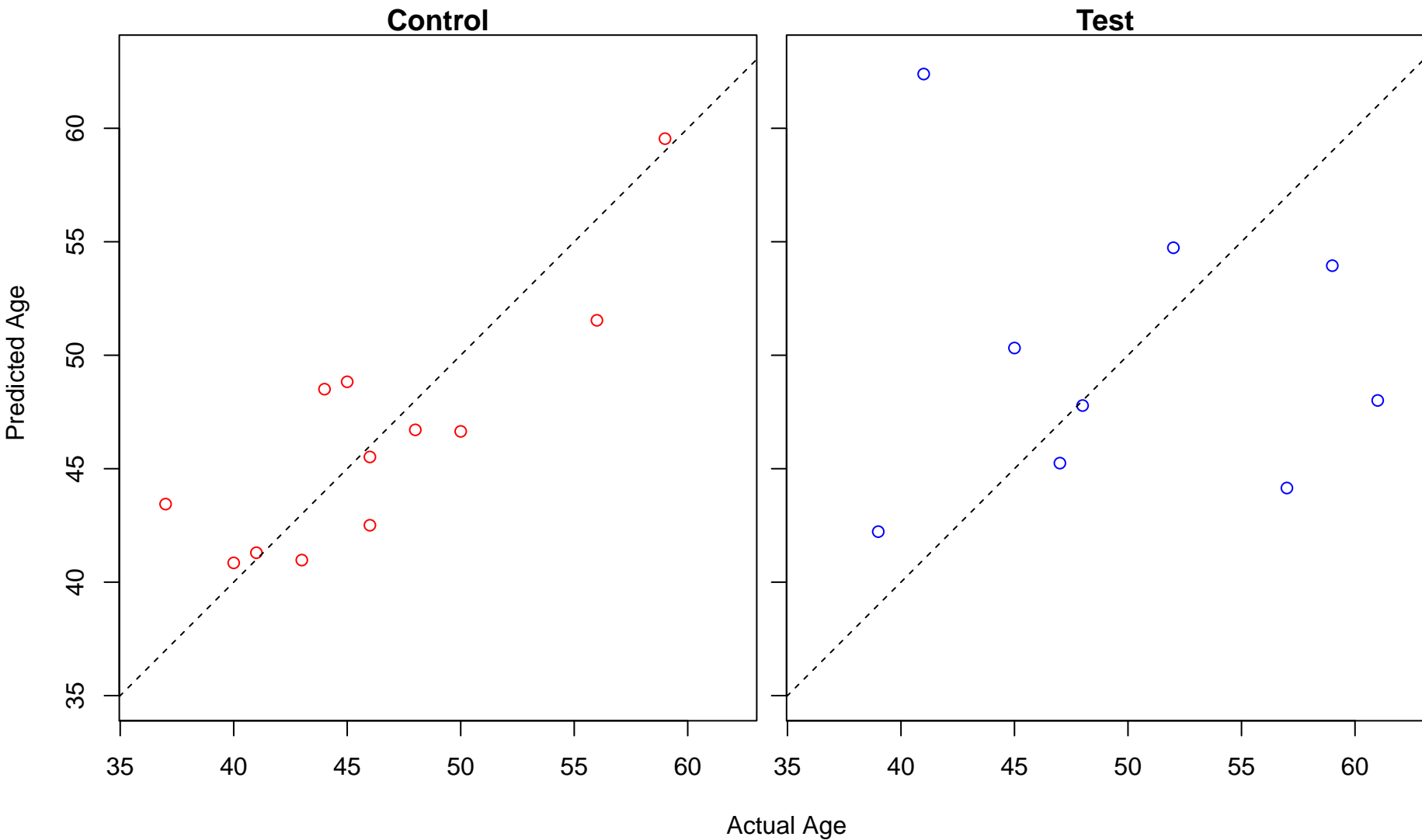
chloride transport (Score: 10.615138)



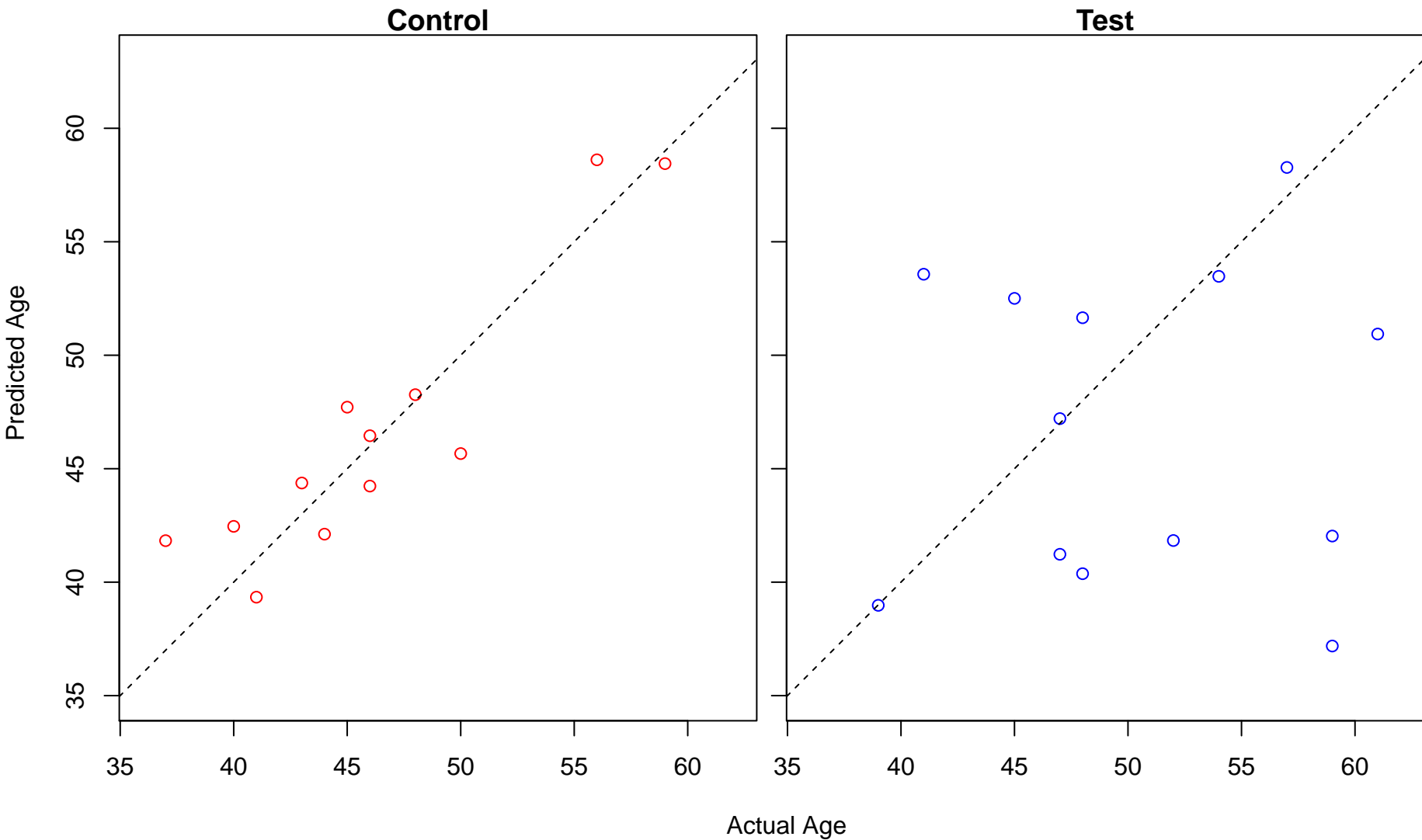
amino acid transport (Score: 10.611467)



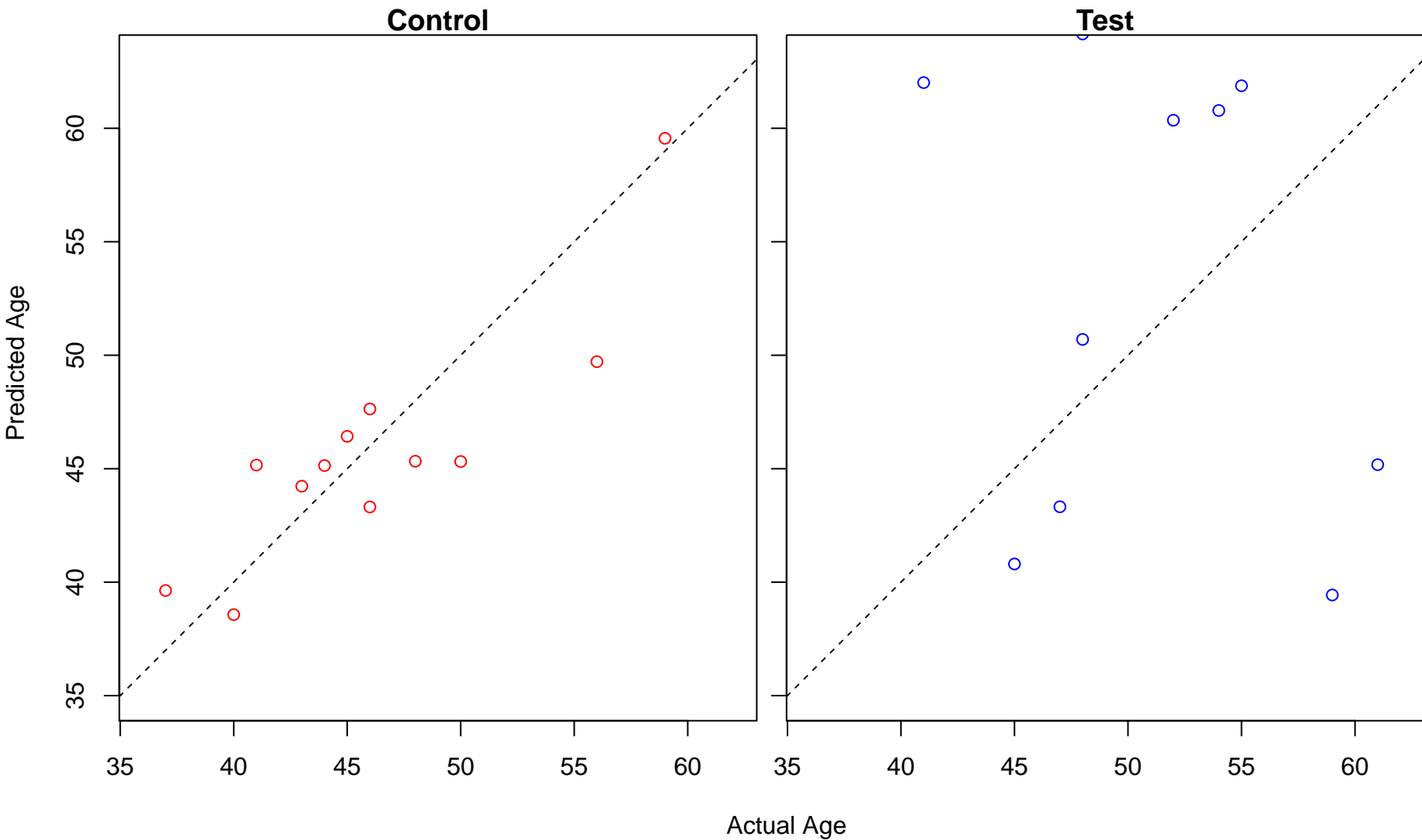
regionalization (Score: 10.604446)



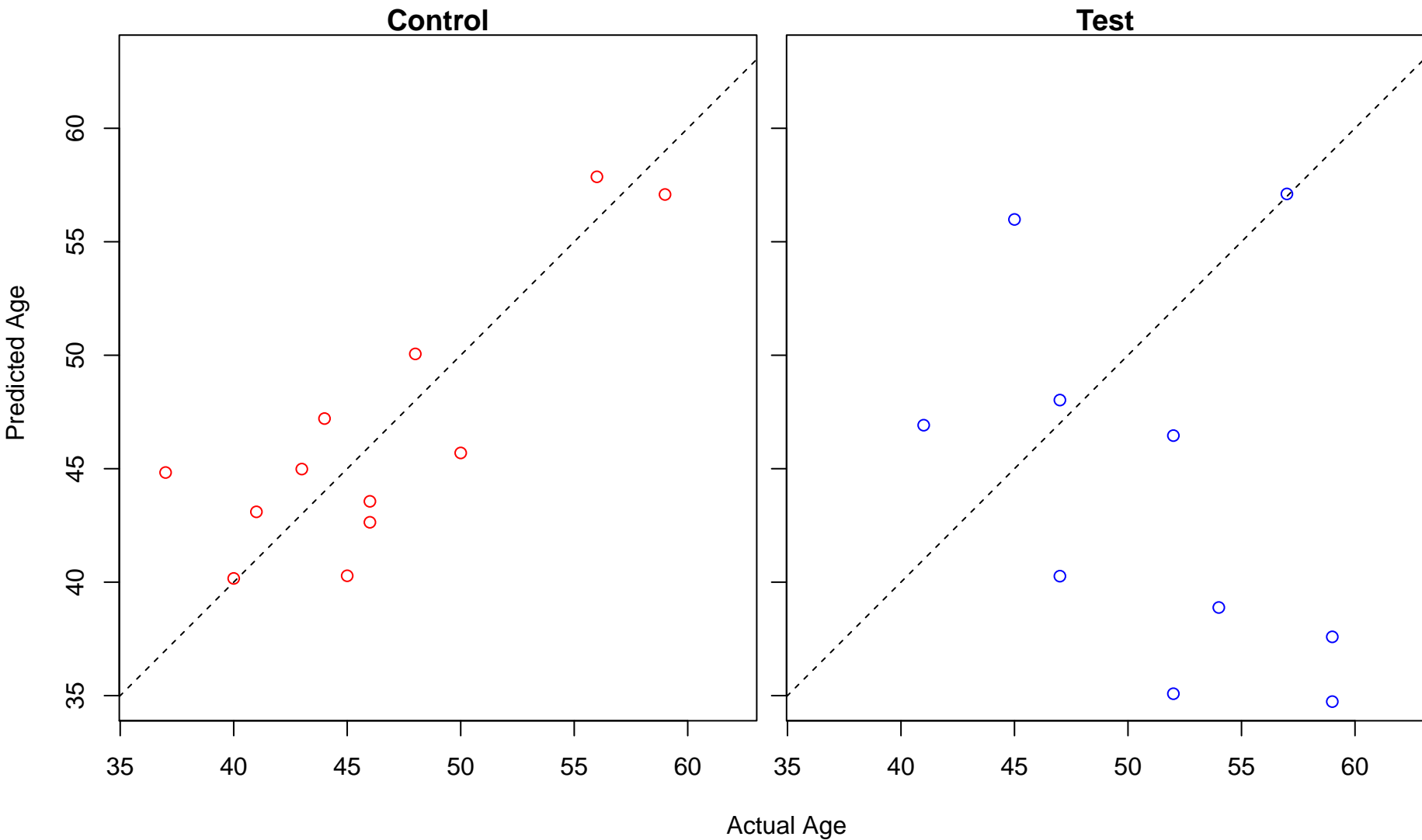
regulation of acute inflammatory response (Score: 10.597021)



chloride transmembrane transport (Score: 10.565443)

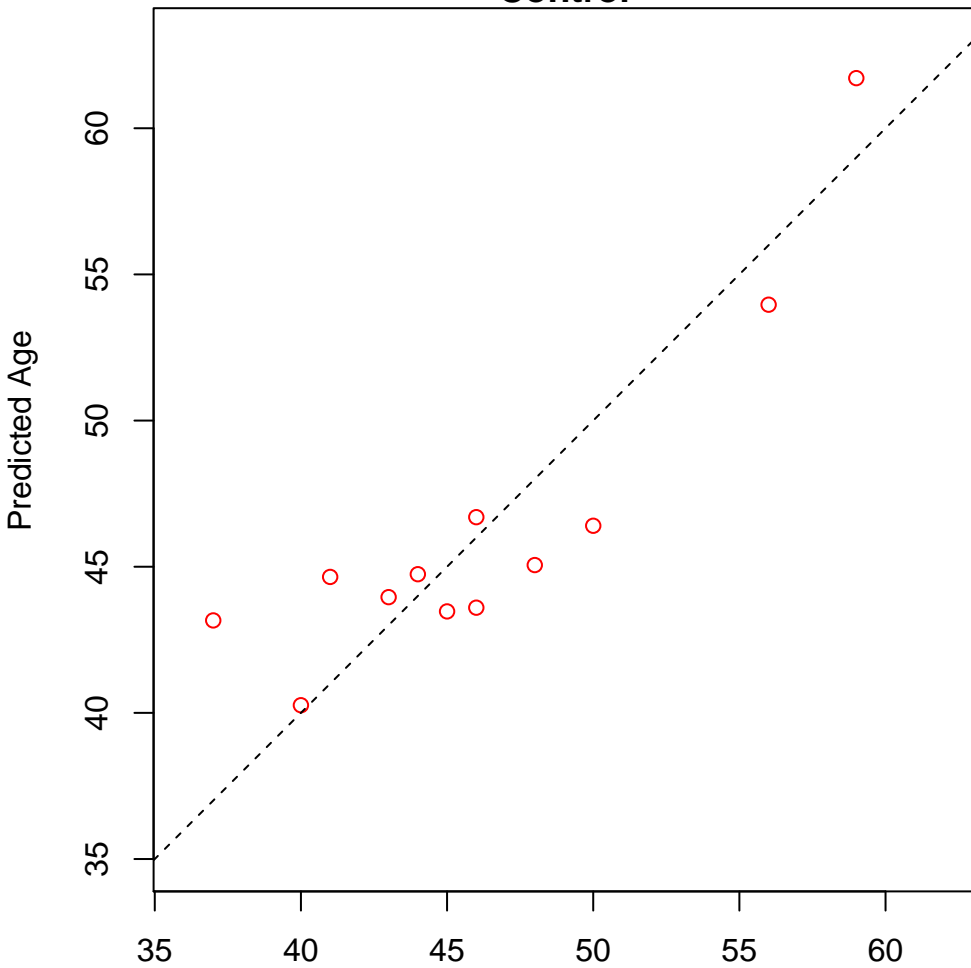


serine family amino acid biosynthetic process (Score: 10.539618)

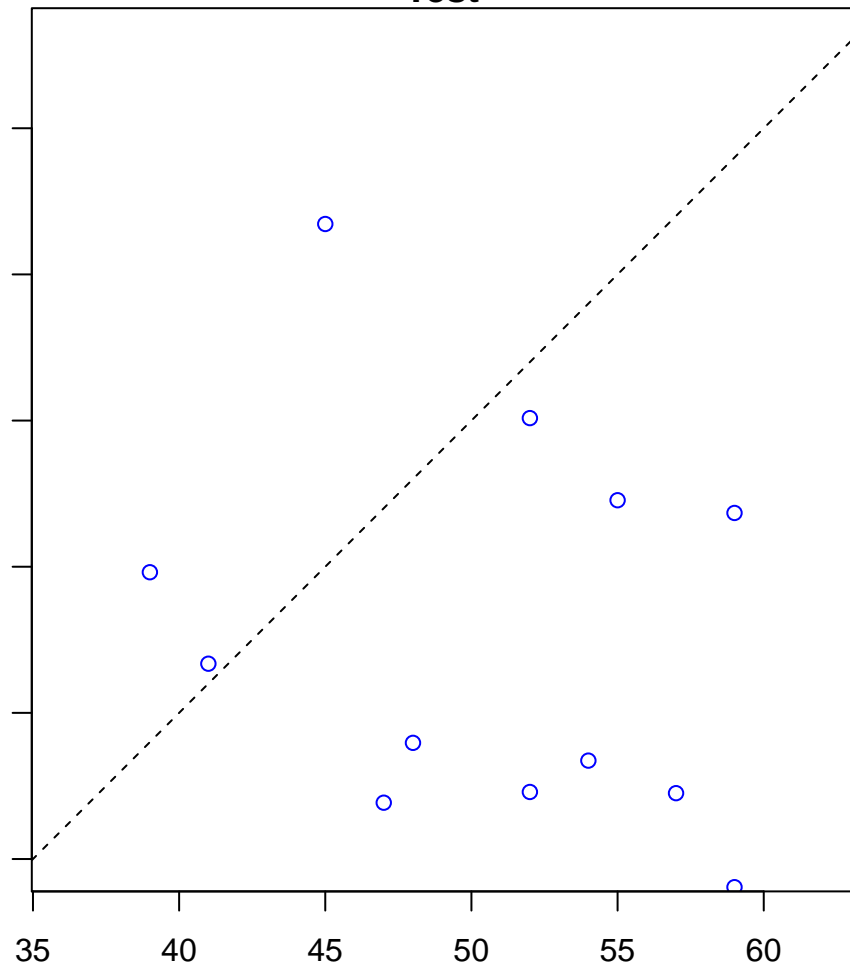


sulfur compound biosynthetic process (Score: 10.527107)

Control

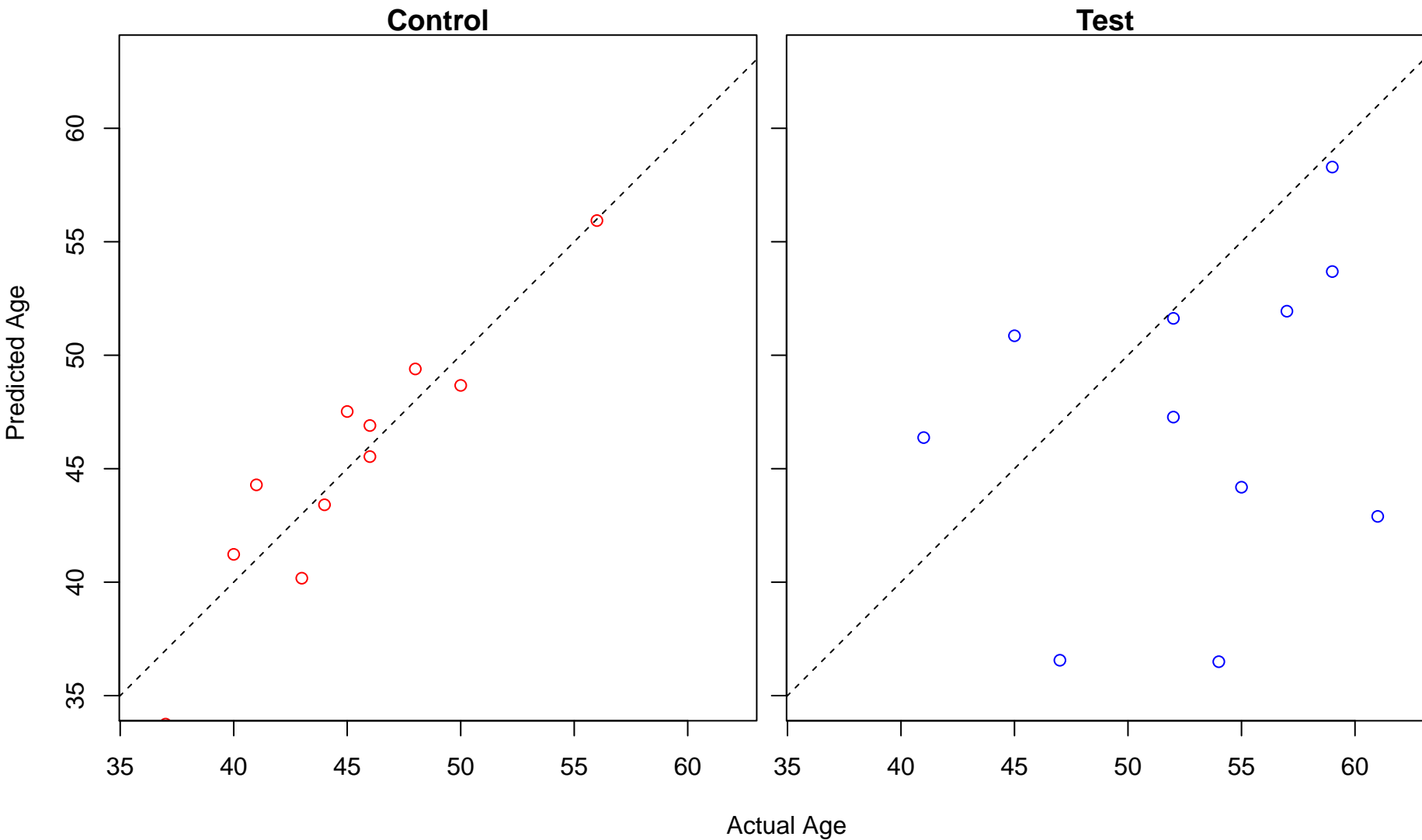


Test

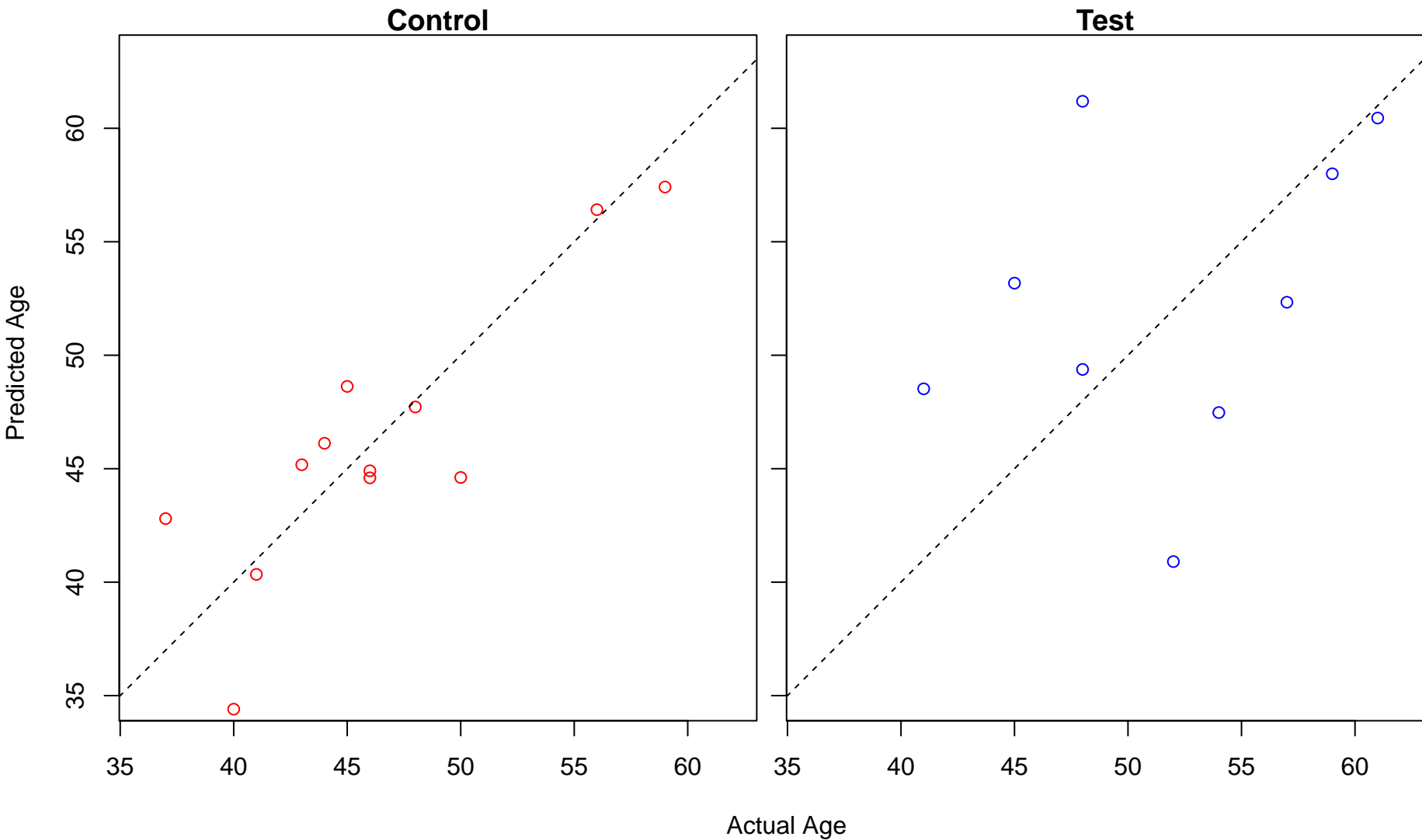


Actual Age

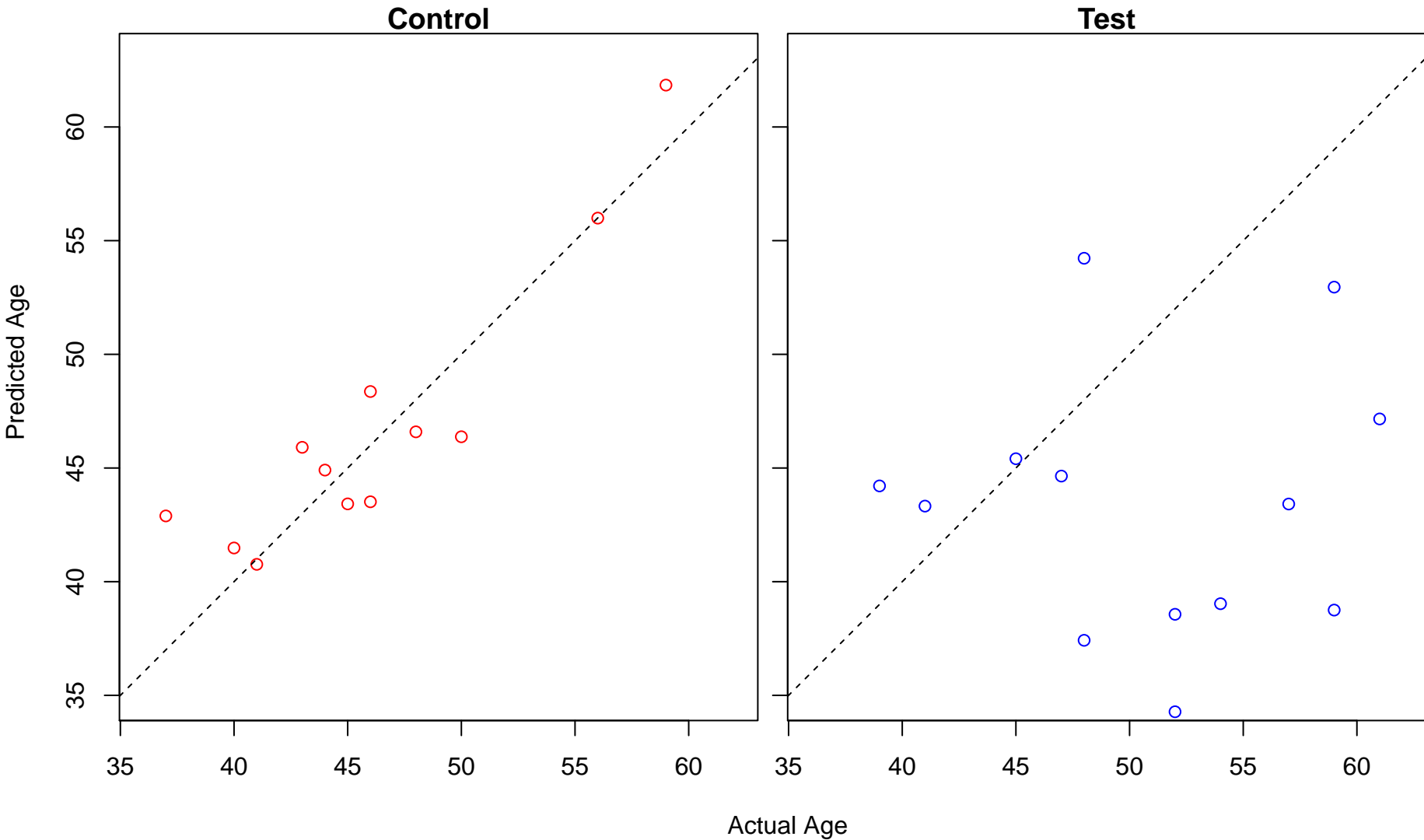
metanephric mesenchyme development (Score: 10.526021)



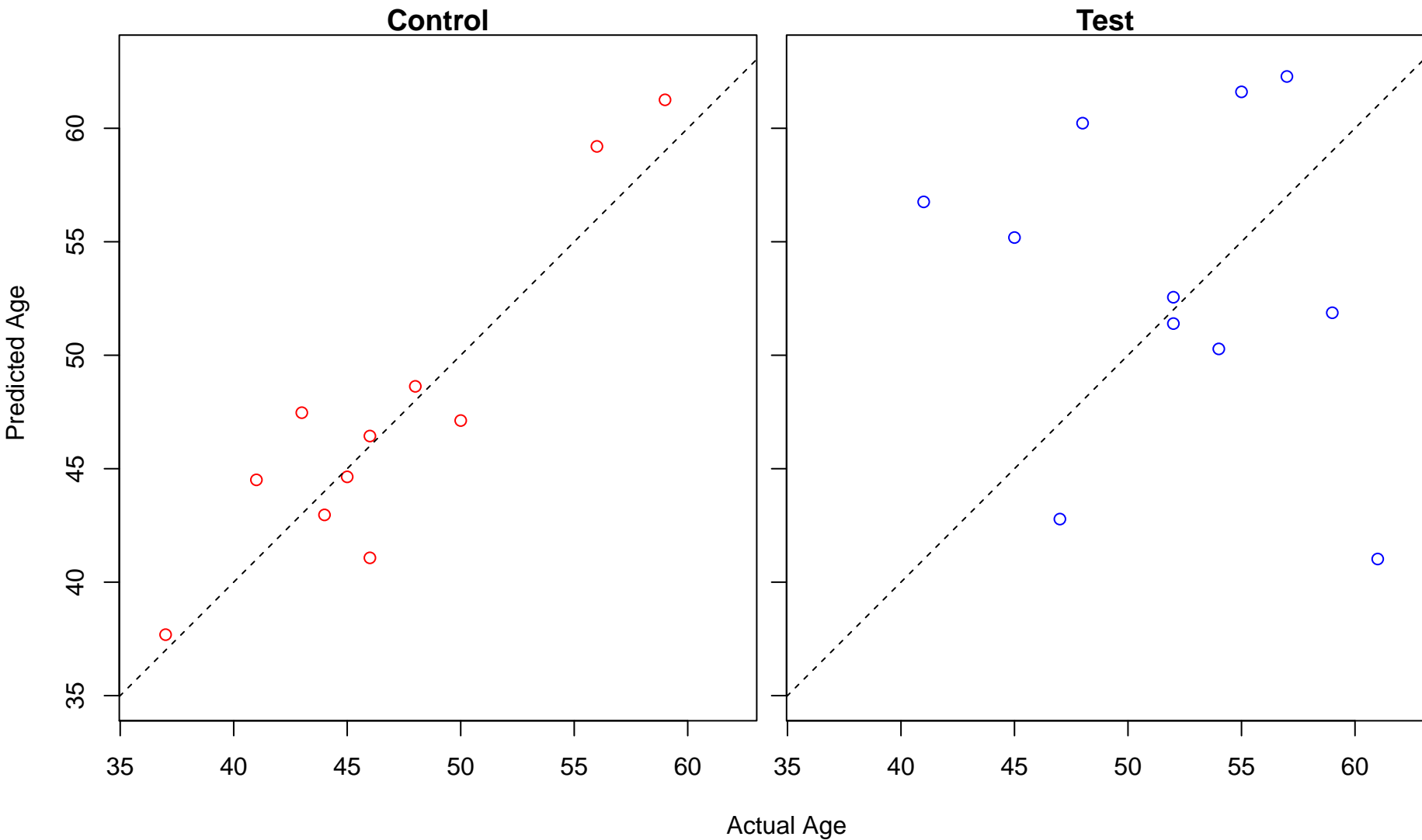
atrial septum morphogenesis (Score: 10.525351)



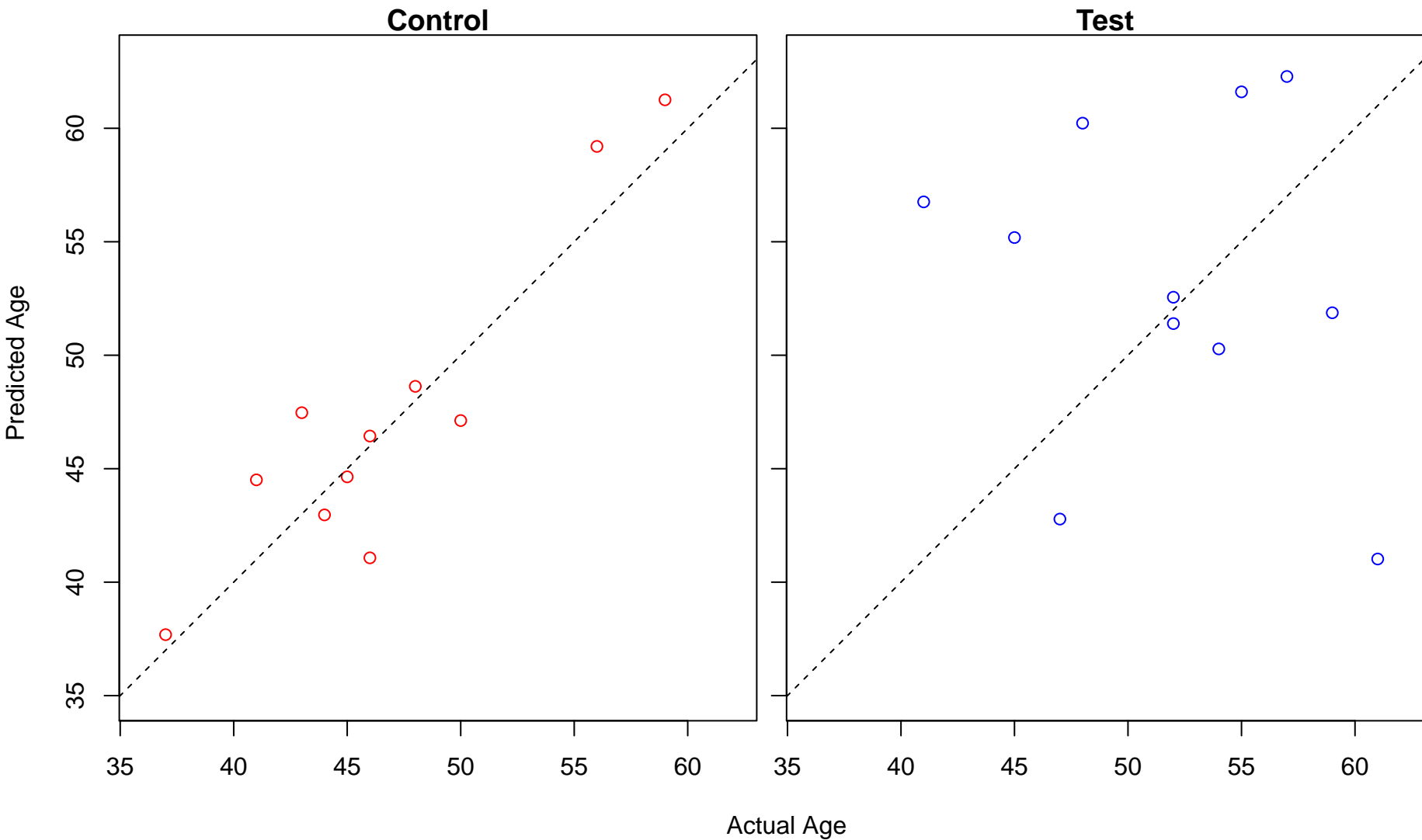
positive regulation of neuron differentiation (Score: 10.524052)



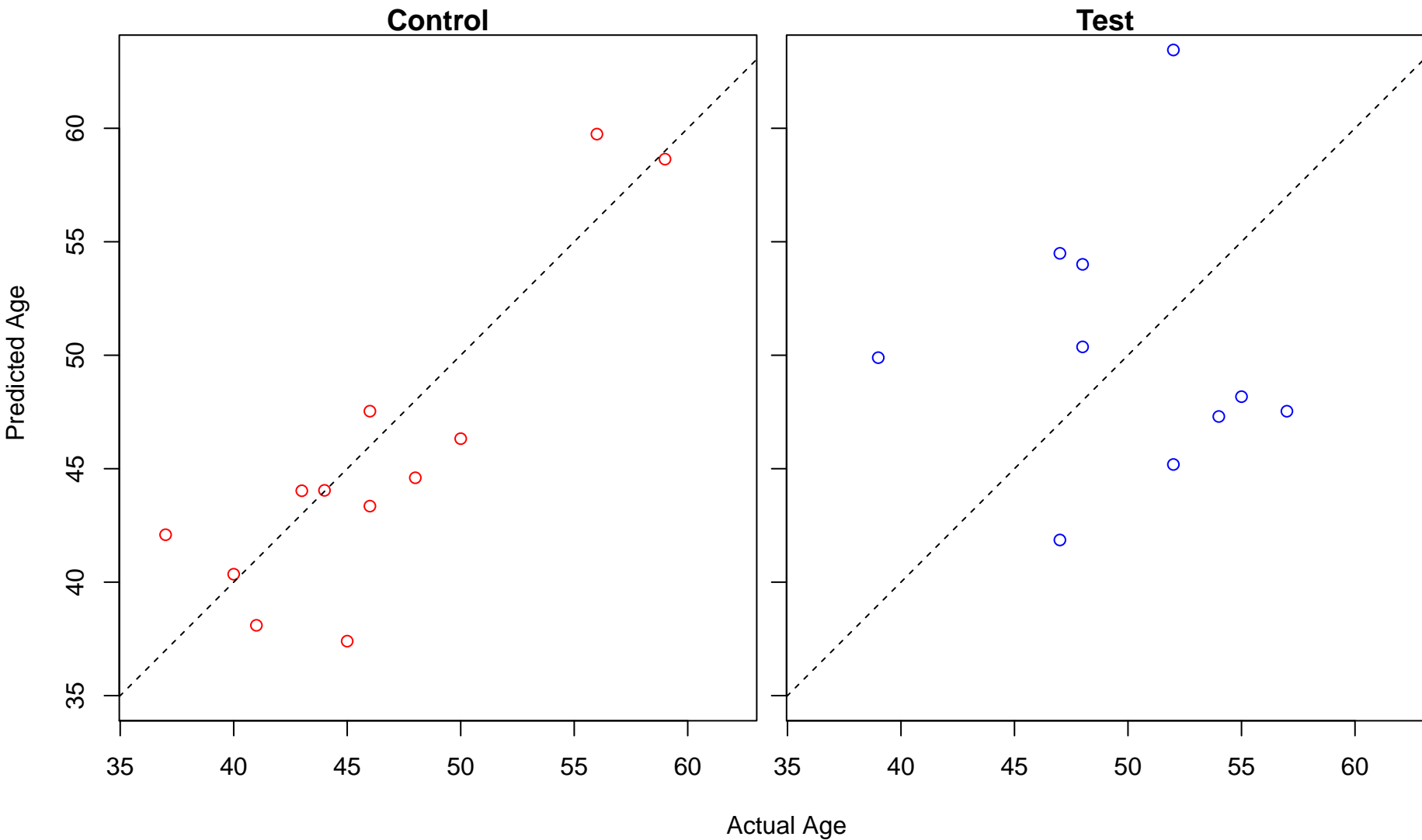
T cell differentiation in thymus (Score: 10.489381)



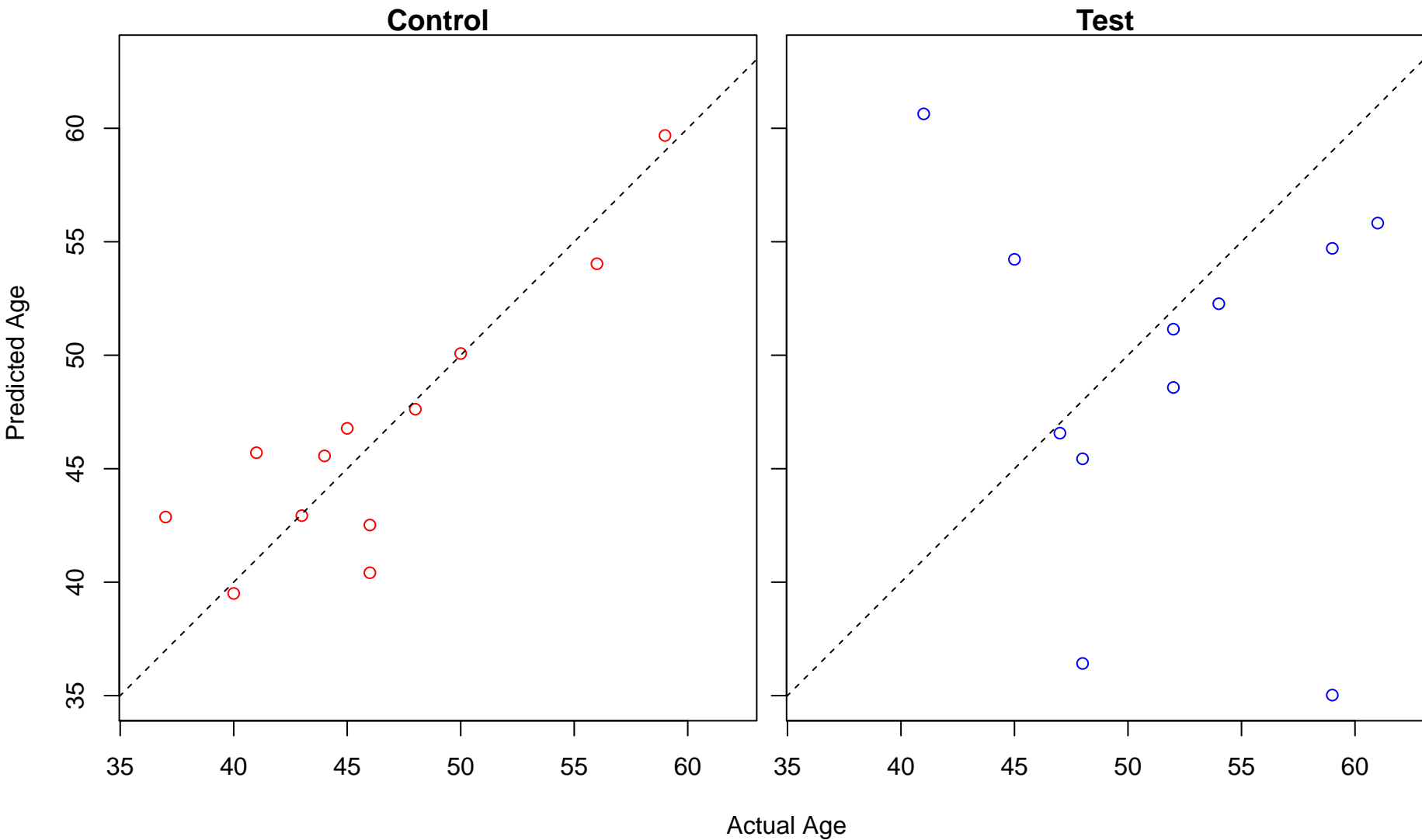
thymocyte aggregation (Score: 10.489381)



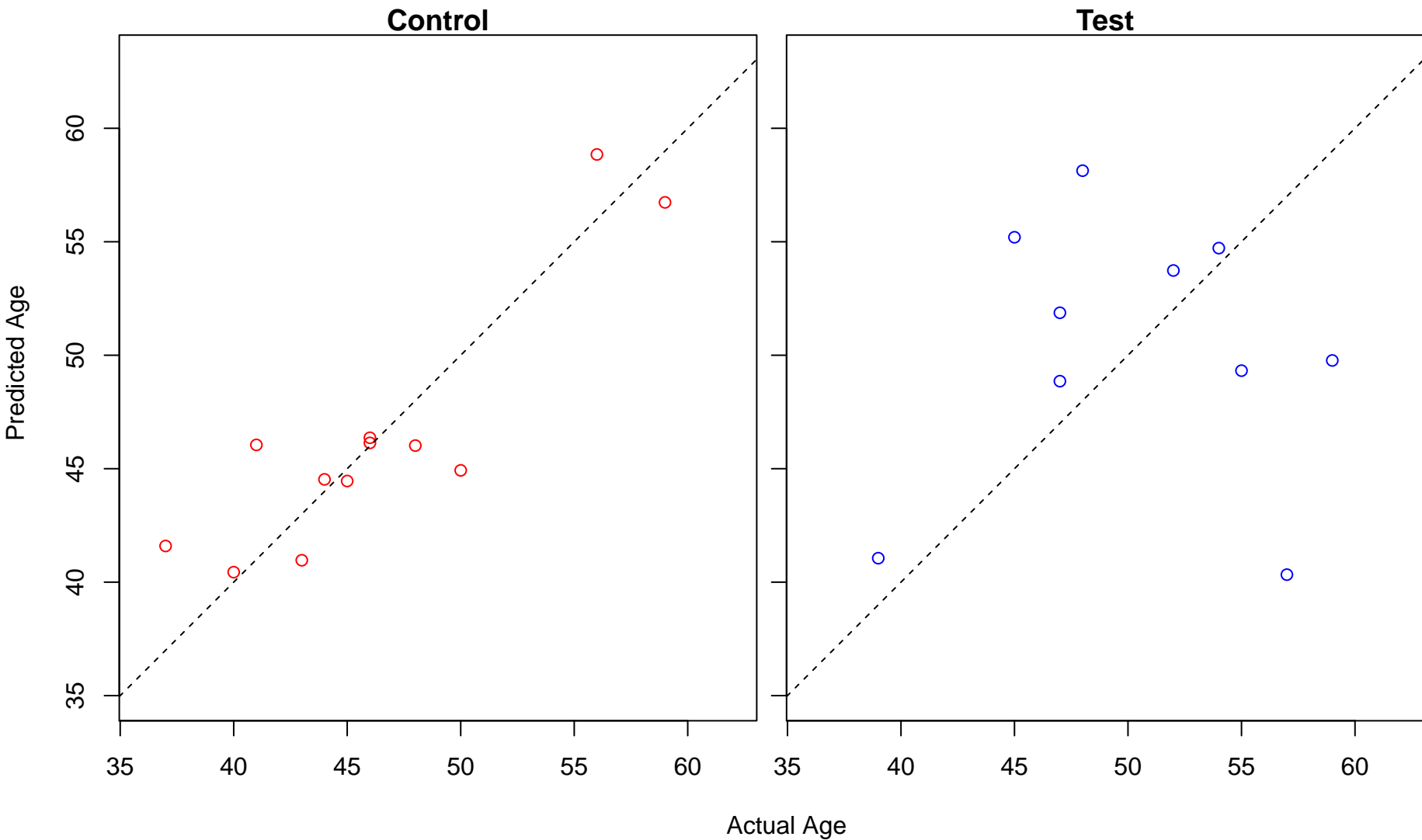
positive regulation of intracellular steroid hormone receptor signaling pathway (Score: 10.475126)



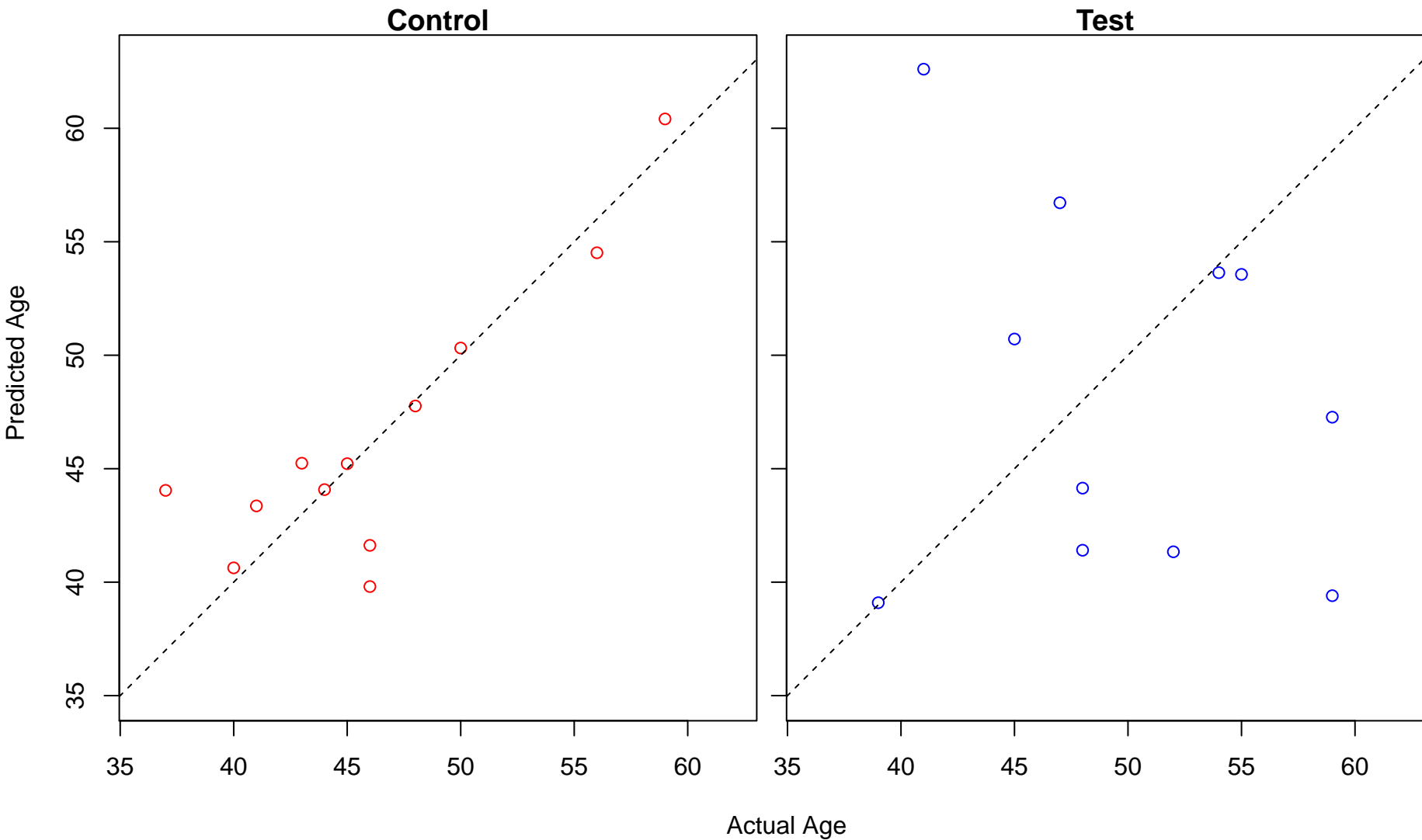
protein homotetramerization (Score: 10.453884)



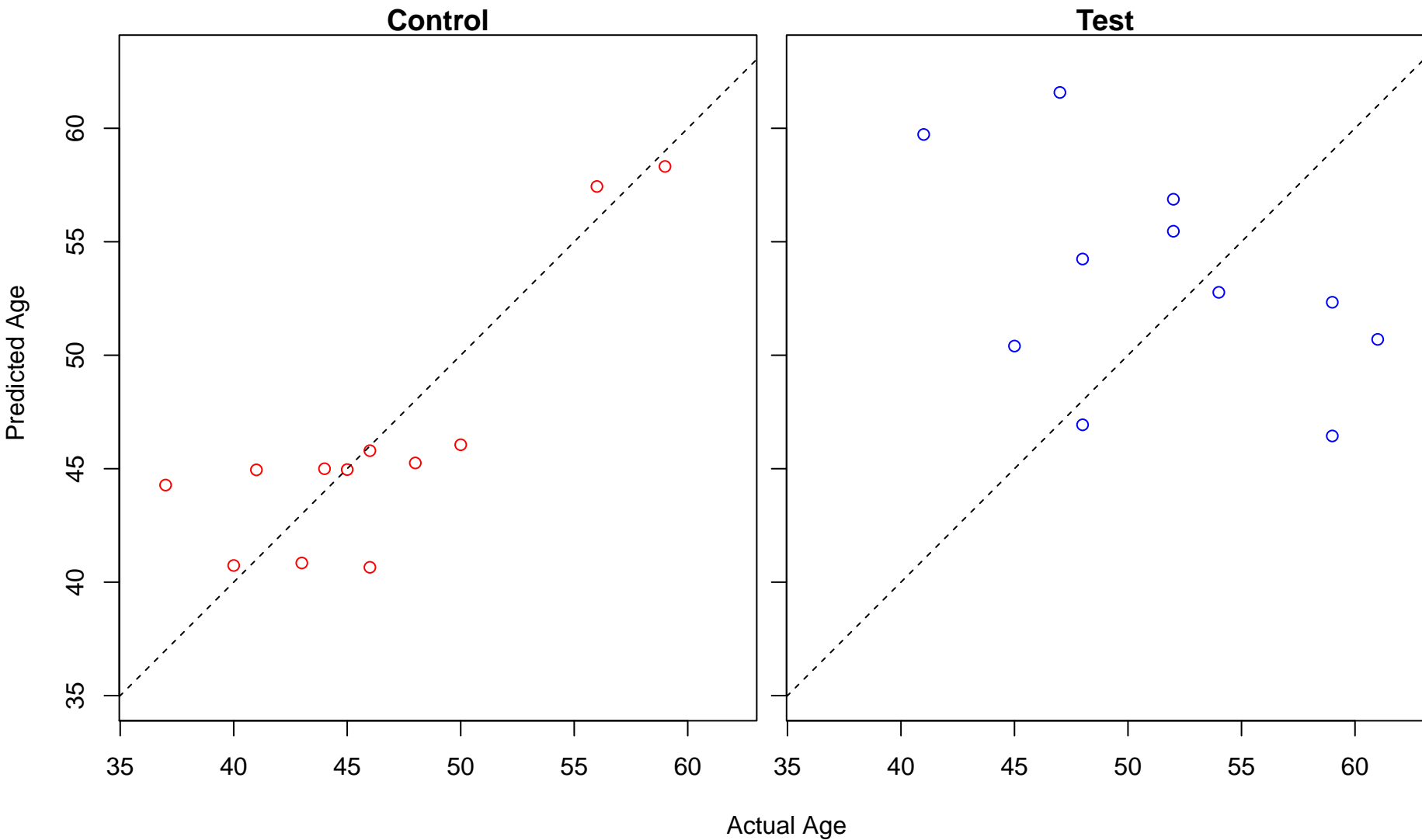
regulation of JUN kinase activity (Score: 10.438708)



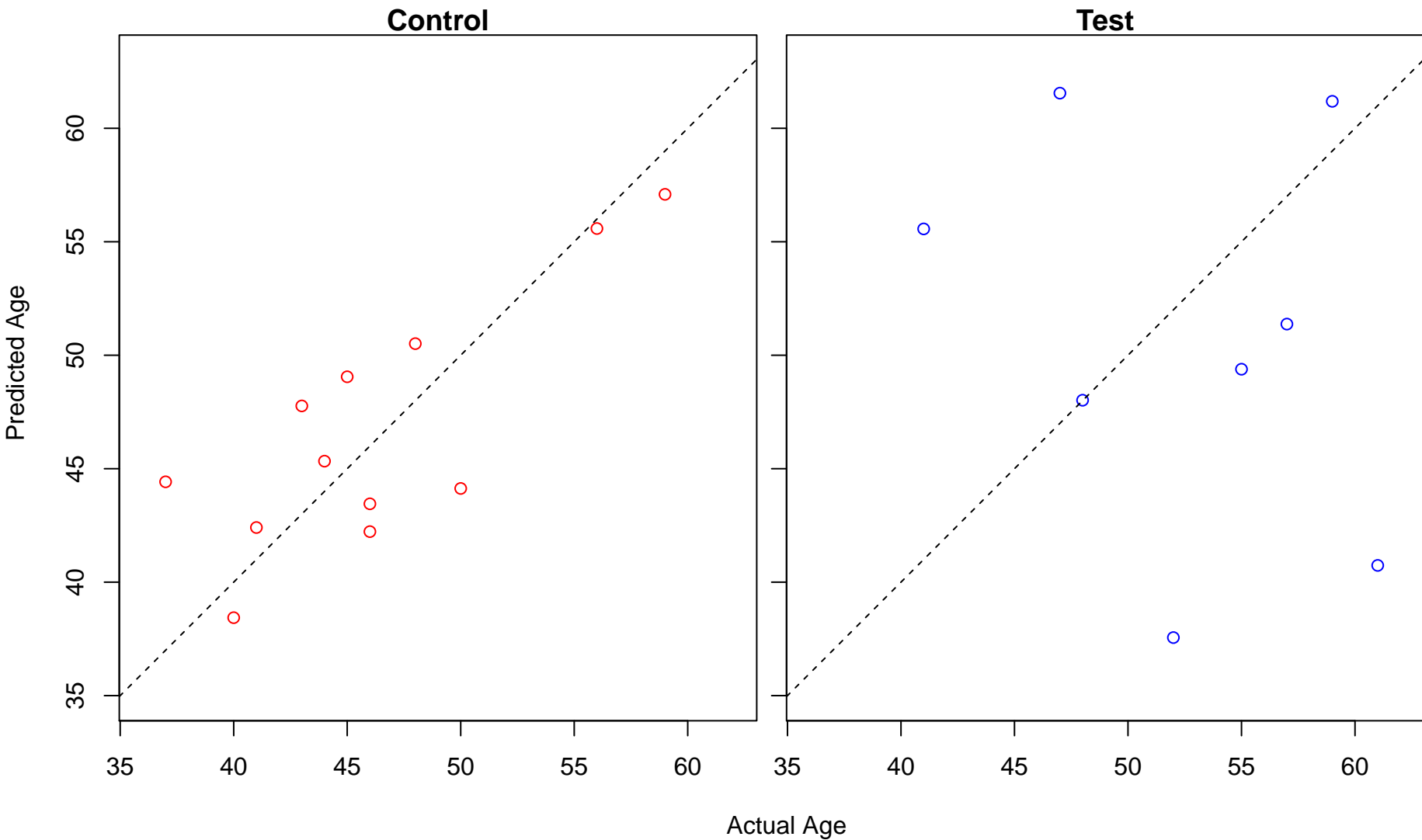
pigment biosynthetic process (Score: 10.436530)



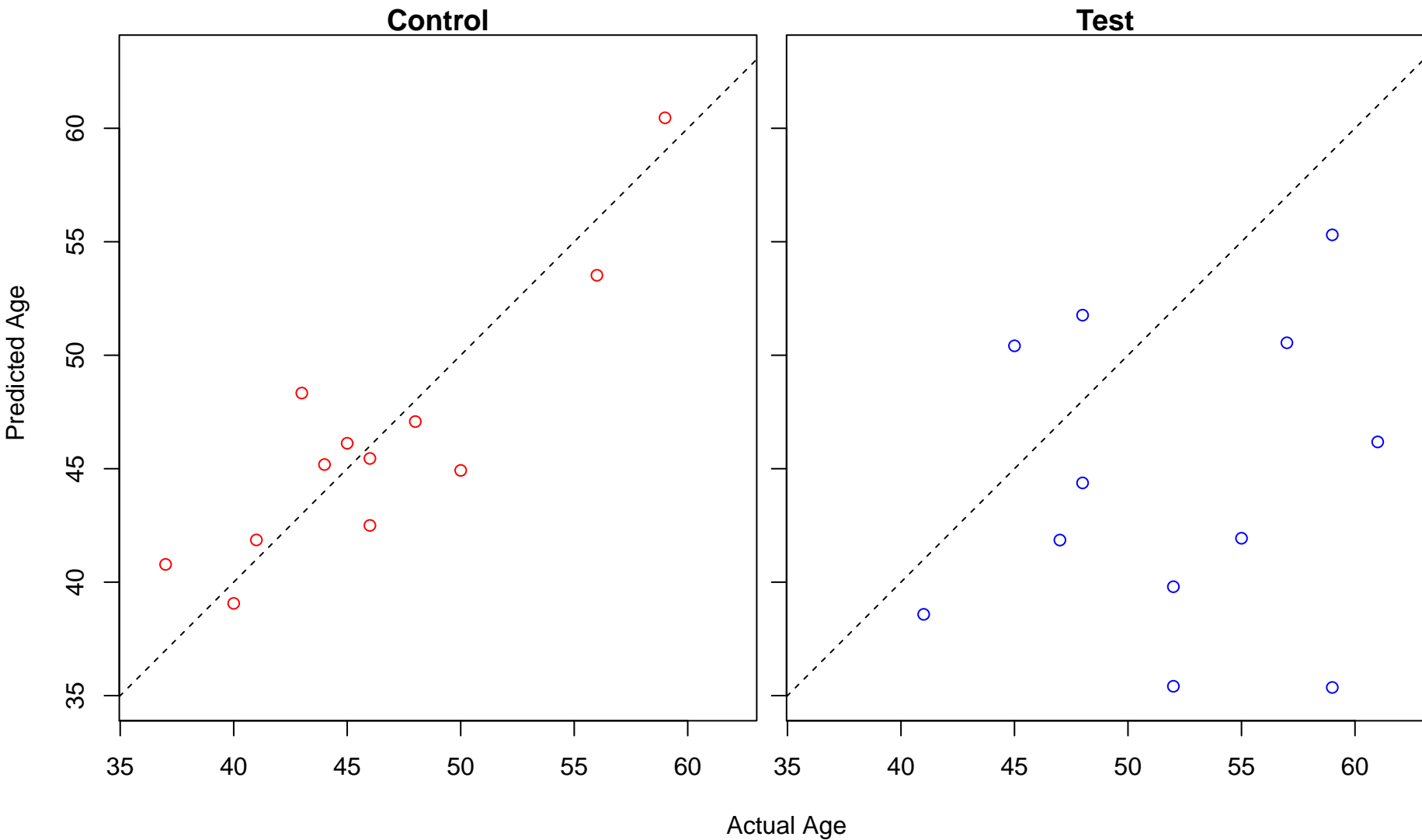
negative regulation of toll-like receptor 4 signaling pathway (Score: 10.435248)



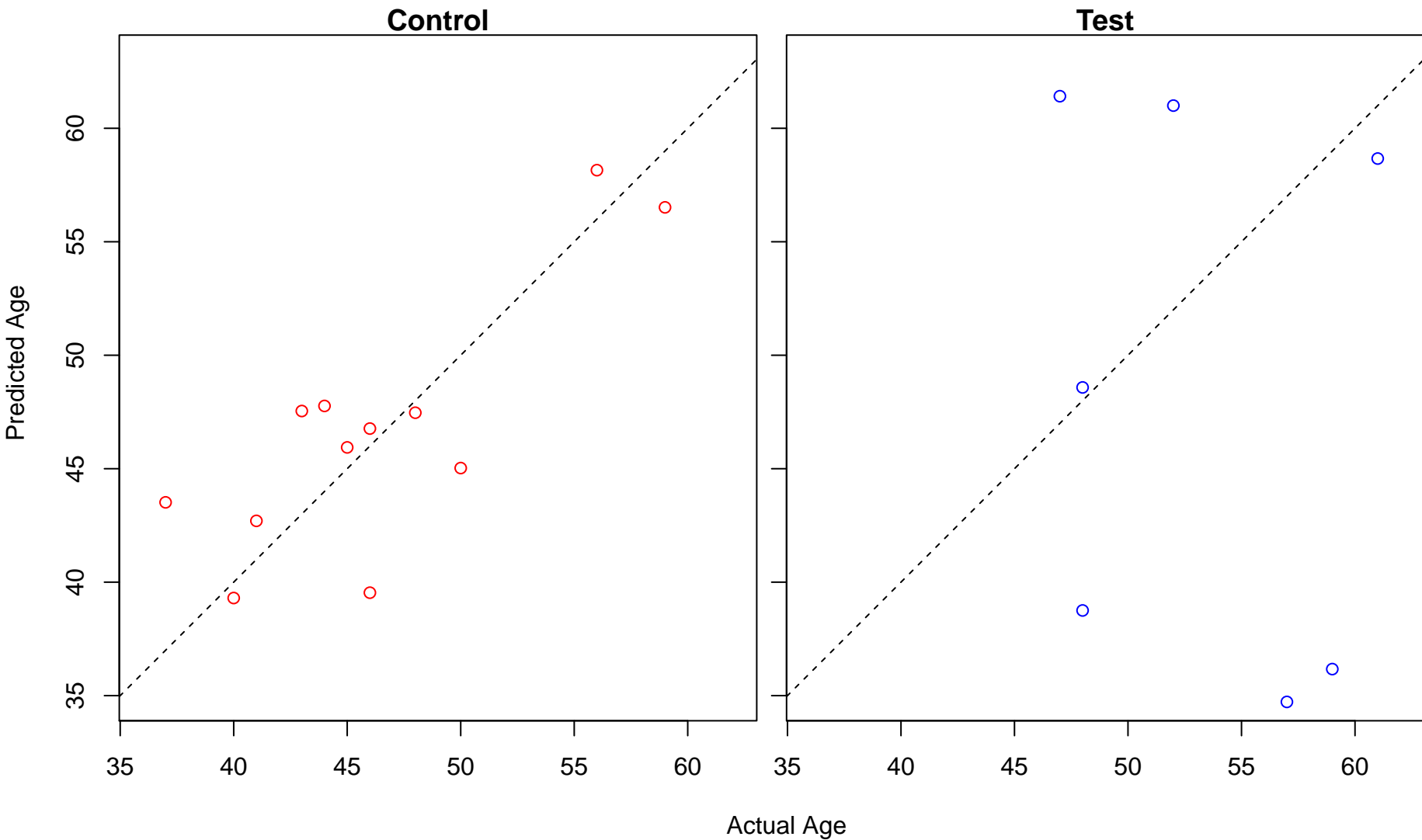
cardiac chamber development (Score: 10.426070)



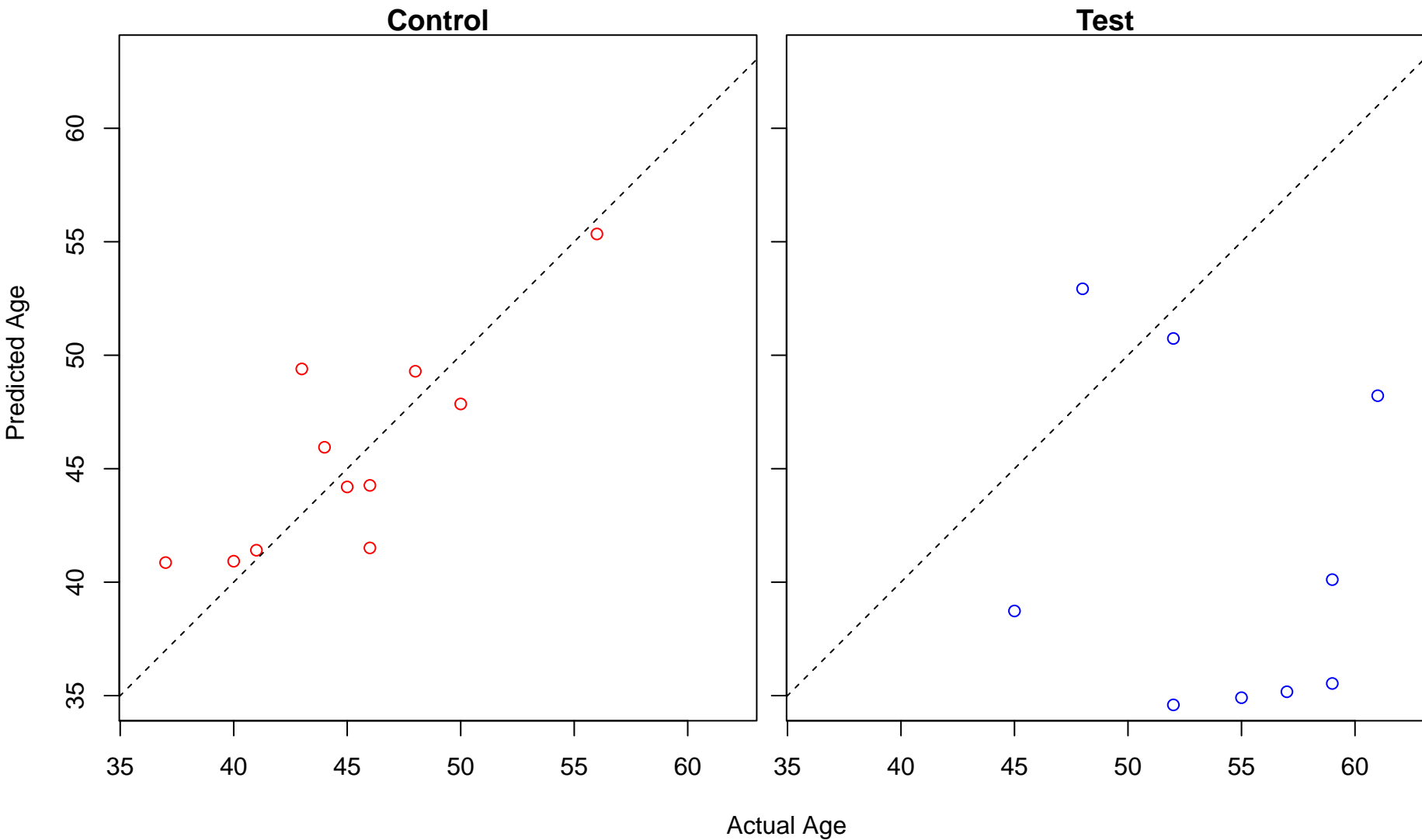
positive regulation of mitochondrion organization (Score: 10.414596)



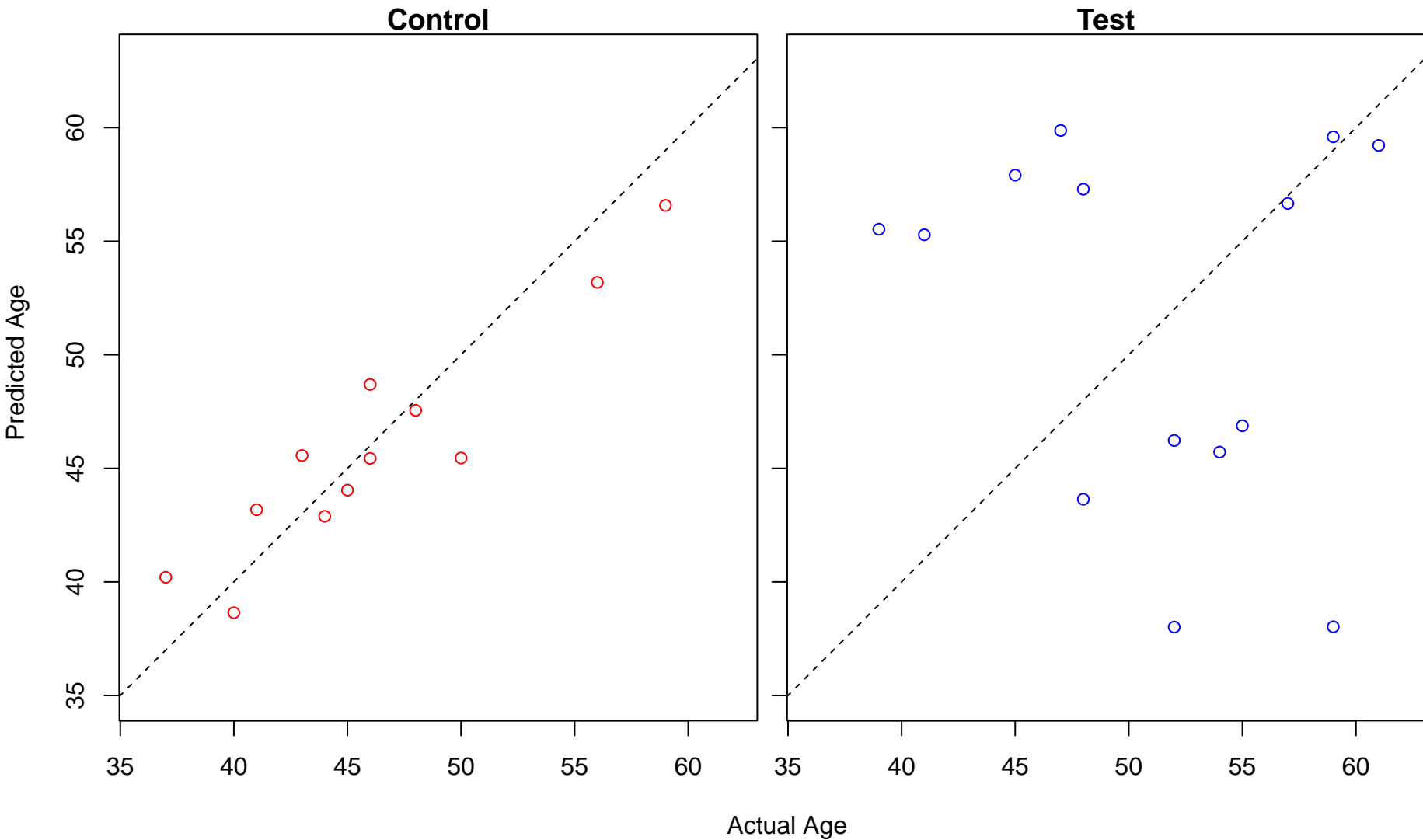
virion assembly (Score: 10.390076)



negative regulation of lyase activity (Score: 10.374977)

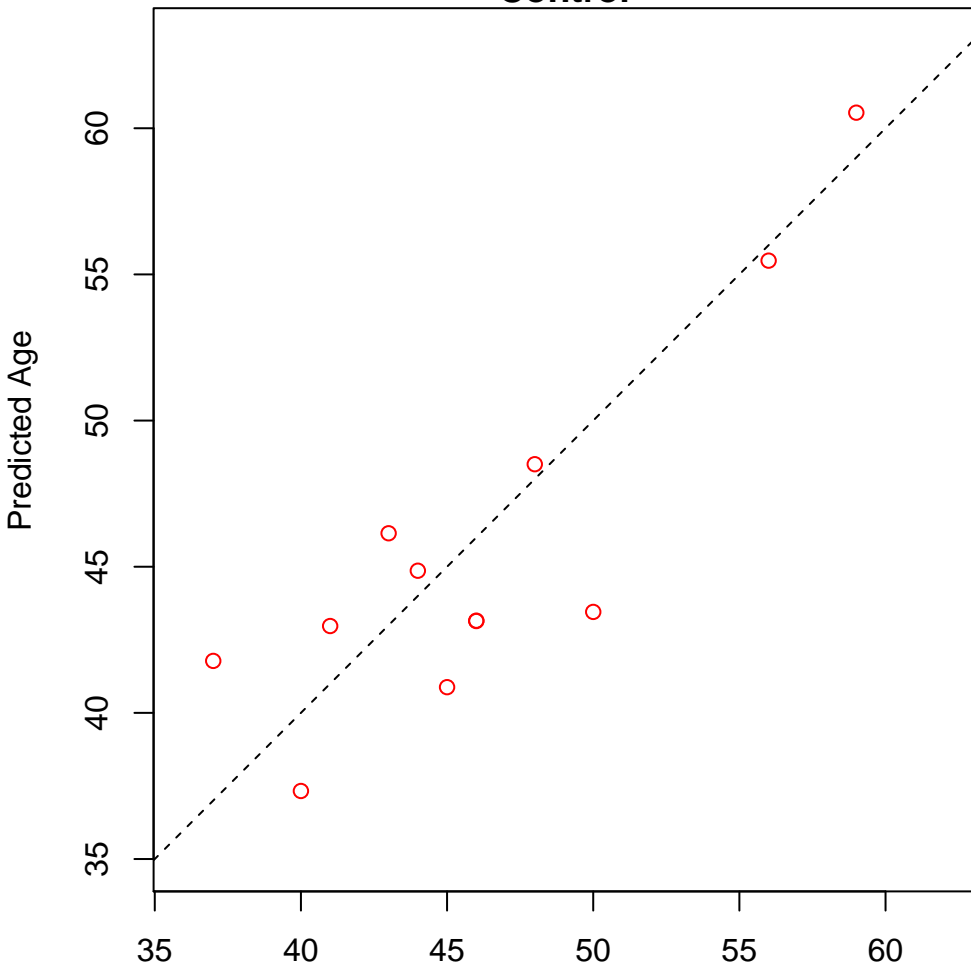


interleukin-1-mediated signaling pathway (Score: 10.342355)

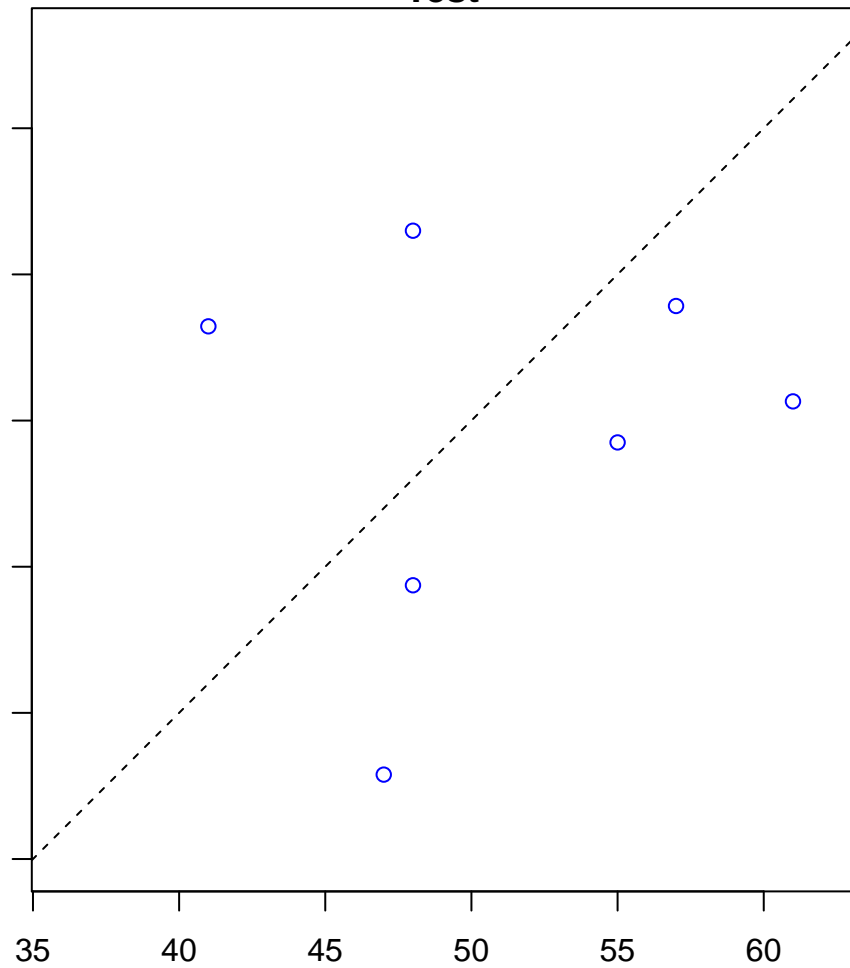


single organism reproductive process (Score: 10.330400)

Control

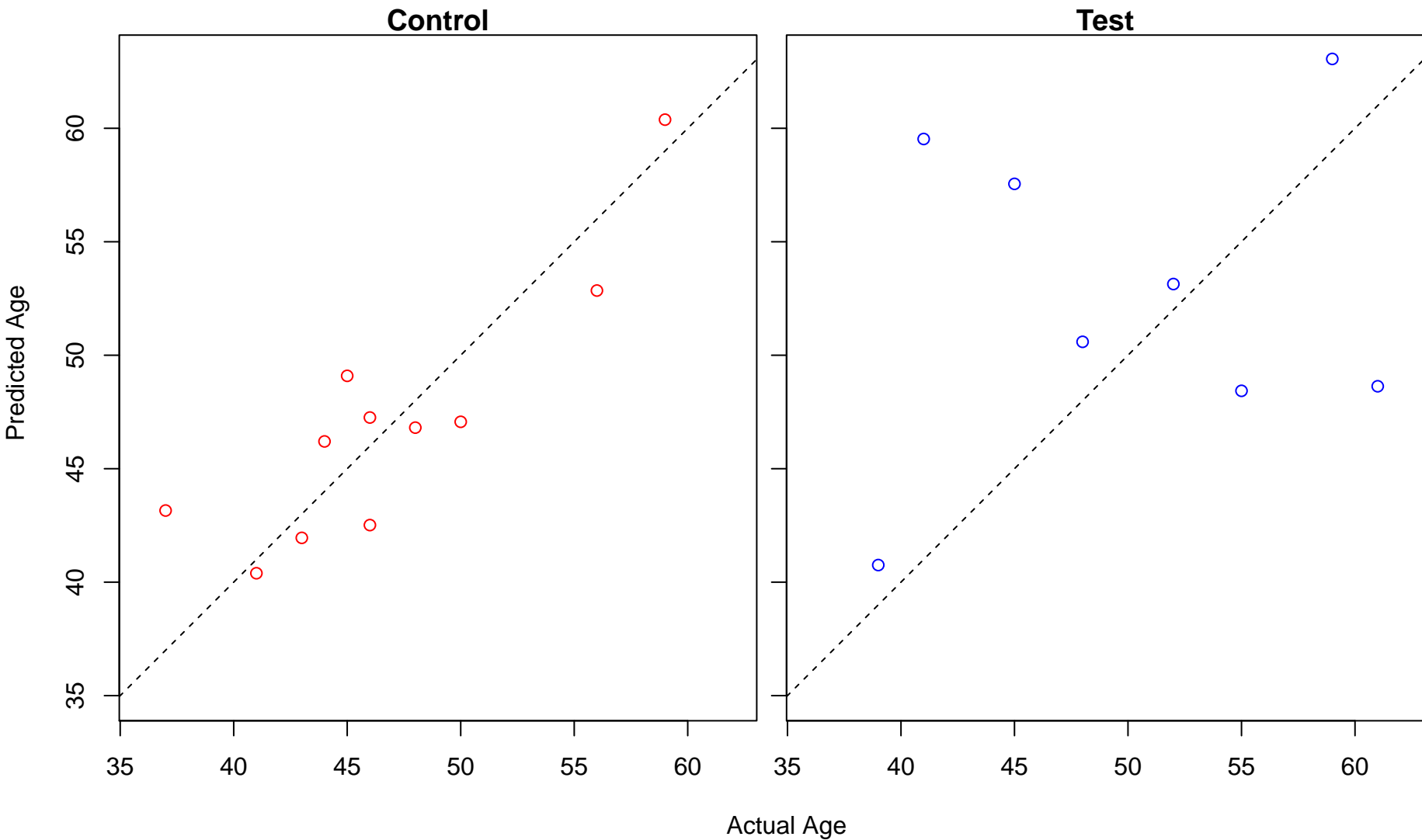


Test

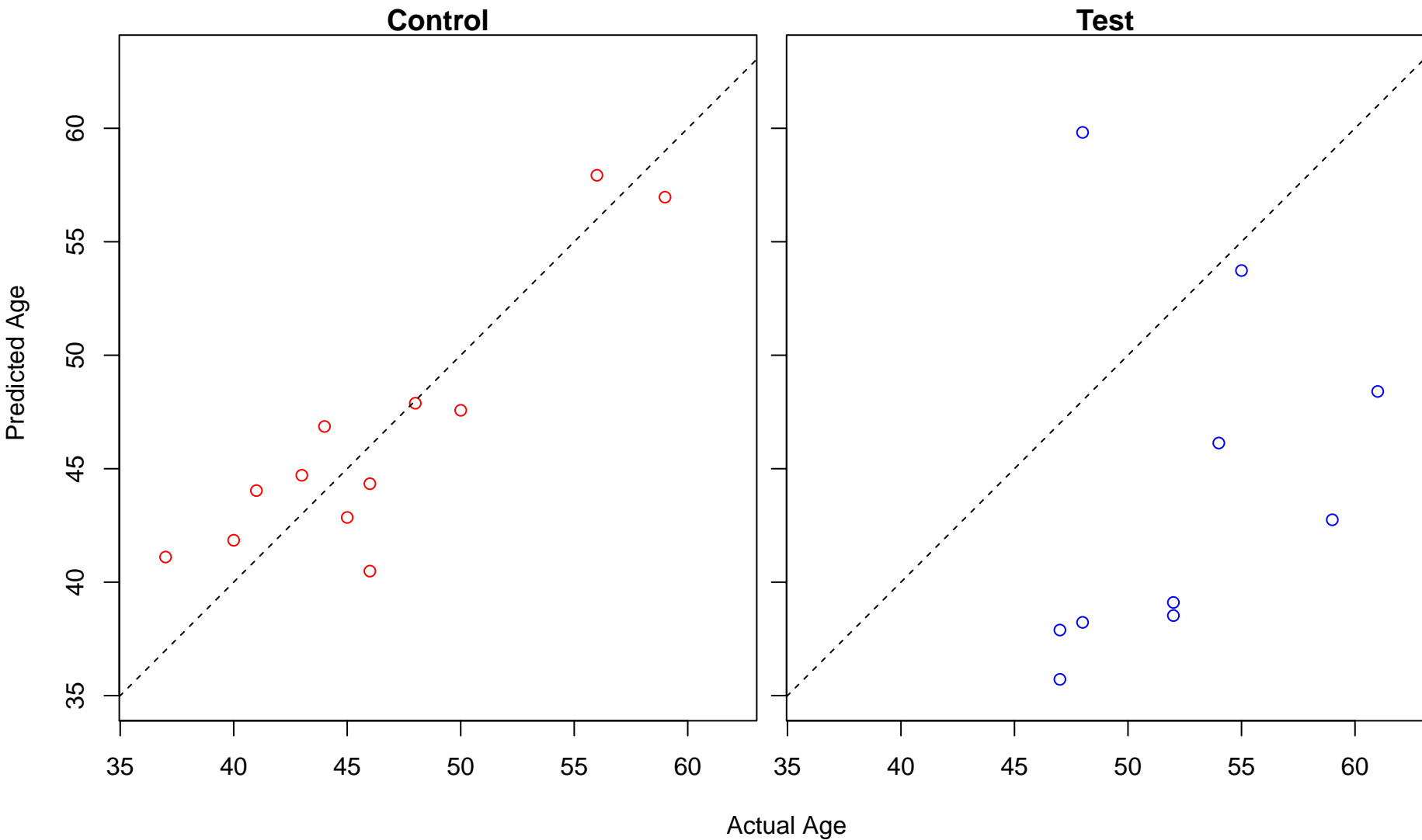


Actual Age

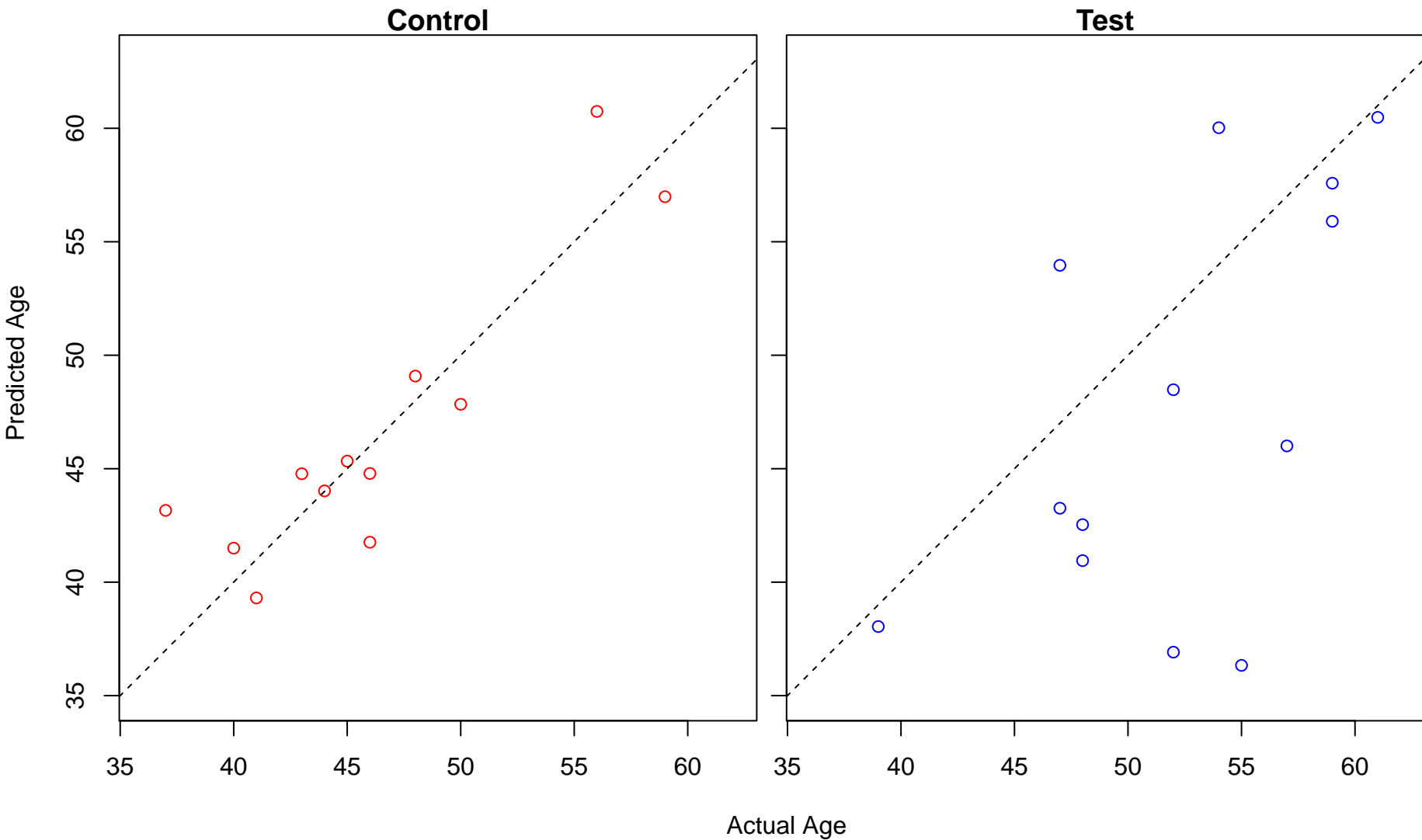
peptide hormone processing (Score: 10.251563)



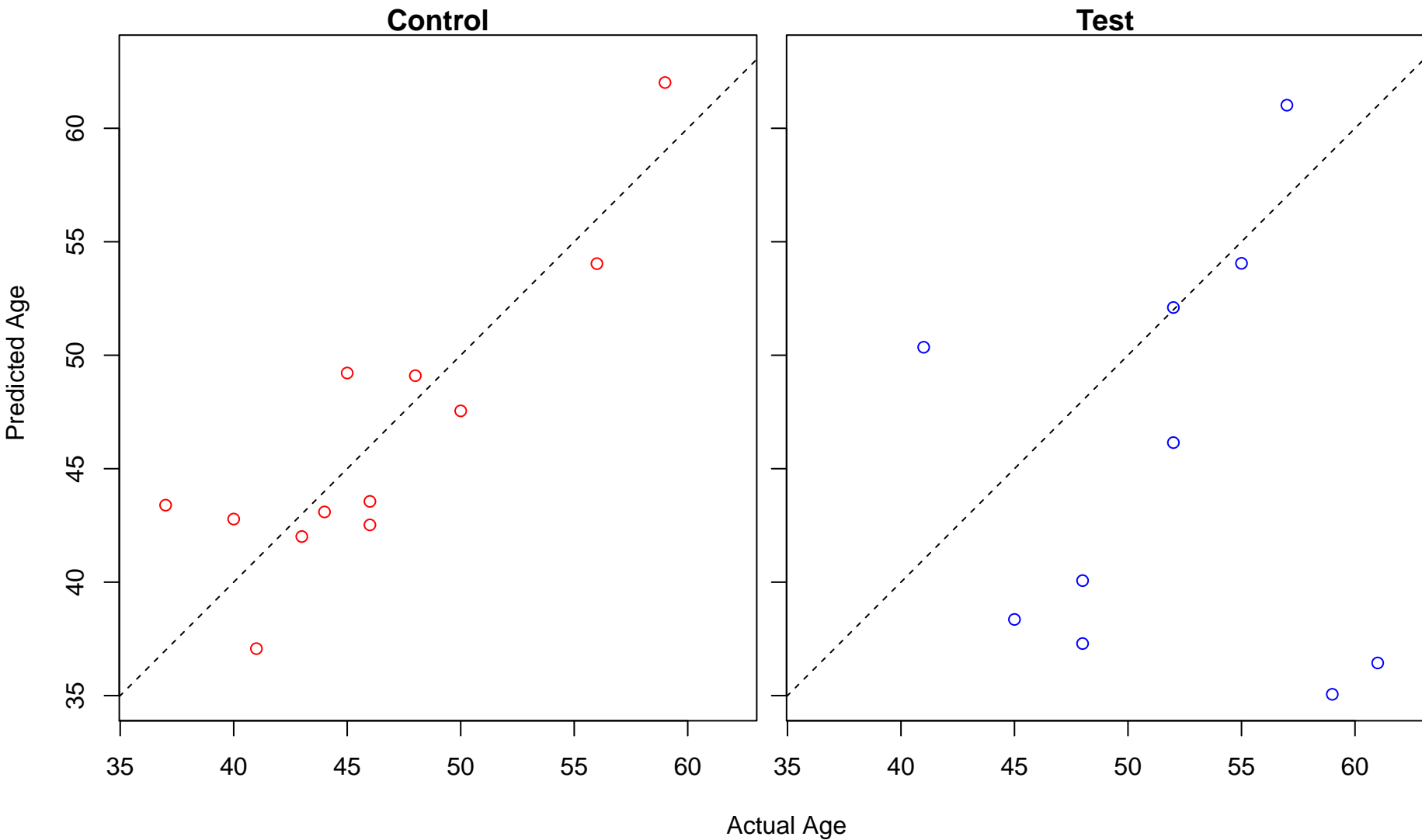
nuclear import (Score: 10.239716)



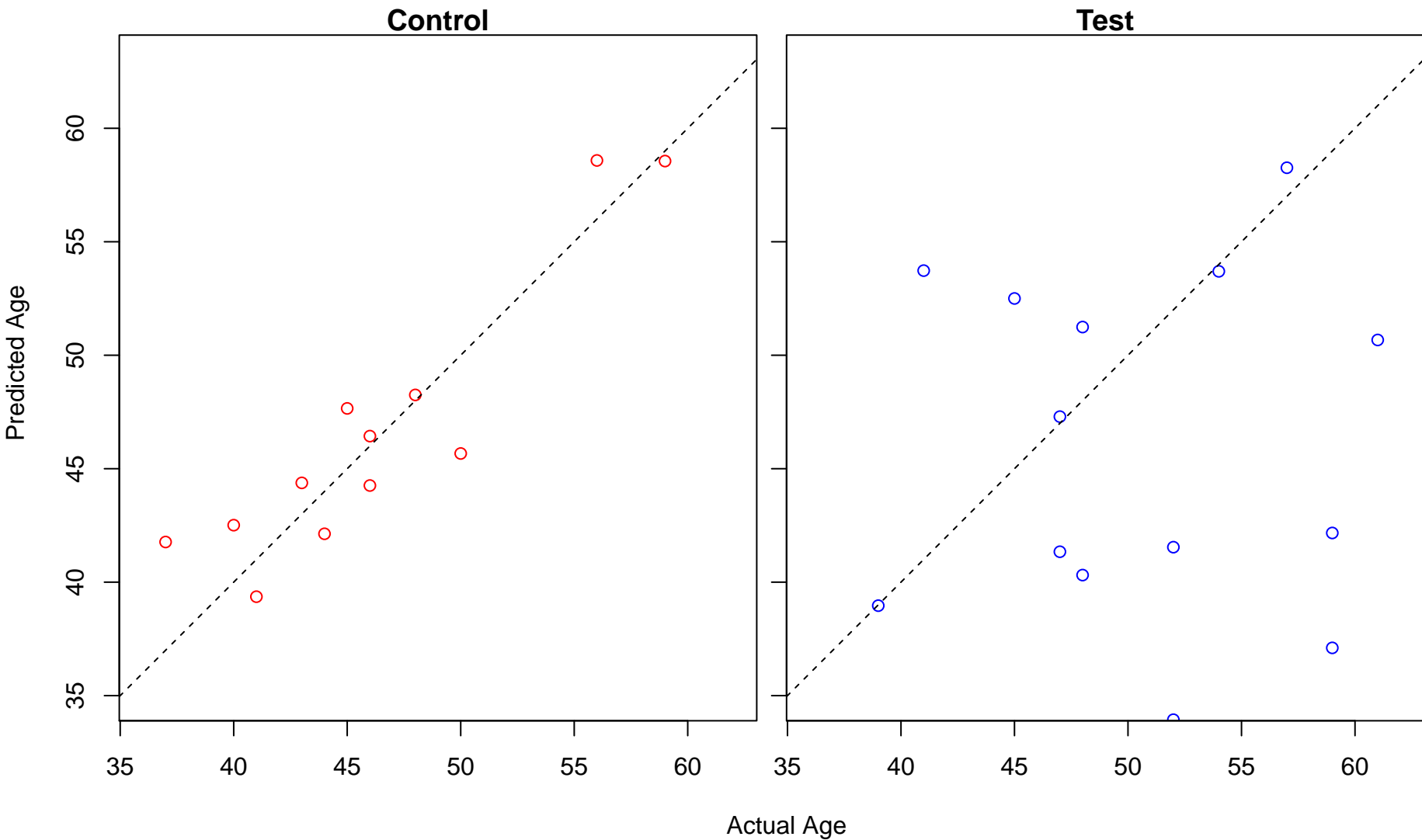
coenzyme catabolic process (Score: 10.237110)



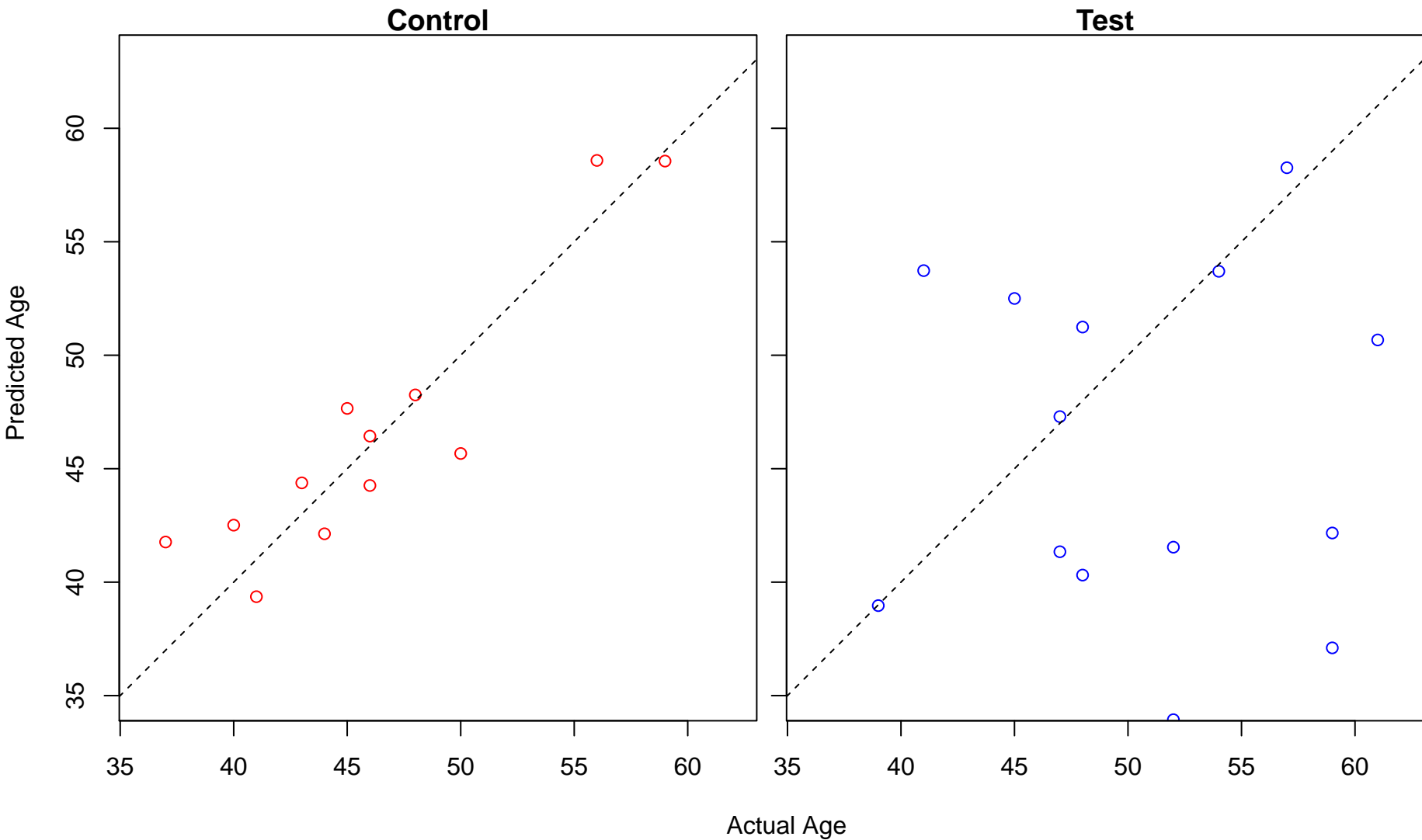
semaphorin-plexin signaling pathway (Score: 10.215519)



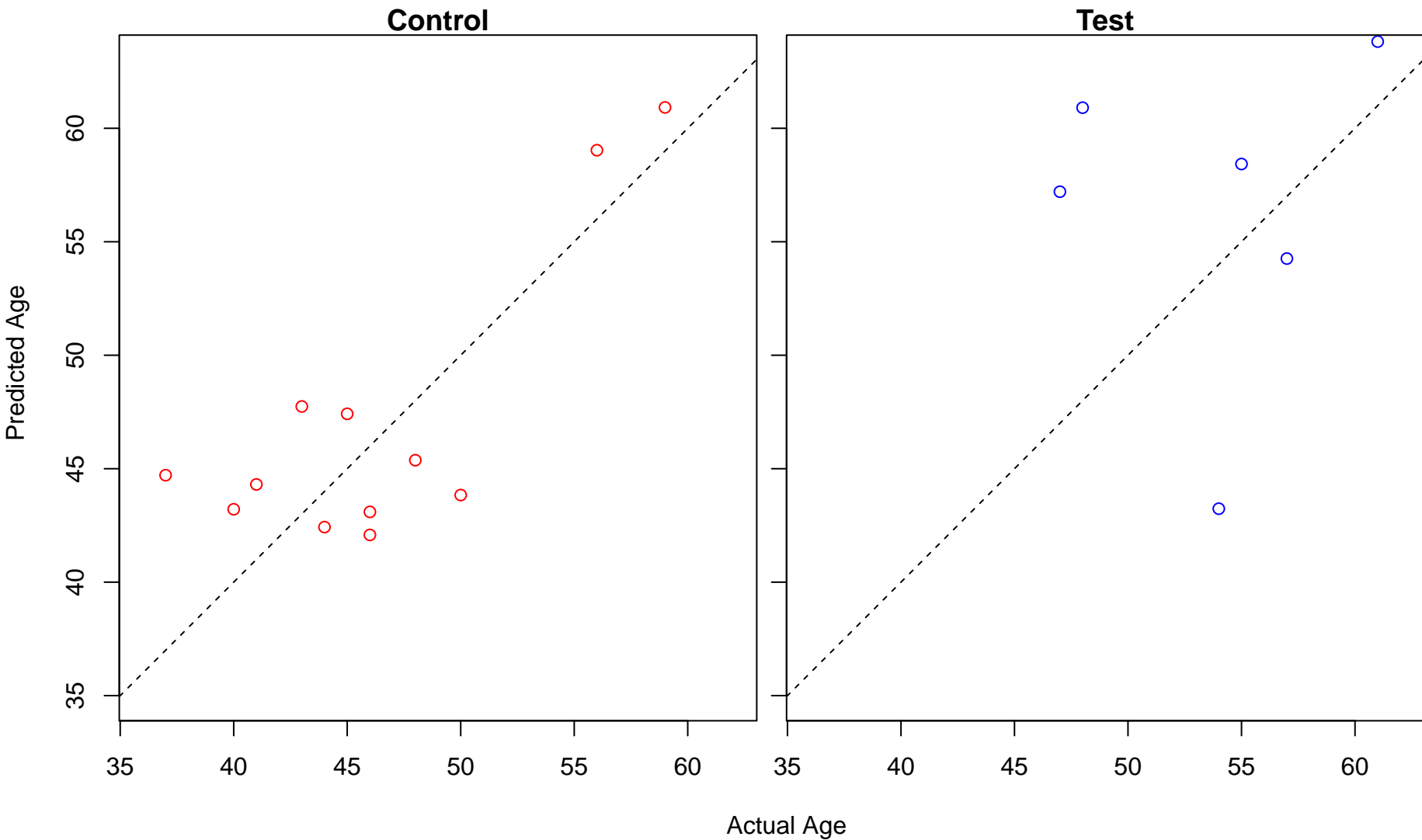
regulation of protein activation cascade (Score: 10.214458)



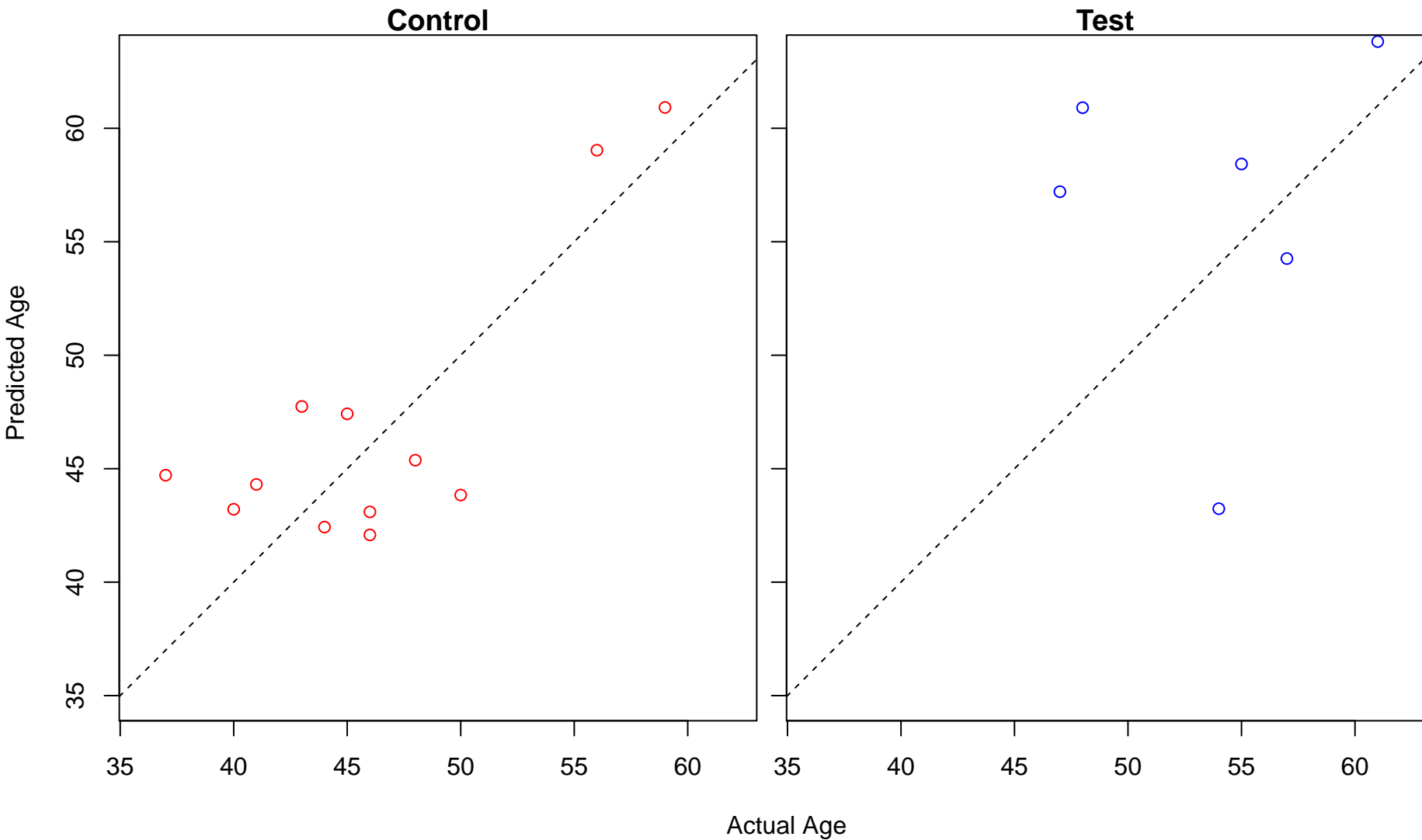
regulation of complement activation (Score: 10.214088)



peptidyl-L-cysteine S-palmitoylation (Score: 10.213858)

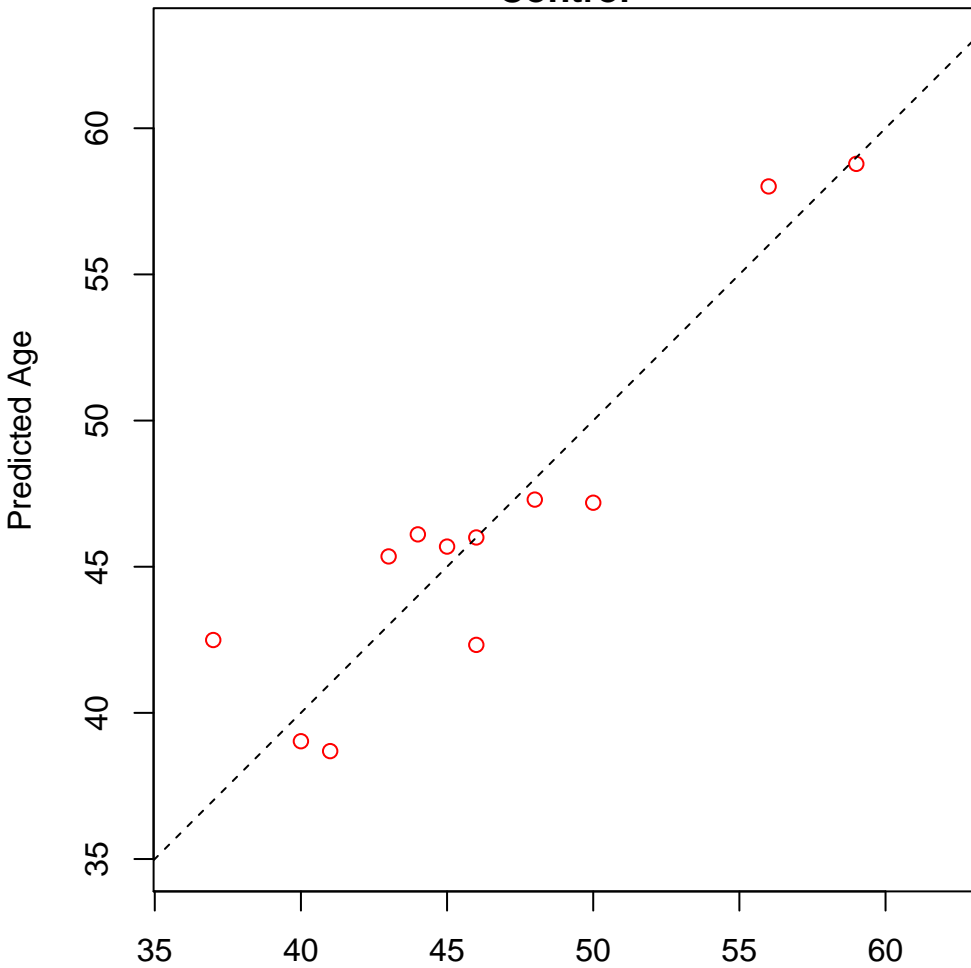


peptidyl-S-diacylglycerol-L-cysteine biosynthetic process from peptidyl-cysteine (Score: 10.21385)

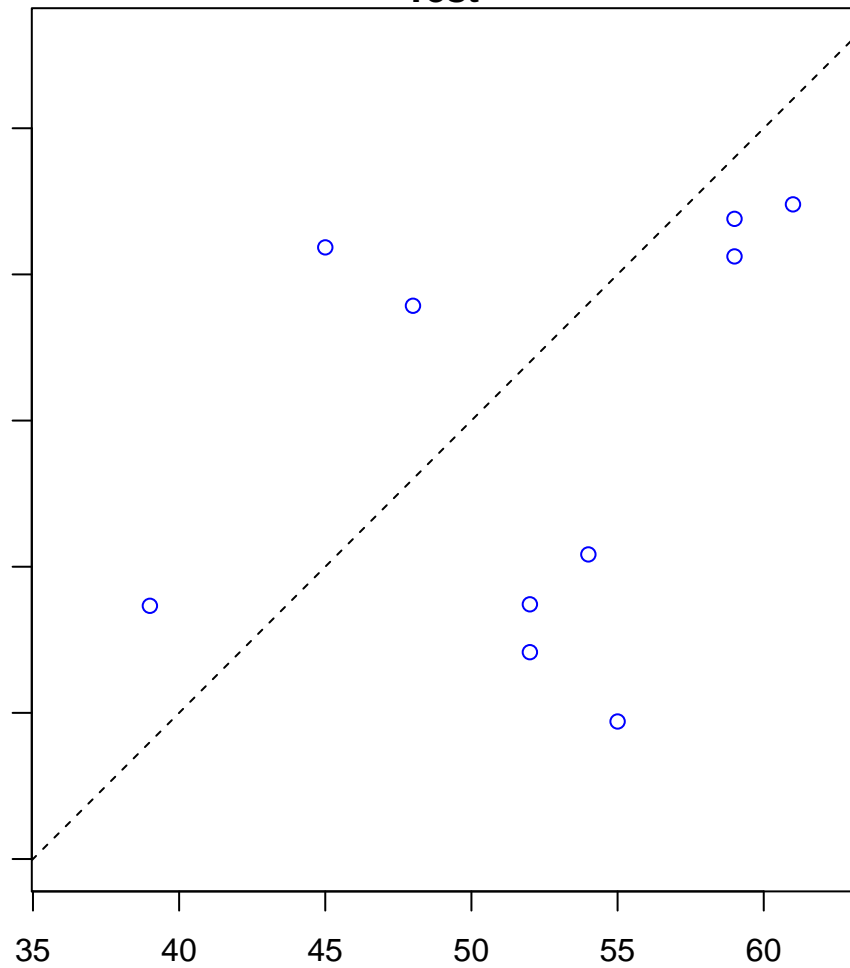


regulation of potassium ion transport (Score: 10.188288)

Control

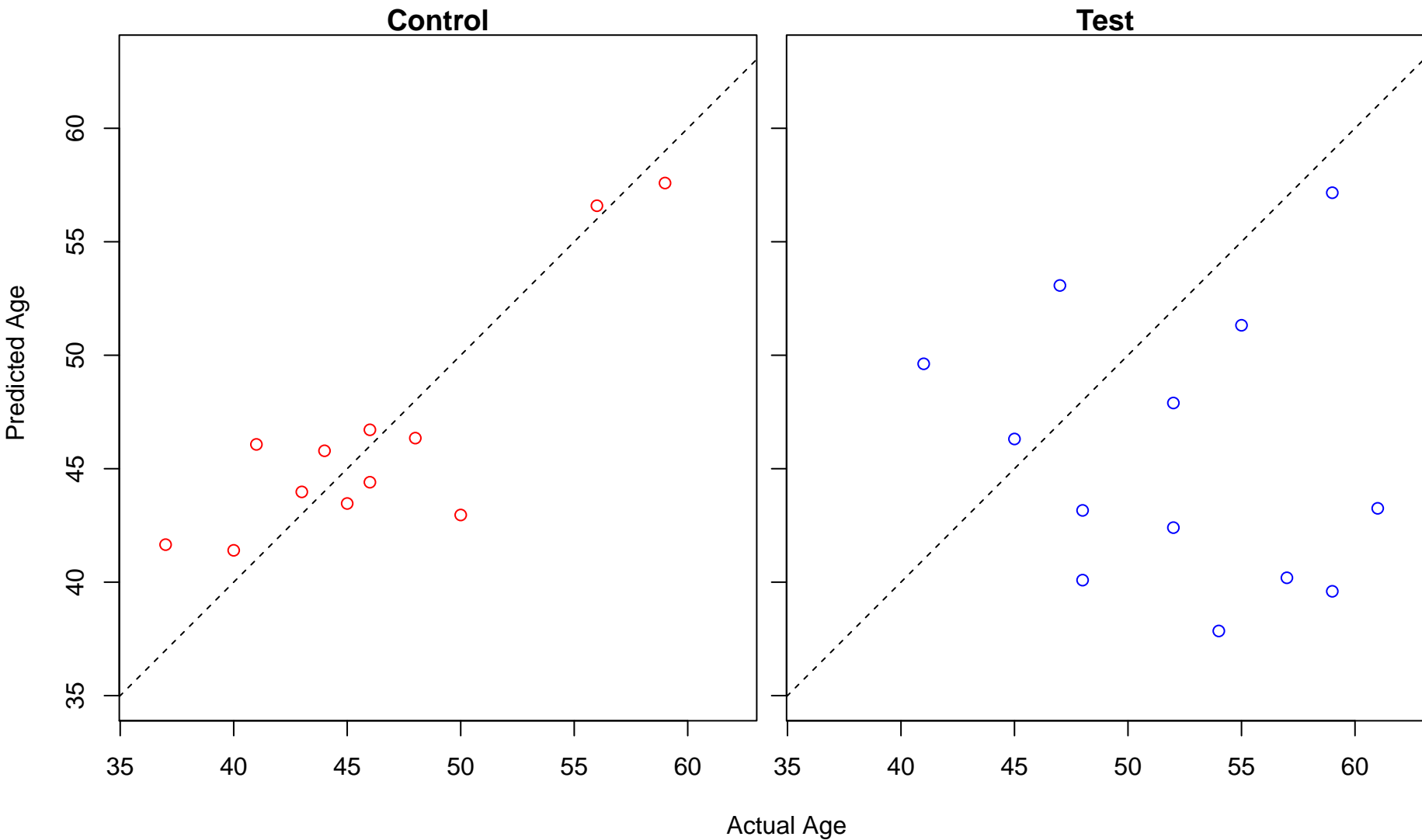


Test

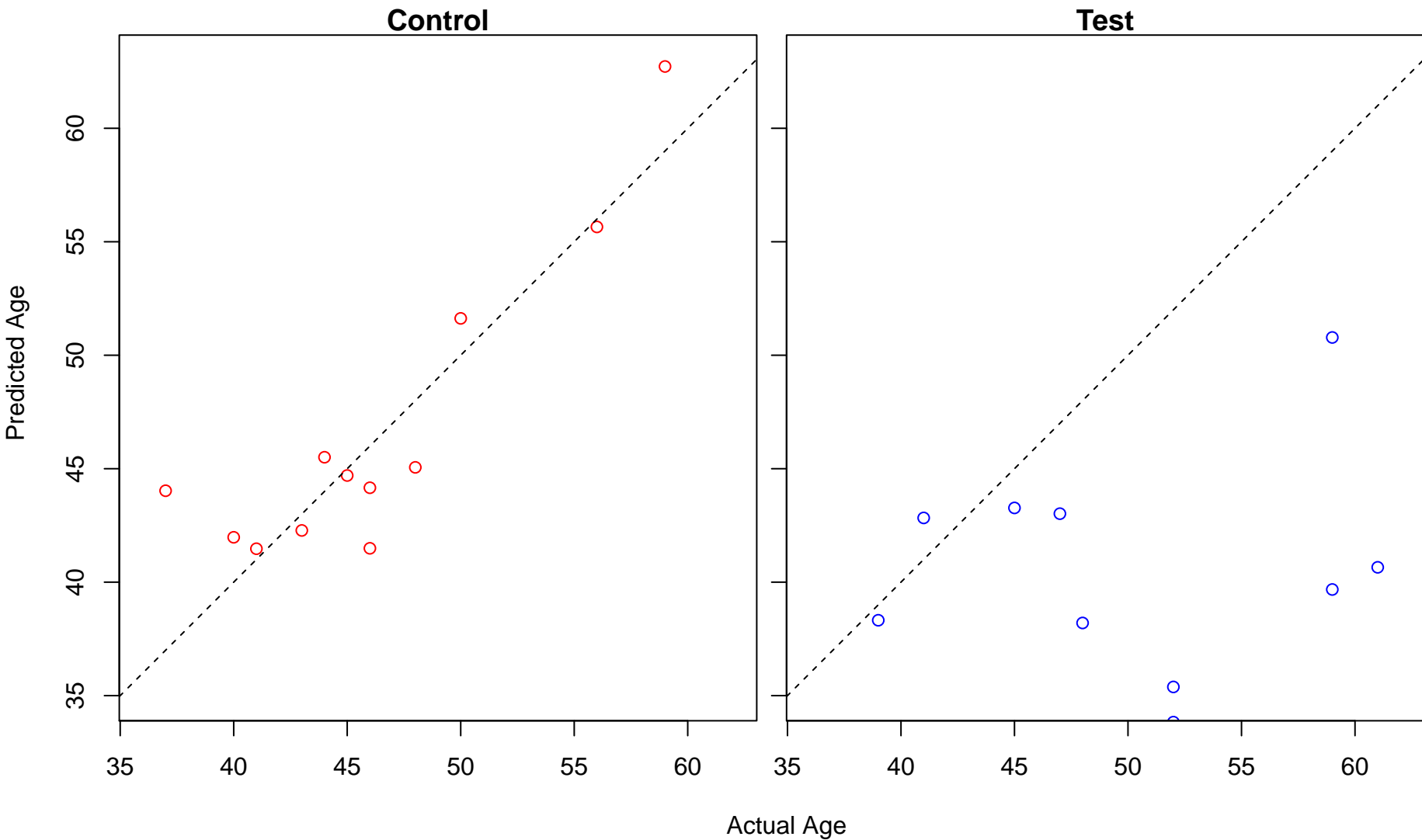


Actual Age

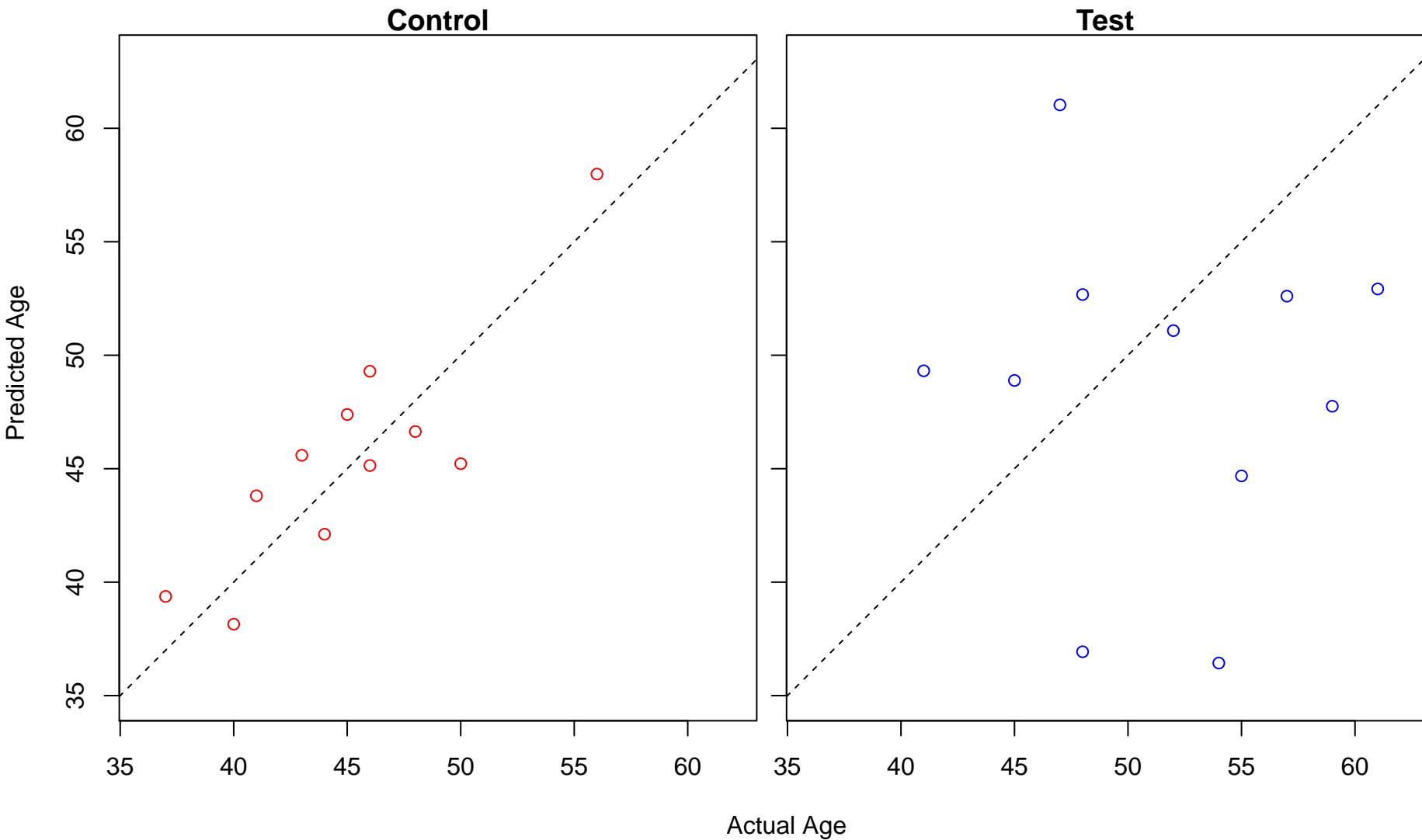
stem cell division (Score: 10.172507)



multicellular organismal signaling (Score: 10.157732)

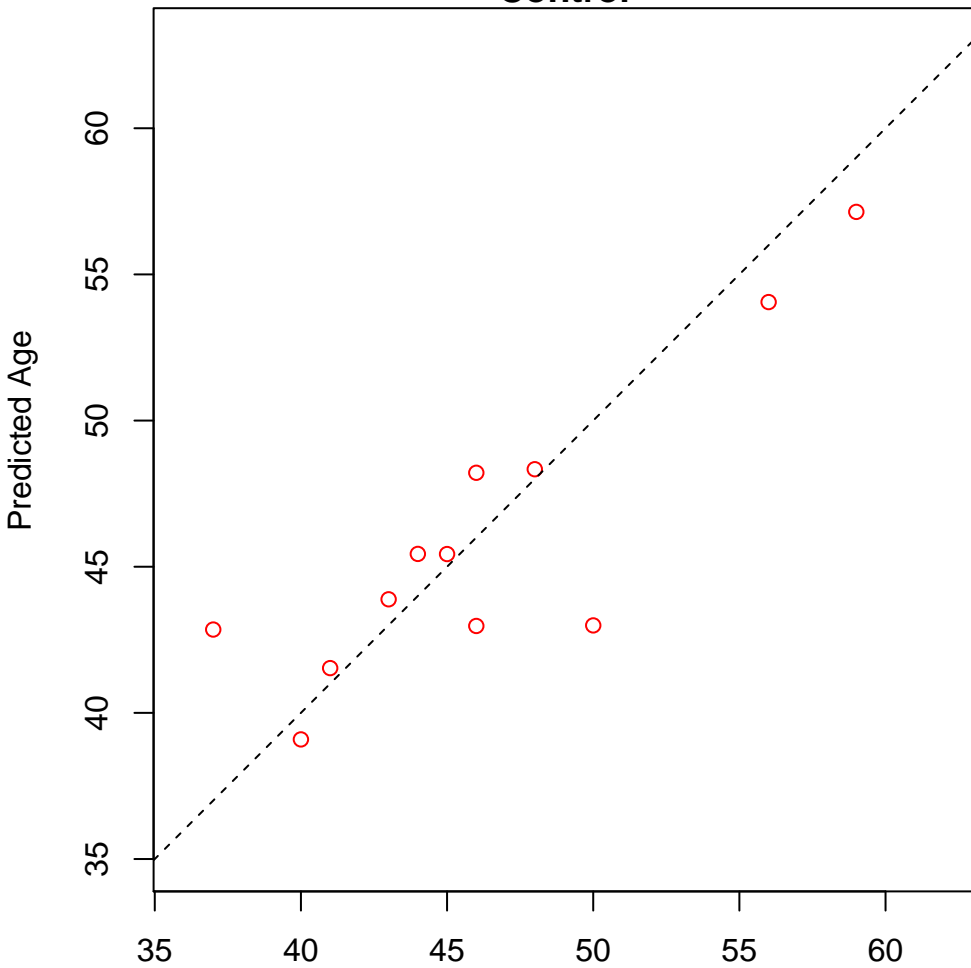


regulation of glomerular mesangial cell proliferation (Score: 10.144351)

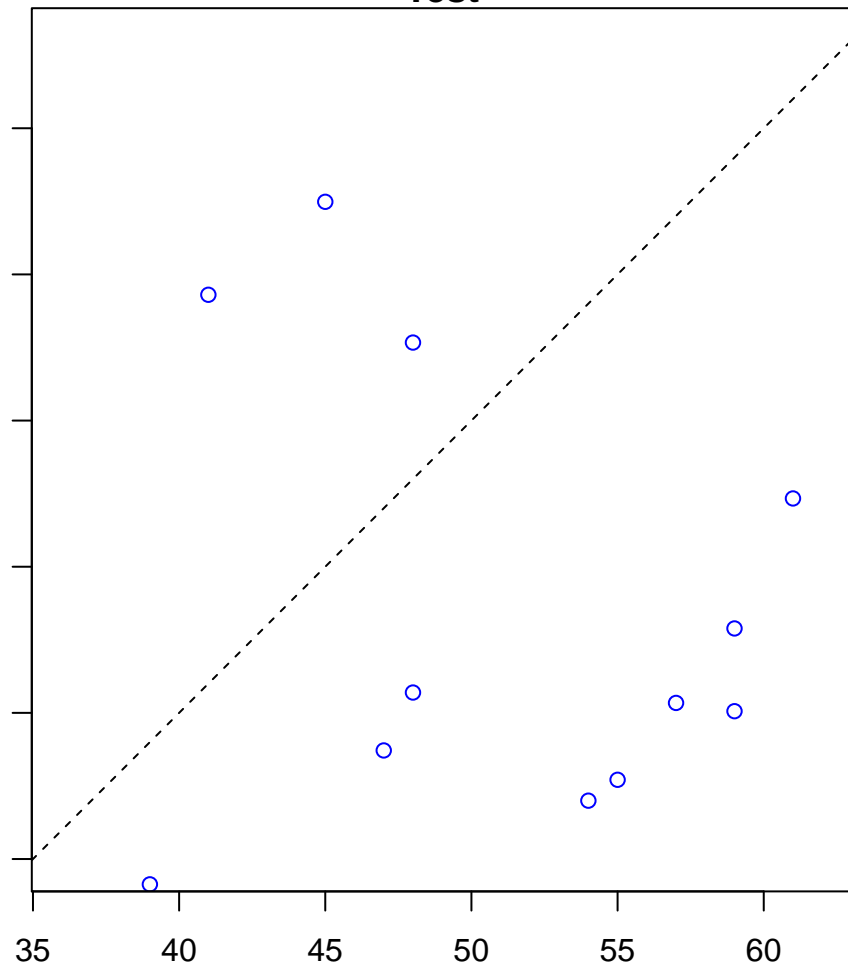


cellular response to ionizing radiation (Score: 10.141958)

Control

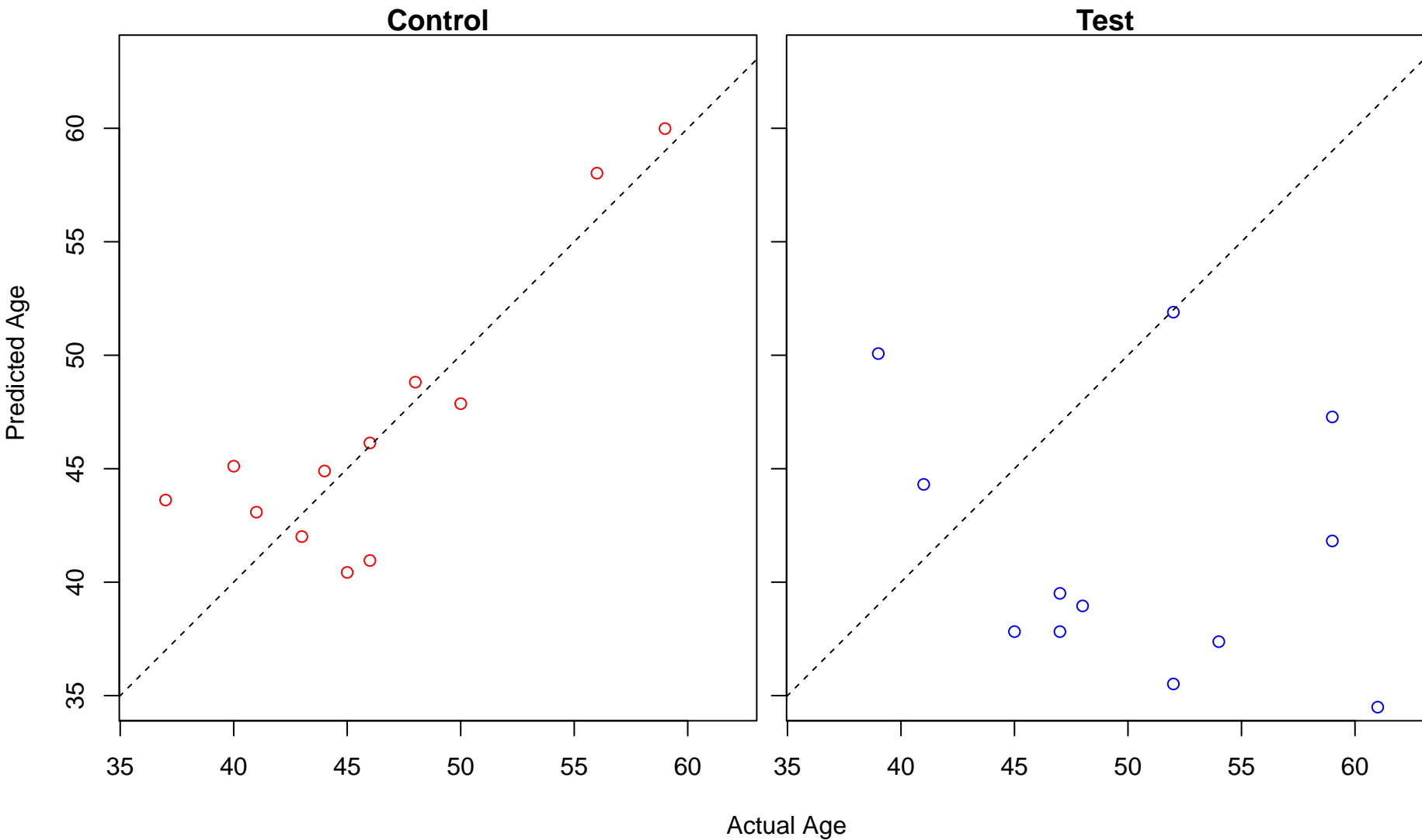


Test

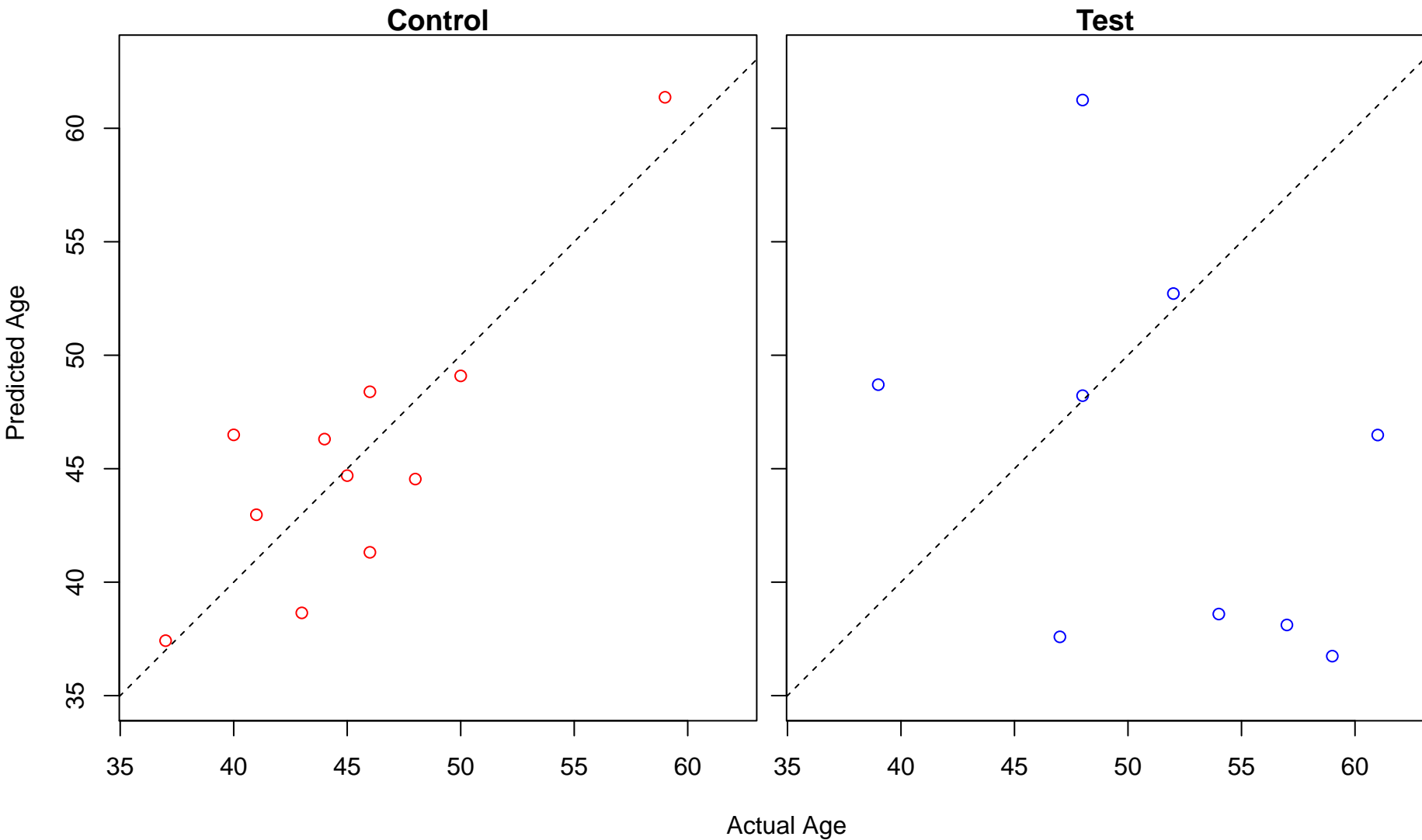


Actual Age

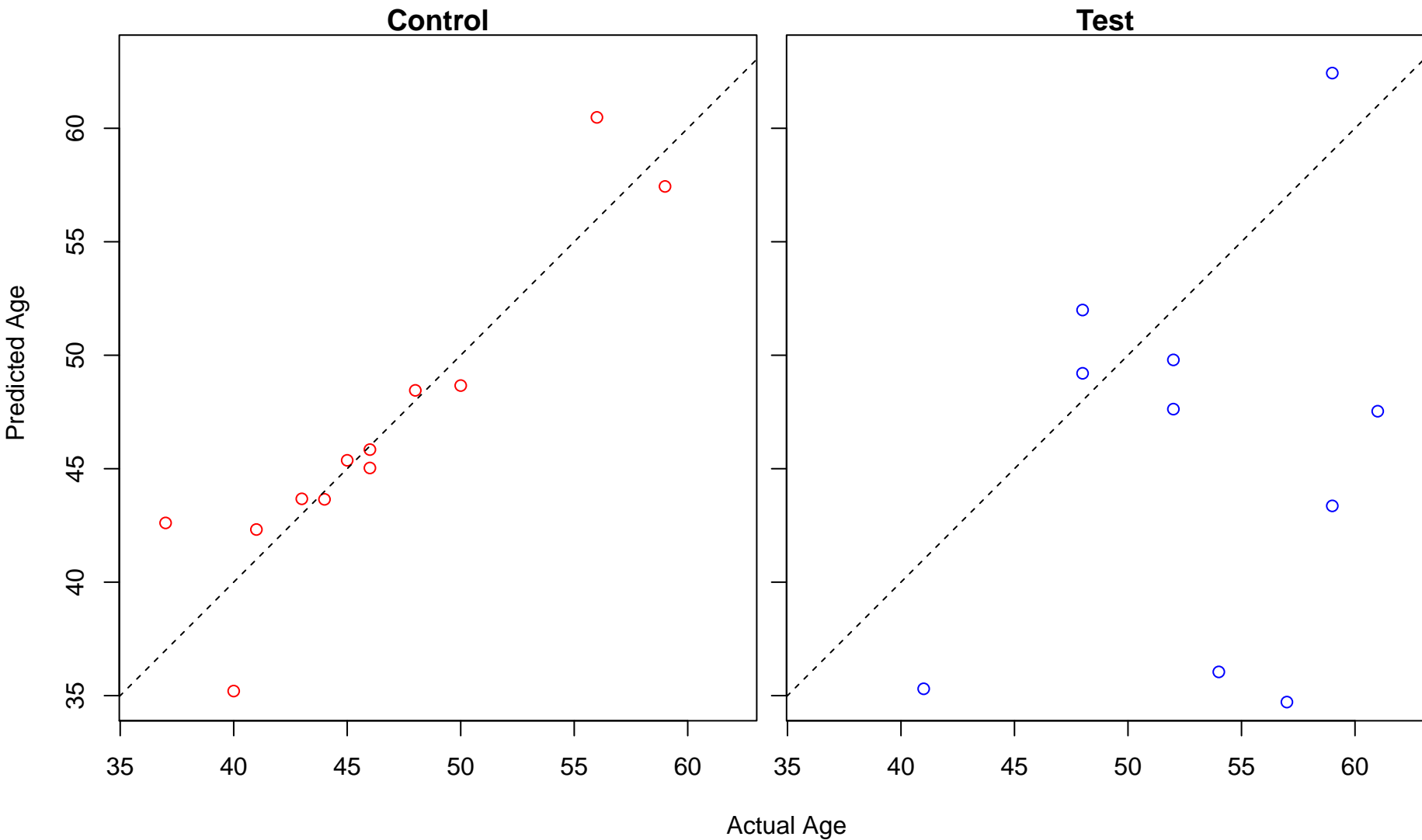
activation of signaling protein activity involved in unfolded protein response (Score: 10.139421)



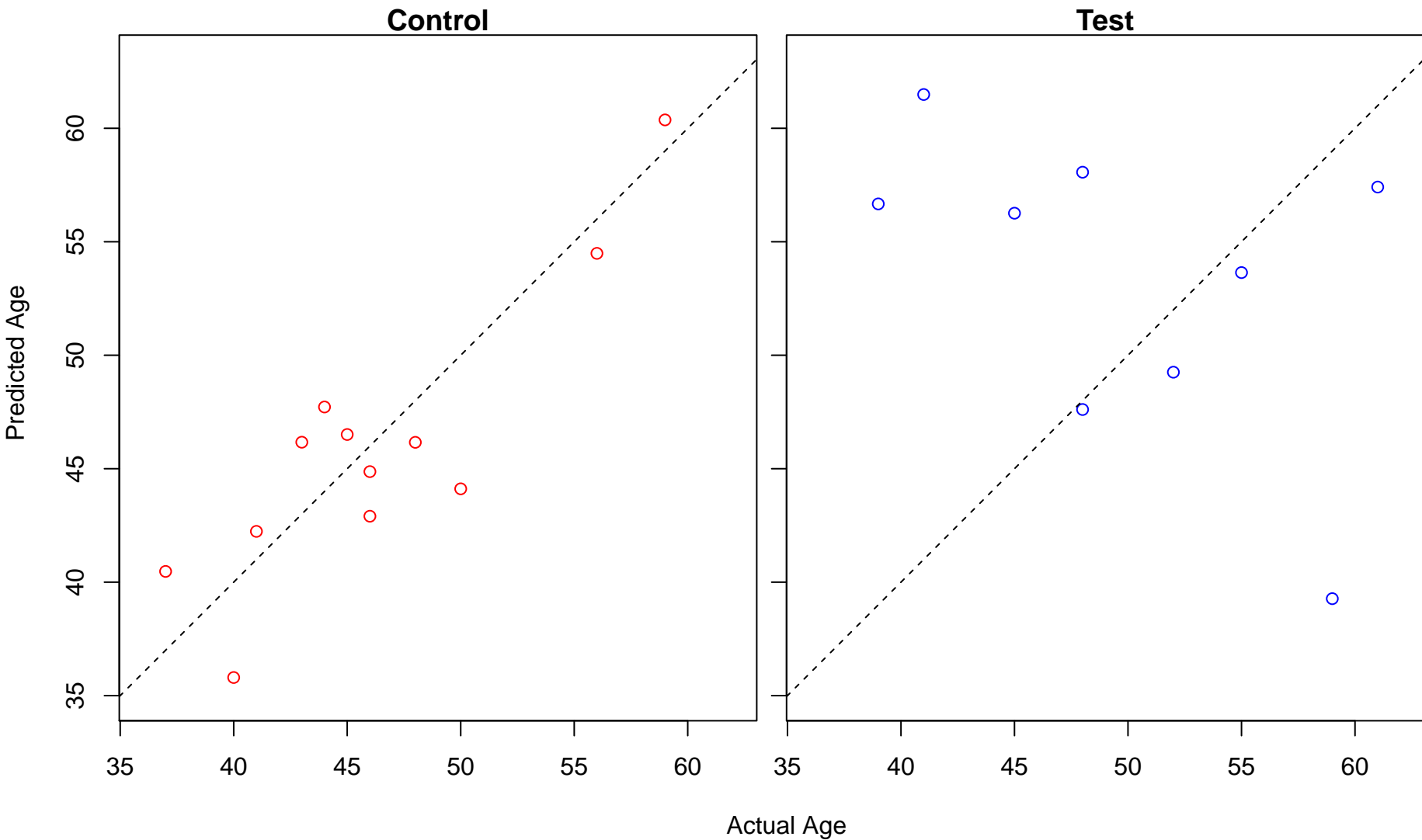
regulation of exit from mitosis (Score: 10.132838)



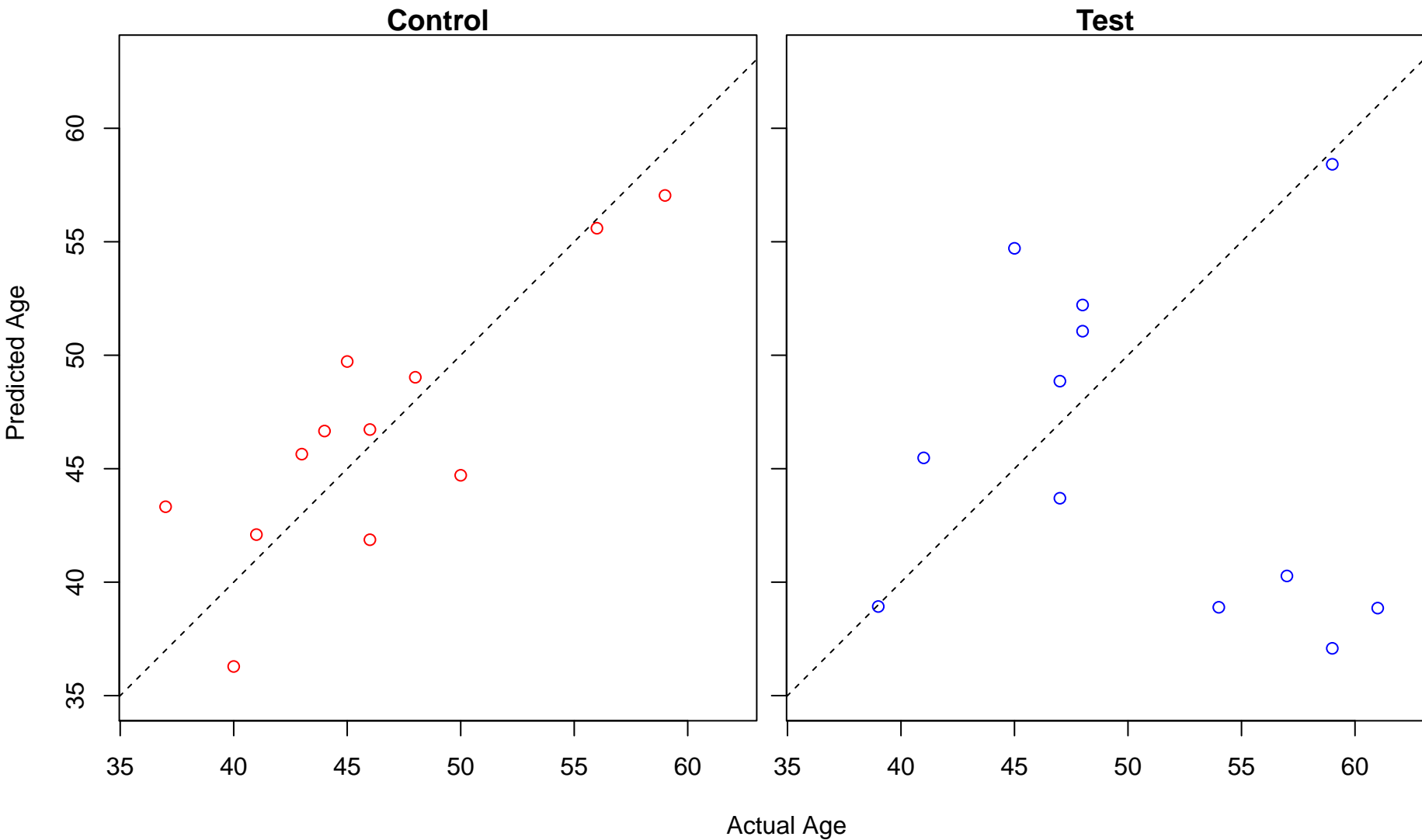
negative regulation of leukocyte chemotaxis (Score: 10.090243)



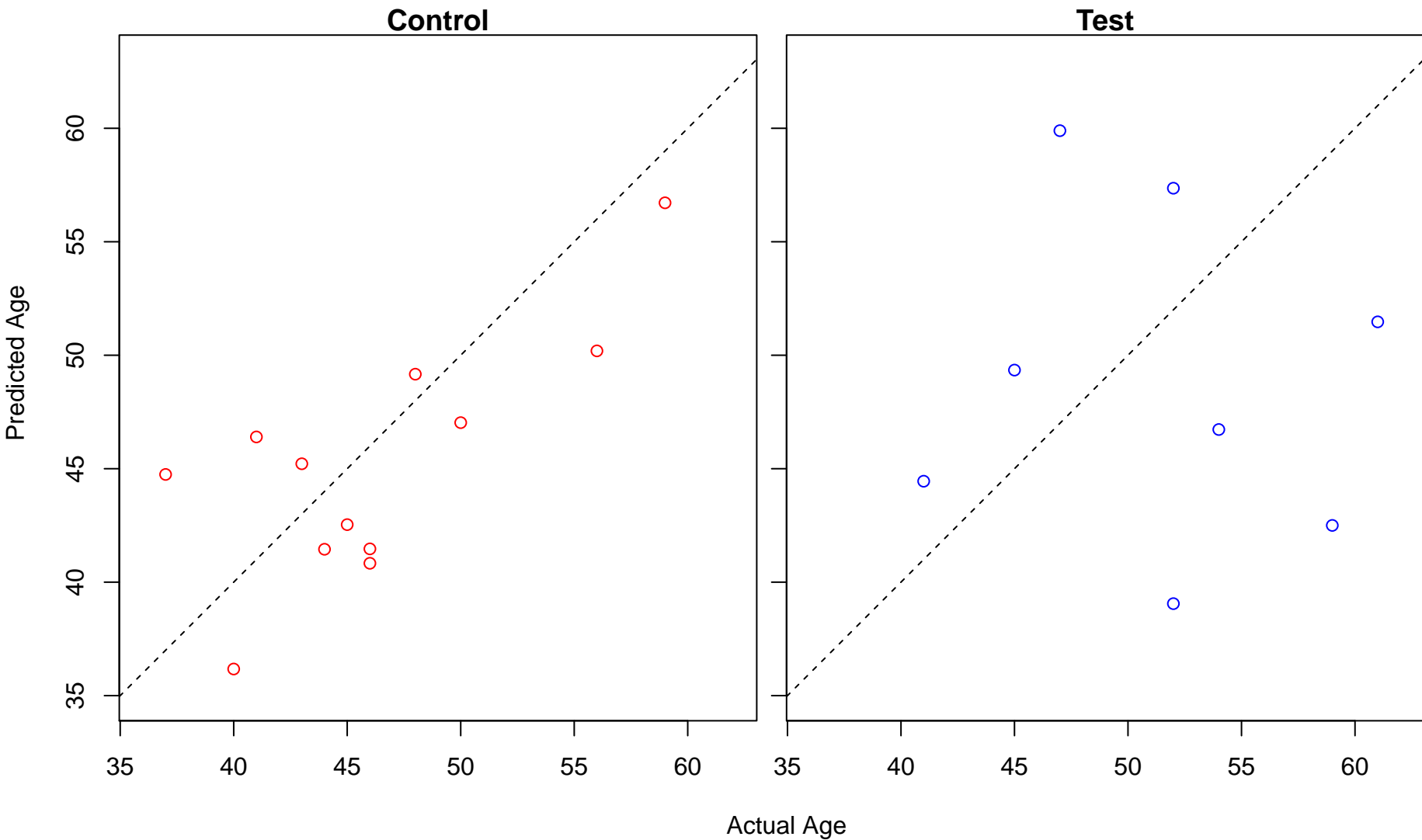
tumor necrosis factor-mediated signaling pathway (Score: 10.088150)



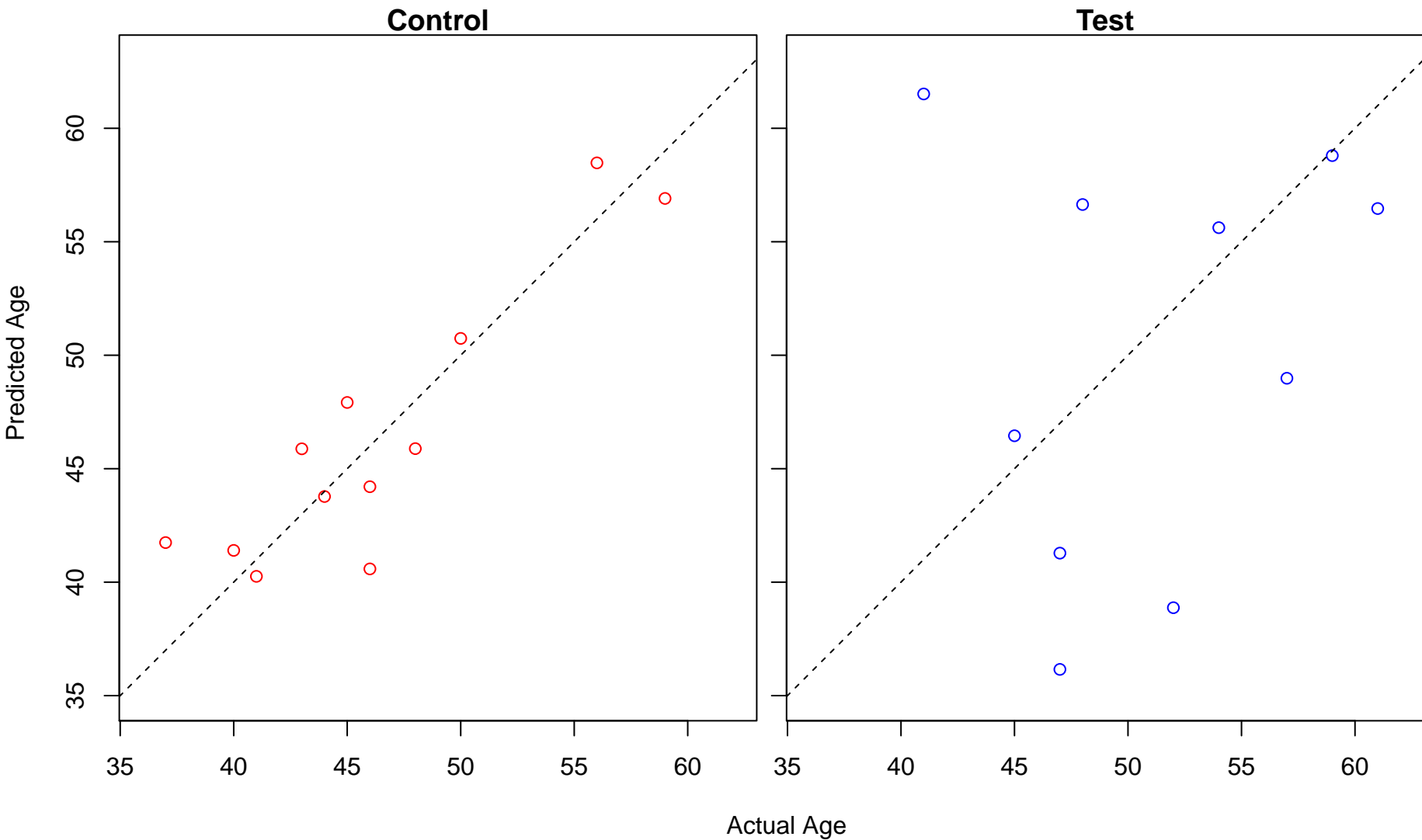
positive regulation of response to external stimulus (Score: 10.080328)



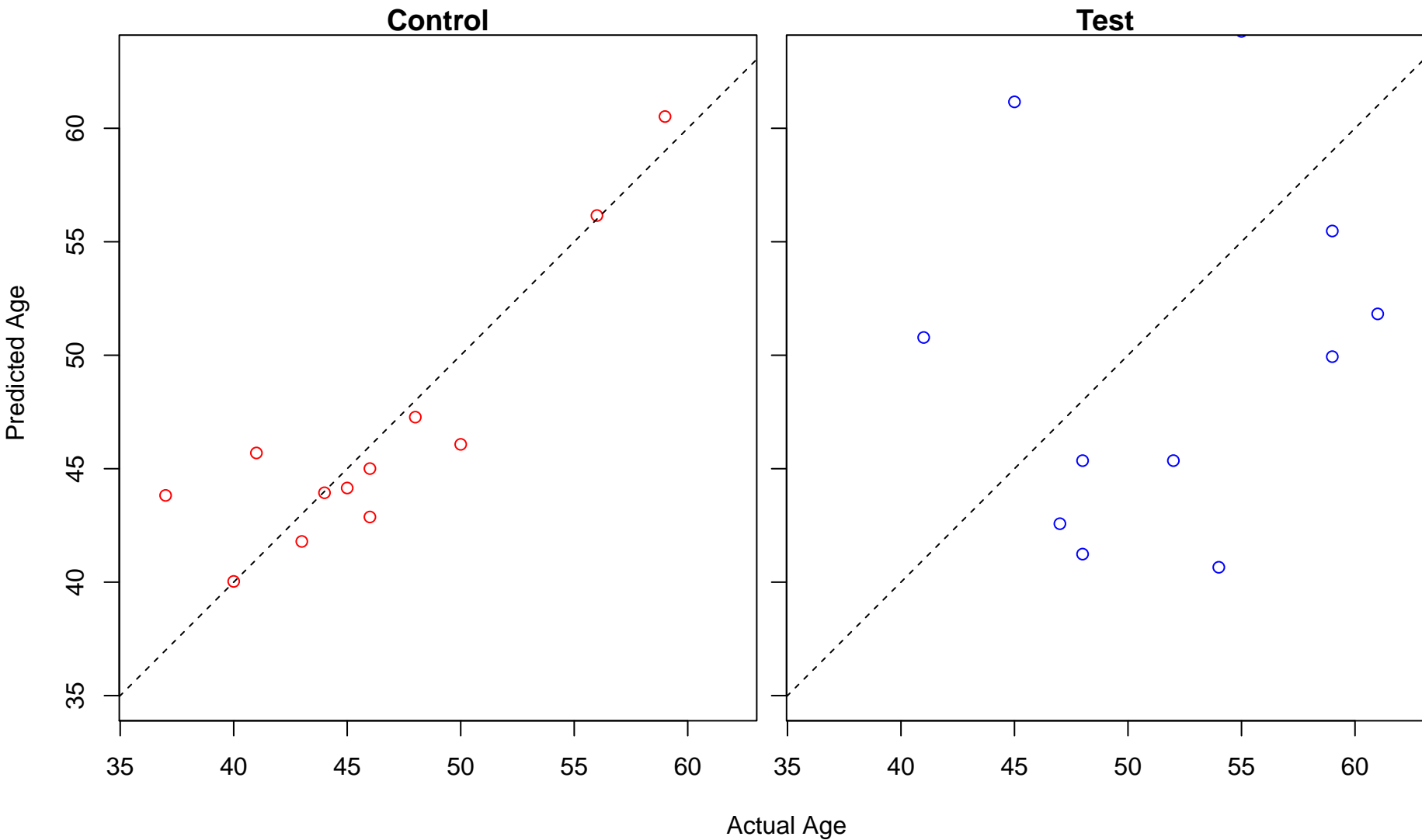
regulation of fibrinolysis (Score: 10.069840)



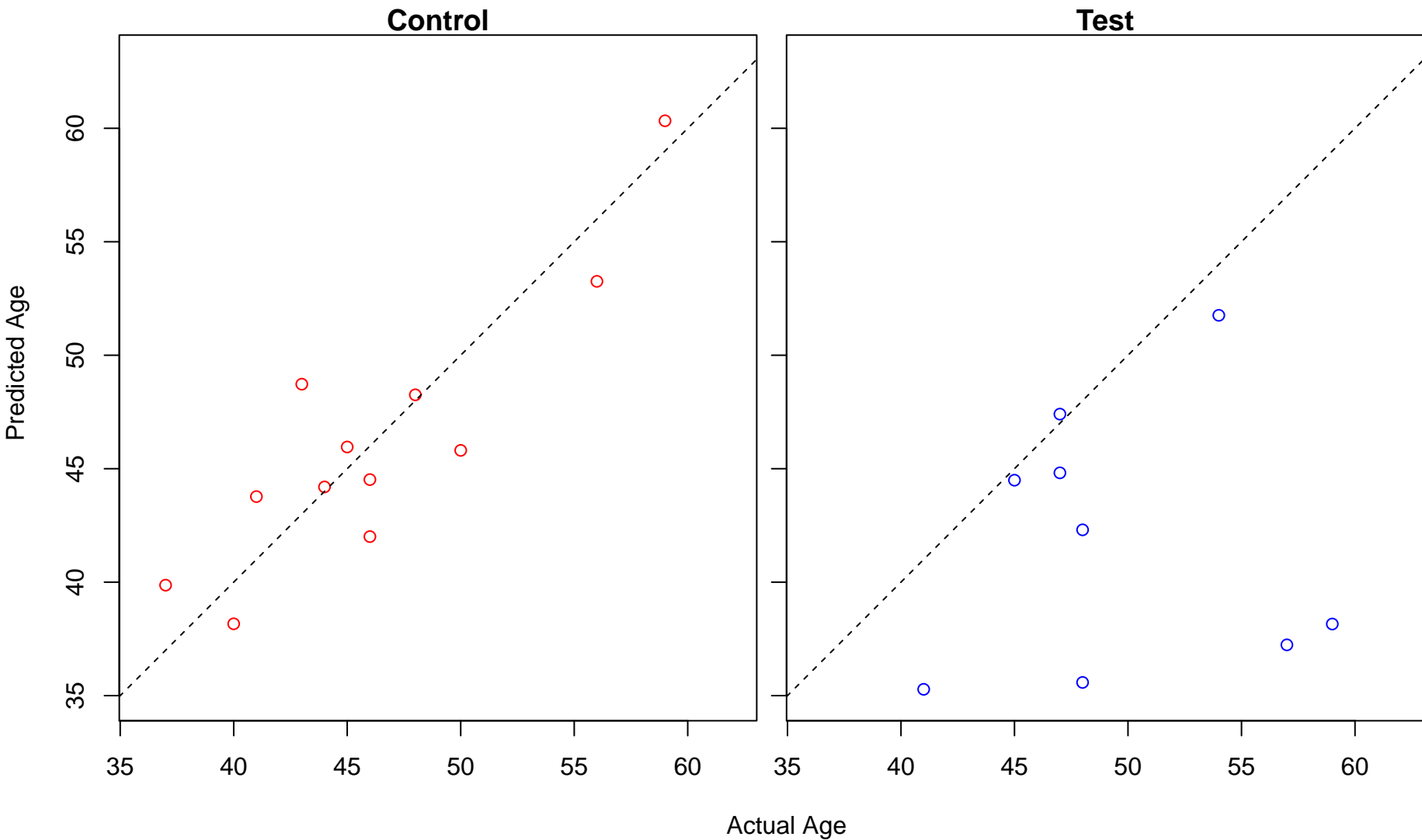
regulation of interleukin-2 secretion (Score: 10.065799)



ossification (Score: 10.049953)

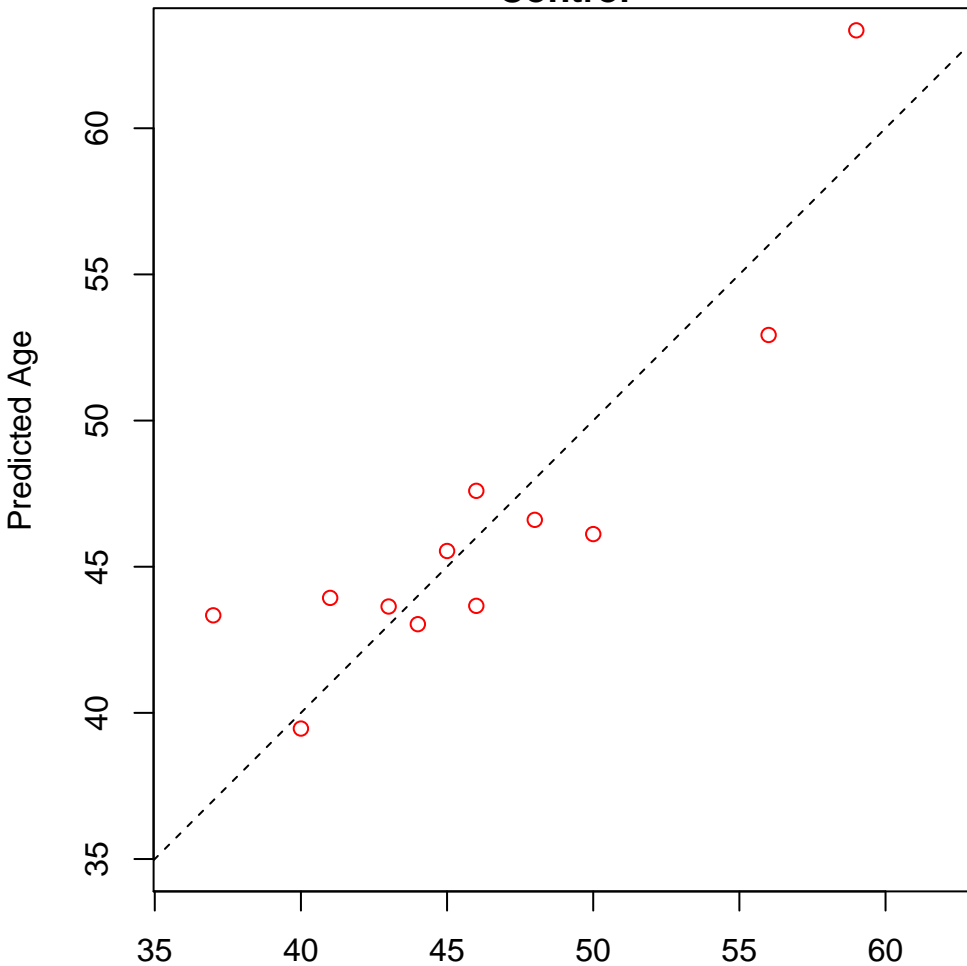


regulation of respiratory burst (Score: 10.032464)

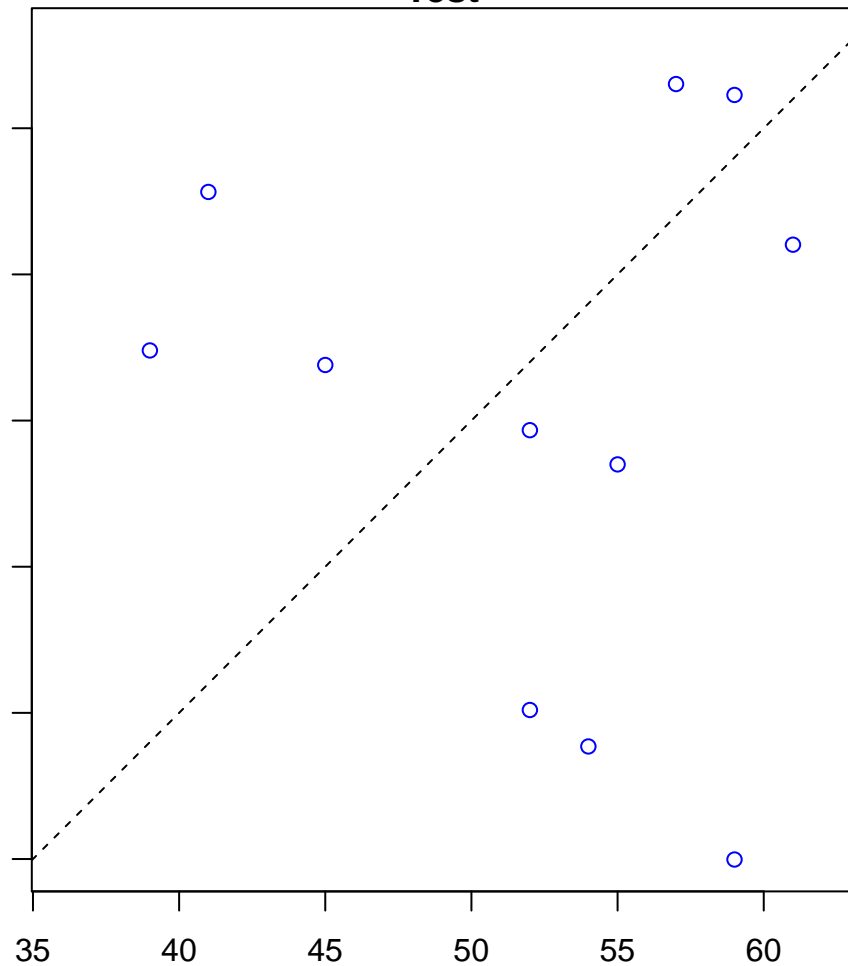


formation of primary germ layer (Score: 10.027464)

Control

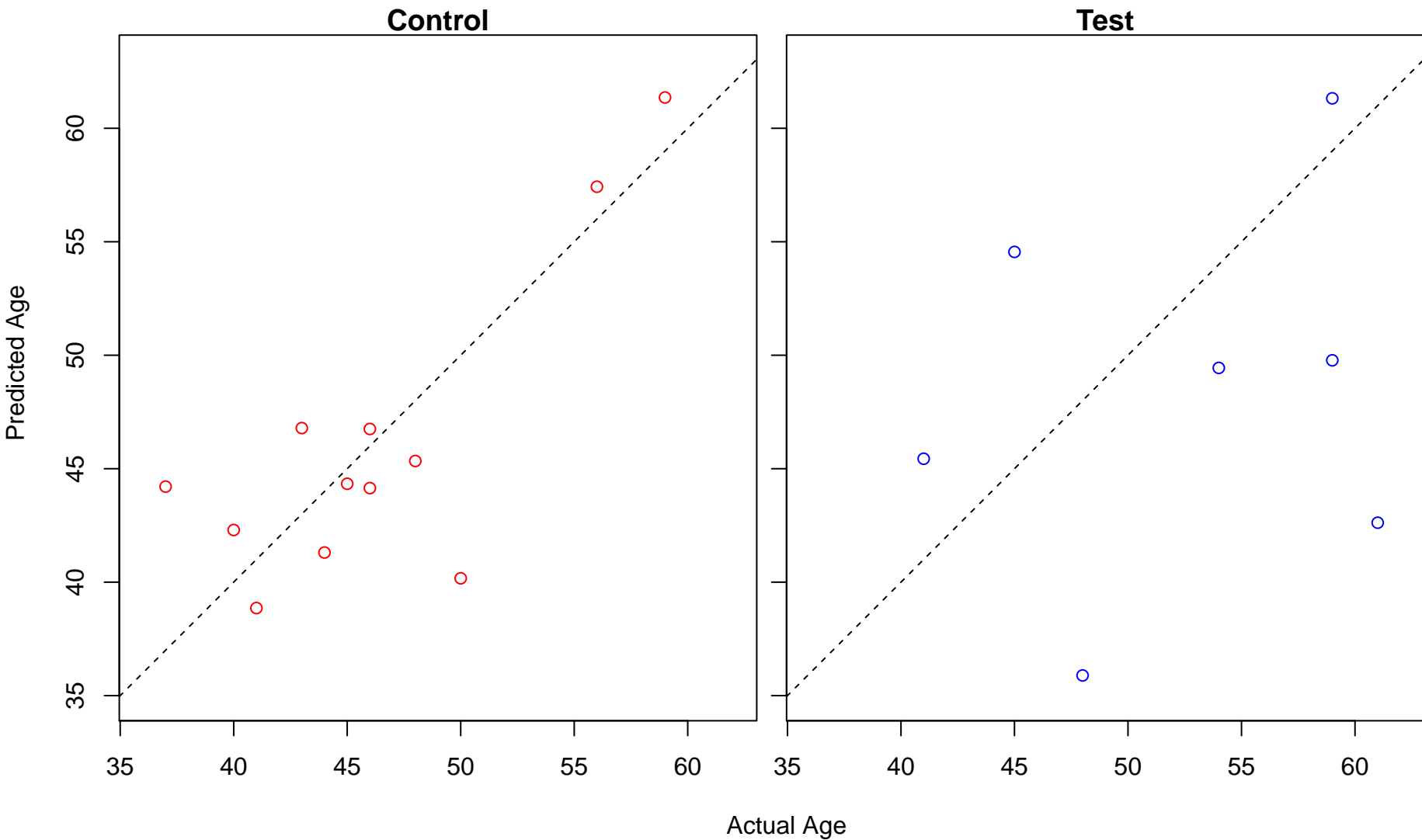


Test

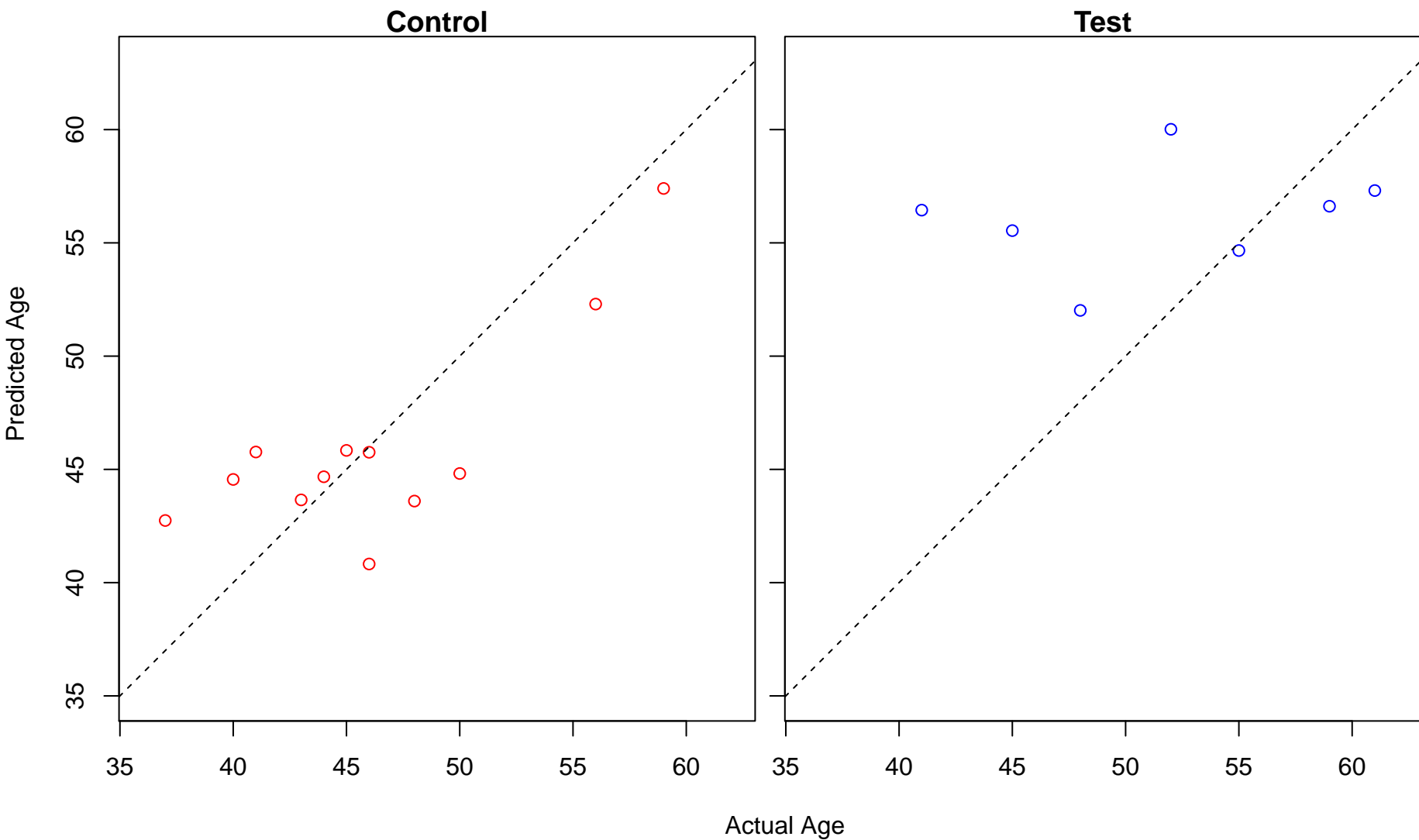


Actual Age

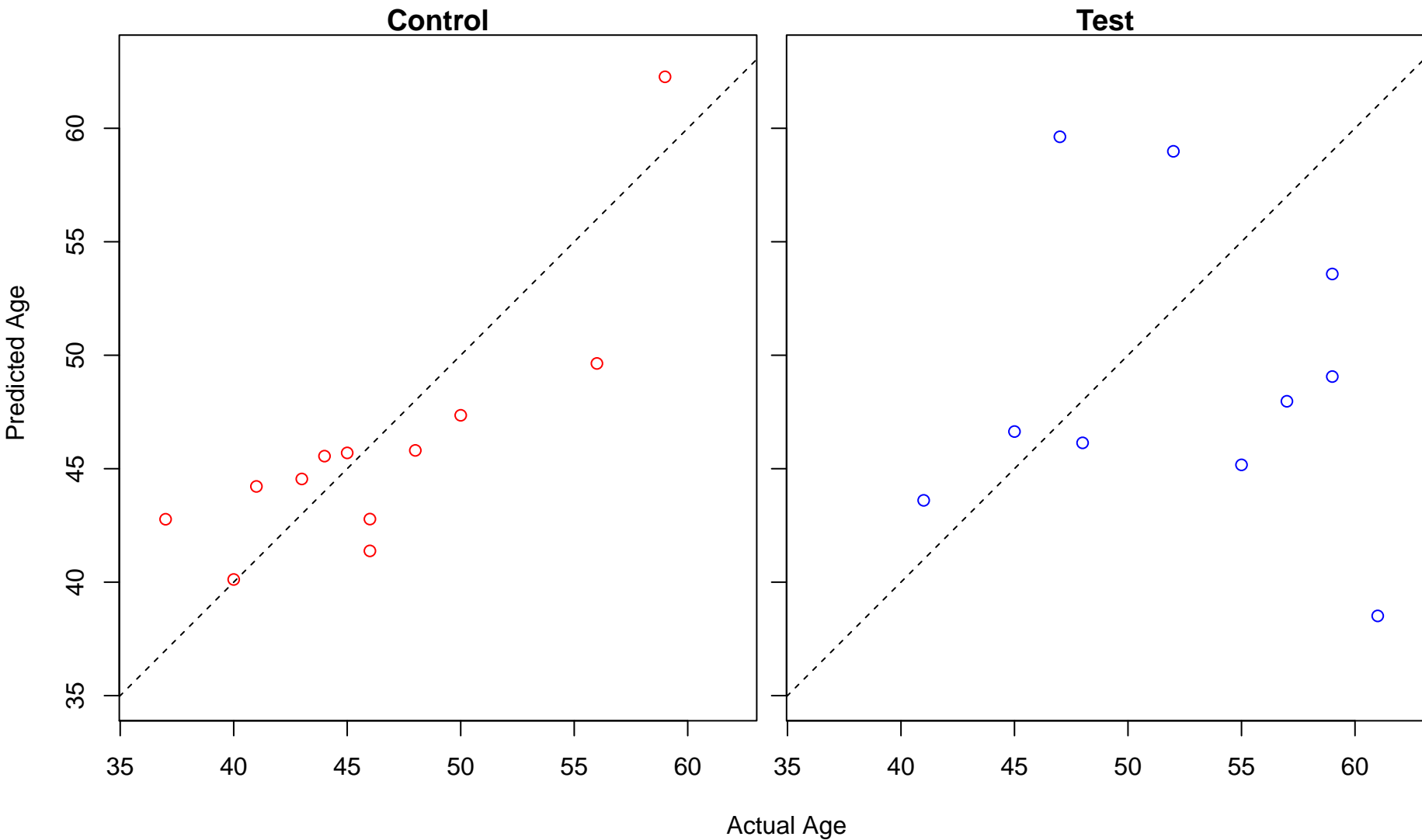
cAMP metabolic process (Score: 10.026355)



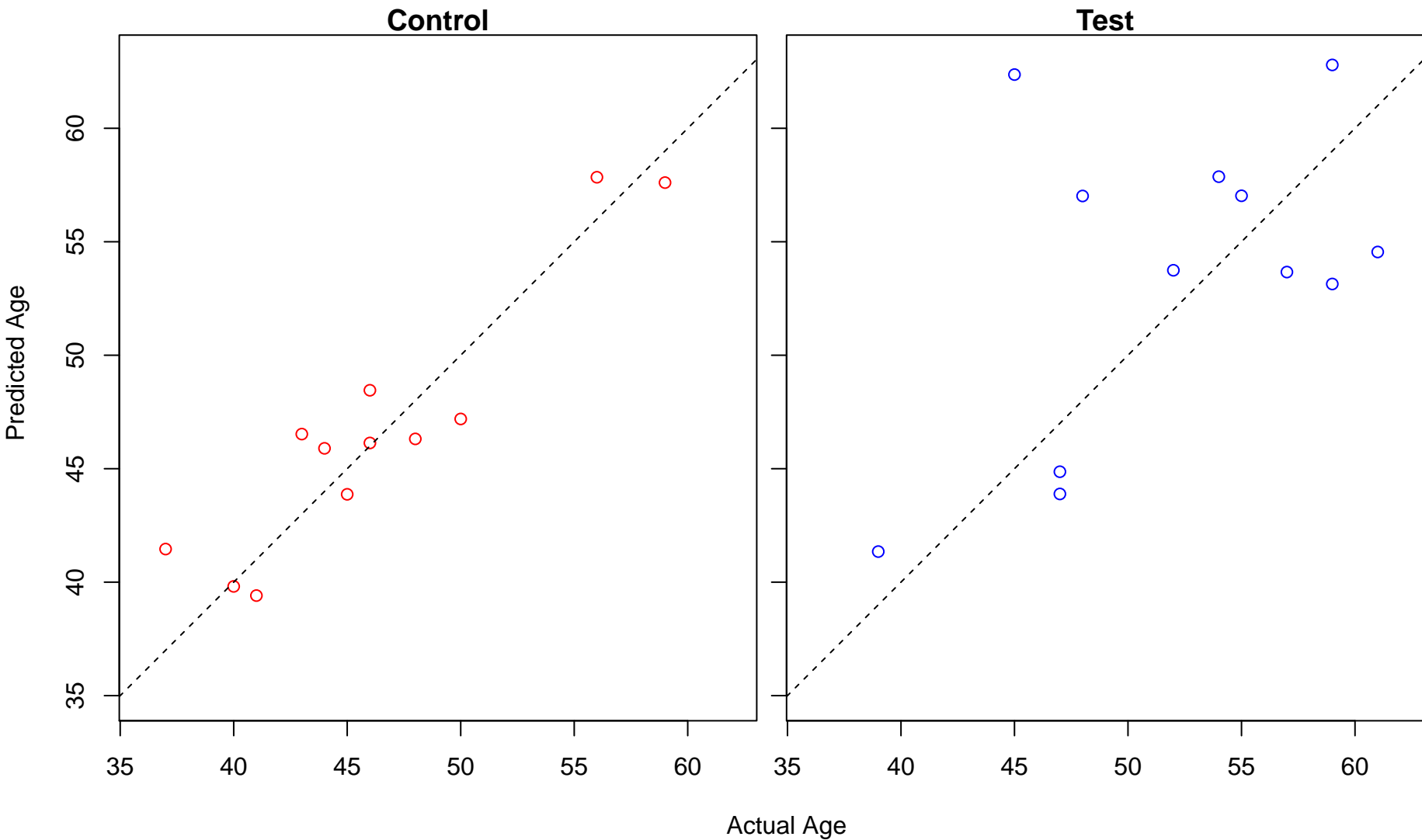
integrin activation (Score: 10.022084)



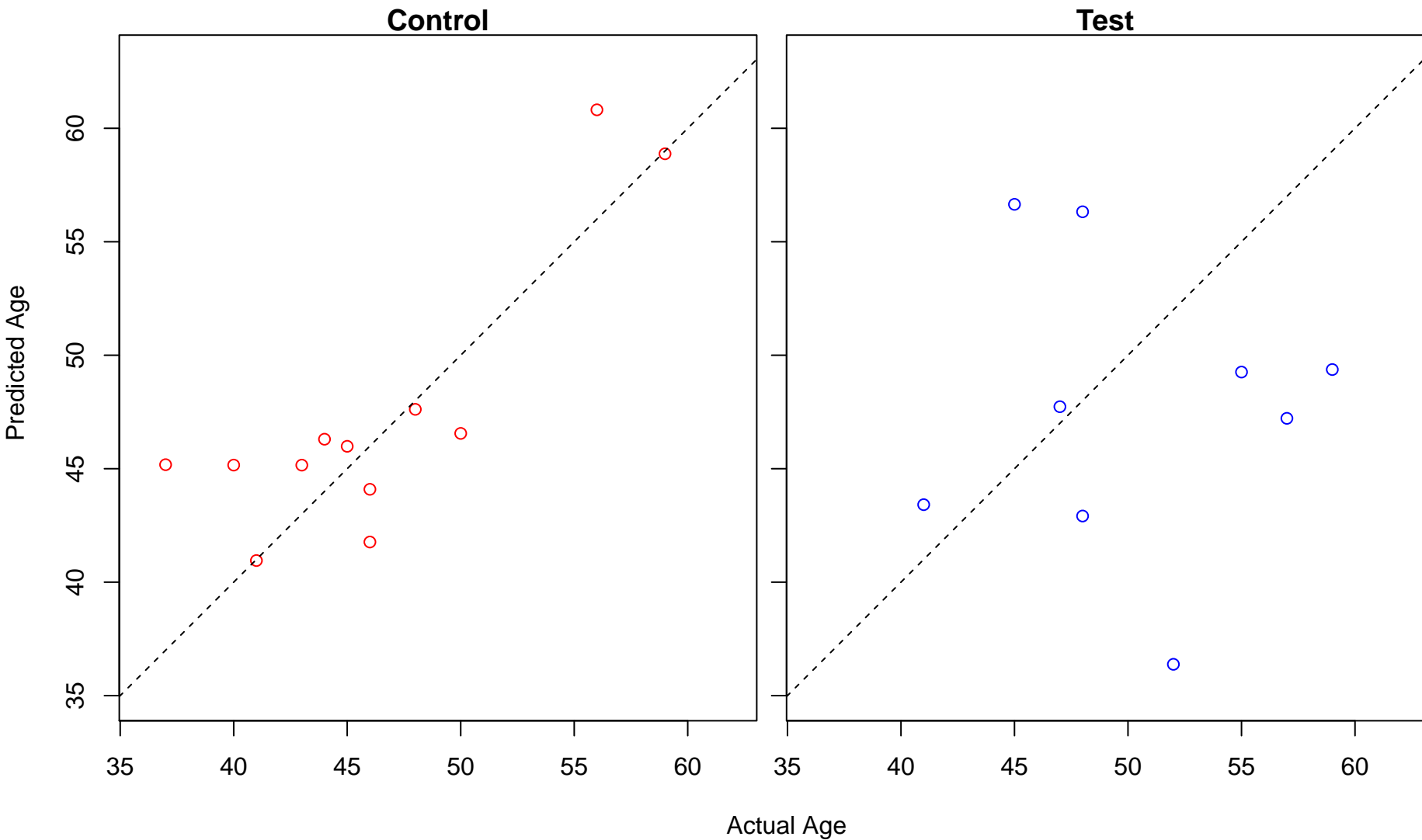
negative regulation of chromosome organization (Score: 10.019770)



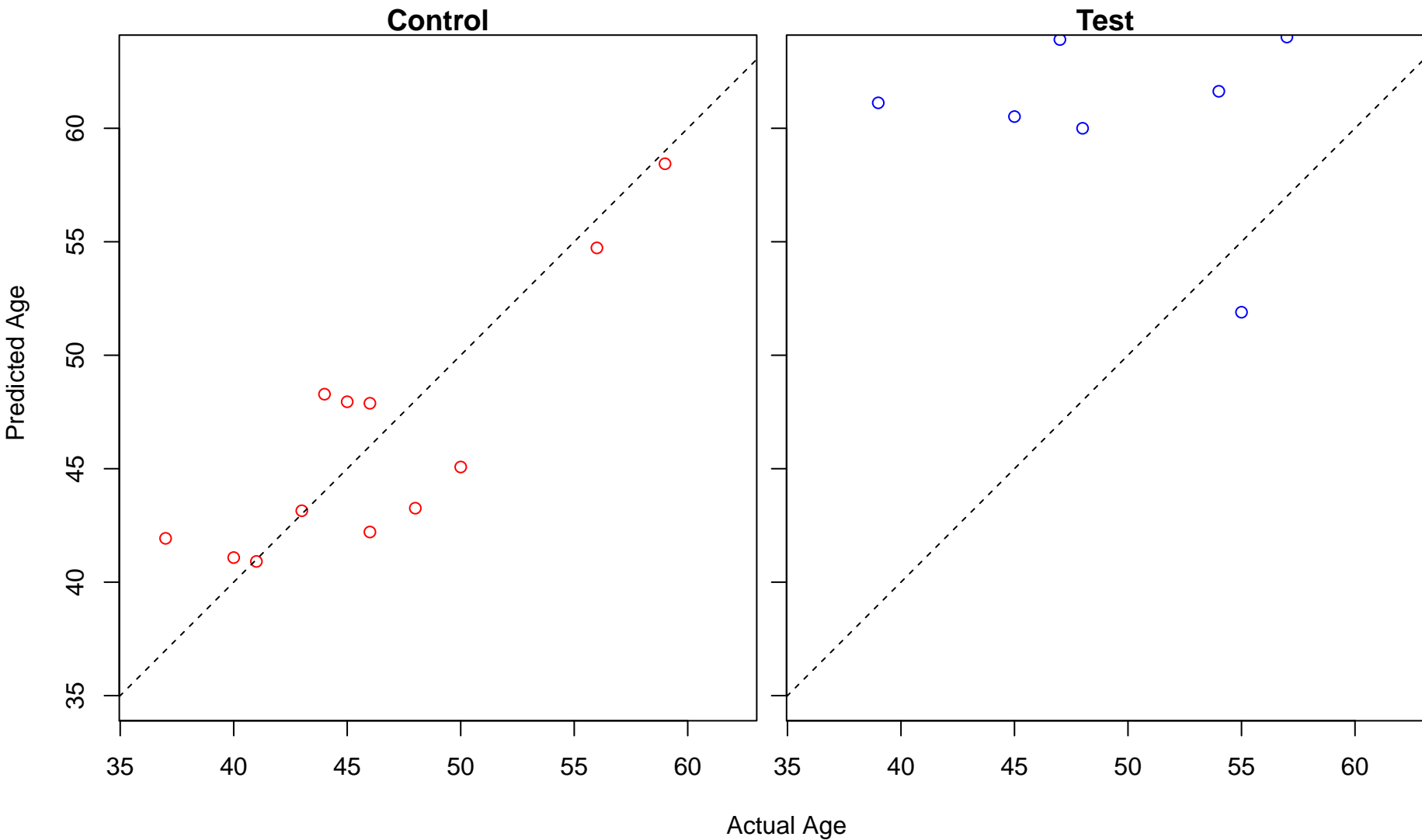
eye morphogenesis (Score: 9.995100)



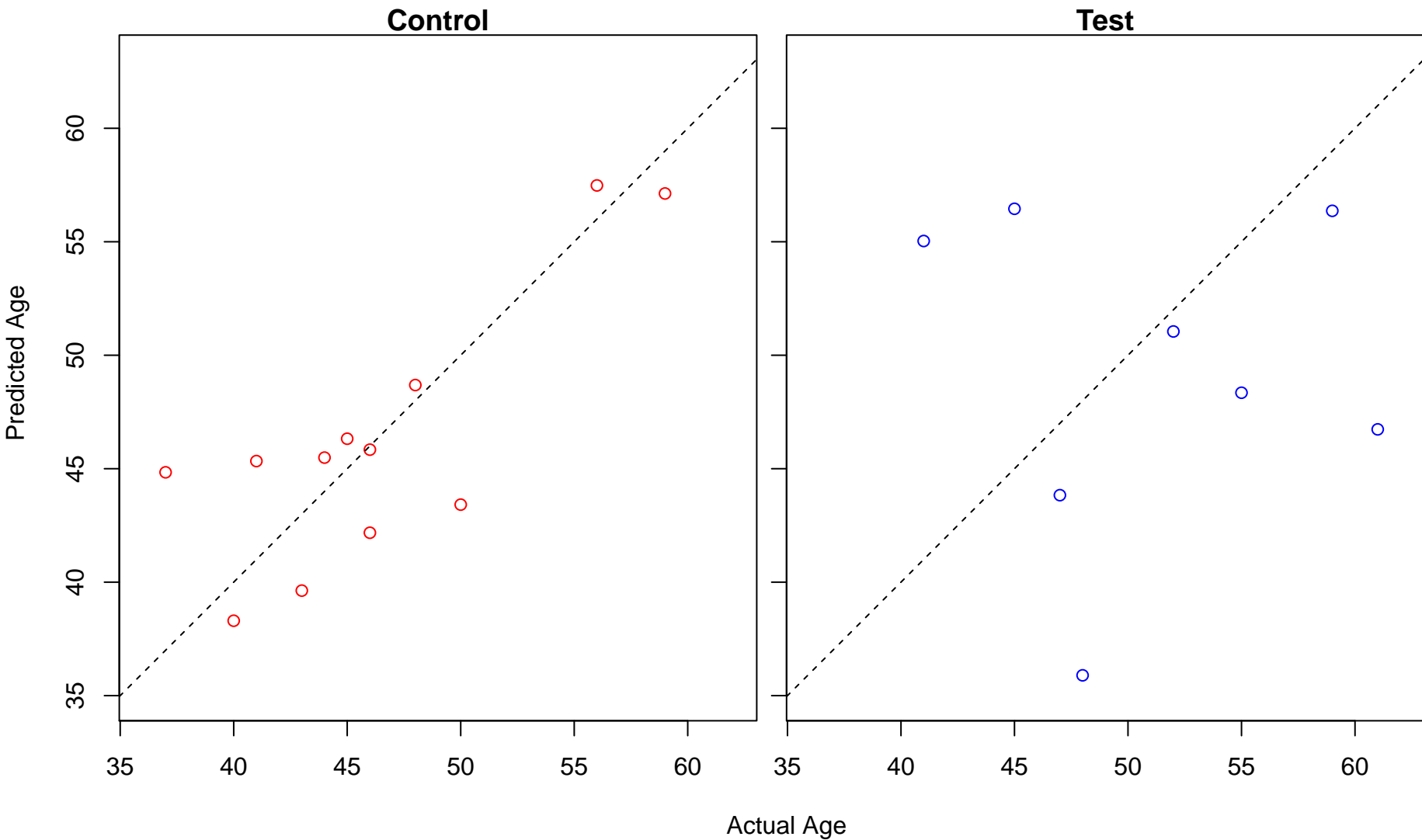
androgen receptor signaling pathway (Score: 9.981513)



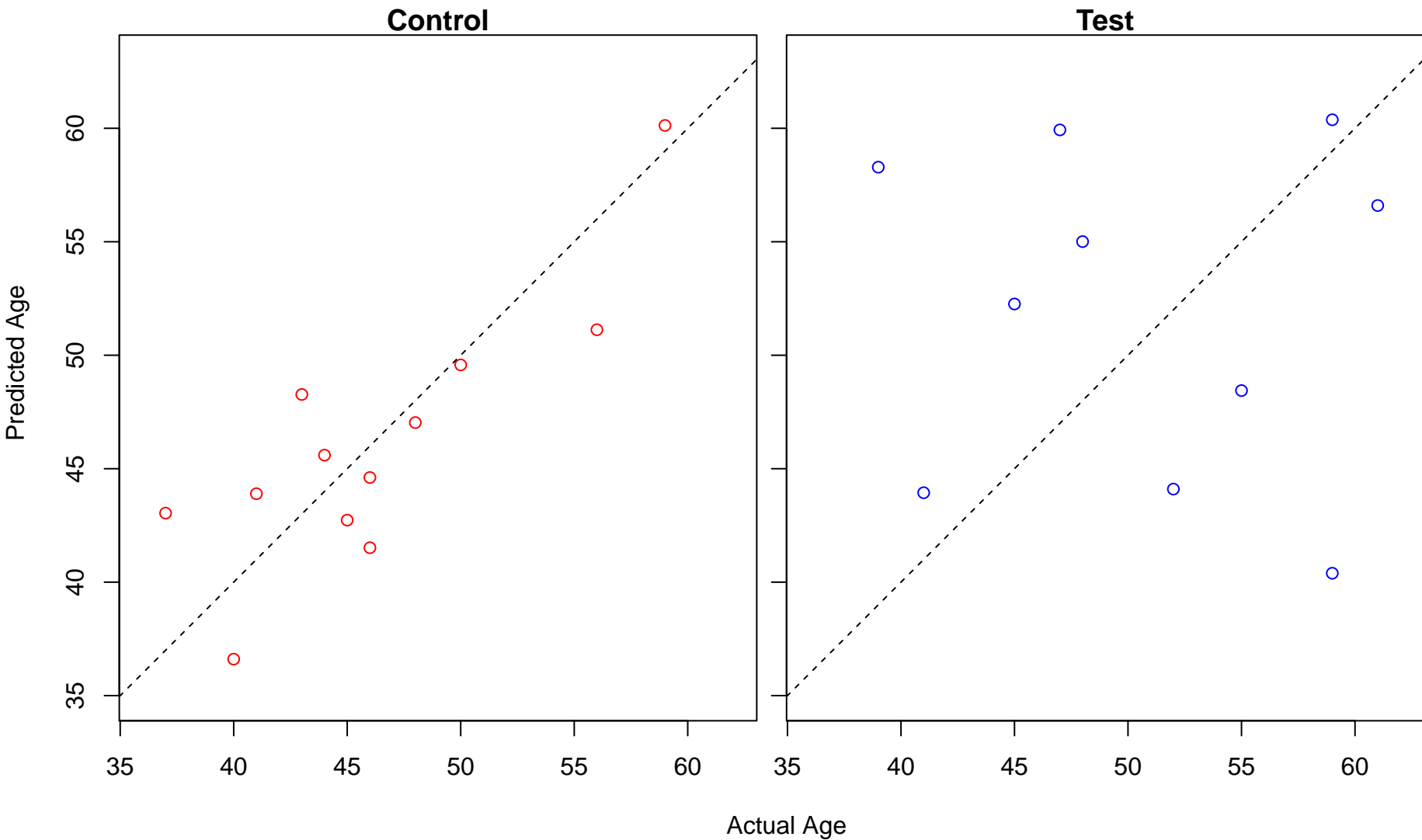
T cell homeostasis (Score: 9.979811)



pancreas development (Score: 9.950020)

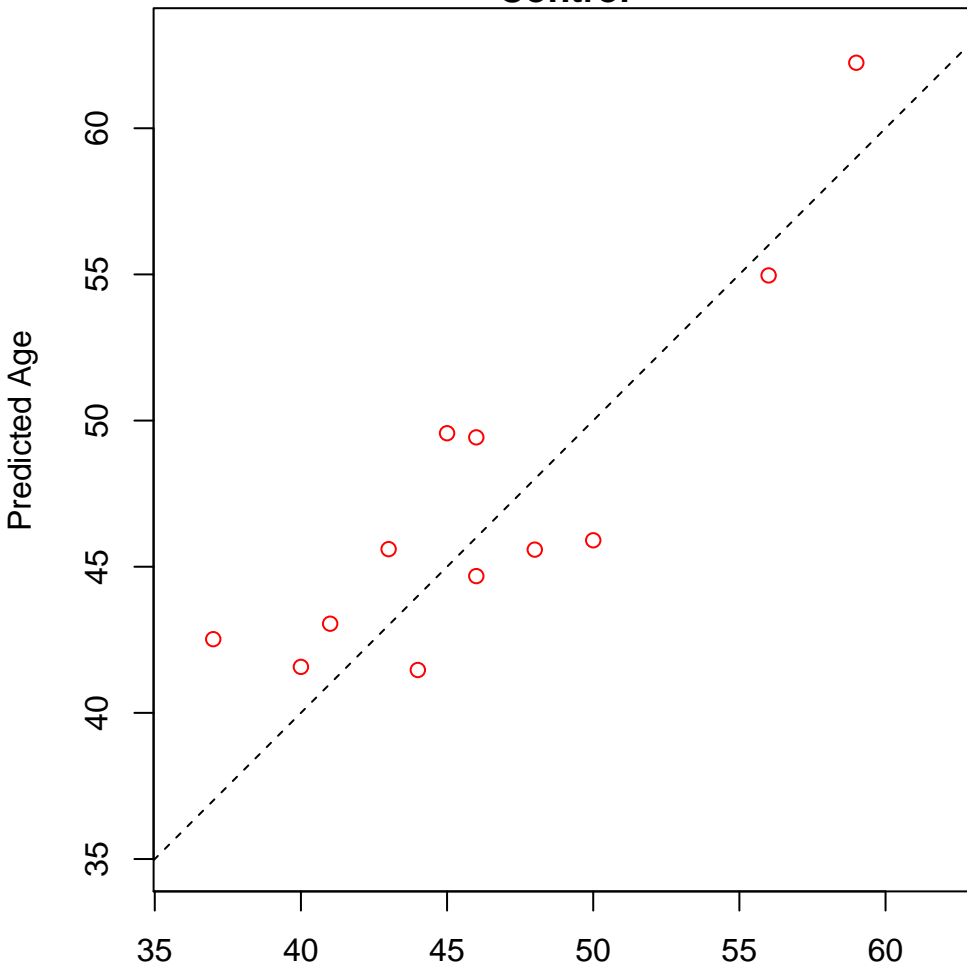


positive regulation of translational initiation (Score: 9.943719)

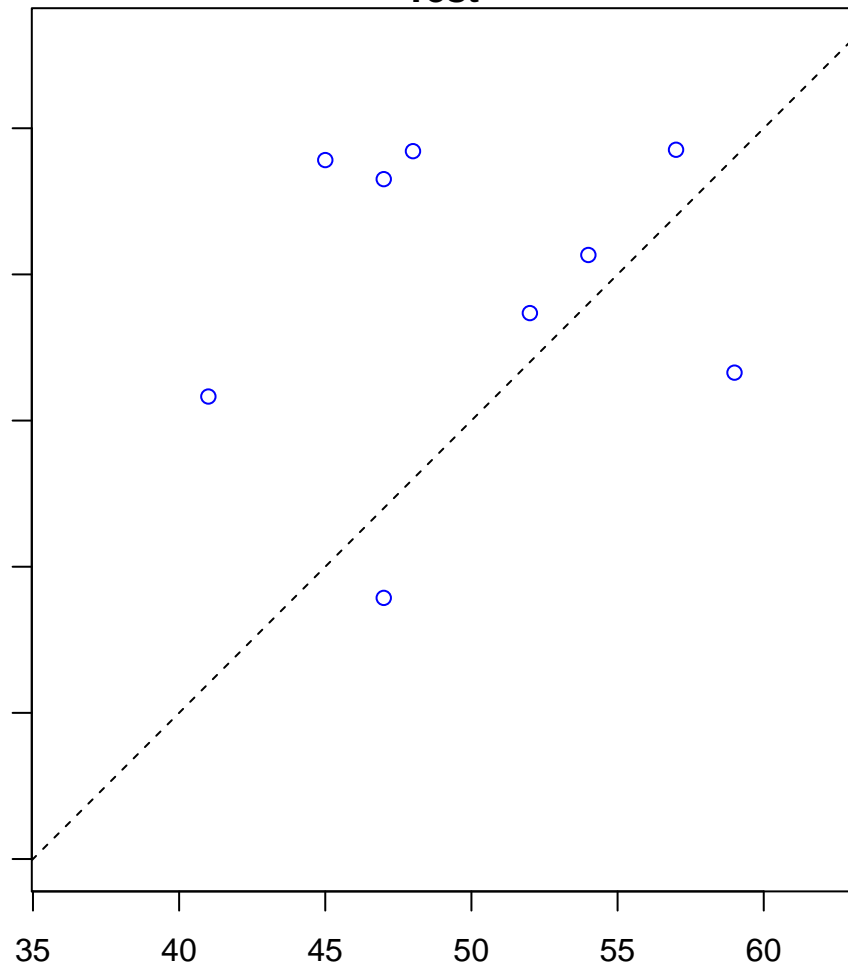


lymphocyte mediated immunity (Score: 9.941745)

Control

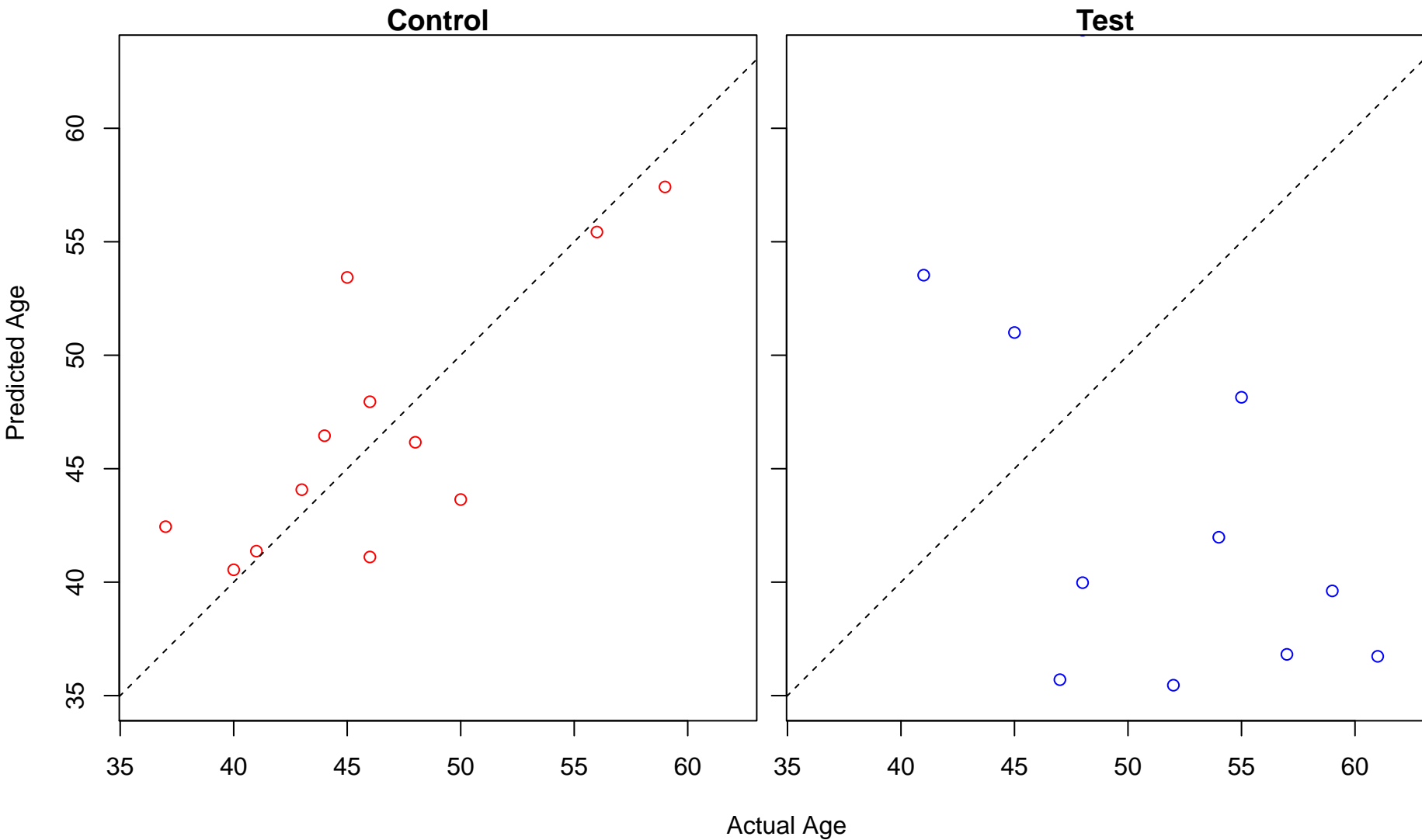


Test

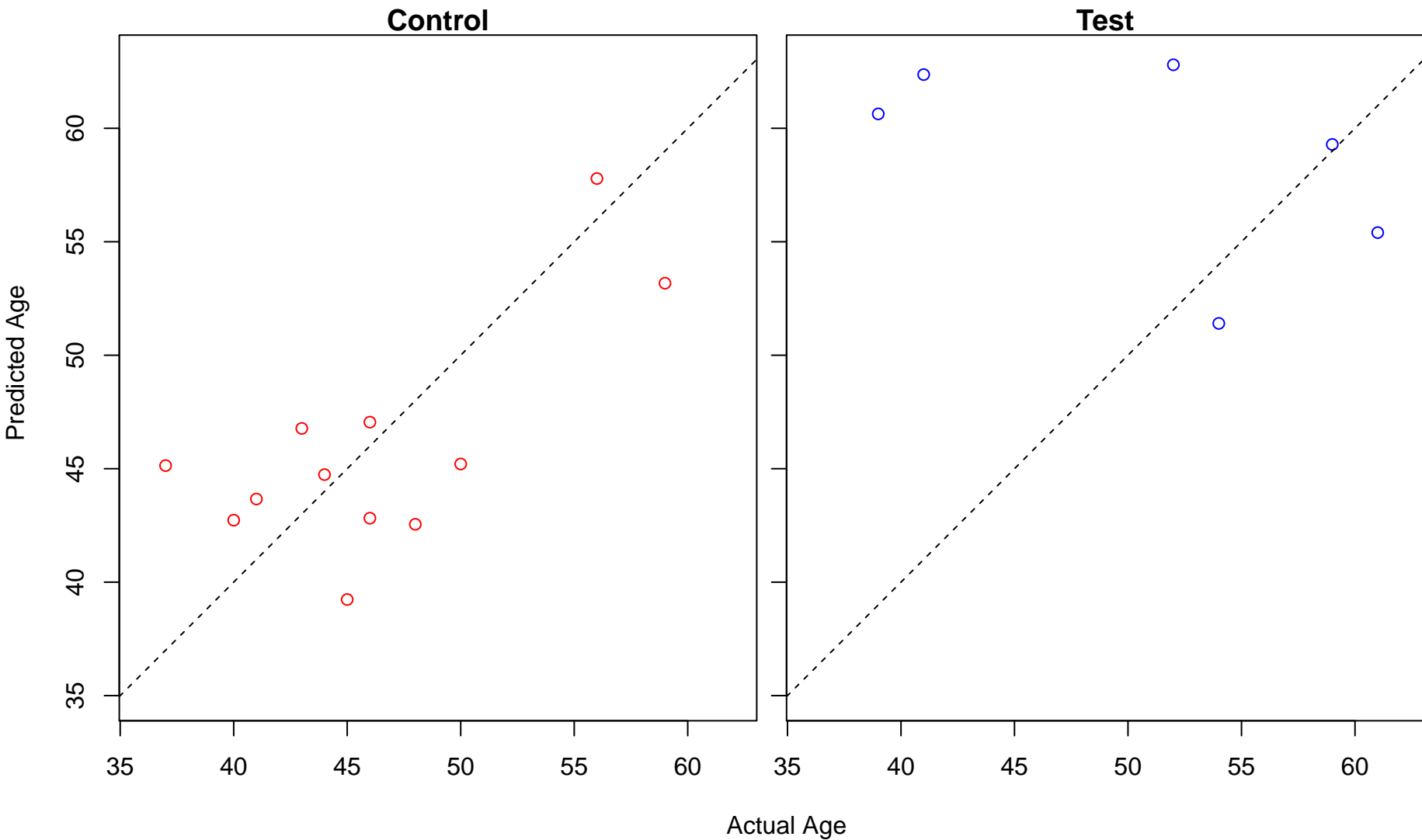


Actual Age

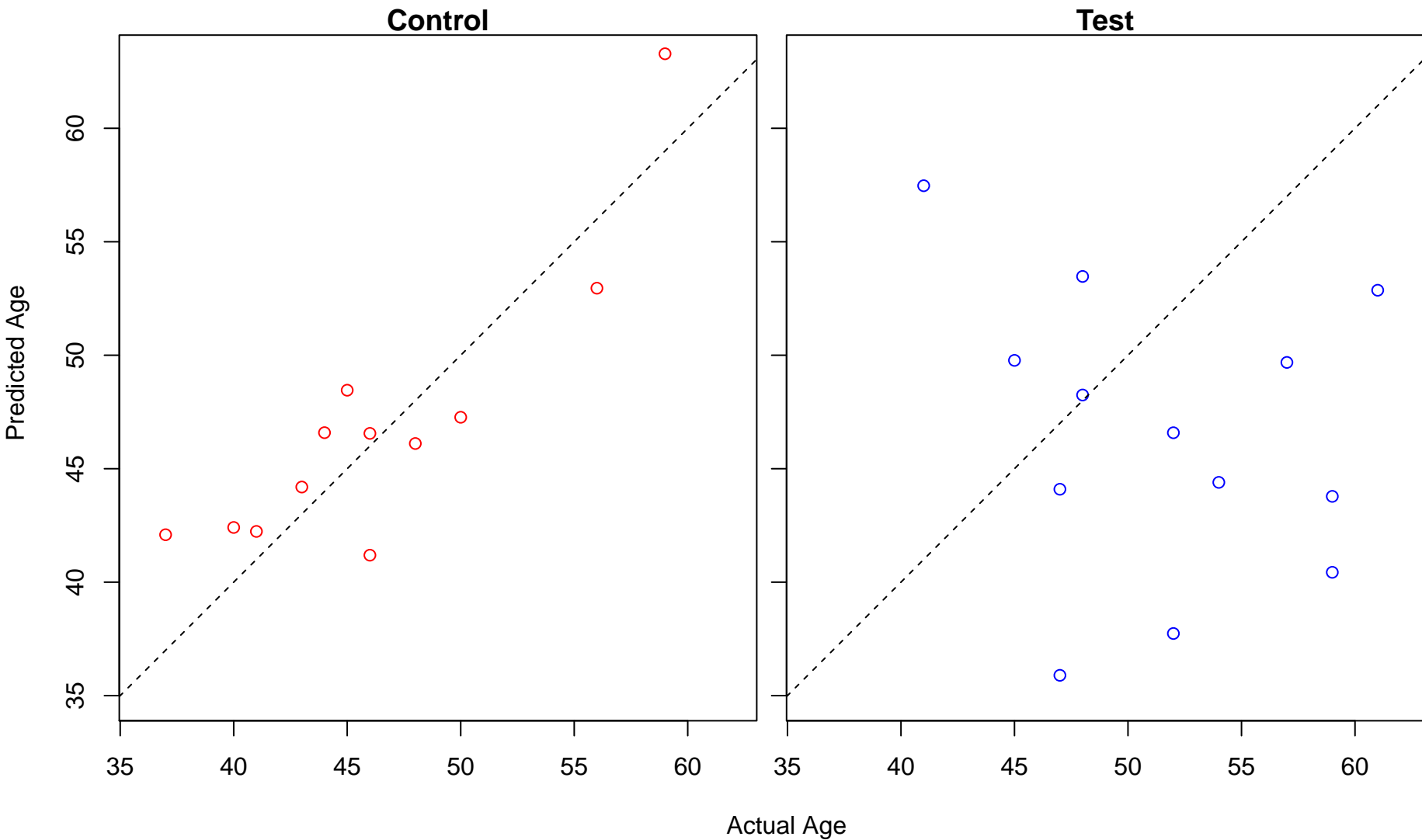
protein autophosphorylation (Score: 9.931577)



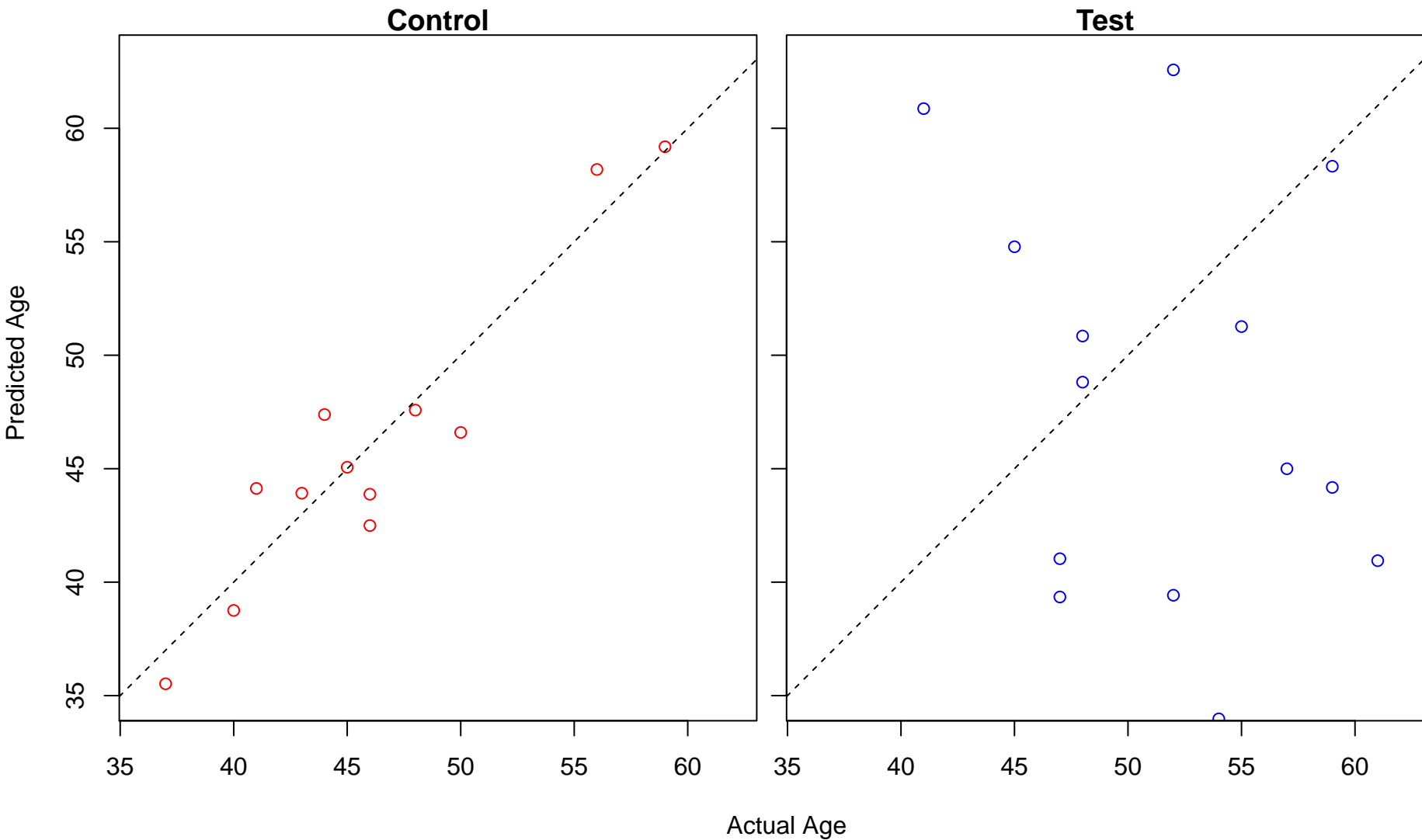
regeneration (Score: 9.928517)



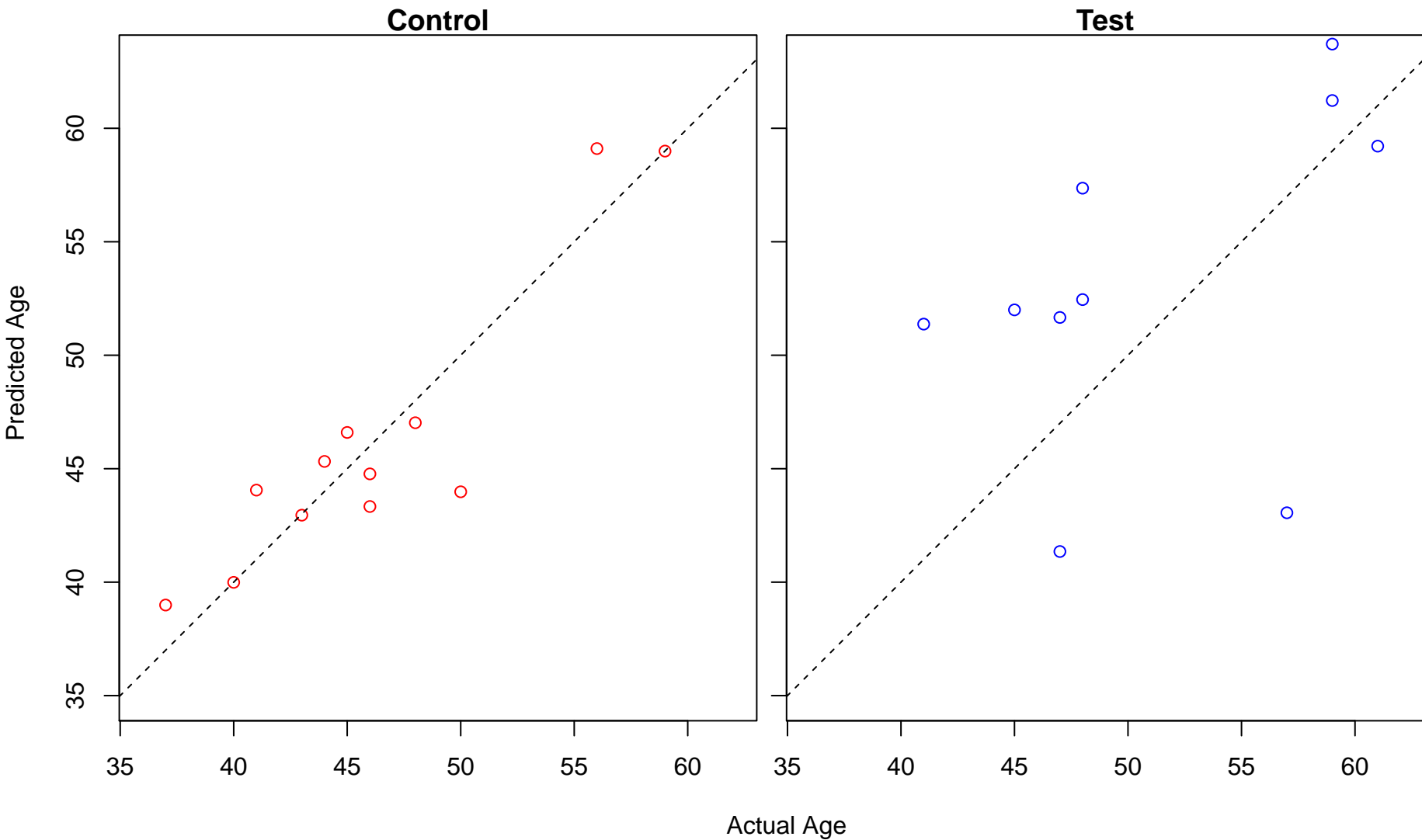
negative regulation of cellular protein localization (Score: 9.919659)



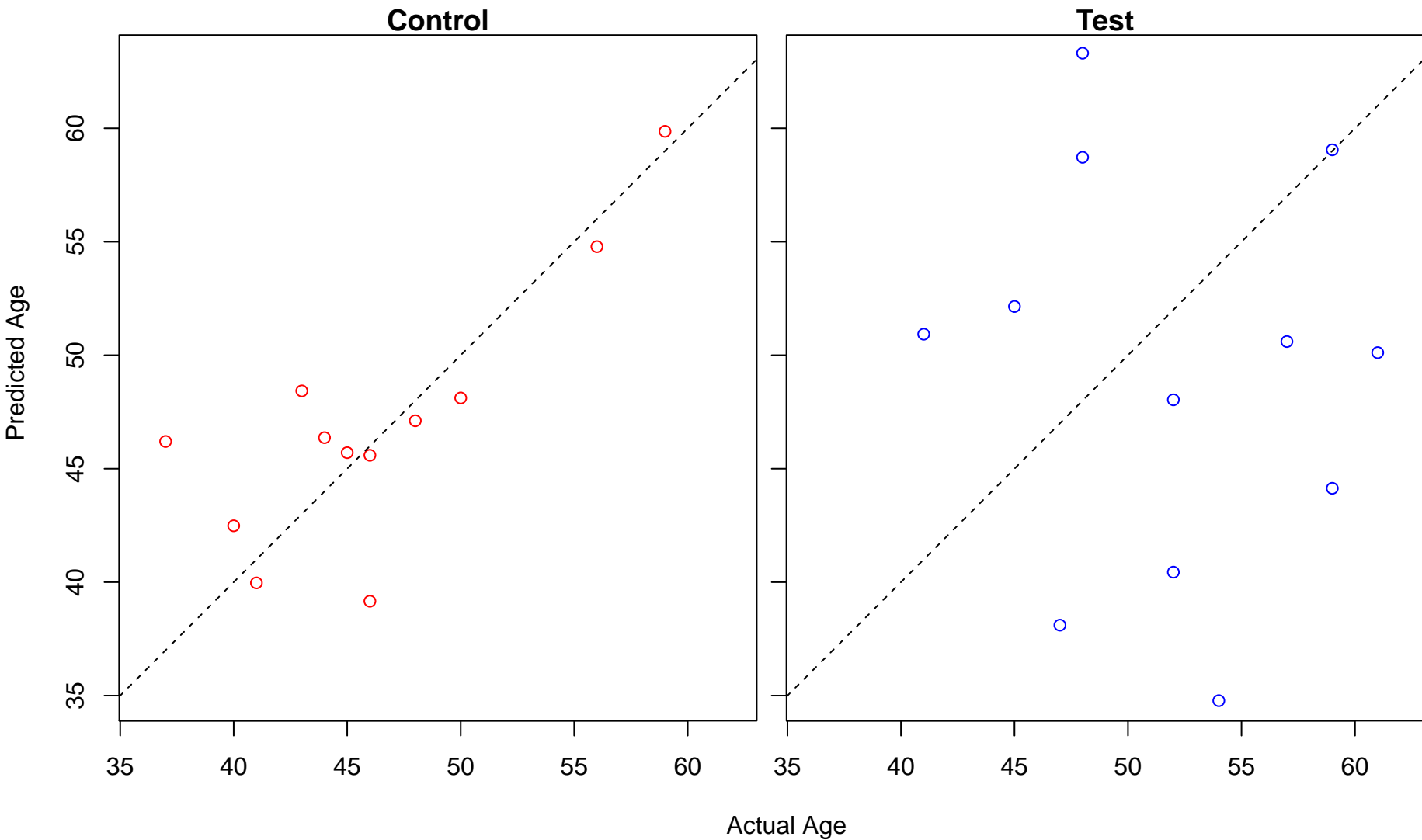
renal tubule development (Score: 9.903231)



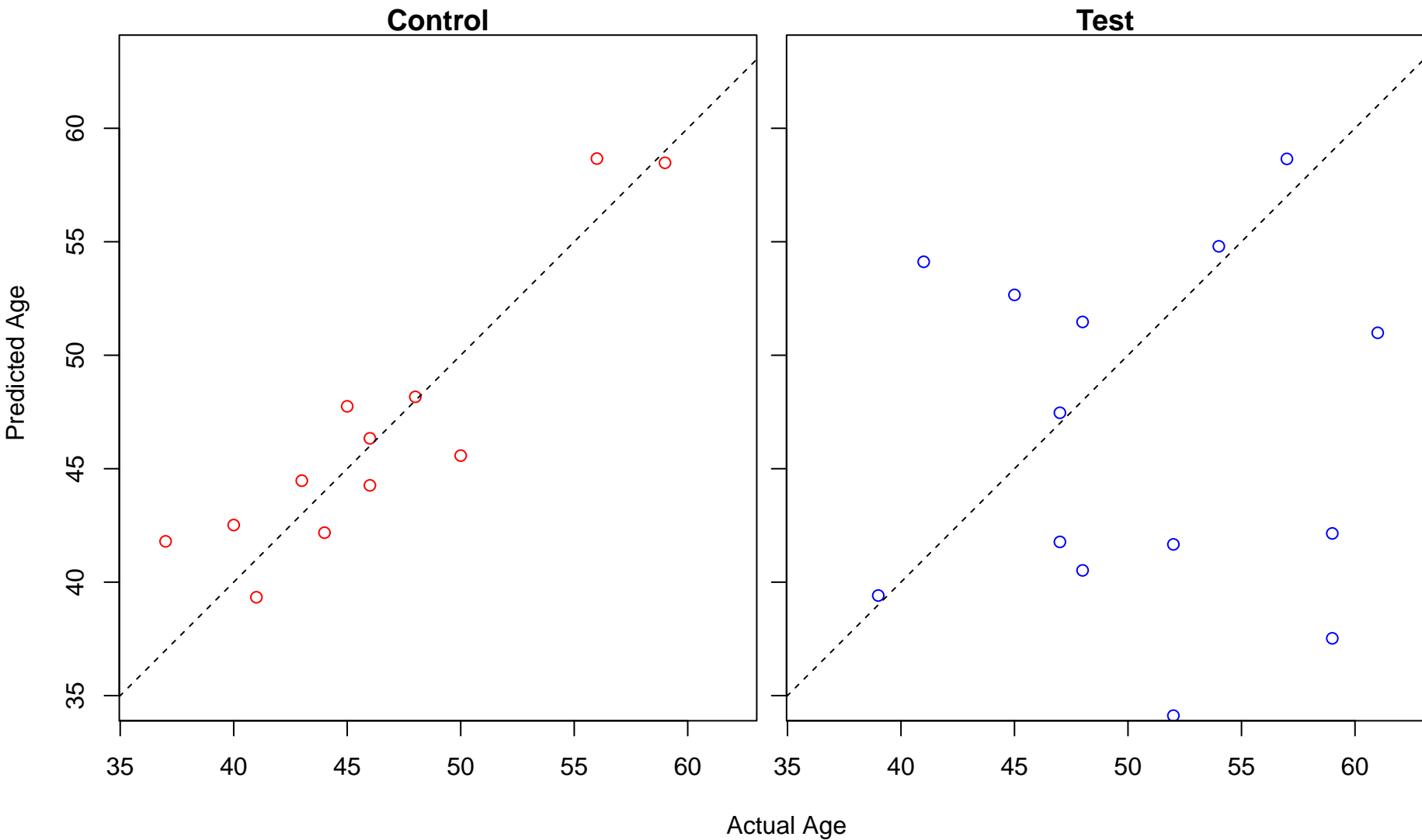
mitotic sister chromatid cohesion (Score: 9.885398)



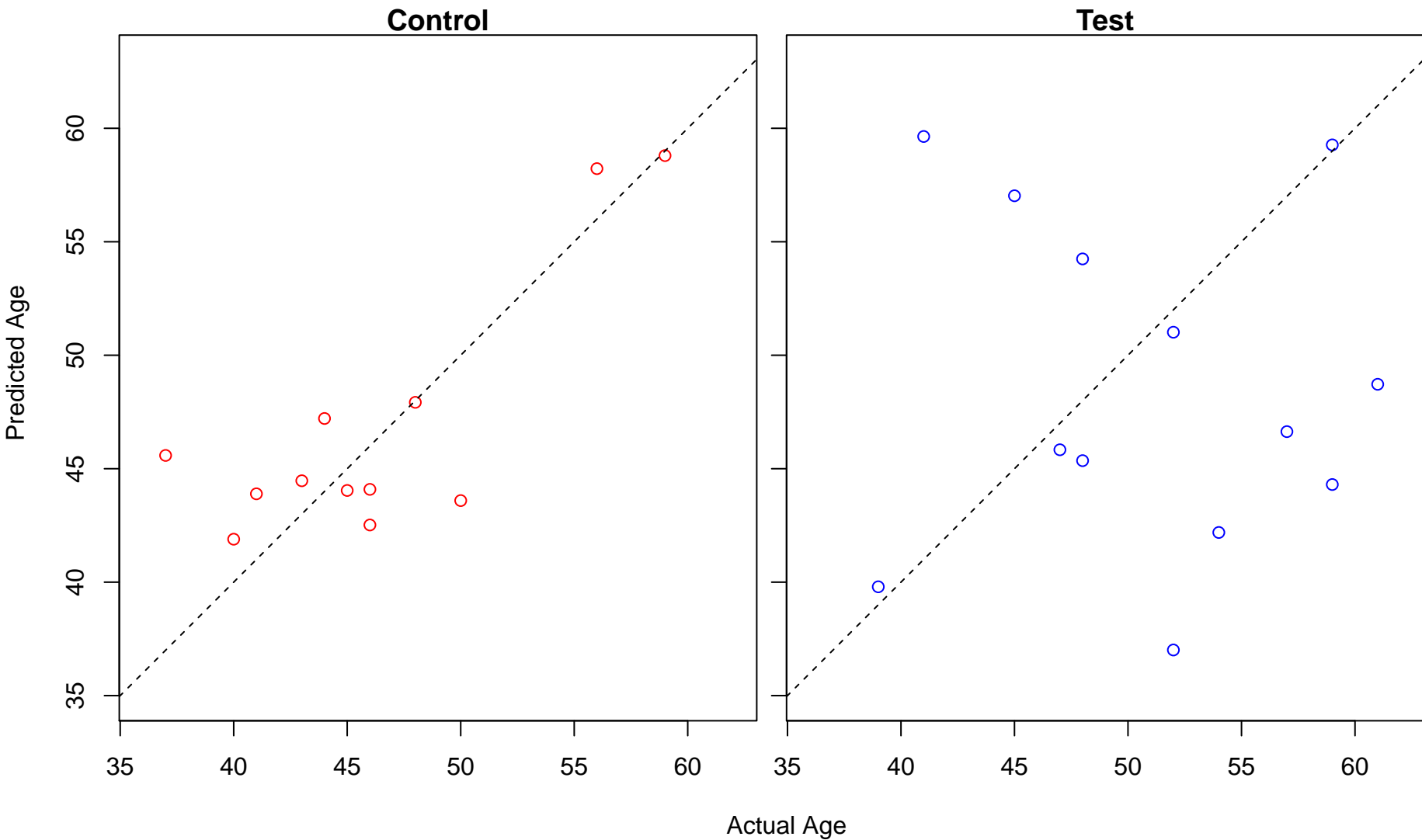
negative regulation of protein transport (Score: 9.840472)



regulation of humoral immune response (Score: 9.745988)

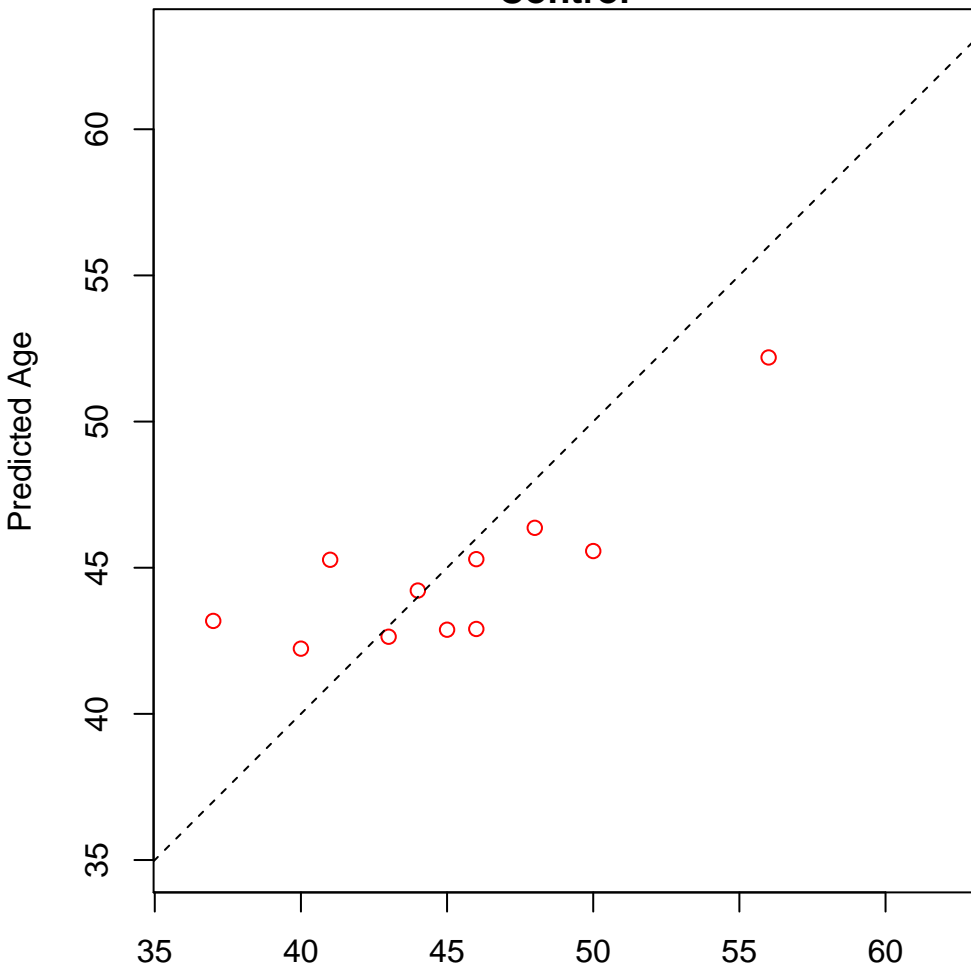


positive regulation of protein complex disassembly (Score: 9.737261)

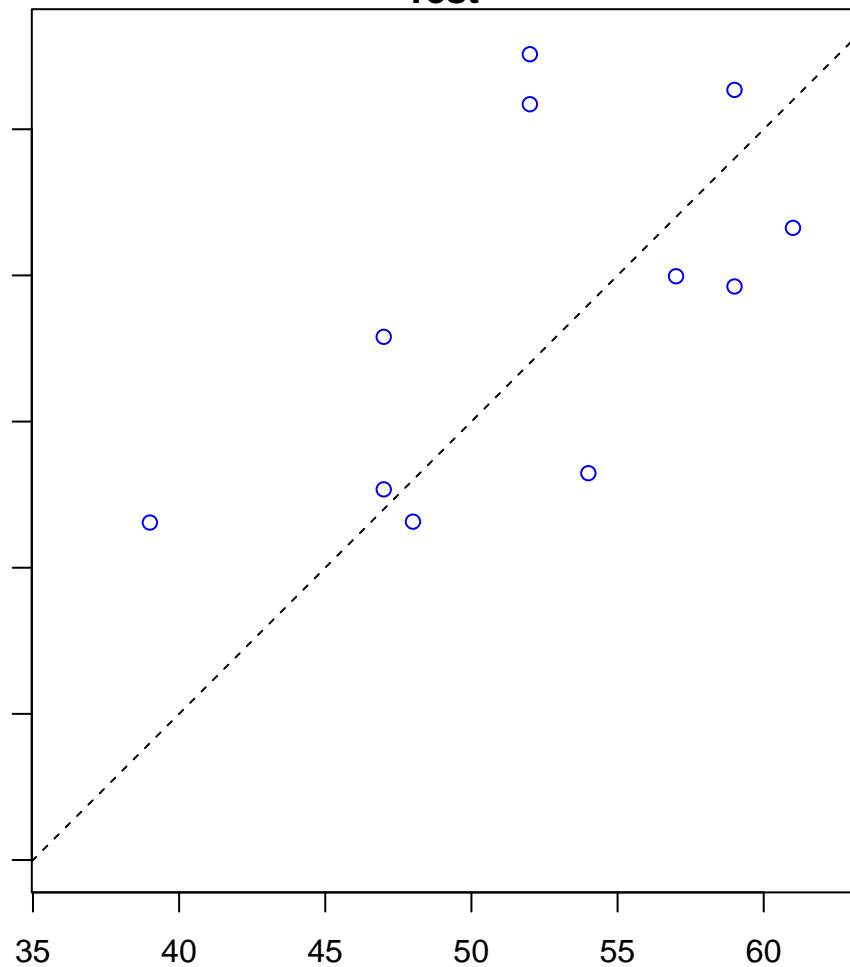


L-glutamate transmembrane transport (Score: 9.701902)

Control

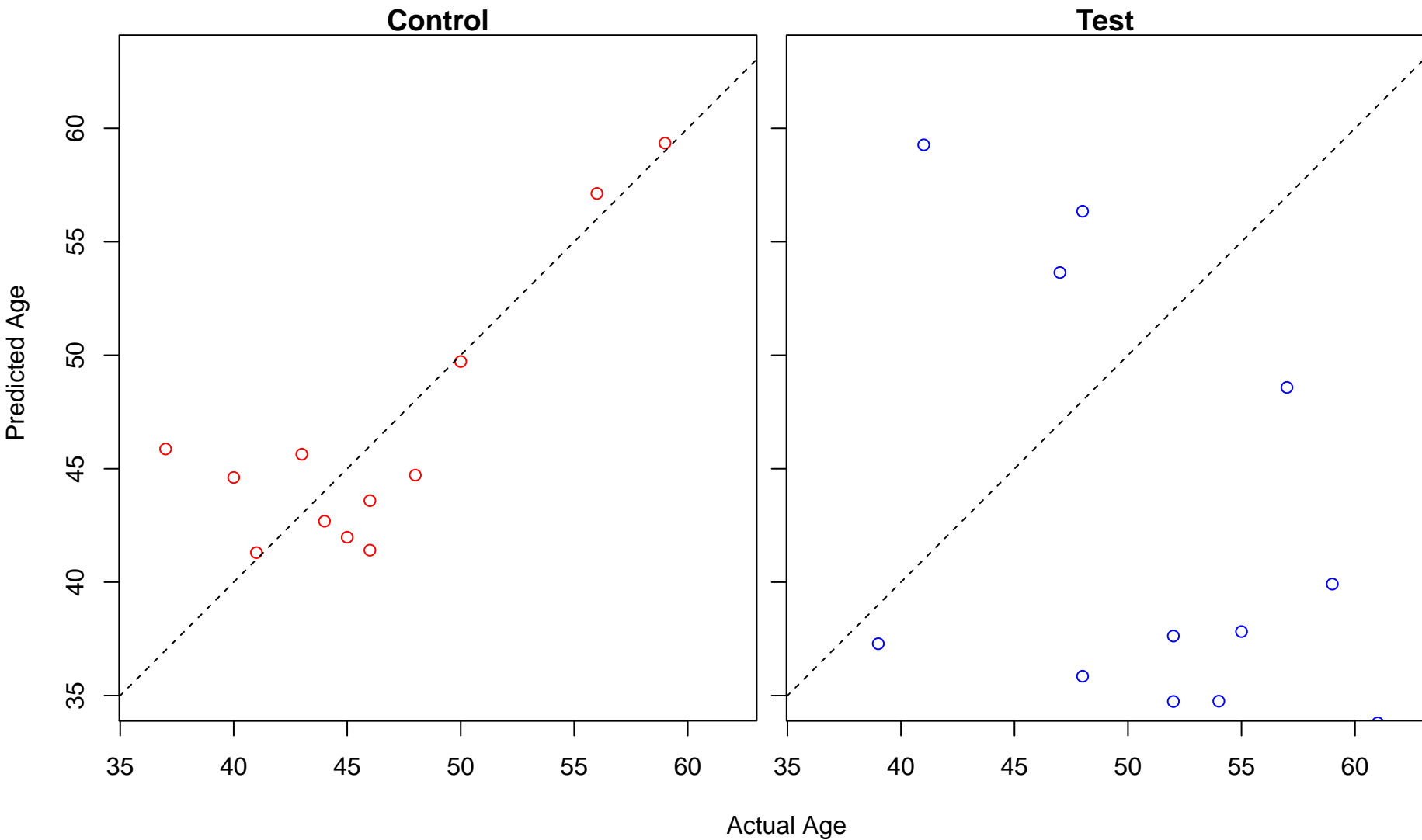


Test

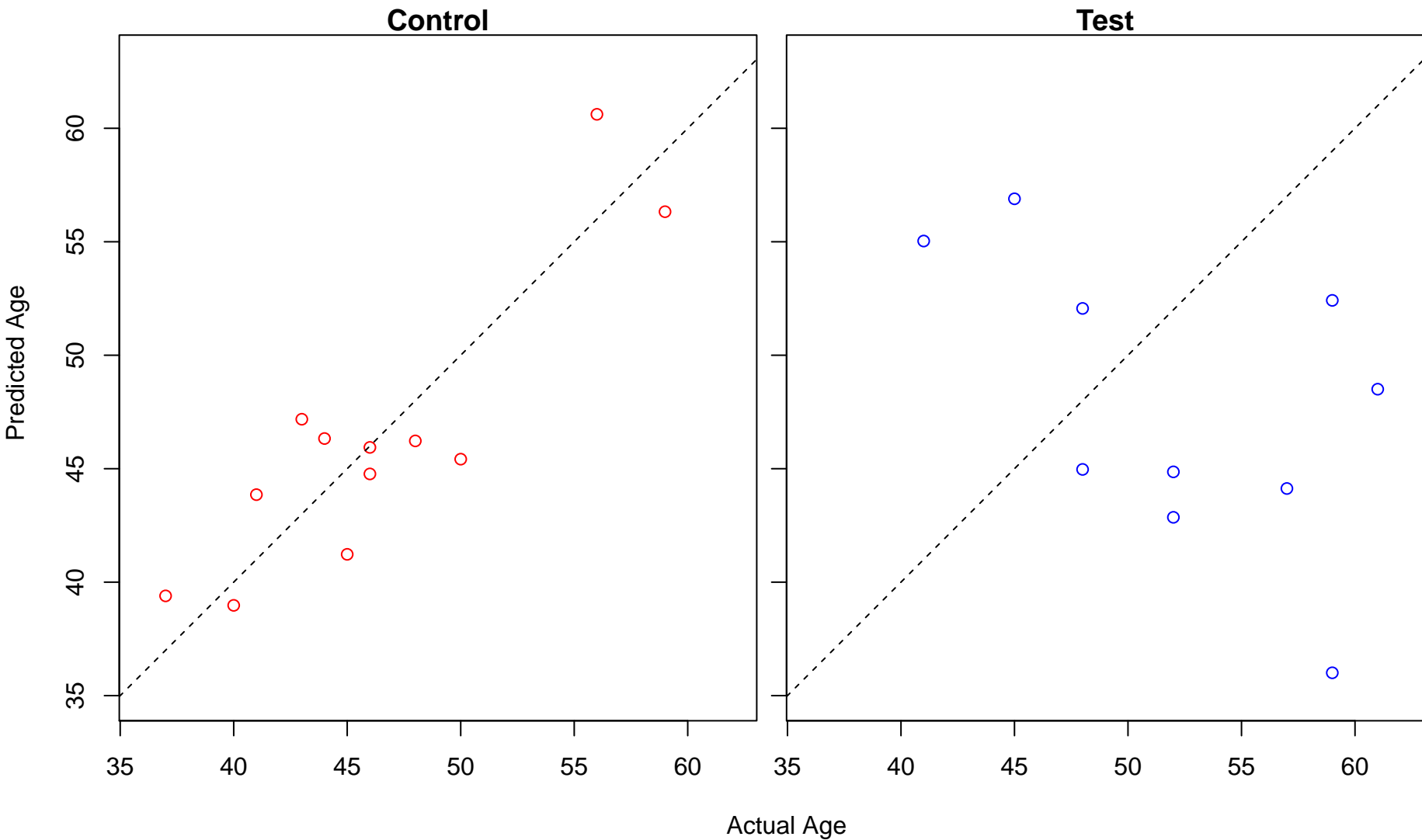


Actual Age

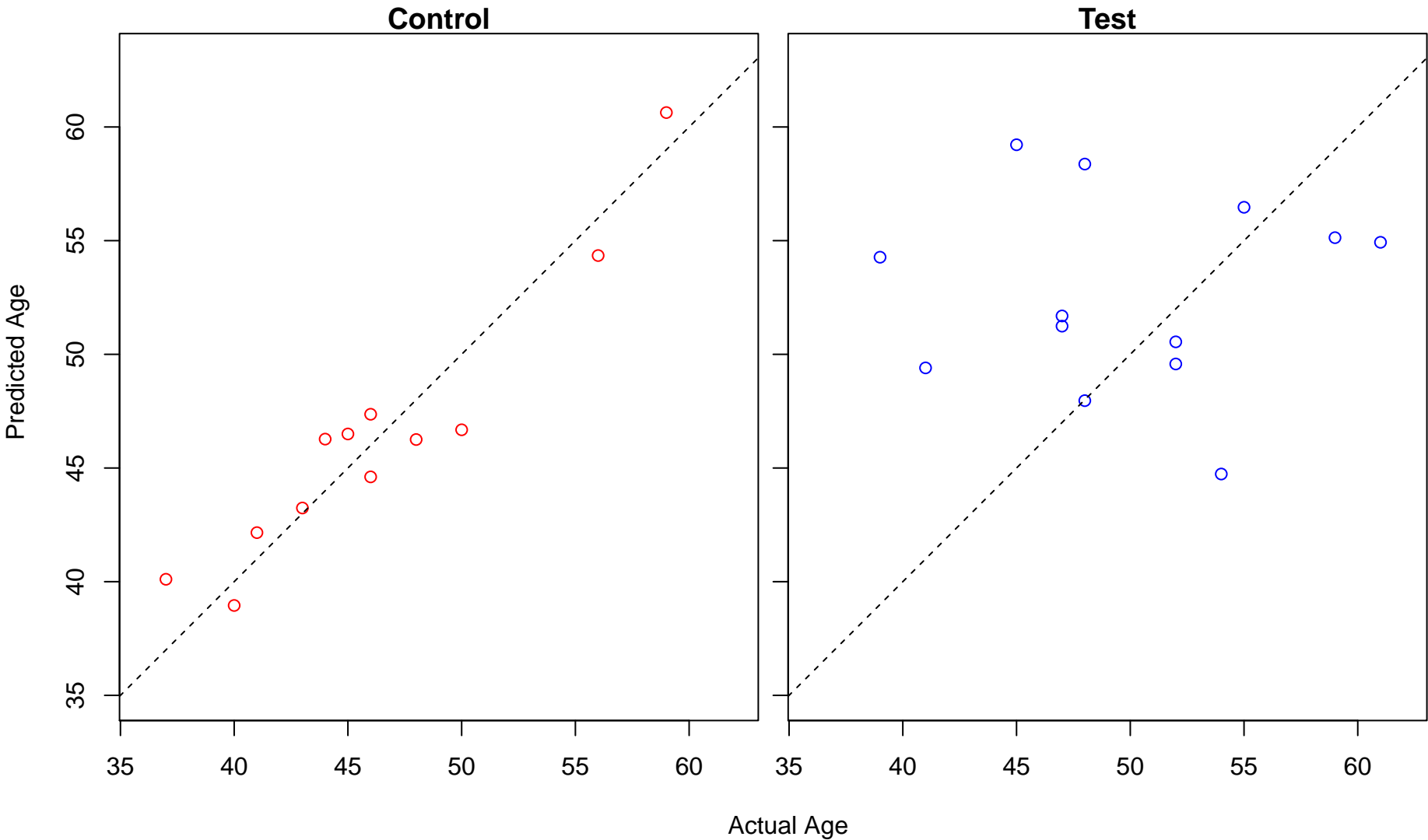
cell-cell junction assembly (Score: 9.695183)



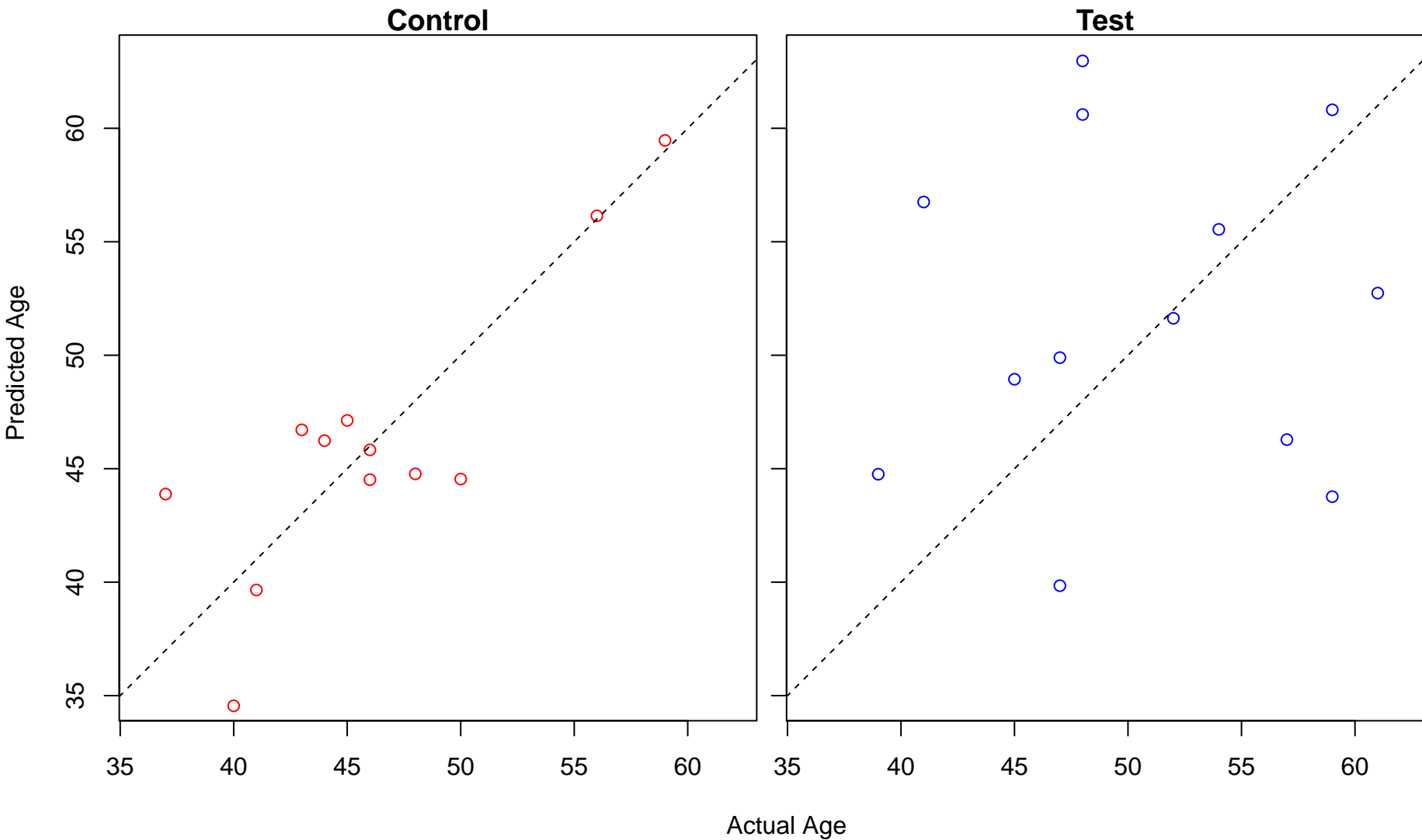
regulation of angiogenesis (Score: 9.693948)



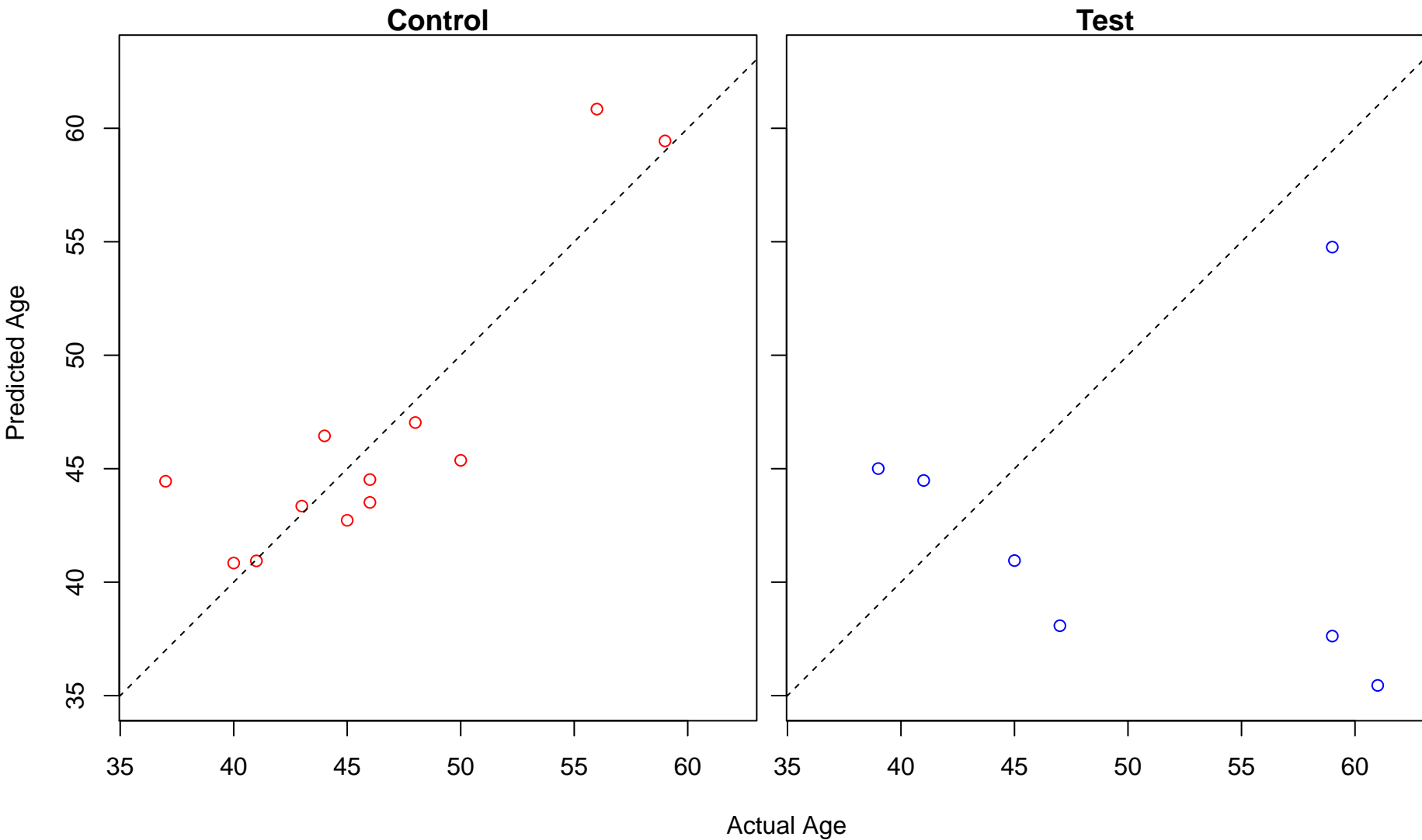
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 9.67)



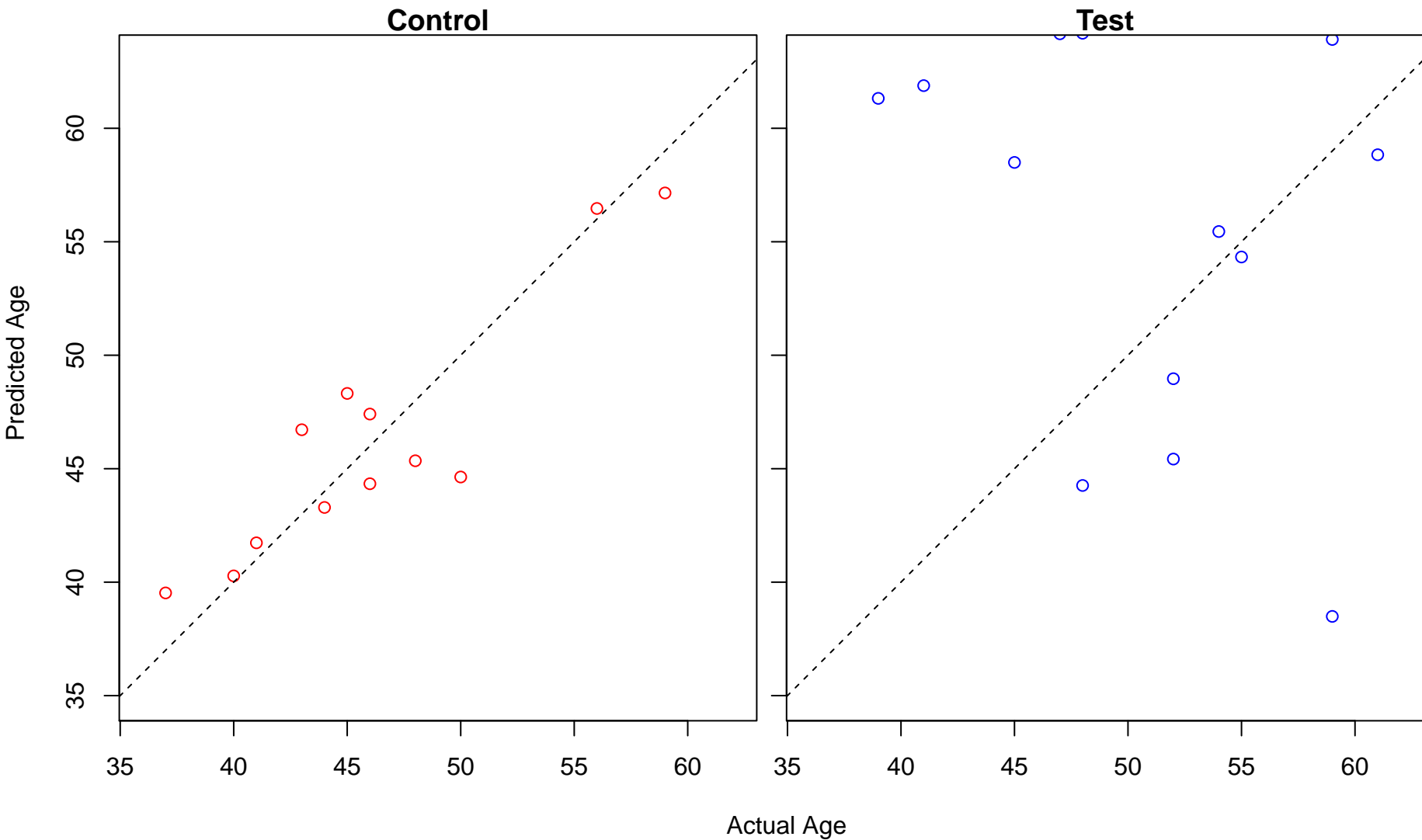
maintenance of protein location in cell (Score: 9.642833)



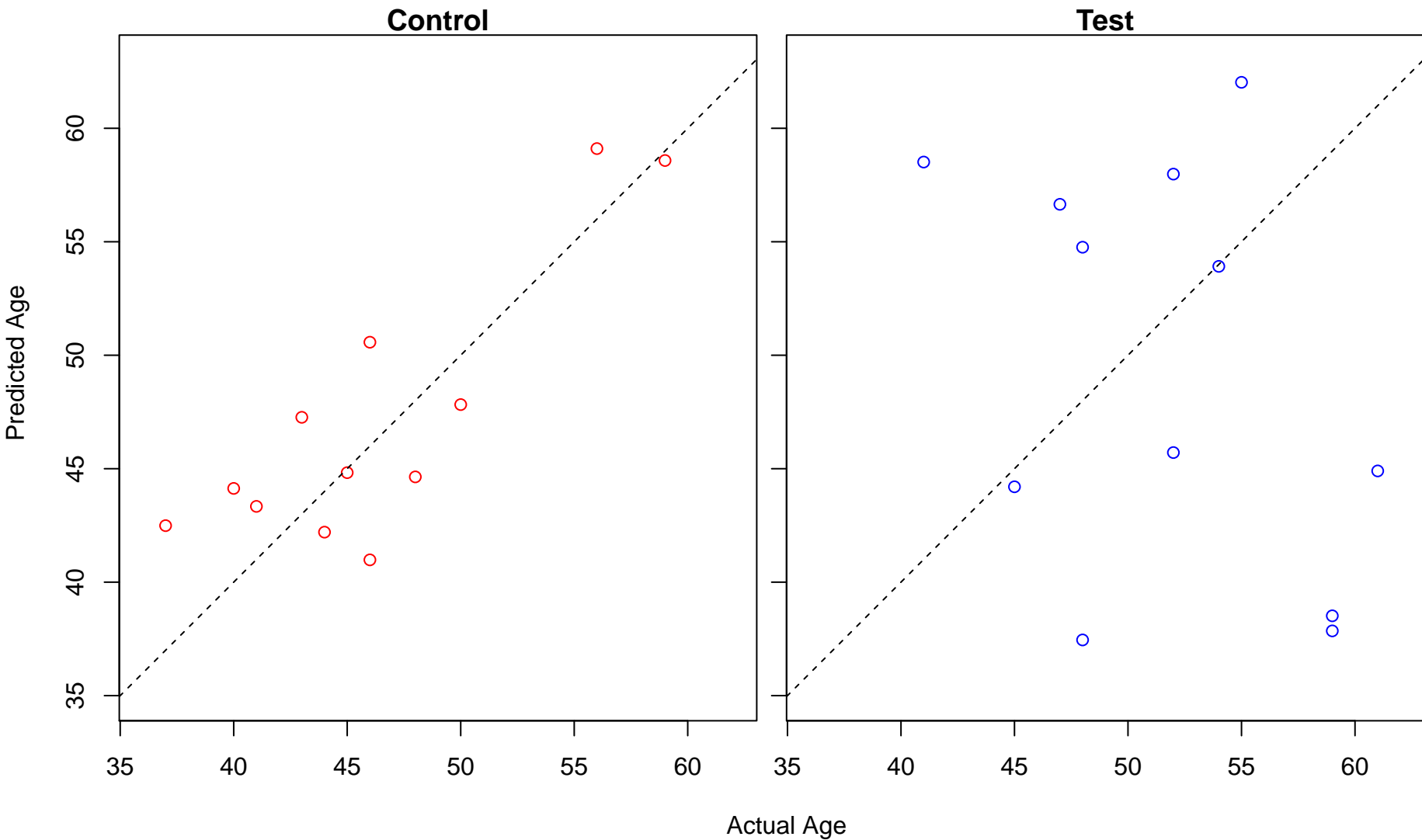
regulation of system process (Score: 9.617243)



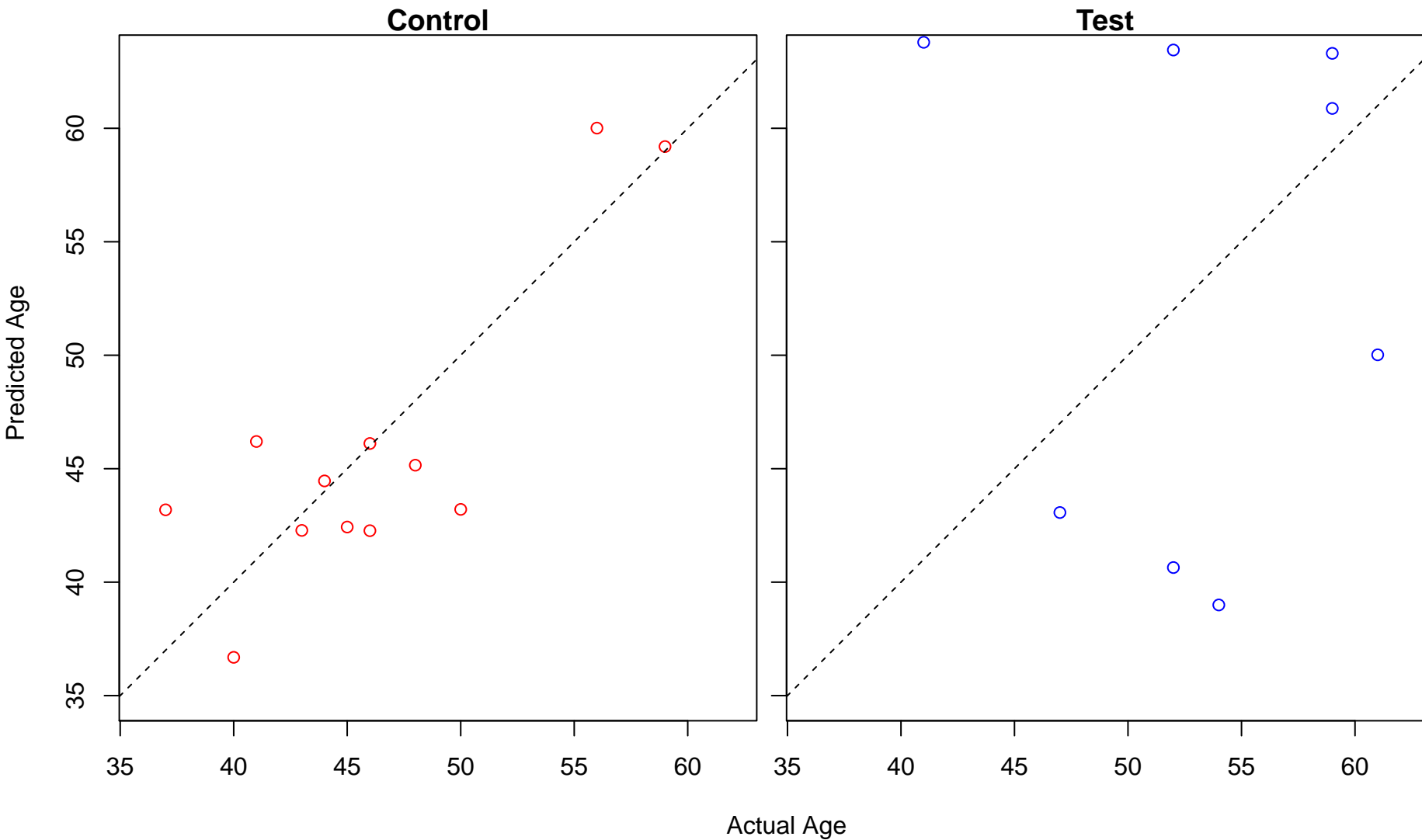
metanephros development (Score: 9.616701)



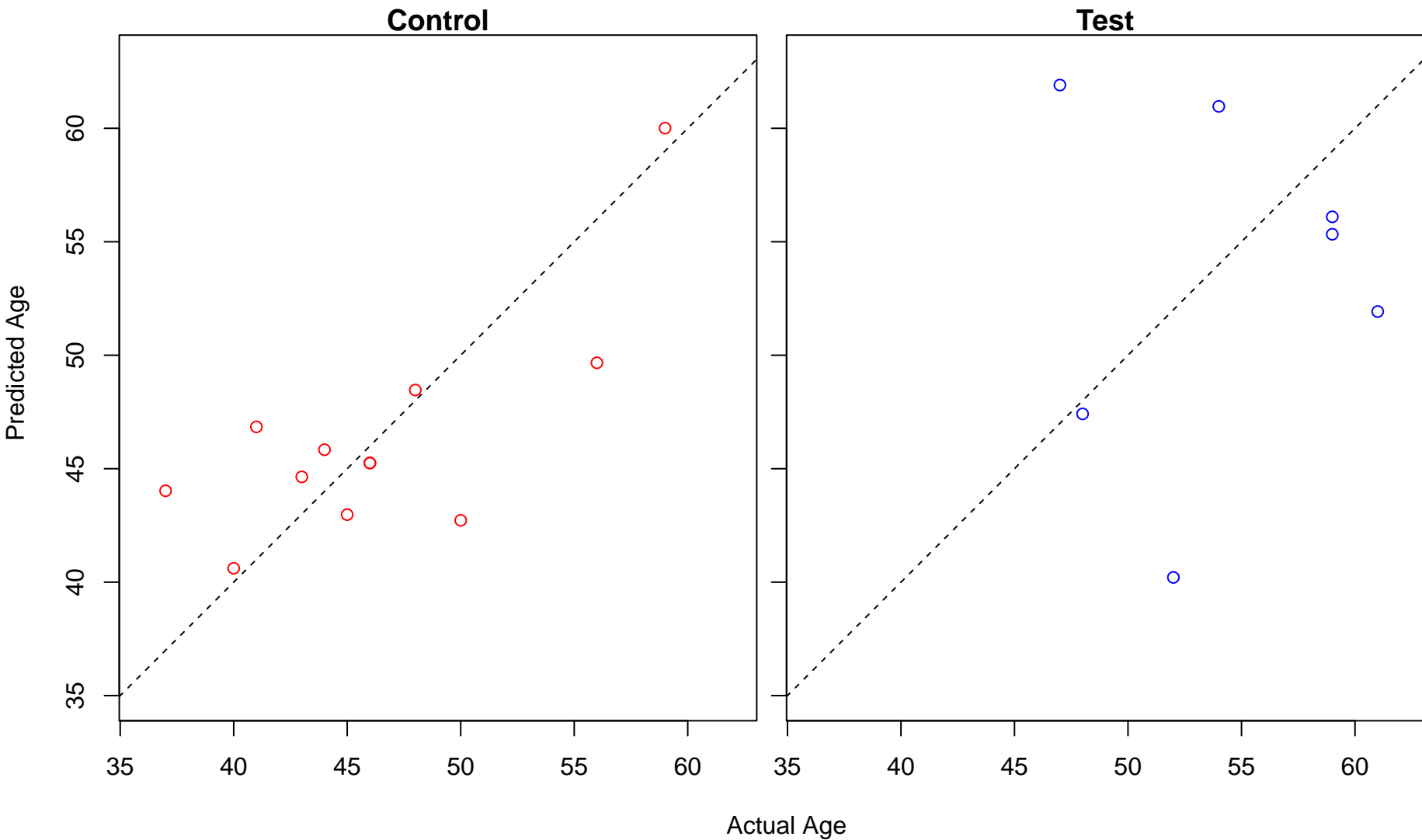
necroptotic process (Score: 9.615751)



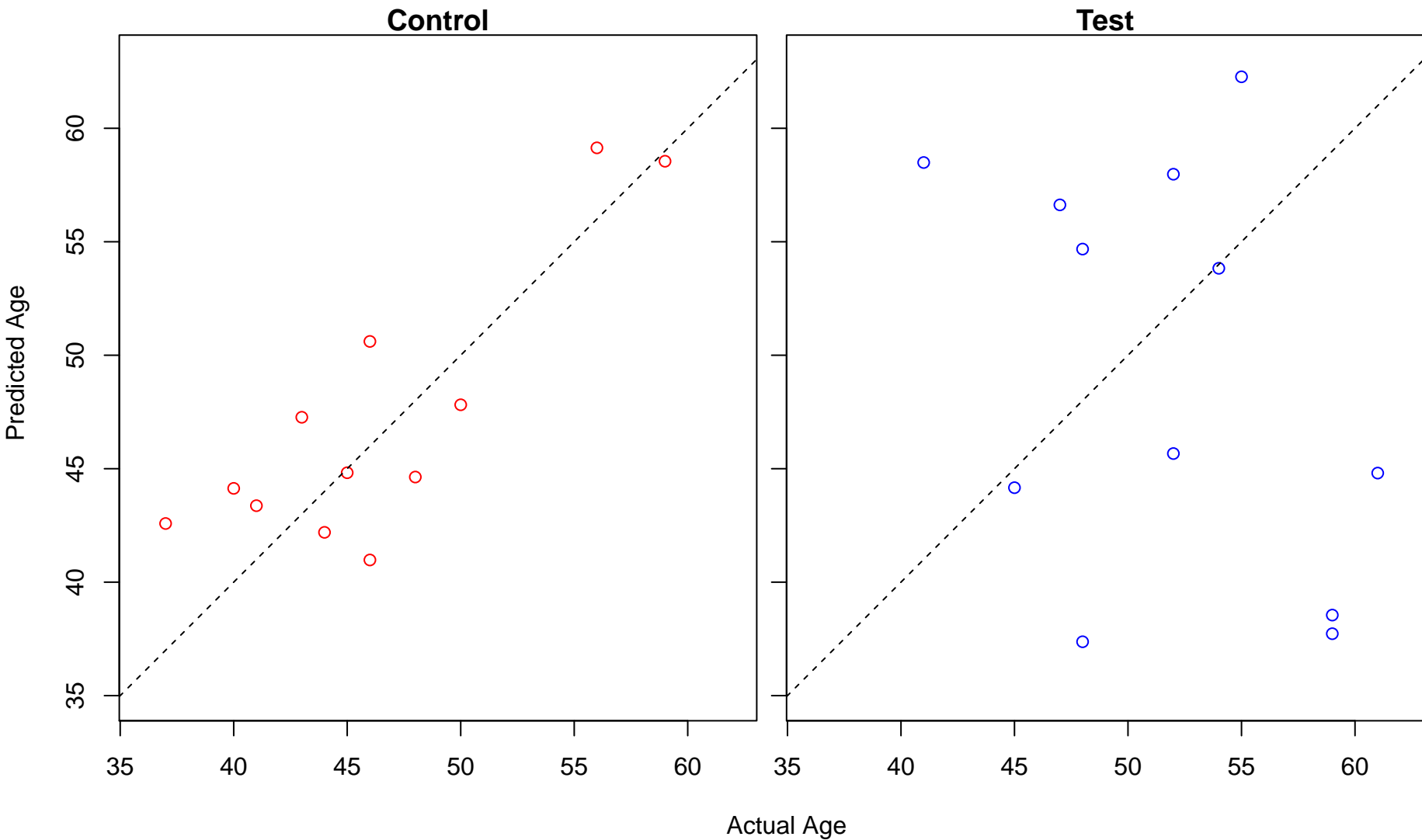
glutathione metabolic process (Score: 9.600966)



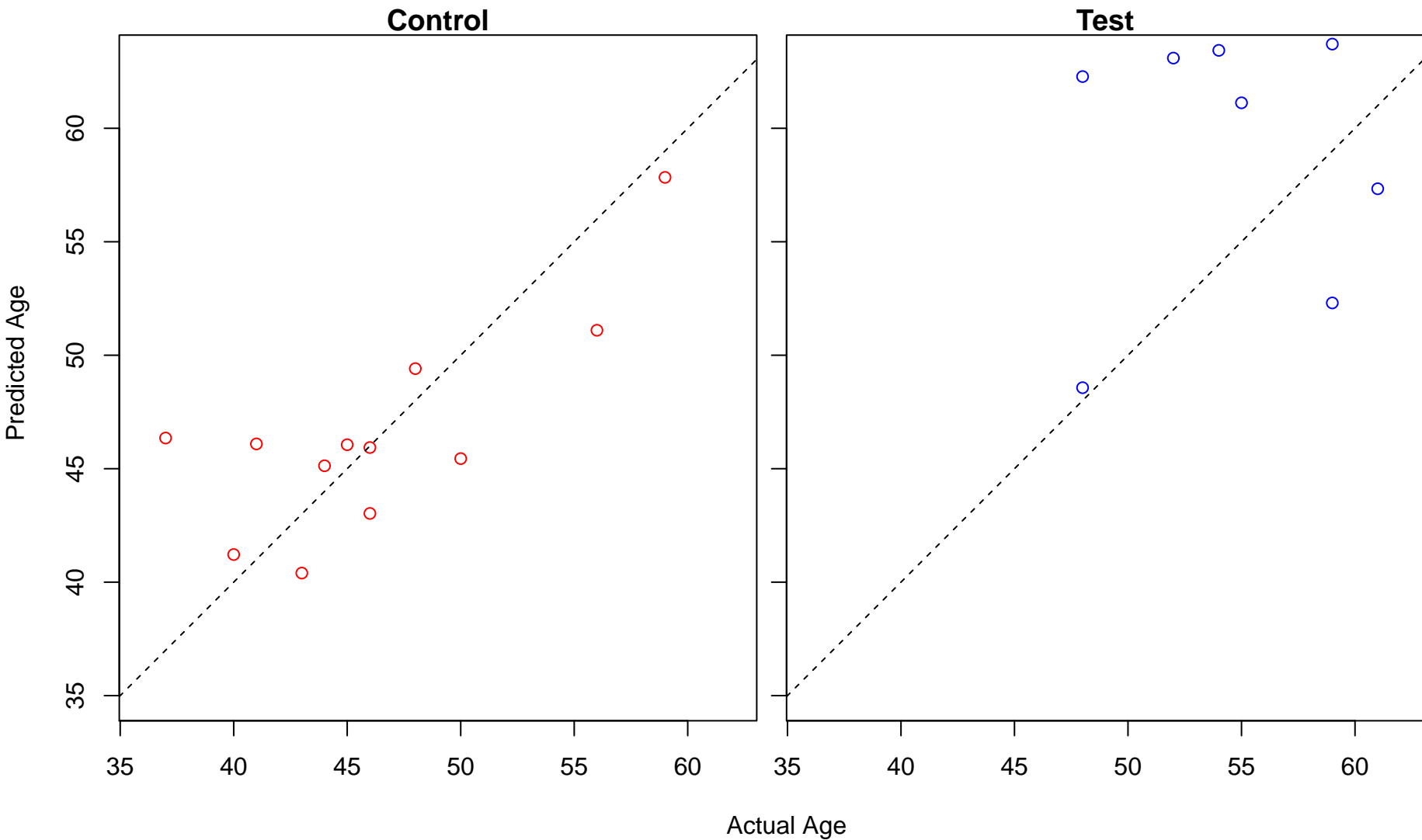
positive regulation of gastrulation (Score: 9.526883)



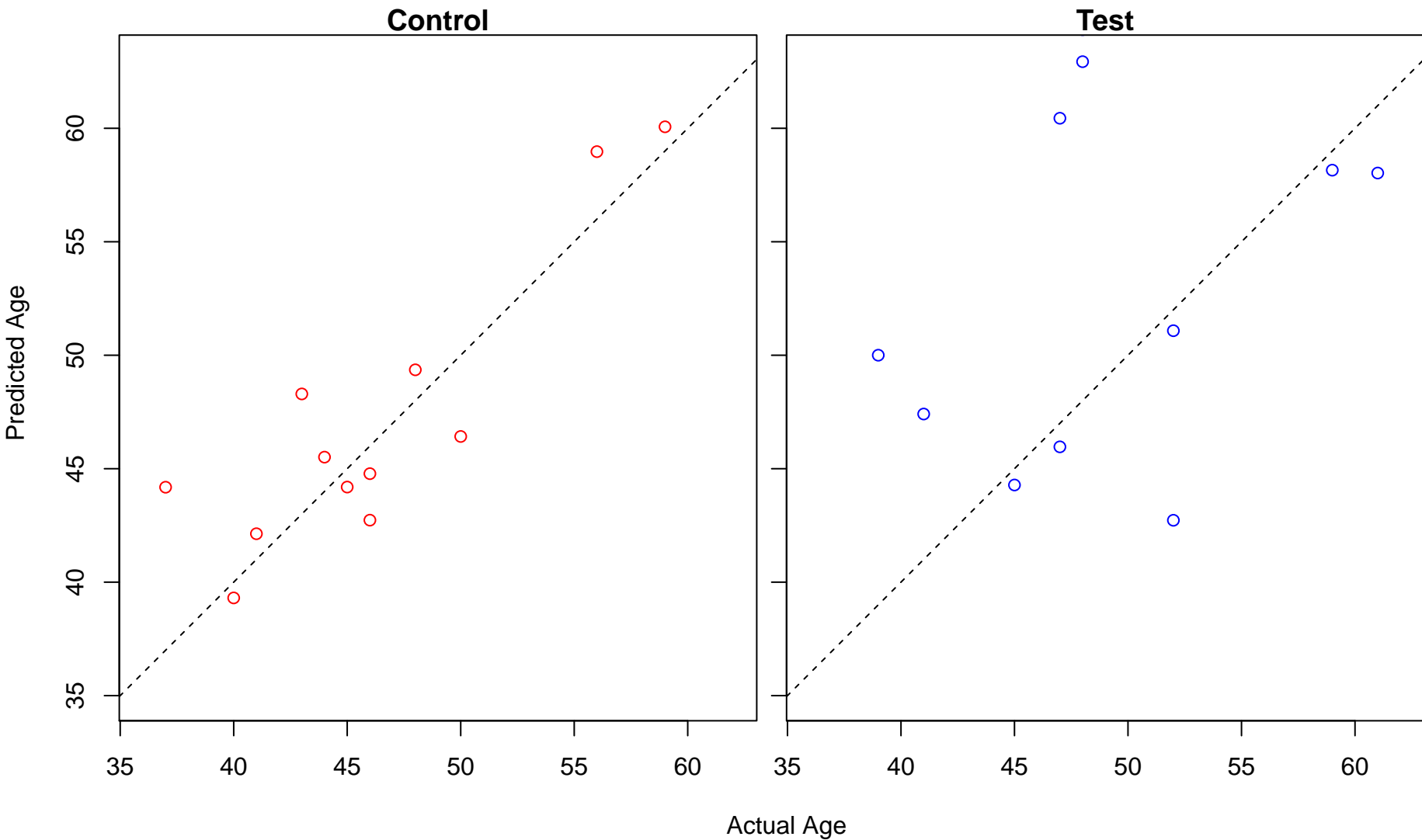
programmed necrotic cell death (Score: 9.514035)



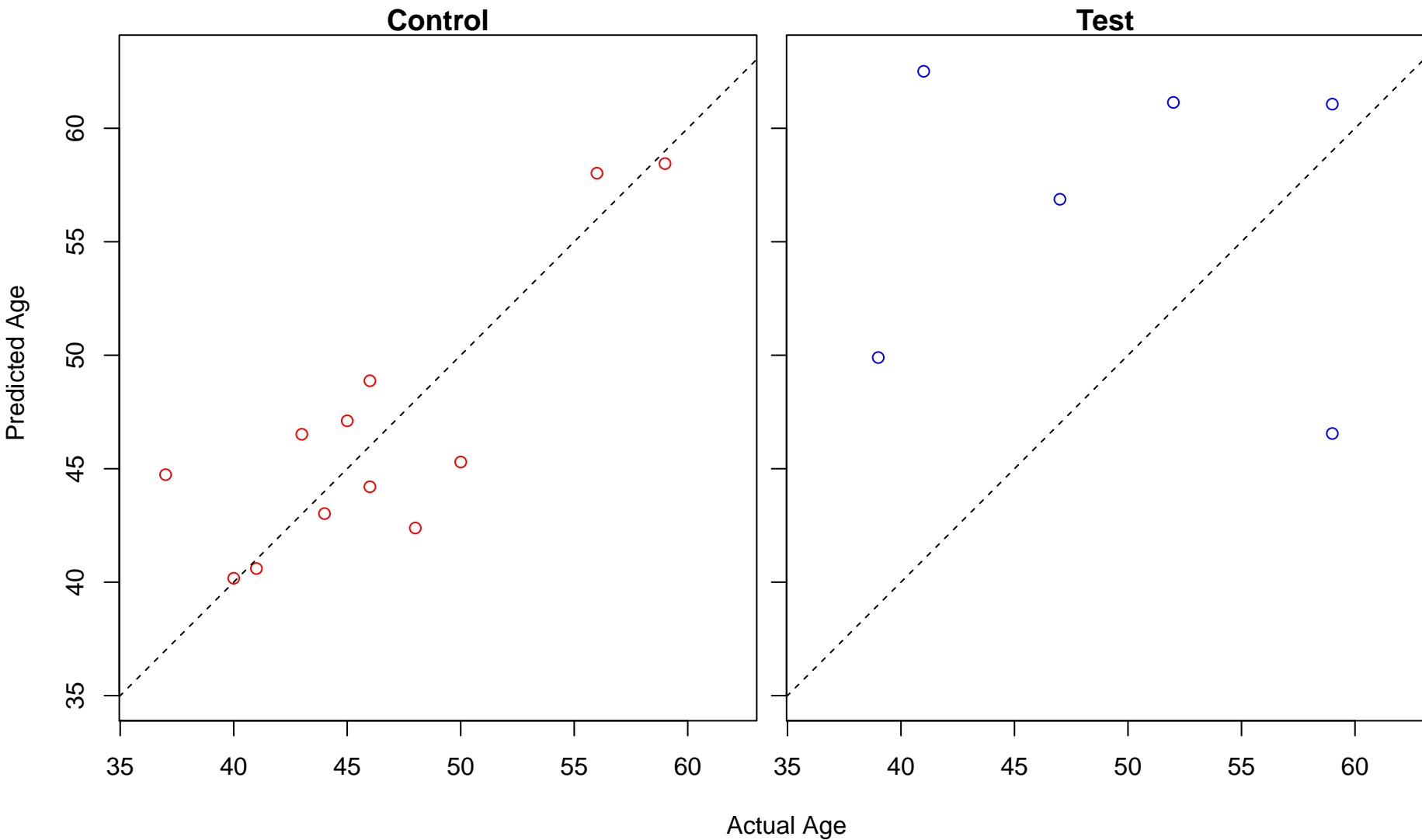
myoblast differentiation (Score: 9.505739)



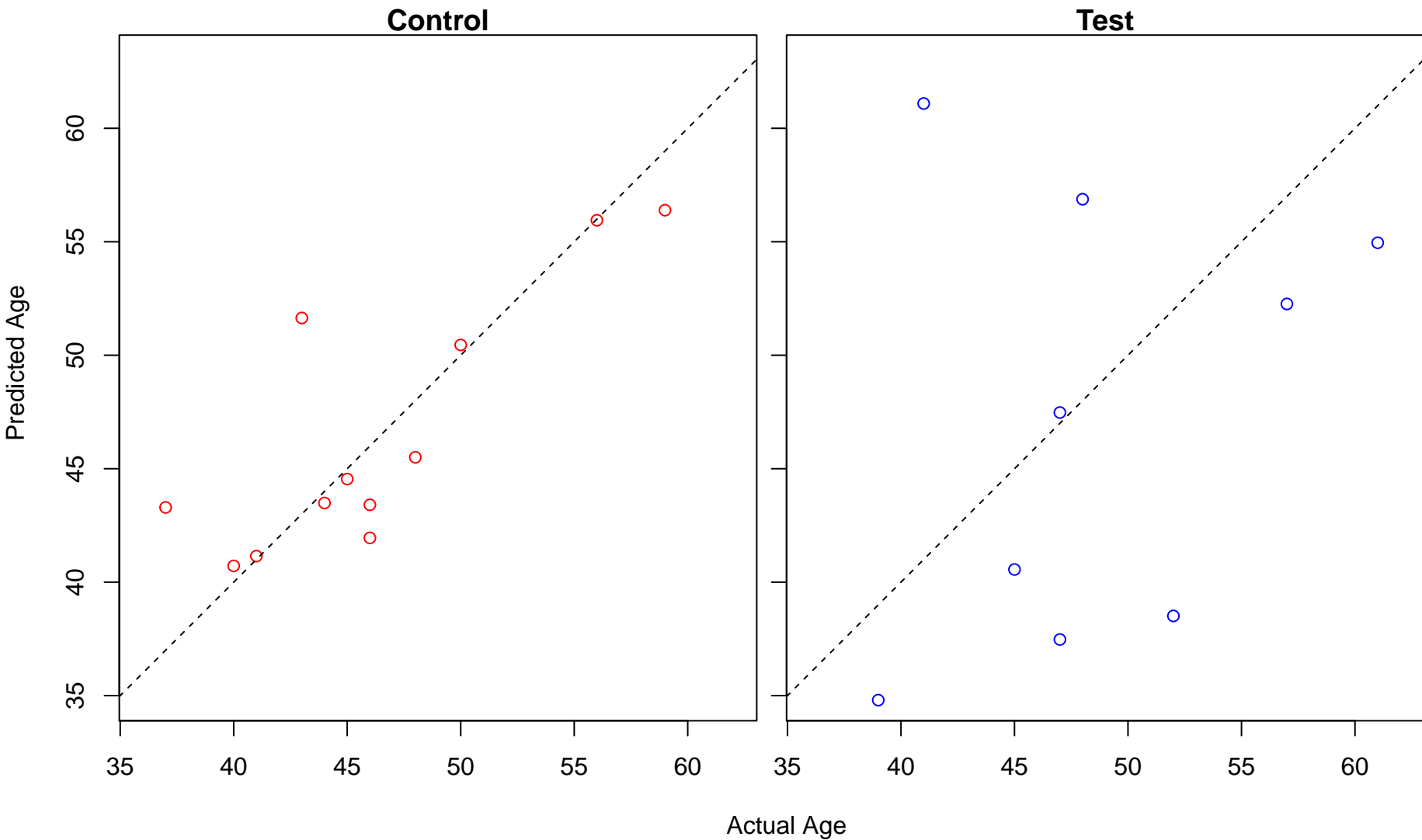
action potential (Score: 9.494820)



regulation of digestive system process (Score: 9.492325)

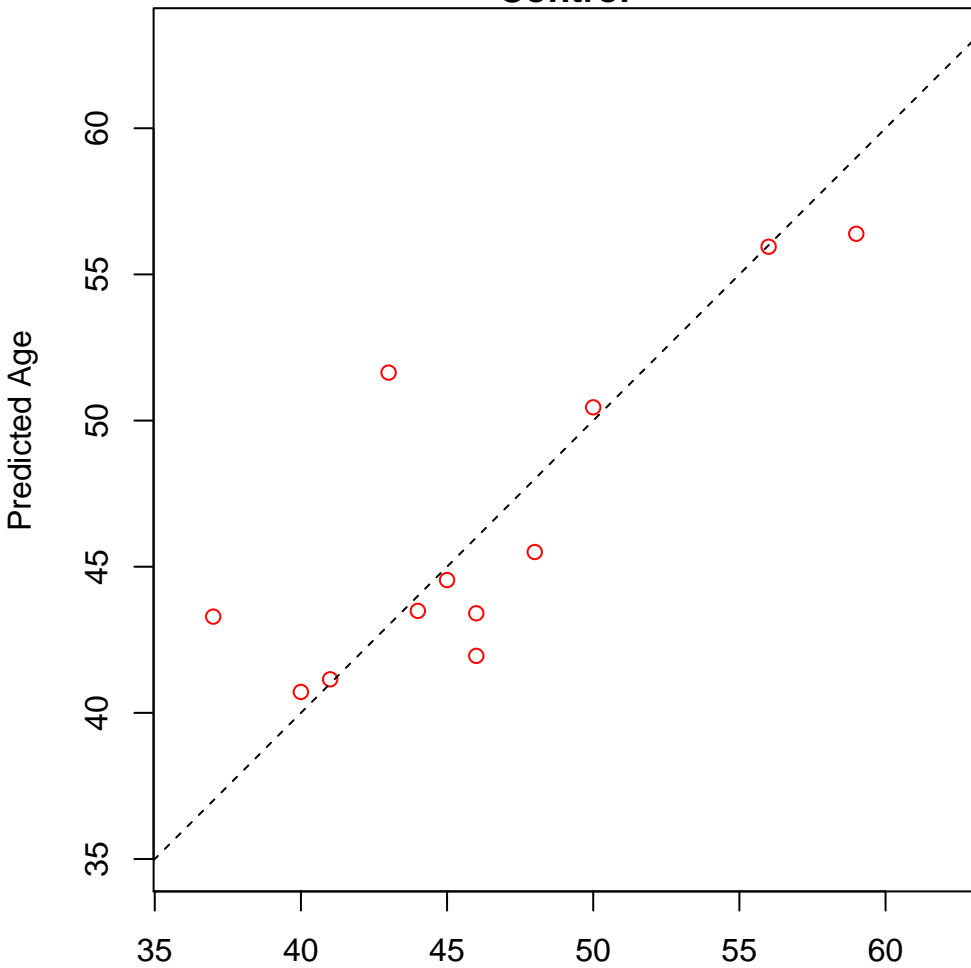


actin filament bundle assembly (Score: 9.447218)

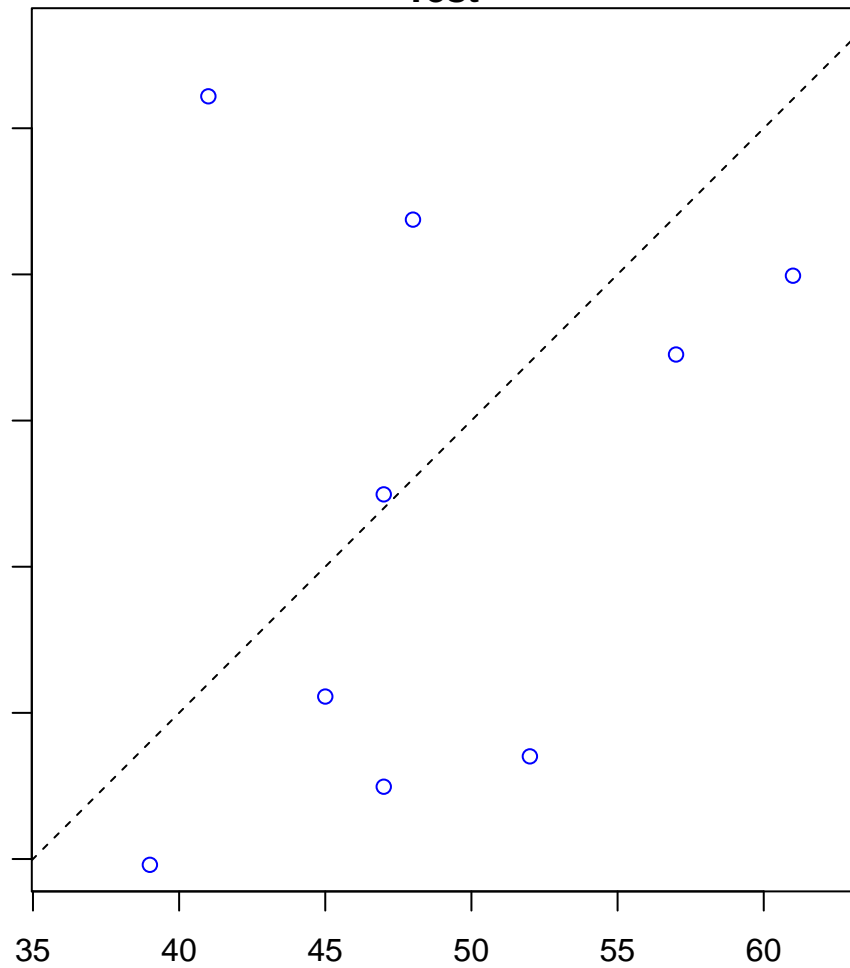


actin filament bundle organization (Score: 9.447218)

Control

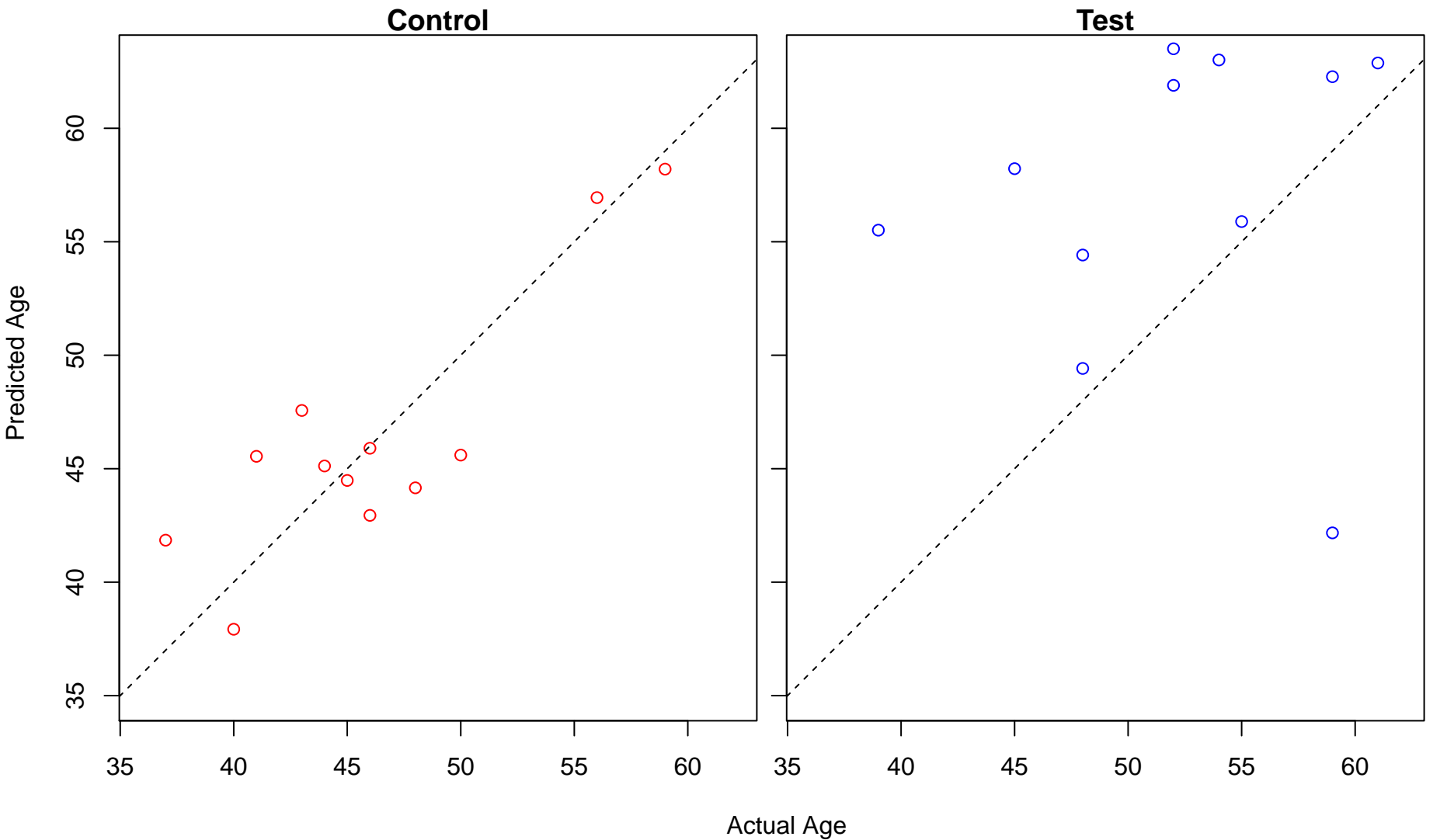


Test

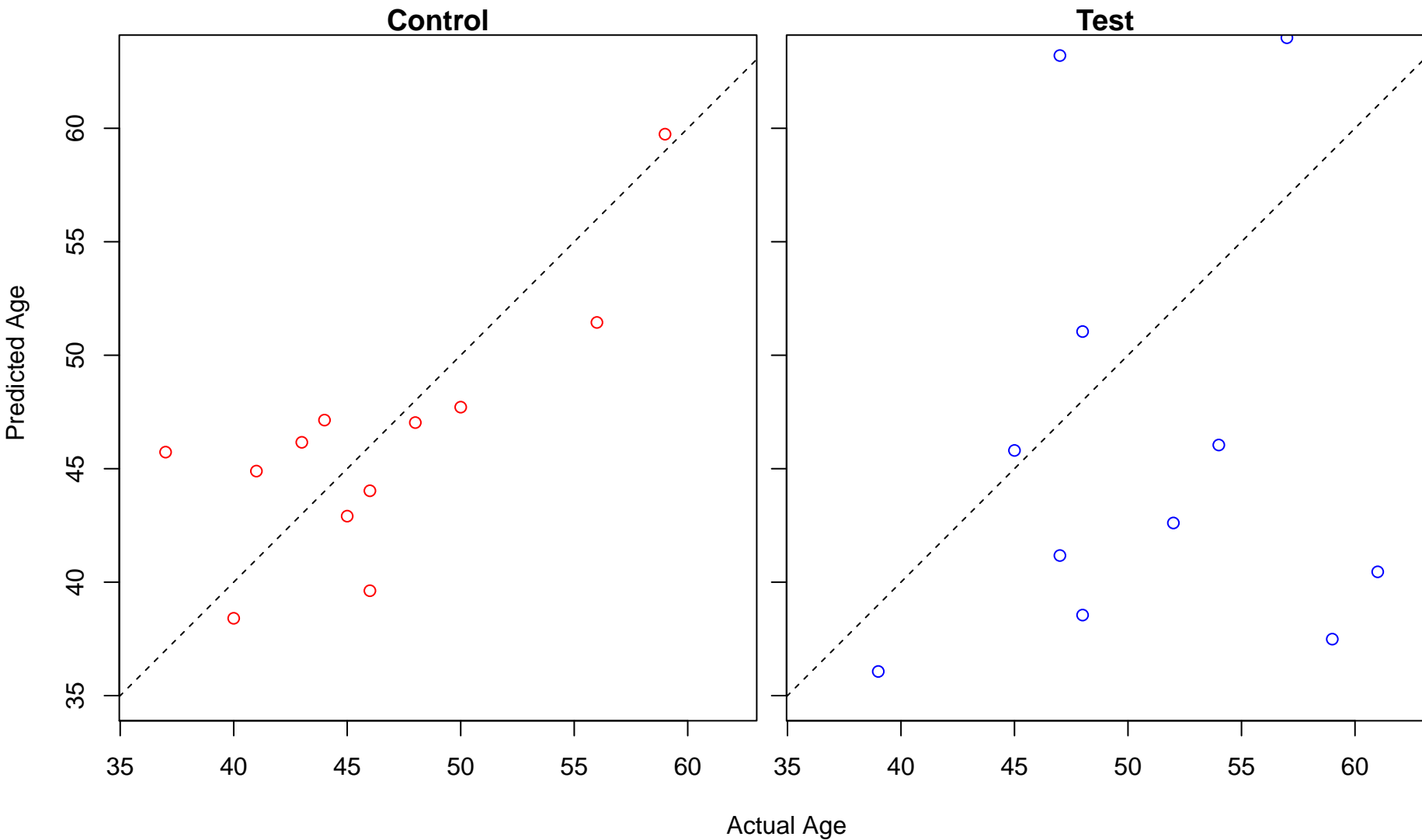


Actual Age

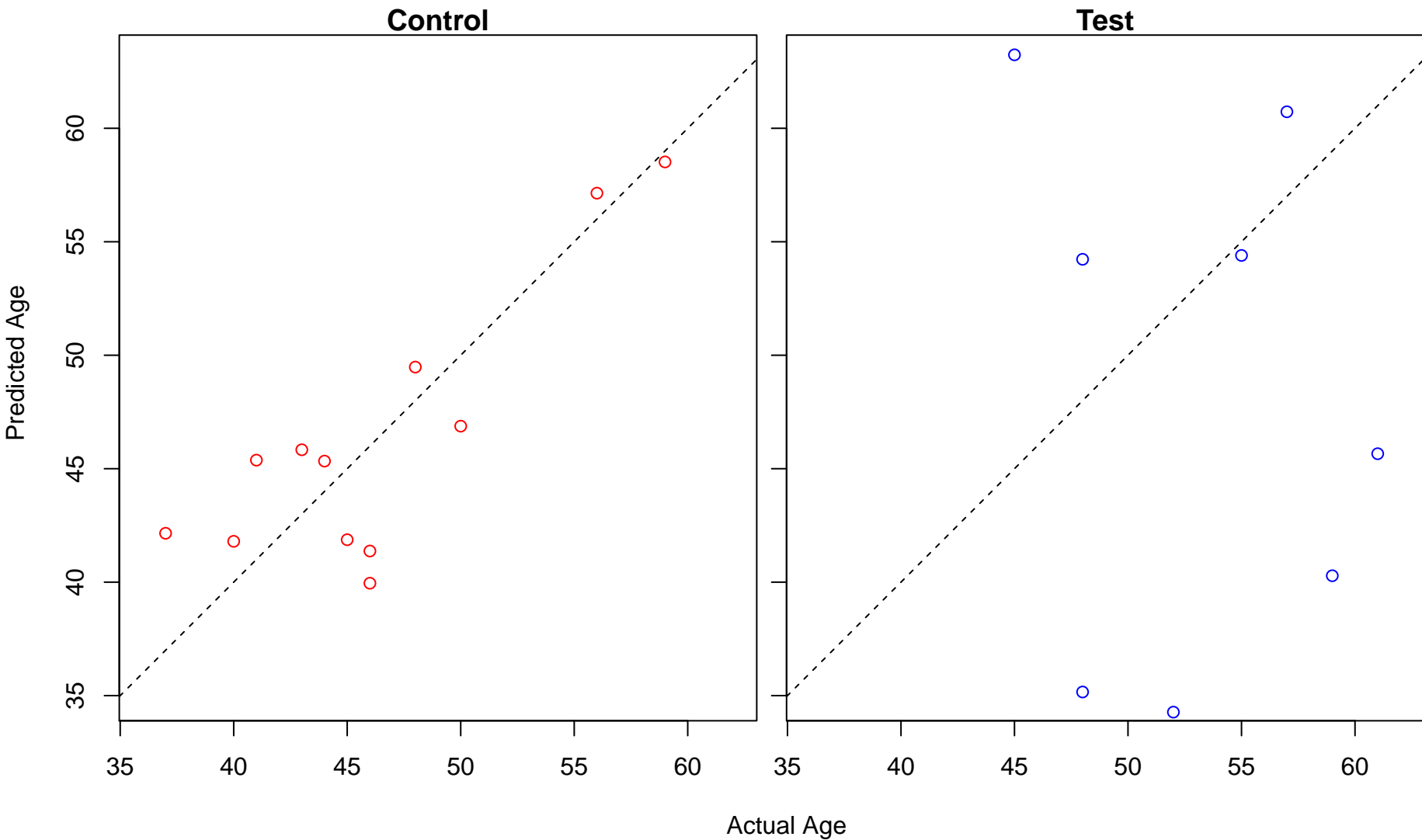
of T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting c



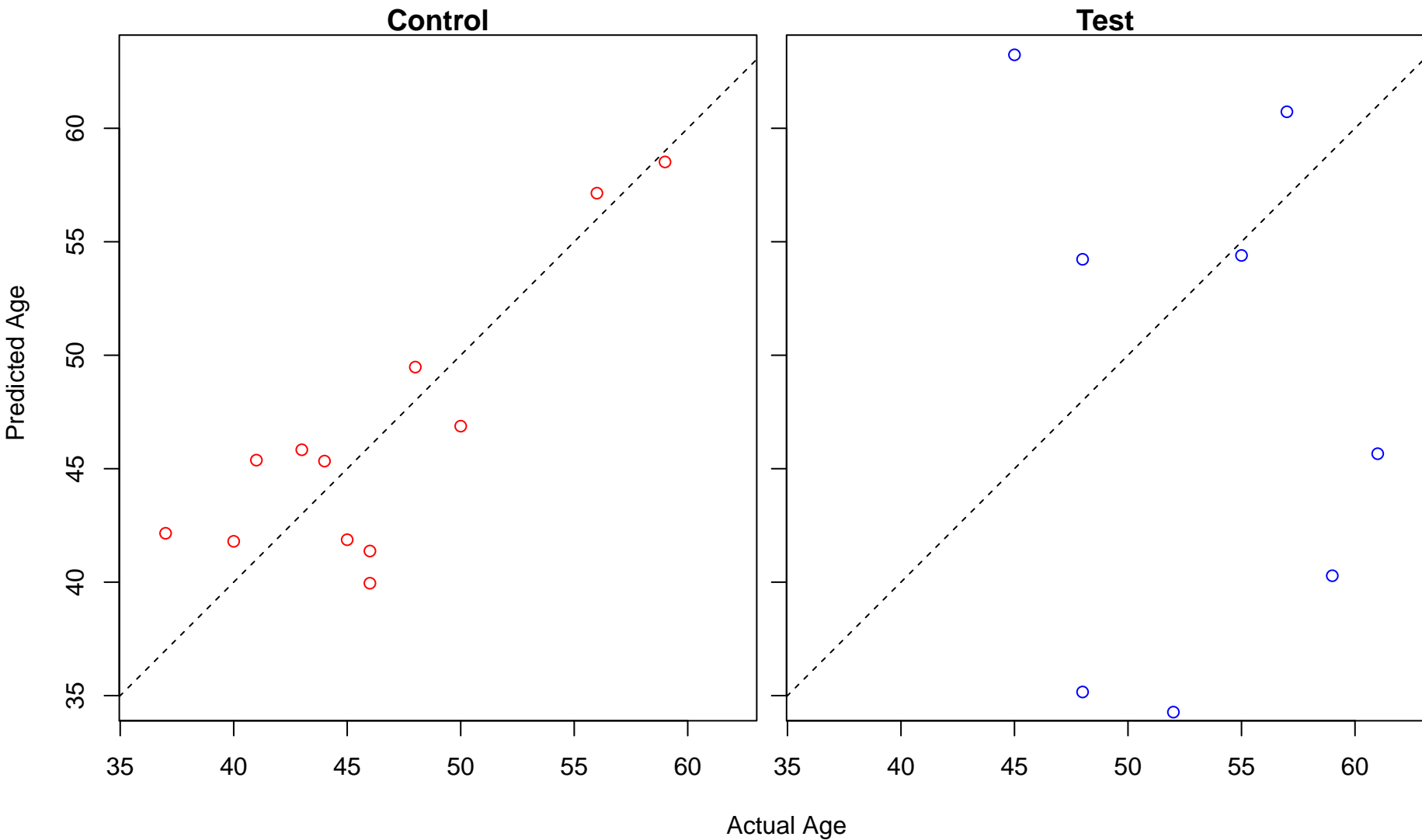
leukocyte migration (Score: 9.397963)



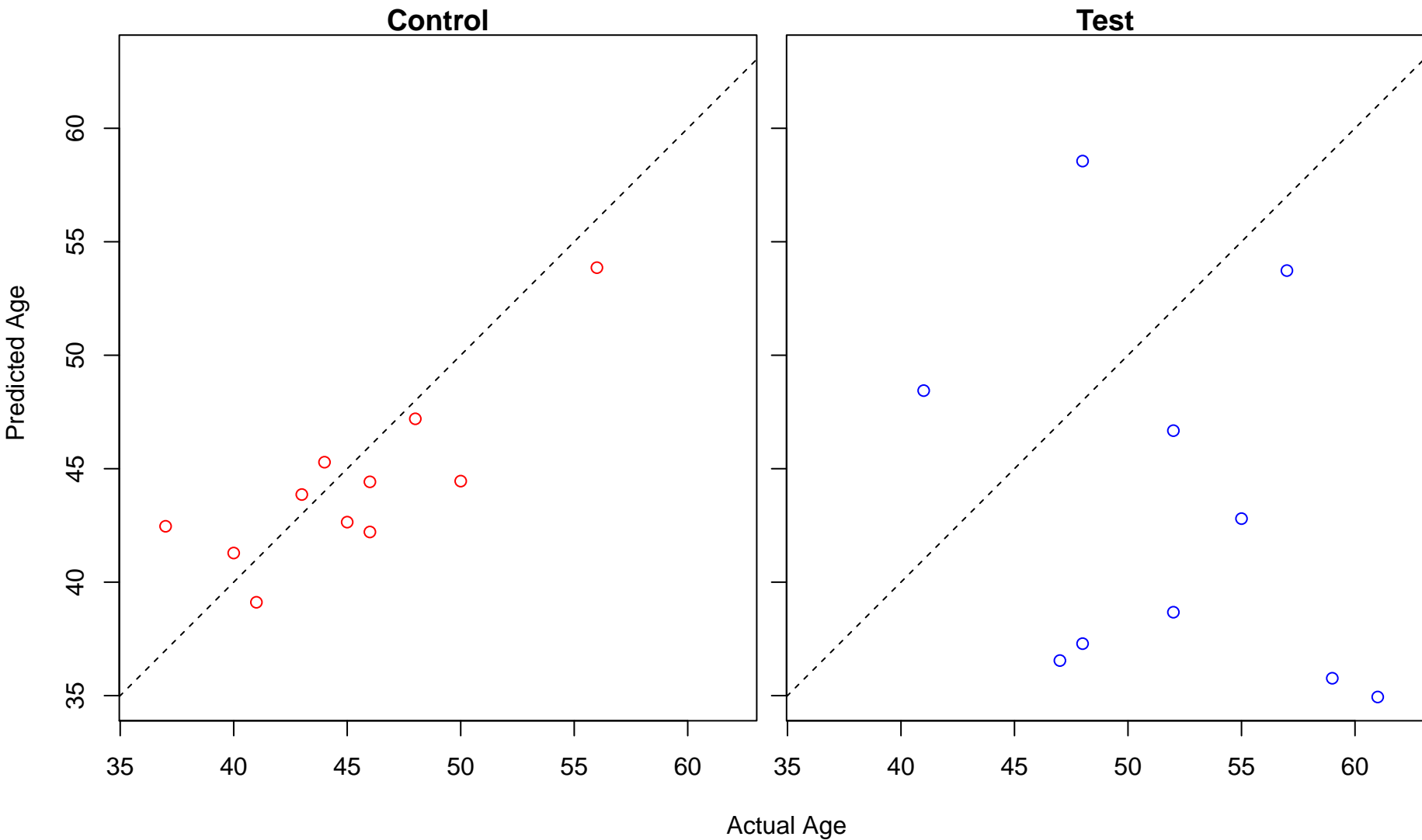
organic acid biosynthetic process (Score: 9.347374)



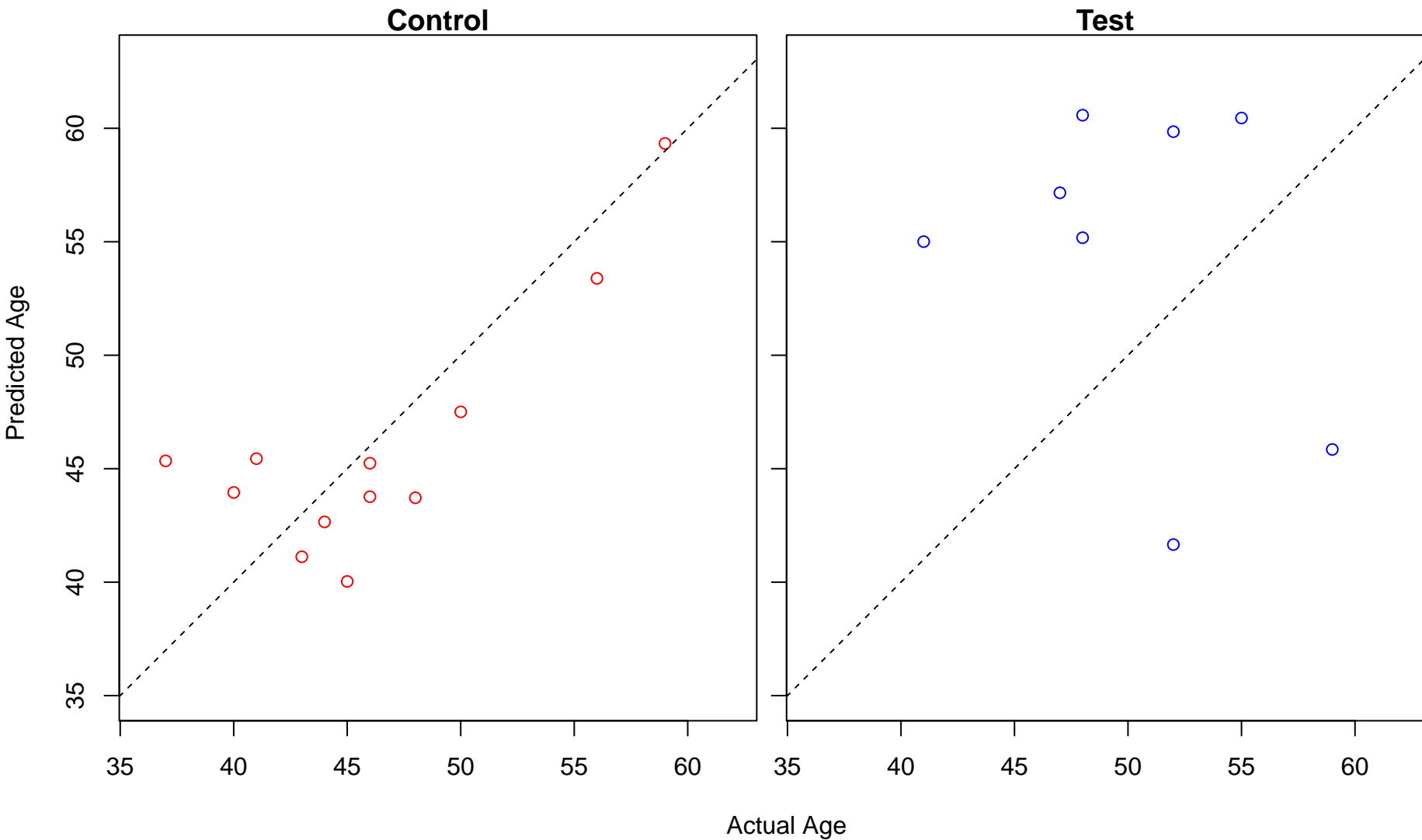
carboxylic acid biosynthetic process (Score: 9.347374)



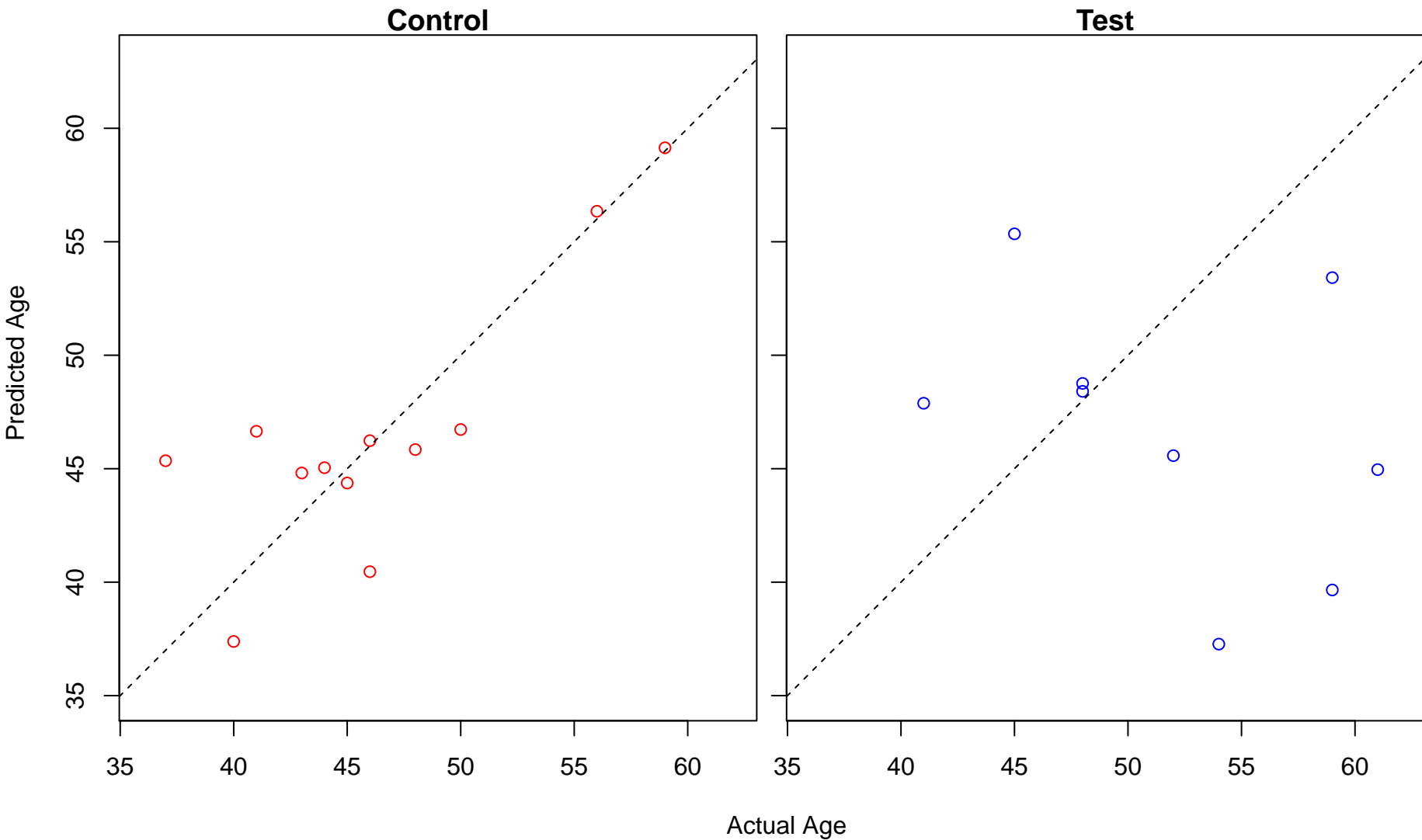
cyclic nucleotide metabolic process (Score: 9.314484)



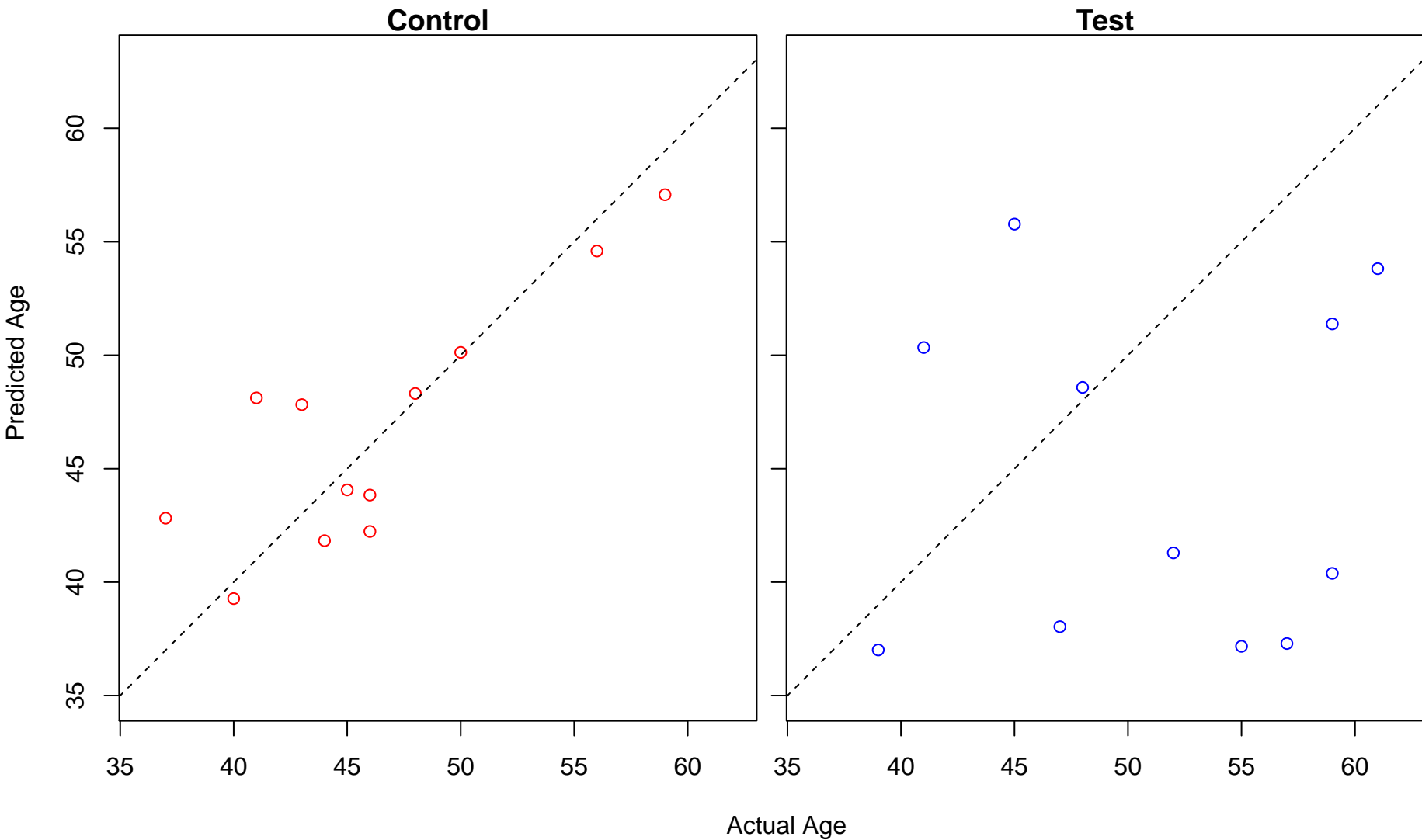
regulation of gliogenesis (Score: 9.309108)



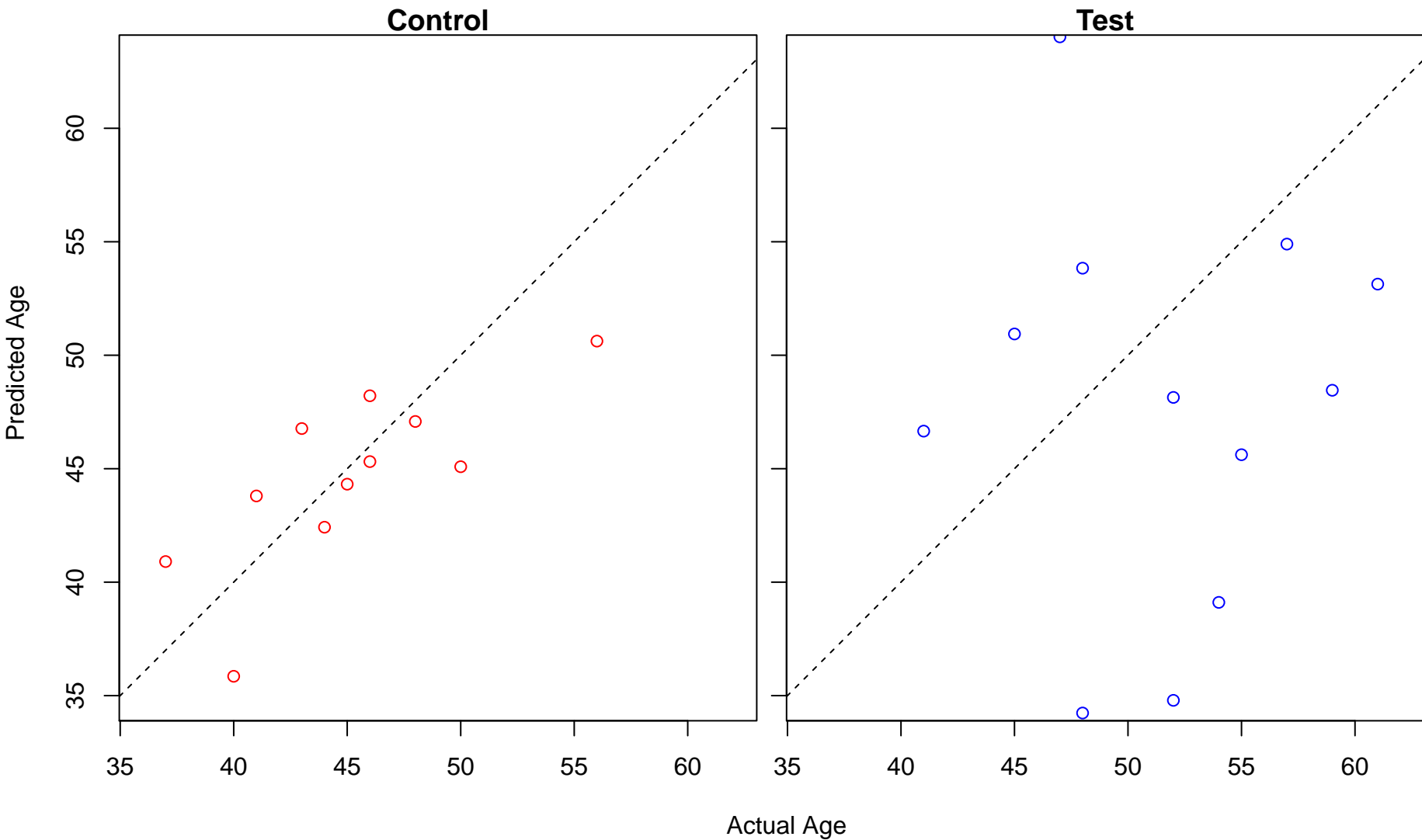
cartilage development (Score: 9.252086)



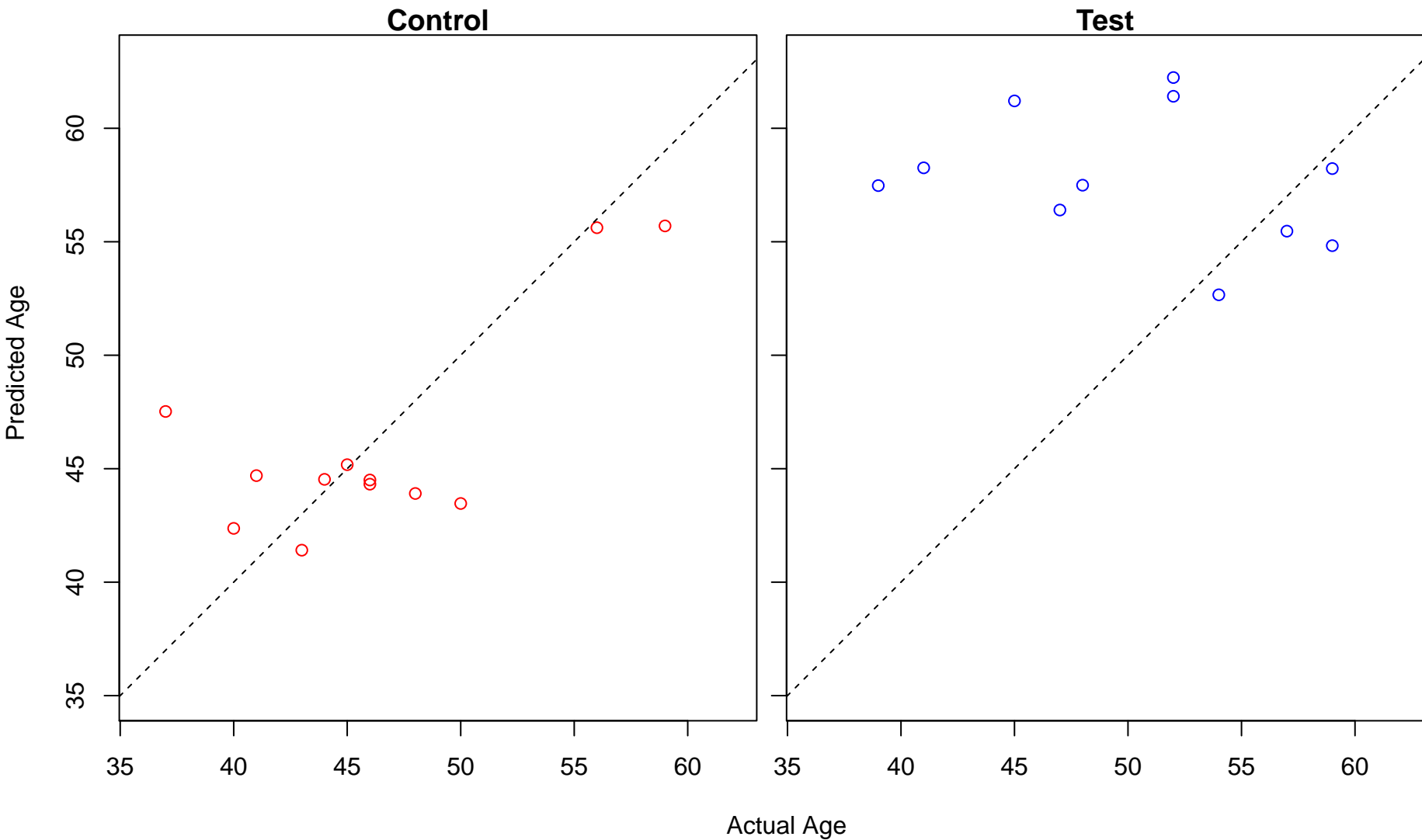
carbohydrate phosphorylation (Score: 9.242240)



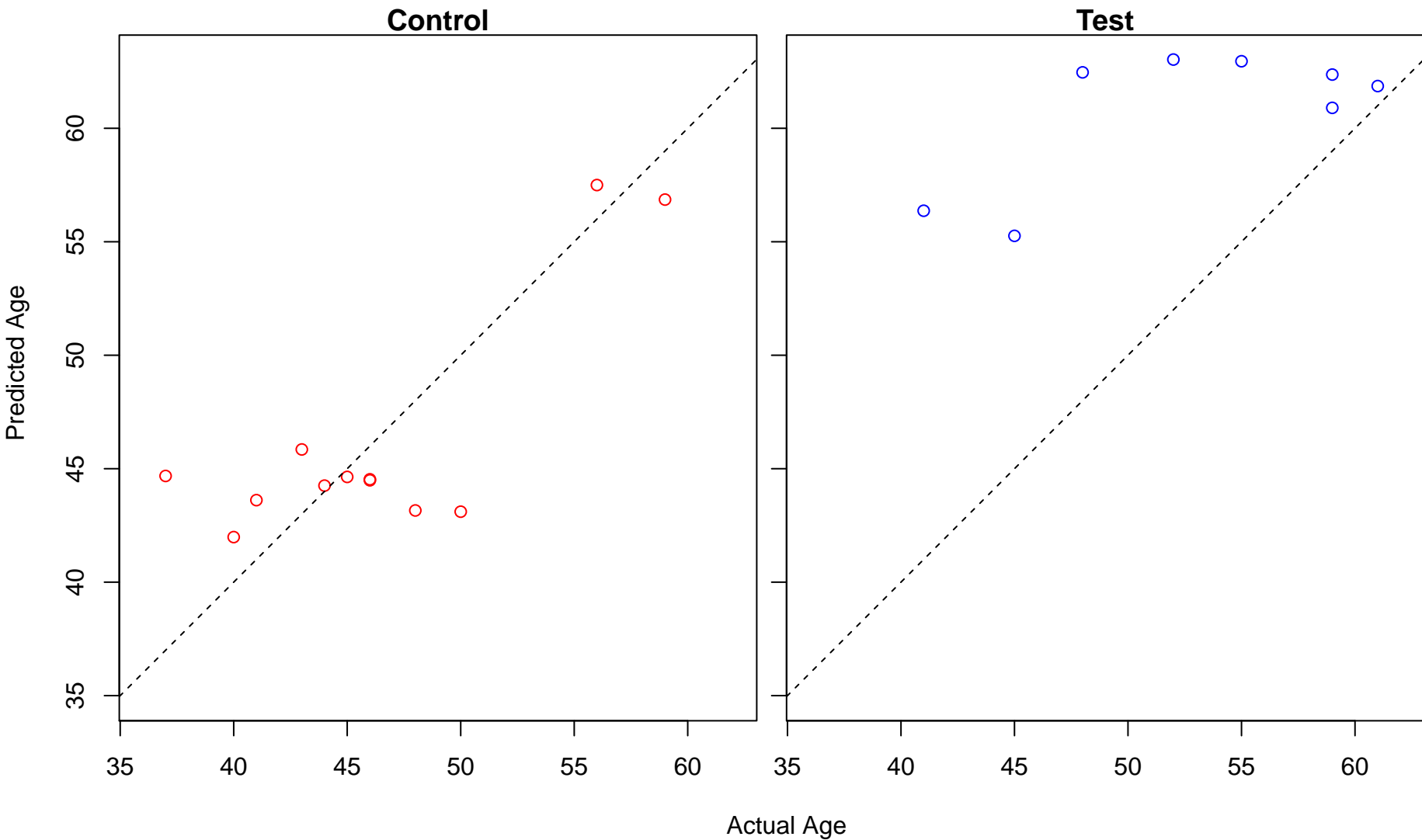
positive regulation of glomerulus development (Score: 9.215717)



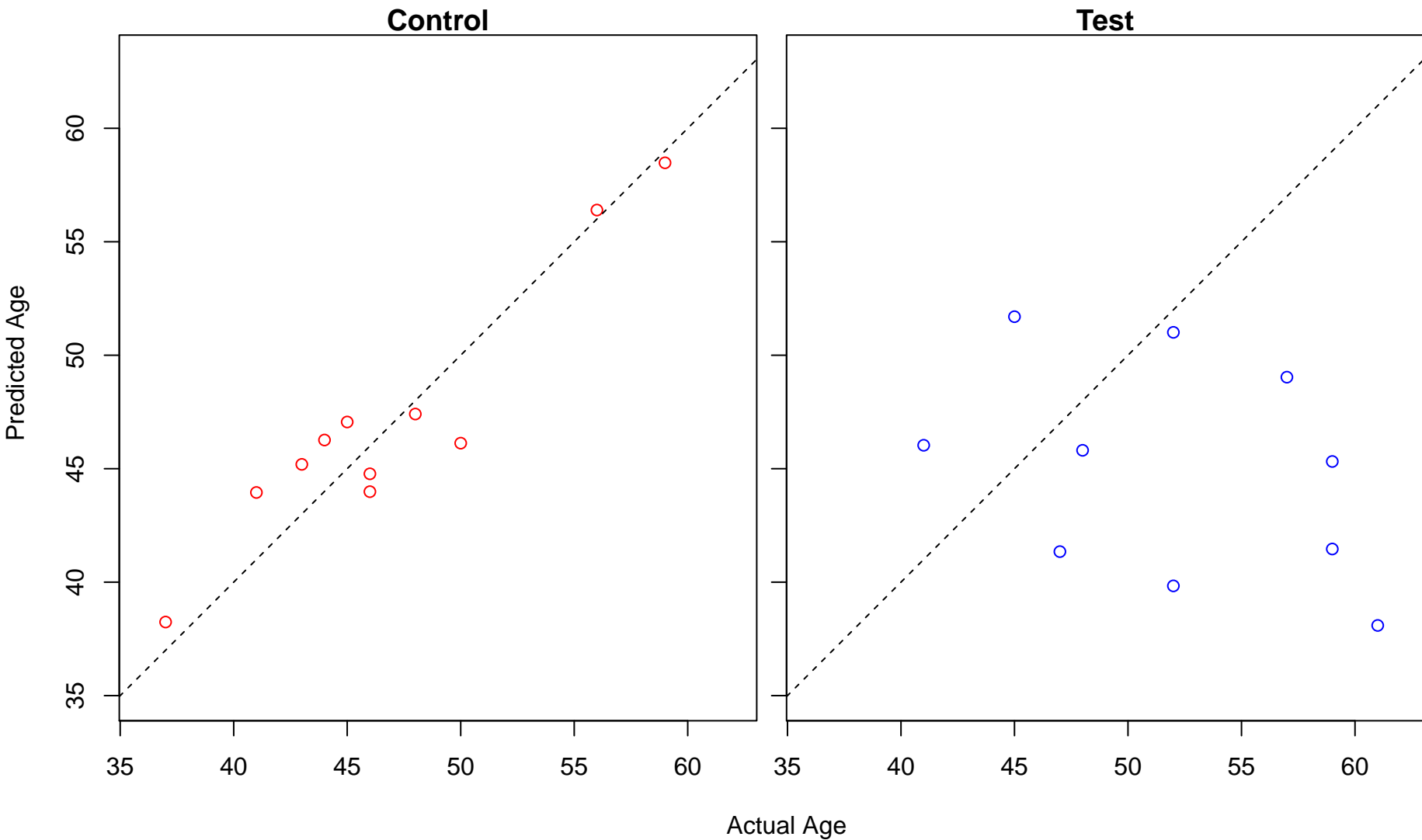
complement receptor mediated signaling pathway (Score: 9.168613)



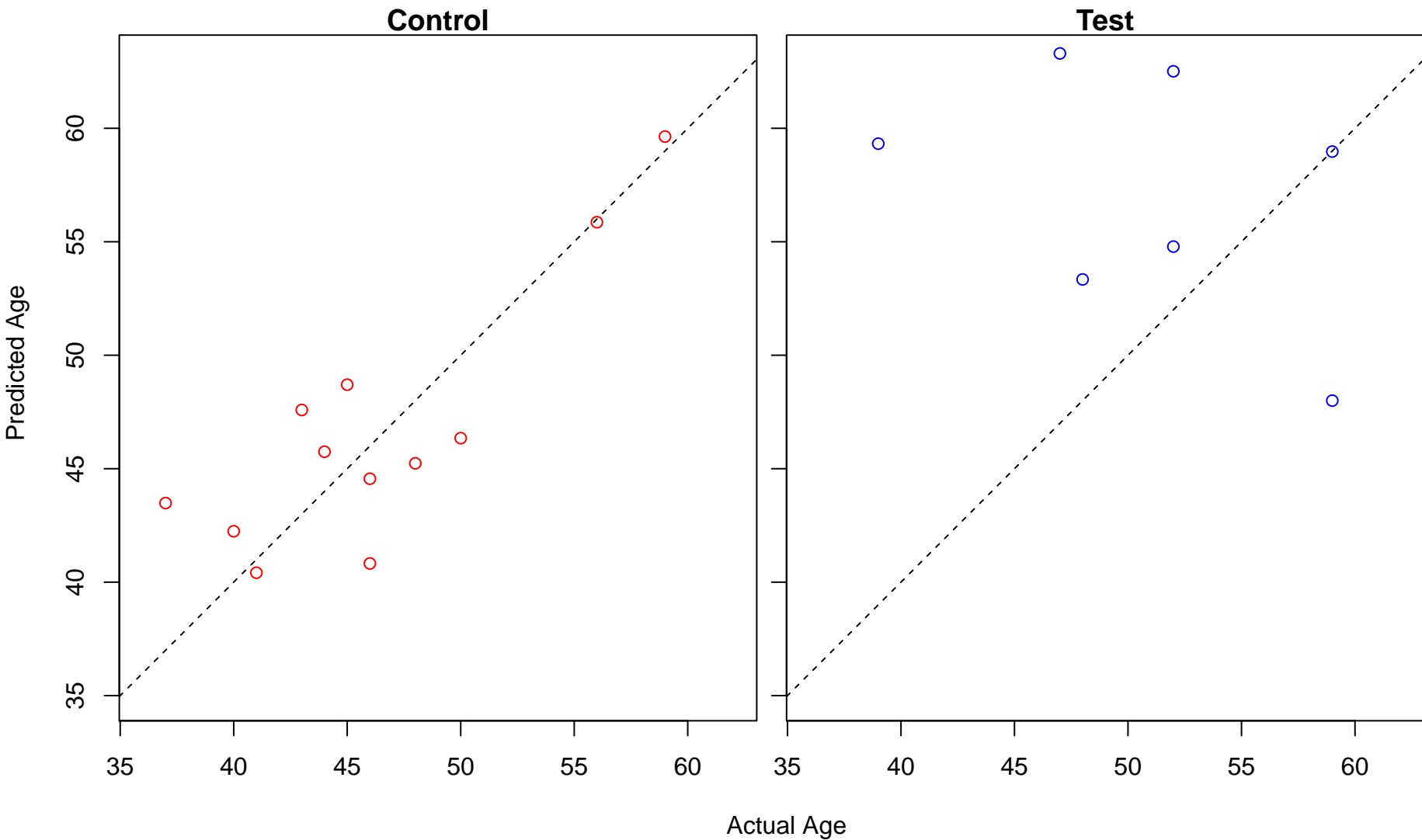
negative regulation of gene silencing by miRNA (Score: 9.157079)



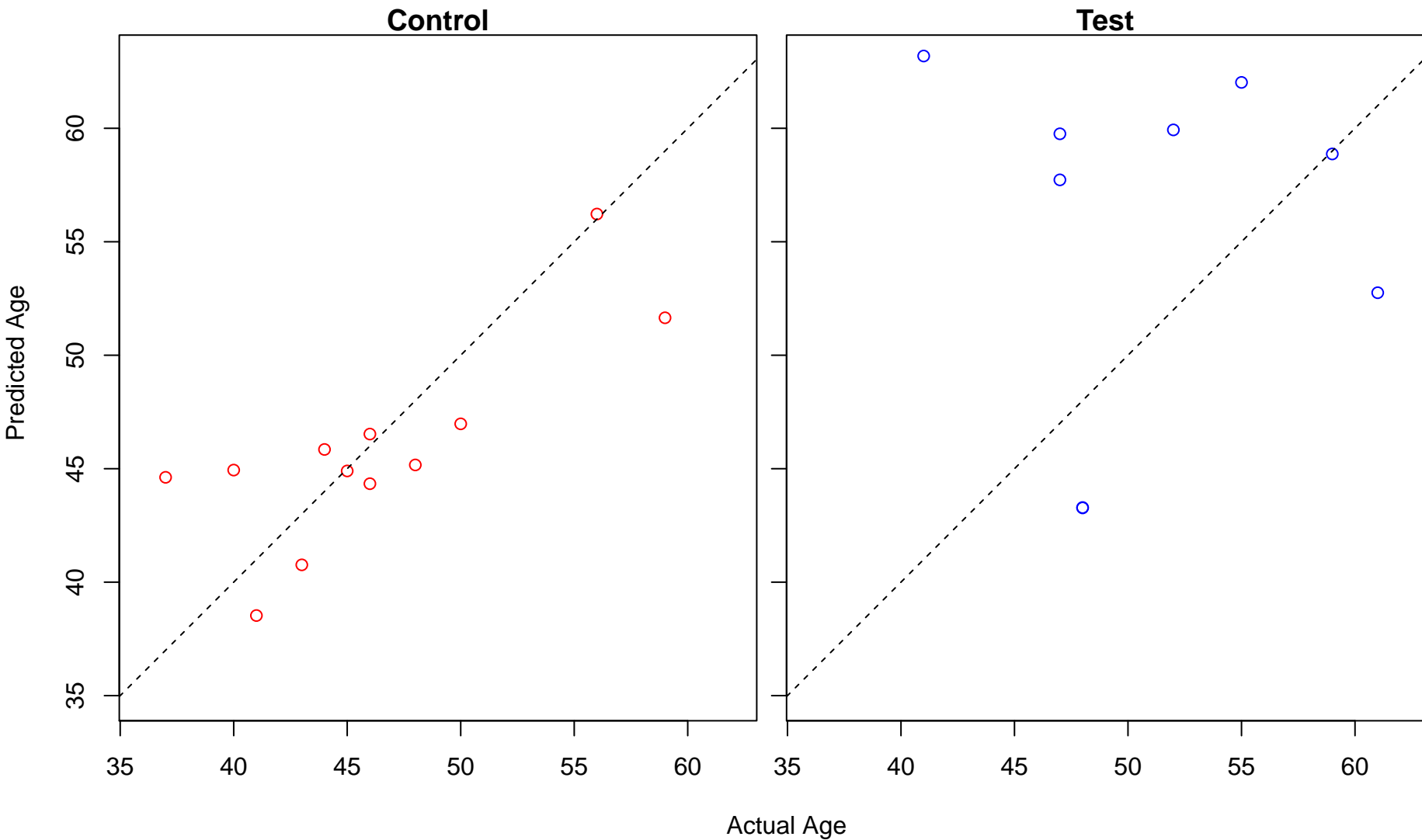
response to interferon-beta (Score: 9.141662)



anatomical structure maturation (Score: 9.116833)

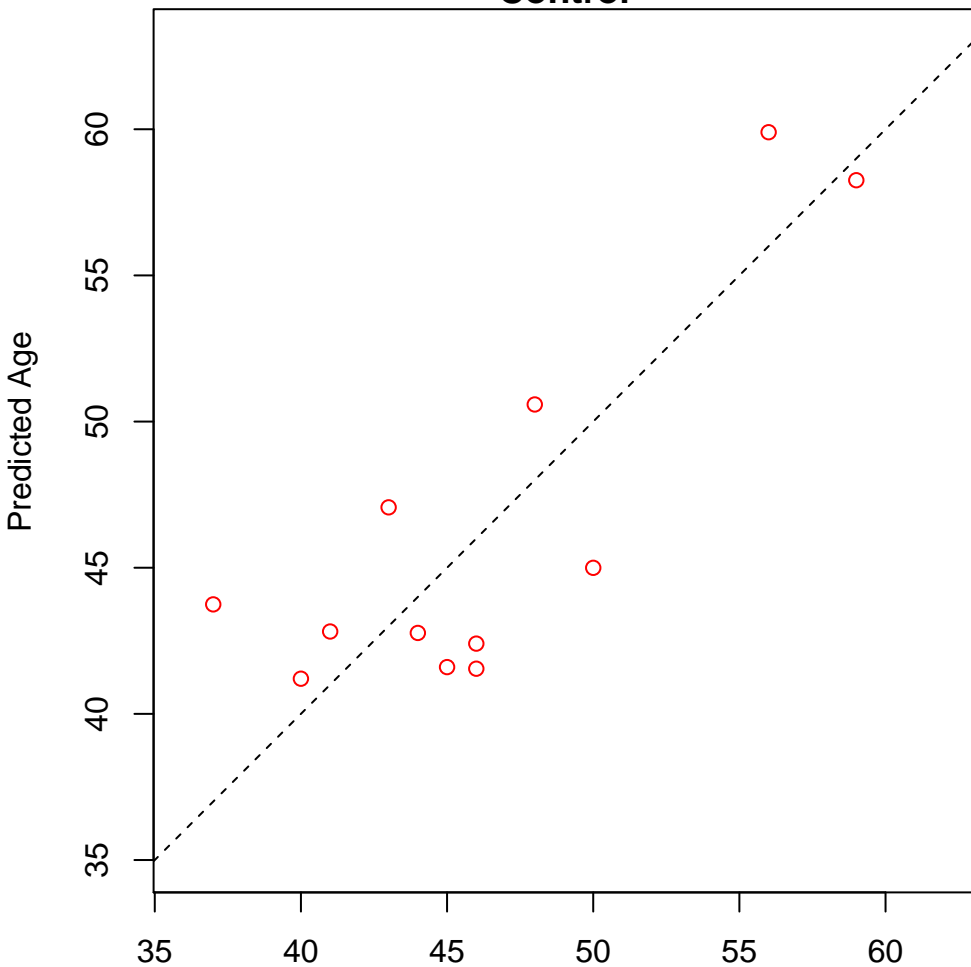


cardiac chamber formation (Score: 9.090494)

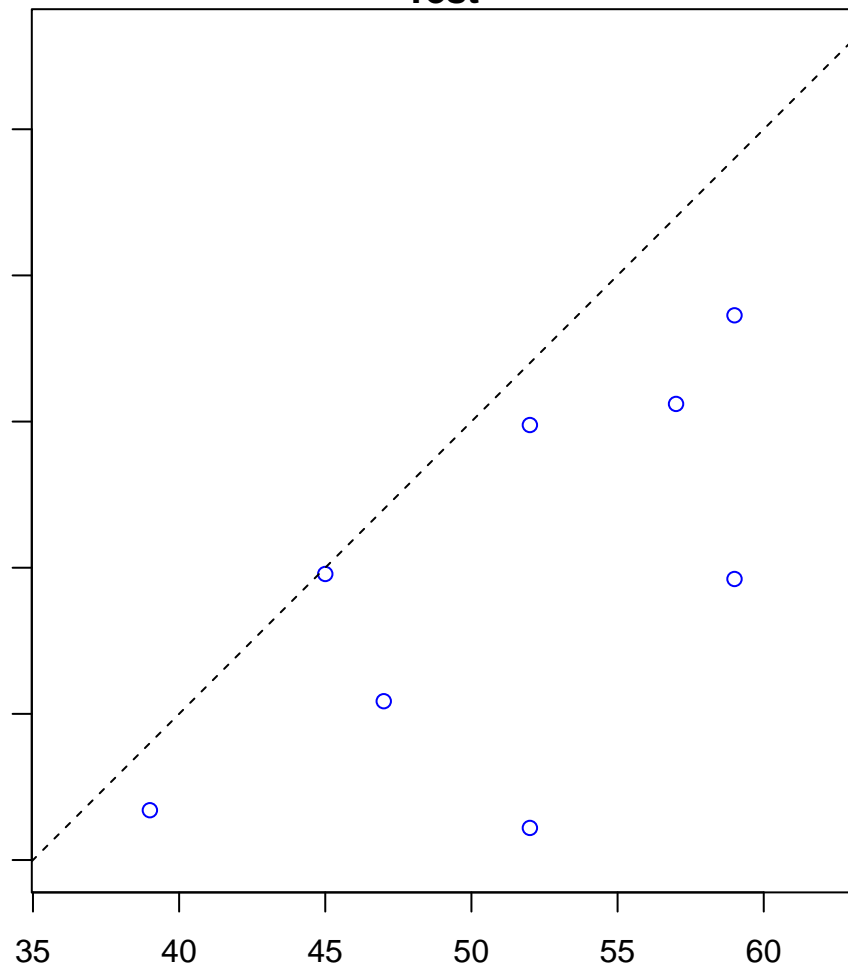


poly(A)+ mRNA export from nucleus (Score: 9.071327)

Control

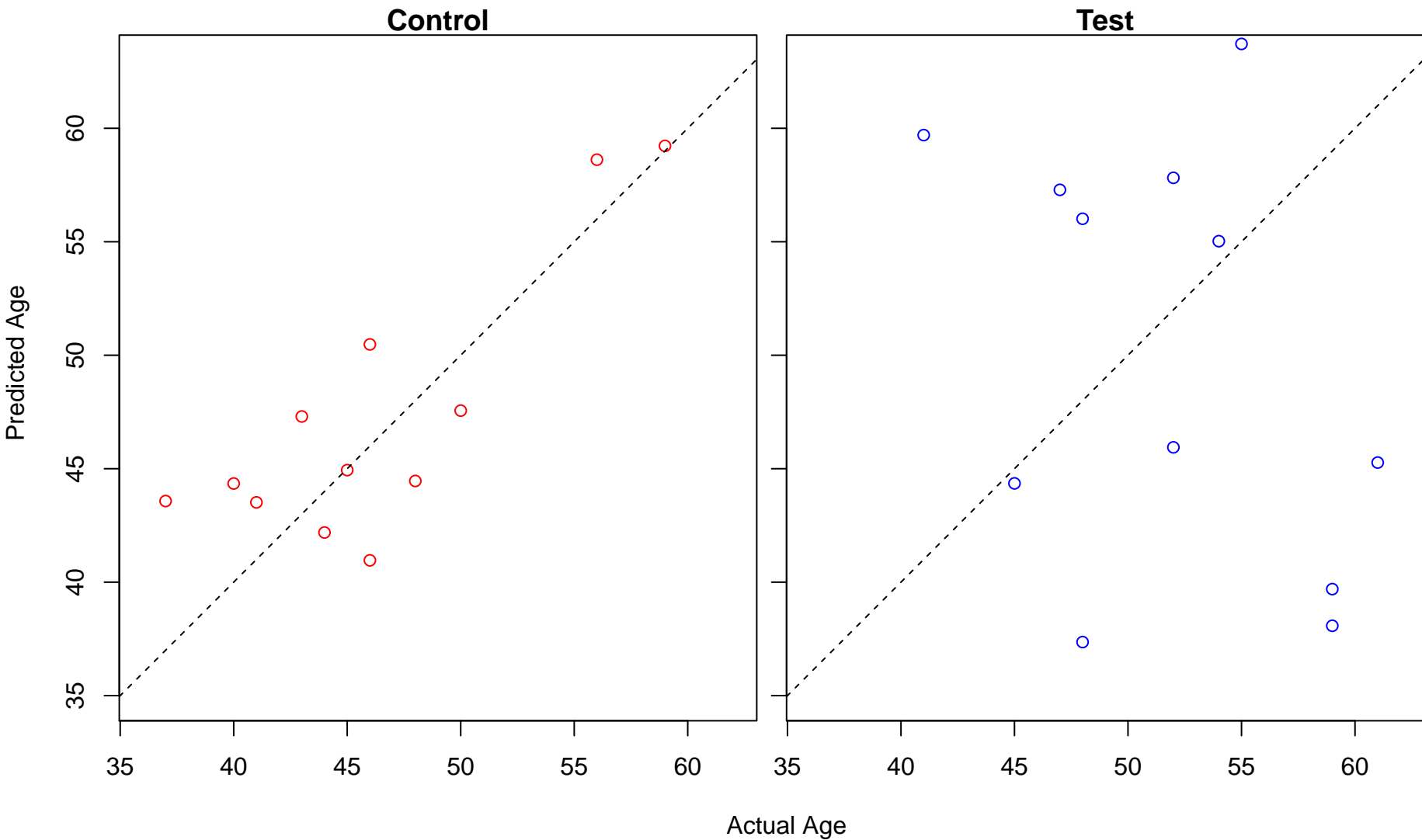


Test

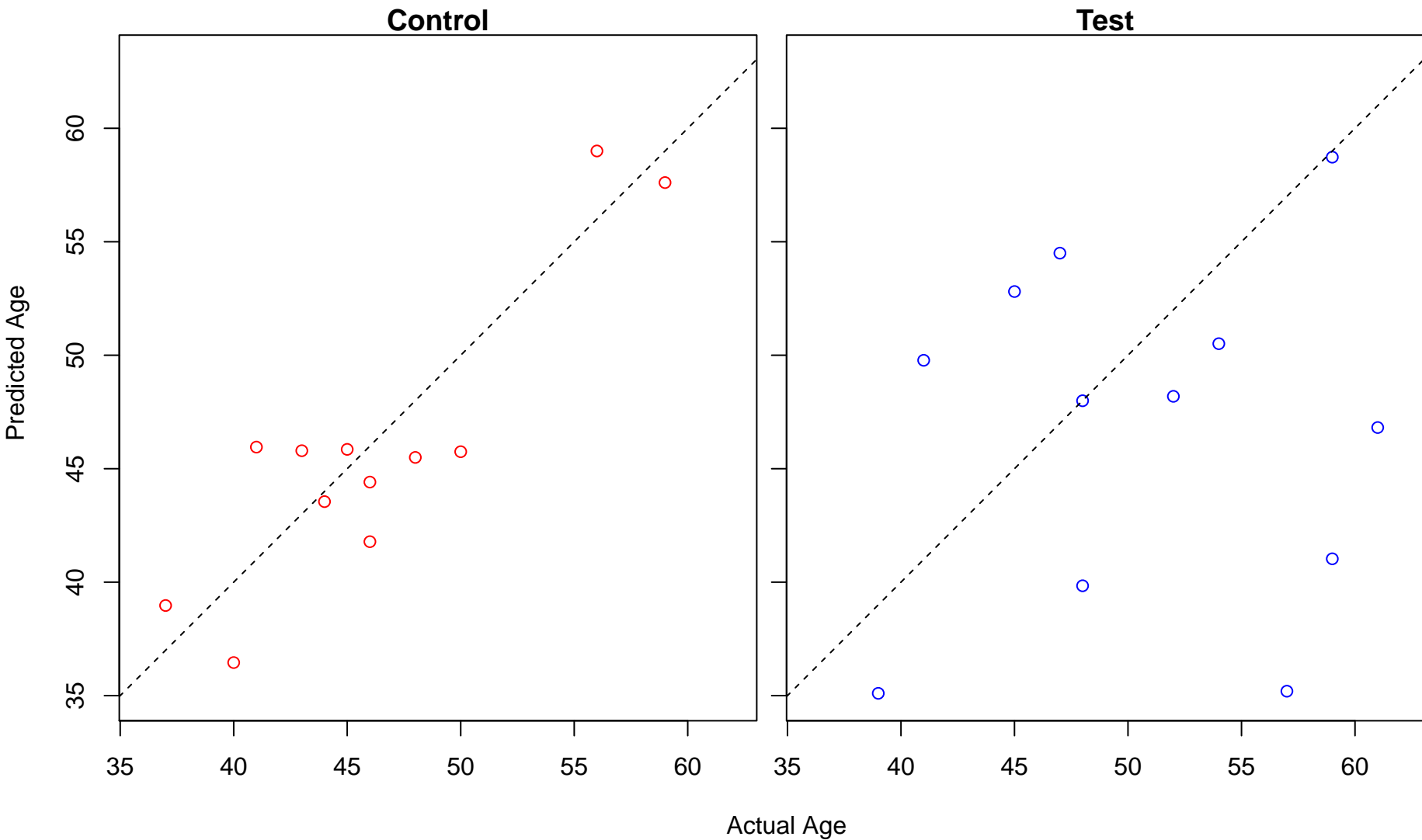


Actual Age

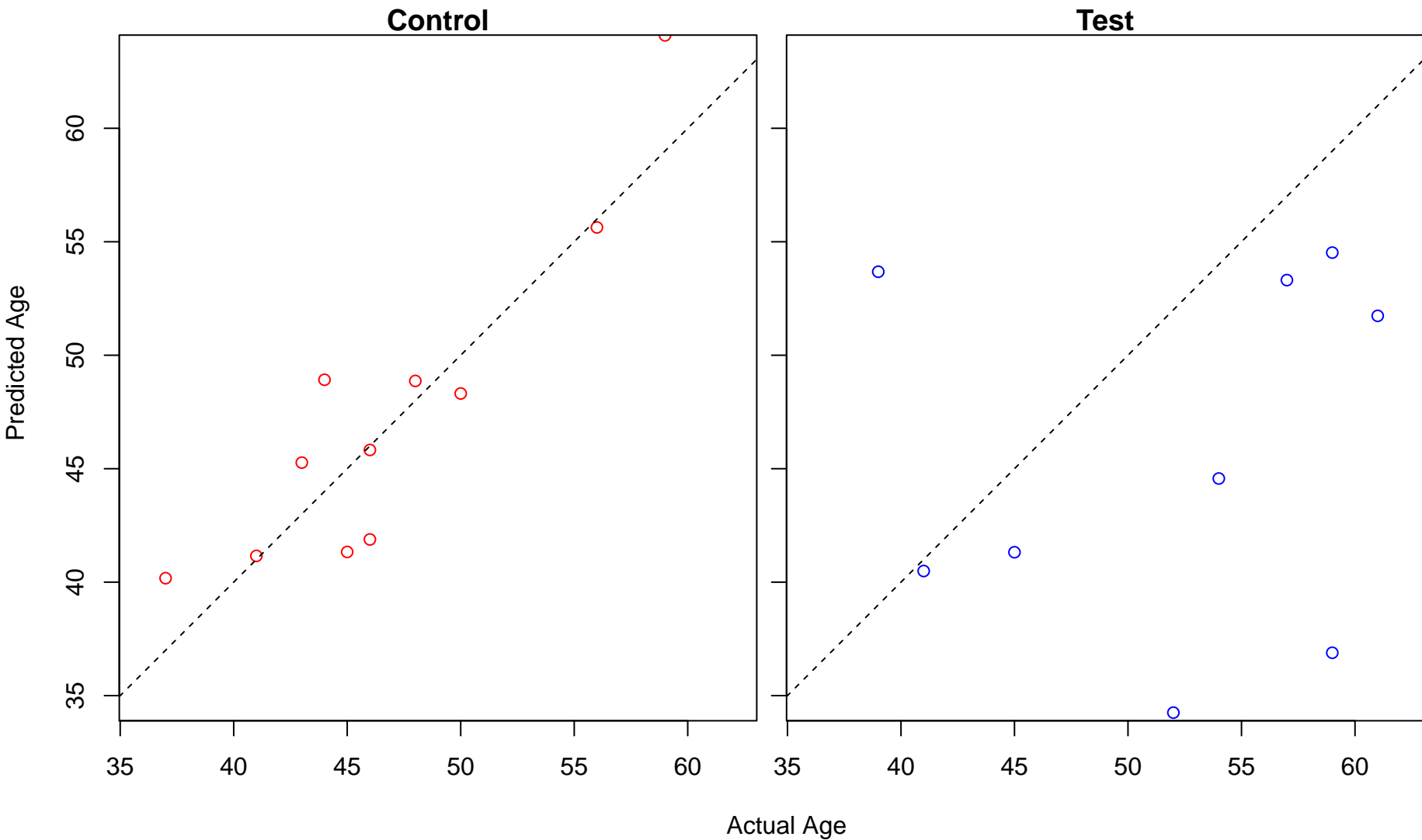
necrotic cell death (Score: 9.071250)



lipoxin metabolic process (Score: 9.062493)

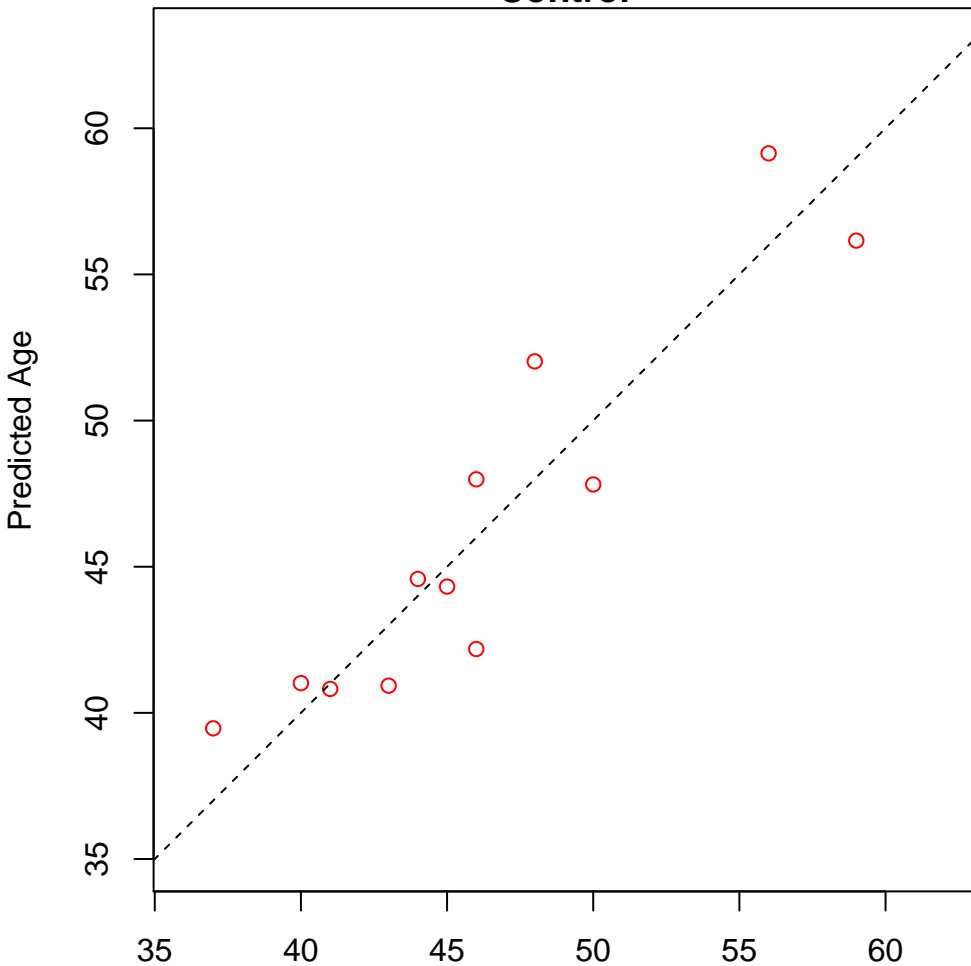


heart formation (Score: 9.031900)

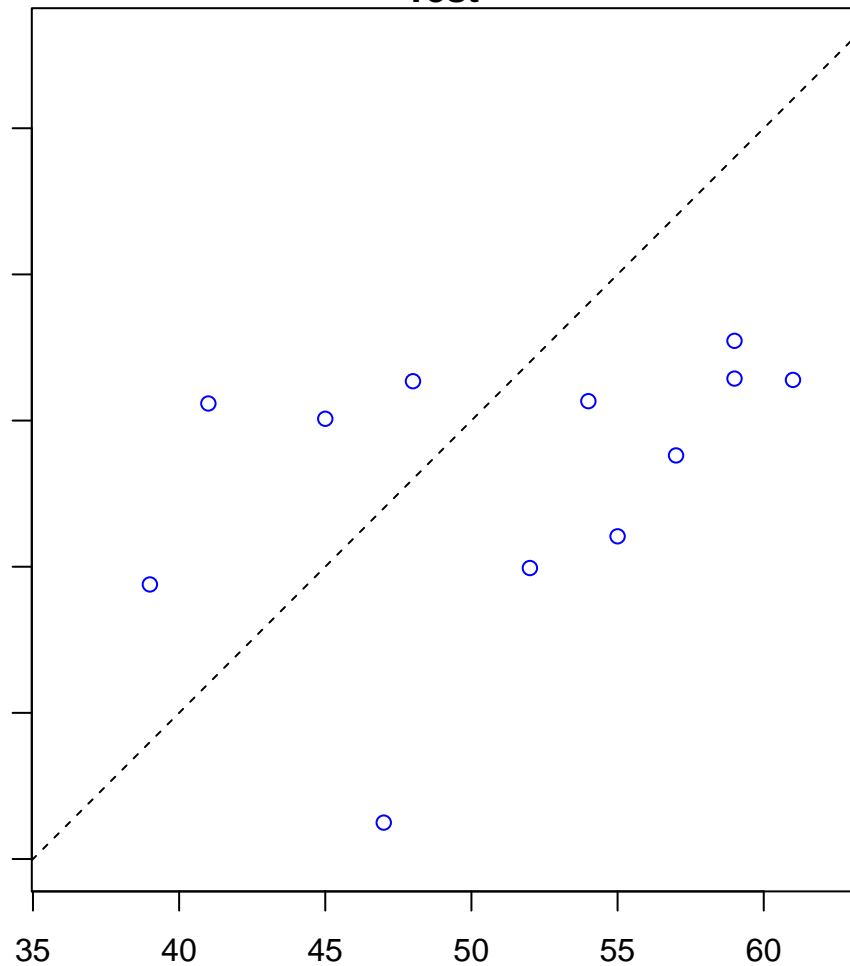


sulfur amino acid catabolic process (Score: 9.008666)

Control

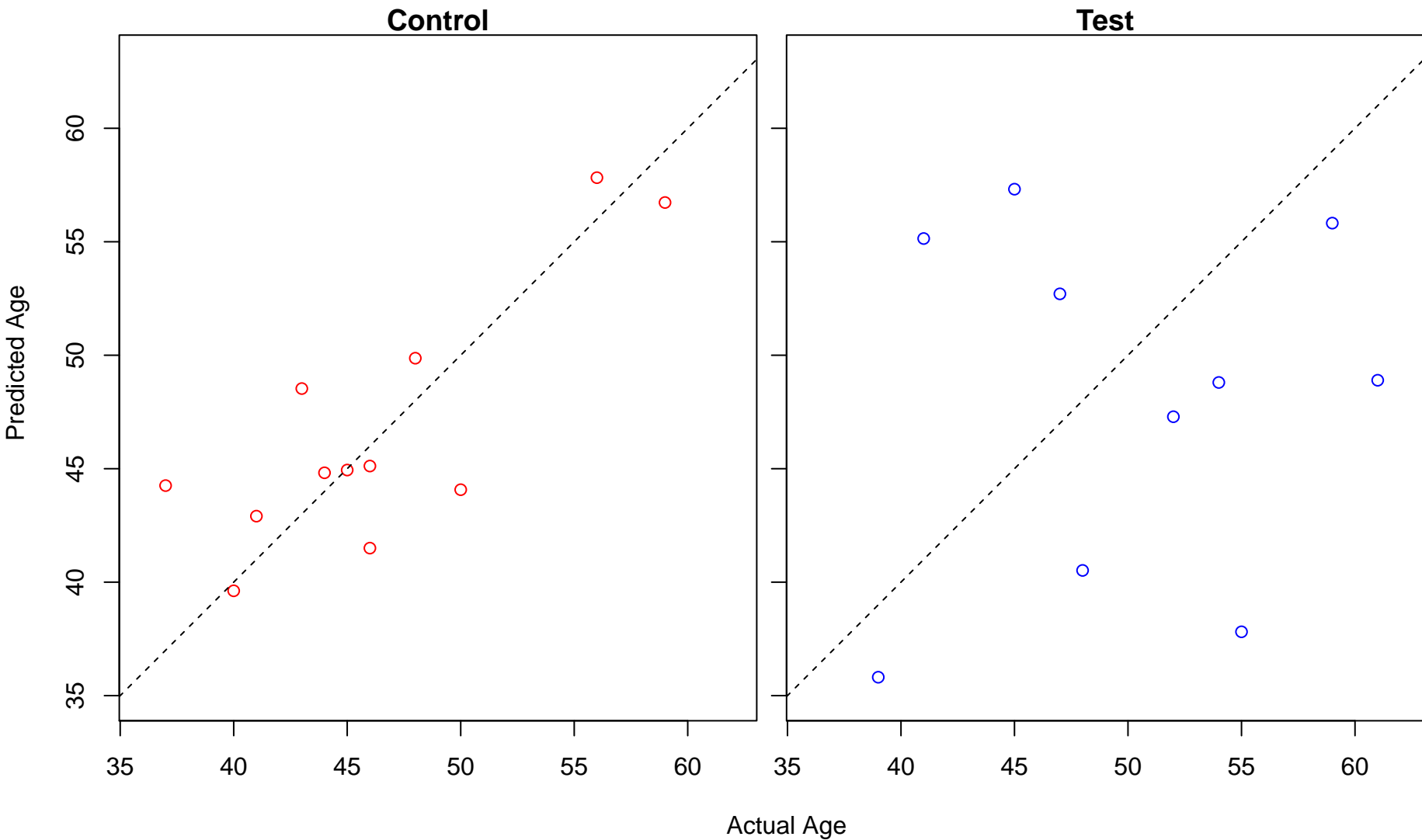


Test

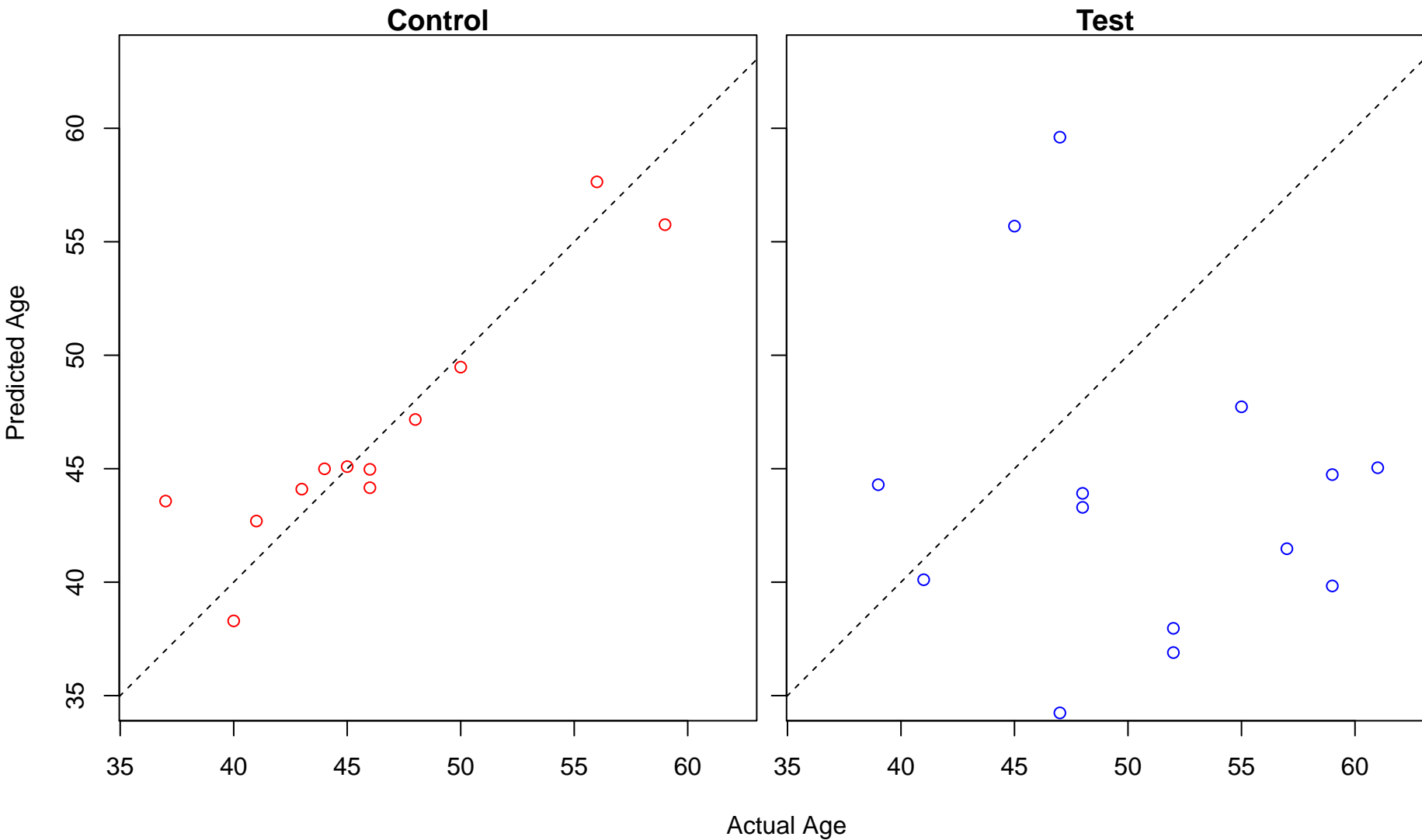


Actual Age

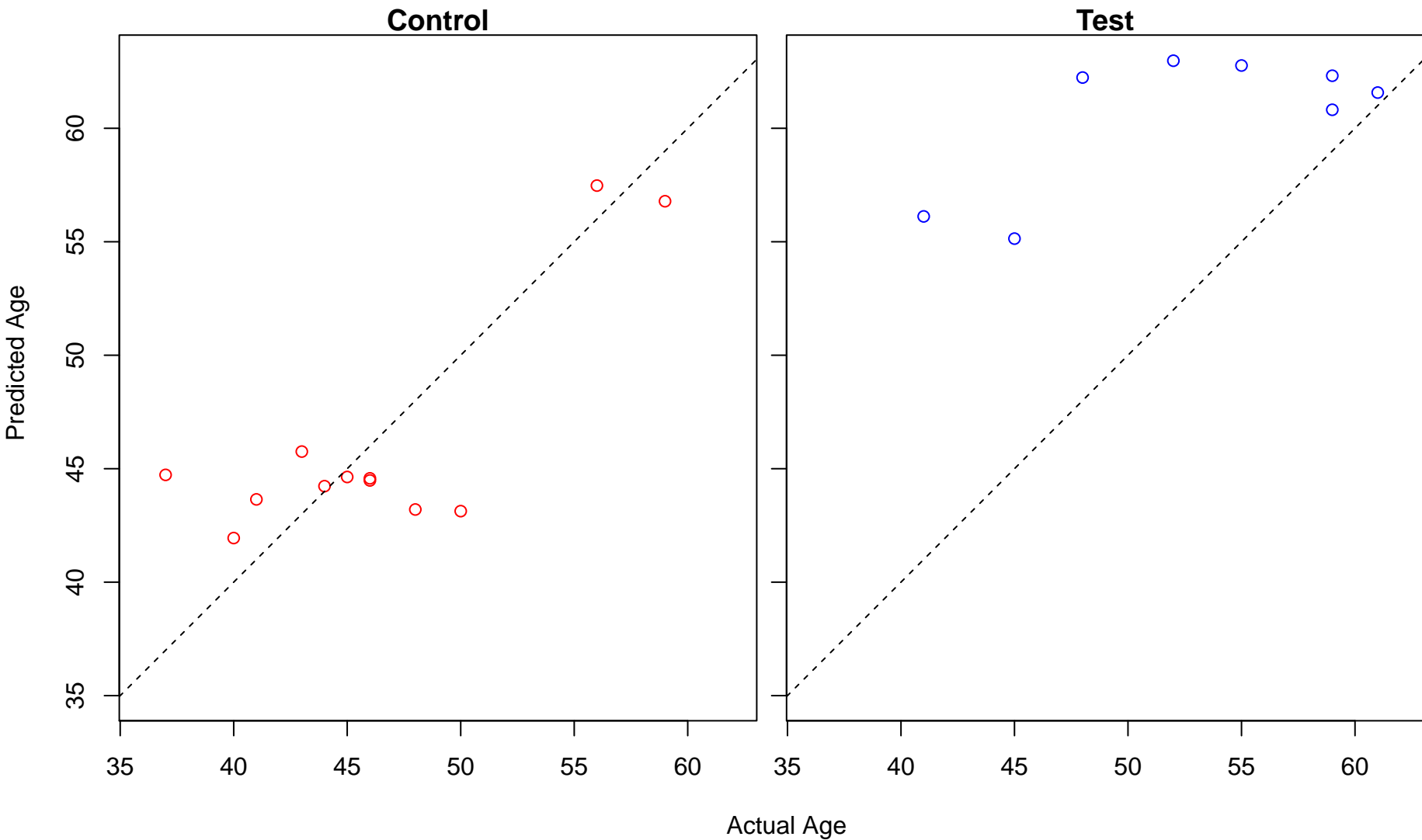
regulation of binding (Score: 8.985099)



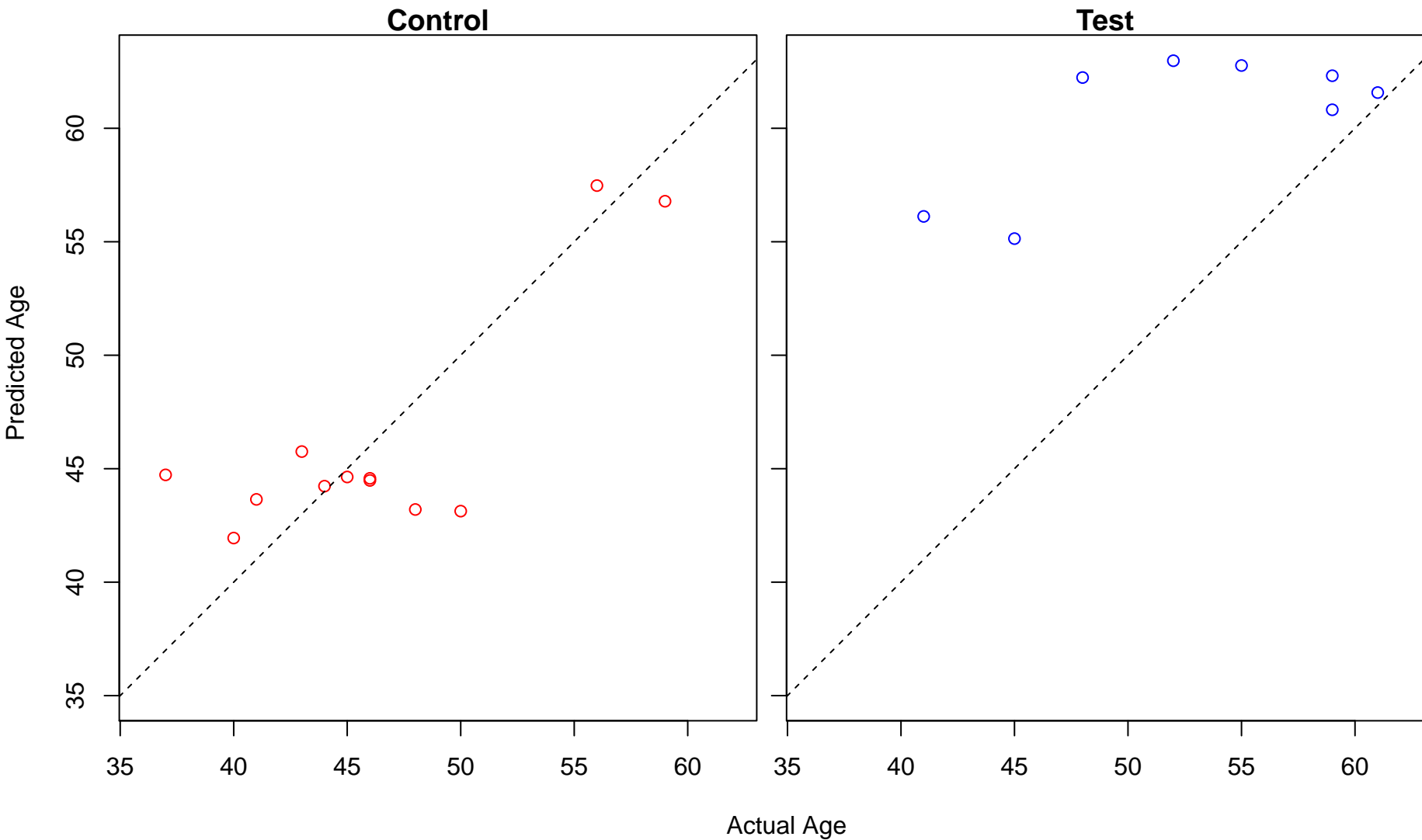
glycosyl compound catabolic process (Score: 8.976473)



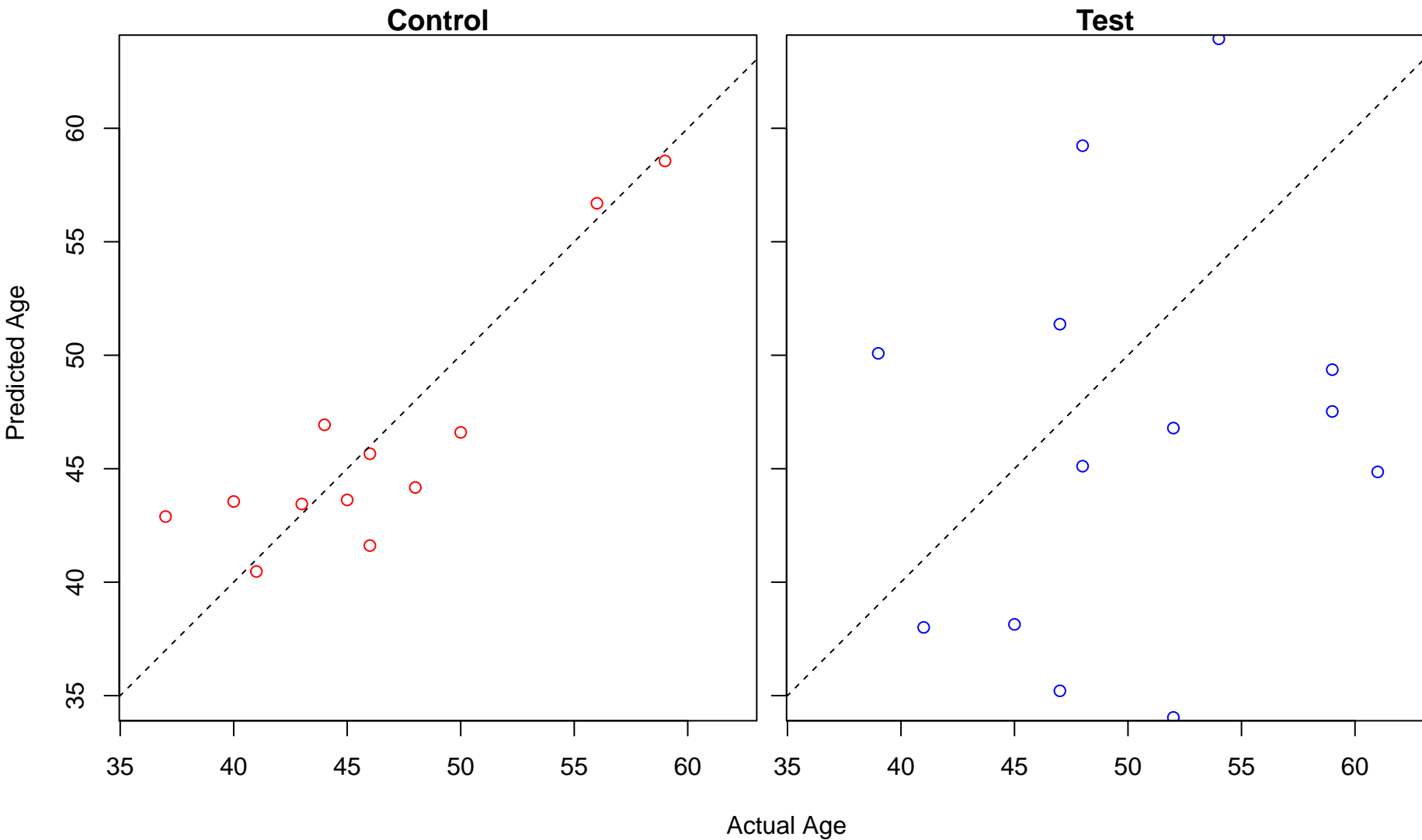
negative regulation of posttranscriptional gene silencing (Score: 8.972171)



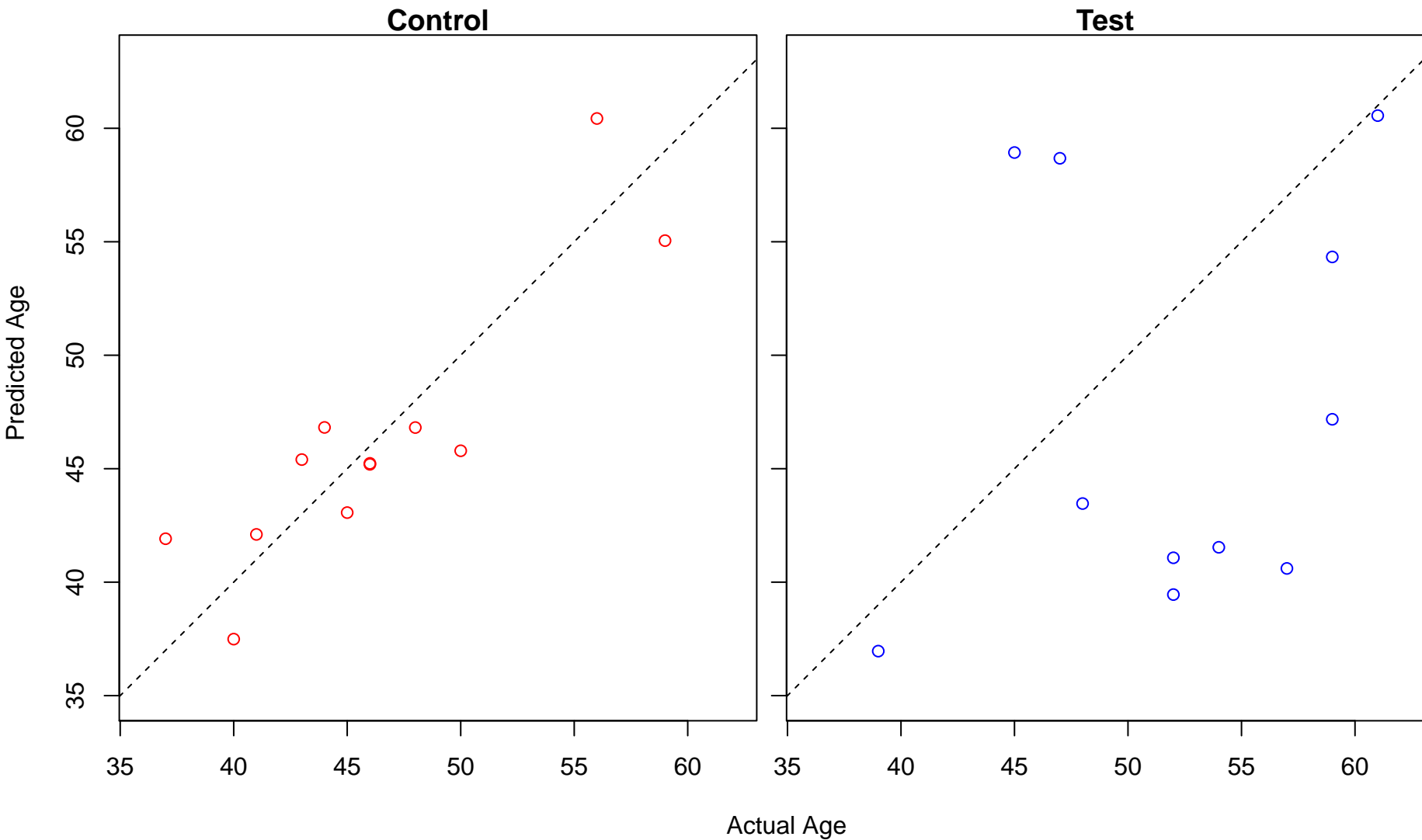
negative regulation of gene silencing by RNA (Score: 8.972171)



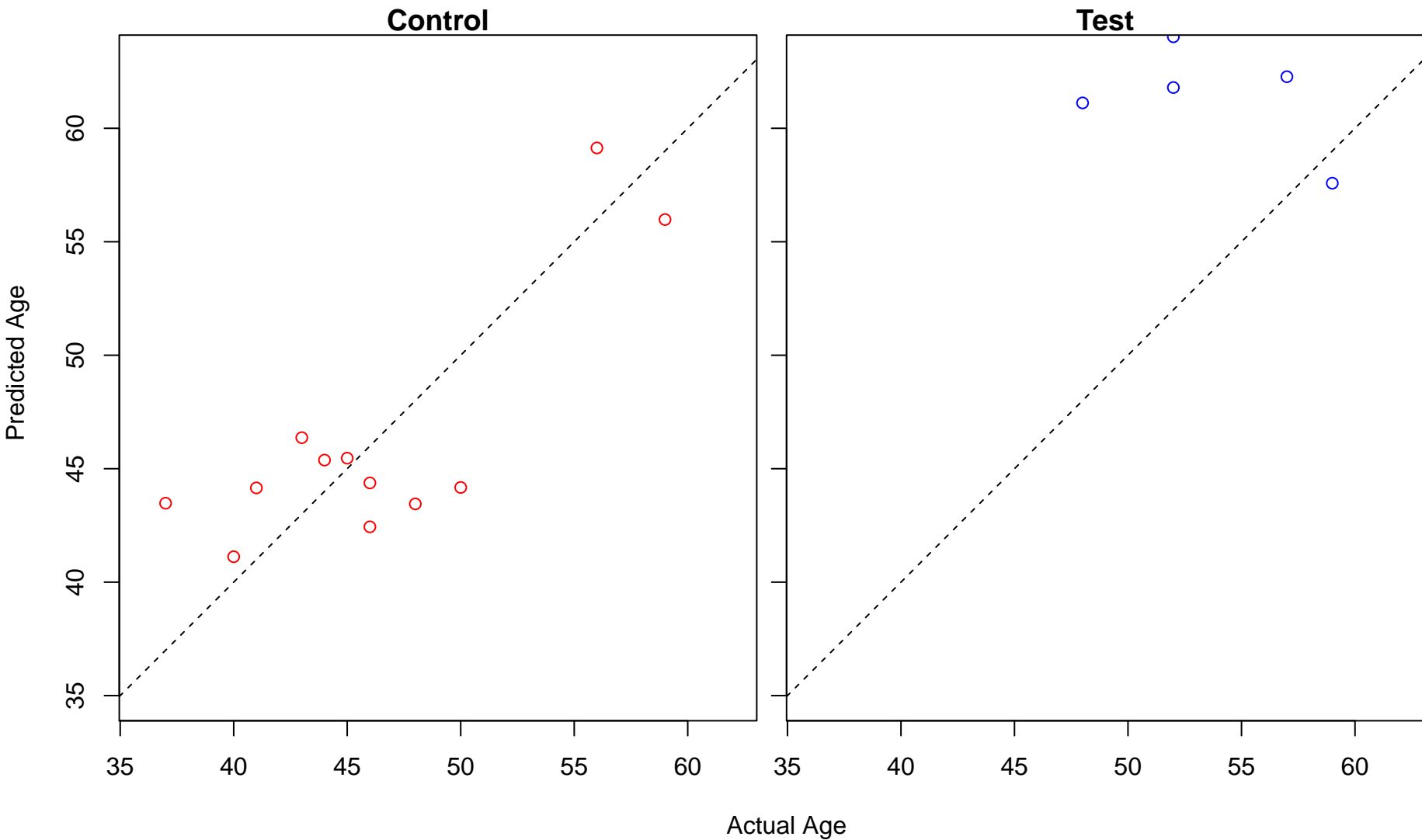
heart process (Score: 8.951575)



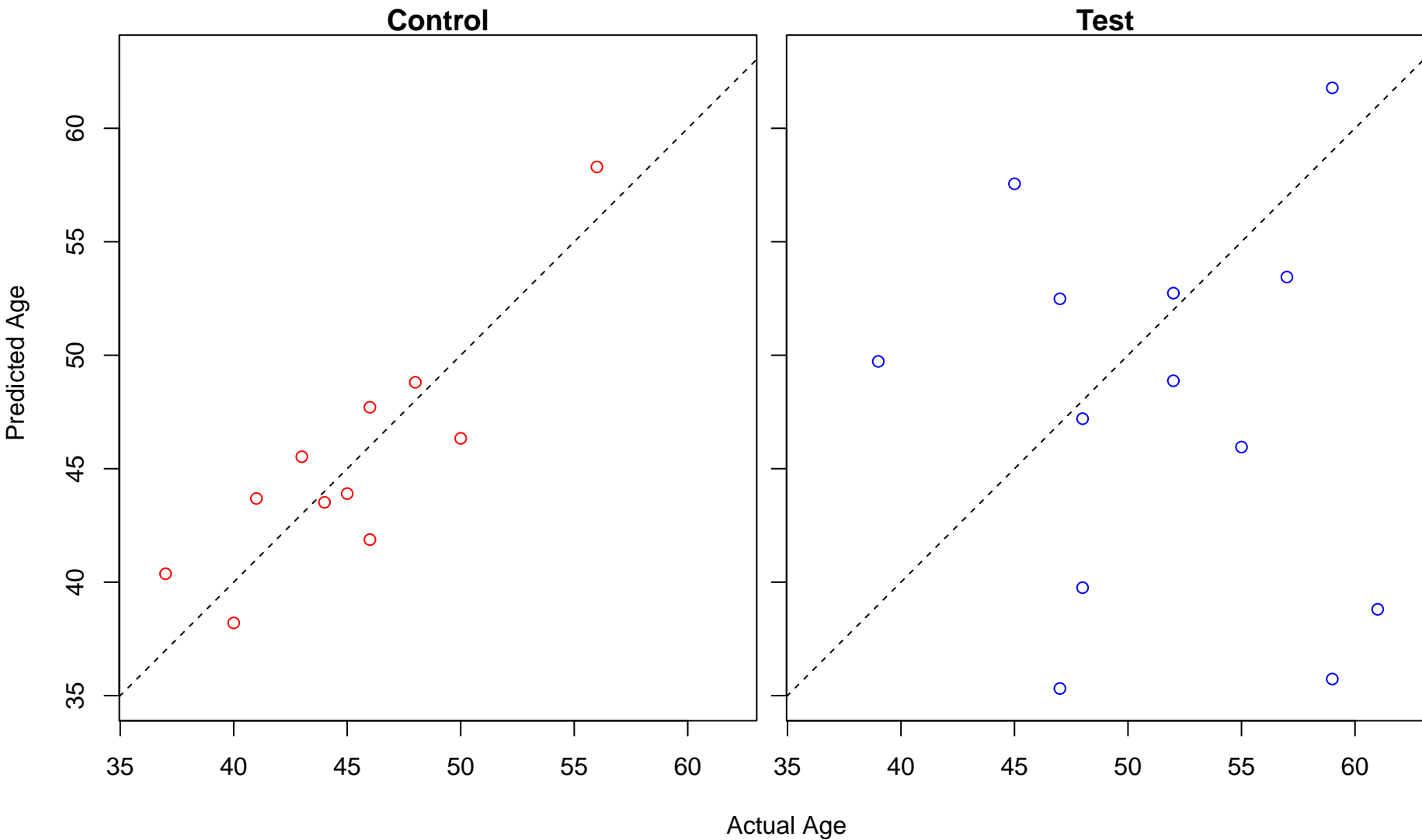
negative regulation of sequence-specific DNA binding transcription factor activity (Score: 8.94263)



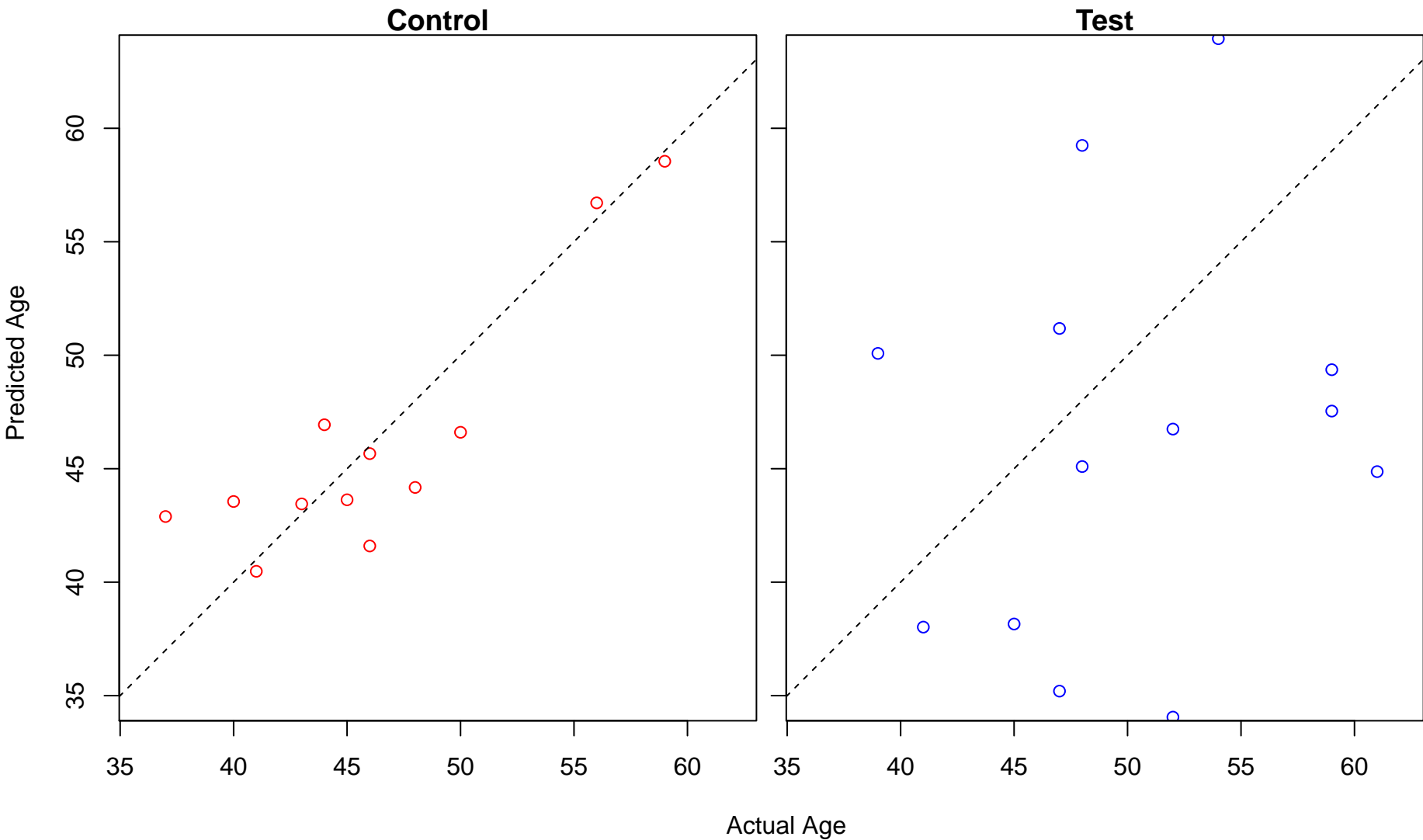
regulation of translational termination (Score: 8.938053)



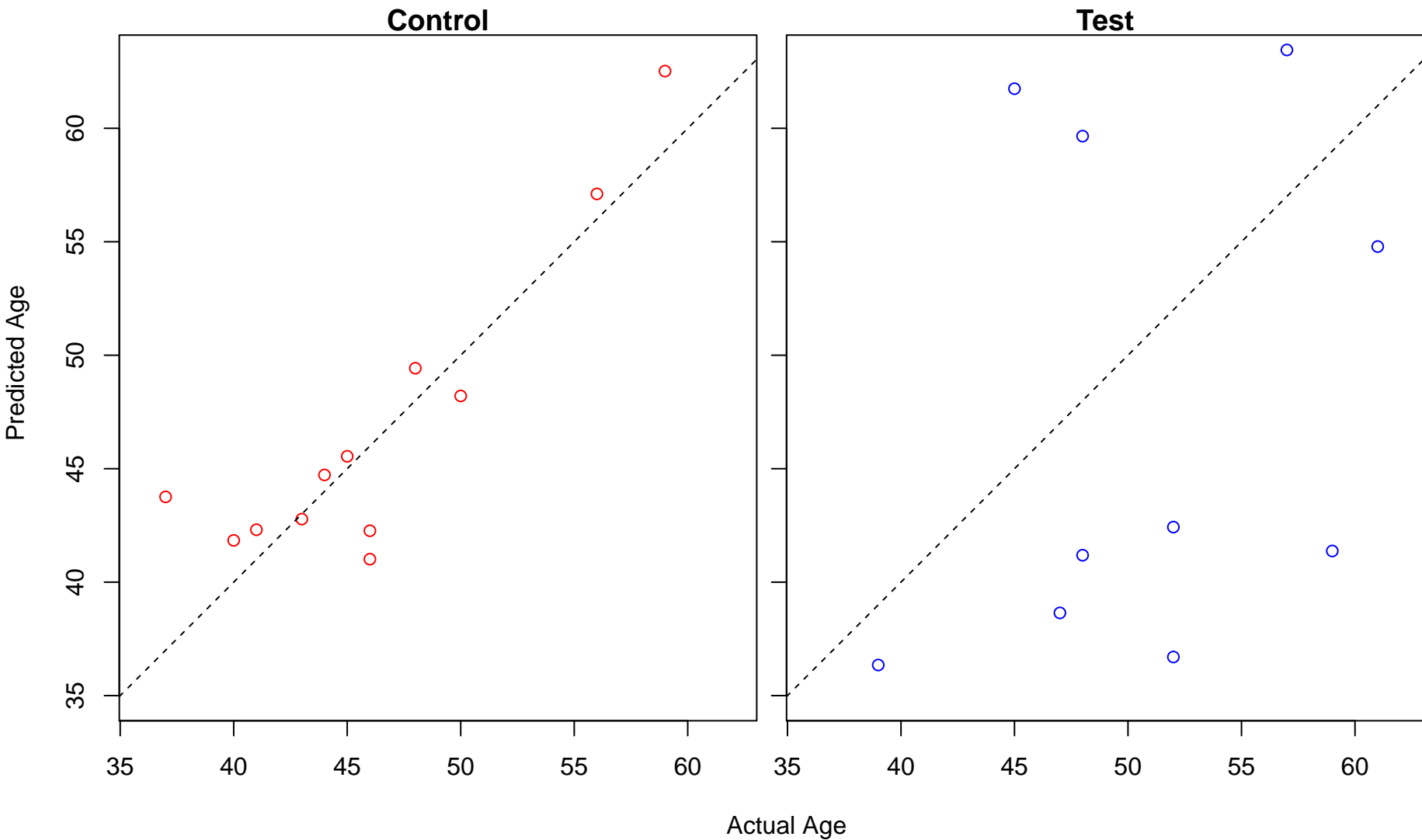
cellular response to alkaloid (Score: 8.933555)



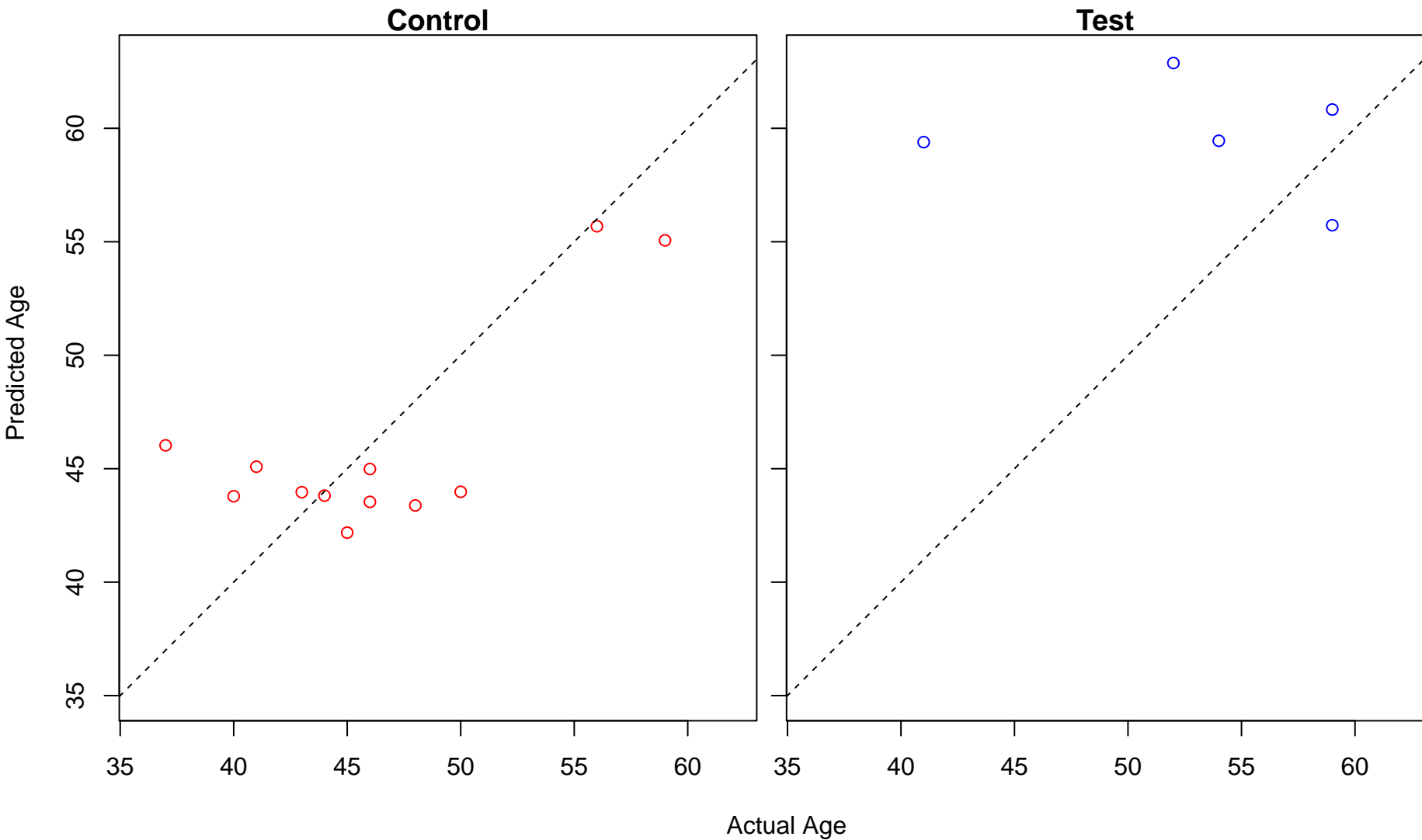
heart contraction (Score: 8.925391)



regulation of cellular ketone metabolic process (Score: 8.918797)

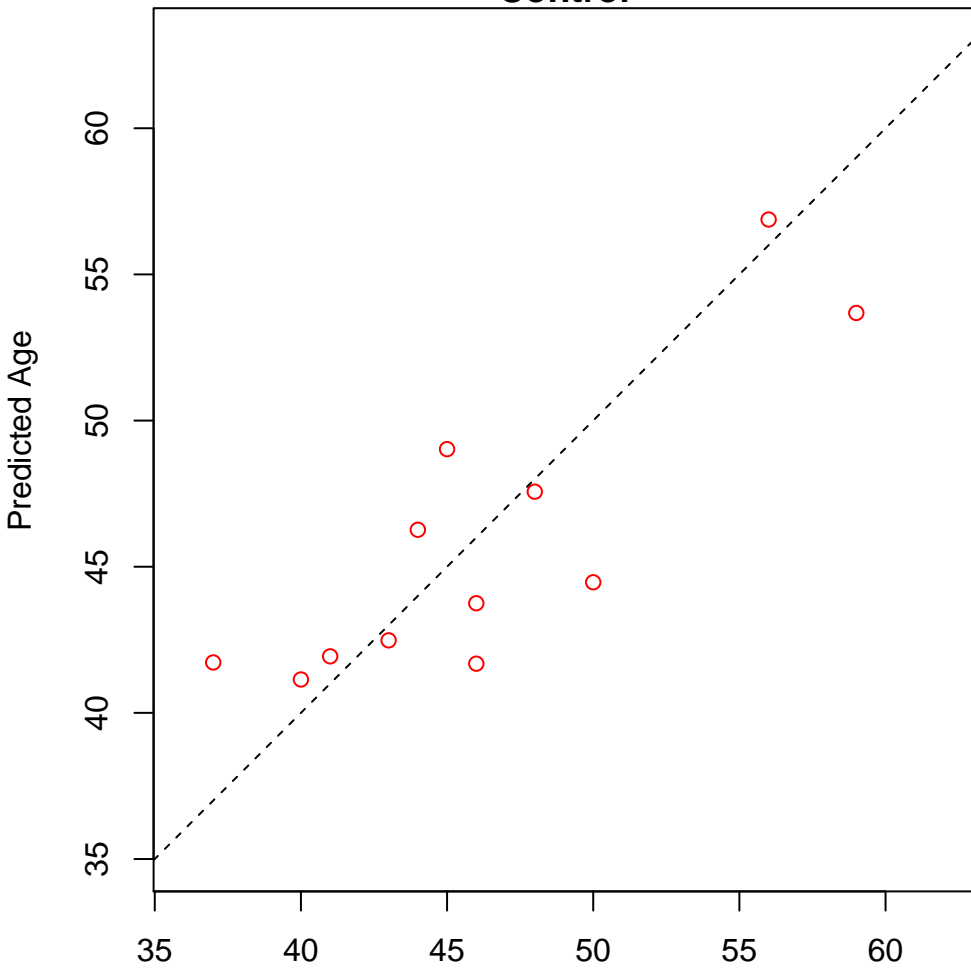


lateral ventricle development (Score: 8.913182)

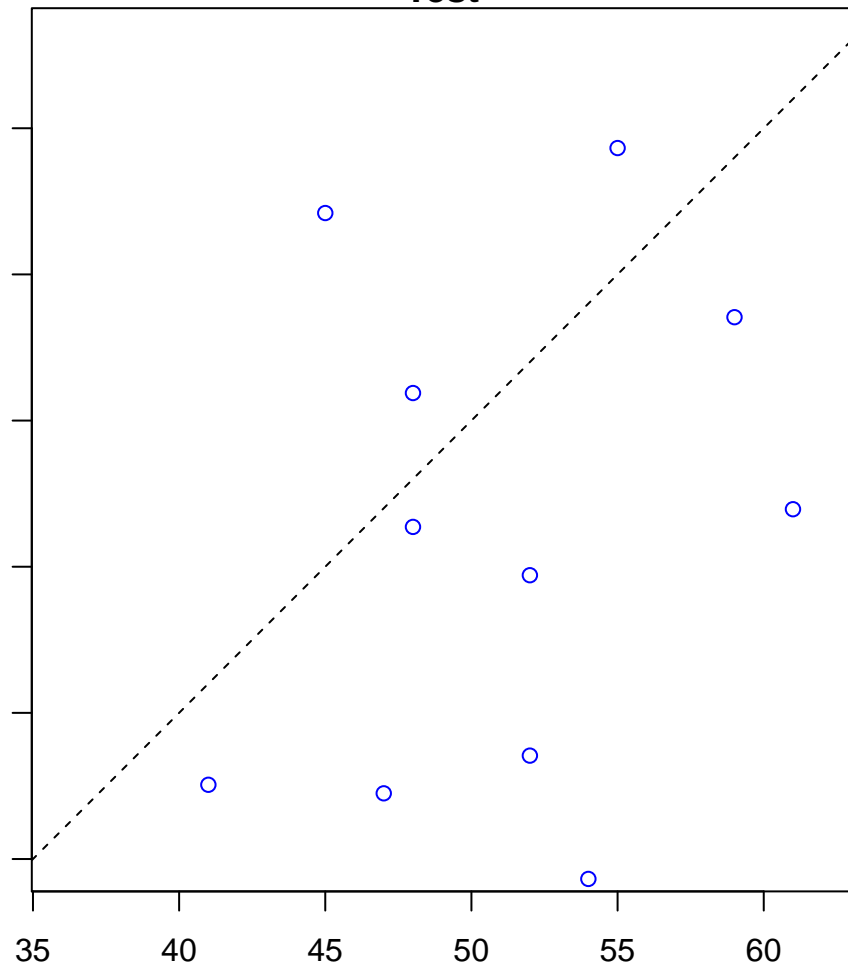


protein peptidyl–prolyl isomerization (Score: 8.910845)

Control

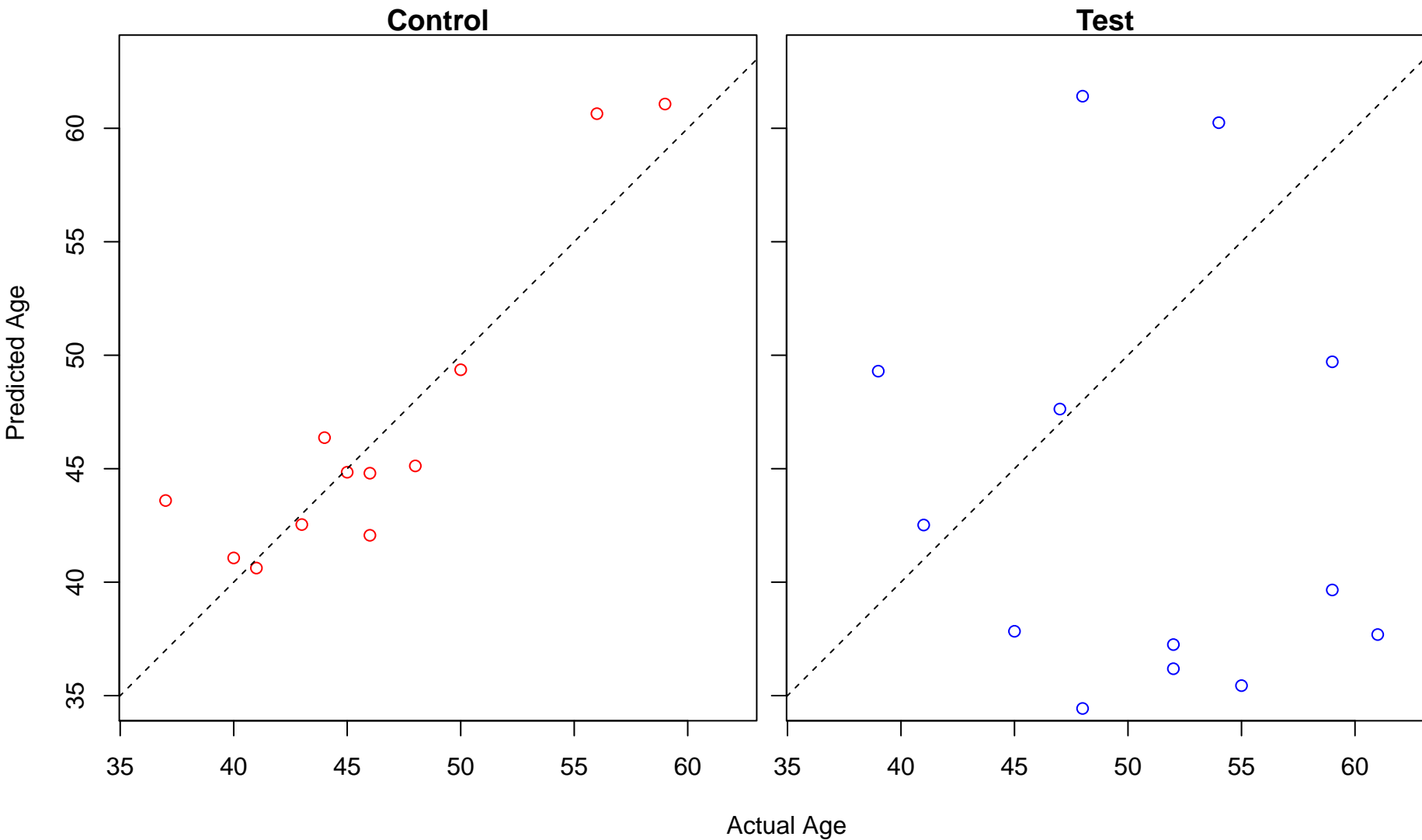


Test

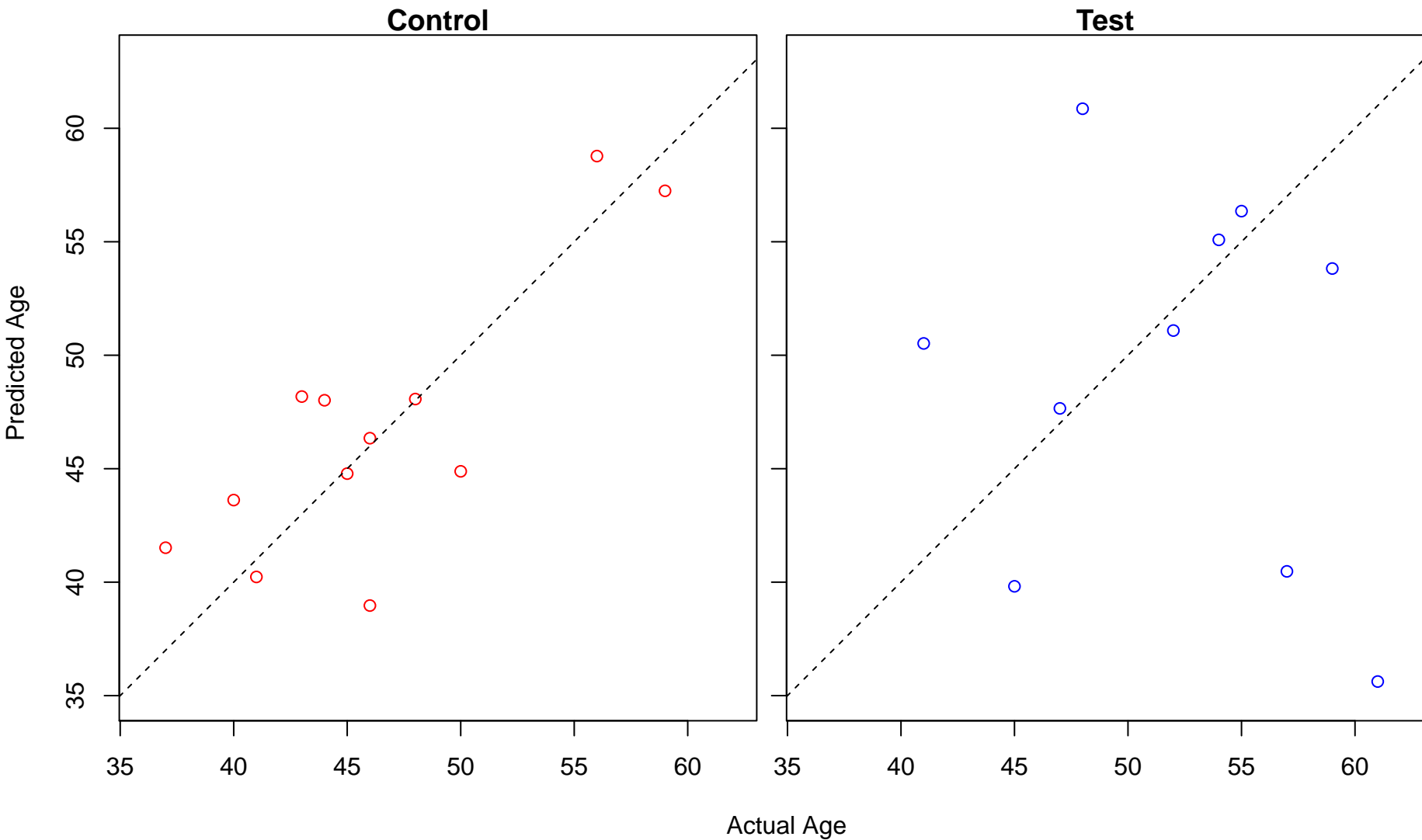


Actual Age

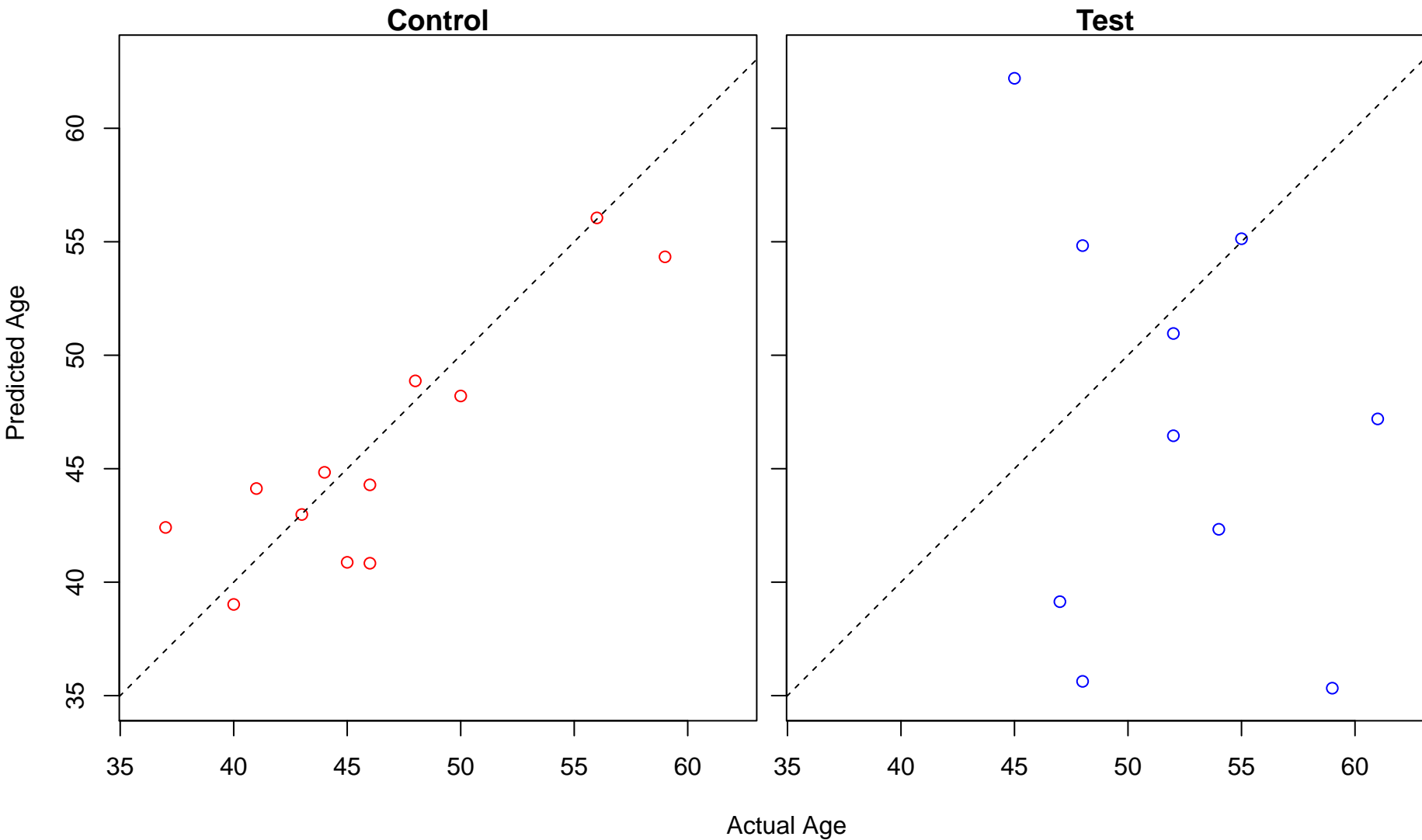
regulation of heart contraction (Score: 8.909617)



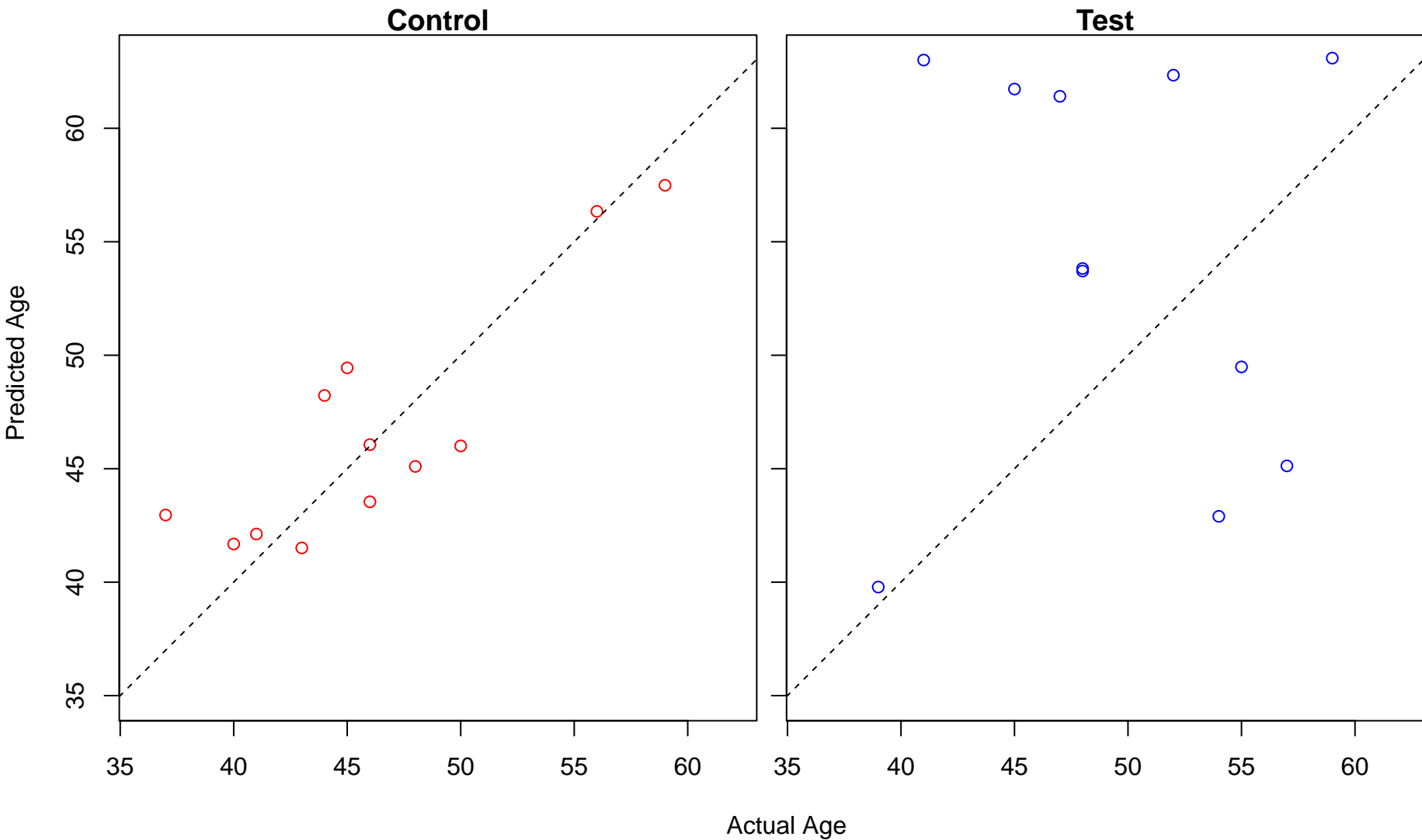
positive regulation of cyclin–dependent protein kinase activity (Score: 8.872876)



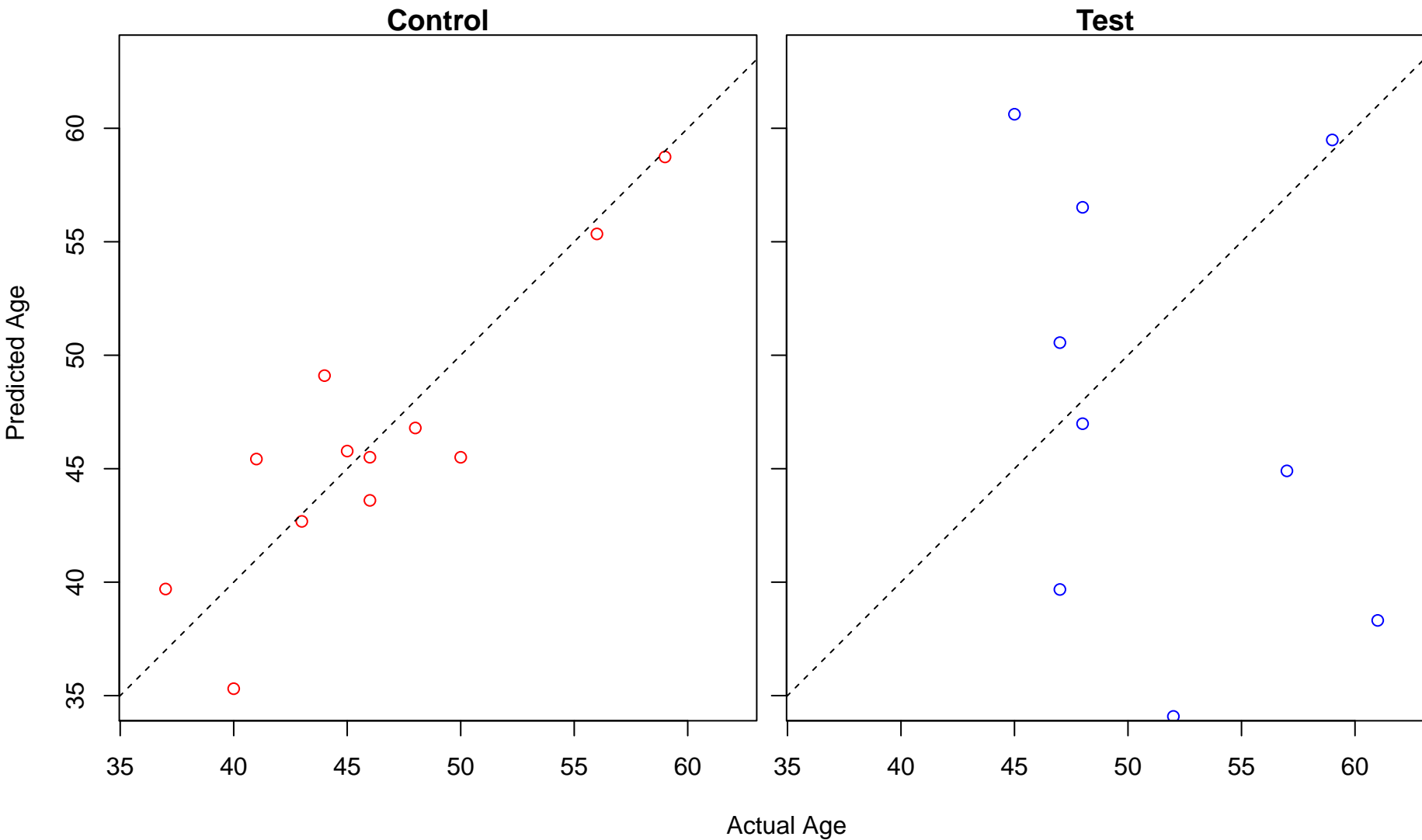
androgen metabolic process (Score: 8.871274)



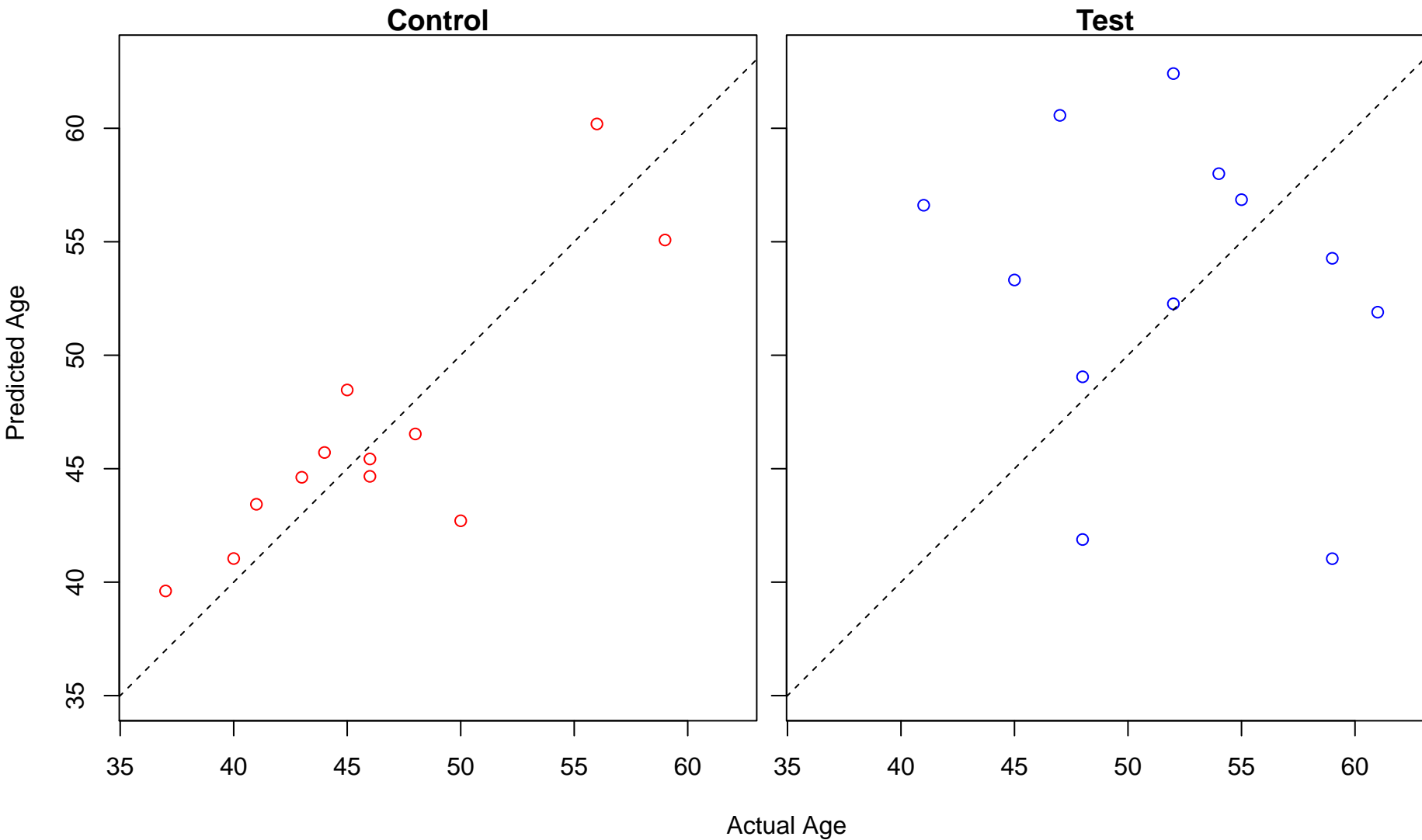
regulation of urine volume (Score: 8.849024)



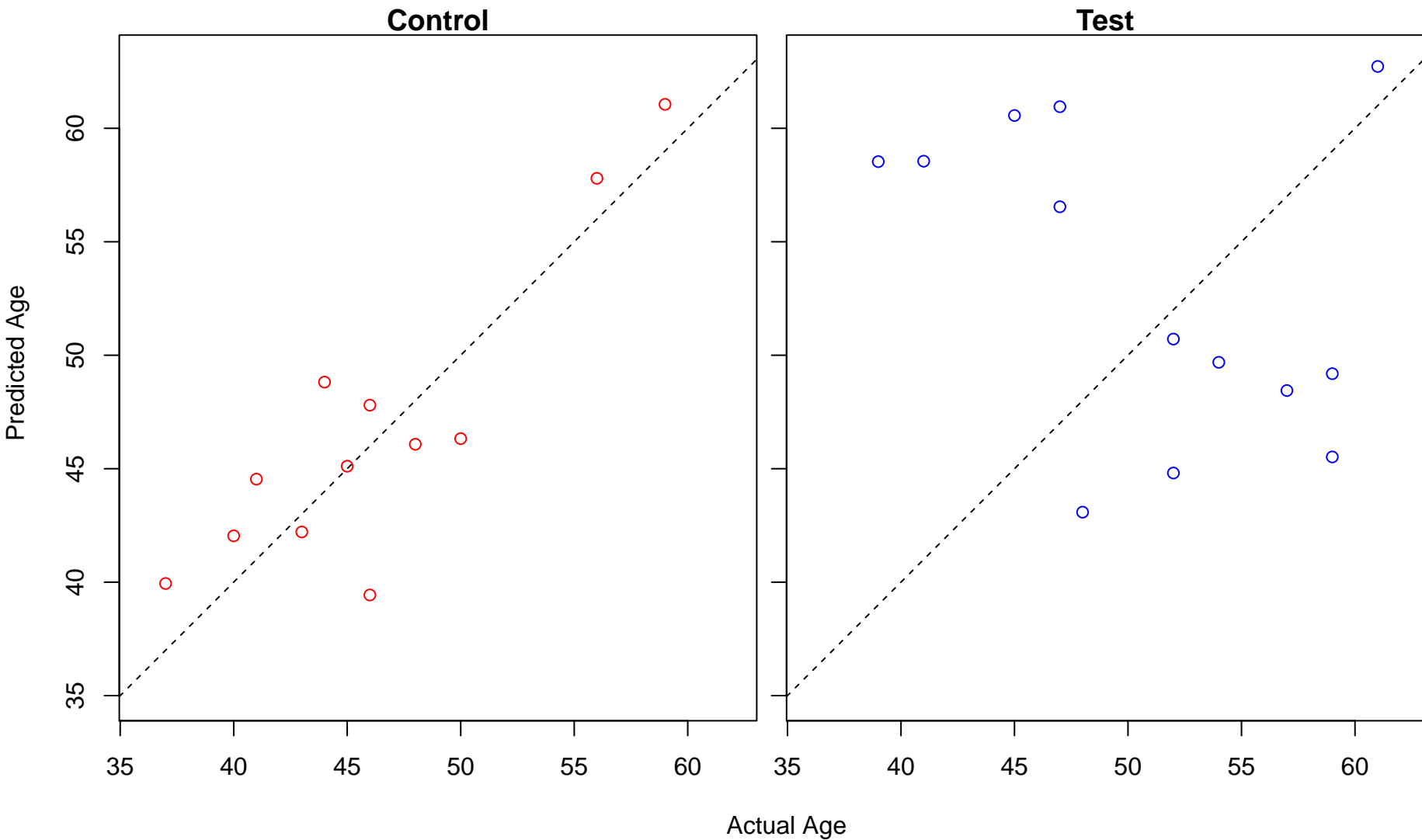
negative regulation of endocytosis (Score: 8.841412)



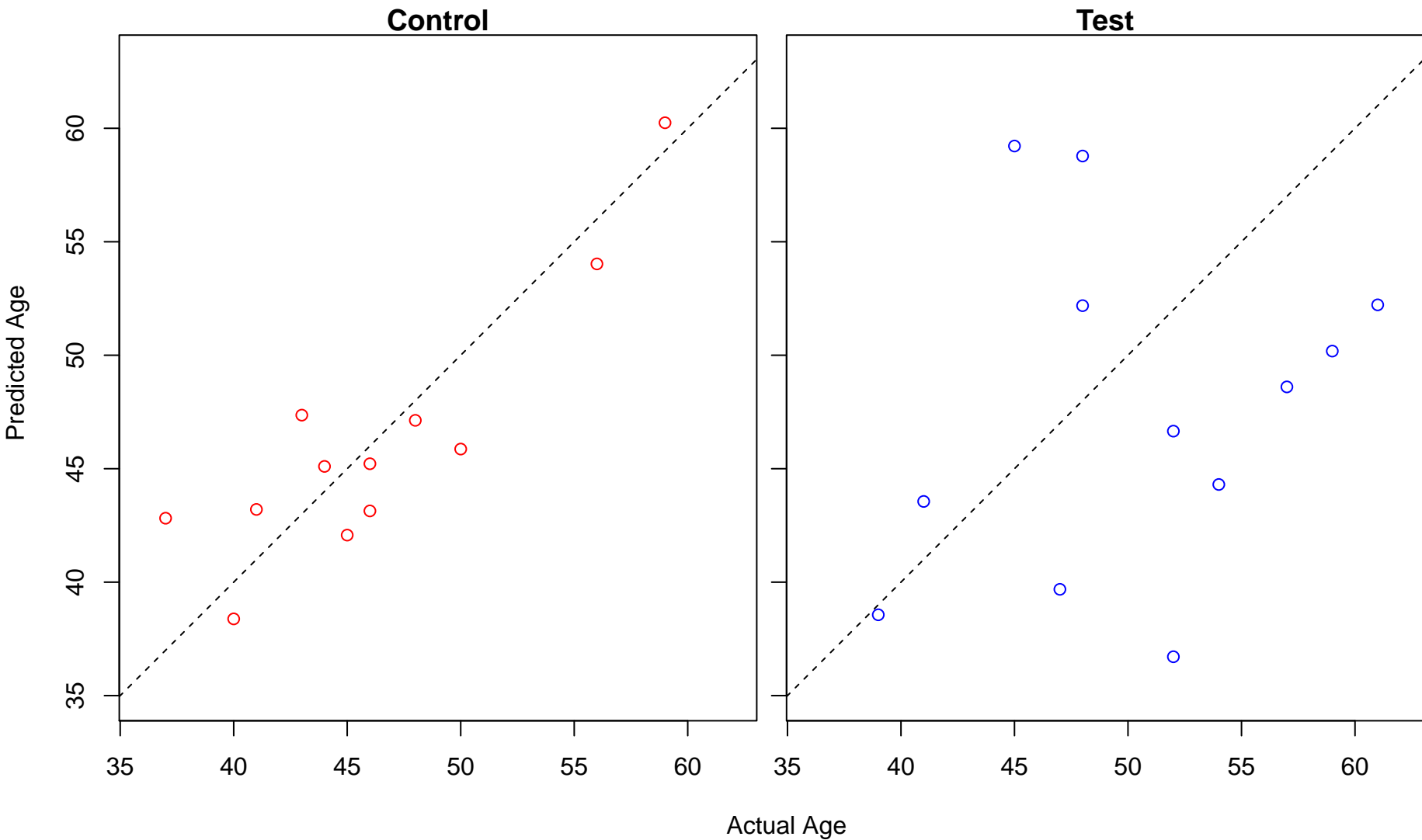
regulation of CD8-positive, alpha-beta T cell activation (Score: 8.828660)



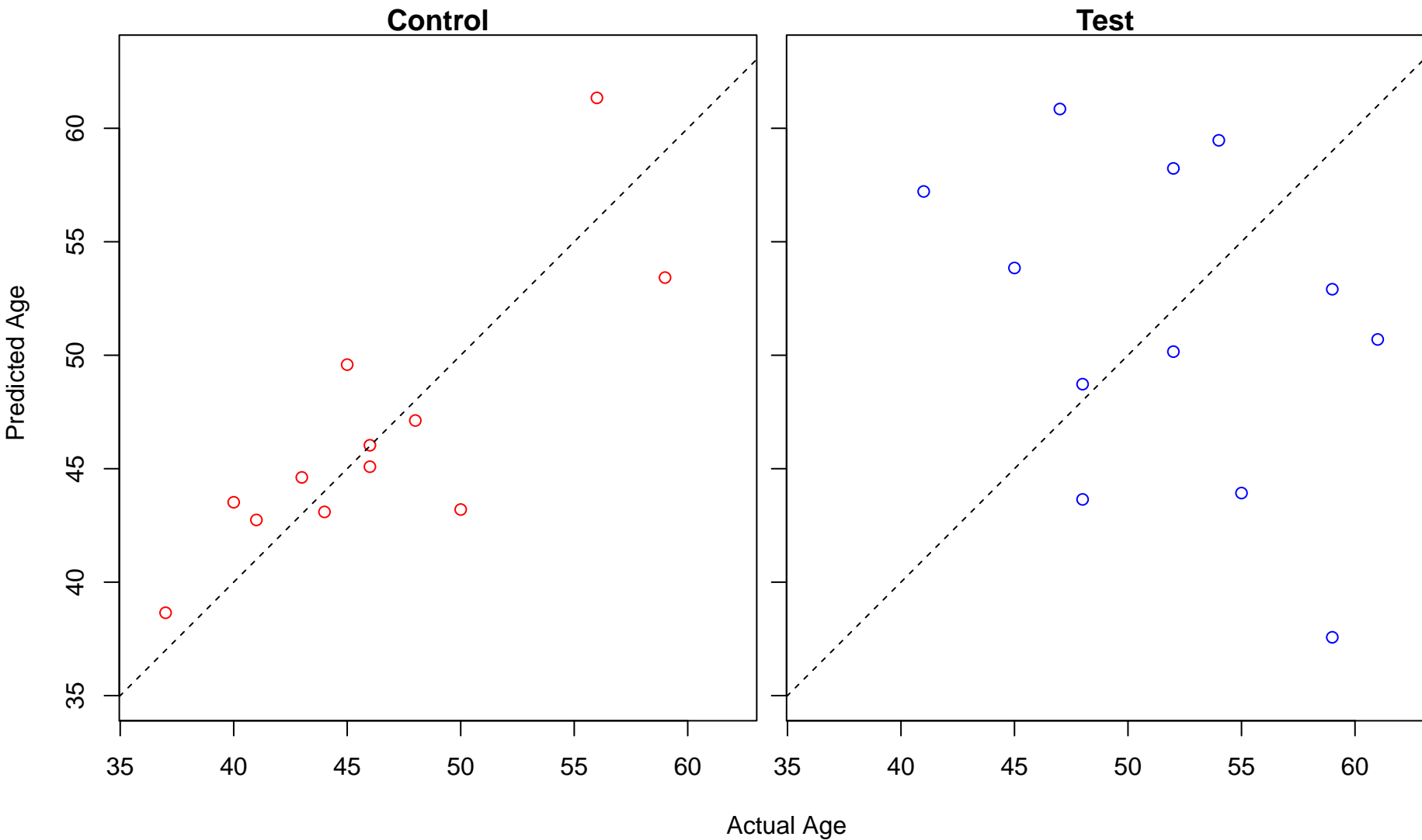
protein folding (Score: 8.812729)



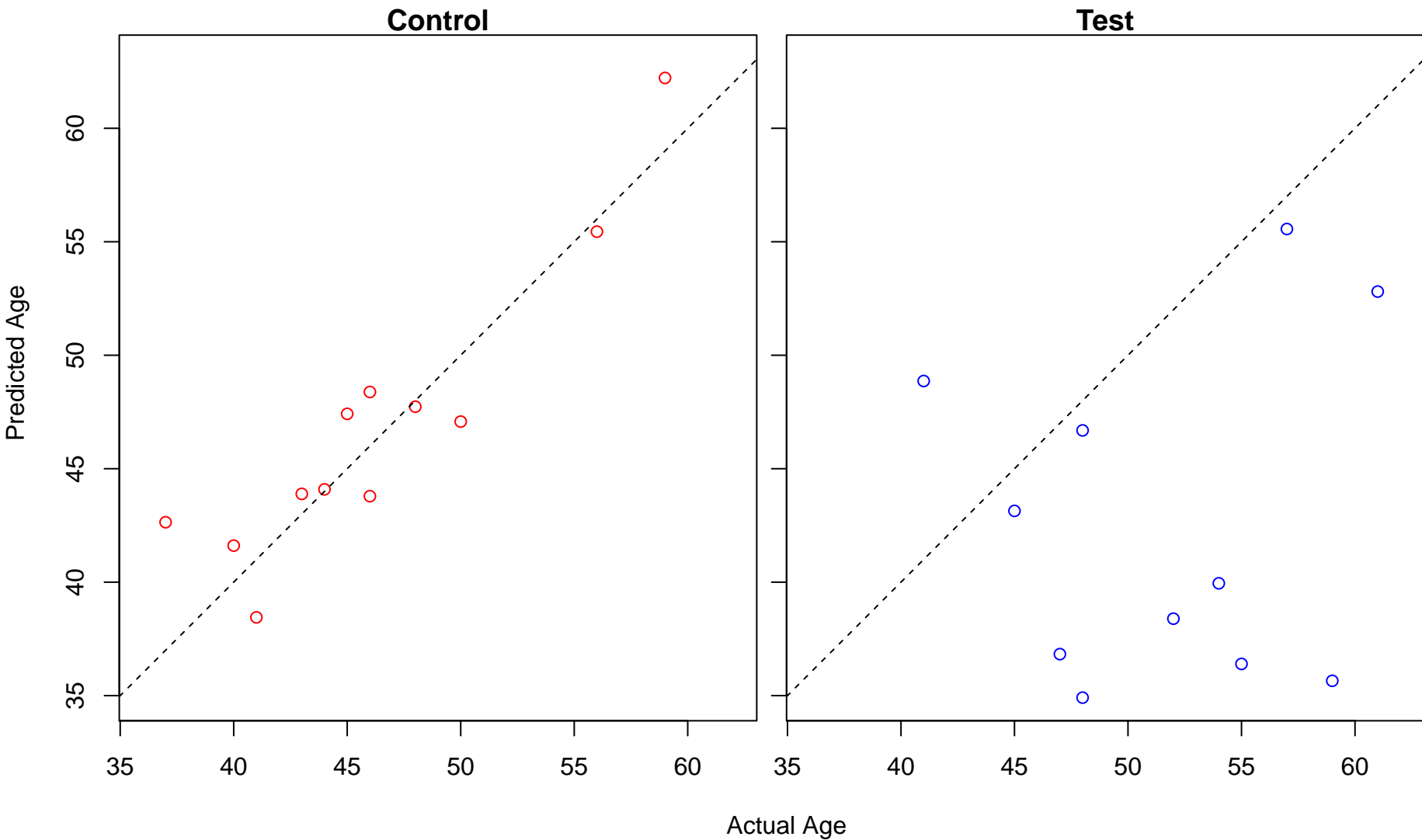
regulation of endopeptidase activity (Score: 8.807391)



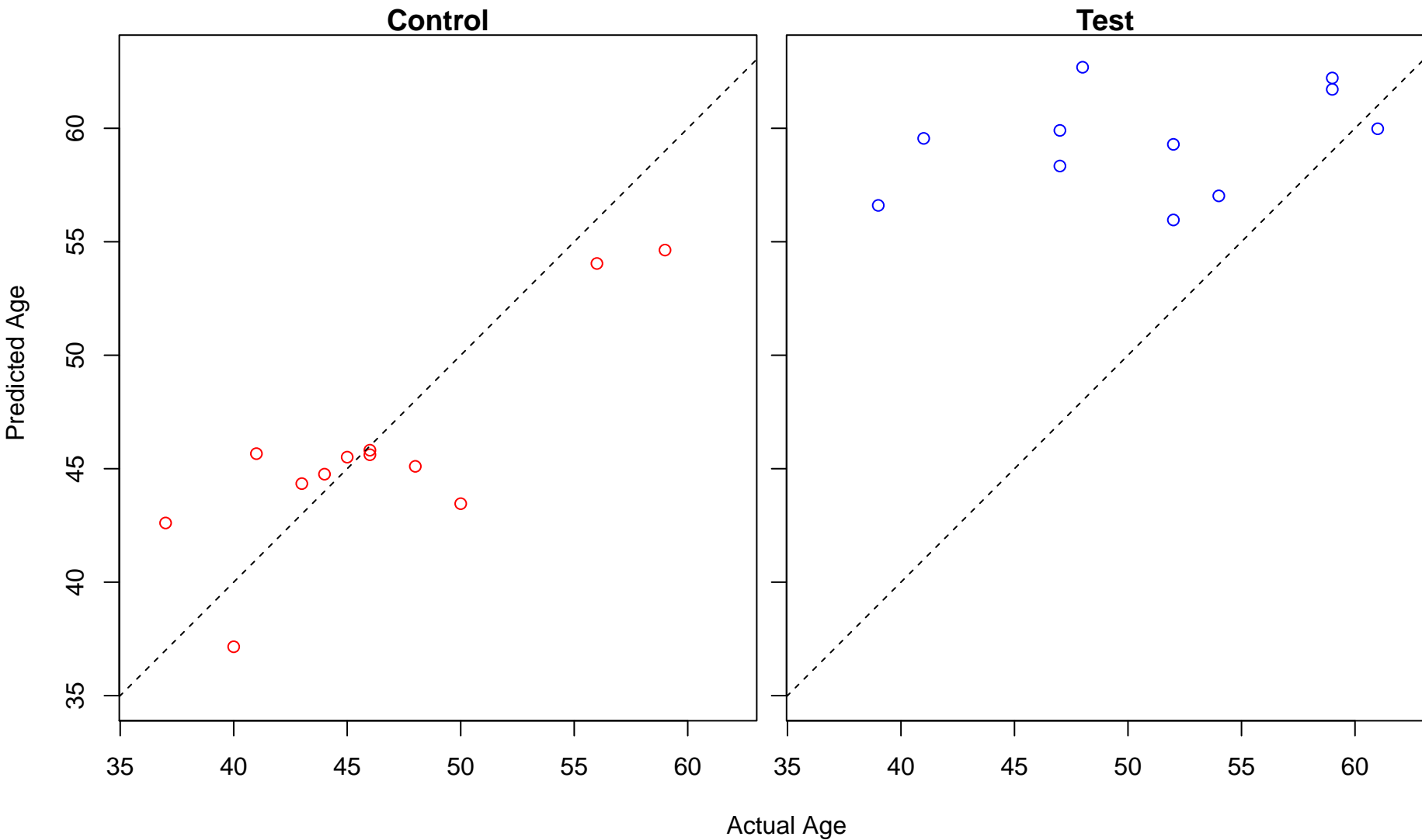
regulation of alpha-beta T cell proliferation (Score: 8.794232)



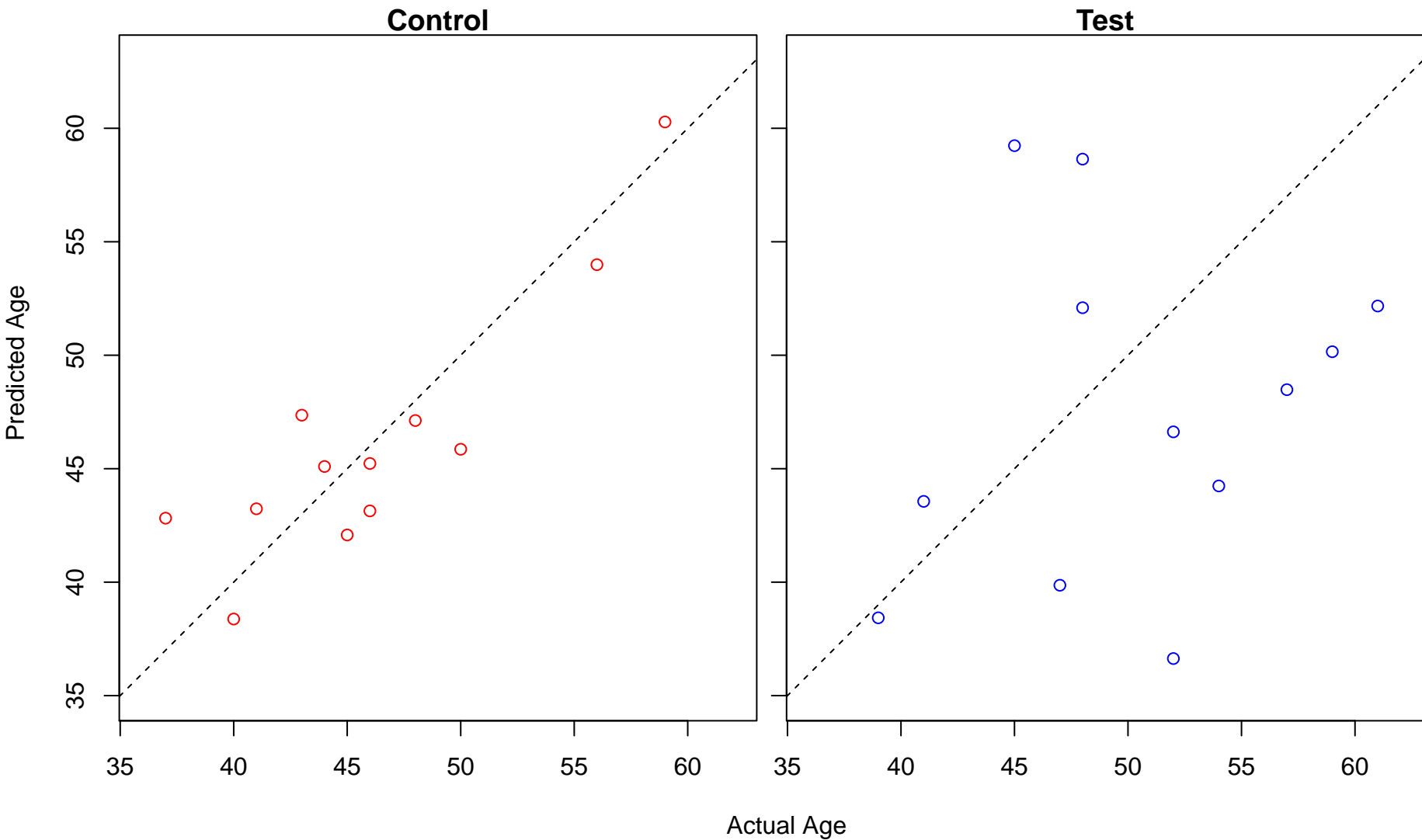
regulation of adherens junction organization (Score: 8.791839)



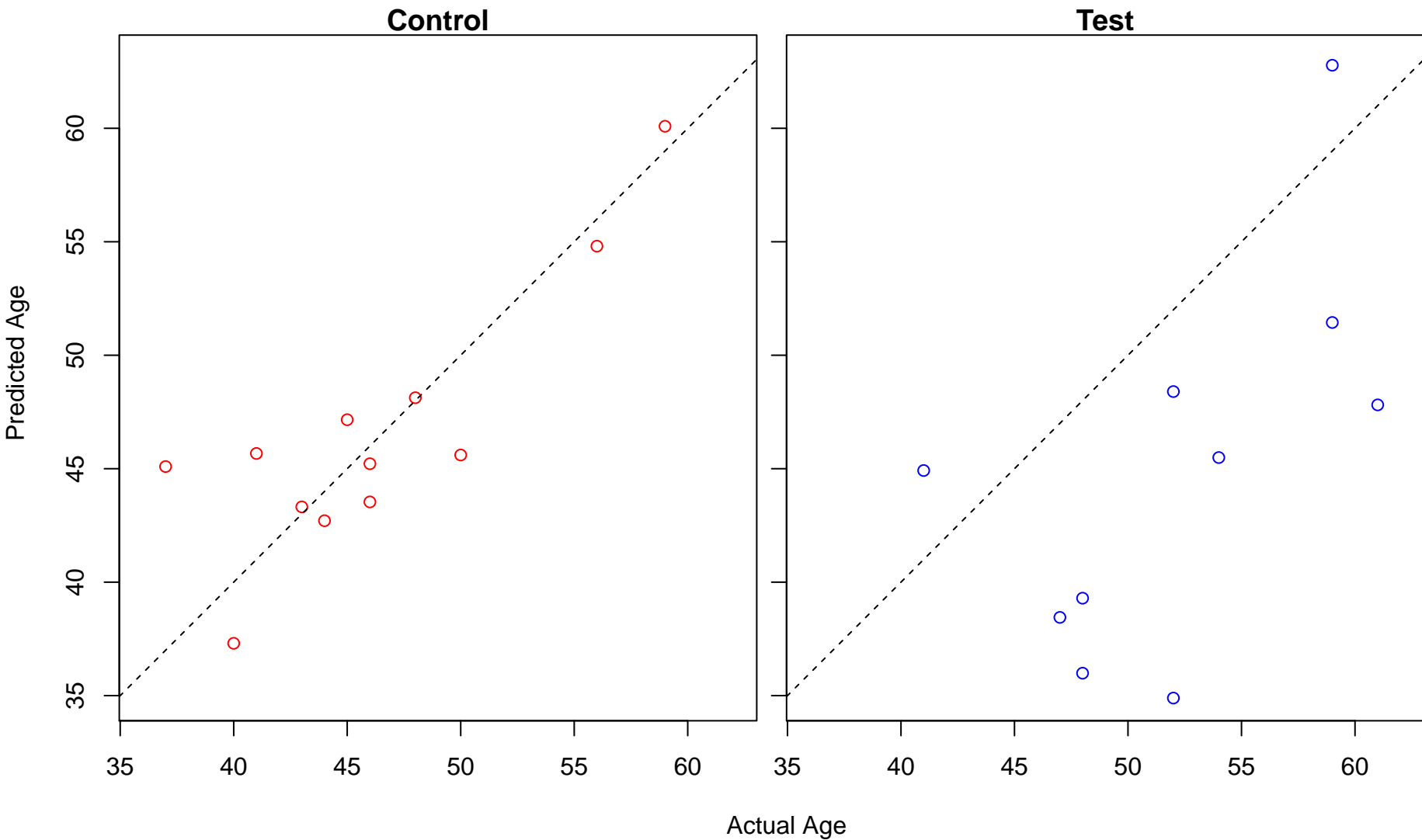
regulation of activation of Janus kinase activity (Score: 8.787582)



regulation of peptidase activity (Score: 8.784709)

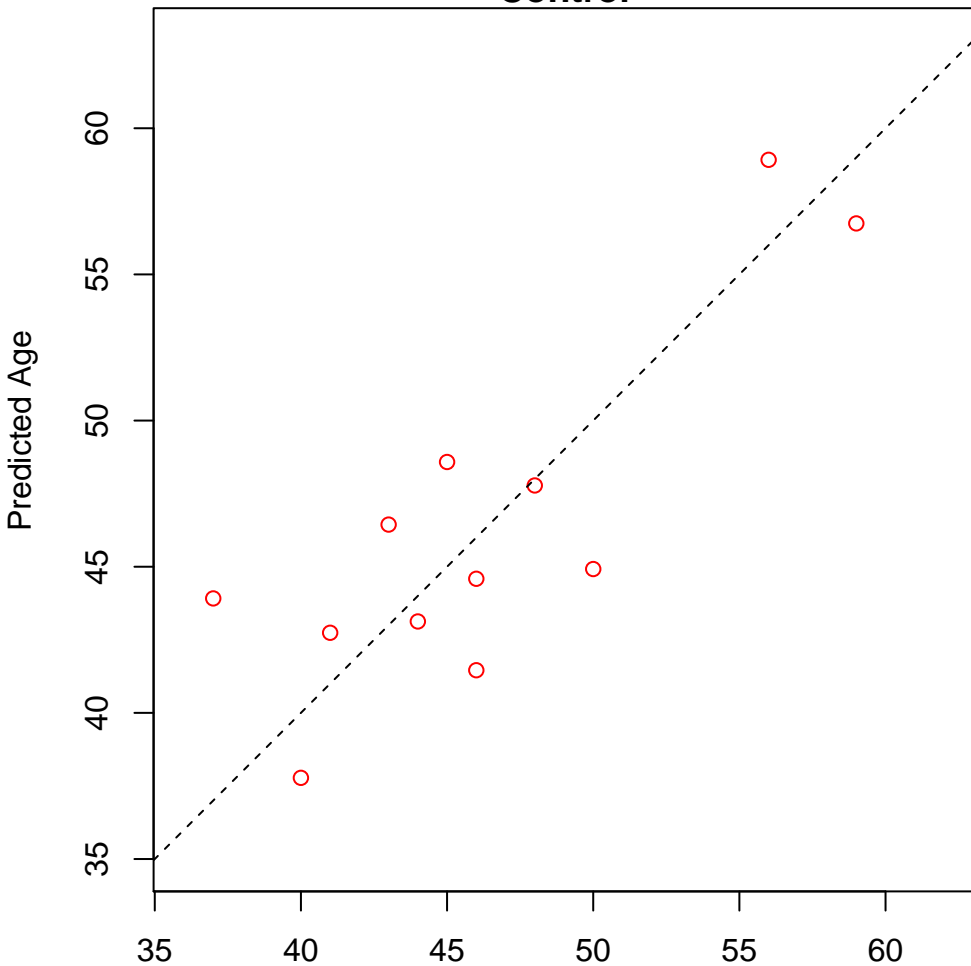


positive regulation of cellular amino acid metabolic process (Score: 8.784515)

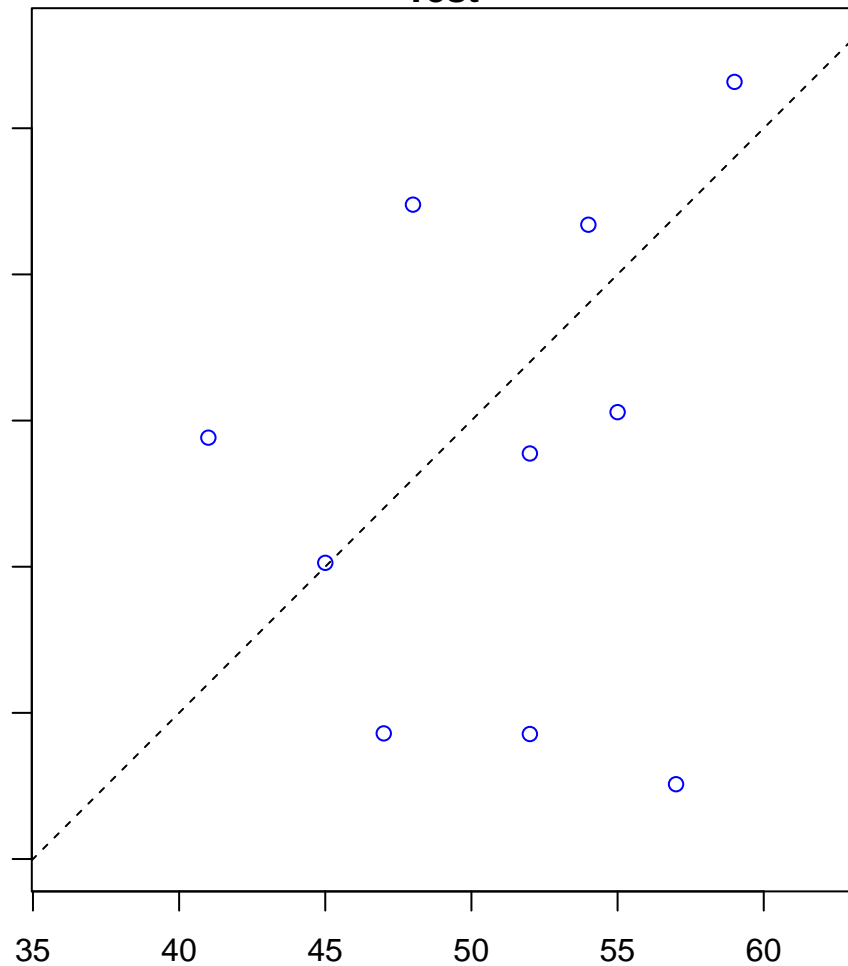


positive regulation of organ growth (Score: 8.777790)

Control

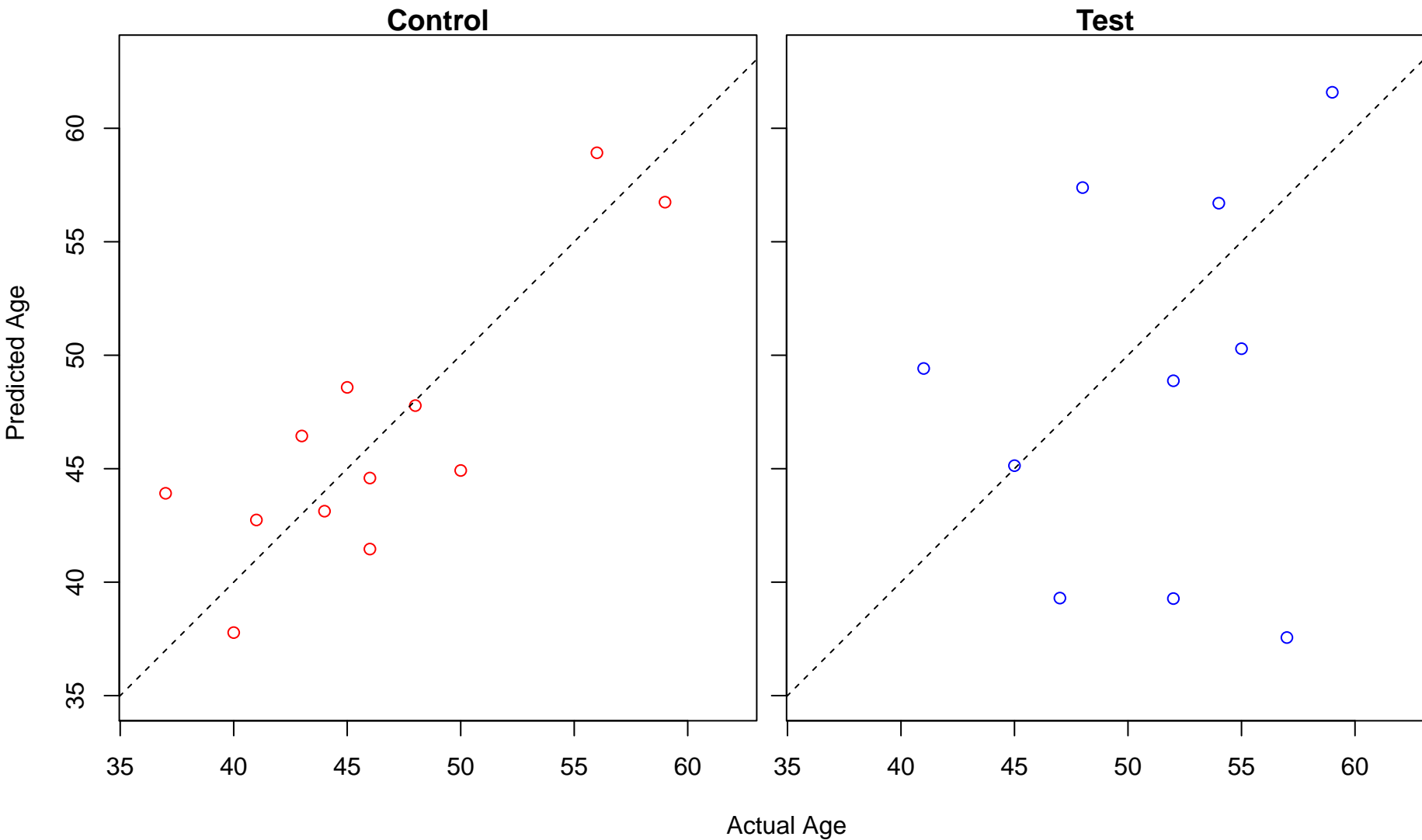


Test

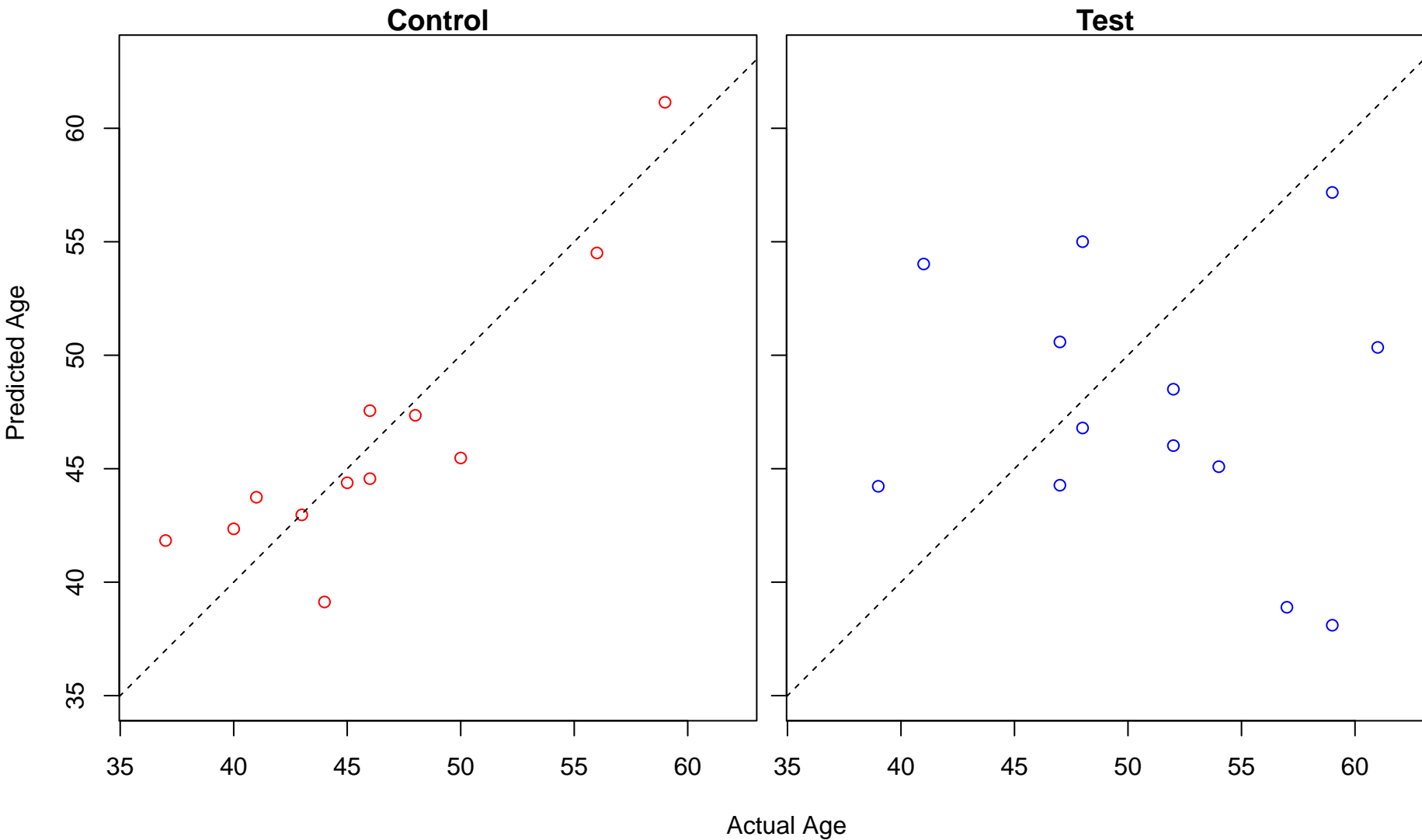


Actual Age

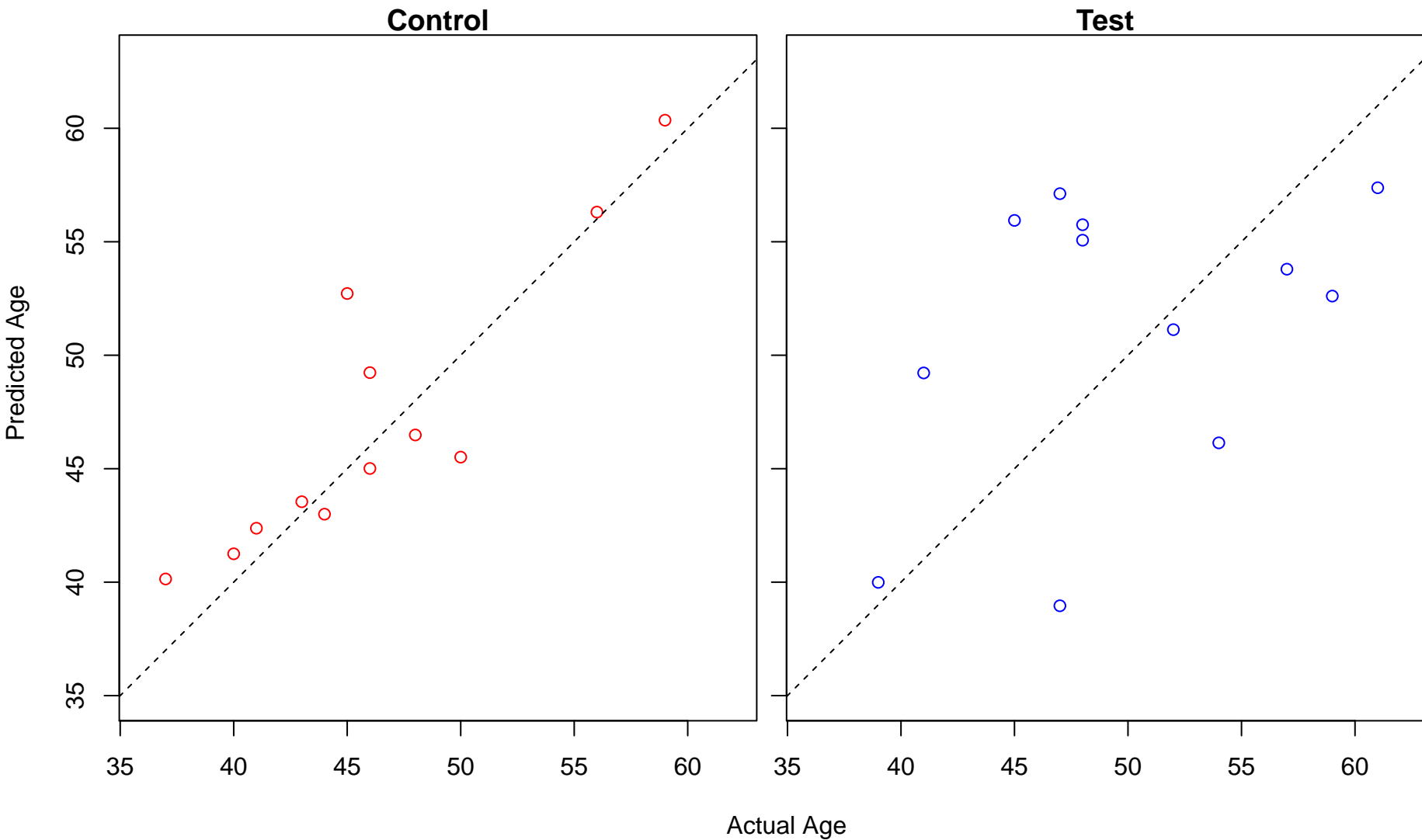
positive regulation of heart growth (Score: 8.777790)



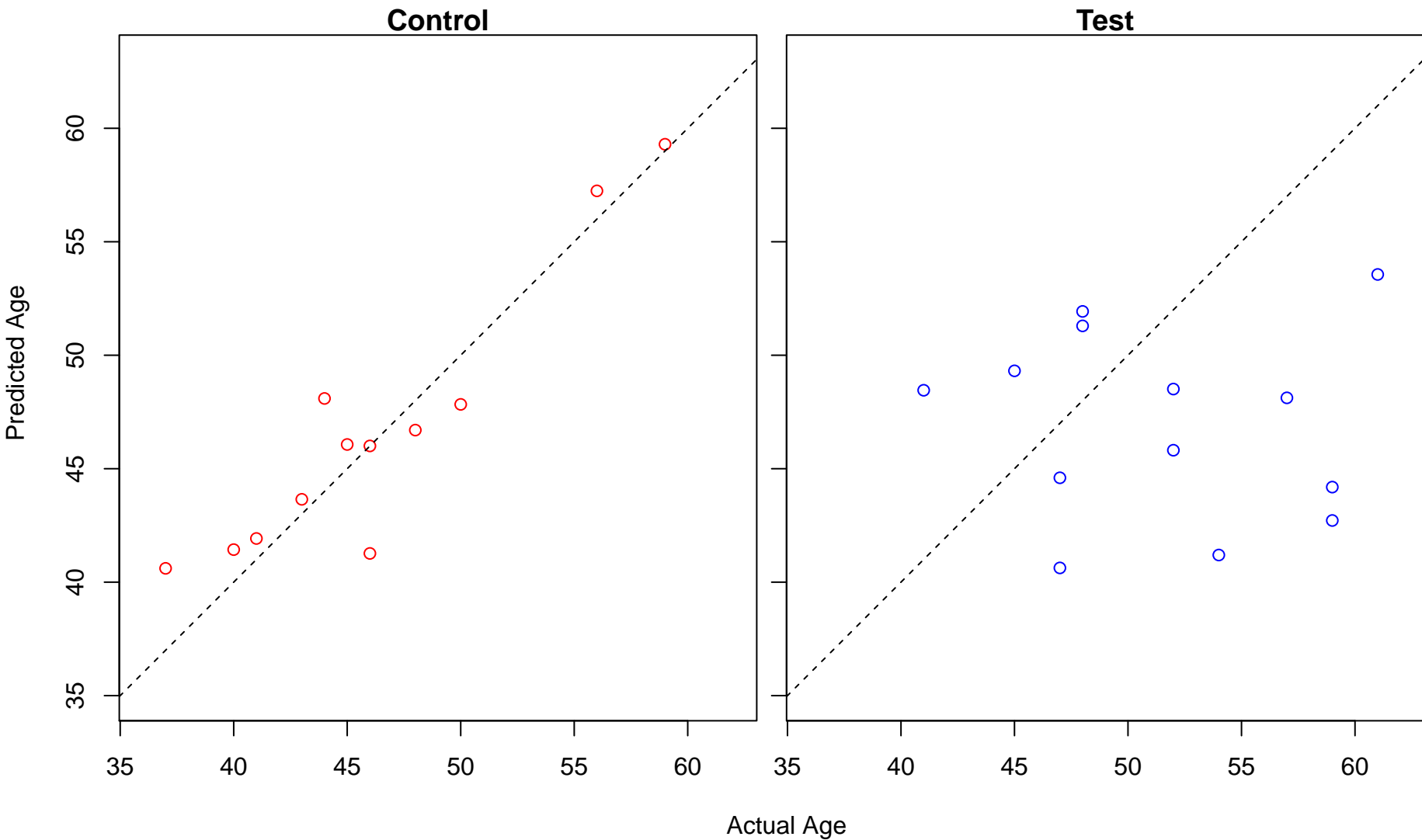
interaction with host (Score: 8.767340)



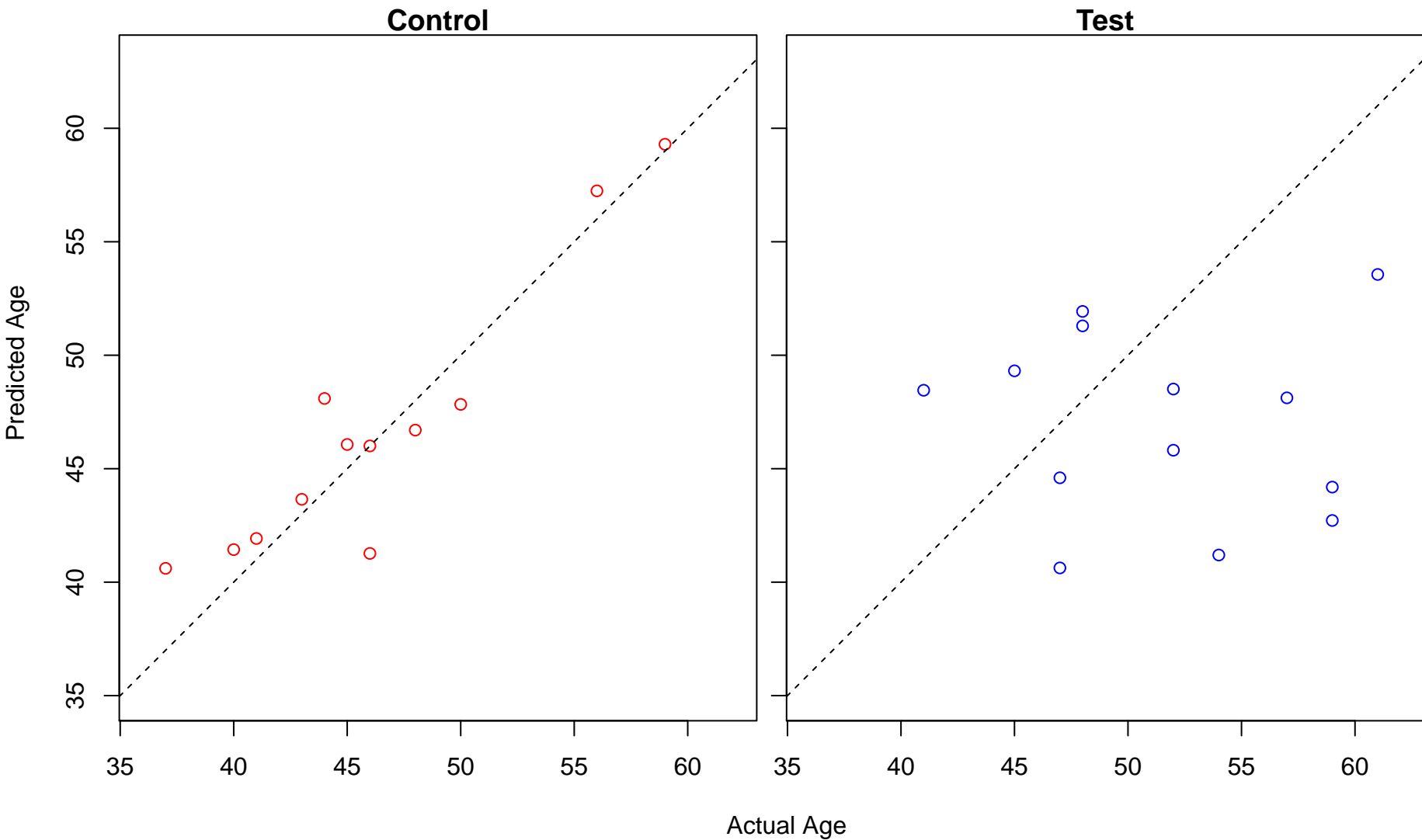
adaptive immune response (Score: 8.766233)



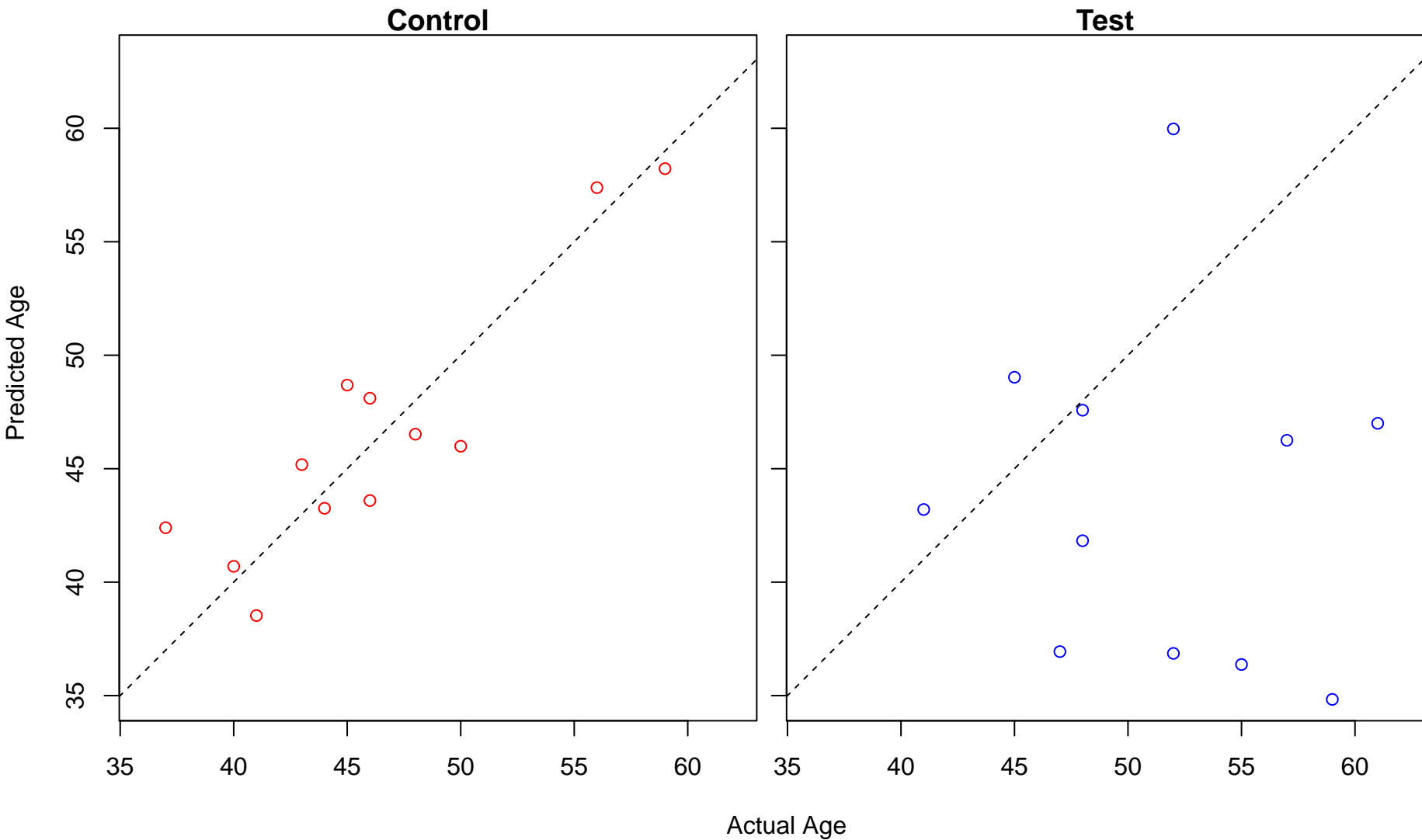
negative regulation of protein localization to plasma membrane (Score: 8.757116)



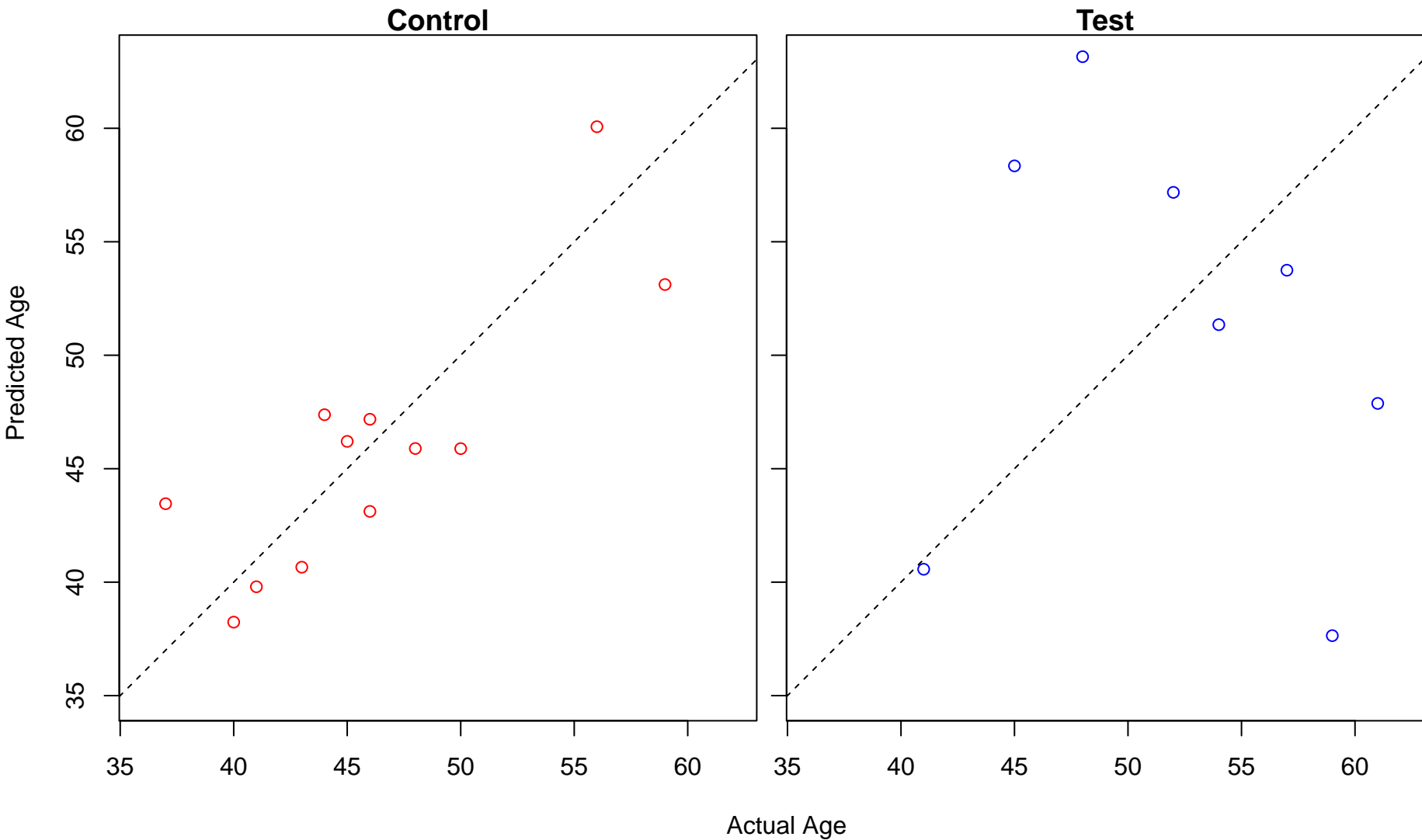
negative regulation of protein localization to cell periphery (Score: 8.757116)



positive regulation of cell-matrix adhesion (Score: 8.751292)

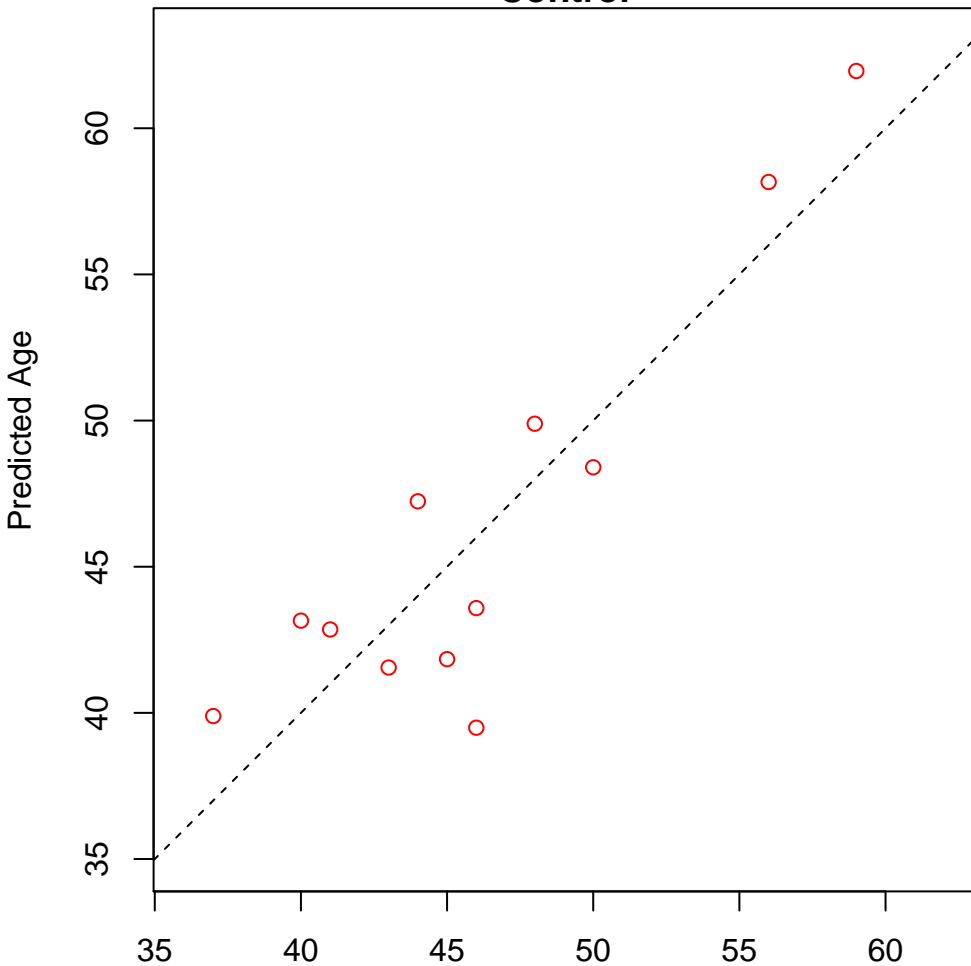


apoptotic cell clearance (Score: 8.742679)

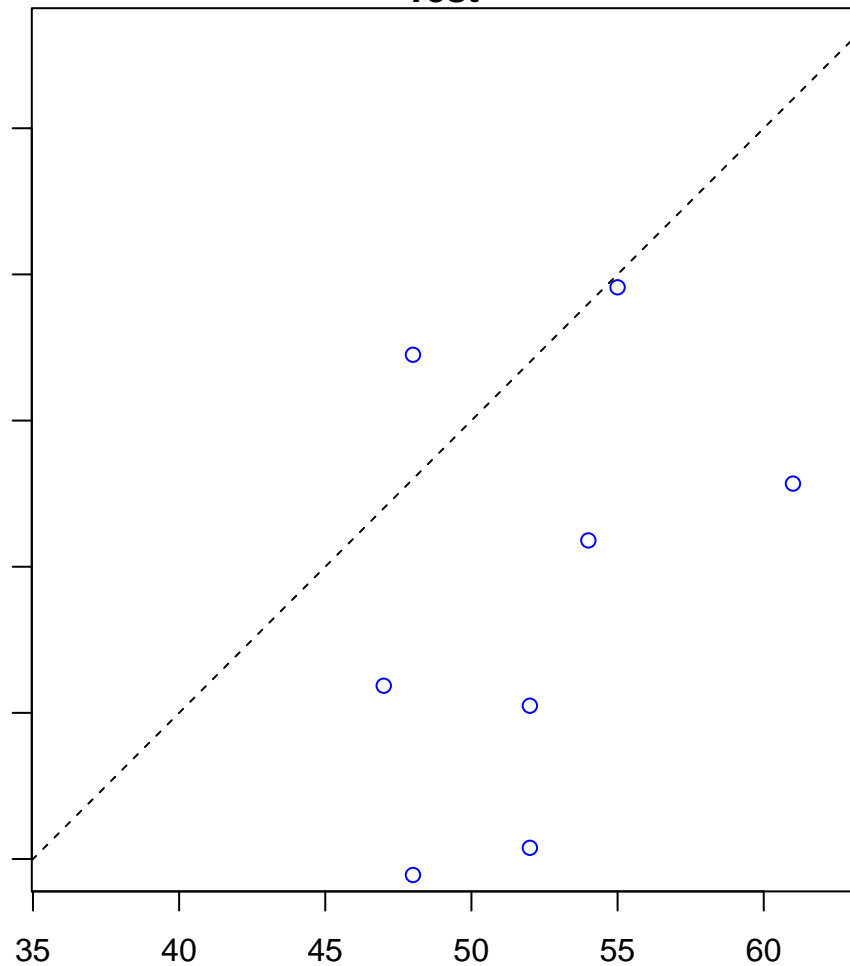


fat-soluble vitamin metabolic process (Score: 8.740510)

Control

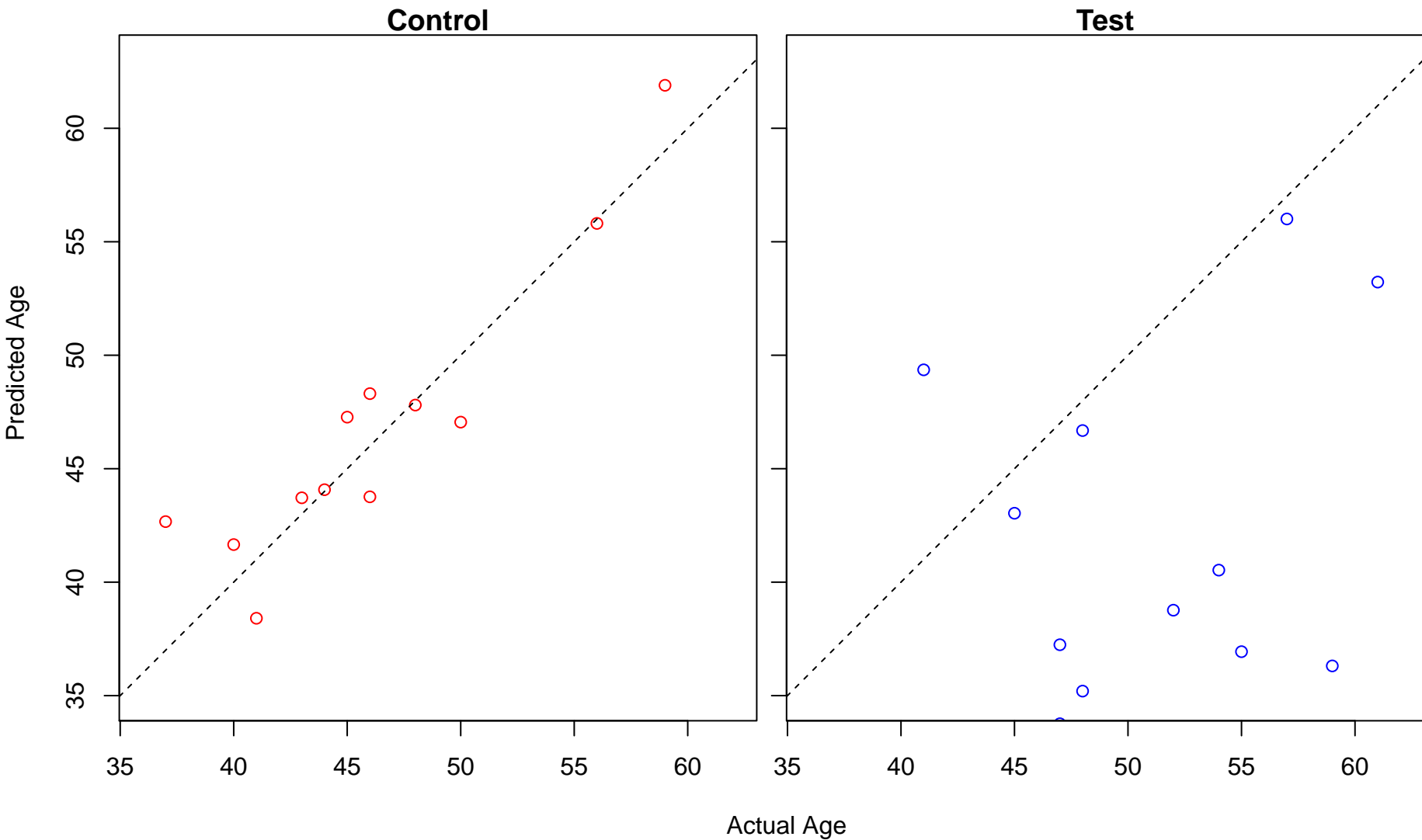


Test

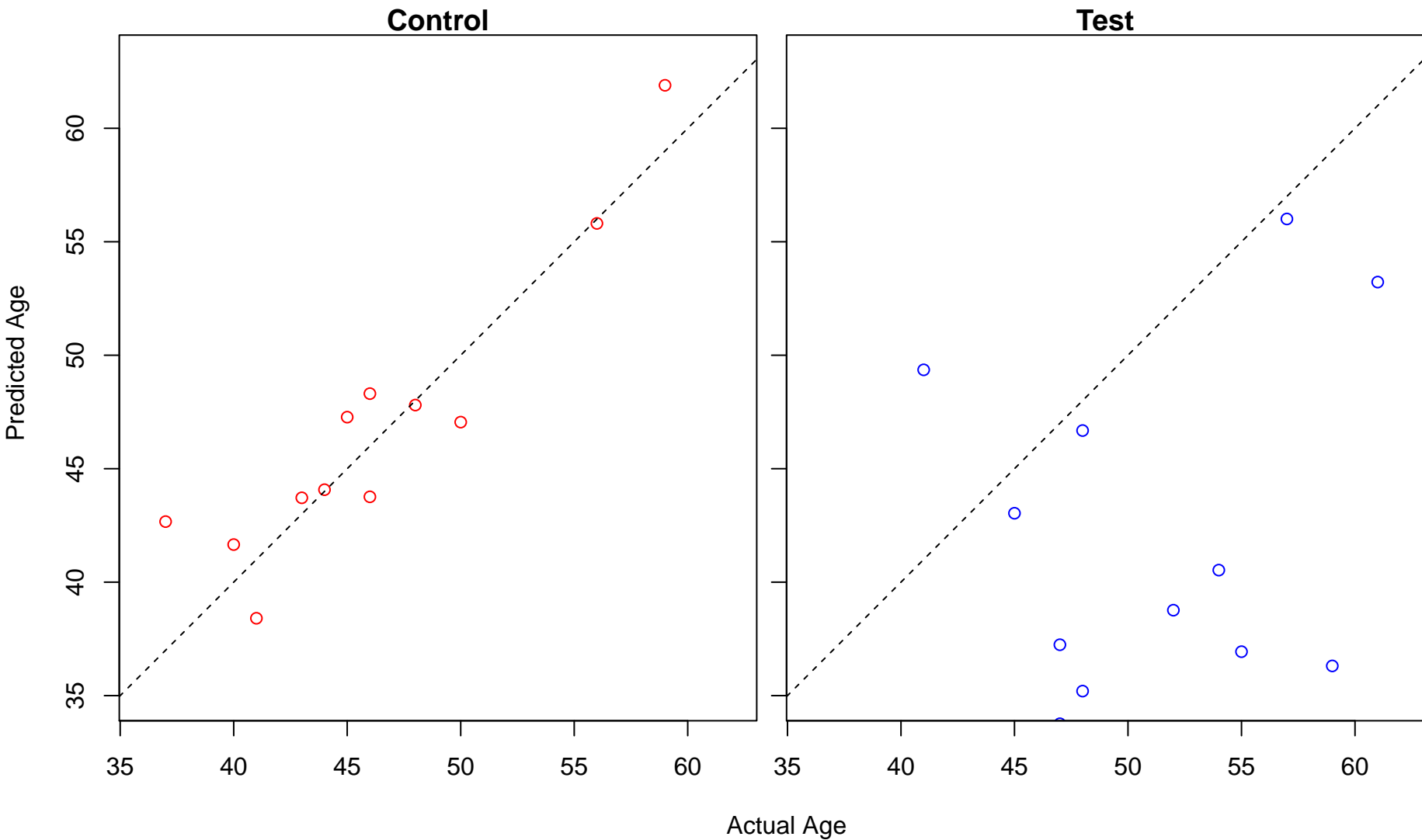


Actual Age

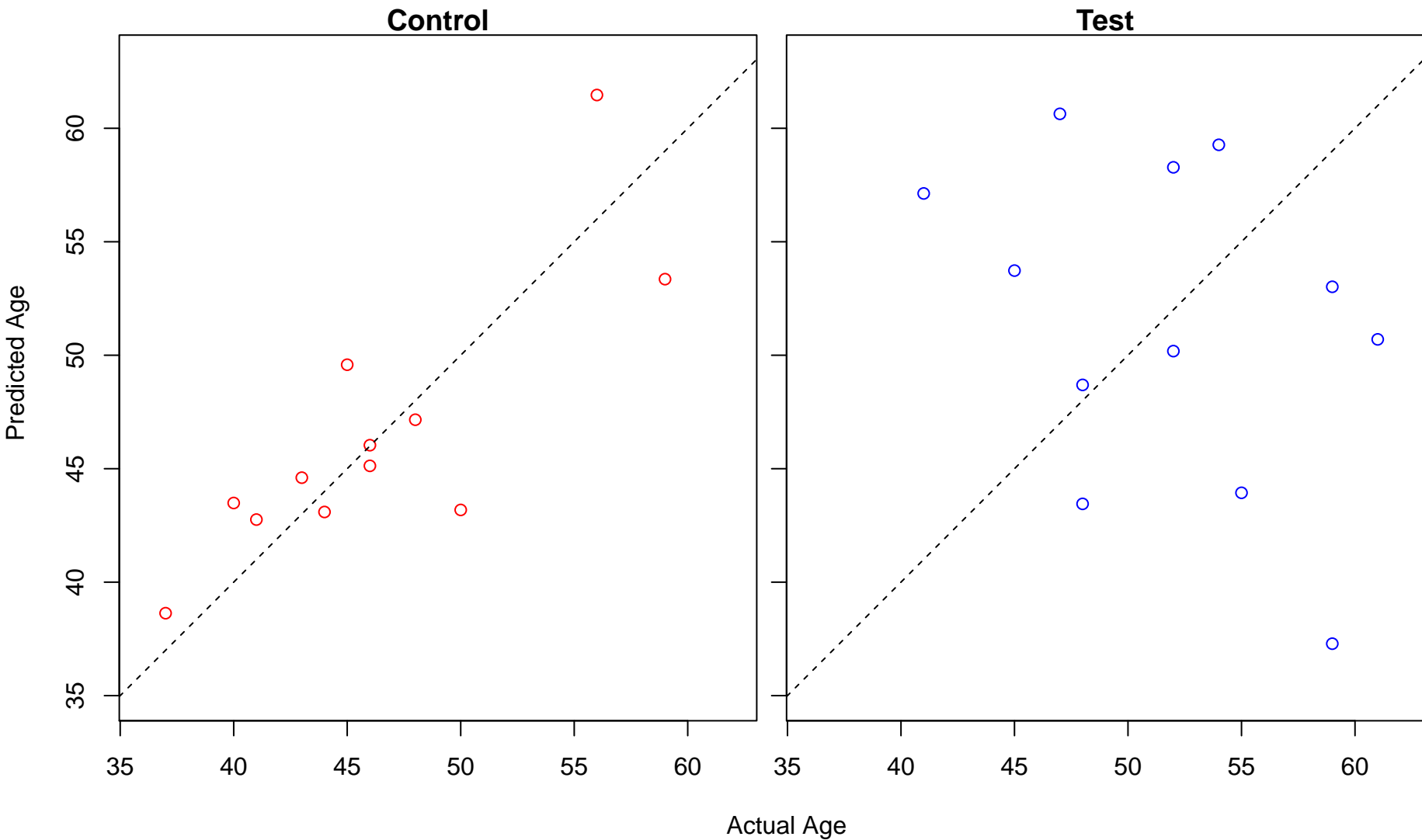
regulation of focal adhesion assembly (Score: 8.728223)



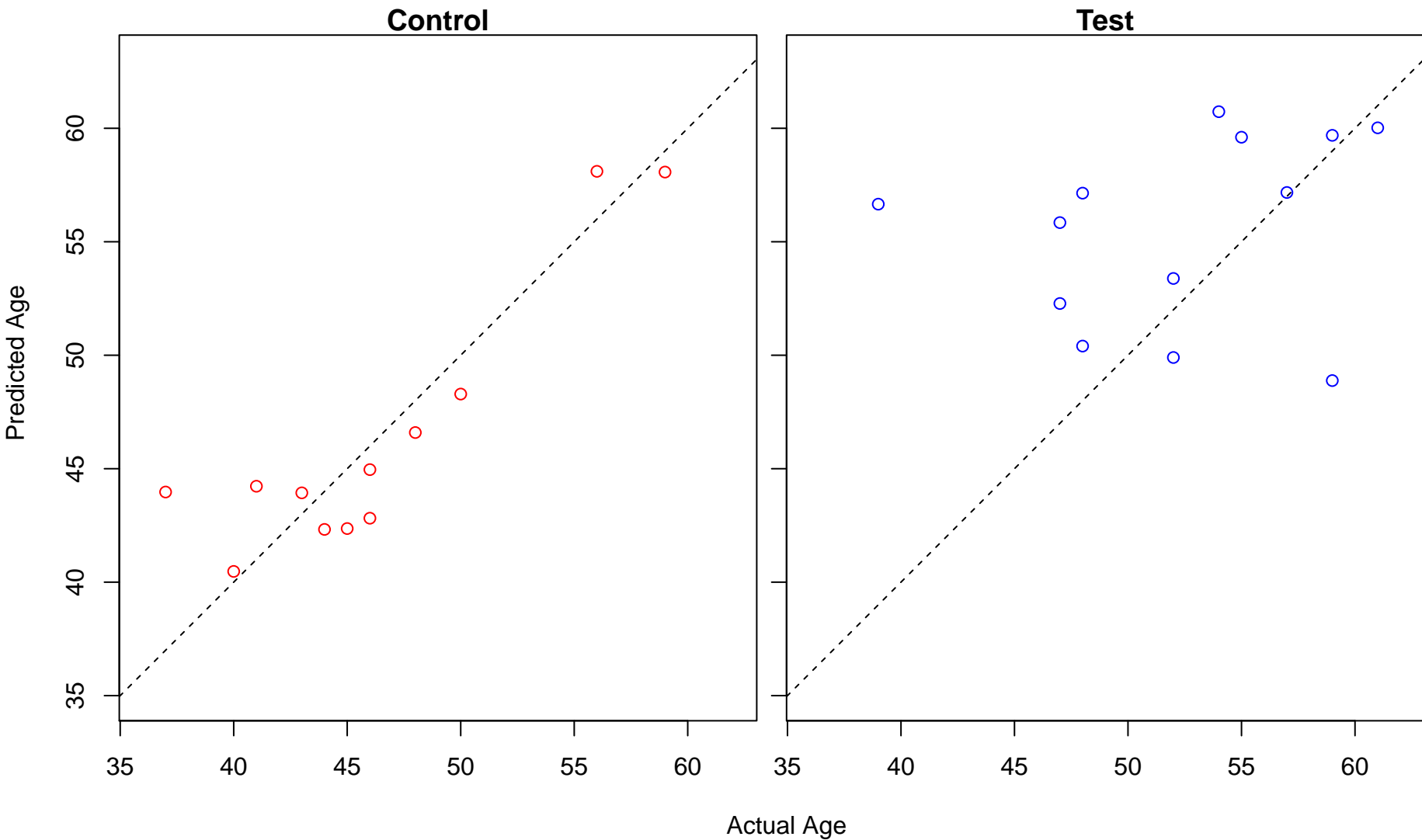
regulation of cell-substrate junction assembly (Score: 8.728223)



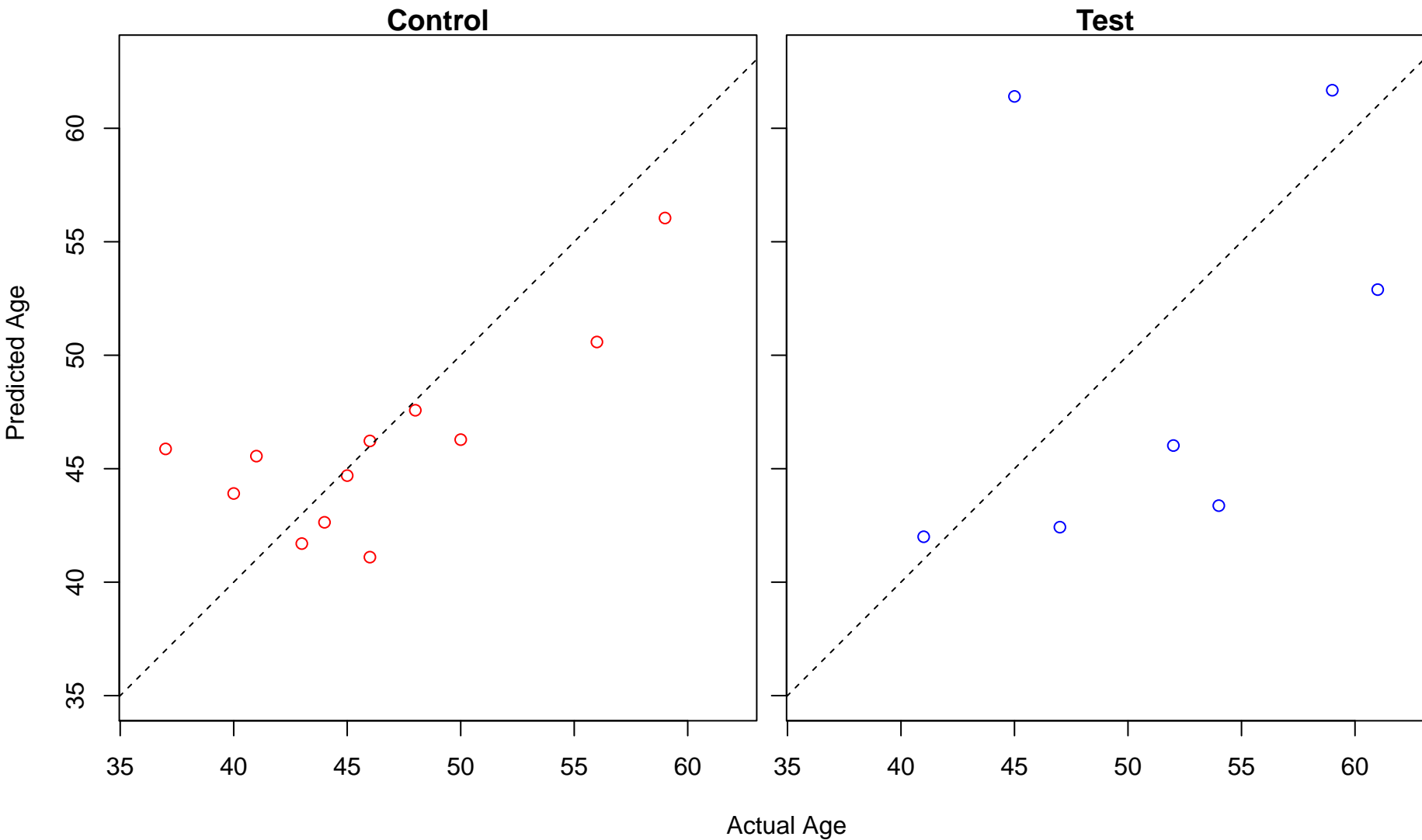
positive regulation of alpha-beta T cell proliferation (Score: 8.709114)



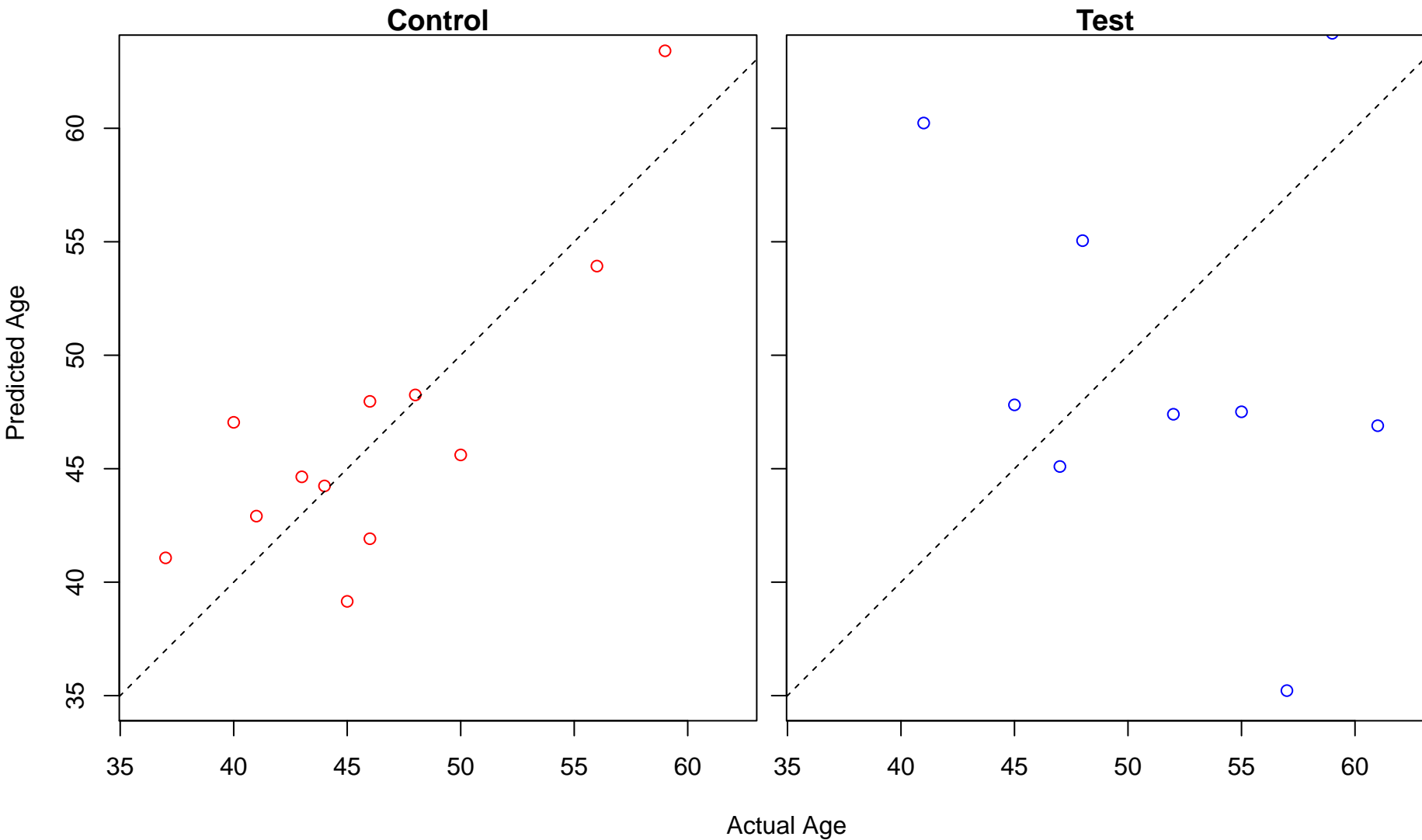
postsynaptic membrane assembly (Score: 8.688860)



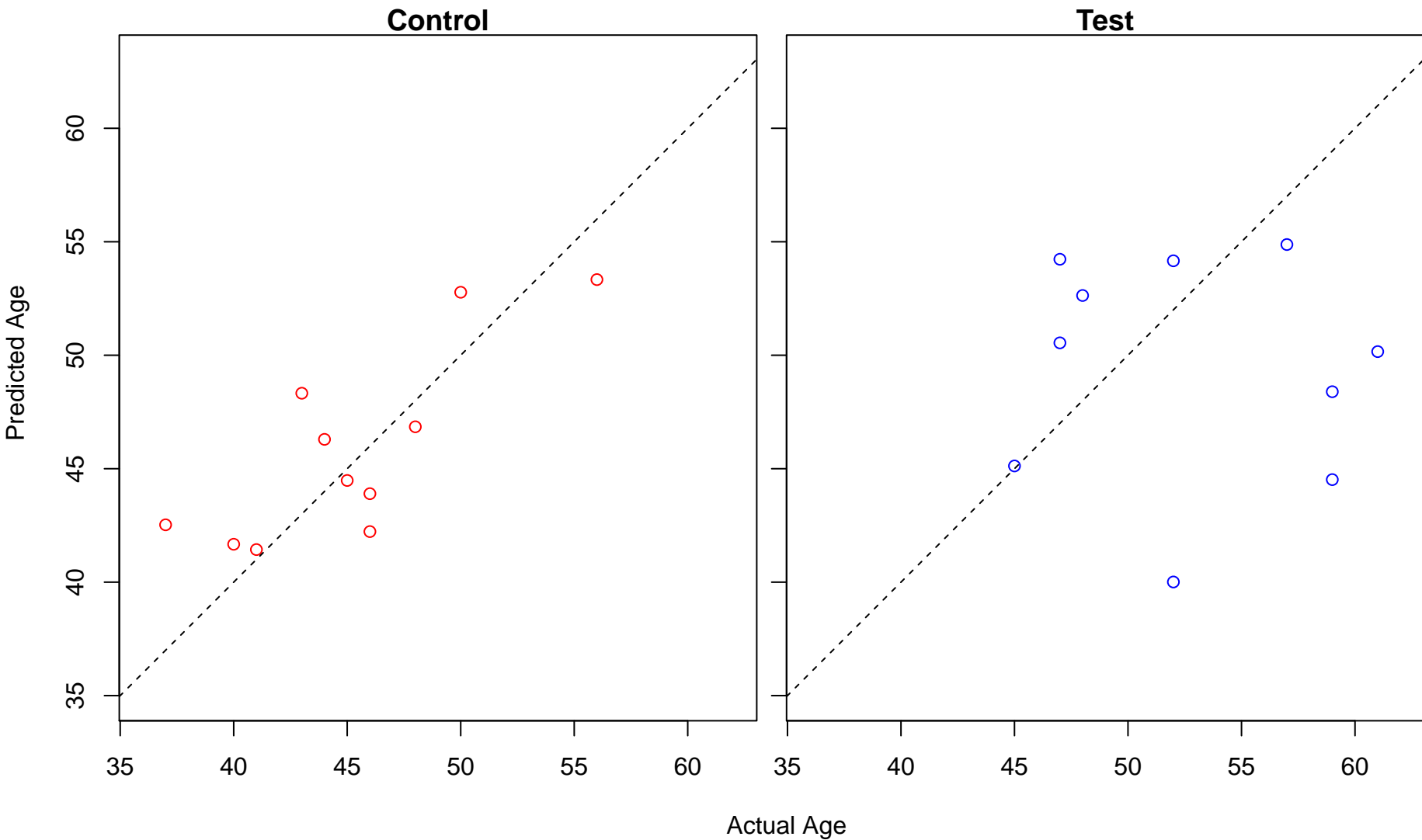
negative regulation of fibrinolysis (Score: 8.687494)



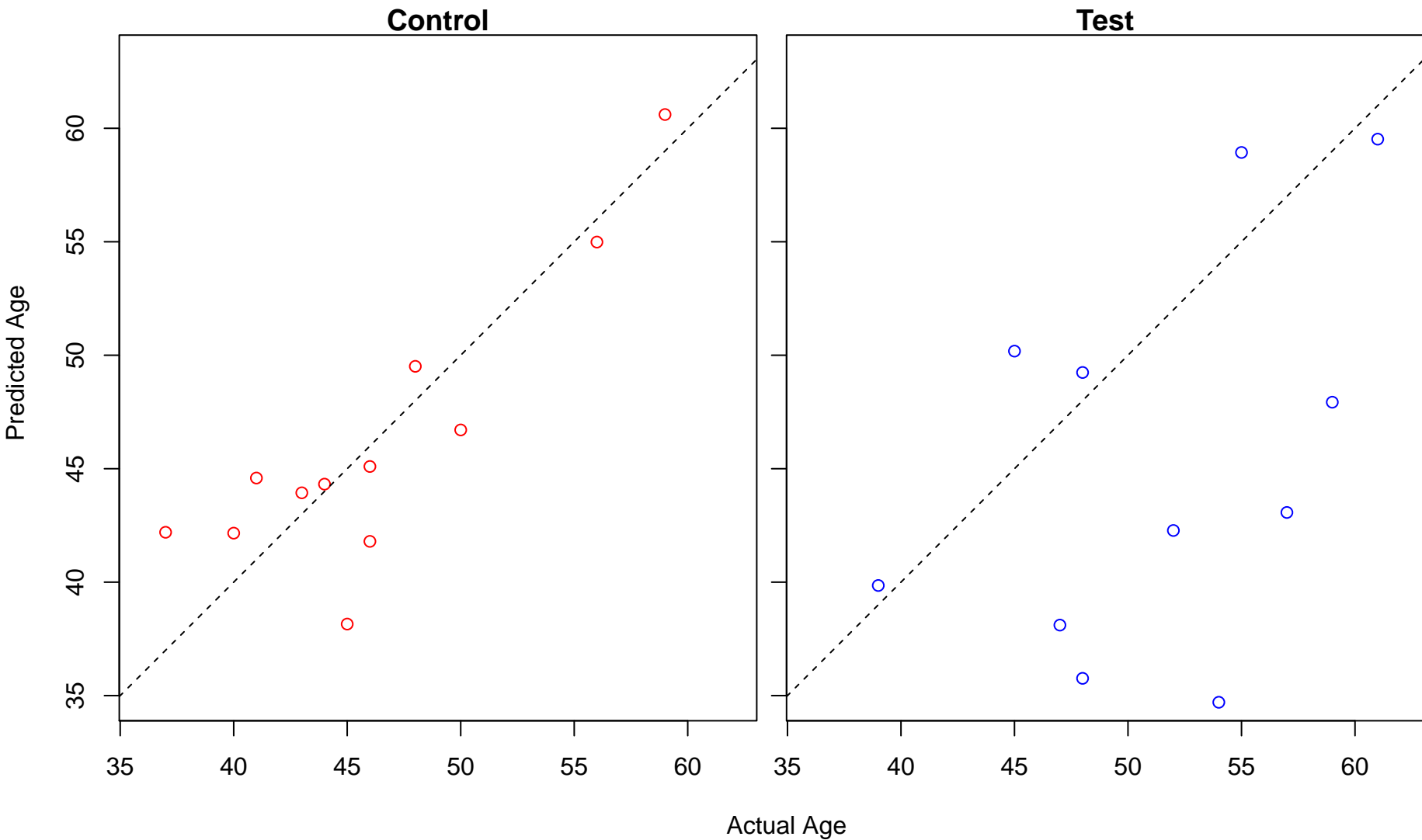
regulation of synaptic vesicle exocytosis (Score: 8.686885)



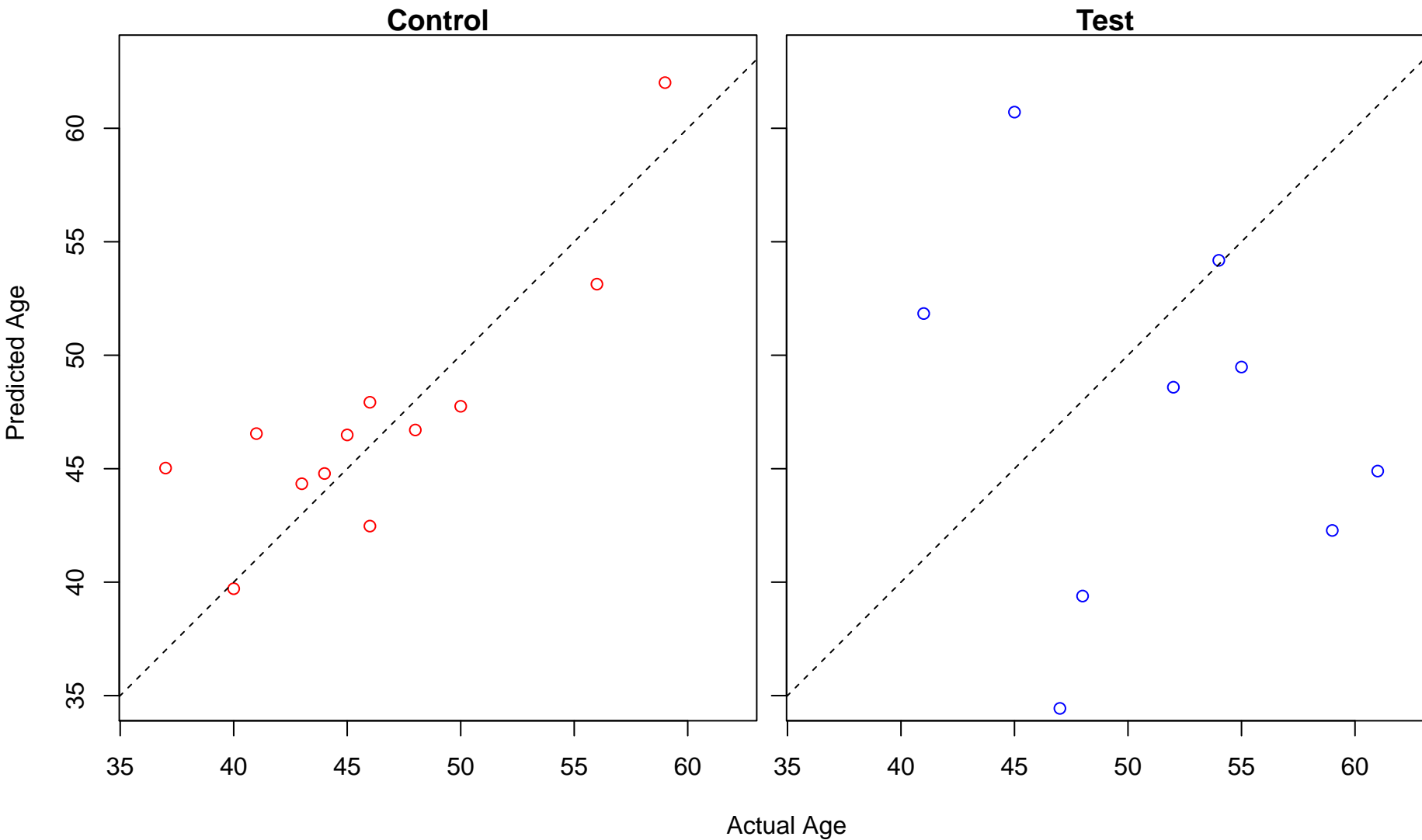
negative regulation of cyclase activity (Score: 8.679835)



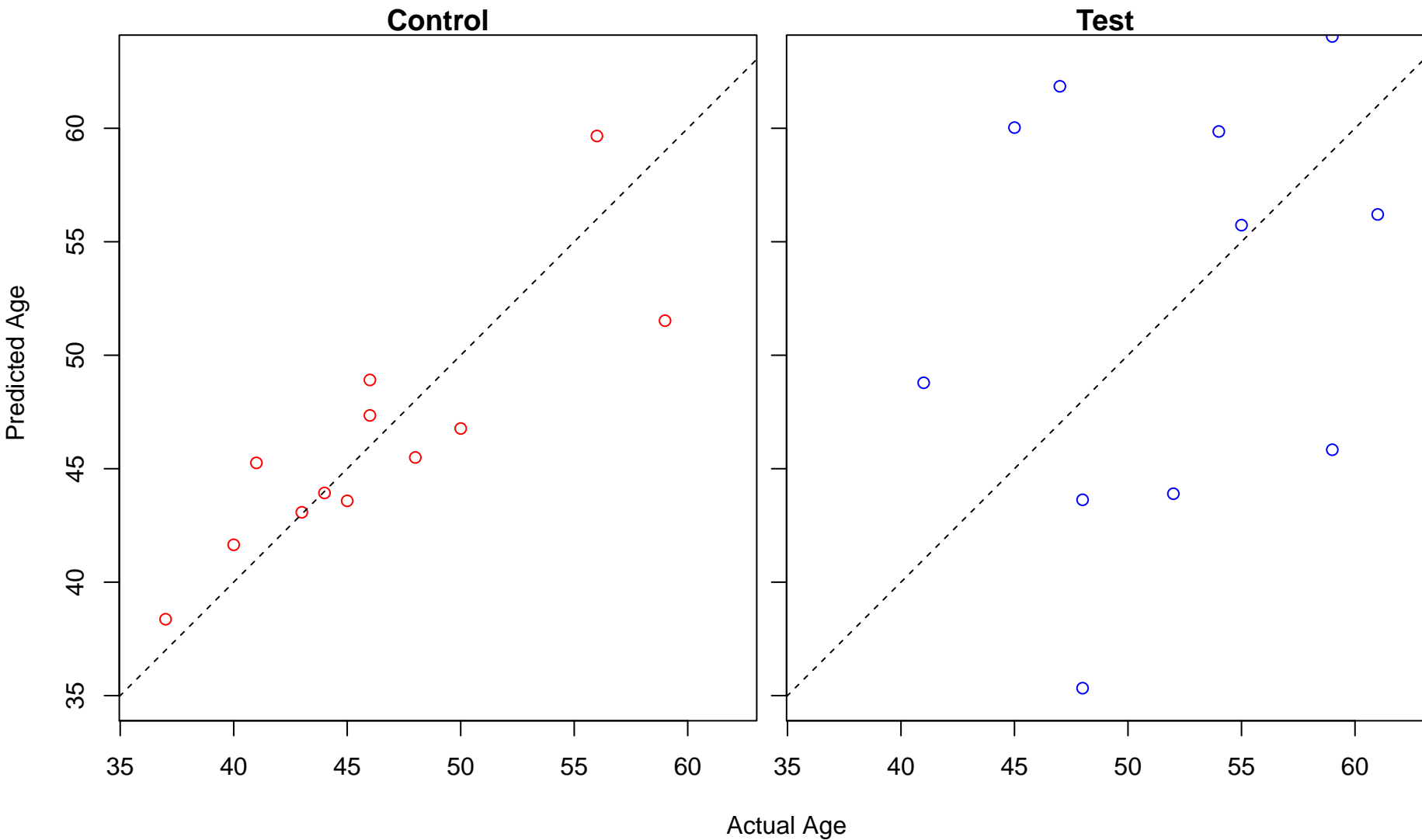
lipid homeostasis (Score: 8.679663)



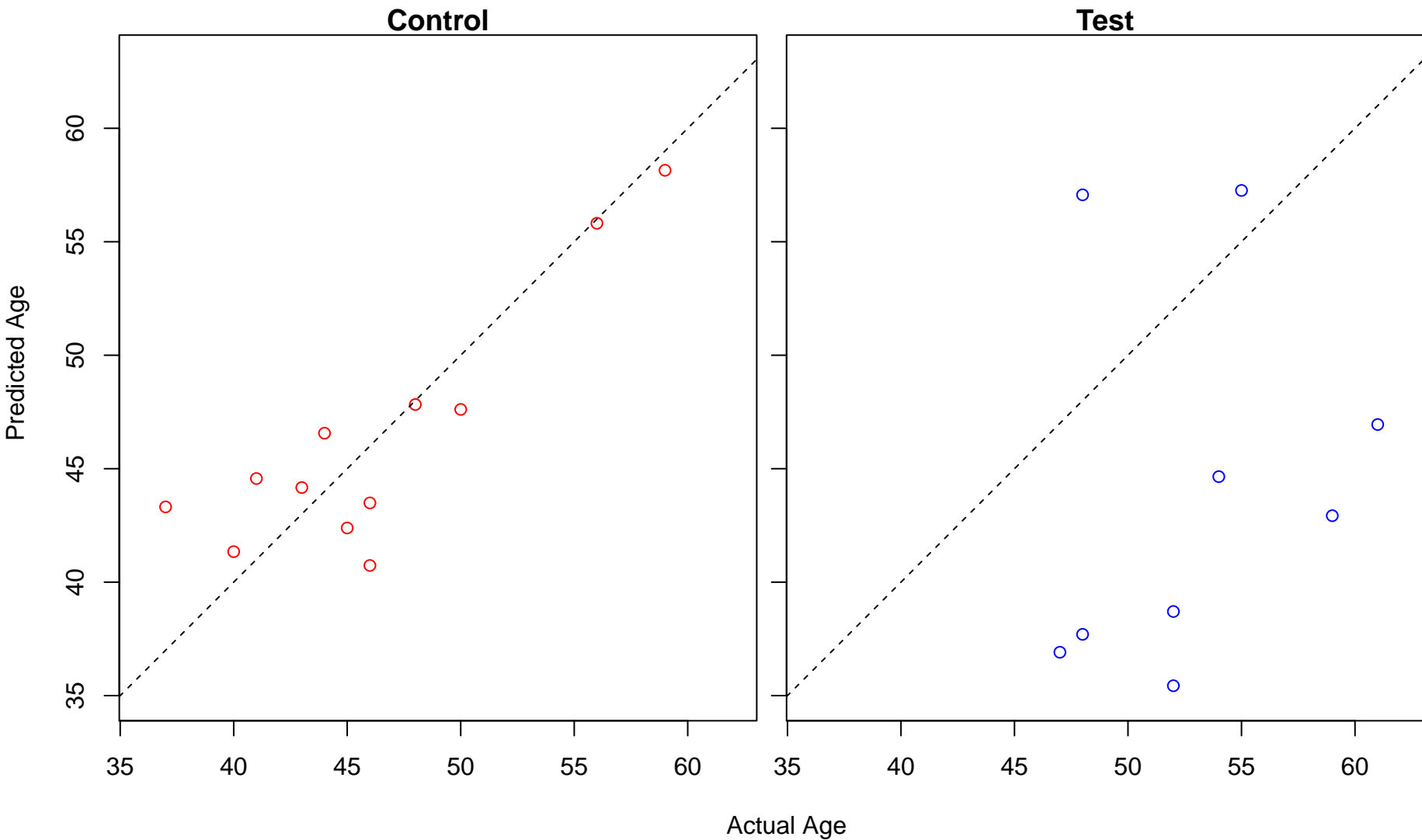
positive regulation of T cell migration (Score: 8.645965)



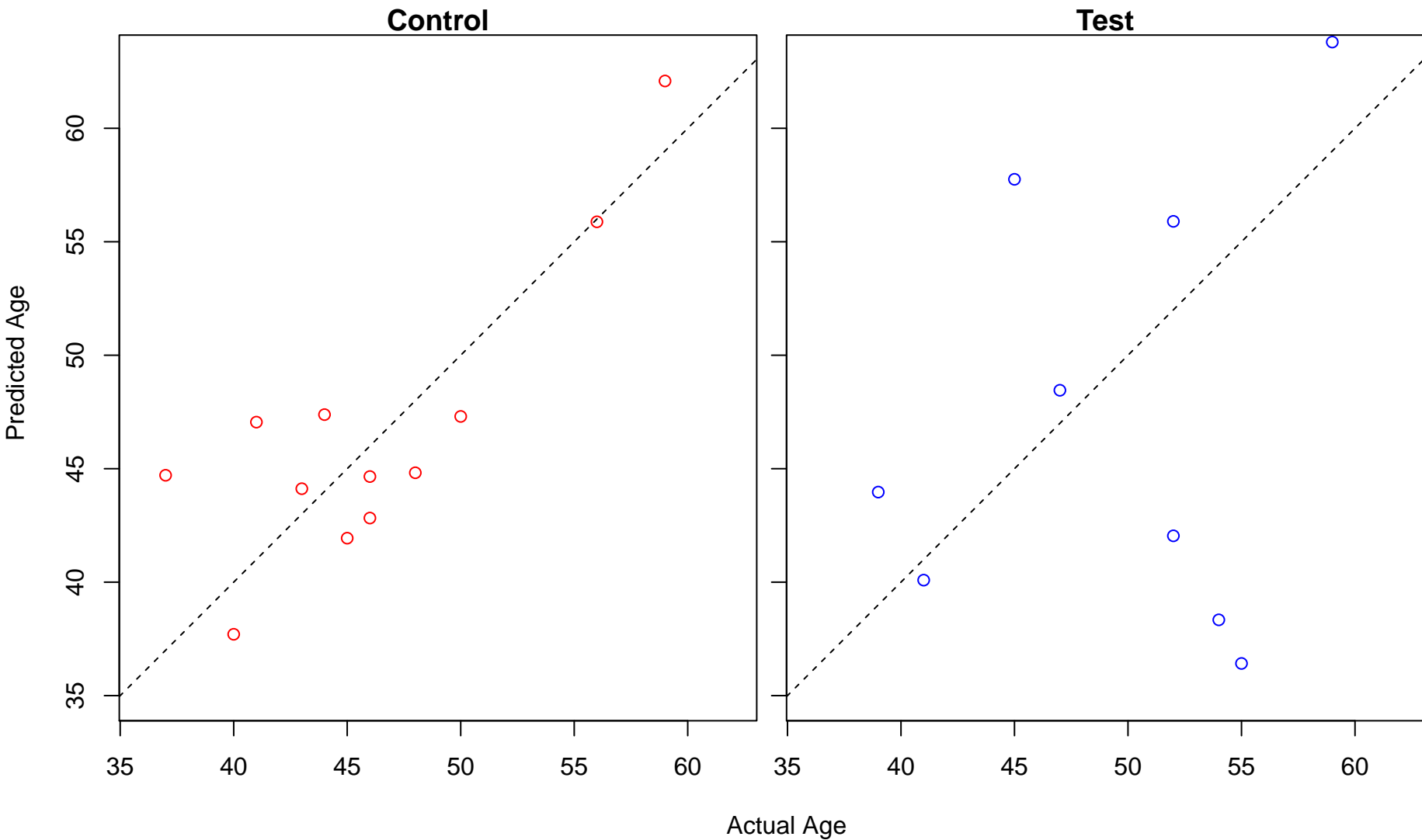
phospholipid efflux (Score: 8.634857)



nucleocytoplasmic transport (Score: 8.601707)

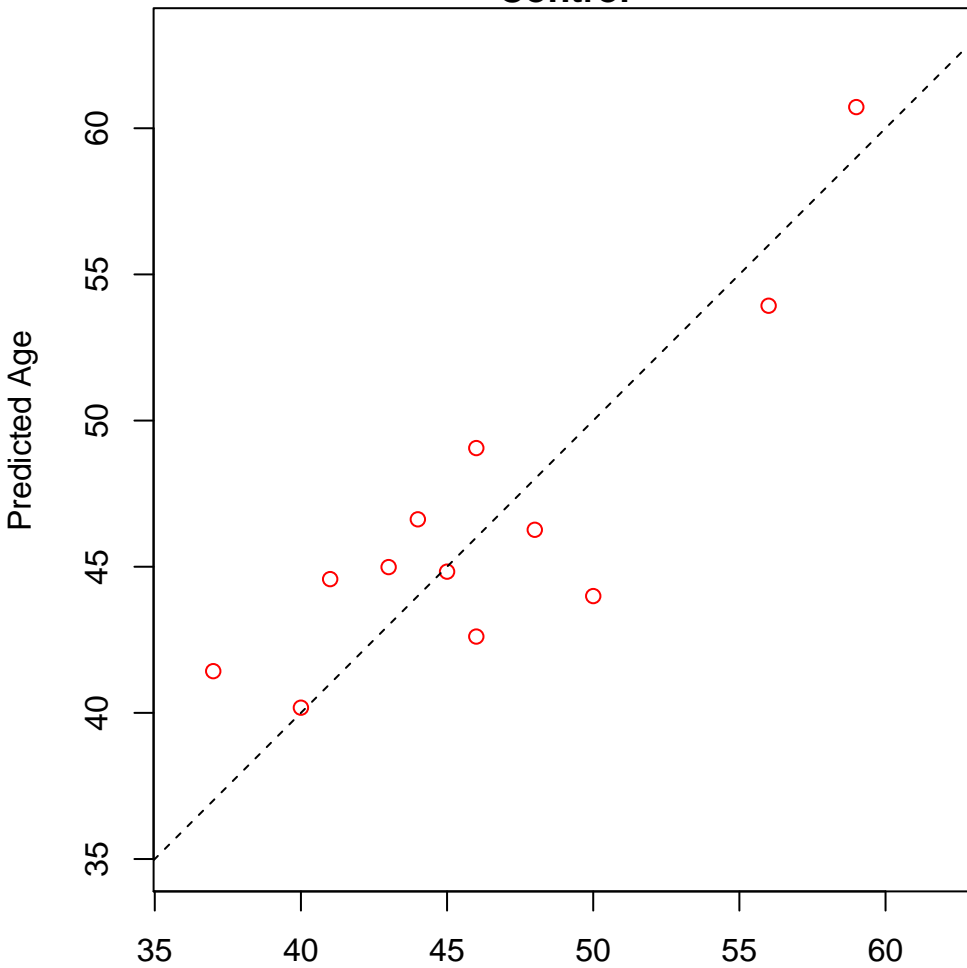


chondroitin sulfate proteoglycan metabolic process (Score: 8.599681)

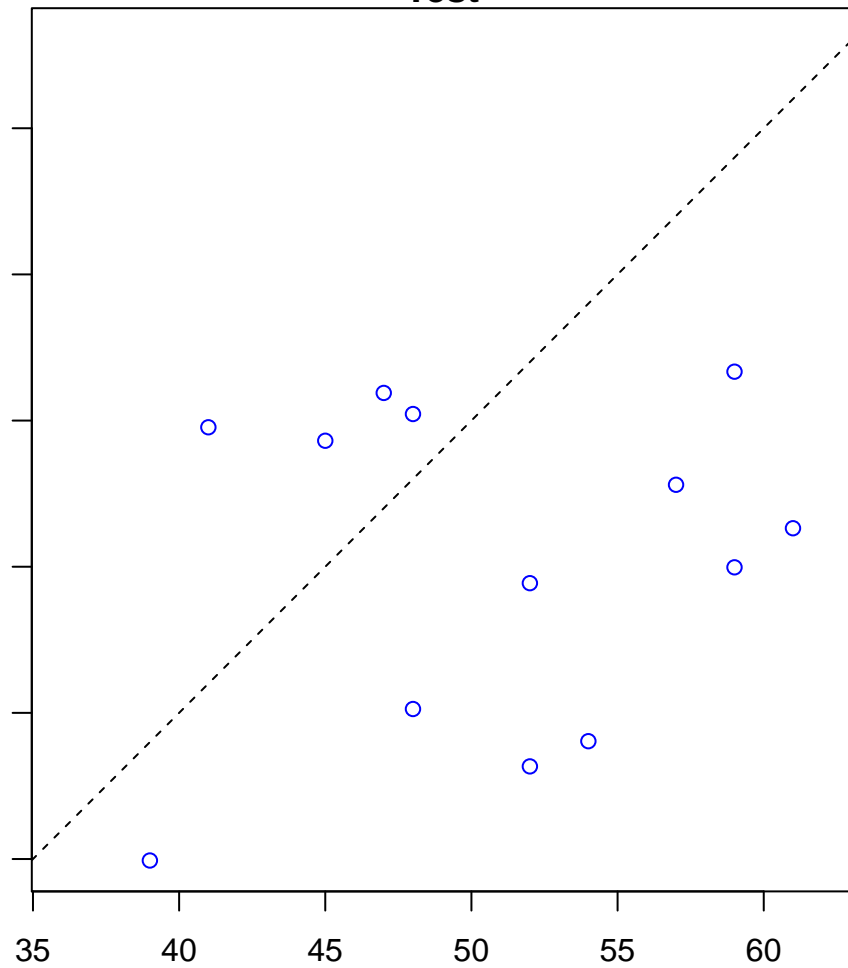


response to molecule of bacterial origin (Score: 8.592279)

Control



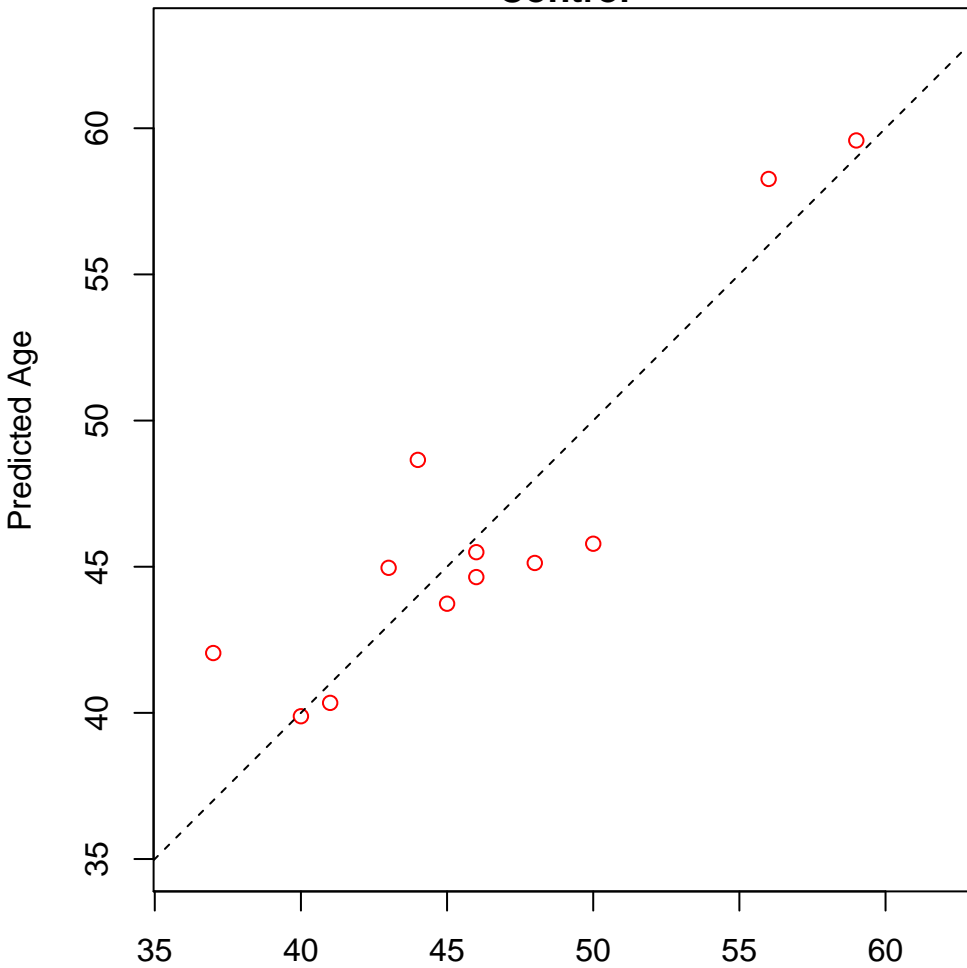
Test



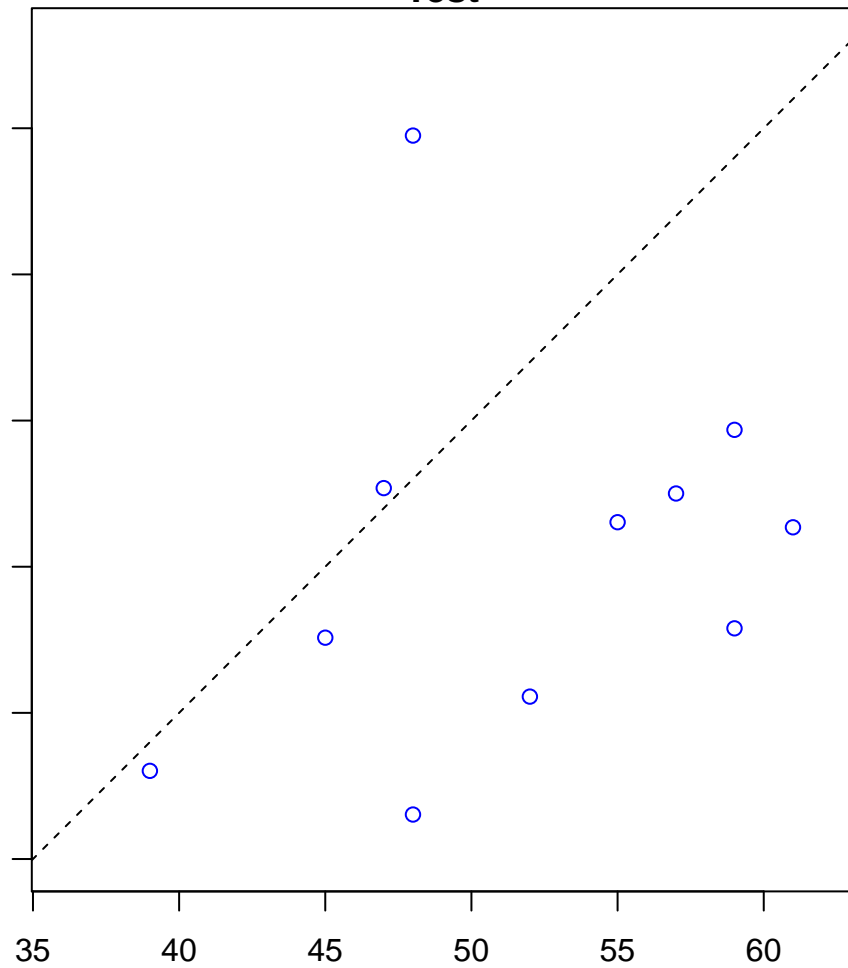
Actual Age

mesonephric epithelium development (Score: 8.588133)

Control



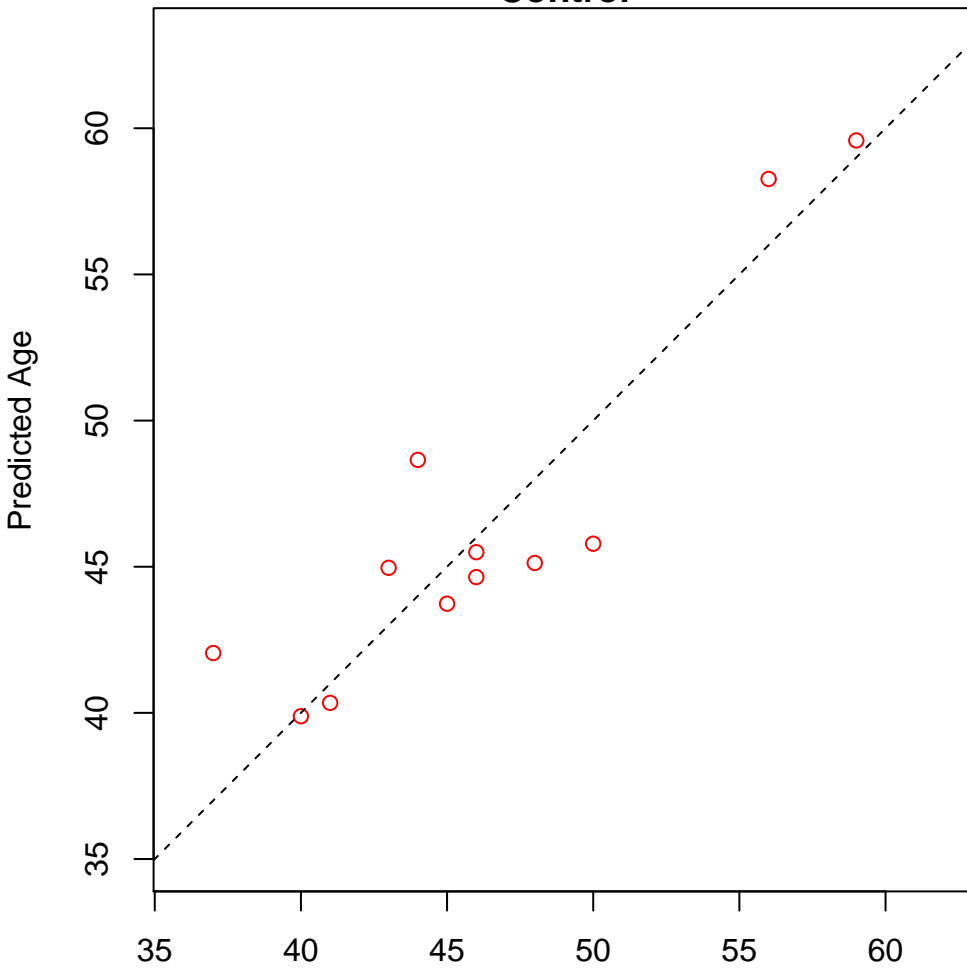
Test



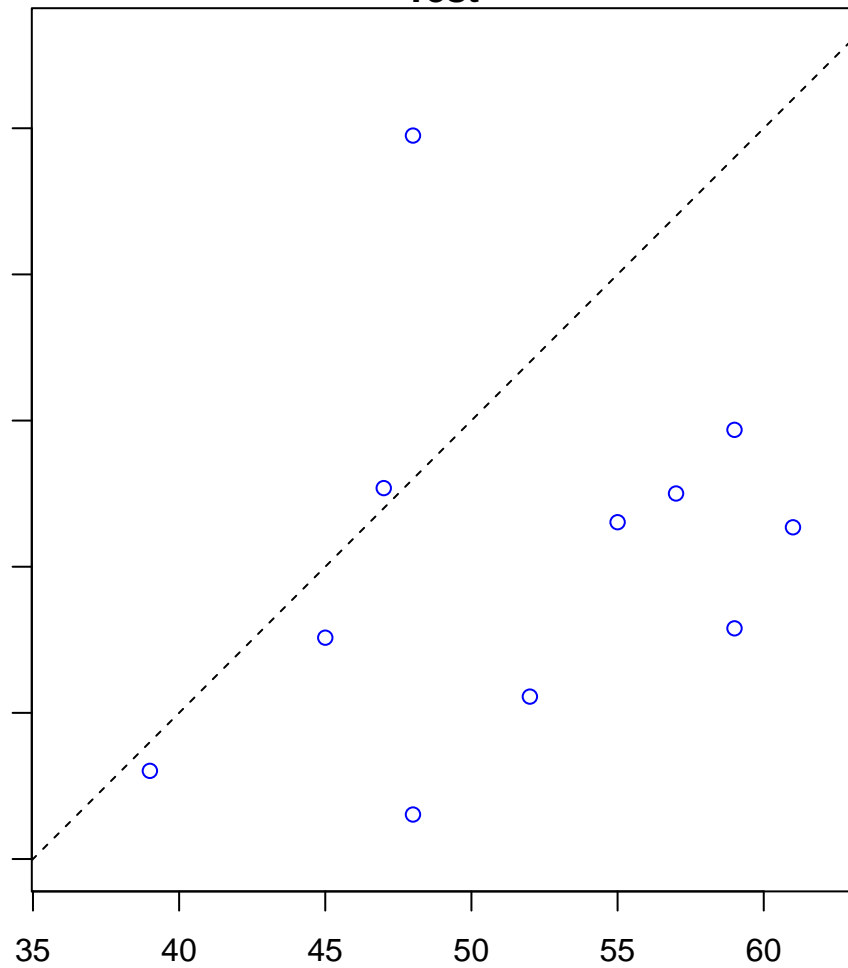
Actual Age

mesonephric tubule development (Score: 8.588133)

Control

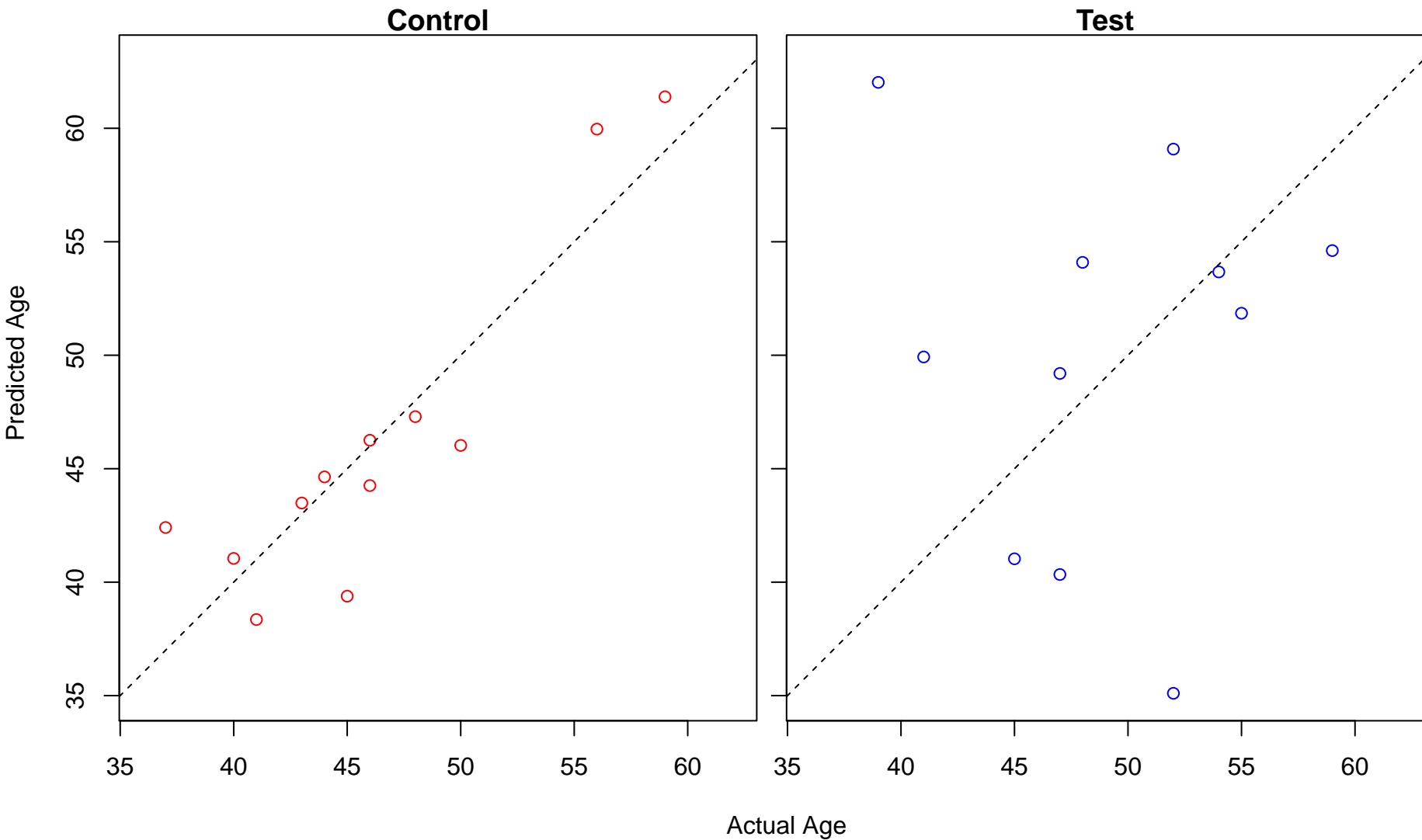


Test

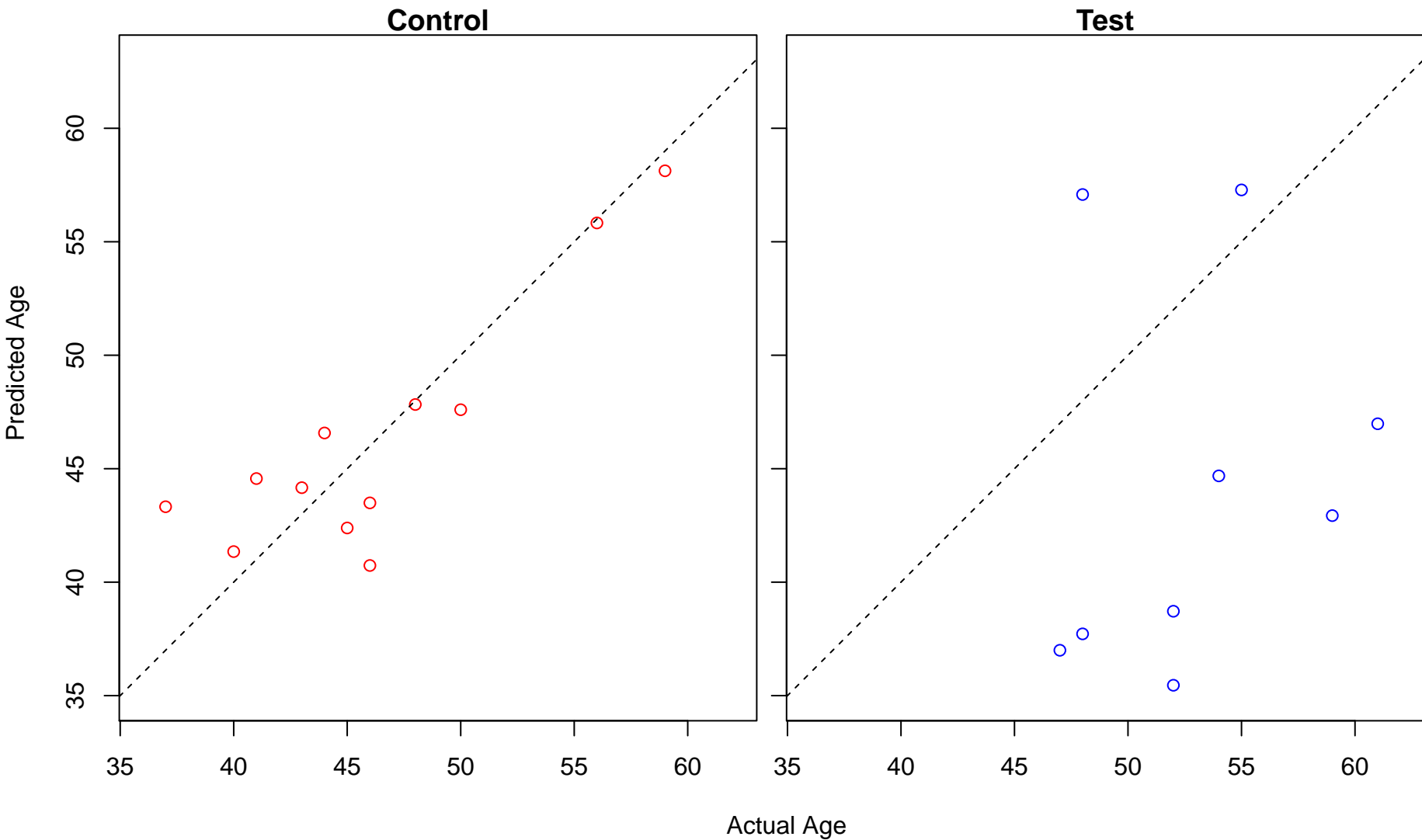


Actual Age

modulation by symbiont of host cellular process (Score: 8.581141)

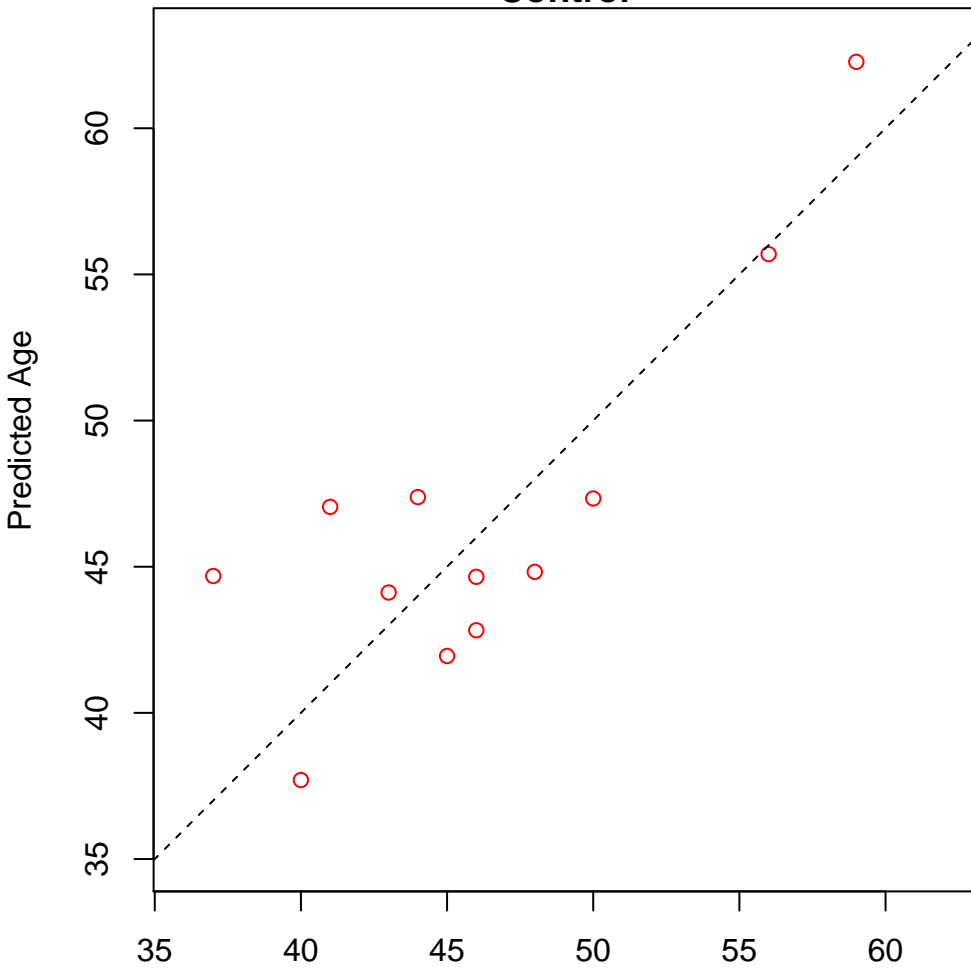


nuclear transport (Score: 8.568069)

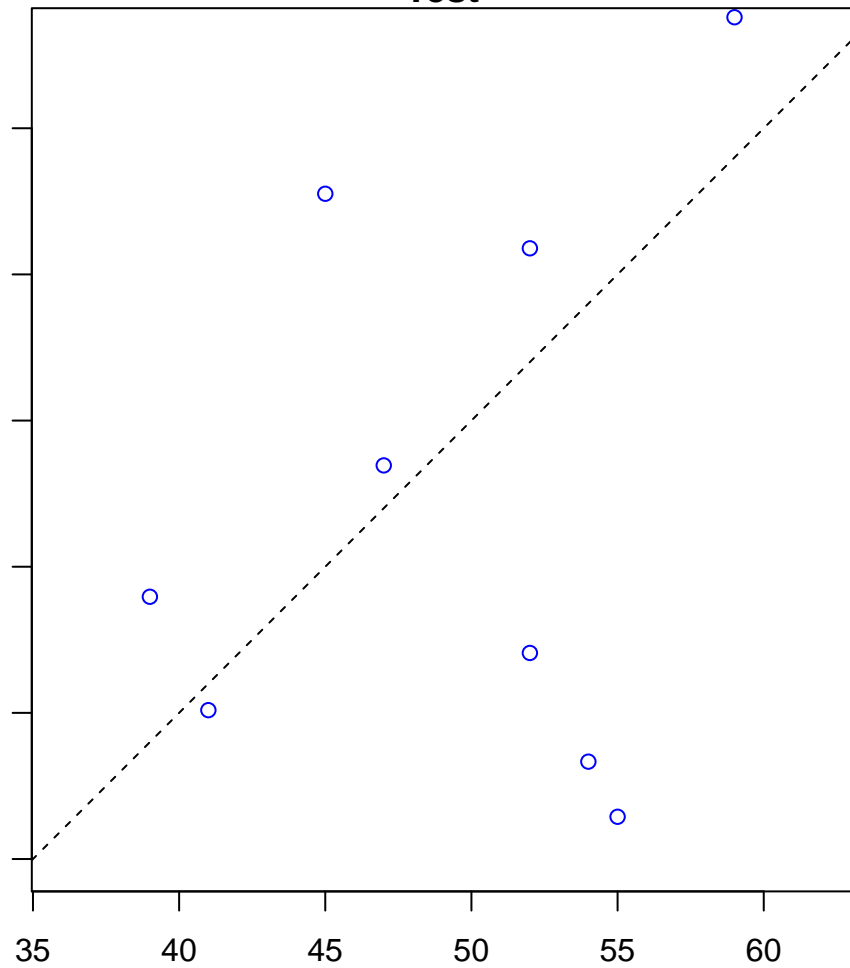


chondroitin sulfate metabolic process (Score: 8.557340)

Control

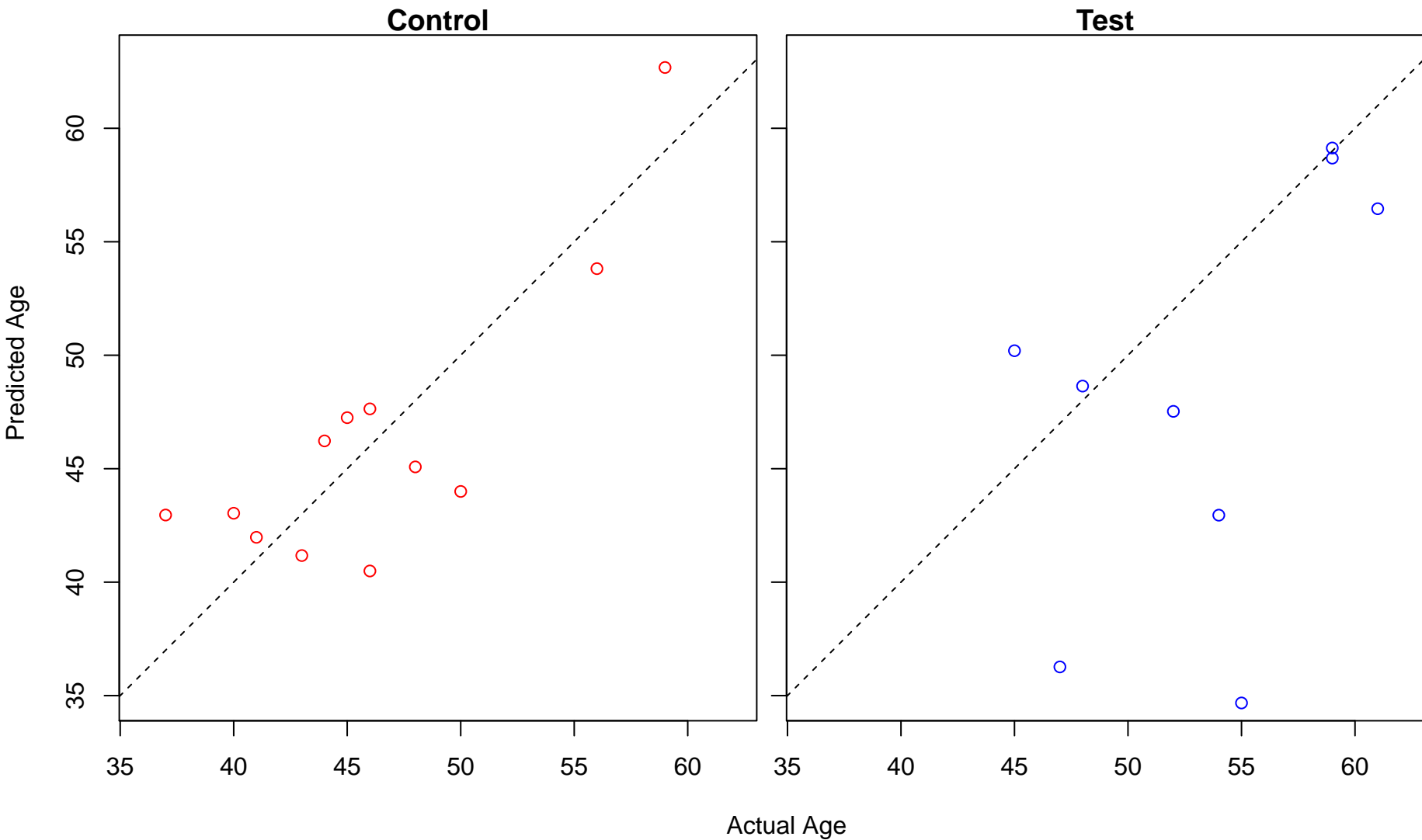


Test

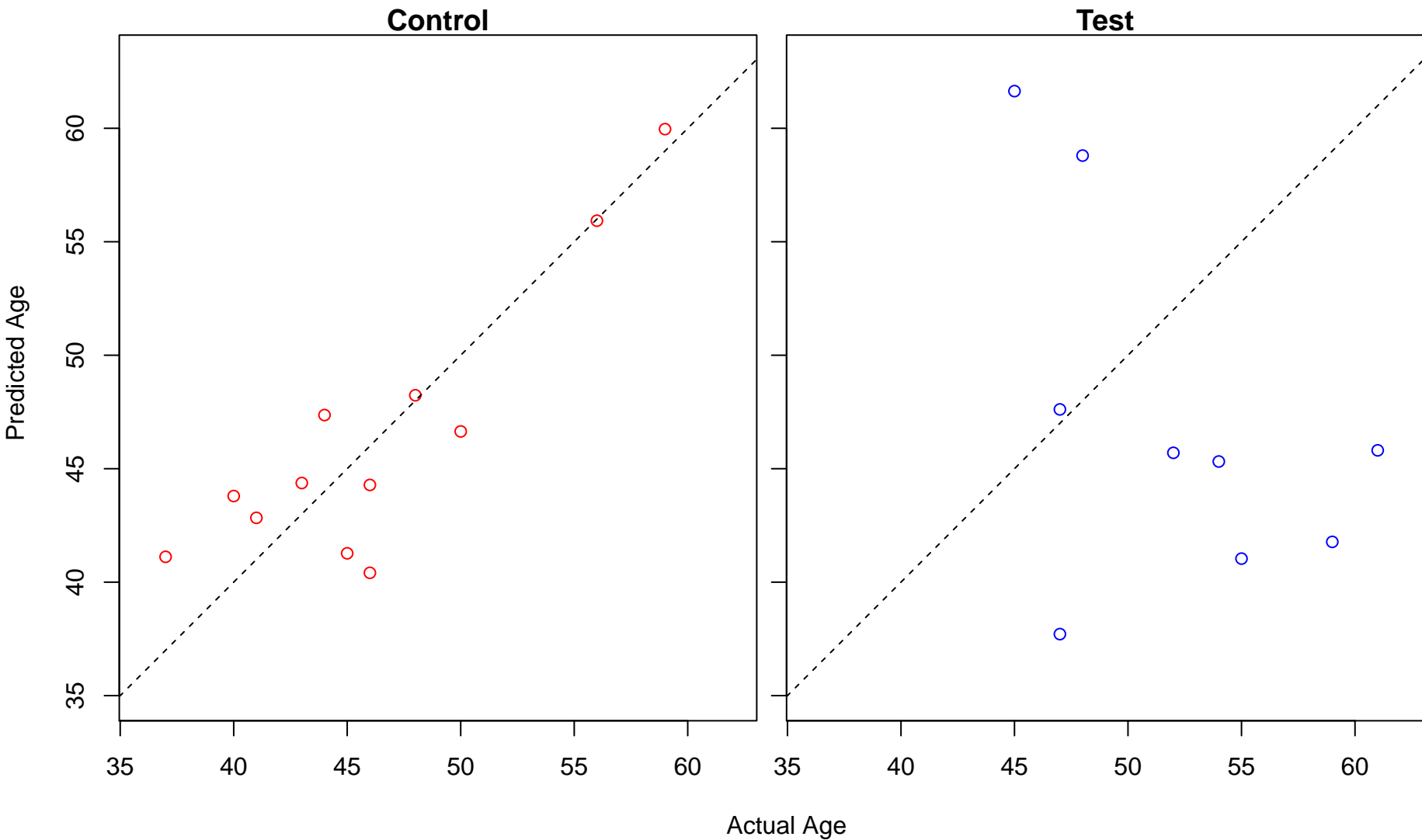


Actual Age

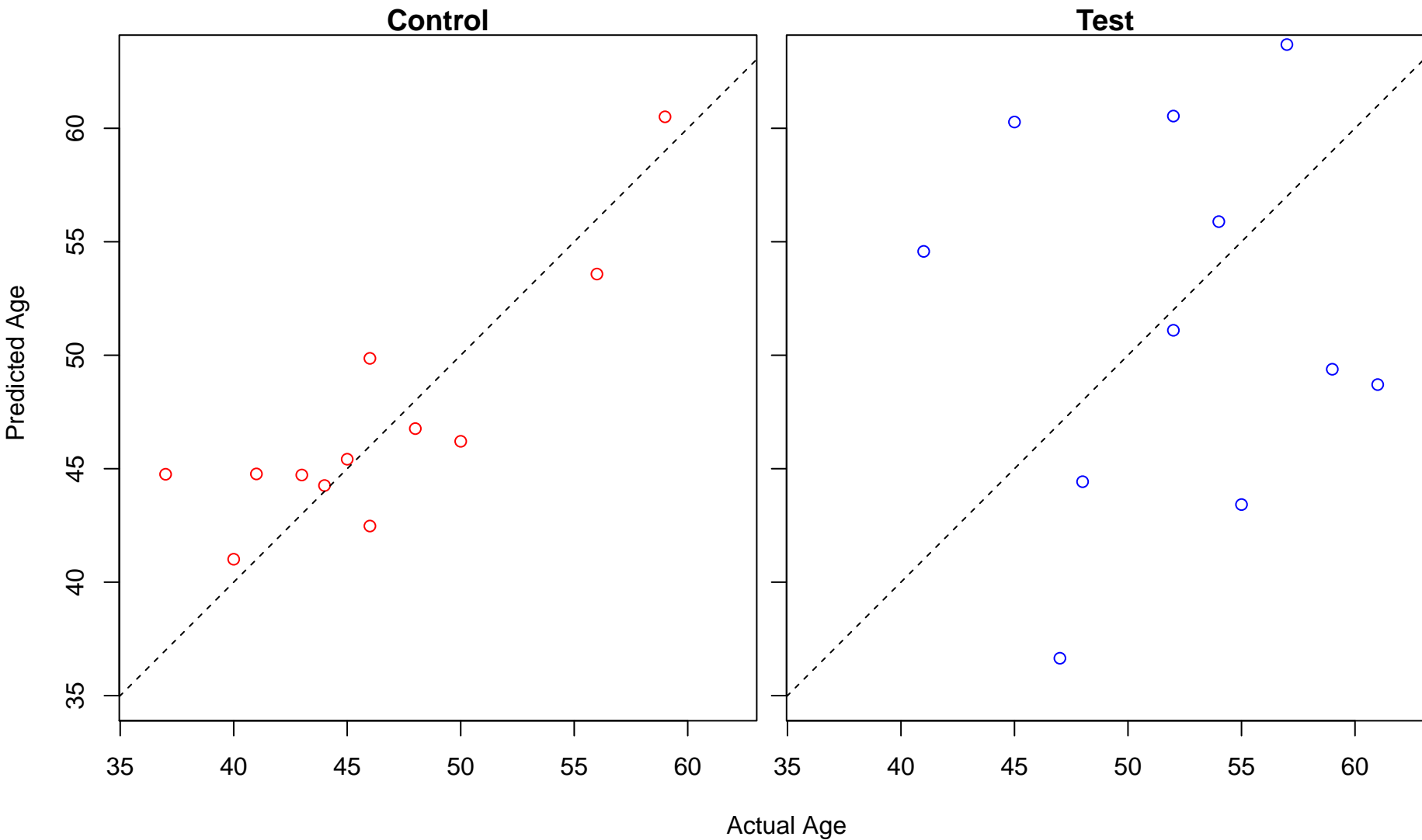
glutamine family amino acid catabolic process (Score: 8.548132)



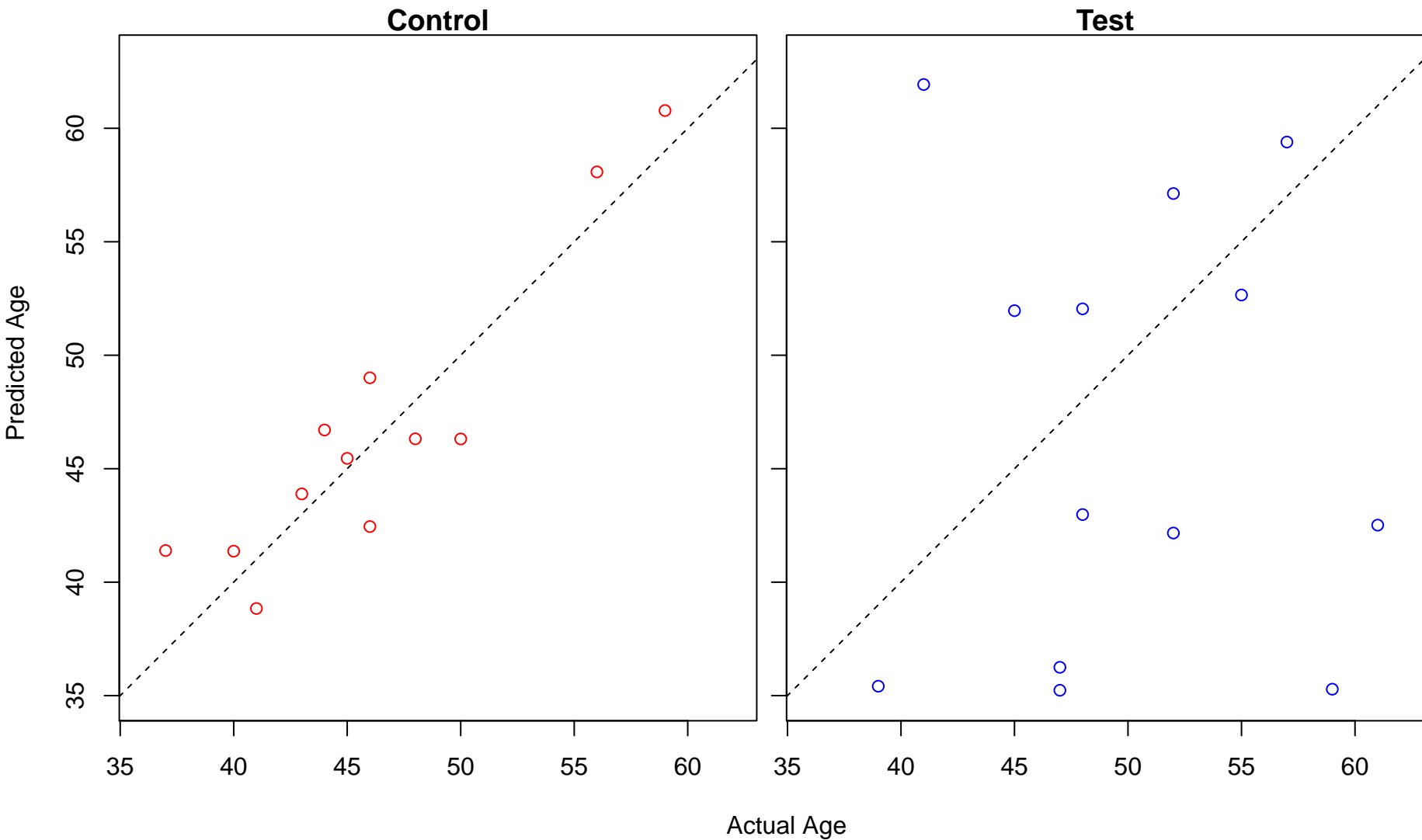
protein import into nucleus, translocation (Score: 8.536828)



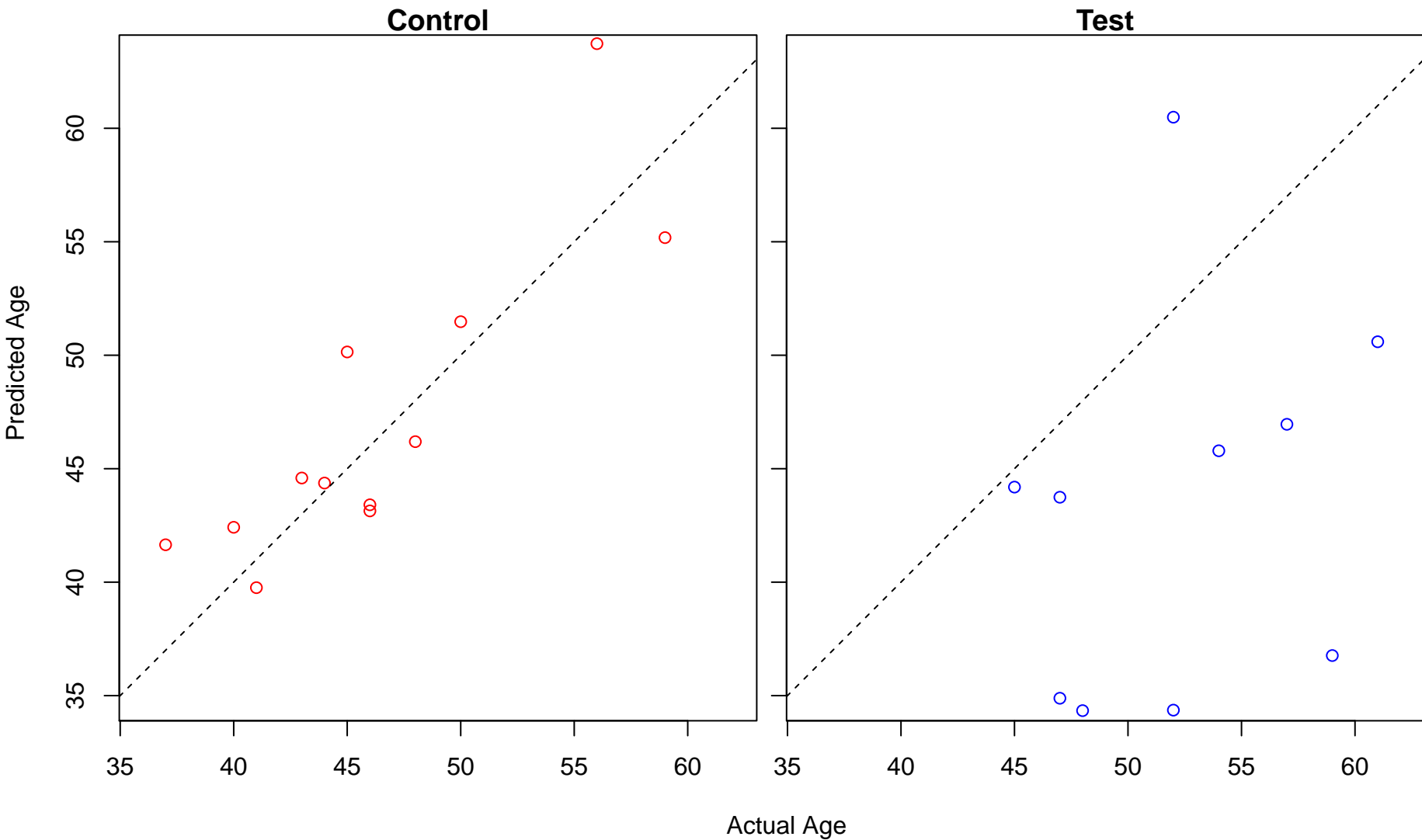
regulation of T cell migration (Score: 8.533683)



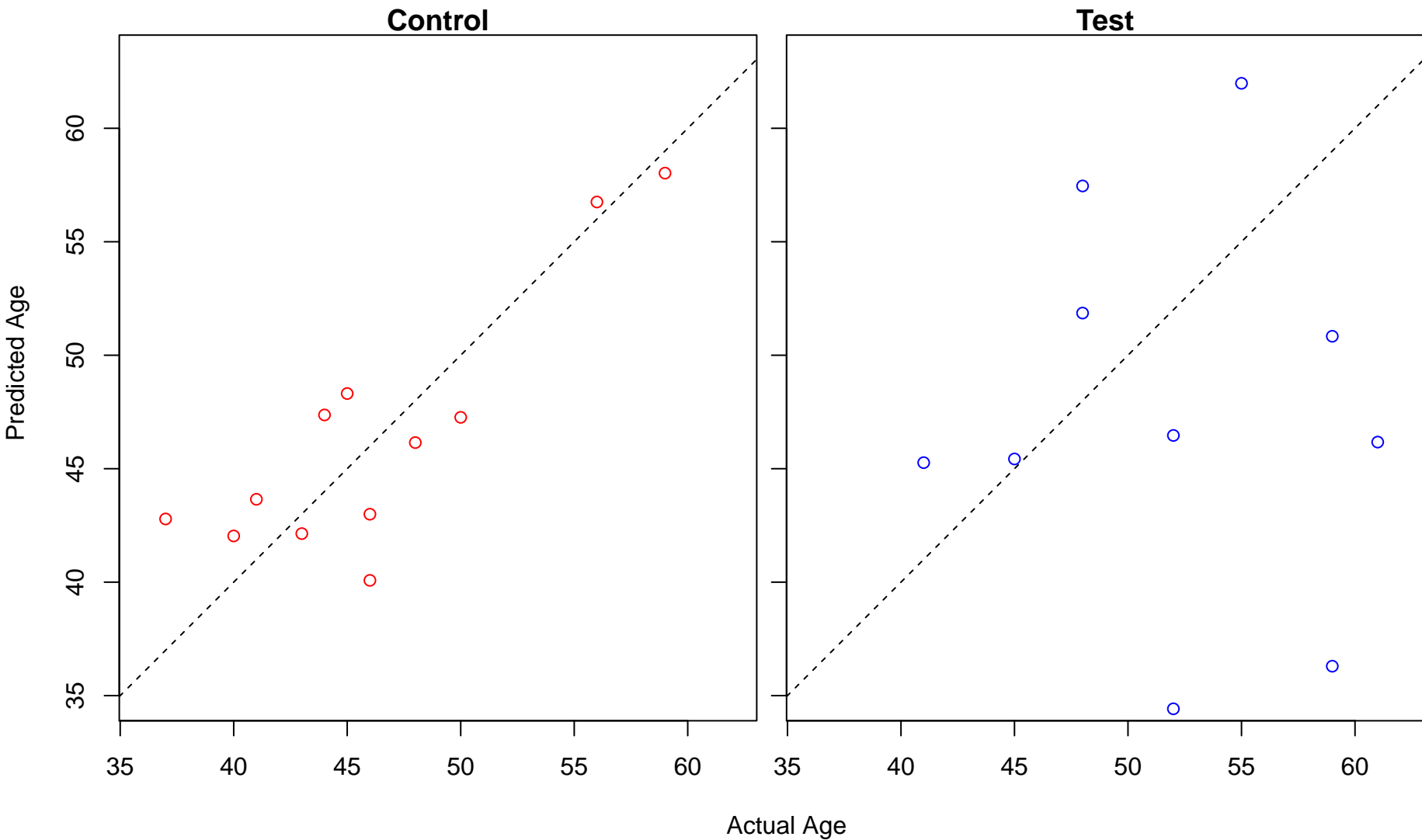
cardiac muscle cell development (Score: 8.532003)



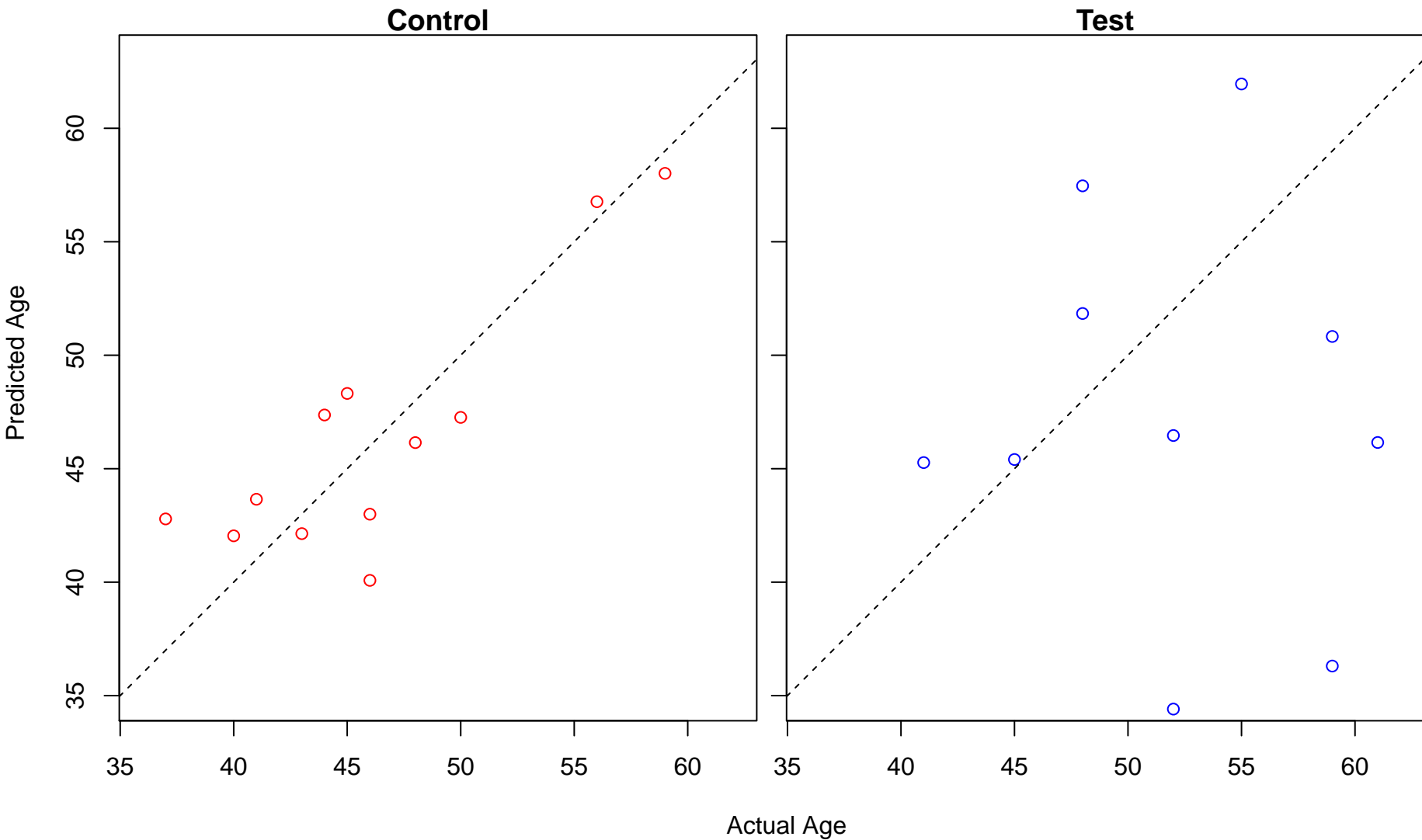
regulation of substrate adhesion-dependent cell spreading (Score: 8.527379)



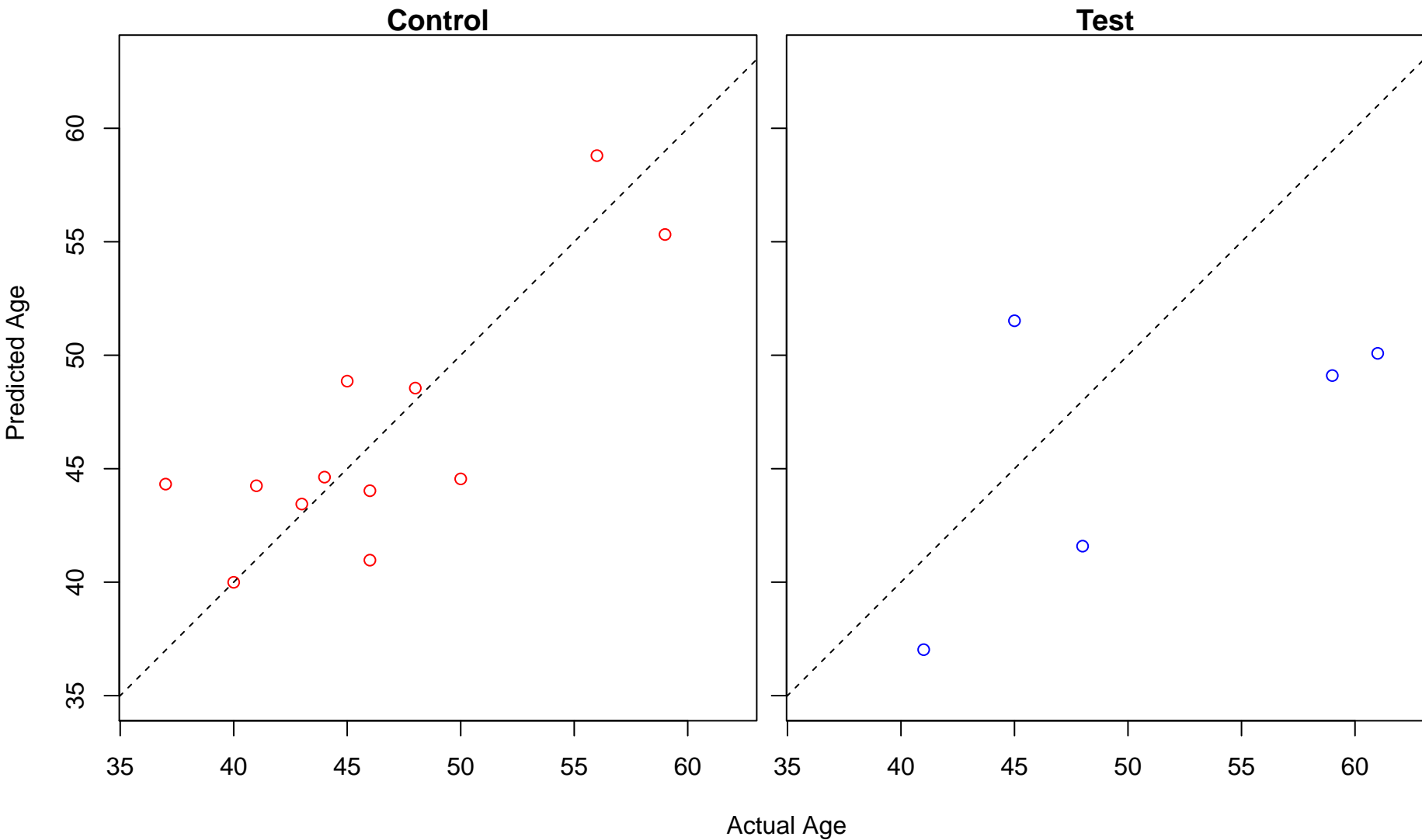
lysosomal transport (Score: 8.510419)



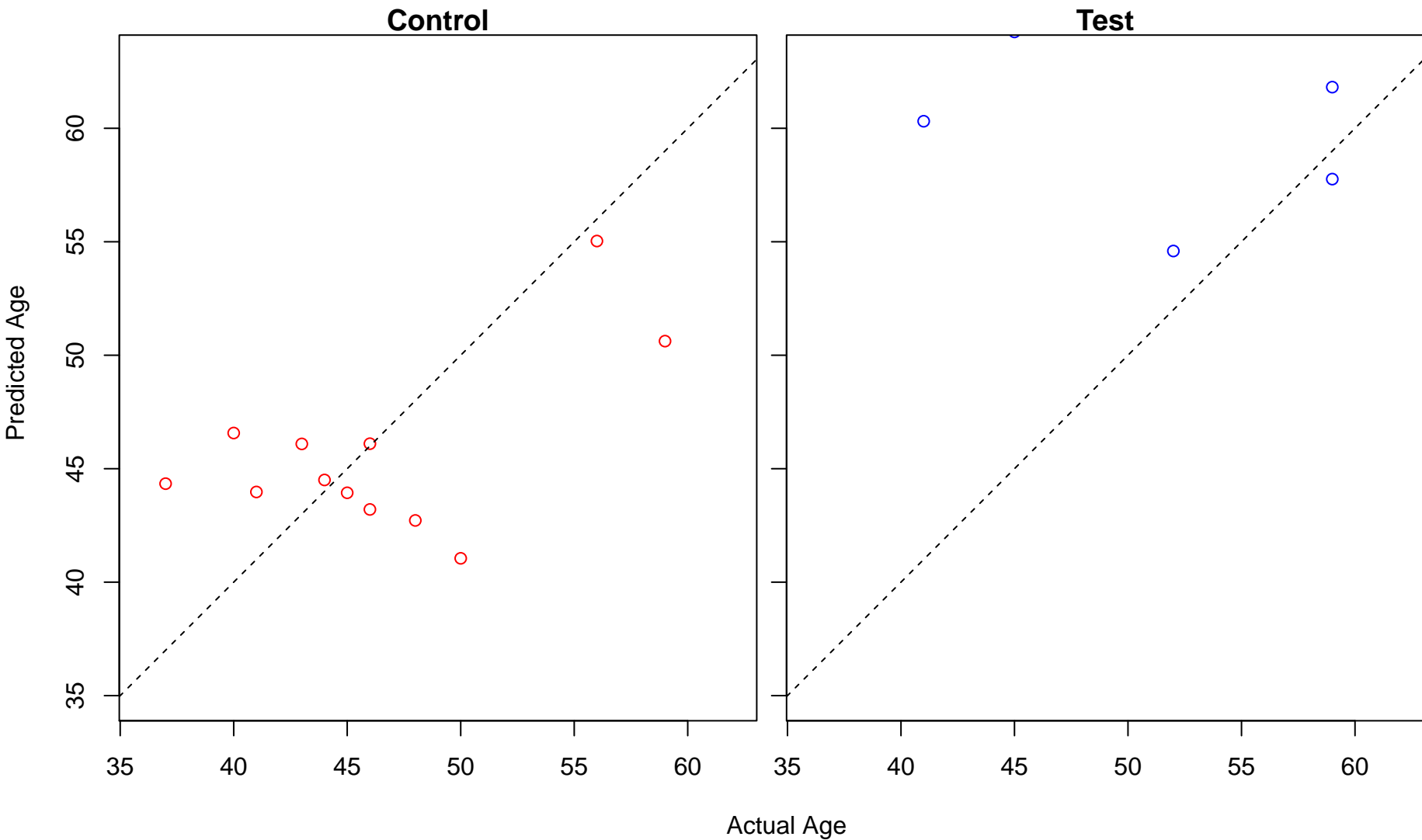
vacuolar transport (Score: 8.501502)



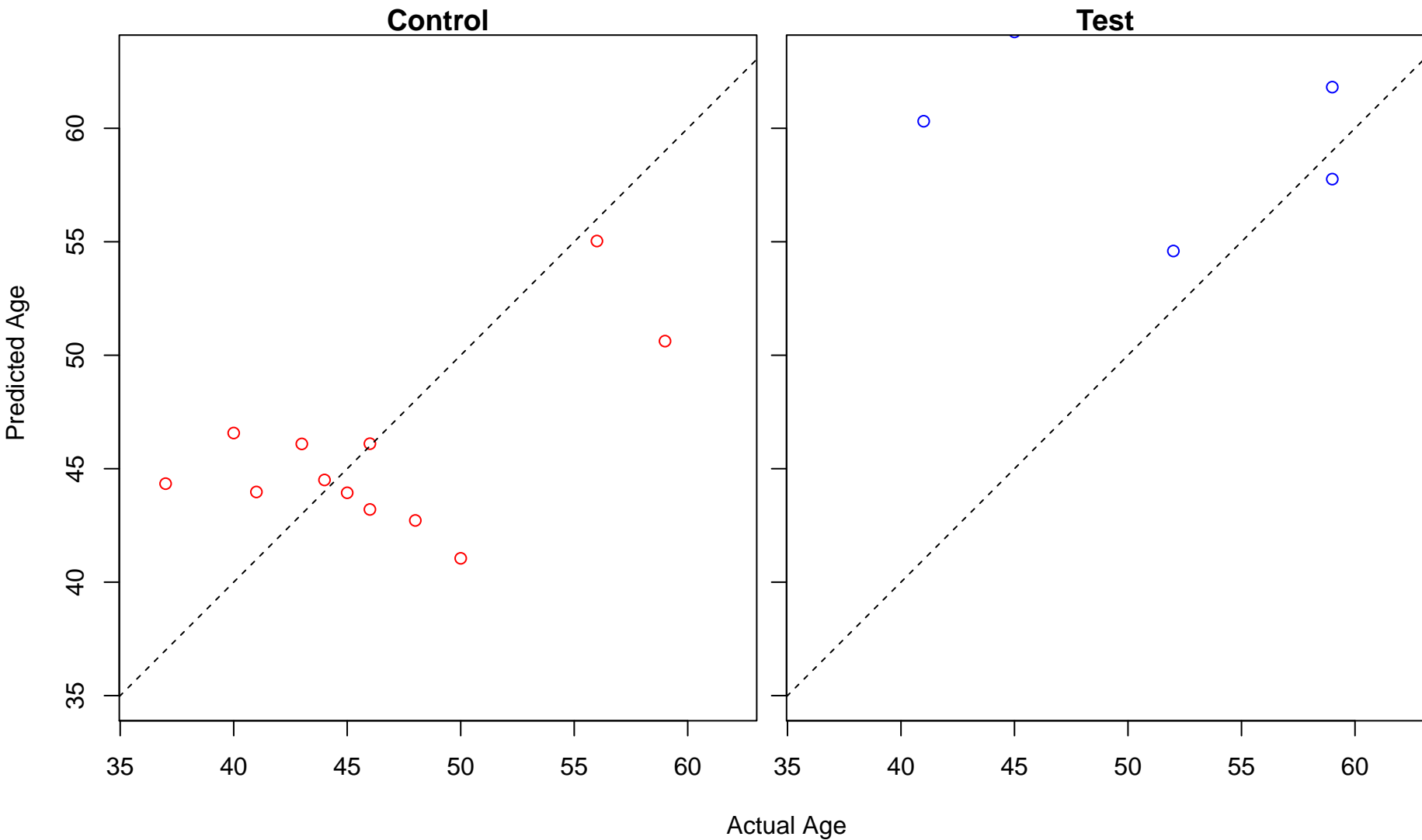
mitral valve morphogenesis (Score: 8.498868)



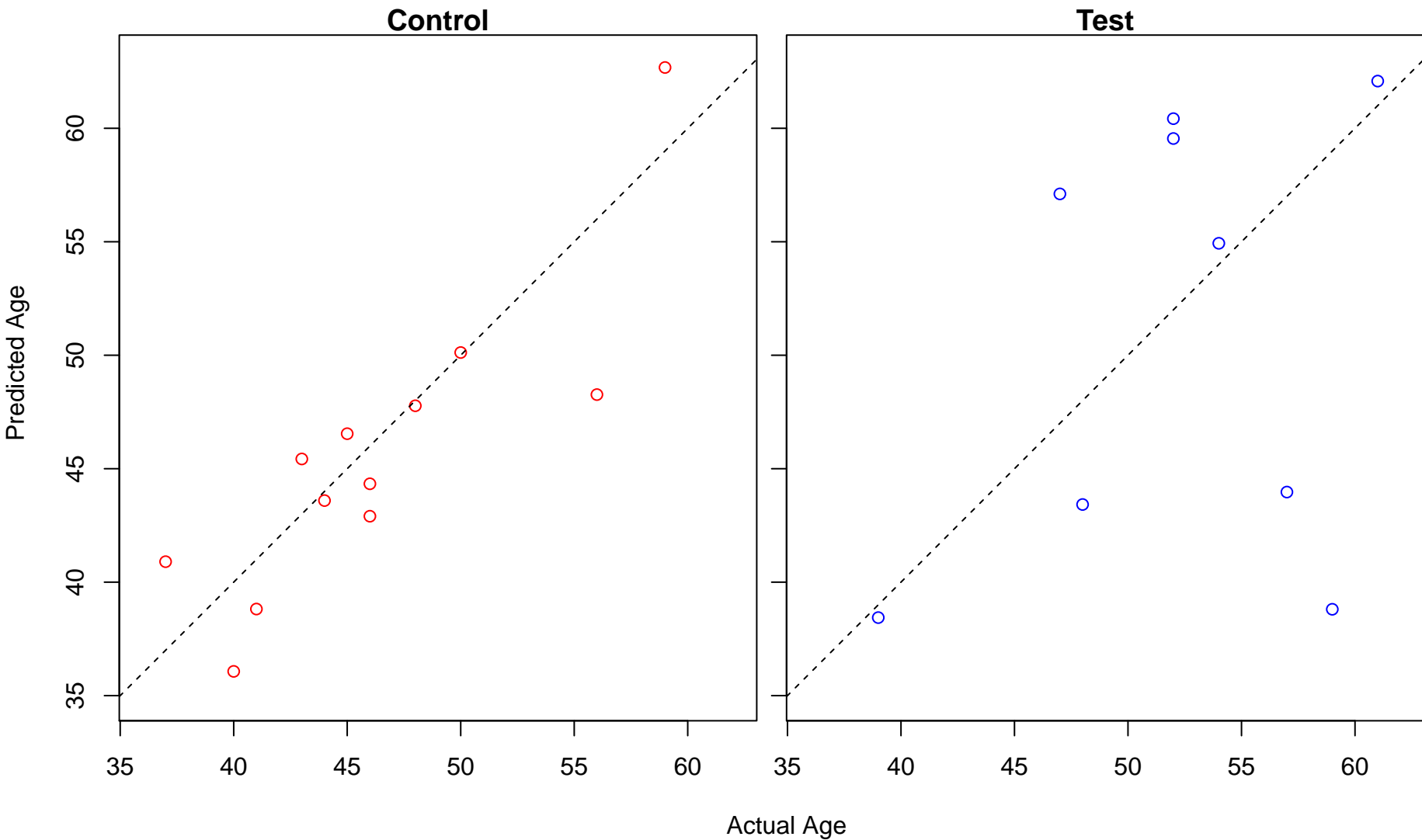
regulation of cell chemotaxis to fibroblast growth factor (Score: 8.493643)



regulation of endothelial cell chemotaxis to fibroblast growth factor (Score: 8.493643)

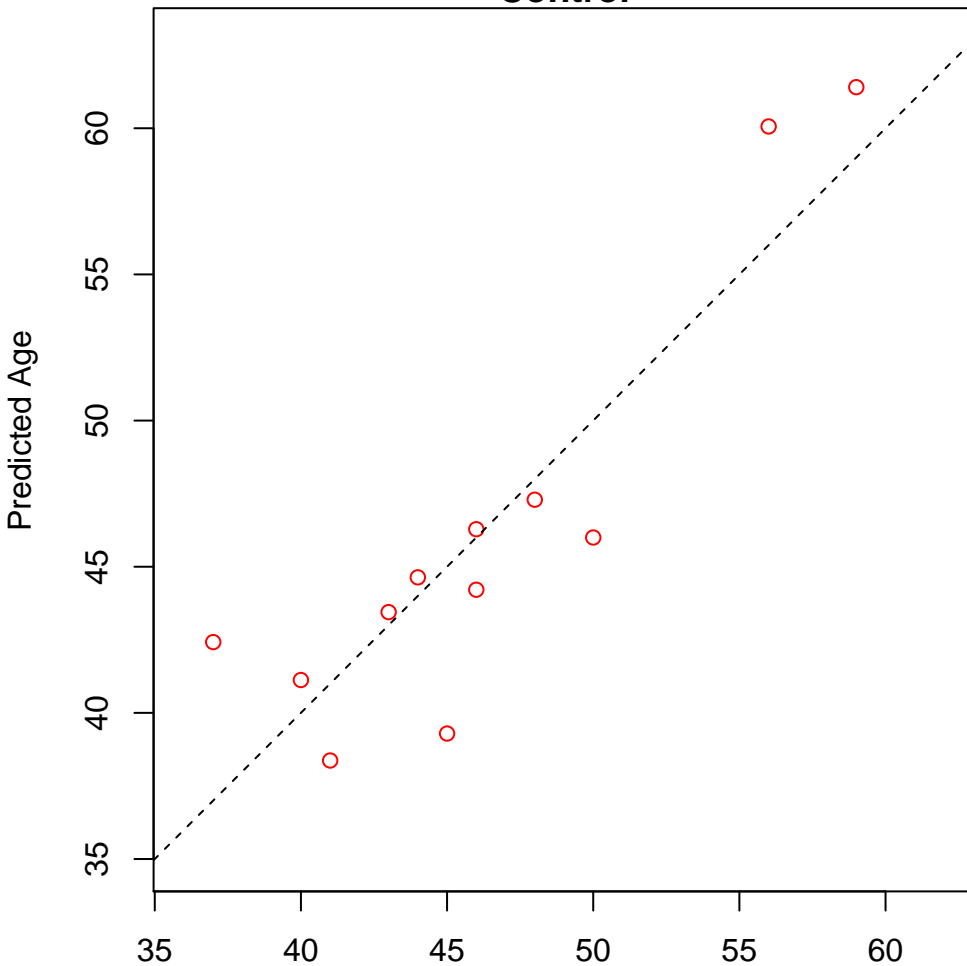


filopodium assembly (Score: 8.491441)

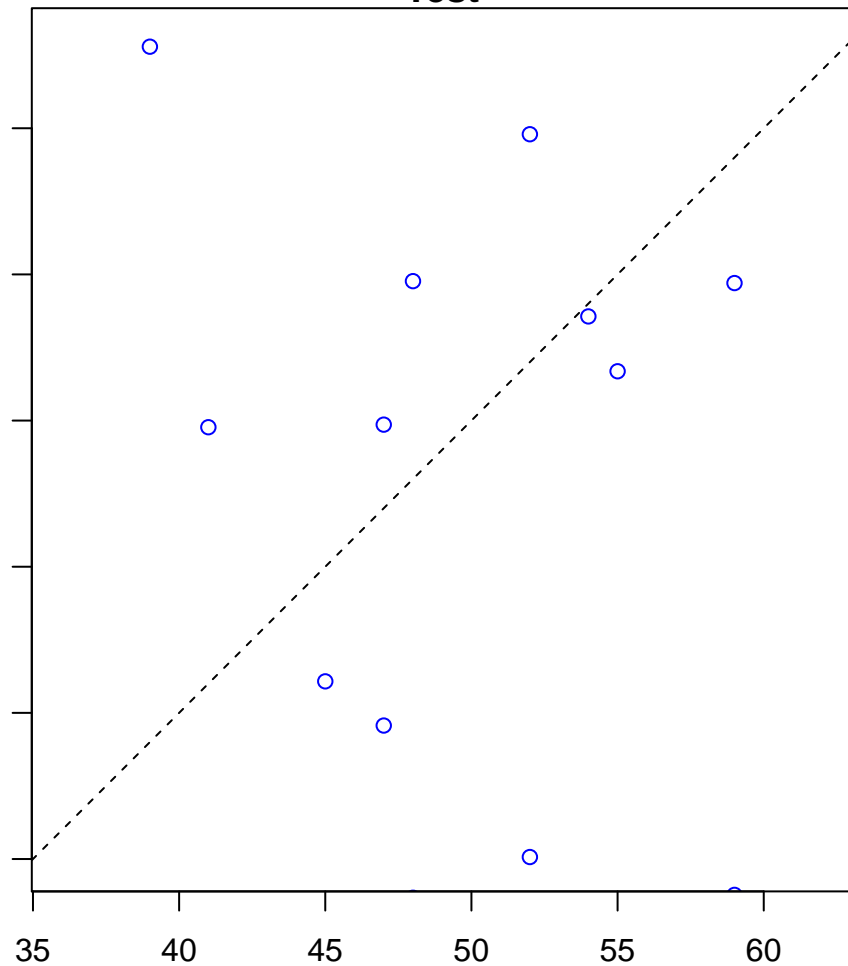


modulation by virus of host process (Score: 8.490736)

Control

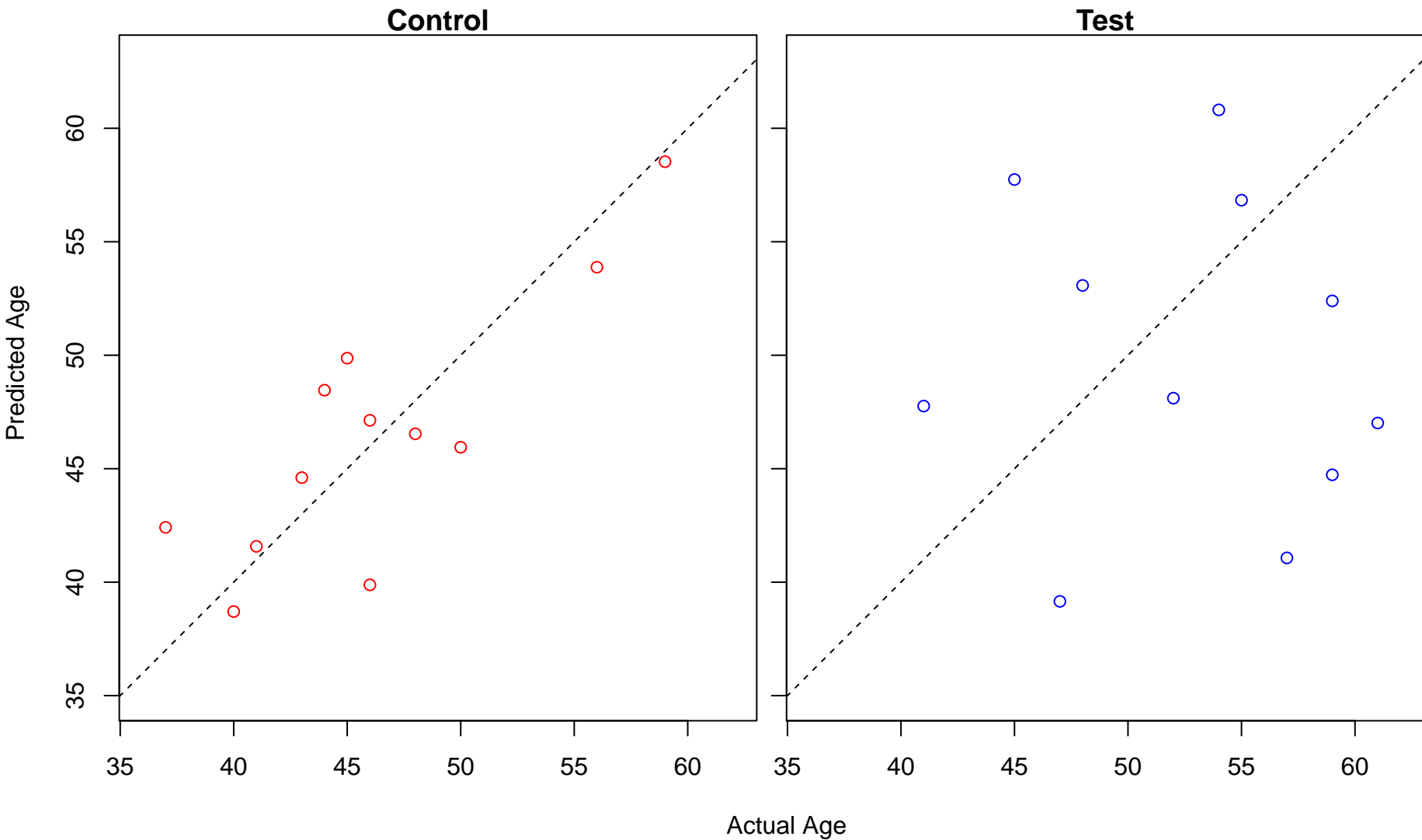


Test

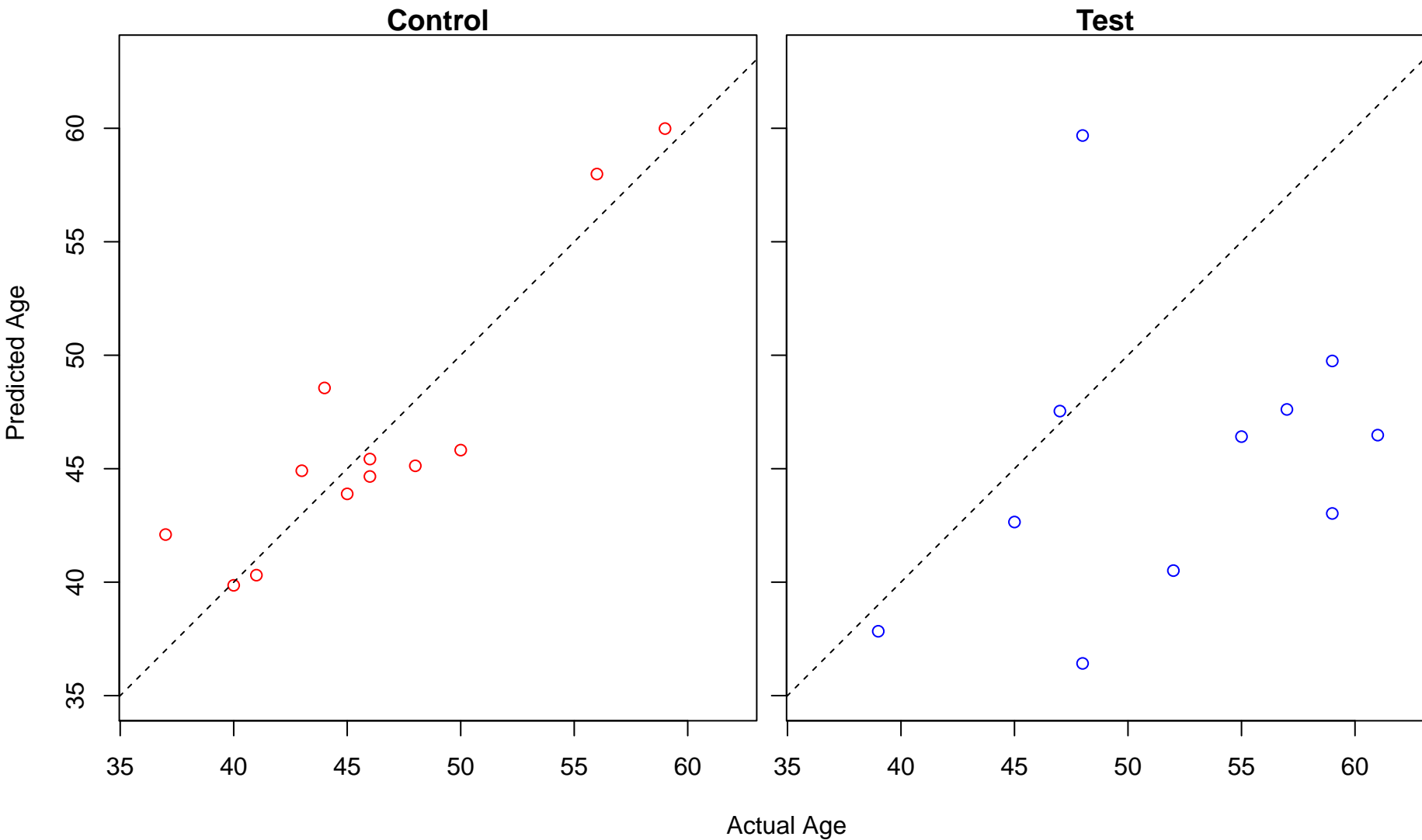


Actual Age

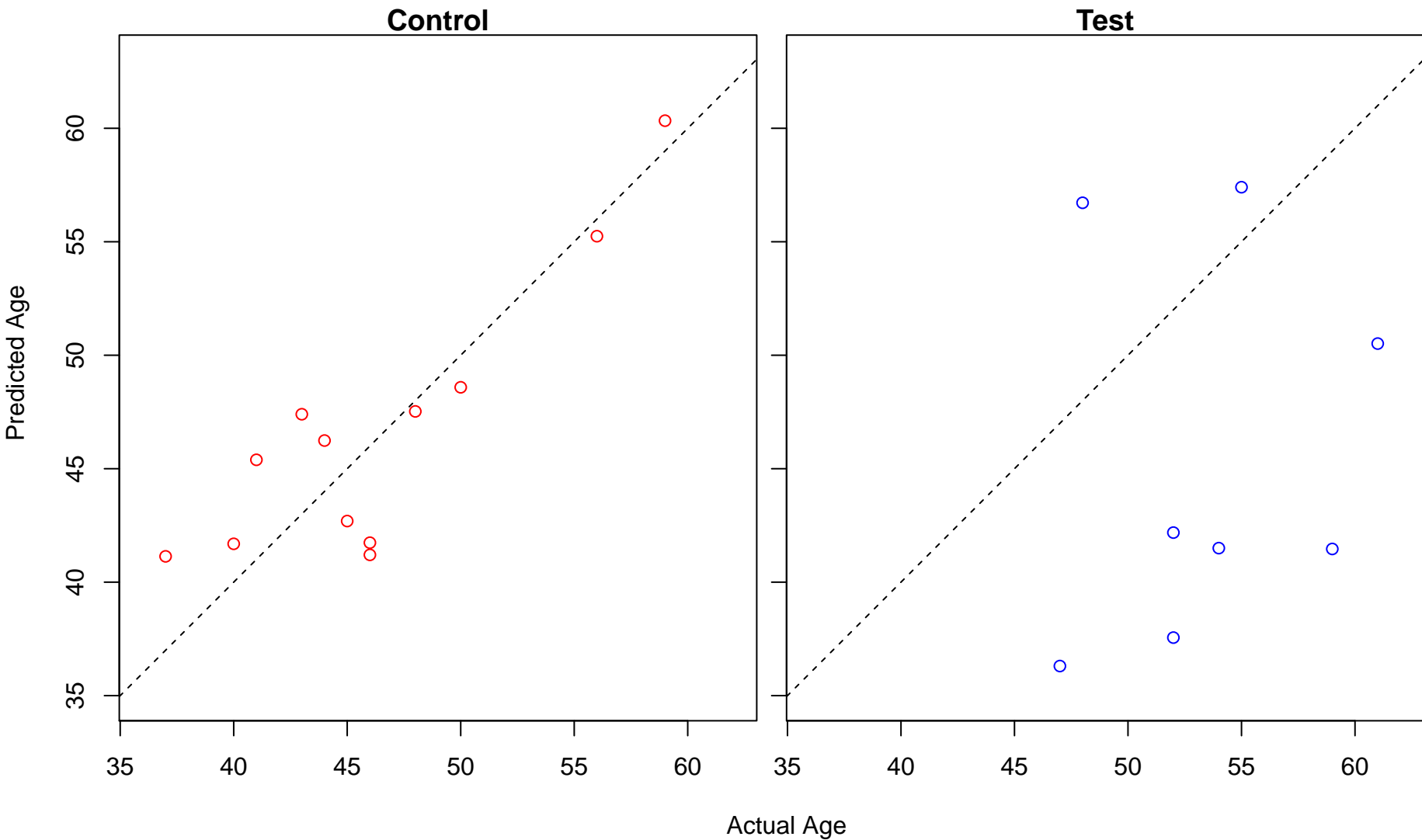
positive regulation of DNA replication (Score: 8.484856)



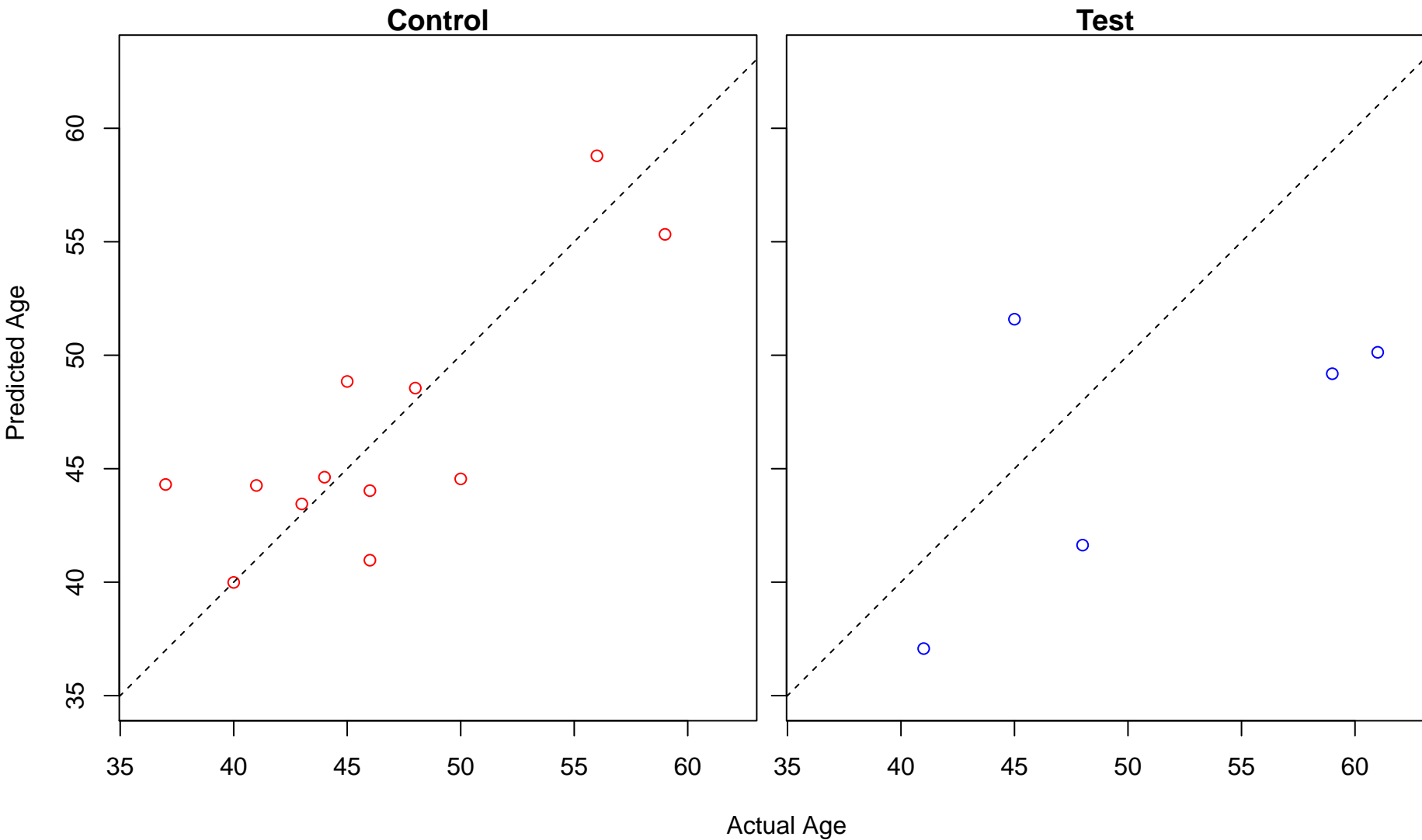
mesonephros development (Score: 8.478152)



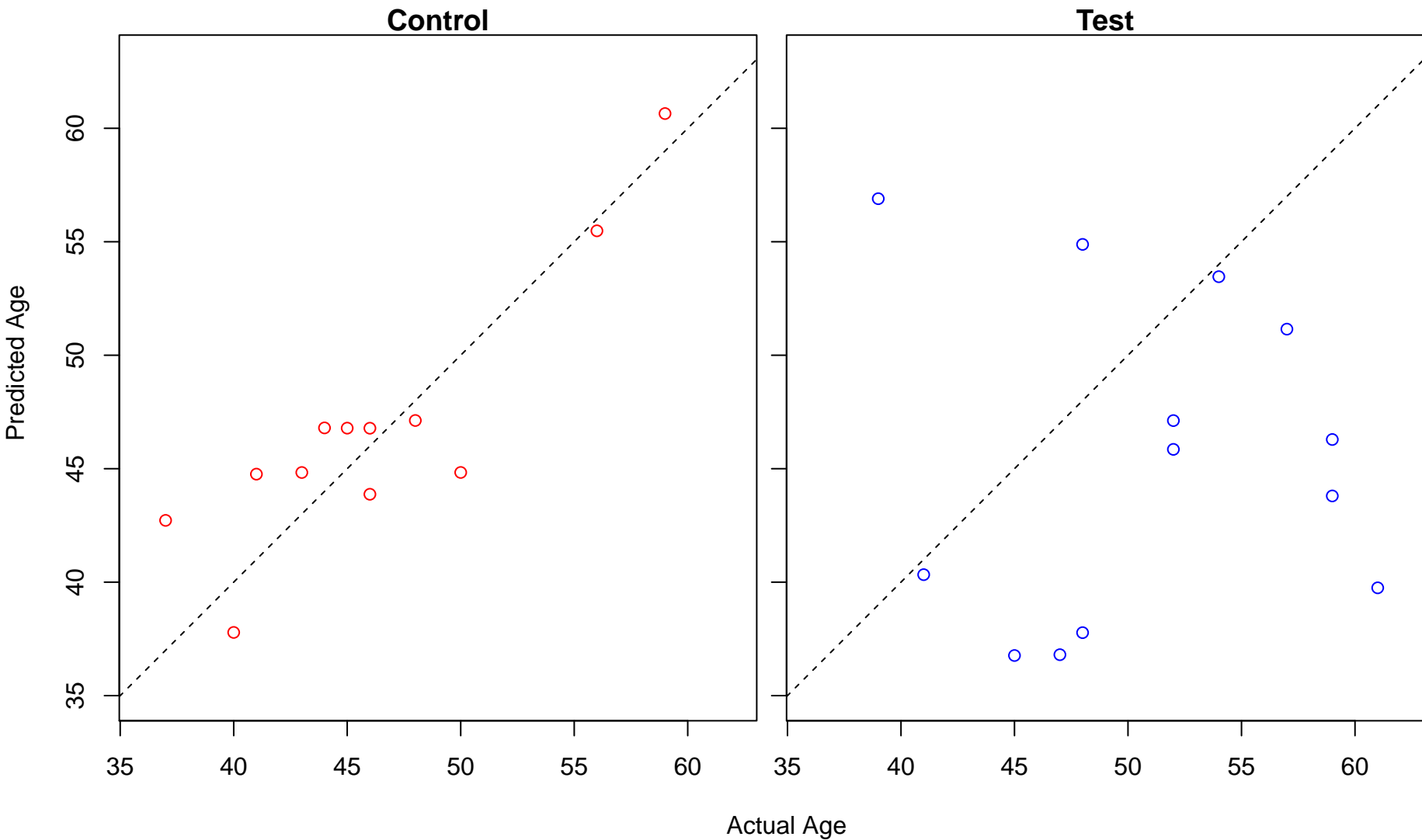
cellular response to steroid hormone stimulus (Score: 8.477508)



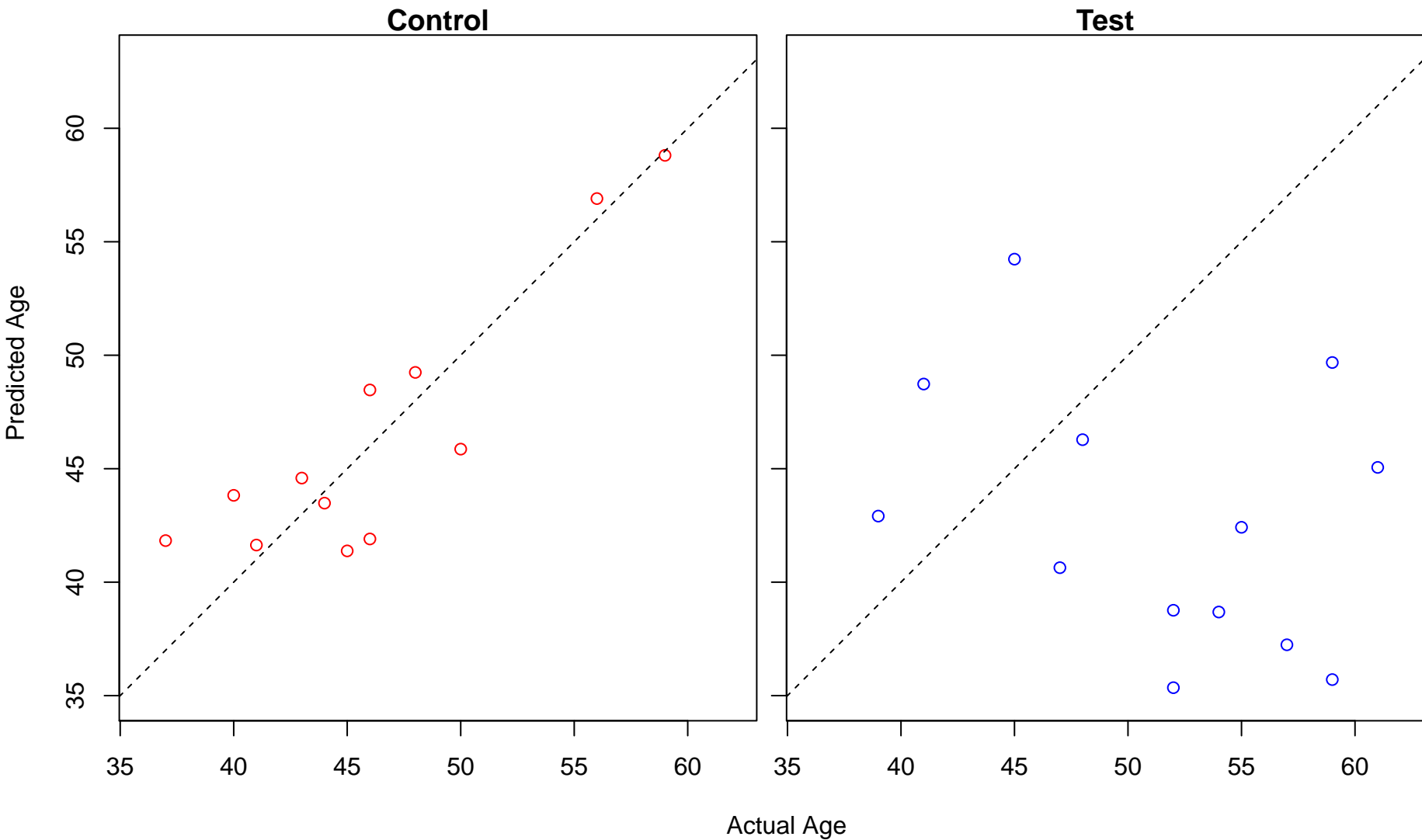
mitral valve development (Score: 8.473815)



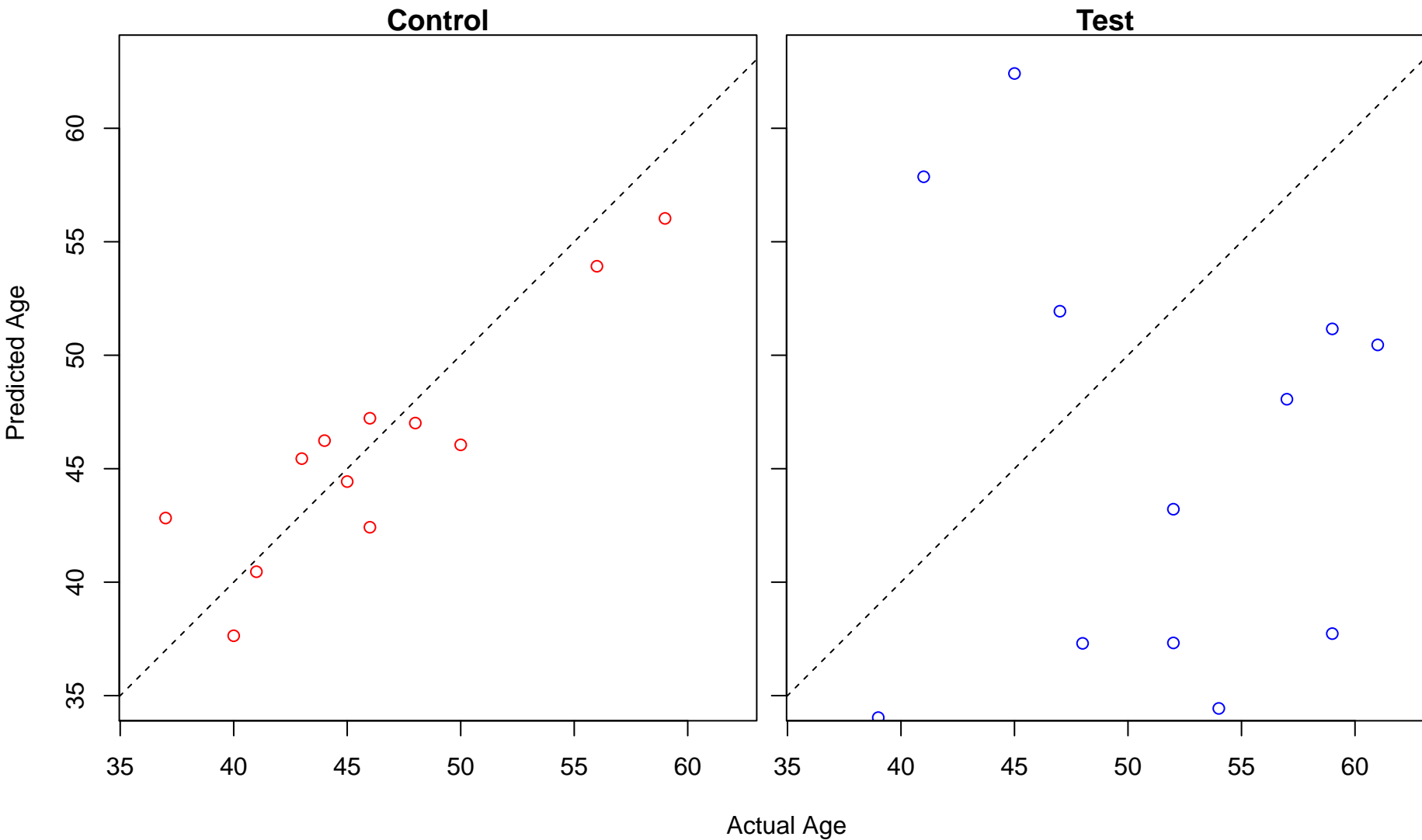
sphingolipid metabolic process (Score: 8.467653)



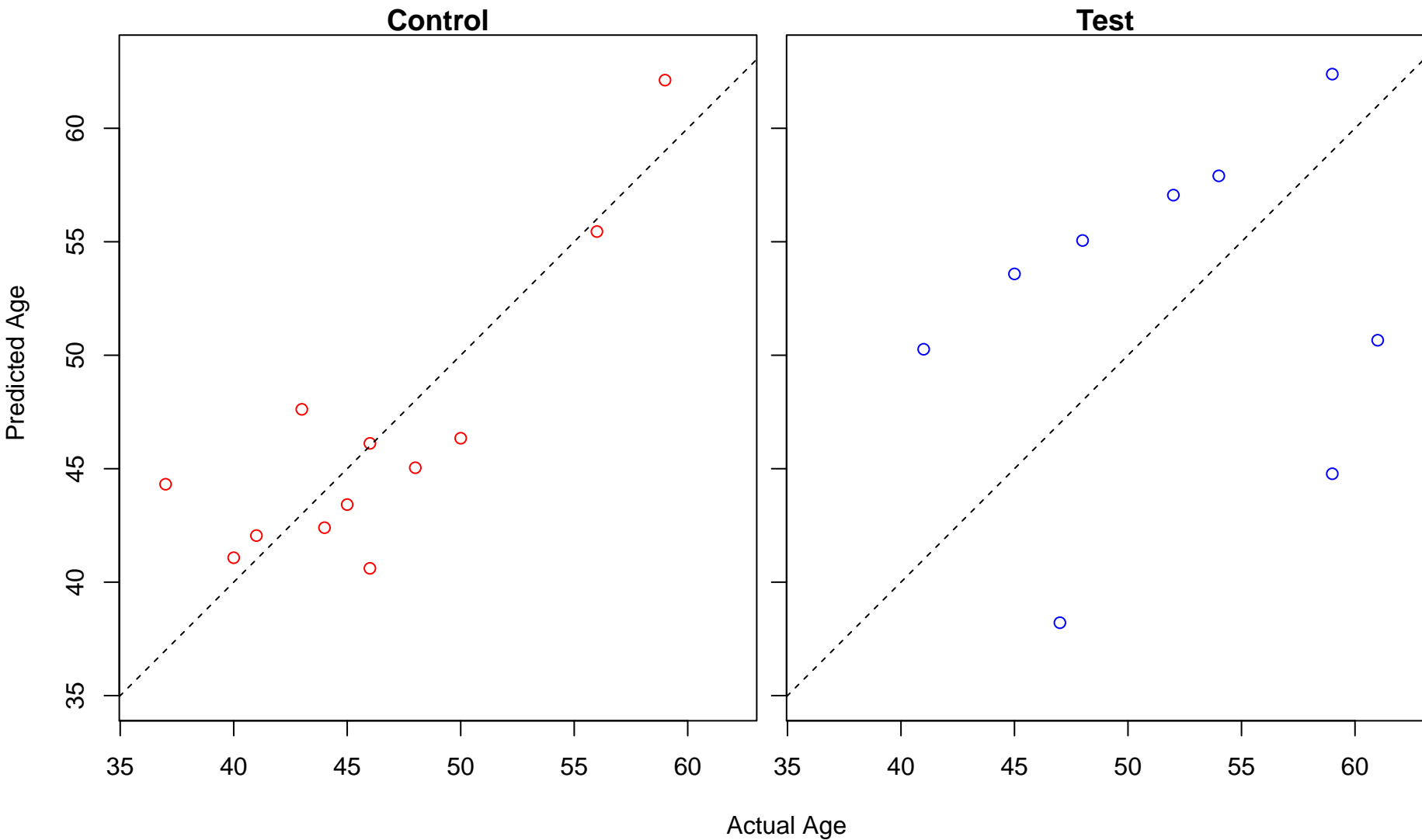
regulation of anion transport (Score: 8.462997)



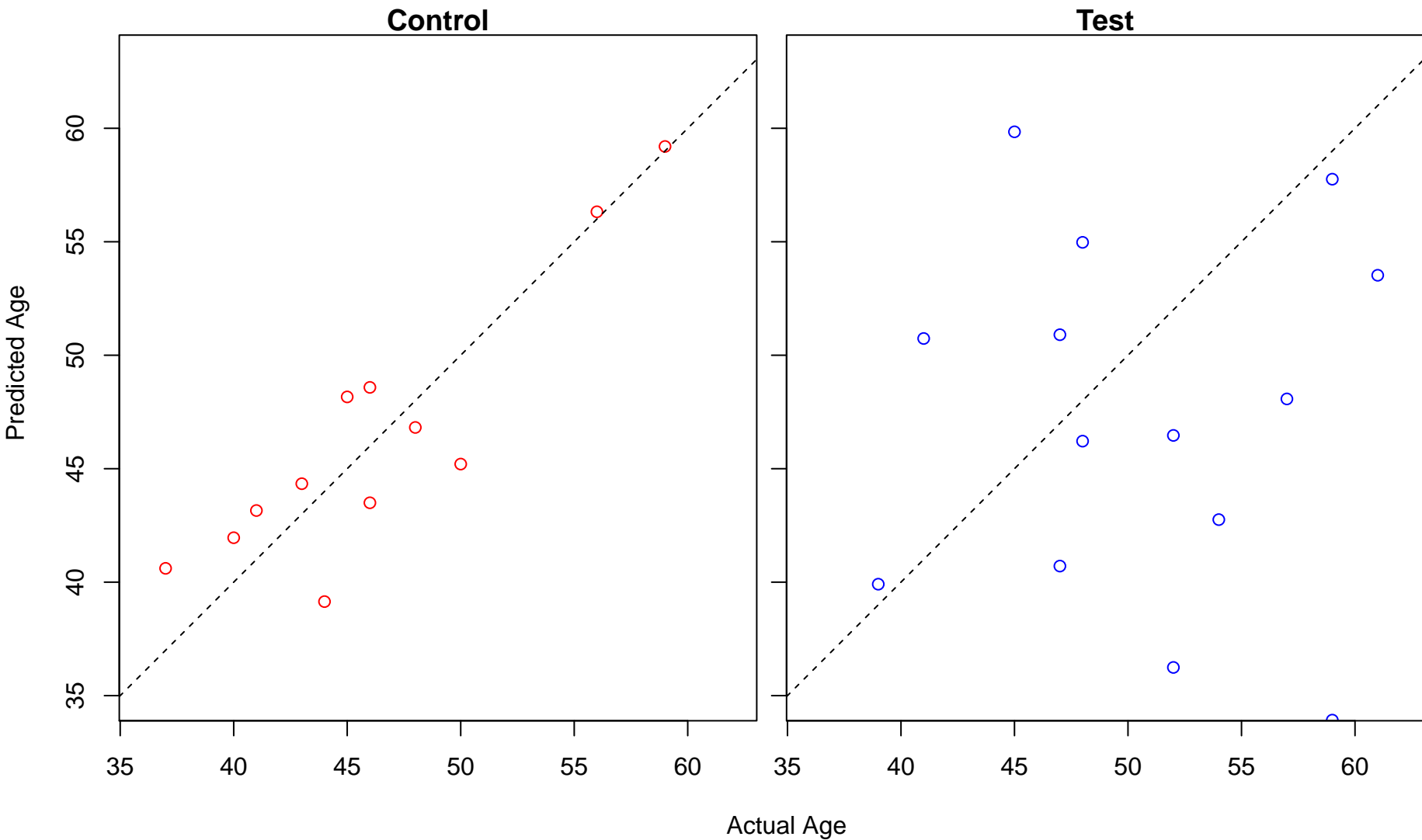
heart development (Score: 8.460356)



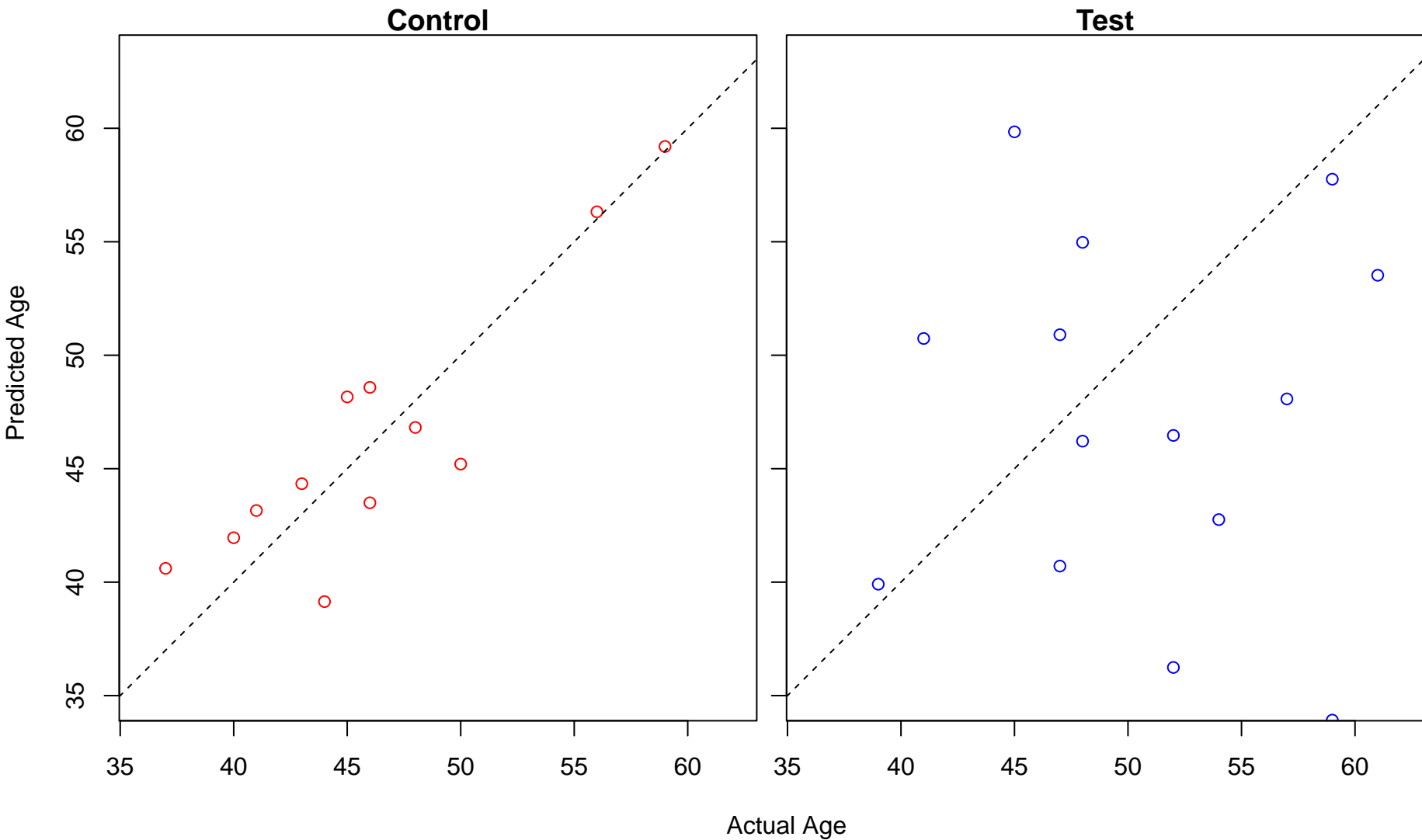
regulation of cell shape (Score: 8.450241)



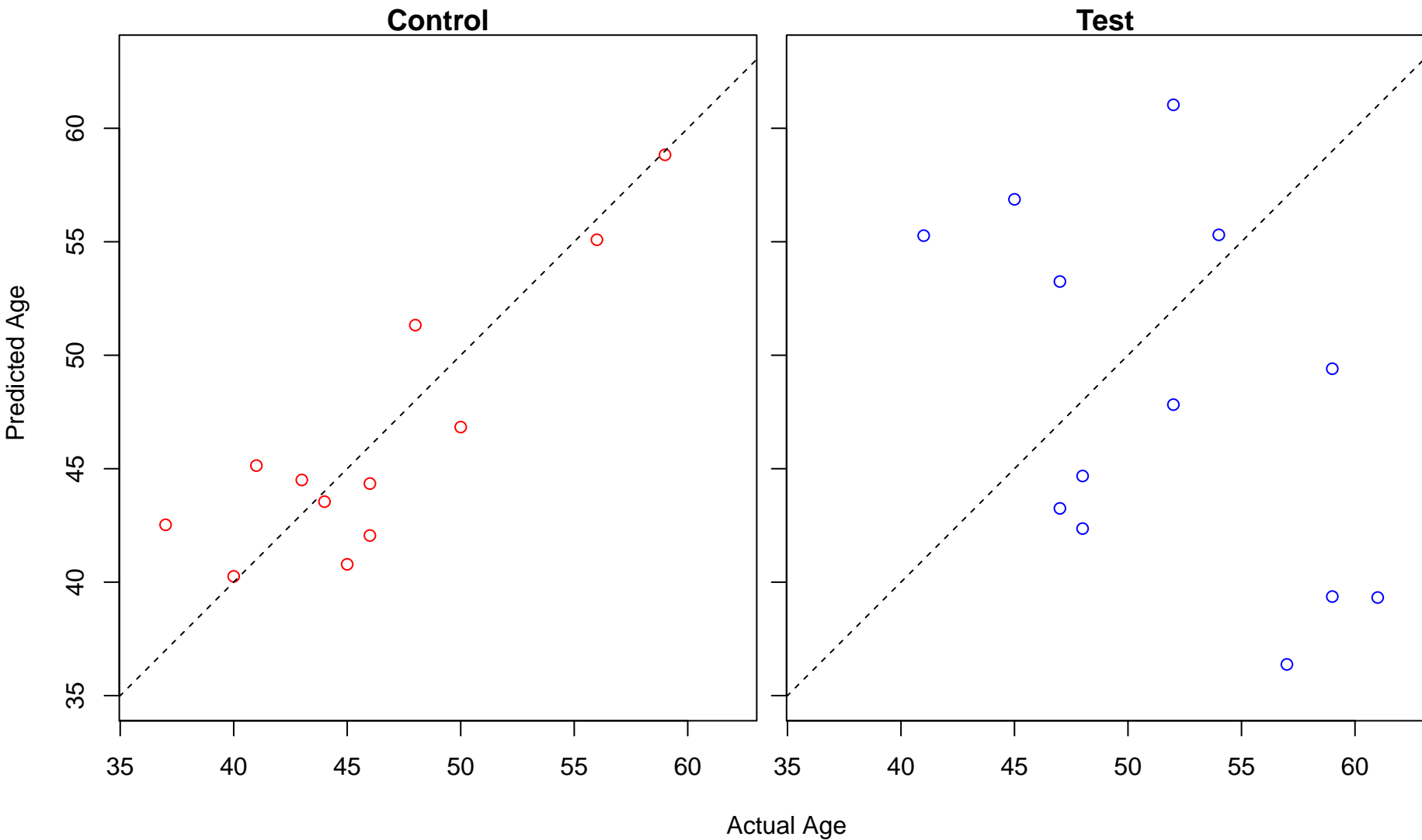
negative regulation of protein processing (Score: 8.426774)



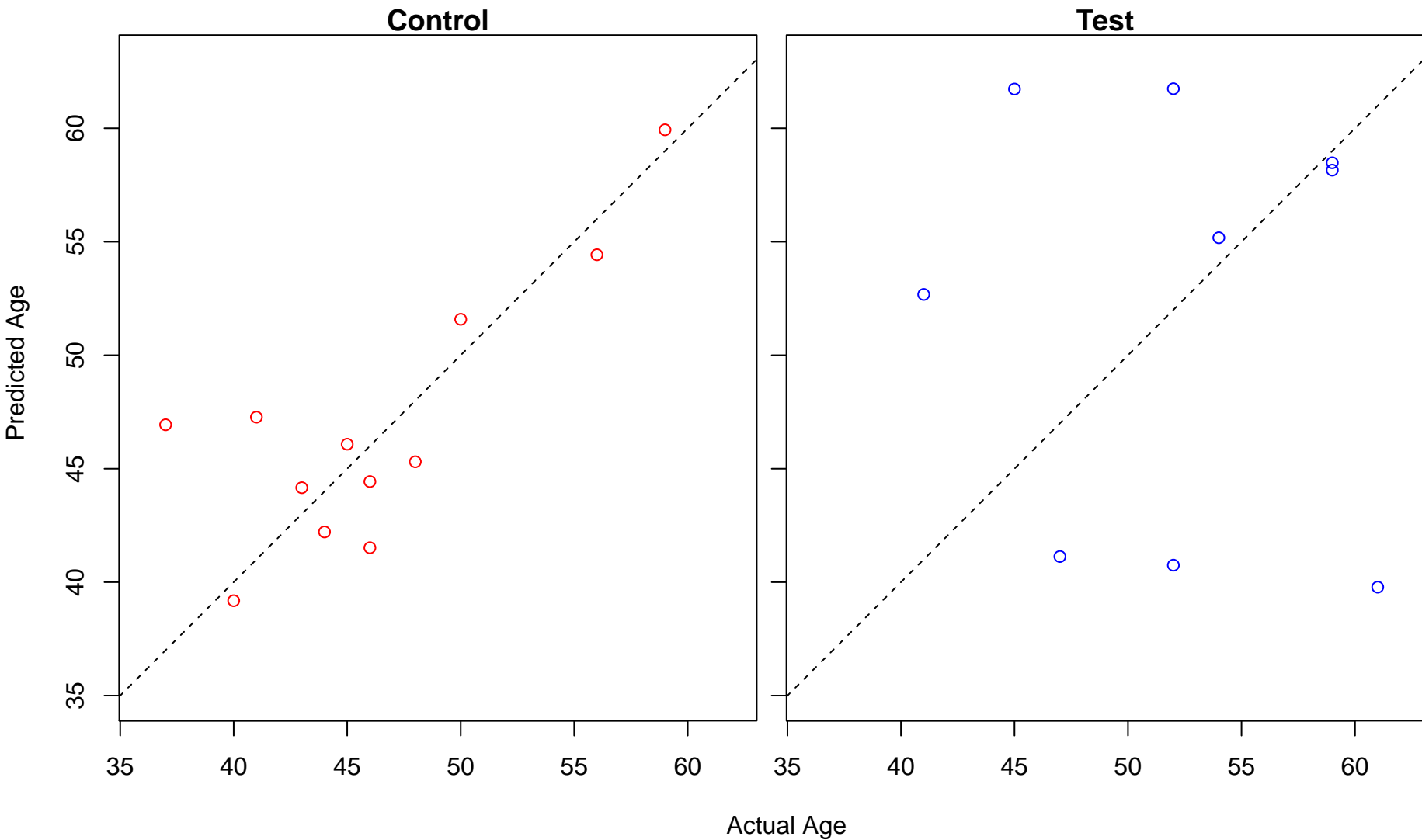
negative regulation of protein maturation (Score: 8.426774)



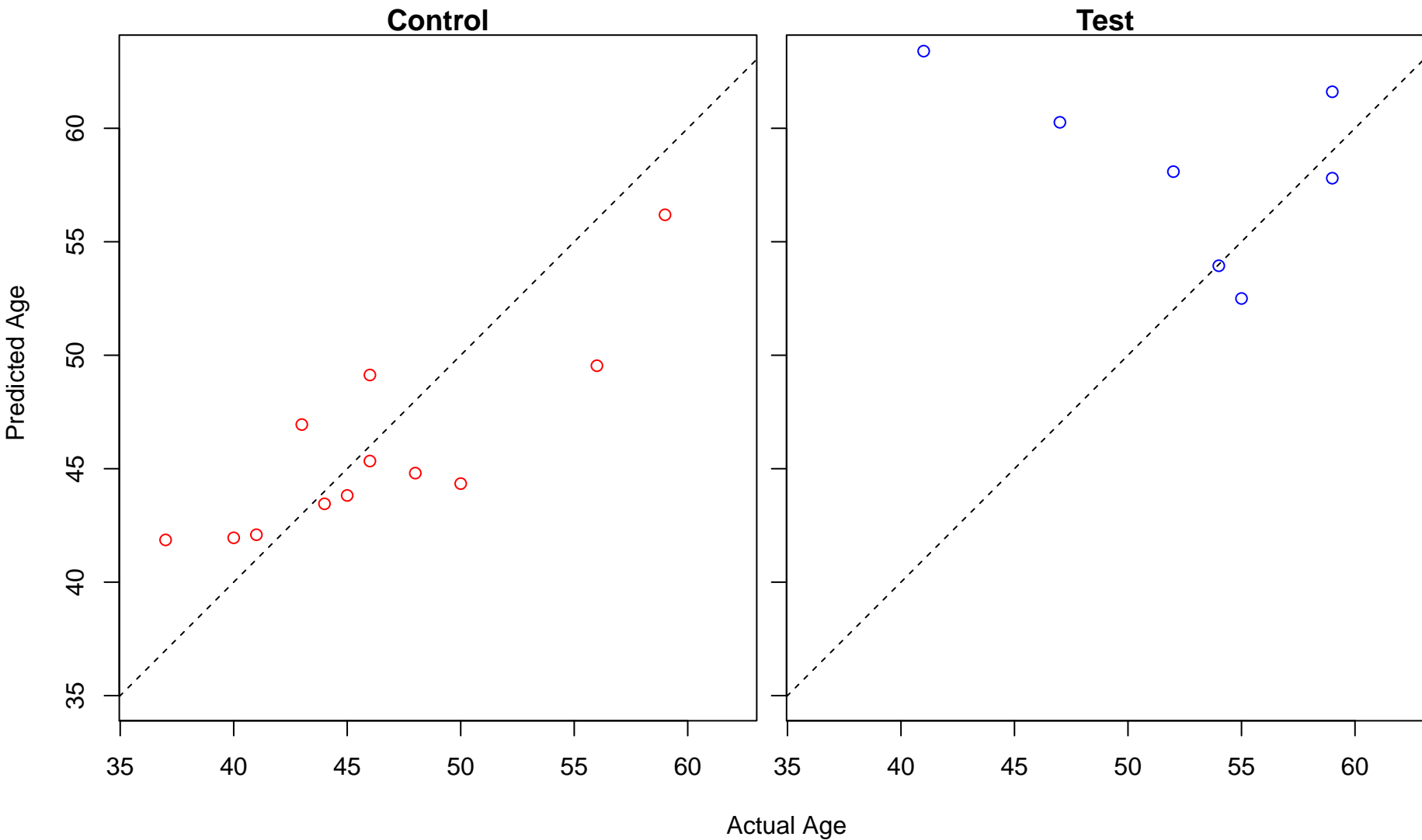
activation of anaphase-promoting complex activity (Score: 8.396997)



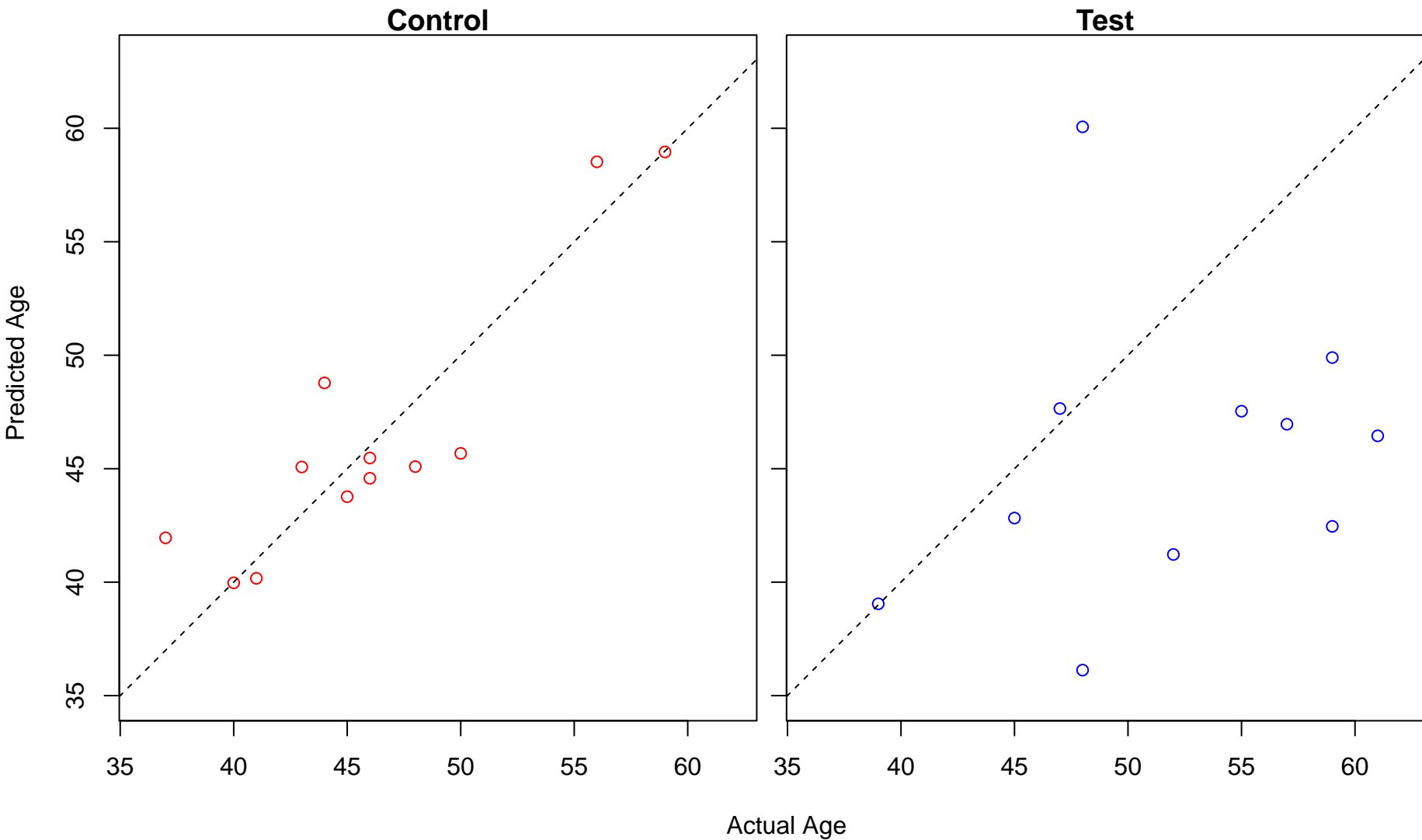
nucleoside salvage (Score: 8.391778)



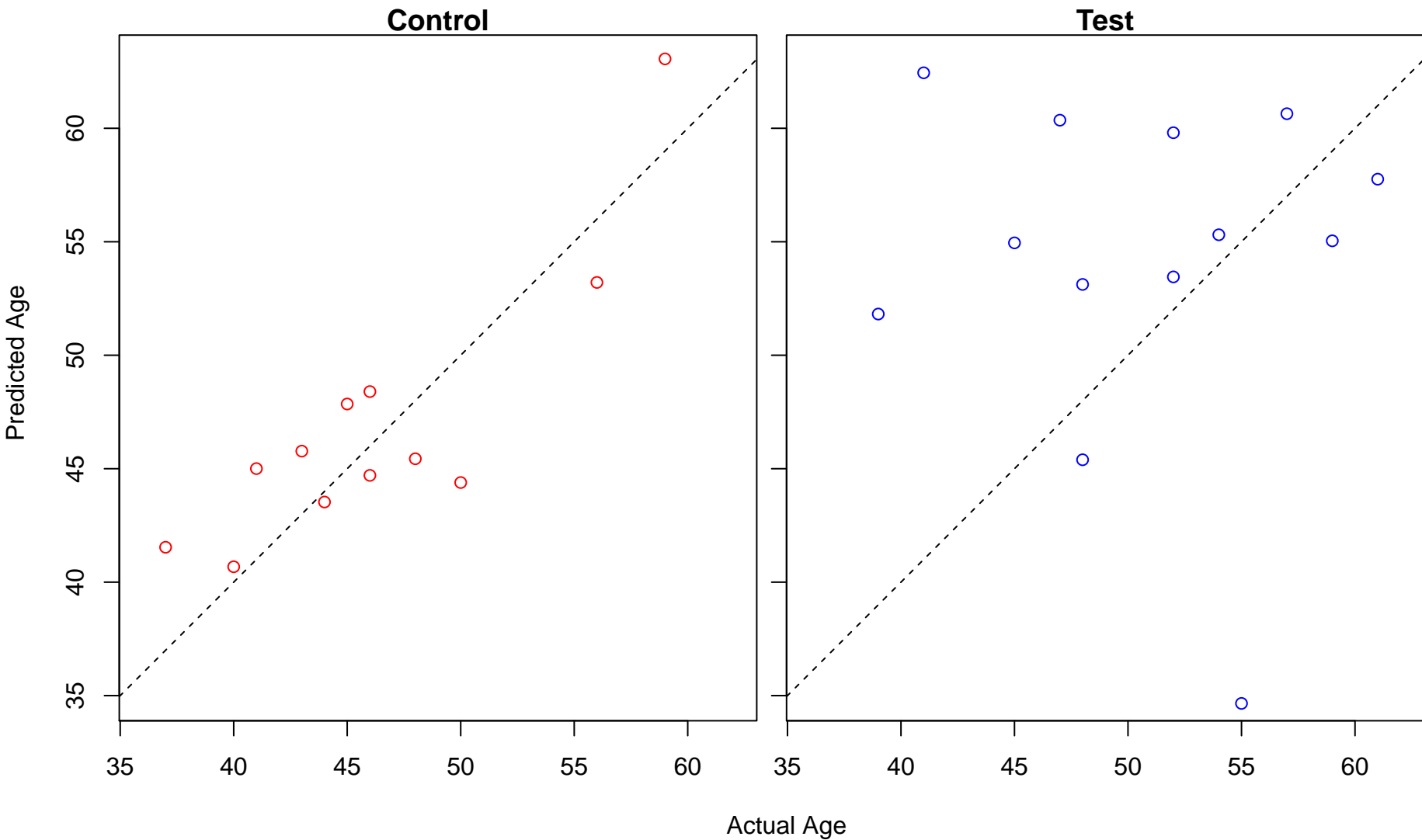
positive regulation of neural precursor cell proliferation (Score: 8.384133)



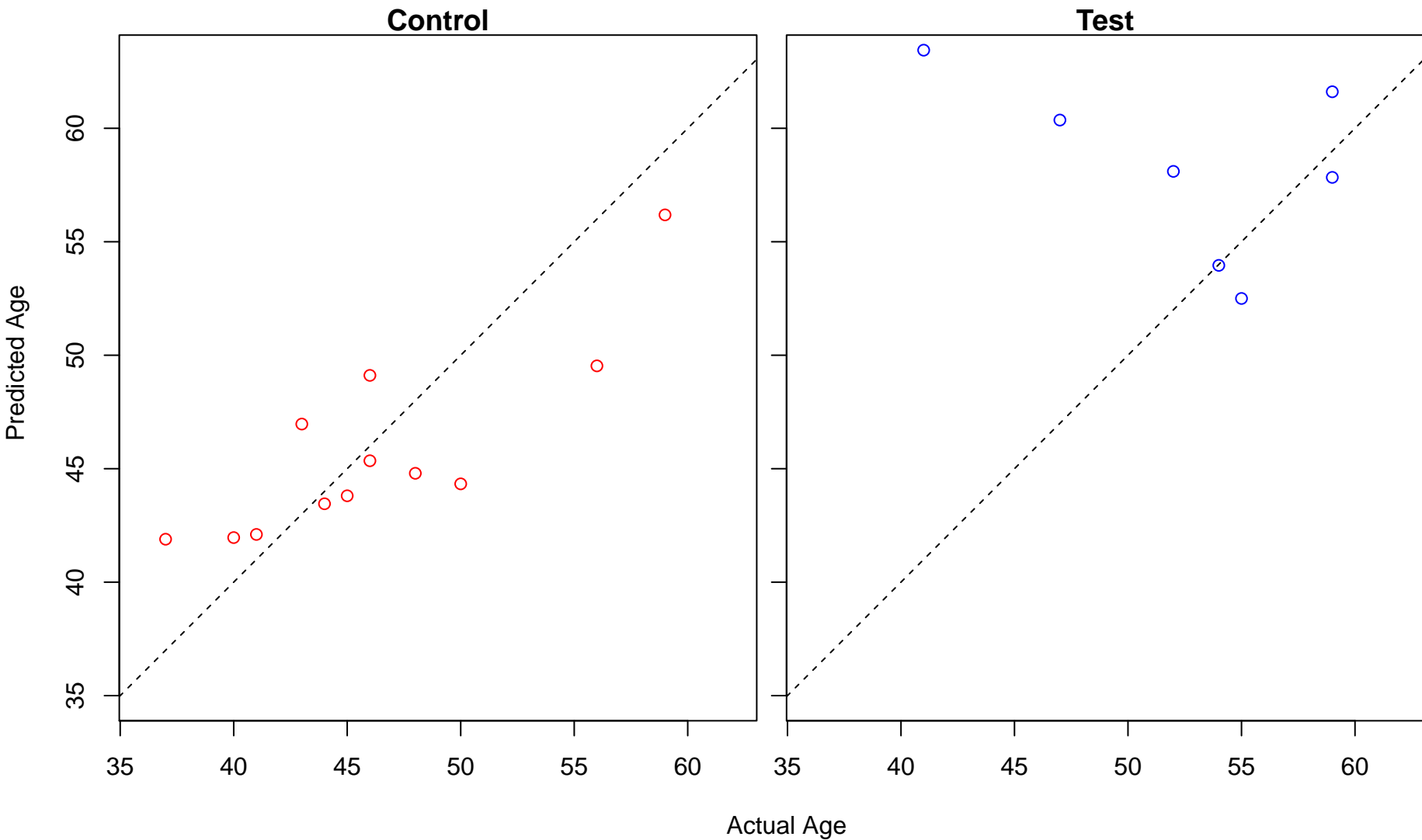
ureteric bud development (Score: 8.381822)



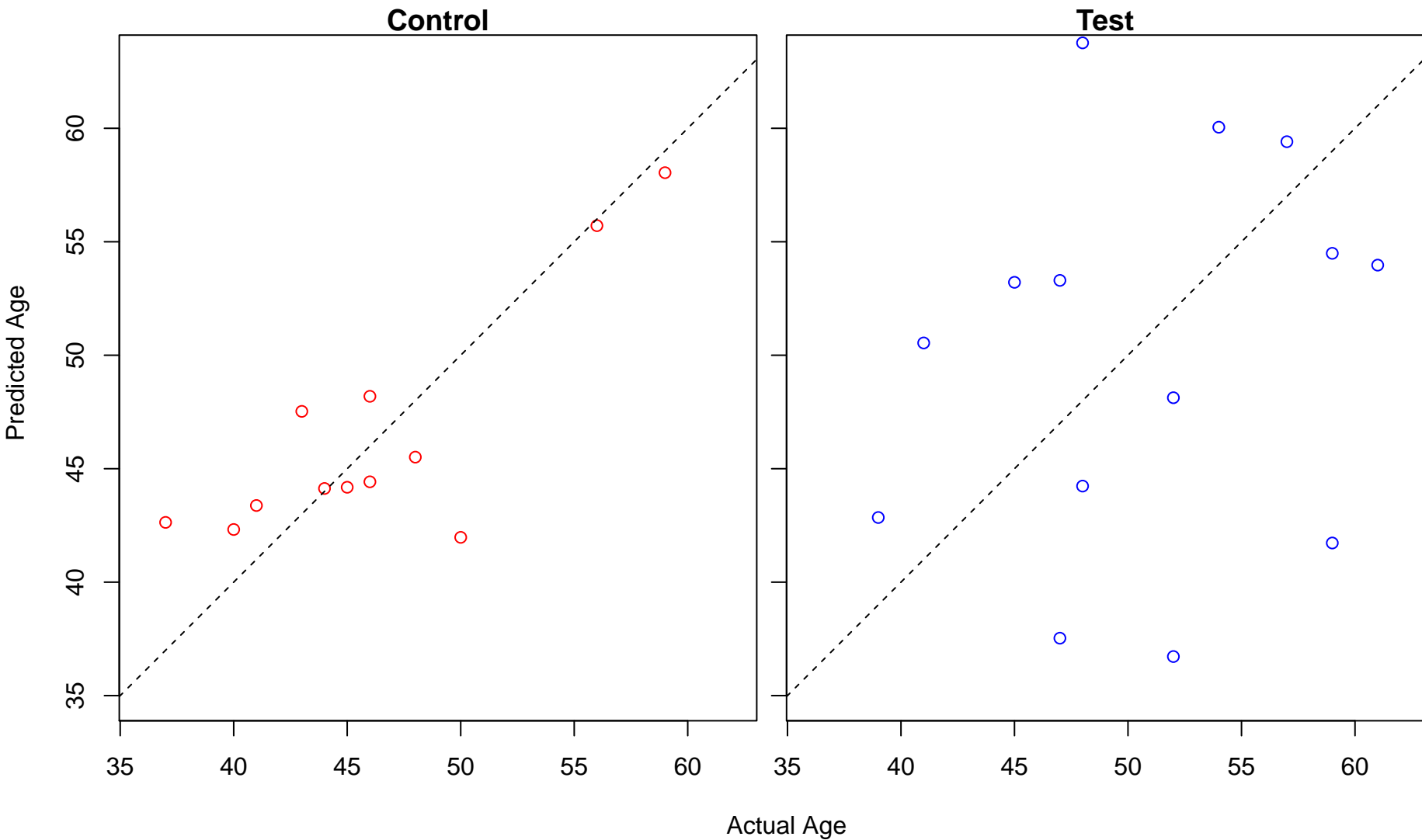
regulation of T cell proliferation (Score: 8.369034)



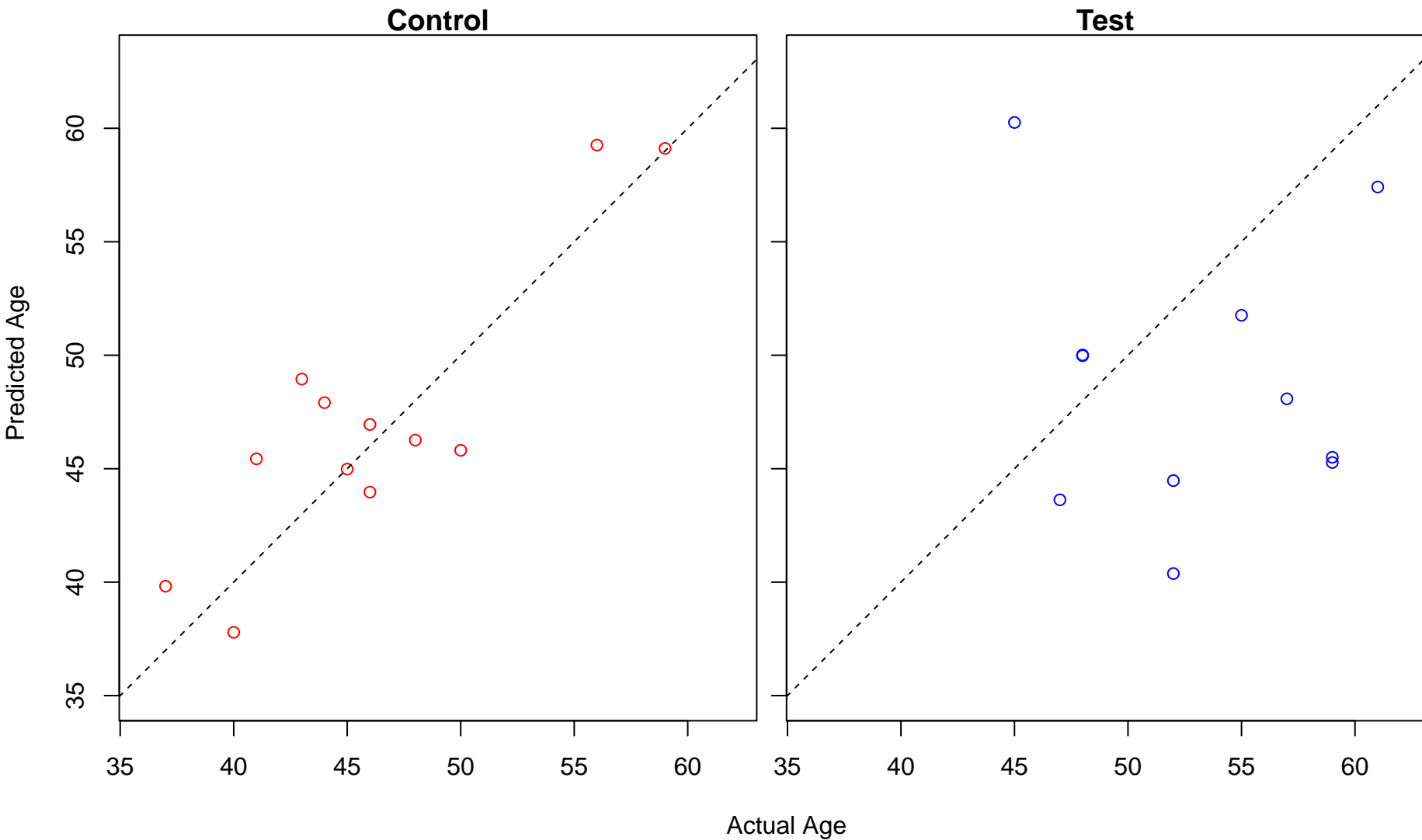
positive regulation of neuroblast proliferation (Score: 8.360574)



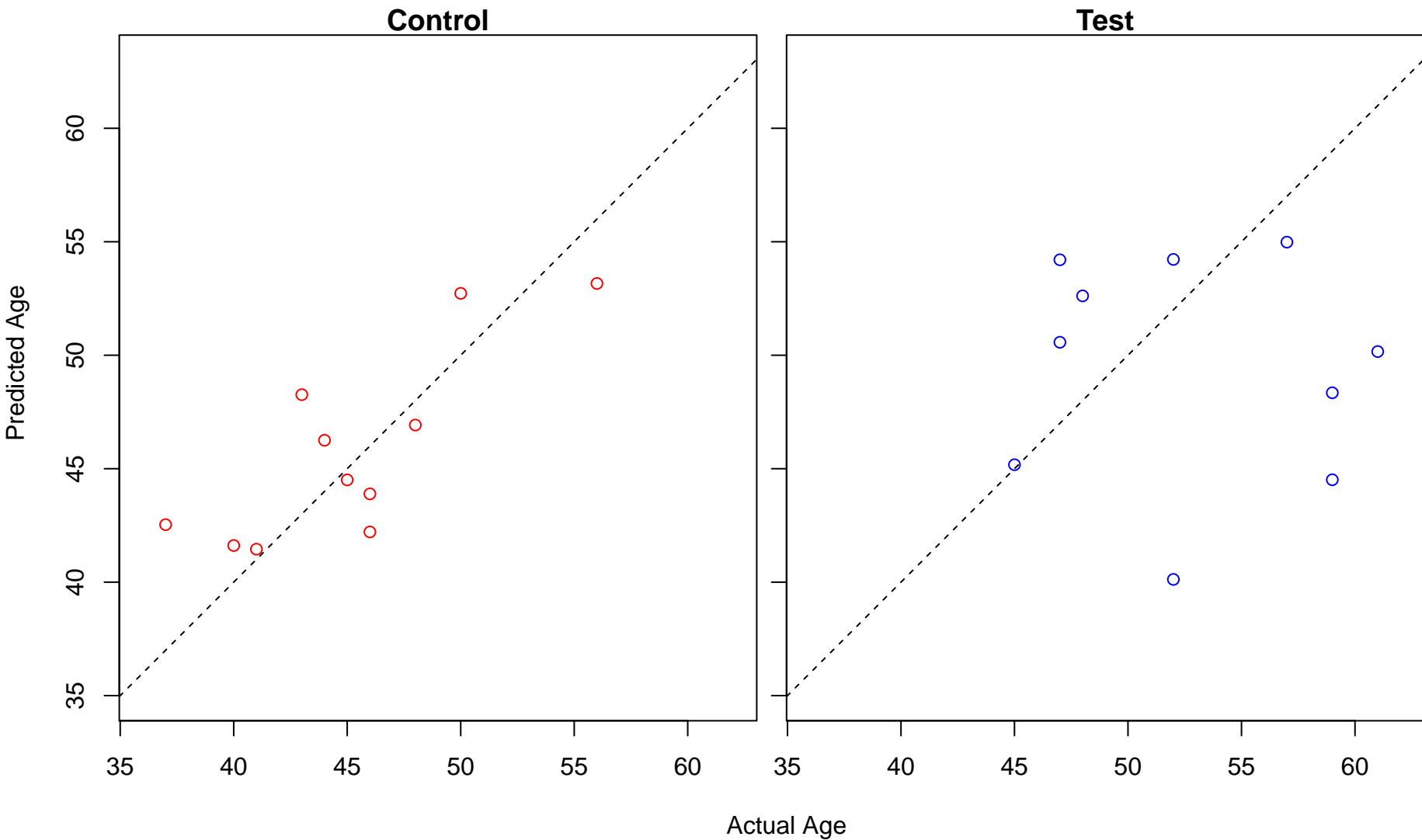
positive regulation of mRNA 3'-end processing (Score: 8.335621)



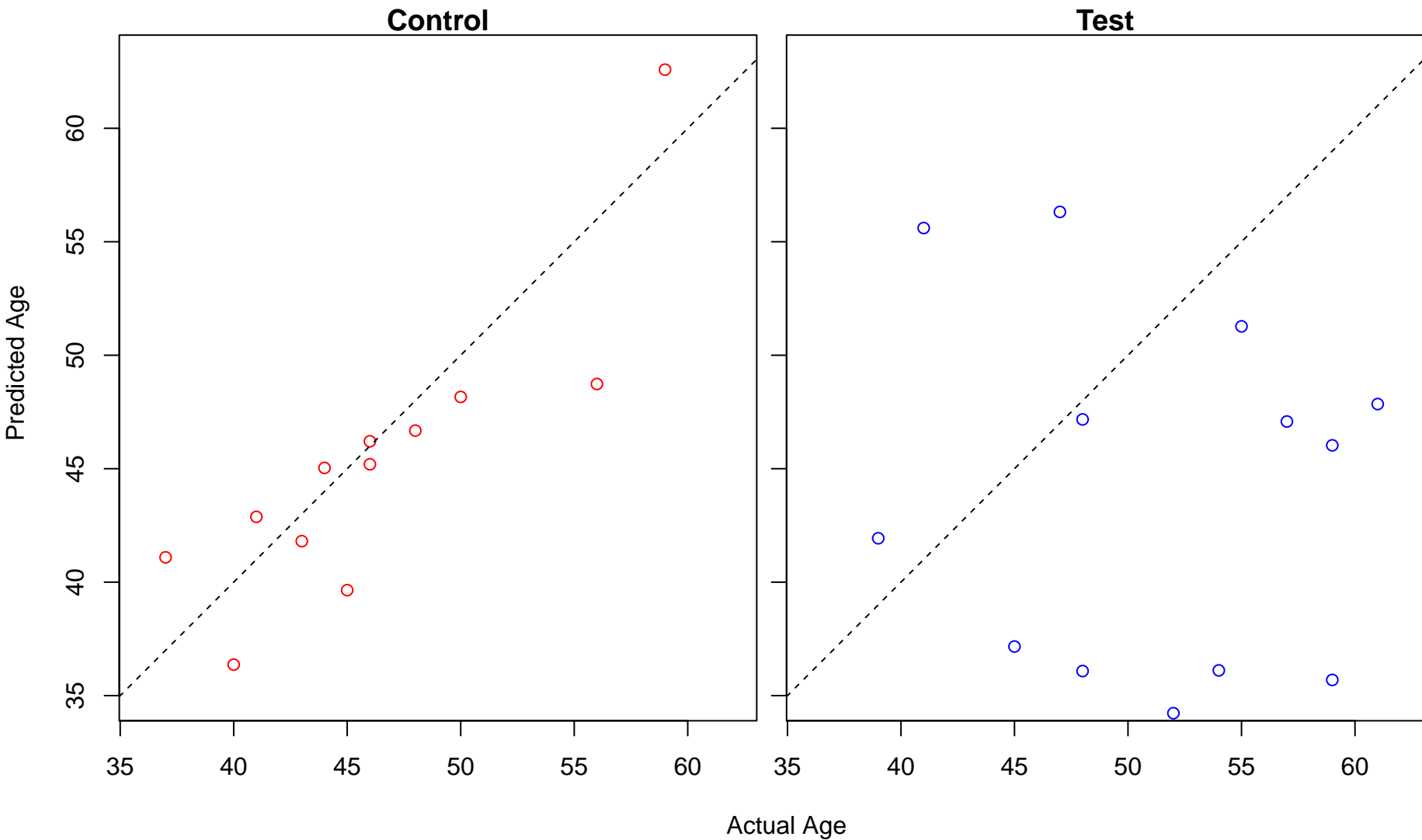
negative regulation of cellular component movement (Score: 8.334542)



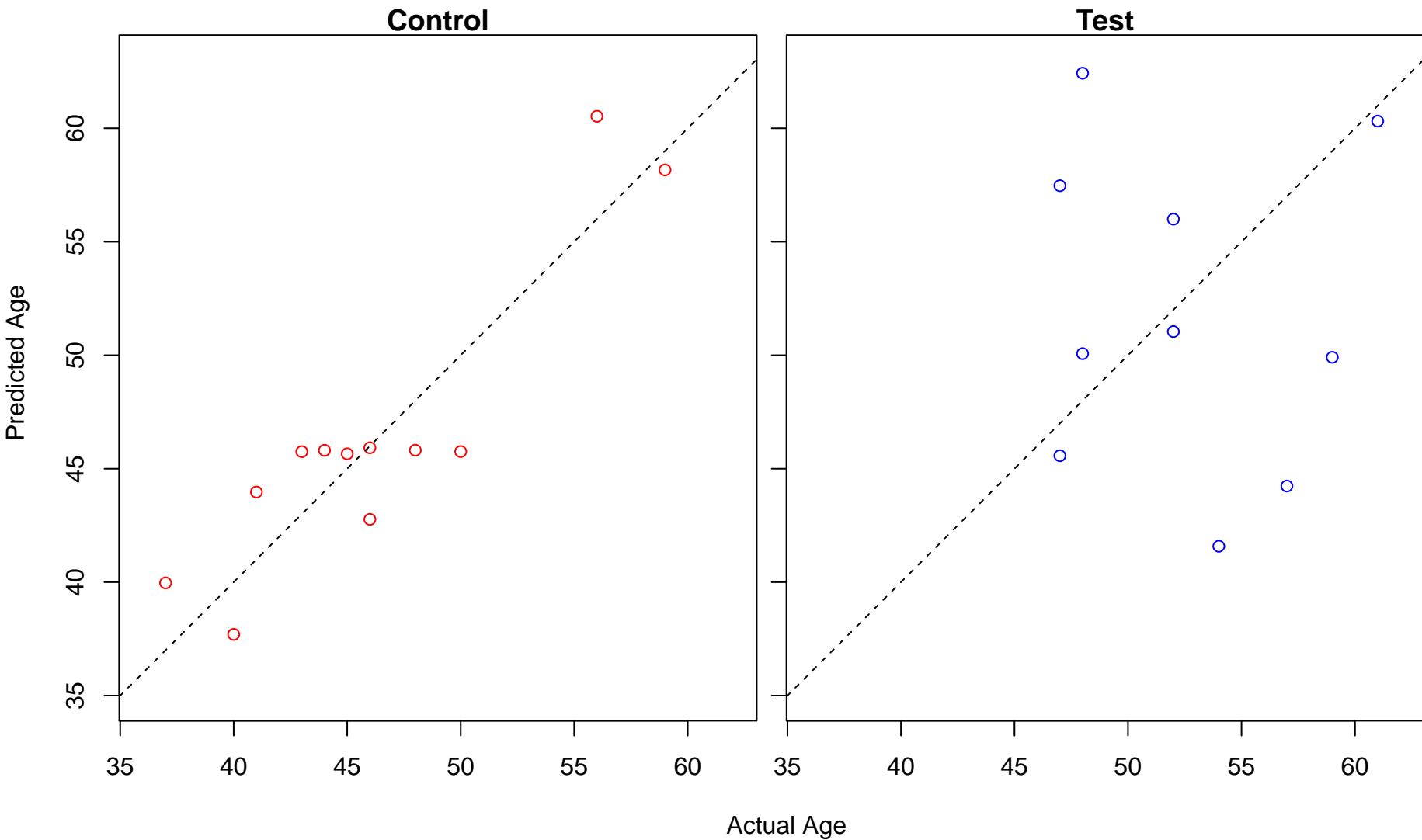
negative regulation of adenylate cyclase activity (Score: 8.298591)



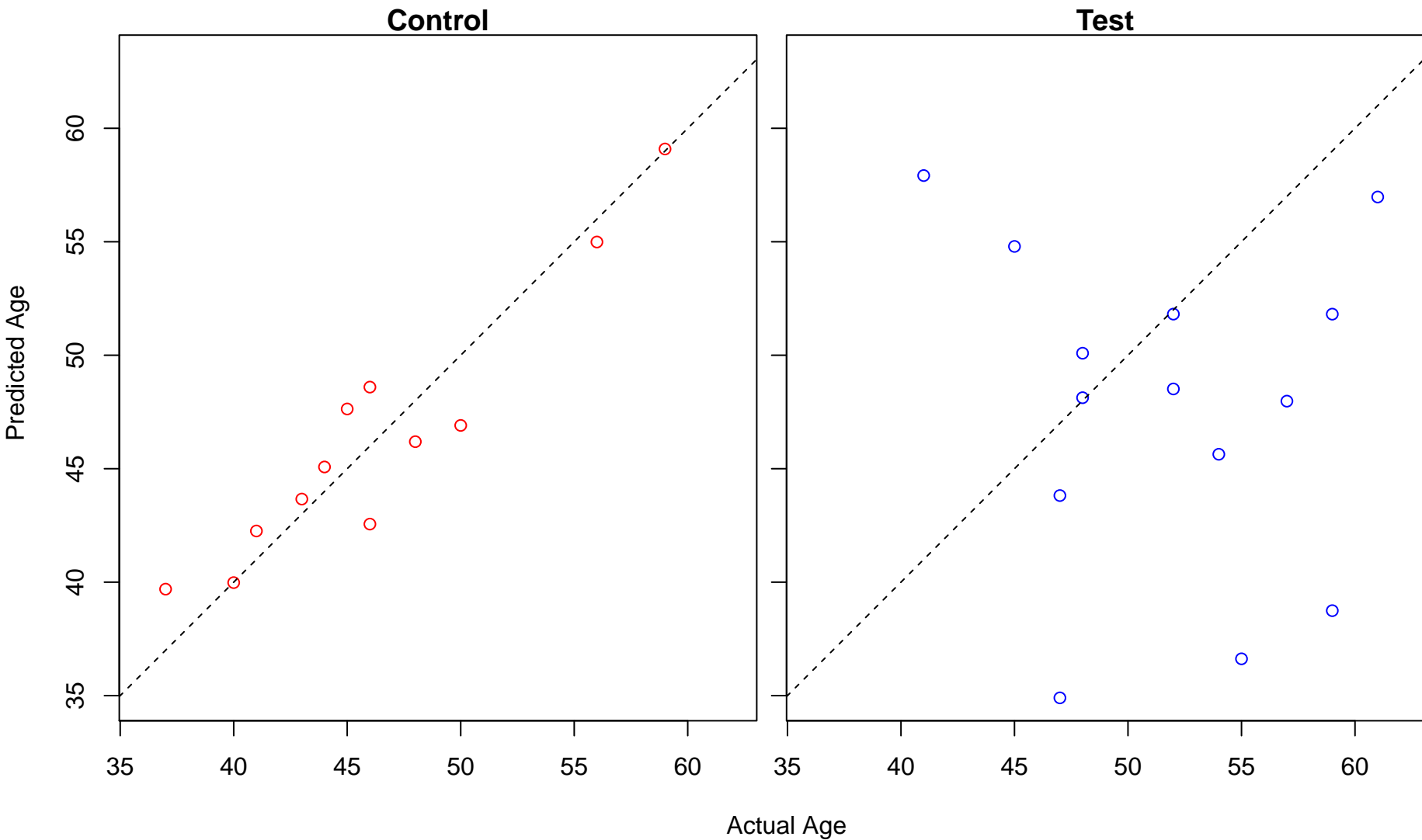
regulation of protein tyrosine kinase activity (Score: 8.292127)



phagocytosis, engulfment (Score: 8.291303)

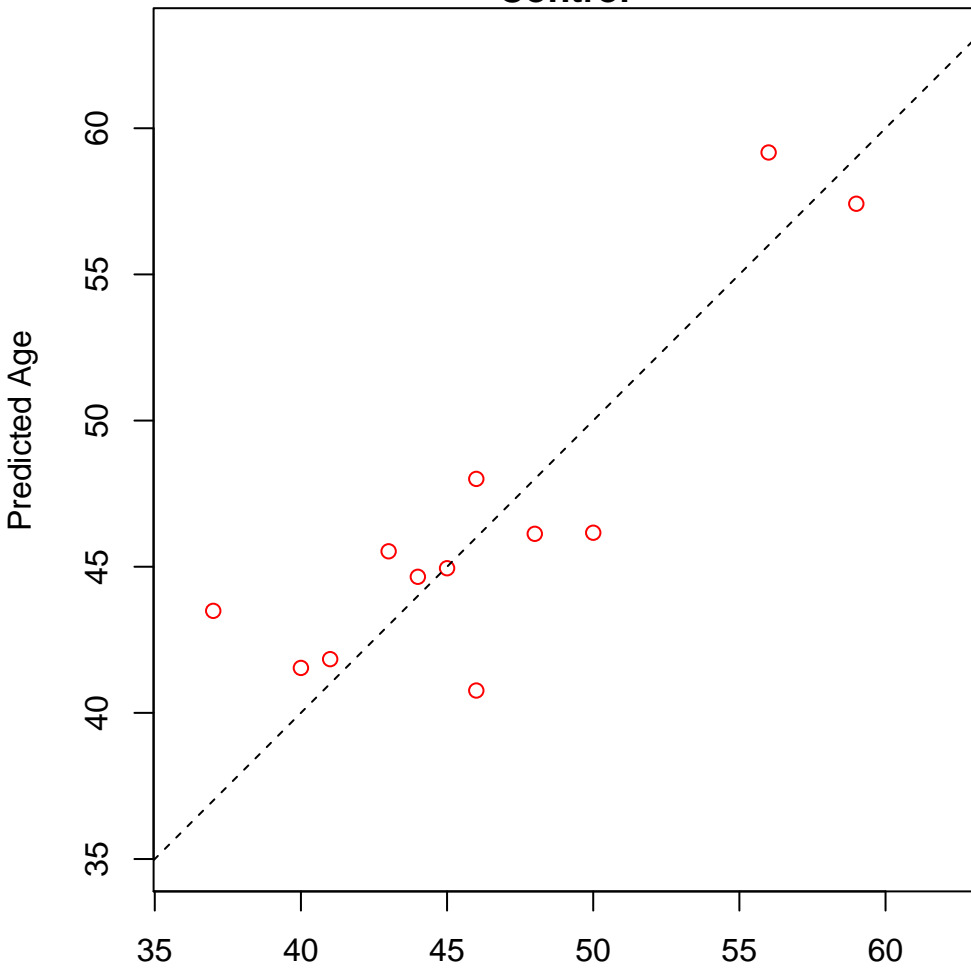


regulation of mesenchymal cell proliferation (Score: 8.277559)

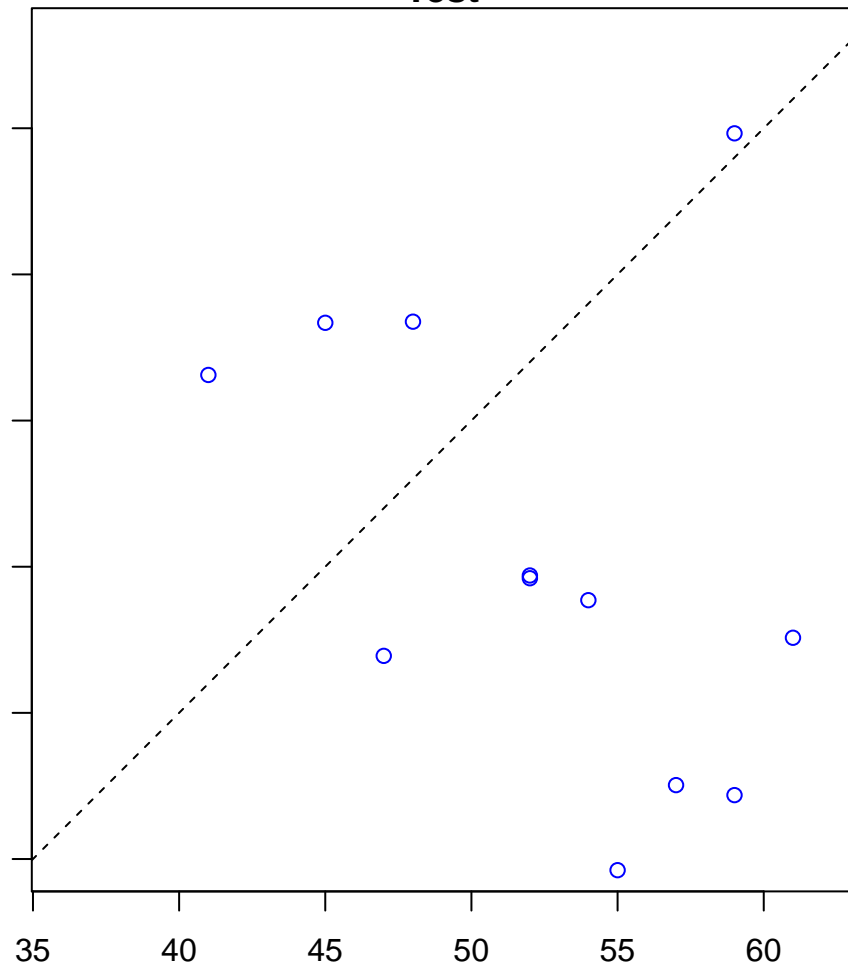


striated muscle tissue development (Score: 8.270937)

Control

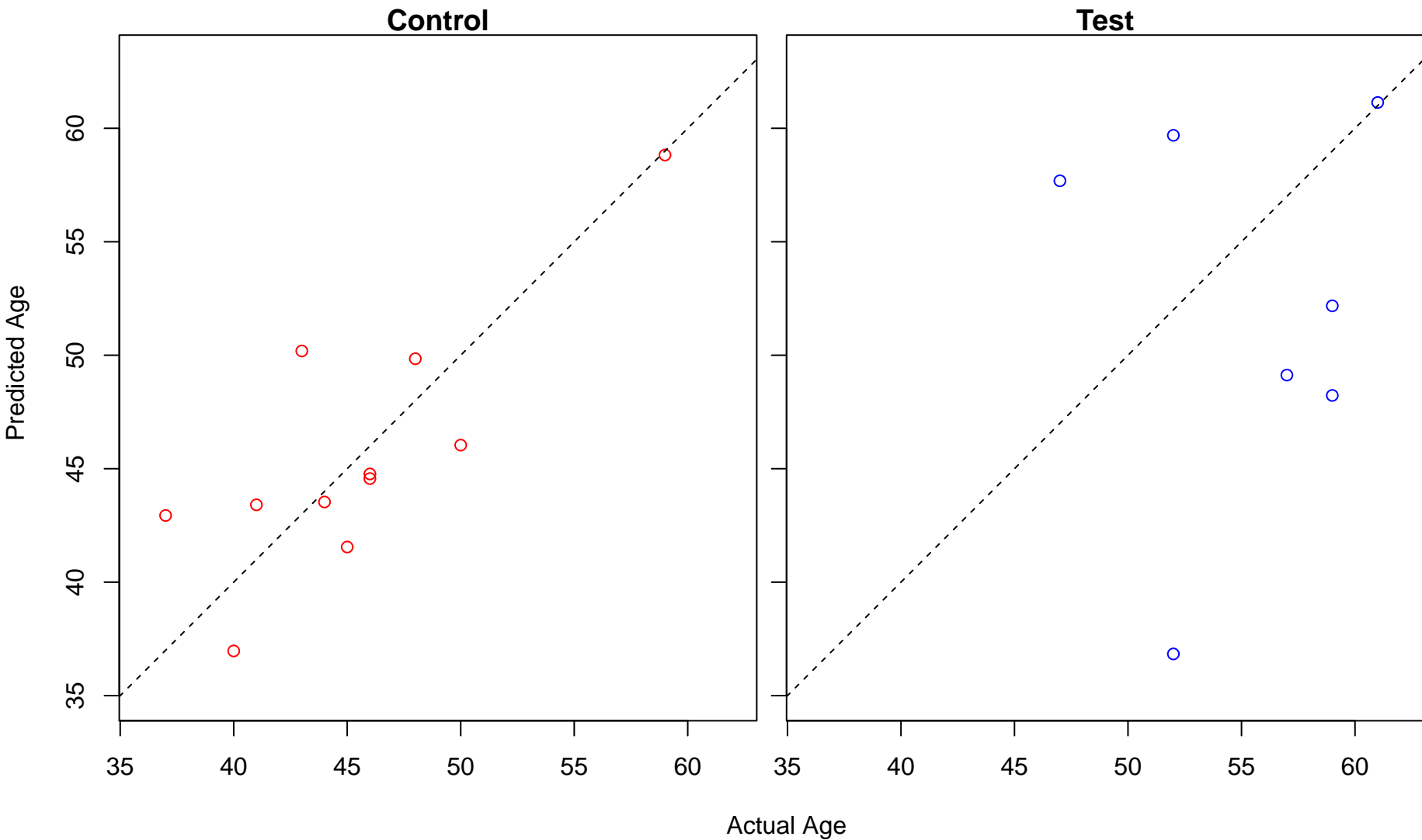


Test

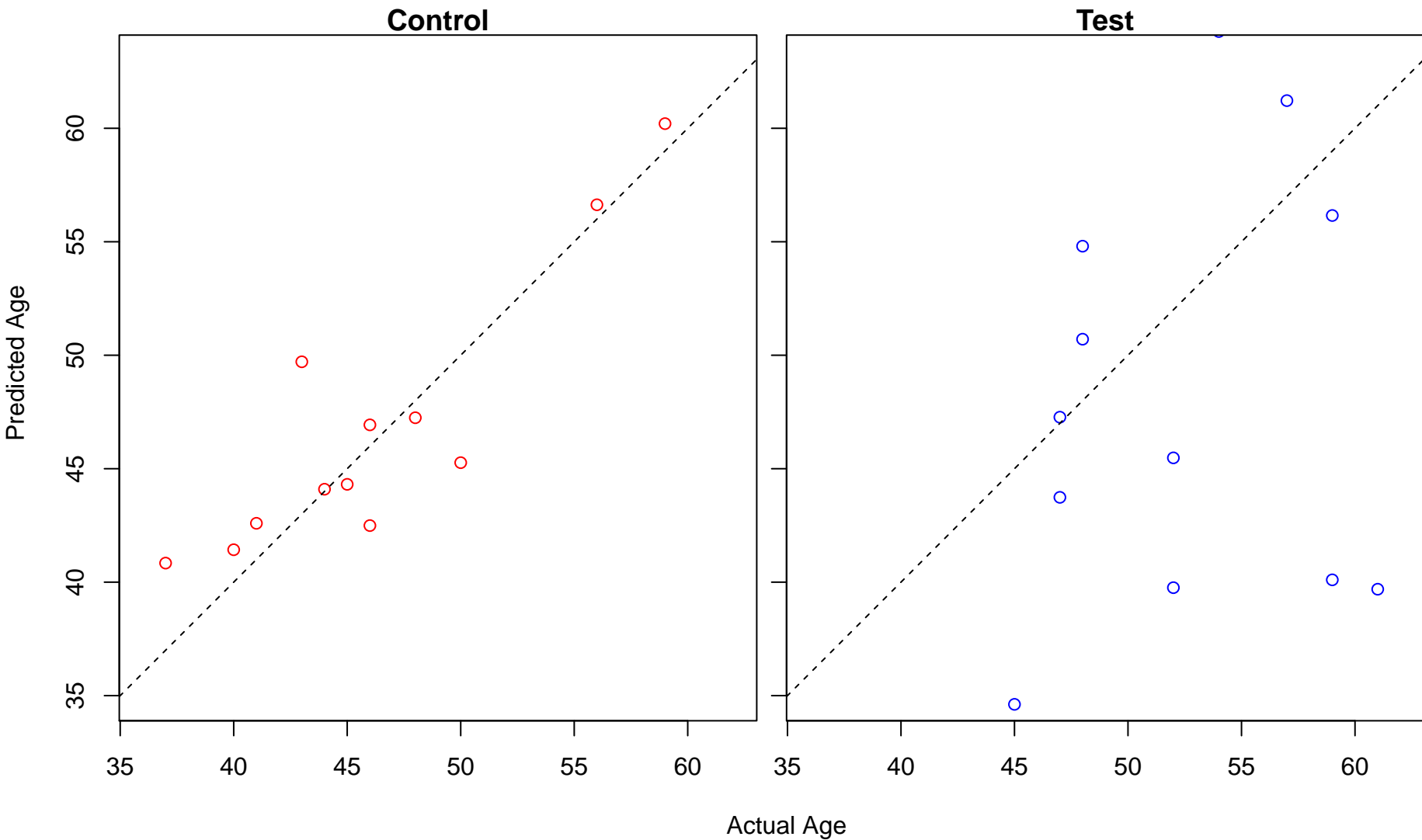


Actual Age

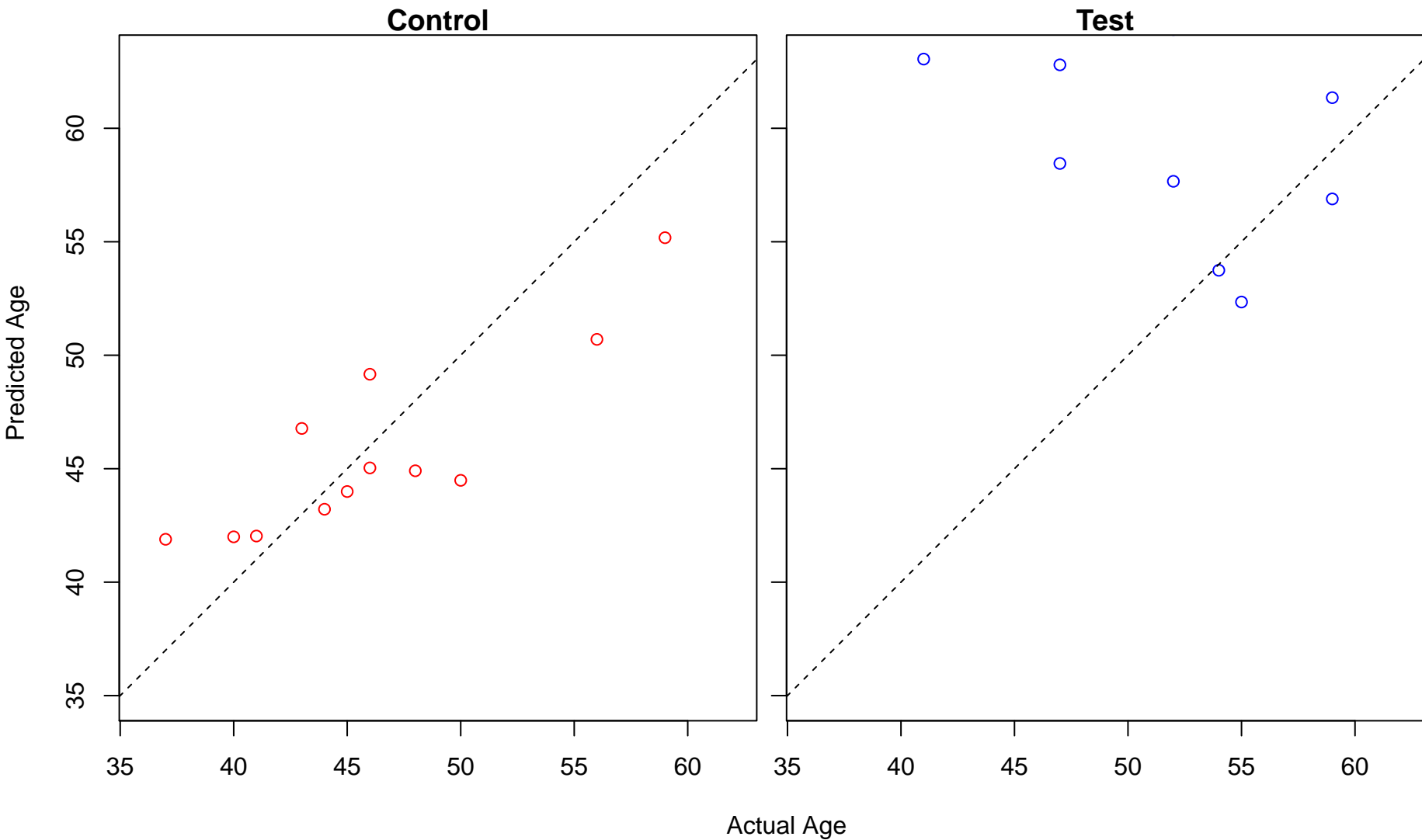
cellular response to vitamin (Score: 8.262886)



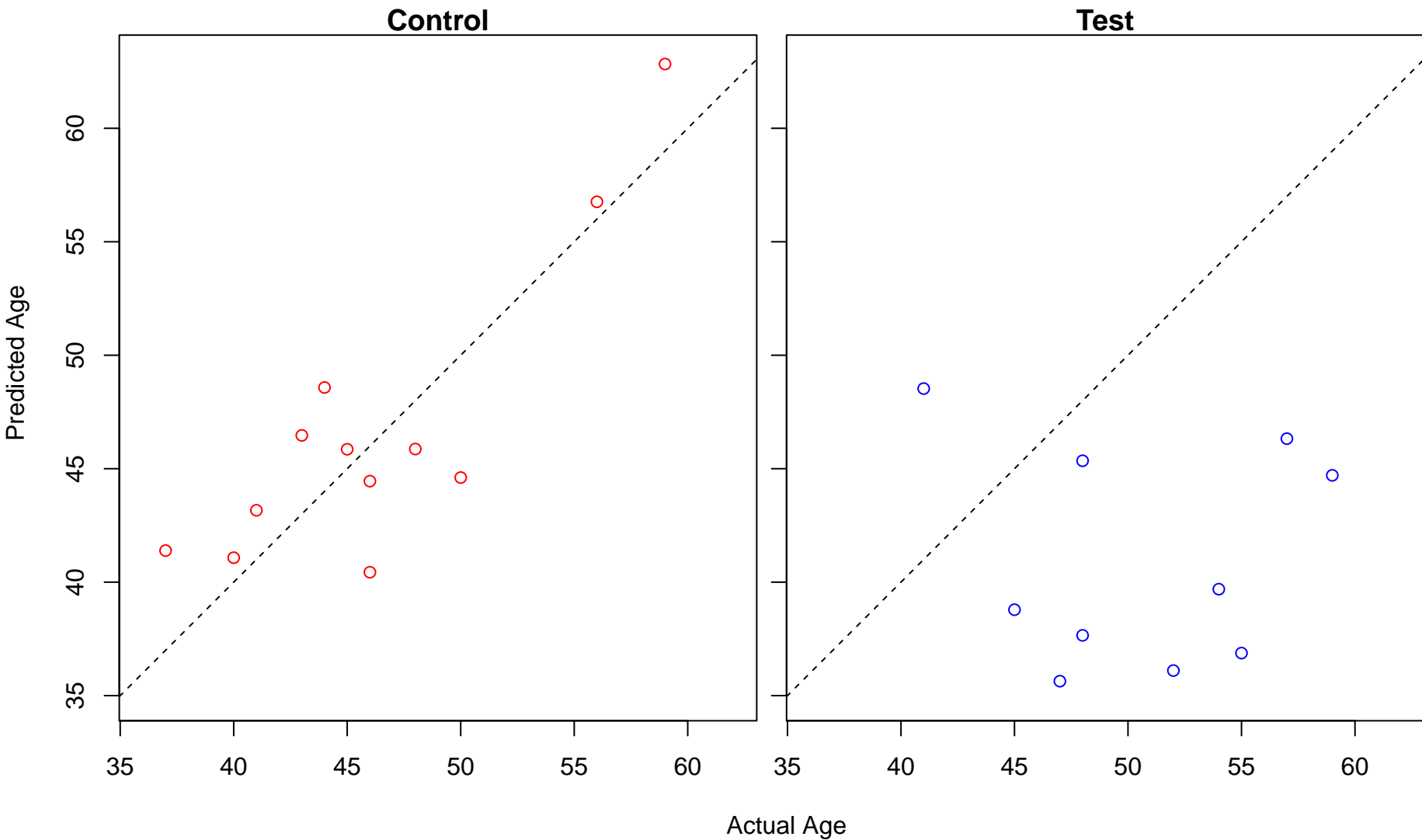
Golgi ribbon formation (Score: 8.253017)



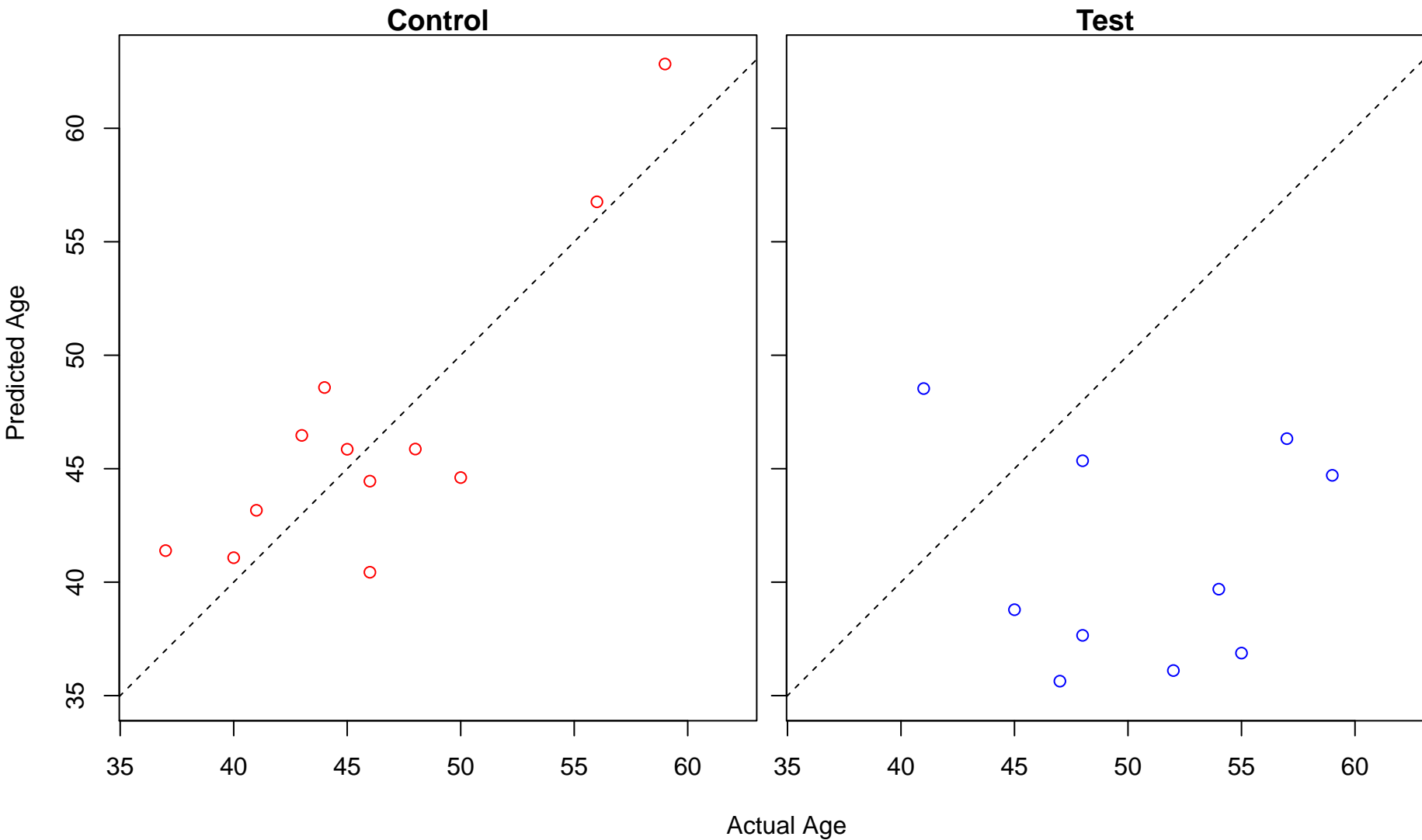
regulation of neuroblast proliferation (Score: 8.245131)



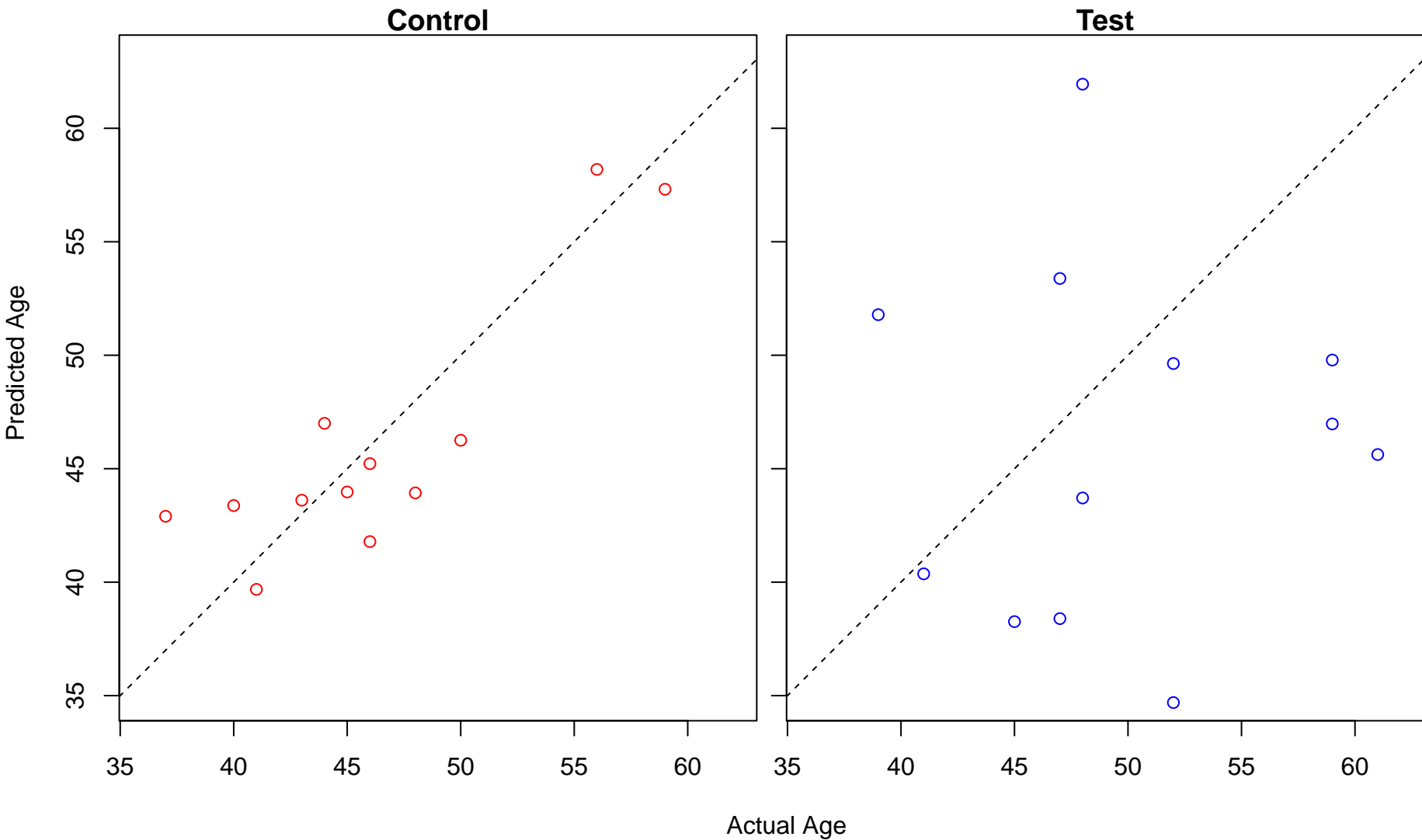
regulation of actin polymerization or depolymerization (Score: 8.244827)



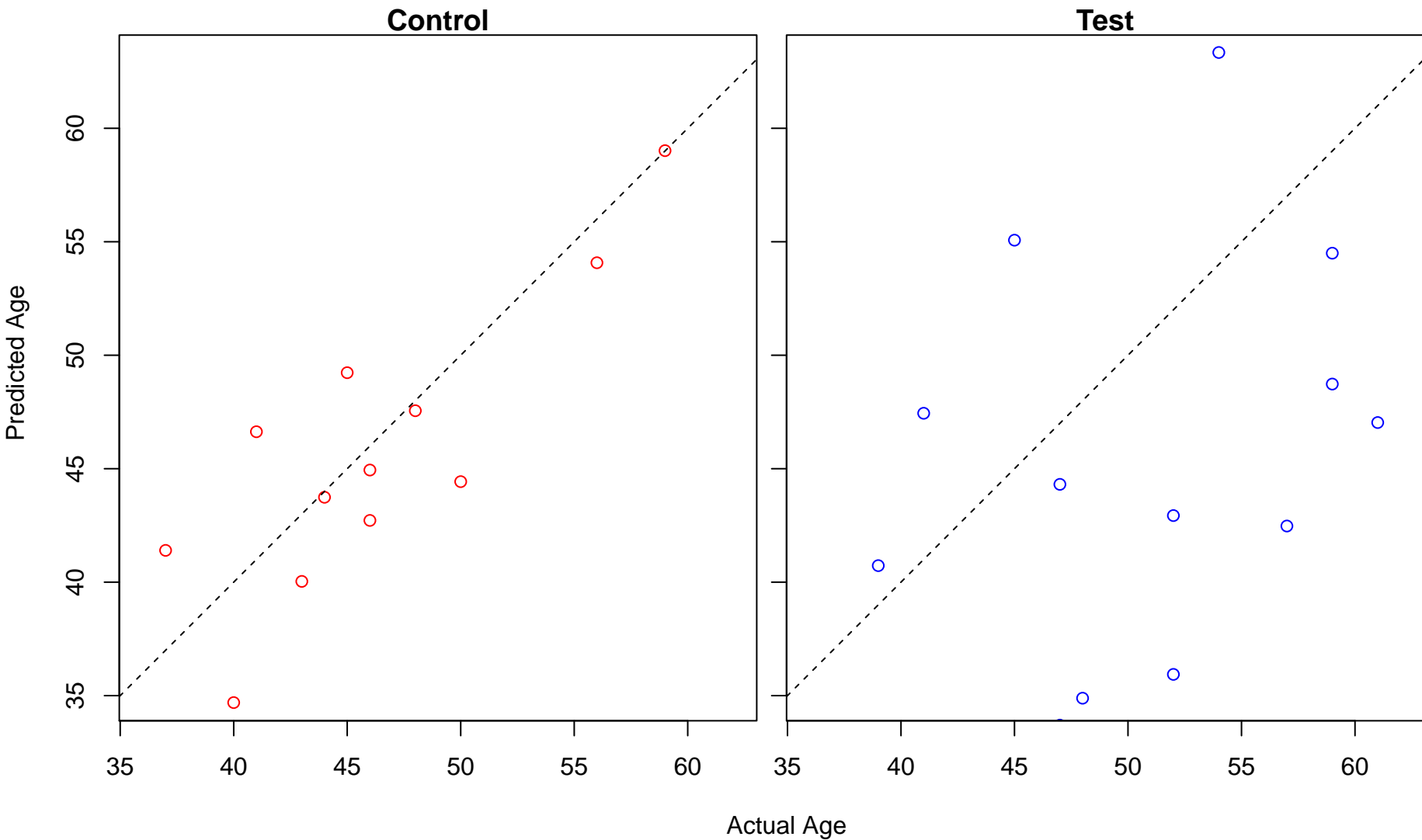
regulation of actin filament length (Score: 8.244827)



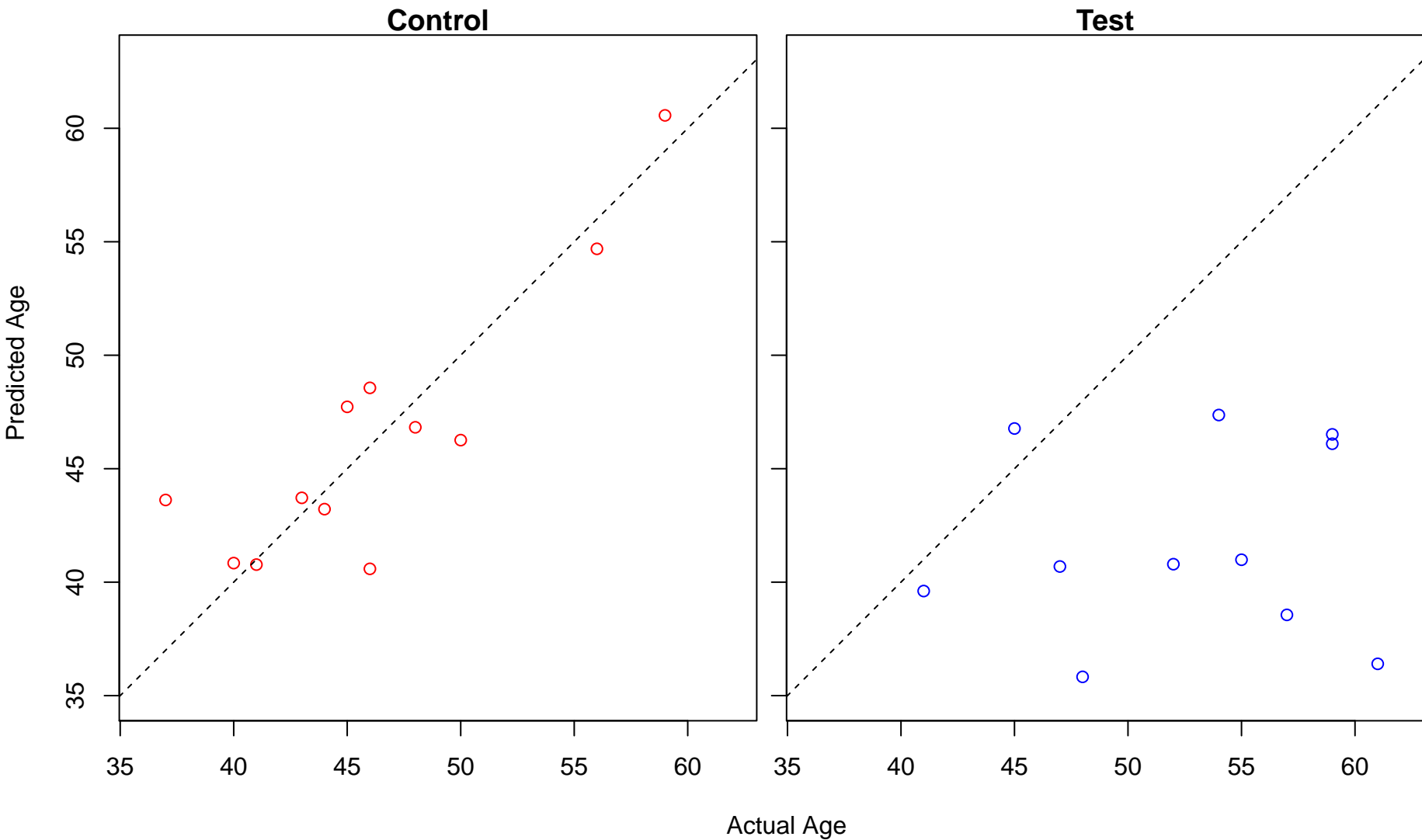
relaxation of muscle (Score: 8.230618)



divalent metal ion transport (Score: 8.216193)

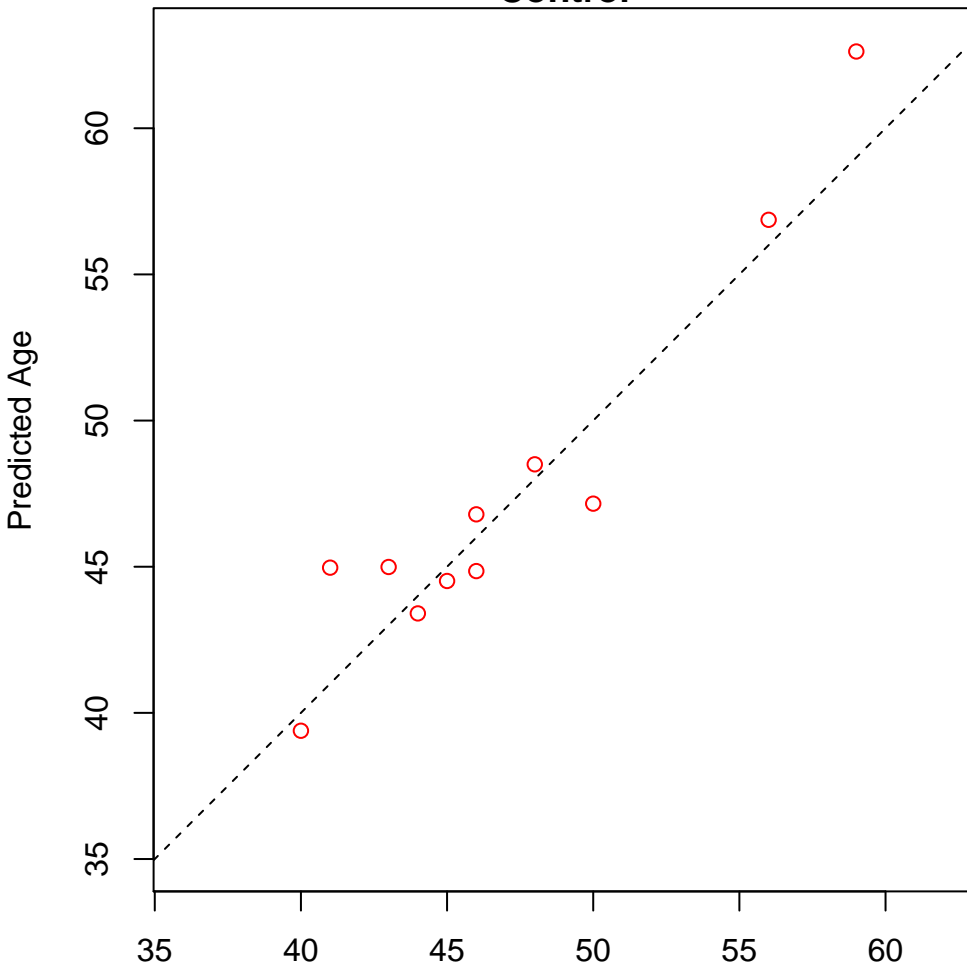


ribosome disassembly (Score: 8.210184)

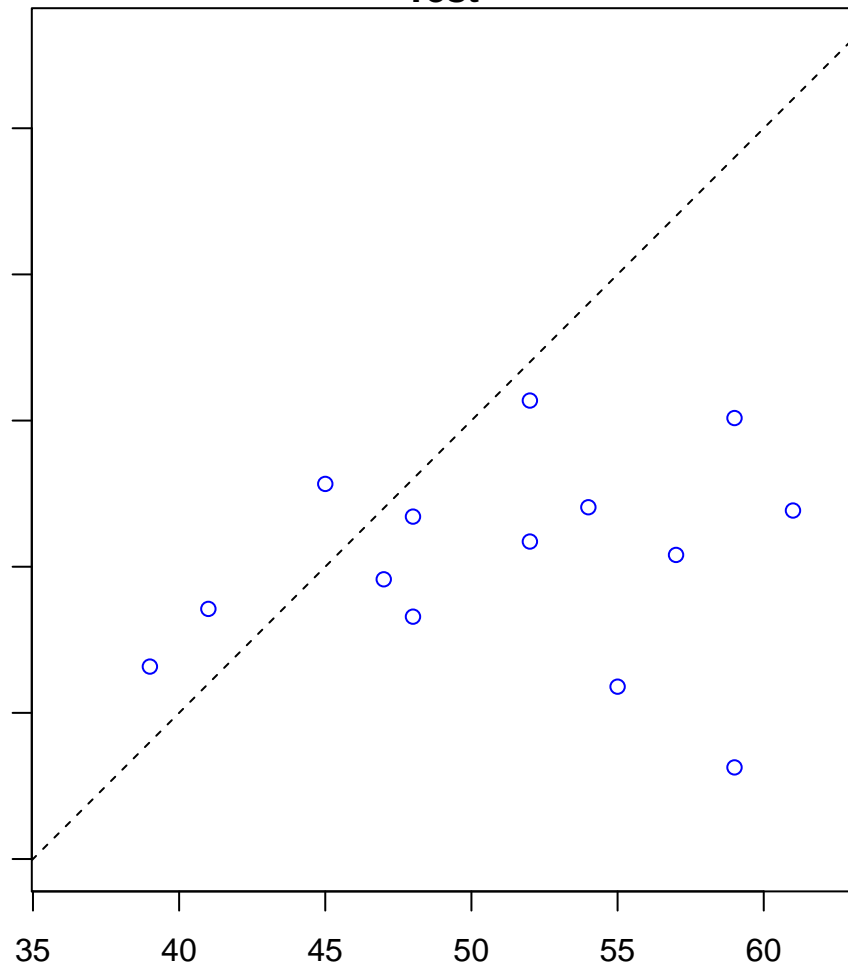


regulation of metanephros development (Score: 8.208550)

Control

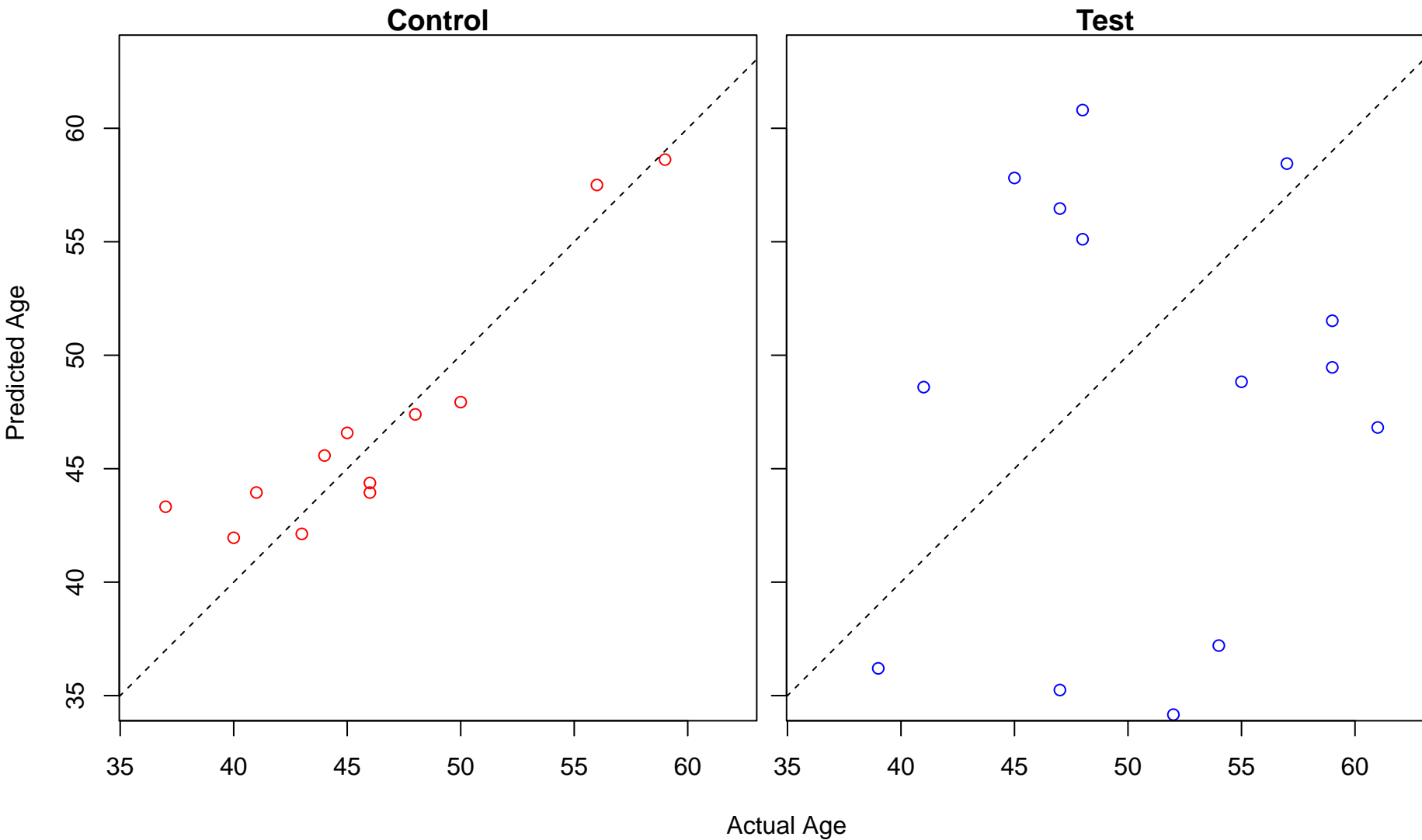


Test

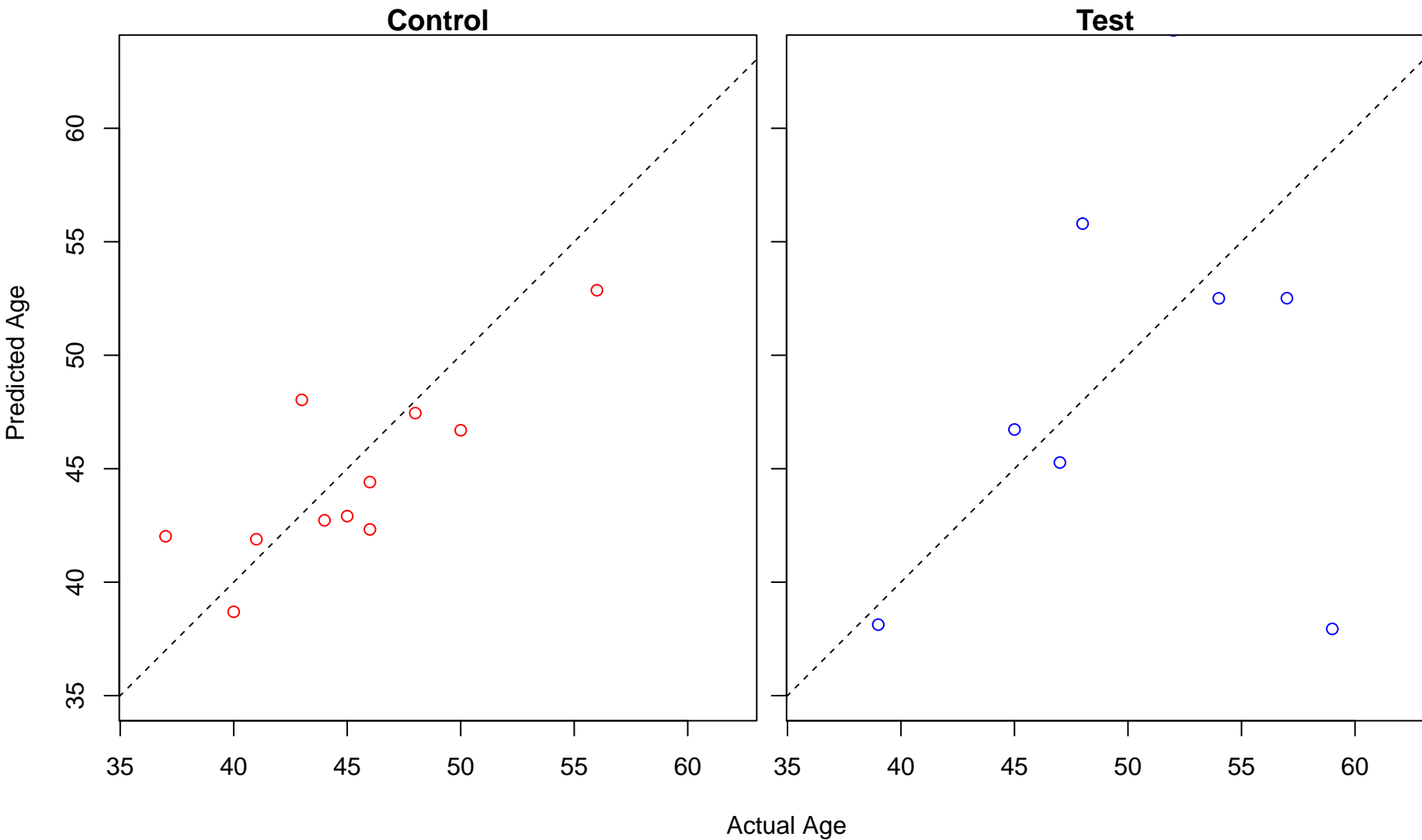


Actual Age

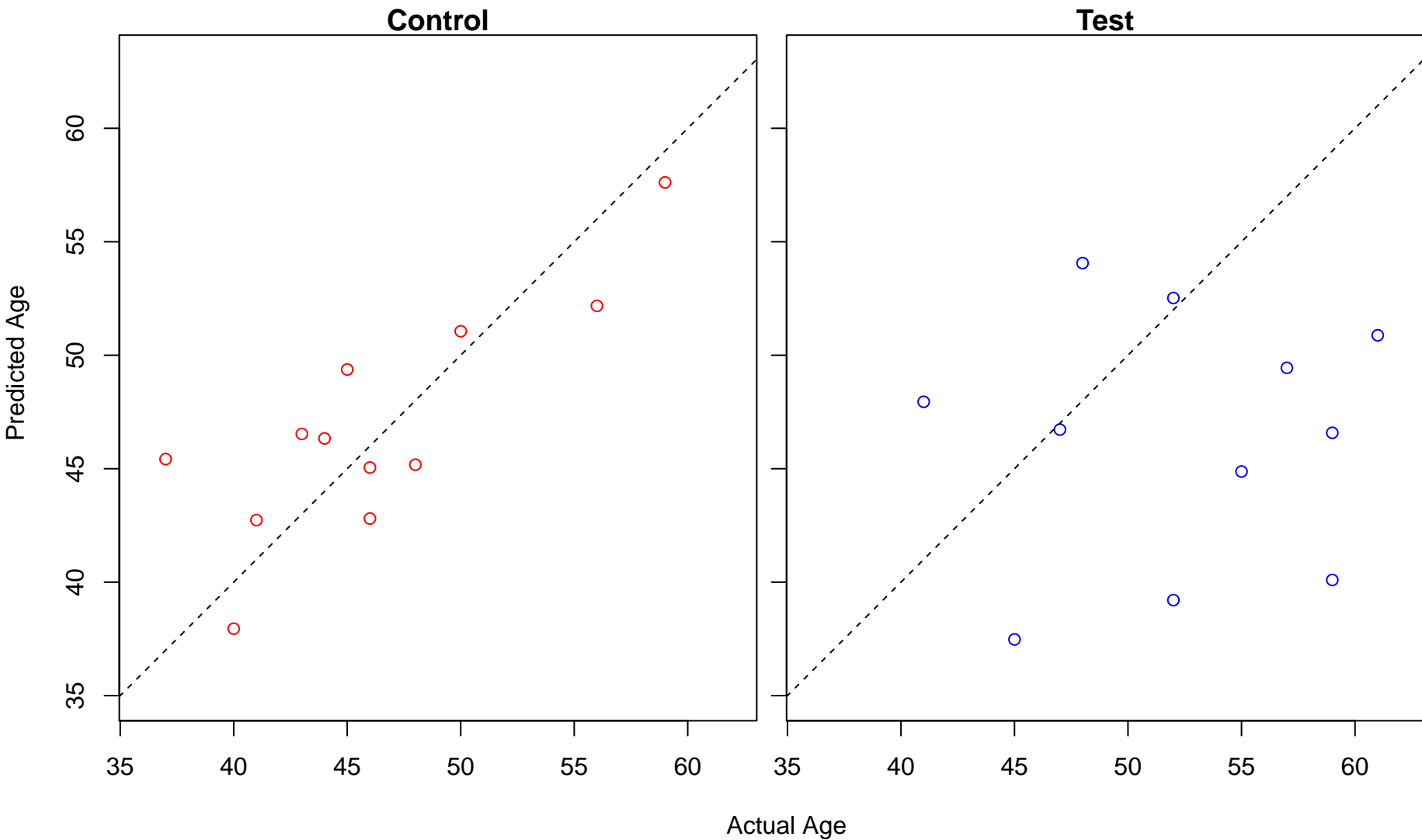
nucleoside catabolic process (Score: 8.207346)



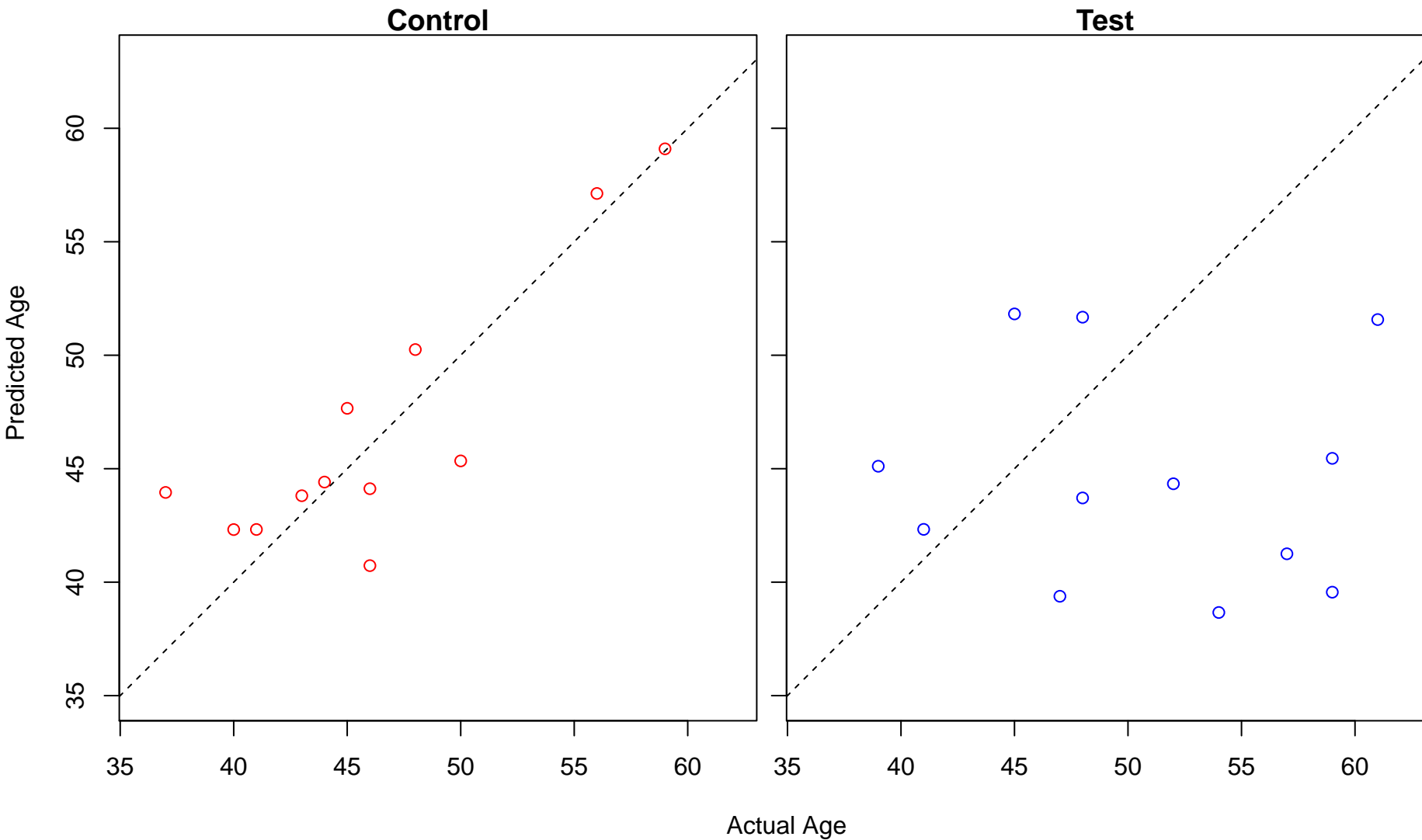
cellular protein complex localization (Score: 8.194041)



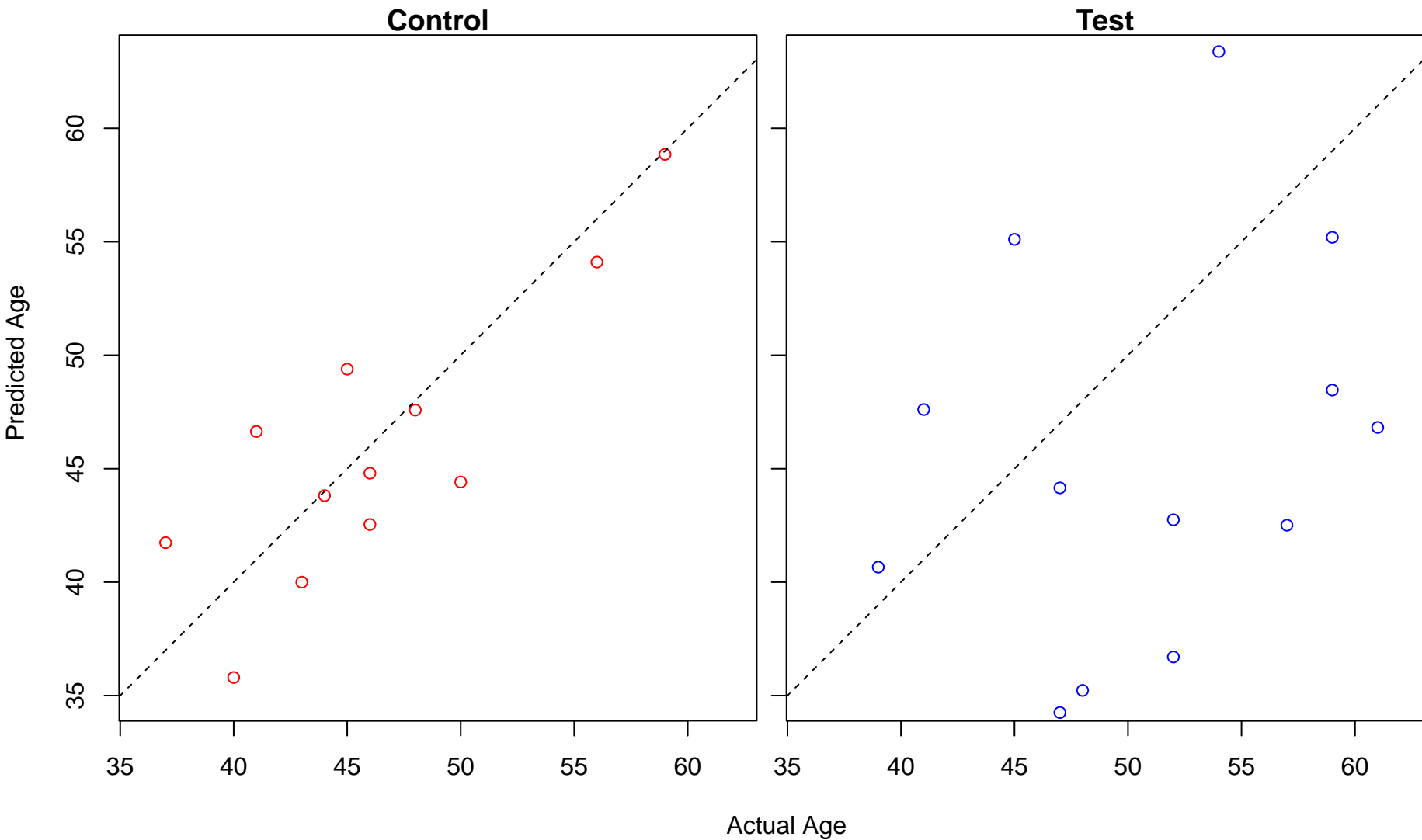
positive regulation of myotube differentiation (Score: 8.186897)



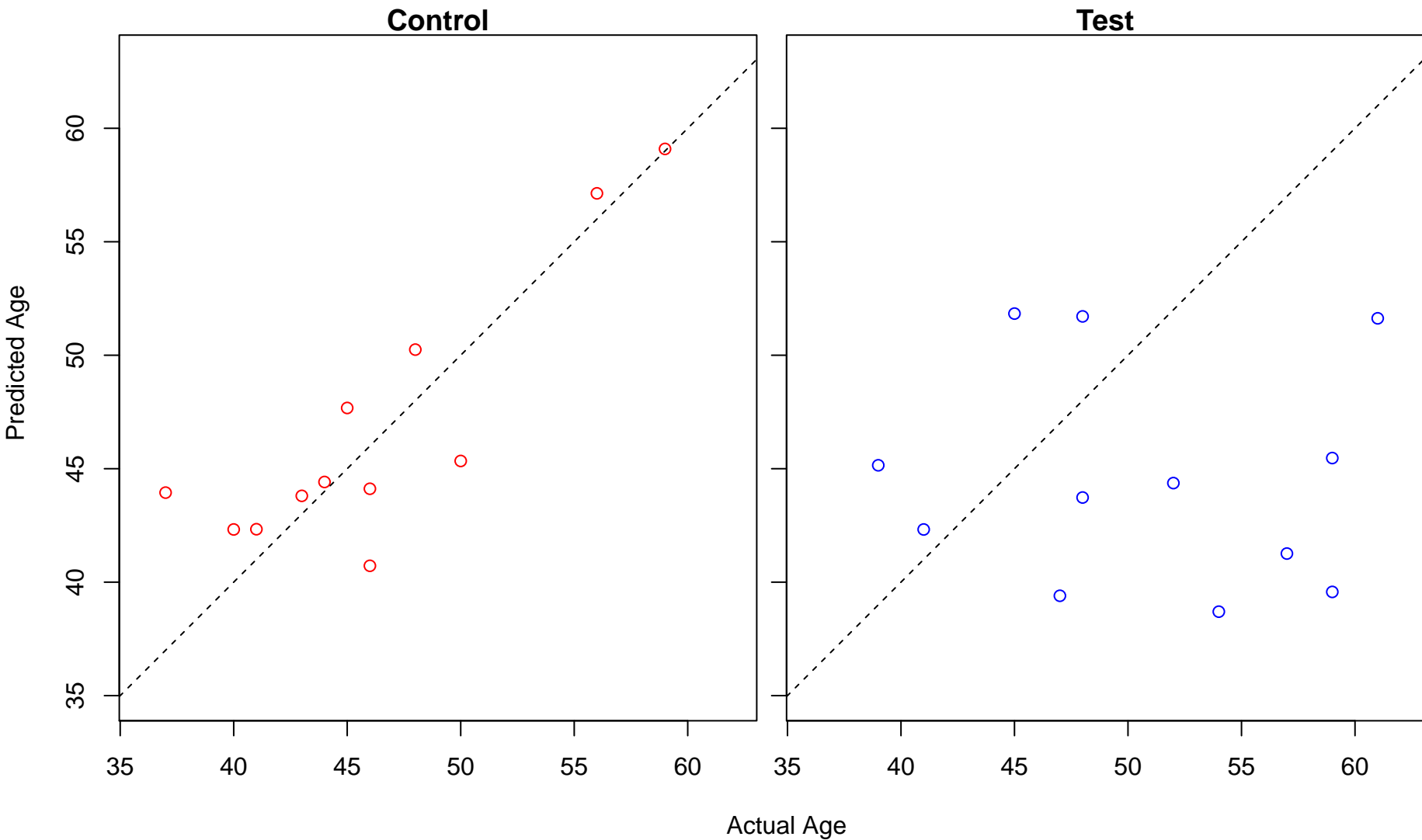
glycosylation (Score: 8.166264)



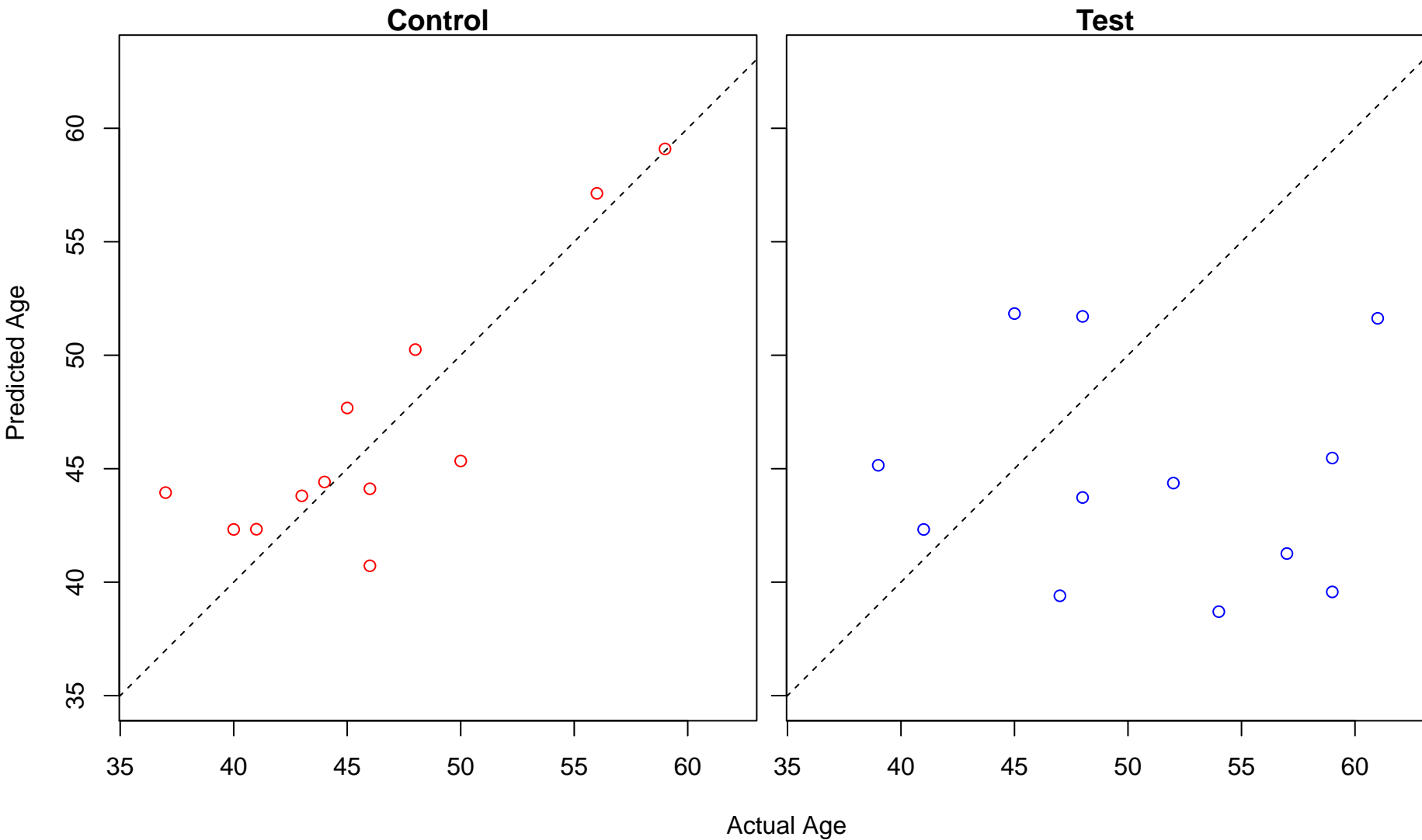
divalent inorganic cation transport (Score: 8.160144)



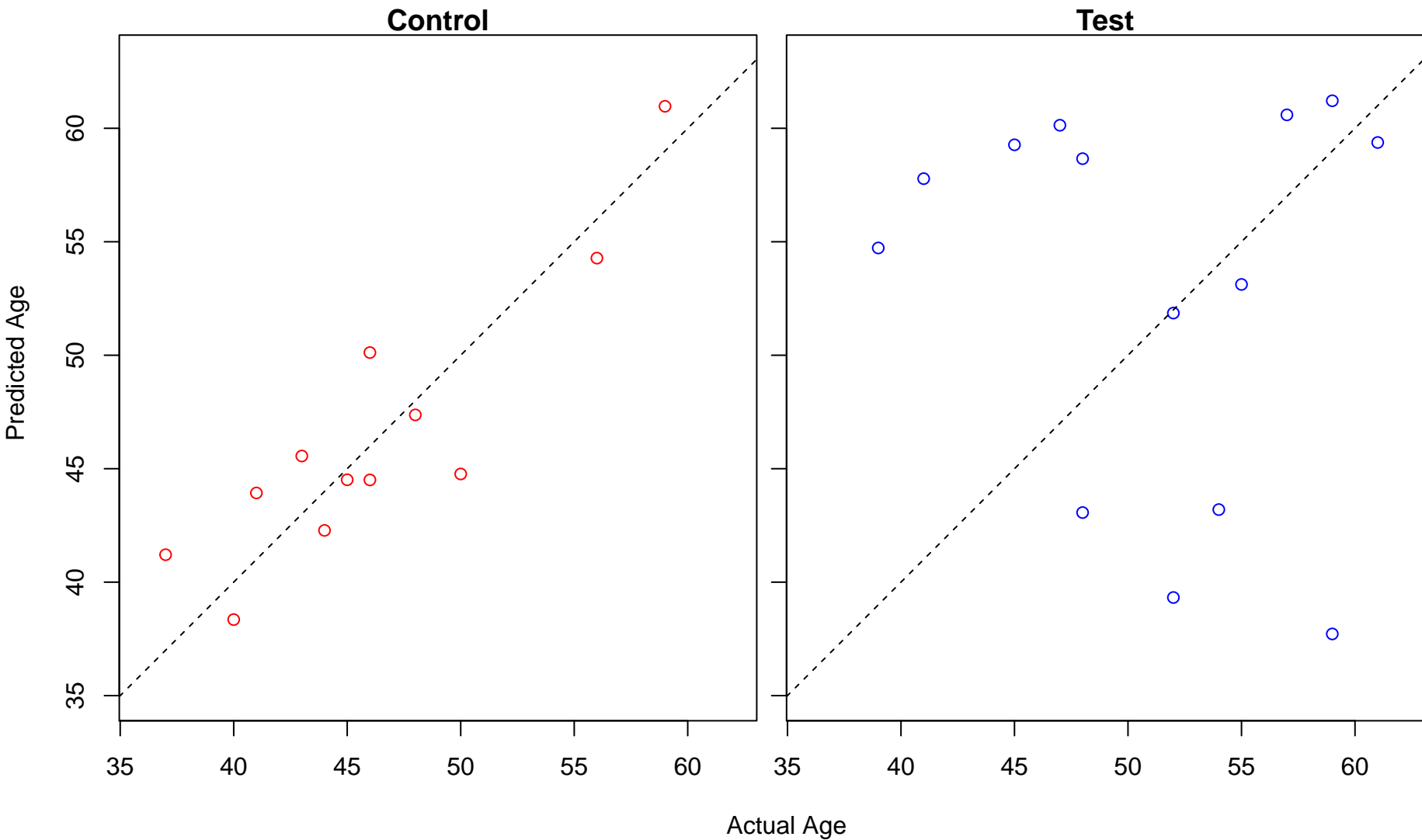
protein glycosylation (Score: 8.148540)



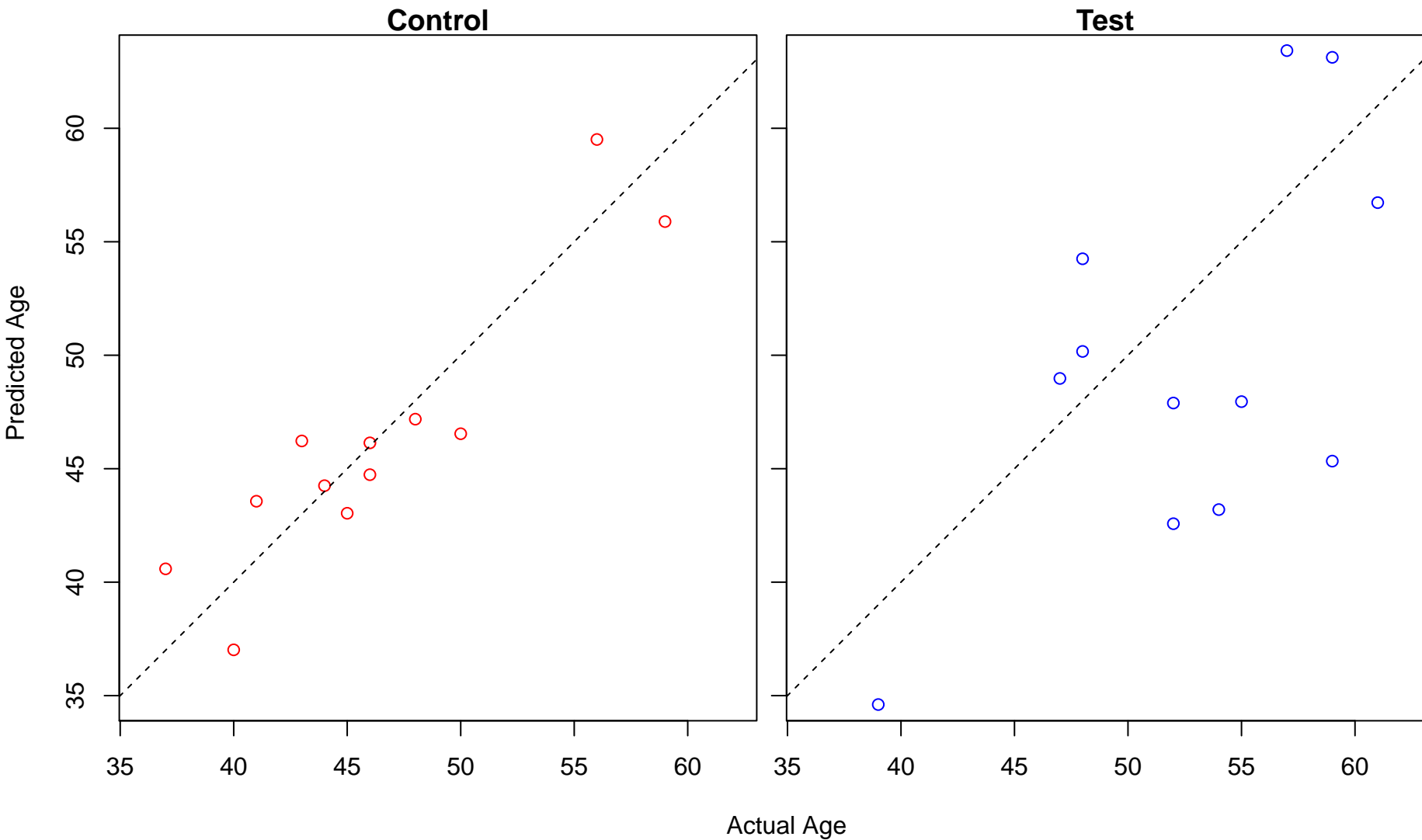
macromolecule glycosylation (Score: 8.148540)



response to interleukin-1 (Score: 8.145281)

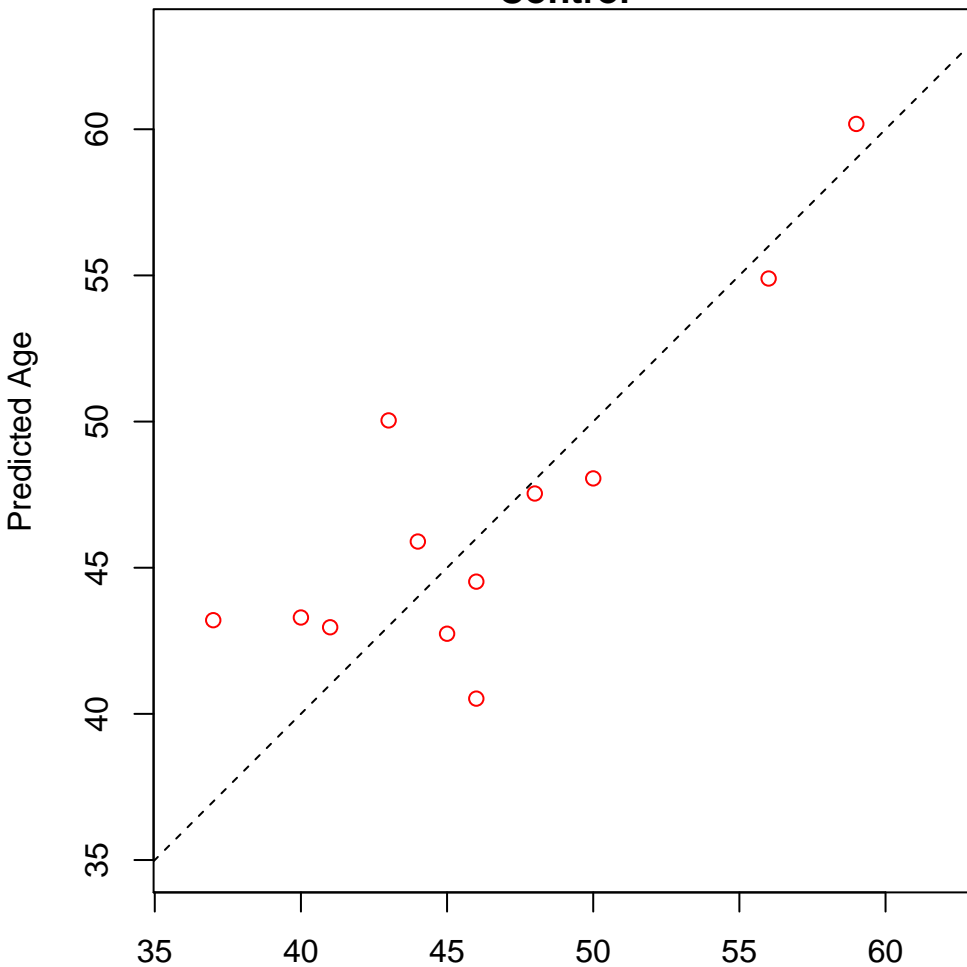


cellular response to organic cyclic compound (Score: 8.129521)

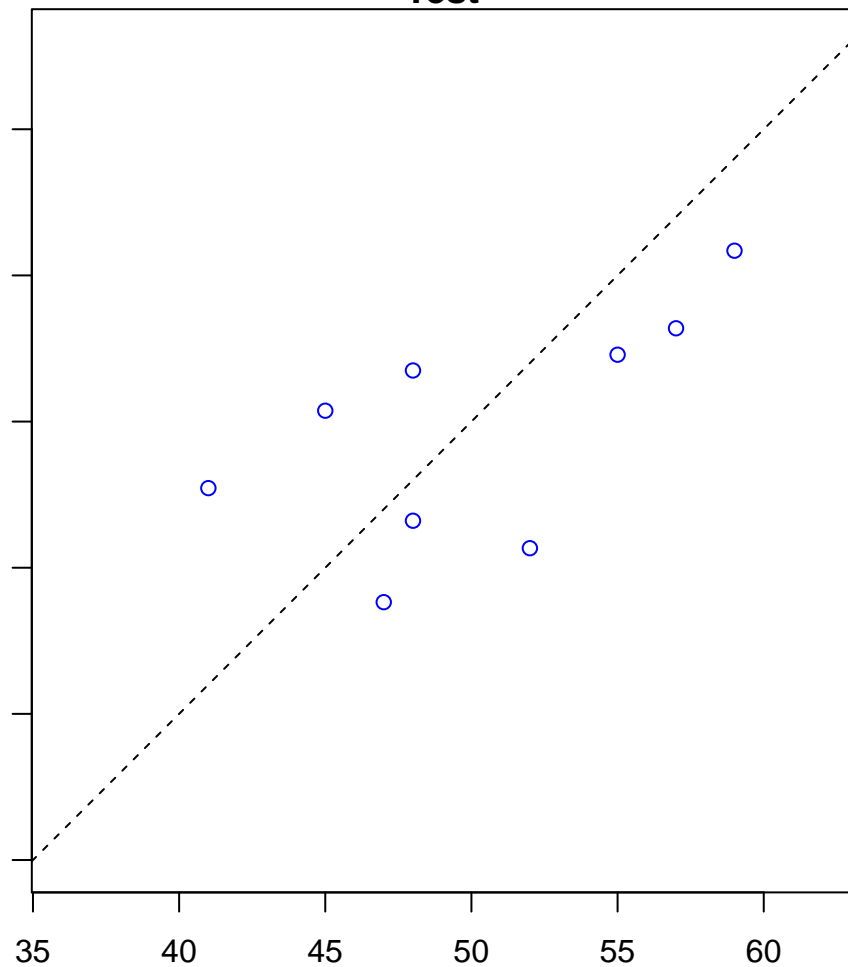


cellular response to estrogen stimulus (Score: 8.114355)

Control

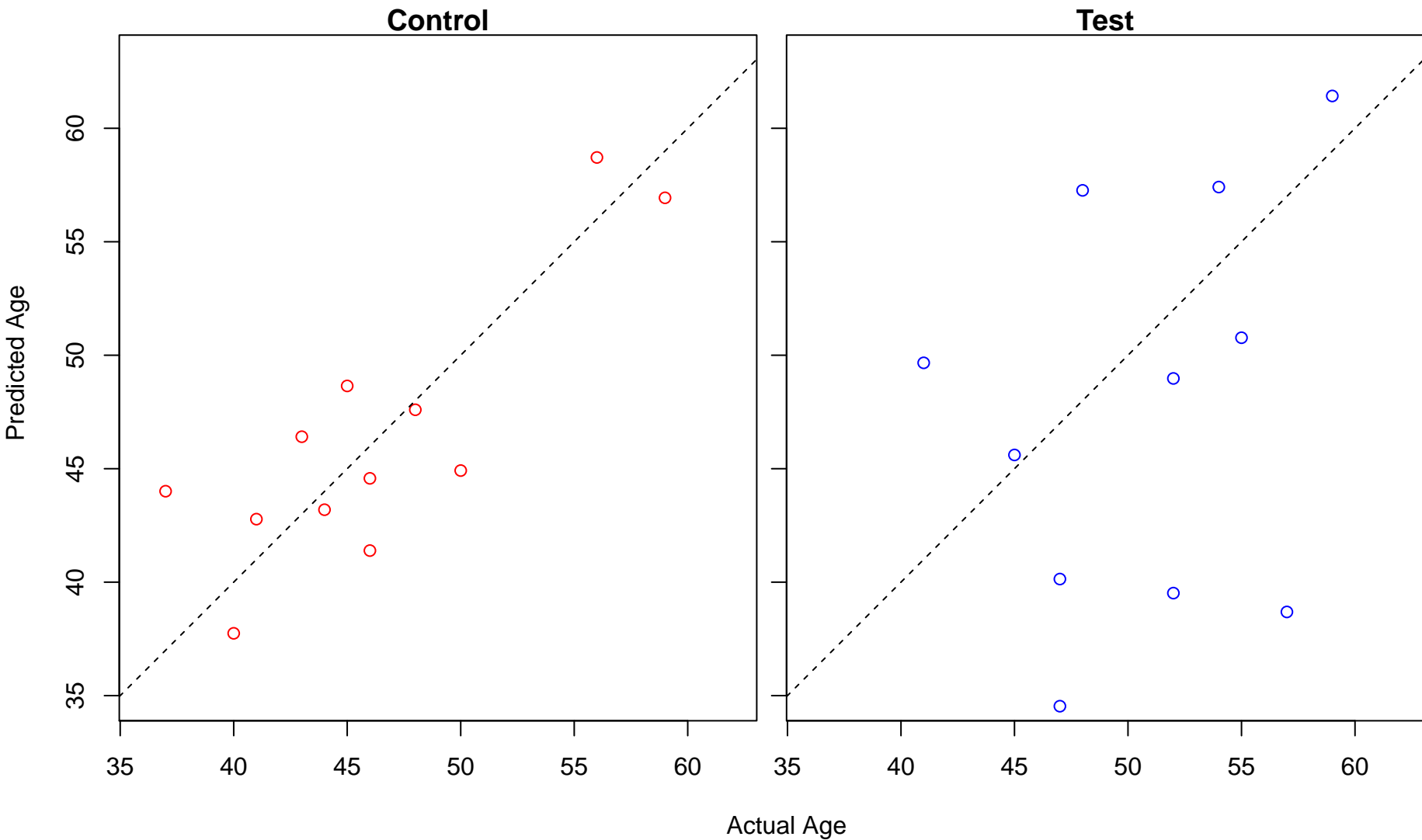


Test

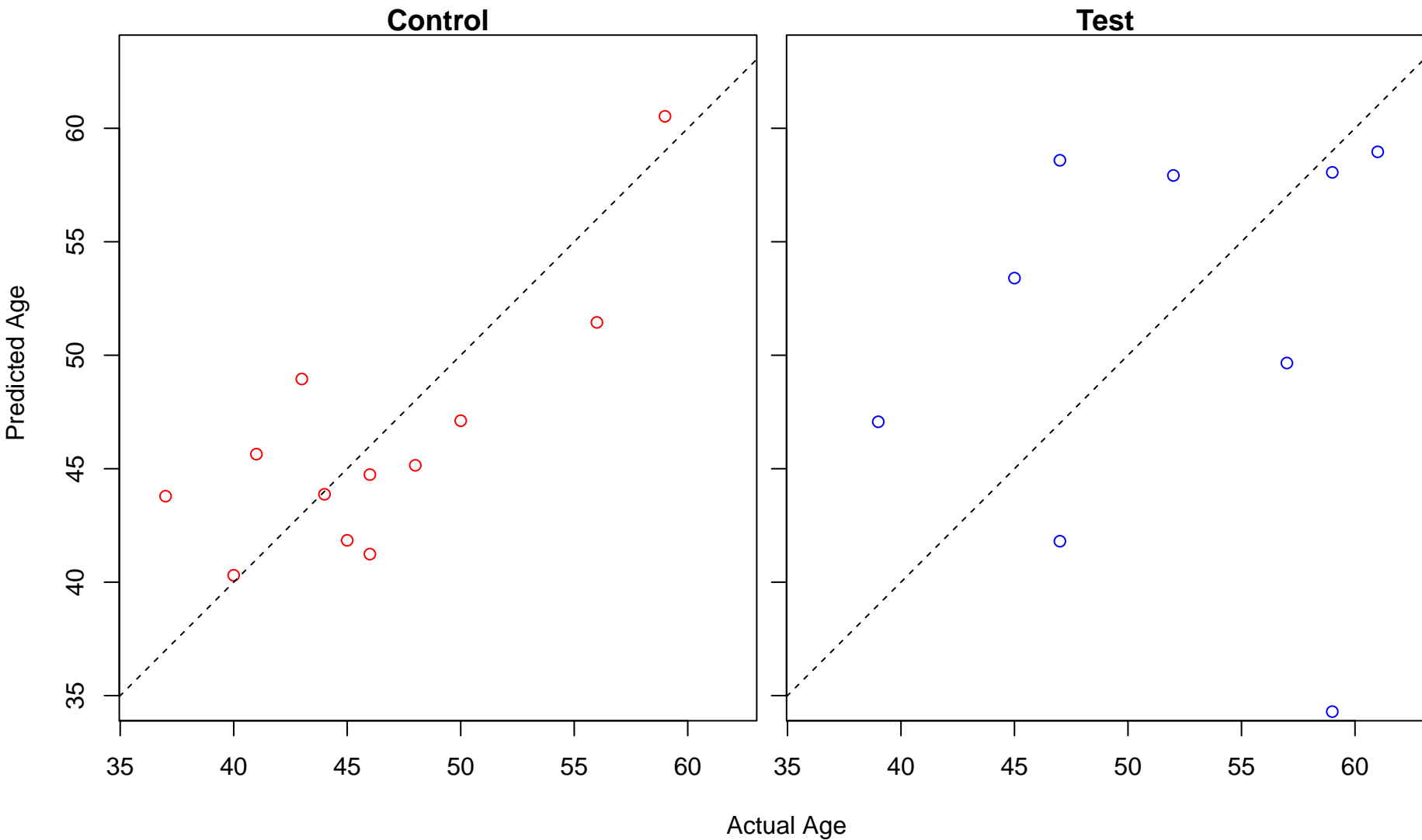


Actual Age

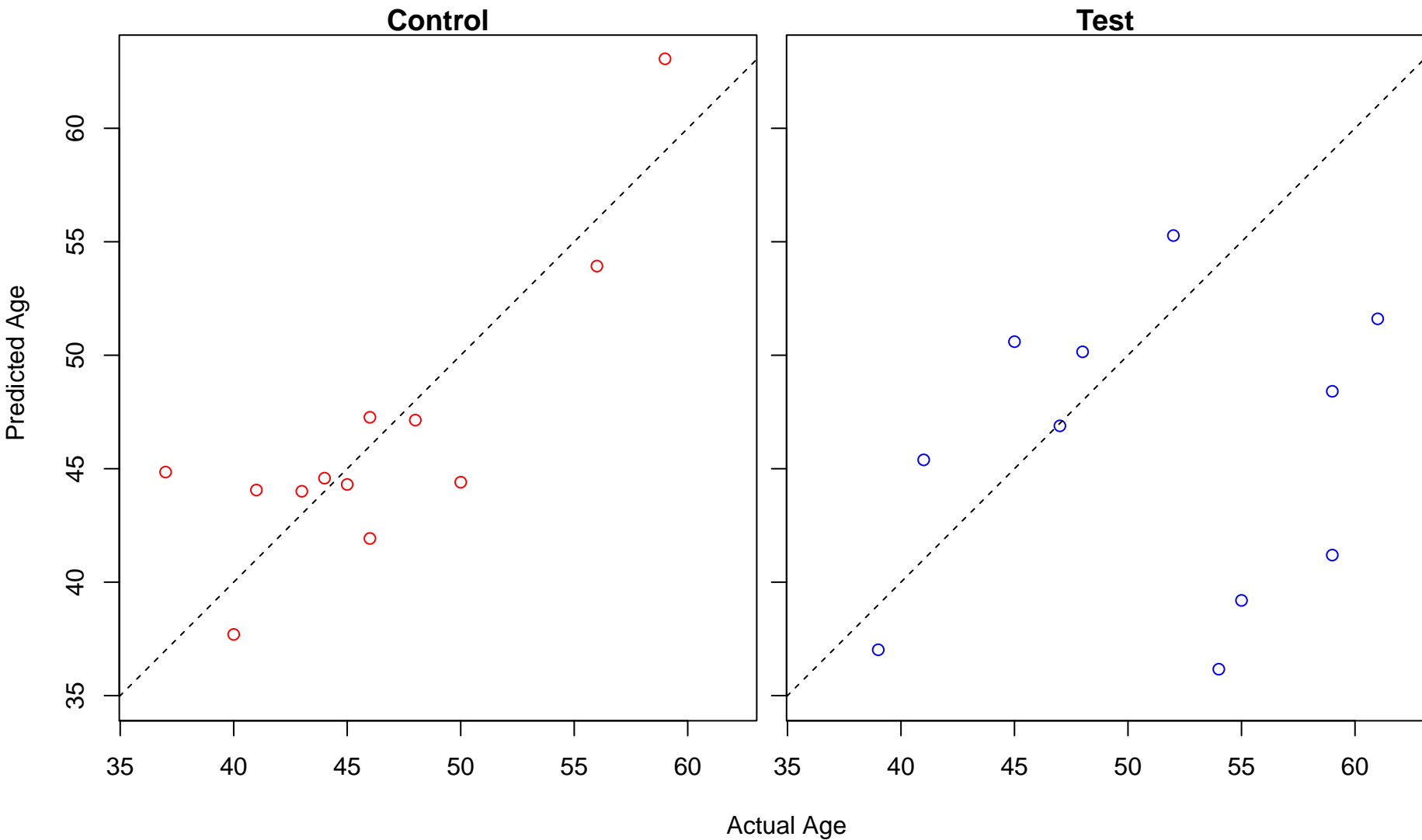
regulation of heart growth (Score: 8.097699)



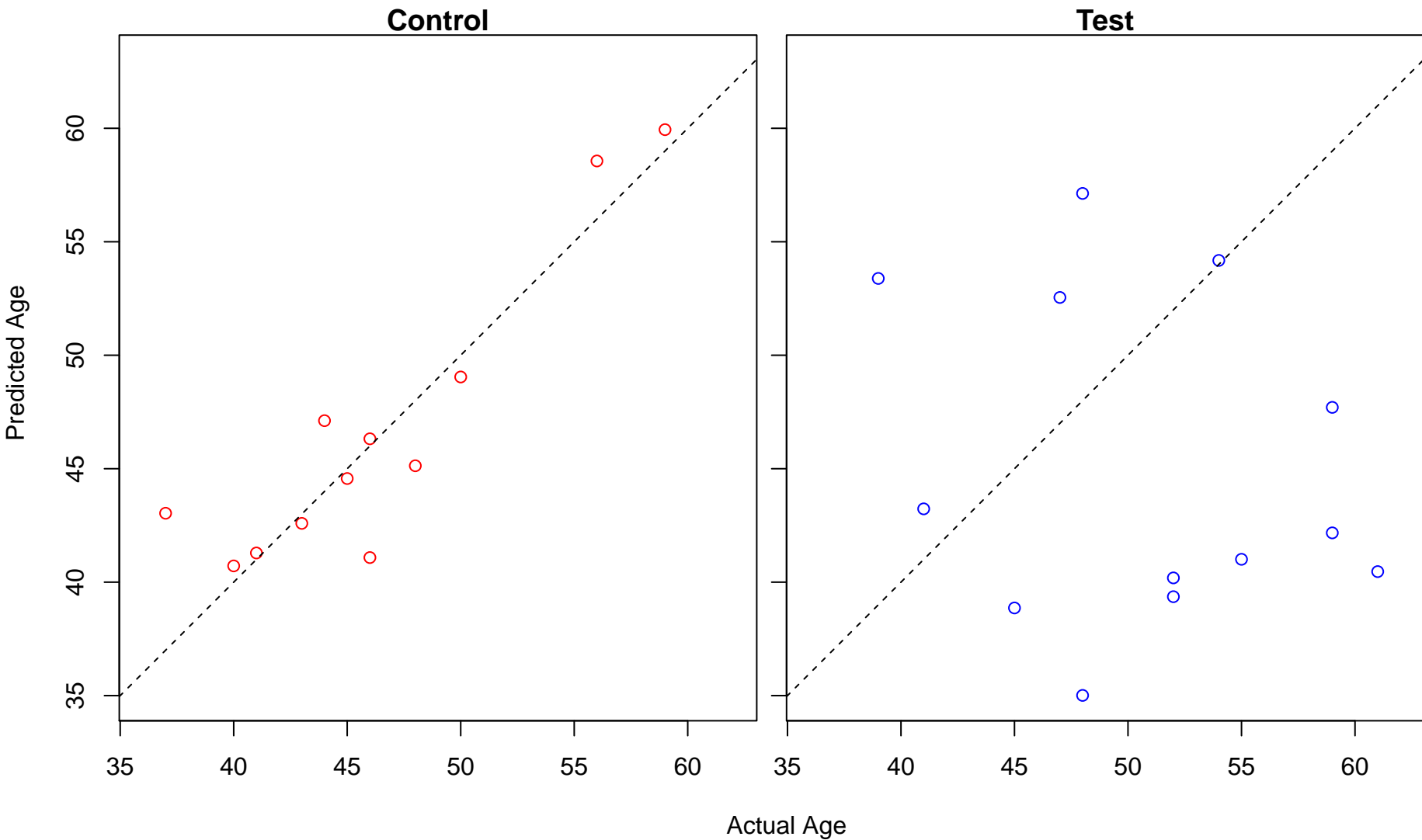
body morphogenesis (Score: 8.067418)



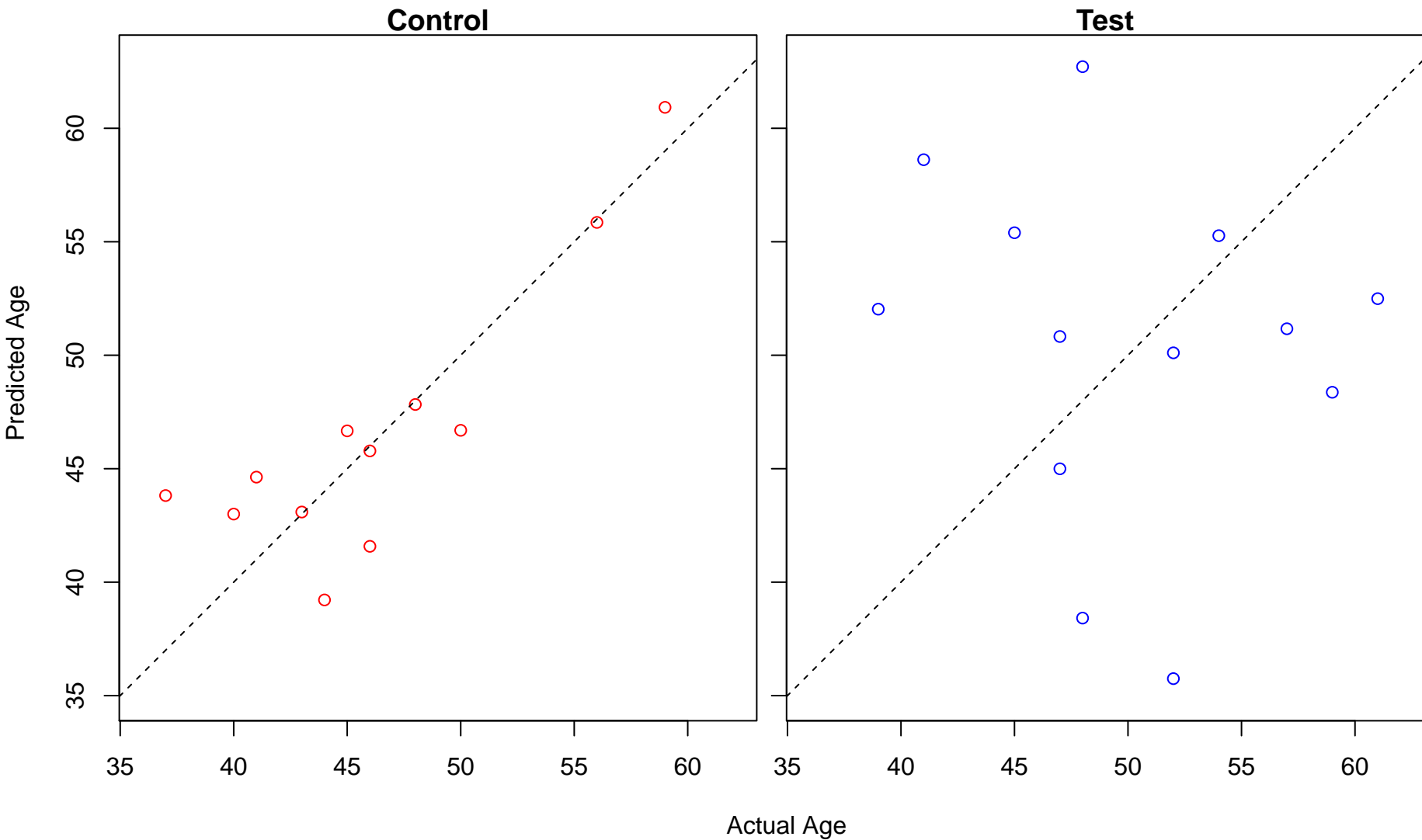
ER-associated ubiquitin-dependent protein catabolic process (Score: 8.065939)



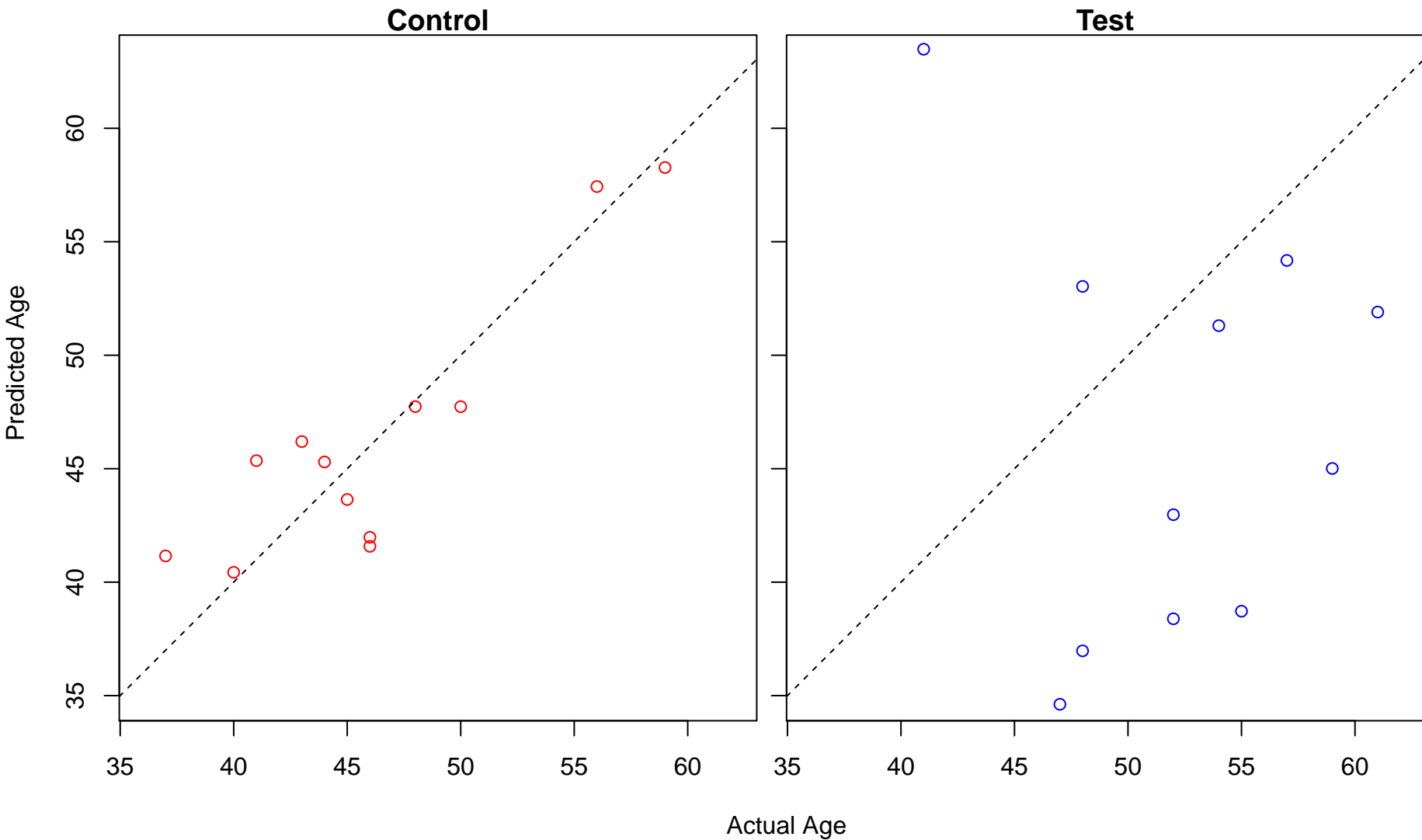
positive regulation of calcium ion transmembrane transporter activity (Score: 8.057080)



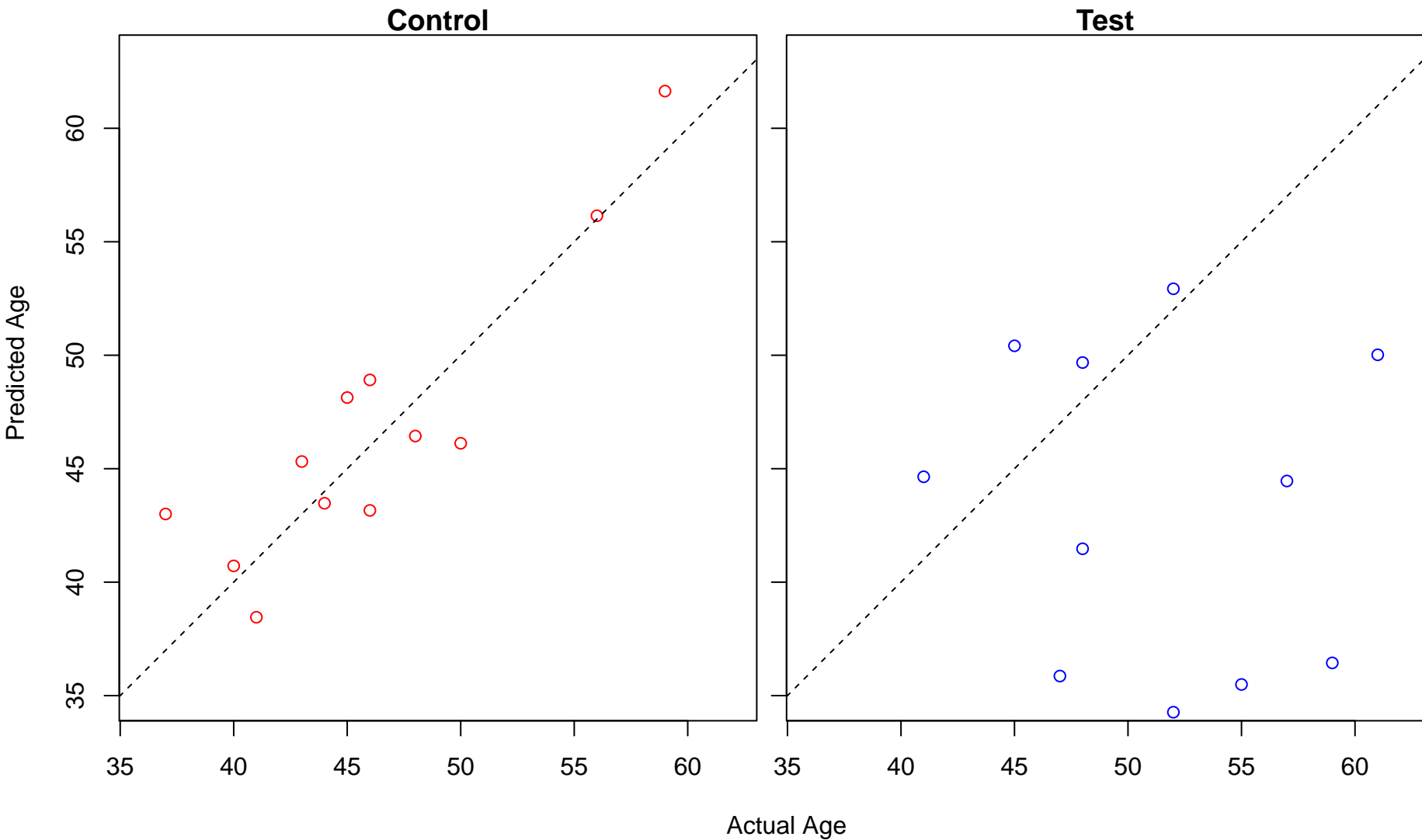
positive regulation of cytosolic calcium ion concentration (Score: 8.044294)



cellular response to metal ion (Score: 8.037511)

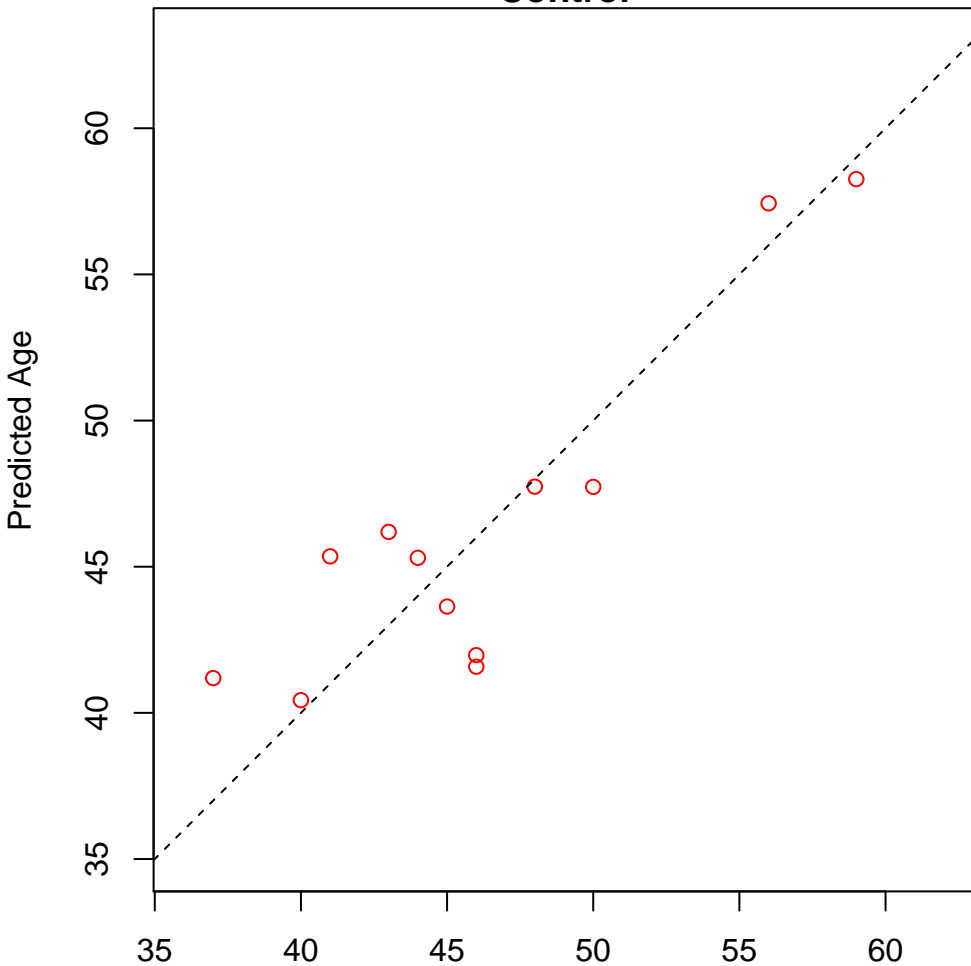


regulation of cell-matrix adhesion (Score: 8.034194)

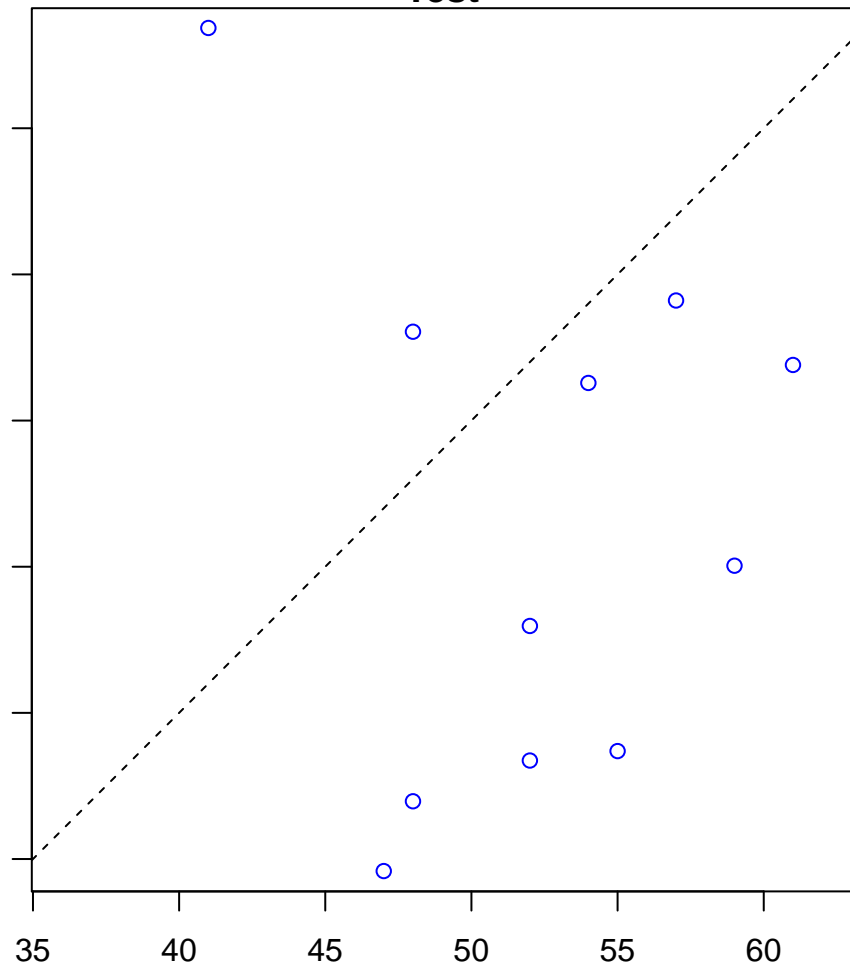


cellular response to inorganic substance (Score: 8.012066)

Control

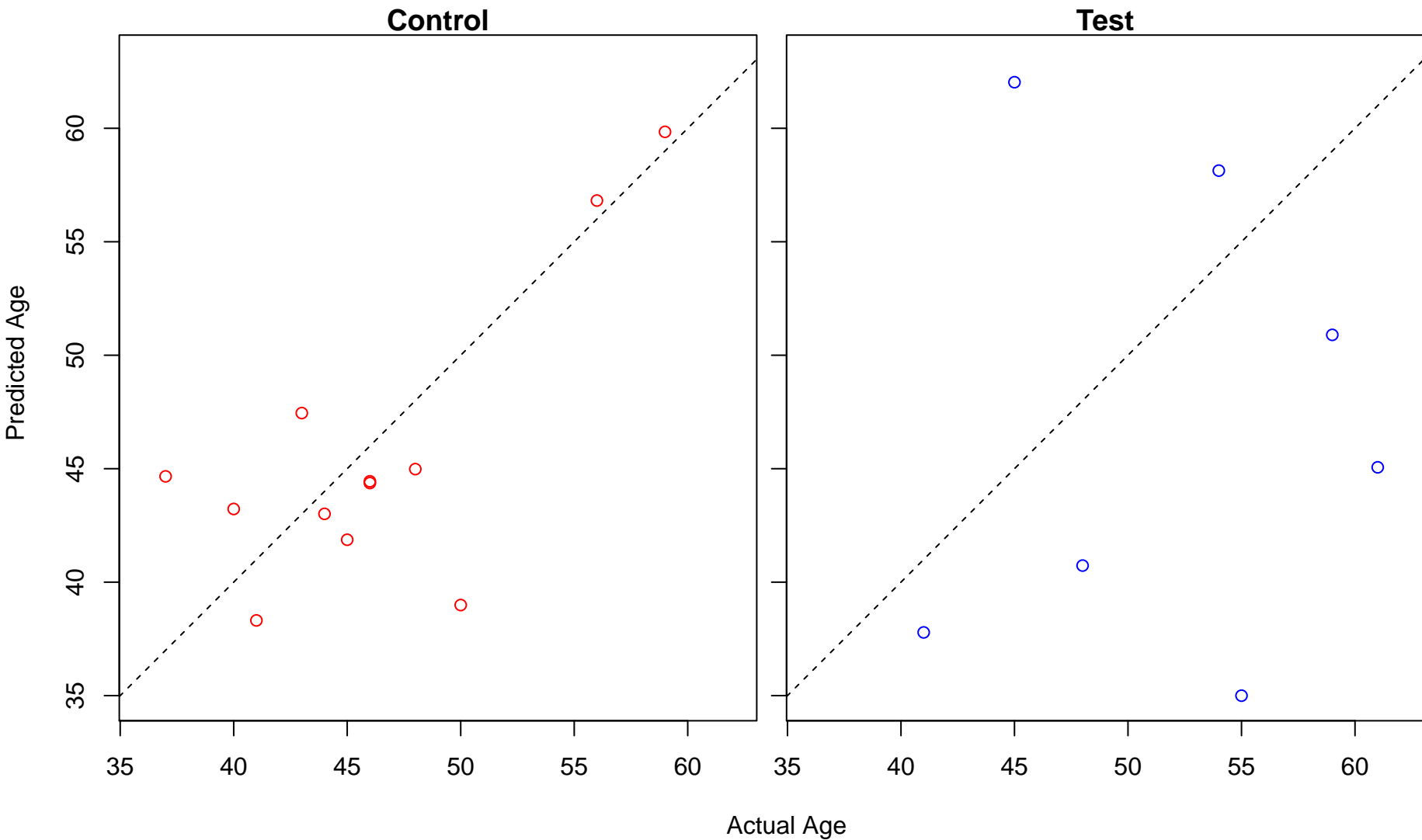


Test

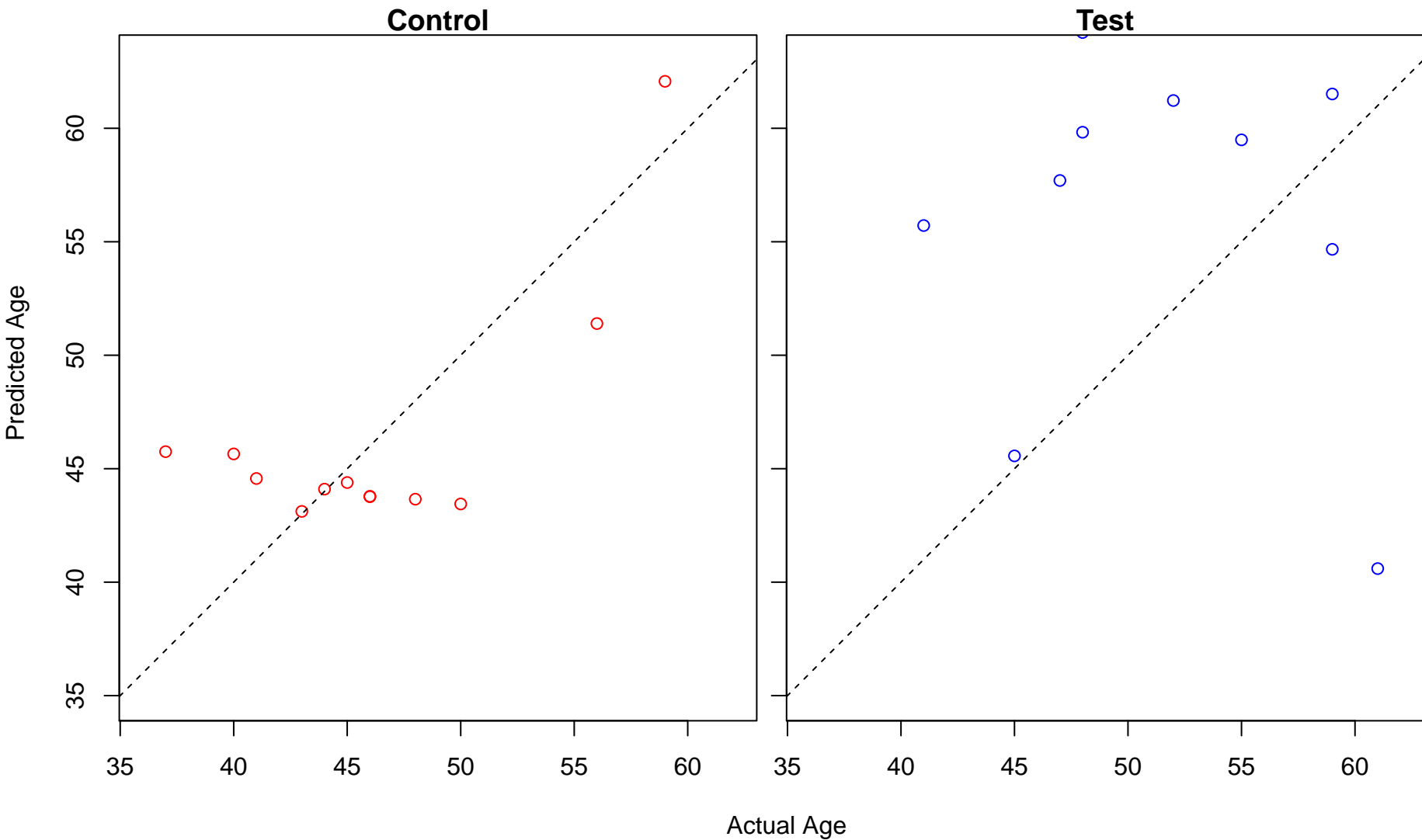


Actual Age

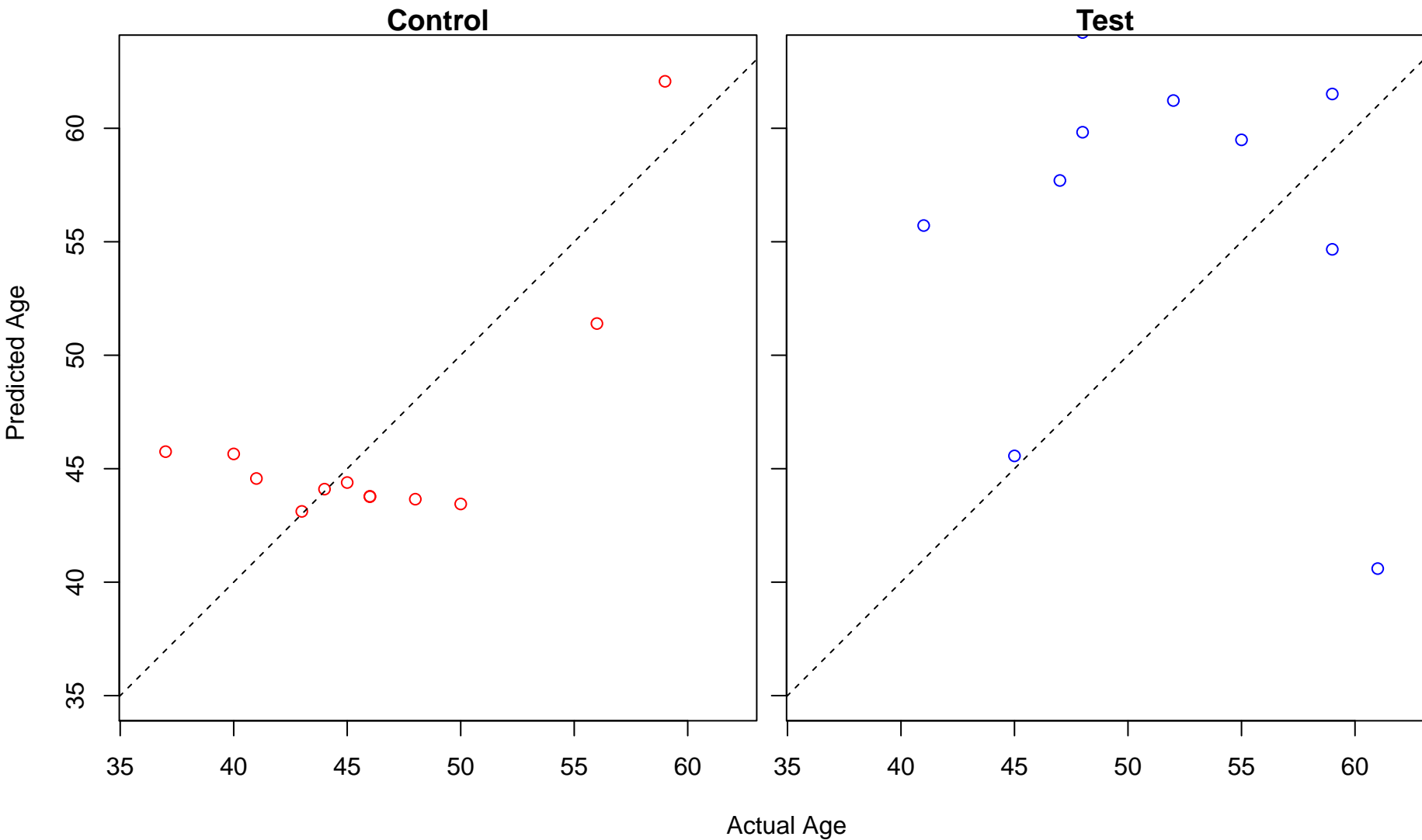
cAMP biosynthetic process (Score: 8.010047)



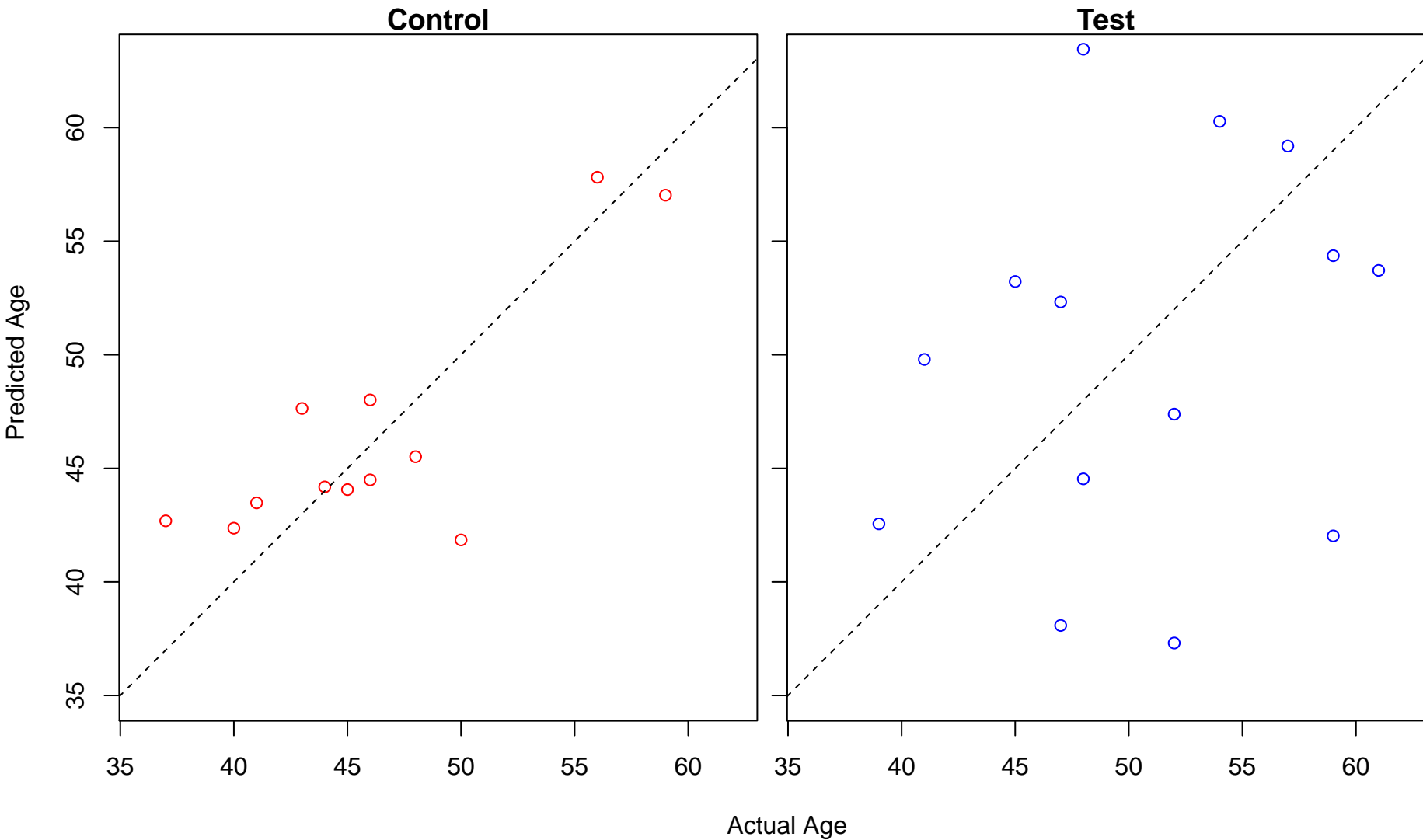
bundle of His cell to Purkinje myocyte signaling (Score: 8.007581)



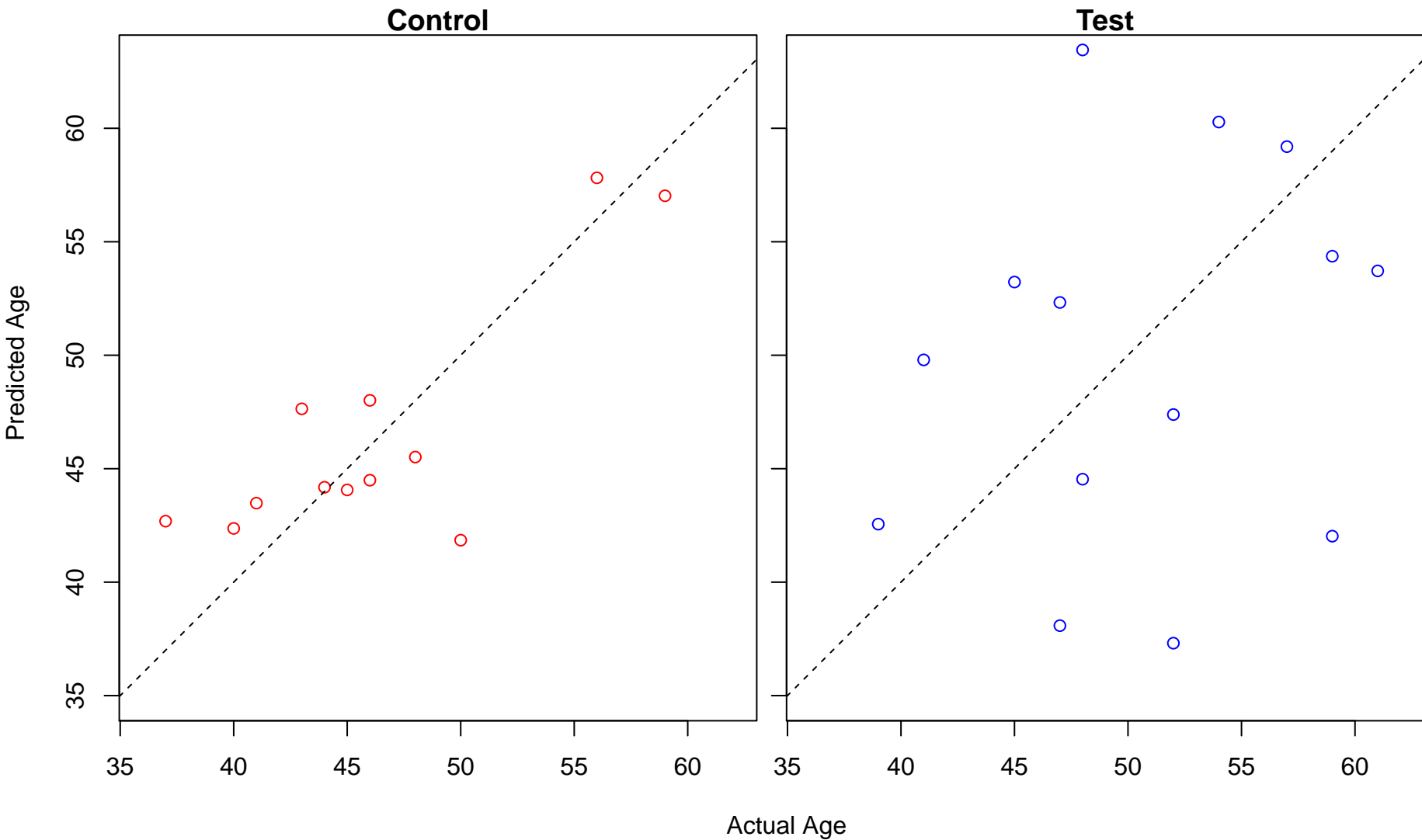
bundle of His cell action potential (Score: 8.007581)



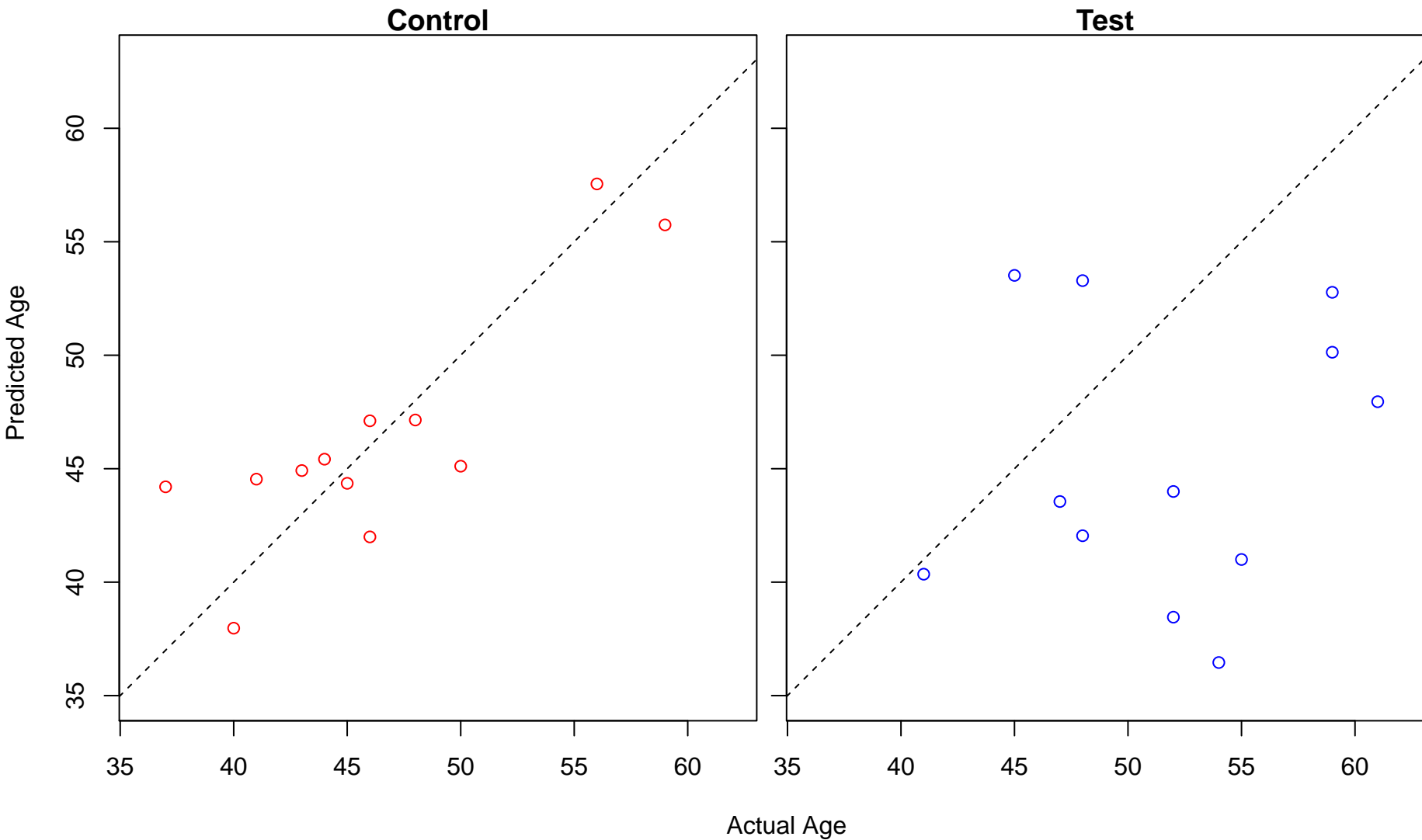
regulation of nuclear-transcribed mRNA poly(A) tail shortening (Score: 8.005612)



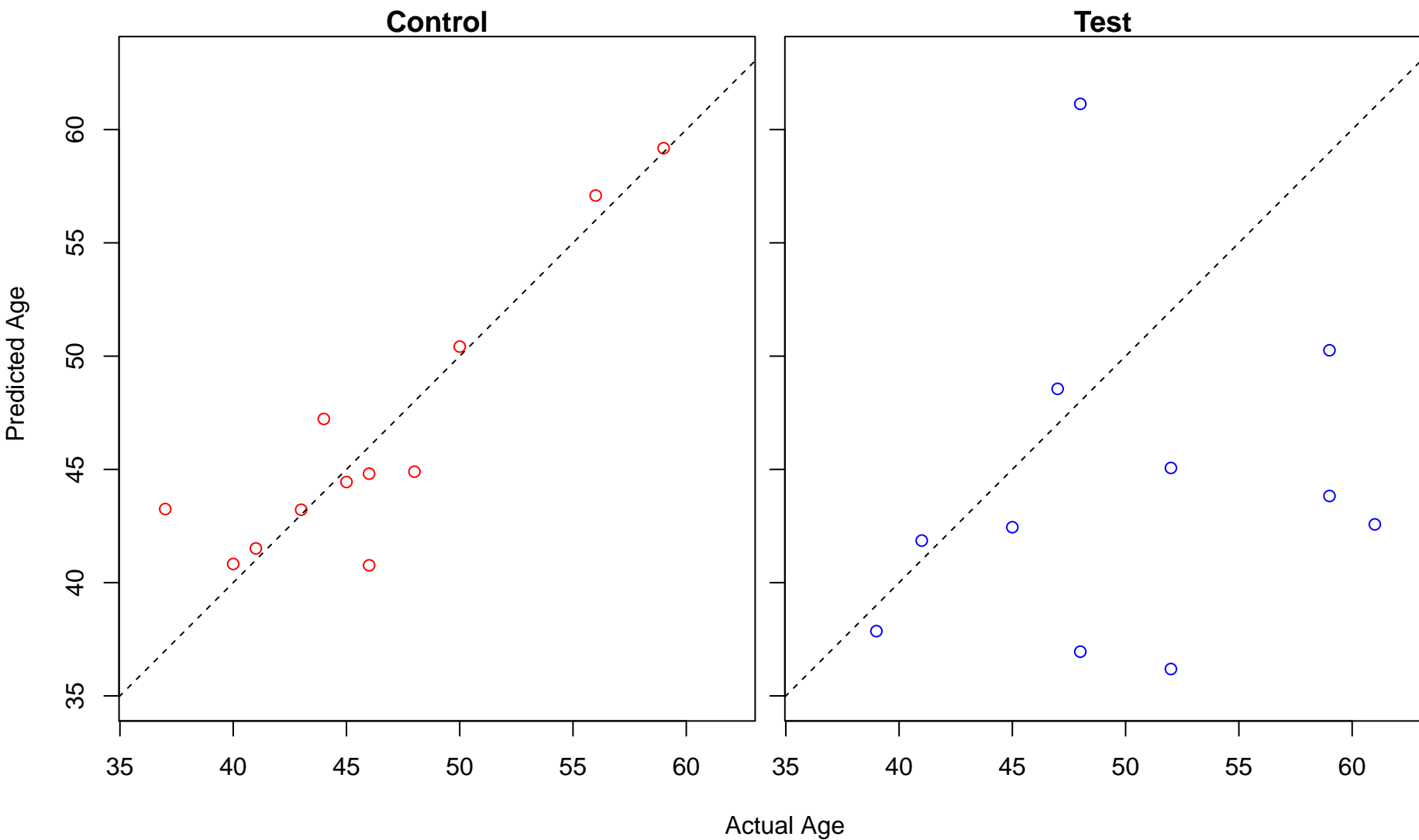
positive regulation of nuclear-transcribed mRNA poly(A) tail shortening (Score: 8.005612)



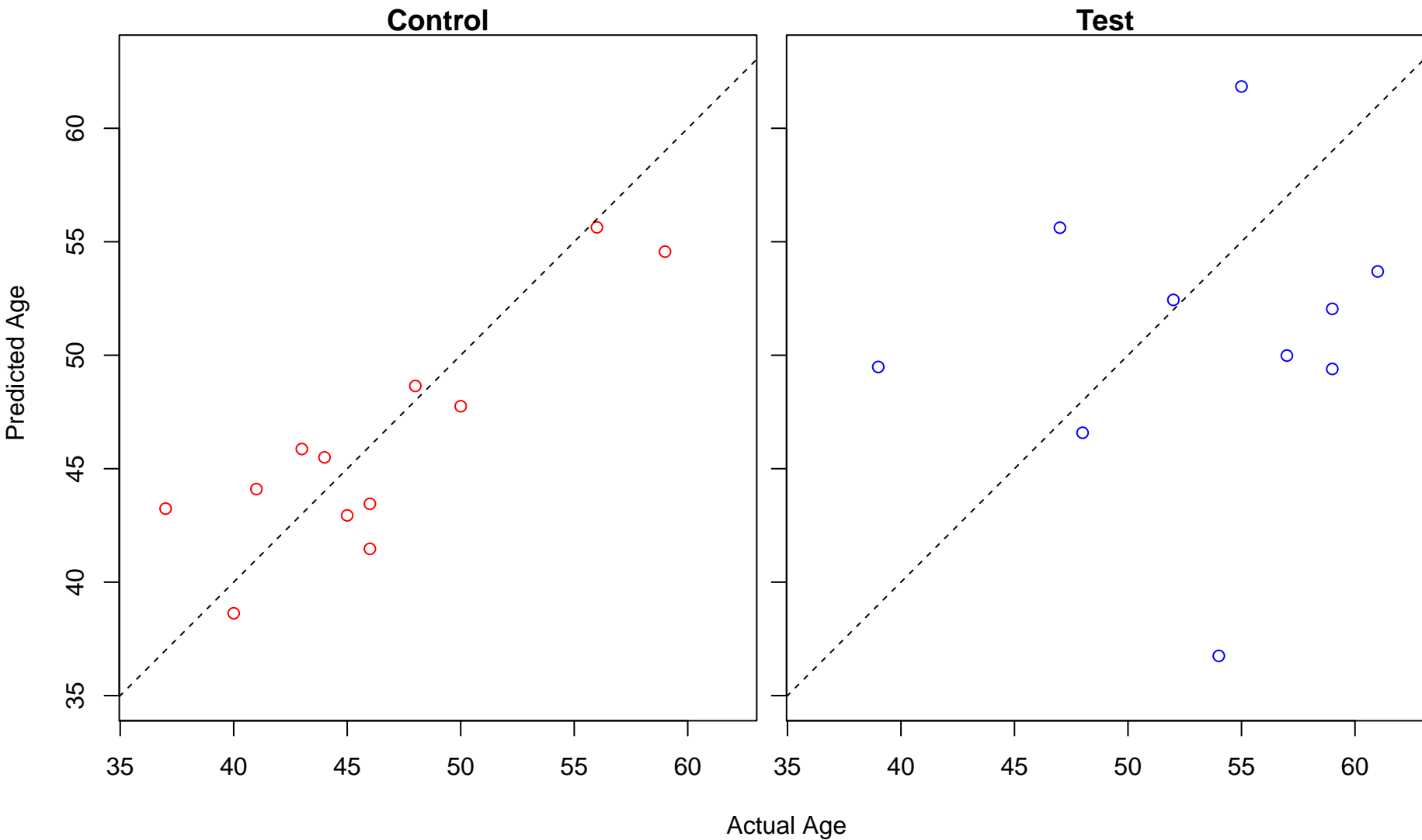
positive regulation of multi-organism process (Score: 8.001571)



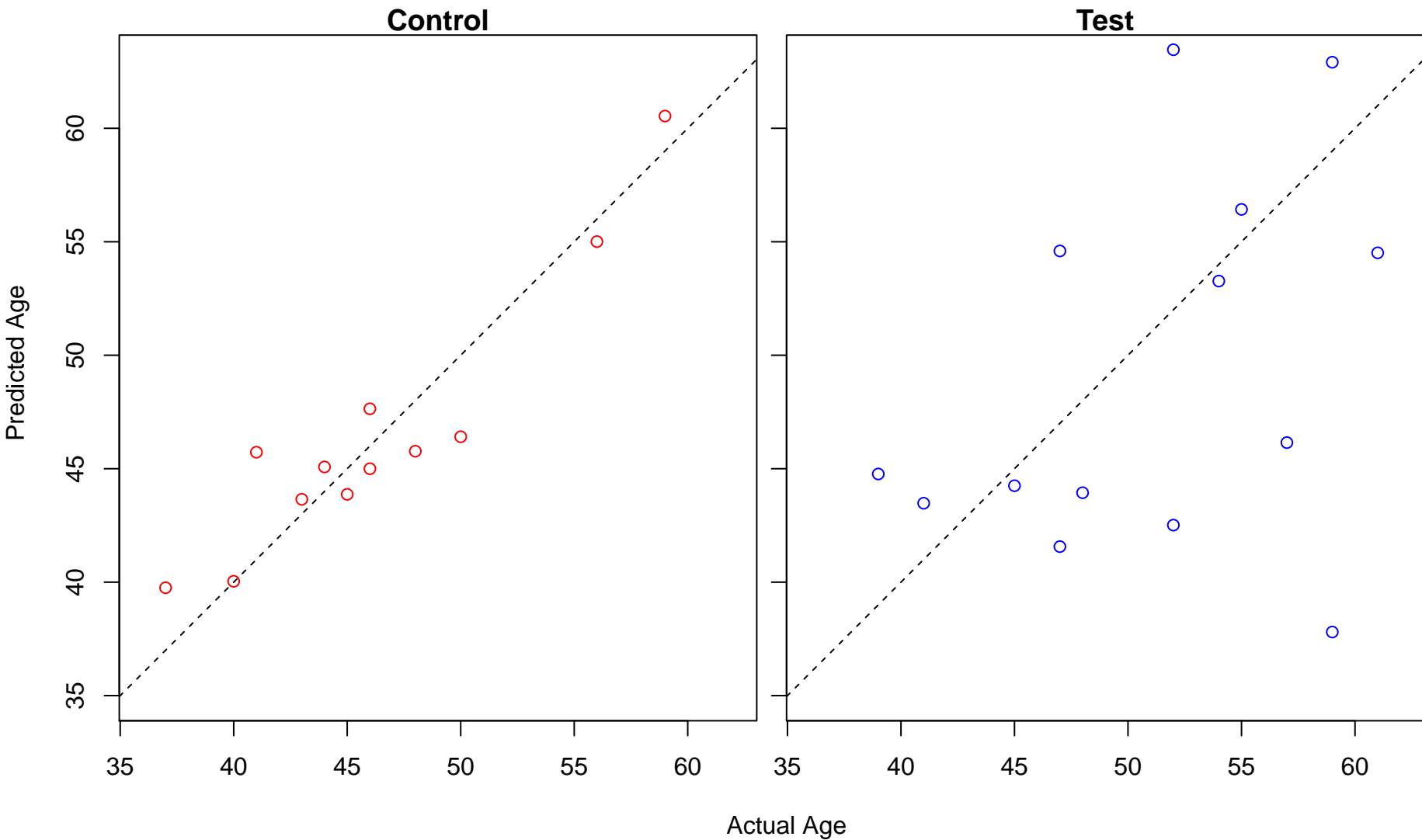
second-messenger-mediated signaling (Score: 7.980276)



mesenchymal cell development (Score: 7.963184)

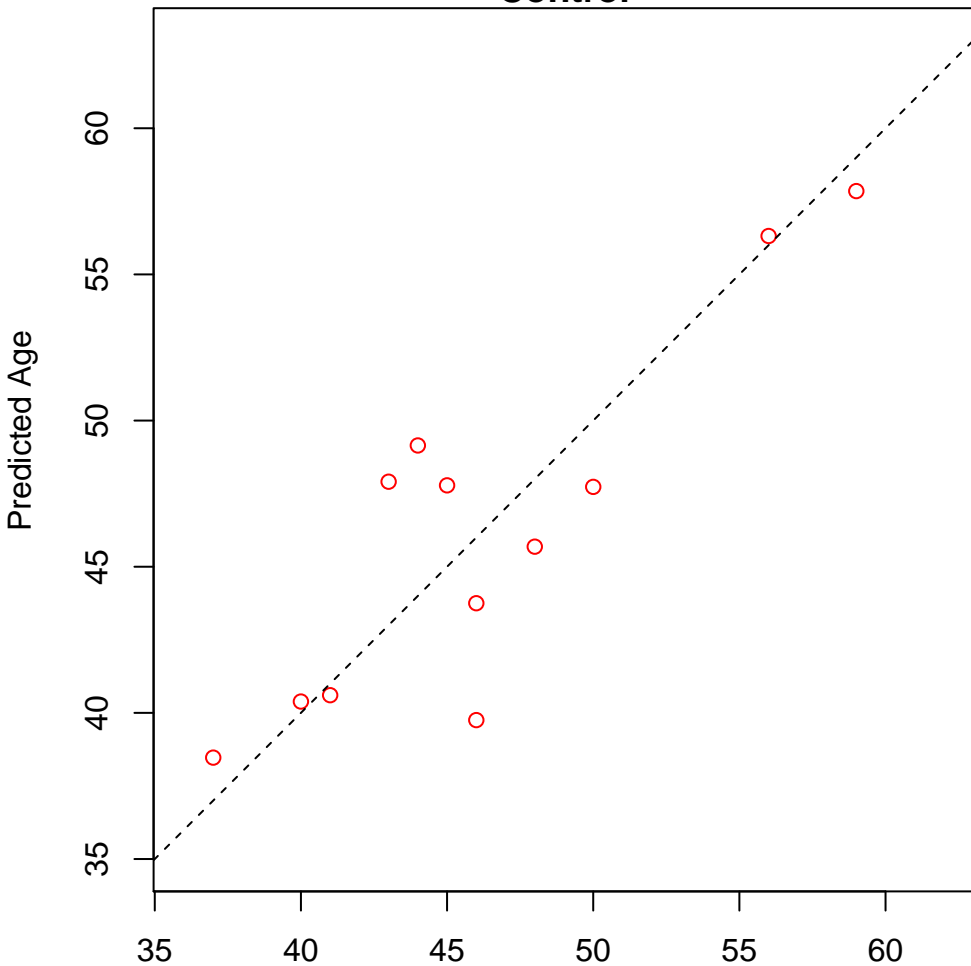


negative regulation of dendritic spine development (Score: 7.957347)

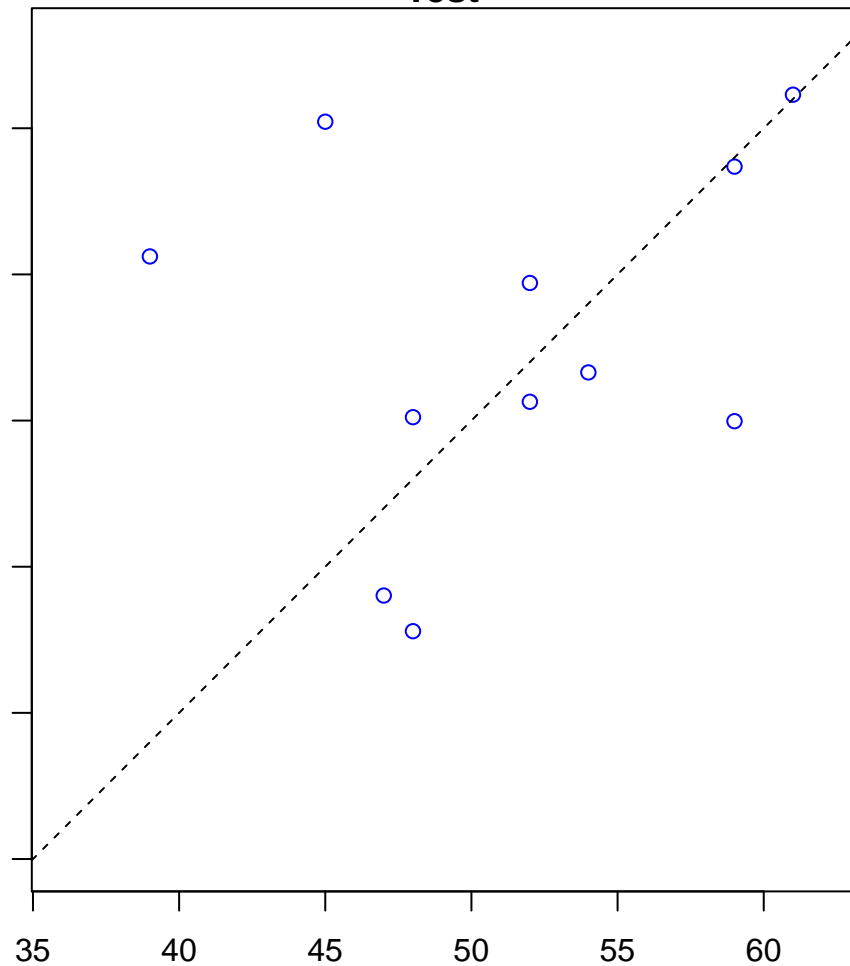


ossification involved in bone maturation (Score: 7.948786)

Control

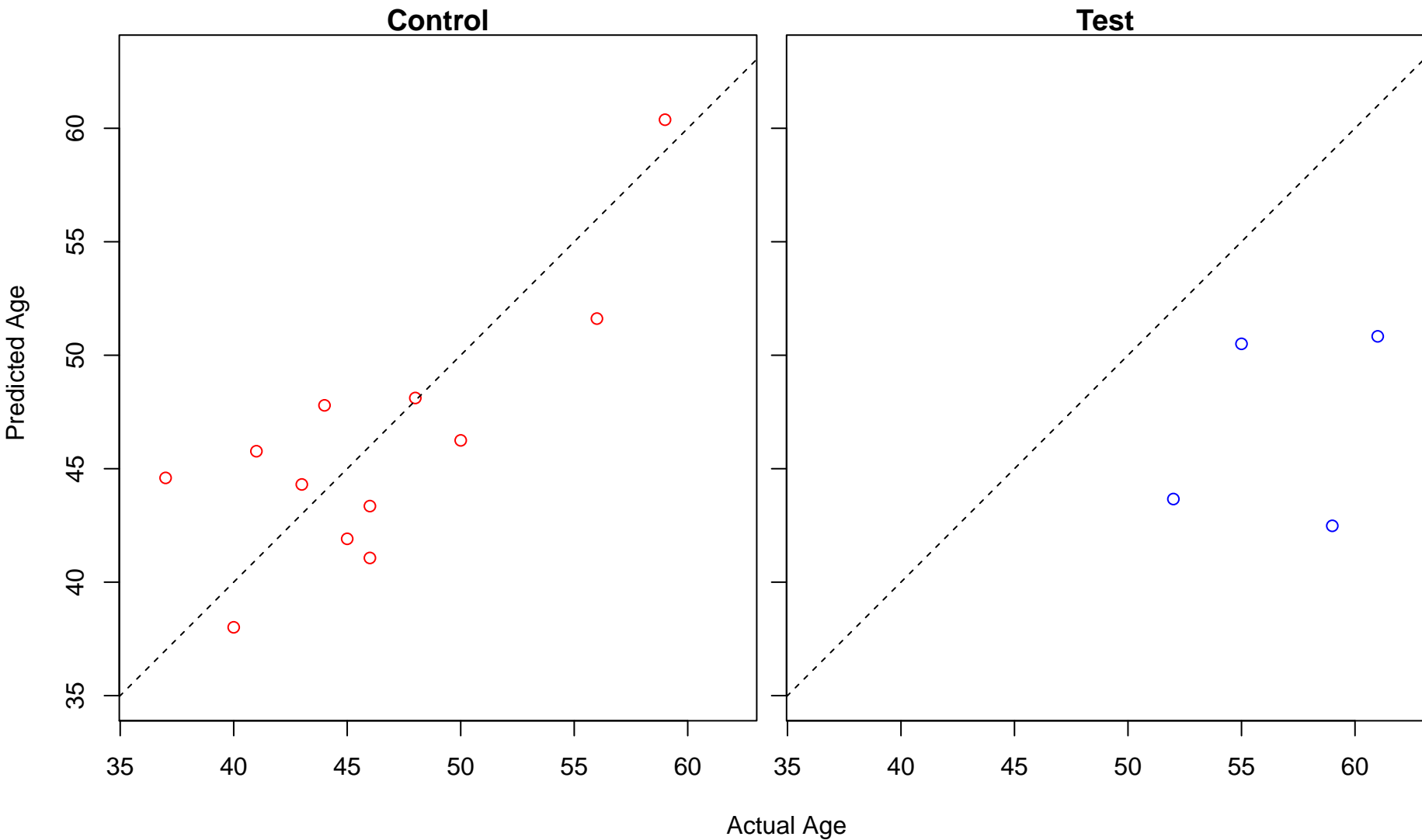


Test

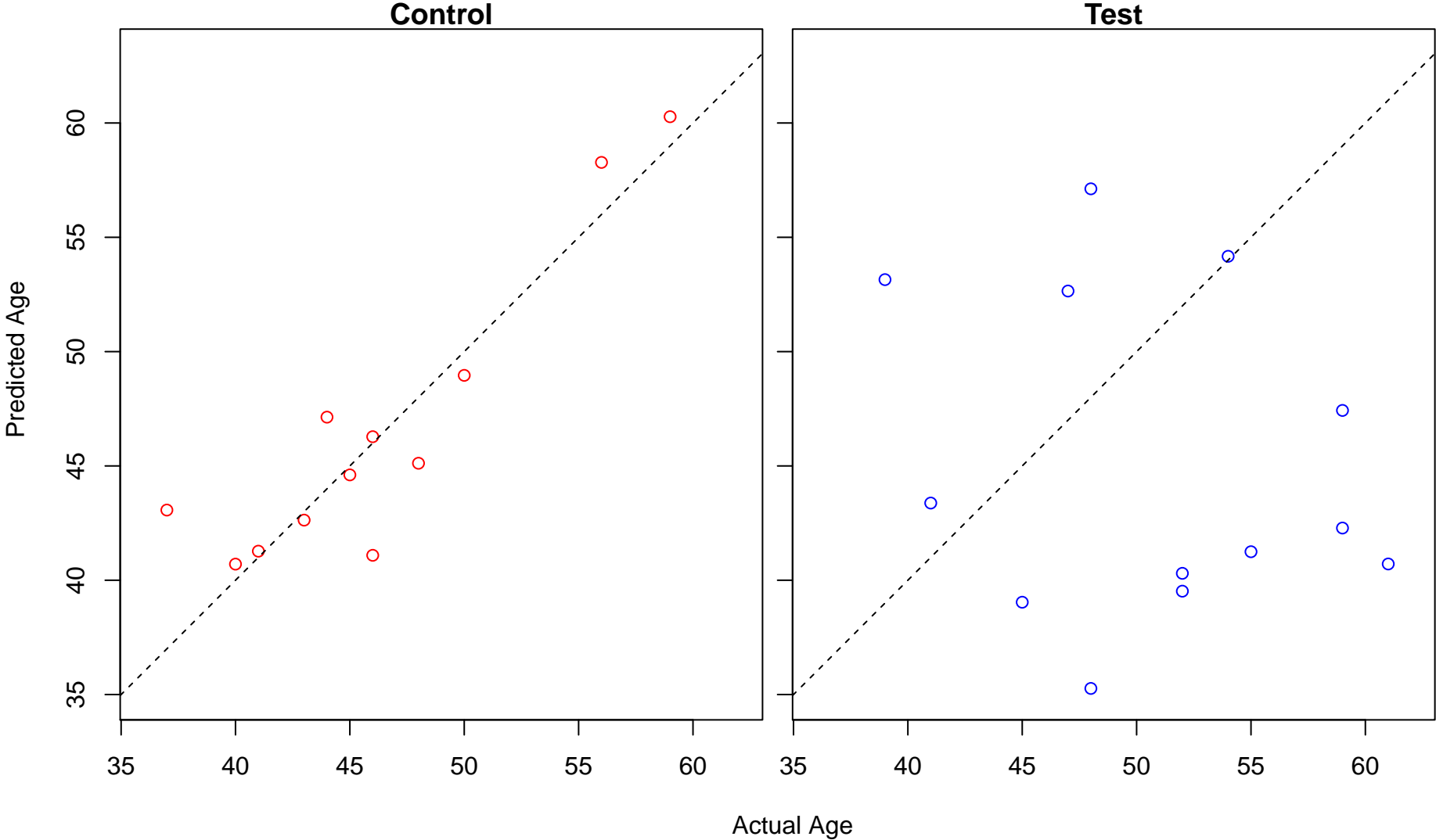


Actual Age

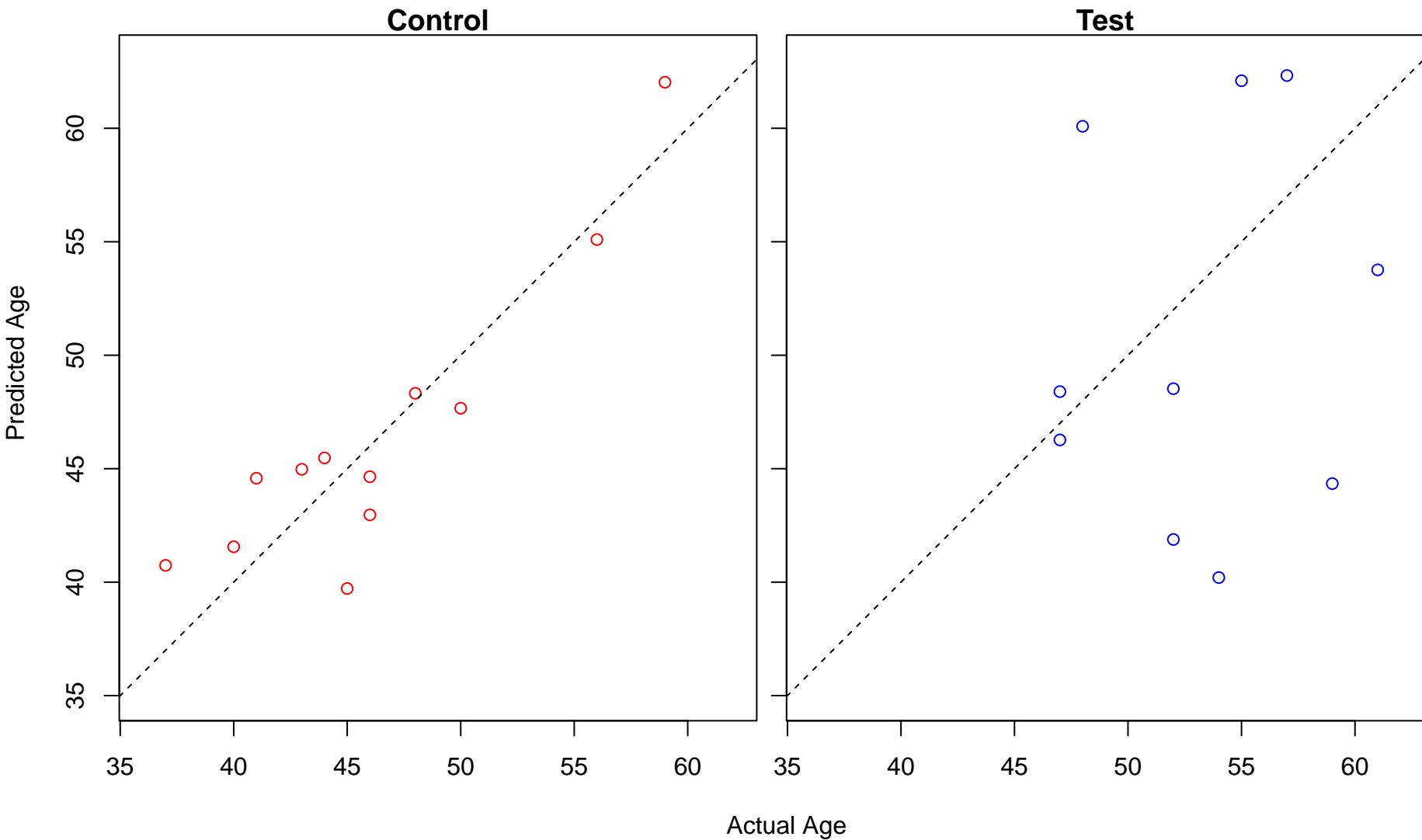
skin development (Score: 7.913816)



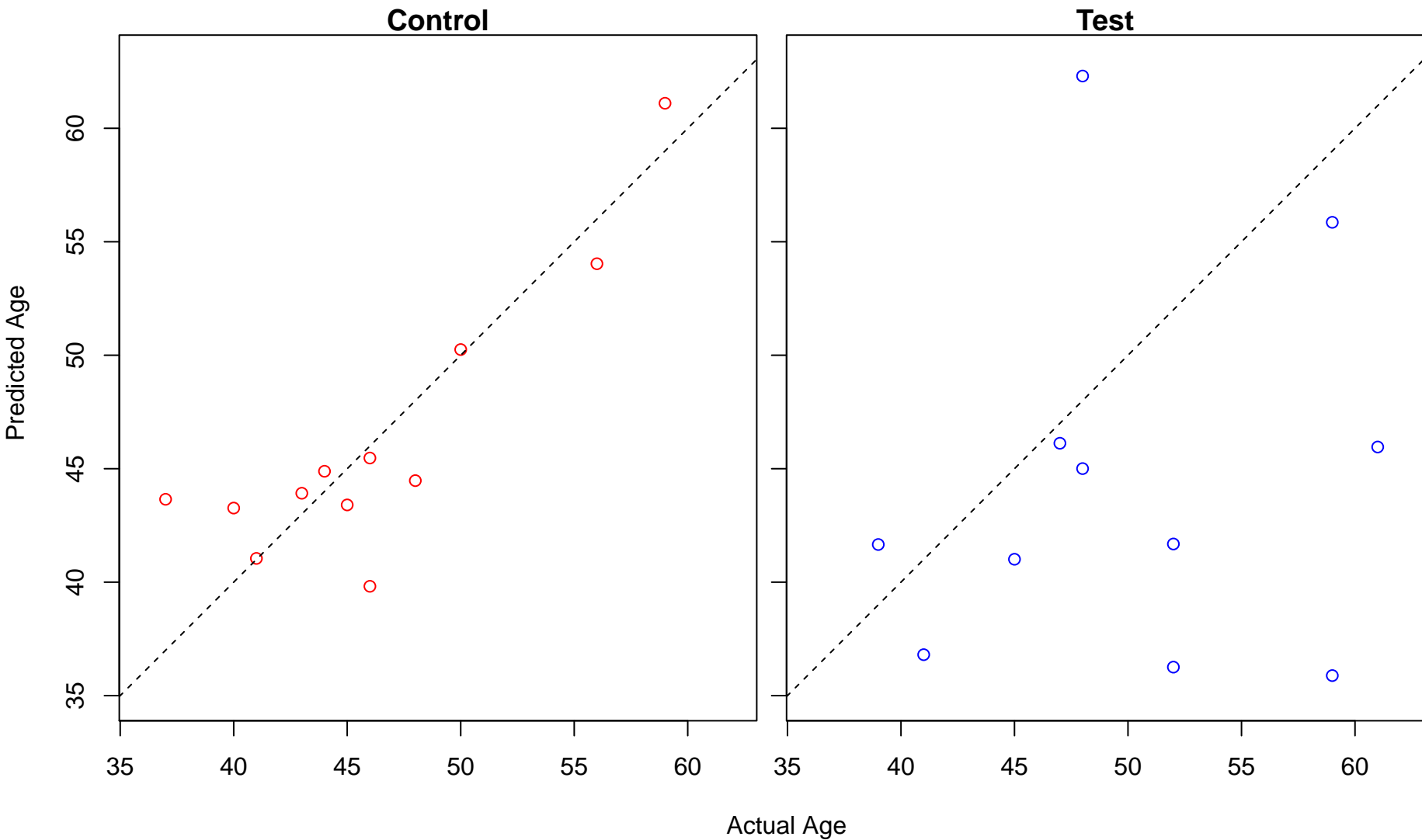
positive regulation of calcium ion transmembrane transport (Score: 7.907459)



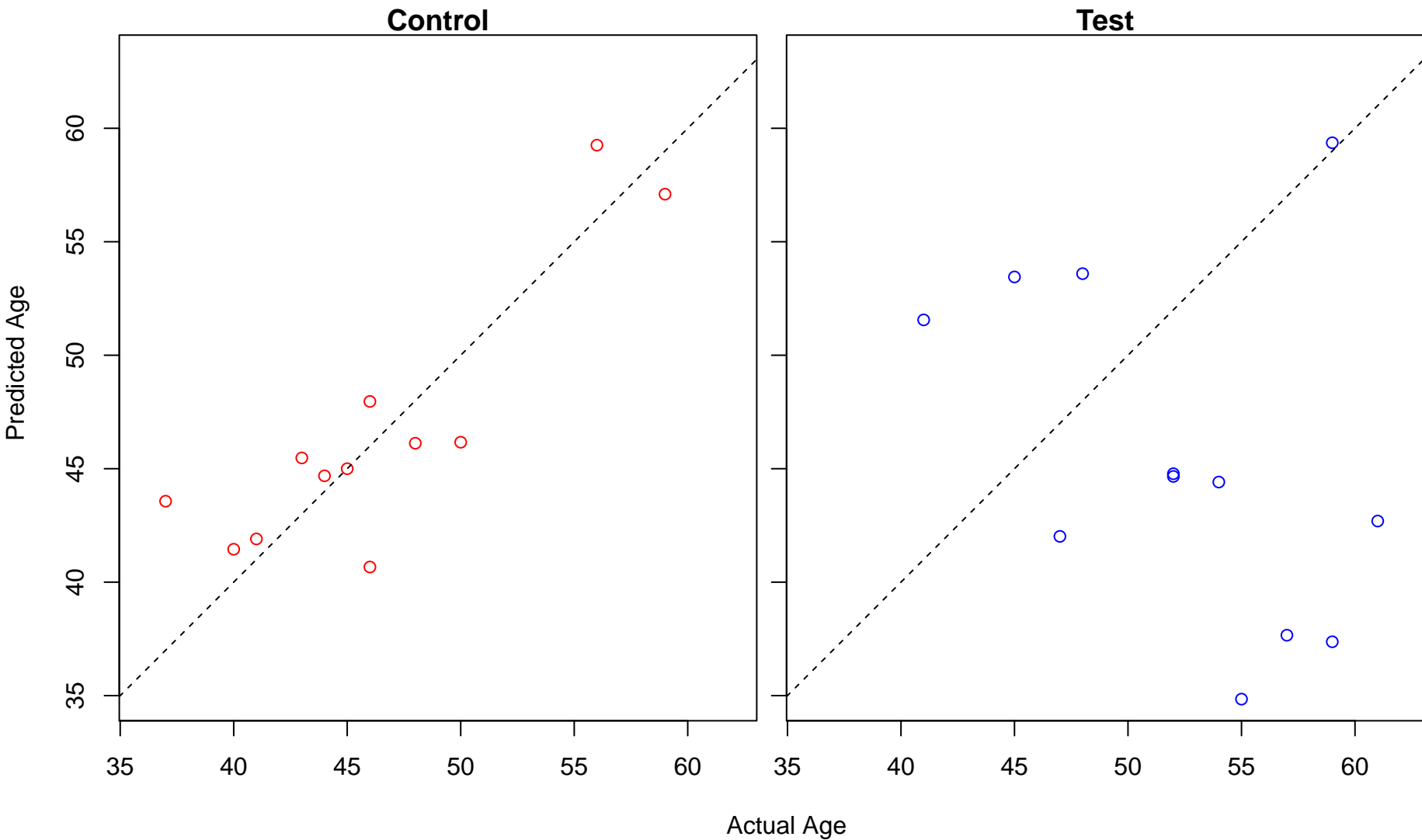
regulation of protein kinase B signaling (Score: 7.888889)



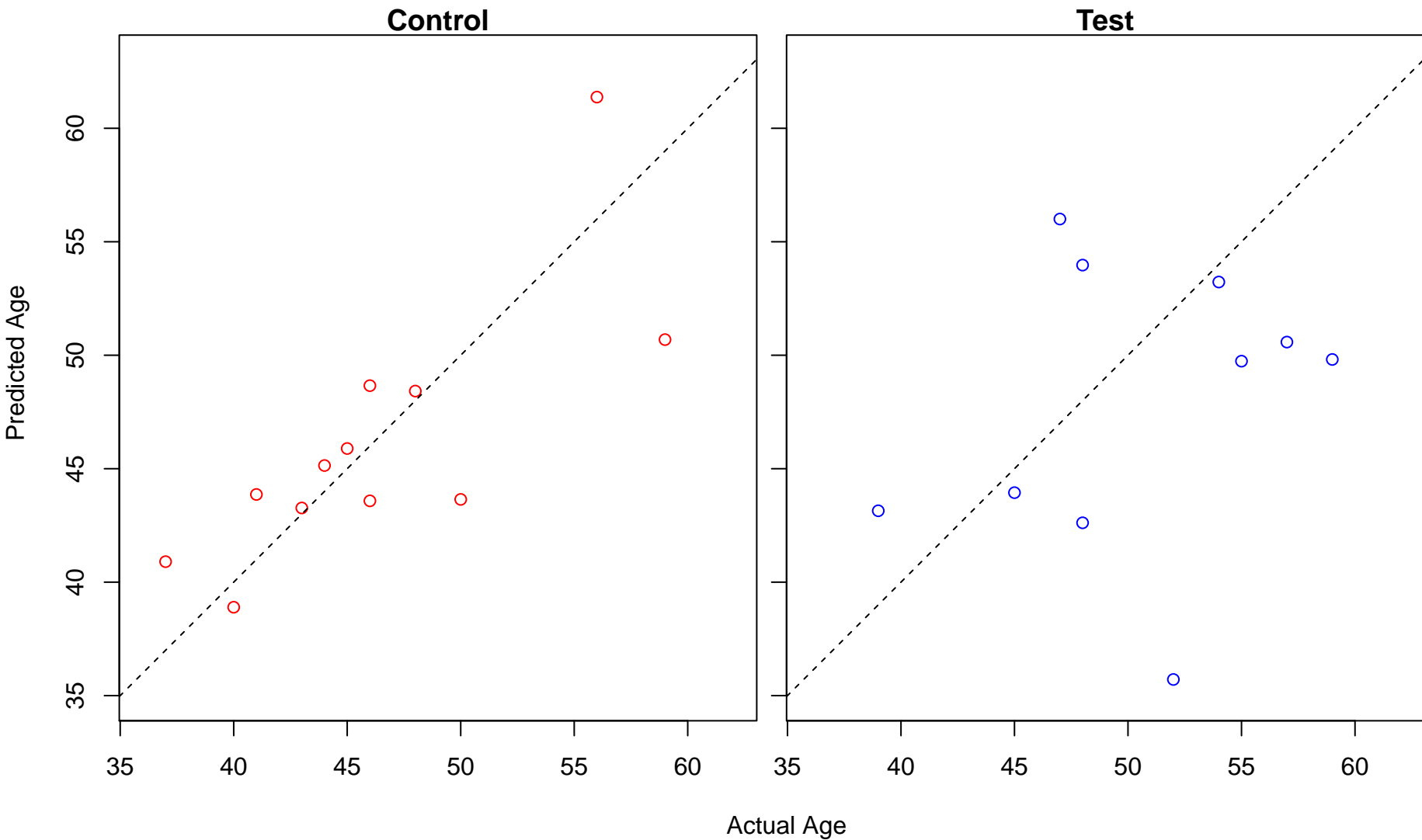
cardiac muscle contraction (Score: 7.877392)



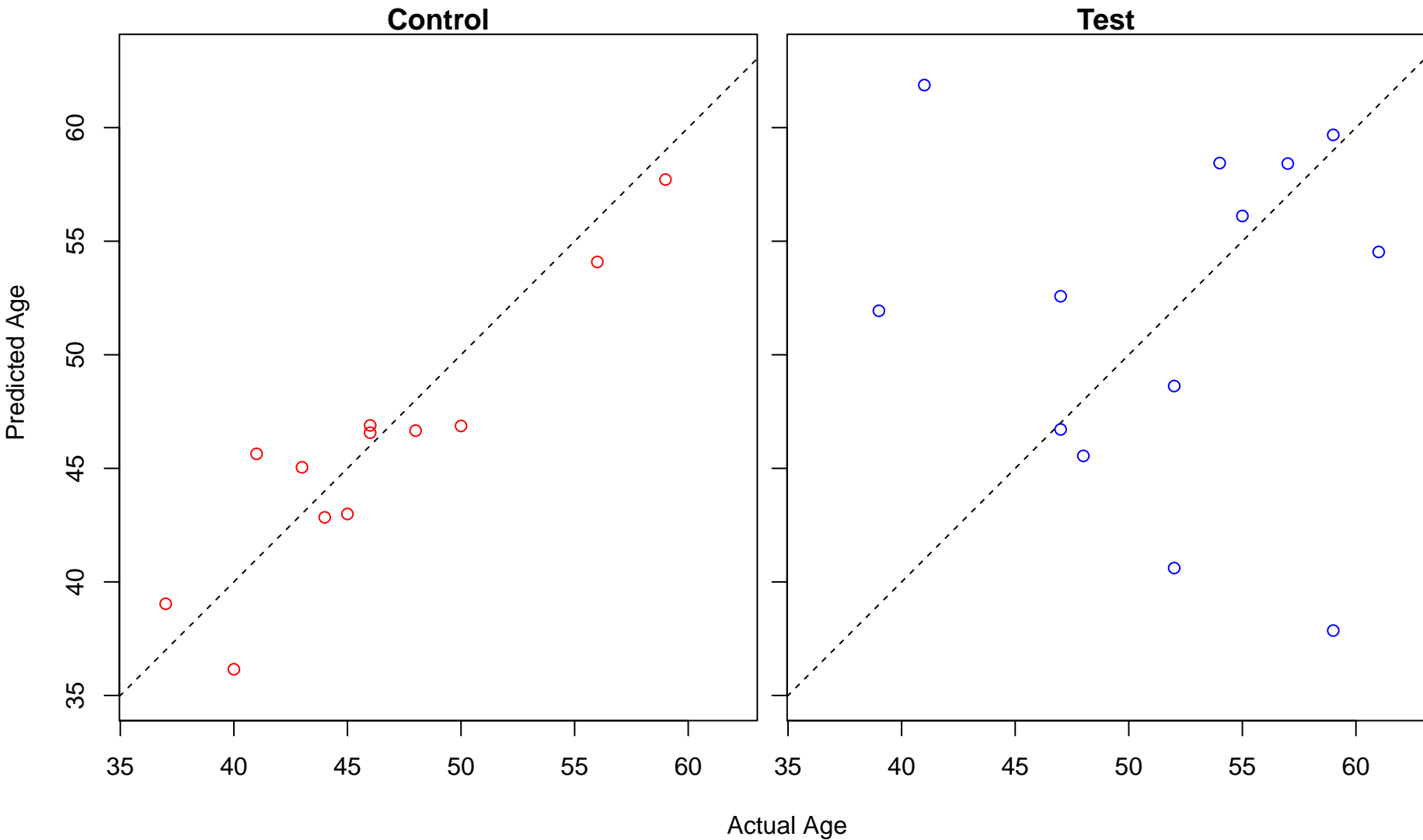
muscle tissue development (Score: 7.874384)



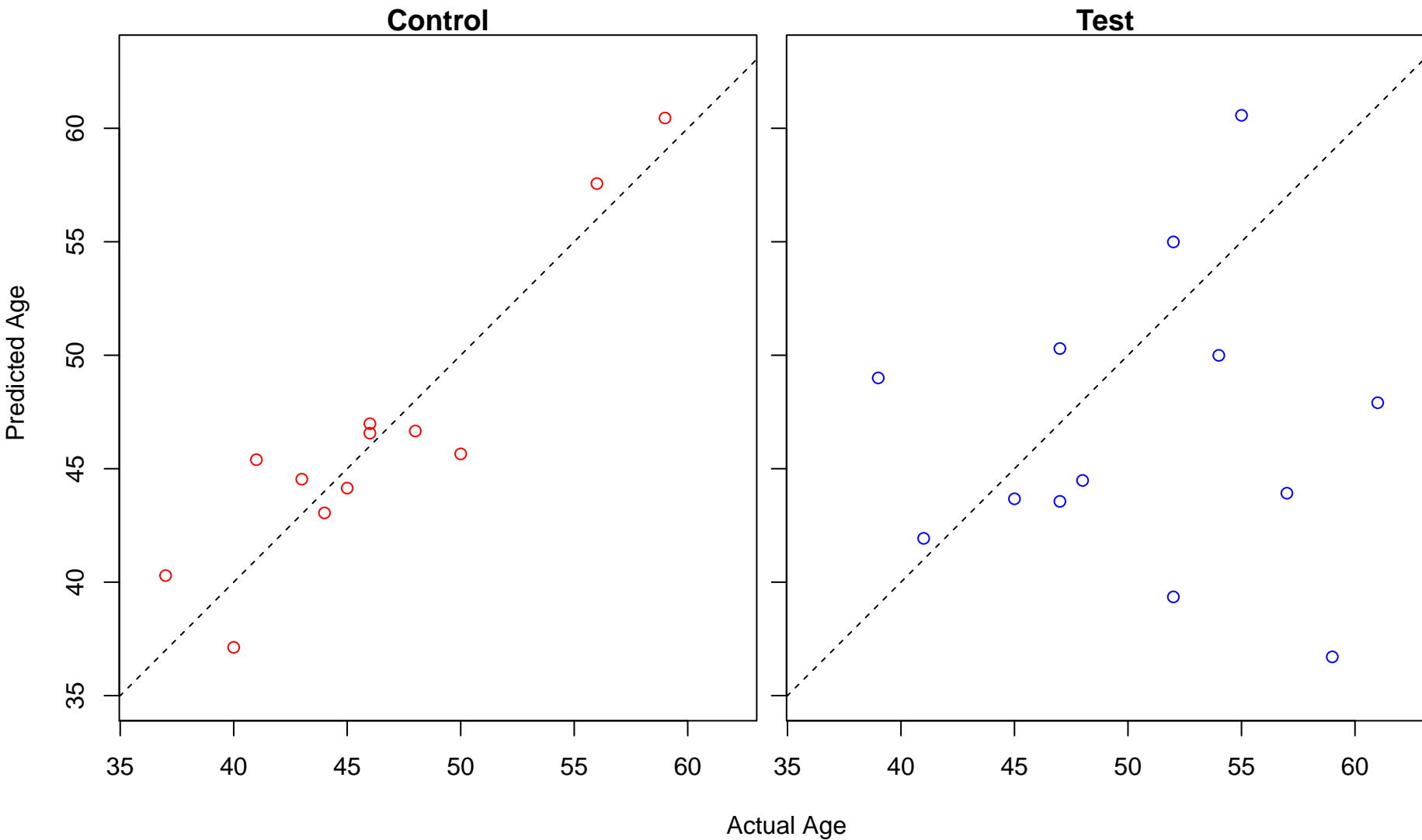
mesodermal cell differentiation (Score: 7.872227)



postsynaptic membrane organization (Score: 7.864252)

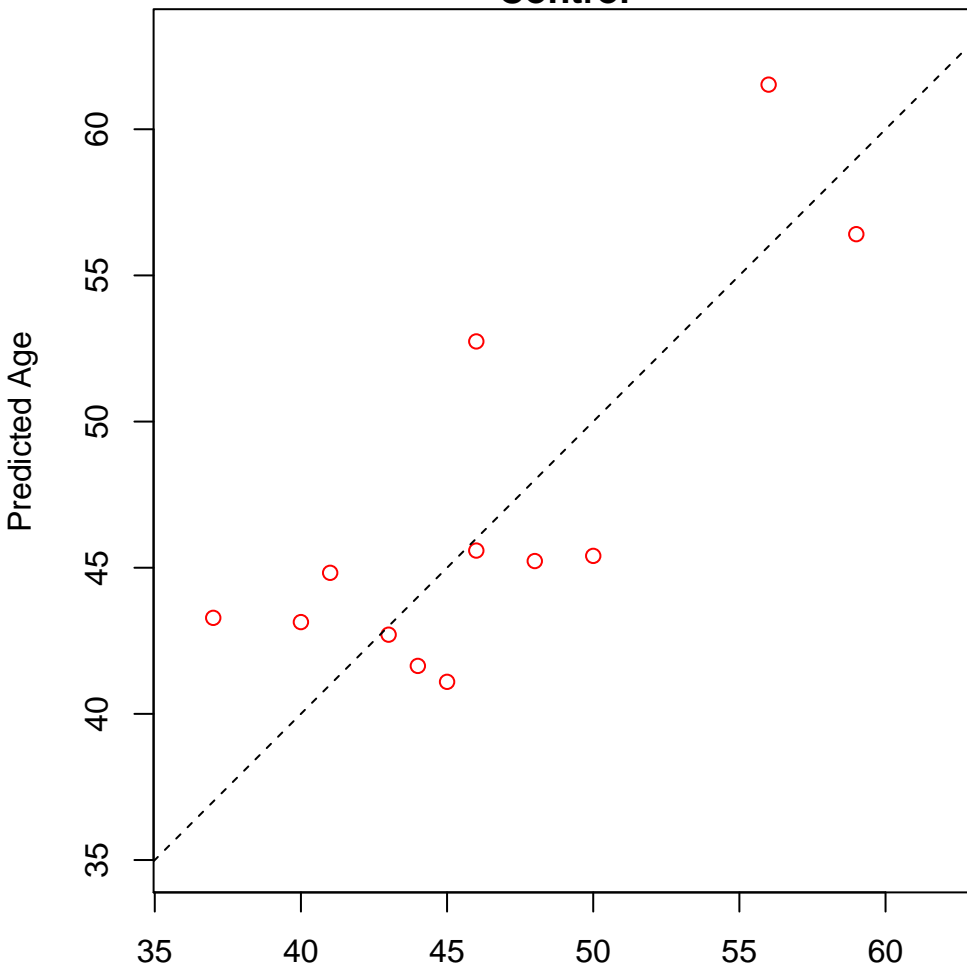


cGMP-mediated signaling (Score: 7.800792)

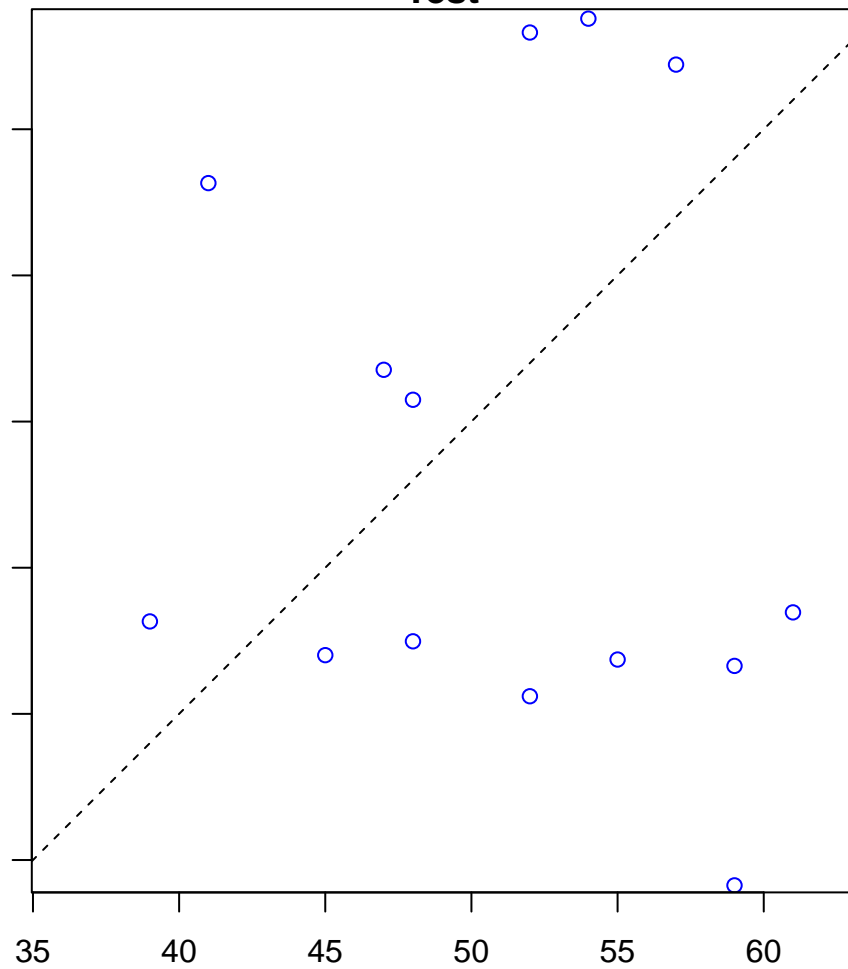


angiotensin-activated signaling pathway (Score: 7.798230)

Control

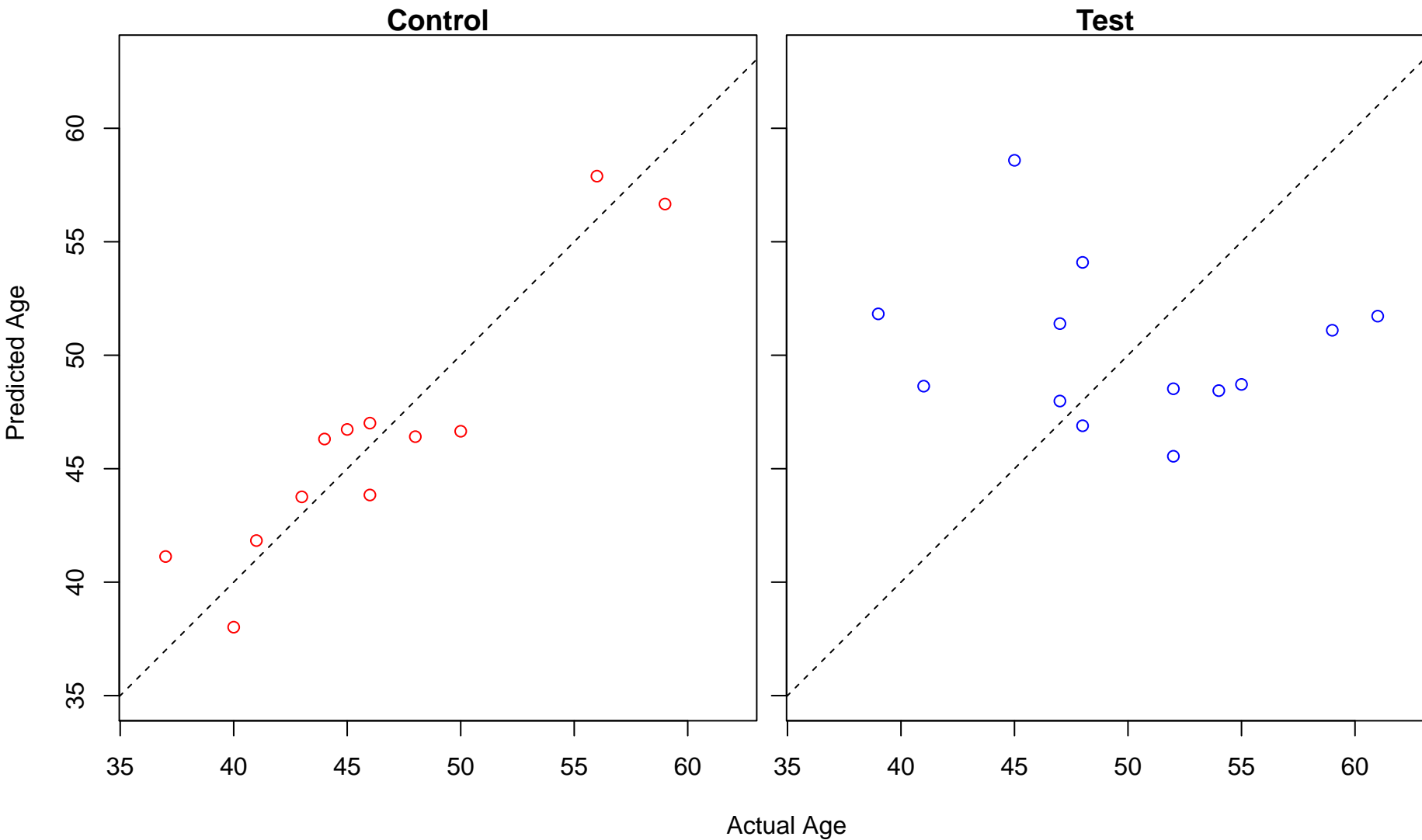


Test

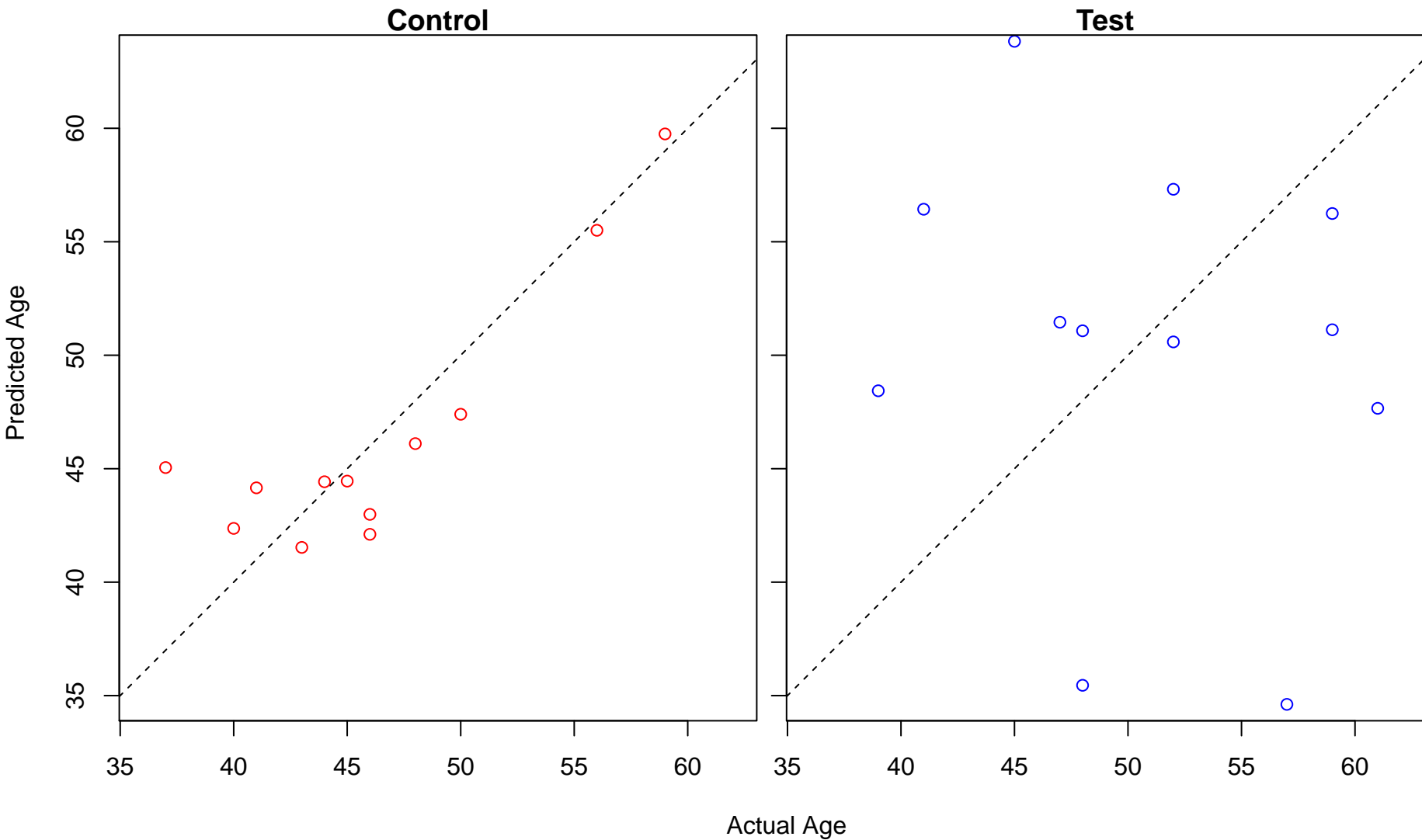


Actual Age

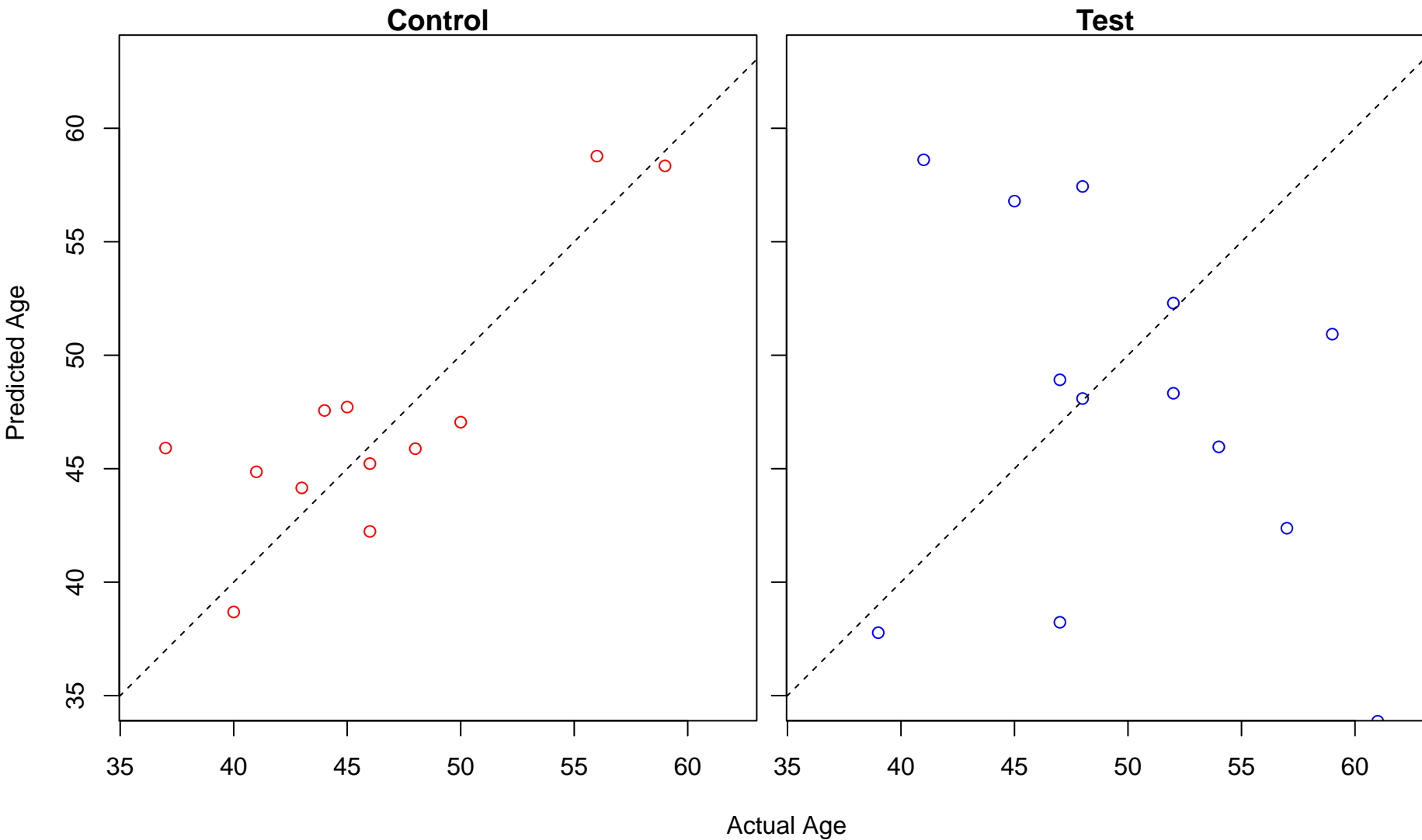
positive regulation of cysteine-type endopeptidase activity (Score: 7.795309)



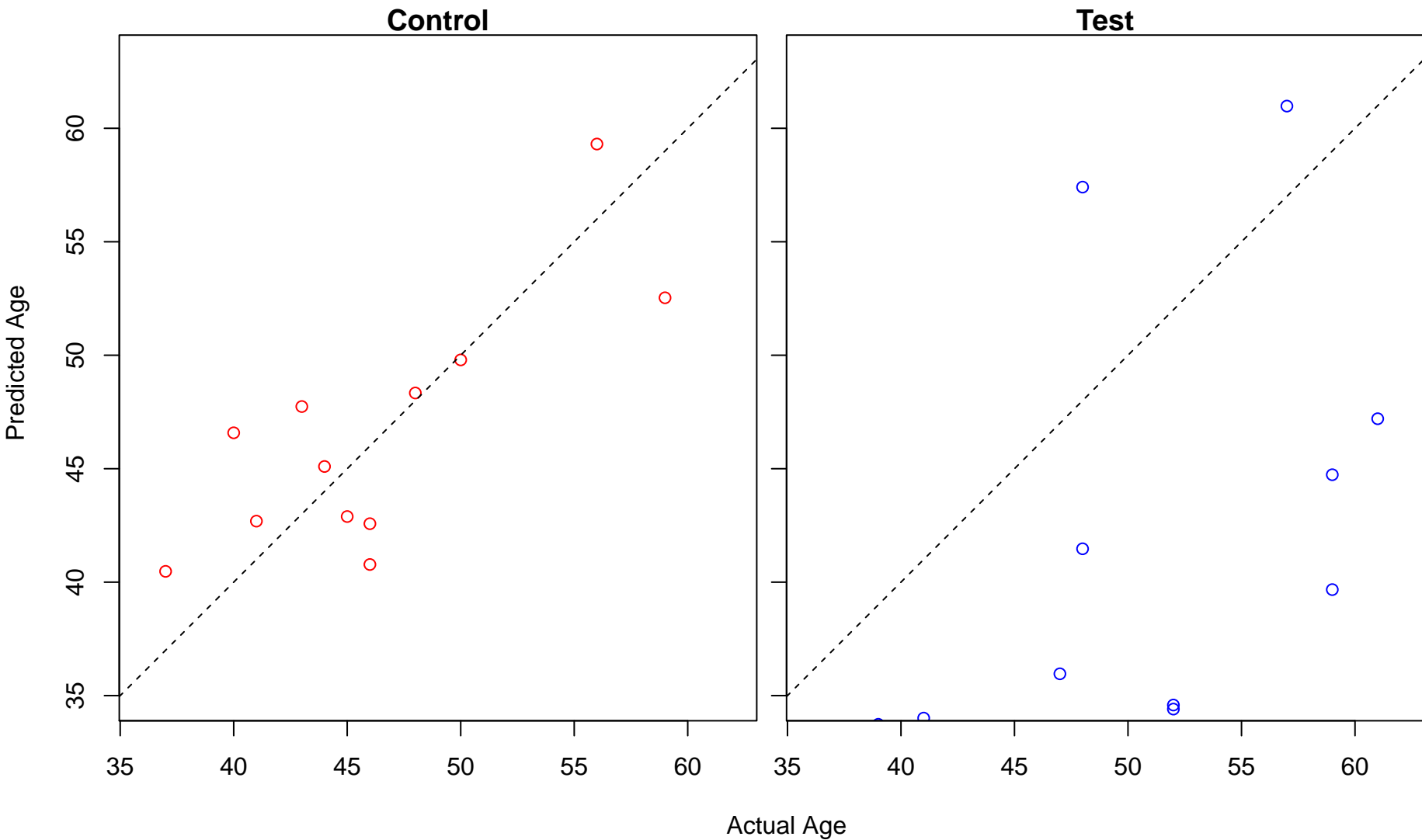
fucosylation (Score: 7.792572)



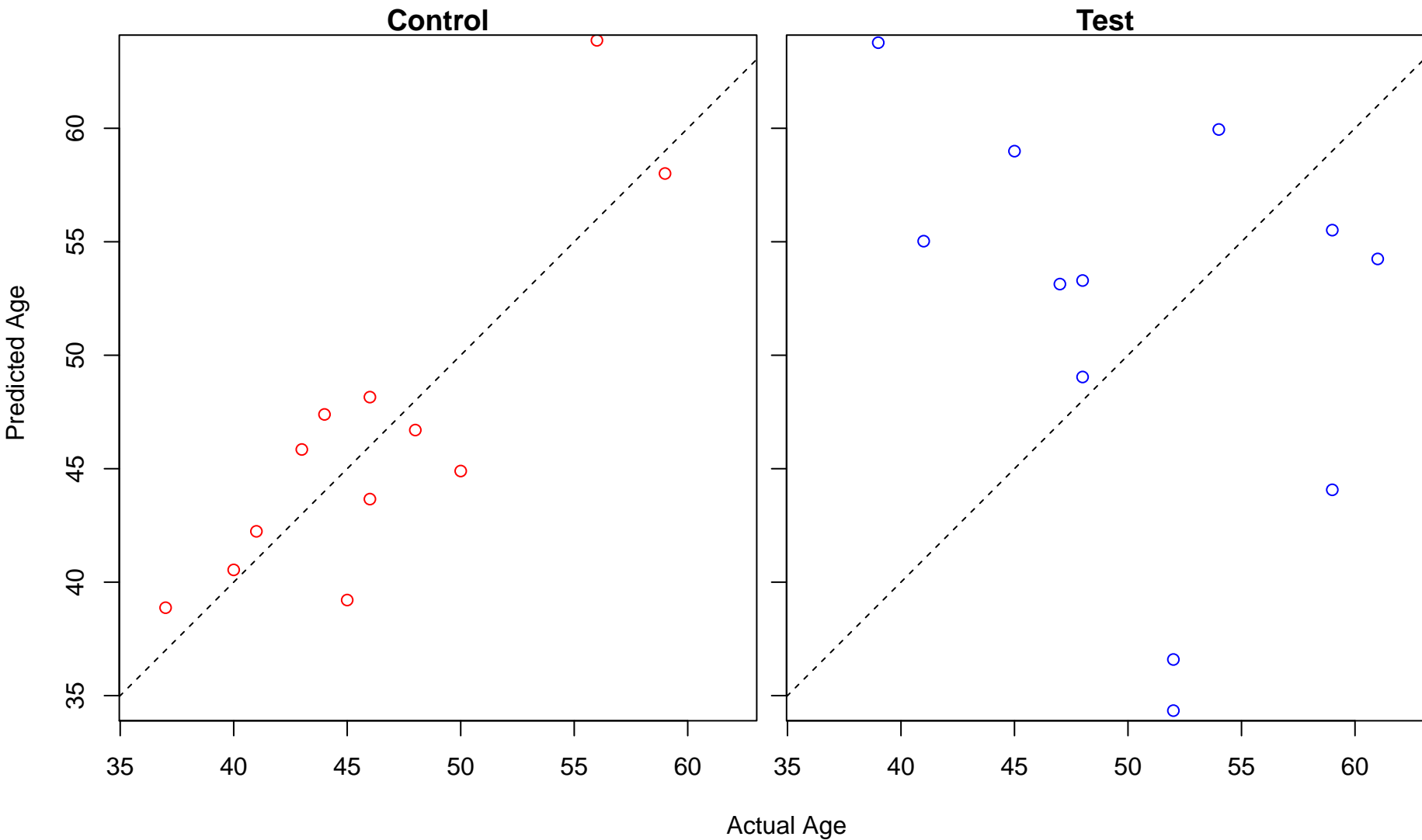
activation of JUN kinase activity (Score: 7.788468)



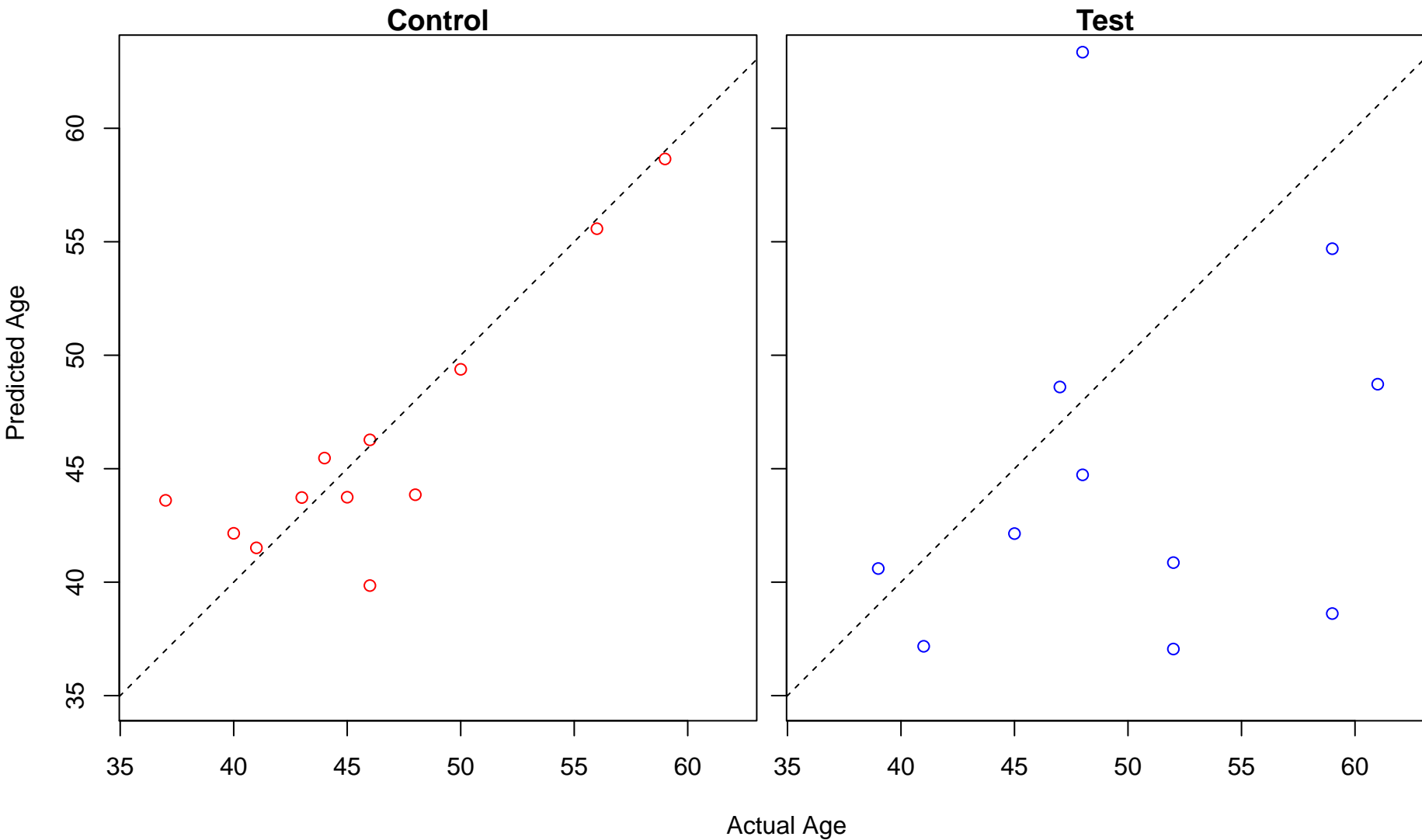
T cell apoptotic process (Score: 7.785923)



leukocyte differentiation (Score: 7.780332)

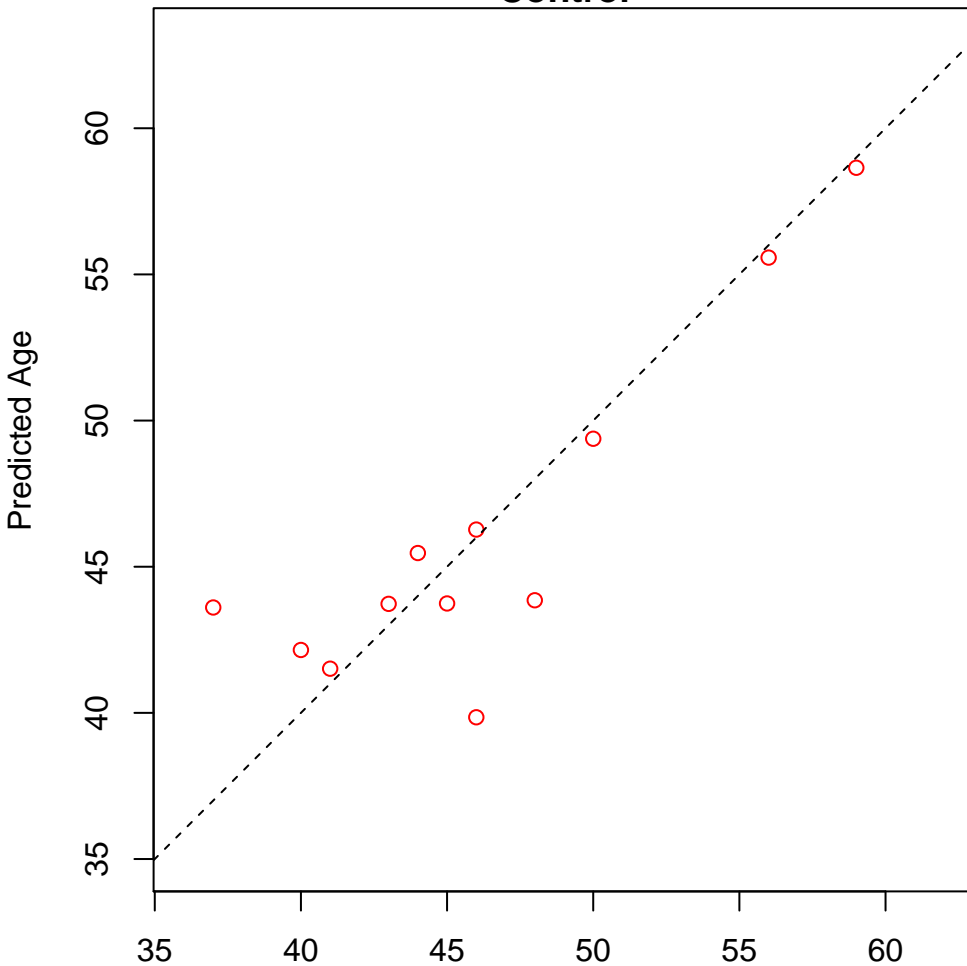


cellular potassium ion transport (Score: 7.777625)

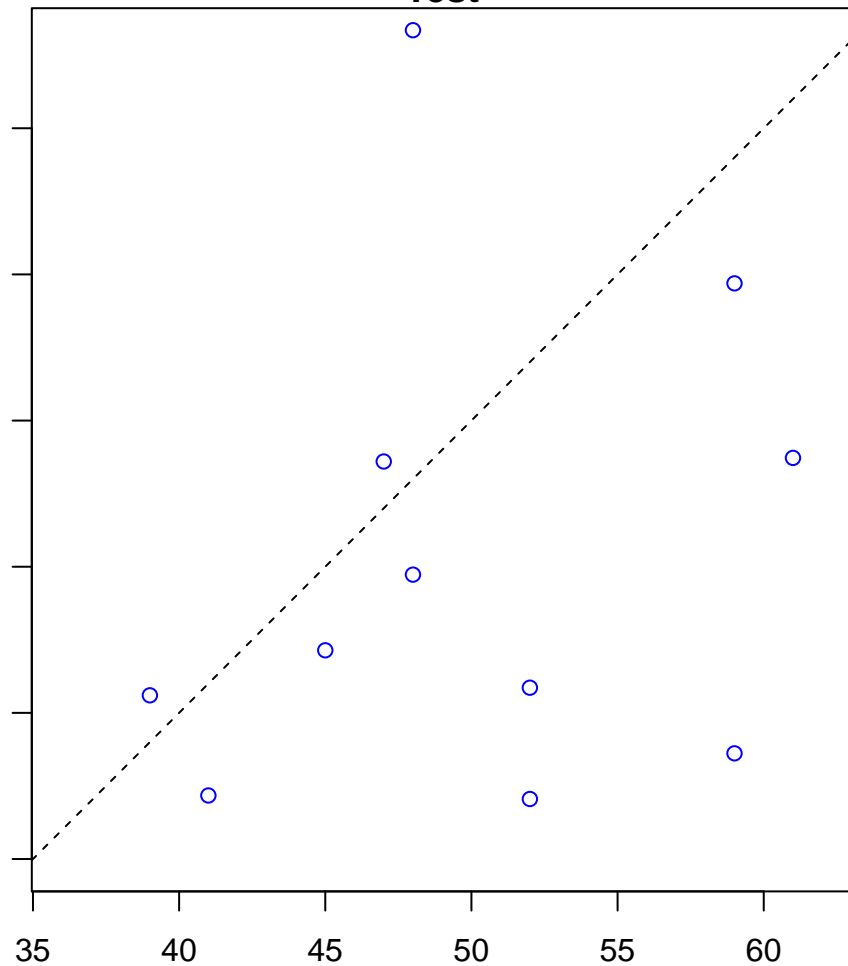


potassium ion transmembrane transport (Score: 7.777625)

Control

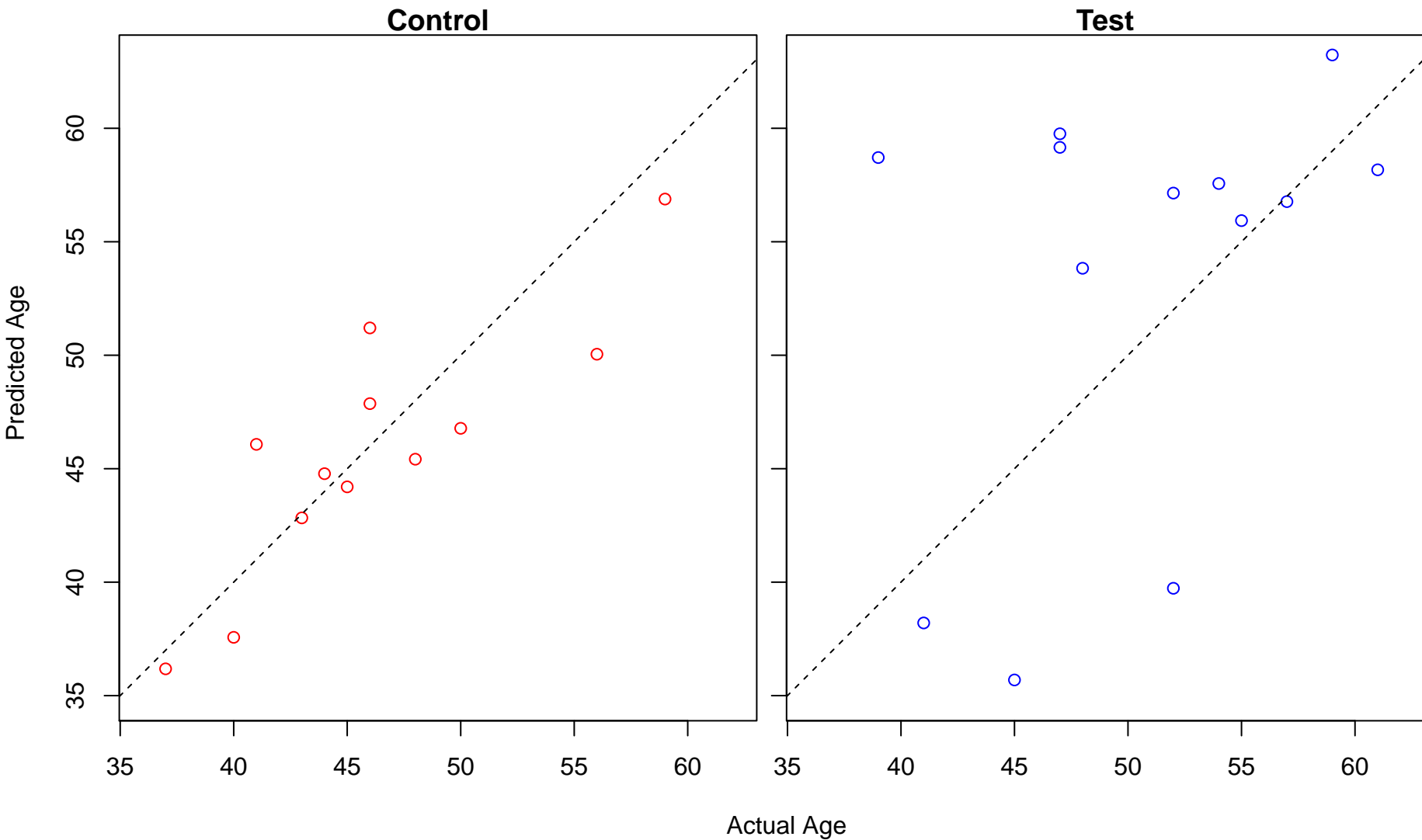


Test

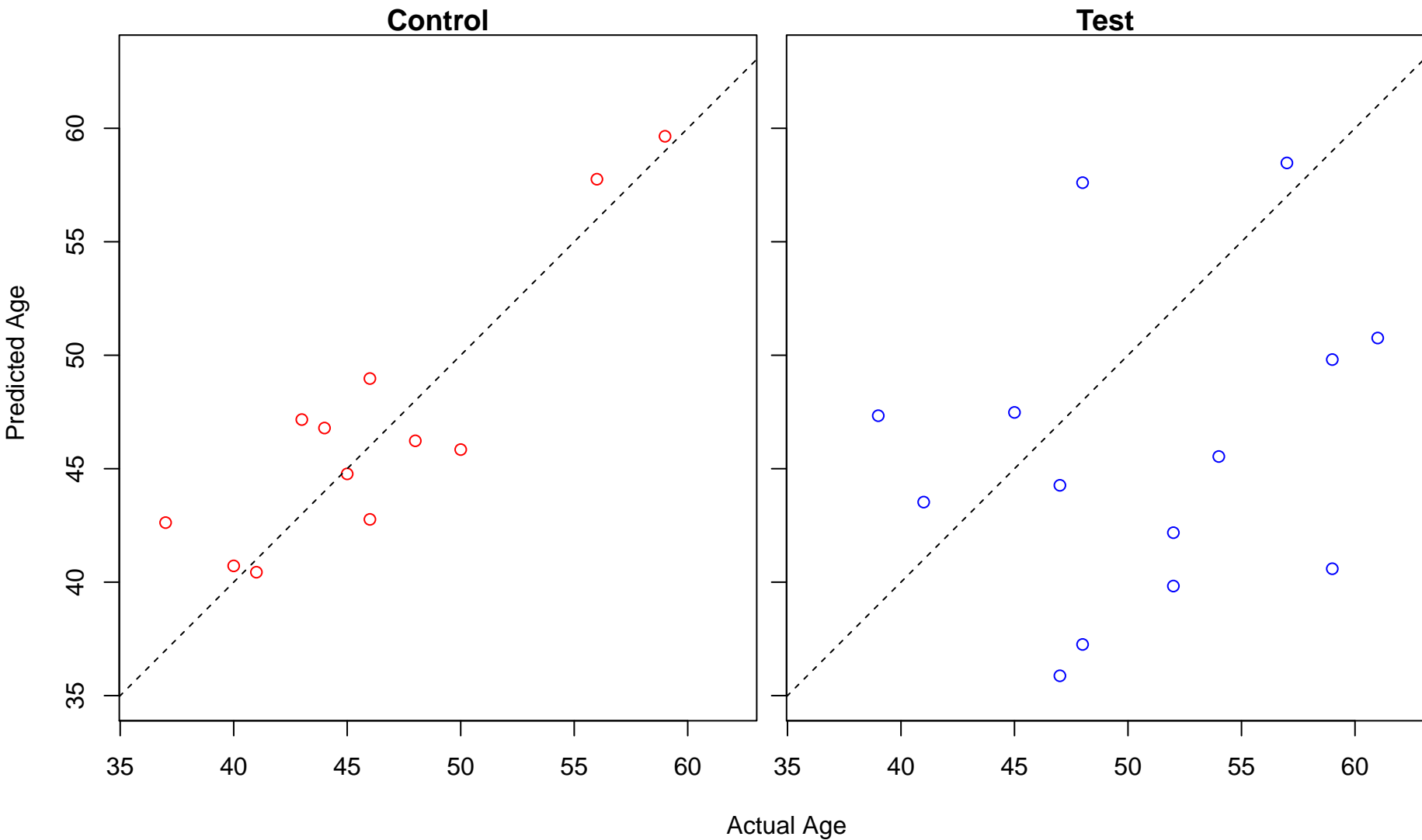


Actual Age

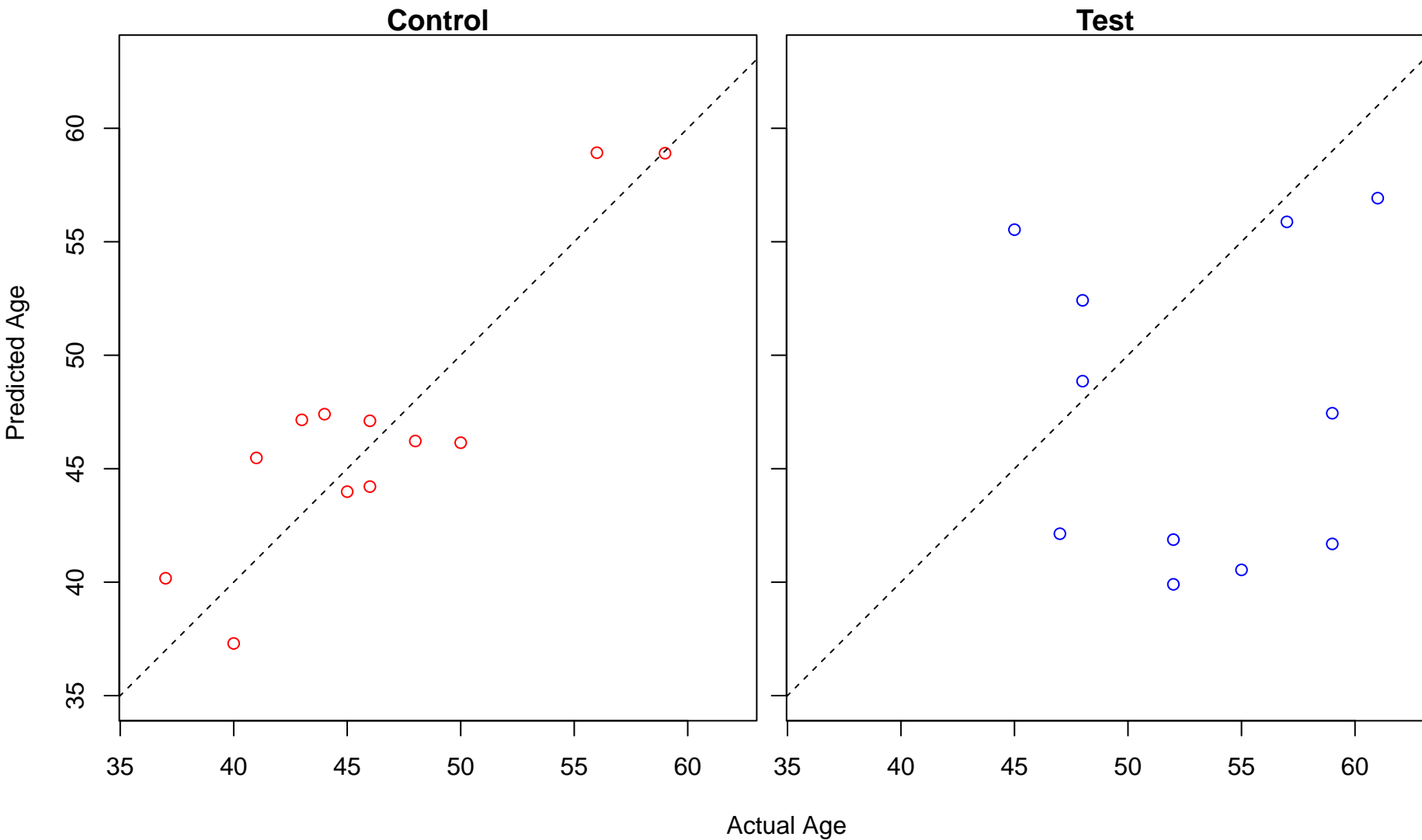
very-low-density lipoprotein particle remodeling (Score: 7.763509)



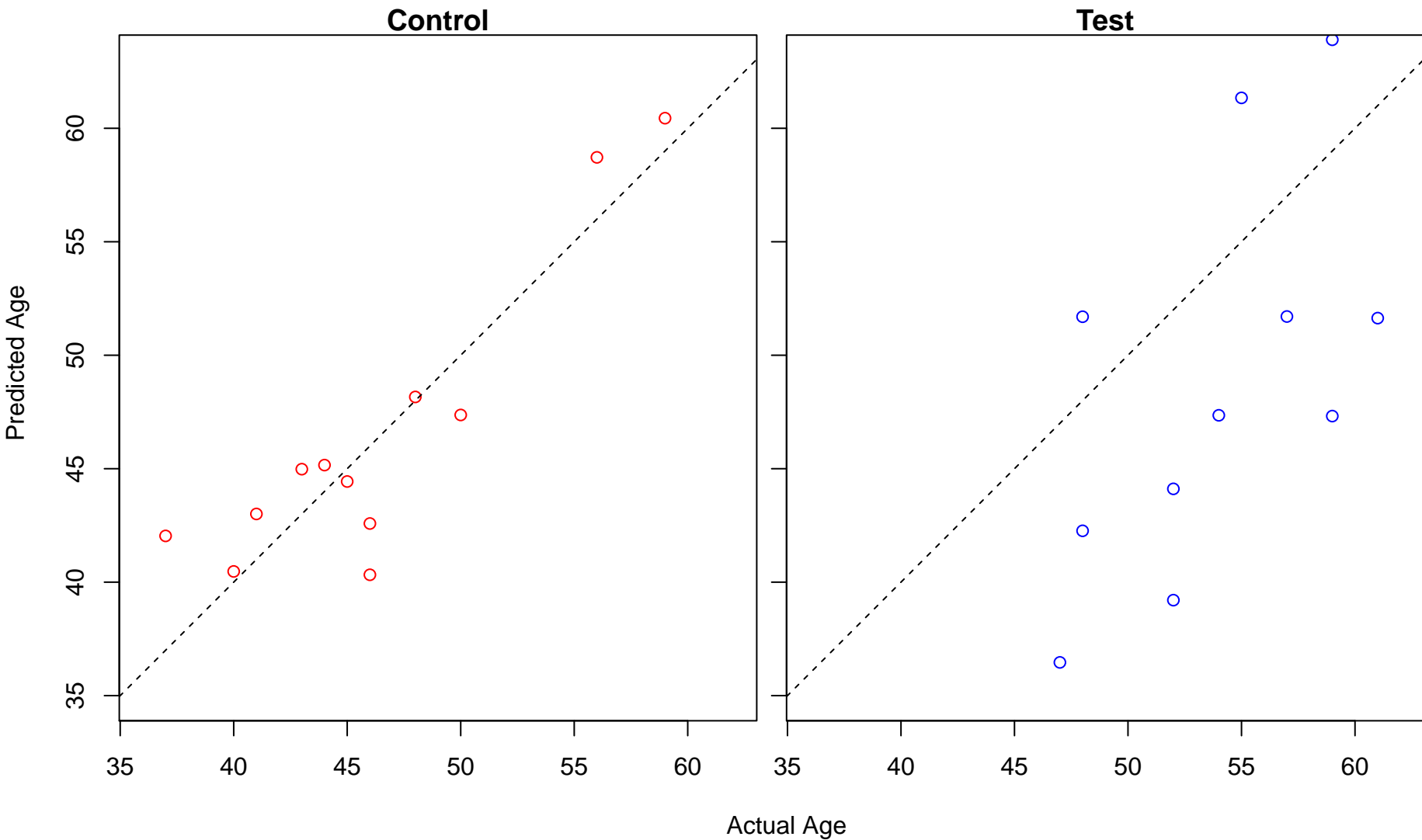
positive regulation of neuron projection development (Score: 7.752214)



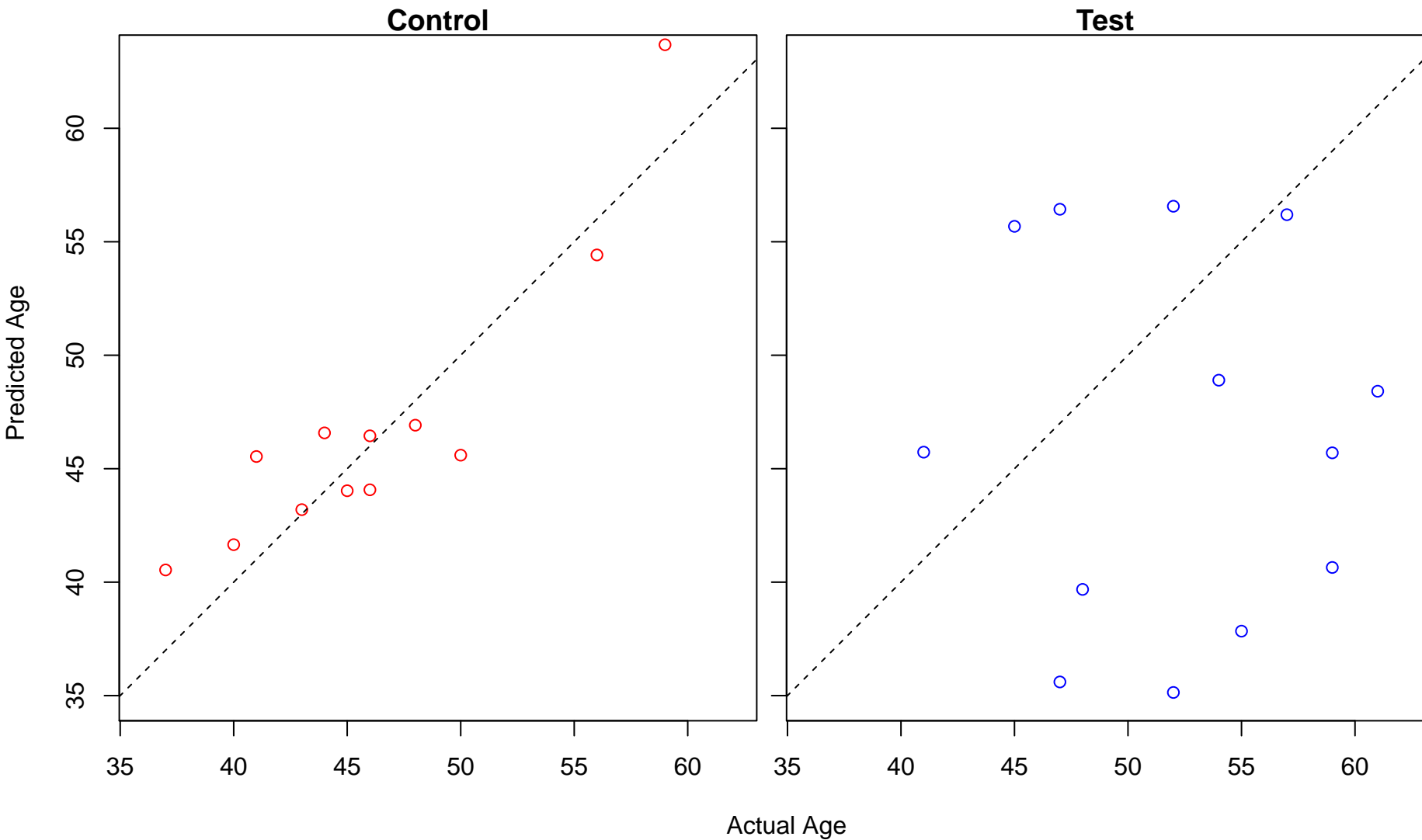
negative regulation of cell migration (Score: 7.723913)



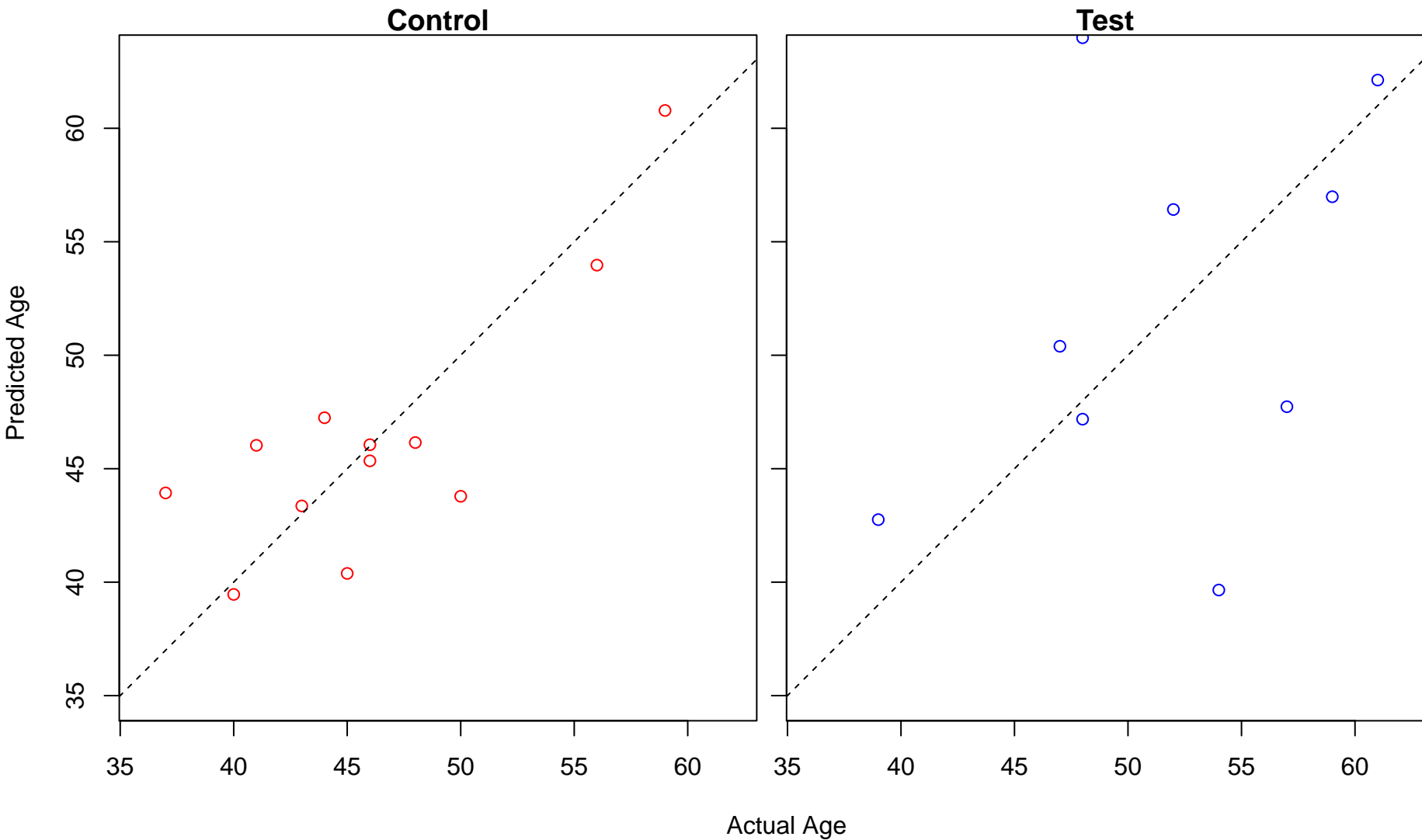
alcohol metabolic process (Score: 7.704105)



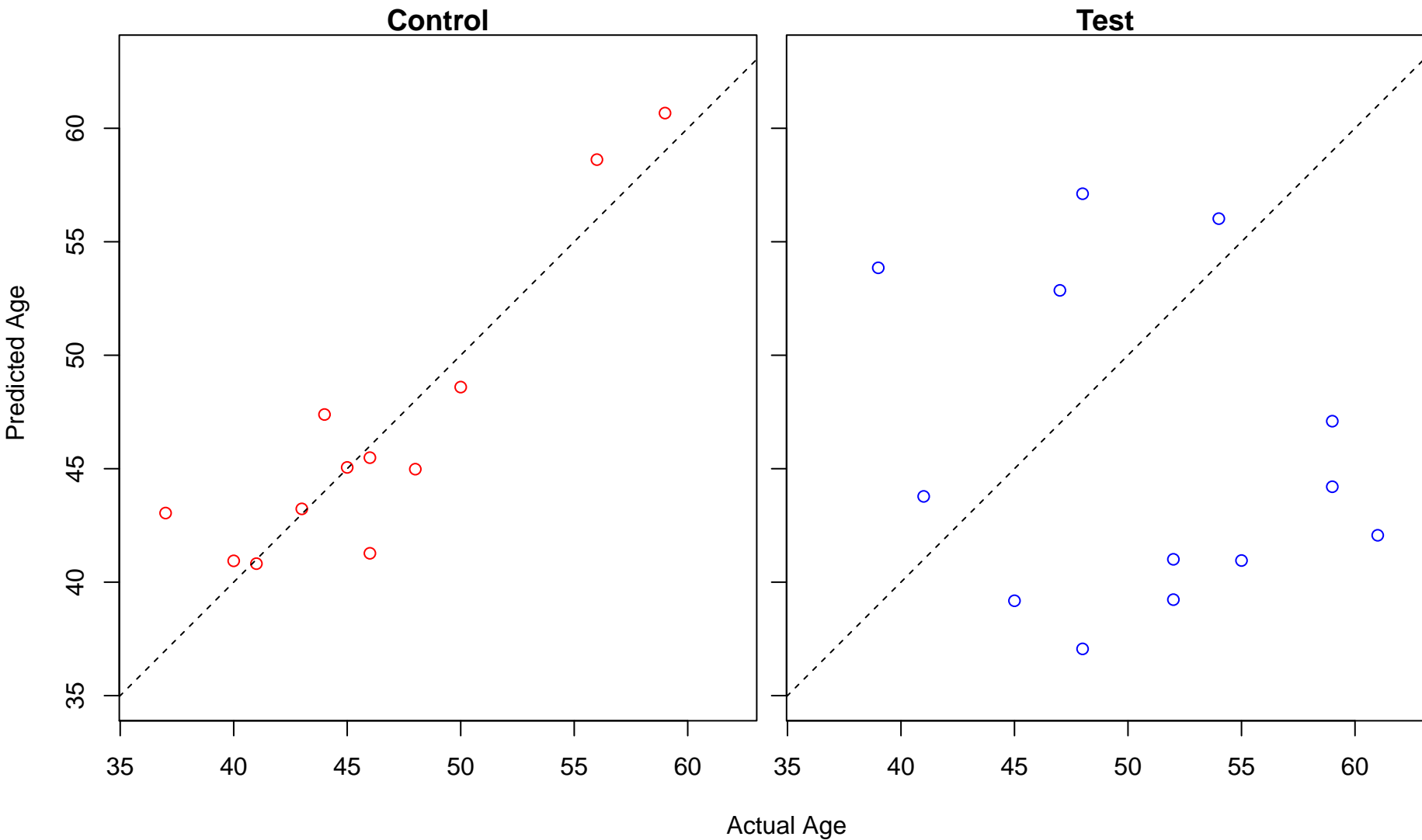
regulation of apoptotic cell clearance (Score: 7.703159)



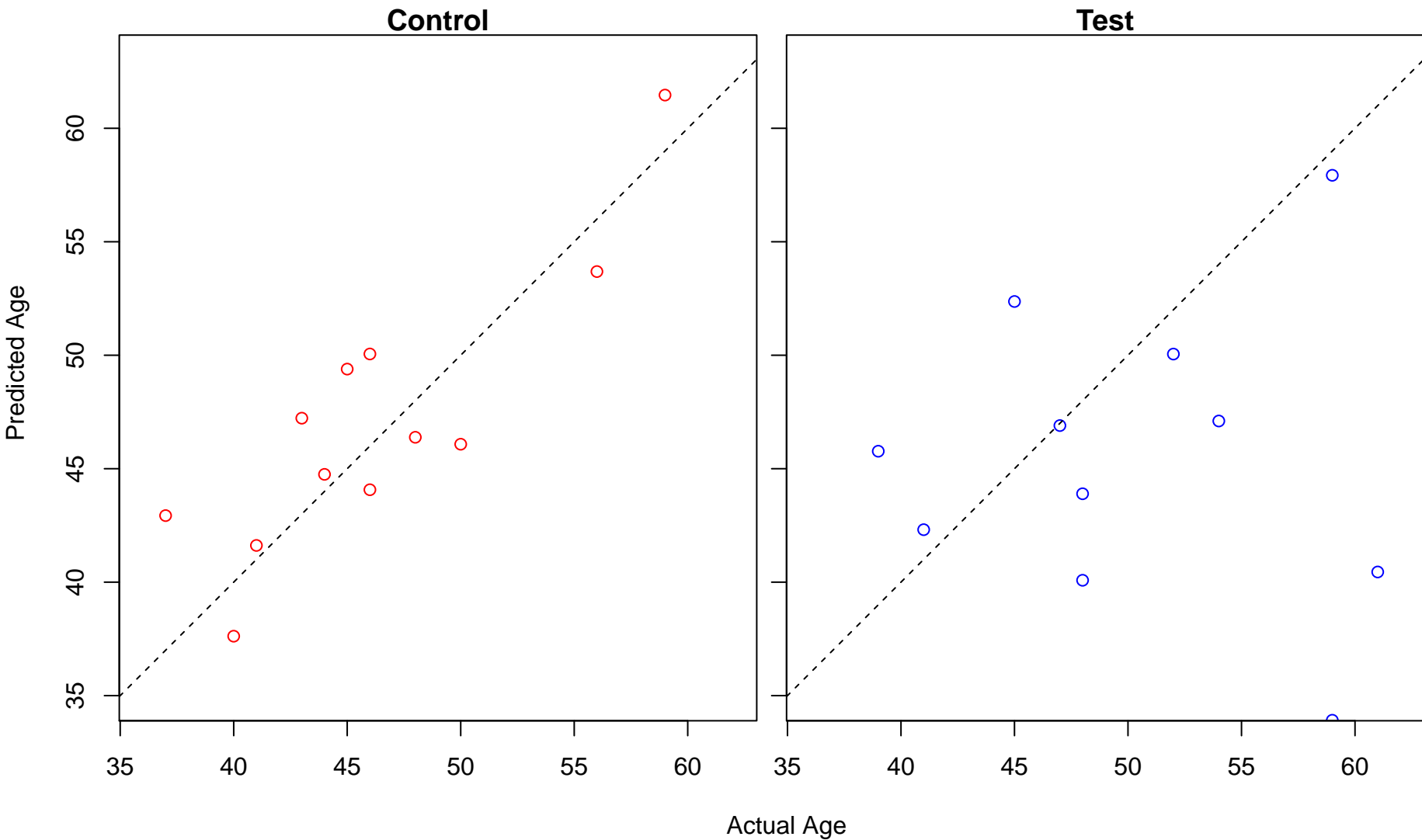
regulation of hydrogen peroxide-induced cell death (Score: 7.696864)



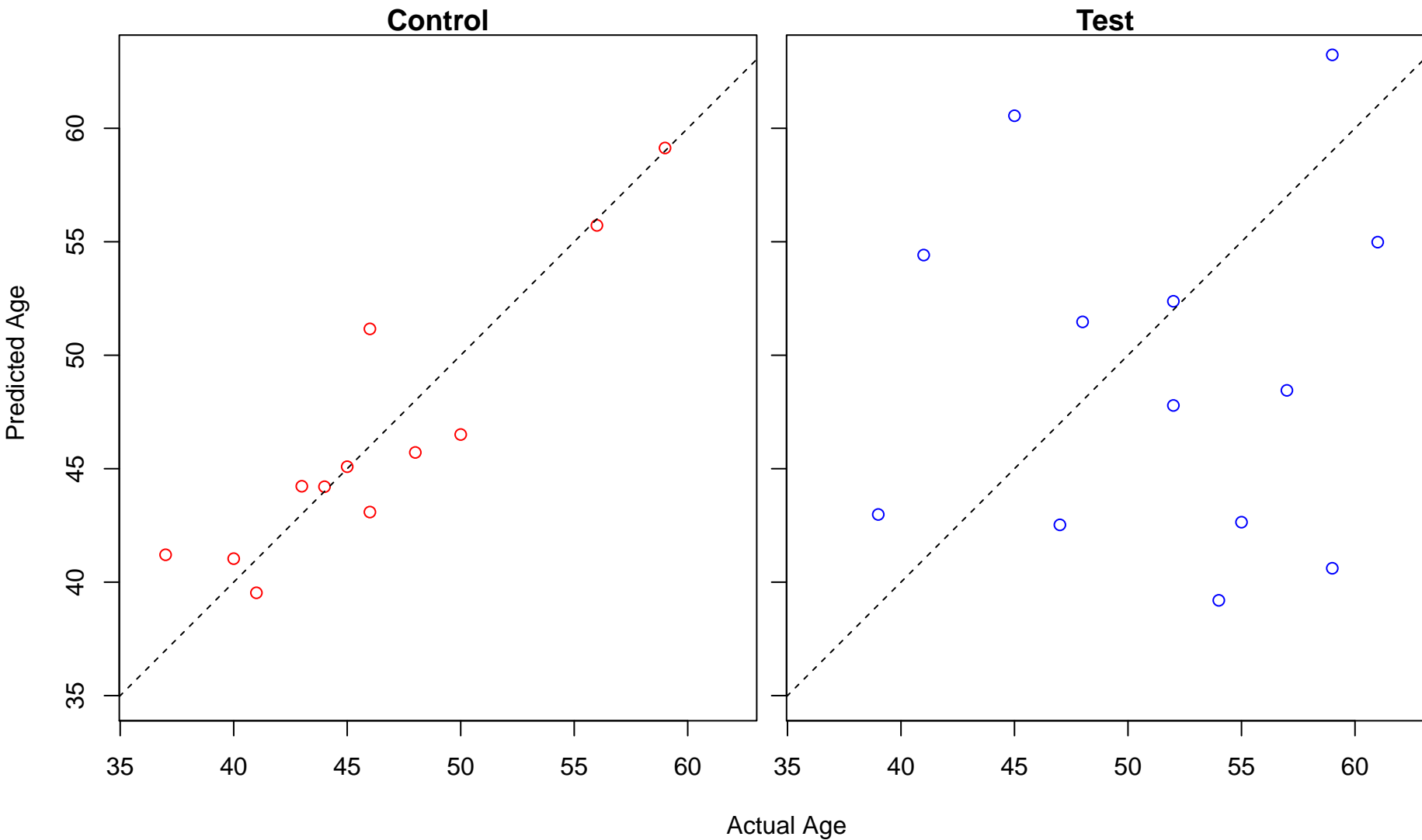
regulation of calcium ion transmembrane transporter activity (Score: 7.692999)



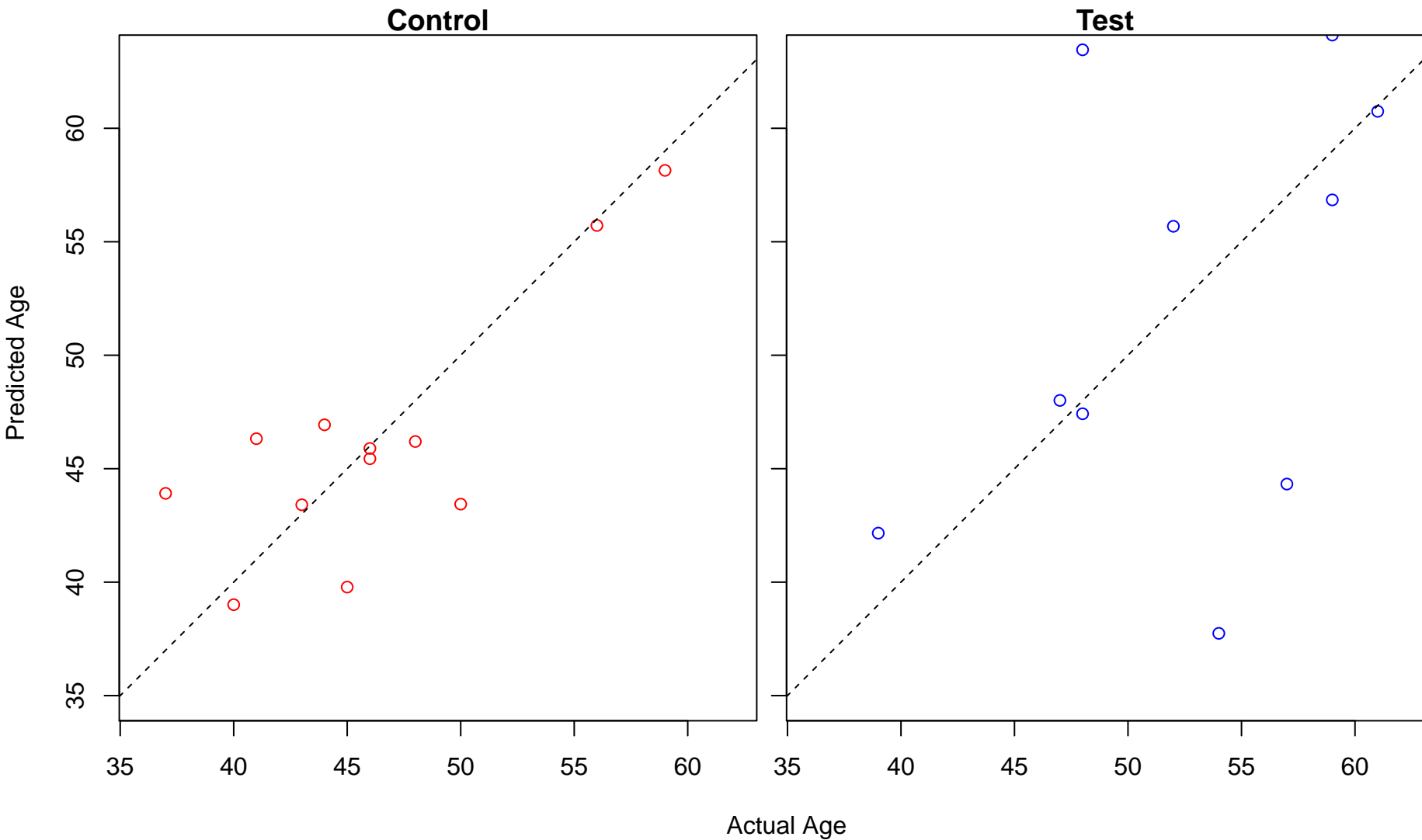
positive regulation of chemotaxis (Score: 7.671197)



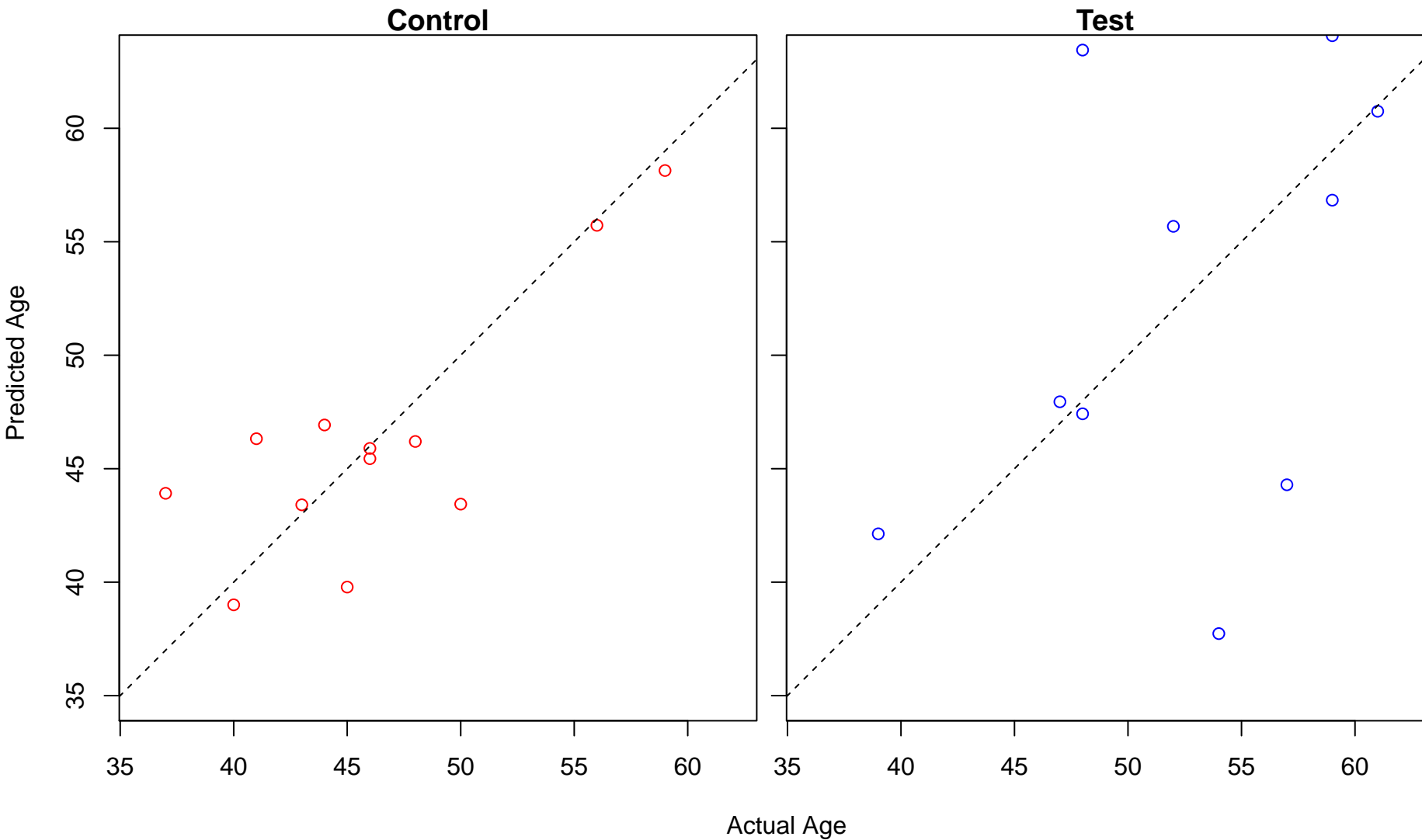
positive regulation of receptor internalization (Score: 7.654923)



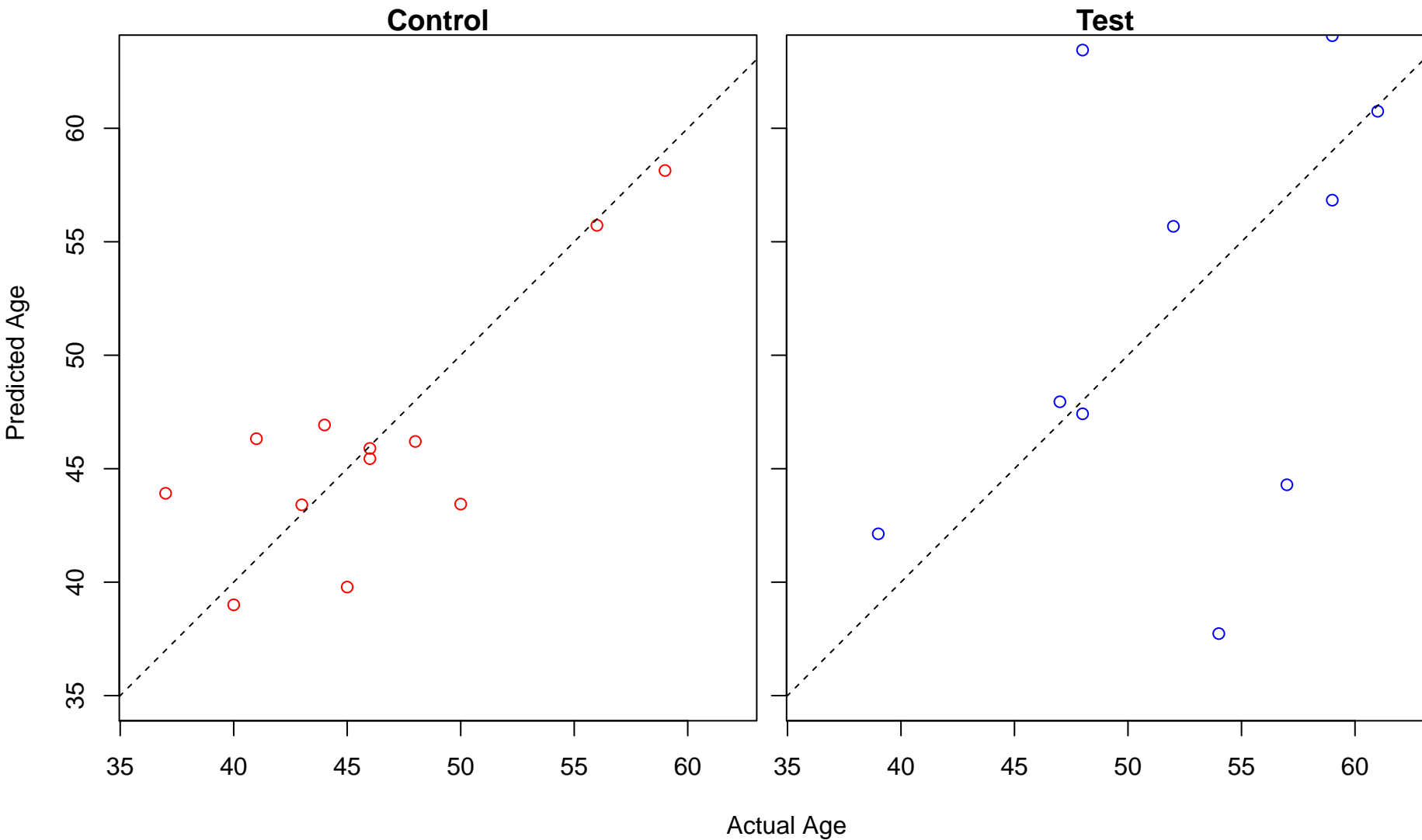
negative regulation of oxidative stress-induced cell death (Score: 7.653361)



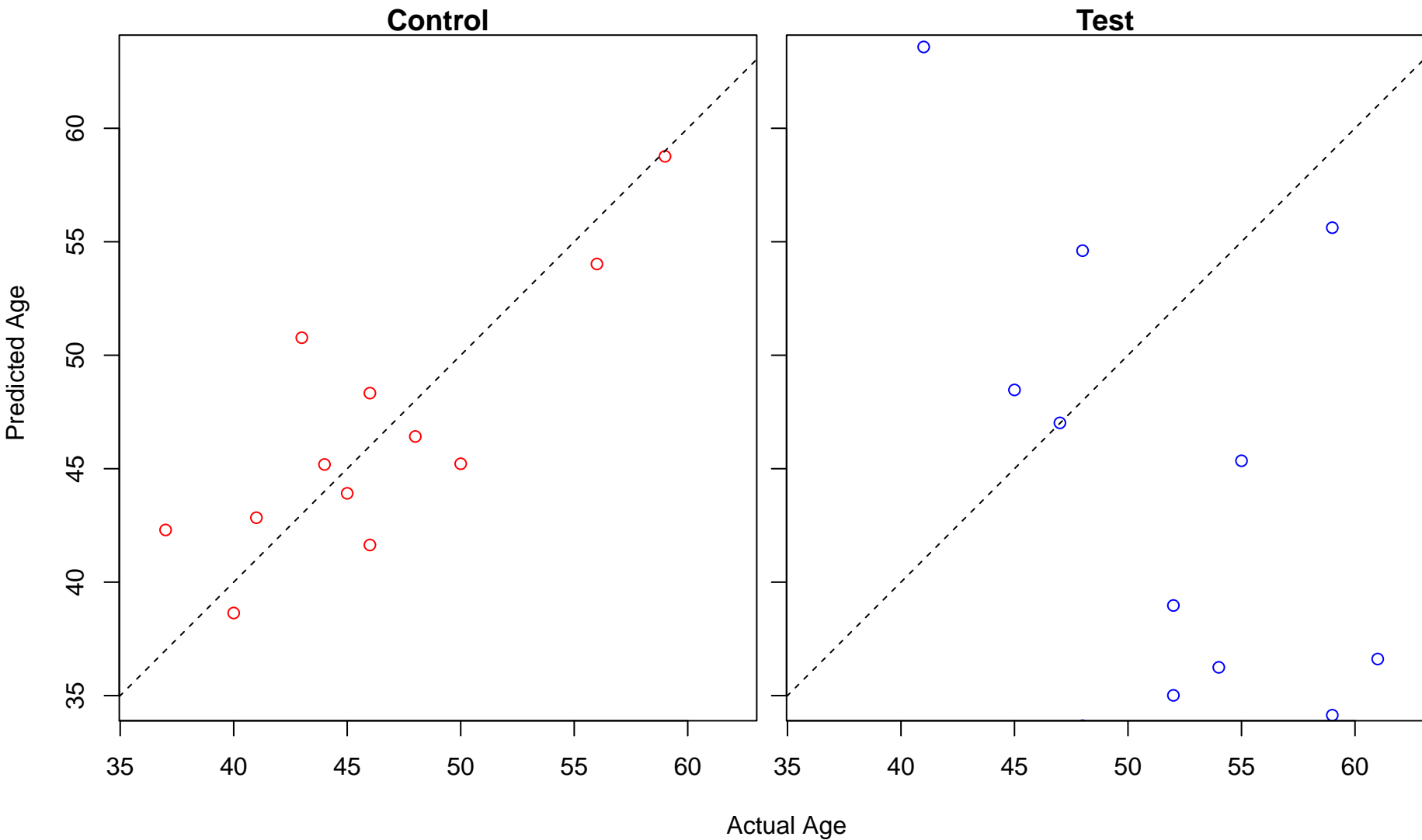
negative regulation of cellular response to oxidative stress (Score: 7.652612)



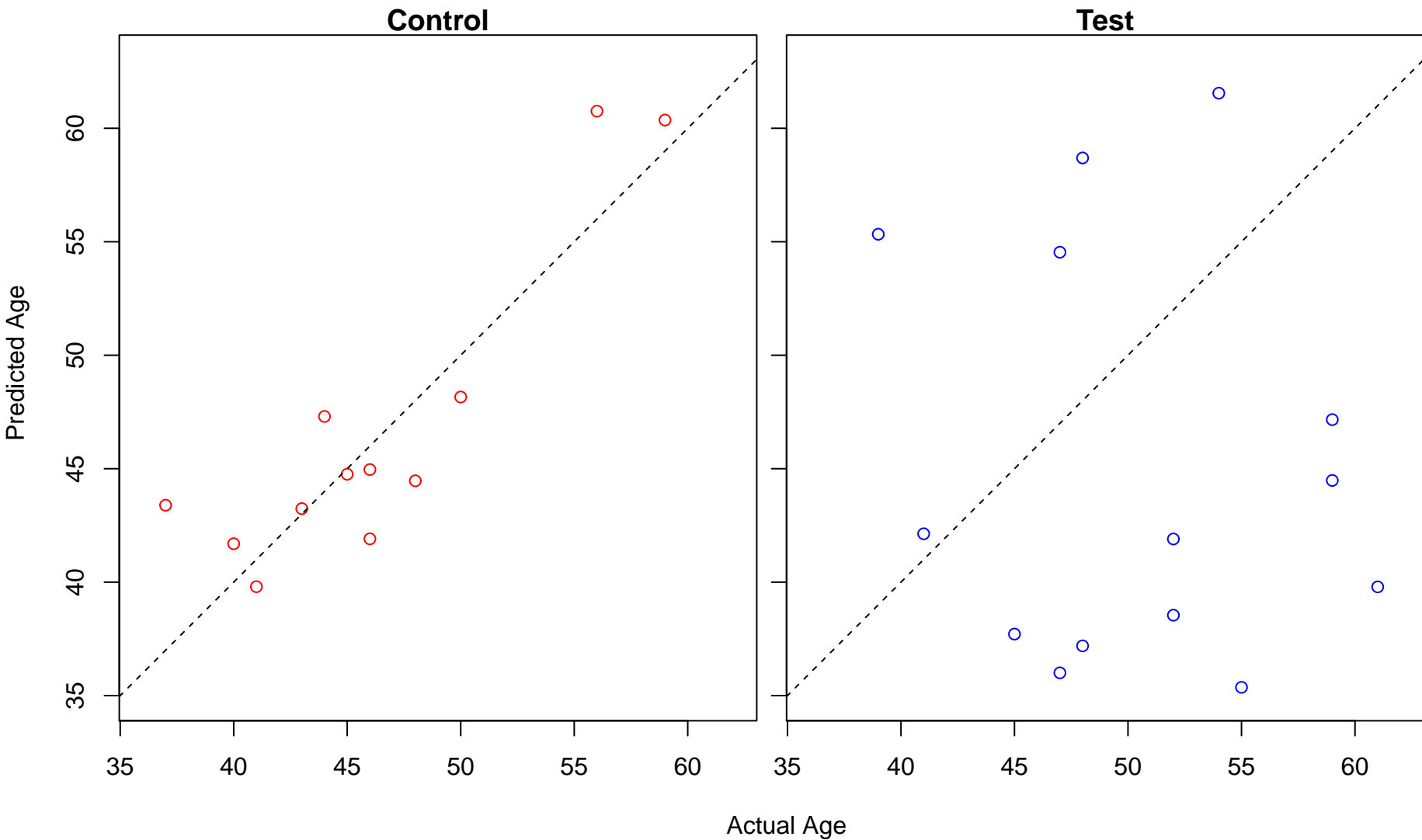
negative regulation of response to oxidative stress (Score: 7.652612)



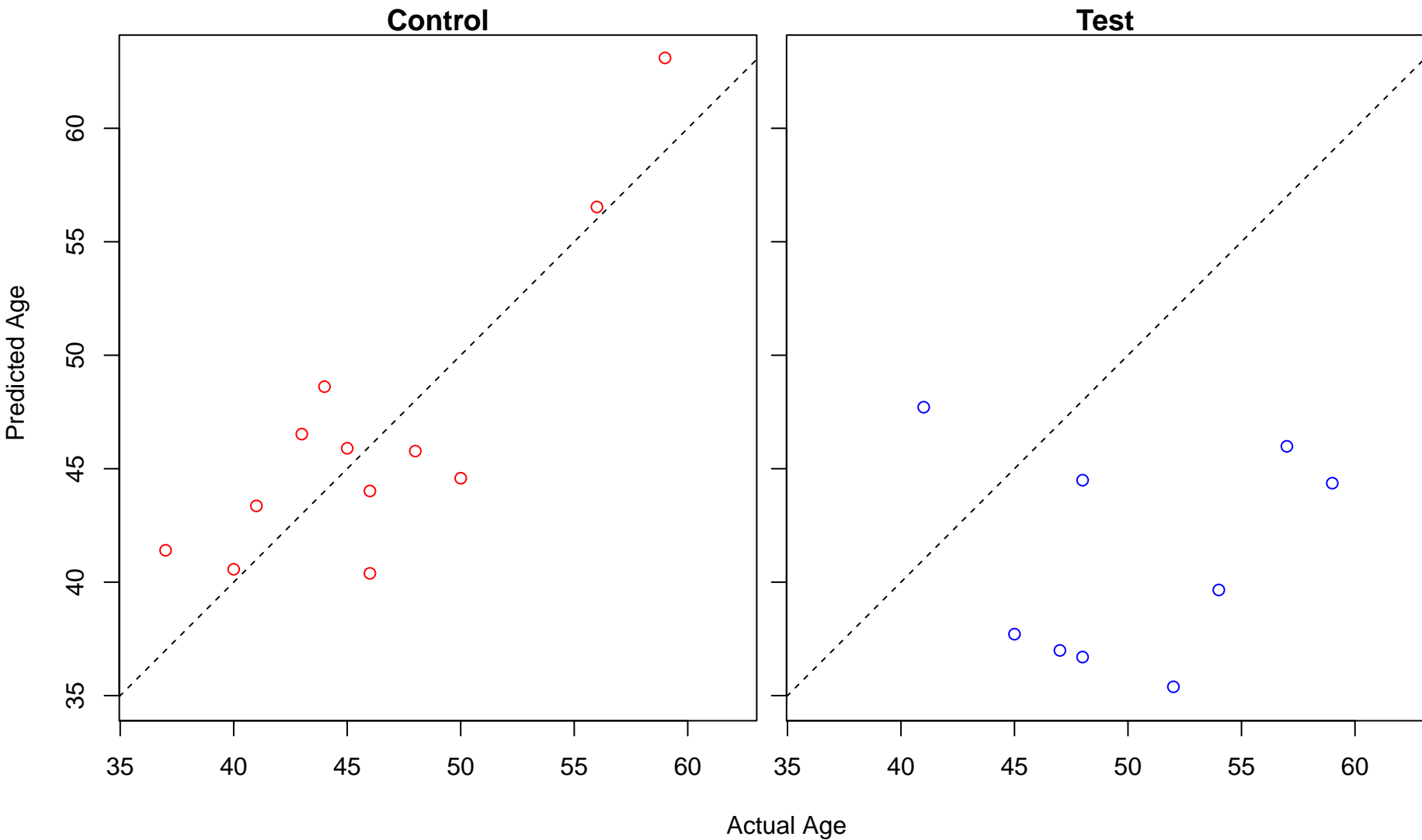
growth (Score: 7.652133)



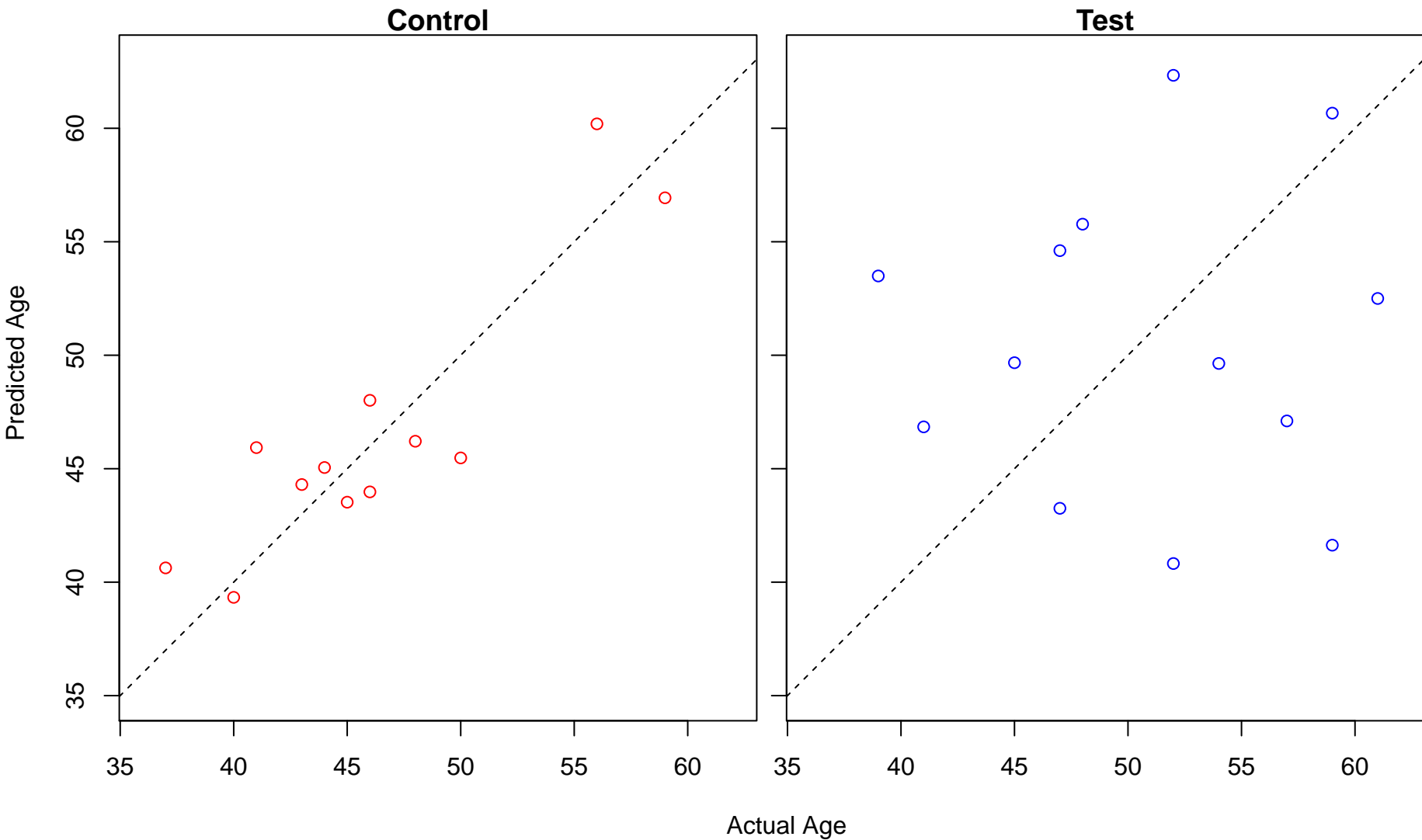
regulation of muscle contraction (Score: 7.640940)



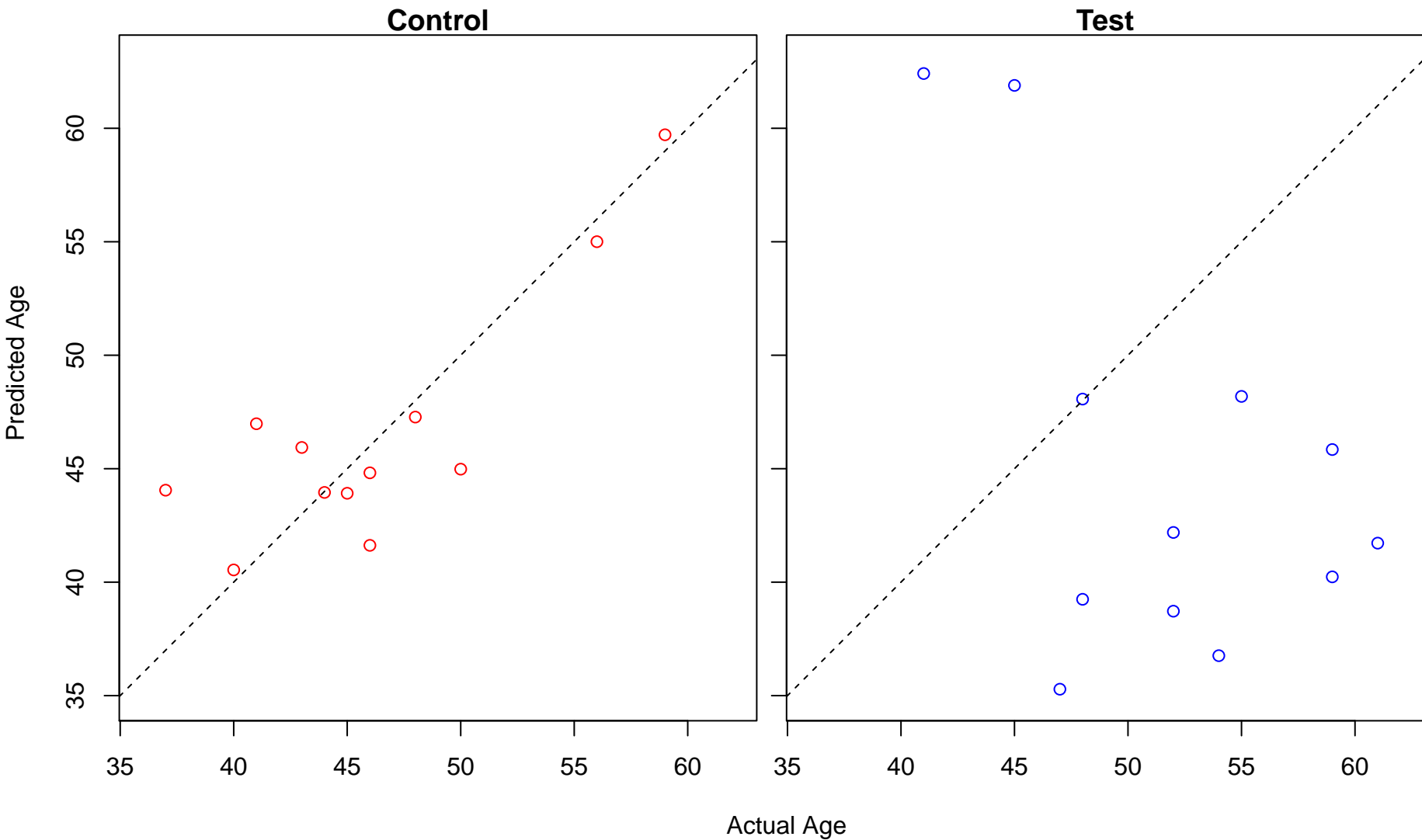
regulation of actin filament polymerization (Score: 7.640735)



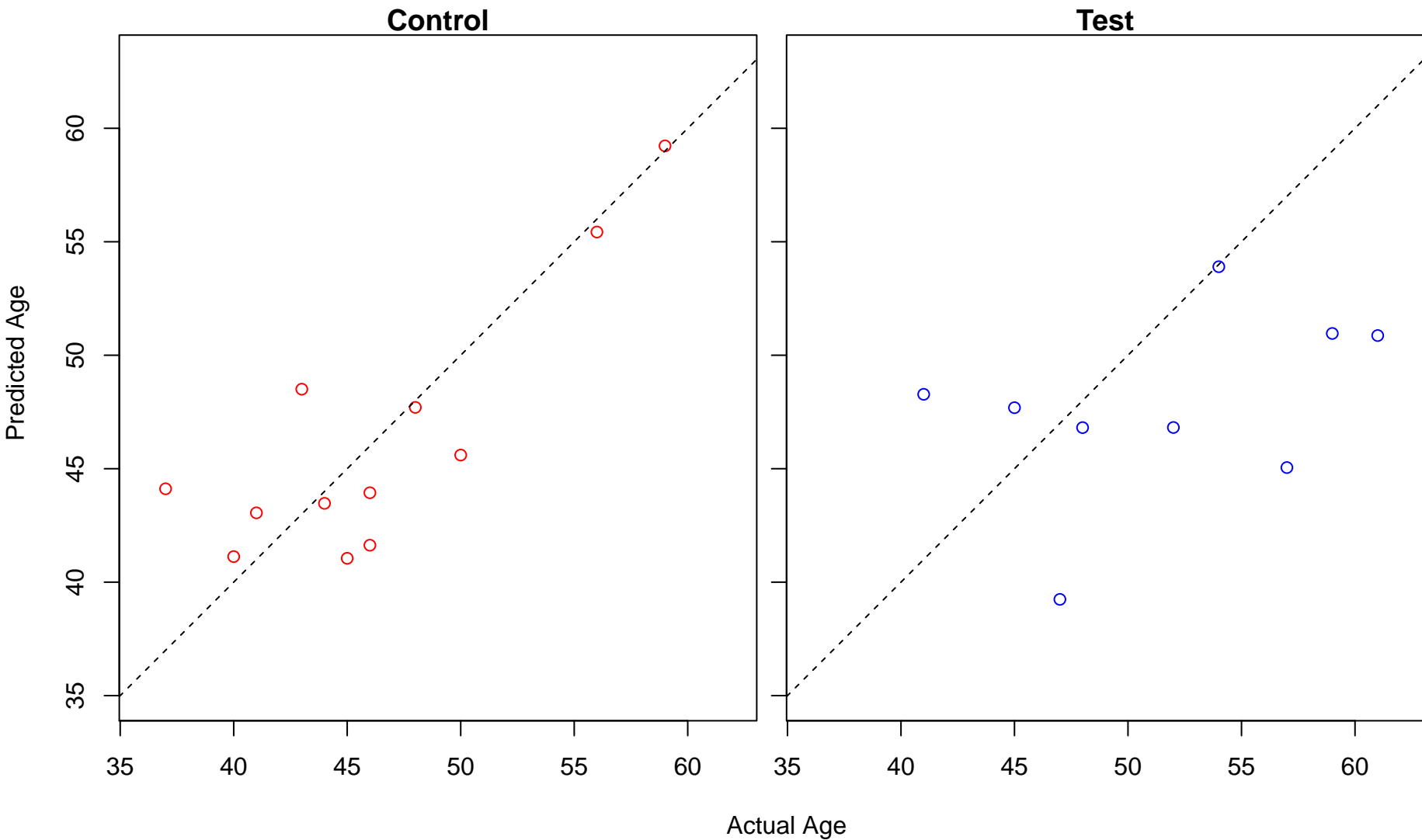
negative regulation of wound healing (Score: 7.635376)



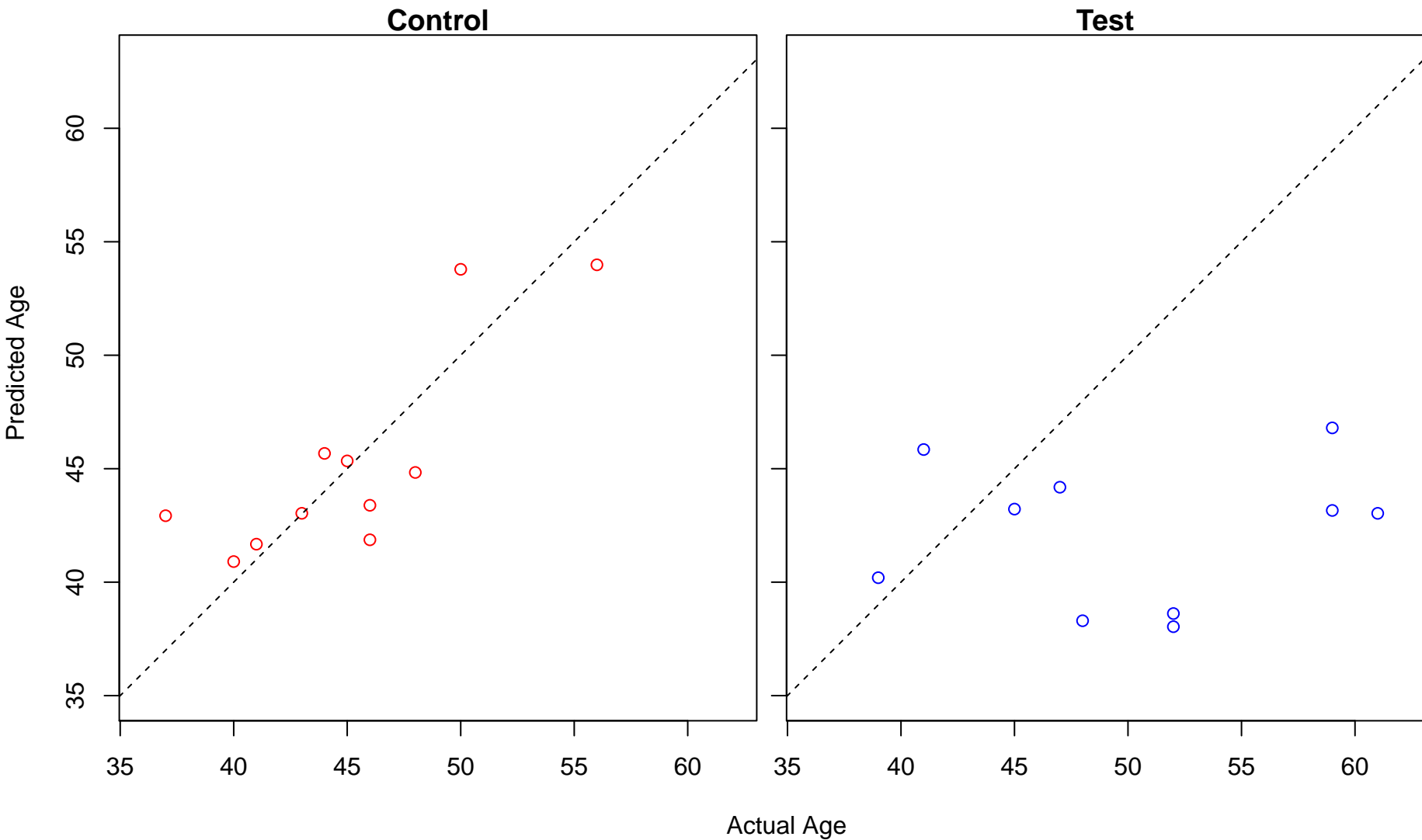
cofactor biosynthetic process (Score: 7.634545)



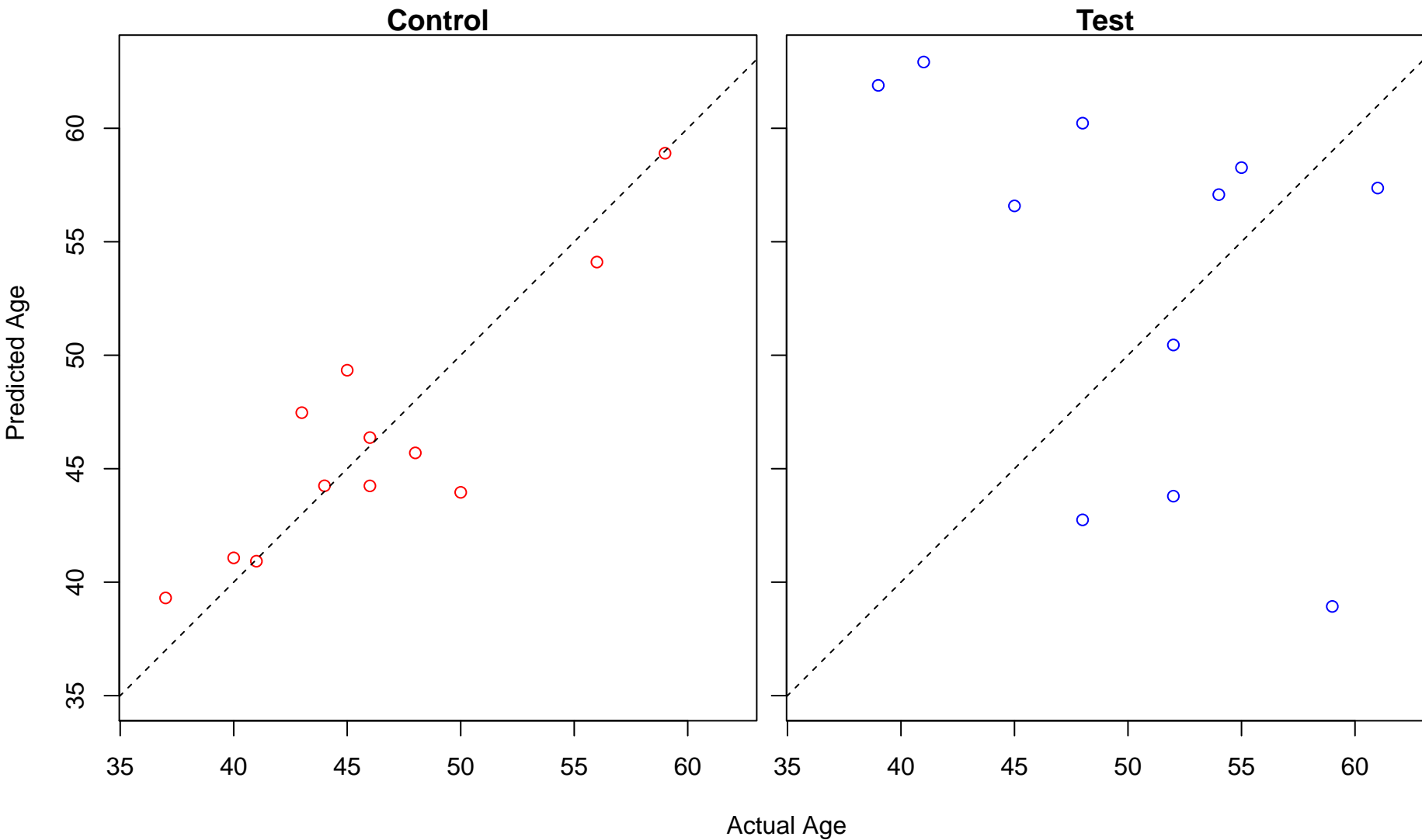
negative regulation of hydrolase activity (Score: 7.631210)



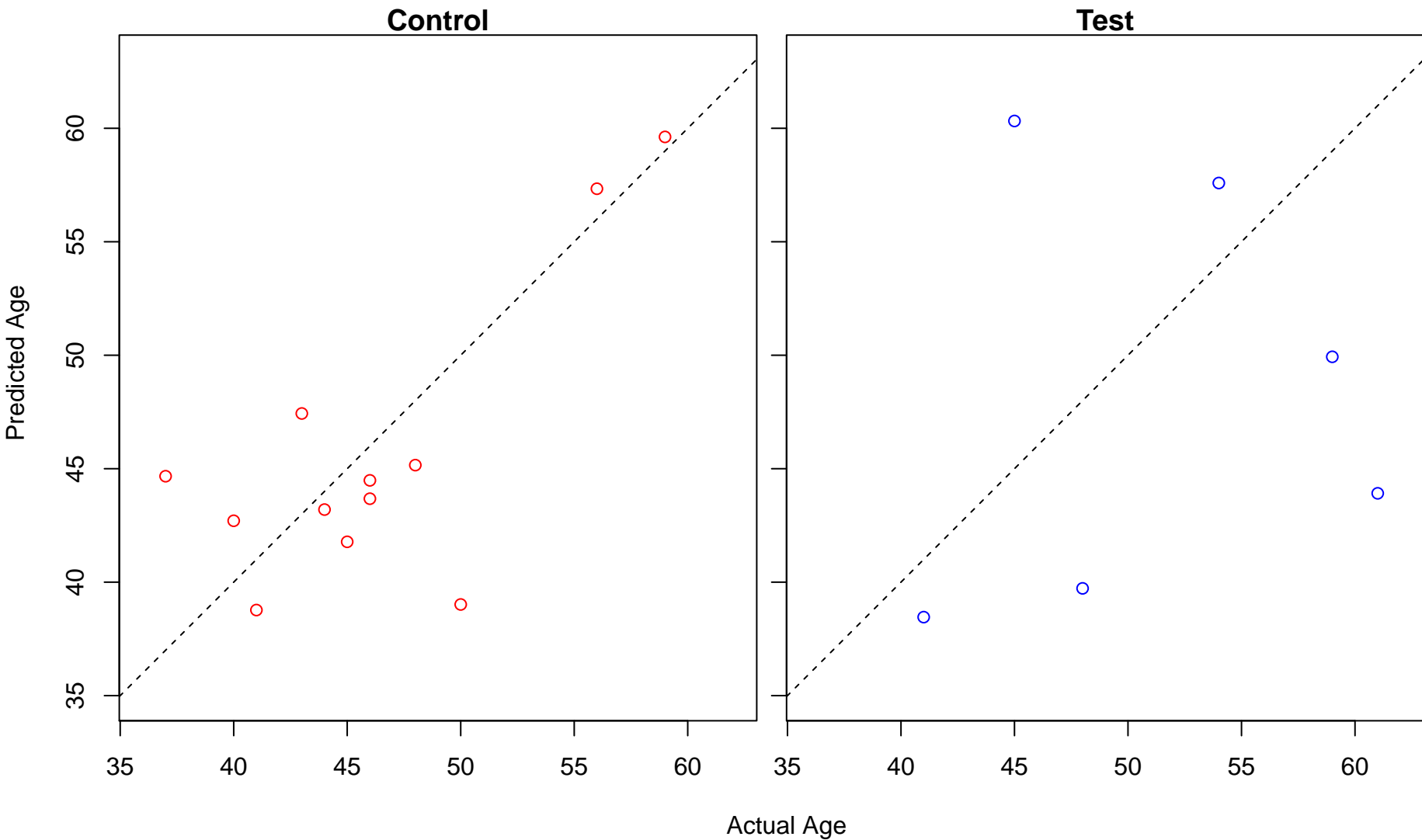
regulation of cardiac conduction (Score: 7.626720)



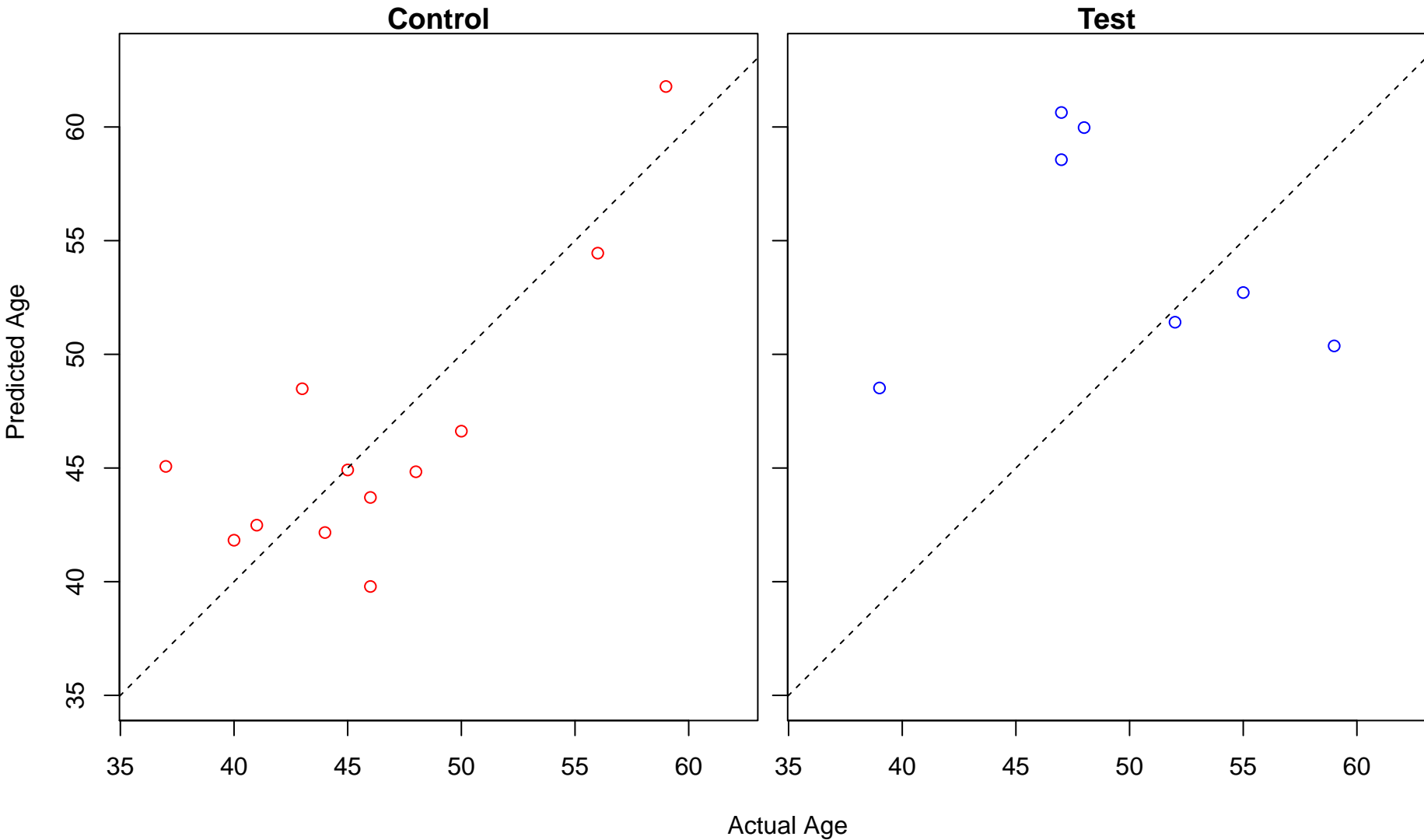
positive regulation of metanephros development (Score: 7.623656)



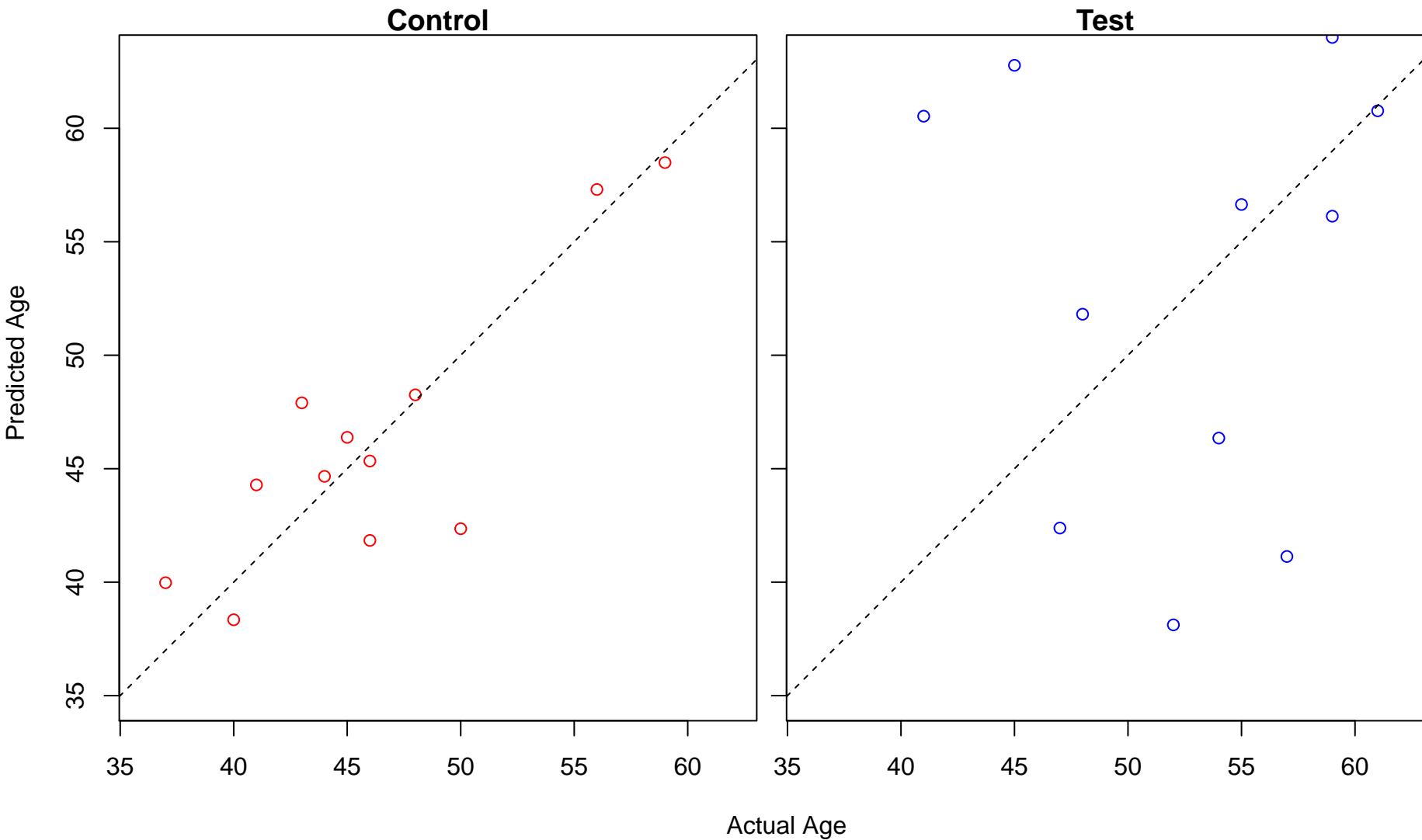
cyclic nucleotide biosynthetic process (Score: 7.609211)



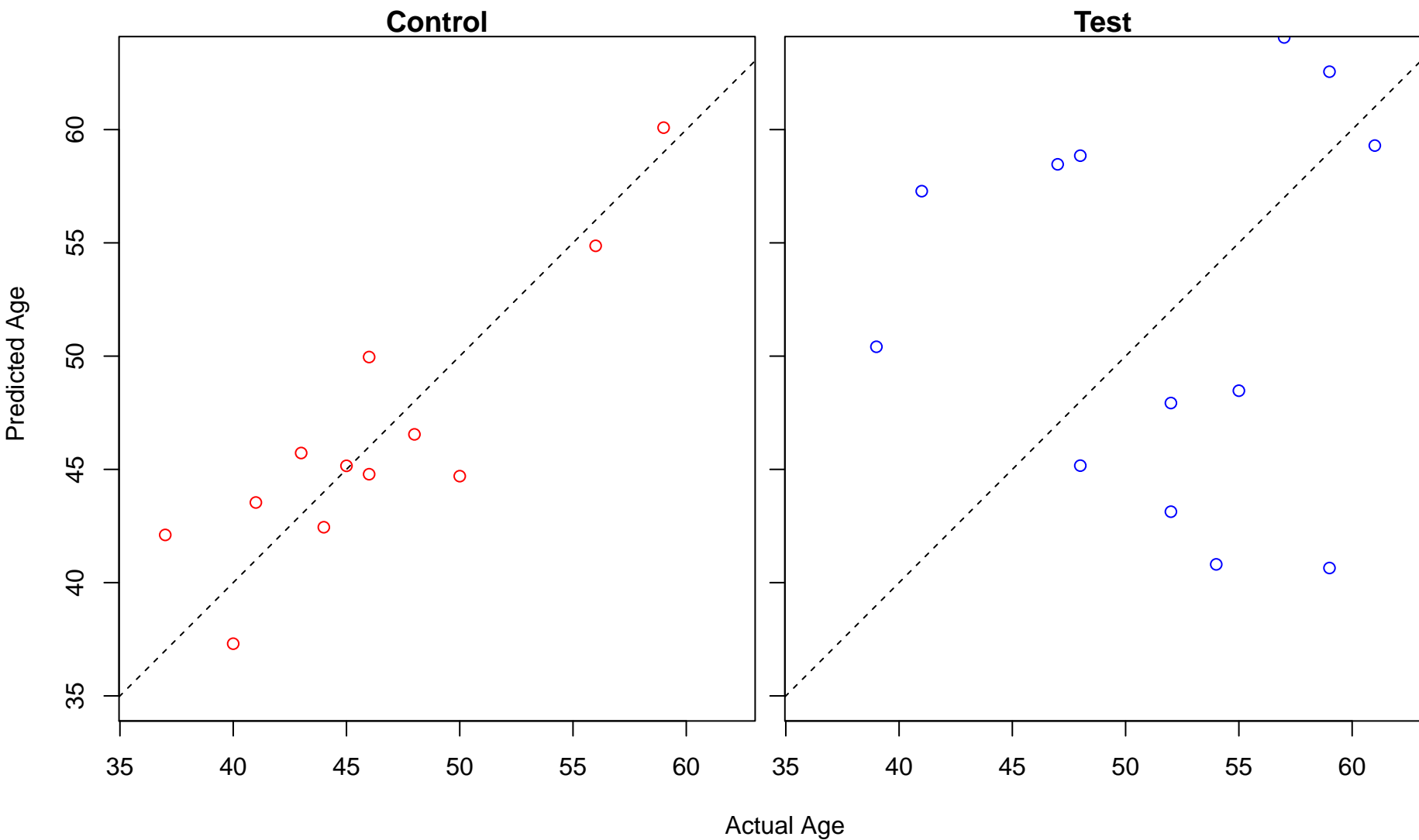
spliceosomal tri-snRNP complex assembly (Score: 7.598920)



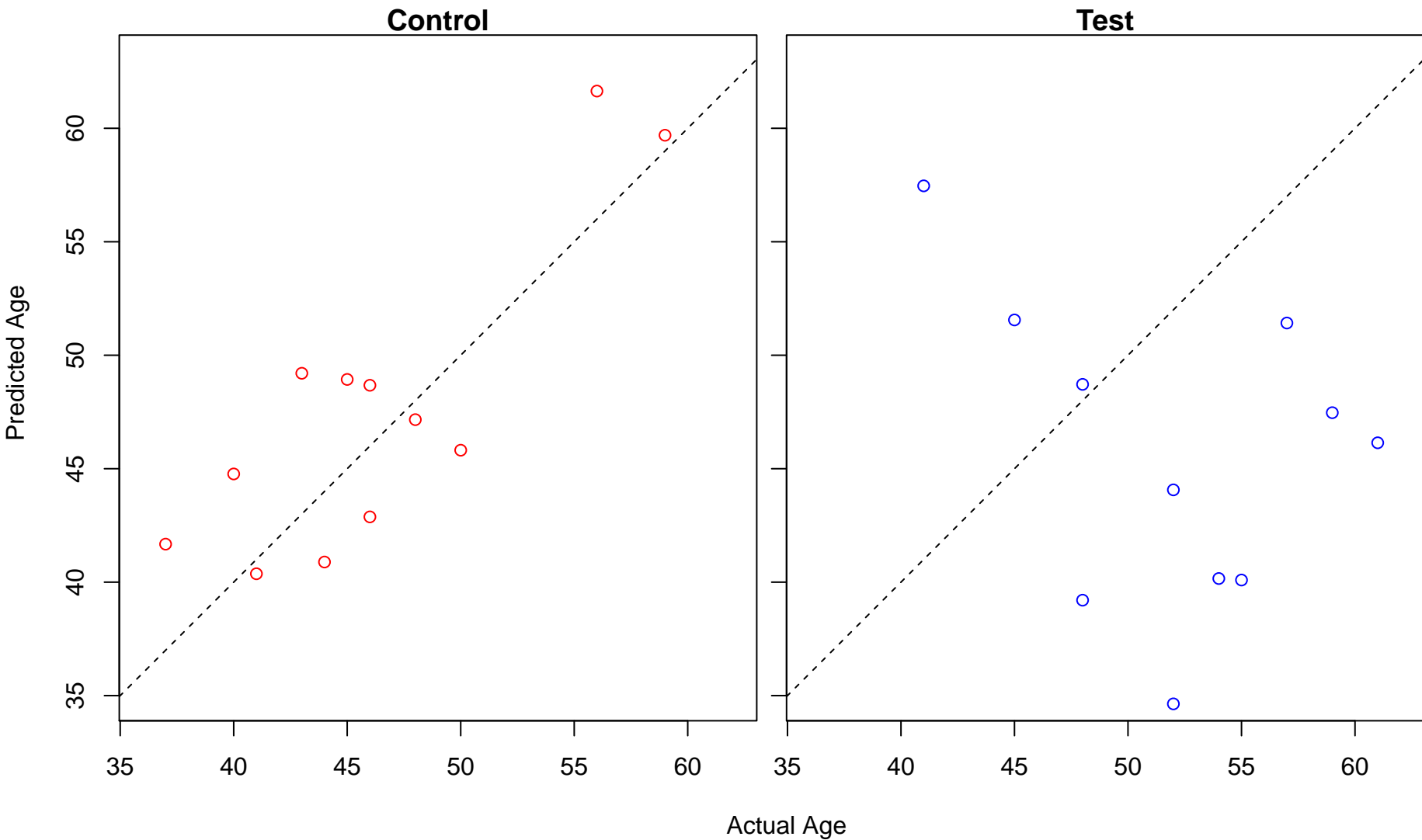
segment specification (Score: 7.596865)



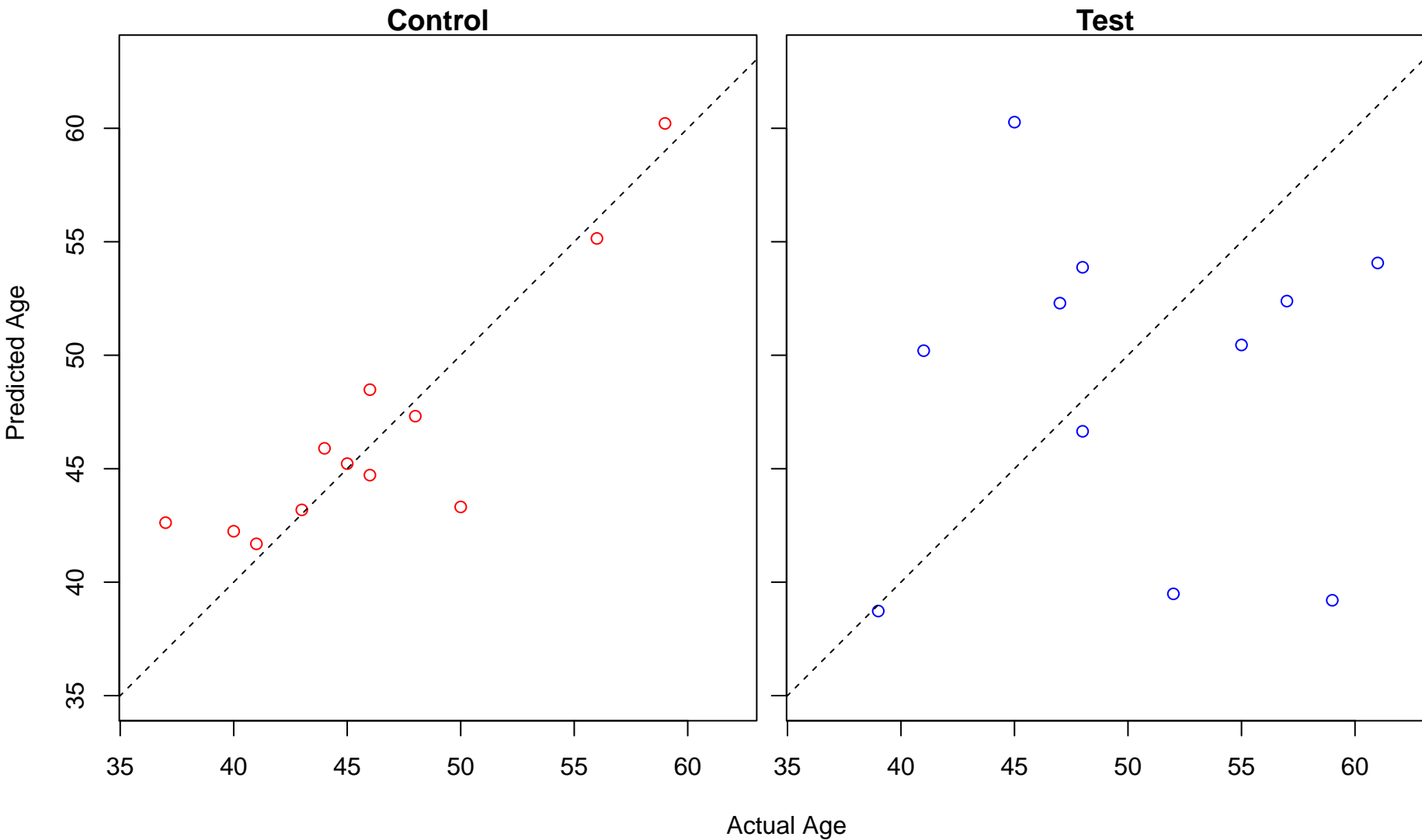
connective tissue development (Score: 7.592730)



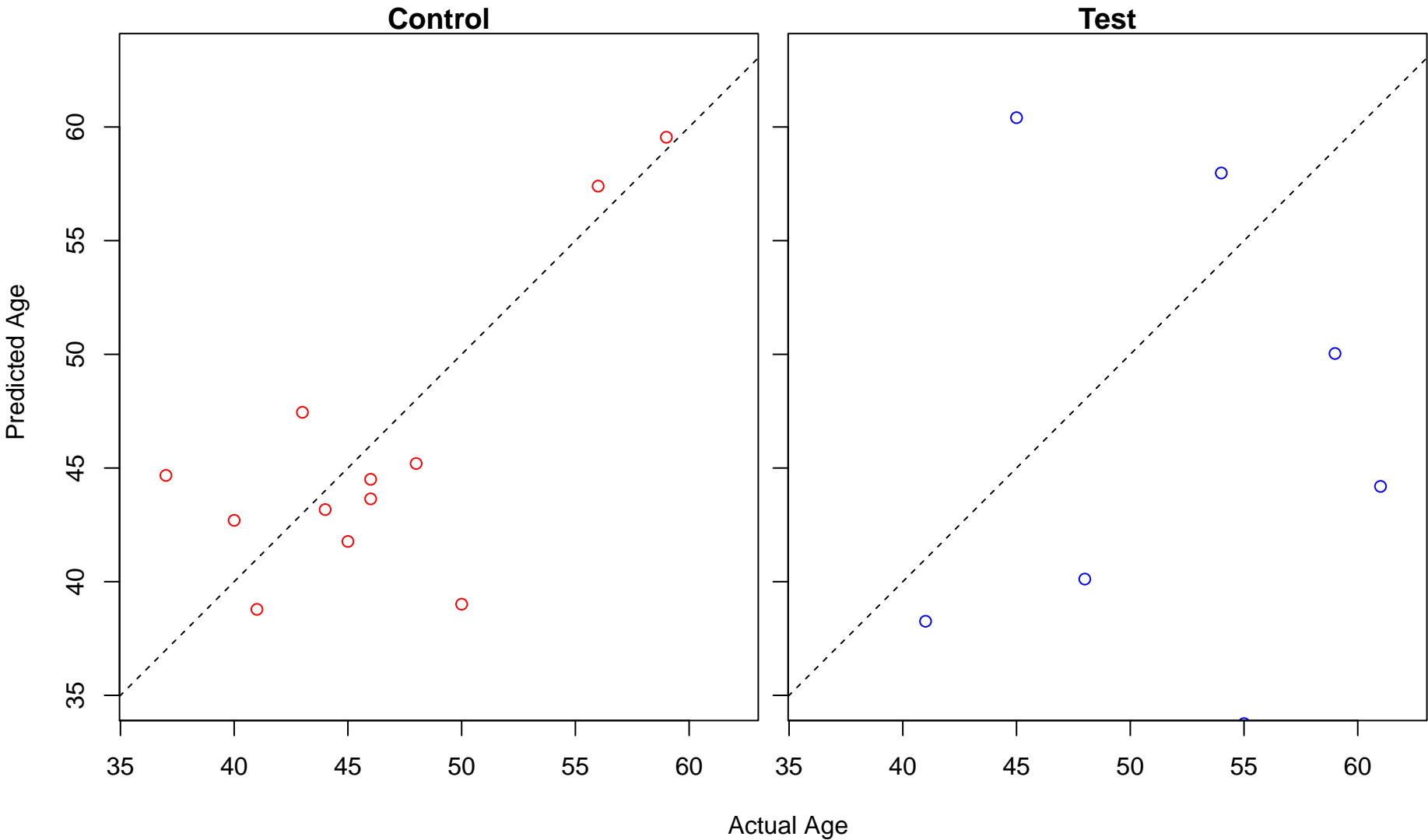
positive regulation of positive chemotaxis (Score: 7.588212)



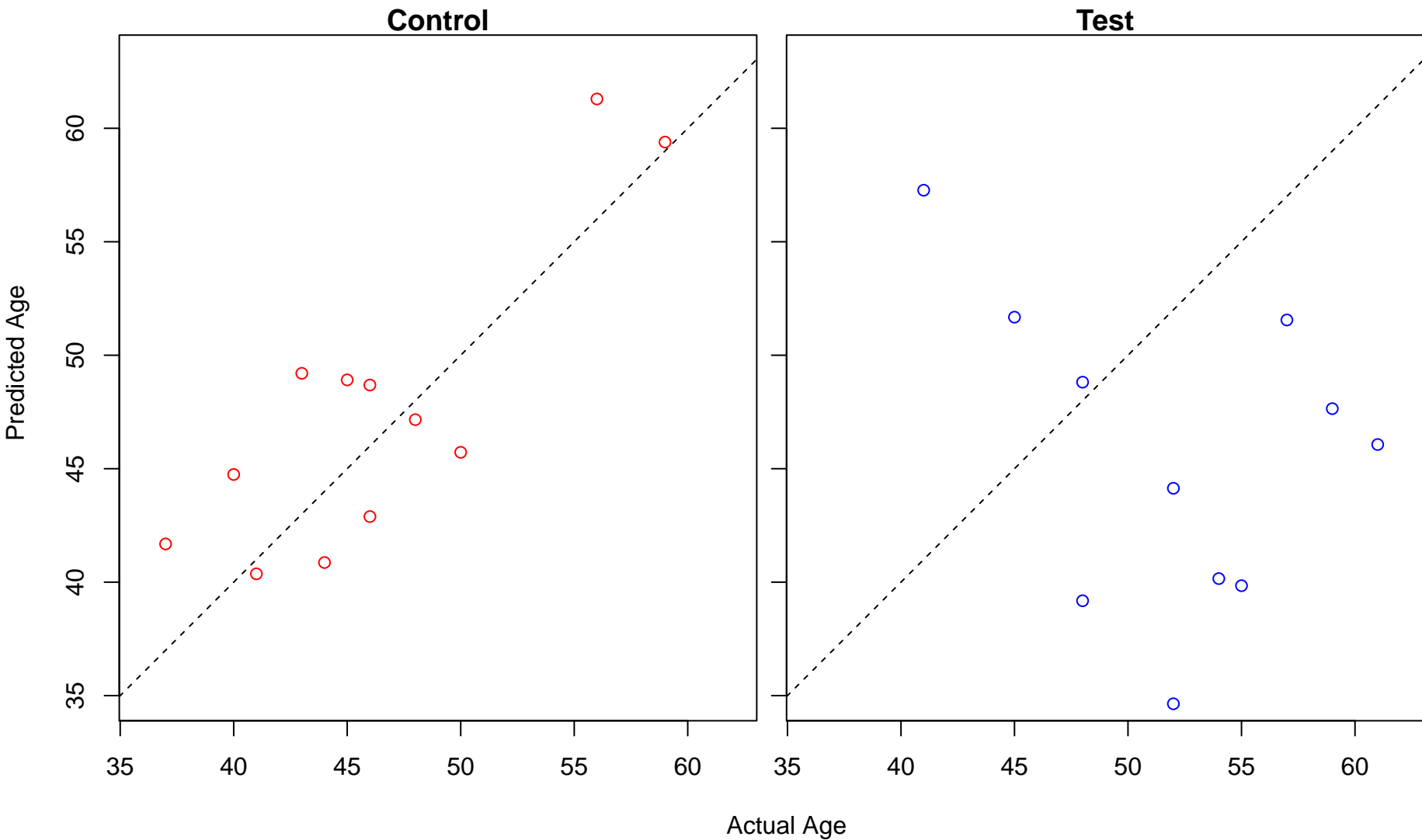
entrainment of circadian clock by photoperiod (Score: 7.563356)



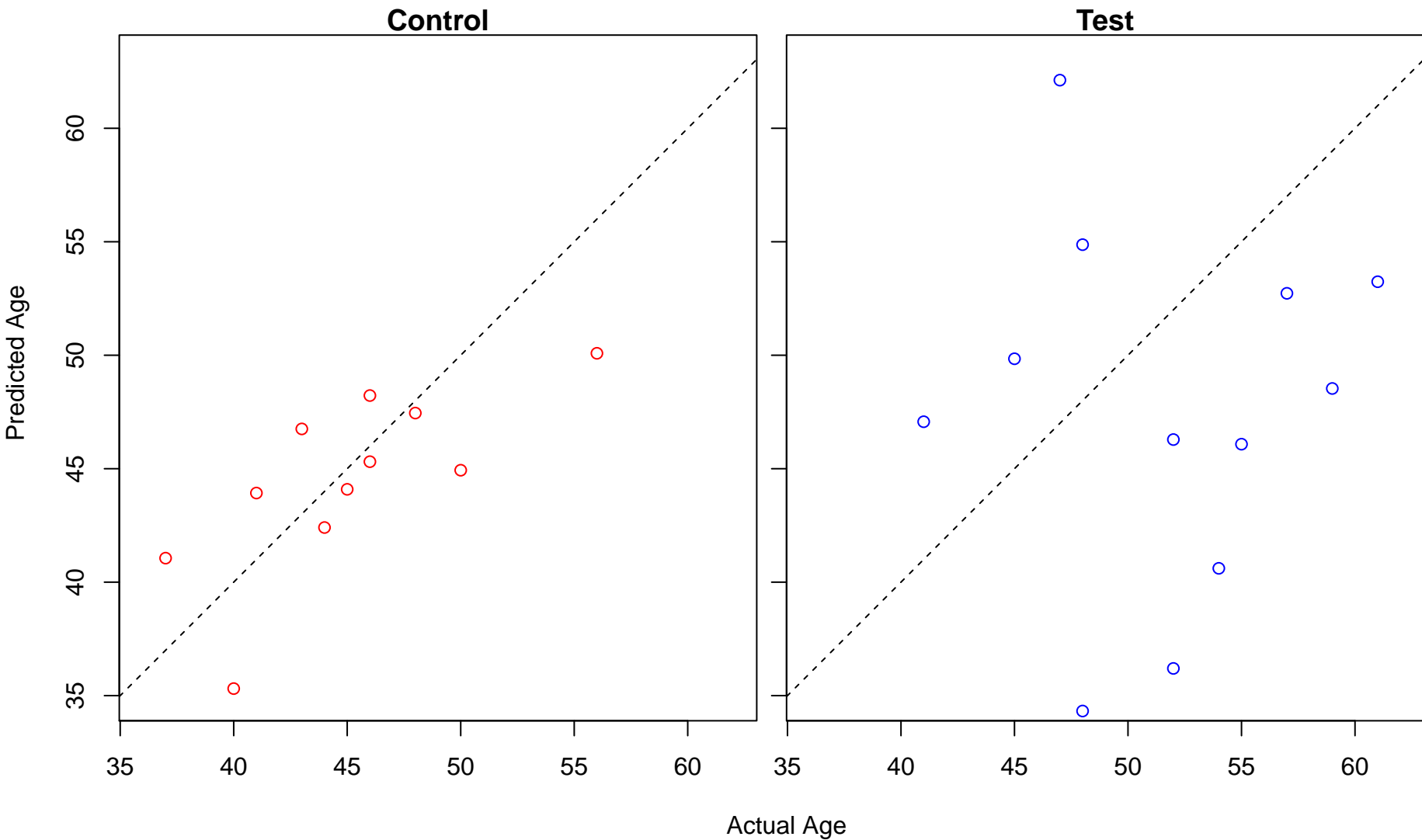
cyclic purine nucleotide metabolic process (Score: 7.560898)



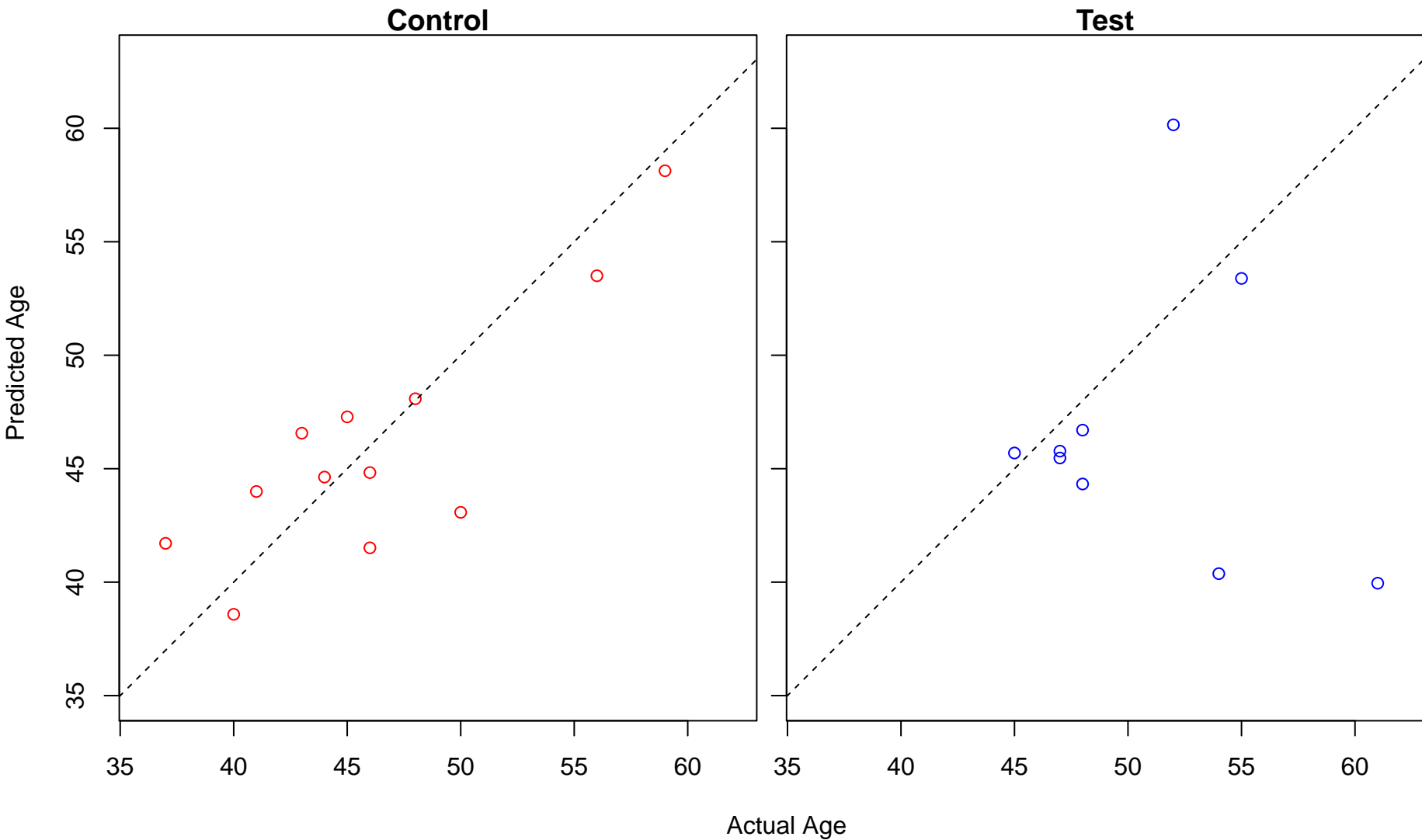
regulation of positive chemotaxis (Score: 7.538186)



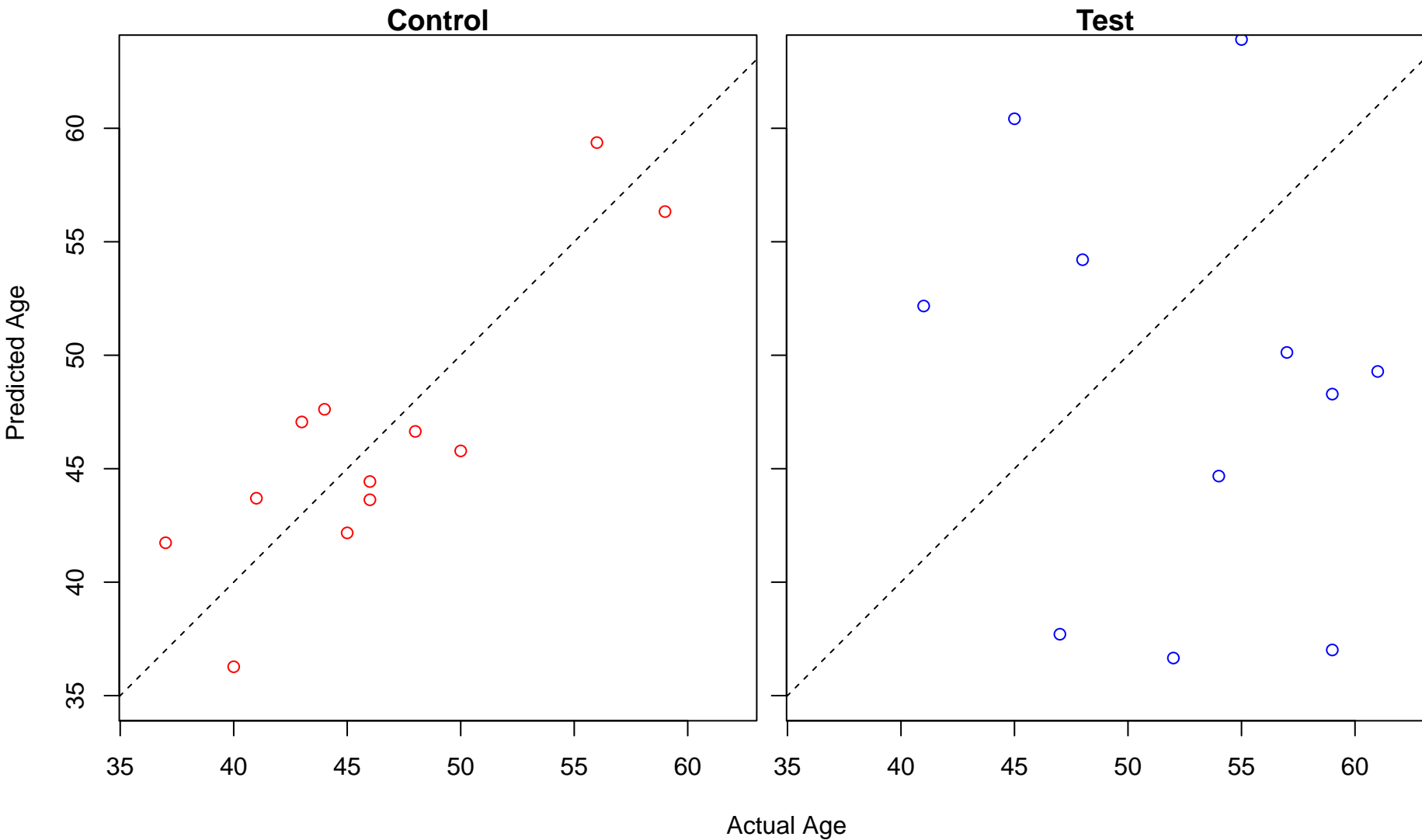
regulation of metanephric glomerulus development (Score: 7.533691)



ribonucleoprotein complex assembly (Score: 7.533337)

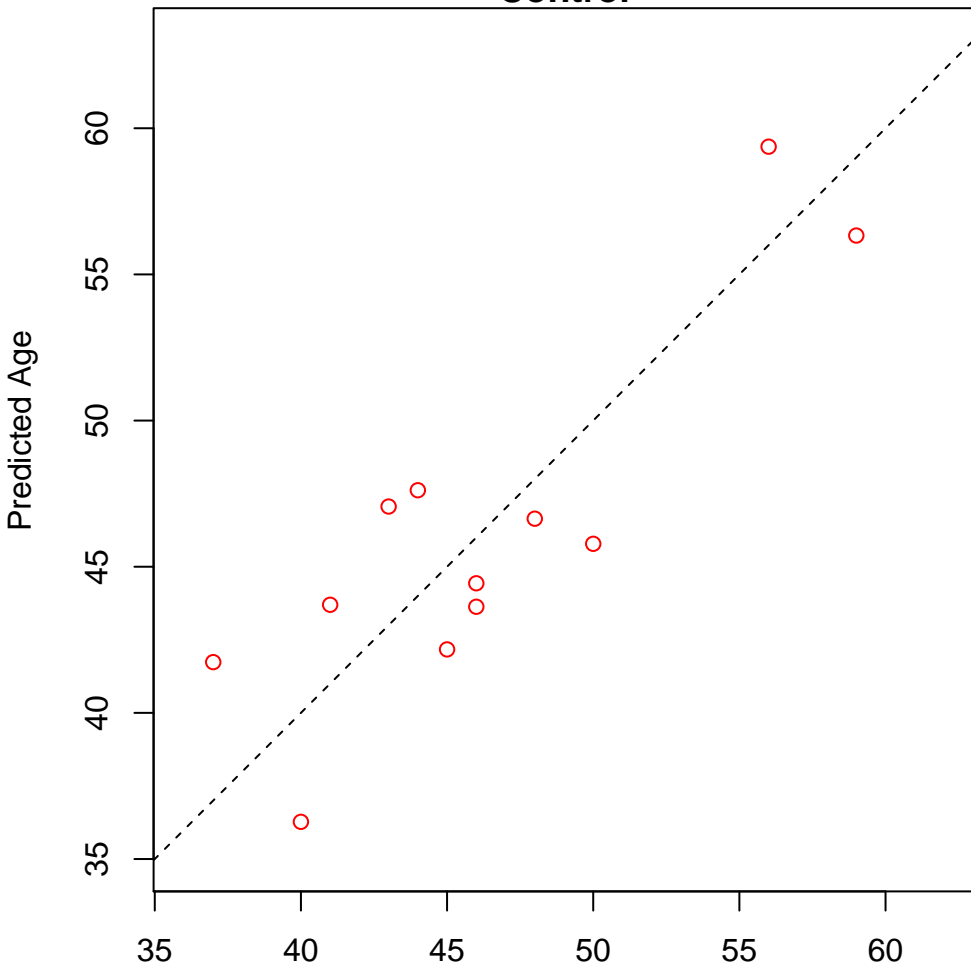


regulation of response to extracellular stimulus (Score: 7.529911)

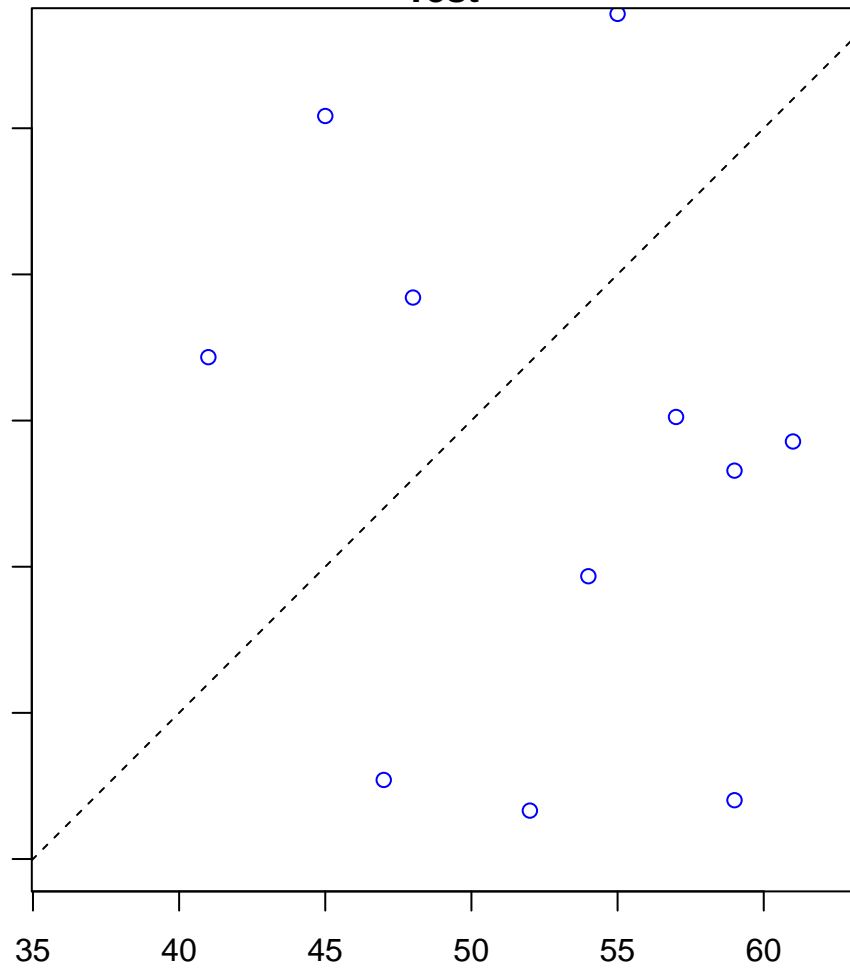


regulation of response to nutrient levels (Score: 7.529911)

Control

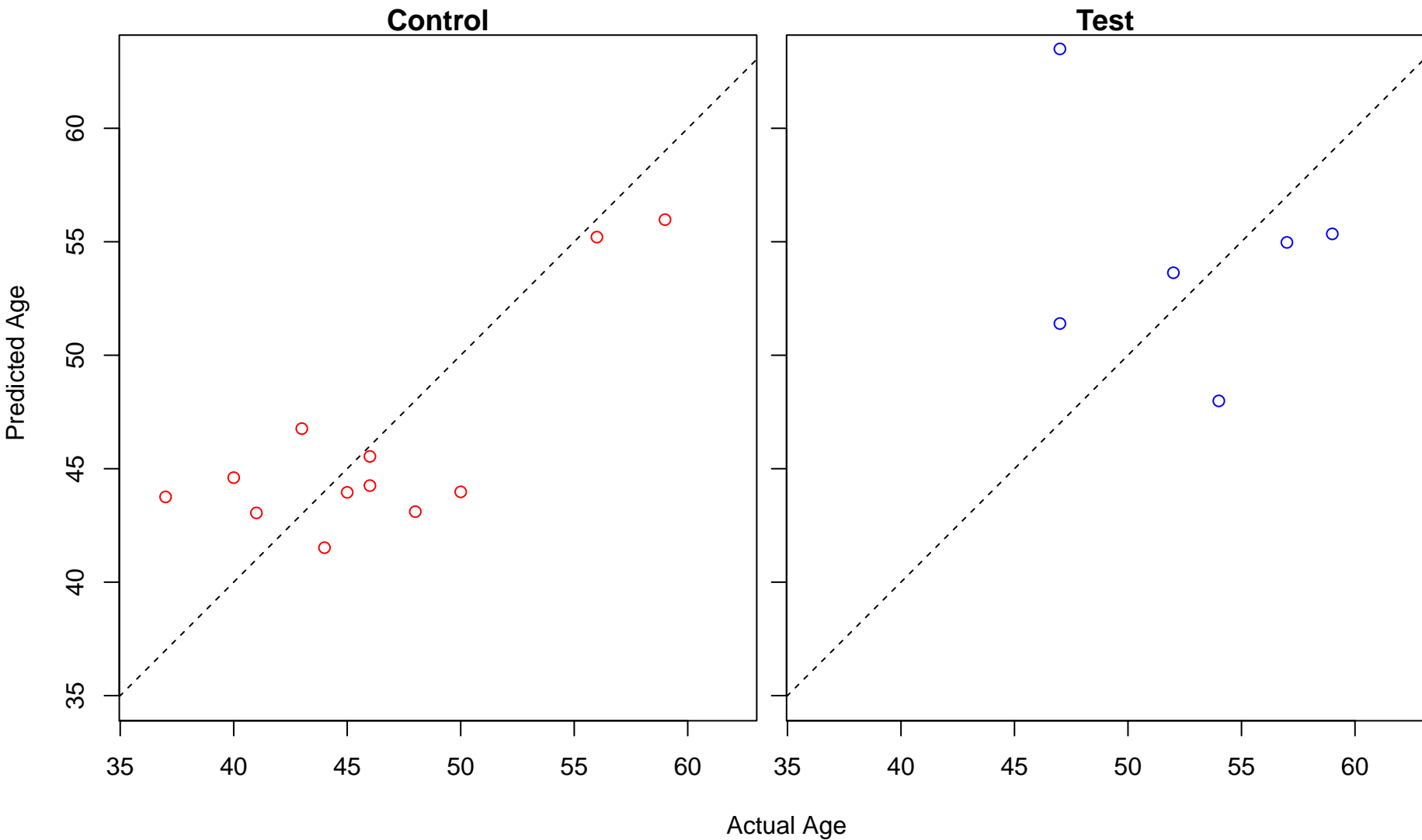


Test

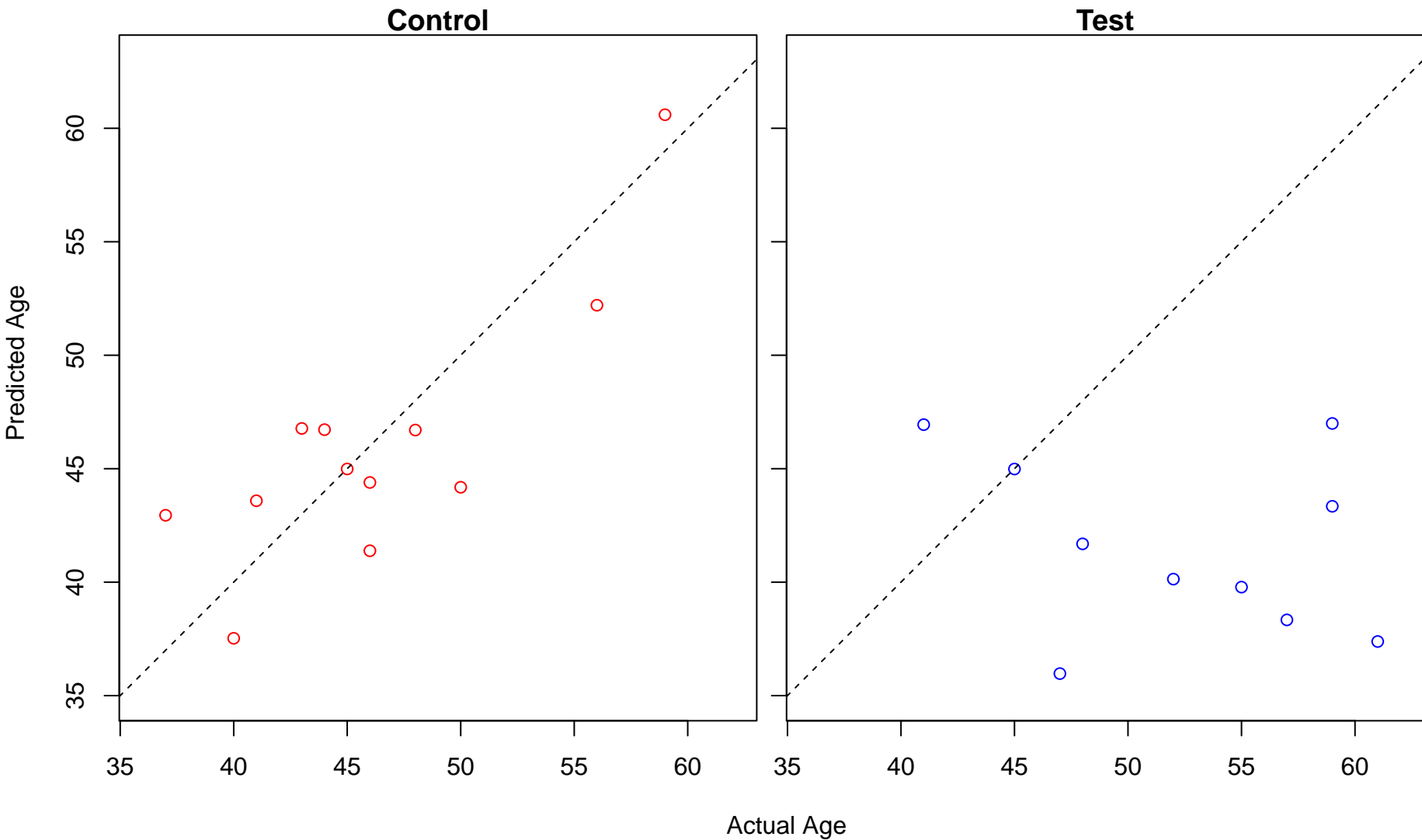


Actual Age

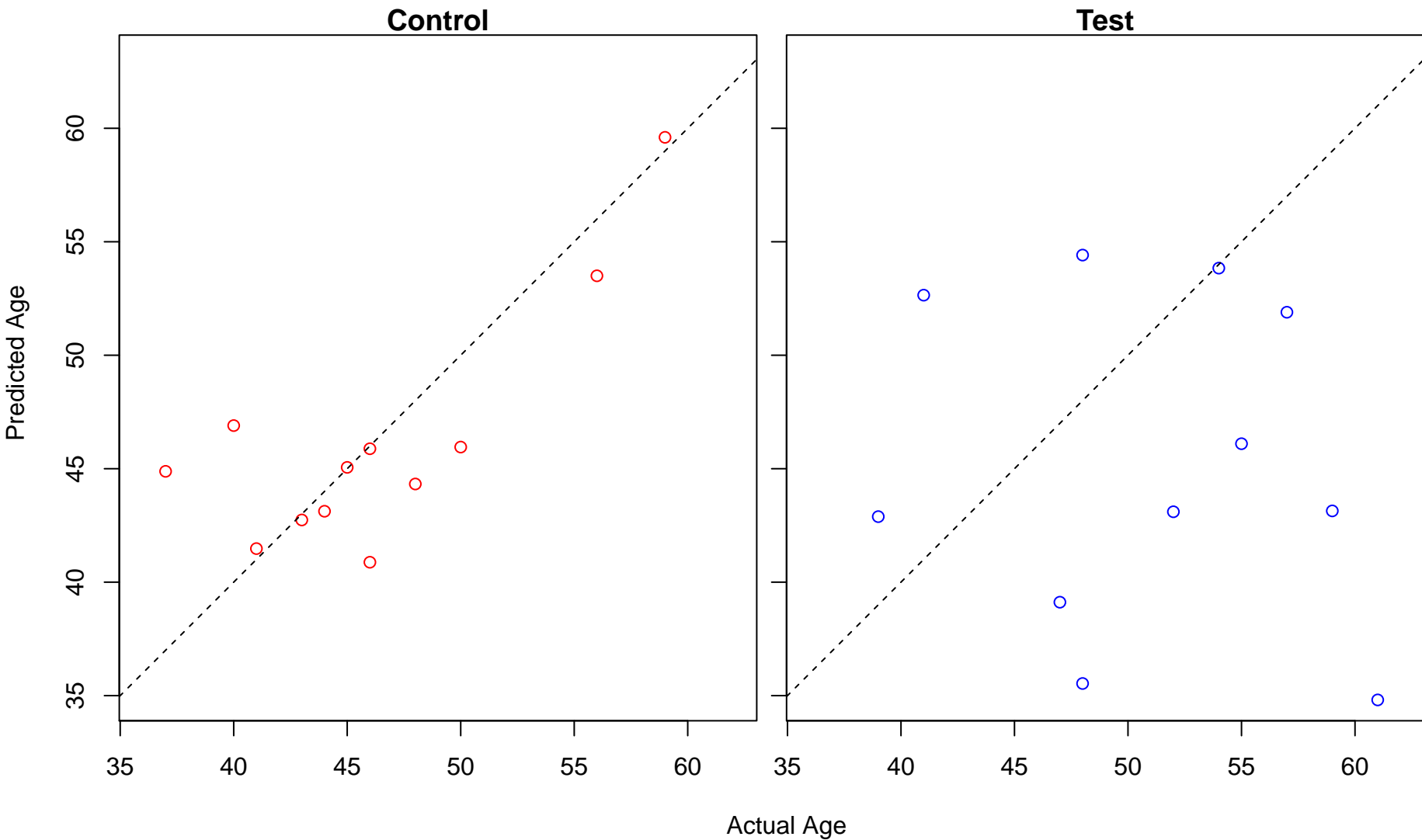
negative regulation of triglyceride metabolic process (Score: 7.527242)



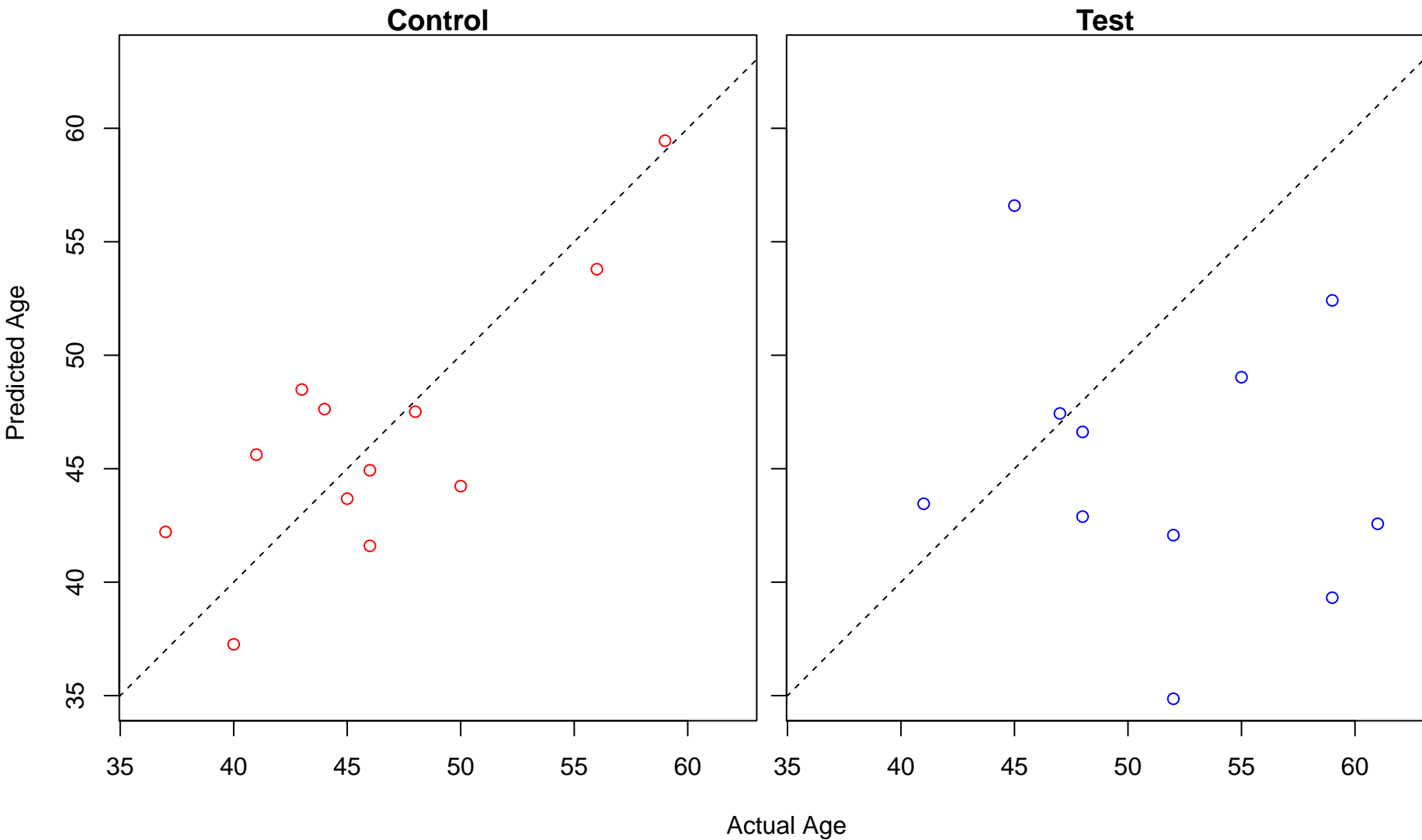
regulation of DNA metabolic process (Score: 7.522880)



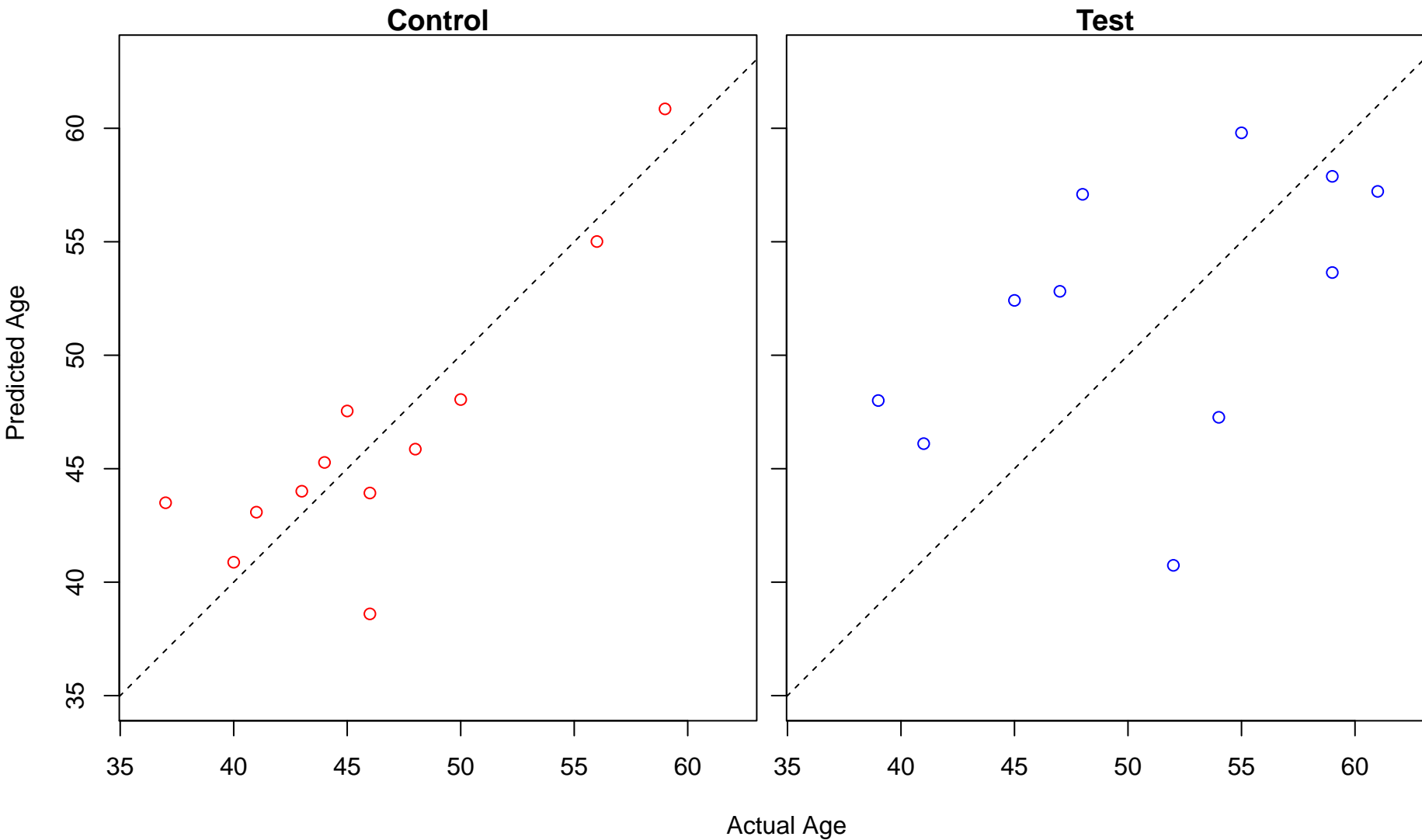
central nervous system projection neuron axonogenesis (Score: 7.519514)



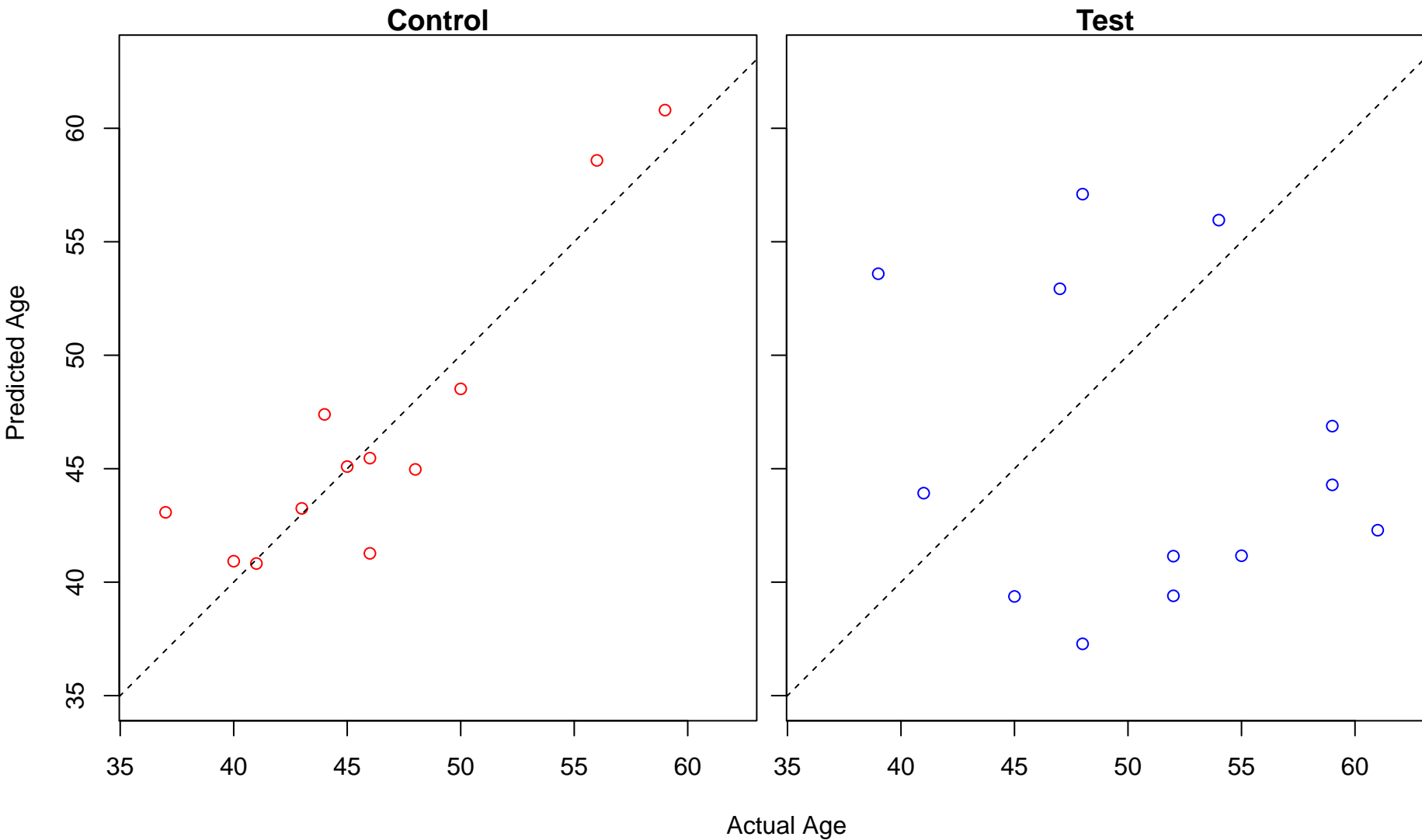
regulation of cell development (Score: 7.509979)



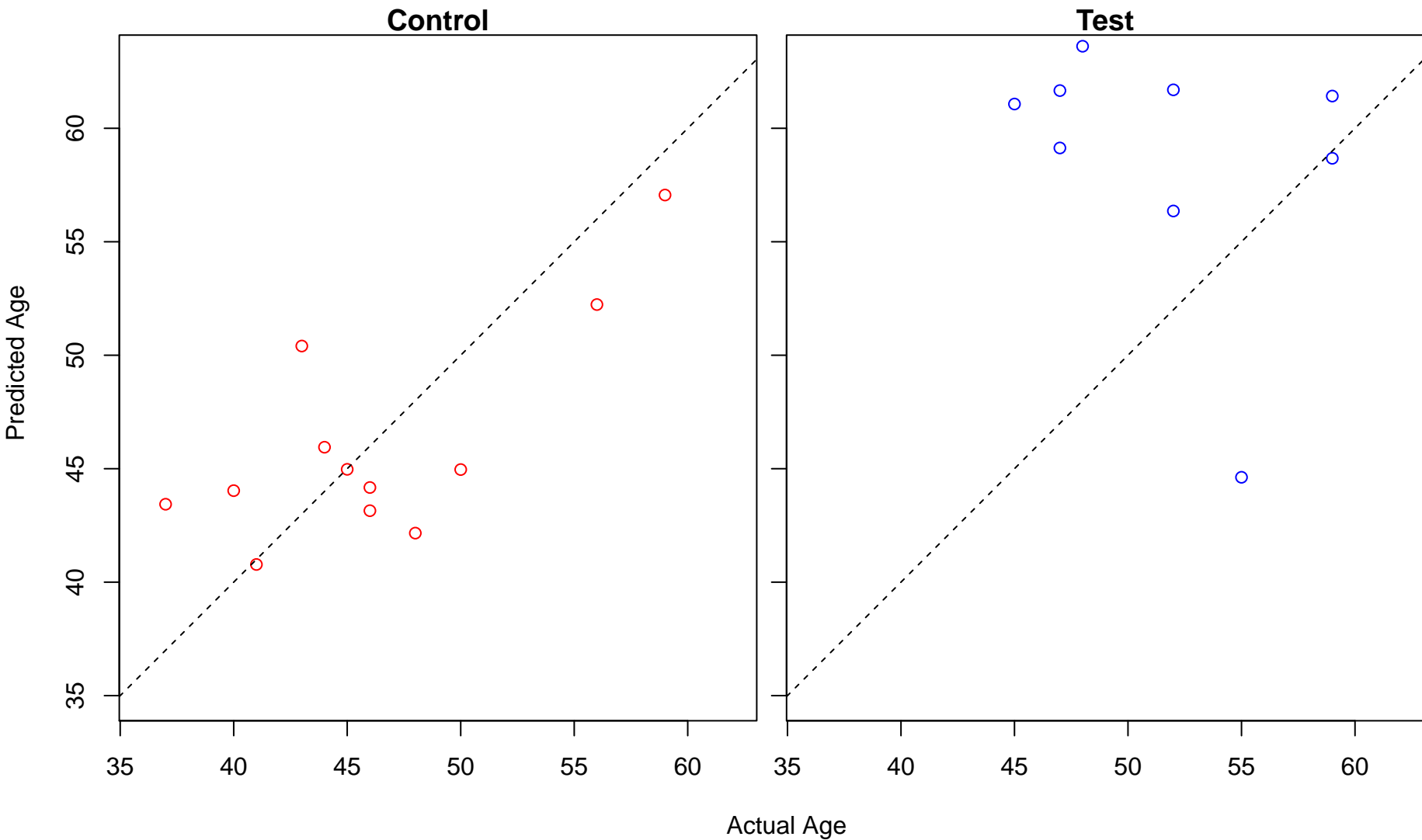
protein targeting to lysosome (Score: 7.504672)



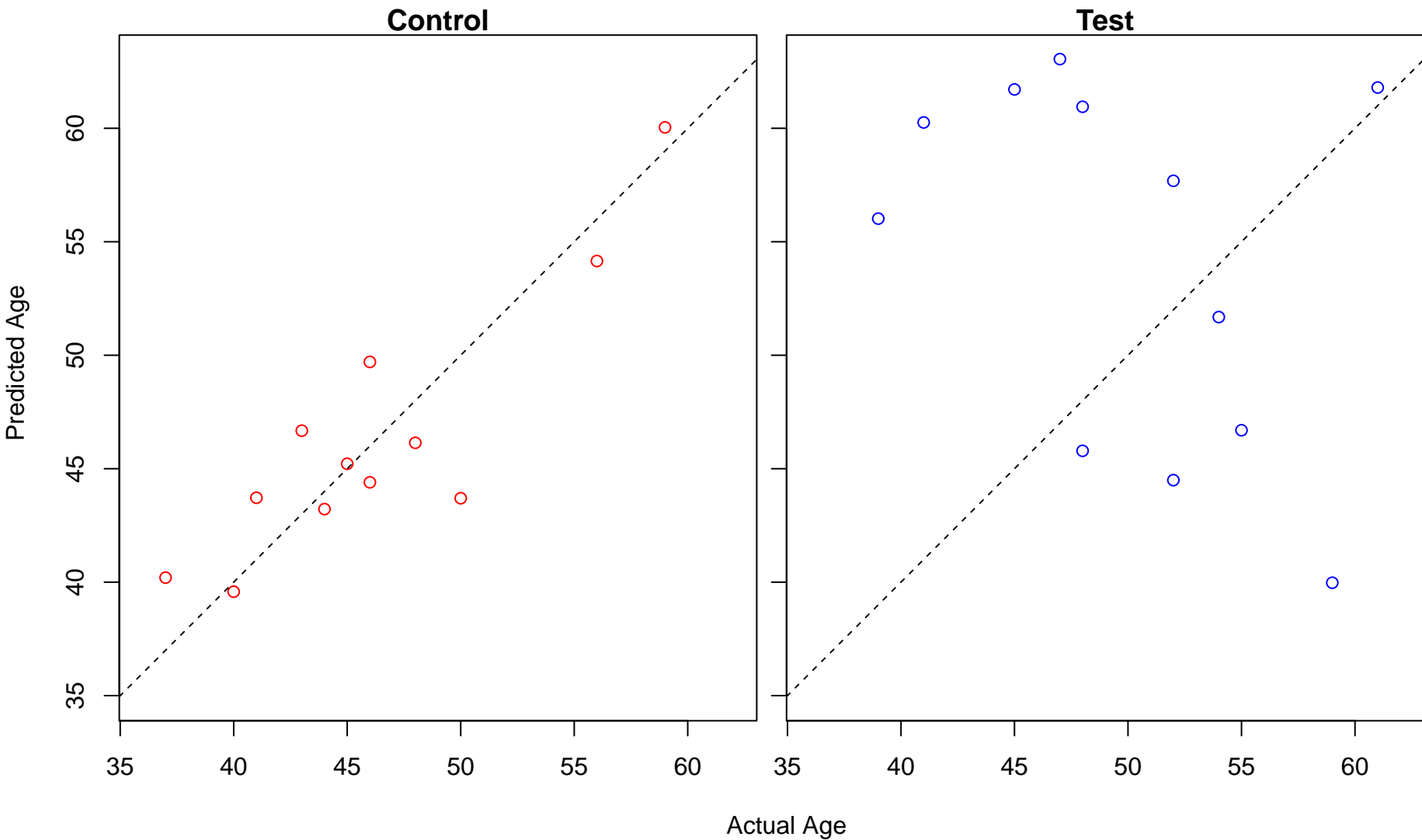
regulation of calcium ion transmembrane transport (Score: 7.486708)



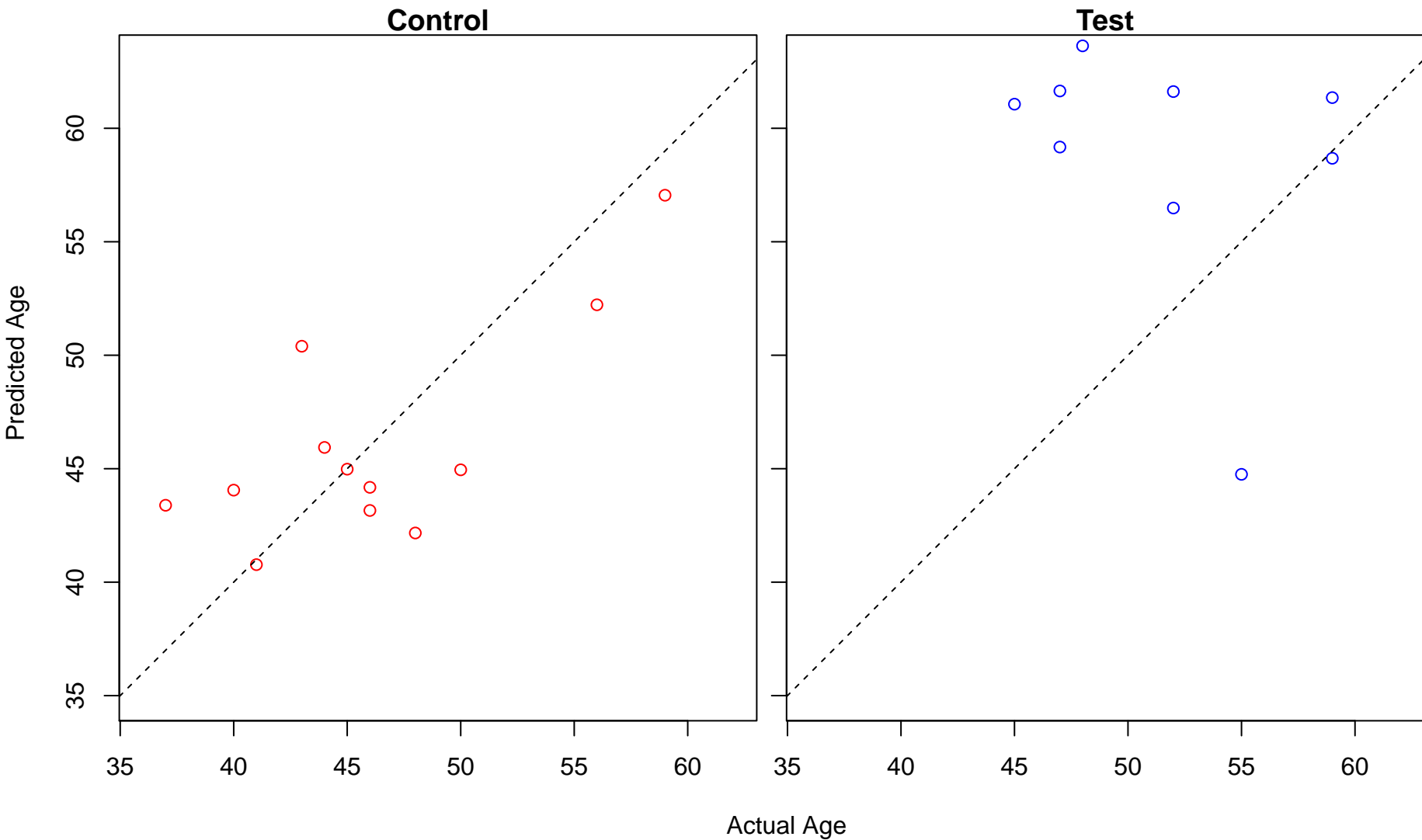
positive regulation of endothelial cell chemotaxis (Score: 7.481687)



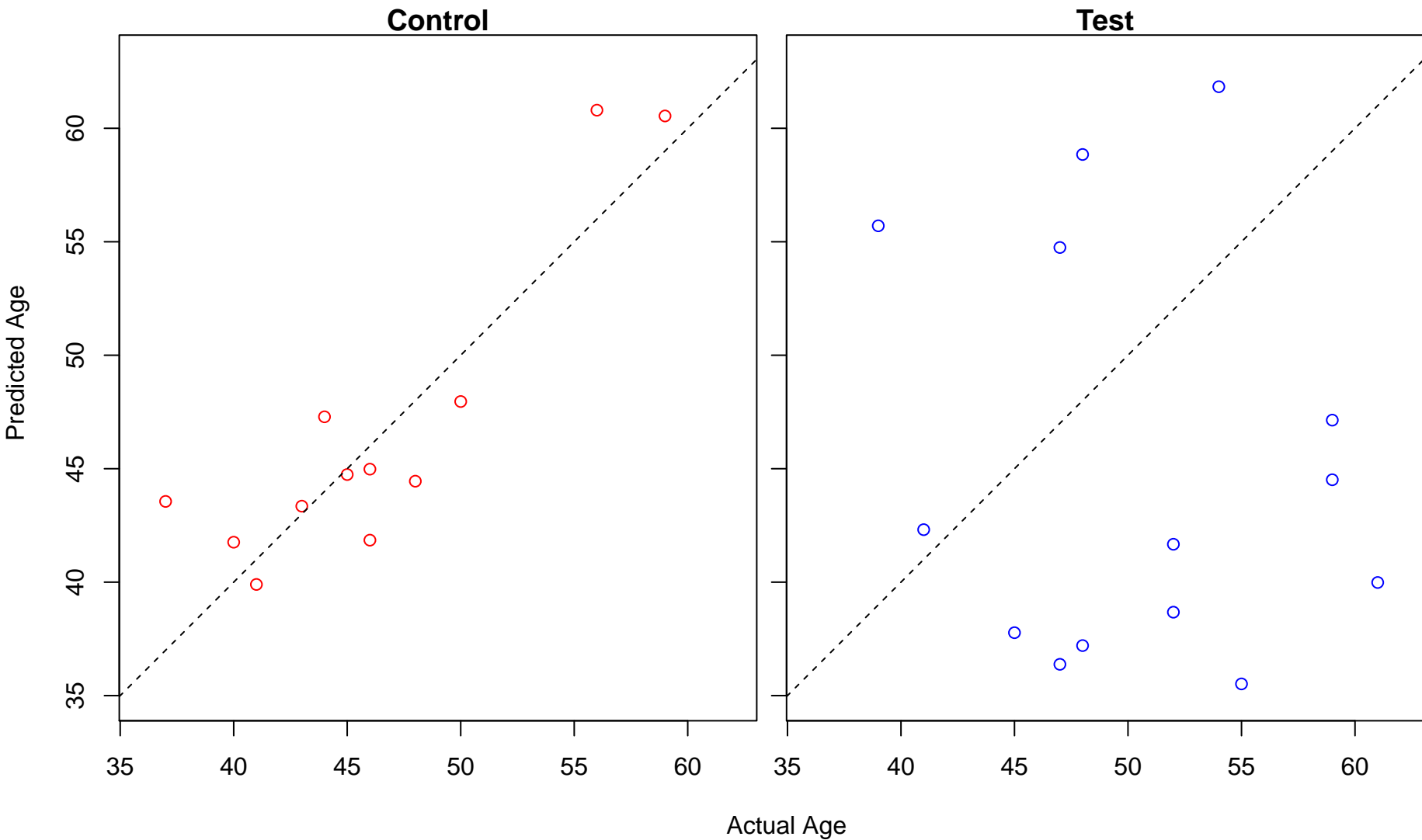
regulation of protein sumoylation (Score: 7.481129)



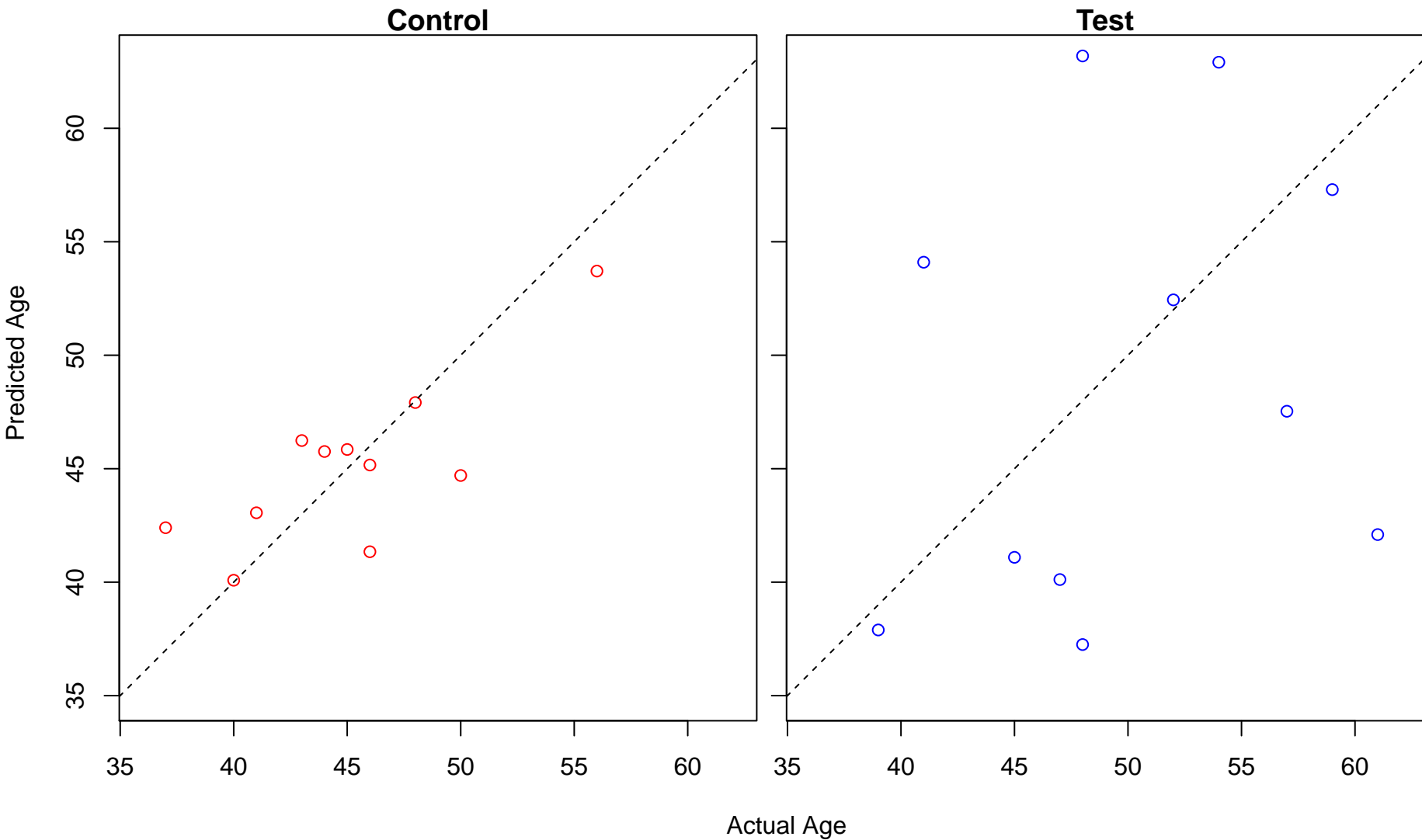
regulation of endothelial cell chemotaxis (Score: 7.478467)



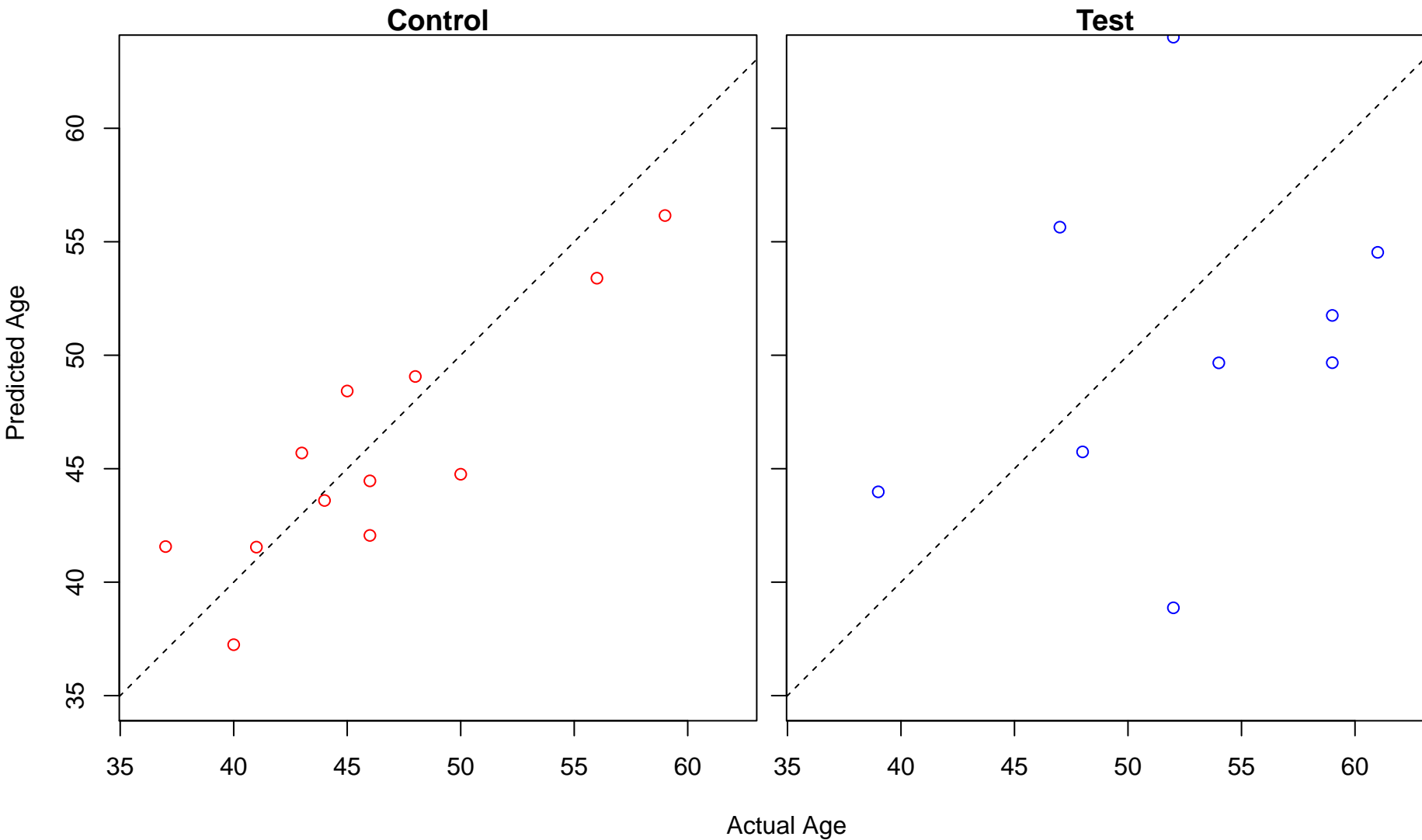
regulation of muscle system process (Score: 7.478091)



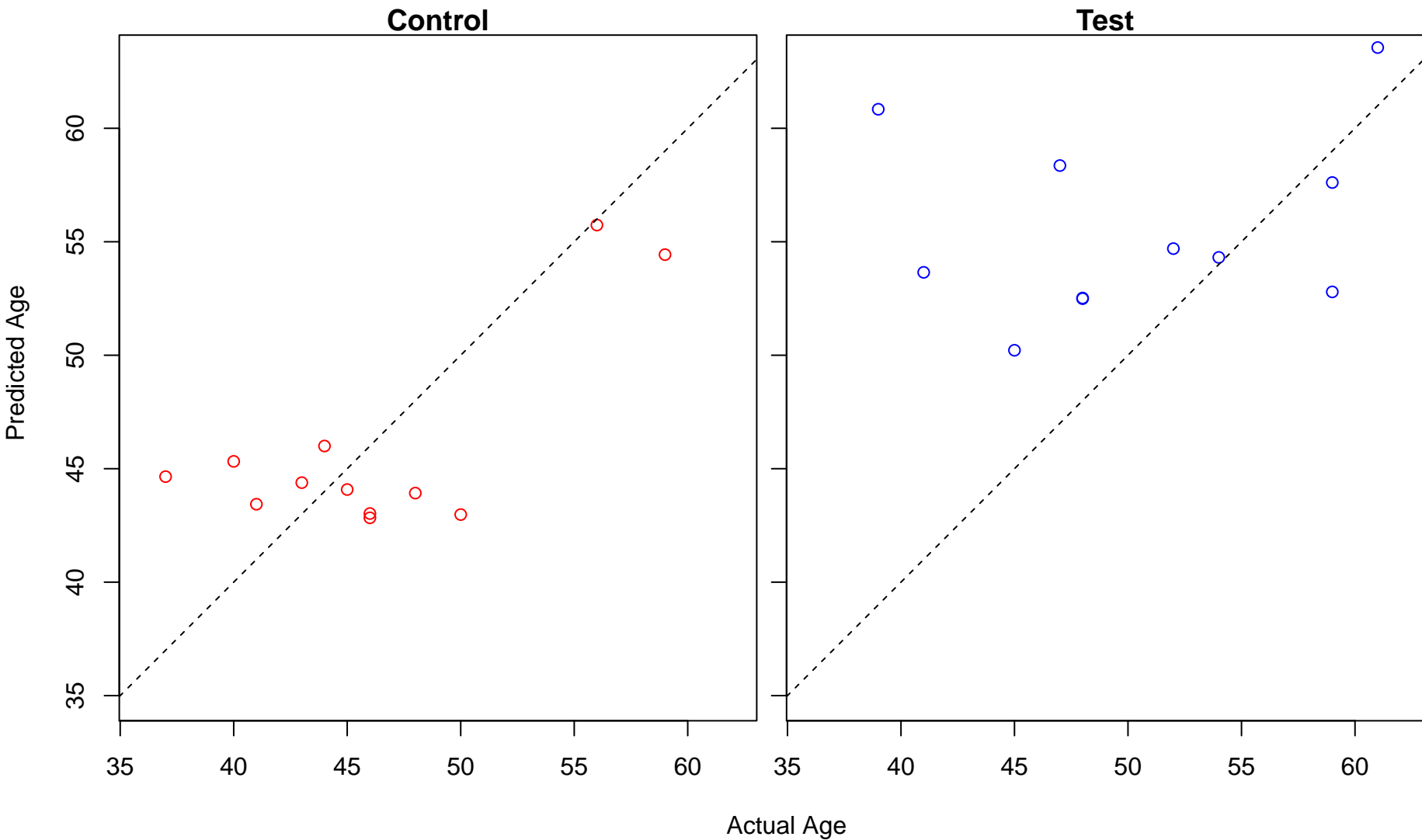
membrane lipid biosynthetic process (Score: 7.475280)



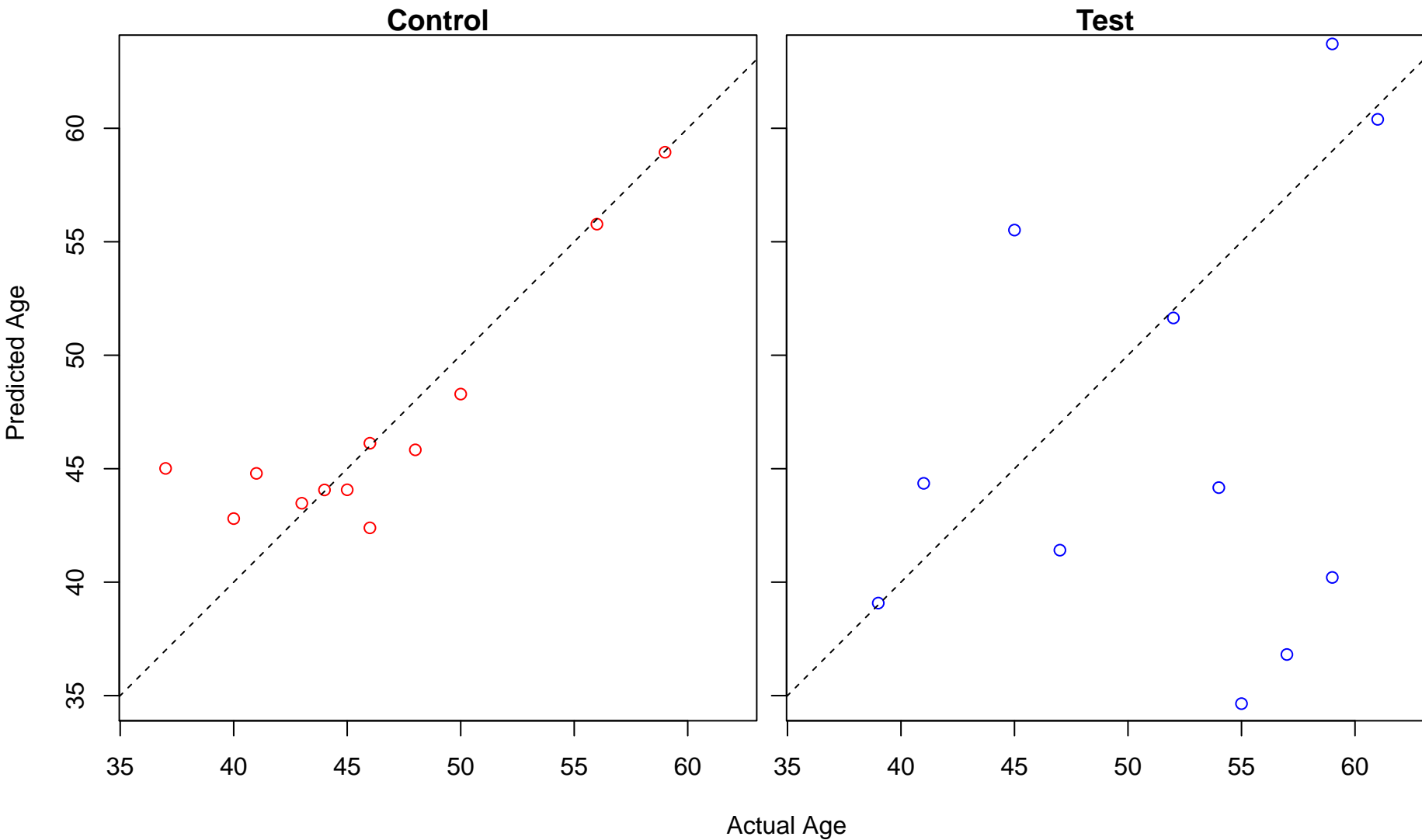
negative regulation of Notch signaling pathway (Score: 7.465384)



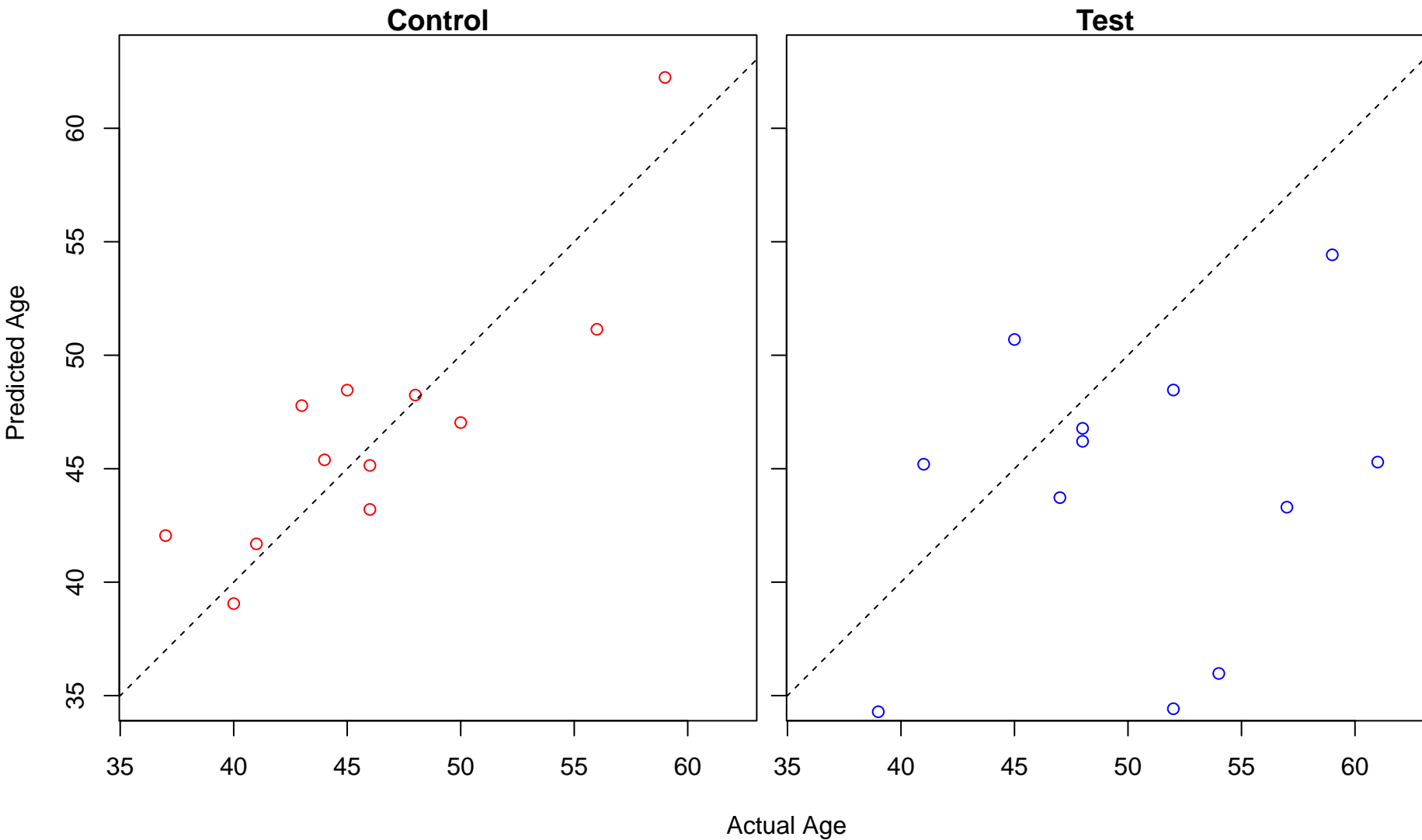
negative regulation of phospholipase activity (Score: 7.461467)



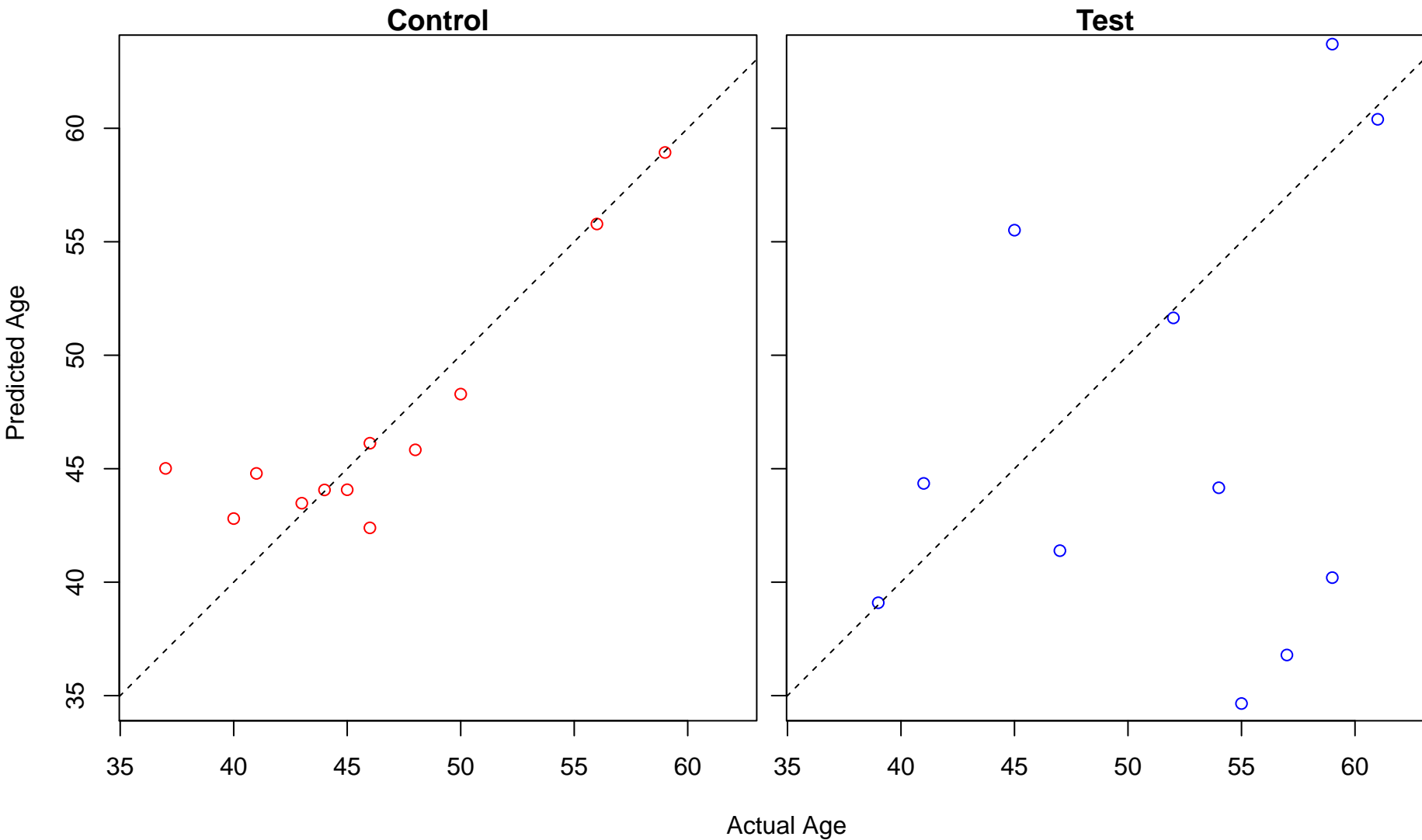
glycosaminoglycan metabolic process (Score: 7.455054)



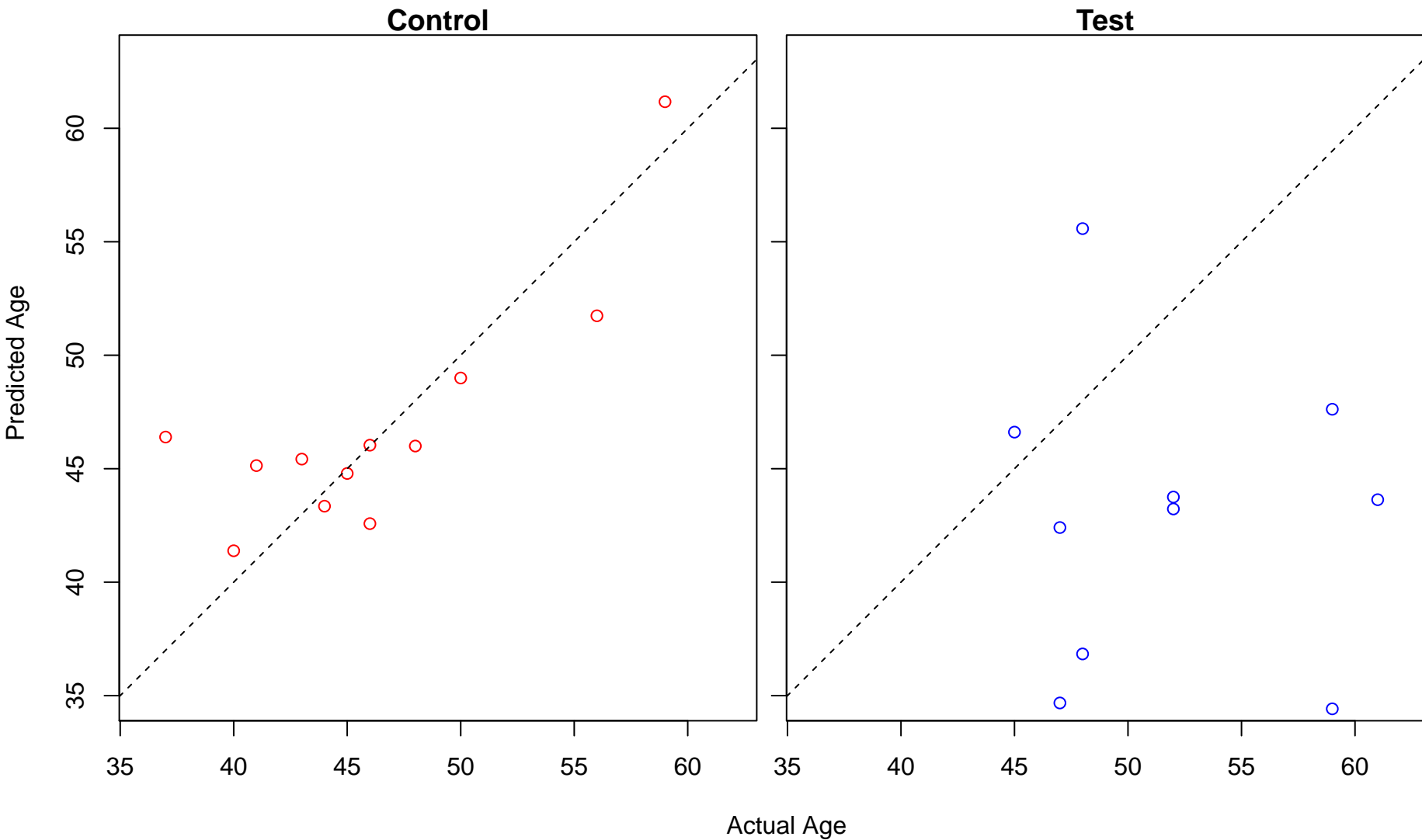
positive regulation of epithelial cell proliferation (Score: 7.454353)



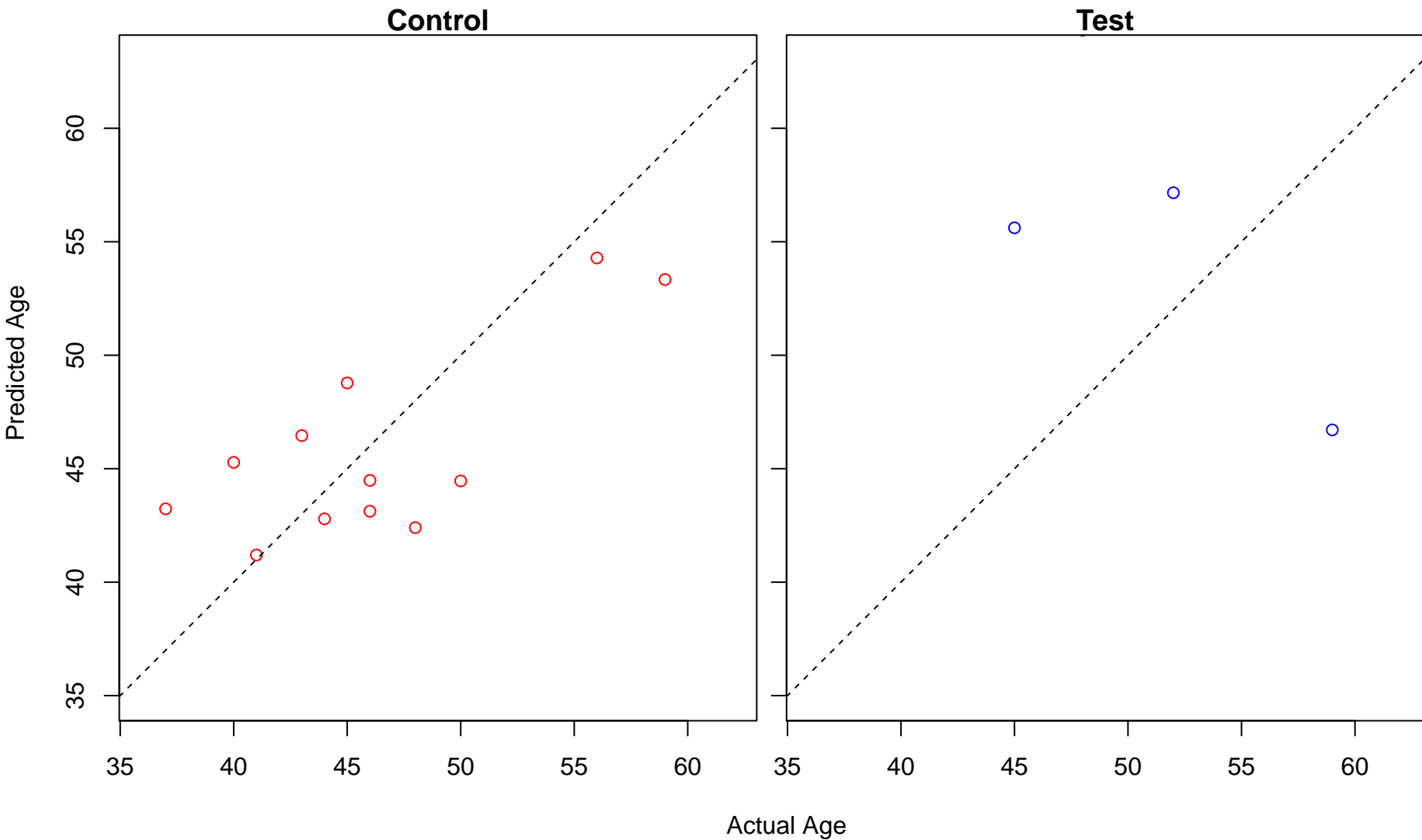
aminoglycan metabolic process (Score: 7.452334)



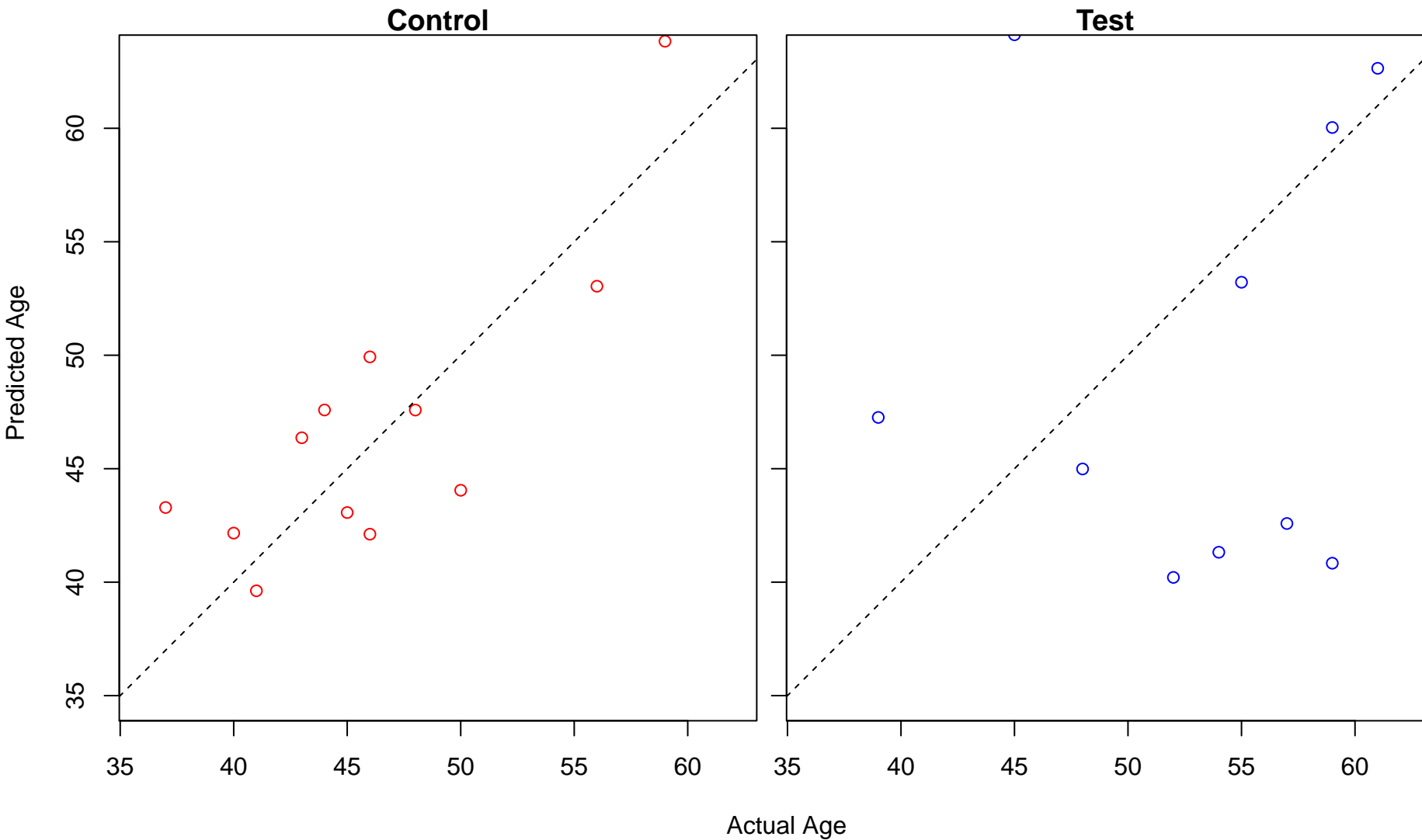
keratan sulfate metabolic process (Score: 7.441757)



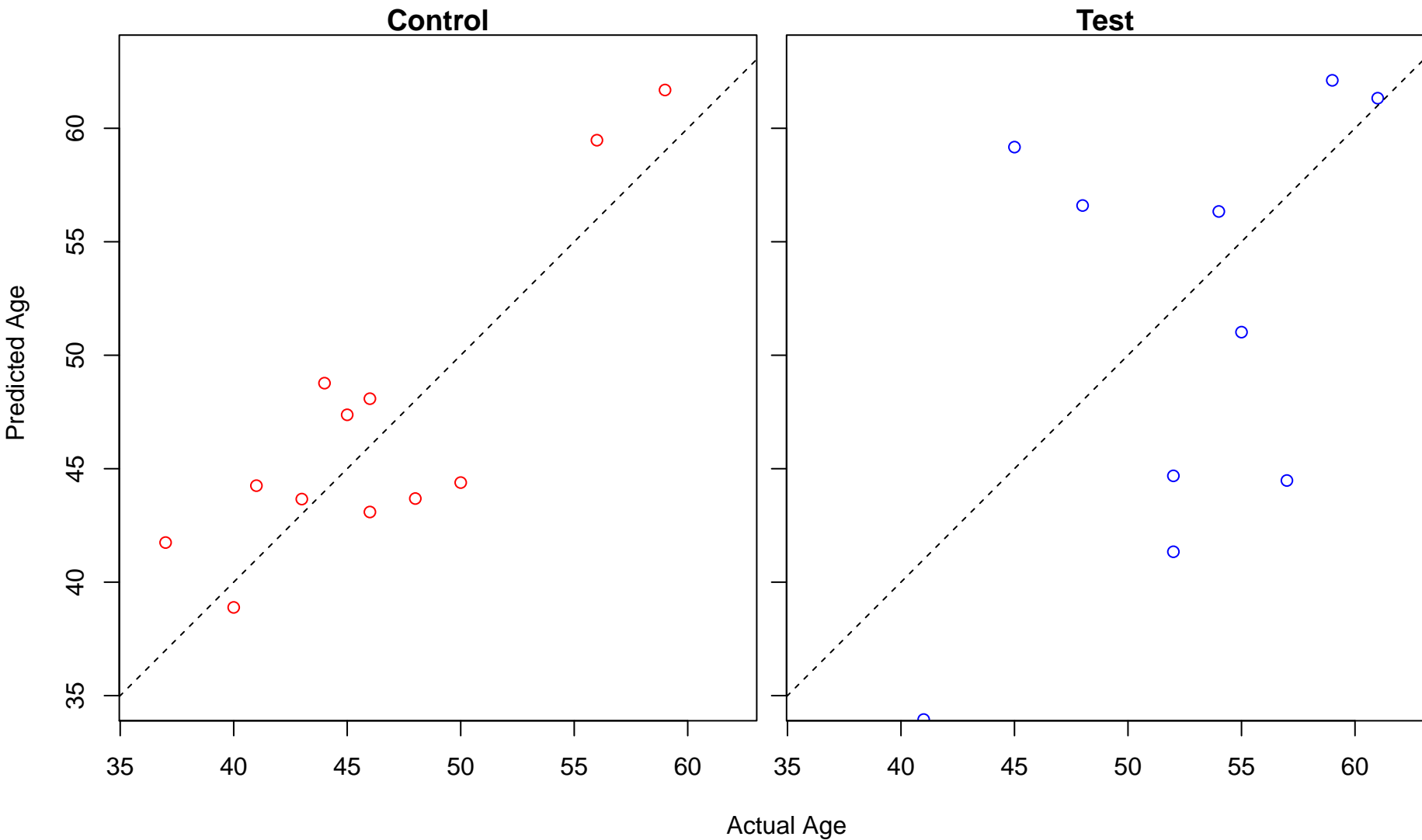
negative regulation of anion transmembrane transport (Score: 7.436763)



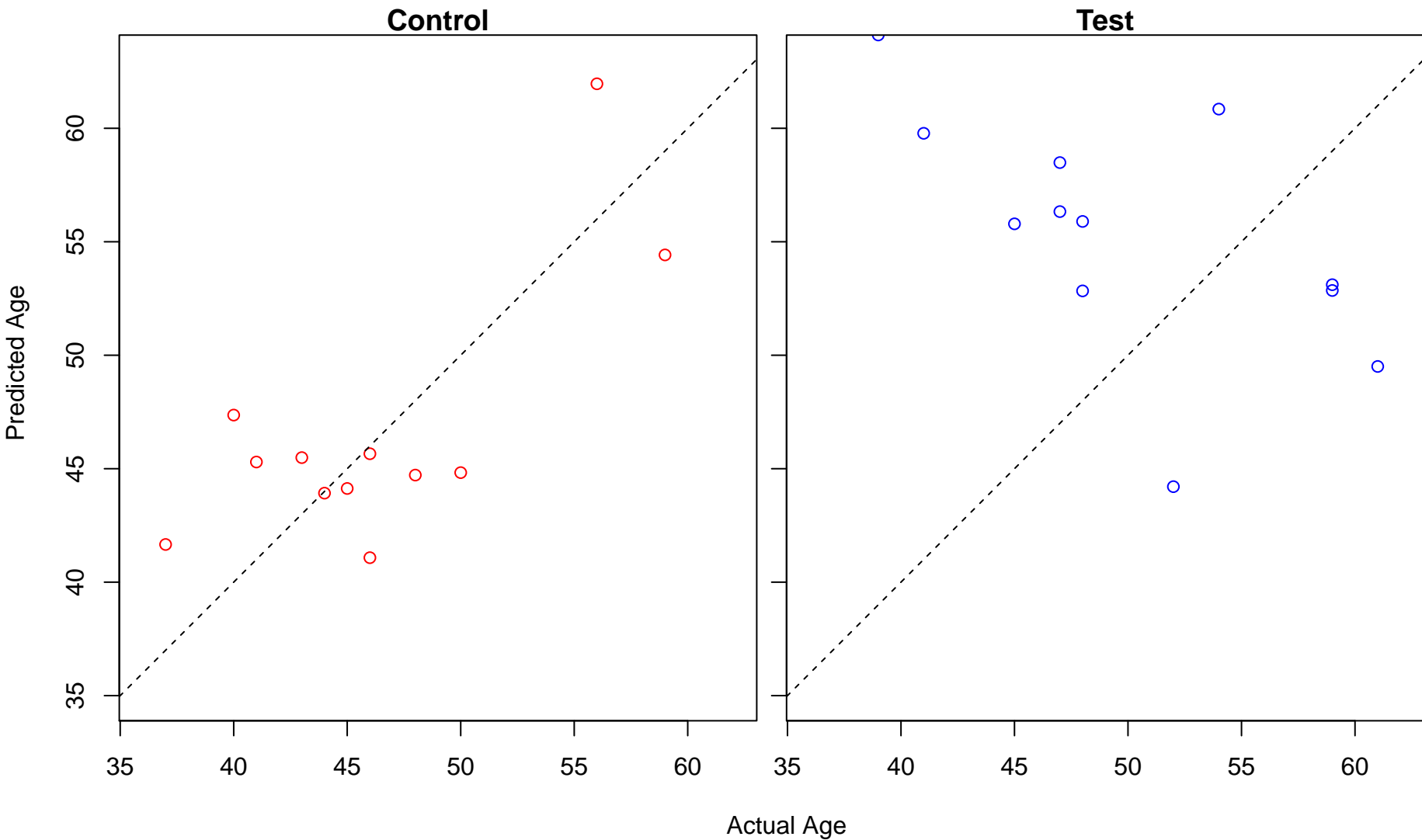
entrainment of circadian clock (Score: 7.432066)



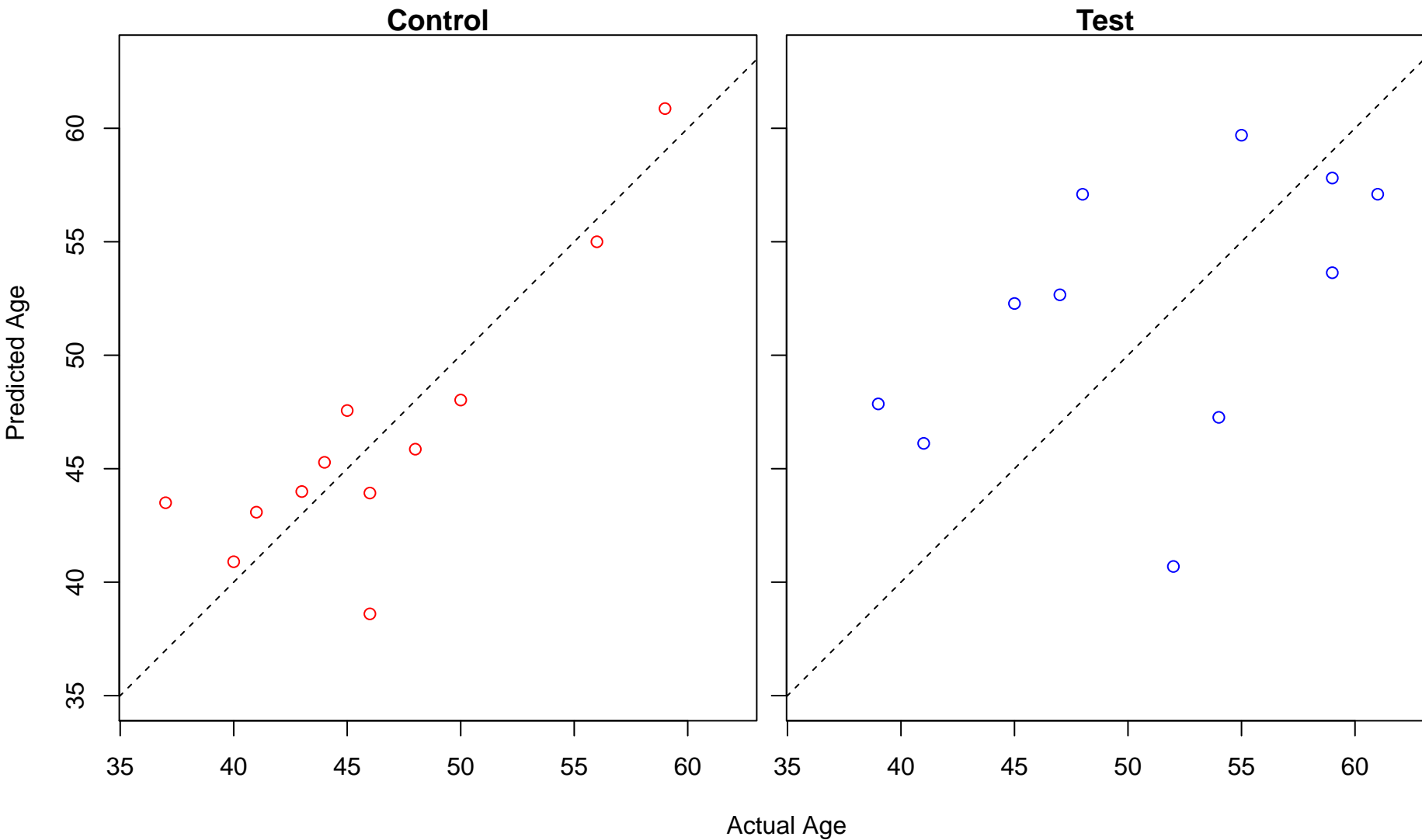
CD4-positive, alpha-beta T cell differentiation (Score: 7.431410)



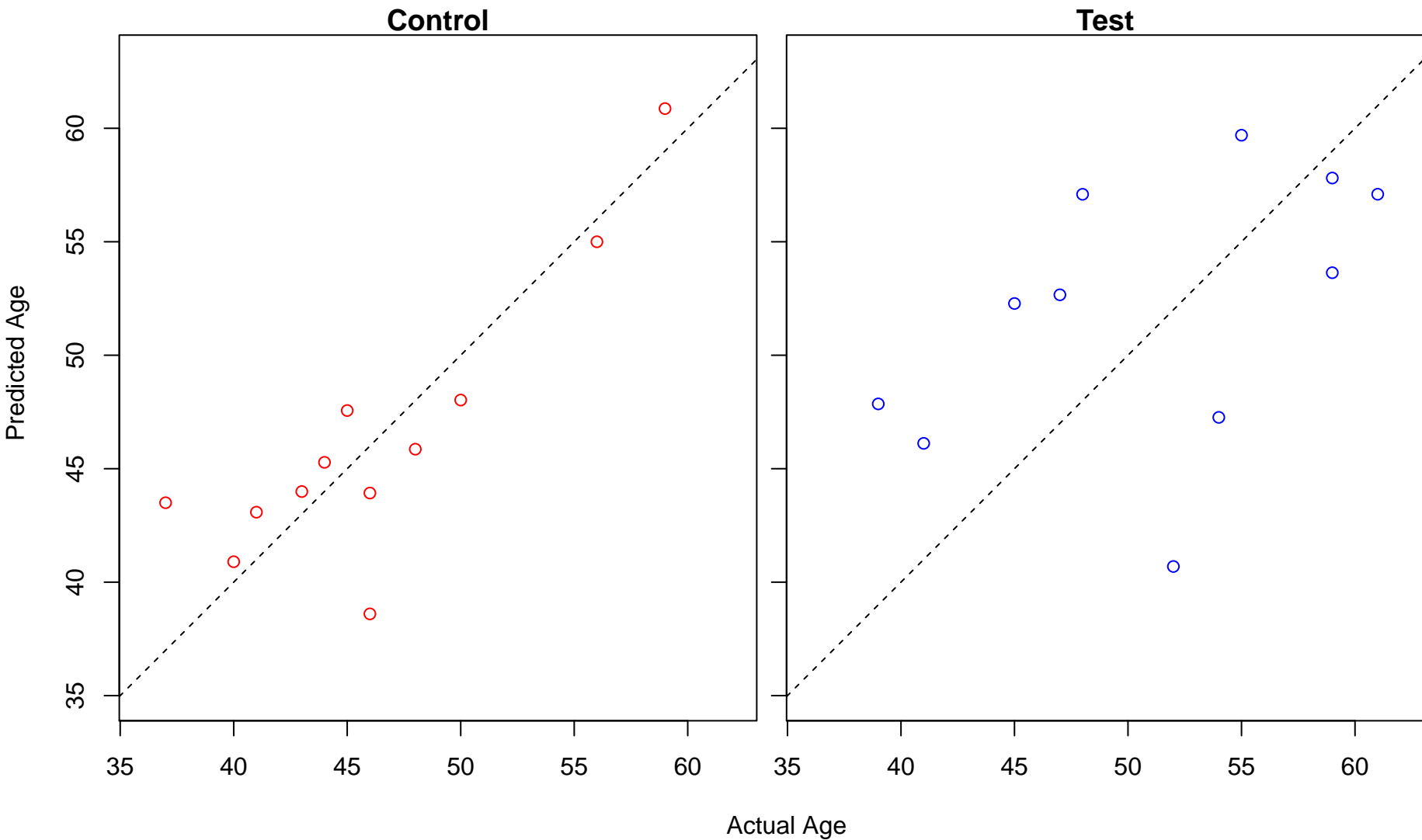
negative regulation of lipase activity (Score: 7.428661)



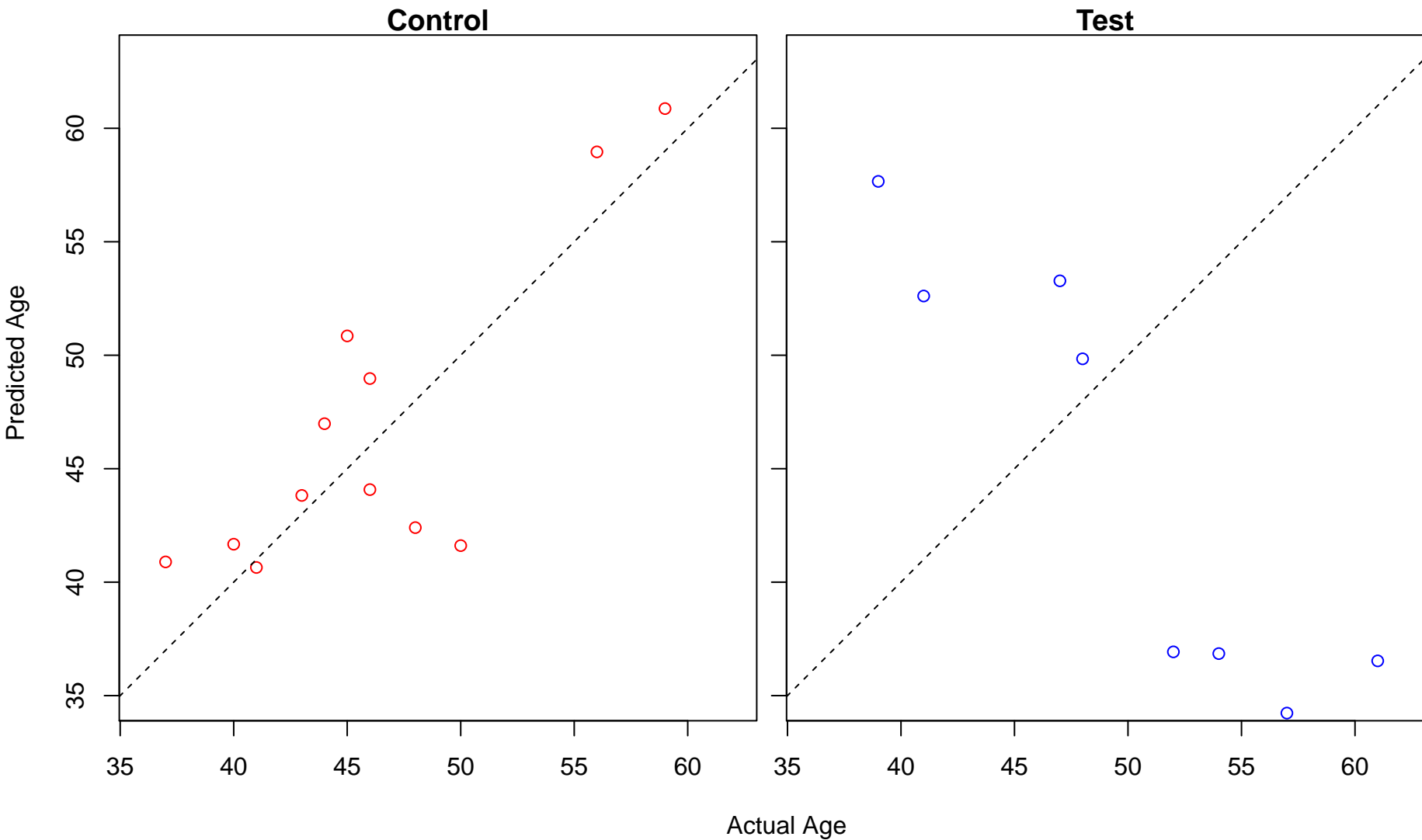
protein targeting to vacuole (Score: 7.423714)



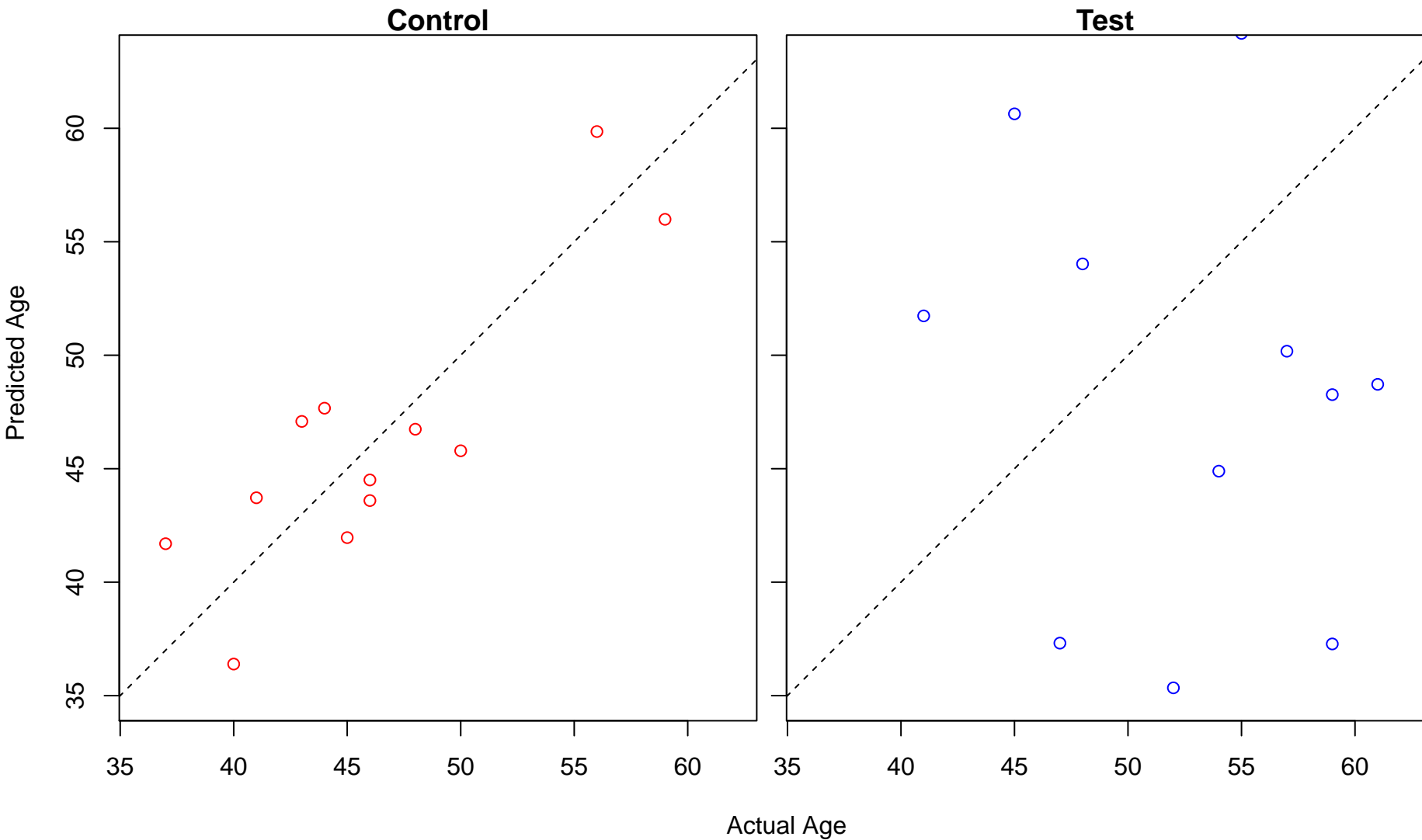
establishment of protein localization to vacuole (Score: 7.423714)



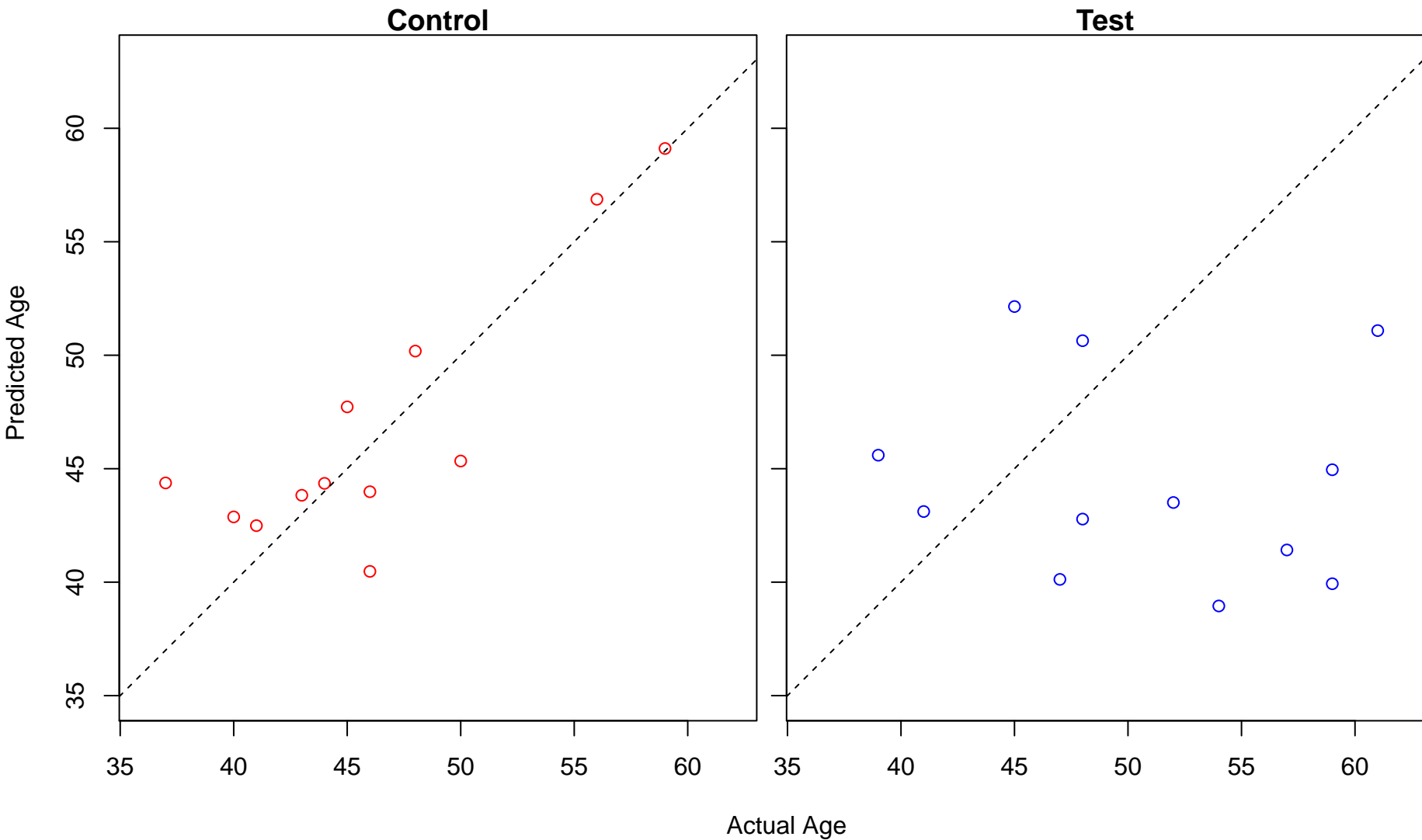
fatty acid alpha-oxidation (Score: 7.419602)



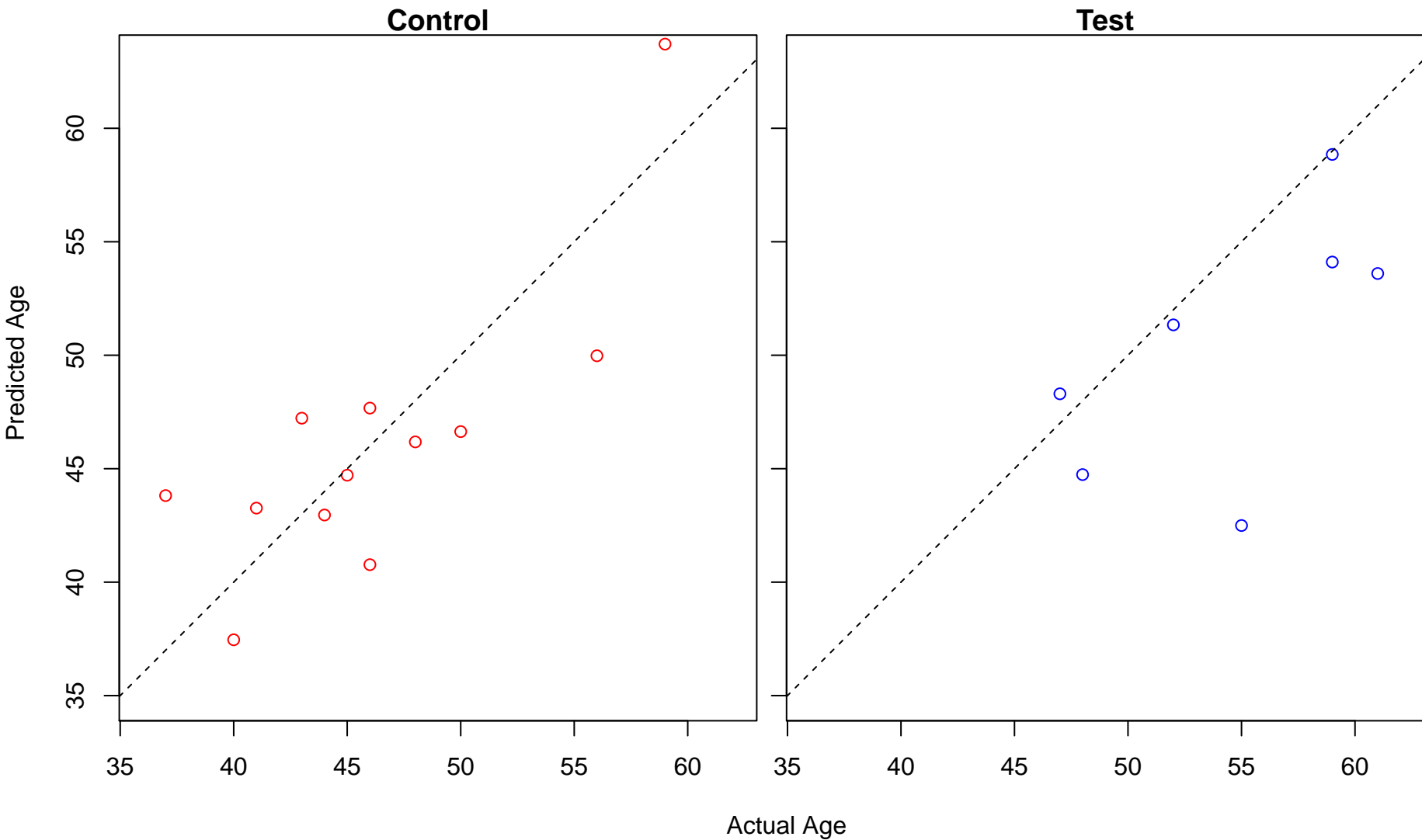
regulation of macroautophagy (Score: 7.396784)



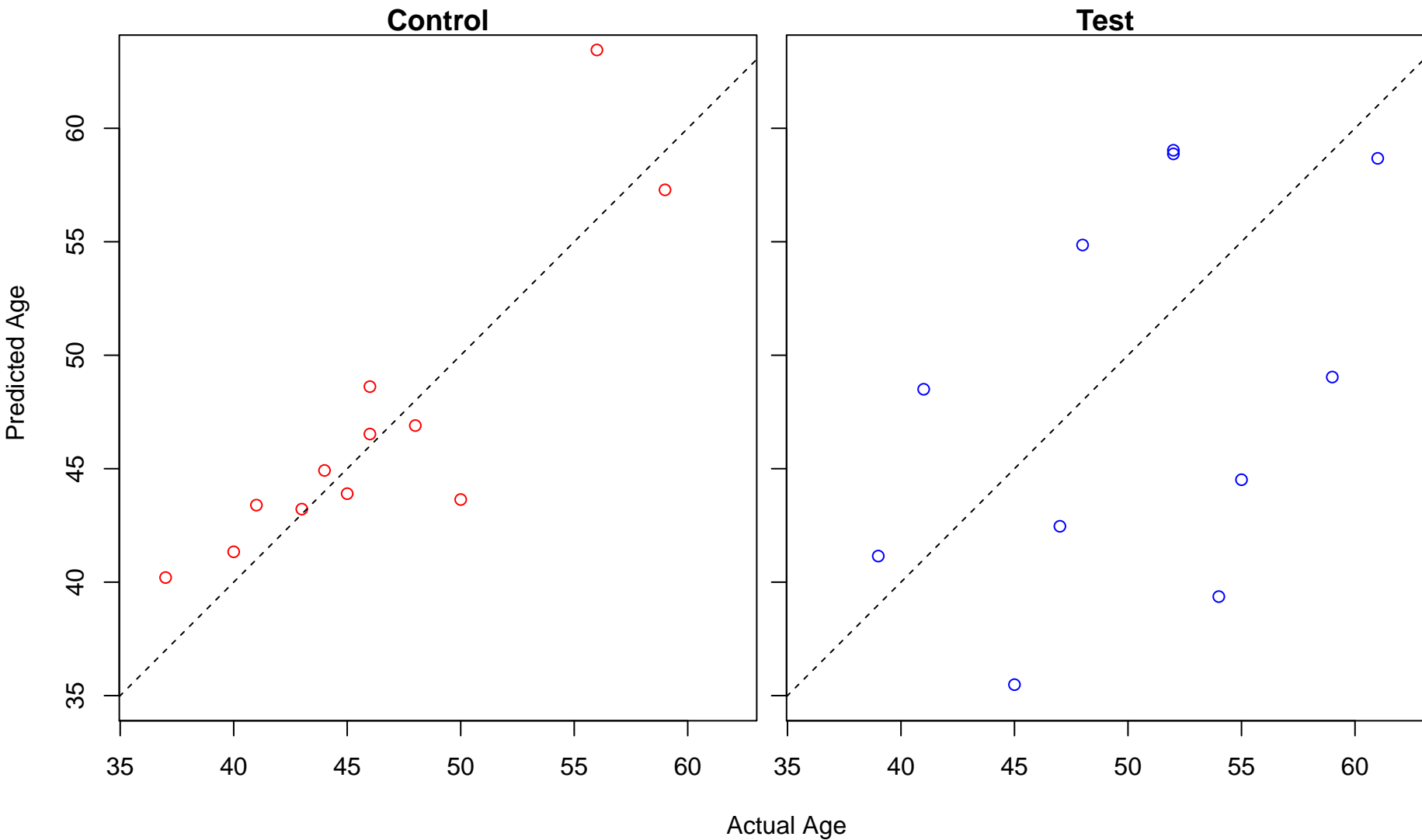
glycoprotein biosynthetic process (Score: 7.379442)



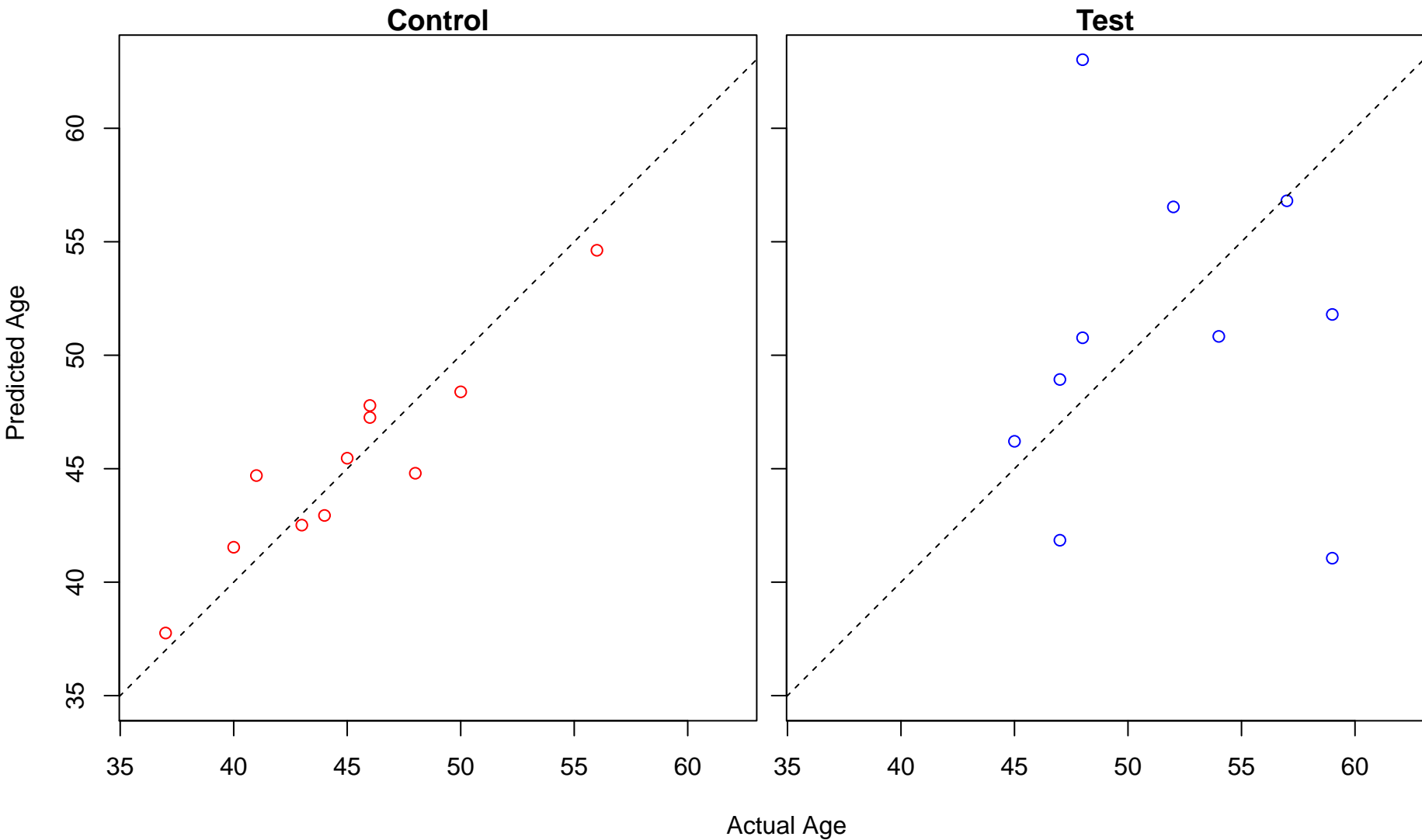
regulation of type B pancreatic cell apoptotic process (Score: 7.370532)



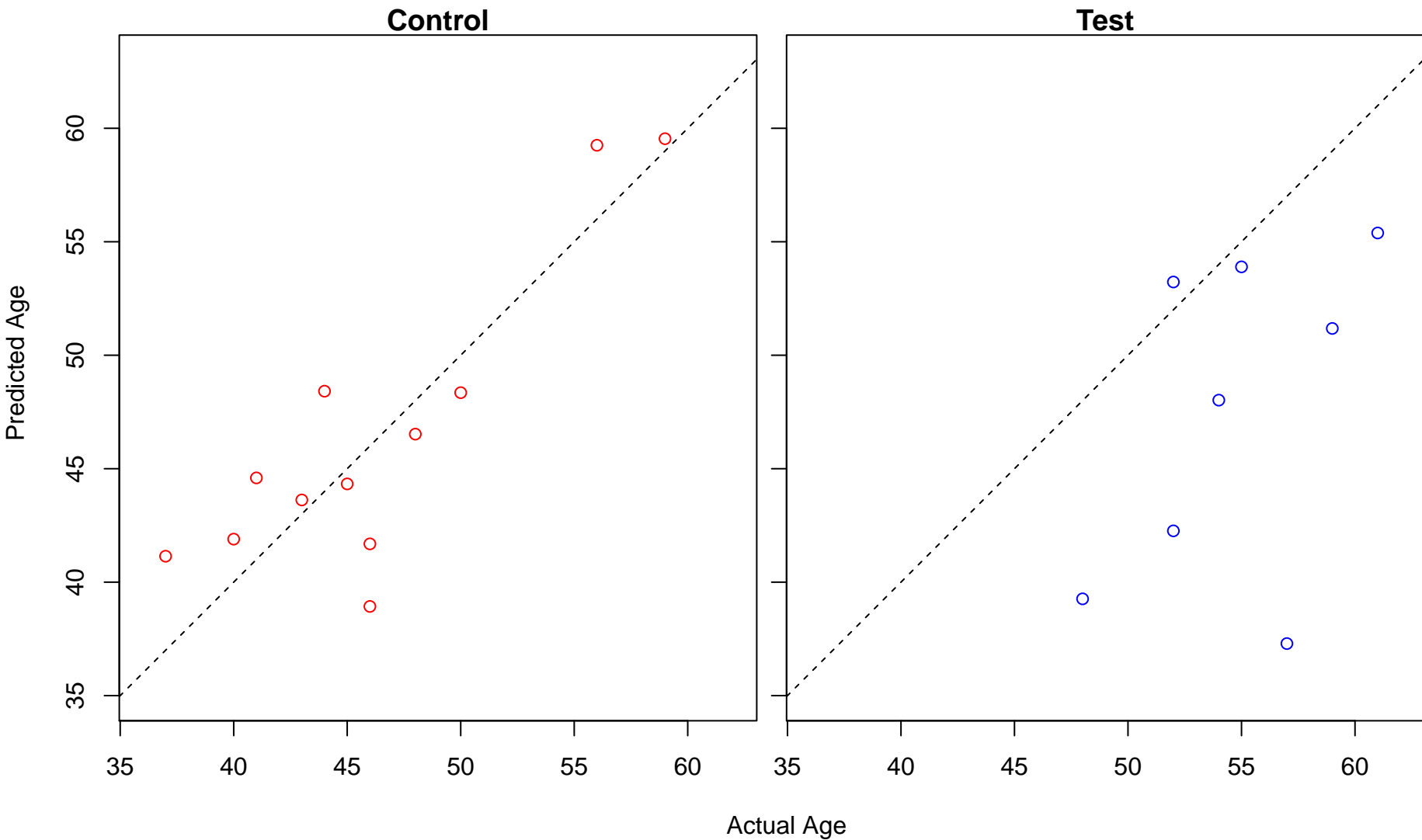
bone development (Score: 7.369980)



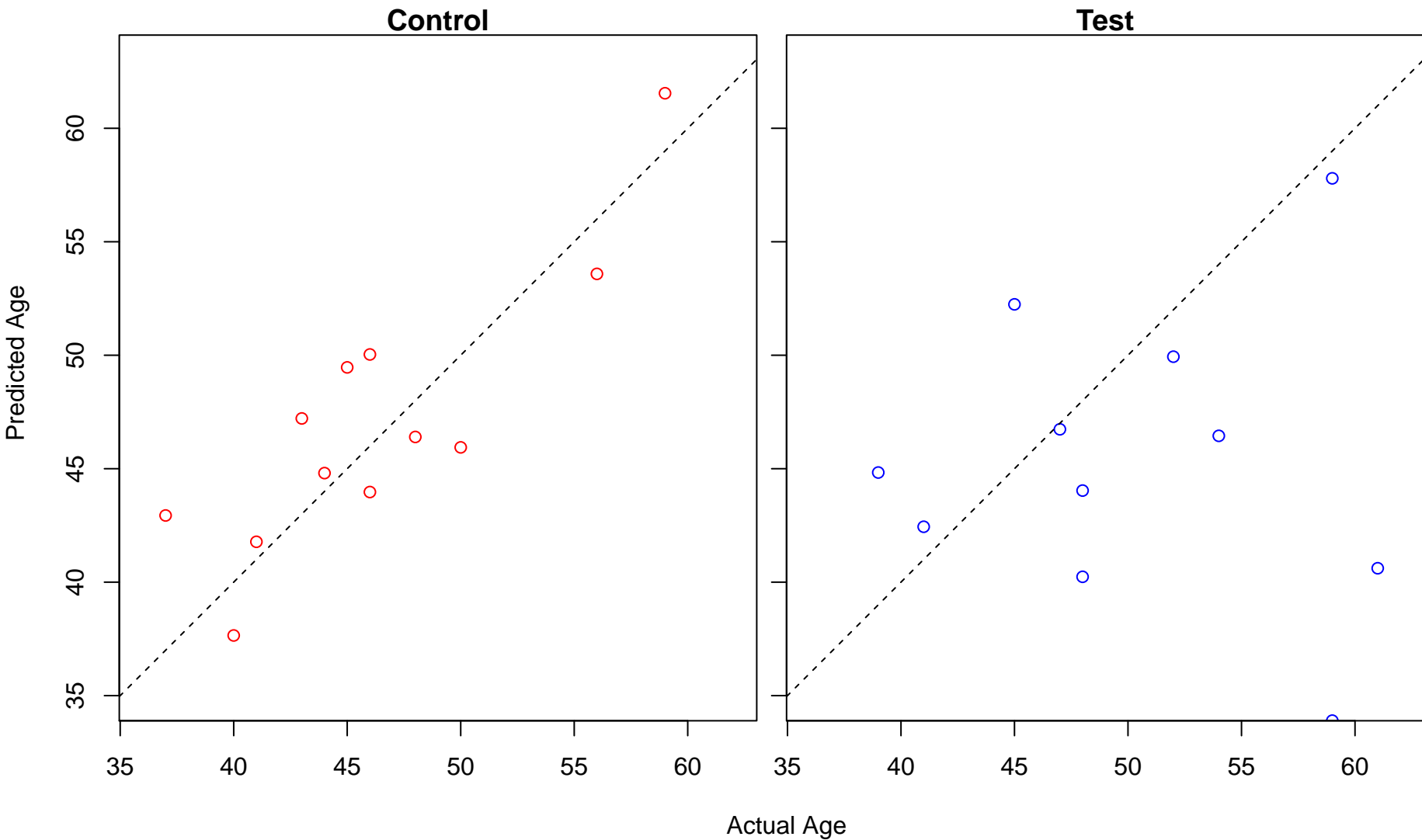
regulation of cholesterol metabolic process (Score: 7.344559)



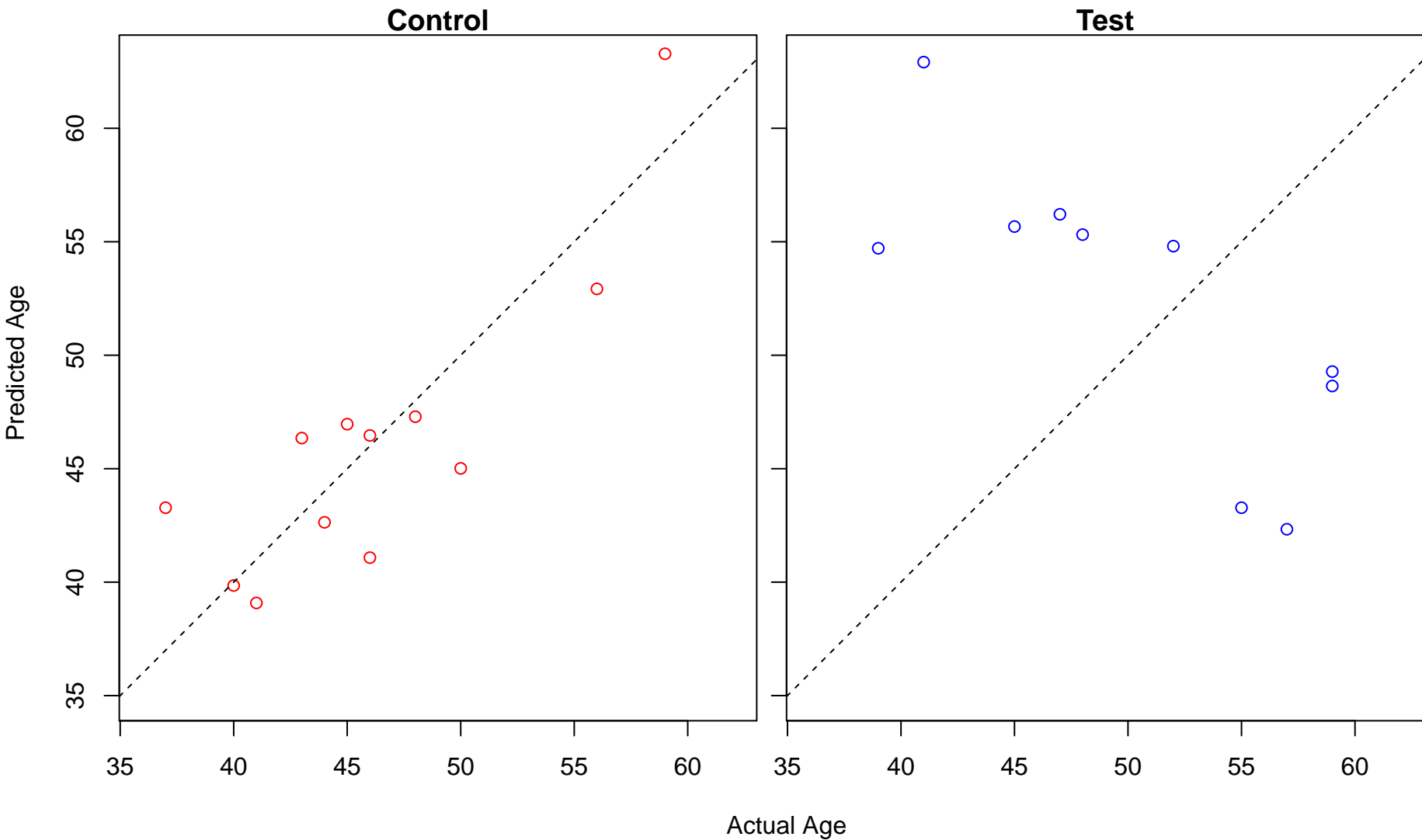
nitric oxide metabolic process (Score: 7.326326)



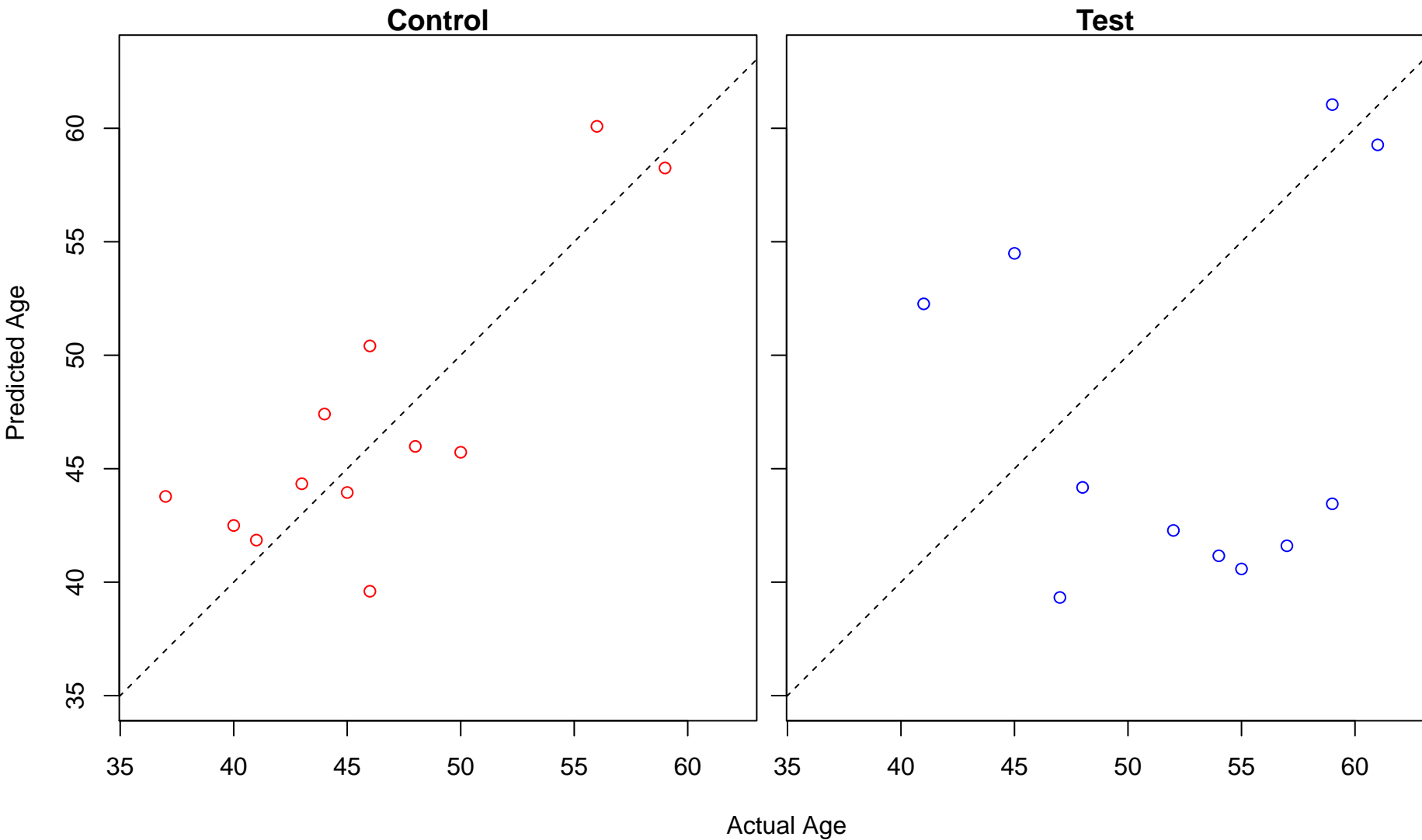
positive regulation of behavior (Score: 7.326194)



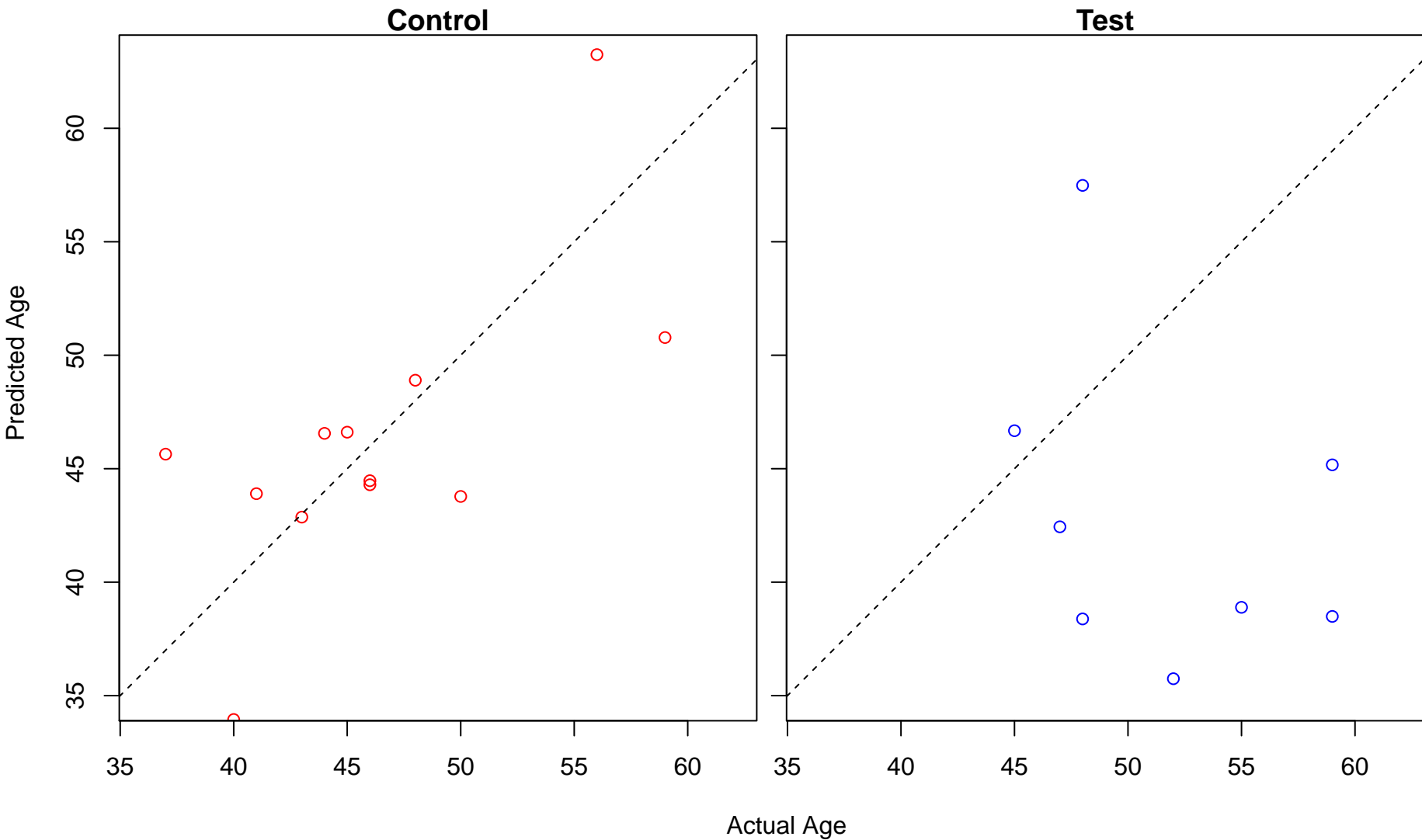
ERAD pathway (Score: 7.319933)



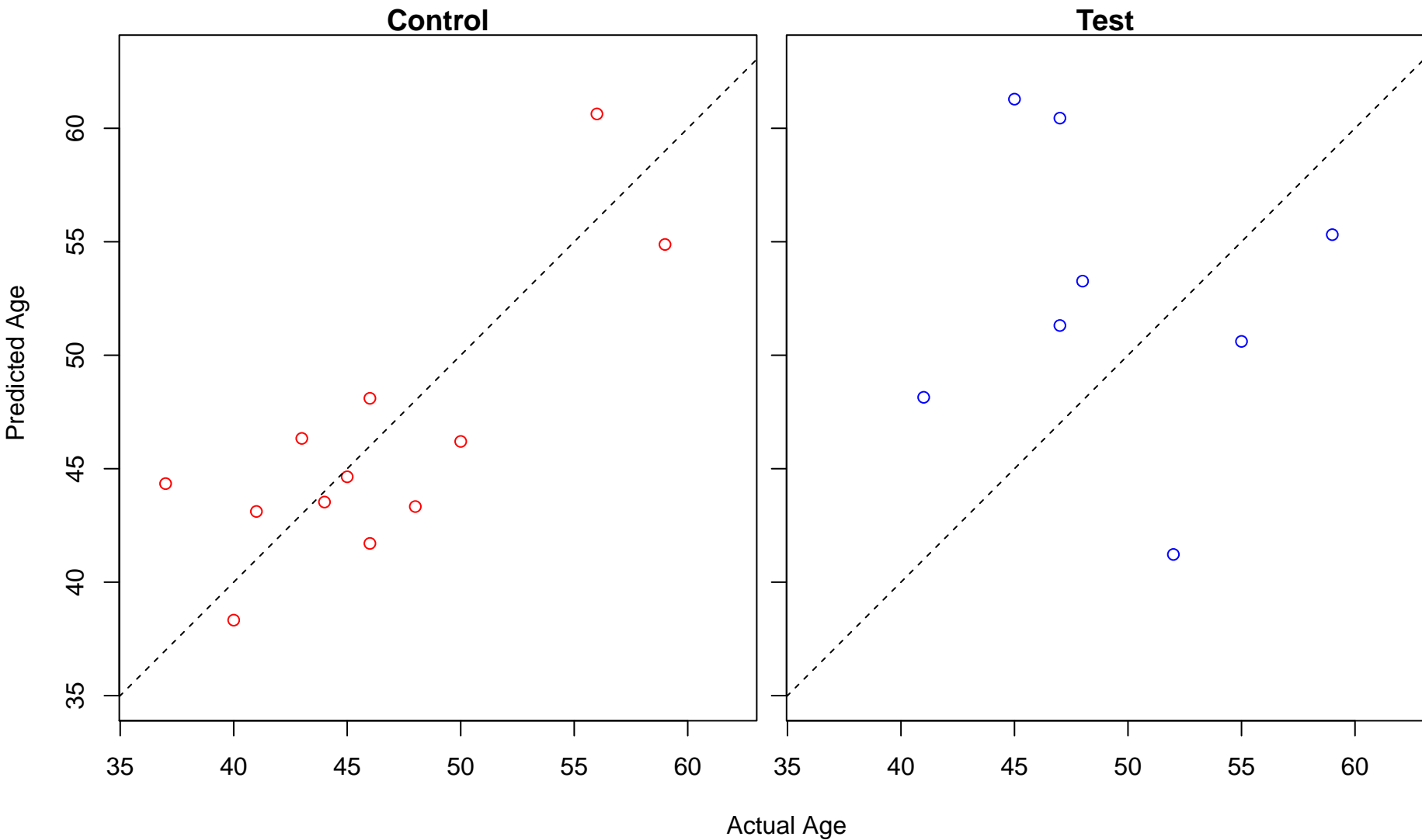
regulation of proteasomal protein catabolic process (Score: 7.318724)



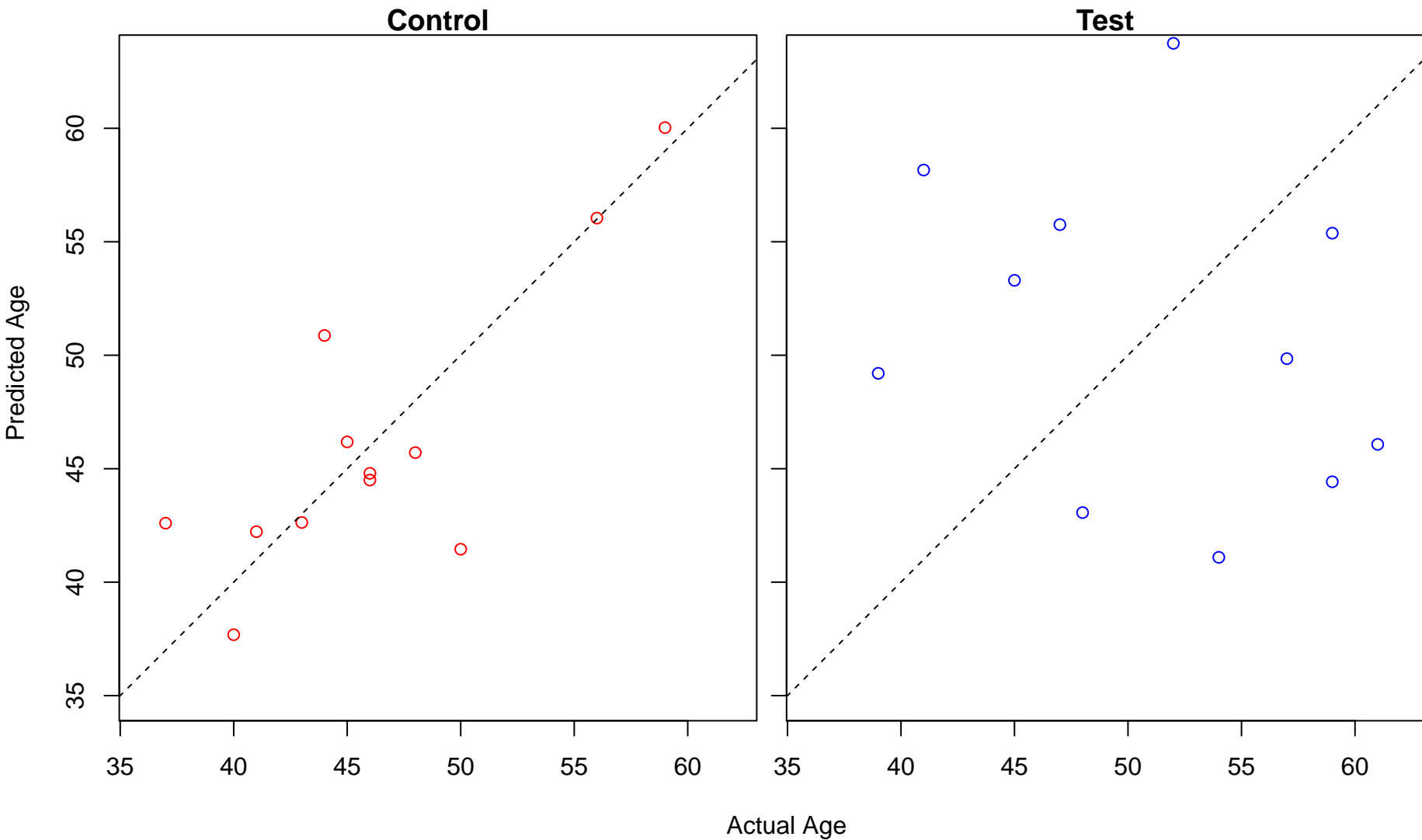
positive regulation of cardiac muscle tissue development (Score: 7.312537)



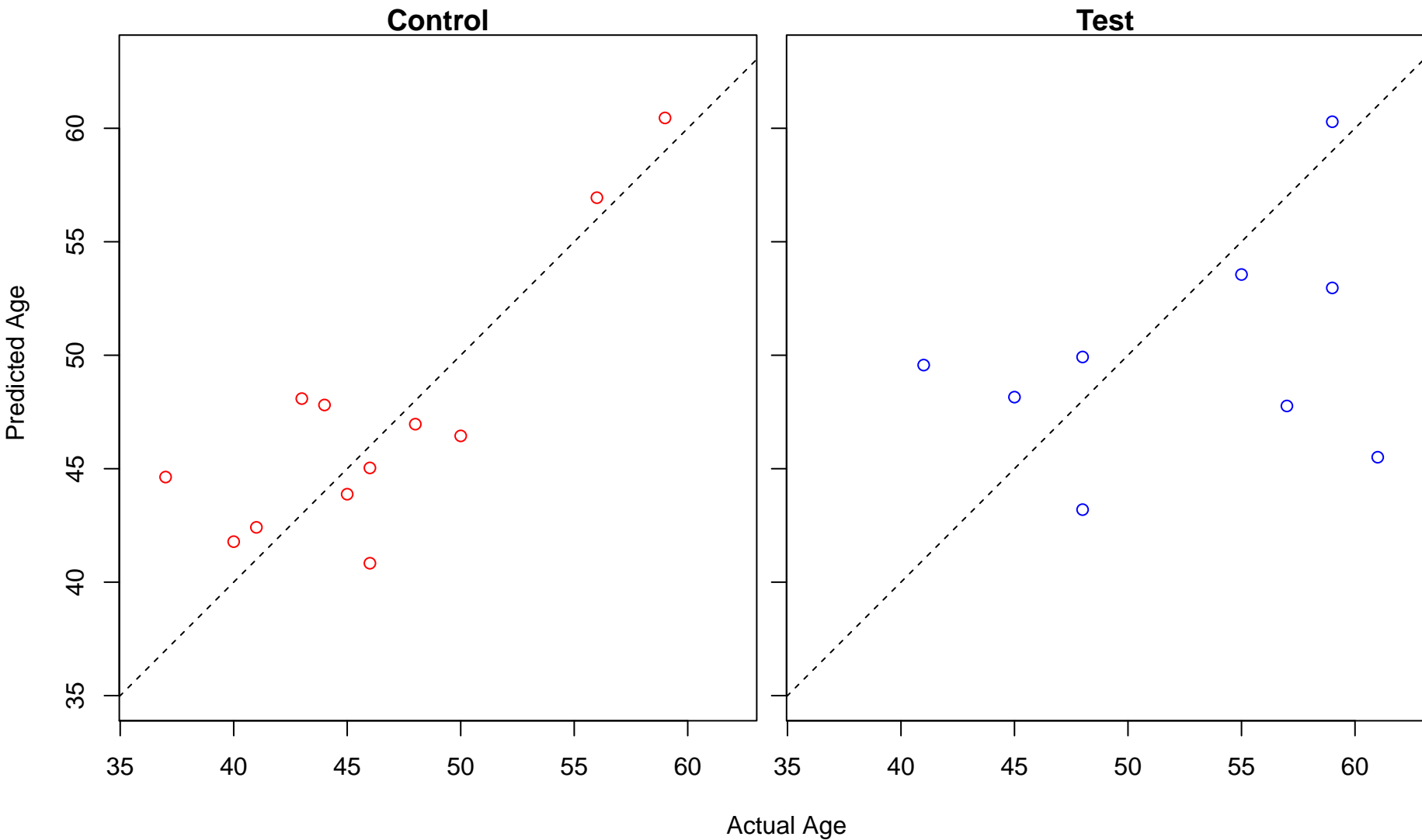
regulation of viral budding via host ESCRT complex (Score: 7.281079)



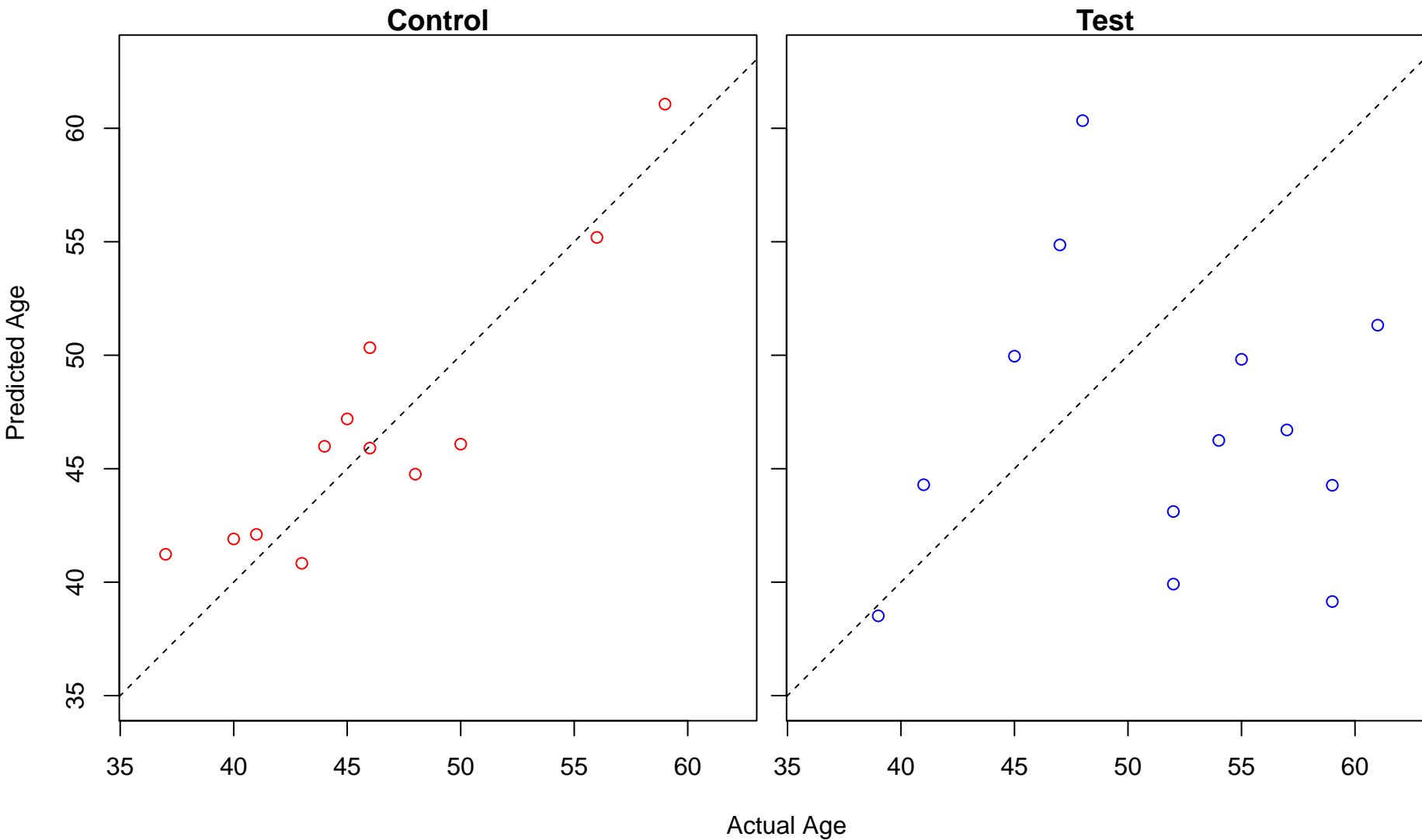
otic vesicle development (Score: 7.278641)



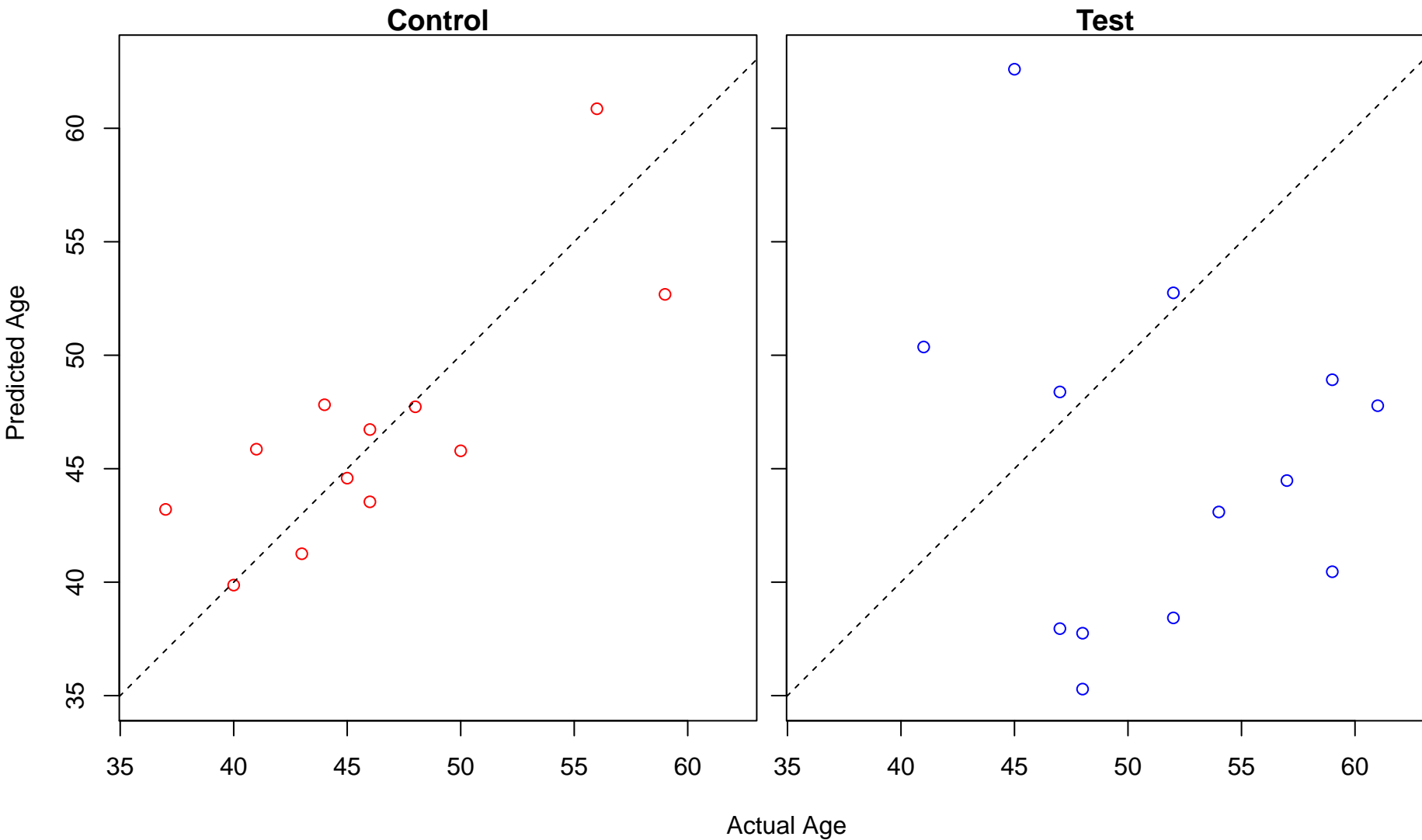
regulation of actin filament bundle assembly (Score: 7.254840)



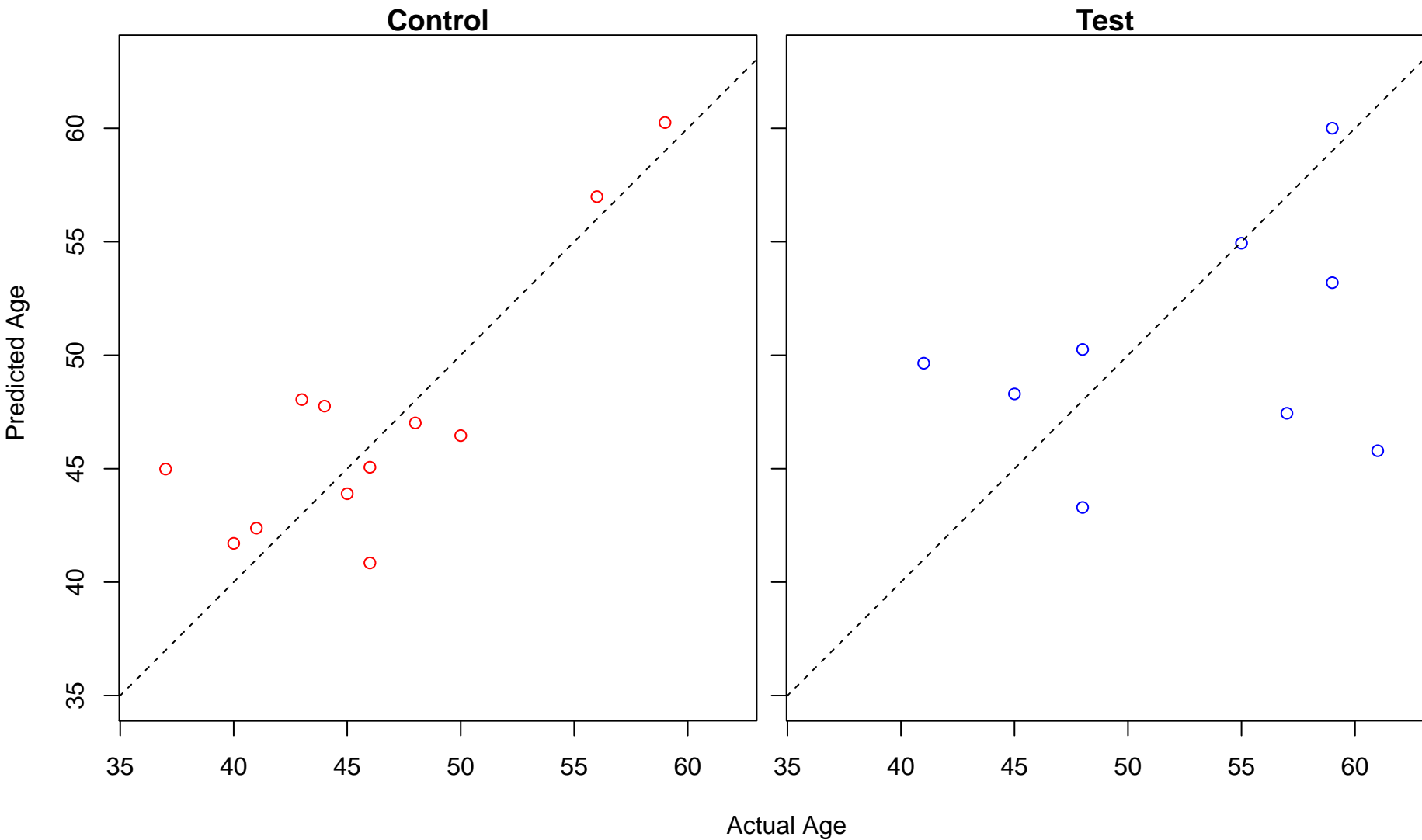
central nervous system neuron differentiation (Score: 7.243936)



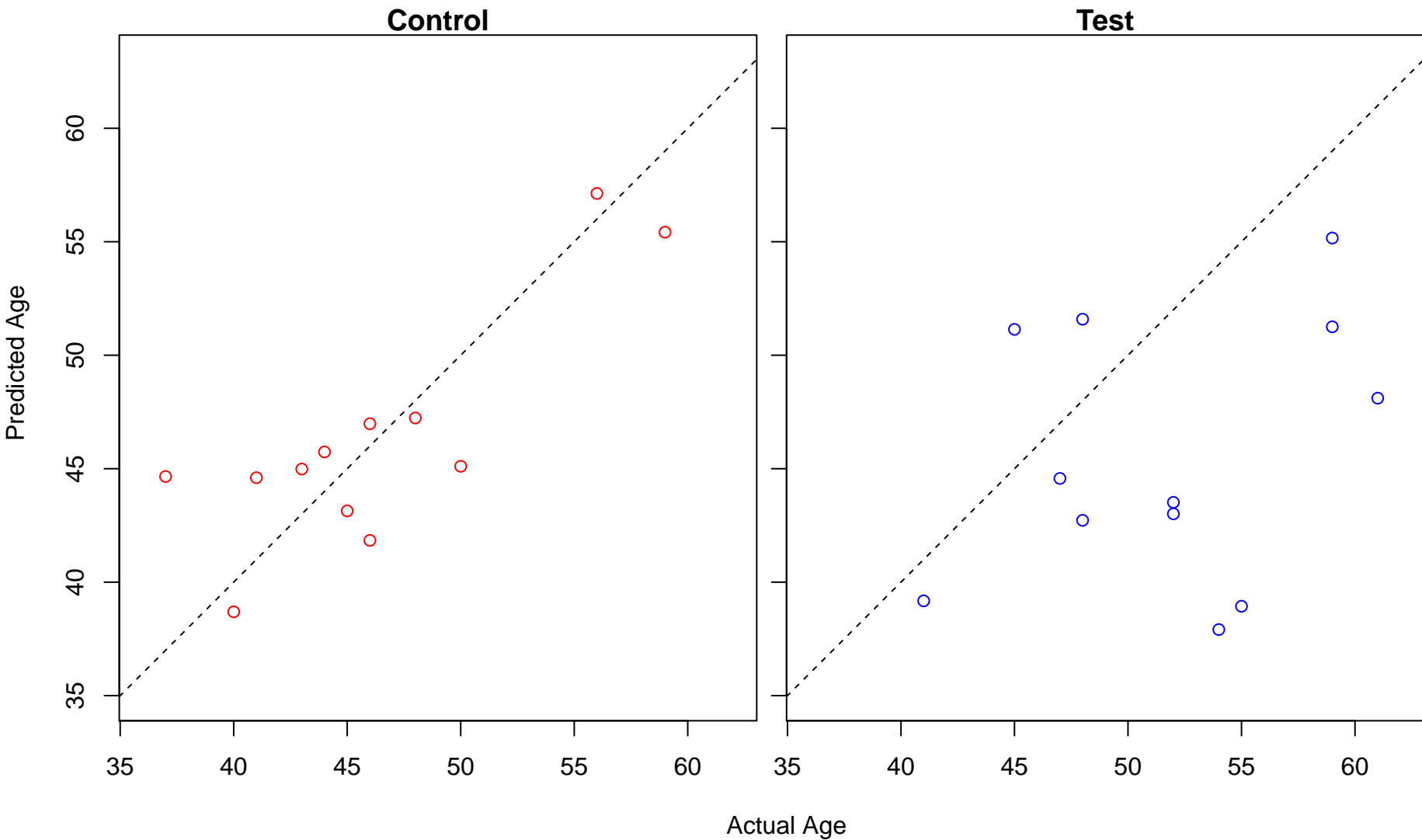
regulation of phagocytosis (Score: 7.242769)



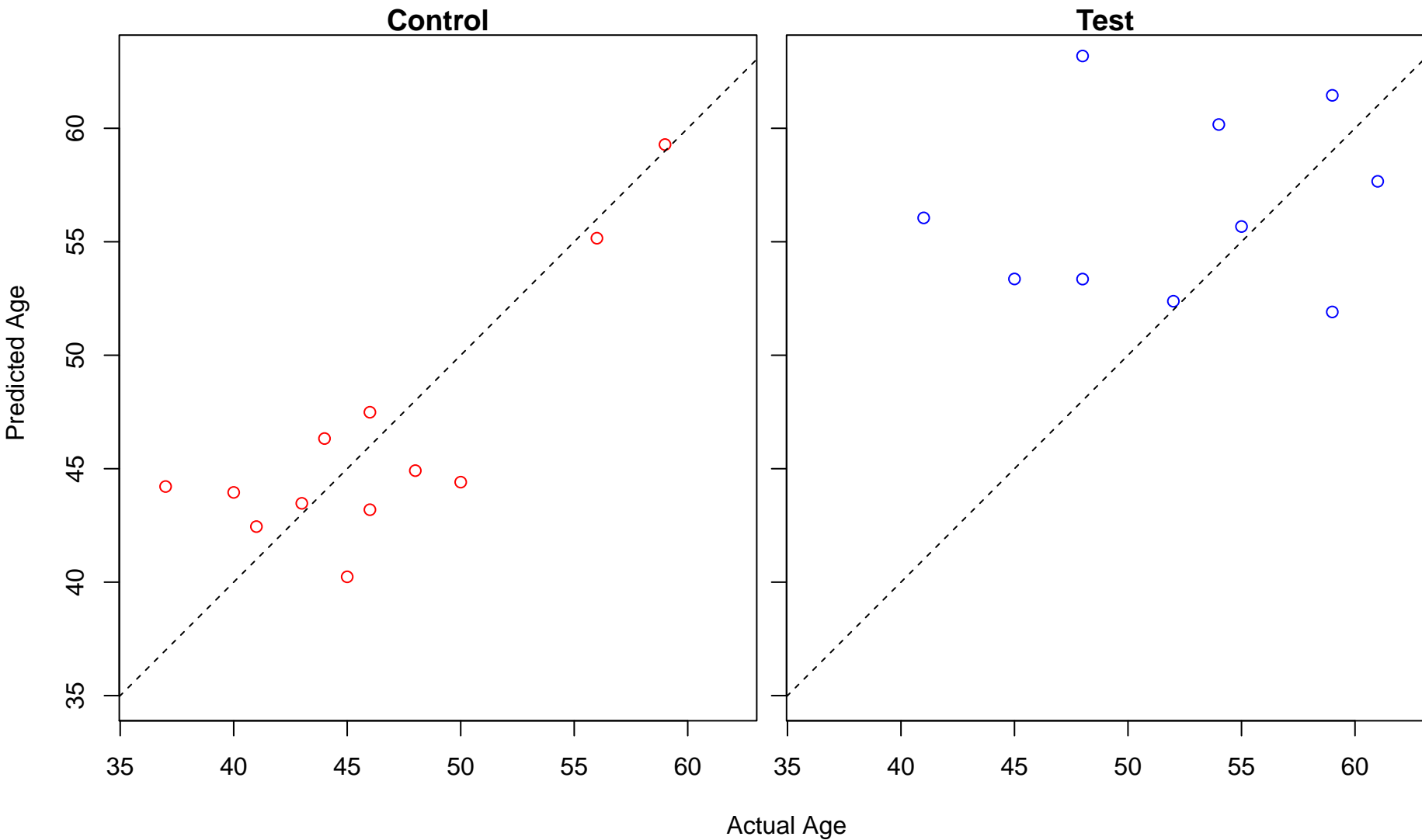
regulation of stress fiber assembly (Score: 7.234987)



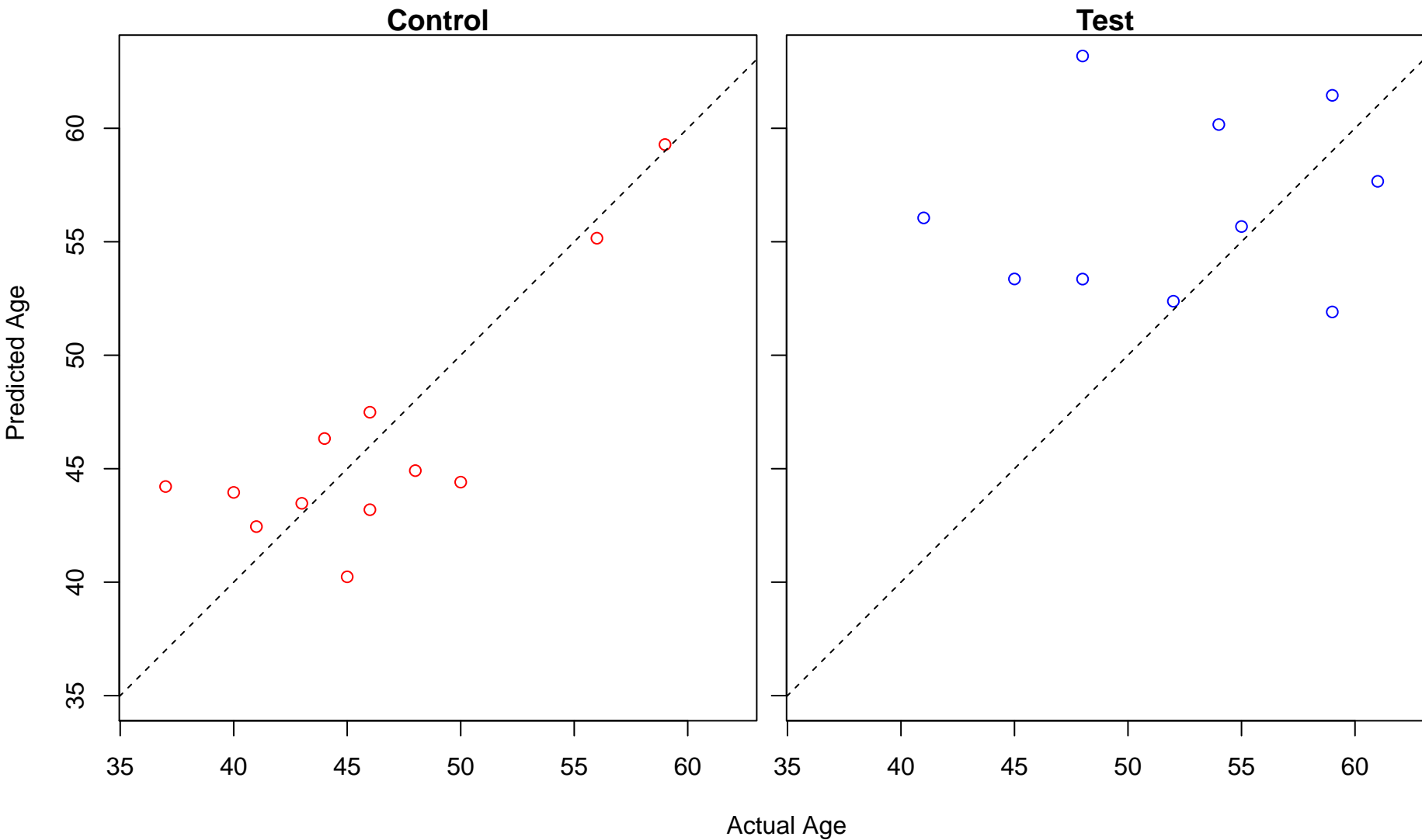
positive regulation of viral process (Score: 7.233856)



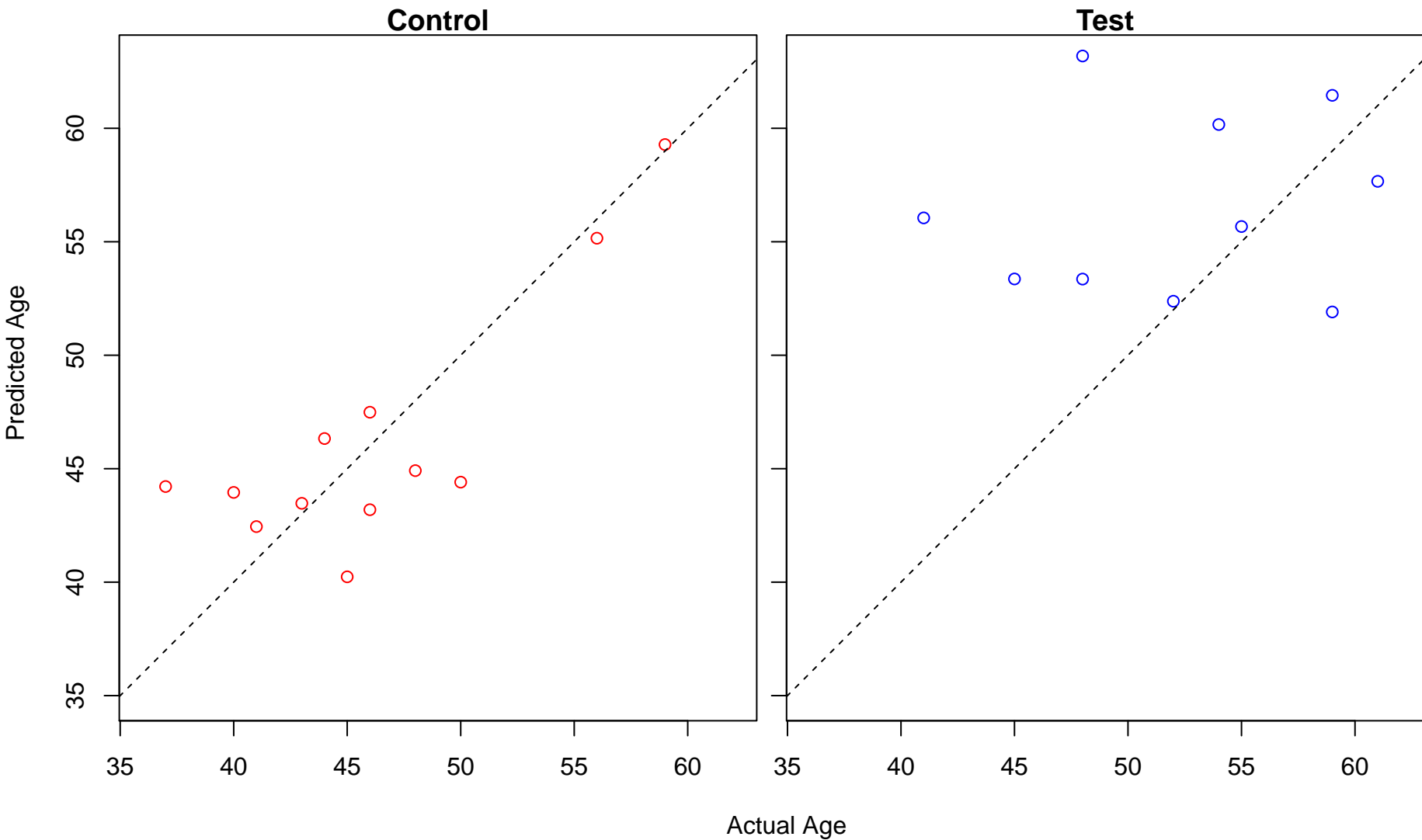
response to cell cycle checkpoint signaling (Score: 7.228753)



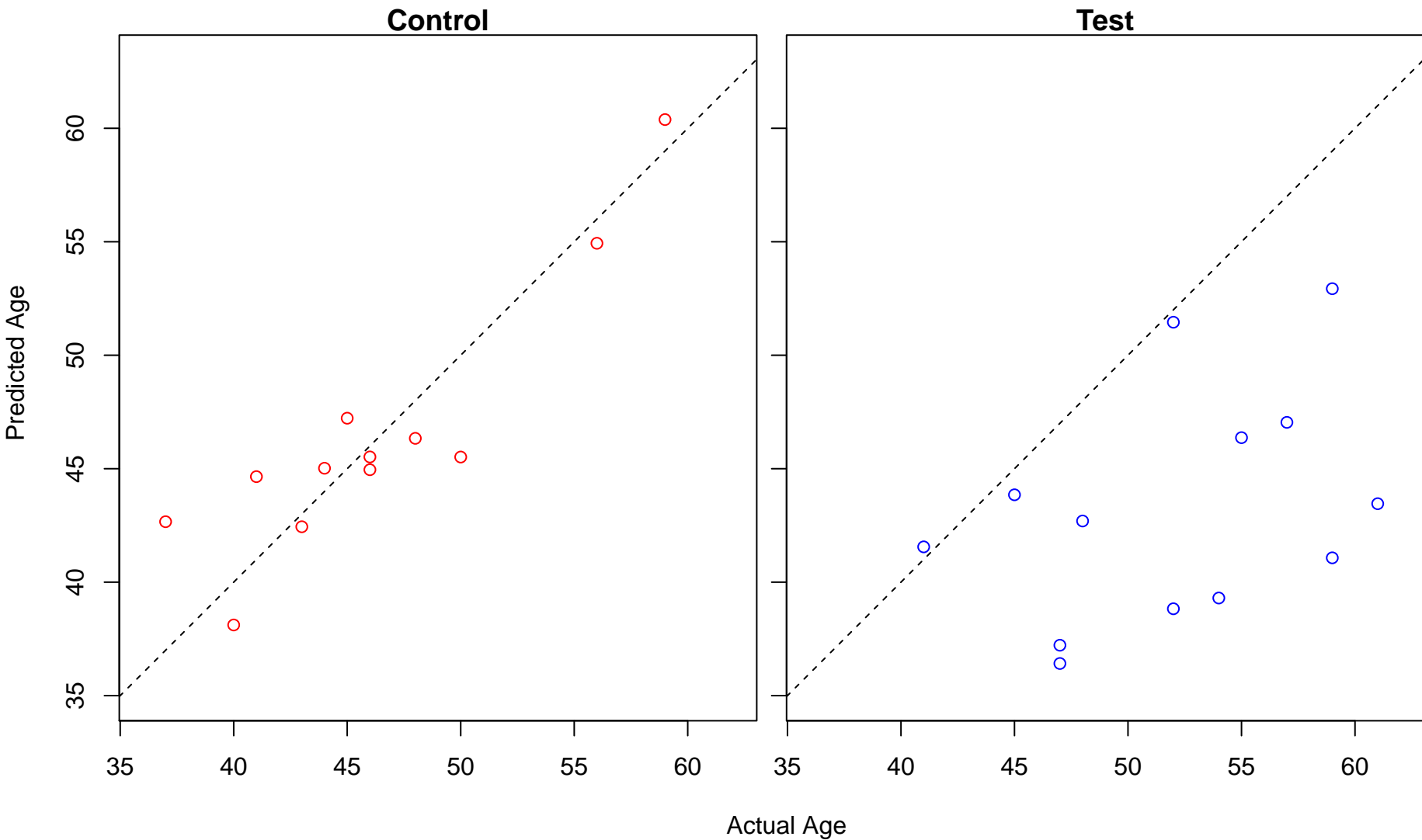
response to DNA integrity checkpoint signaling (Score: 7.228753)



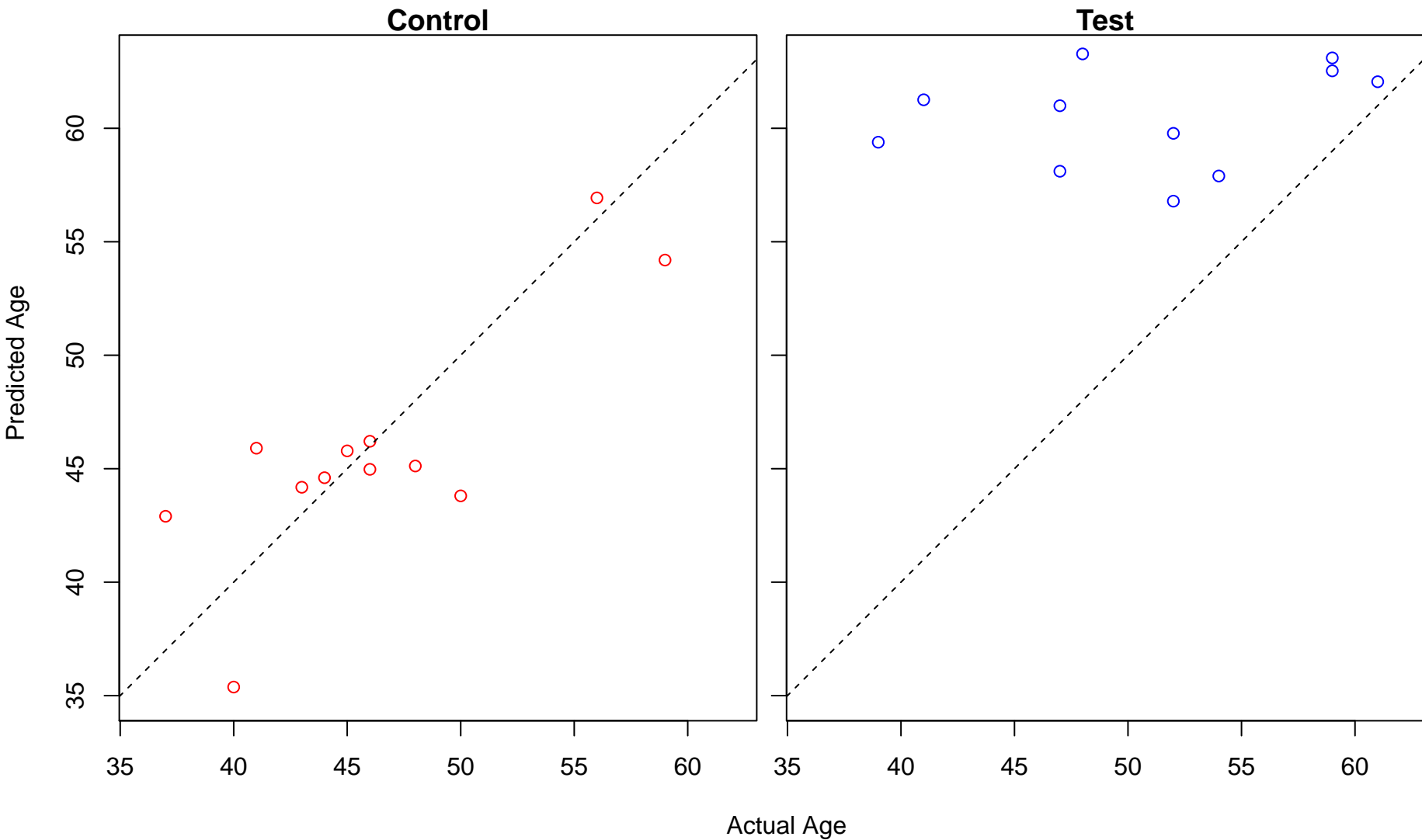
response to DNA damage checkpoint signaling (Score: 7.228753)



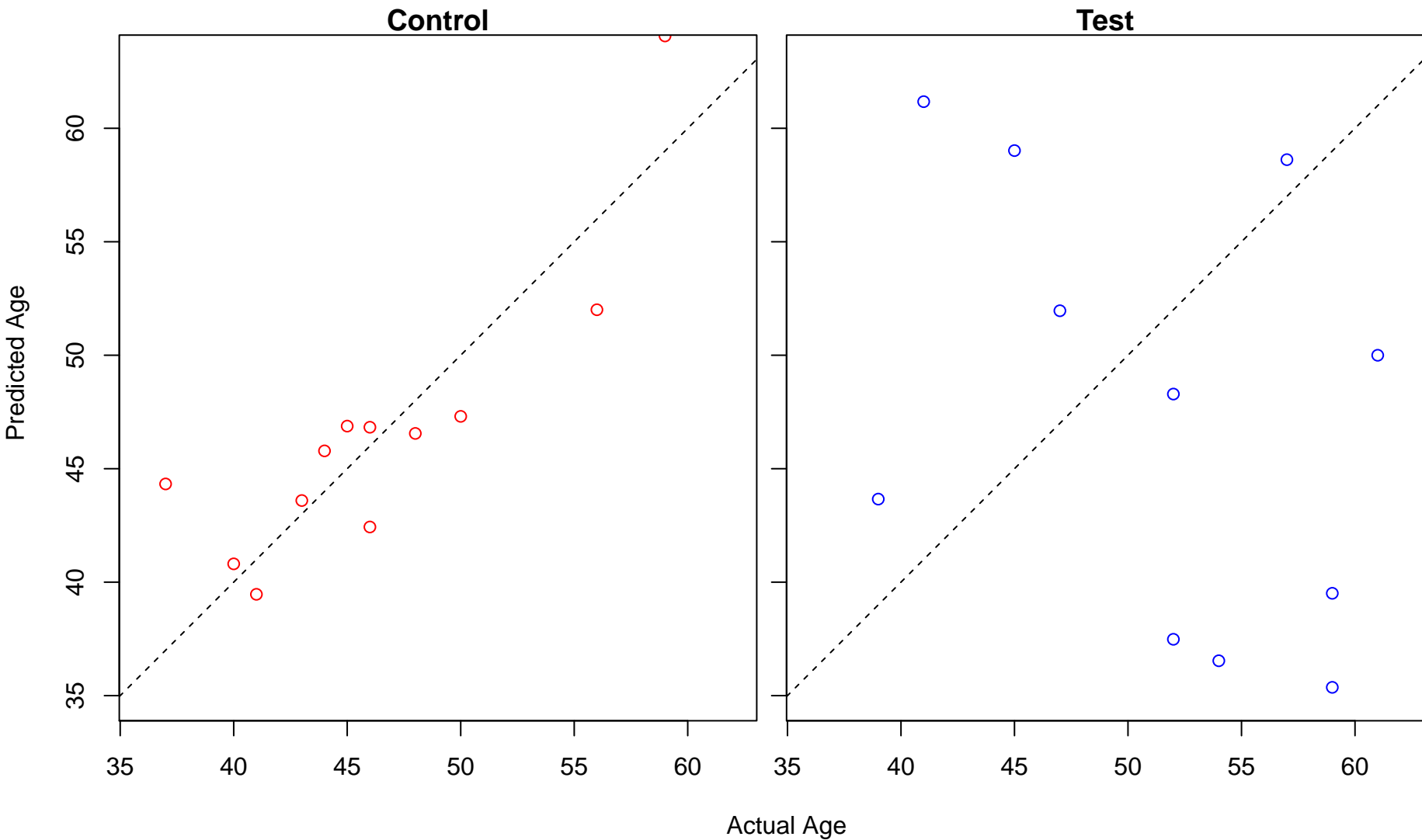
regulation of Ras protein signal transduction (Score: 7.227263)



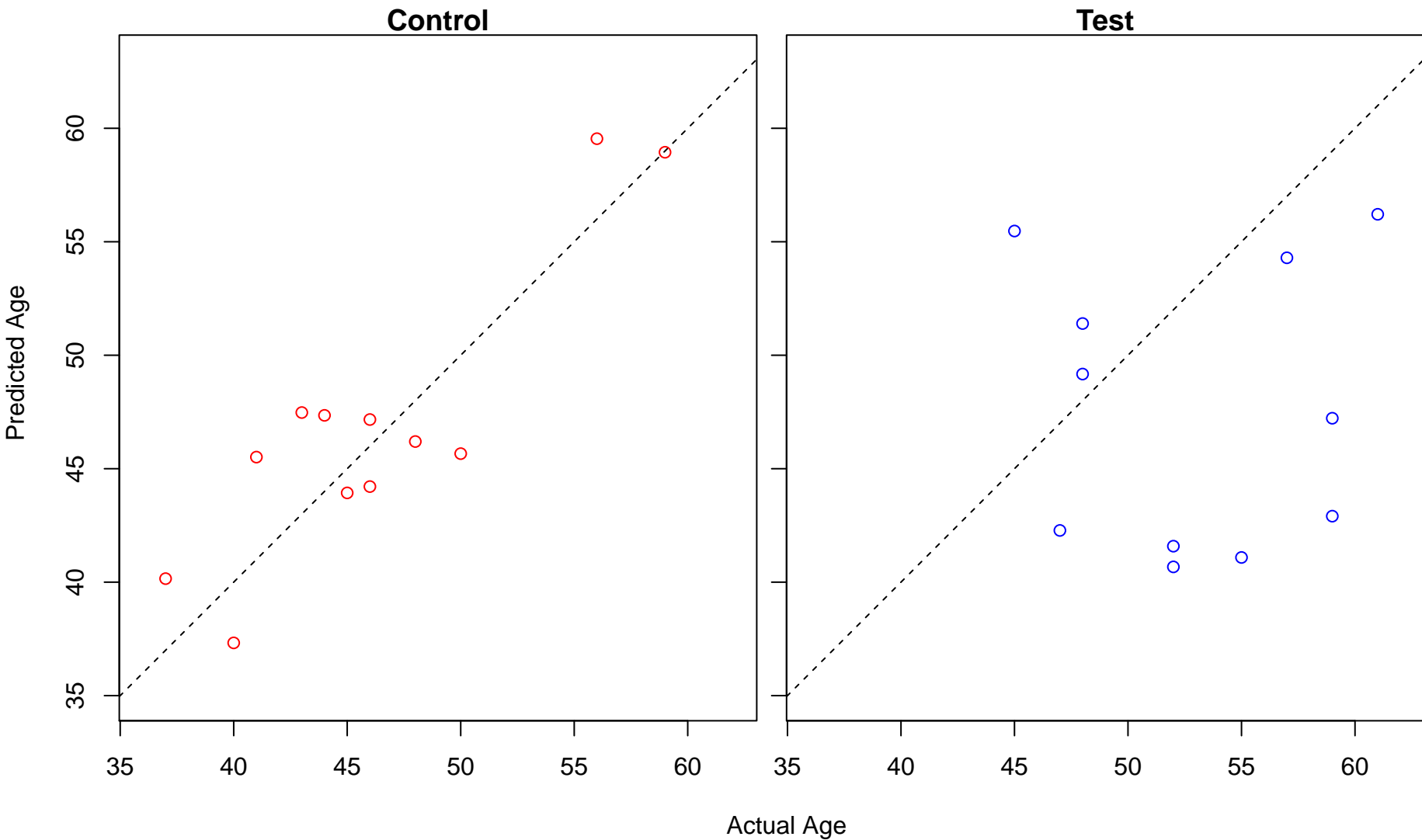
positive regulation of activation of Janus kinase activity (Score: 7.224043)



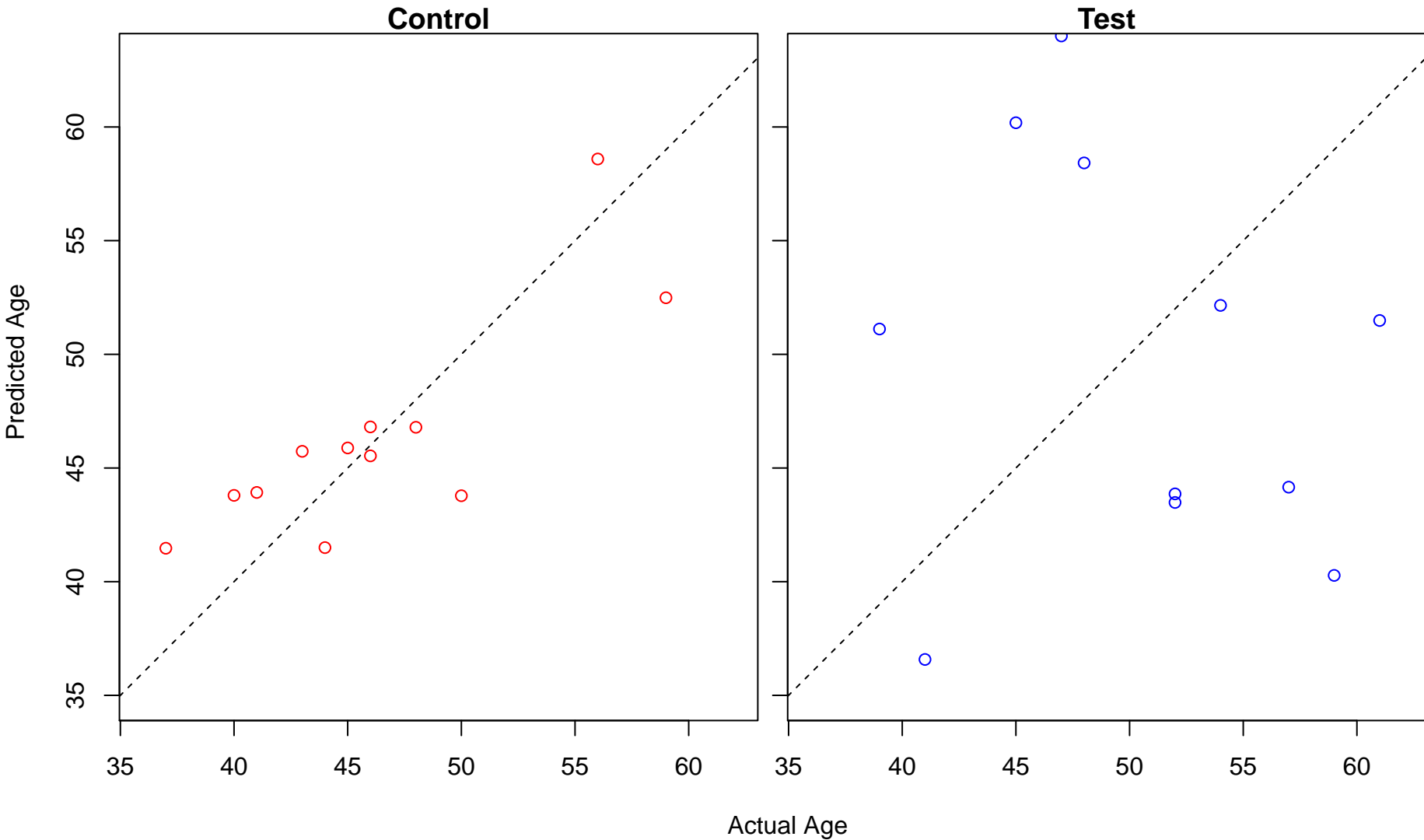
tube morphogenesis (Score: 7.215632)



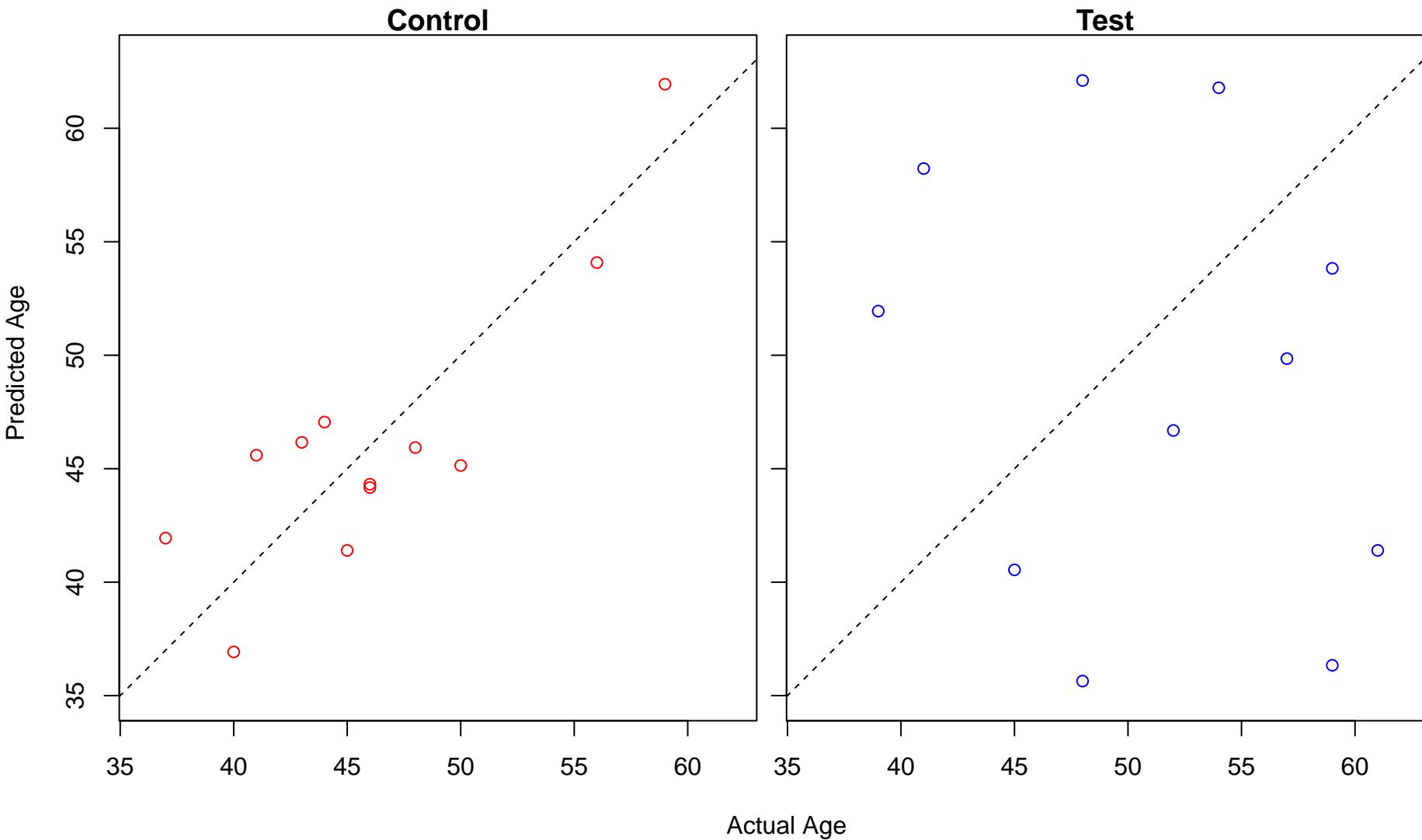
negative regulation of cell motility (Score: 7.201137)



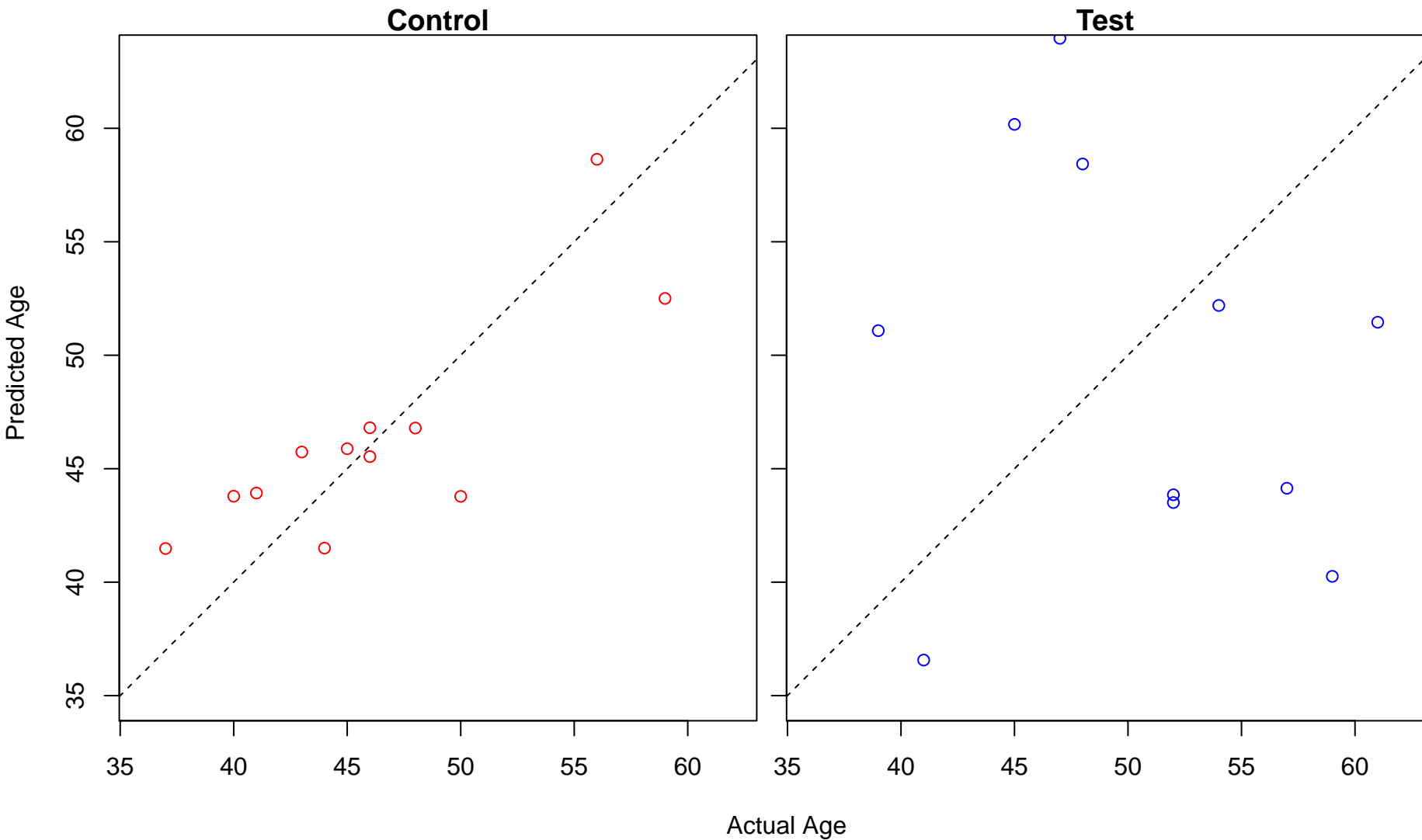
negative regulation of protein activation cascade (Score: 7.200531)



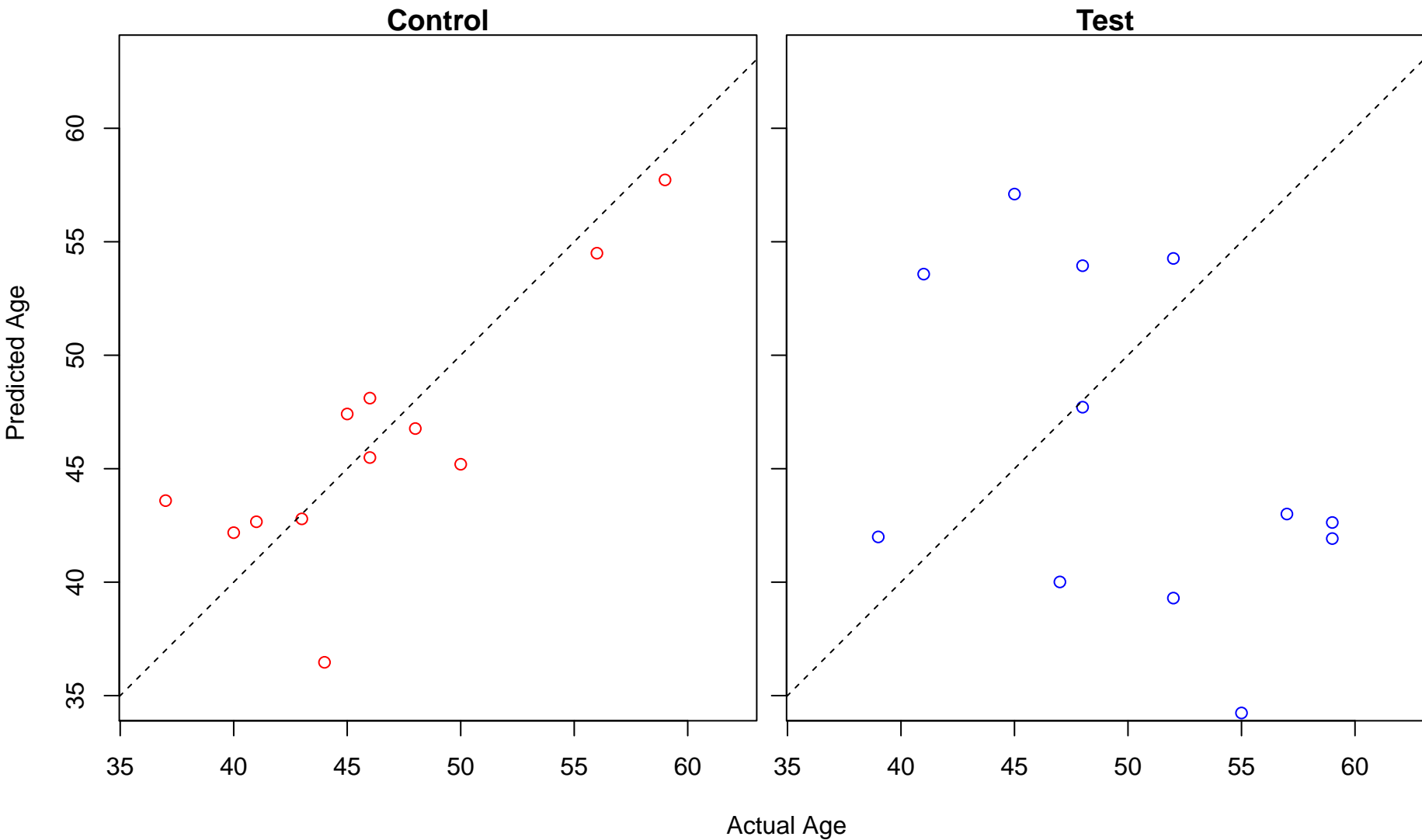
membrane lipid metabolic process (Score: 7.200357)



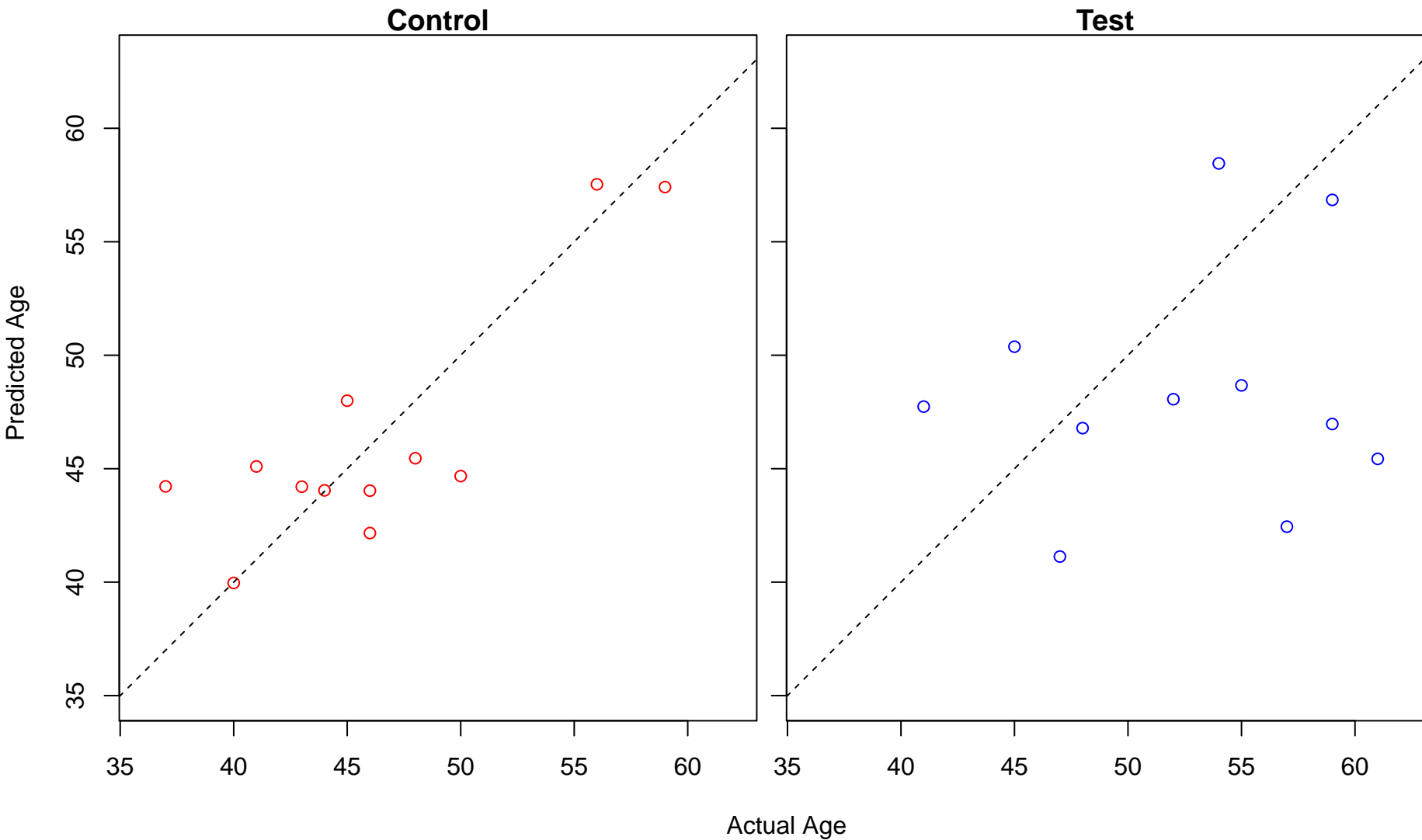
negative regulation of complement activation (Score: 7.199241)



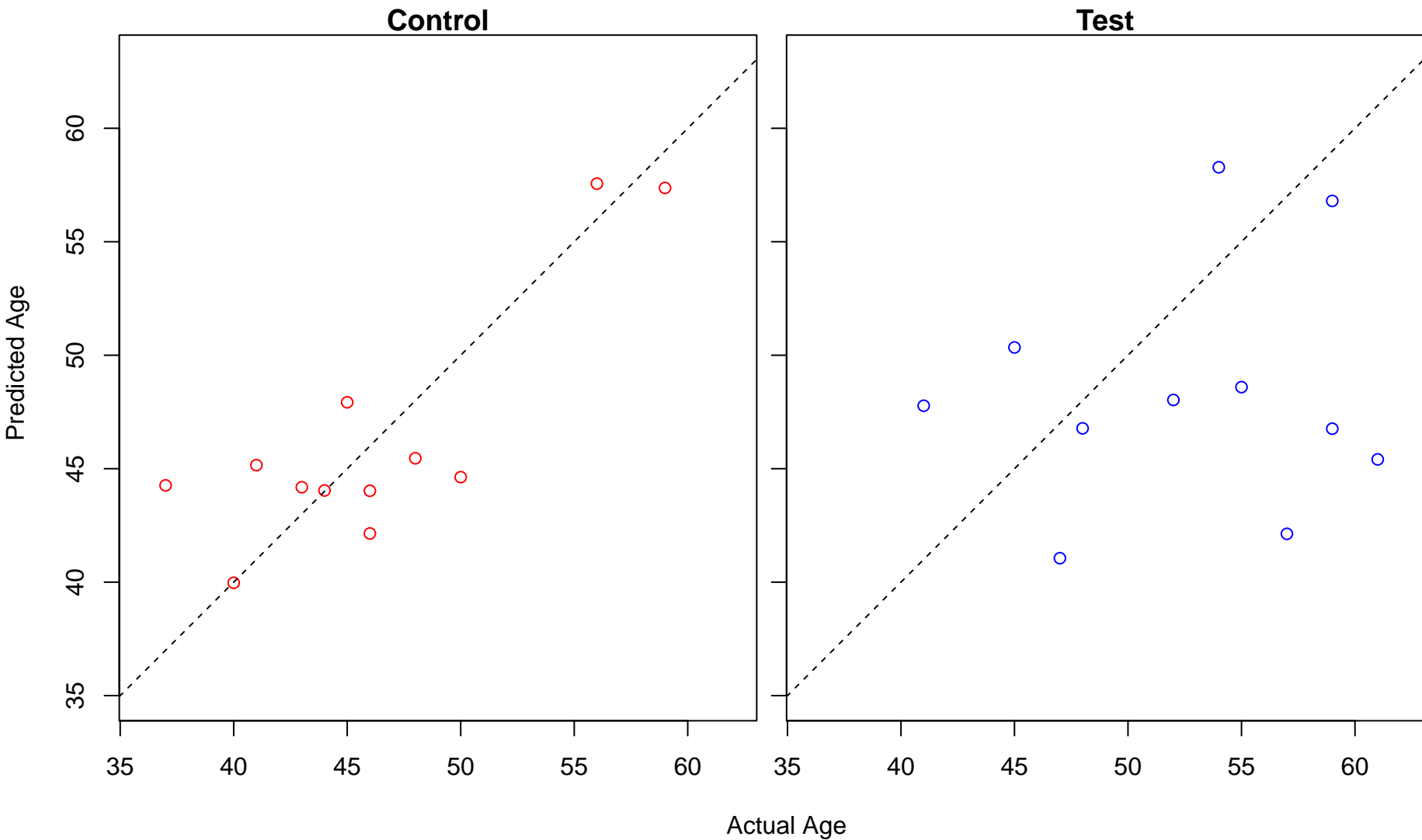
parturition (Score: 7.195845)



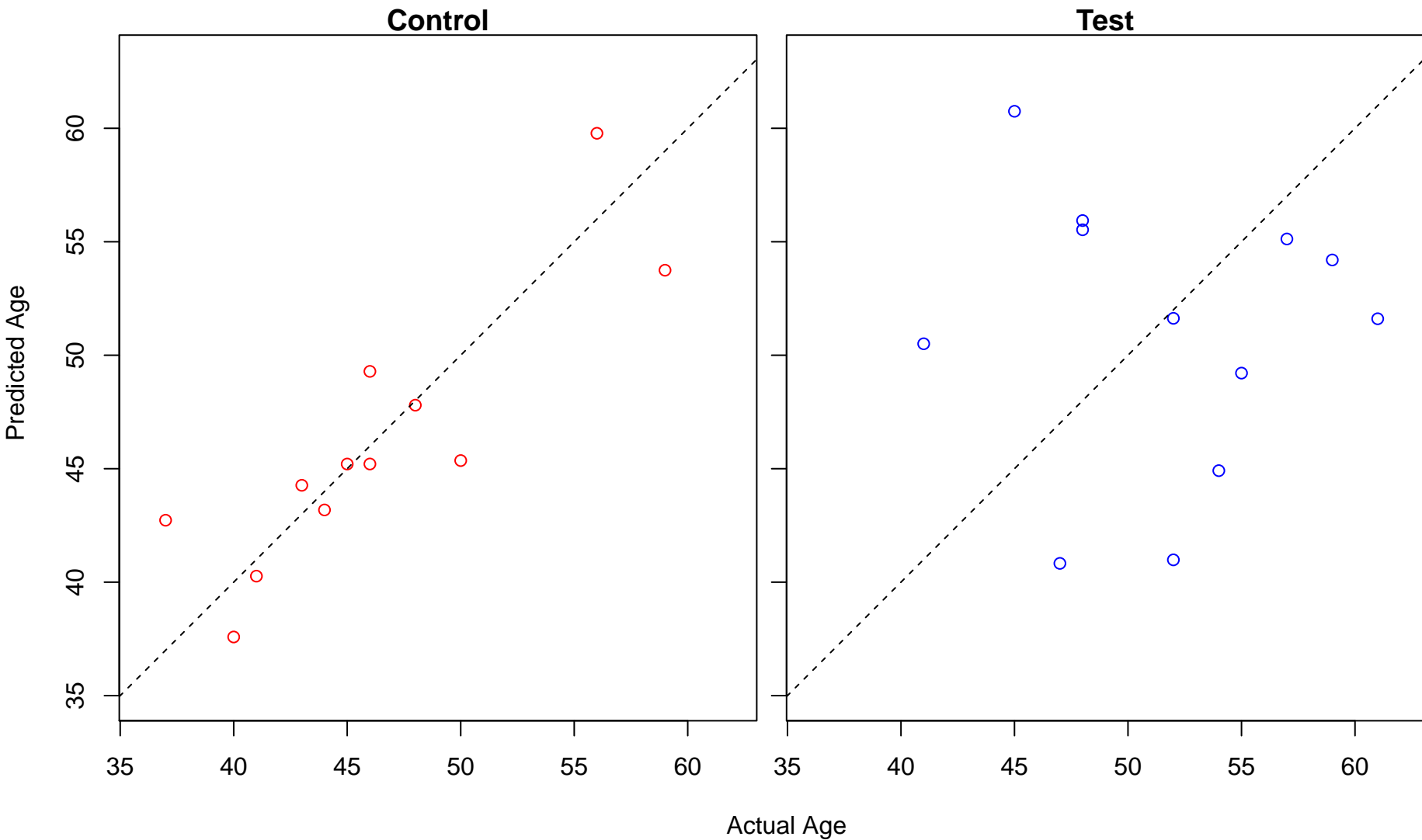
regulation of telomere maintenance via telomerase (Score: 7.184204)



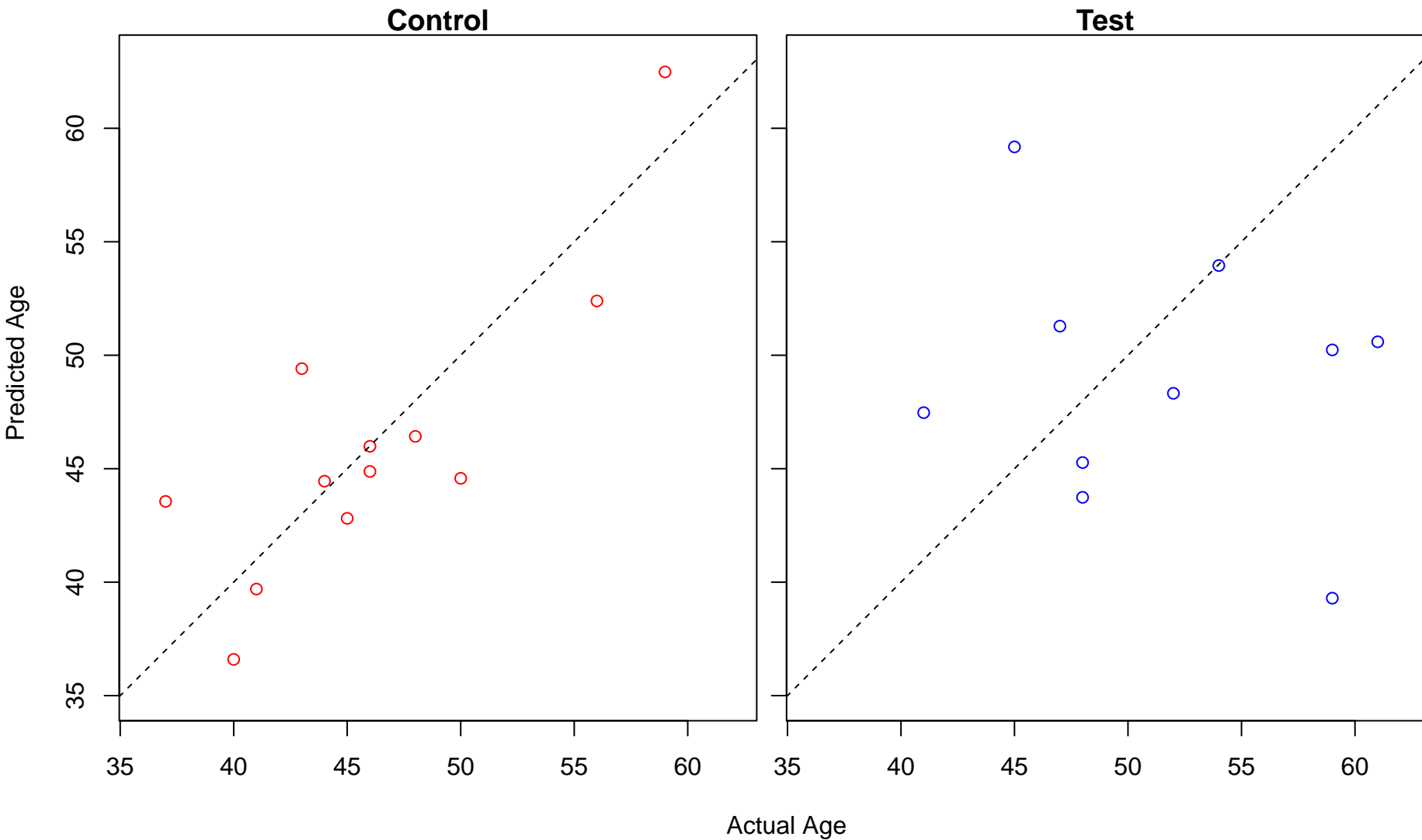
regulation of telomere maintenance via telomere lengthening (Score: 7.174645)



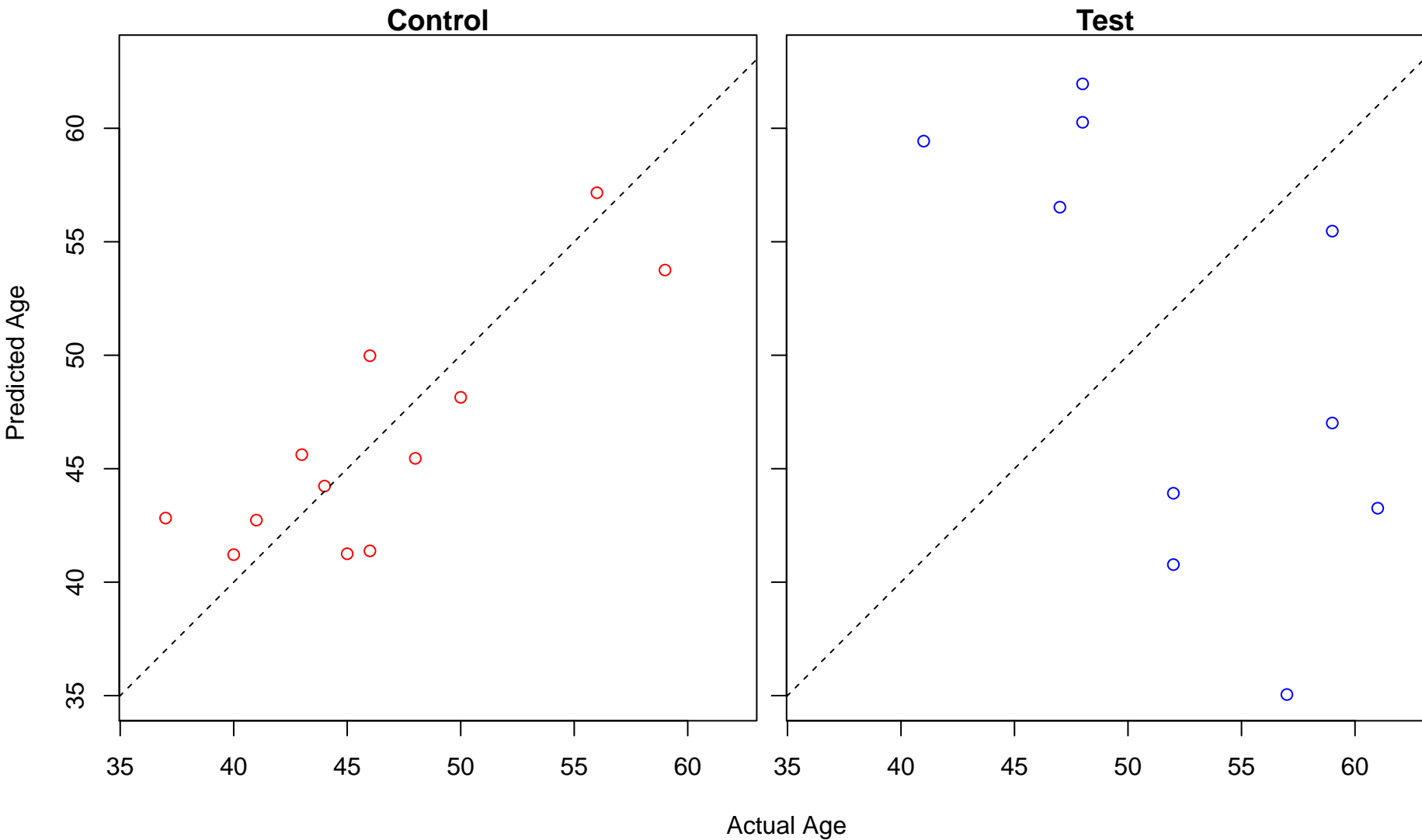
positive regulation of release of cytochrome c from mitochondria (Score: 7.174434)



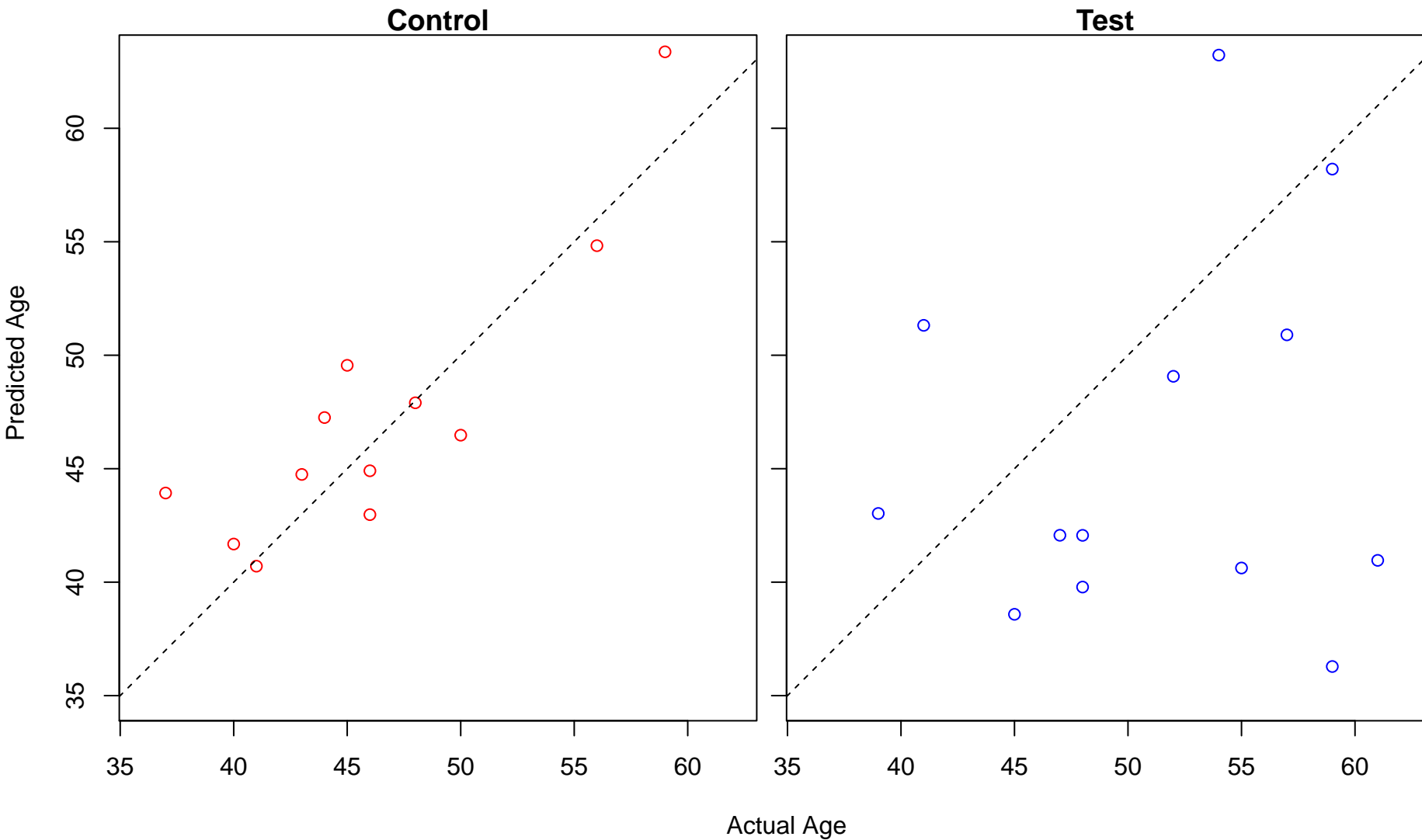
negative regulation of multi-organism process (Score: 7.160791)



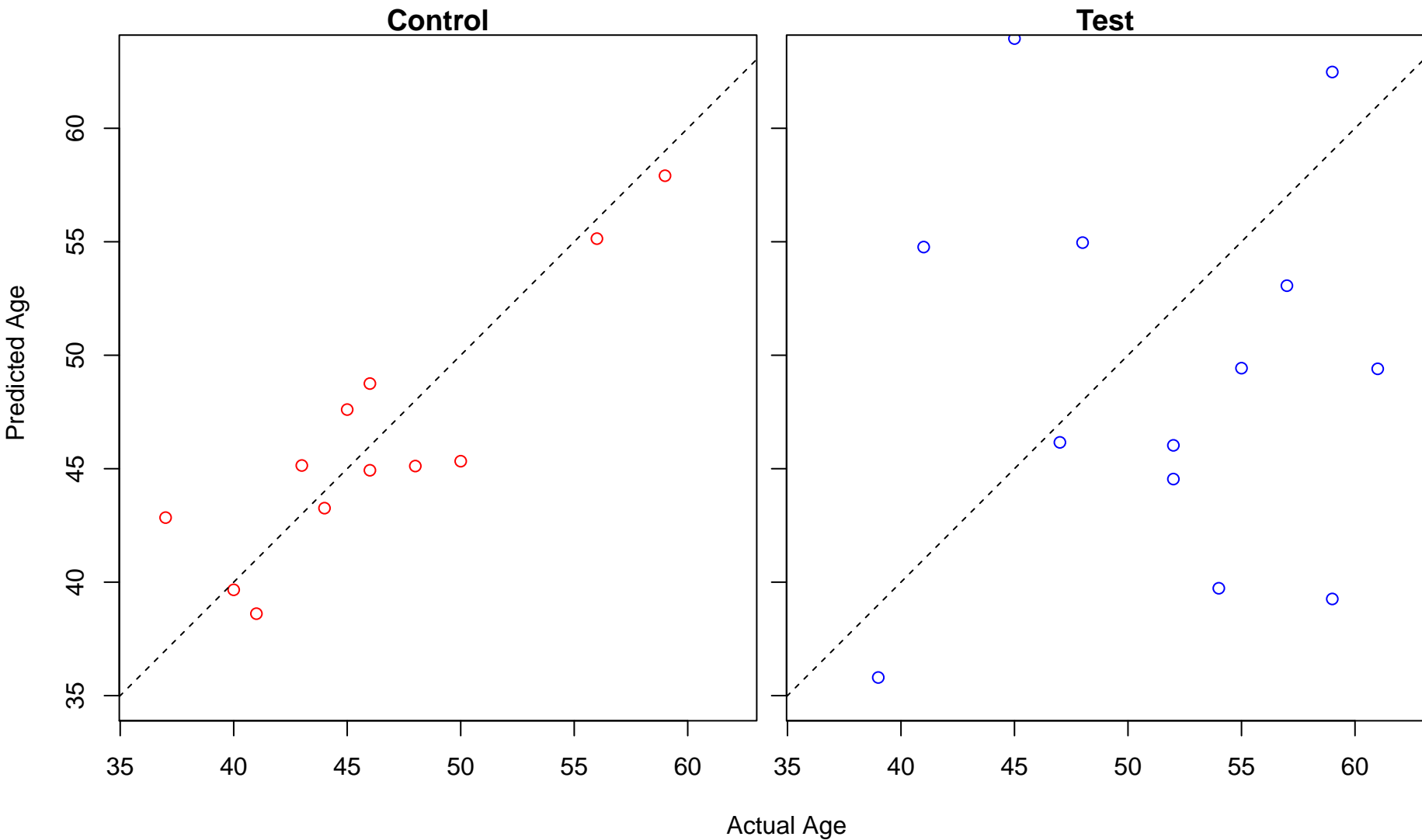
positive regulation of protein homooligomerization (Score: 7.157232)



negative regulation of dephosphorylation (Score: 7.151977)

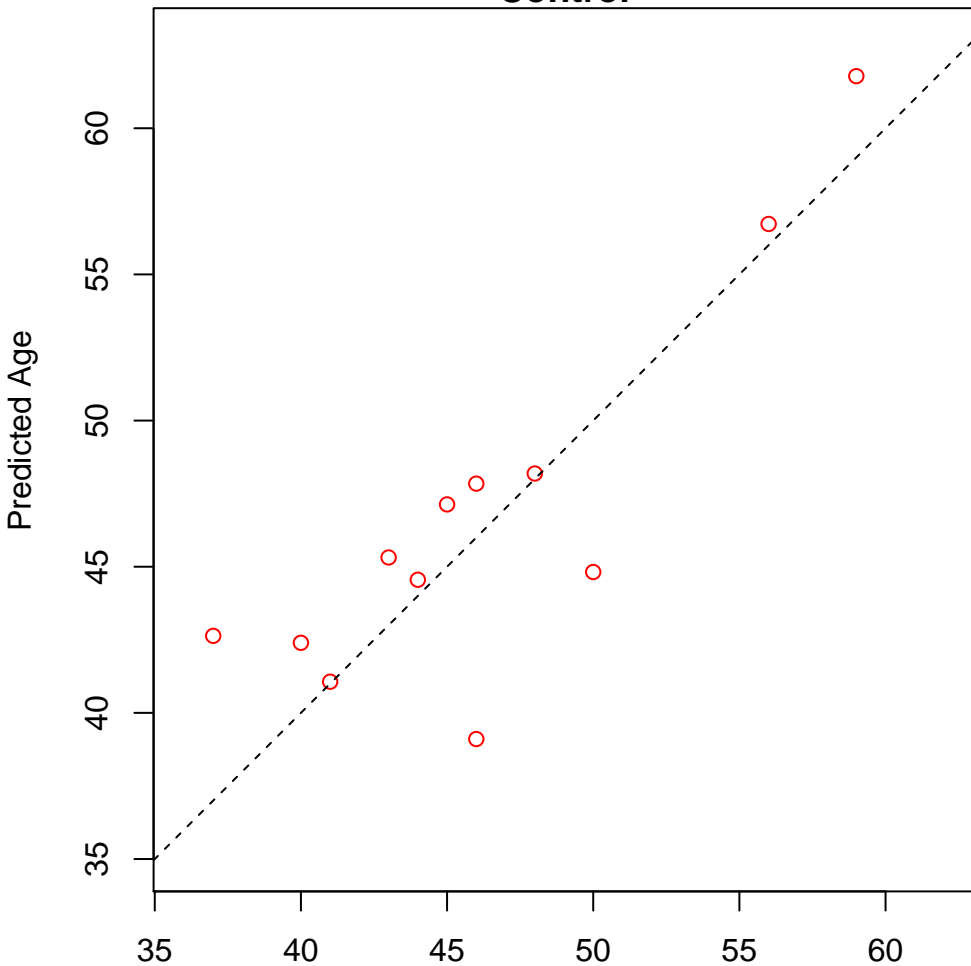


in utero embryonic development (Score: 7.138452)

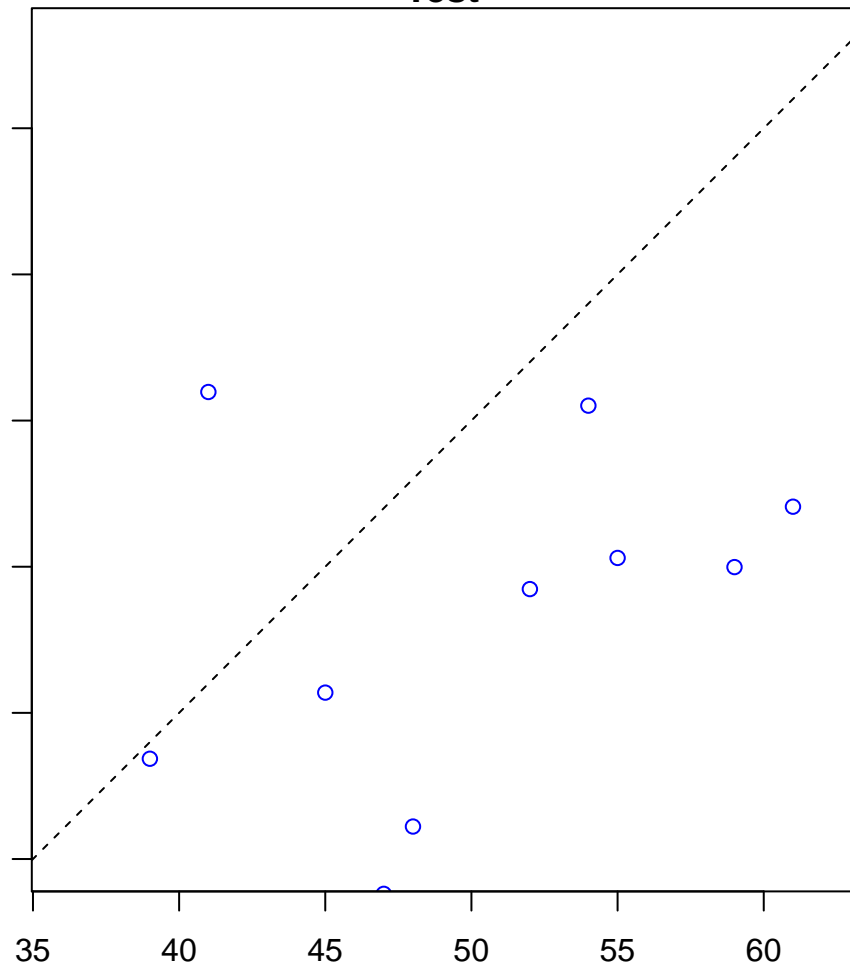


negative regulation of catabolic process (Score: 7.133404)

Control

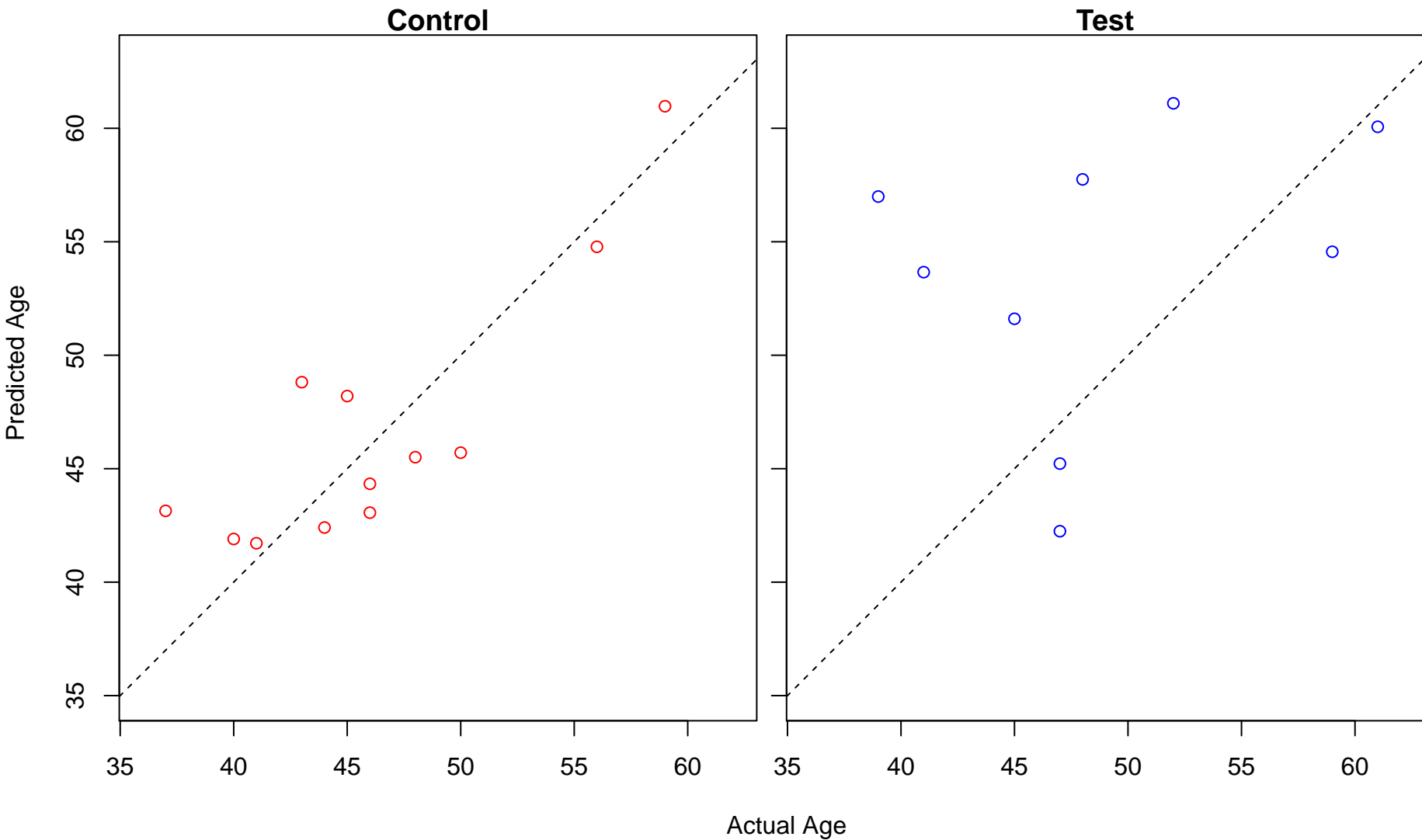


Test

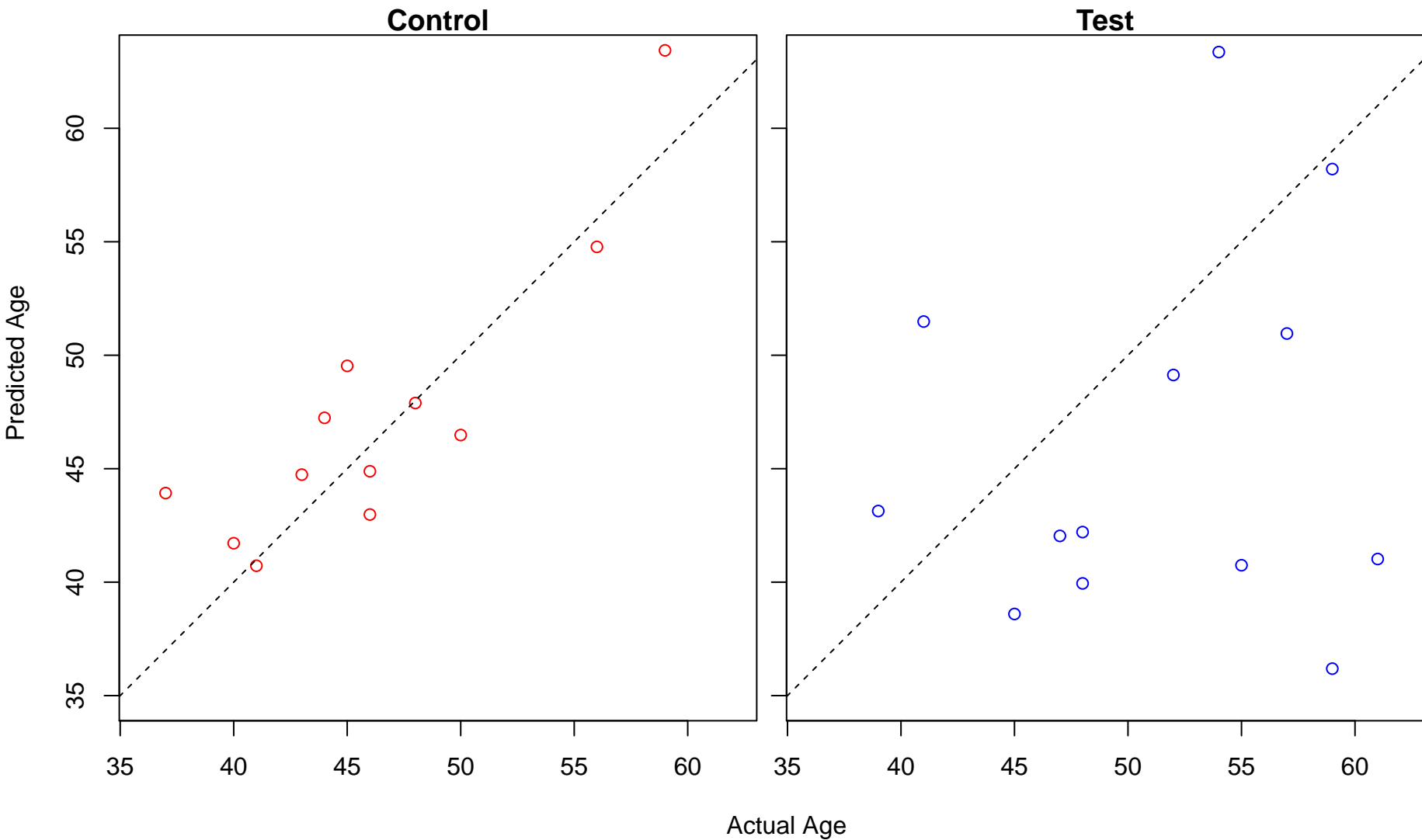


Actual Age

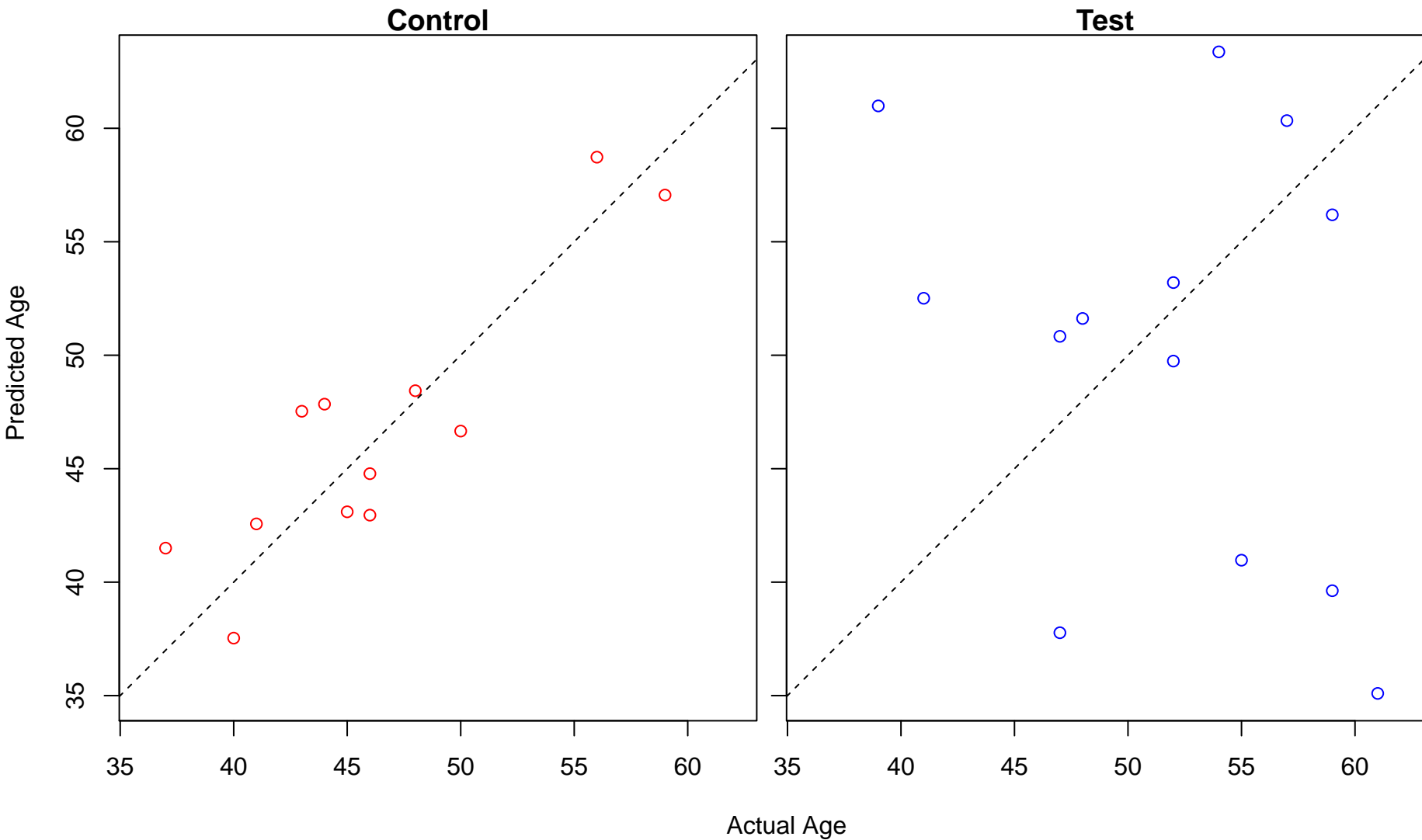
negative regulation of cysteine-type endopeptidase activity (Score: 7.128300)



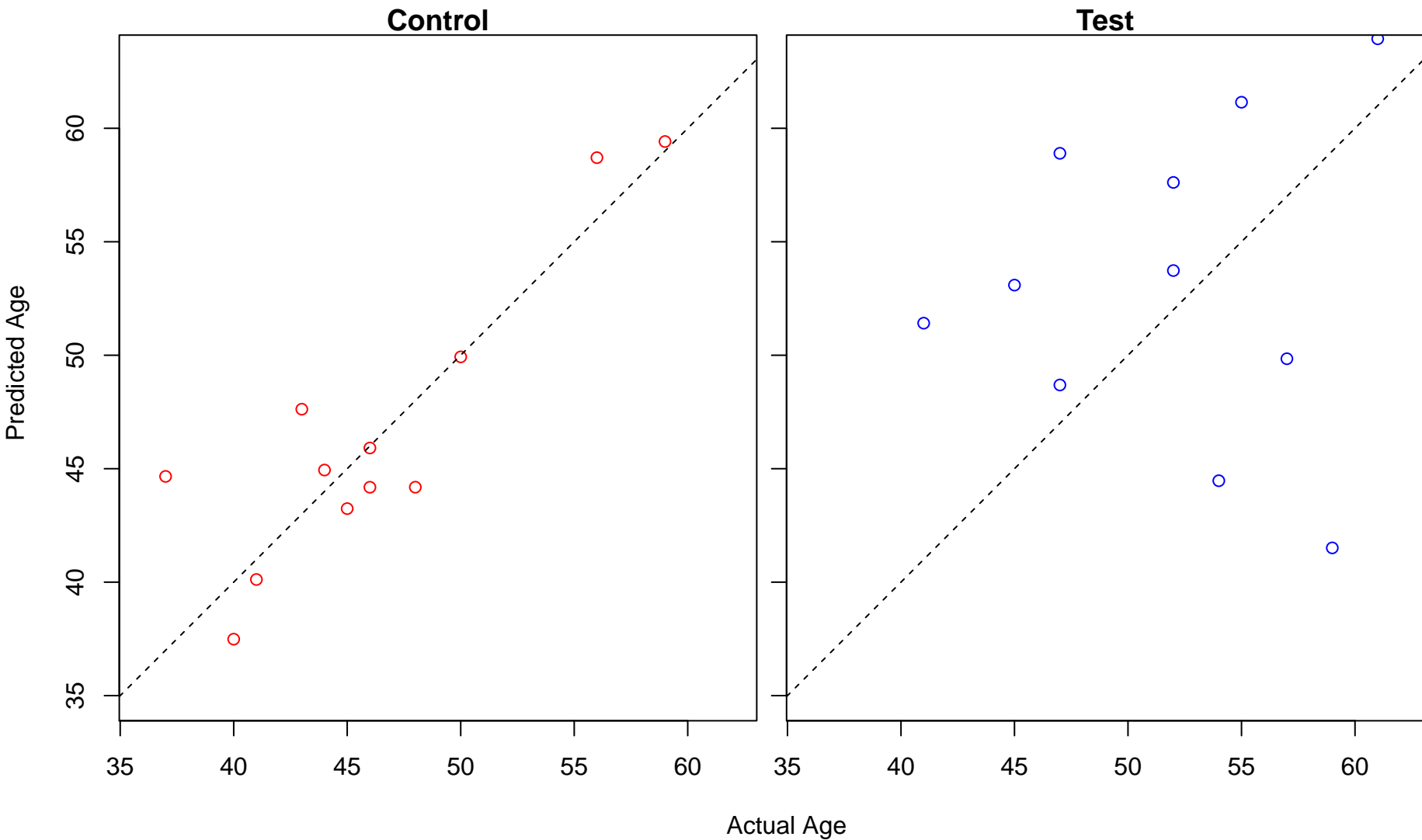
negative regulation of protein dephosphorylation (Score: 7.128106)



vocalization behavior (Score: 7.099663)

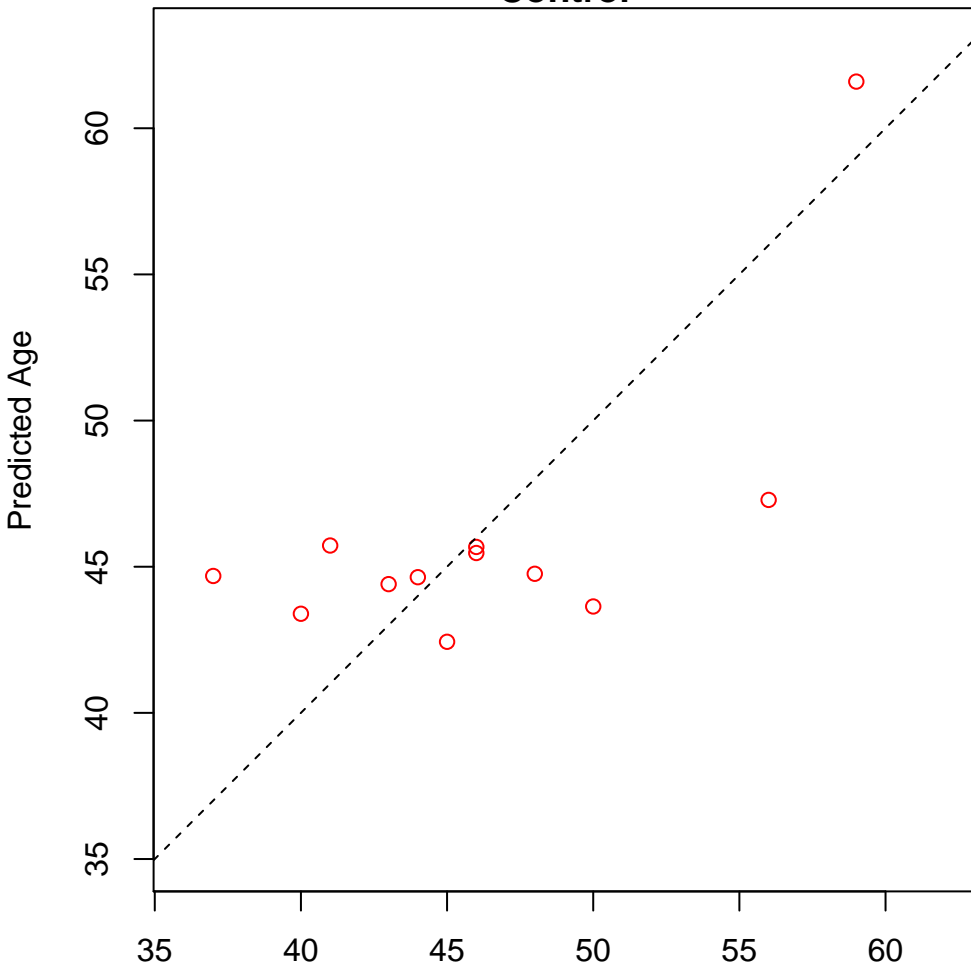


regulation of retrograde protein transport, ER to cytosol (Score: 7.098603)

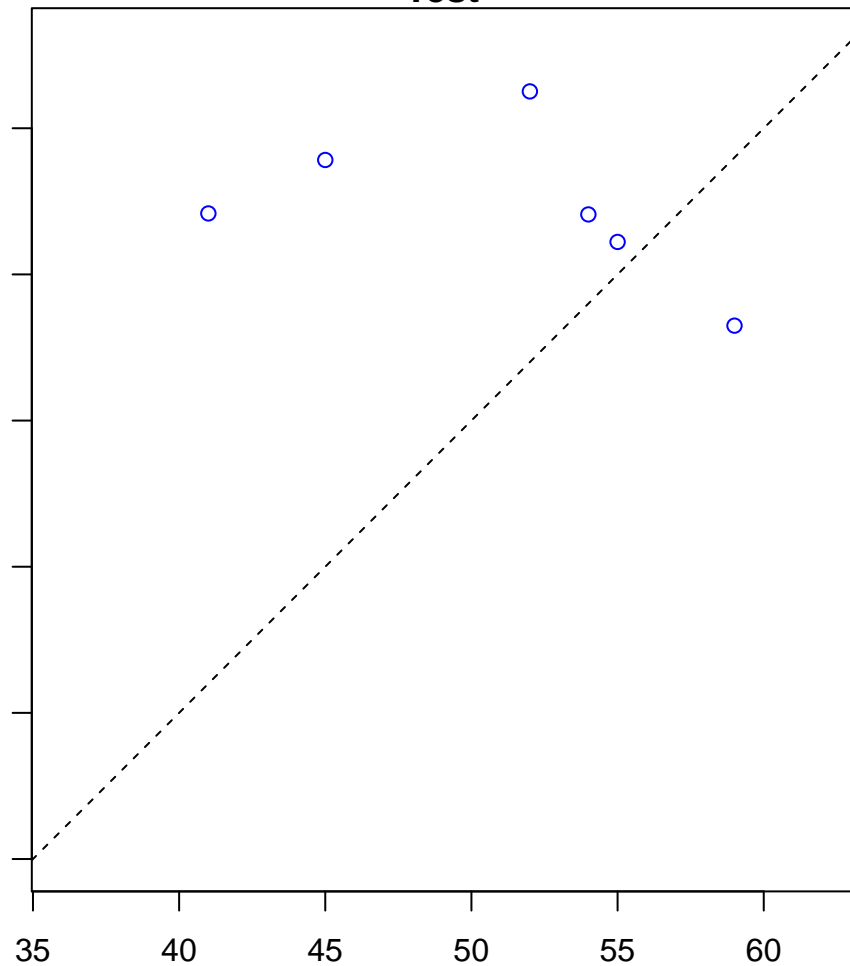


embryonic skeletal joint morphogenesis (Score: 7.092104)

Control

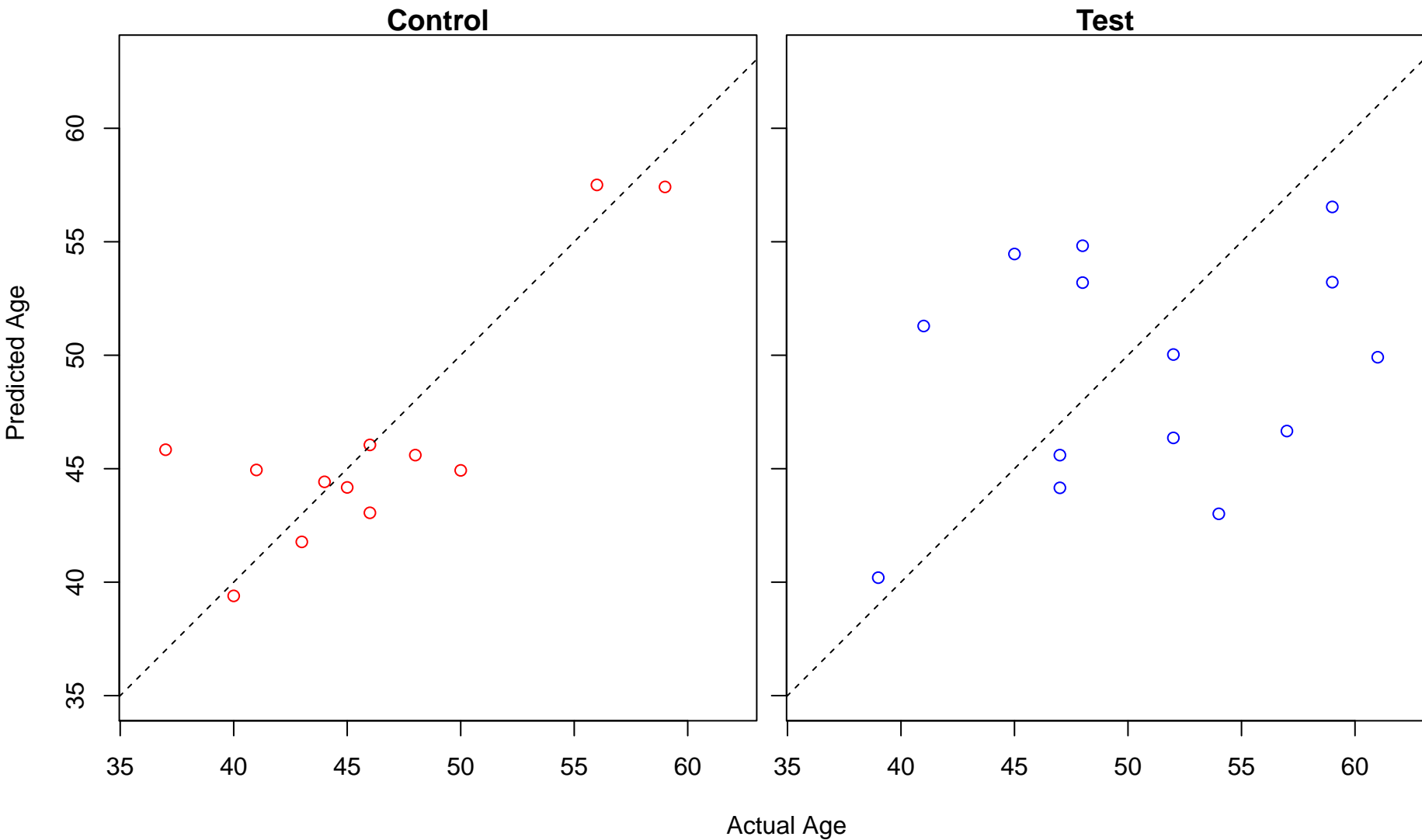


Test

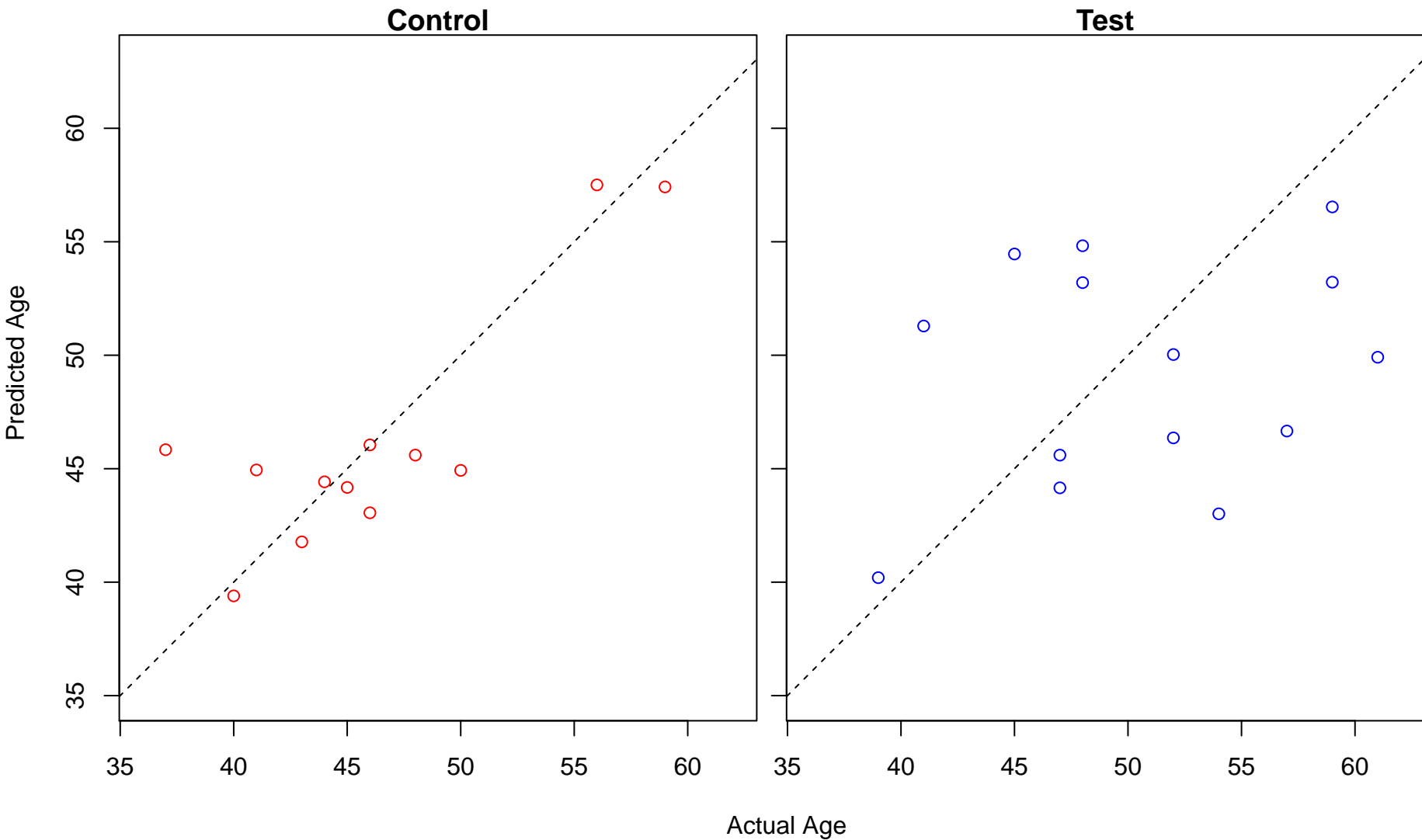


Actual Age

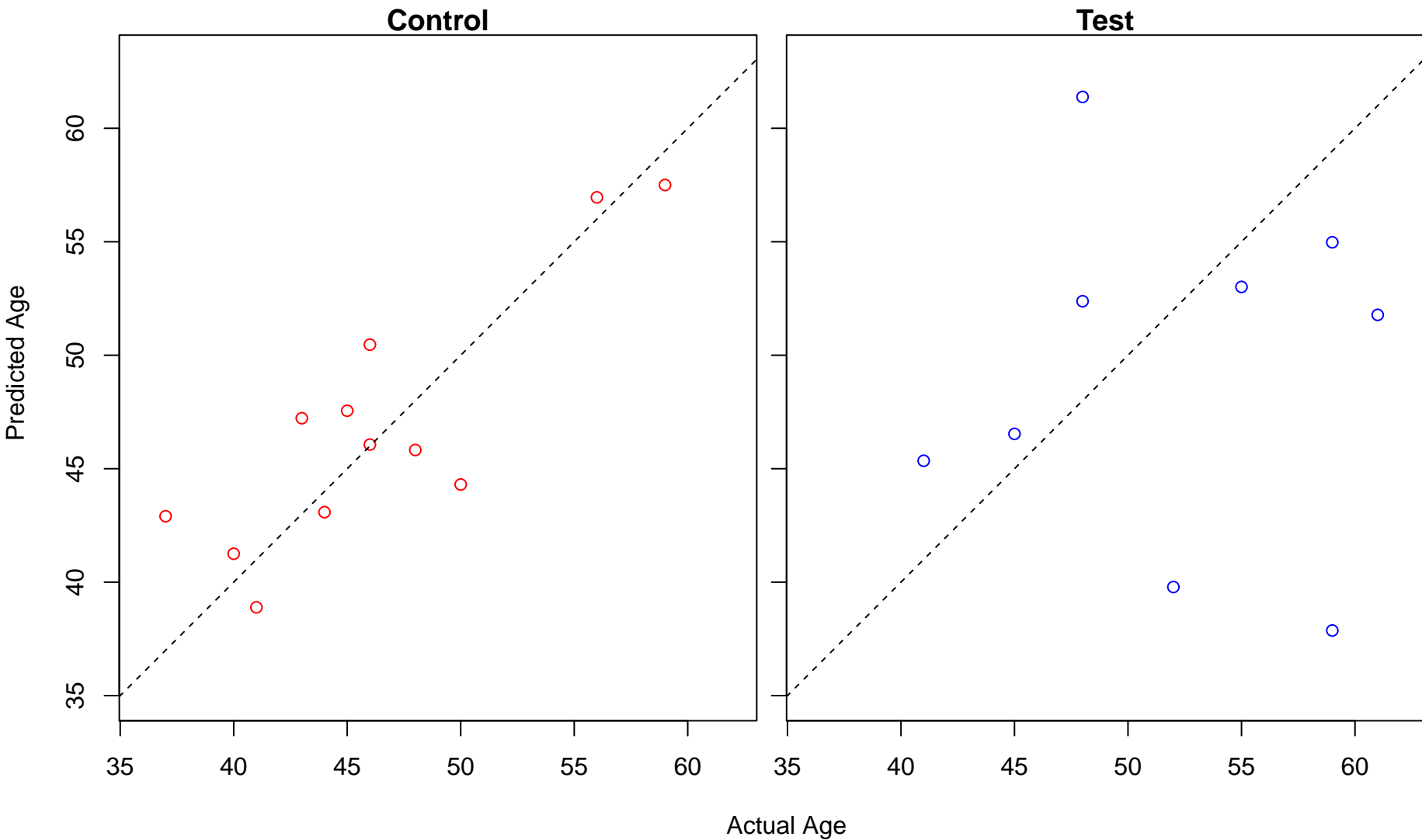
negative regulation of protein import into nucleus (Score: 7.079577)



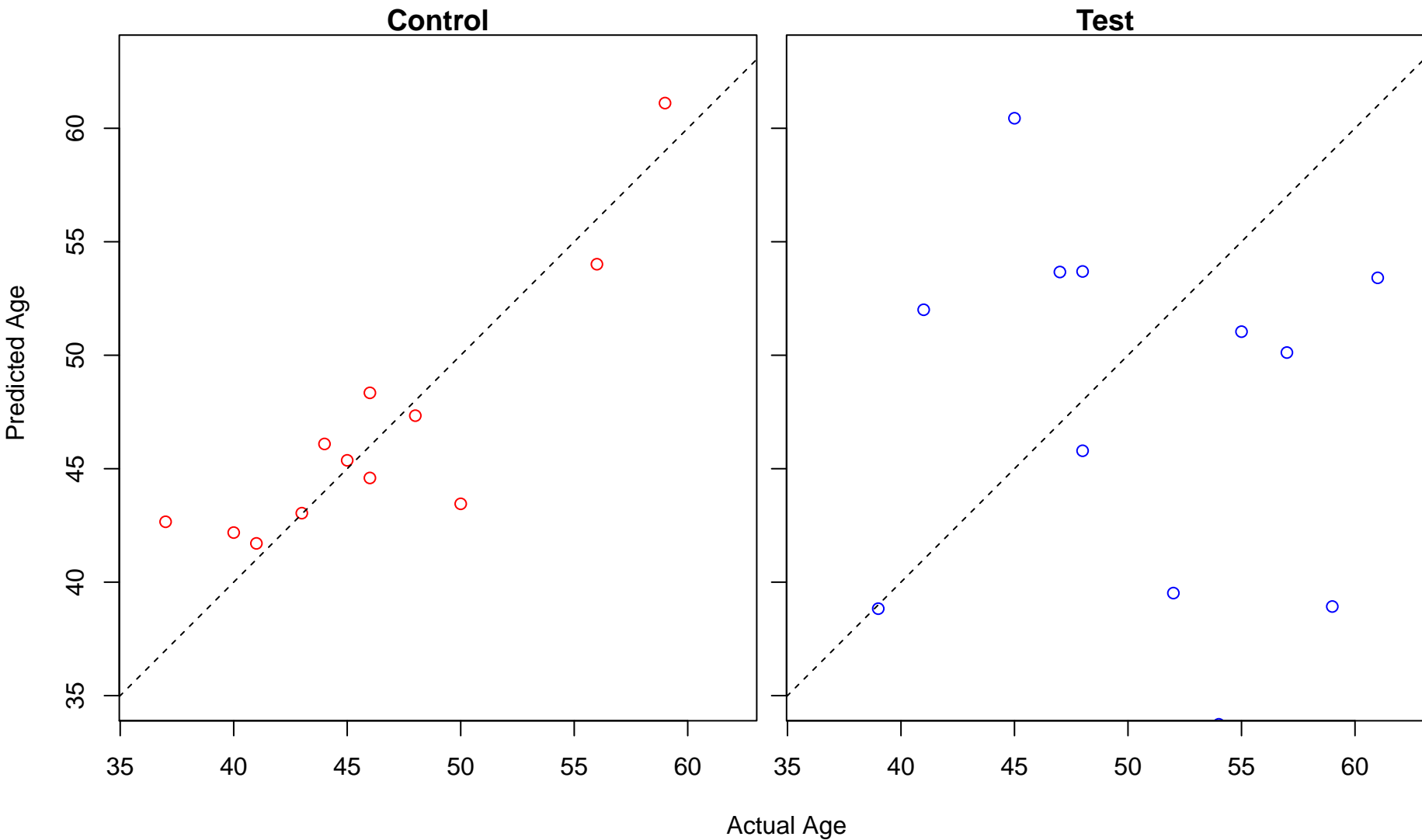
negative regulation of protein import (Score: 7.079577)



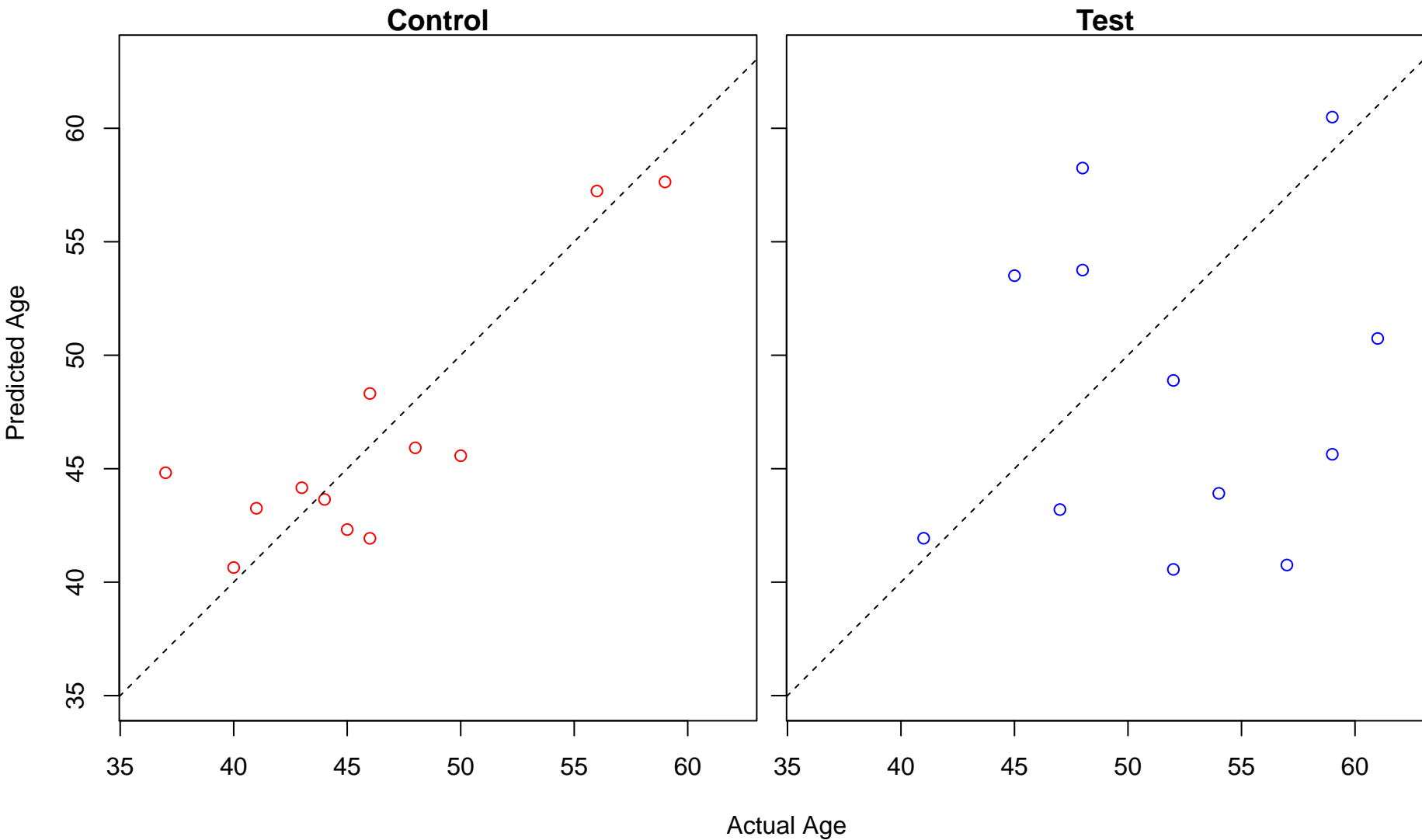
positive regulation of blood vessel endothelial cell migration (Score: 7.078386)



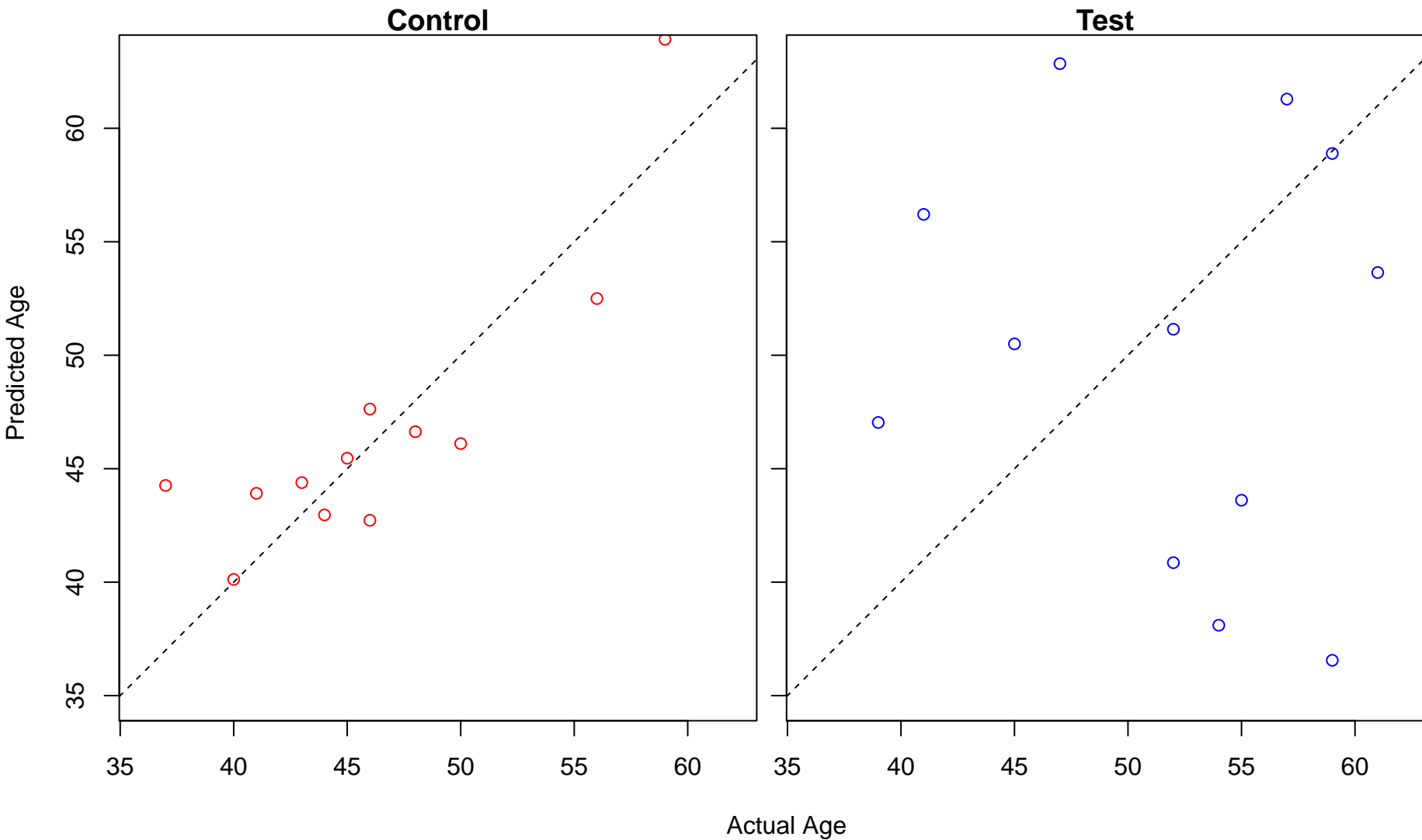
photoperiodism (Score: 7.060564)



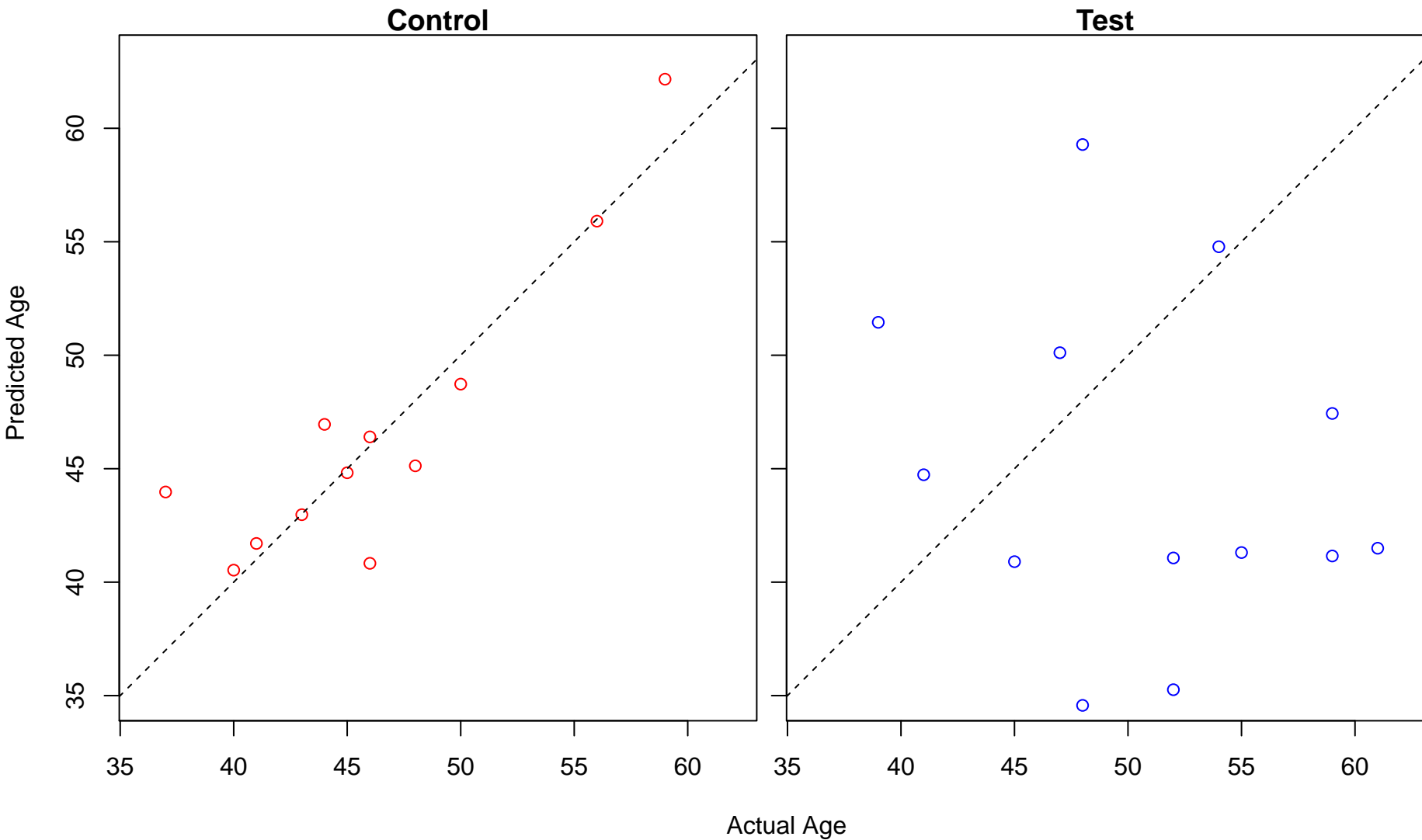
Rho protein signal transduction (Score: 7.058174)



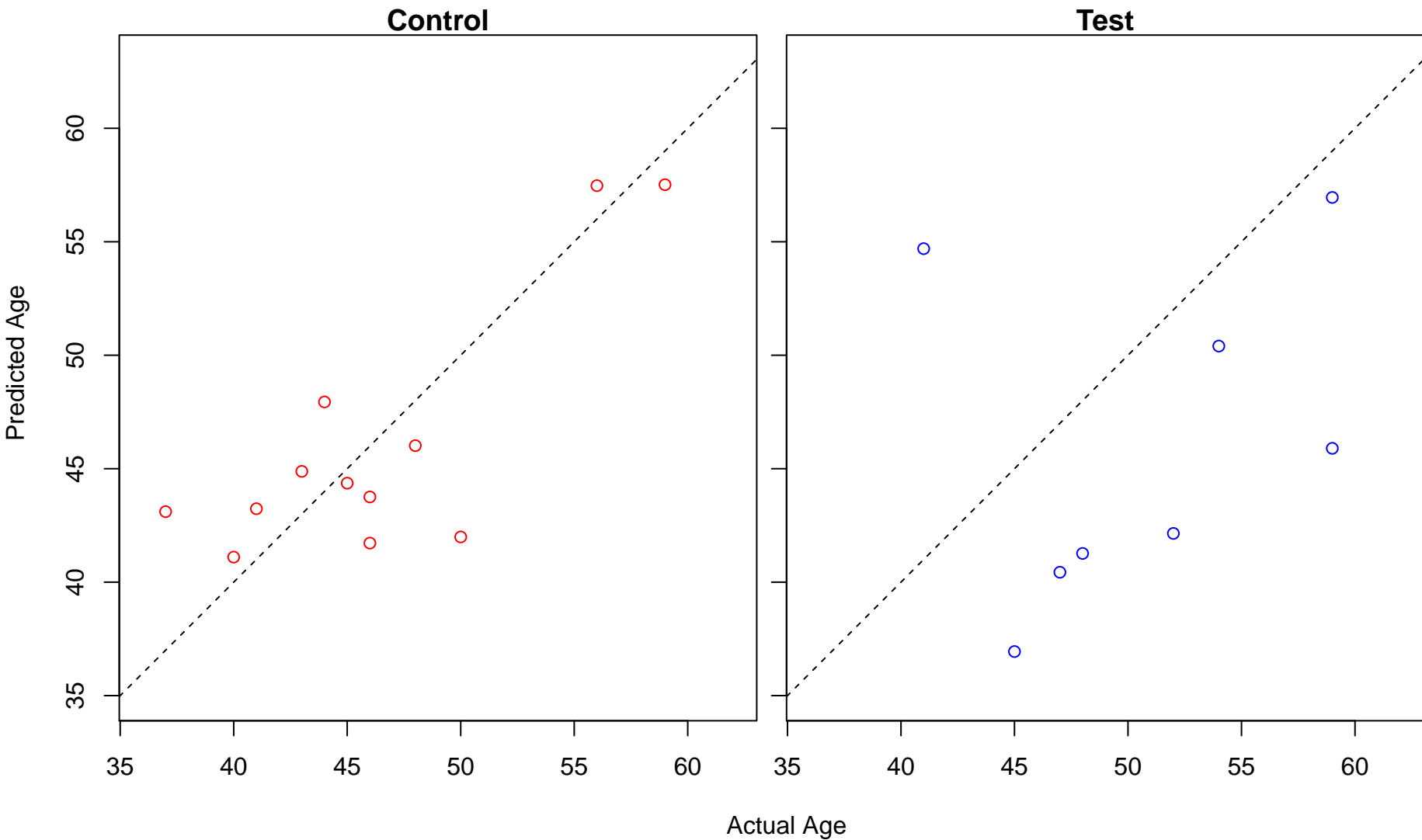
gastrulation (Score: 7.053088)



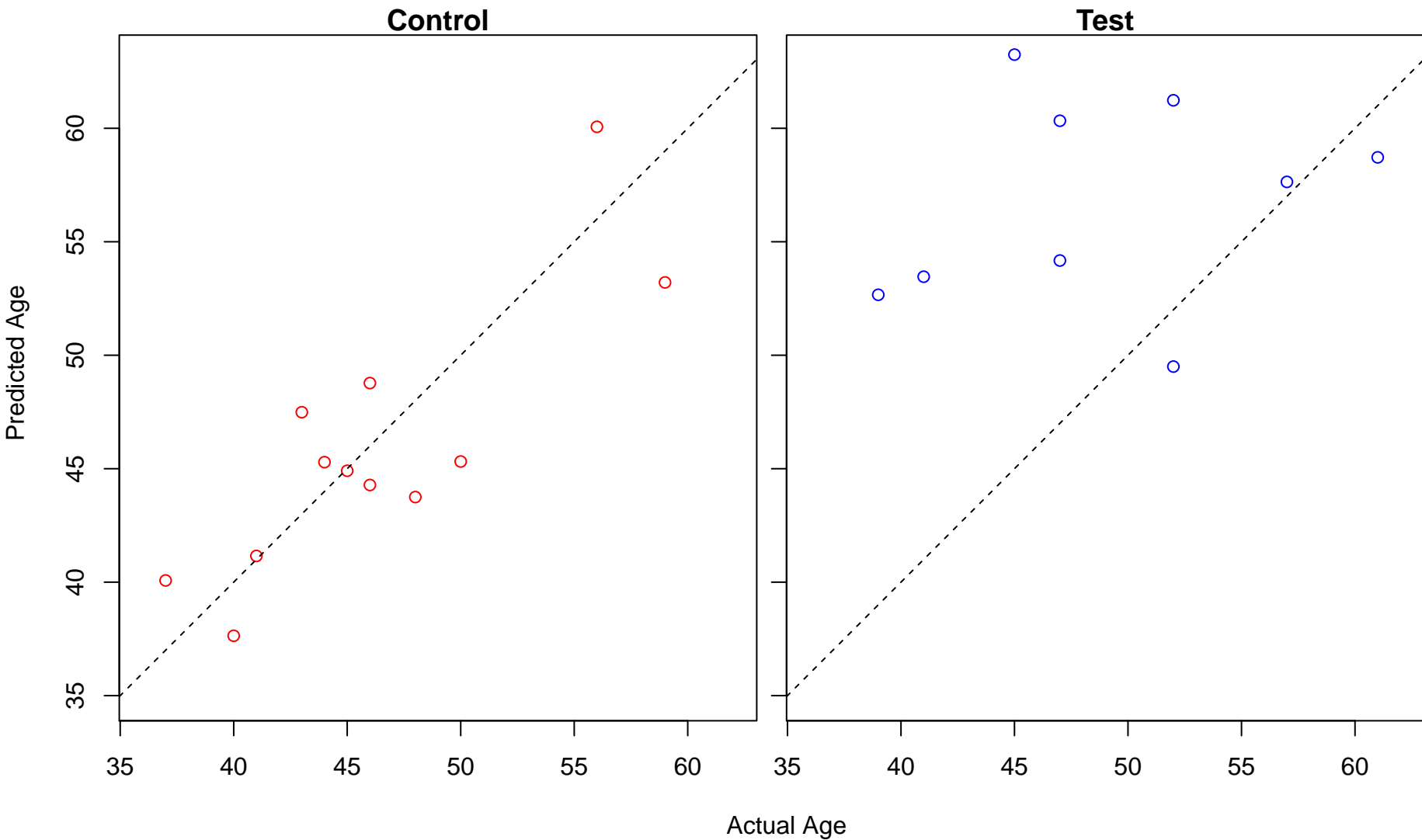
positive regulation of ion transmembrane transporter activity (Score: 7.048846)



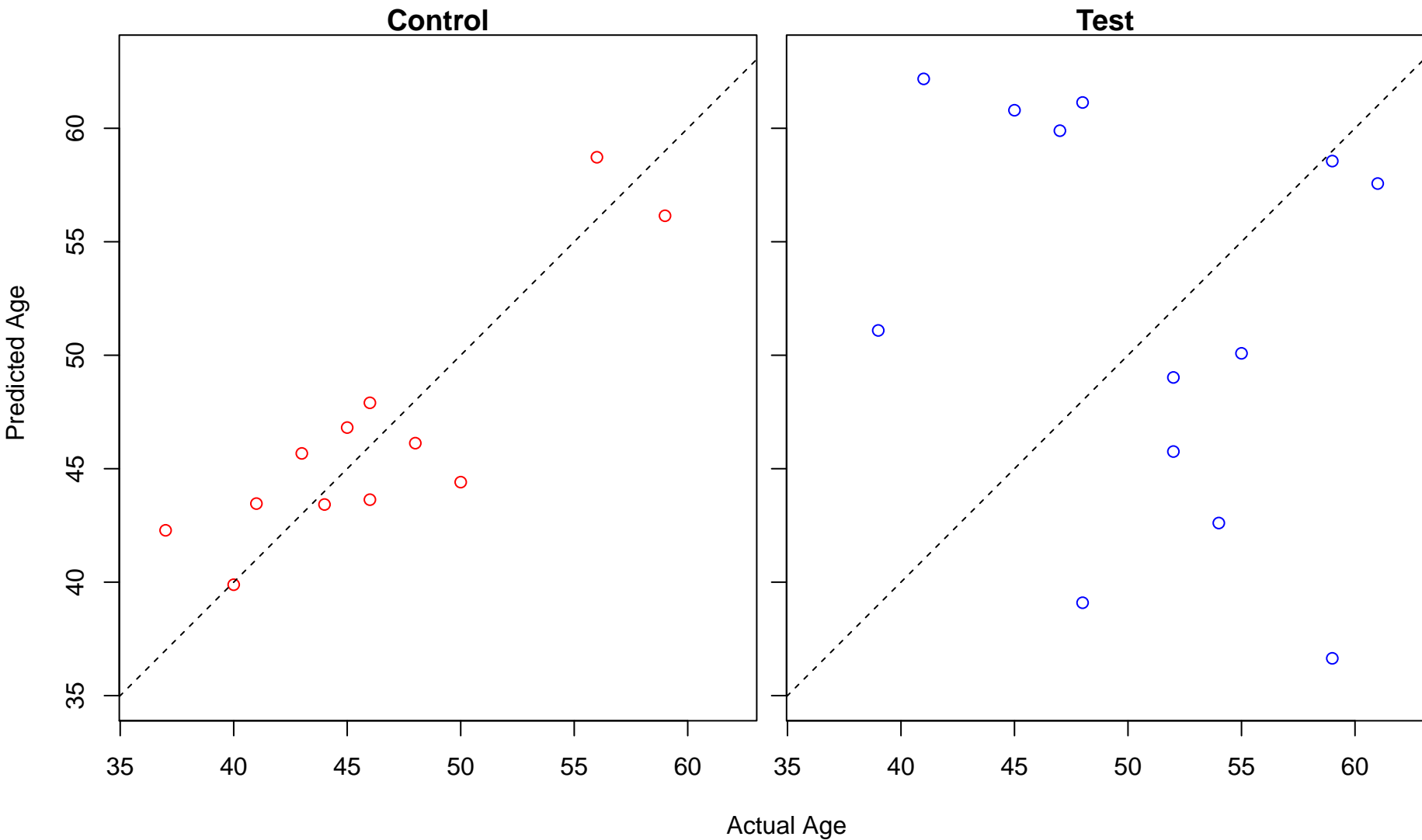
RNA localization (Score: 7.036336)



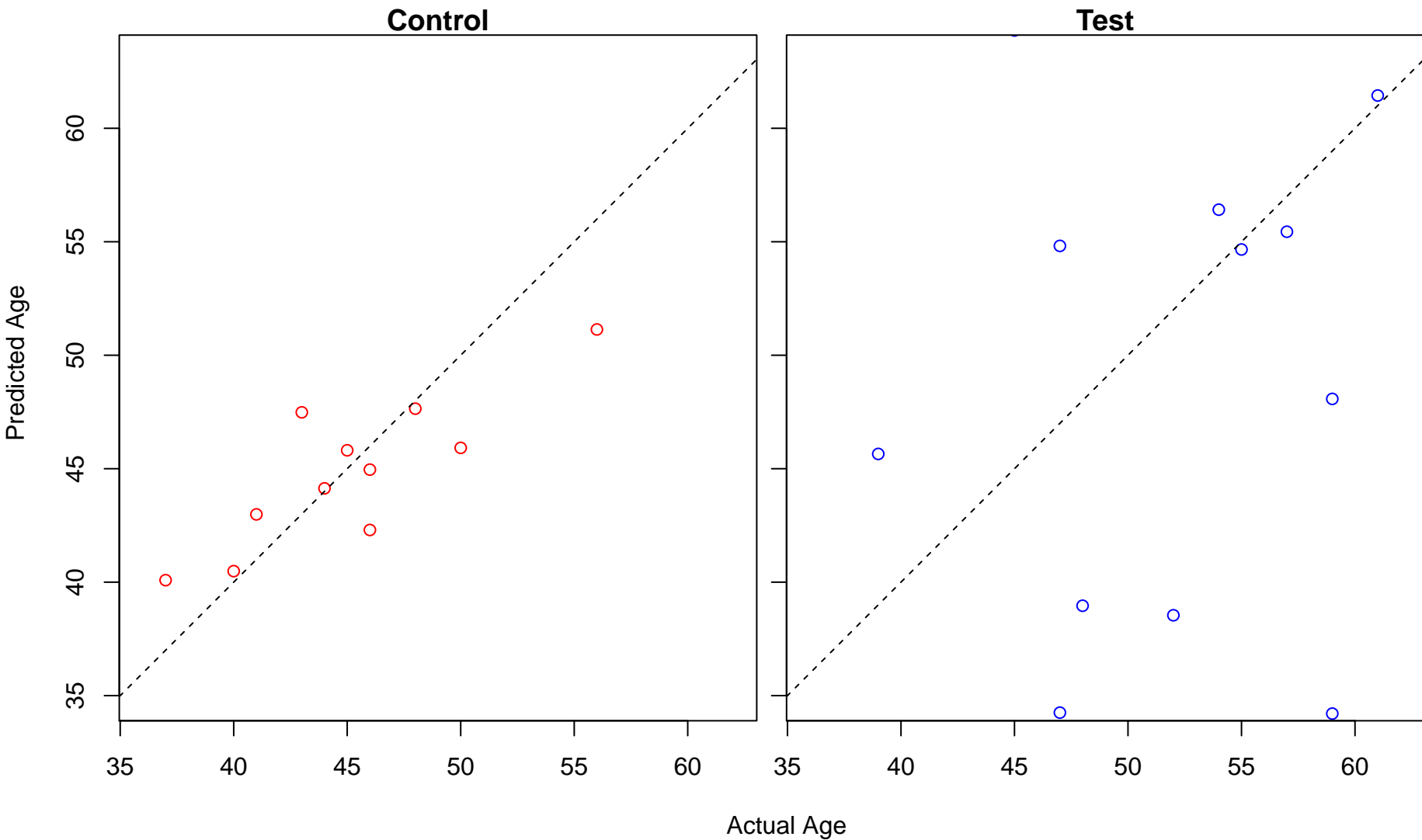
positive regulation of alpha-beta T cell differentiation (Score: 7.033333)



kidney development (Score: 7.032303)

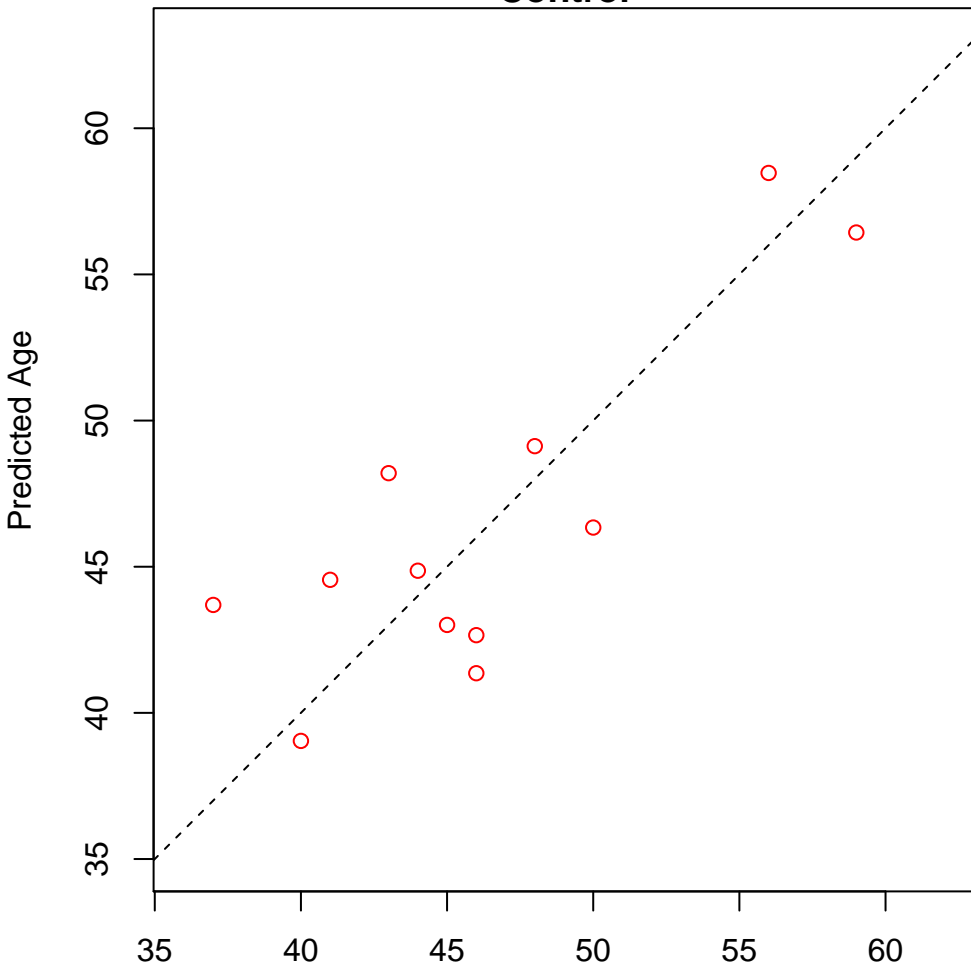


regulation of mRNA metabolic process (Score: 7.025849)

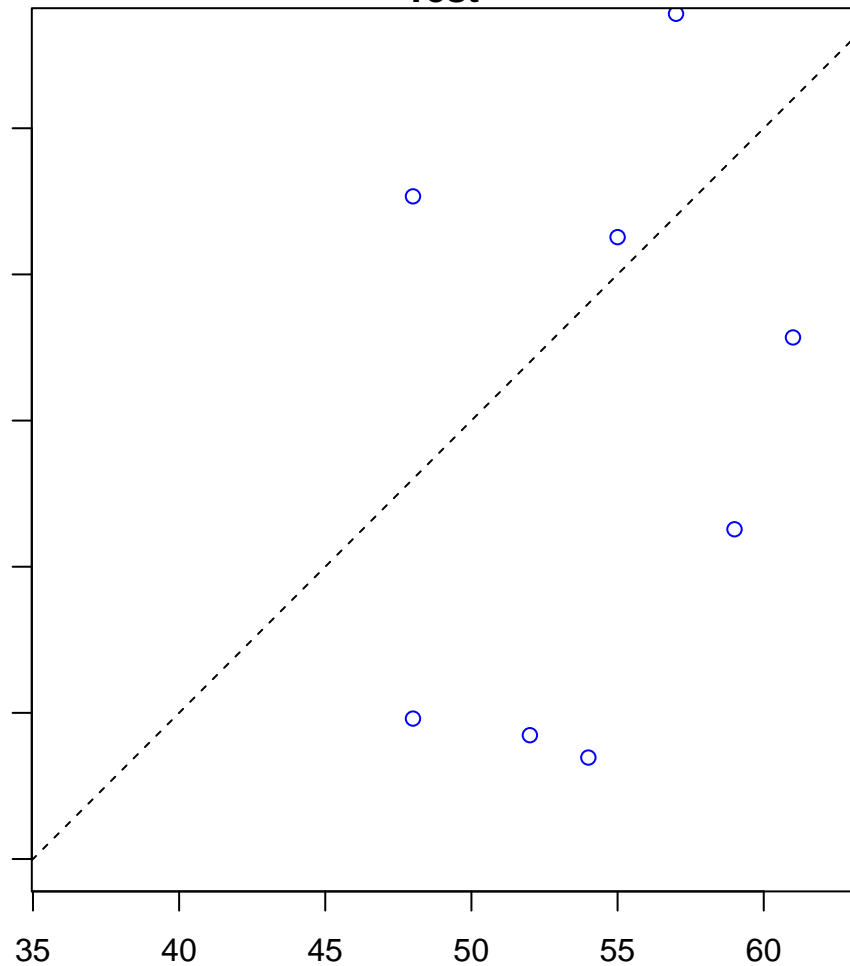


small molecule biosynthetic process (Score: 7.022461)

Control

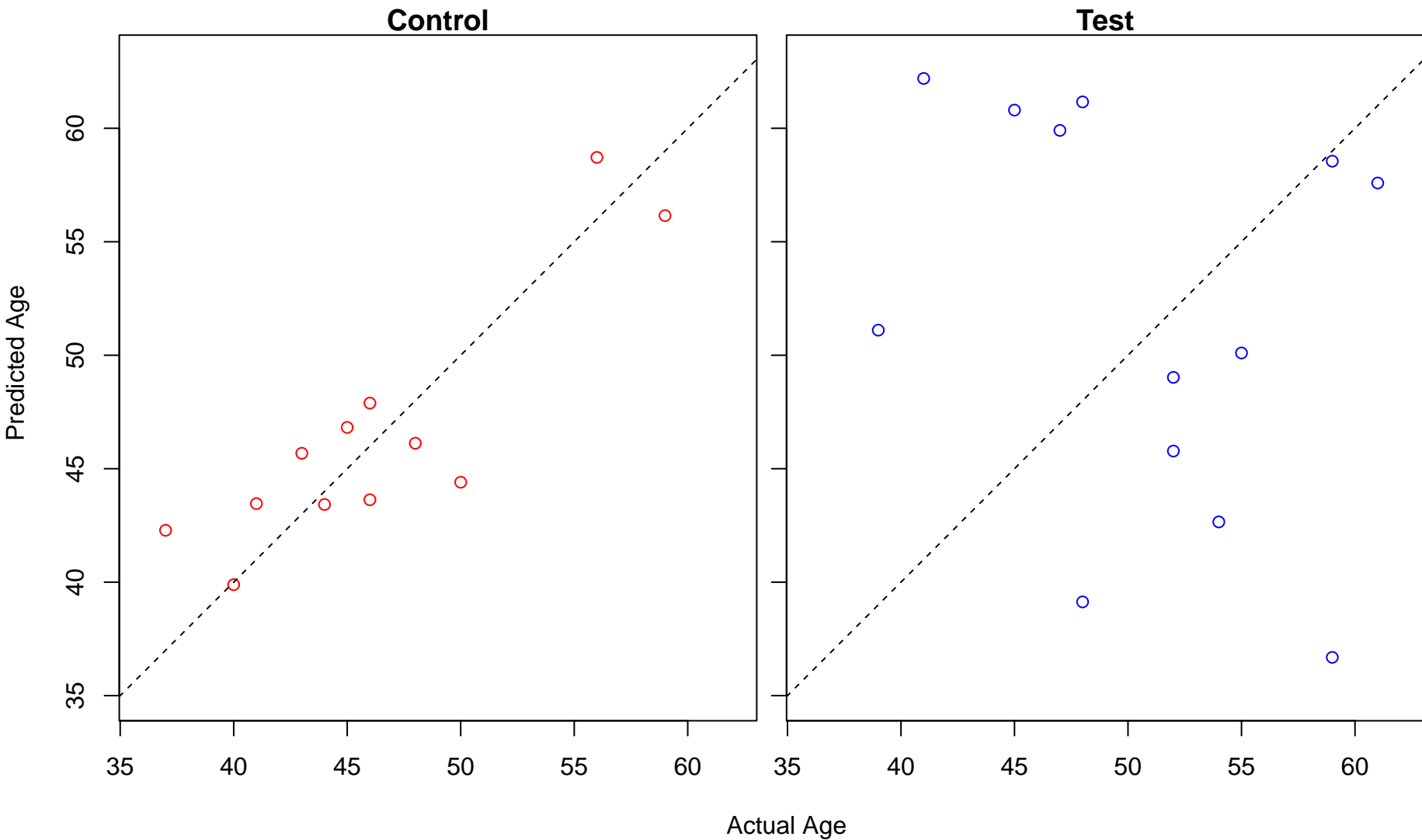


Test

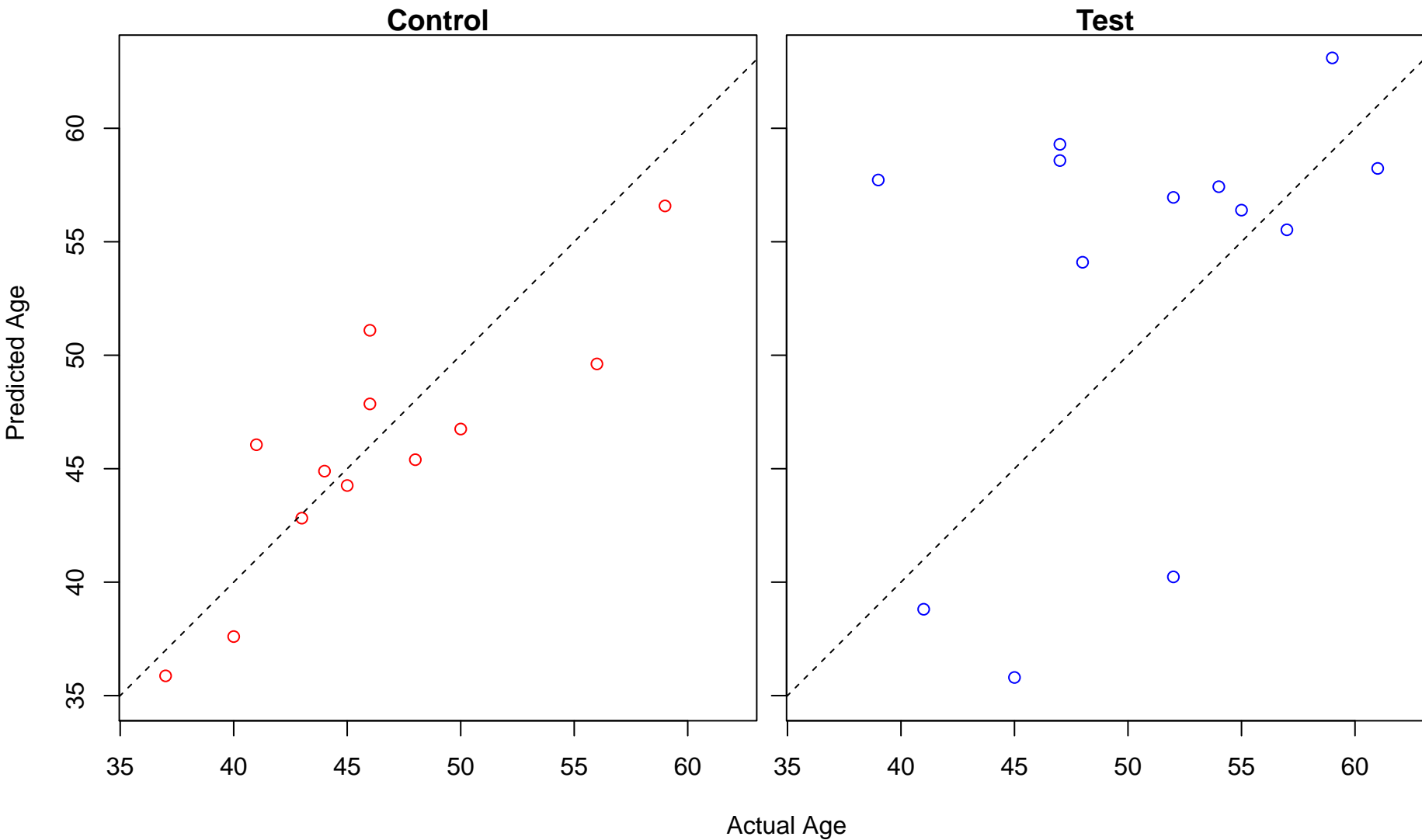


Actual Age

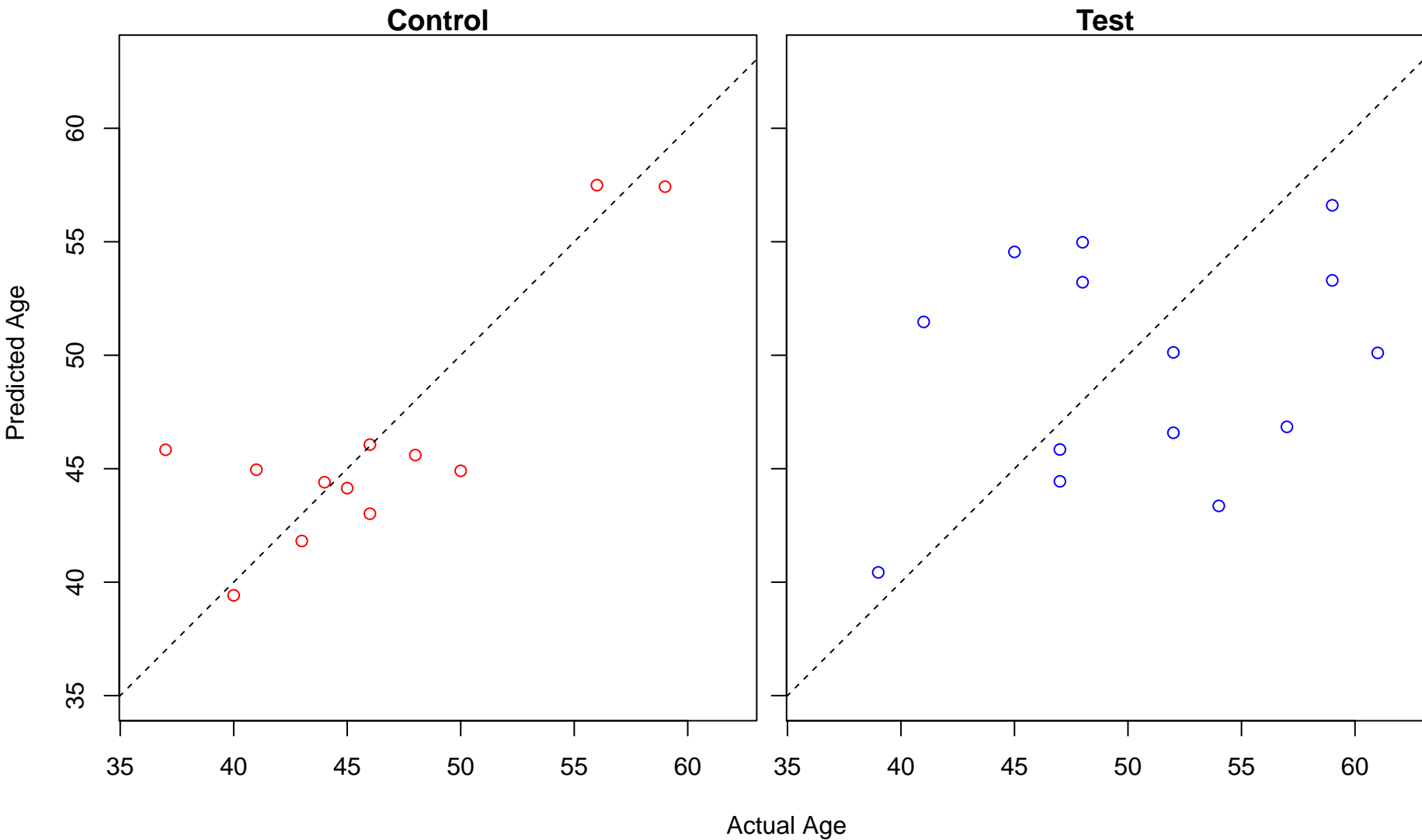
renal system development (Score: 7.022374)



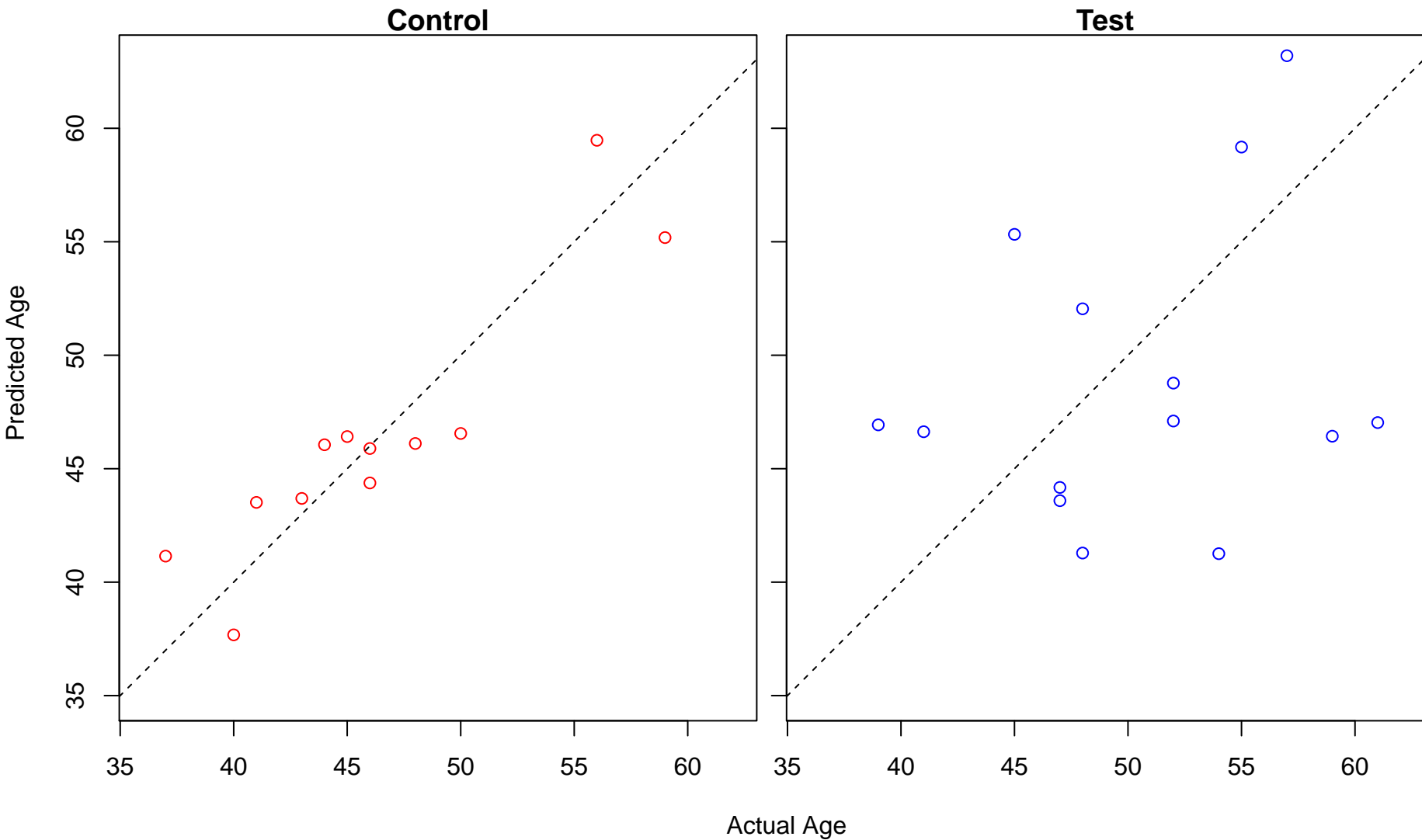
triglyceride-rich lipoprotein particle remodeling (Score: 7.009380)



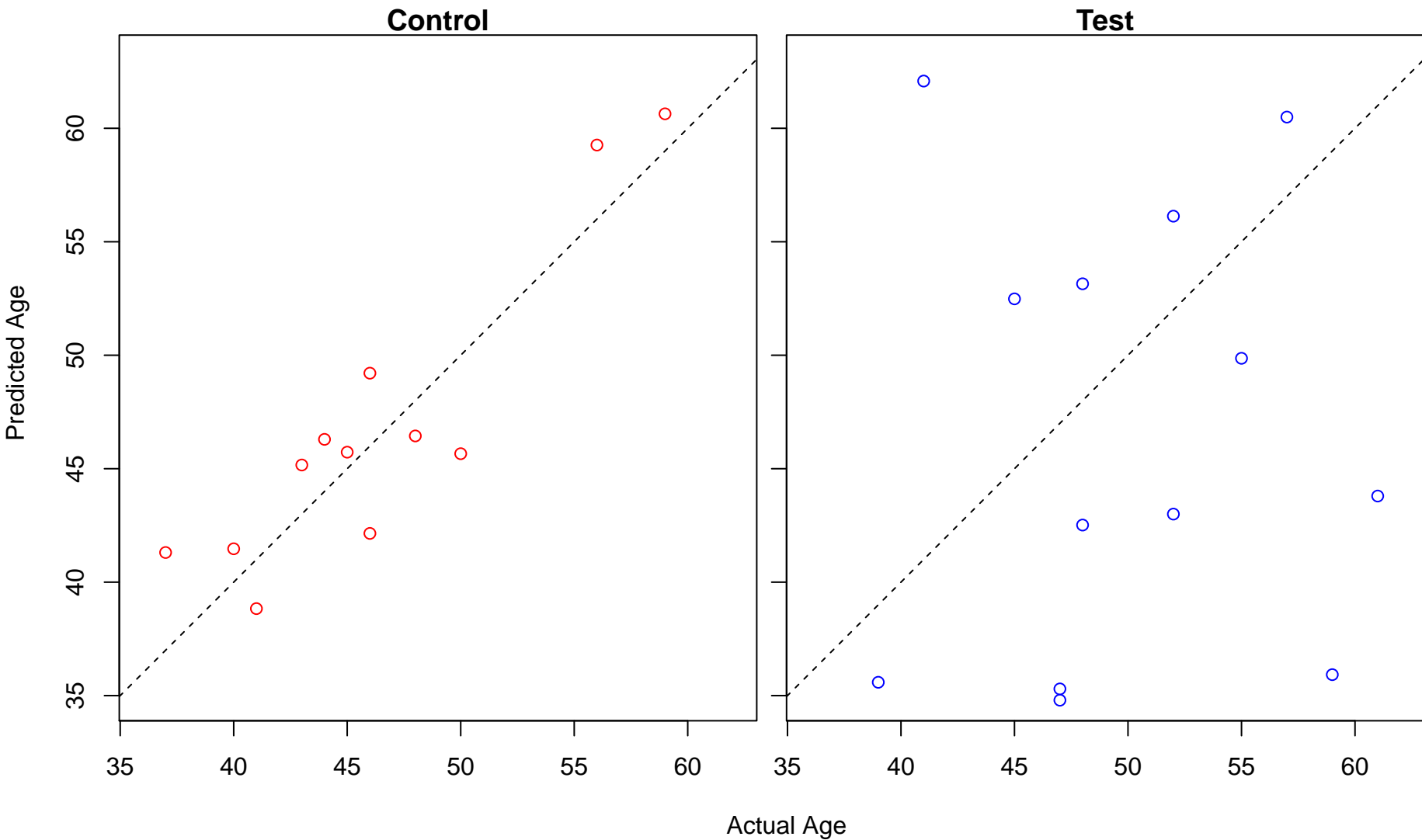
negative regulation of protein localization to nucleus (Score: 6.990188)



positive regulation of endopeptidase activity (Score: 6.982455)

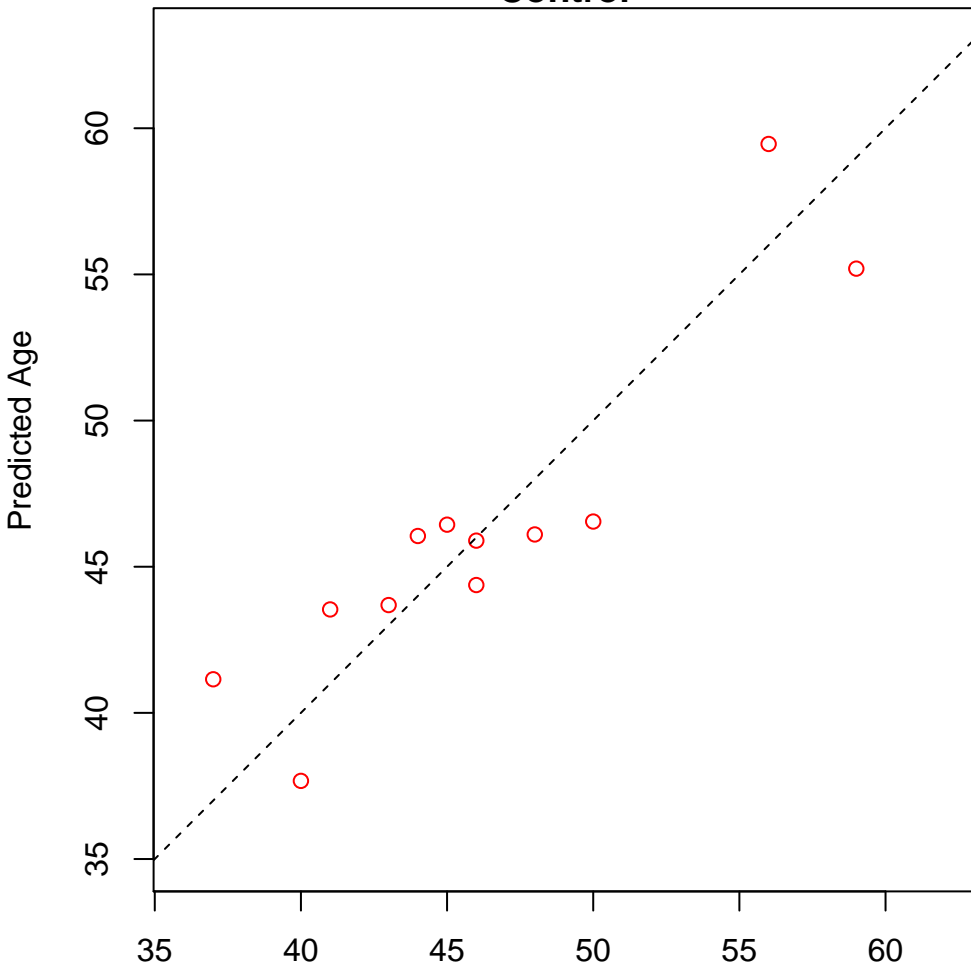


cardiac muscle cell differentiation (Score: 6.967867)

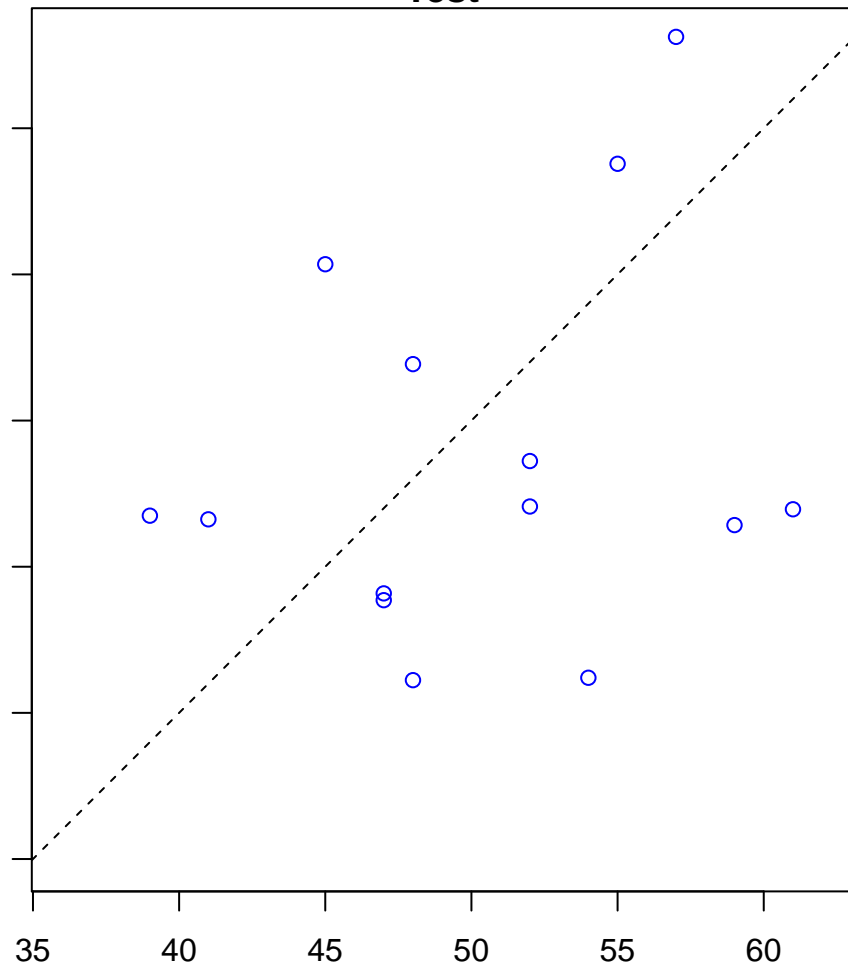


positive regulation of peptidase activity (Score: 6.960380)

Control



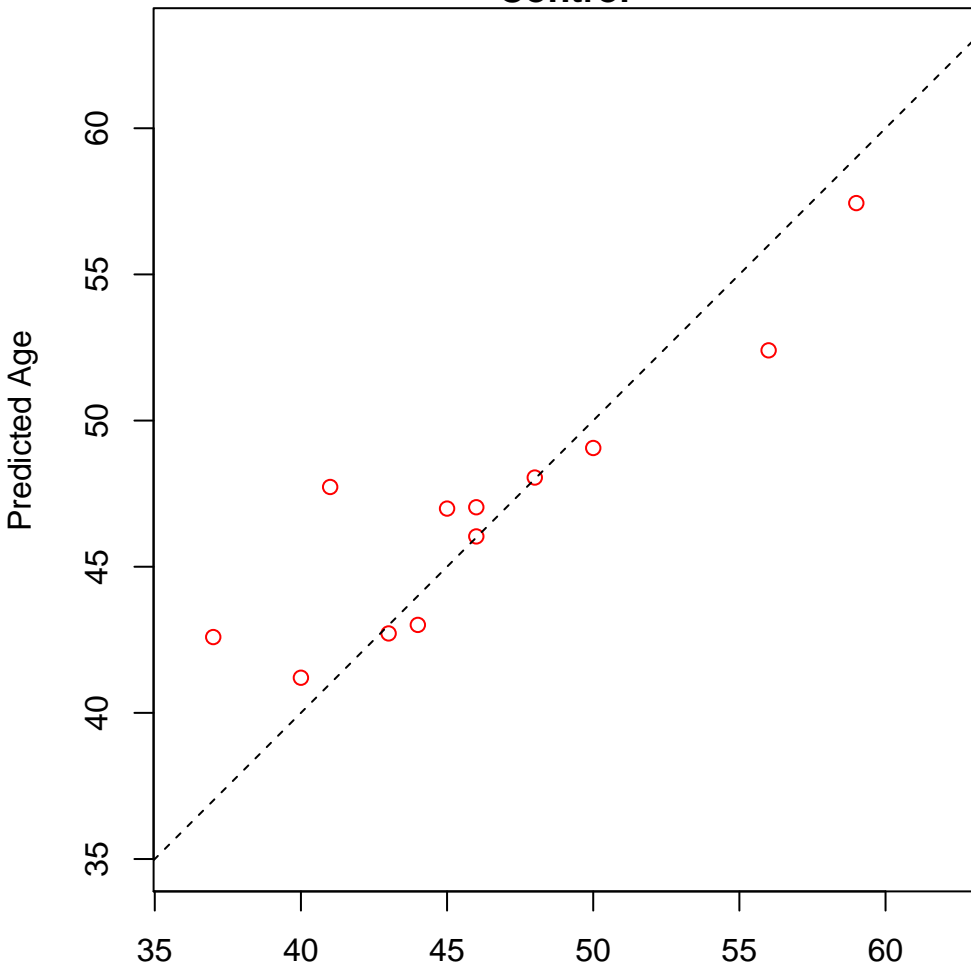
Test



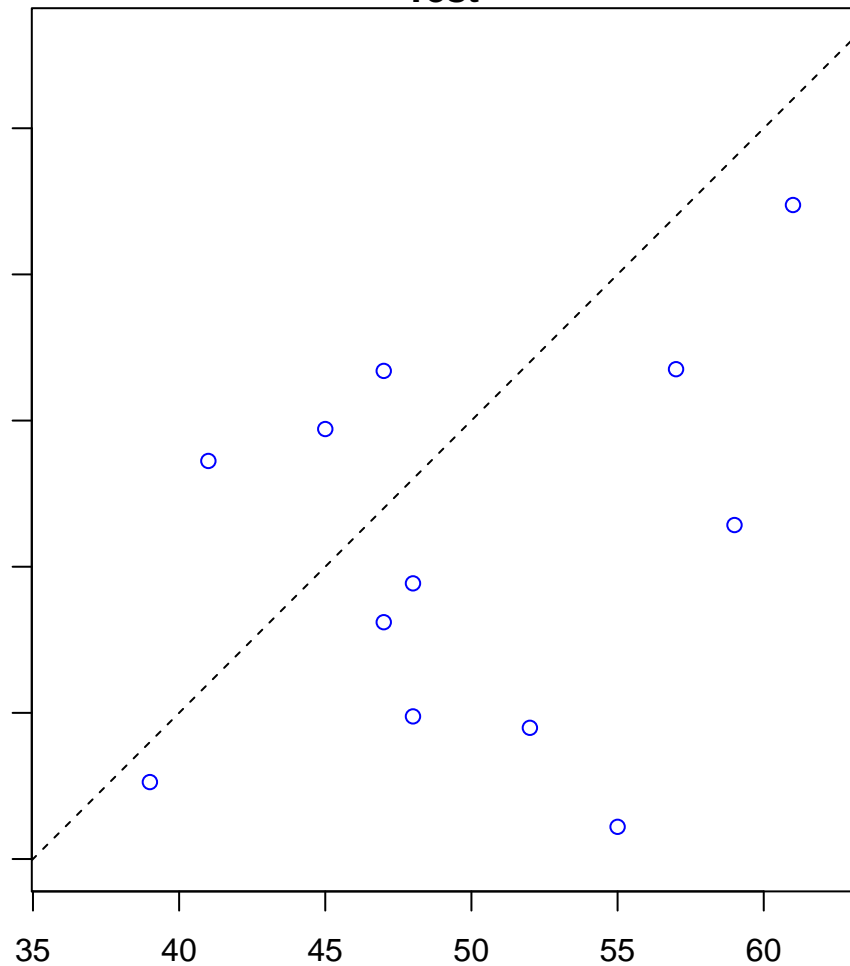
Actual Age

regulation of cGMP metabolic process (Score: 6.959170)

Control

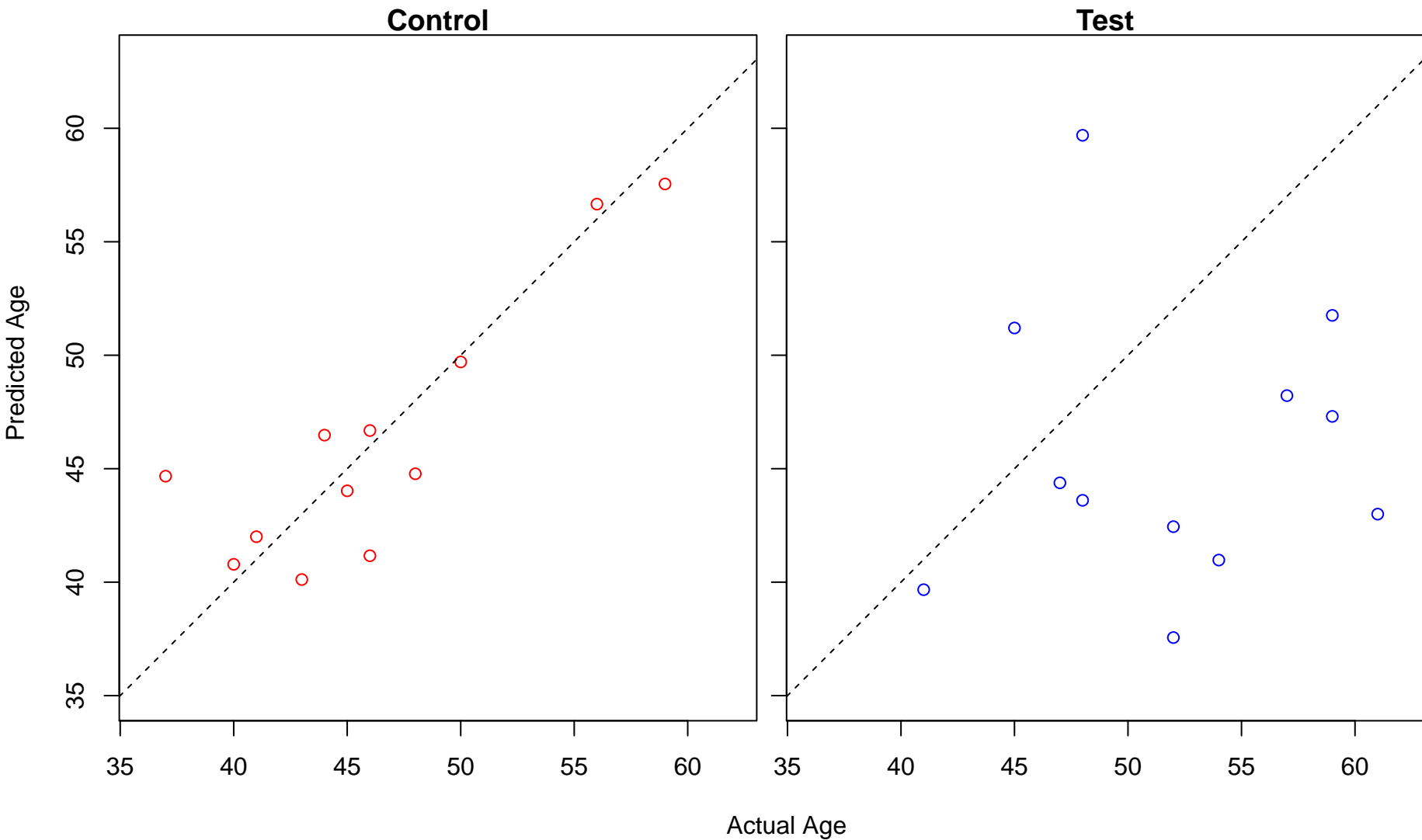


Test

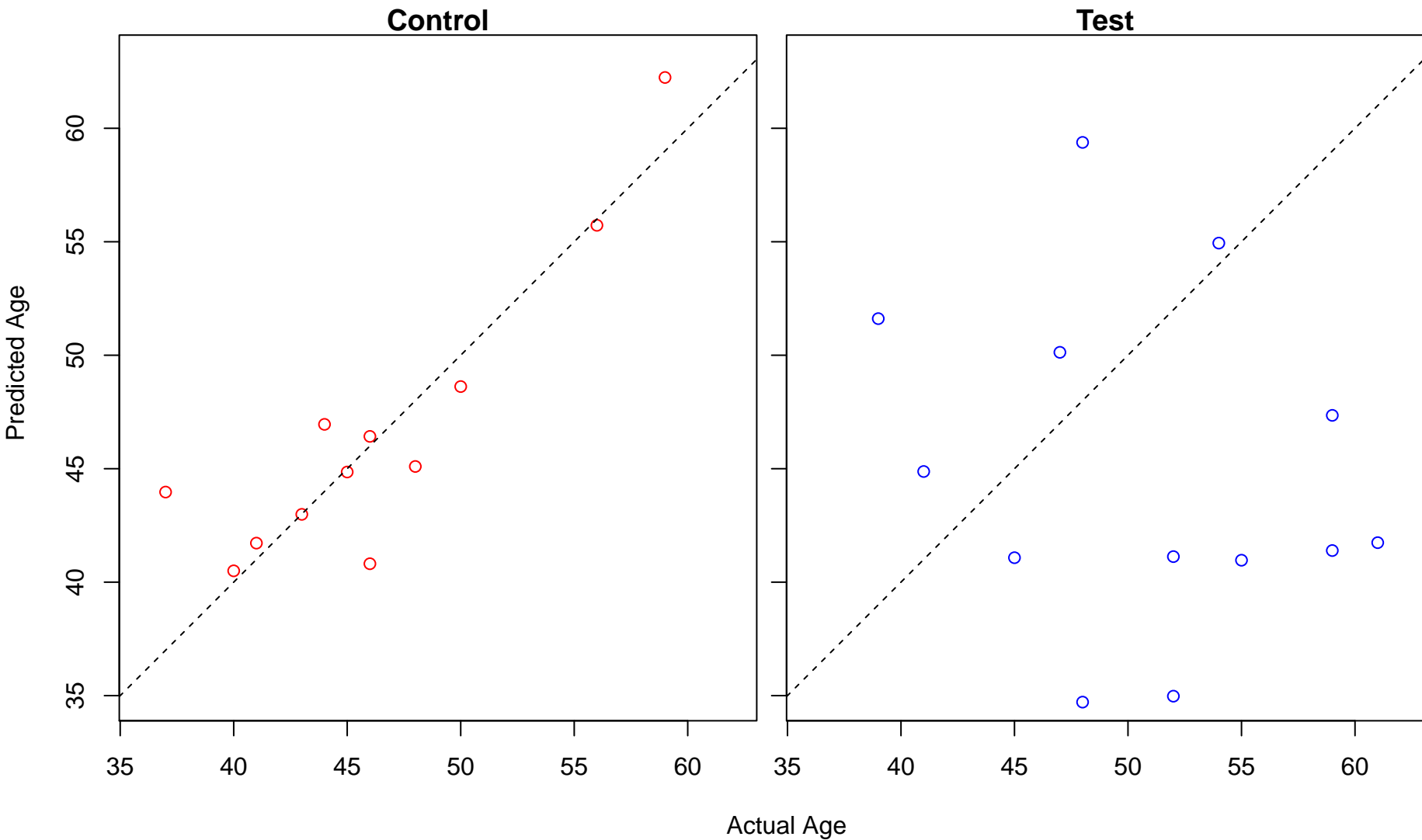


Actual Age

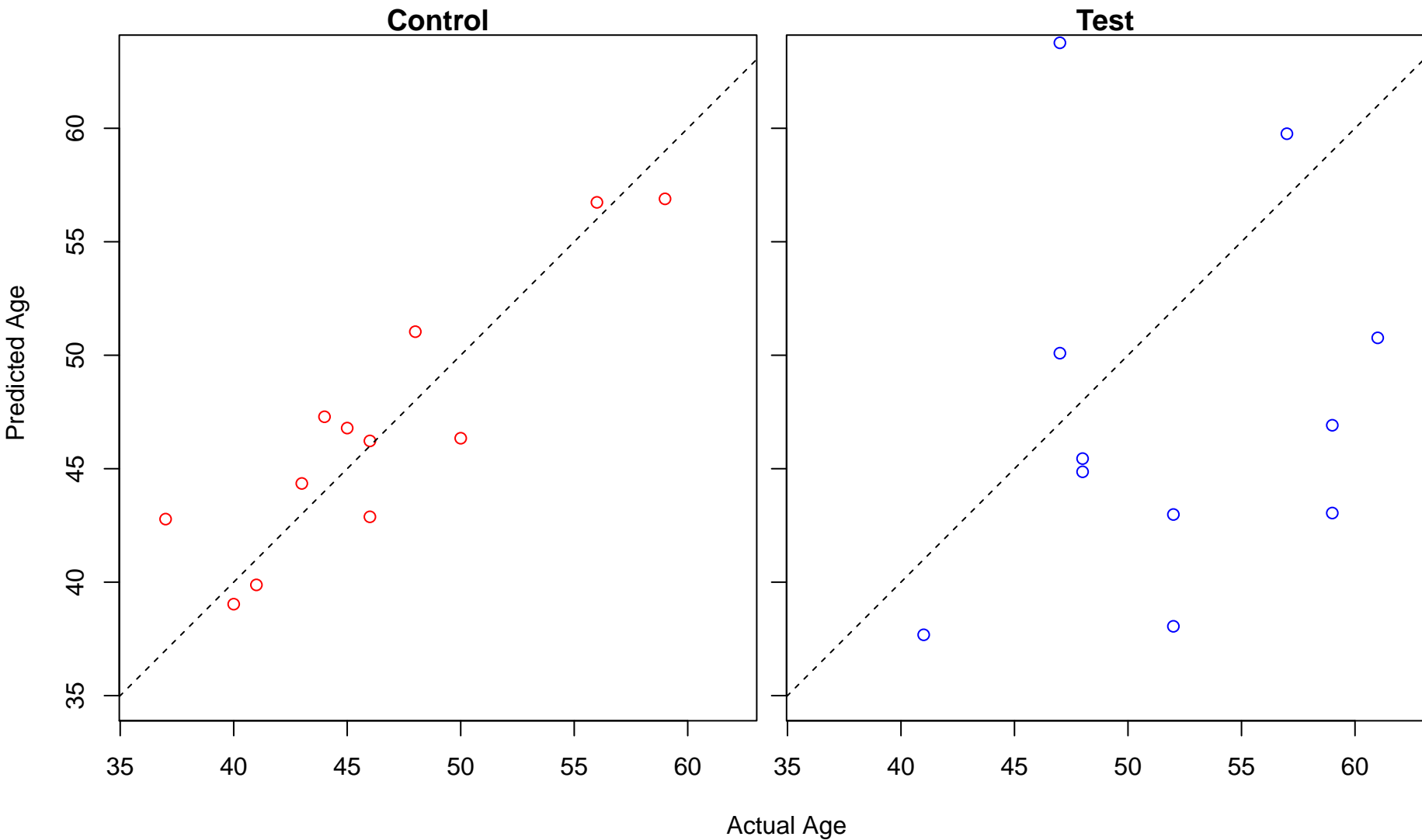
positive regulation of potassium ion transport (Score: 6.945181)



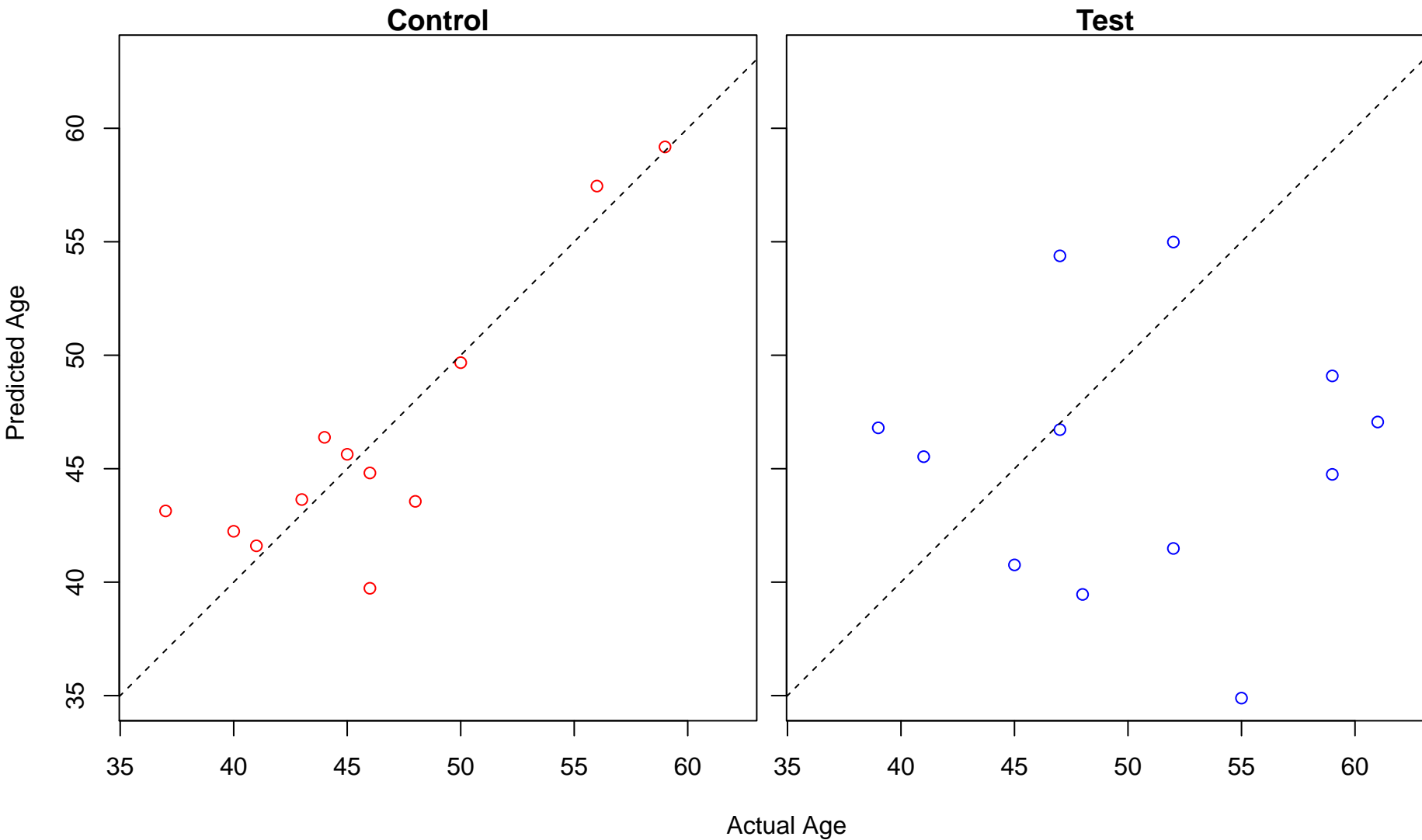
positive regulation of transporter activity (Score: 6.936704)



regulation of cytoplasmic translation (Score: 6.934386)

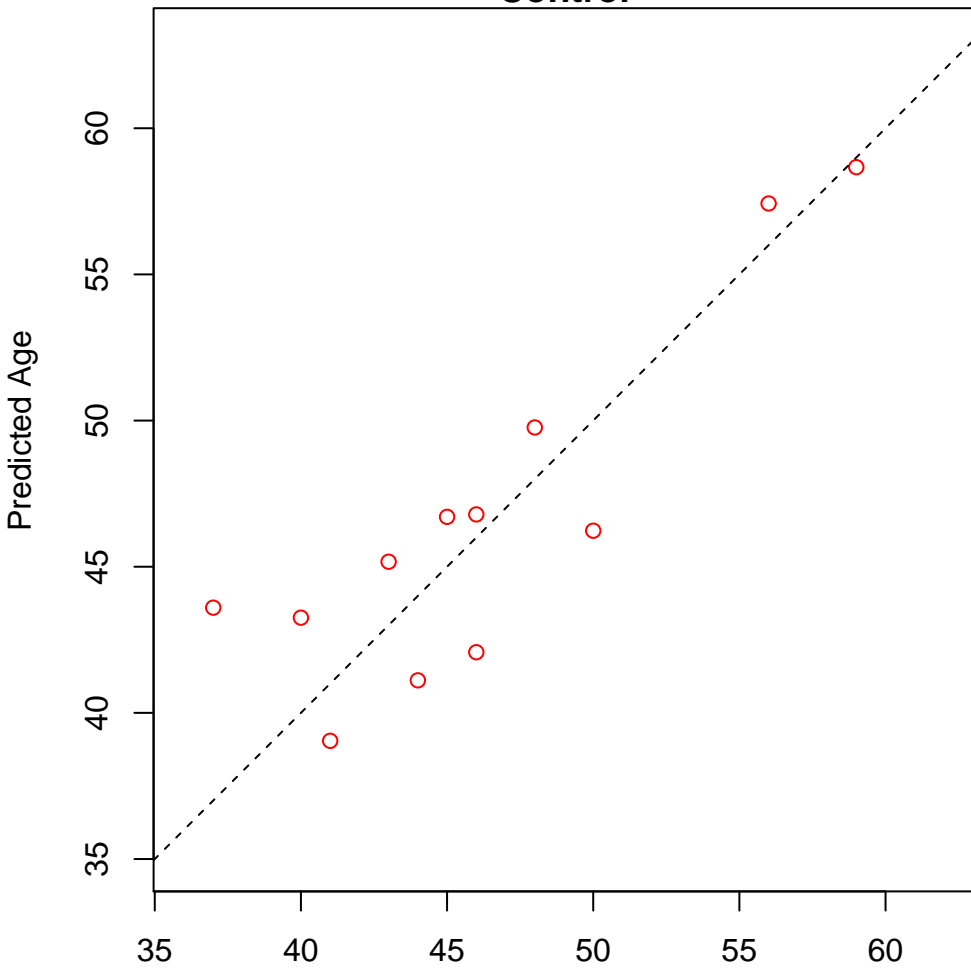


relaxation of cardiac muscle (Score: 6.930398)

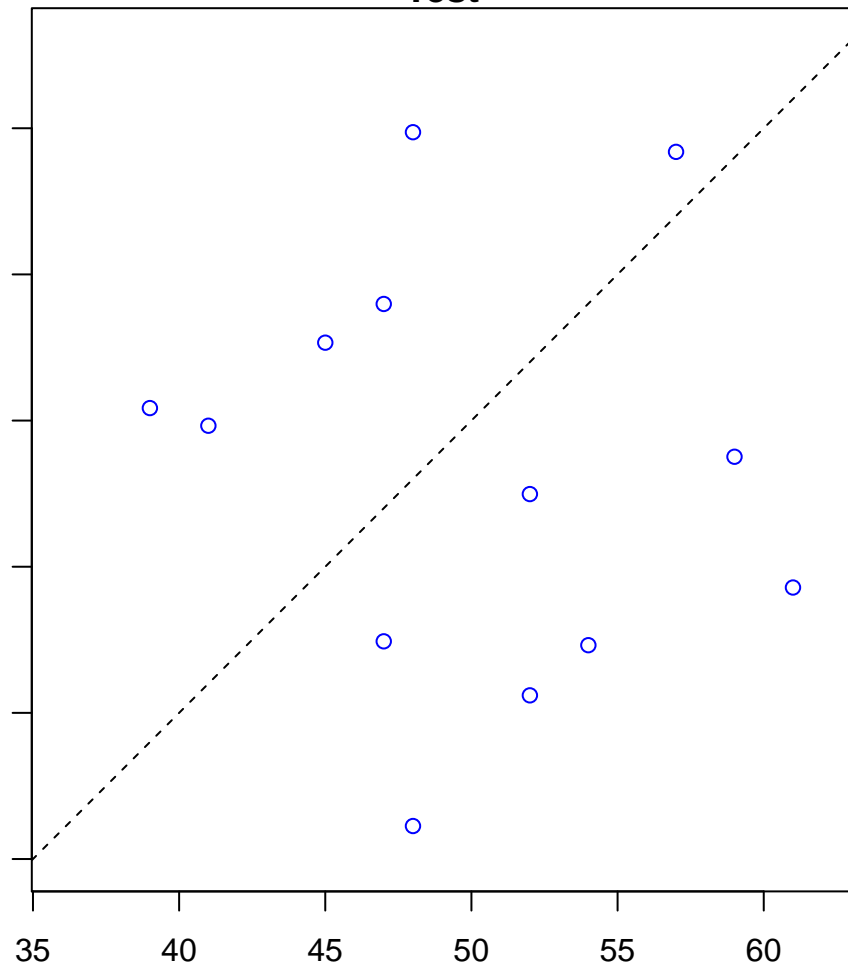


ER to Golgi vesicle-mediated transport (Score: 6.929138)

Control

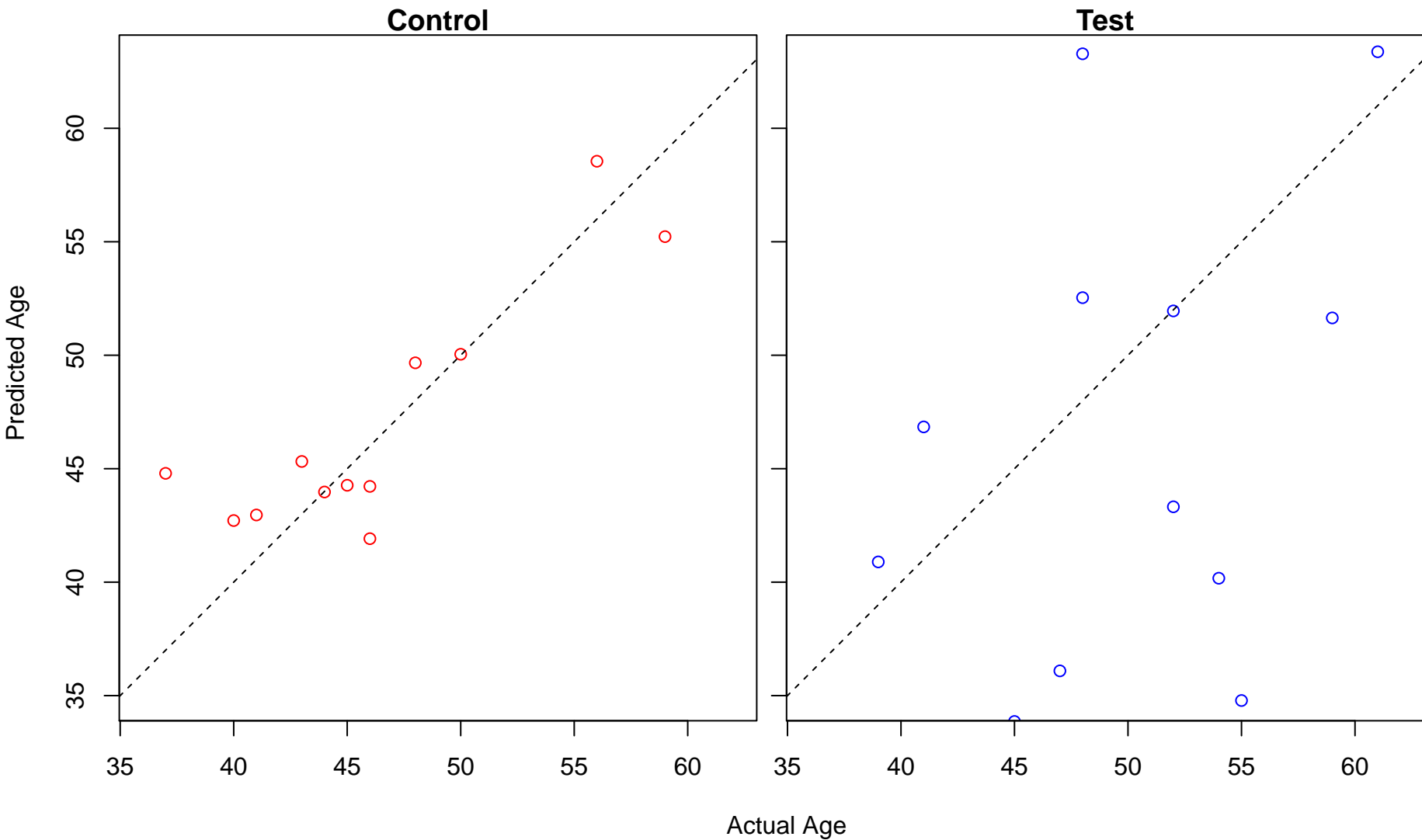


Test

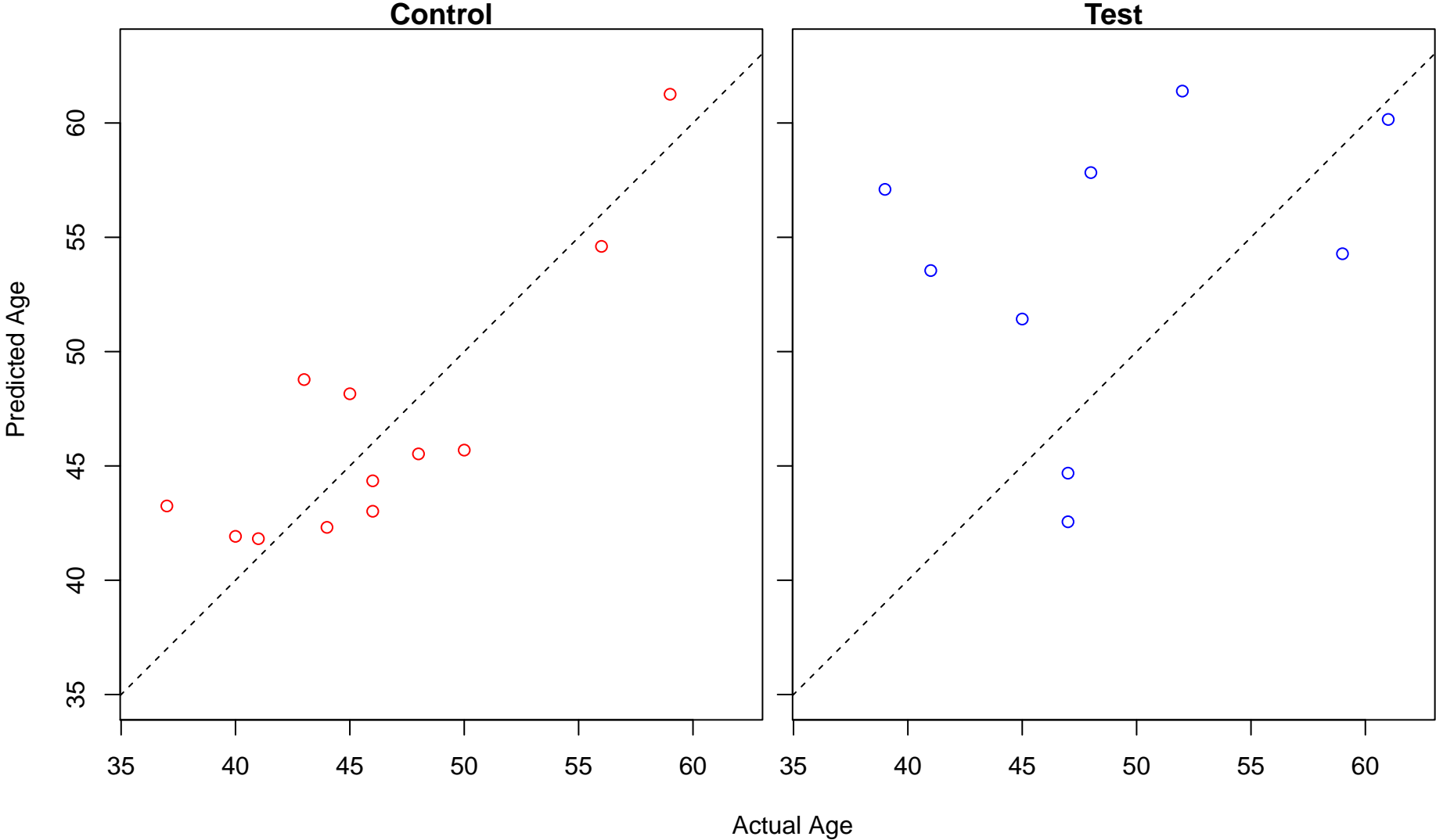


Actual Age

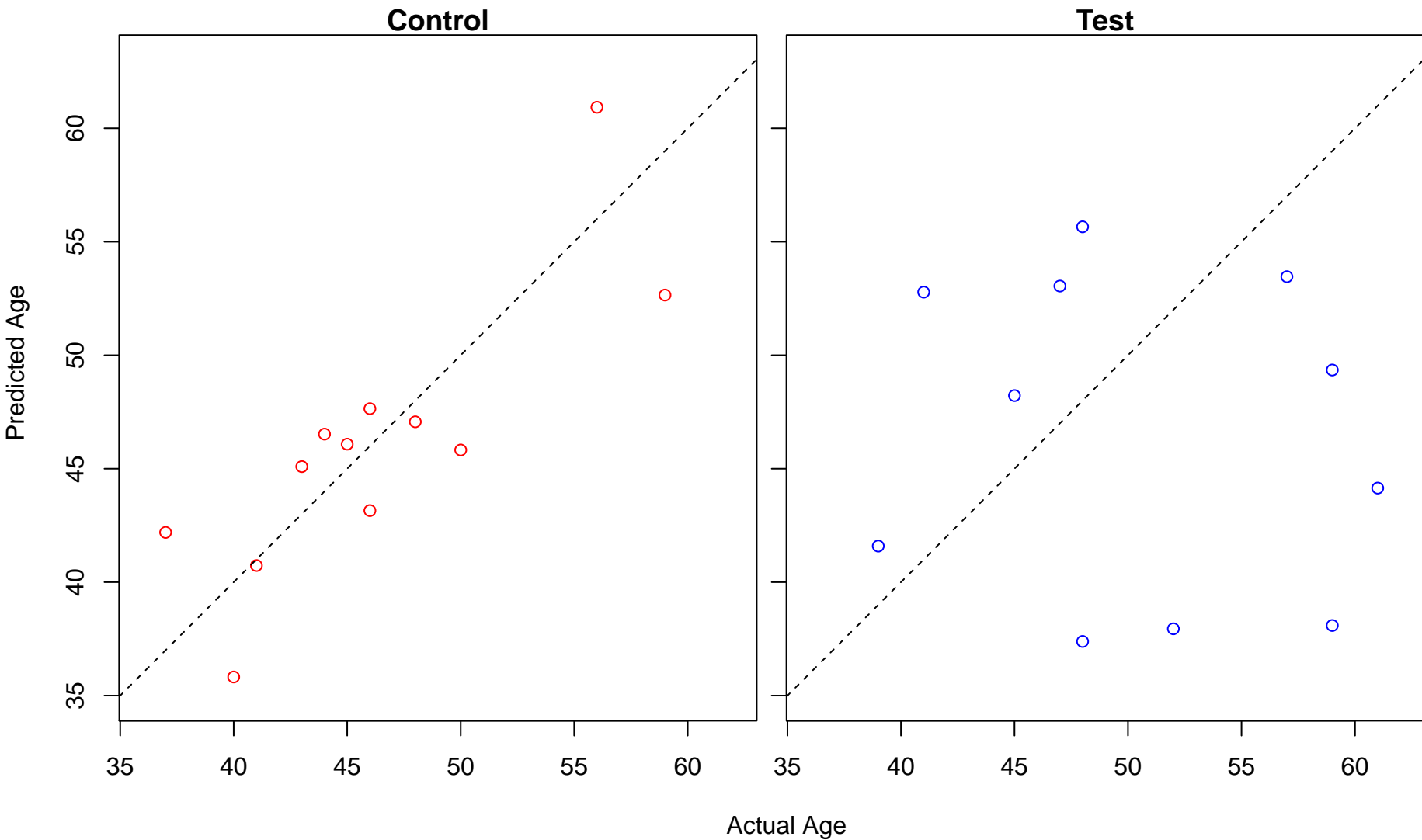
negative regulation of leukocyte migration (Score: 6.917905)



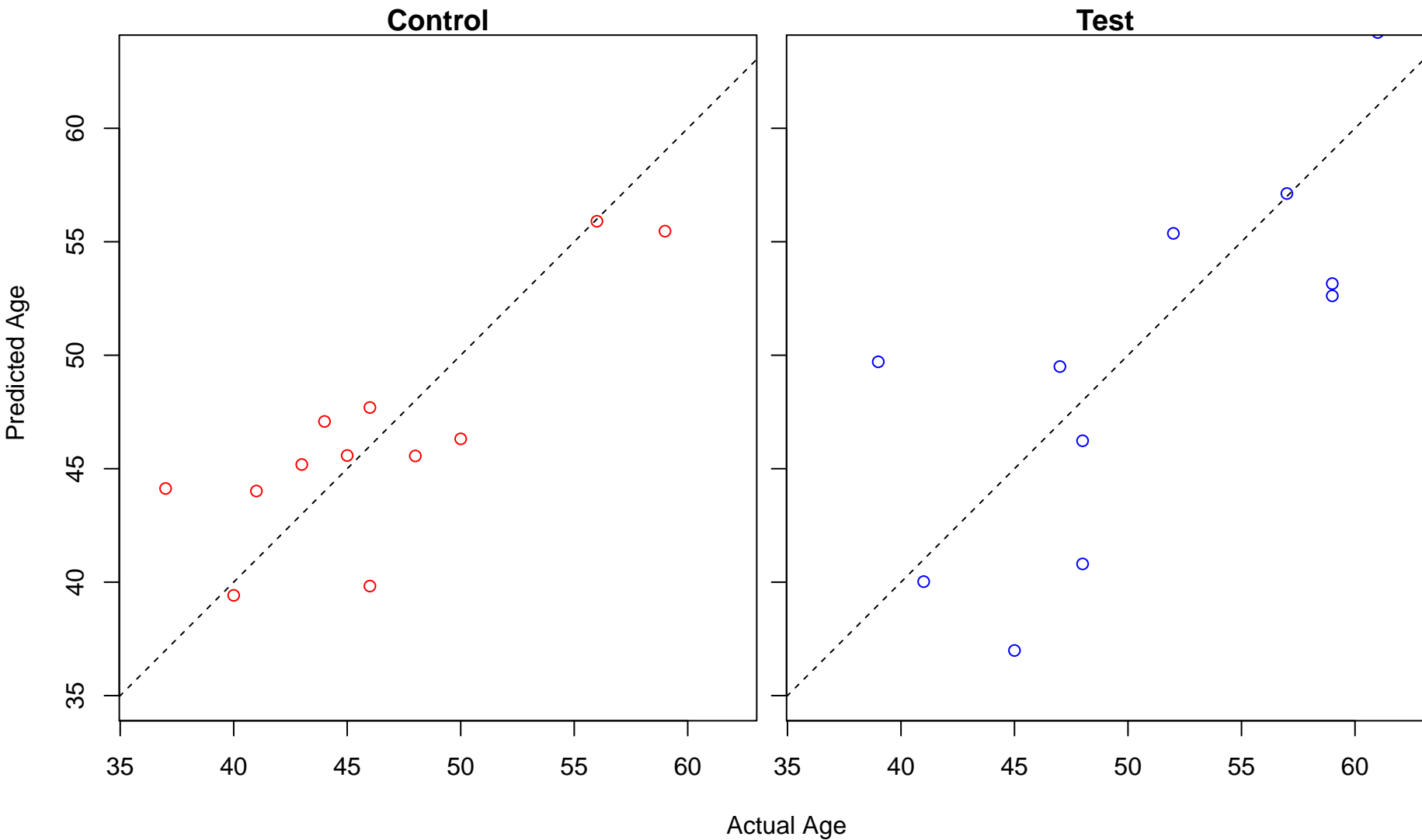
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 6.90)



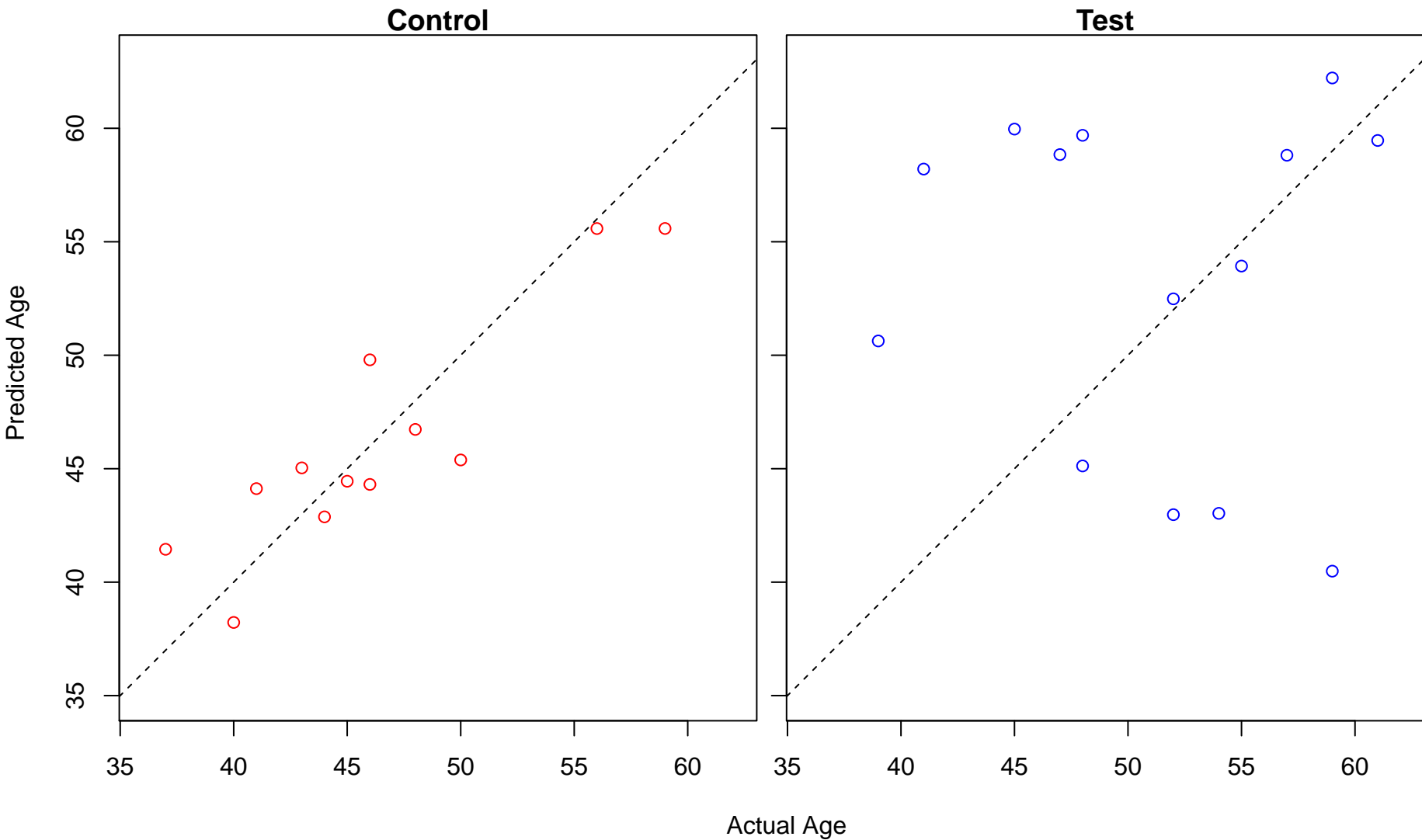
regulation of peptidyl-tyrosine phosphorylation (Score: 6.905915)



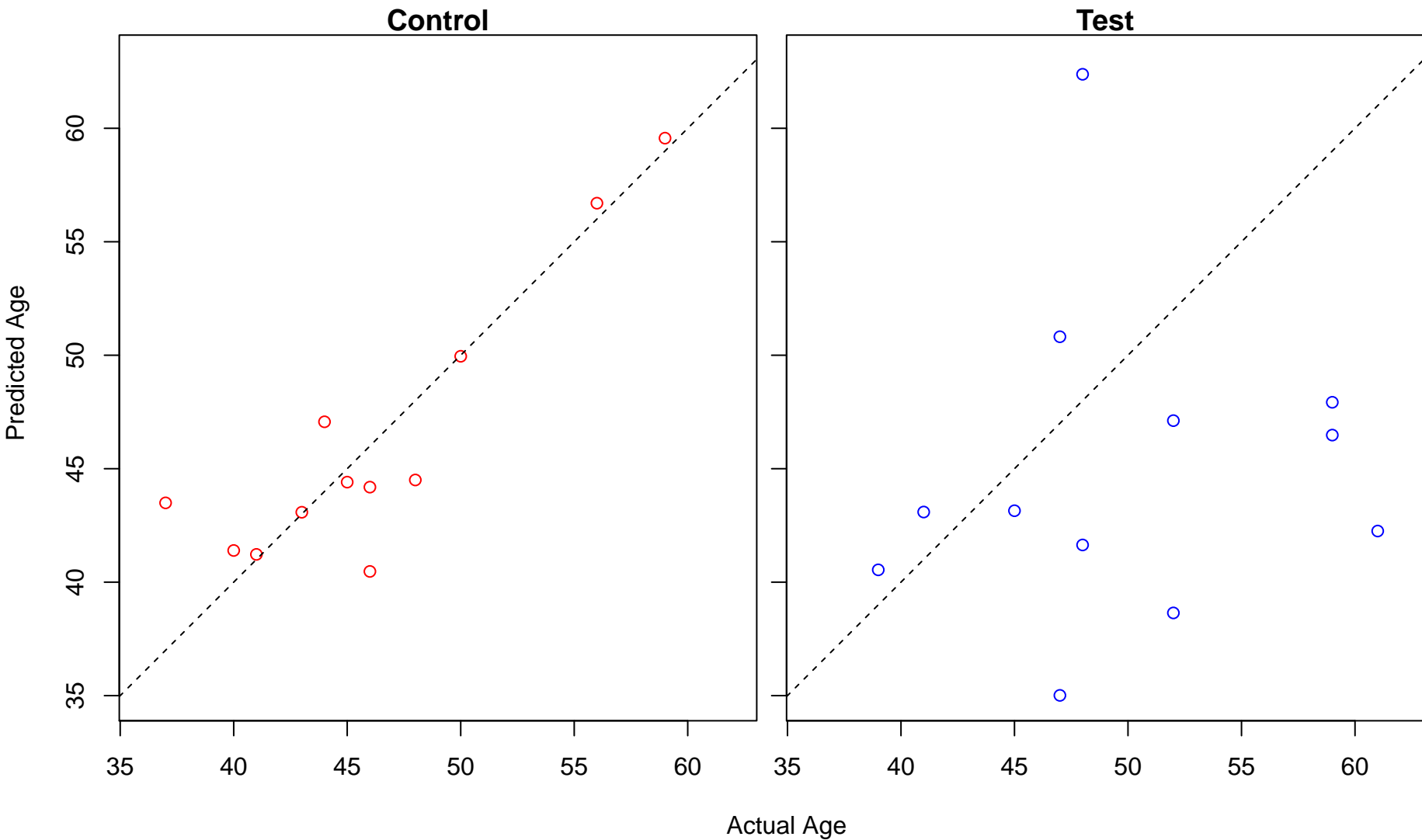
positive regulation of transforming growth factor beta production (Score: 6.886806)



cellular response to interleukin-1 (Score: 6.883506)

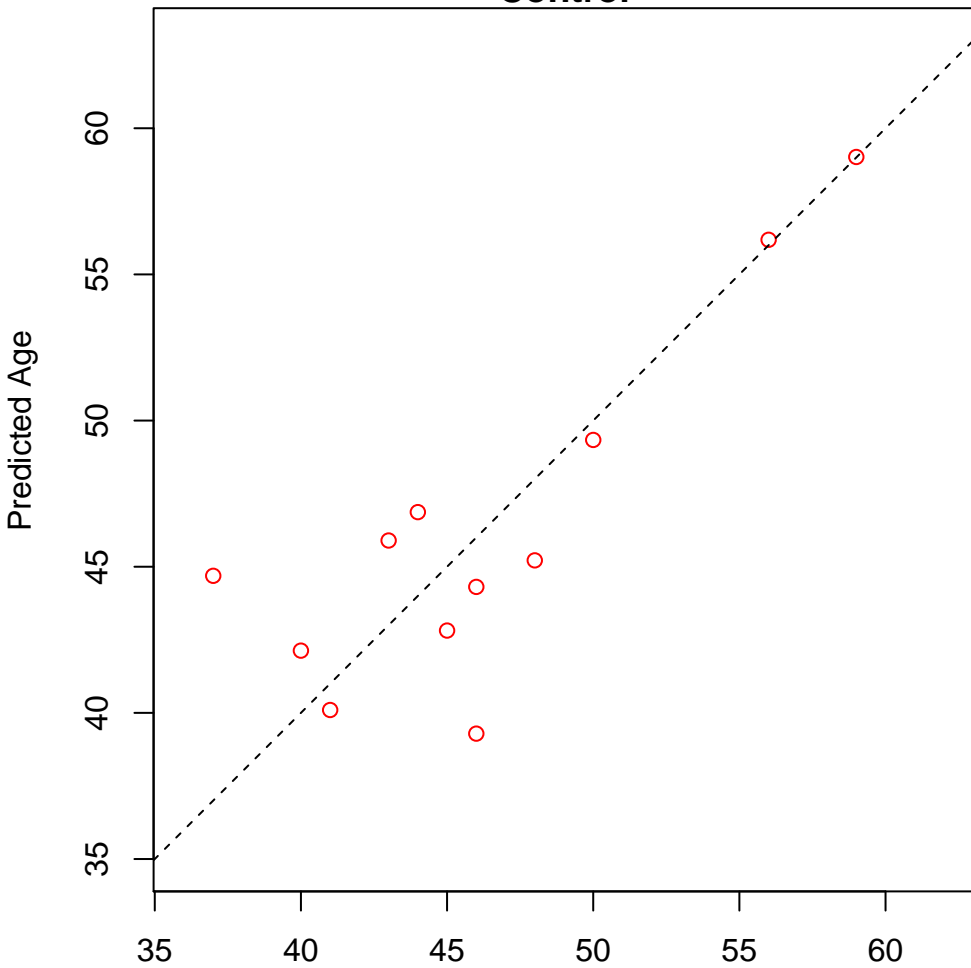


calcium-mediated signaling (Score: 6.873434)

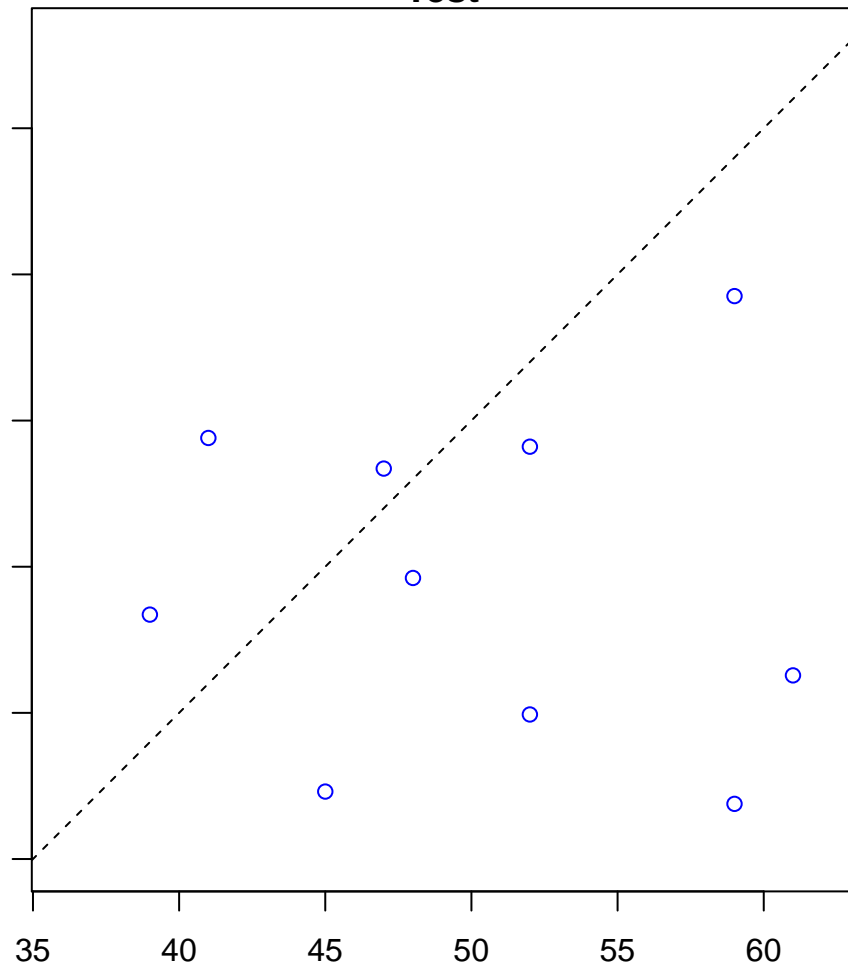


protein localization to plasma membrane (Score: 6.864204)

Control



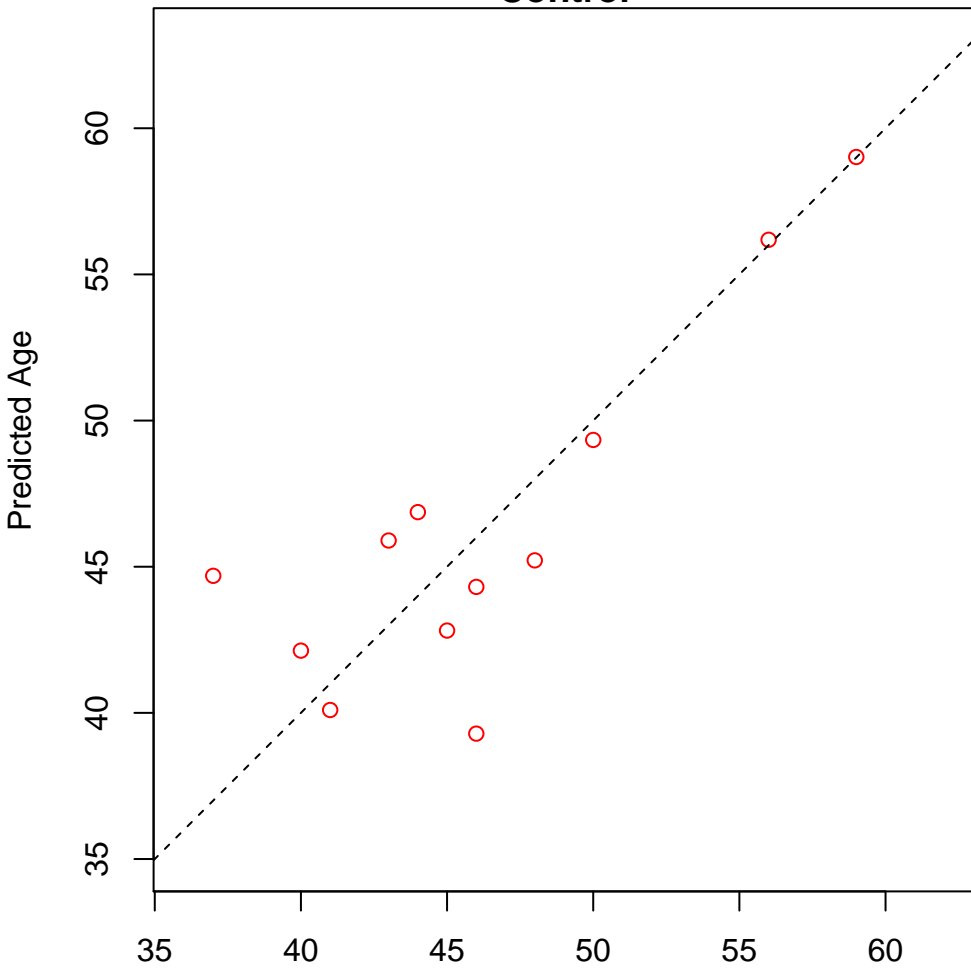
Test



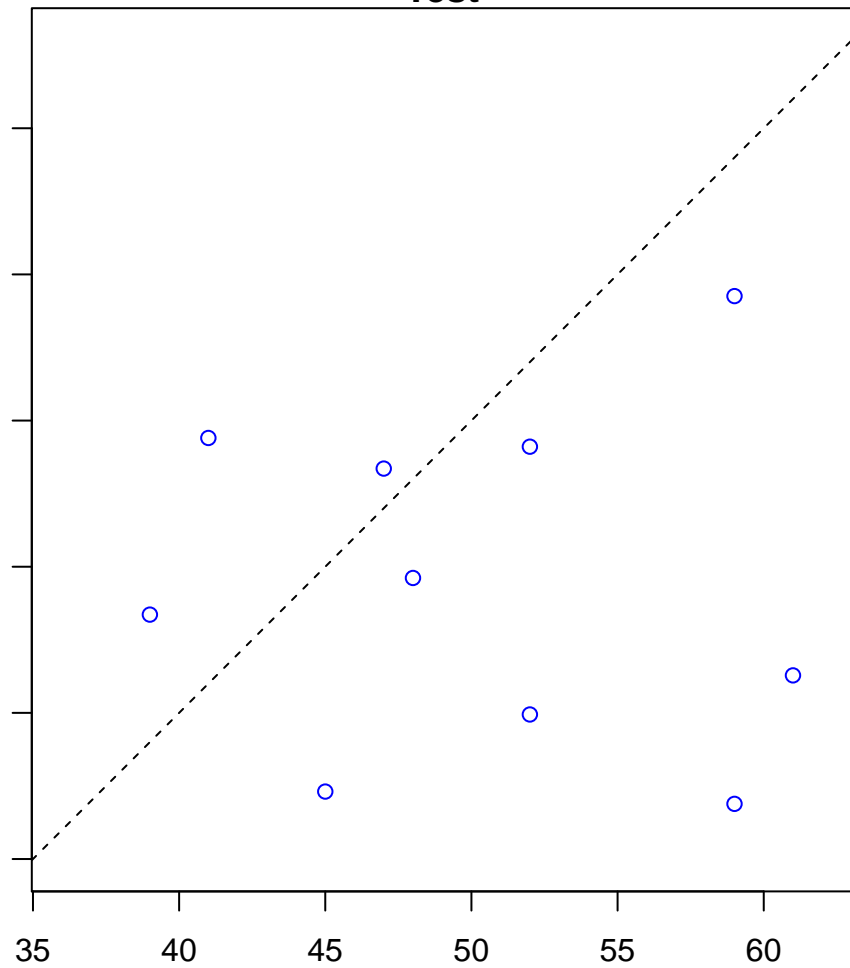
Actual Age

protein localization to cell periphery (Score: 6.864204)

Control

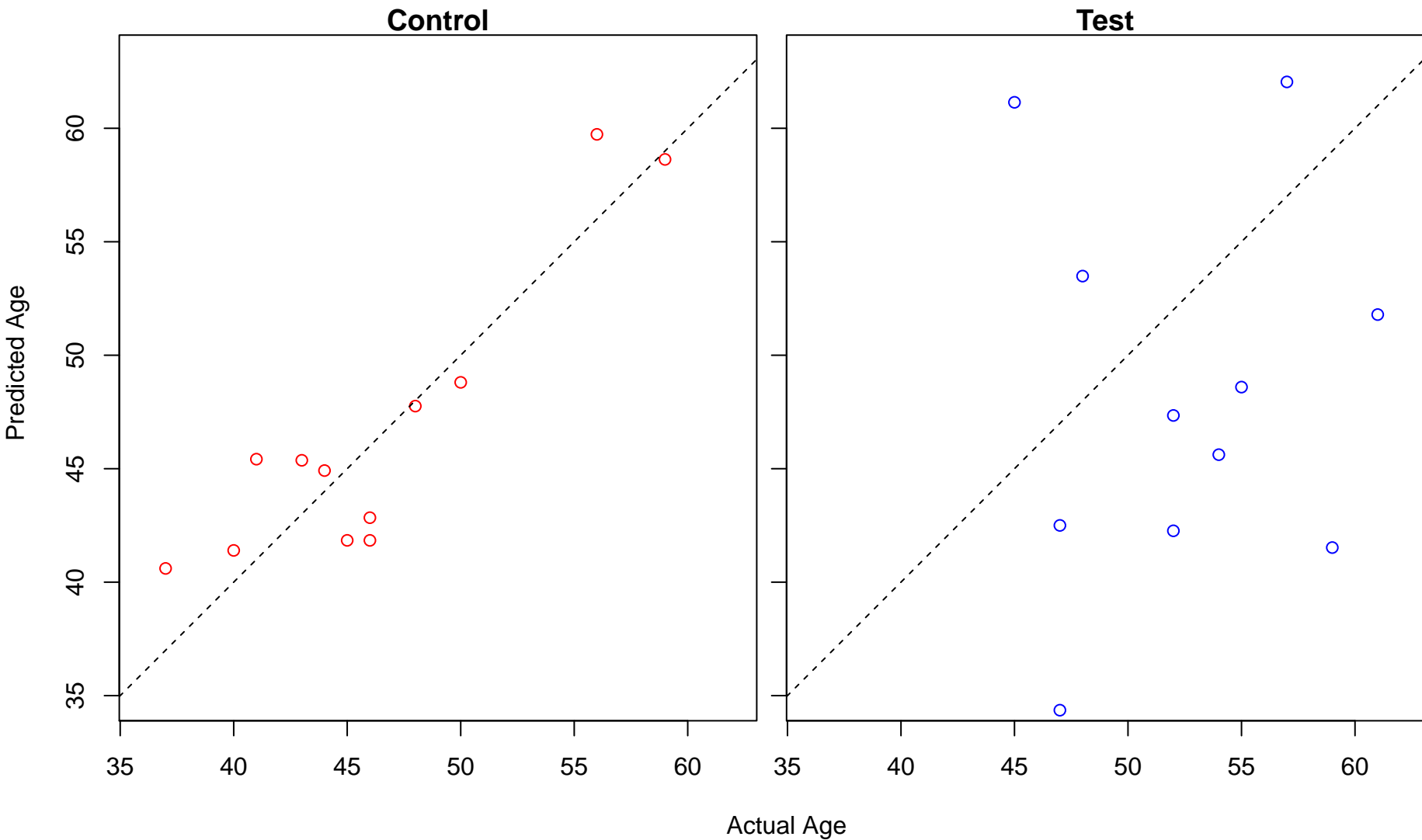


Test

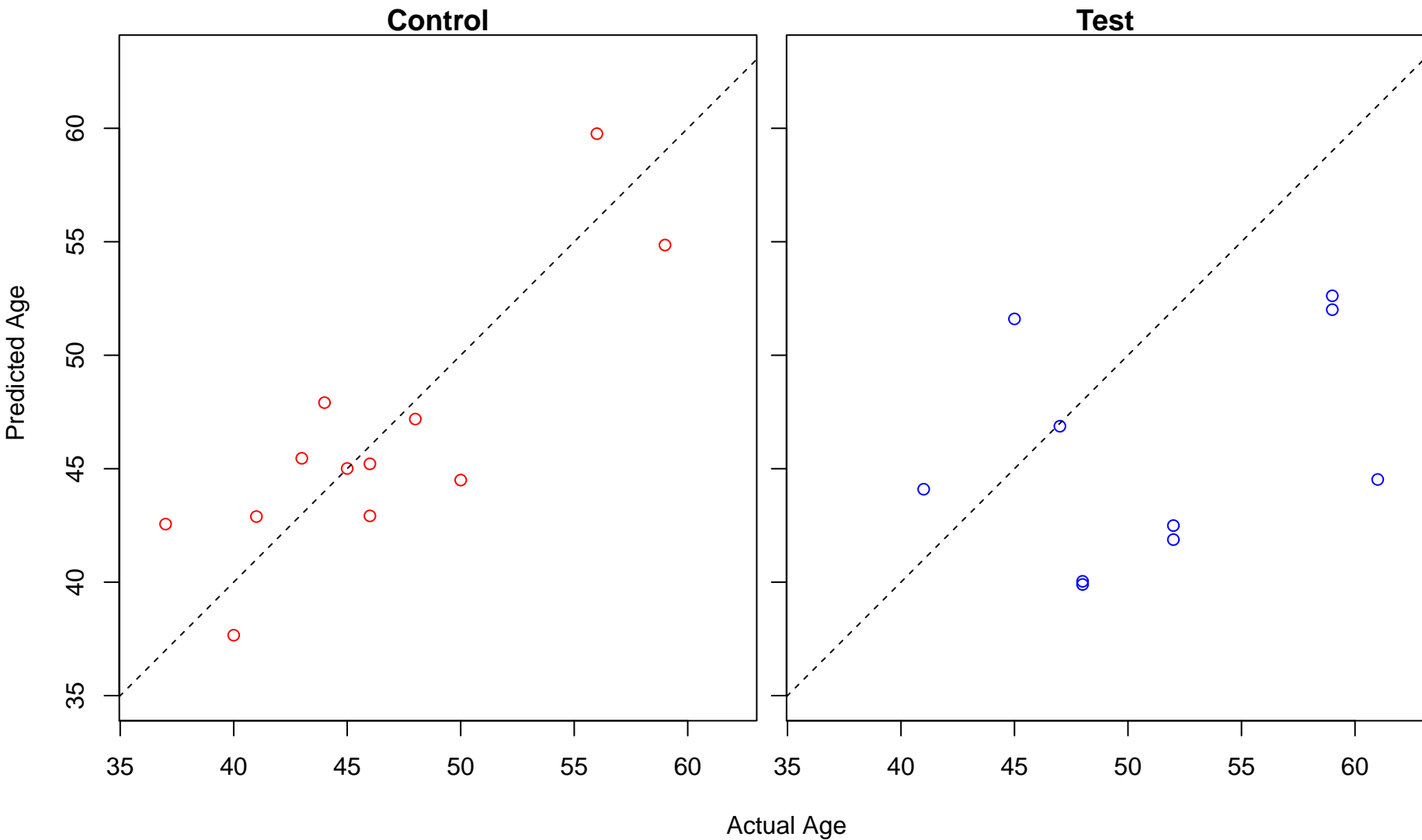


Actual Age

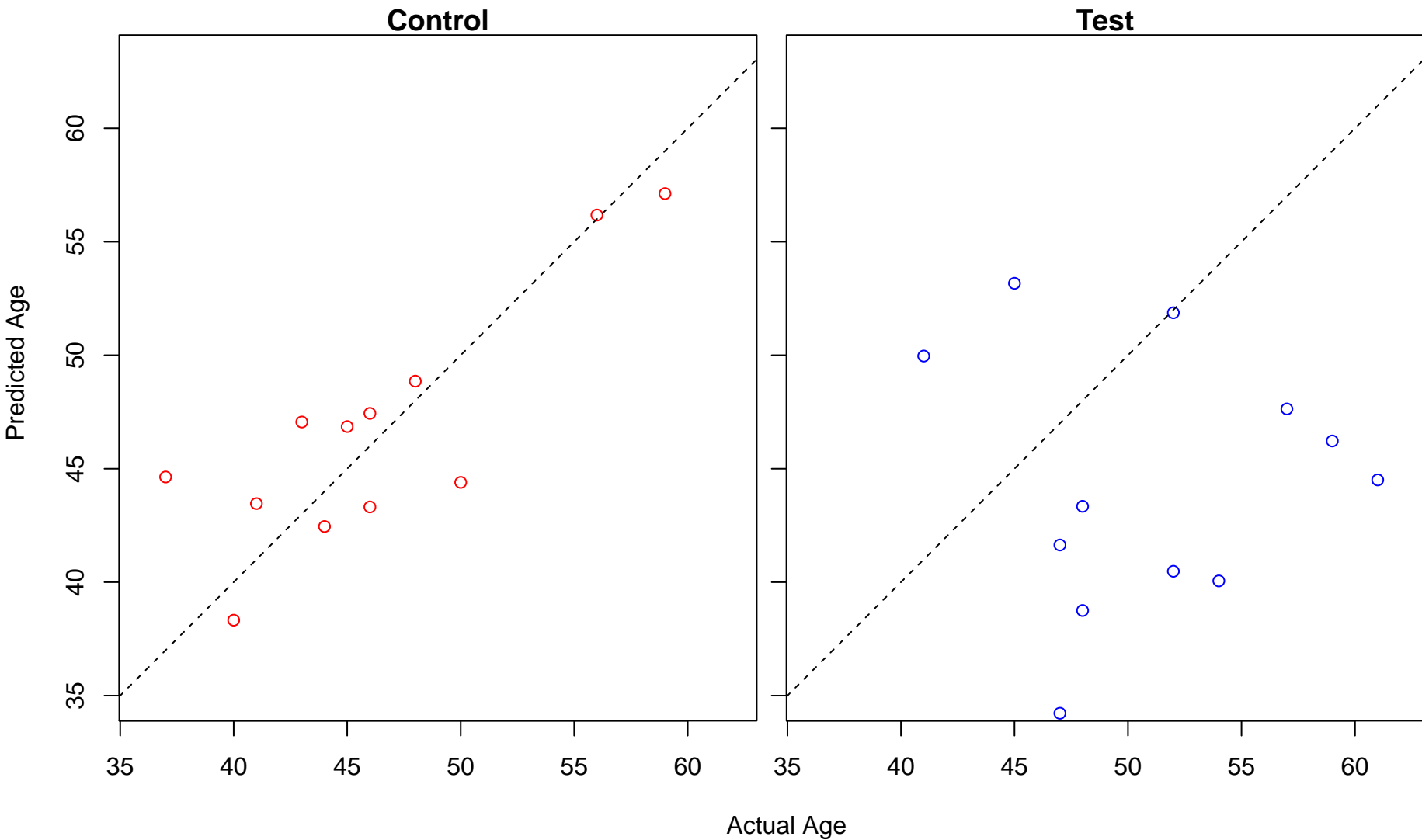
negative regulation of lipid metabolic process (Score: 6.863455)



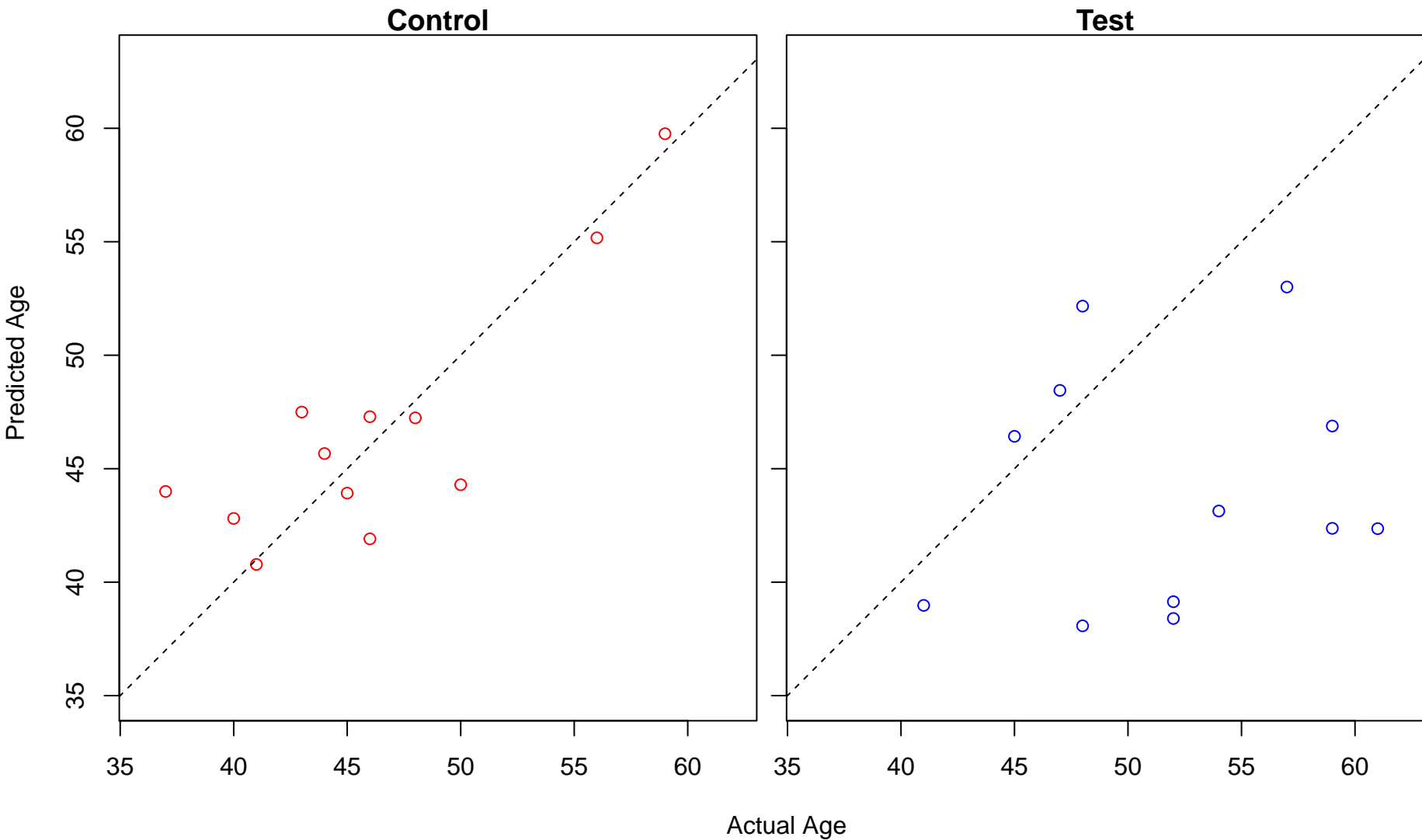
regulation of viral life cycle (Score: 6.863154)



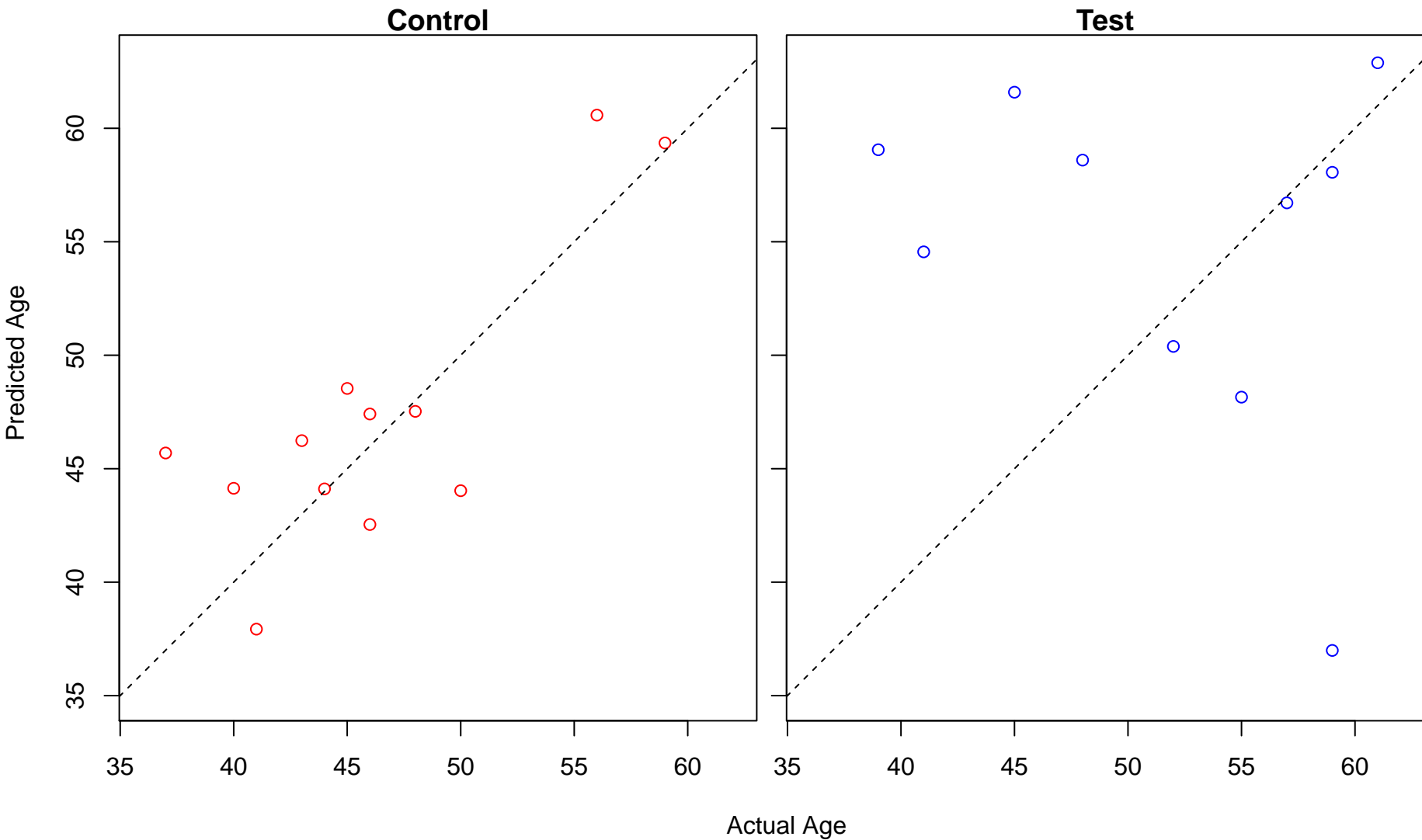
regulation of inflammatory response (Score: 6.850885)



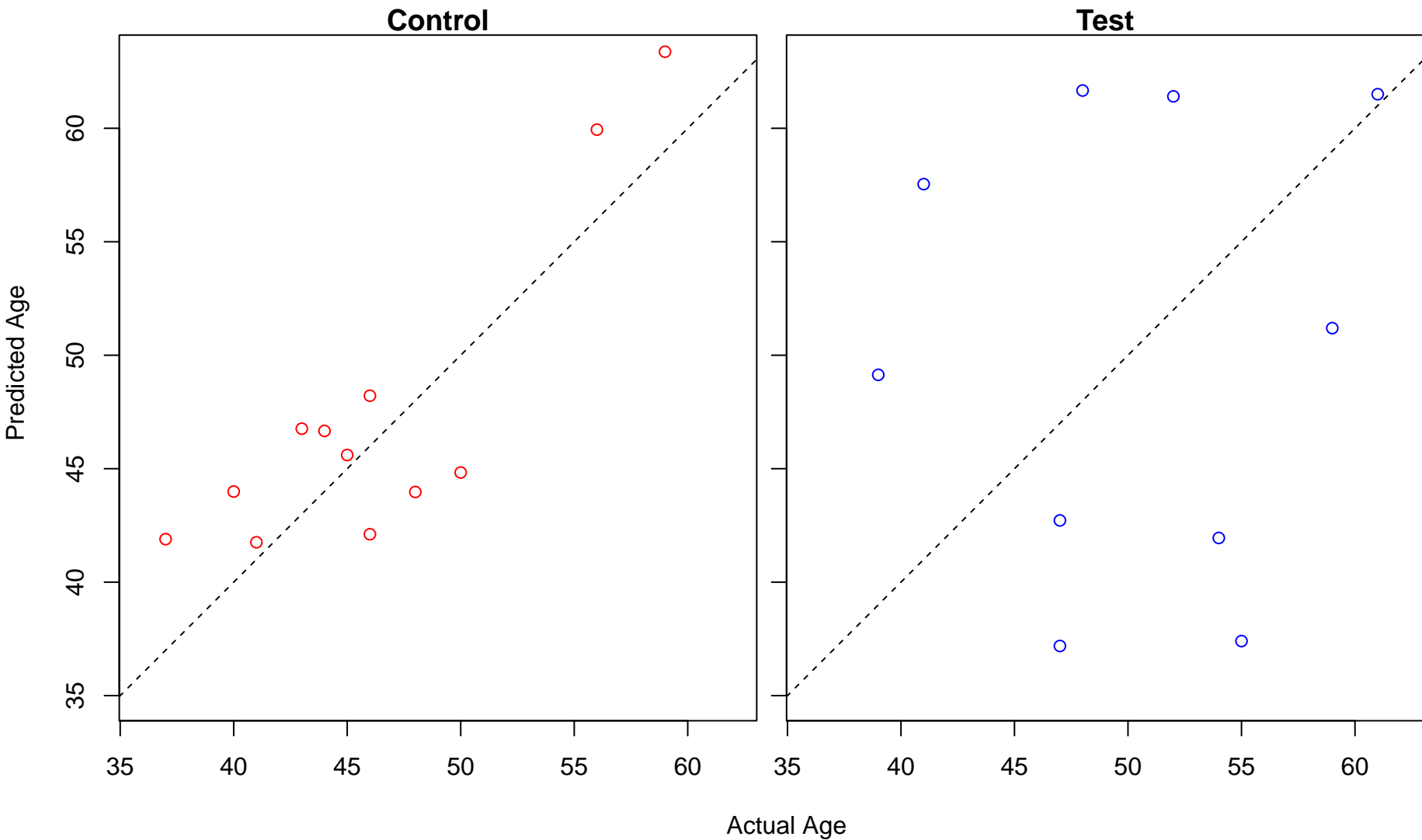
regulation of multi-organism process (Score: 6.848769)



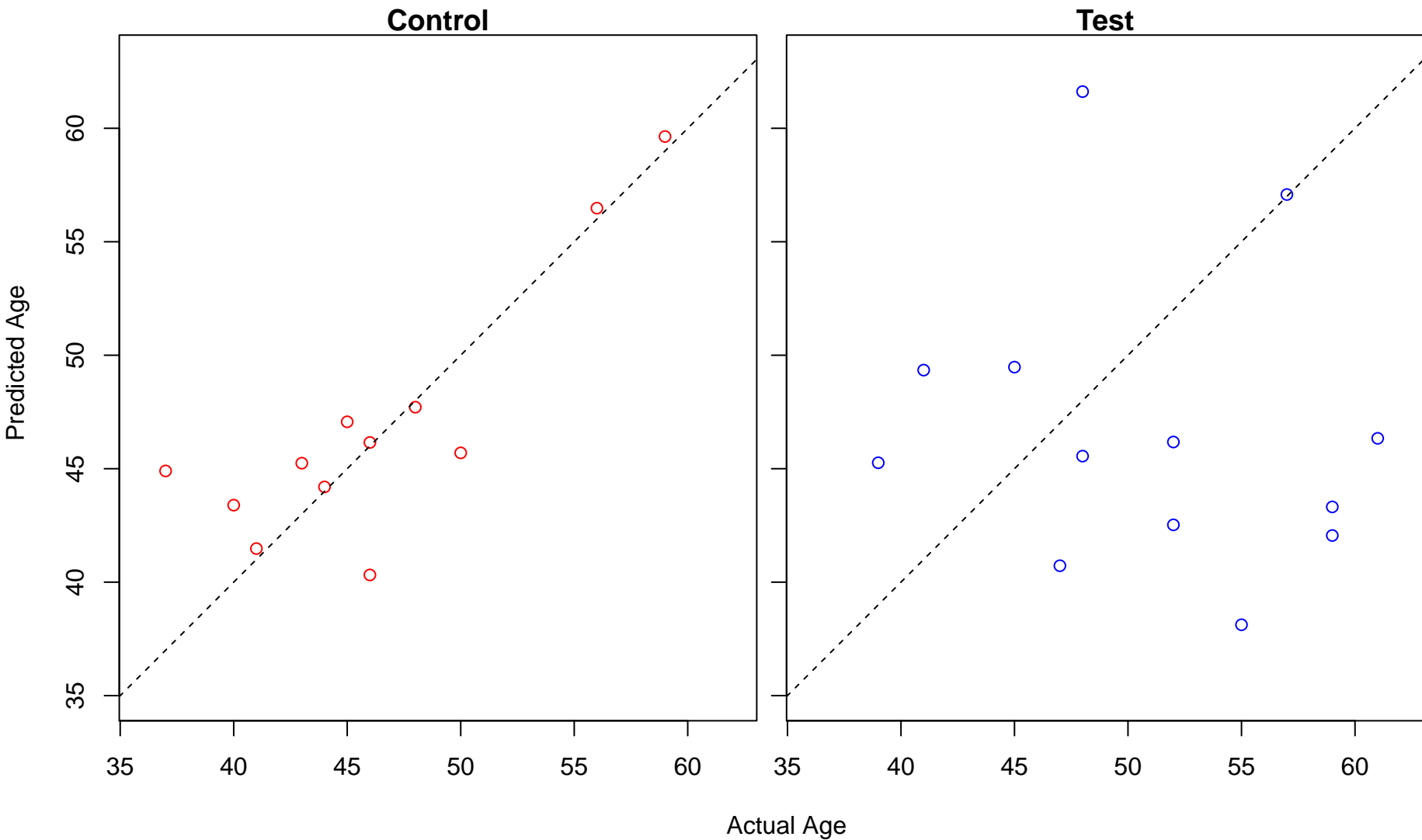
regulation of fatty acid oxidation (Score: 6.826218)



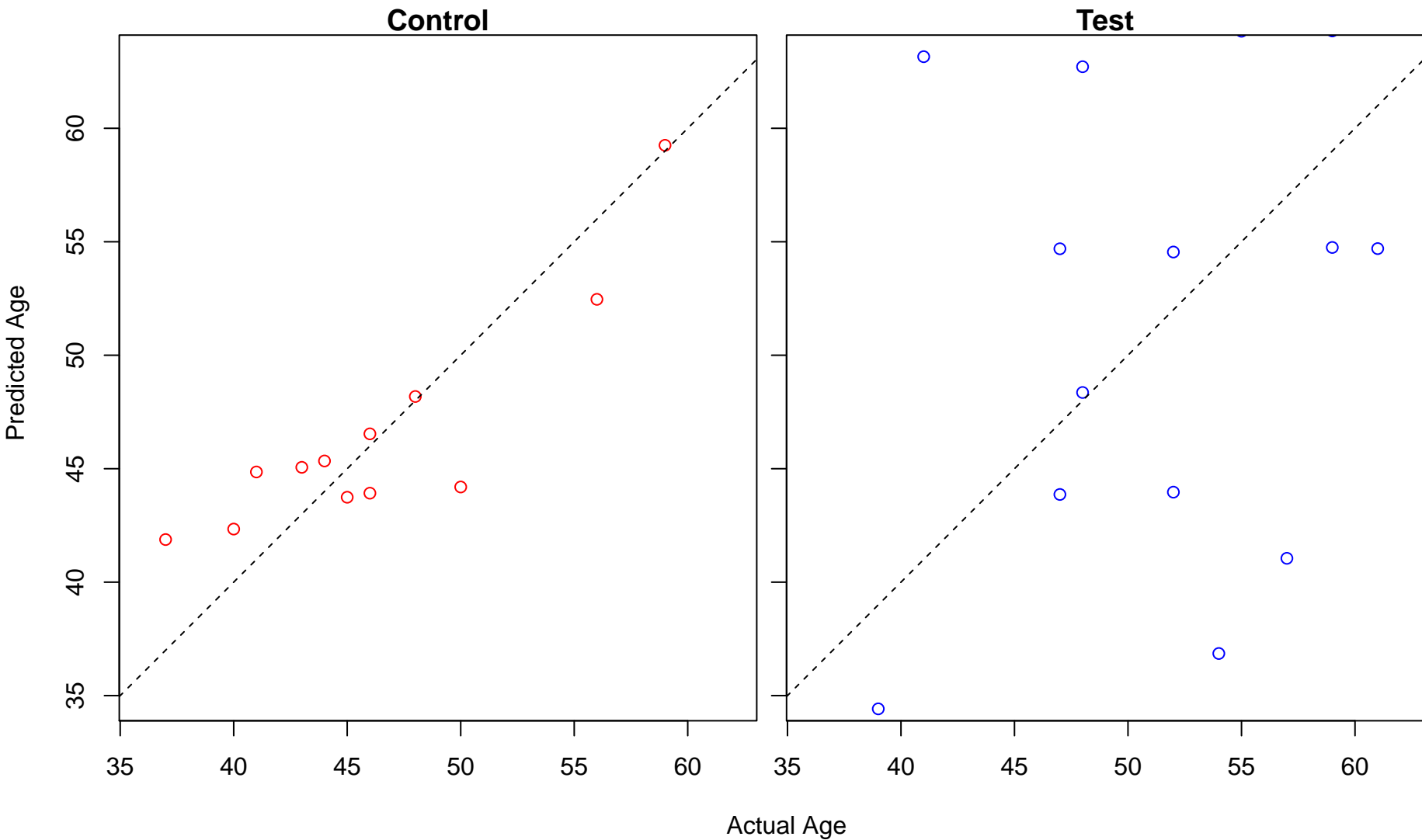
nuclear envelope organization (Score: 6.812214)



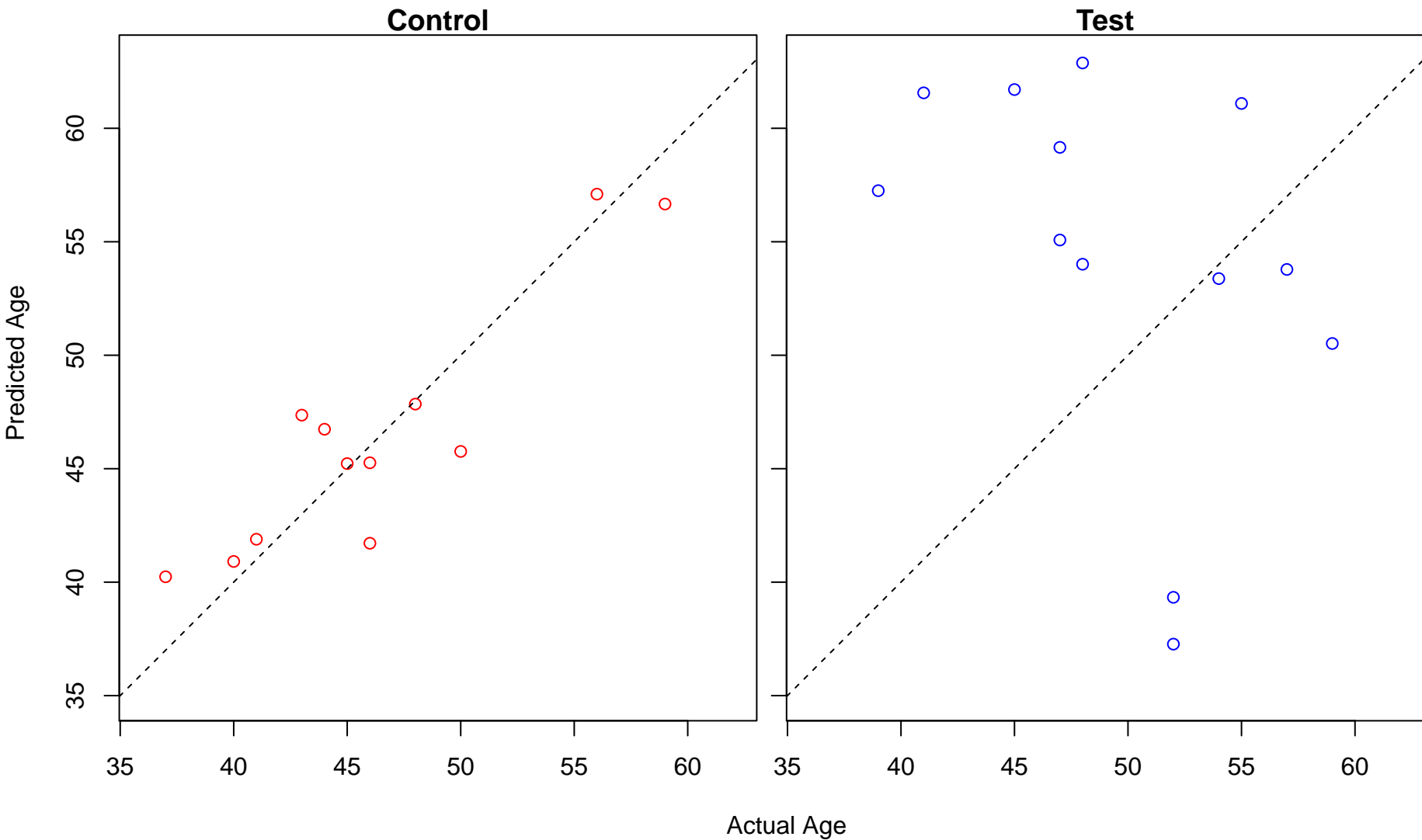
Golgi vesicle transport (Score: 6.799732)



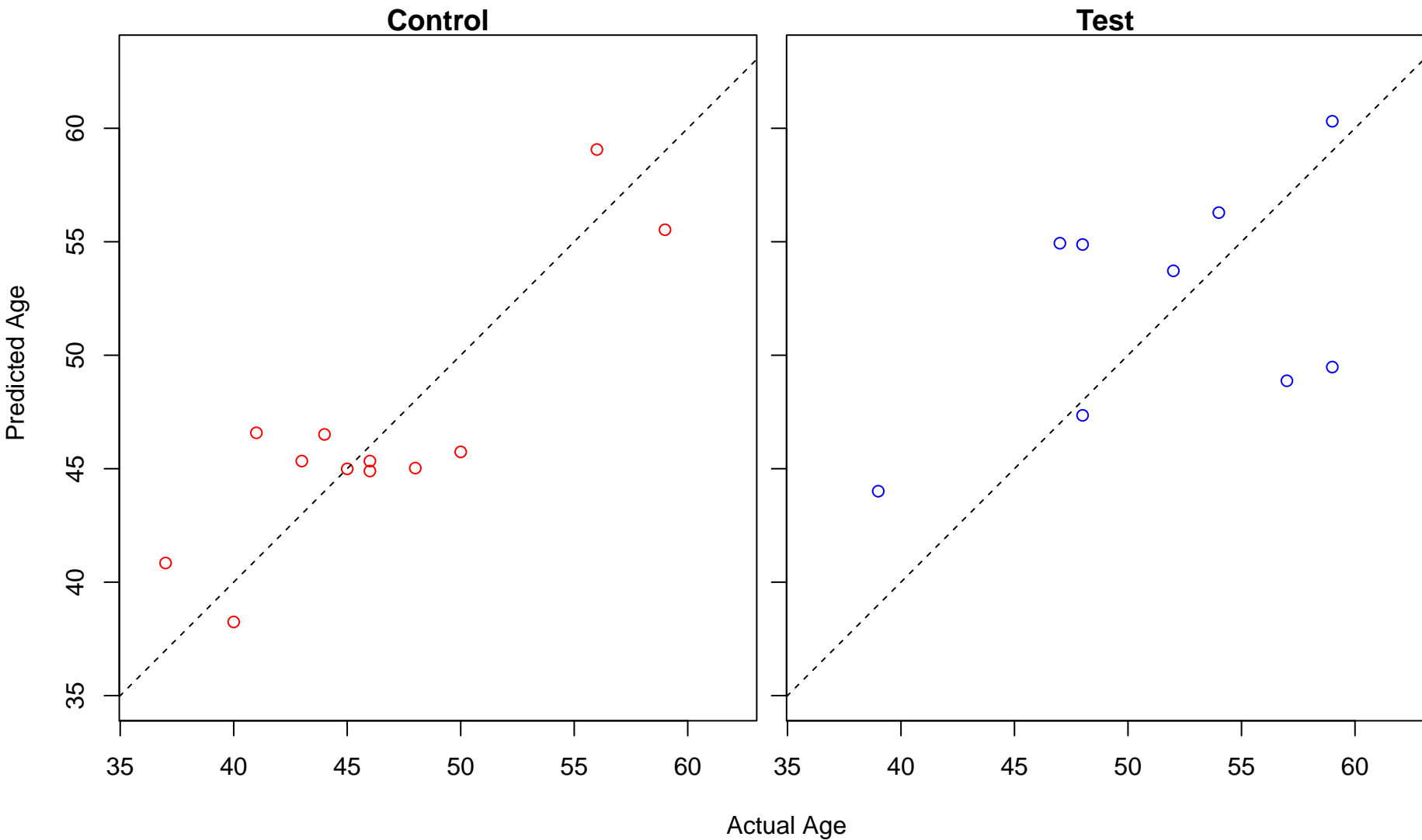
response to carbohydrate (Score: 6.780100)



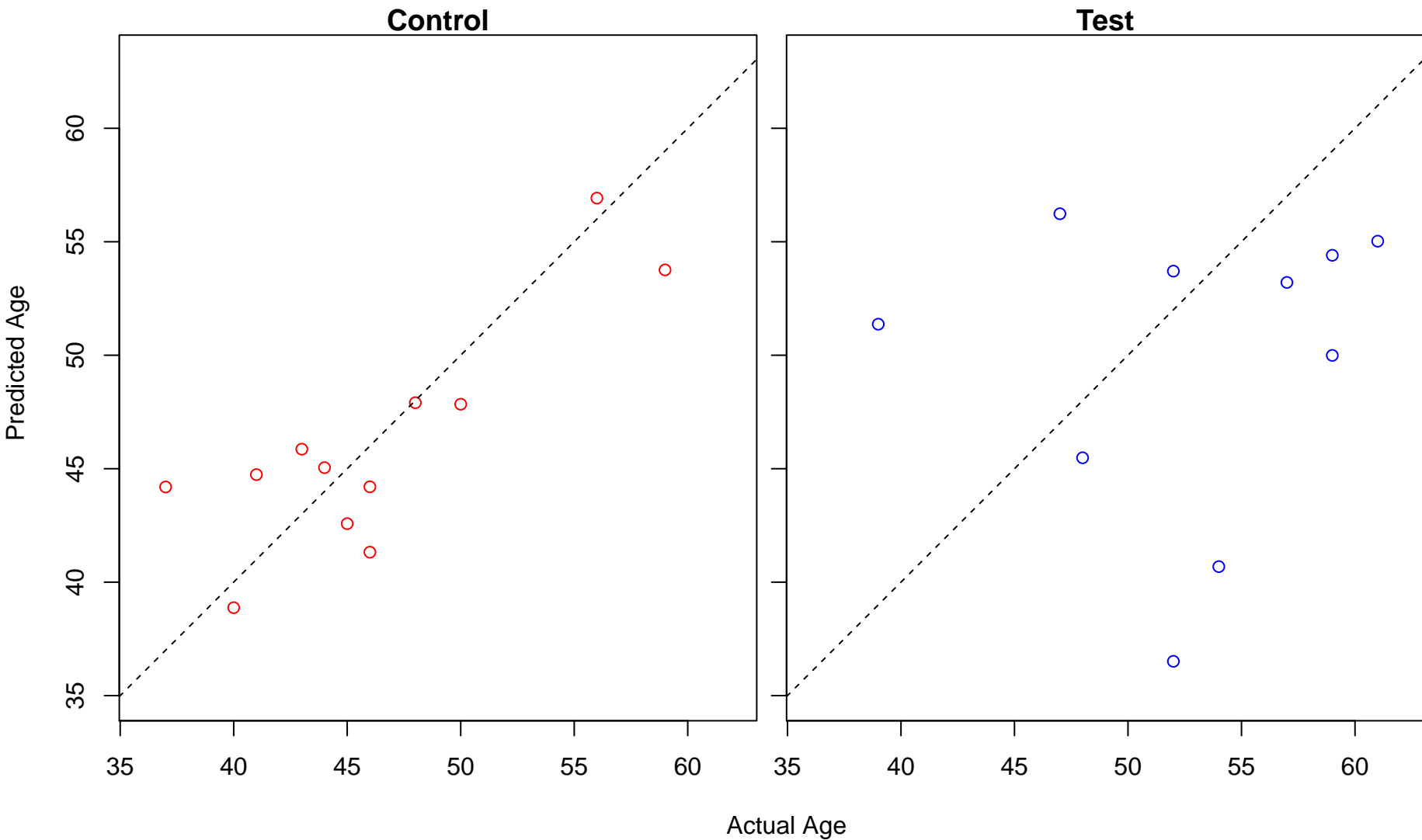
regulation of cytokine-mediated signaling pathway (Score: 6.777139)



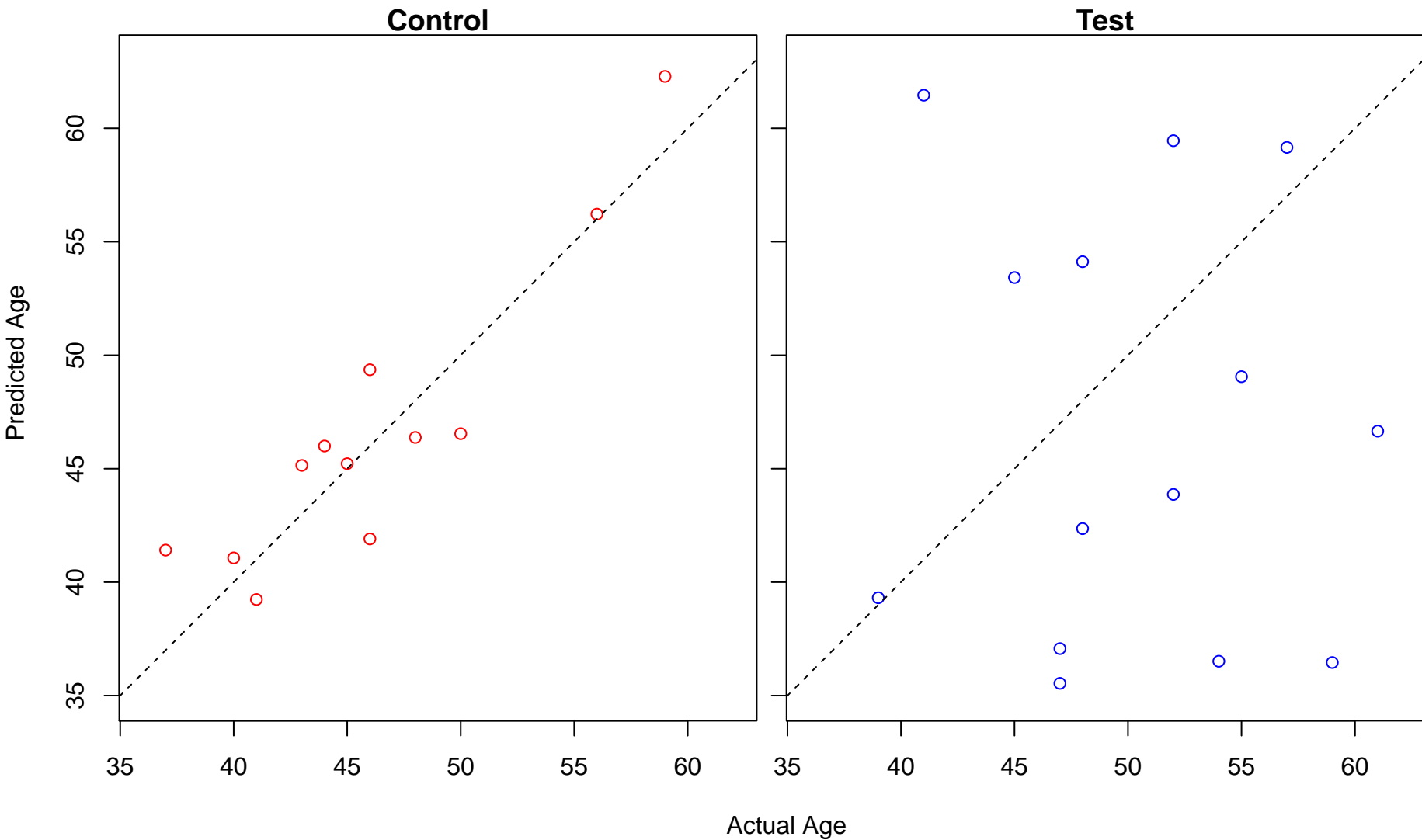
negative regulation of cell adhesion (Score: 6.767207)



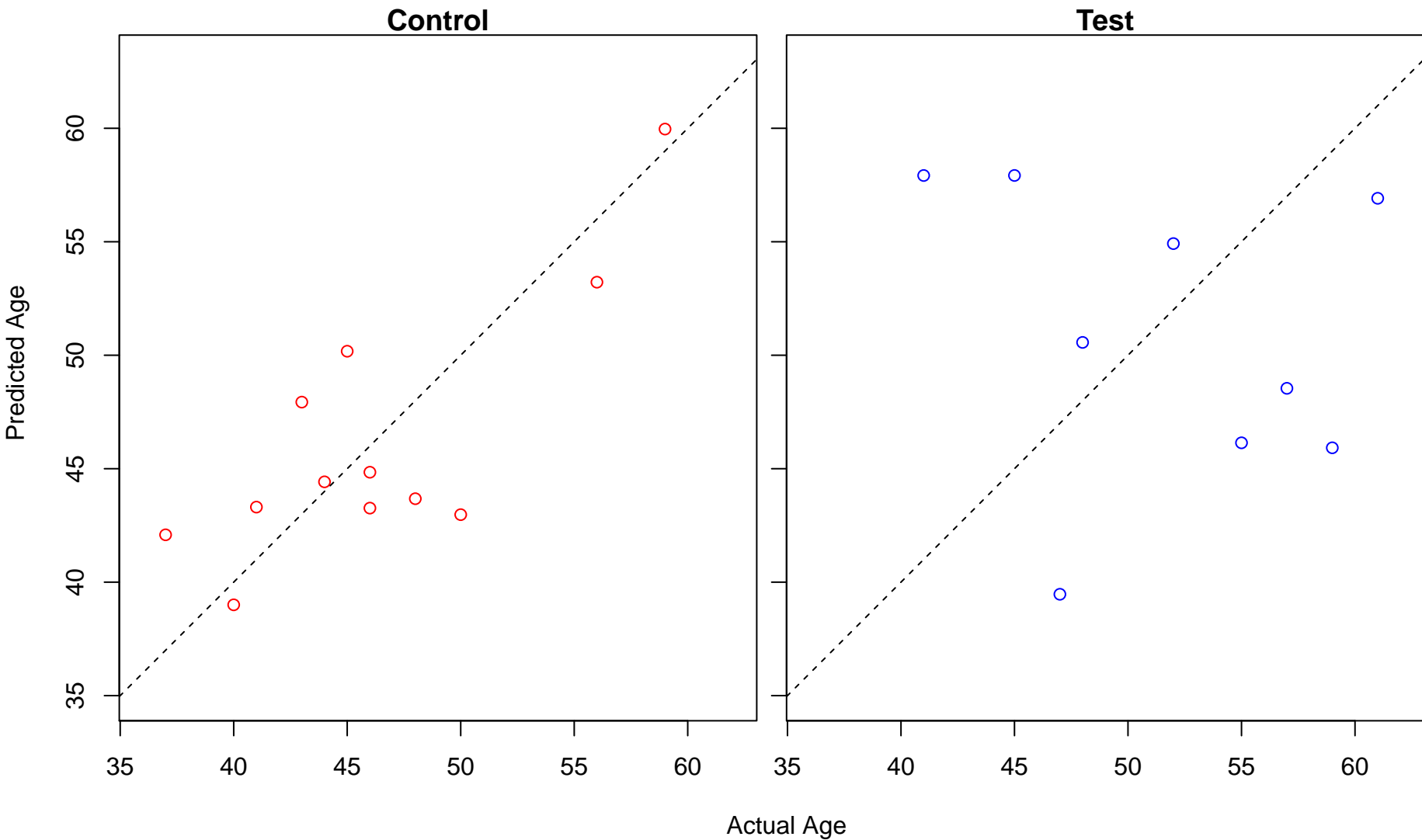
stem cell development (Score: 6.745763)



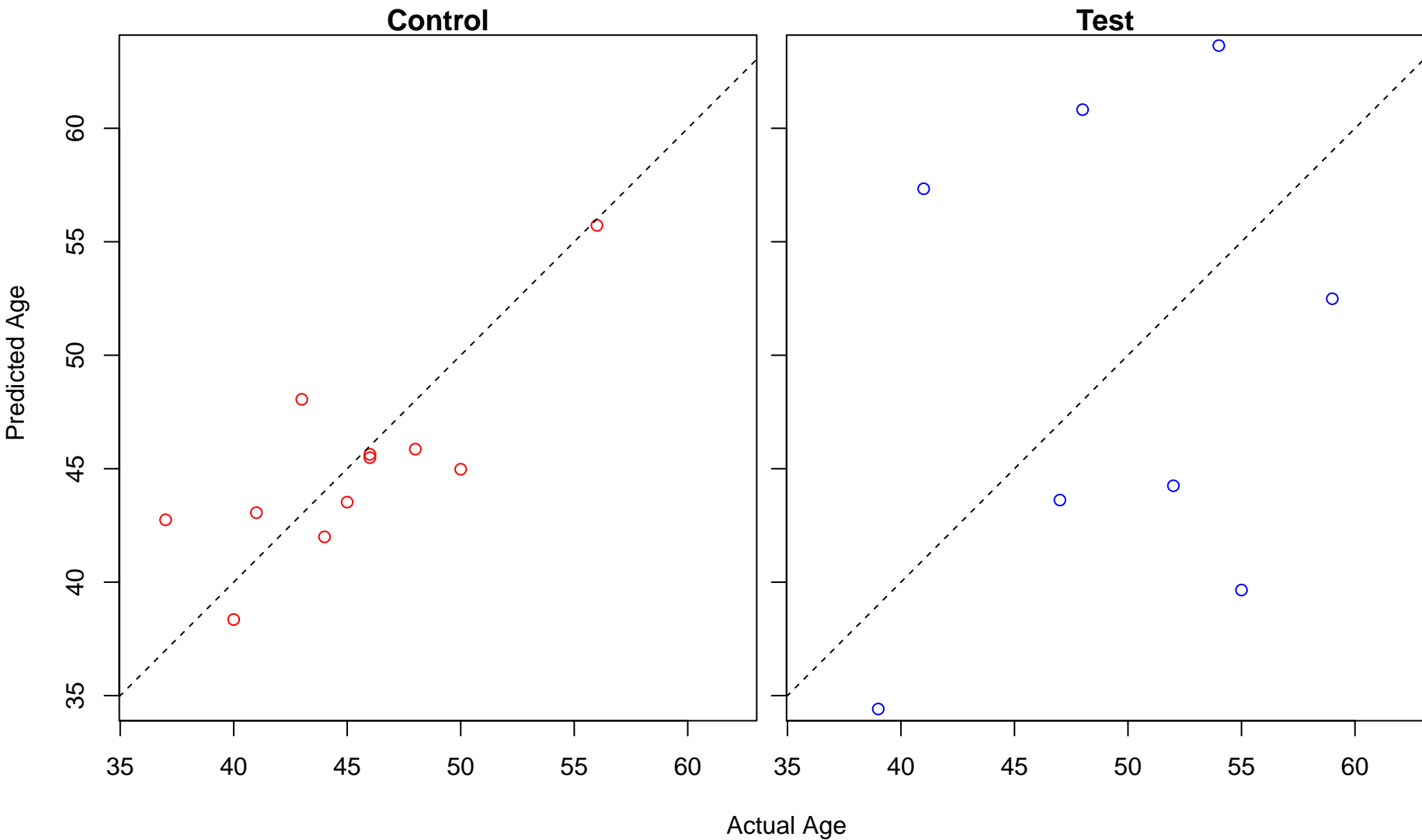
cardiac cell development (Score: 6.738251)



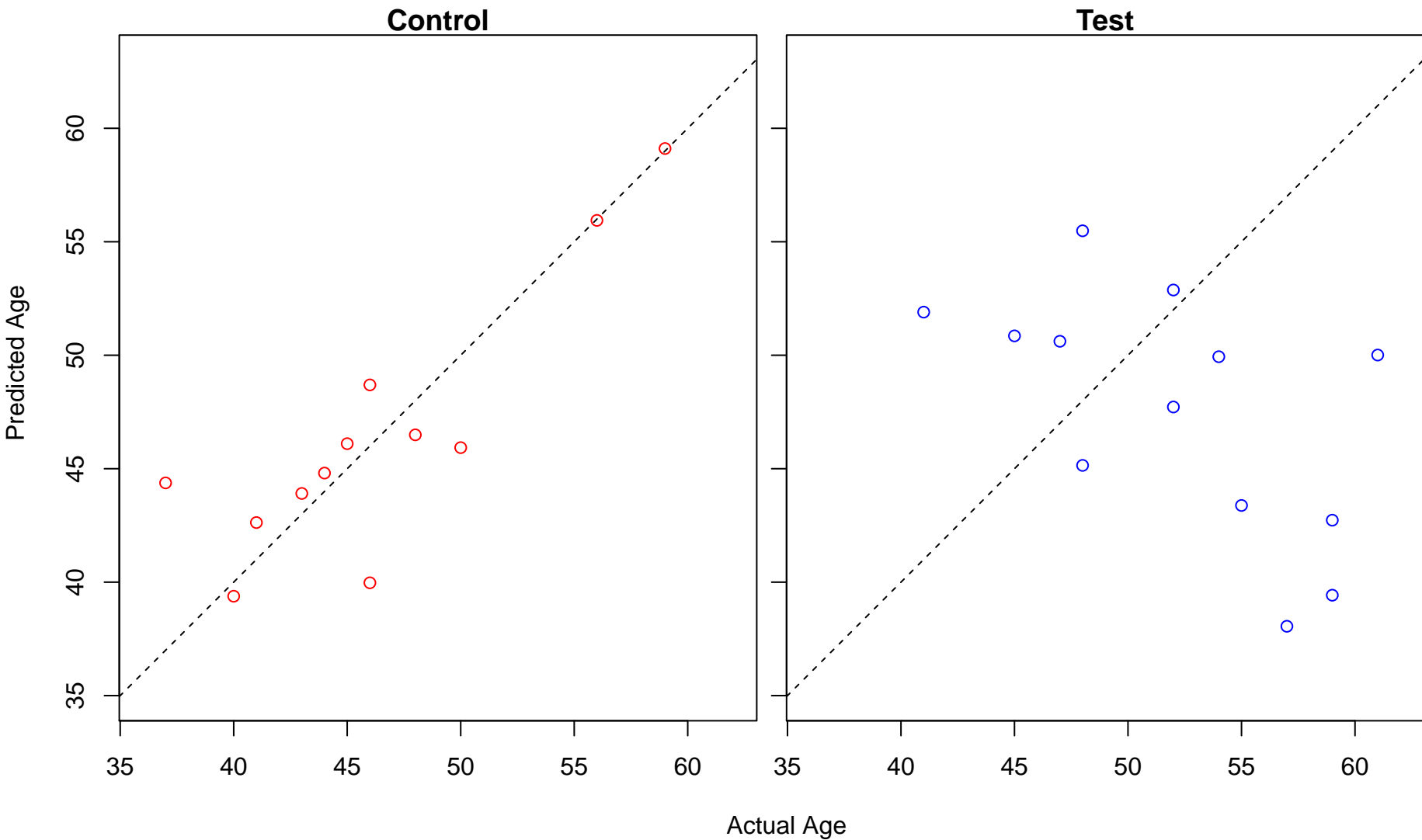
positive regulation of protein acetylation (Score: 6.737684)



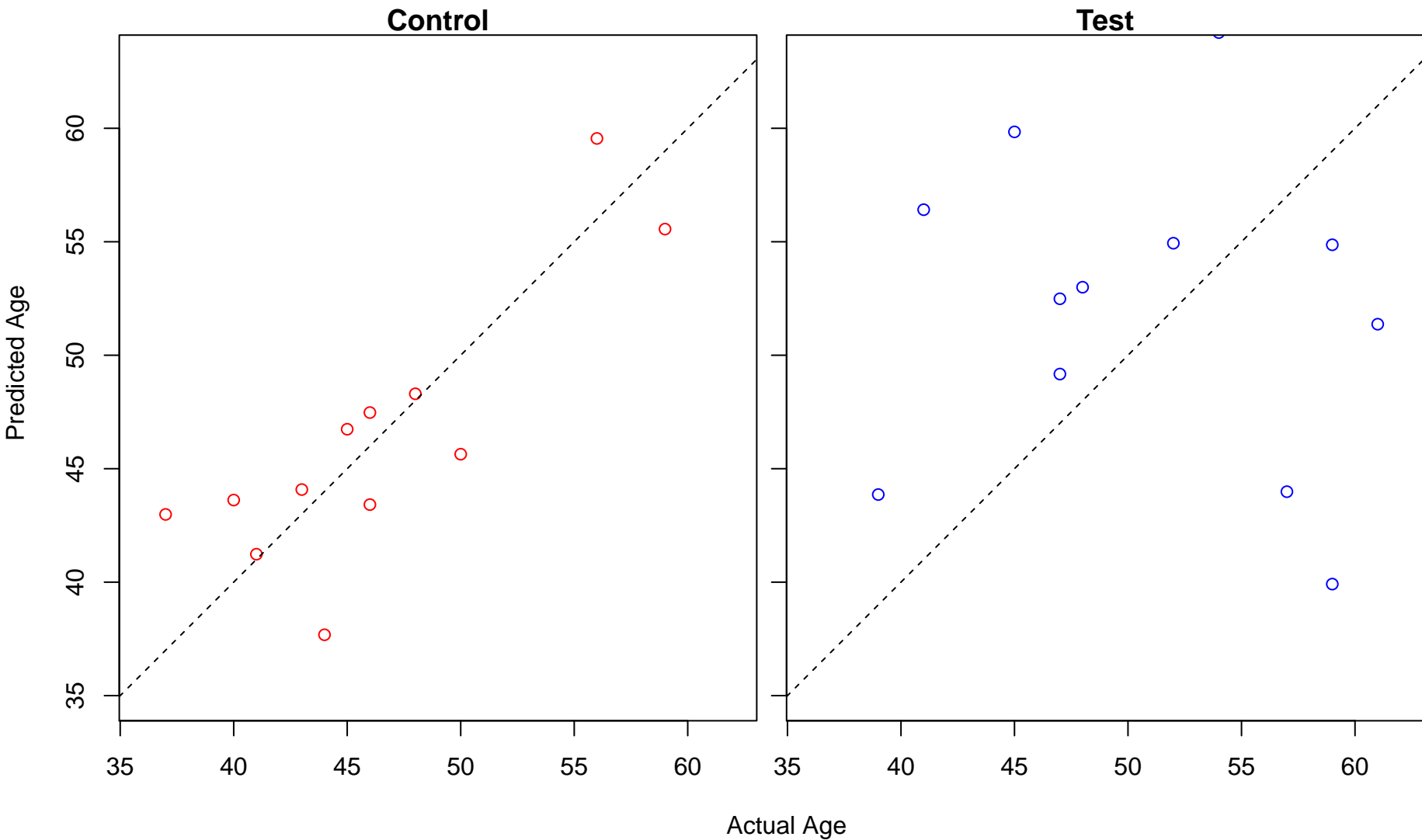
protein complex localization (Score: 6.725916)



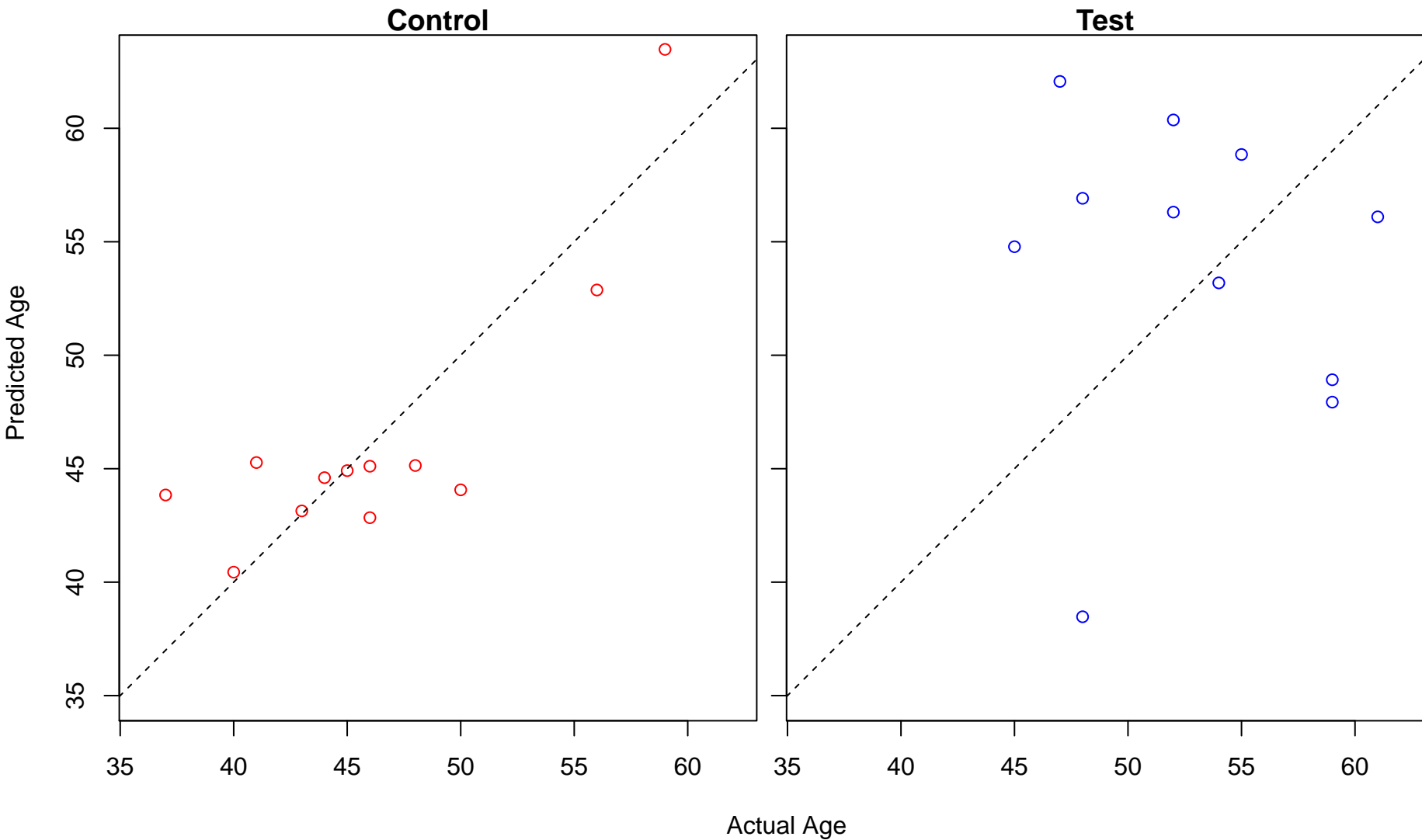
negative regulation of androgen receptor signaling pathway (Score: 6.725422)



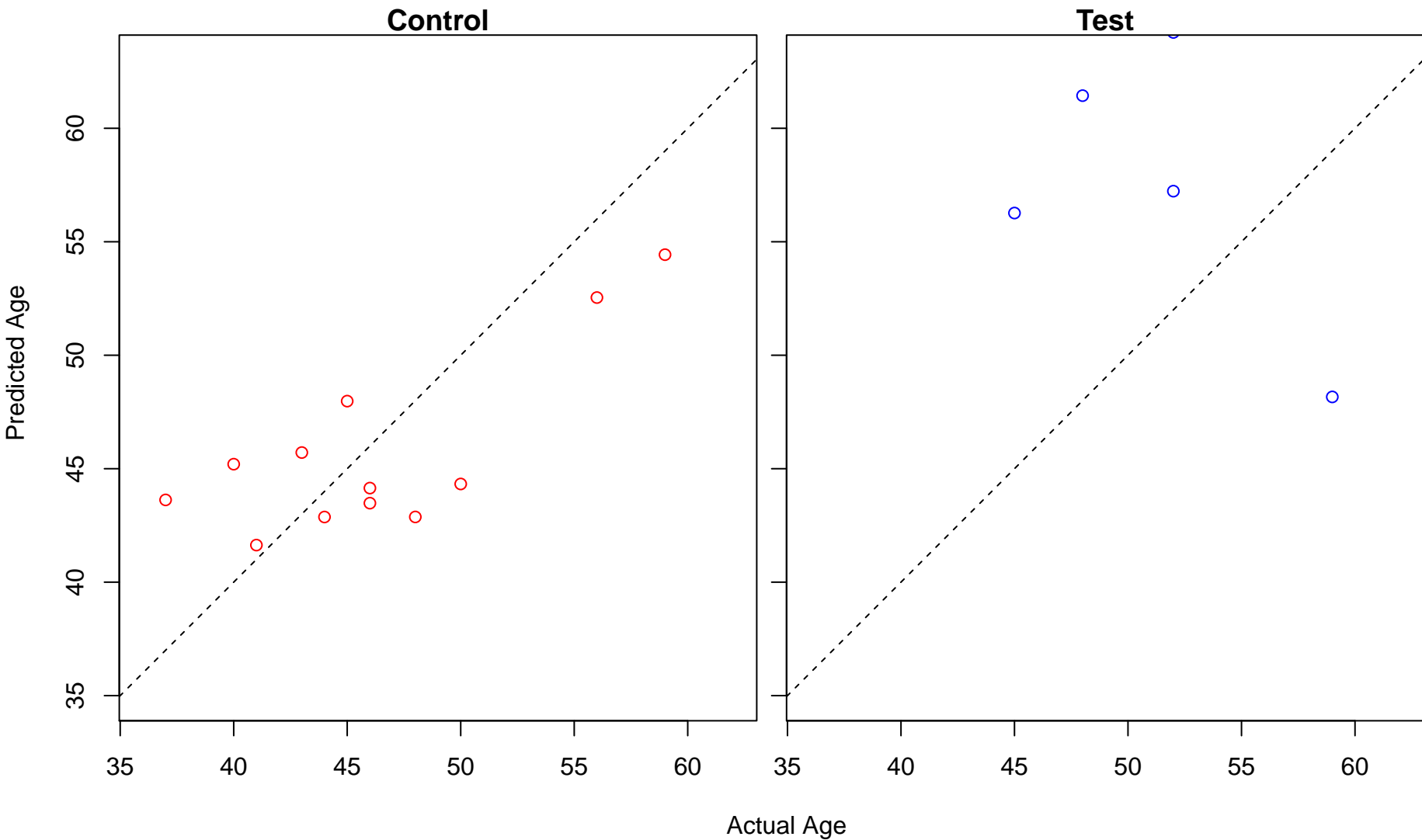
positive regulation of CD4-positive, alpha-beta T cell activation (Score: 6.697341)



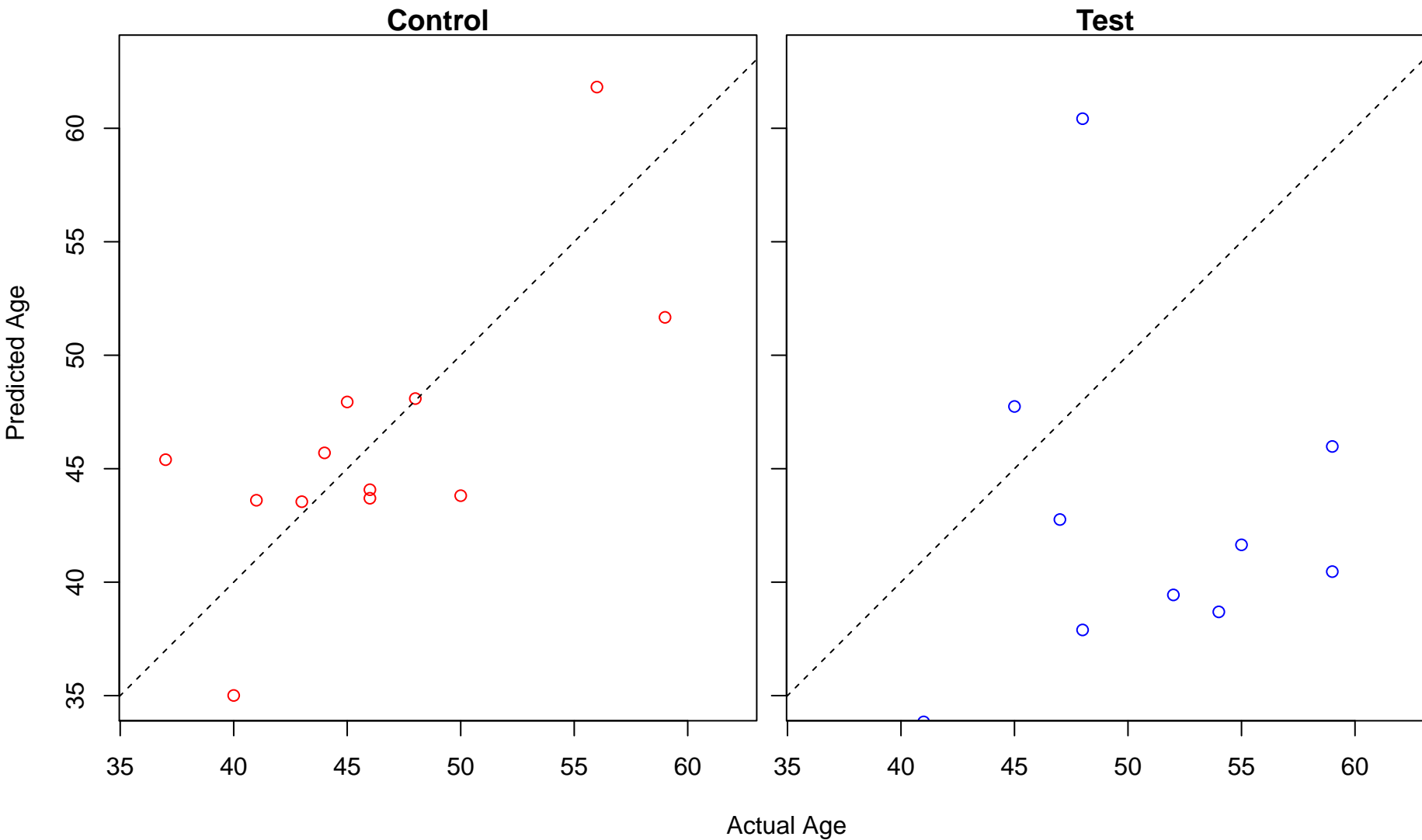
regulation of toll-like receptor 4 signaling pathway (Score: 6.687378)



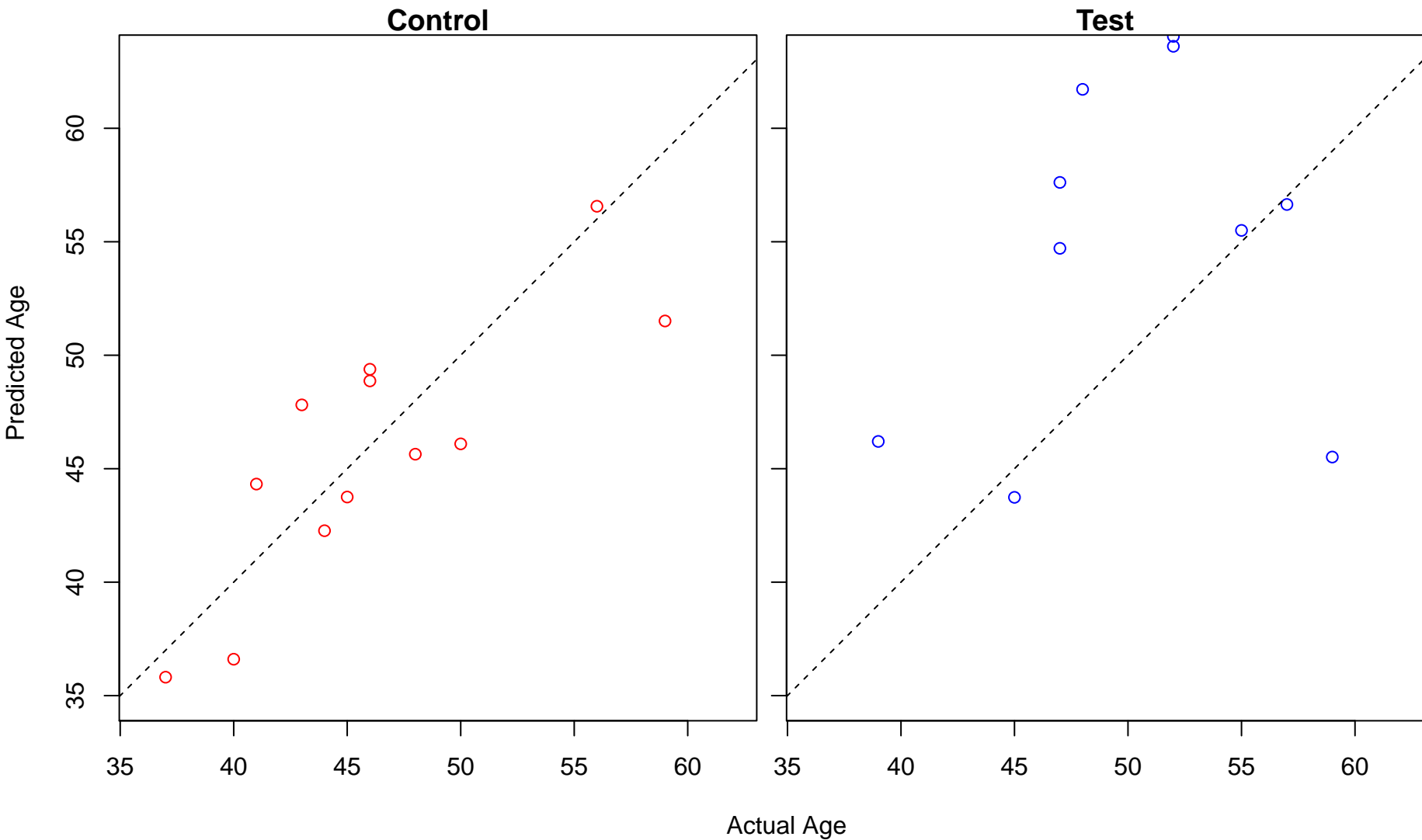
negative regulation of fatty acid transport (Score: 6.685842)



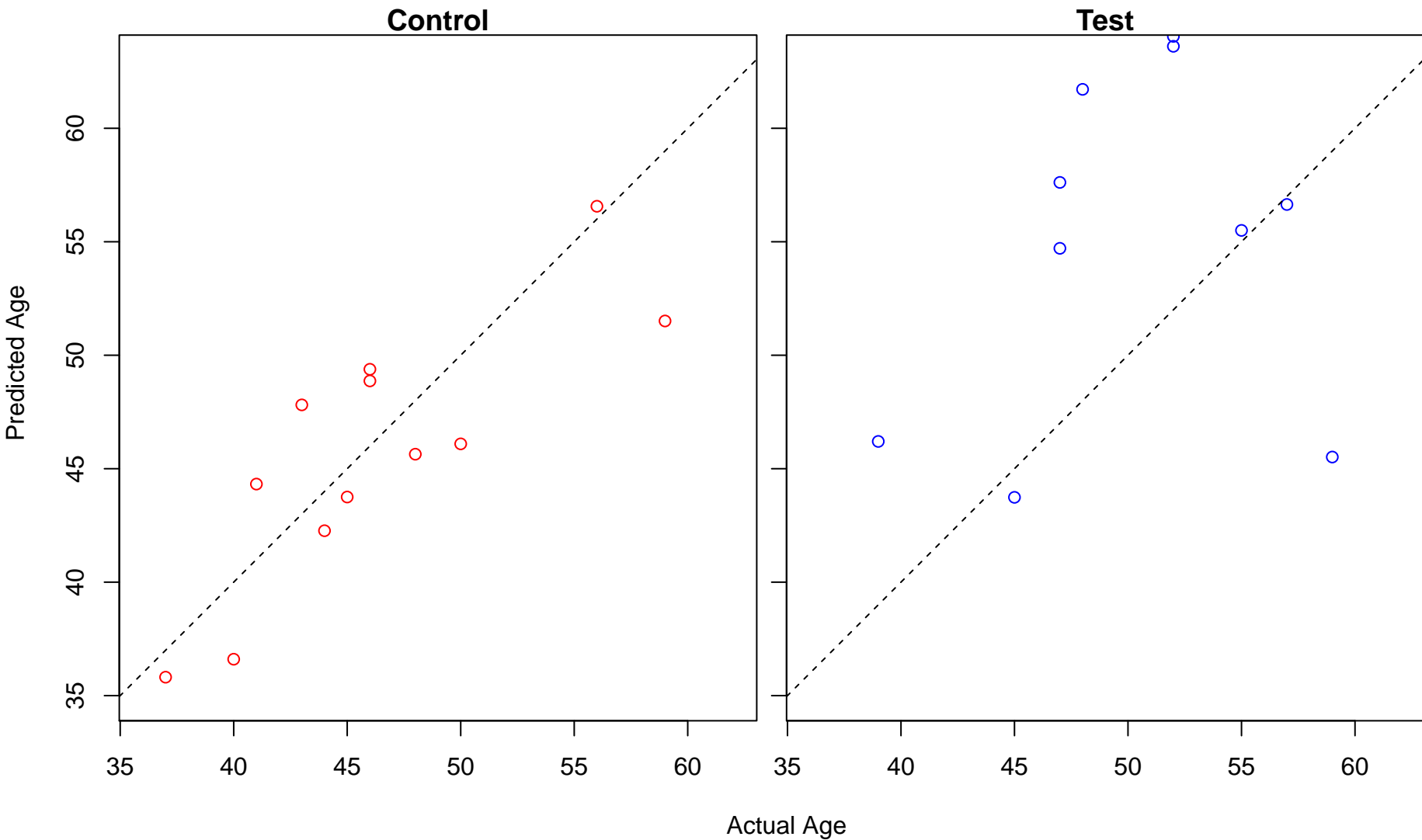
regulation of cardiac muscle tissue development (Score: 6.685639)



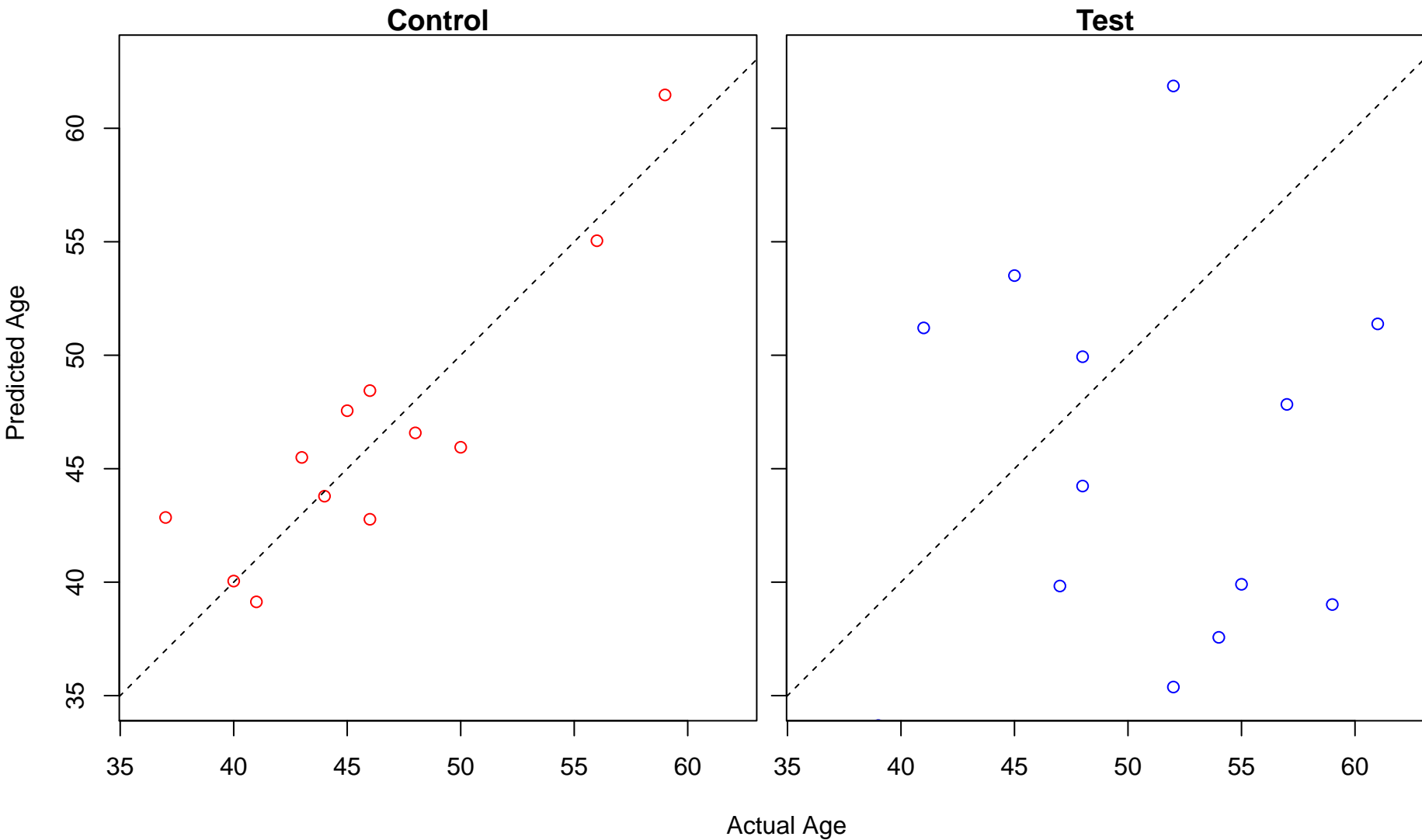
hyperosmotic response (Score: 6.677187)



cellular hyperosmotic response (Score: 6.677187)

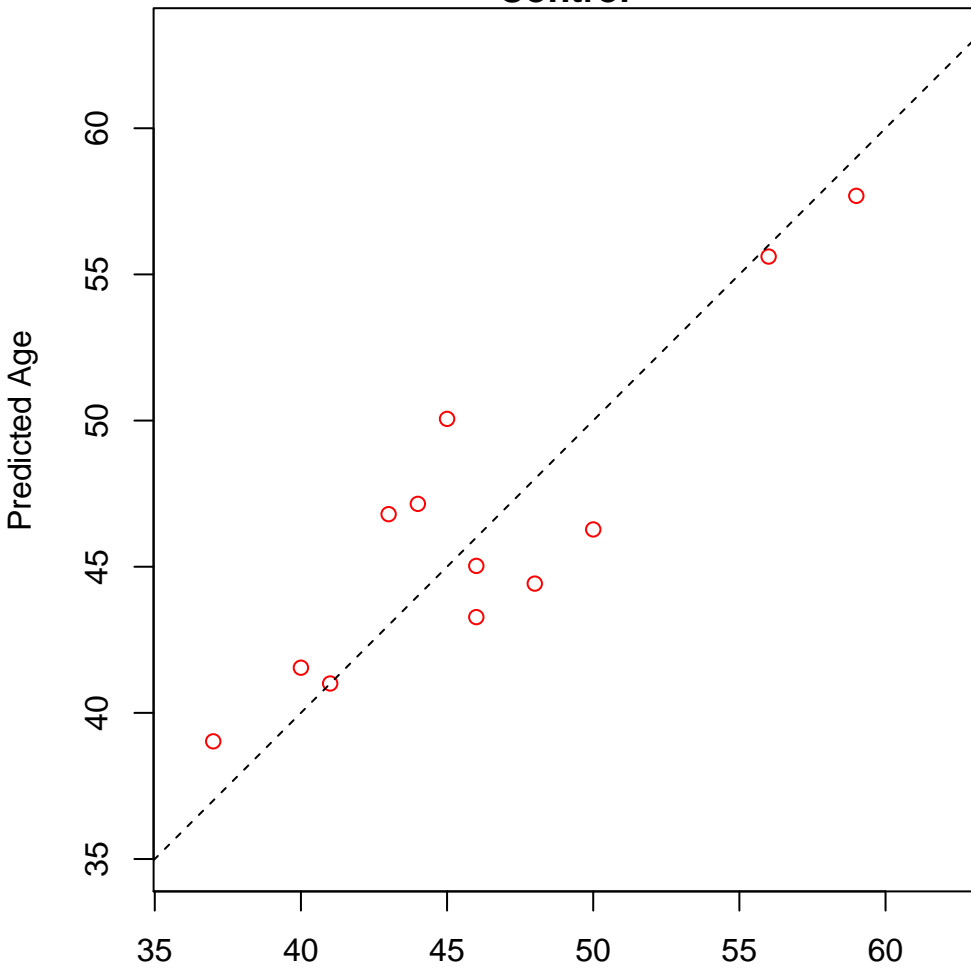


regulation of cell junction assembly (Score: 6.668162)

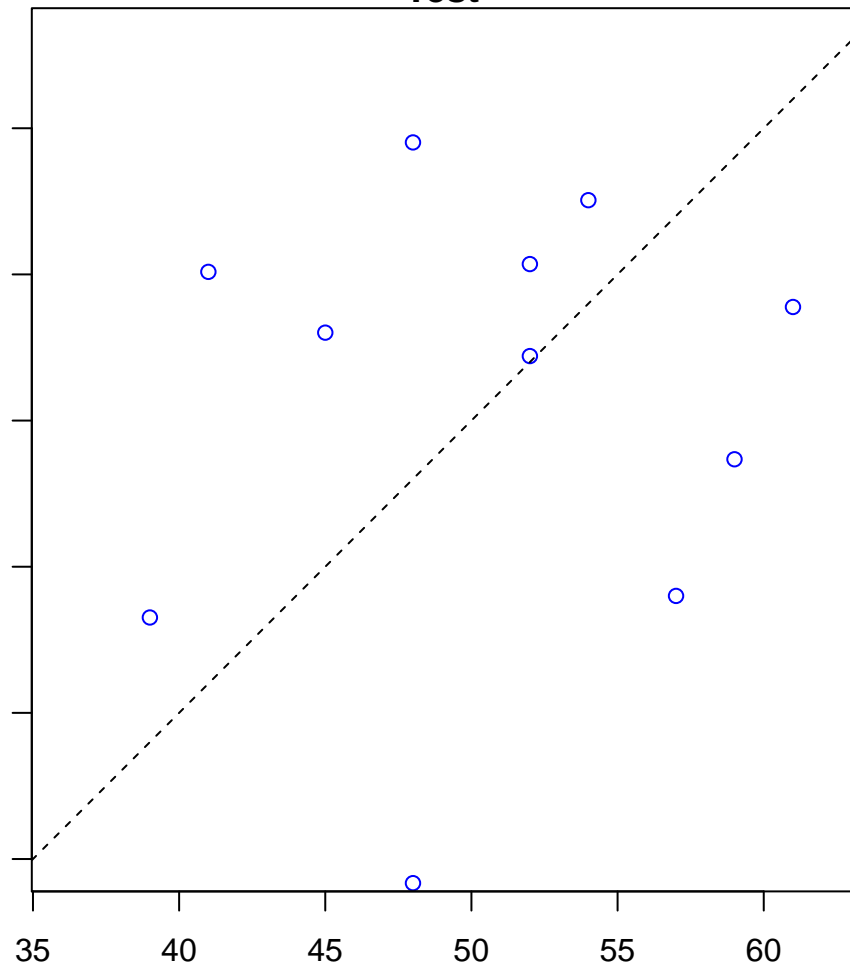


regulation of interleukin-4 production (Score: 6.667833)

Control

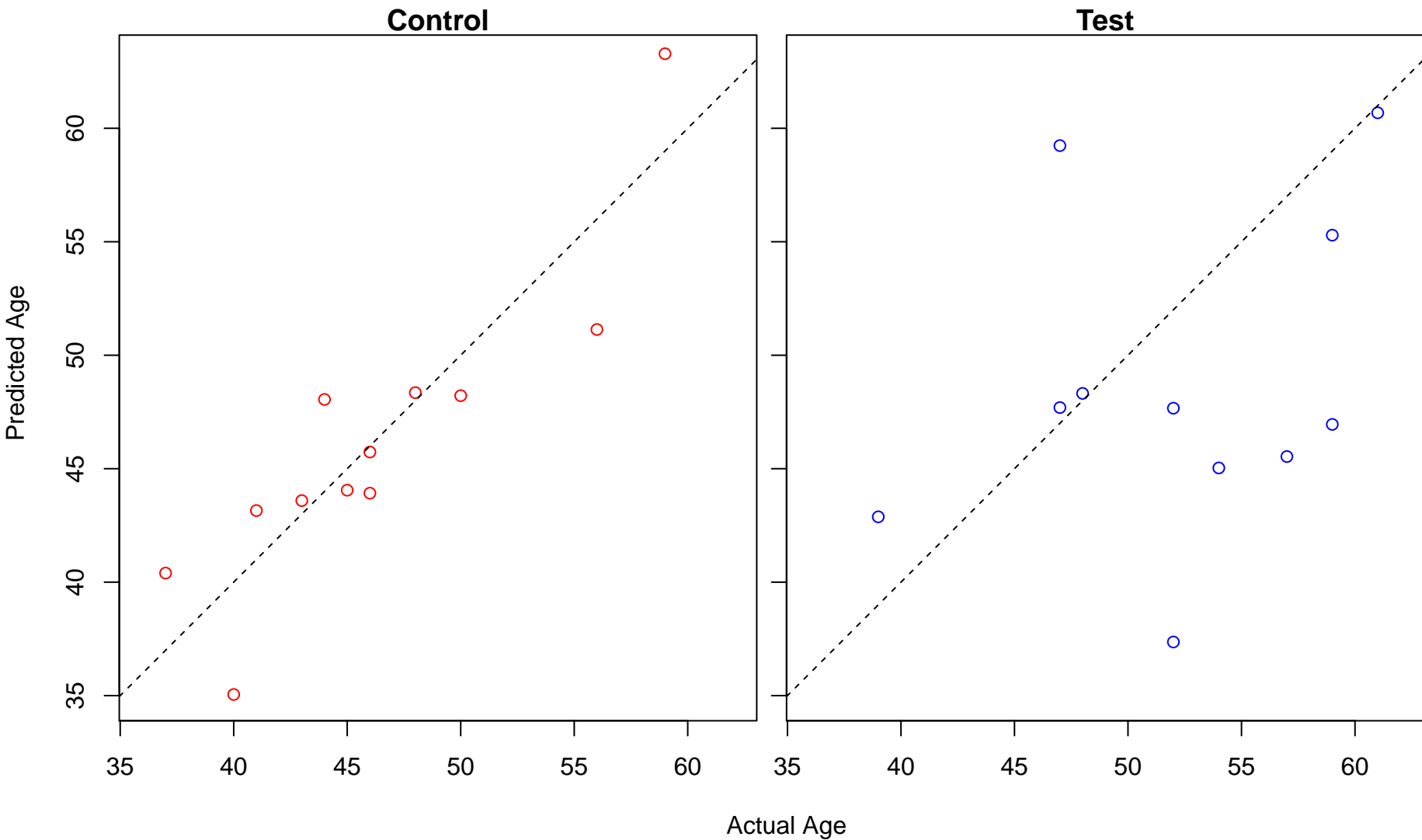


Test

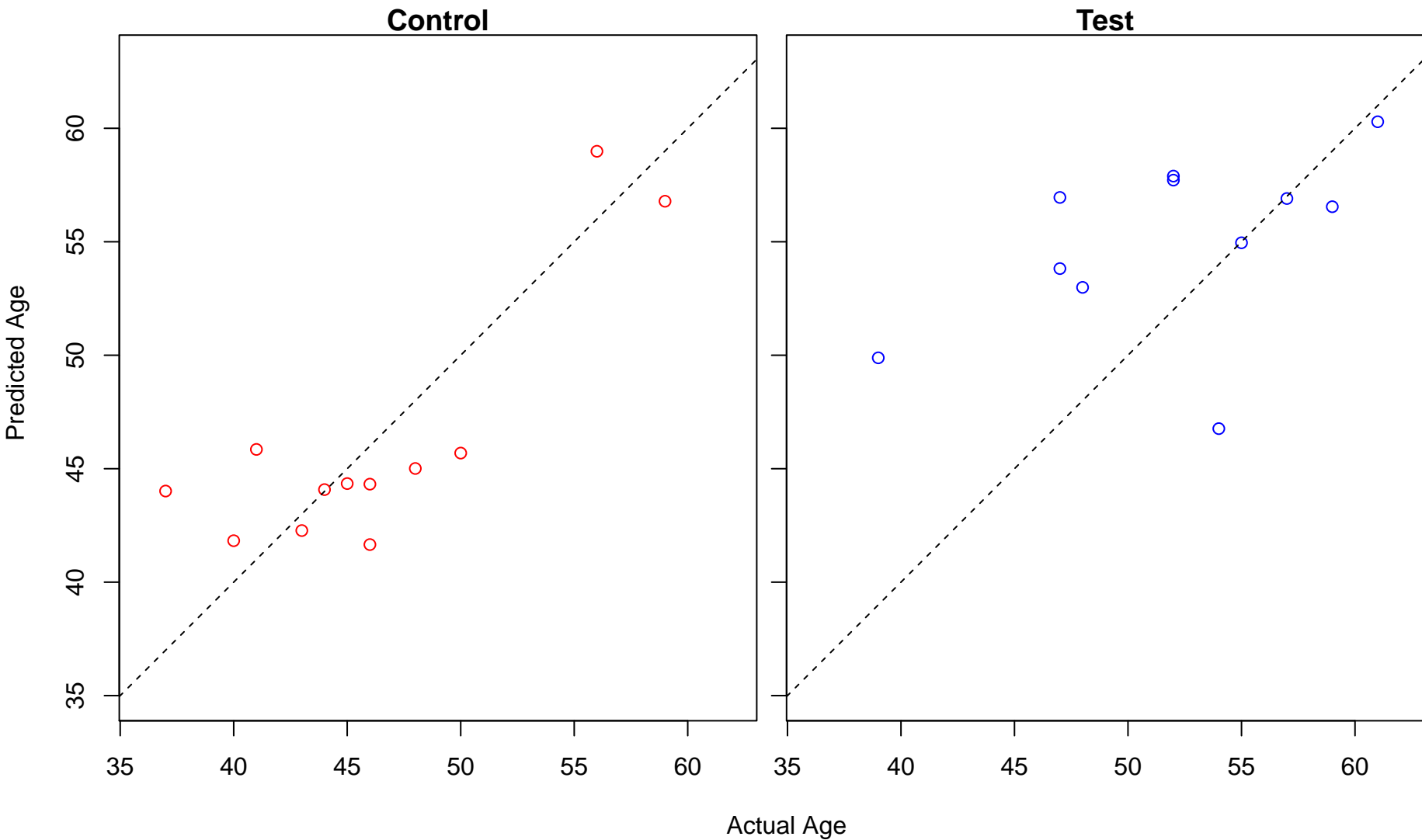


Actual Age

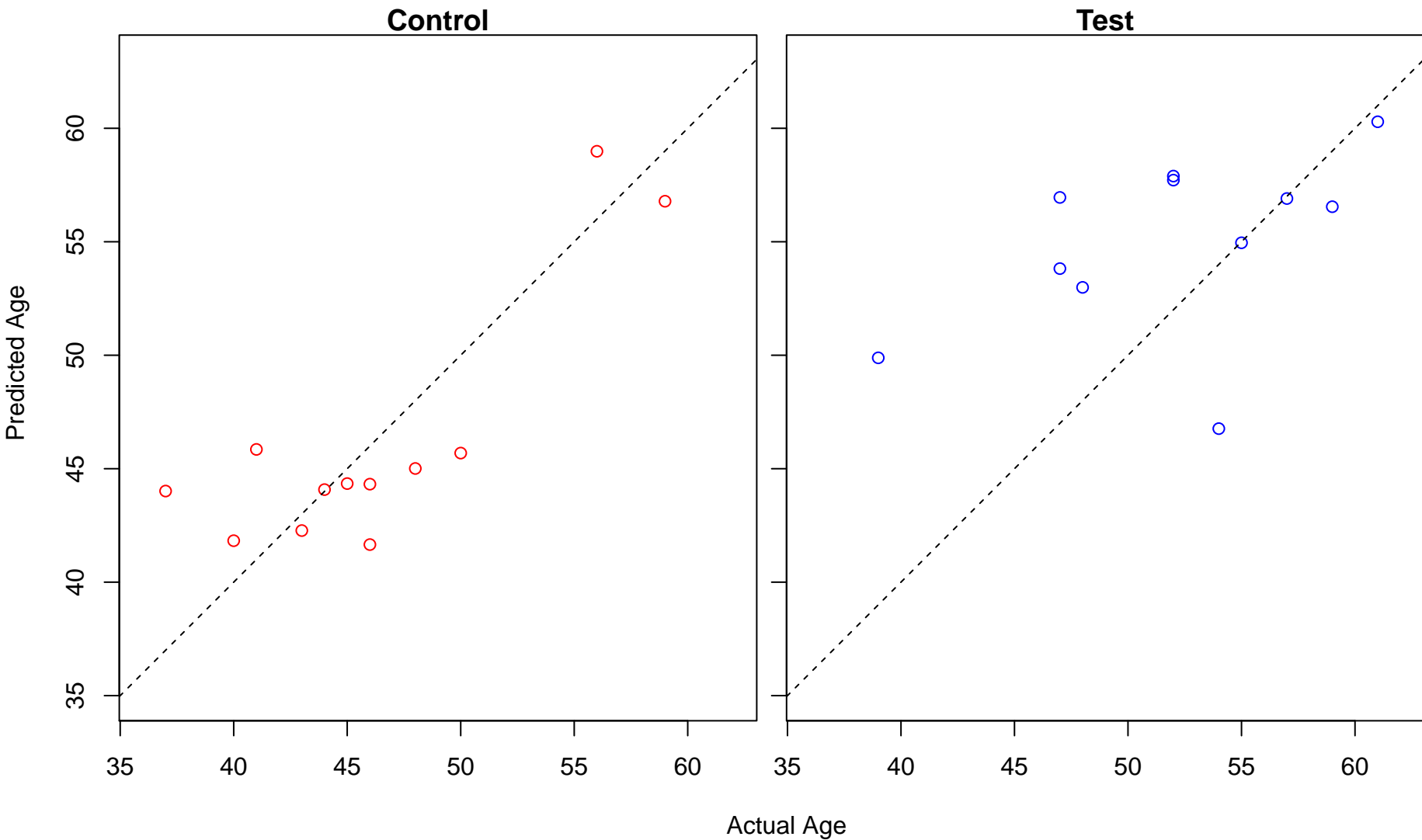
regulation of endoplasmic reticulum unfolded protein response (Score: 6.659370)



activation of store-operated calcium channel activity (Score: 6.653757)

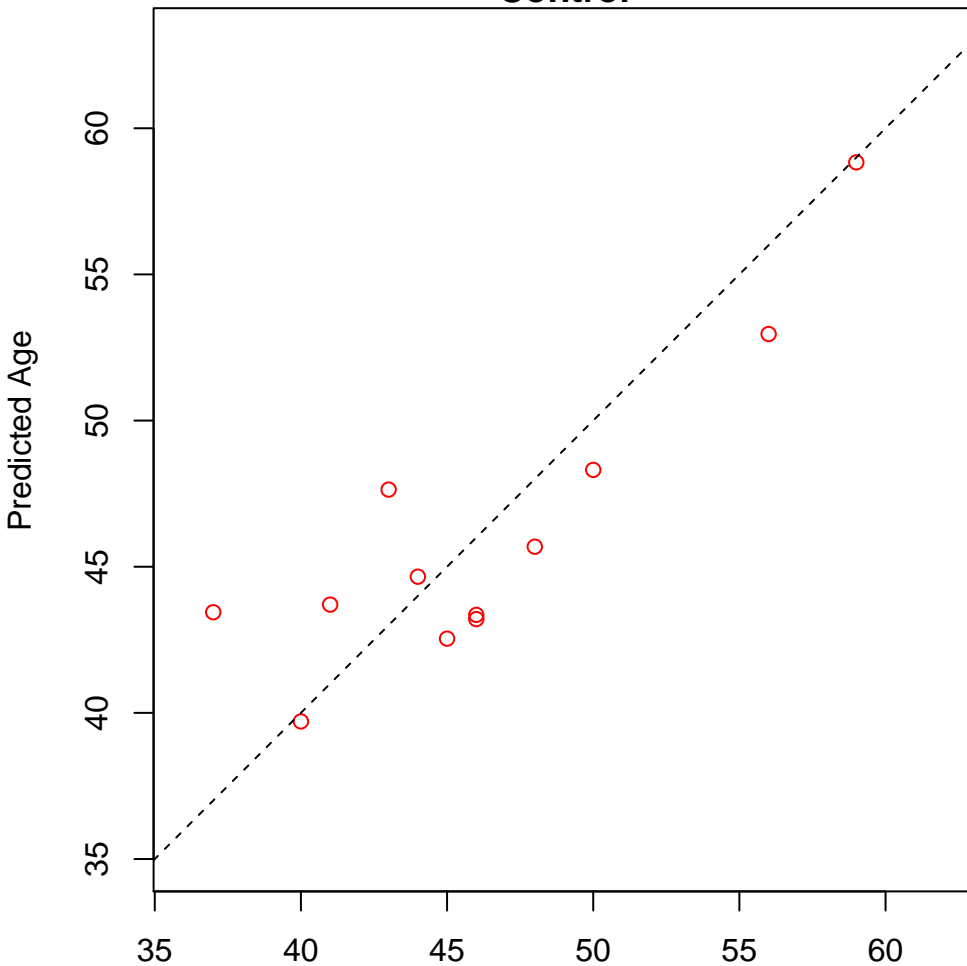


positive regulation of store-operated calcium channel activity (Score: 6.653757)

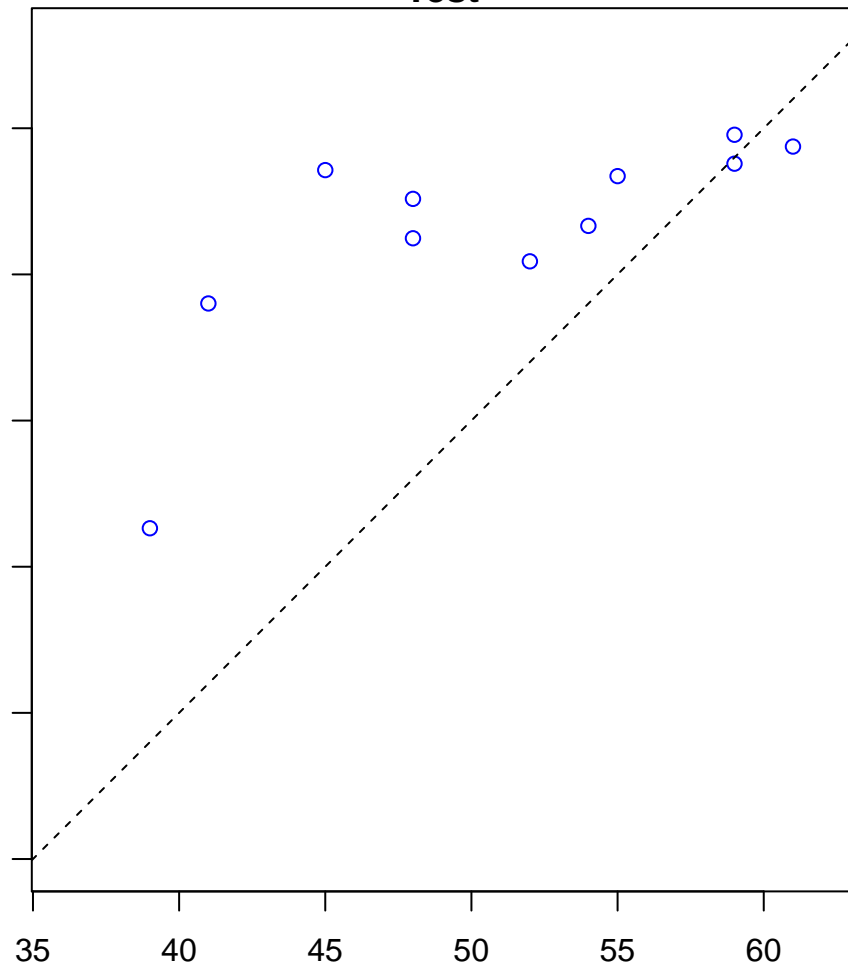


hematopoietic stem cell proliferation (Score: 6.635271)

Control

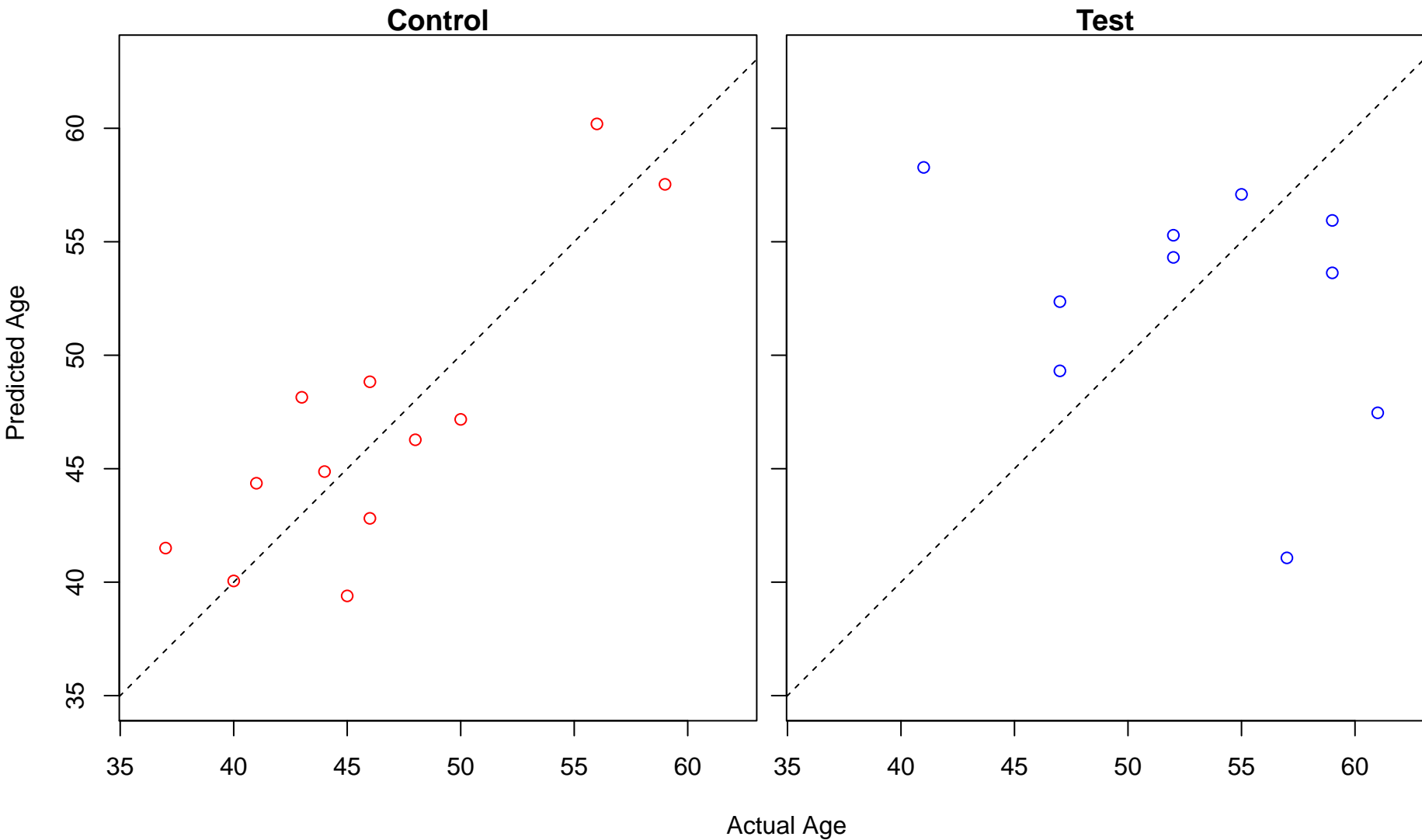


Test

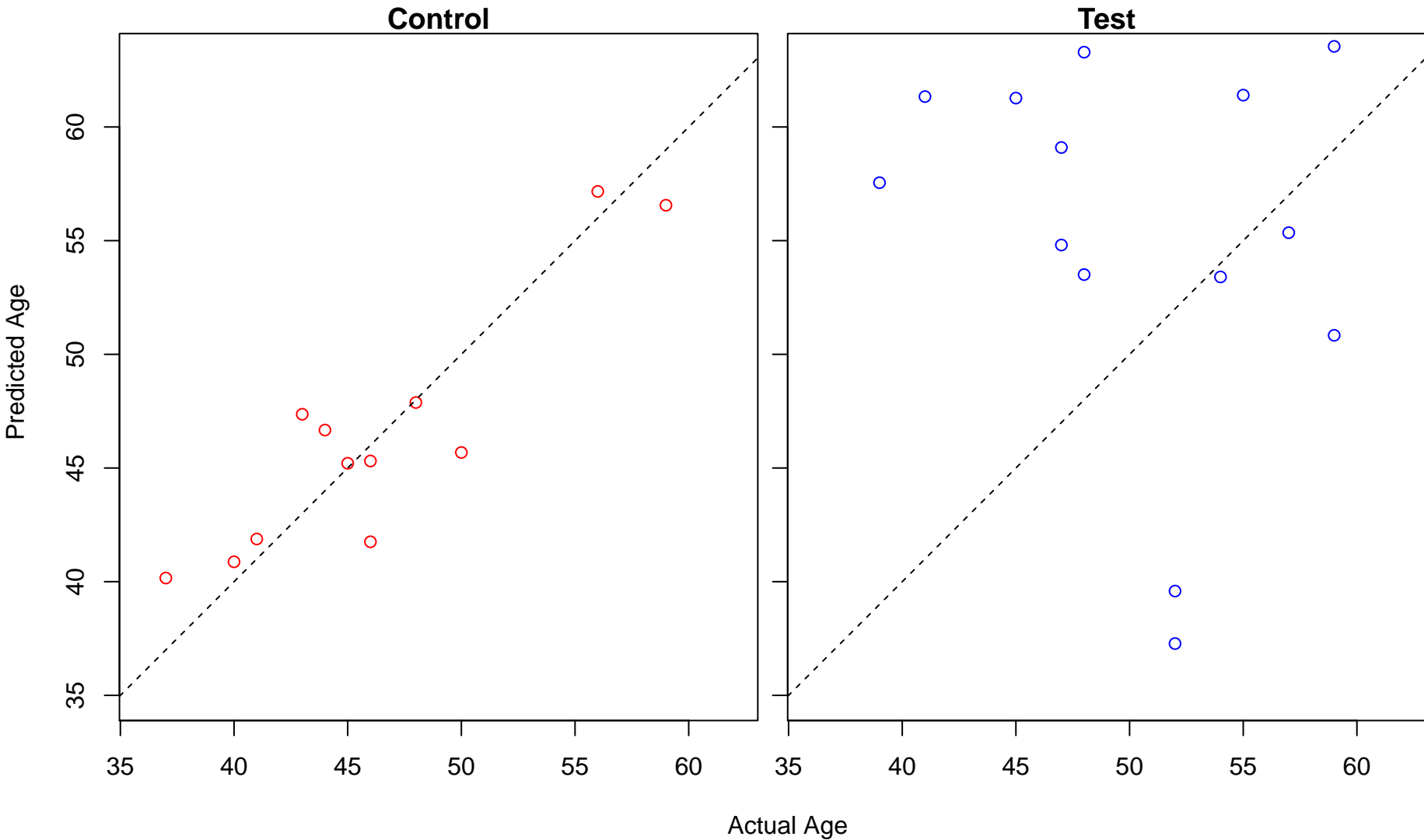


Actual Age

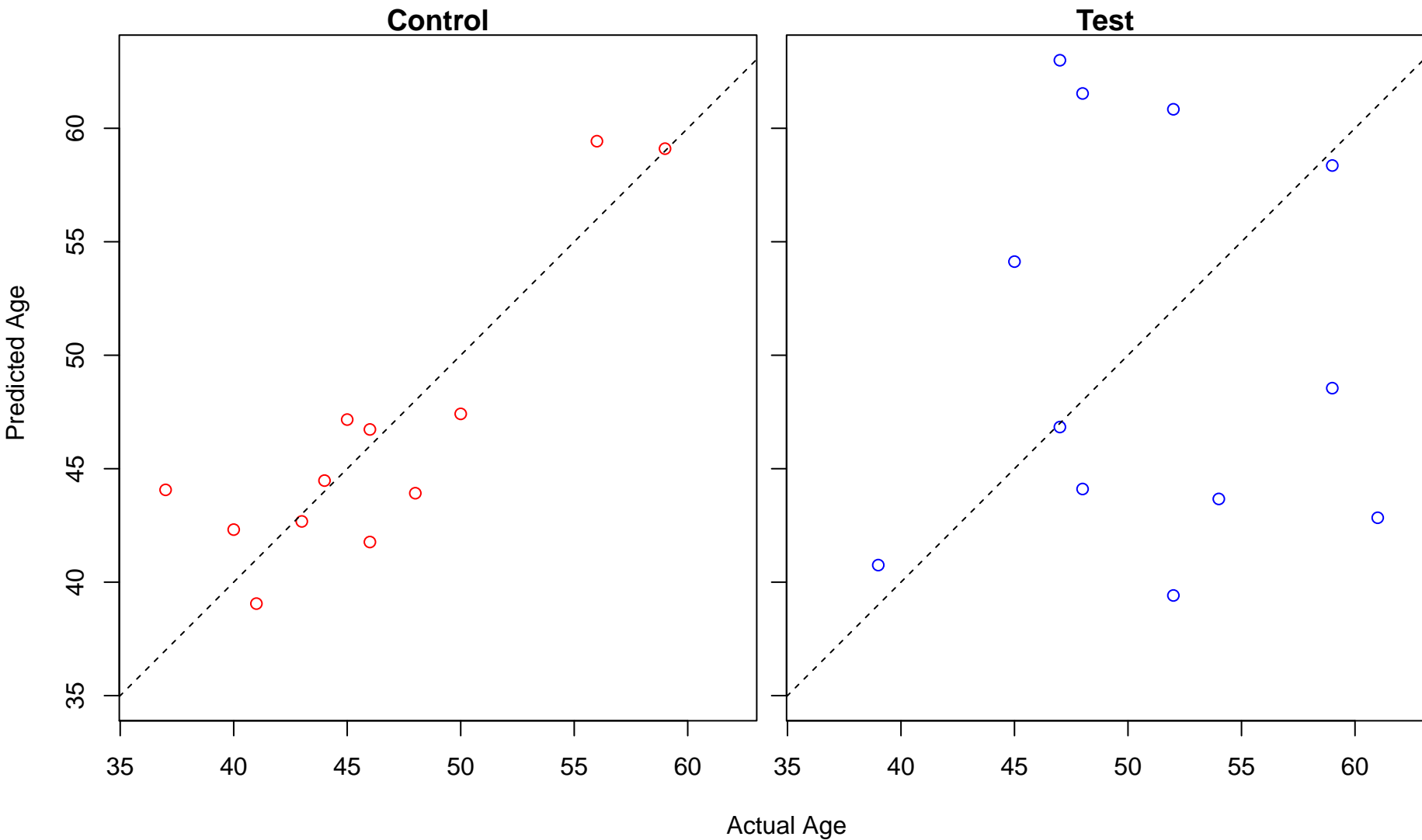
neural crest cell migration (Score: 6.630125)



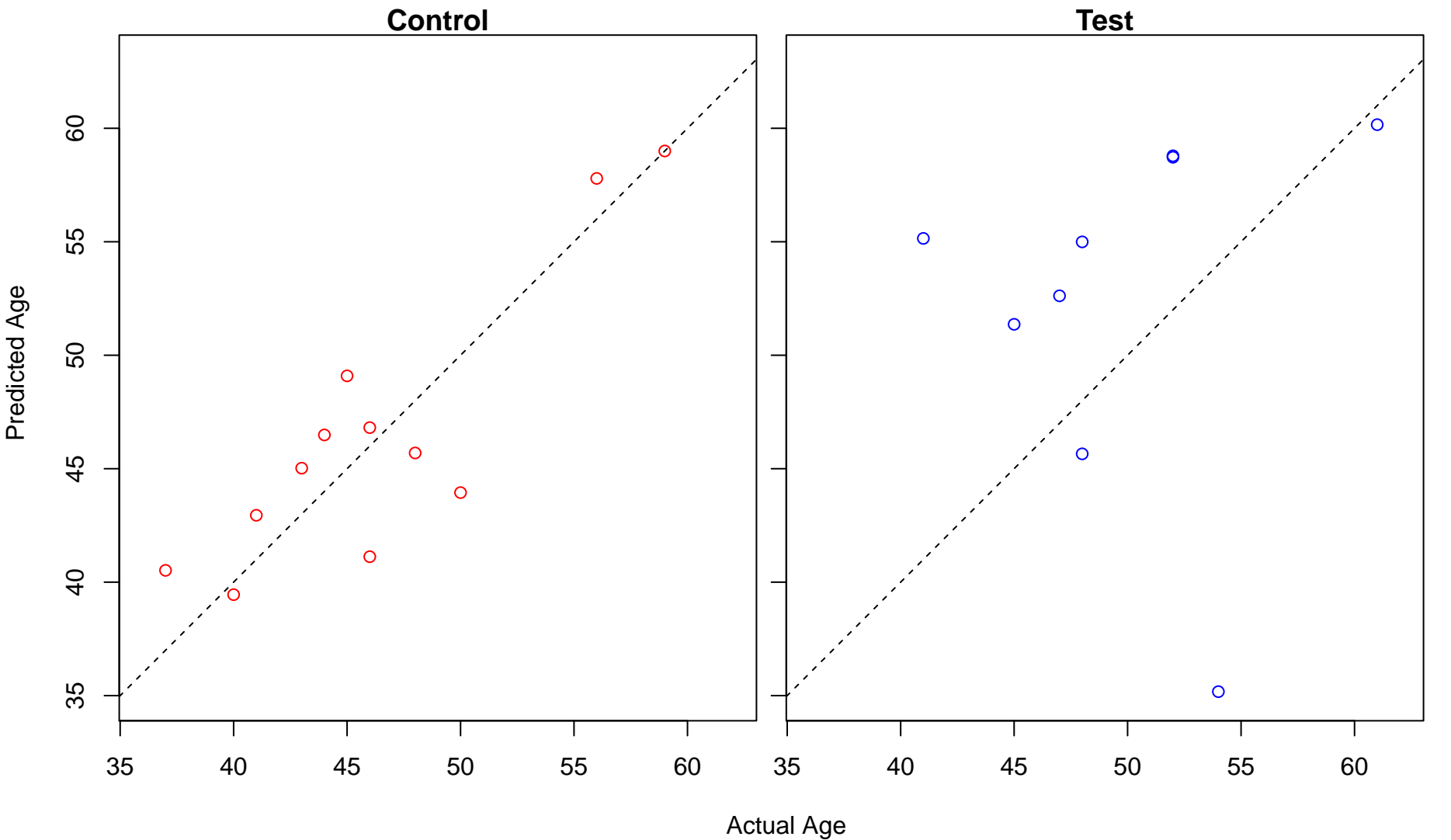
regulation of response to cytokine stimulus (Score: 6.626312)



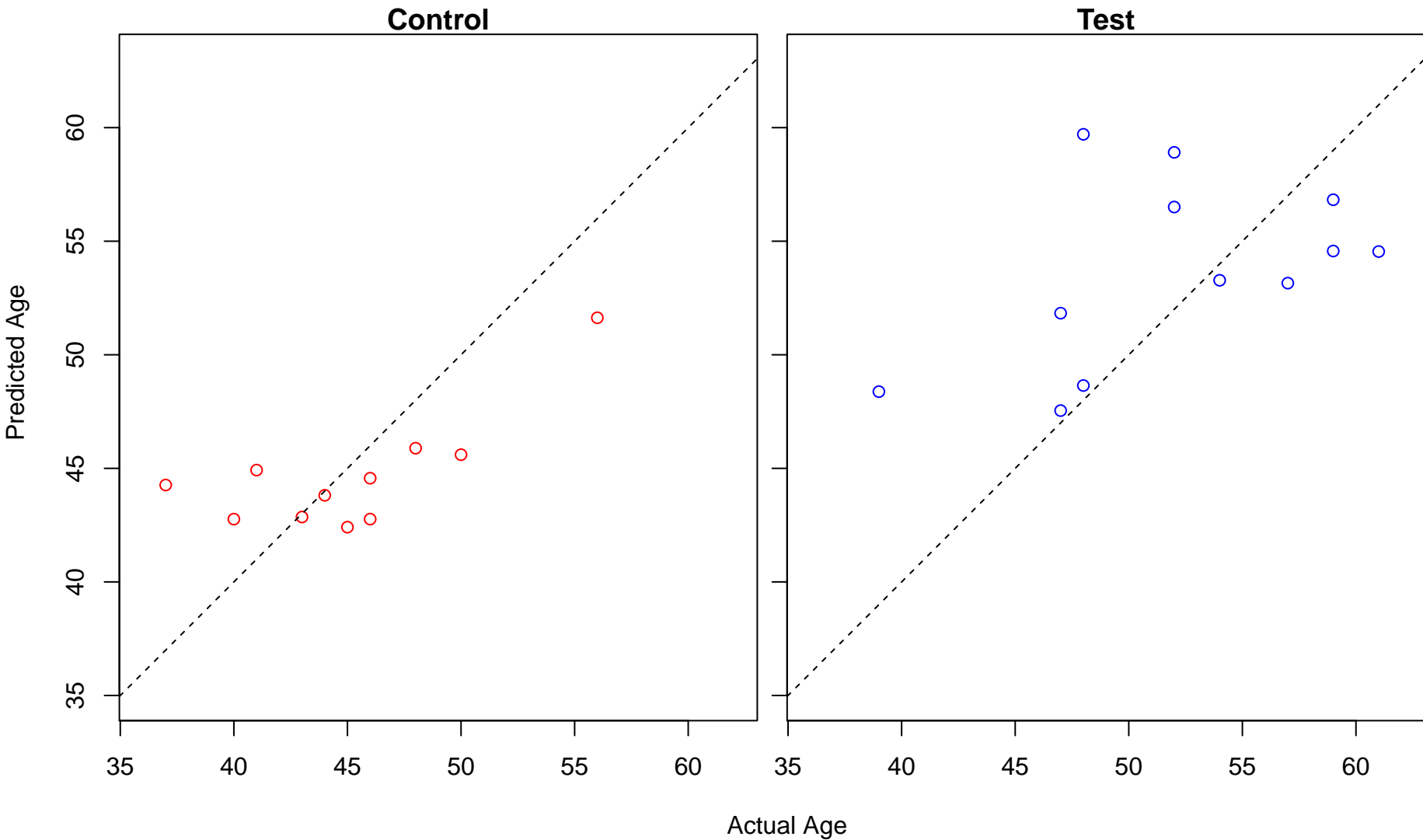
adherens junction organization (Score: 6.616282)



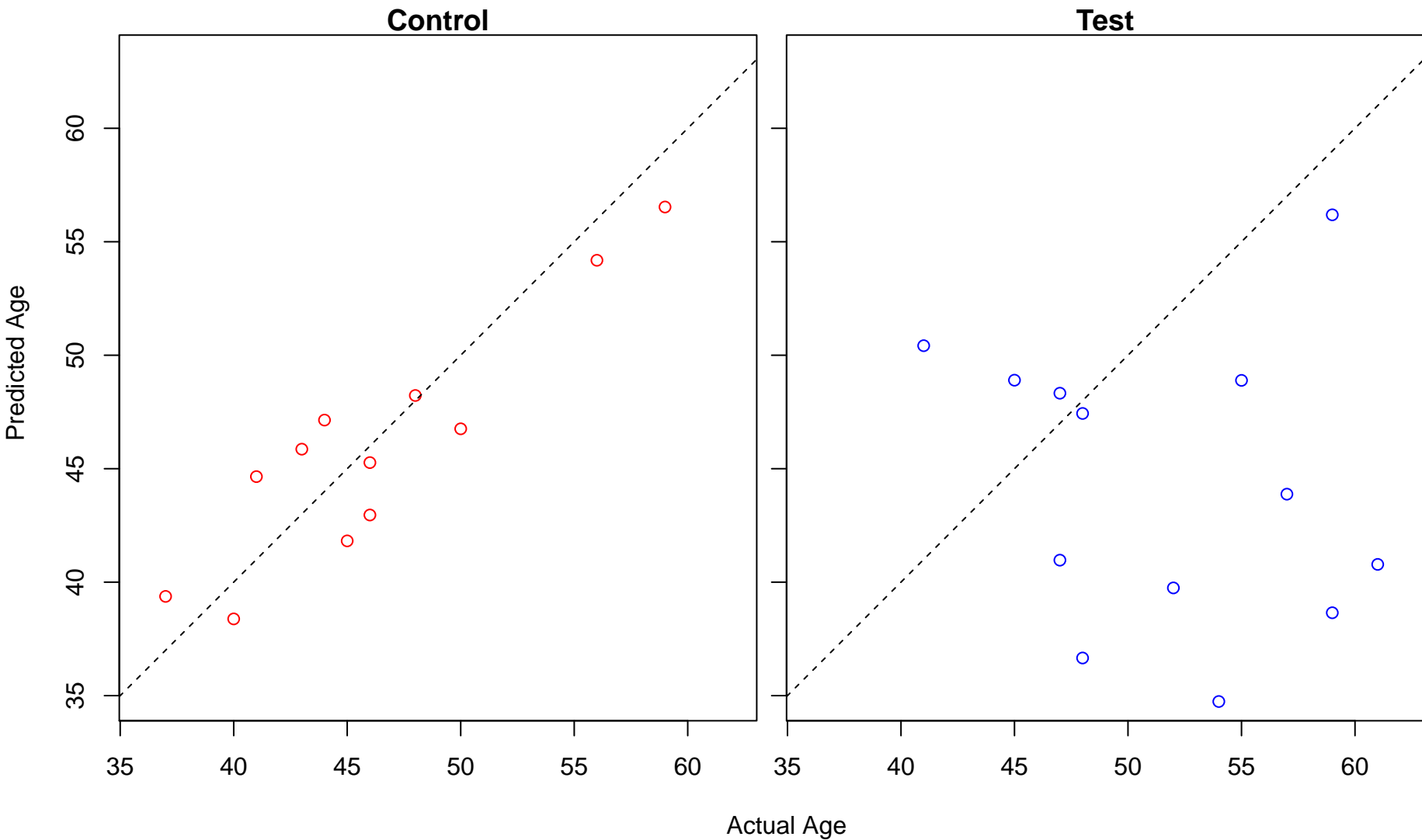
Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (Score



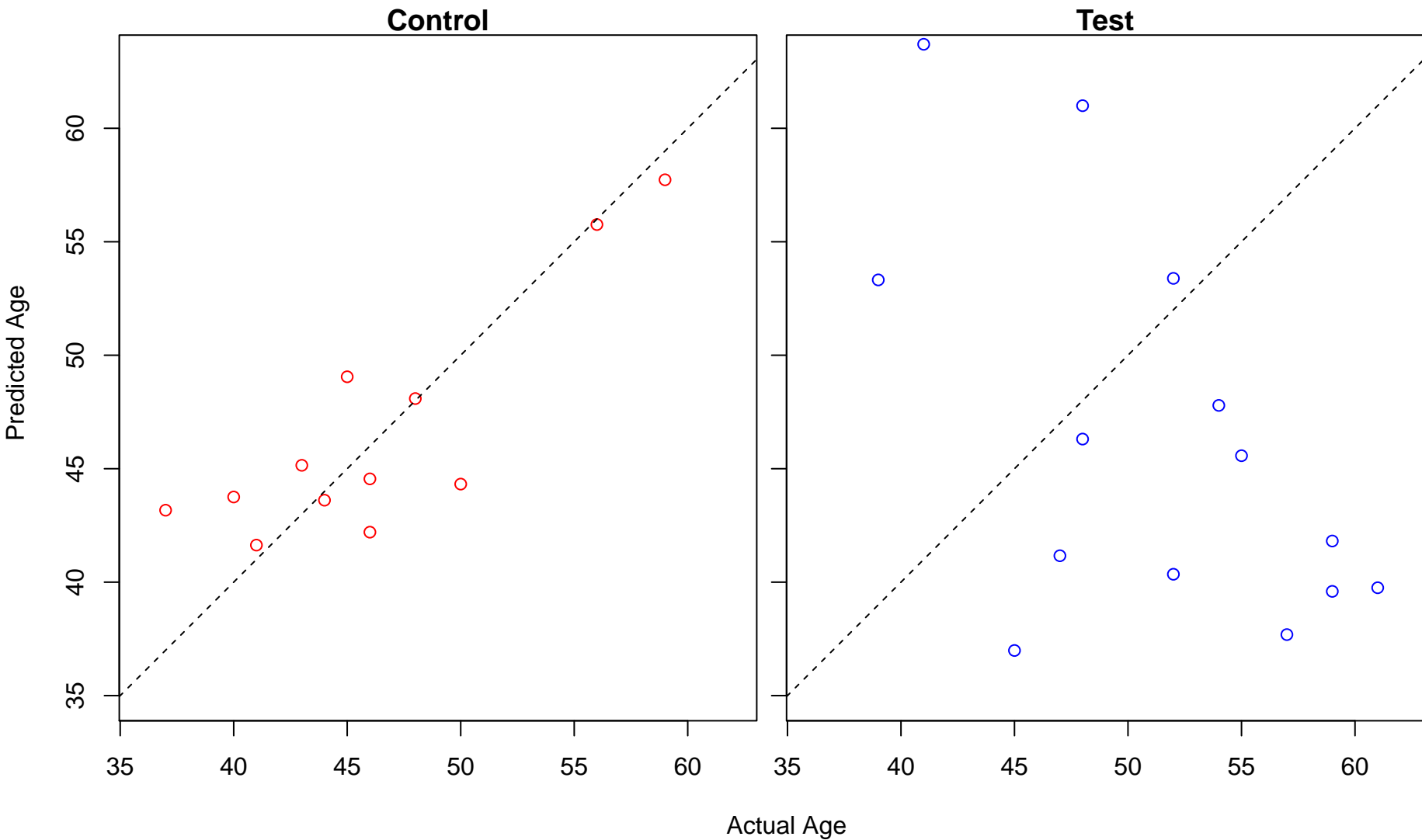
amino acid transmembrane transport (Score: 6.611272)



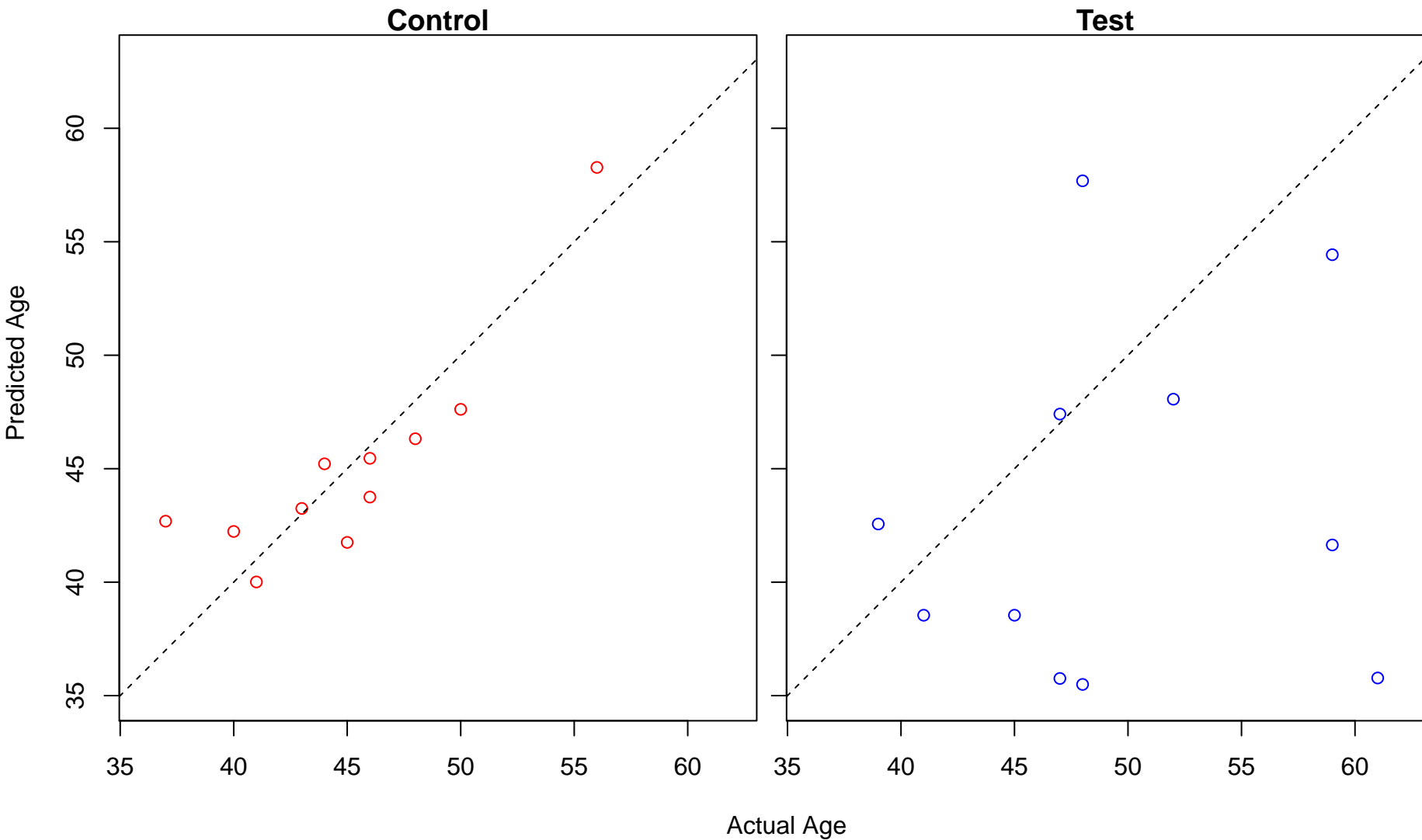
negative regulation of endothelial cell proliferation (Score: 6.605195)



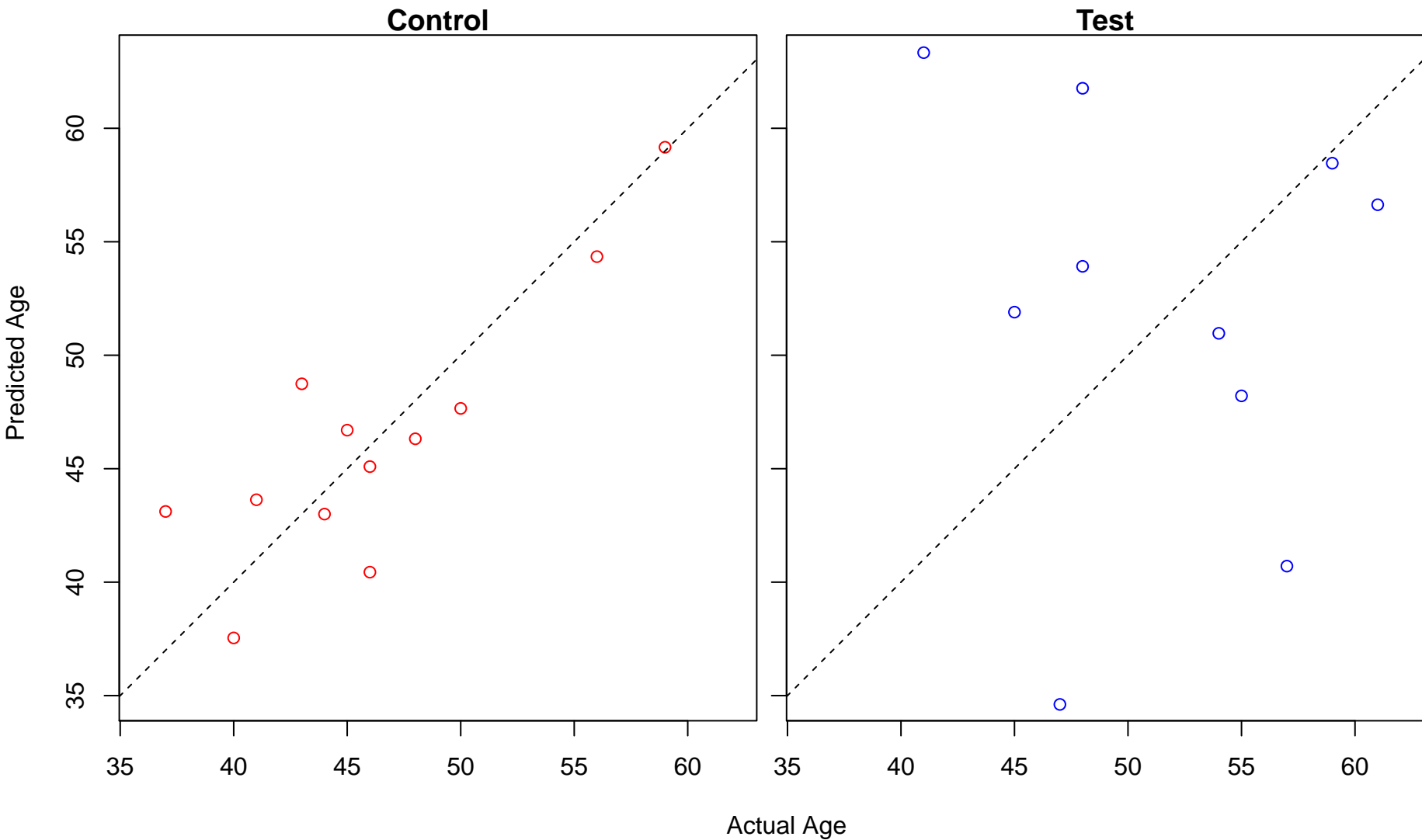
IRE1-mediated unfolded protein response (Score: 6.601998)



modification by symbiont of host morphology or physiology (Score: 6.590988)

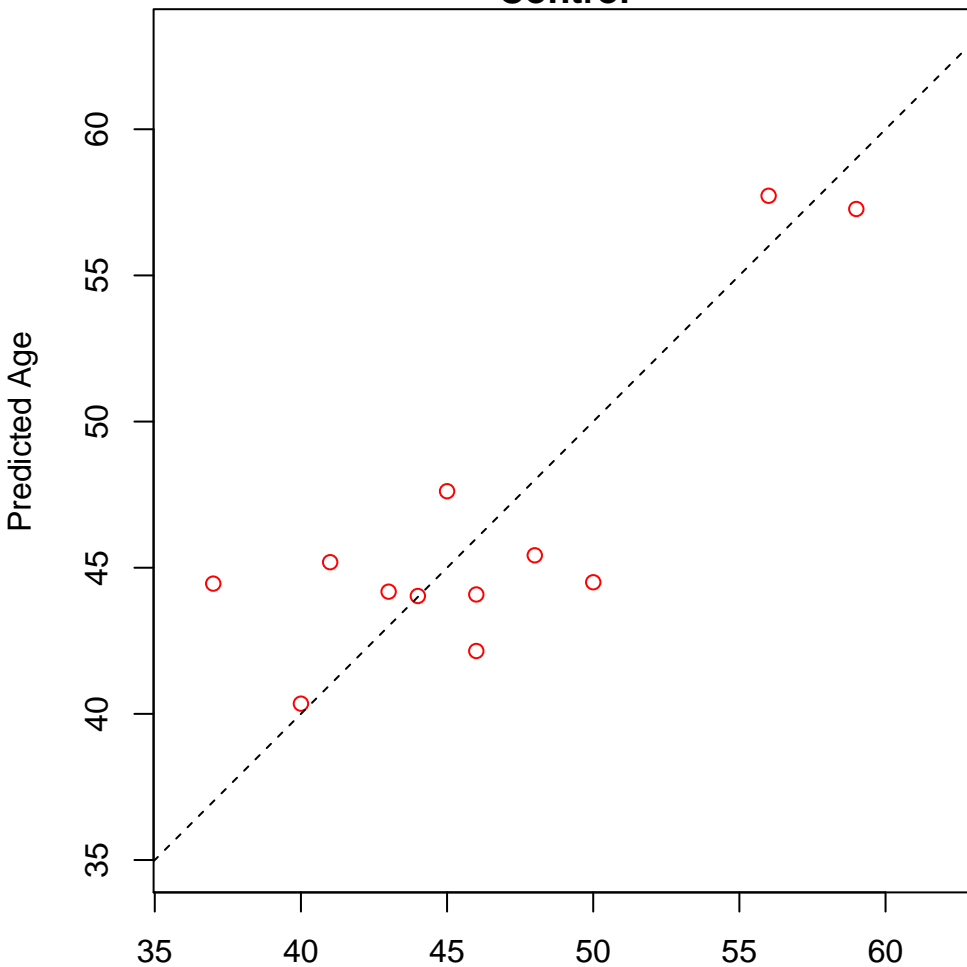


response to cAMP (Score: 6.589718)

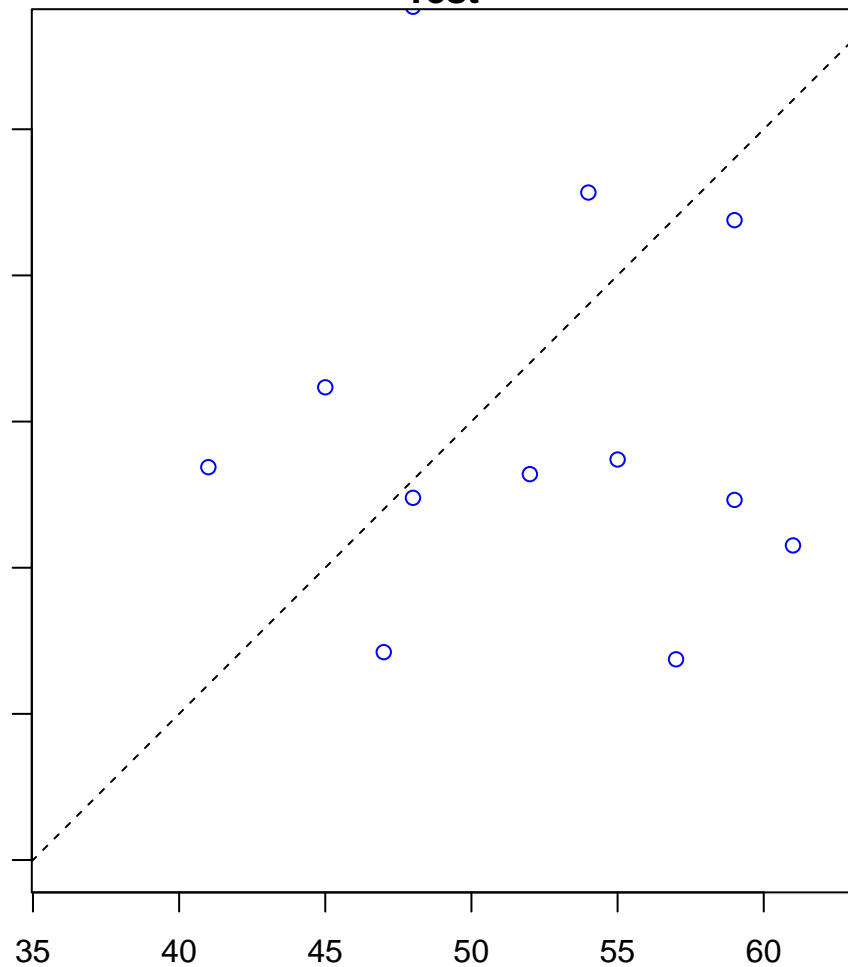


regulation of telomere maintenance (Score: 6.586030)

Control

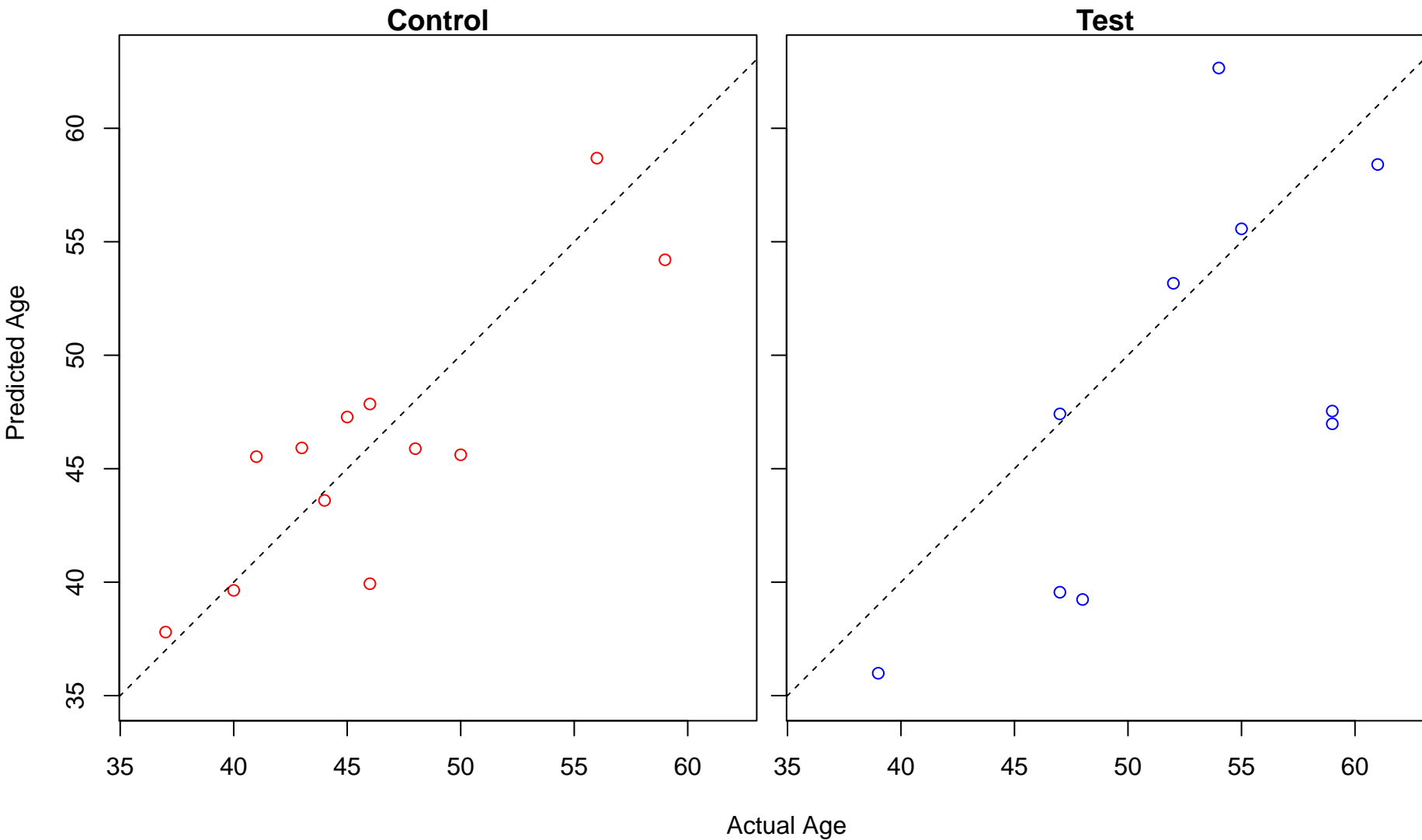


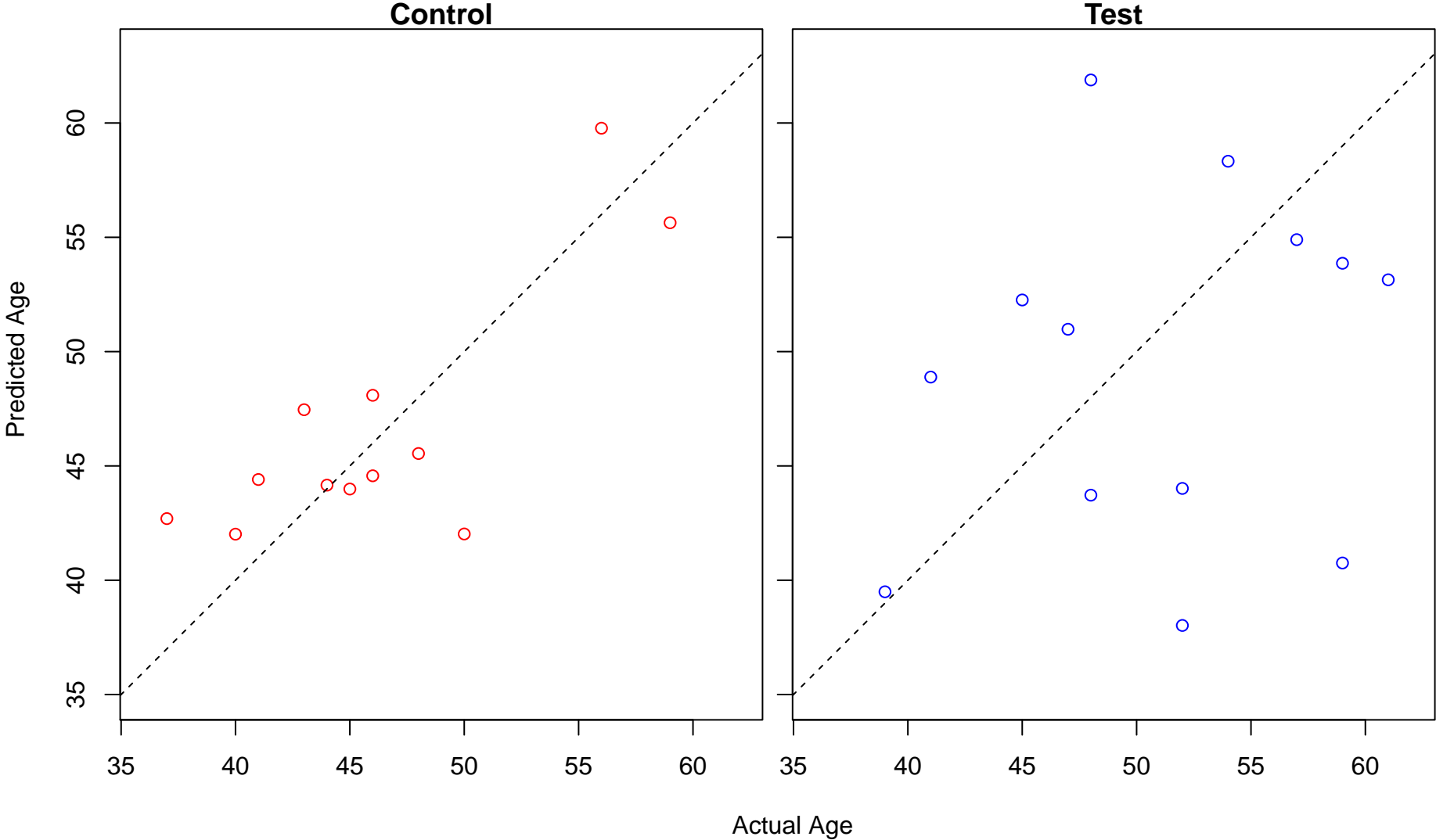
Test



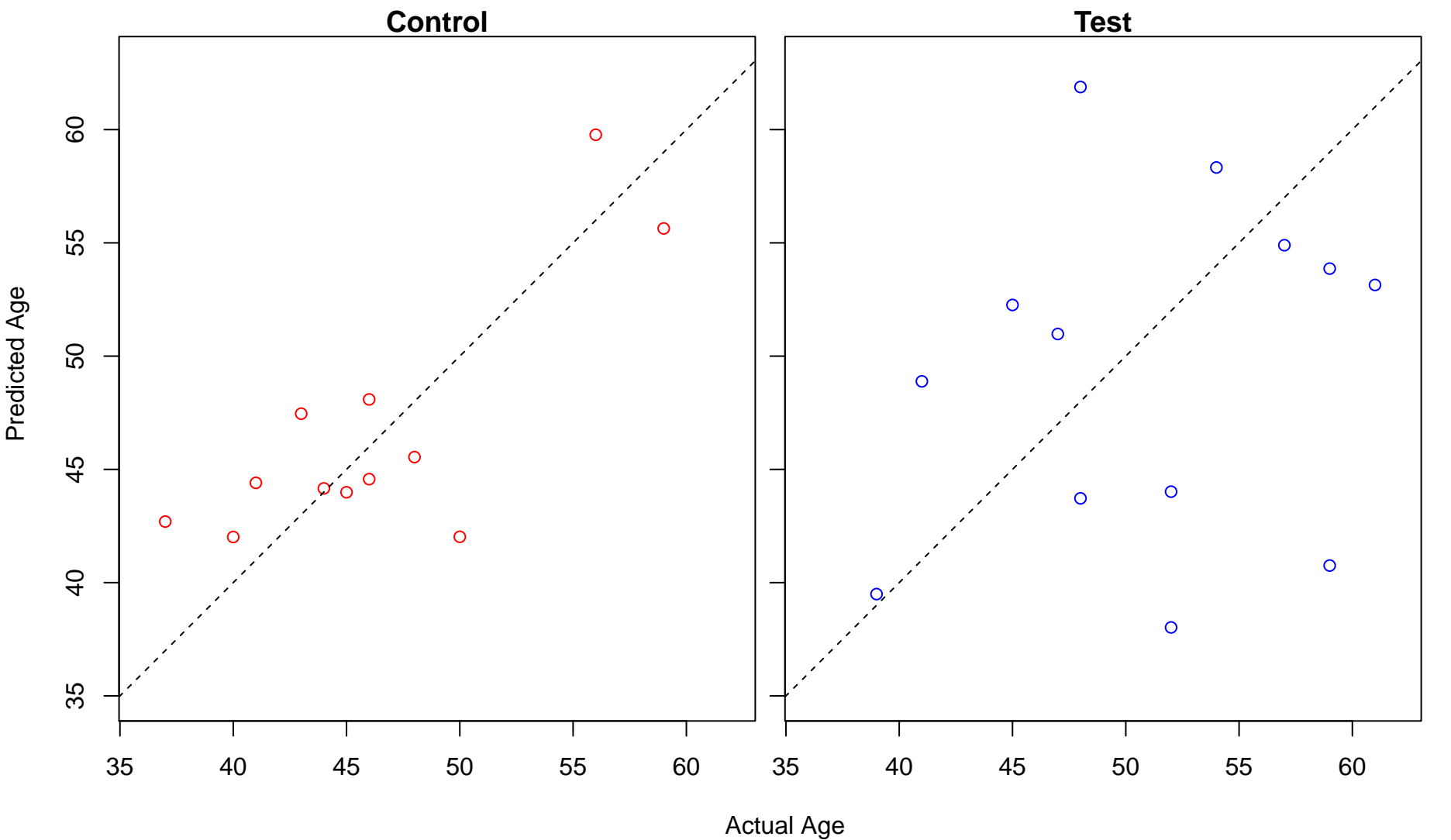
Actual Age

positive regulation of membrane potential (Score: 6.584243)



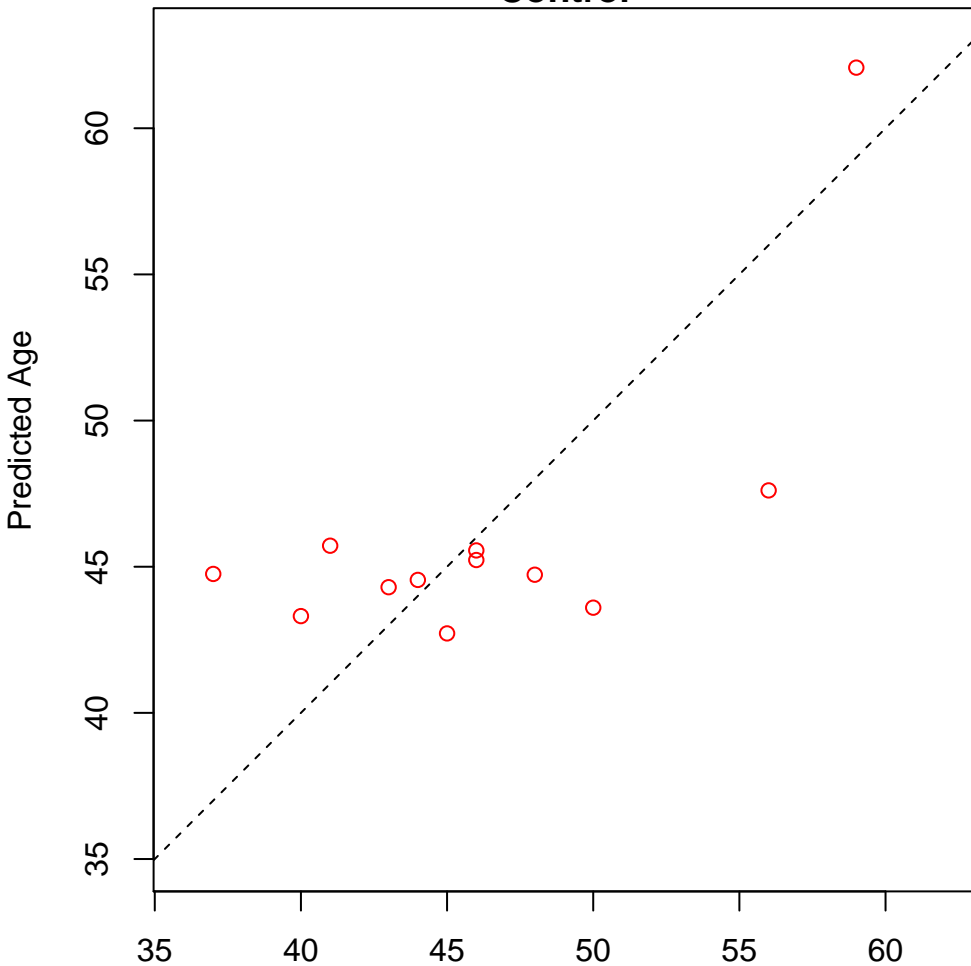


Positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay (Score

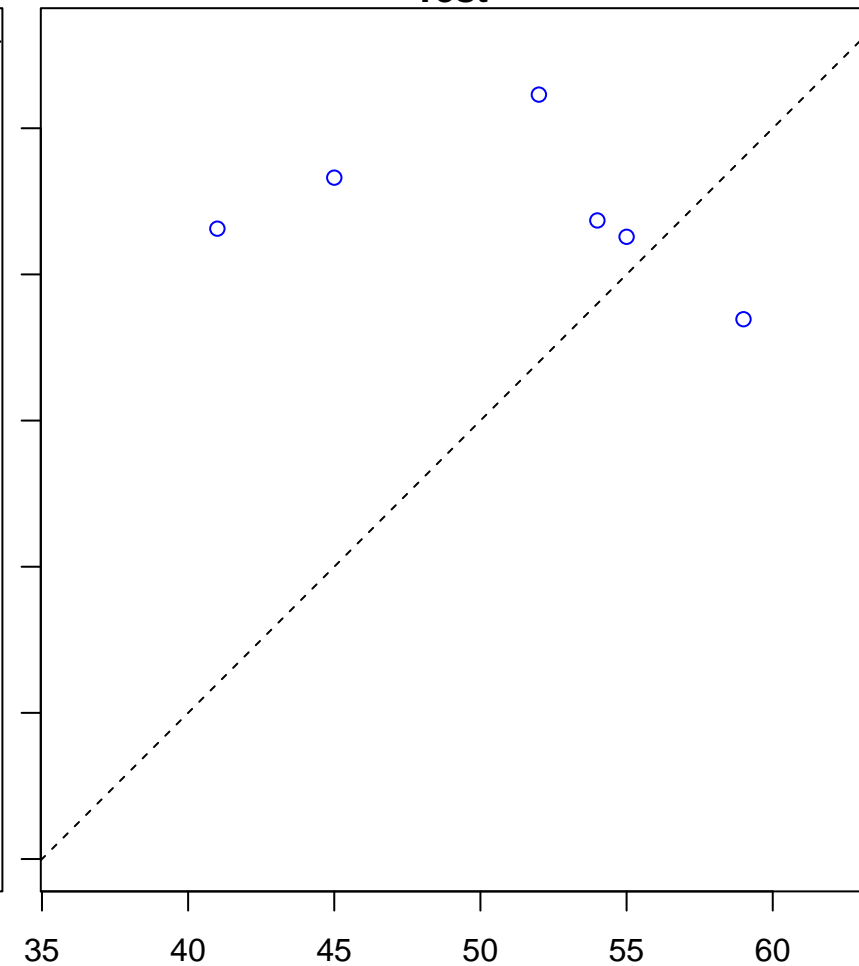


embryonic skeletal joint development (Score: 6.572970)

Control

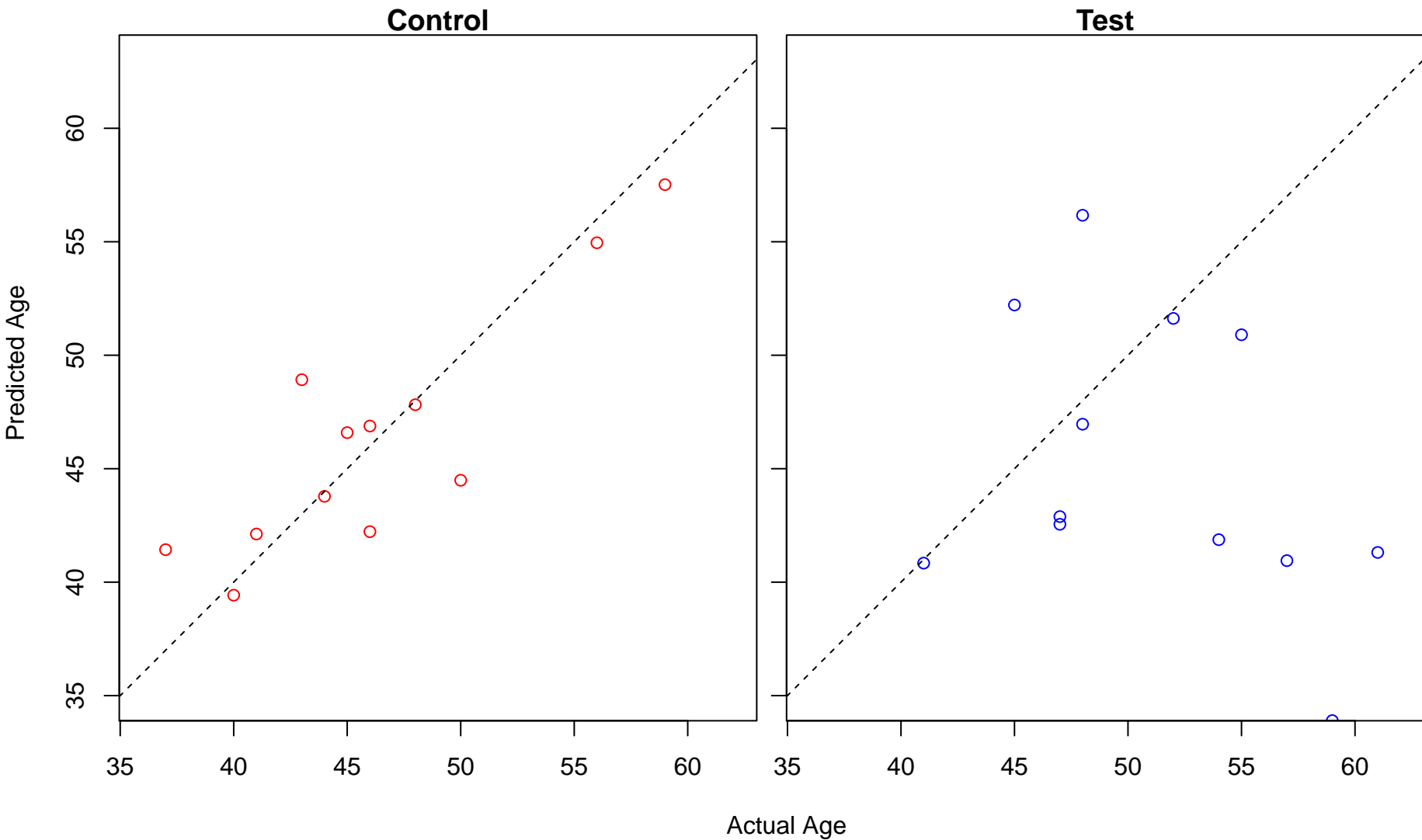


Test

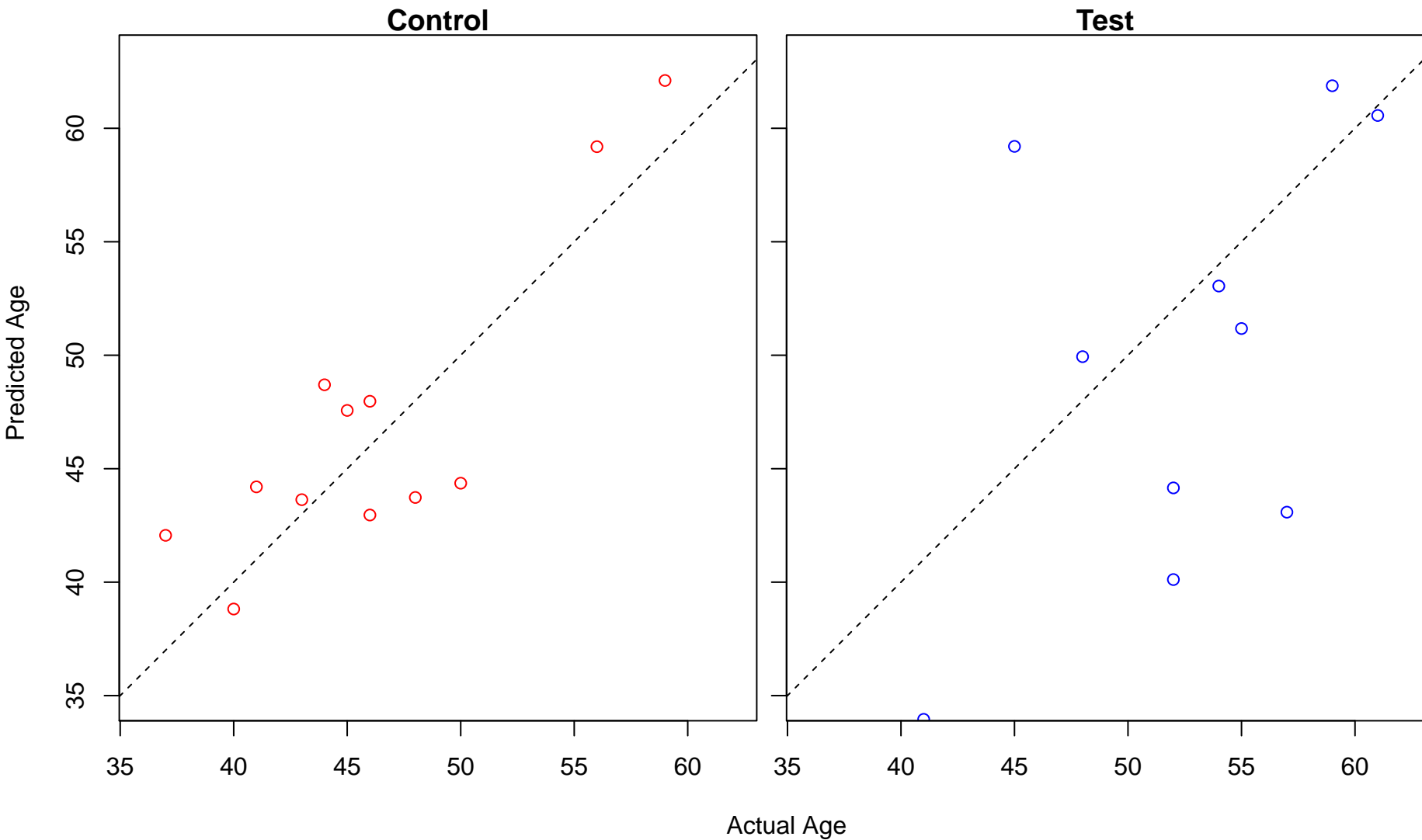


Actual Age

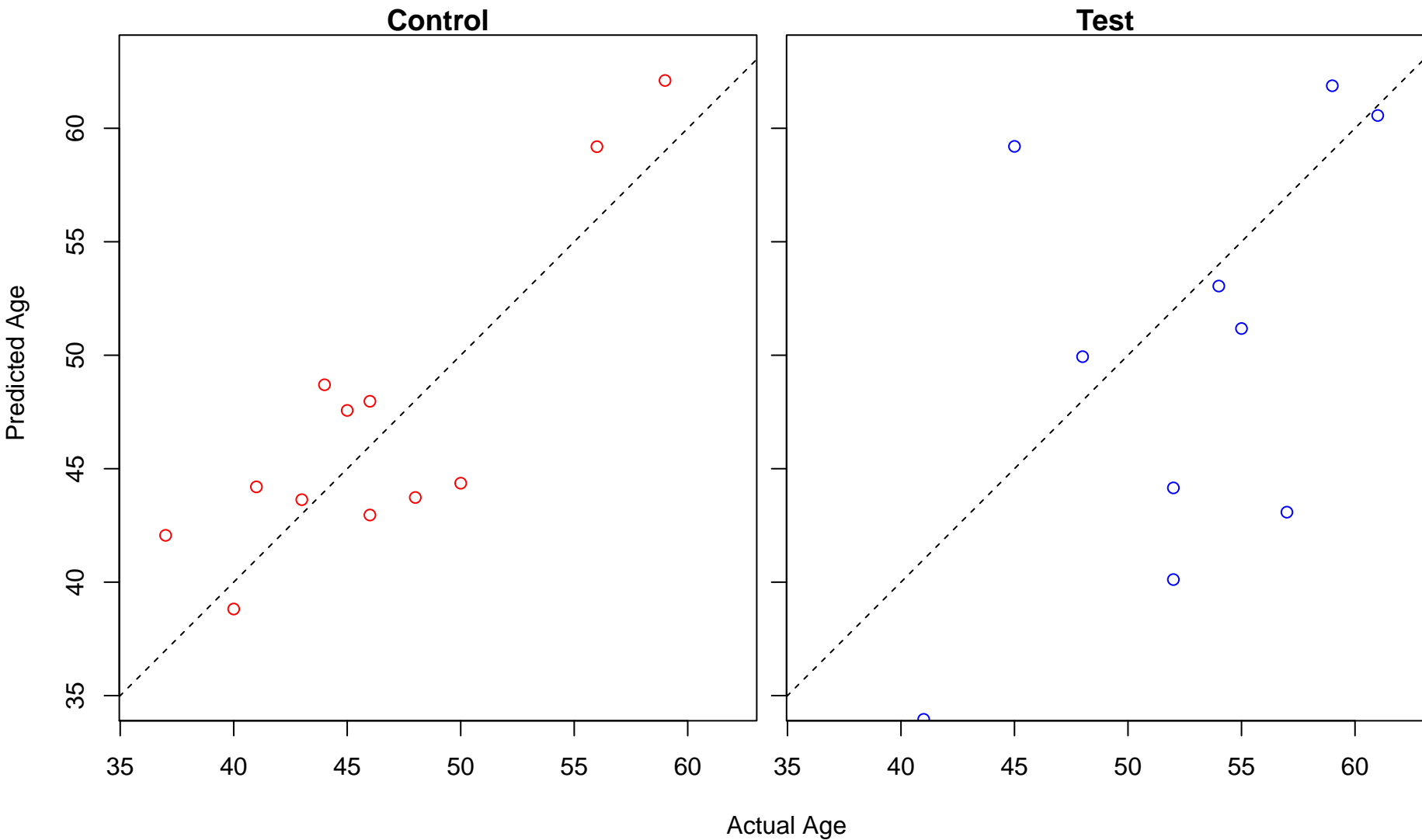
myeloid cell homeostasis (Score: 6.569541)



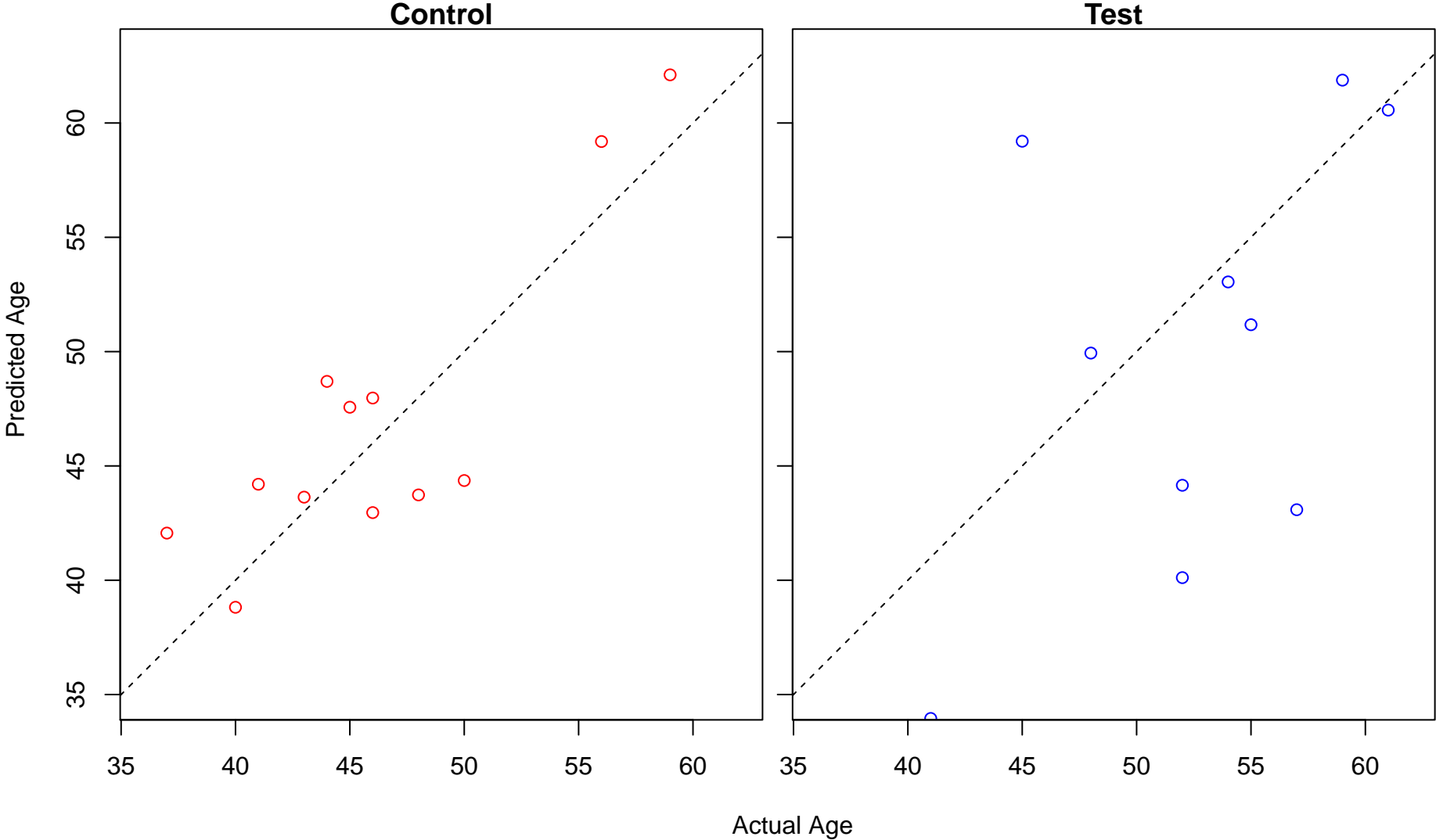
alpha-beta T cell activation involved in immune response (Score: 6.562515)



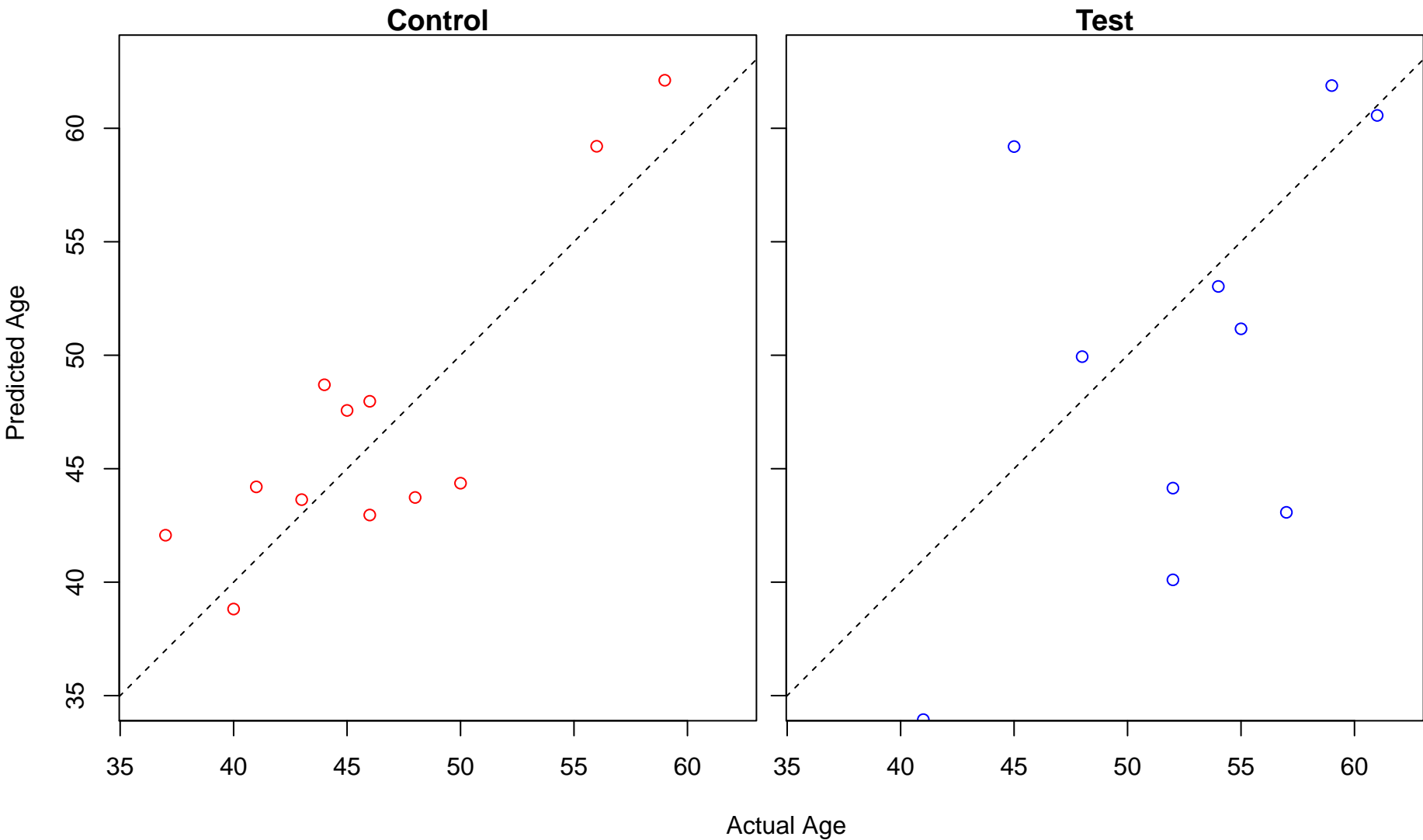
T cell differentiation involved in immune response (Score: 6.562515)



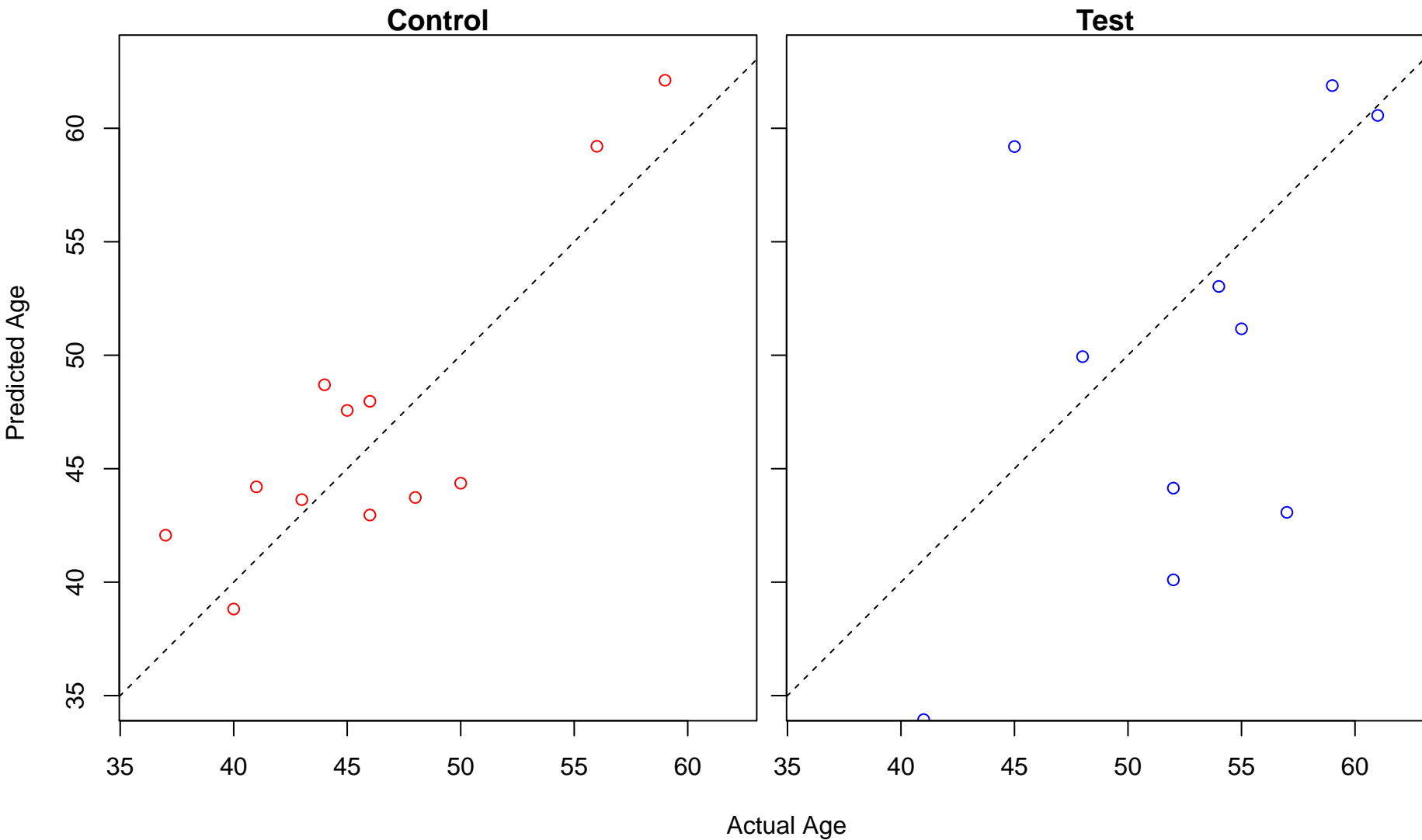
alpha-beta T cell differentiation involved in immune response (Score: 6.562515)



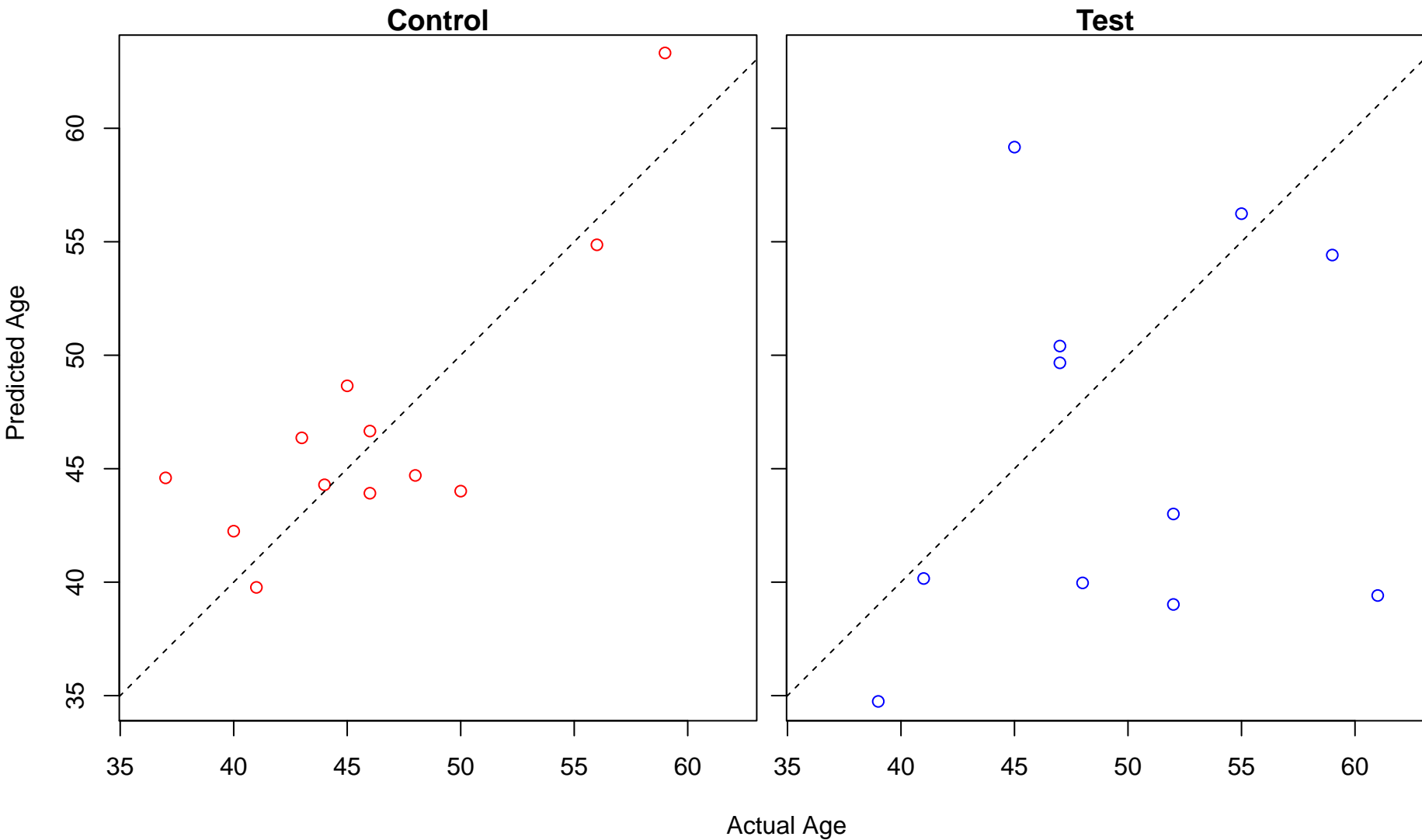
CD4-positive, alpha-beta T cell differentiation involved in immune response (Score: 6.560967)



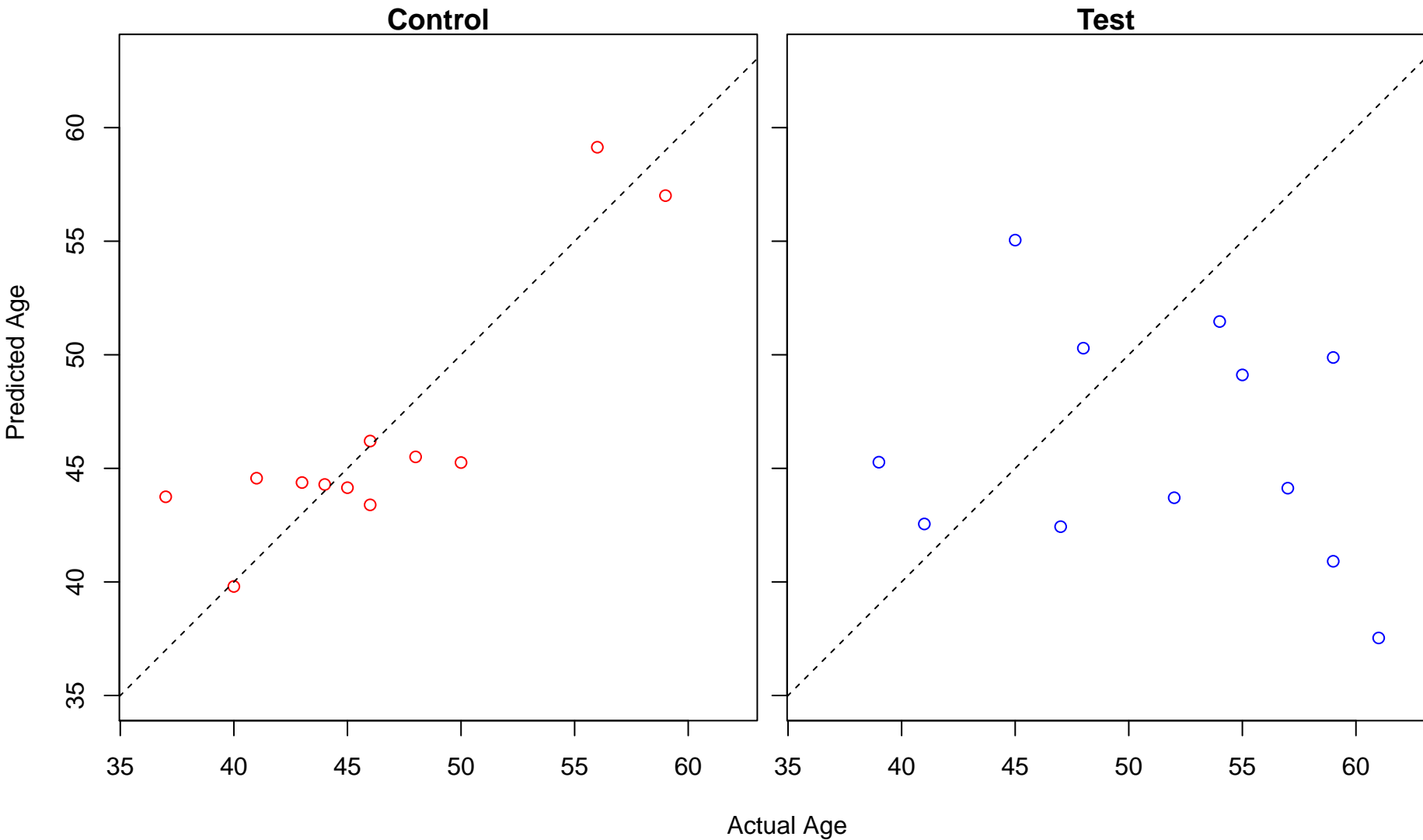
T-helper cell differentiation (Score: 6.560967)



regulation of DNA-templated transcription, elongation (Score: 6.558339)

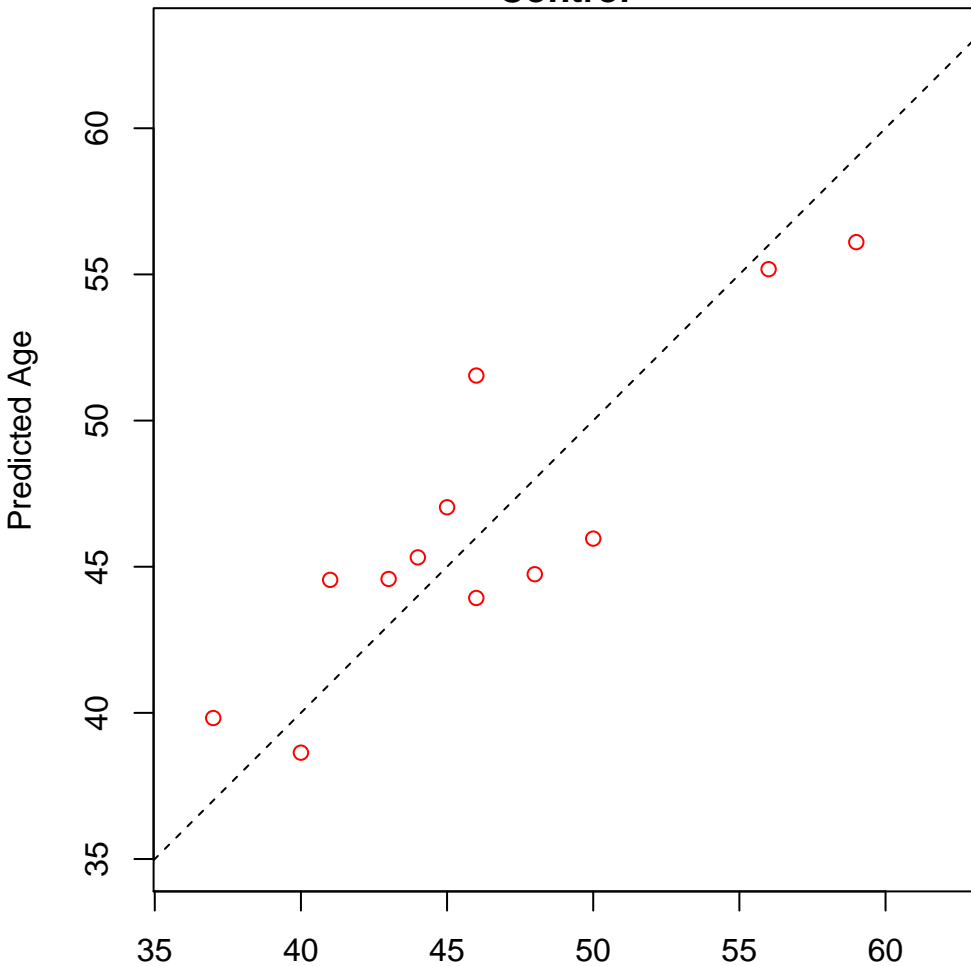


sulfur compound metabolic process (Score: 6.549658)

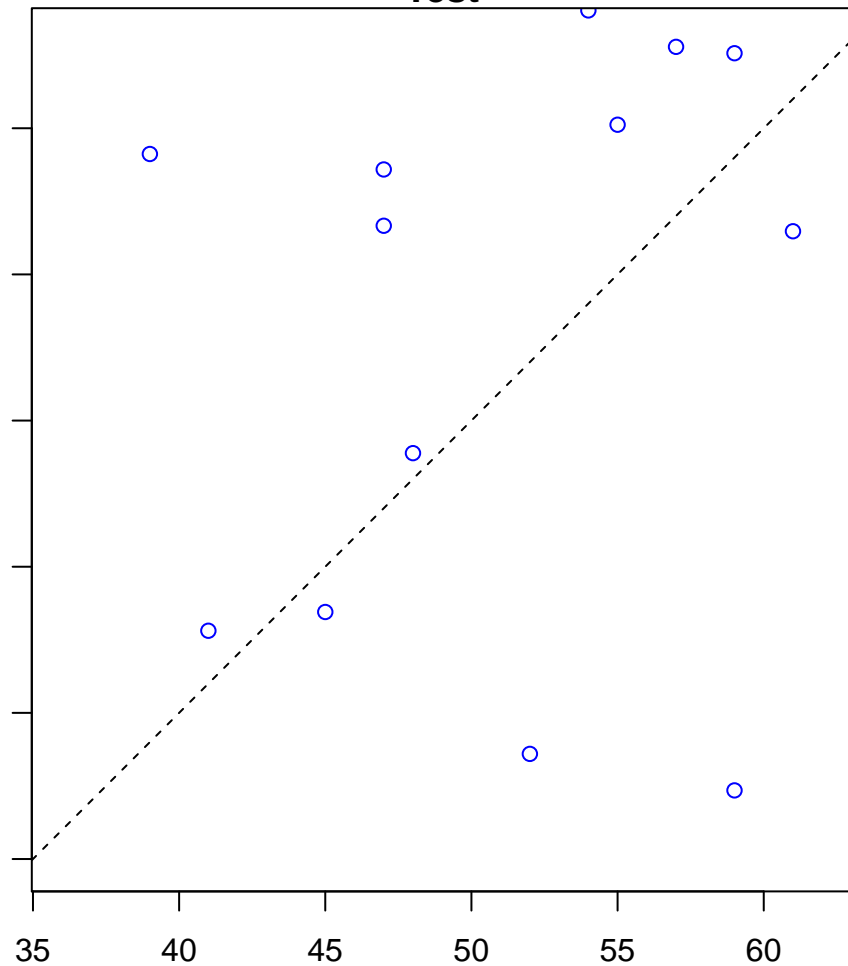


negative regulation of platelet activation (Score: 6.532617)

Control

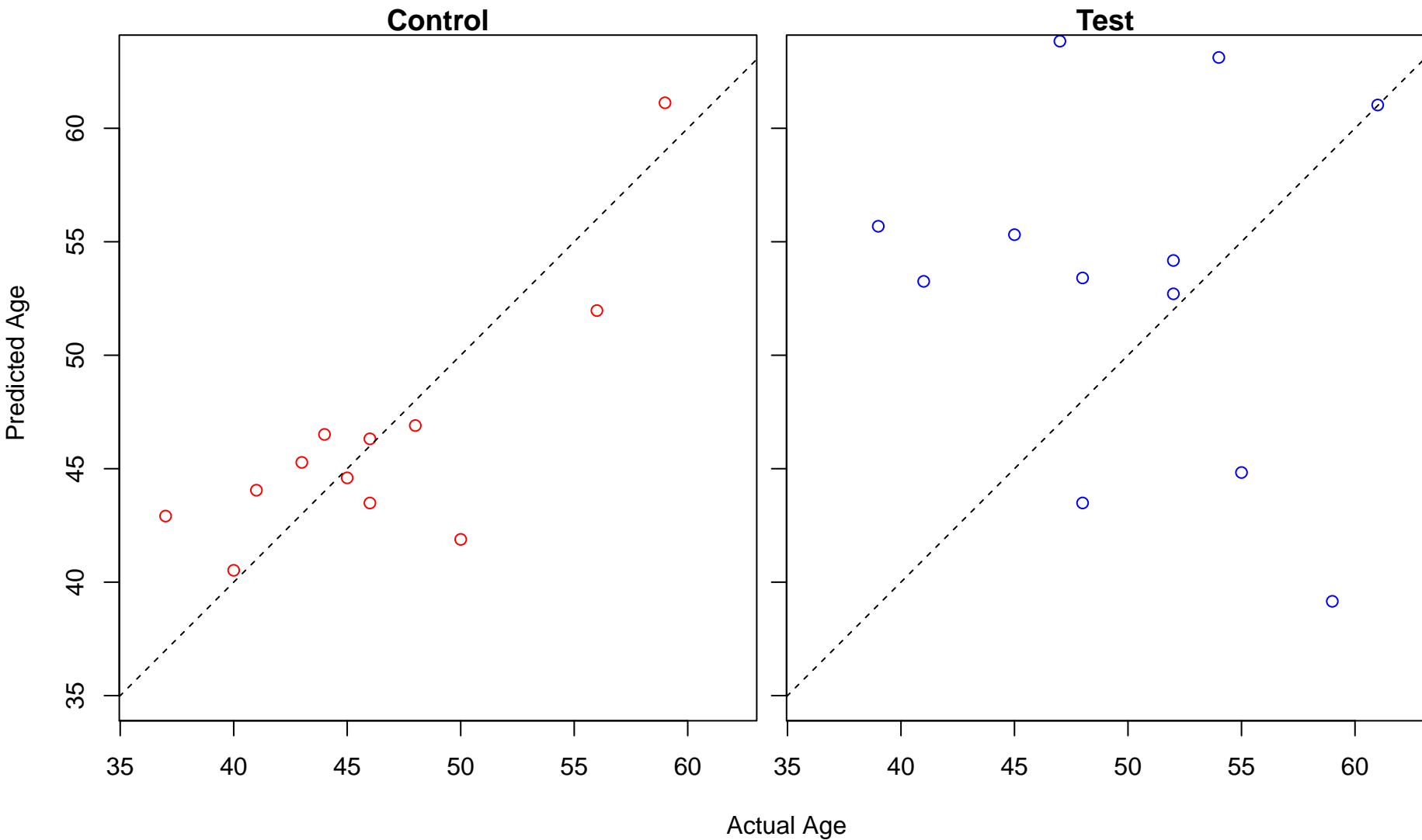


Test

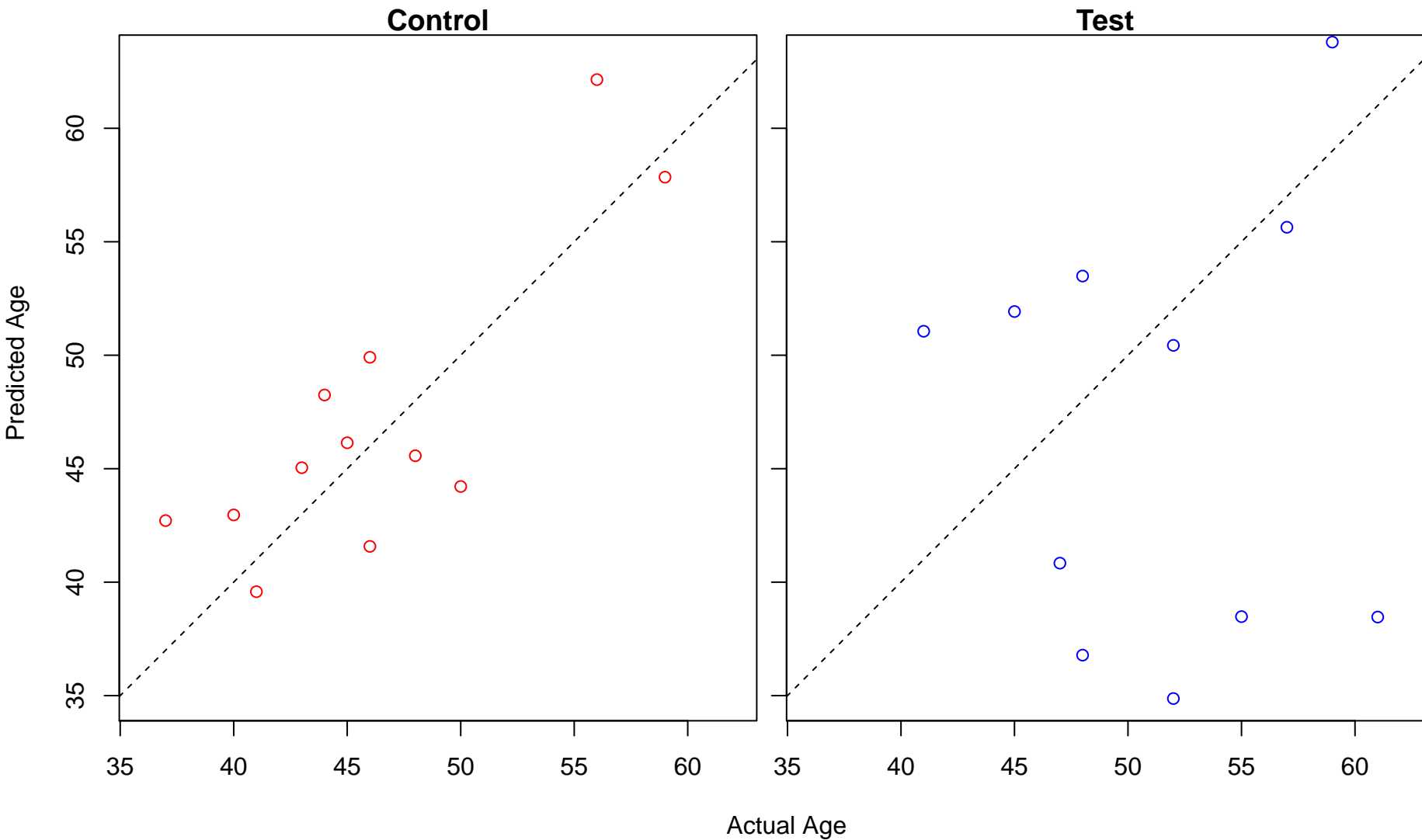


Actual Age

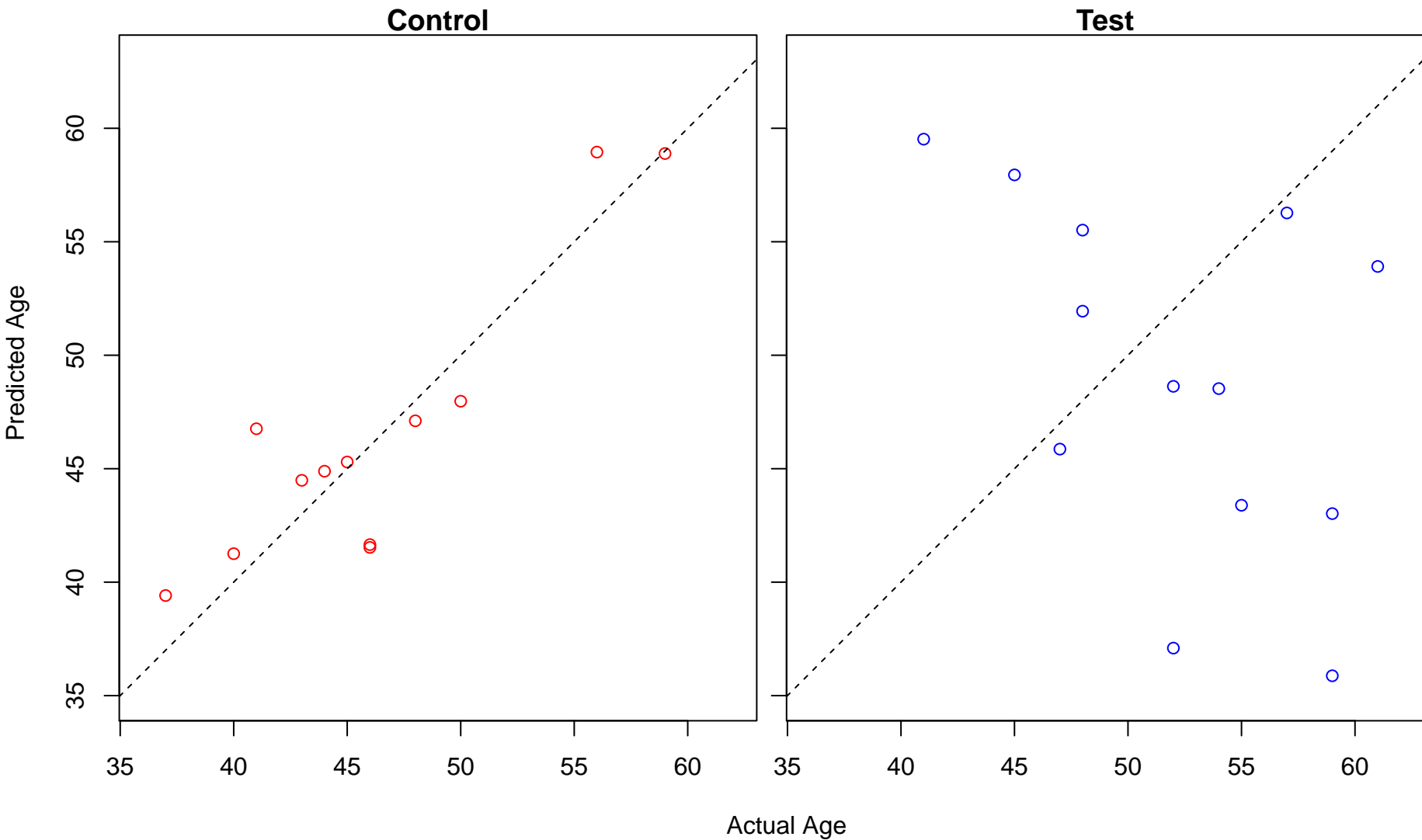
positive regulation of natural killer cell mediated immunity (Score: 6.528626)



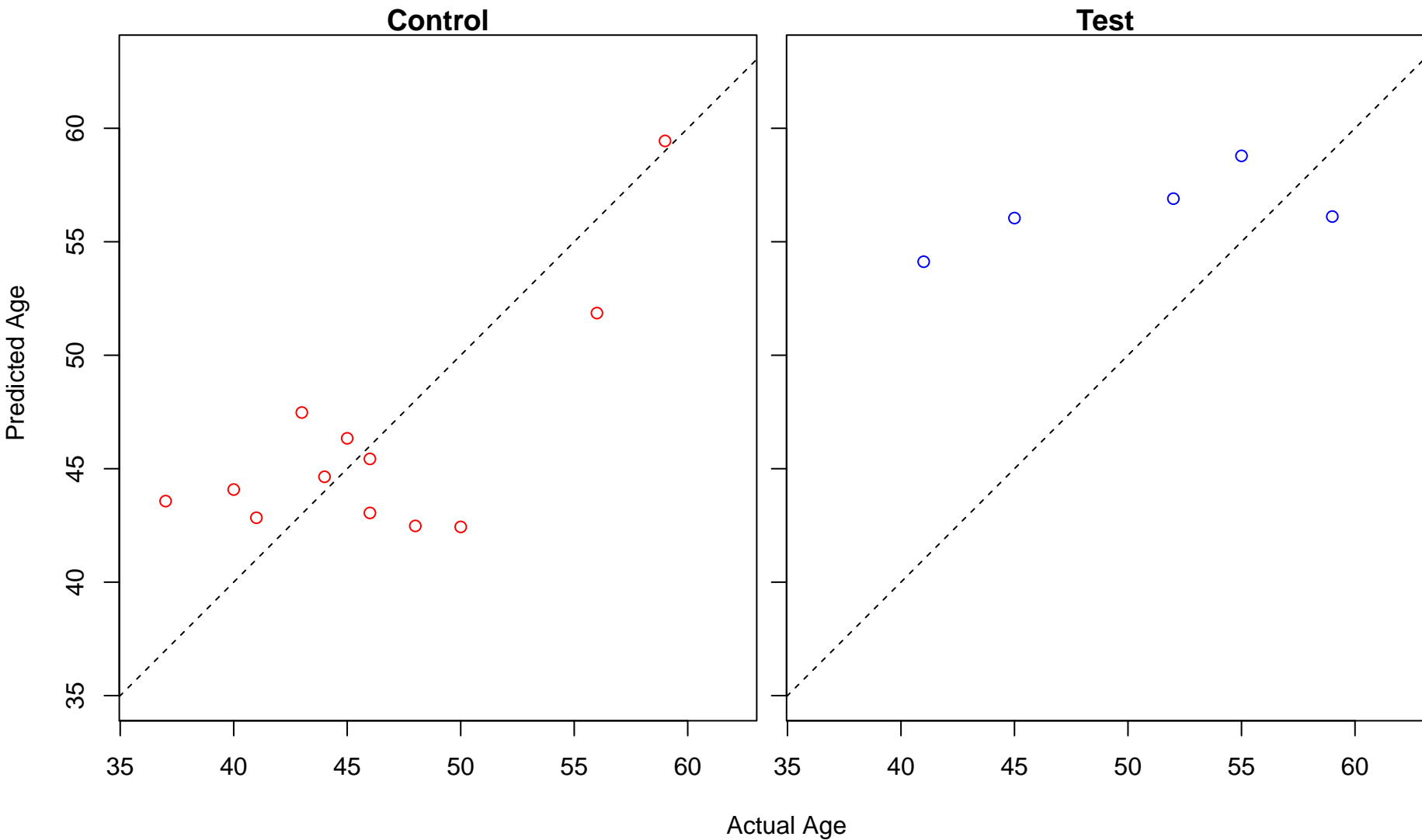
muscle cell development (Score: 6.527241)



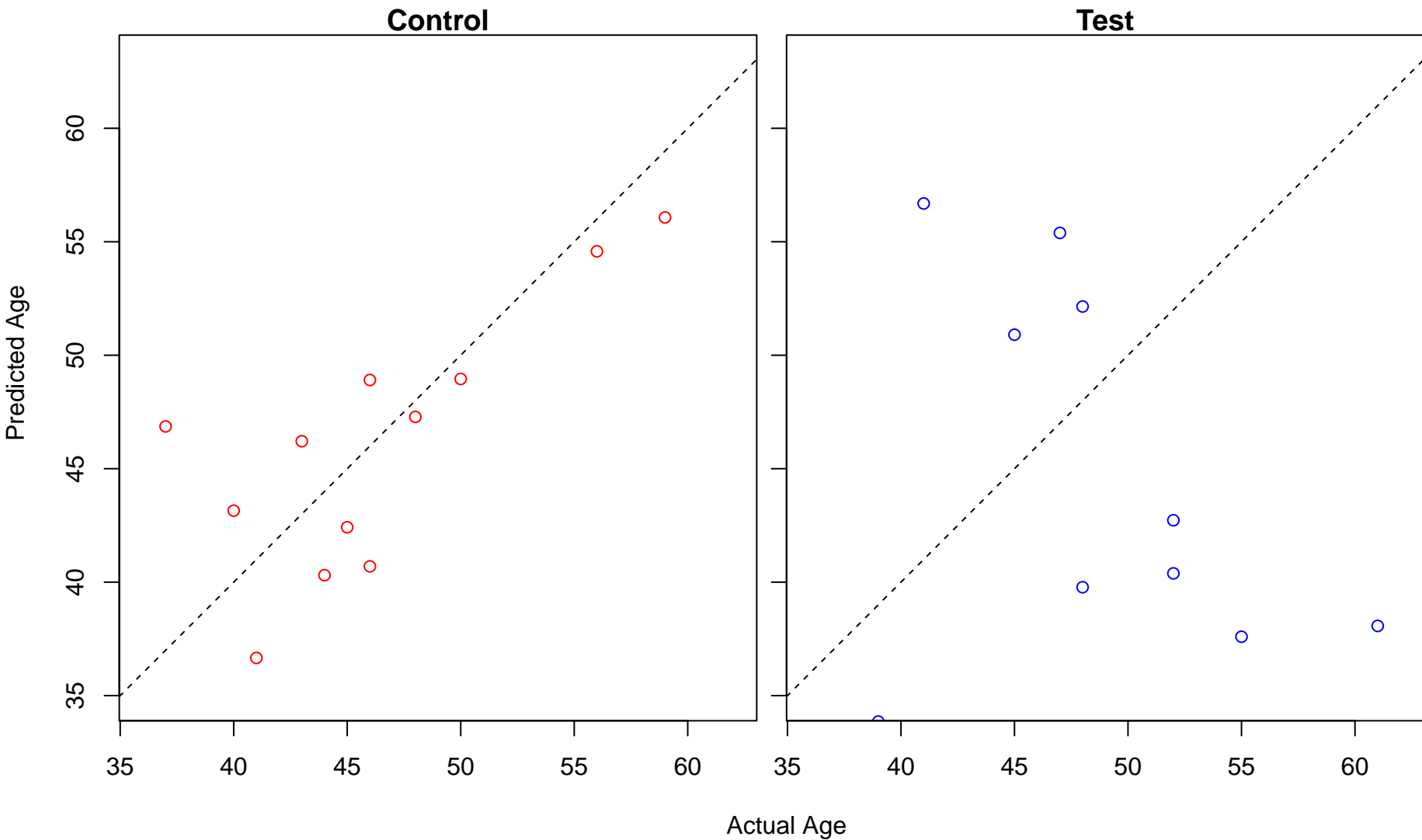
ERK1 and ERK2 cascade (Score: 6.518206)



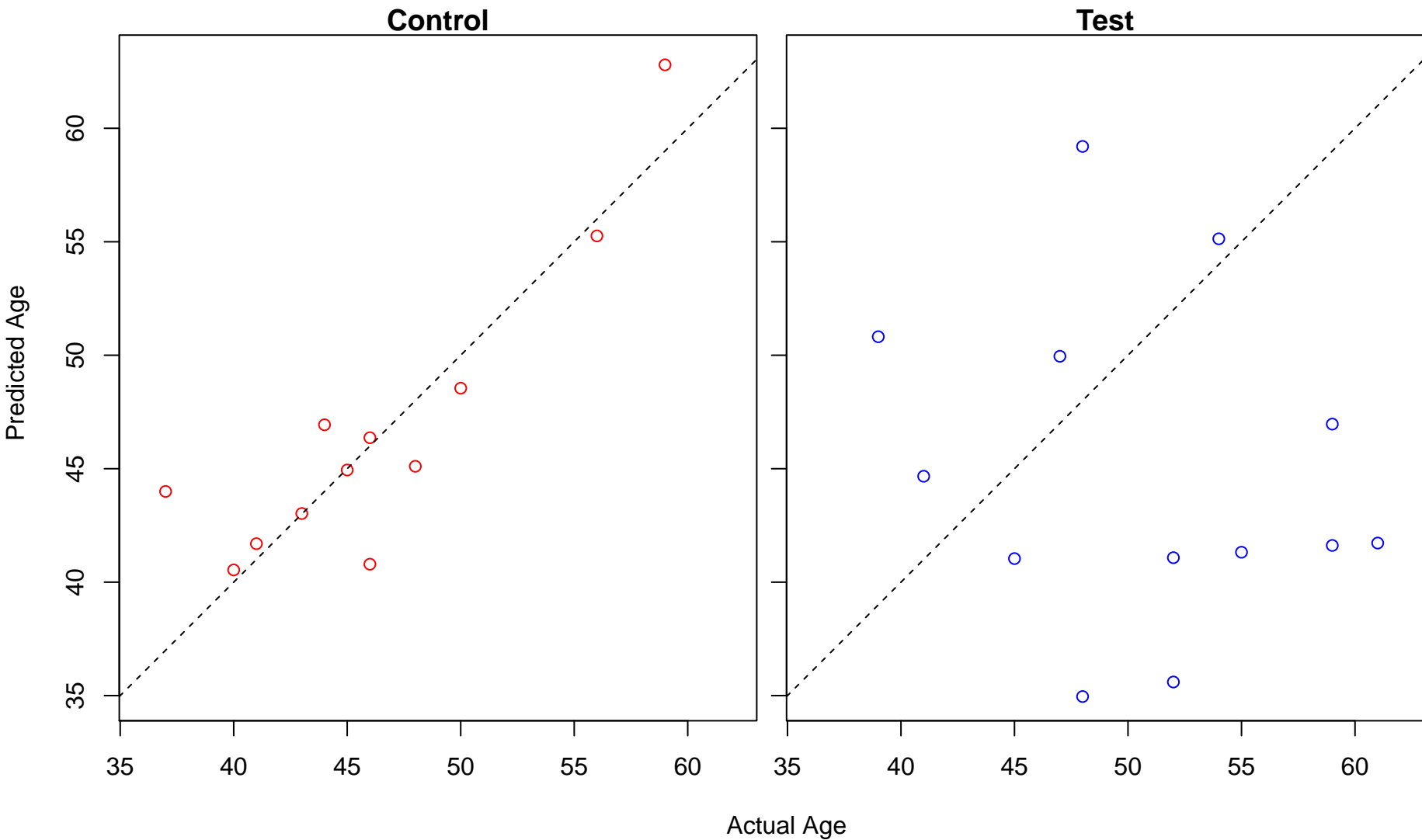
regulation of hexokinase activity (Score: 6.517542)



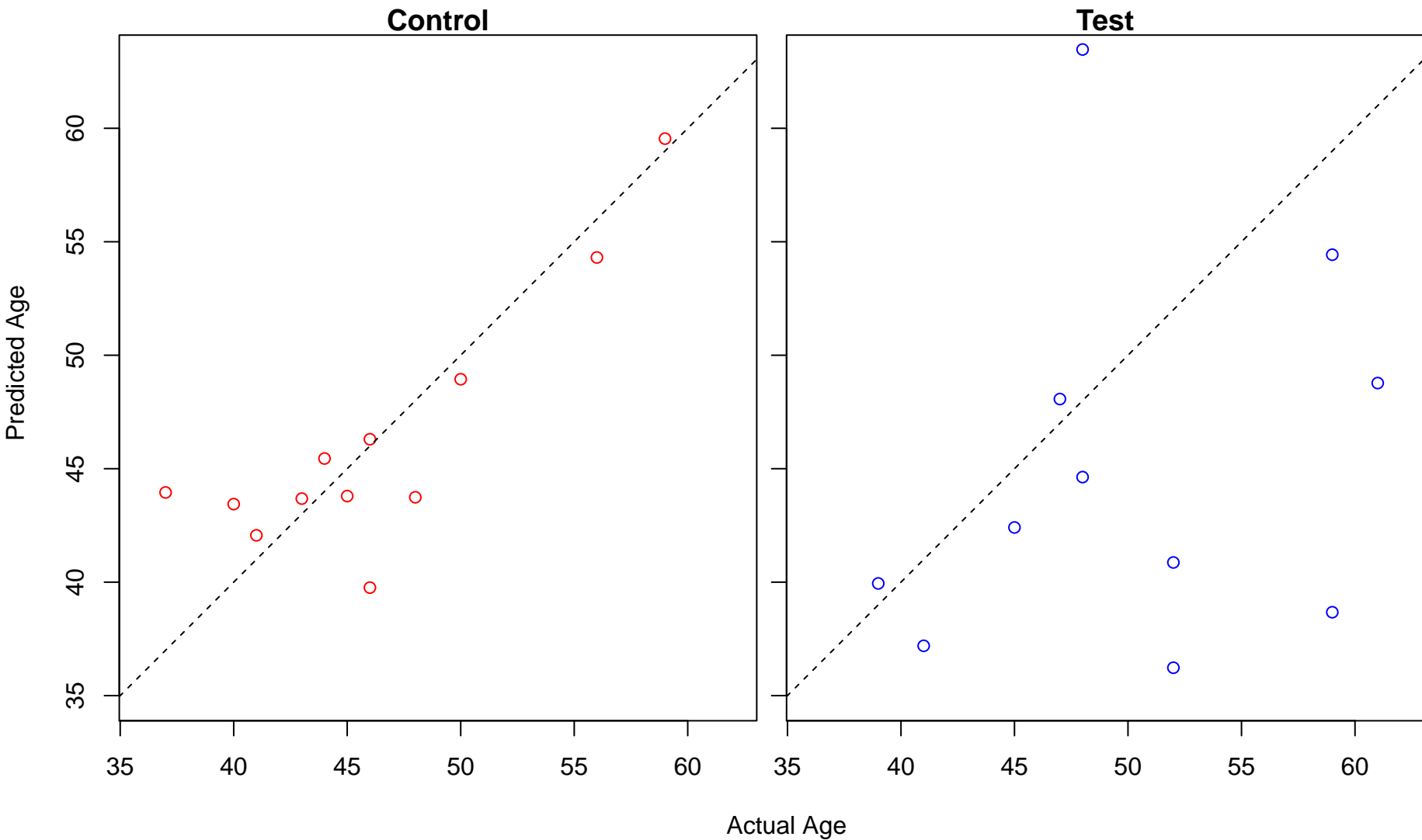
positive regulation of extrinsic apoptotic signaling pathway (Score: 6.505912)



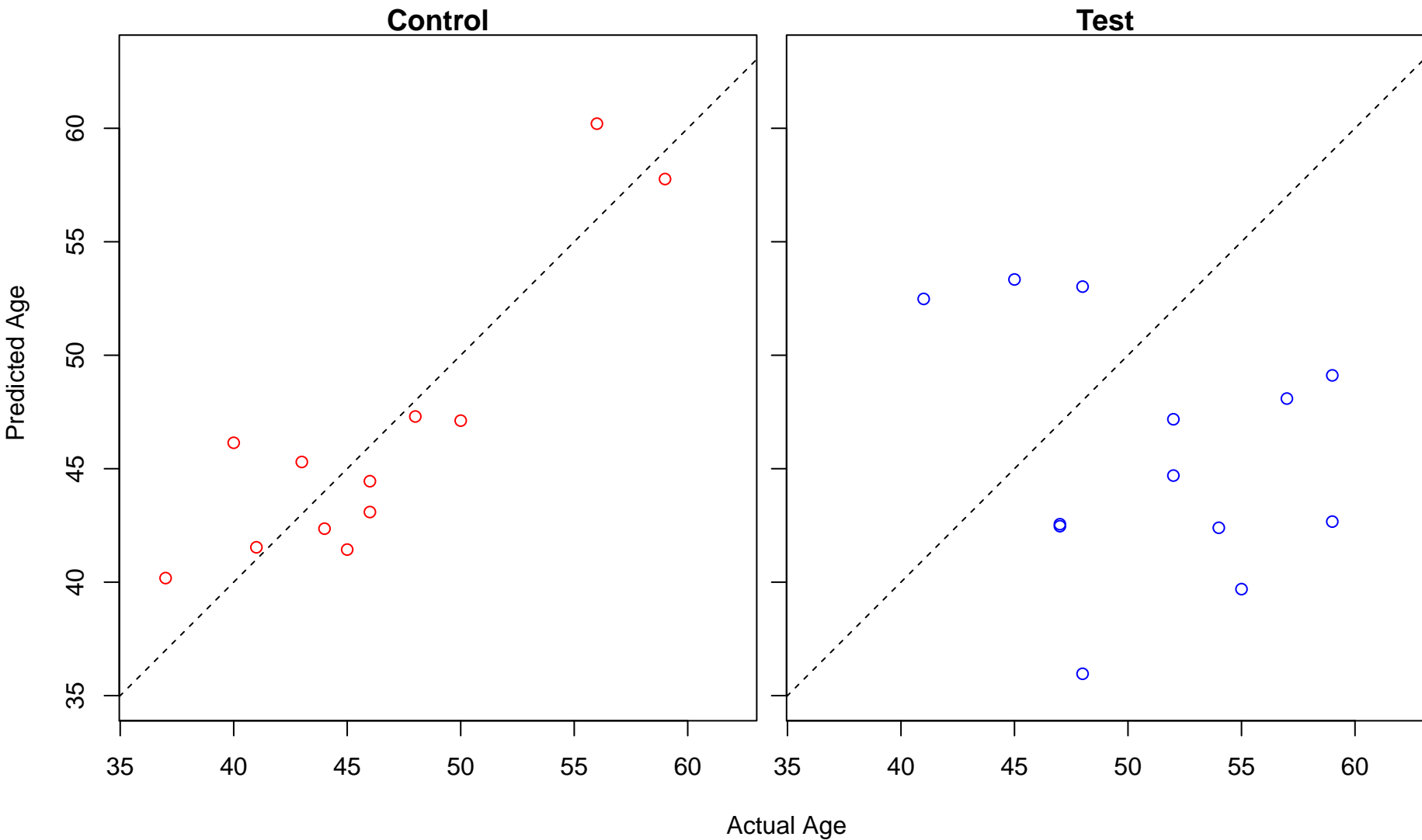
positive regulation of cation transmembrane transport (Score: 6.501205)



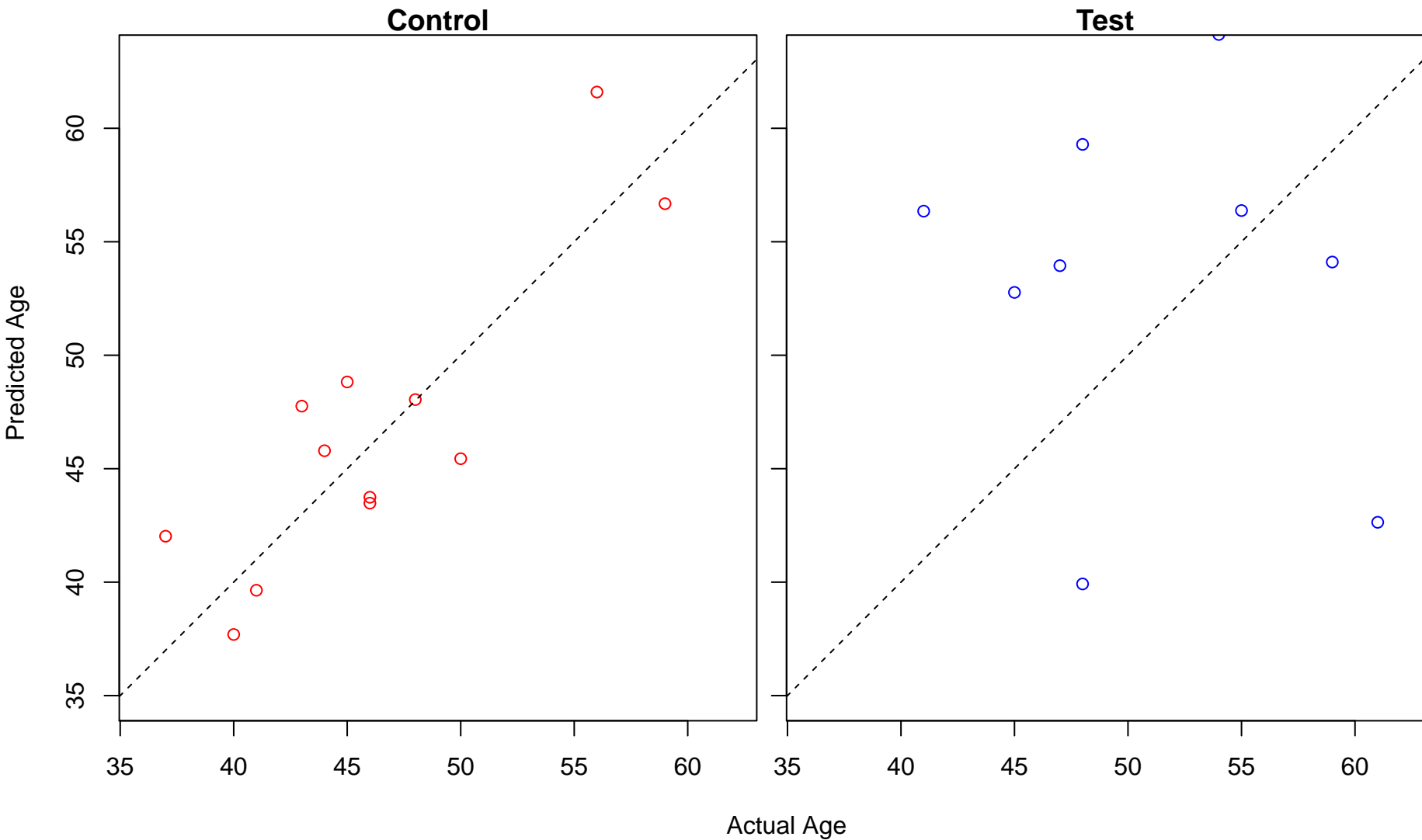
potassium ion transport (Score: 6.499044)



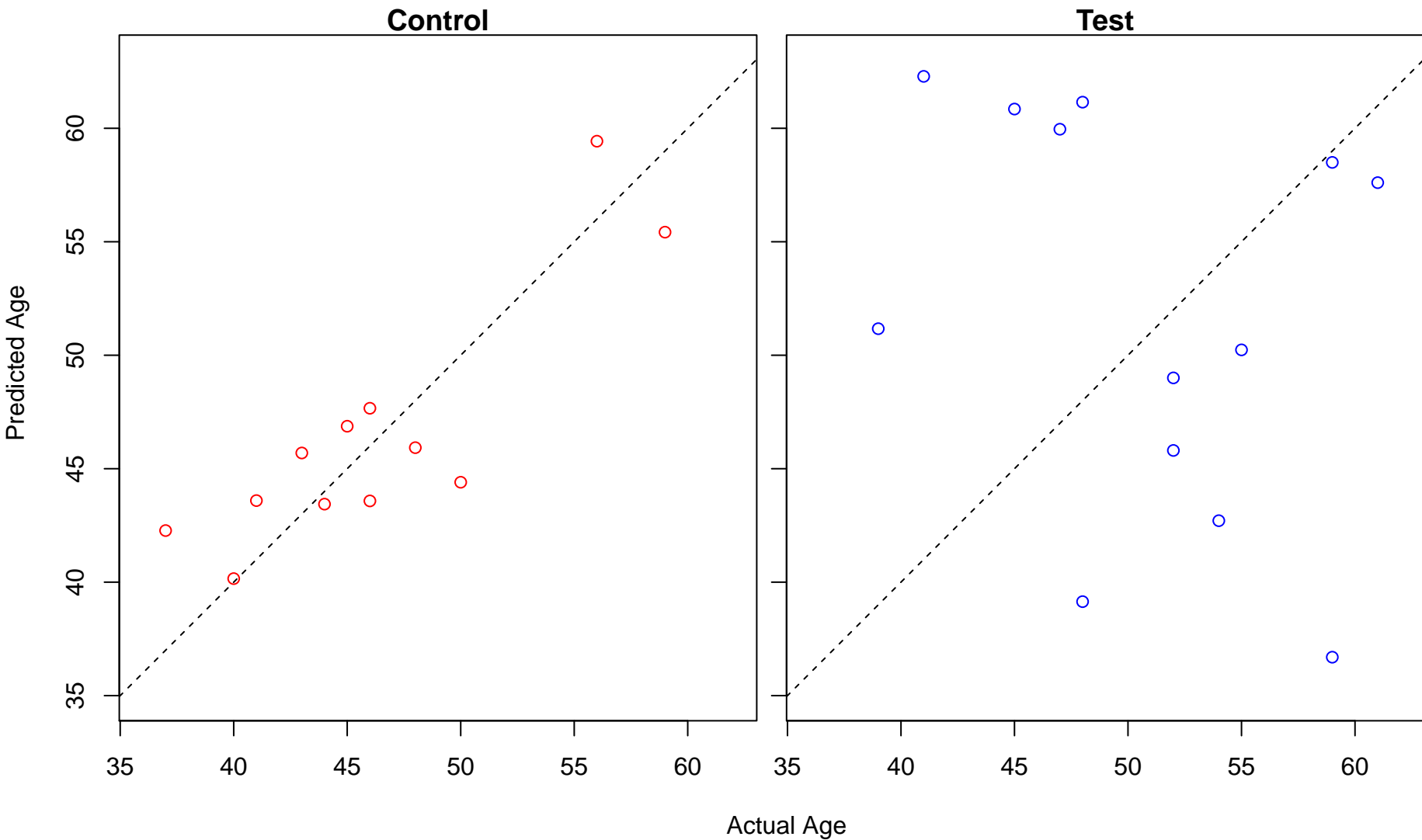
drug metabolic process (Score: 6.496510)



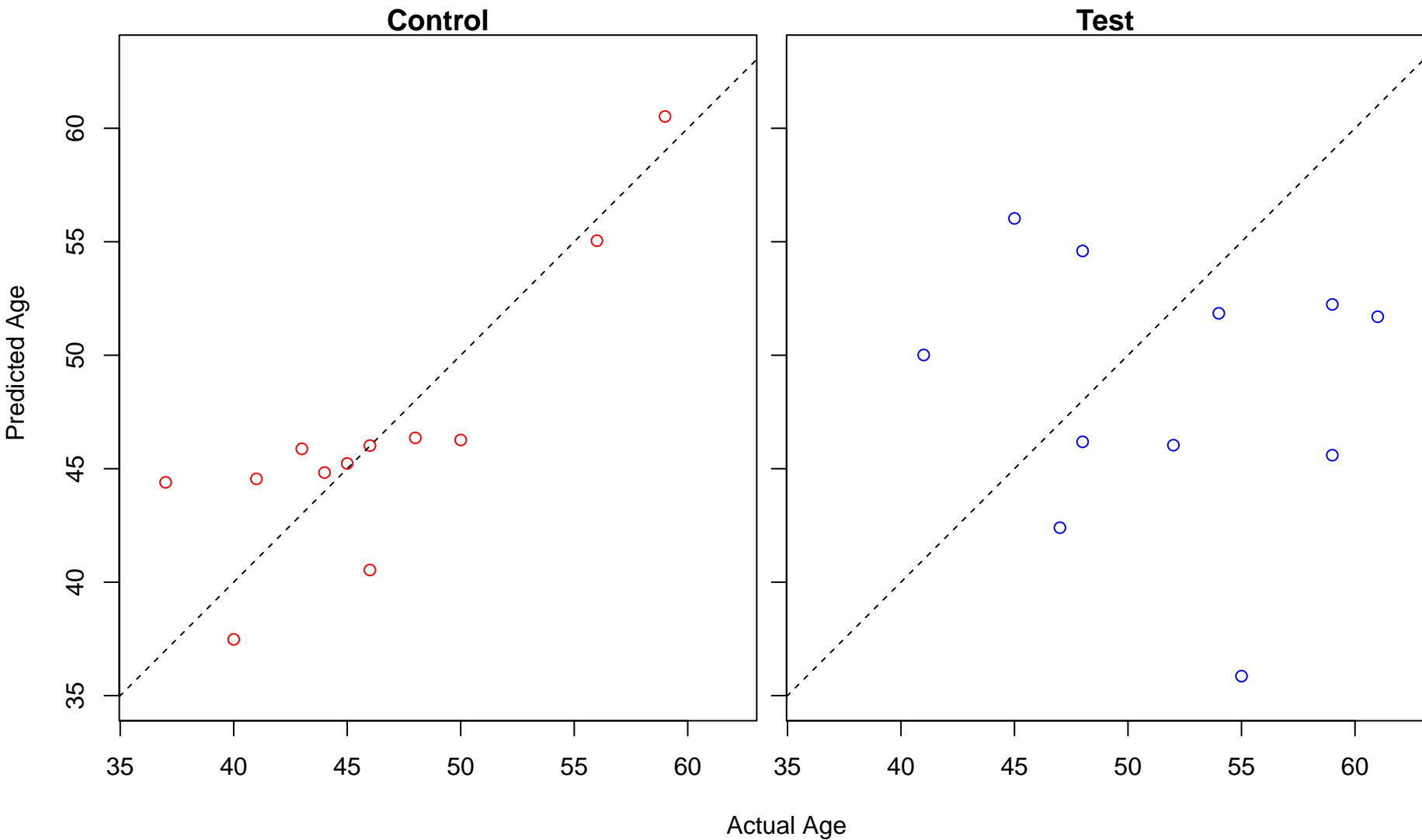
somitogenesis (Score: 6.493926)



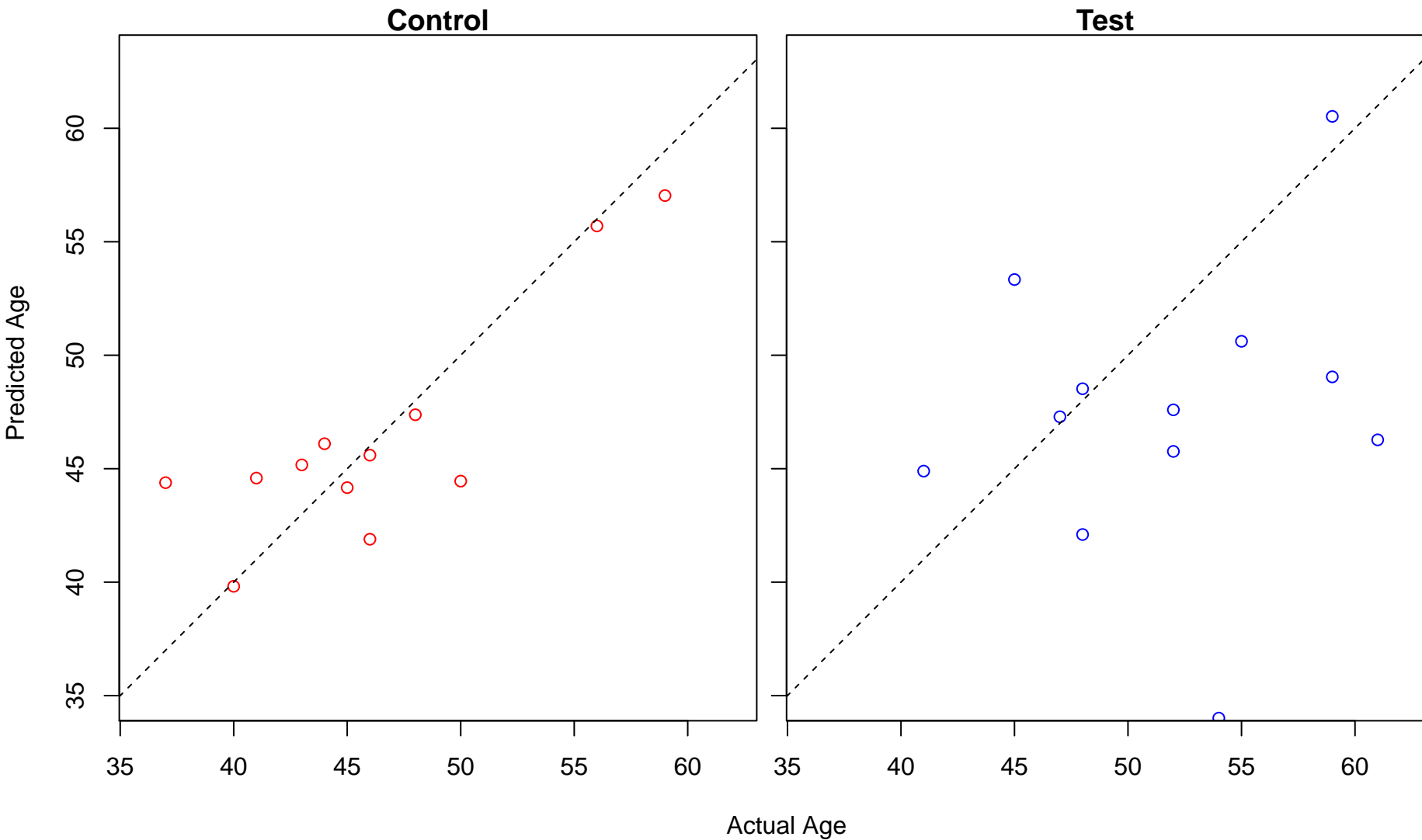
urogenital system development (Score: 6.486967)



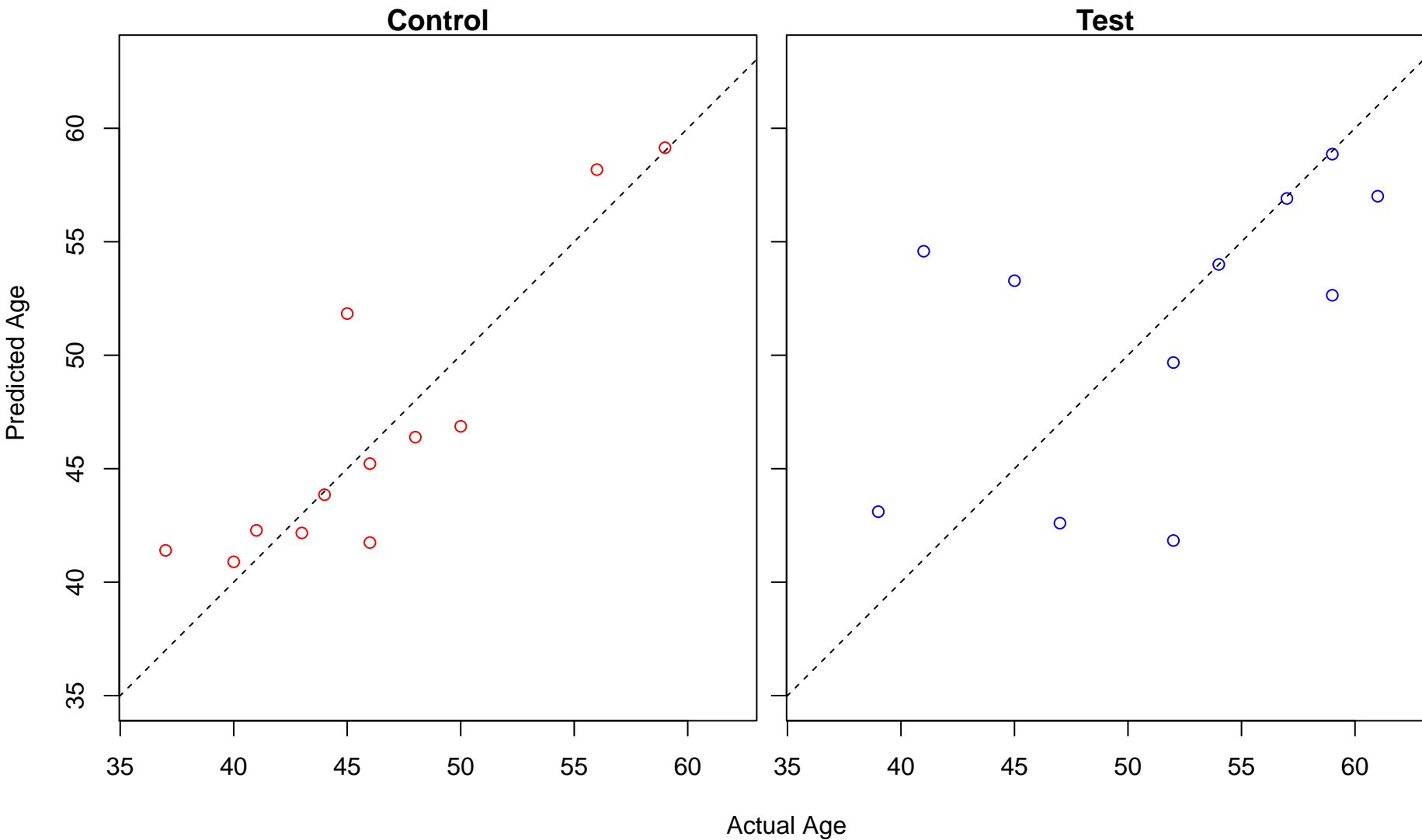
regulation of cellular protein localization (Score: 6.485118)



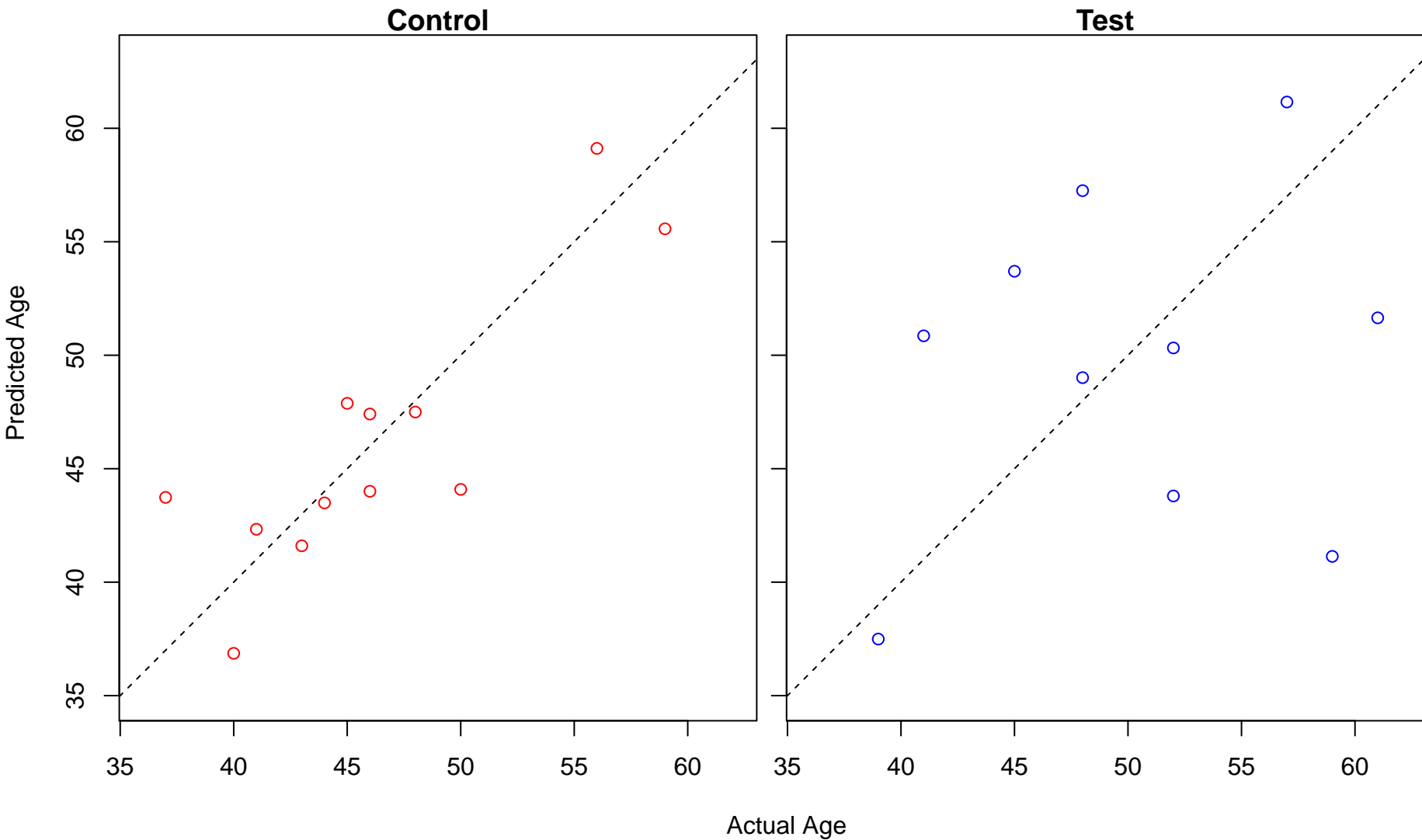
positive regulation of viral life cycle (Score: 6.482095)



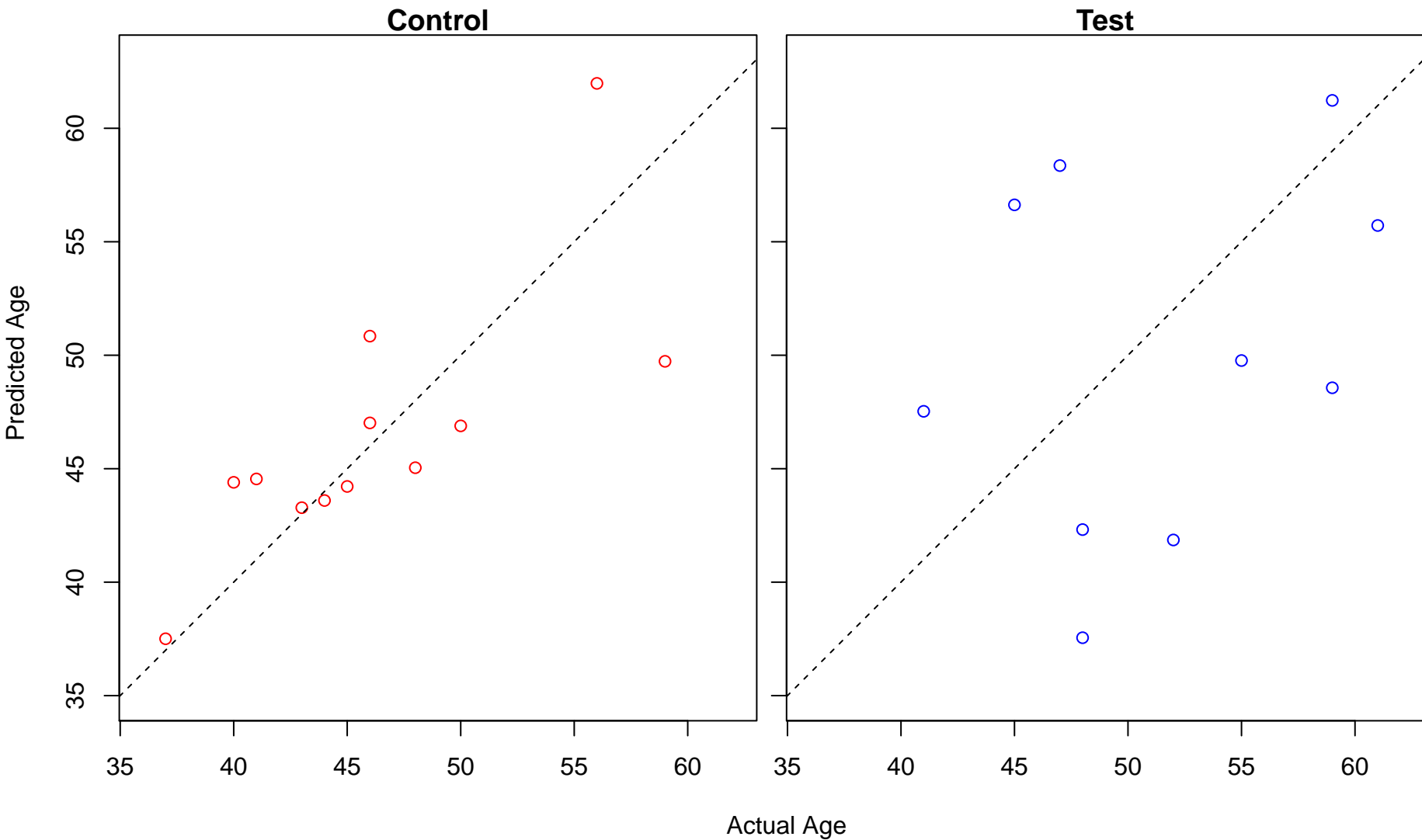
regulation of Notch signaling pathway (Score: 6.470485)



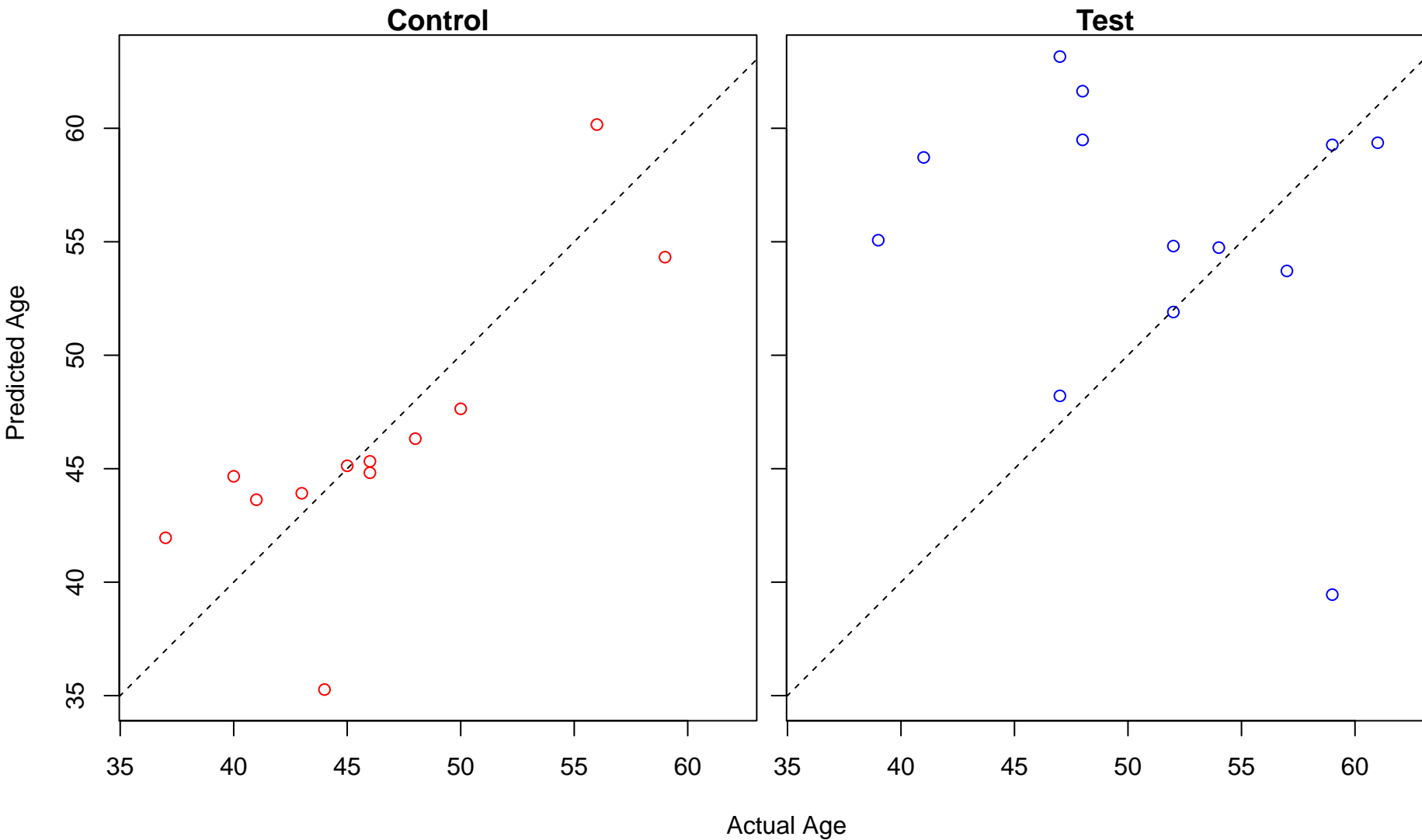
regulation of cytokine production involved in inflammatory response (Score: 6.466744)



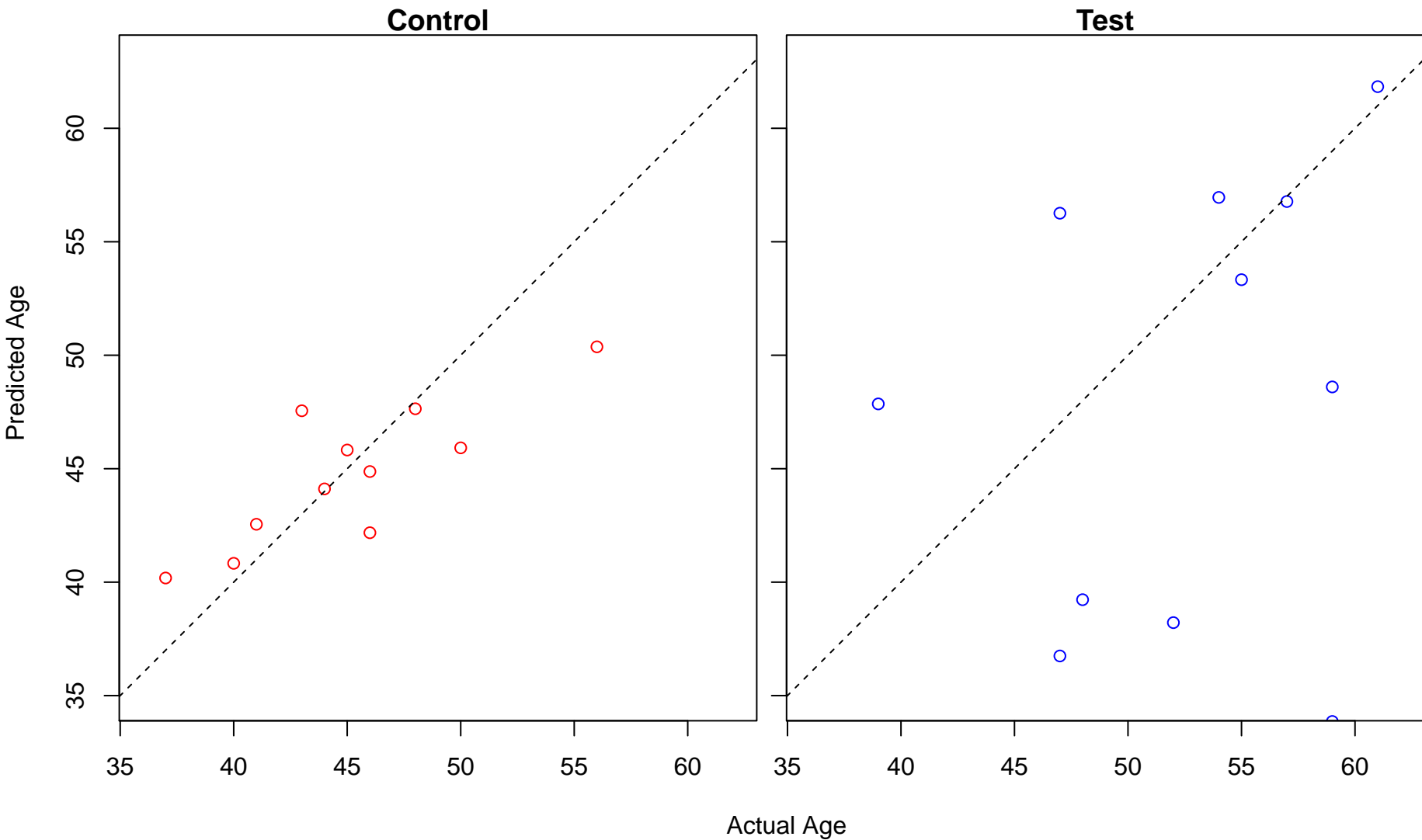
regulation of cholesterol esterification (Score: 6.457905)



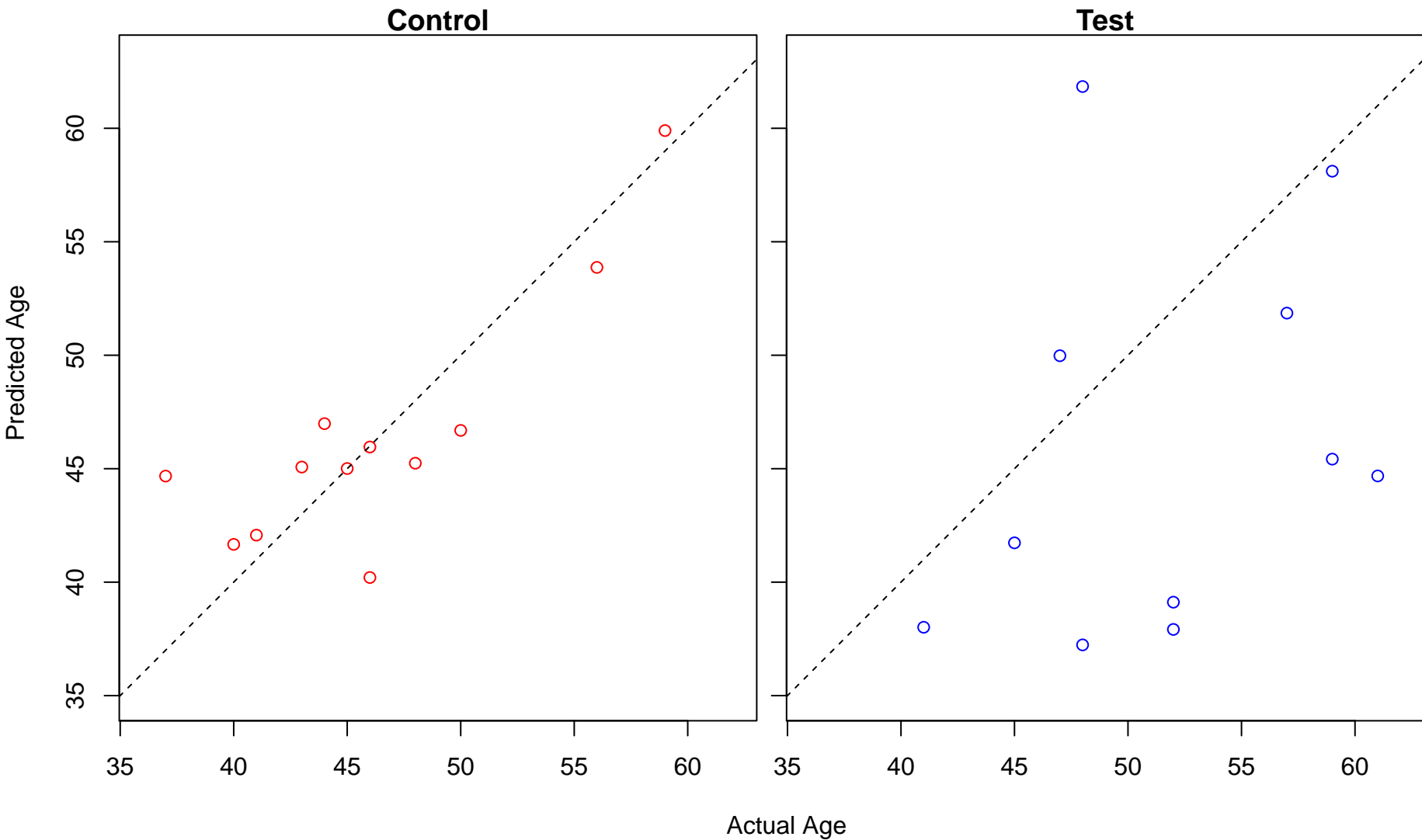
viral entry into host cell (Score: 6.453902)



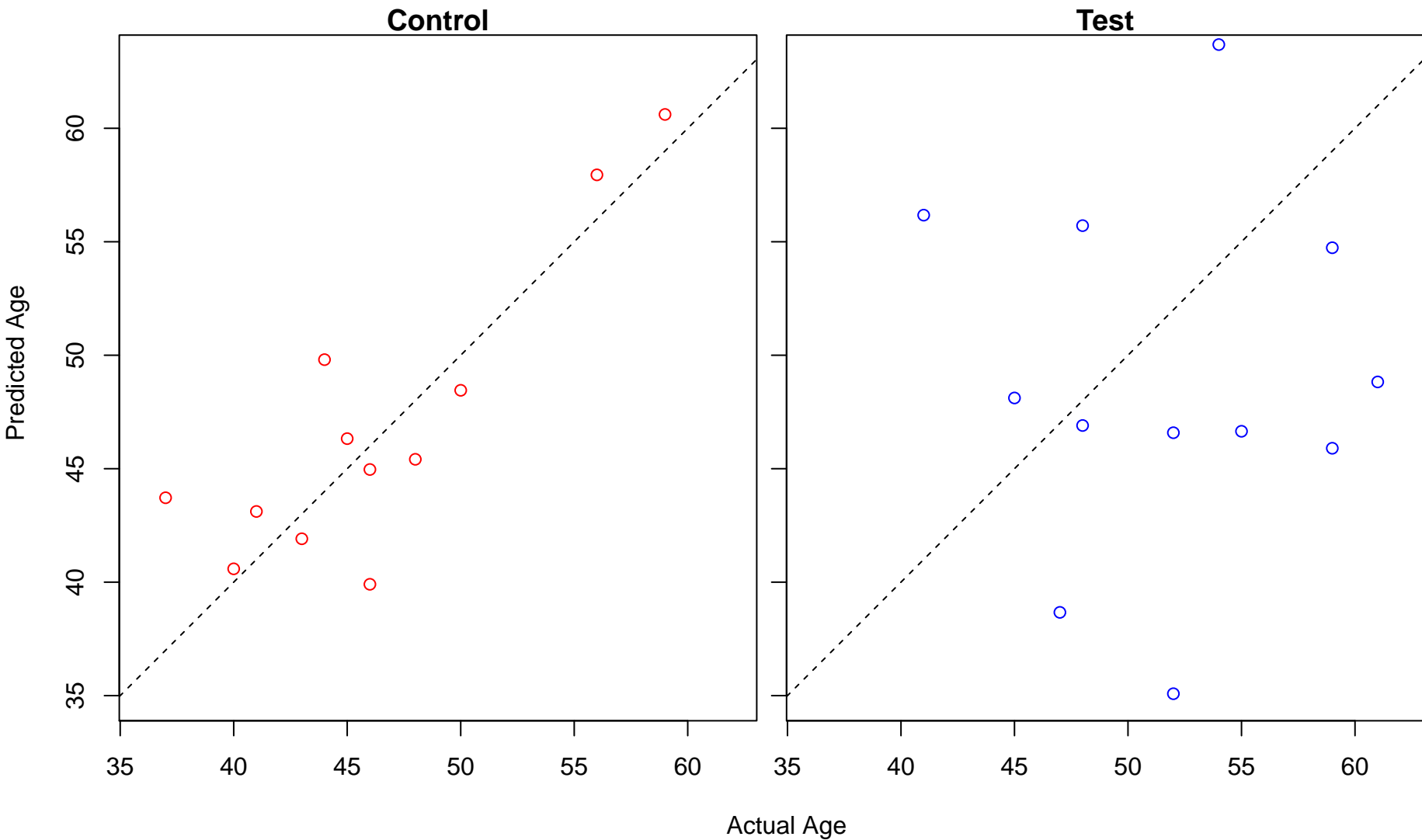
regulation of mRNA processing (Score: 6.426329)



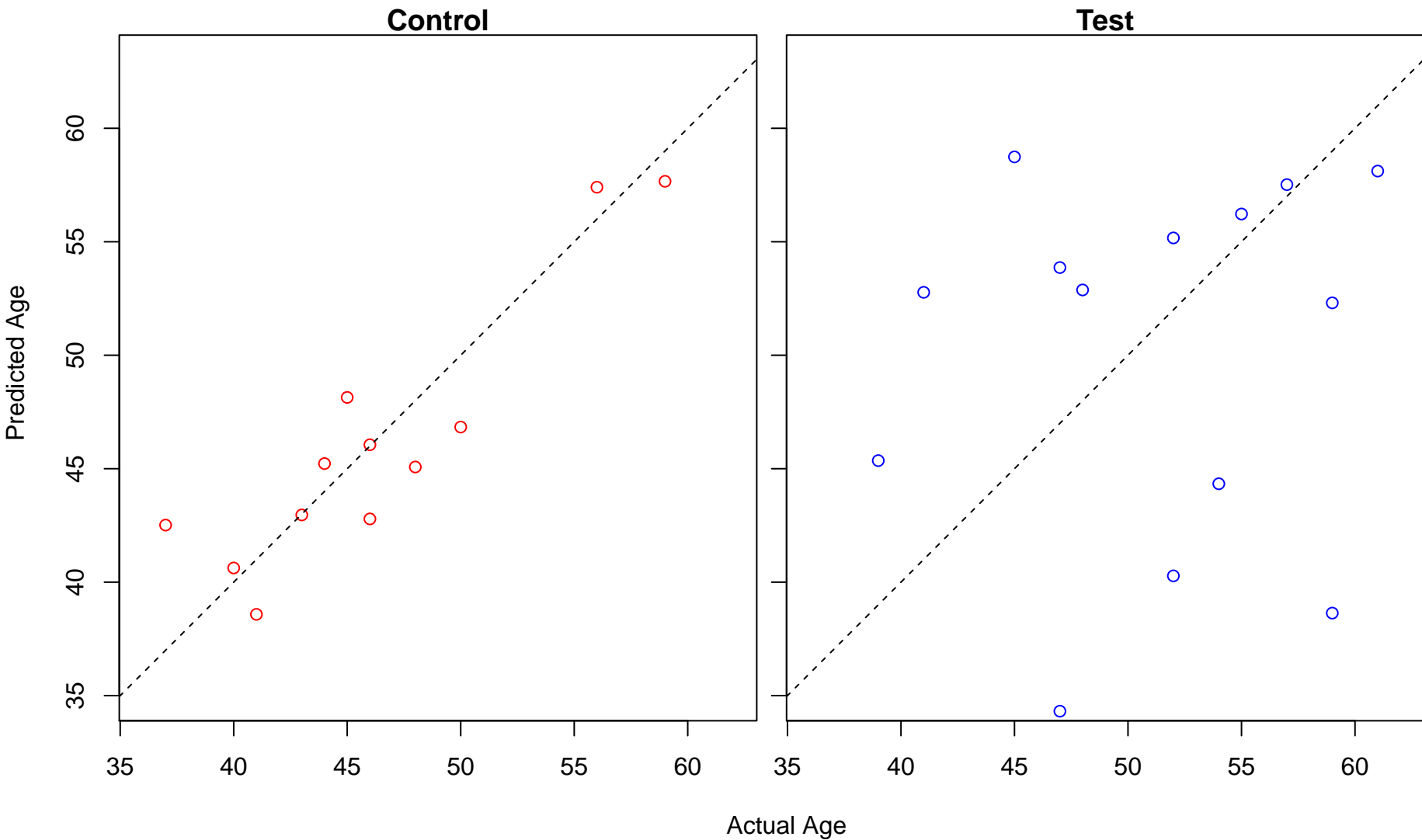
xenophagy (Score: 6.421414)



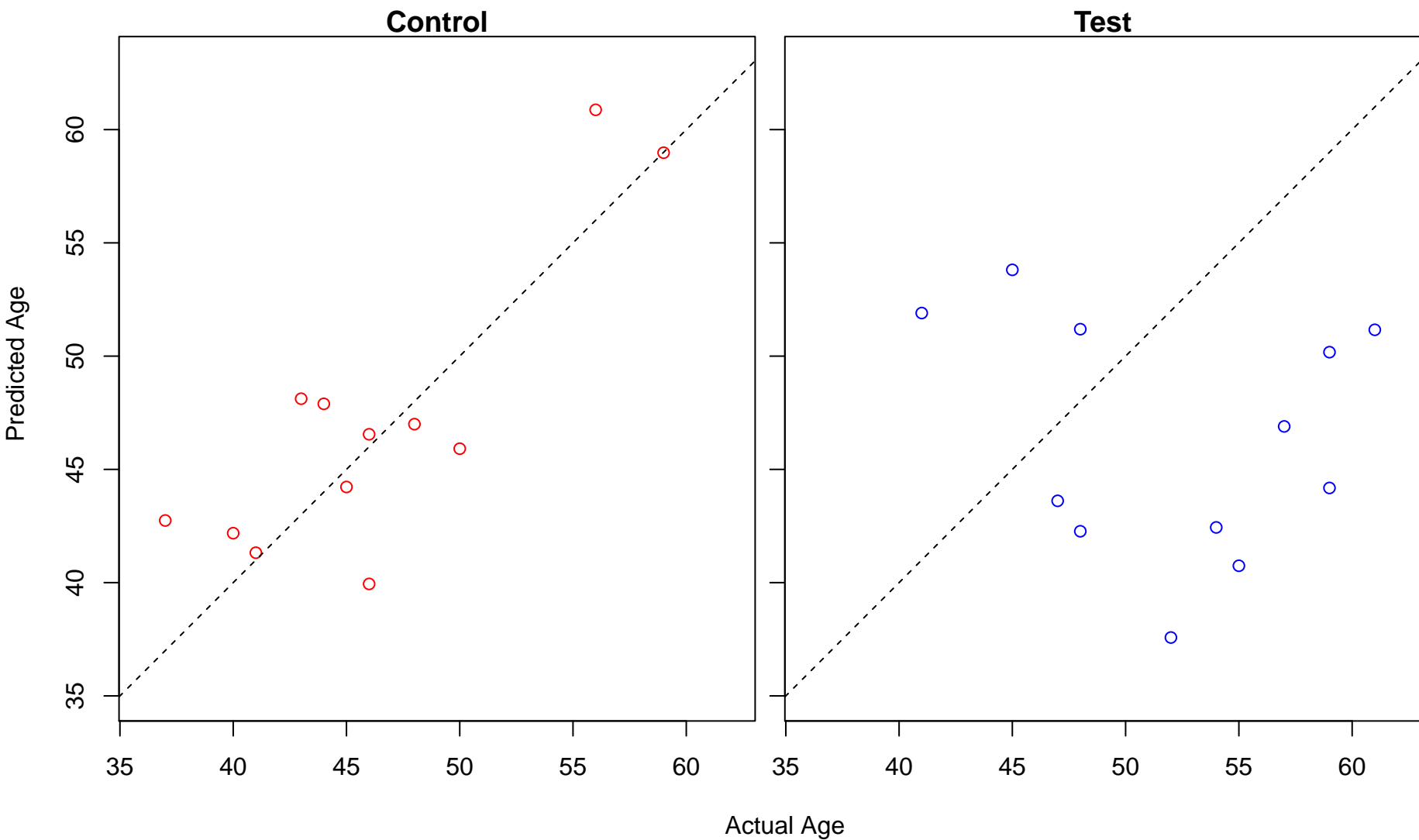
regulation of monooxygenase activity (Score: 6.419314)



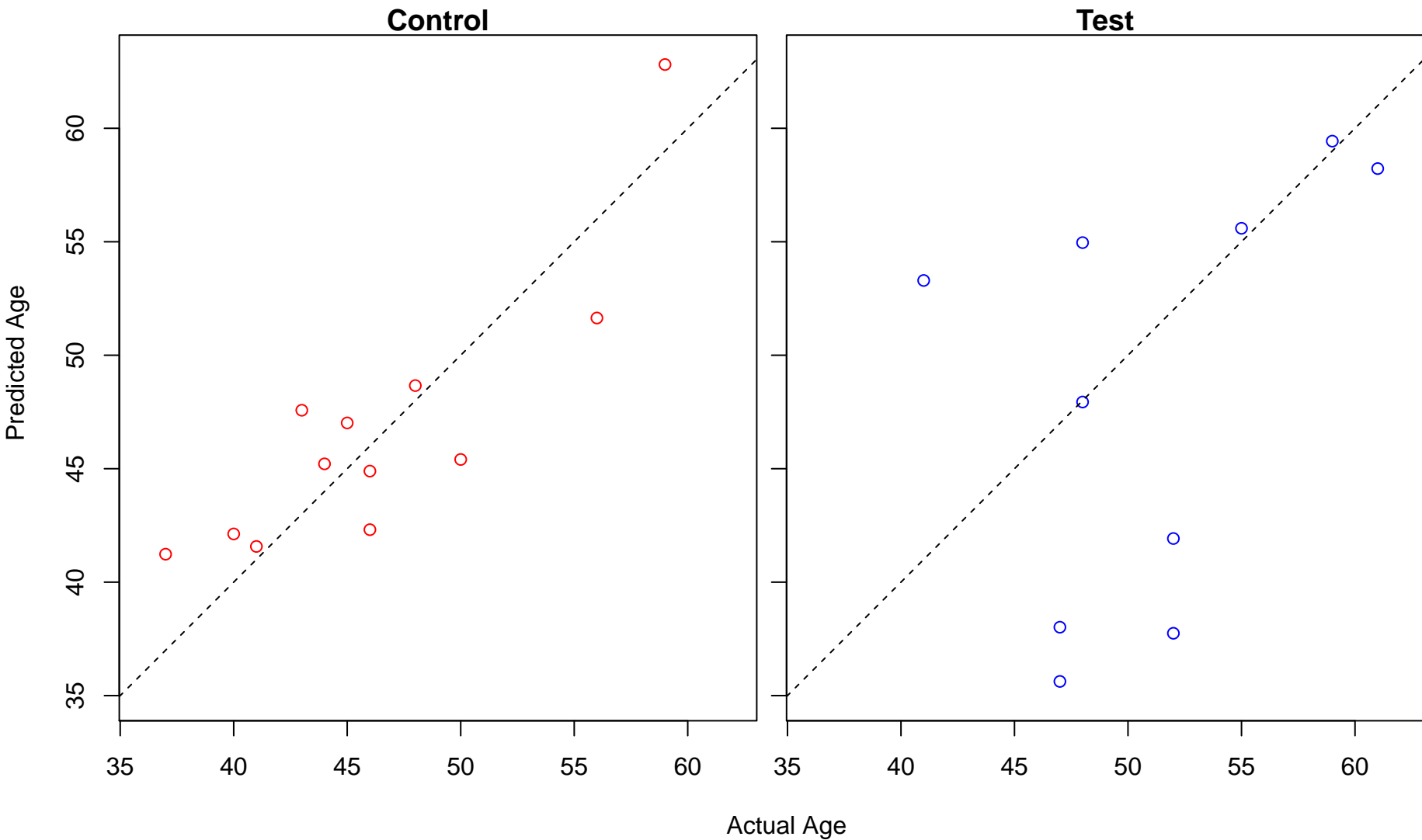
lung development (Score: 6.376199)



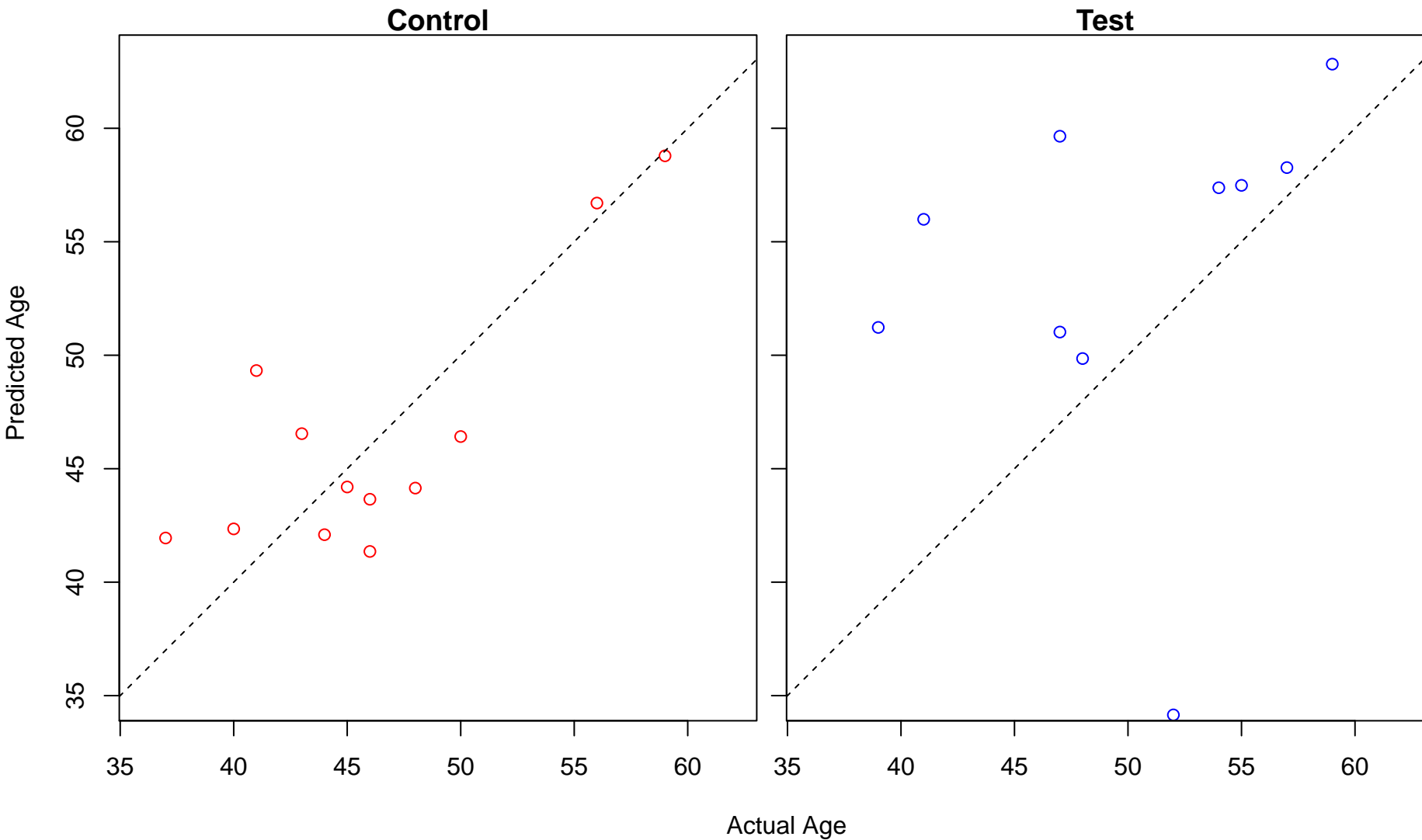
regulation of cell projection organization (Score: 6.350334)



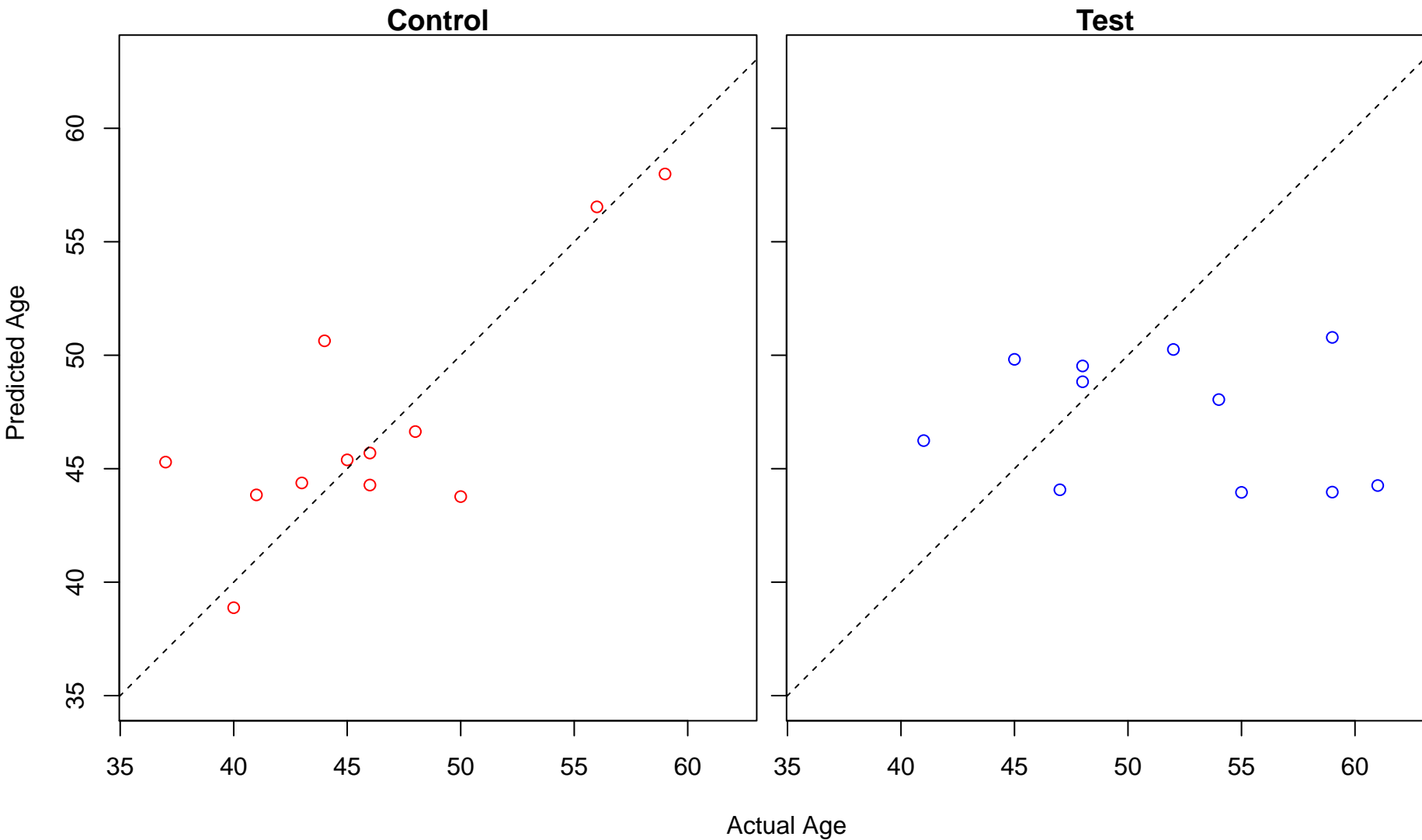
regulation of mitochondrion organization (Score: 6.339556)



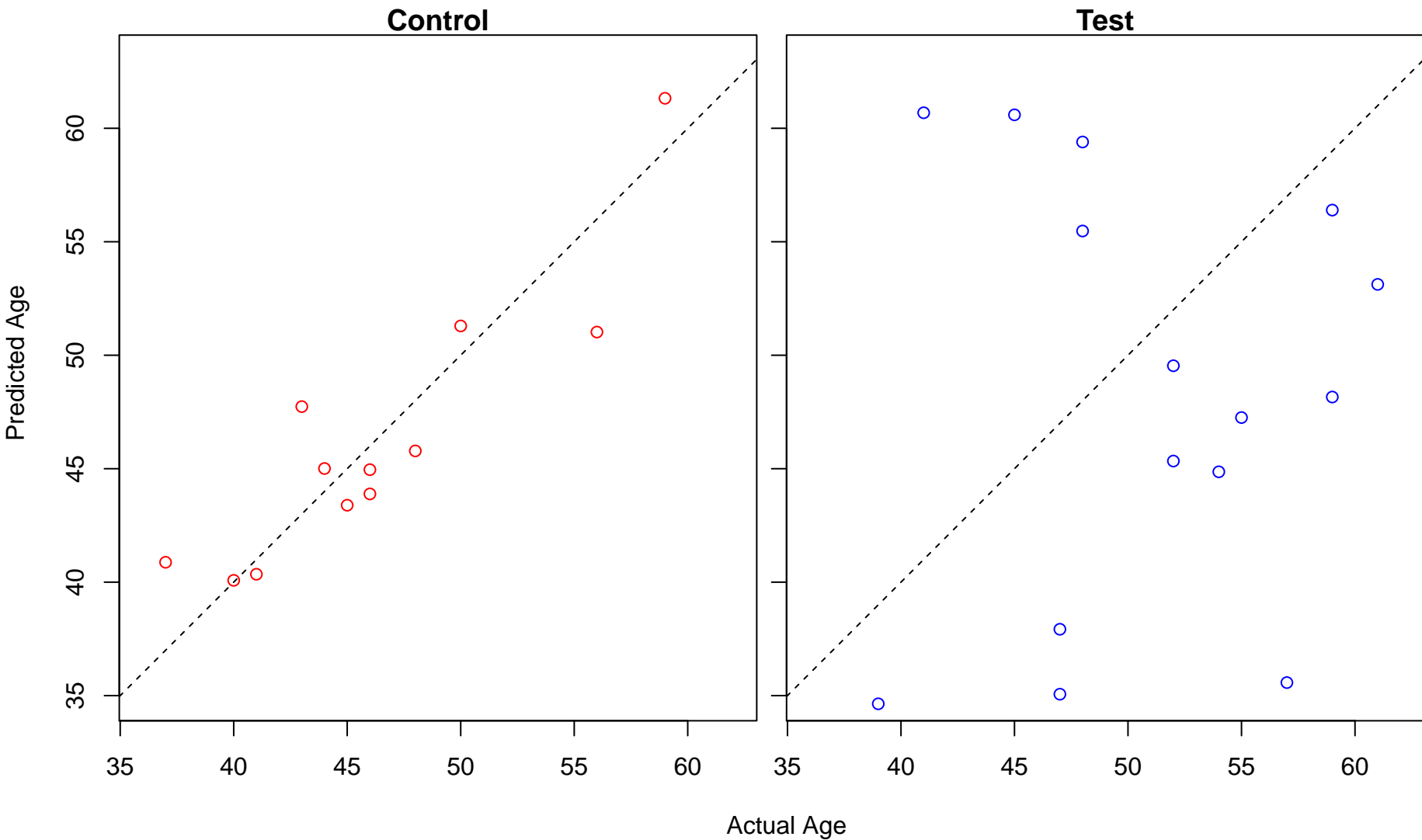
positive regulation of mitochondrial translation (Score: 6.314720)



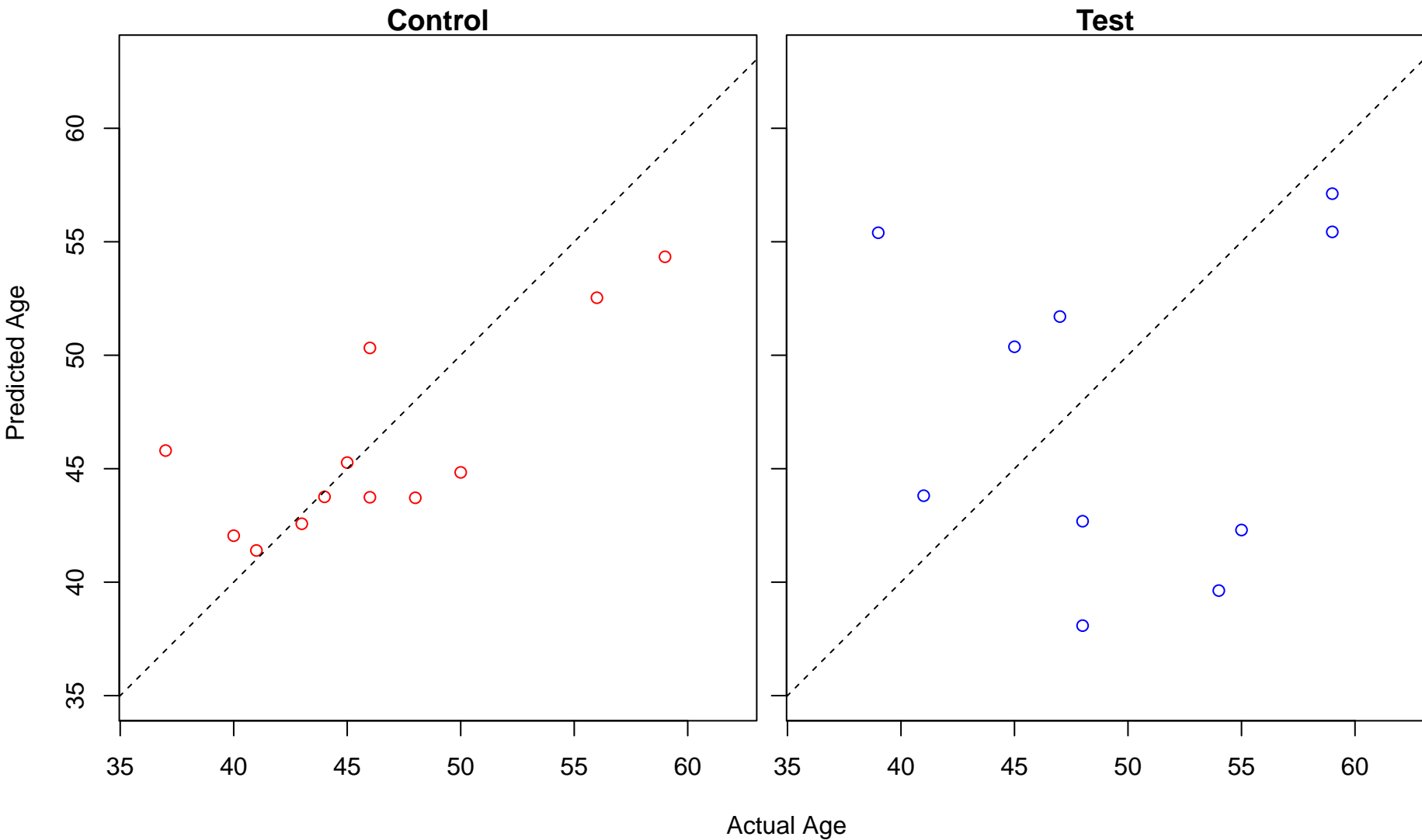
positive regulation of G2/M transition of mitotic cell cycle (Score: 6.306709)



ameboidal-type cell migration (Score: 6.291313)

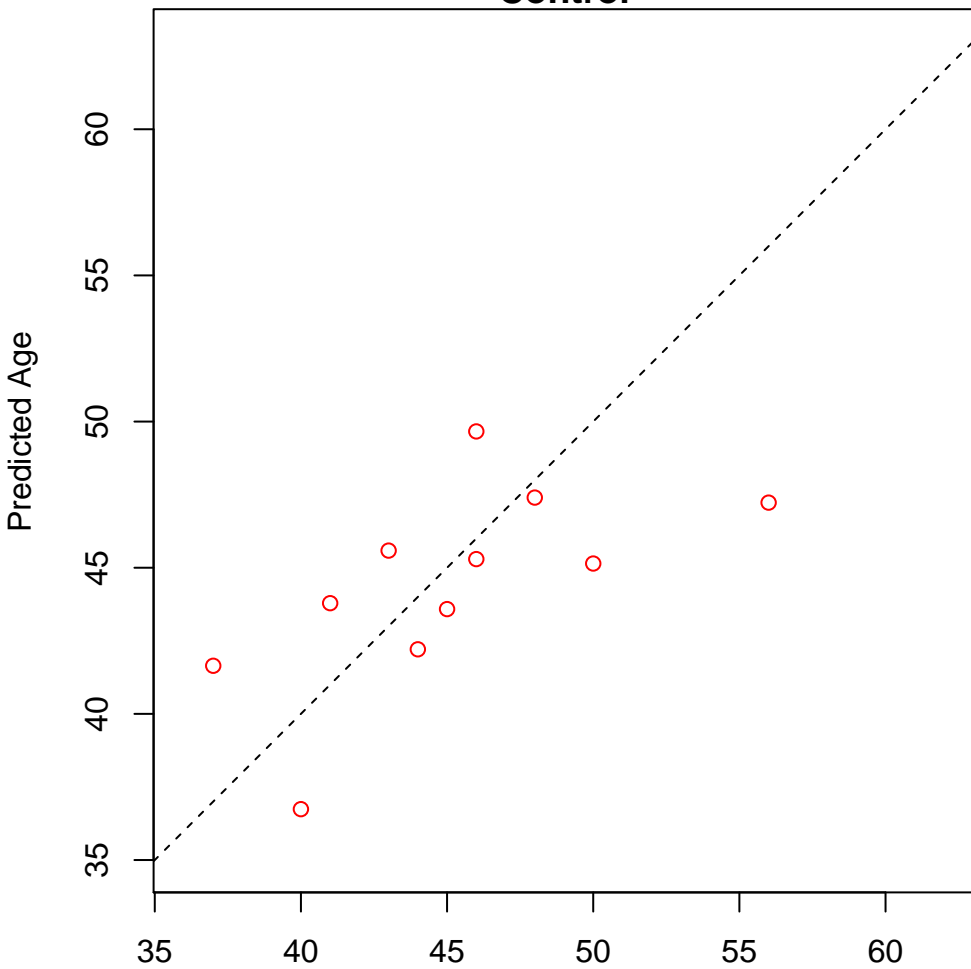


regulation of synapse structural plasticity (Score: 6.280439)

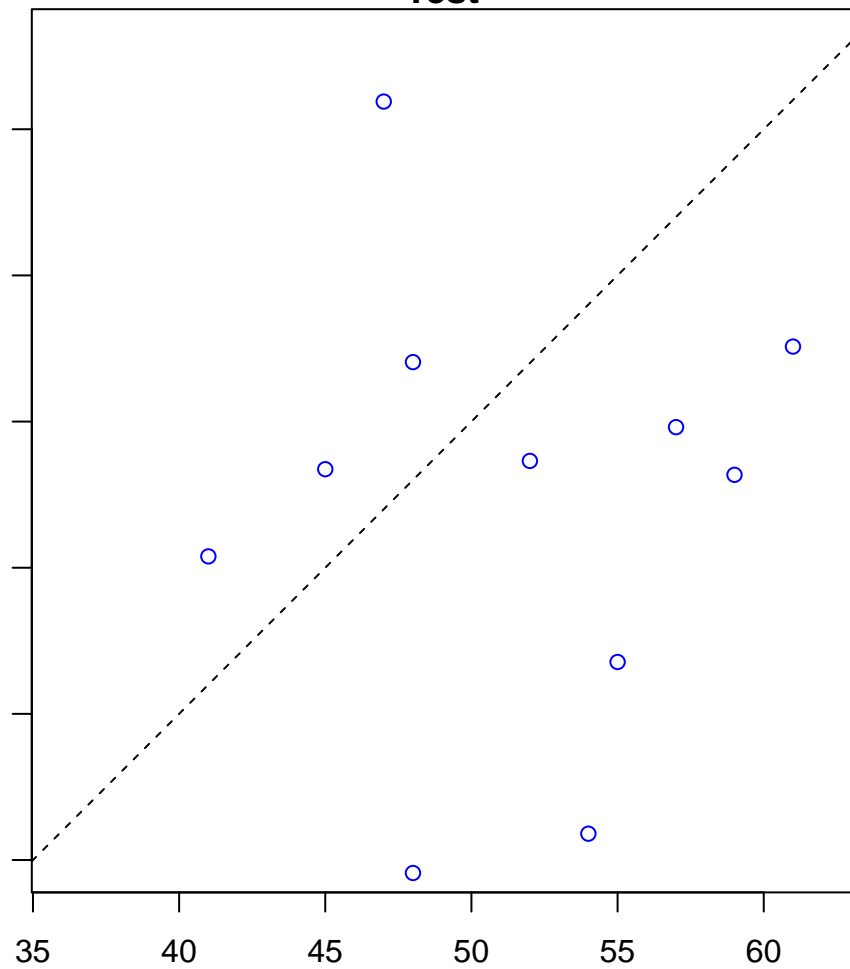


regulation of glomerulus development (Score: 6.271214)

Control

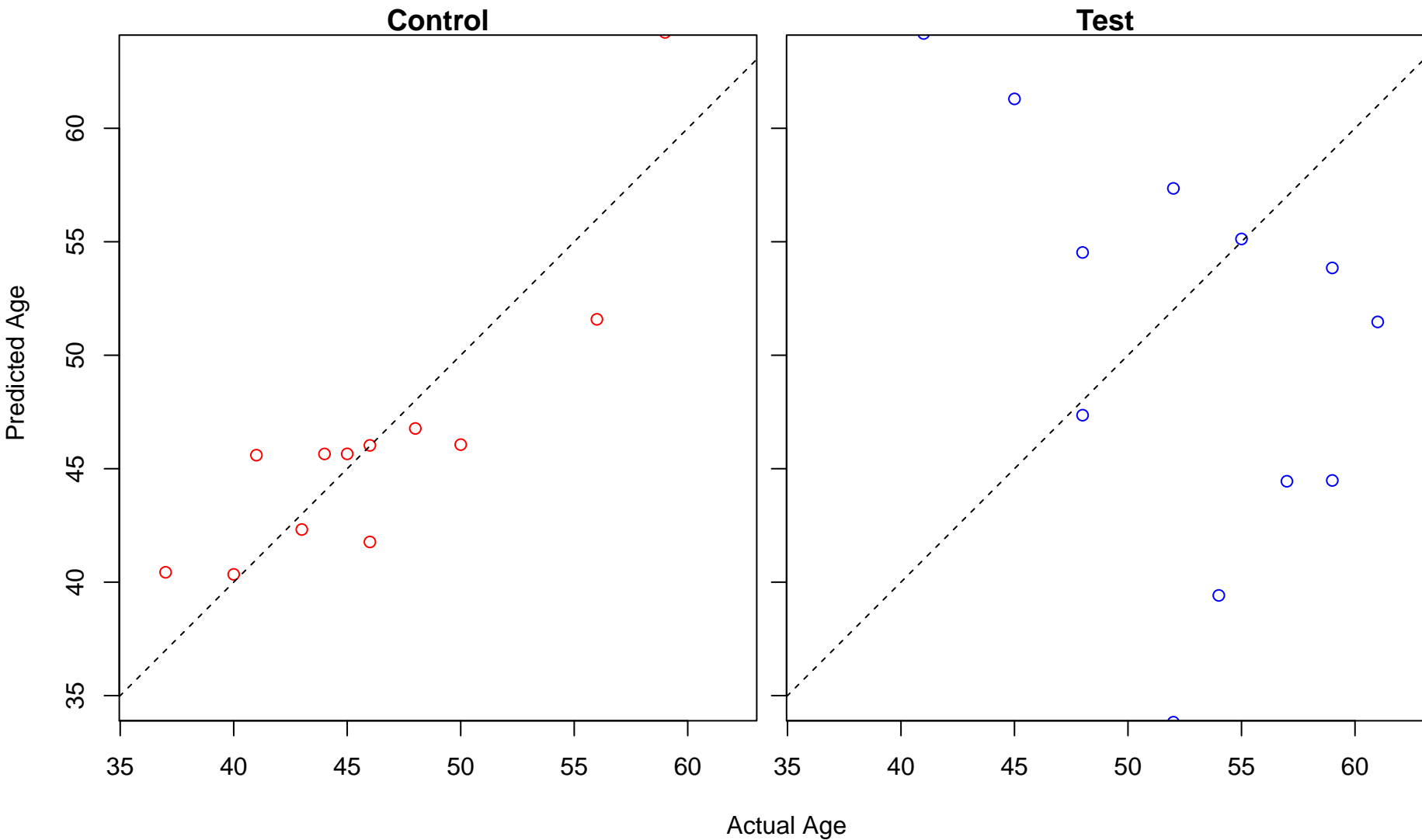


Test

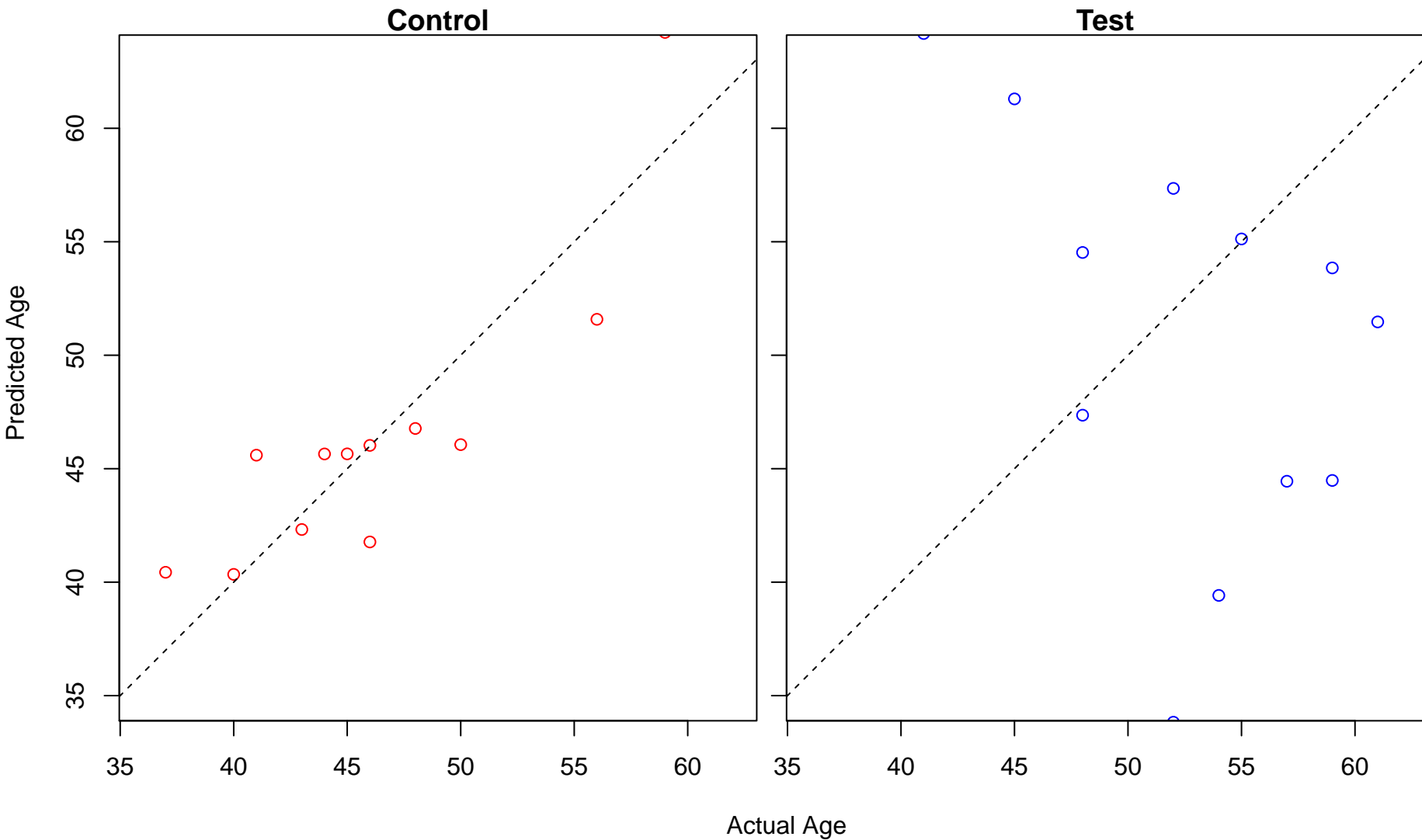


Actual Age

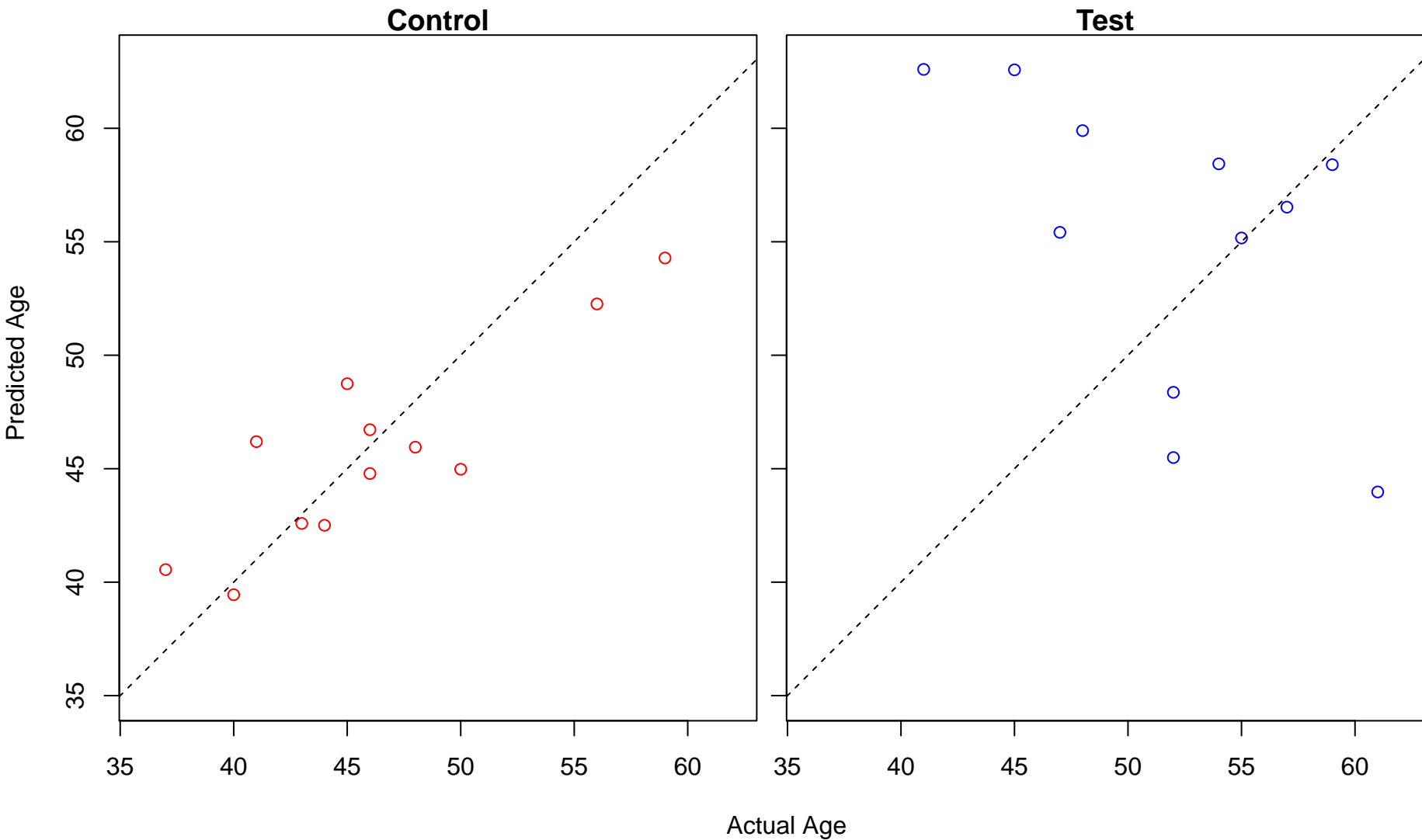
regulation of MHC class I biosynthetic process (Score: 6.262434)



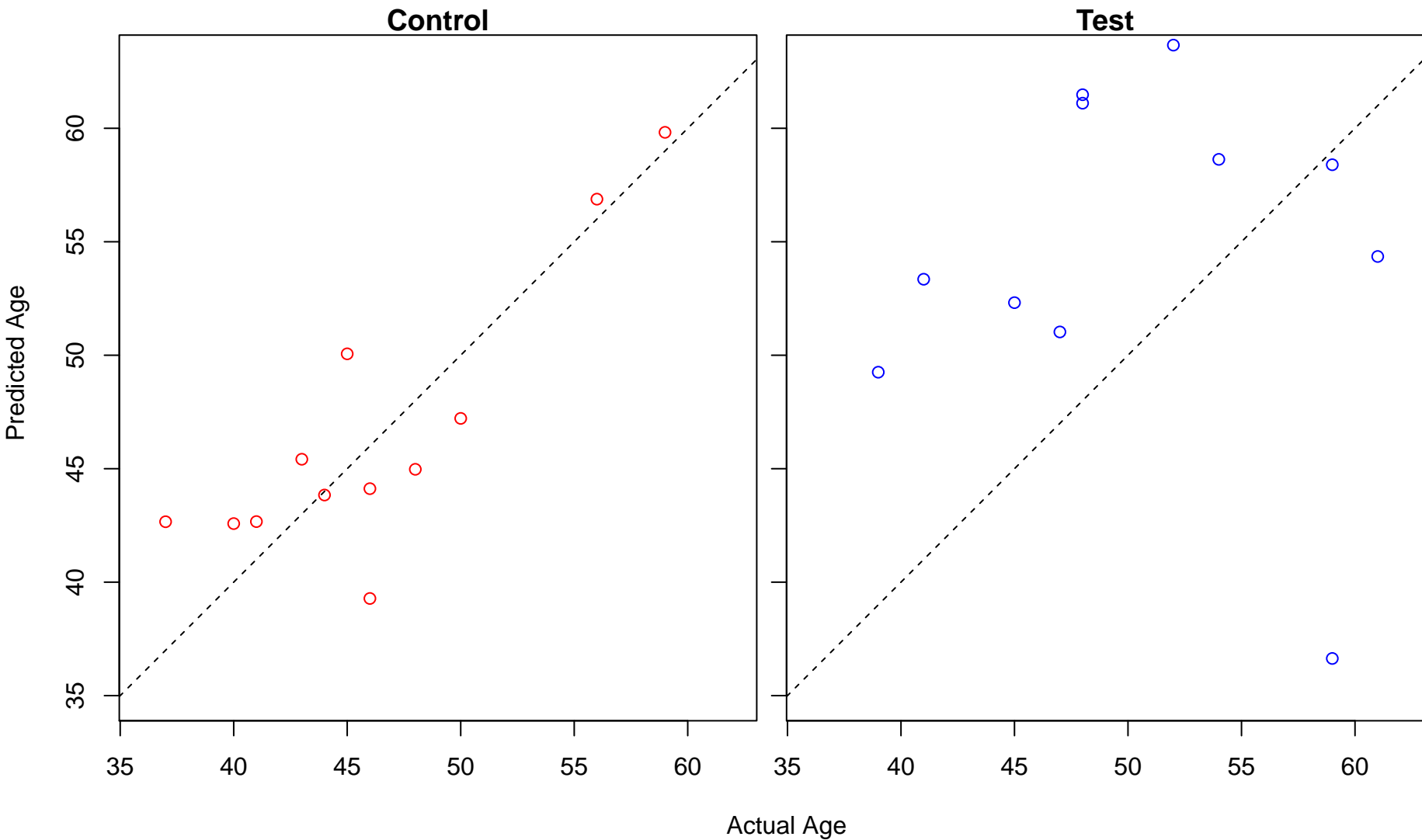
positive regulation of MHC class I biosynthetic process (Score: 6.262434)



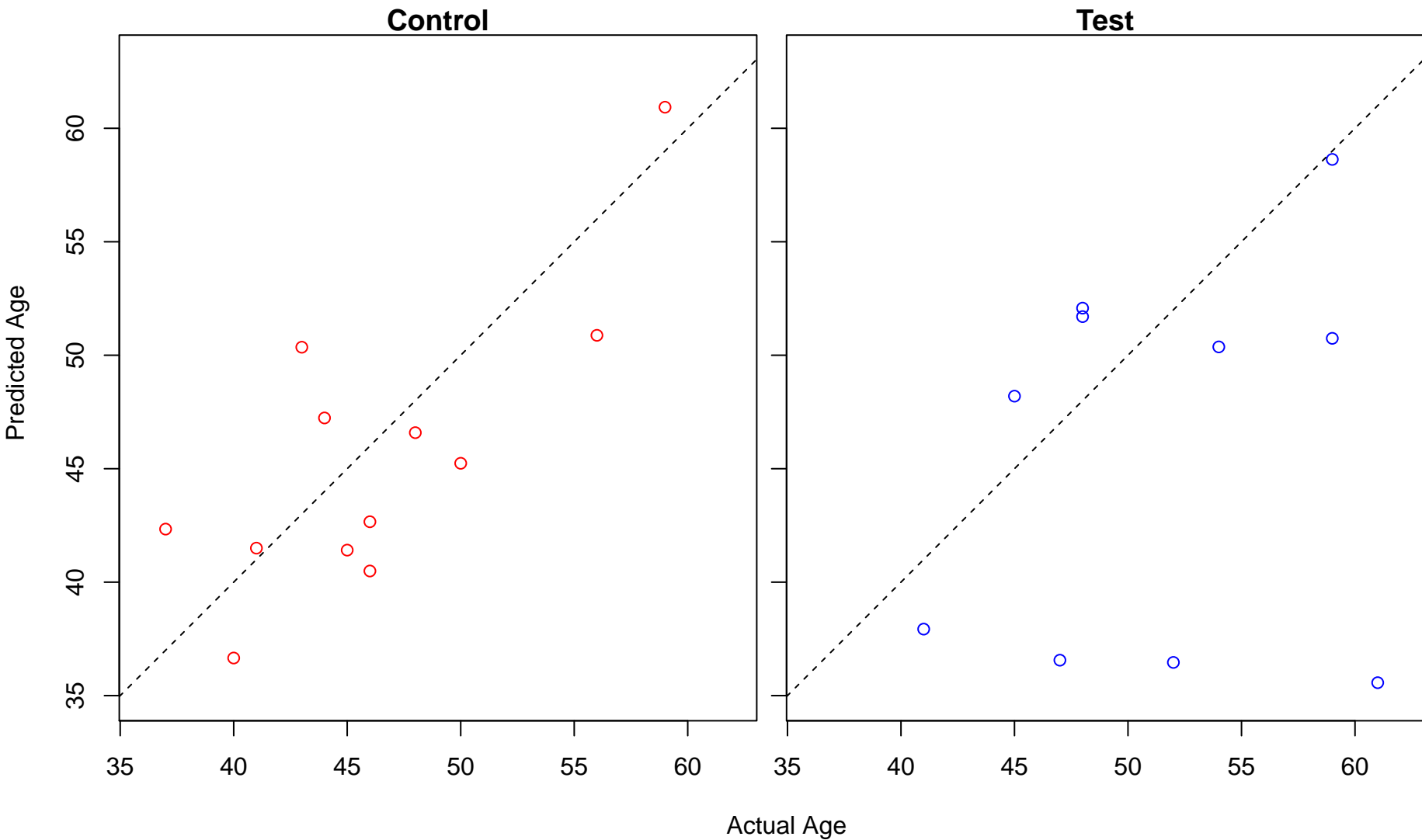
negative regulation of T cell apoptotic process (Score: 6.249793)



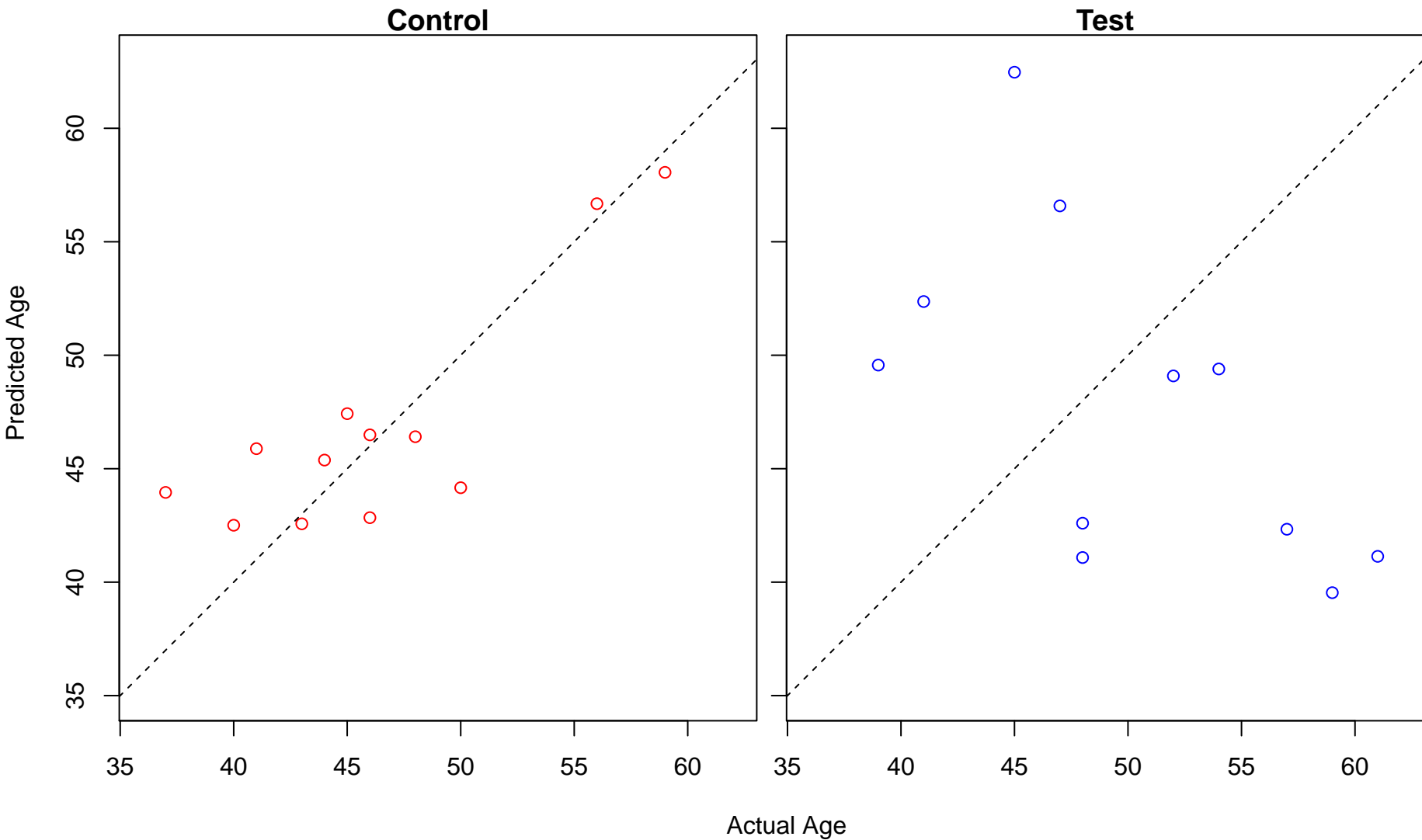
neurotransmitter secretion (Score: 6.243812)



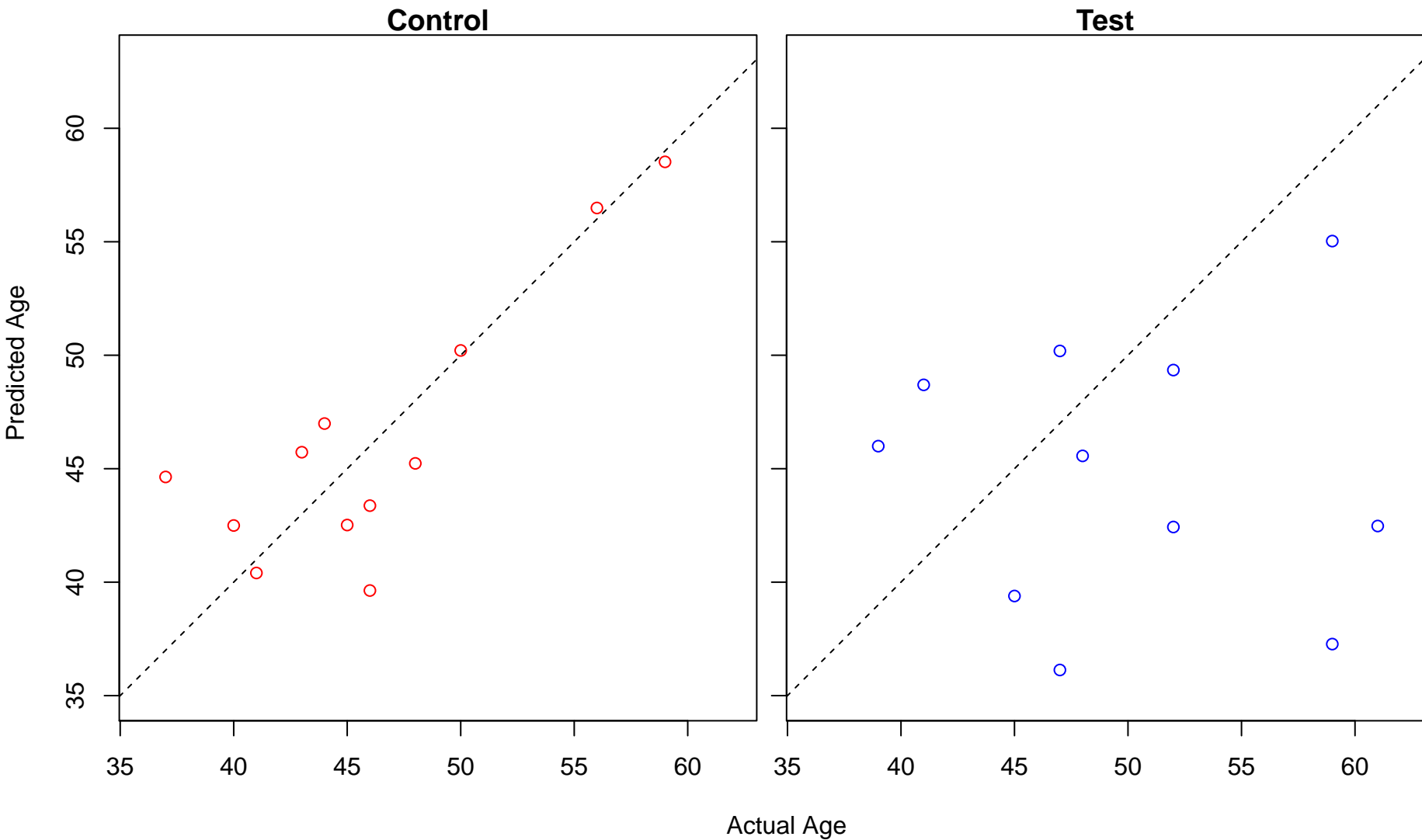
protein-DNA complex assembly (Score: 6.241321)



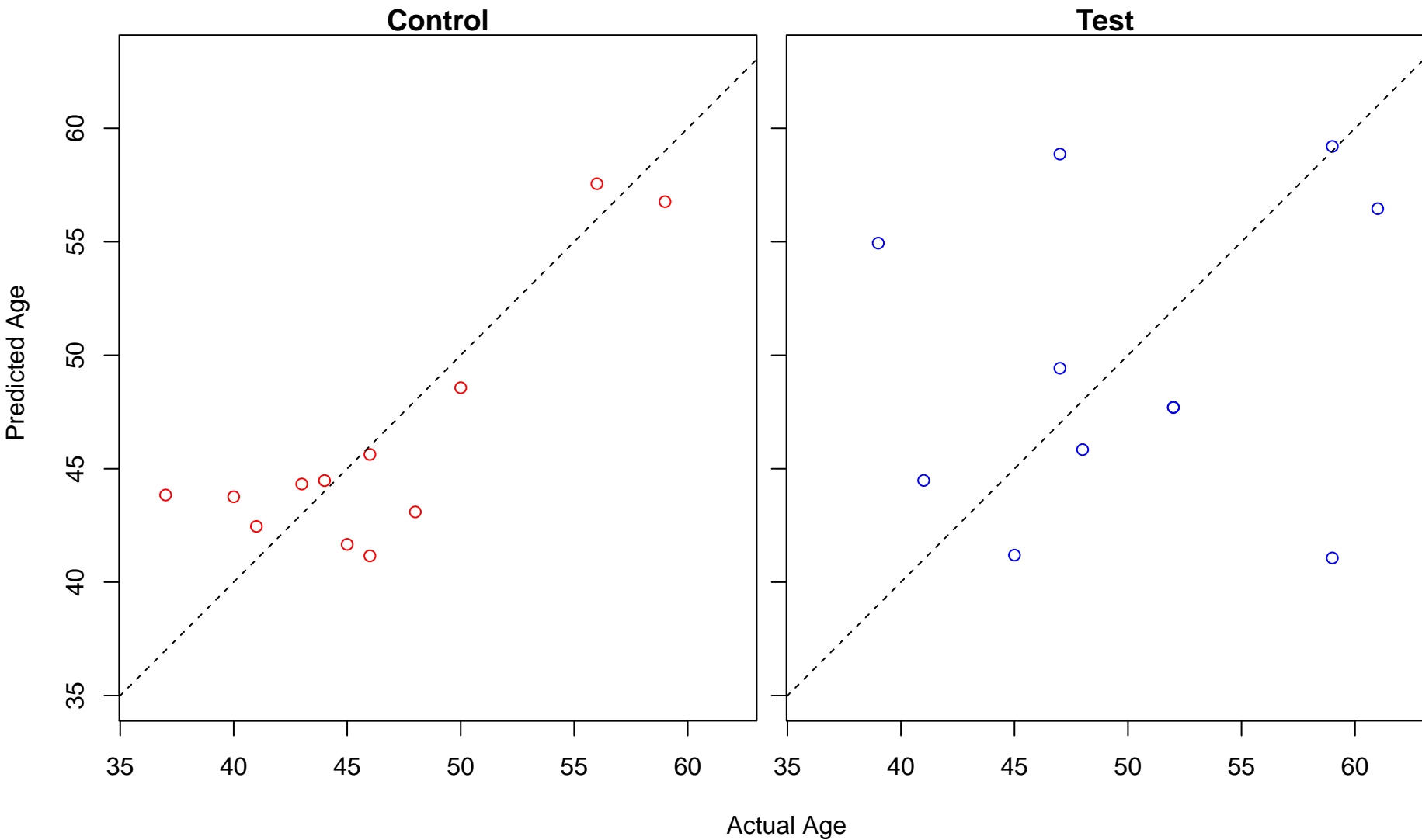
wound healing, spreading of epidermal cells (Score: 6.239220)



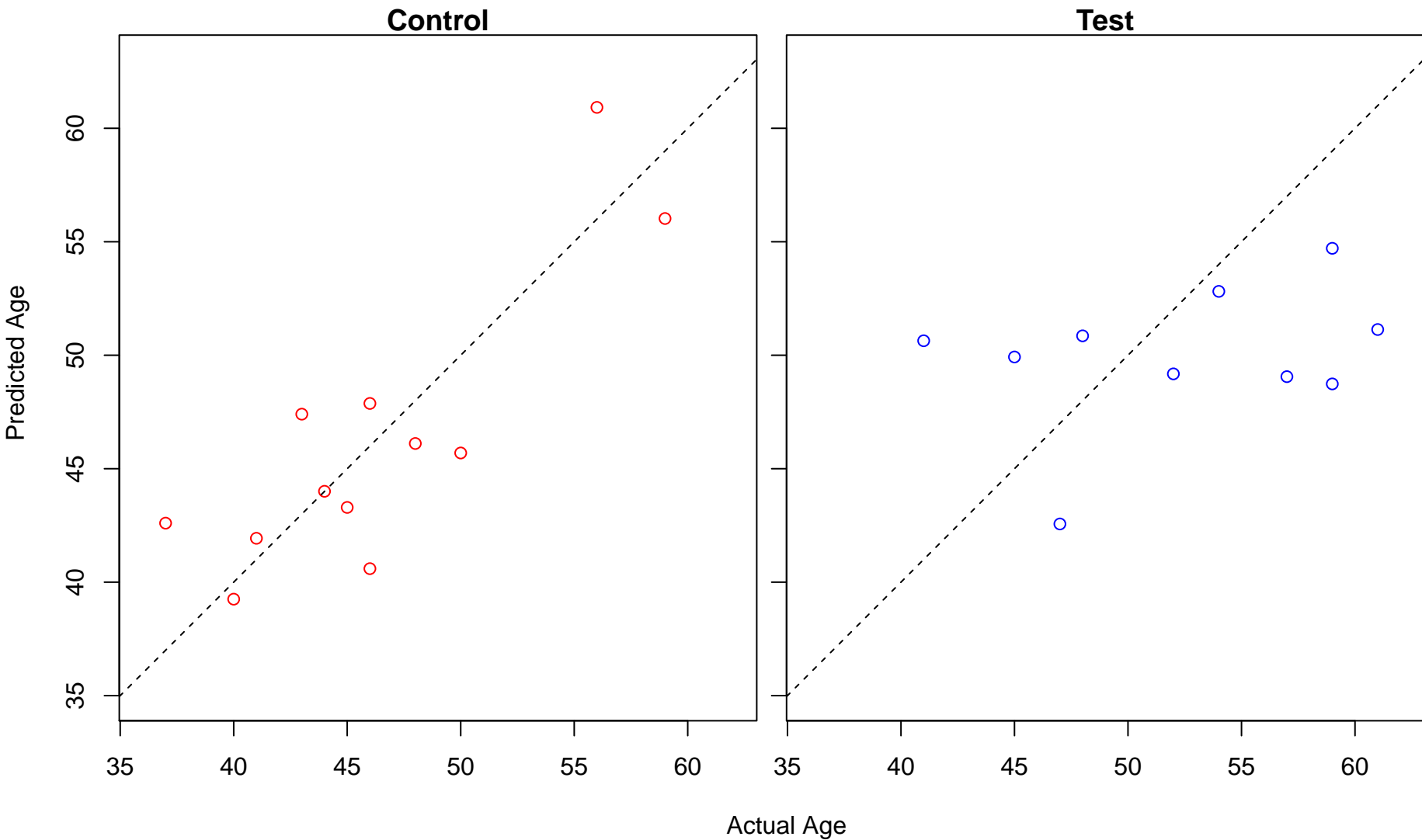
establishment of protein localization to plasma membrane (Score: 6.237121)



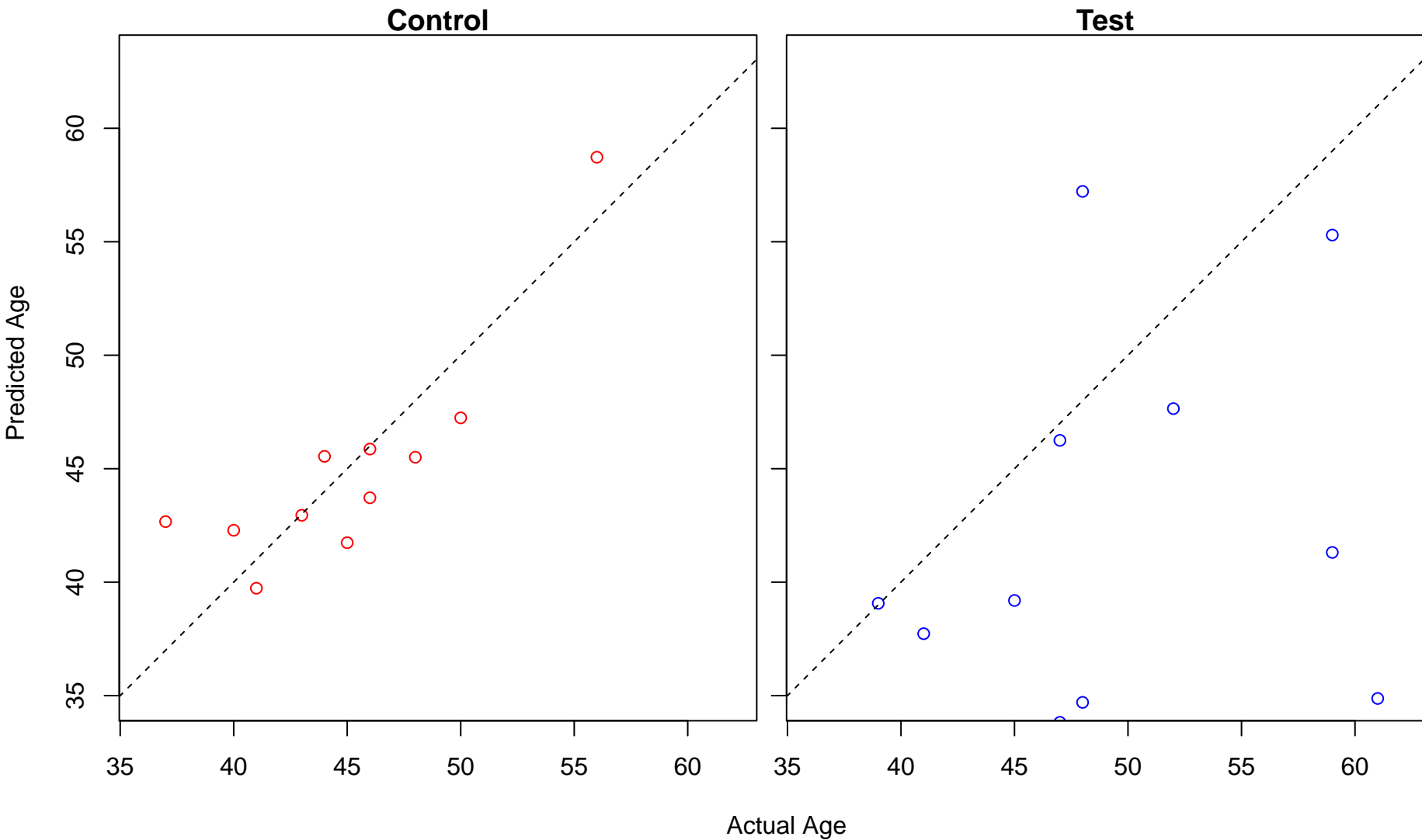
import across plasma membrane (Score: 6.225819)



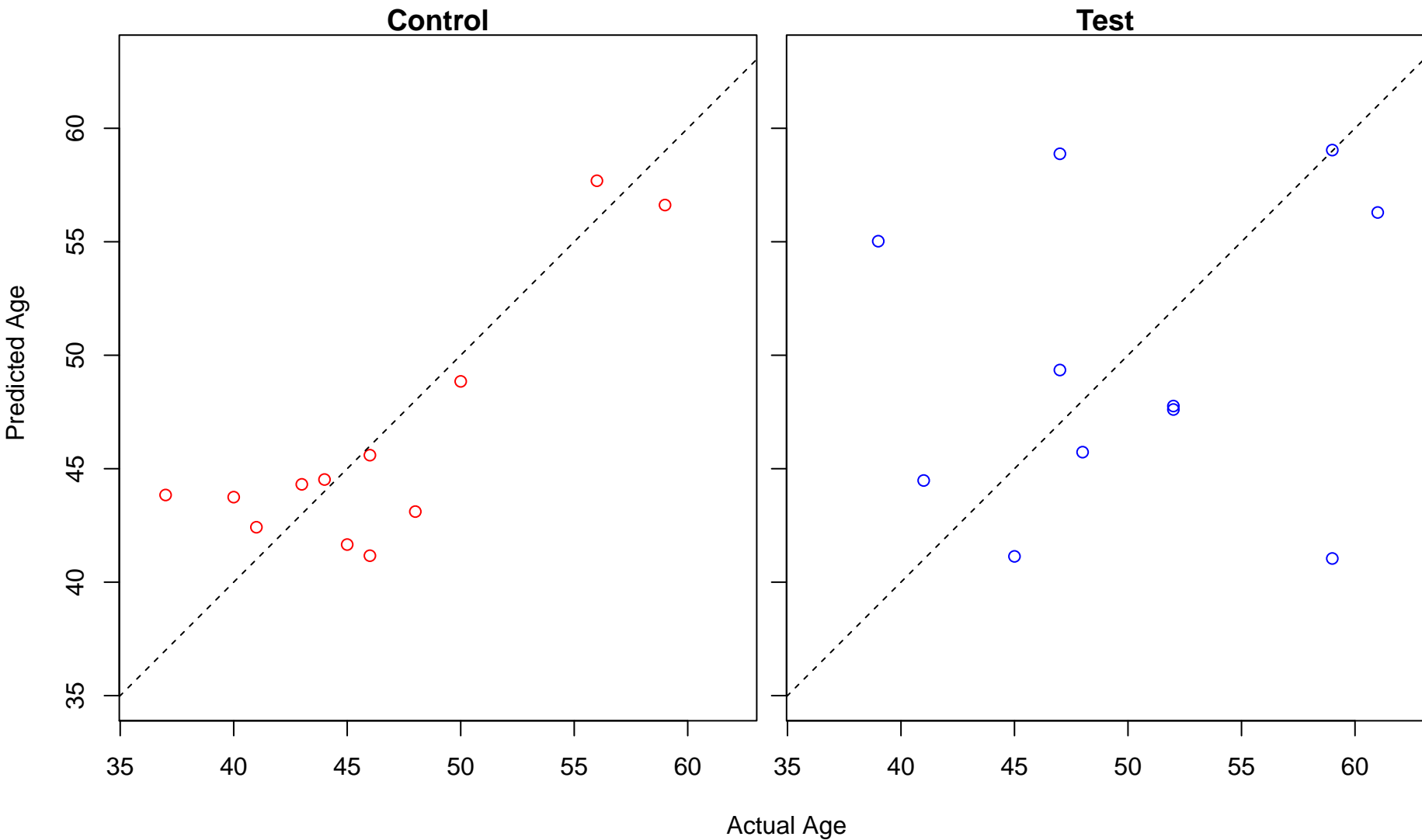
actin cytoskeleton organization (Score: 6.224342)



modulation by virus of host morphology or physiology (Score: 6.222654)

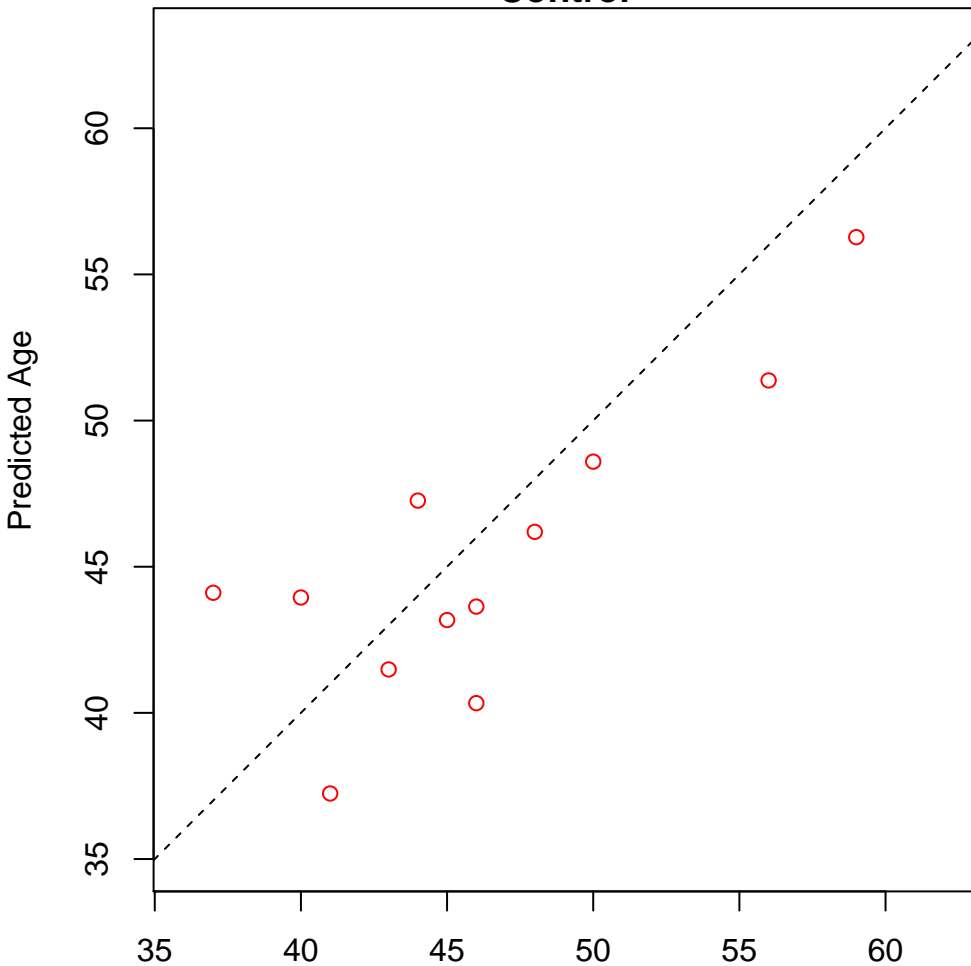


cell communication by electrical coupling involved in cardiac conduction (Score: 6.215804)

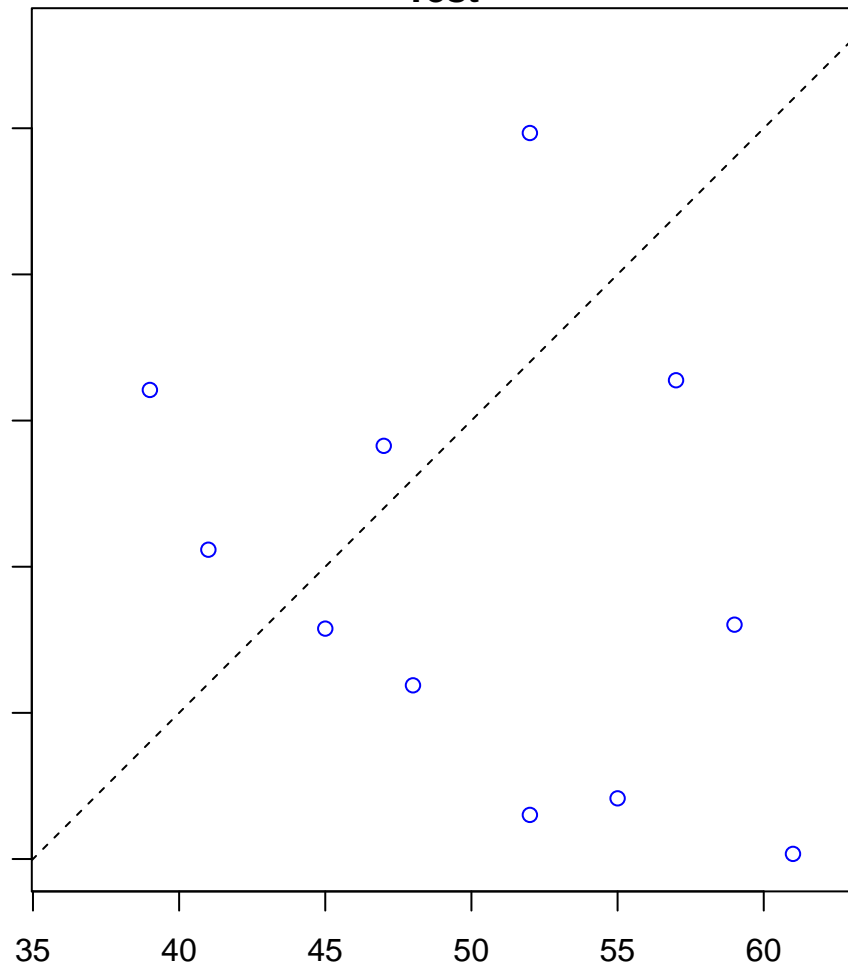


hydrogen ion transmembrane transport (Score: 6.214818)

Control

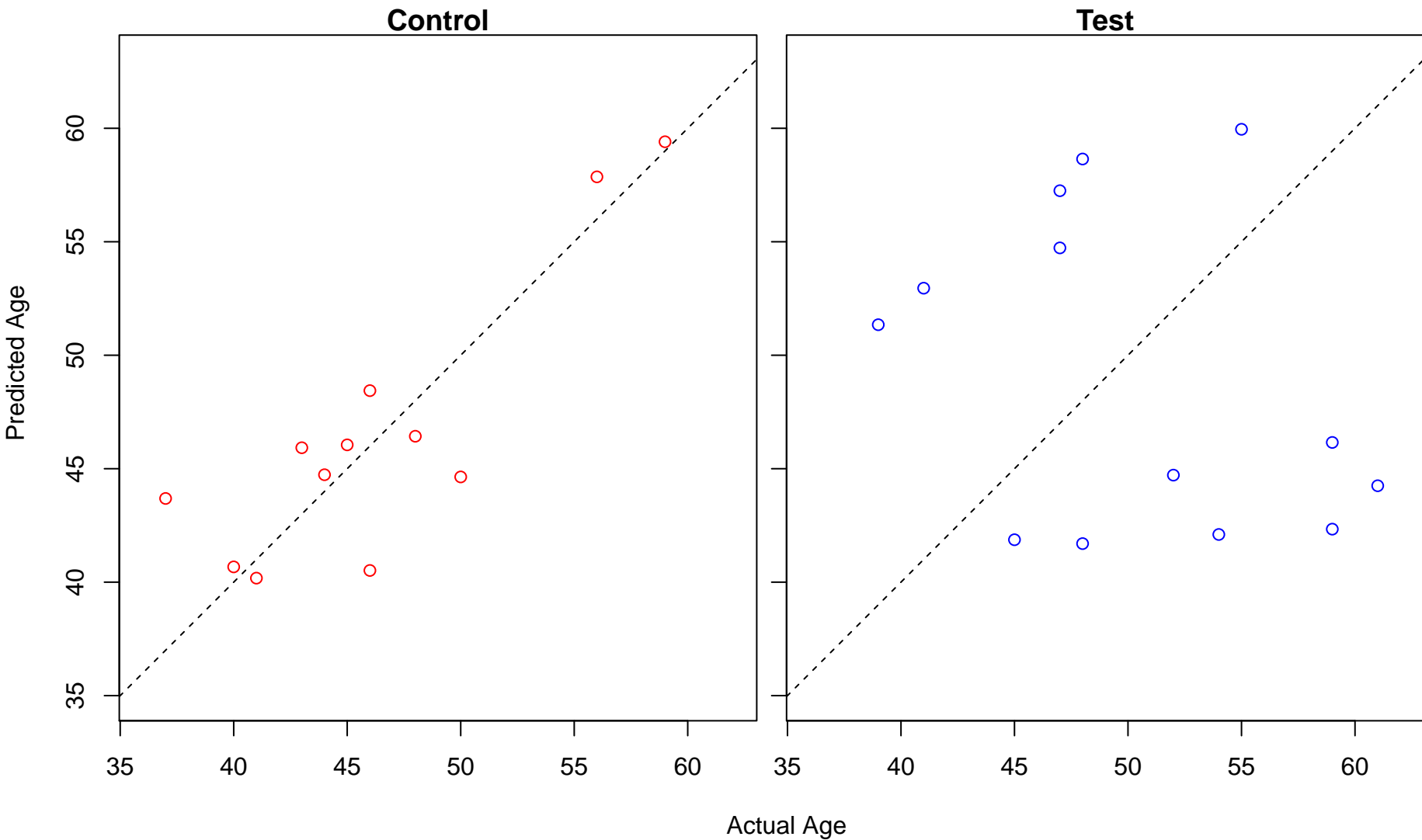


Test

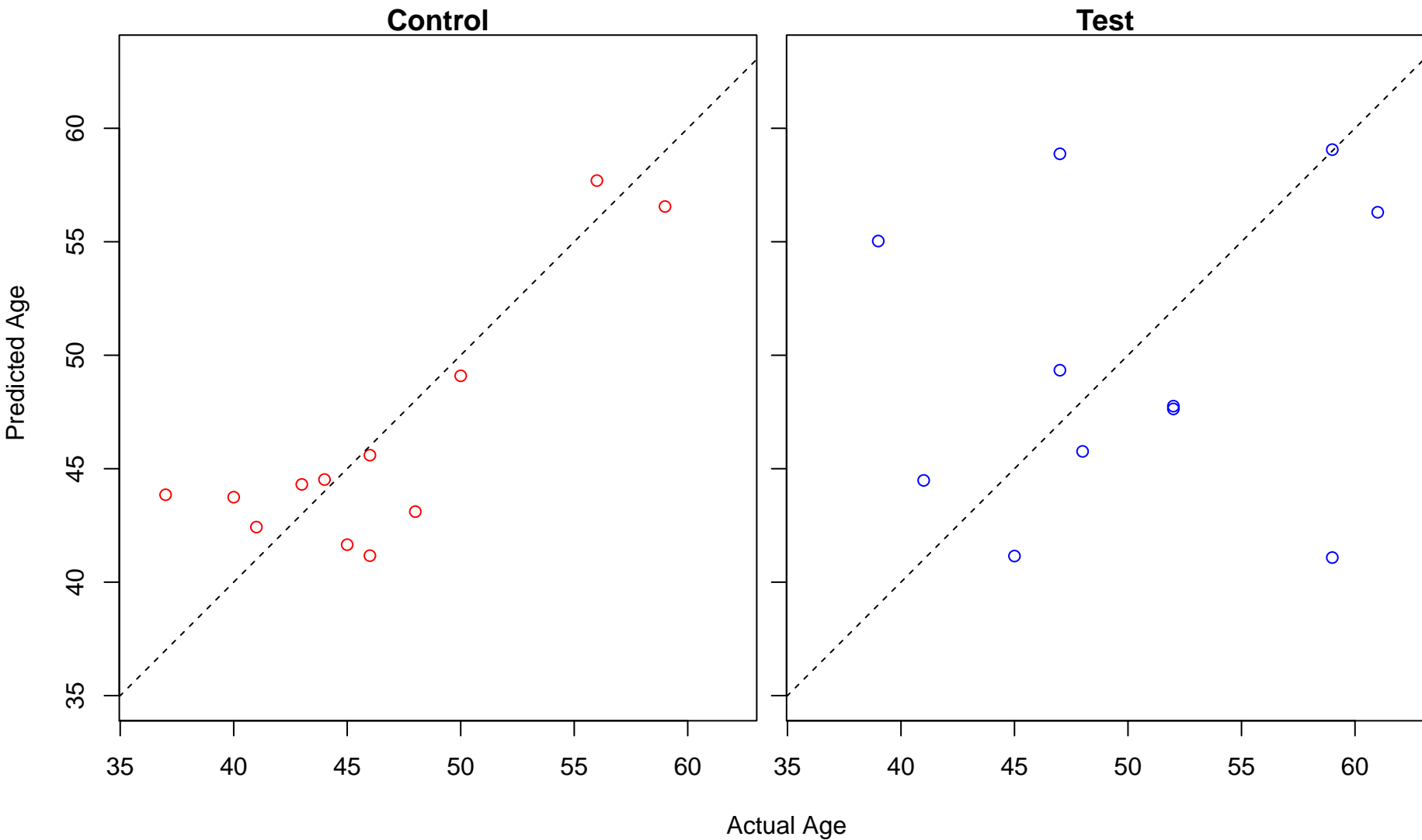


Actual Age

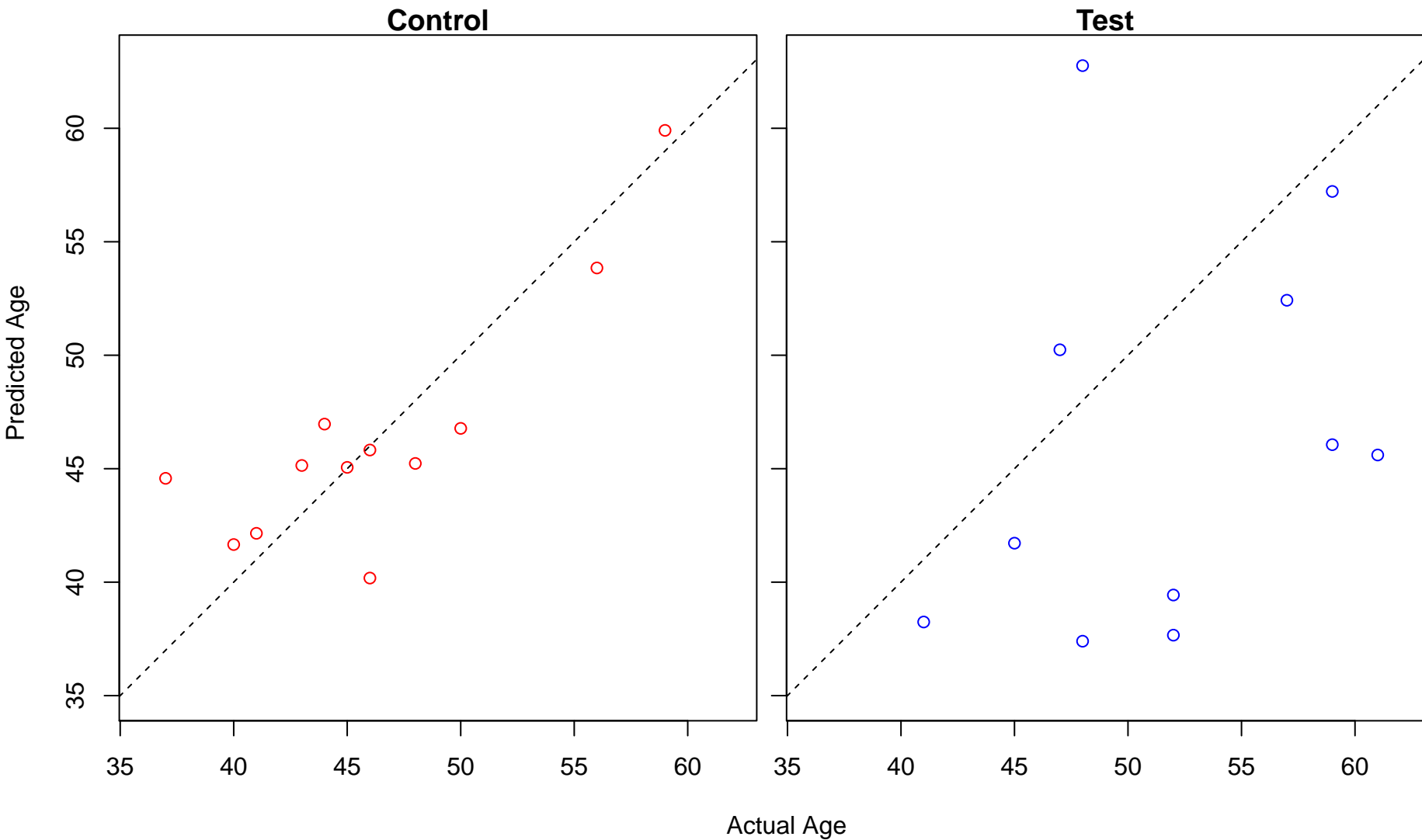
positive regulation of I-kappaB kinase/NF-kappaB signaling (Score: 6.213518)



cell communication by electrical coupling (Score: 6.212590)

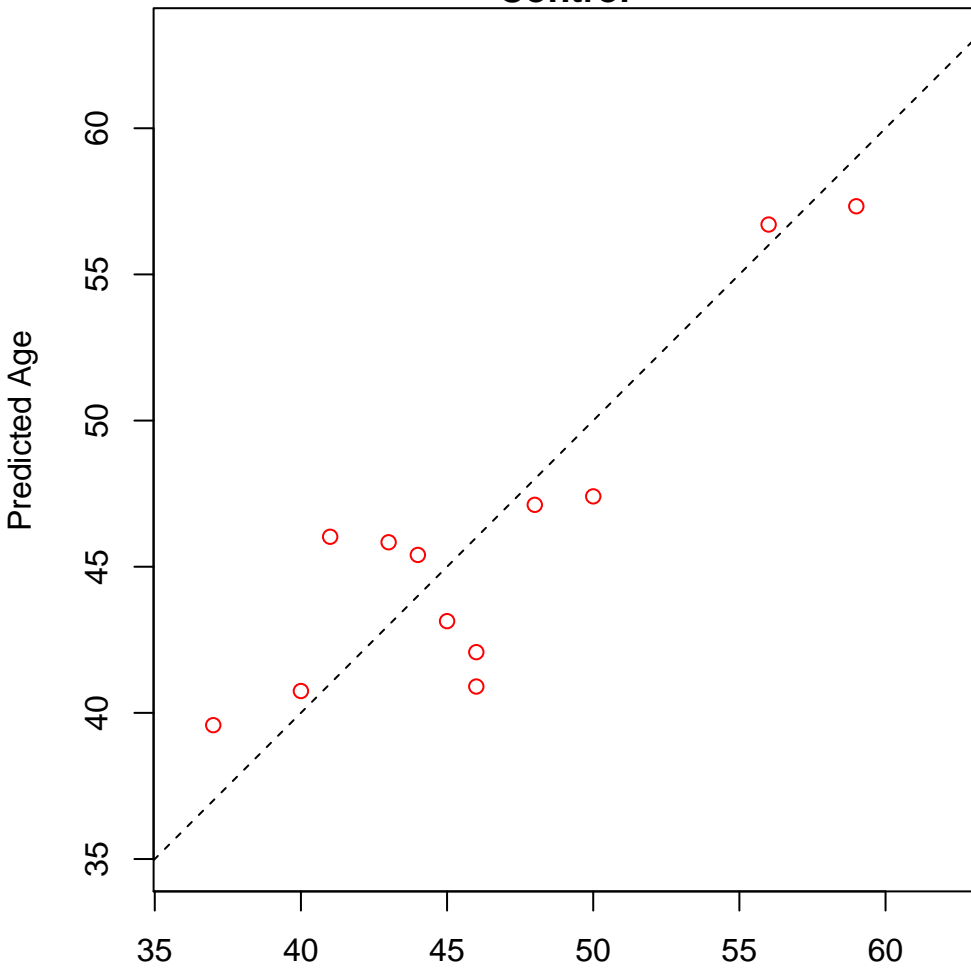


positive regulation of defense response to virus by host (Score: 6.202383)

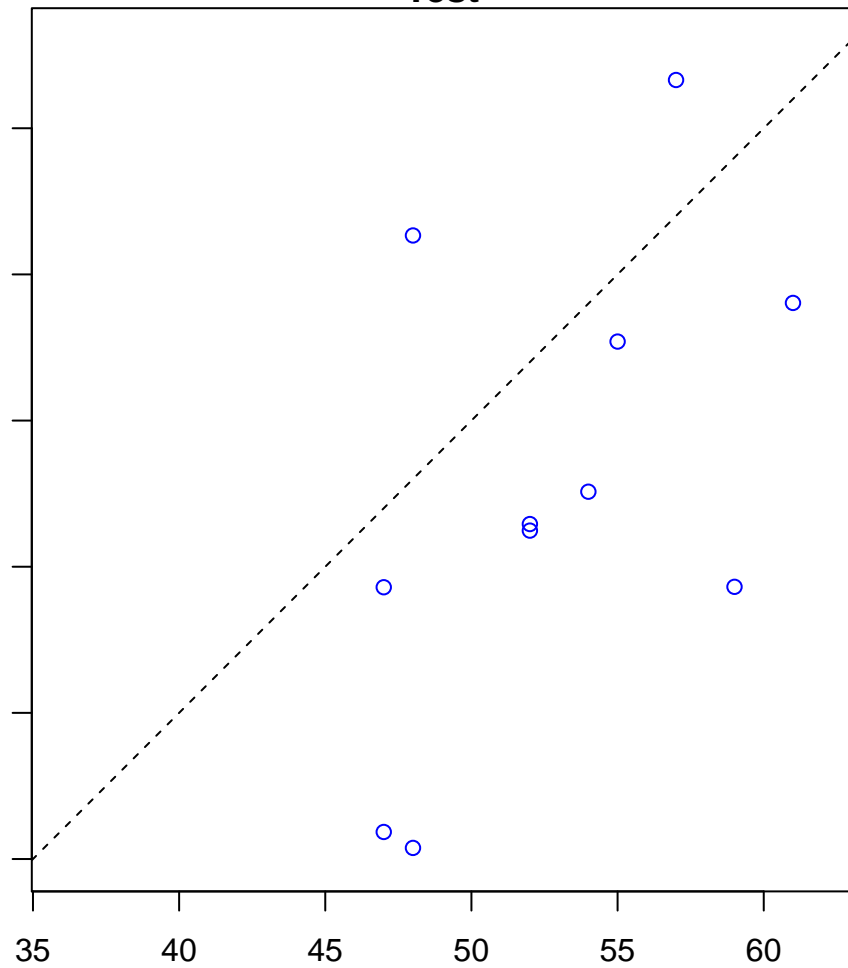


long-chain fatty acid metabolic process (Score: 6.196195)

Control

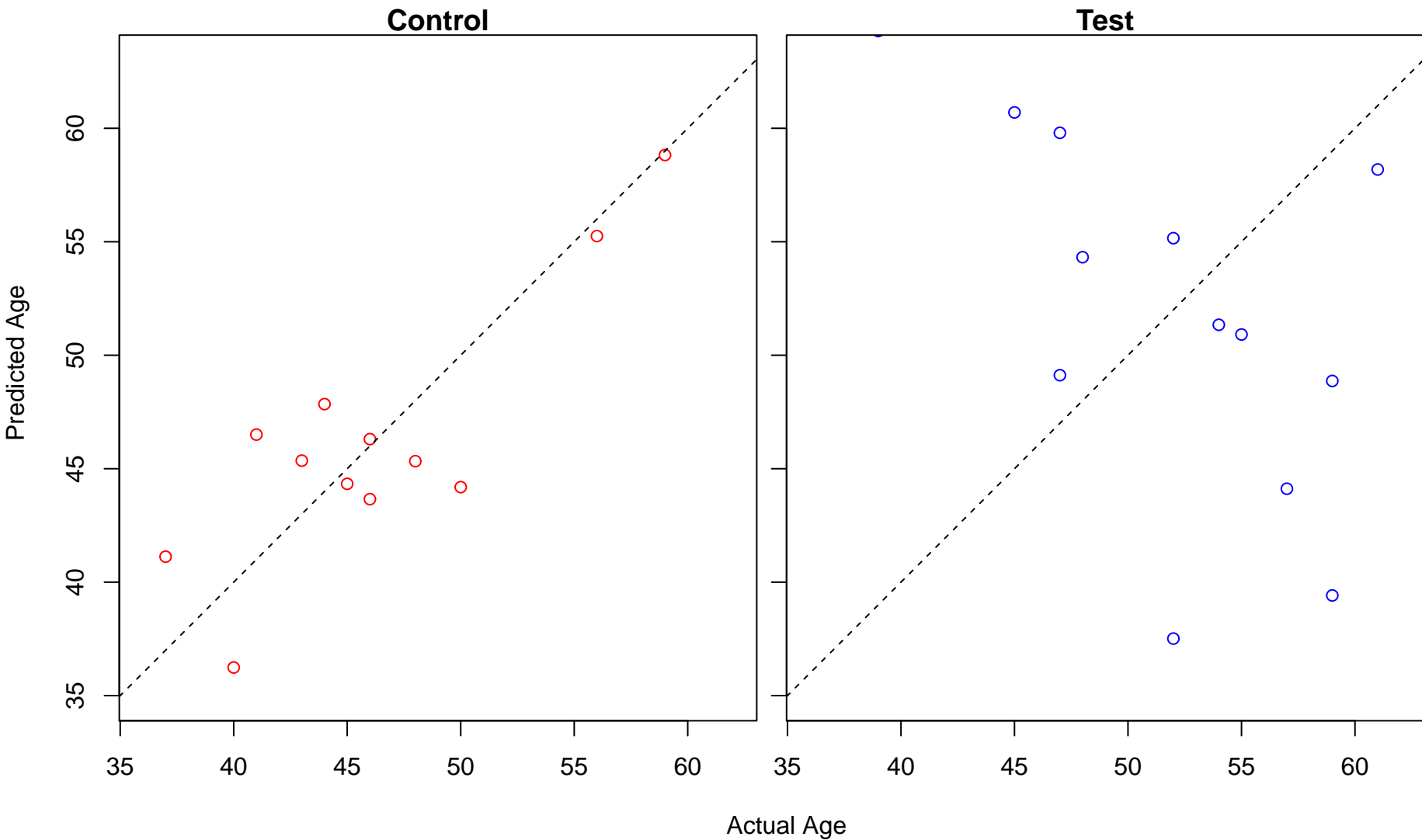


Test

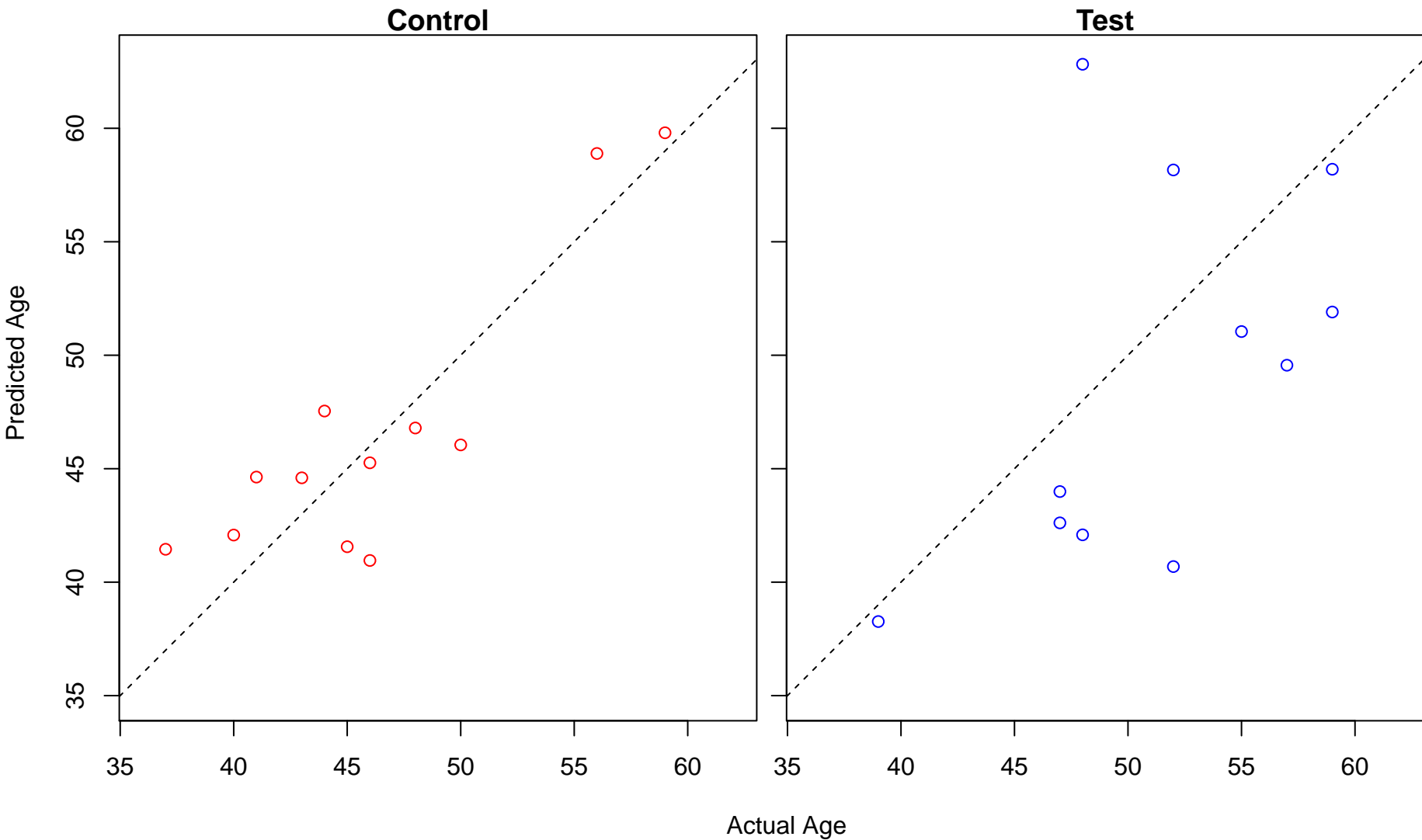


Actual Age

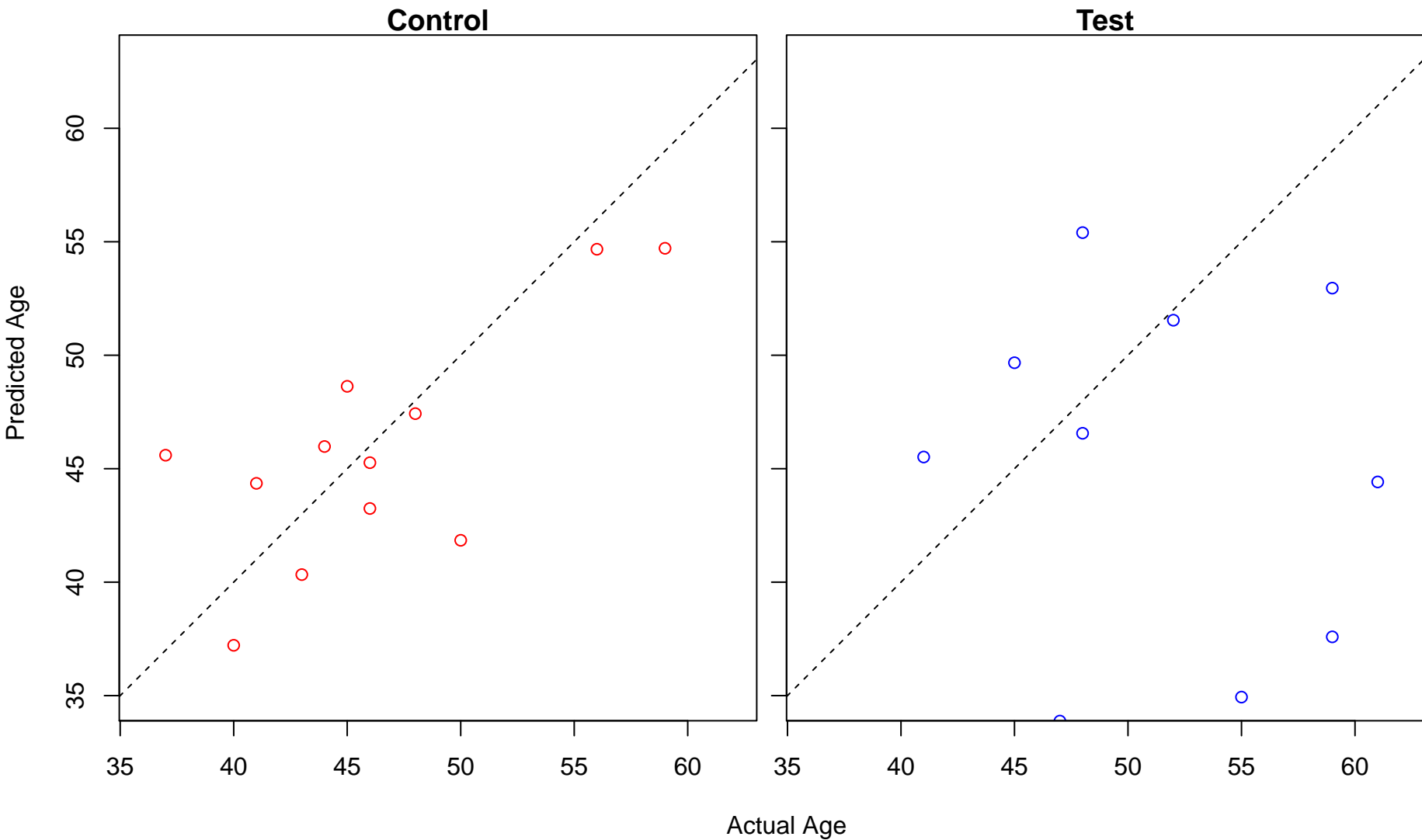
protein secretion (Score: 6.180923)



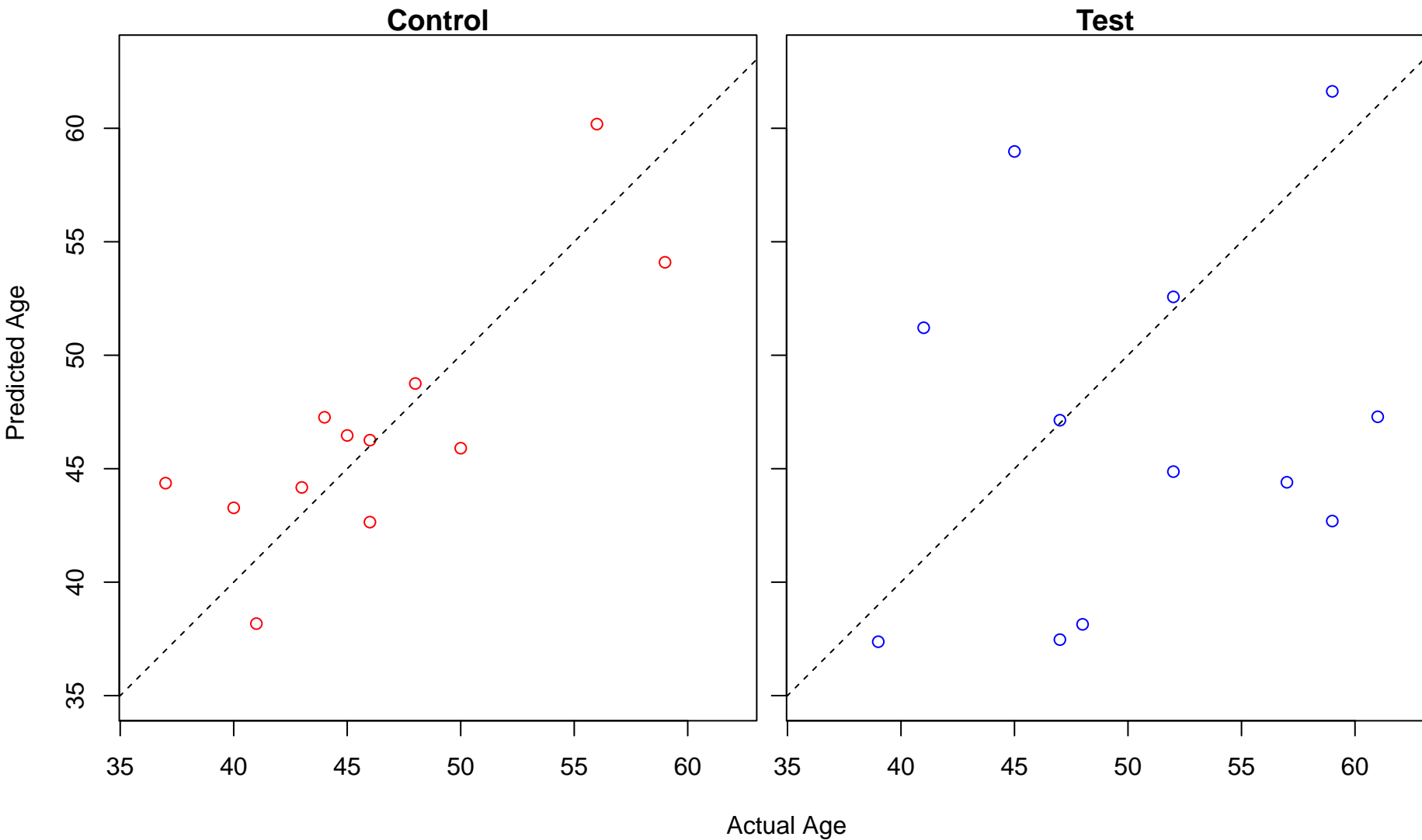
estrogen metabolic process (Score: 6.175470)



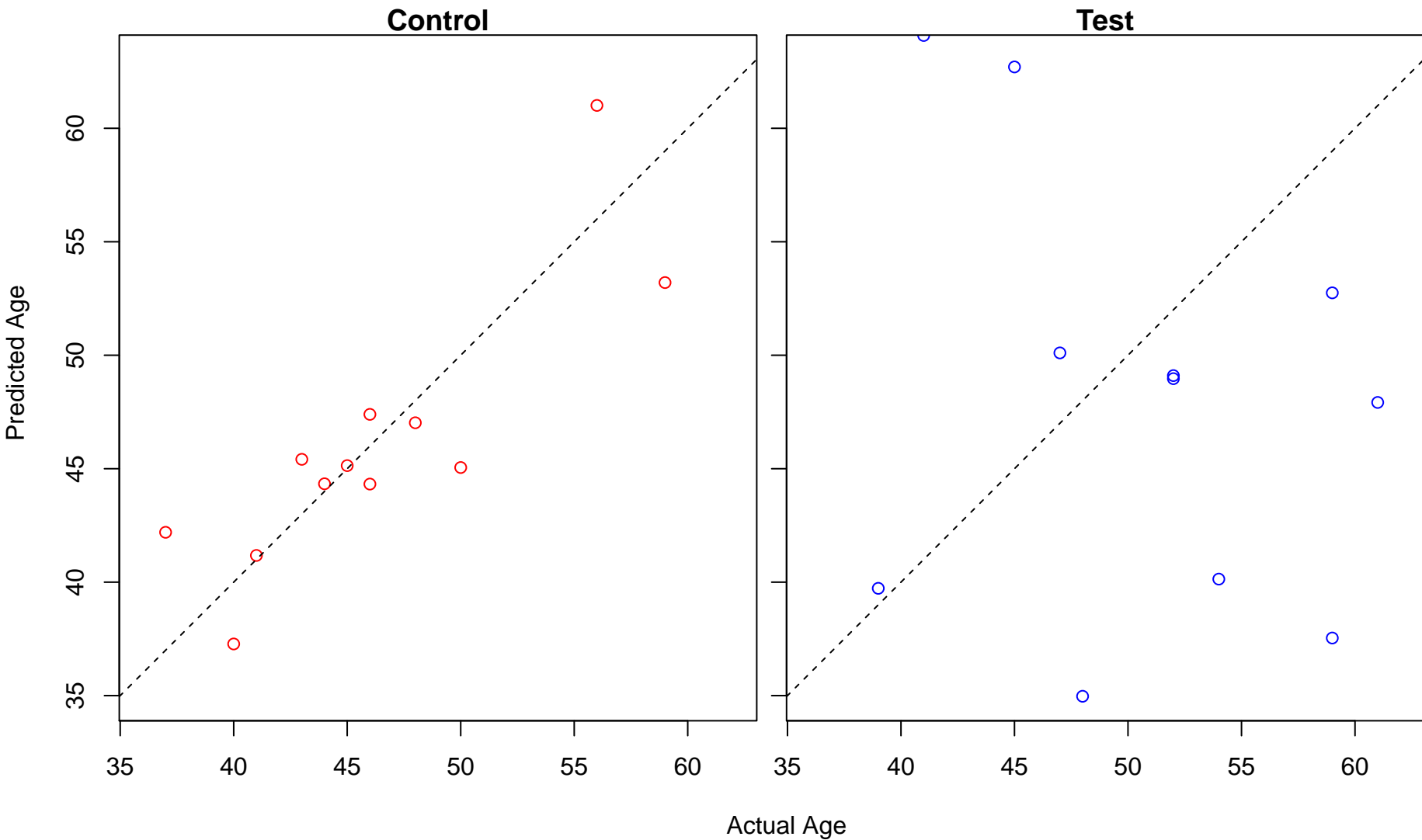
bone remodeling (Score: 6.160410)



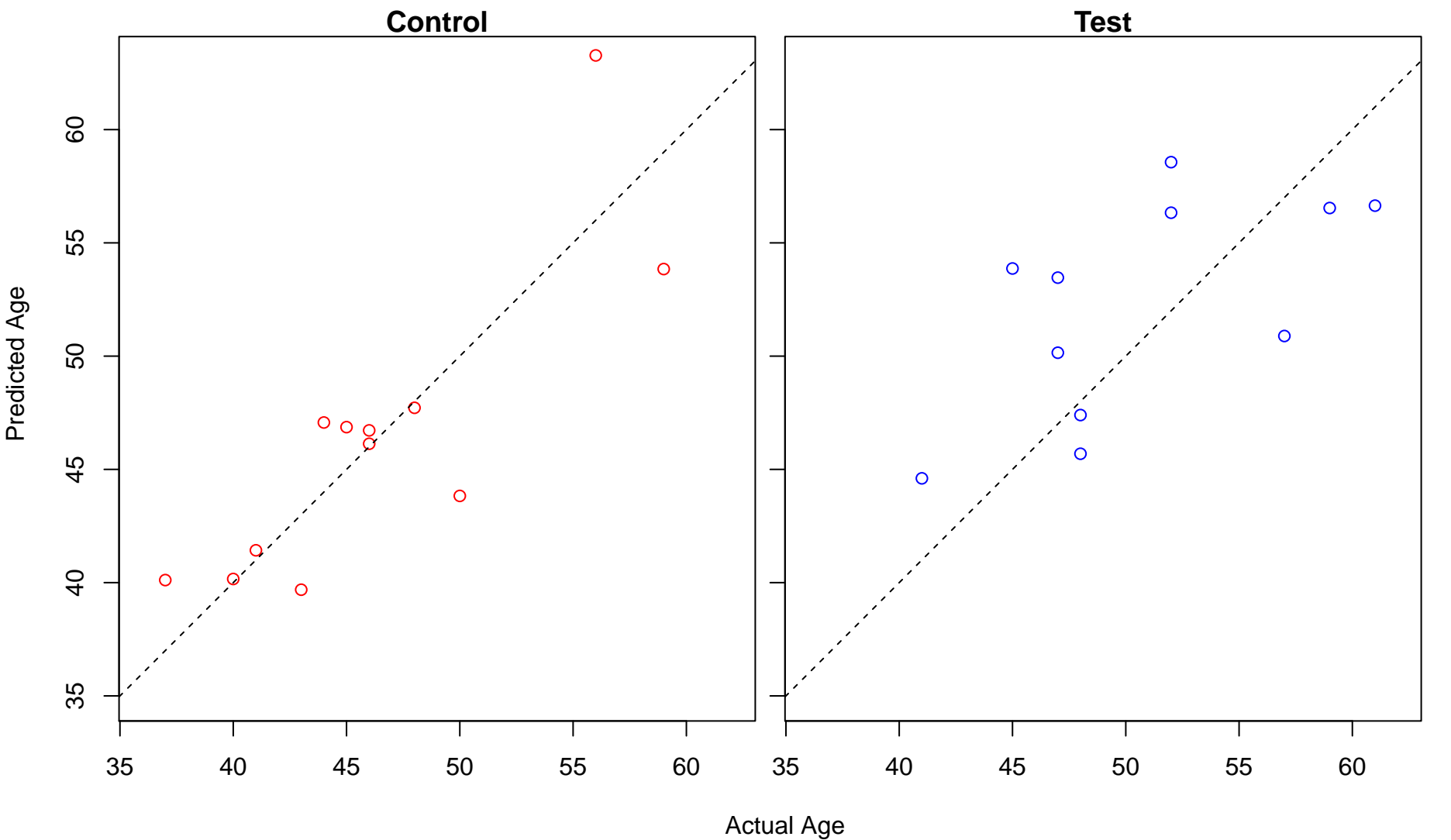
apoptotic mitochondrial changes (Score: 6.138443)



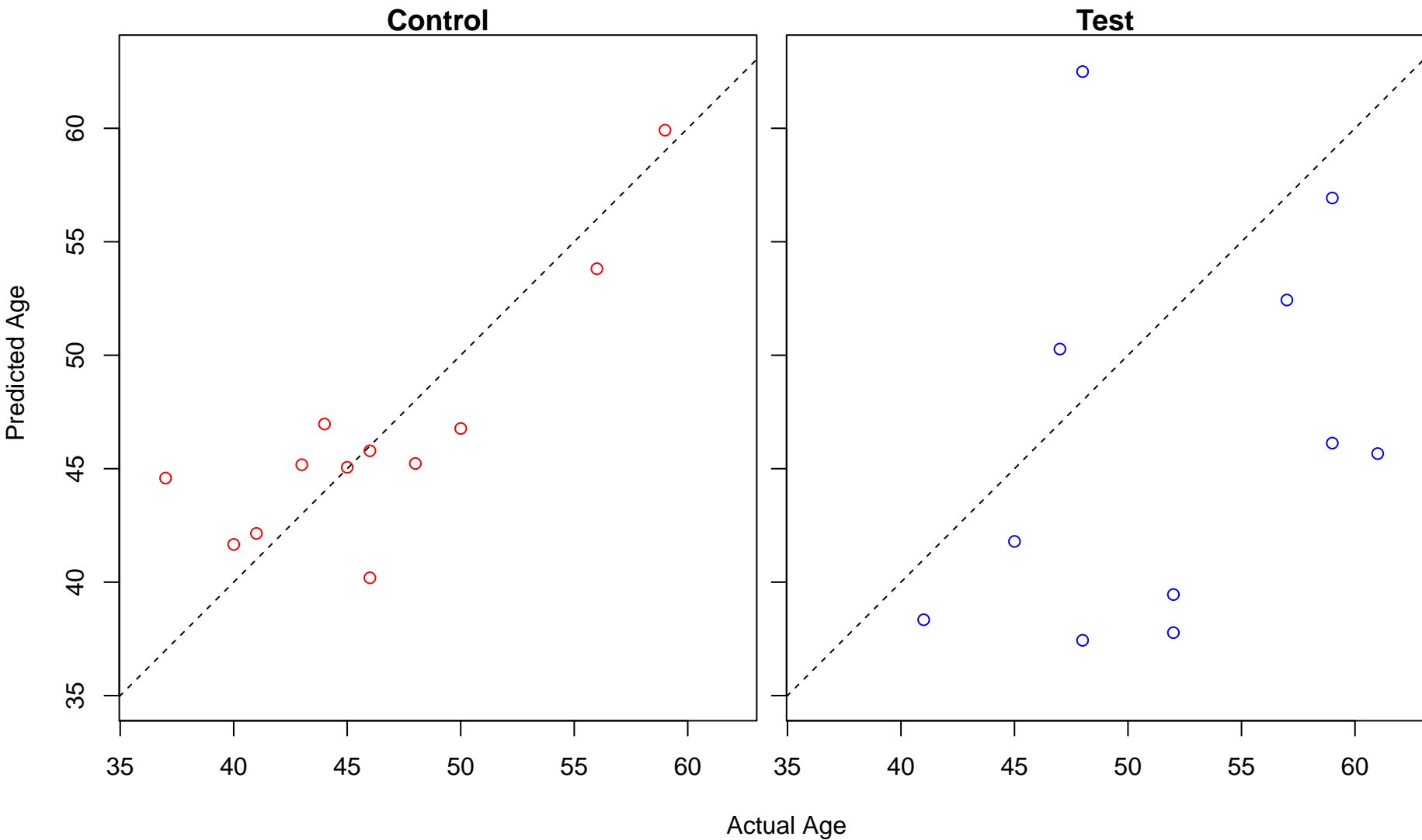
embryonic organ development (Score: 6.135299)



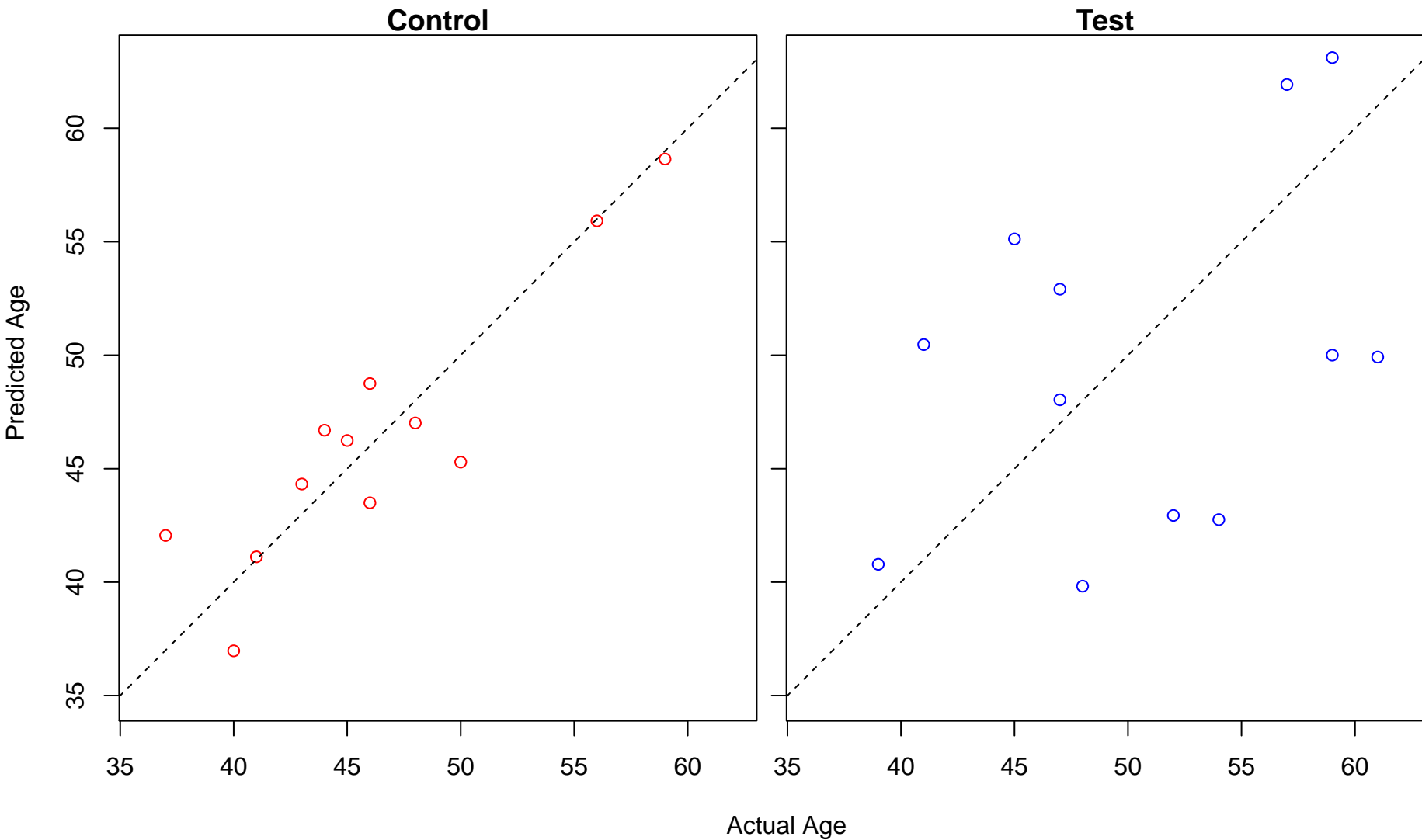
Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent (Score



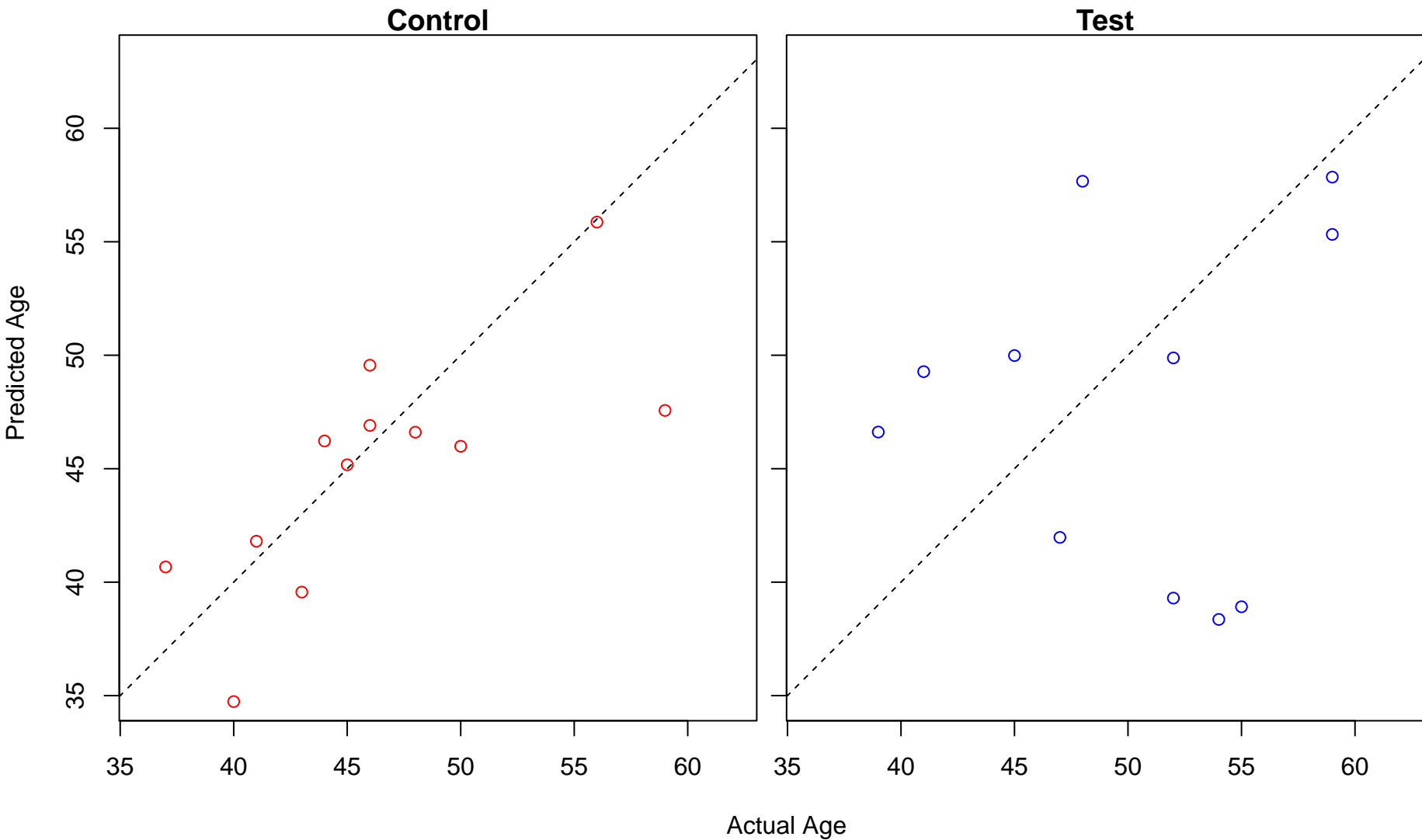
regulation of defense response to virus by host (Score: 6.124861)



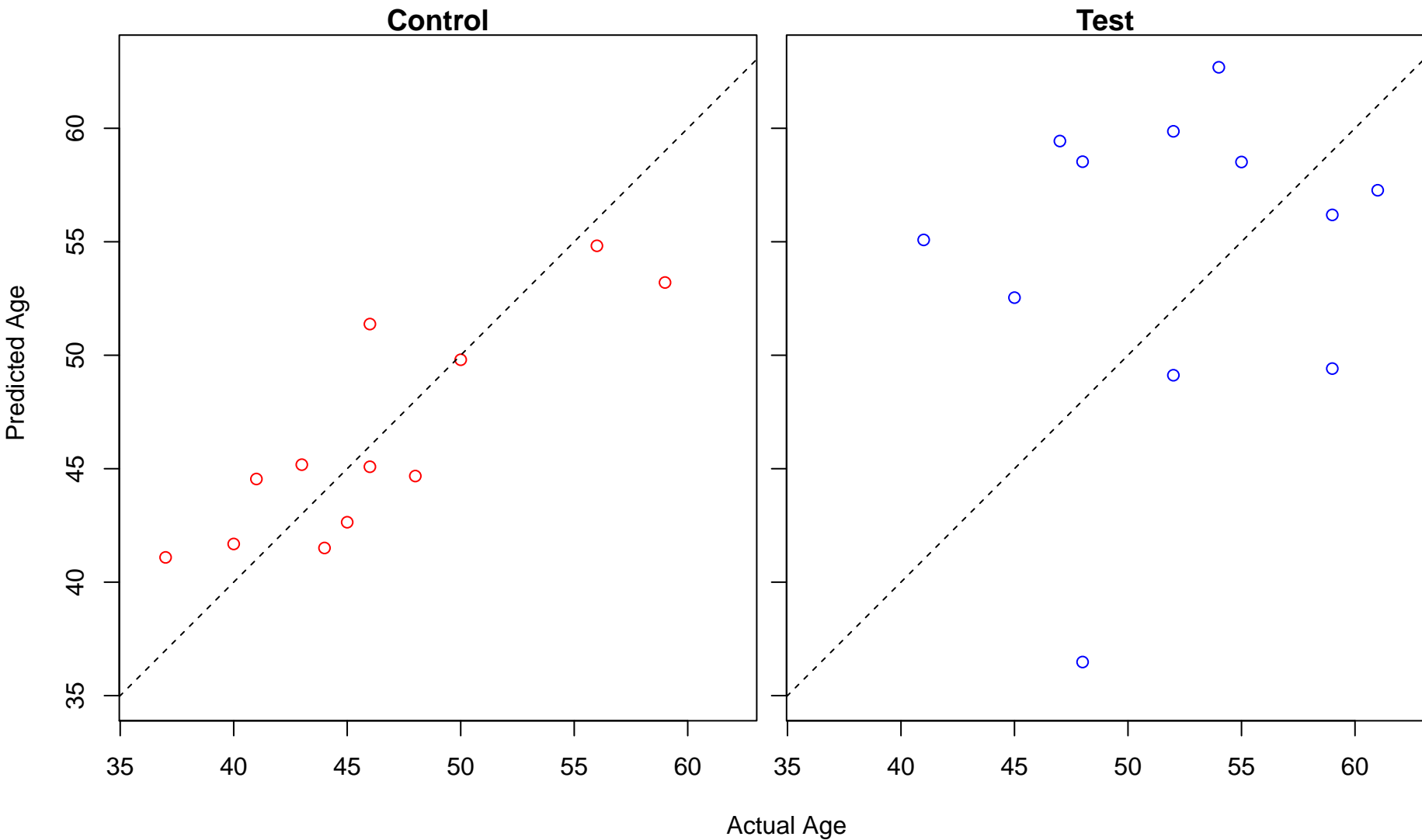
regulation of cyclic nucleotide metabolic process (Score: 6.118260)



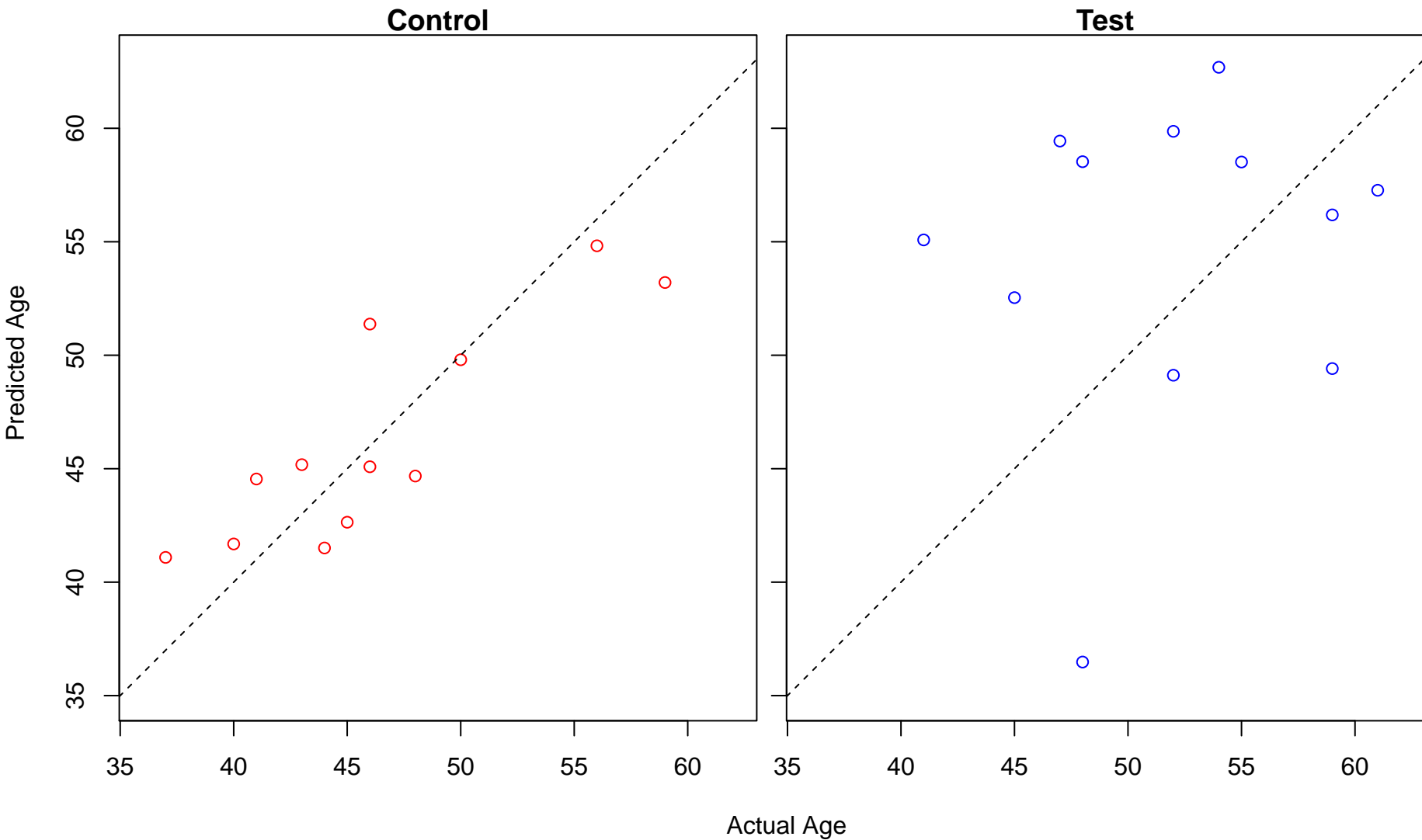
detection of stimulus involved in sensory perception (Score: 6.115574)



negative regulation of sterol transport (Score: 6.107341)

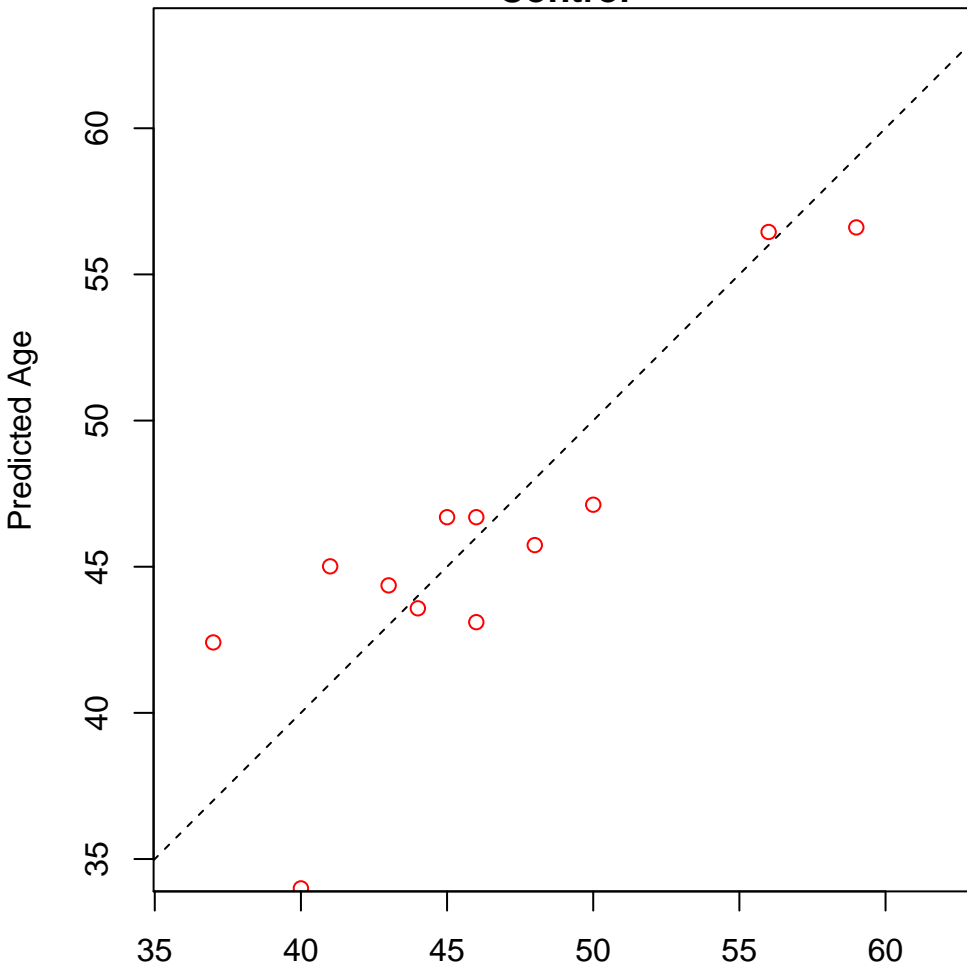


negative regulation of cholesterol transport (Score: 6.107341)

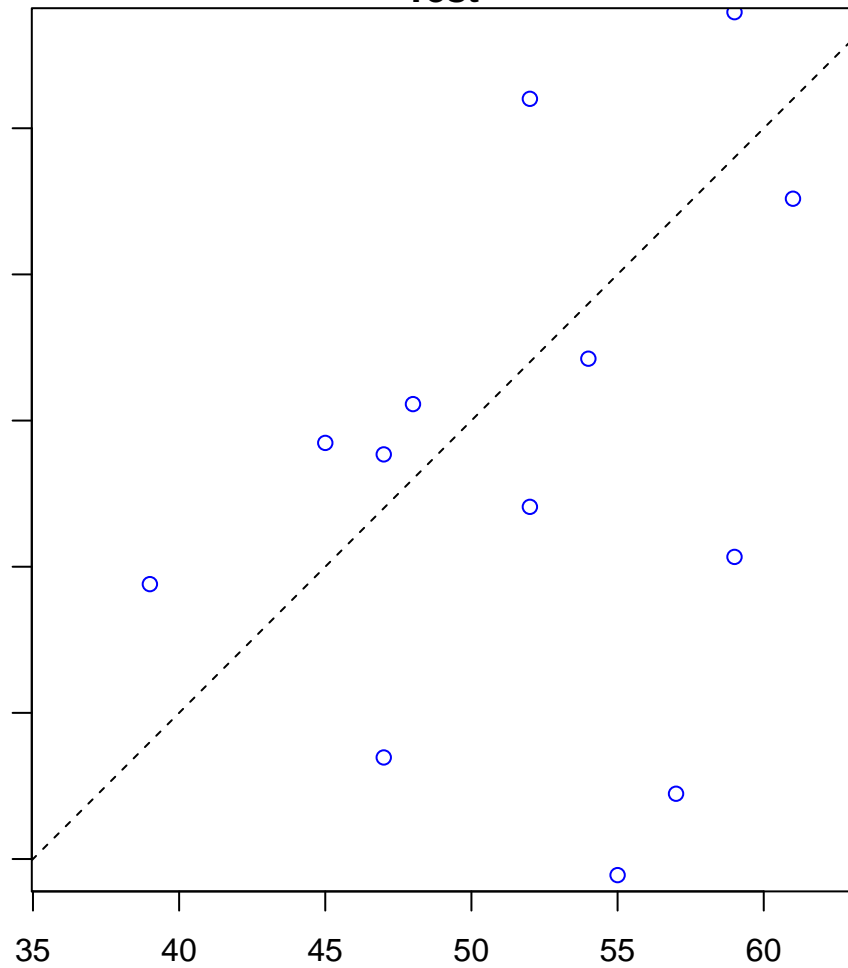


cellular response to muramyl dipeptide (Score: 6.102505)

Control

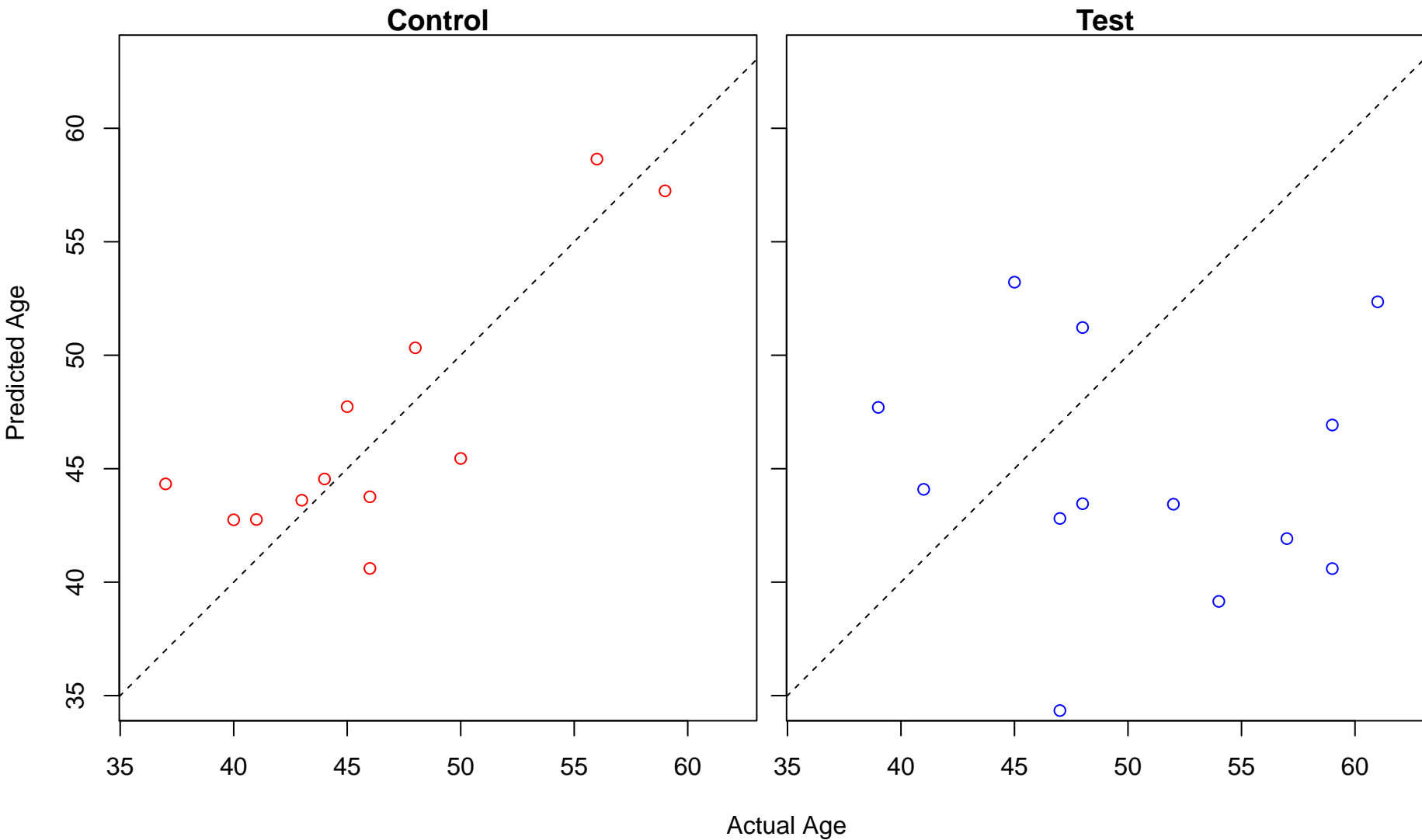


Test

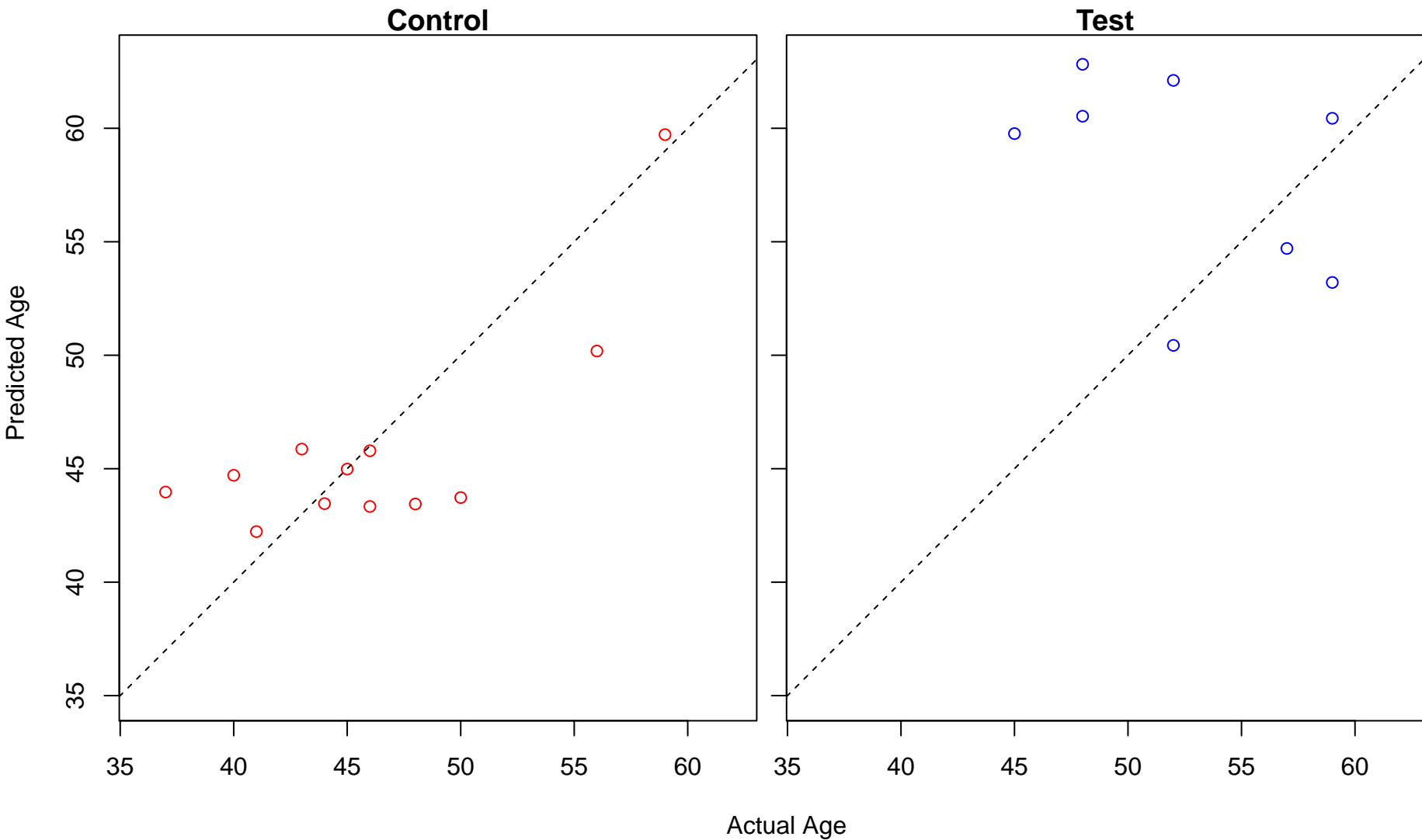


Actual Age

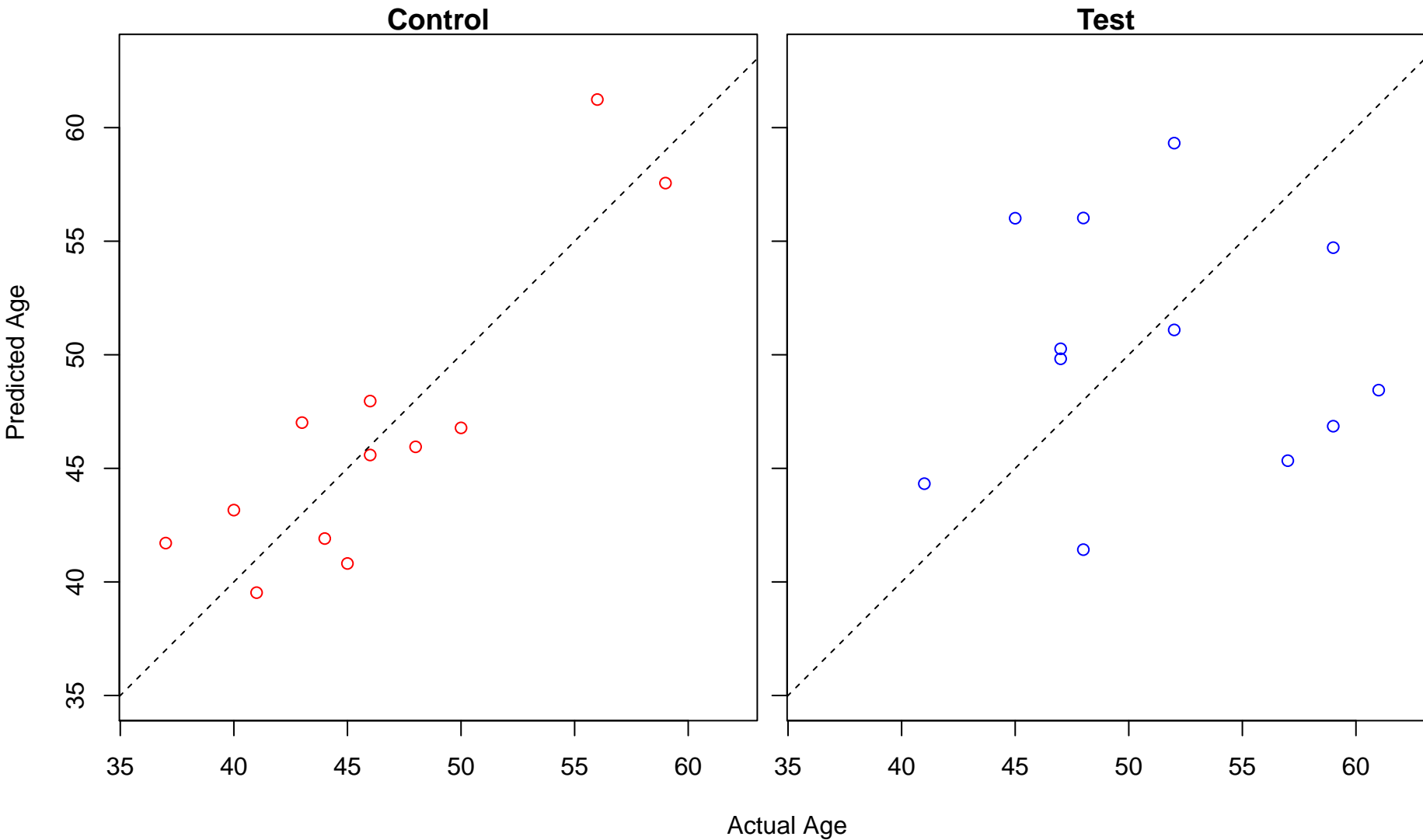
glycoprotein metabolic process (Score: 6.095865)



positive regulation of fatty acid beta-oxidation (Score: 6.088208)

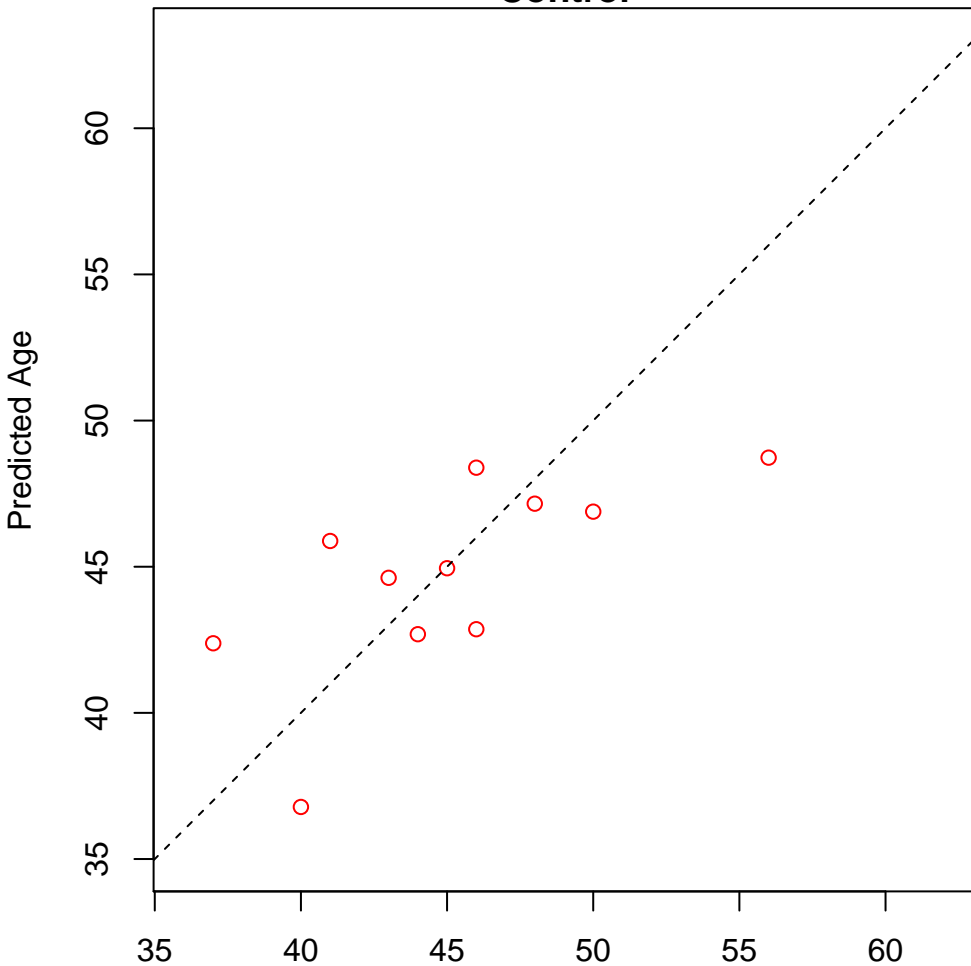


inositol phosphate catabolic process (Score: 6.074138)

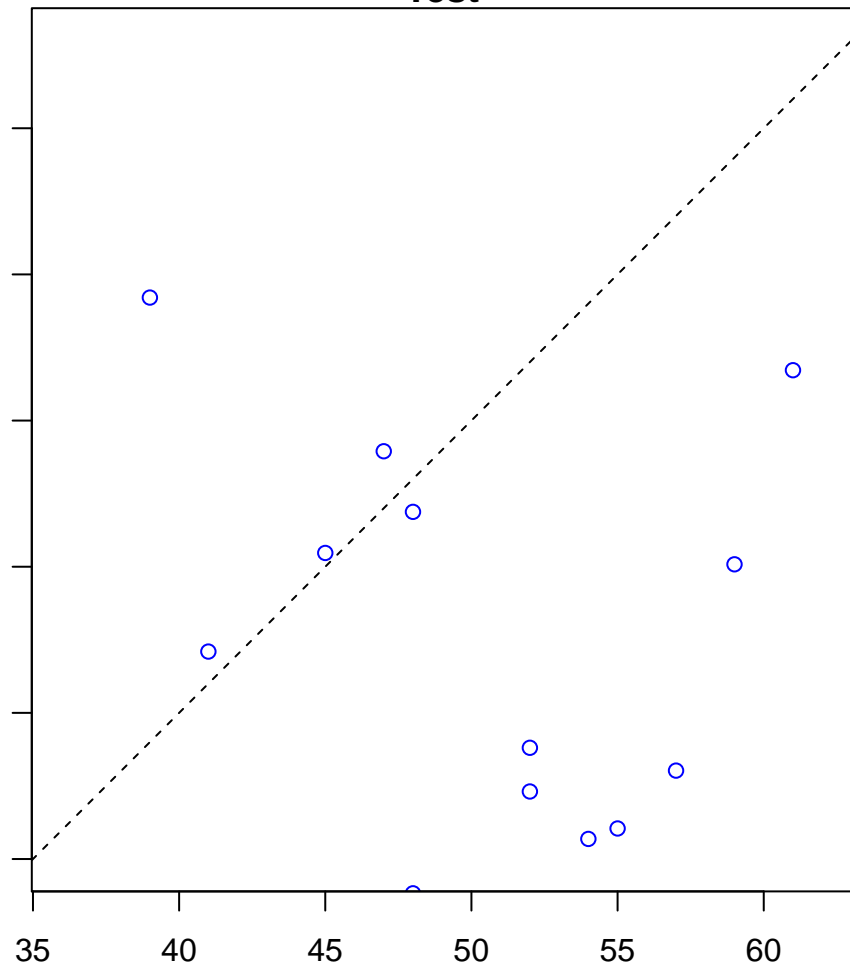


glomerulus vasculature development (Score: 6.072624)

Control

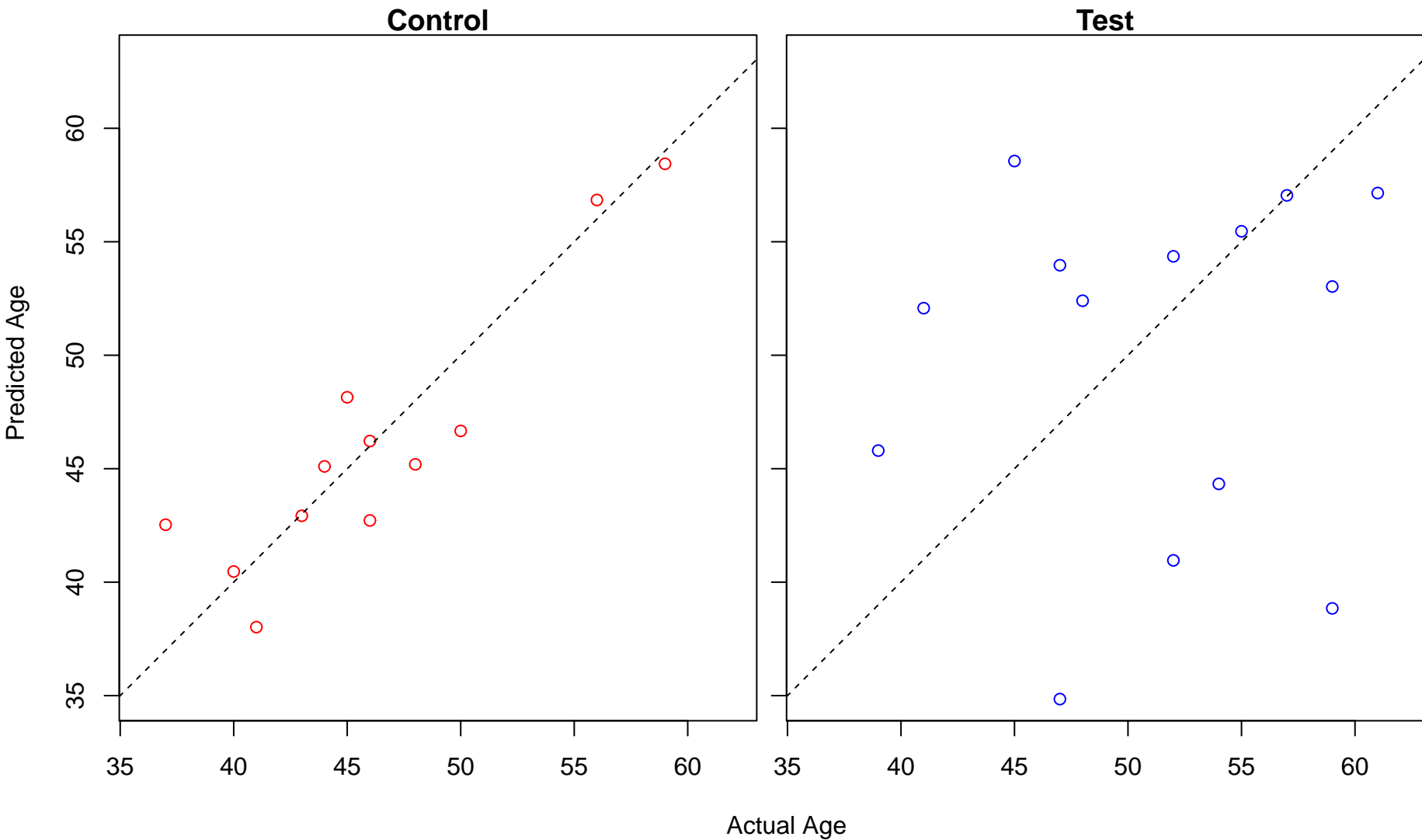


Test

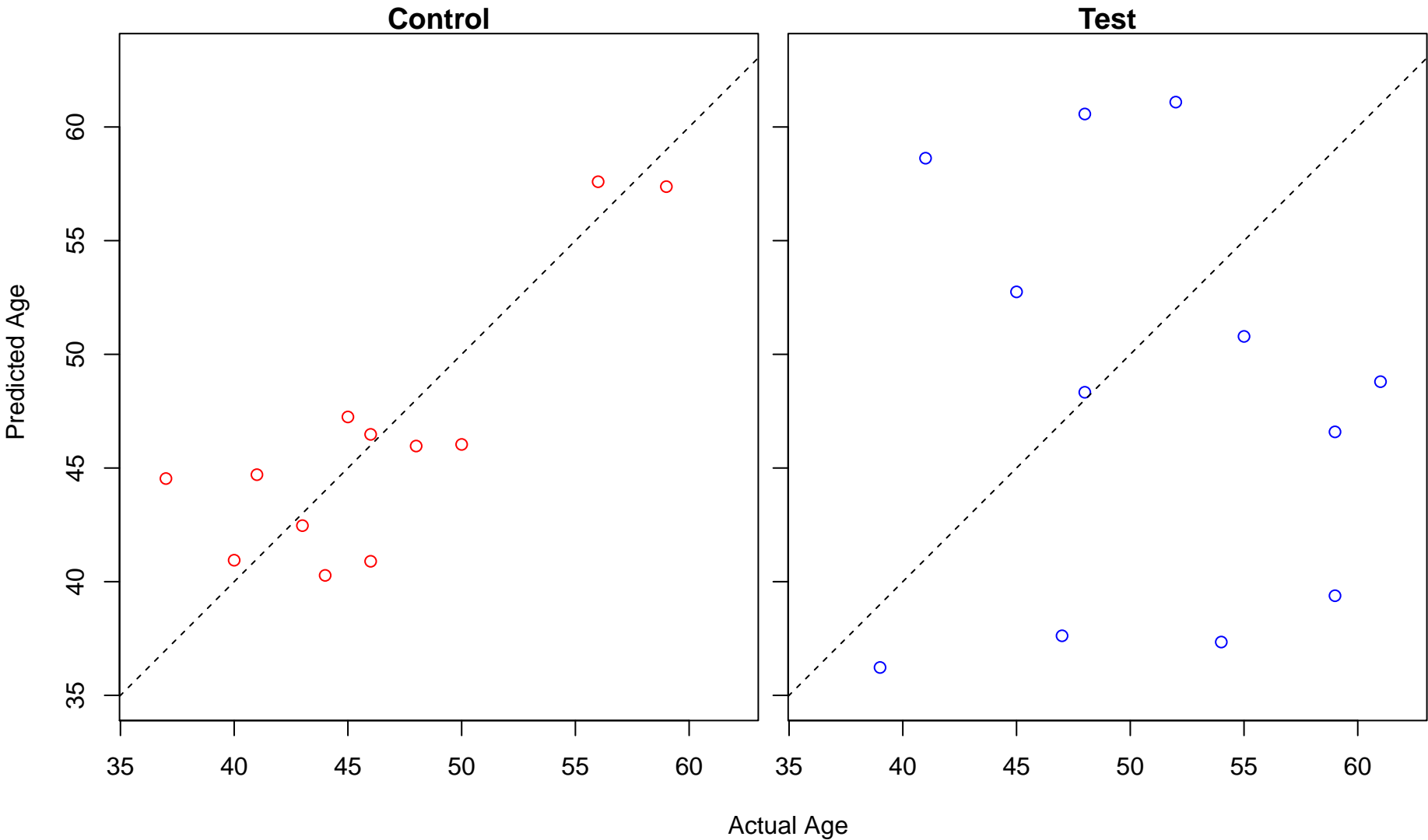


Actual Age

respiratory tube development (Score: 6.071828)

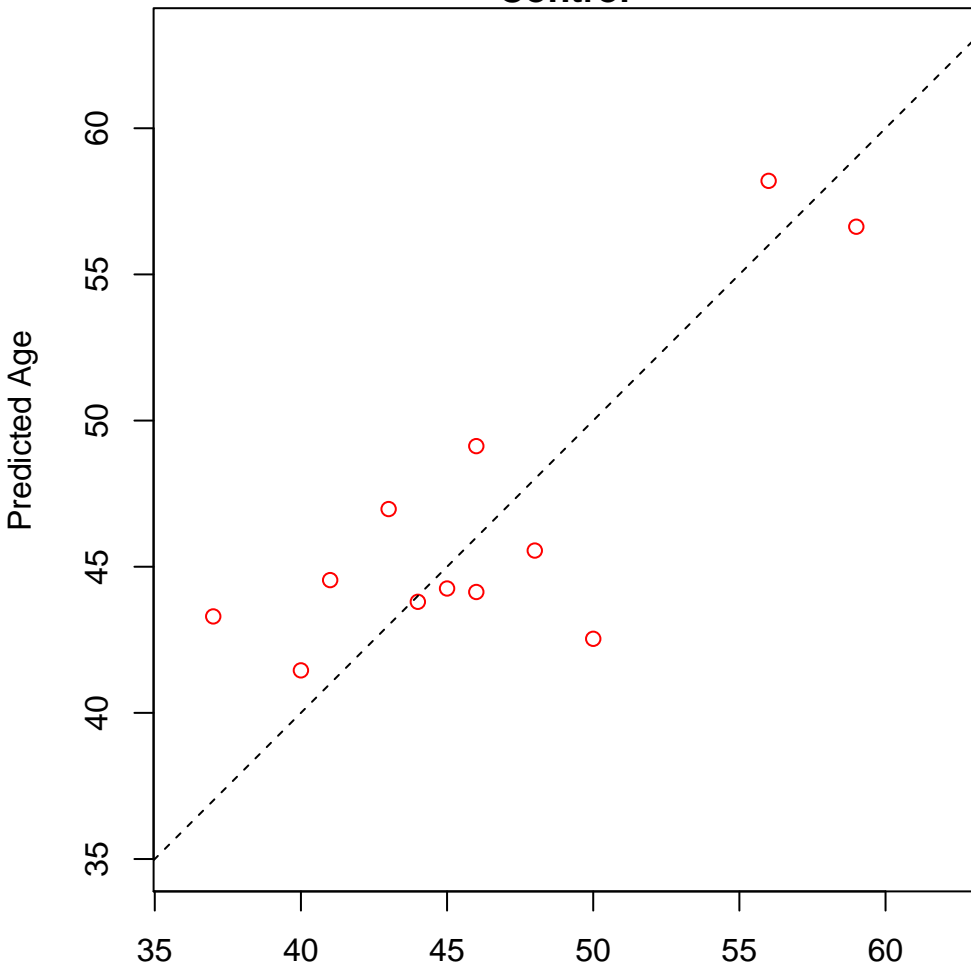


maintenance of protein location in nucleus (Score: 6.064014)

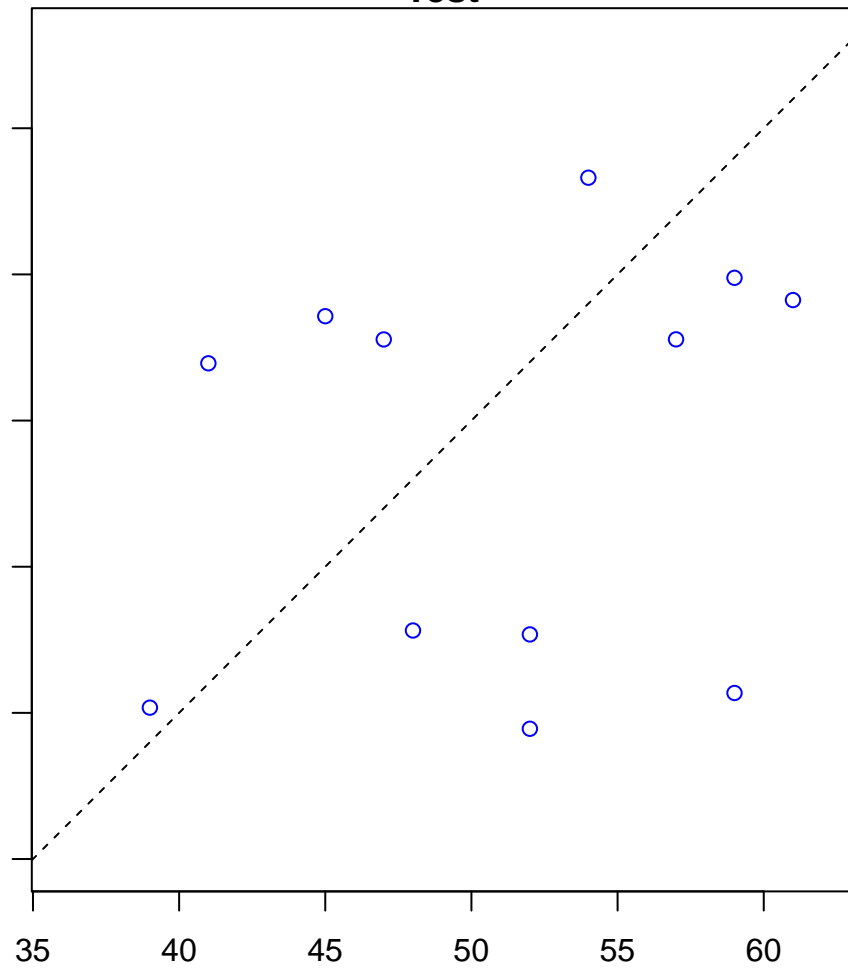


regulation of mRNA catabolic process (Score: 6.062754)

Control

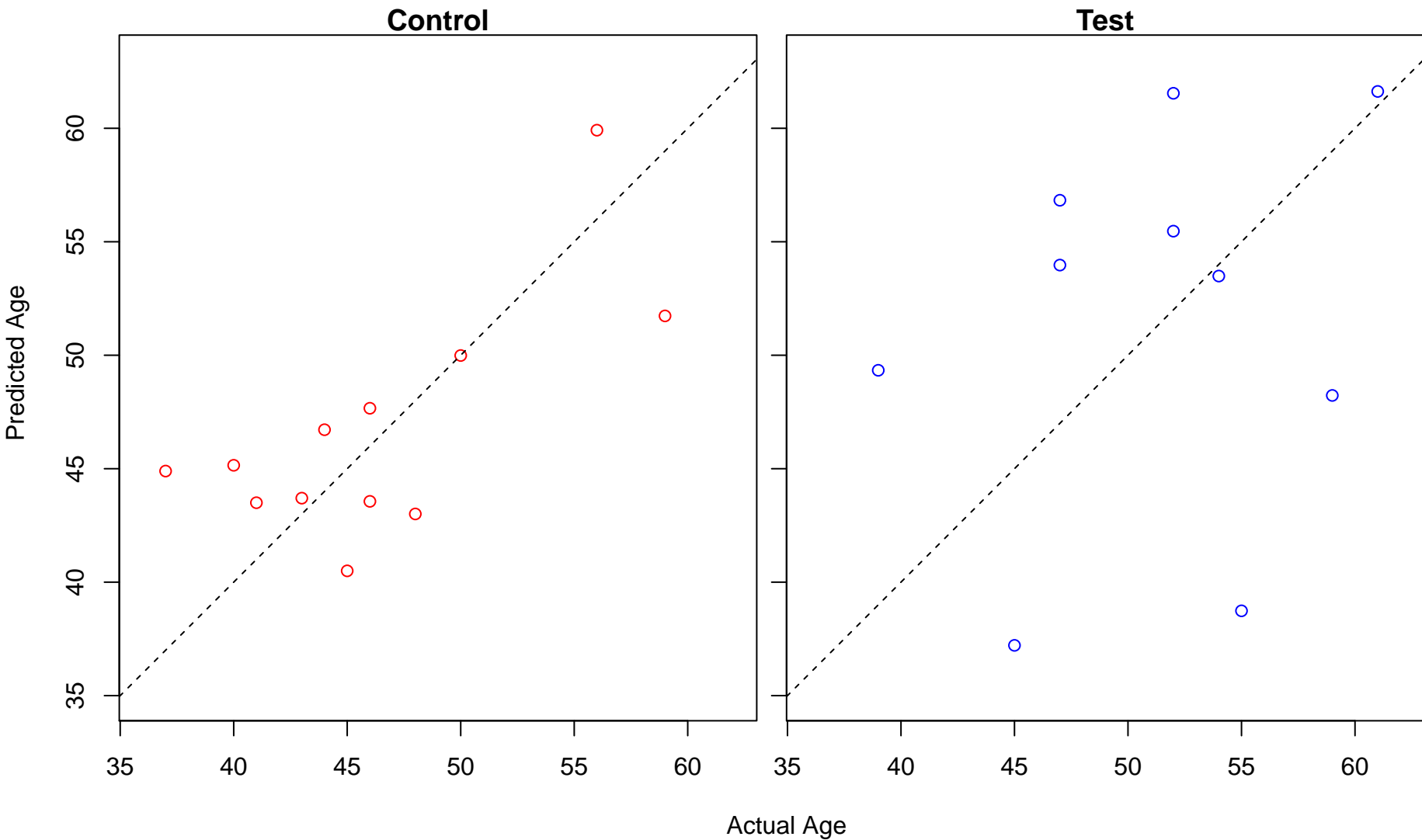


Test

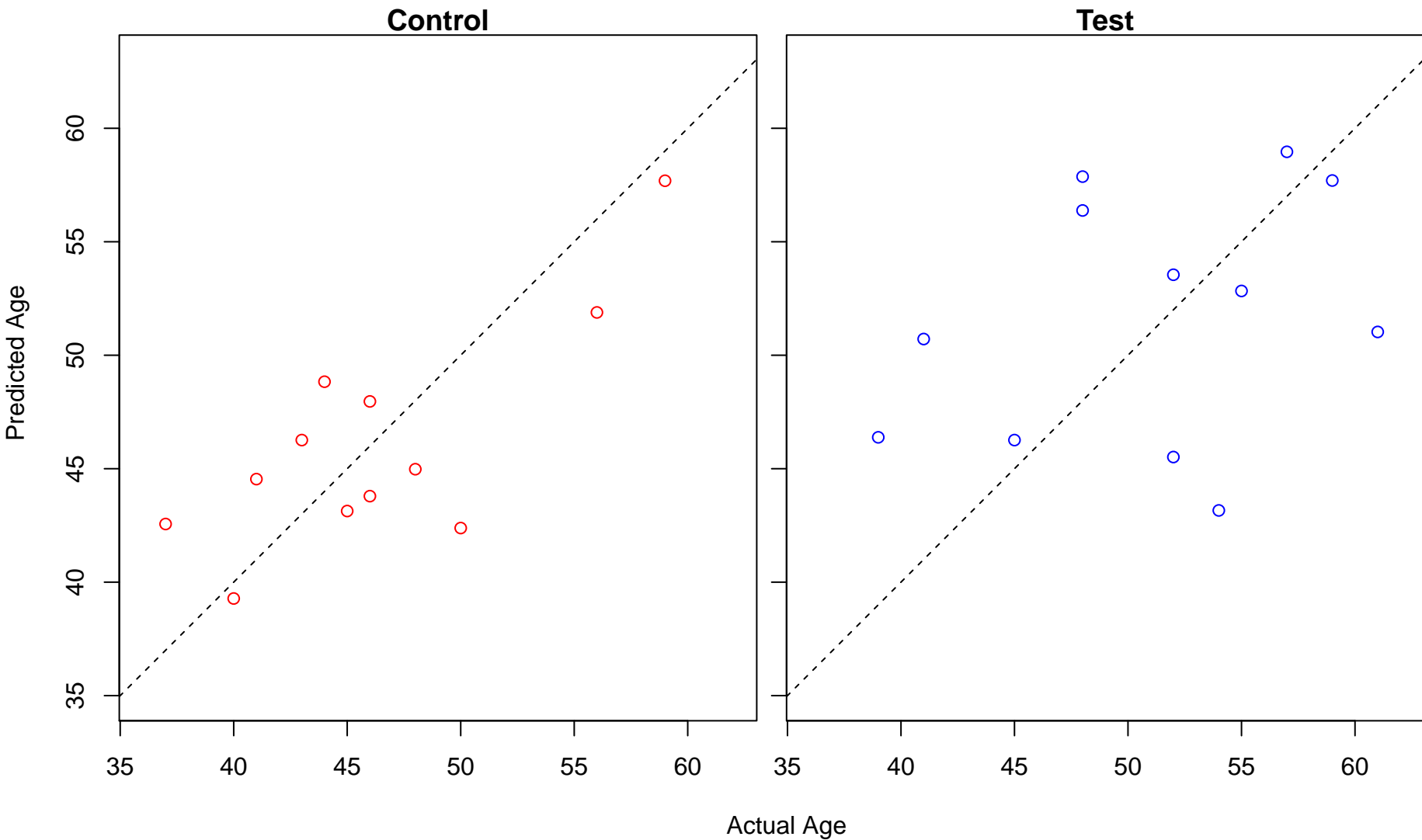


Actual Age

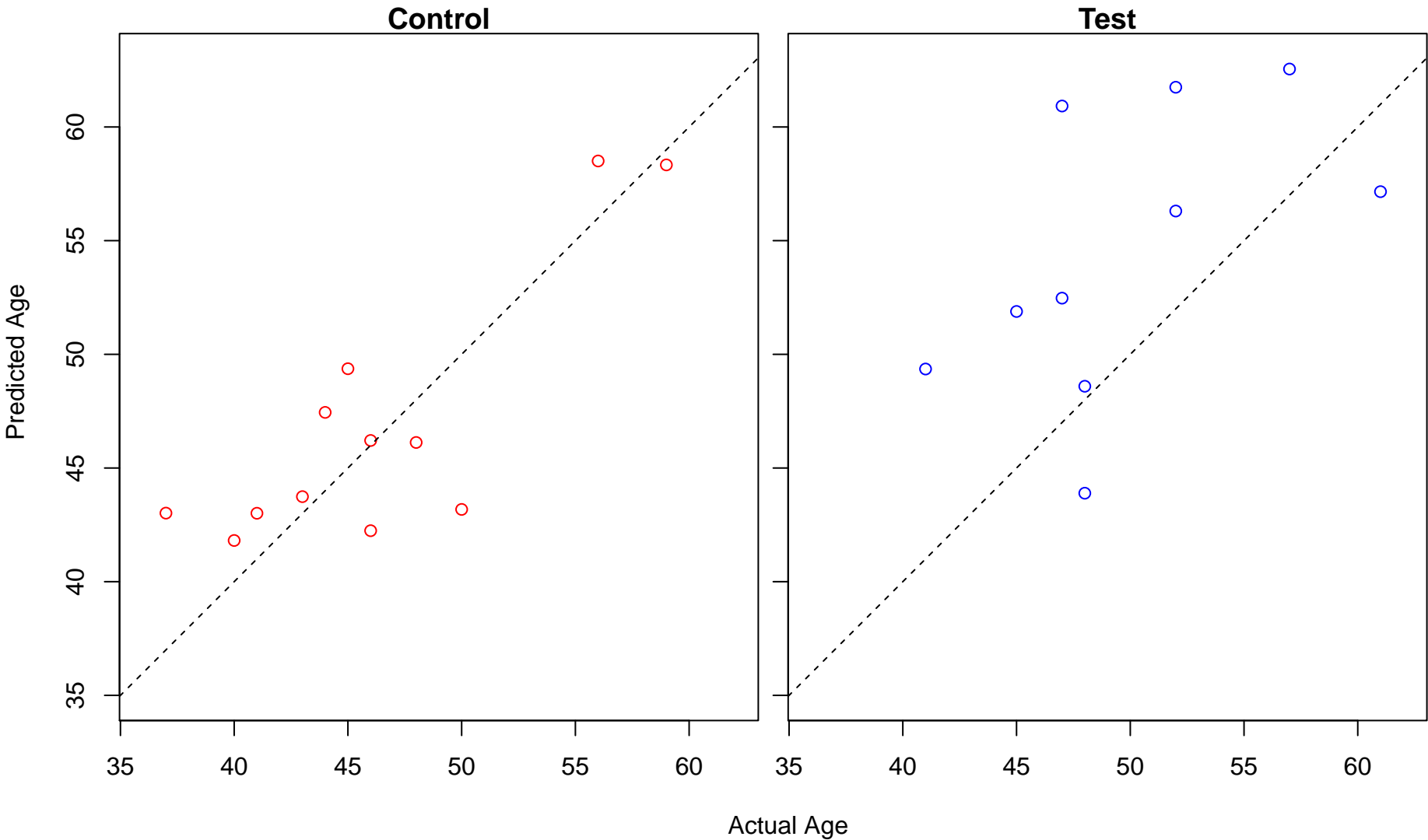
negative regulation of striated muscle contraction (Score: 6.062091)



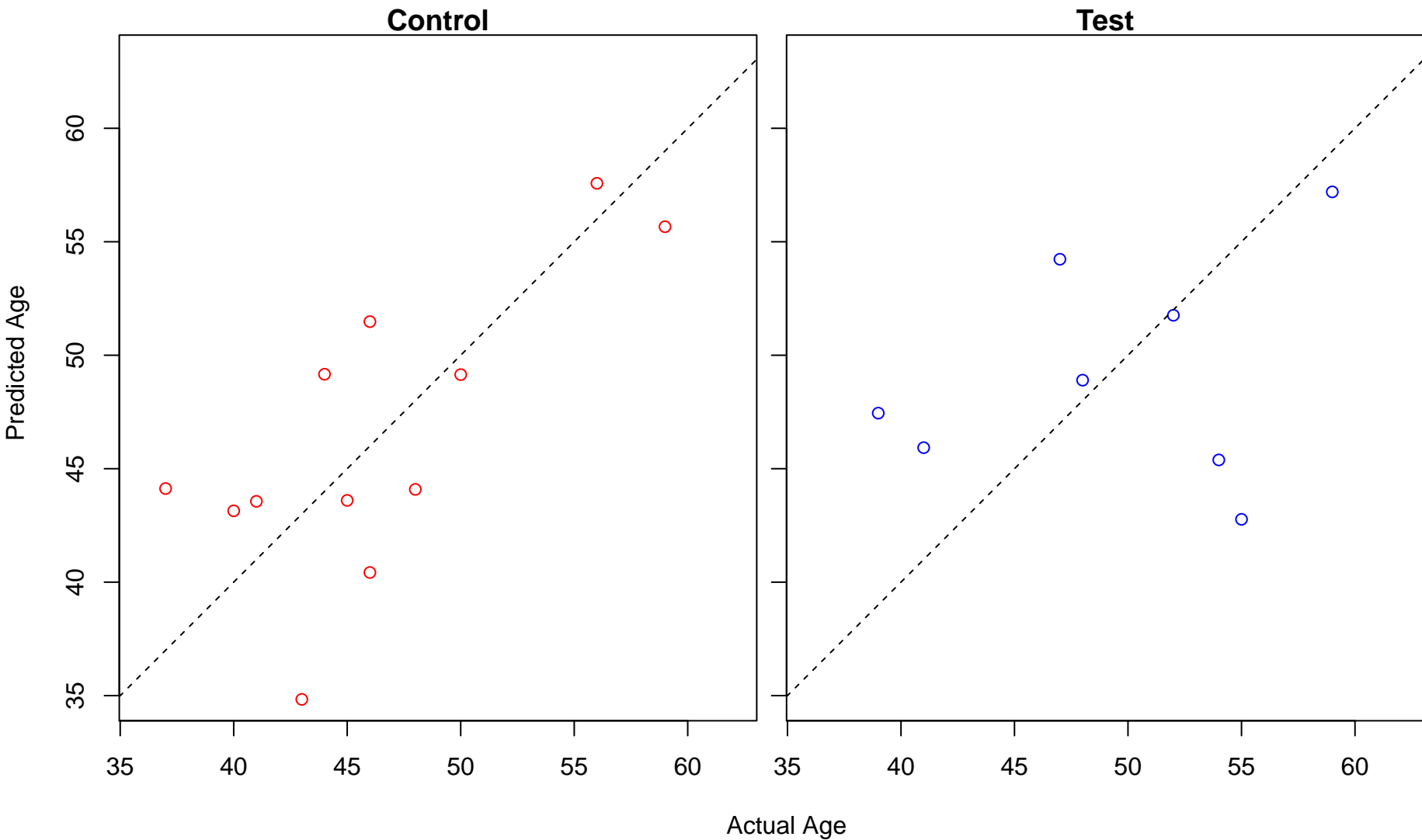
regulation of regulated secretory pathway (Score: 6.039745)



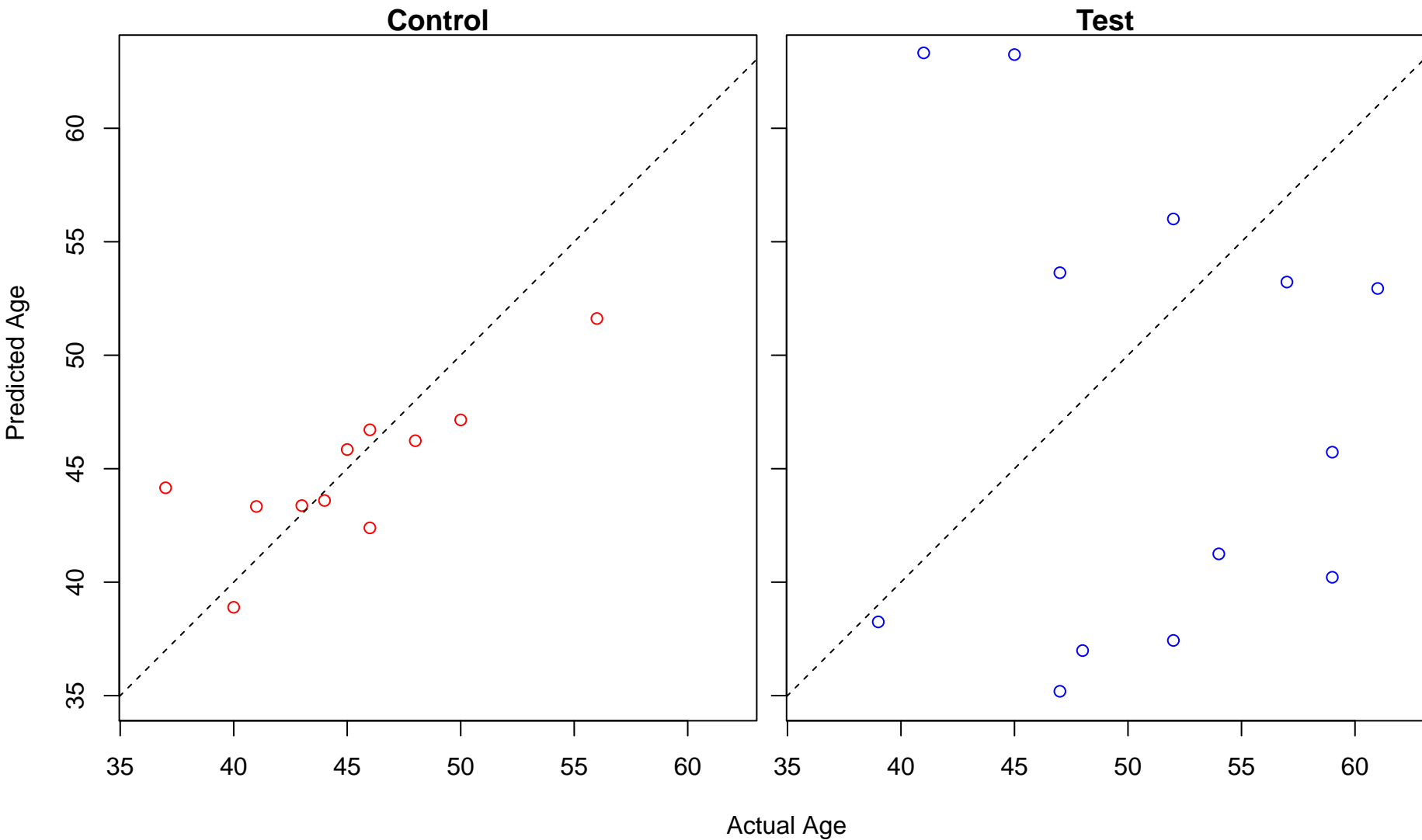
antigen processing and presentation of exogenous peptide antigen via MHC class I (Score: 6.03900)



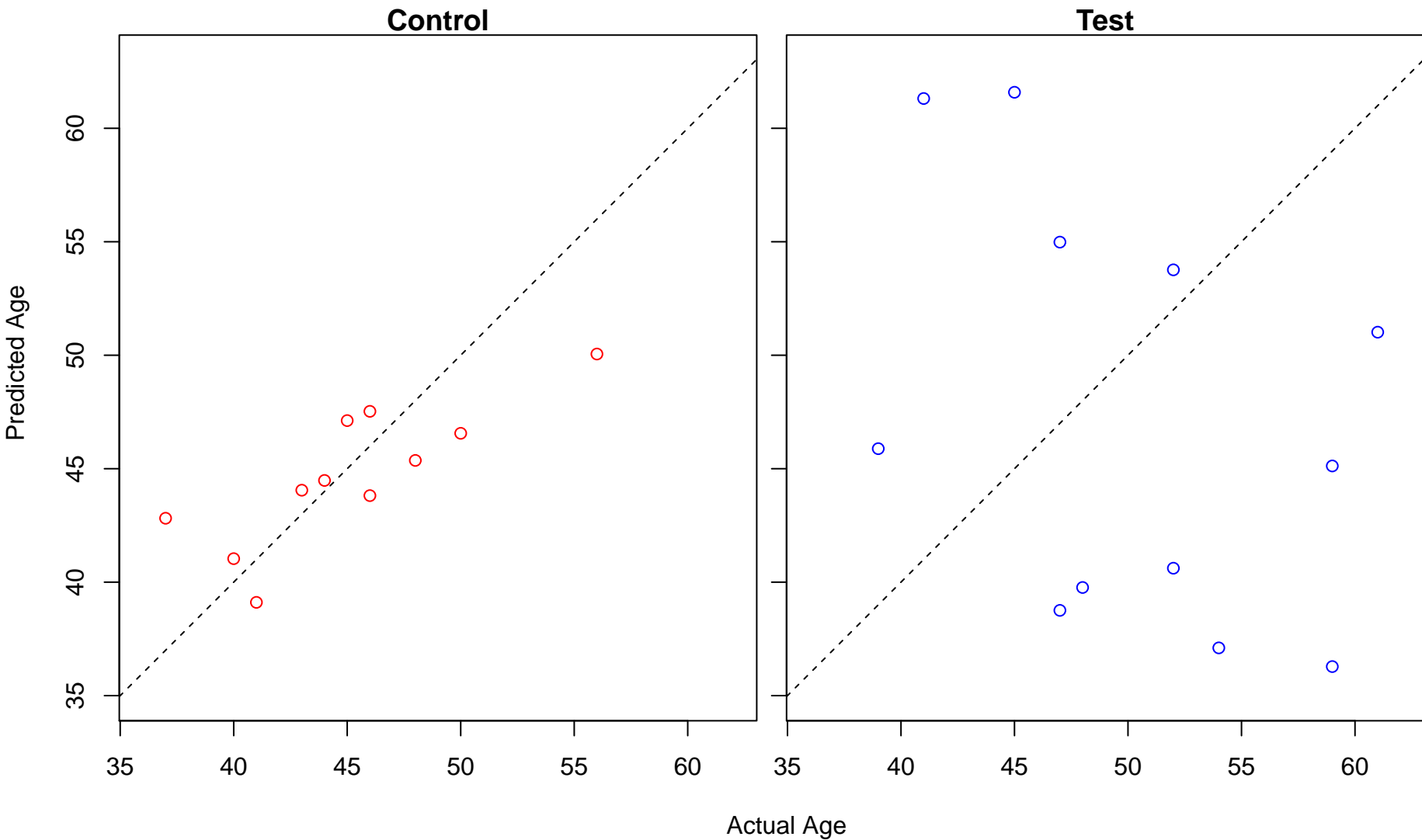
omega-hydroxylase P450 pathway (Score: 6.037897)



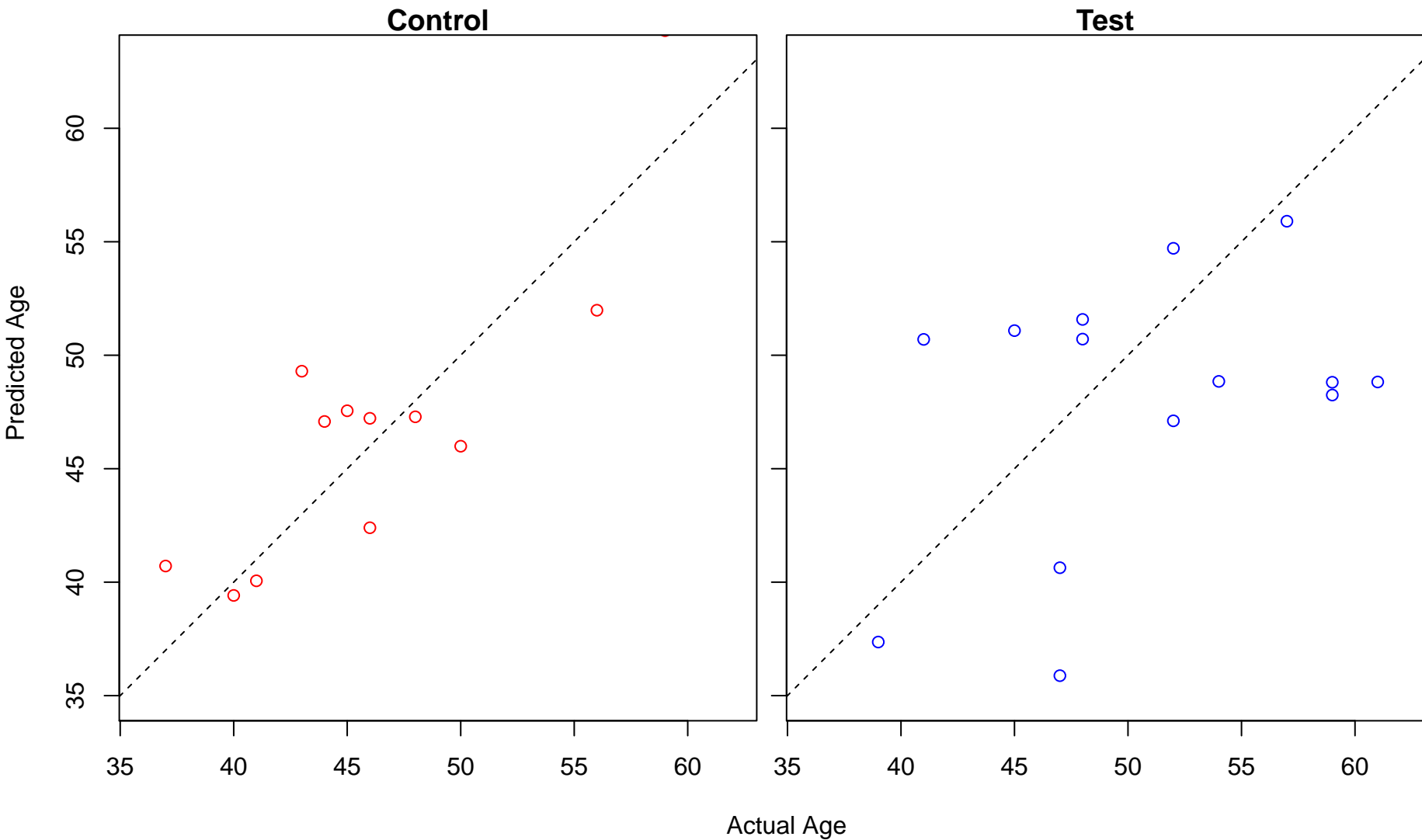
epithelial tube morphogenesis (Score: 6.036519)



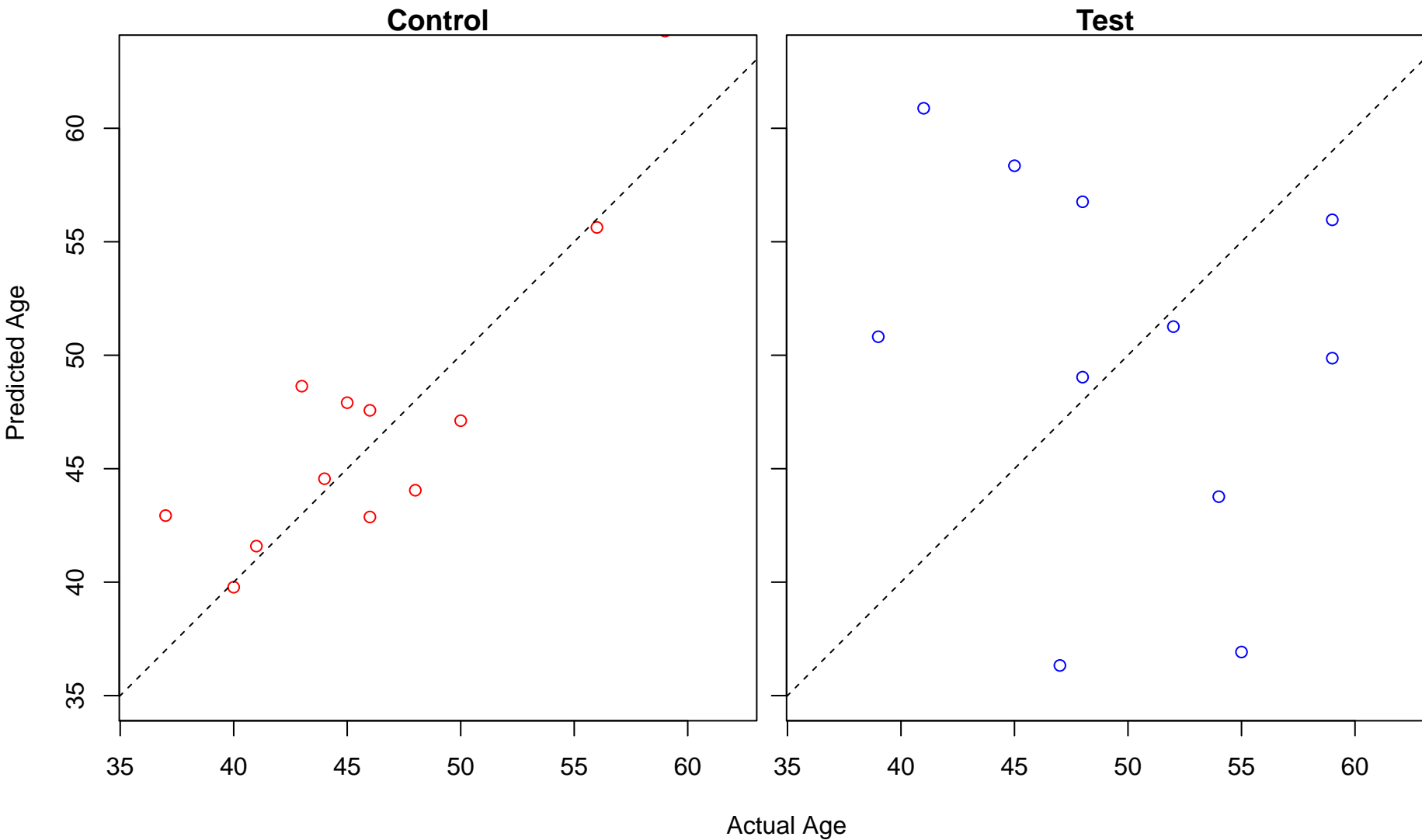
morphogenesis of an epithelium (Score: 6.019158)



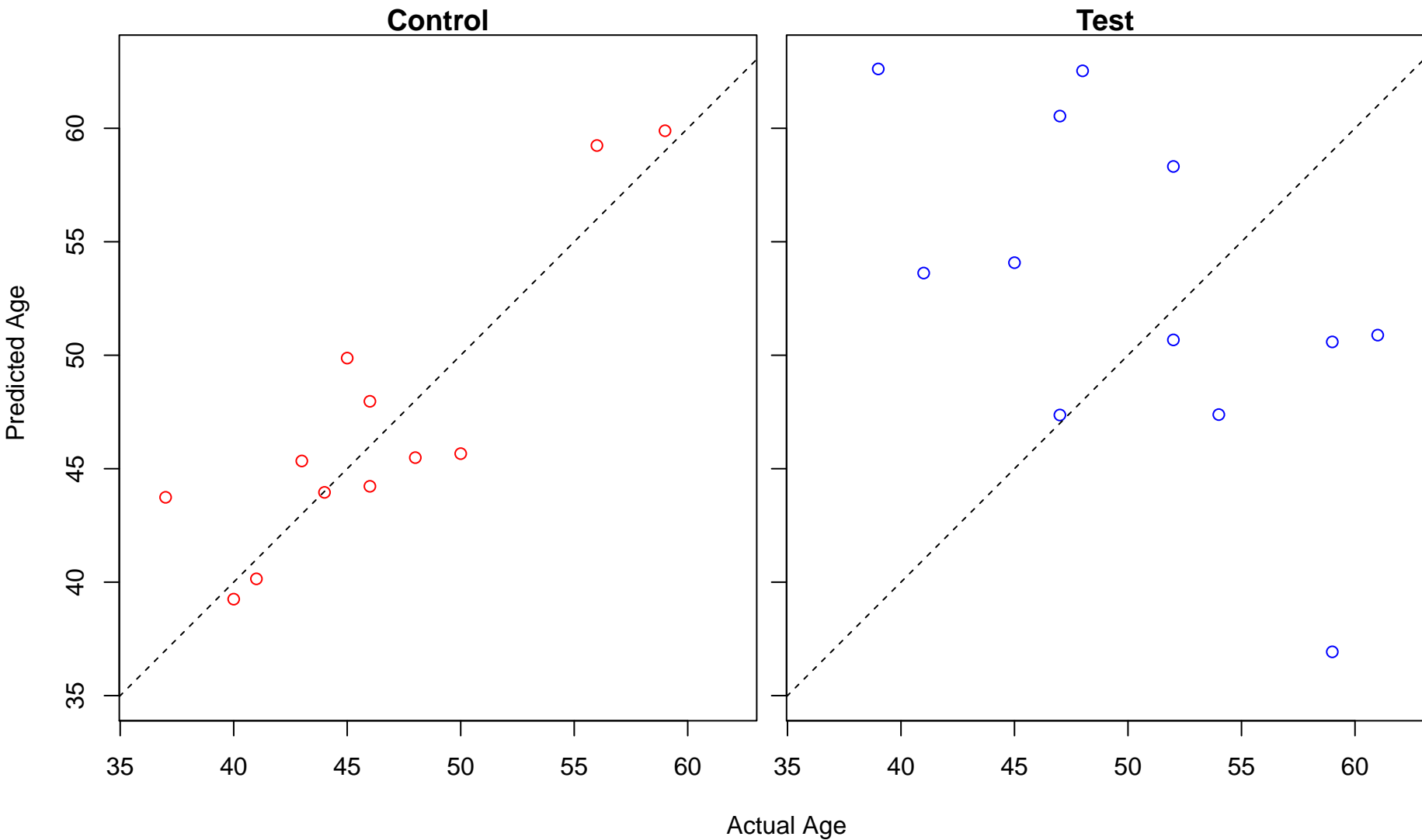
JAK-STAT cascade involved in growth hormone signaling pathway (Score: 6.012779)



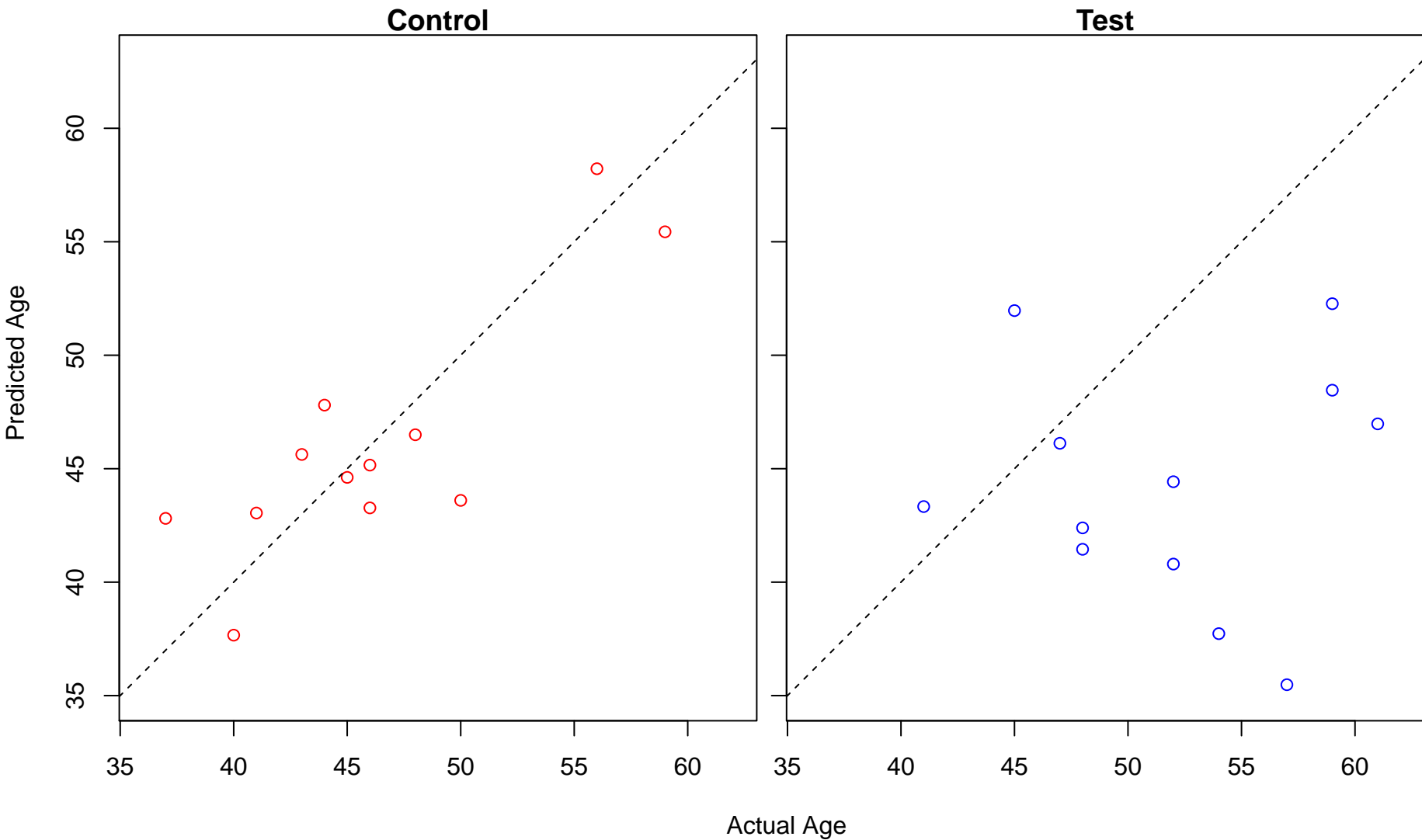
negative regulation of cyclin-dependent protein kinase activity (Score: 6.012405)



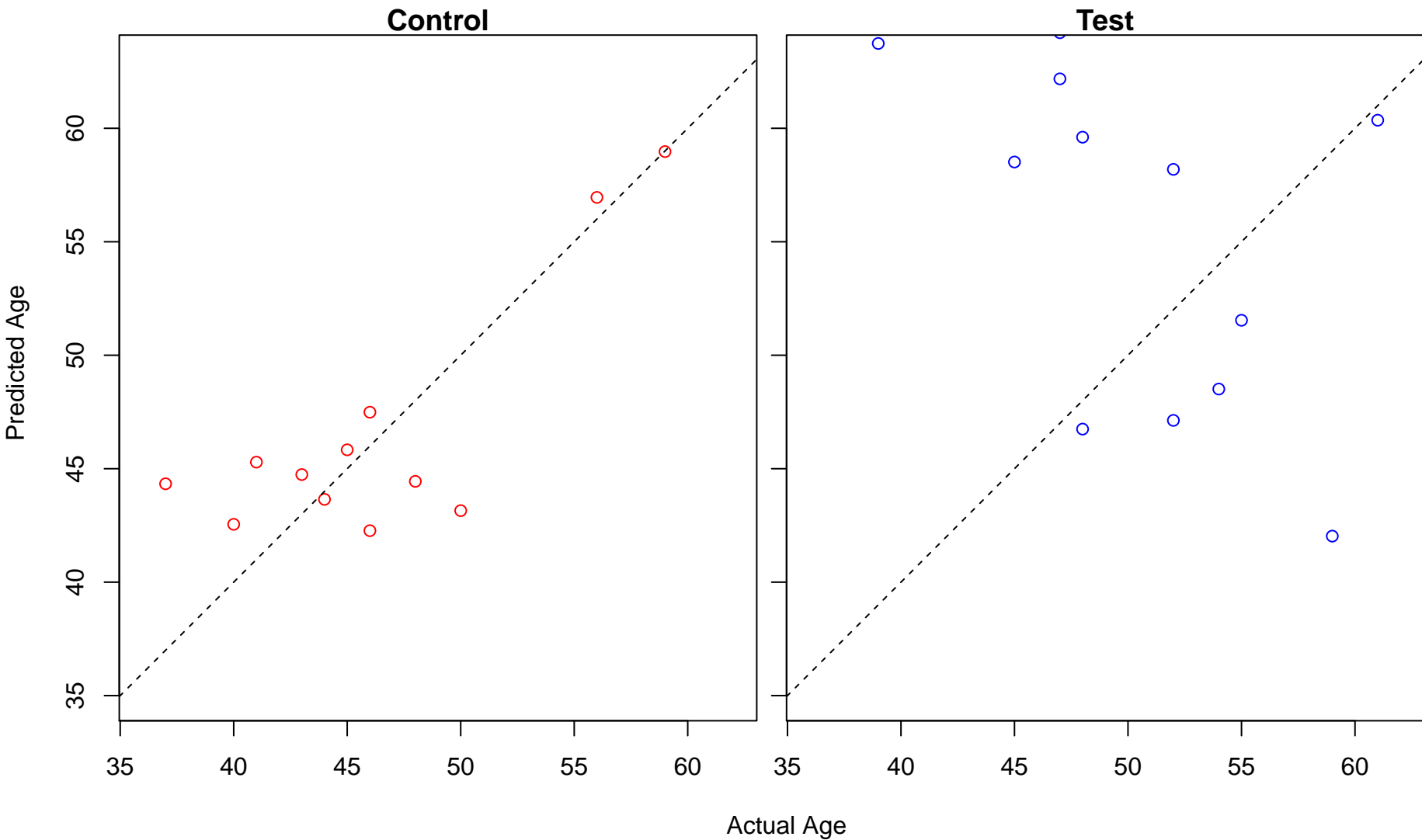
midbrain development (Score: 6.004761)



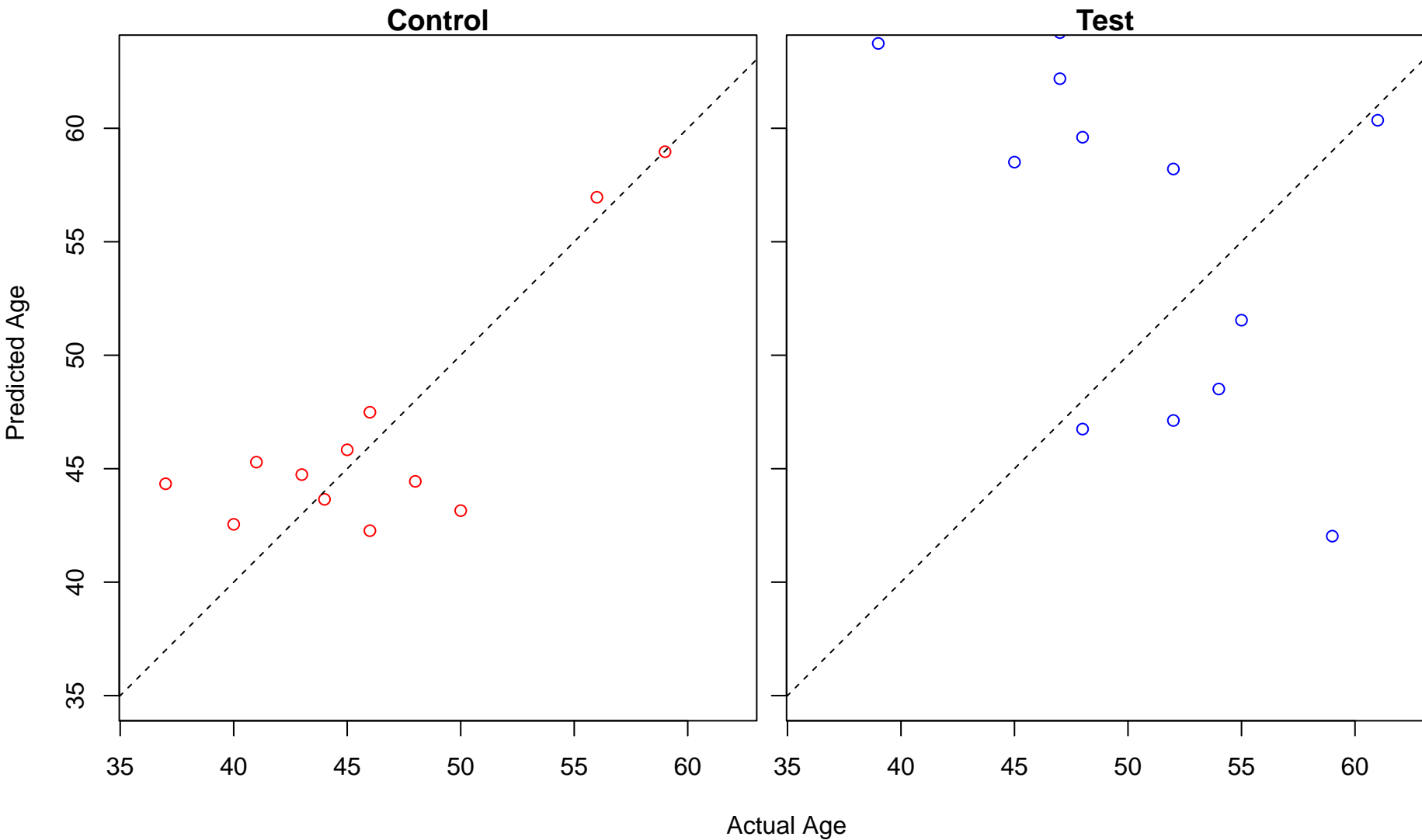
regulation of viral process (Score: 6.001621)



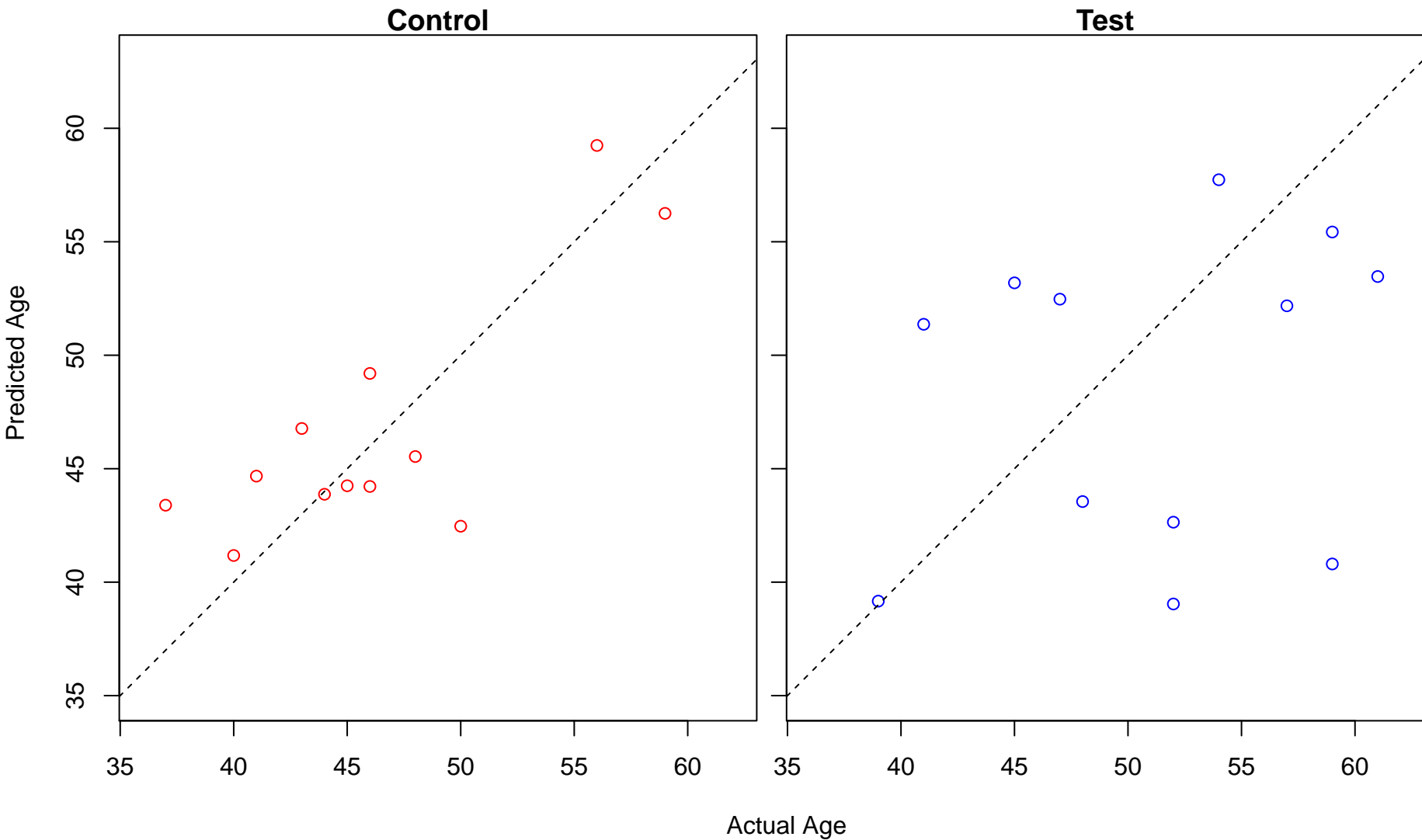
regulation of ubiquitin–protein transferase activity (Score: 5.994195)



regulation of ligase activity (Score: 5.994105)

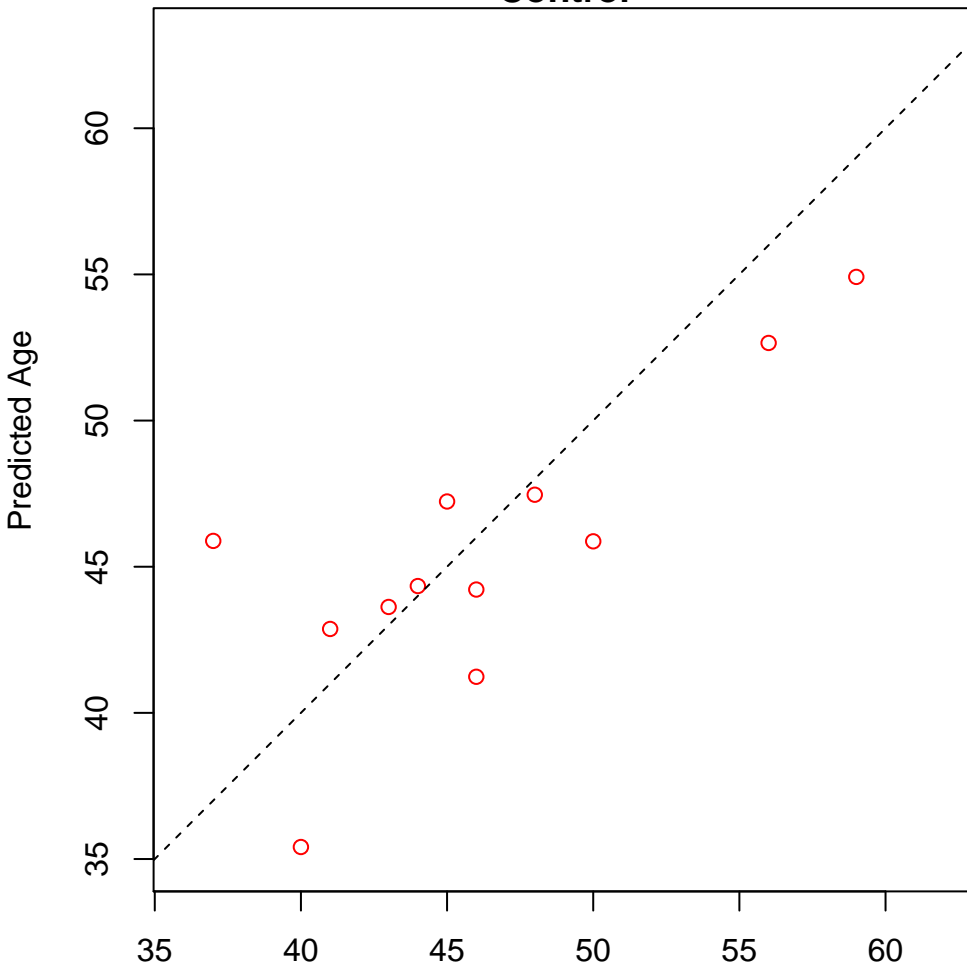


positive regulation of mRNA catabolic process (Score: 5.986469)

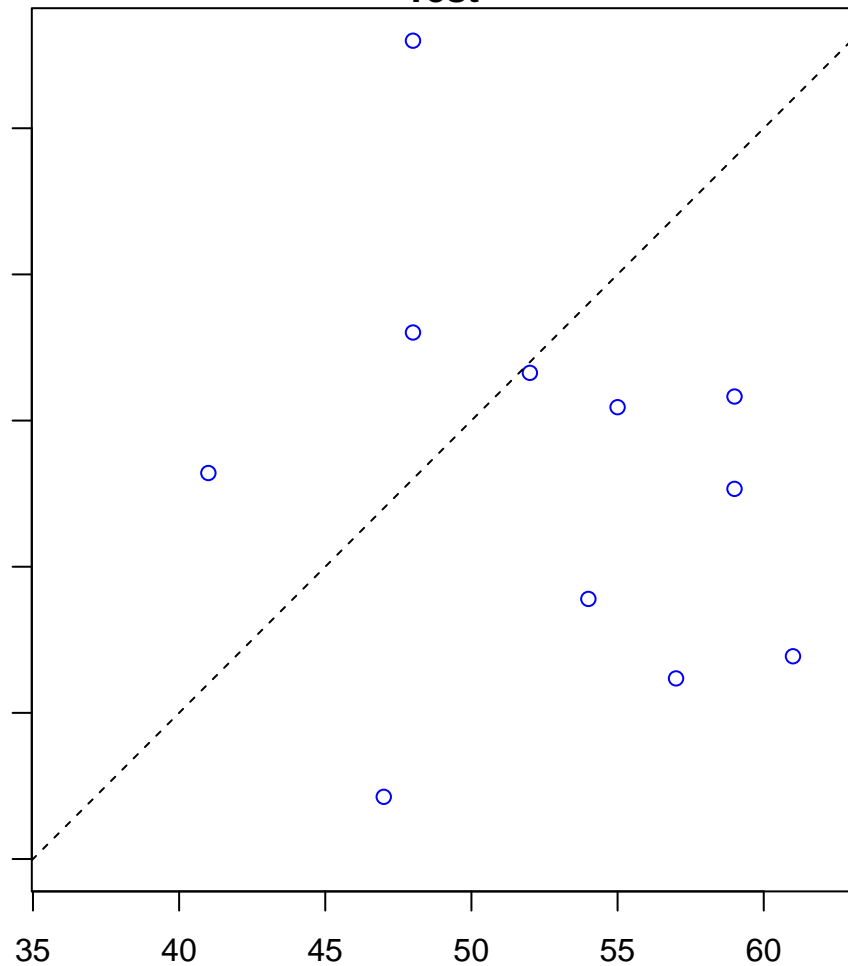


placenta blood vessel development (Score: 5.985246)

Control

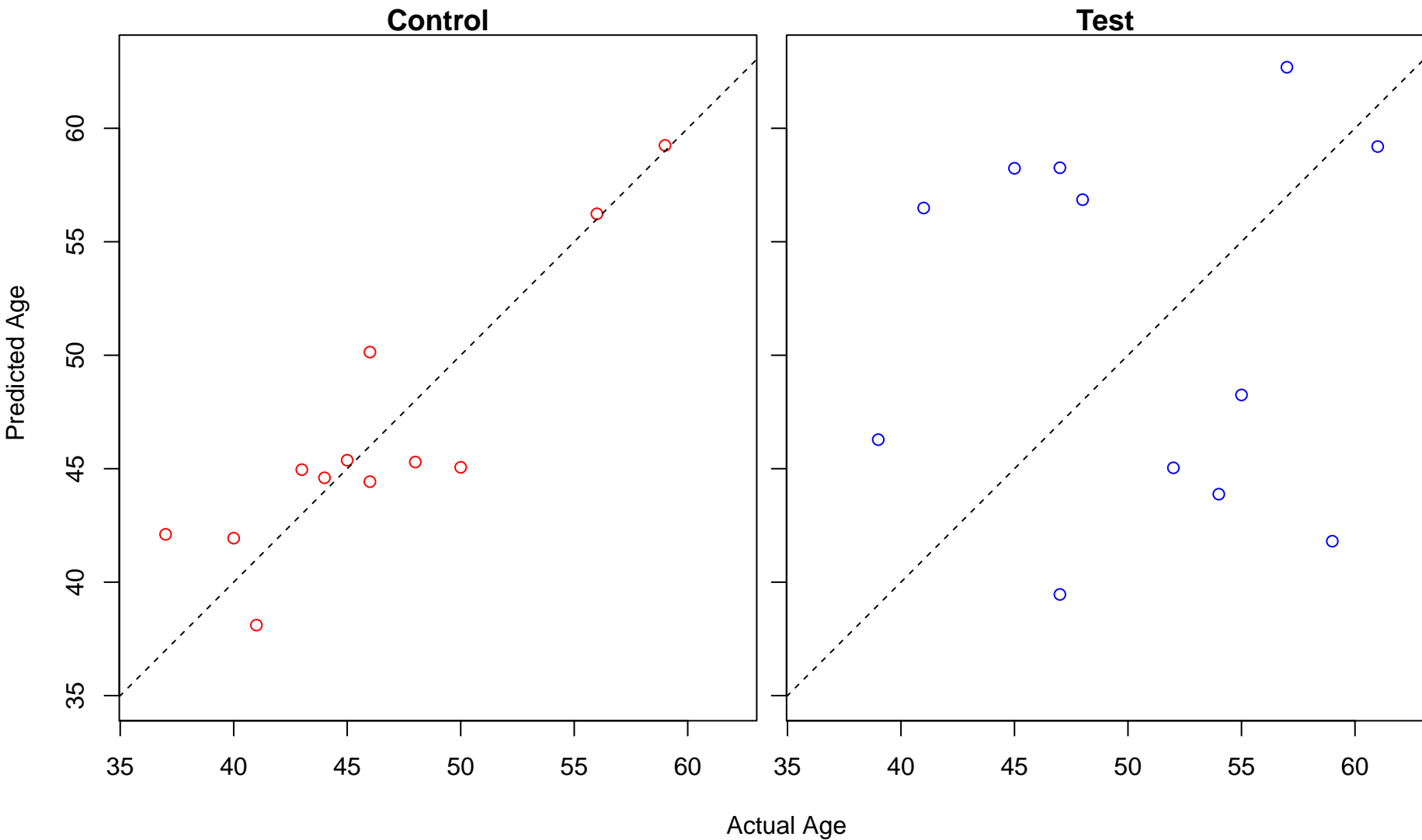


Test

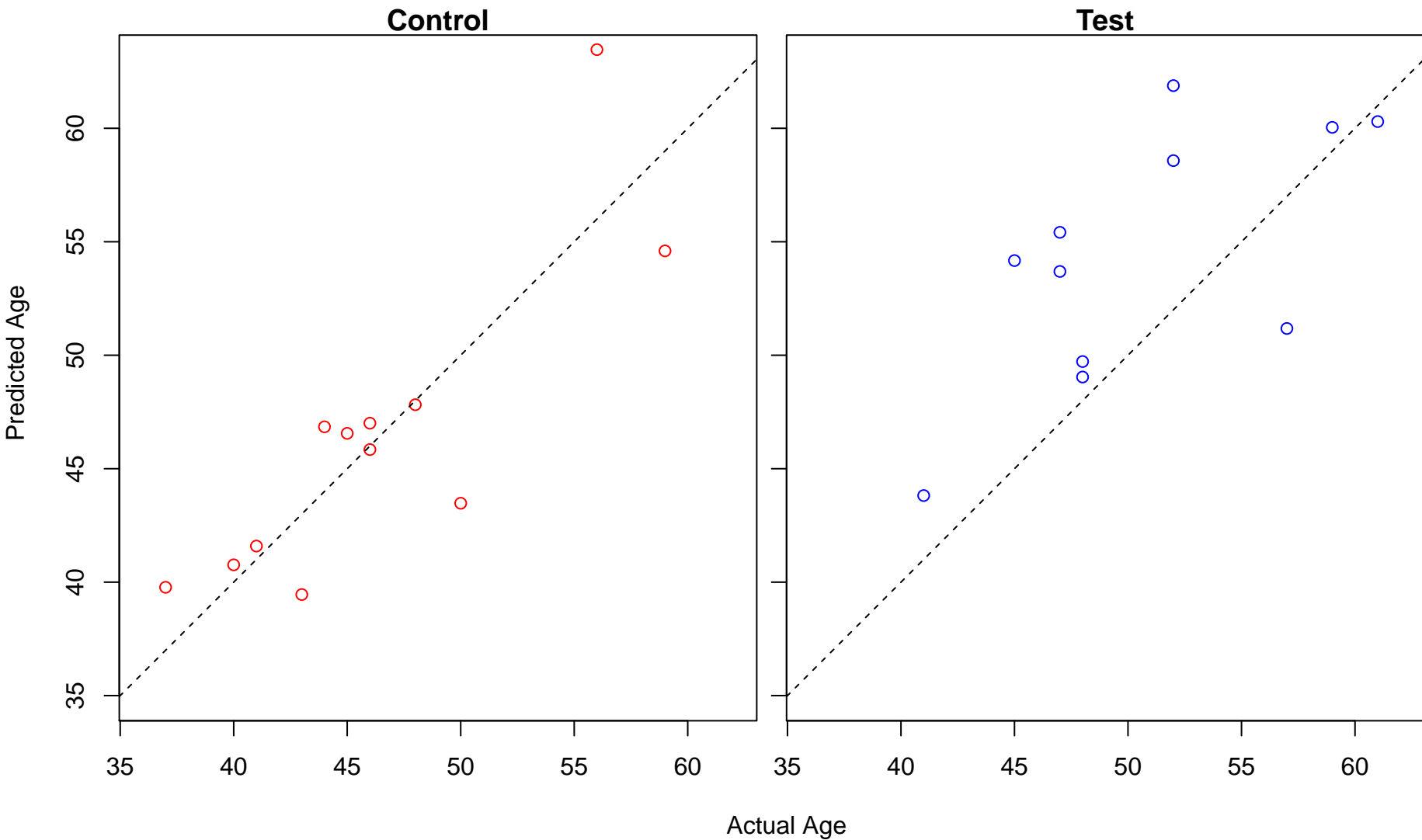


Actual Age

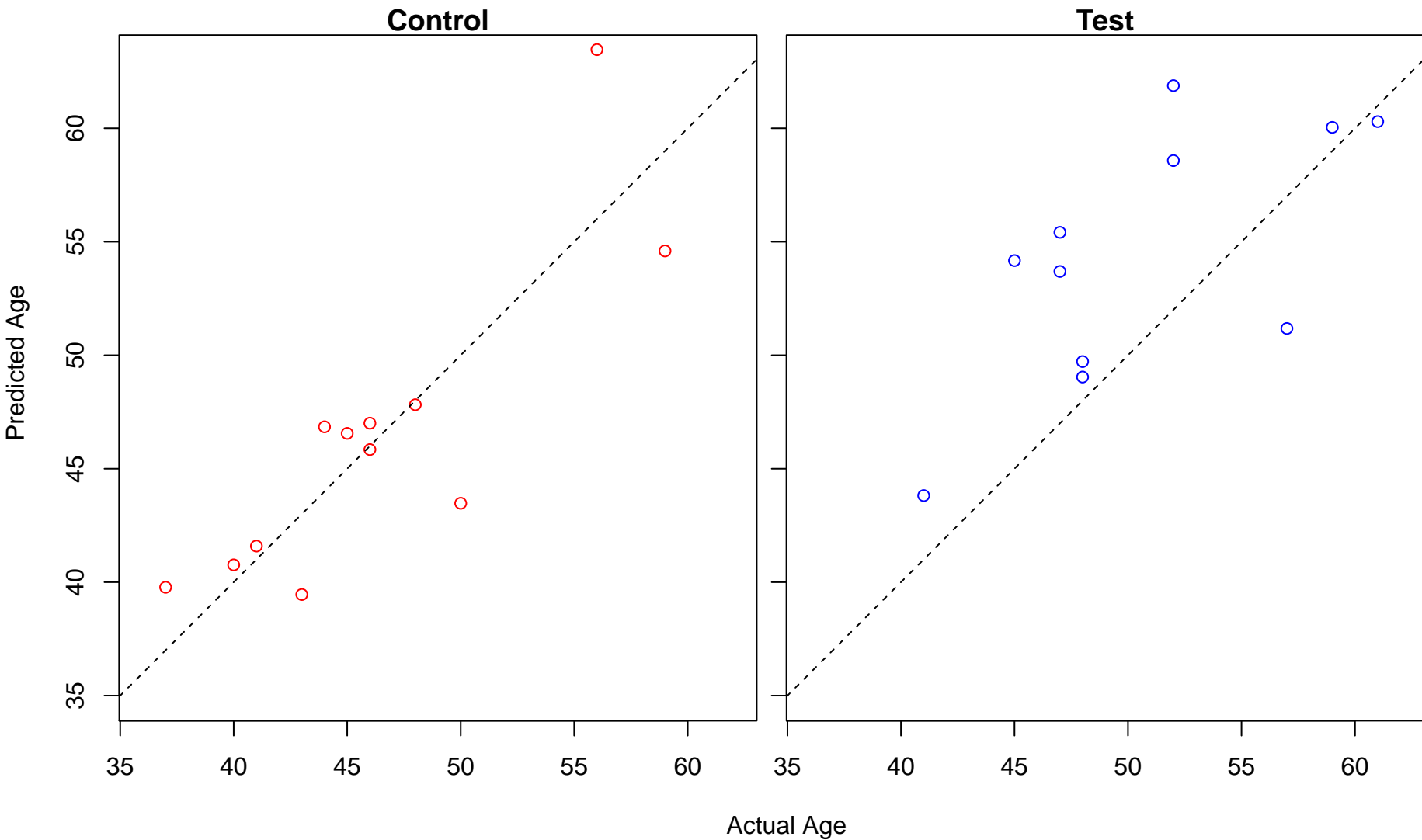
vasculogenesis (Score: 5.984993)



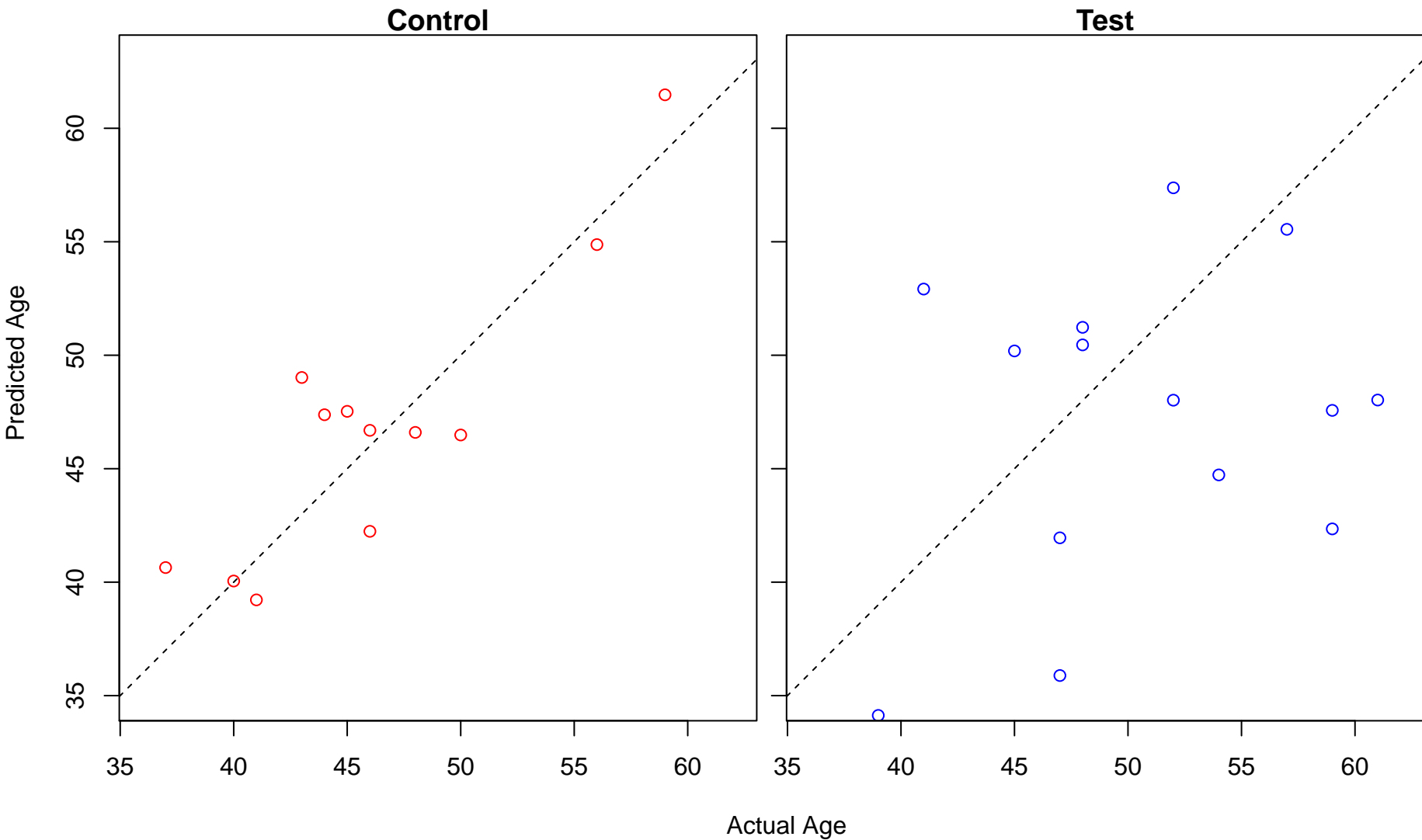
antigen processing and presentation of endogenous peptide antigen (Score: 5.978708)



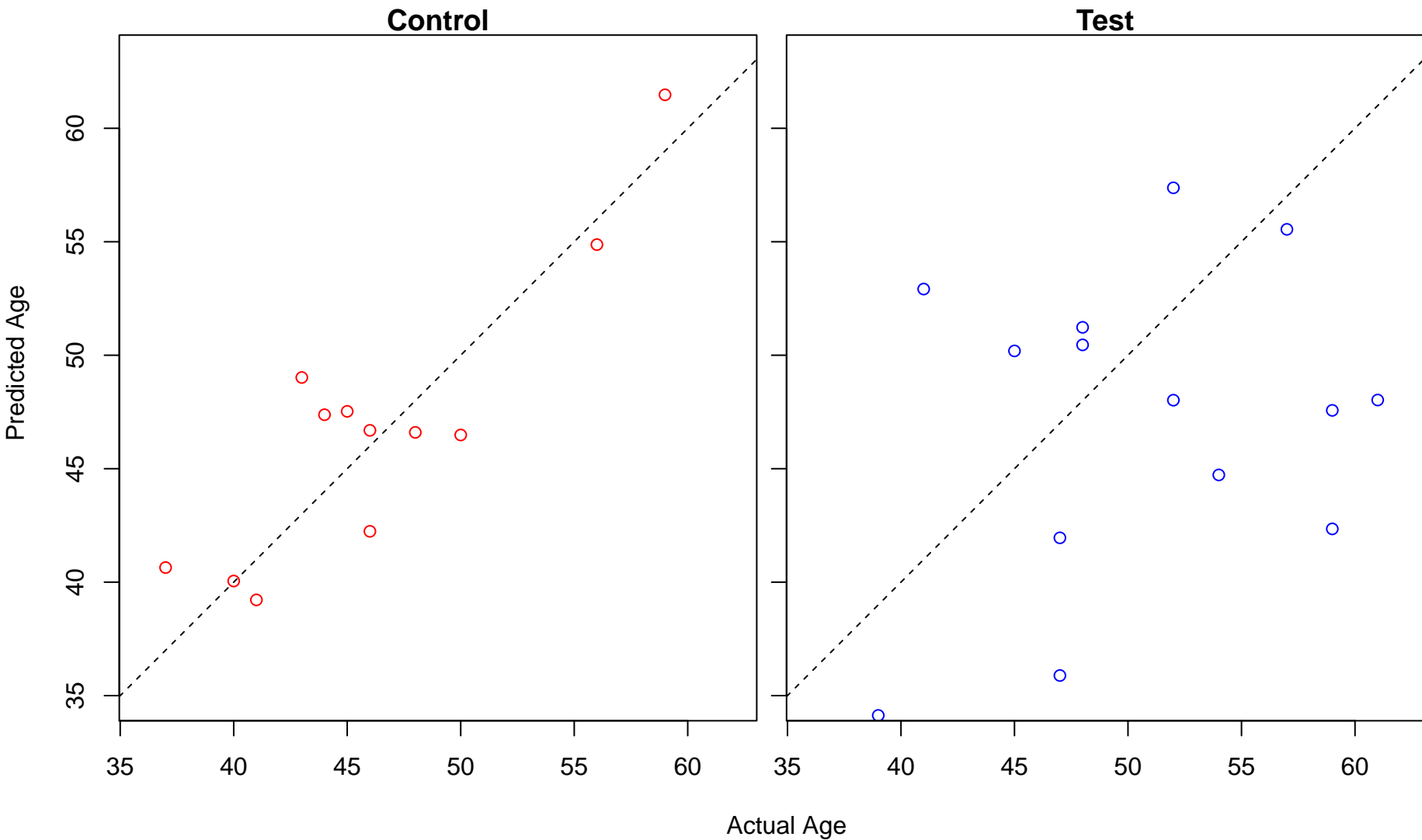
antigen processing and presentation of endogenous antigen (Score: 5.977756)



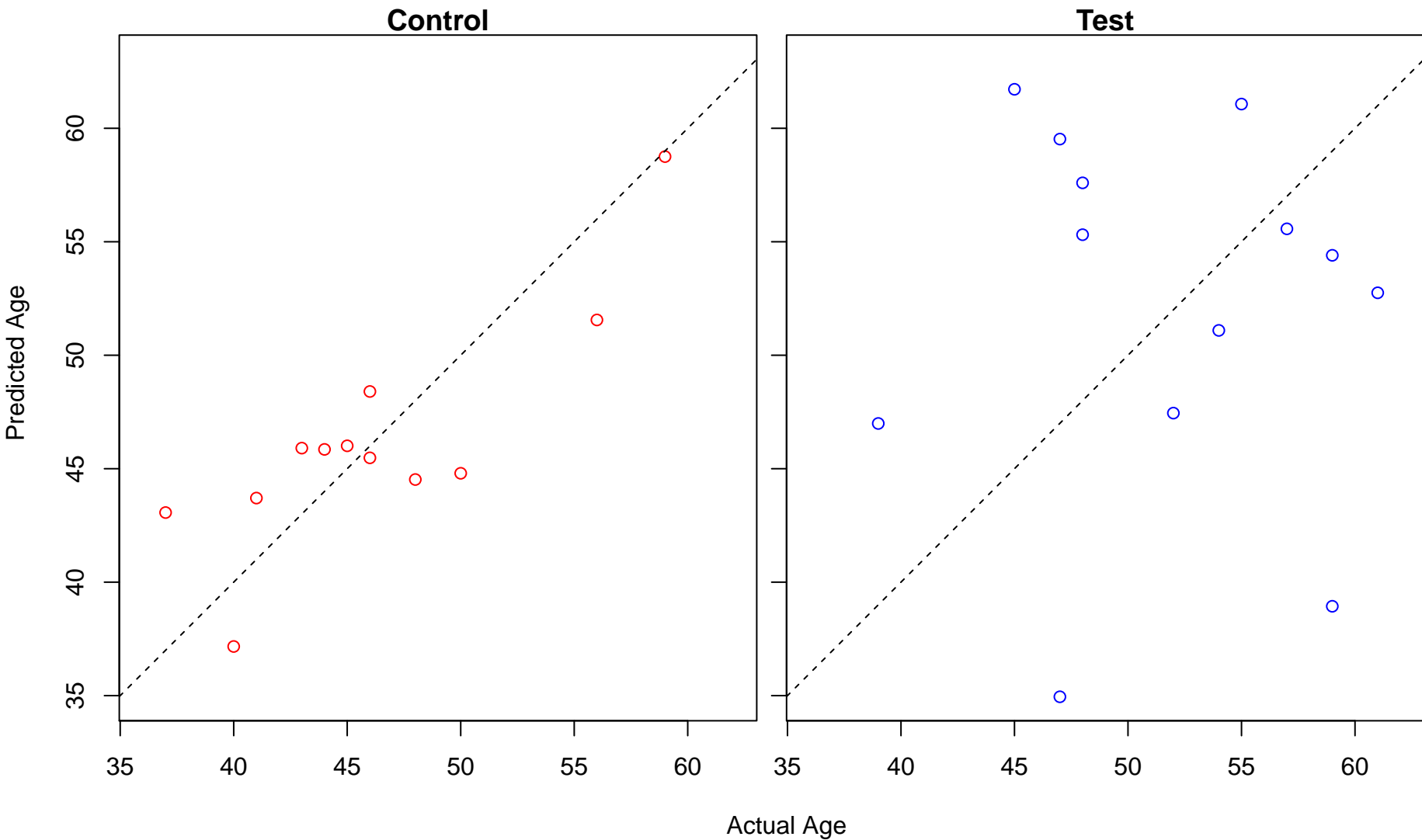
growth hormone receptor signaling pathway (Score: 5.973337)



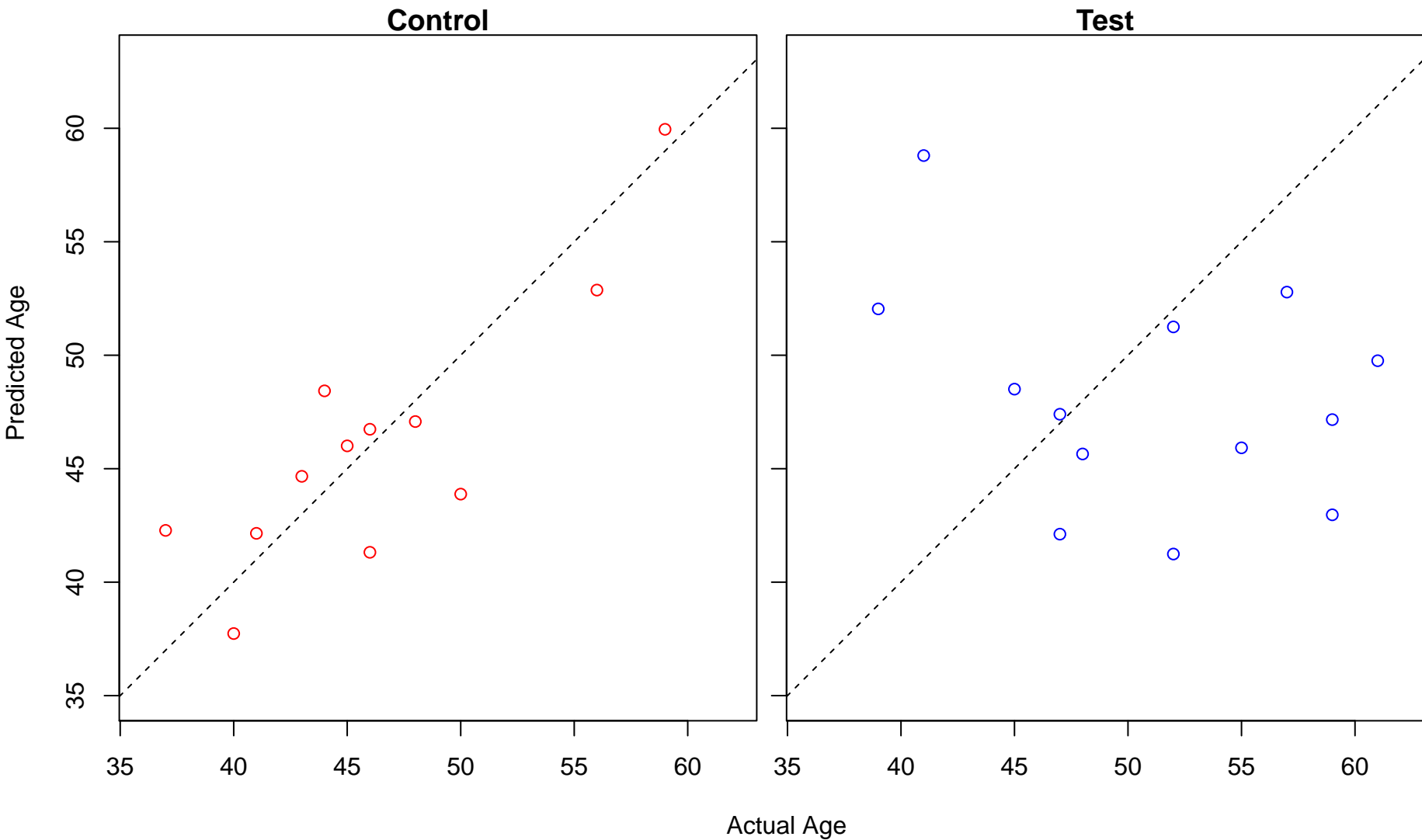
cellular response to growth hormone stimulus (Score: 5.973337)



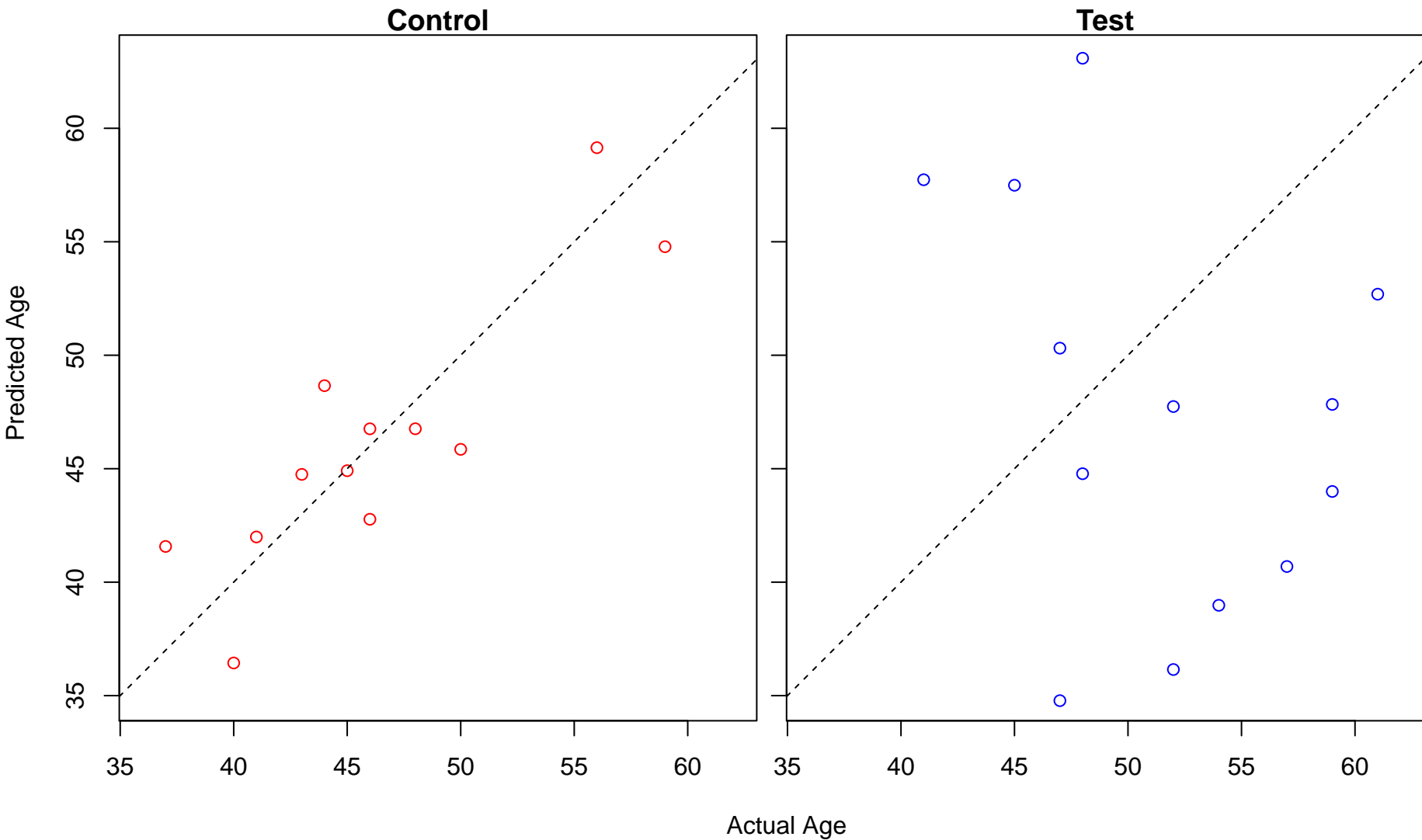
lung alveolus development (Score: 5.946783)



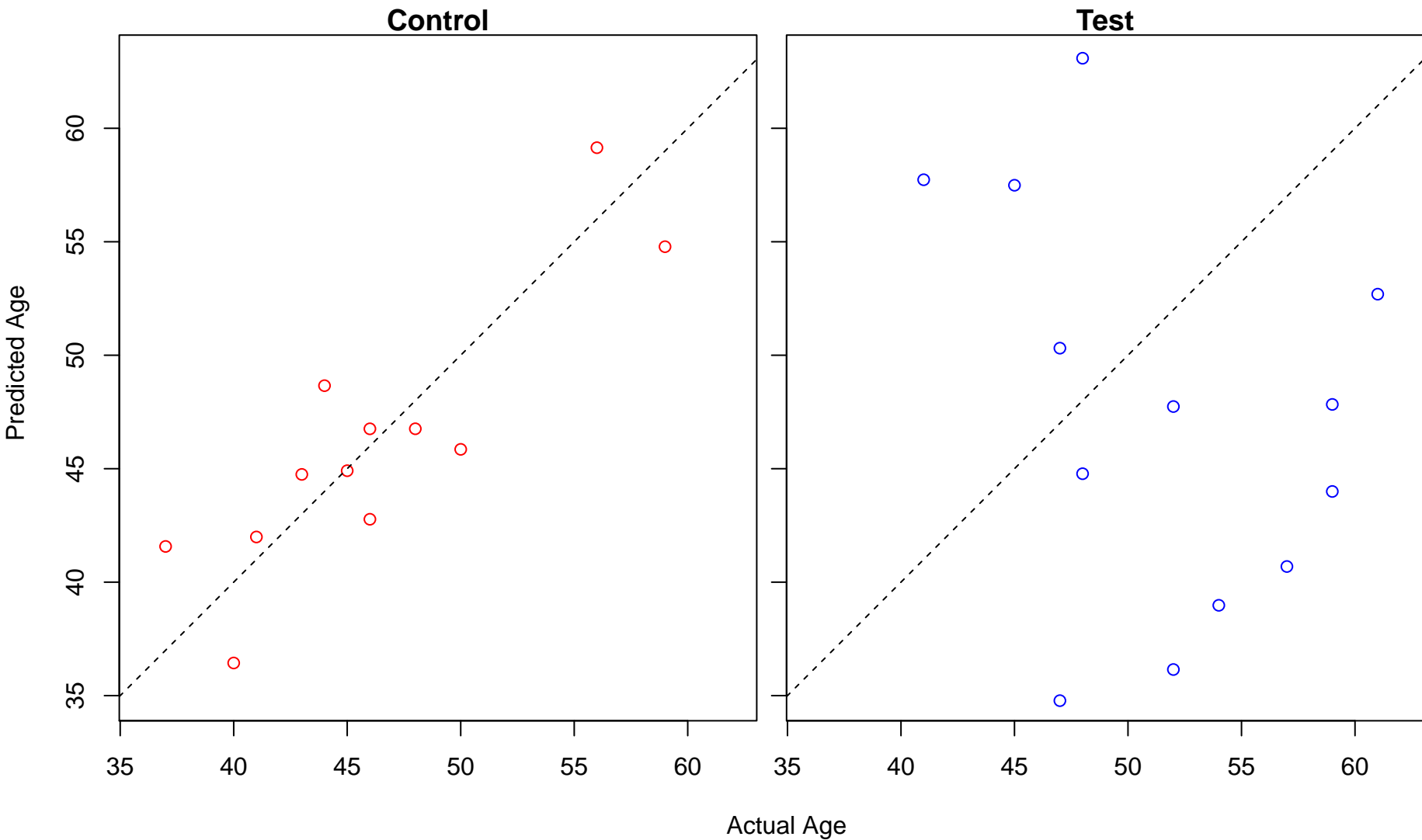
positive regulation of DNA metabolic process (Score: 5.934748)



regulation of protein localization to plasma membrane (Score: 5.929485)

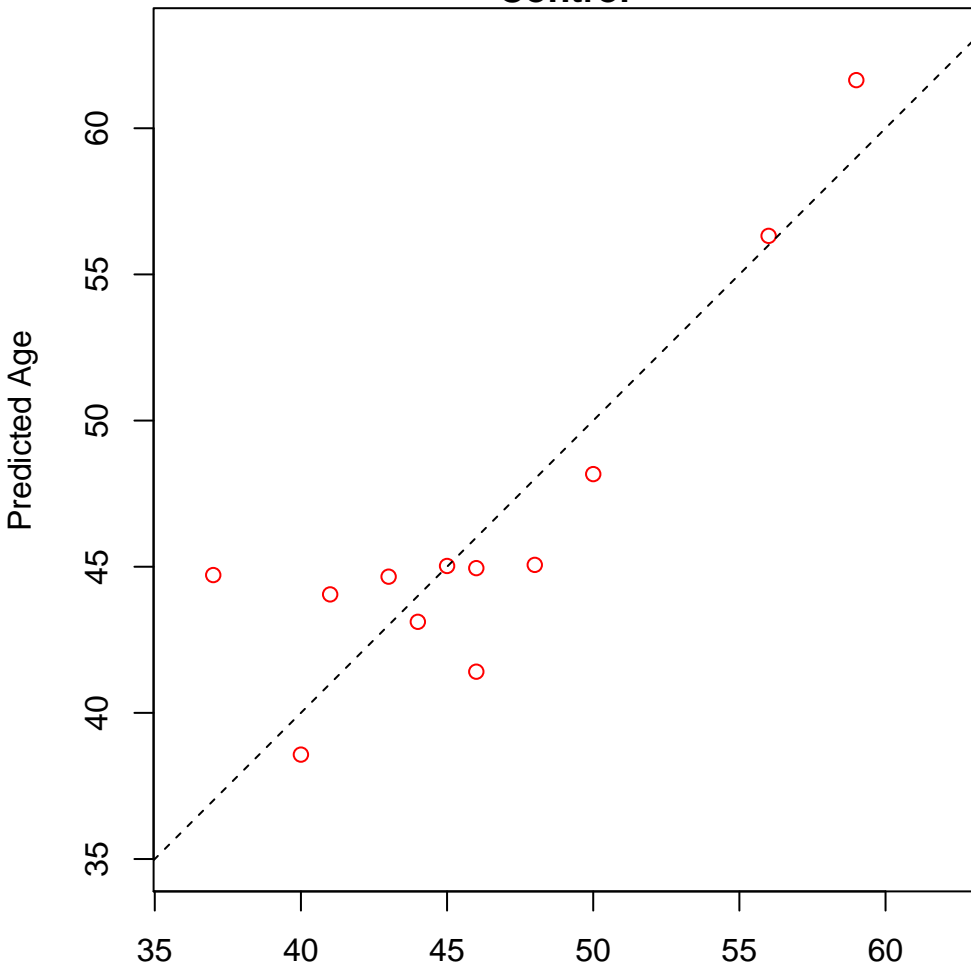


regulation of protein localization to cell periphery (Score: 5.929485)

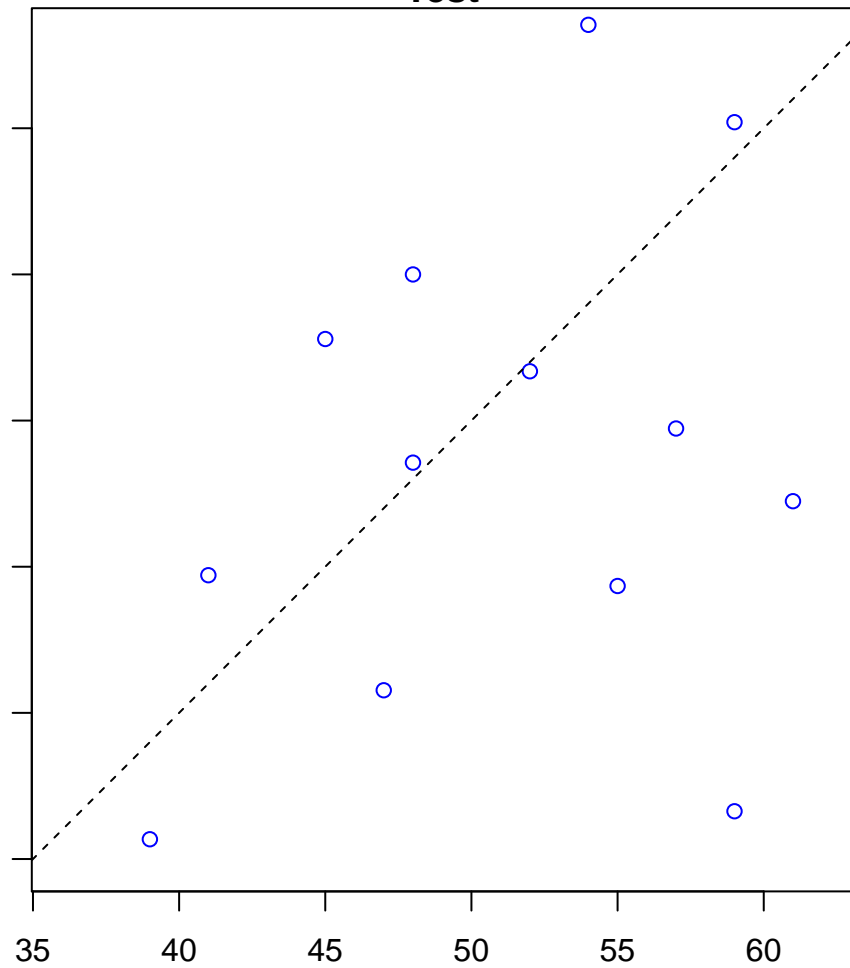


ATP-dependent chromatin remodeling (Score: 5.925304)

Control

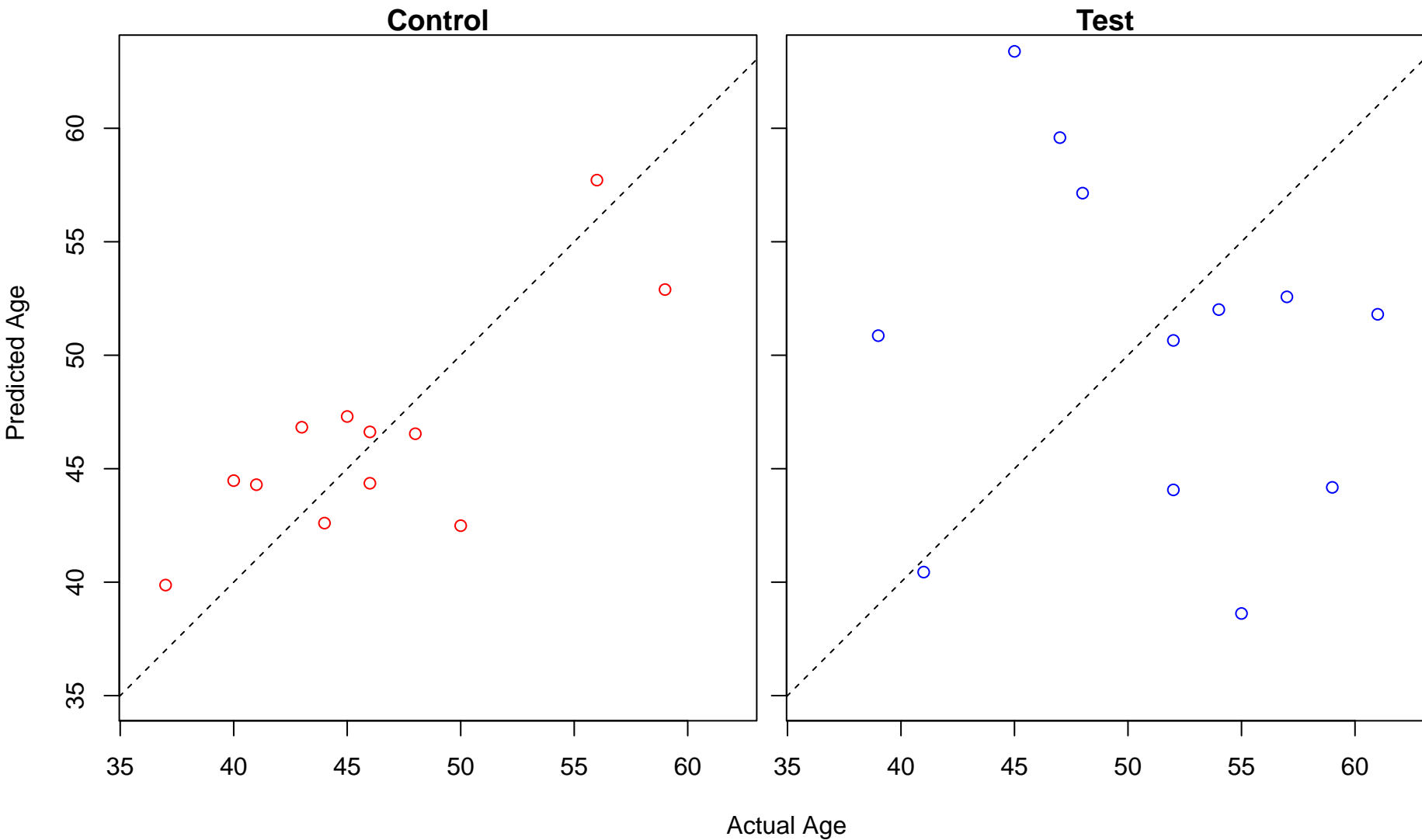


Test

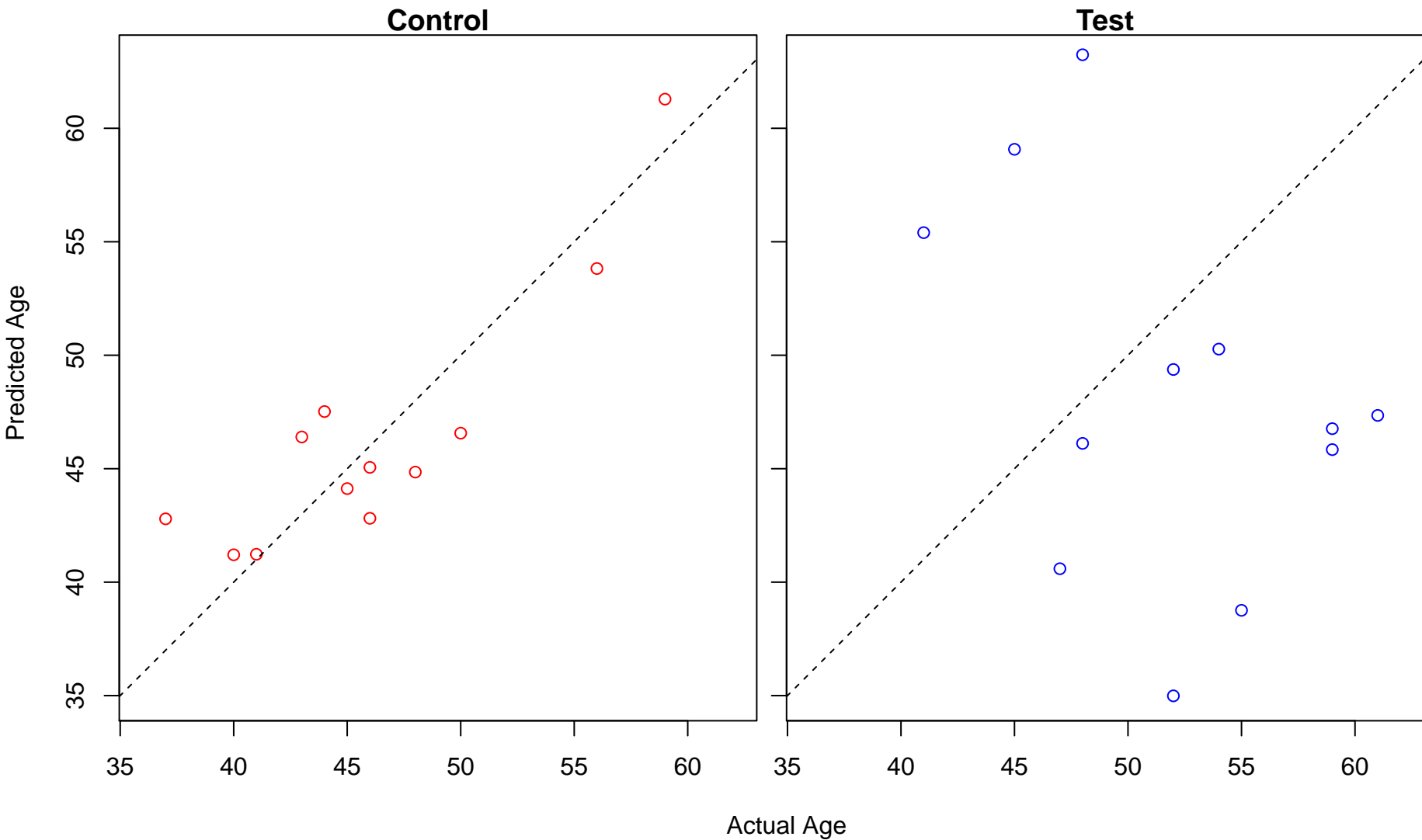


Actual Age

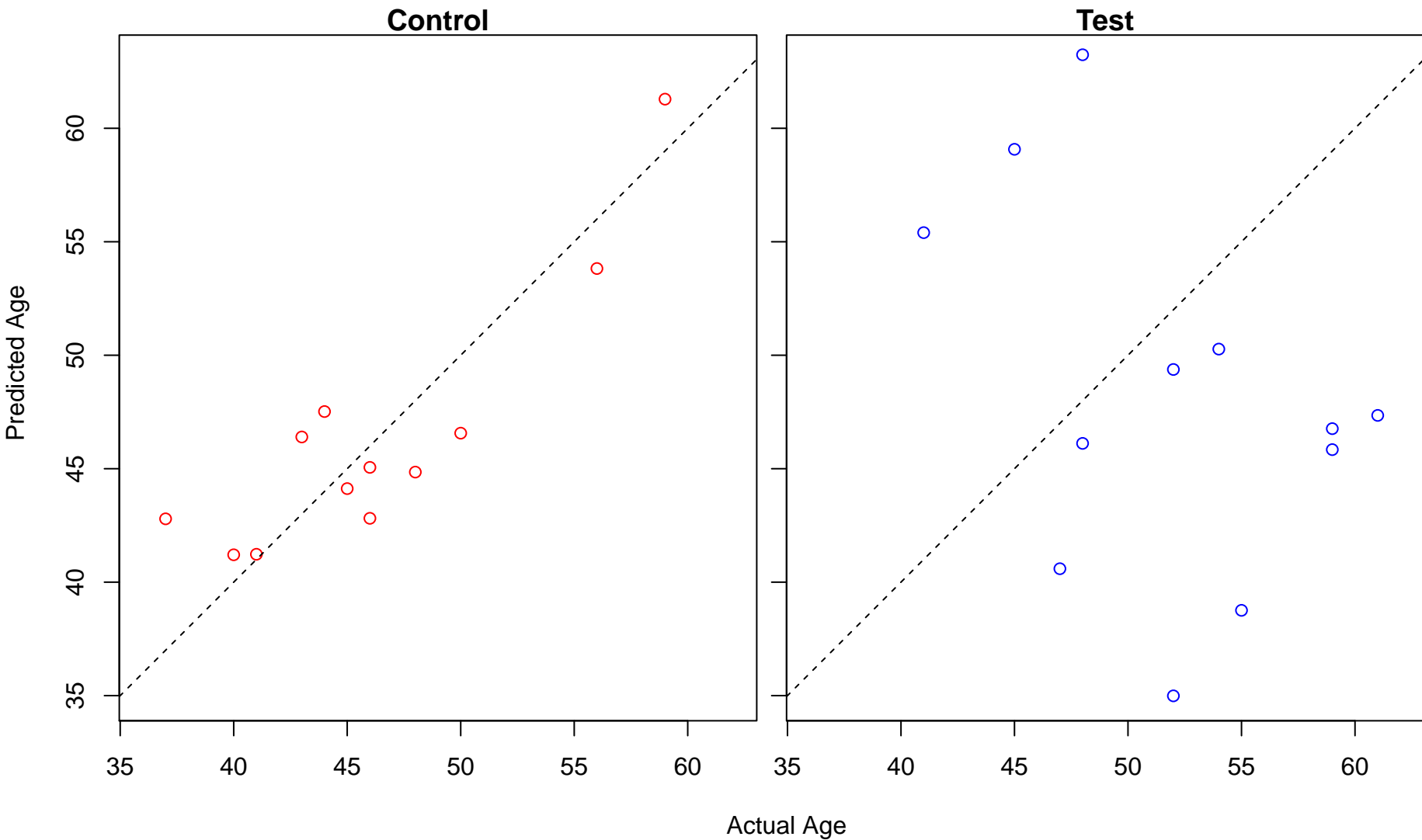
negative regulation of humoral immune response (Score: 5.914444)



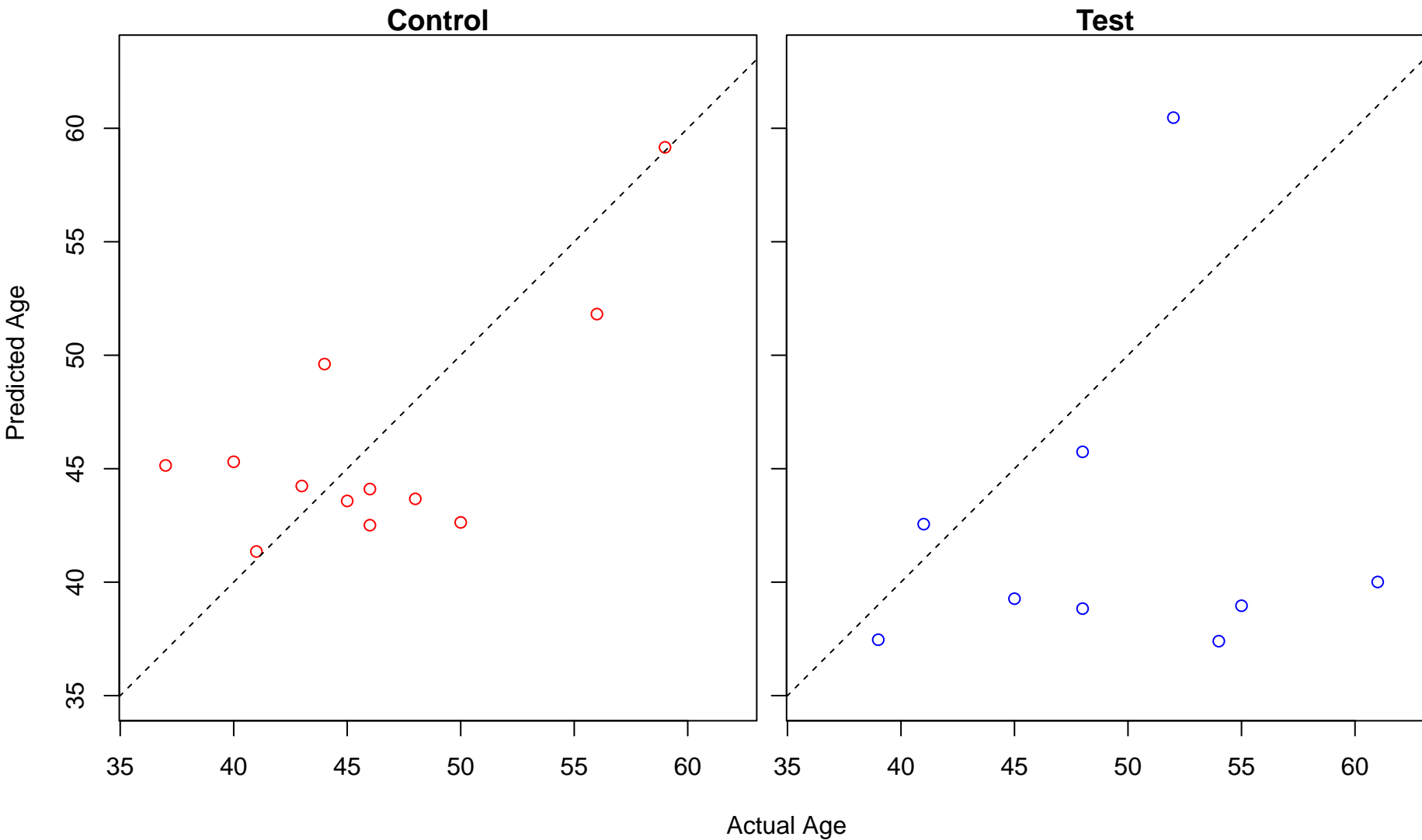
blood circulation (Score: 5.906936)



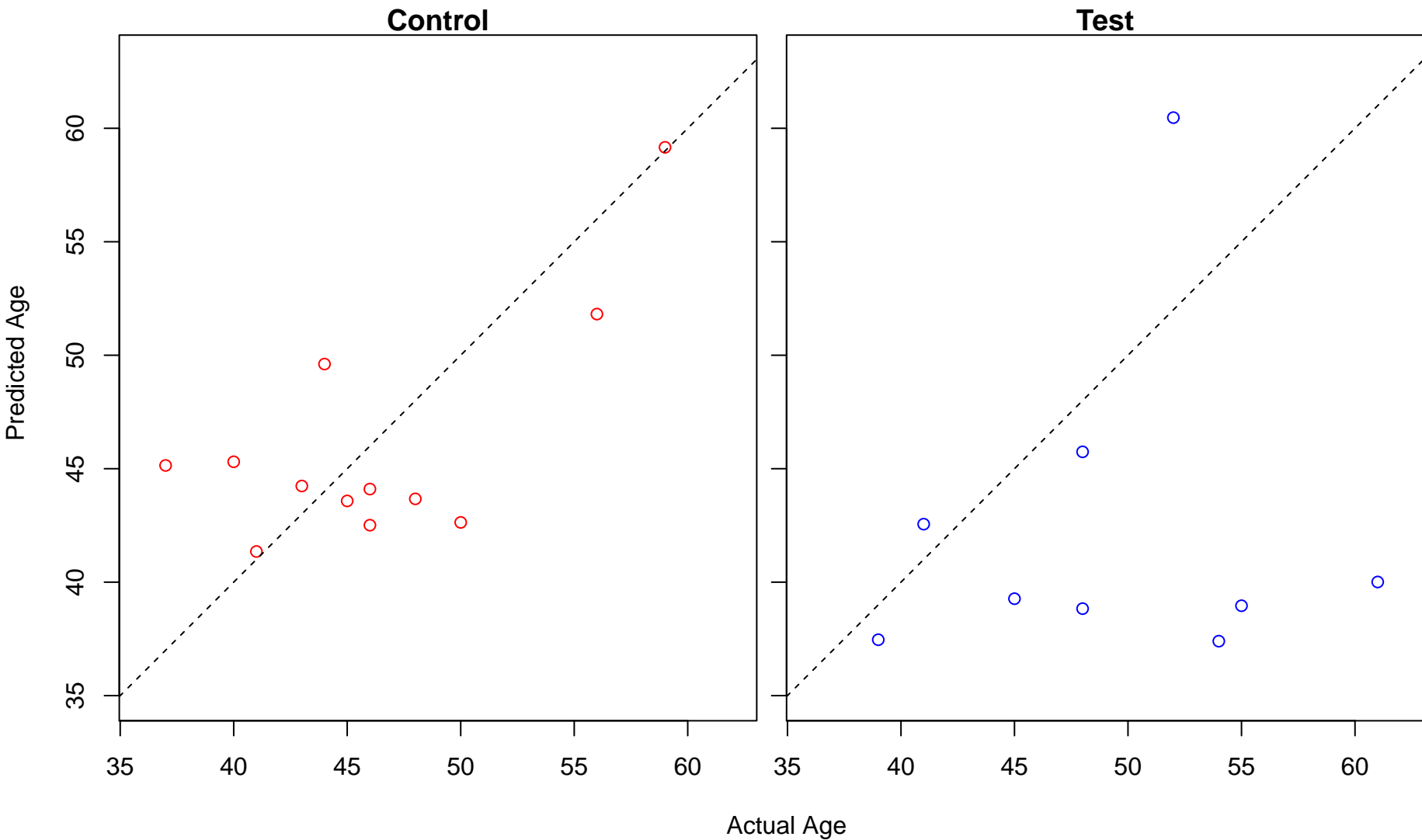
circulatory system process (Score: 5.906900)



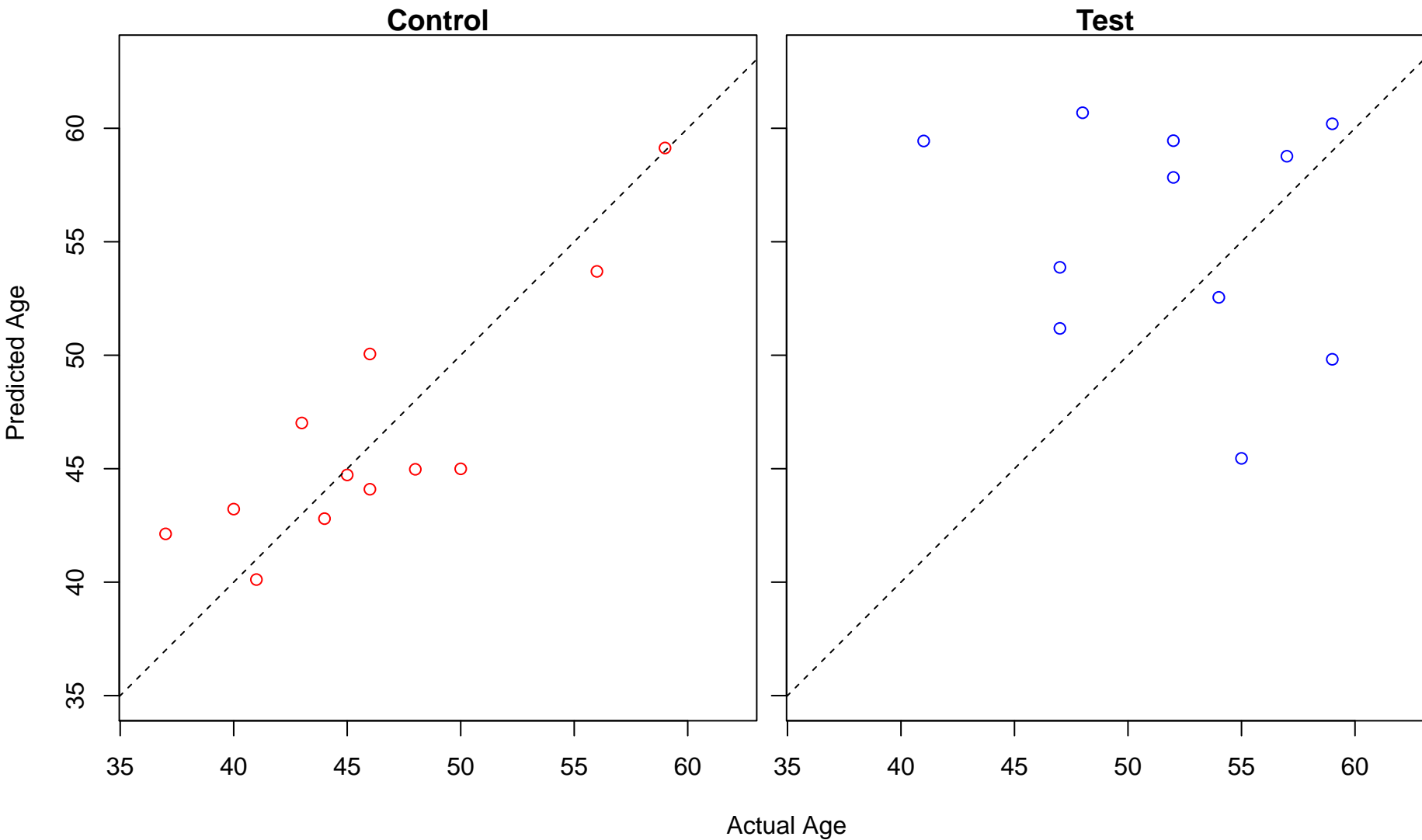
immune response–inhibiting signal transduction (Score: 5.892443)



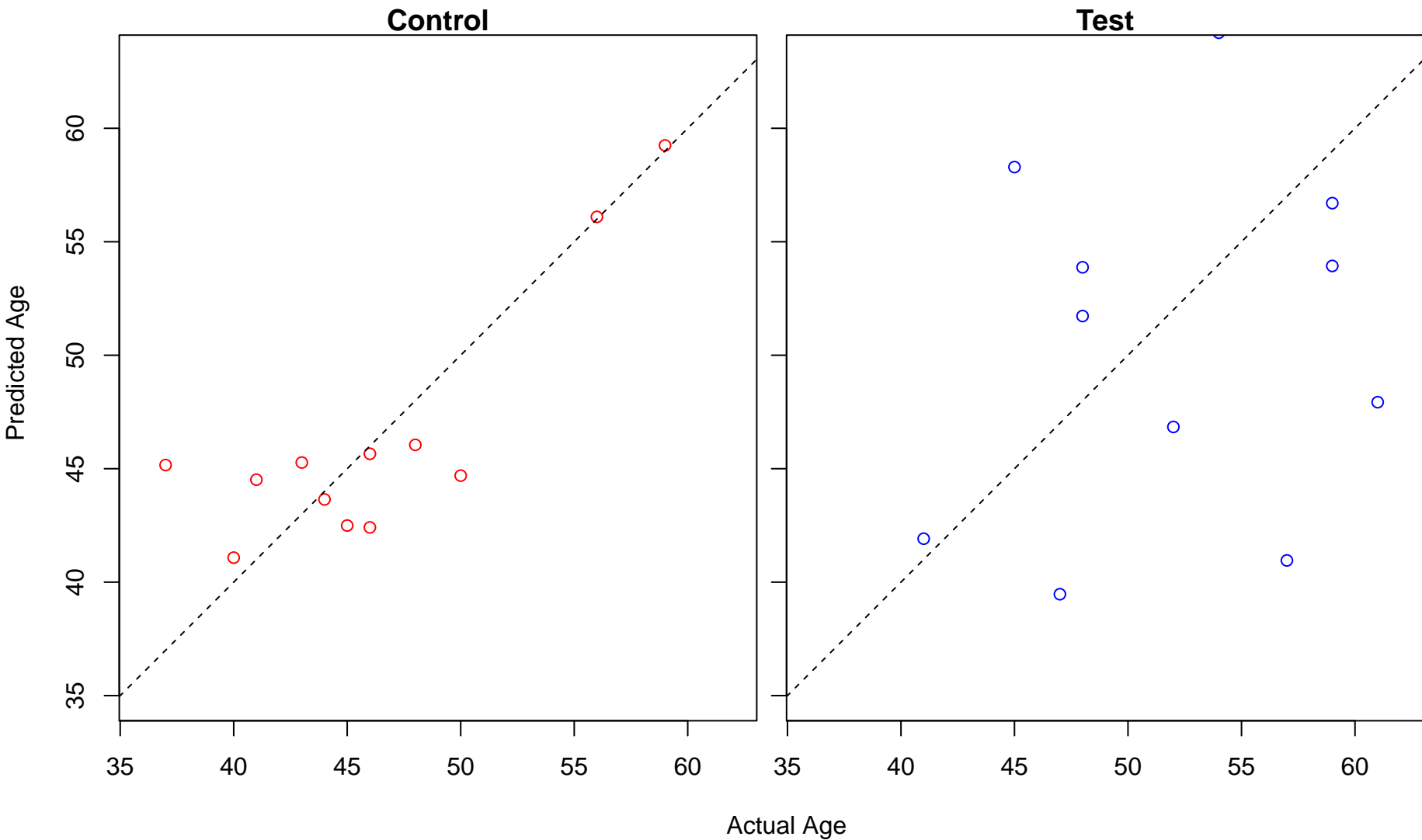
immune response–inhibiting cell surface receptor signaling pathway (Score: 5.892443)



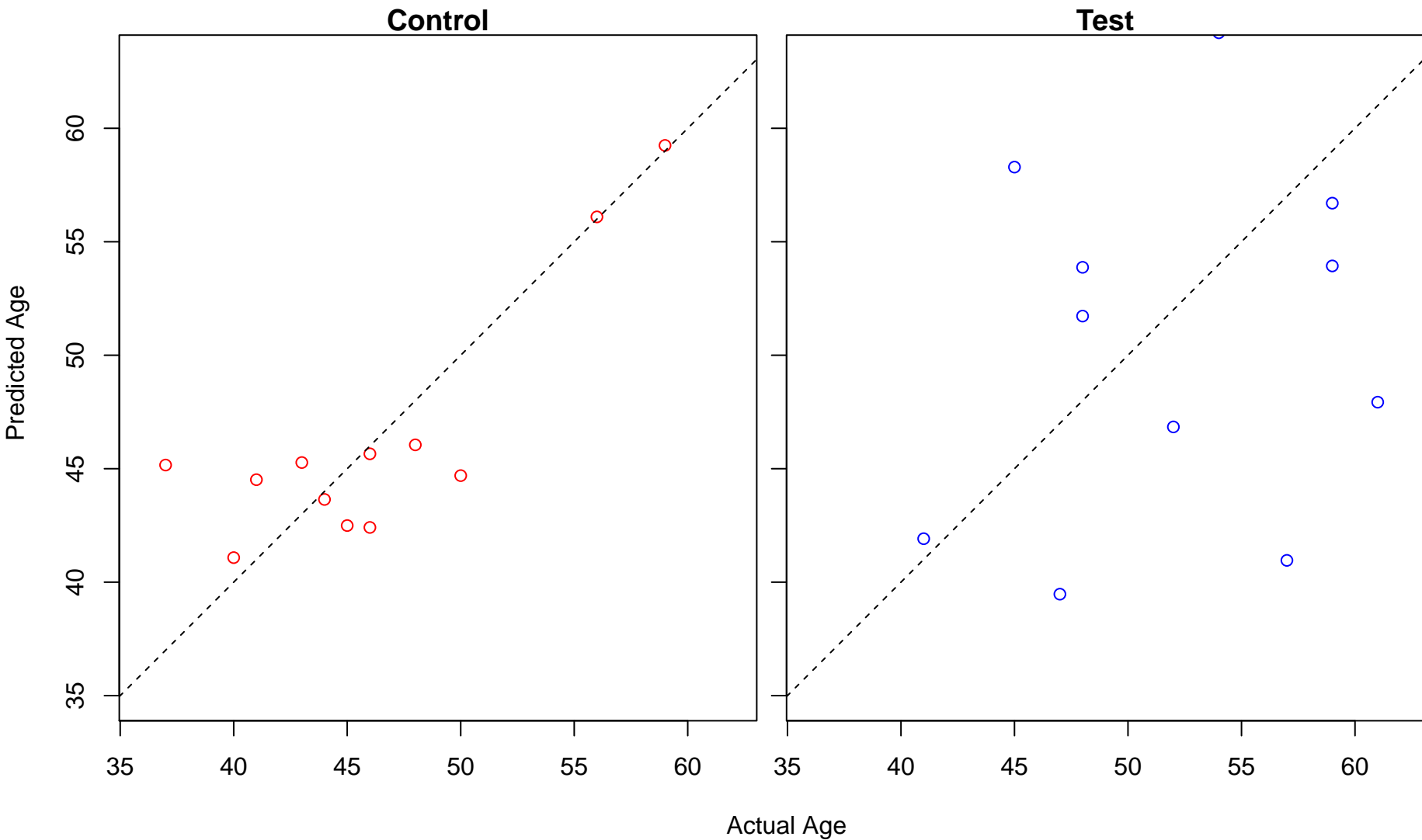
regulation of neural precursor cell proliferation (Score: 5.890796)



histone modification (Score: 5.887353)

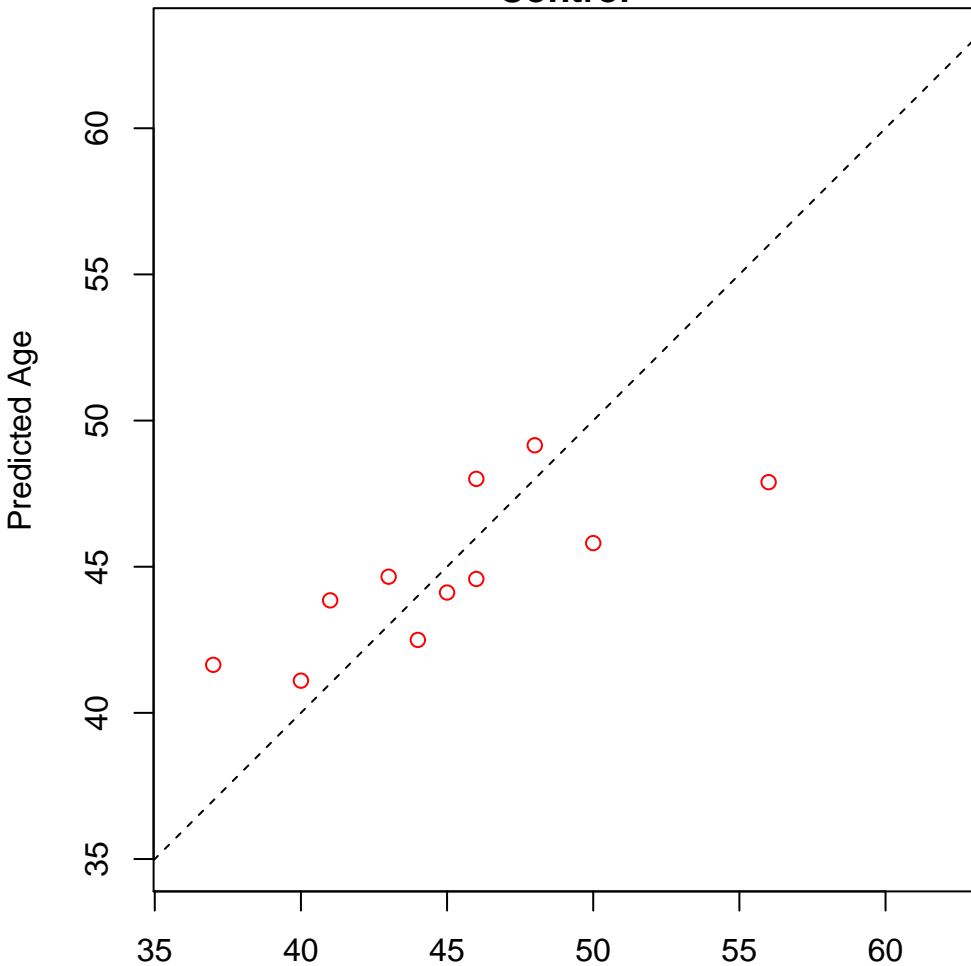


covalent chromatin modification (Score: 5.886227)

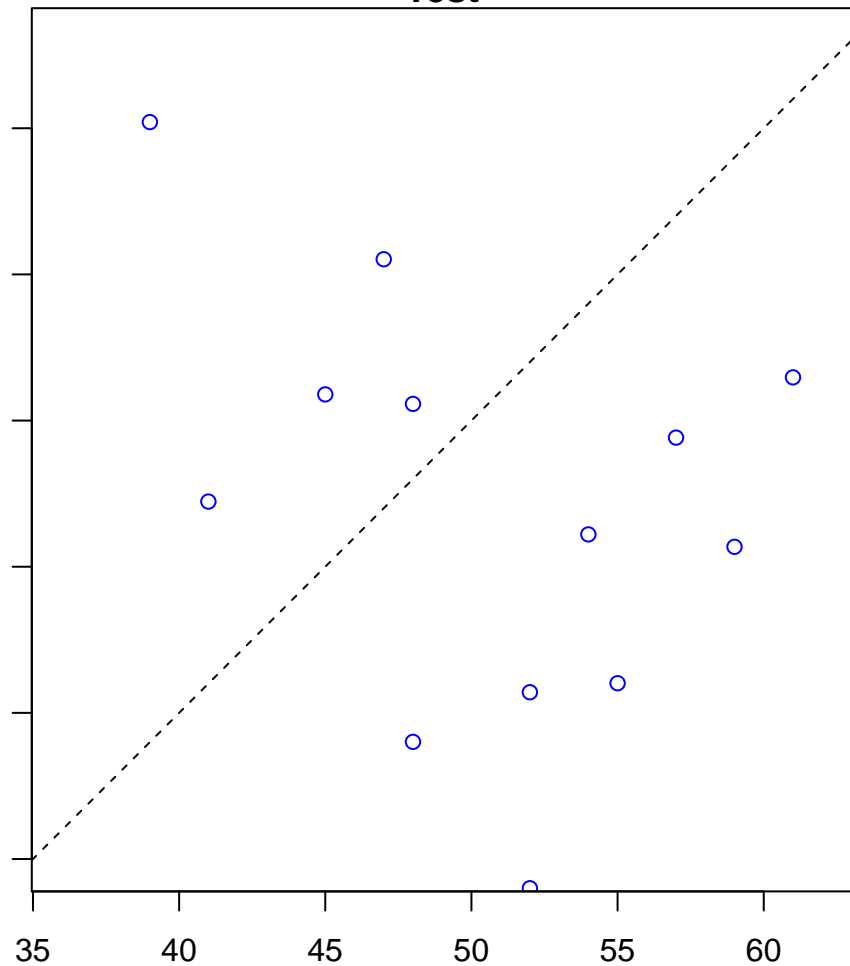


renal system vasculature development (Score: 5.875206)

Control

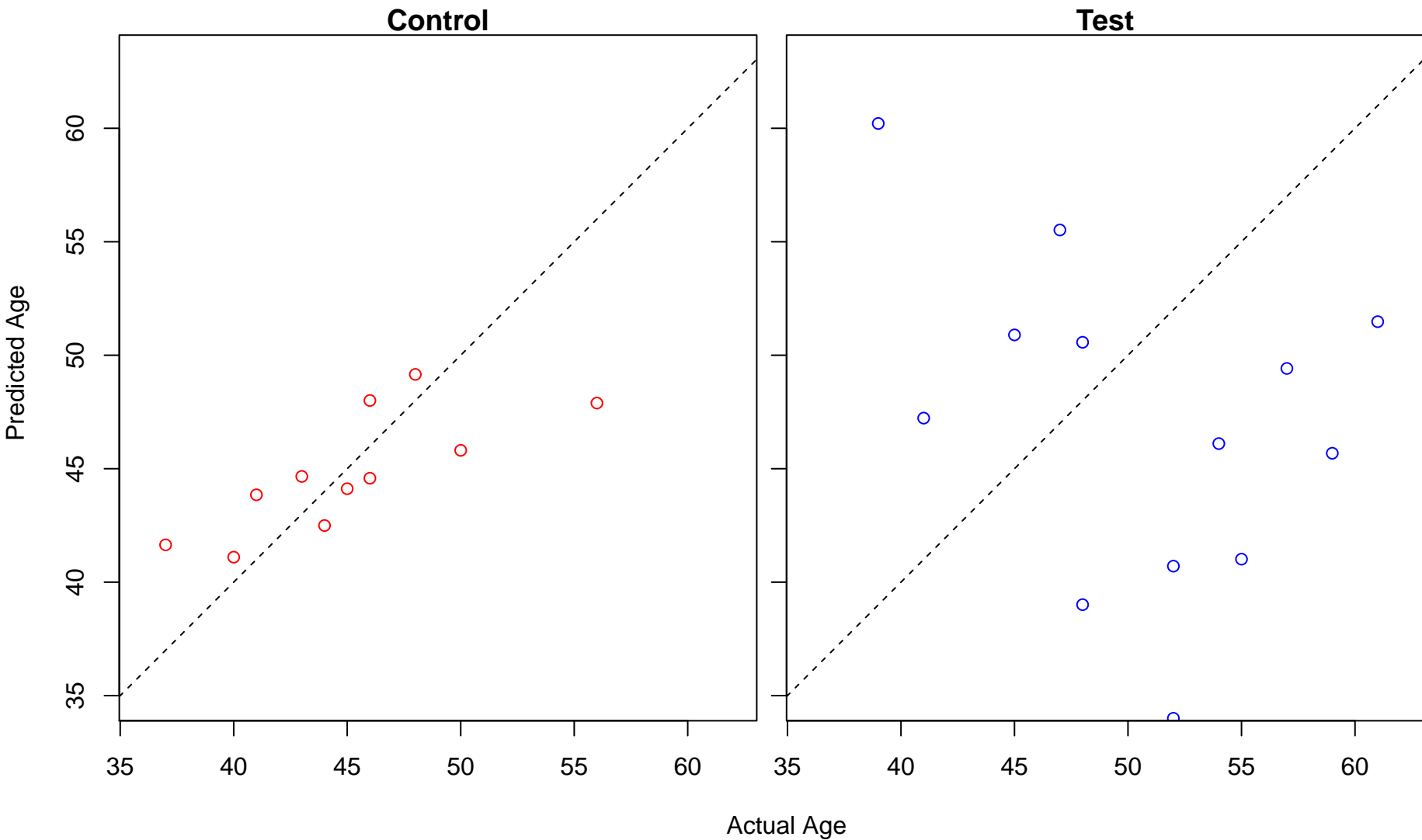


Test

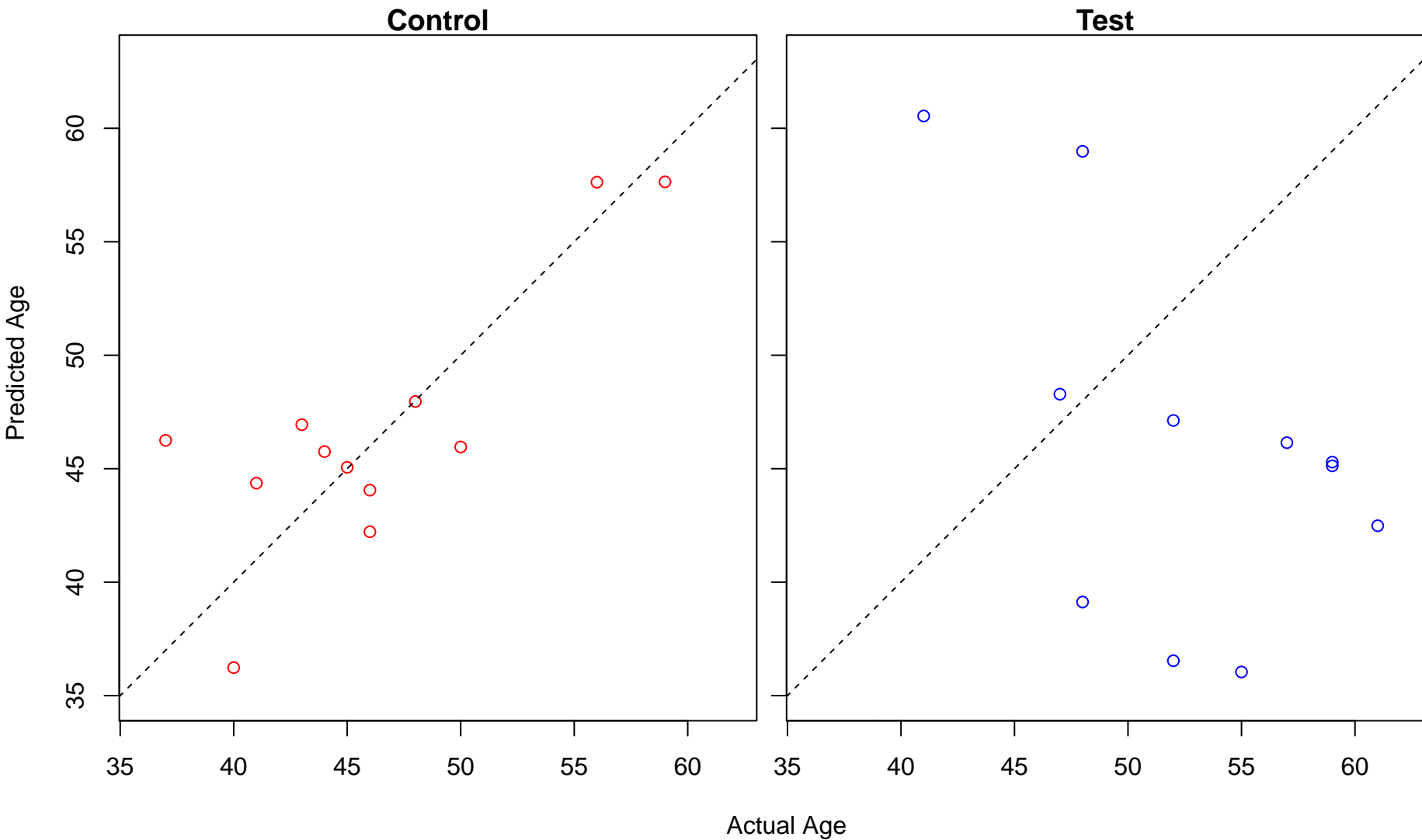


Actual Age

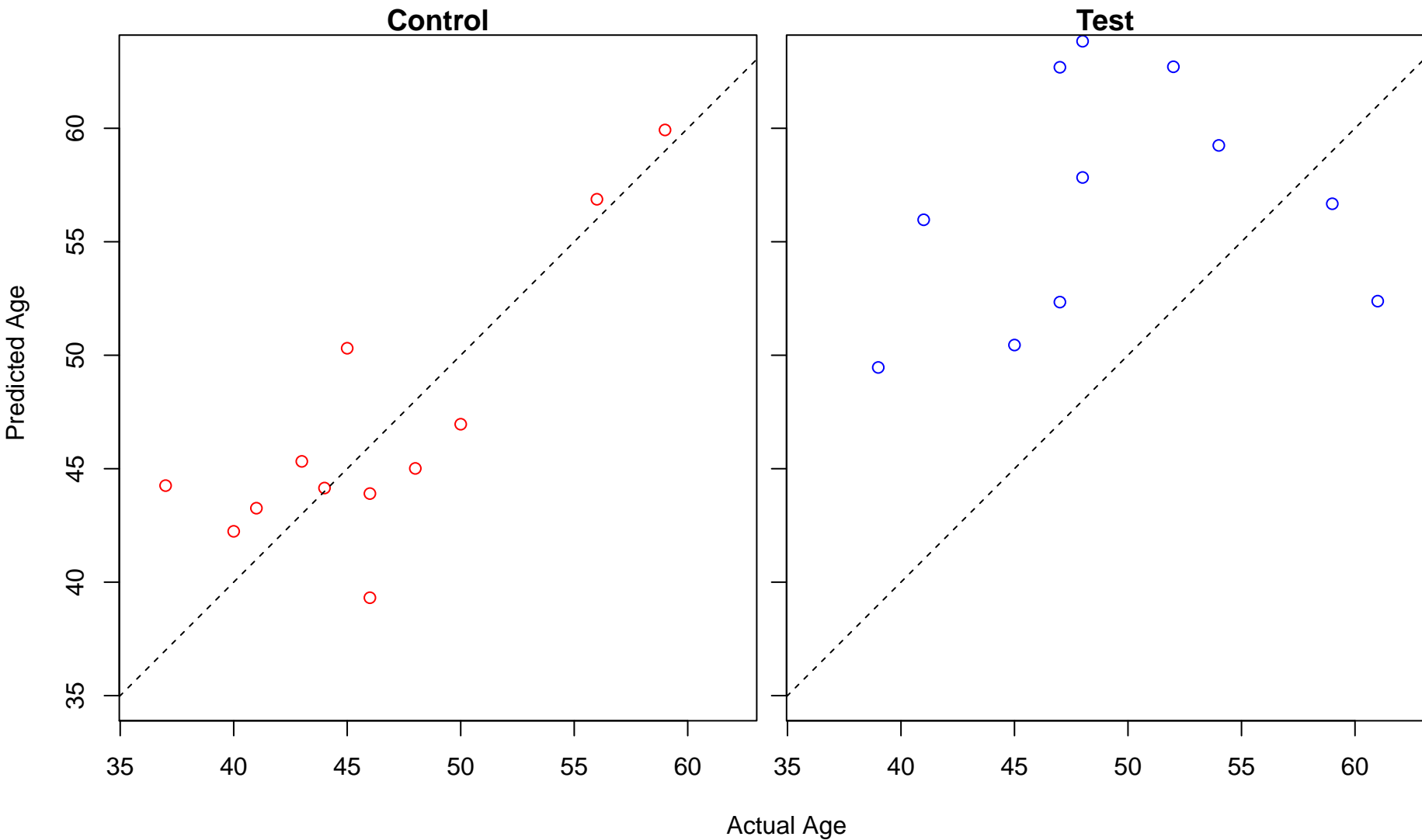
kidney vasculature development (Score: 5.875206)



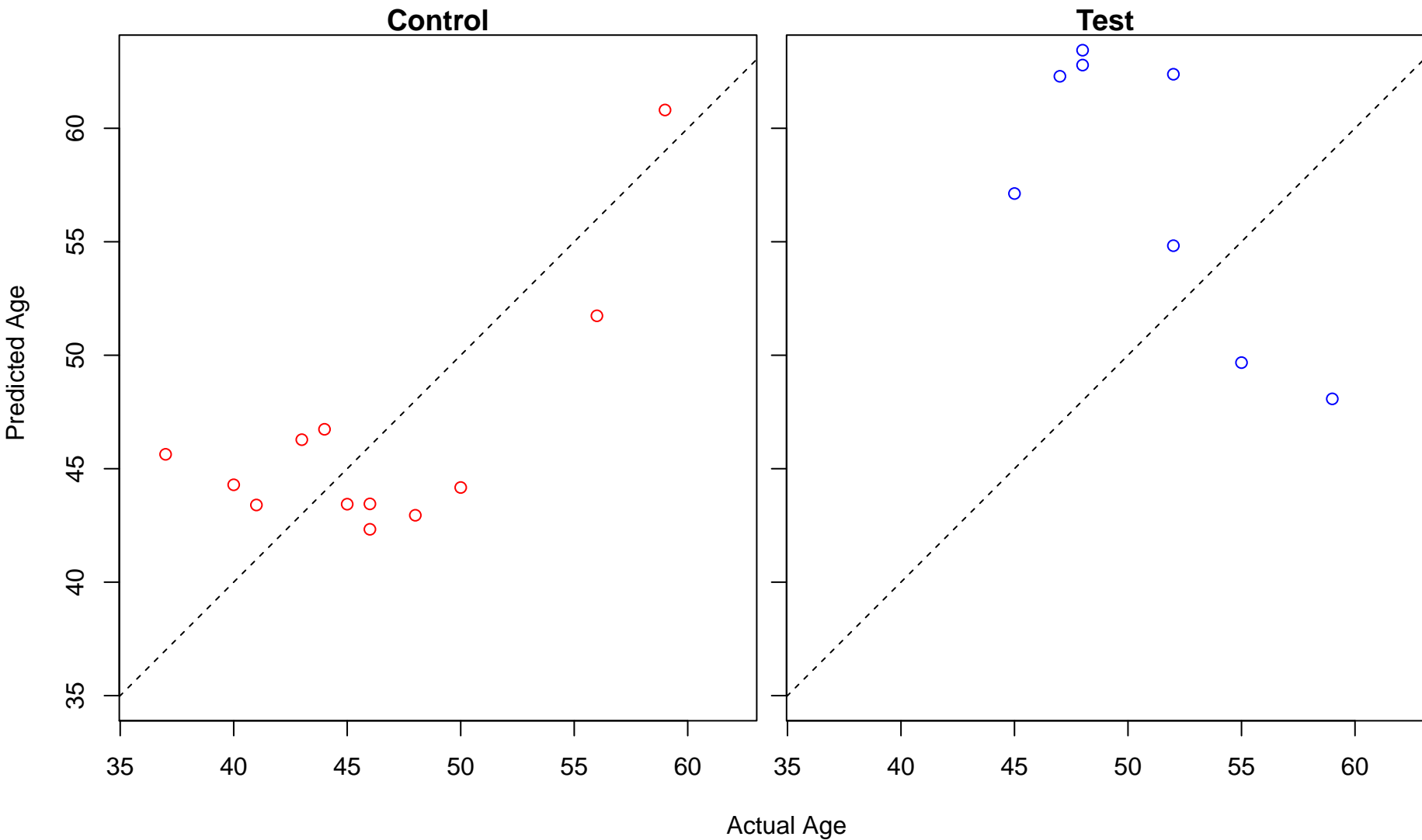
stem cell differentiation (Score: 5.872497)



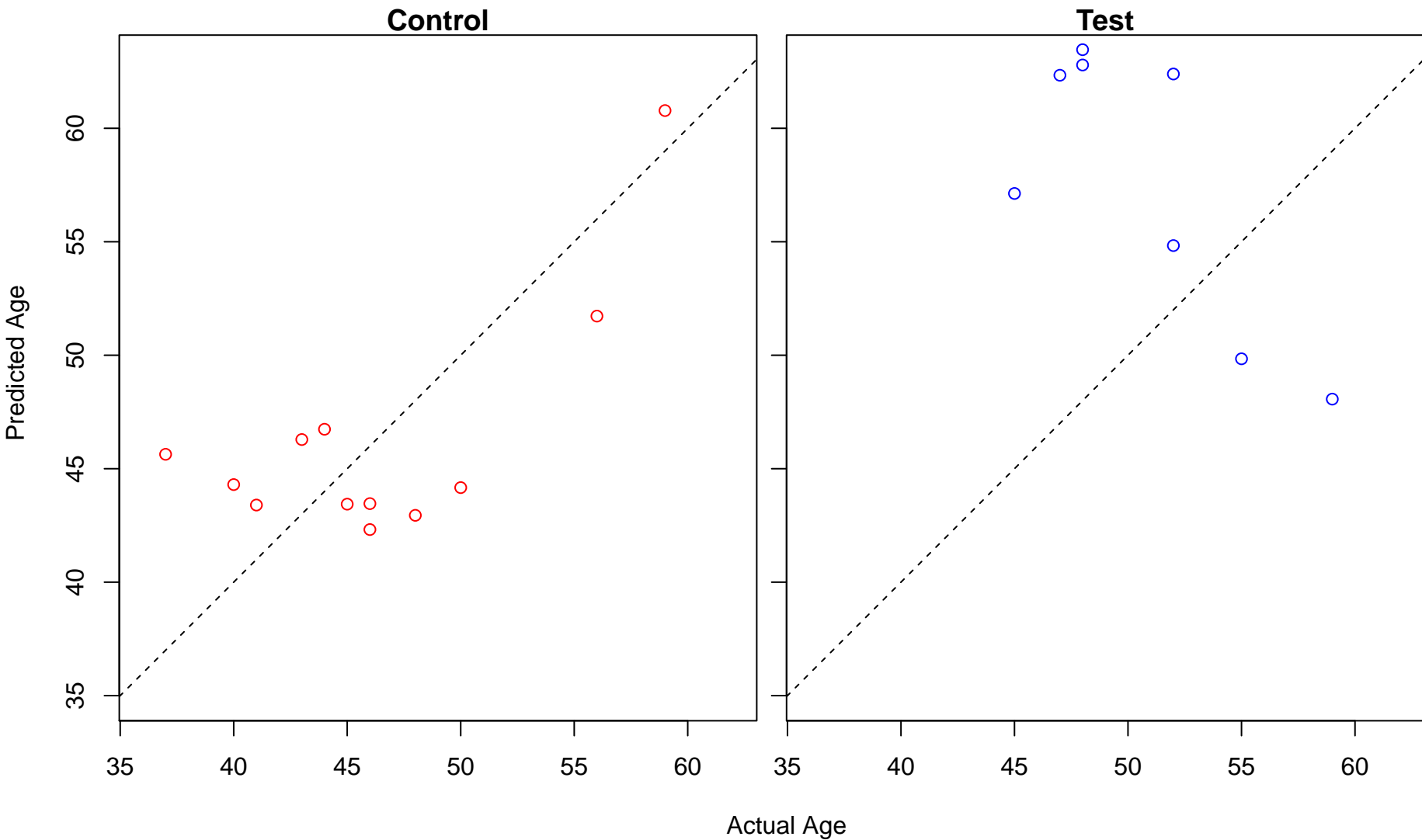
signal release (Score: 5.871429)



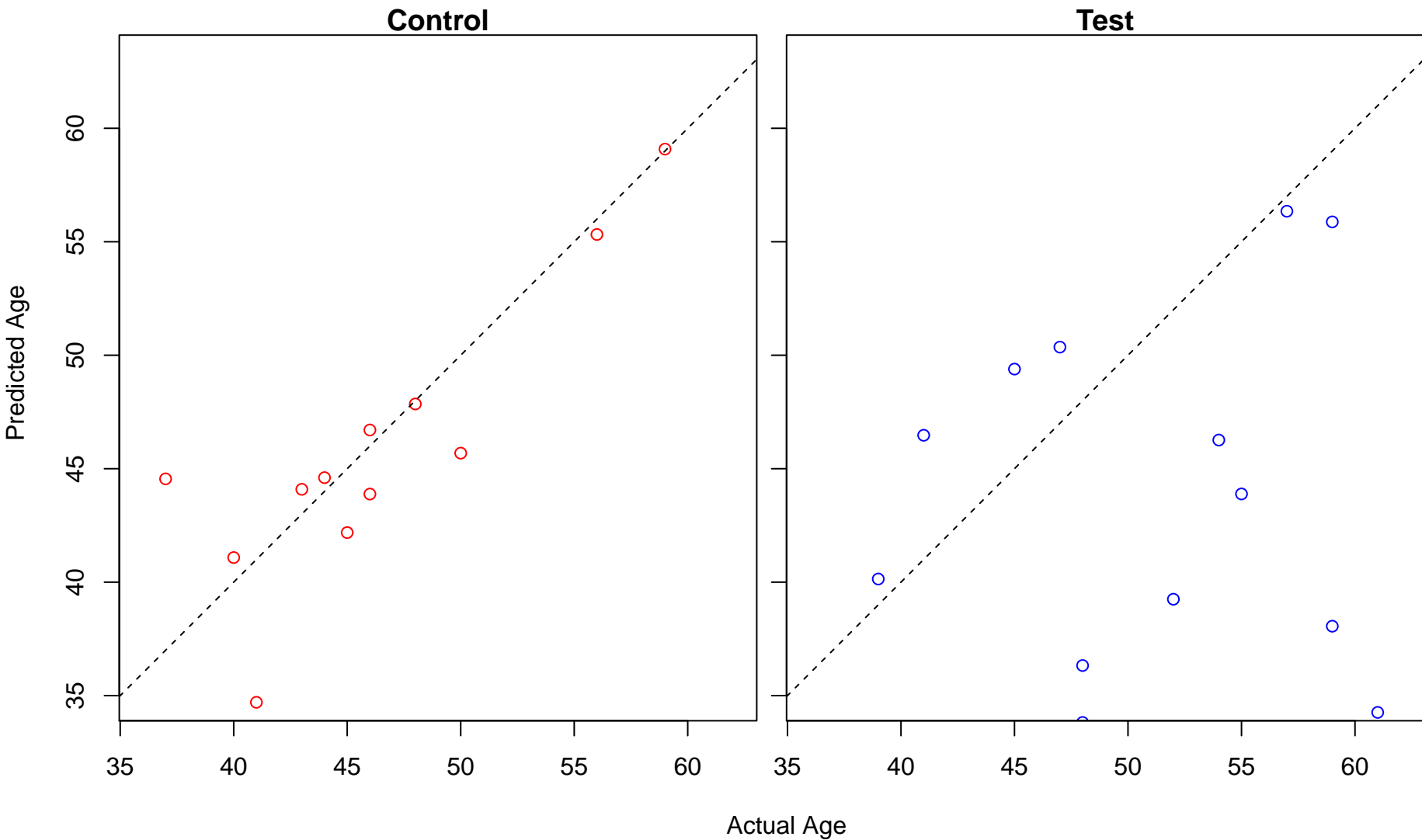
regulation of tumor necrosis factor biosynthetic process (Score: 5.870255)



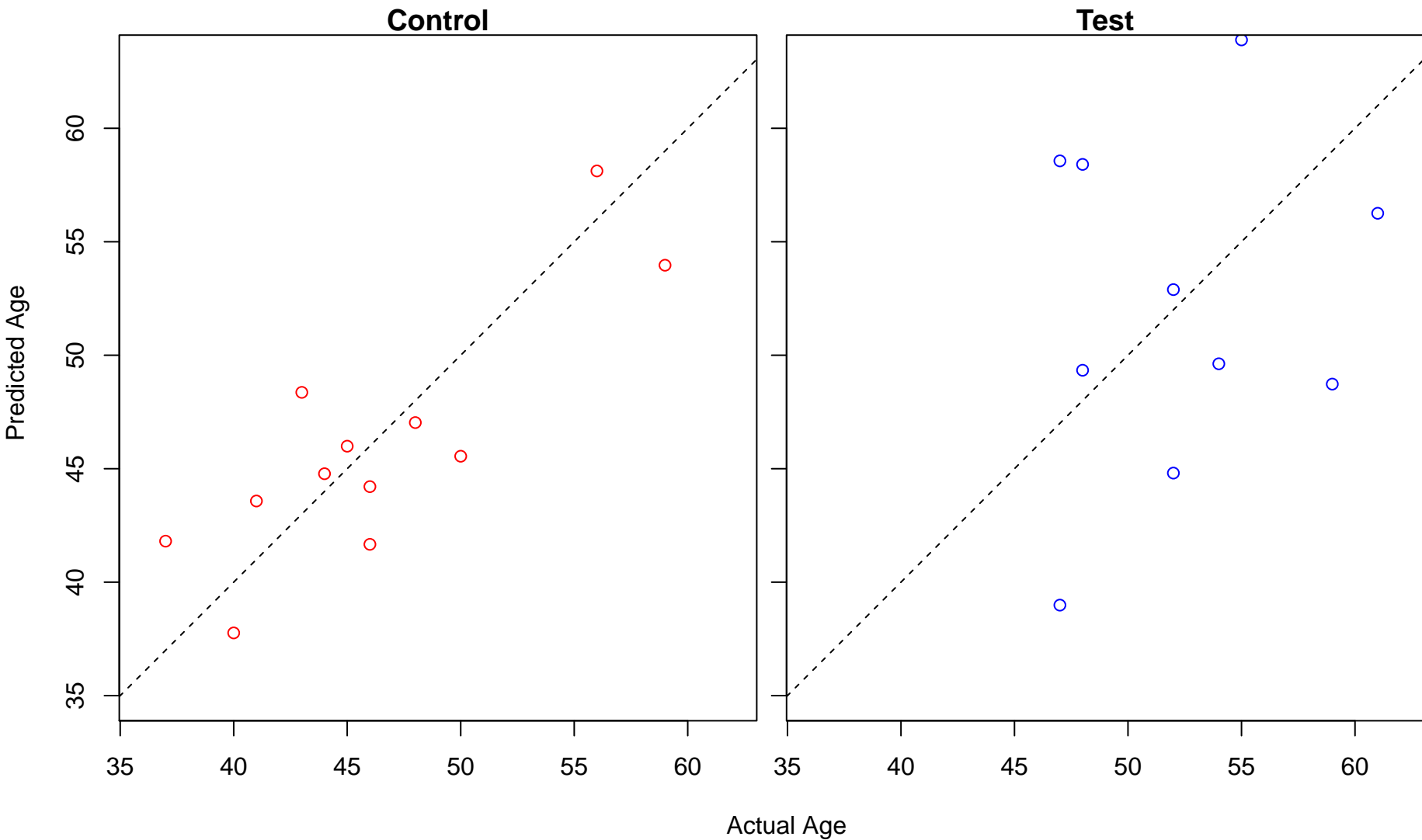
positive regulation of tumor necrosis factor biosynthetic process (Score: 5.865765)



AV node cell to bundle of His cell communication (Score: 5.862635)

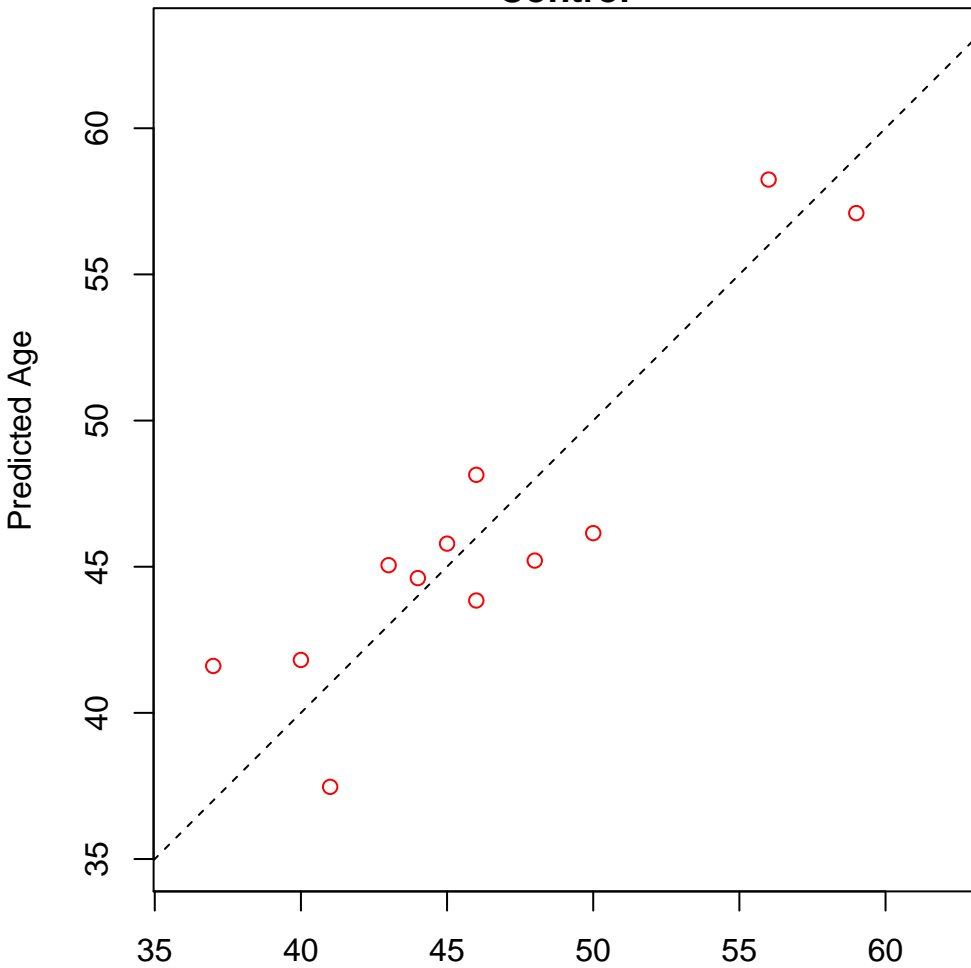


negative regulation of translation (Score: 5.857666)

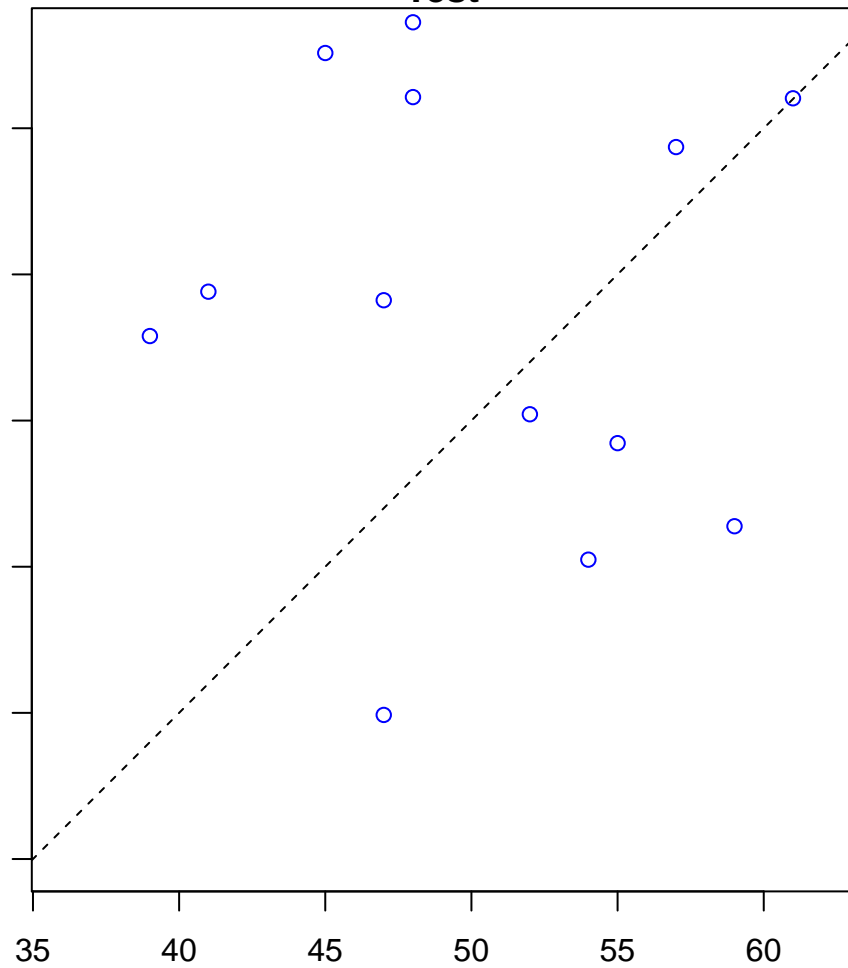


regulation of vascular permeability (Score: 5.850494)

Control

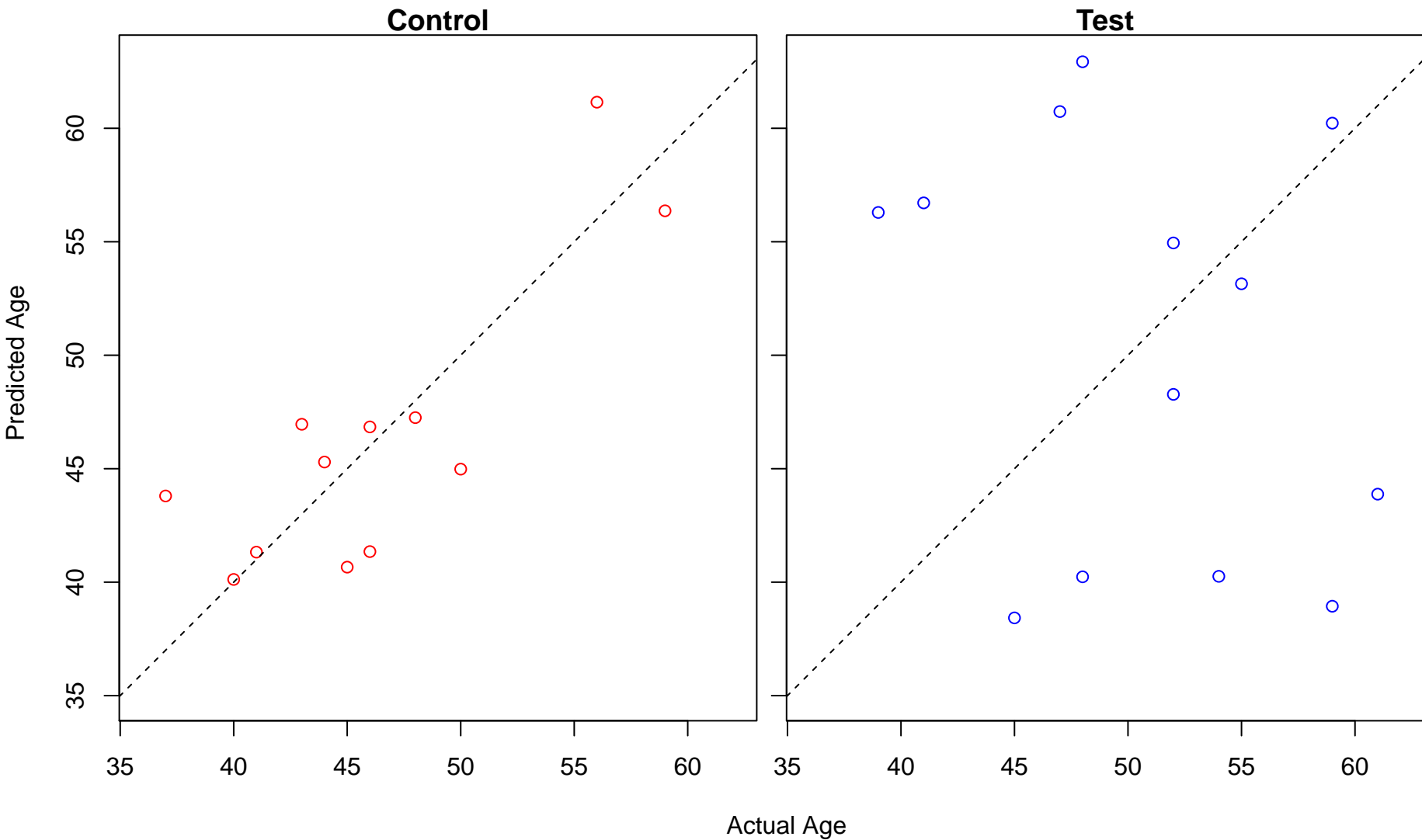


Test

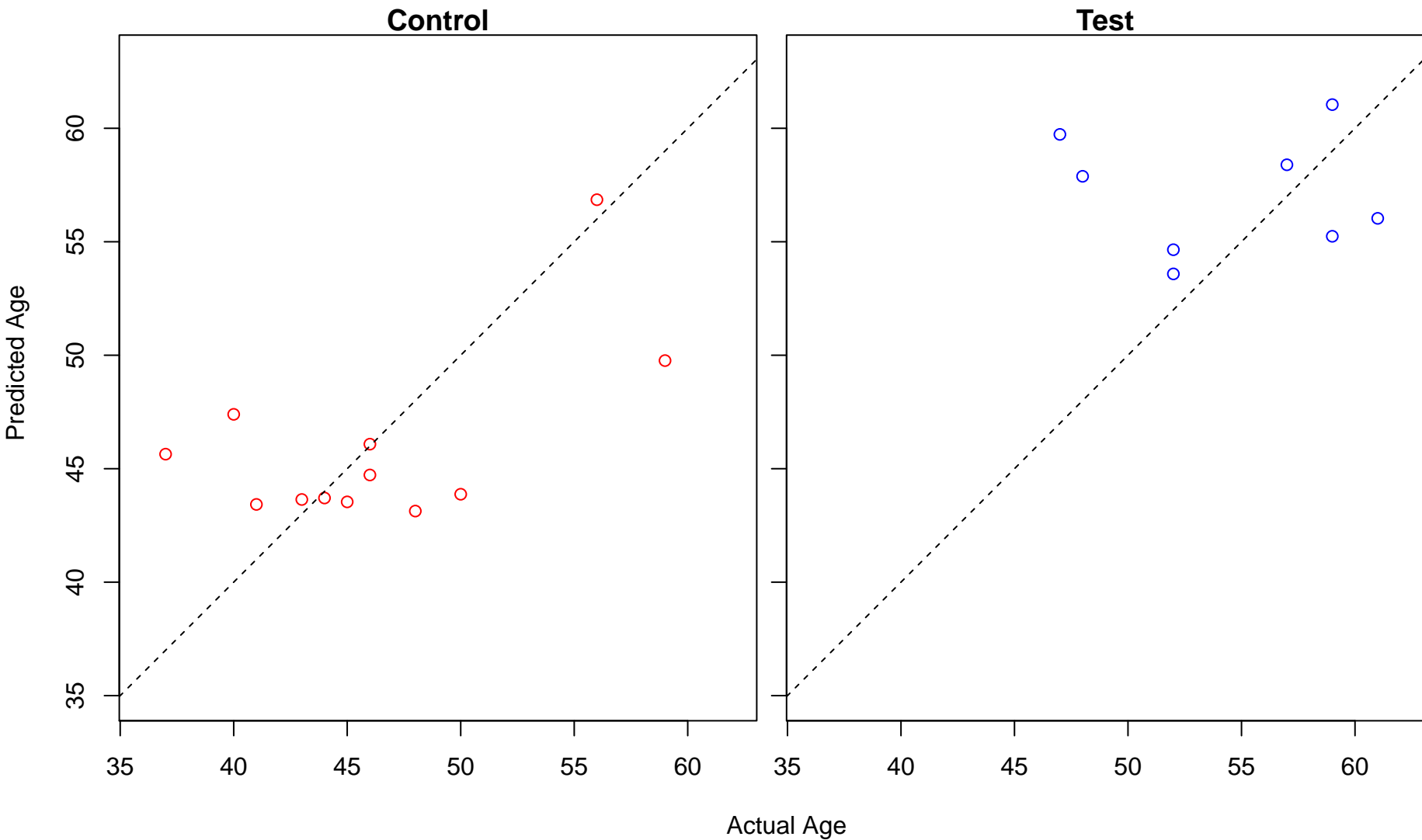


Actual Age

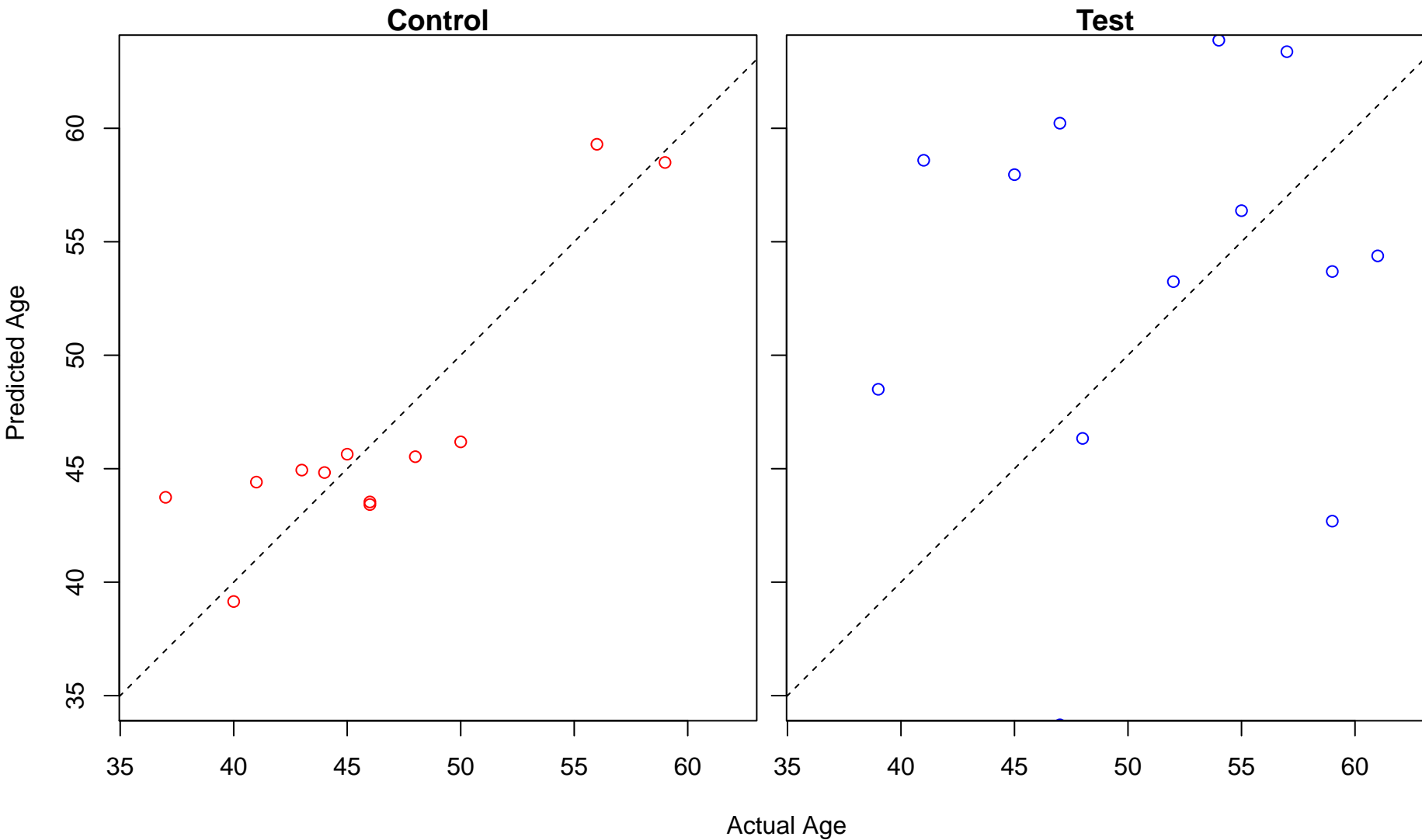
positive regulation of protein catabolic process (Score: 5.844221)



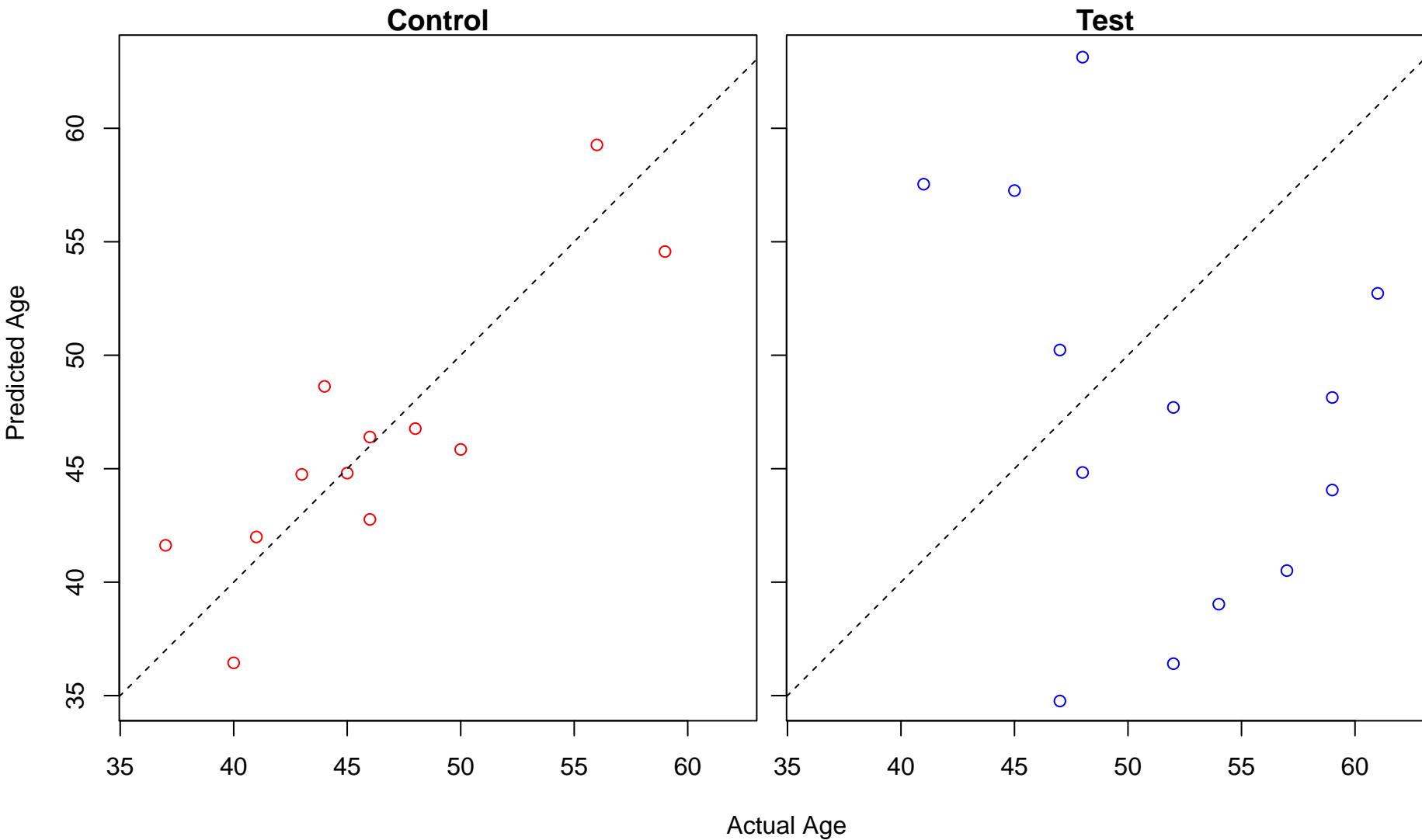
regulation of cell maturation (Score: 5.839769)



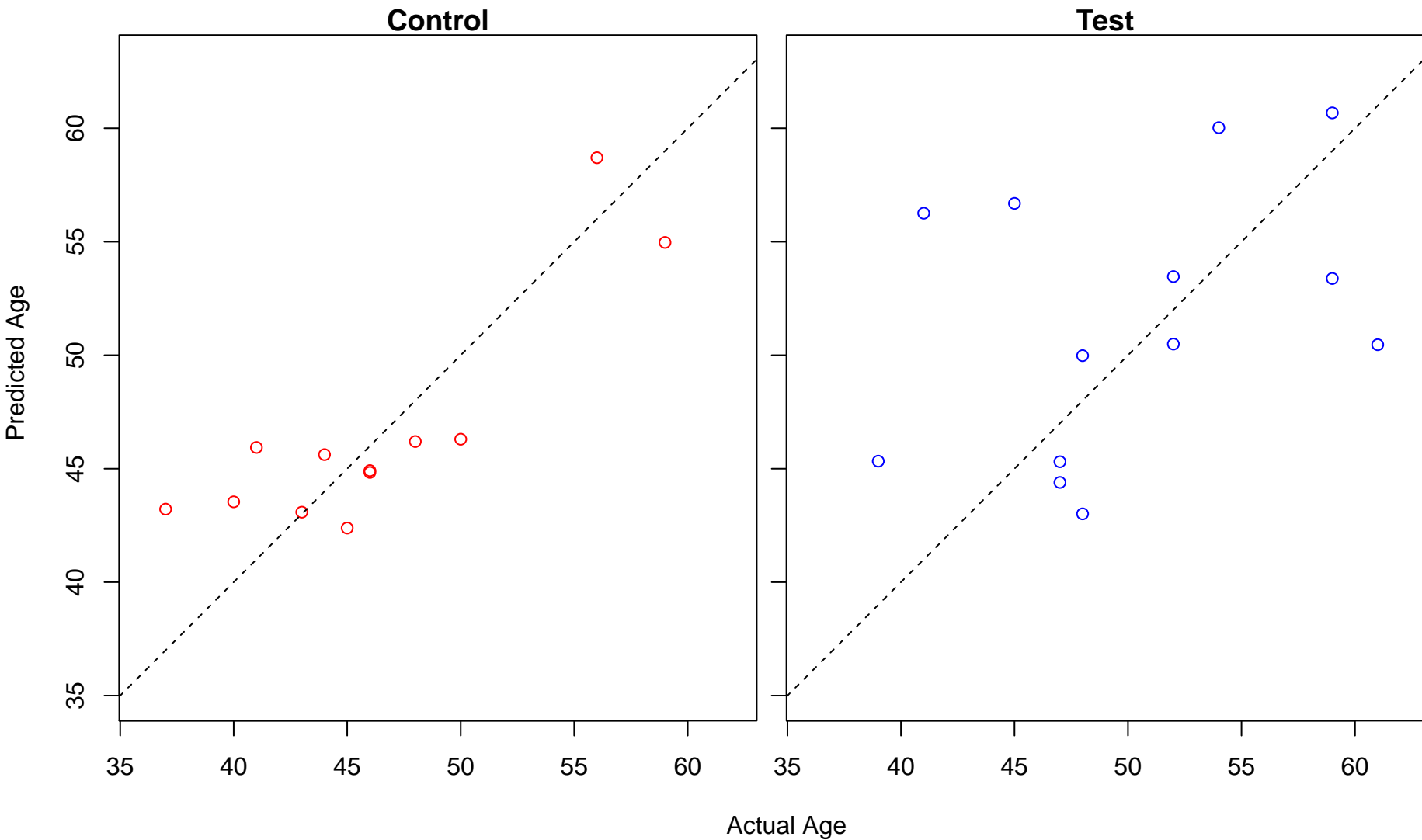
negative regulation of homeostatic process (Score: 5.839310)



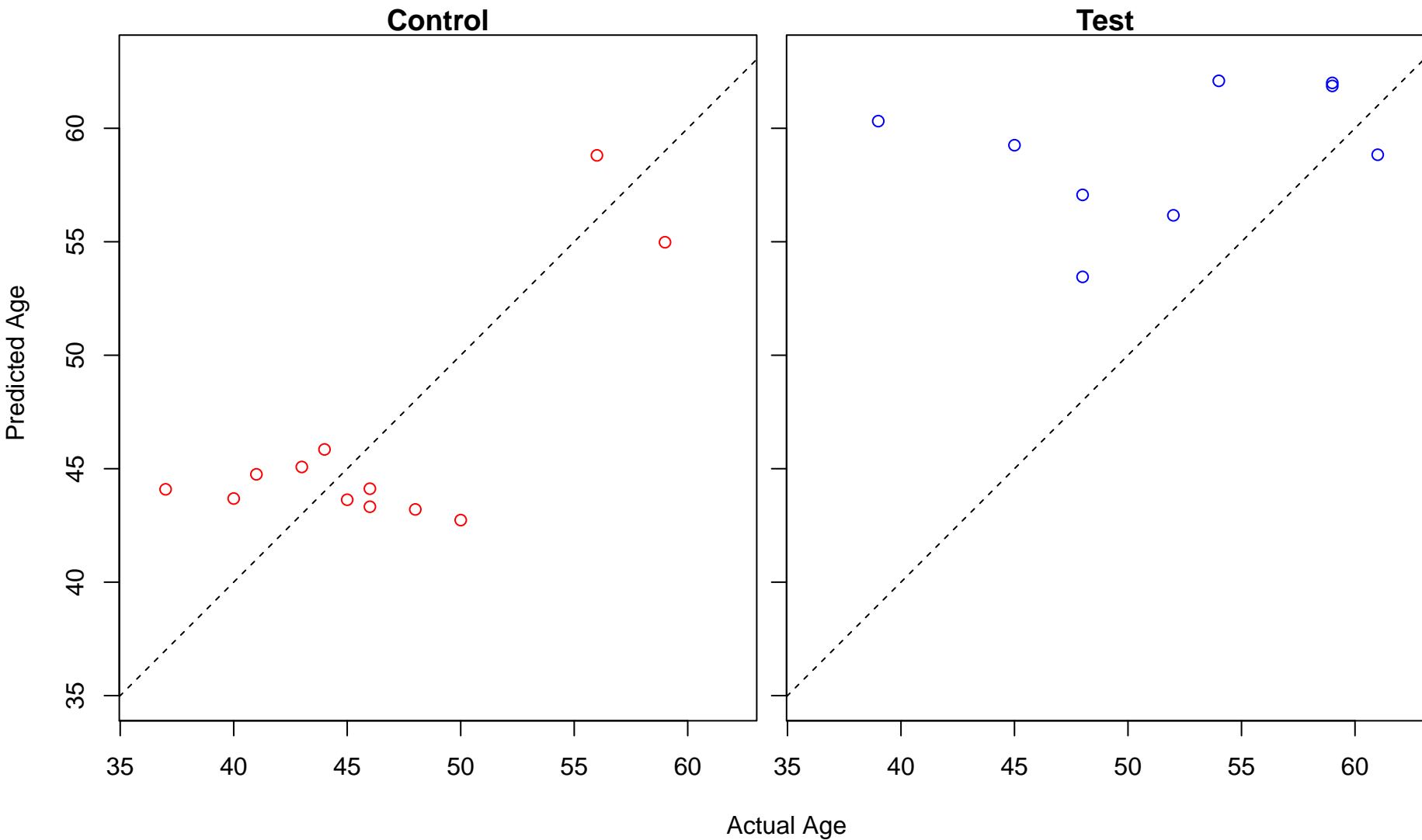
regulation of plasma membrane organization (Score: 5.819945)



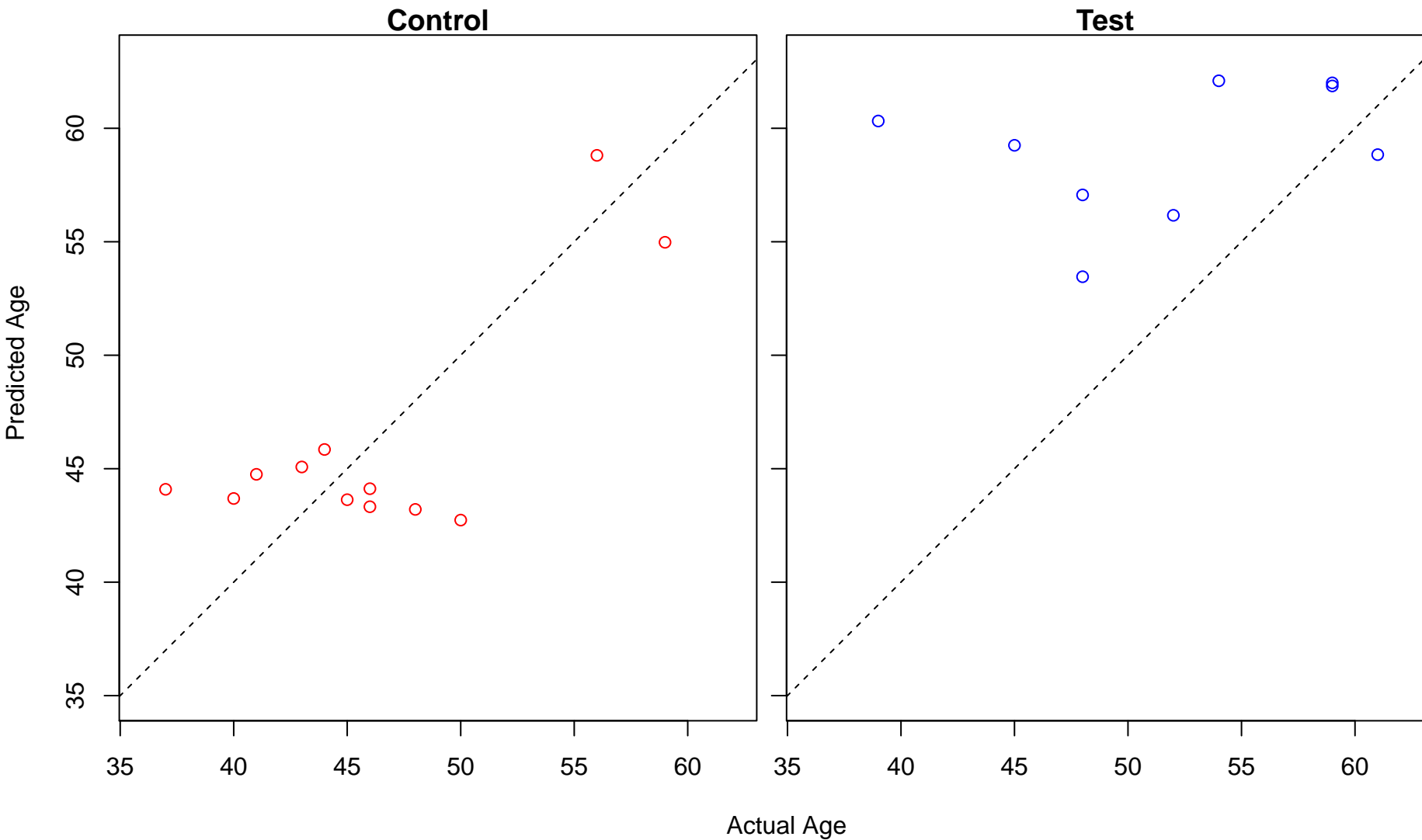
superoxide anion generation (Score: 5.817206)



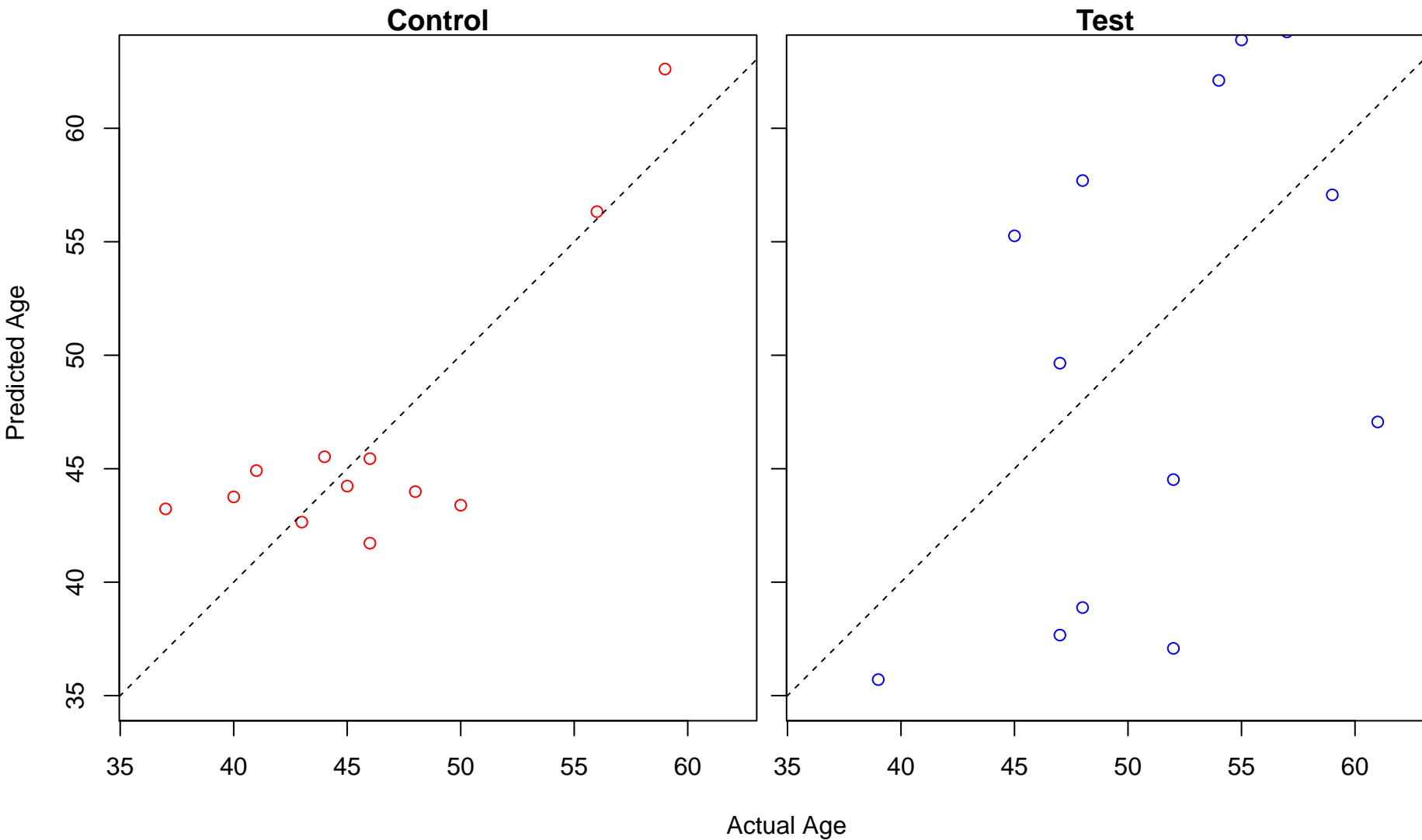
negative regulation of myotube differentiation (Score: 5.803323)



negative regulation of striated muscle cell differentiation (Score: 5.800060)

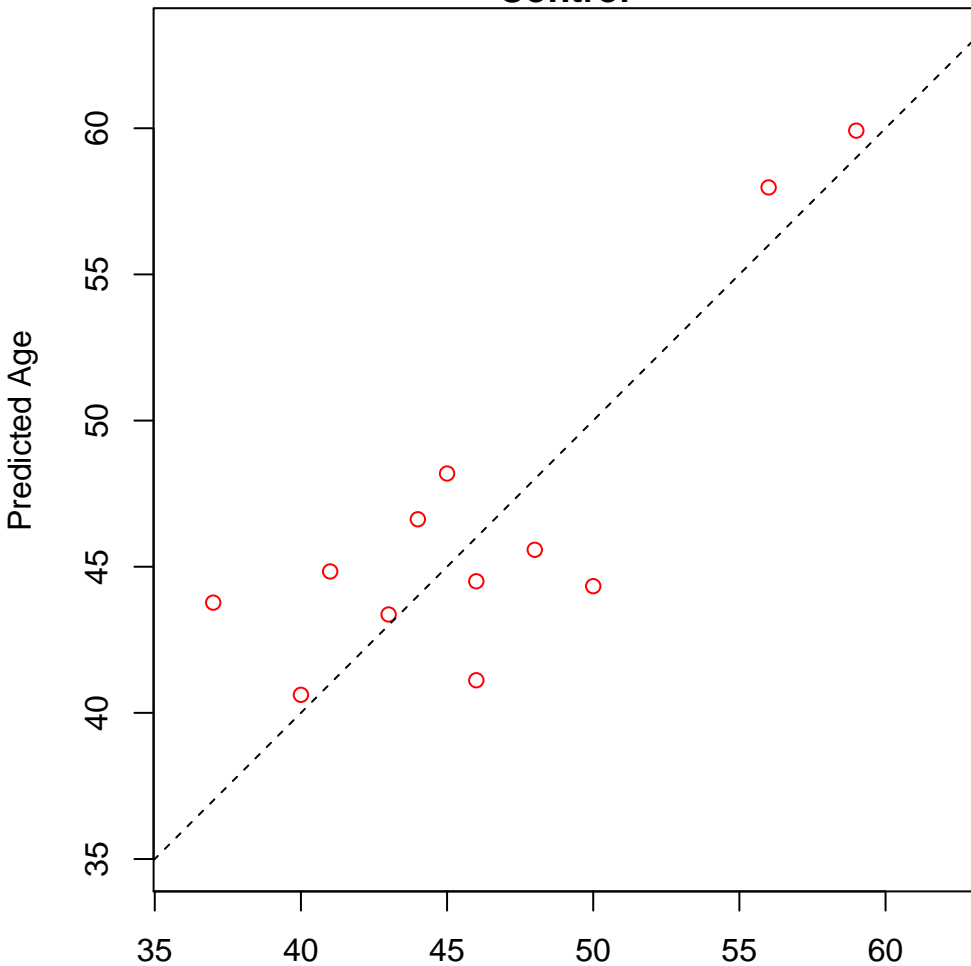


cell redox homeostasis (Score: 5.783055)

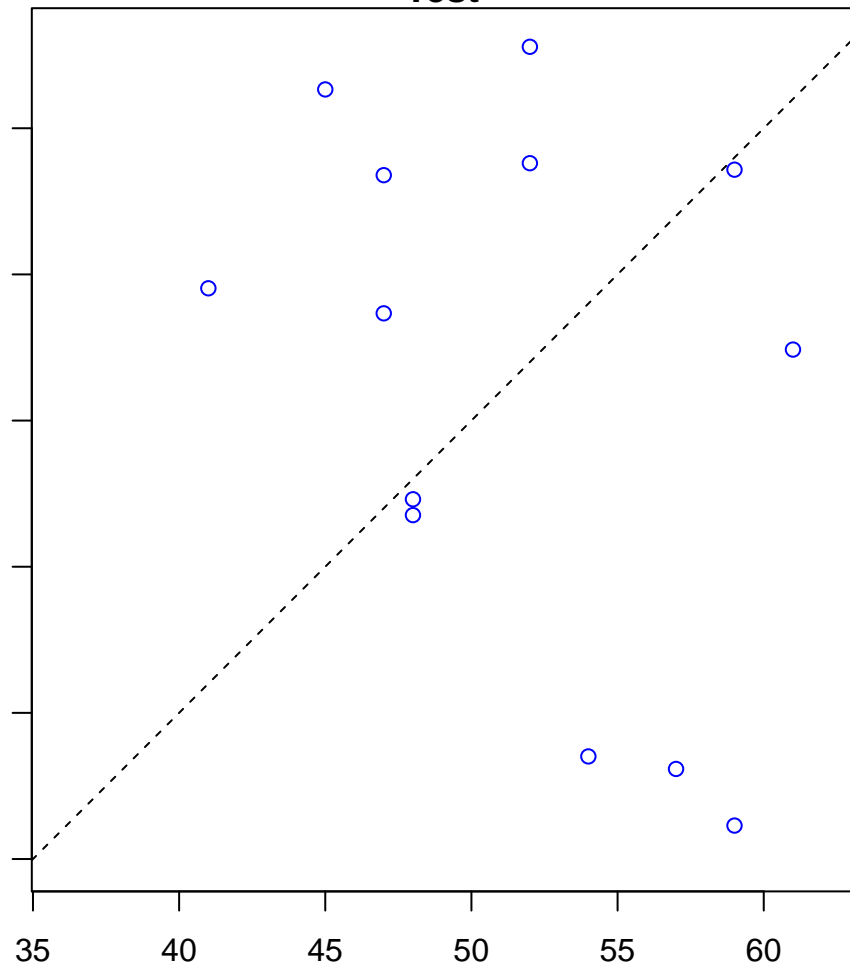


cellular response to interferon- γ (Score: 5.780755)

Control

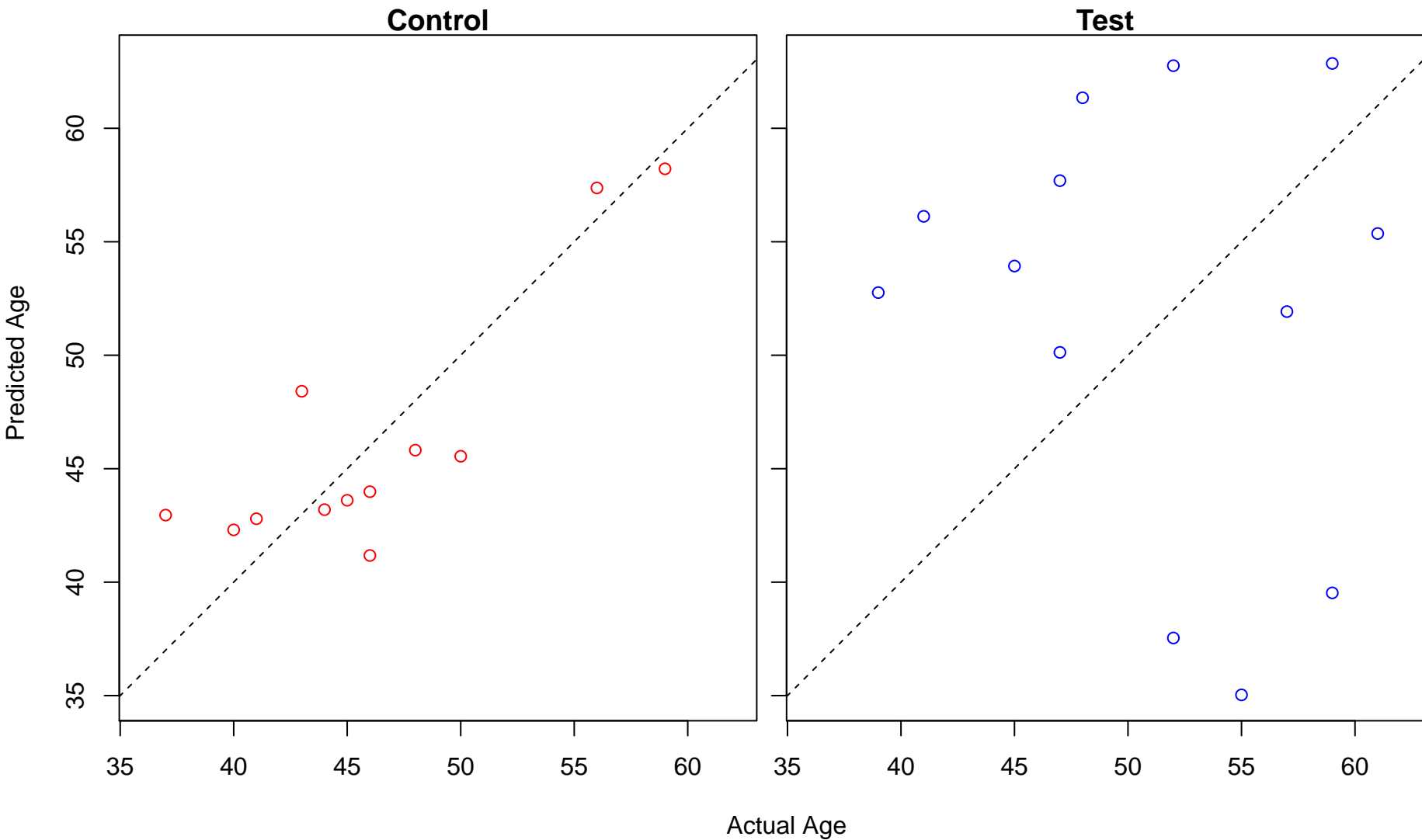


Test

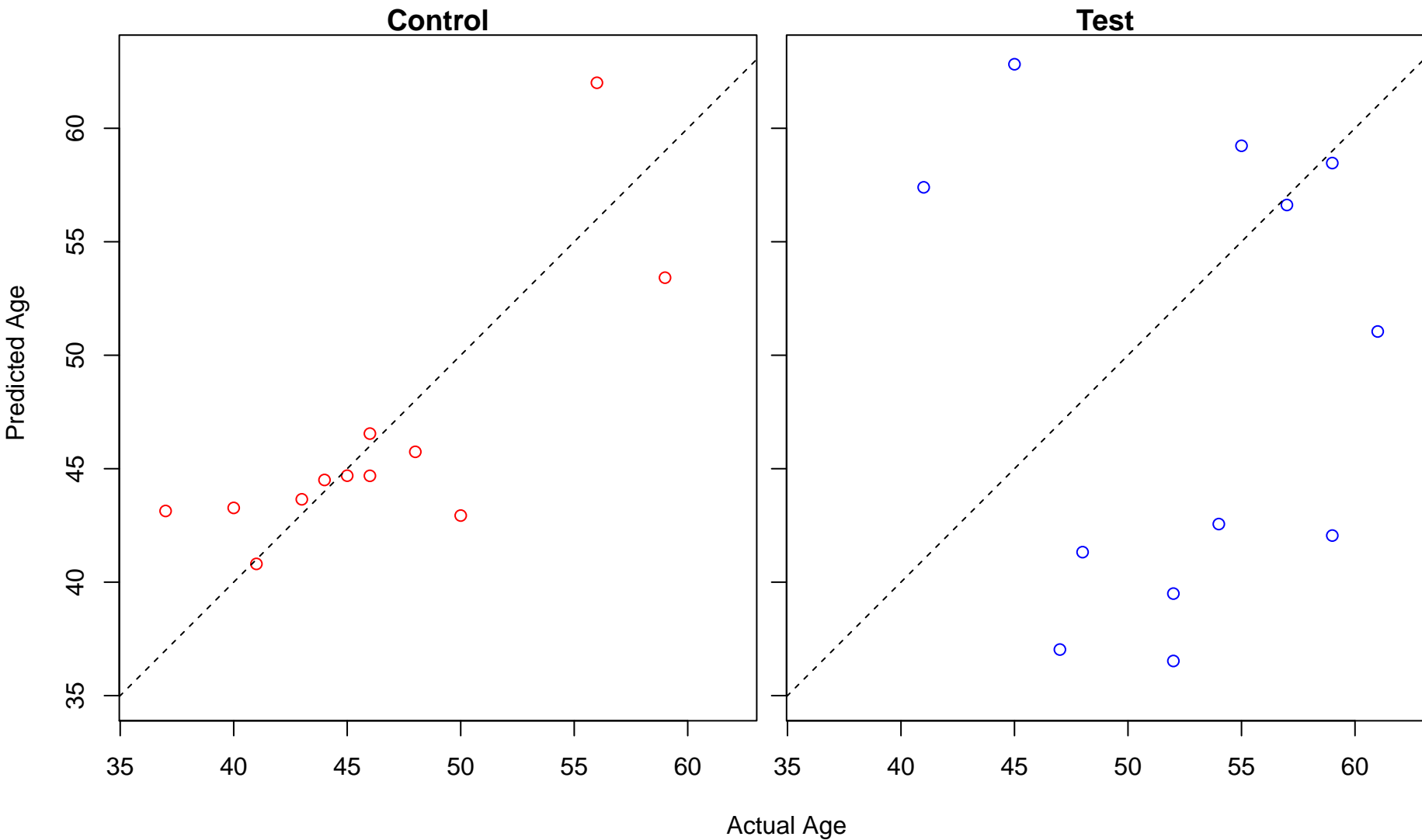


Actual Age

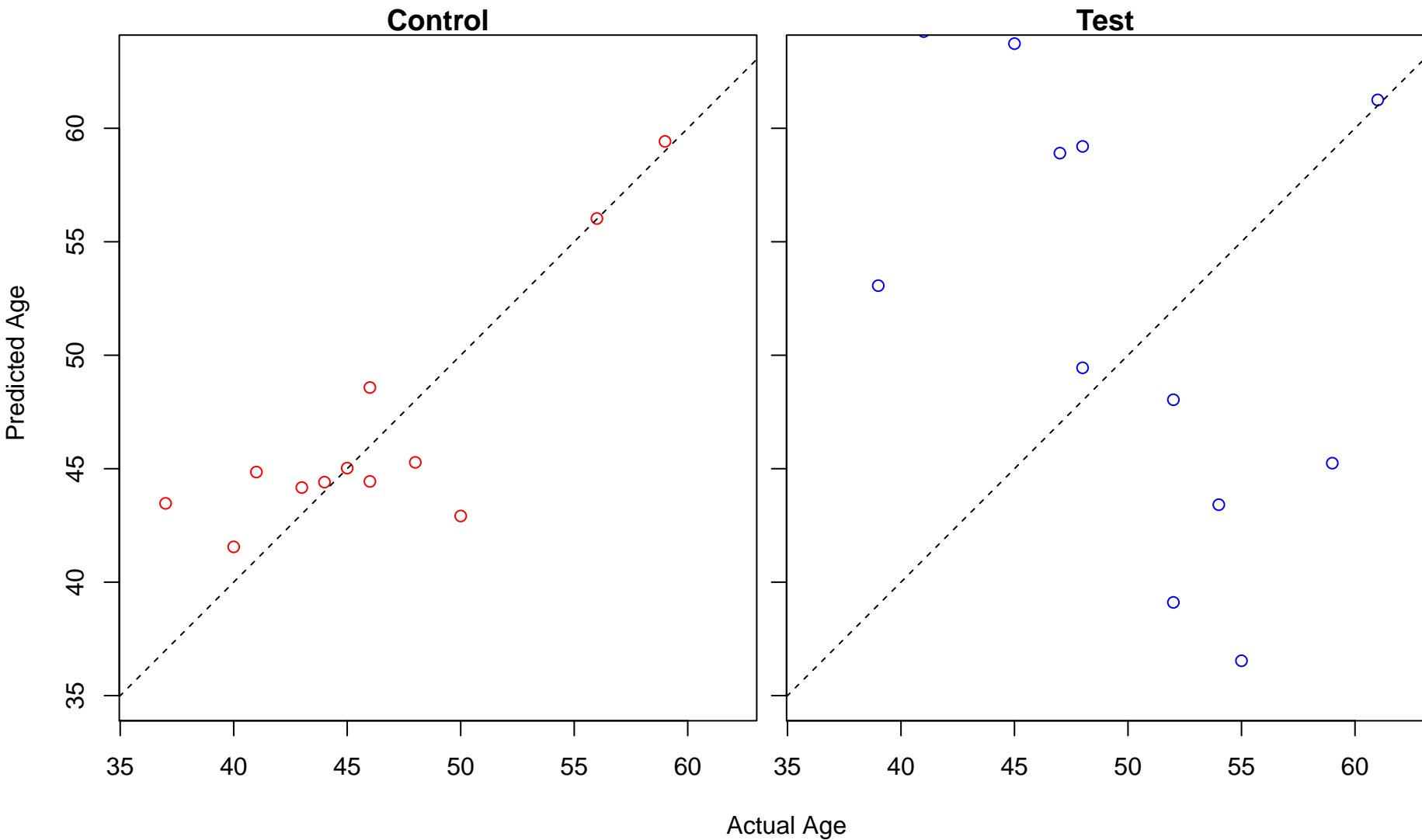
regulation of interleukin-2 production (Score: 5.778927)



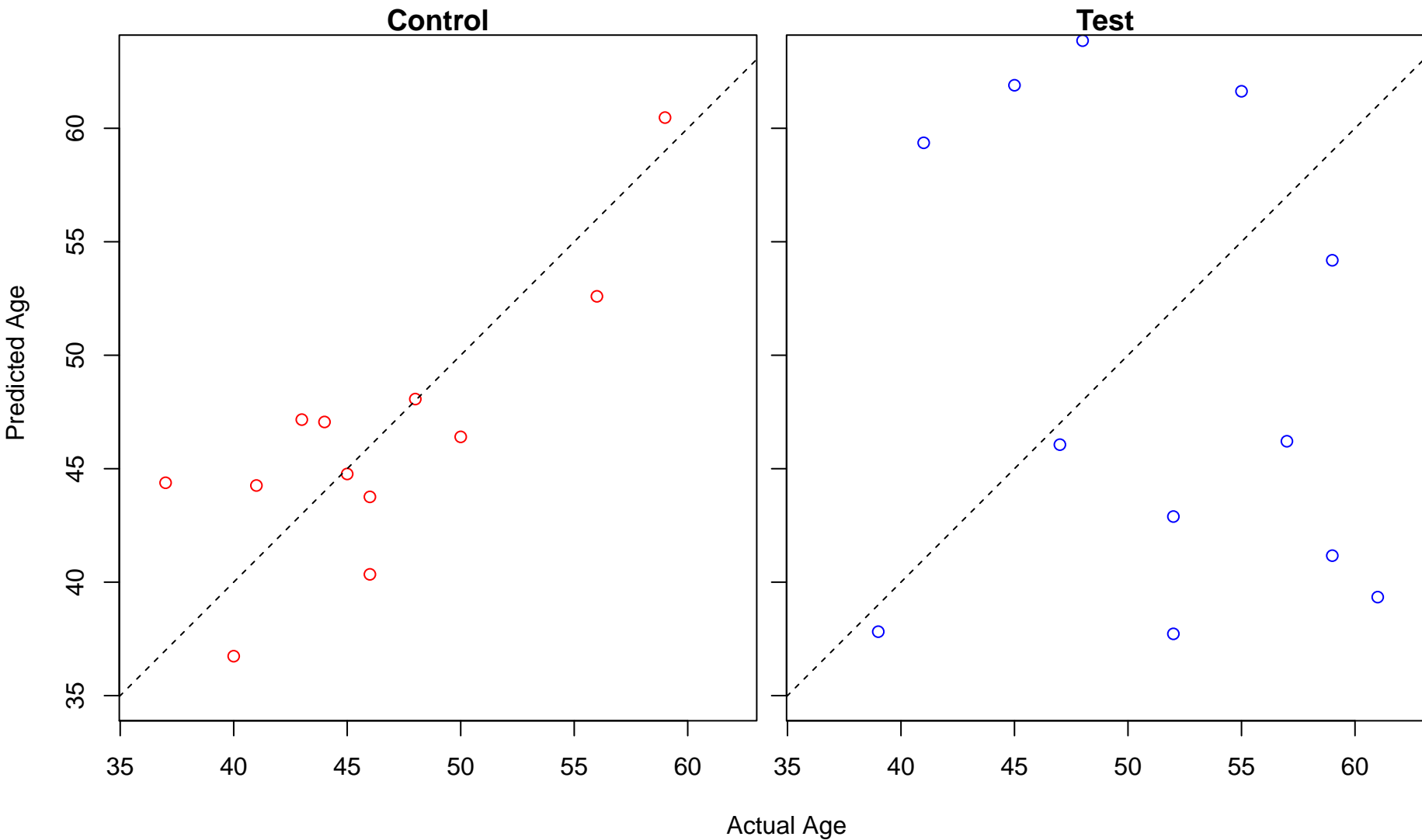
organ morphogenesis (Score: 5.772559)



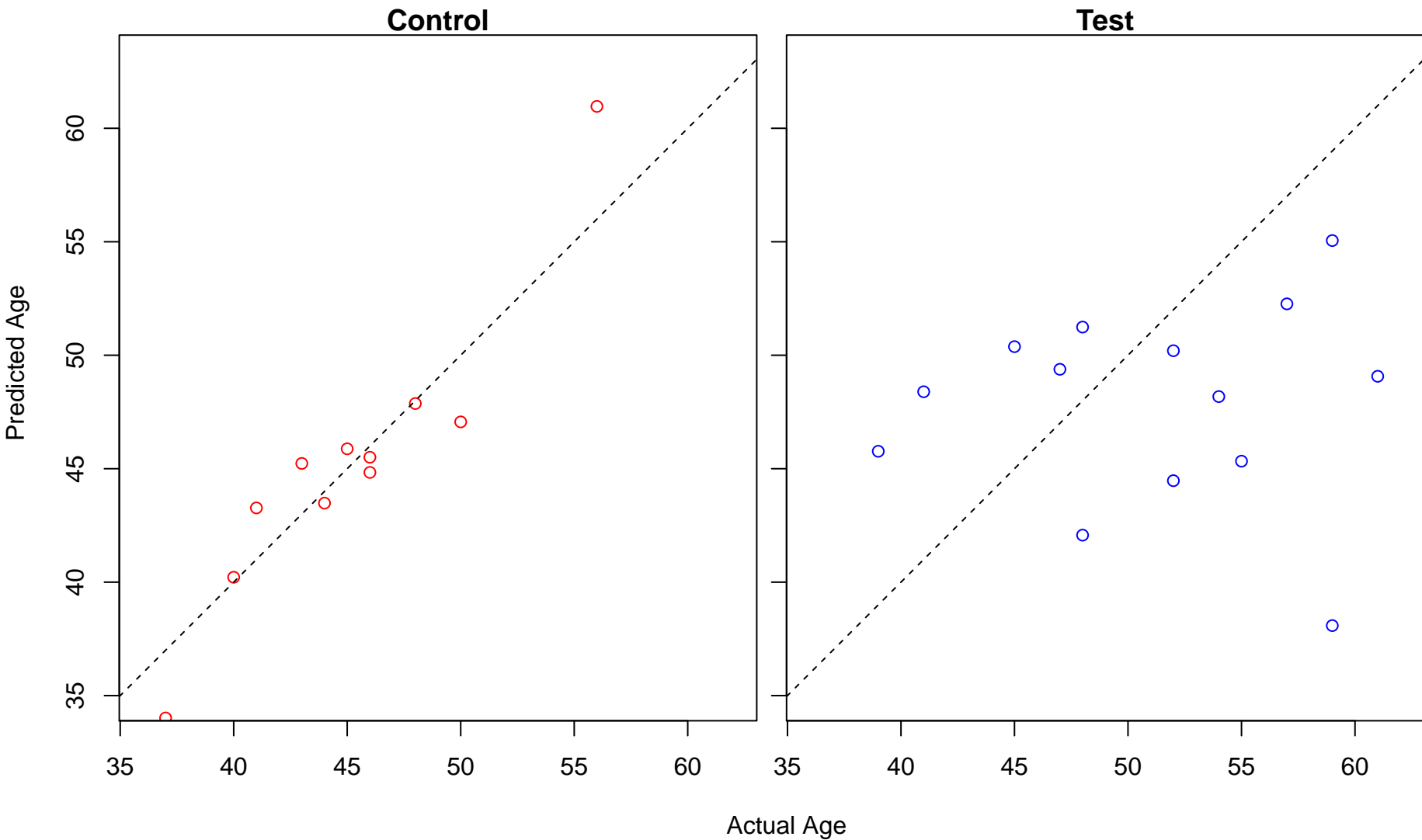
cell cycle arrest (Score: 5.761904)



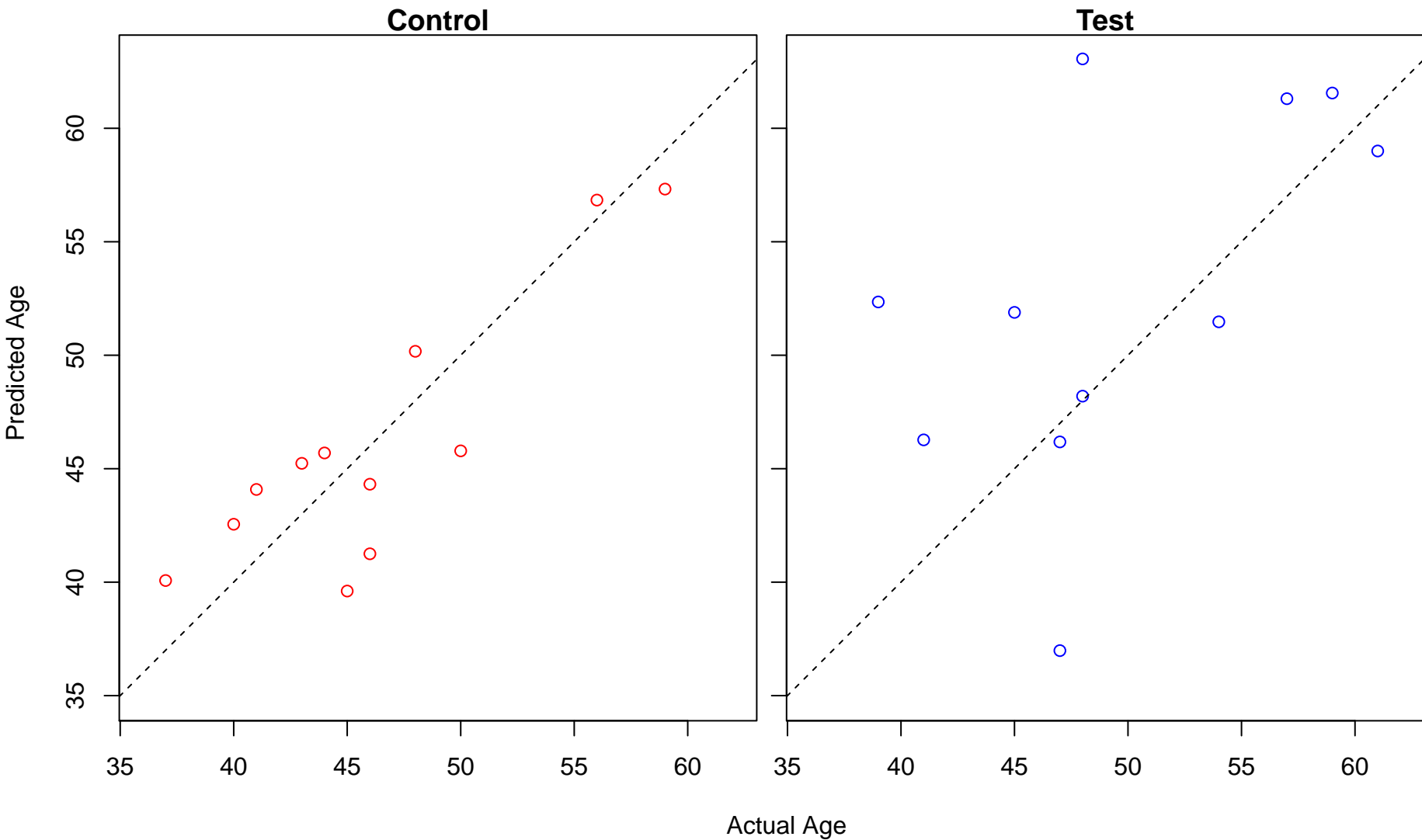
mesenchyme development (Score: 5.754770)



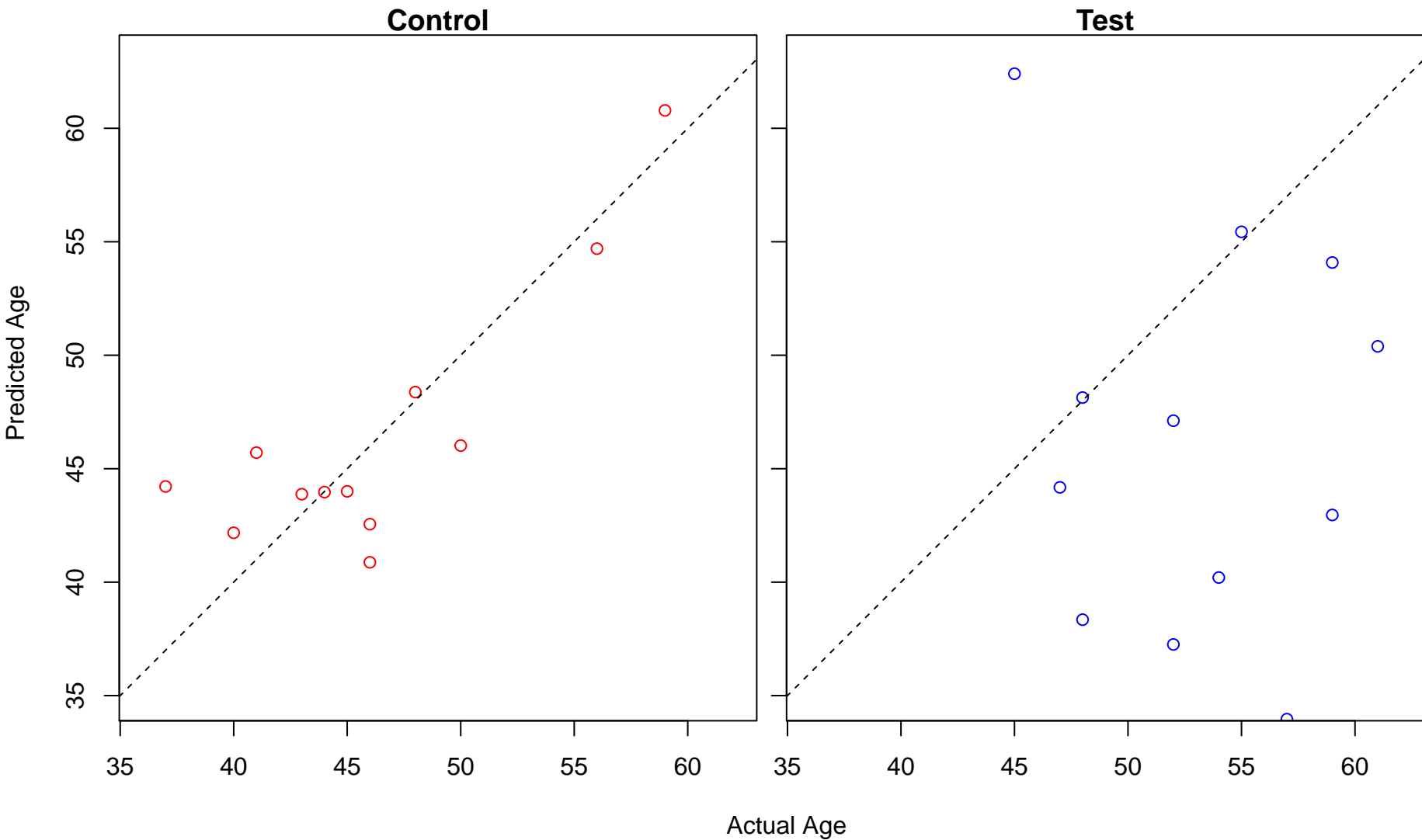
cell proliferation involved in kidney development (Score: 5.738250)



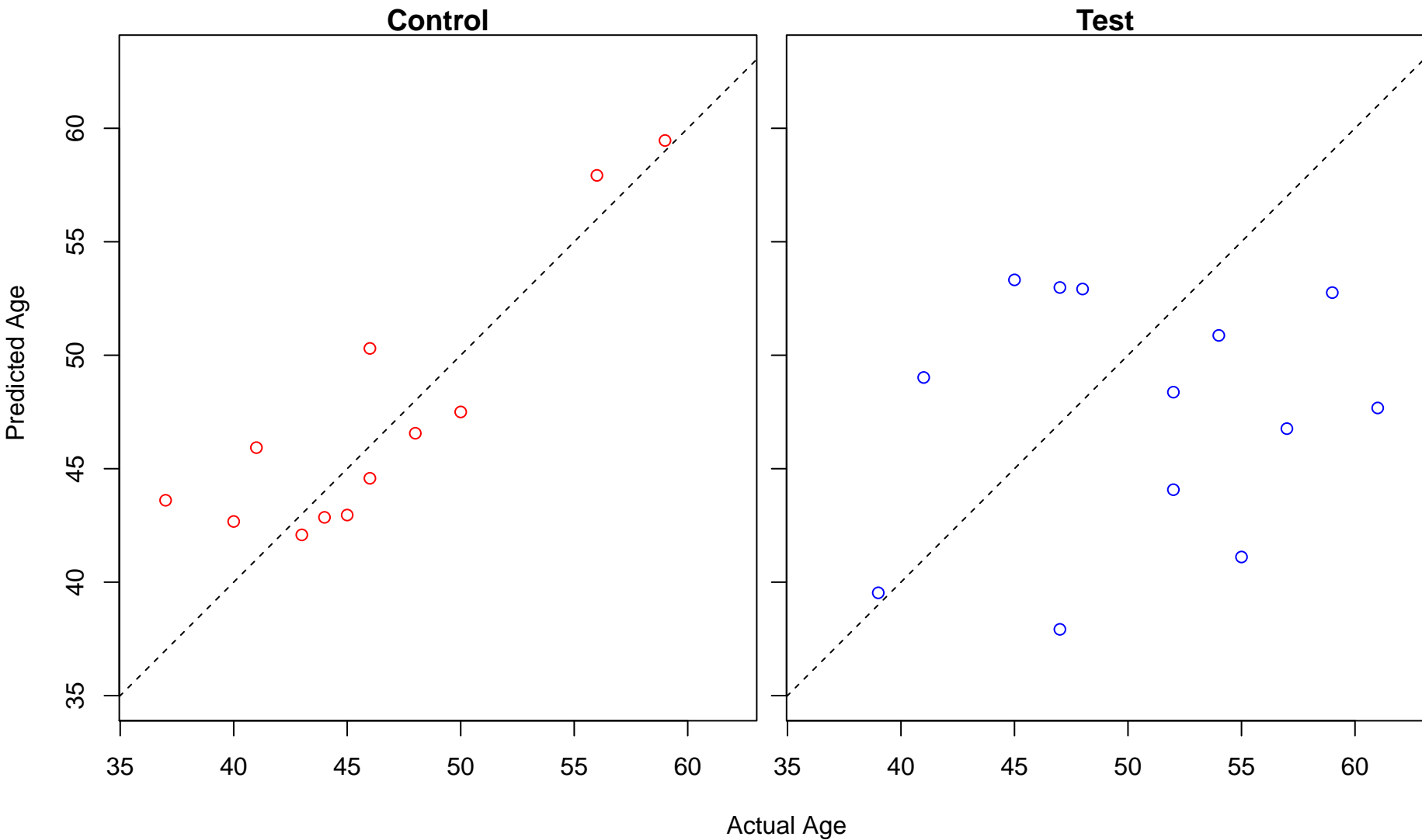
negative regulation of intrinsic apoptotic signaling pathway (Score: 5.729728)



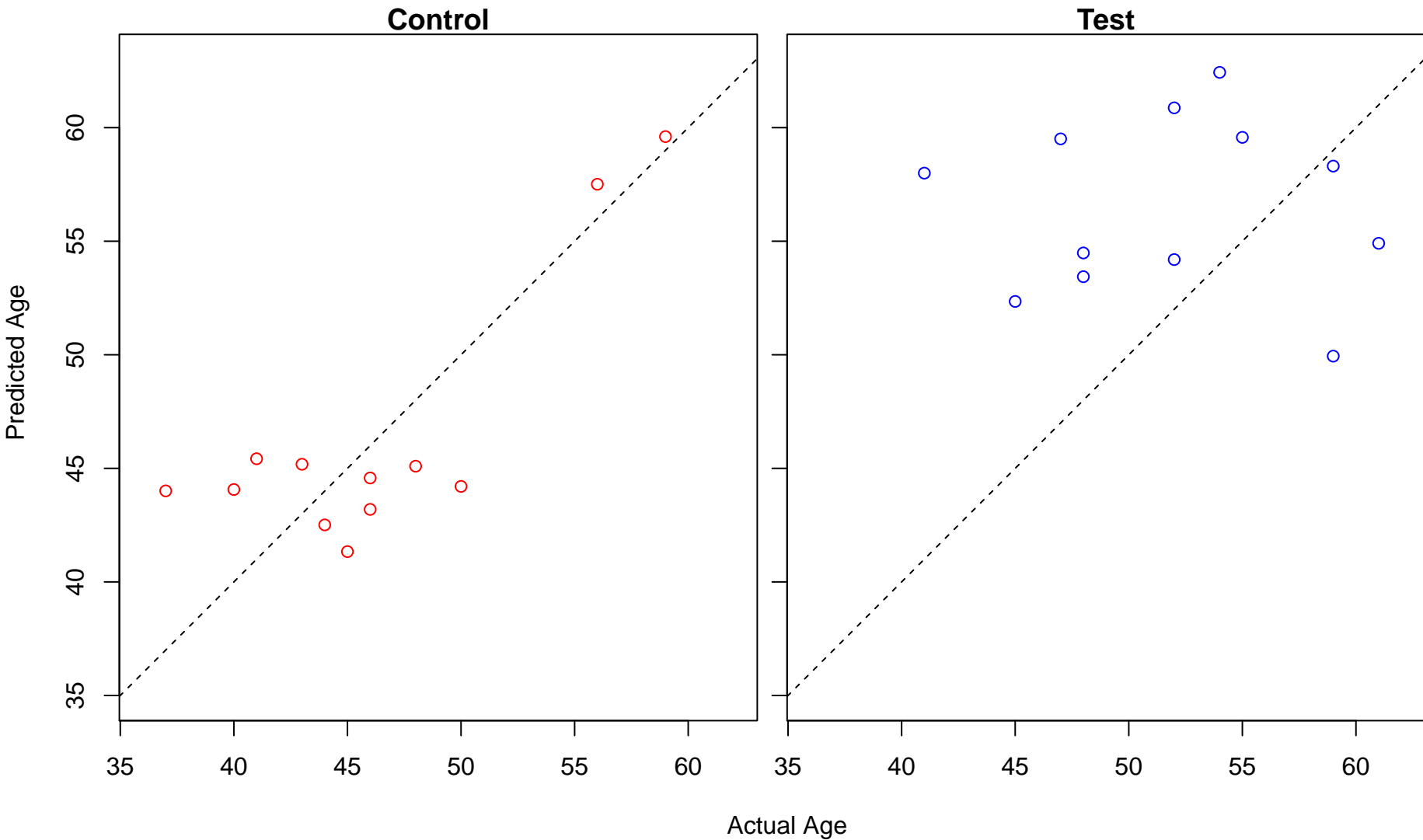
pigment metabolic process (Score: 5.725189)



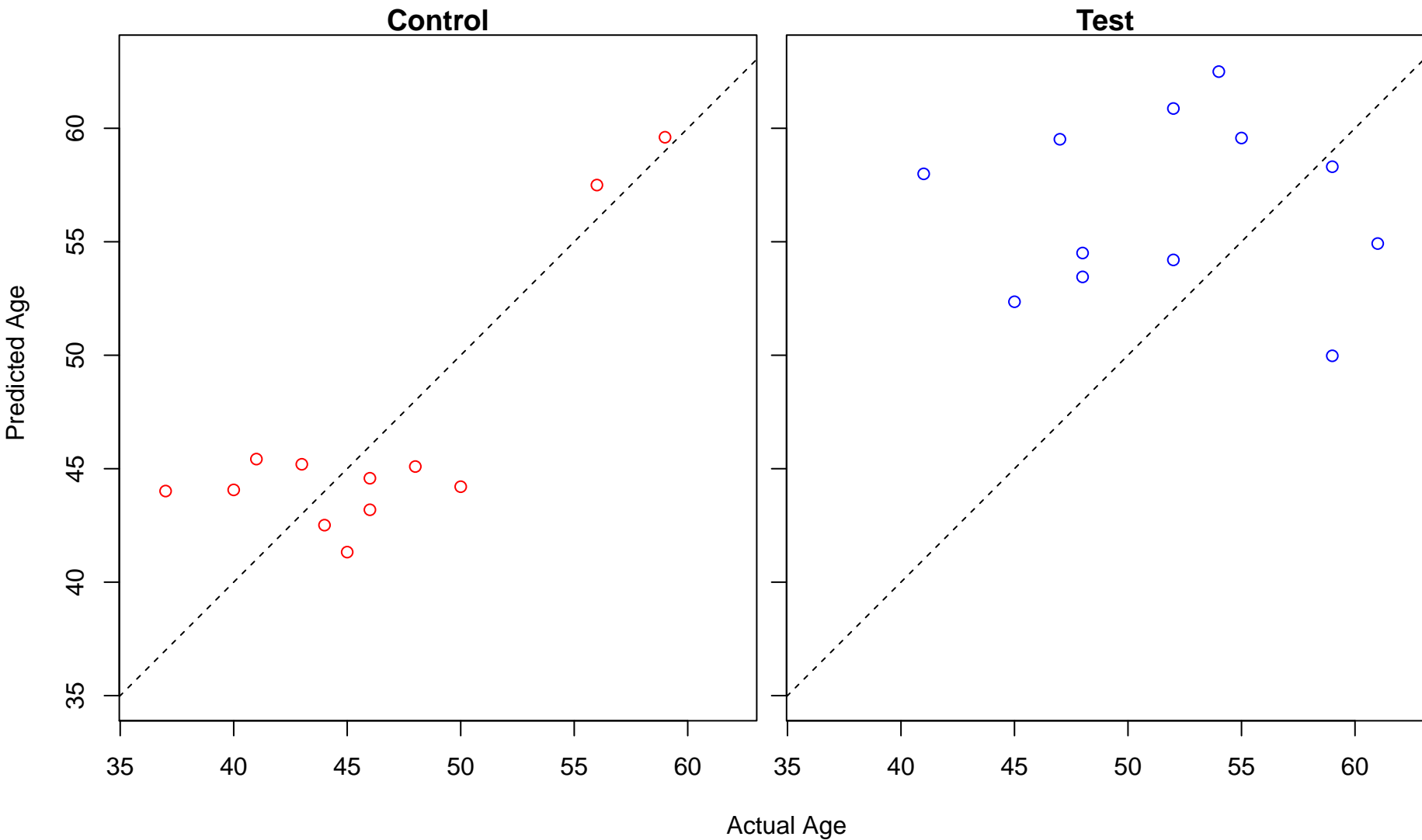
striated muscle cell proliferation (Score: 5.722024)



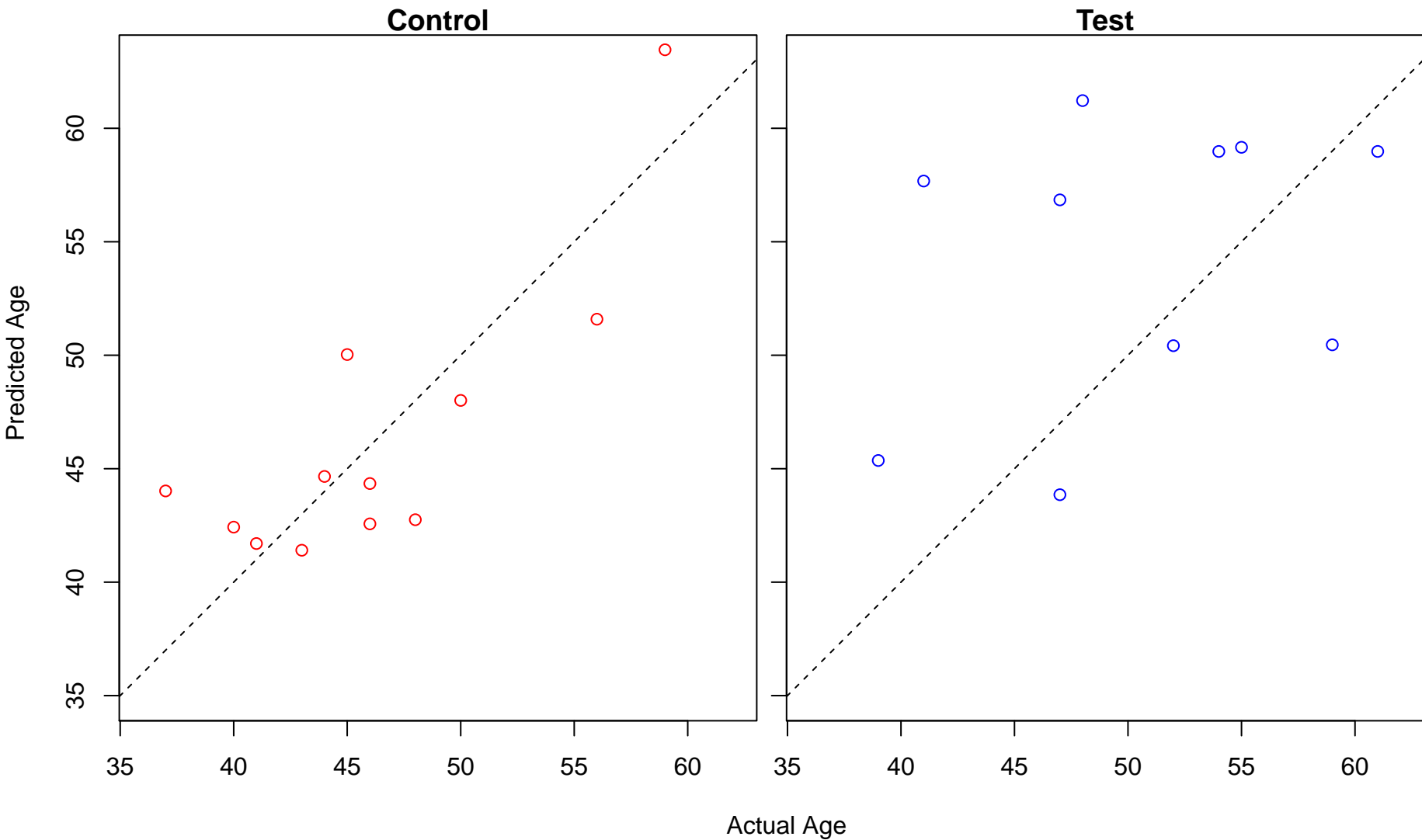
positive regulation of vesicle fusion (Score: 5.687607)



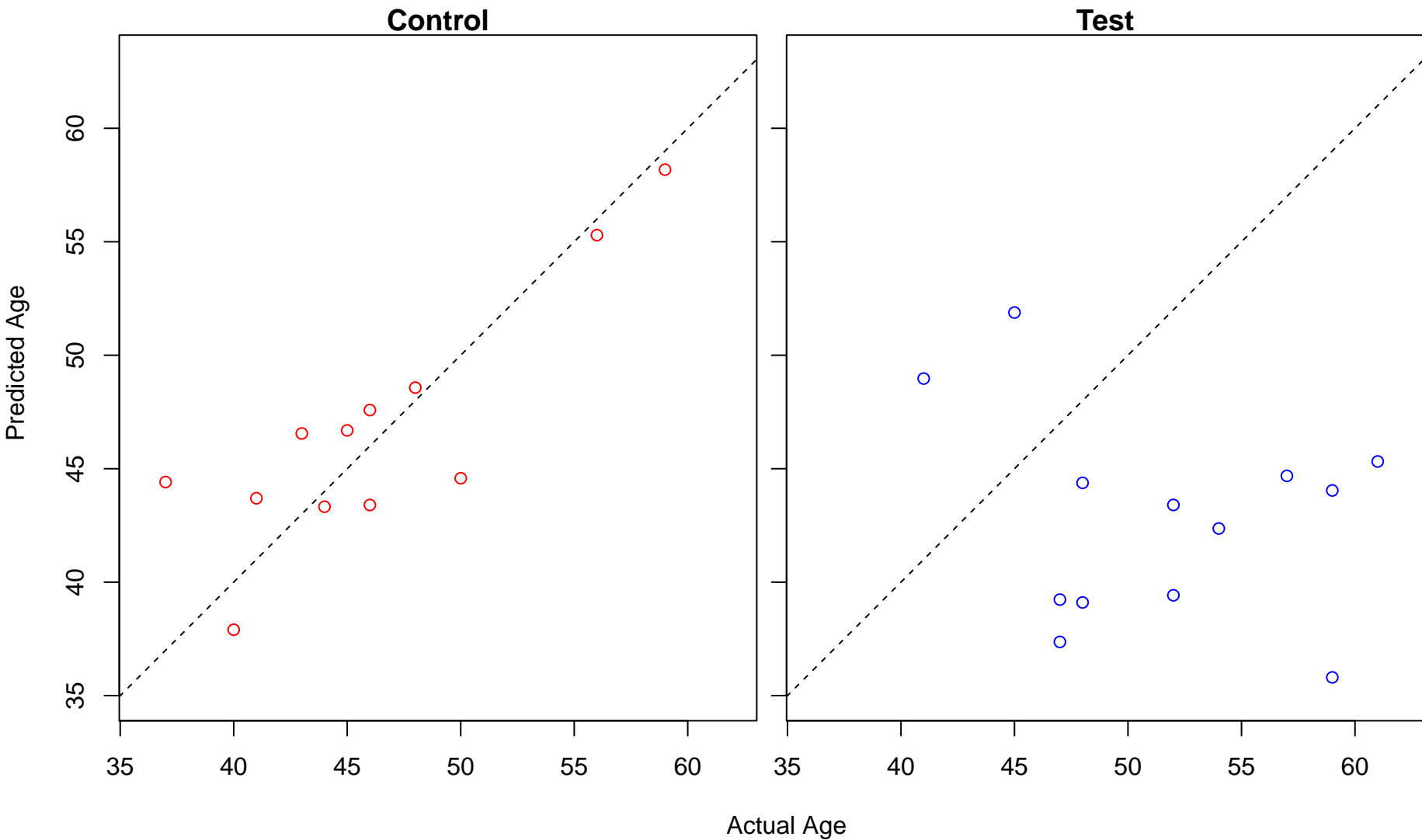
regulation of vesicle fusion (Score: 5.682805)



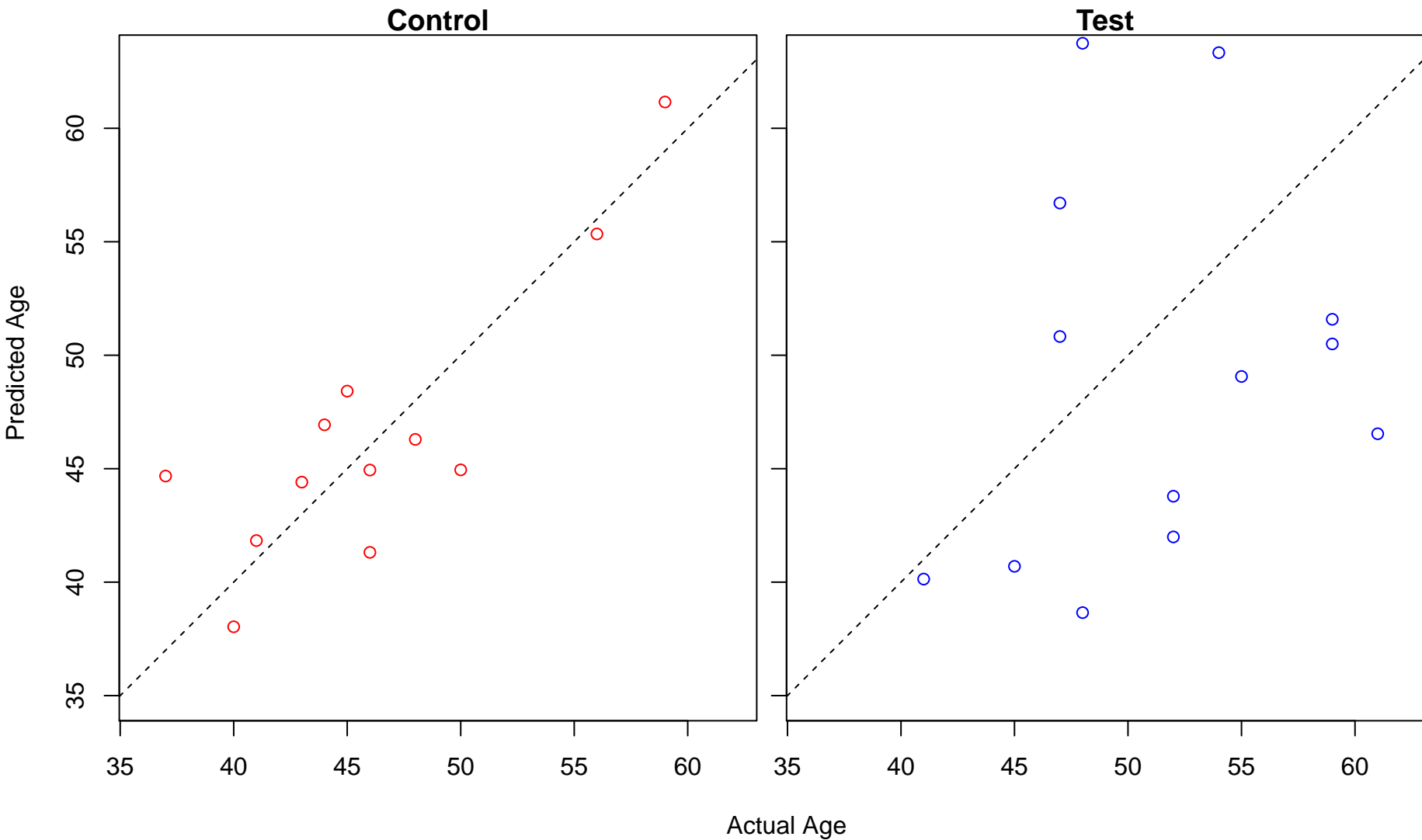
negative regulation of neurological system process (Score: 5.671534)



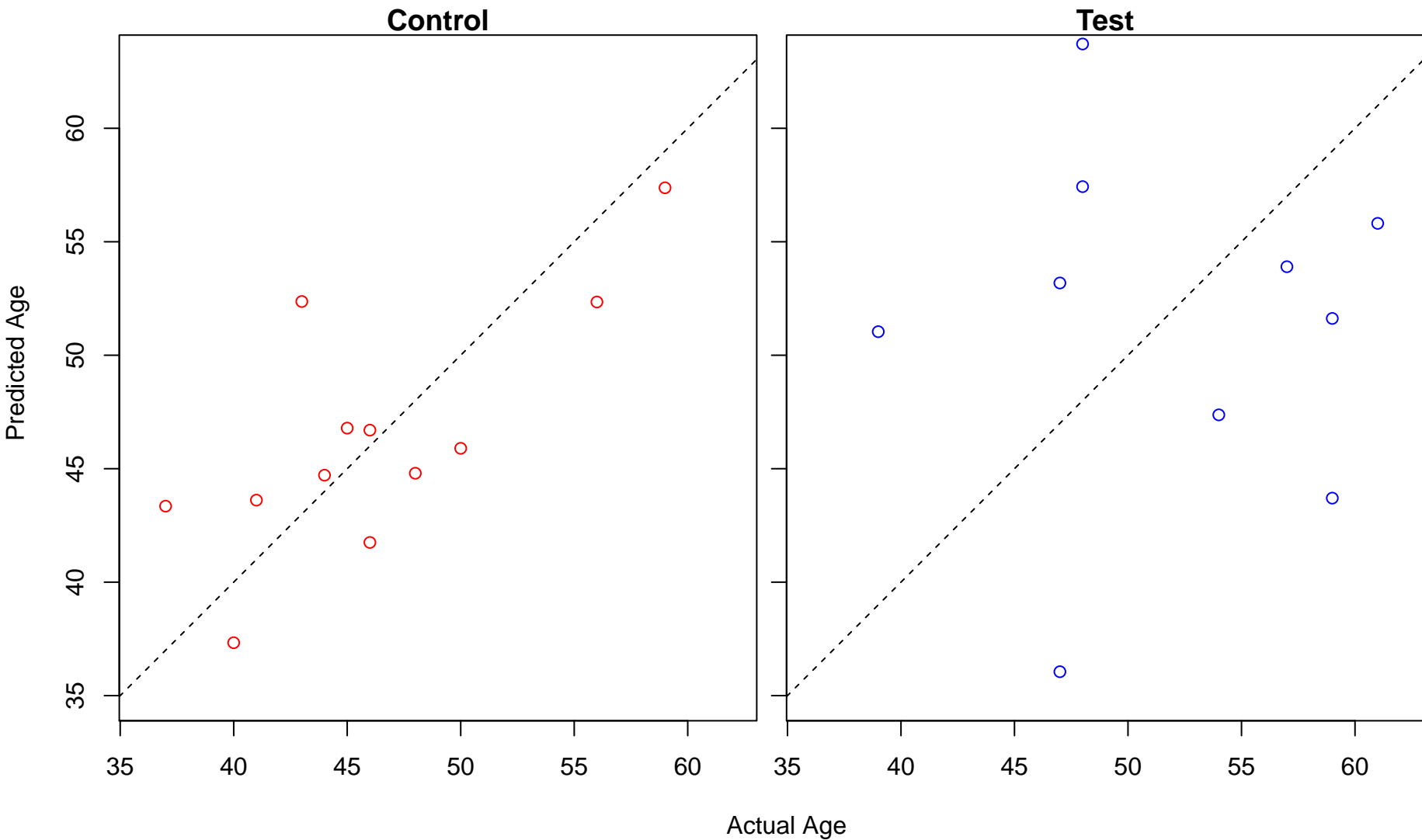
regulation of response to wounding (Score: 5.666985)



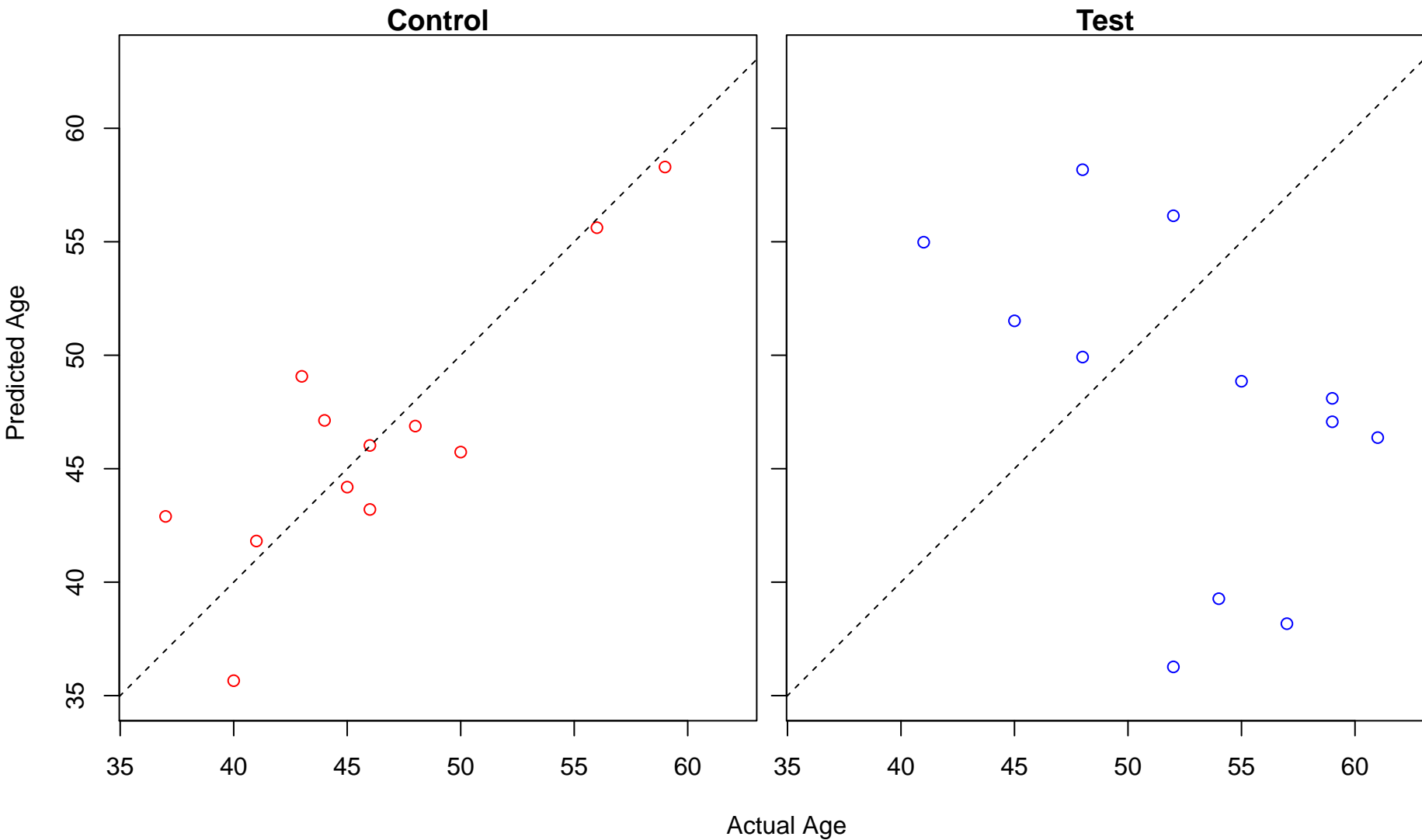
regulation of phosphatase activity (Score: 5.659497)



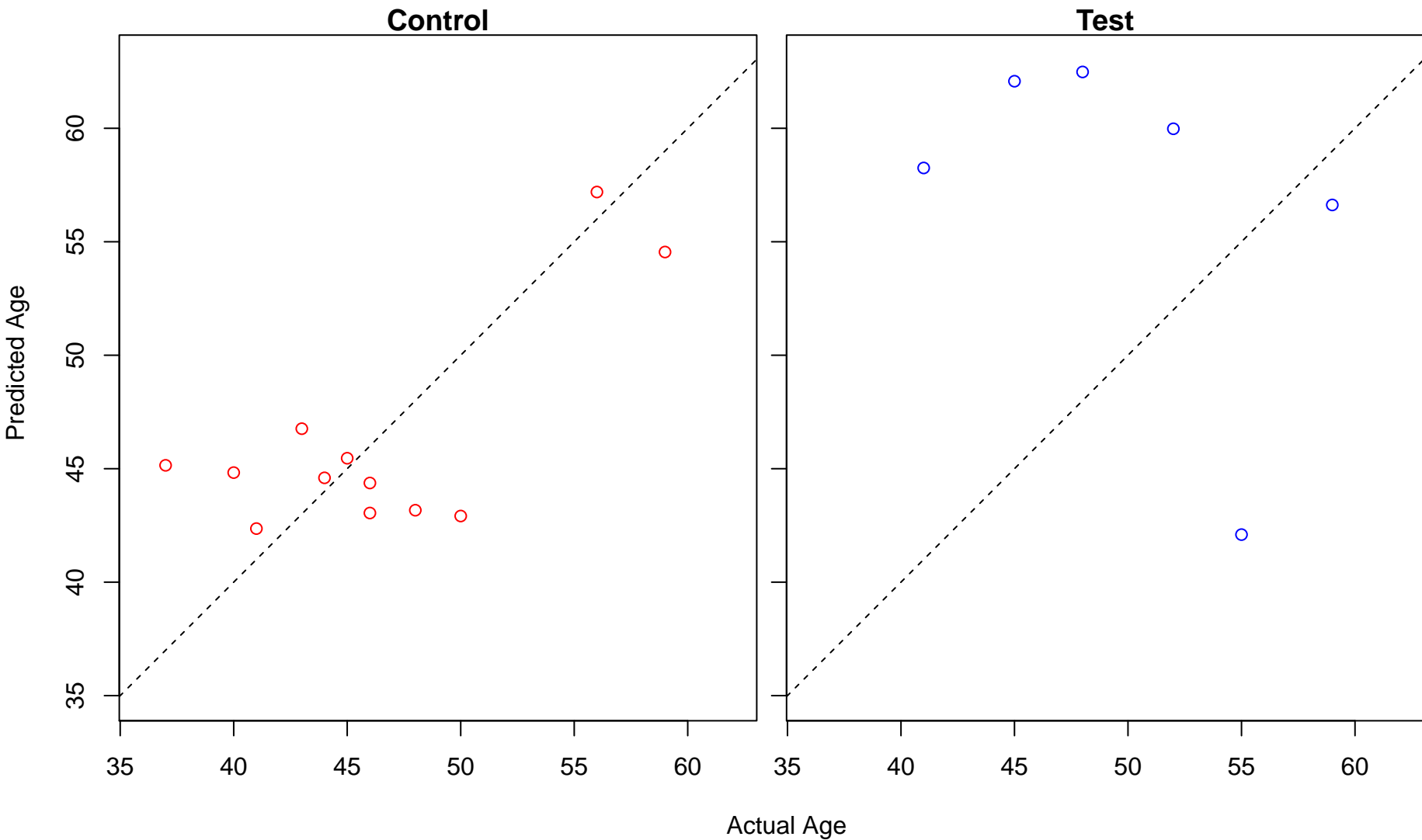
hair follicle morphogenesis (Score: 5.658788)



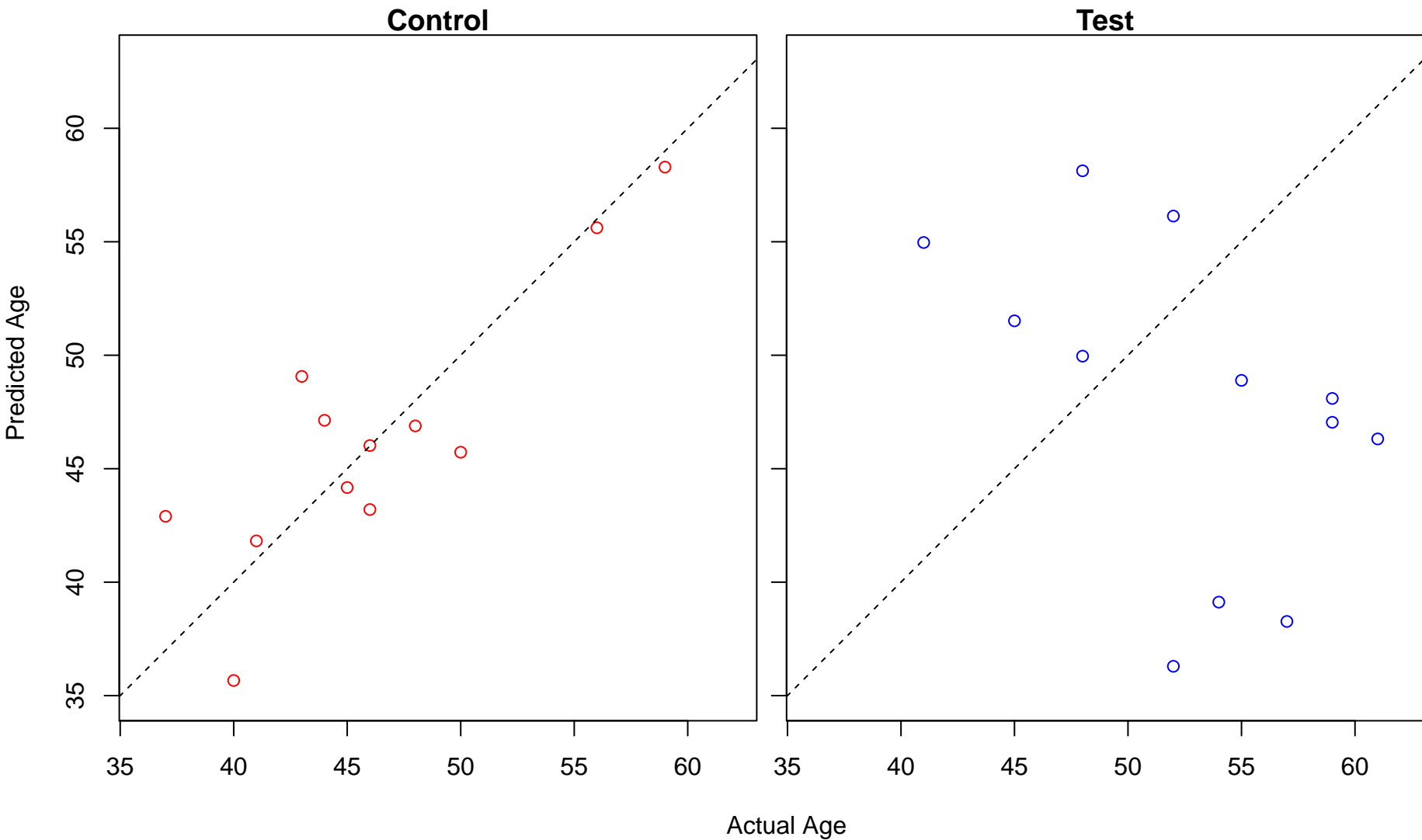
negative regulation of angiogenesis (Score: 5.648797)



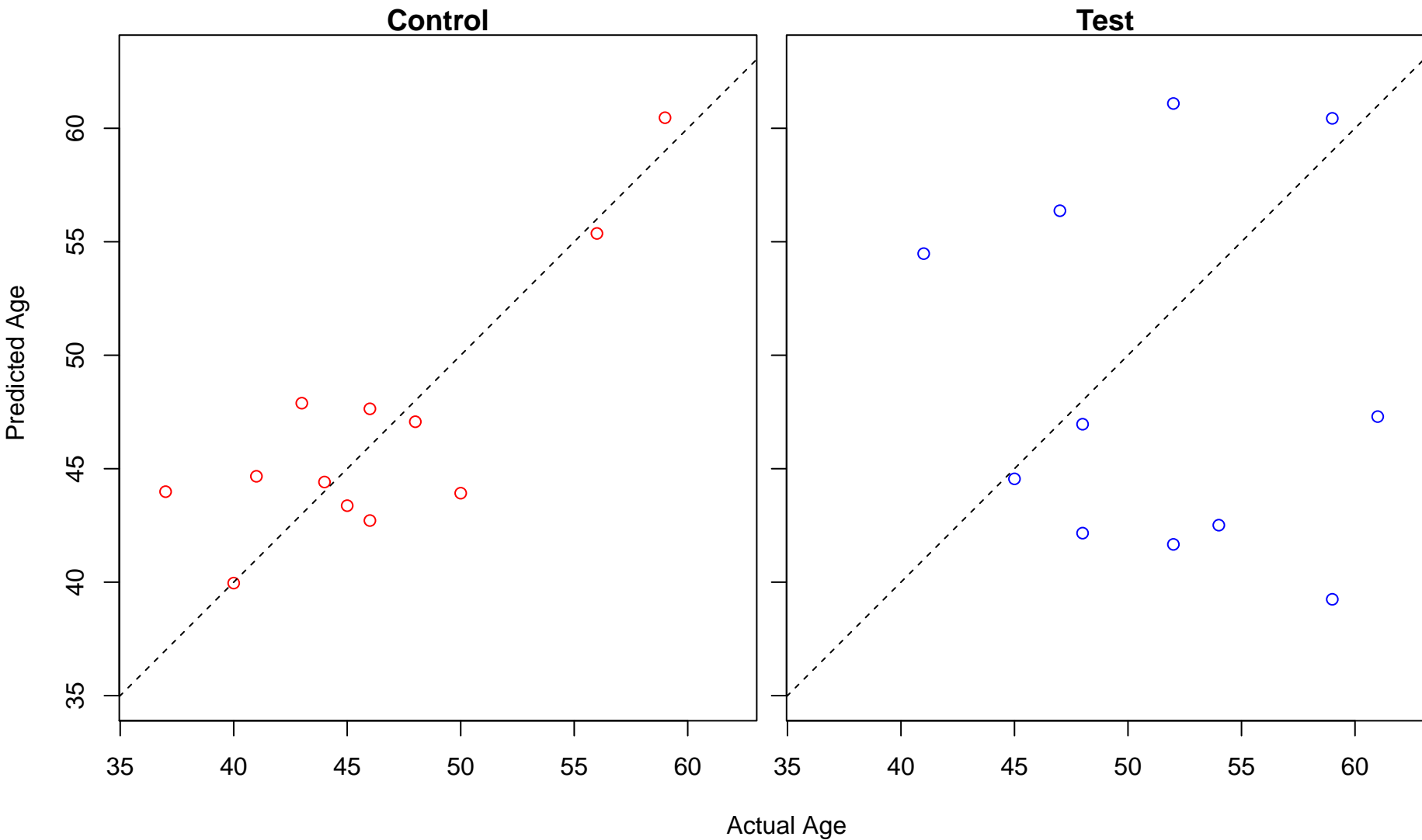
pteridine-containing compound biosynthetic process (Score: 5.643175)



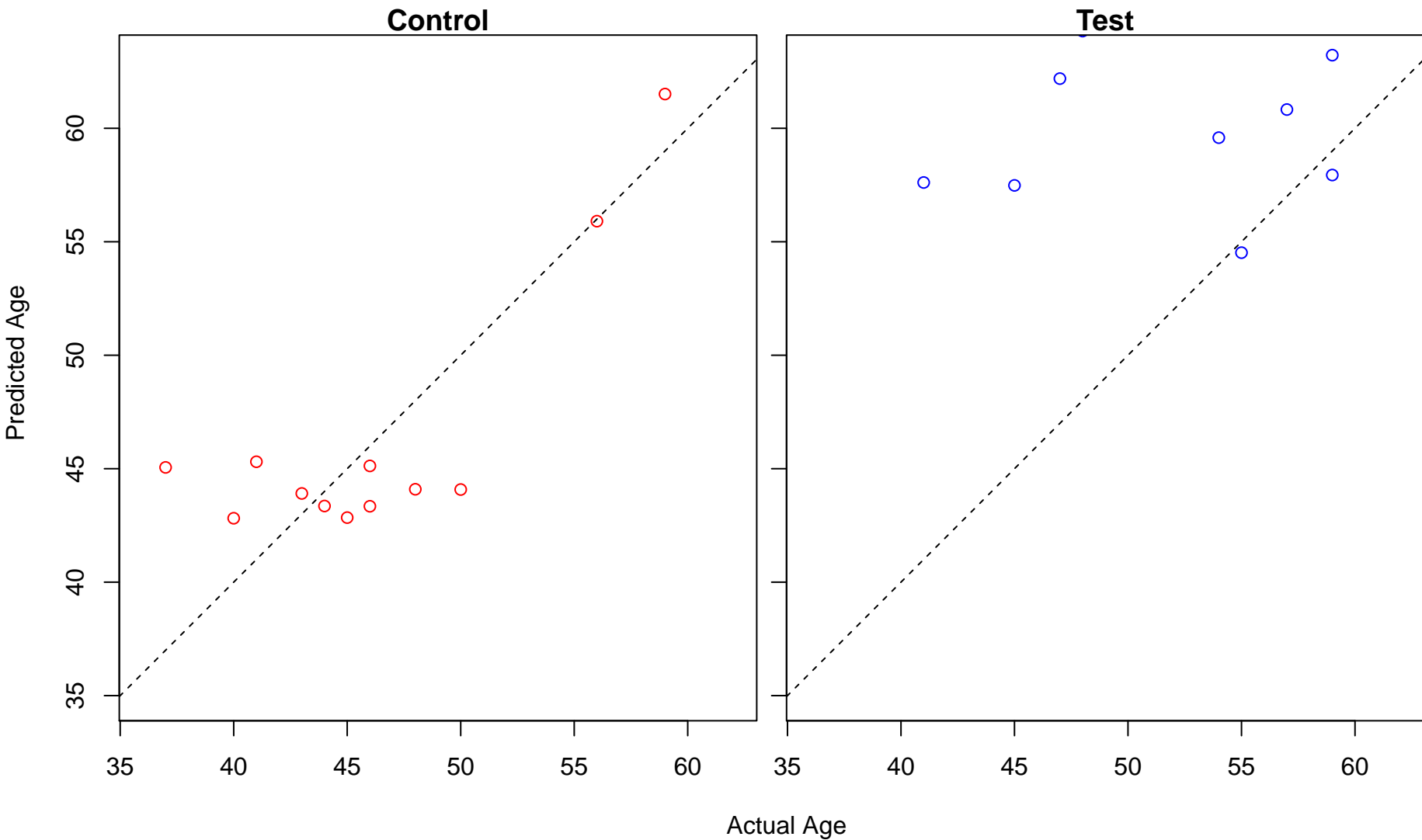
negative regulation of blood vessel morphogenesis (Score: 5.642997)



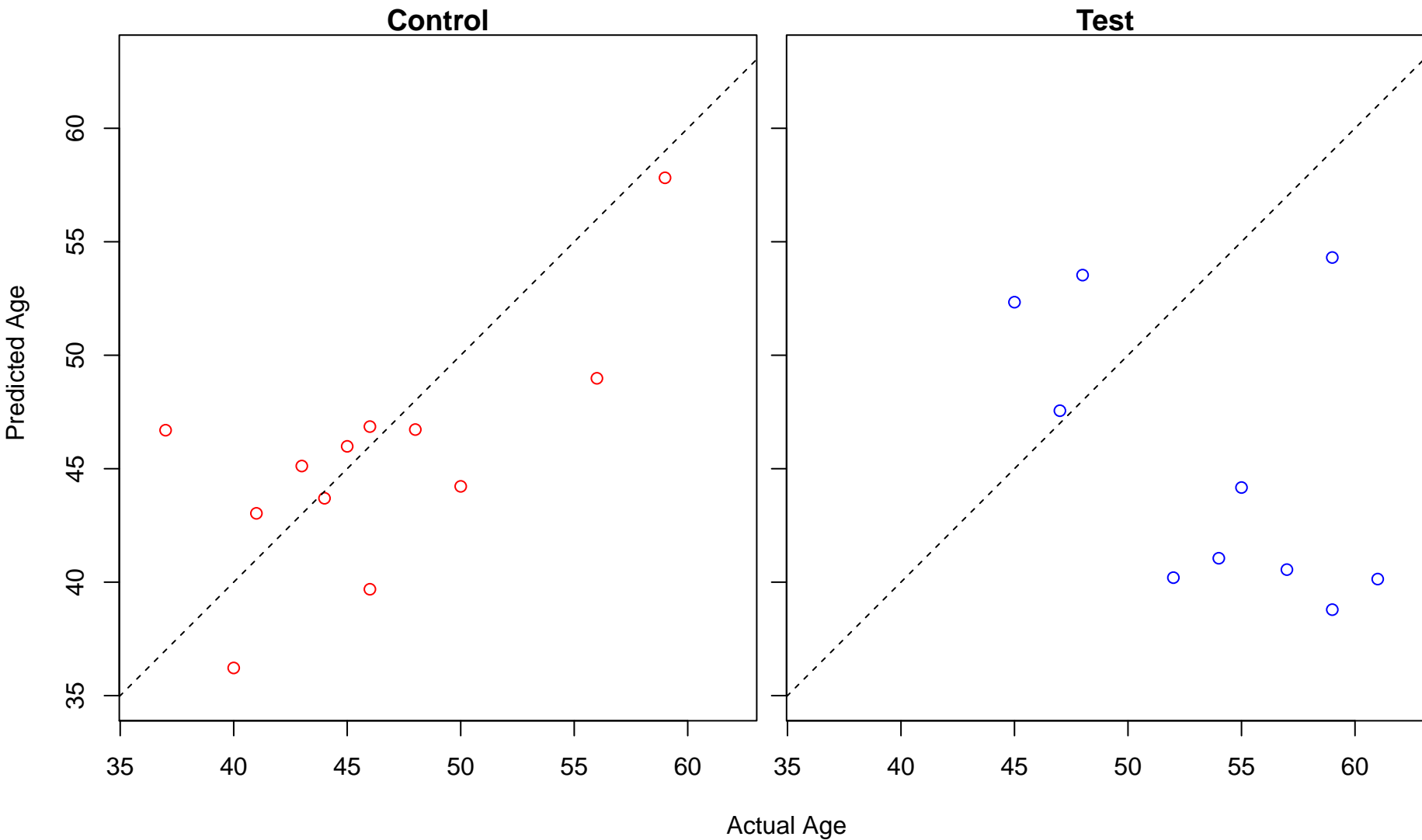
regulation of receptor-mediated endocytosis (Score: 5.620195)



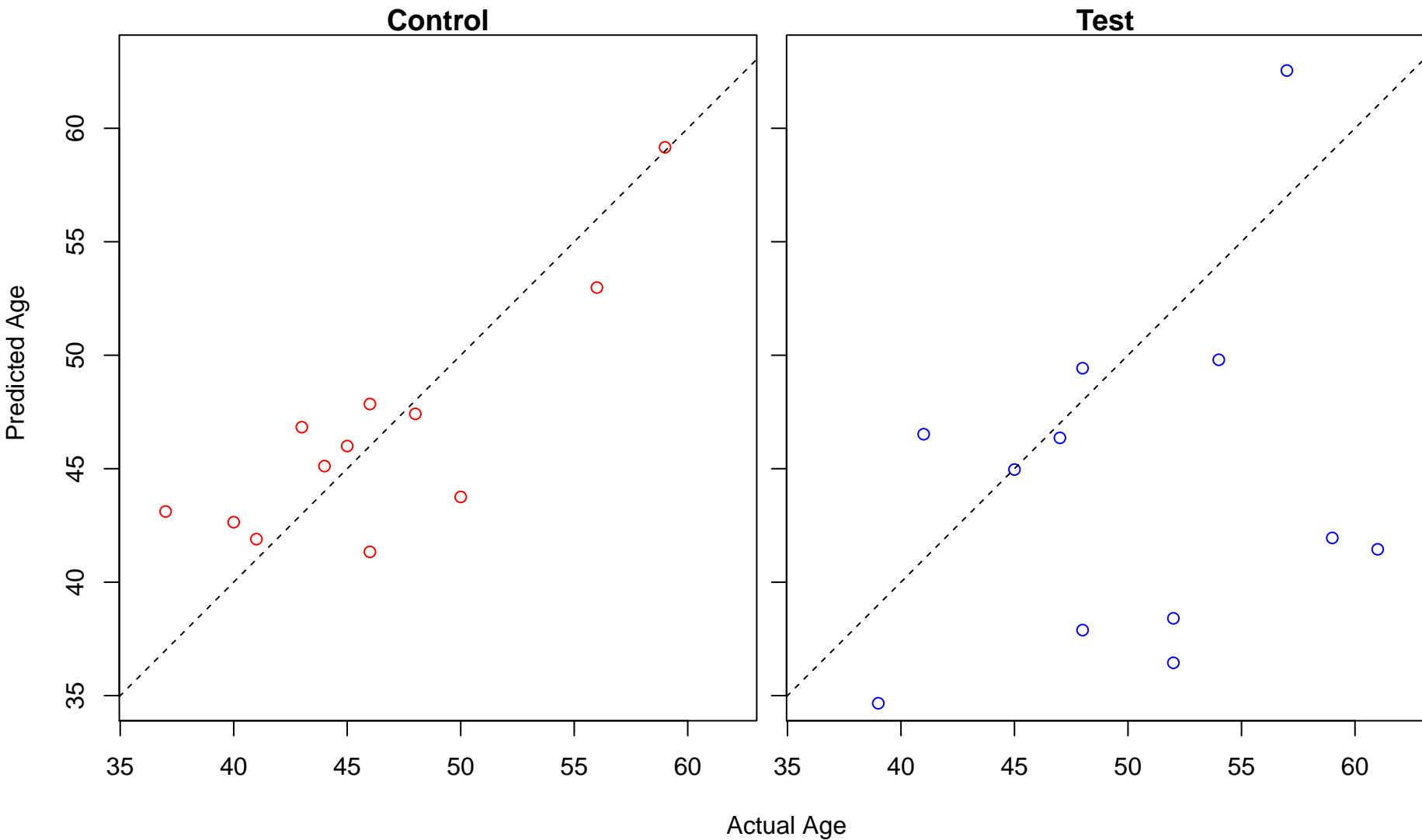
autonomic nervous system development (Score: 5.600848)



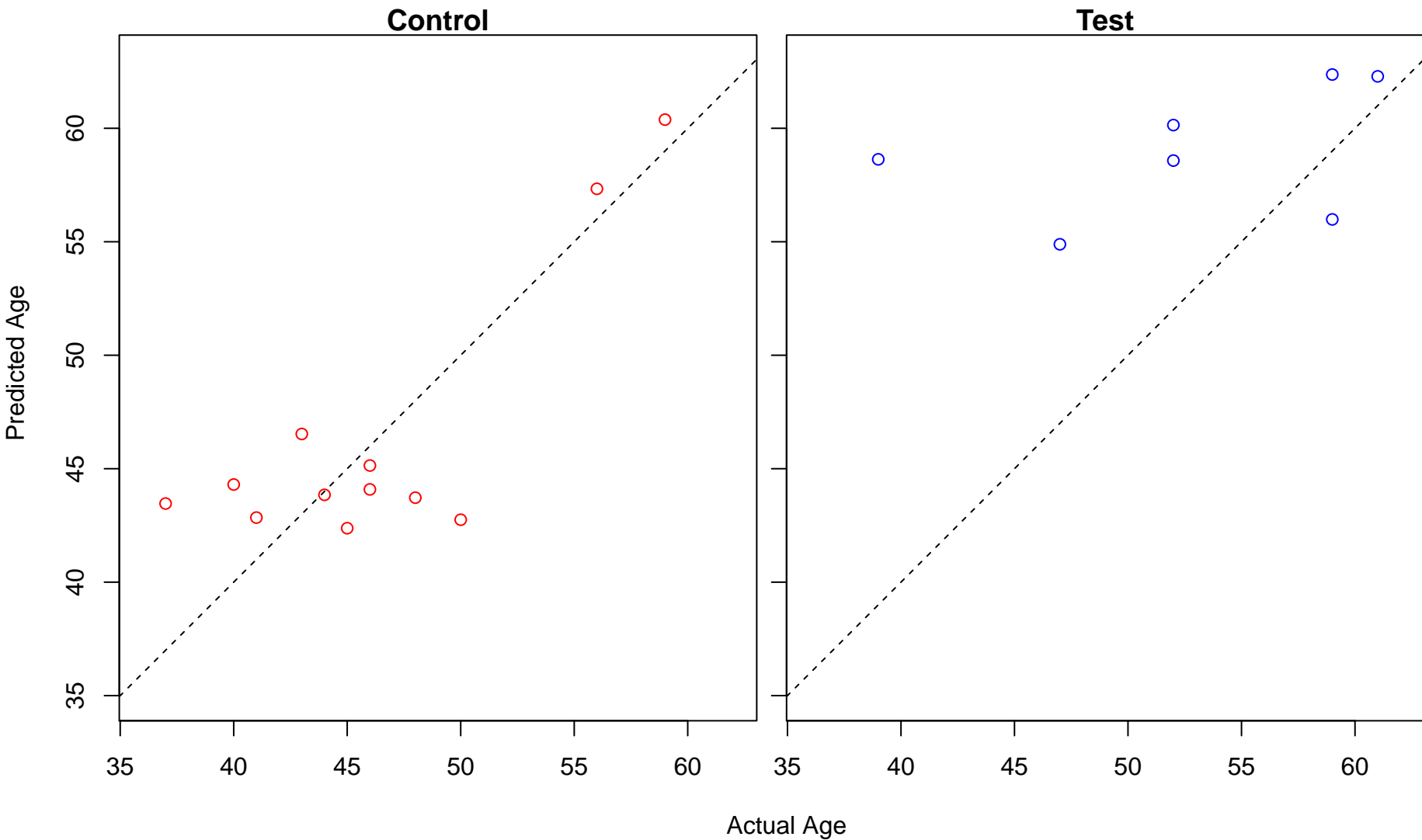
labyrinthine layer development (Score: 5.600617)



regulation of immune effector process (Score: 5.594055)

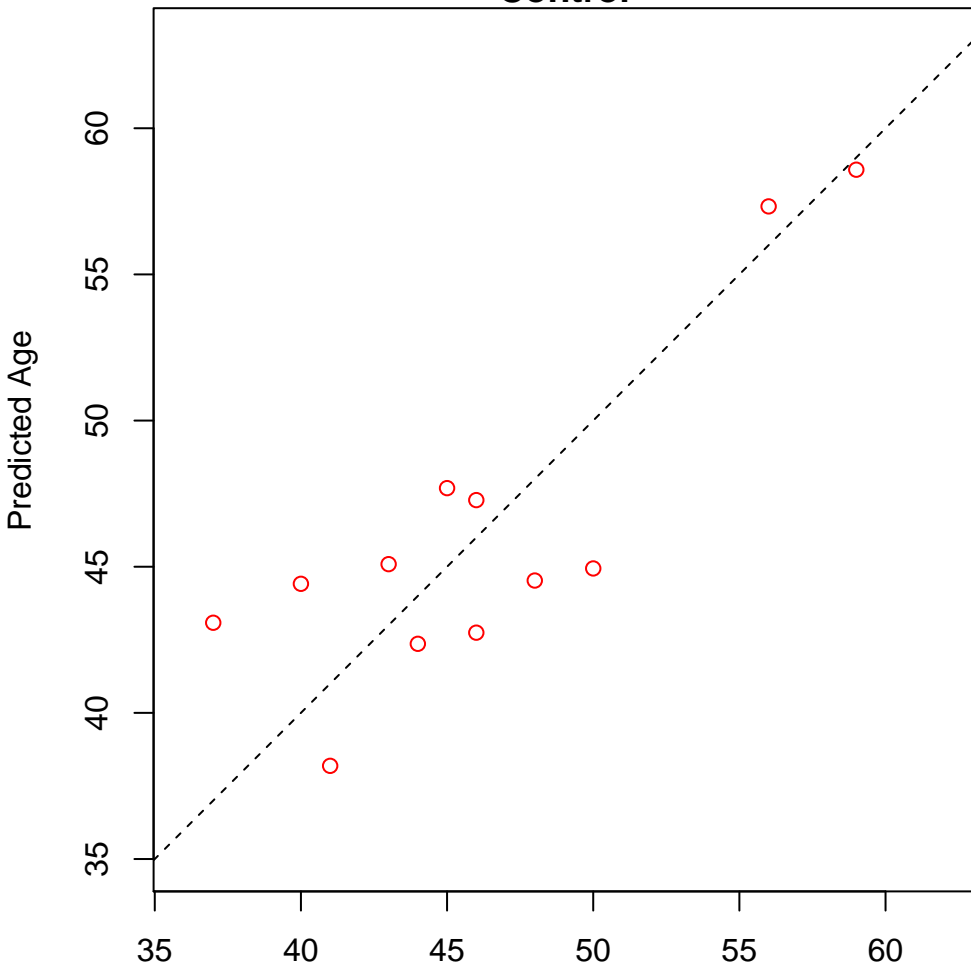


regulation of T-helper cell differentiation (Score: 5.576162)

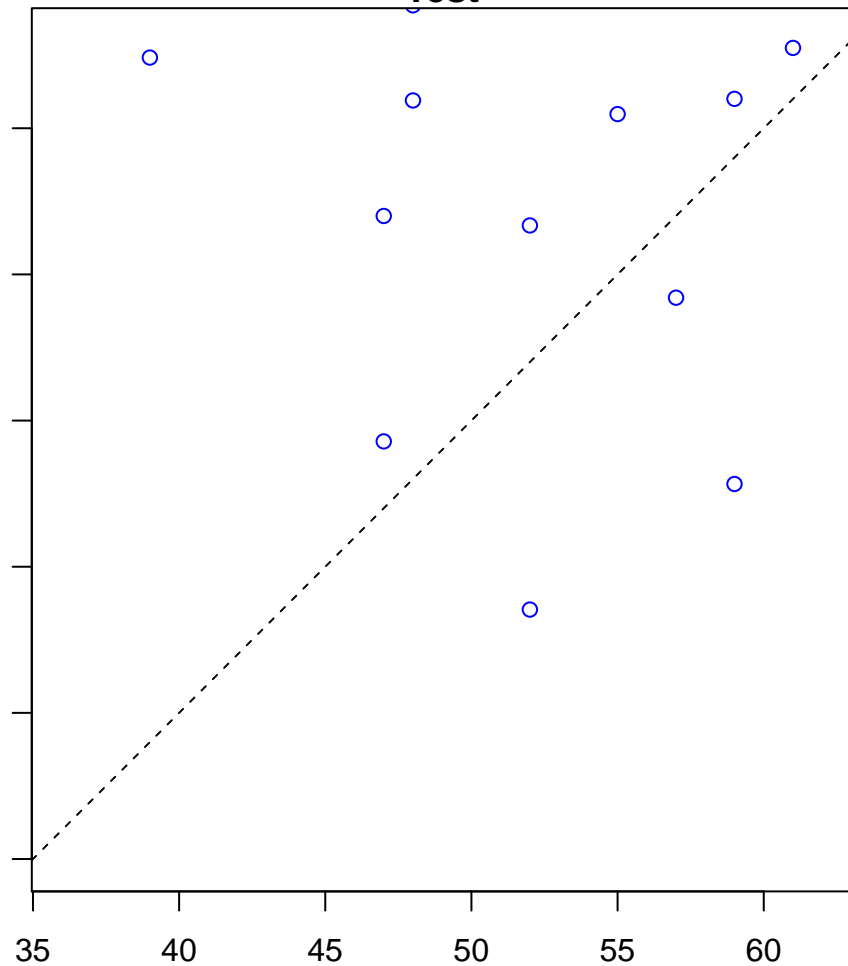


regulation of fatty acid beta-oxidation (Score: 5.565190)

Control

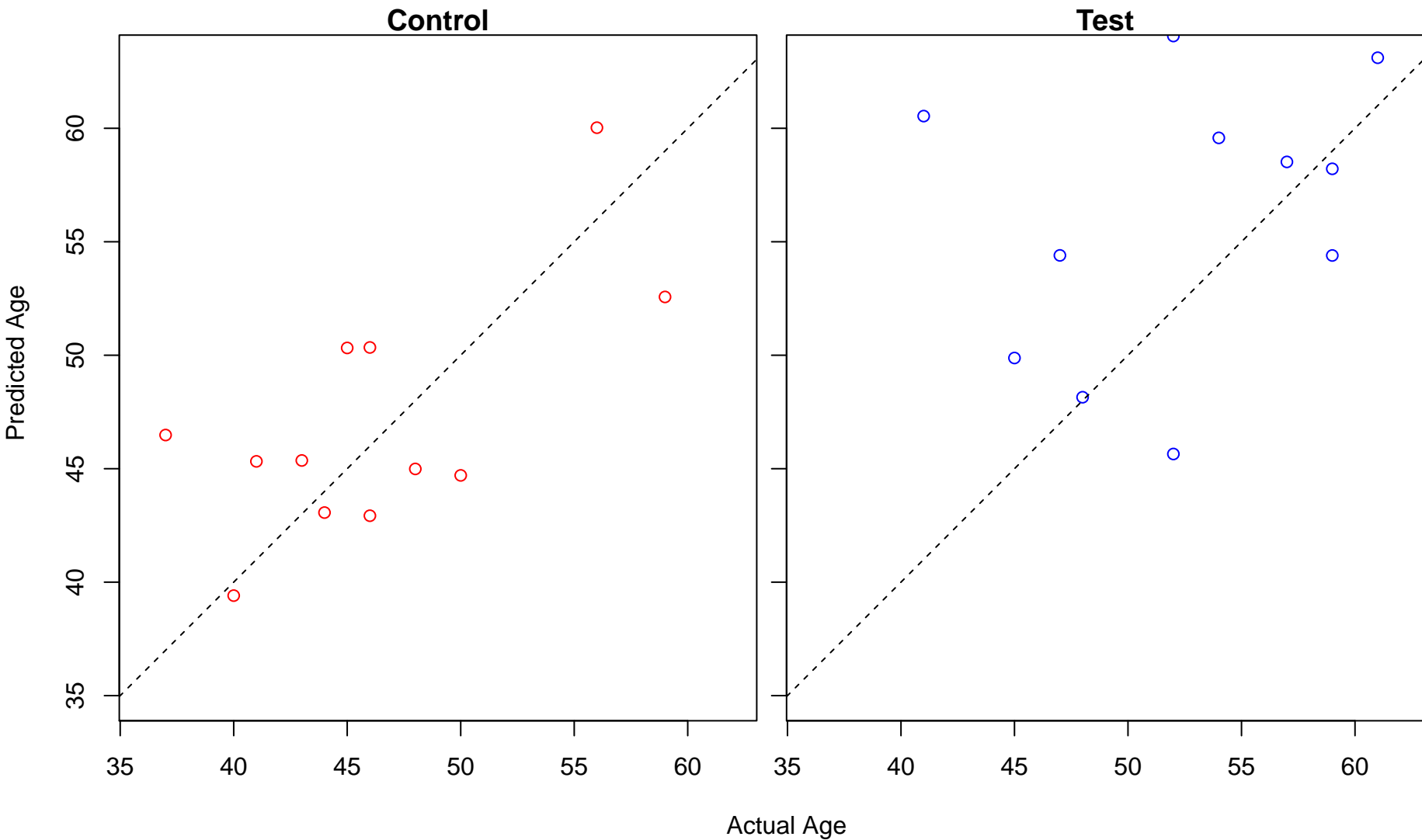


Test



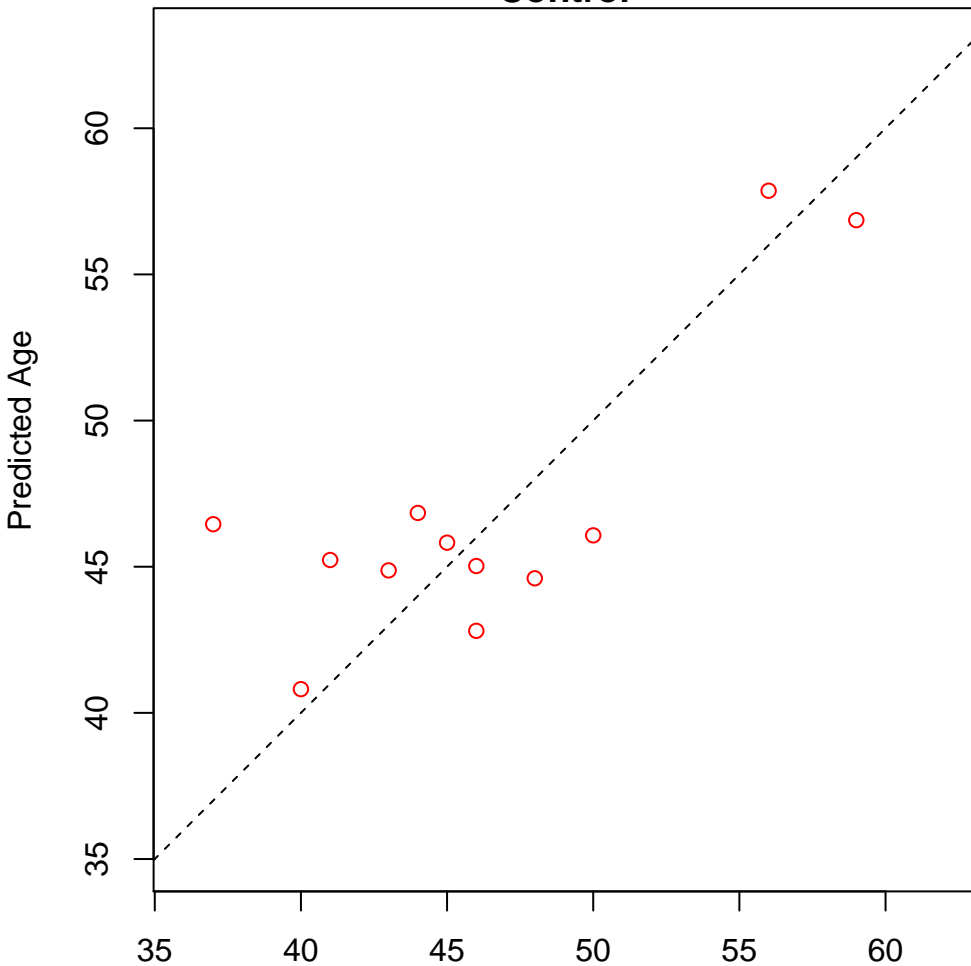
Actual Age

cellular response to UV-B (Score: 5.562504)

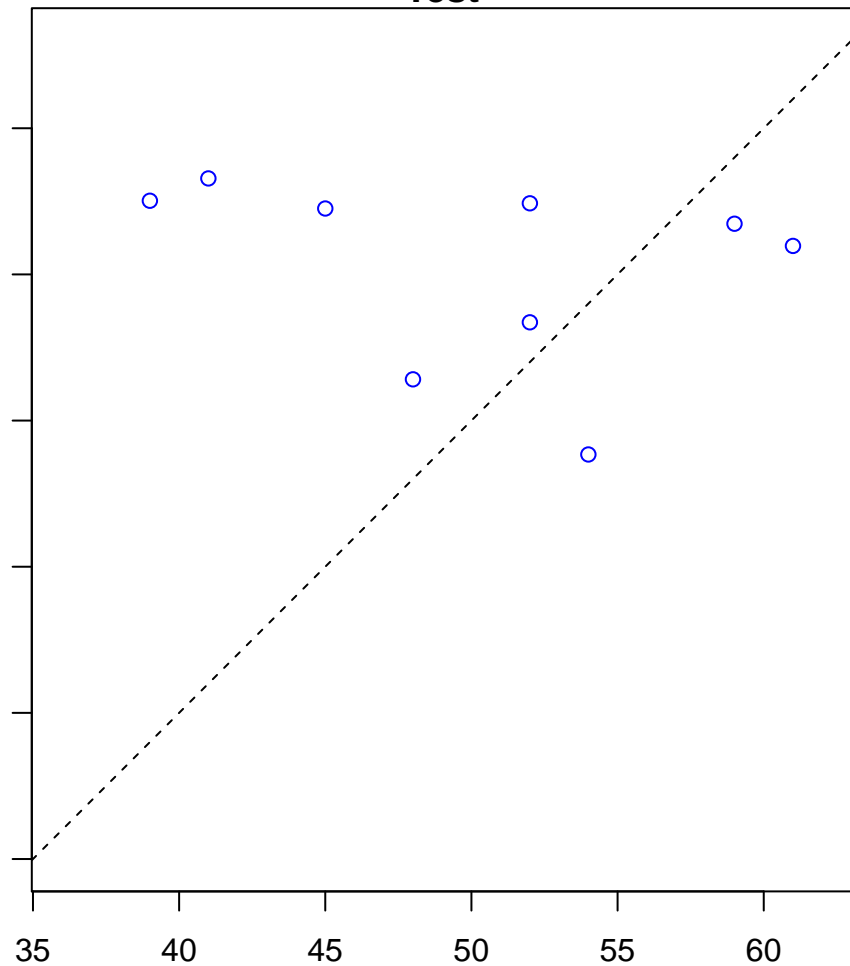


regulation of angiotensin levels in blood (Score: 5.558666)

Control

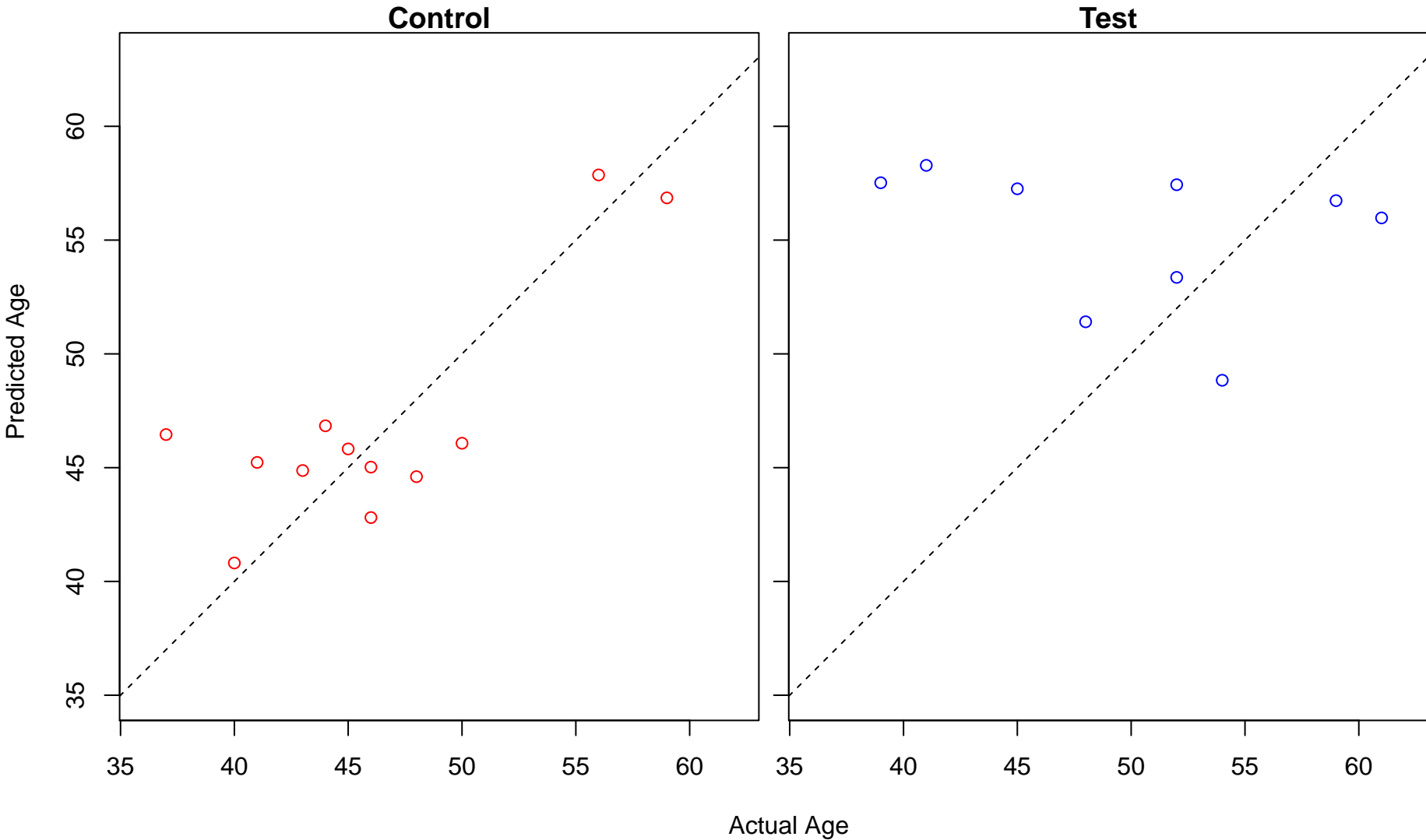


Test

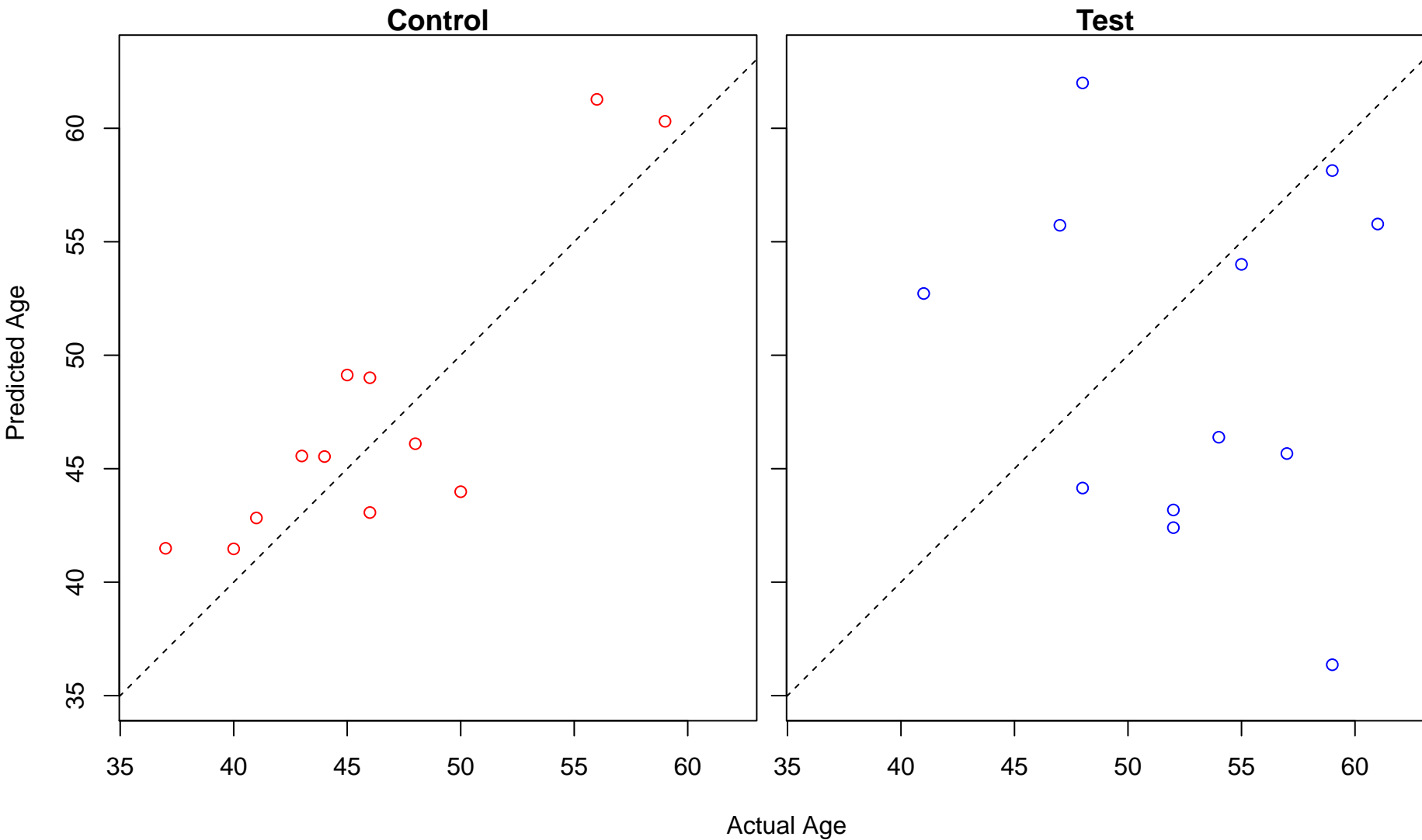


Actual Age

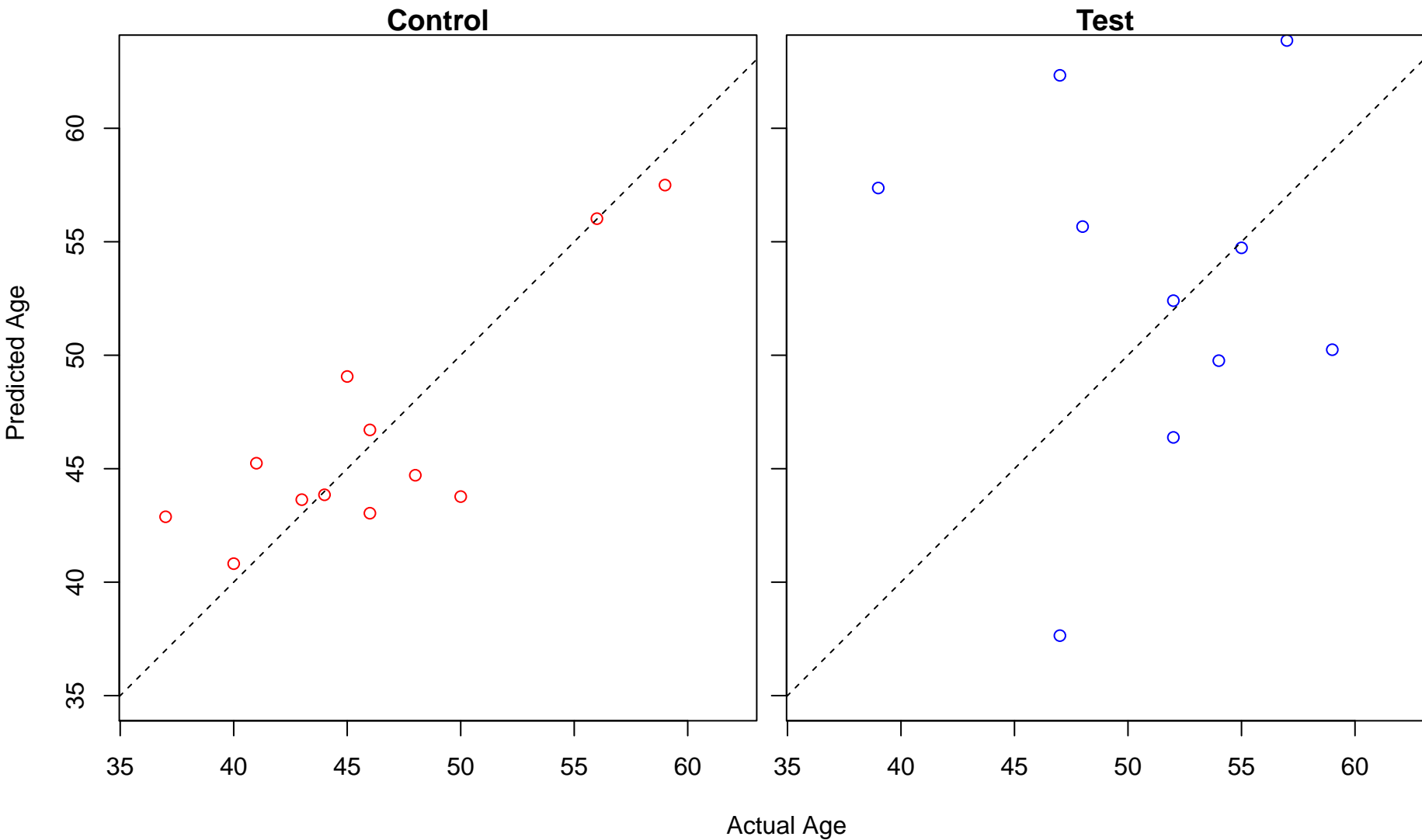
regulation of angiotensin metabolic process (Score: 5.558666)



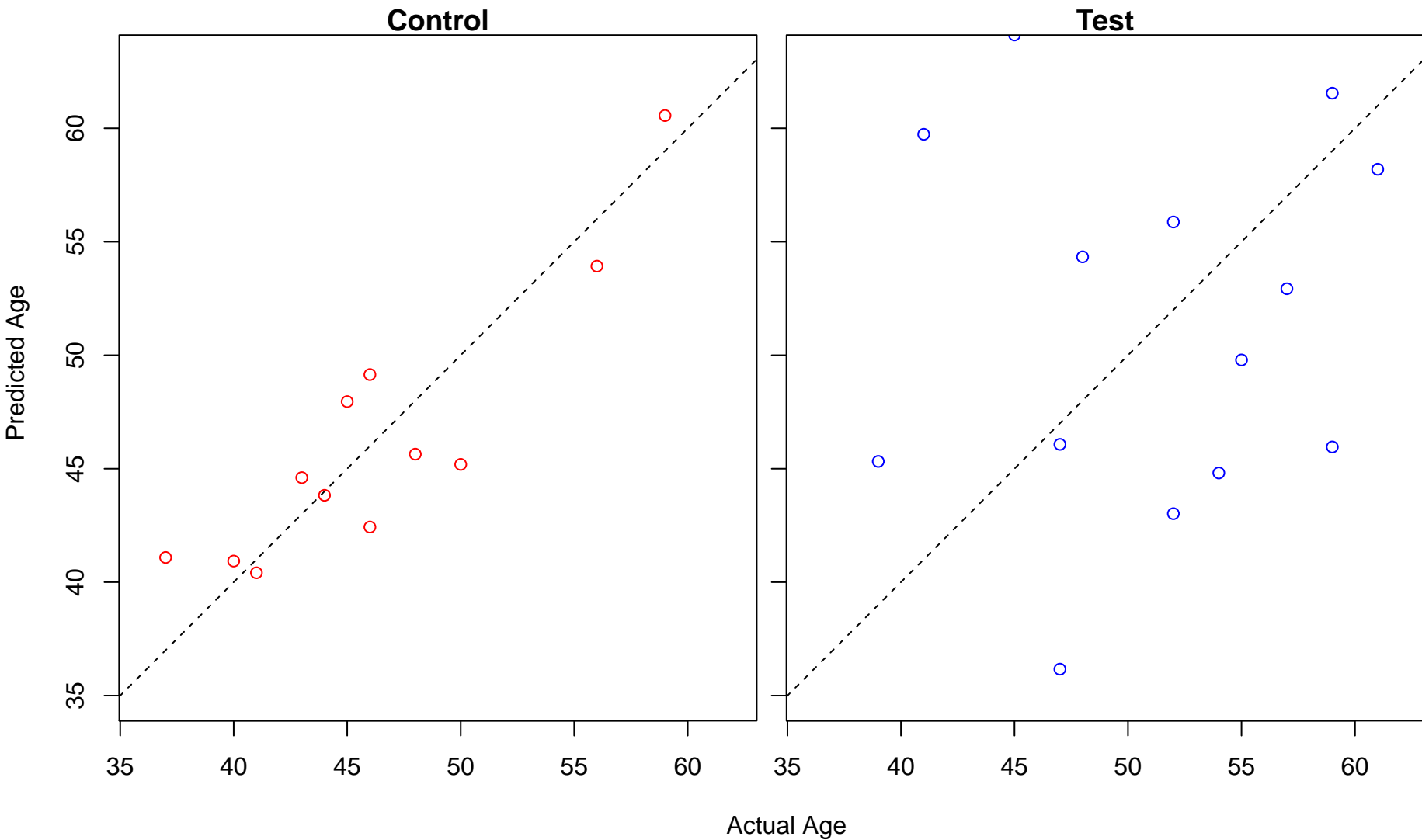
fat cell differentiation (Score: 5.549189)



regulation of cell cycle checkpoint (Score: 5.532215)

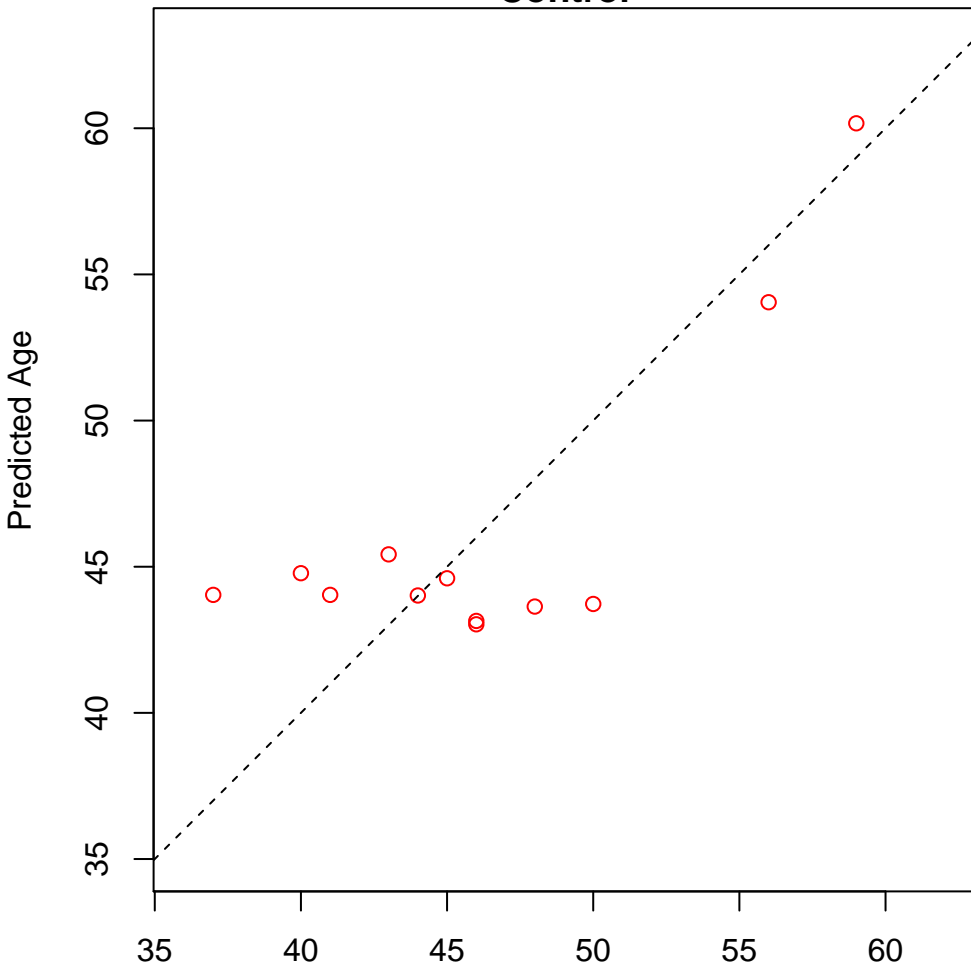


photoreceptor cell development (Score: 5.531225)

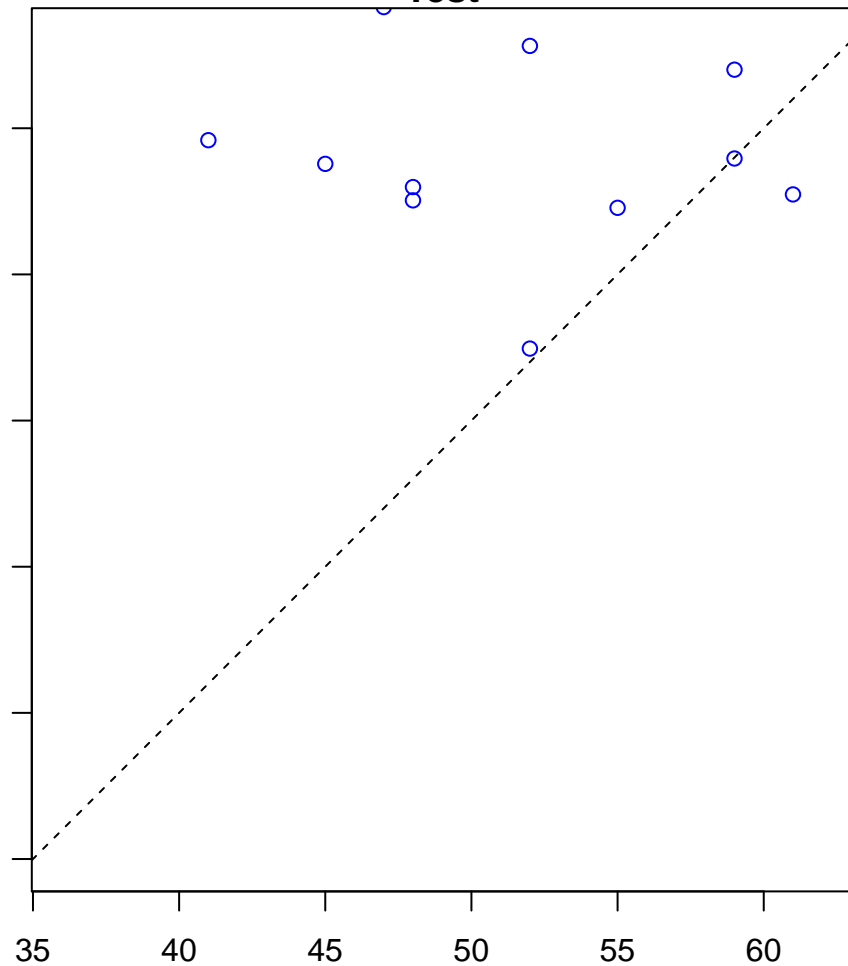


negative regulation of cilium assembly (Score: 5.528712)

Control

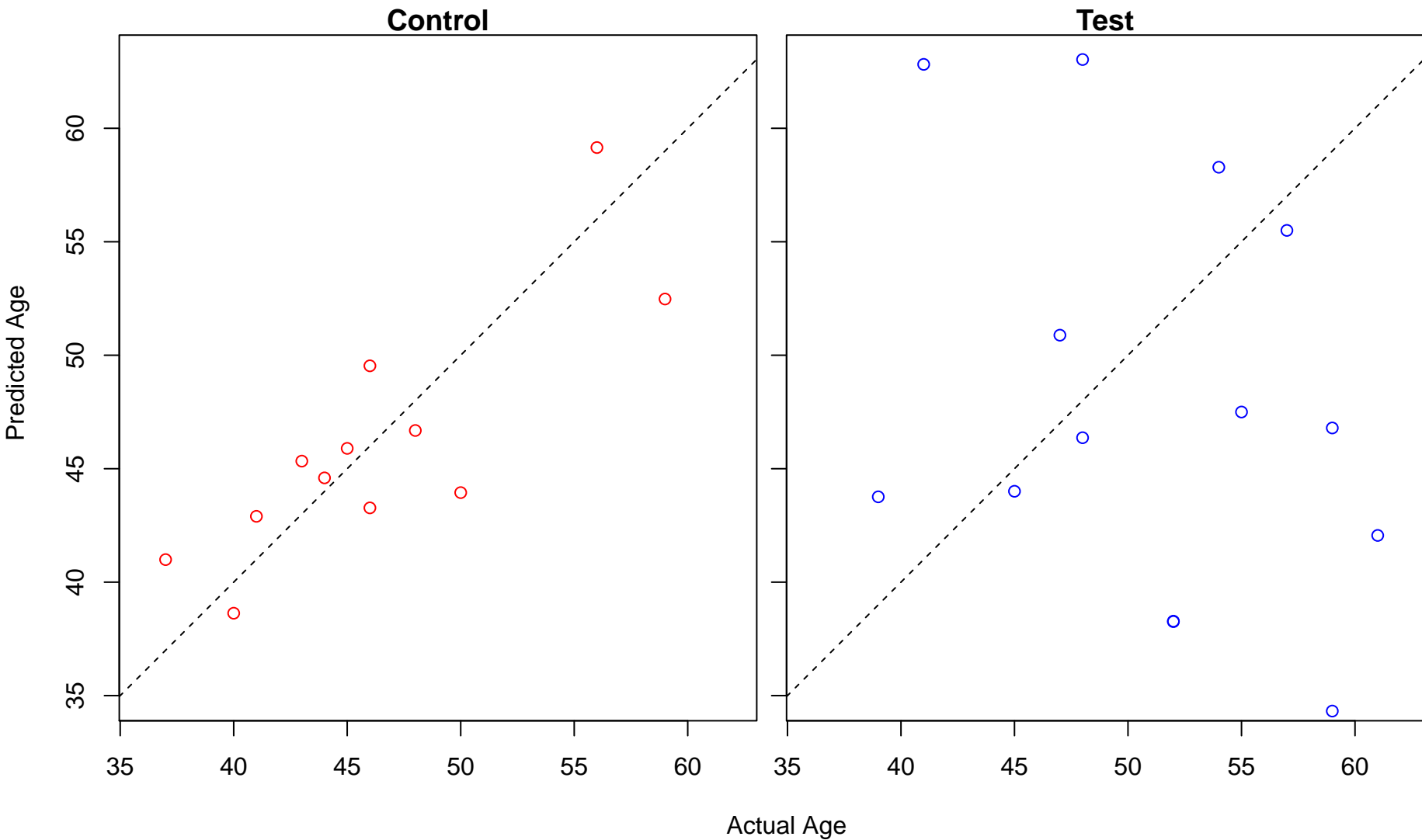


Test



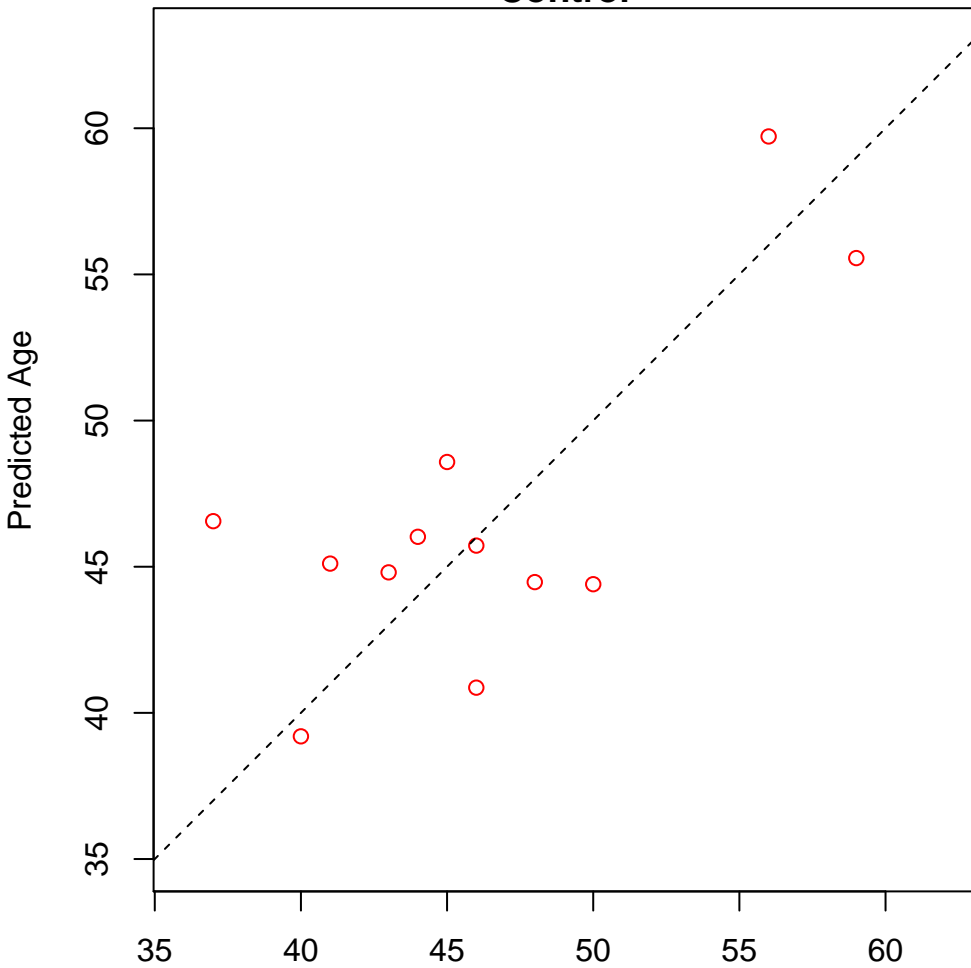
Actual Age

mesoderm morphogenesis (Score: 5.516400)

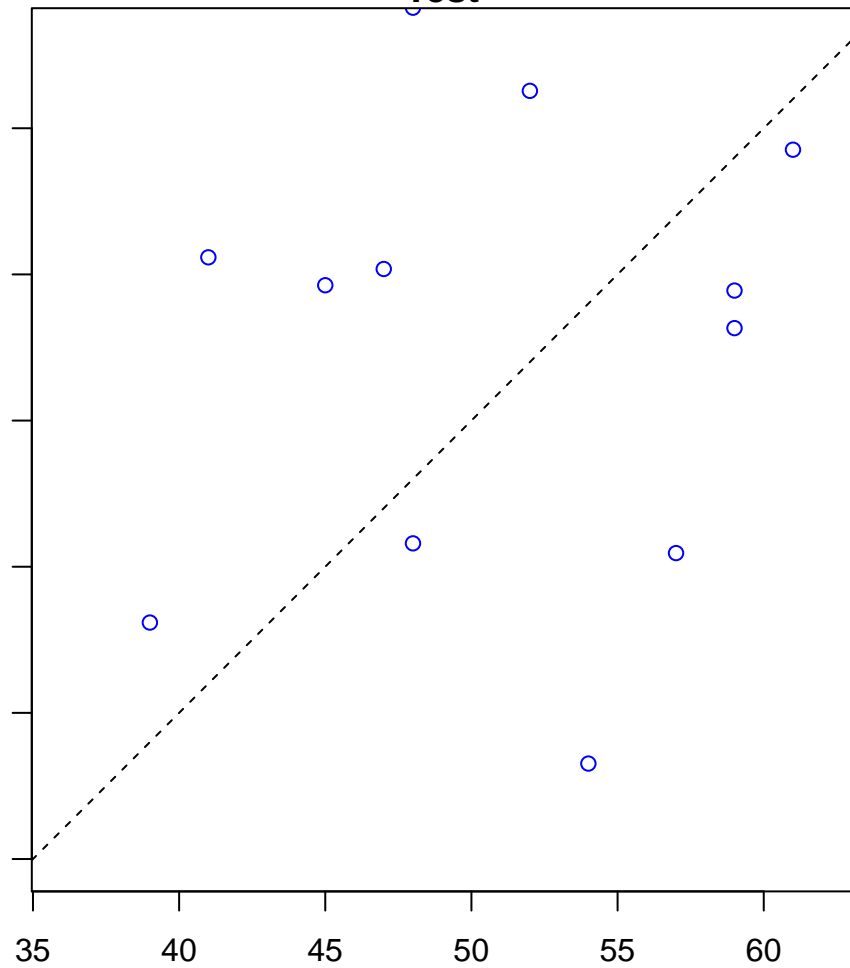


response to UV-B (Score: 5.509524)

Control

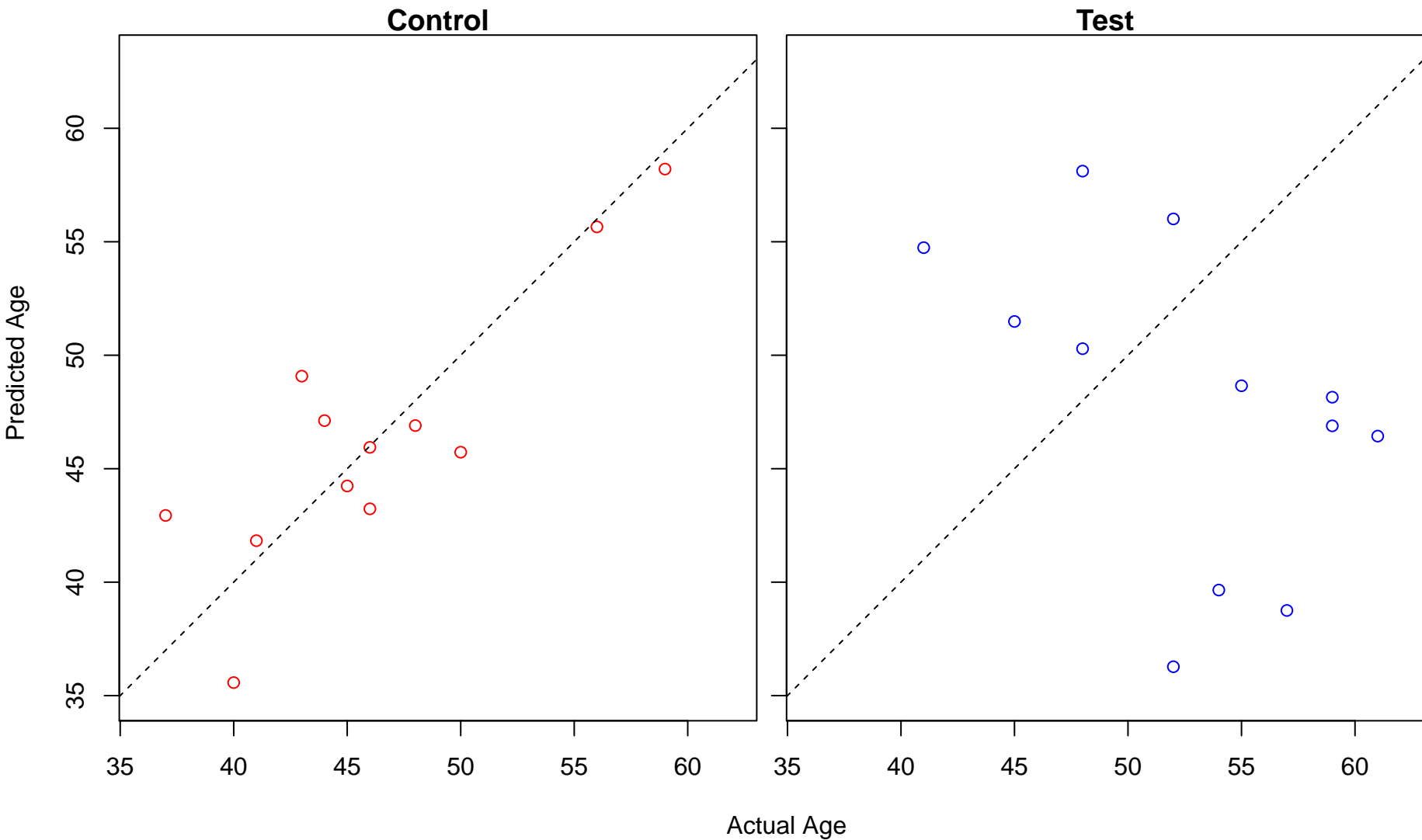


Test

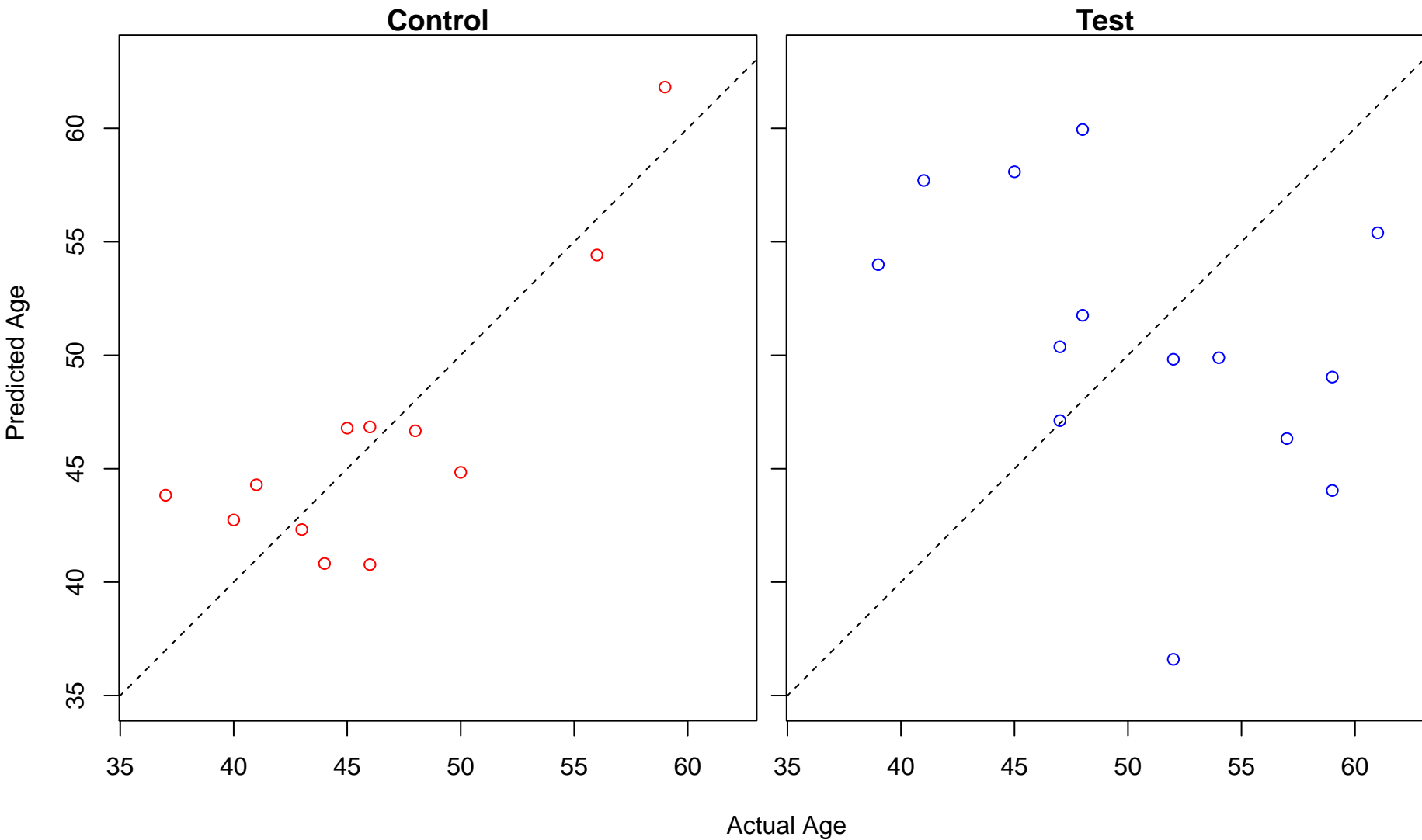


Actual Age

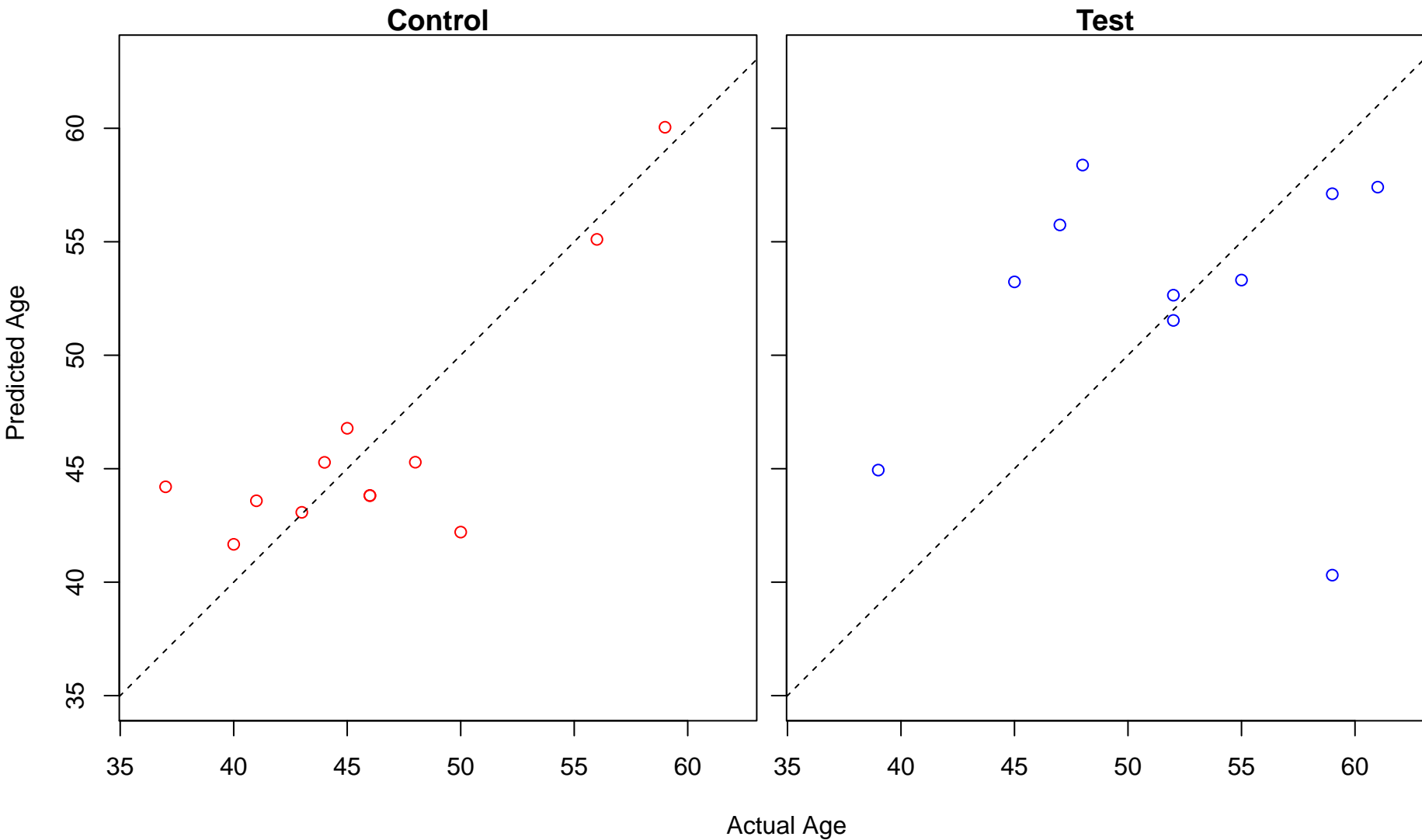
negative regulation of vasculature development (Score: 5.506577)



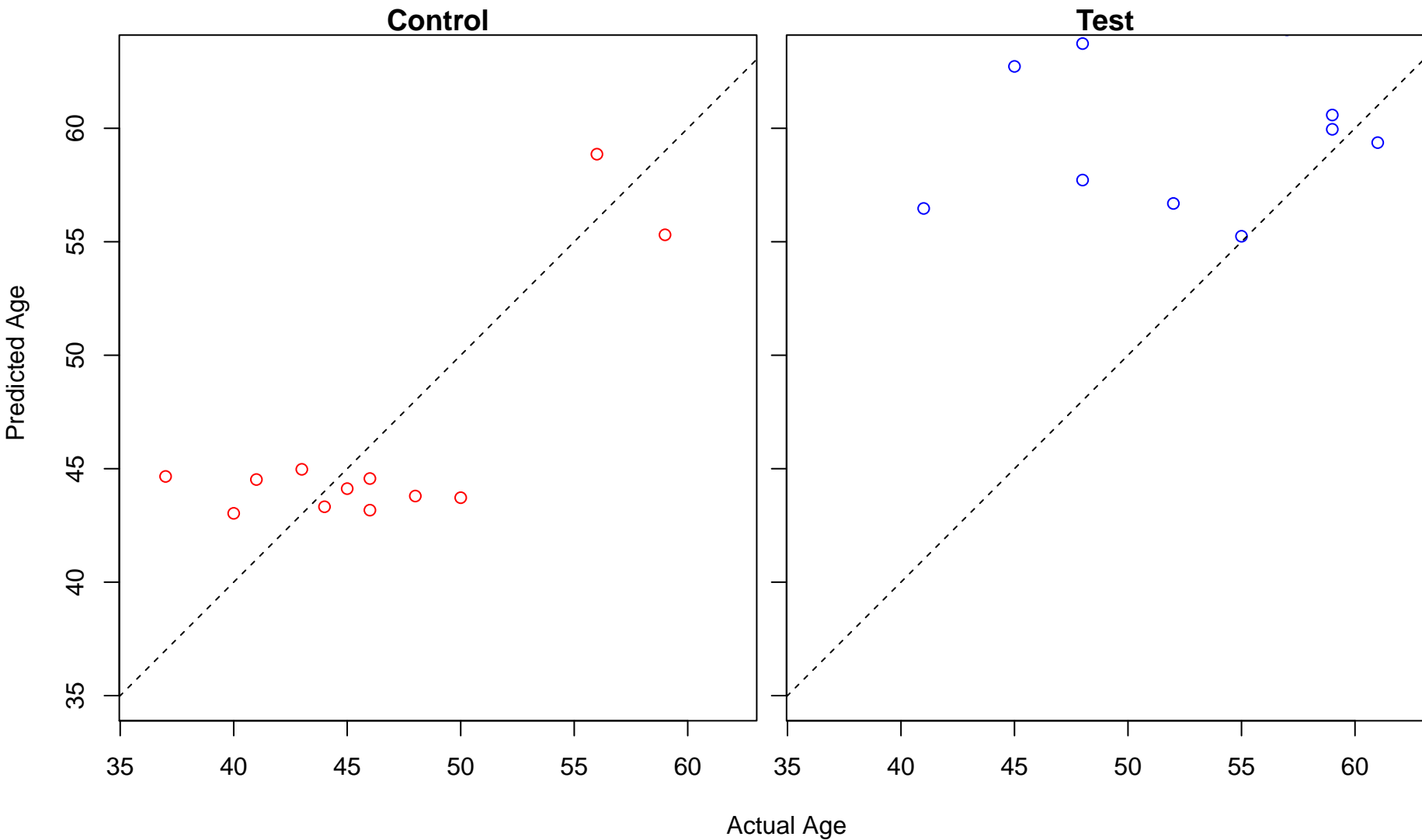
cytokine production (Score: 5.503816)



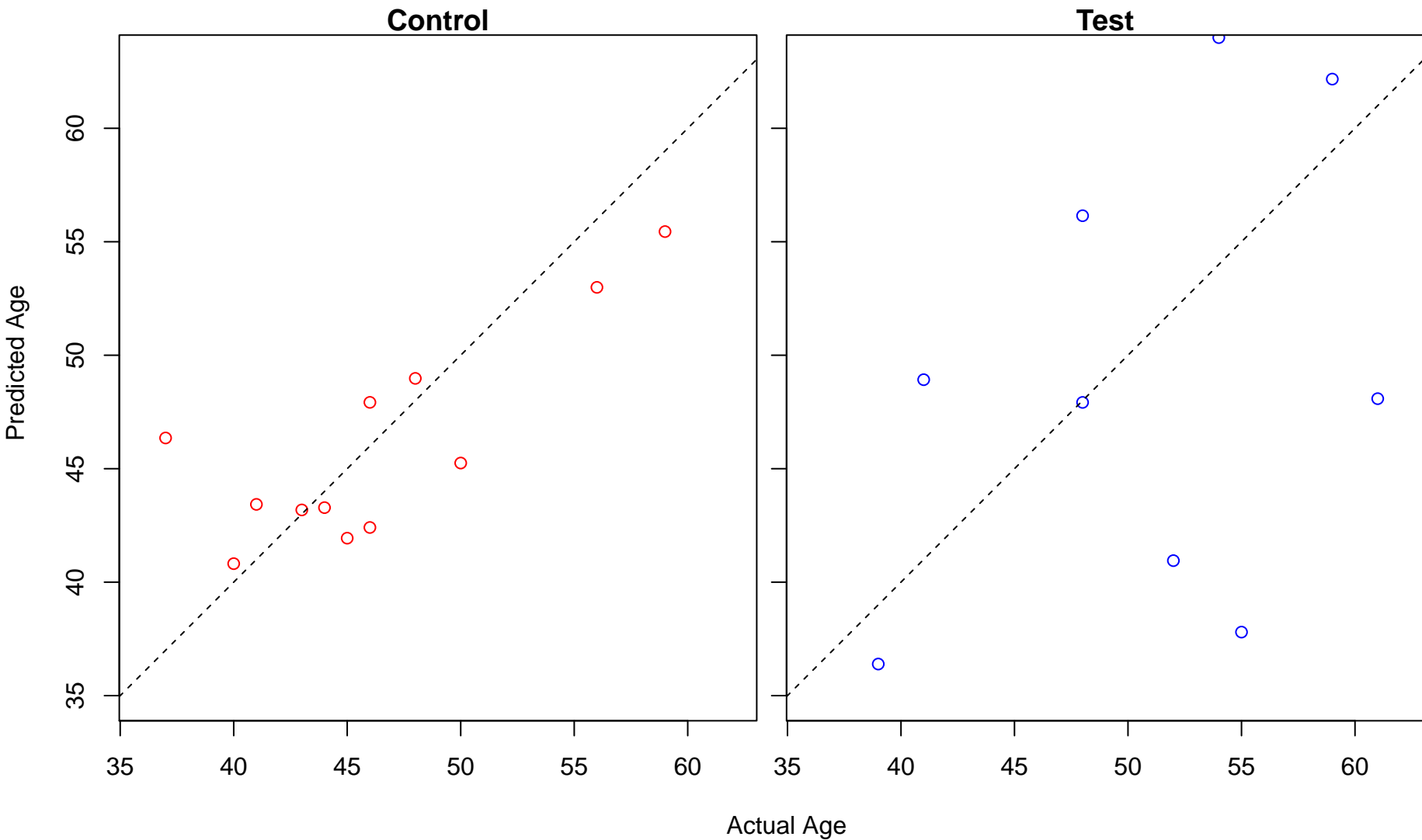
regulation of bone development (Score: 5.502537)



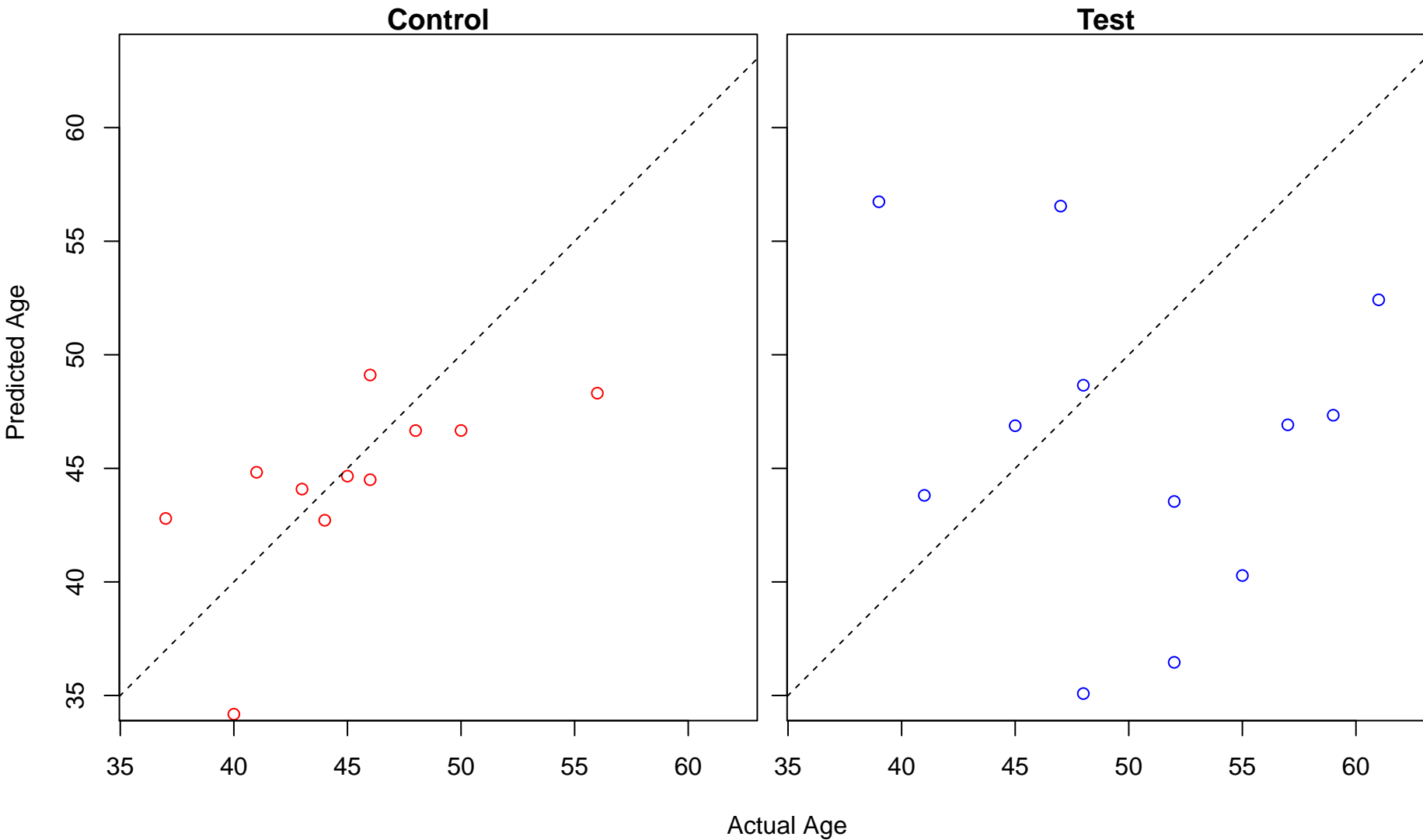
osteoblast development (Score: 5.501694)



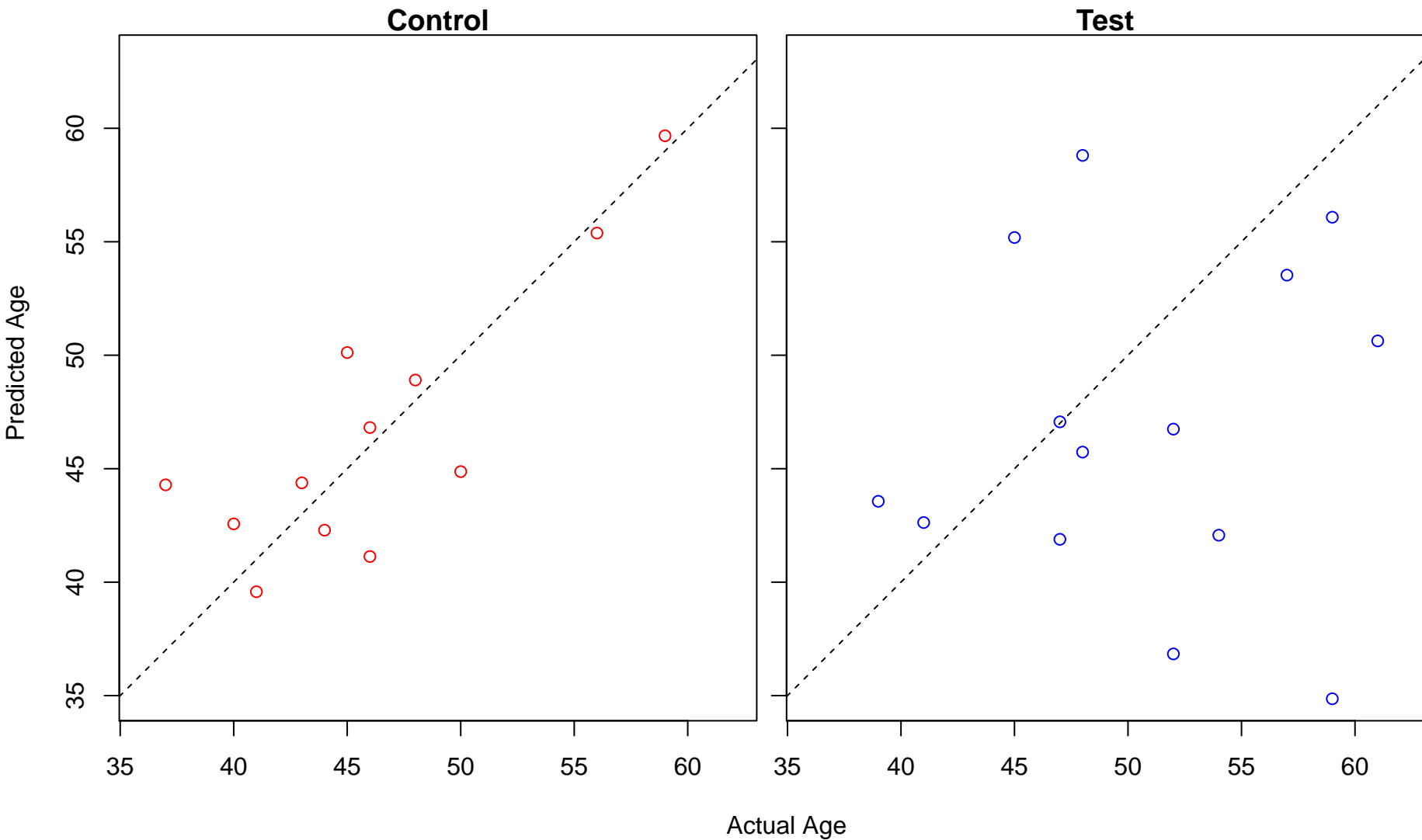
tetrahydrofolate interconversion (Score: 5.501151)



regulation of cell proliferation involved in kidney development (Score: 5.495607)

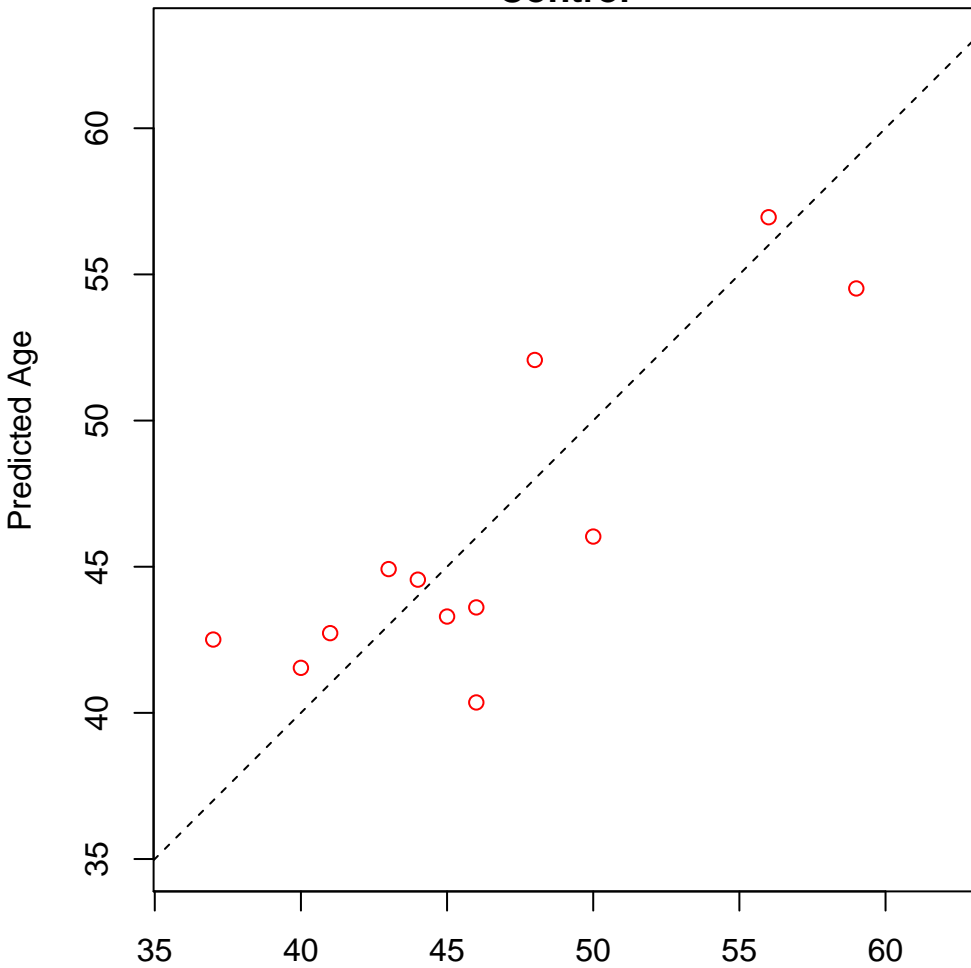


protein N-linked glycosylation via asparagine (Score: 5.494946)

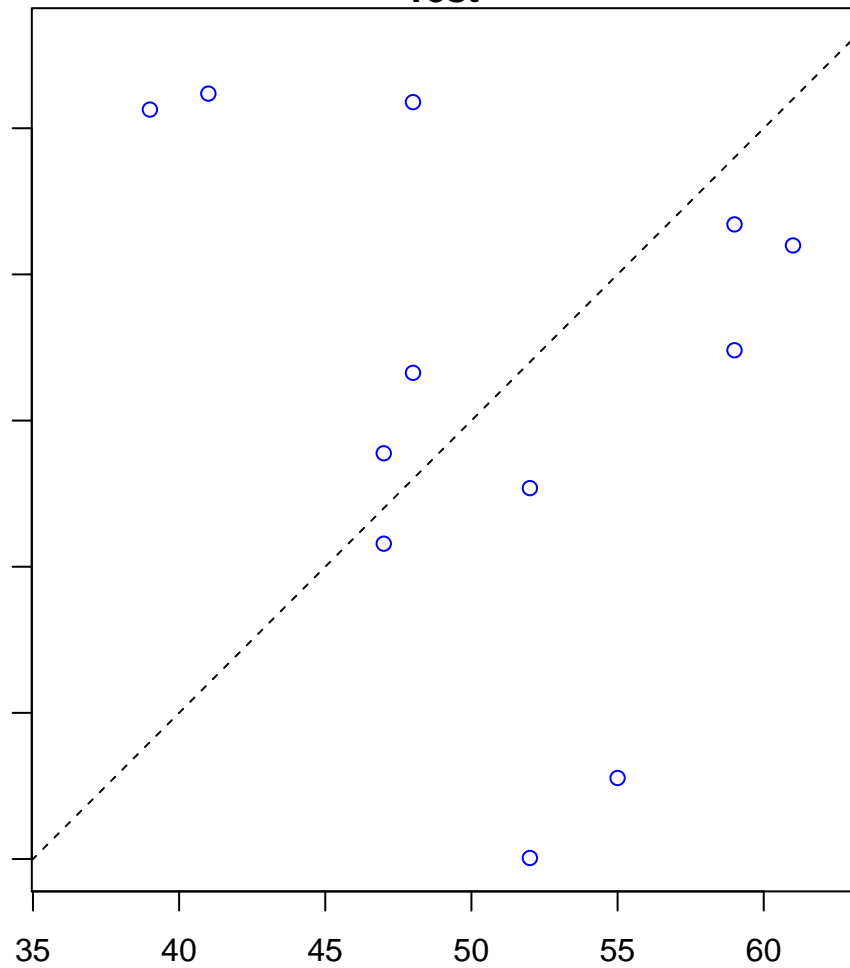


regulation of neurotransmitter transport (Score: 5.492434)

Control

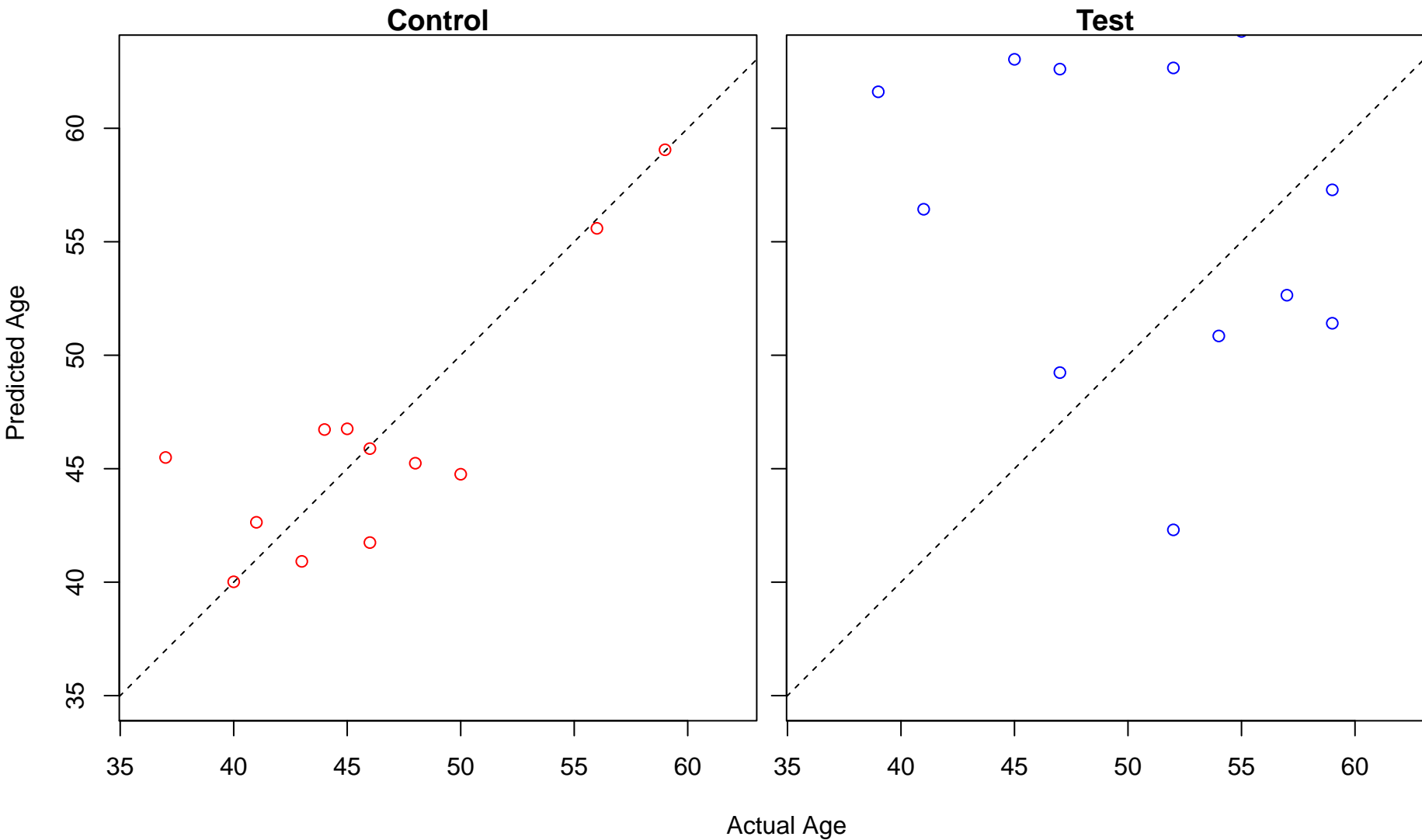


Test

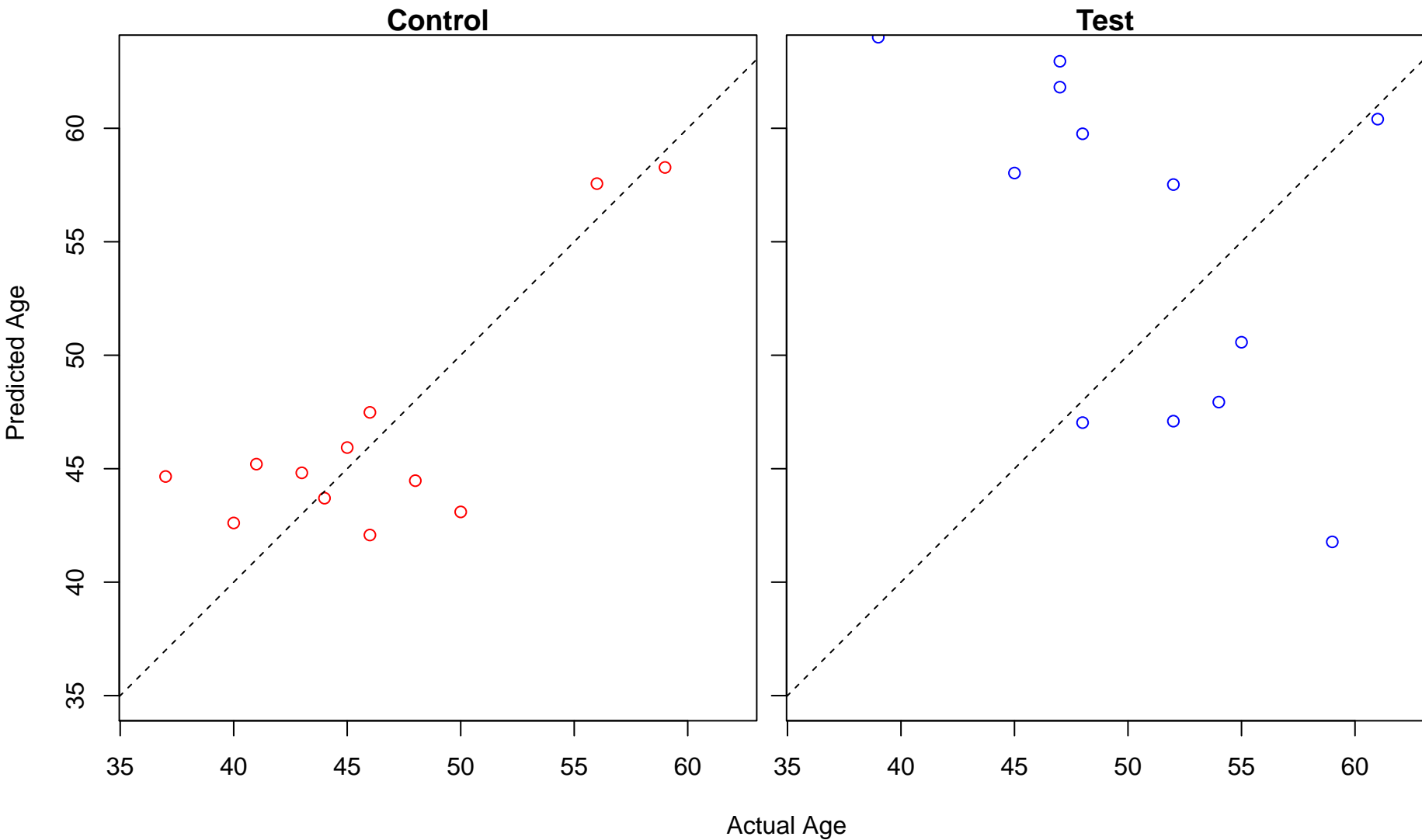


Actual Age

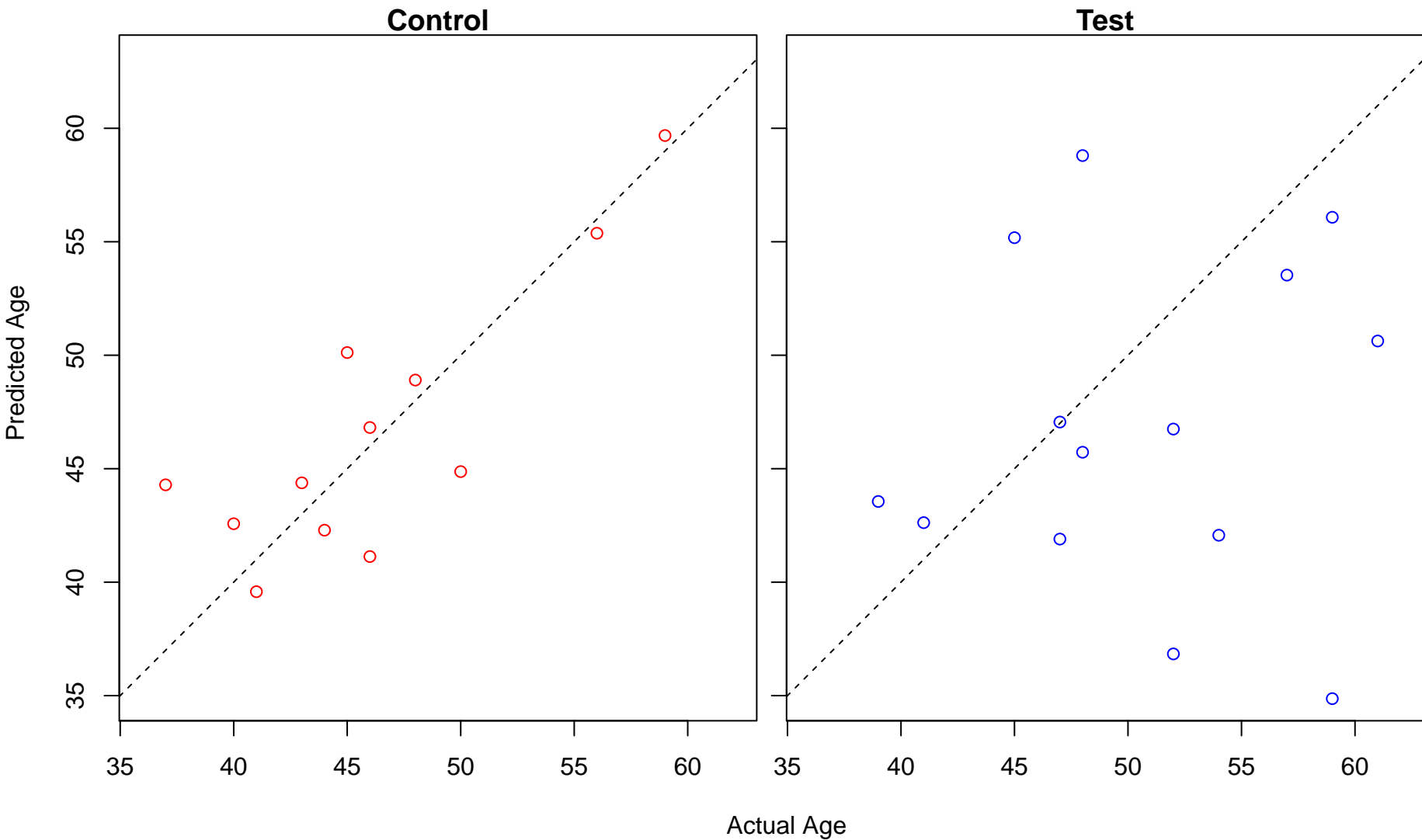
negative regulation of pathway-restricted SMAD protein phosphorylation (Score: 5.492004)



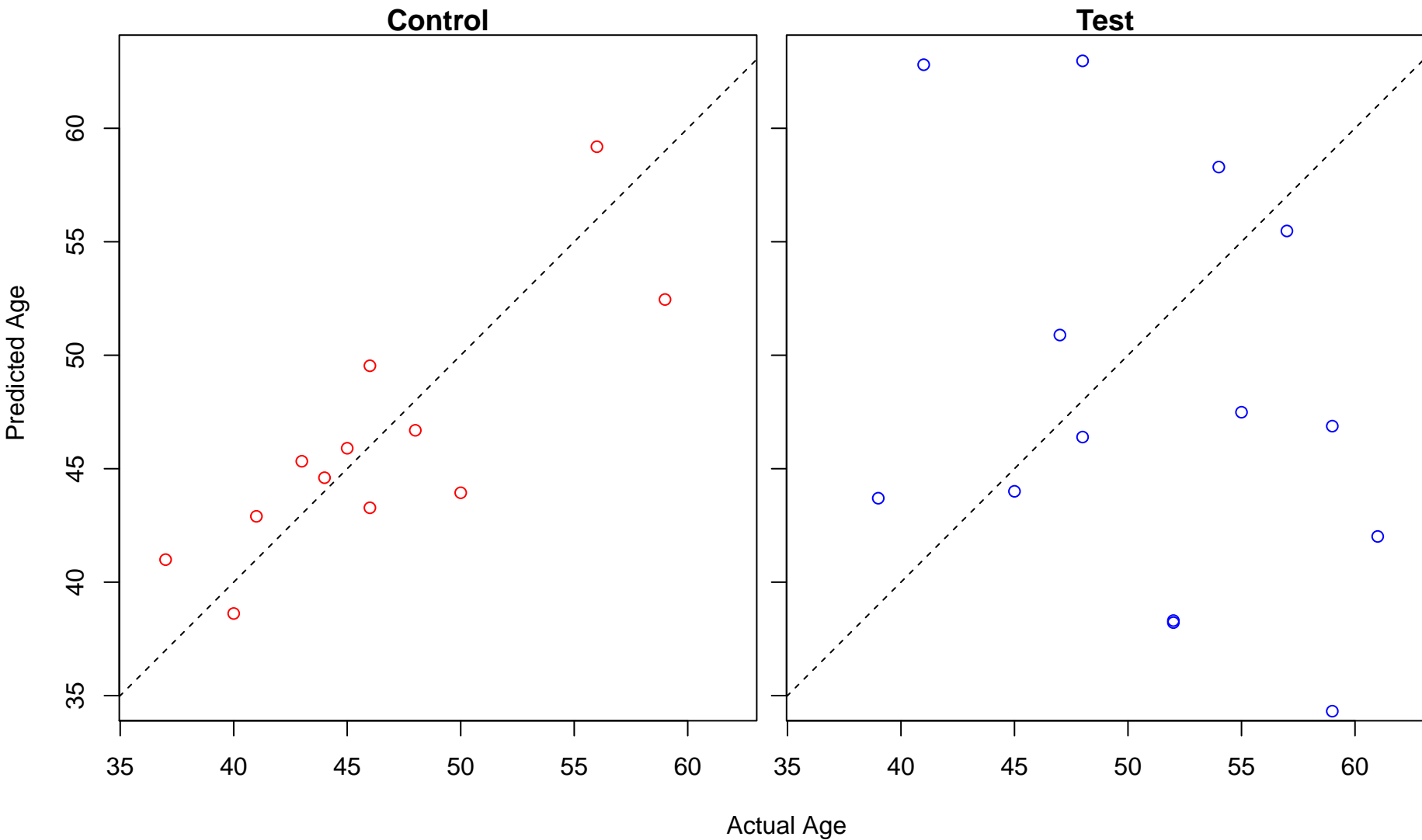
regulation of mitotic cell cycle phase transition (Score: 5.490741)



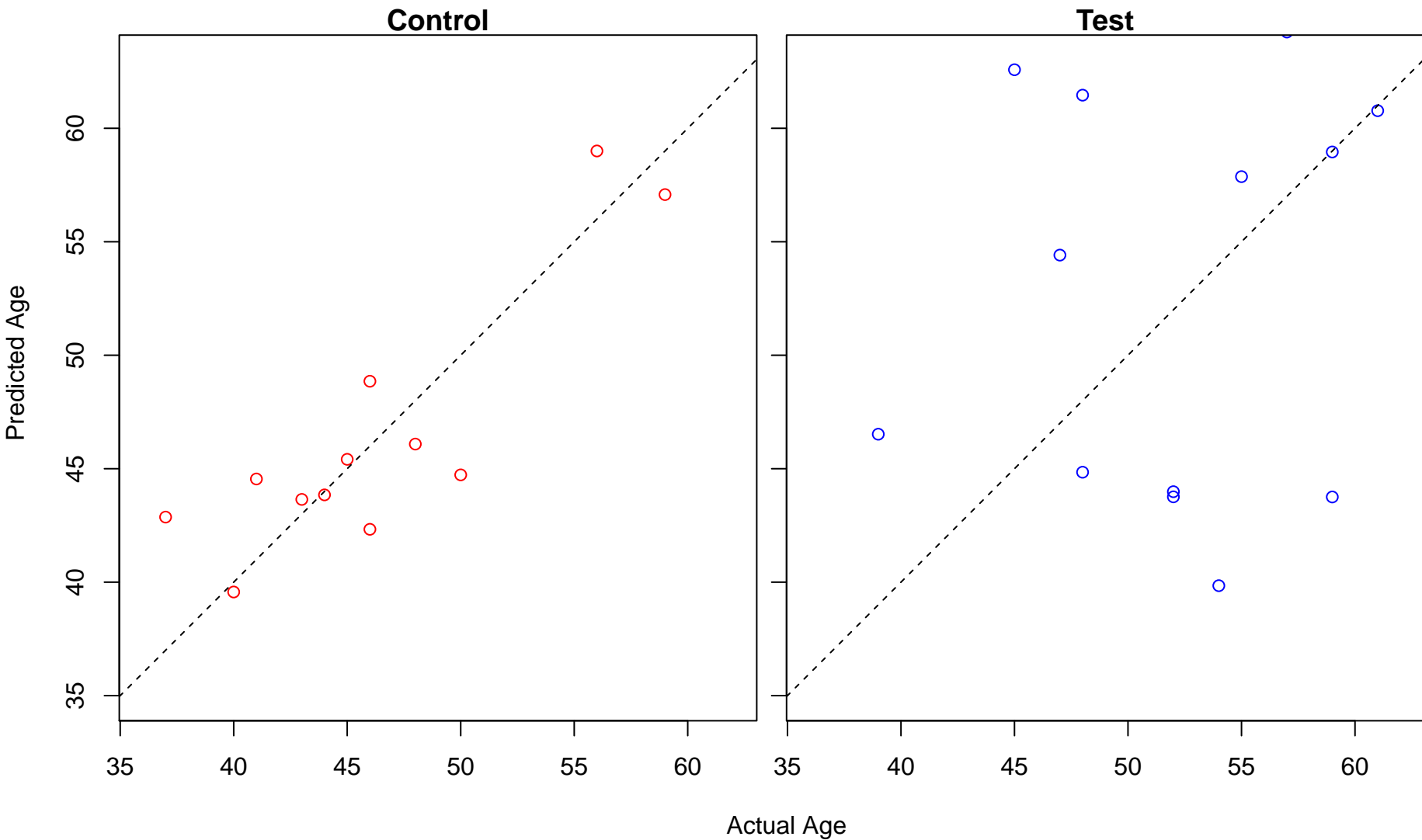
peptidyl-asparagine modification (Score: 5.490417)



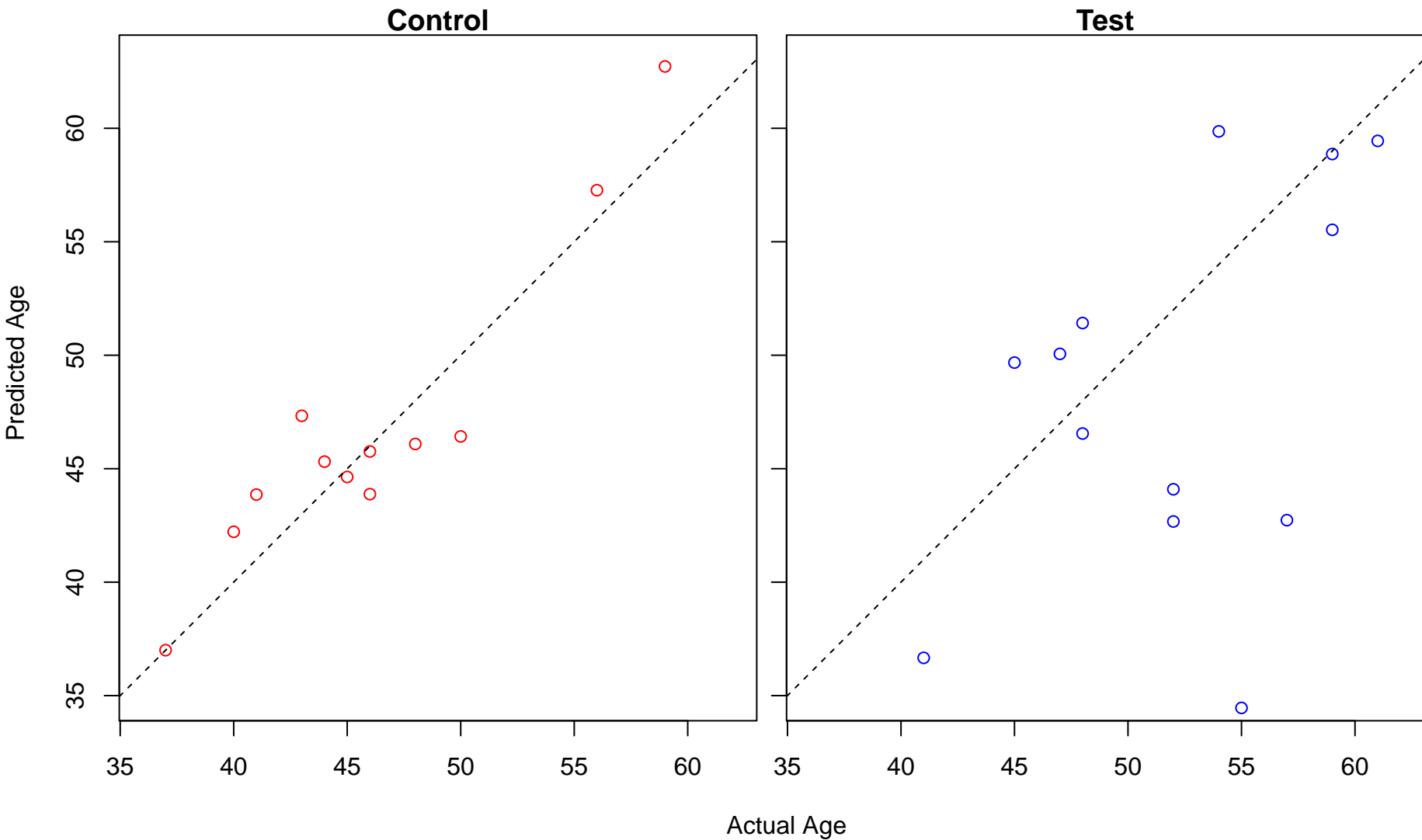
mesoderm formation (Score: 5.490094)



regulation of protein modification by small protein conjugation or removal (Score: 5.469022)

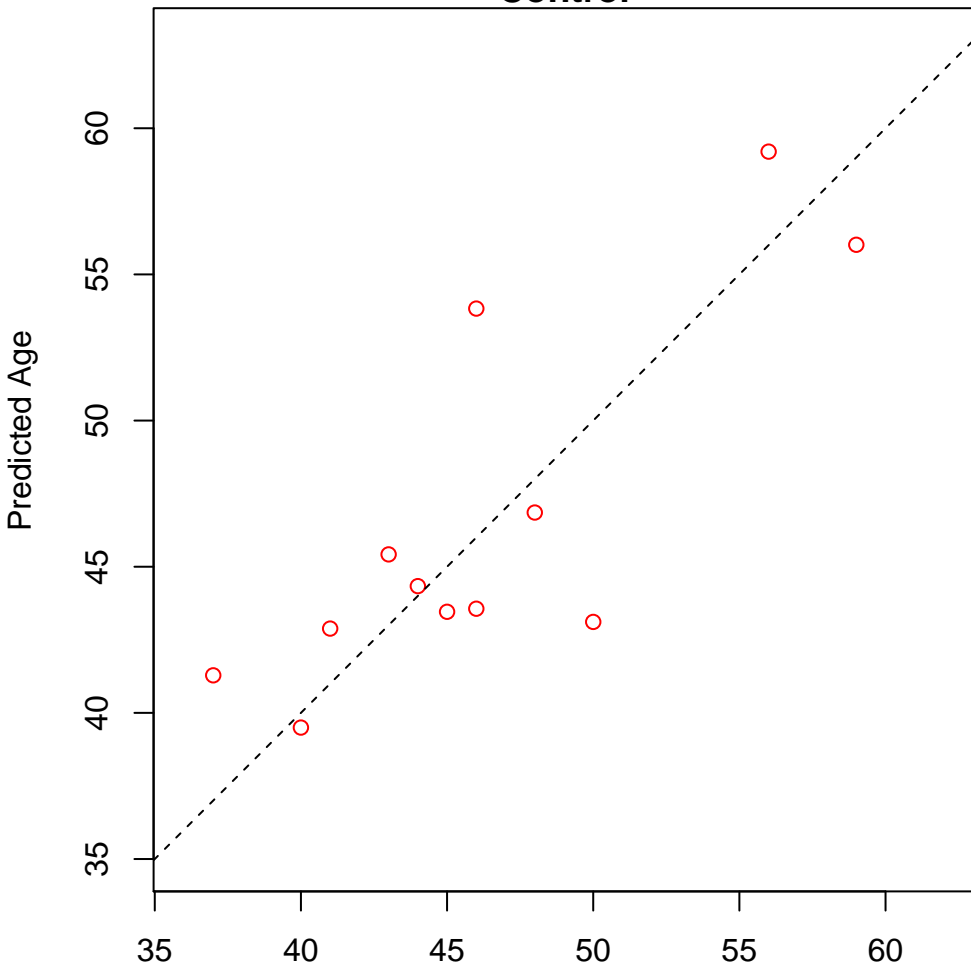


negative regulation of adherens junction organization (Score: 5.465877)

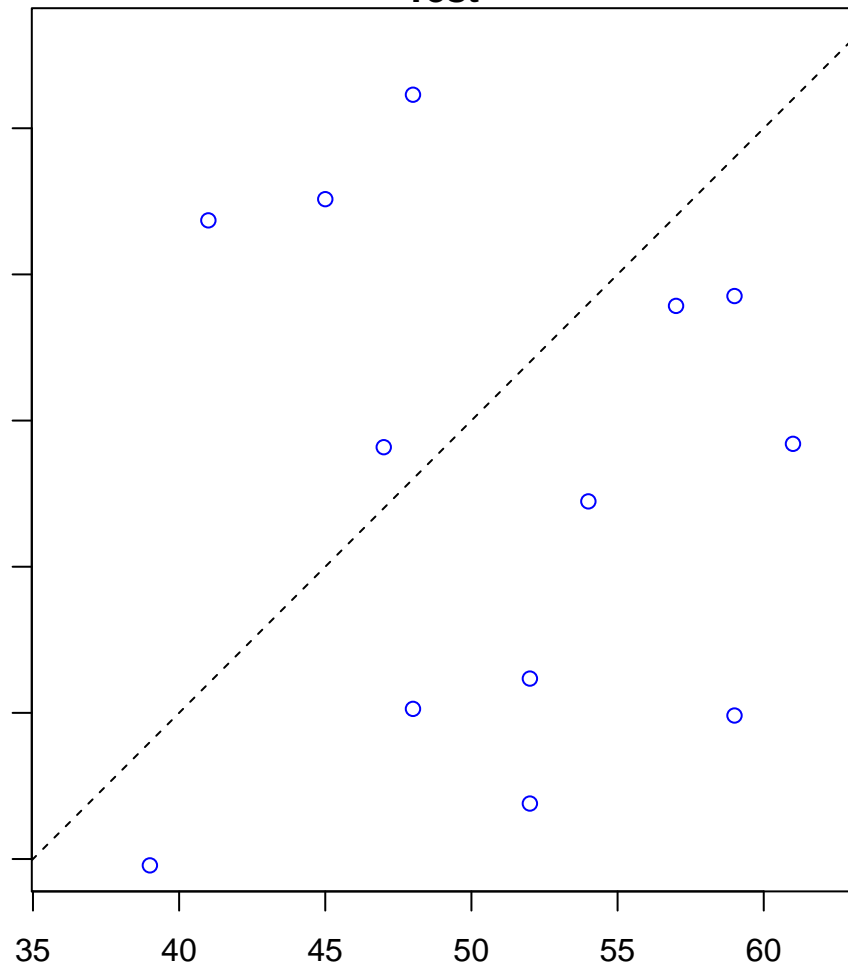


regulation of mRNA 3'-end processing (Score: 5.462613)

Control

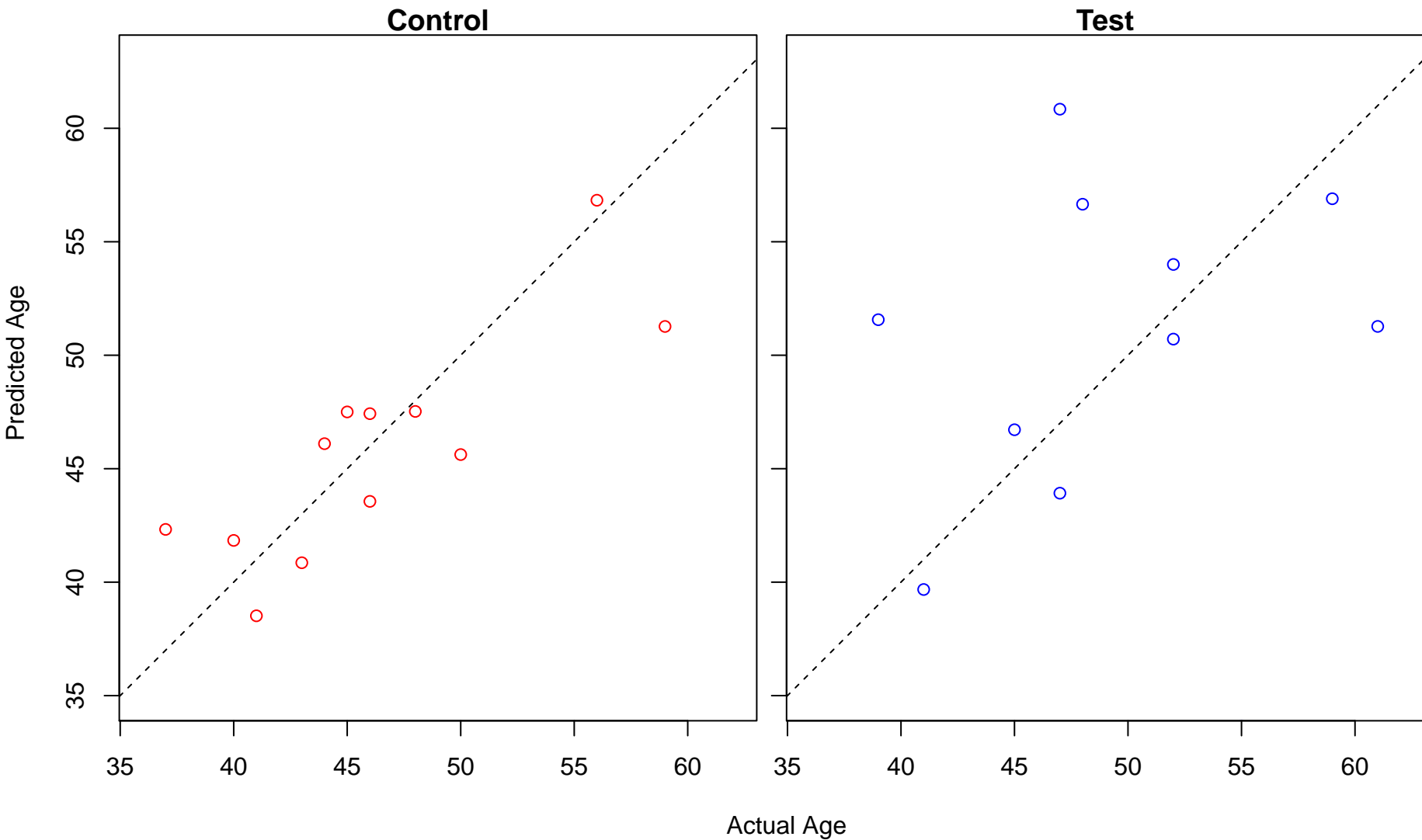


Test

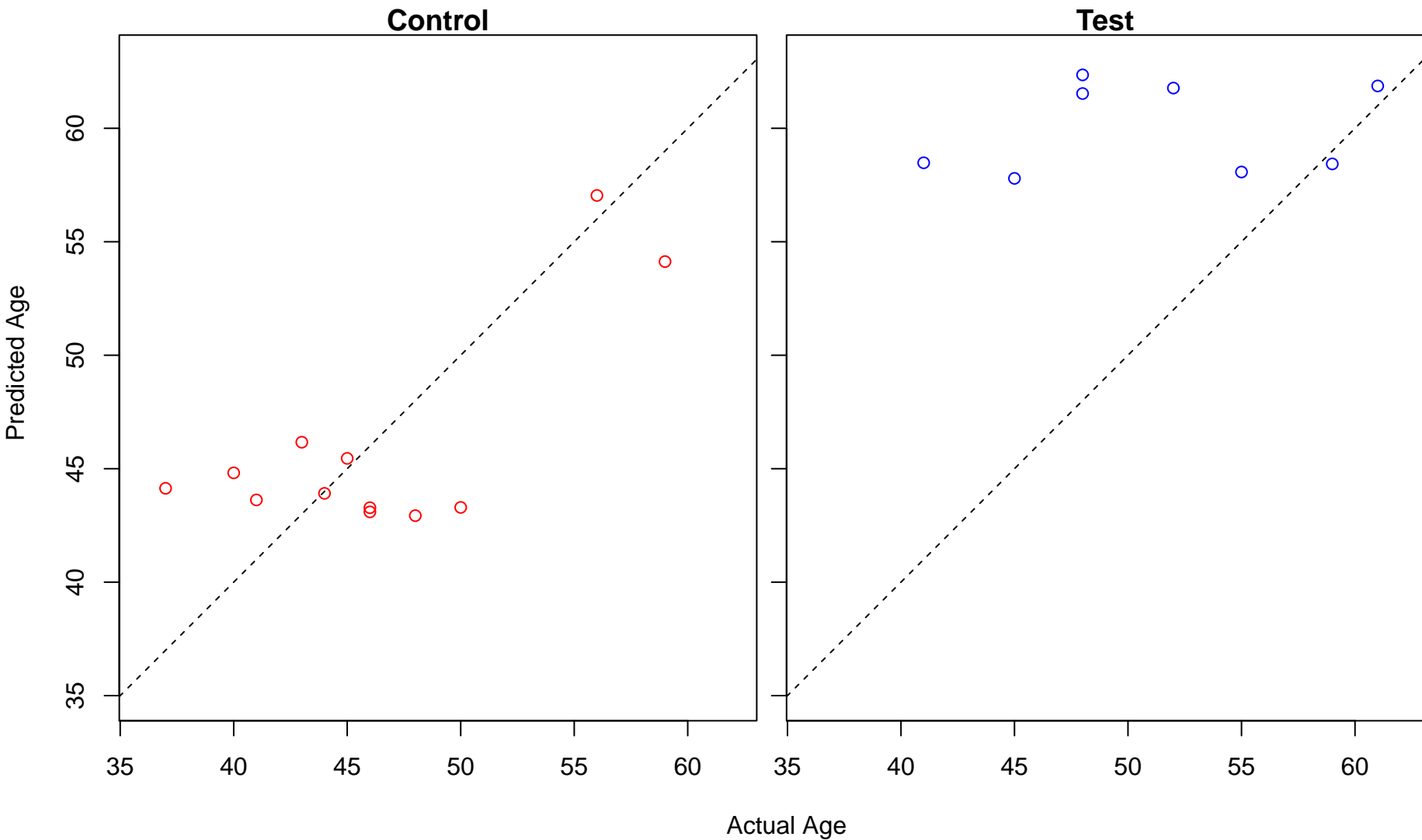


Actual Age

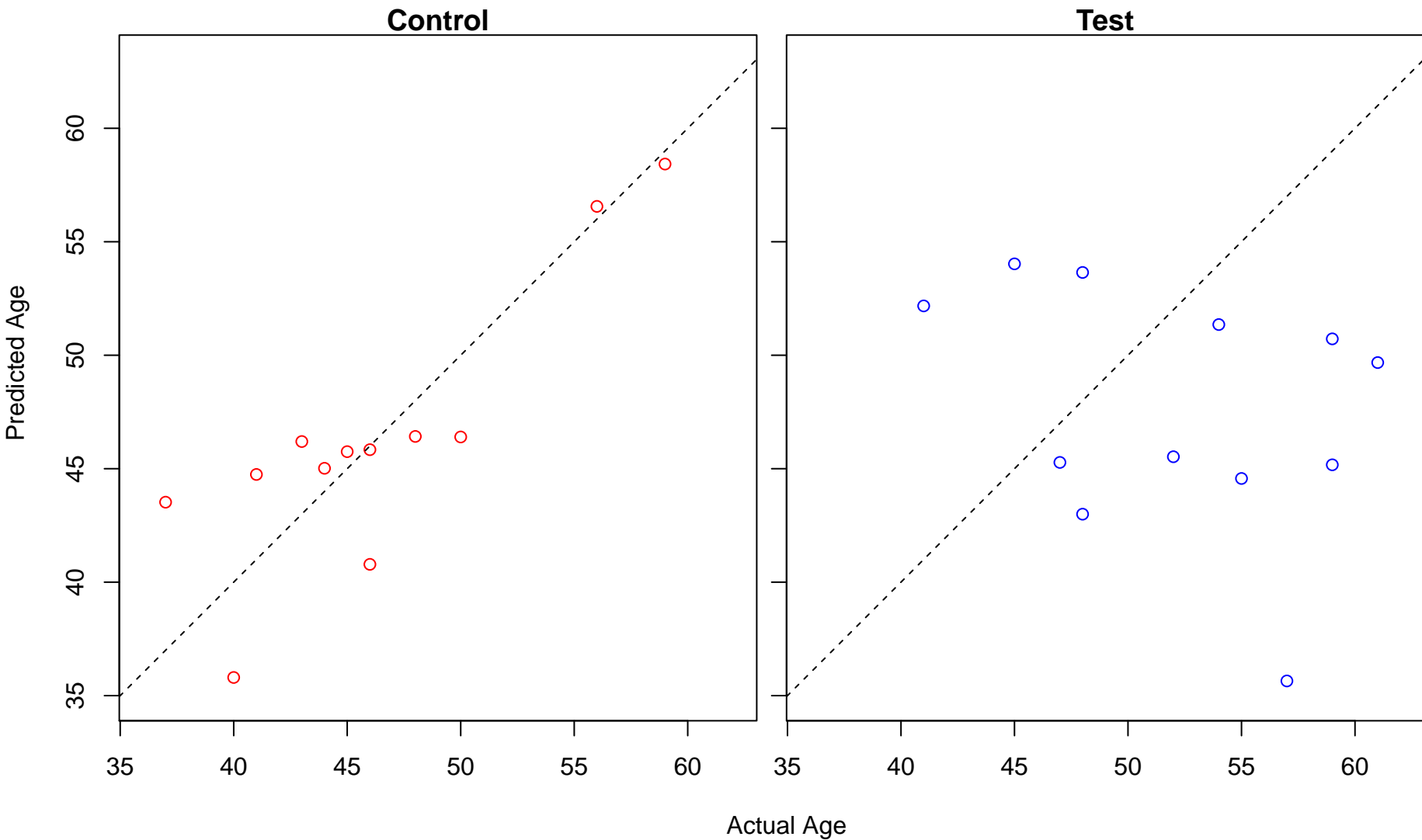
regulation of protein heterodimerization activity (Score: 5.460110)



peroxisome proliferator activated receptor signaling pathway (Score: 5.452450)

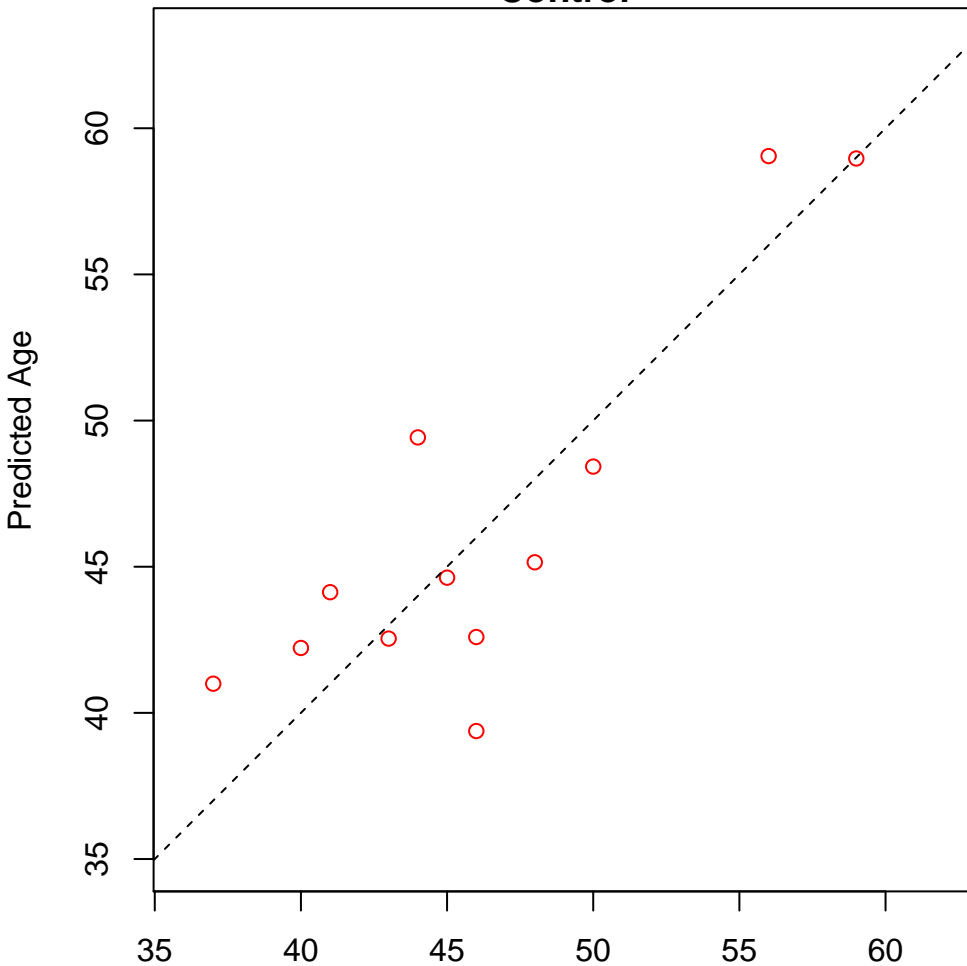


regulation of cytoplasmic transport (Score: 5.451712)

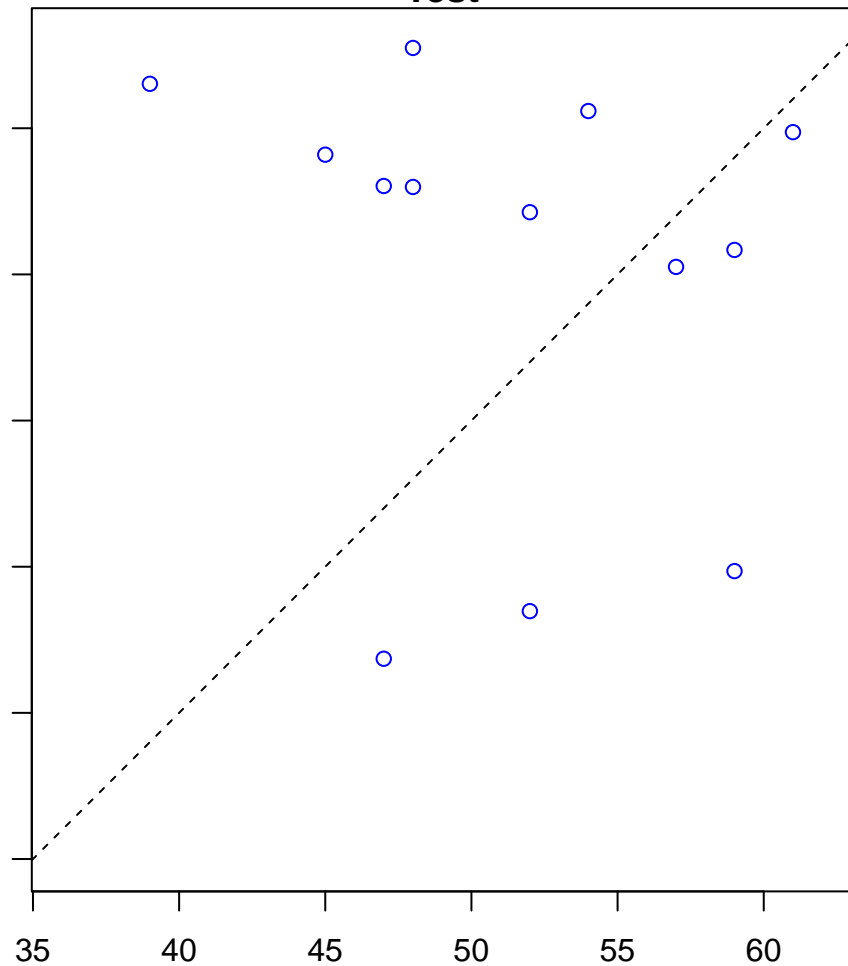


protein localization to mitochondrion (Score: 5.450205)

Control

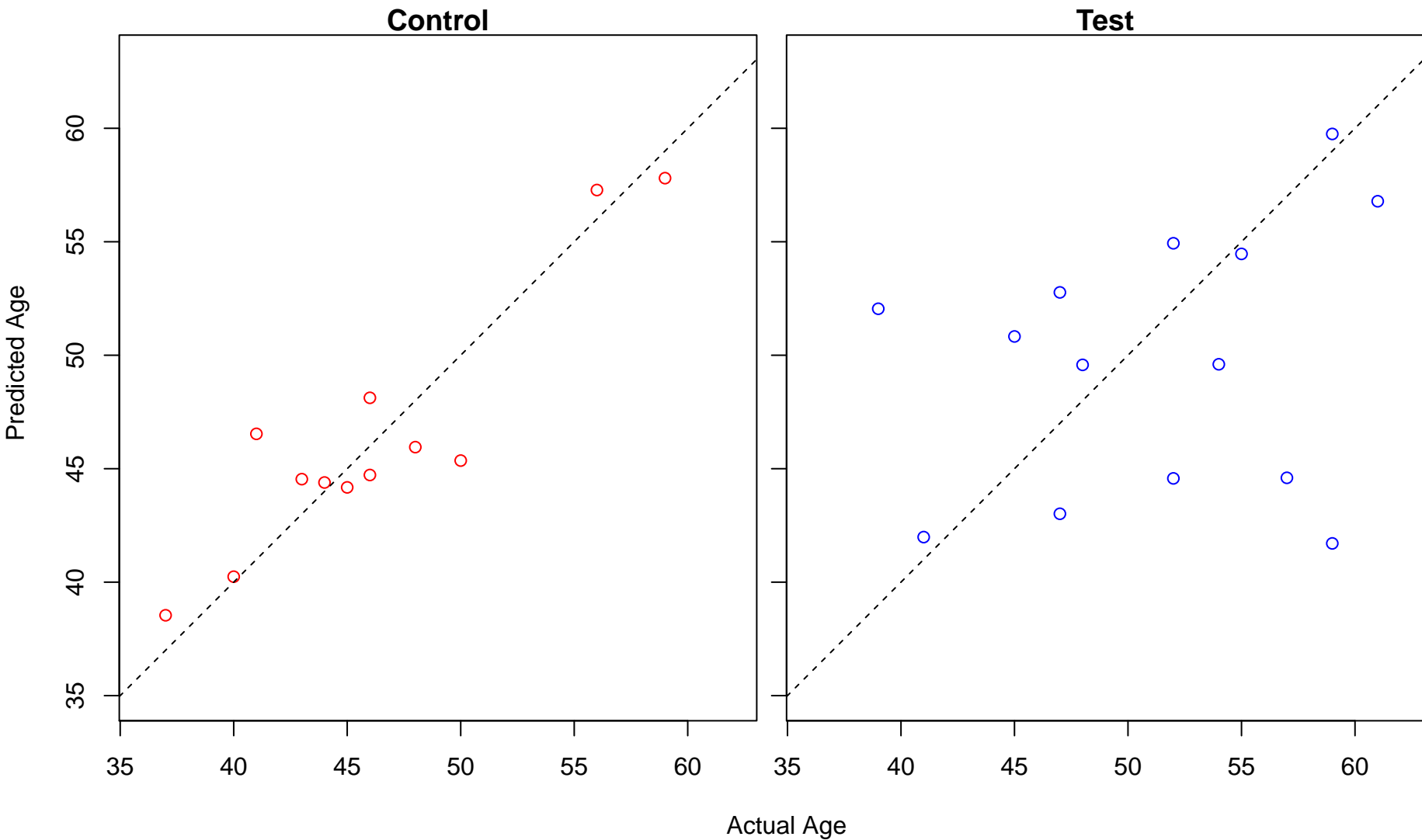


Test

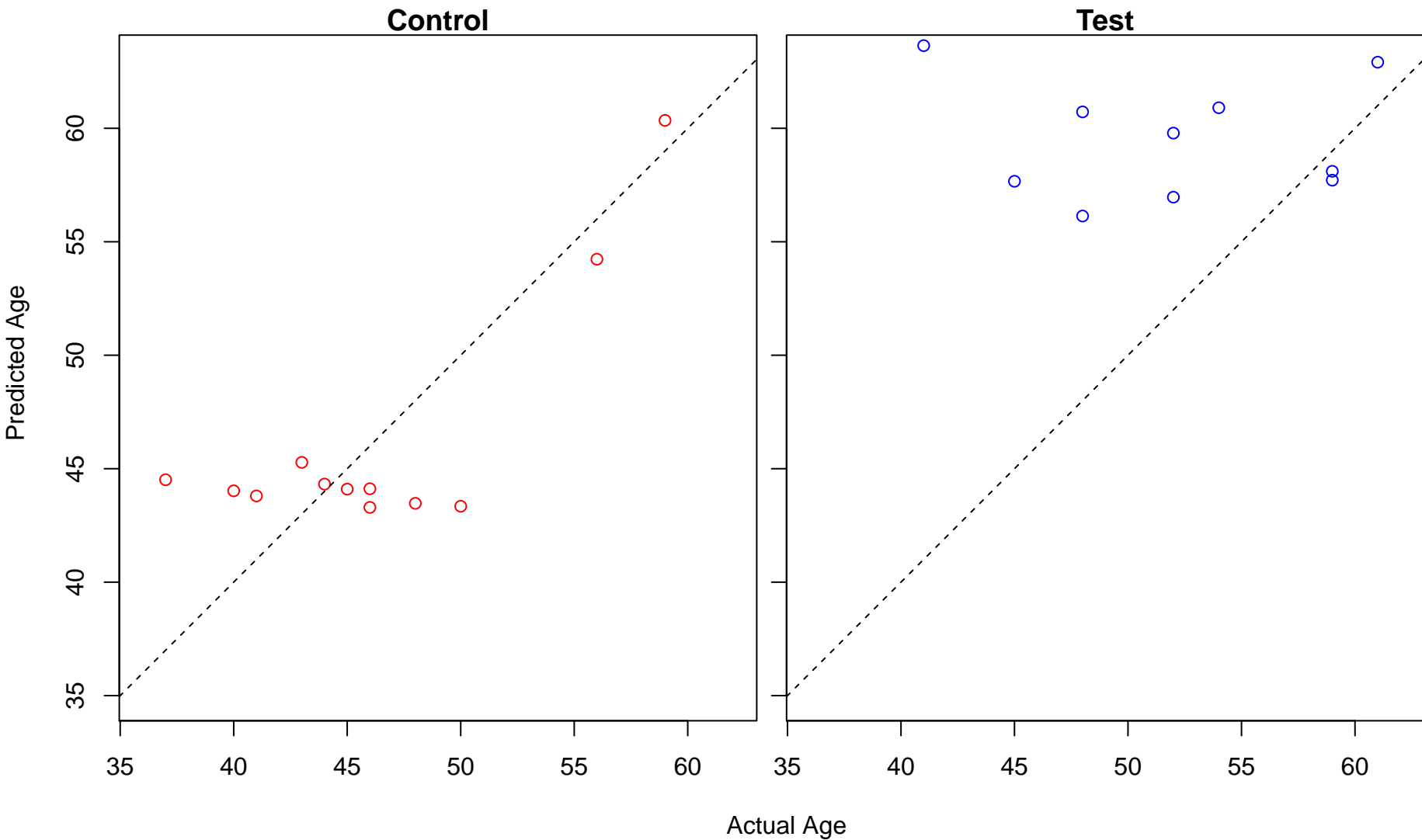


Actual Age

fatty acid homeostasis (Score: 5.441906)

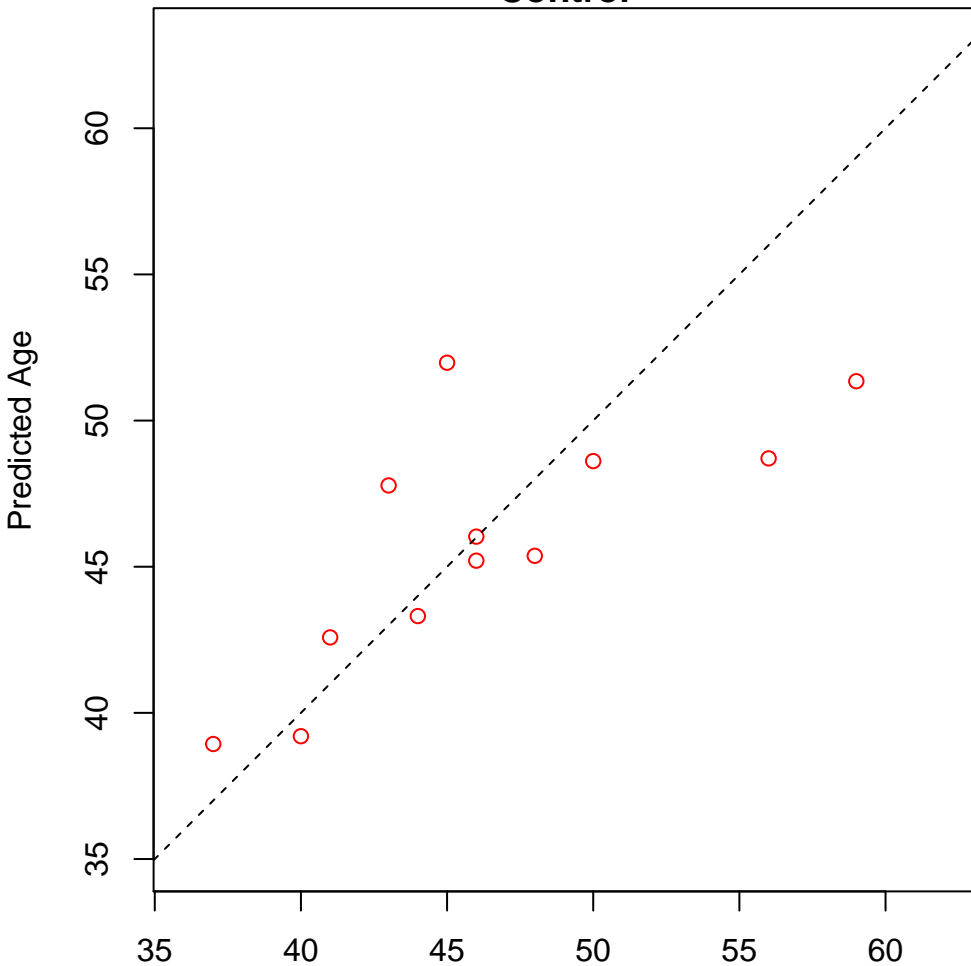


negative regulation of fibroblast proliferation (Score: 5.441679)

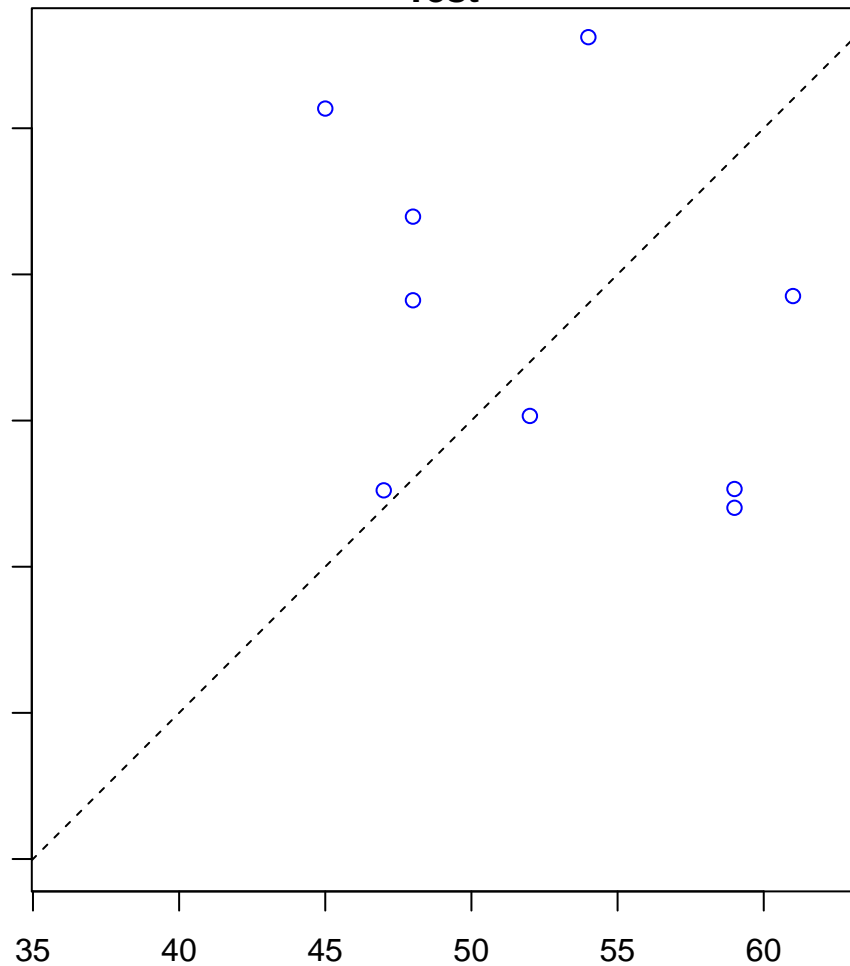


base conversion or substitution editing (Score: 5.436338)

Control

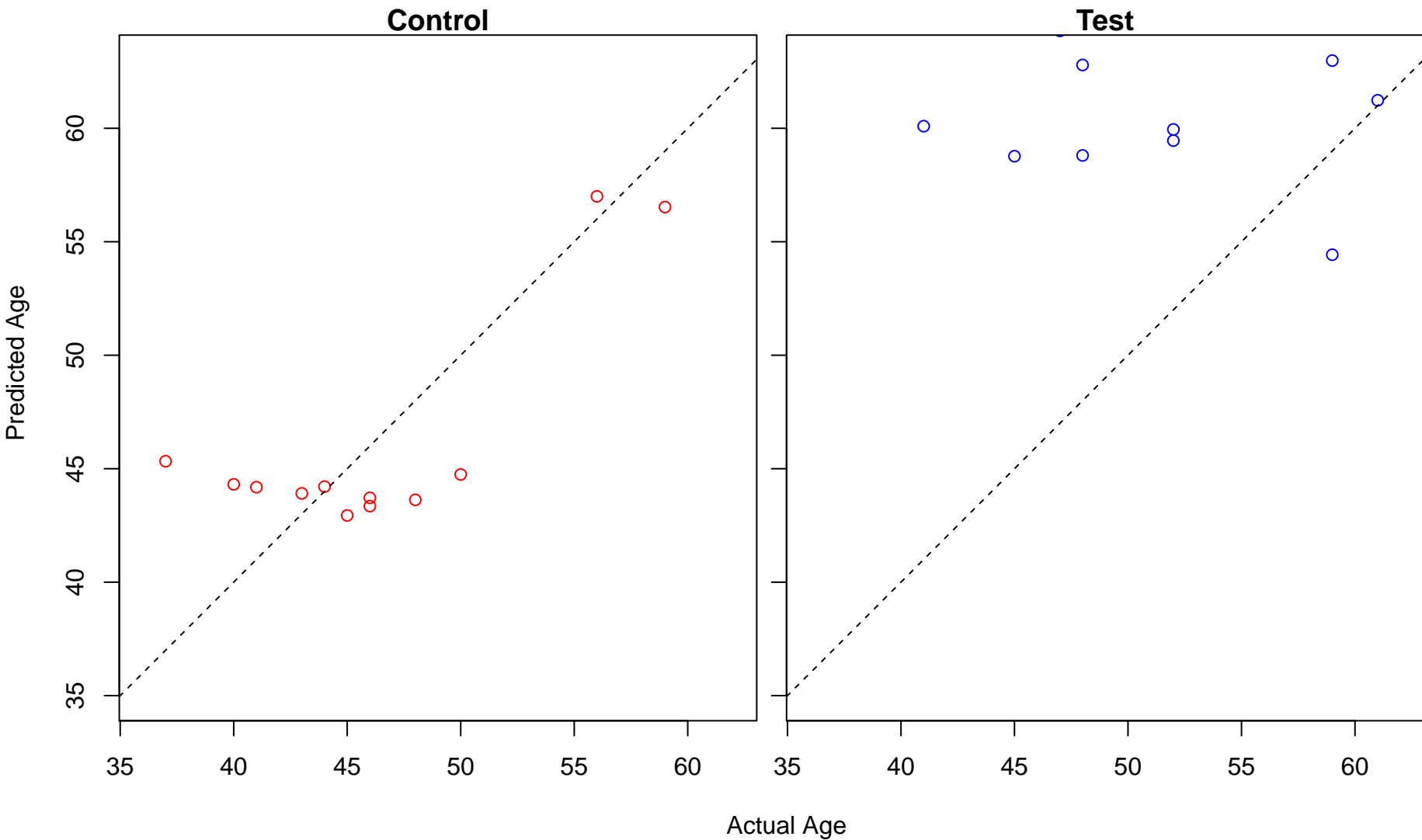


Test

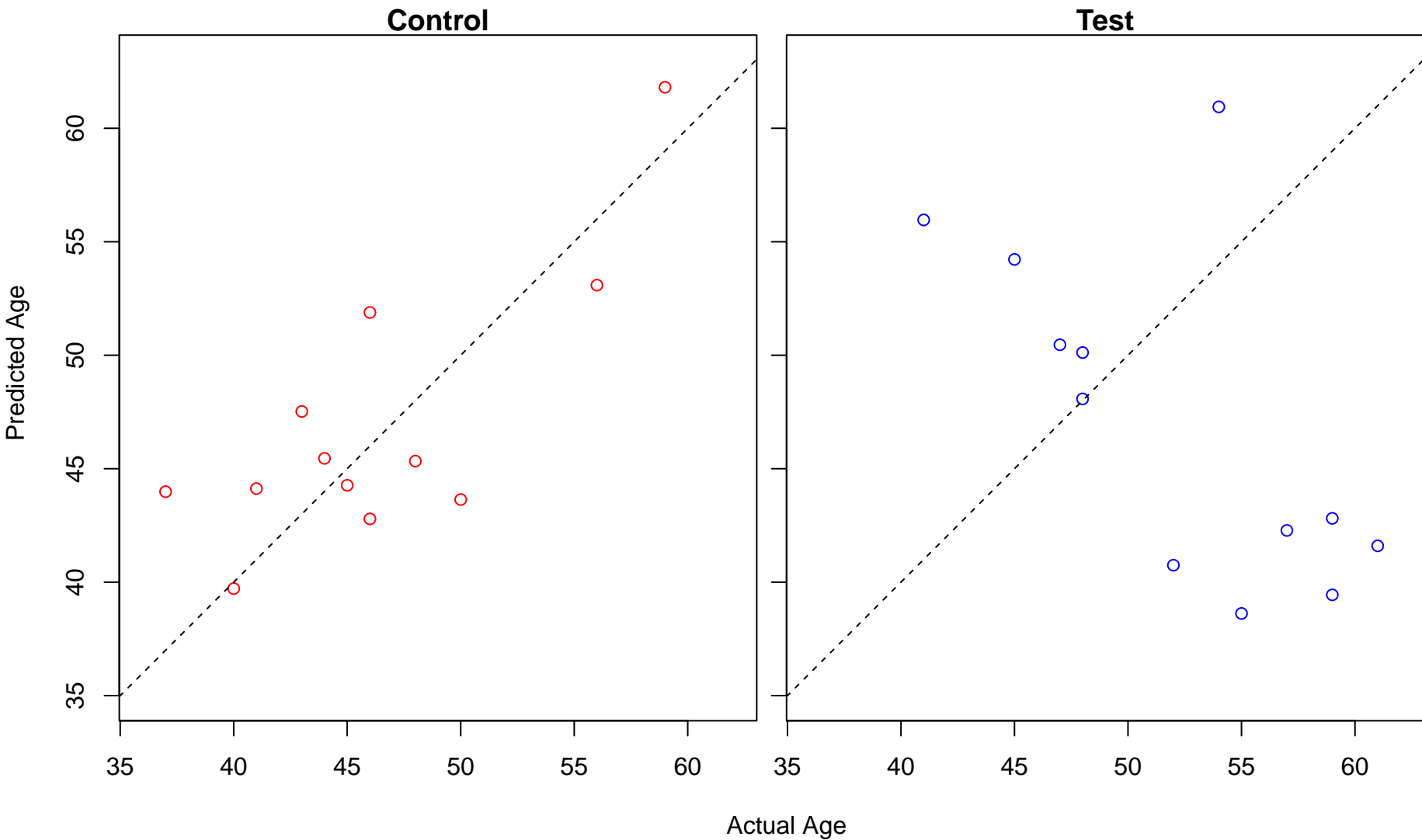


Actual Age

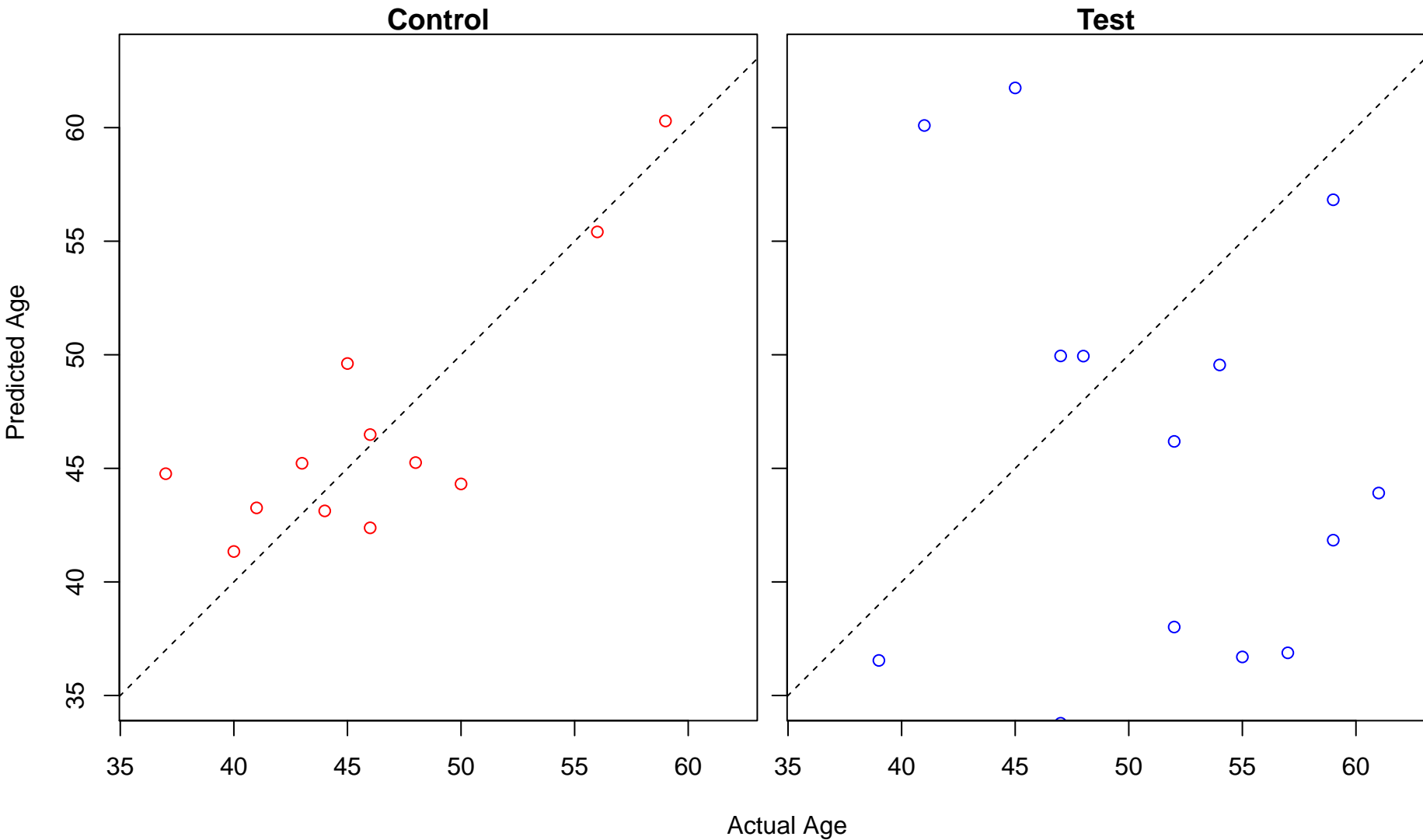
cellular lactam metabolic process (Score: 5.427632)



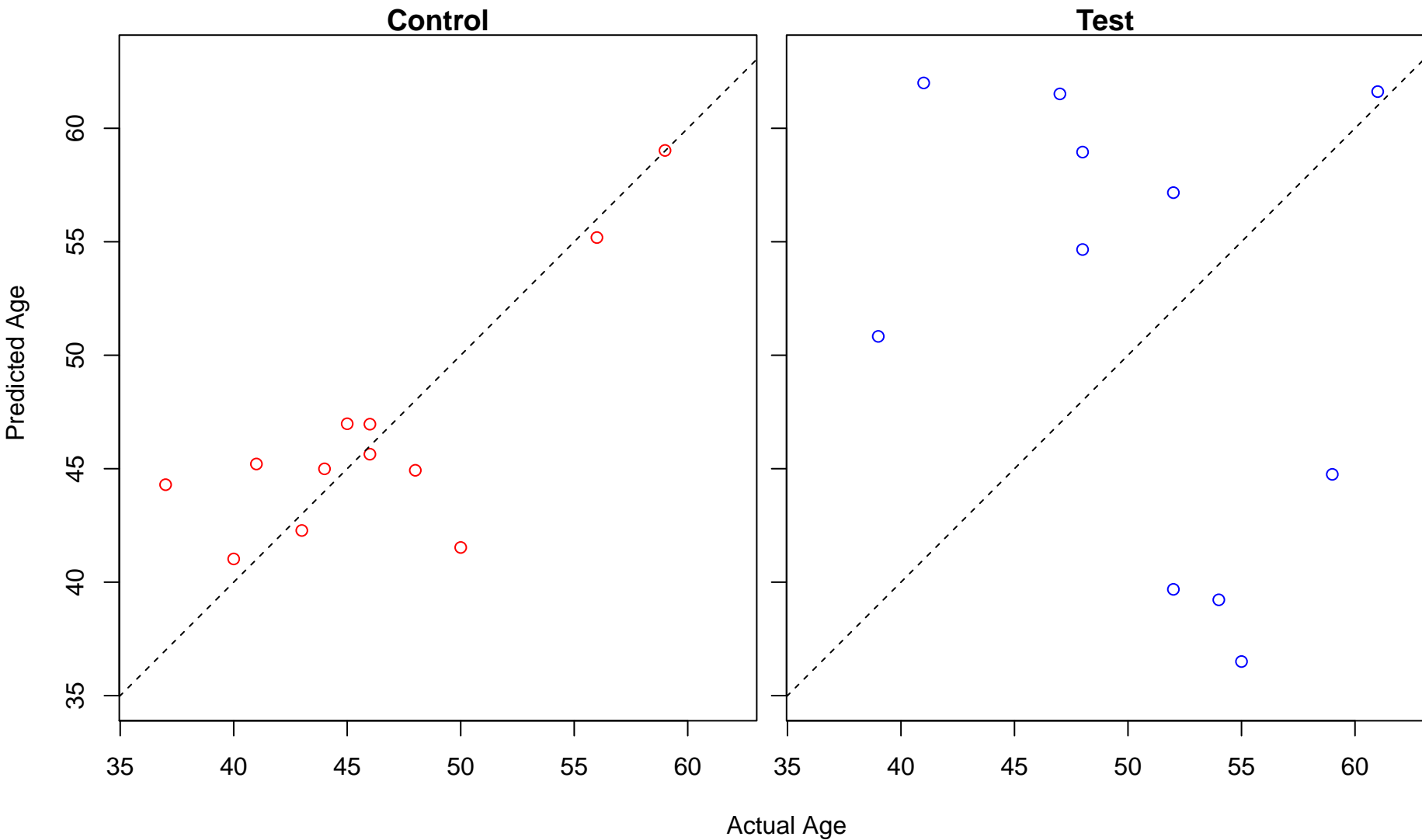
RNA polyadenylation (Score: 5.418398)



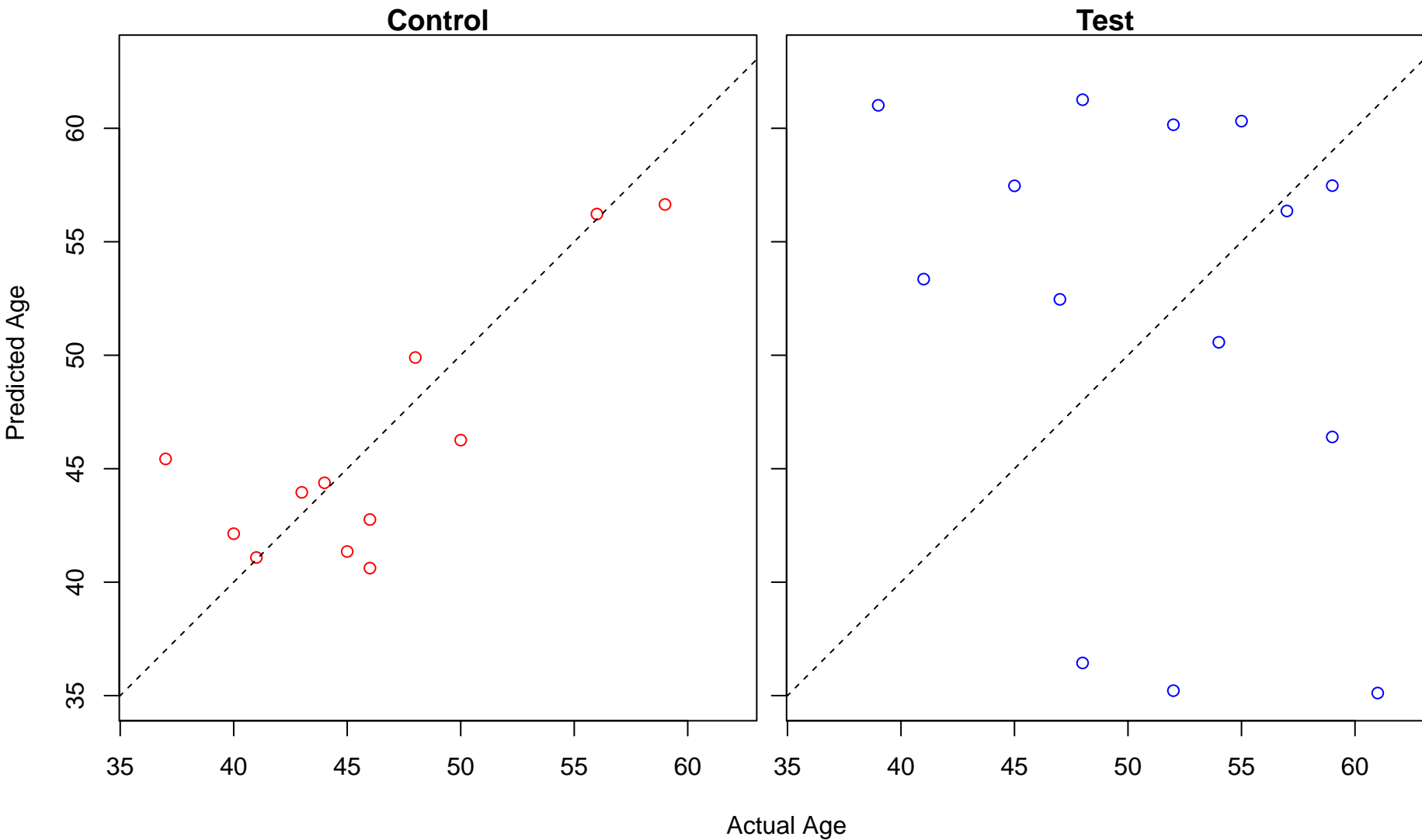
positive regulation of stress-activated protein kinase signaling cascade (Score: 5.409029)



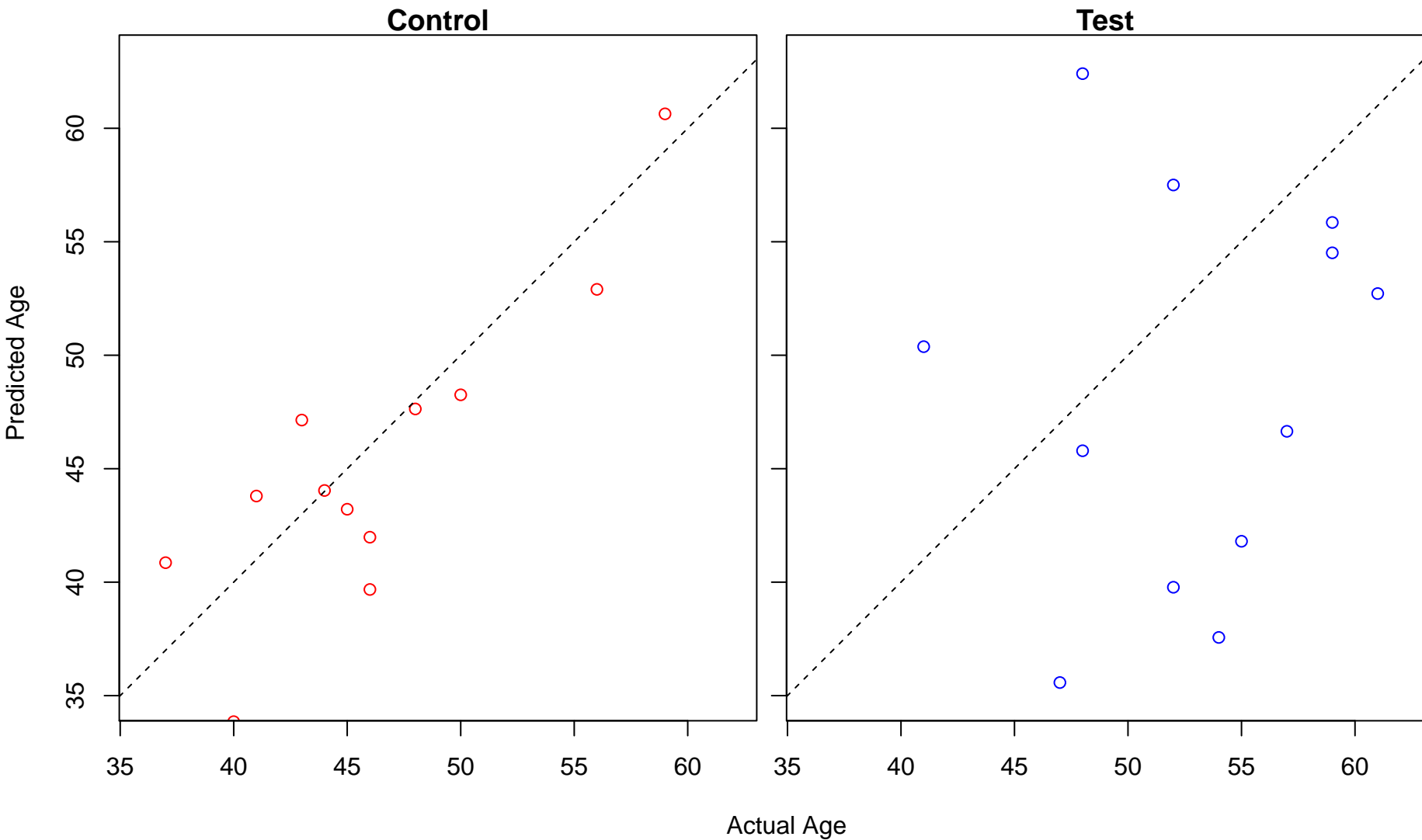
mitotic cell cycle arrest (Score: 5.408390)



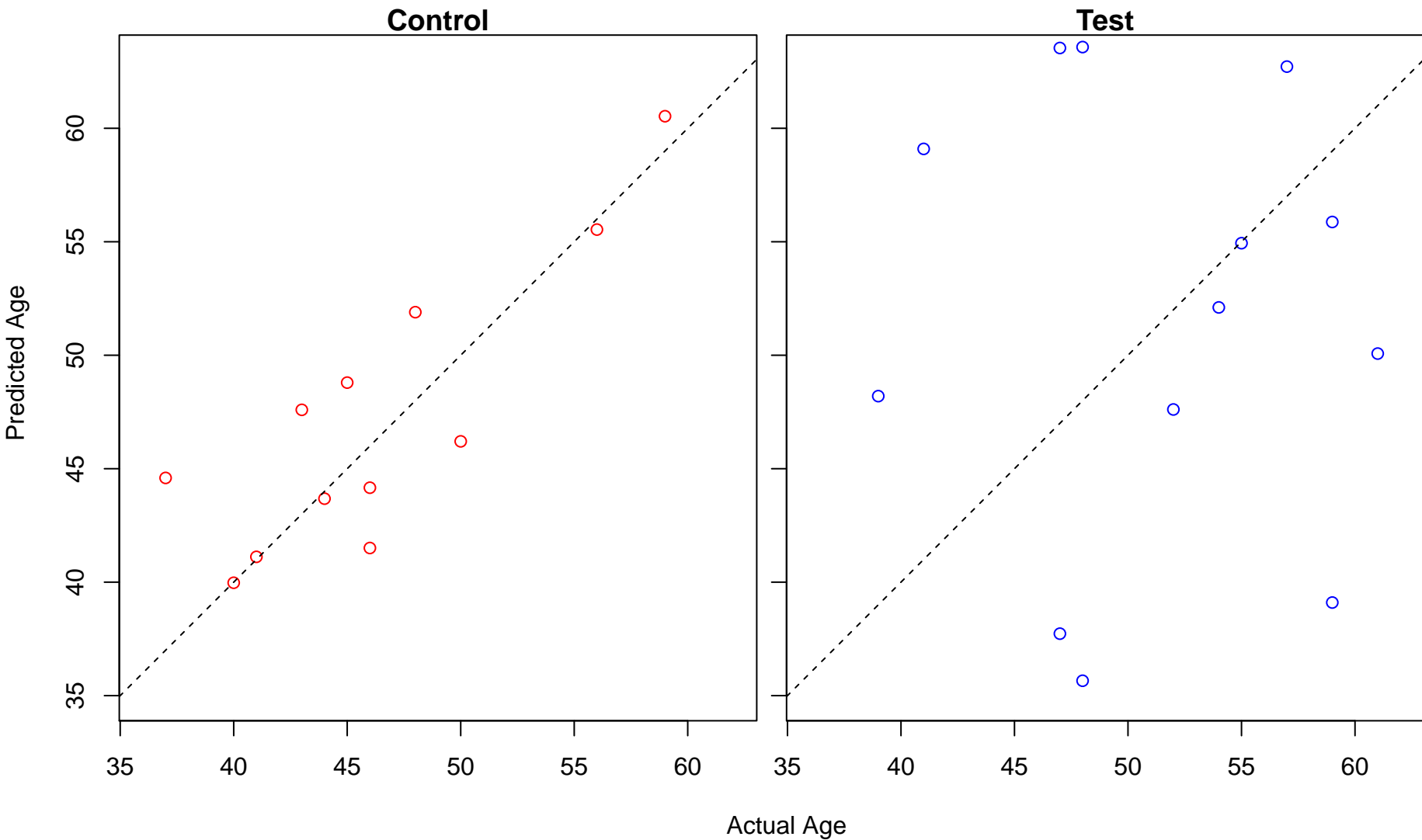
membrane depolarization (Score: 5.387512)



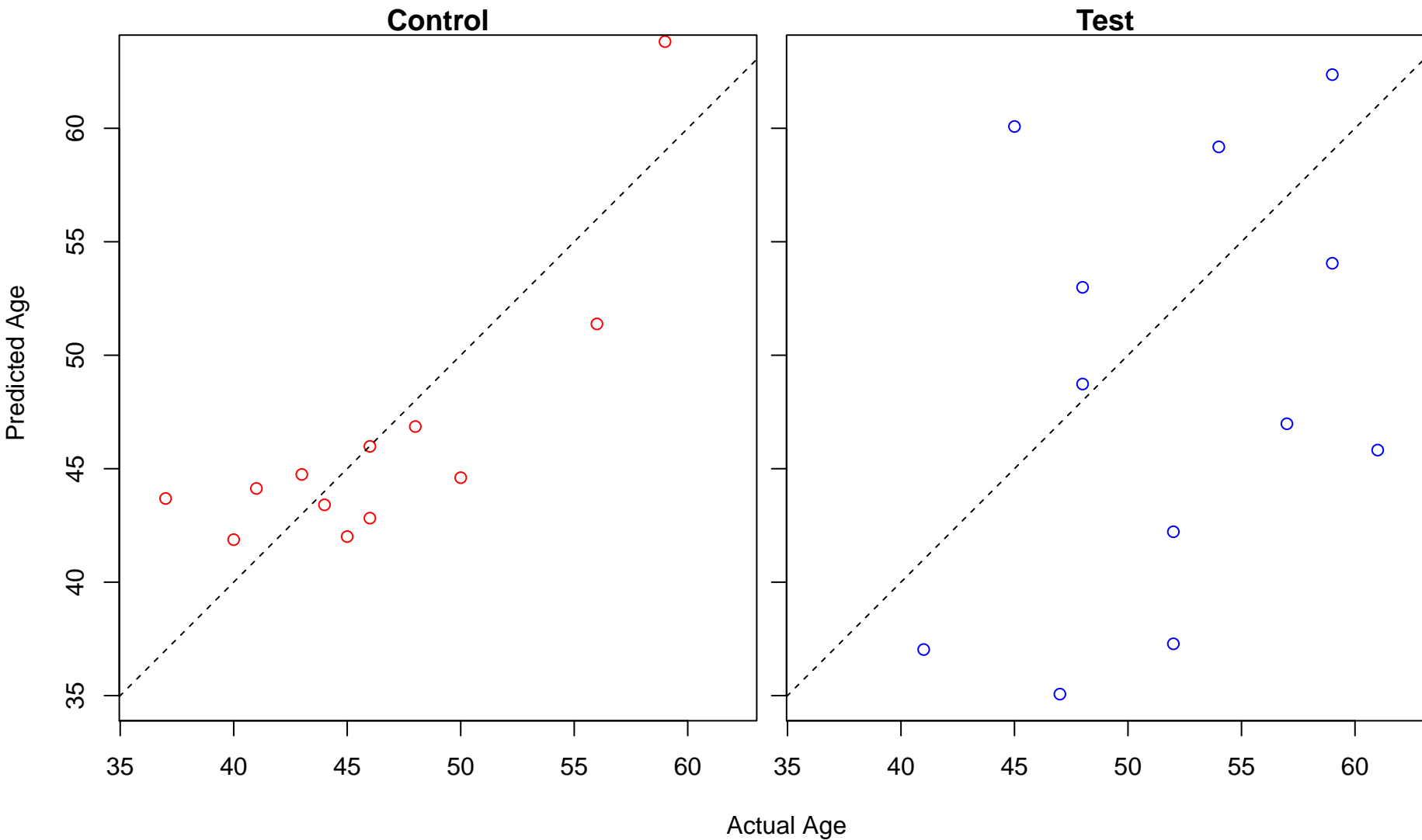
sulfur amino acid metabolic process (Score: 5.382516)



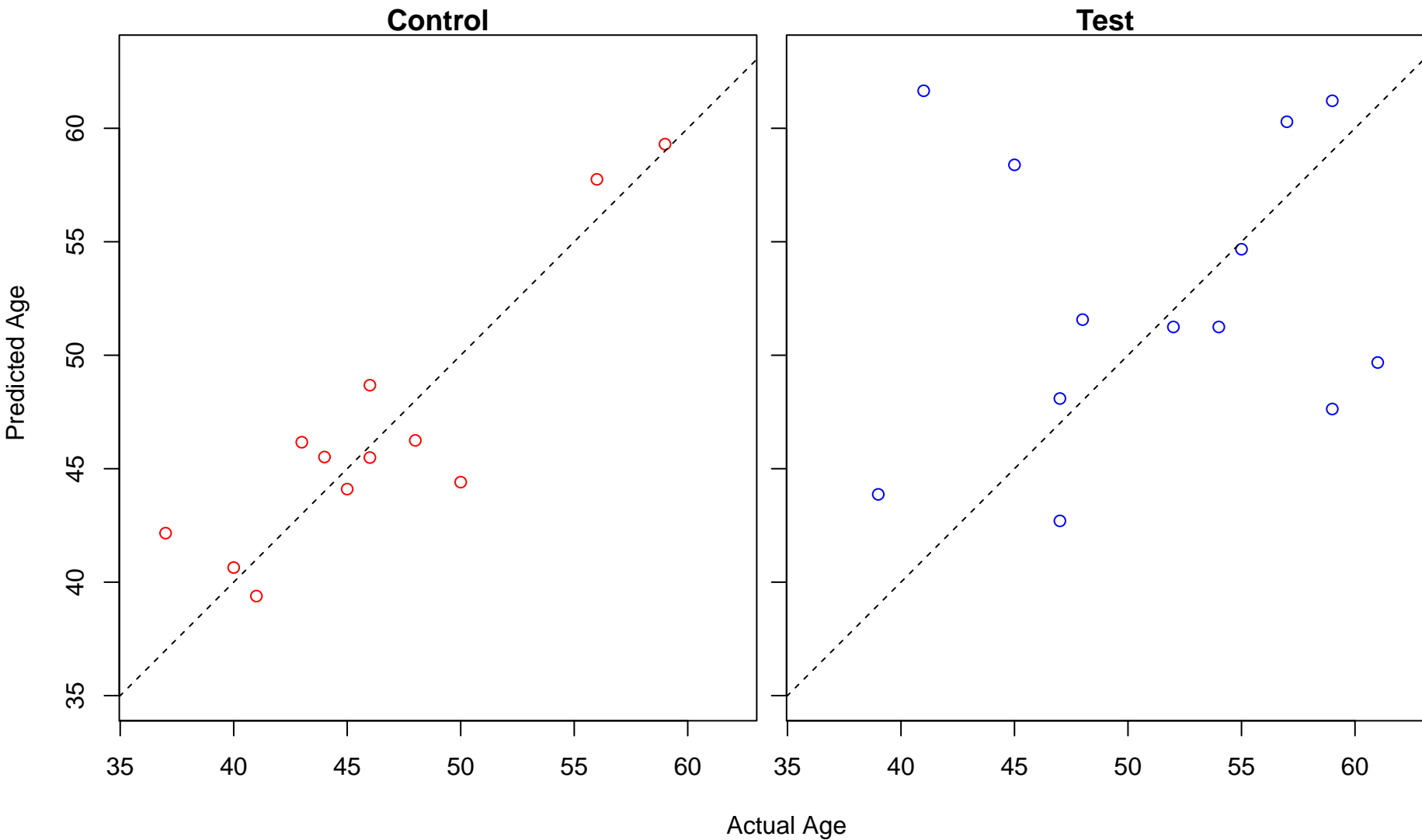
cardiac ventricle morphogenesis (Score: 5.379935)



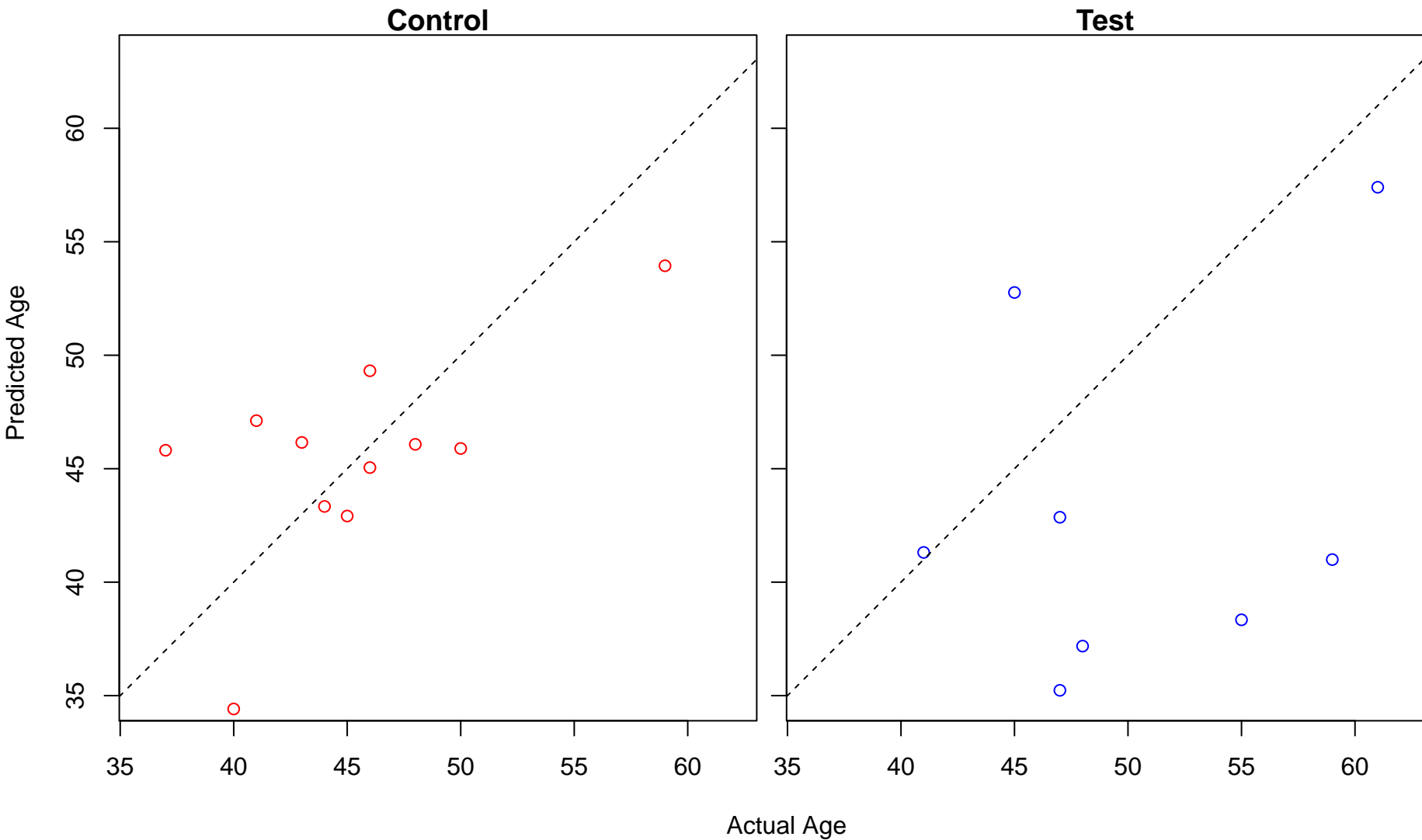
protein monoubiquitination (Score: 5.366463)



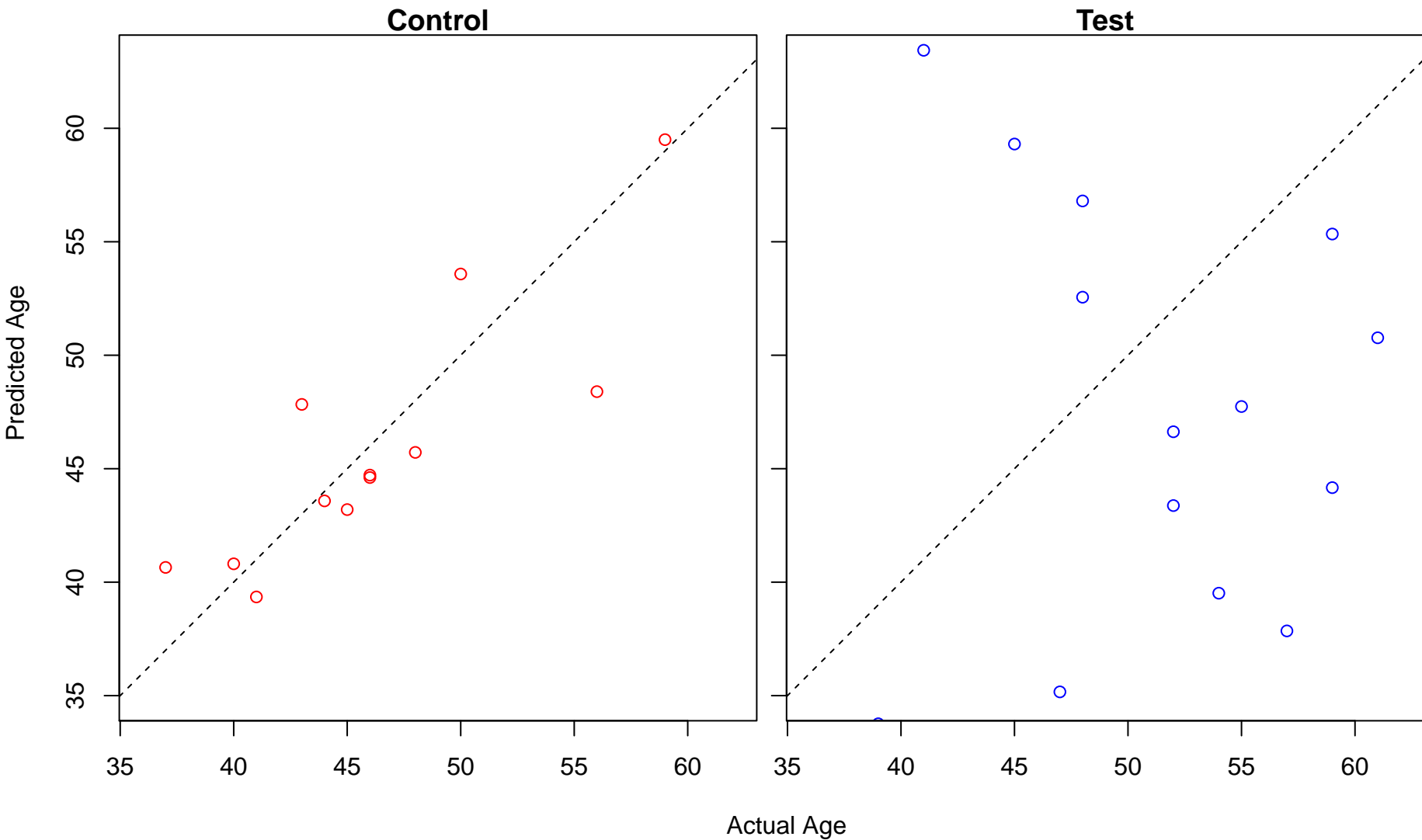
sensory organ morphogenesis (Score: 5.363657)



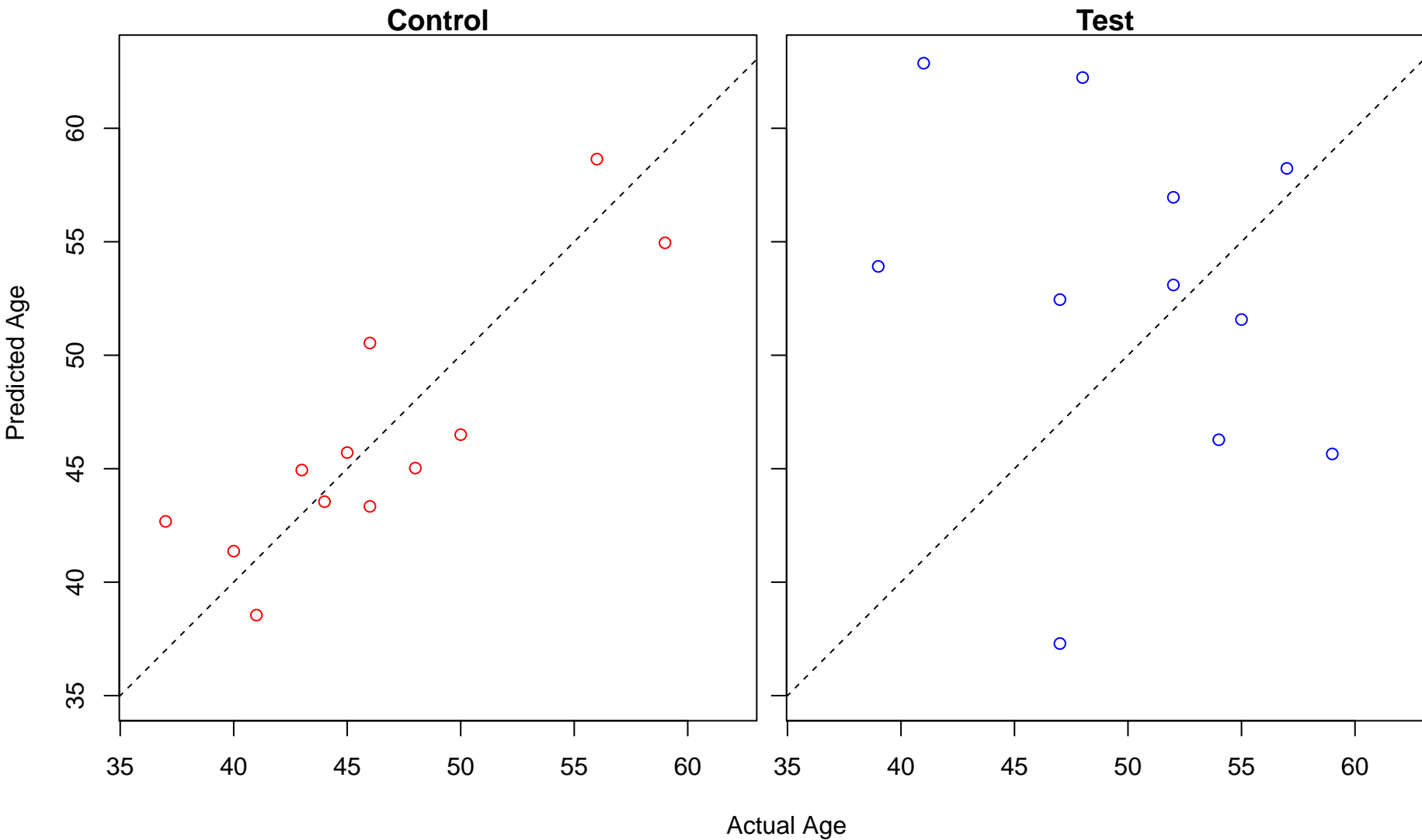
glycerolipid catabolic process (Score: 5.363015)



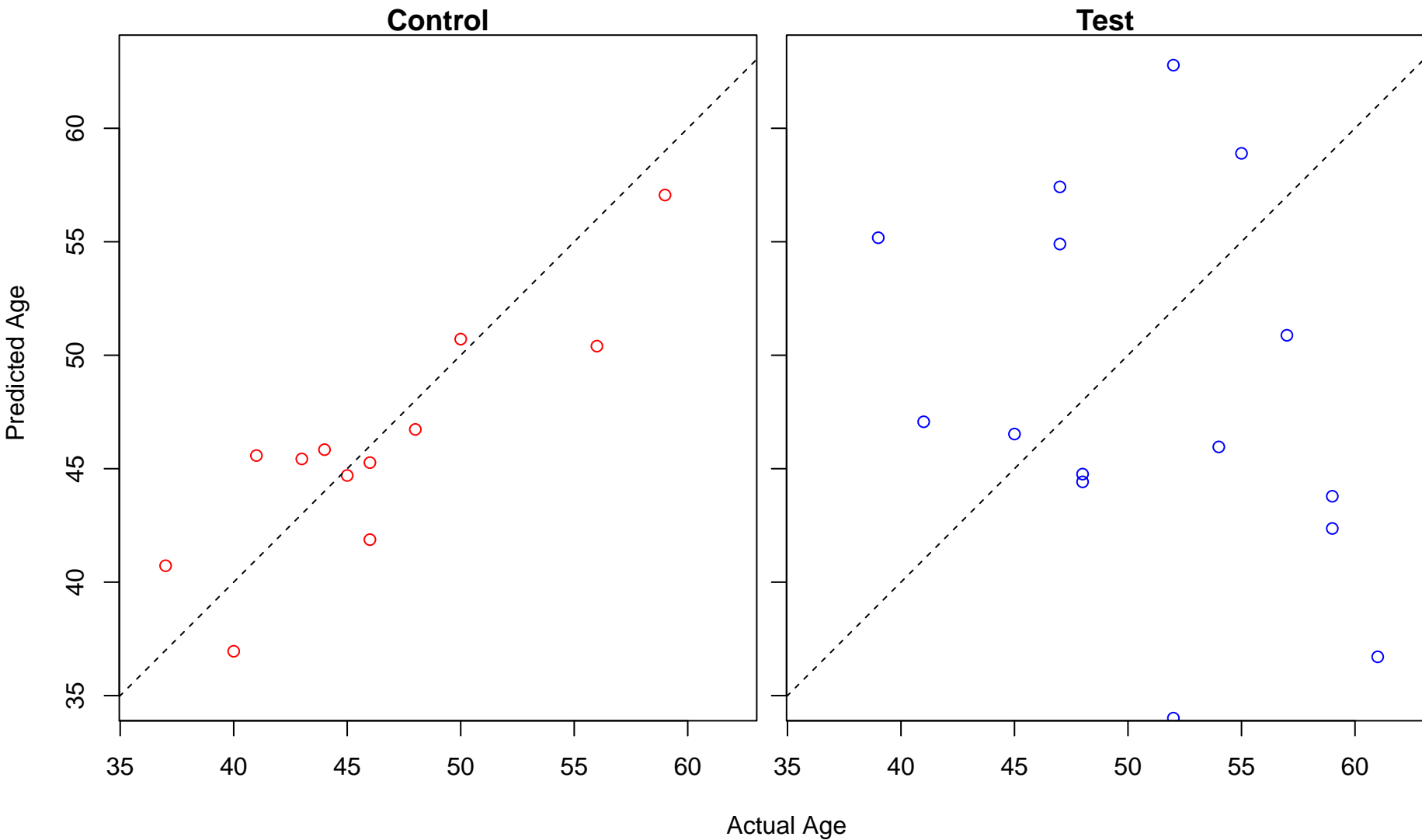
endothelial cell migration (Score: 5.337660)



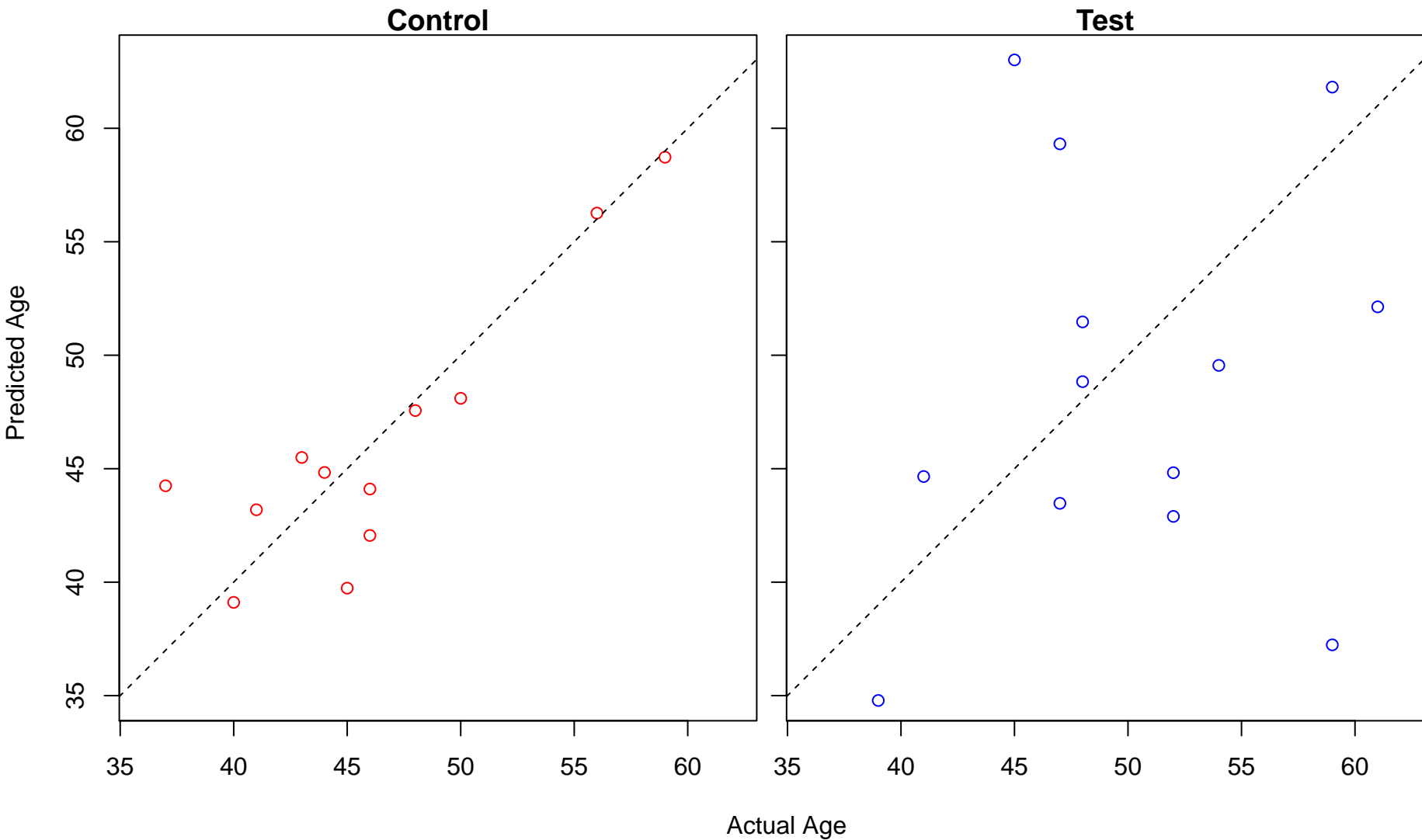
platelet-derived growth factor receptor signaling pathway (Score: 5.332891)



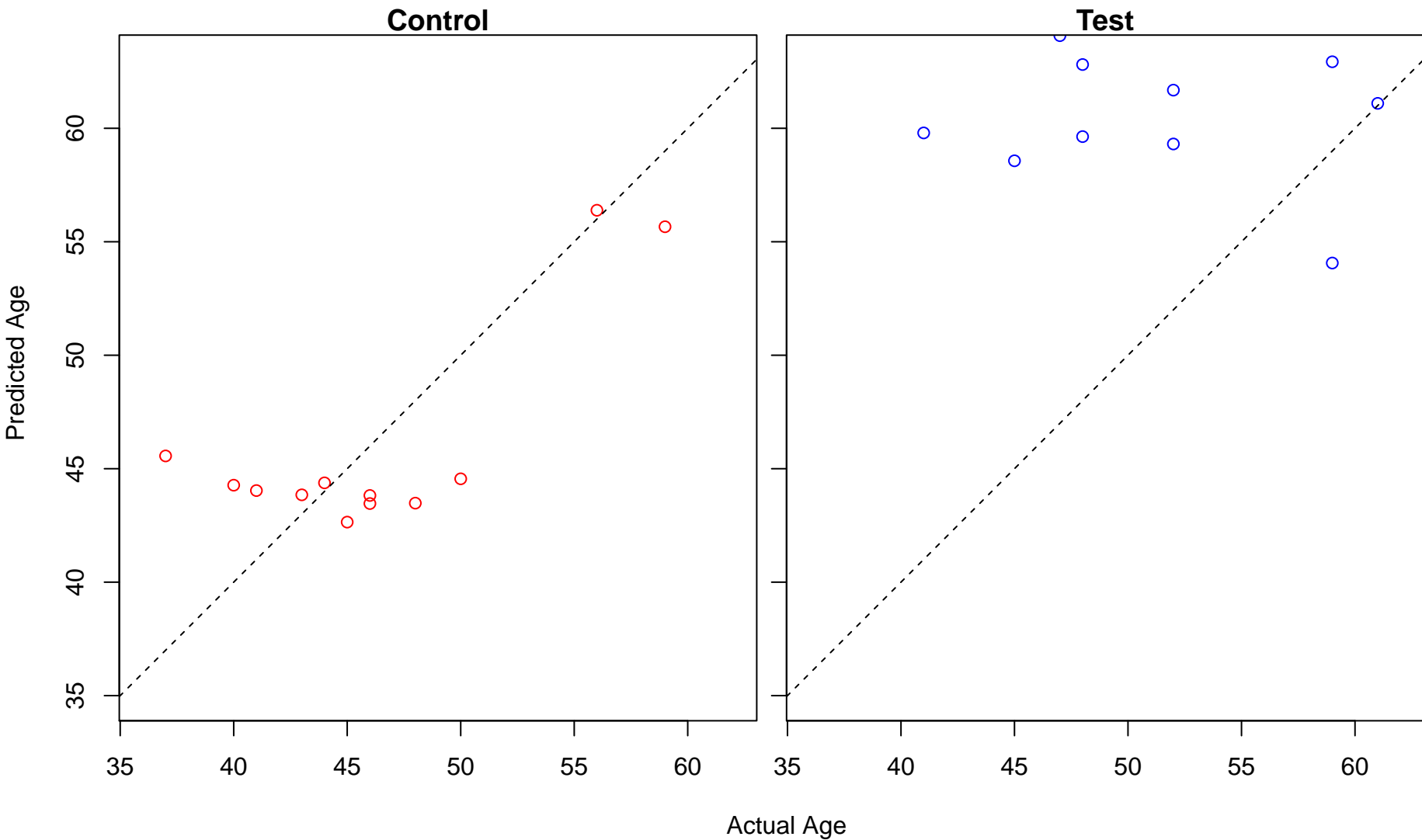
iron ion import (Score: 5.324053)



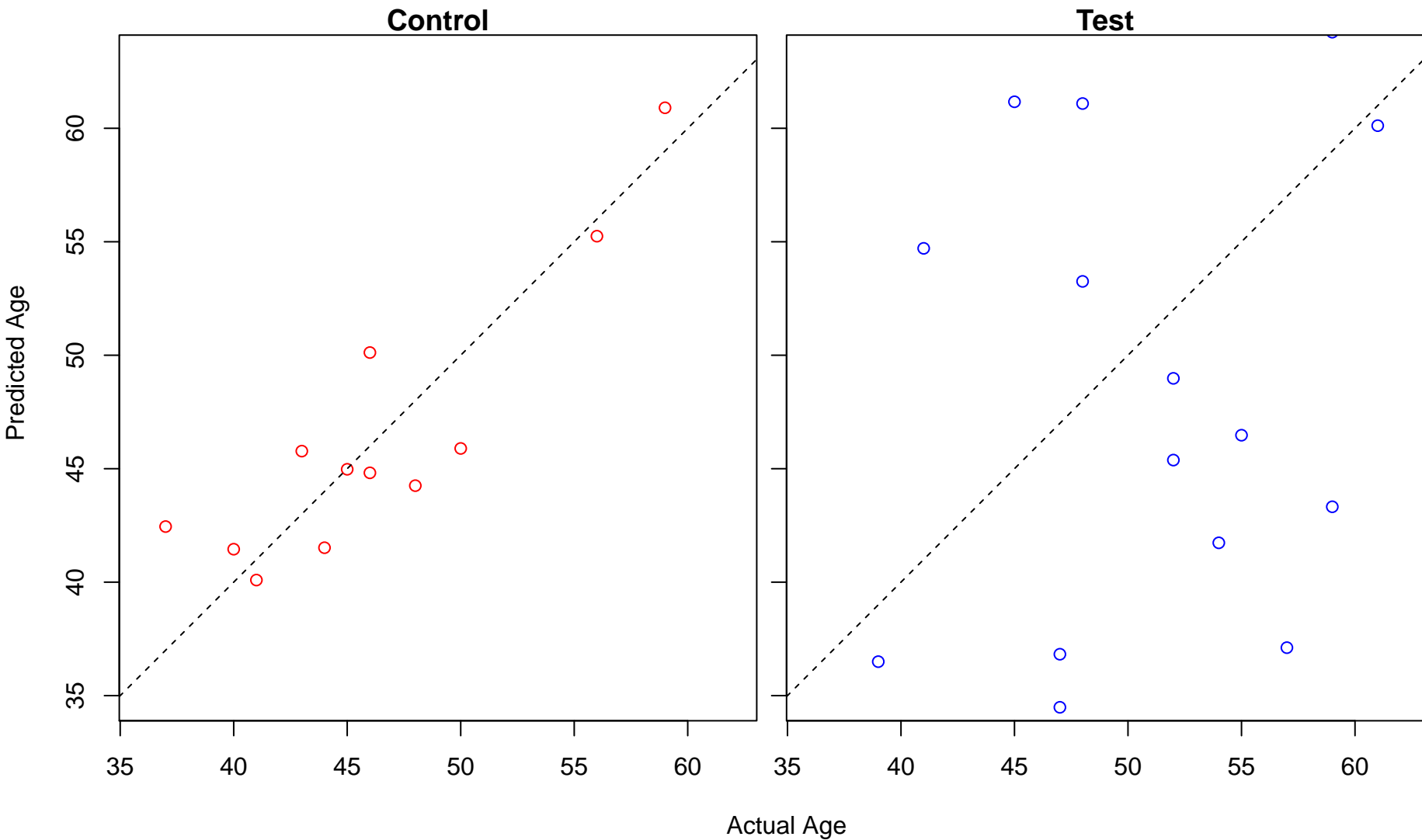
regulation of skeletal muscle tissue development (Score: 5.319381)



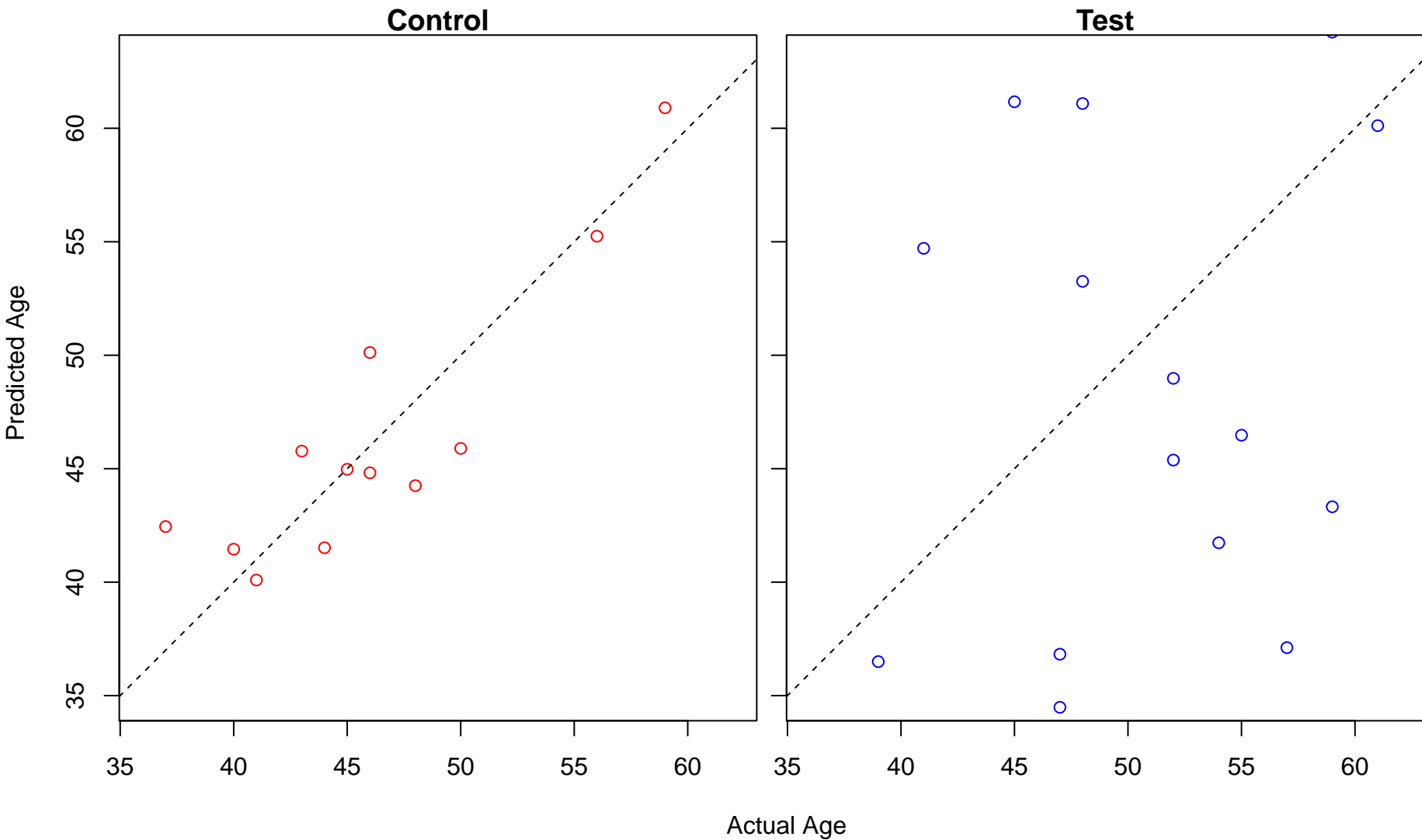
taurine metabolic process (Score: 5.318062)



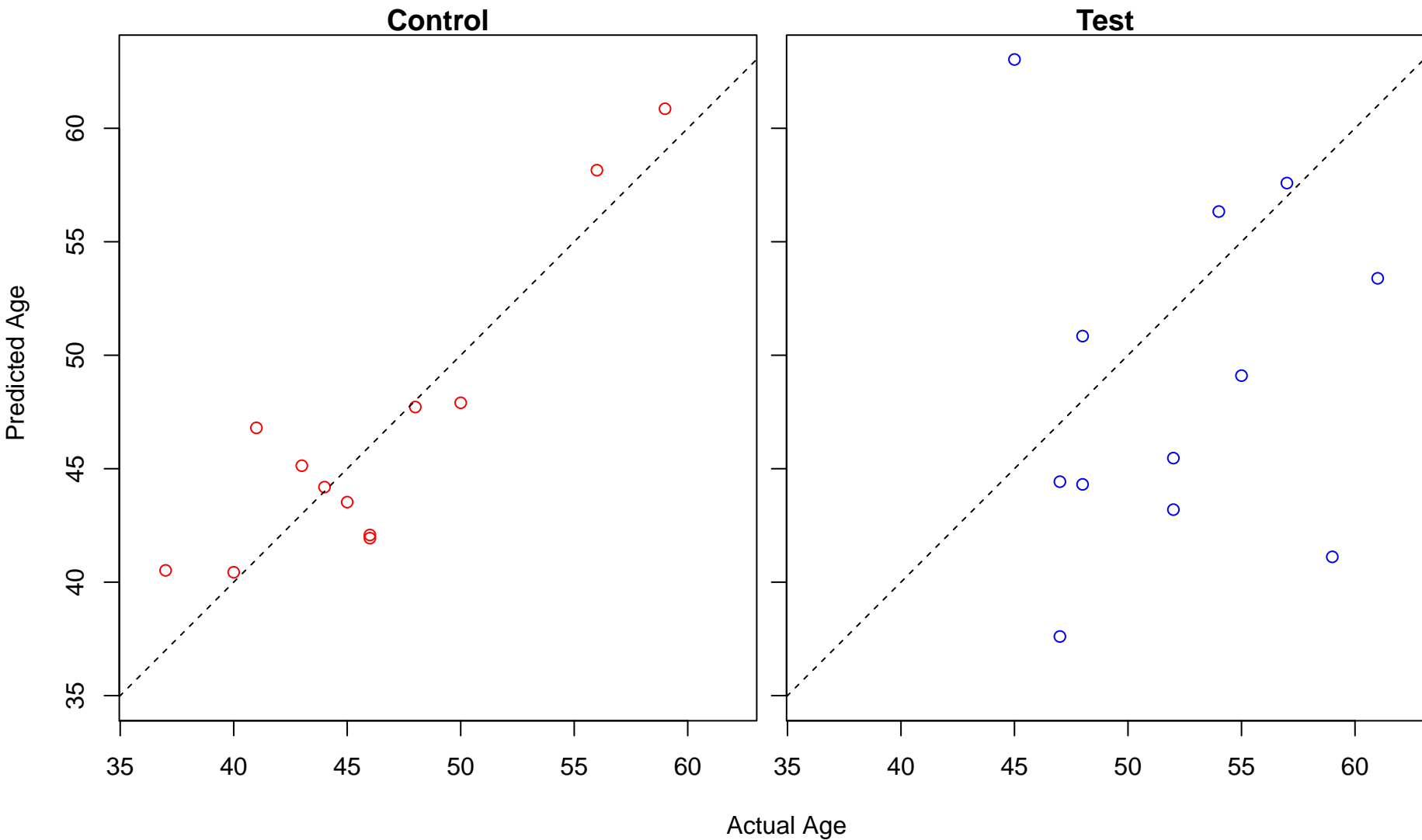
female gonad development (Score: 5.314564)



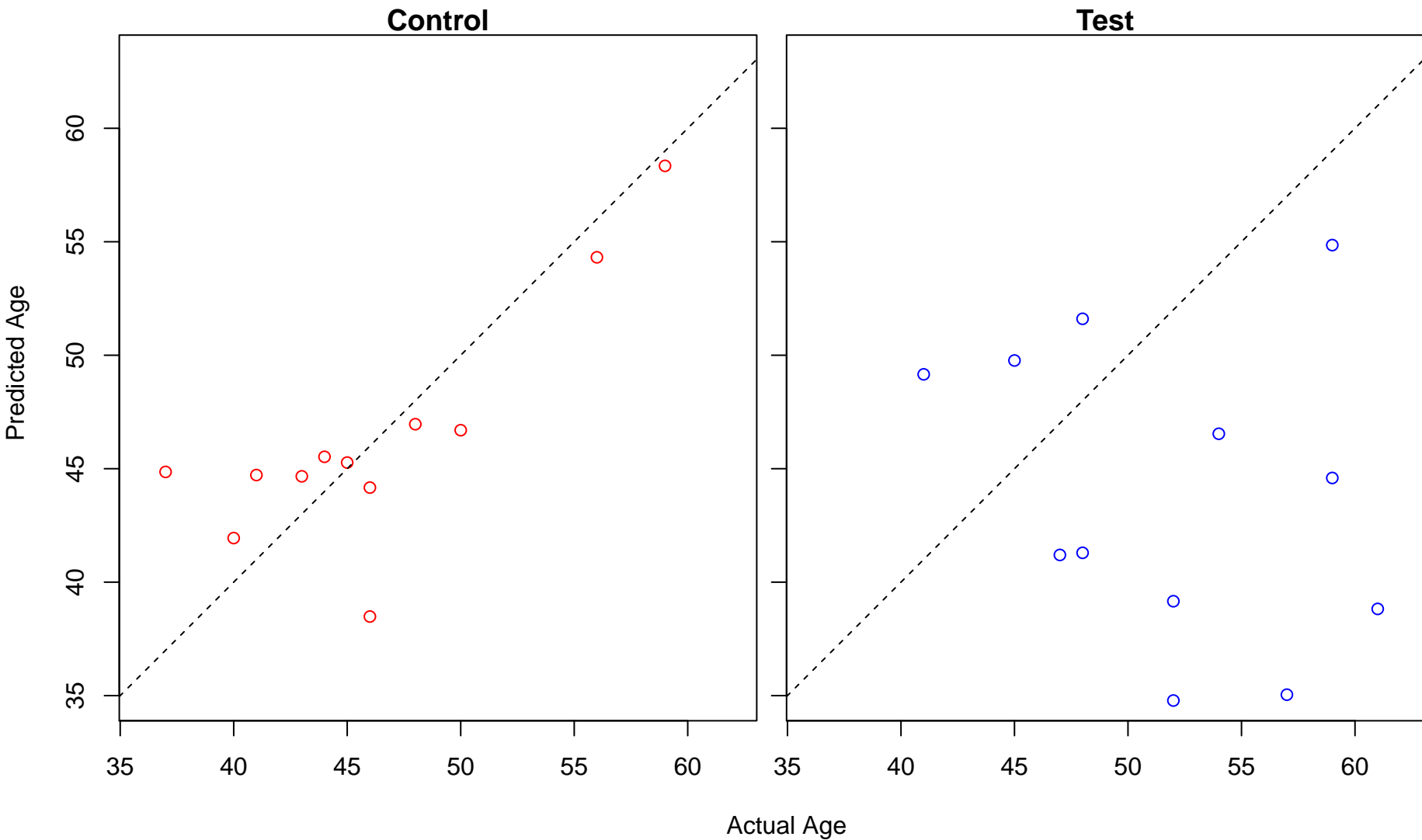
development of primary female sexual characteristics (Score: 5.314564)



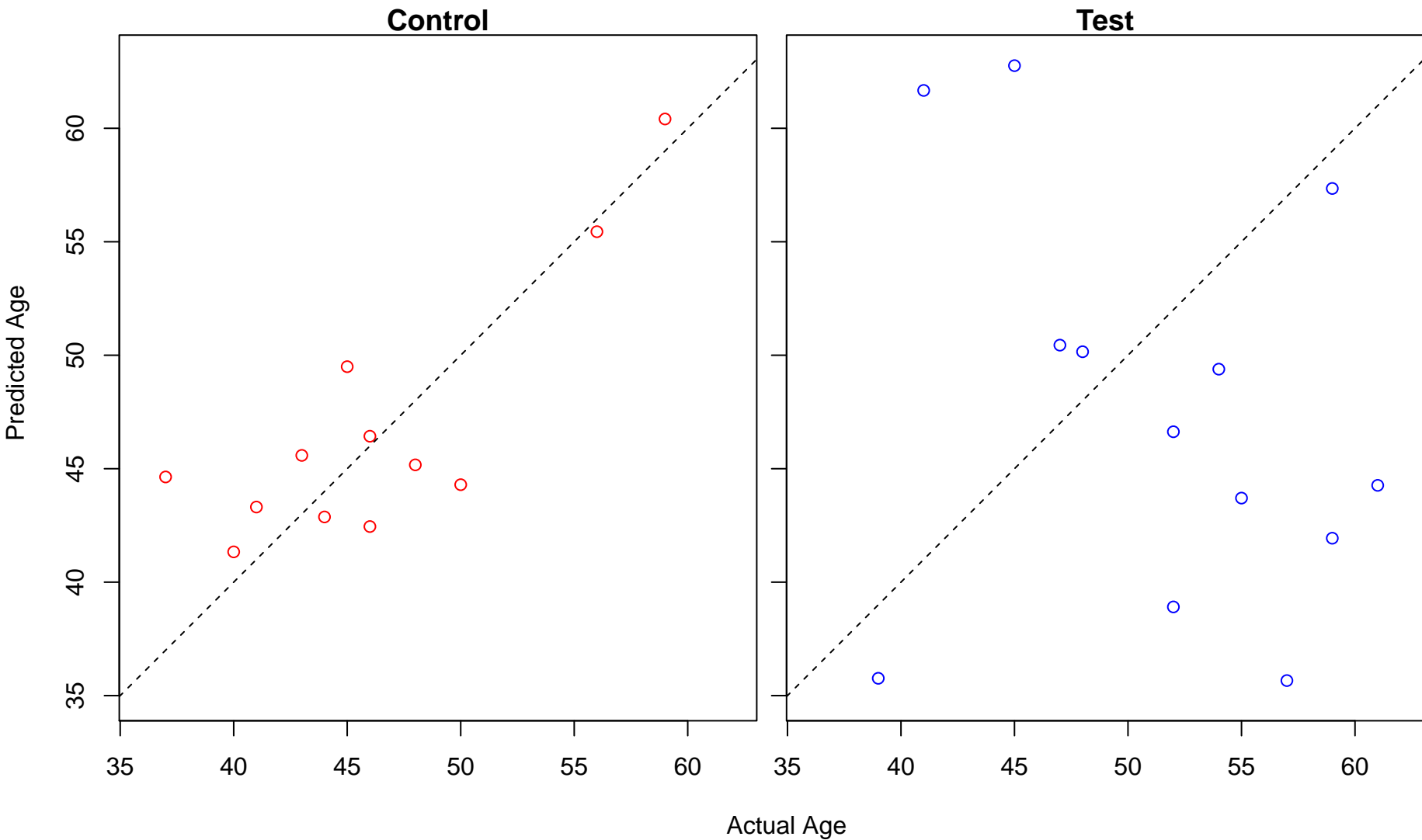
cellular response to calcium ion (Score: 5.304754)



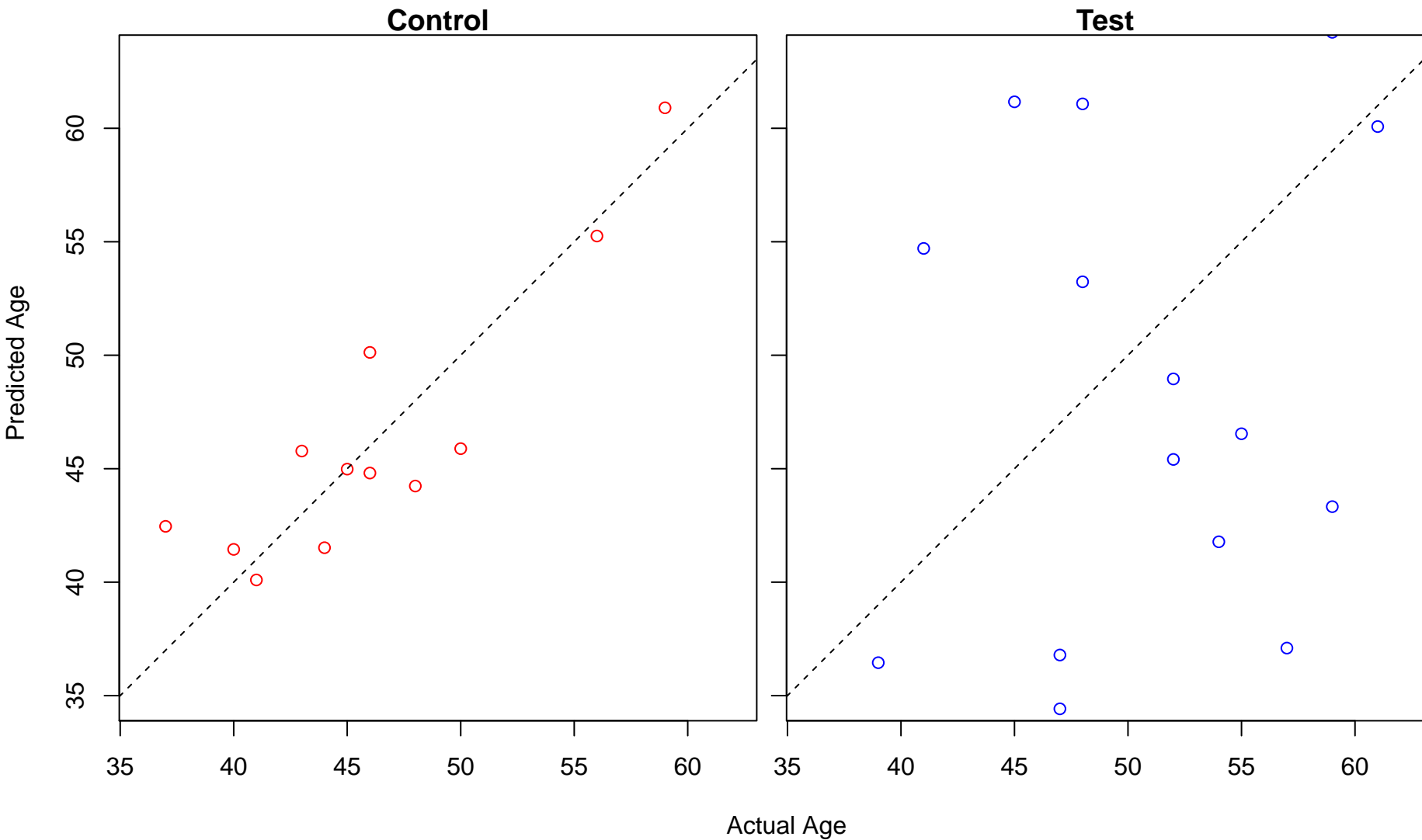
RNA processing (Score: 5.303719)



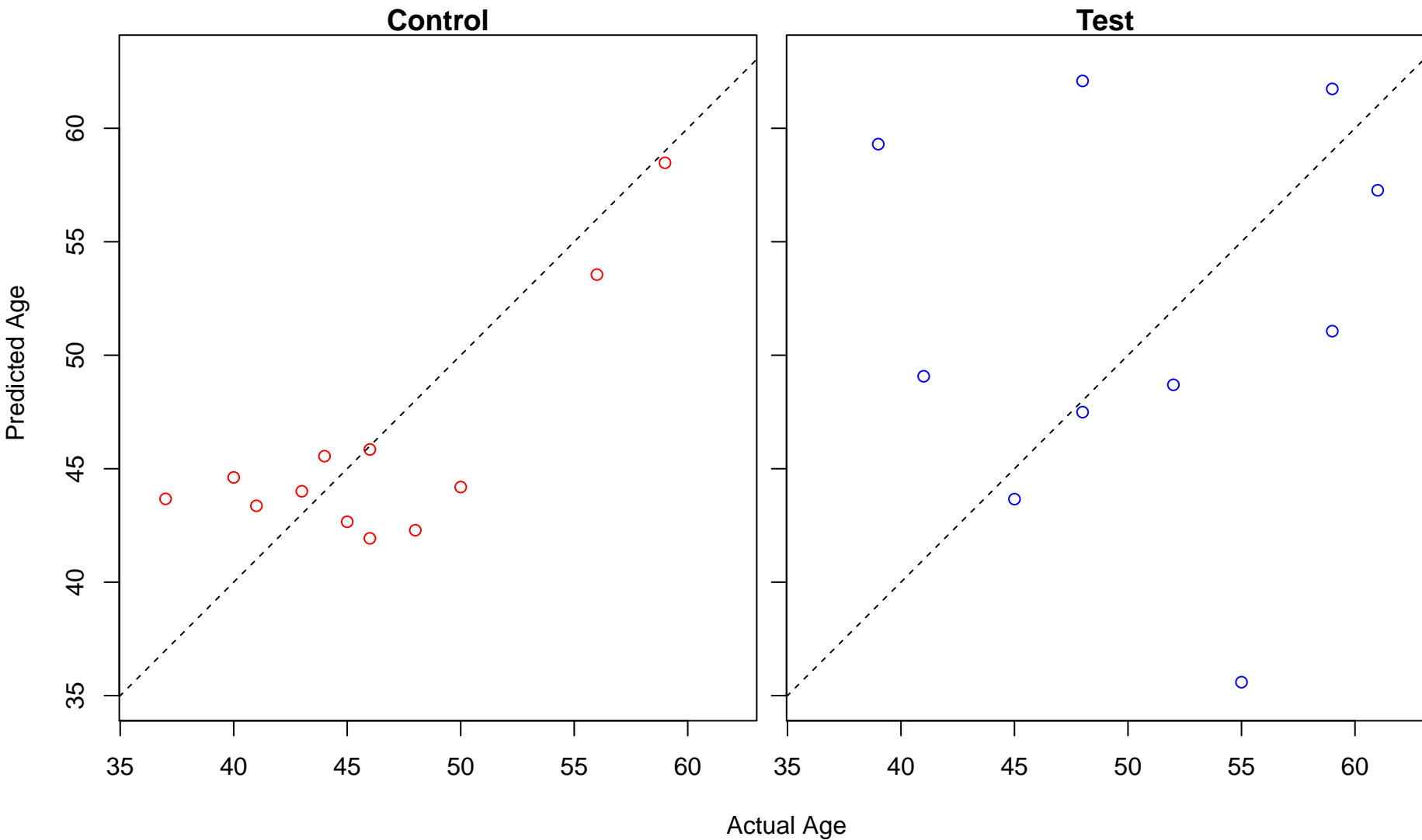
positive regulation of stress-activated MAPK cascade (Score: 5.303492)



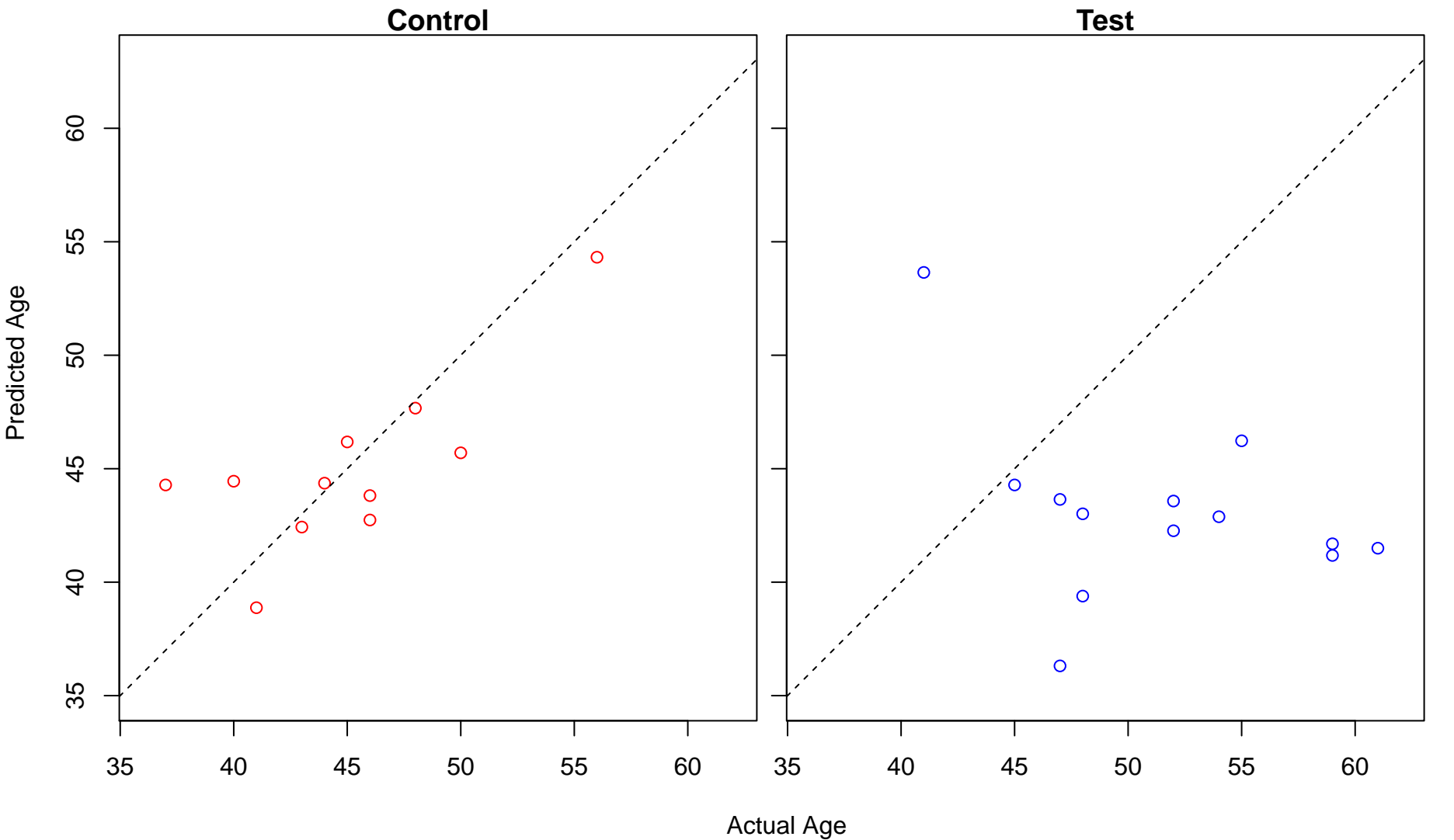
female sex differentiation (Score: 5.301774)



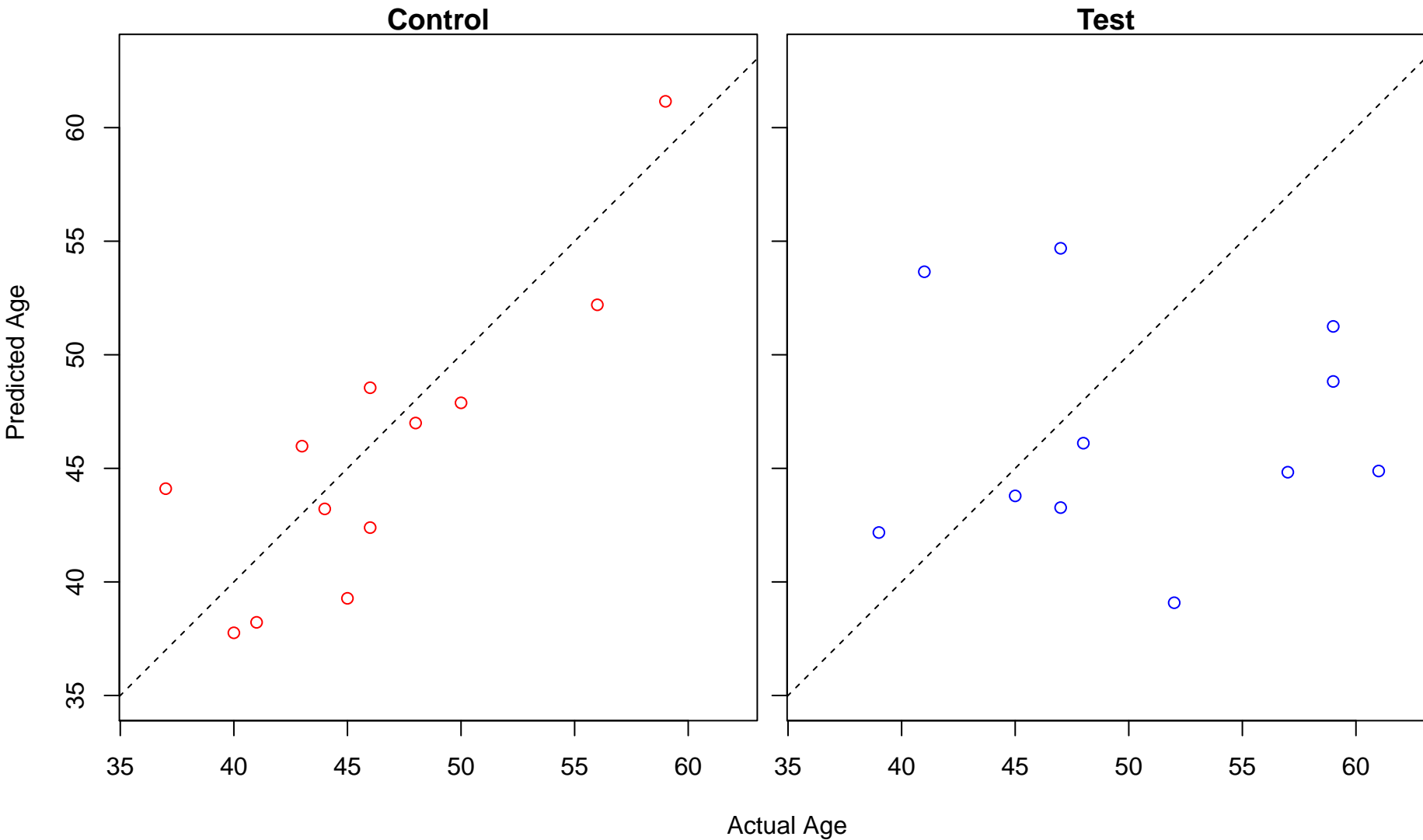
sodium ion homeostasis (Score: 5.297558)



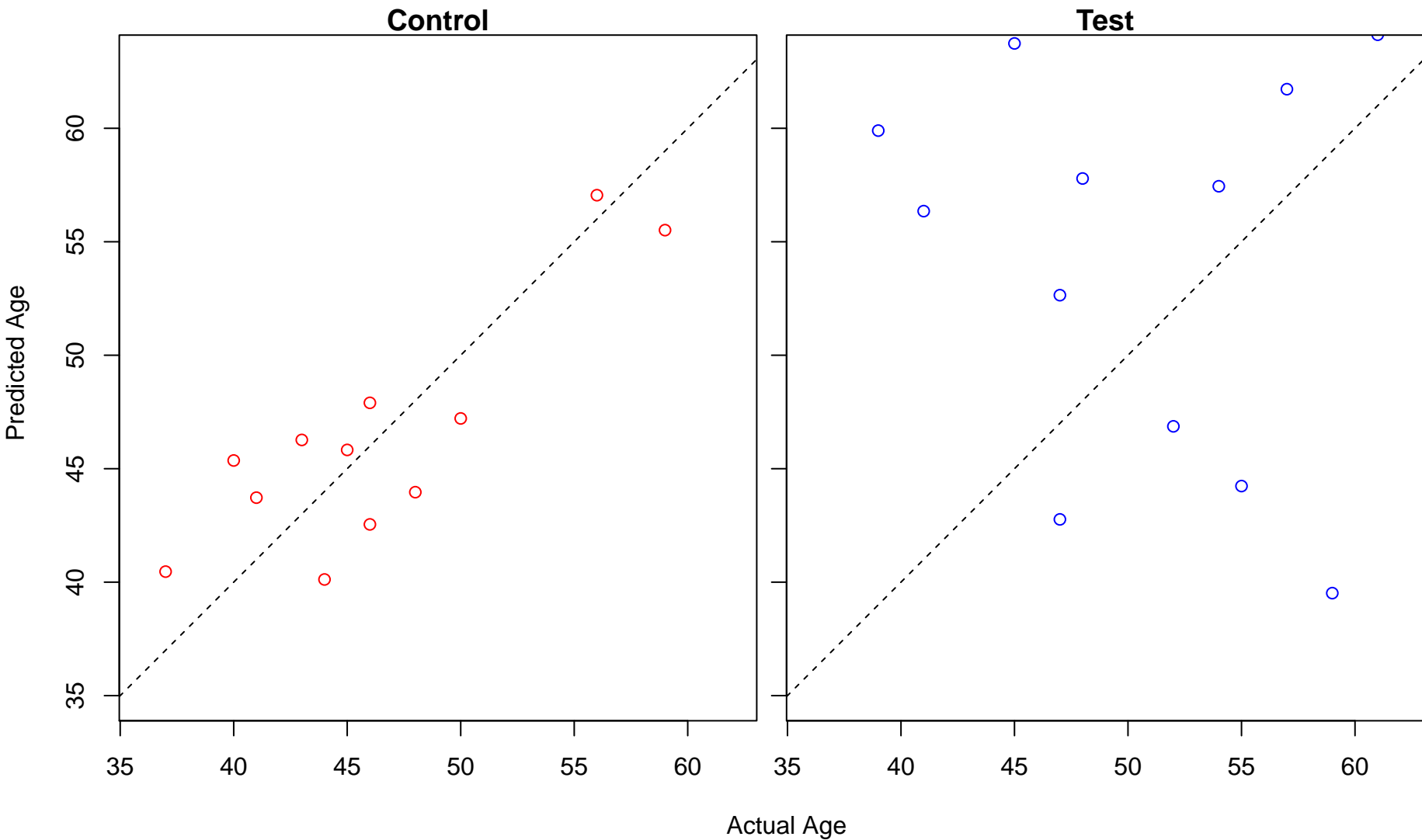
nucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay (Score)



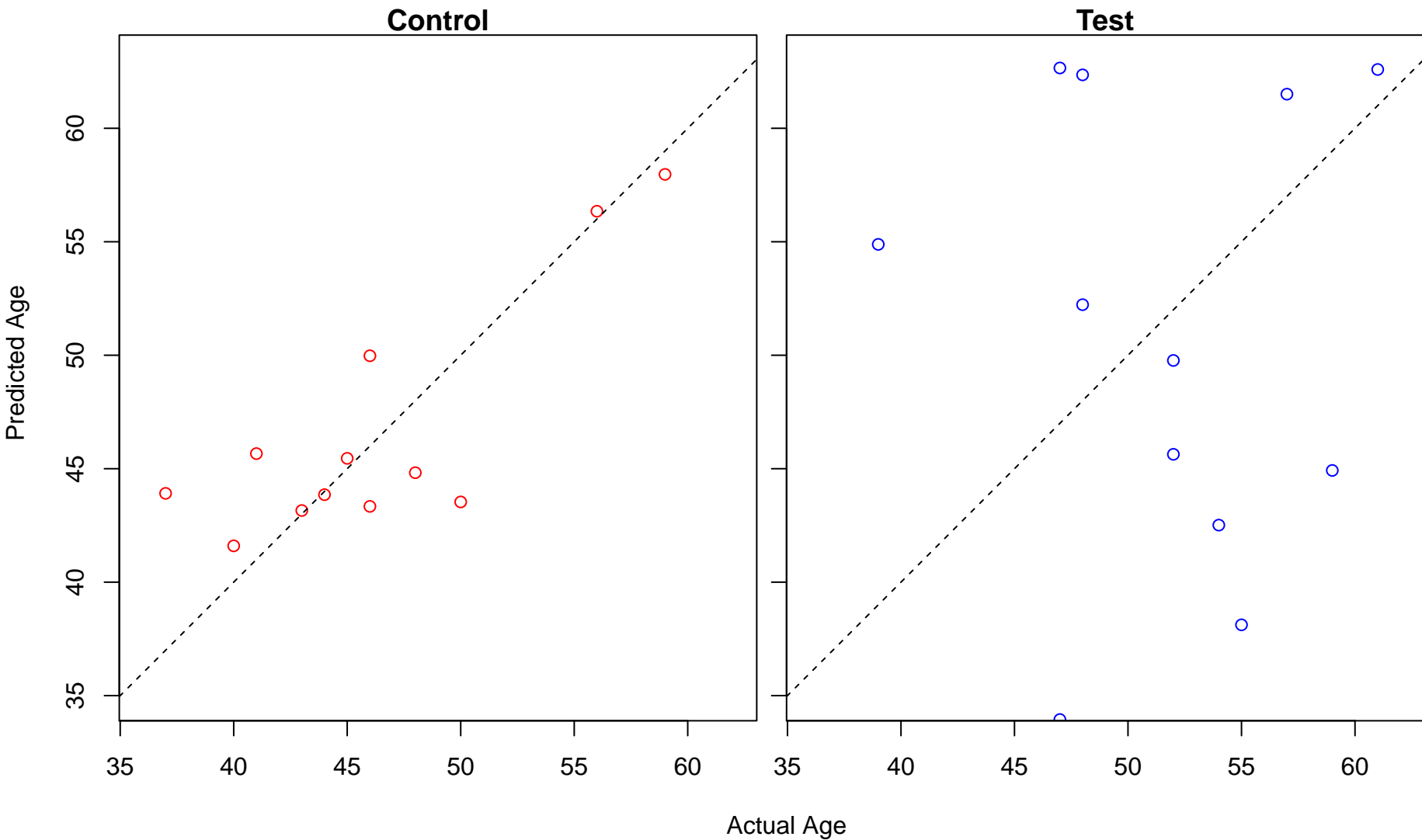
positive regulation of sodium ion transport (Score: 5.288827)



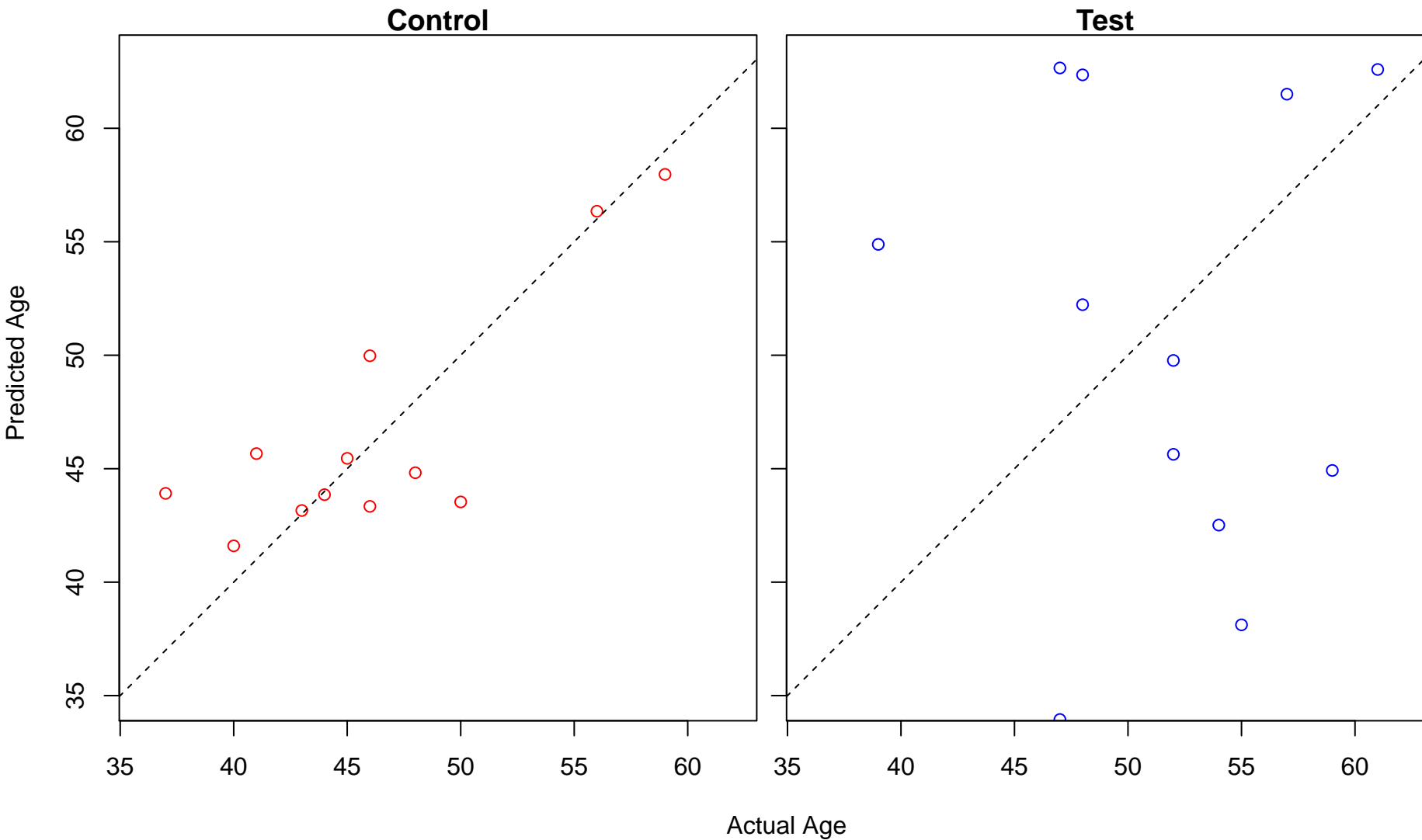
positive regulation of protein kinase C signaling (Score: 5.286821)



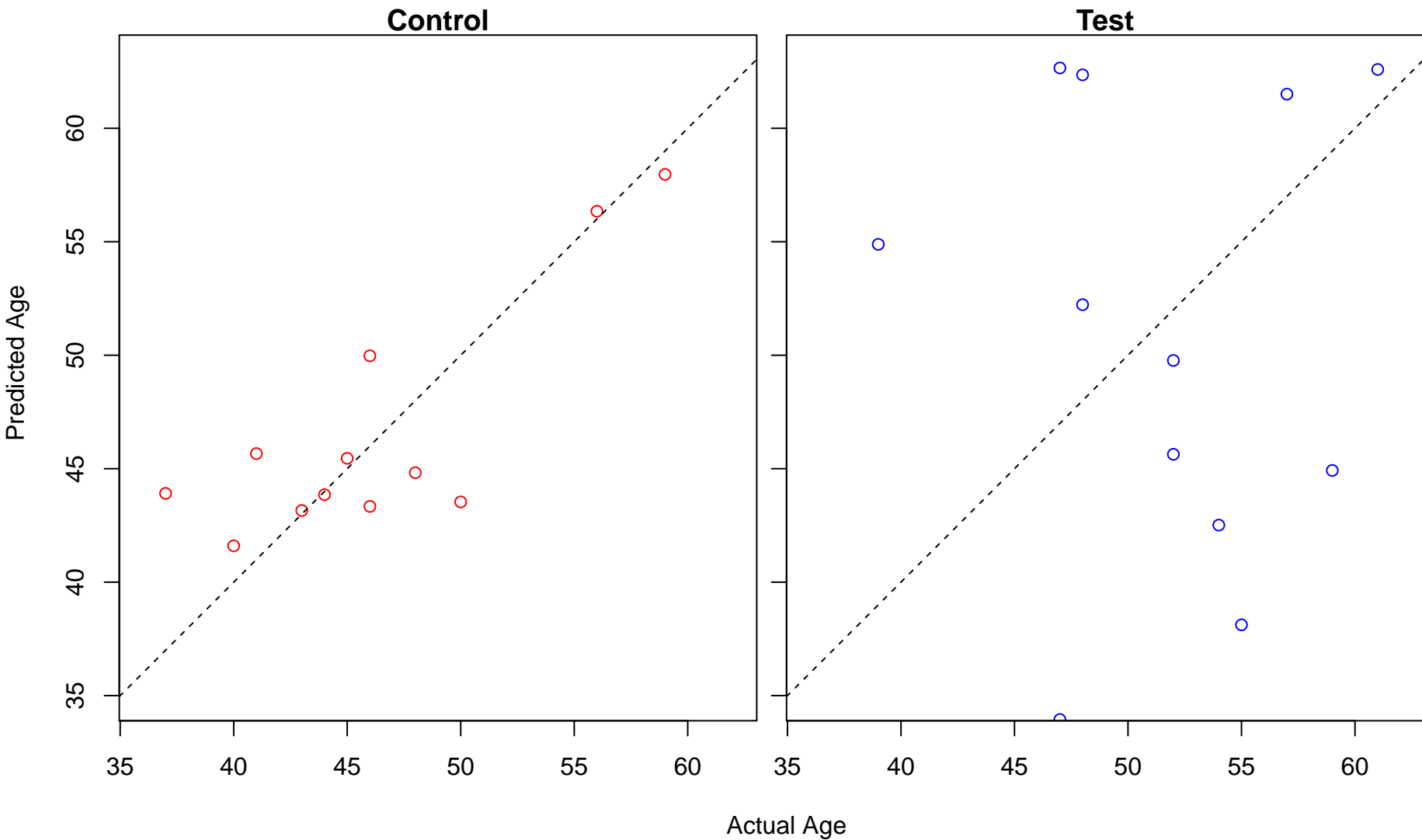
regulation of mitotic metaphase/anaphase transition (Score: 5.281898)



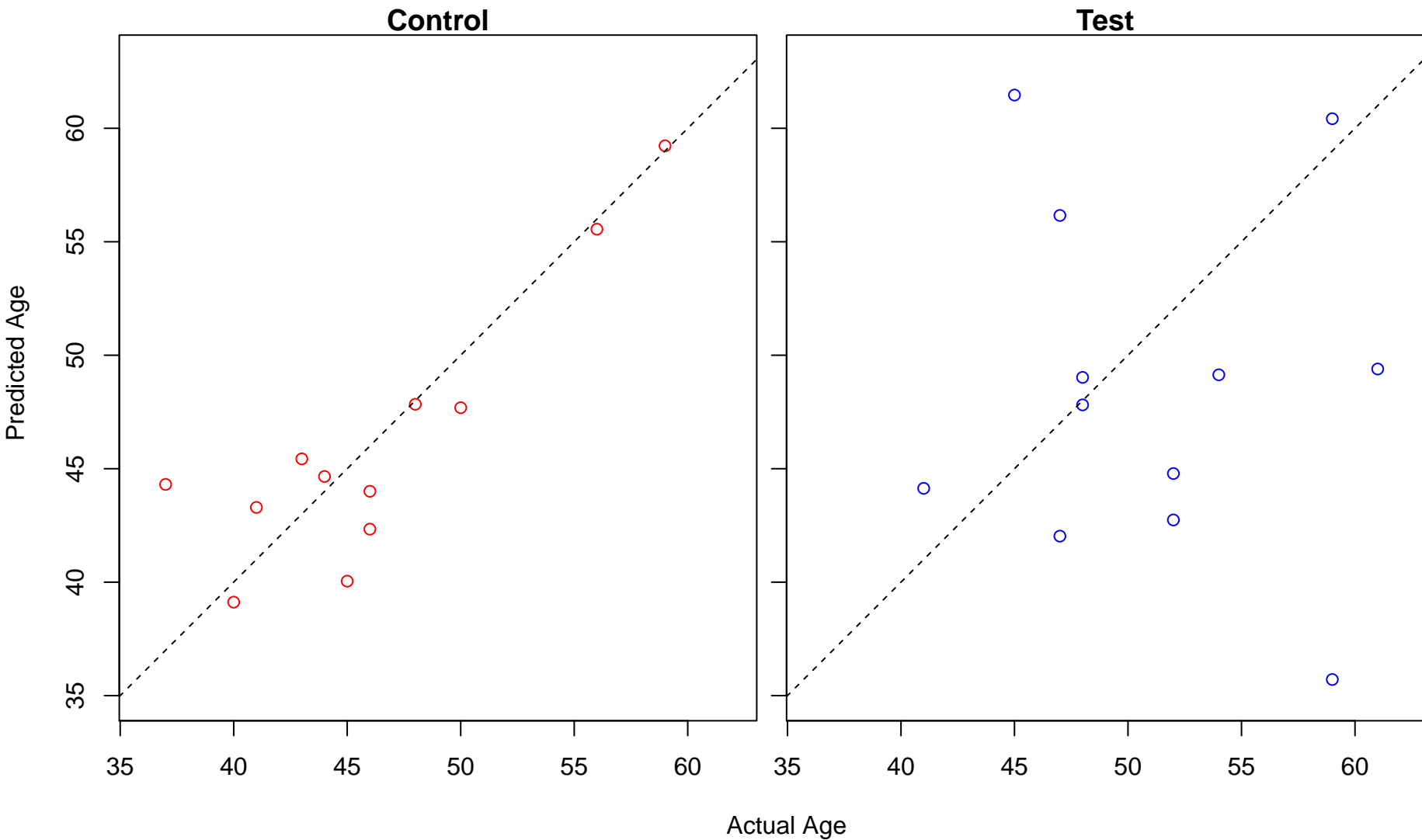
regulation of metaphase/anaphase transition of cell cycle (Score: 5.281891)



regulation of mitotic sister chromatid separation (Score: 5.281890)

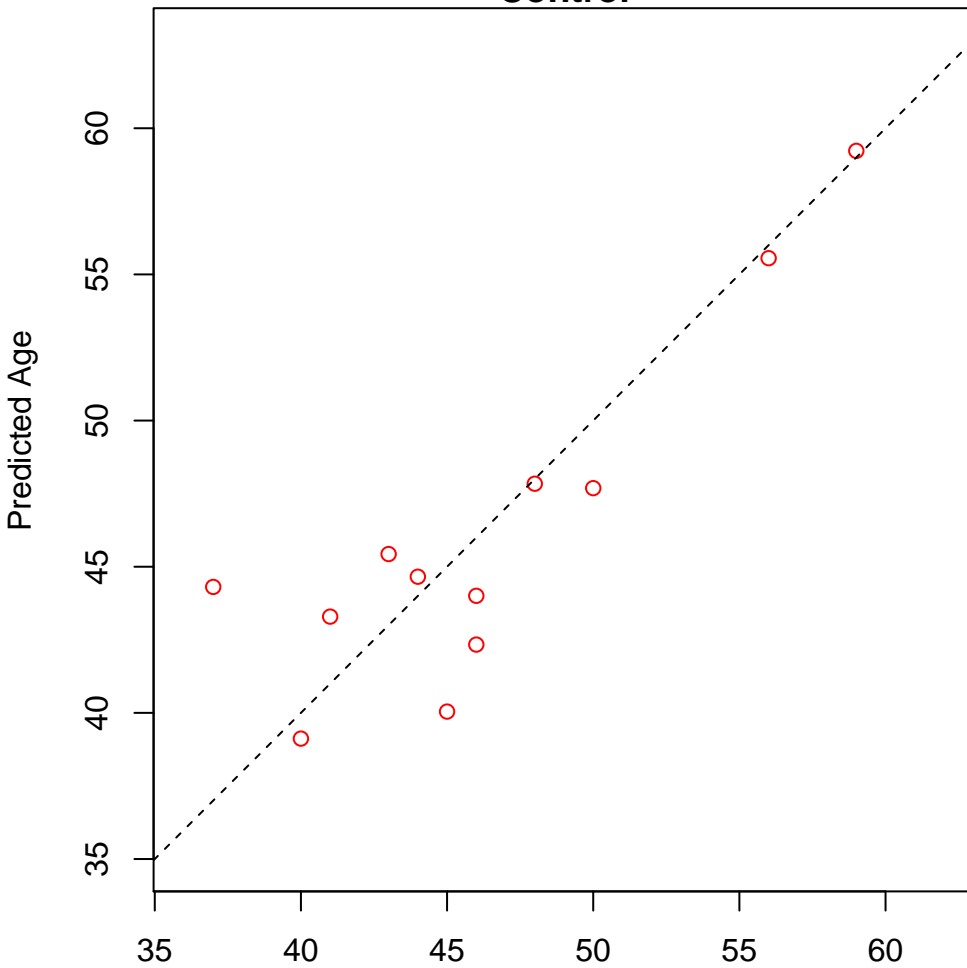


regulation of striated muscle tissue development (Score: 5.281845)

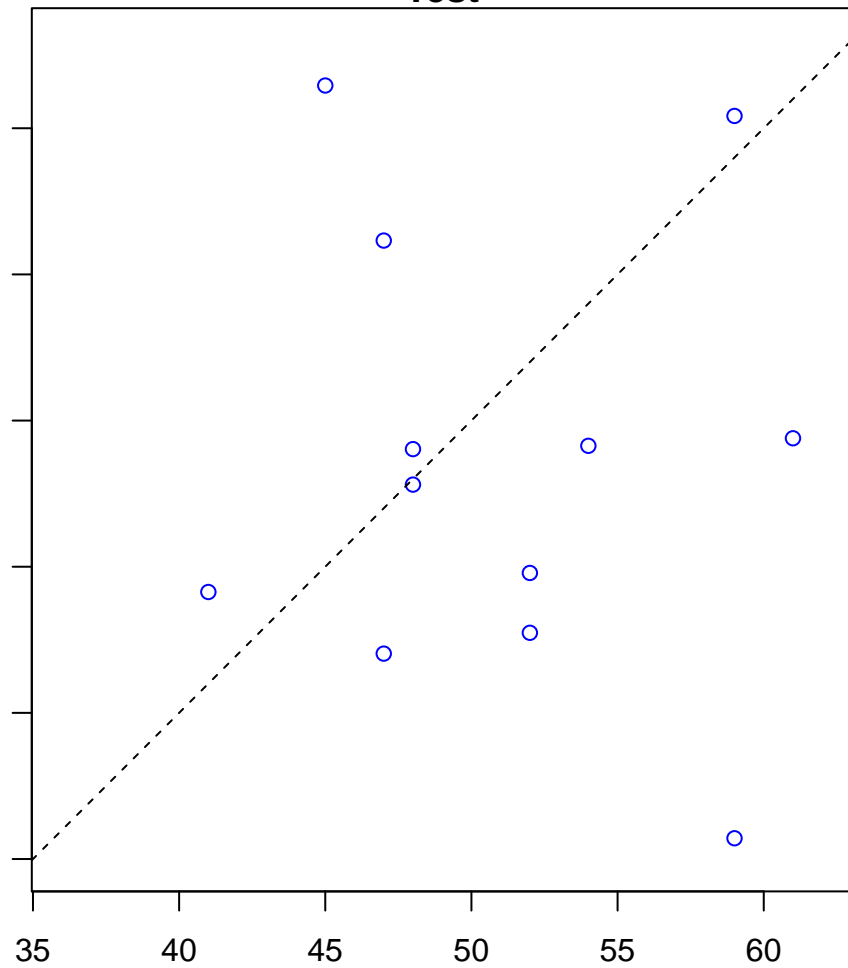


regulation of muscle tissue development (Score: 5.281625)

Control



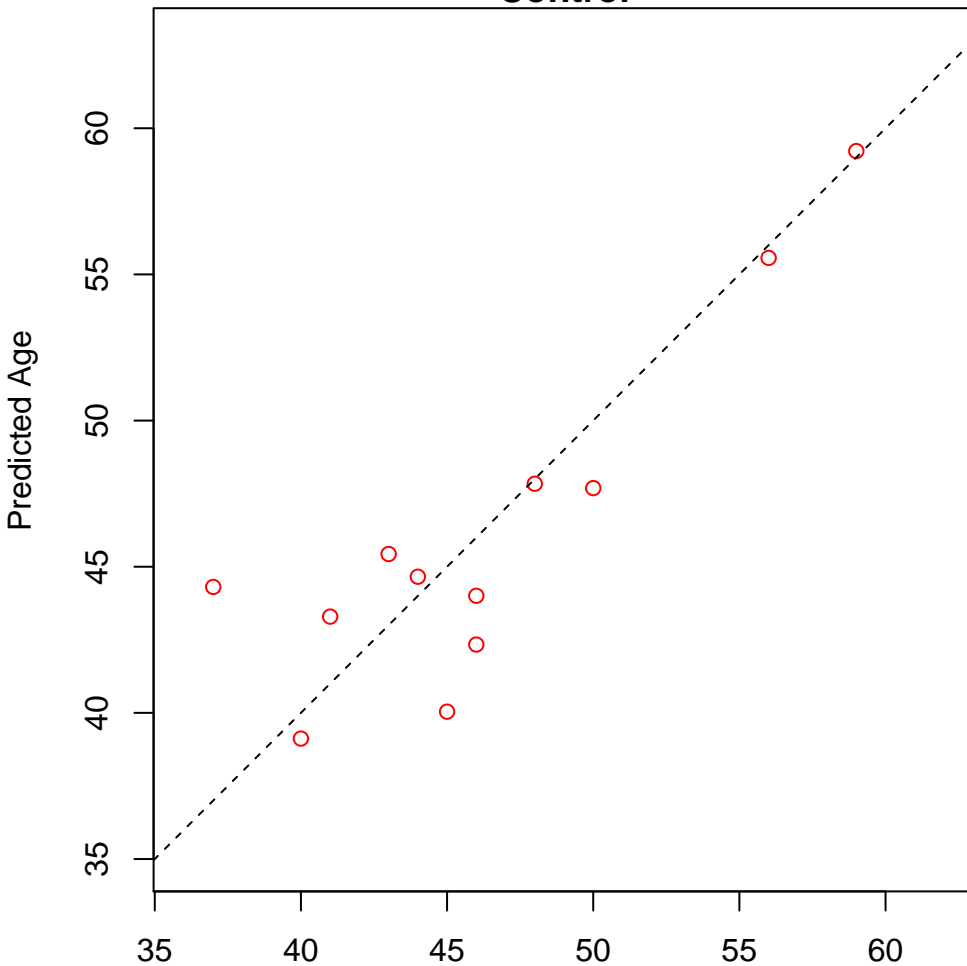
Test



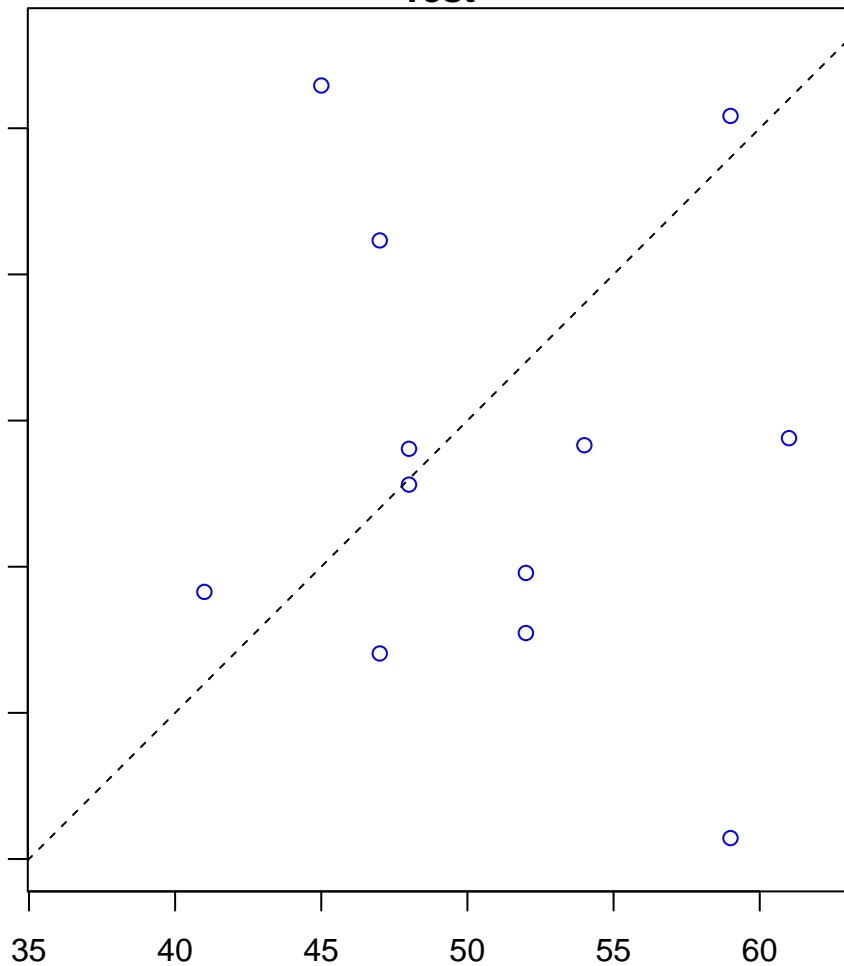
Actual Age

regulation of muscle organ development (Score: 5.281015)

Control

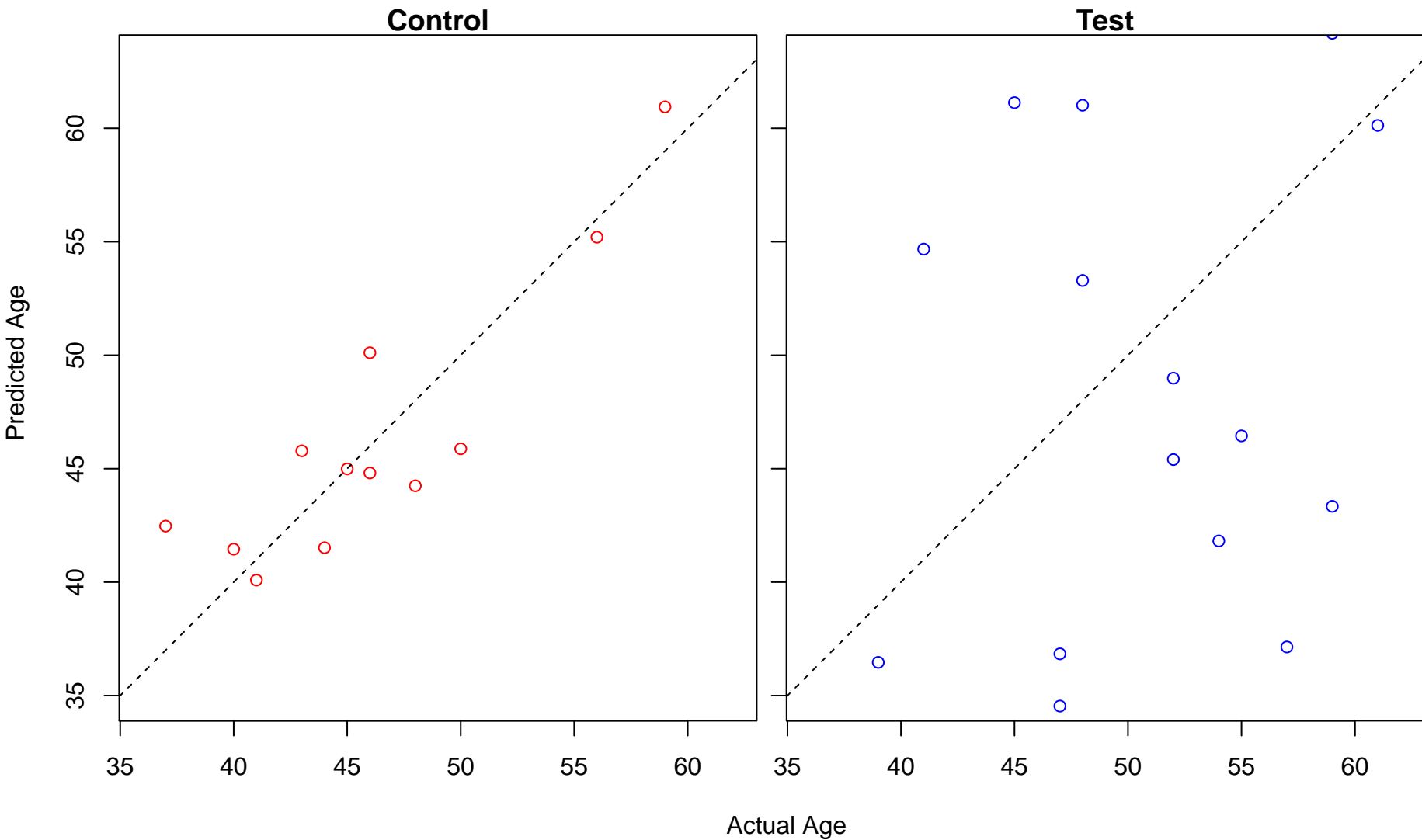


Test

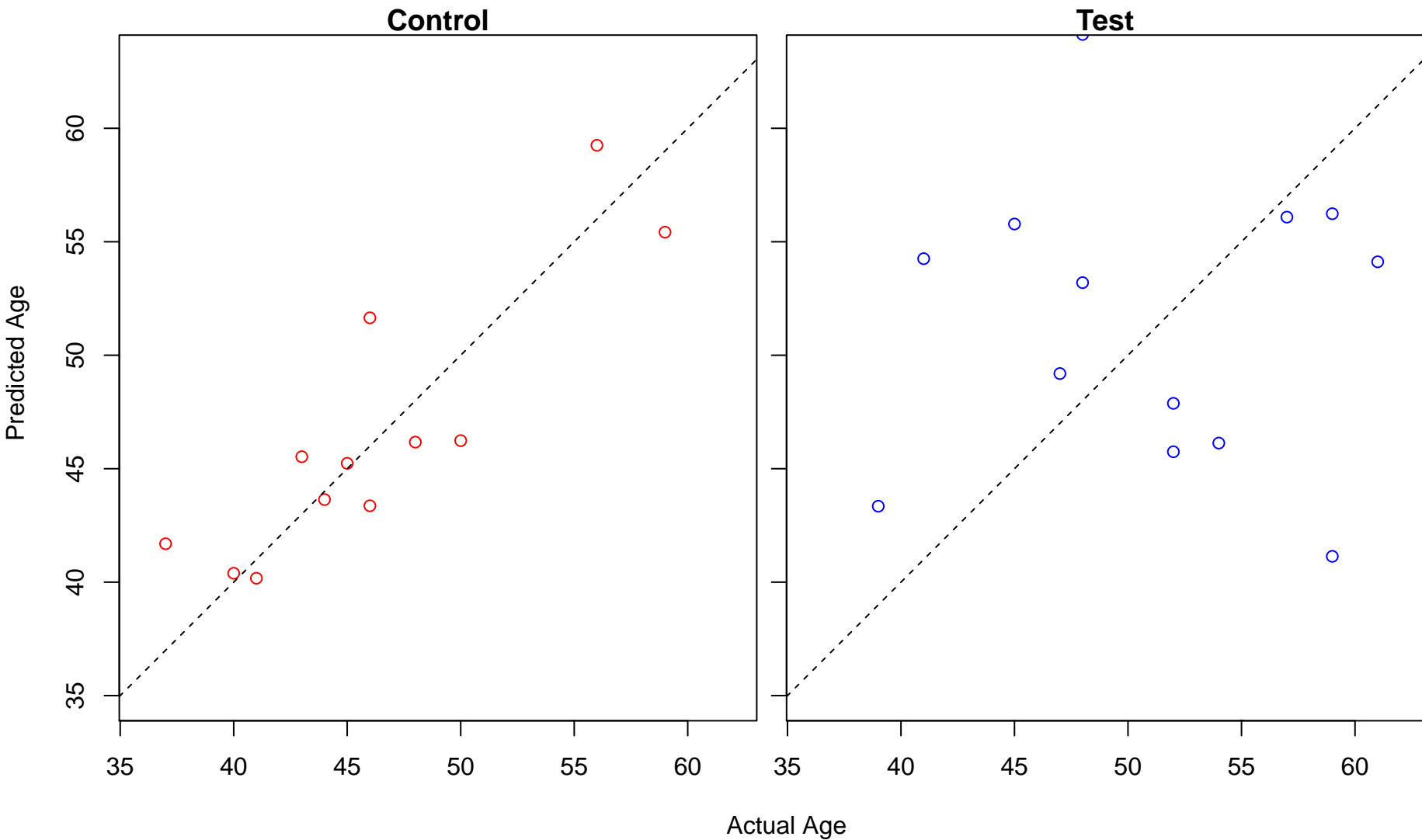


Actual Age

ovulation cycle process (Score: 5.262871)

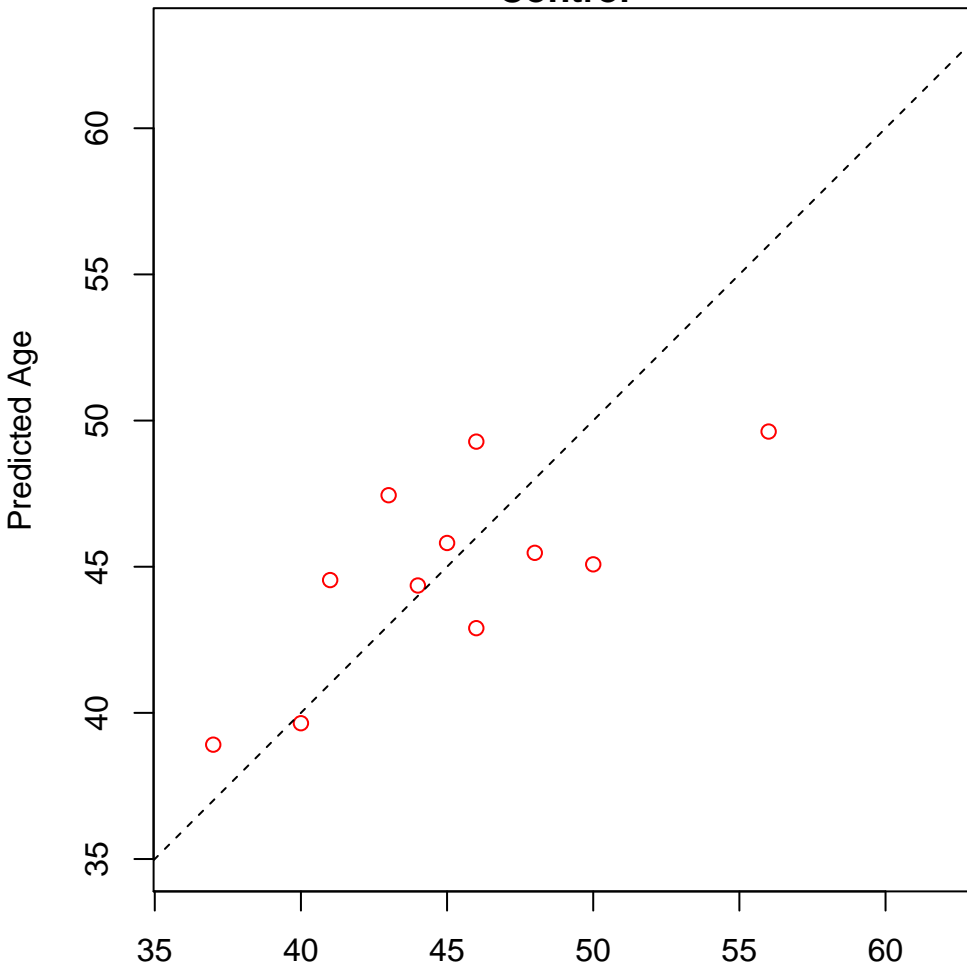


mesoderm development (Score: 5.262443)

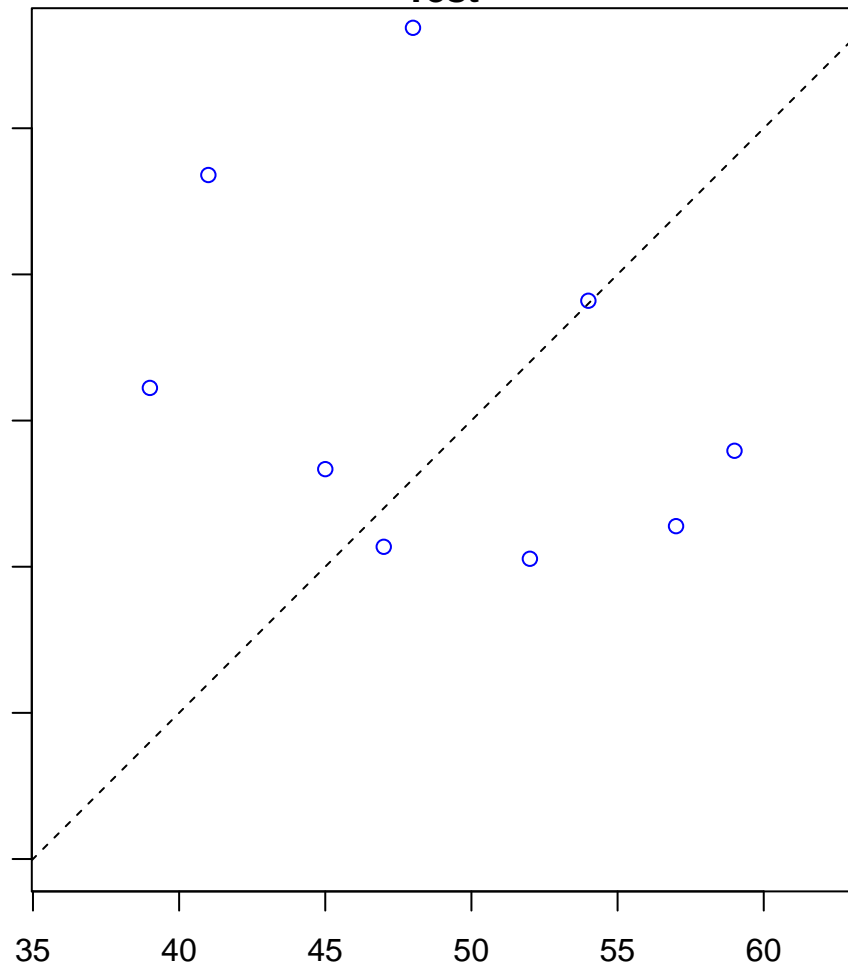


regulation of response to osmotic stress (Score: 5.262375)

Control

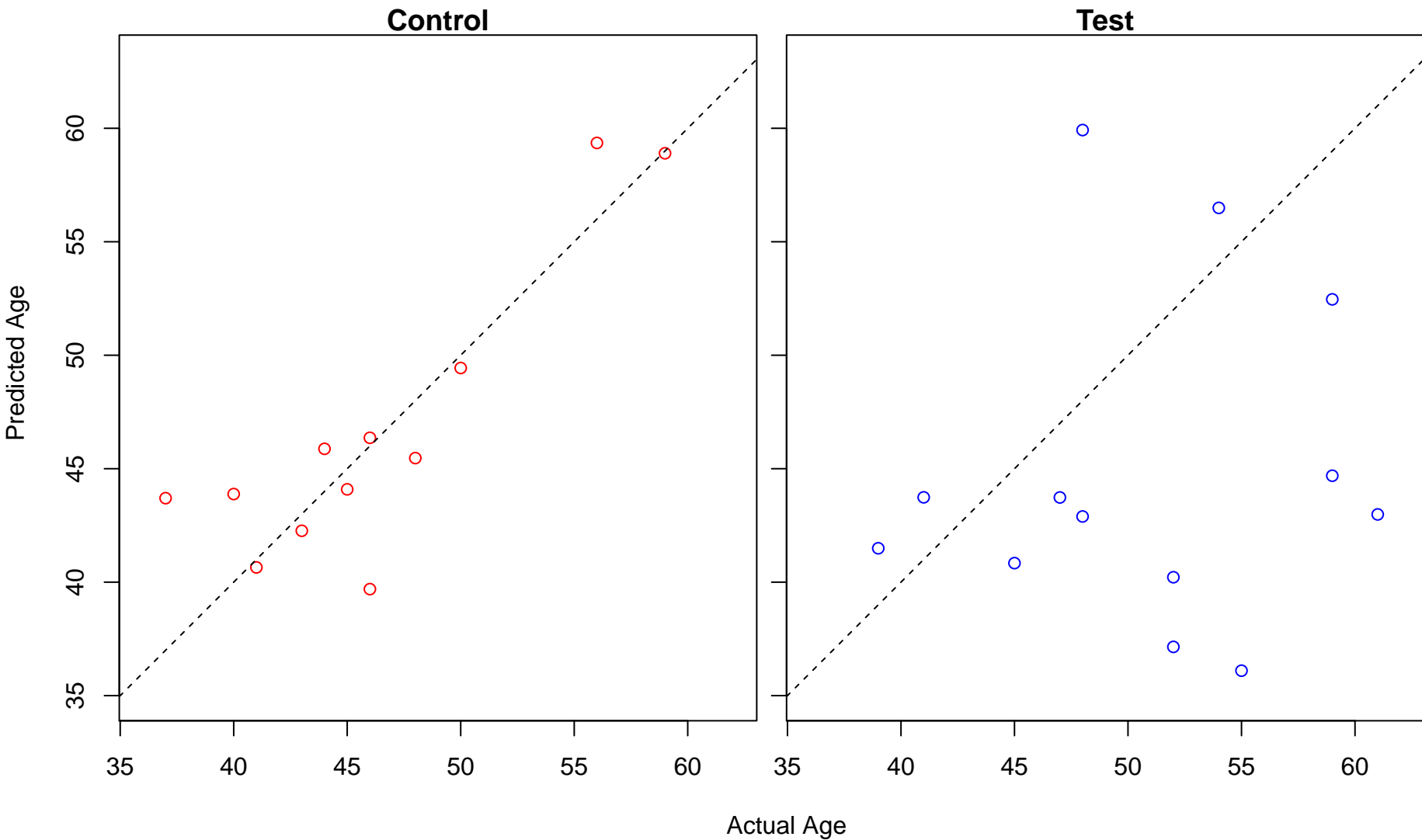


Test

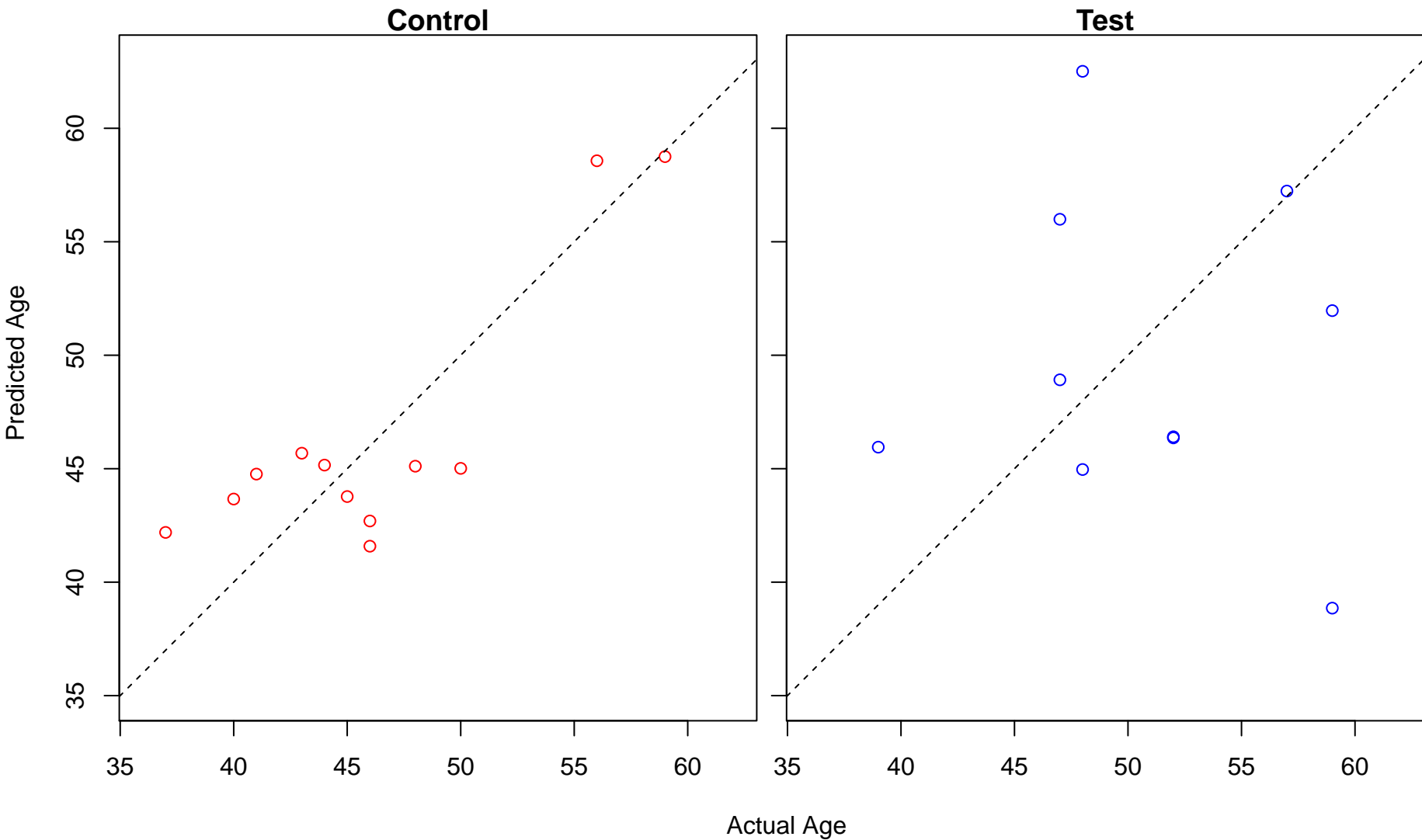


Actual Age

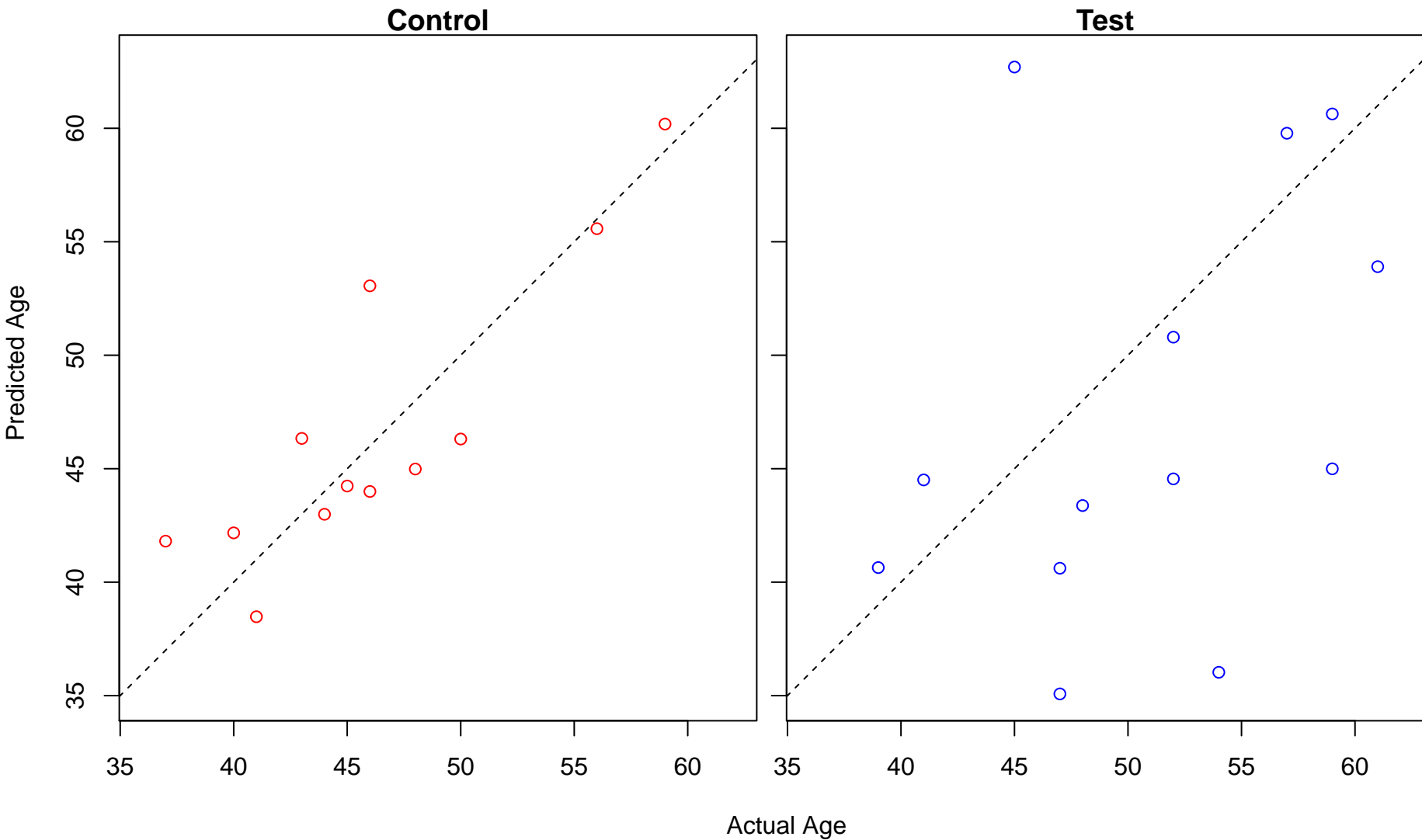
positive regulation of ATPase activity (Score: 5.253314)



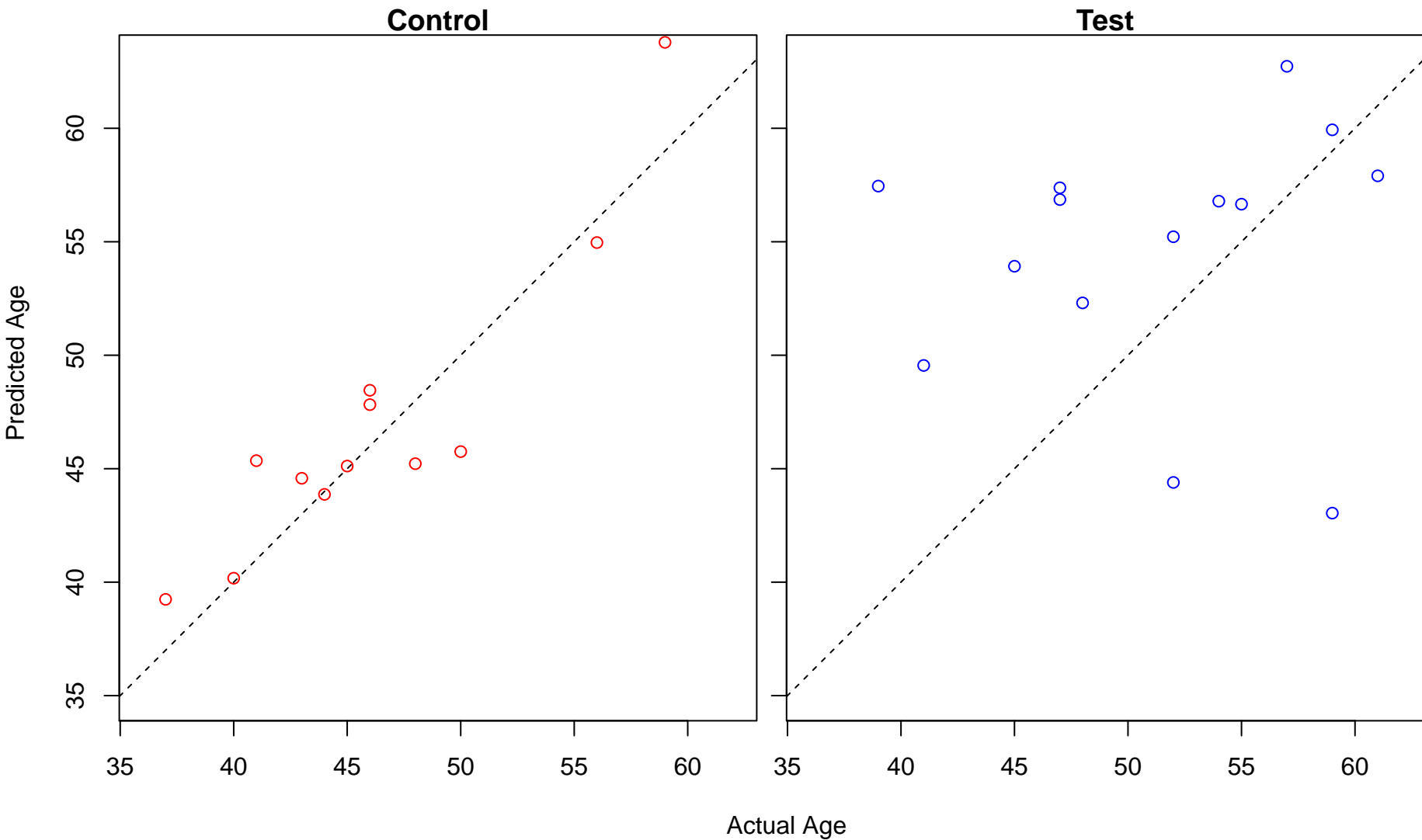
heme transport (Score: 5.252514)



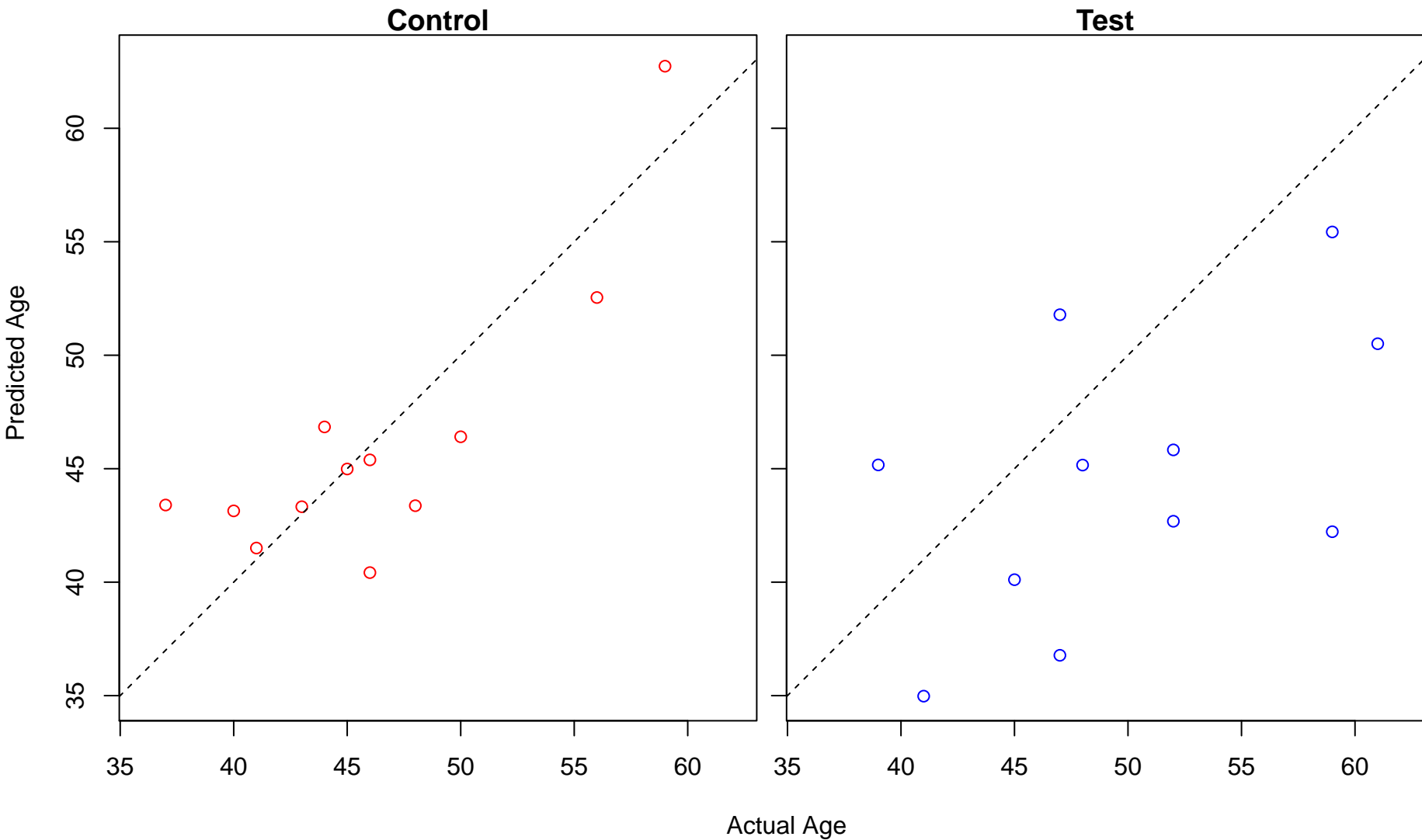
positive regulation of mesonephros development (Score: 5.250598)



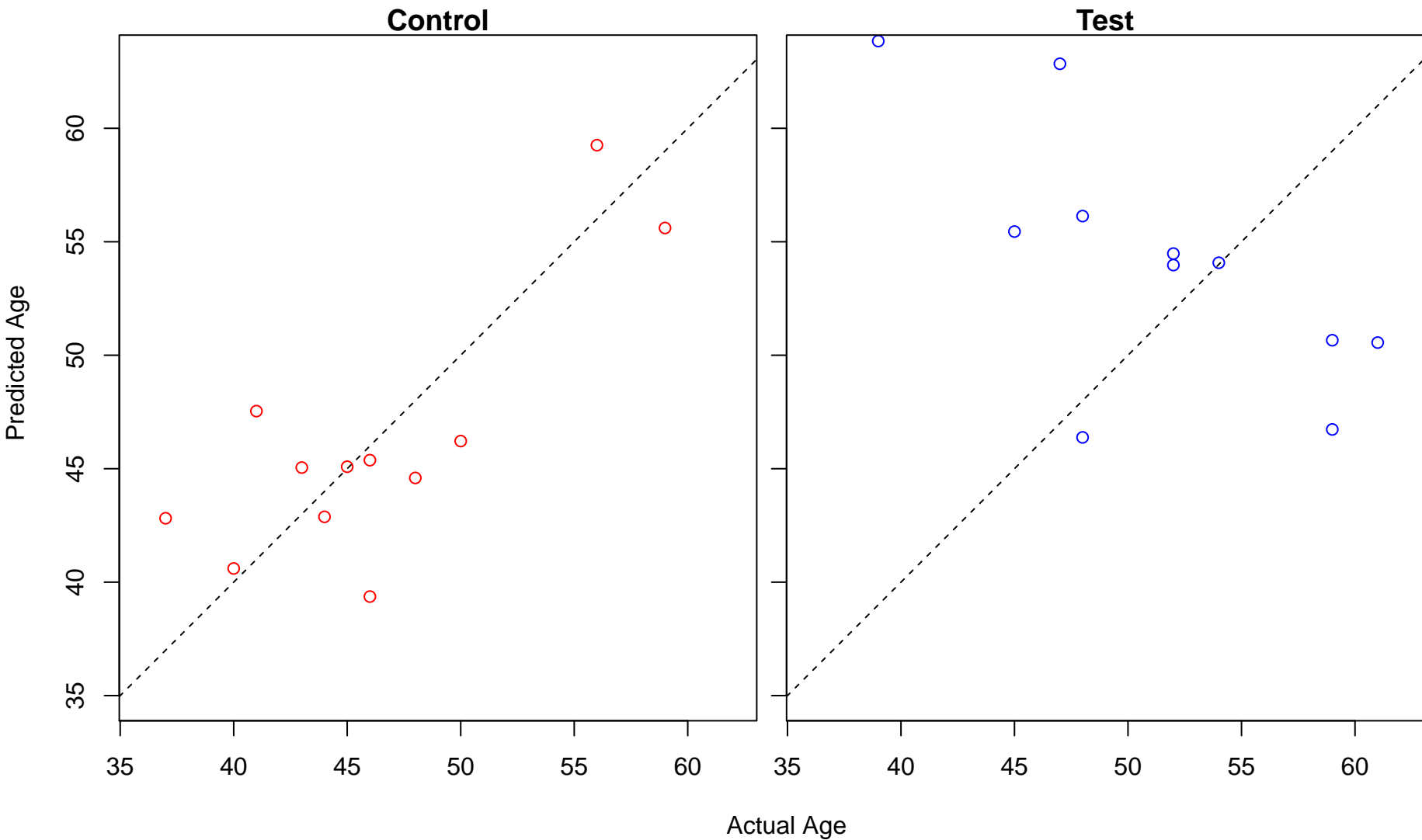
high-density lipoprotein particle remodeling (Score: 5.248527)



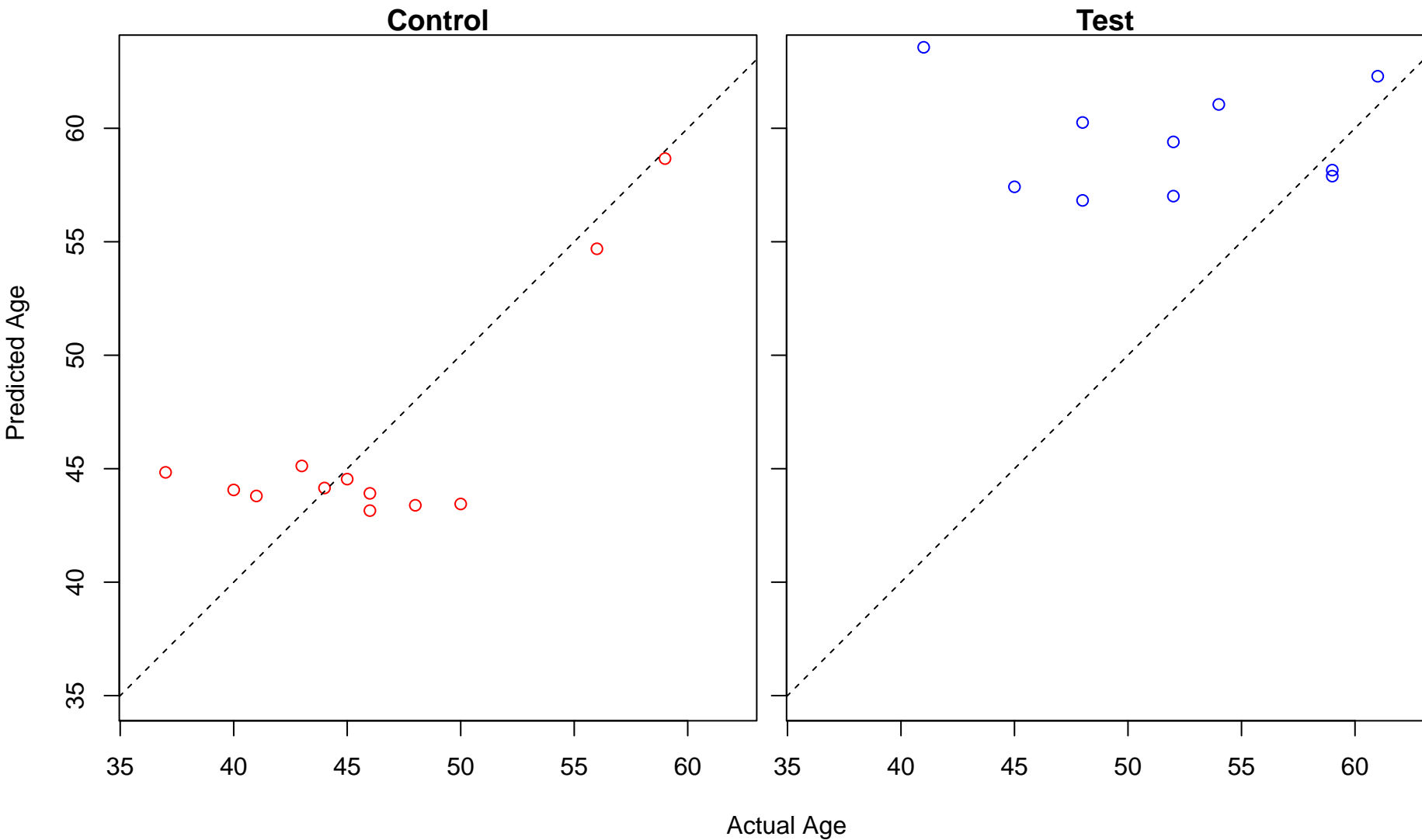
striated muscle contraction (Score: 5.246160)



innate immune response in mucosa (Score: 5.242872)

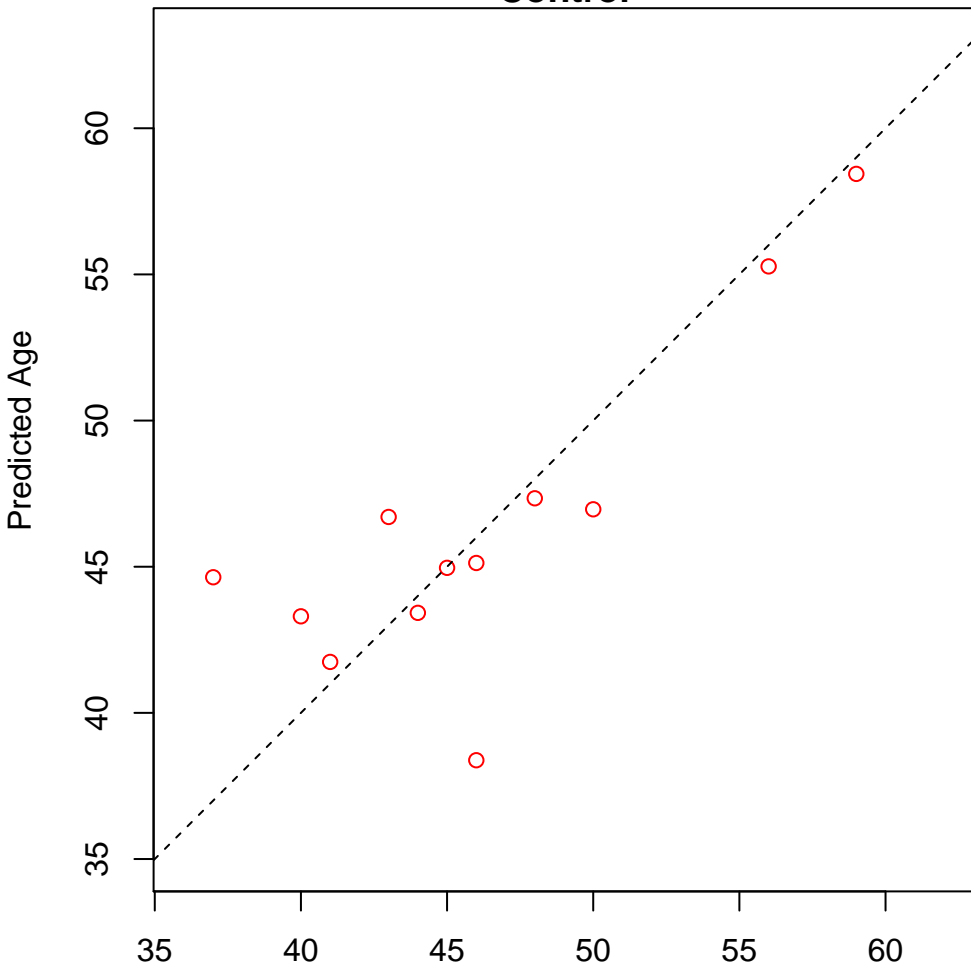


regulation of fibroblast proliferation (Score: 5.237797)

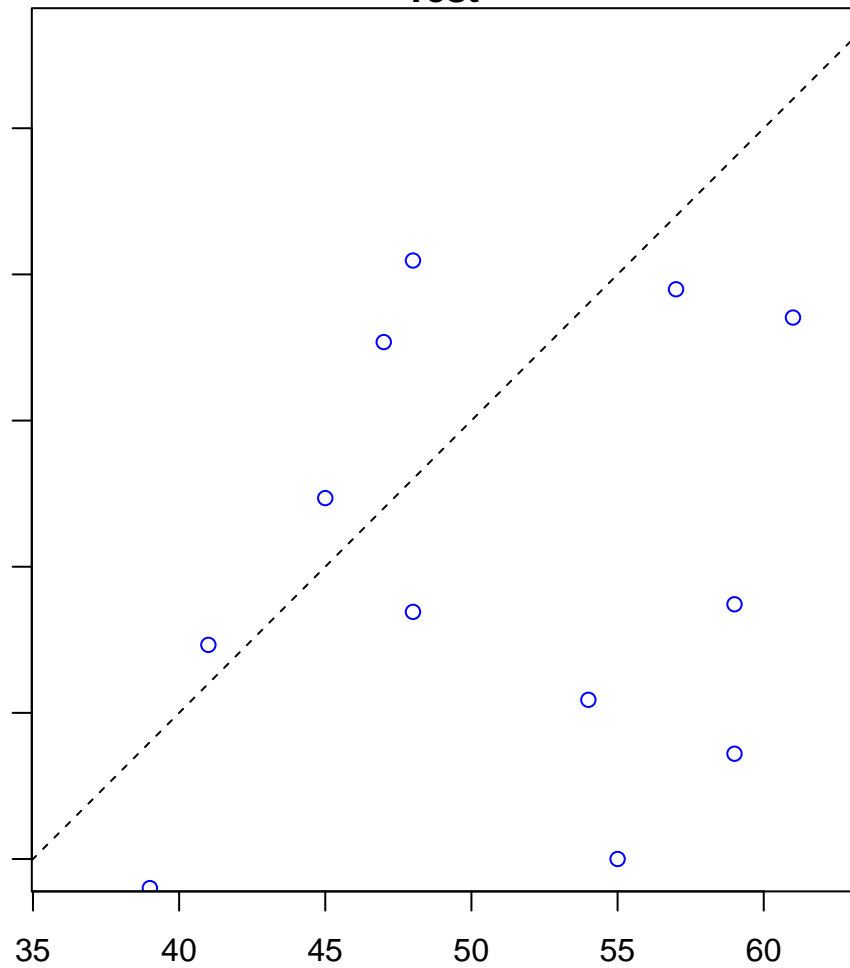


protein exit from endoplasmic reticulum (Score: 5.230049)

Control



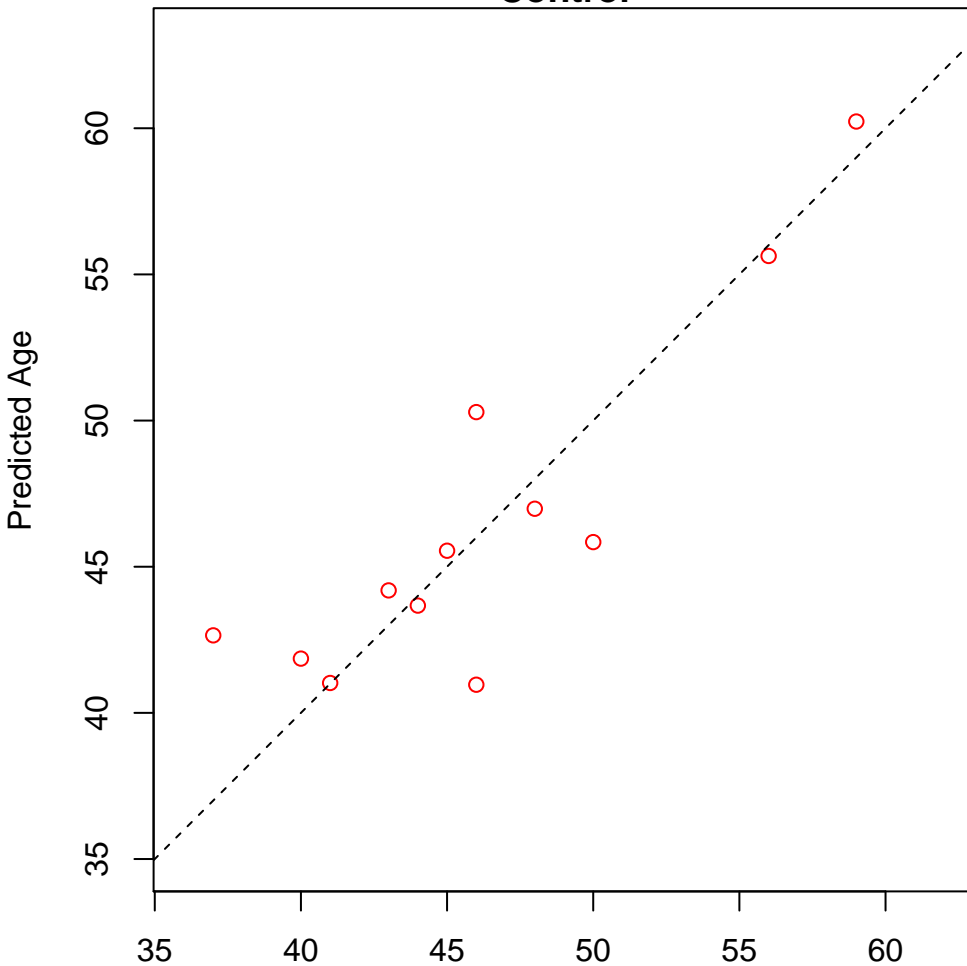
Test



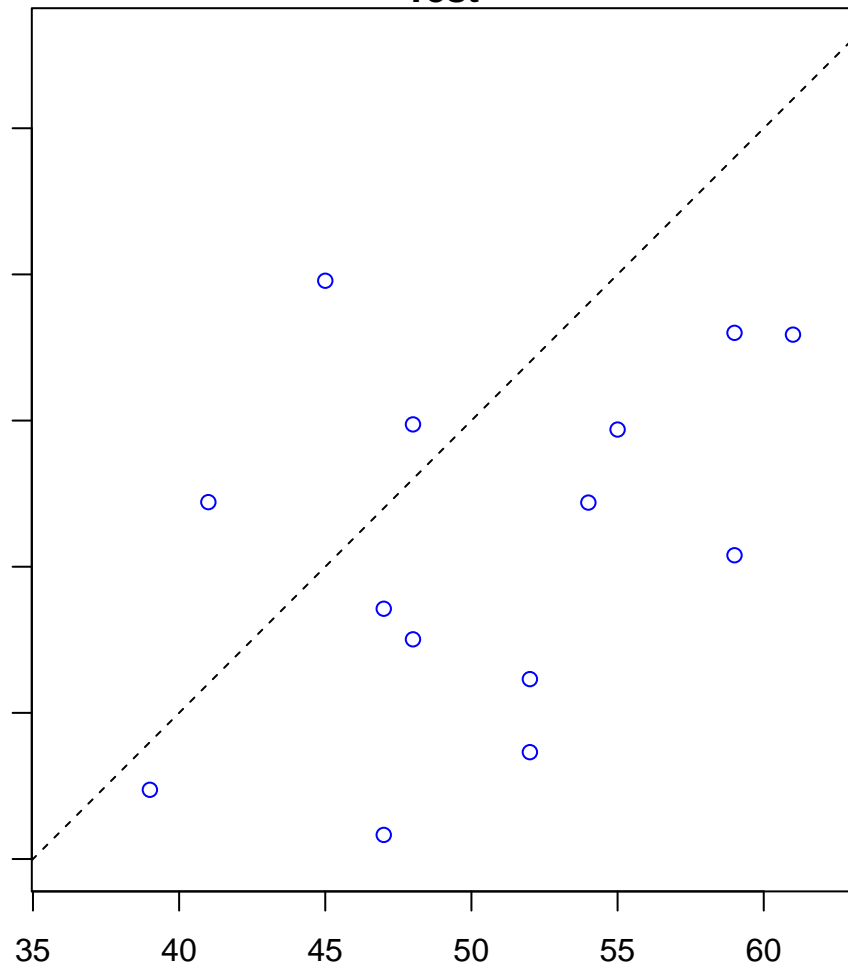
Actual Age

positive regulation of glucose import (Score: 5.227314)

Control

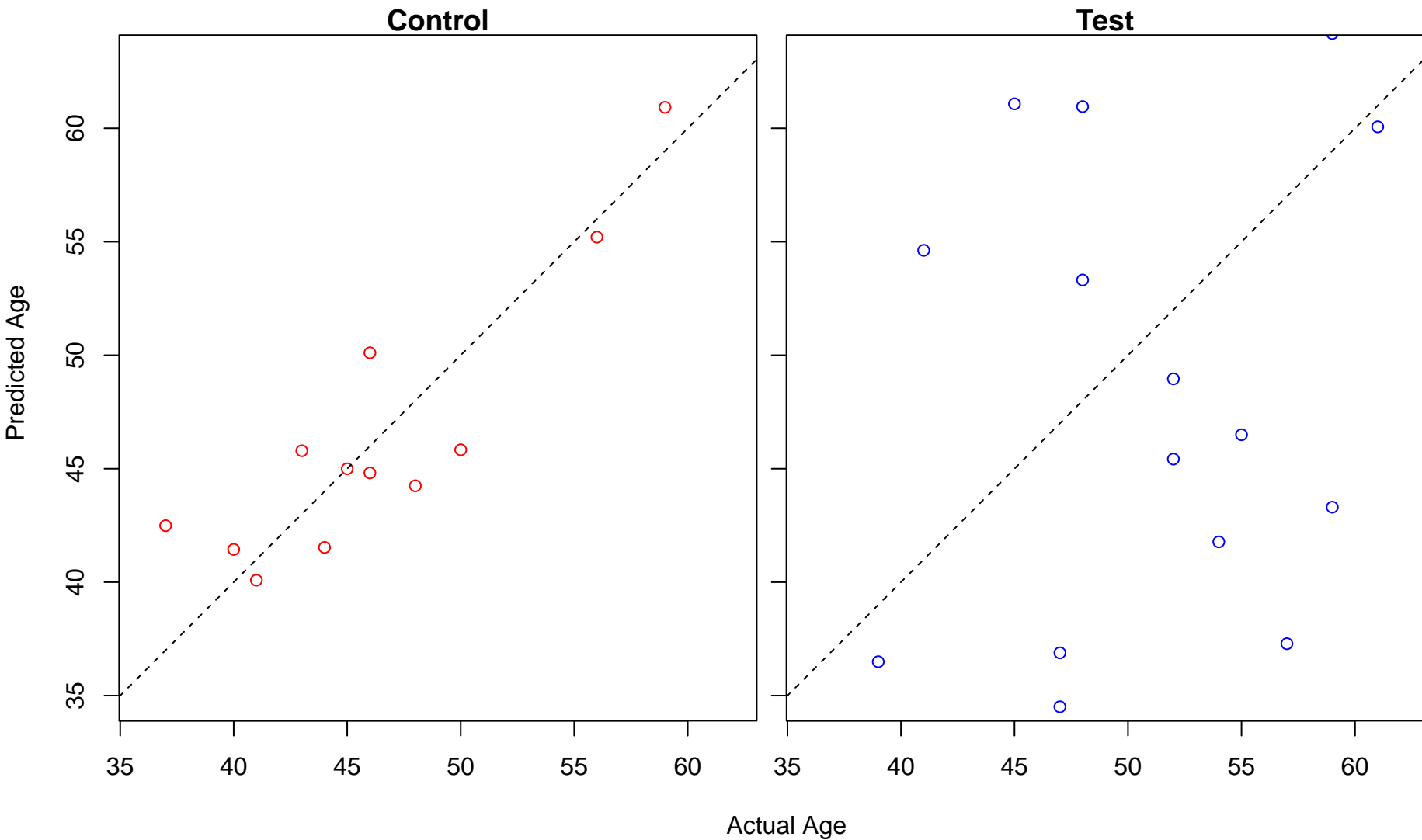


Test

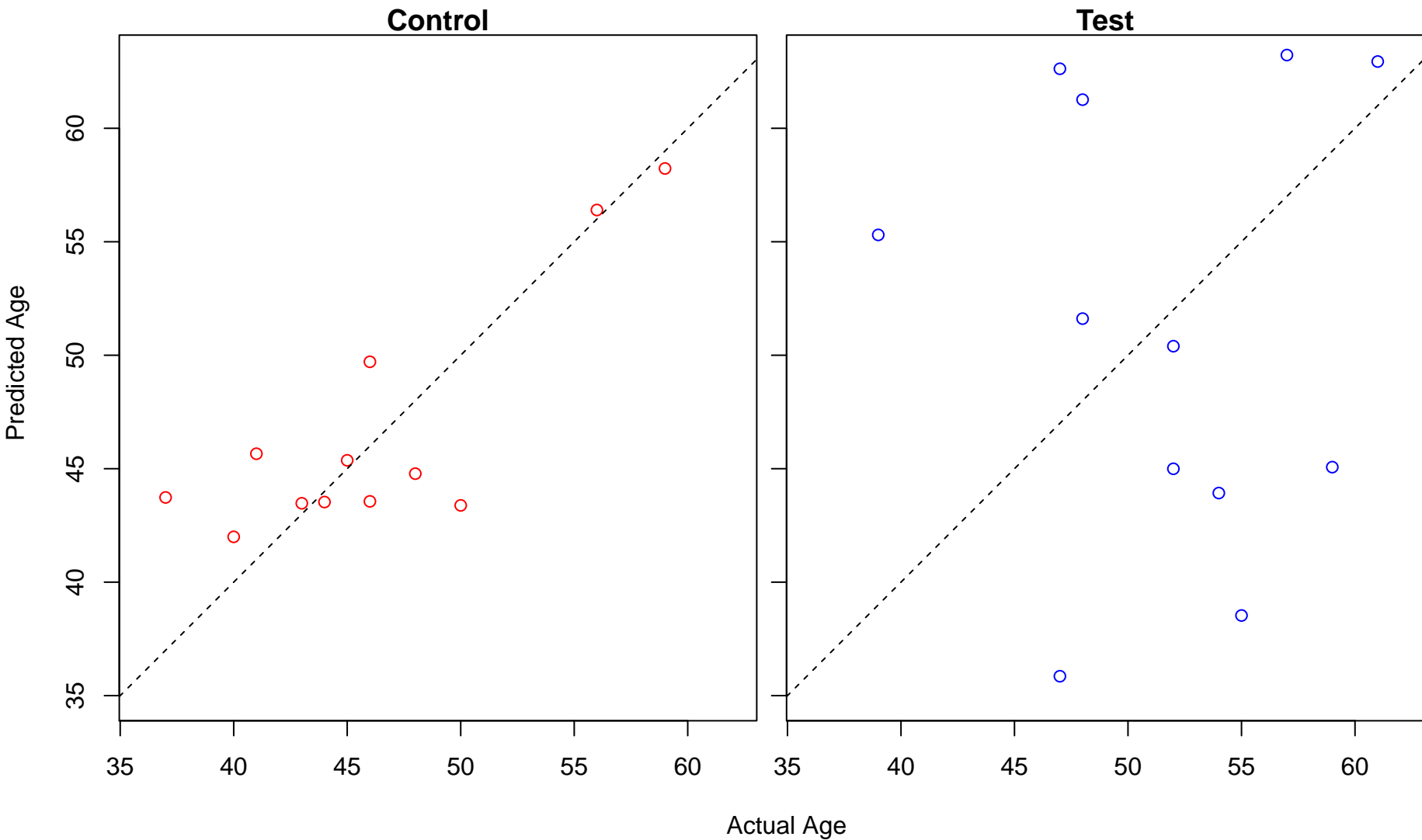


Actual Age

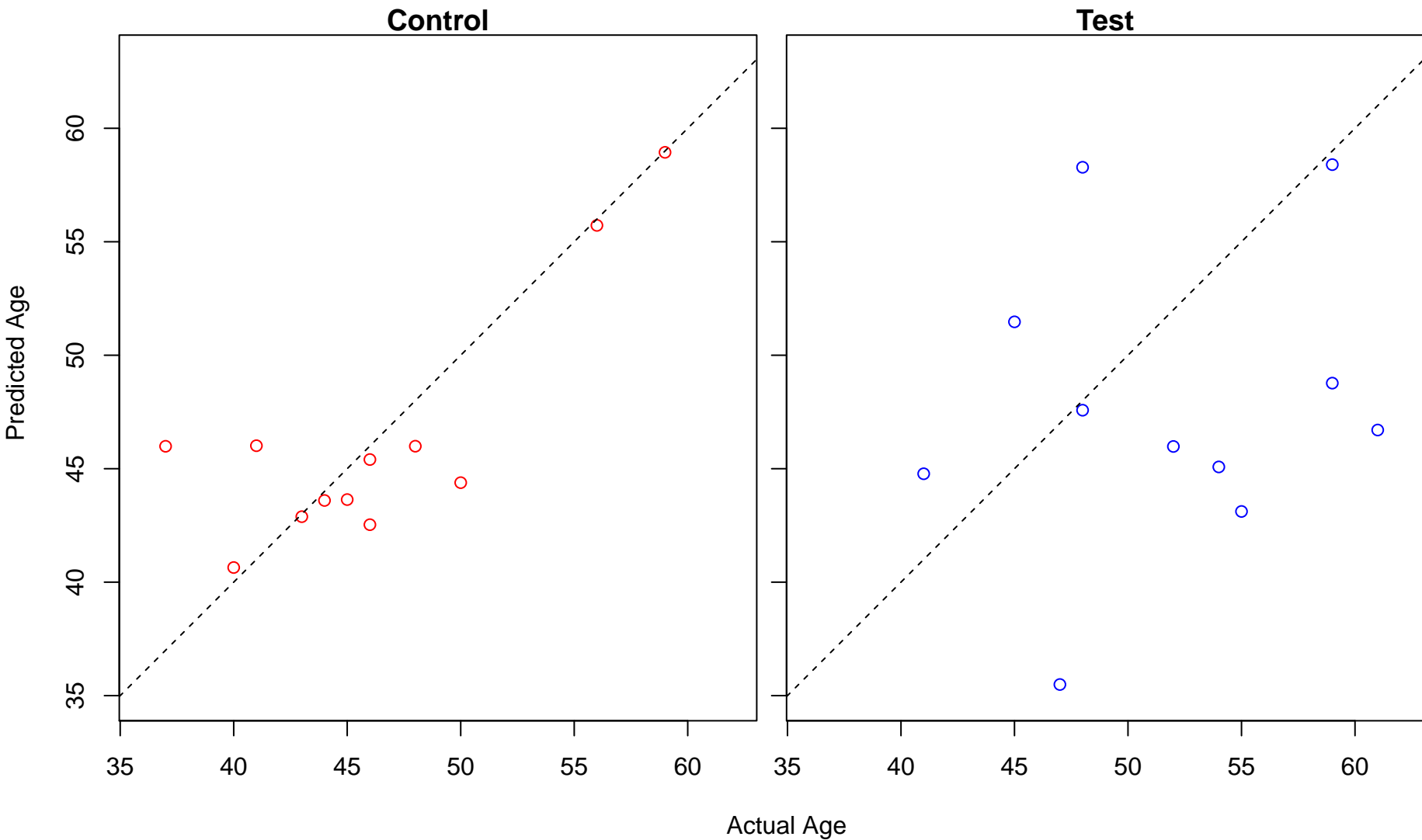
ovulation cycle (Score: 5.225991)



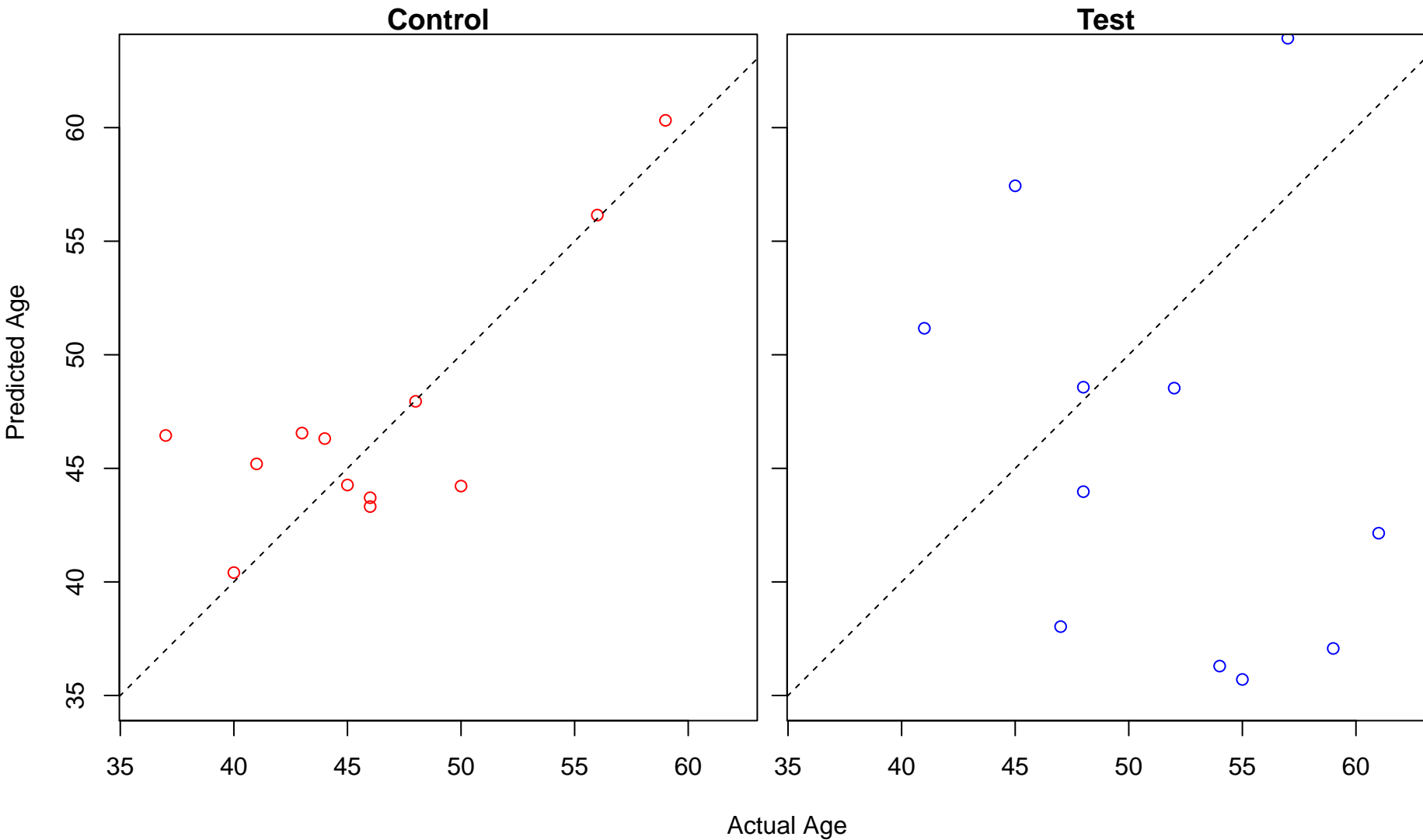
regulation of mitotic sister chromatid segregation (Score: 5.22053)



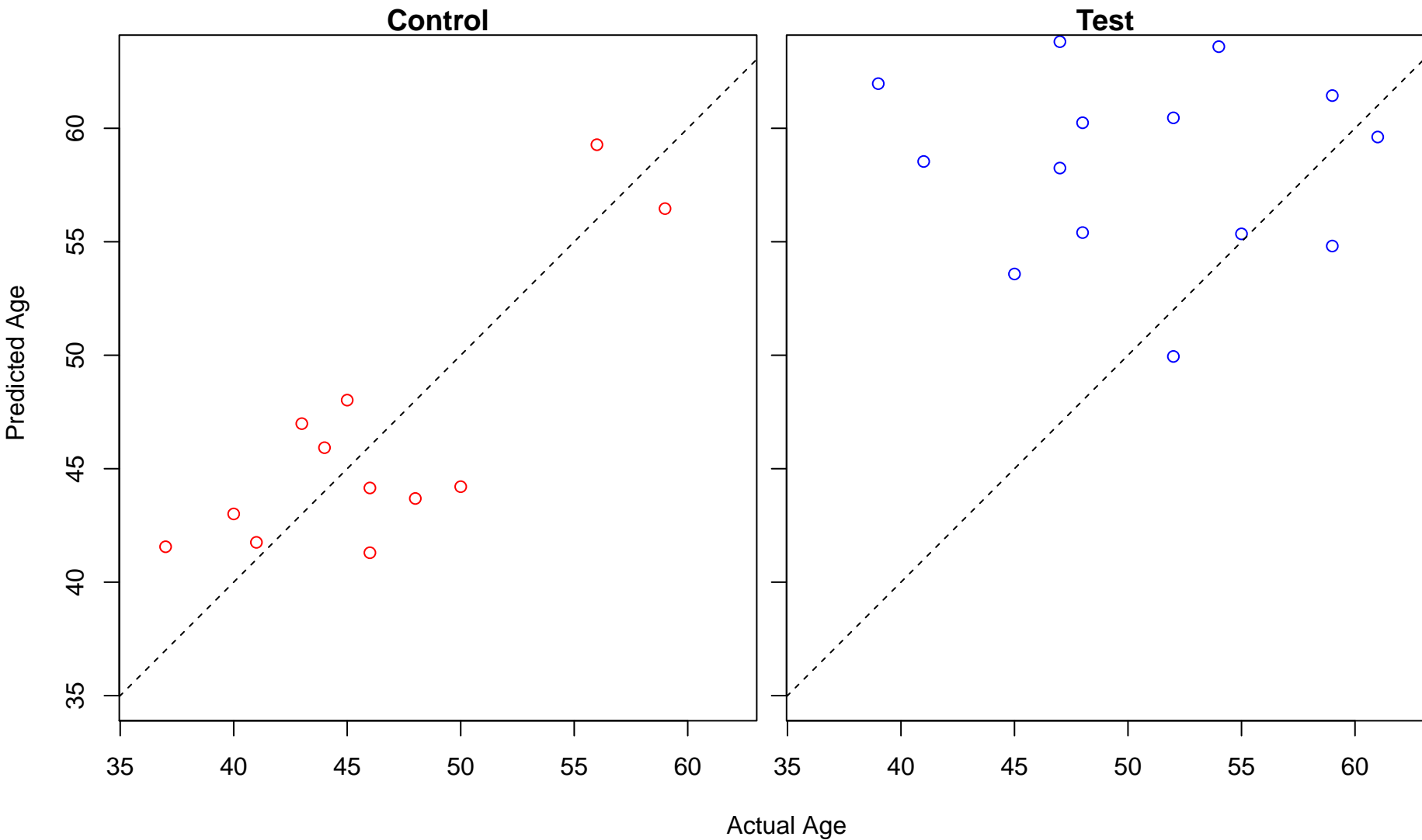
regulation of DNA replication (Score: 5.221822)



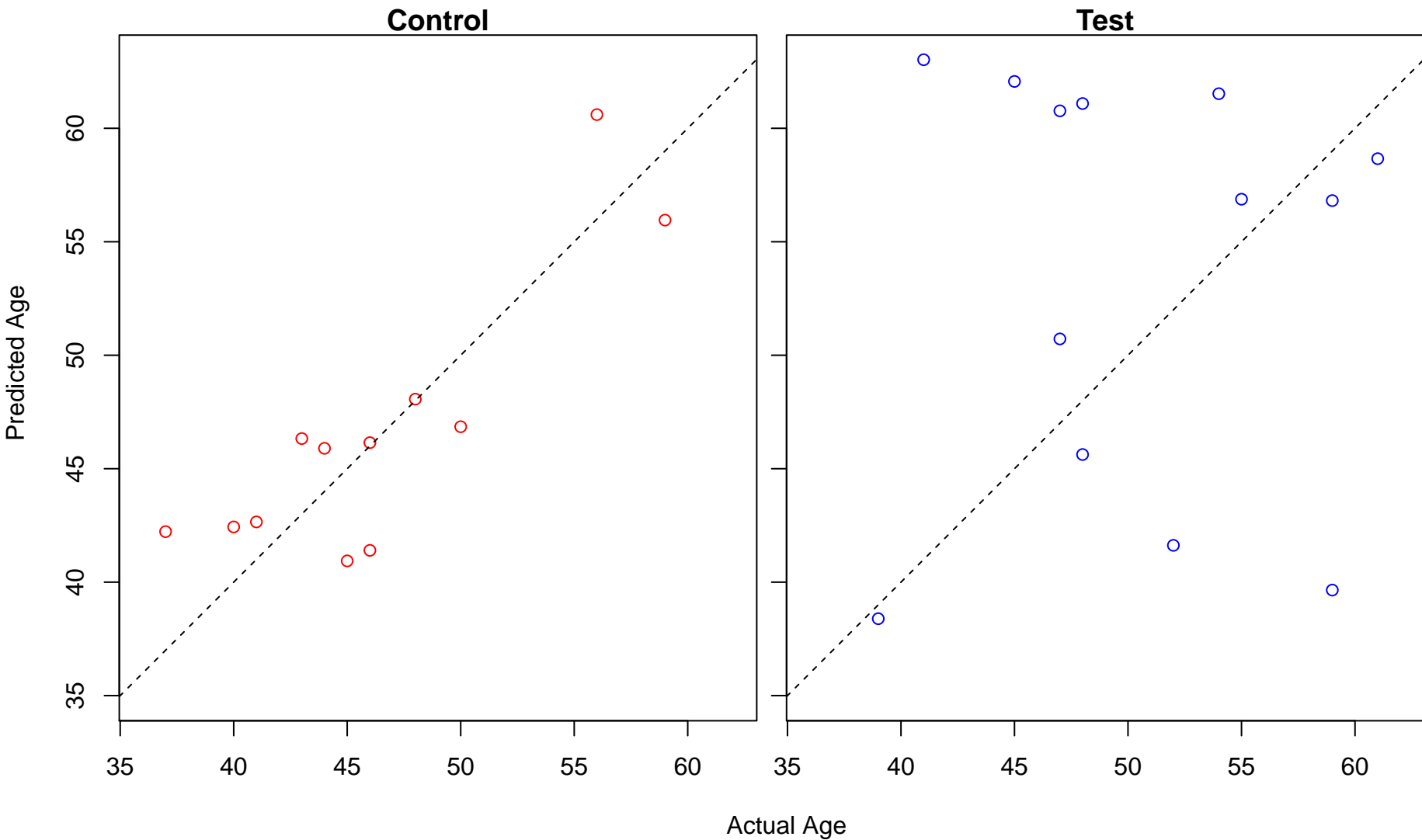
regulation of G2/M transition of mitotic cell cycle (Score: 5.204359)



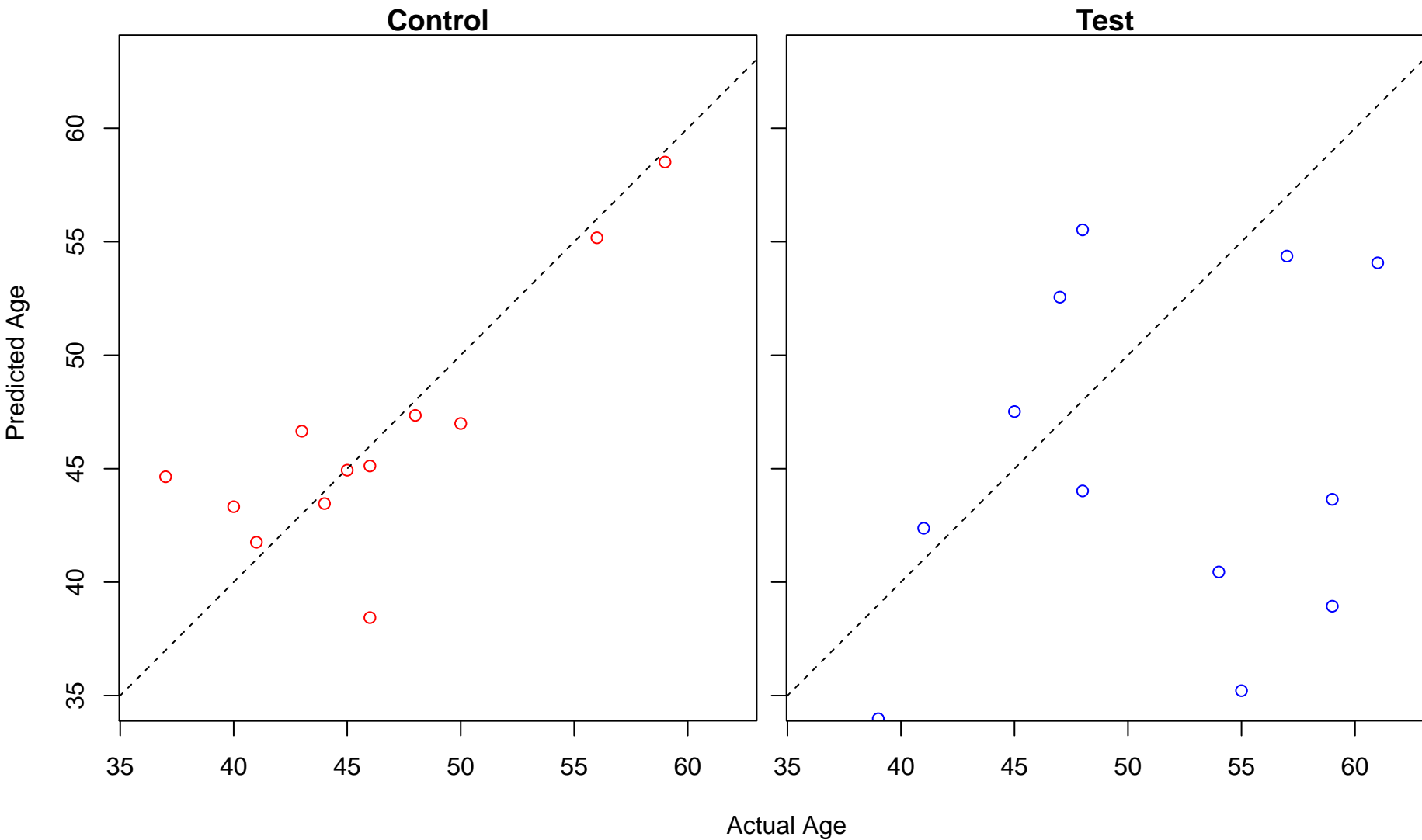
regulation of voltage-gated calcium channel activity (Score: 5.201976)



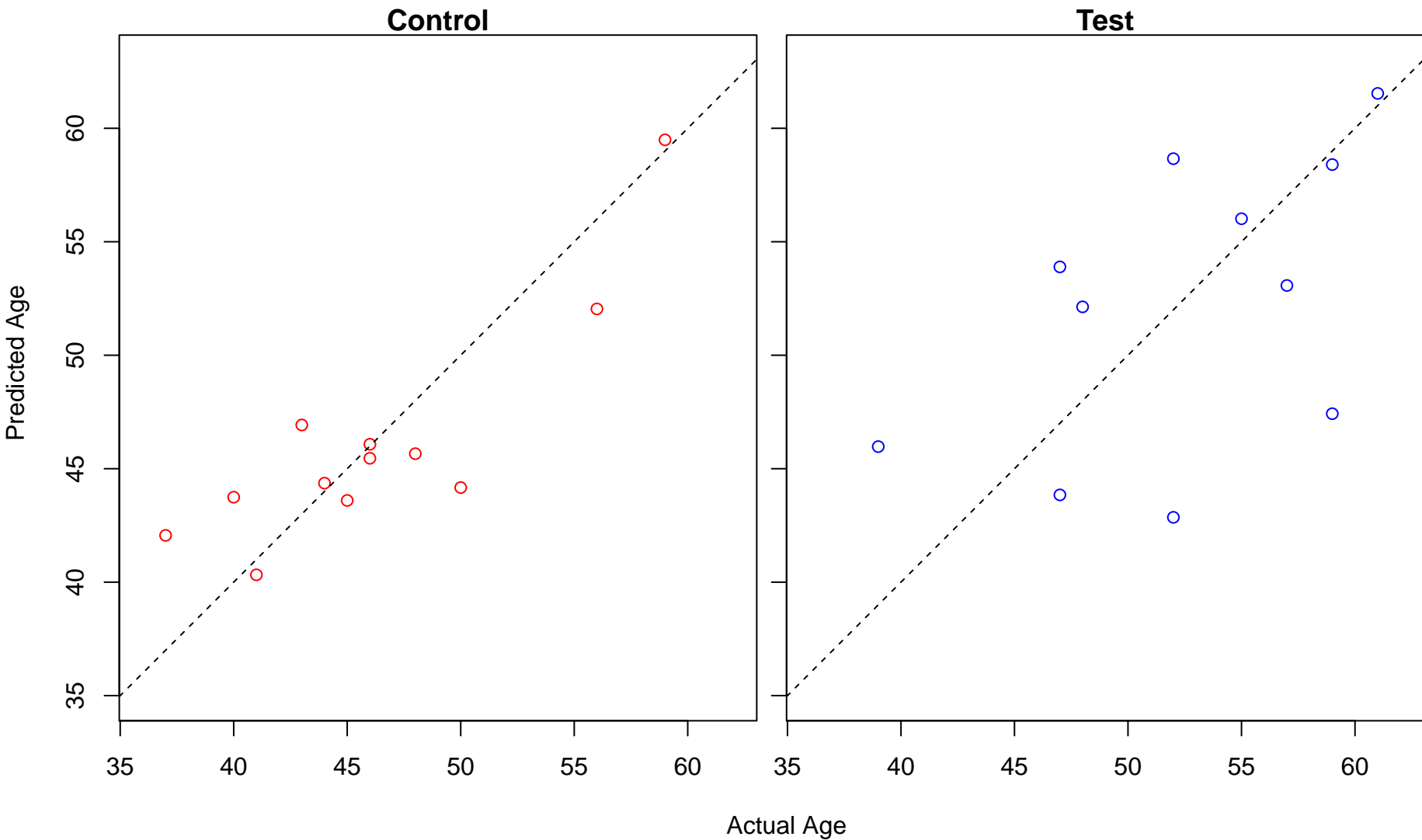
negative regulation of apoptotic signaling pathway (Score: 5.200950)



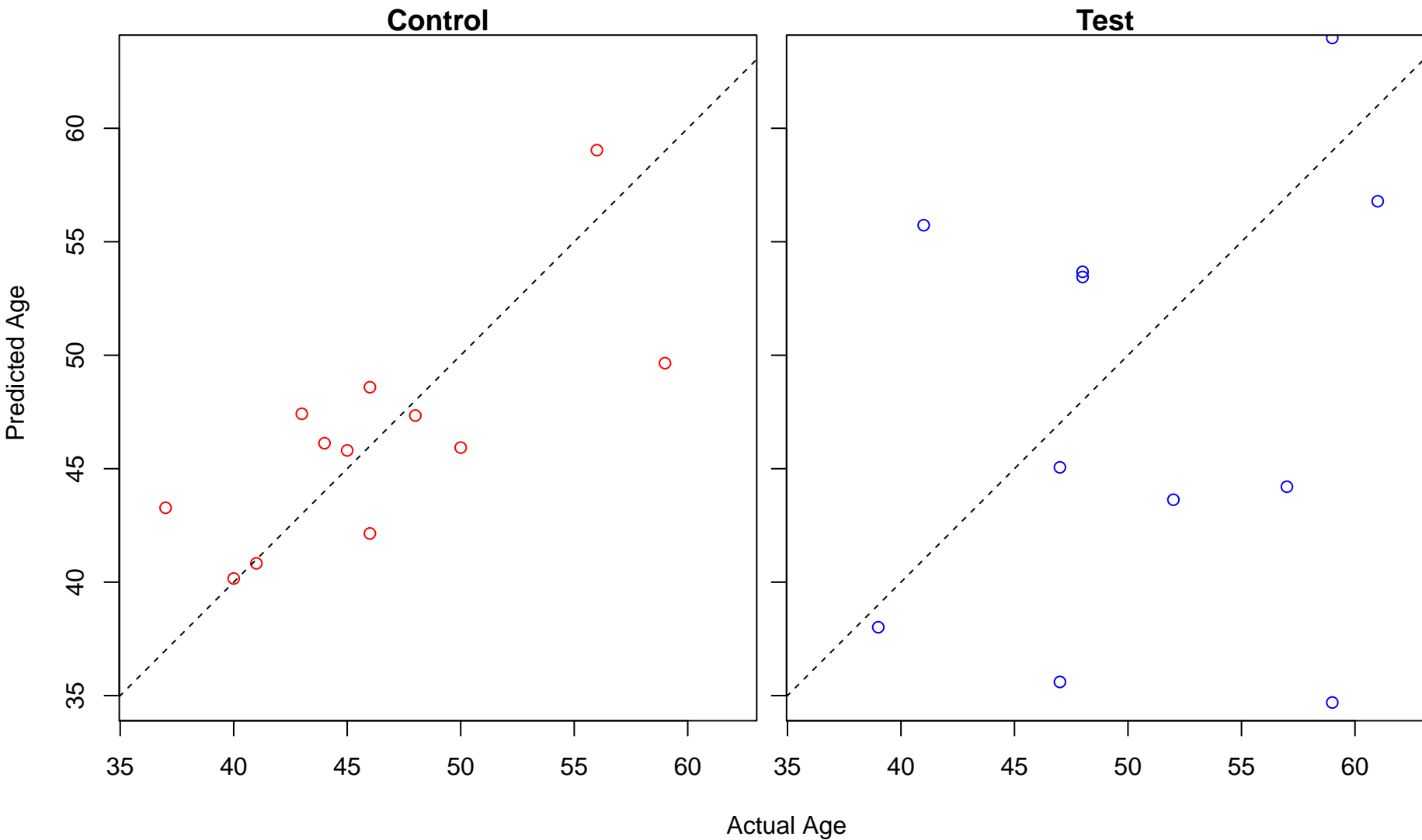
retrograde protein transport, ER to cytosol (Score: 5.199766)



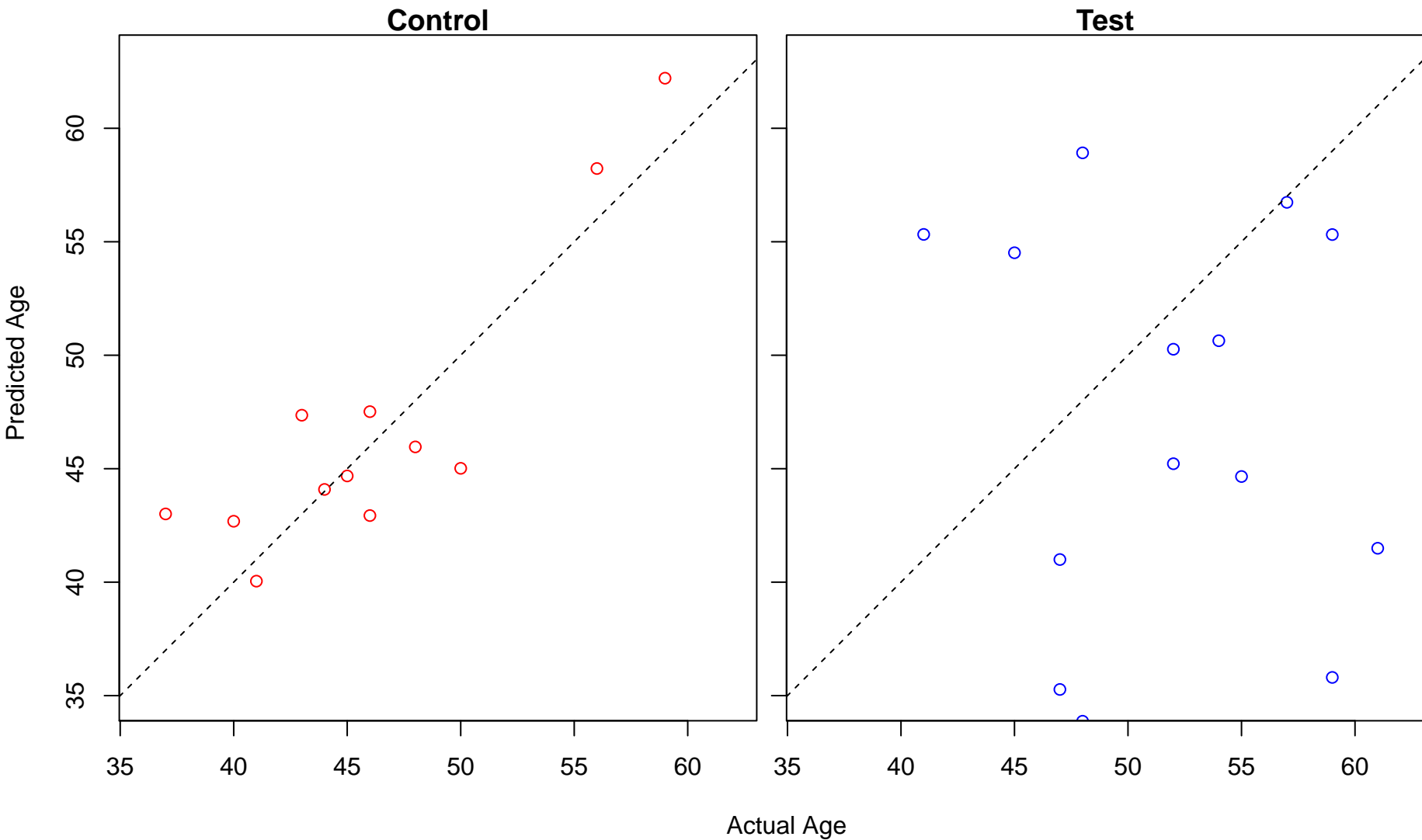
aromatic amino acid family metabolic process (Score: 5.196406)



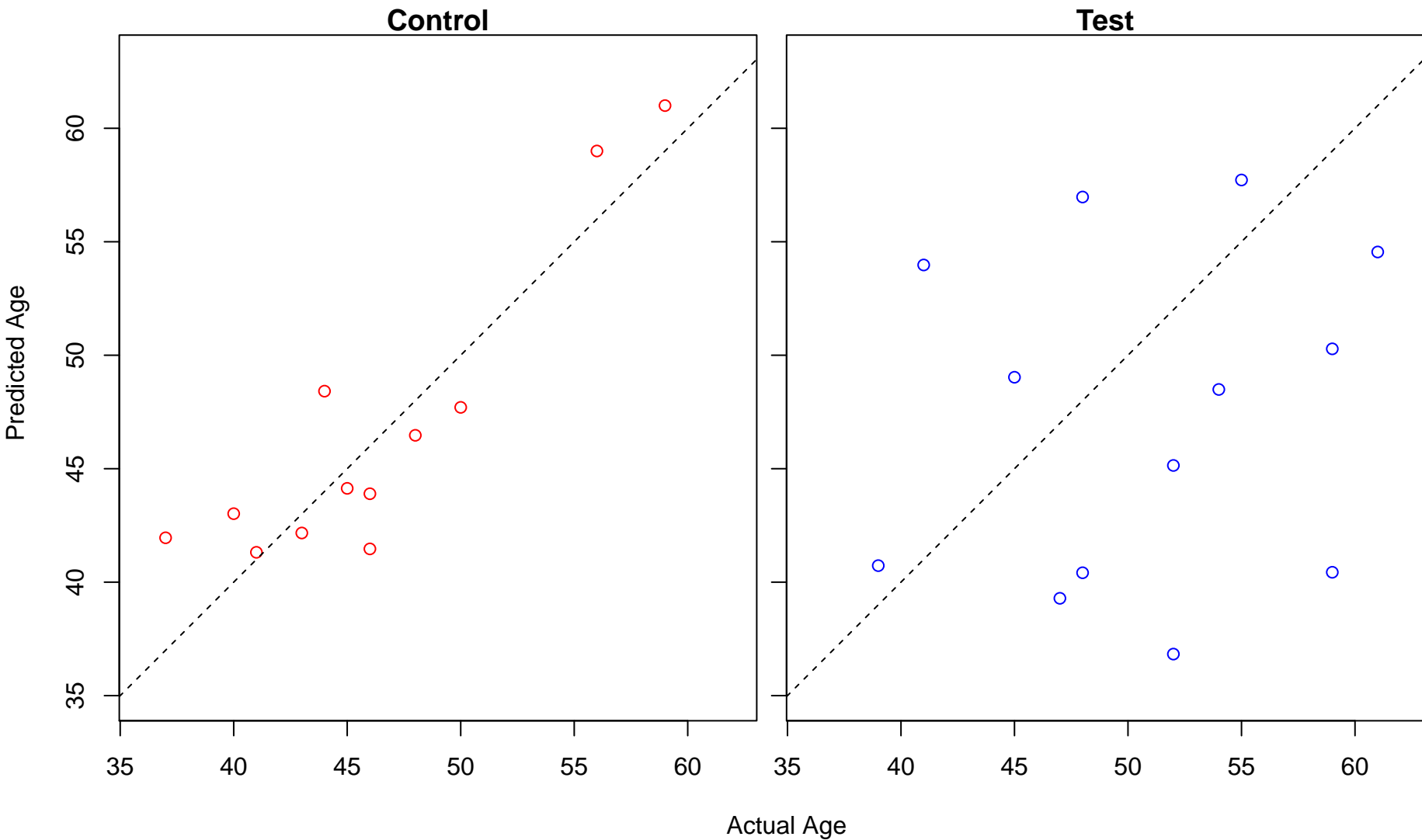
cellular response to glucose starvation (Score: 5.189578)



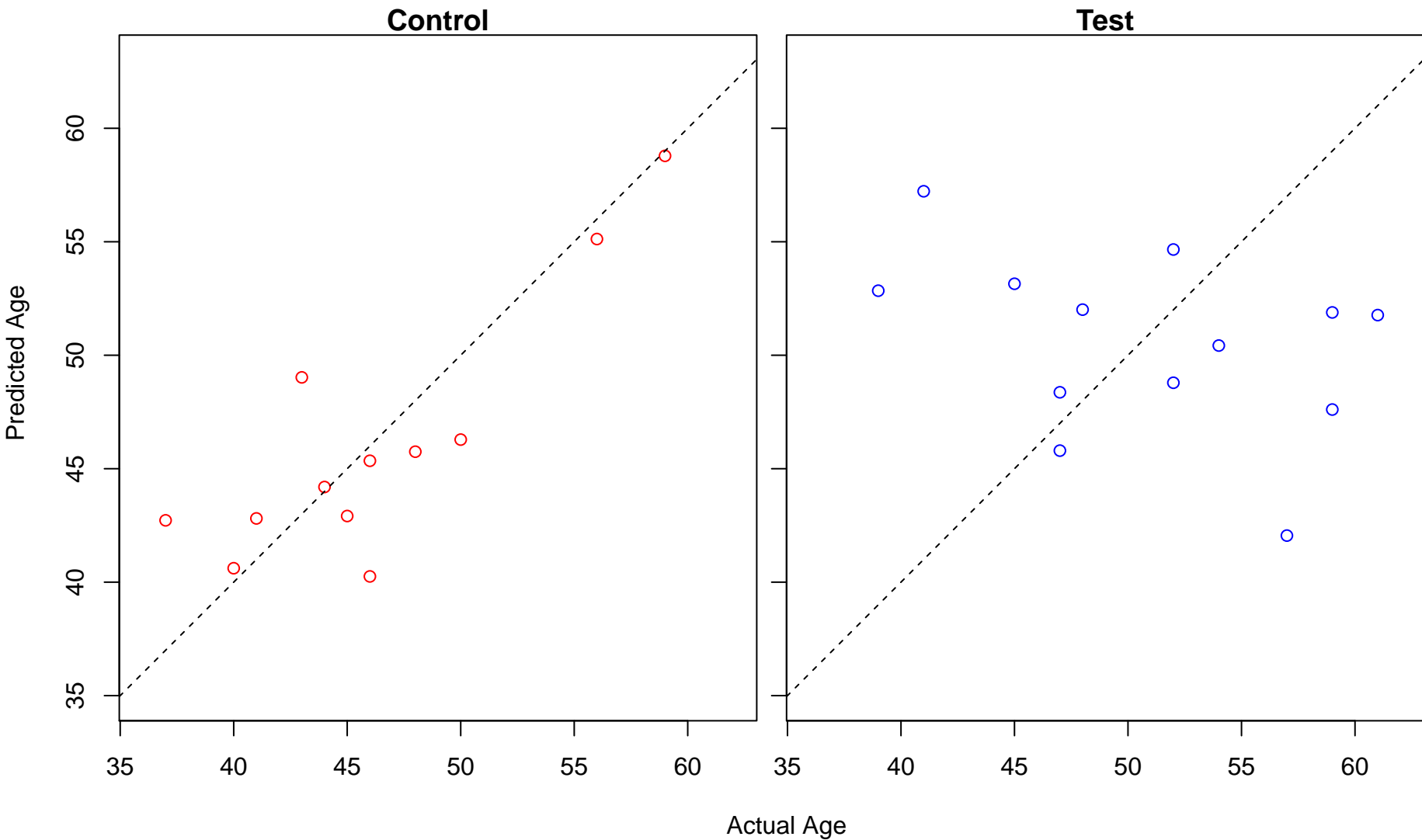
cardiac muscle tissue development (Score: 5.186178)



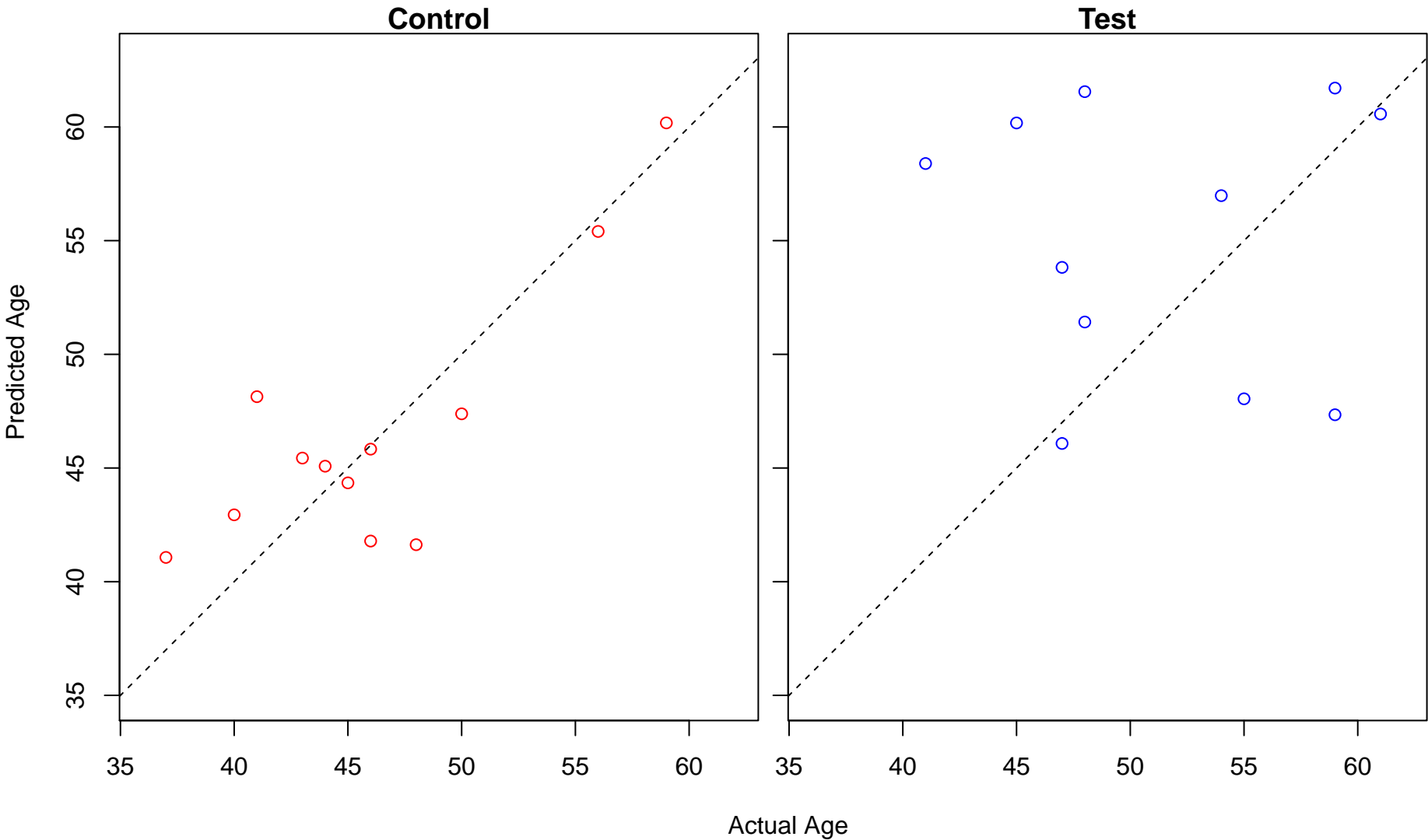
protein stabilization (Score: 5.183870)



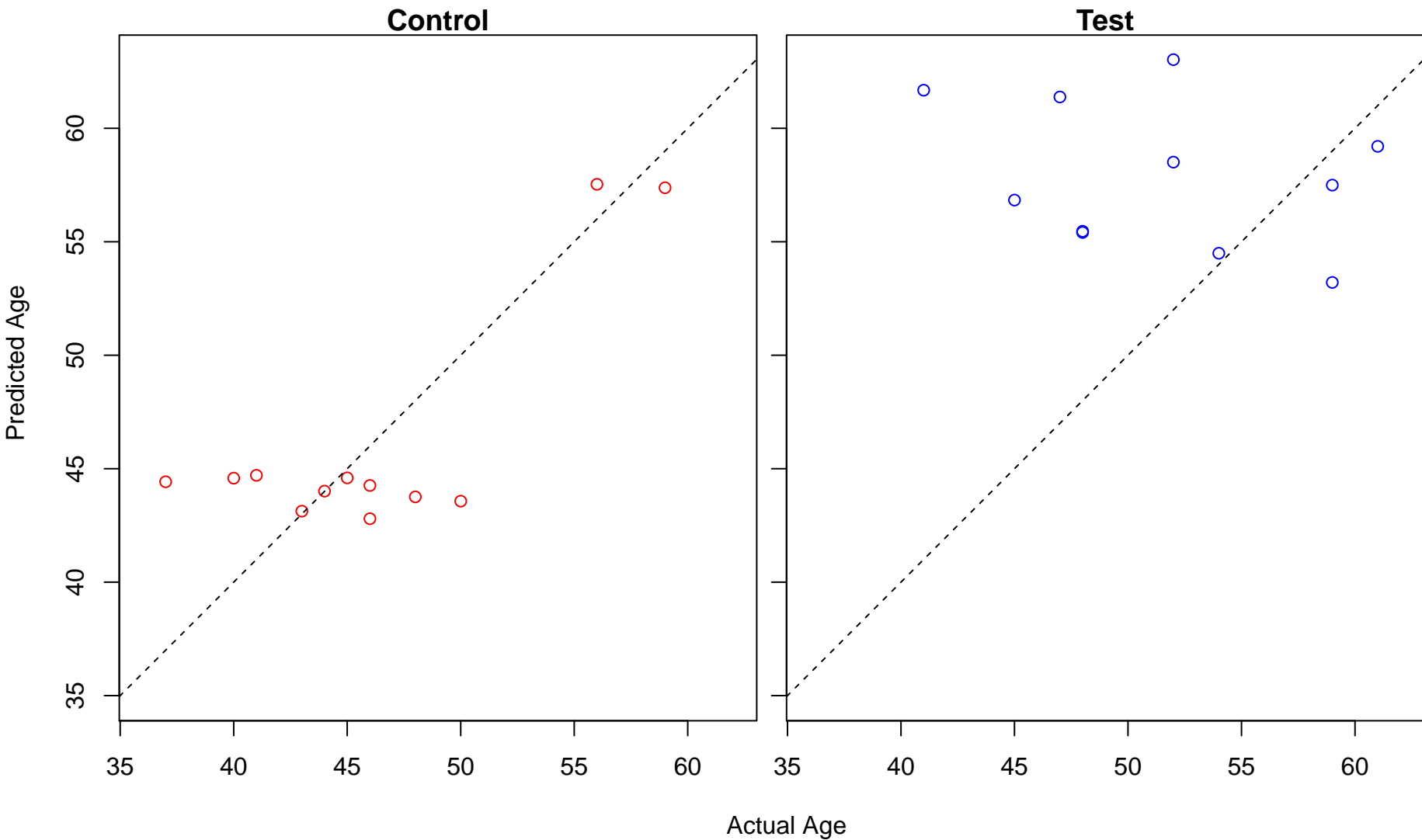
regulation of stress-activated protein kinase signaling cascade (Score: 5.183127)



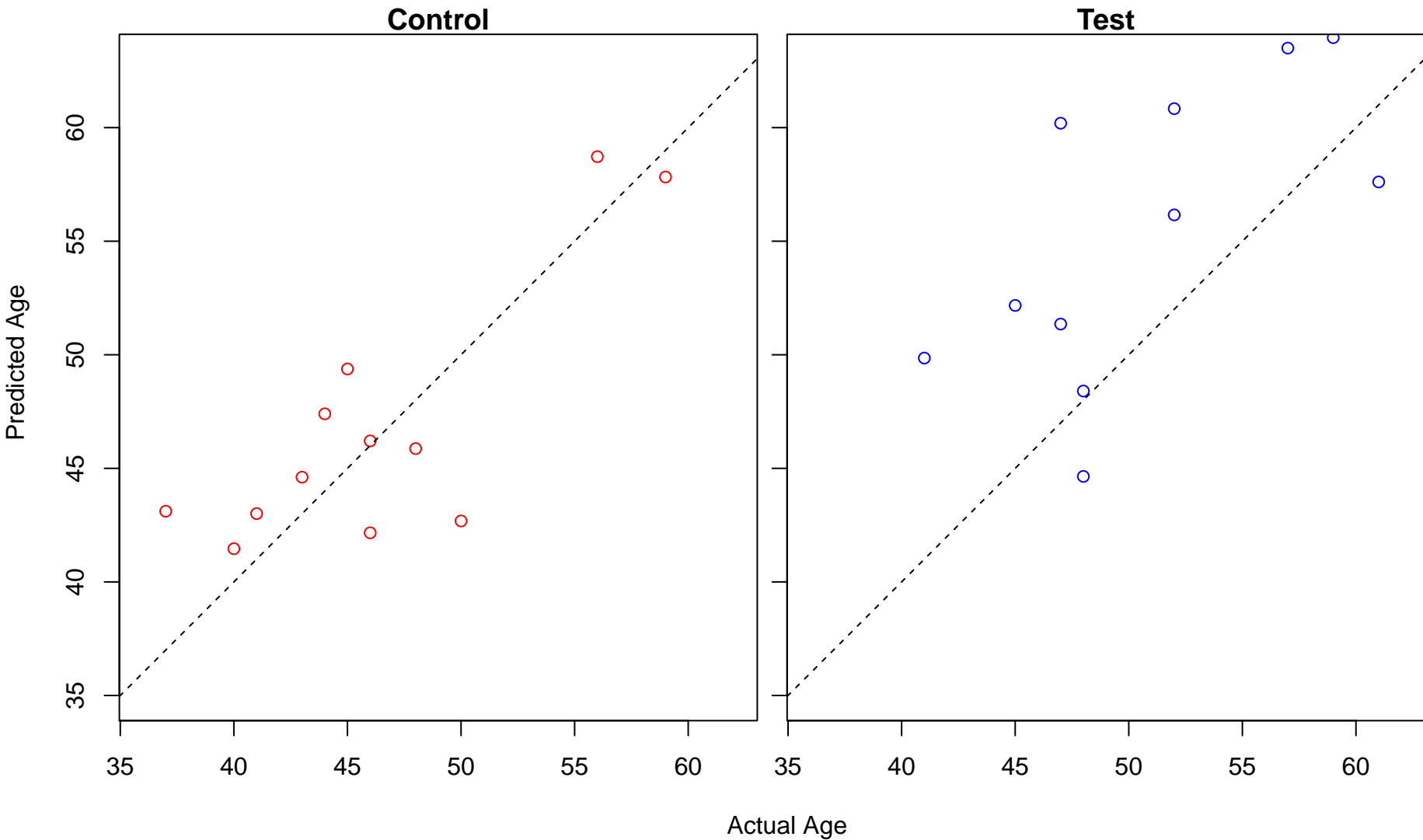
regulation of insulin secretion involved in cellular response to glucose stimulus (Score: 5.18232)



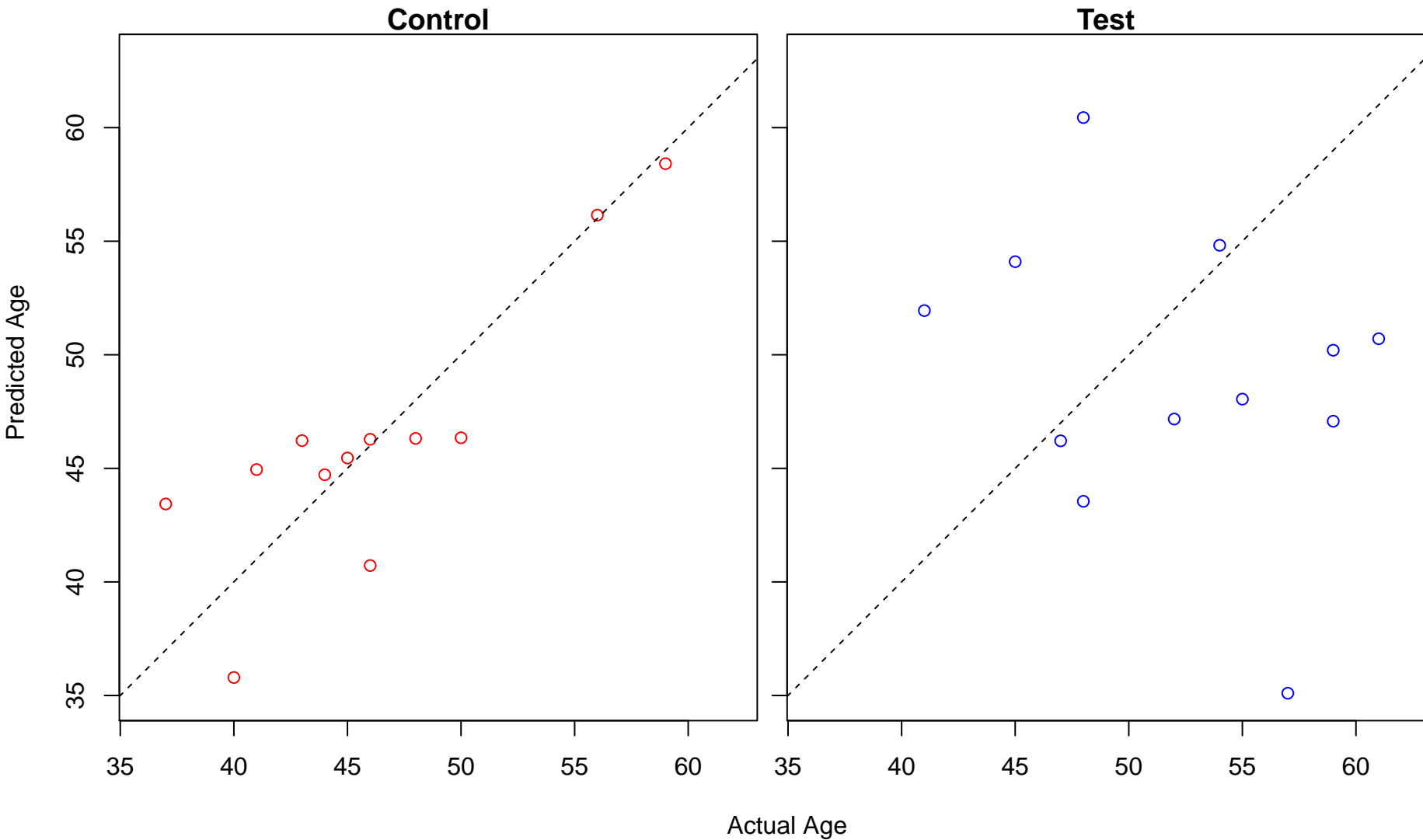
alternative mRNA splicing, via spliceosome (Score: 5.173041)



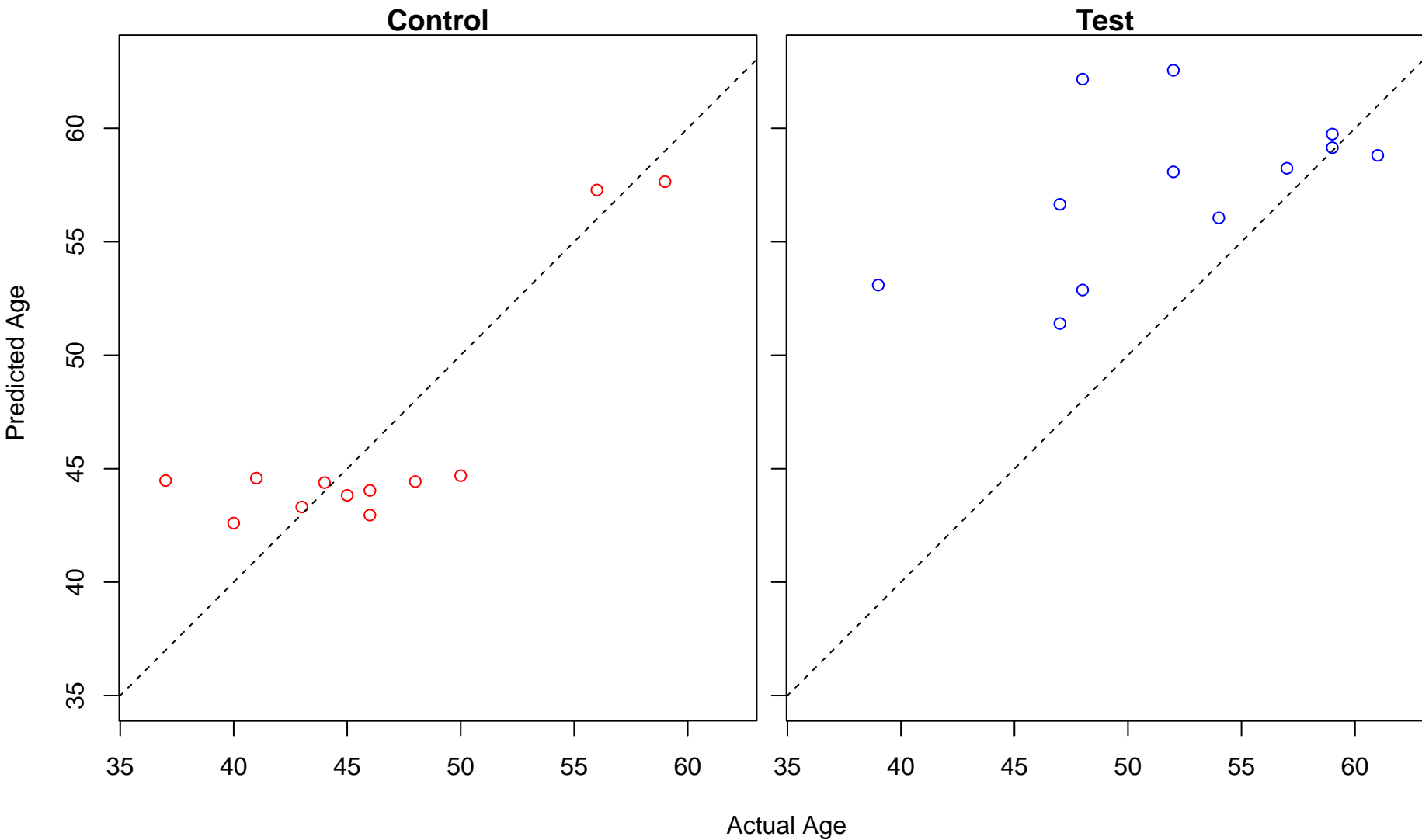
antigen processing and presentation of peptide antigen via MHC class I (Score: 5.165208)



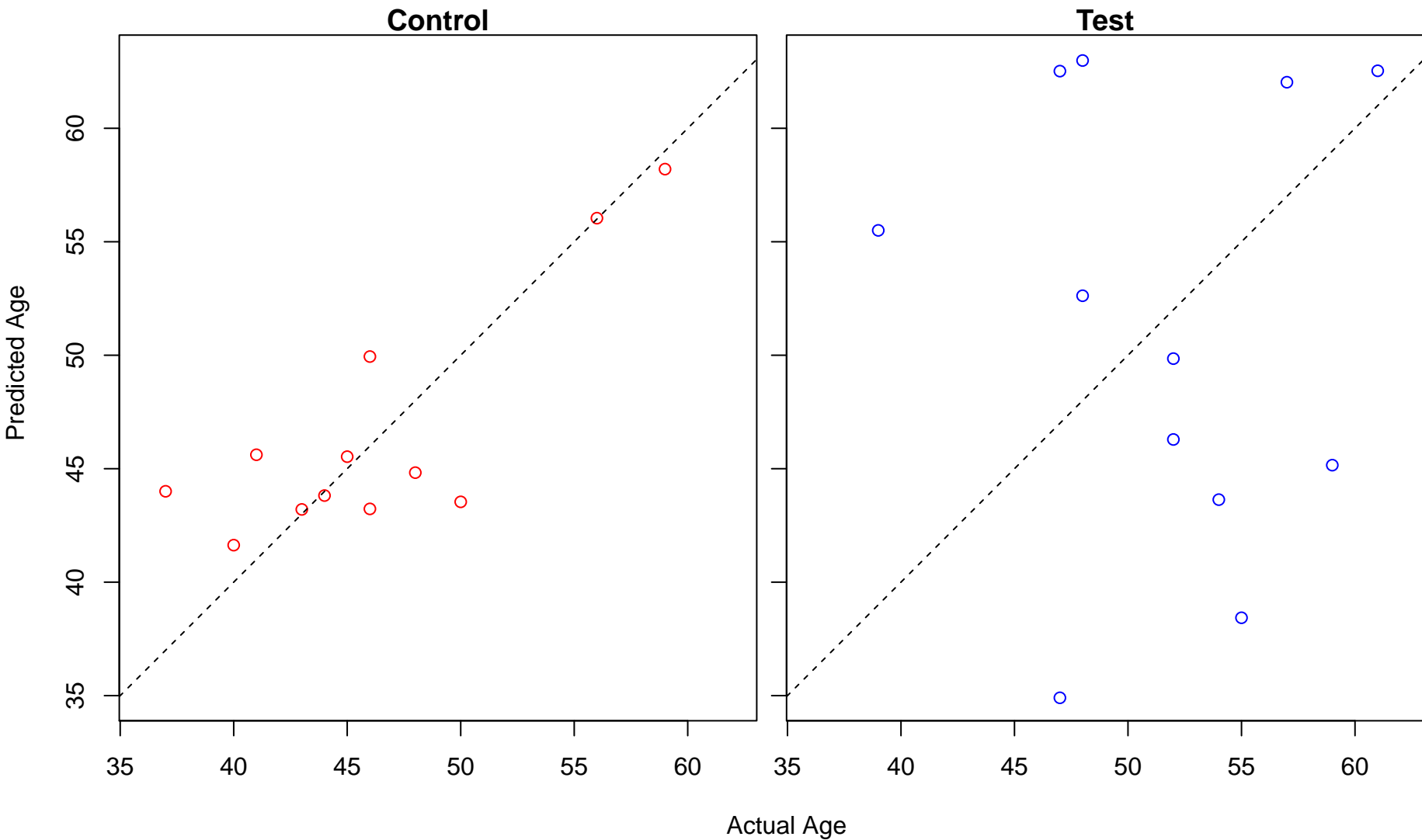
positive regulation of cytoplasmic transport (Score: 5.161804)



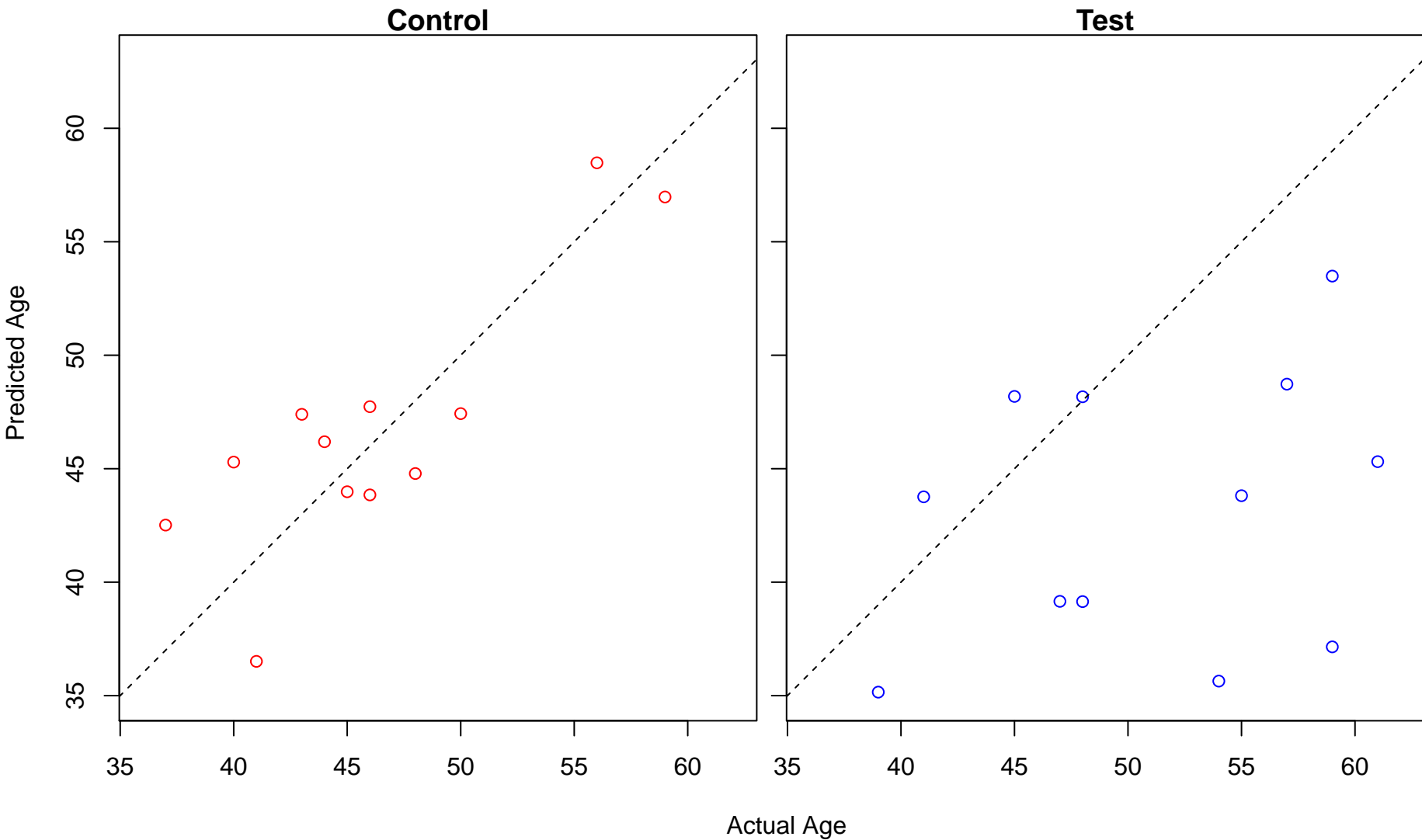
neutral amino acid transport (Score: 5.159319)



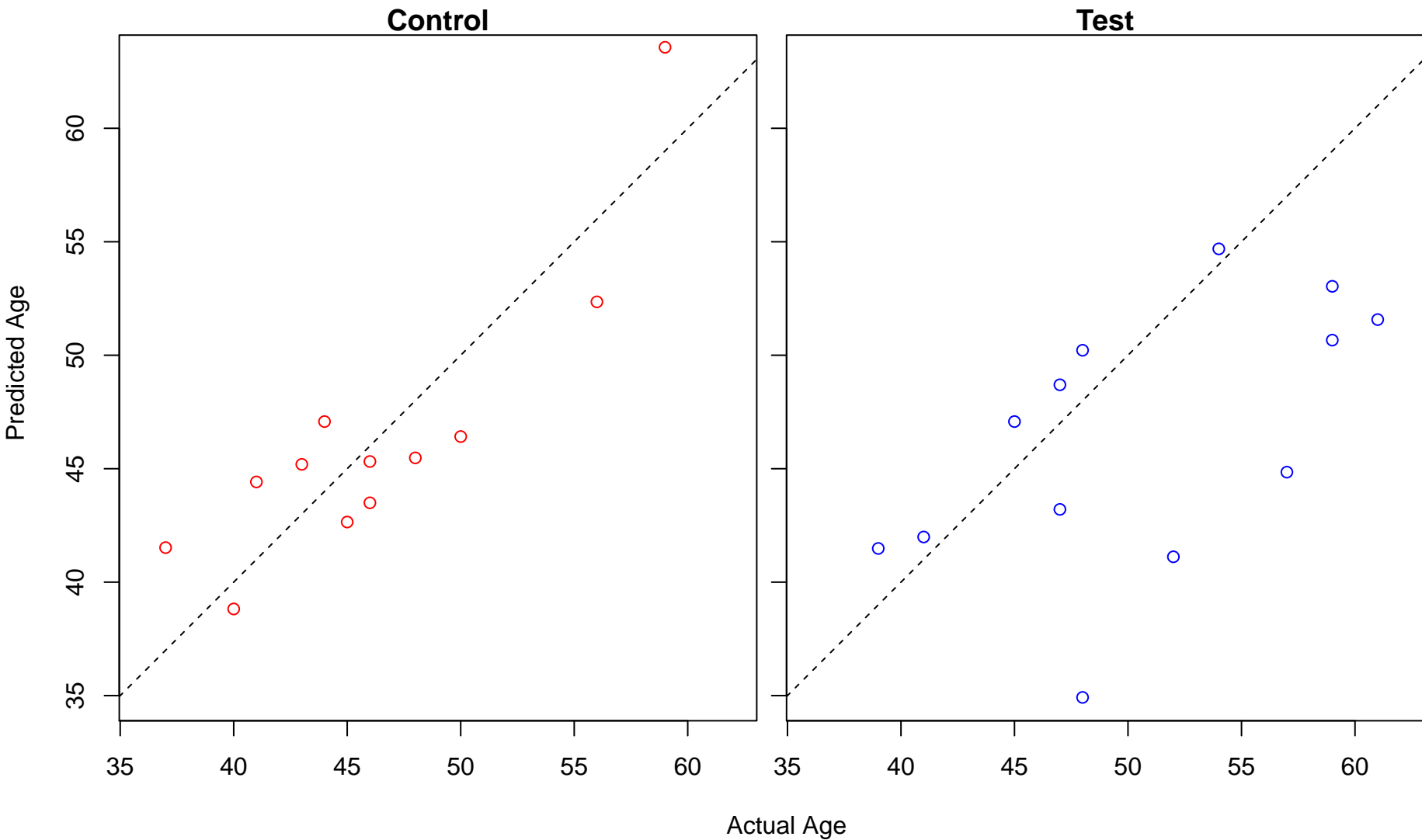
regulation of ubiquitin protein ligase activity (Score: 5.158150)



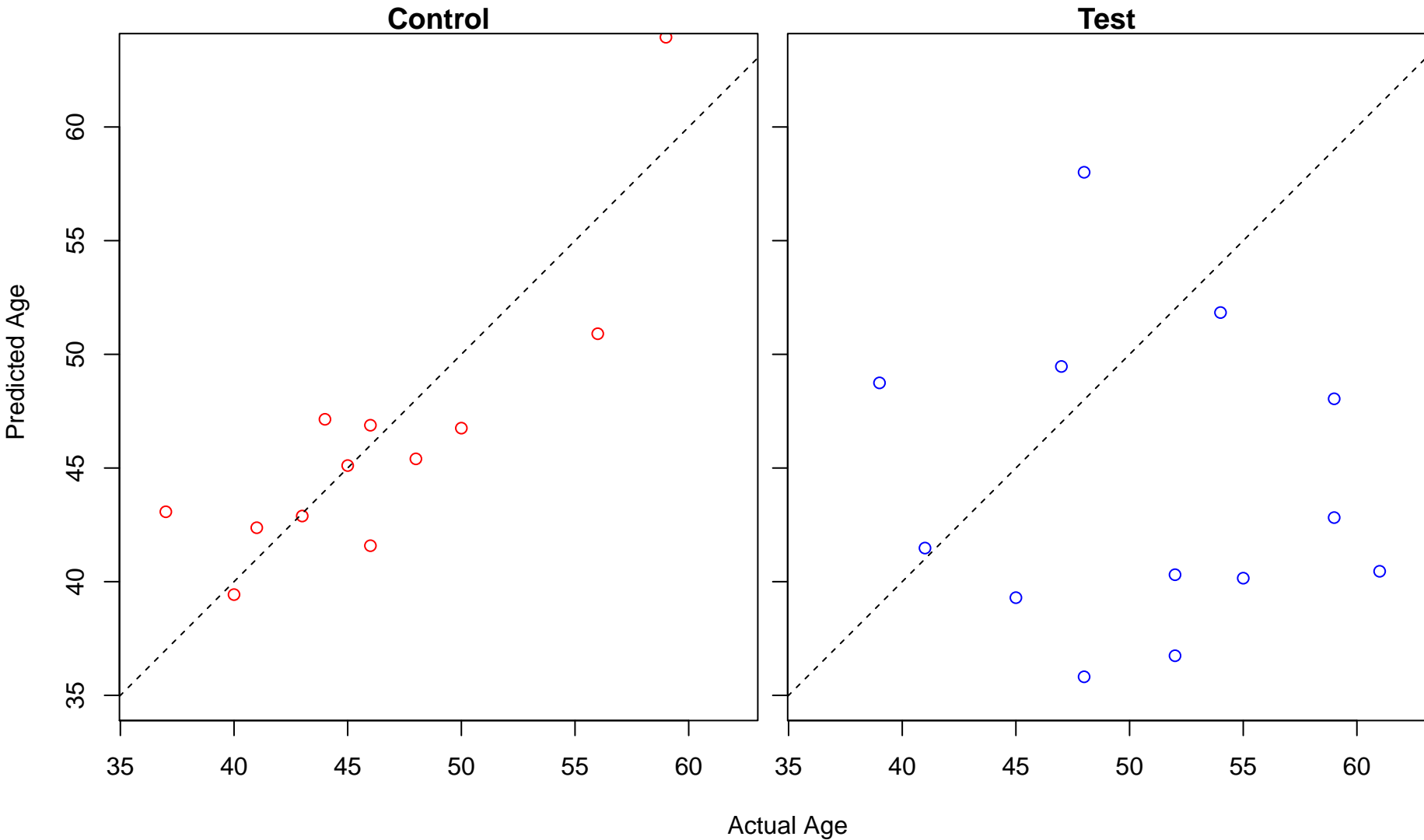
branching morphogenesis of an epithelial tube (Score: 5.155164)



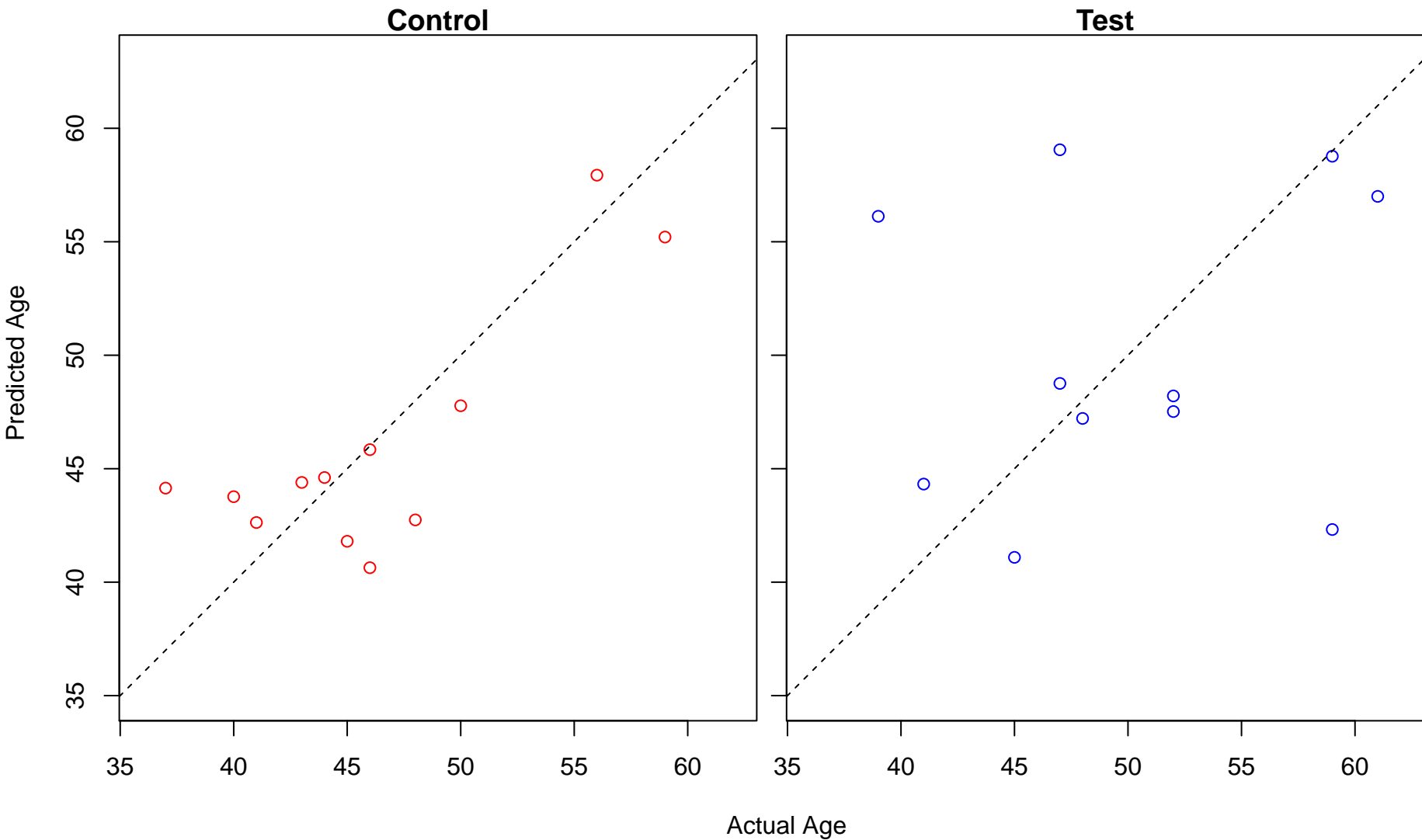
regulation of wound healing (Score: 5.153243)



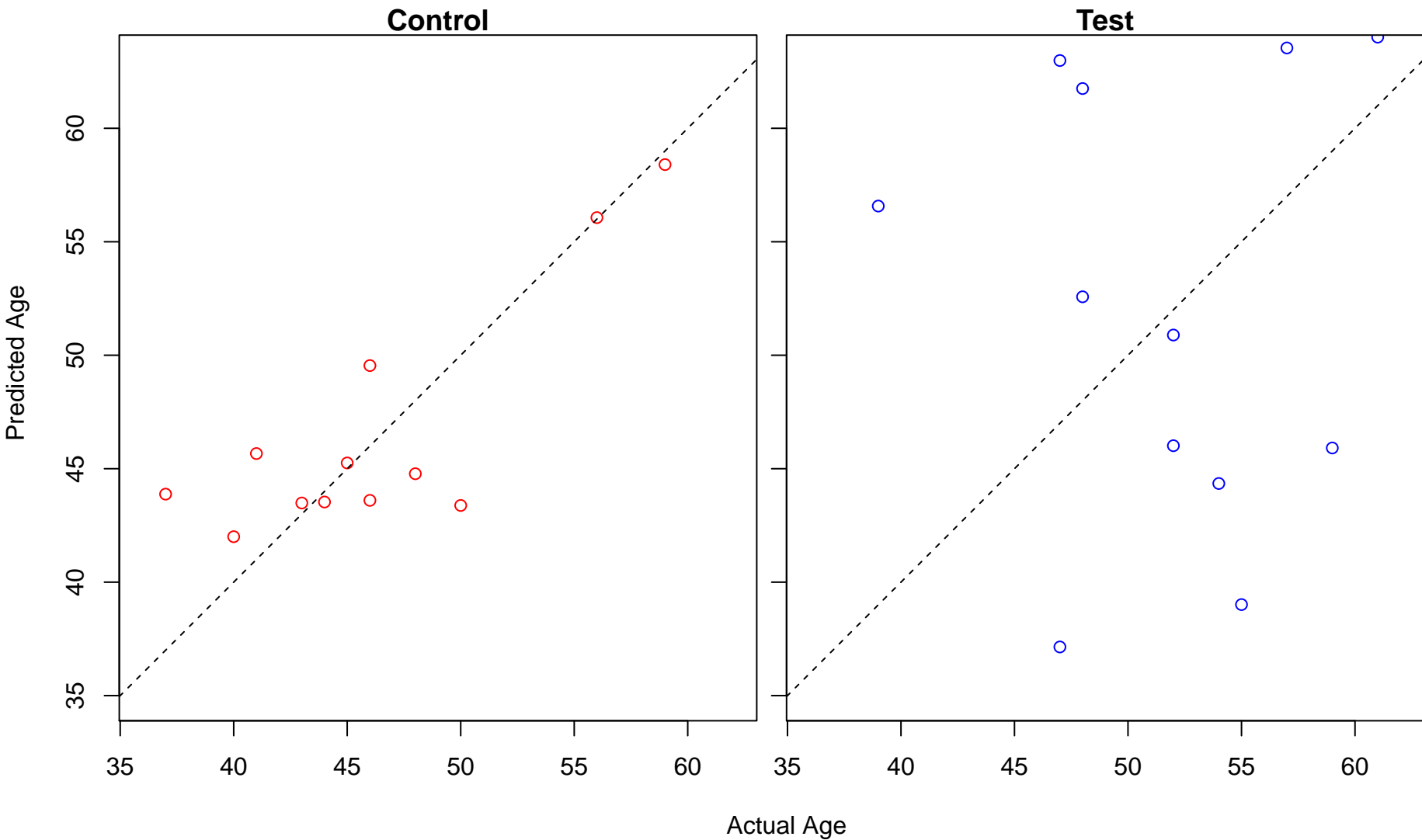
positive regulation of calcium ion transport (Score: 5.151657)



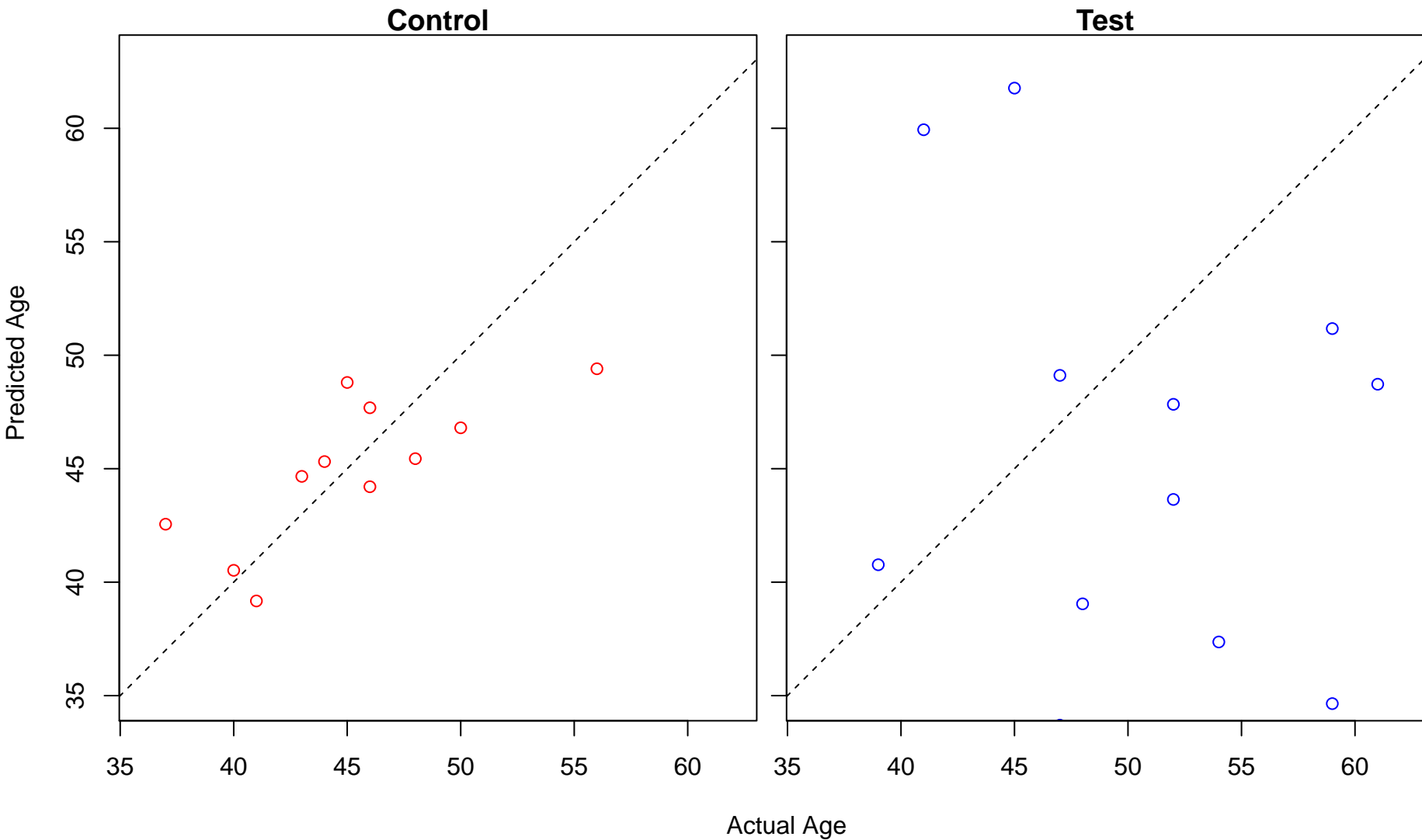
cellular sodium ion homeostasis (Score: 5.149540)



regulation of sister chromatid segregation (Score: 5.136350)

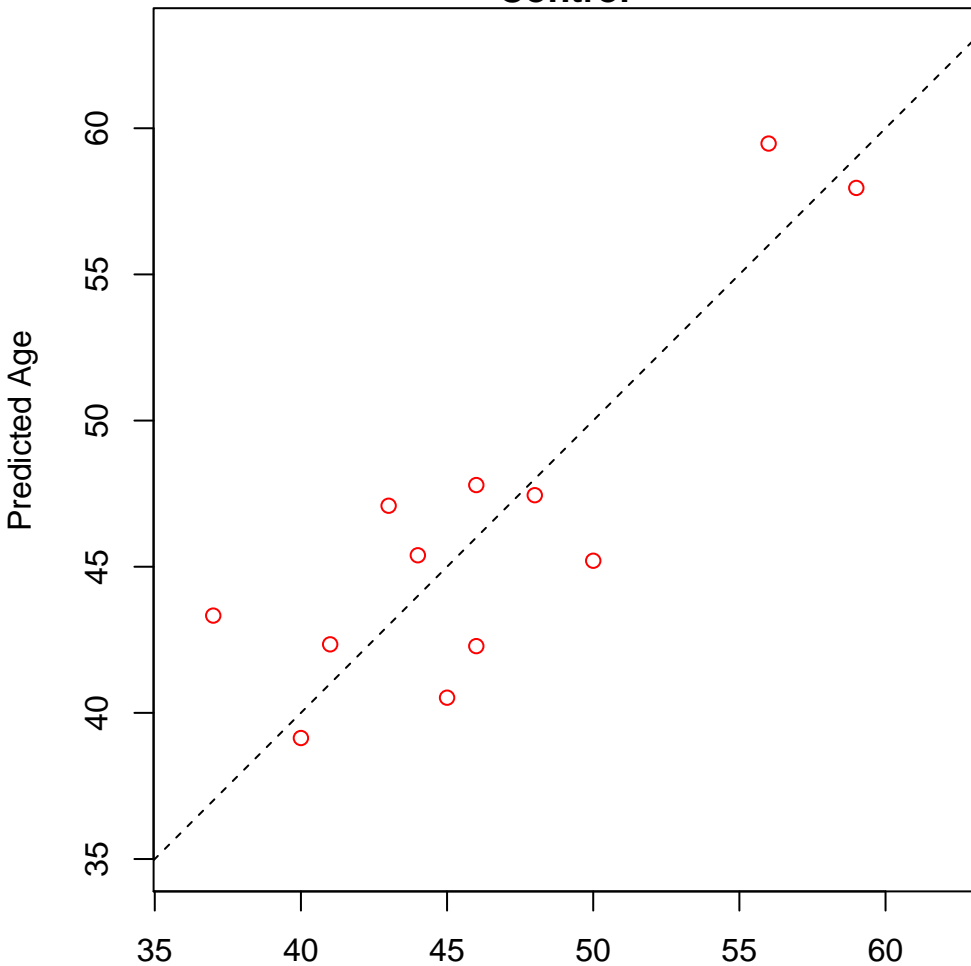


tissue morphogenesis (Score: 5.134991)

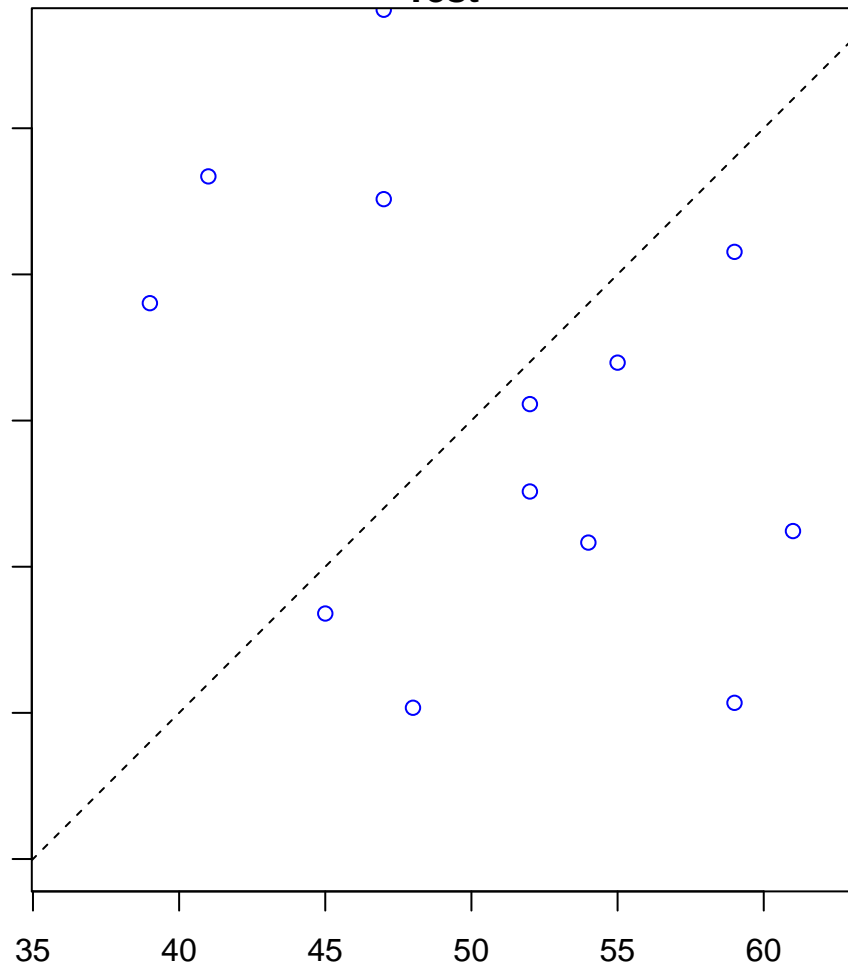


positive regulation of catabolic process (Score: 5.112564)

Control

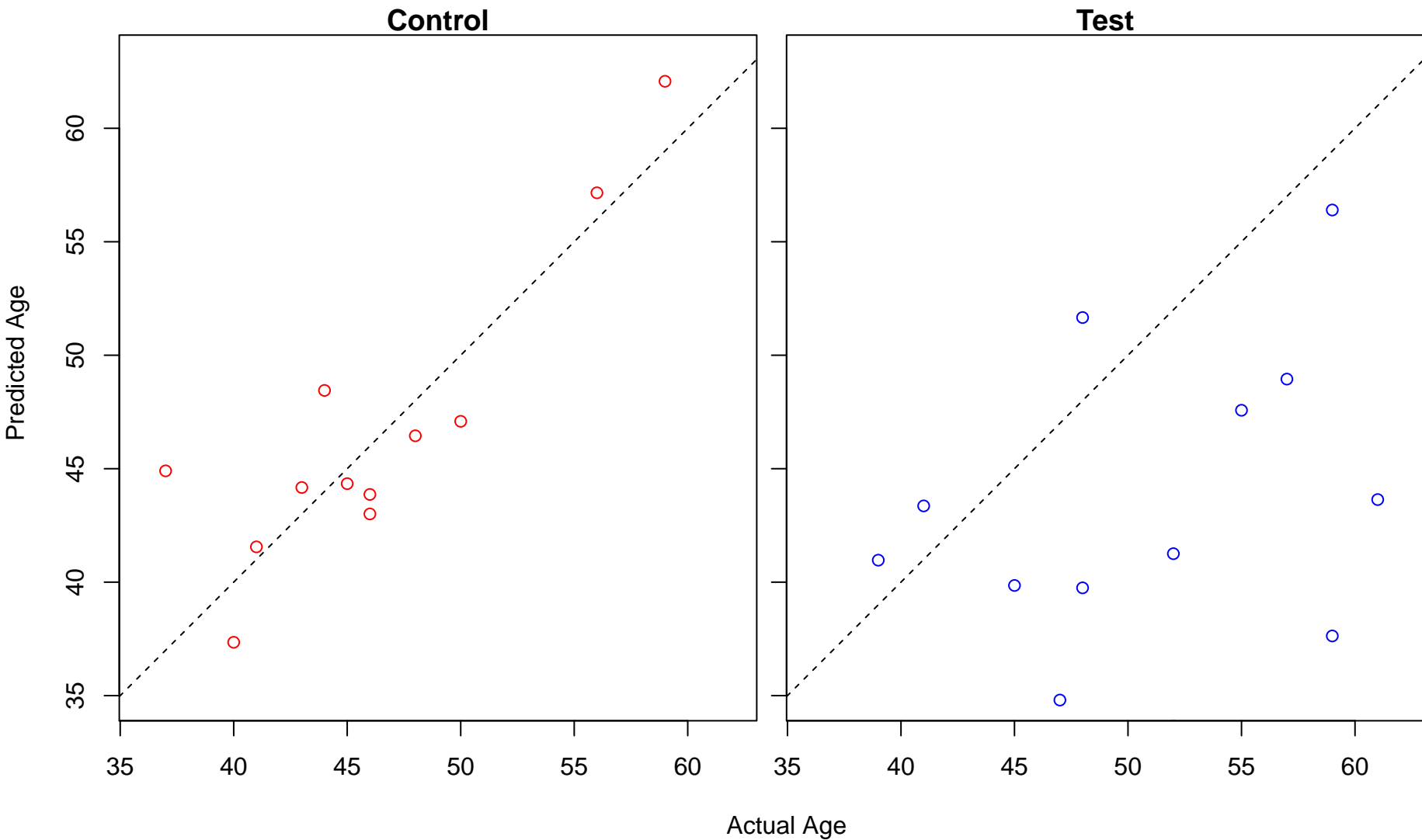


Test

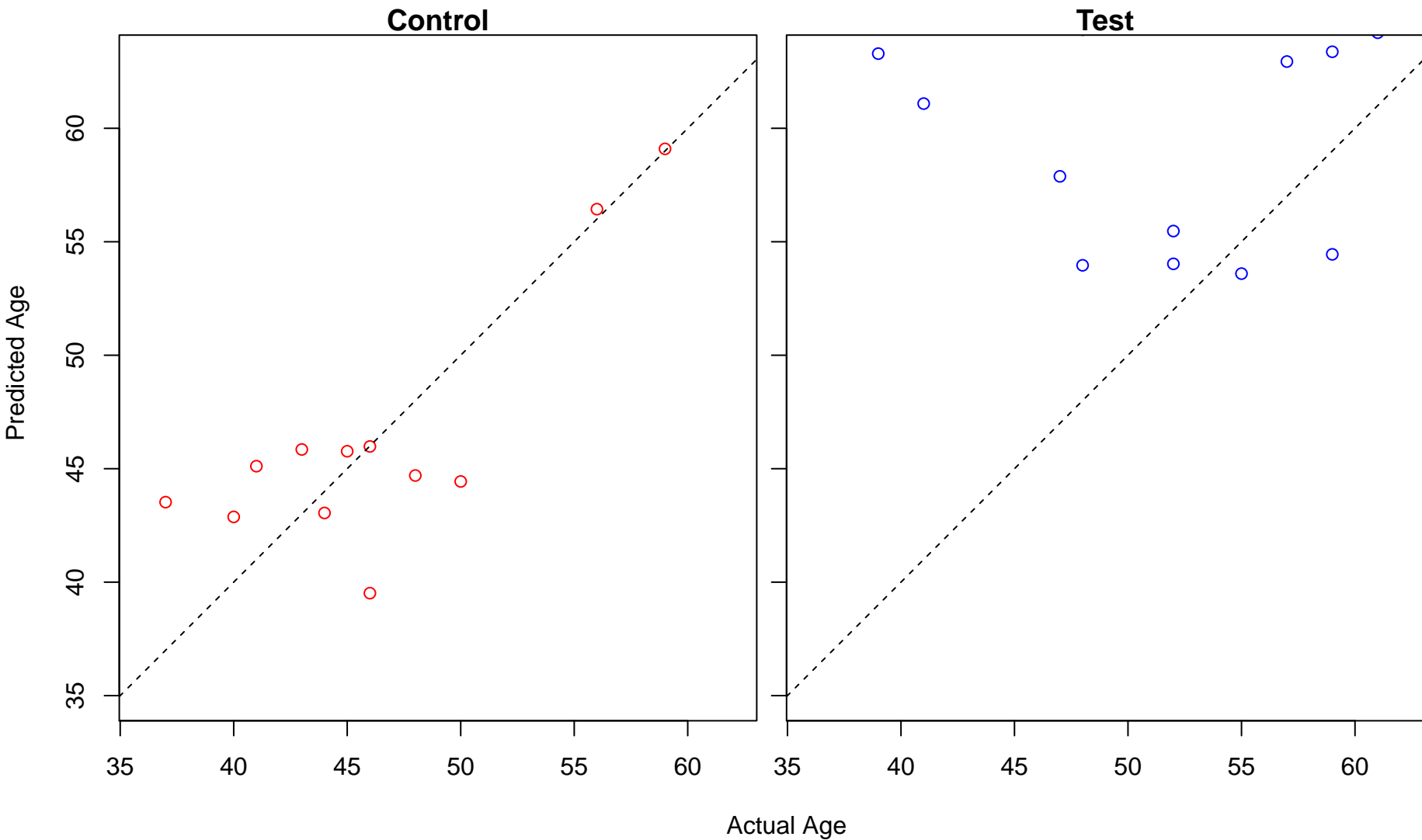


Actual Age

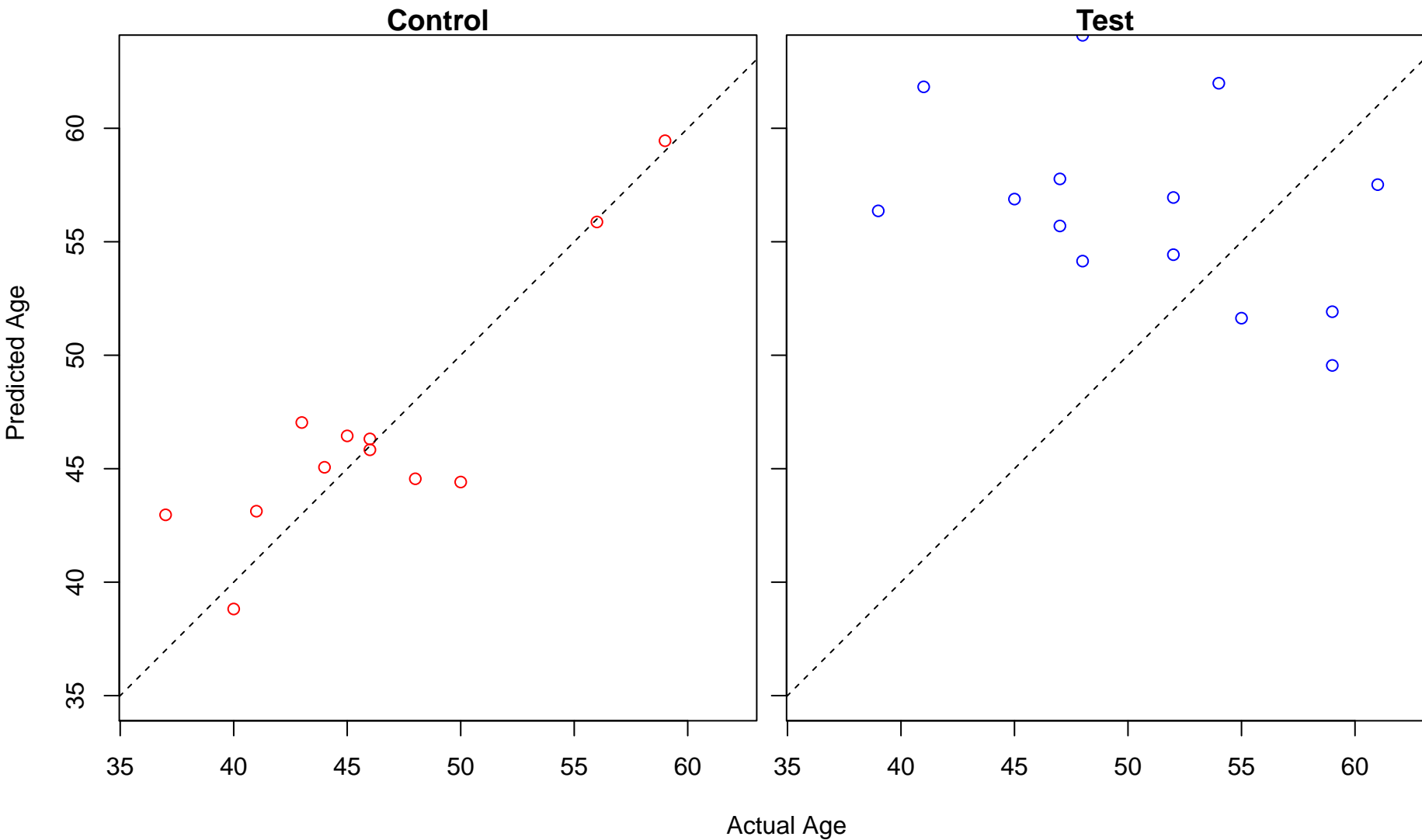
negative regulation of phosphatase activity (Score: 5.104693)



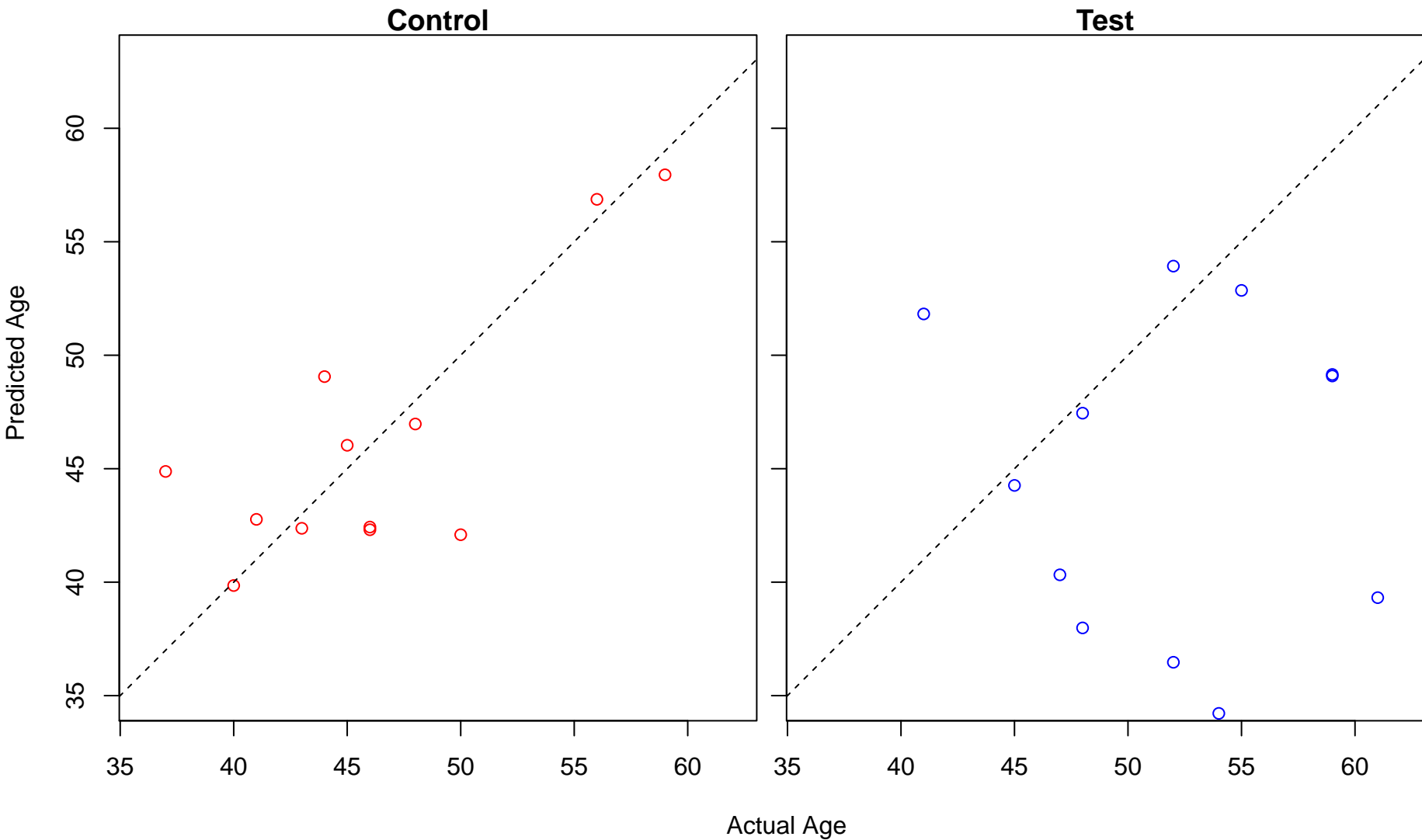
negative regulation of lipoprotein particle clearance (Score: 5.102614)



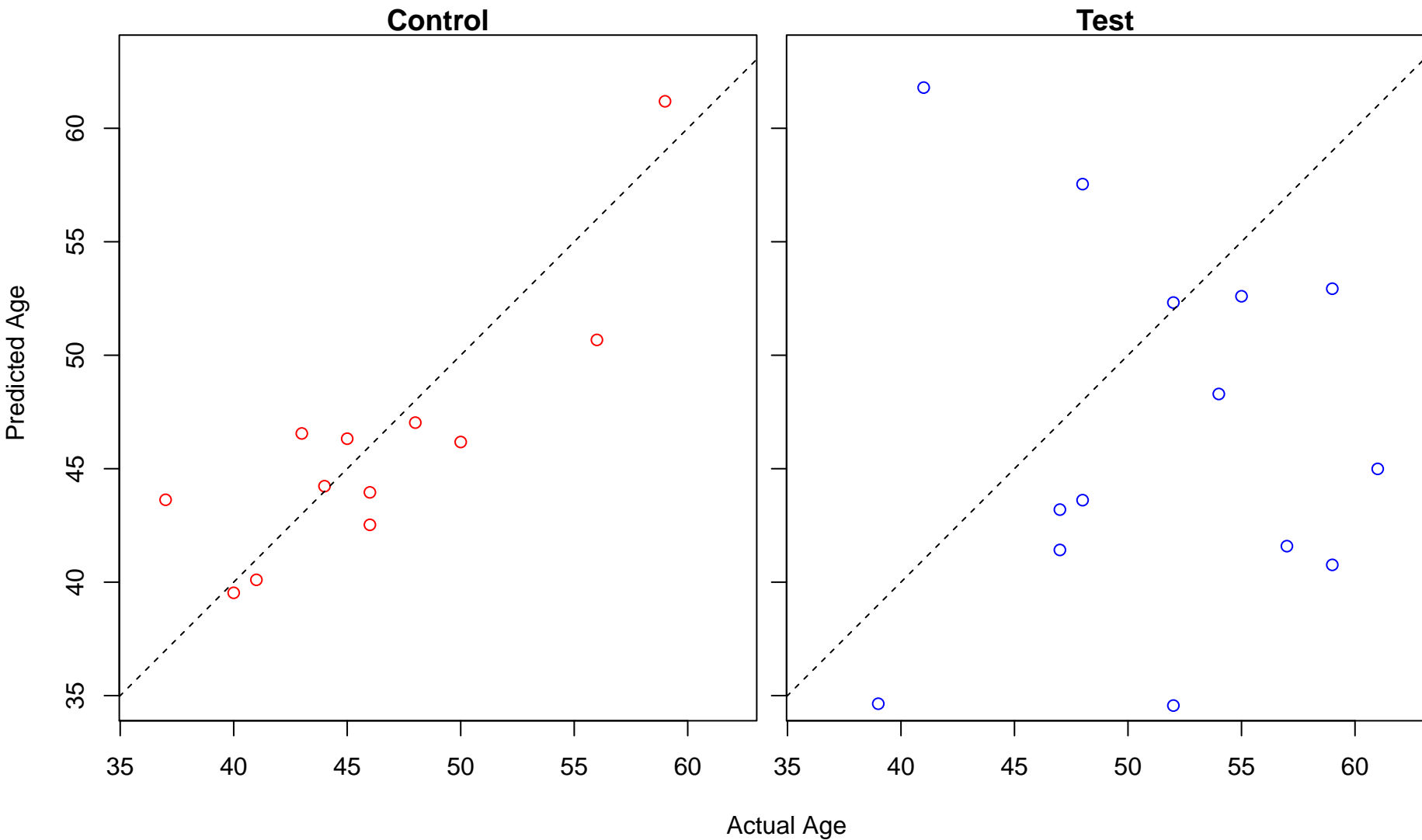
positive chemotaxis (Score: 5.098829)



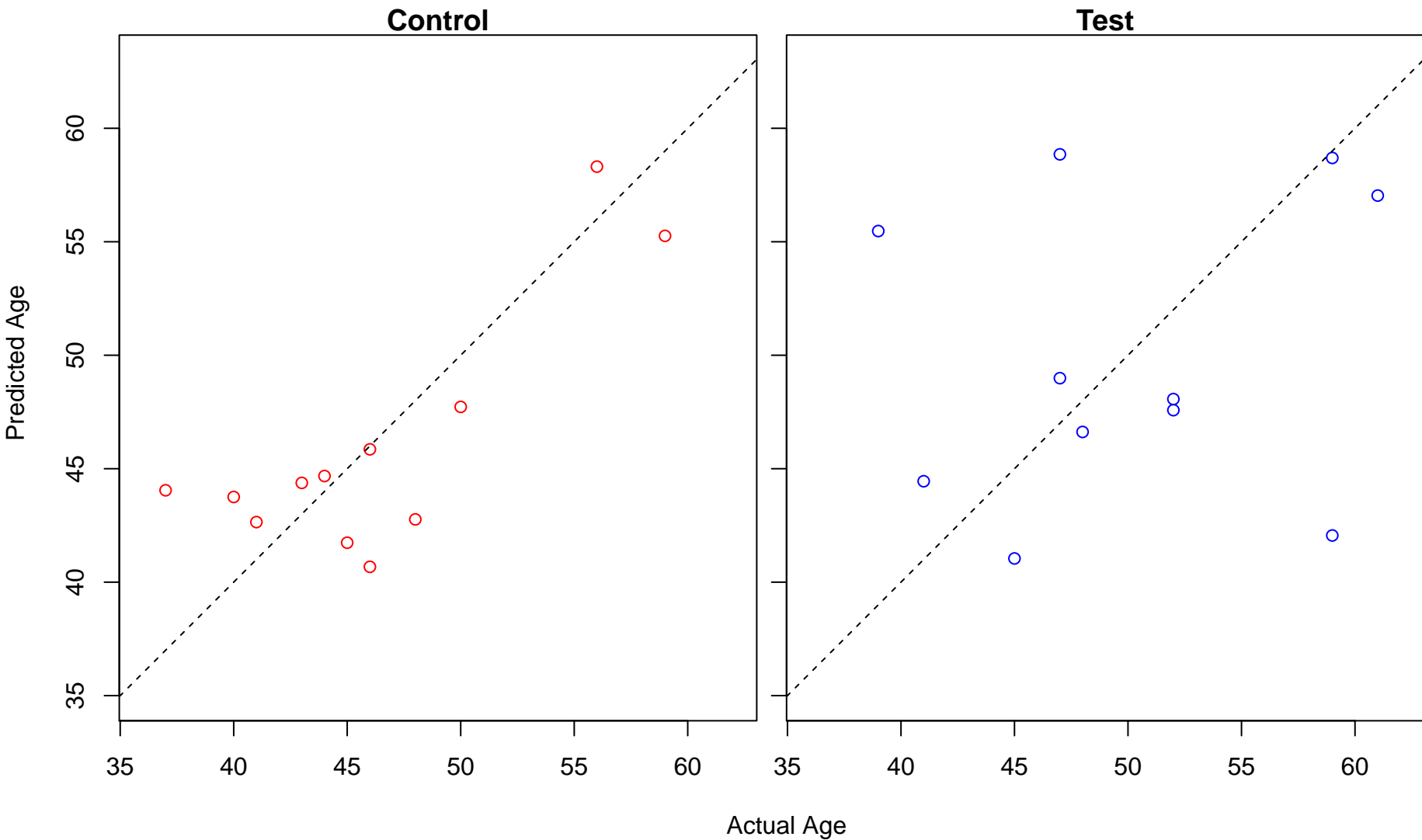
histone mRNA metabolic process (Score: 5.094836)



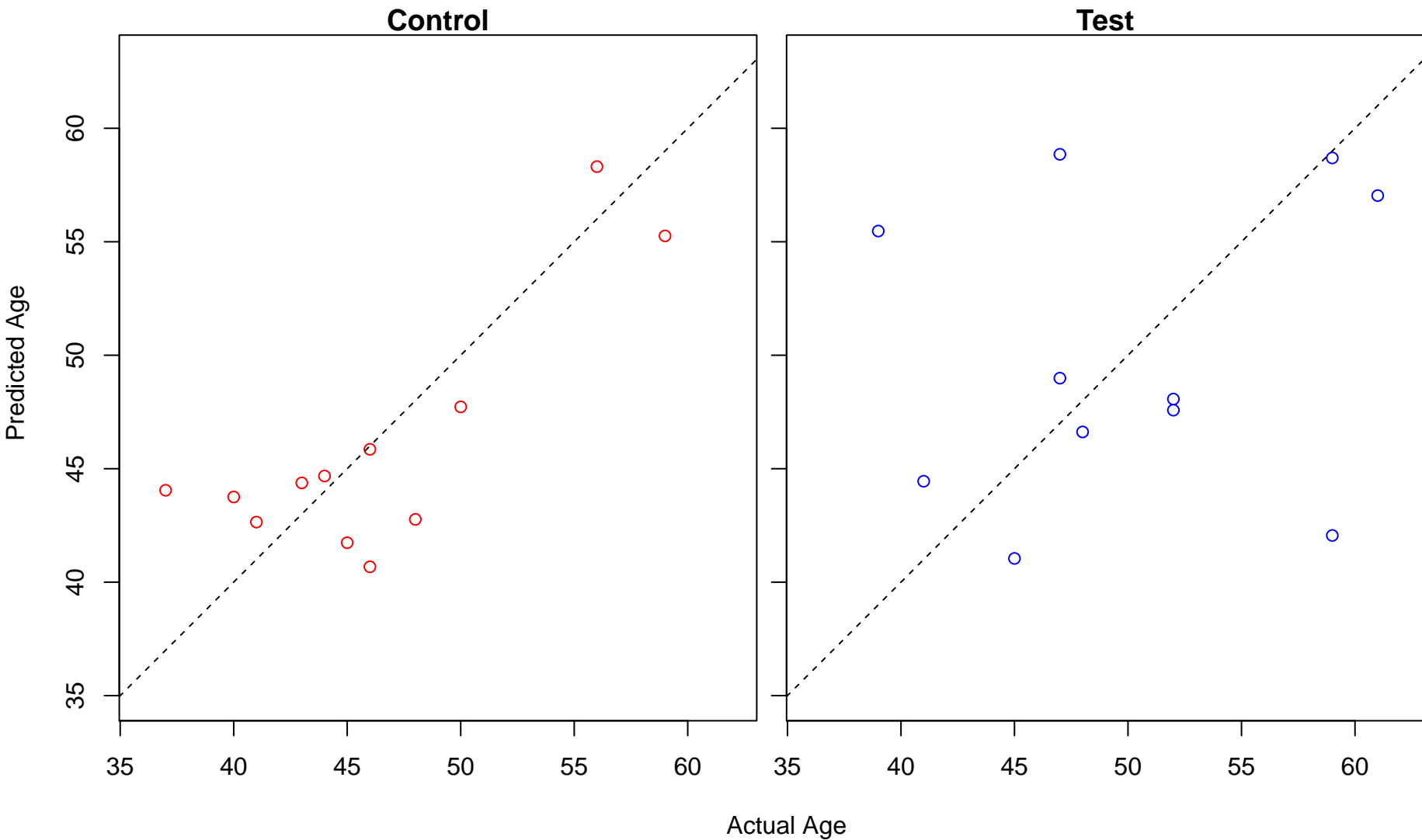
nitrogen compound transport (Score: 5.094601)



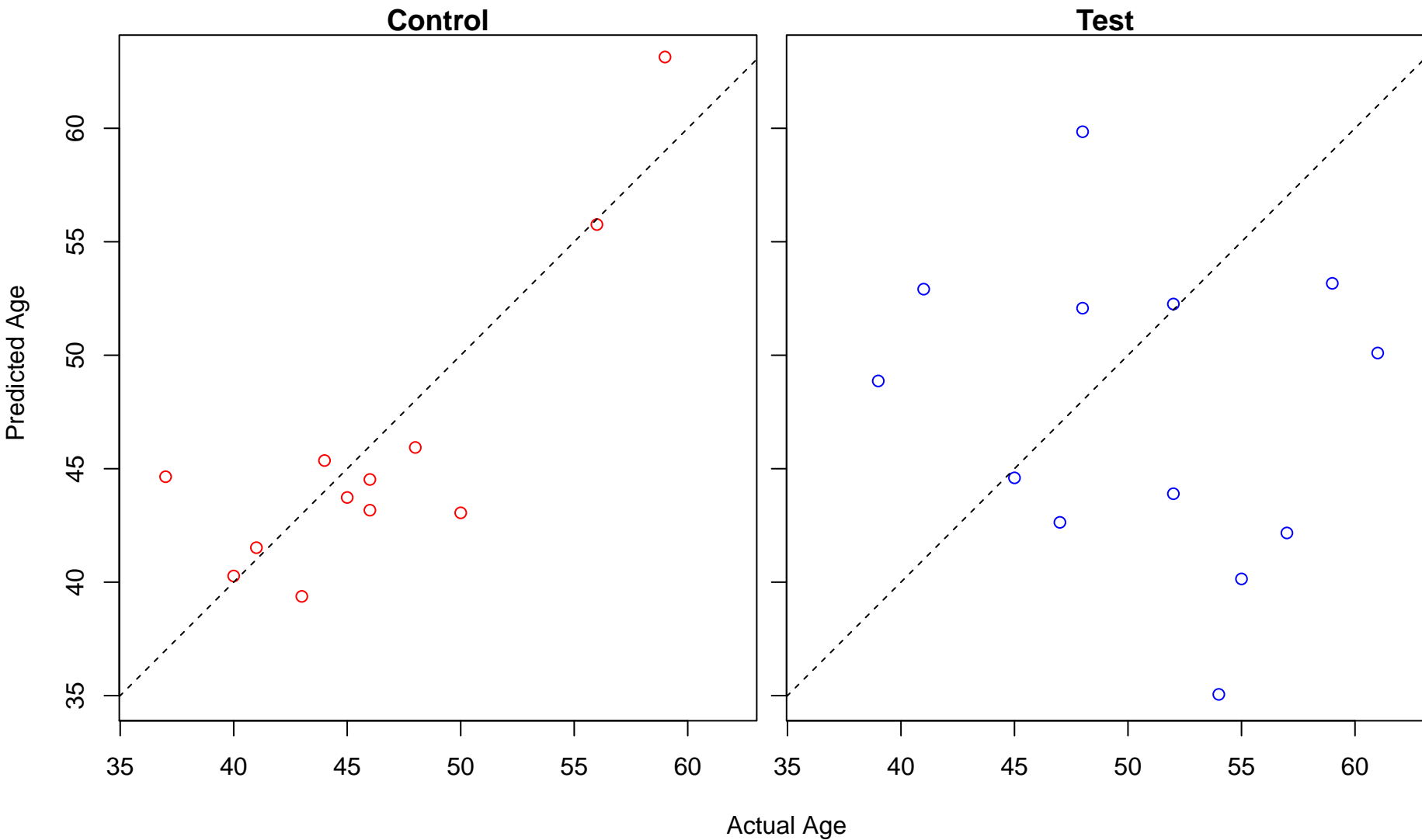
sodium ion export from cell (Score: 5.092898)



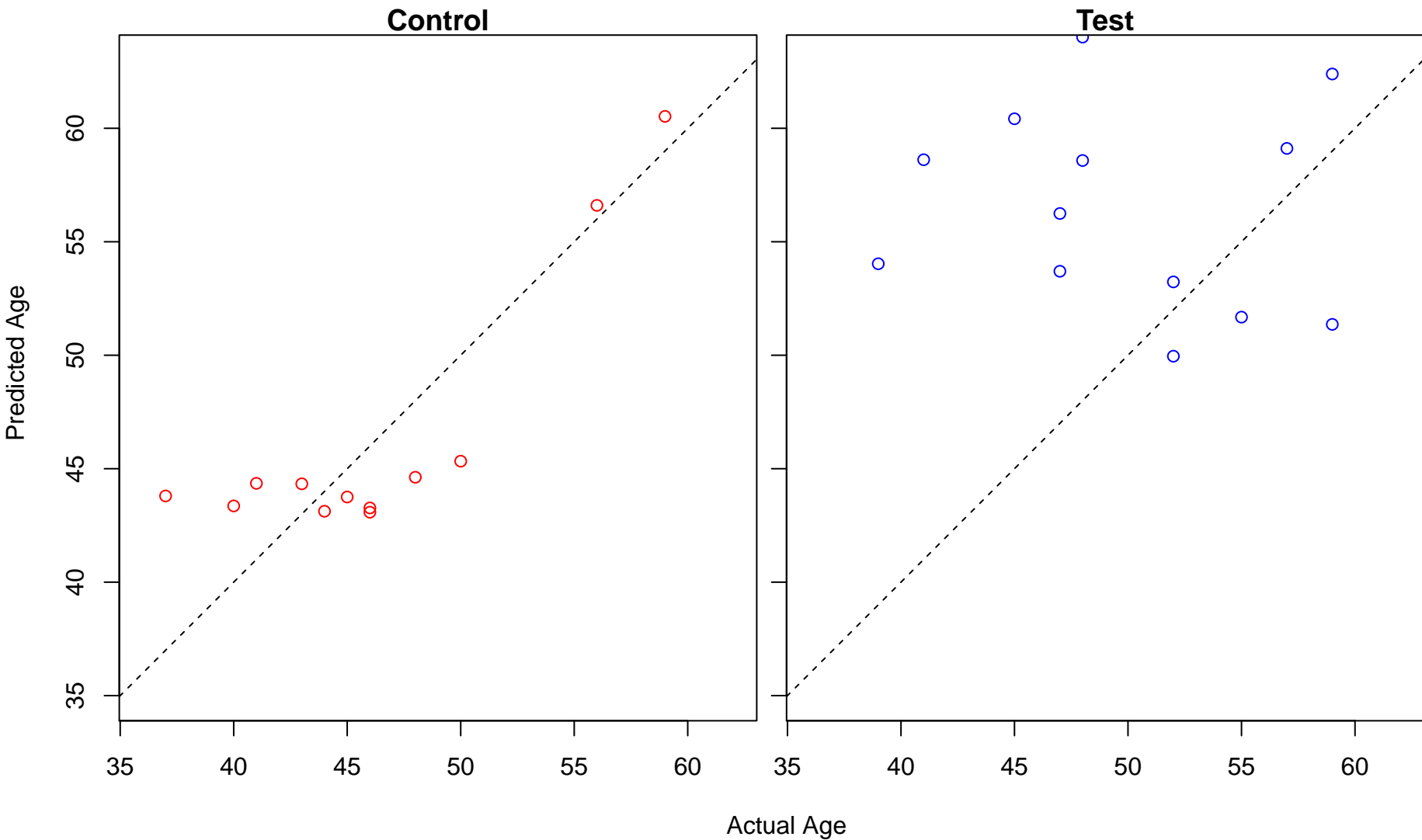
ATP hydrolysis coupled transmembrane transport (Score: 5.092895)



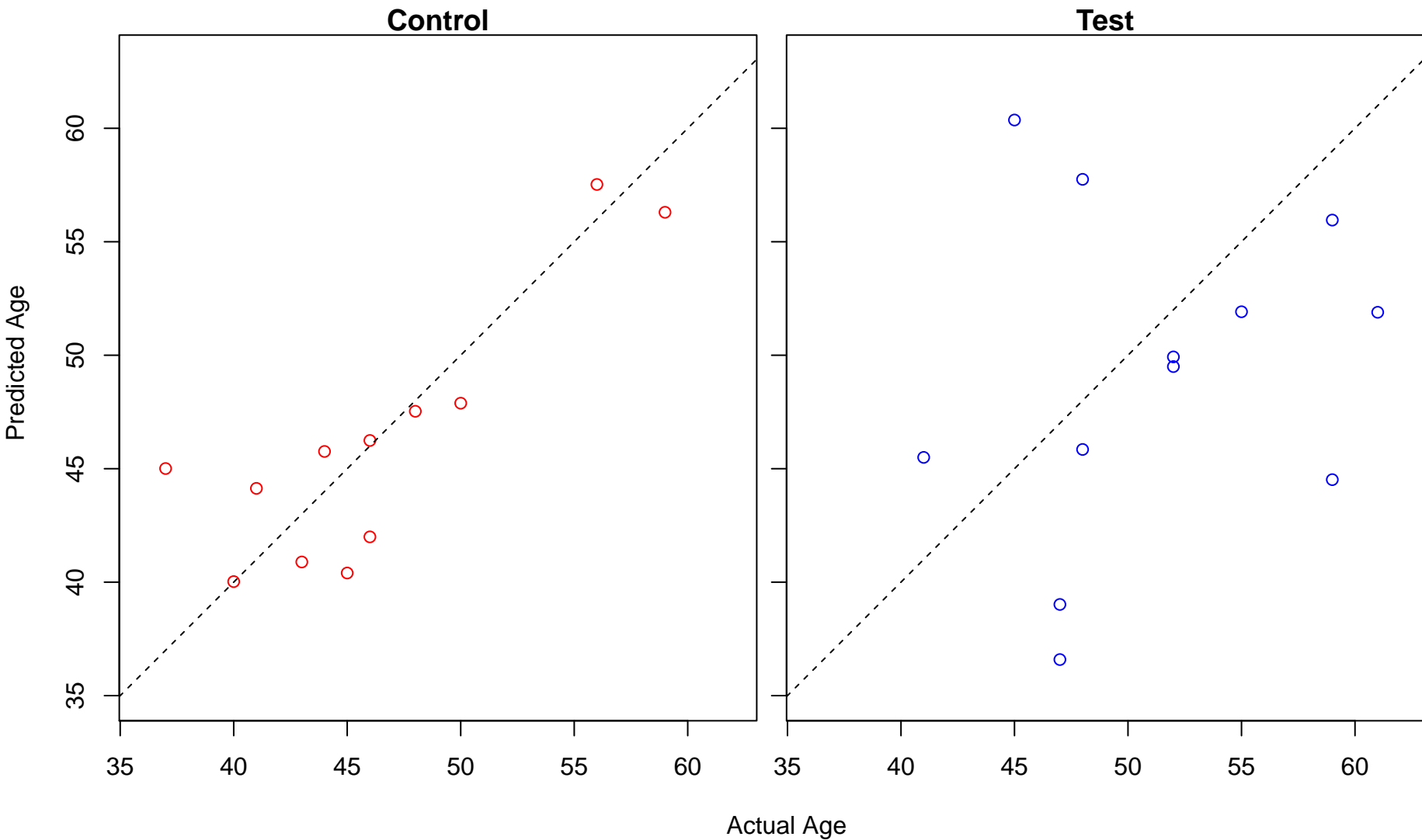
GMP metabolic process (Score: 5.091384)



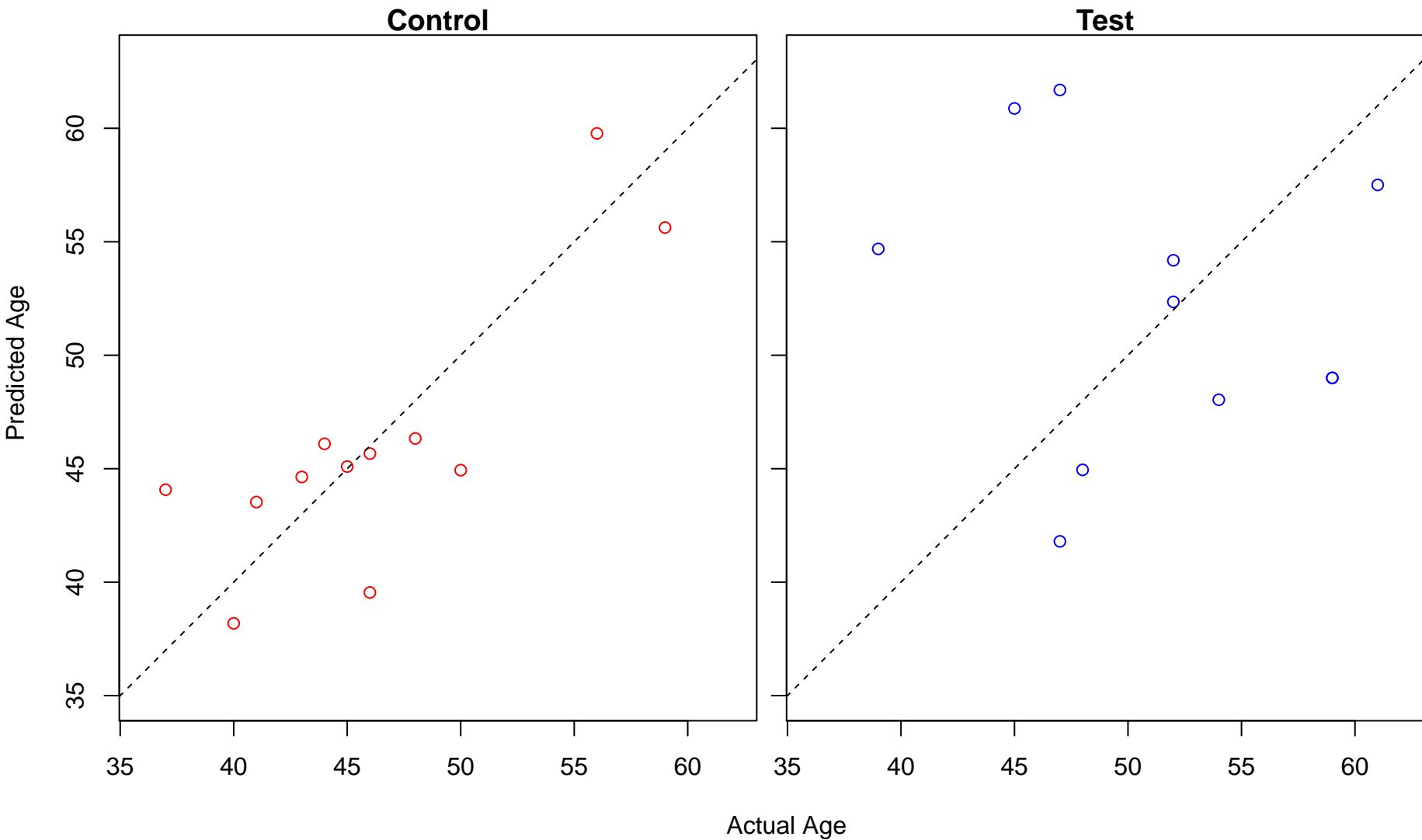
sulfation (Score: 5.089530)



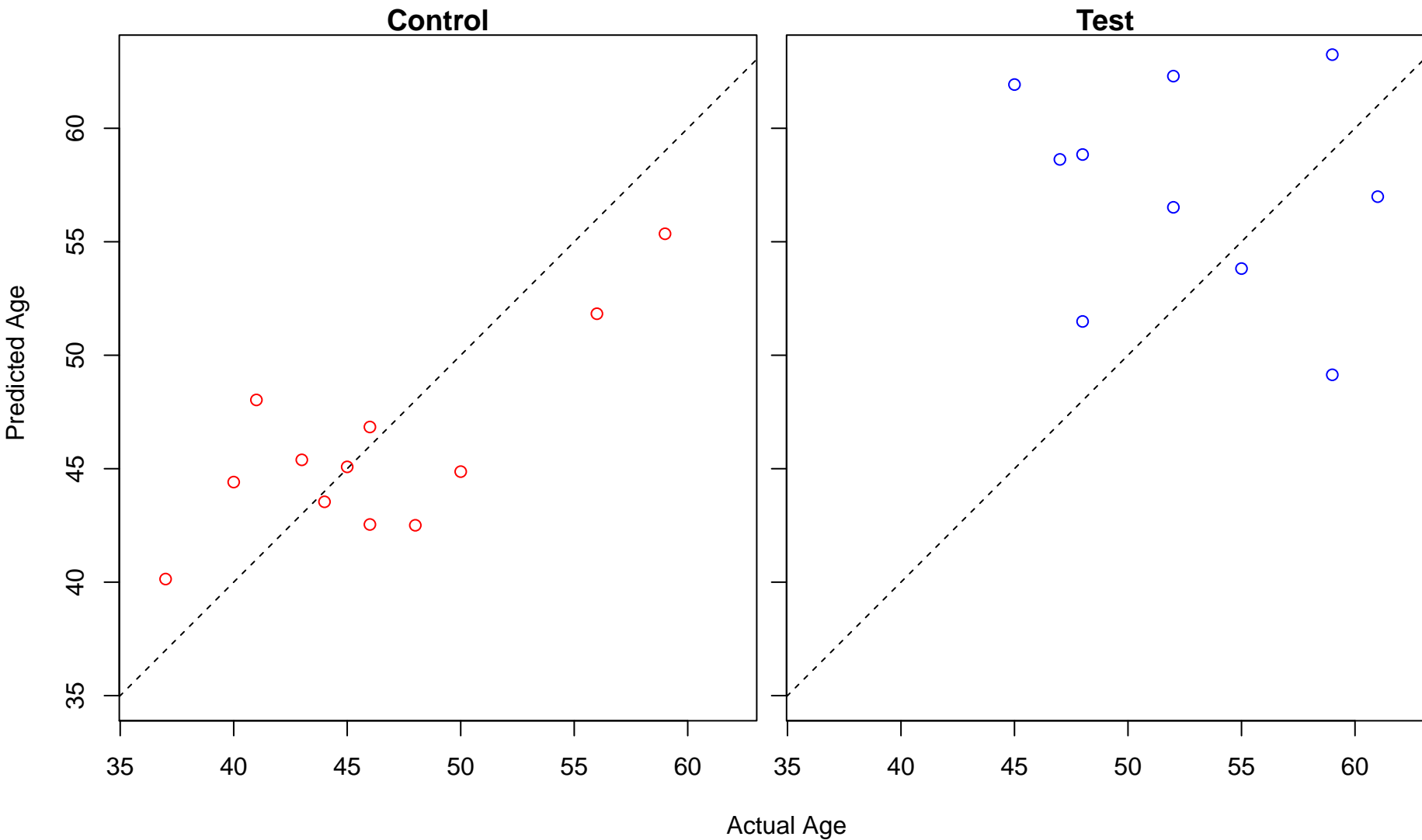
carbohydrate derivative transport (Score: 5.087426)



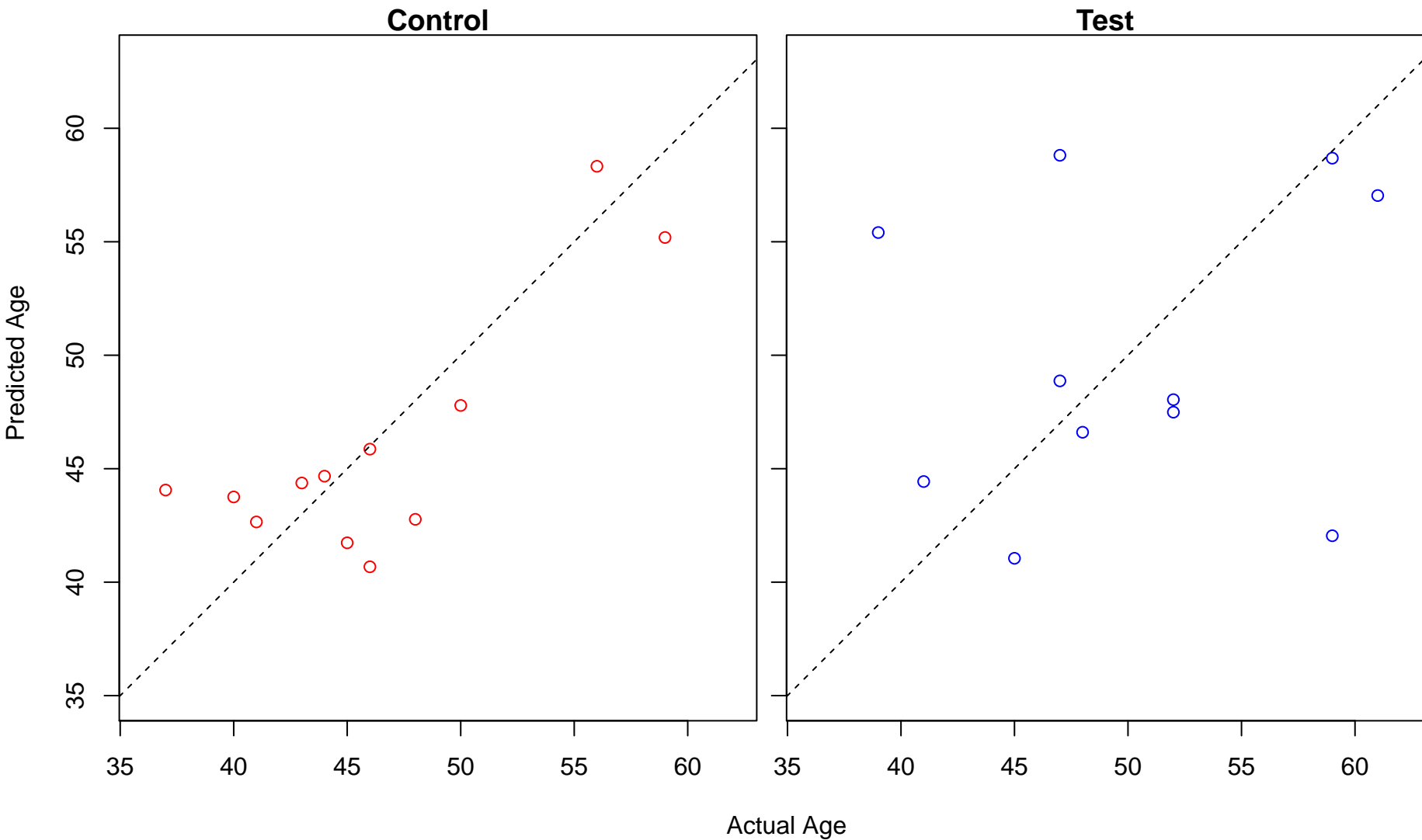
embryonic morphogenesis (Score: 5.083184)



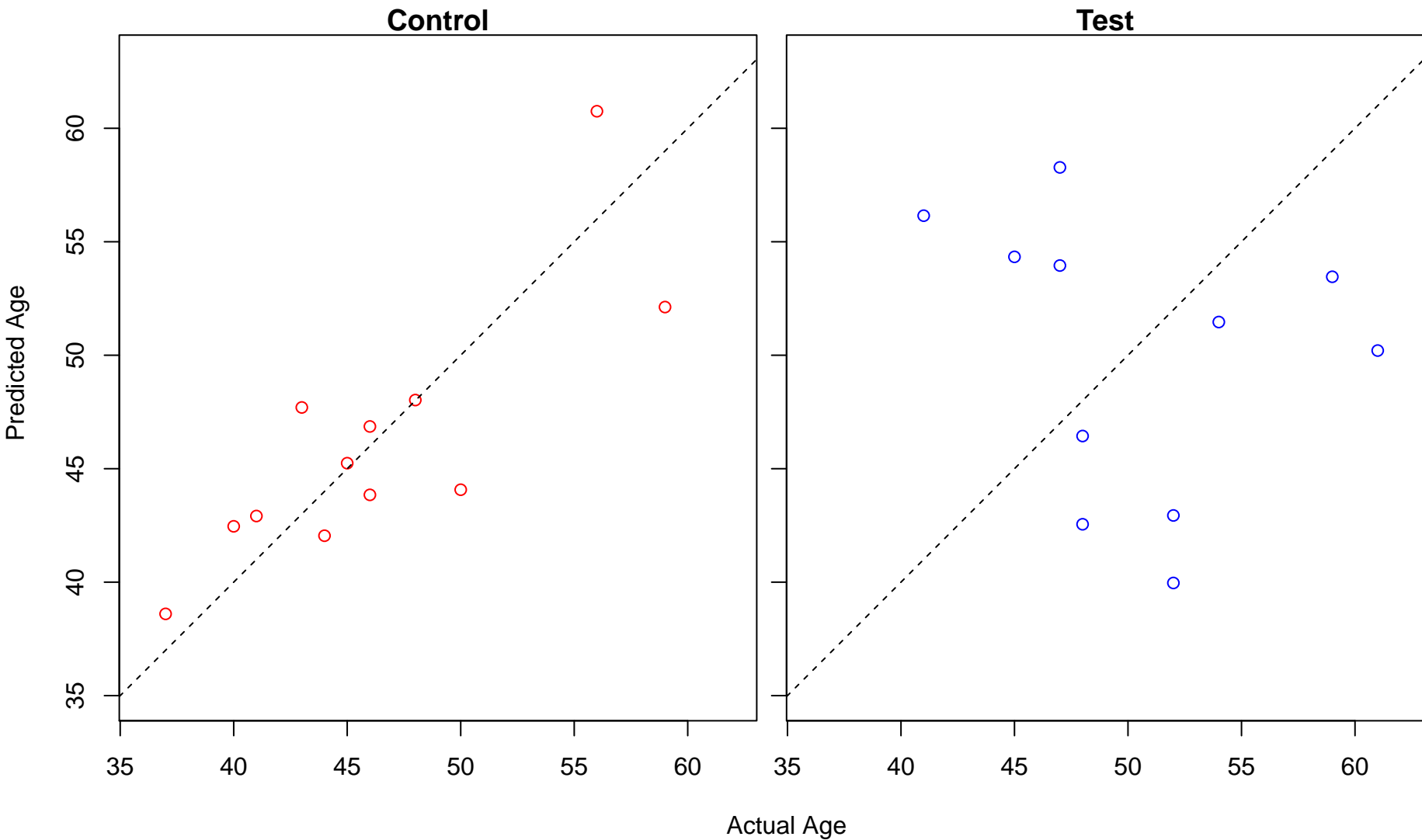
regulation of interleukin-10 secretion (Score: 5.076370)



sodium ion export (Score: 5.065914)

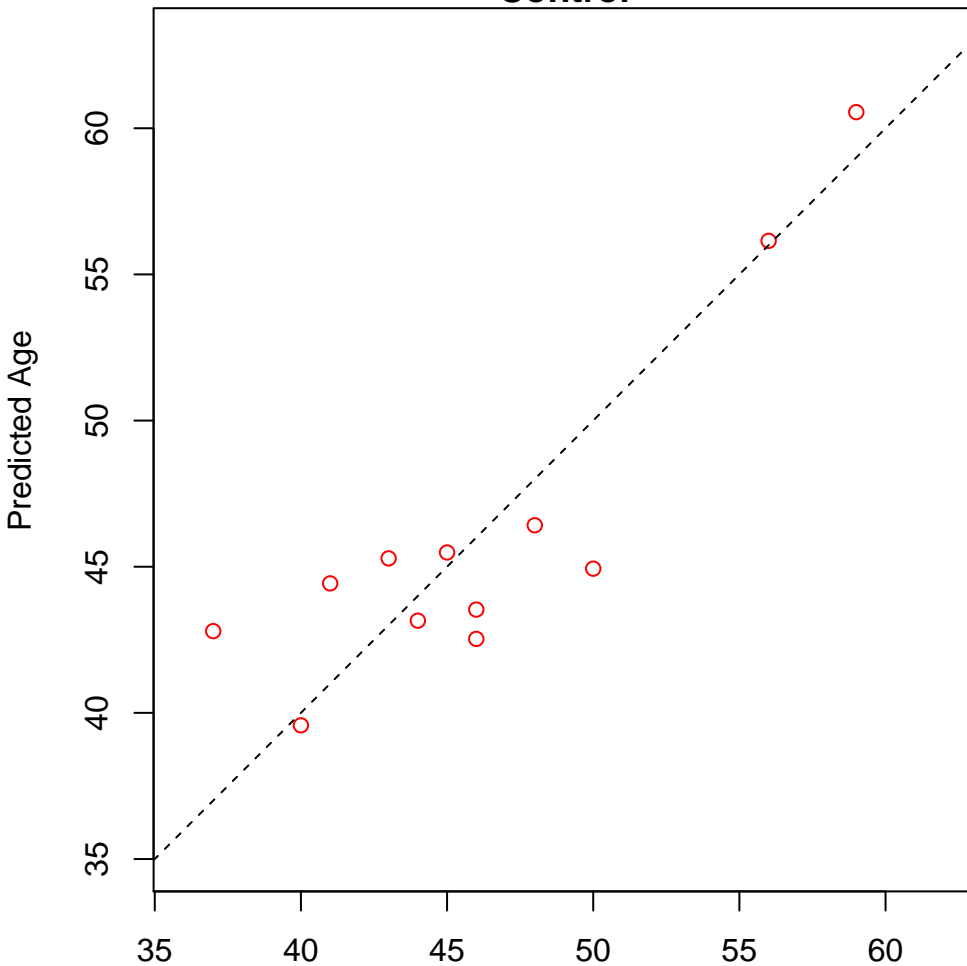


negative regulation of immune effector process (Score: 5.048863)

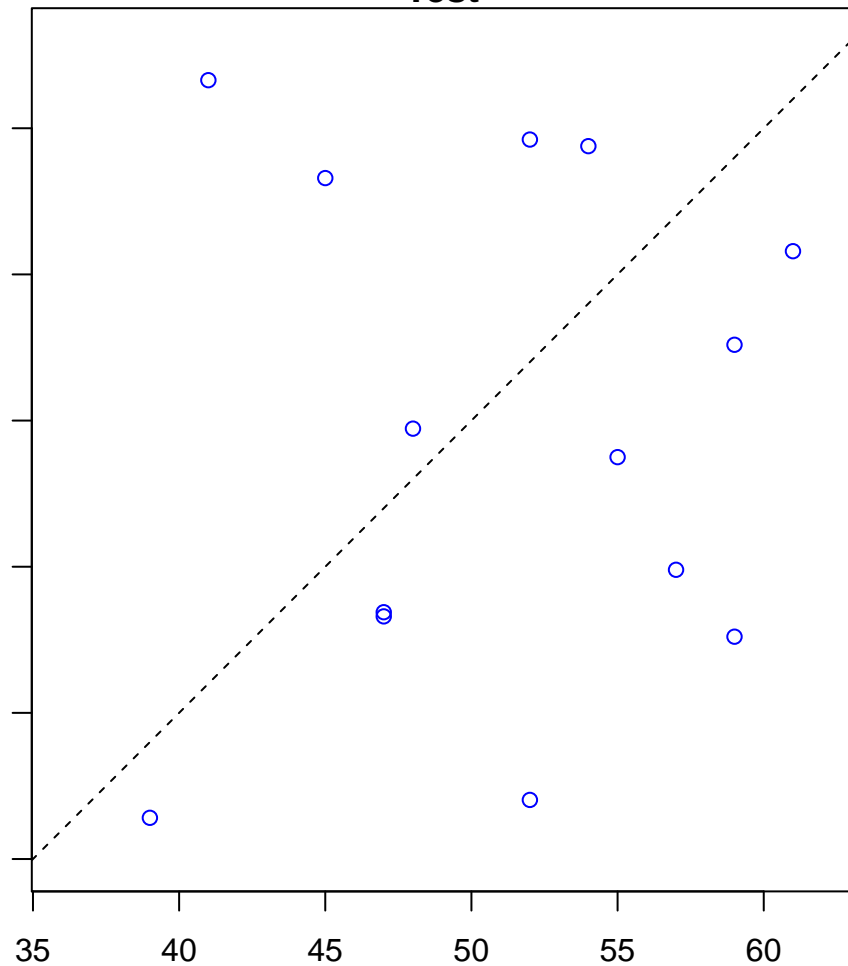


response to purine-containing compound (Score: 5.048060)

Control

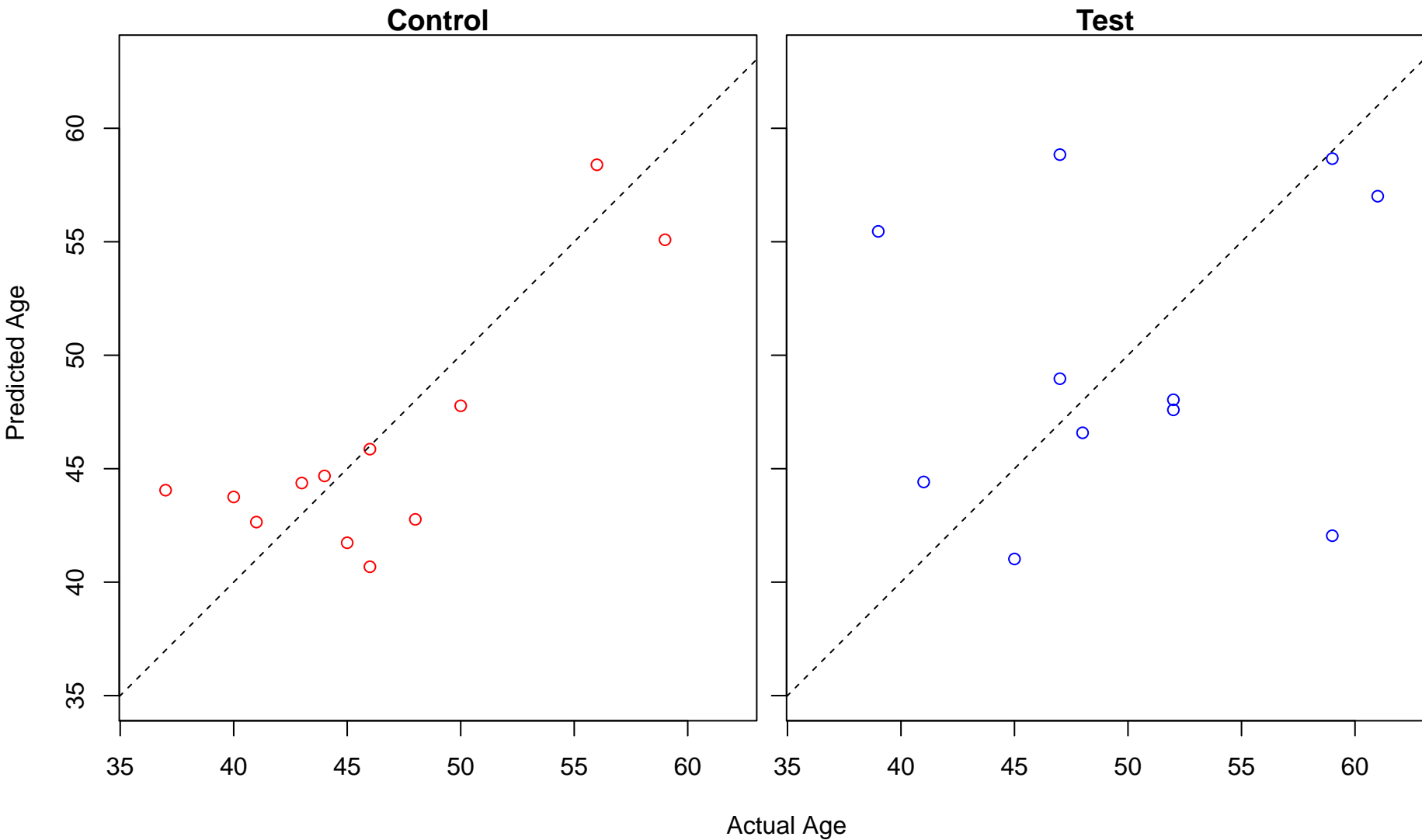


Test

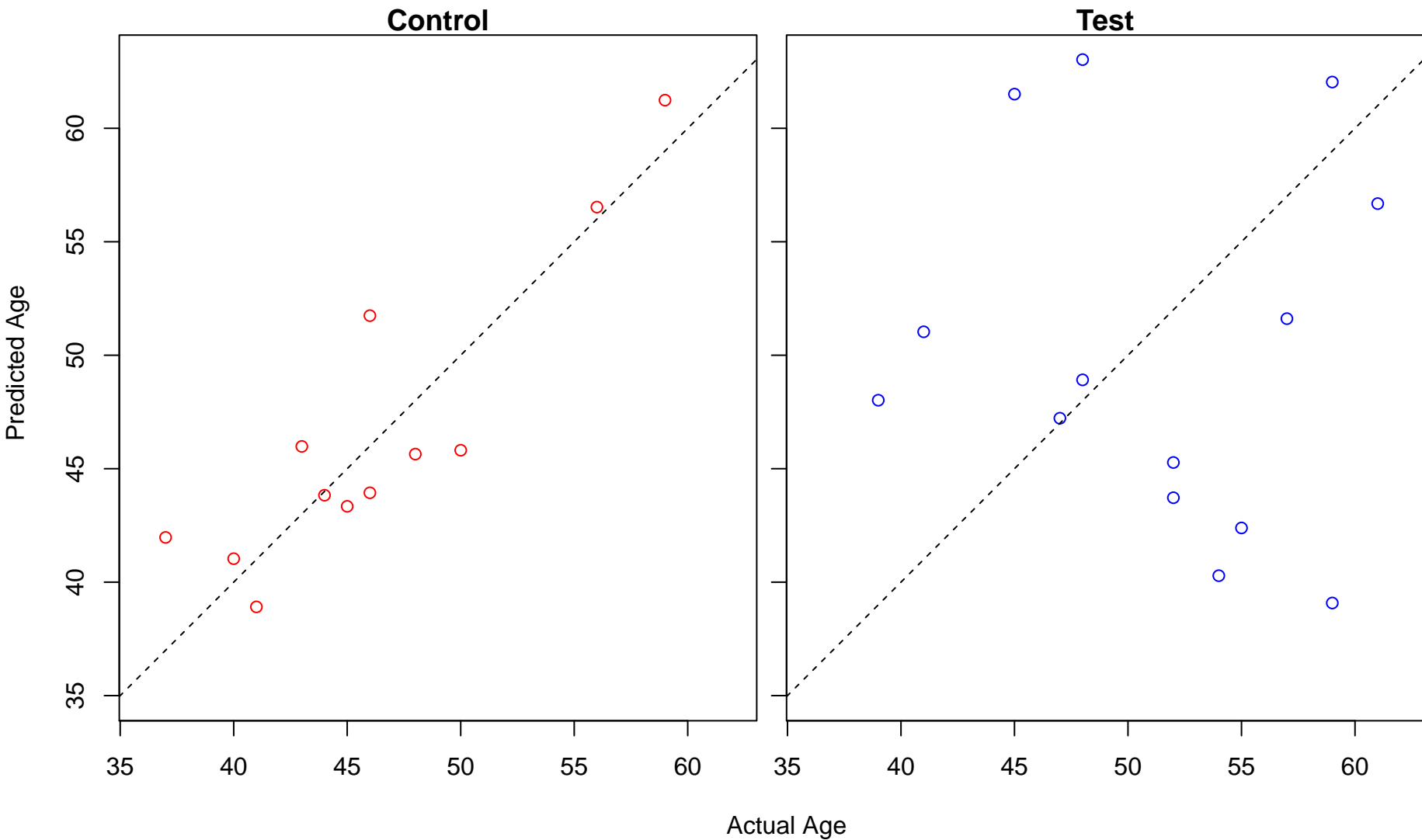


Actual Age

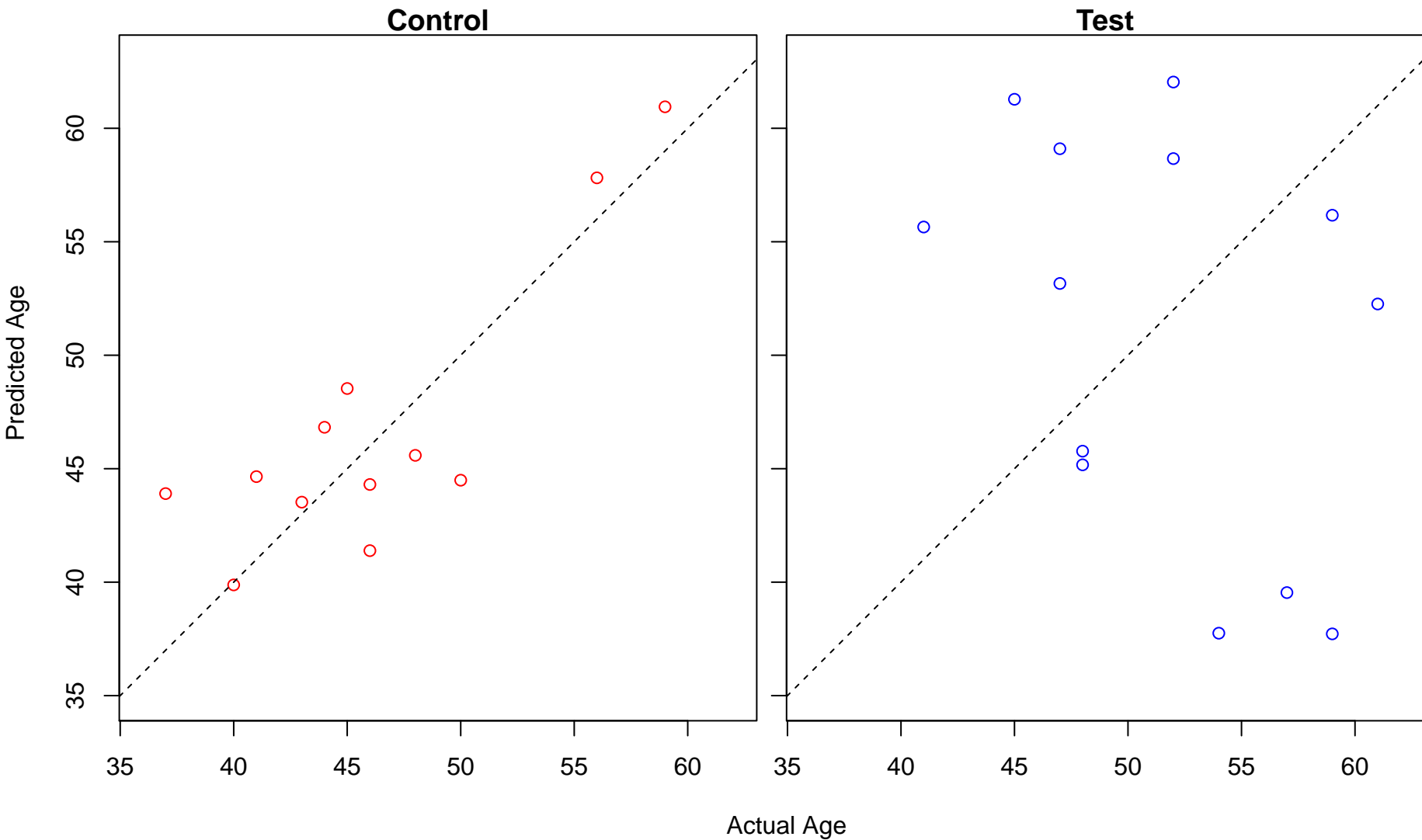
establishment or maintenance of transmembrane electrochemical gradient (Score: 5.044378)



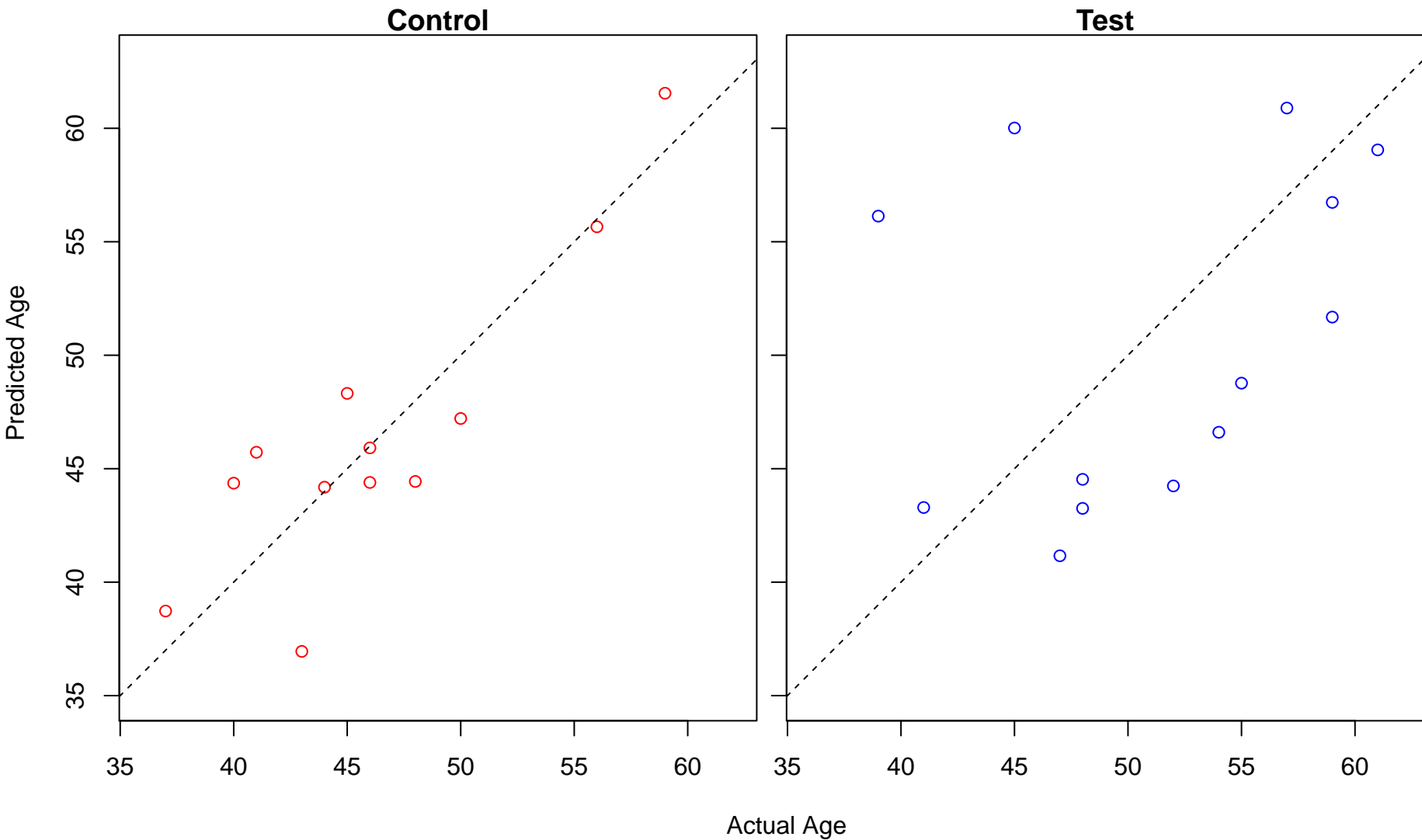
positive regulation of axonogenesis (Score: 5.041575)



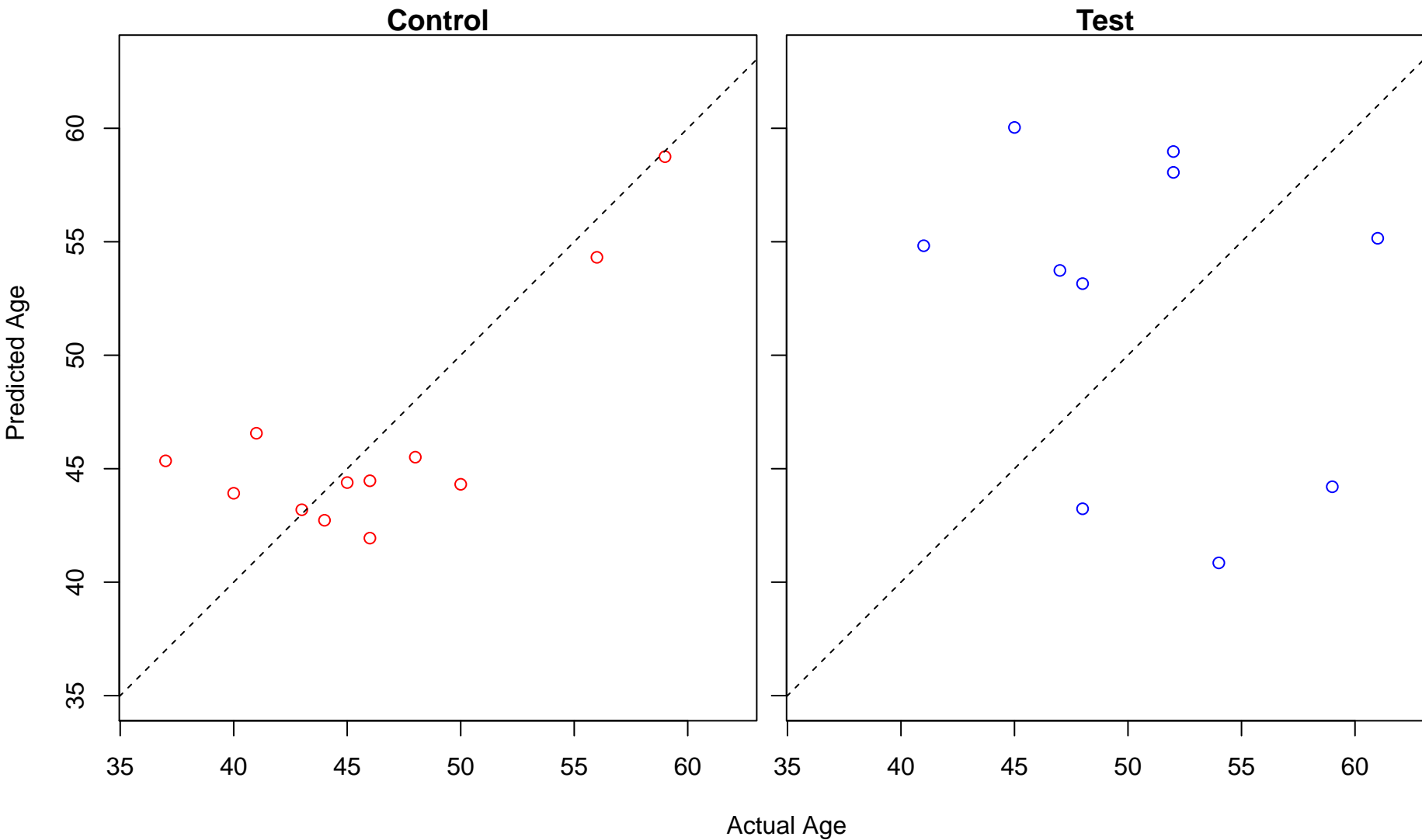
response to interferon-gamma (Score: 5.040697)



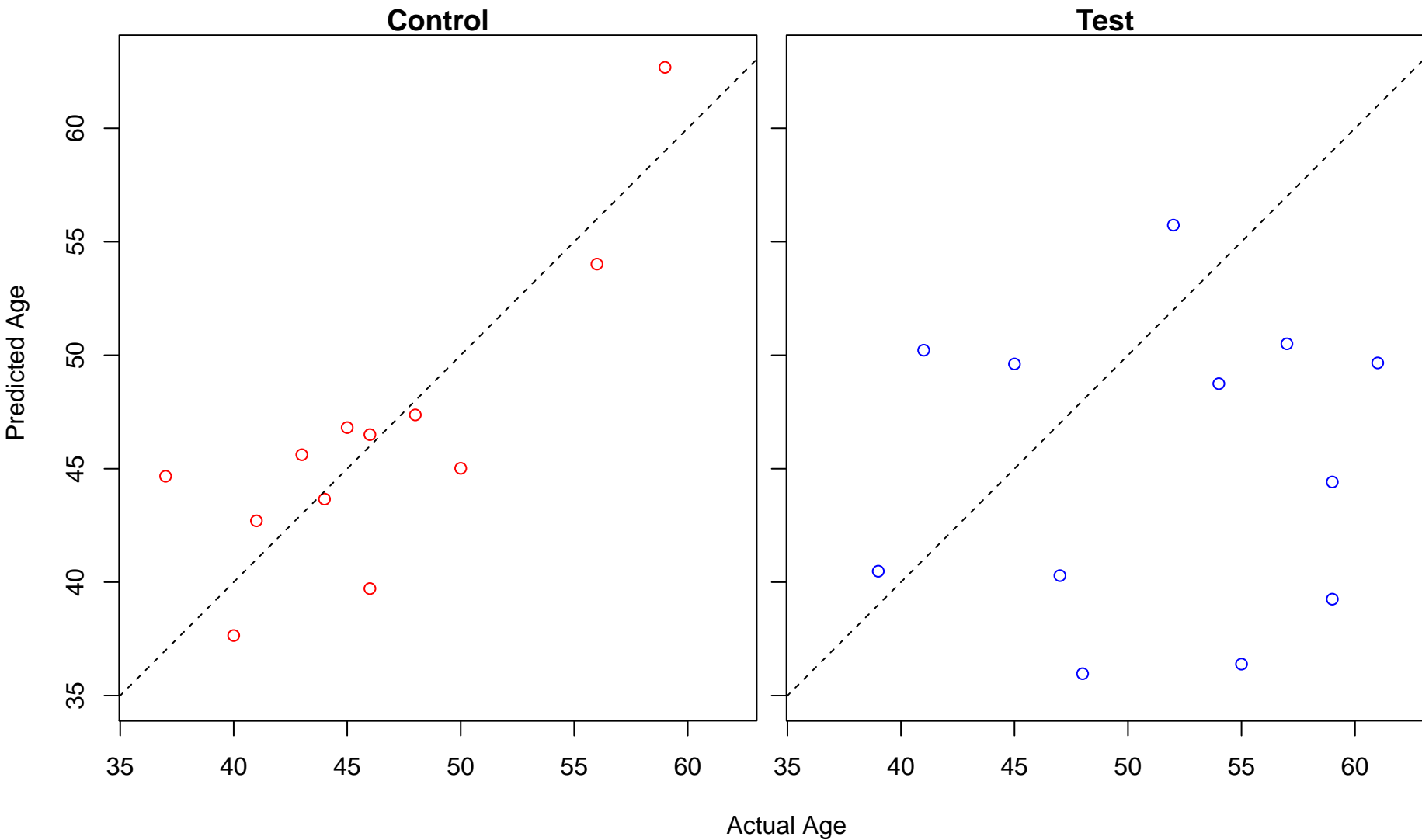
regulation of phagocytosis, engulfment (Score: 5.035389)



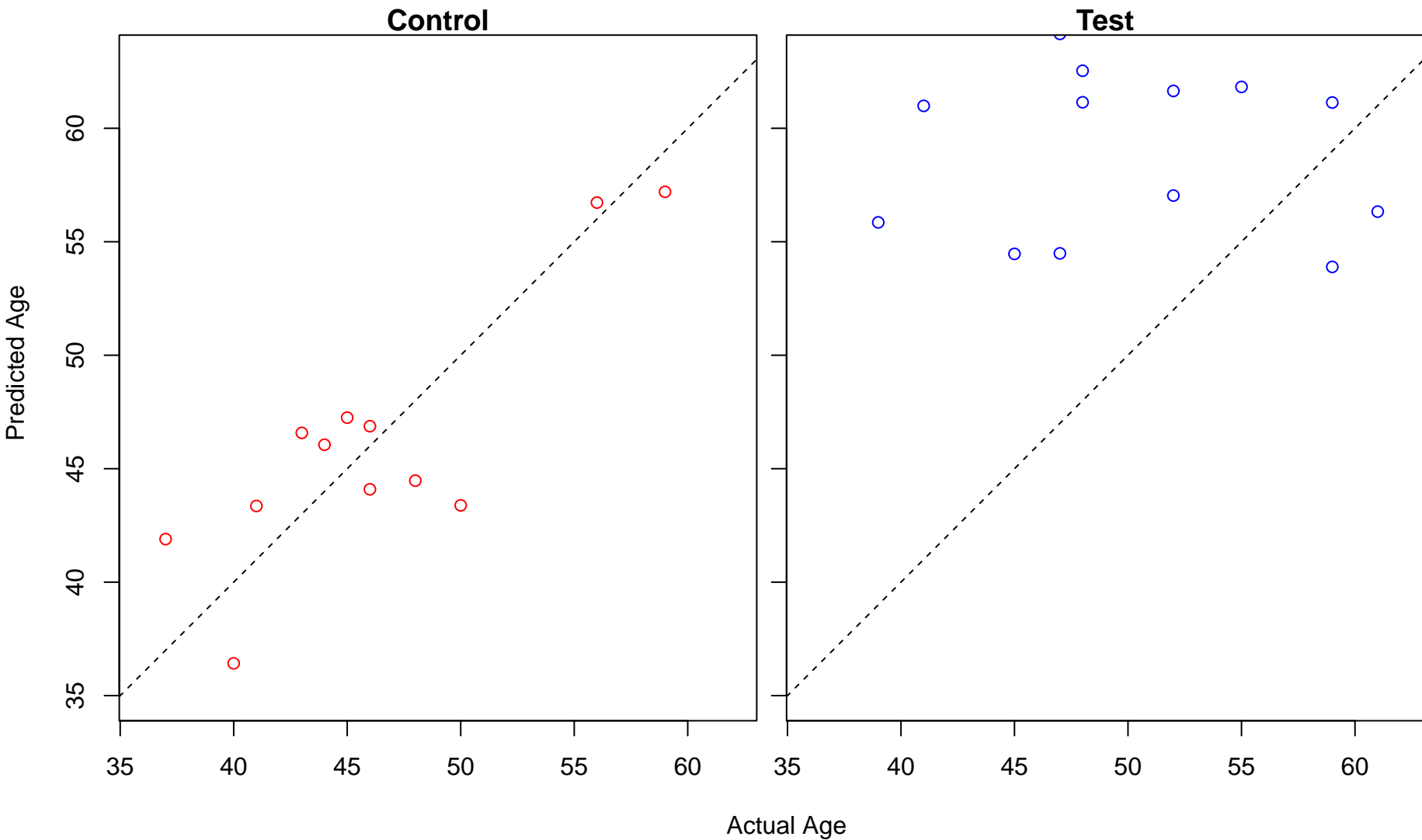
phospholipid homeostasis (Score: 5.034205)



single-organism membrane budding (Score: 5.025902)

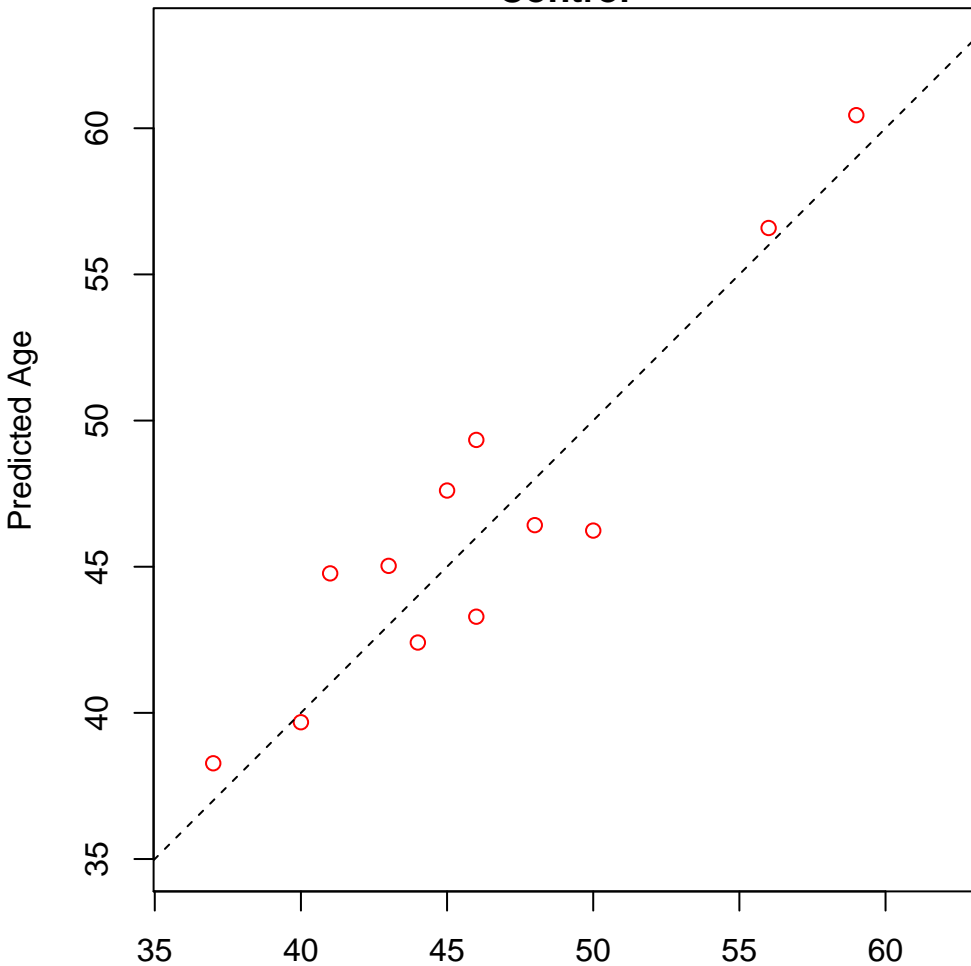


positive regulation of T cell apoptotic process (Score: 5.025646)

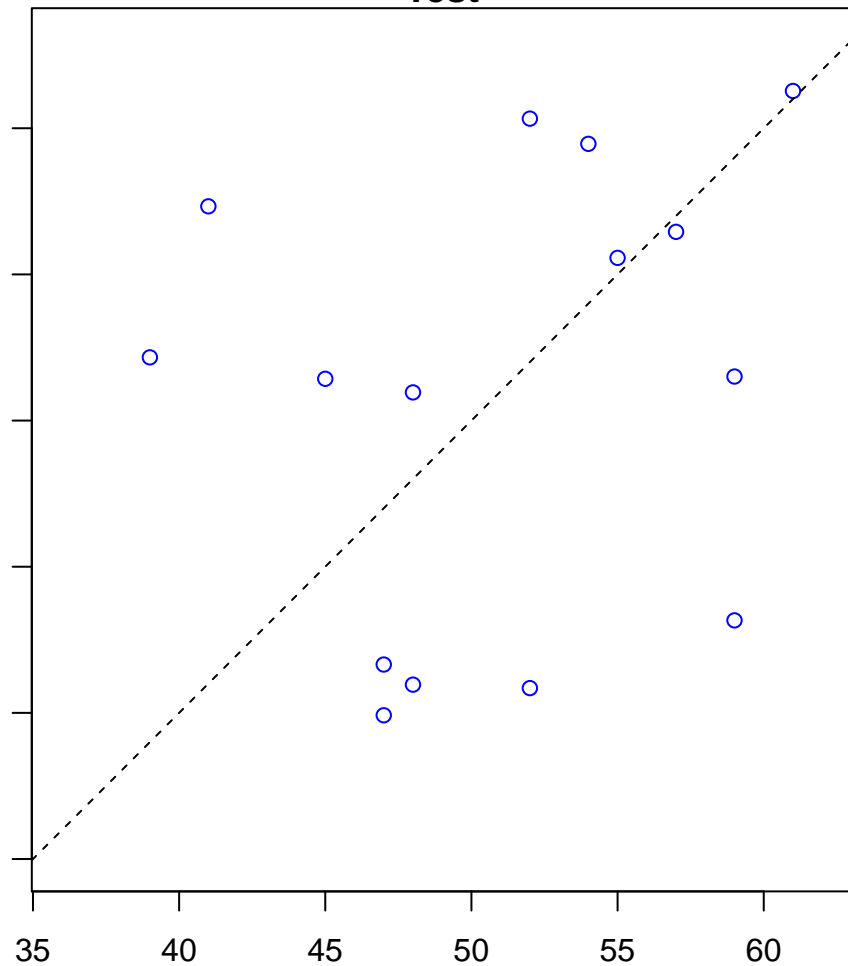


negative regulation of anion transport (Score: 5.011958)

Control

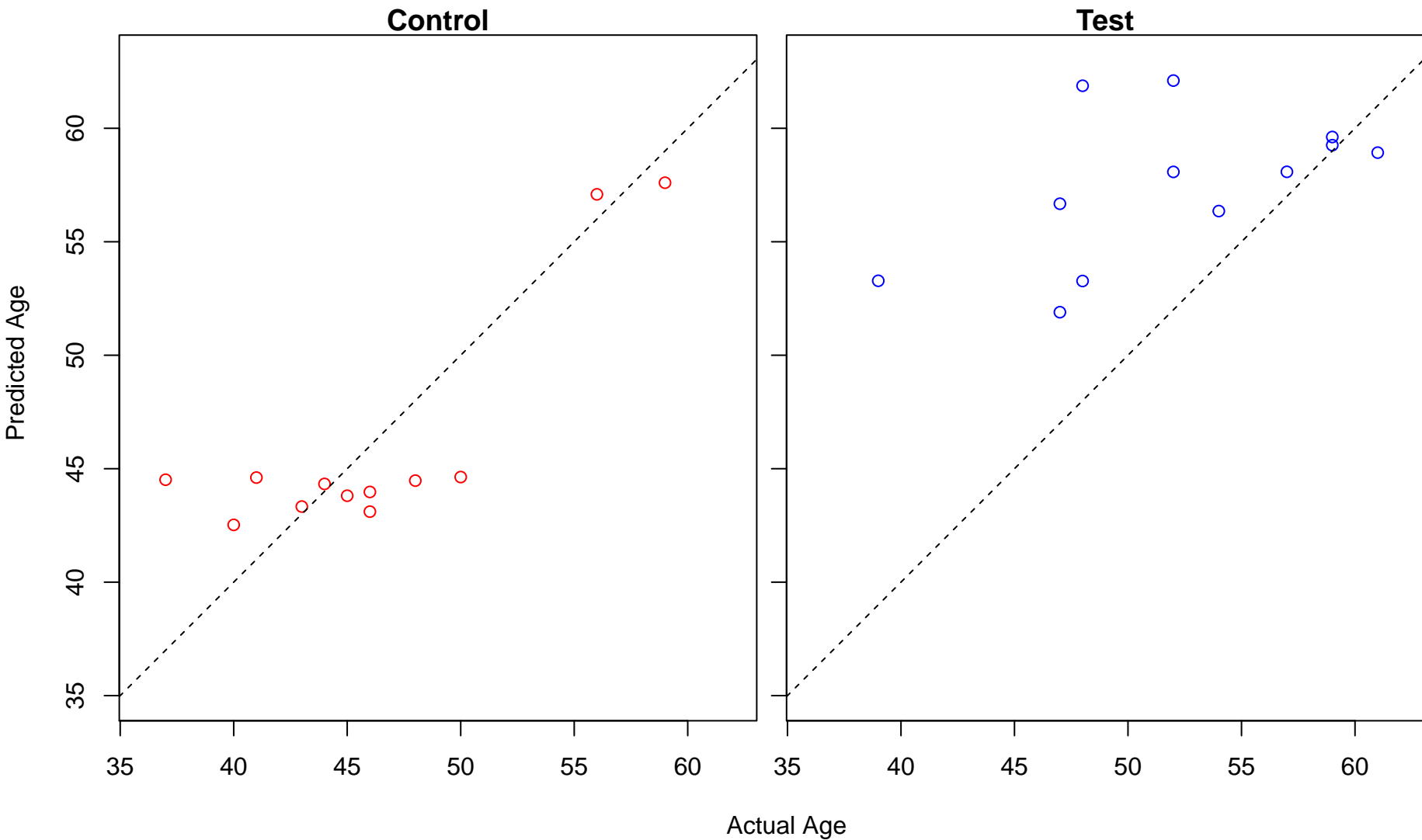


Test



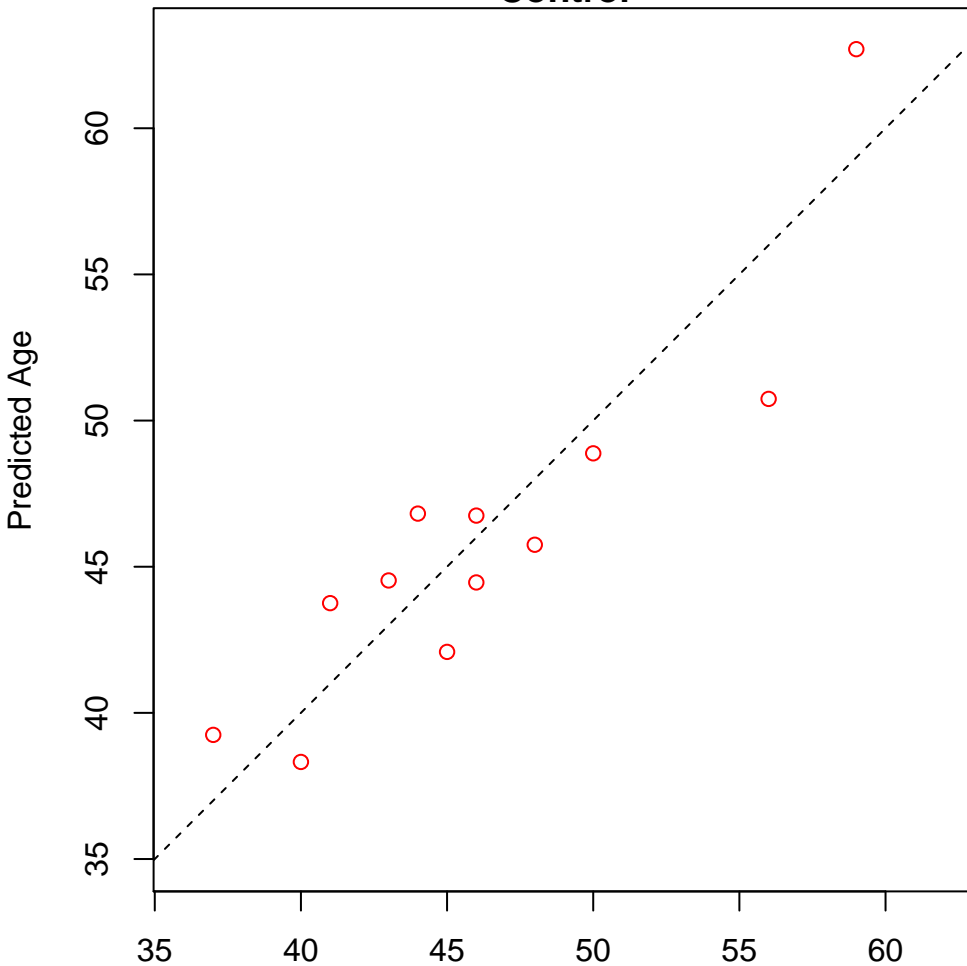
Actual Age

L-alpha-amino acid transmembrane transport (Score: 5.005313)

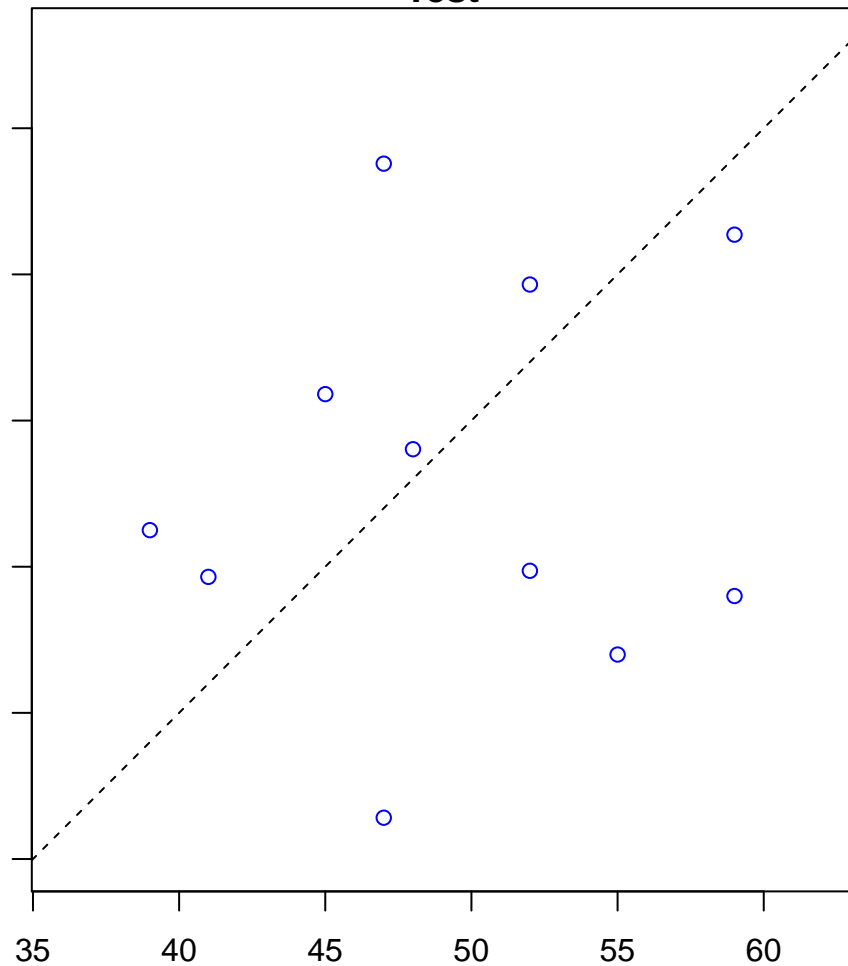


regulation of synapse organization (Score: 4.999167)

Control

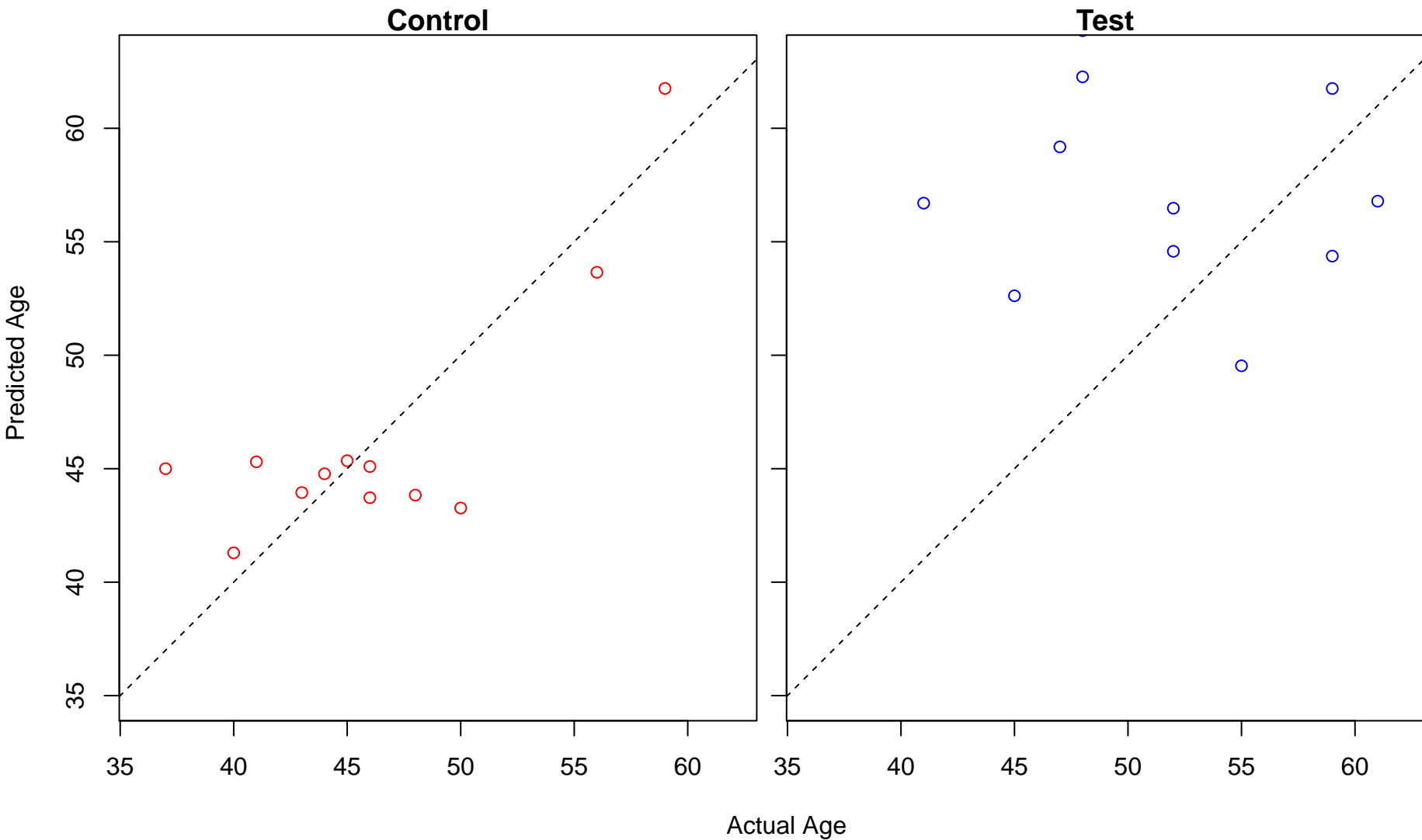


Test

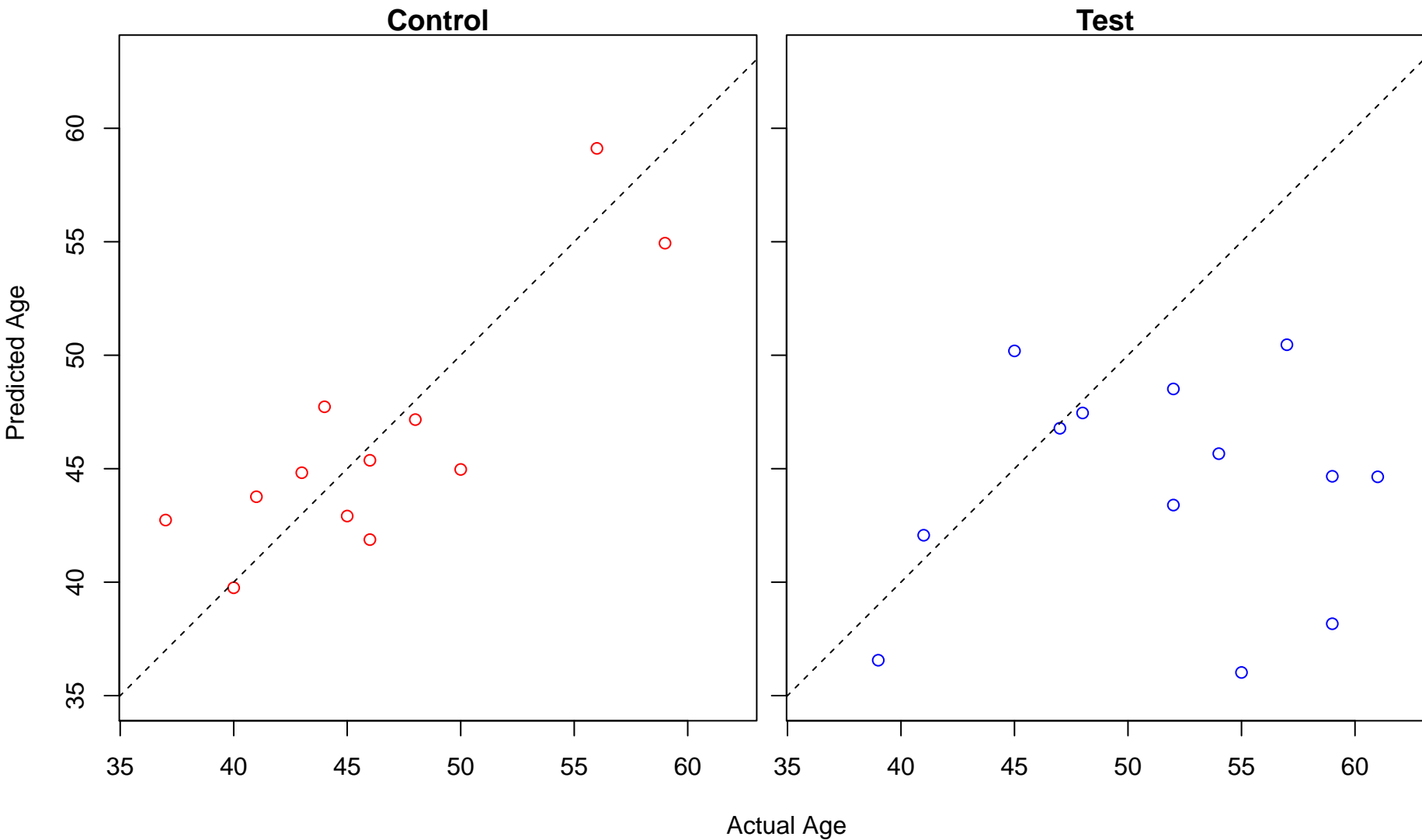


Actual Age

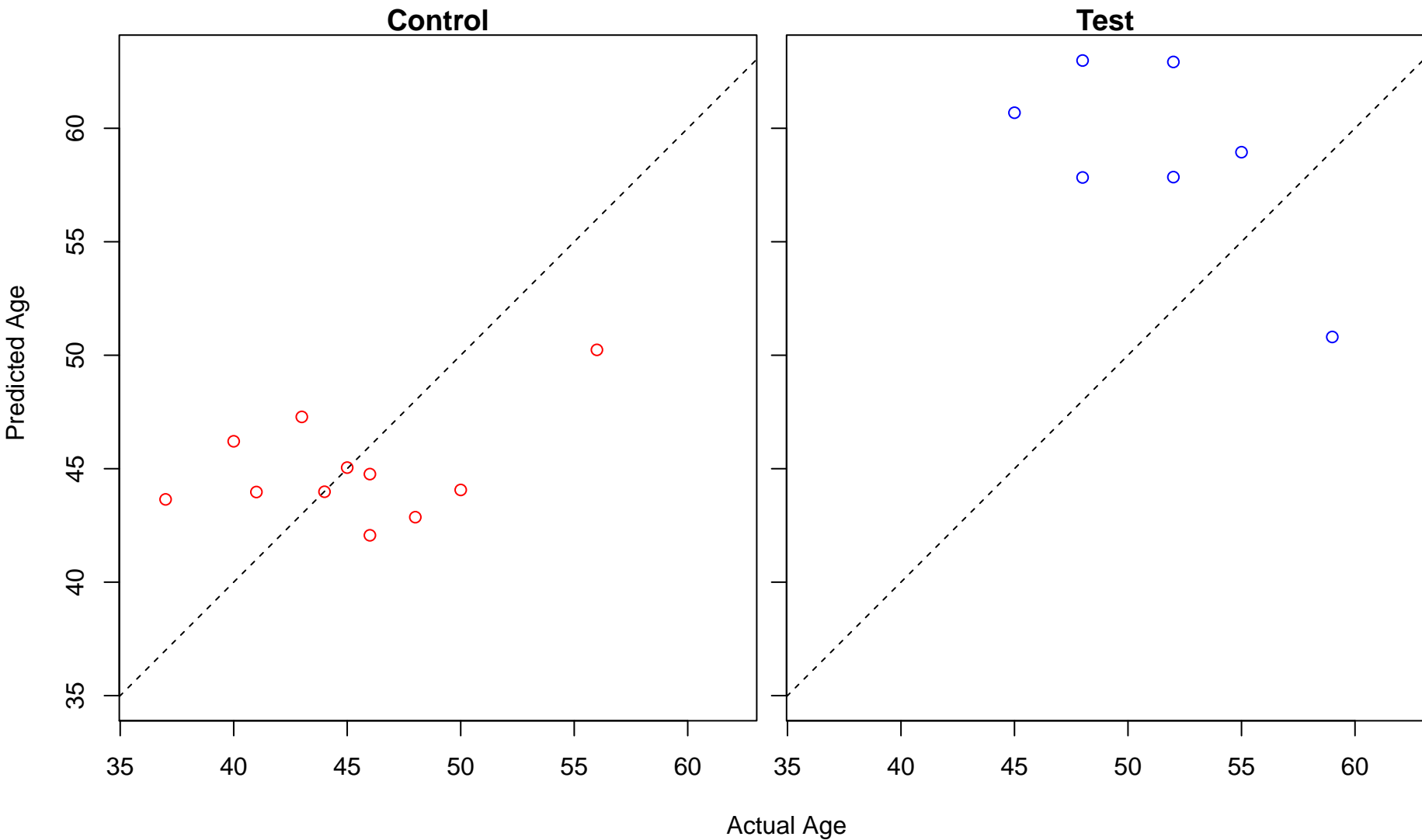
regulation of transcription by glucose (Score: 4.997759)



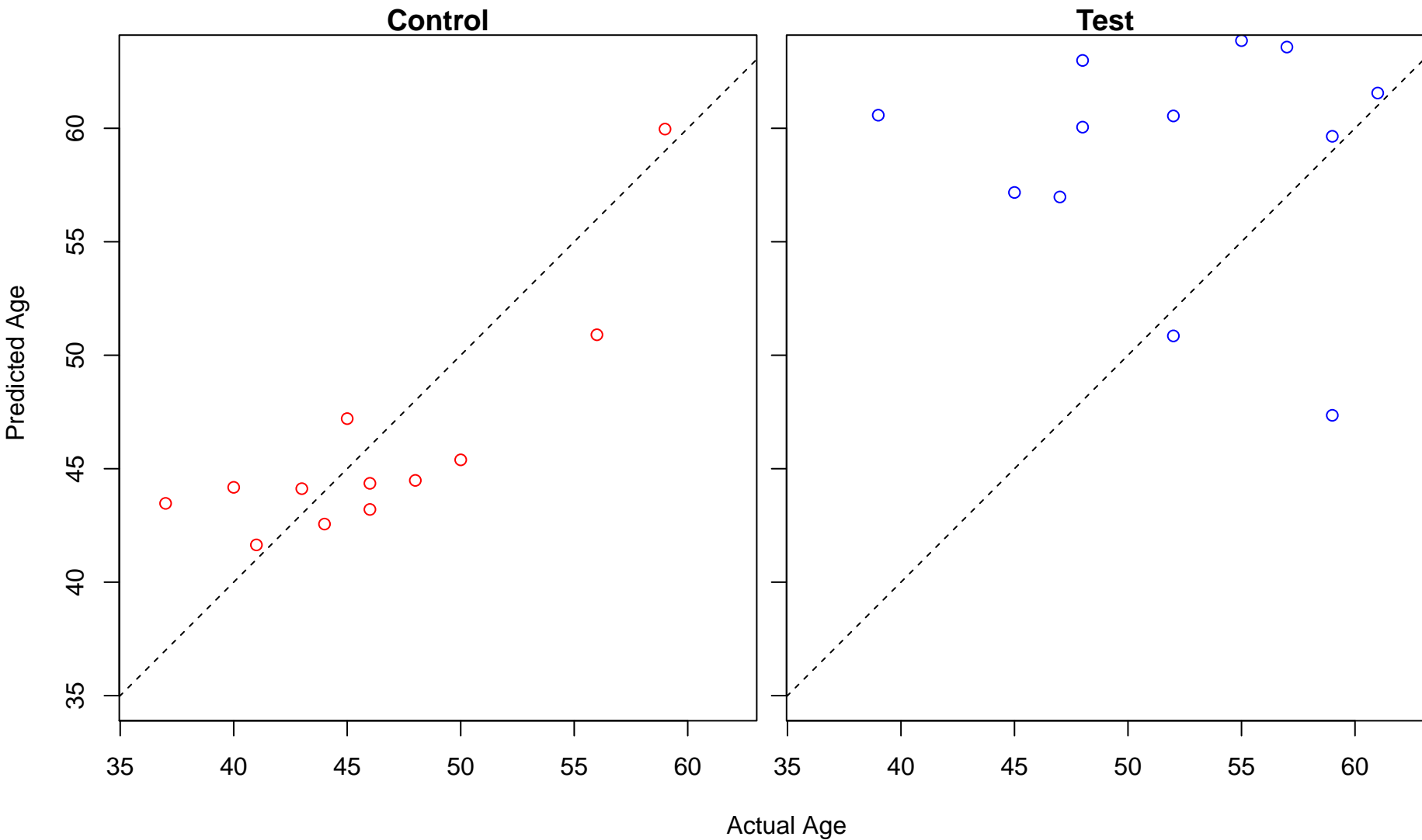
vacuole organization (Score: 4.989360)



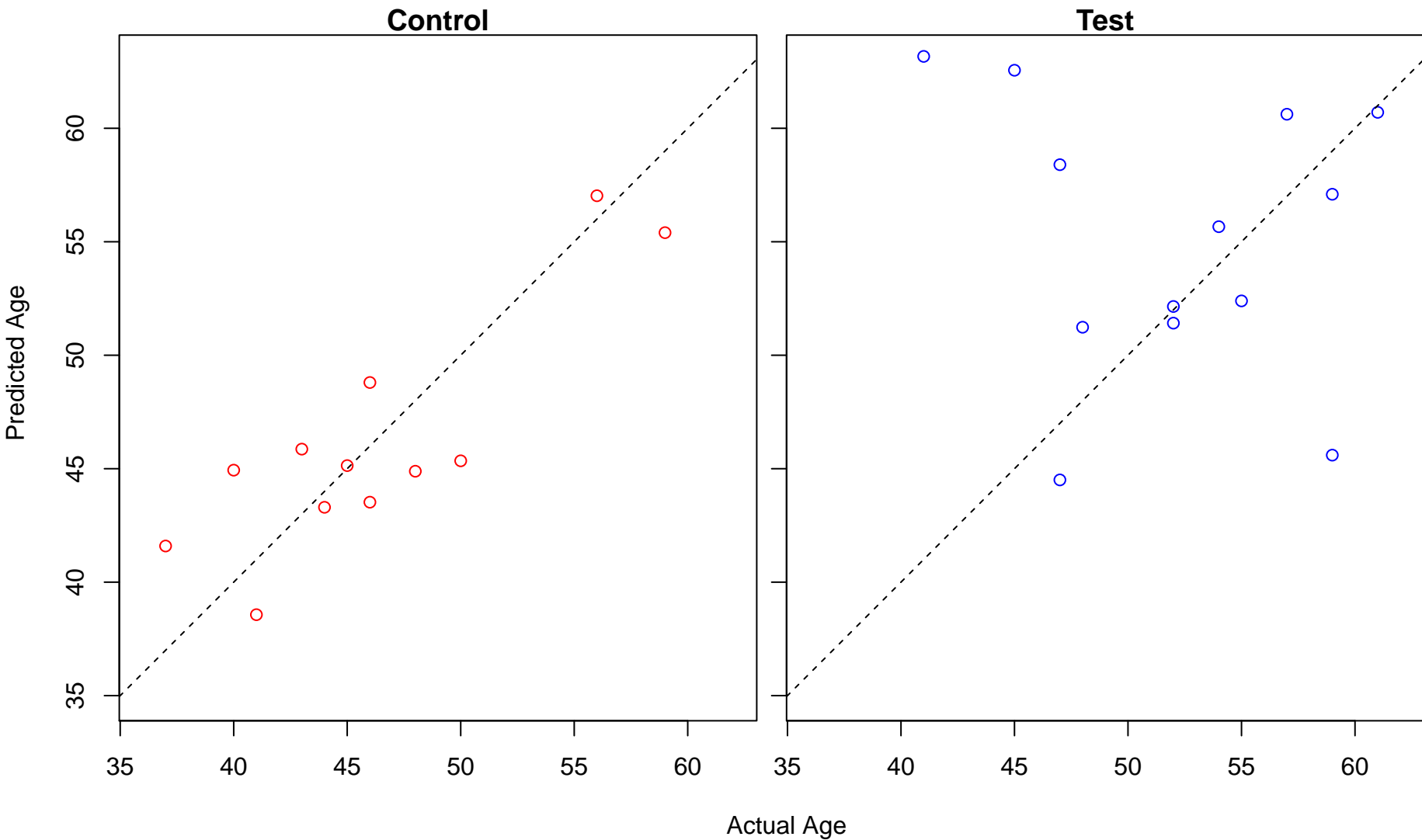
fructose 1,6-bisphosphate metabolic process (Score: 4.977368)



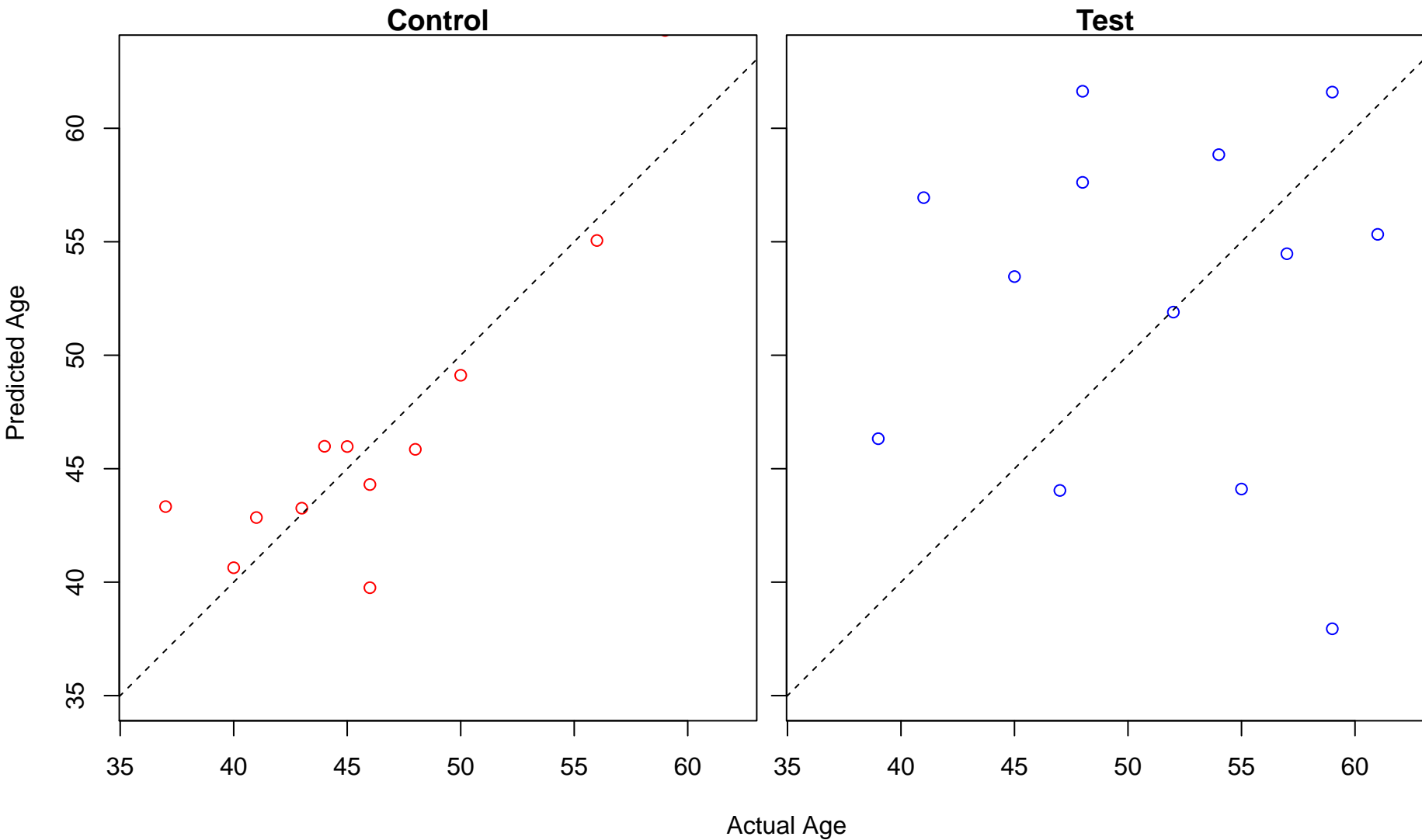
negative regulation of organic acid transport (Score: 4.966621)



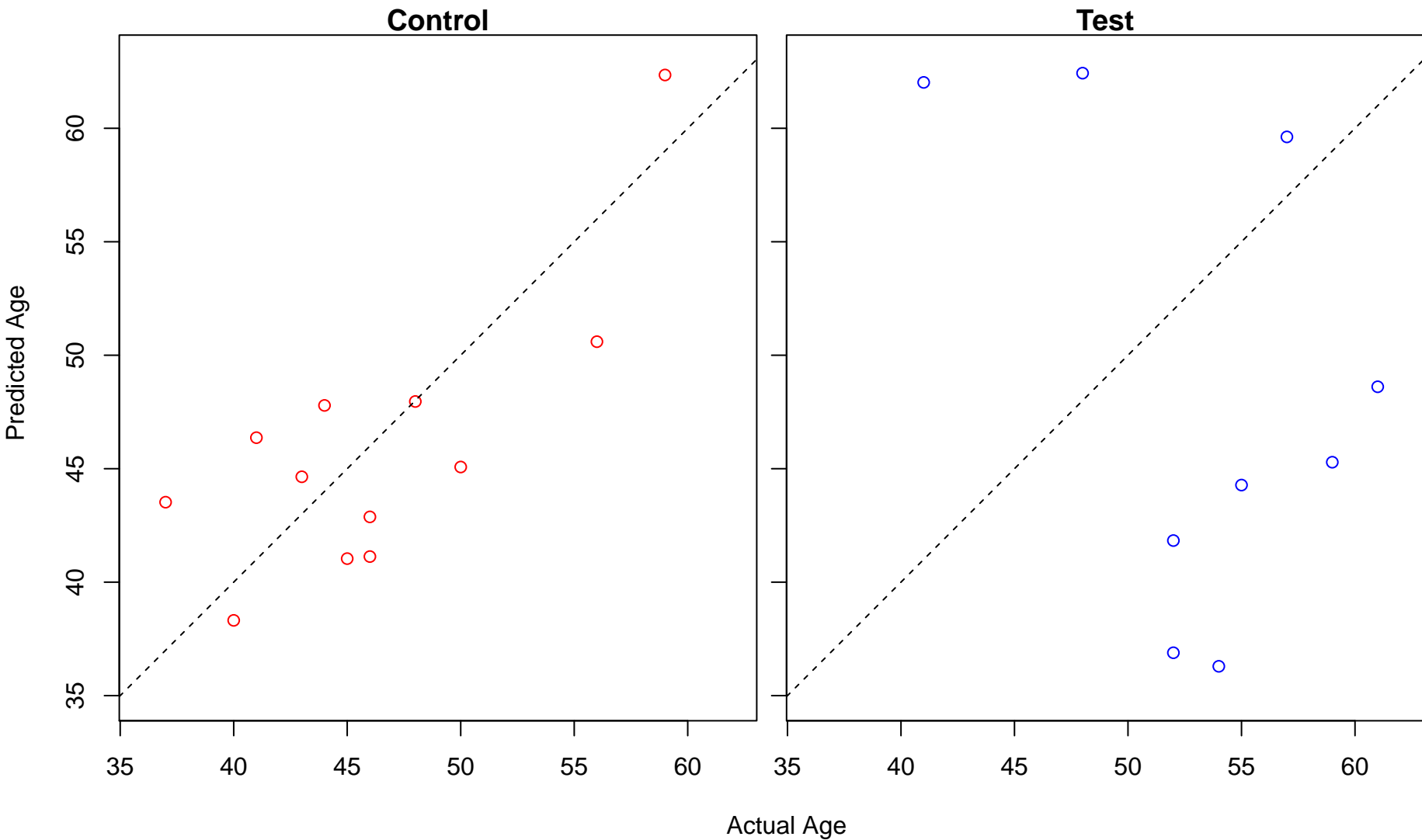
embryonic hemopoiesis (Score: 4.962588)



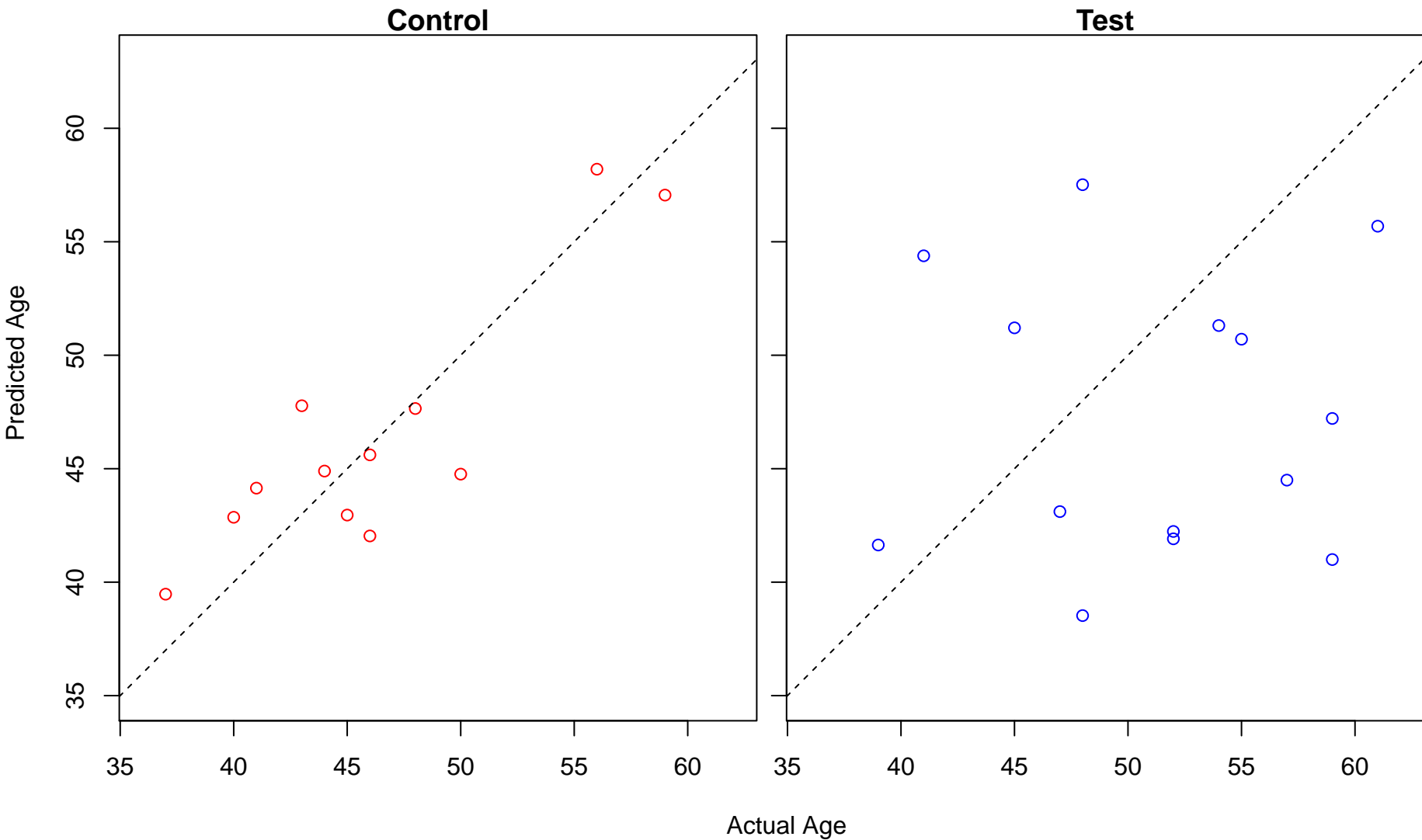
regulation of oxidoreductase activity (Score: 4.955131)



epidermis development (Score: 4.954017)

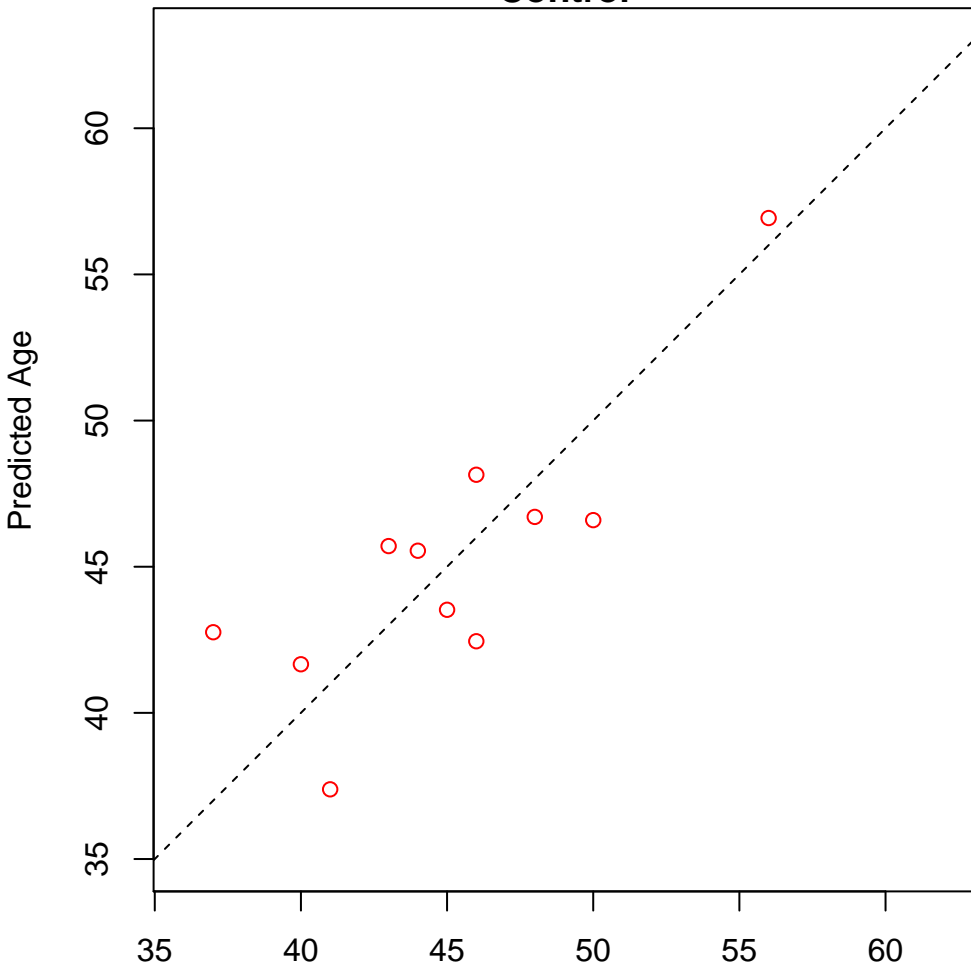


modulation of synaptic transmission (Score: 4.953200)

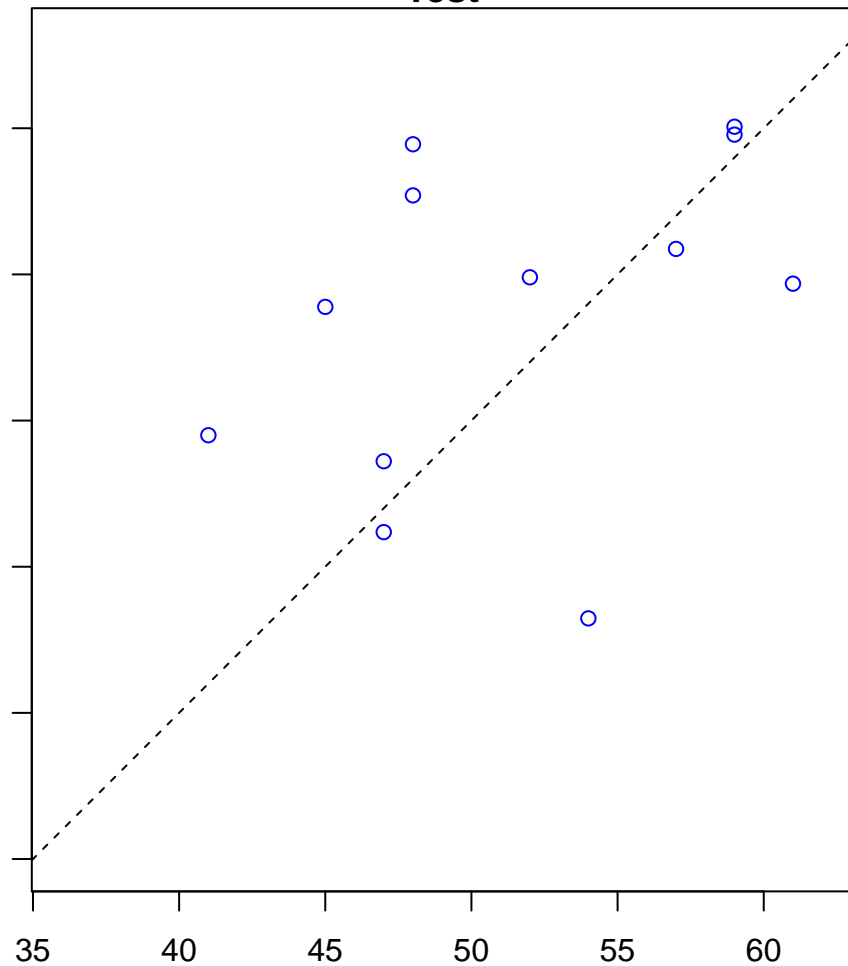


NLS-bearing protein import into nucleus (Score: 4.944394)

Control

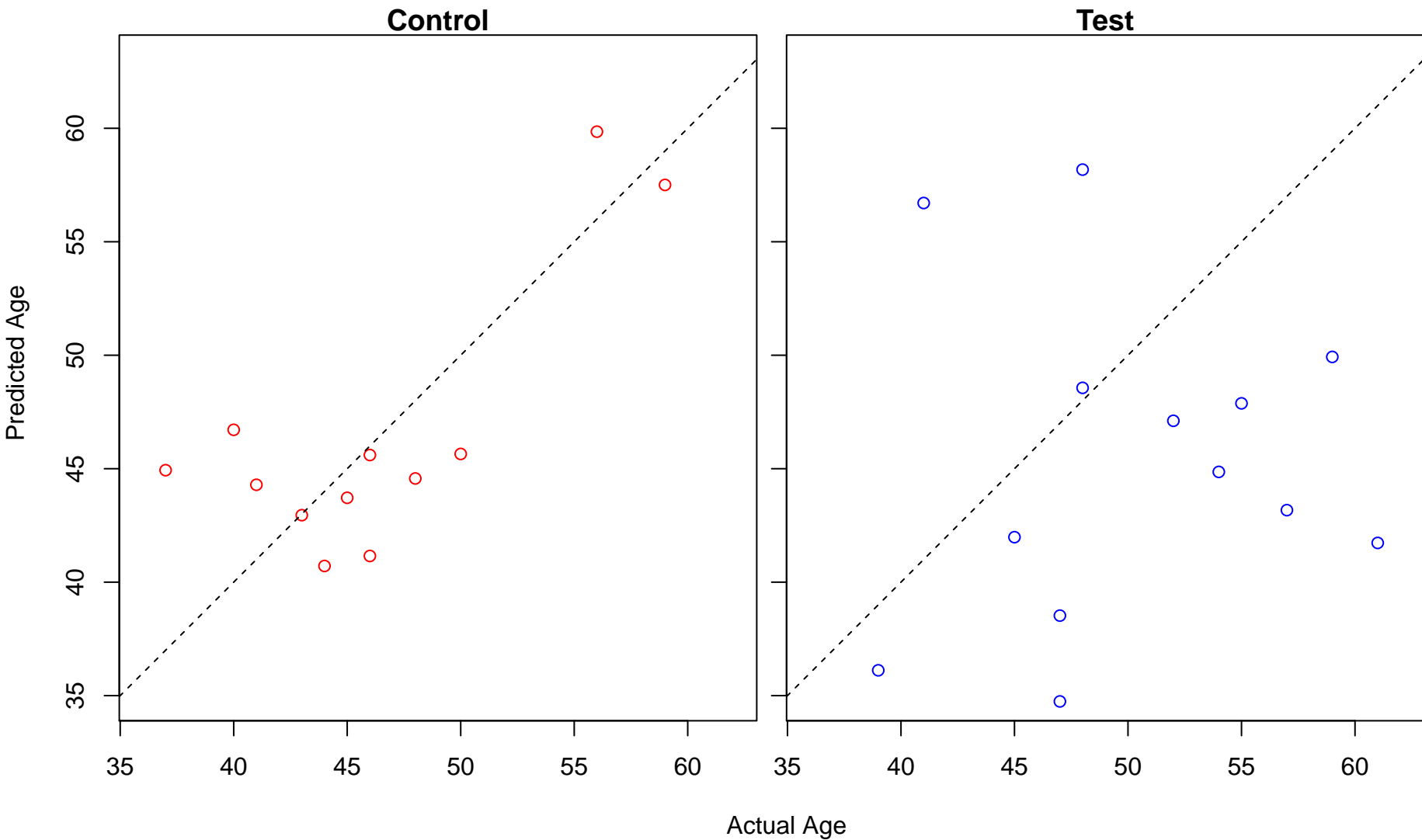


Test



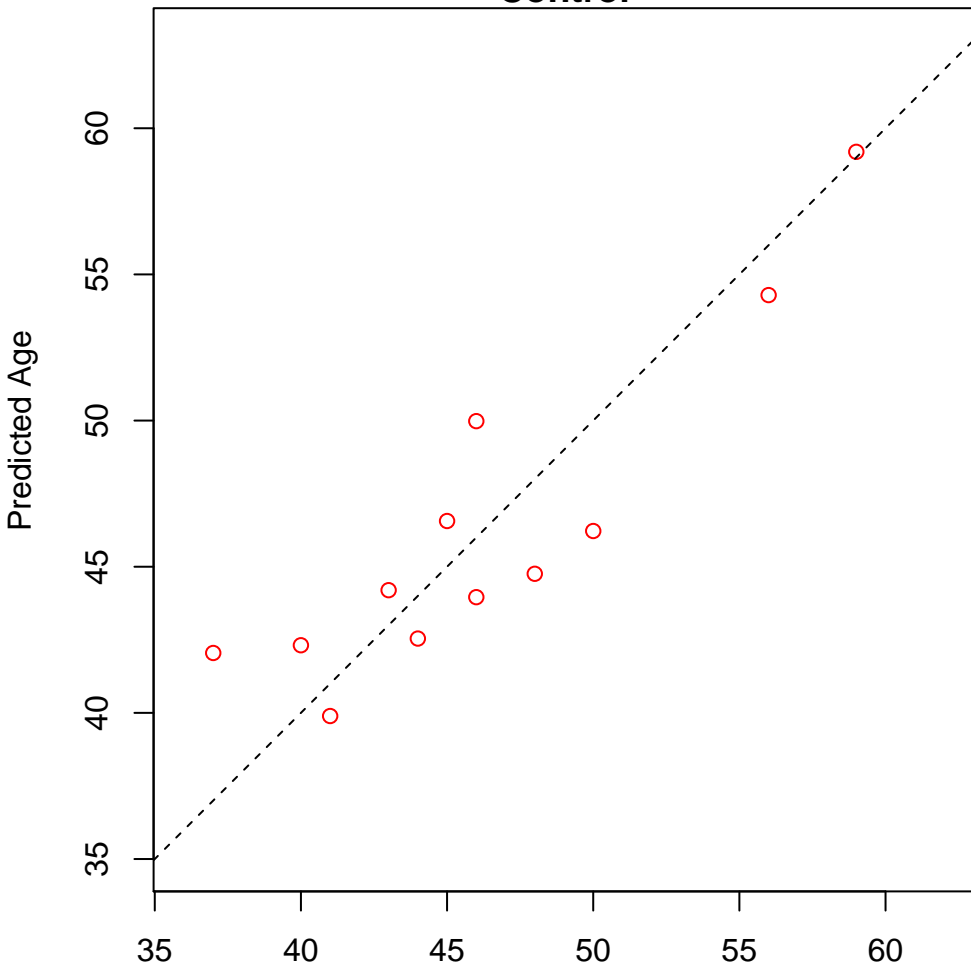
Actual Age

retrograde axonal transport (Score: 4.938694)

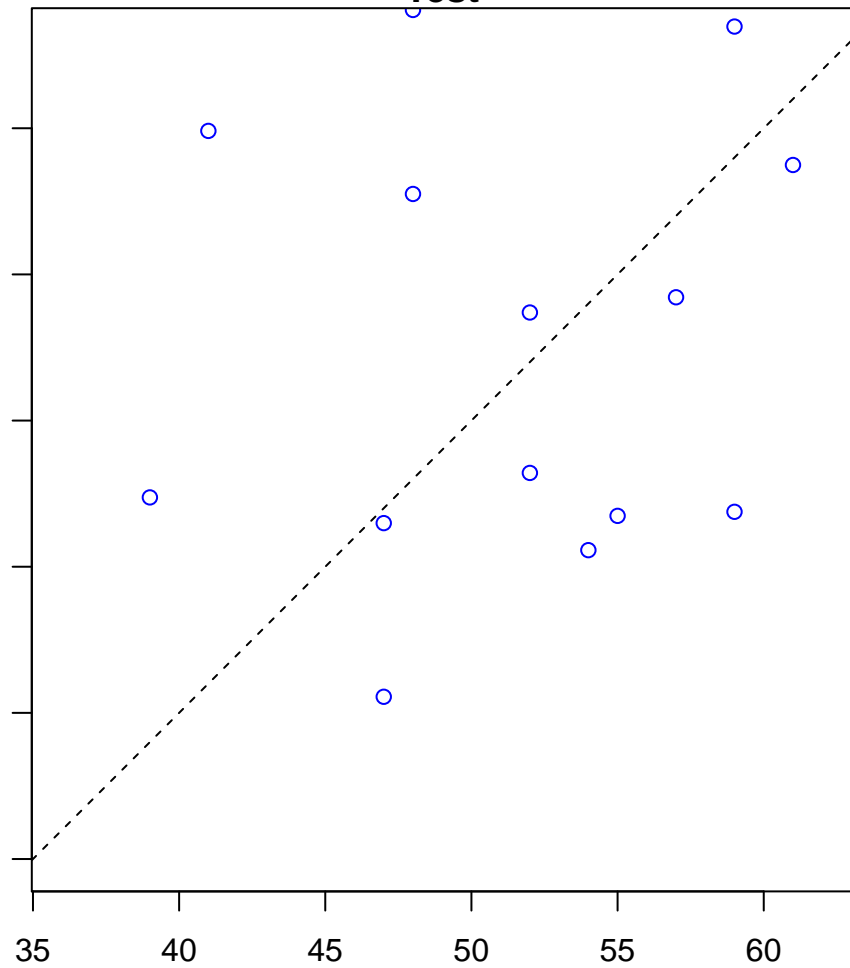


venous blood vessel development (Score: 4.926698)

Control

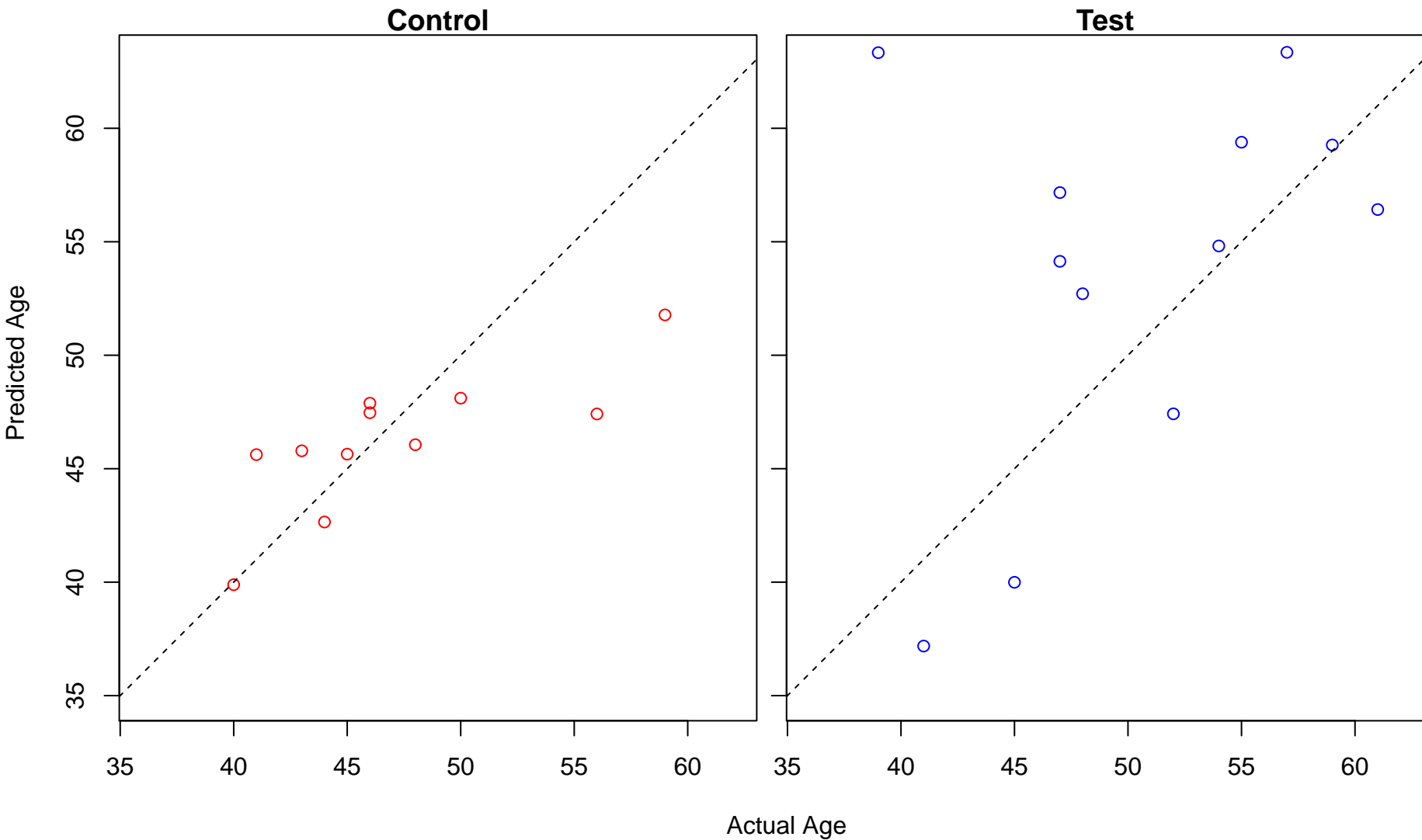


Test

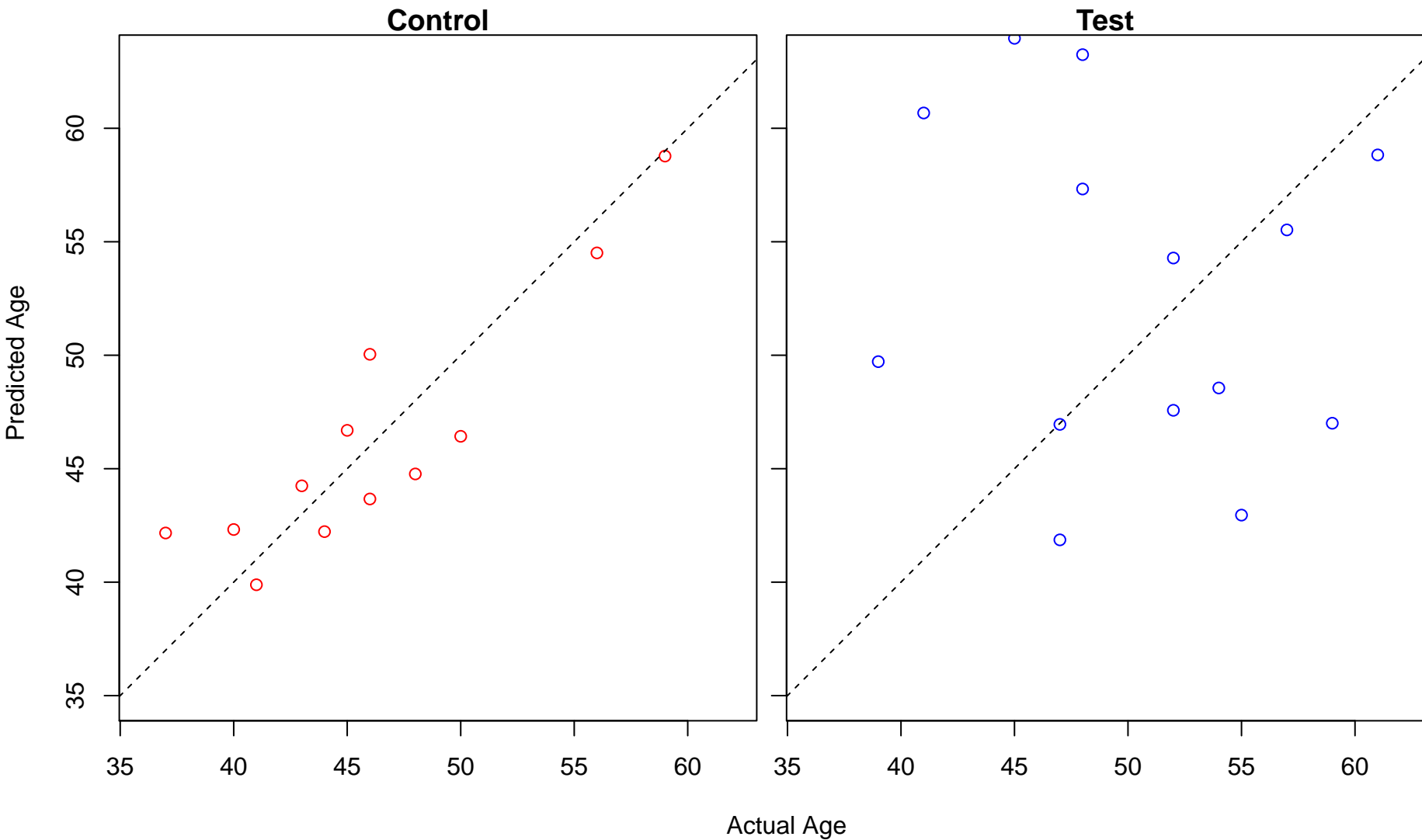


Actual Age

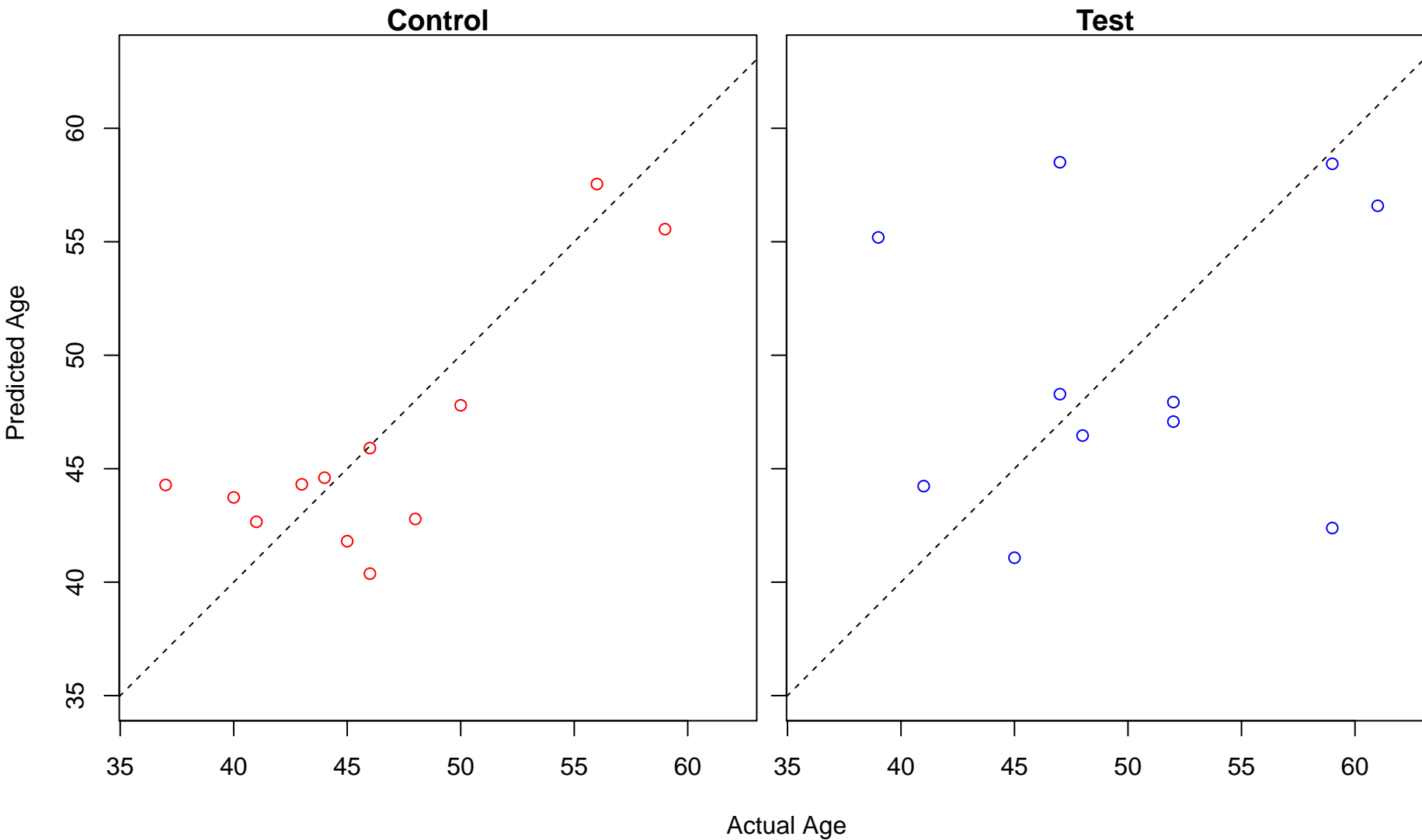
regulation of cGMP biosynthetic process (Score: 4.926373)



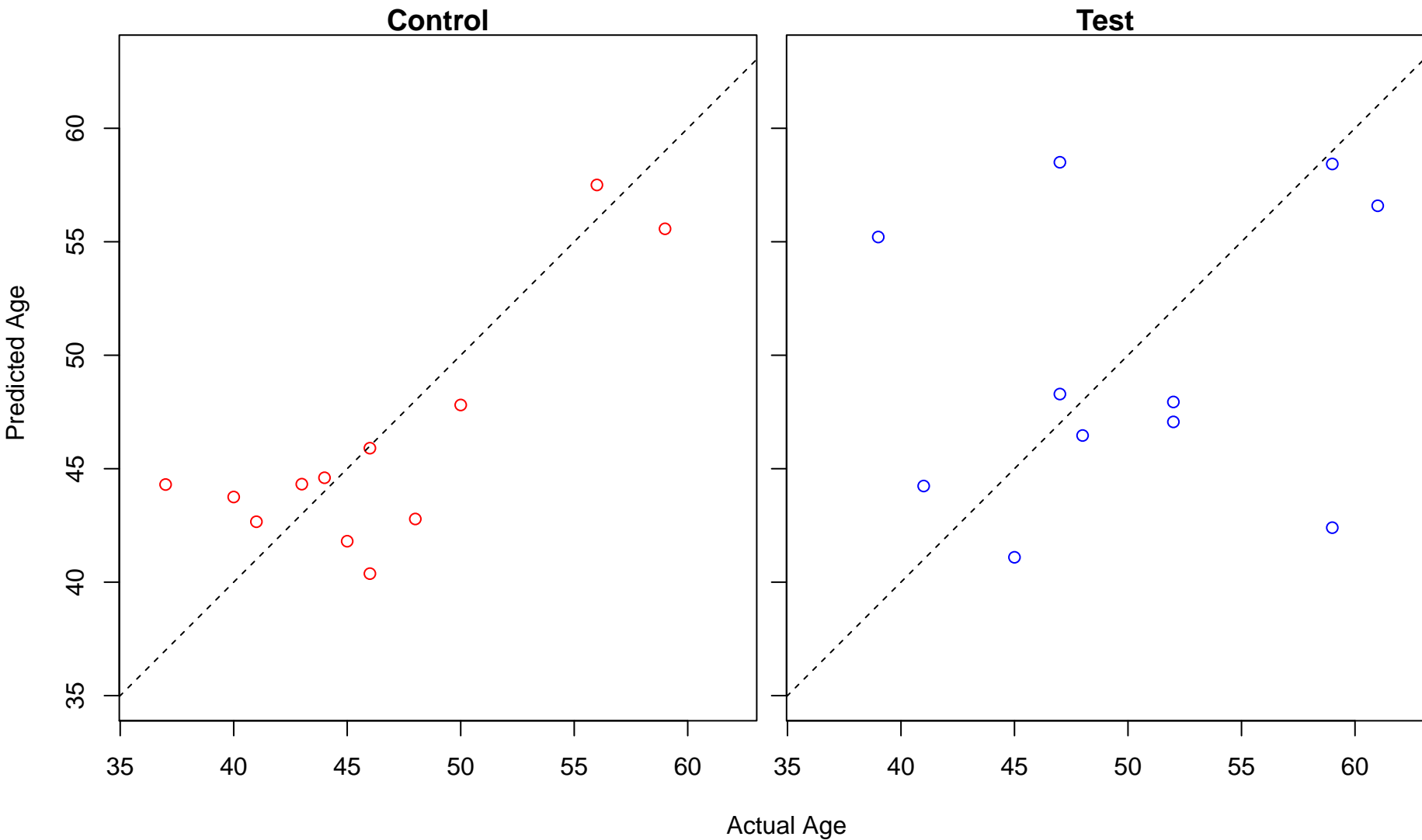
lymph vessel morphogenesis (Score: 4.917586)



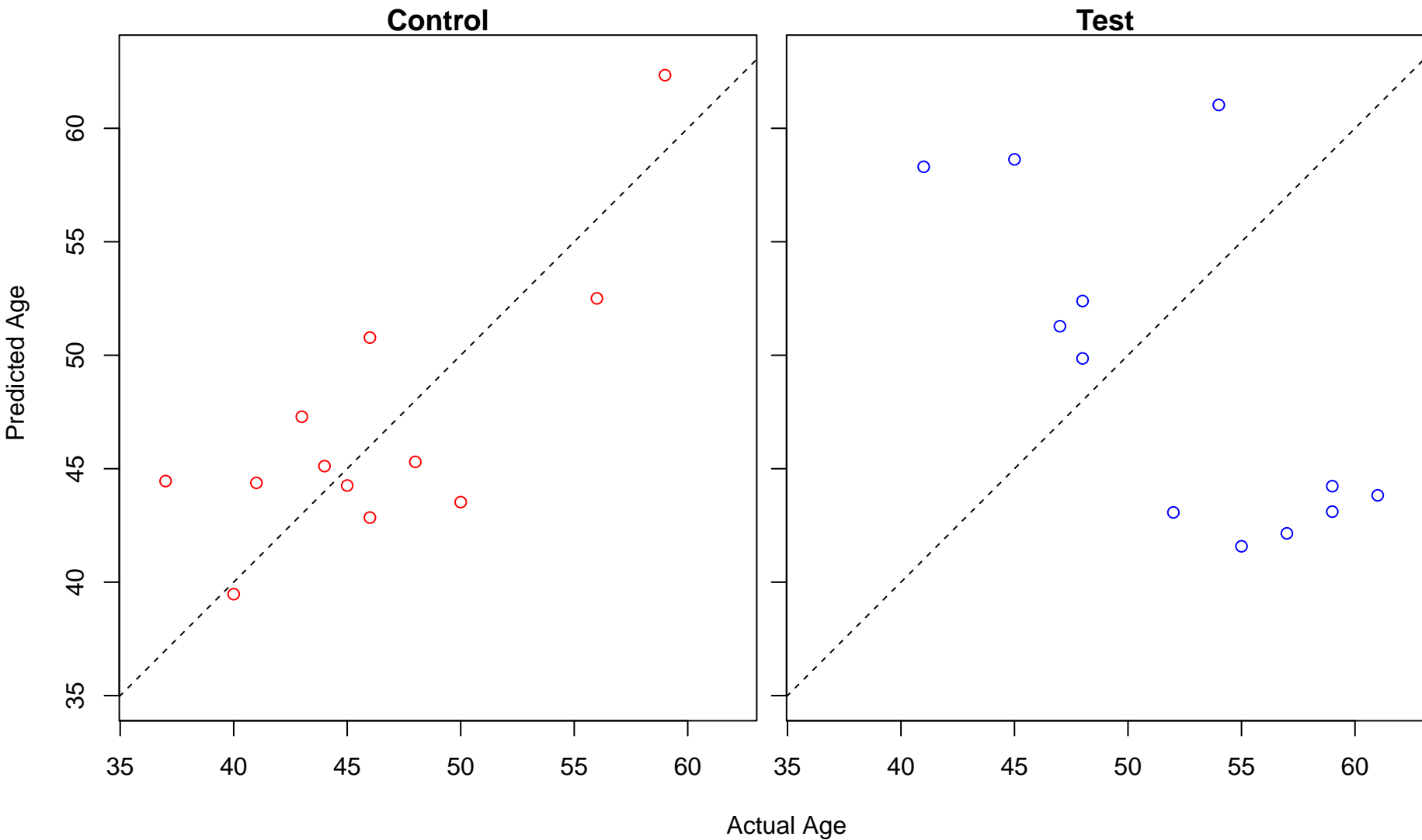
cellular potassium ion homeostasis (Score: 4.906267)



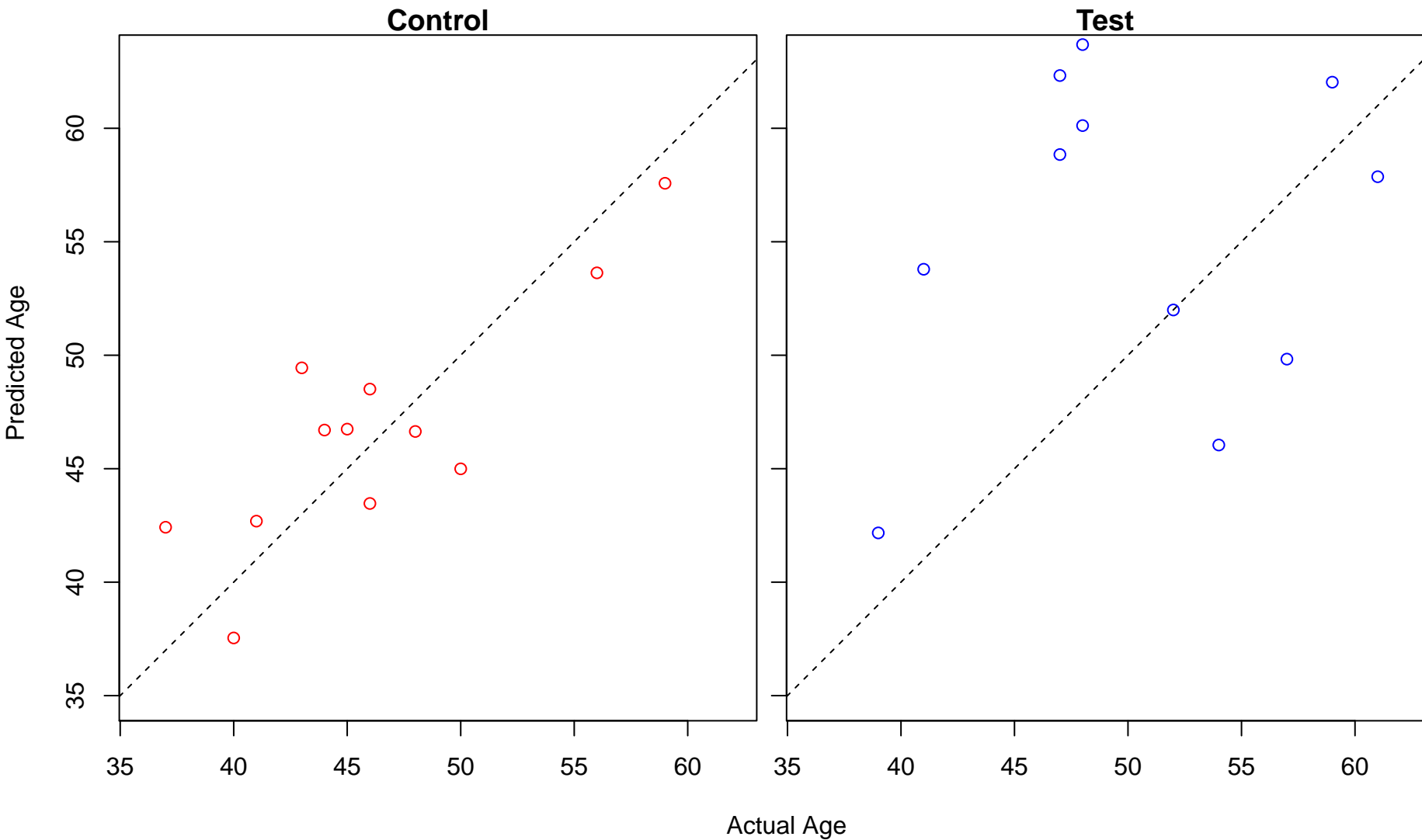
potassium ion homeostasis (Score: 4.903113)



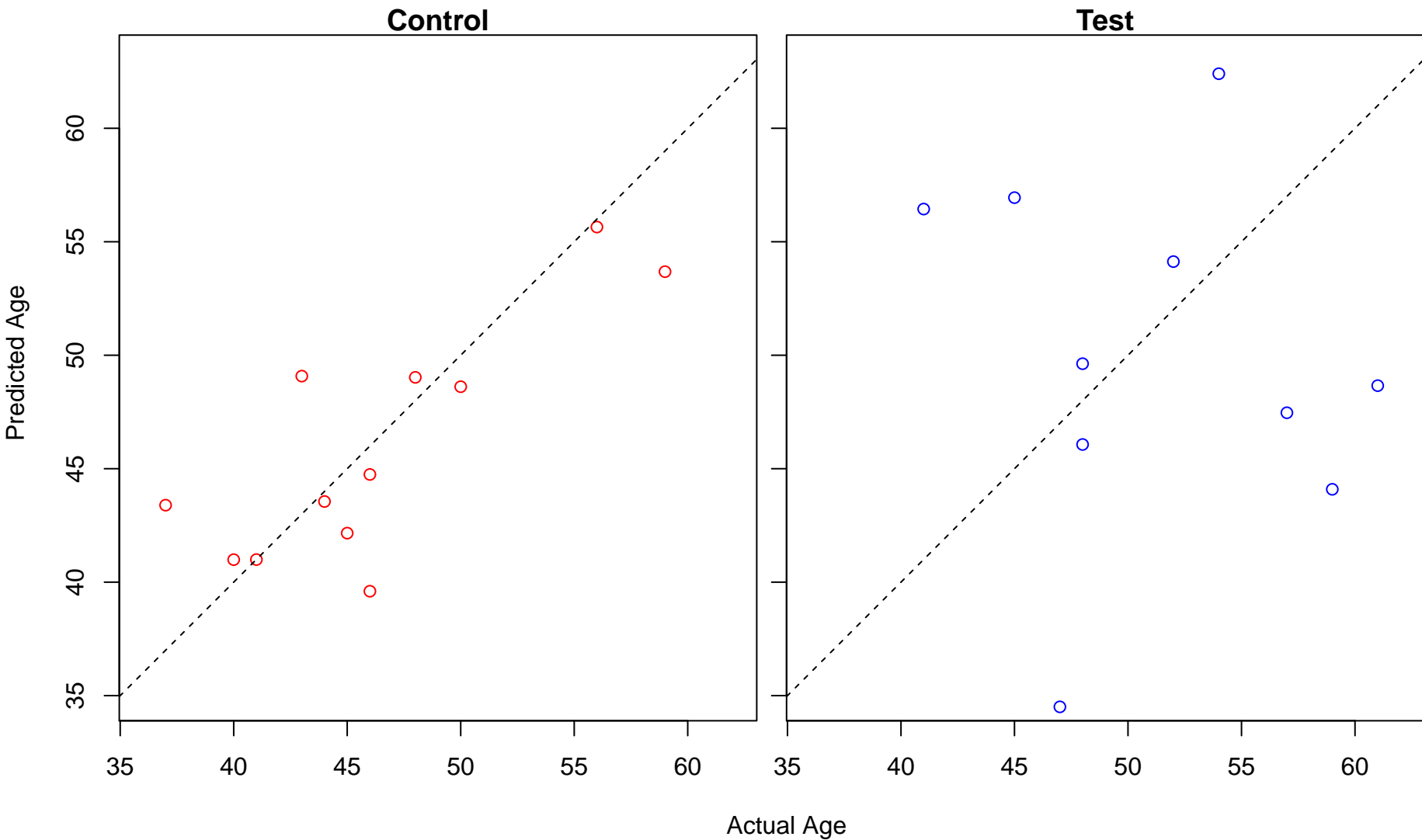
mRNA polyadenylation (Score: 4.900930)



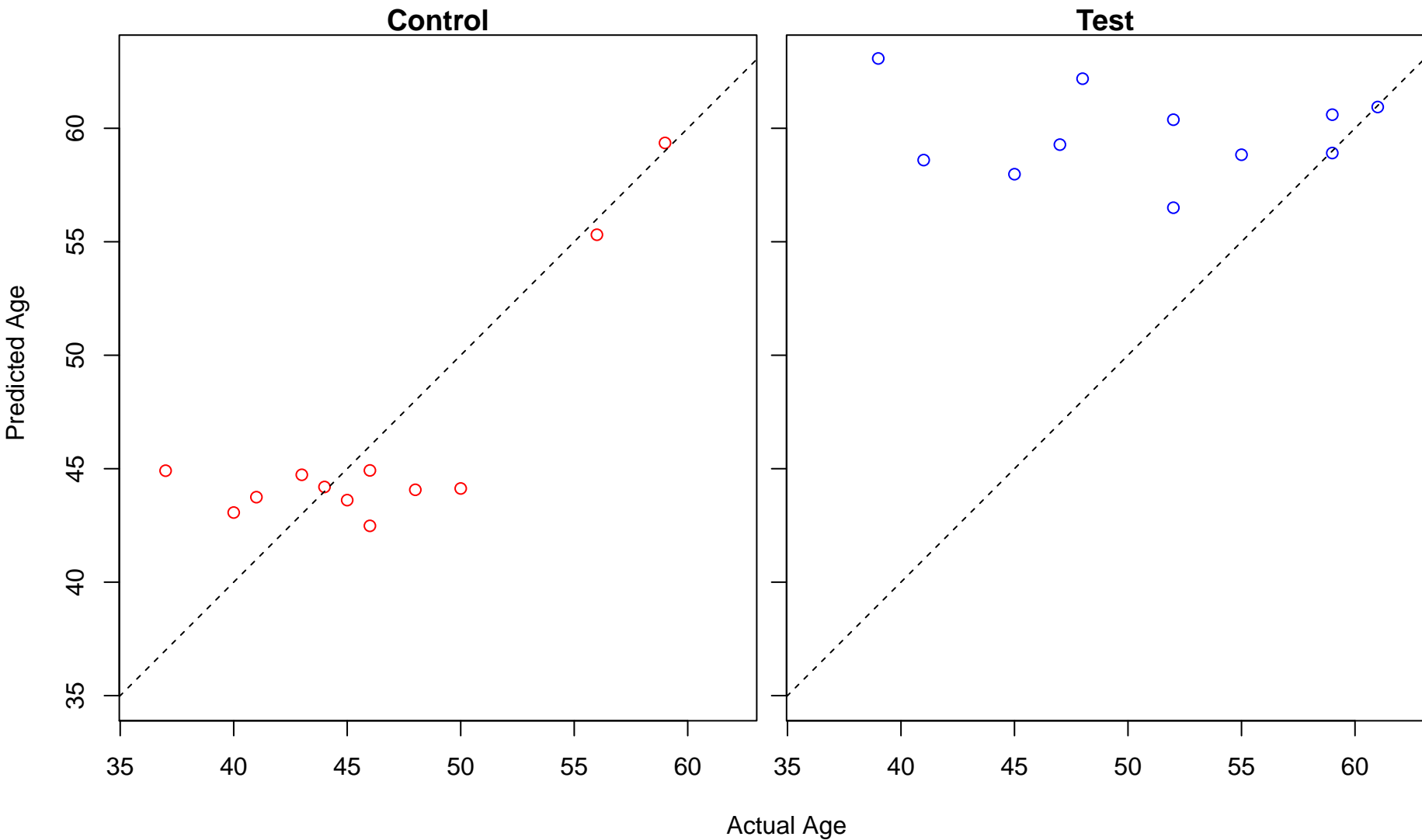
response to glucose (Score: 4.895220)



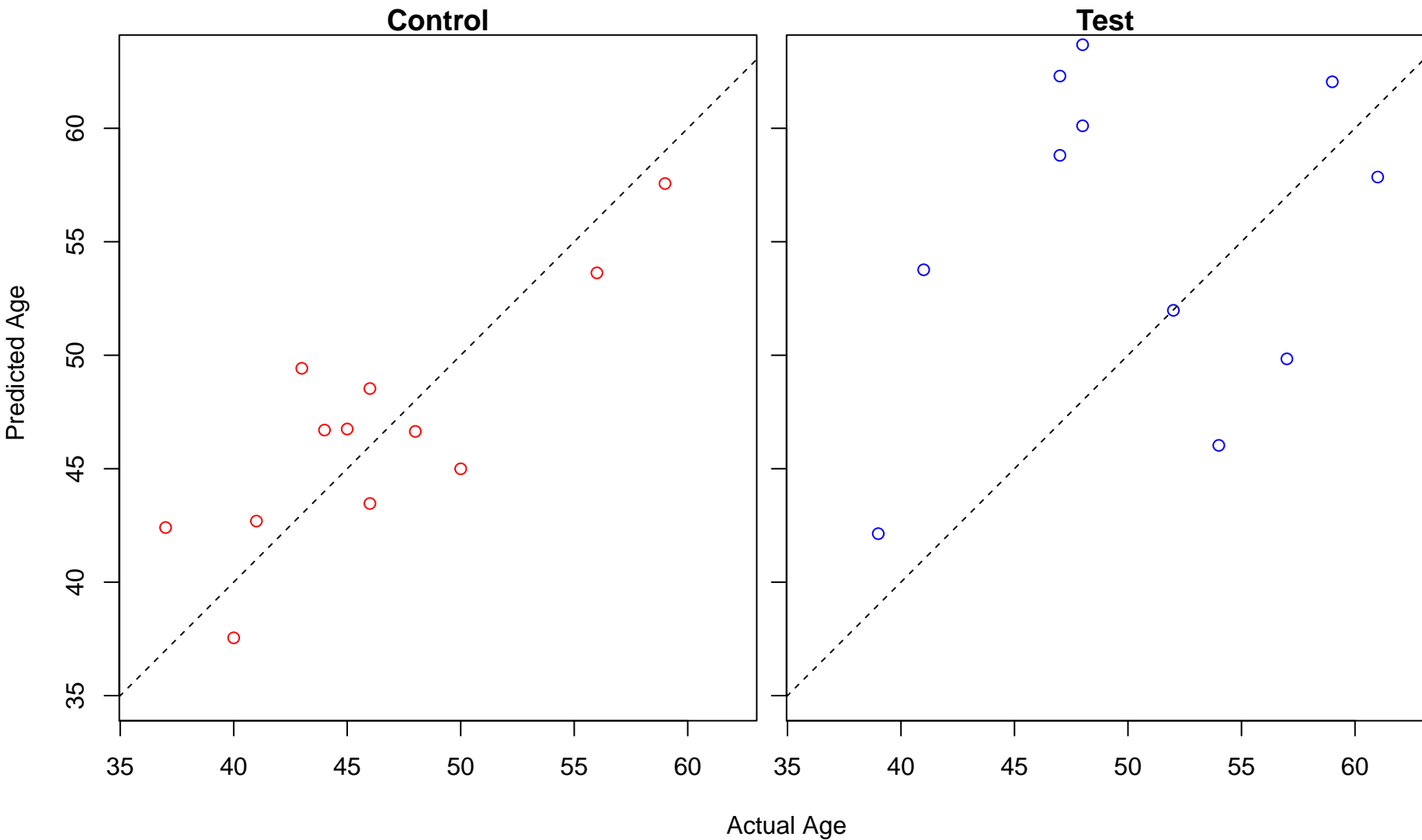
ethanolamine-containing compound metabolic process (Score: 4.892113)



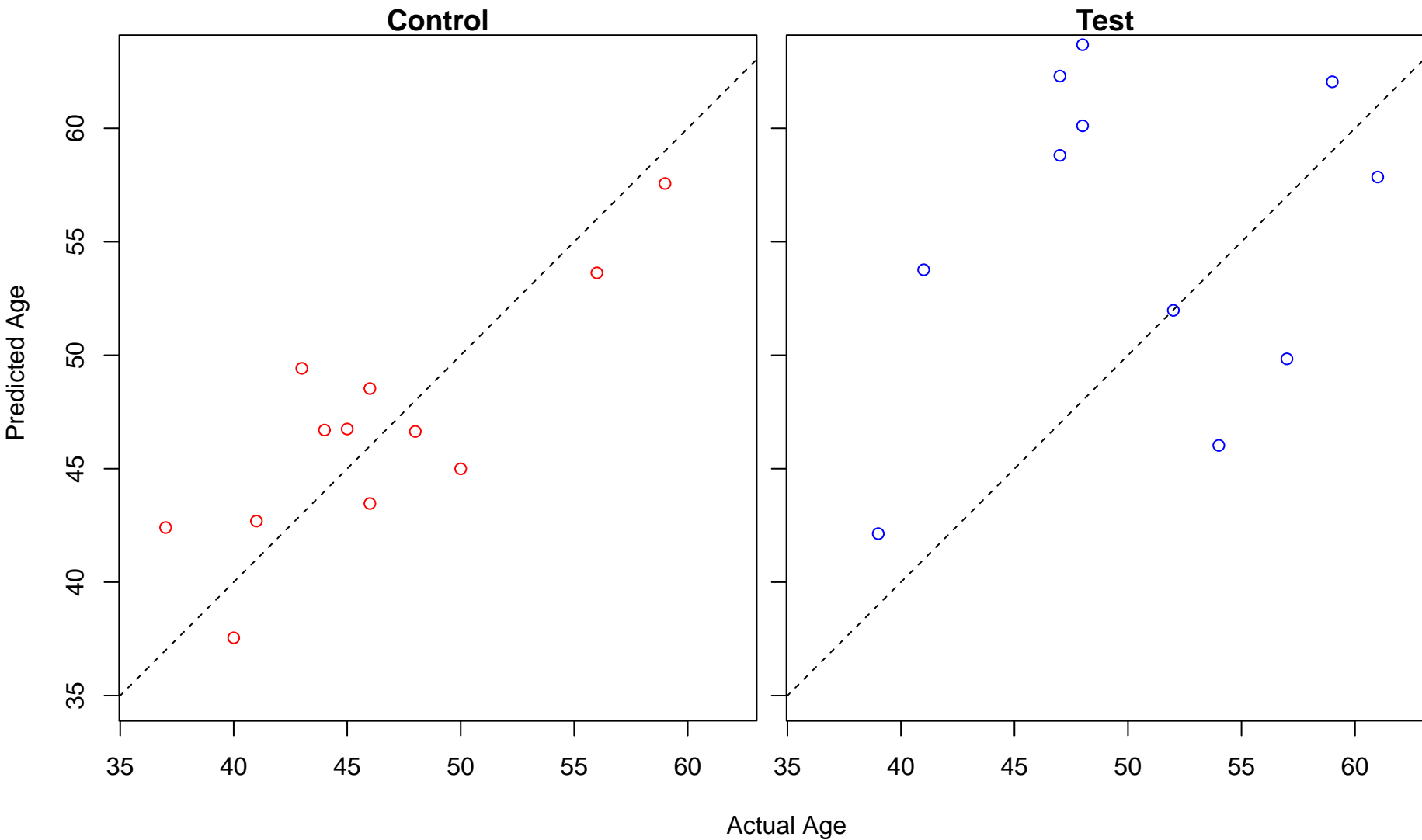
DNA methylation involved in gamete generation (Score: 4.892053)



response to hexose (Score: 4.891512)

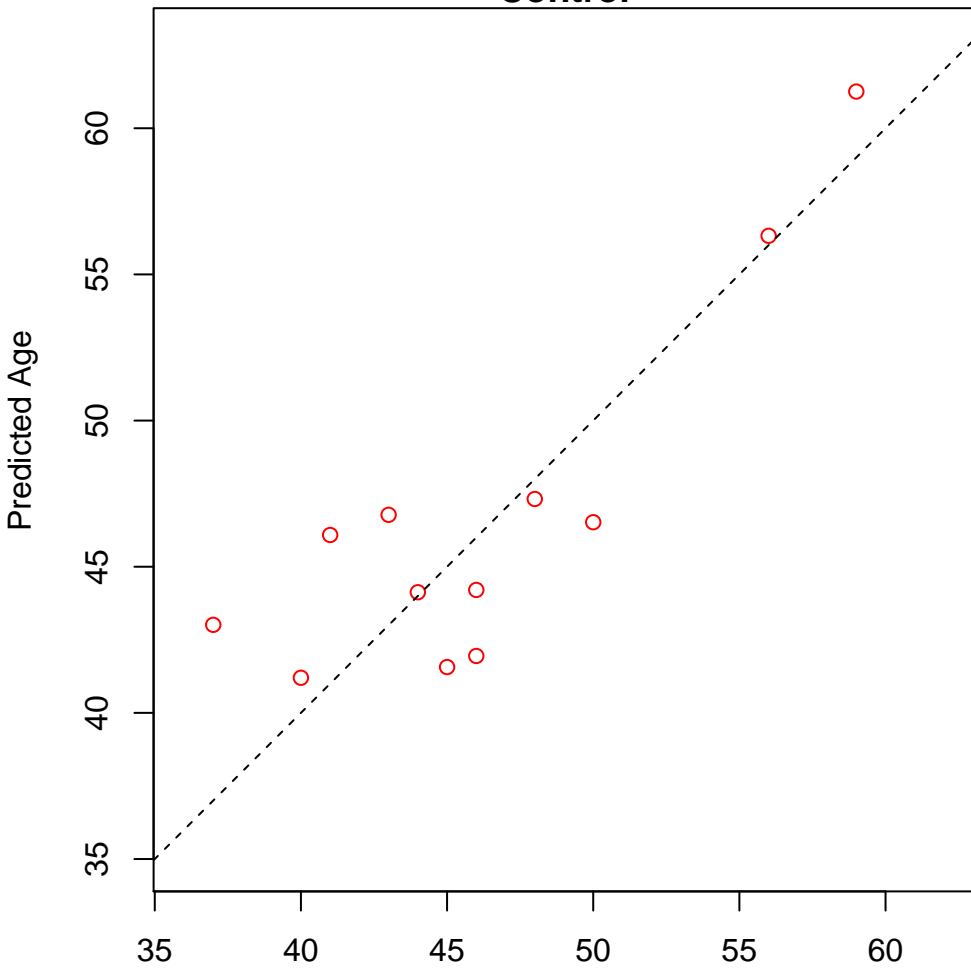


response to monosaccharide (Score: 4.891512)

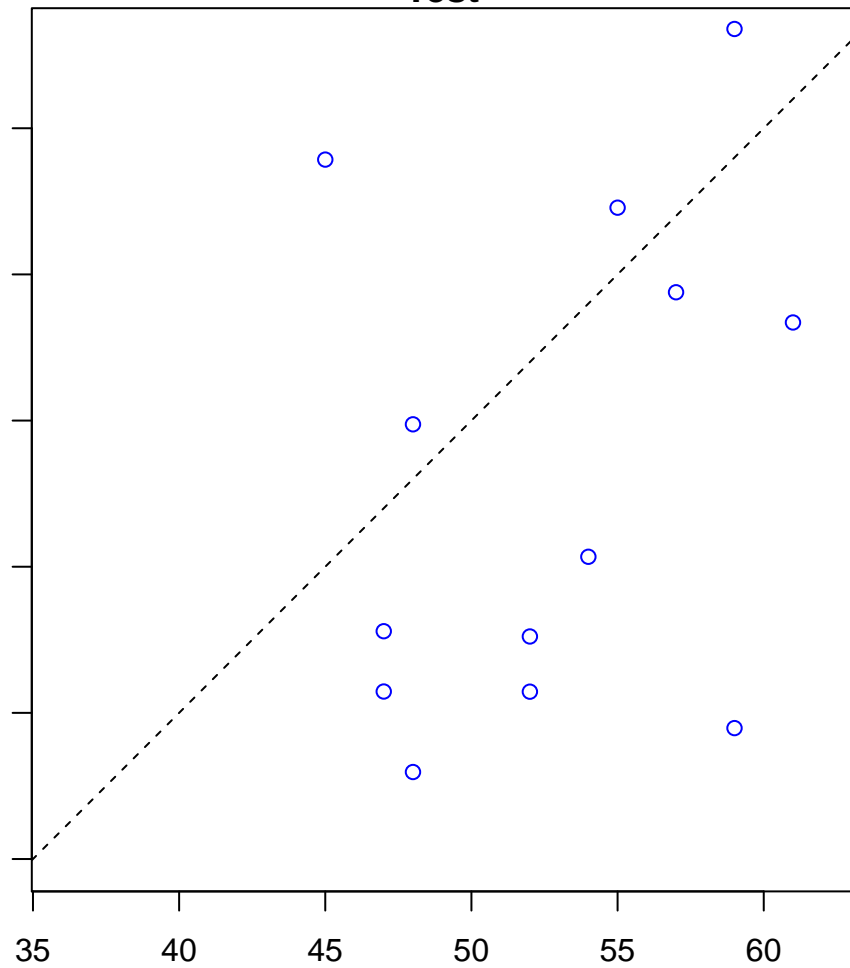


cellular response to hormone stimulus (Score: 4.890332)

Control



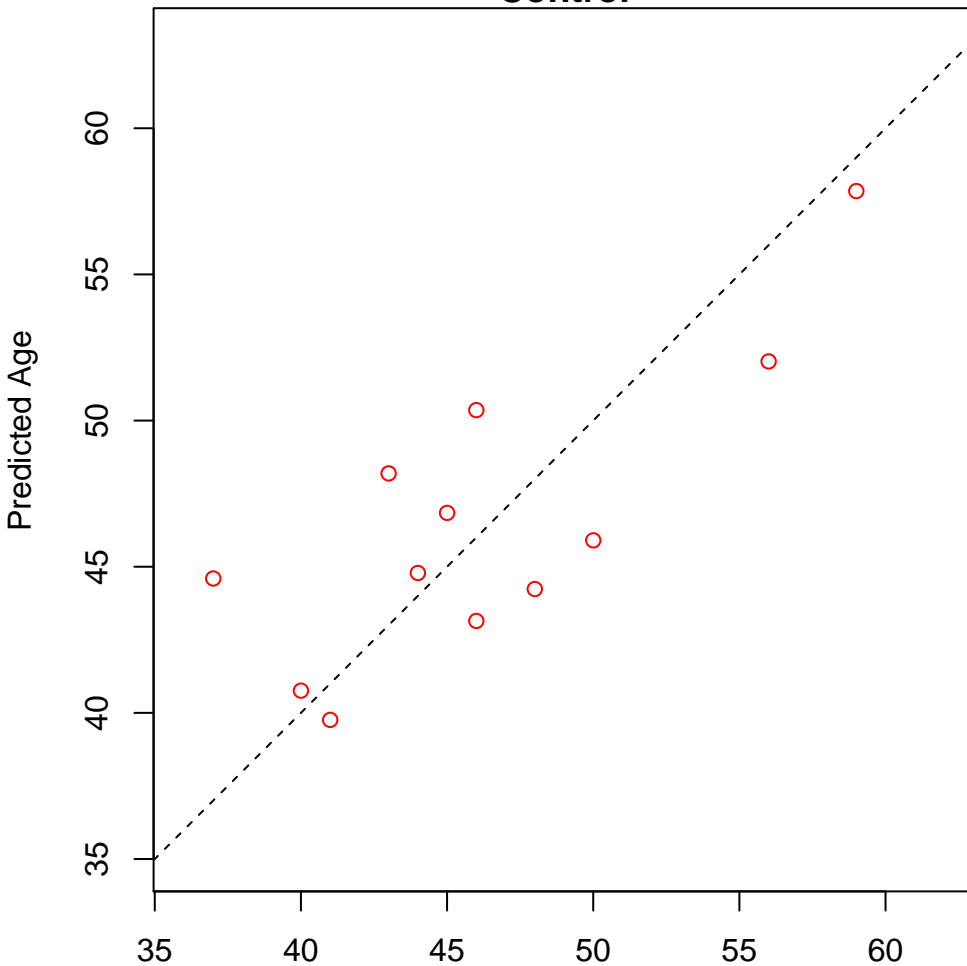
Test



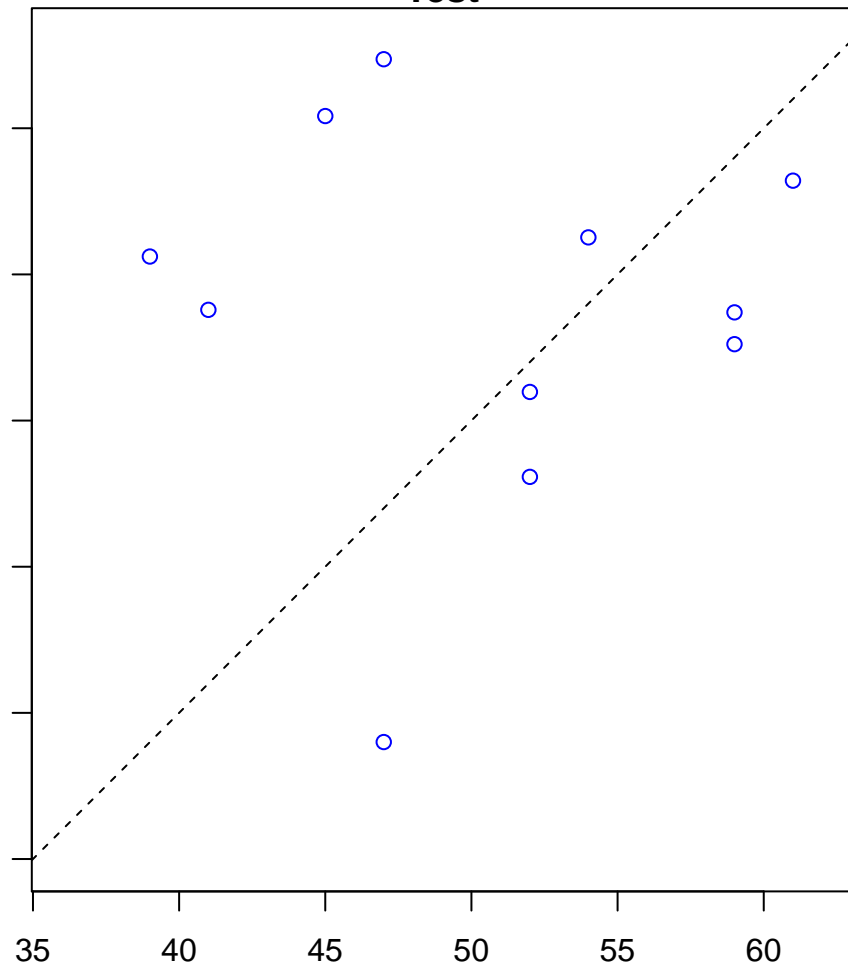
Actual Age

coronary vasculature development (Score: 4.887461)

Control



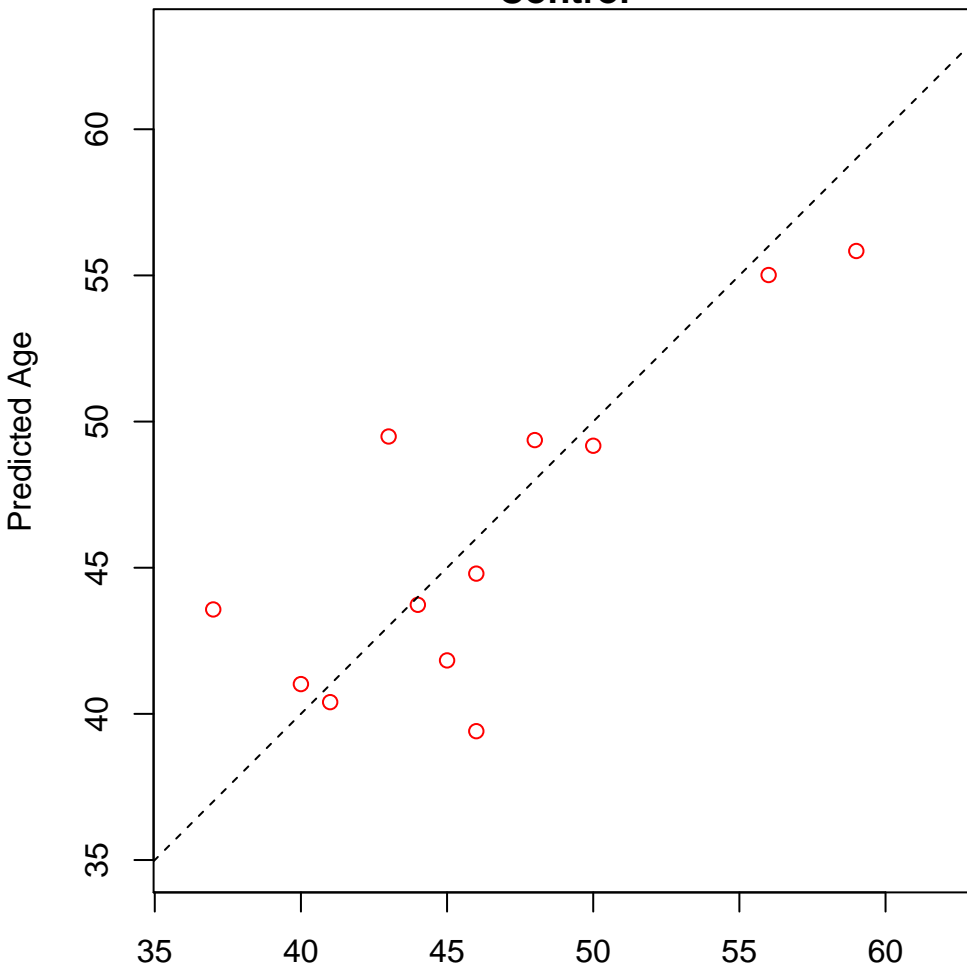
Test



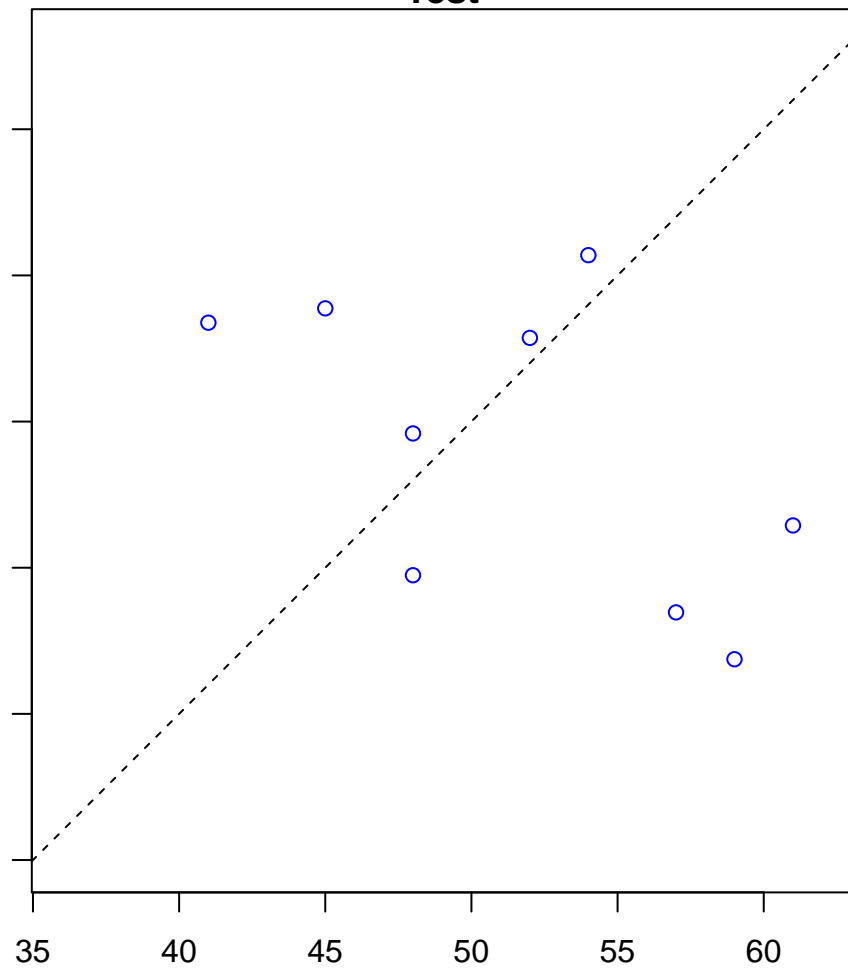
Actual Age

phosphatidylcholine metabolic process (Score: 4.877646)

Control

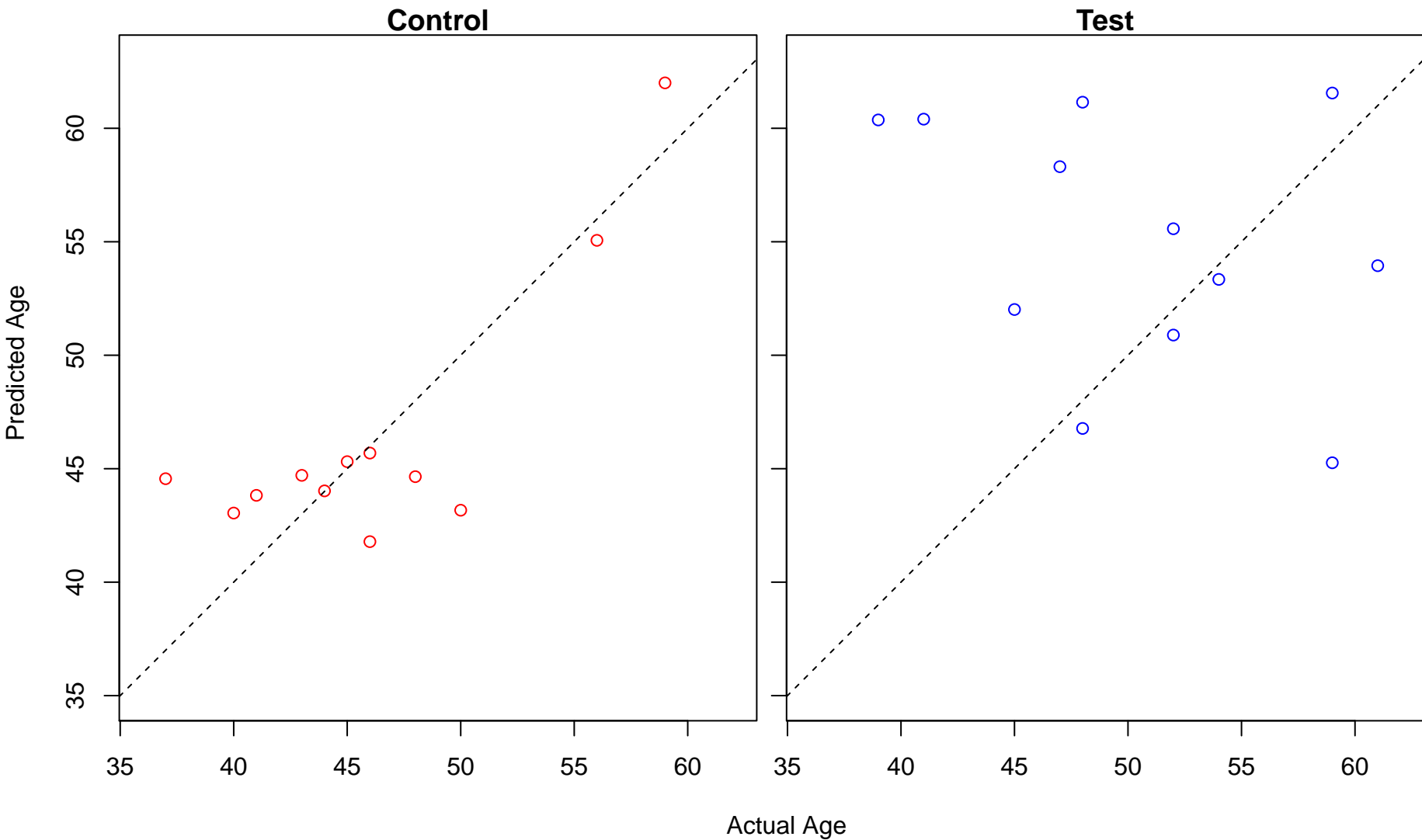


Test

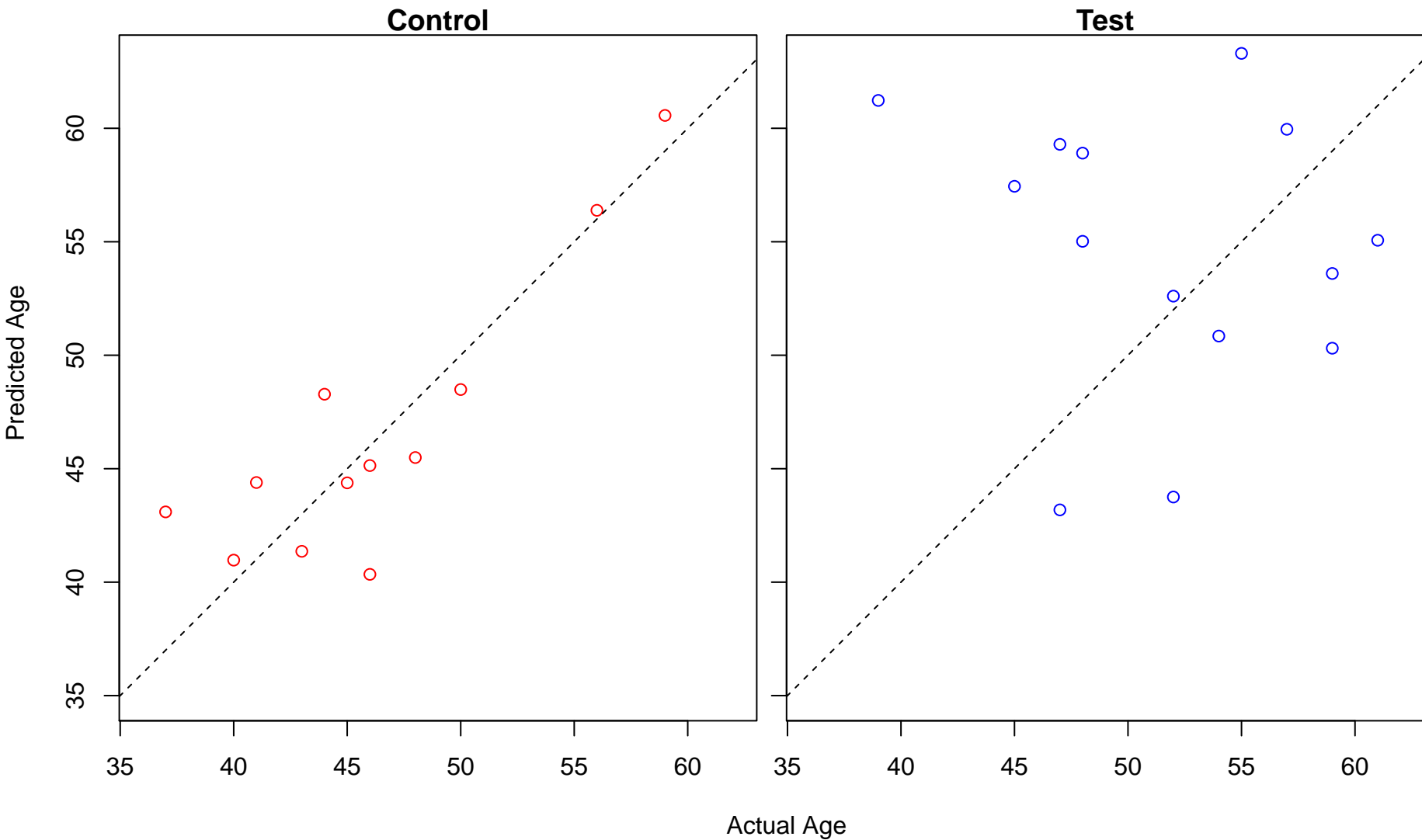


Actual Age

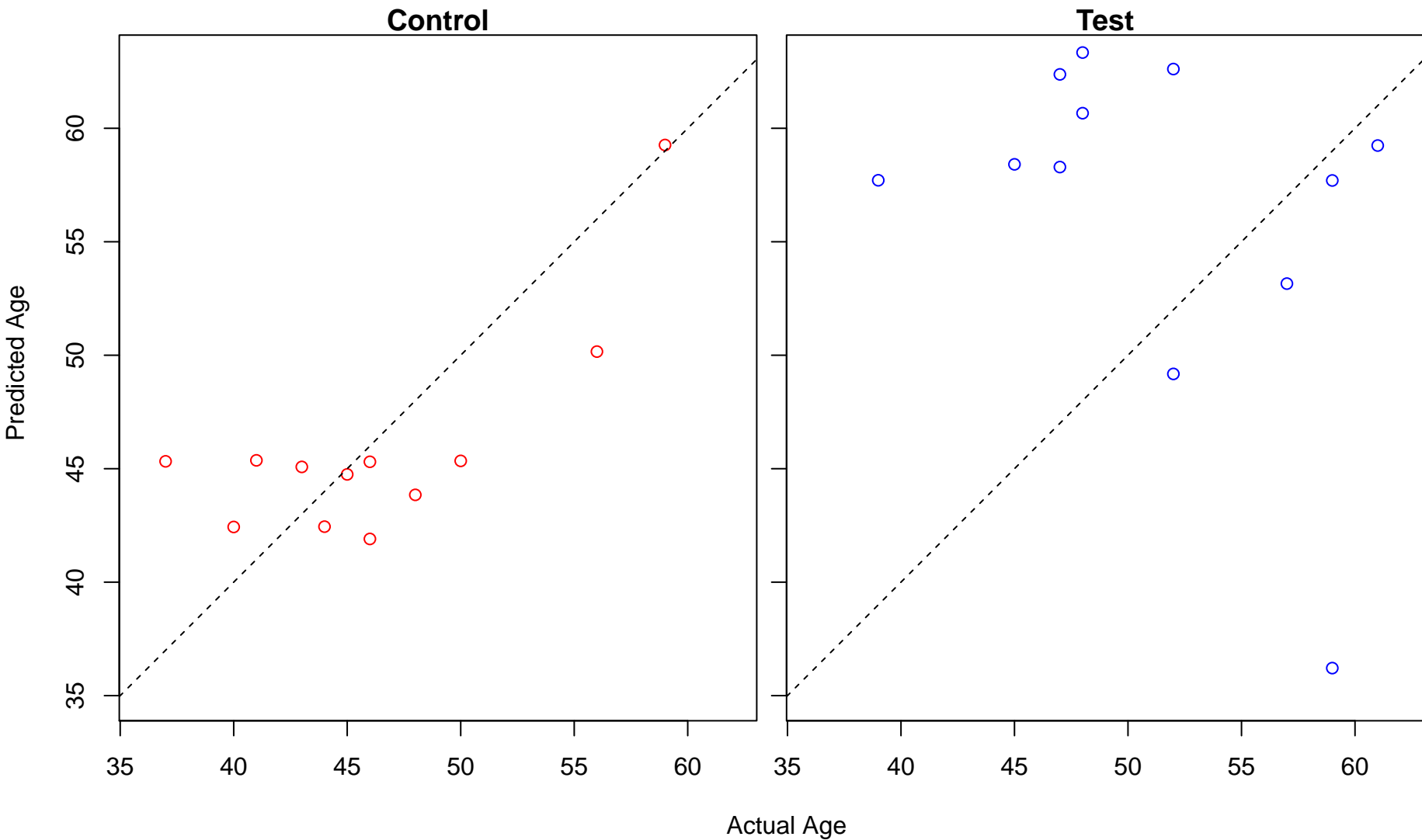
regulation of transcription from RNA polymerase II promoter in response to stress (Score: 4.87275)



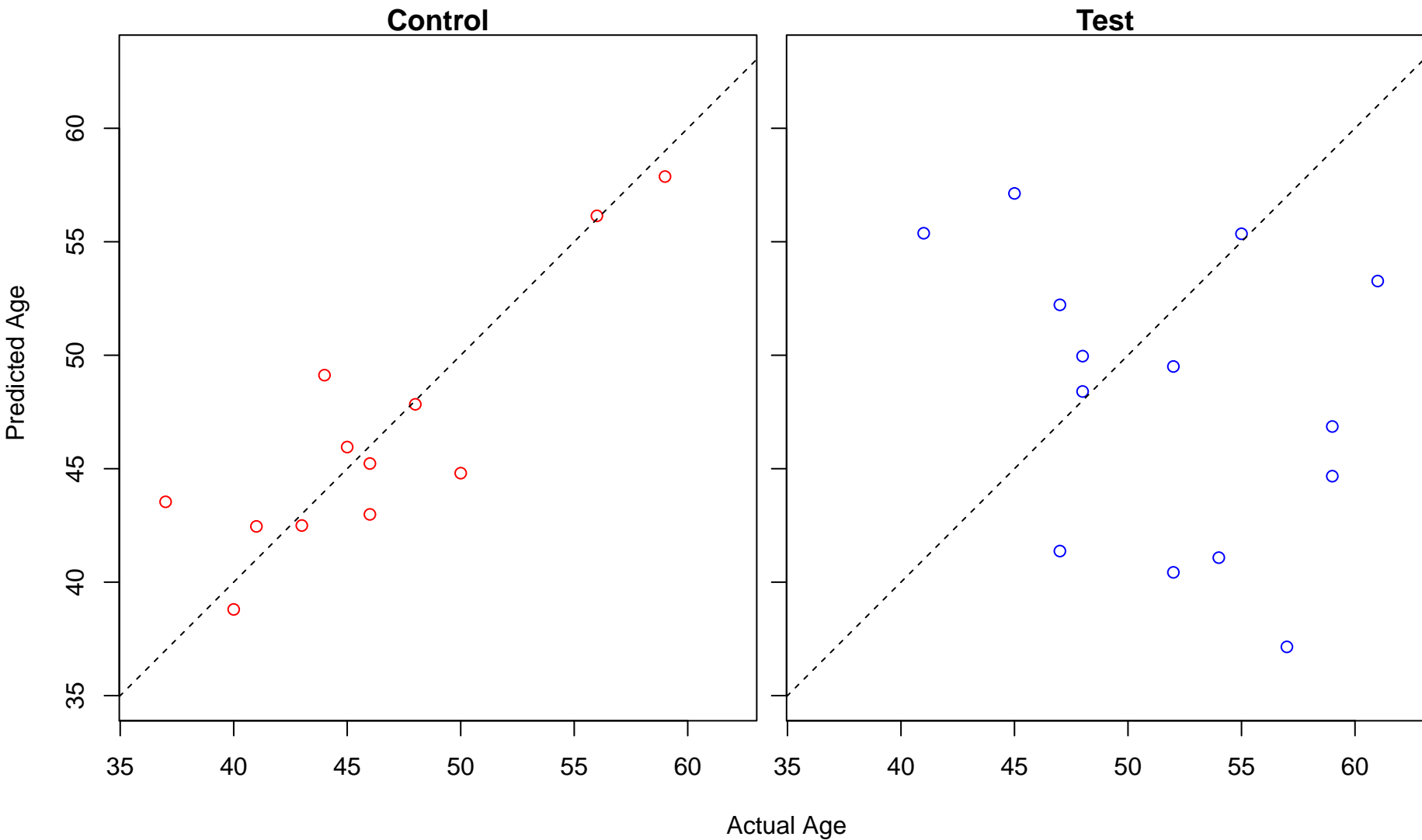
protein transmembrane transport (Score: 4.864618)



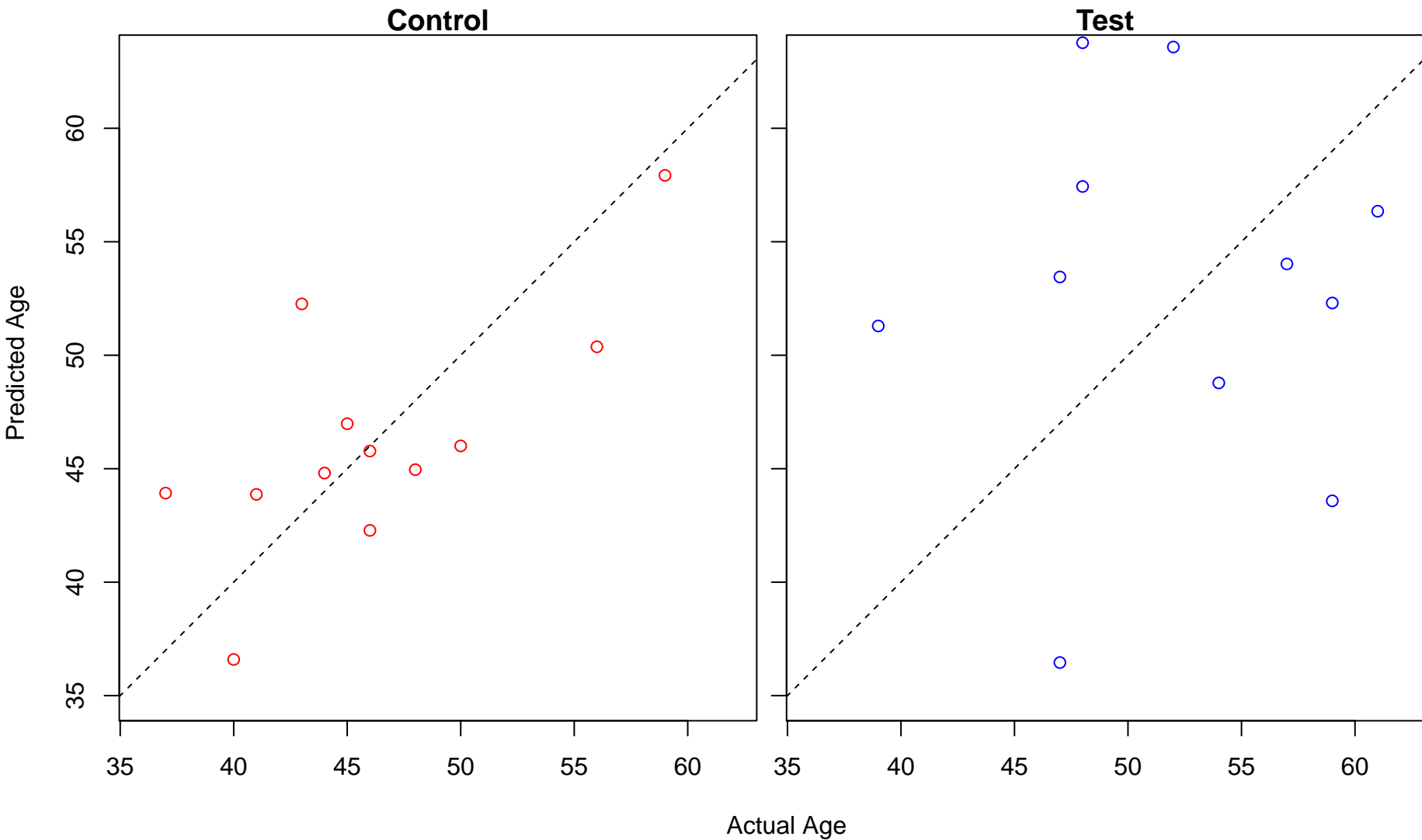
positive regulation of interleukin-23 production (Score: 4.863923)



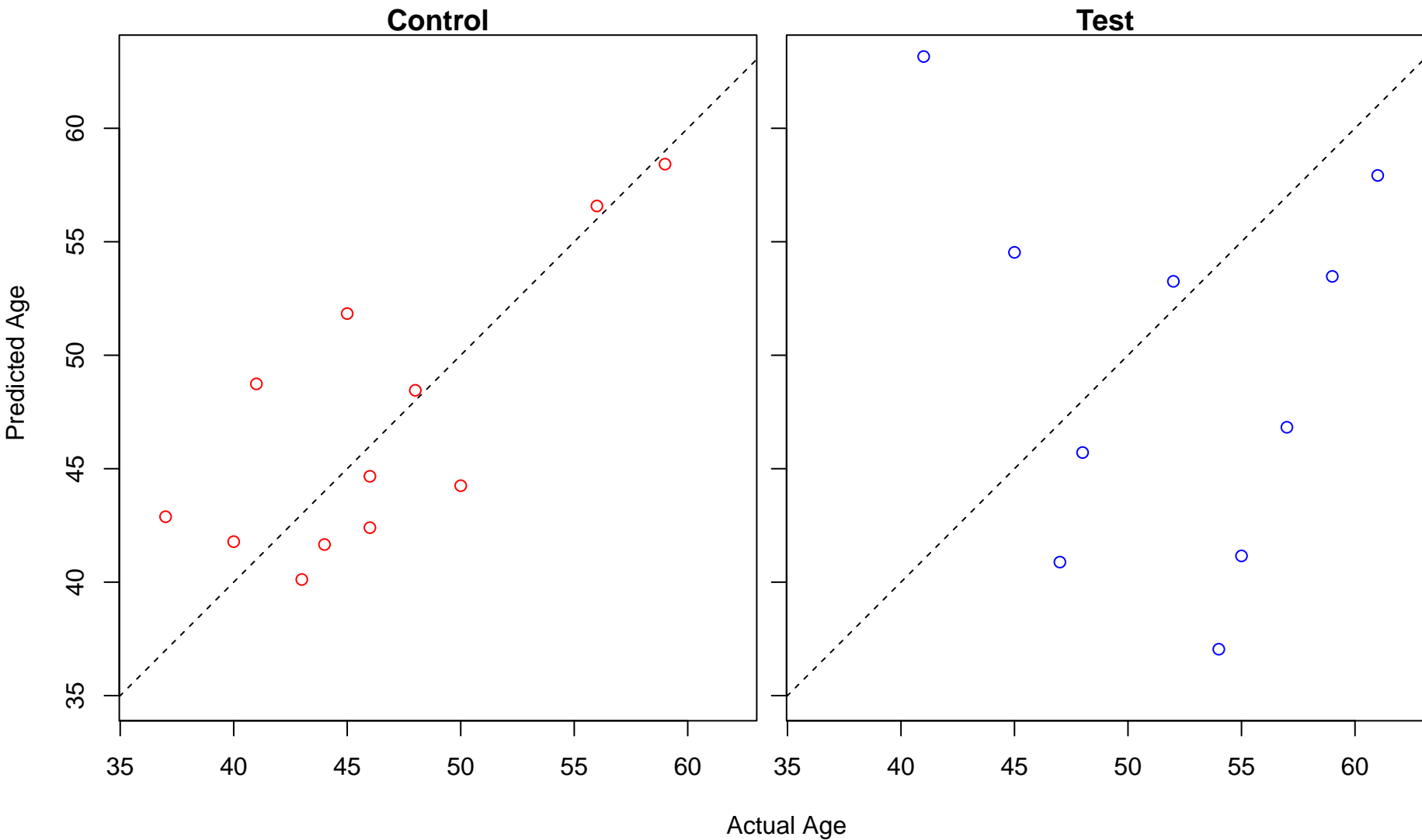
tRNA aminoacylation for protein translation (Score: 4.861311)



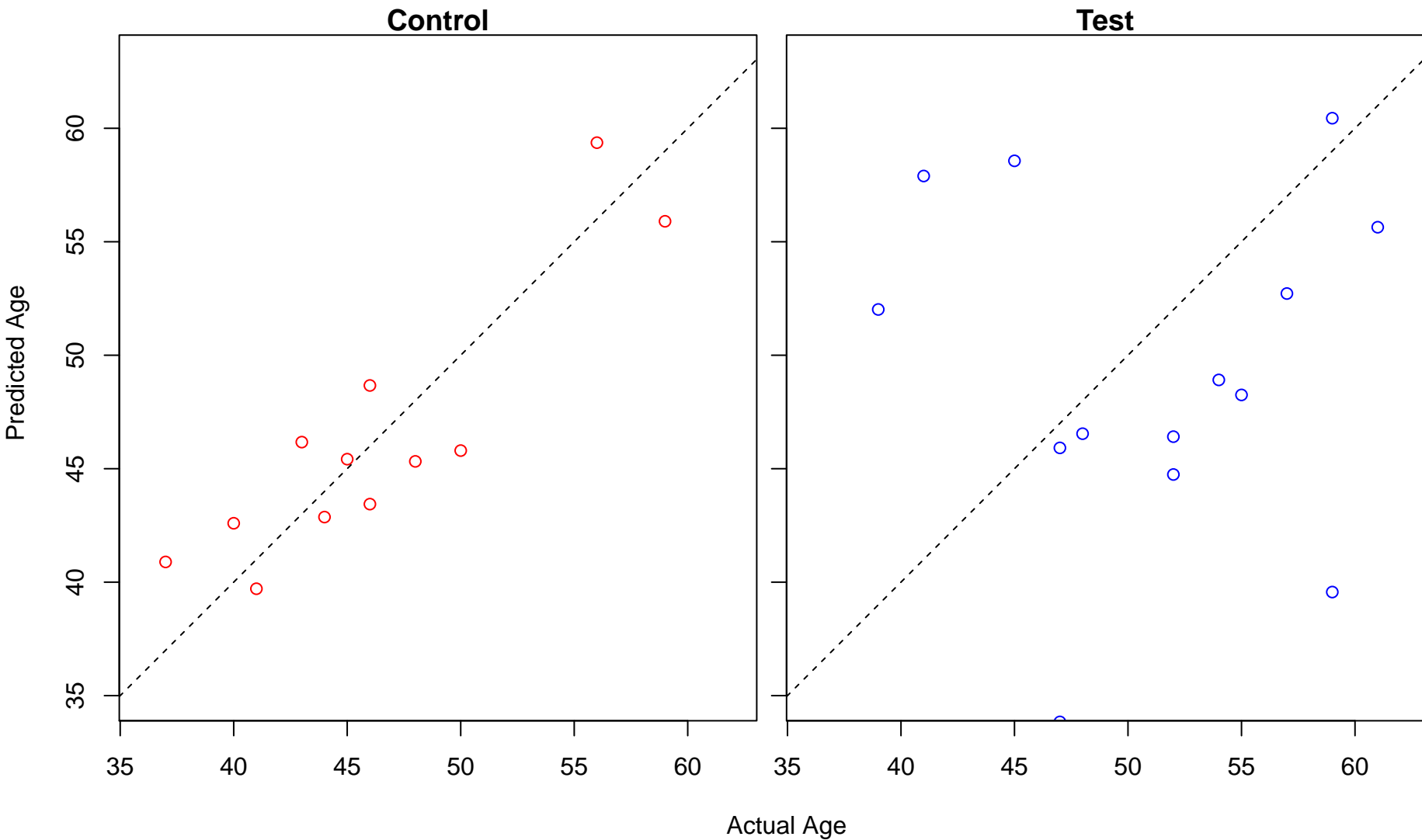
epidermis morphogenesis (Score: 4.860765)



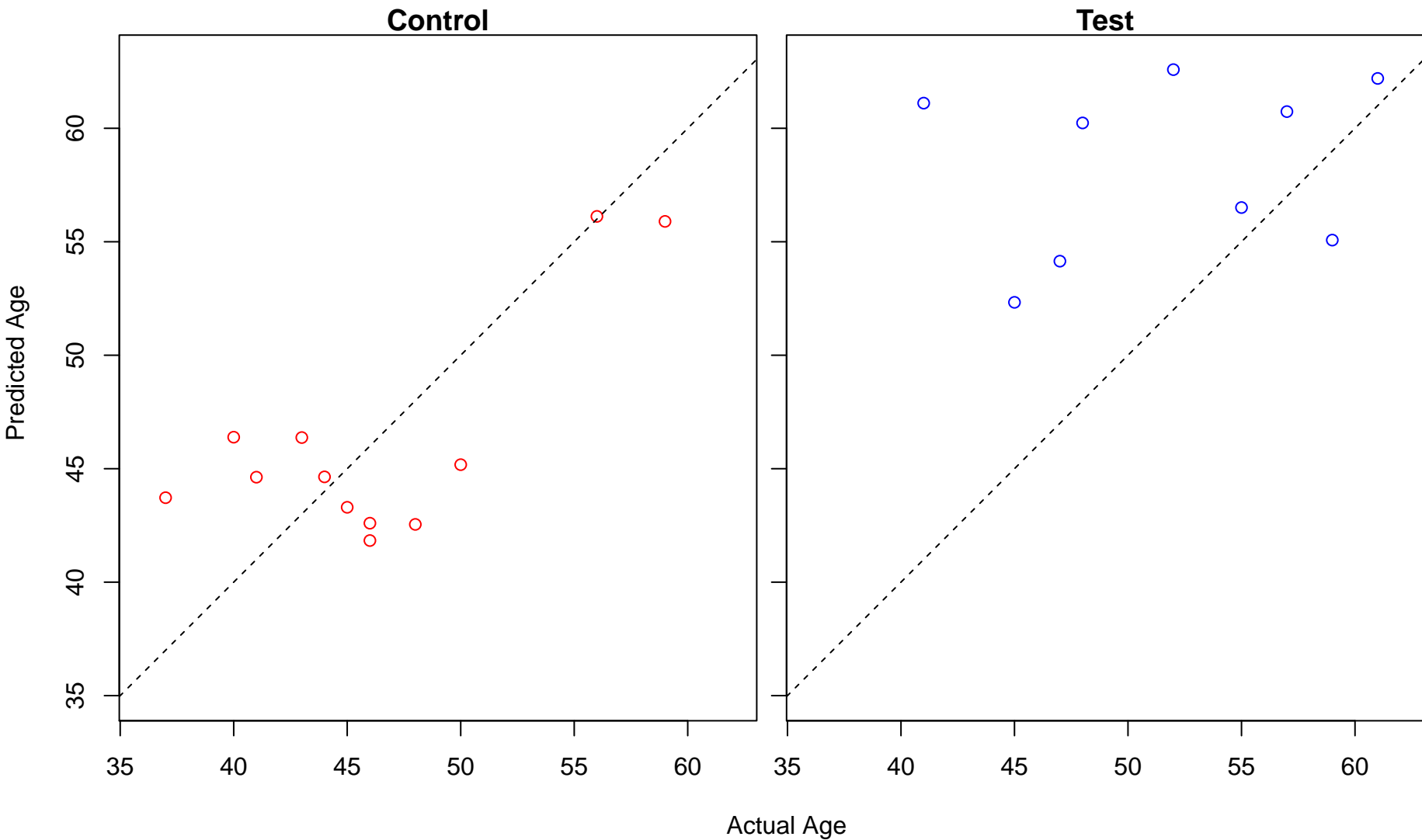
negative regulation of MAP kinase activity (Score: 4.860432)



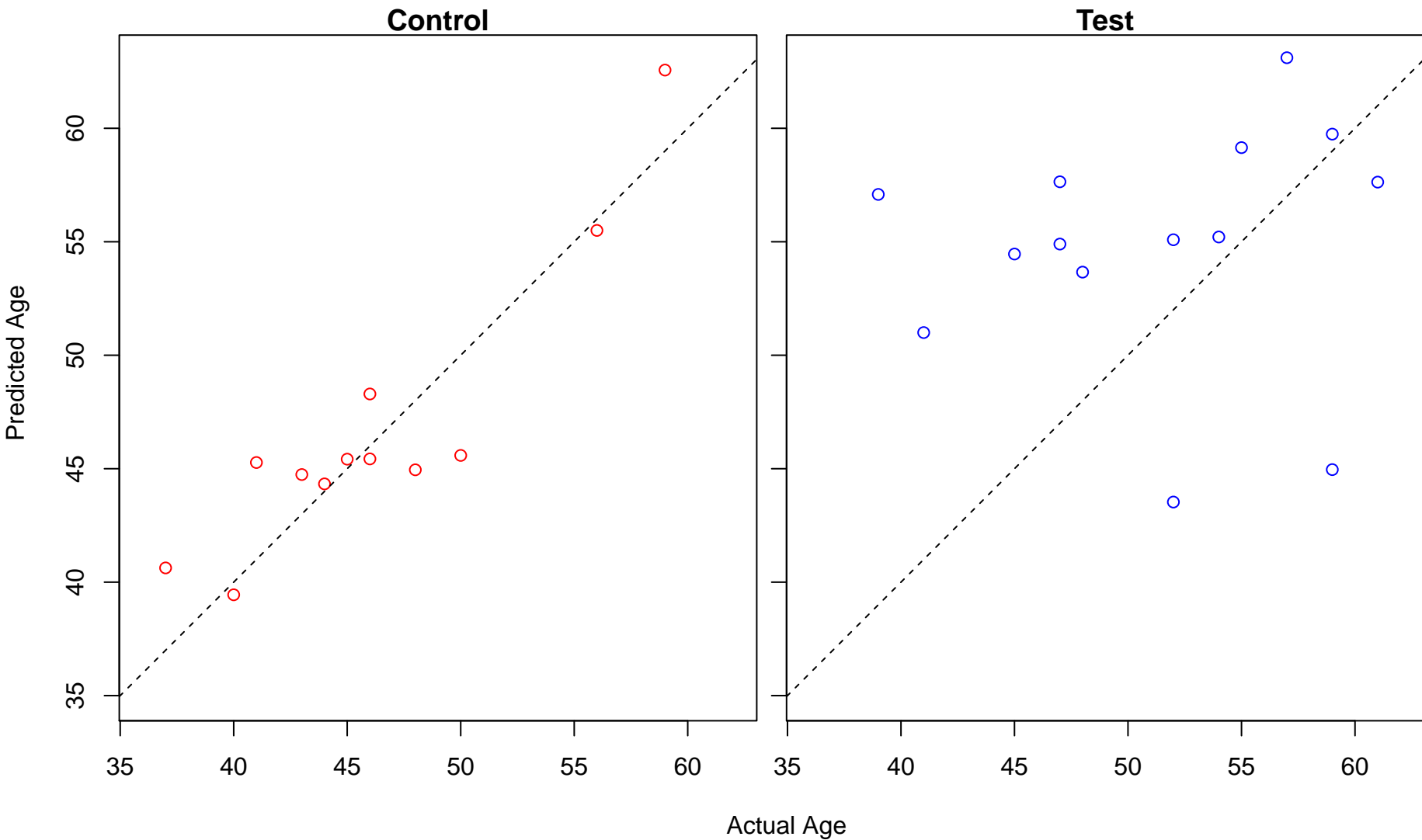
positive regulation of axon extension (Score: 4.857904)



oligopeptide transport (Score: 4.852319)

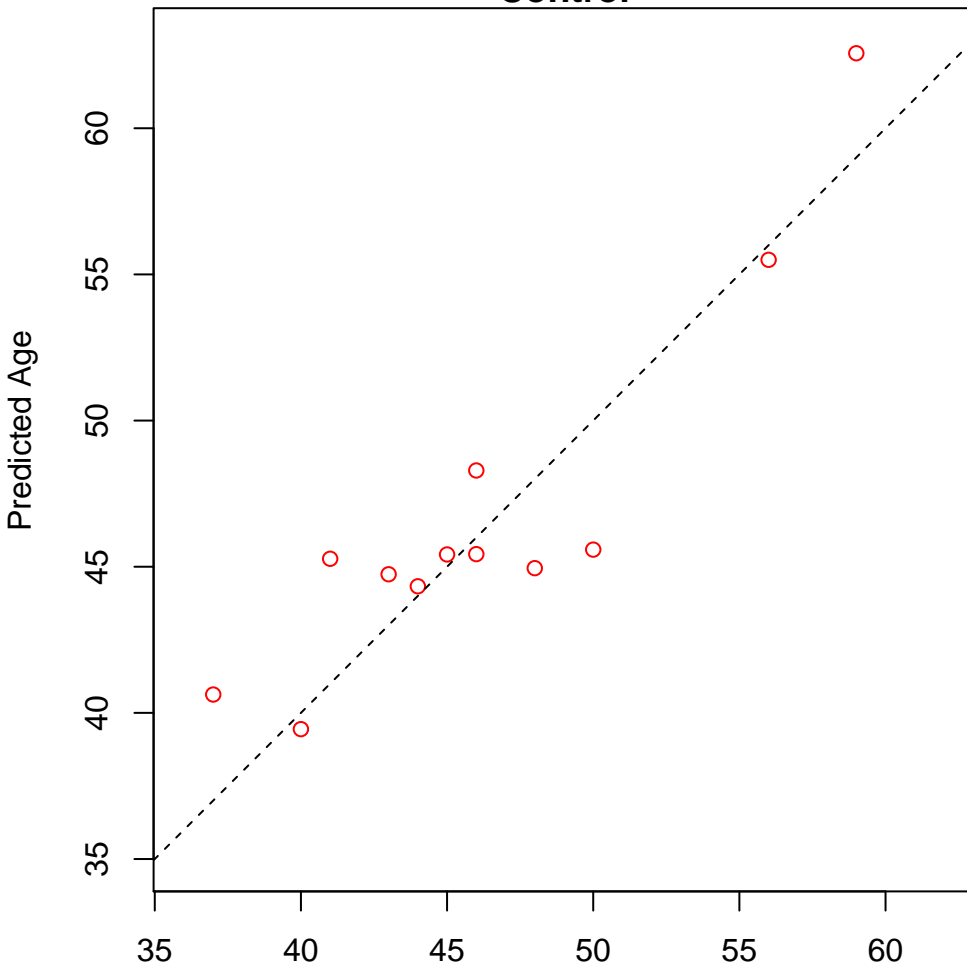


macromolecular complex remodeling (Score: 4.851297)

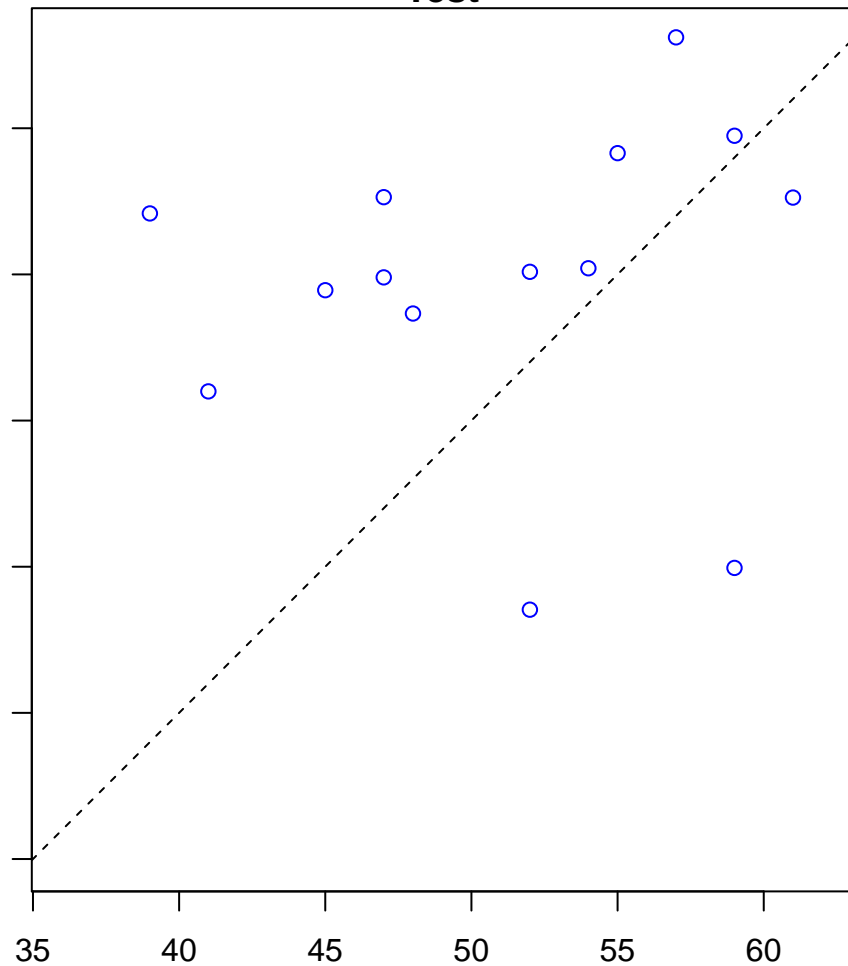


protein-lipid complex remodeling (Score: 4.851297)

Control



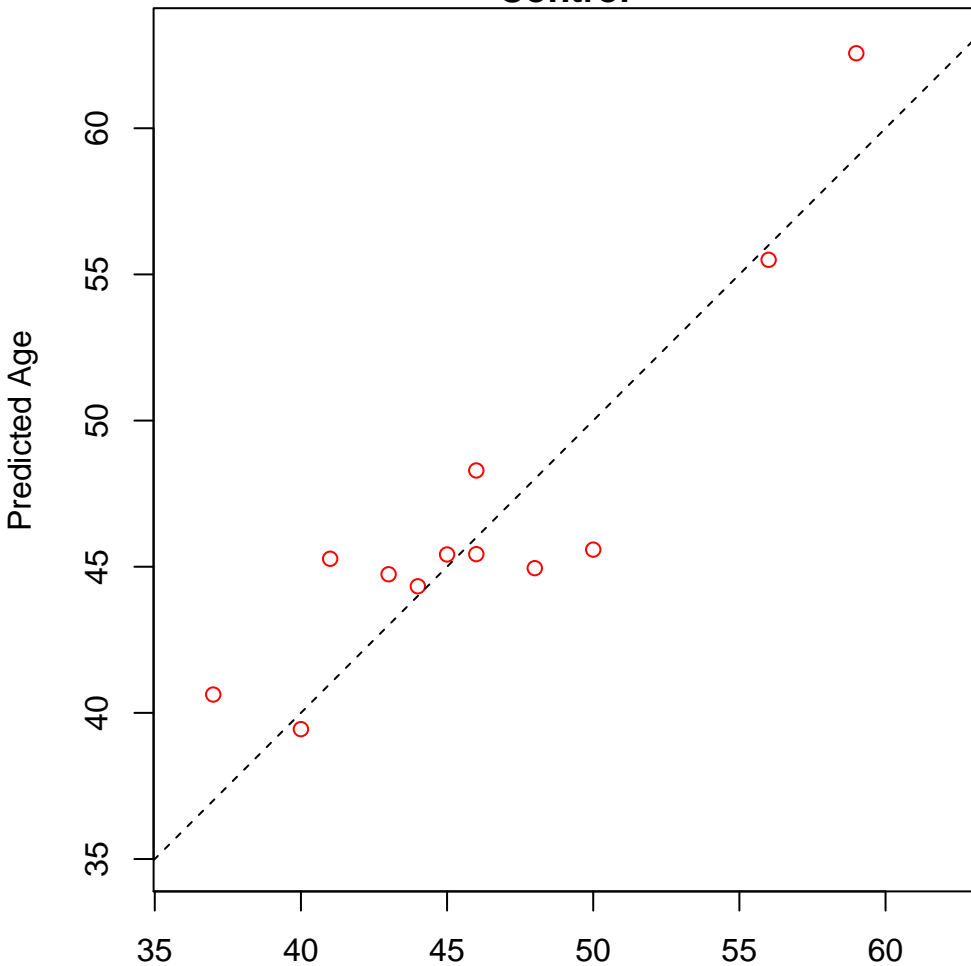
Test



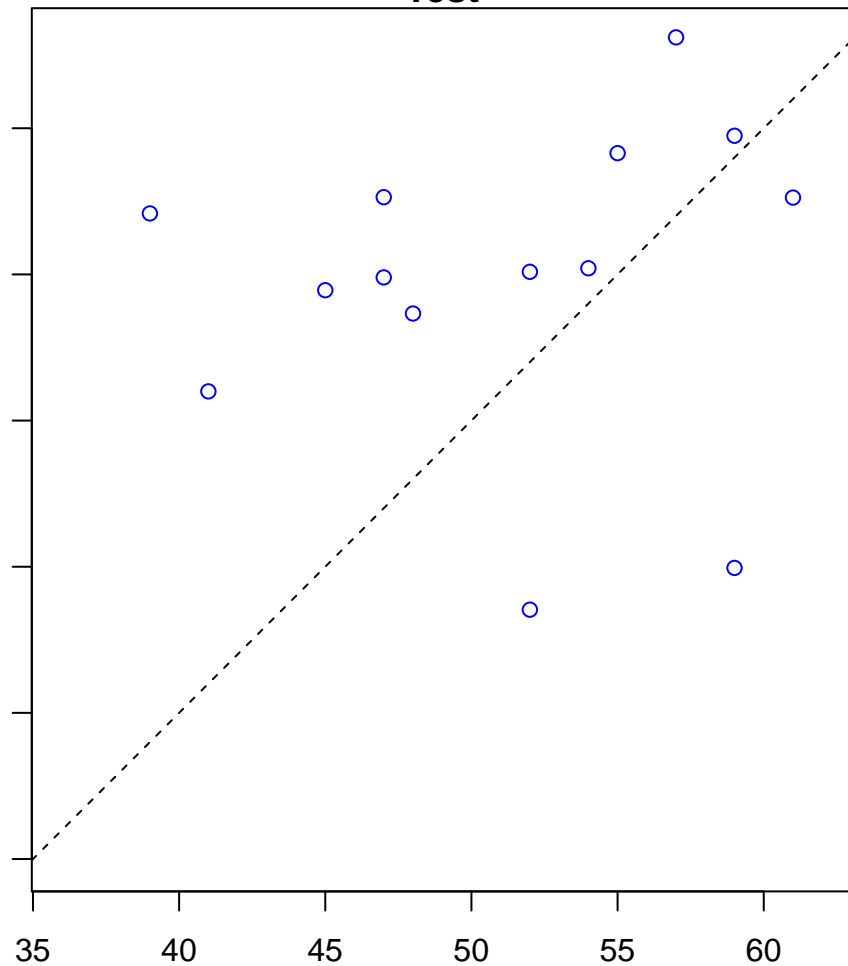
Actual Age

plasma lipoprotein particle remodeling (Score: 4.851297)

Control

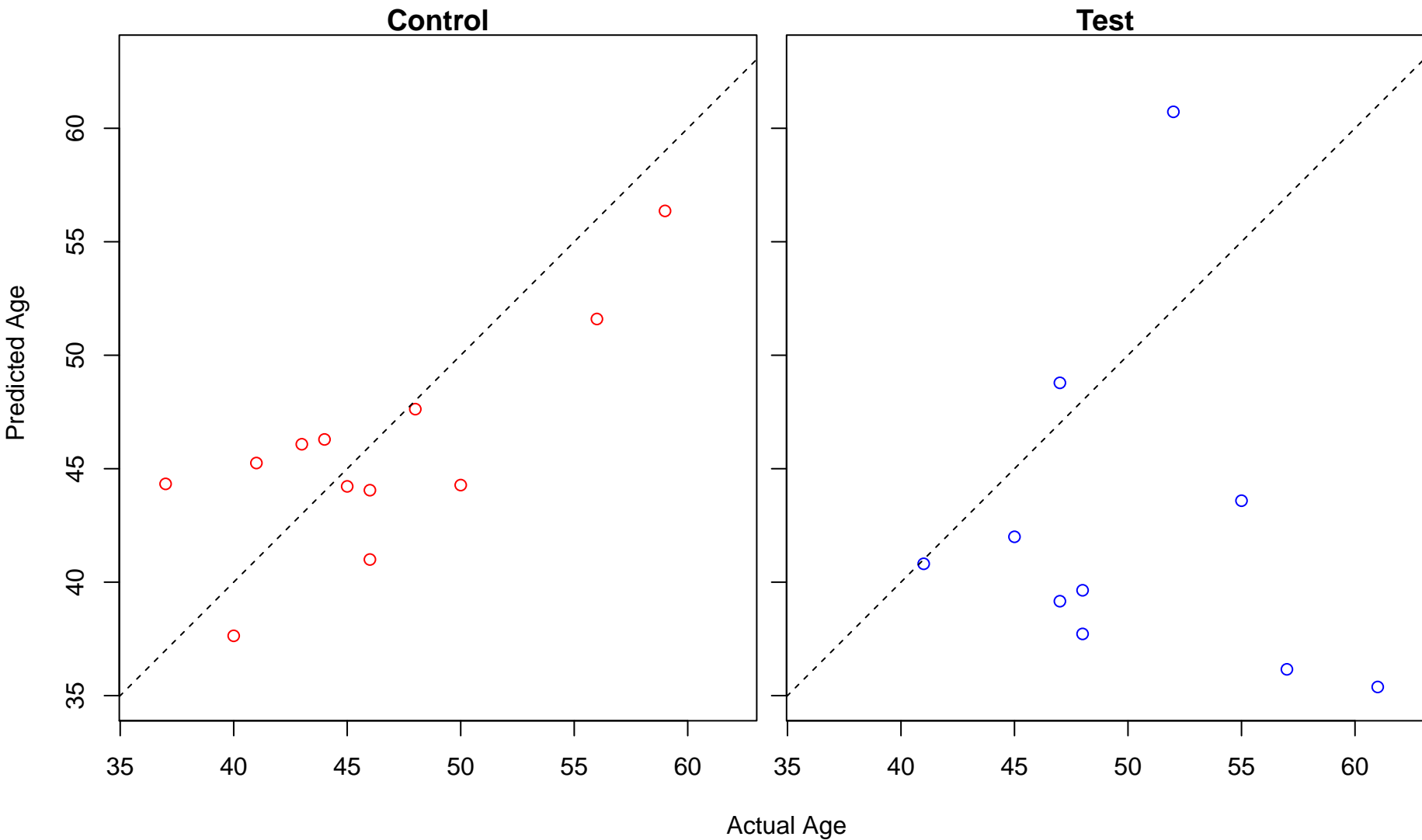


Test

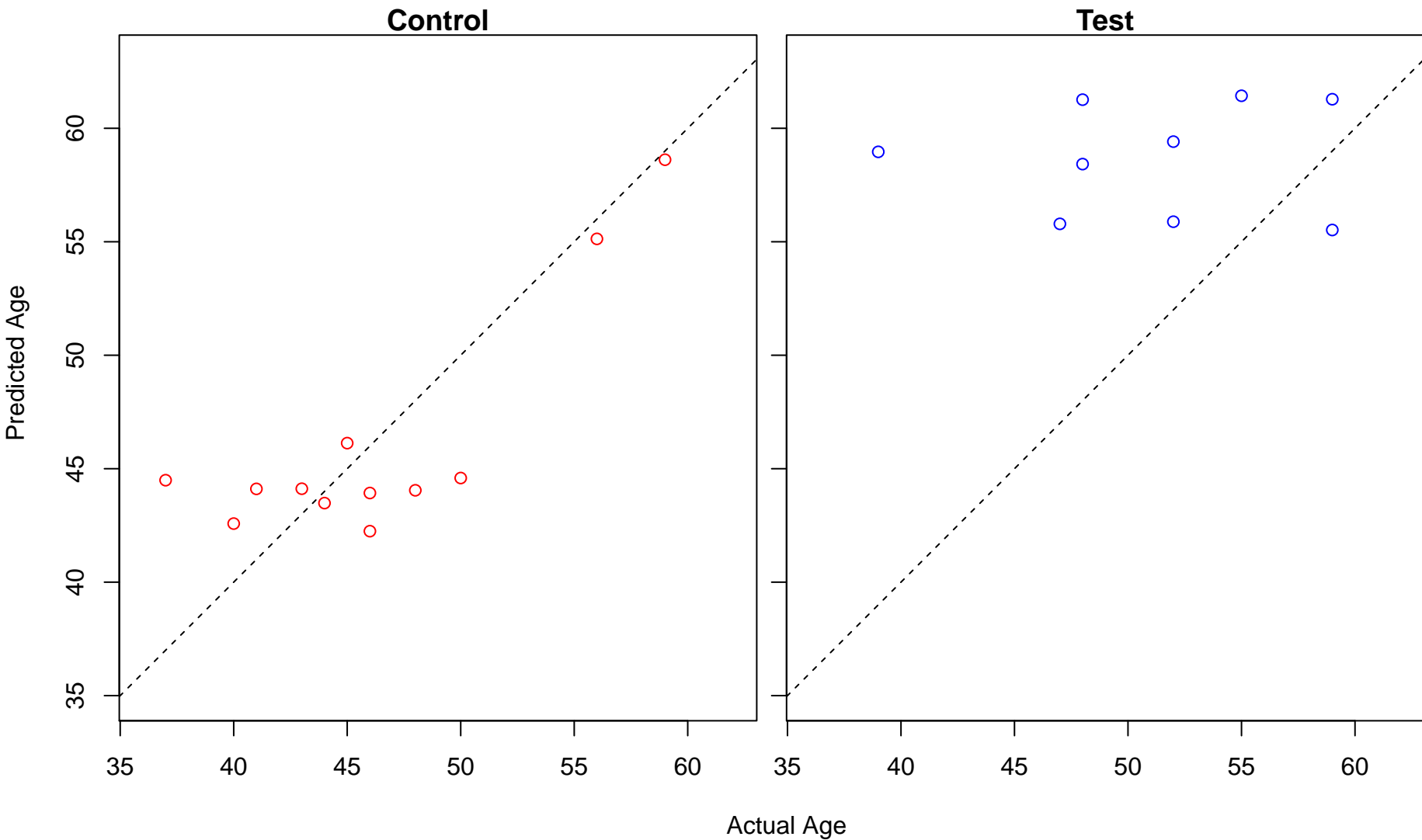


Actual Age

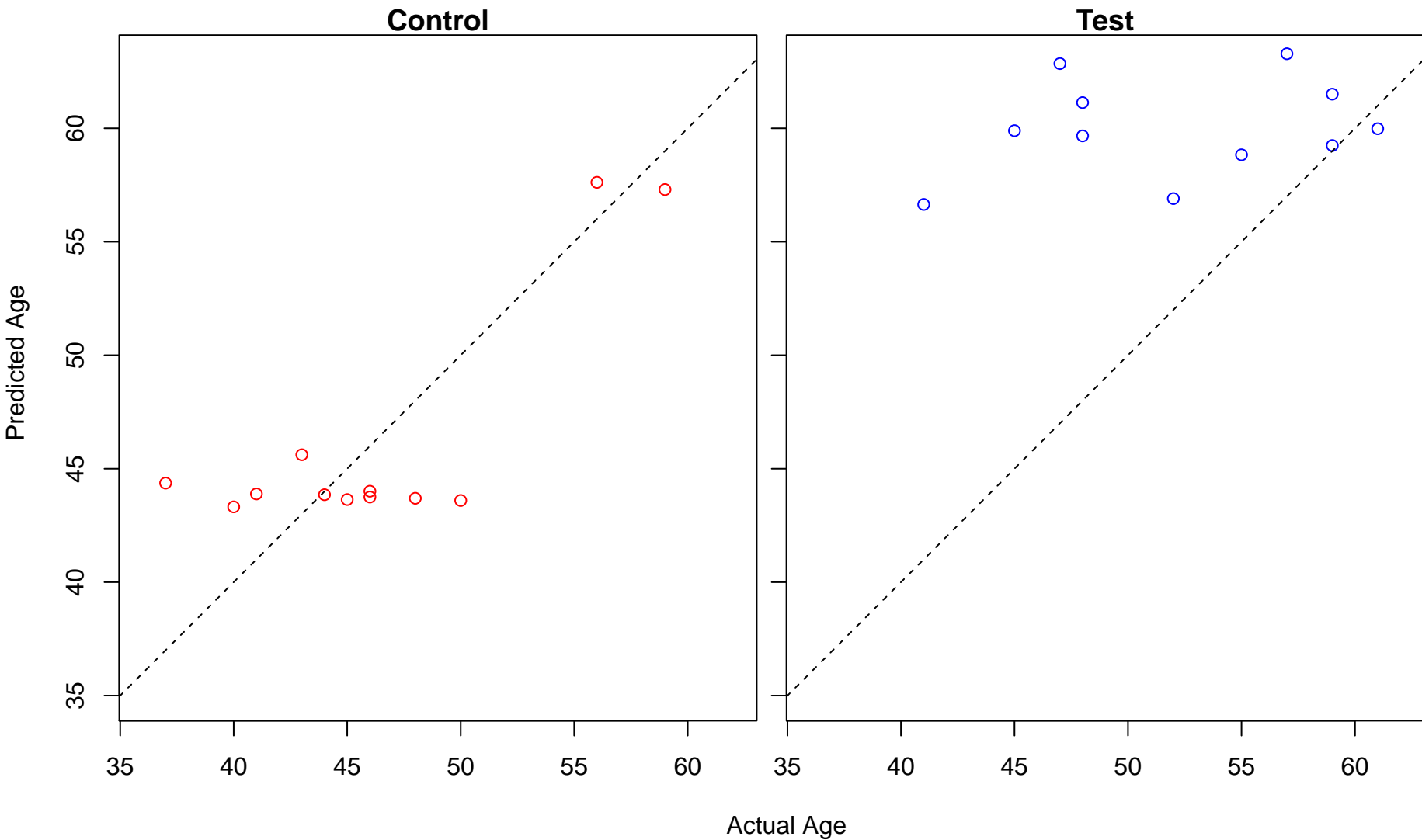
cellular modified amino acid metabolic process (Score: 4.845789)



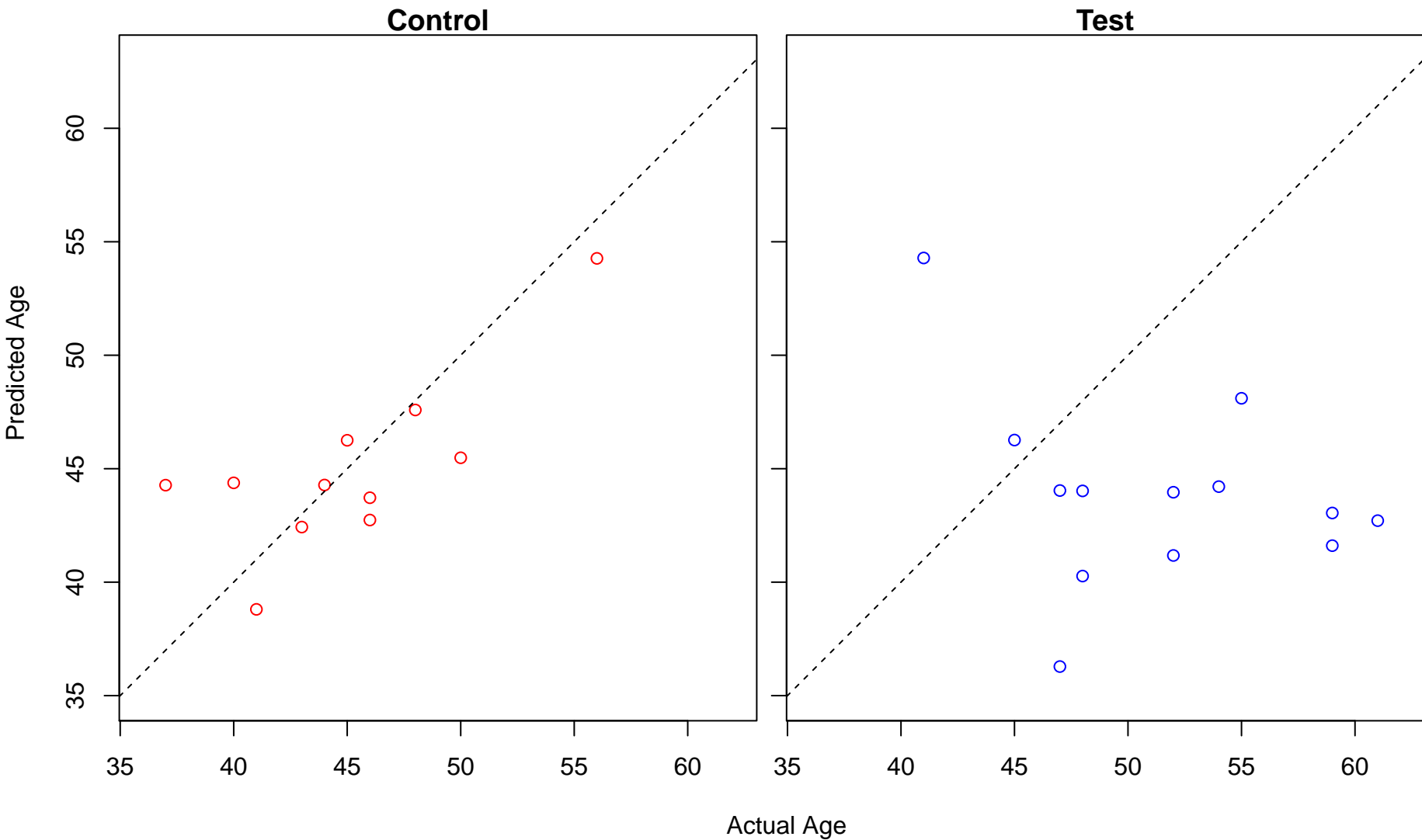
regulation of inclusion body assembly (Score: 4.837699)



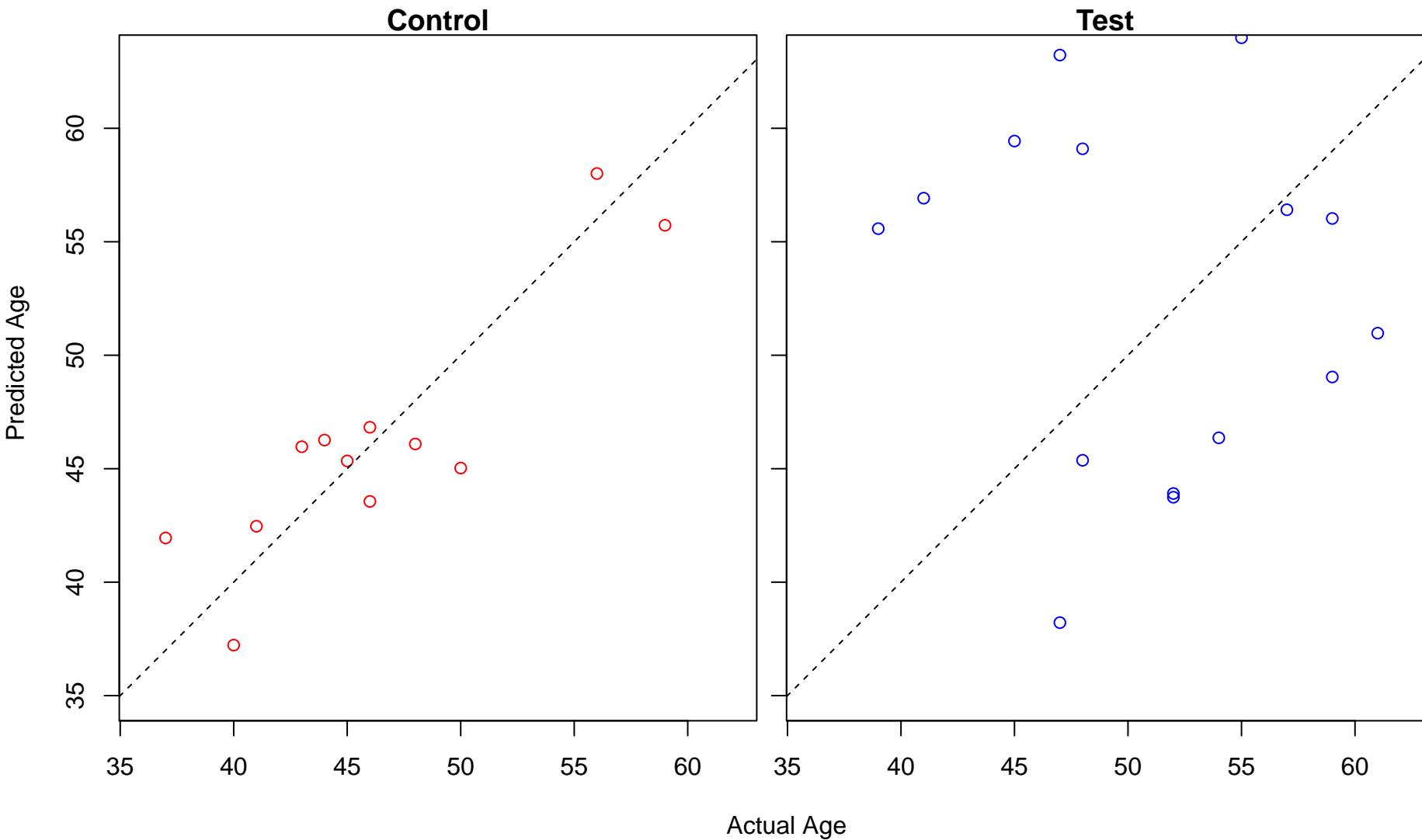
negative regulation of hippo signaling (Score: 4.815864)



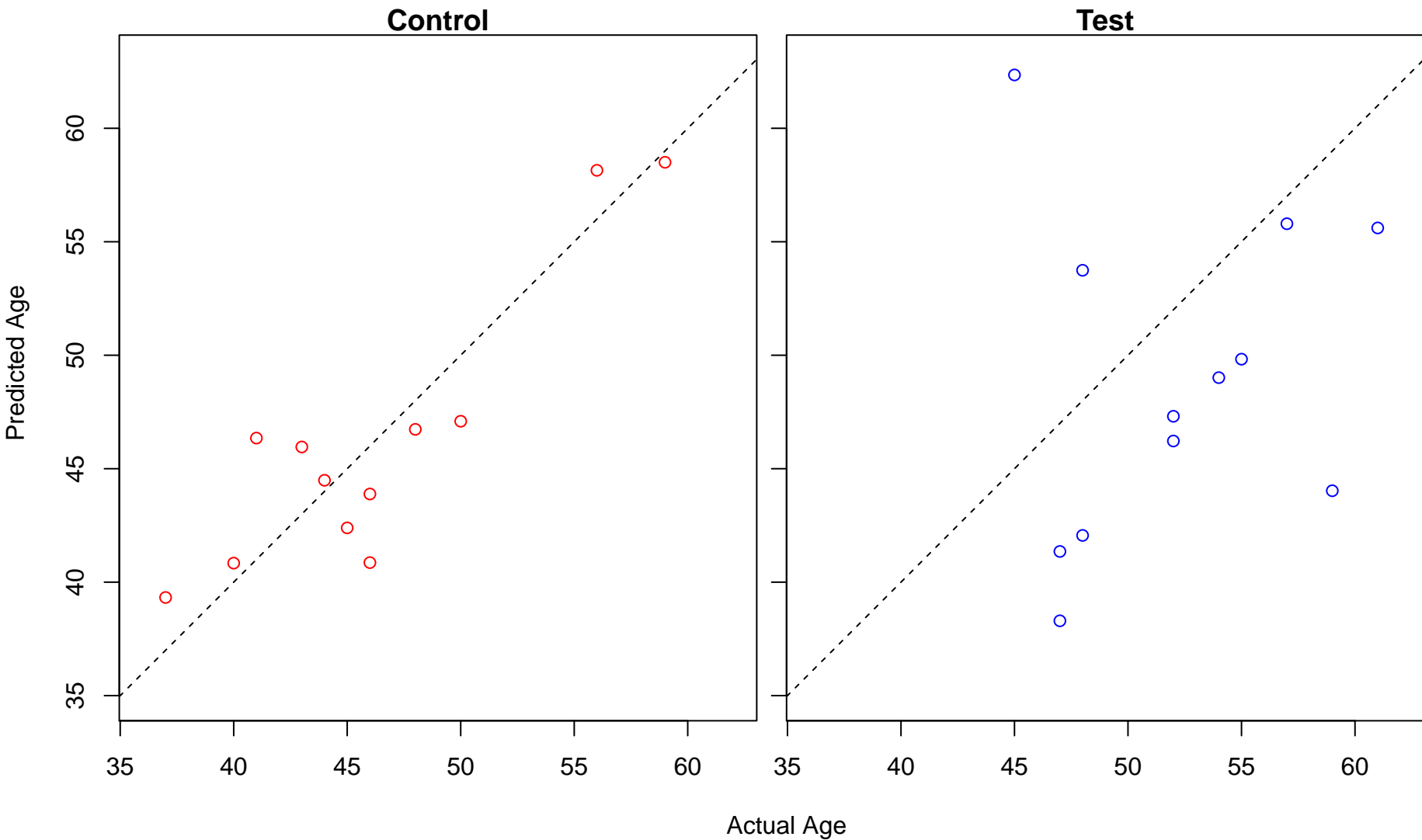
nuclear-transcribed mRNA catabolic process, exonucleolytic (Score: 4.810669)



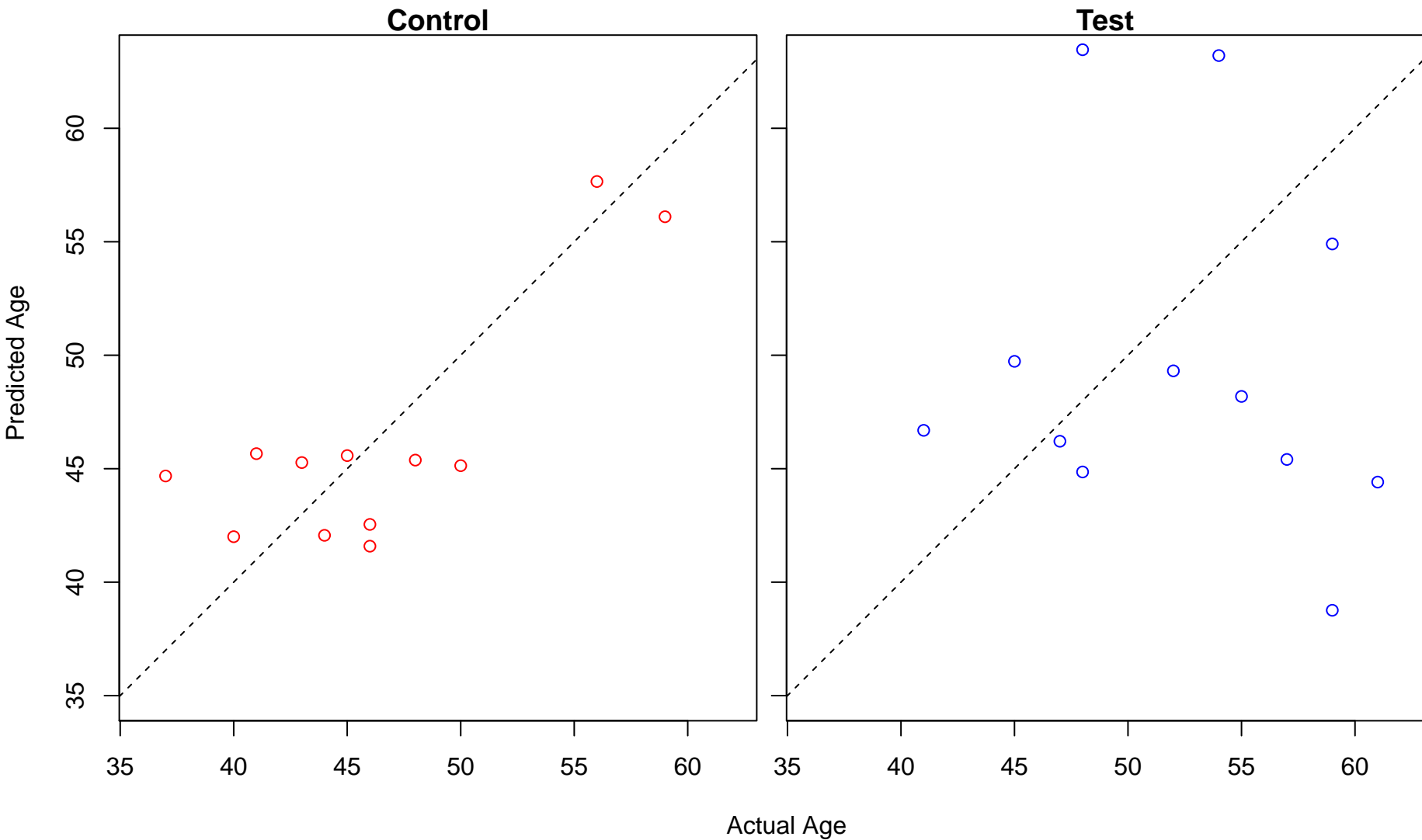
regulation of nucleotide metabolic process (Score: 4.804994)



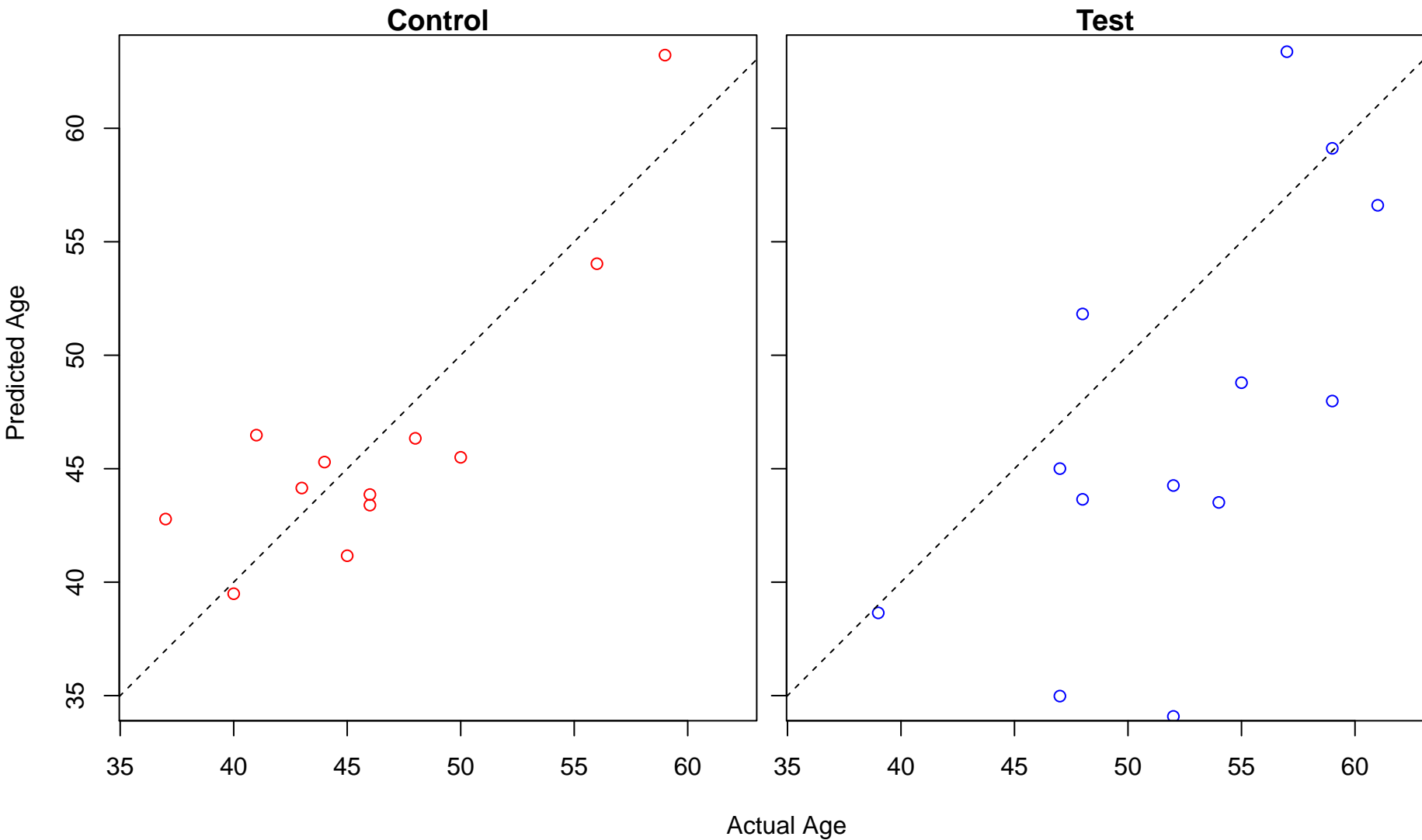
fatty acid biosynthetic process (Score: 4.803083)



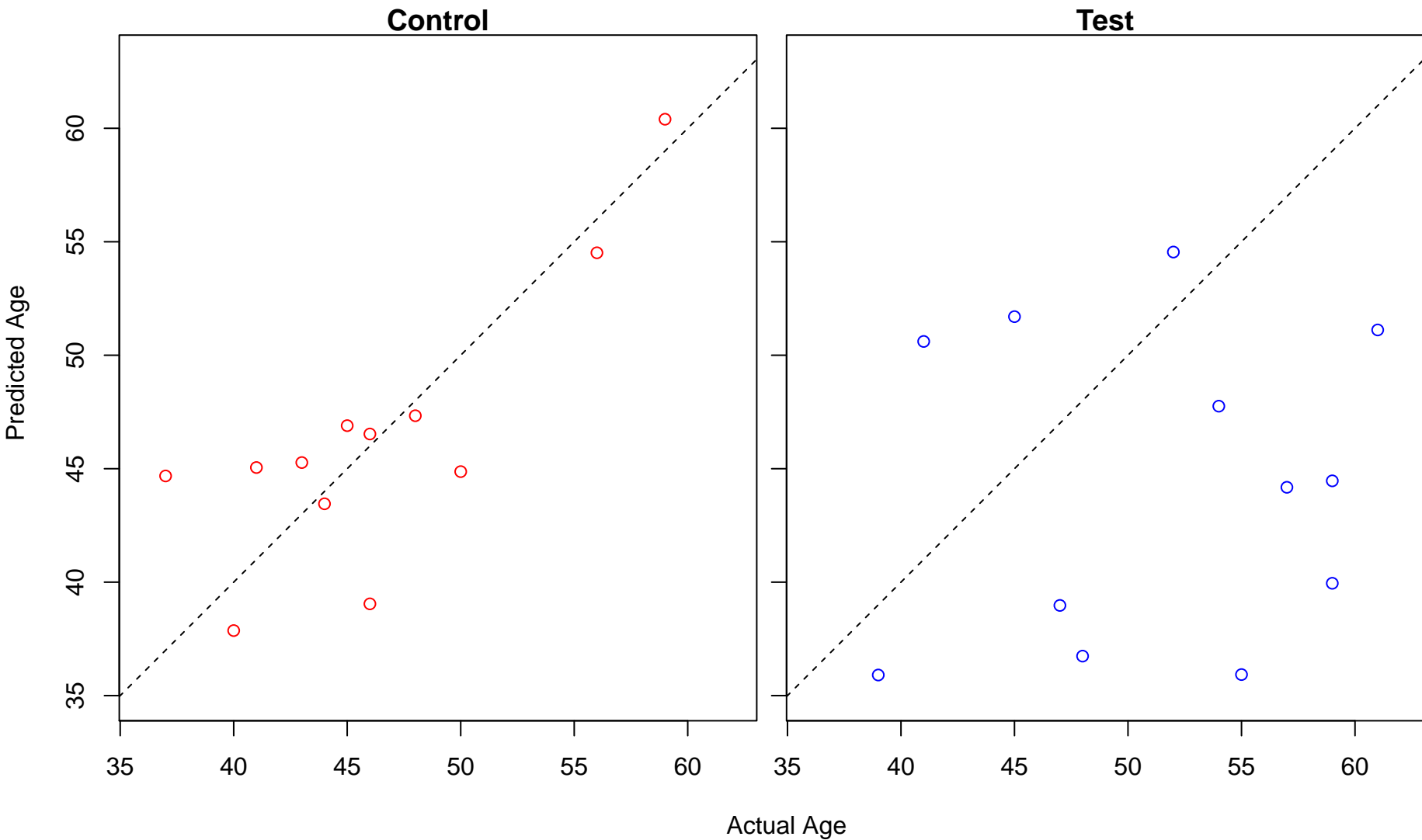
negative regulation of telomere maintenance (Score: 4.800675)



response to oxidative stress (Score: 4.800598)

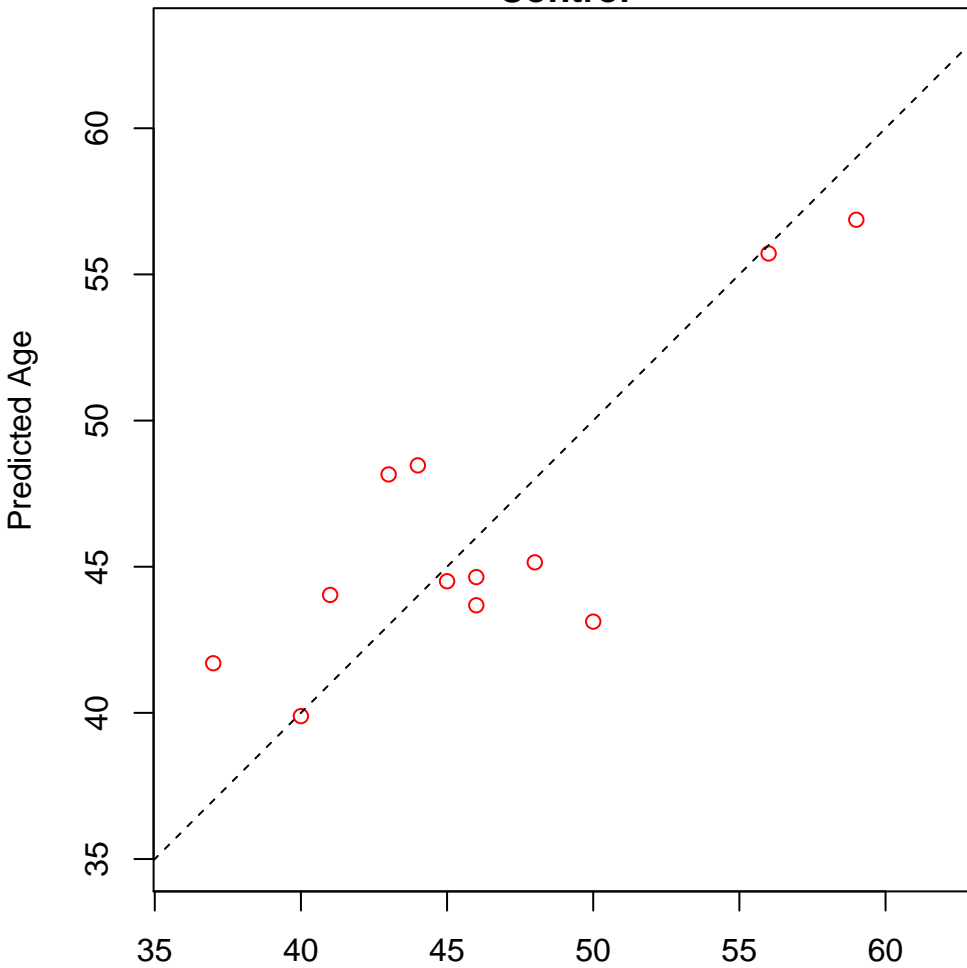


vesicle targeting, to, from or within Golgi (Score: 4.800202)

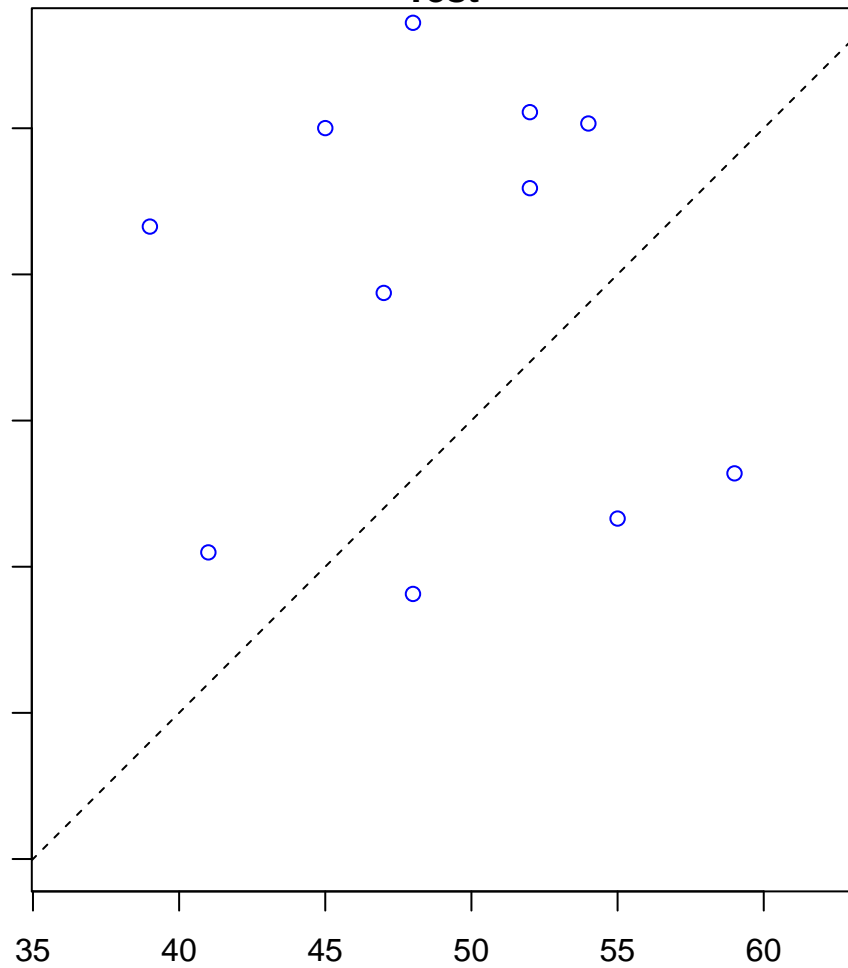


regulation of immunoglobulin secretion (Score: 4.793053)

Control

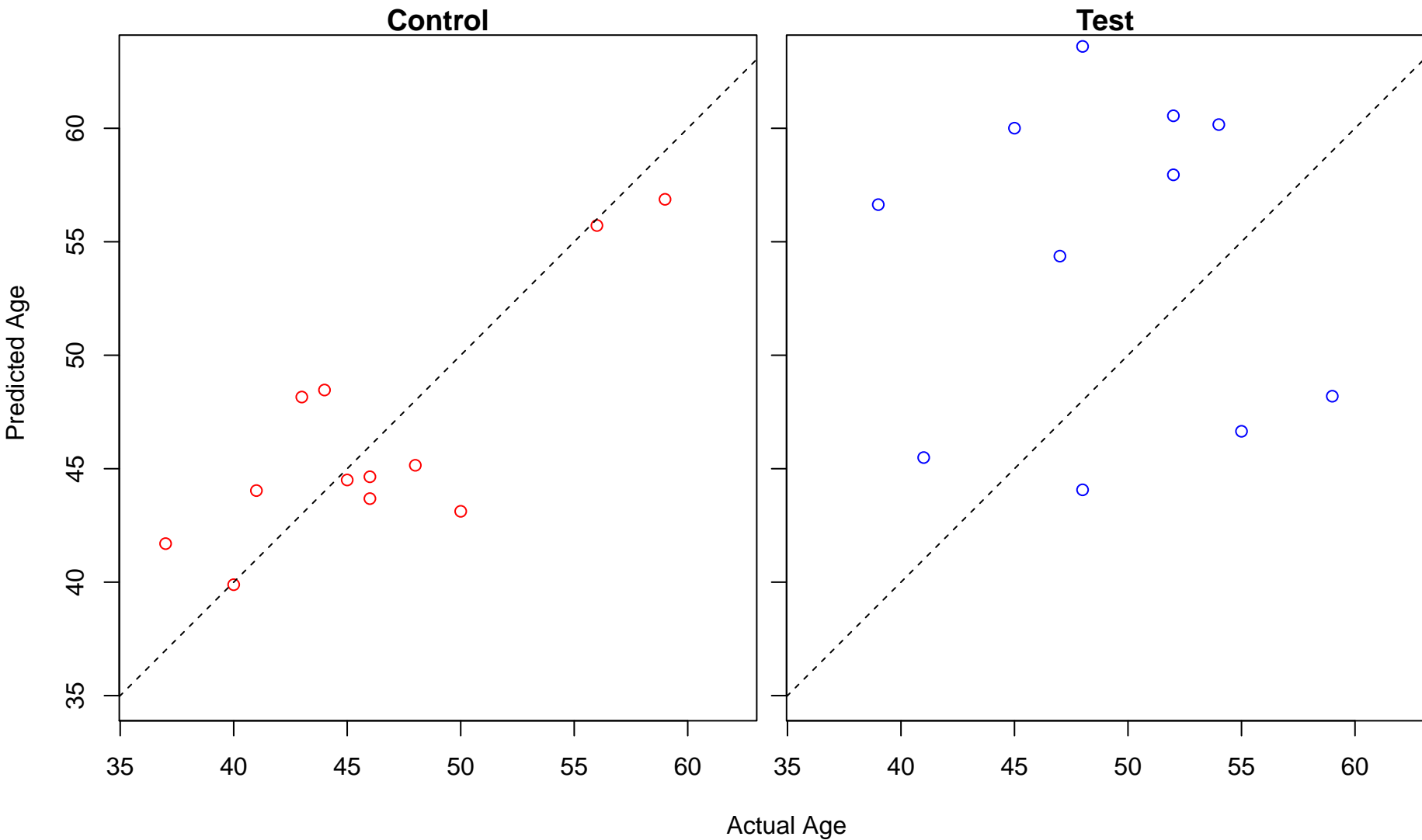


Test

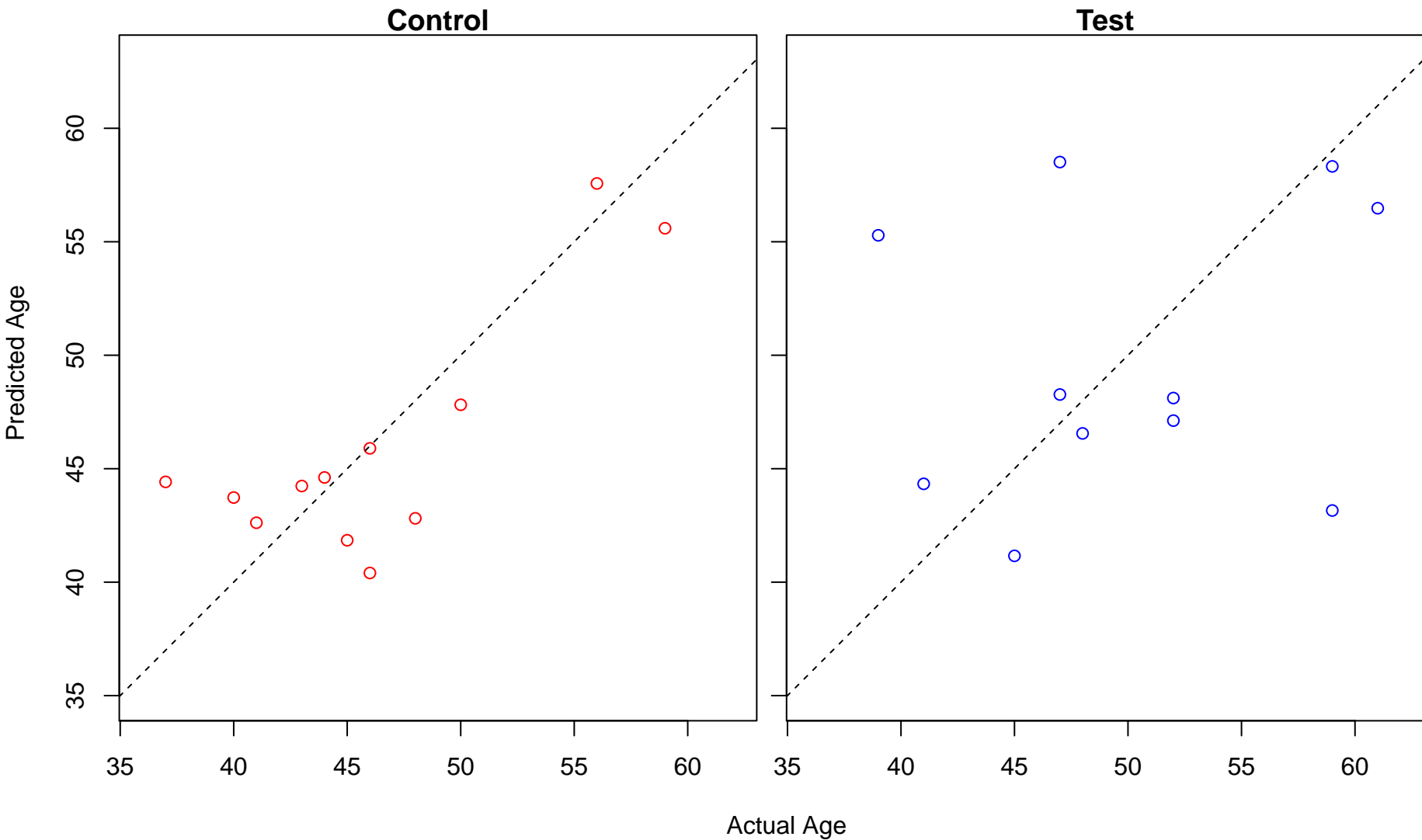


Actual Age

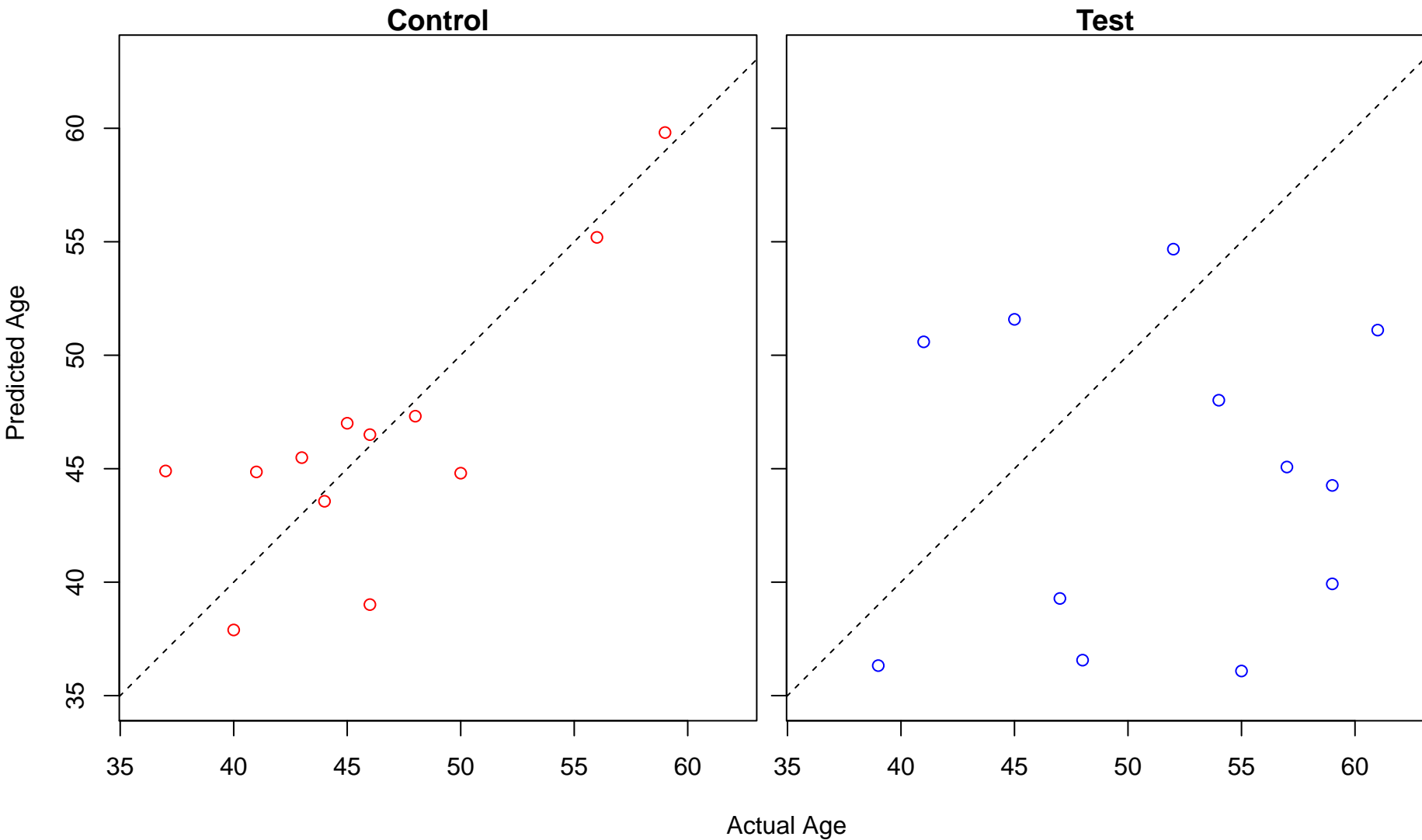
positive regulation of immunoglobulin secretion (Score: 4.793053)



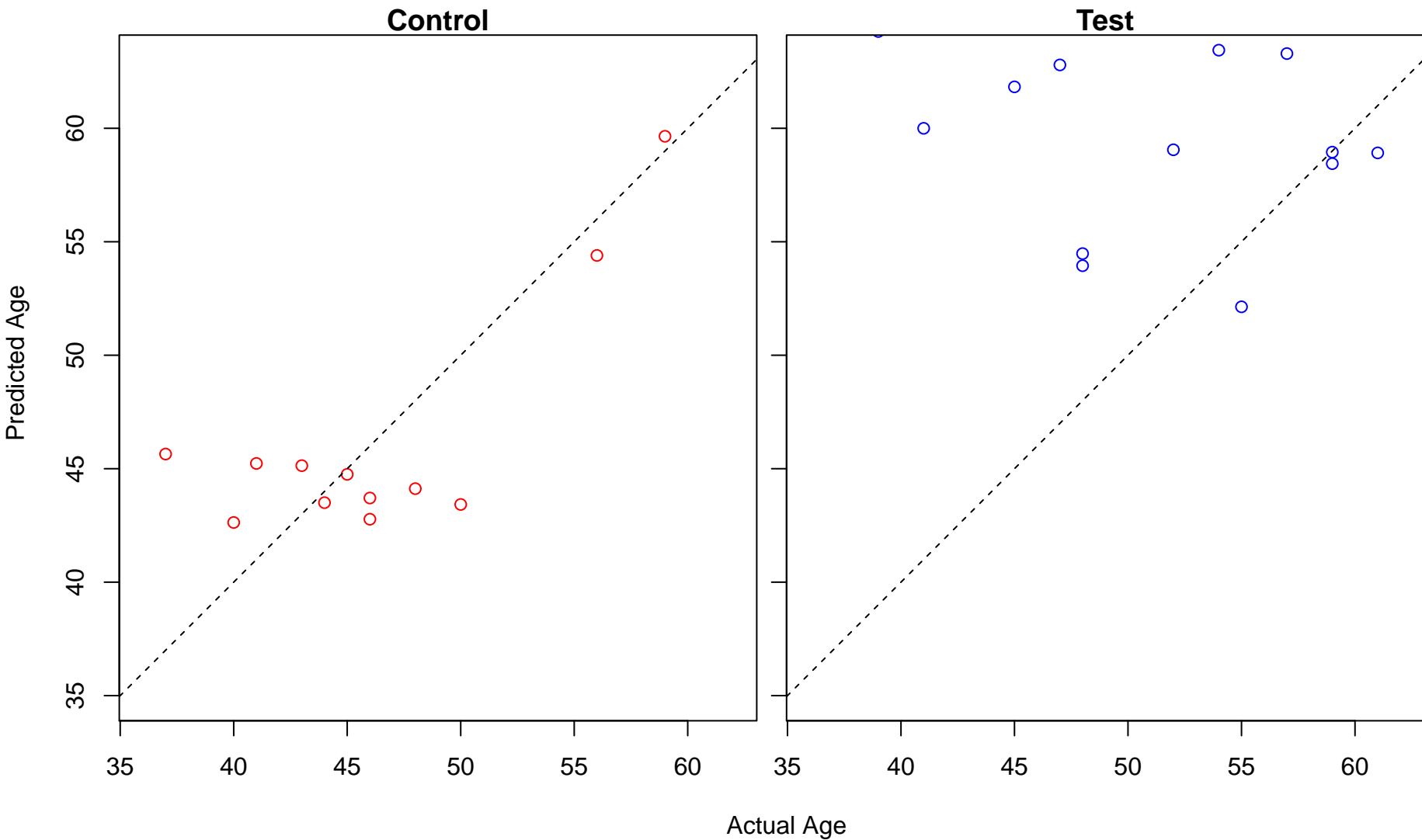
potassium ion import (Score: 4.786074)



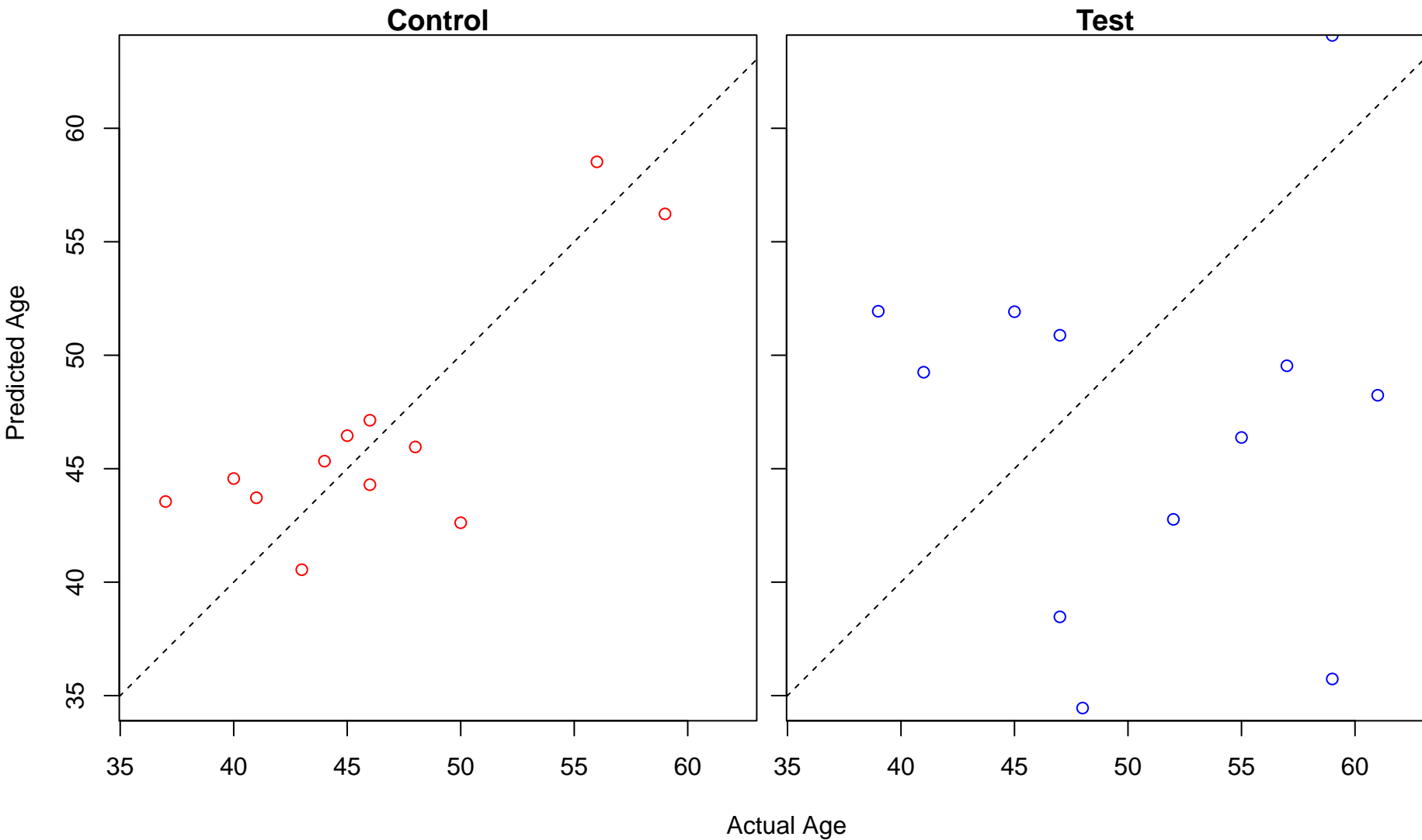
vesicle coating (Score: 4.785122)



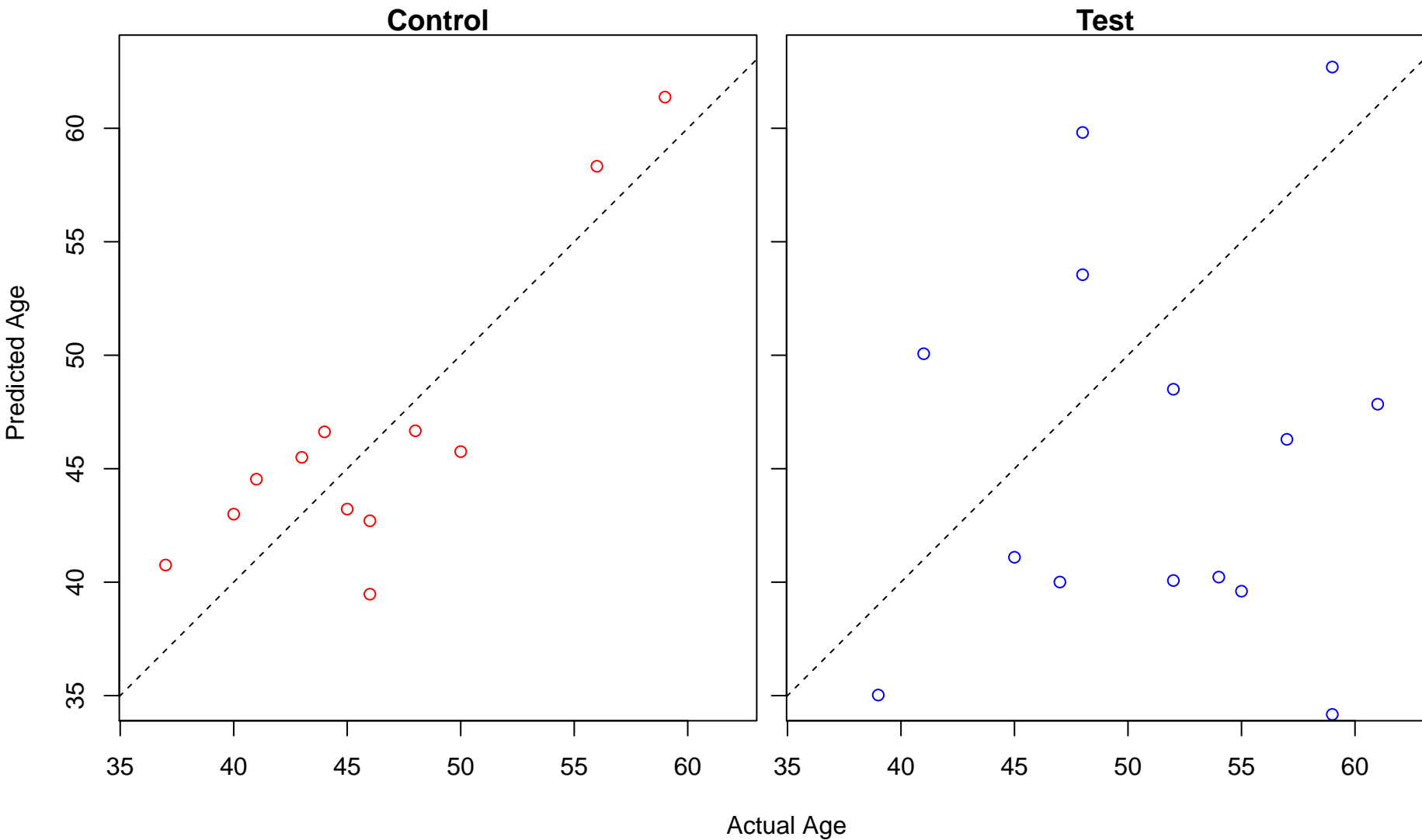
response to vitamin D (Score: 4.778226)



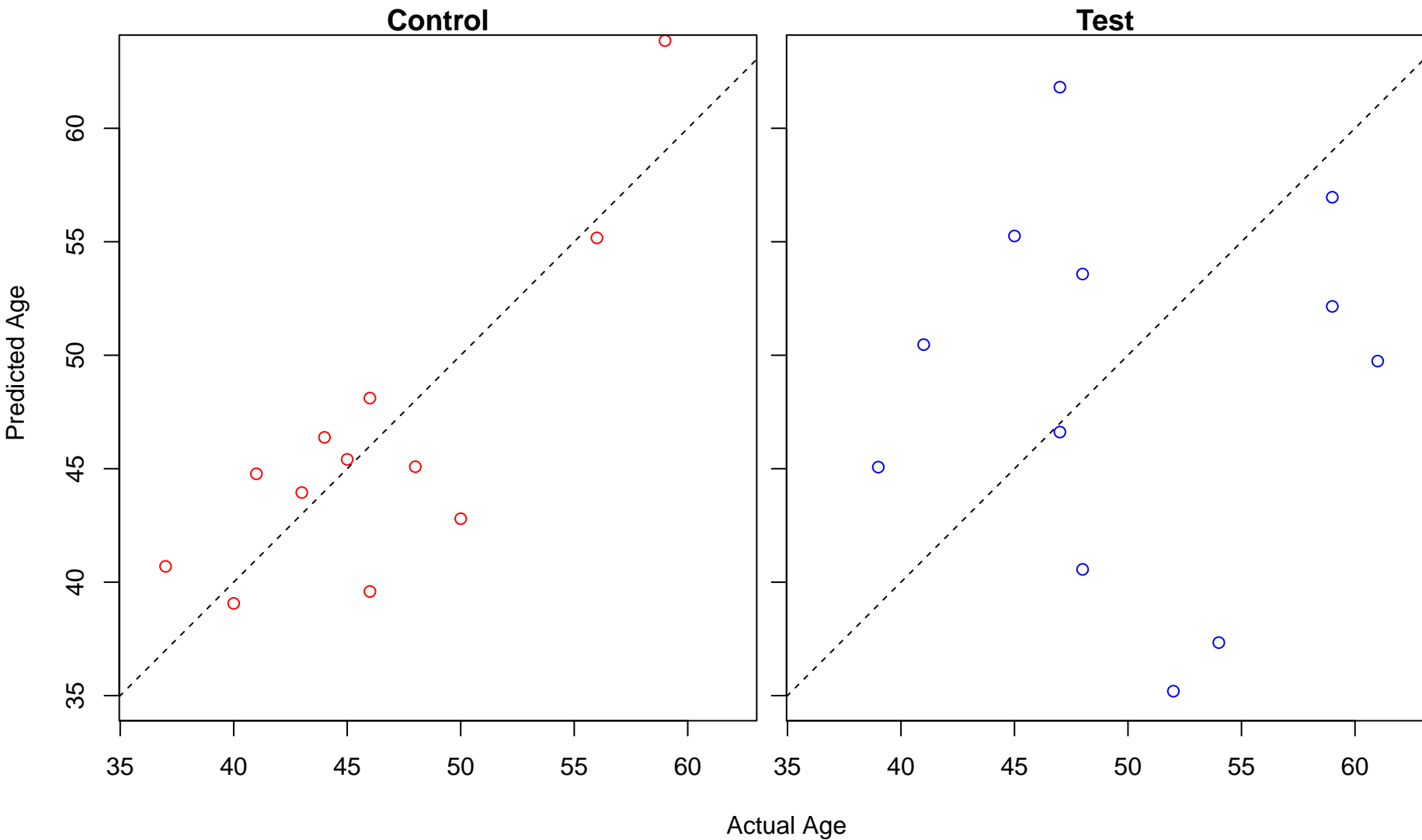
anion homeostasis (Score: 4.776952)



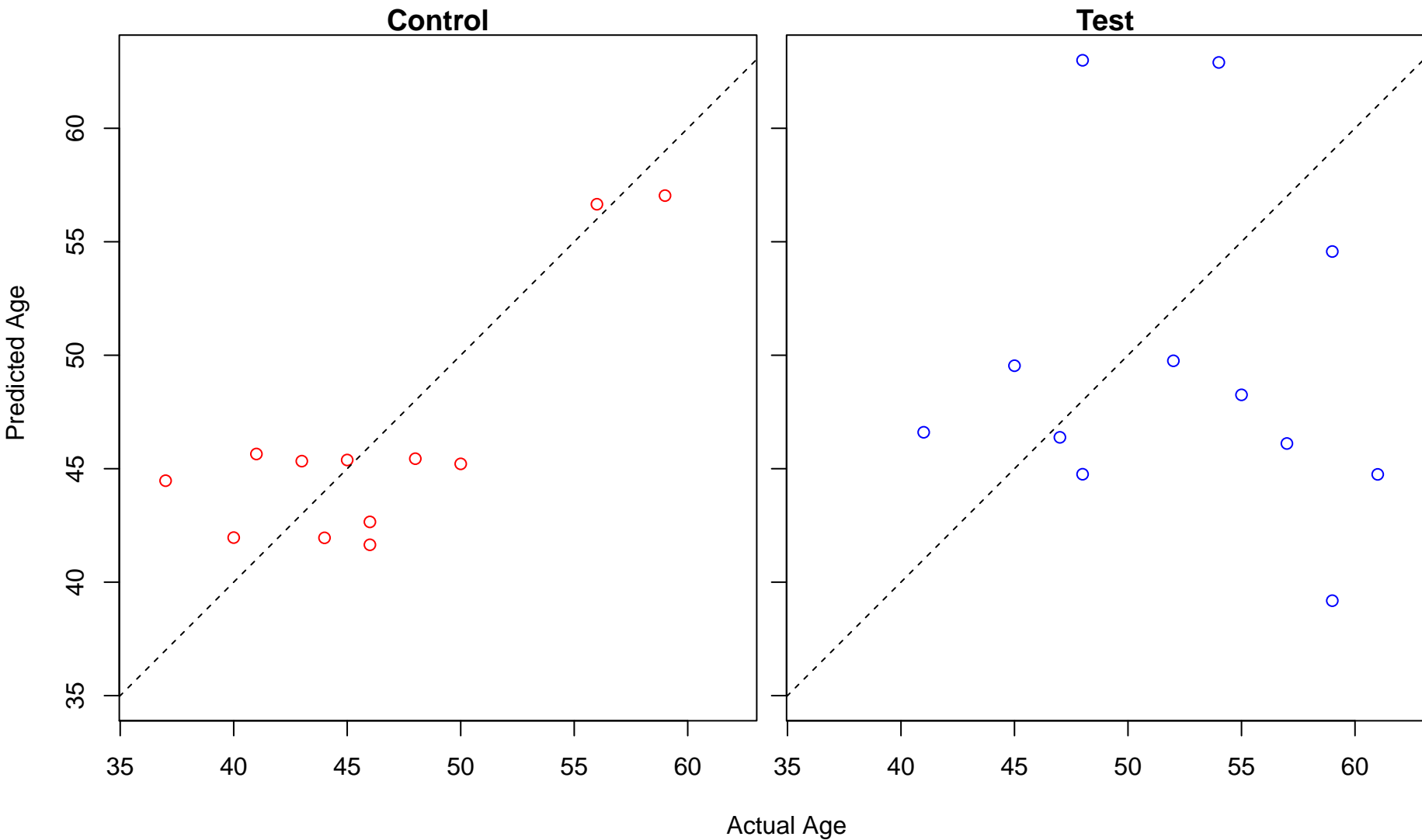
positive regulation of actin filament polymerization (Score: 4.775146)



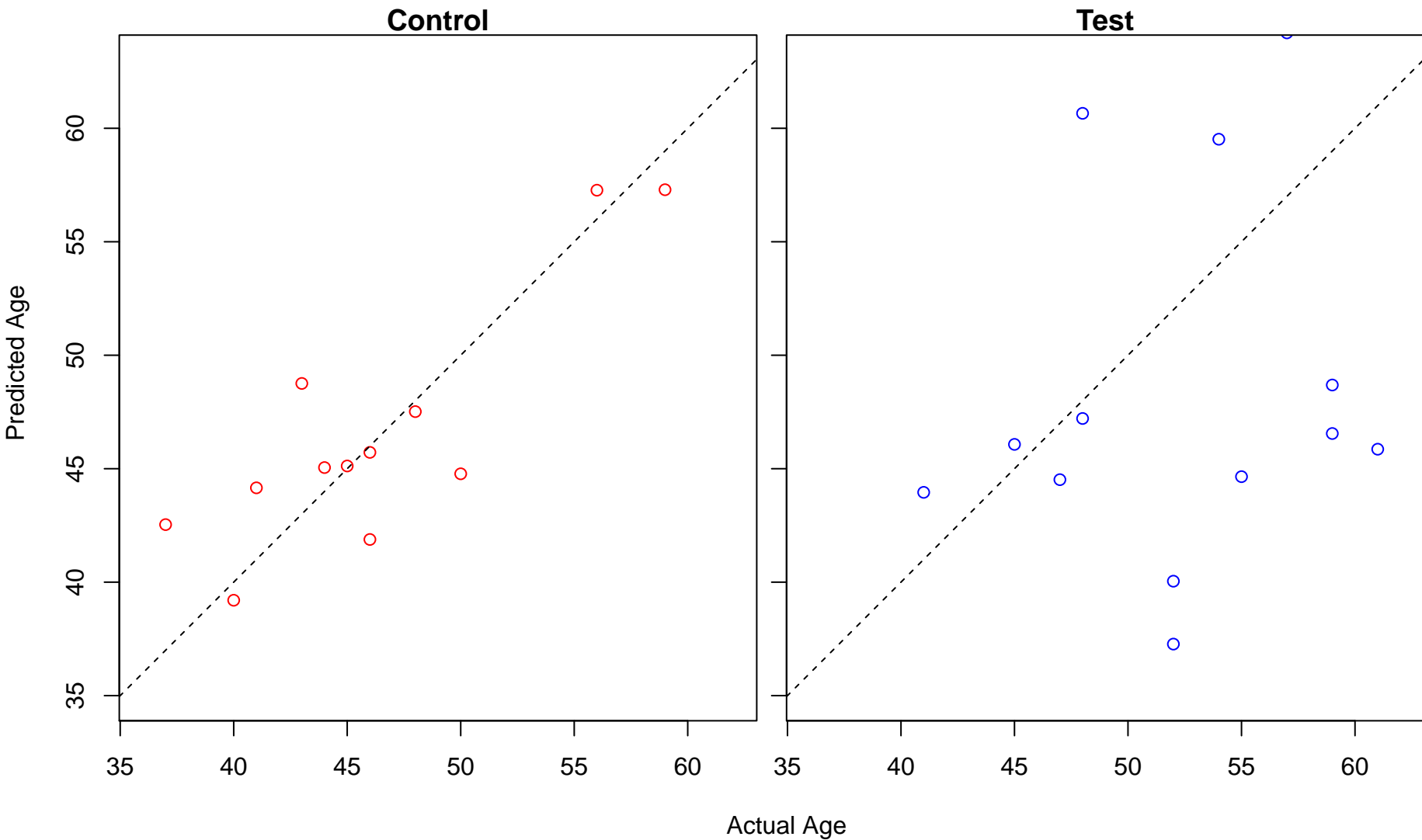
cellular extravasation (Score: 4.774020)



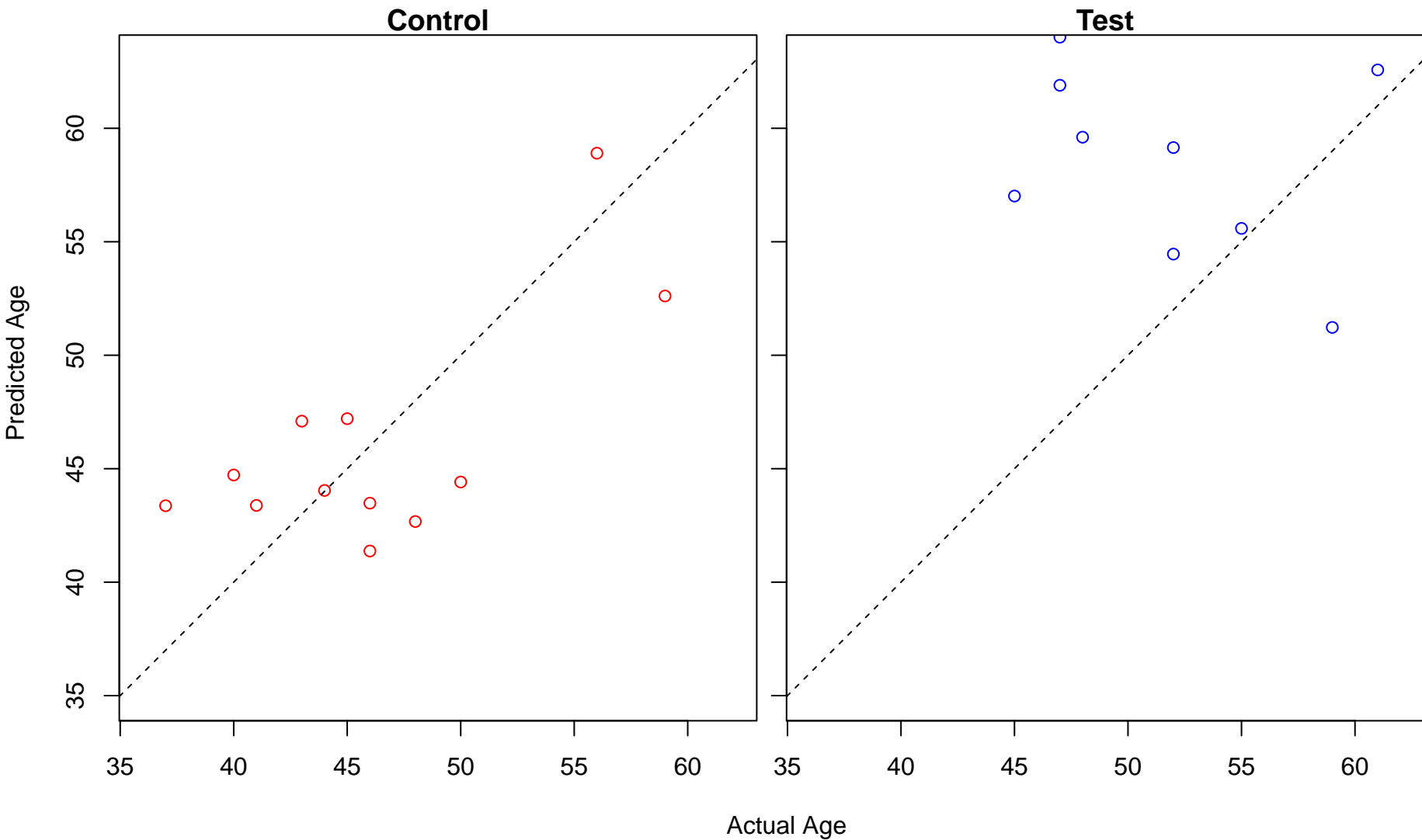
negative regulation of telomere maintenance via telomere lengthening (Score: 4.773808)



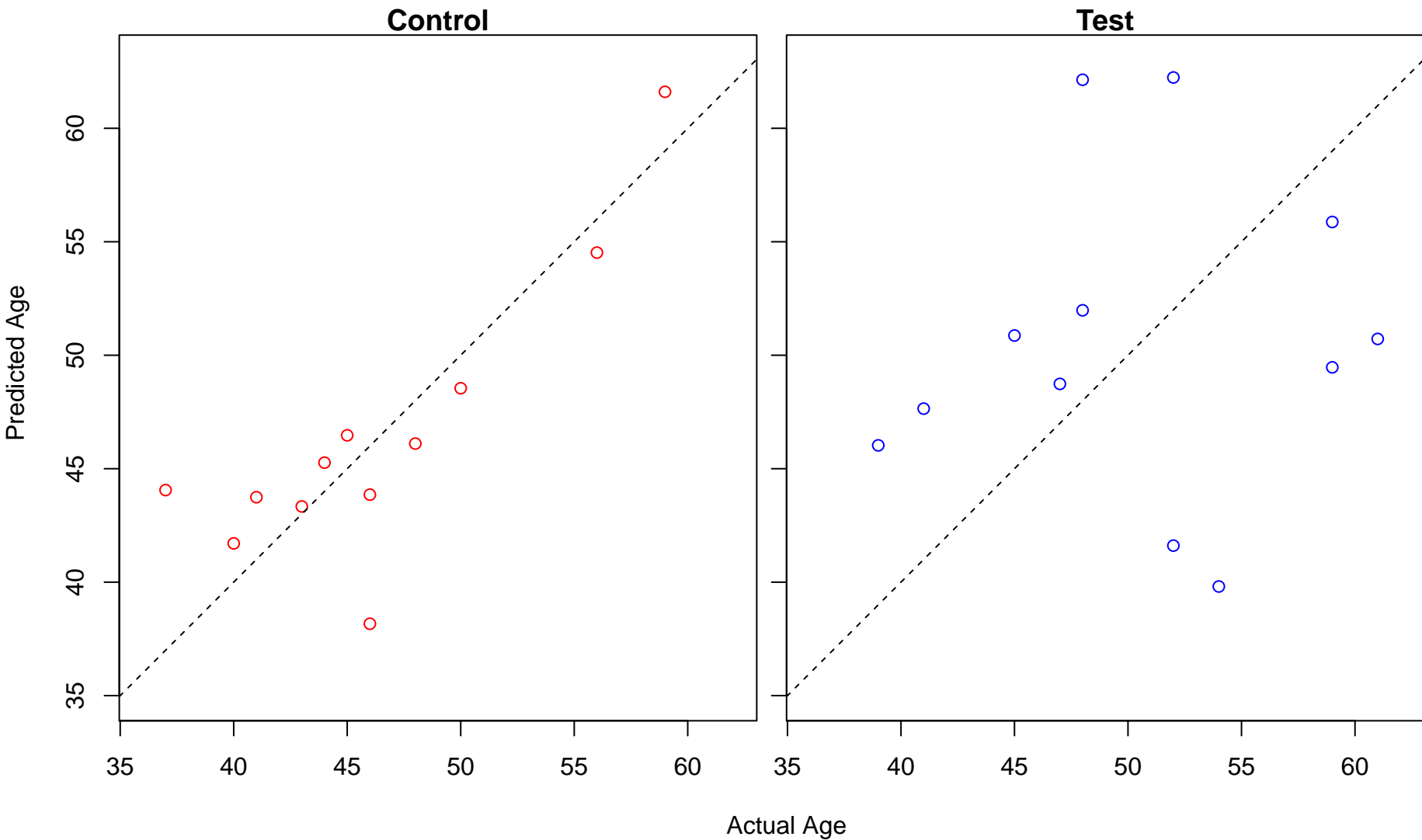
positive regulation of organelle organization (Score: 4.773089)



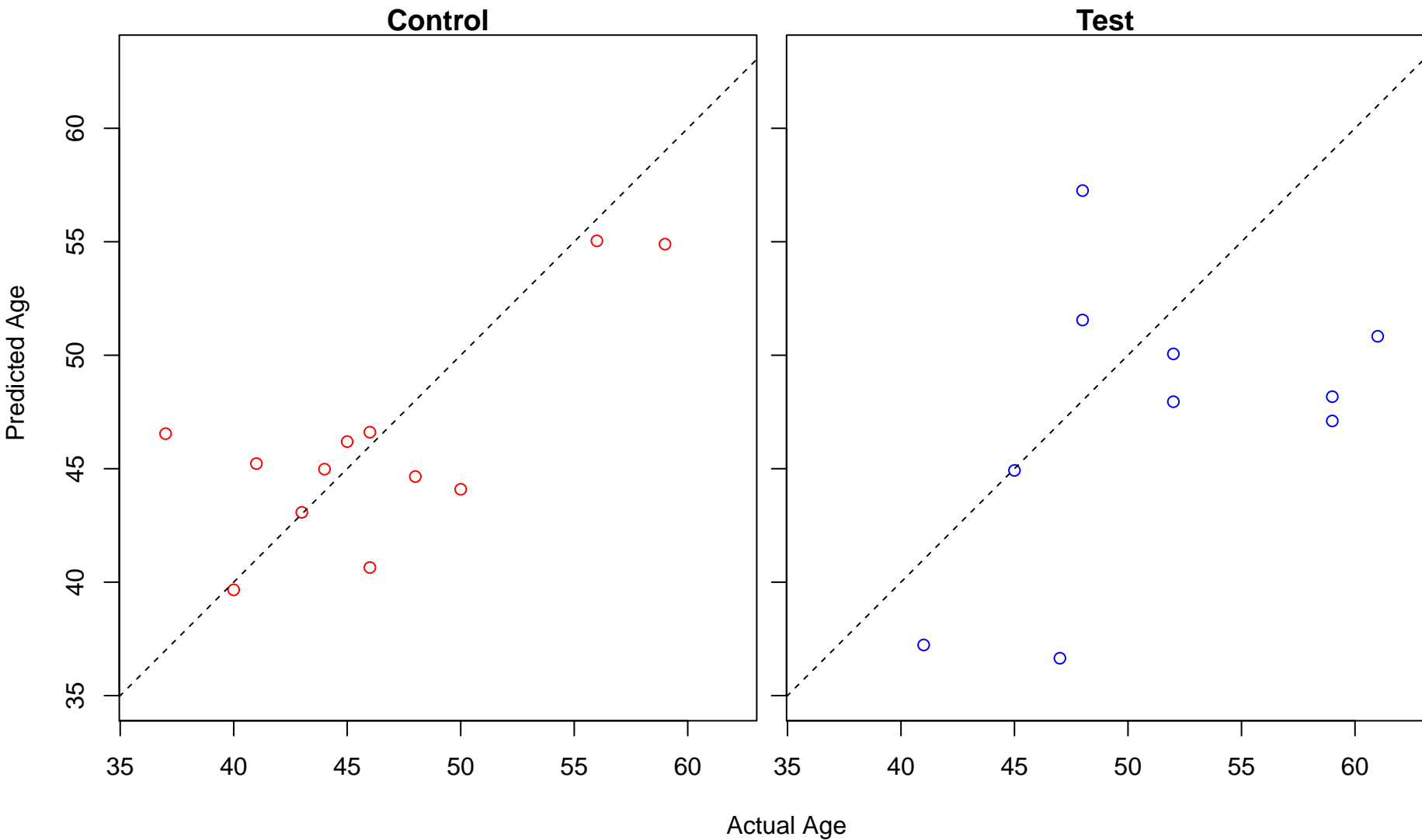
establishment of apical/basal cell polarity (Score: 4.766799)



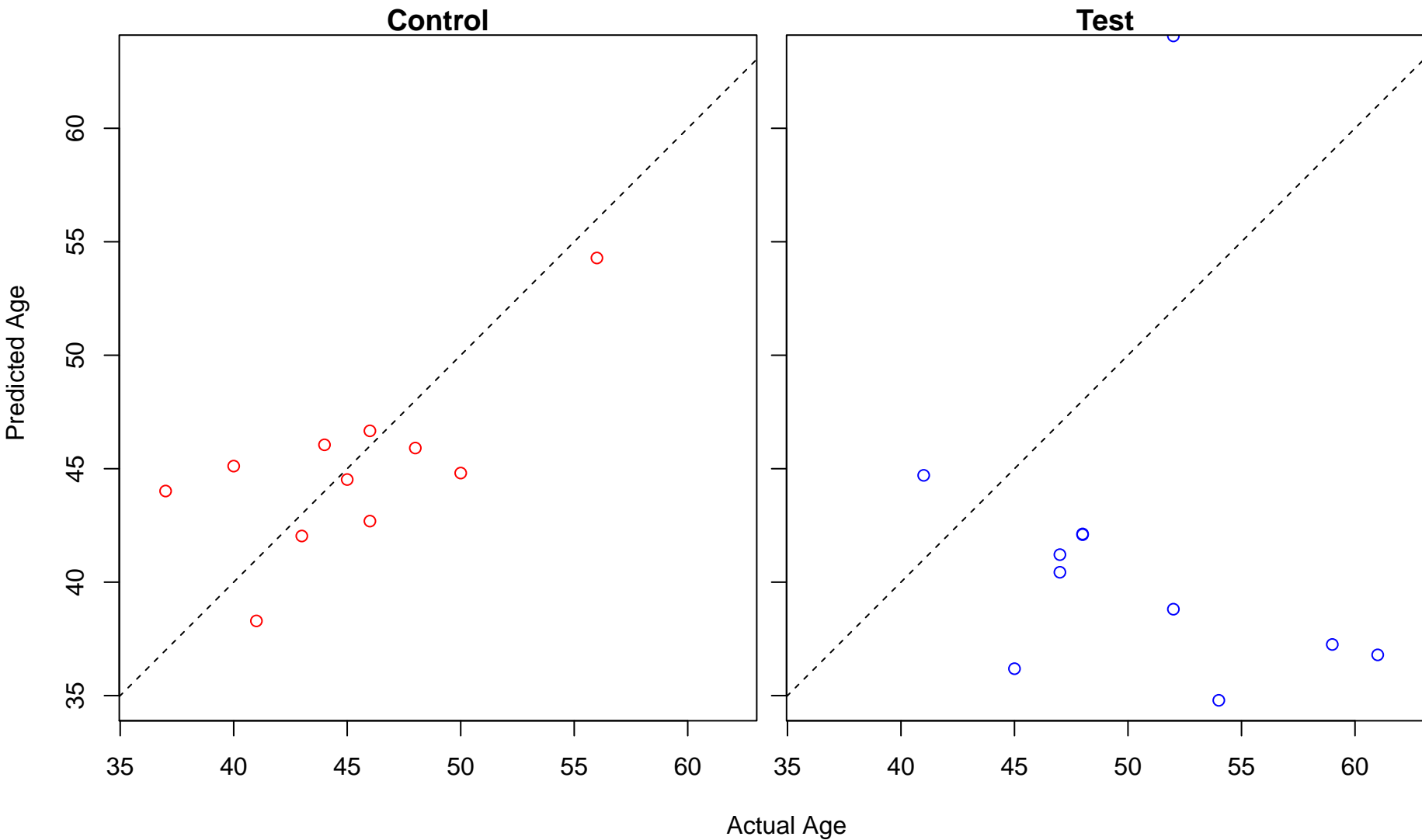
protein localization to lysosome (Score: 4.765873)



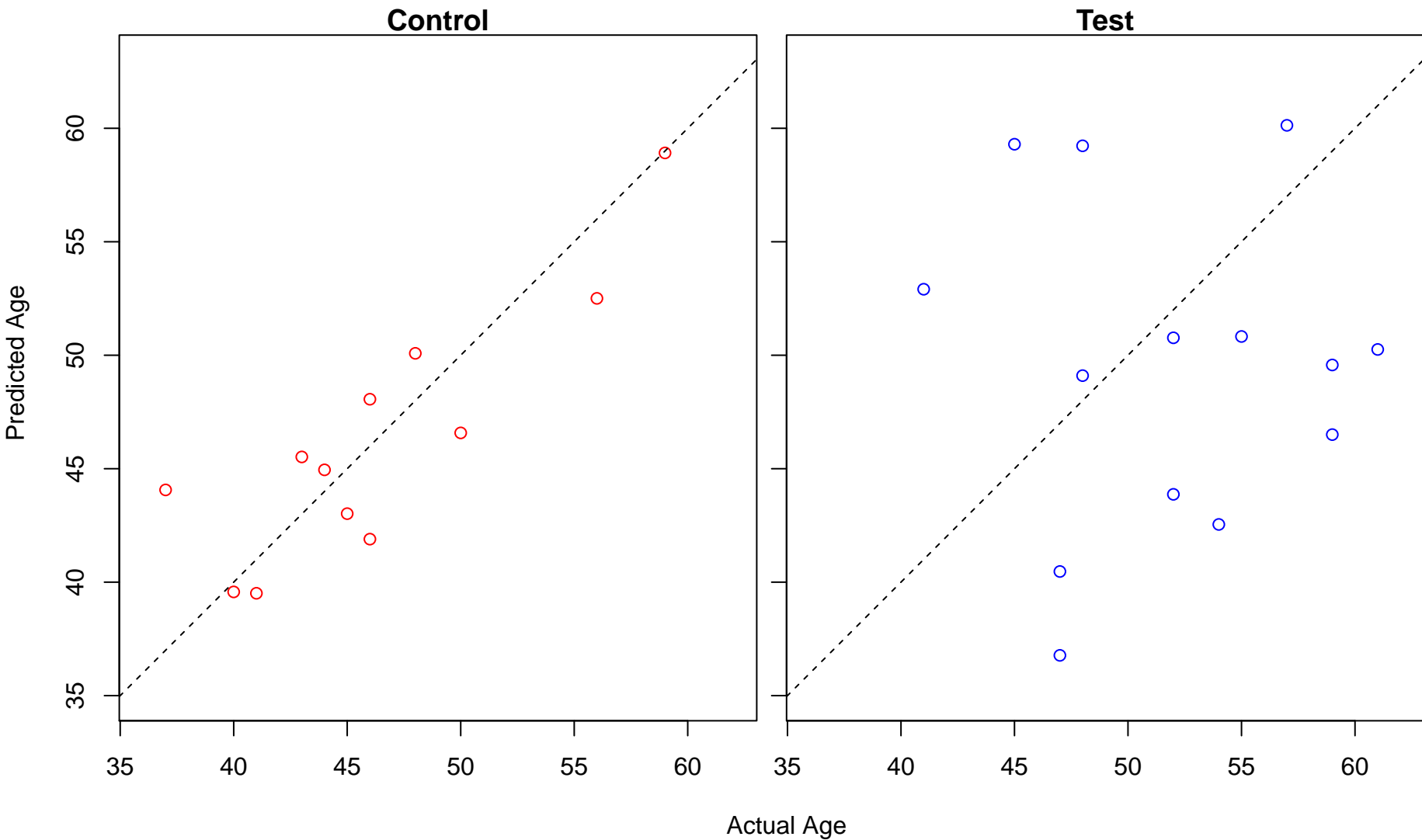
regulation of chemokine (C-X-C motif) ligand 2 production (Score: 4.762620)



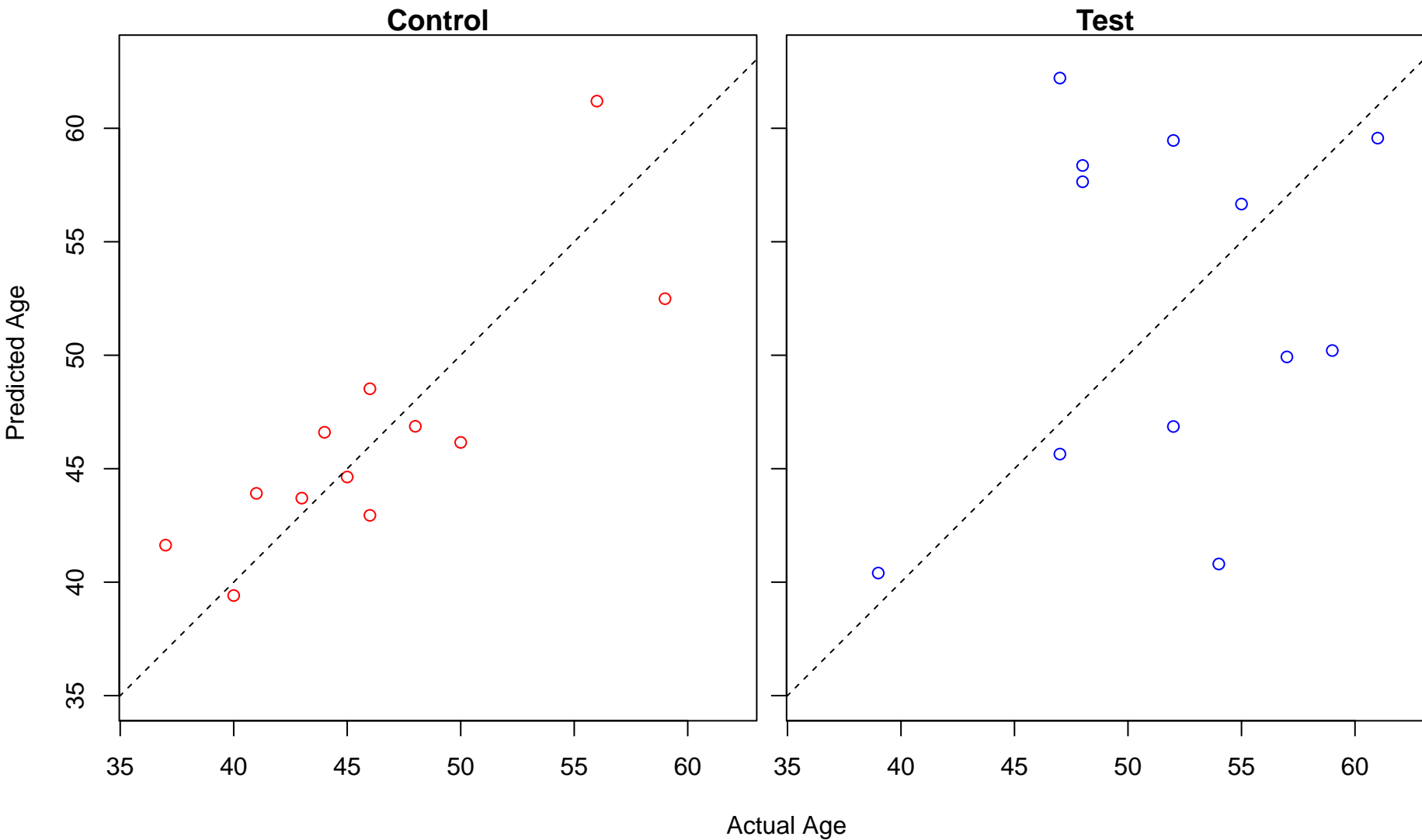
sister chromatid segregation (Score: 4.762497)



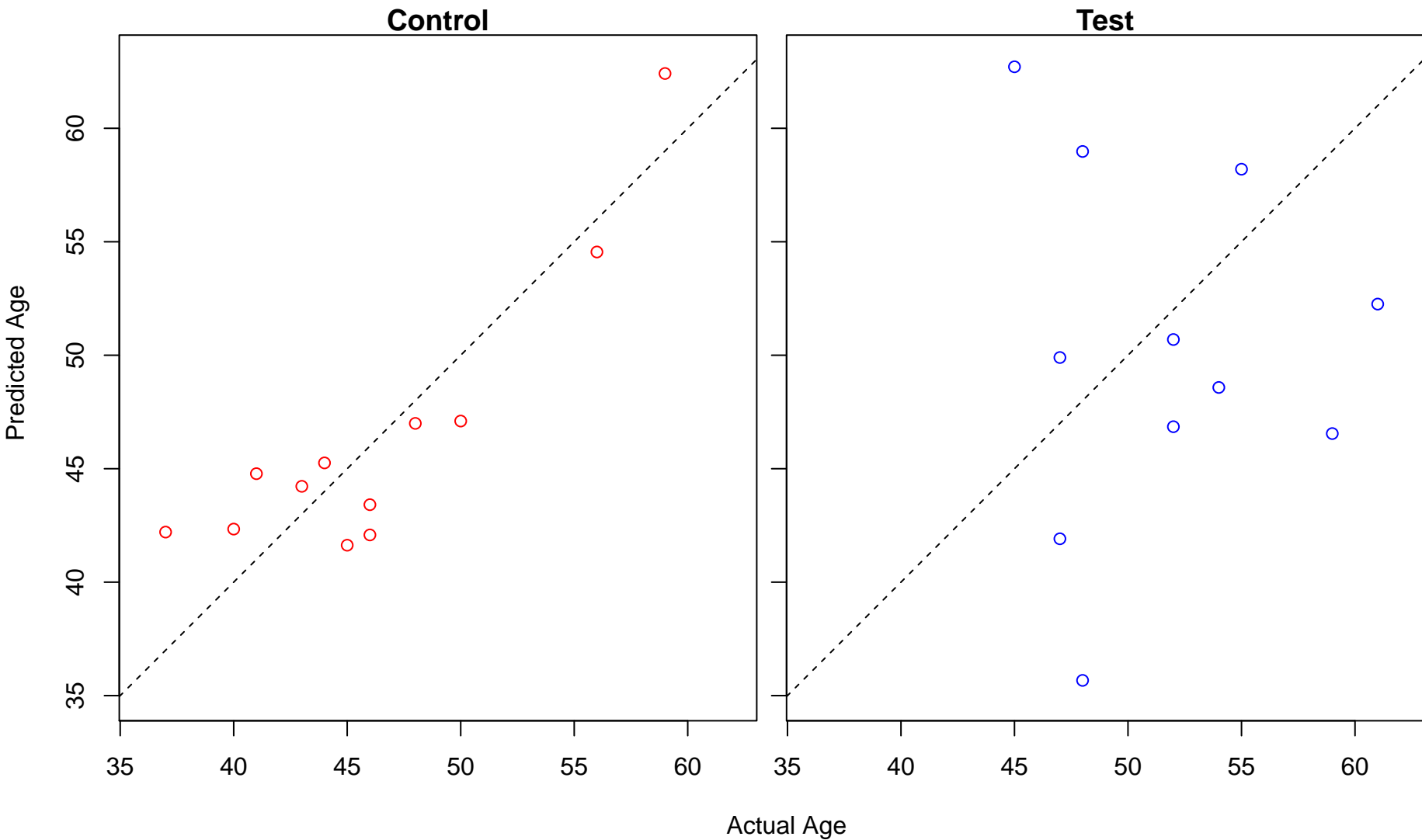
NADP metabolic process (Score: 4.755738)



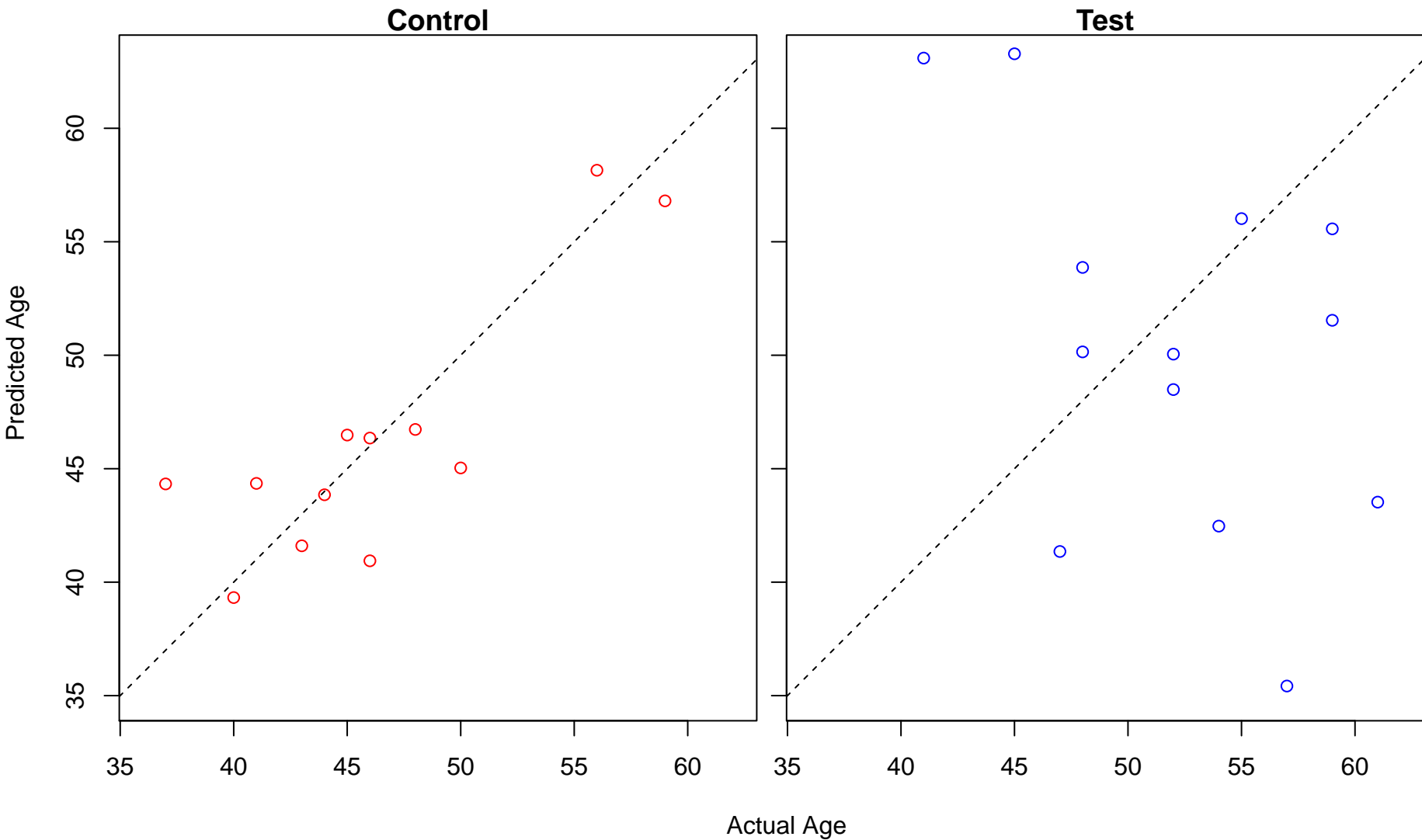
regulation of peptidyl-serine phosphorylation (Score: 4.755724)



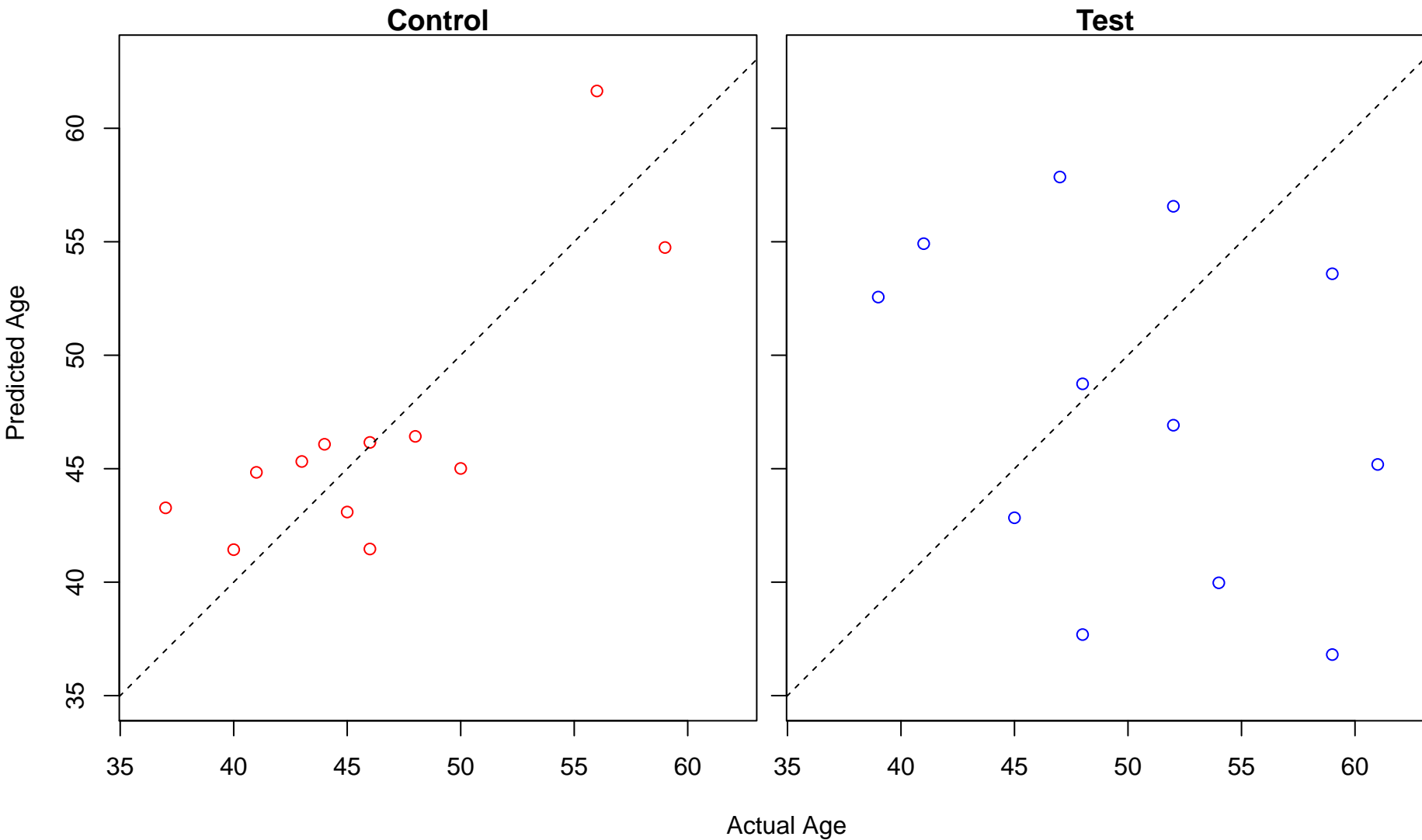
negative regulation of lipid biosynthetic process (Score: 4.752159)



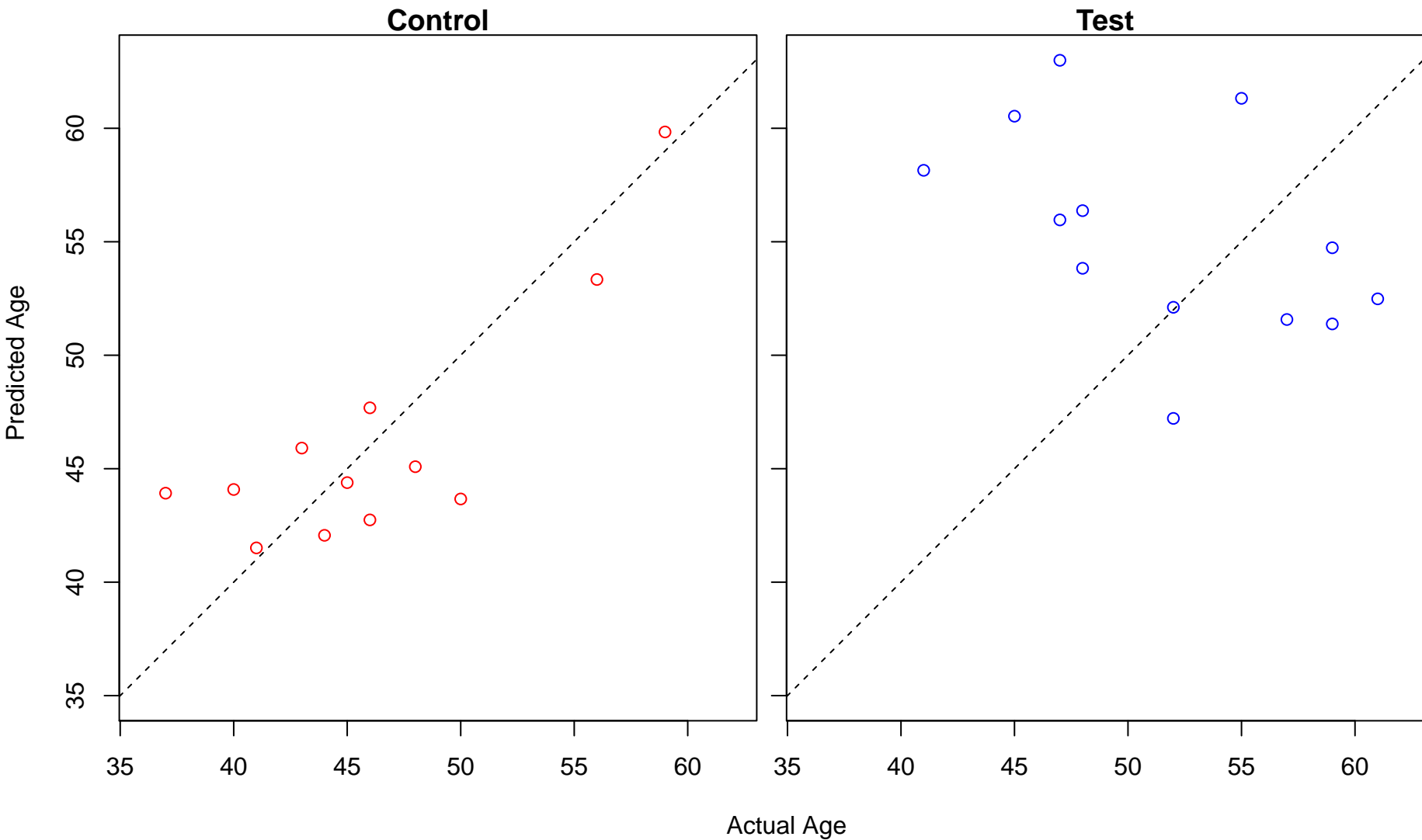
UDP-N-acetylglucosamine biosynthetic process (Score: 4.750718)



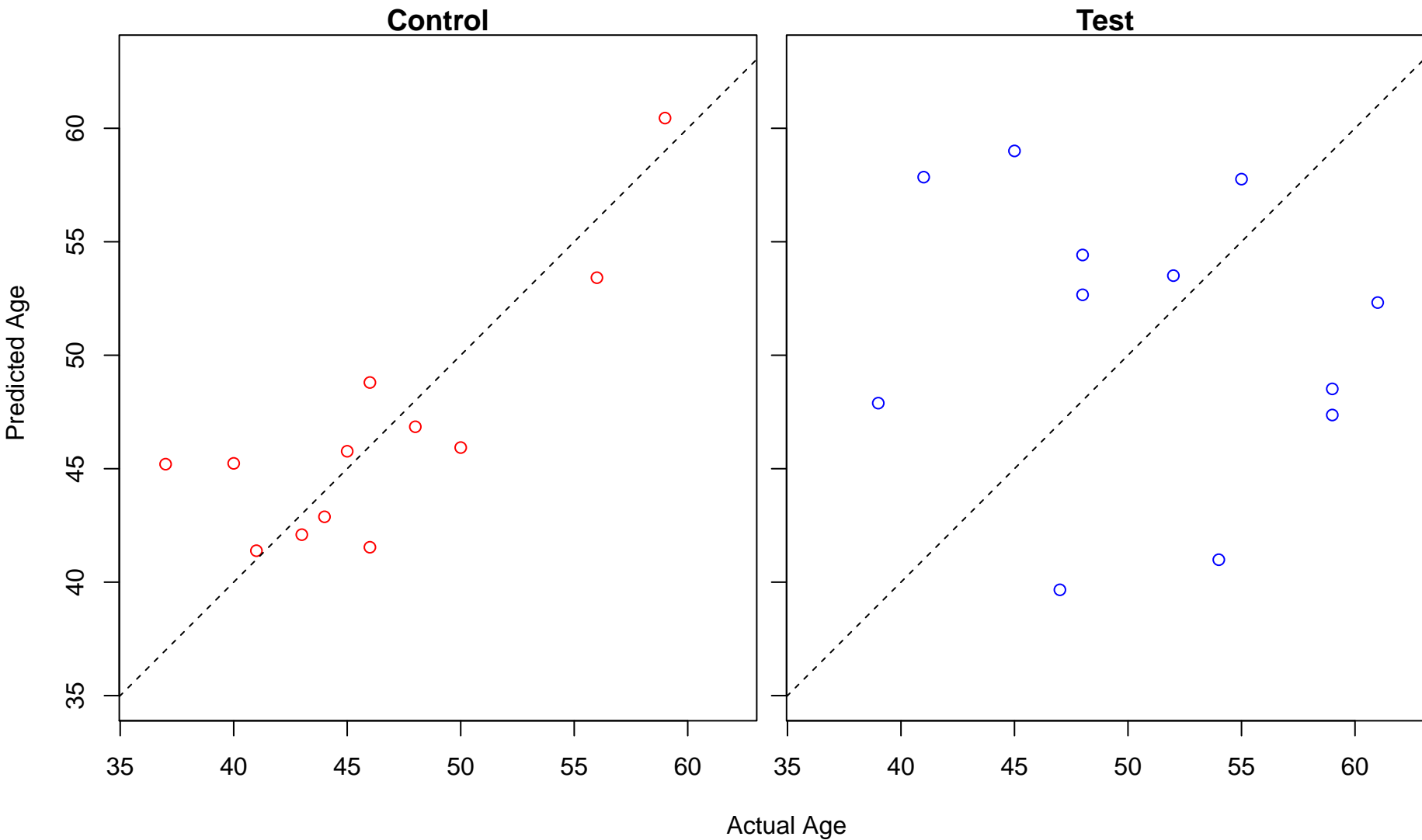
positive regulation of proteolysis (Score: 4.750504)



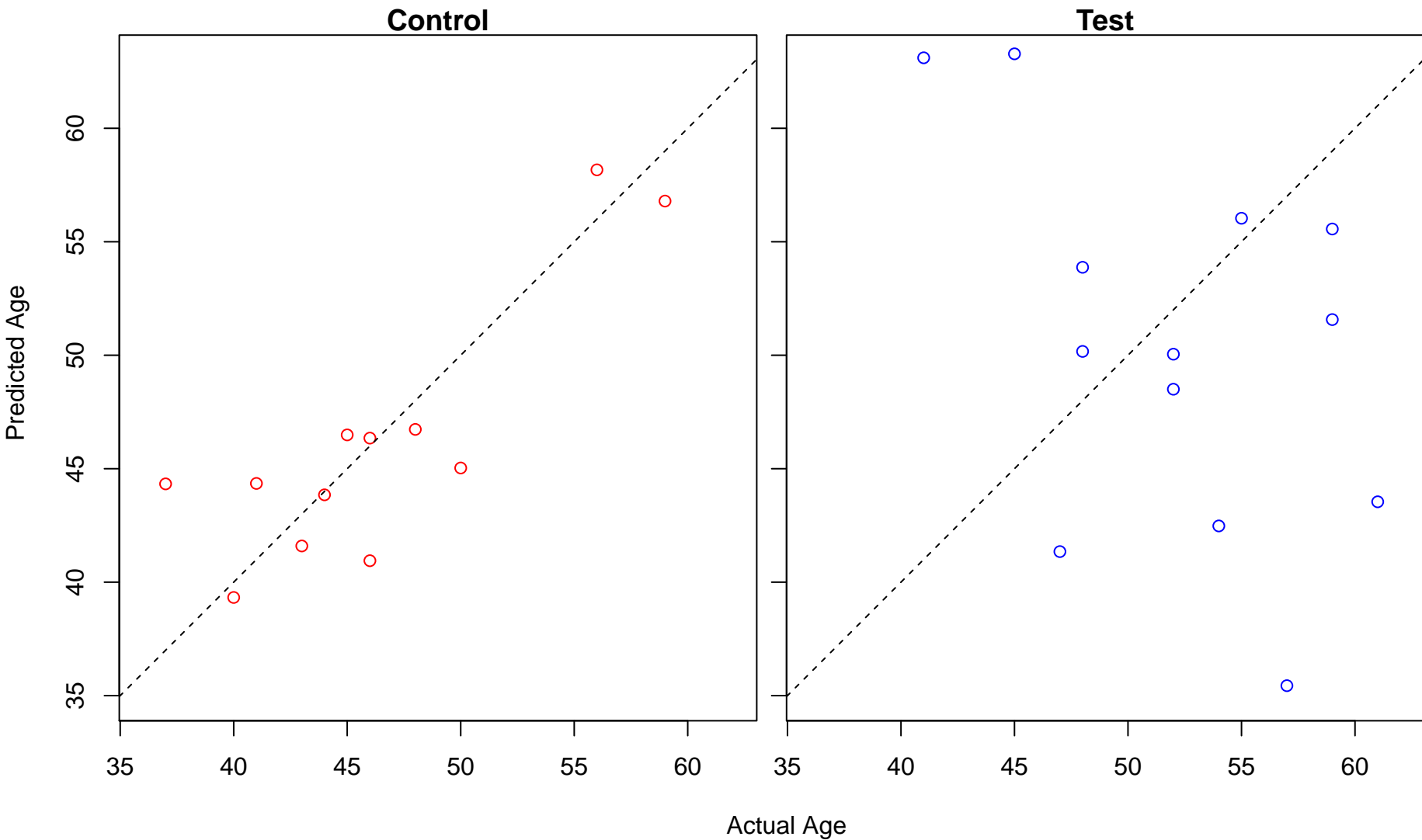
positive regulation of glycogen metabolic process (Score: 4.749825)



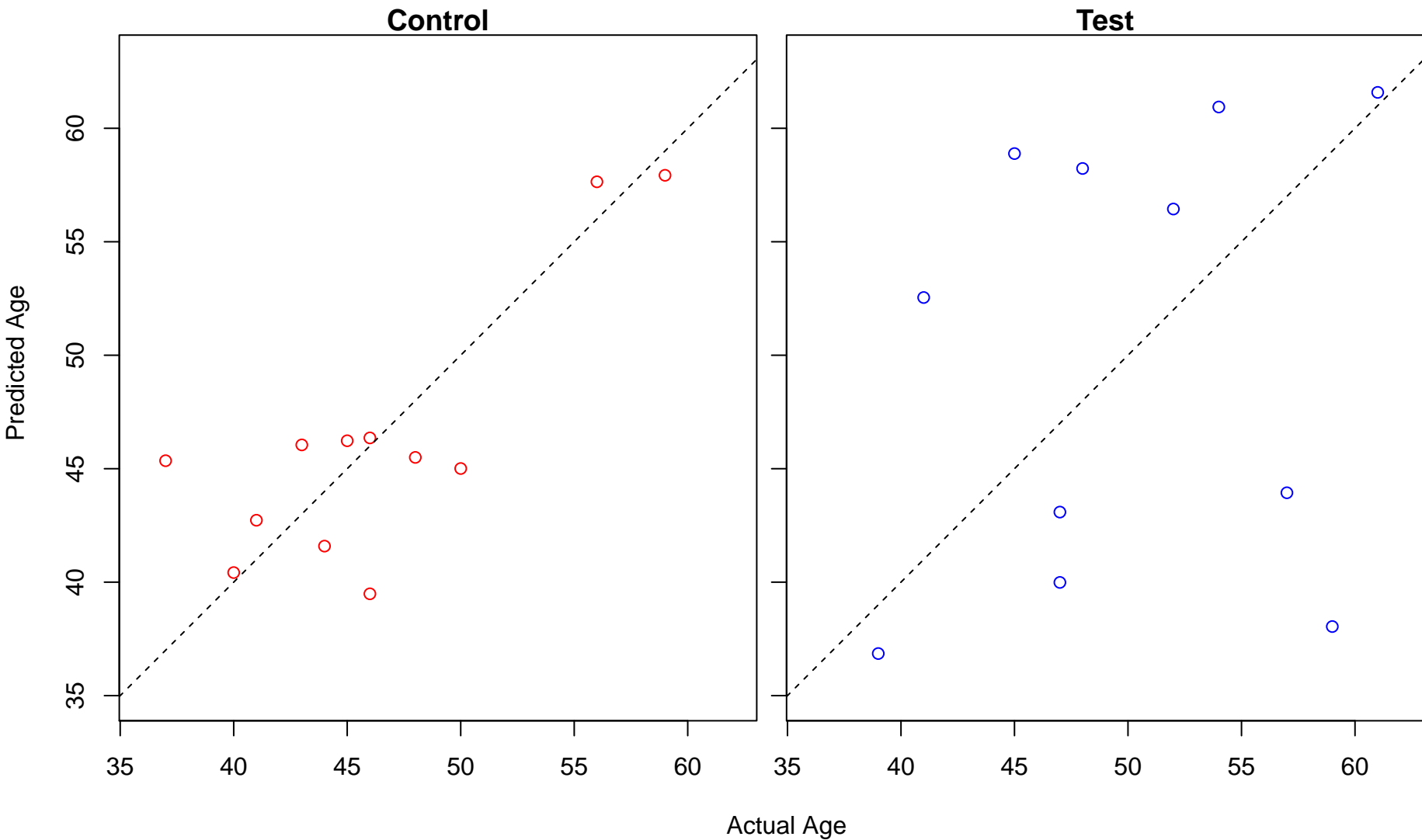
positive regulation of carbohydrate metabolic process (Score: 4.744253)



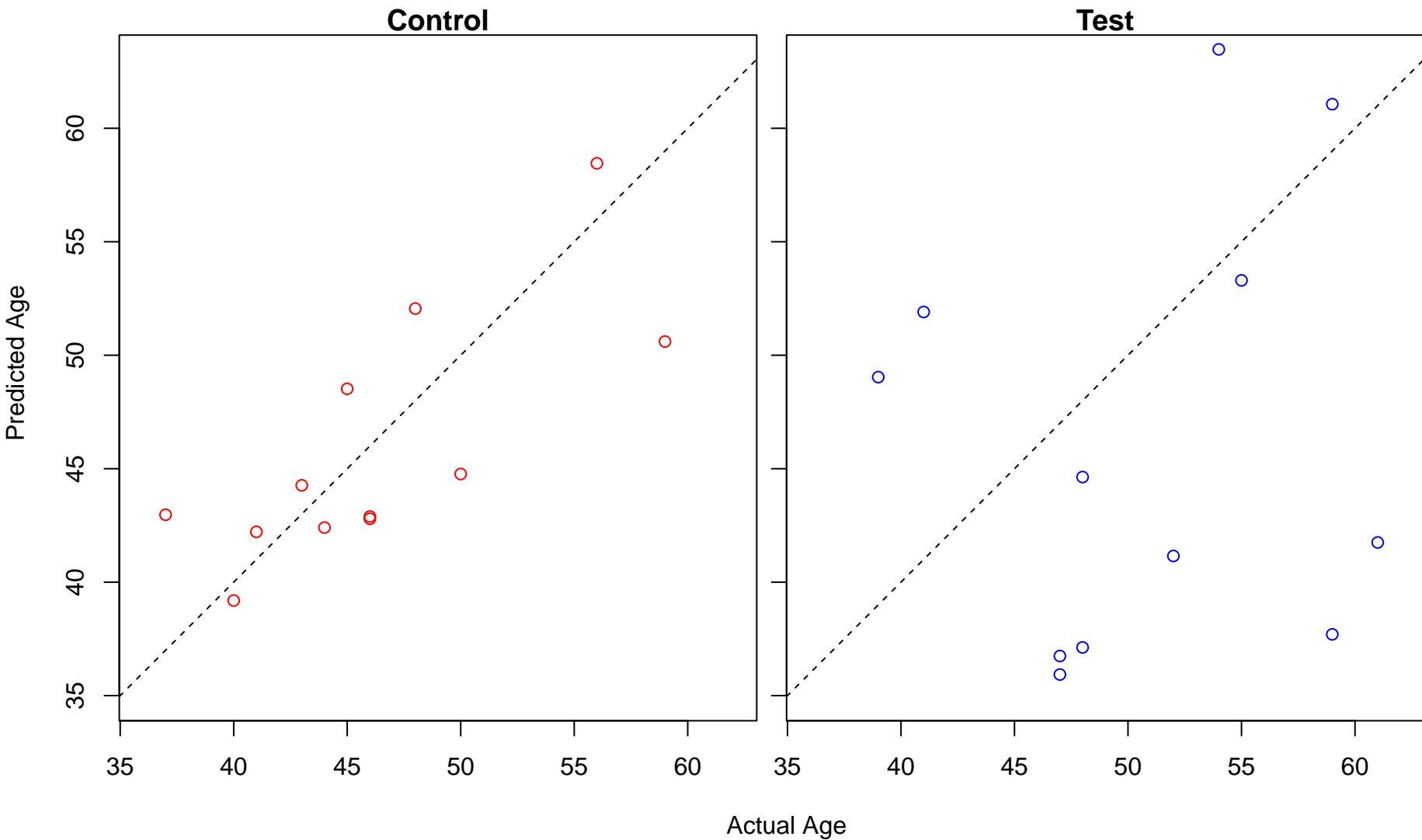
amino sugar biosynthetic process (Score: 4.743827)



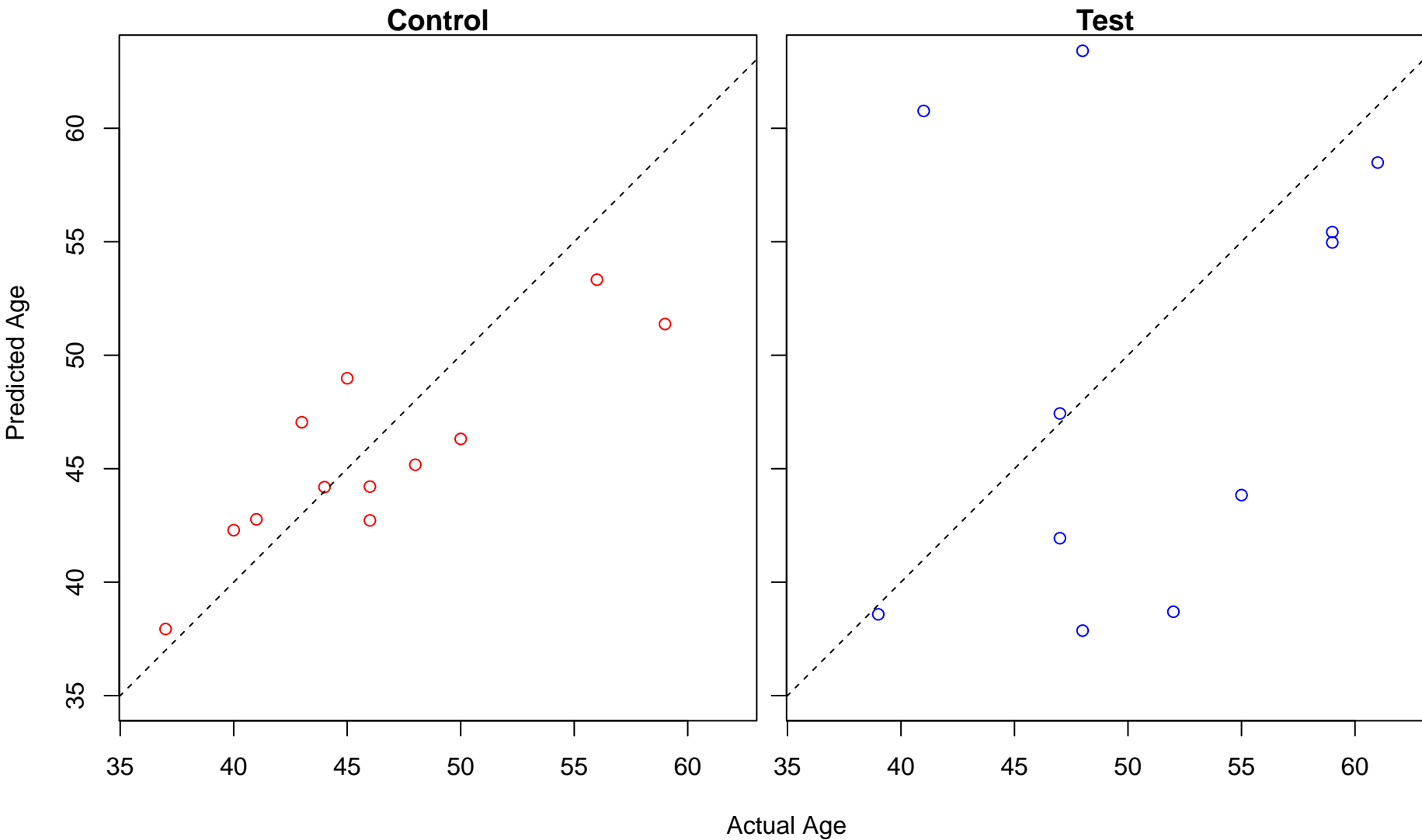
positive regulation of cell growth (Score: 4.724375)



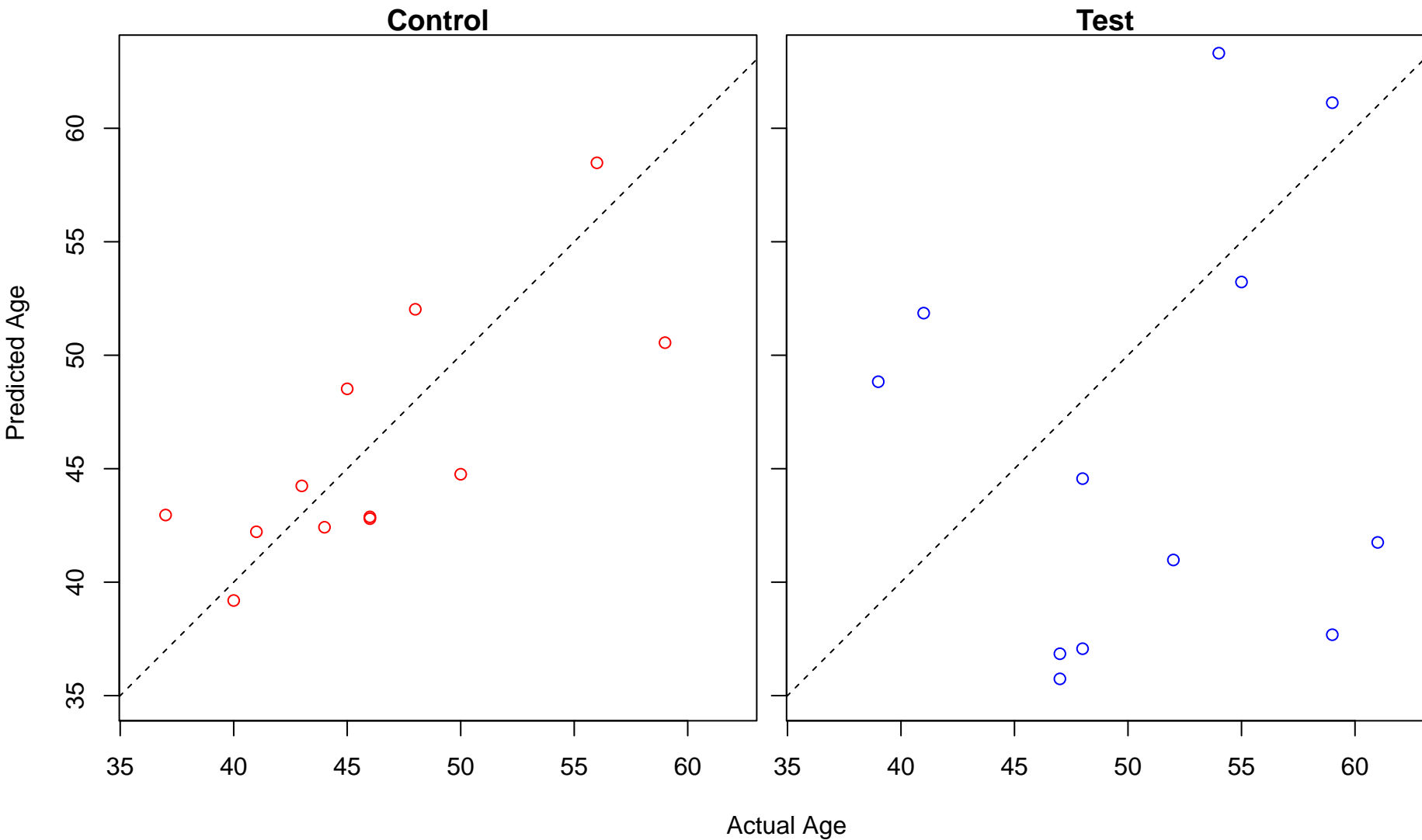
atrioventricular valve morphogenesis (Score: 4.723062)



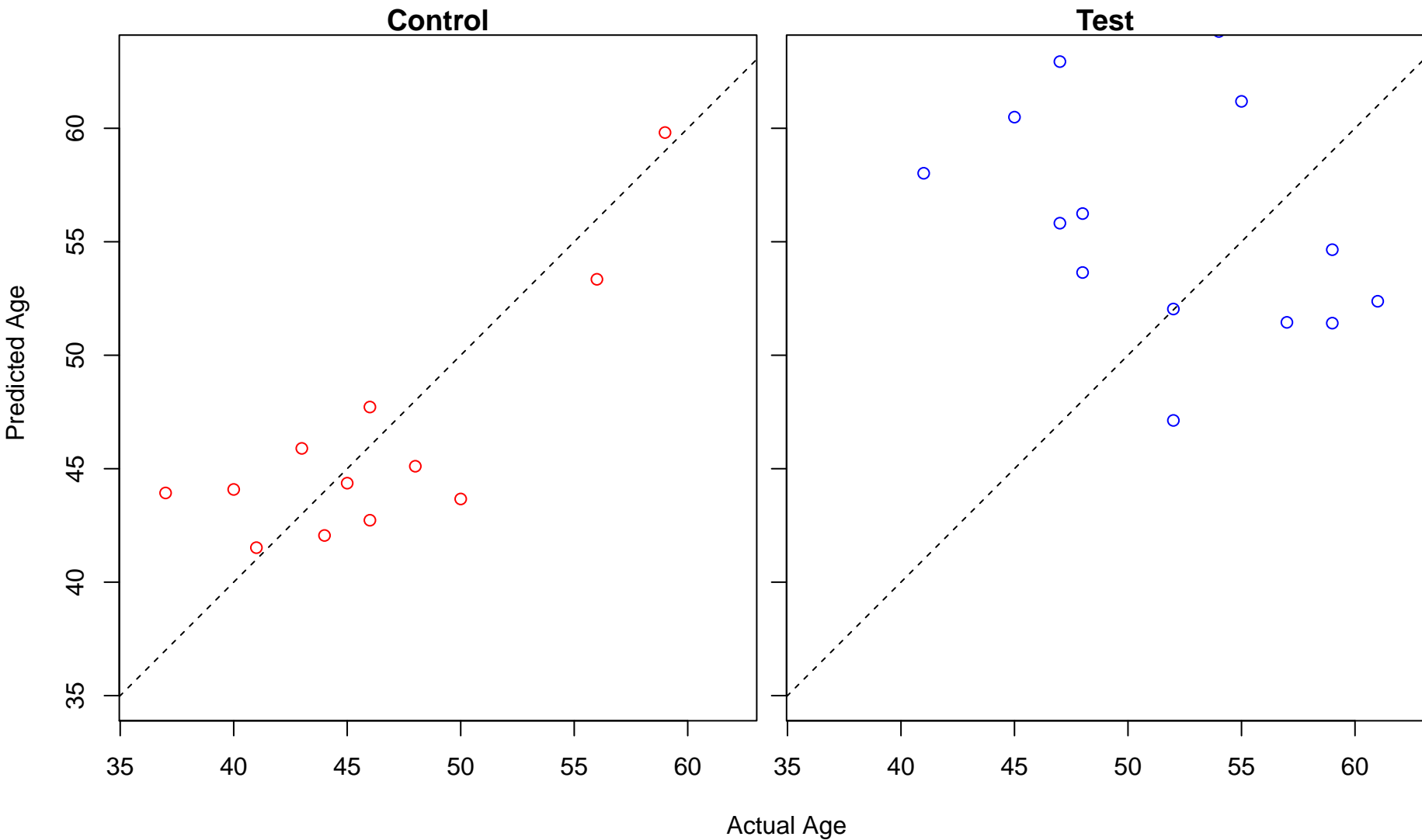
monocyte differentiation (Score: 4.718296)



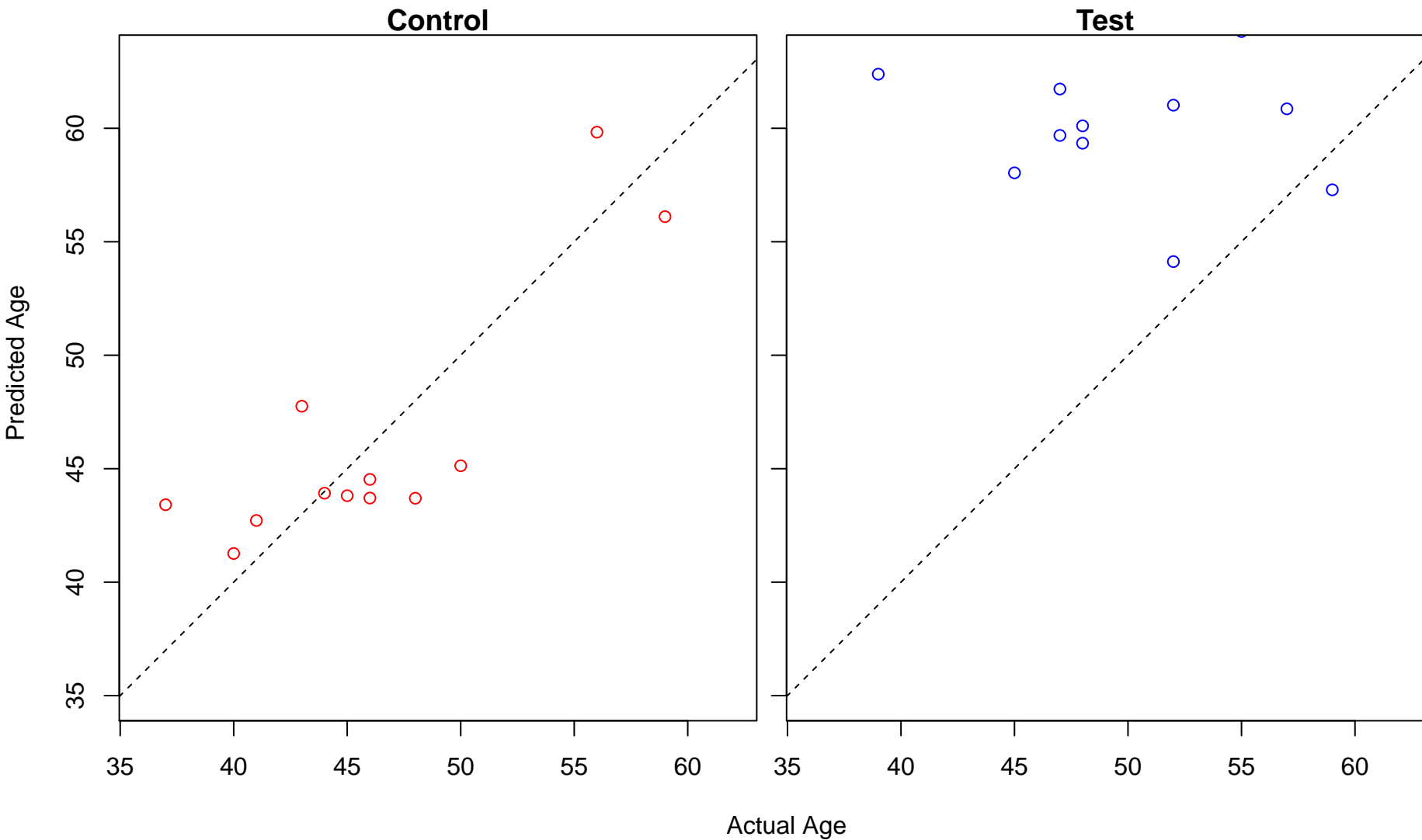
atrioventricular valve development (Score: 4.703717)



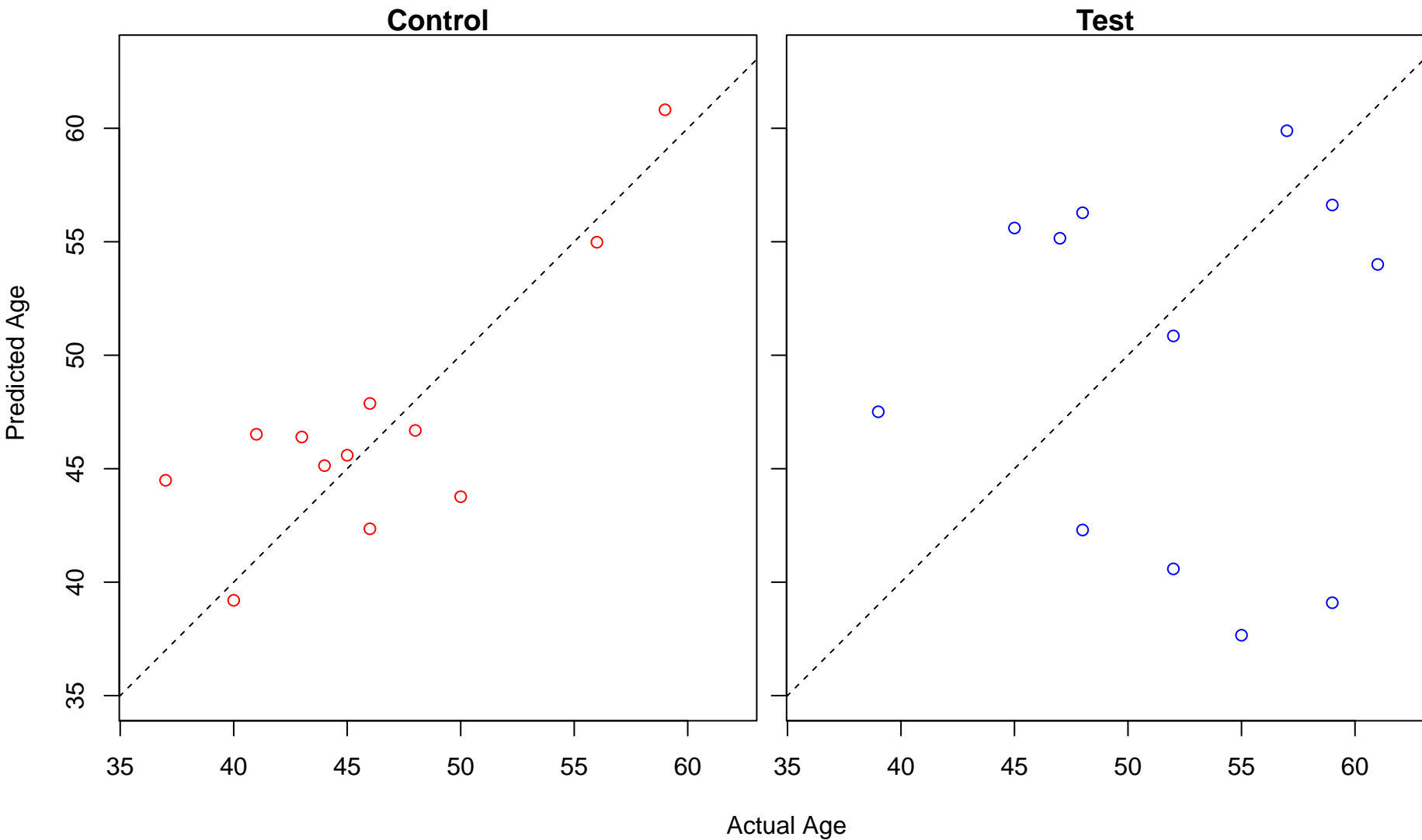
positive regulation of glycogen biosynthetic process (Score: 4.699960)



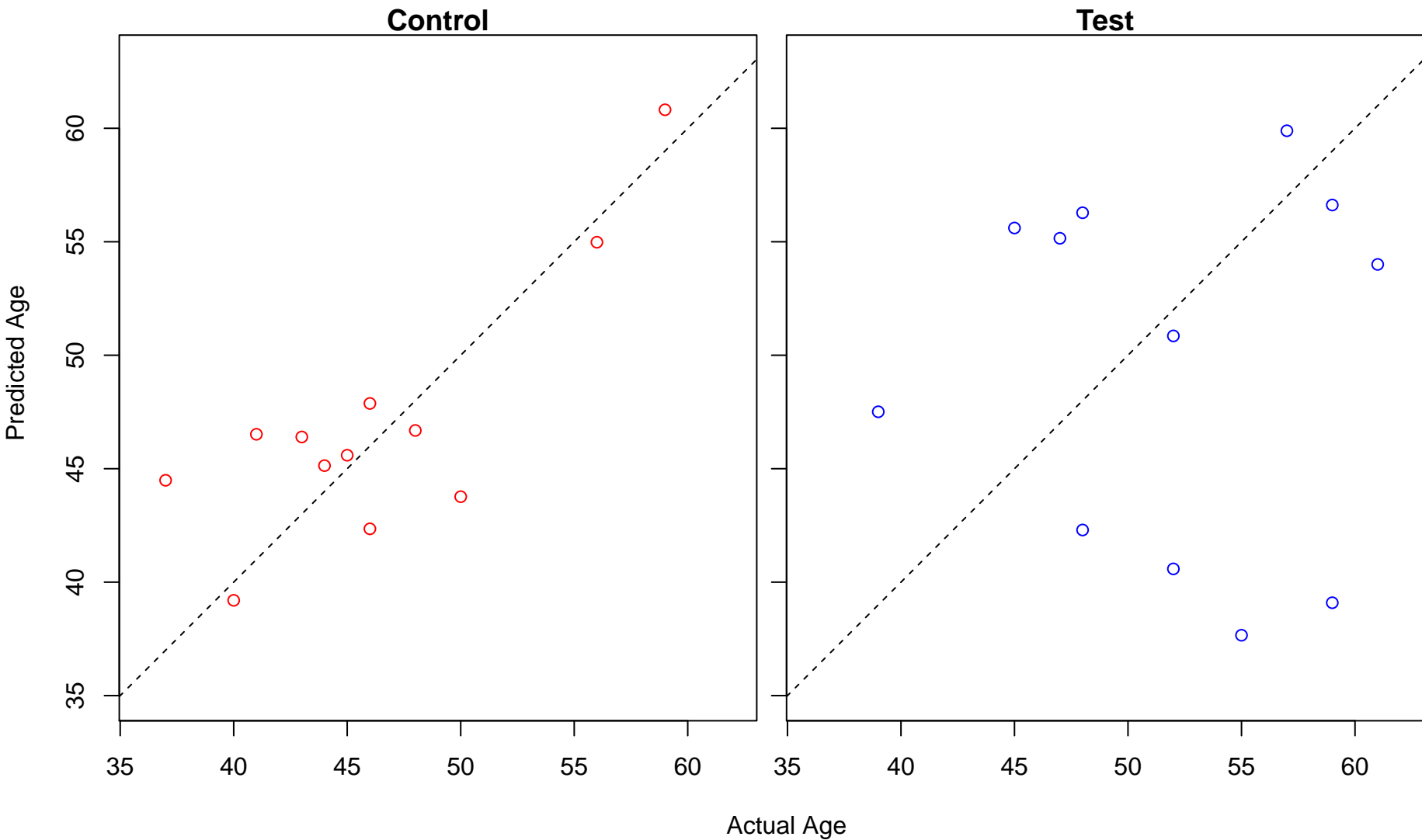
negative regulation of insulin-like growth factor receptor signaling pathway (Score: 4.698462)



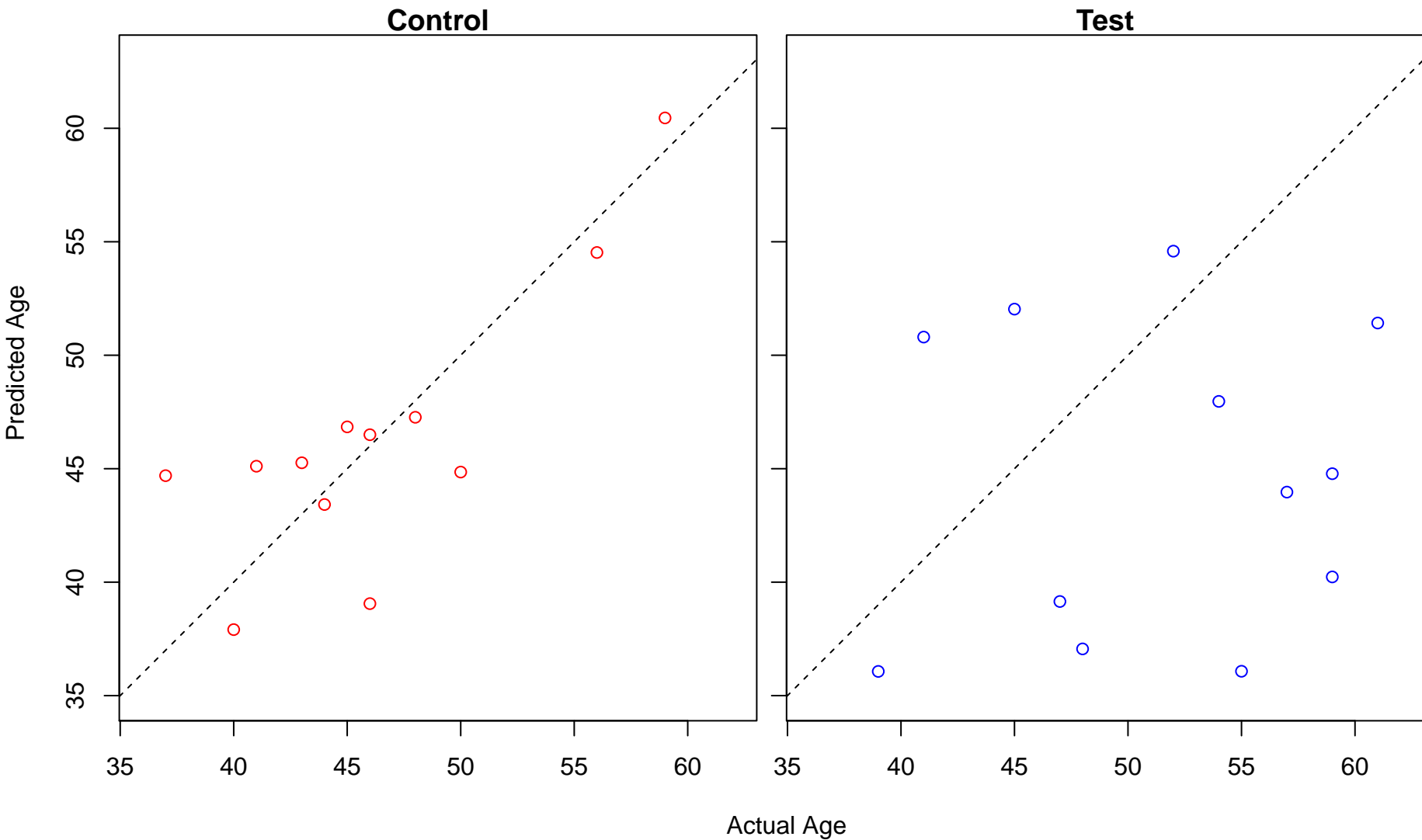
negative regulation of phosphorus metabolic process (Score: 4.698140)



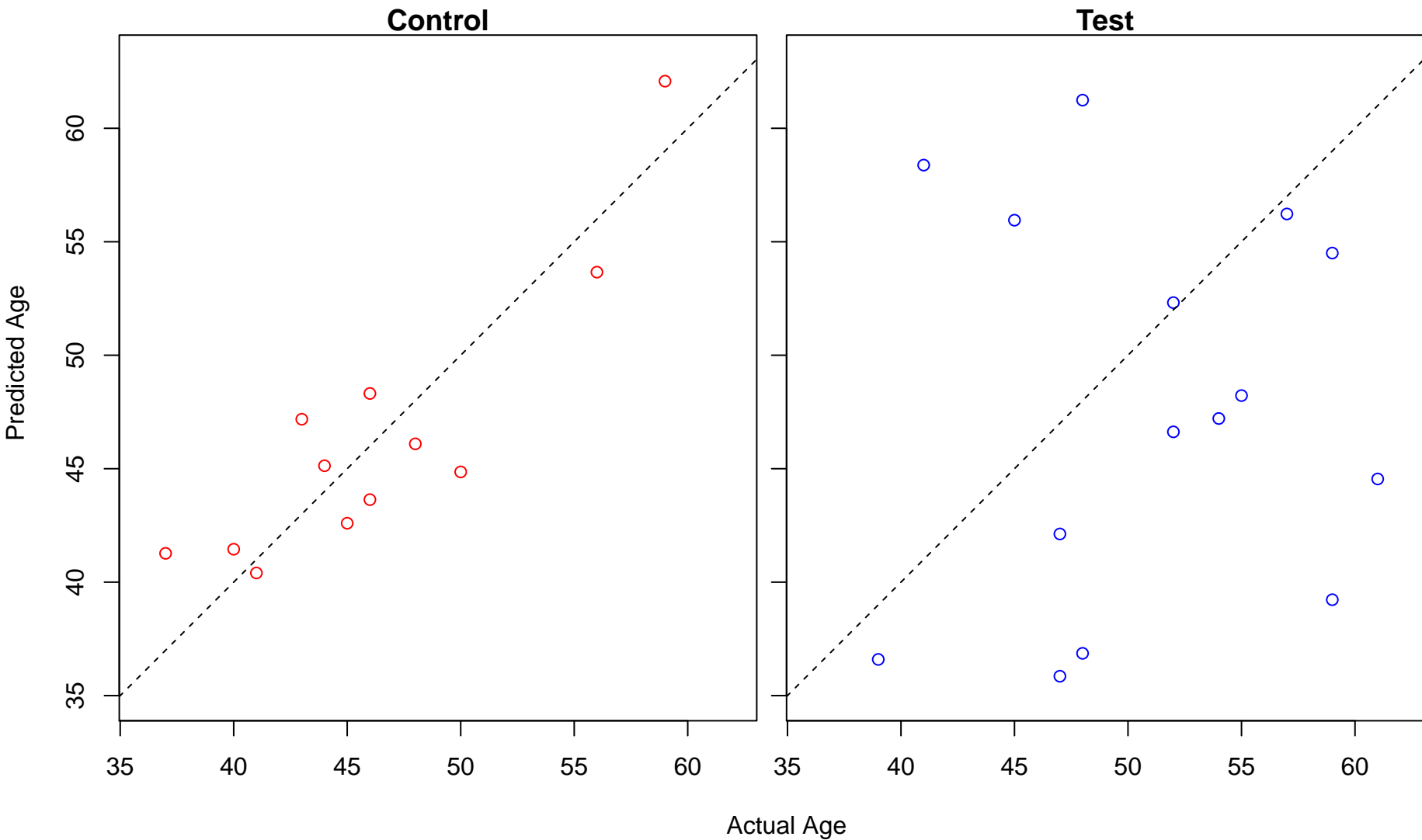
negative regulation of phosphate metabolic process (Score: 4.698140)



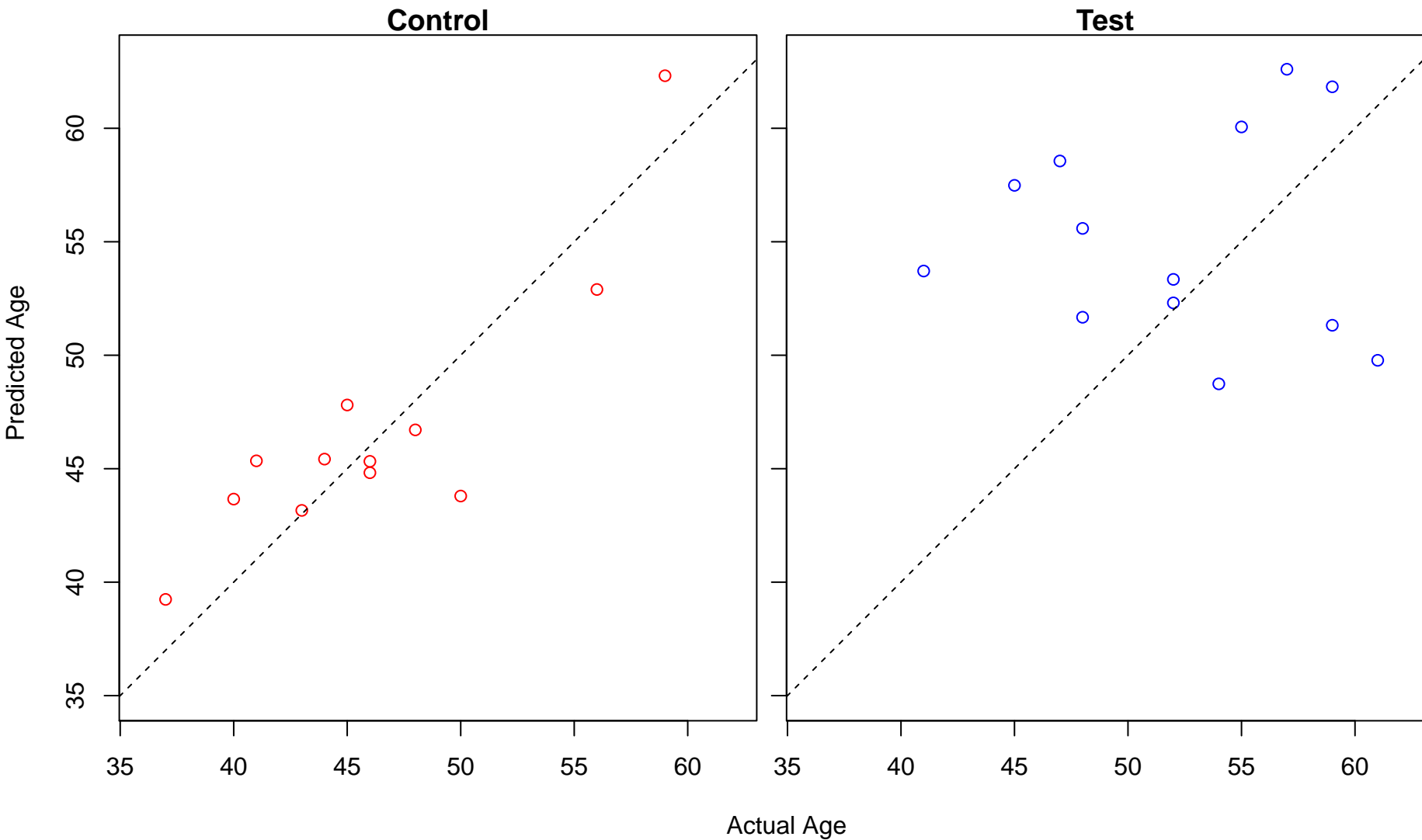
vesicle targeting (Score: 4.690416)



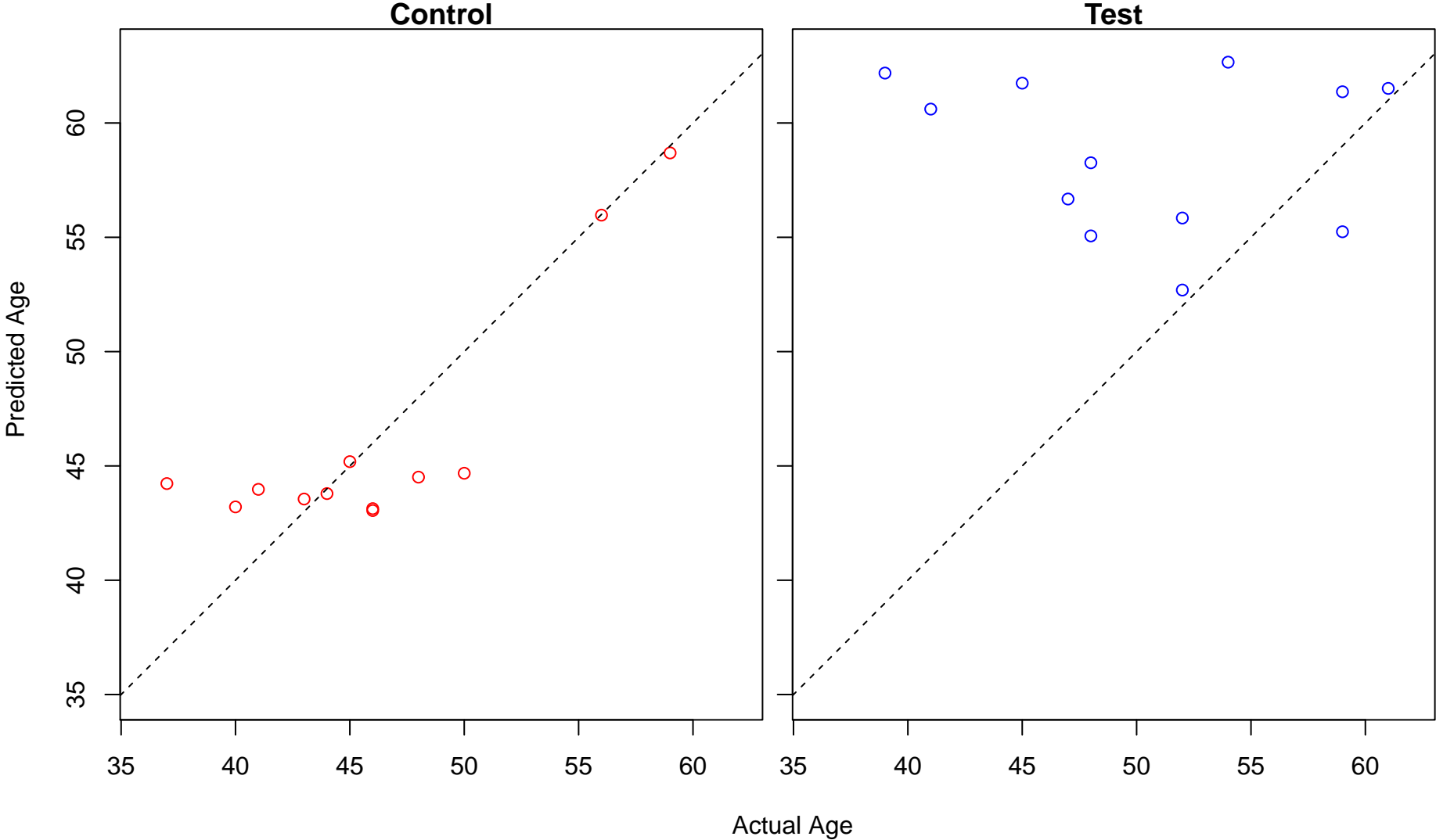
cardiocyte differentiation (Score: 4.688537)



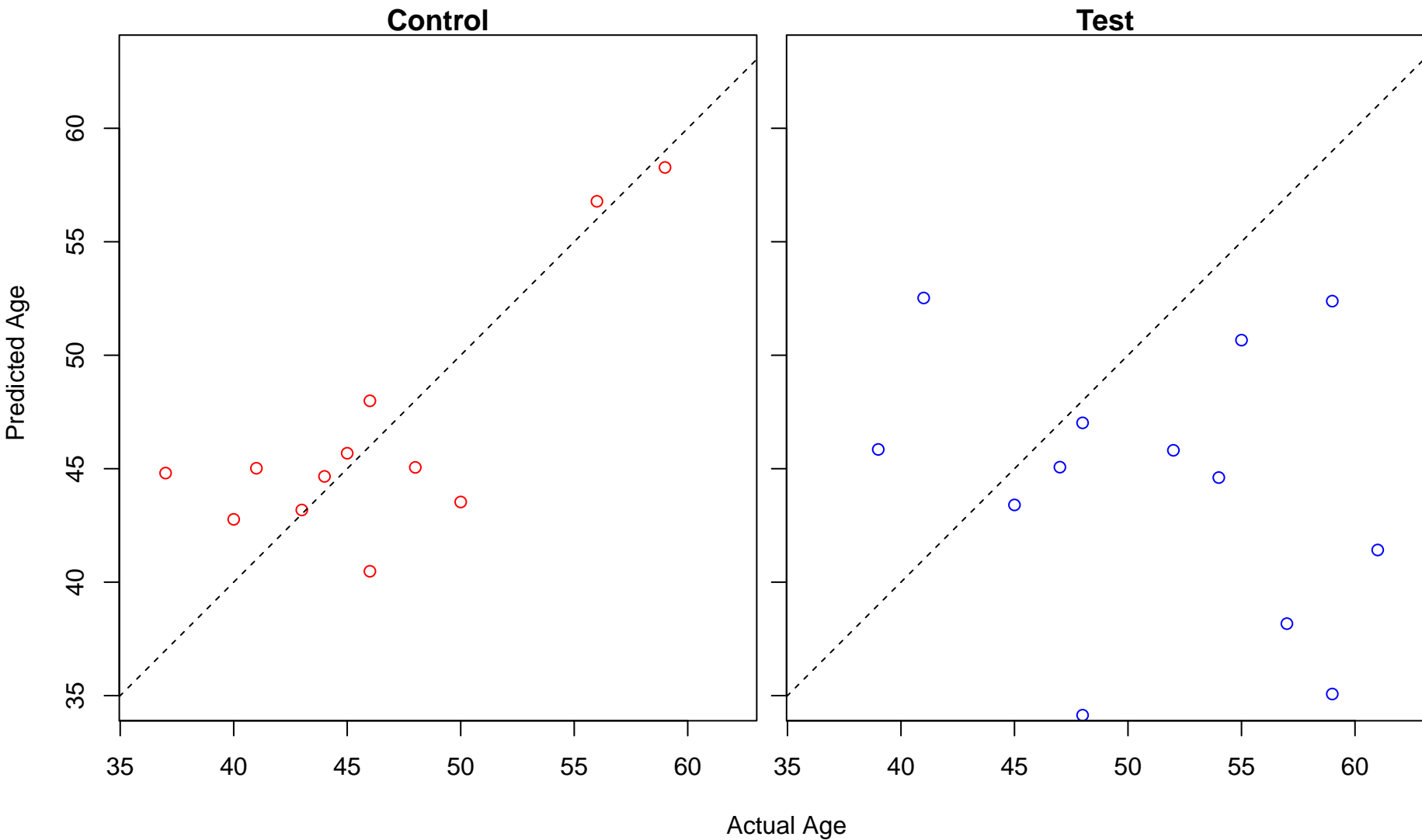
regulation of macrophage chemotaxis (Score: 4.688071)



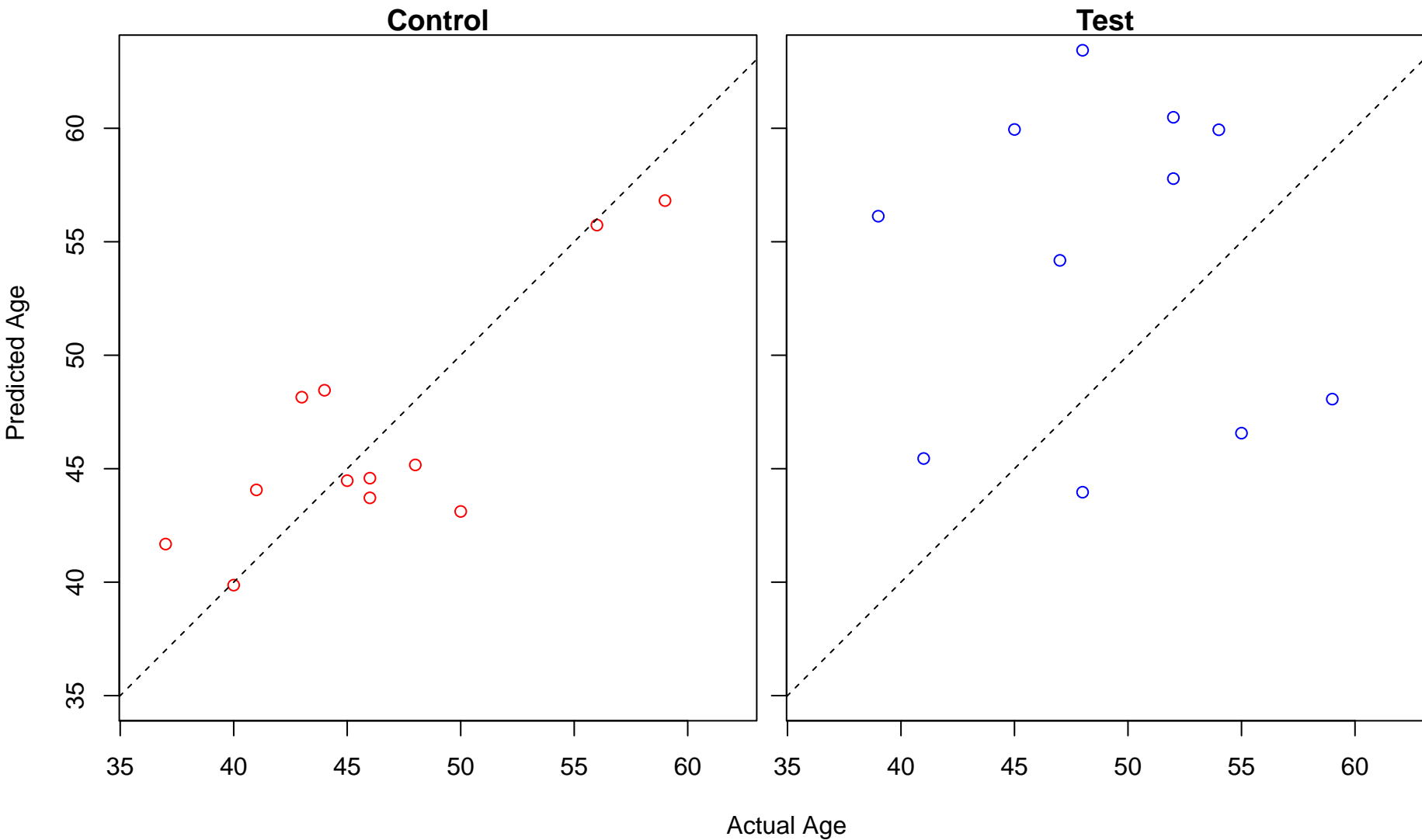
positive regulation of cytokine-mediated signaling pathway (Score: 4.685356)



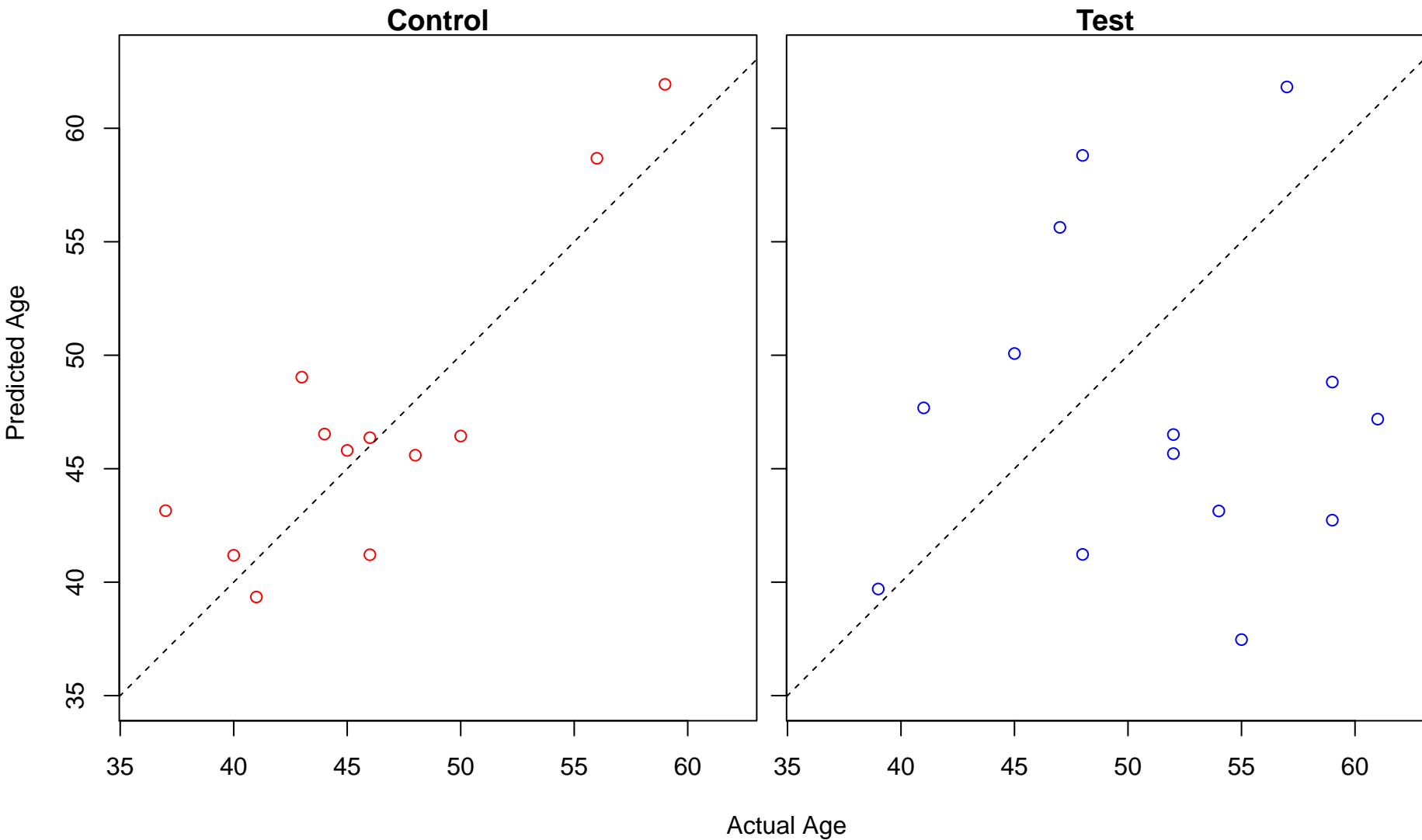
spleen development (Score: 4.684724)



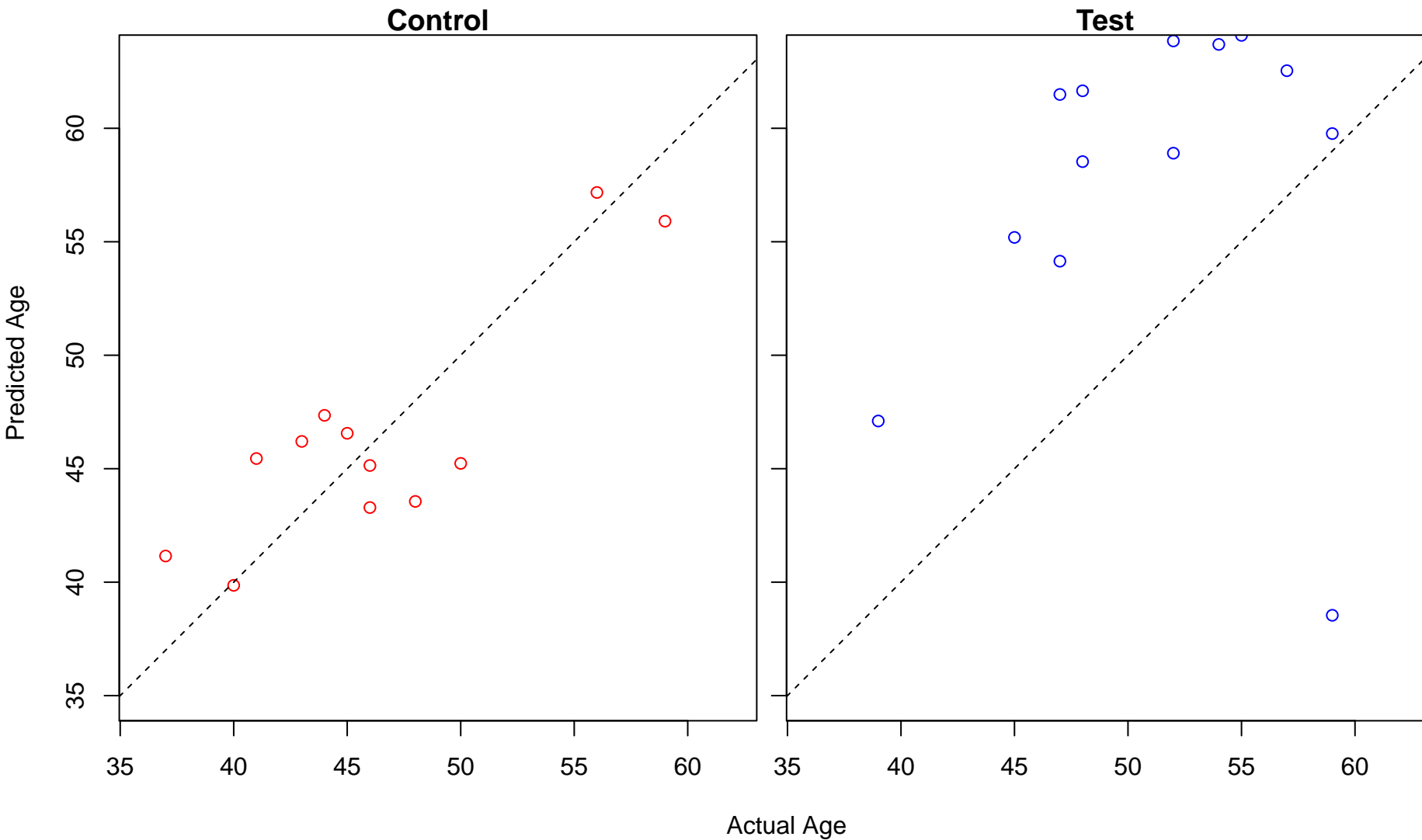
positive regulation of immunoglobulin production (Score: 4.682723)



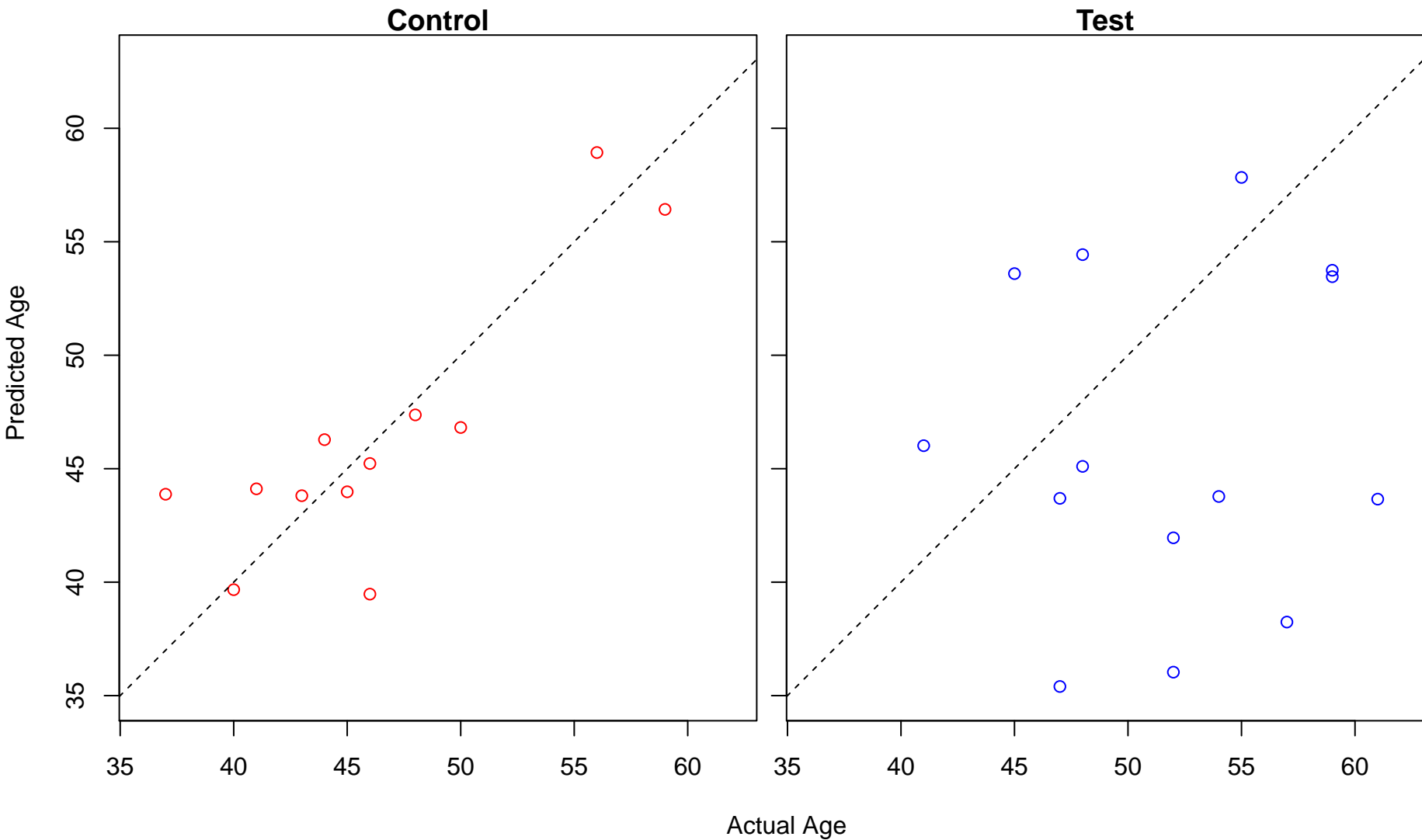
regulation of cyclin-dependent protein kinase activity (Score: 4.678594)



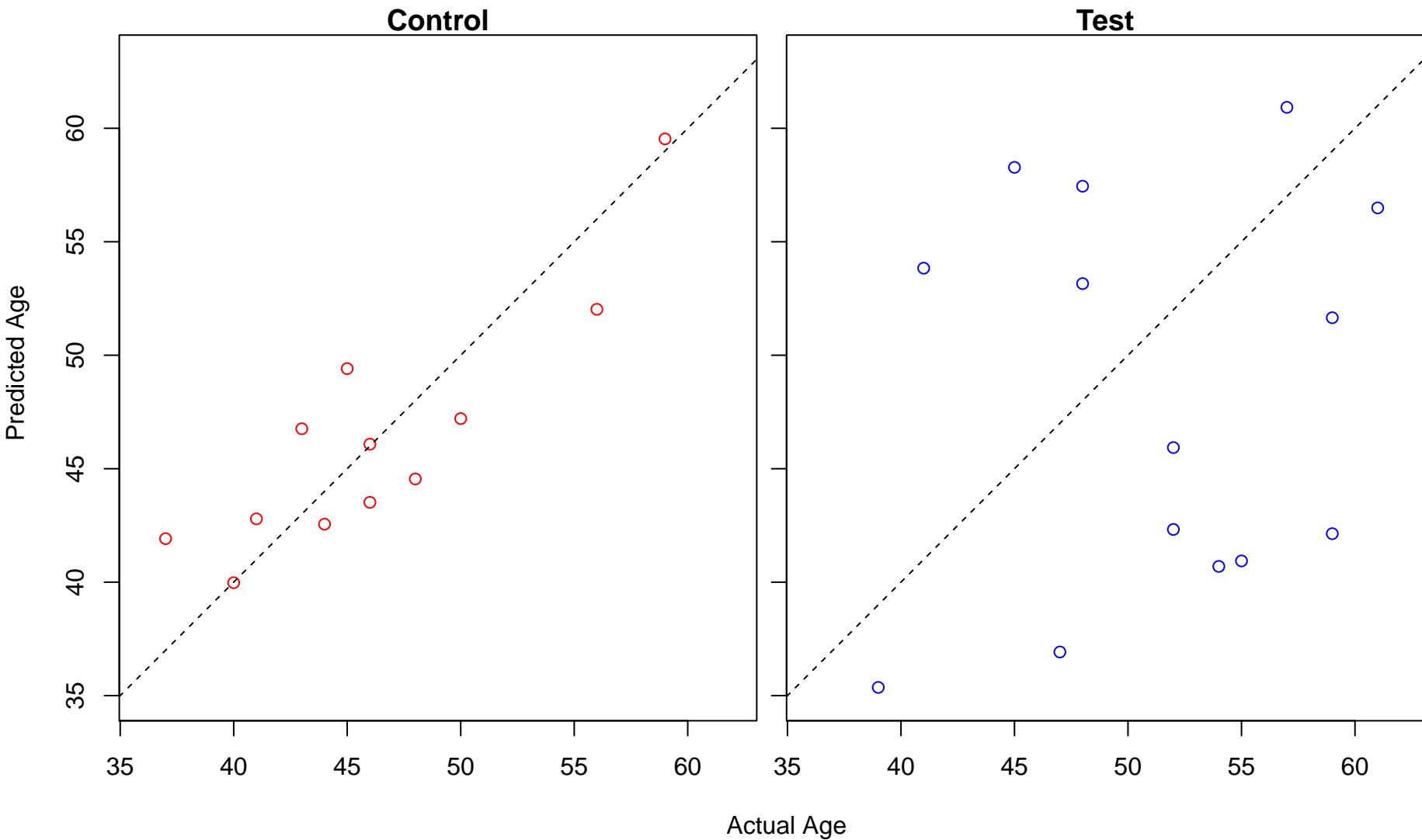
interferon-gamma secretion (Score: 4.676476)



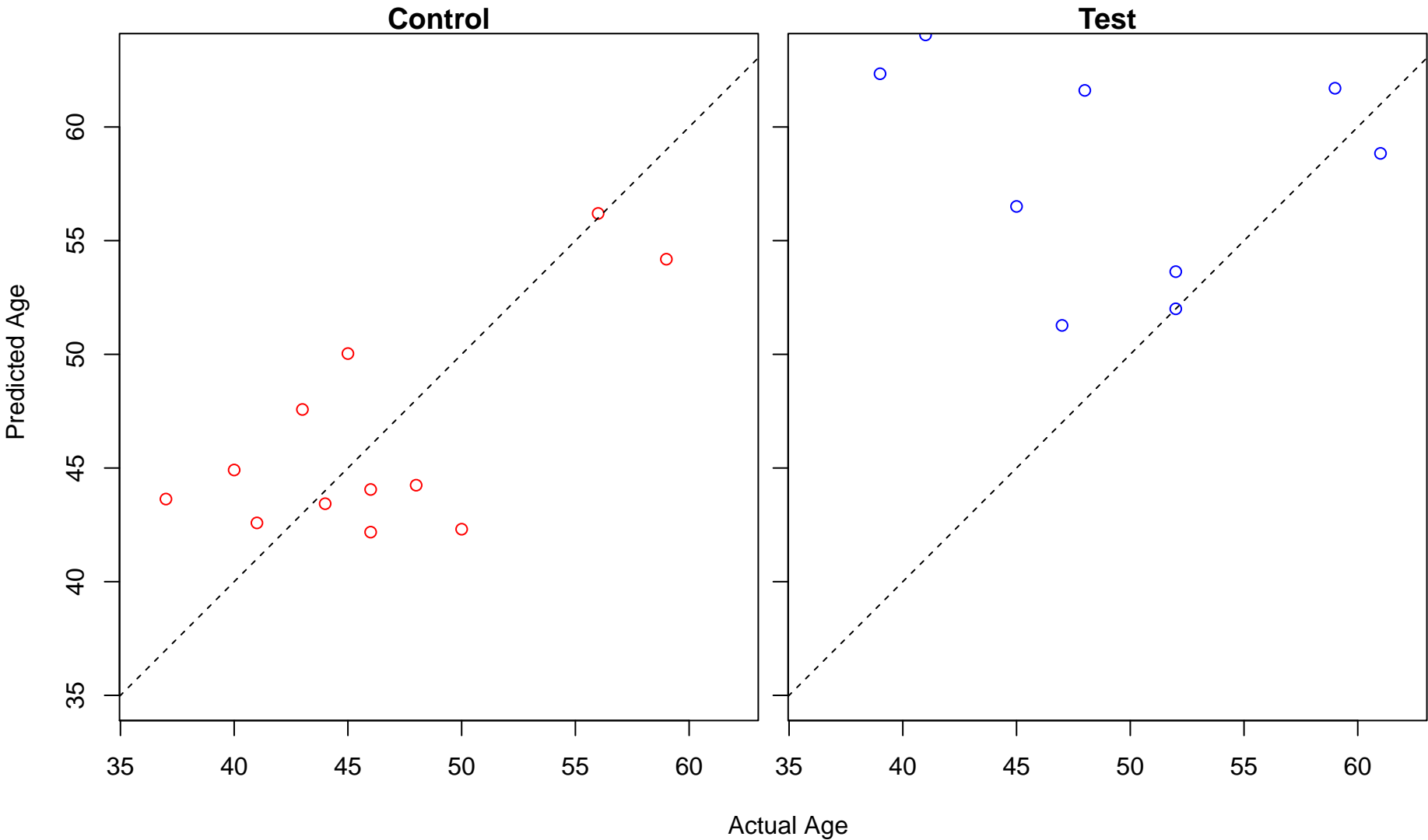
regulation of cellular component biogenesis (Score: 4.674348)



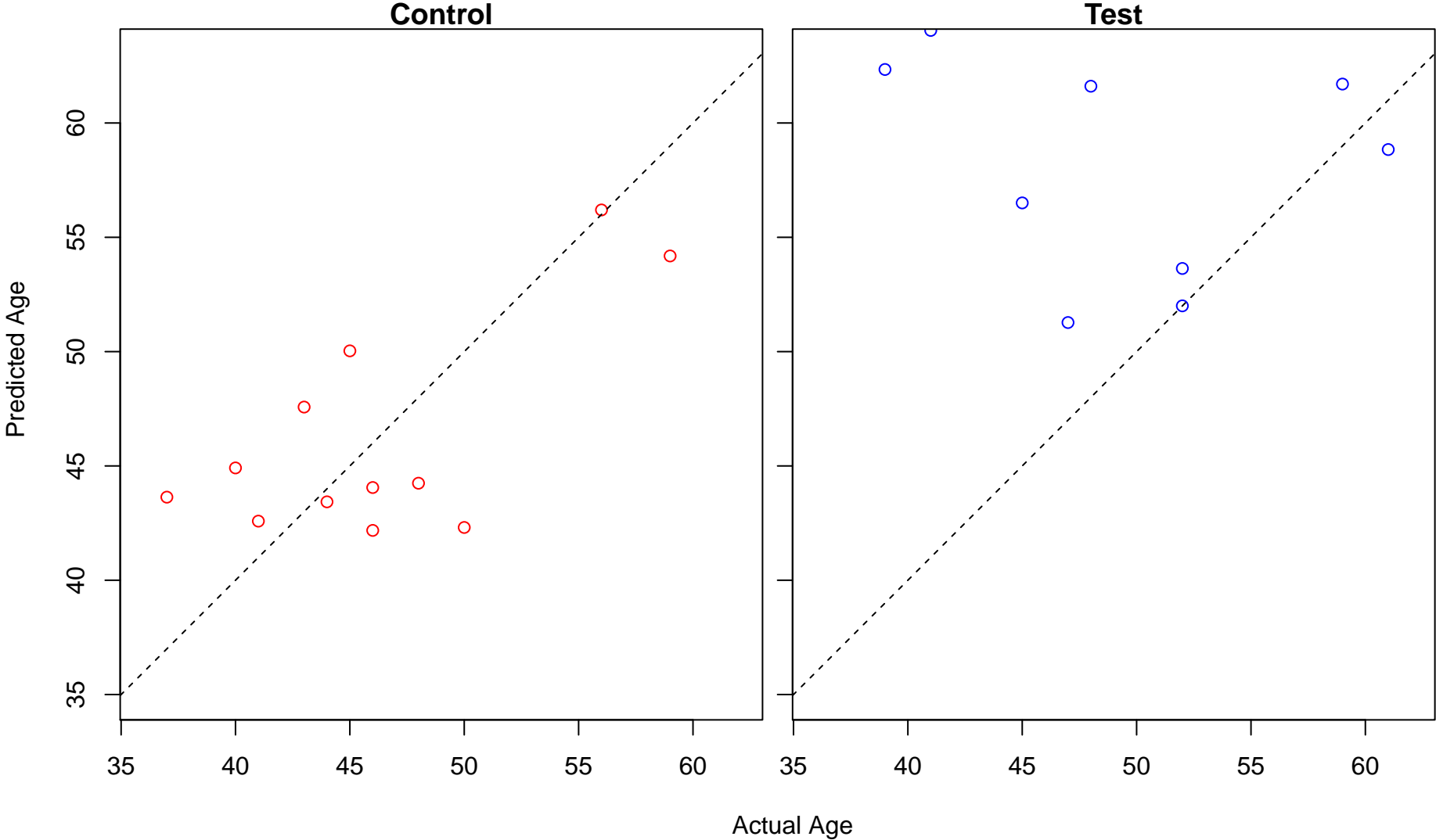
regulation of vascular endothelial growth factor receptor signaling pathway (Score: 4.669773)



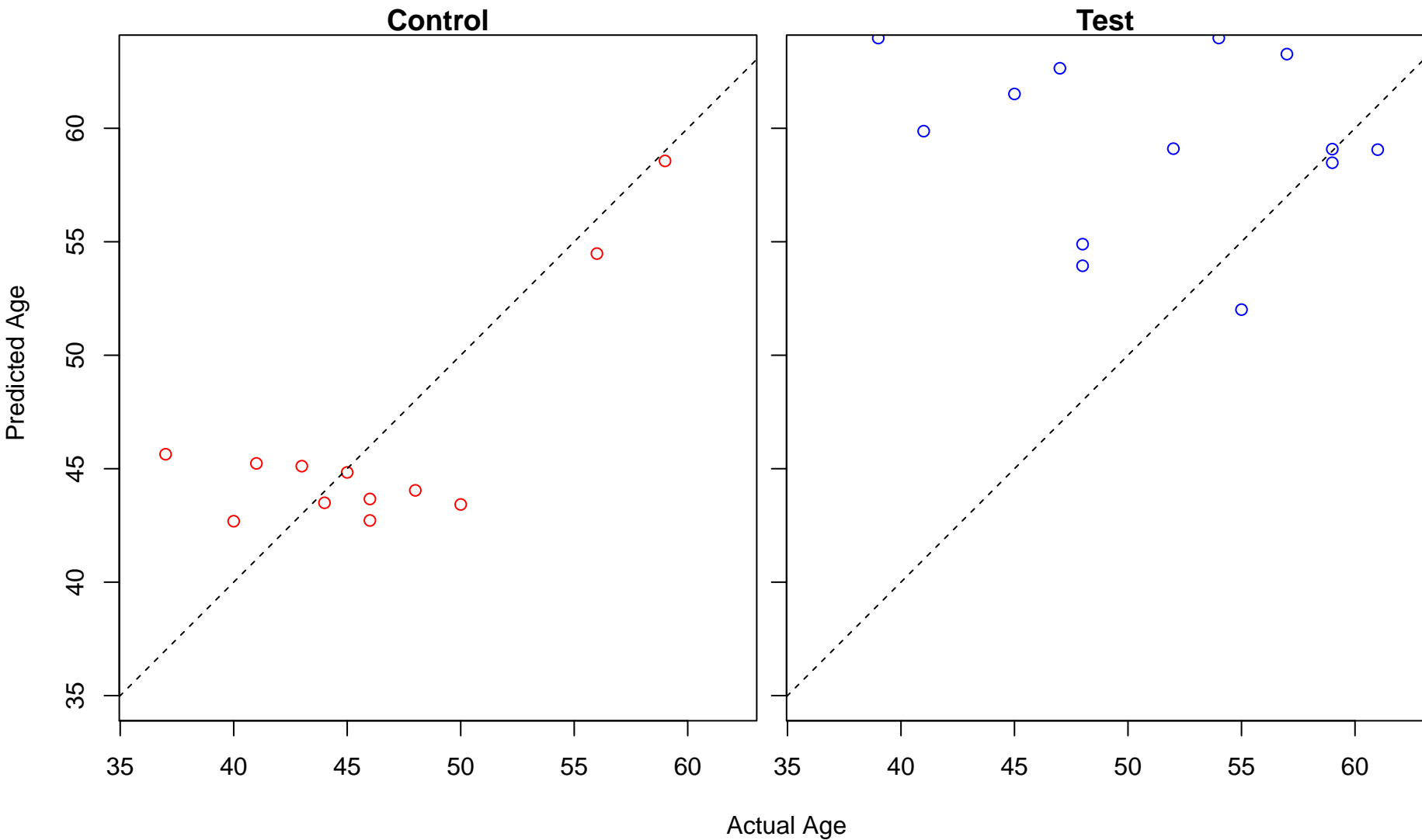
regulation of humoral immune response mediated by circulating immunoglobulin (Score: 4.668884)



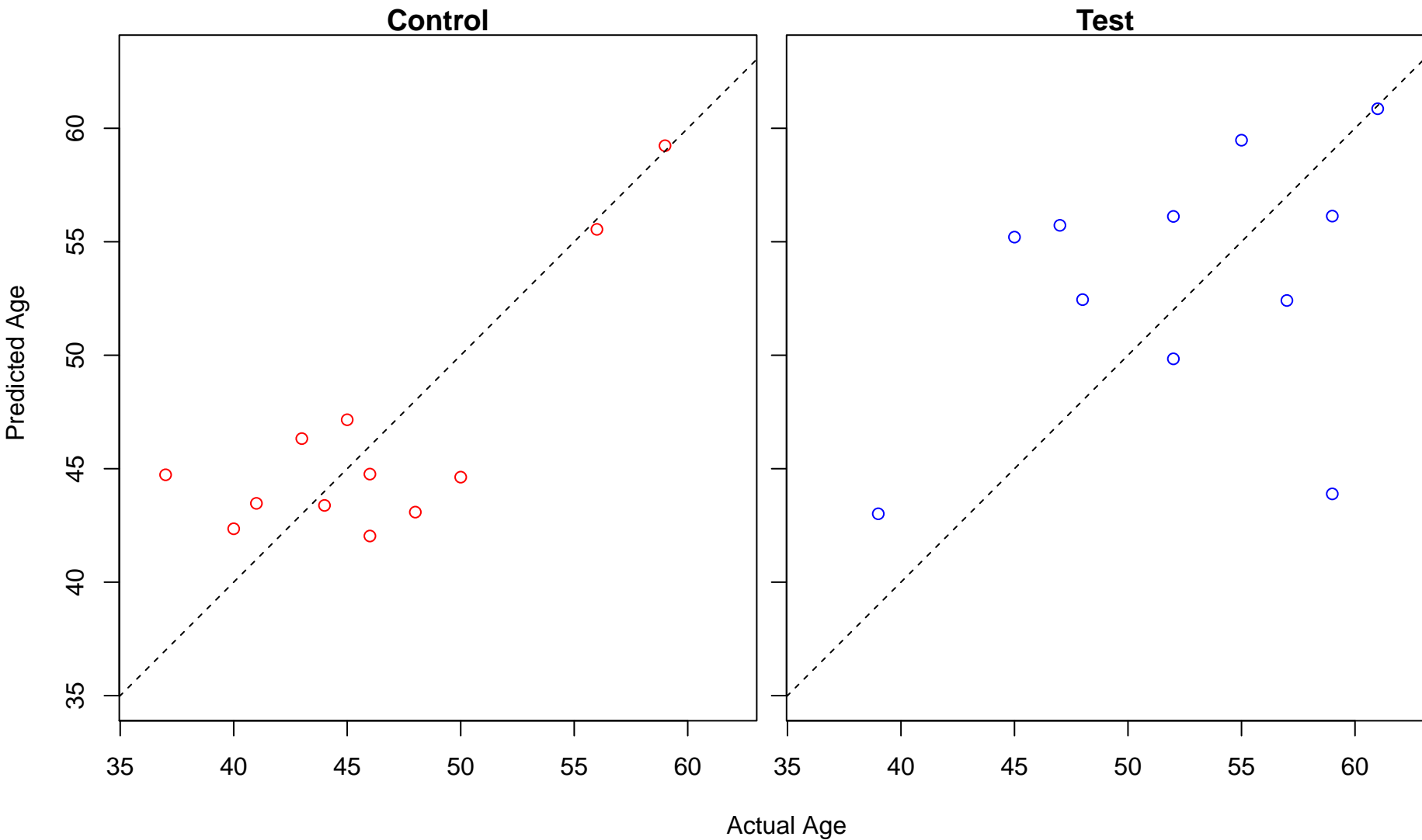
negative regulation of humoral immune response mediated by circulating immunoglobulin (Score: 4.66)



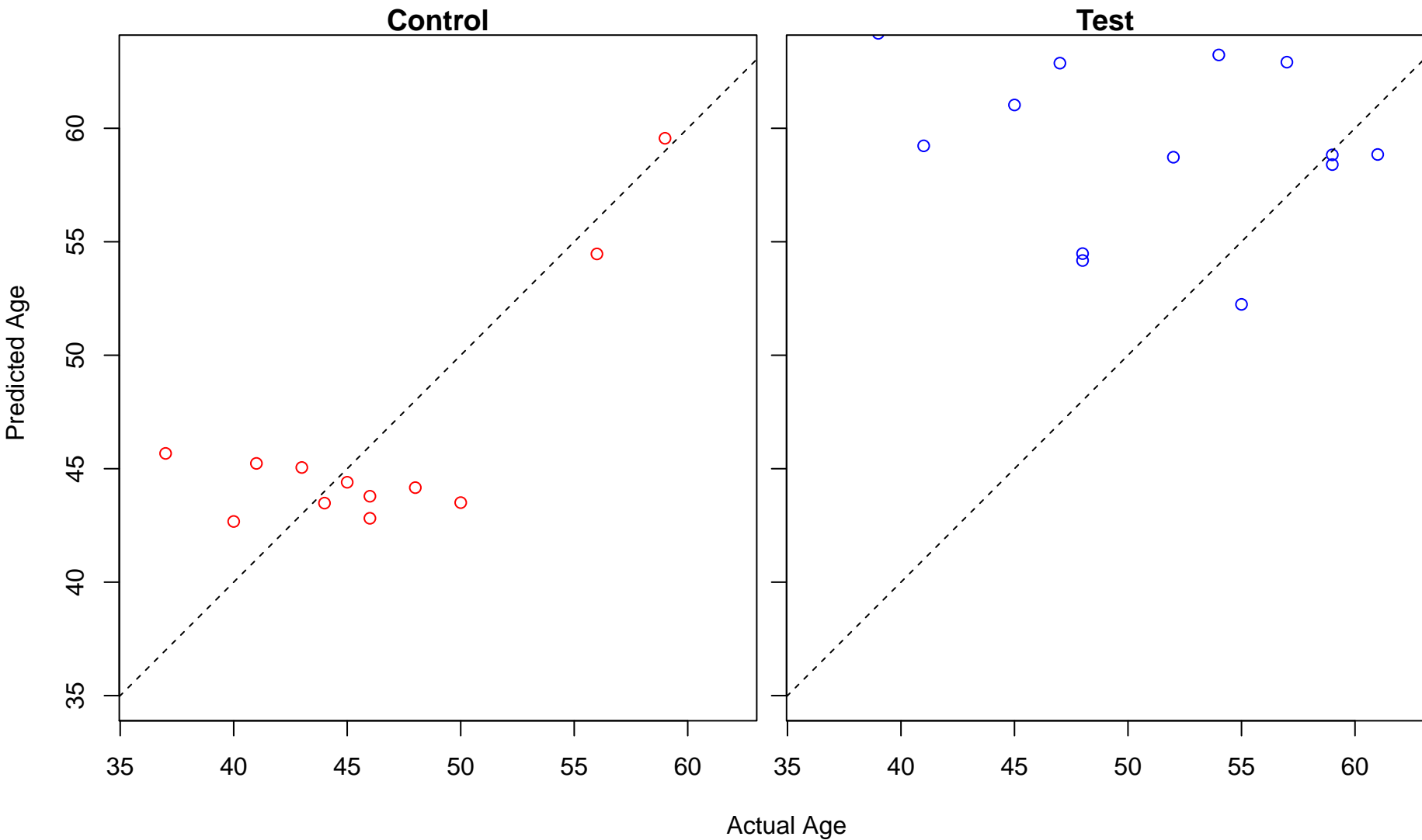
response to vitamin (Score: 4.661038)



negative regulation of protein autophosphorylation (Score: 4.660726)

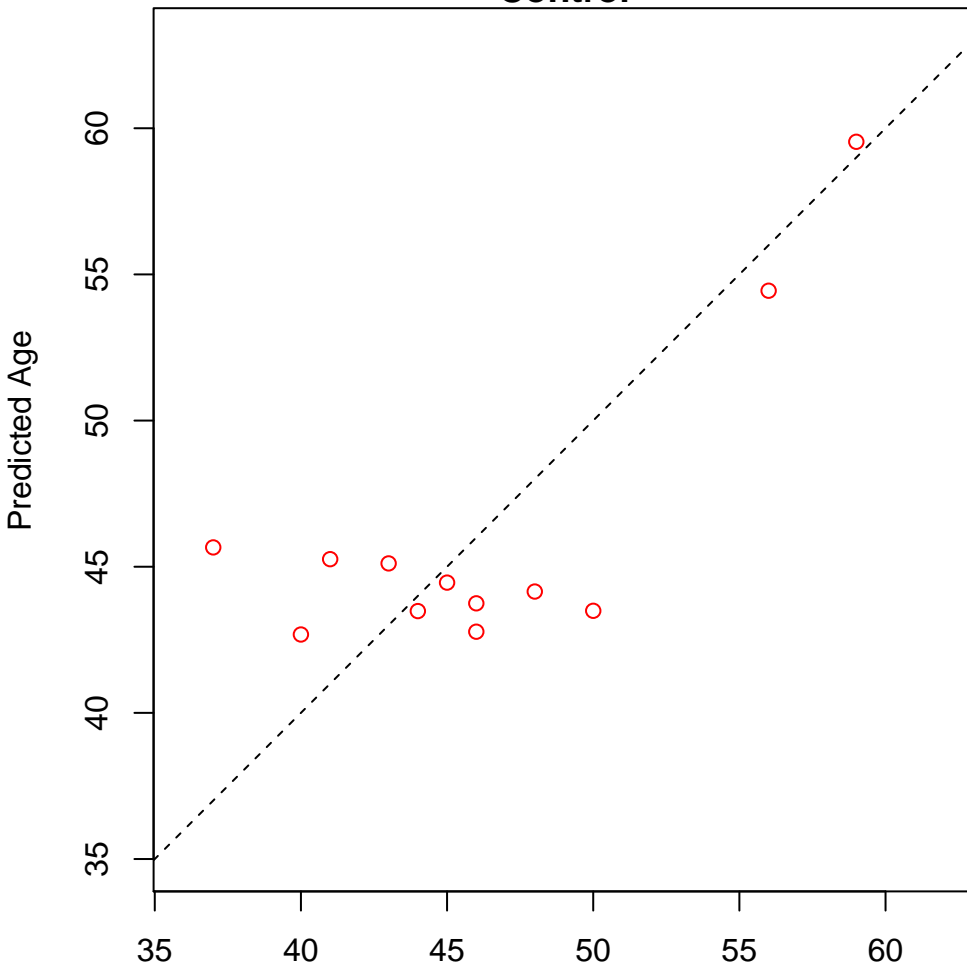


polyol transport (Score: 4.658726)

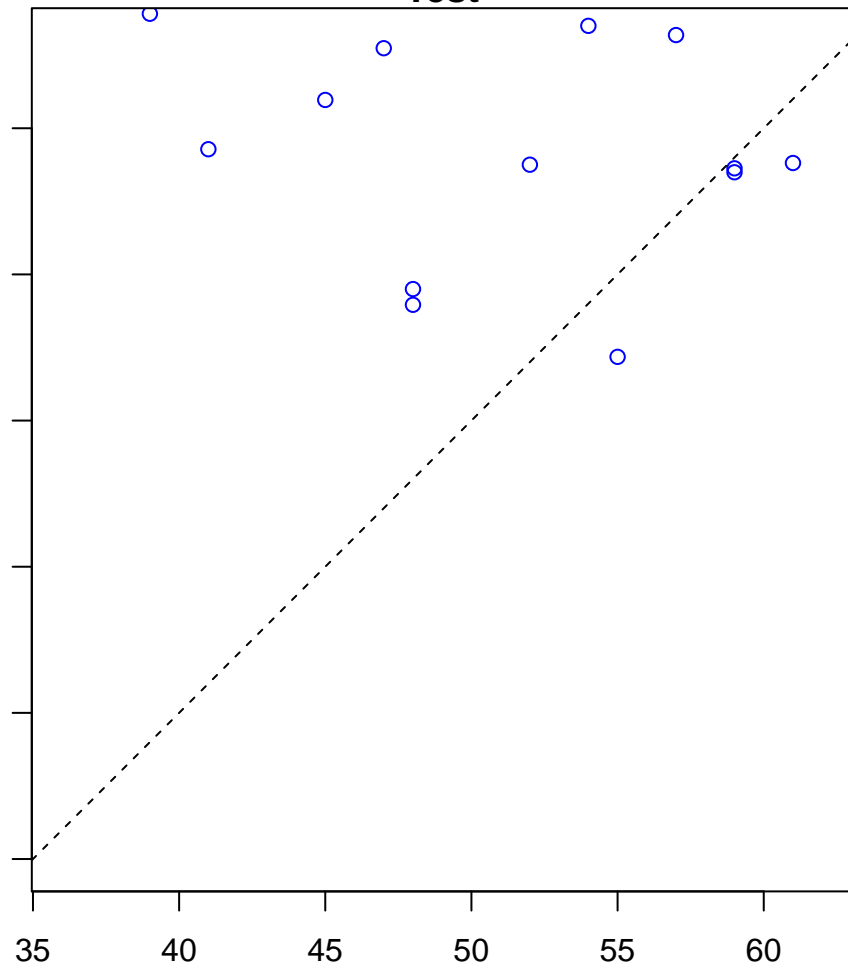


carbohydrate transmembrane transport (Score: 4.658069)

Control

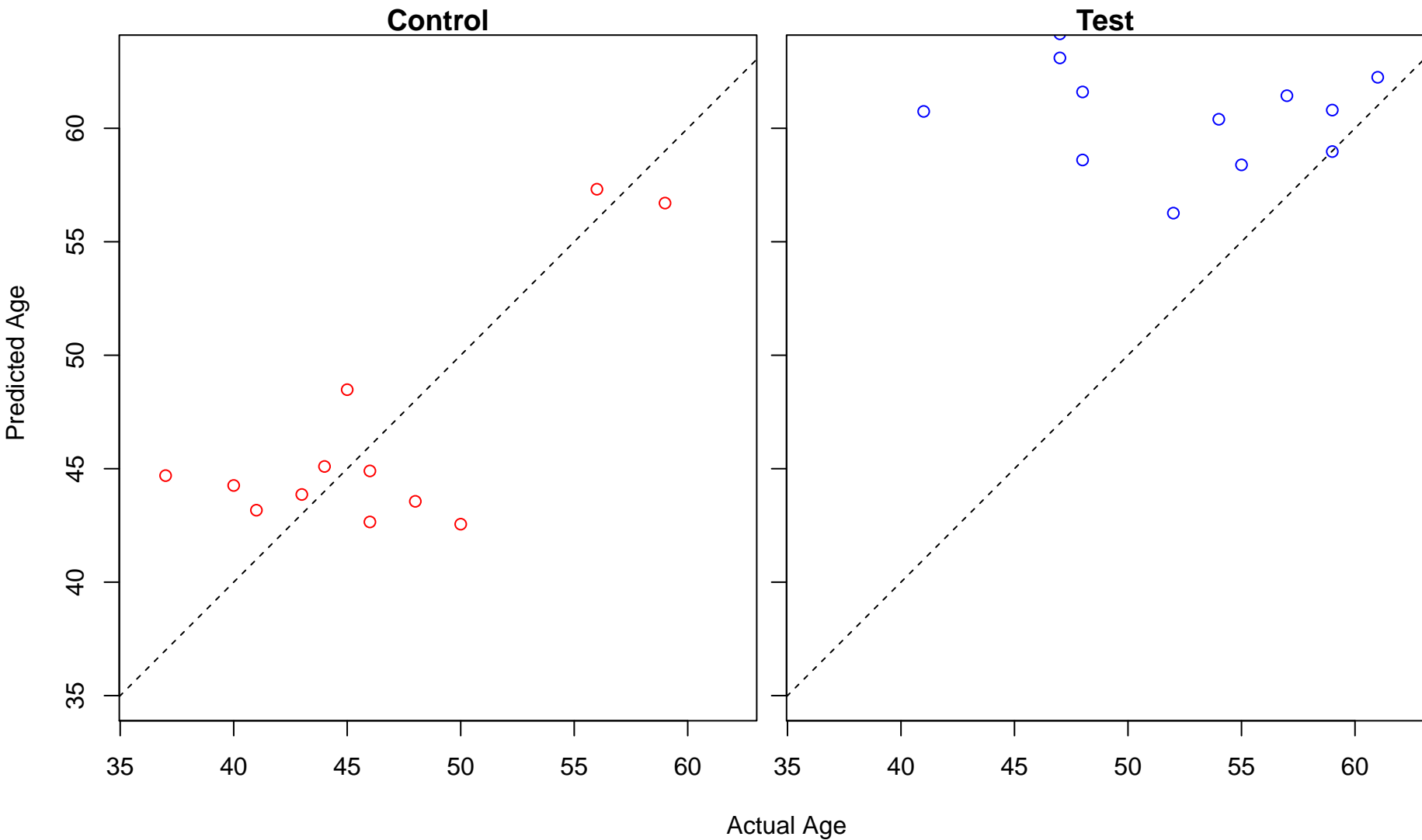


Test

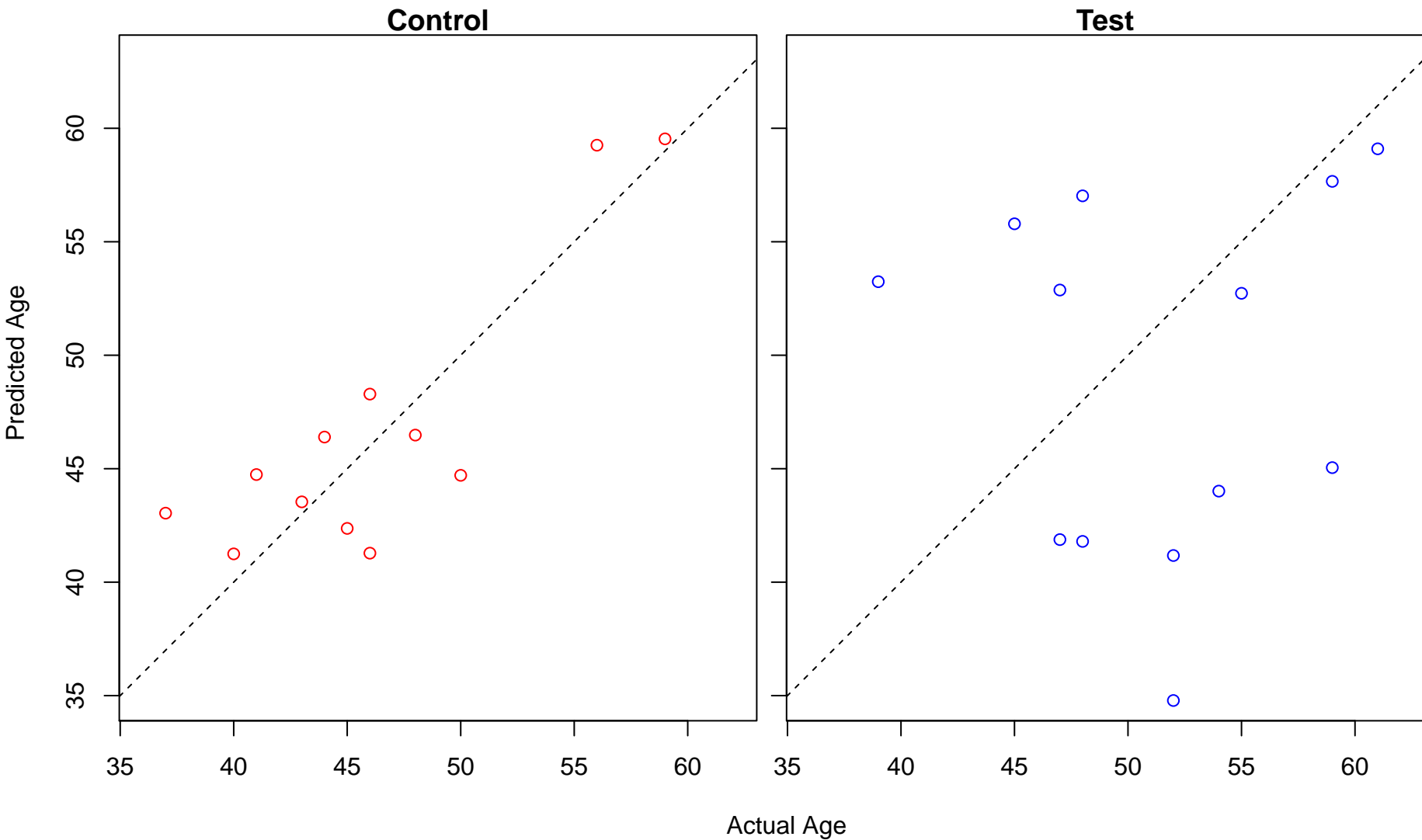


Actual Age

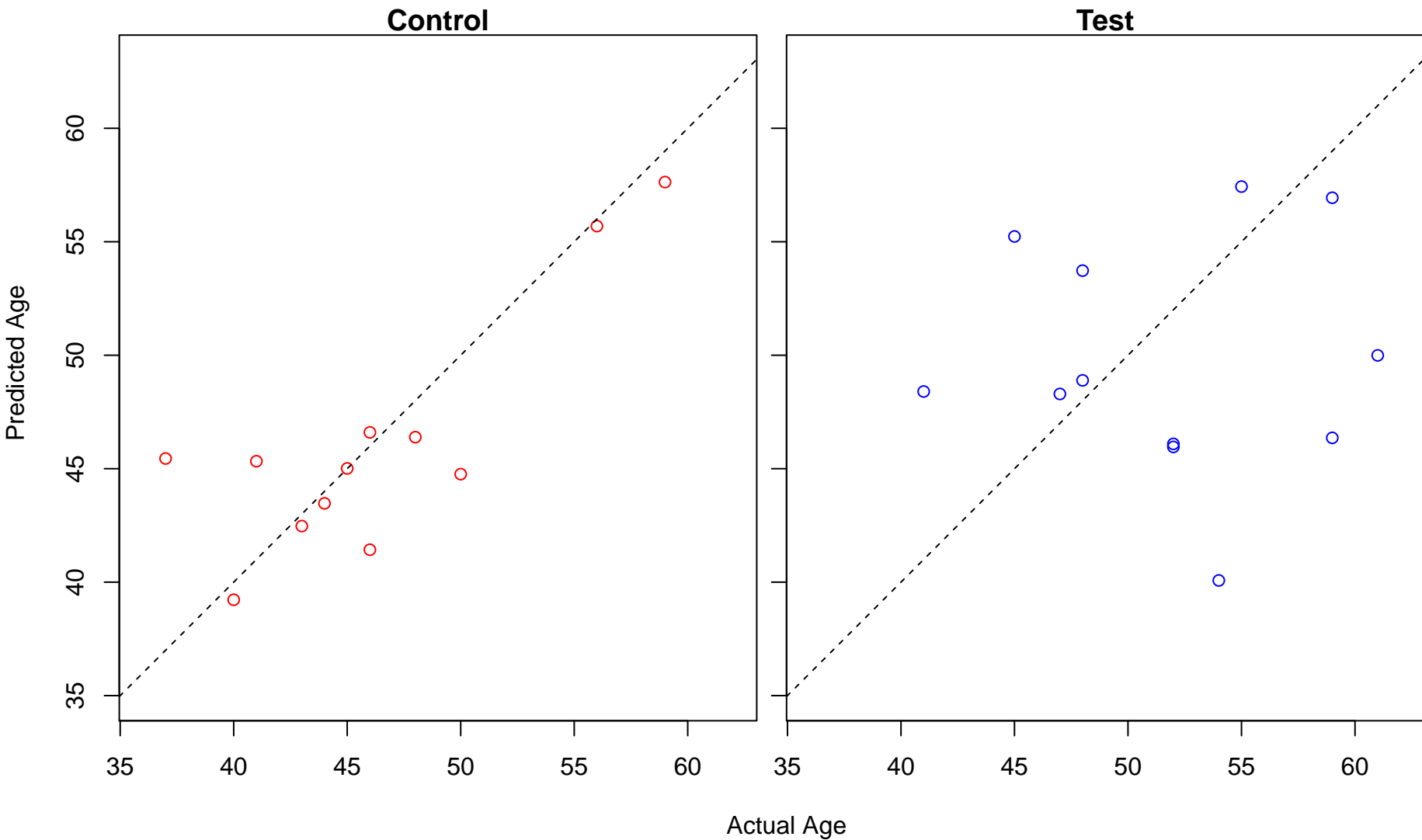
maternal placenta development (Score: 4.654600)



regulation of protein ubiquitination (Score: 4.653221)

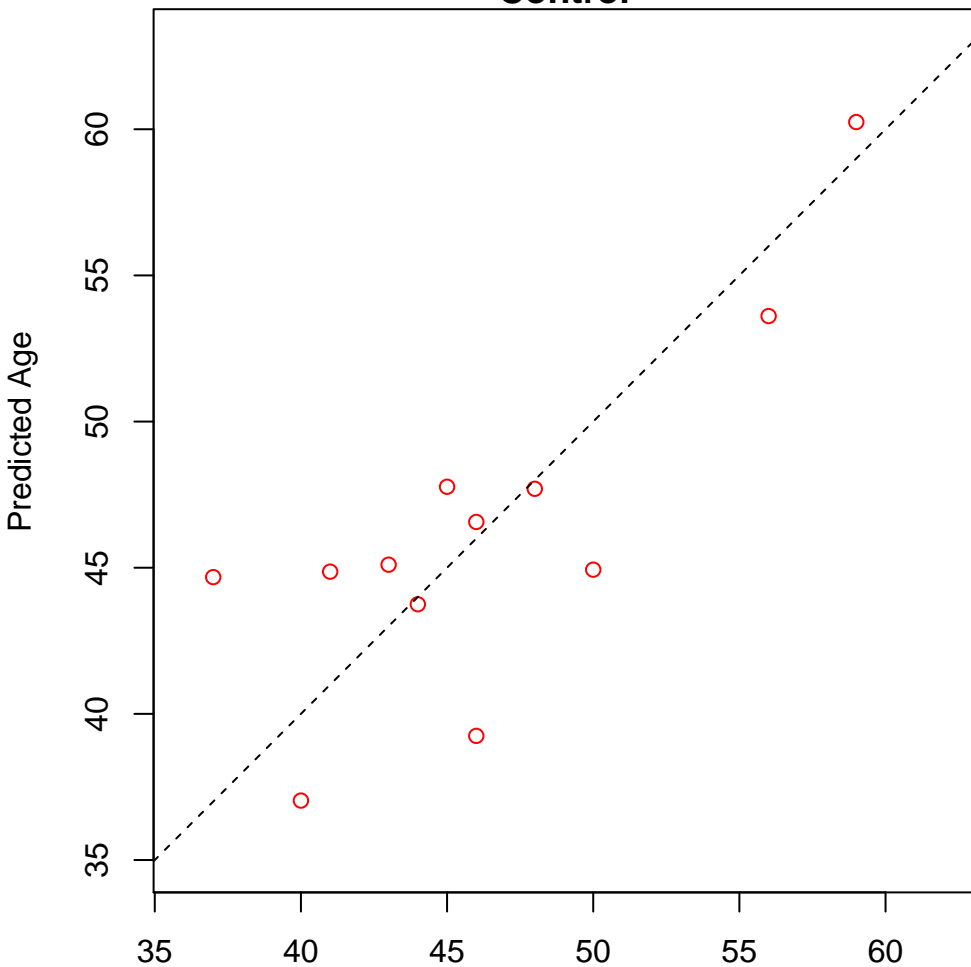


ribonucleoprotein complex subunit organization (Score: 4.652322)

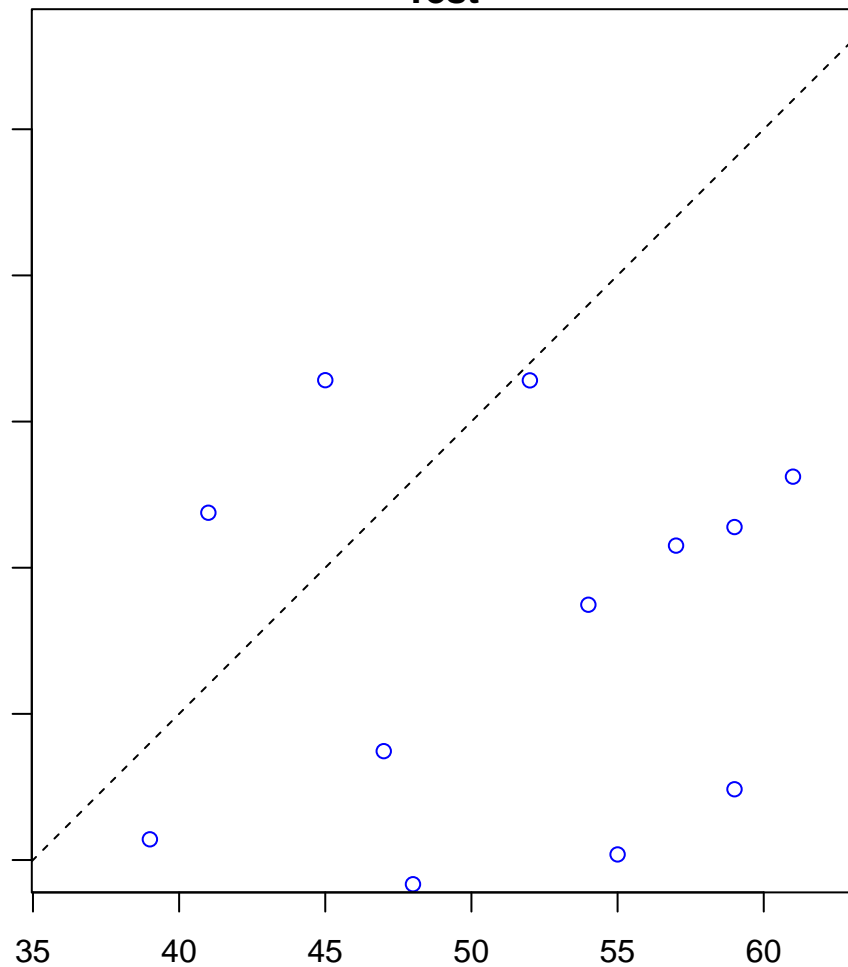


vesicle targeting, rough ER to cis-Golgi (Score: 4.646568)

Control

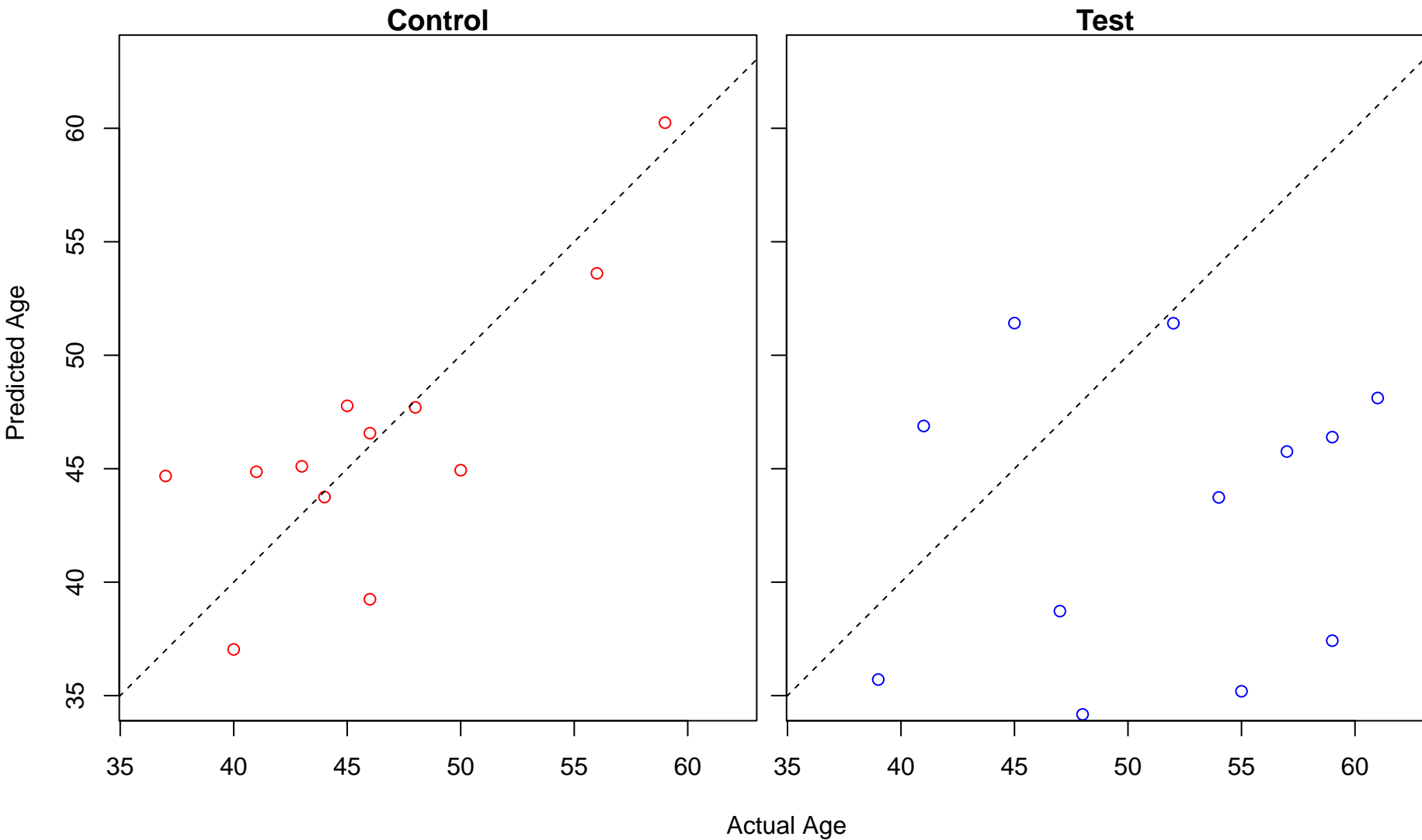


Test

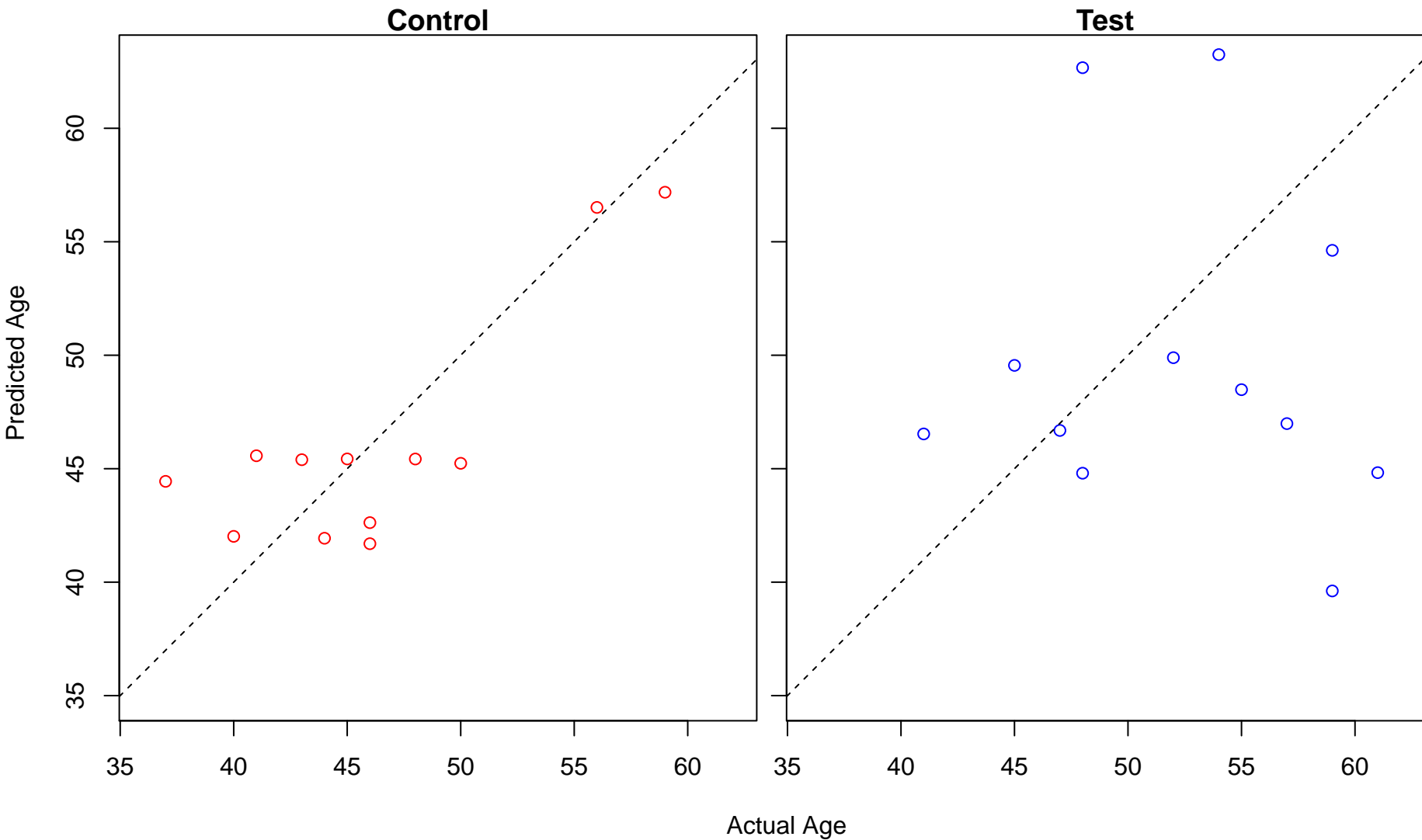


Actual Age

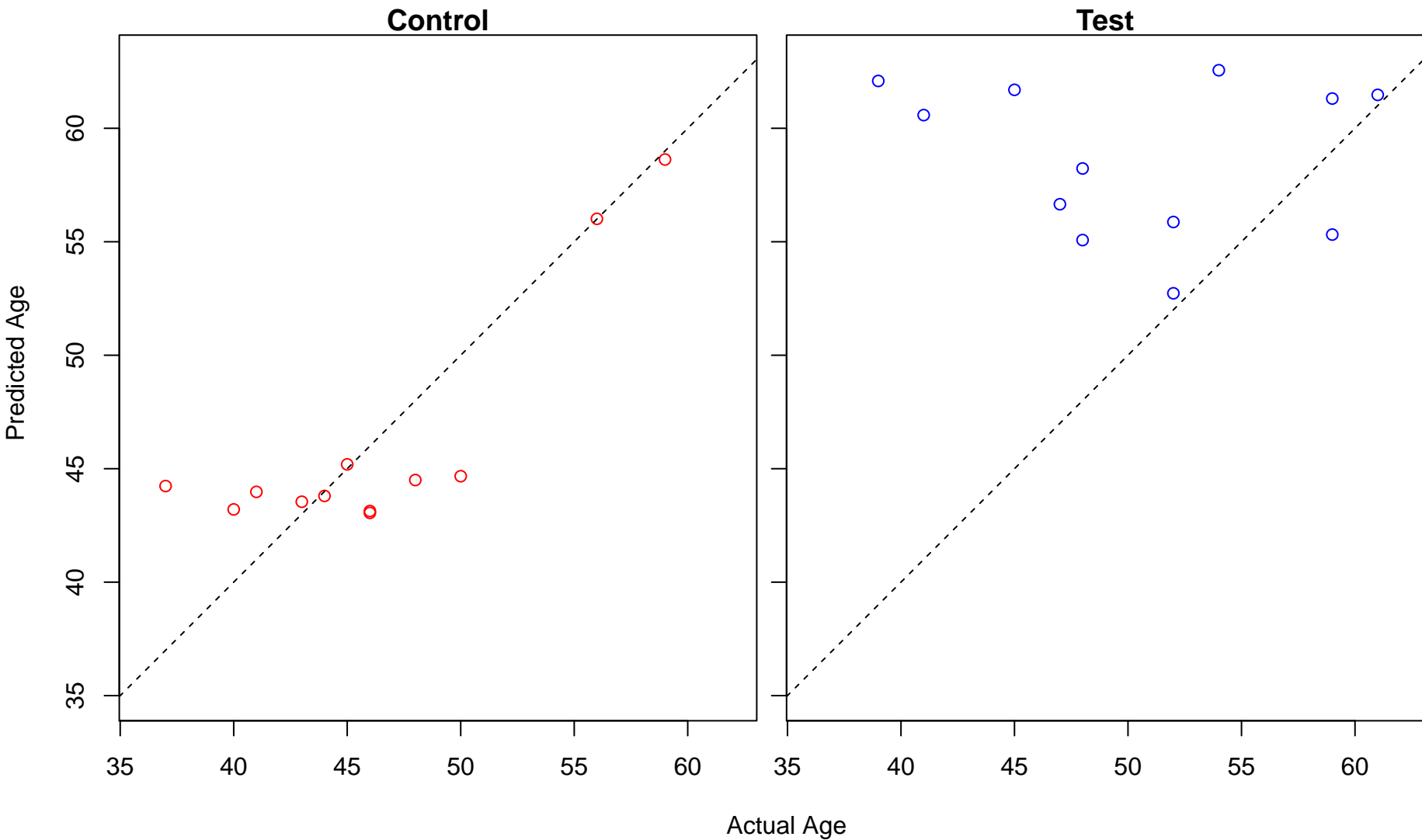
COP2 vesicle coating (Score: 4.646568)



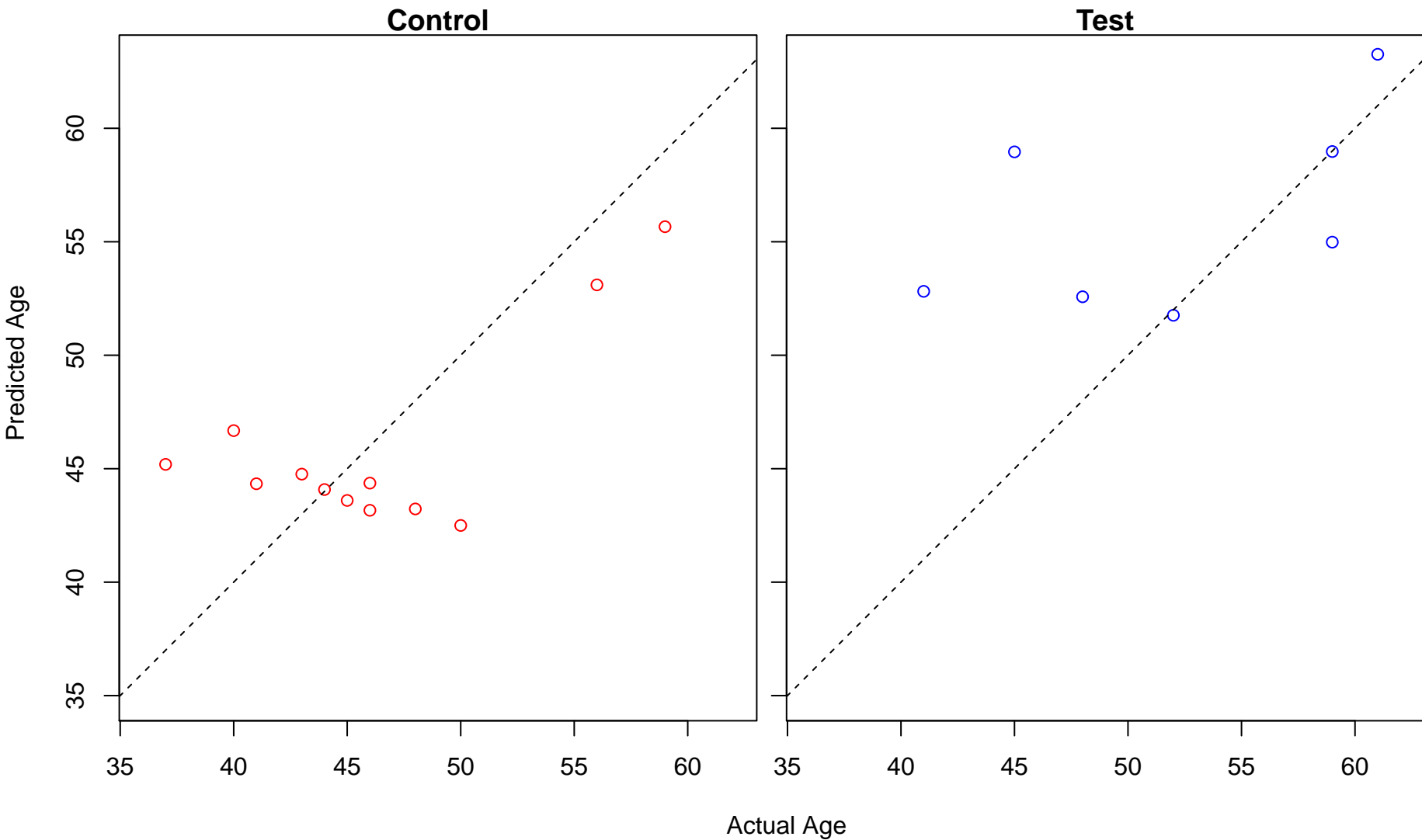
negative regulation of telomere maintenance via telomerase (Score: 4.642452)



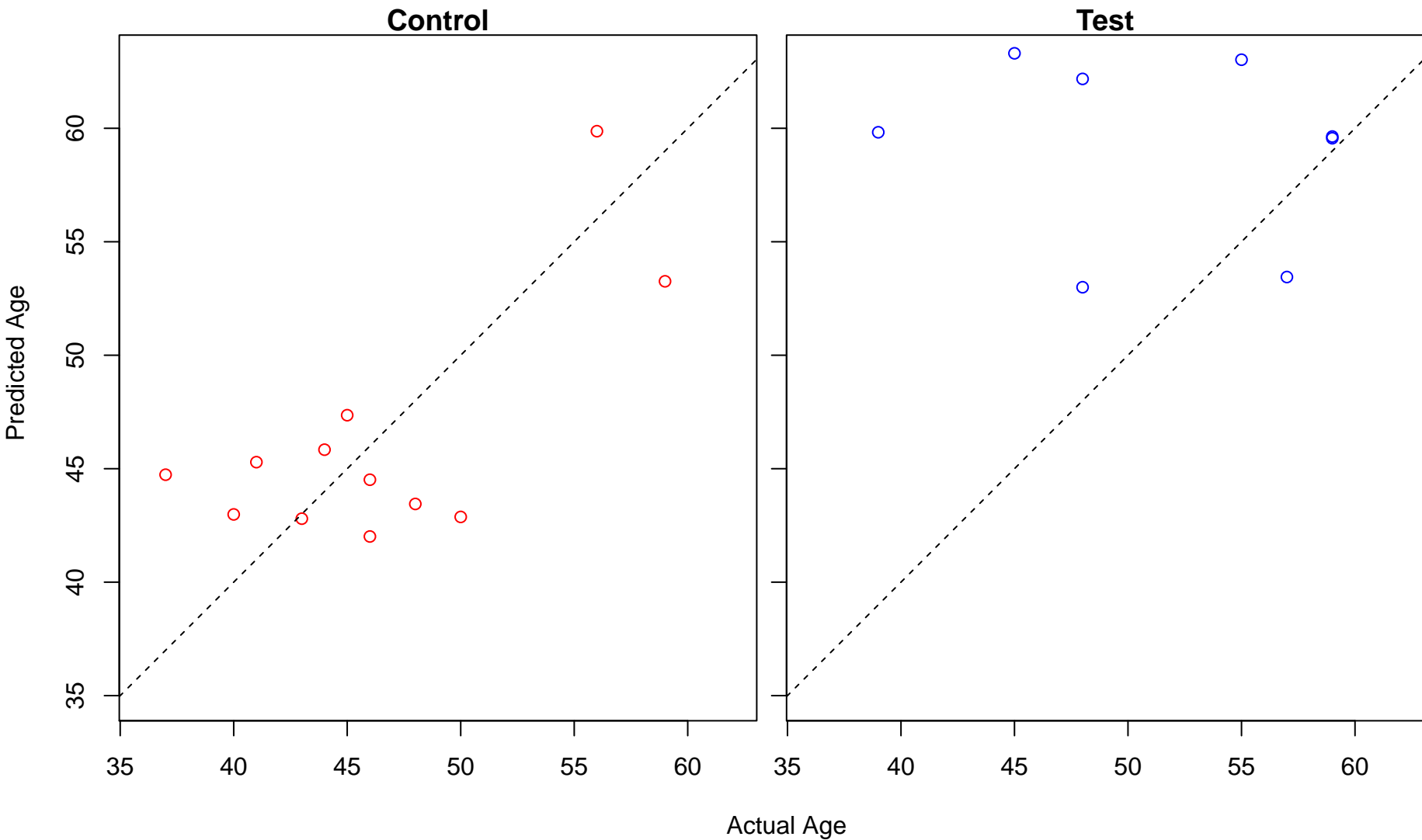
positive regulation of response to cytokine stimulus (Score: 4.639252)



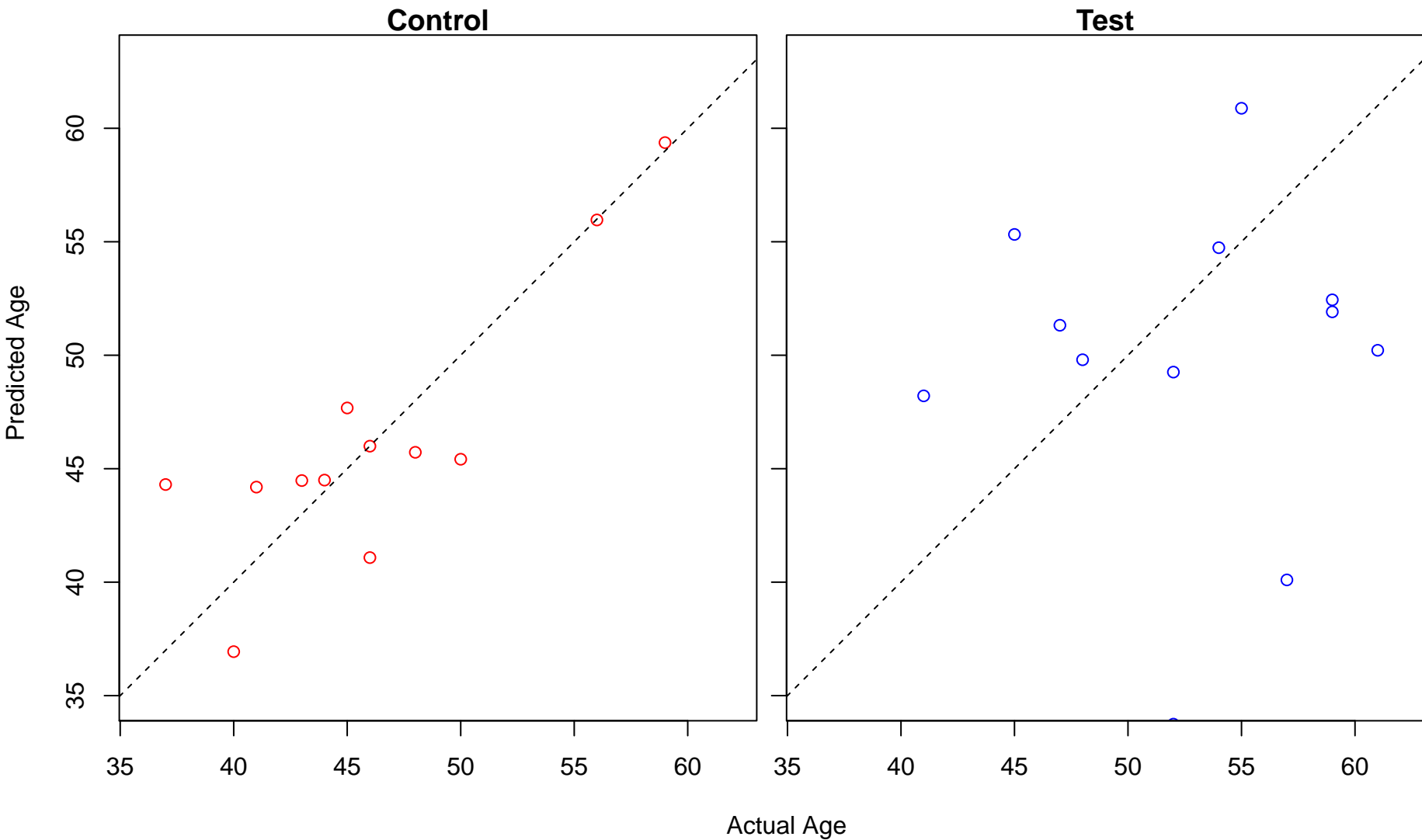
negative regulation of endothelial cell chemotaxis (Score: 4.632438)



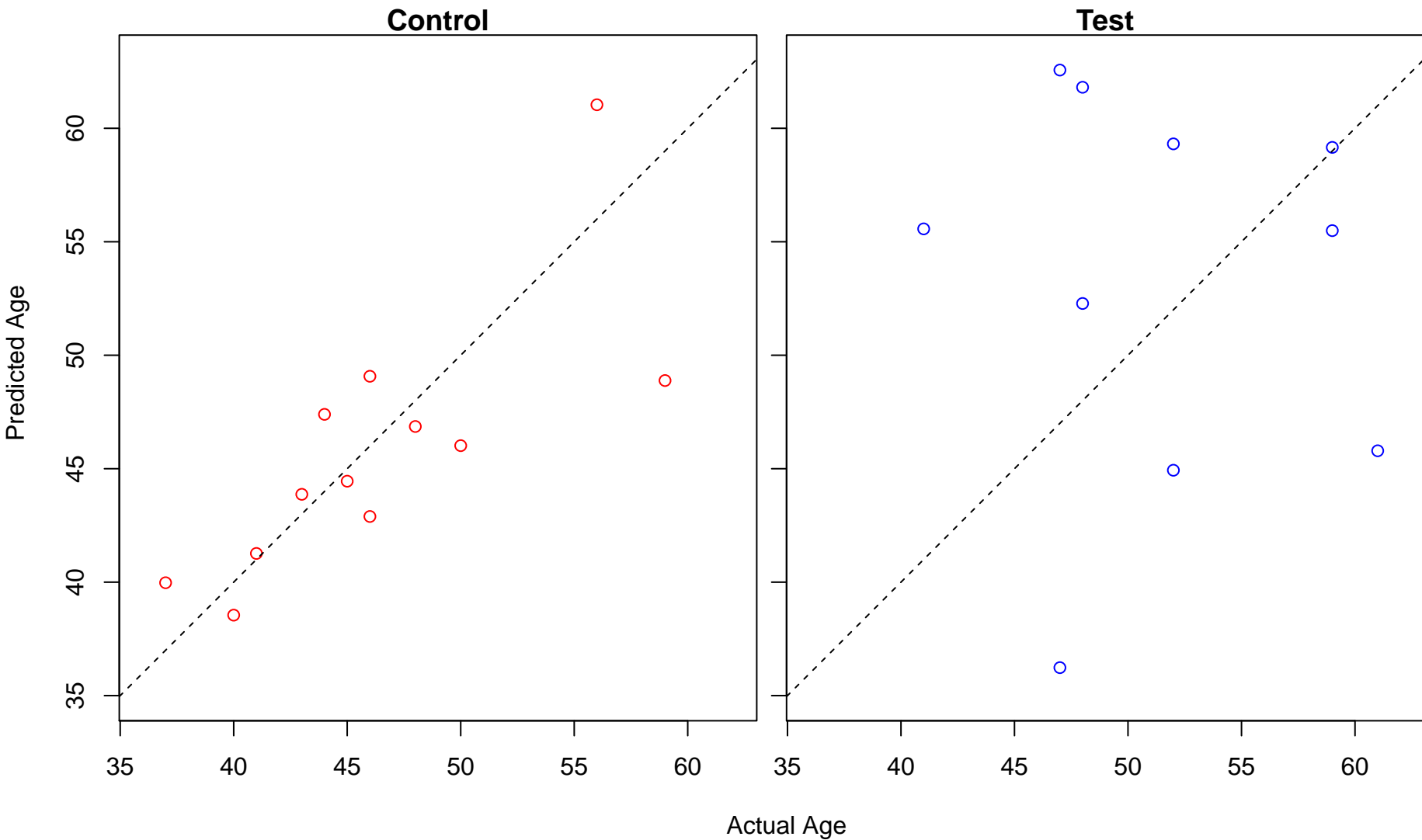
positive regulation of ruffle assembly (Score: 4.623506)



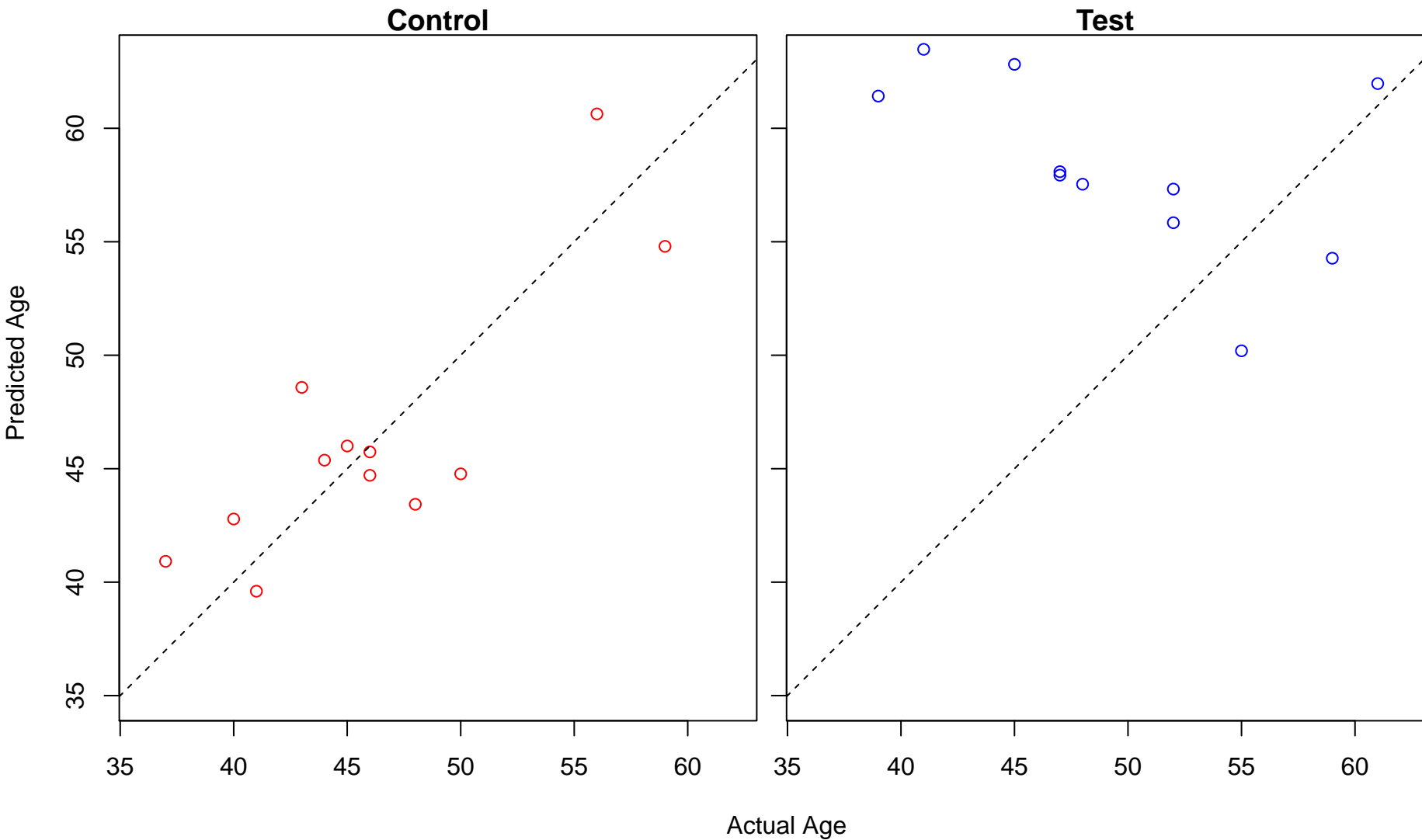
organelle assembly (Score: 4.610322)



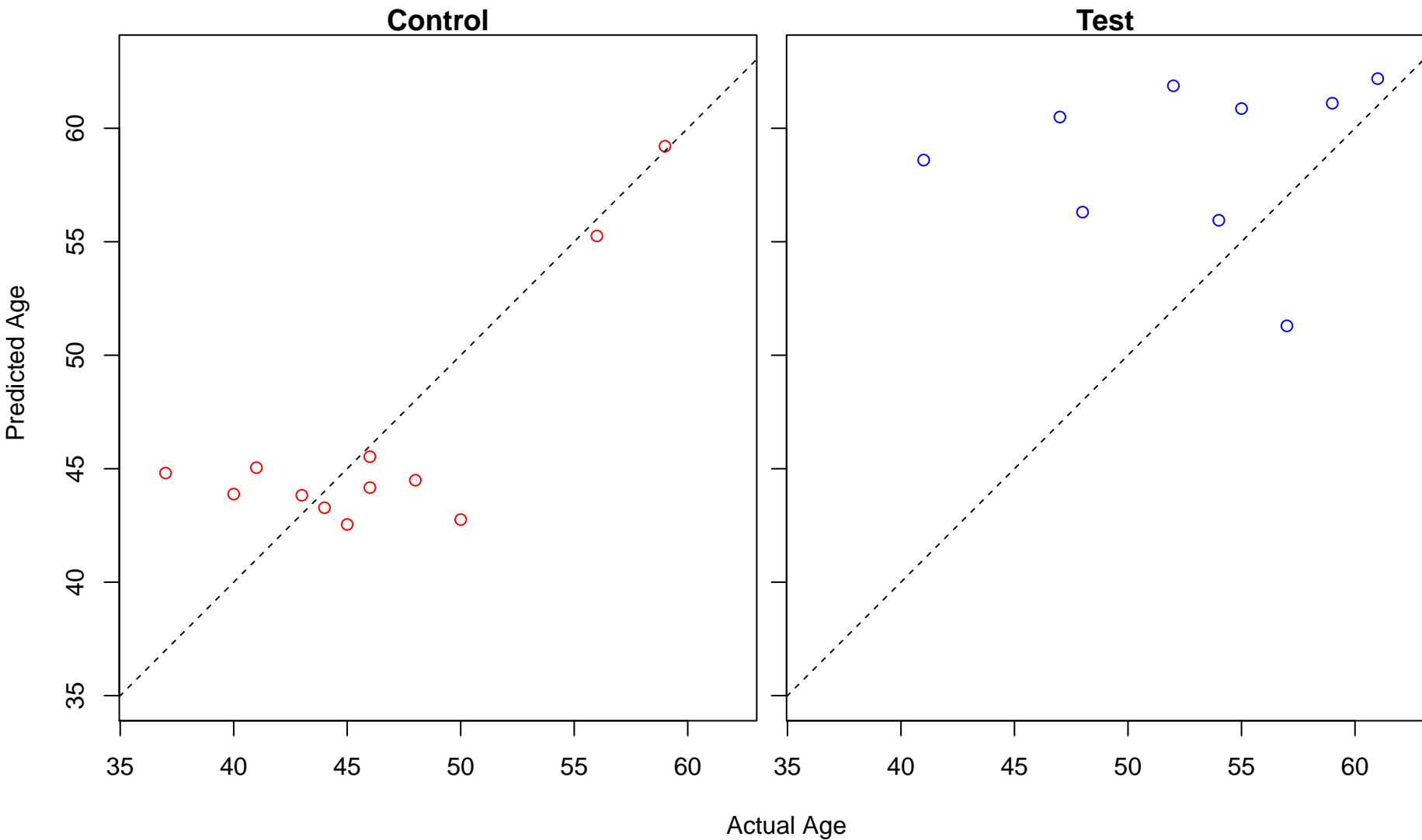
positive regulation of protein oligomerization (Score: 4.610314)



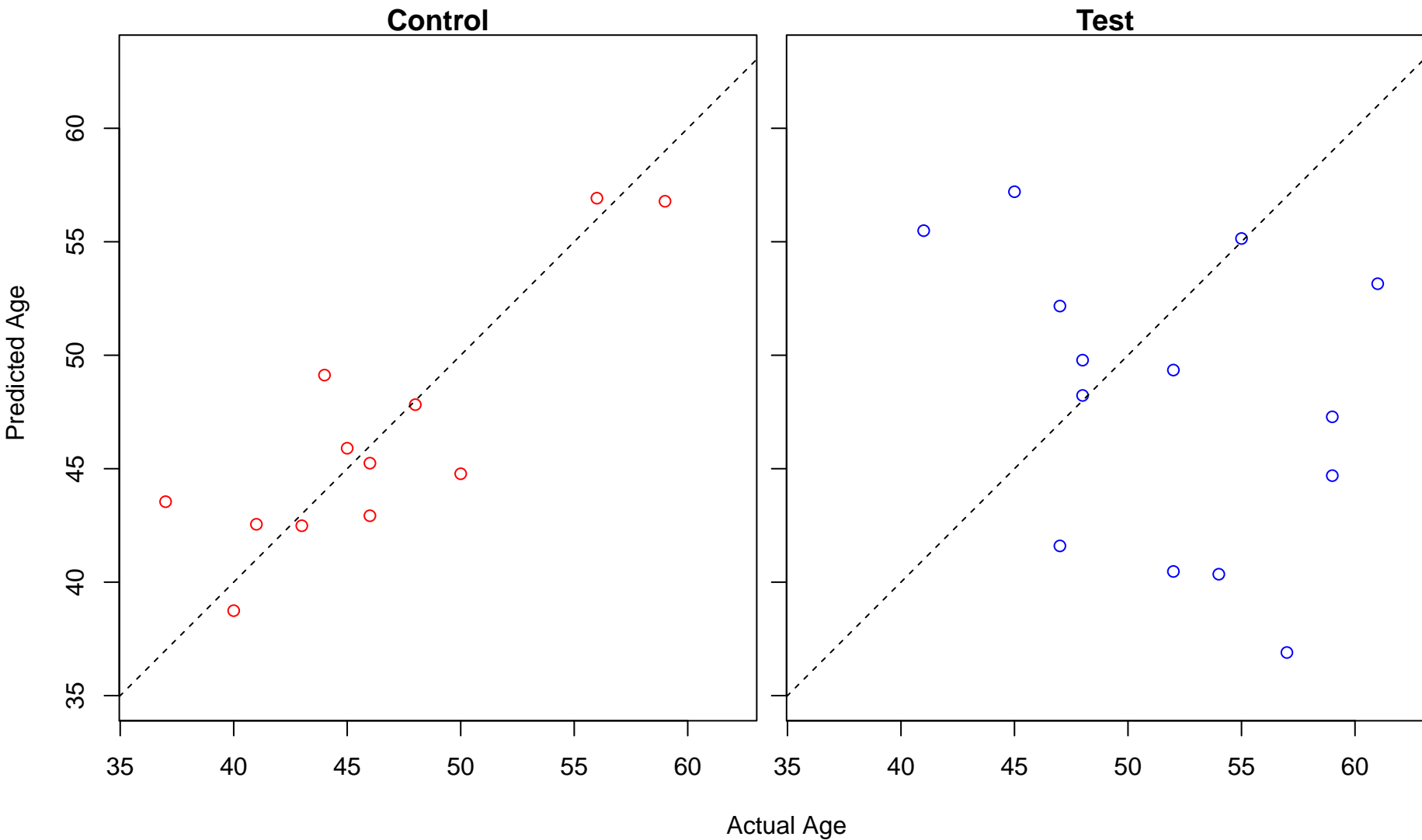
positive regulation of CREB transcription factor activity (Score: 4.608901)



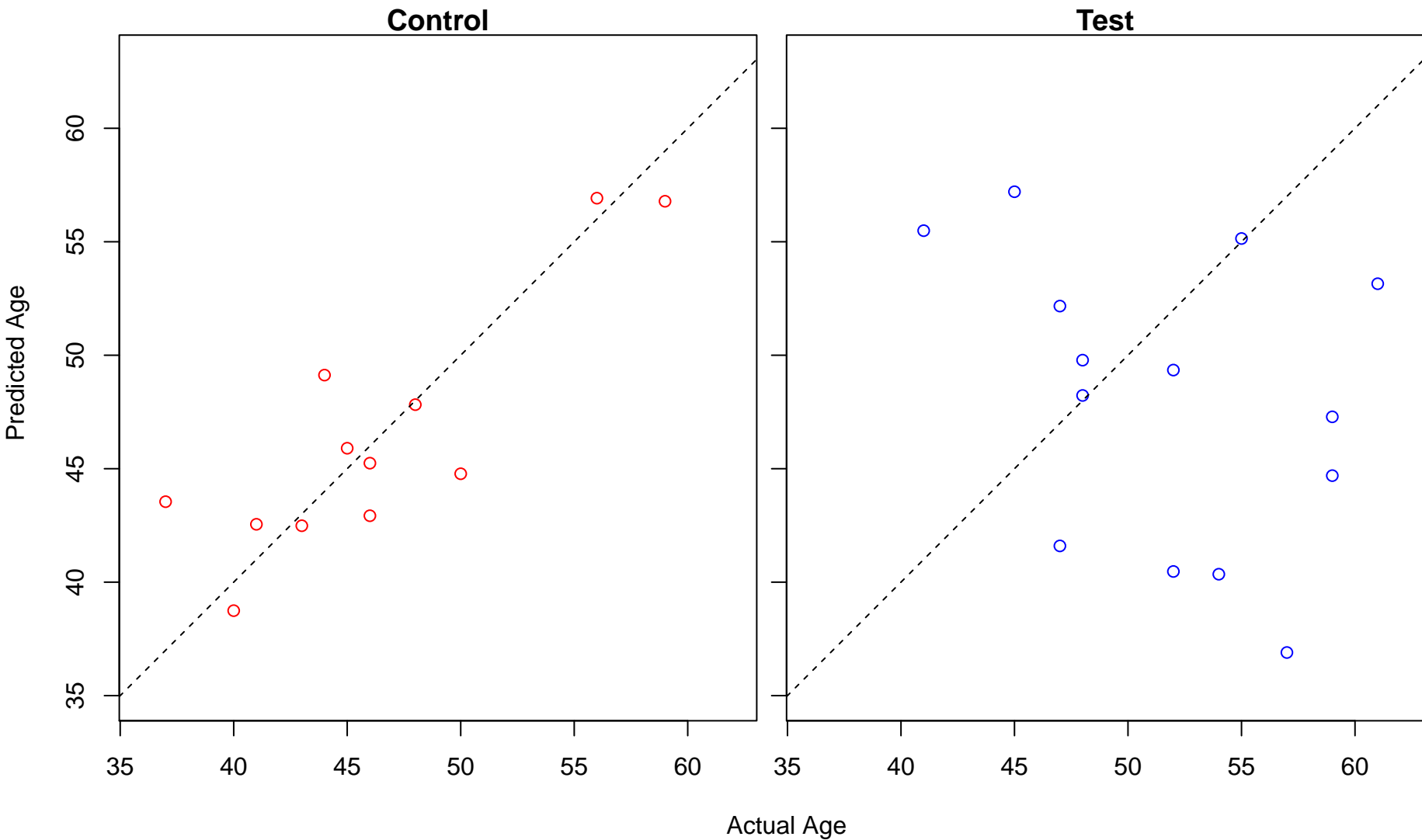
positive regulation of glial cell differentiation (Score: 4.606169)



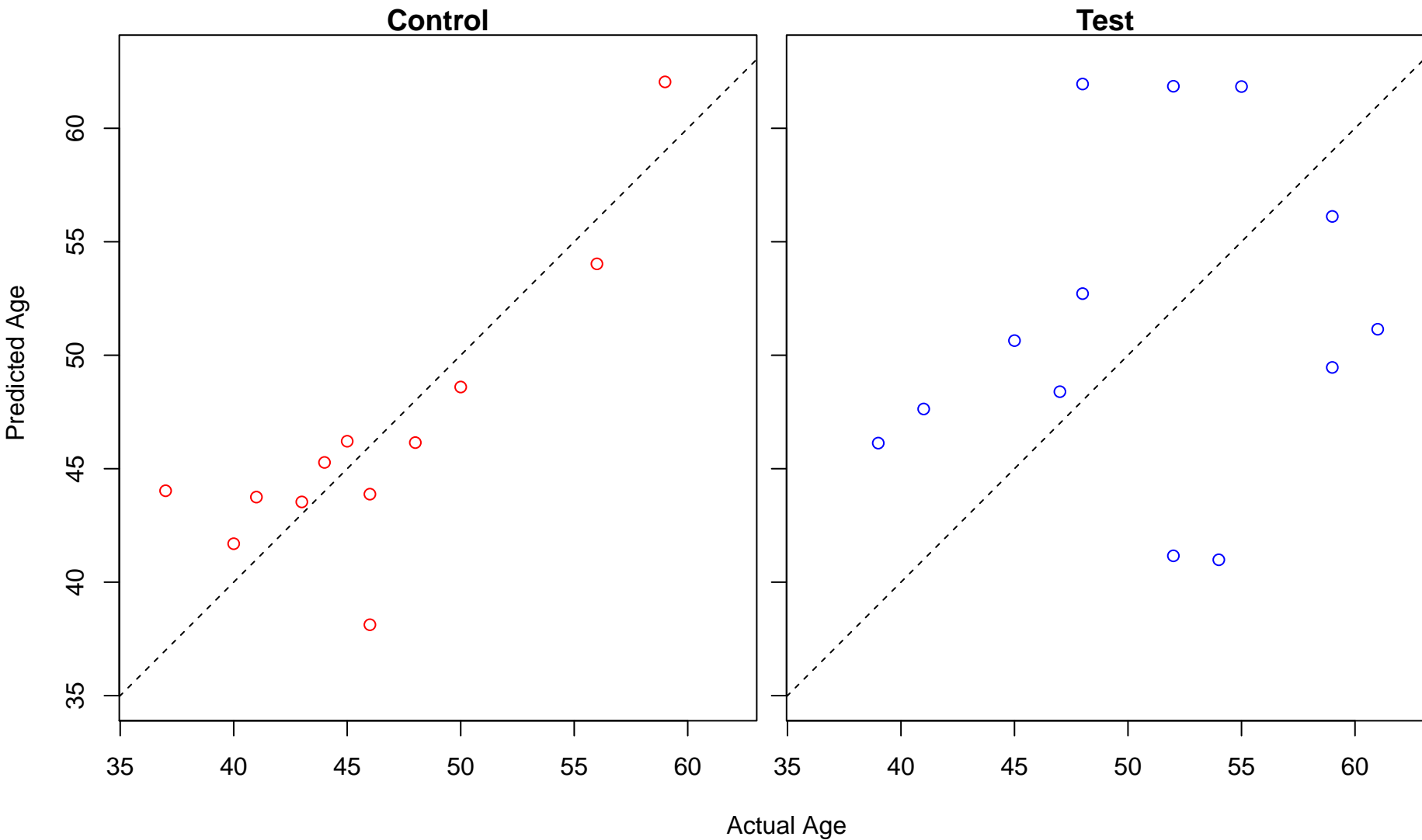
amino acid activation (Score: 4.605859)



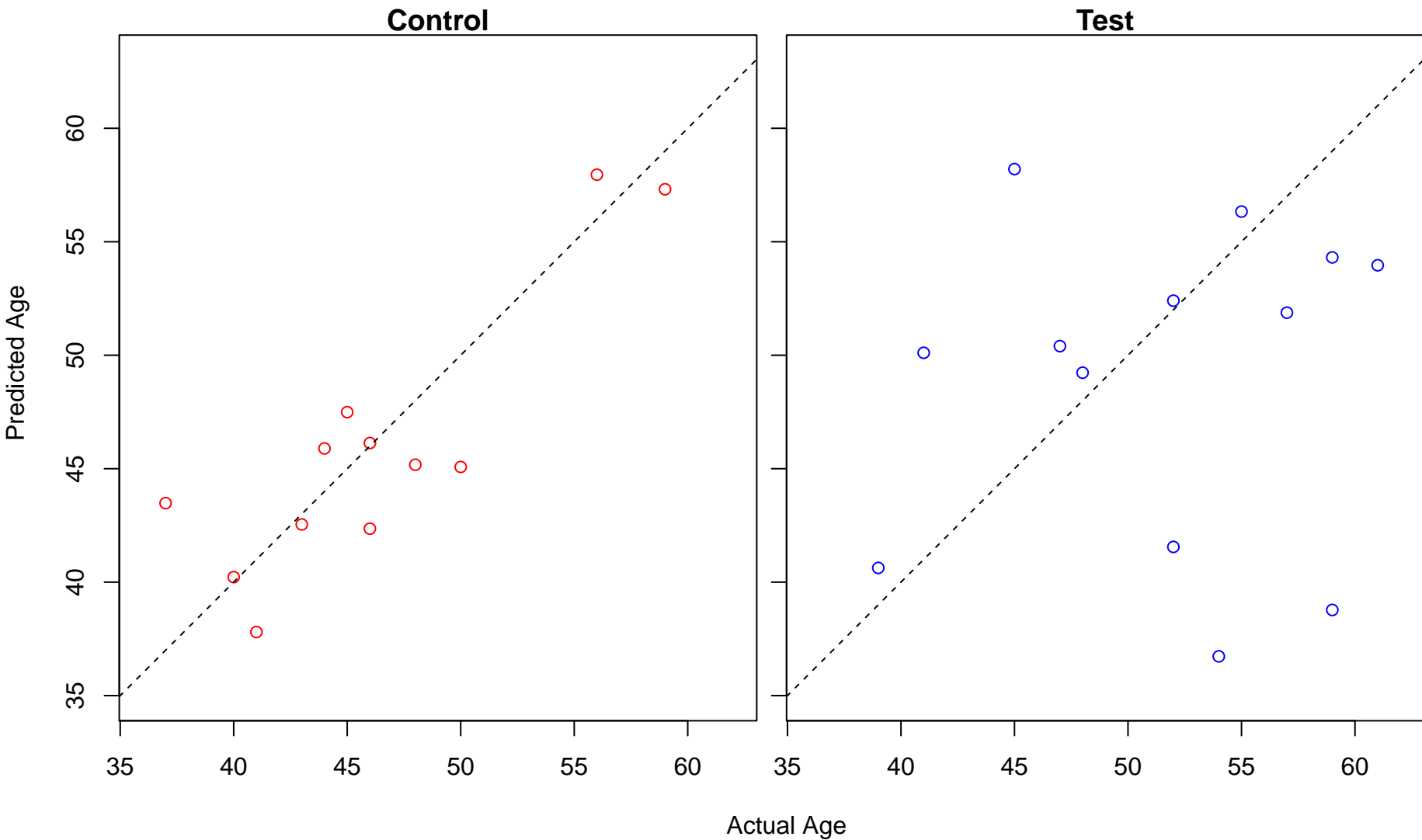
tRNA aminoacylation (Score: 4.605859)



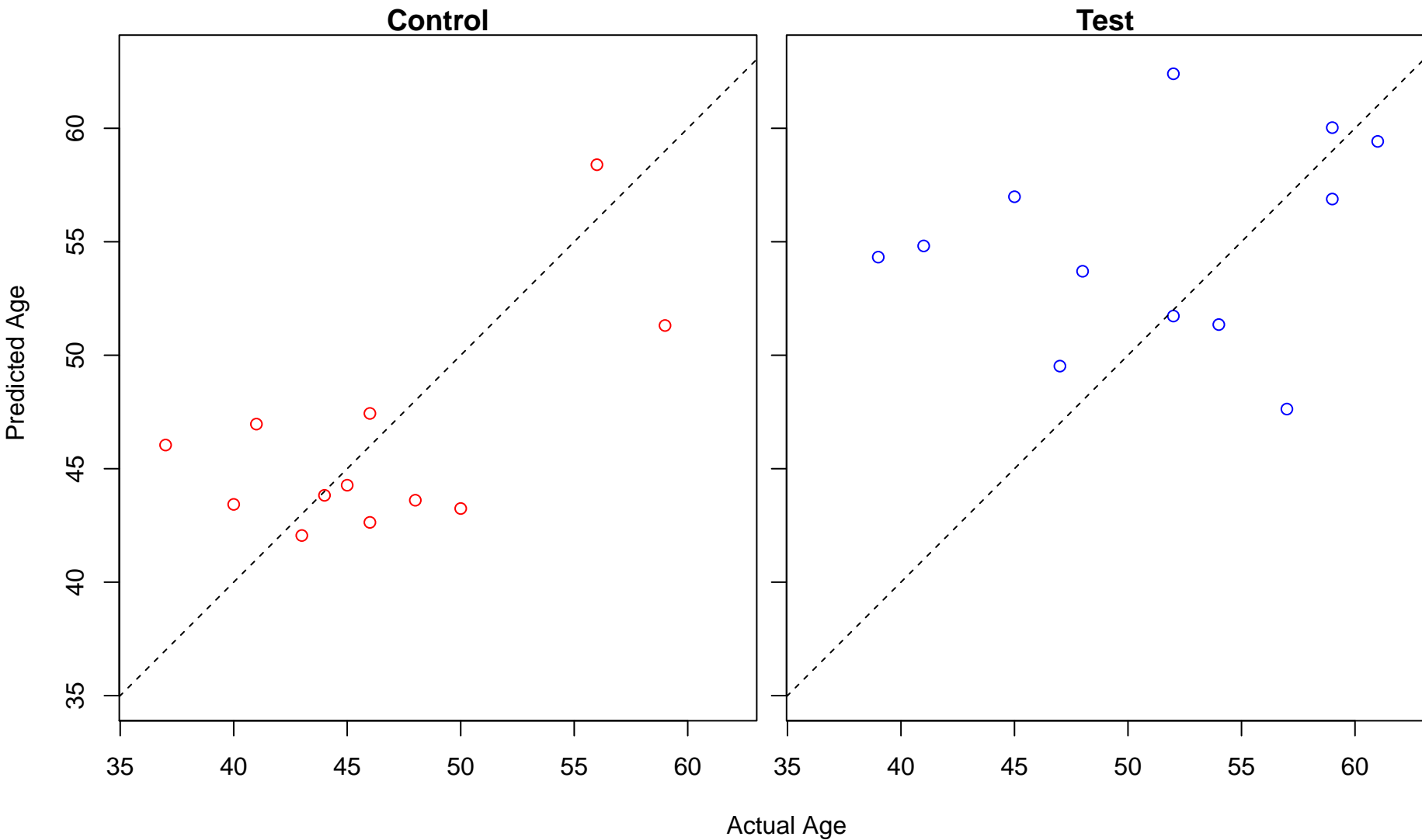
protein localization to vacuole (Score: 4.603799)



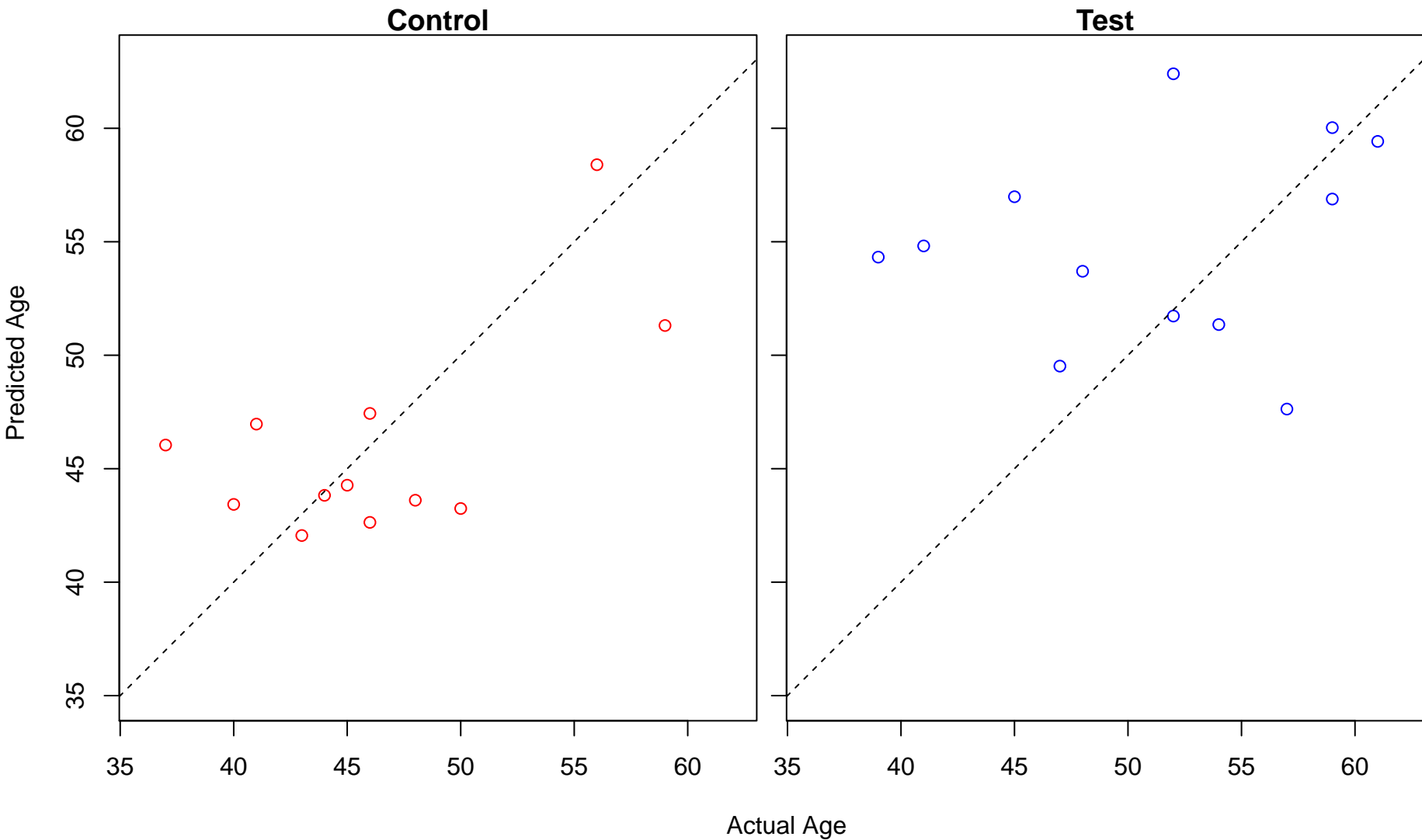
respiratory system development (Score: 4.592784)



positive regulation of T cell differentiation in thymus (Score: 4.591622)

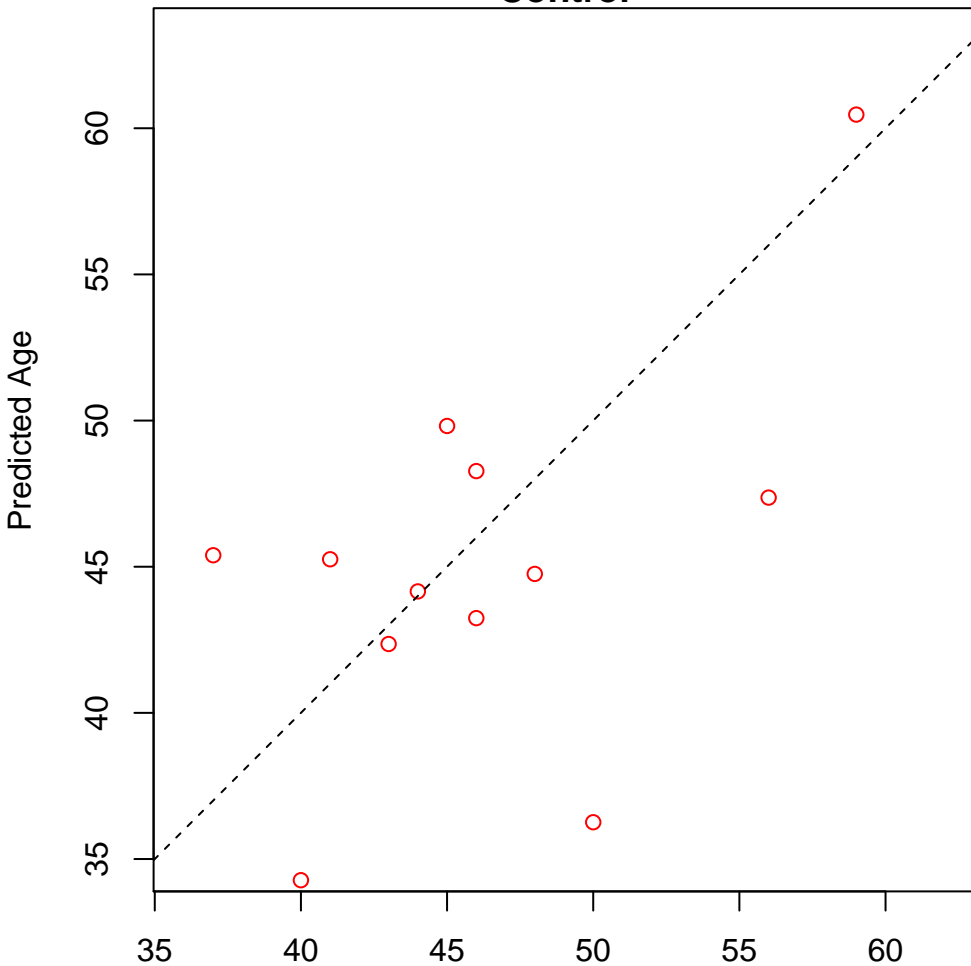


positive regulation of thymocyte aggregation (Score: 4.591622)

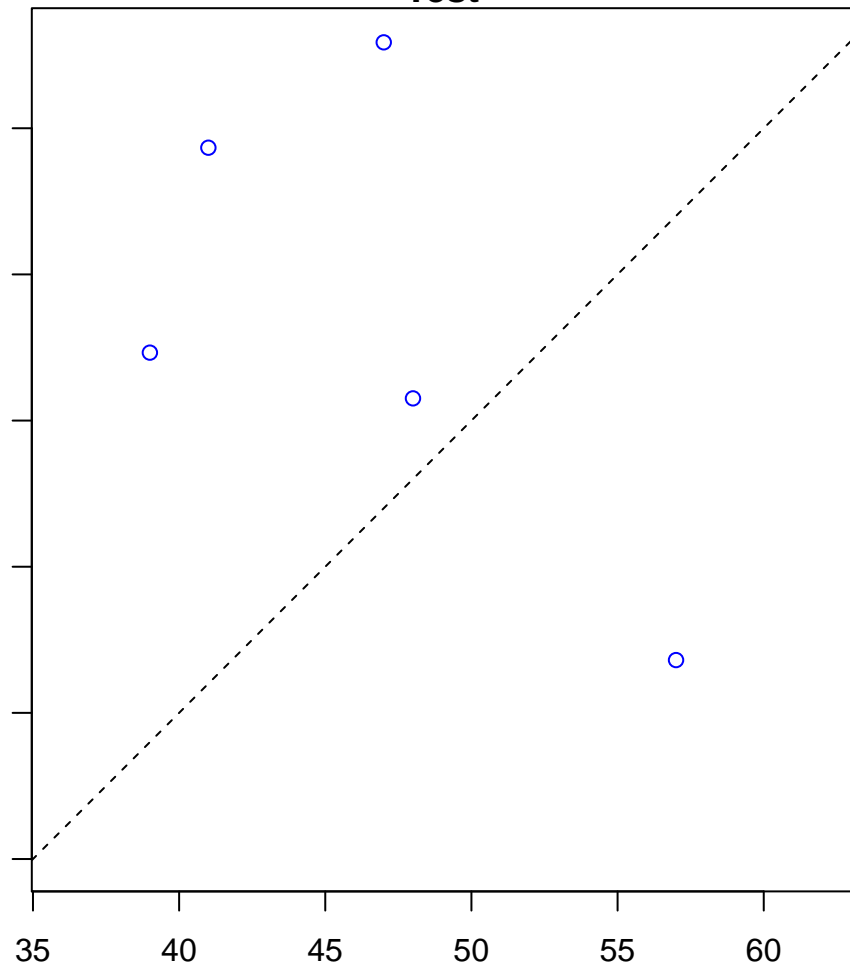


N-acetylneuraminate metabolic process (Score: 4.588416)

Control



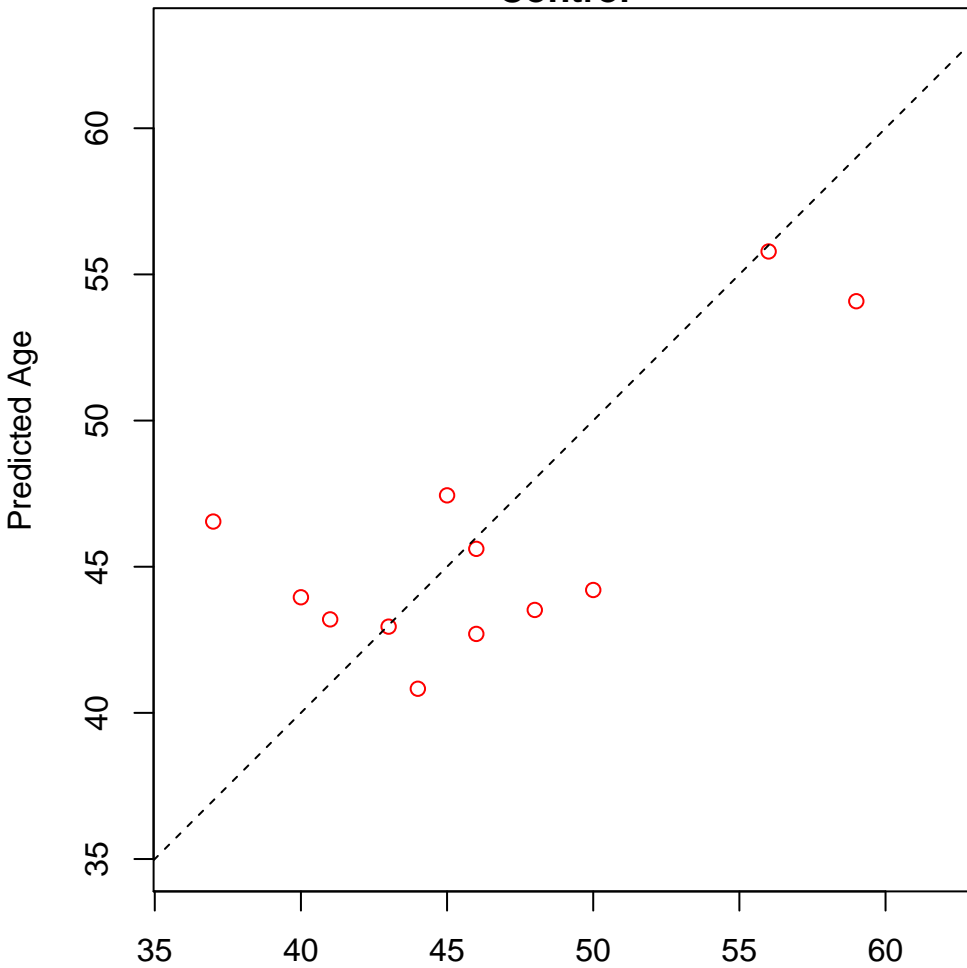
Test



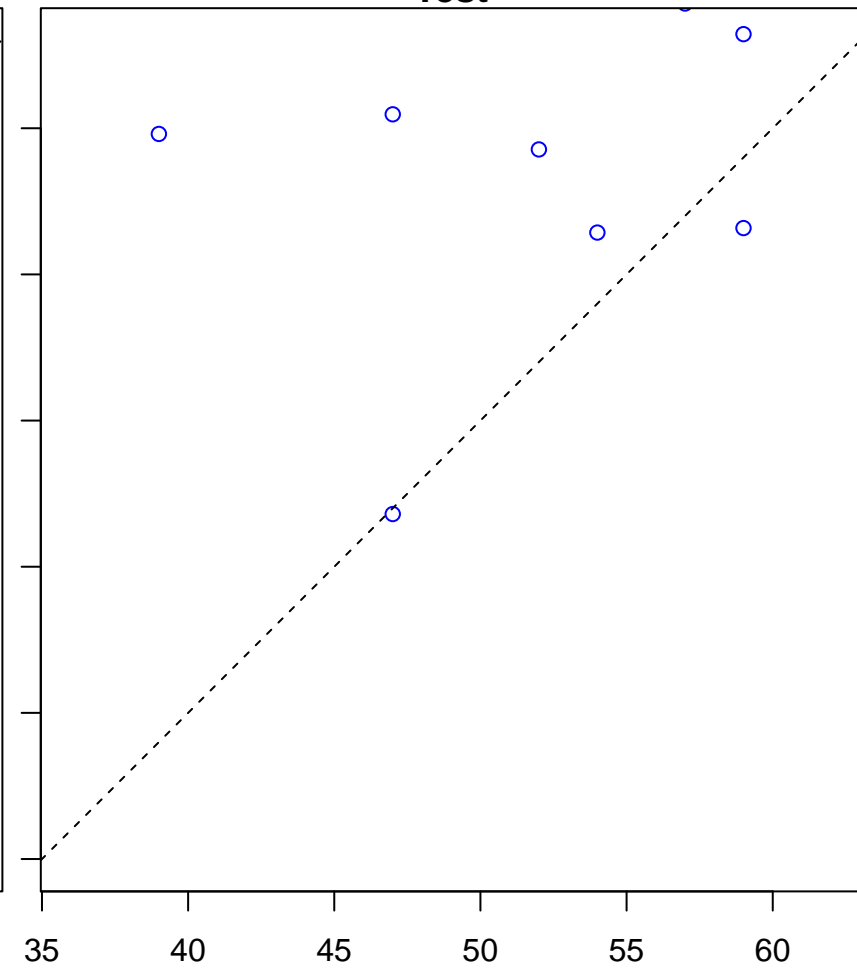
Actual Age

negative regulation of gluconeogenesis (Score: 4.585169)

Control



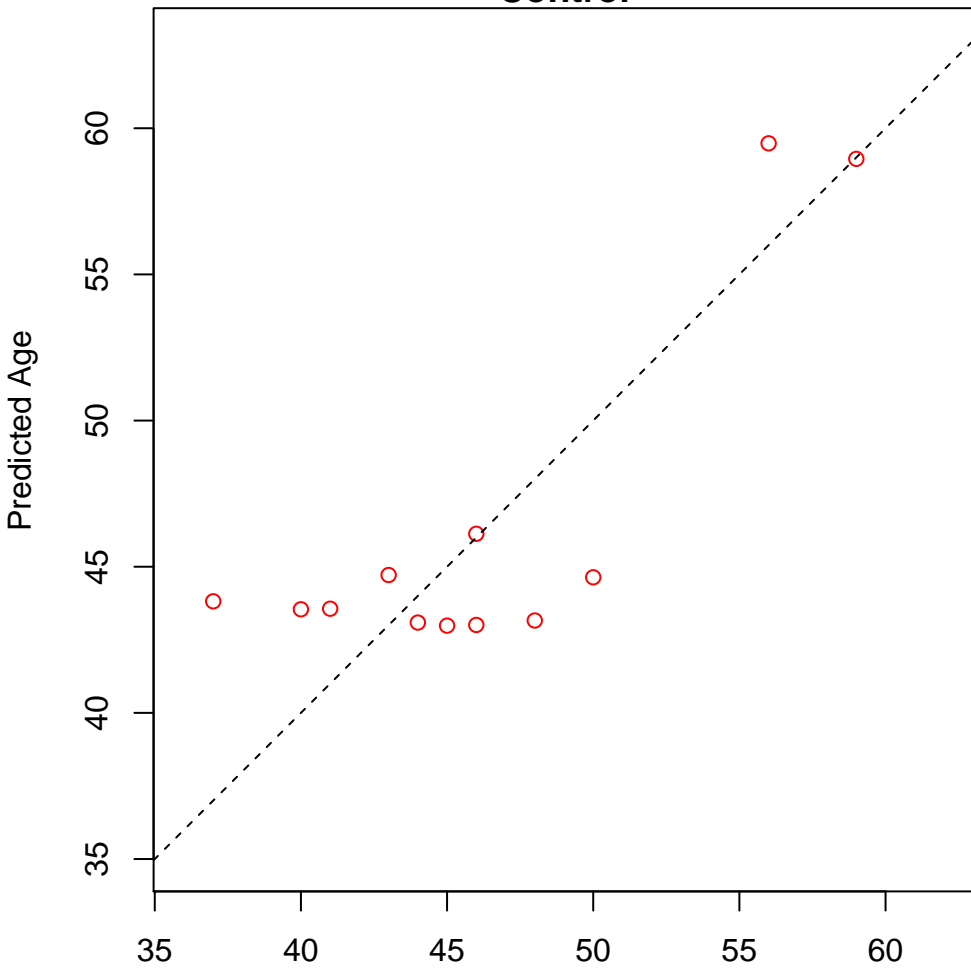
Test



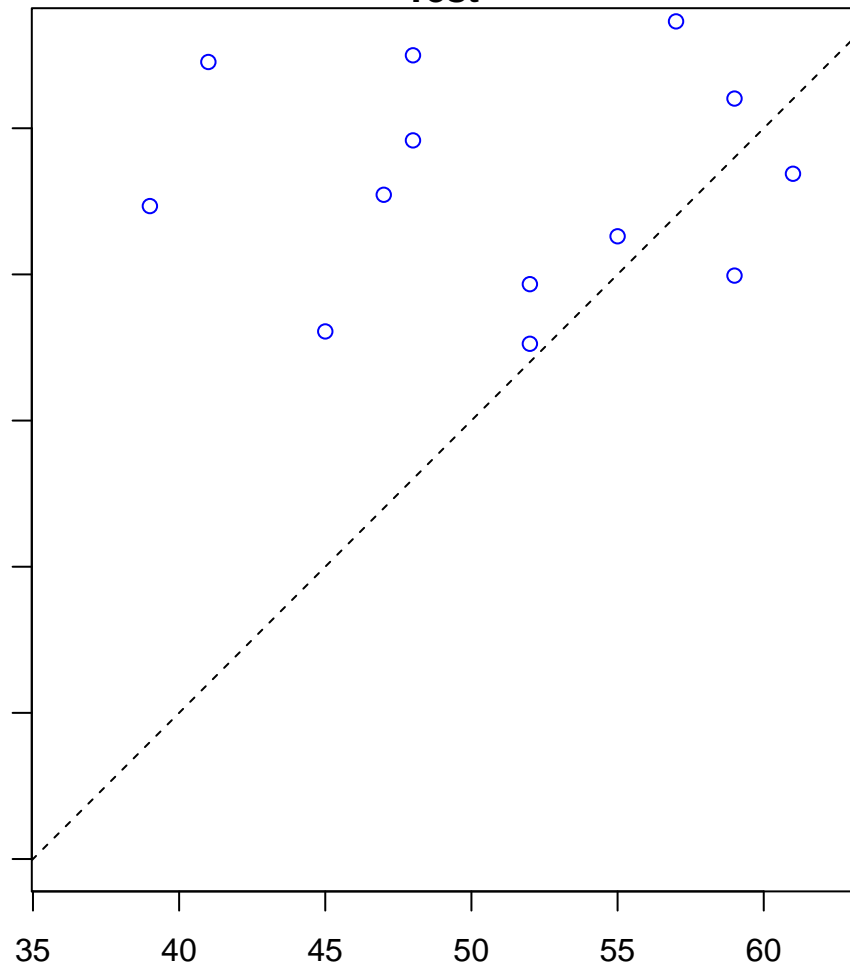
Actual Age

one-carbon compound transport (Score: 4.582095)

Control

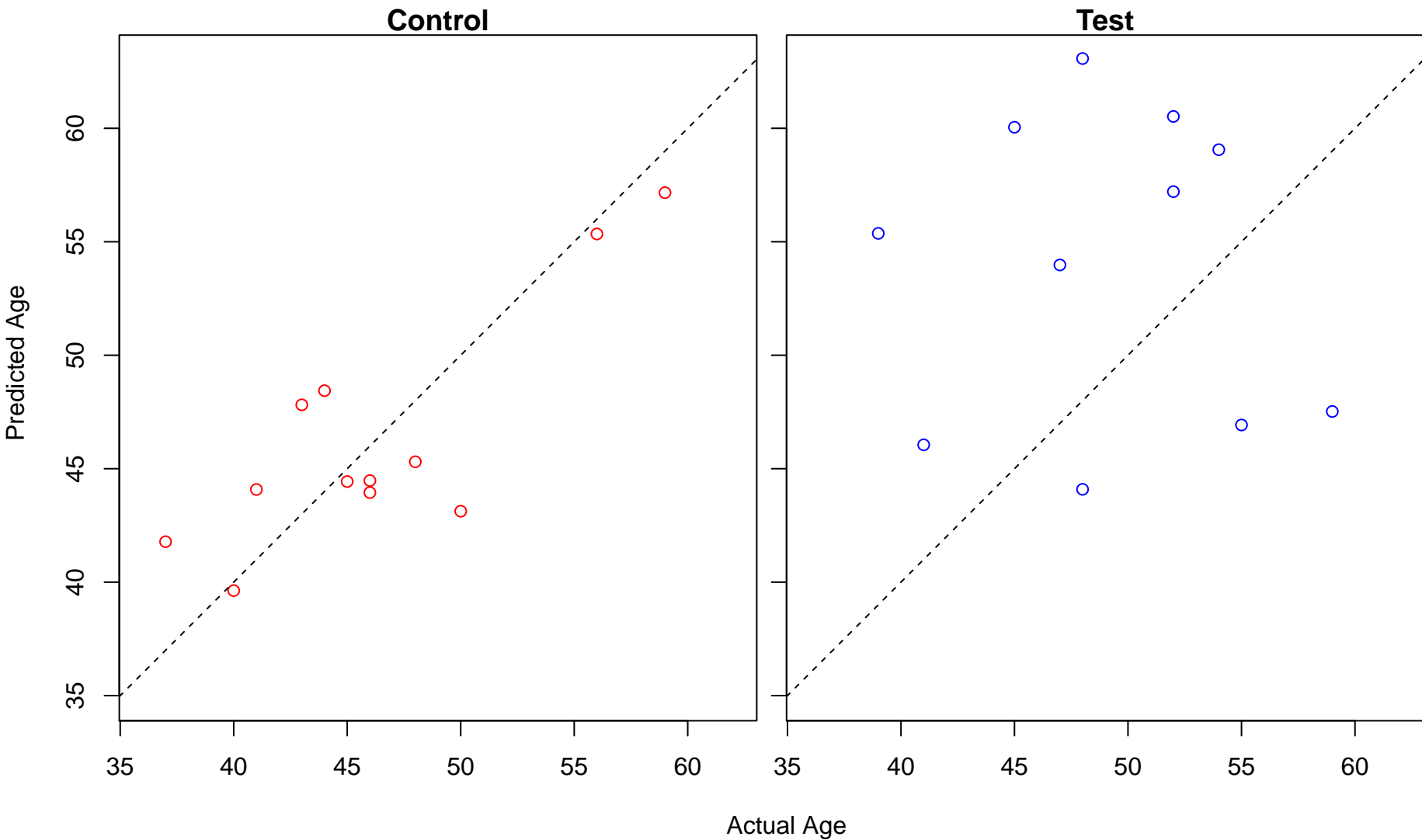


Test

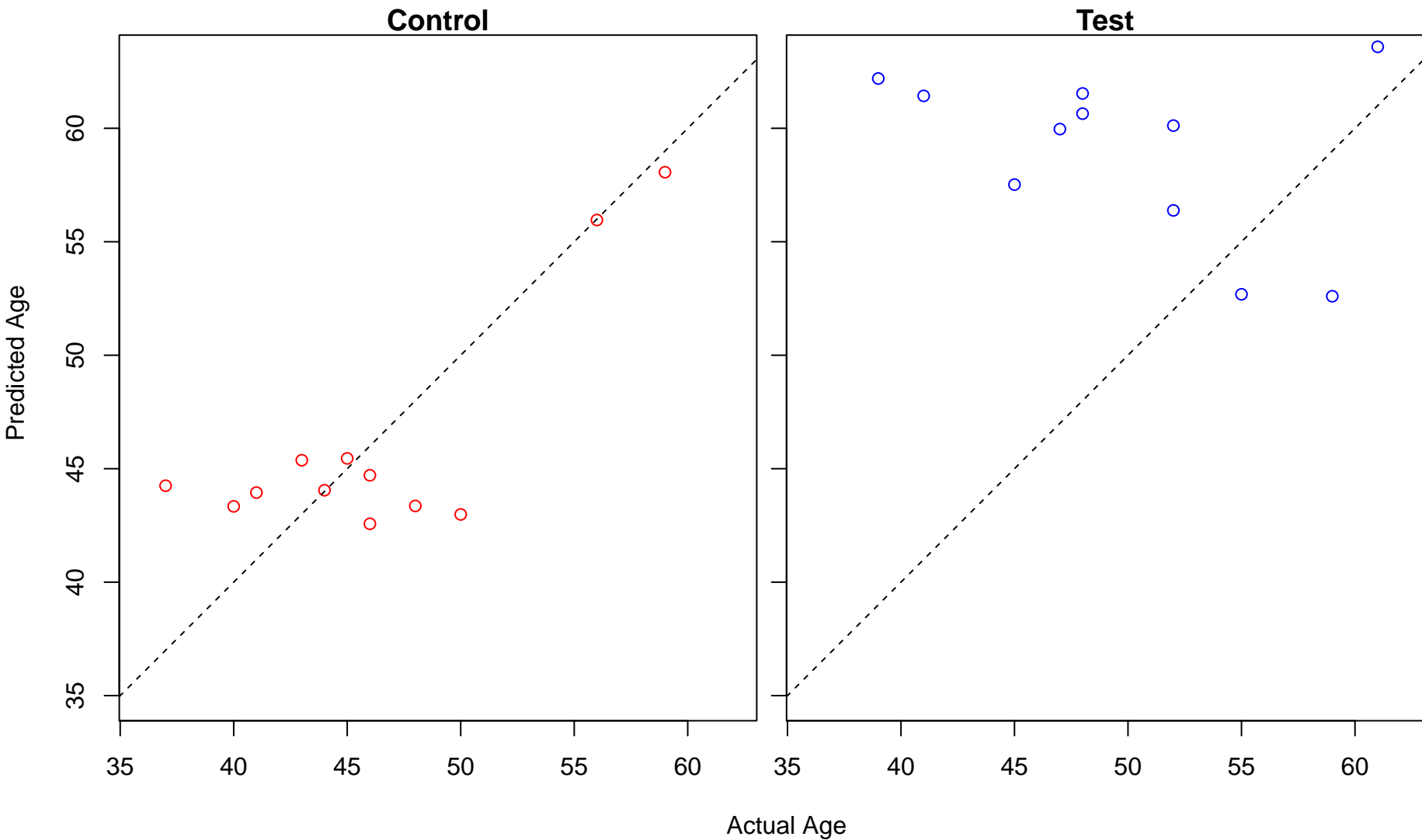


Actual Age

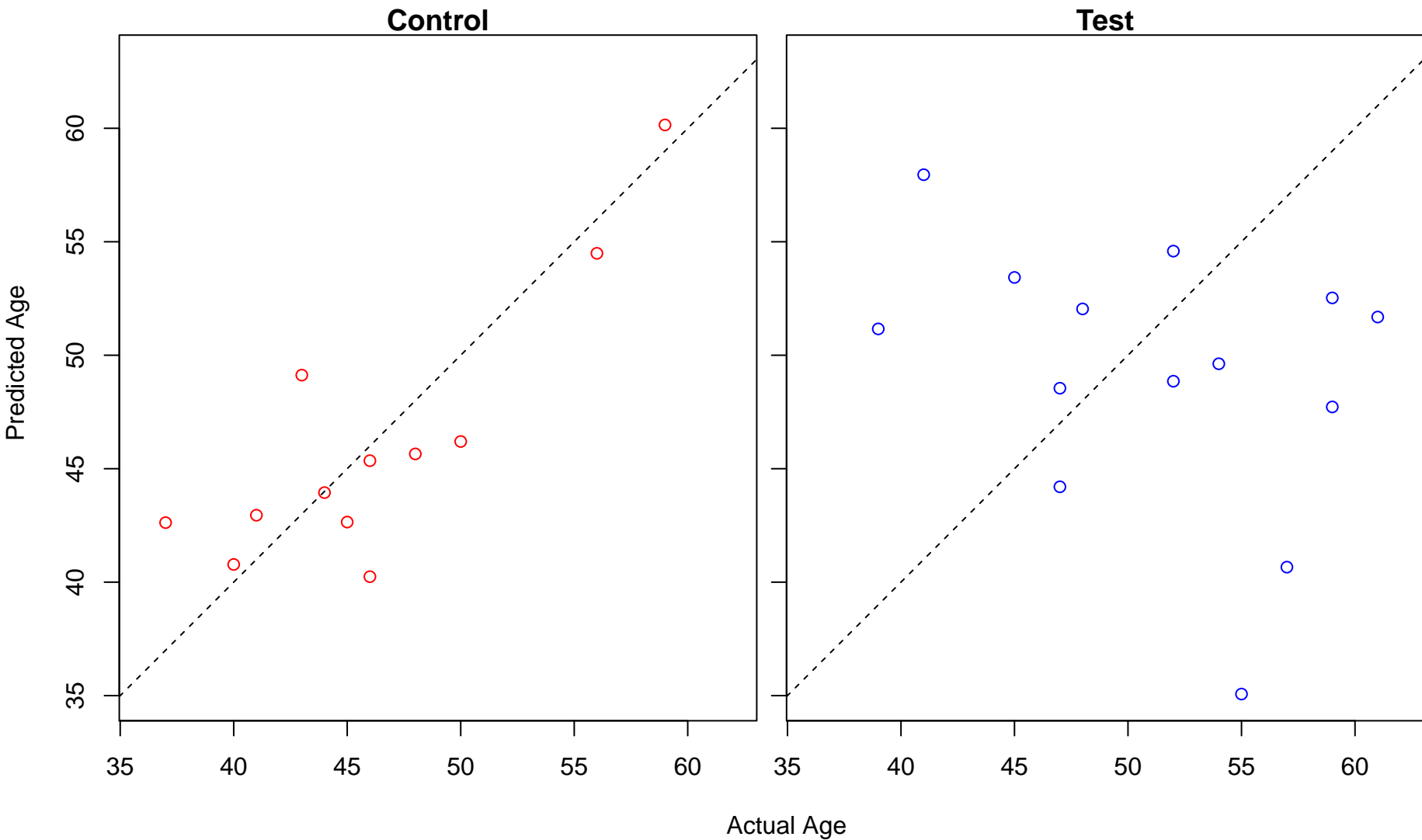
regulation of immunoglobulin production (Score: 4.573434)



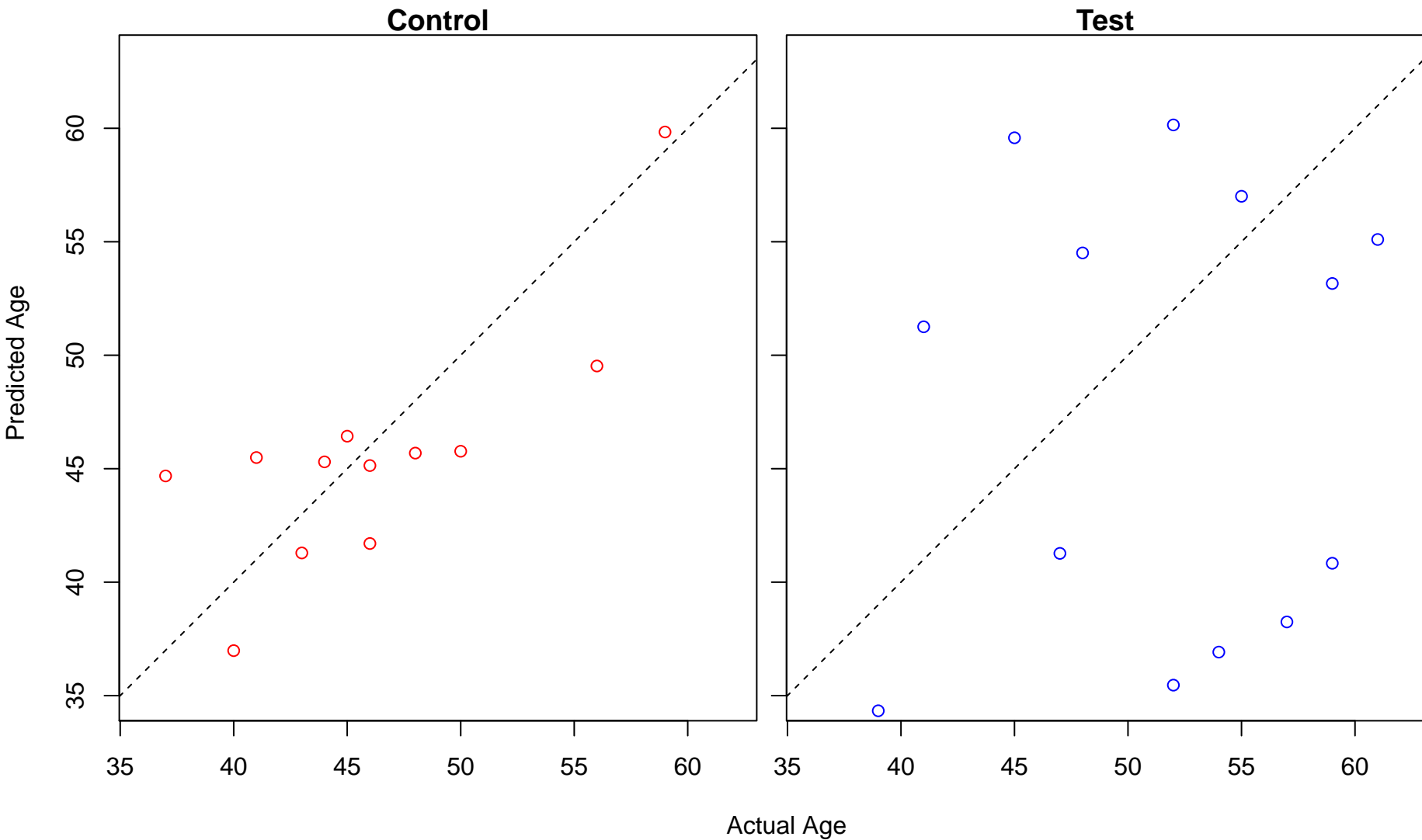
calcium-mediated signaling using intracellular calcium source (Score: 4.570685)



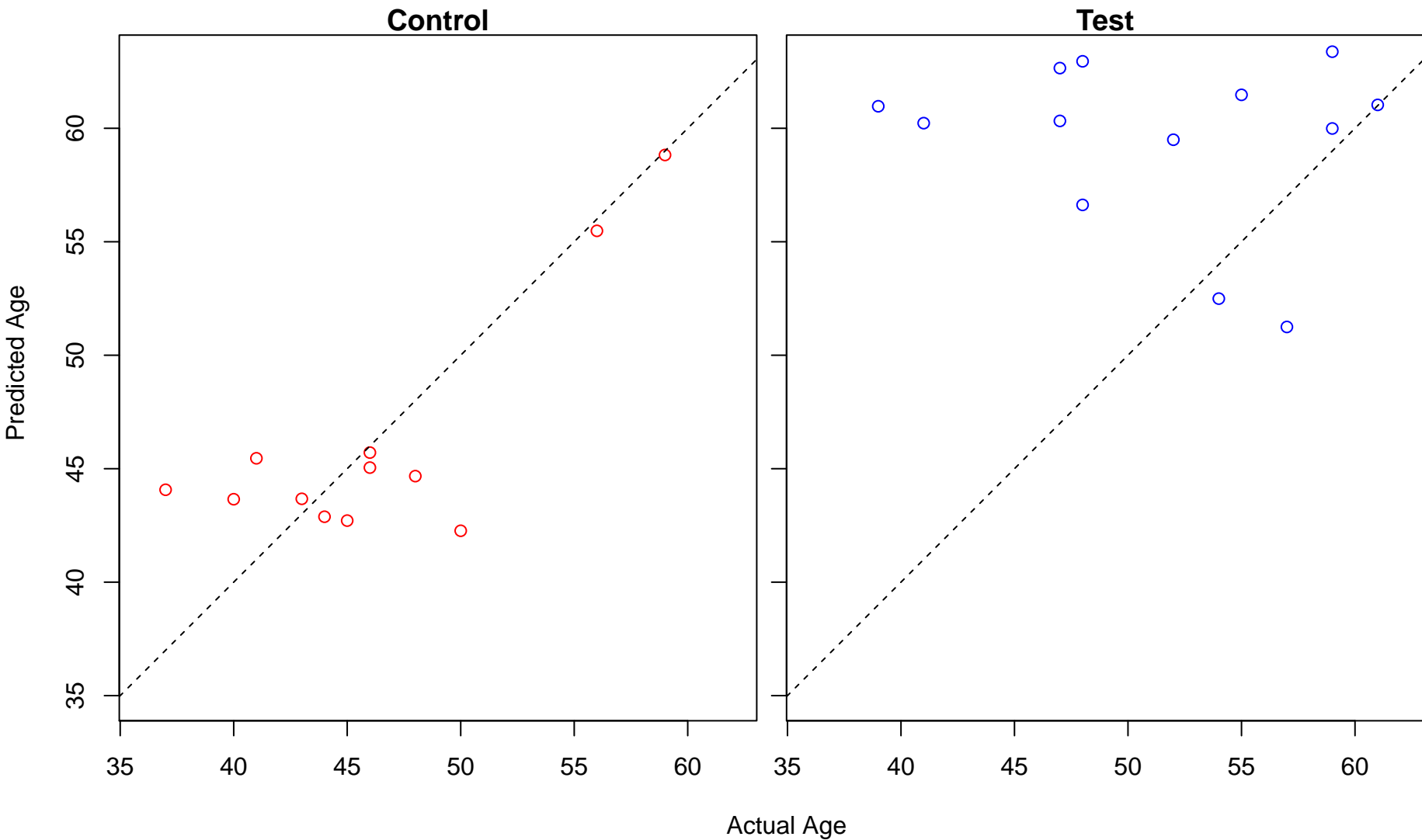
regulation of stress-activated MAPK cascade (Score: 4.566538)



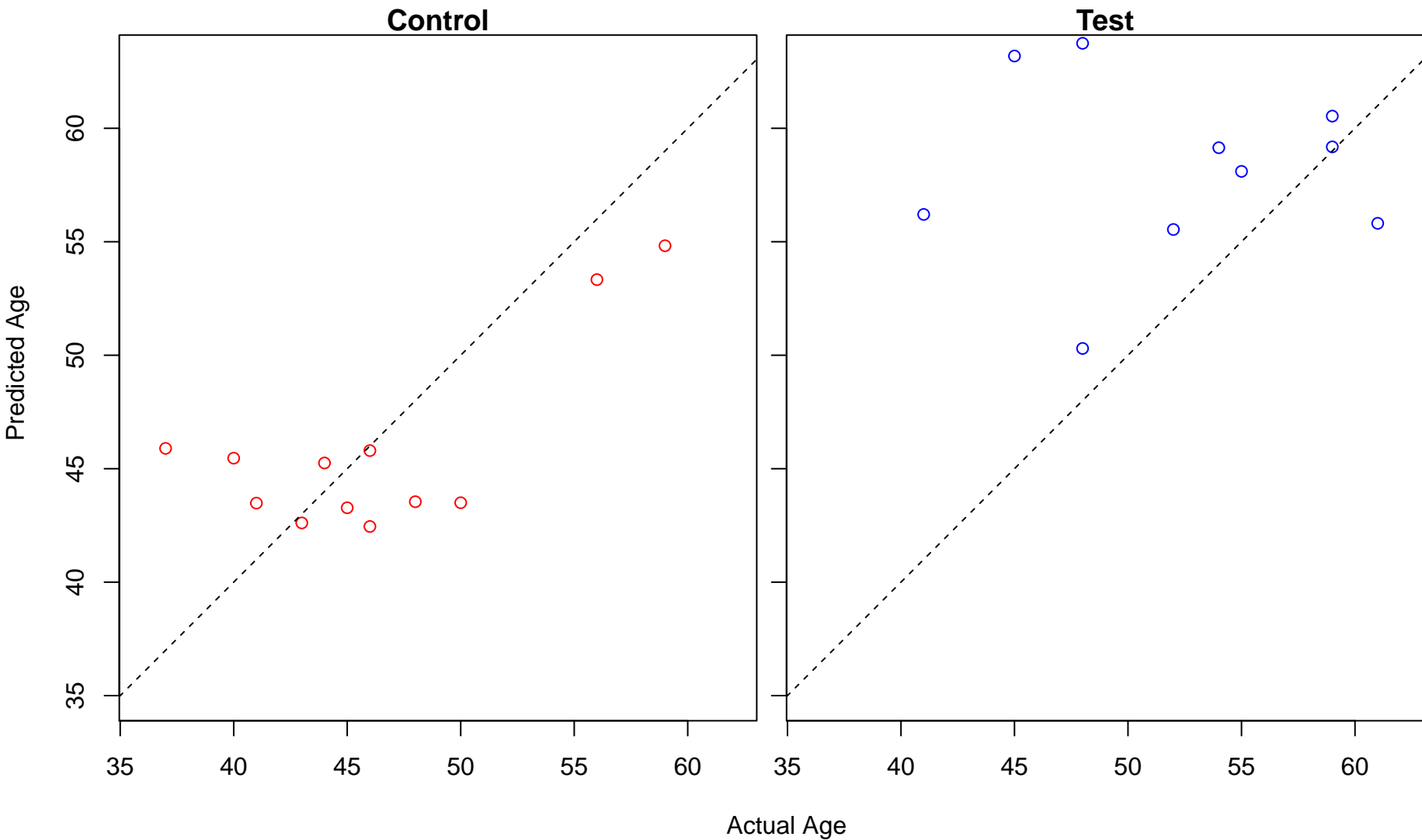
regulation of microtubule-based movement (Score: 4.566097)



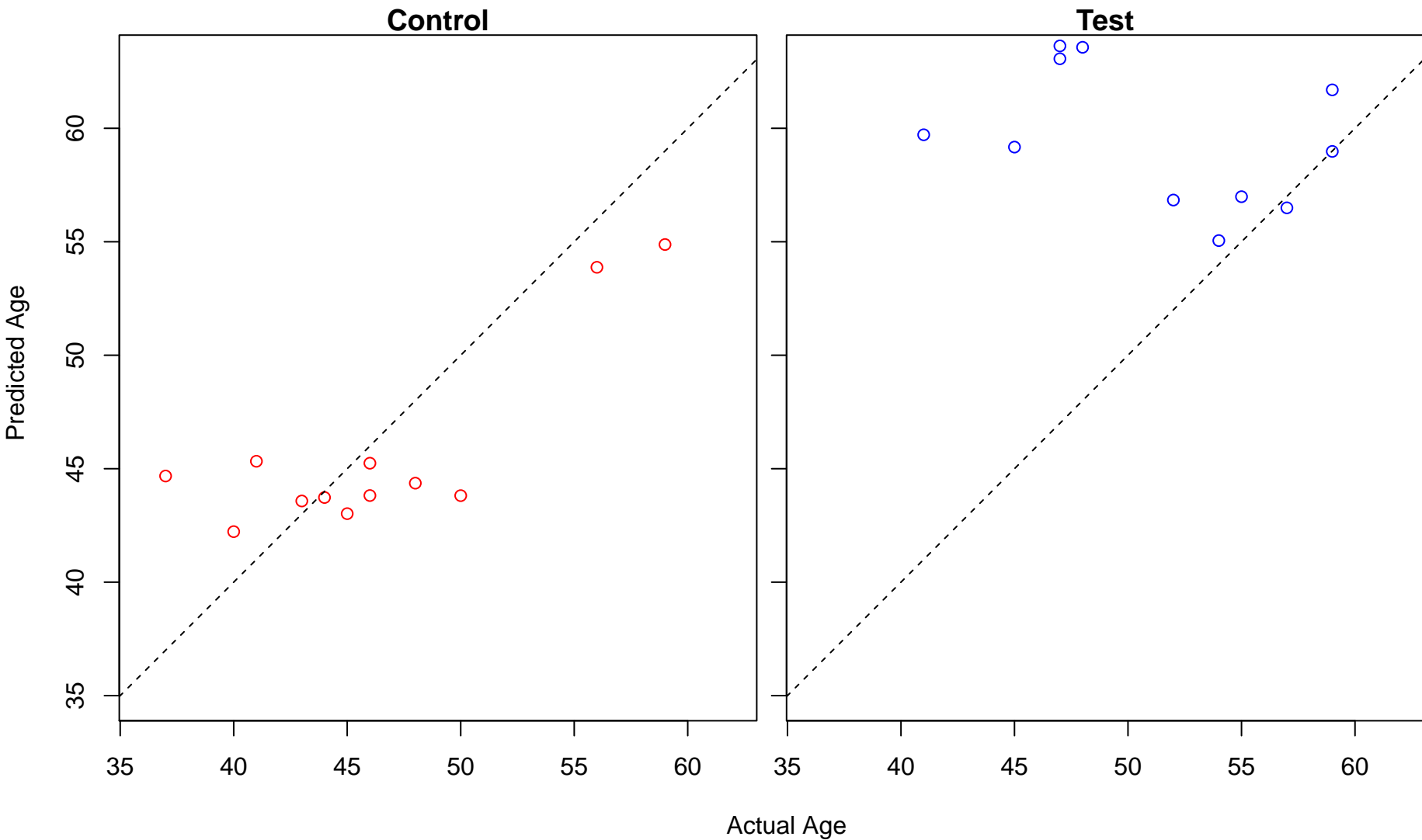
production of siRNA involved in RNA interference (Score: 4.565411)



low-density lipoprotein particle remodeling (Score: 4.562504)

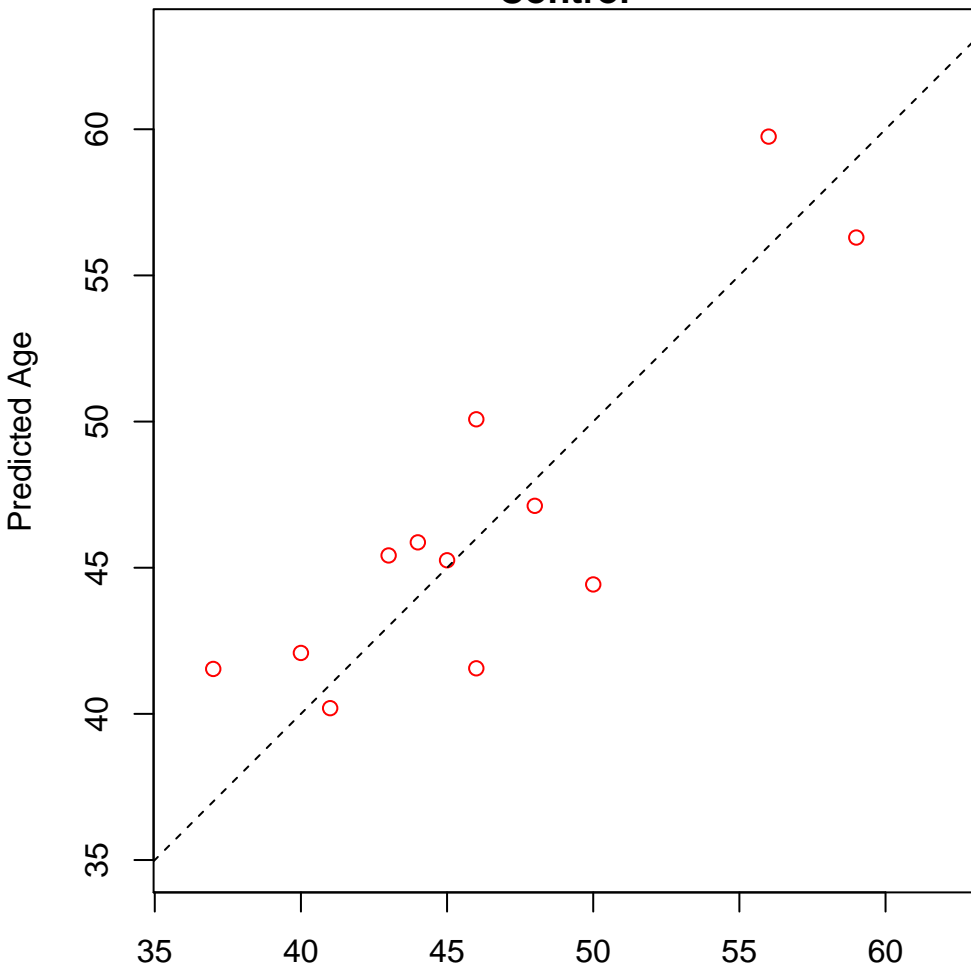


negative regulation of embryonic development (Score: 4.552886)

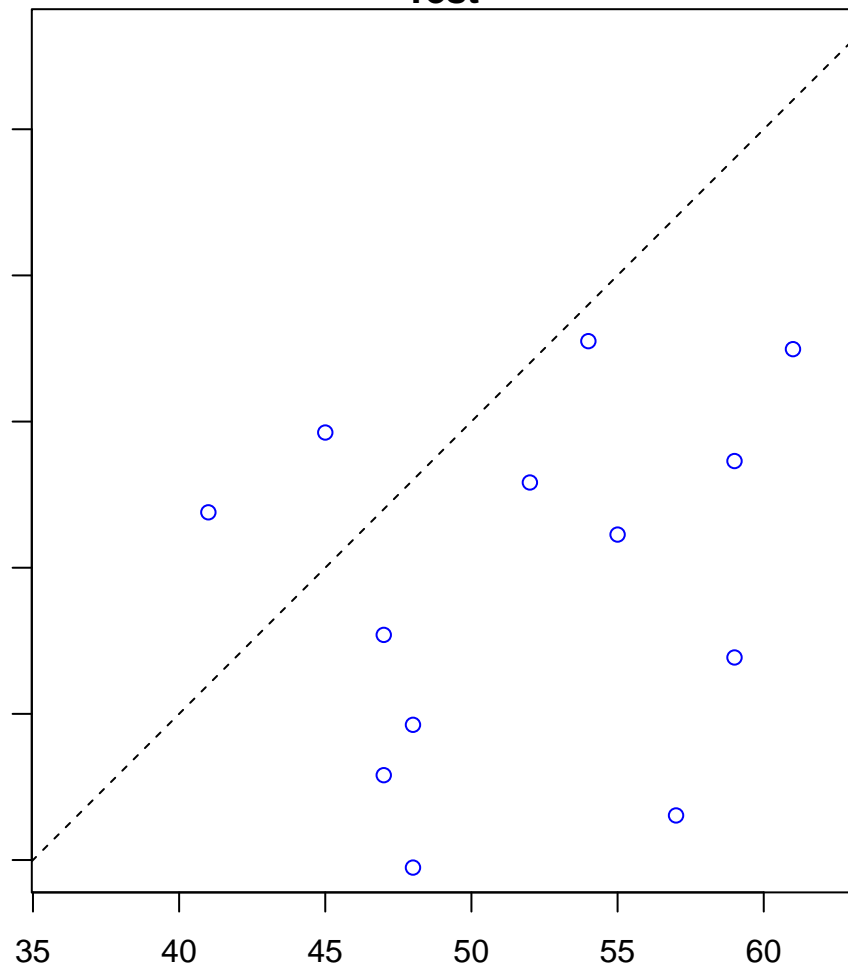


positive regulation of glucose transport (Score: 4.549937)

Control

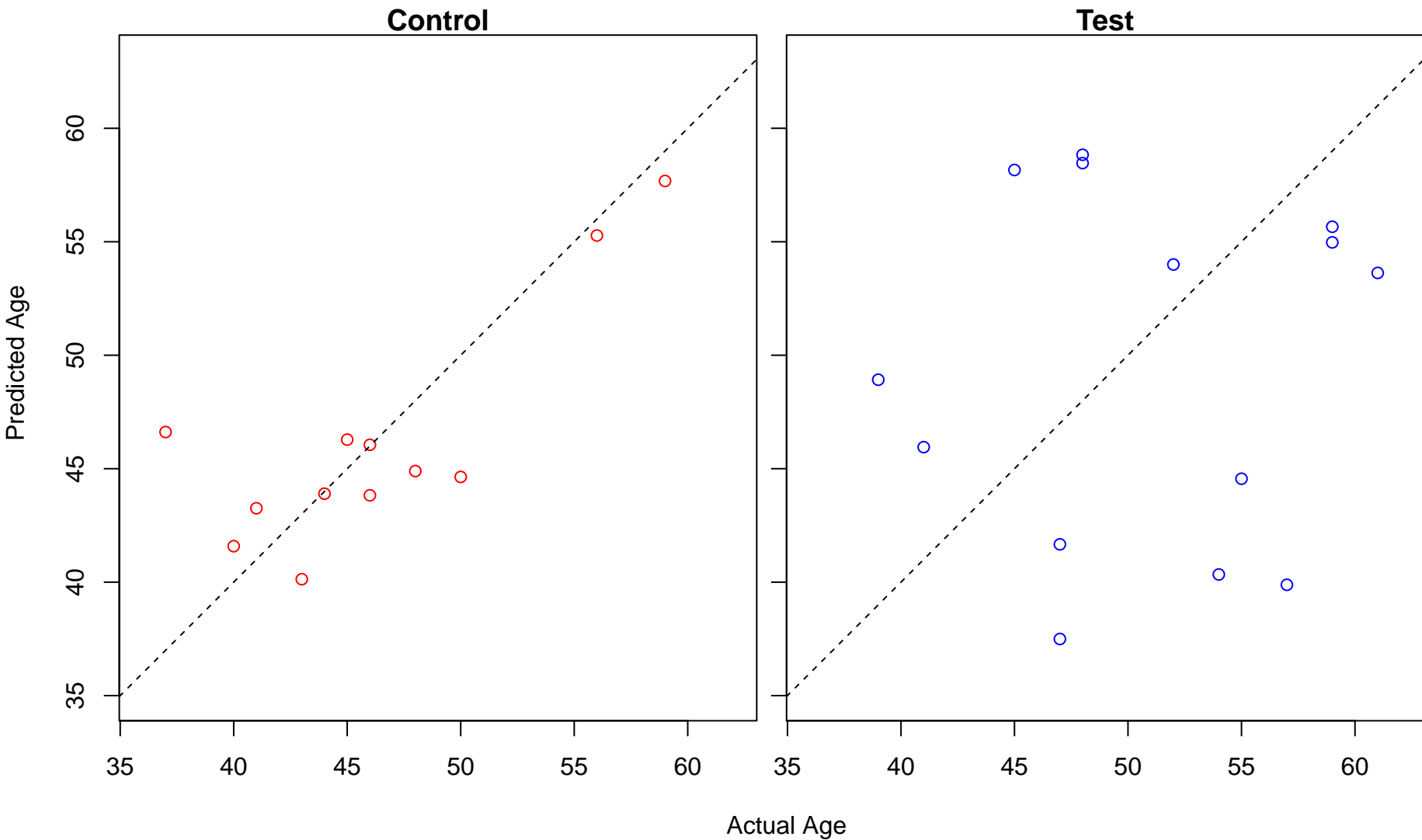


Test

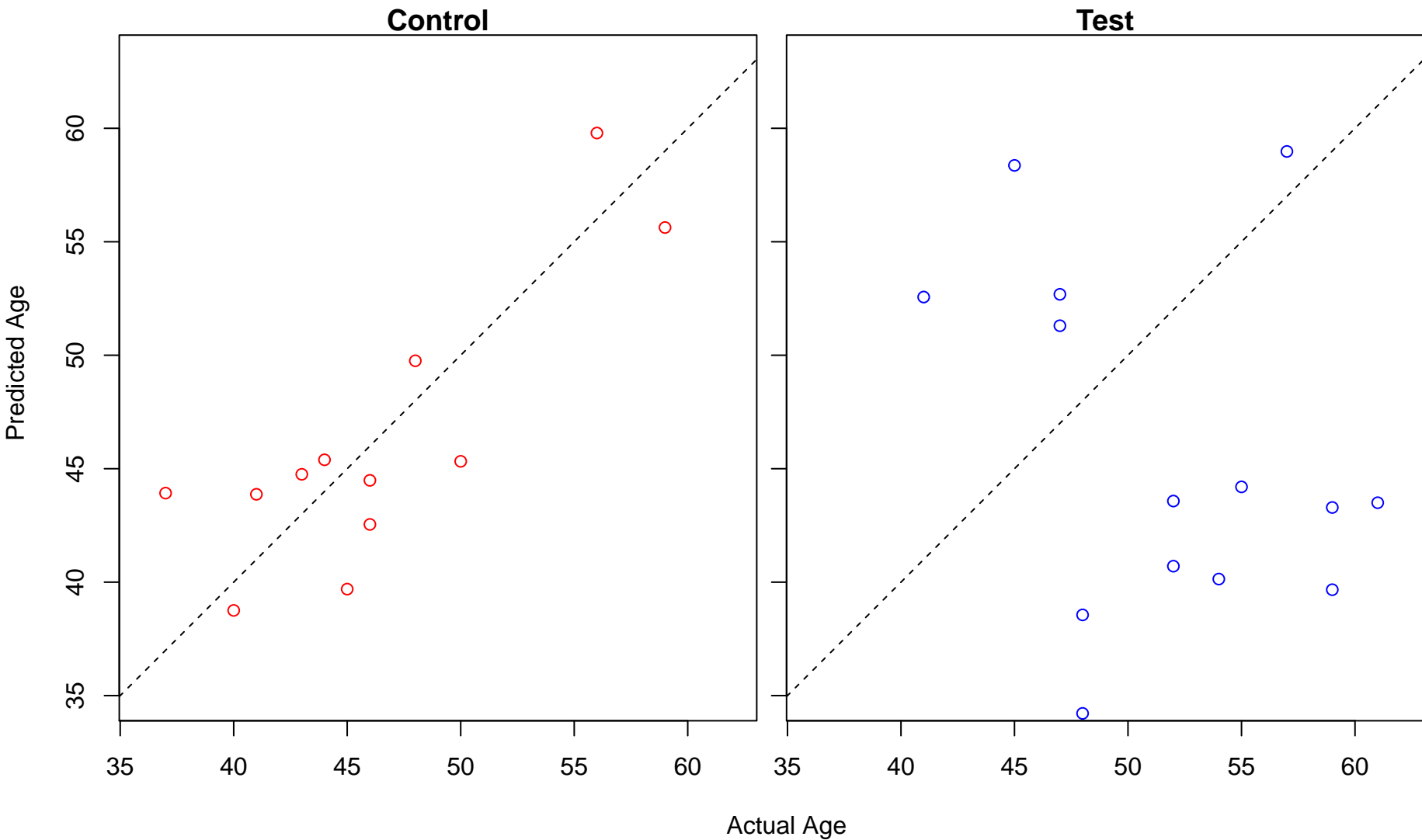


Actual Age

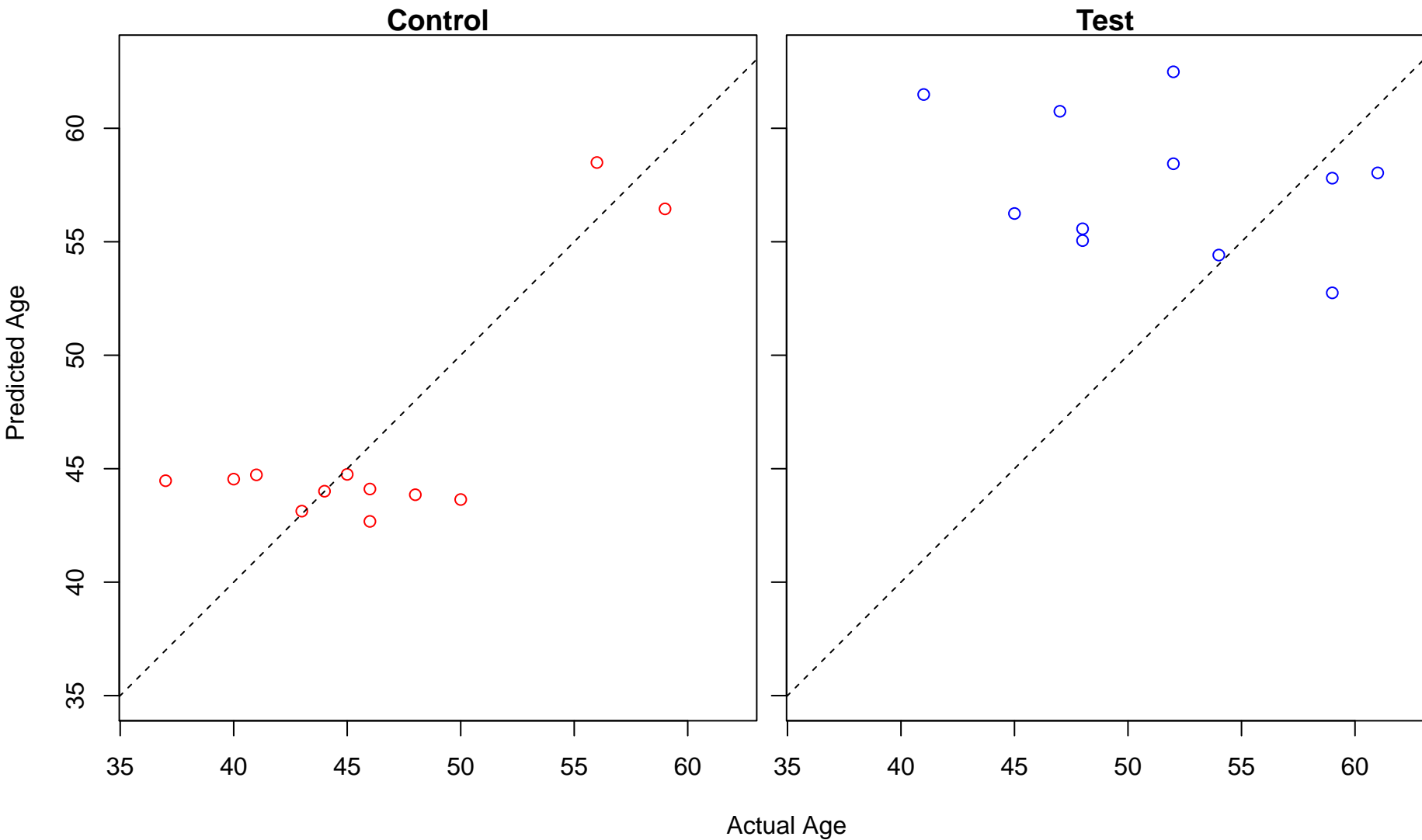
negative regulation of epidermal growth factor-activated receptor activity (Score: 4.540467)



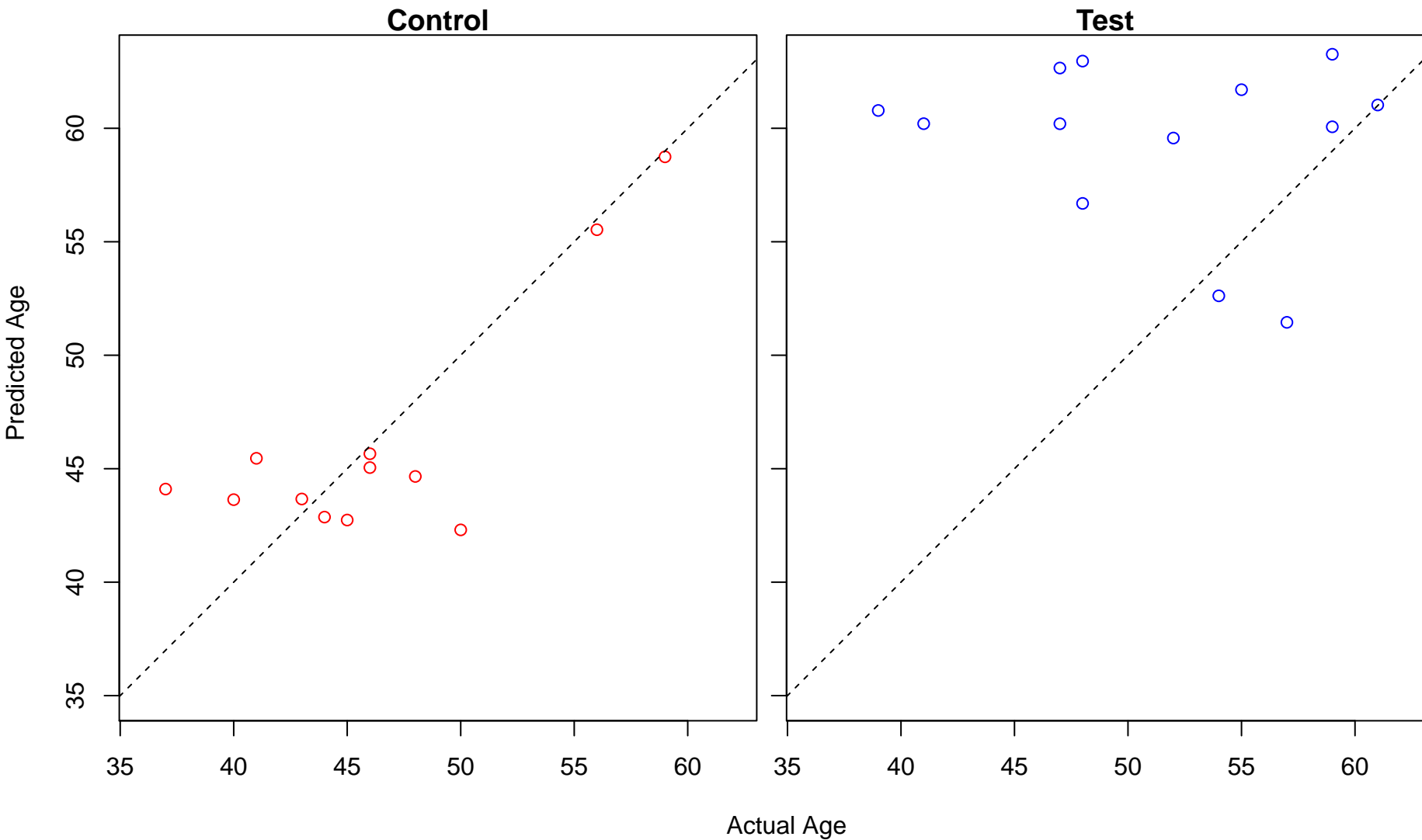
L-serine metabolic process (Score: 4.539534)



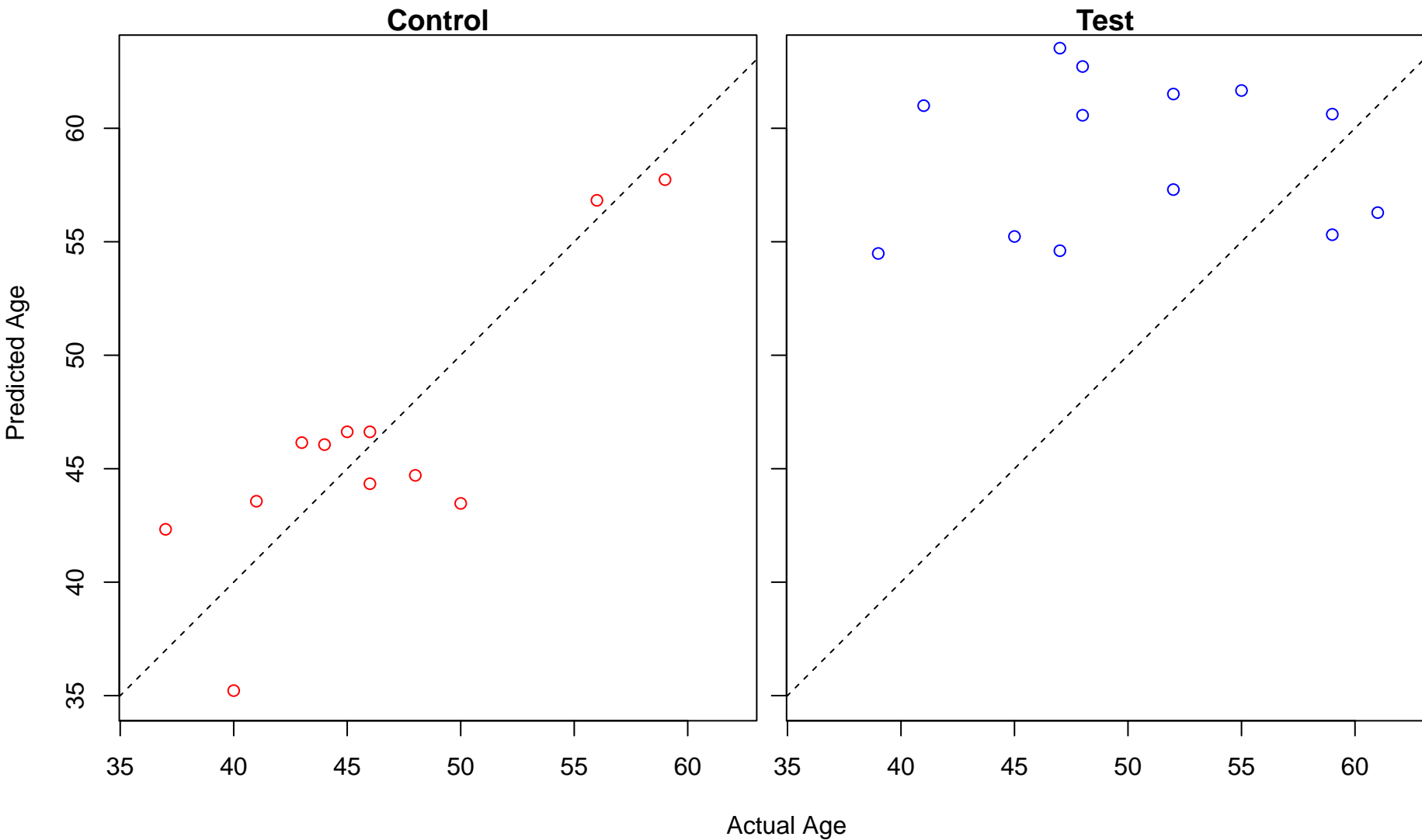
negative regulation of cell division (Score: 4.539379)



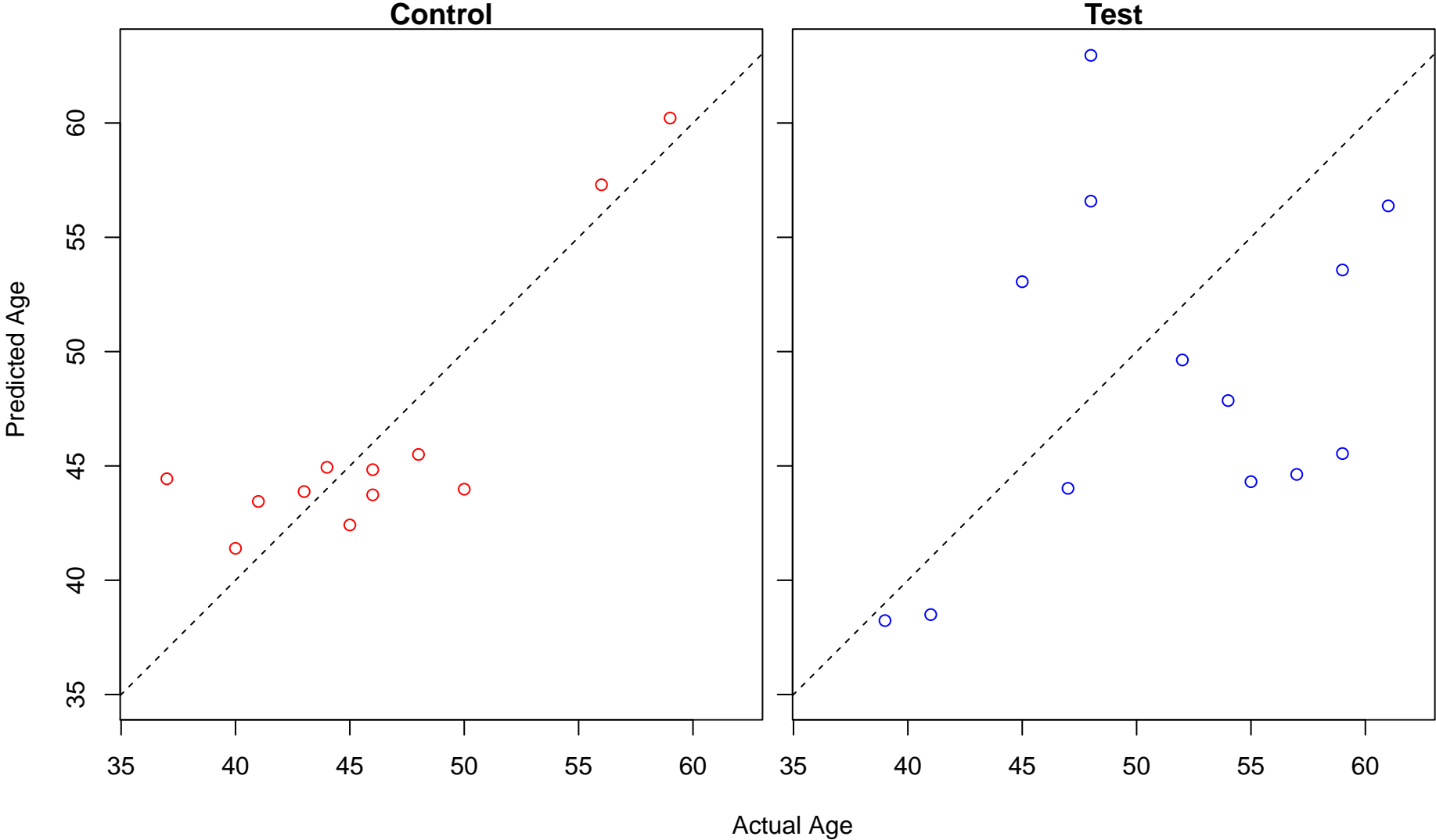
RNA interference (Score: 4.537710)



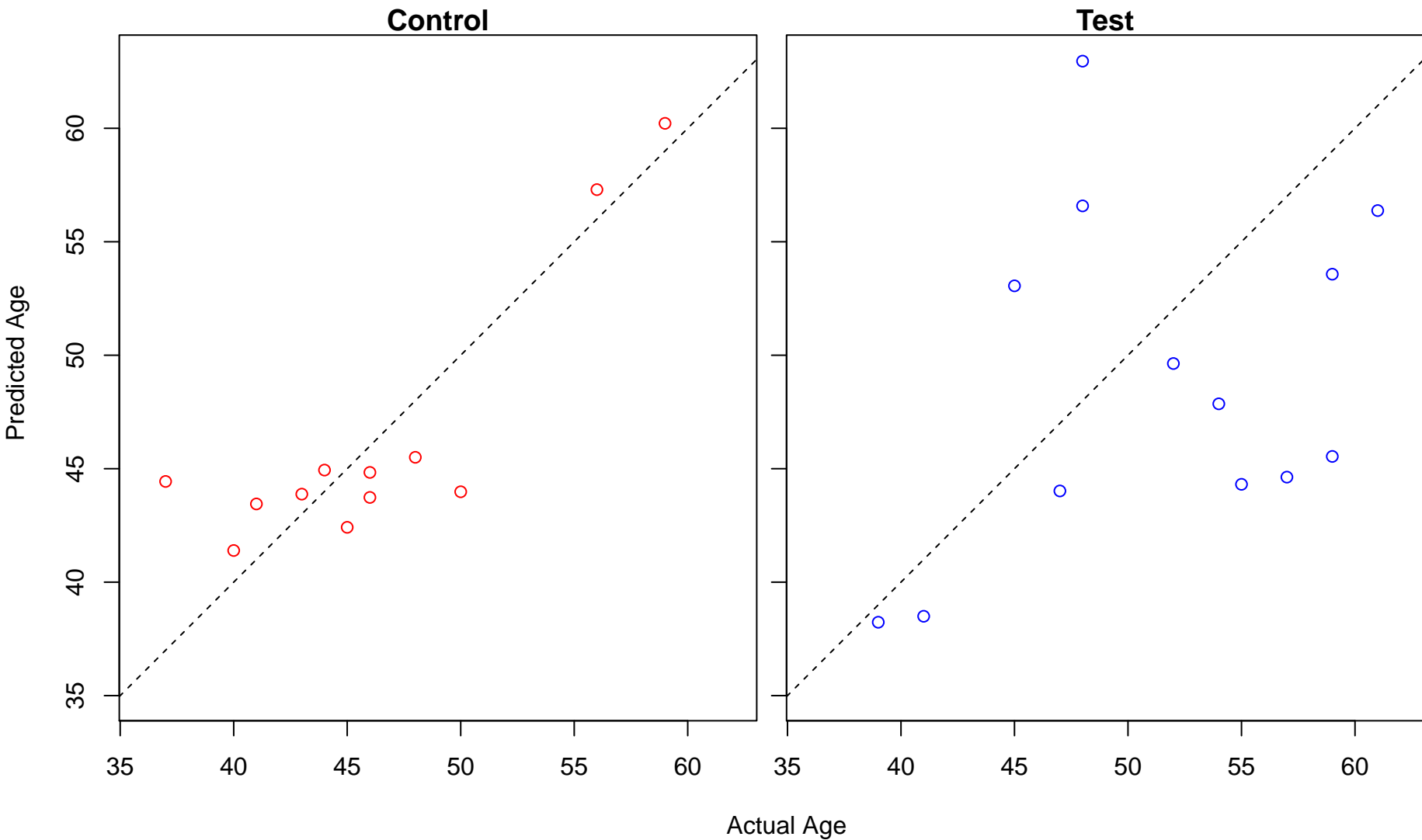
positive regulation of lymphocyte apoptotic process (Score: 4.535738)



spermatogenesis (Score: 4.531029)

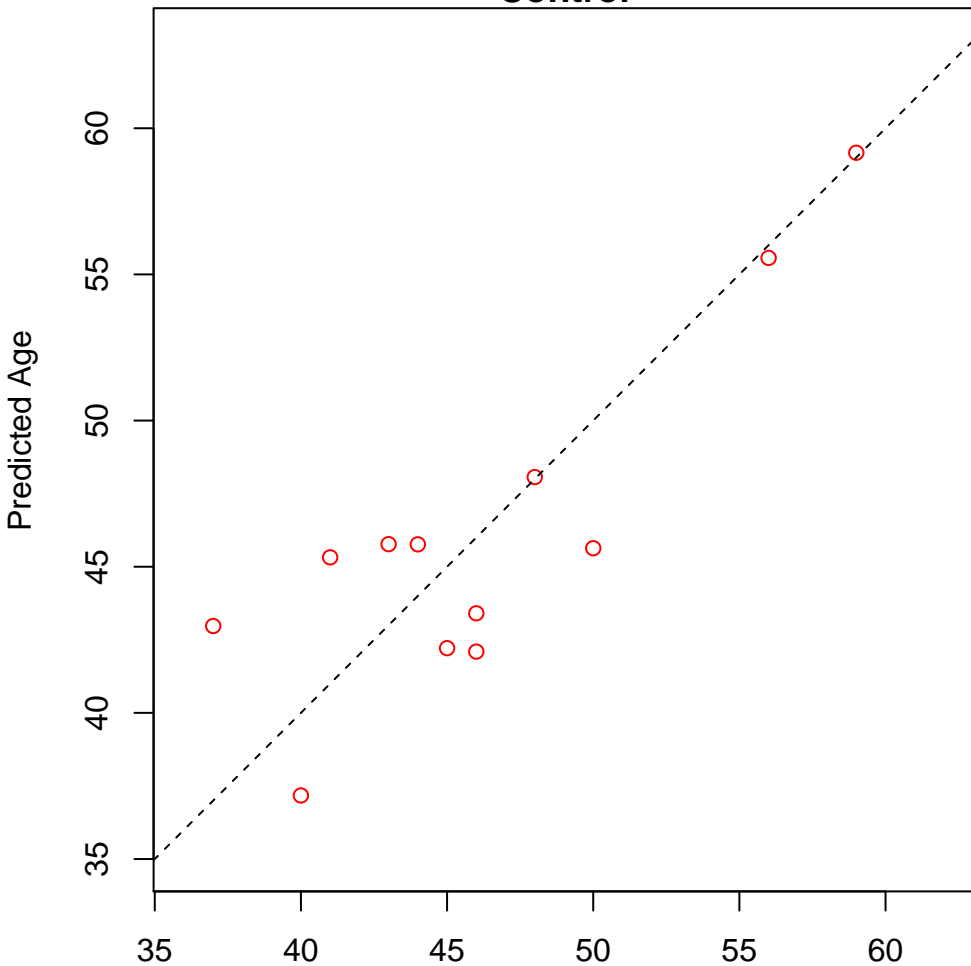


male gamete generation (Score: 4.530875)

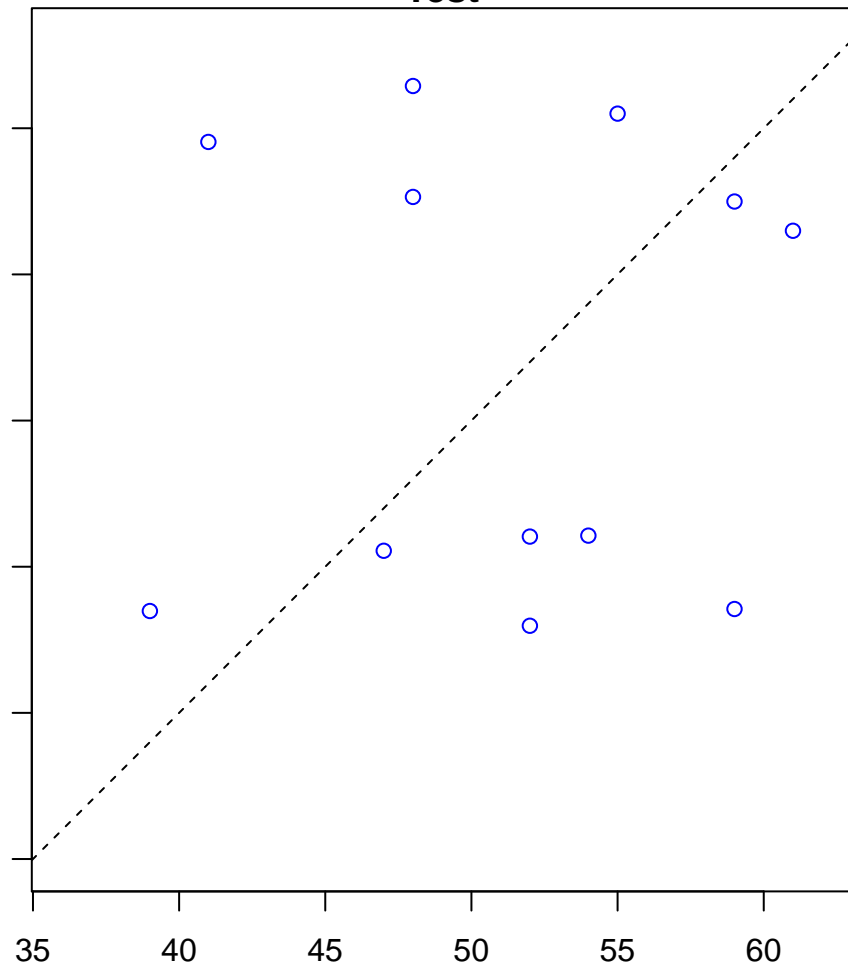


positive regulation of macroautophagy (Score: 4.530096)

Control

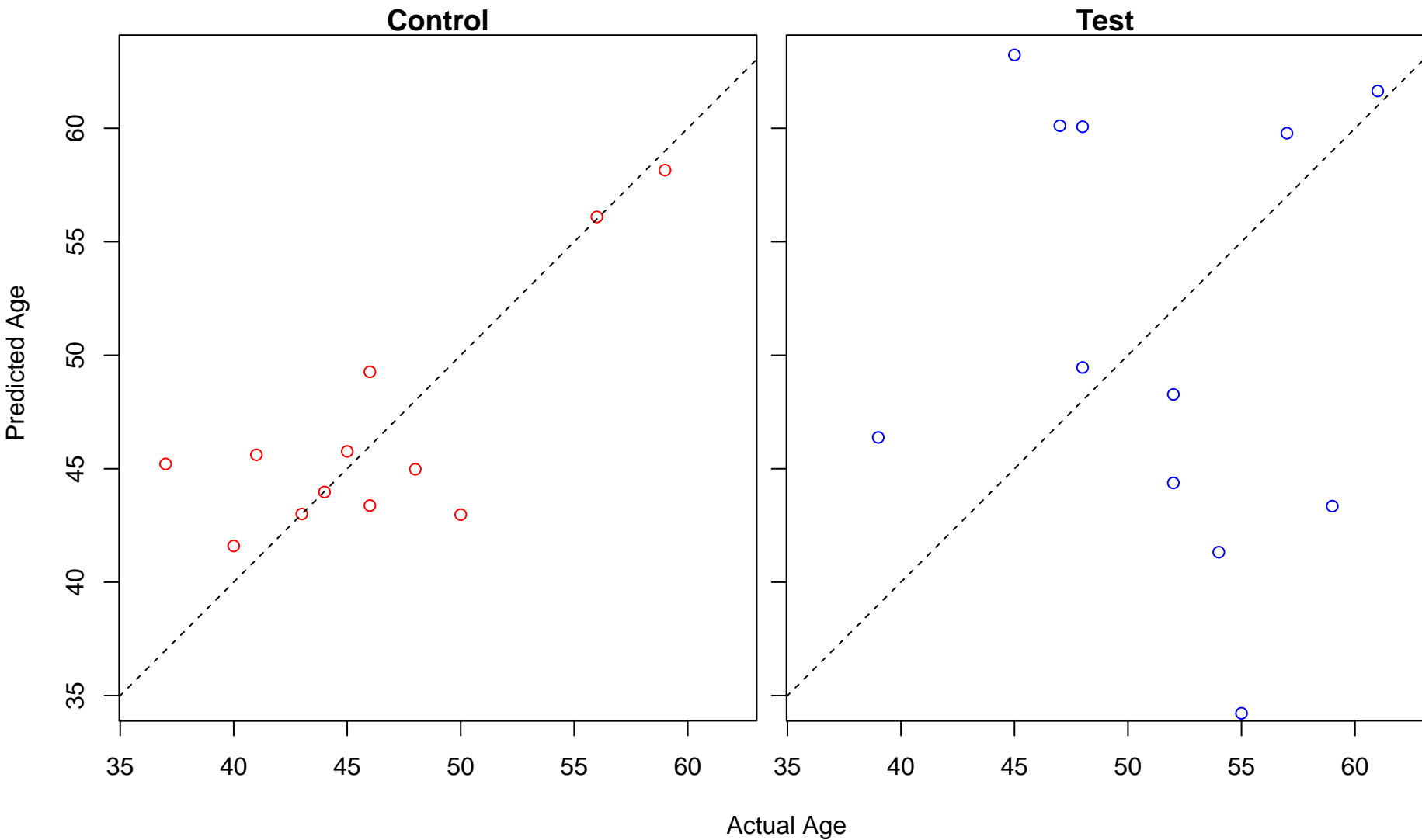


Test

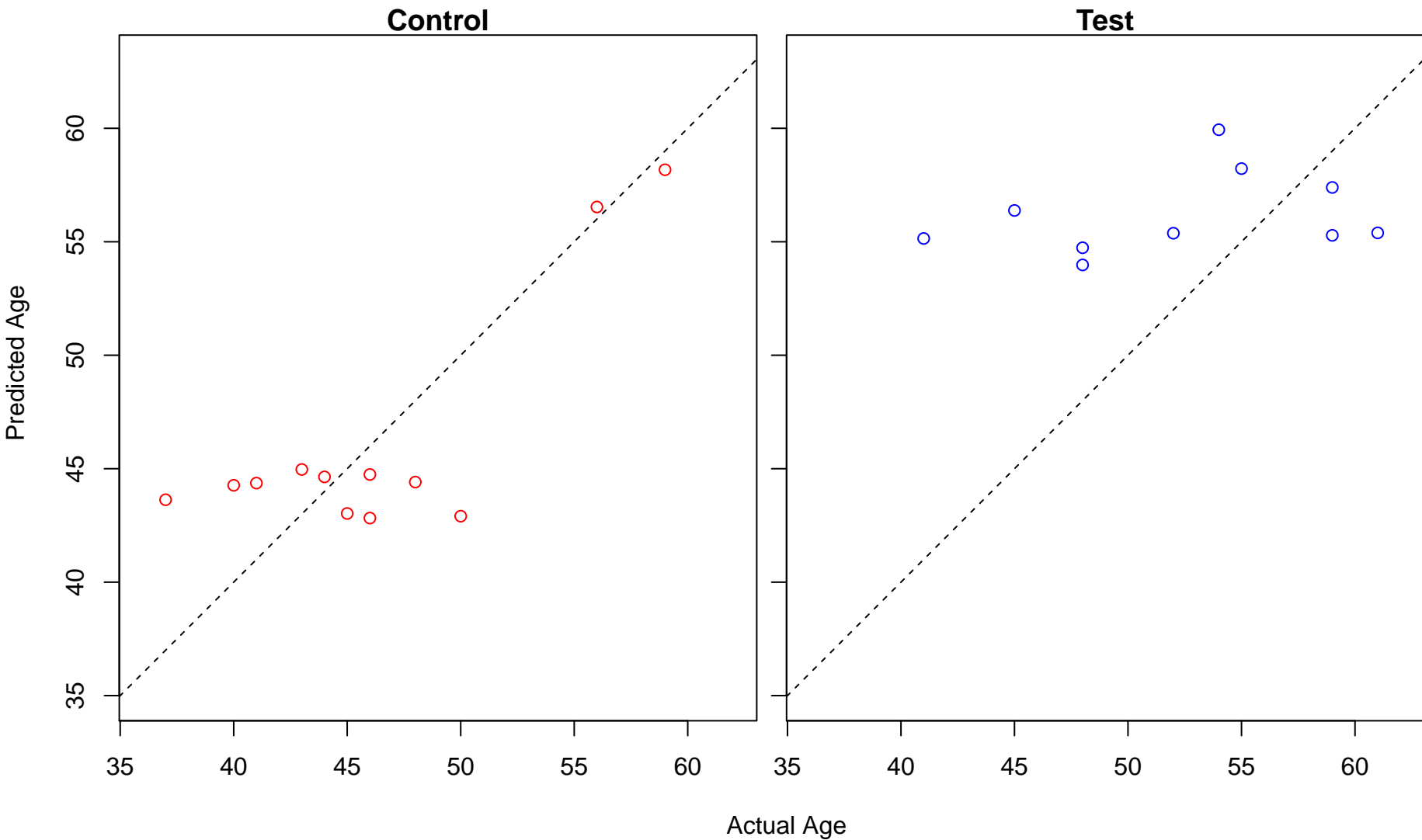


Actual Age

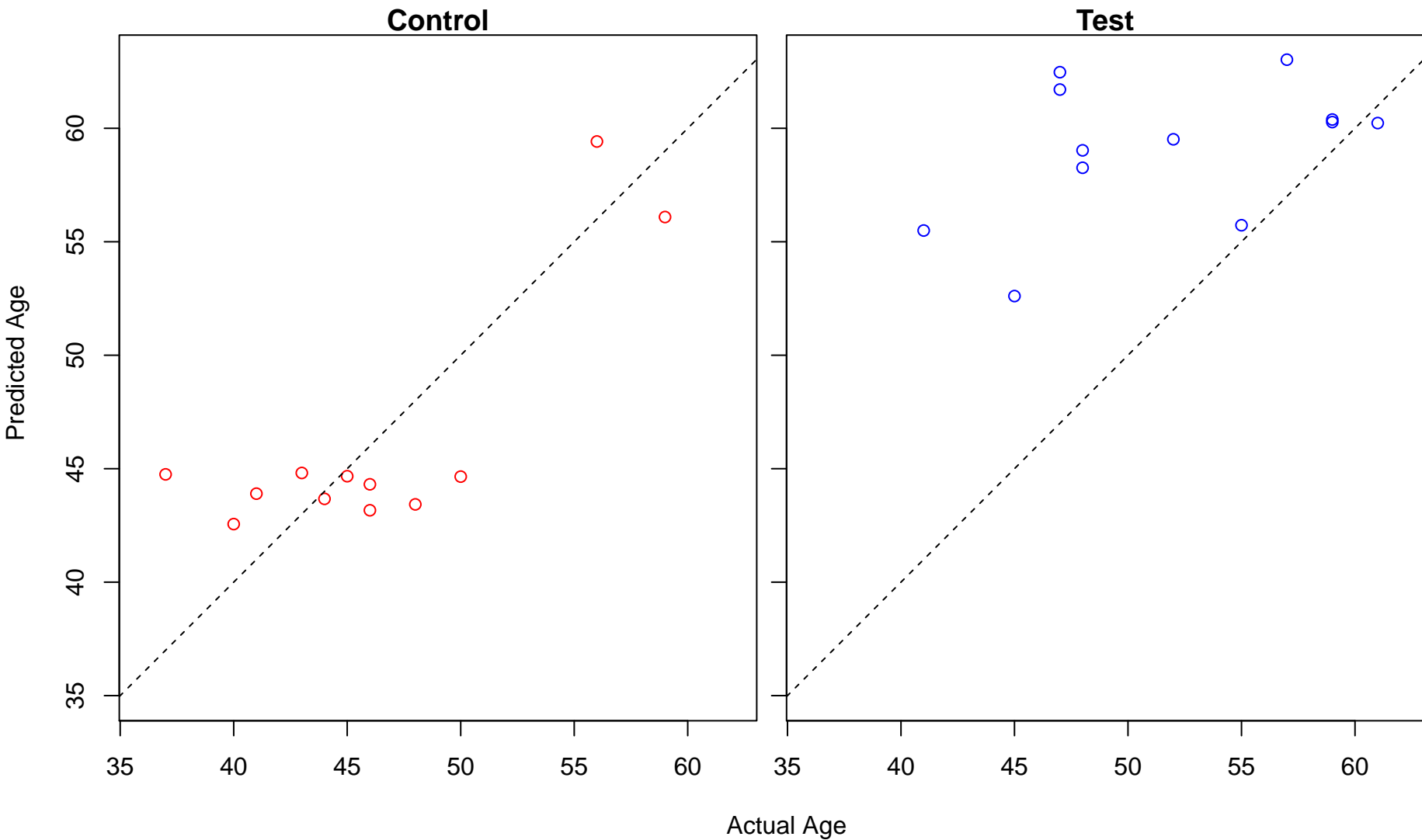
regulation of mitotic nuclear division (Score: 4.529503)



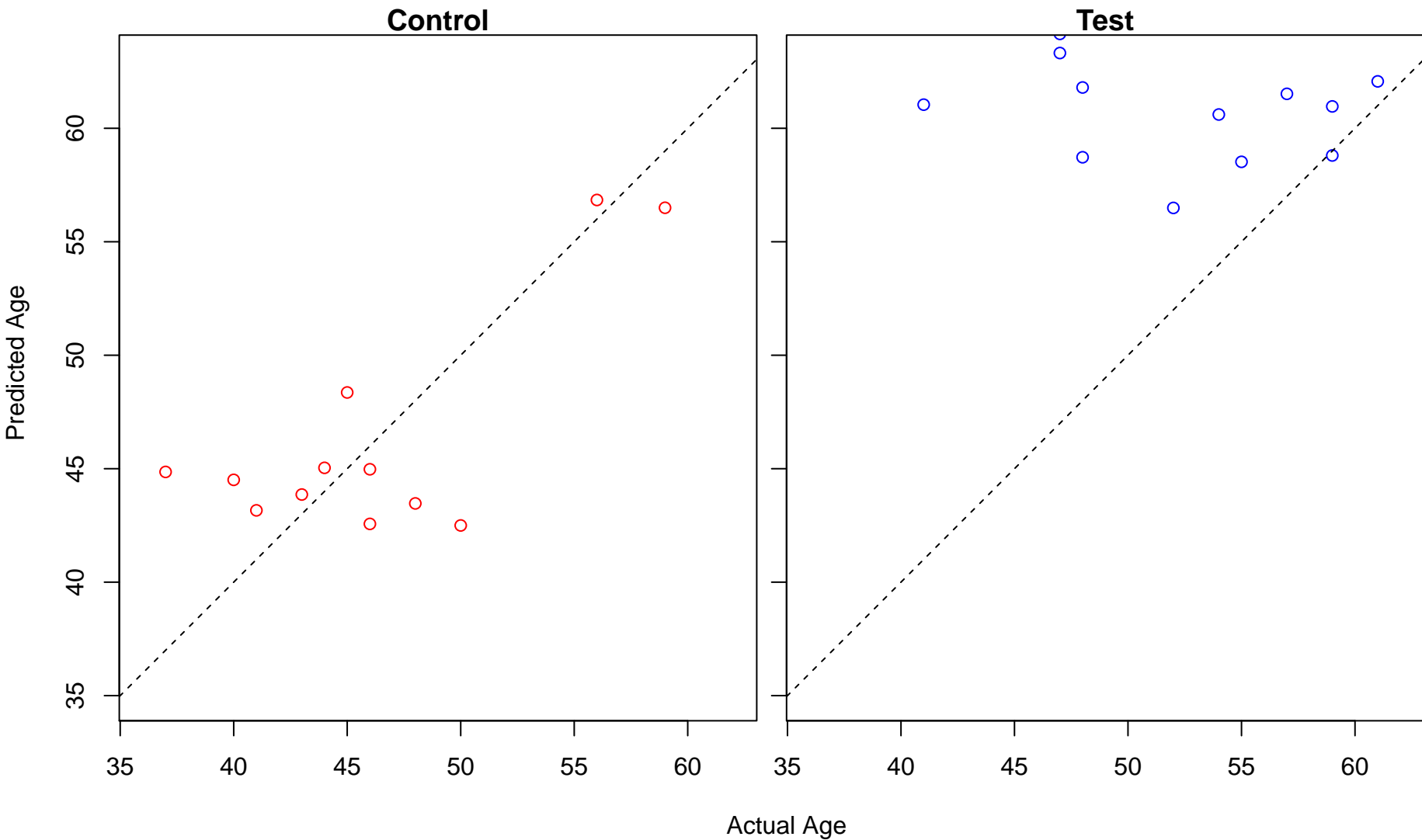
white fat cell differentiation (Score: 4.527565)



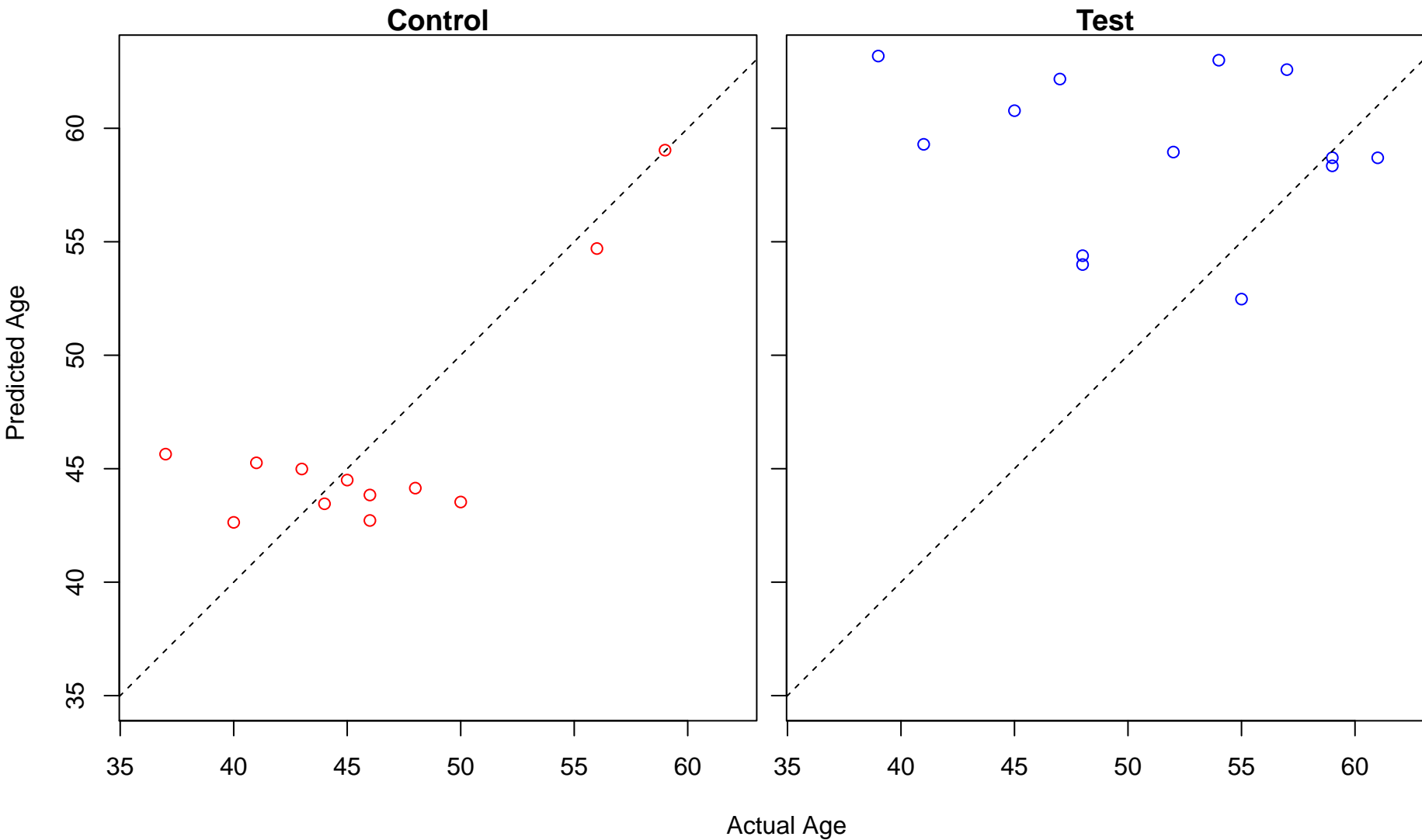
negative regulation of gene silencing (Score: 4.519748)



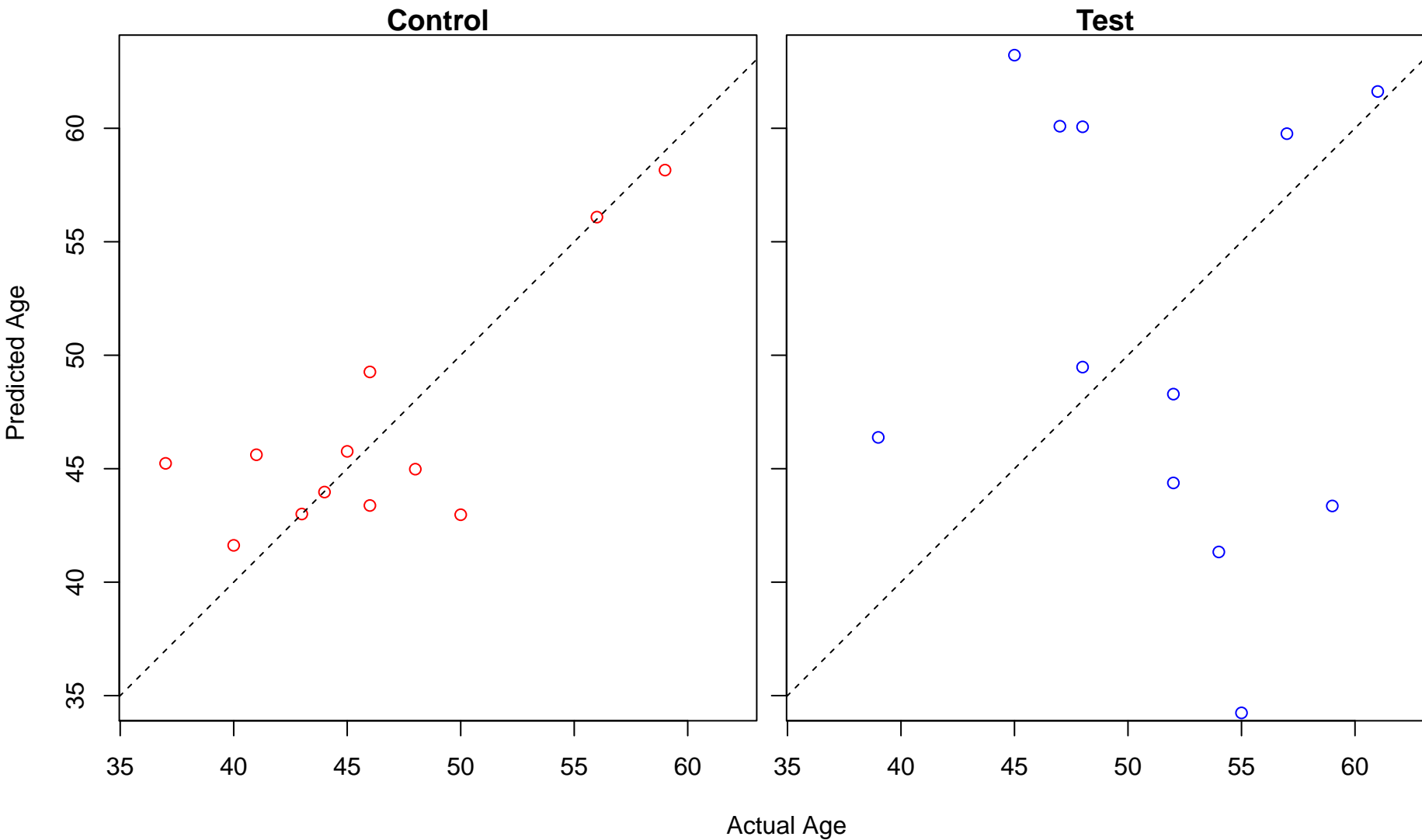
maternal process involved in female pregnancy (Score: 4.519080)



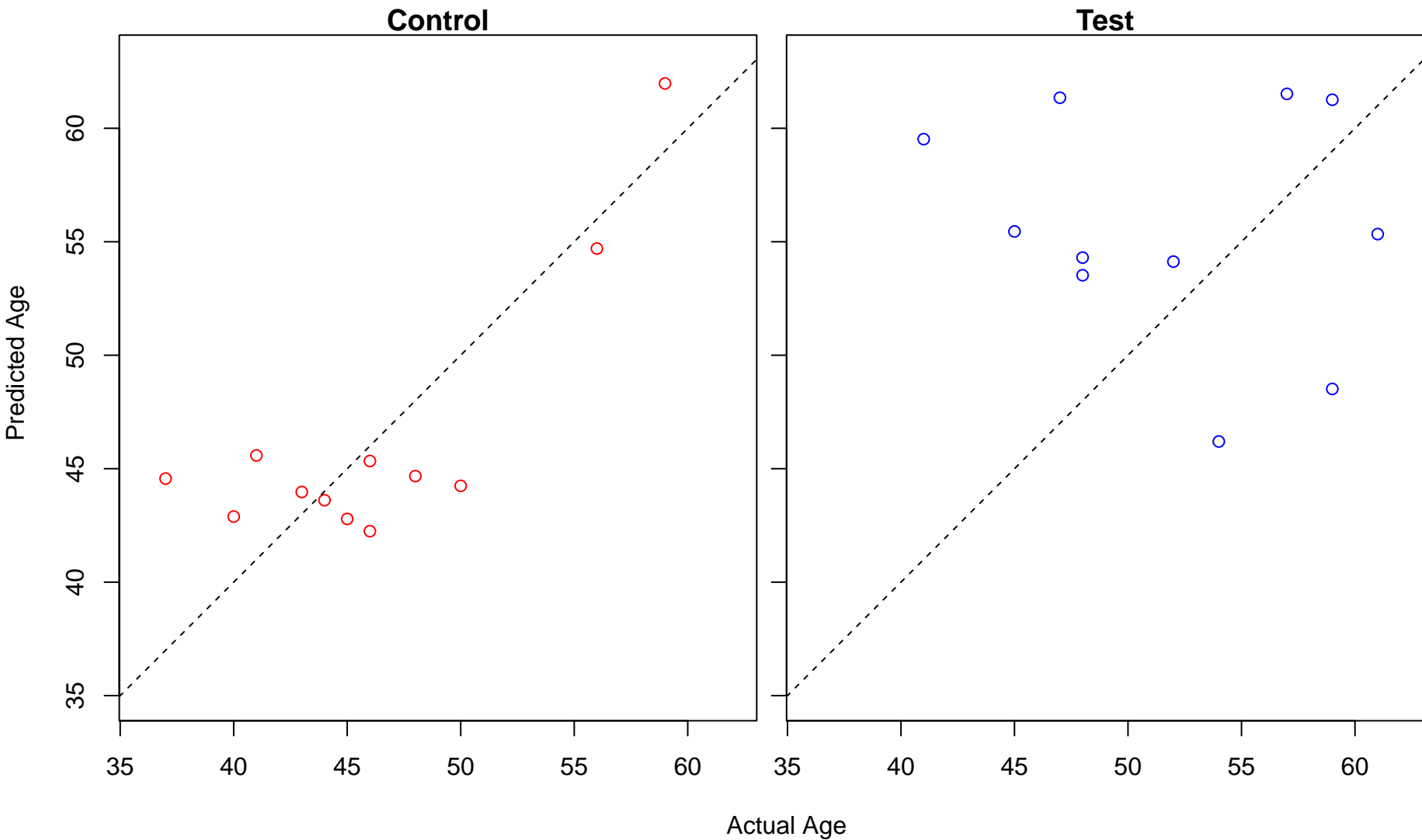
excretion (Score: 4.512621)



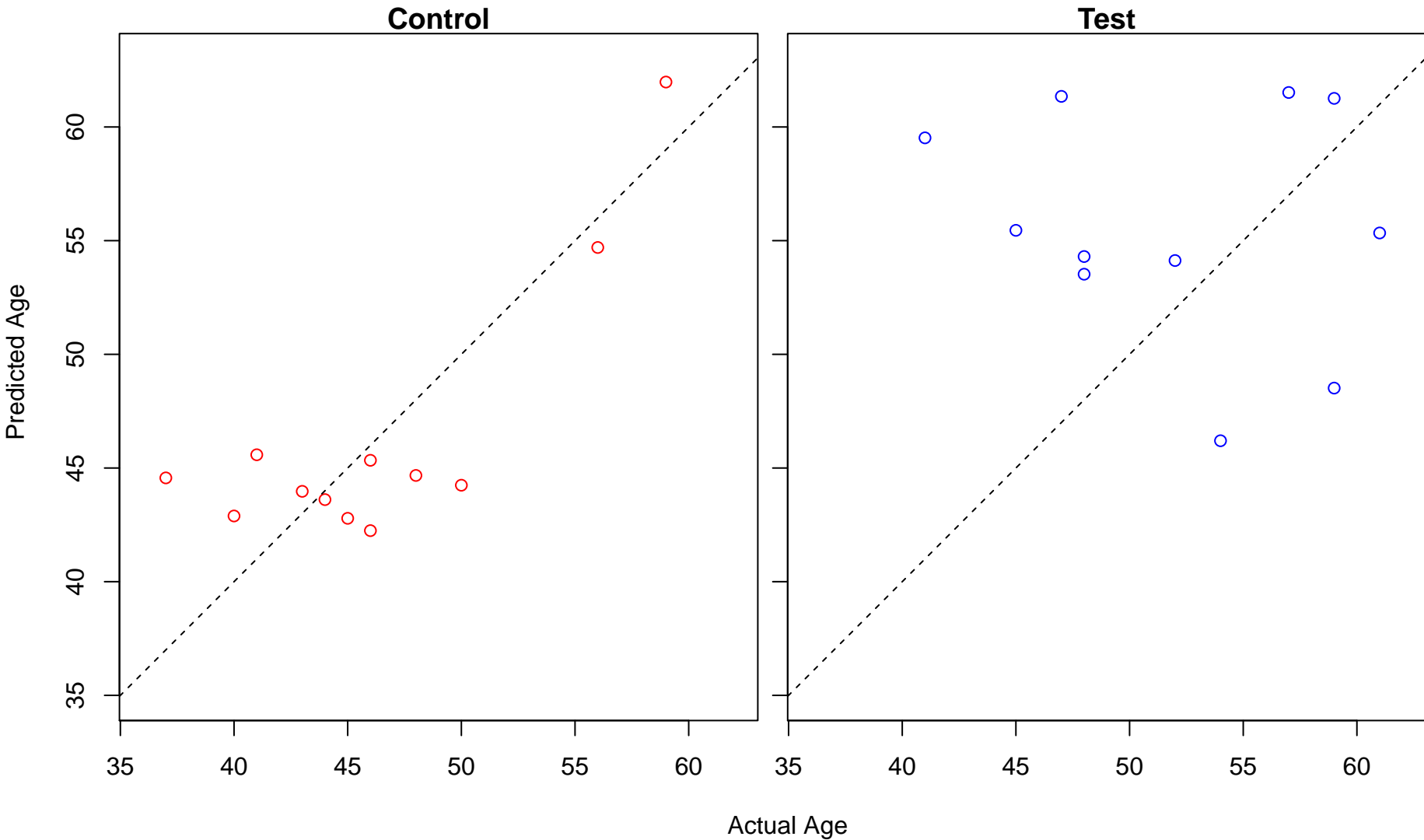
regulation of nuclear division (Score: 4.508926)



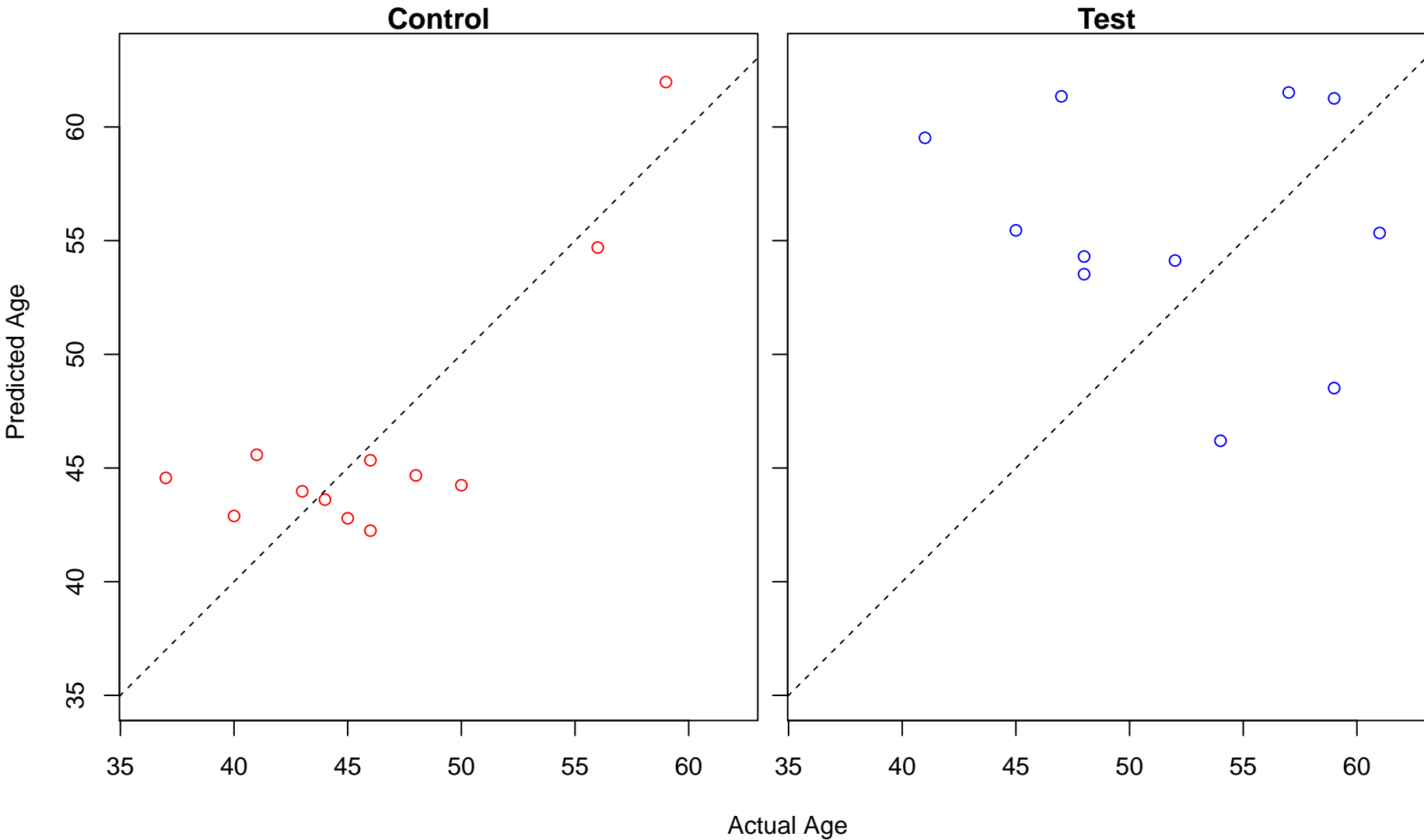
establishment of mitochondrion localization, microtubule-mediated (Score: 4.506904)



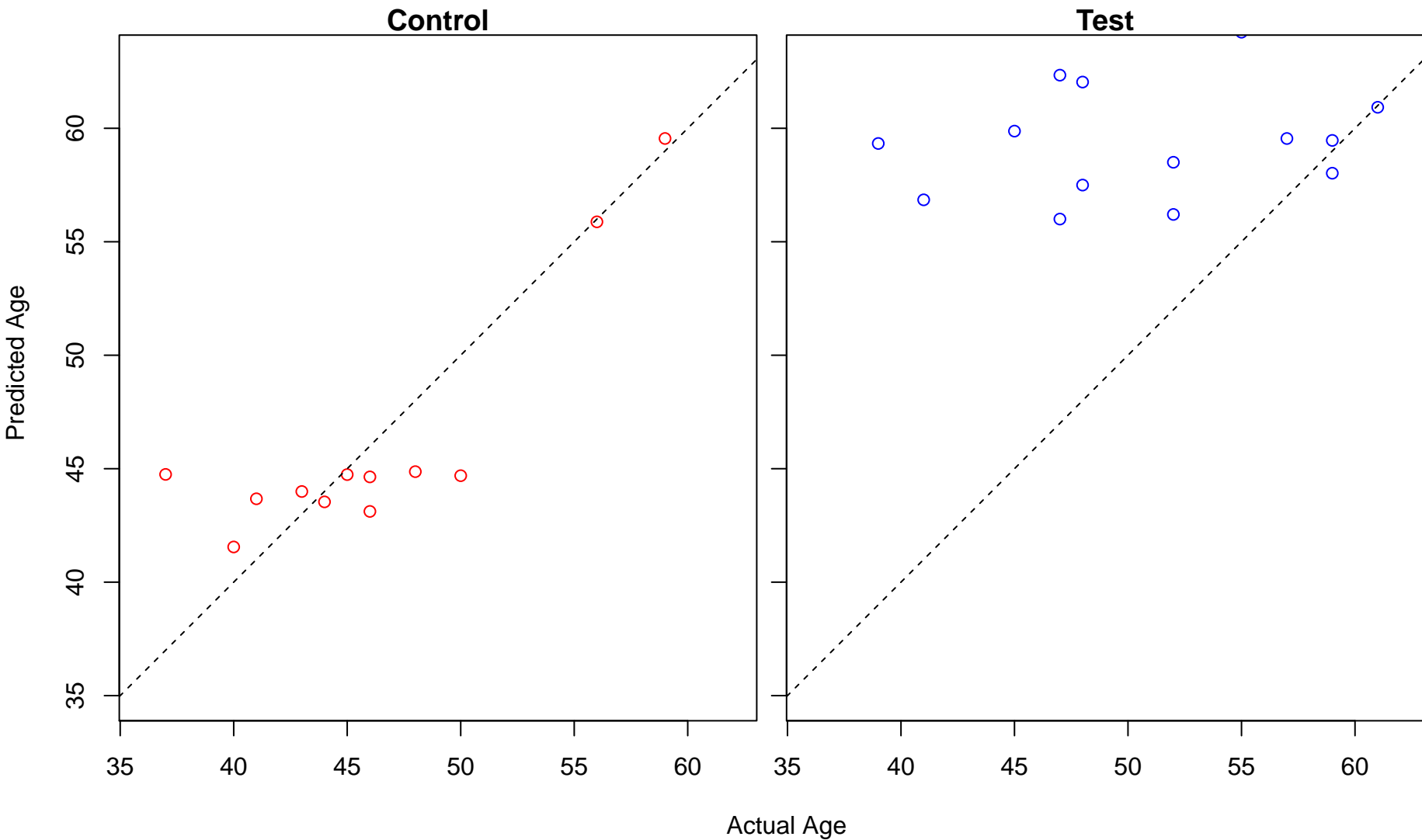
mitochondrion transport along microtubule (Score: 4.506904)



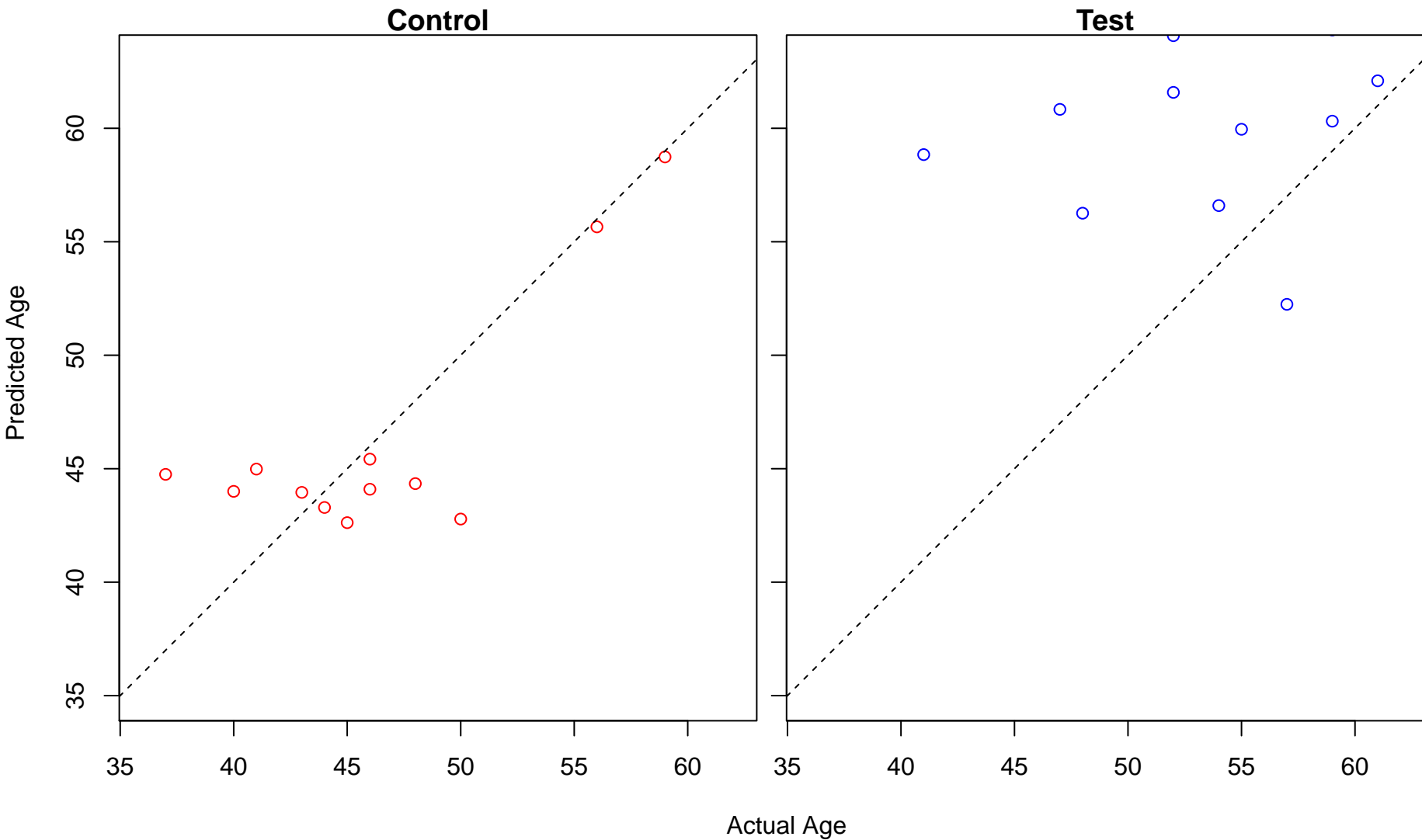
establishment of mitochondrion localization (Score: 4.506904)



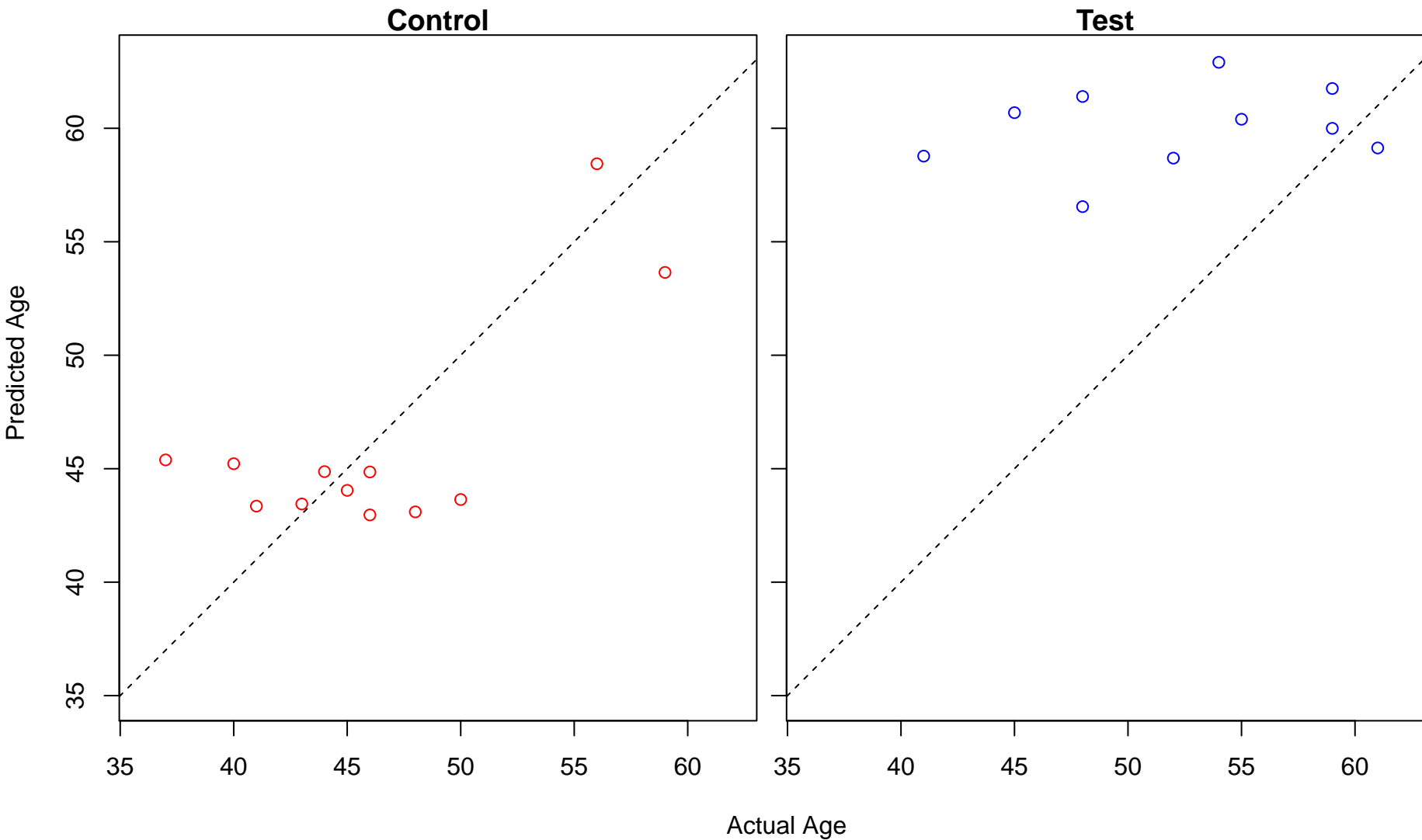
sodium-independent organic anion transport (Score: 4.501103)



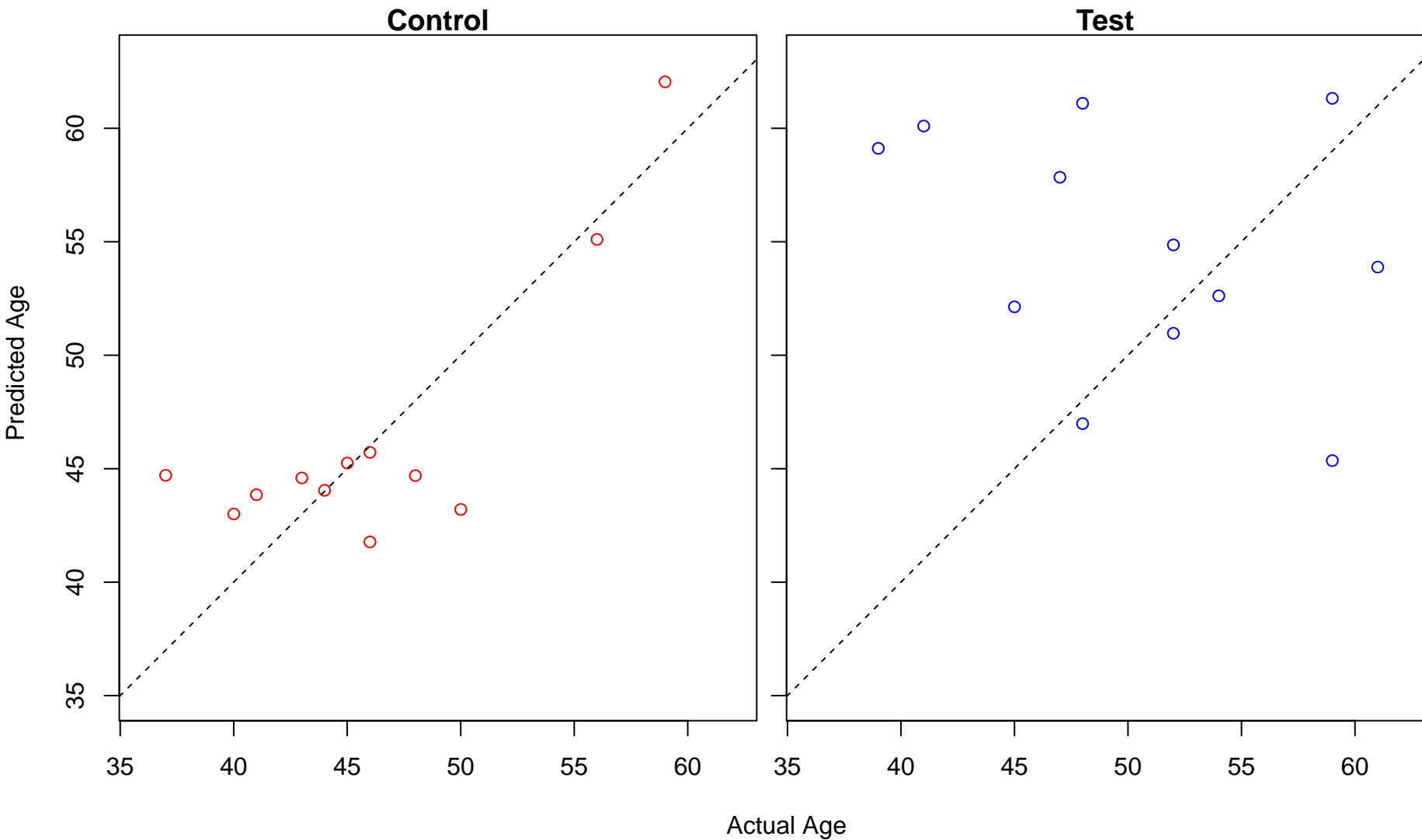
negative regulation of glial cell proliferation (Score: 4.491157)



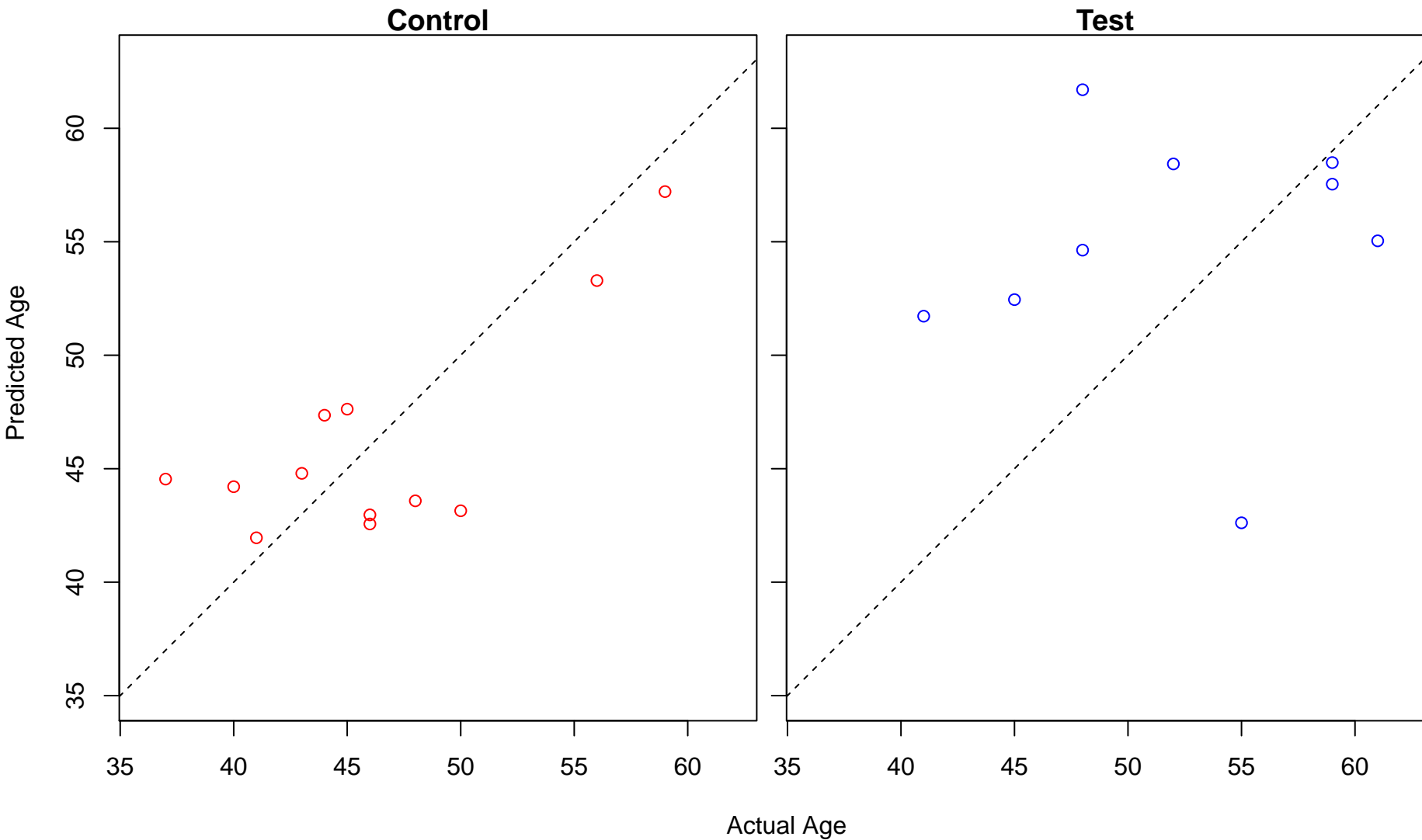
negative regulation of cholesterol storage (Score: 4.489997)



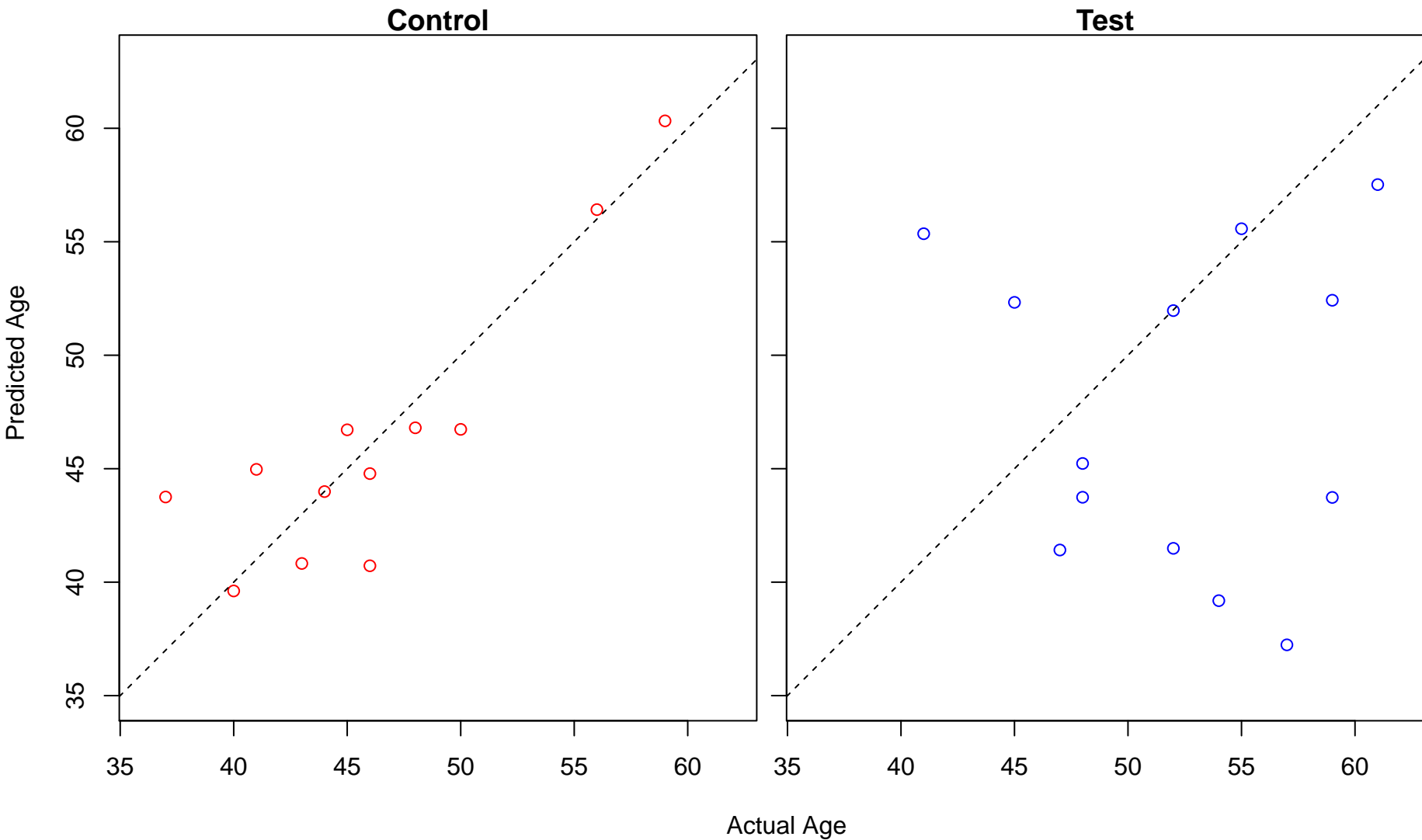
regulation of DNA-templated transcription in response to stress (Score: 4.488645)



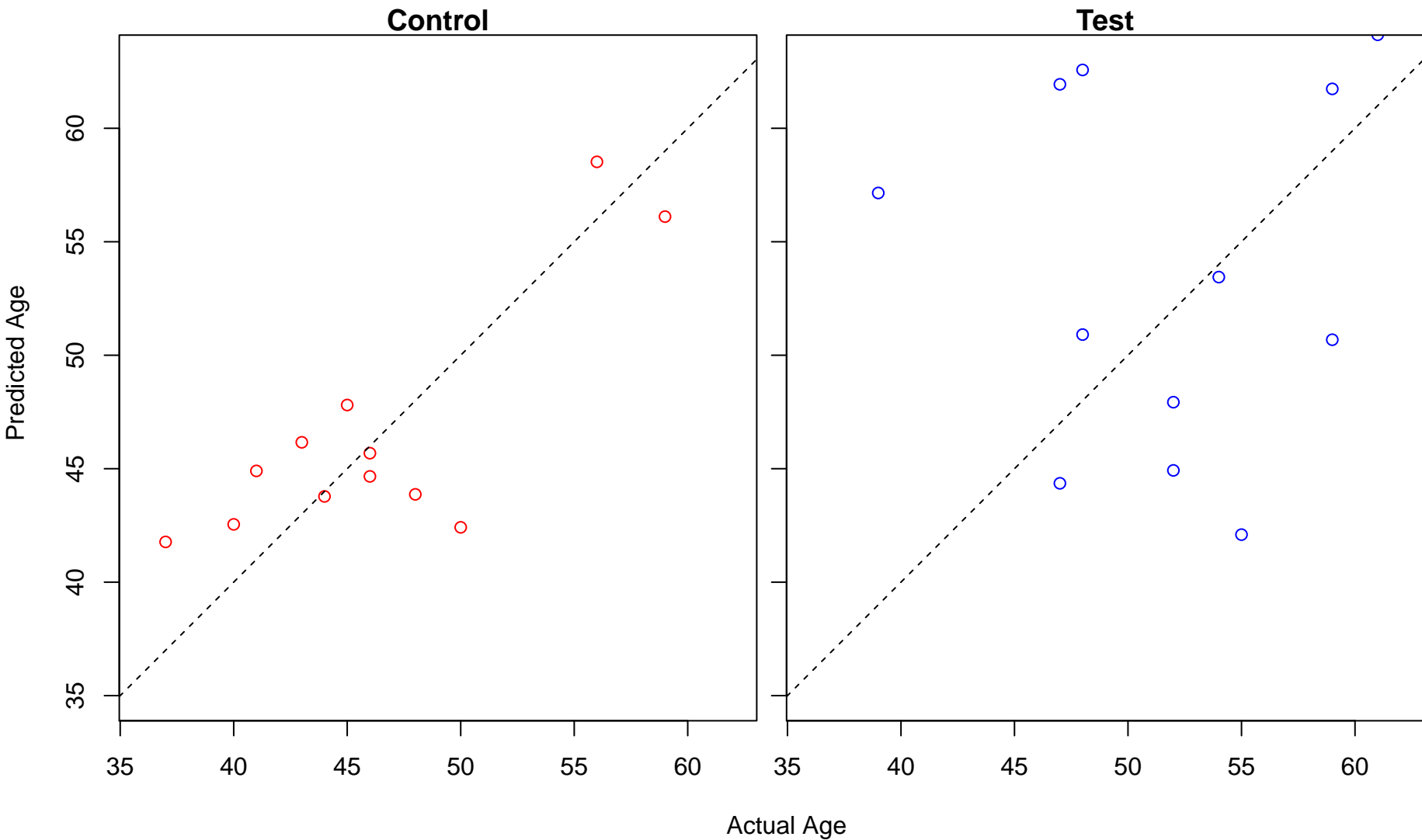
regulation of platelet aggregation (Score: 4.487520)



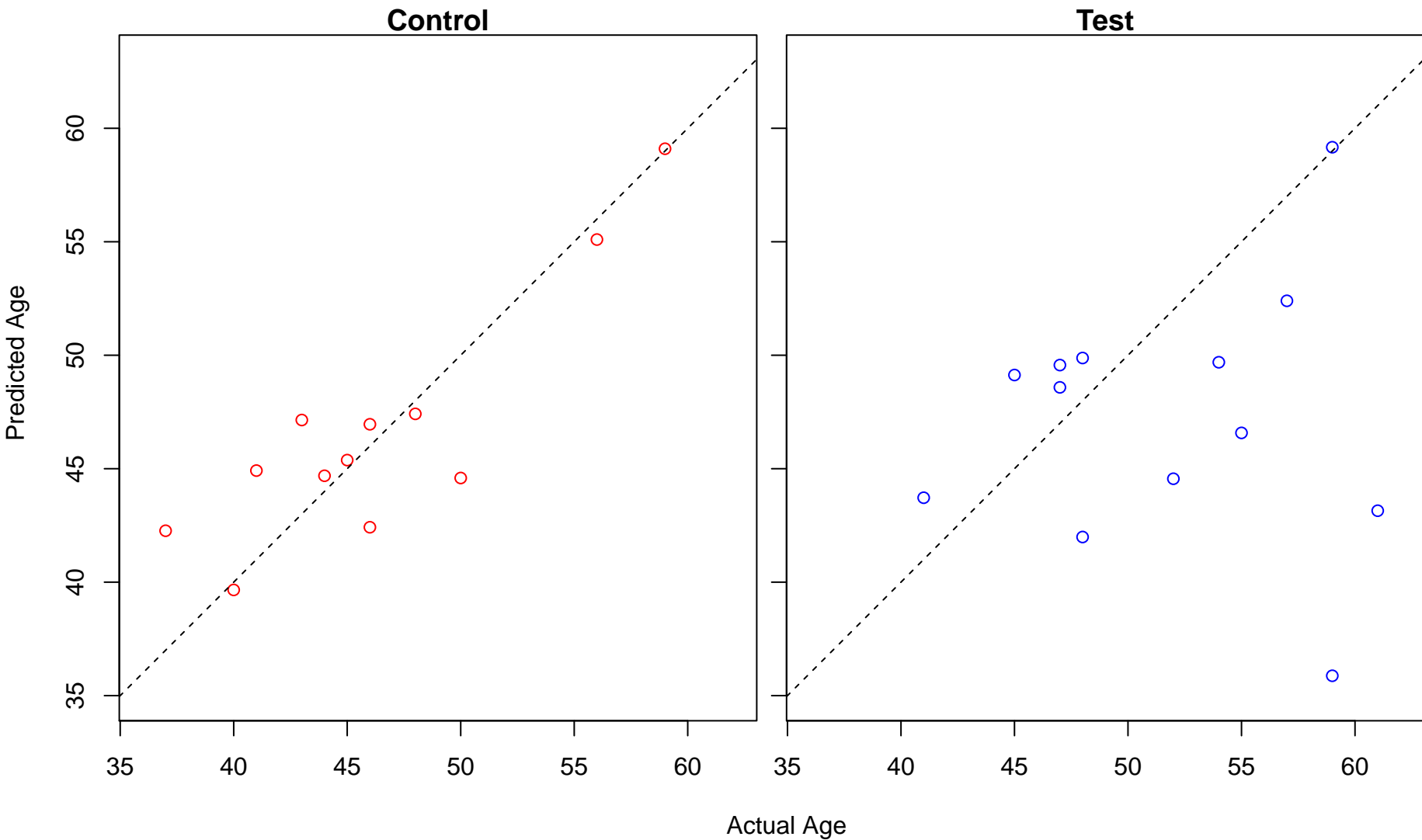
nucleobase metabolic process (Score: 4.486011)



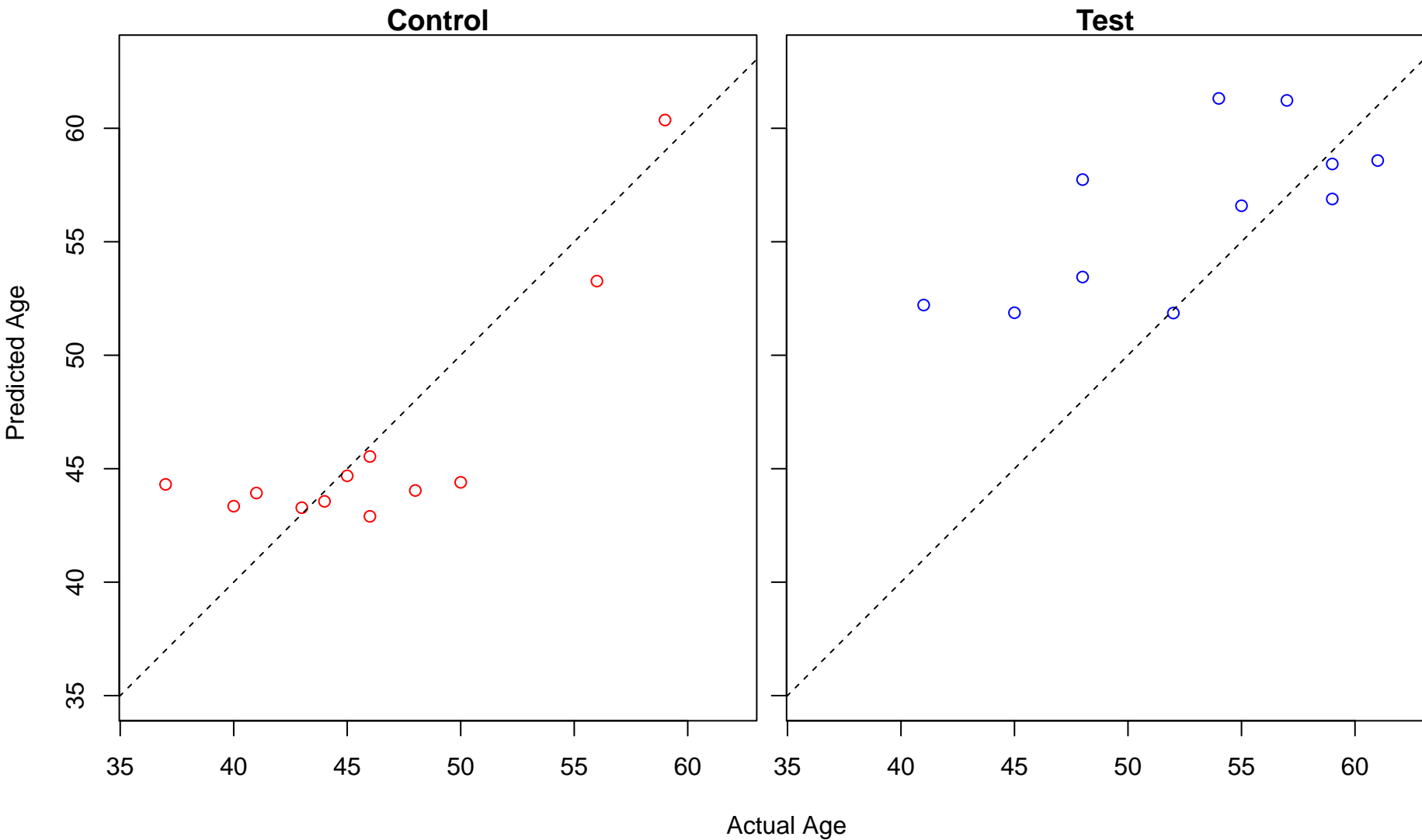
regulation of reproductive process (Score: 4.485136)



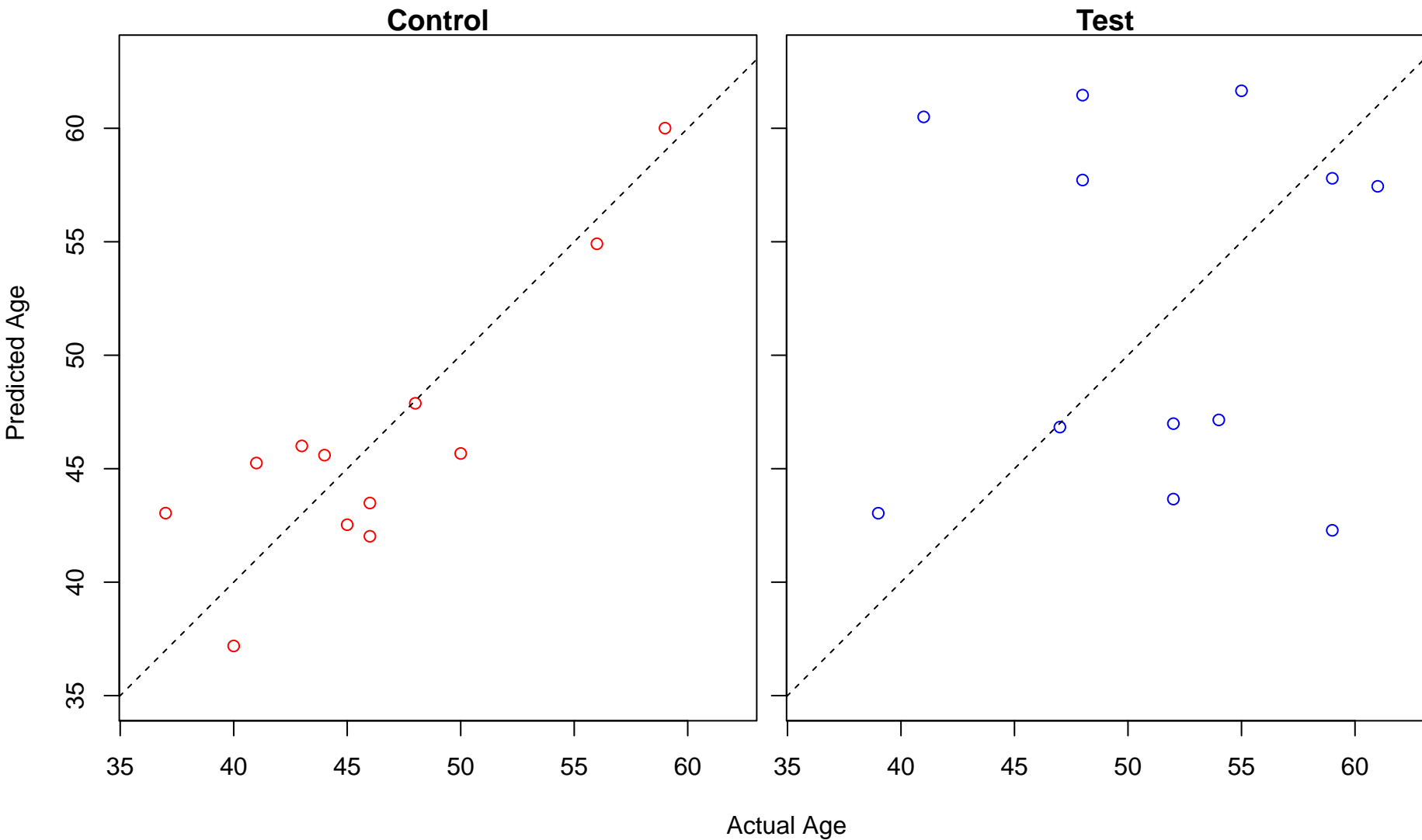
immune system development (Score: 4.482642)



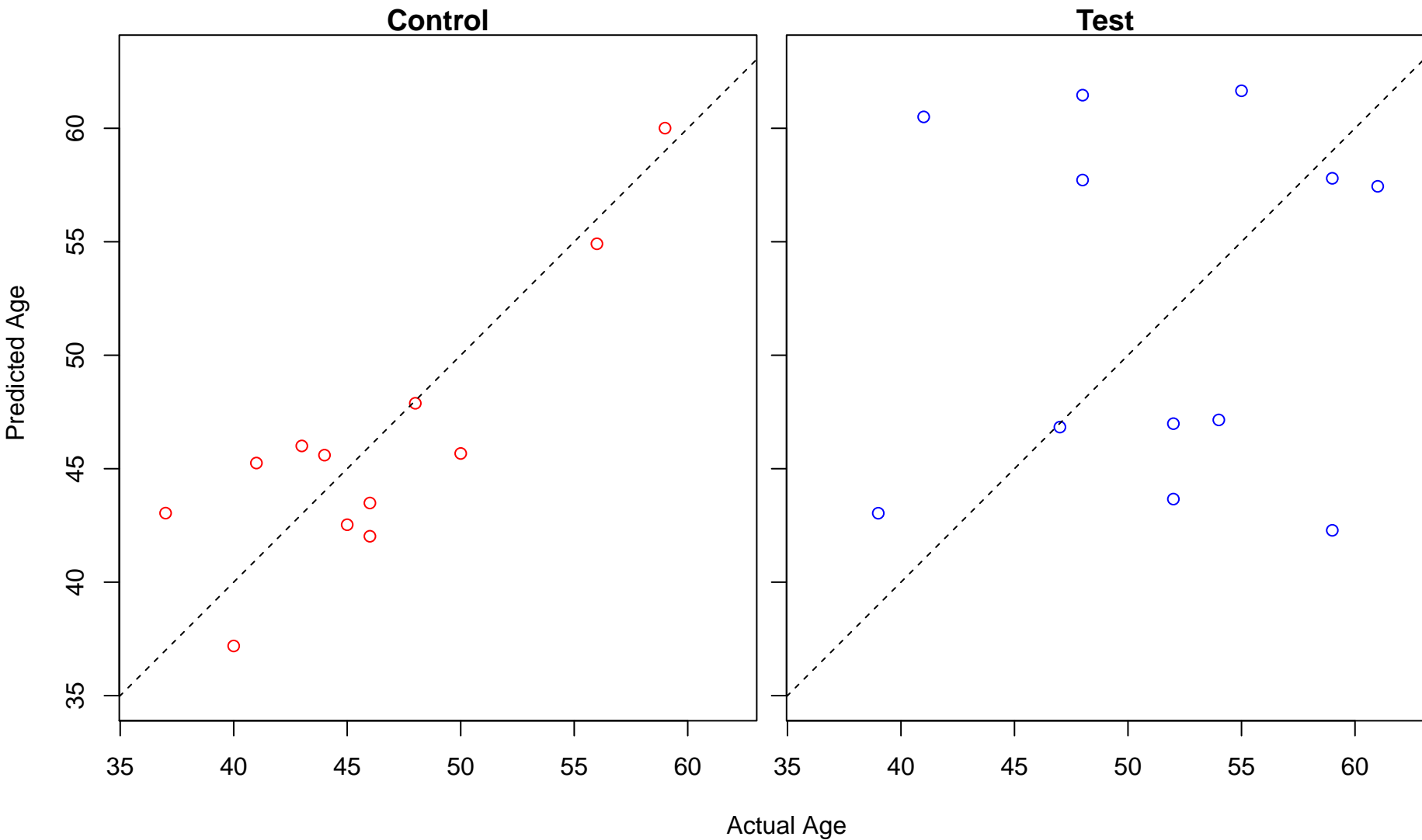
negative regulation of cell proliferation involved in kidney development (Score: 4.482262)



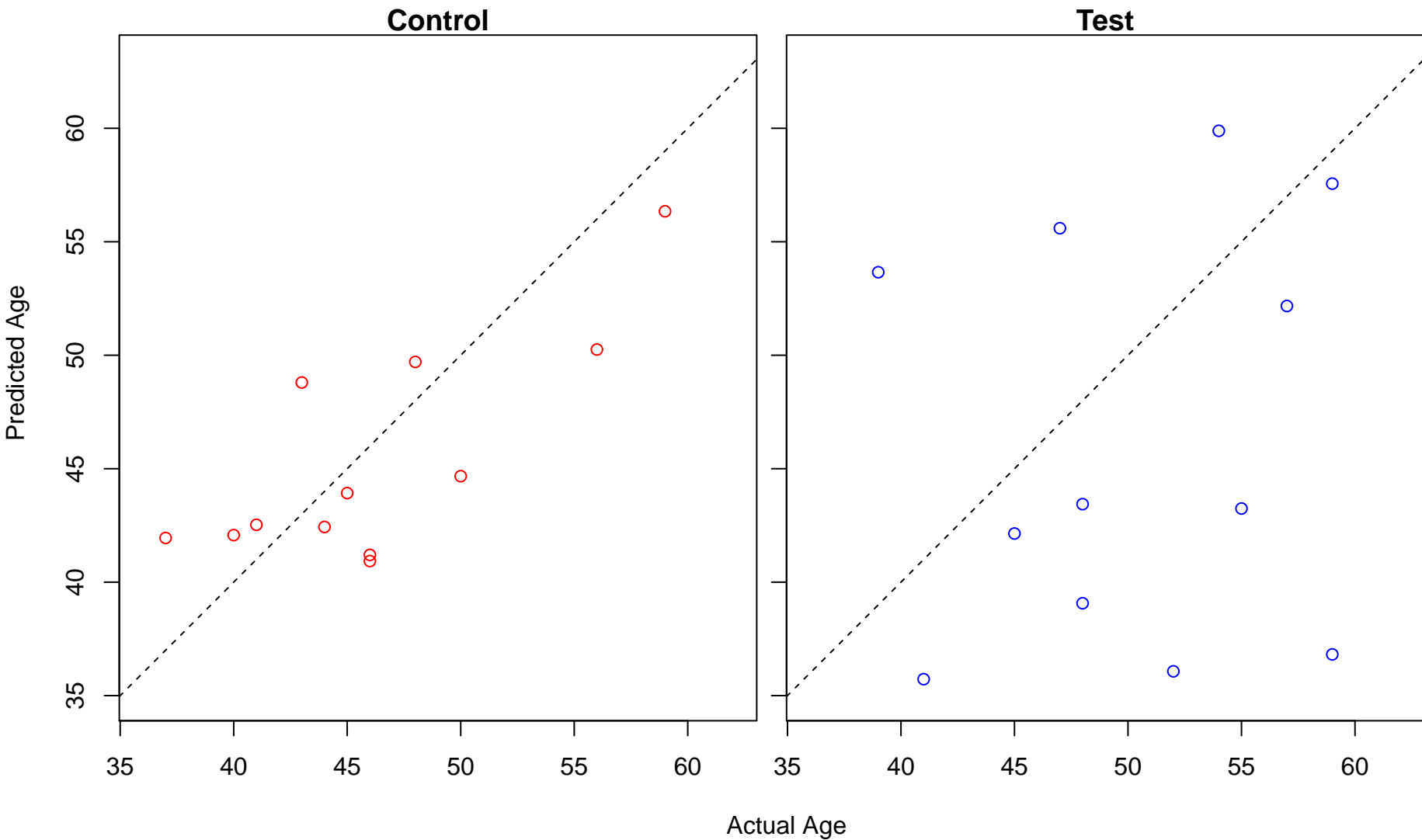
positive regulation of response to extracellular stimulus (Score: 4.481982)



positive regulation of response to nutrient levels (Score: 4.481982)

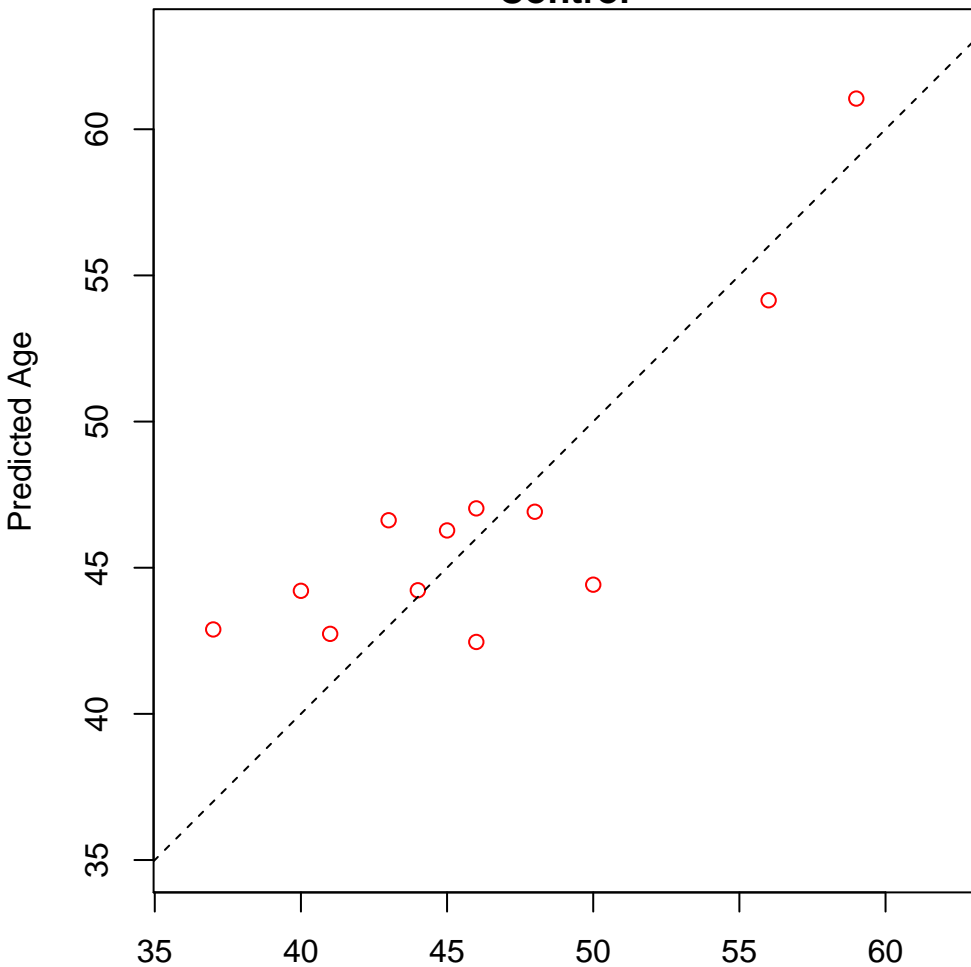


copper ion transmembrane transport (Score: 4.476901)

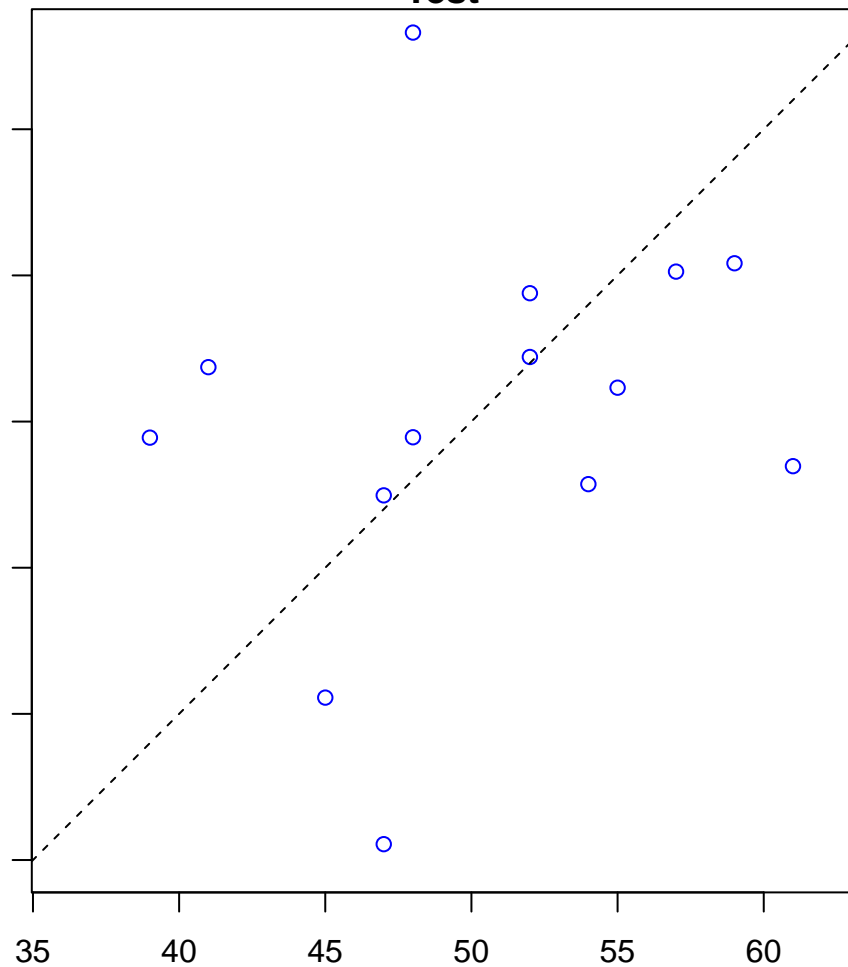


cellular response to unfolded protein (Score: 4.466583)

Control

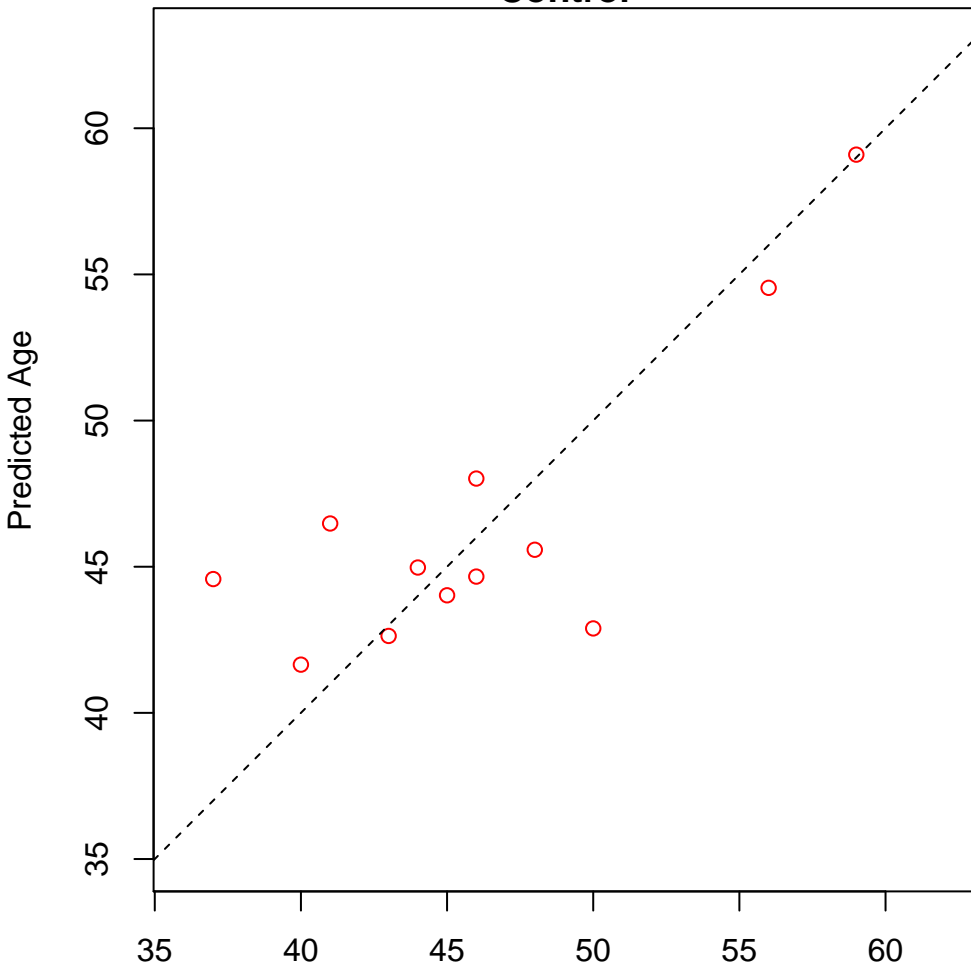


Test

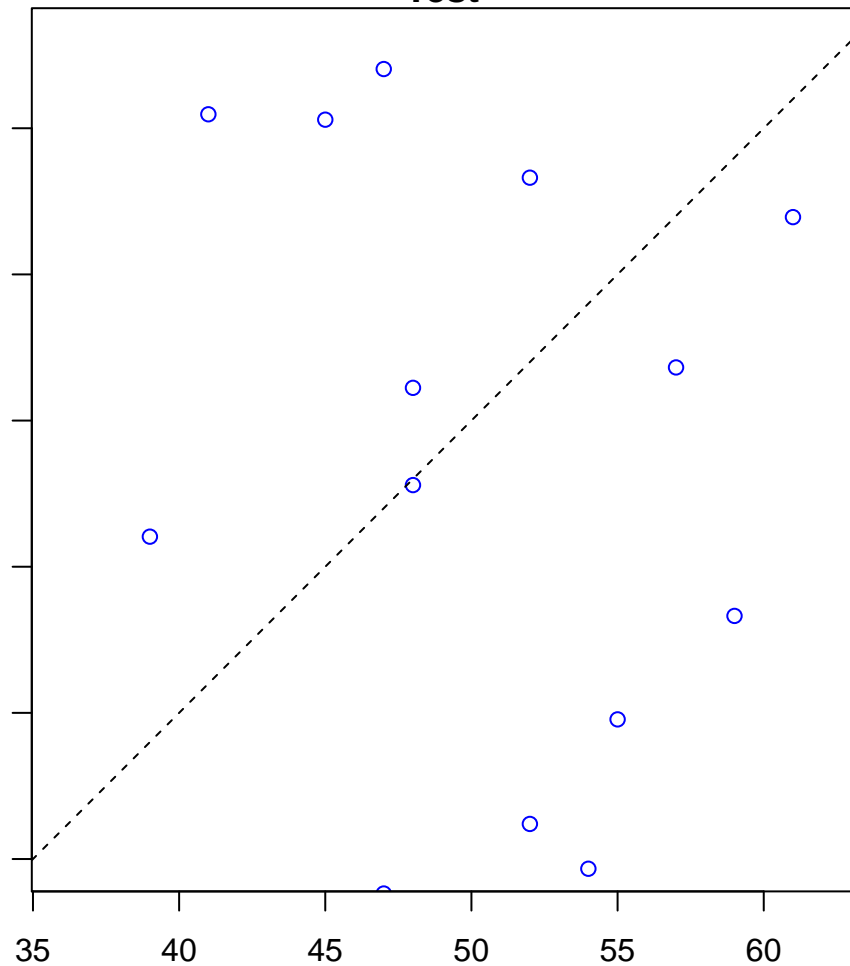


peptidyl-threonine dephosphorylation (Score: 4.459392)

Control

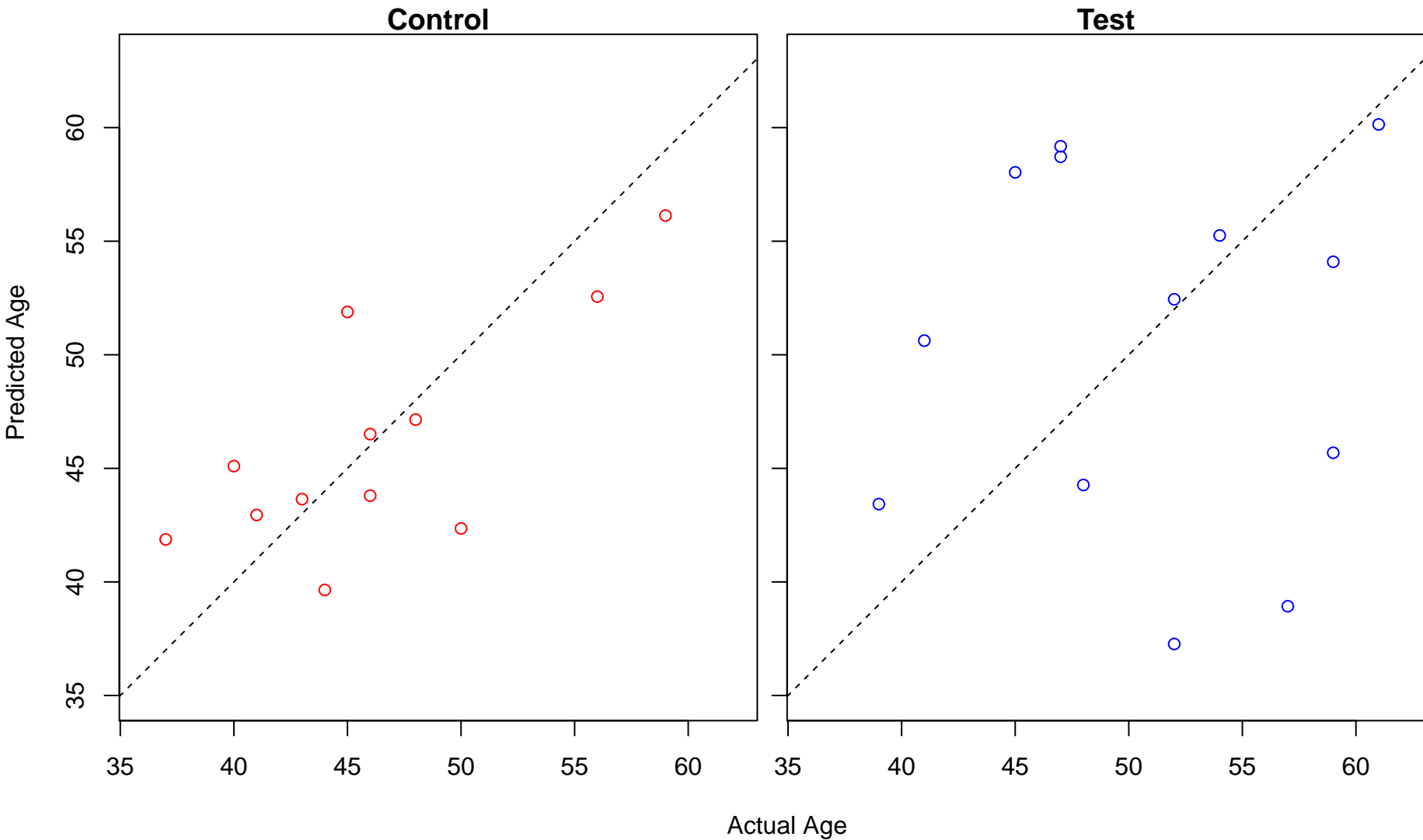


Test

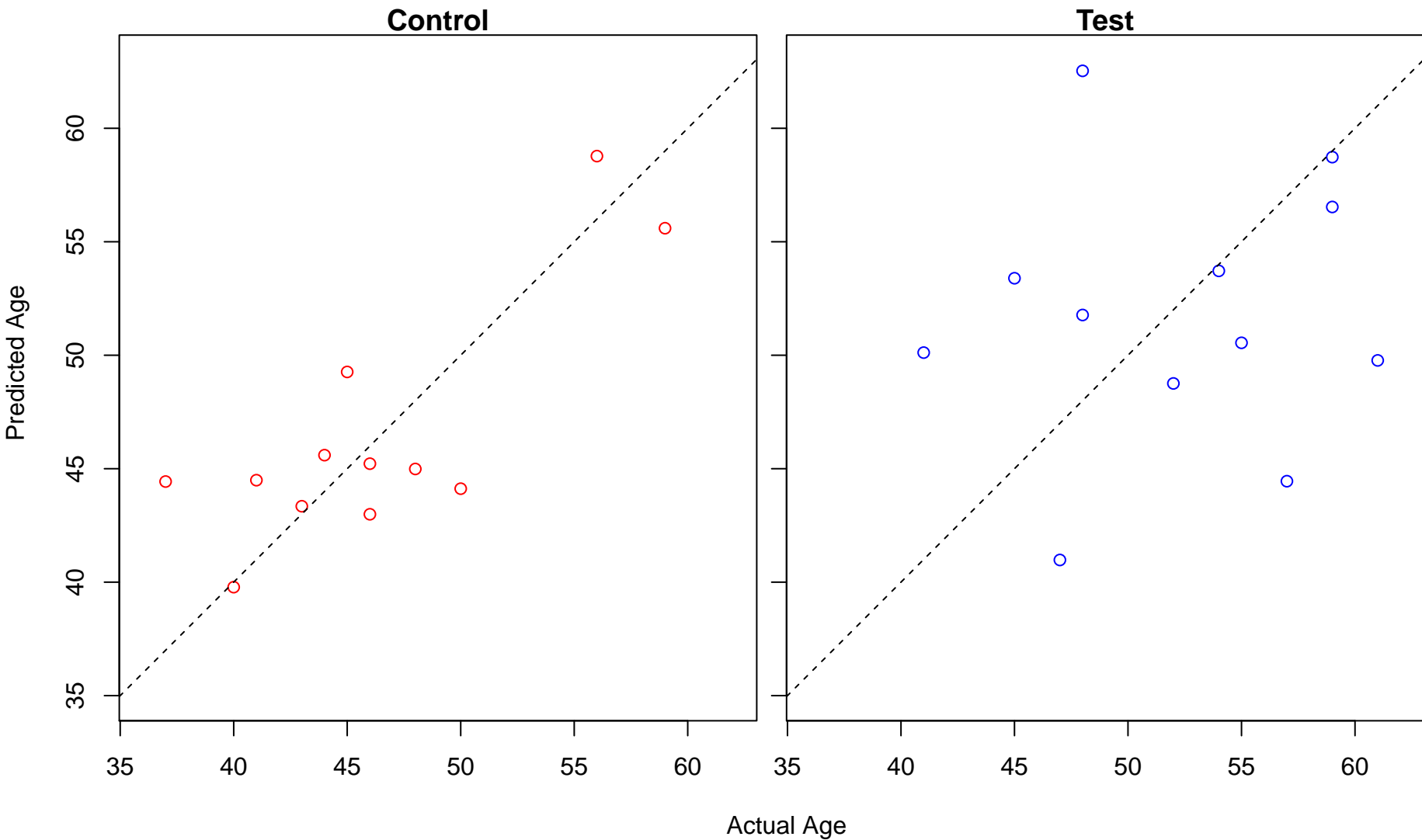


Actual Age

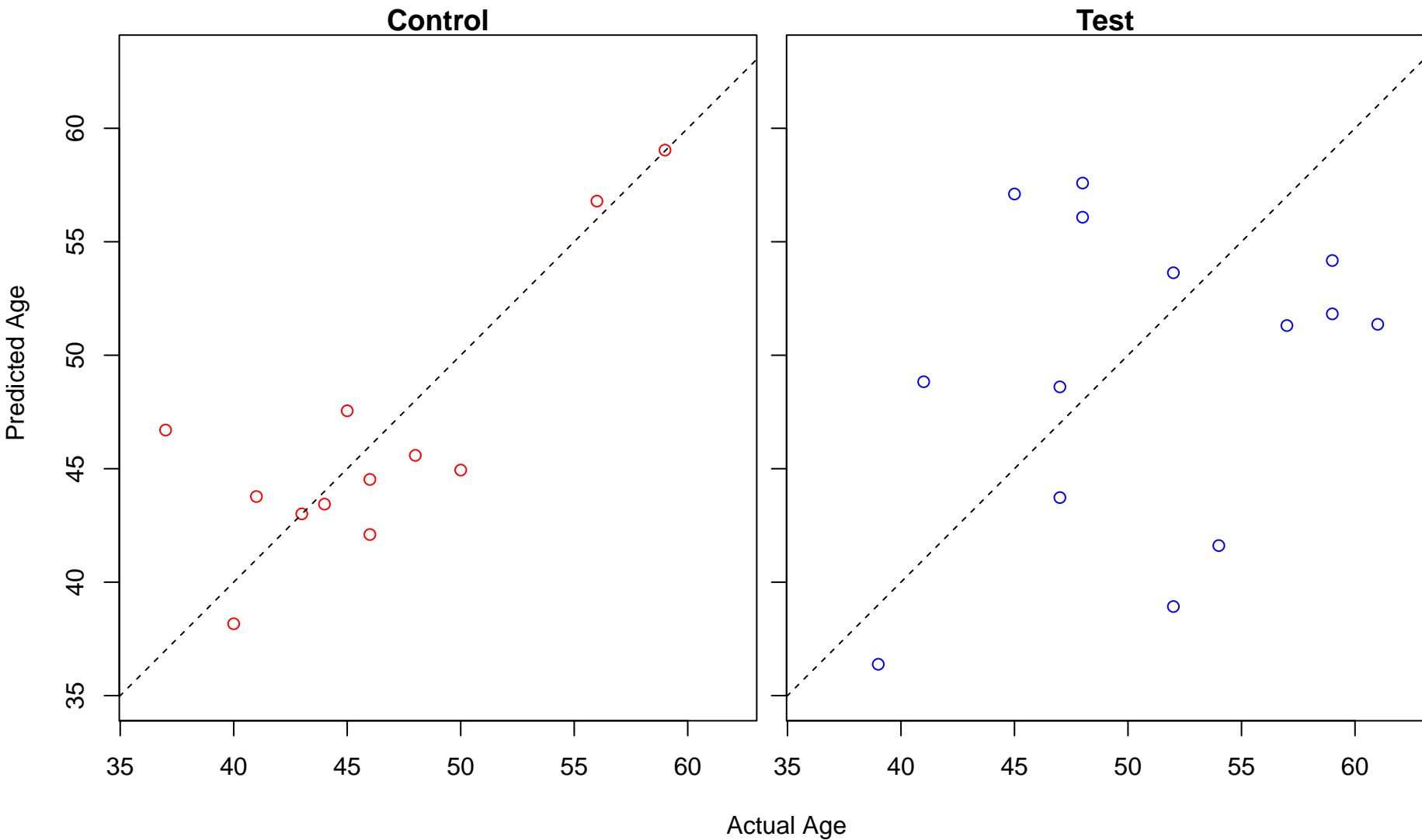
regulation of lipopolysaccharide-mediated signaling pathway (Score: 4.454352)



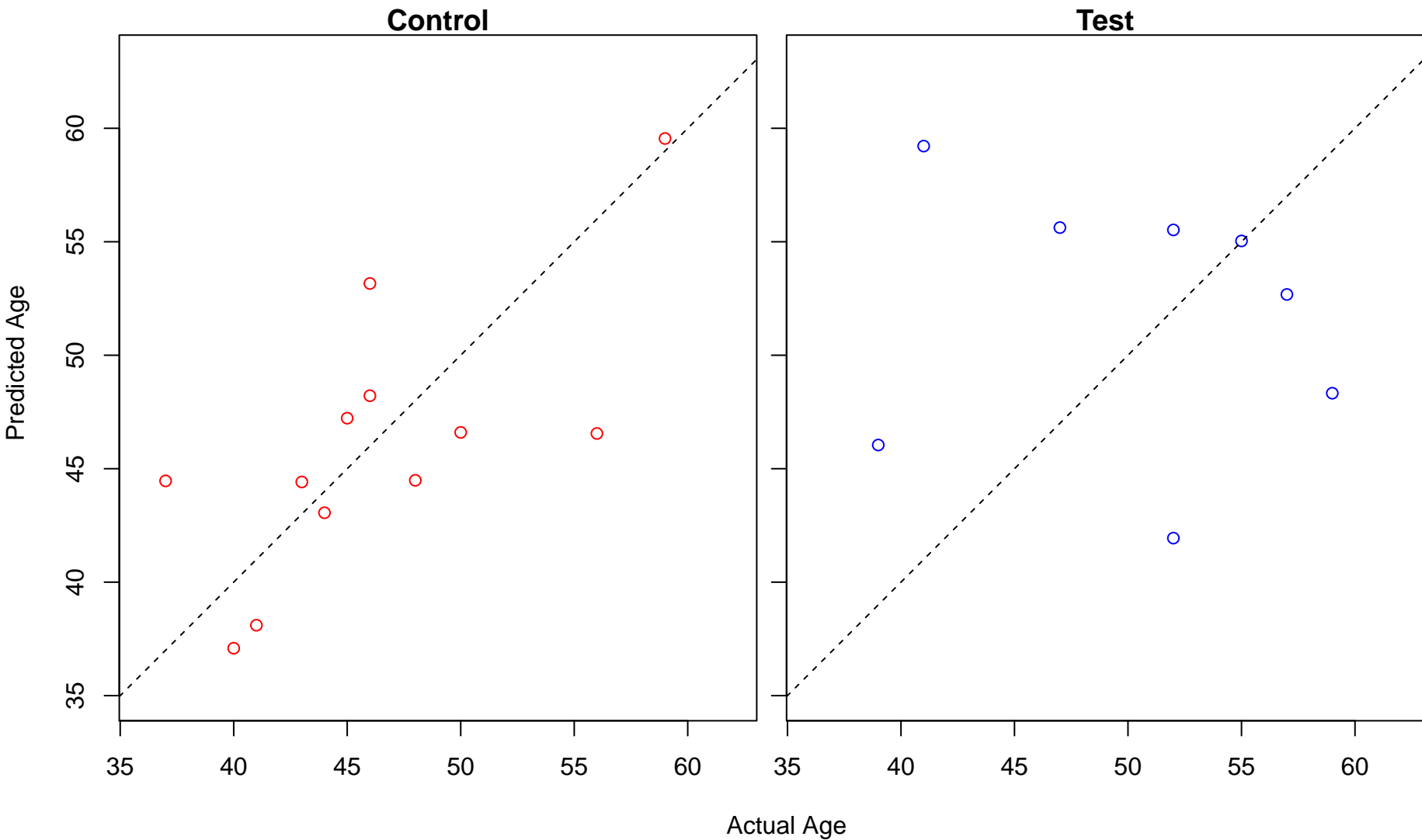
positive regulation of telomere maintenance via telomerase (Score: 4.453573)



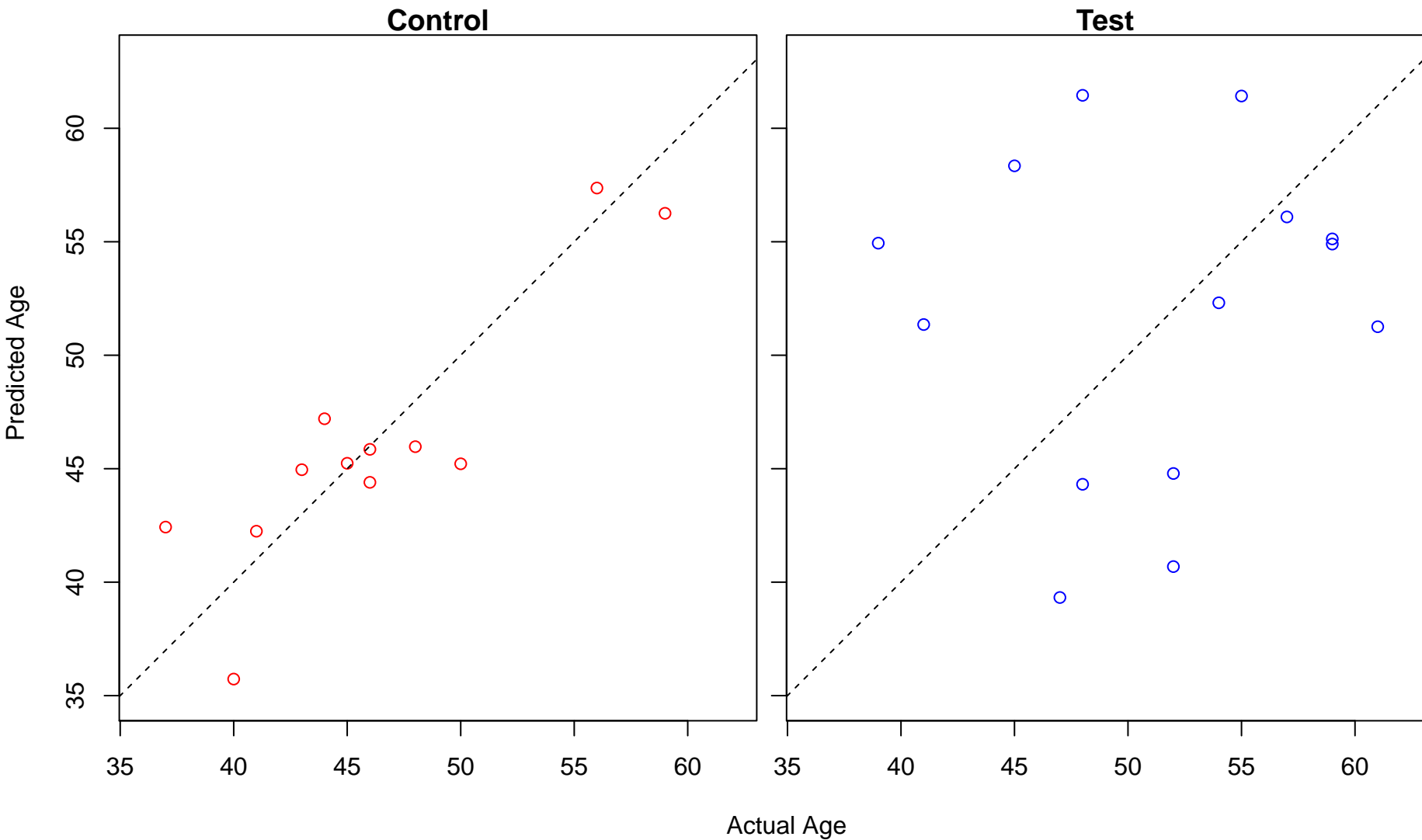
regulation of protein exit from endoplasmic reticulum (Score: 4.452428)



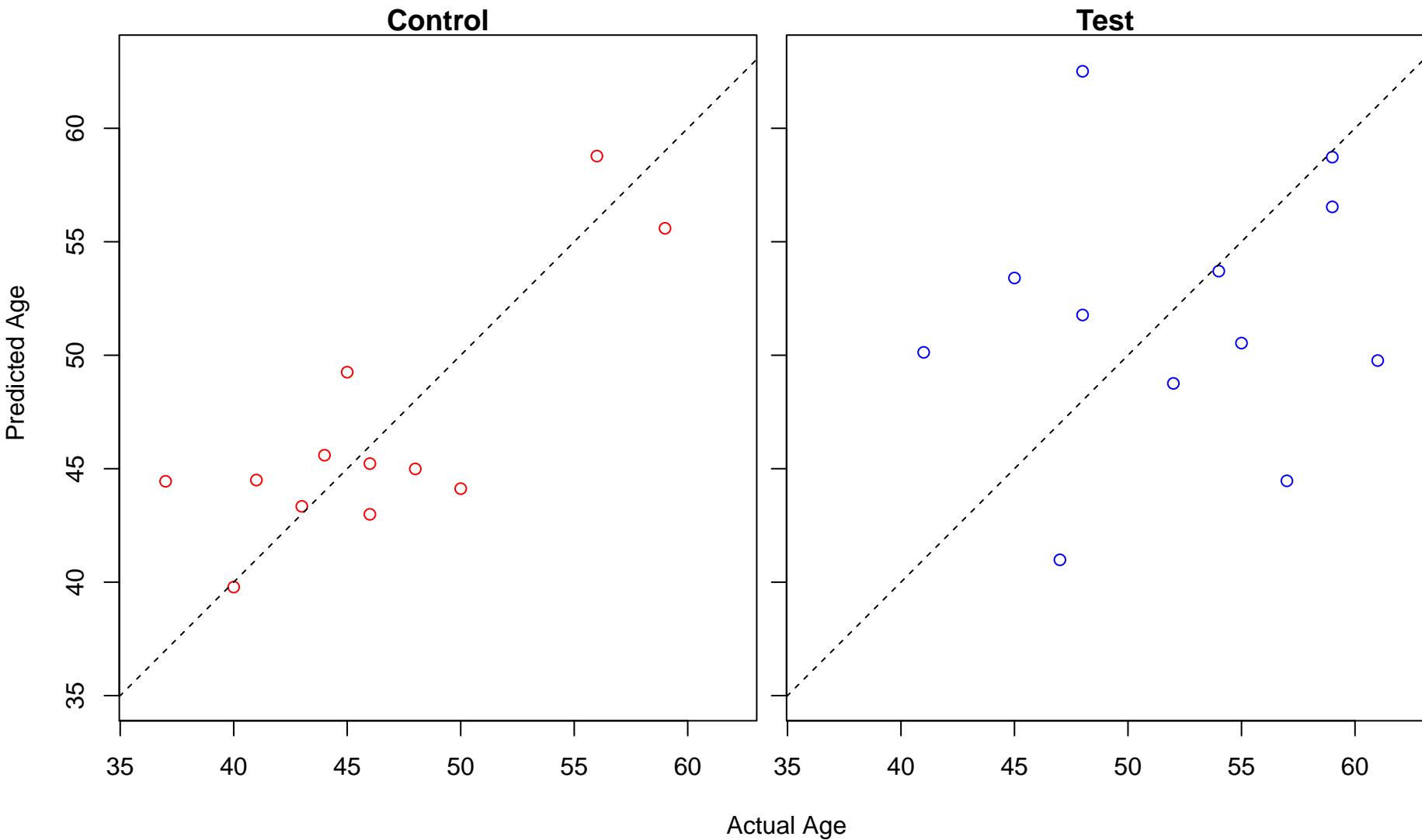
outflow tract morphogenesis (Score: 4.452331)



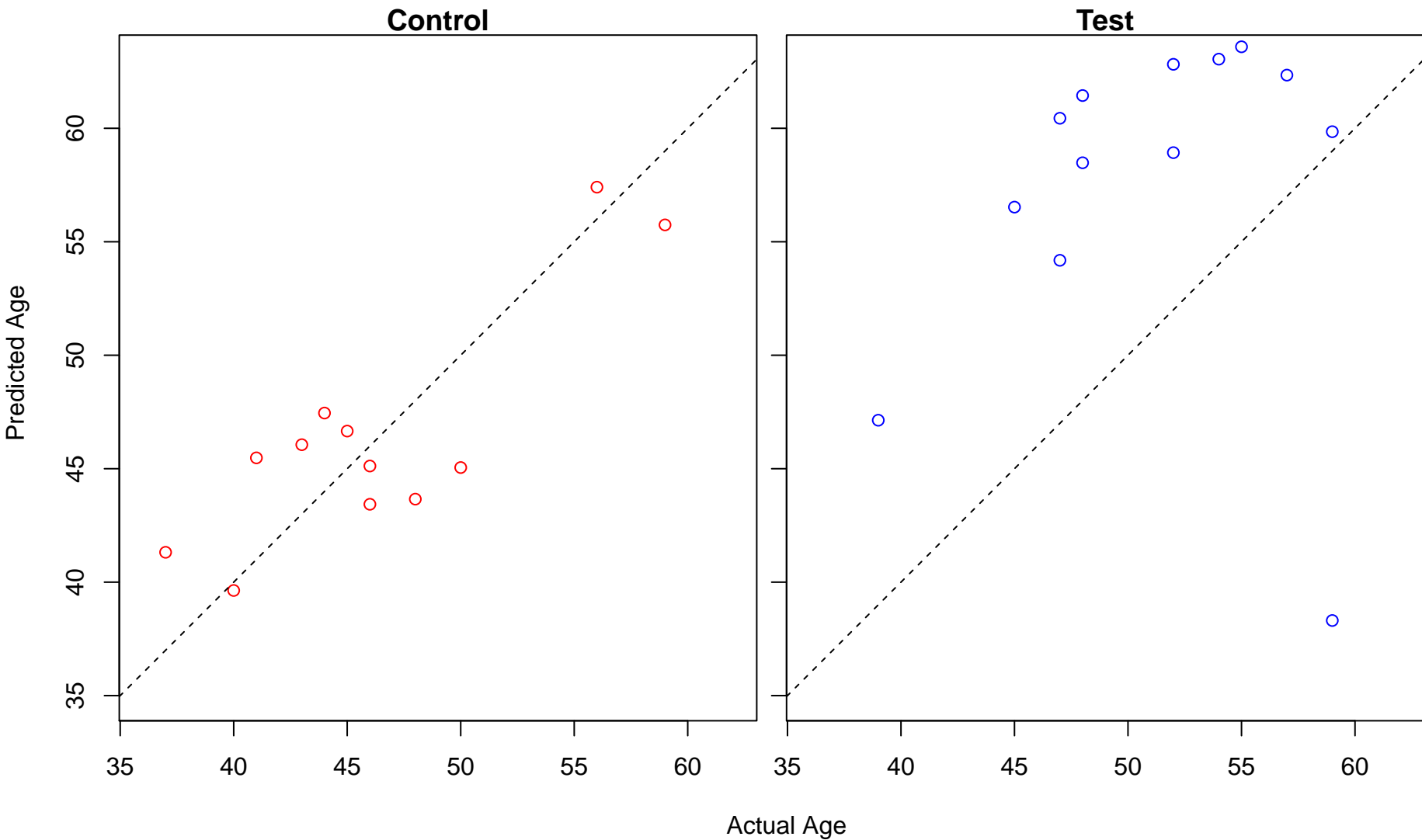
positive regulation of nucleotide metabolic process (Score: 4.443370)



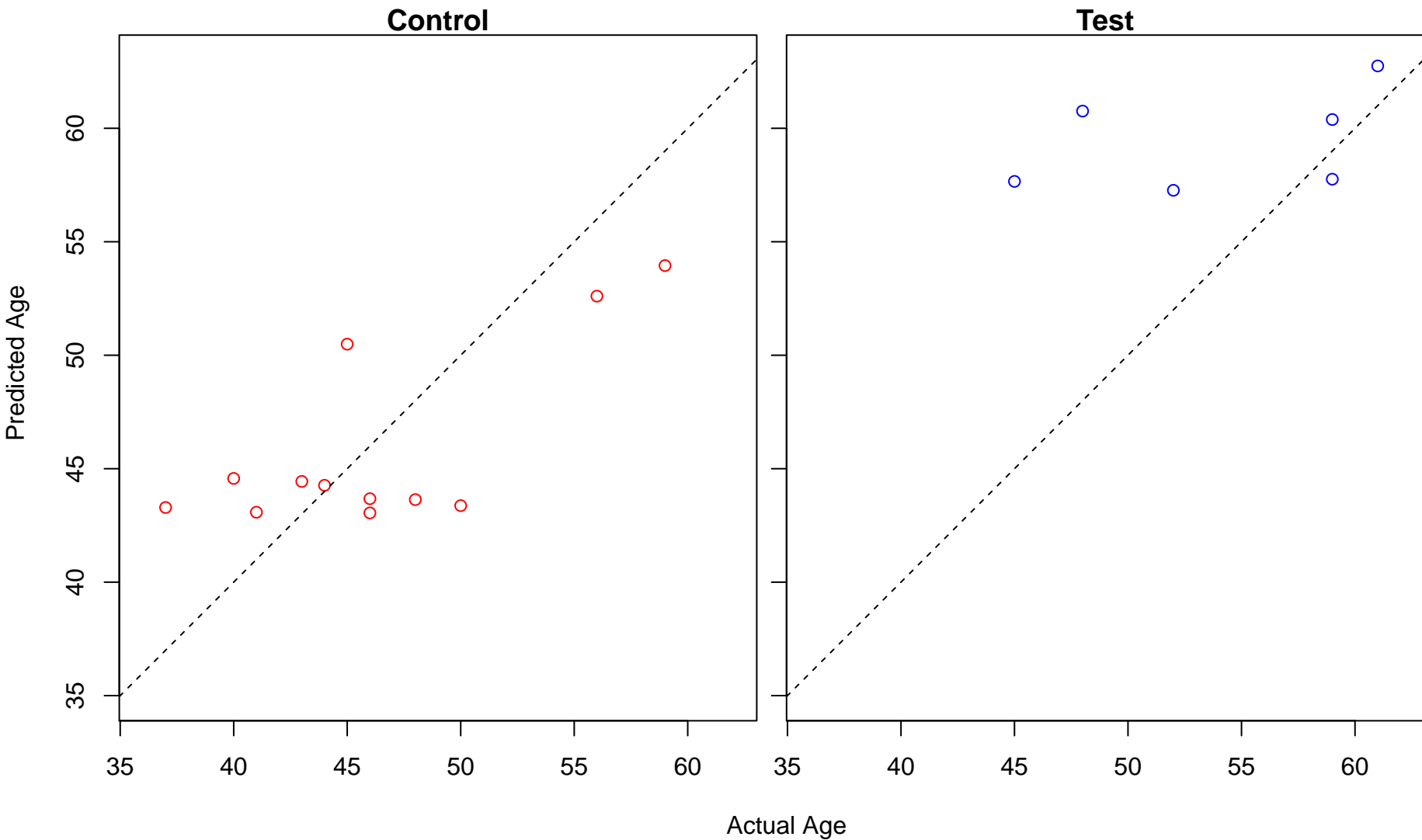
positive regulation of telomere maintenance via telomere lengthening (Score: 4.442867)



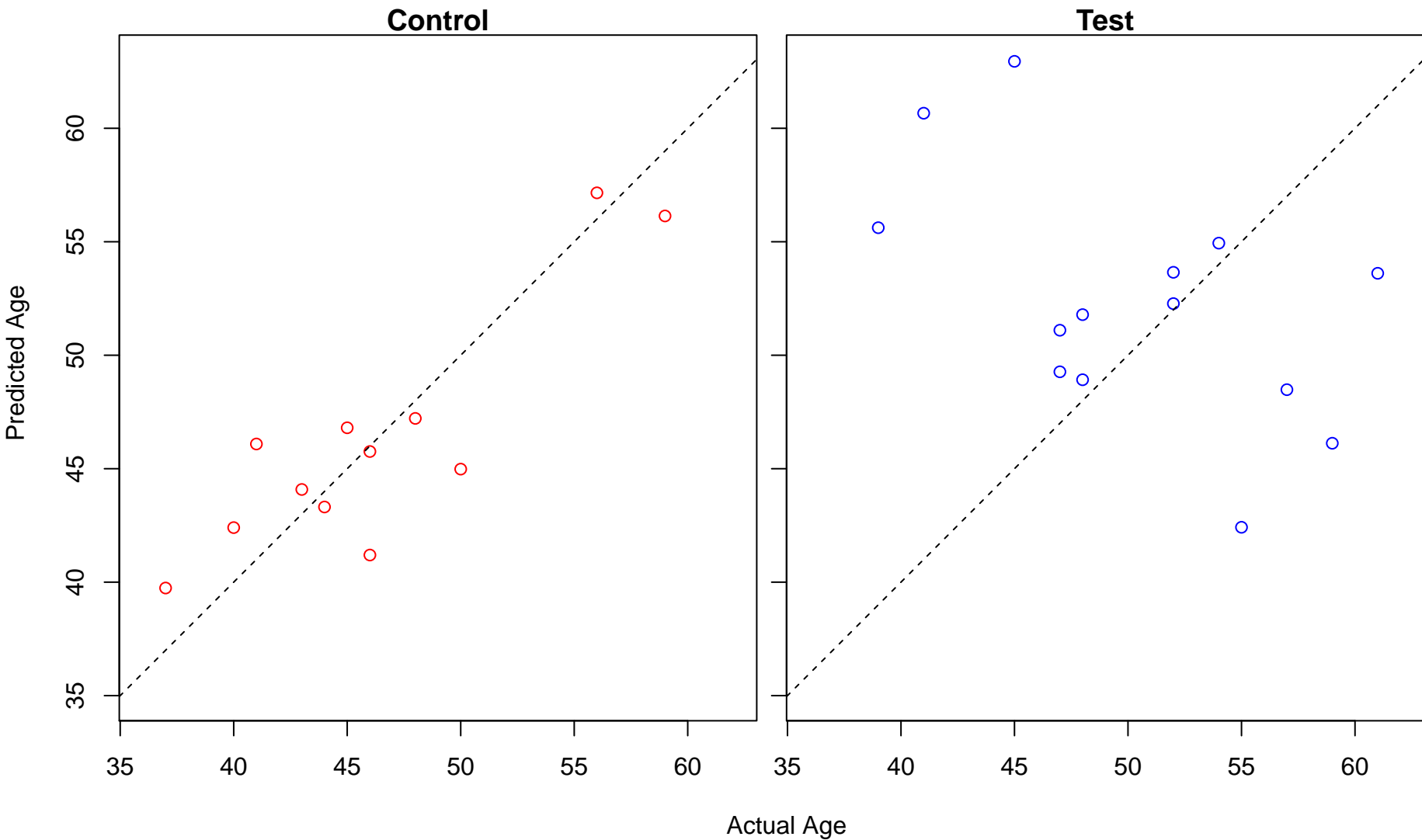
interferon-gamma production (Score: 4.439706)



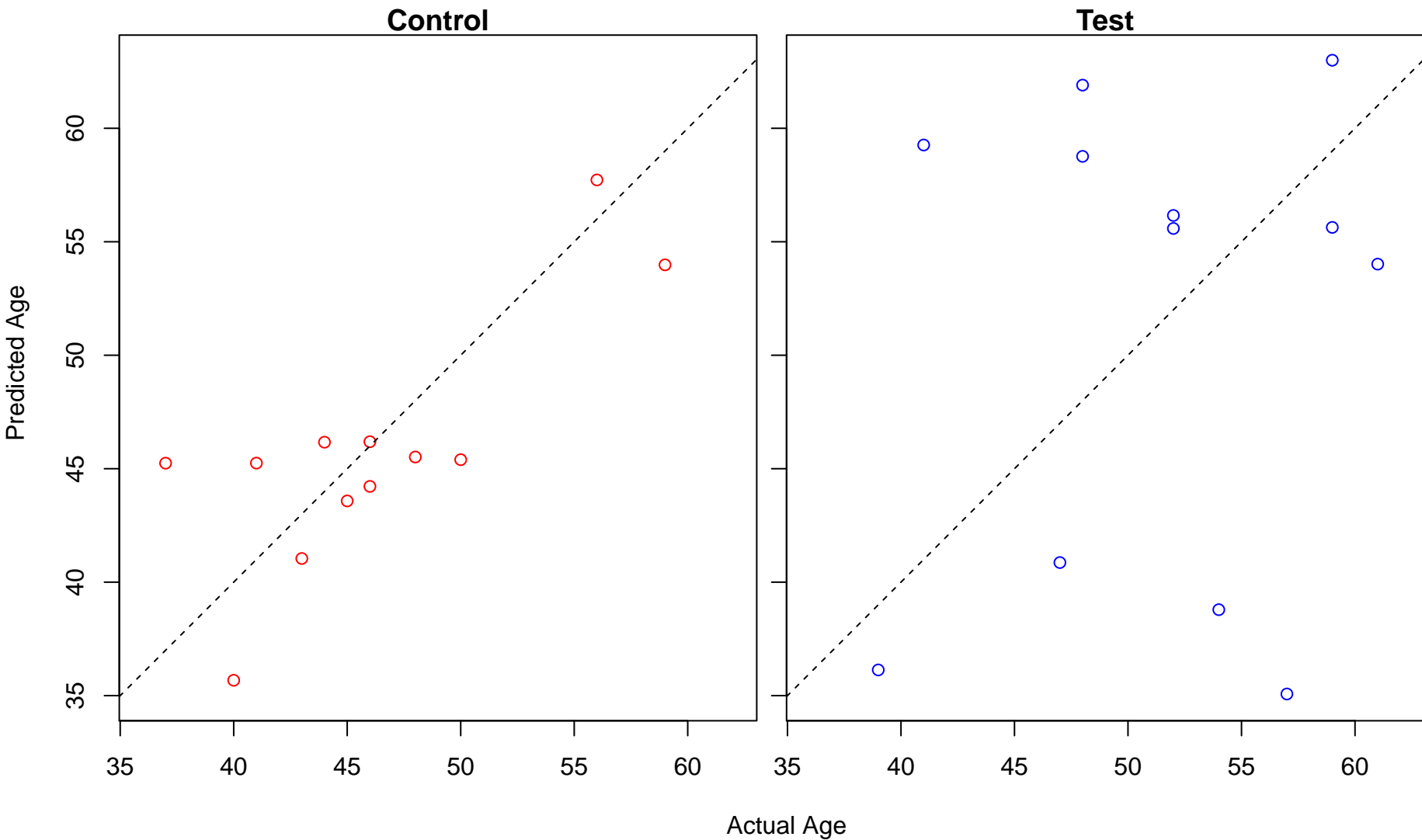
positive regulation of fatty acid metabolic process (Score: 4.427312)



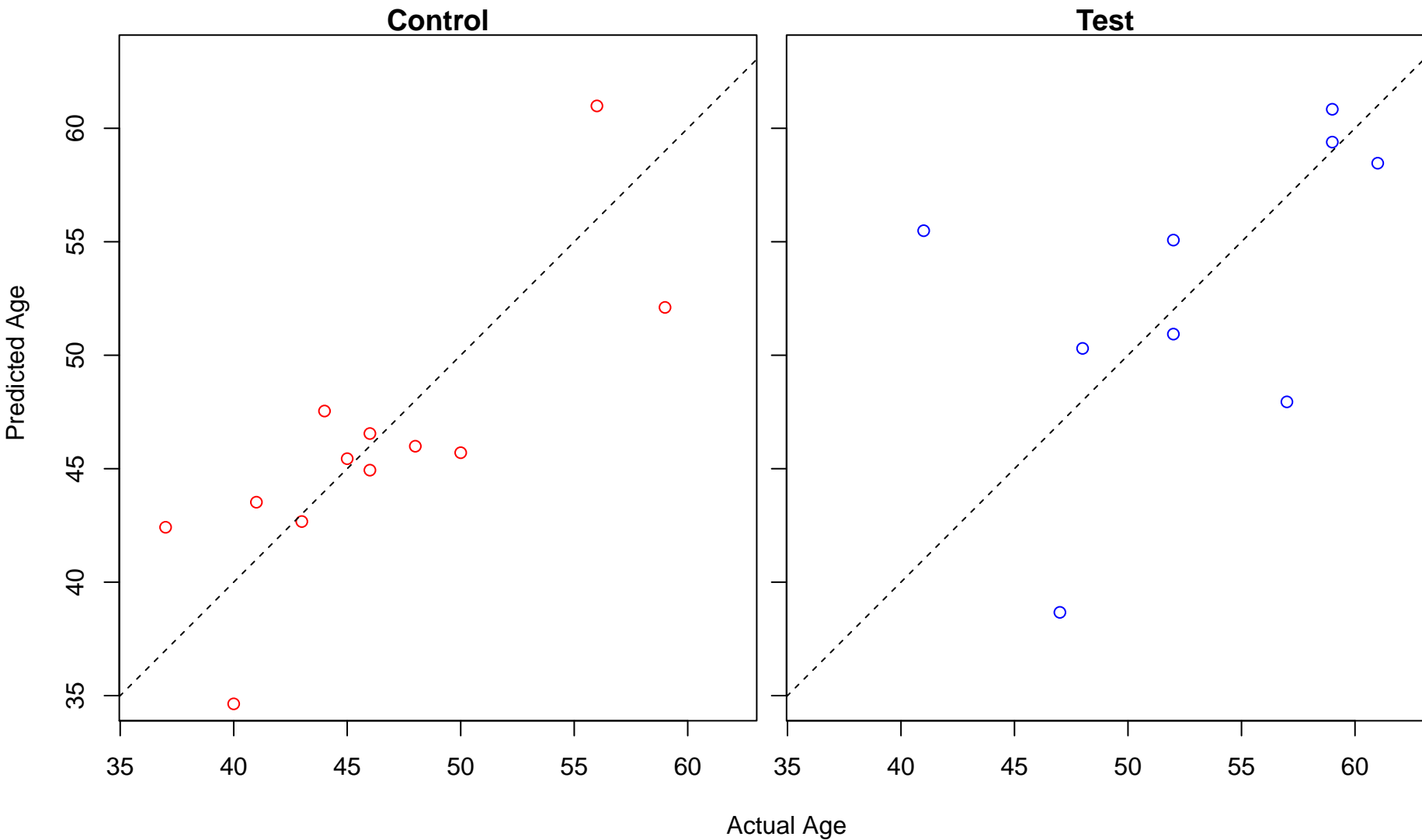
positive regulation of epithelial cell proliferation involved in wound healing (Score: 4.420039)



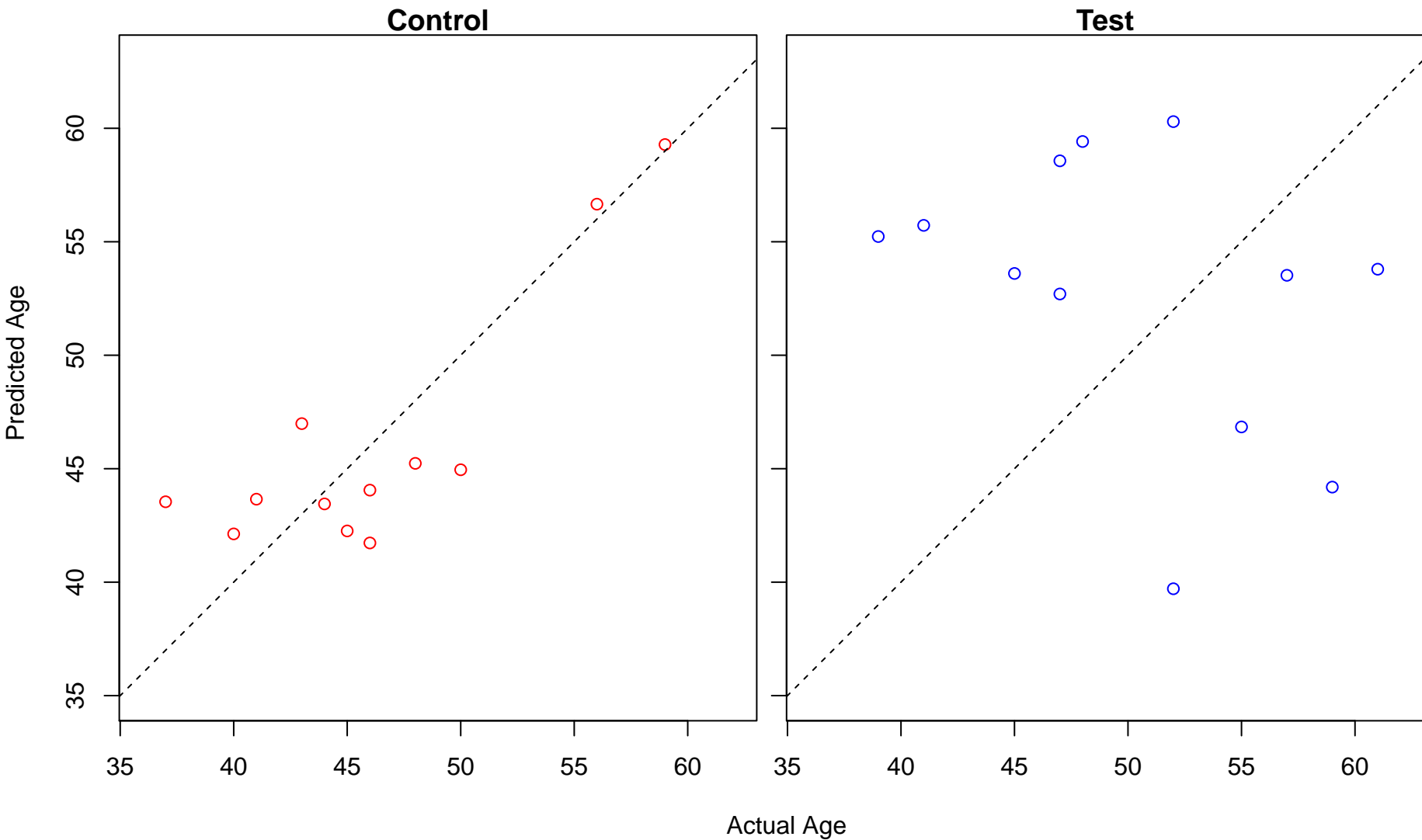
negative regulation of peptidyl-tyrosine phosphorylation (Score: 4.417270)



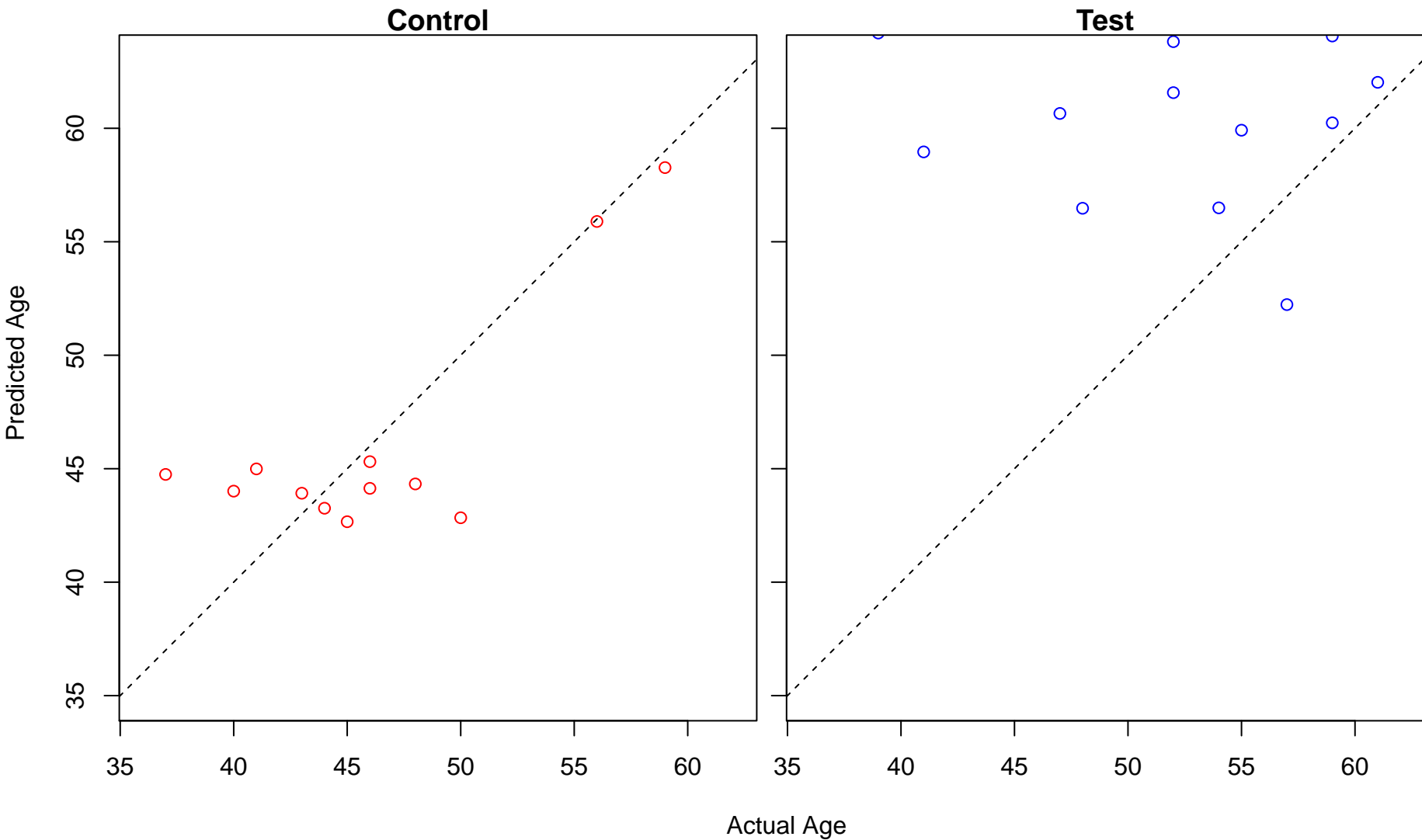
negative regulation of protein kinase B signaling (Score: 4.414950)



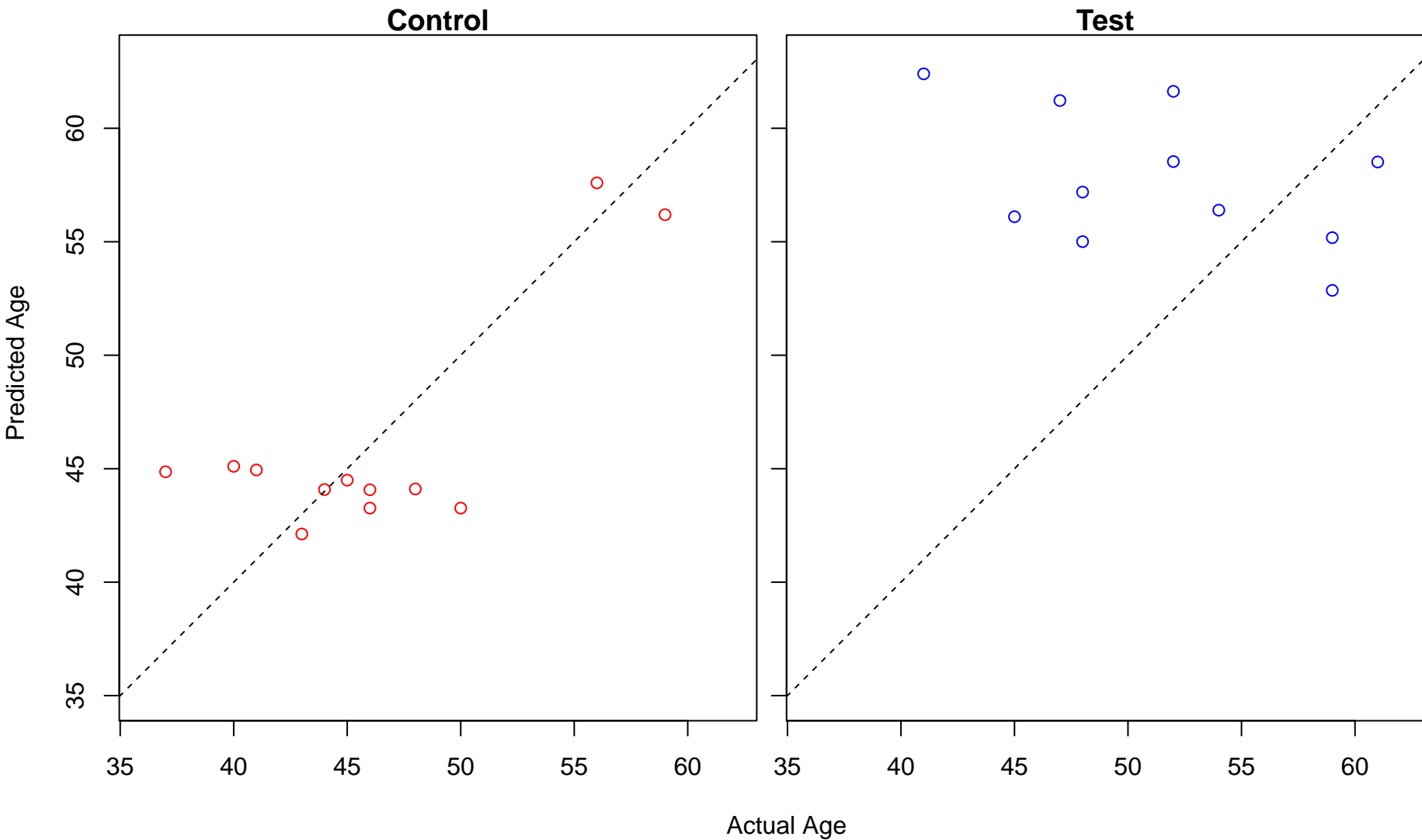
actin cytoskeleton reorganization (Score: 4.414545)



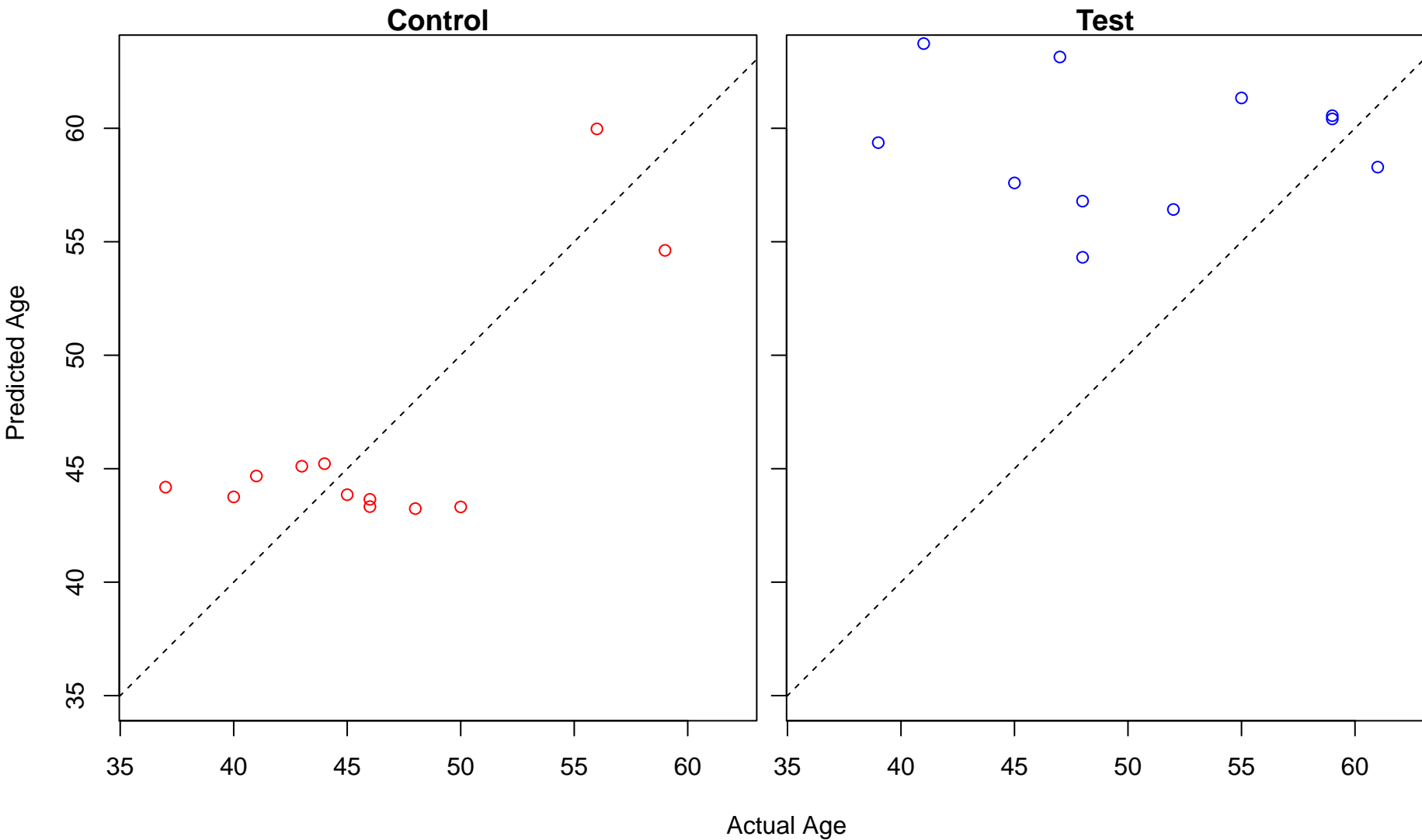
negative regulation of gliogenesis (Score: 4.409008)



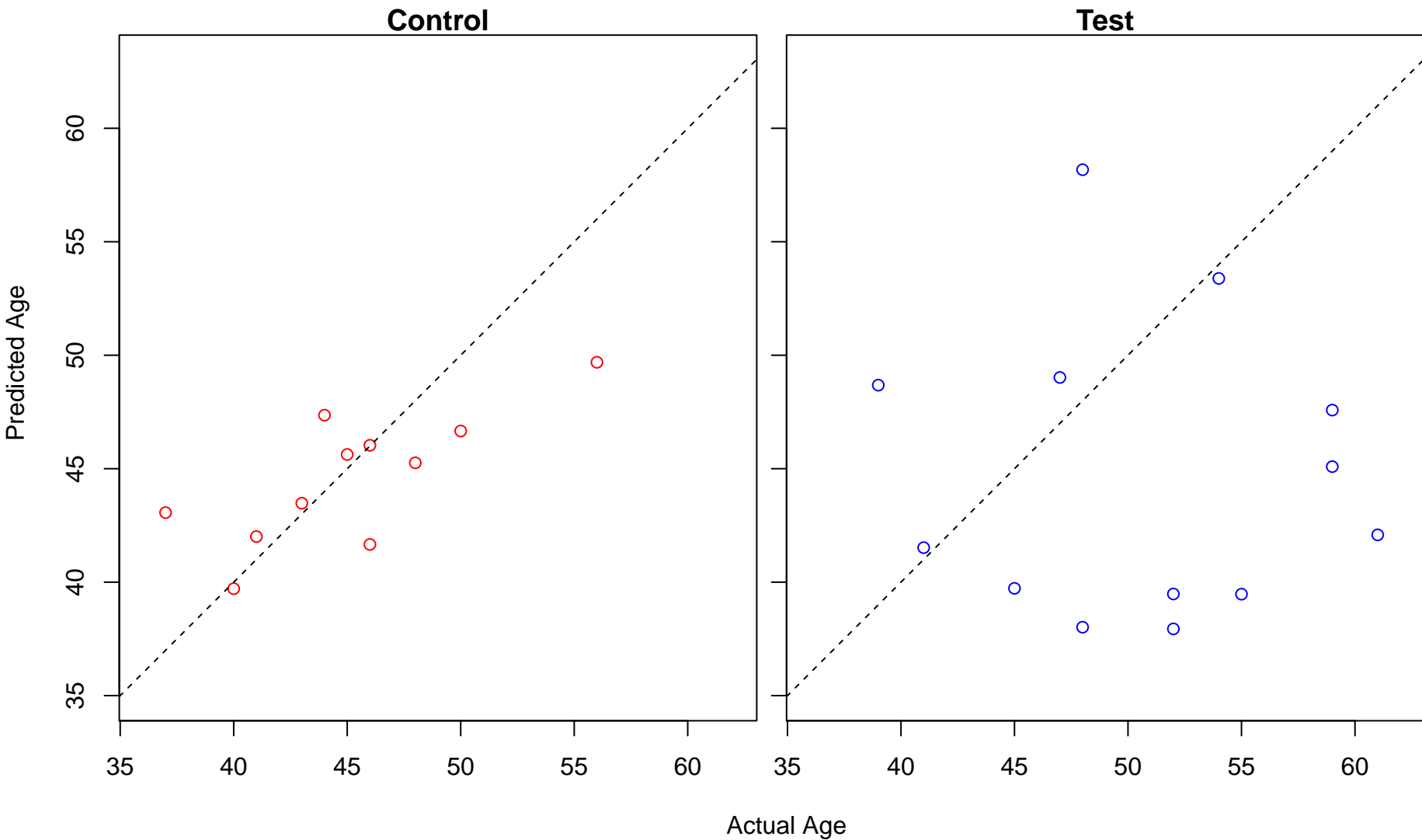
negative regulation of I-kappaB kinase/NF-kappaB signaling (Score: 4.405011)



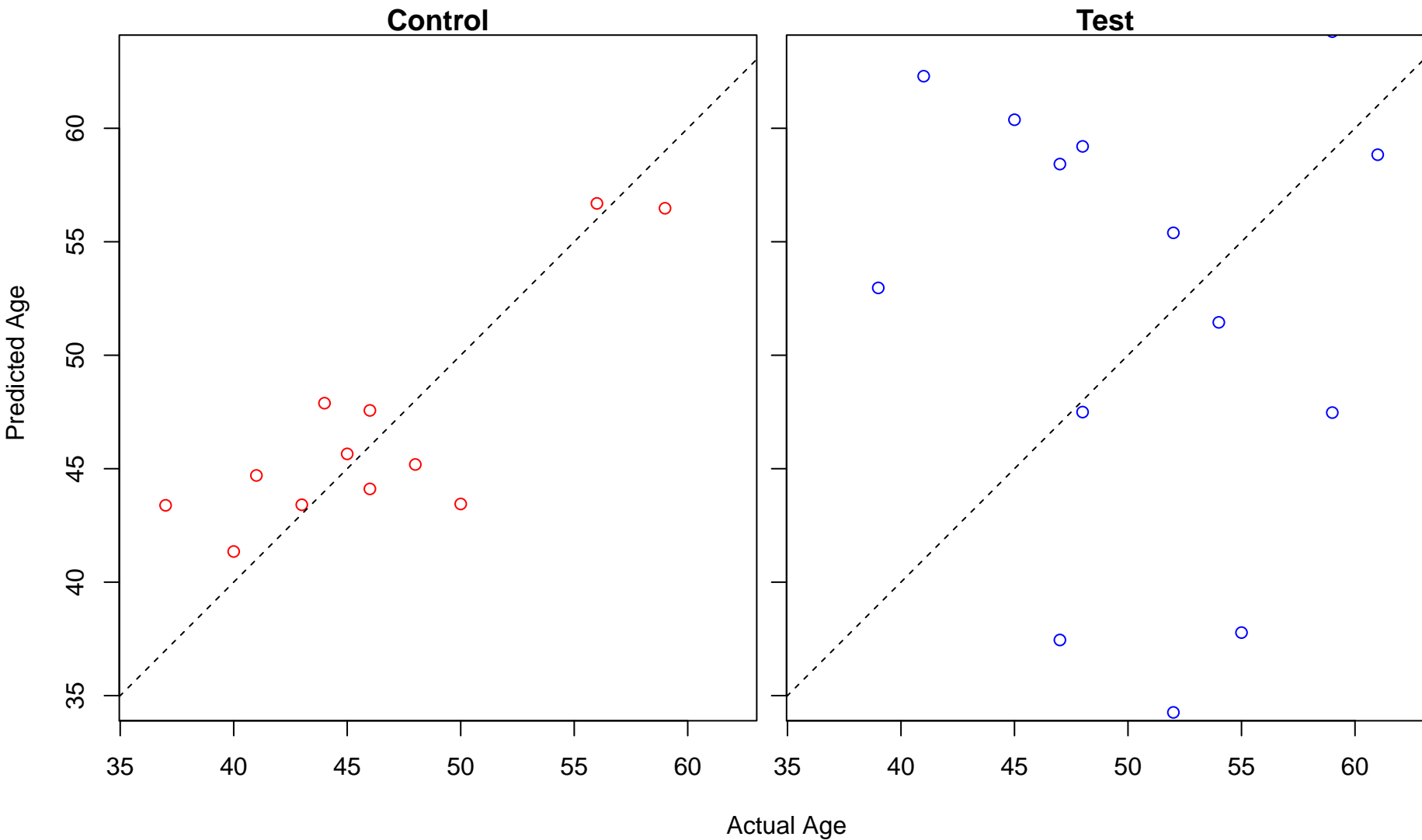
negative regulation of muscle cell differentiation (Score: 4.404965)



regulation of calcium ion transport (Score: 4.393894)

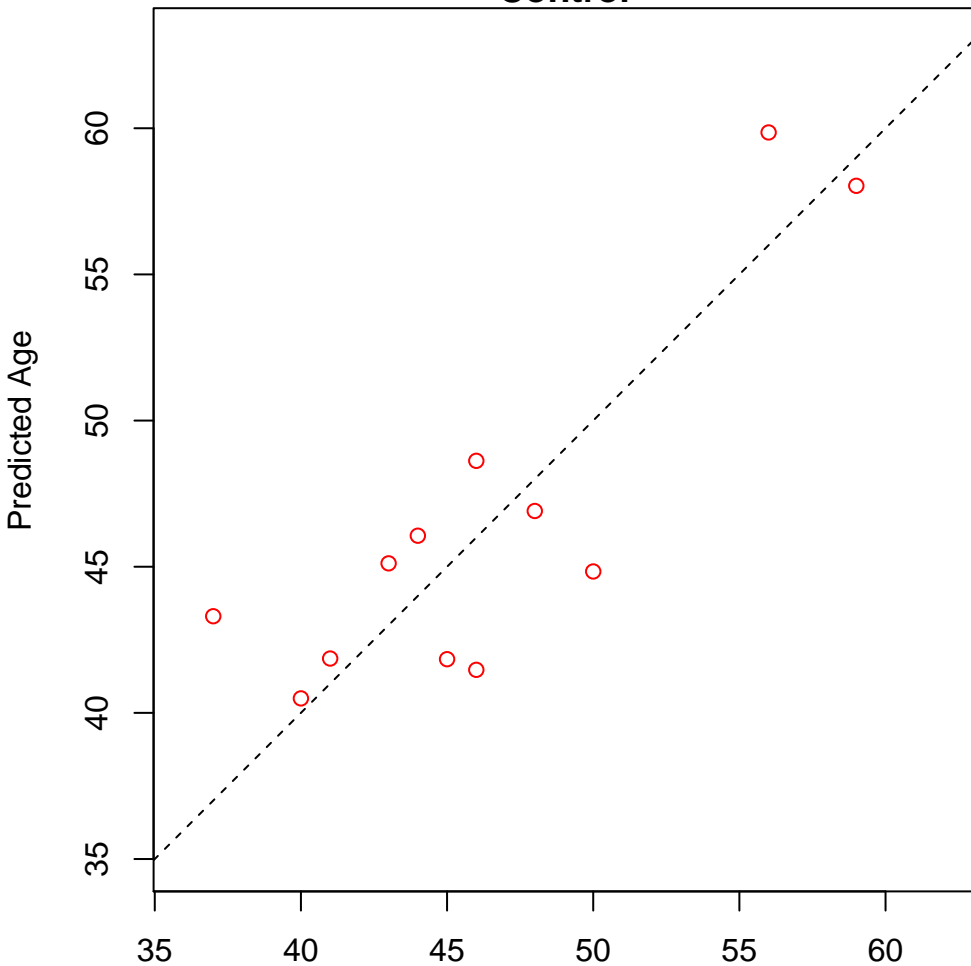


regulation of spindle checkpoint (Score: 4.389608)

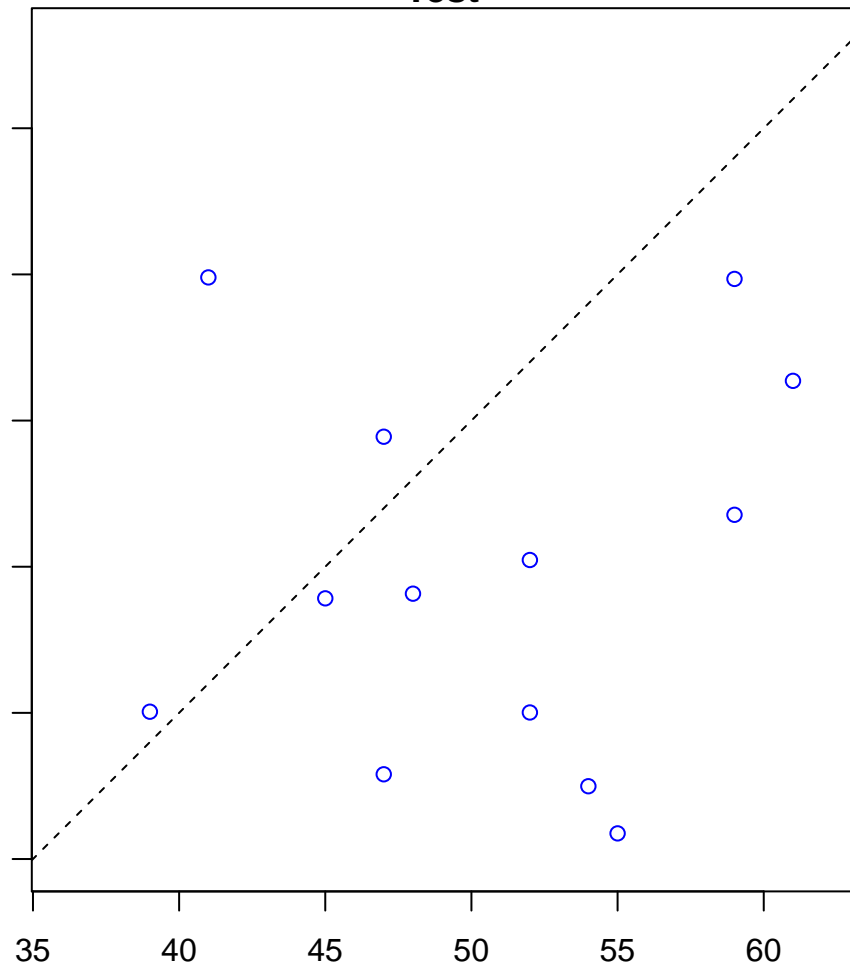


regulation of protein catabolic process (Score: 4.389321)

Control

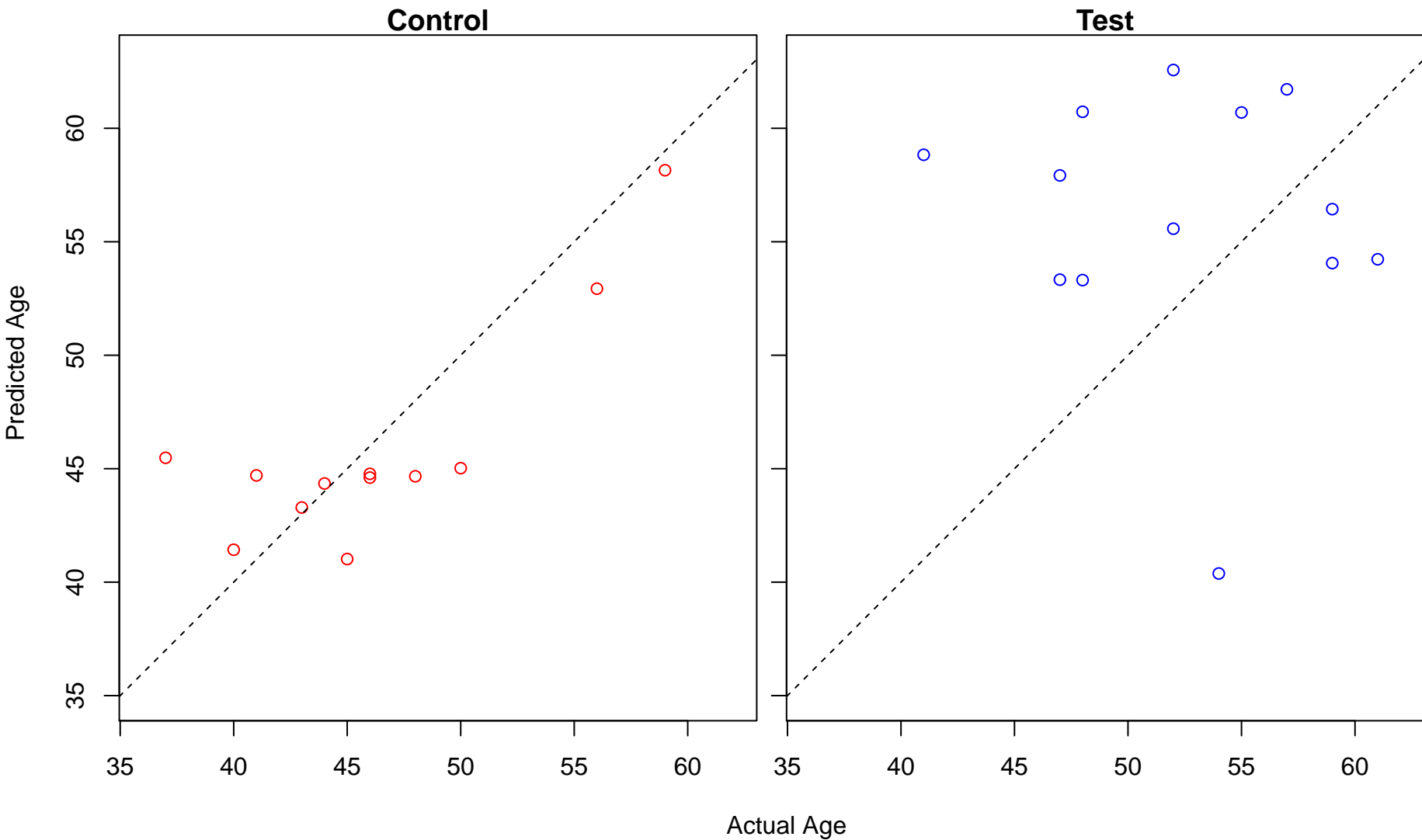


Test

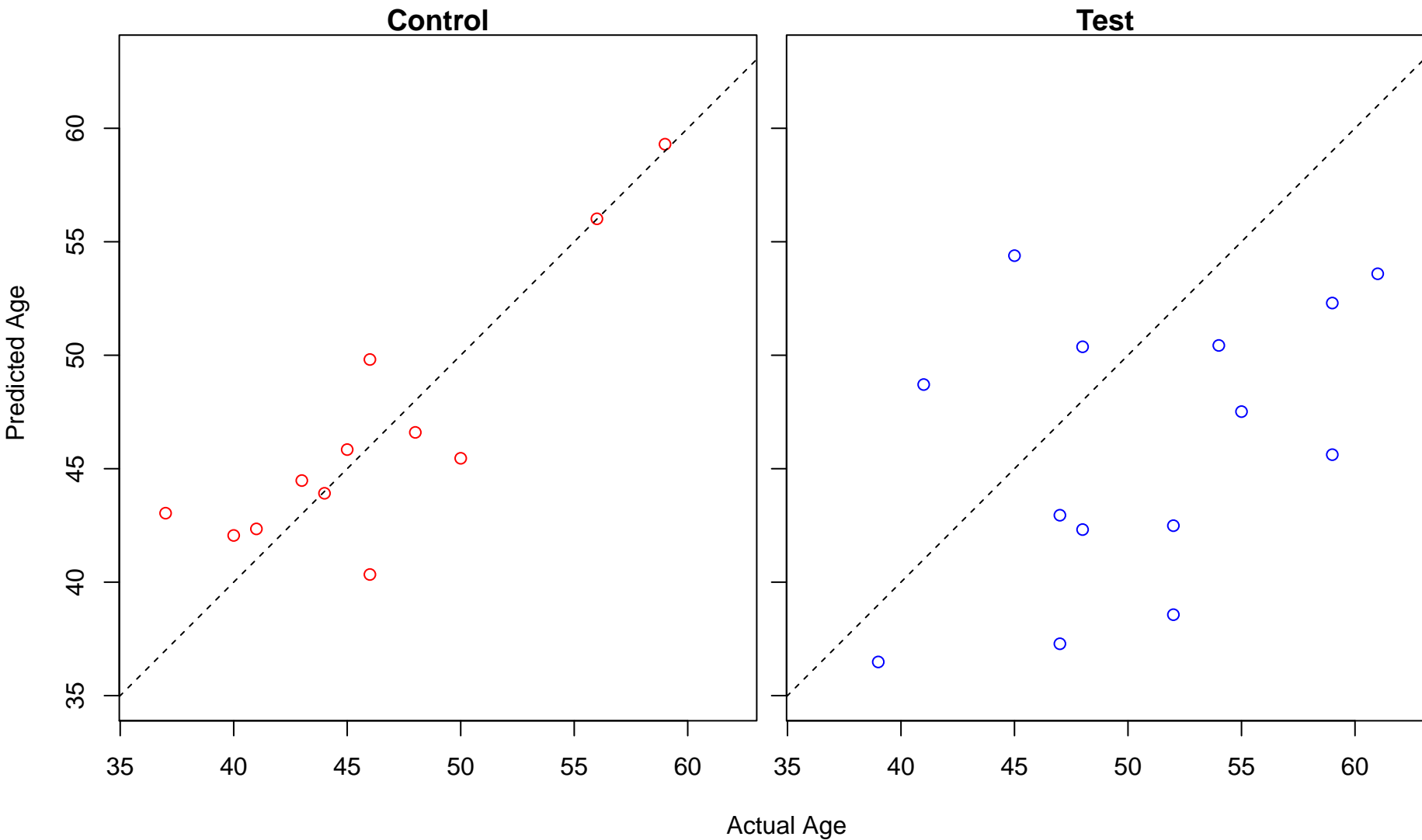


Actual Age

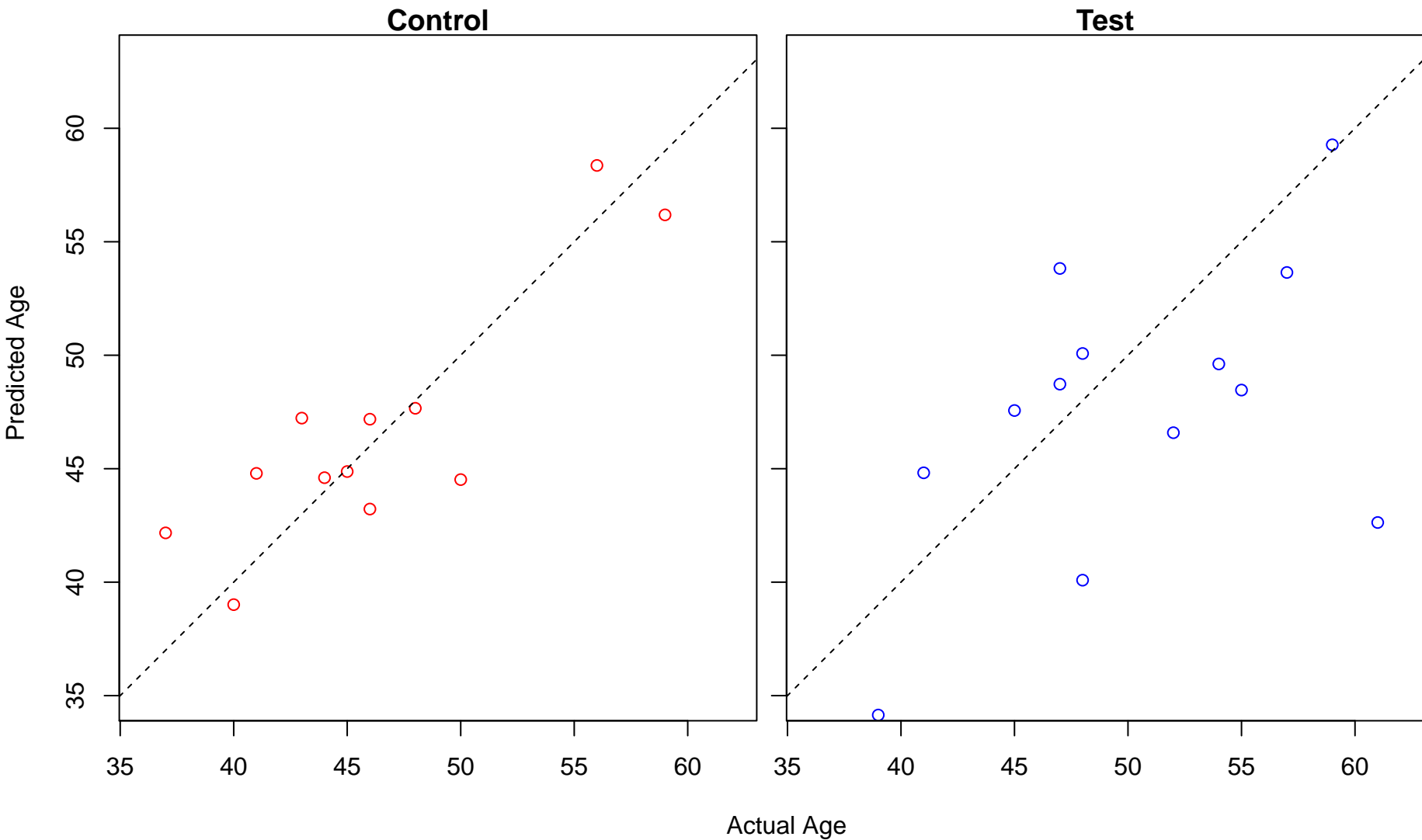
folic acid transport (Score: 4.388529)



regulation of glucose import (Score: 4.388094)

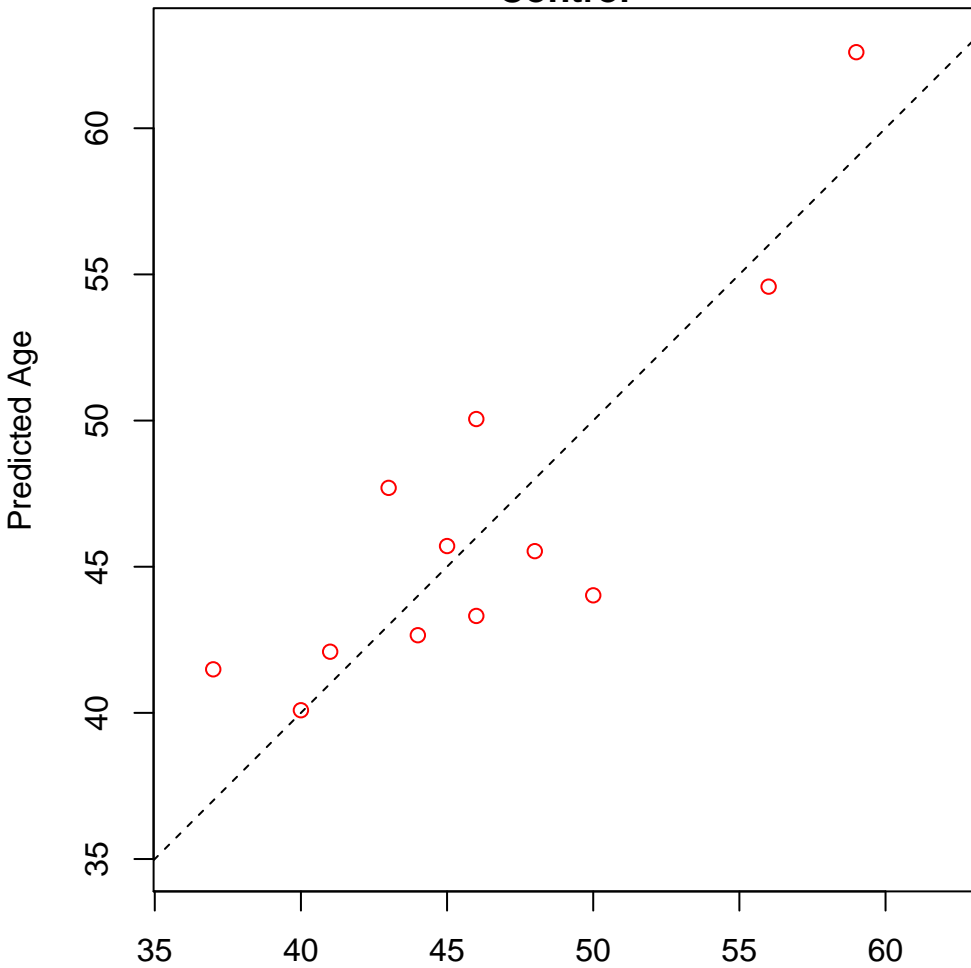


hemopoiesis (Score: 4.375418)

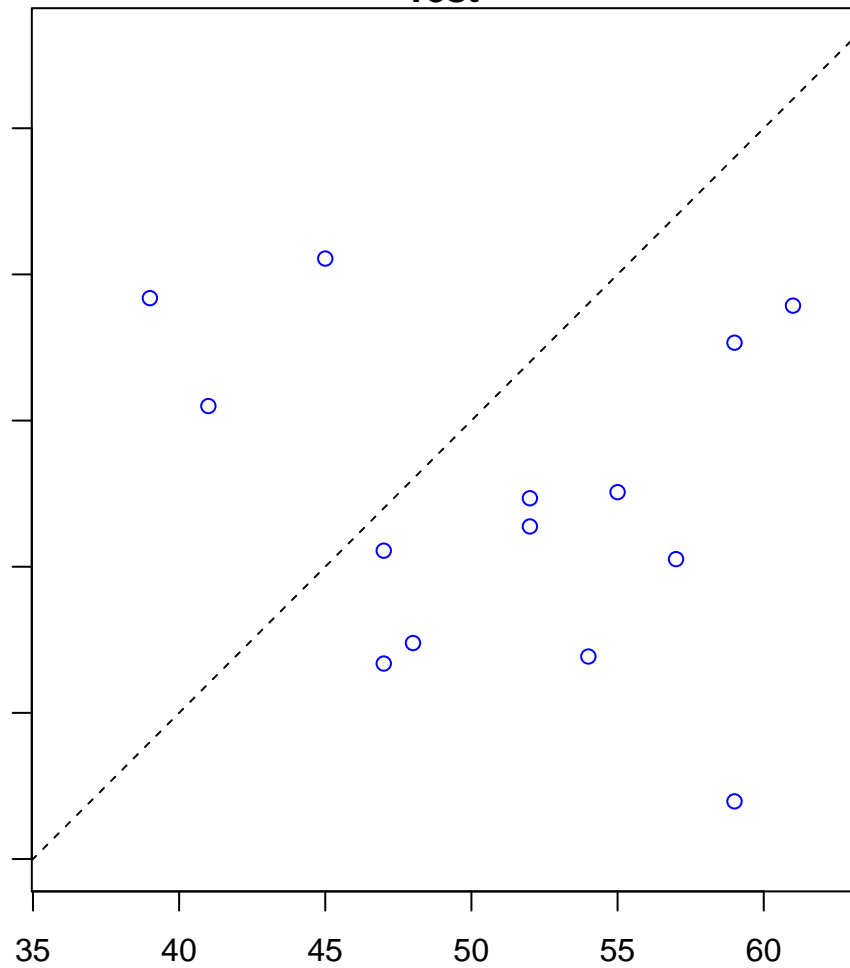


regulation of endothelial cell migration (Score: 4.373662)

Control

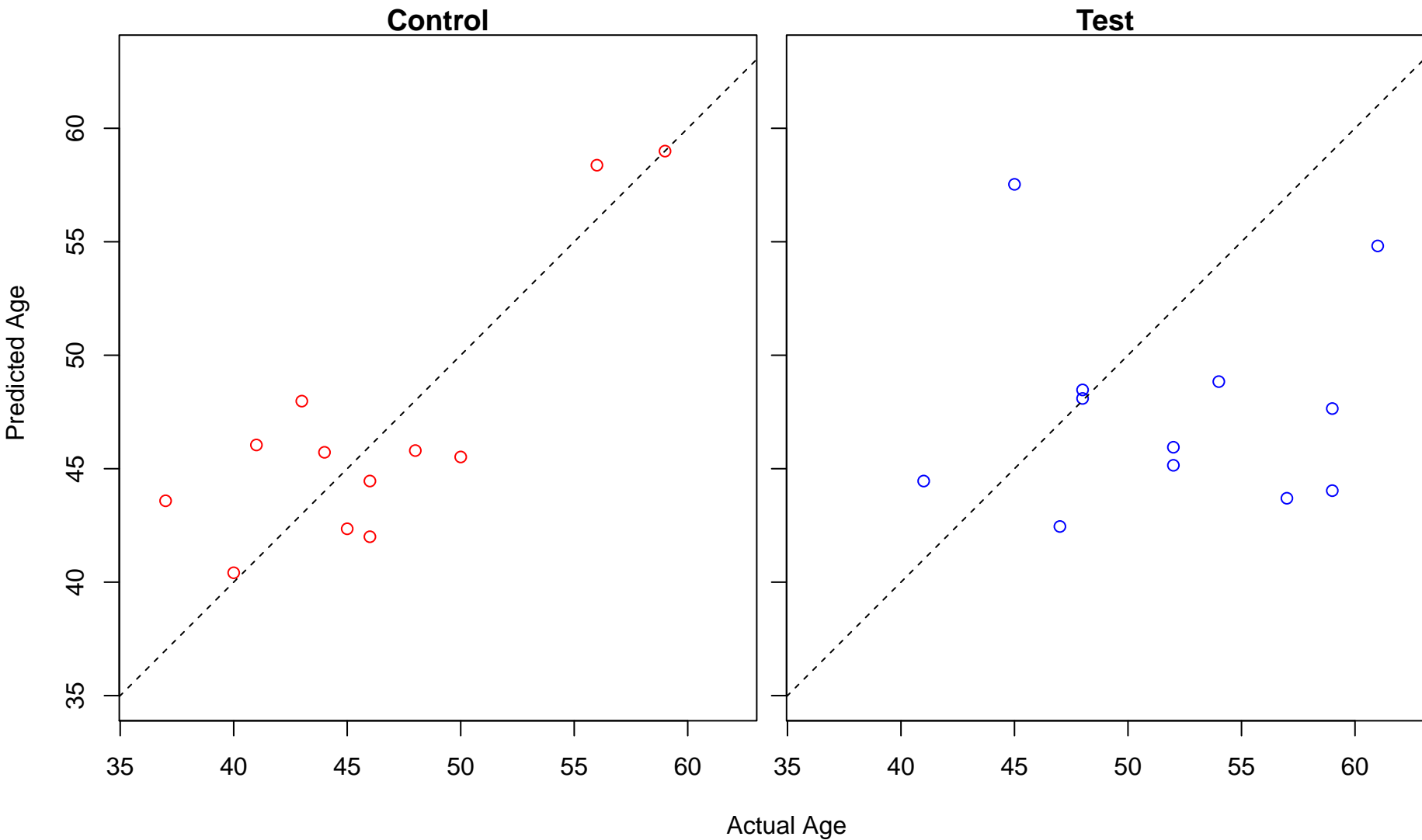


Test

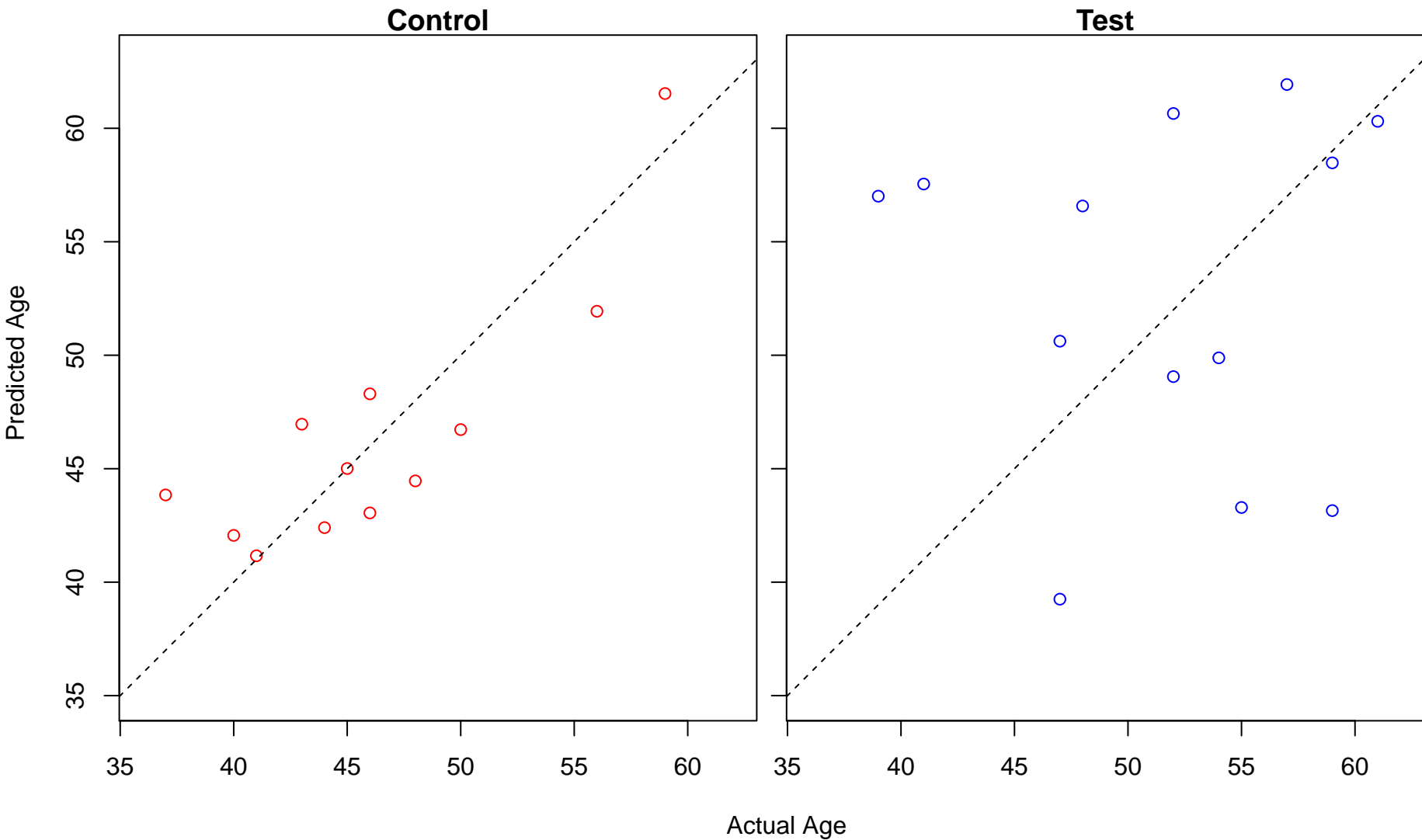


Actual Age

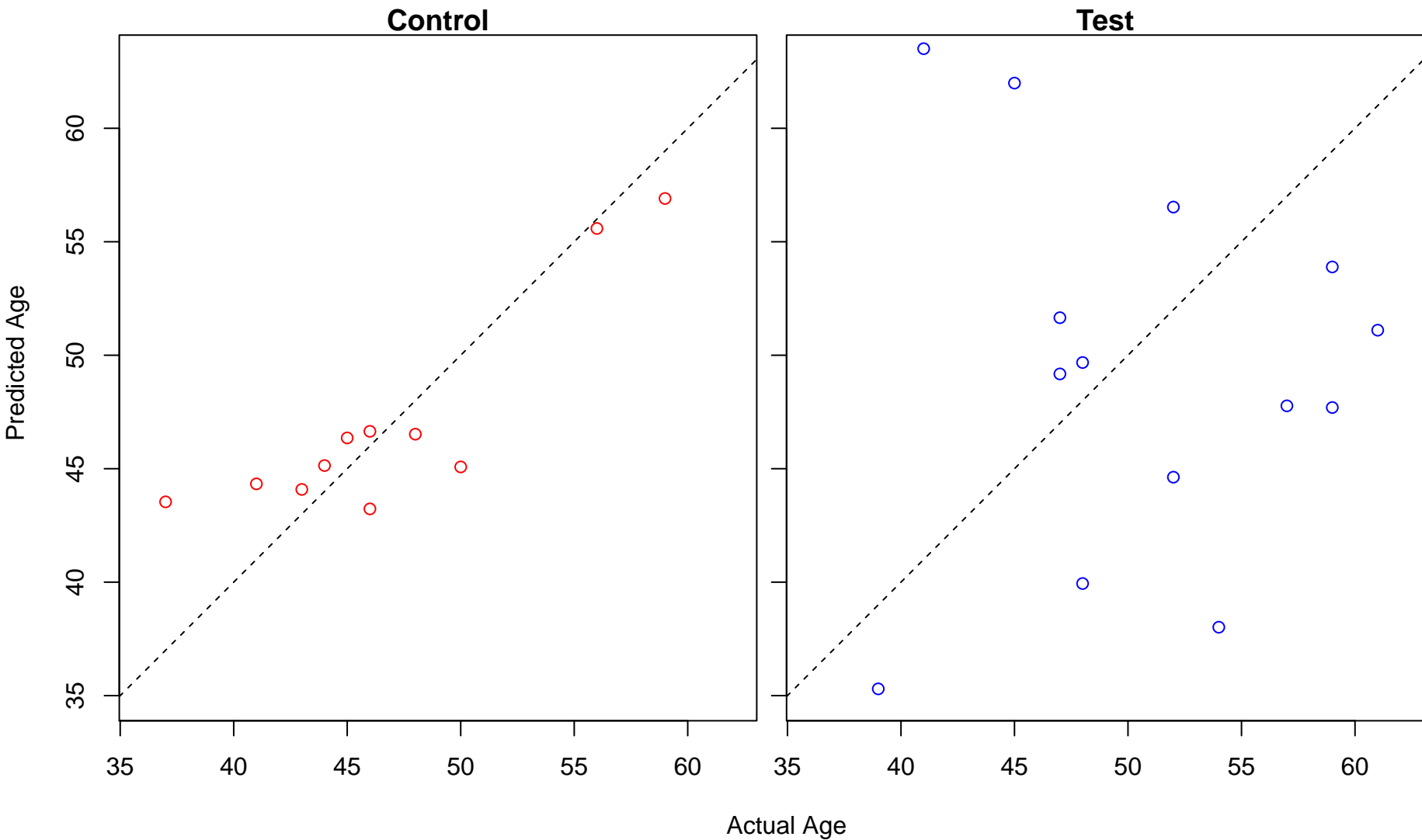
regulation of cell morphogenesis involved in differentiation (Score: 4.372883)



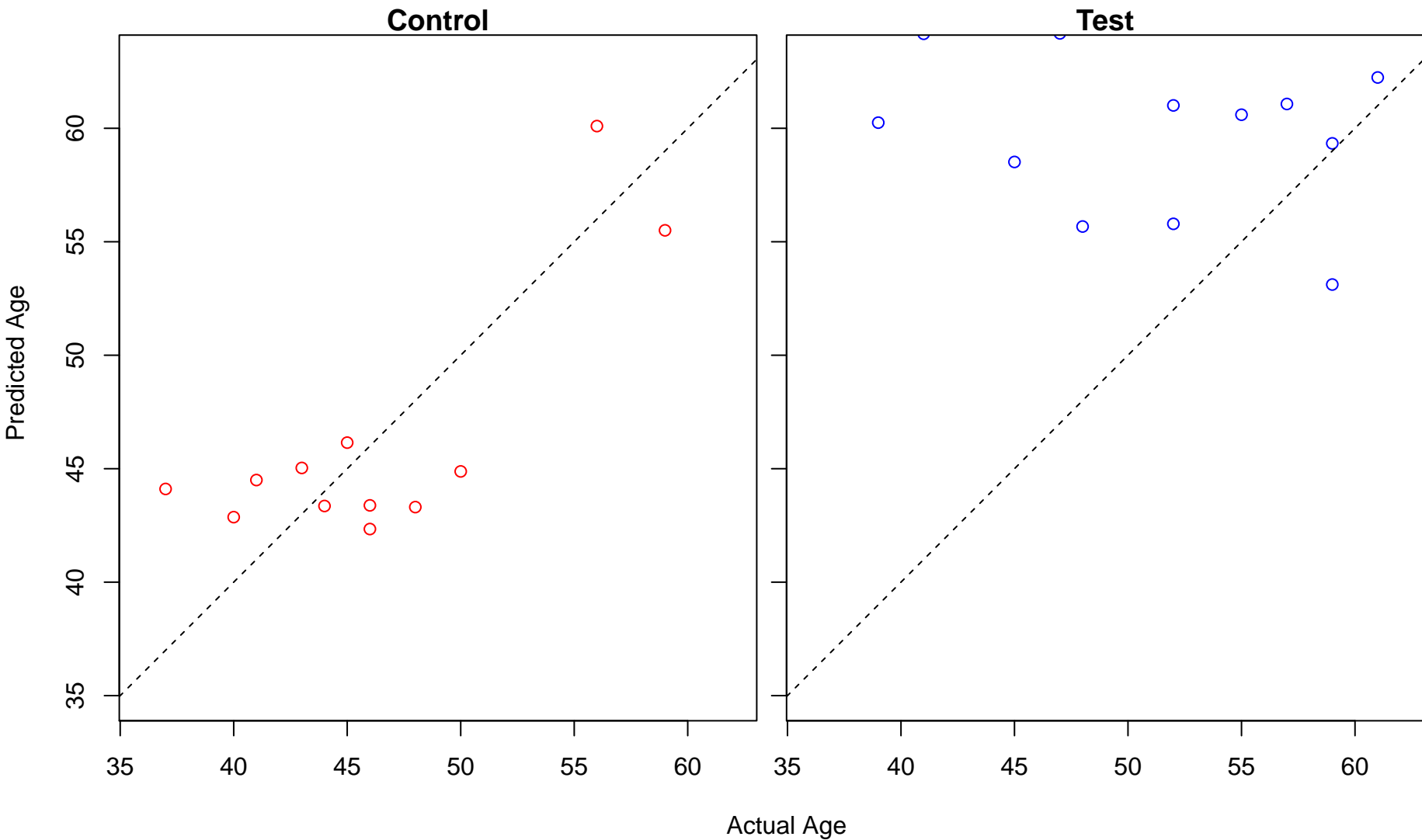
artery morphogenesis (Score: 4.364163)



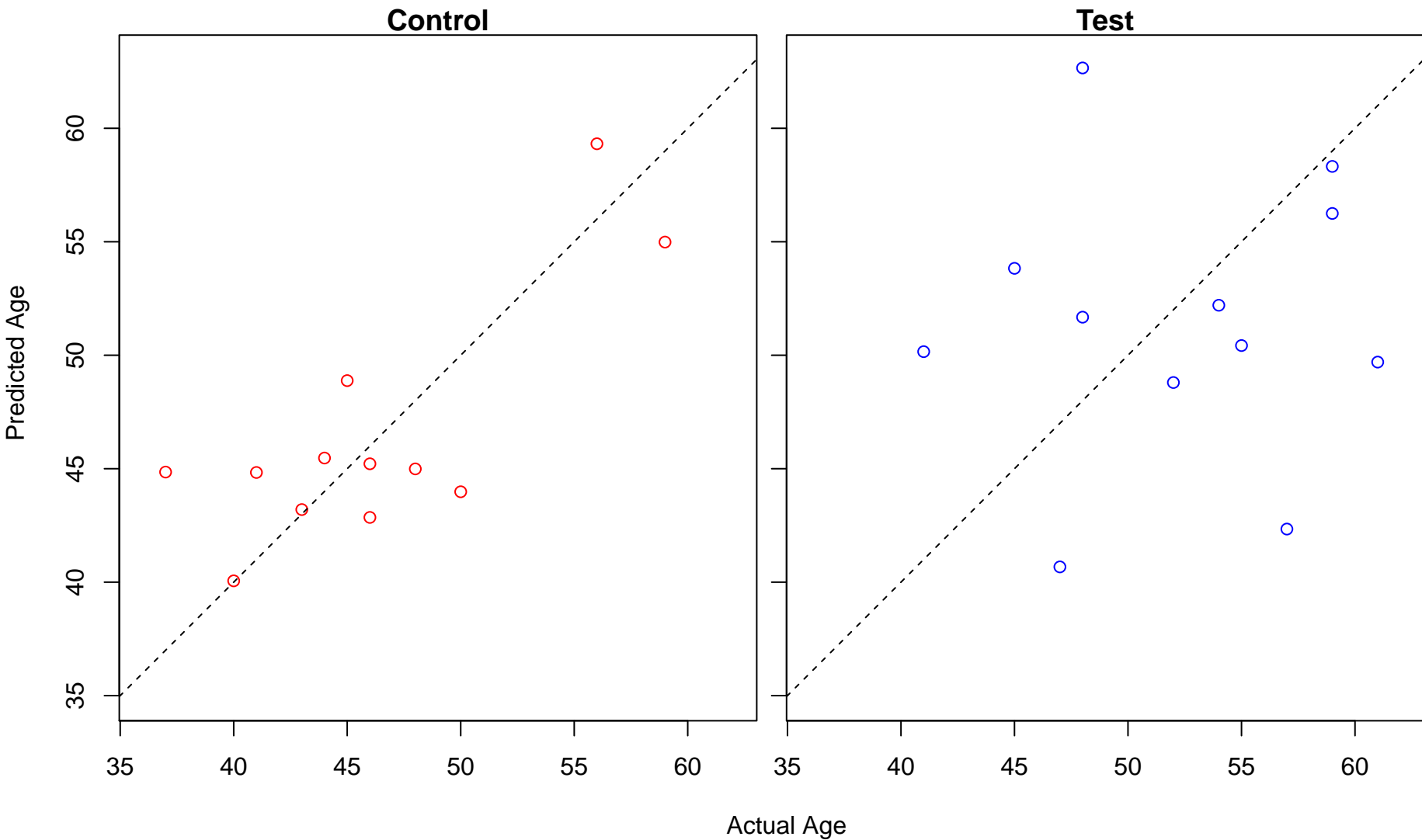
response to interferon-alpha (Score: 4.362376)



regulation of neuron migration (Score: 4.359855)

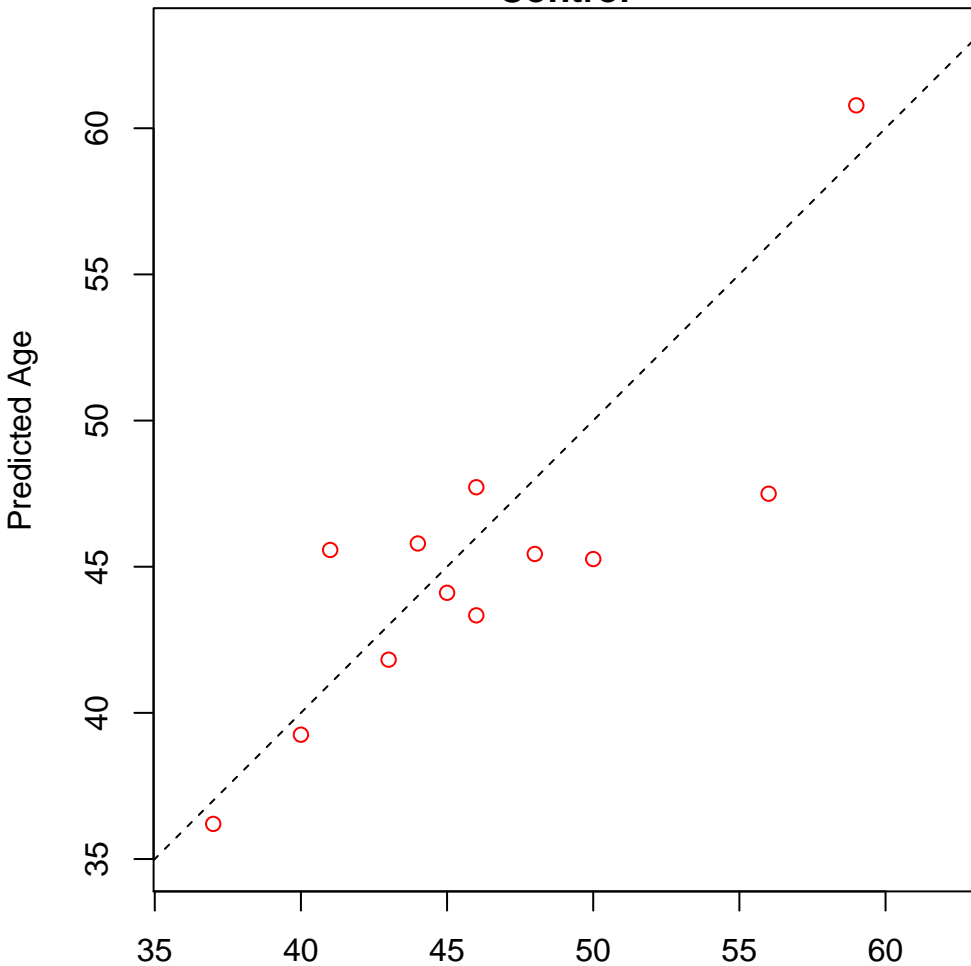


positive regulation of telomere maintenance (Score: 4.359853)

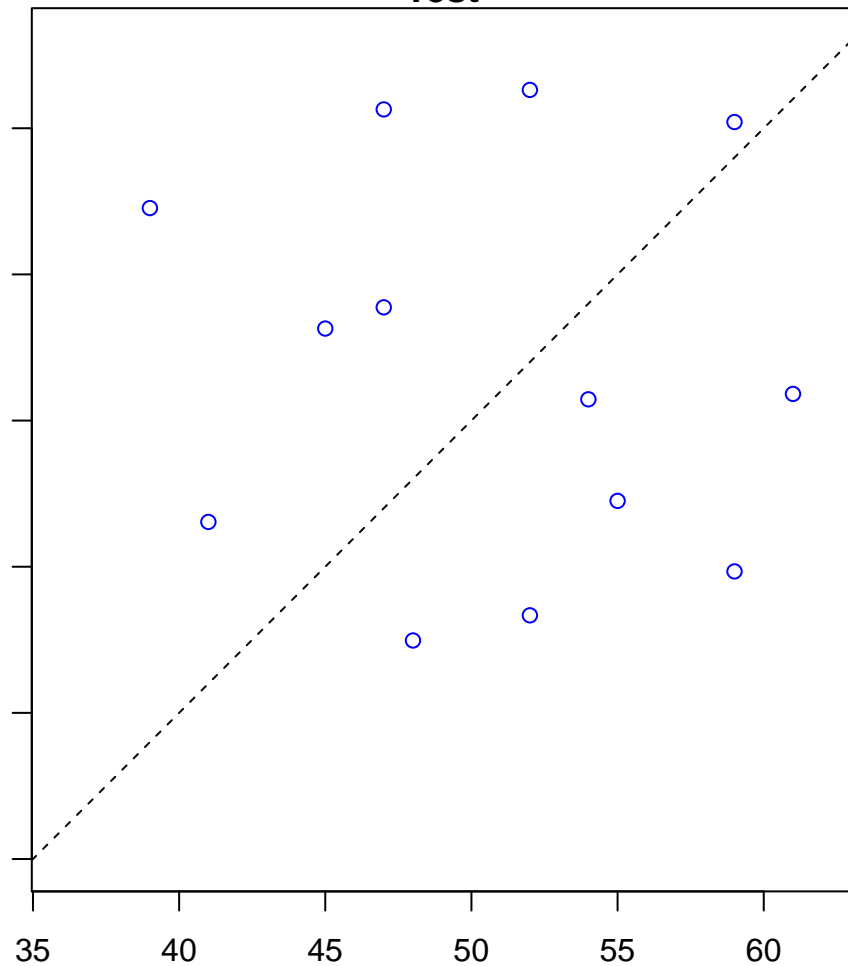


plasma lipoprotein particle assembly (Score: 4.354116)

Control

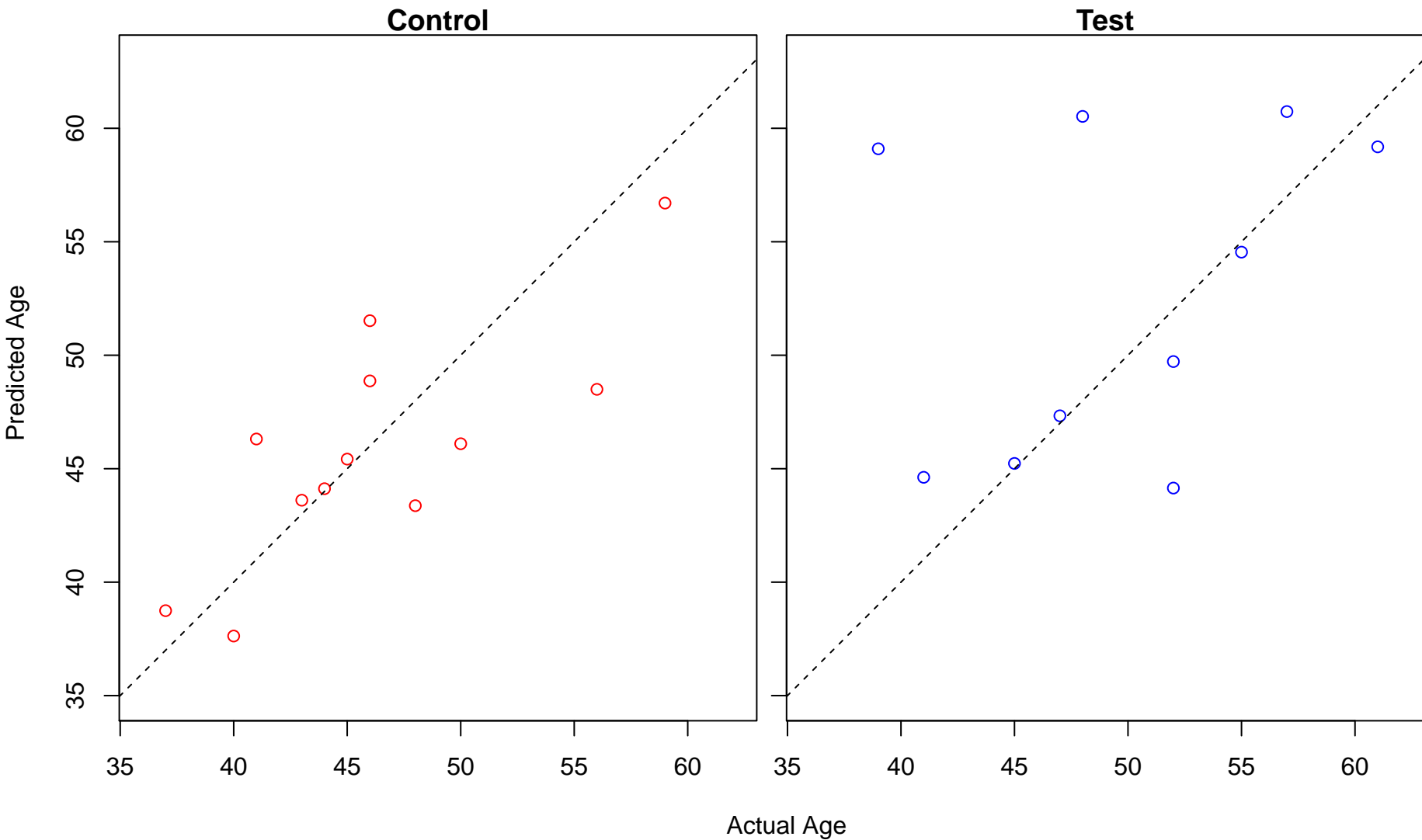


Test

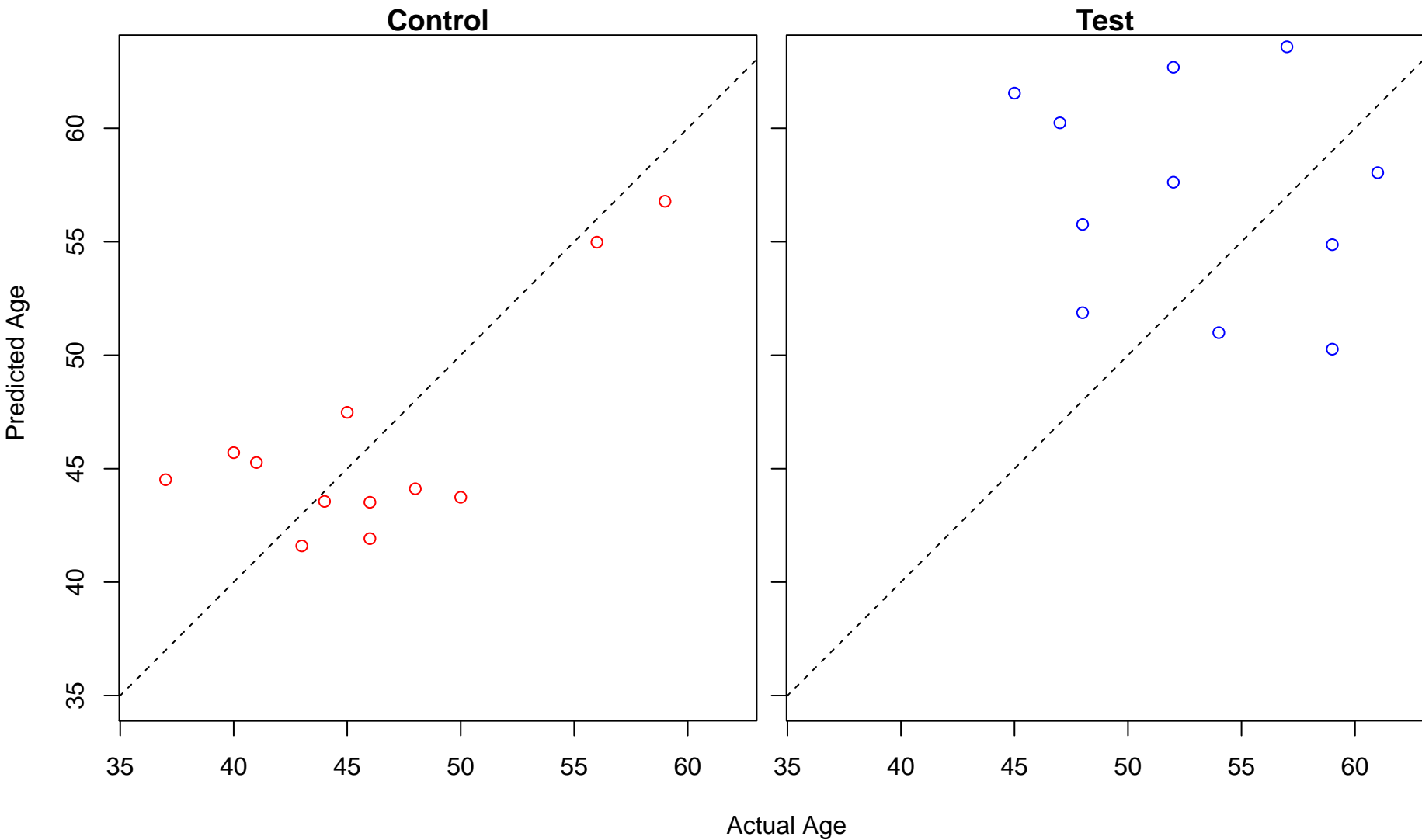


Actual Age

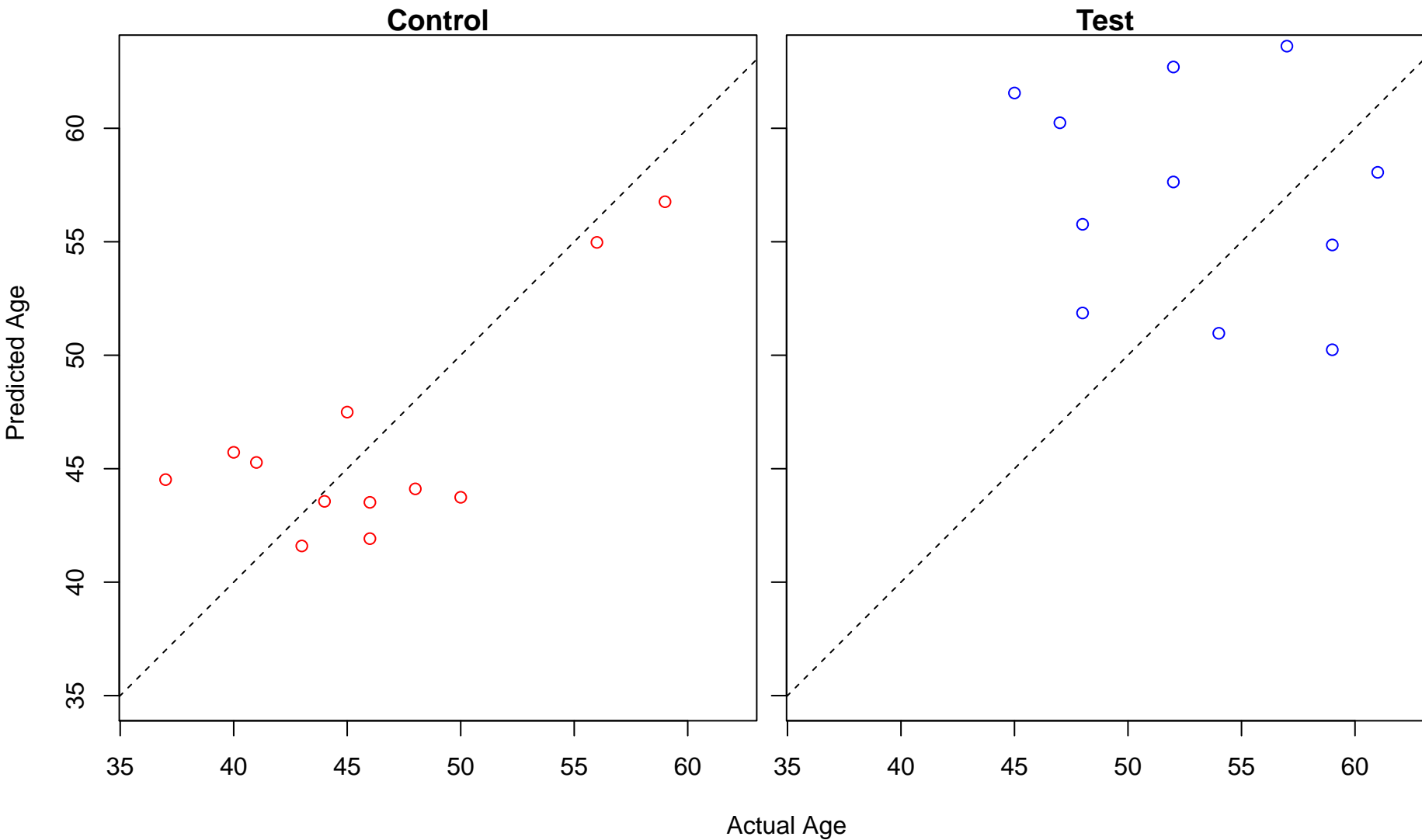
triglyceride-rich lipoprotein particle clearance (Score: 4.349976)



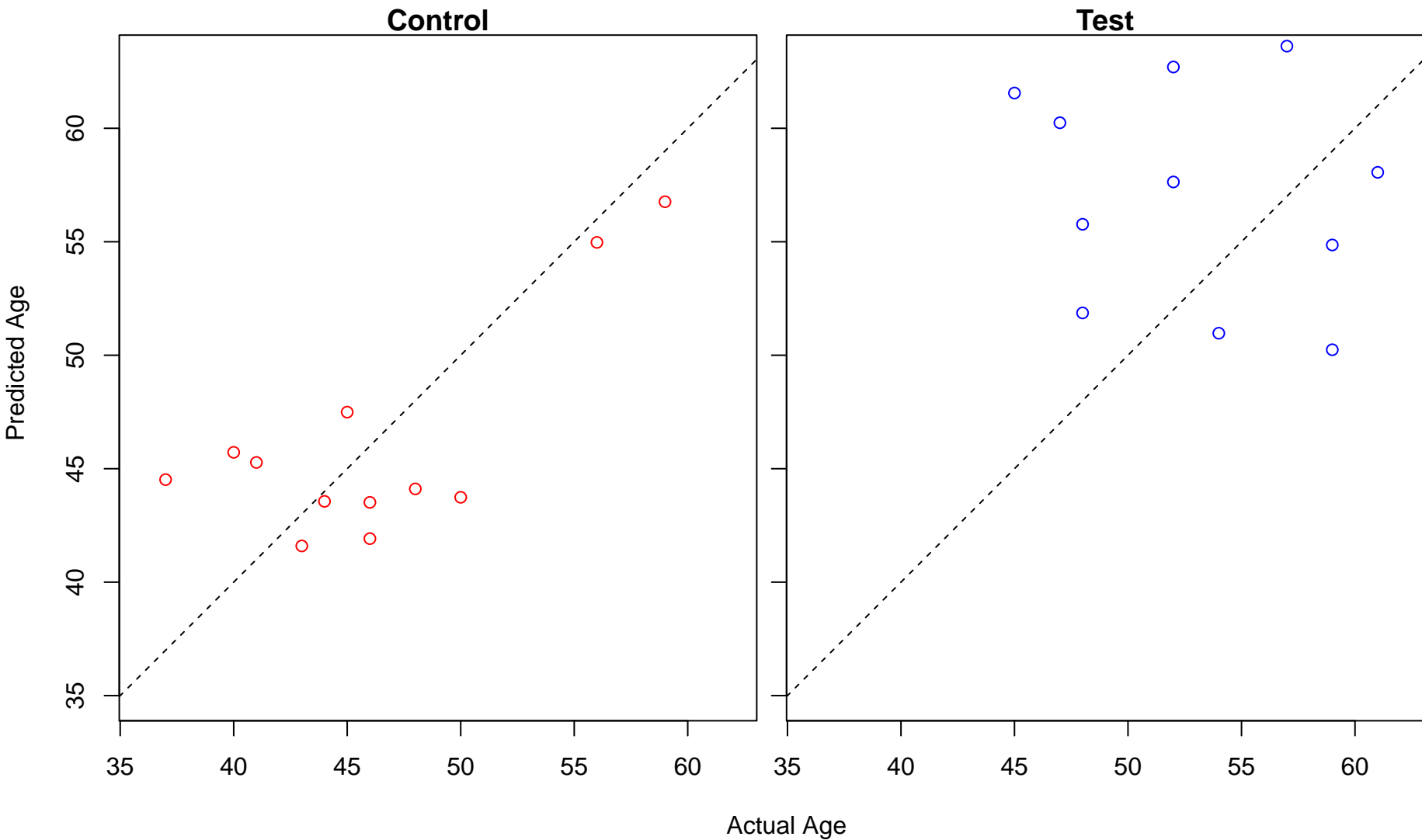
renal system process involved in regulation of systemic arterial blood pressure (Score: 4.348703)



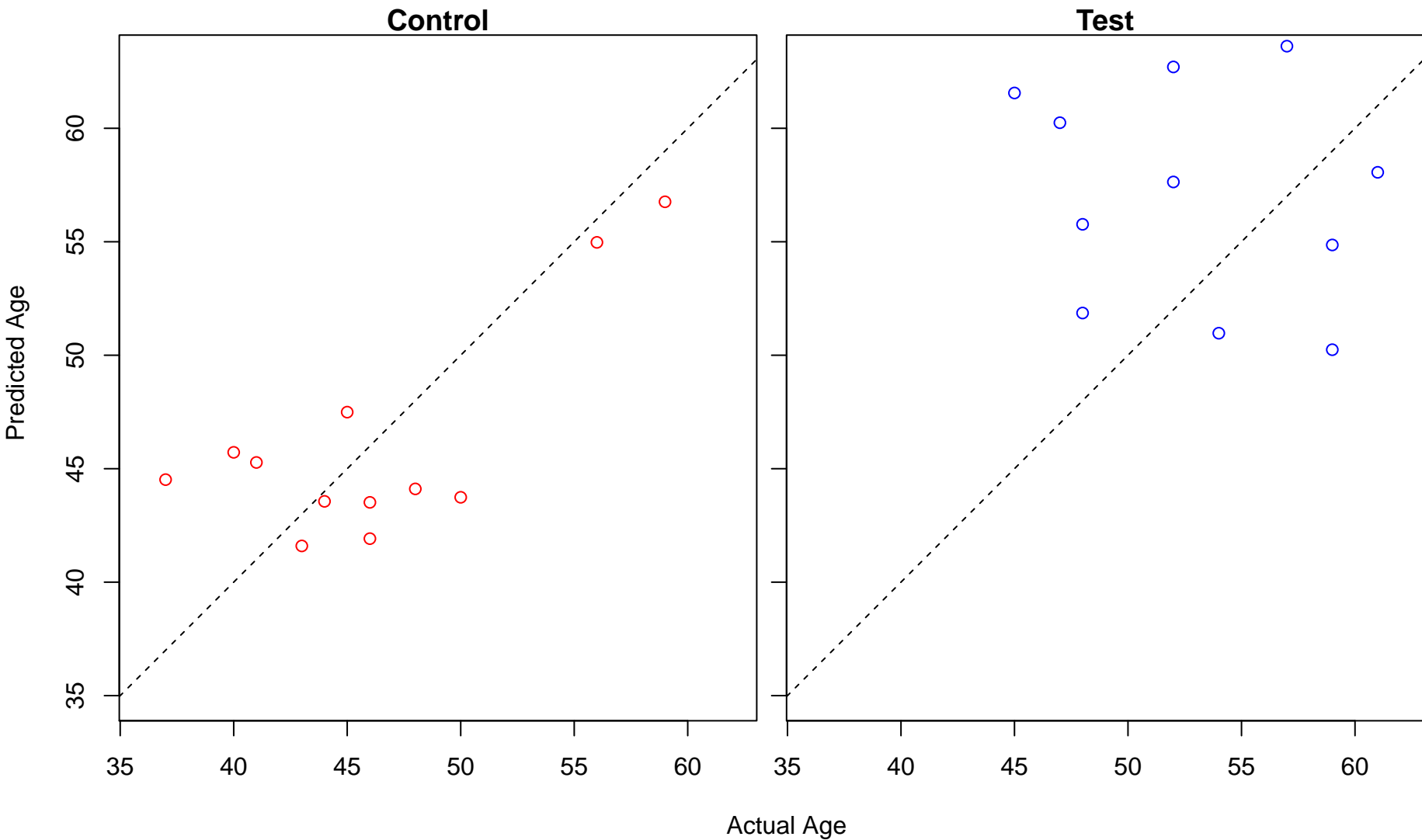
regulation of glomerular filtration (Score: 4.346414)



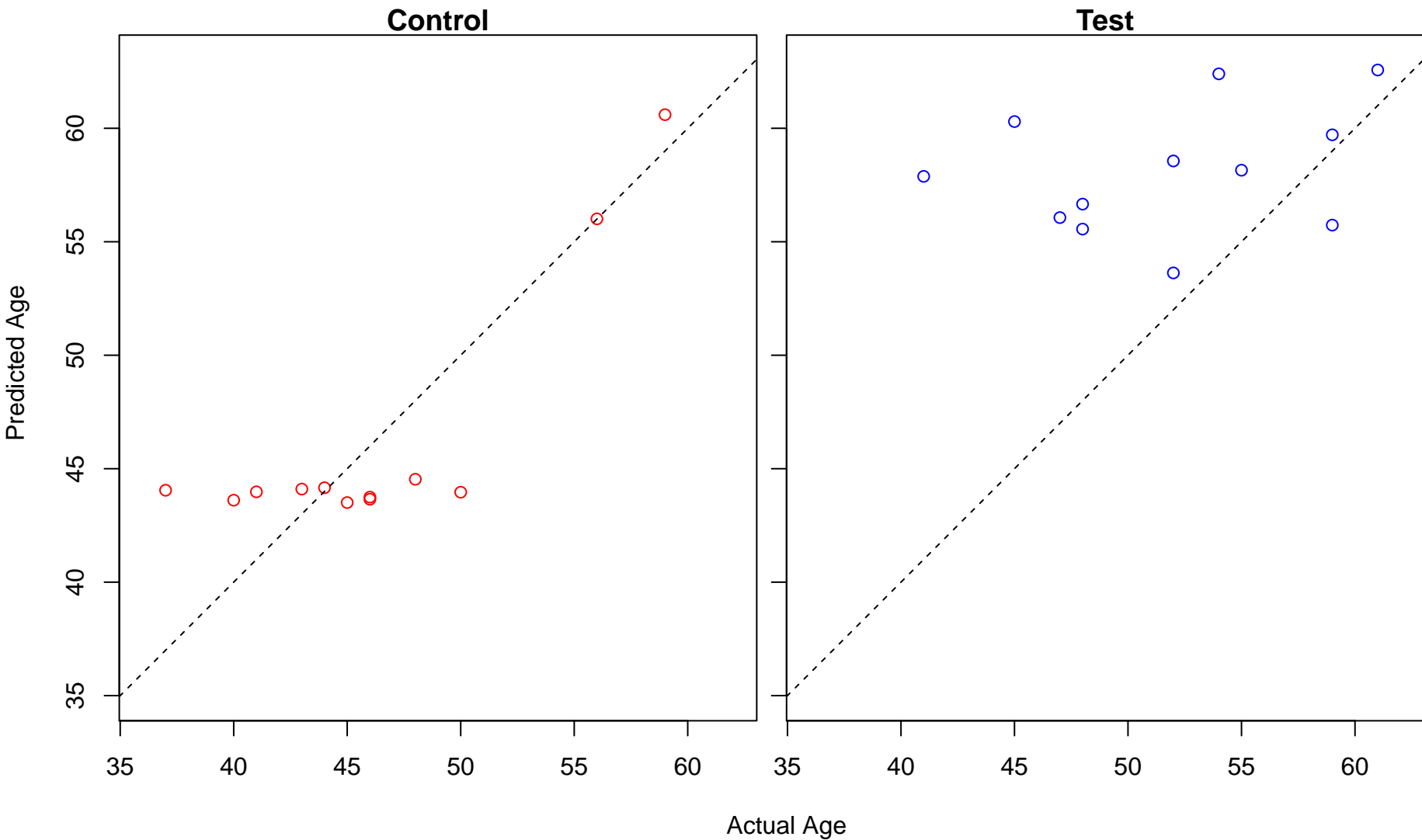
regulation of renal system process (Score: 4.346181)



renal system process involved in regulation of blood volume (Score: 4.345985)

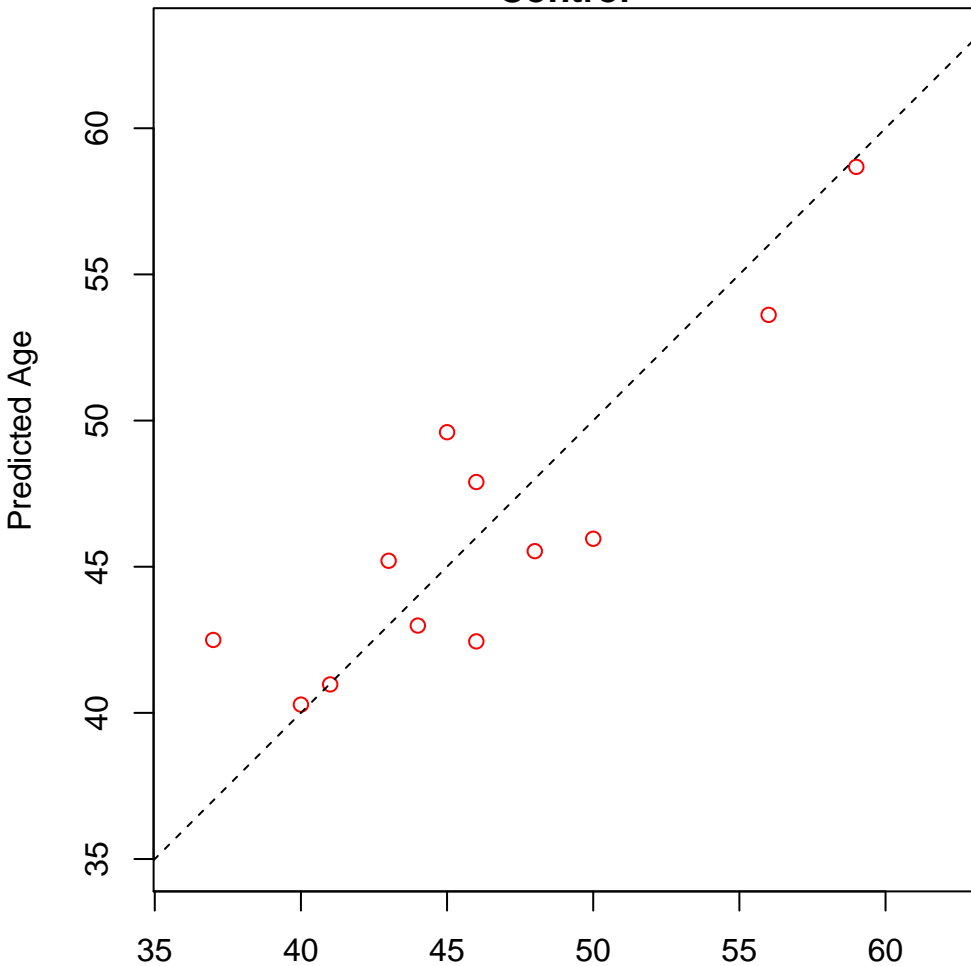


positive regulation of nuclease activity (Score: 4.342016)

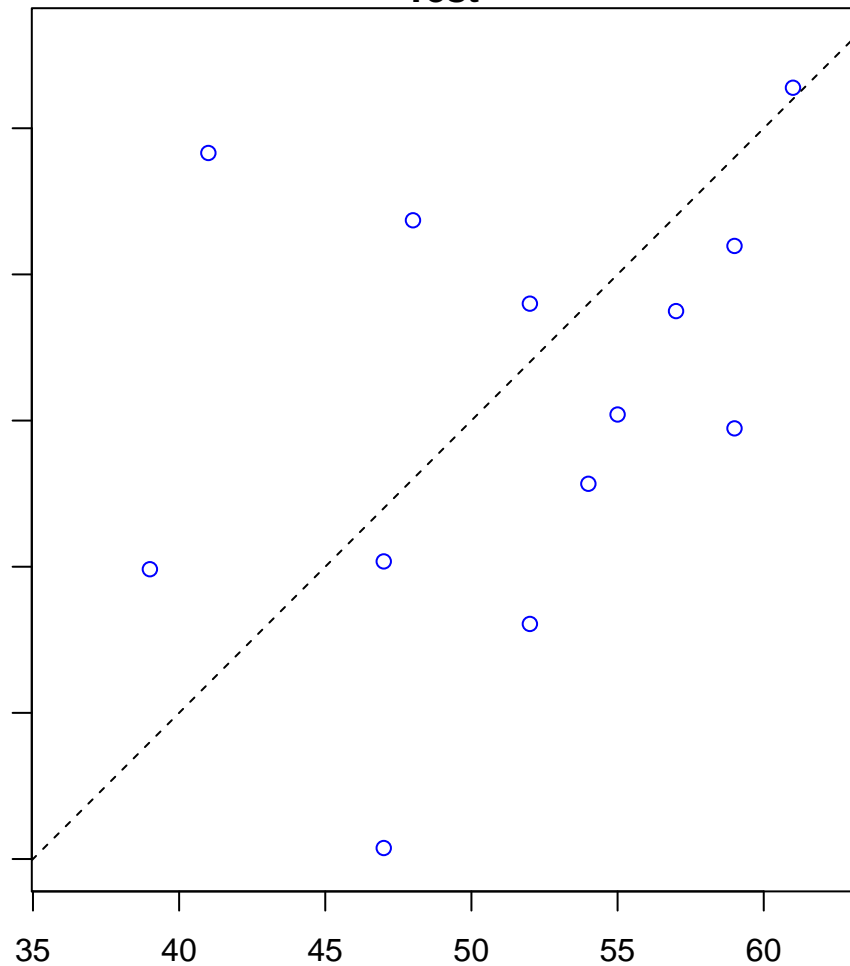


eye photoreceptor cell development (Score: 4.33550)

Control

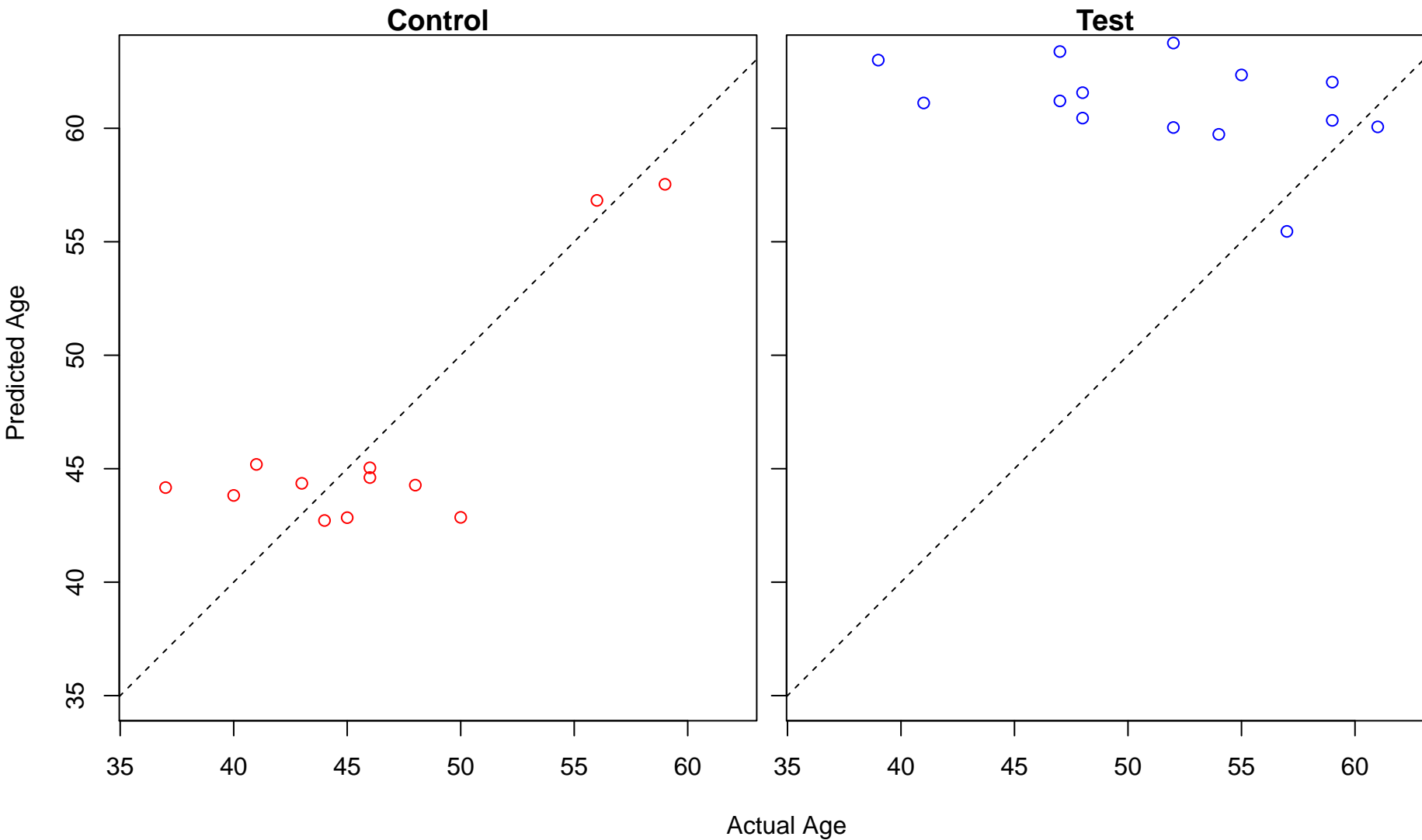


Test

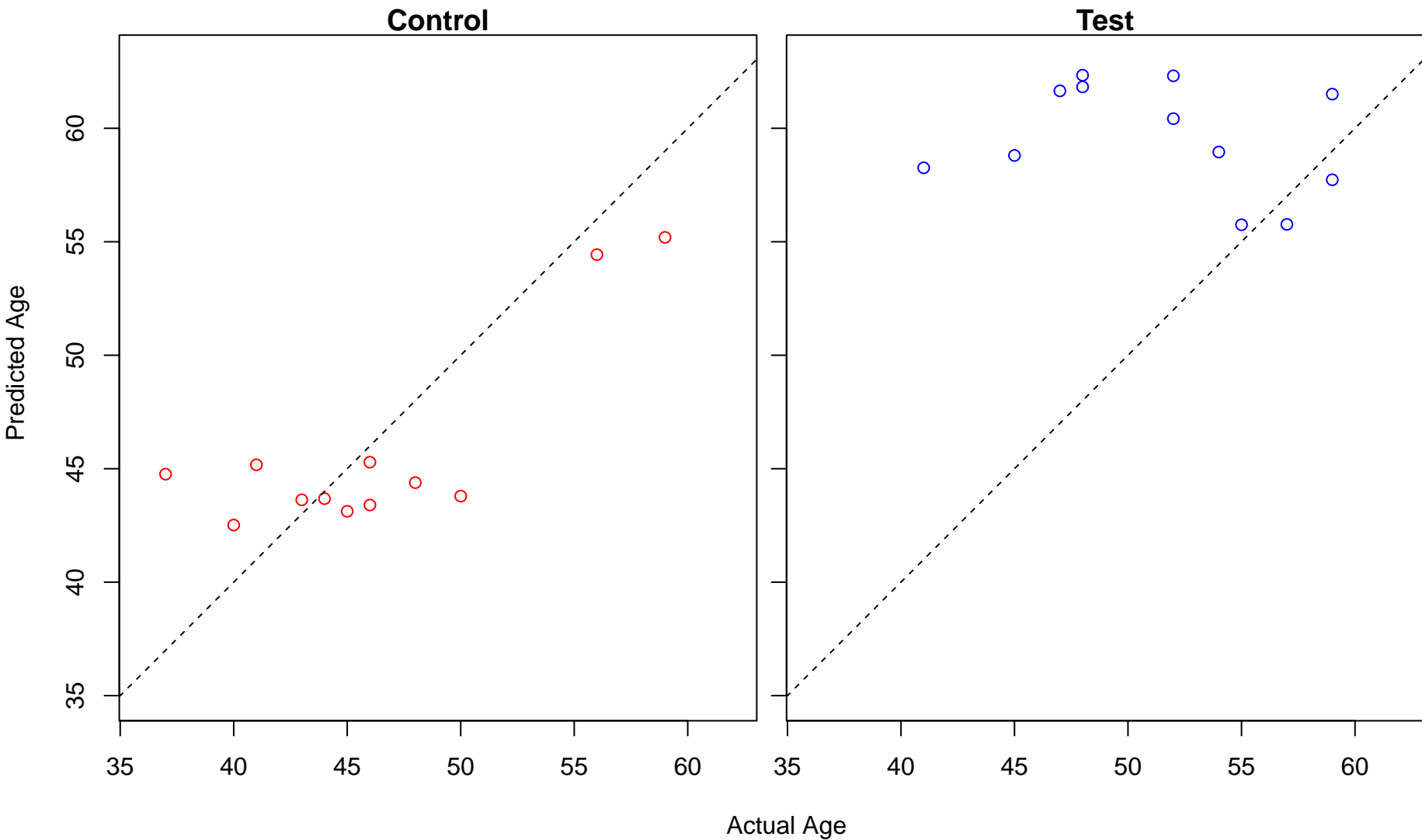


Actual Age

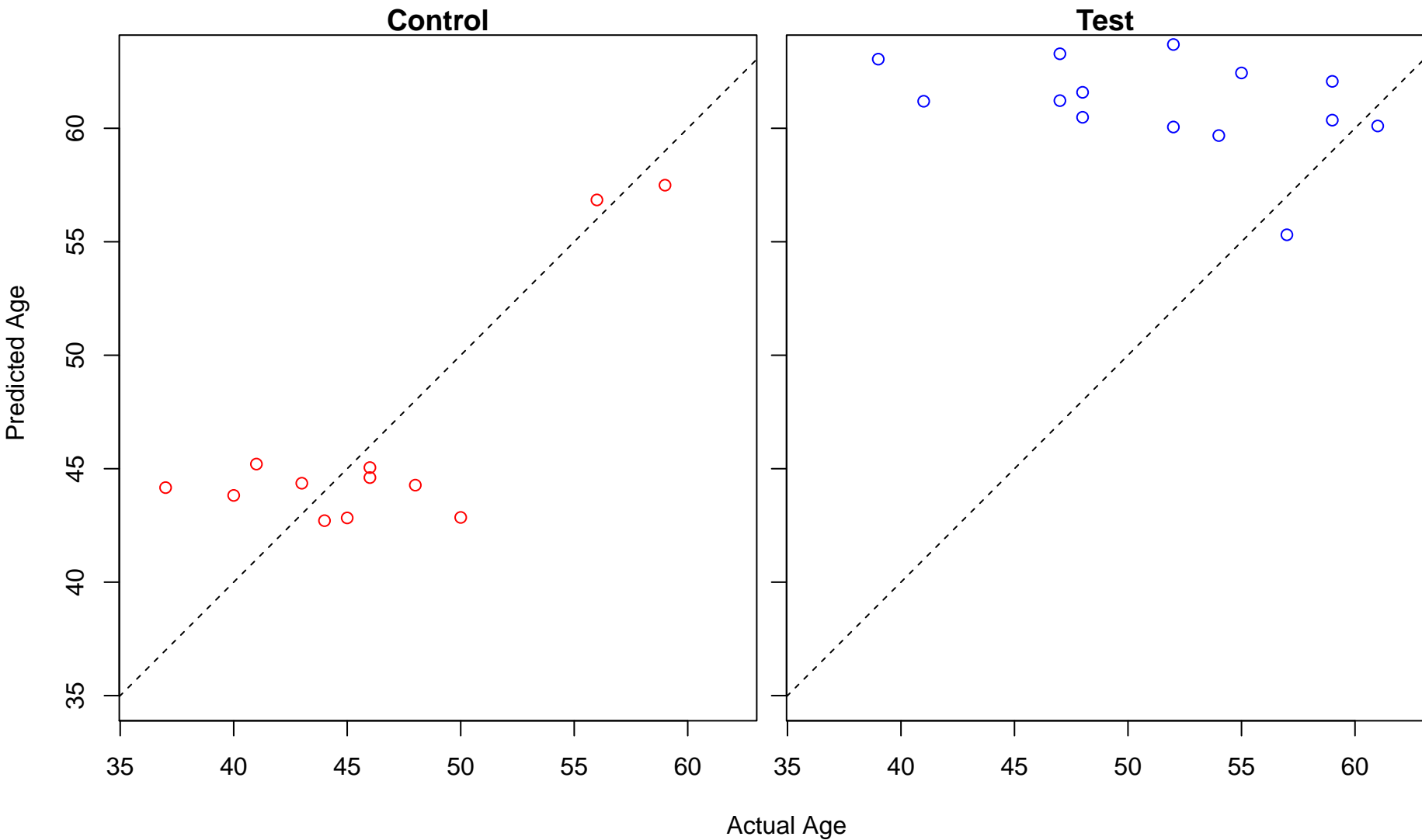
small RNA loading onto RISC (Score: 4.333386)



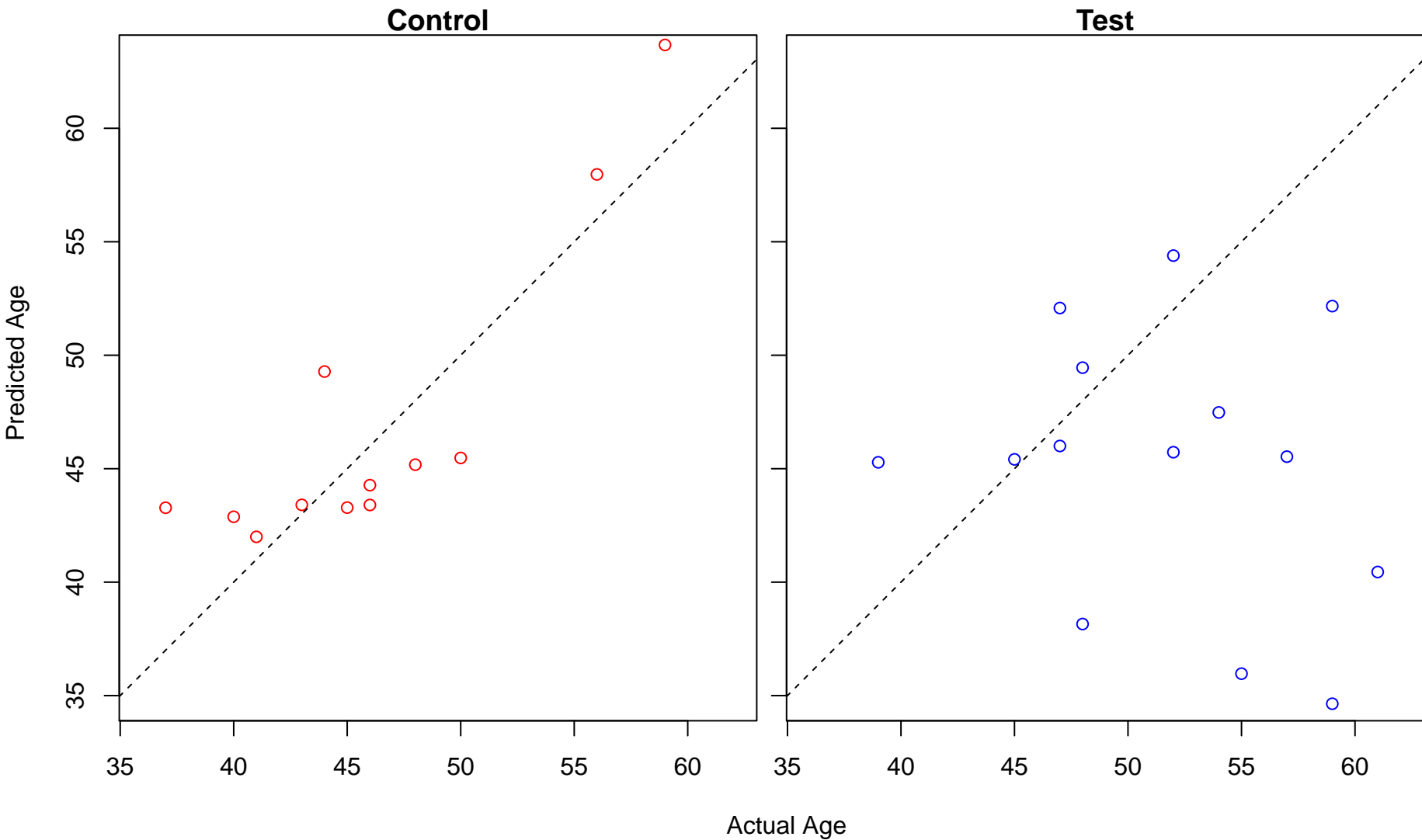
sympathetic ganglion development (Score: 4.333064)



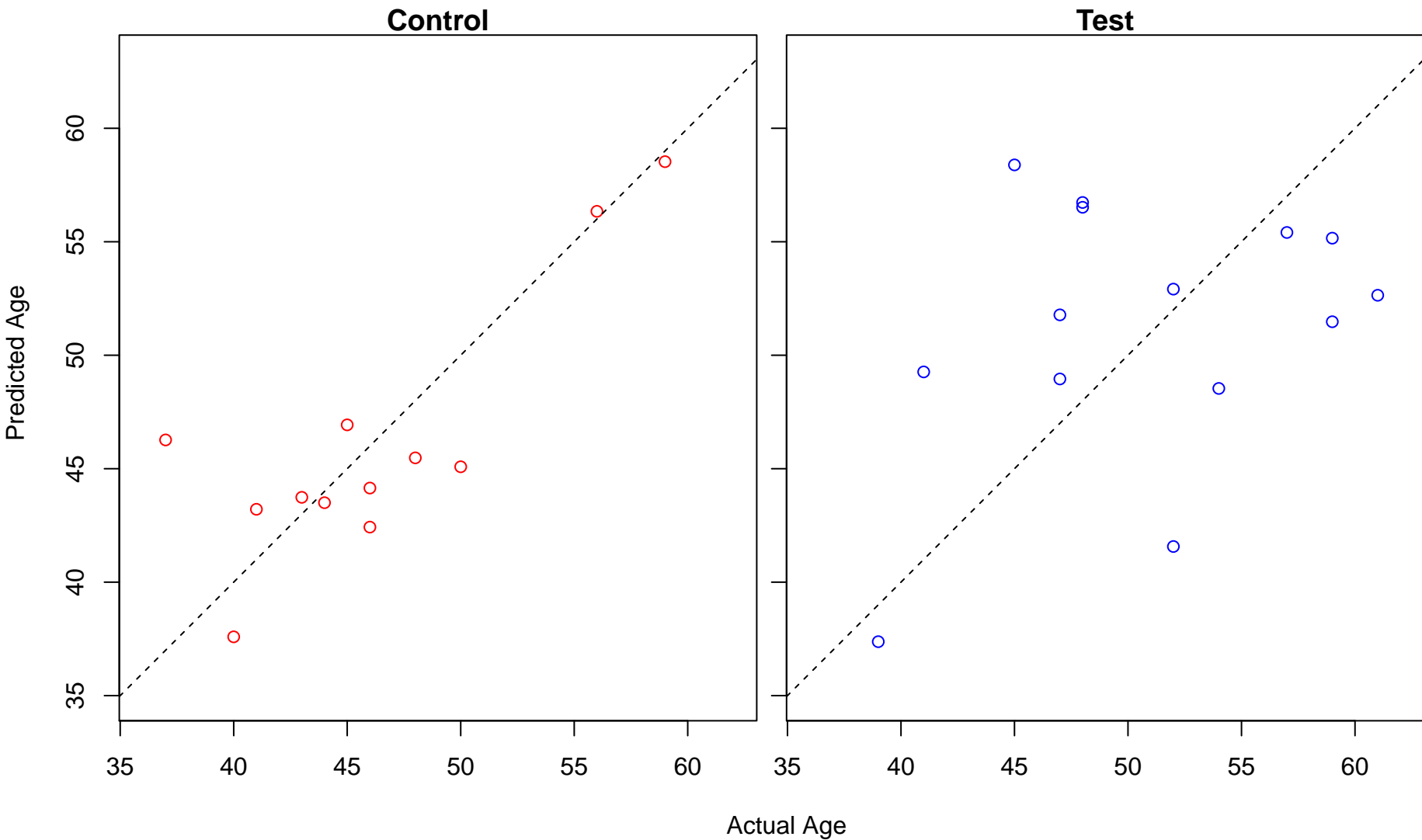
miRNA loading onto RISC involved in gene silencing by miRNA (Score: 4.331838)



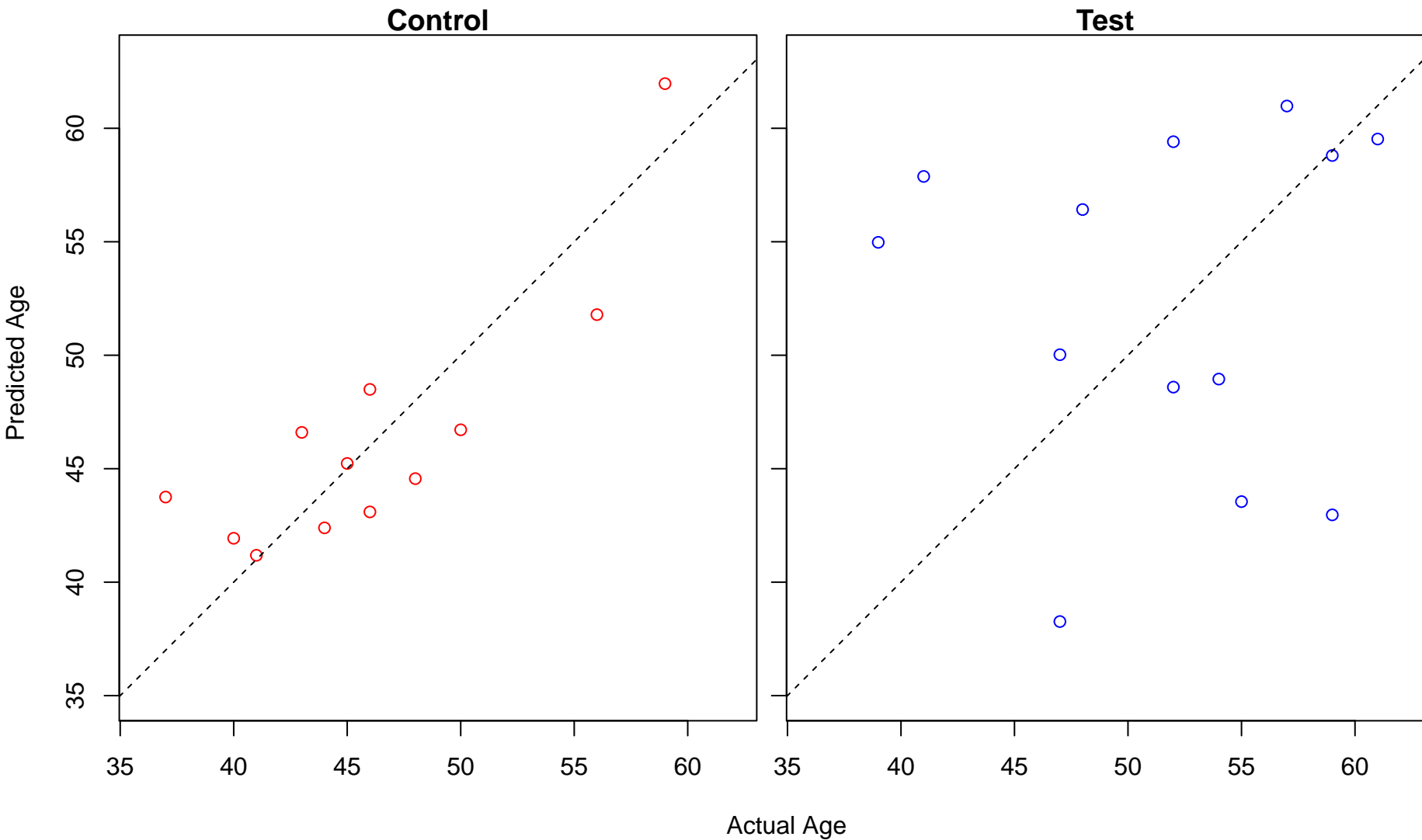
dendrite morphogenesis (Score: 4.331816)



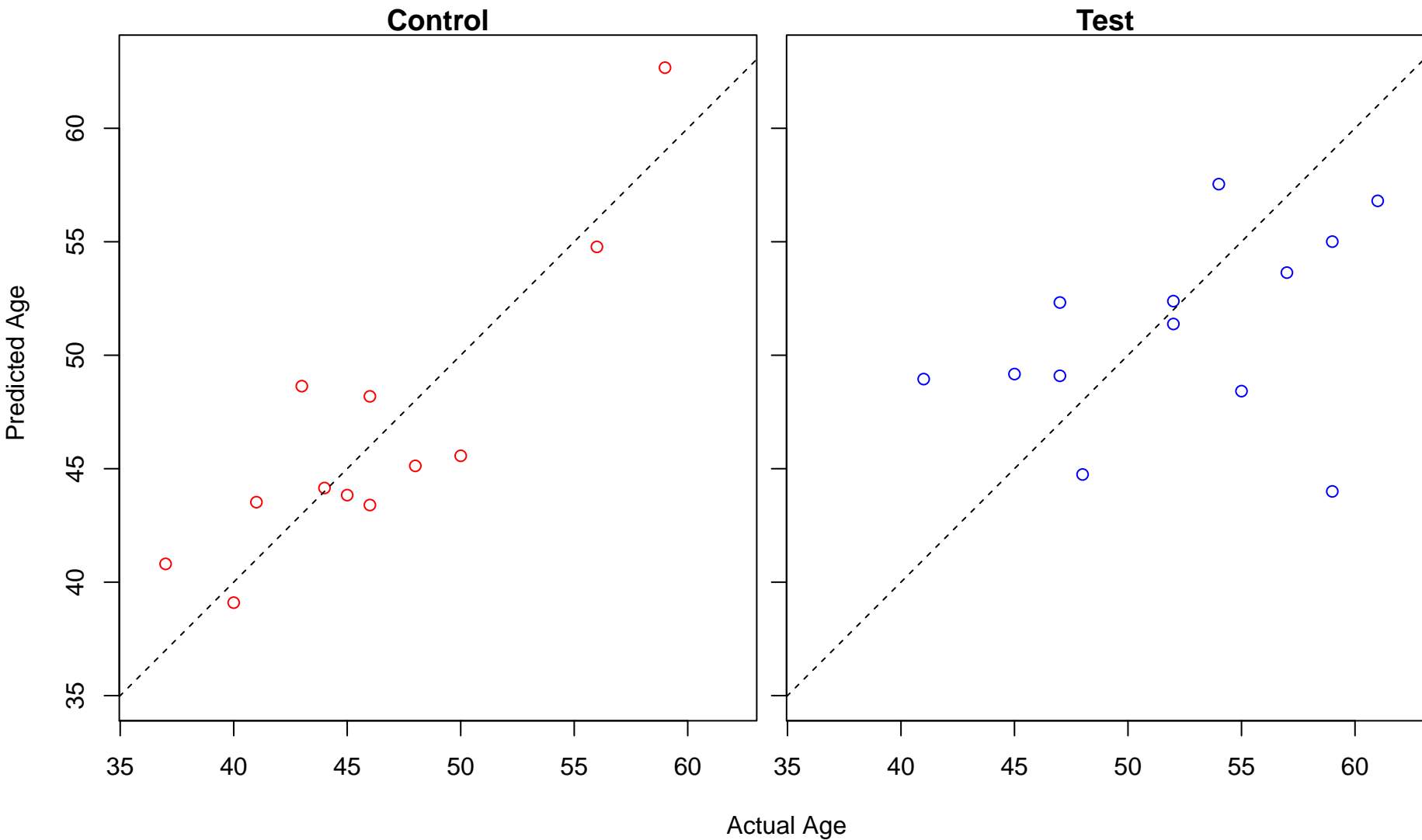
positive regulation of protein exit from endoplasmic reticulum (Score: 4.327262)



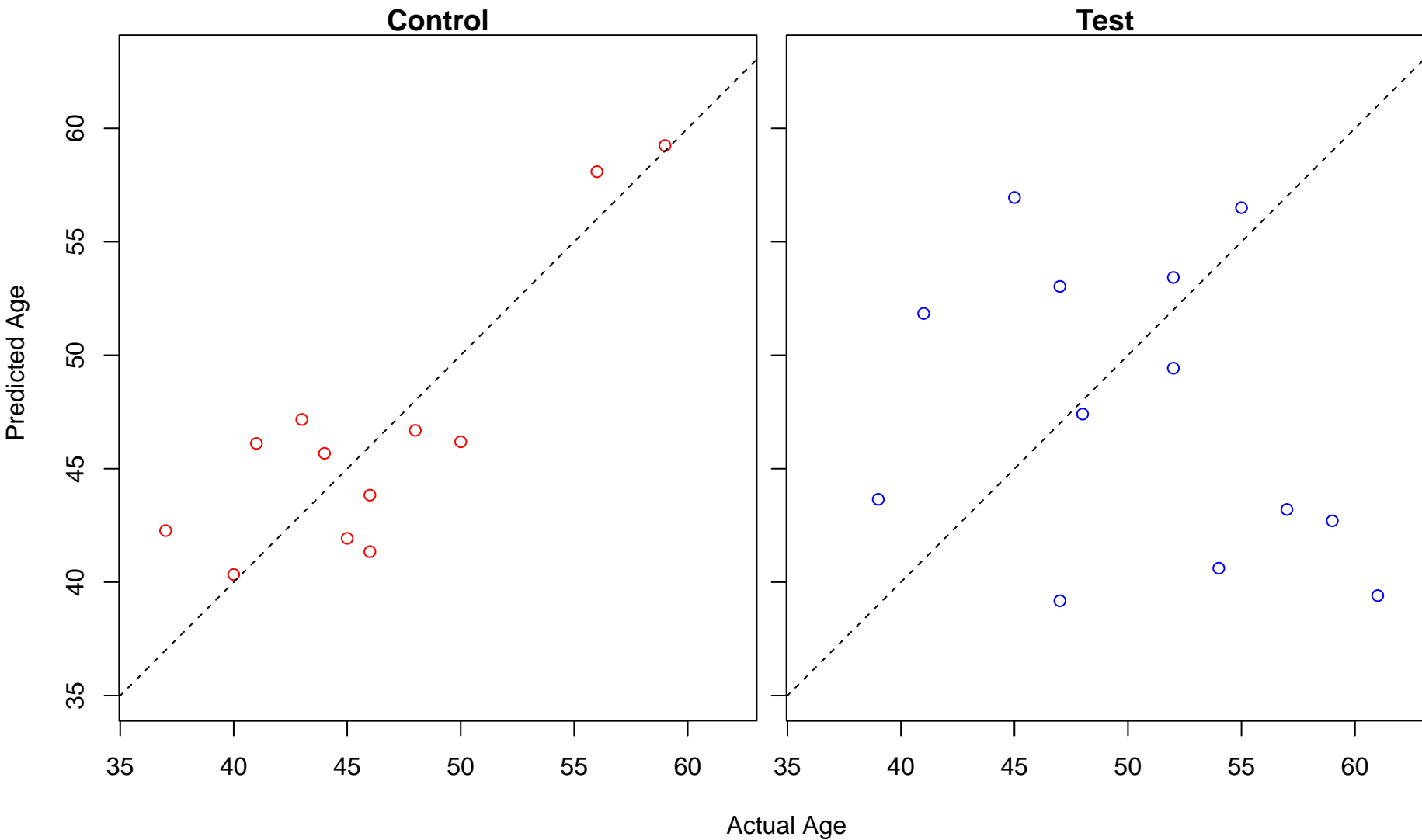
artery development (Score: 4.325879)



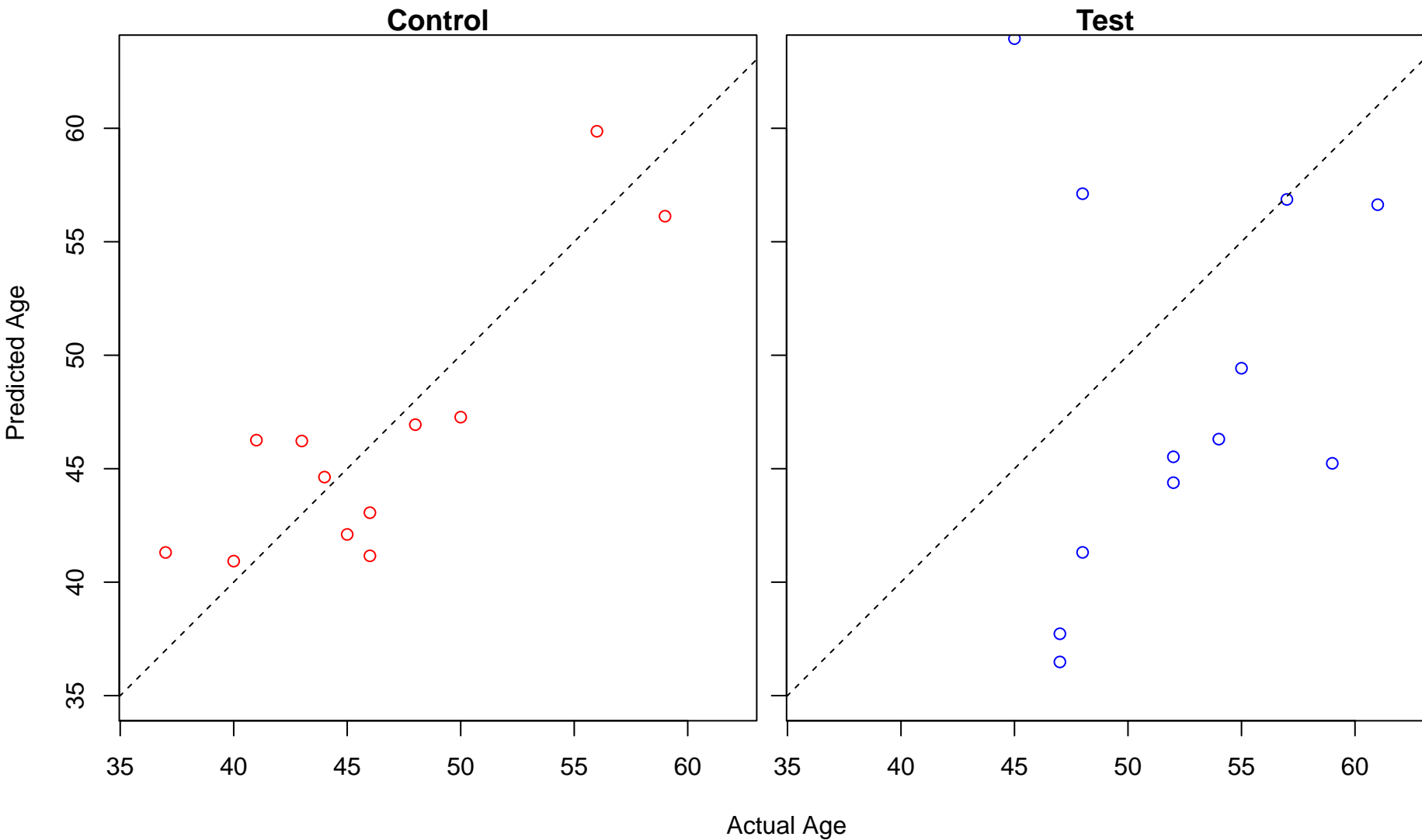
negative regulation of endothelial cell migration (Score: 4.325813)



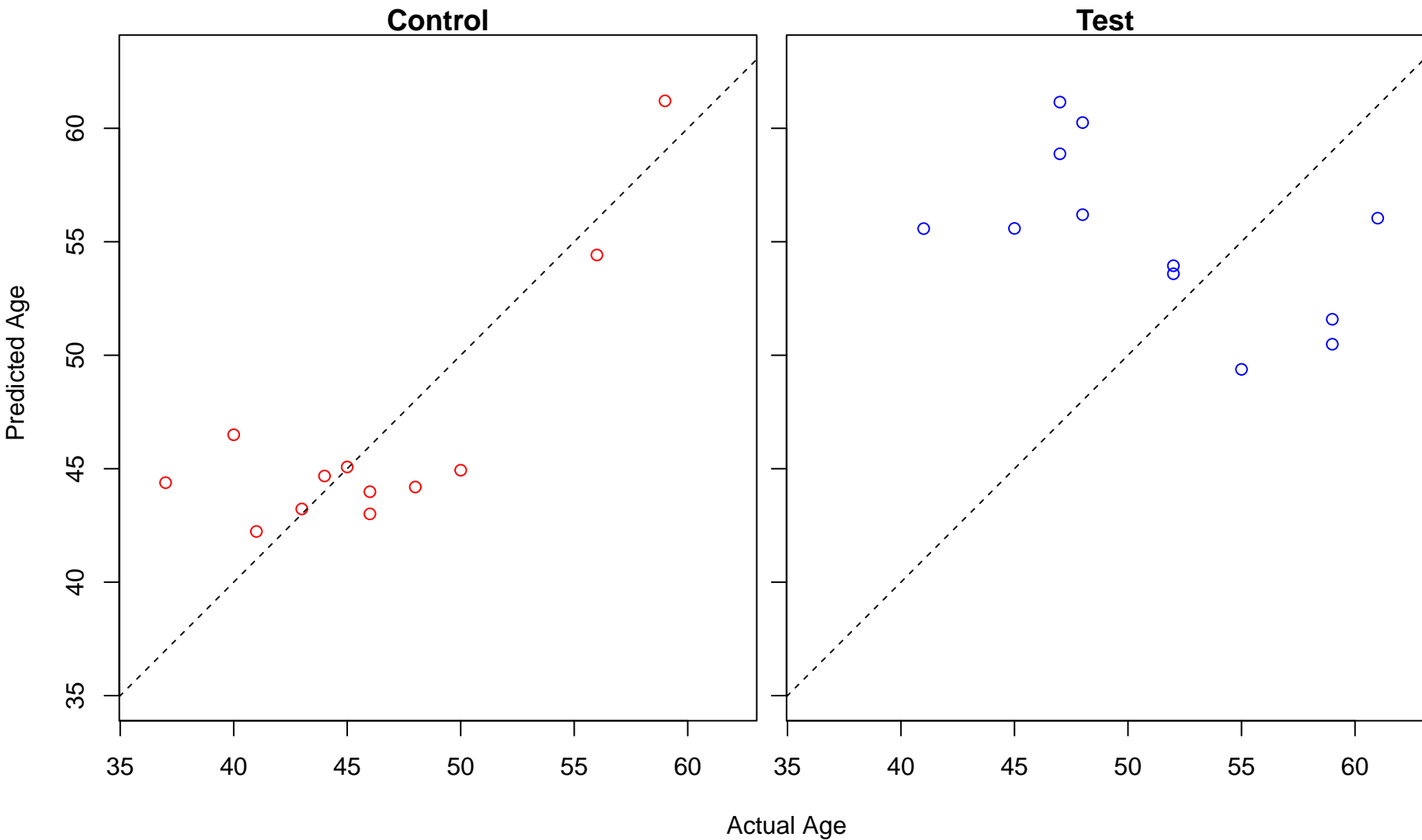
Arp2/3 complex-mediated actin nucleation (Score: 4.323402)



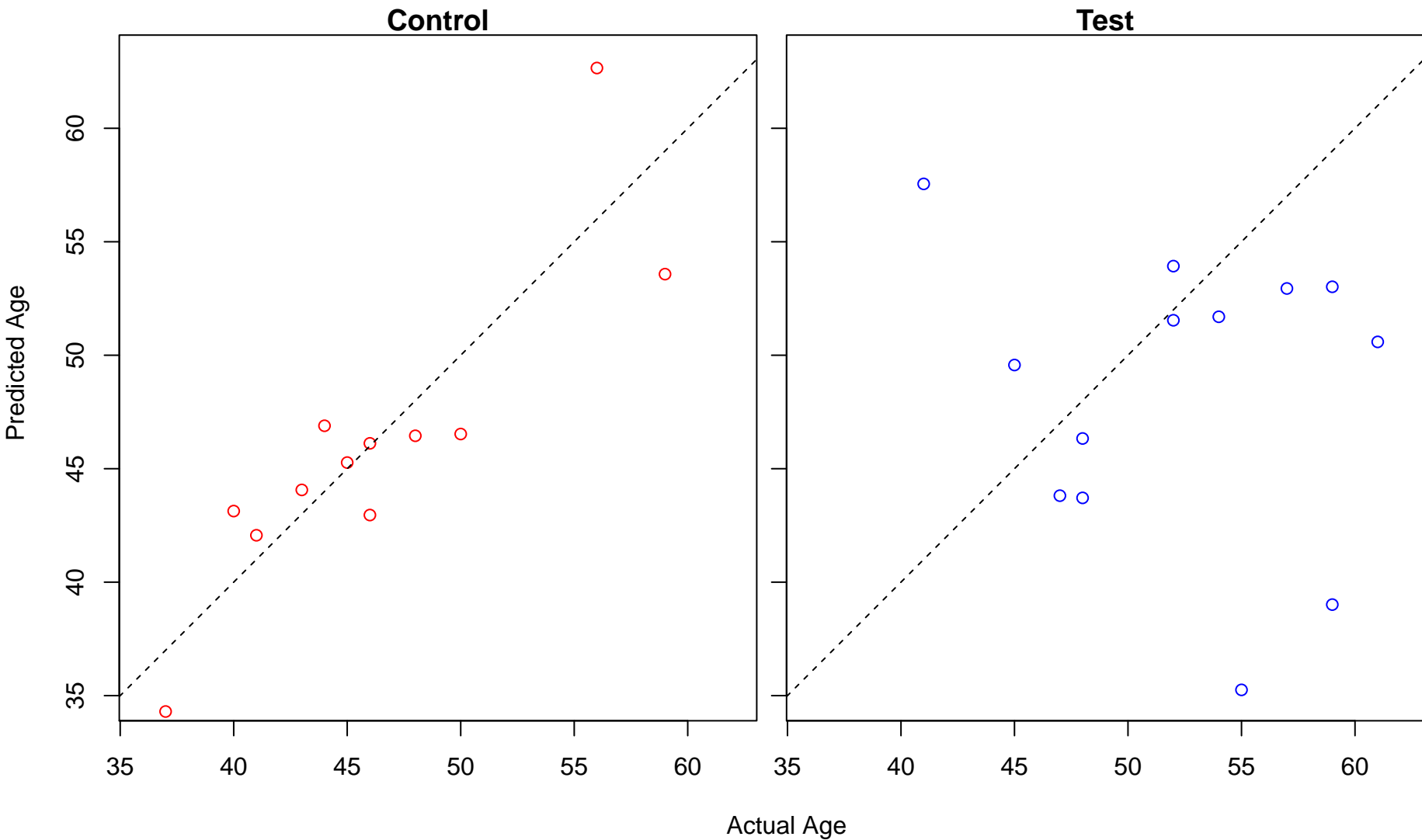
monocarboxylic acid biosynthetic process (Score: 4.321062)



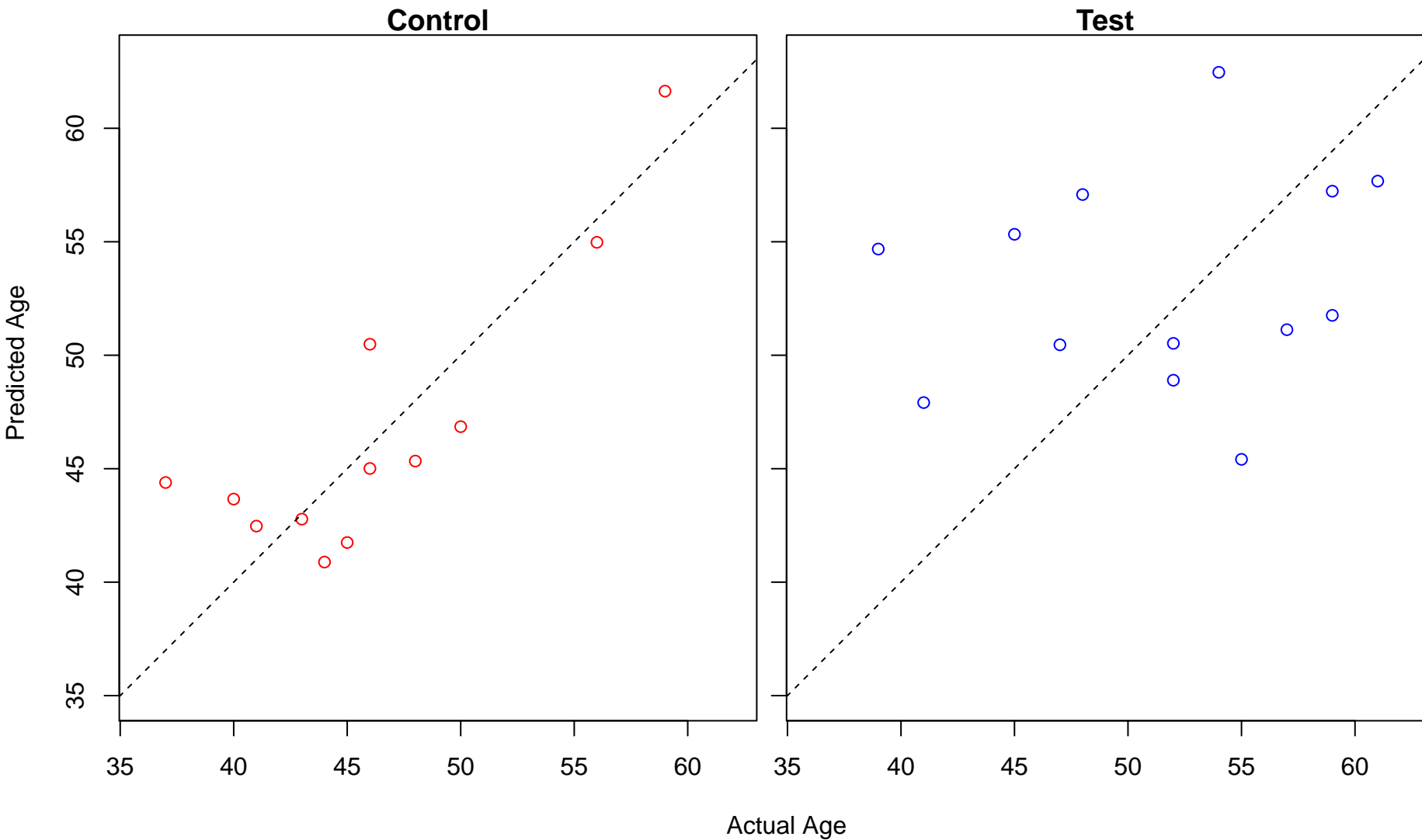
sulfur compound transport (Score: 4.320962)



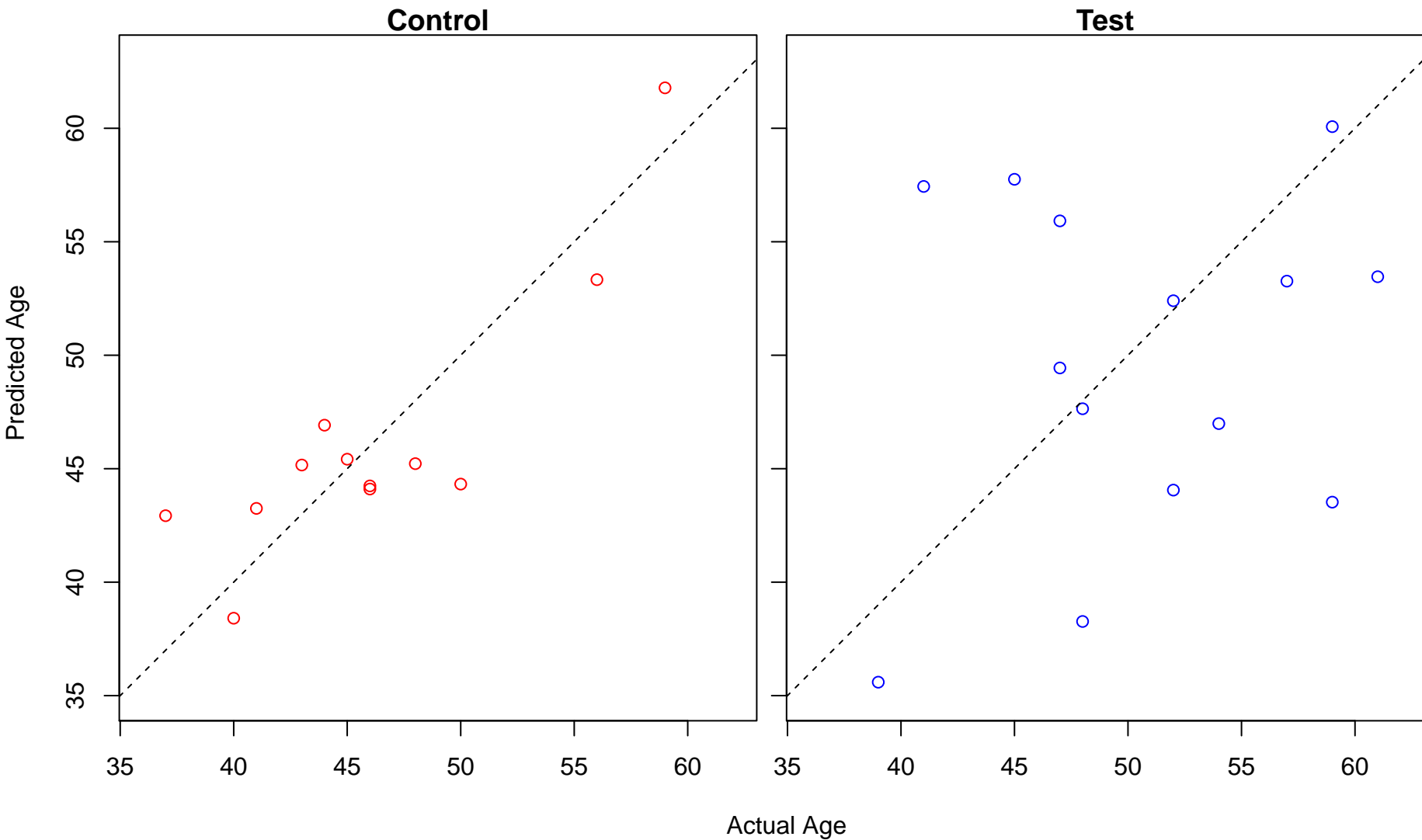
positive regulation of mesenchymal cell proliferation (Score: 4.320916)



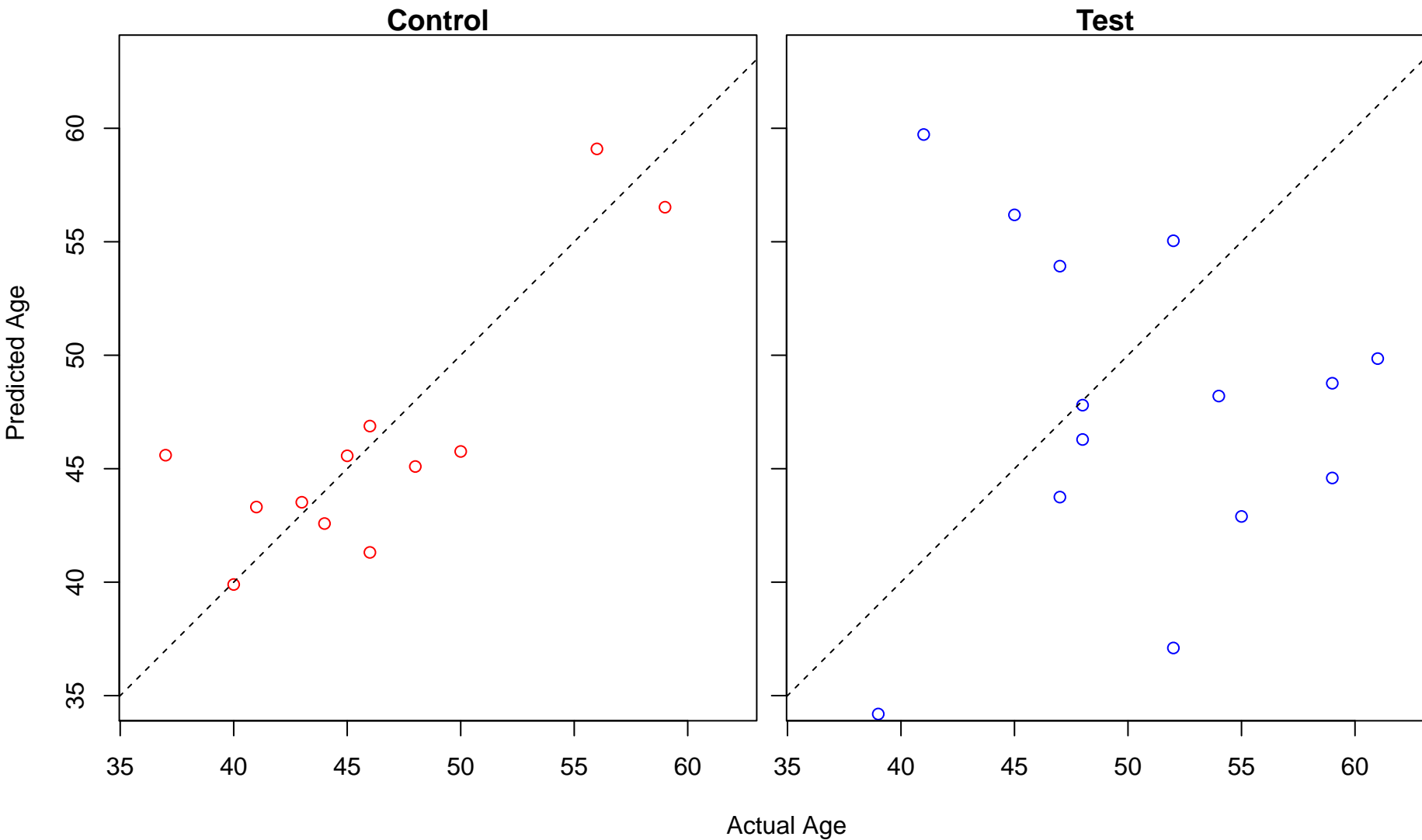
muscle cell proliferation (Score: 4.320419)



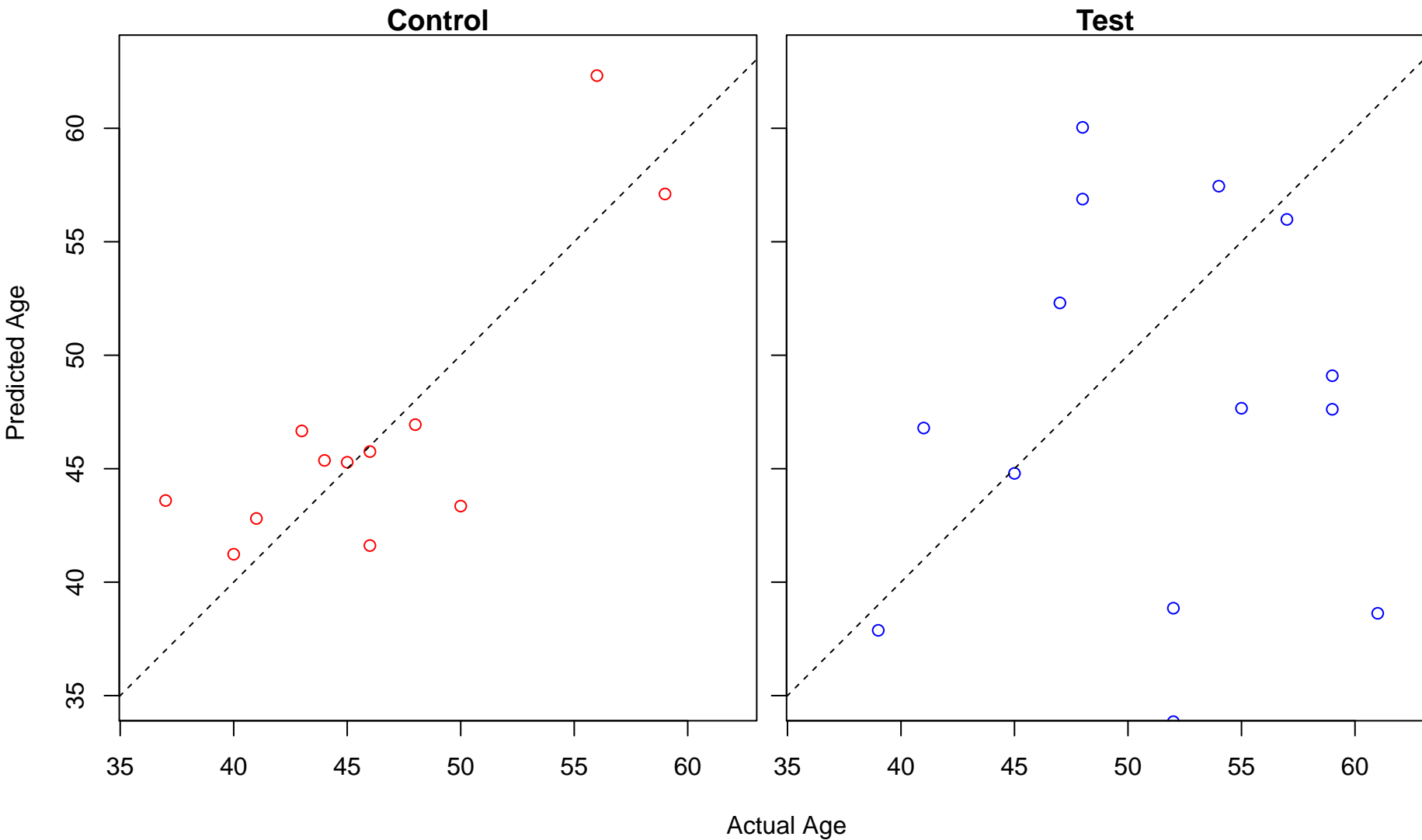
regulation of viral entry into host cell (Score: 4.320294)



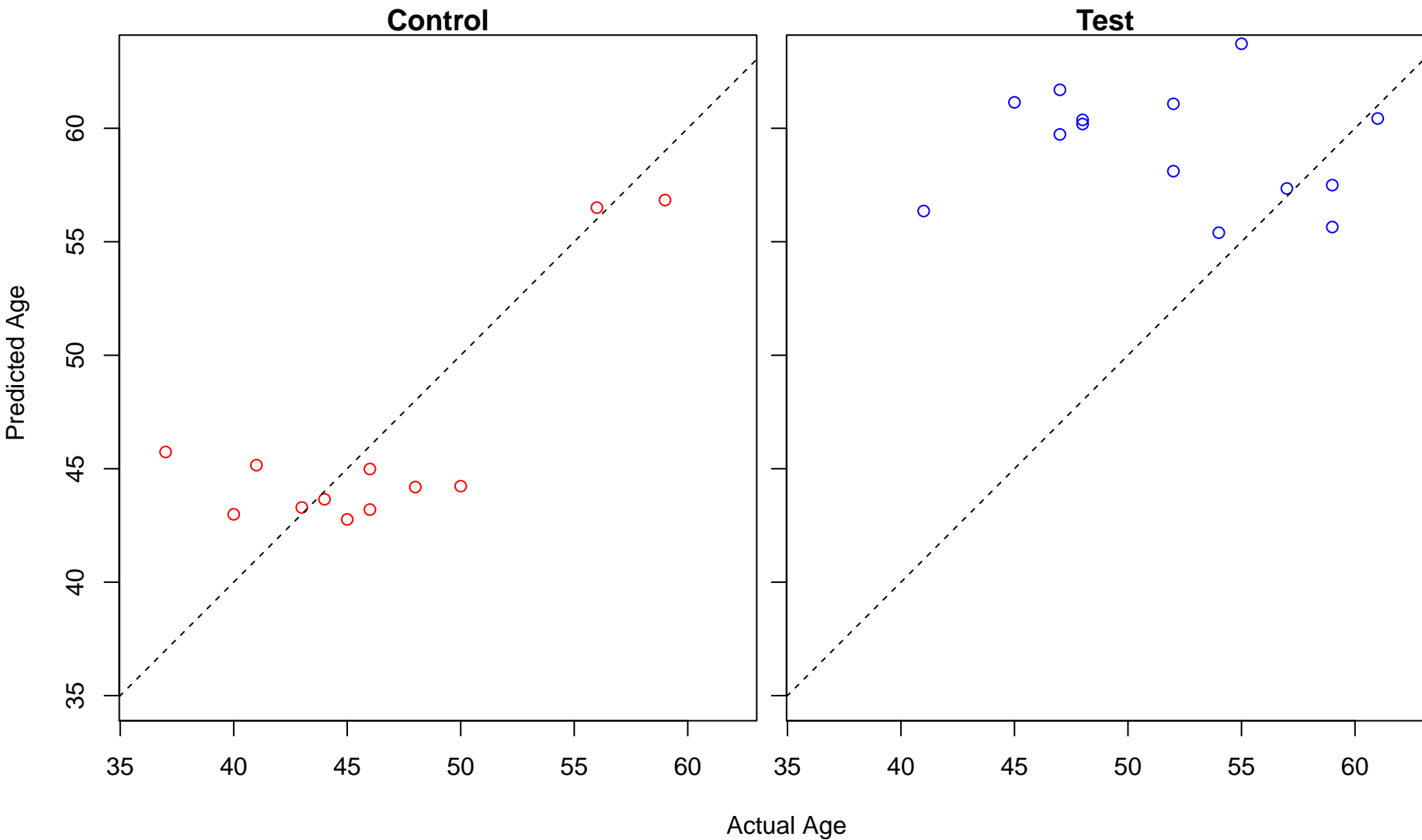
cellular copper ion homeostasis (Score: 4.319256)



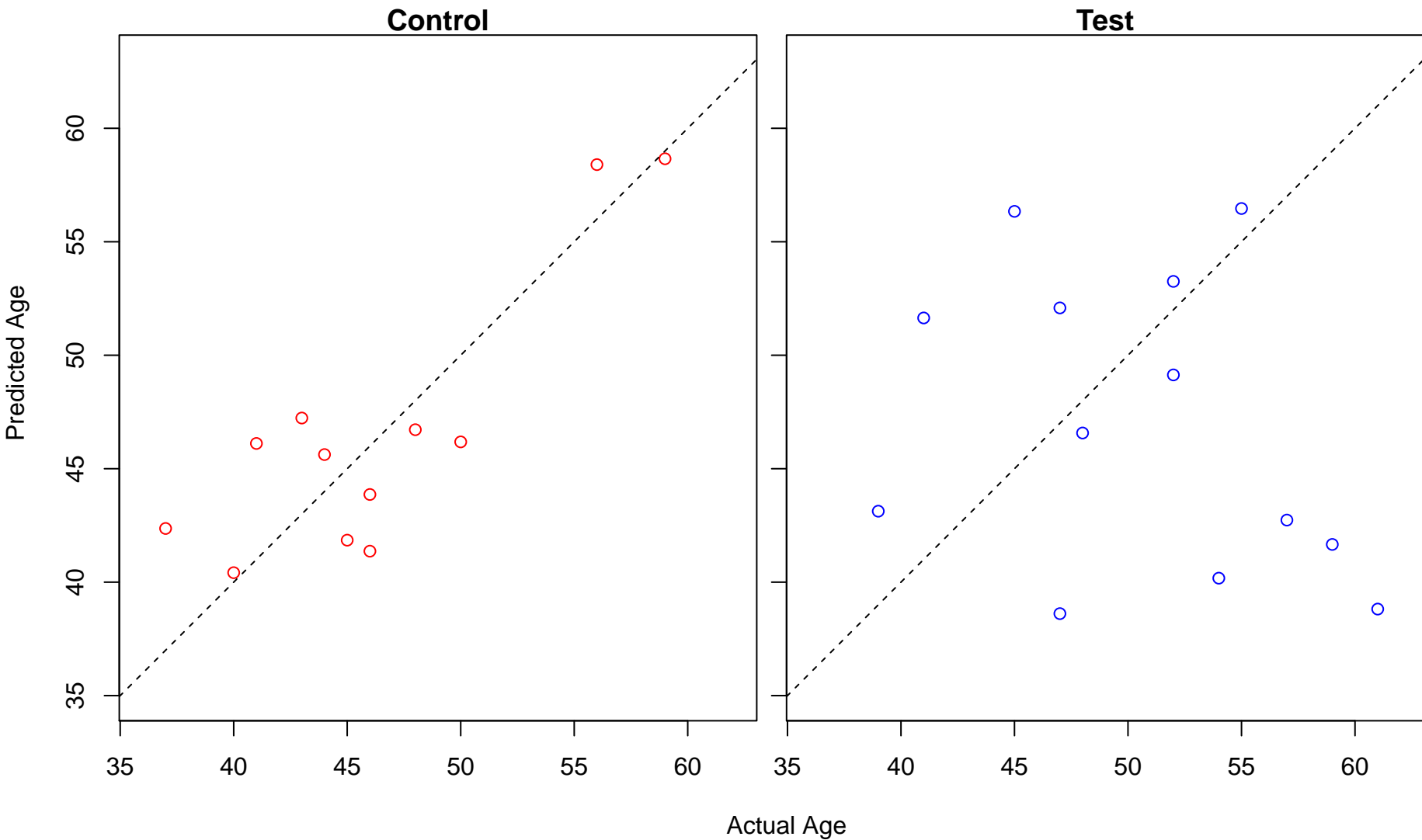
behavior (Score: 4.312771)



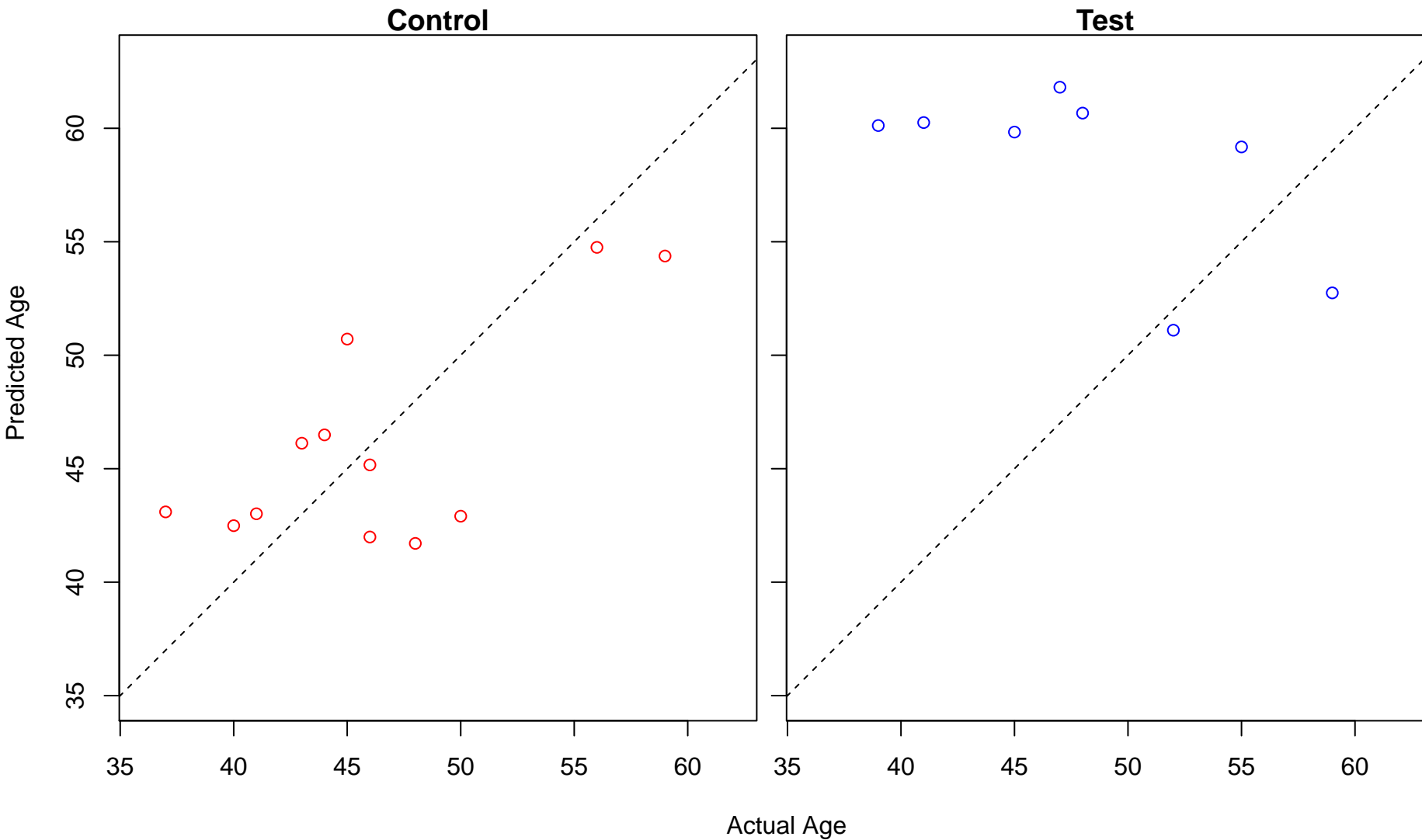
ventricular system development (Score: 4.310401)



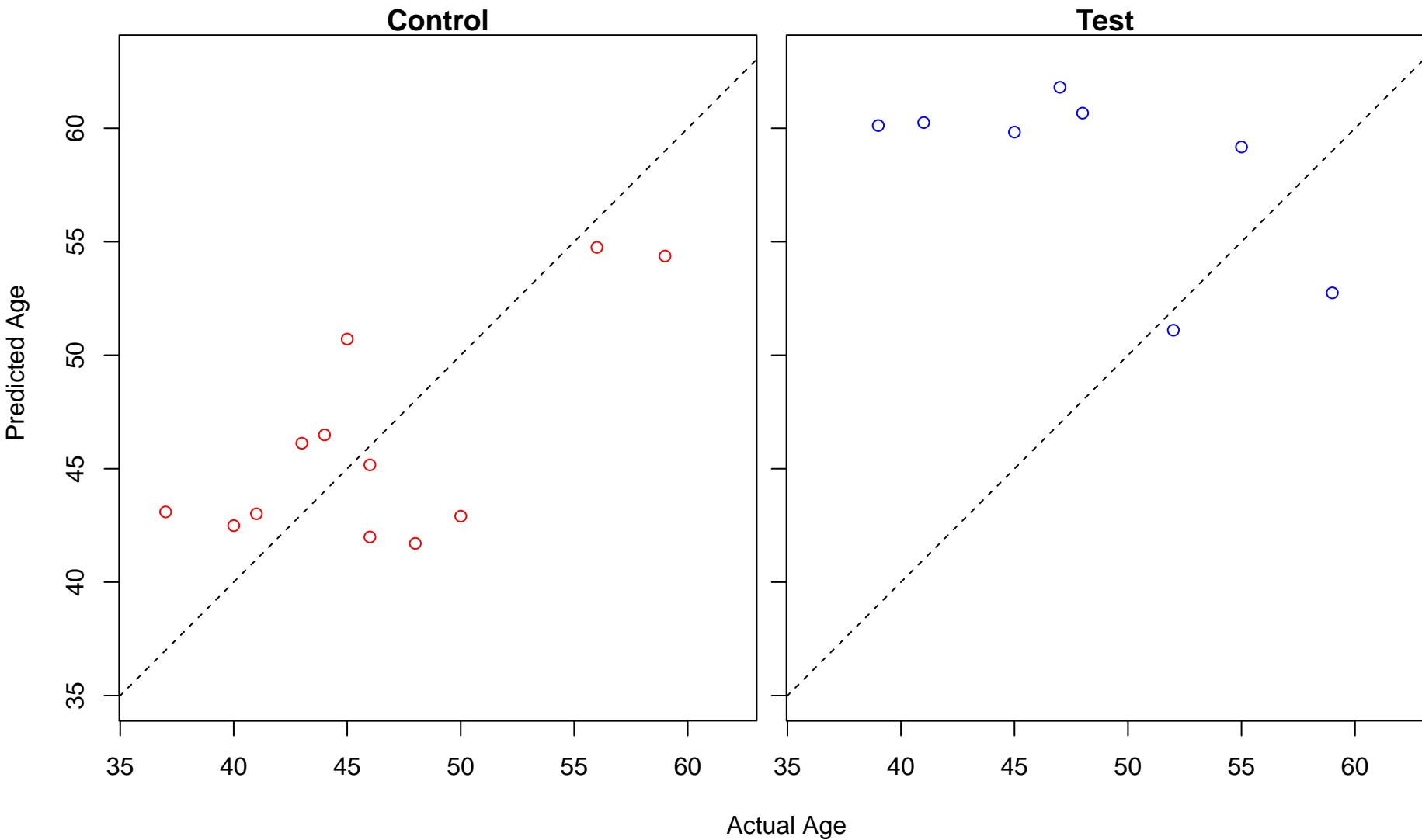
actin nucleation (Score: 4.309519)



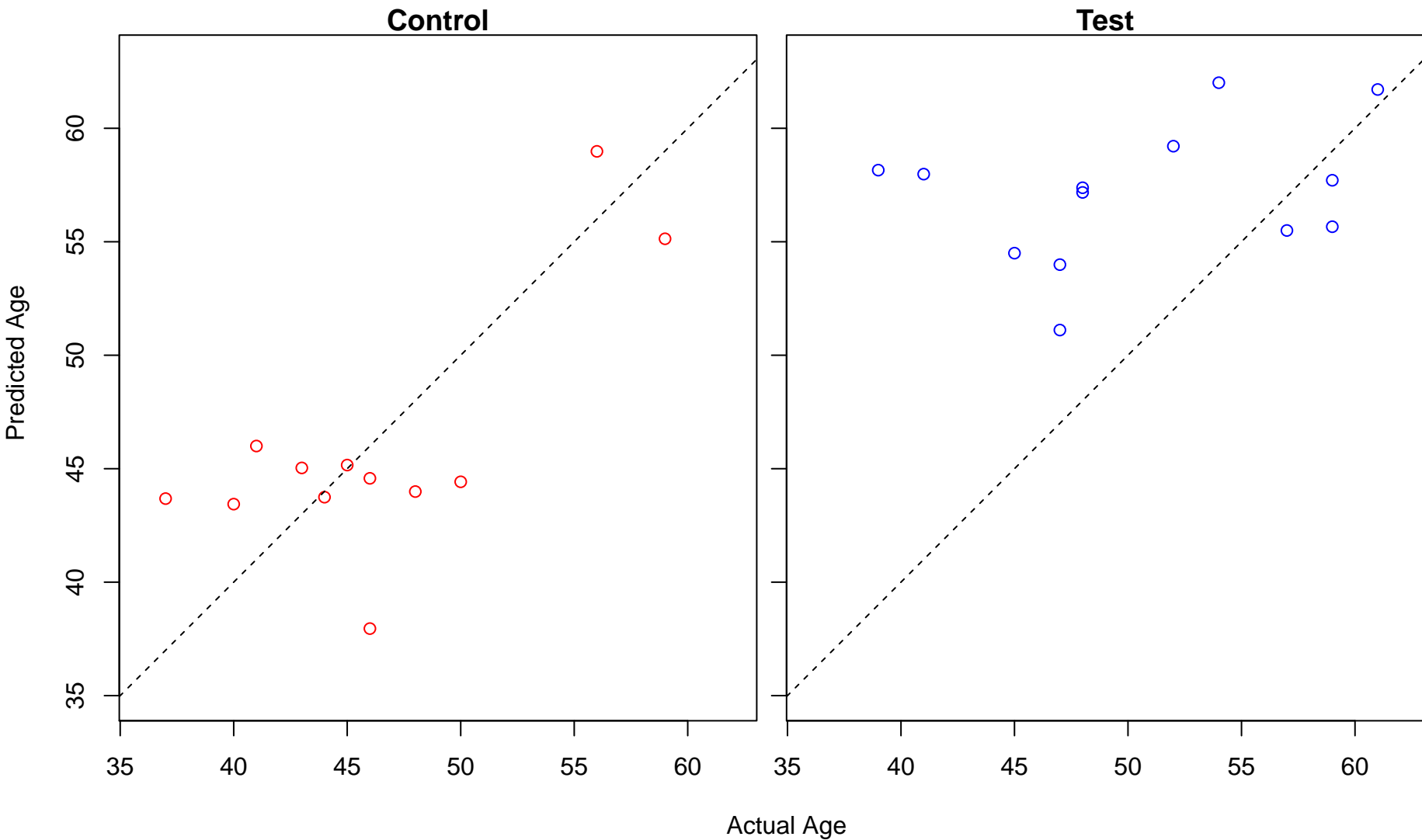
multicellular organismal movement (Score: 4.309111)



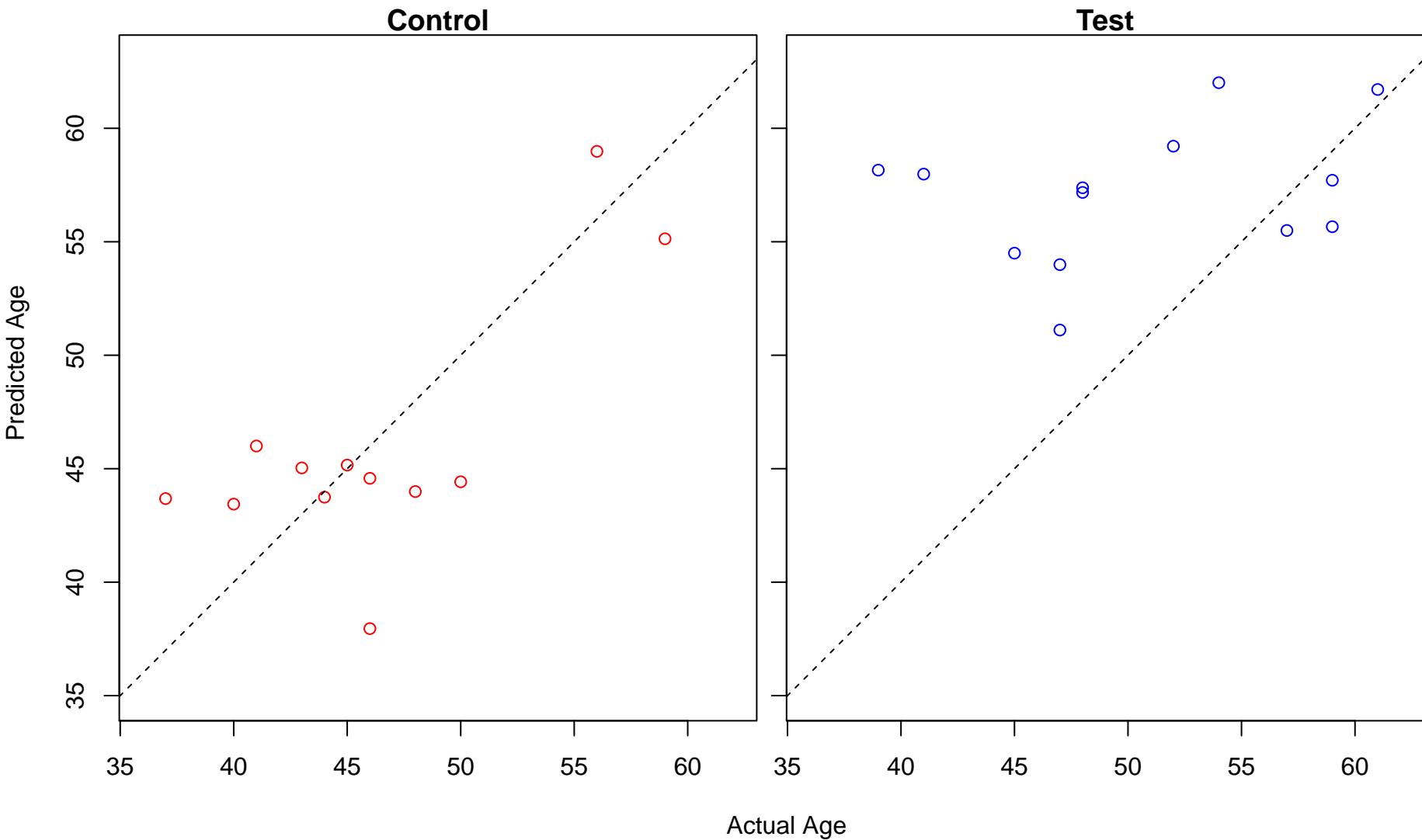
musculoskeletal movement (Score: 4.309111)



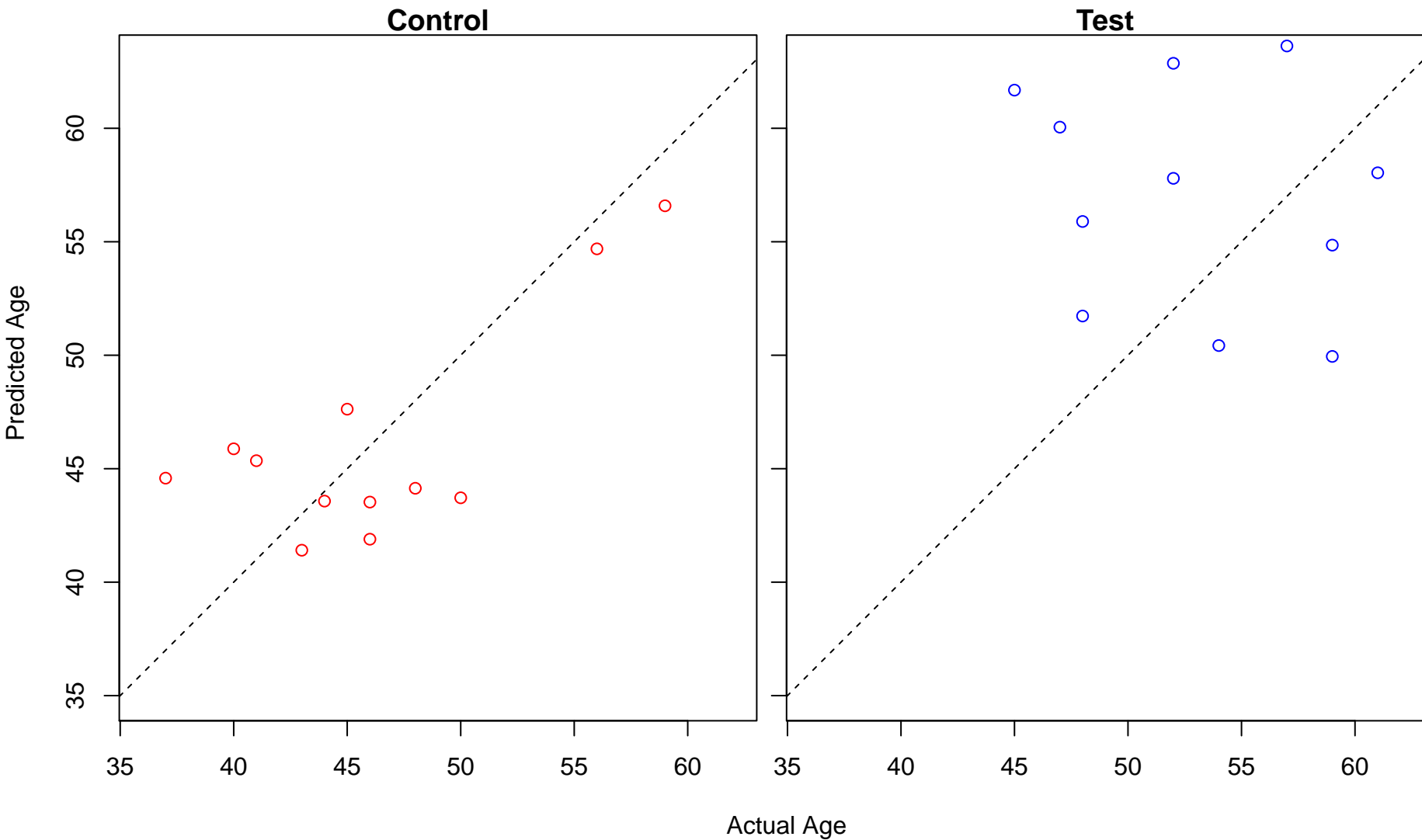
negative regulation of nucleoside metabolic process (Score: 4.303784)



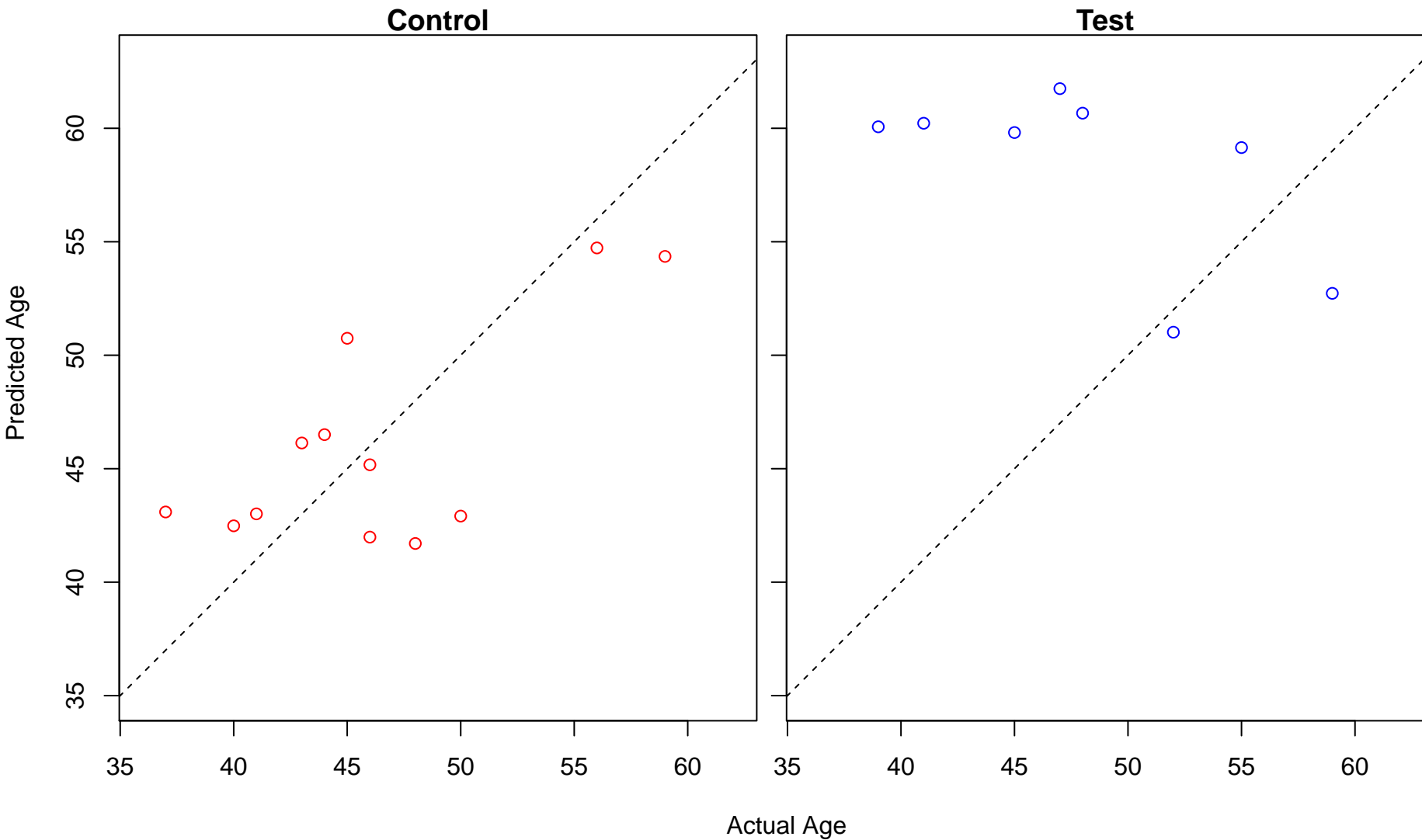
negative regulation of ATP metabolic process (Score: 4.303784)



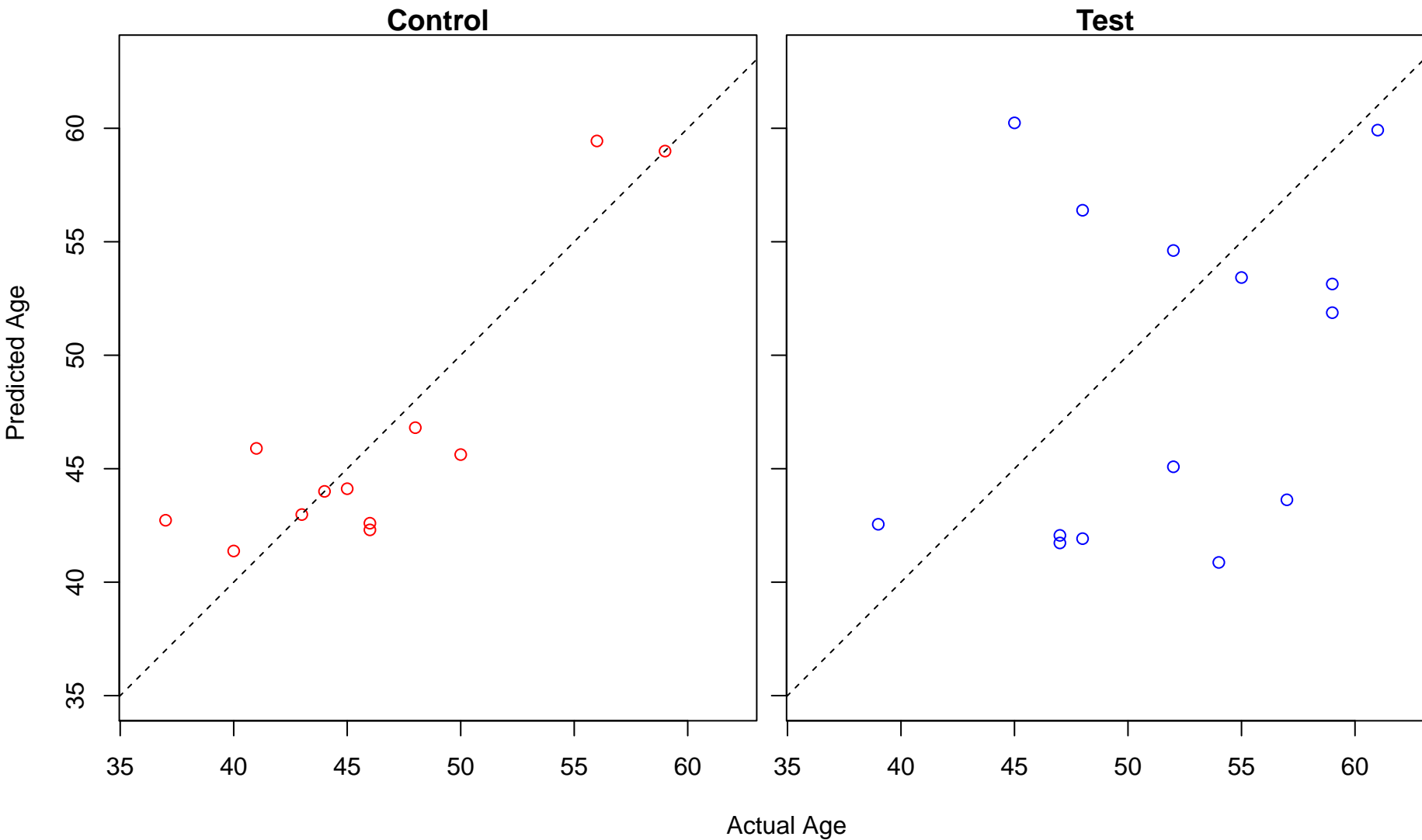
regulation of axon guidance (Score: 4.302058)



skeletal muscle contraction (Score: 4.298937)

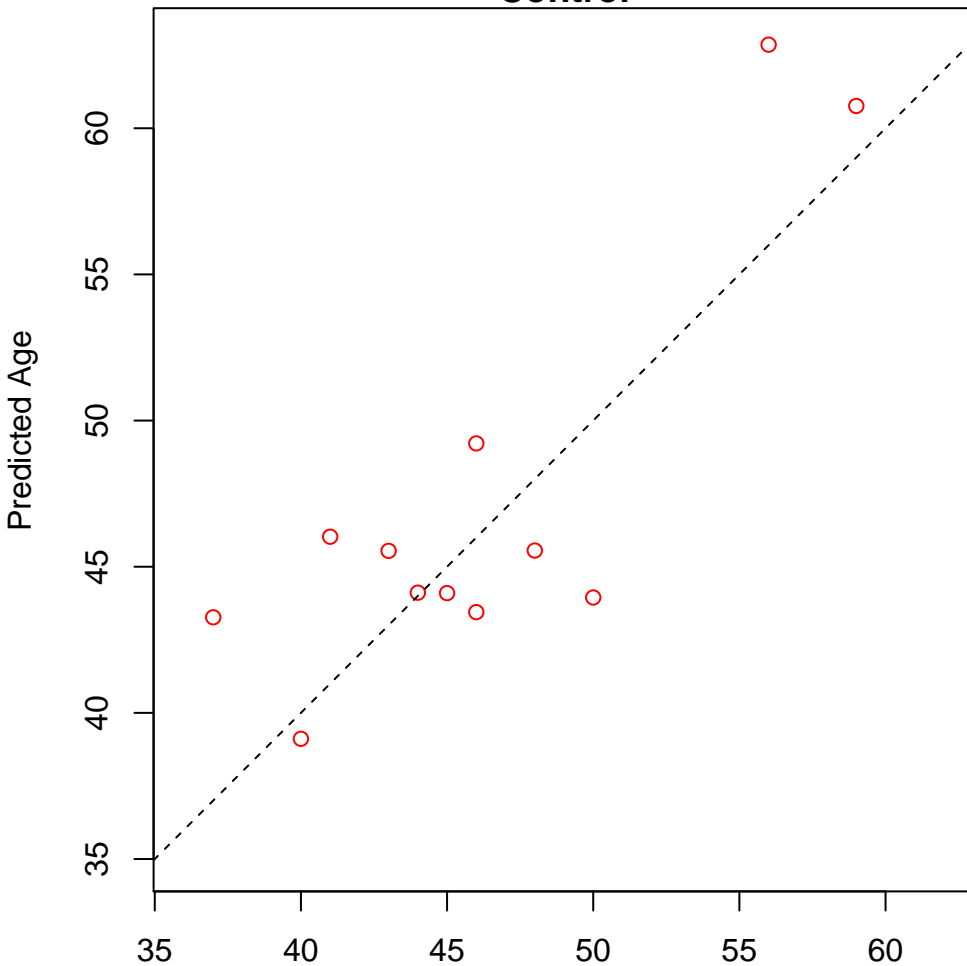


negative regulation of glucuronosyltransferase activity (Score: 4.296534)

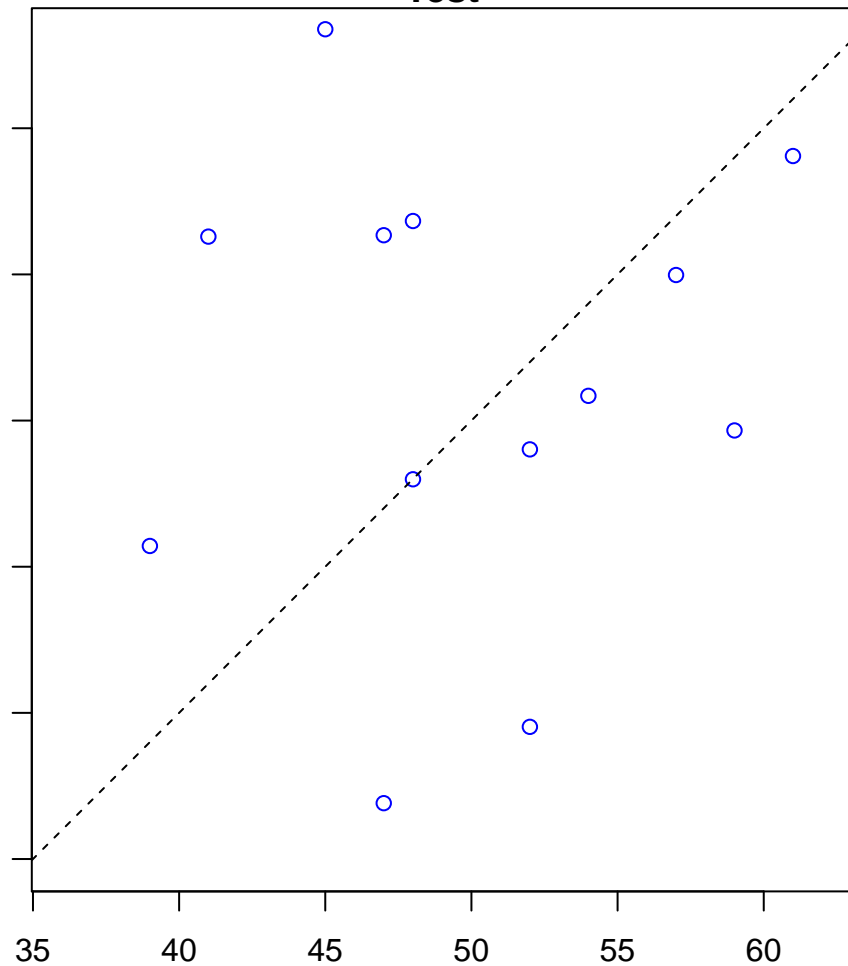


peptidyl-tyrosine dephosphorylation (Score: 4.295232)

Control

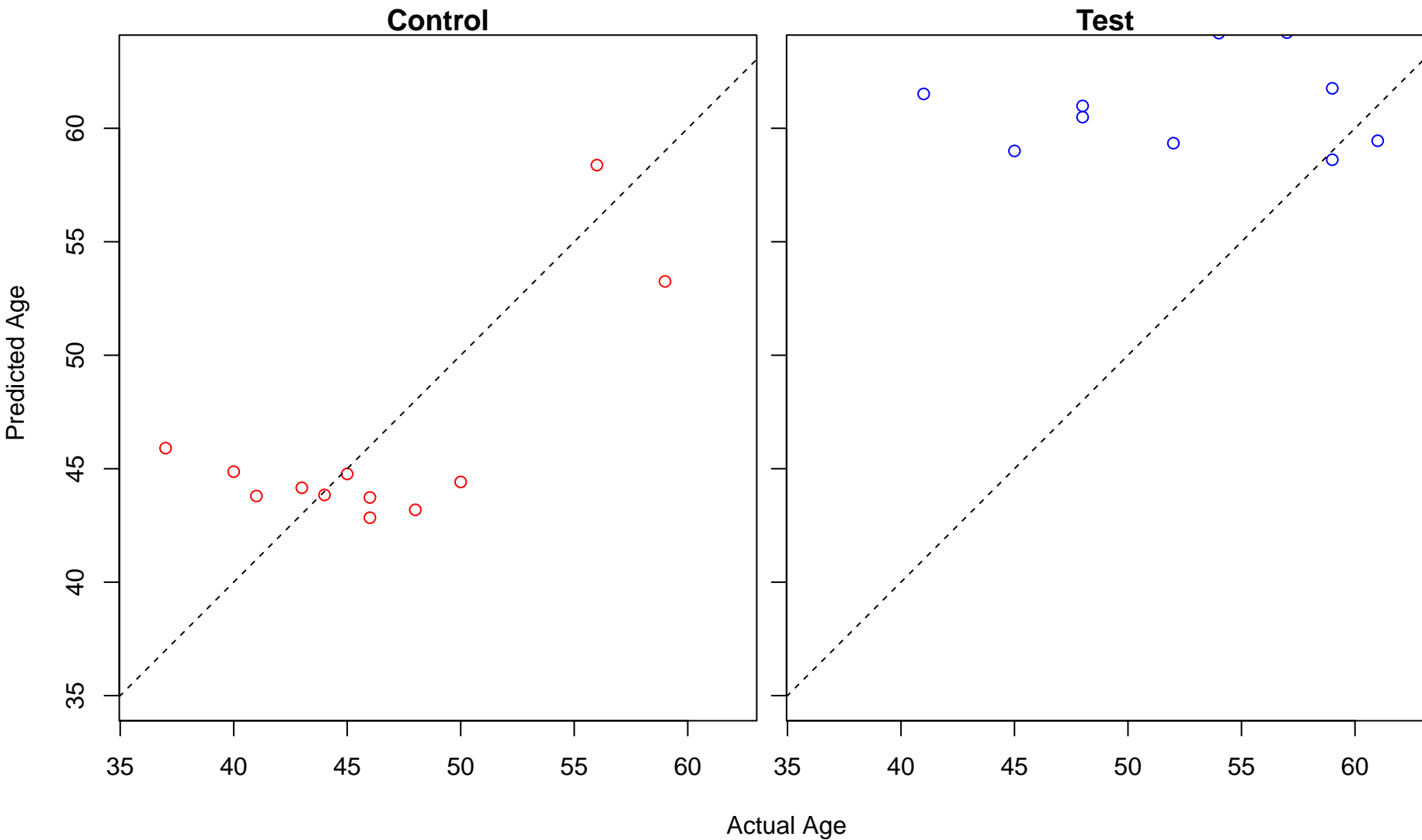


Test

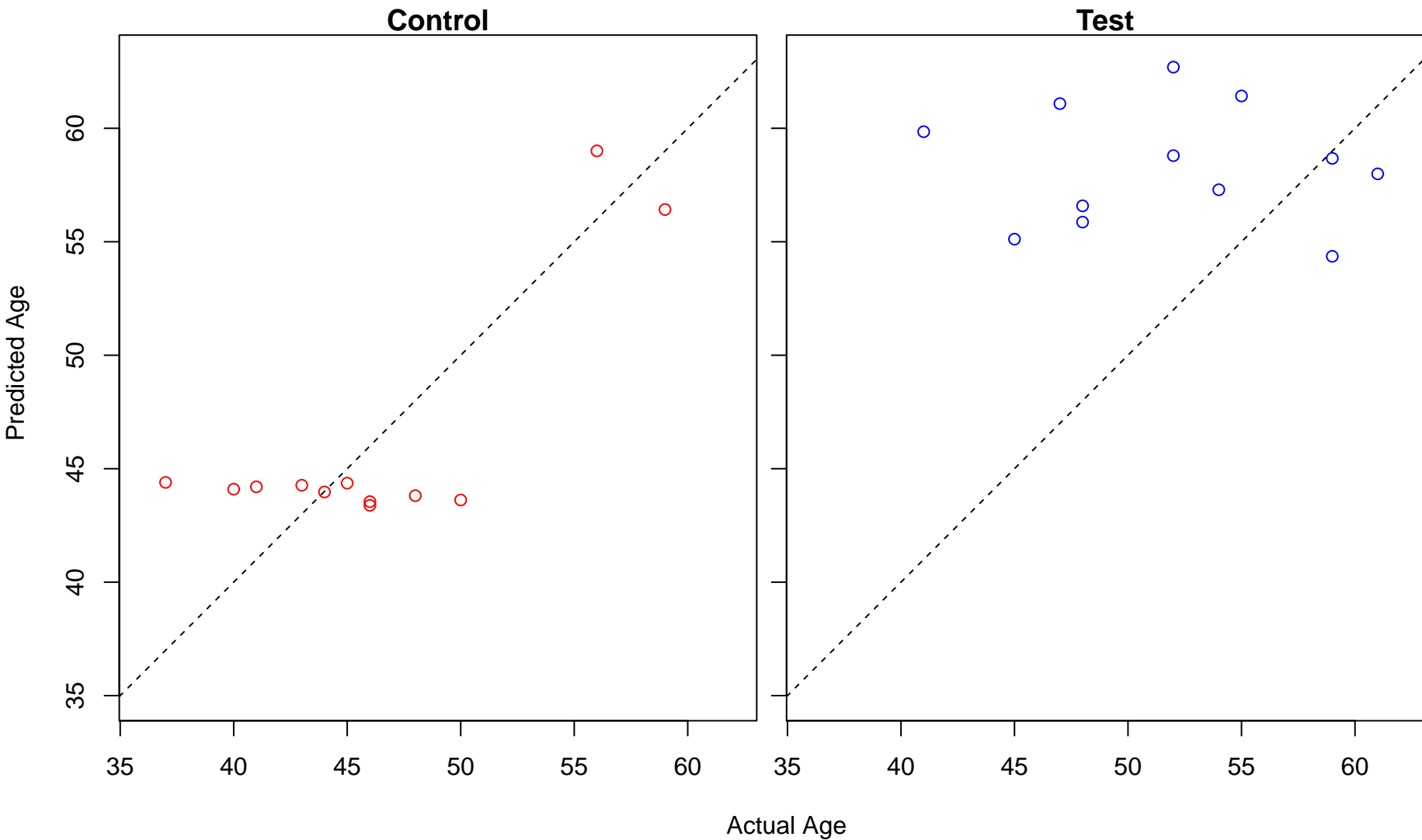


Actual Age

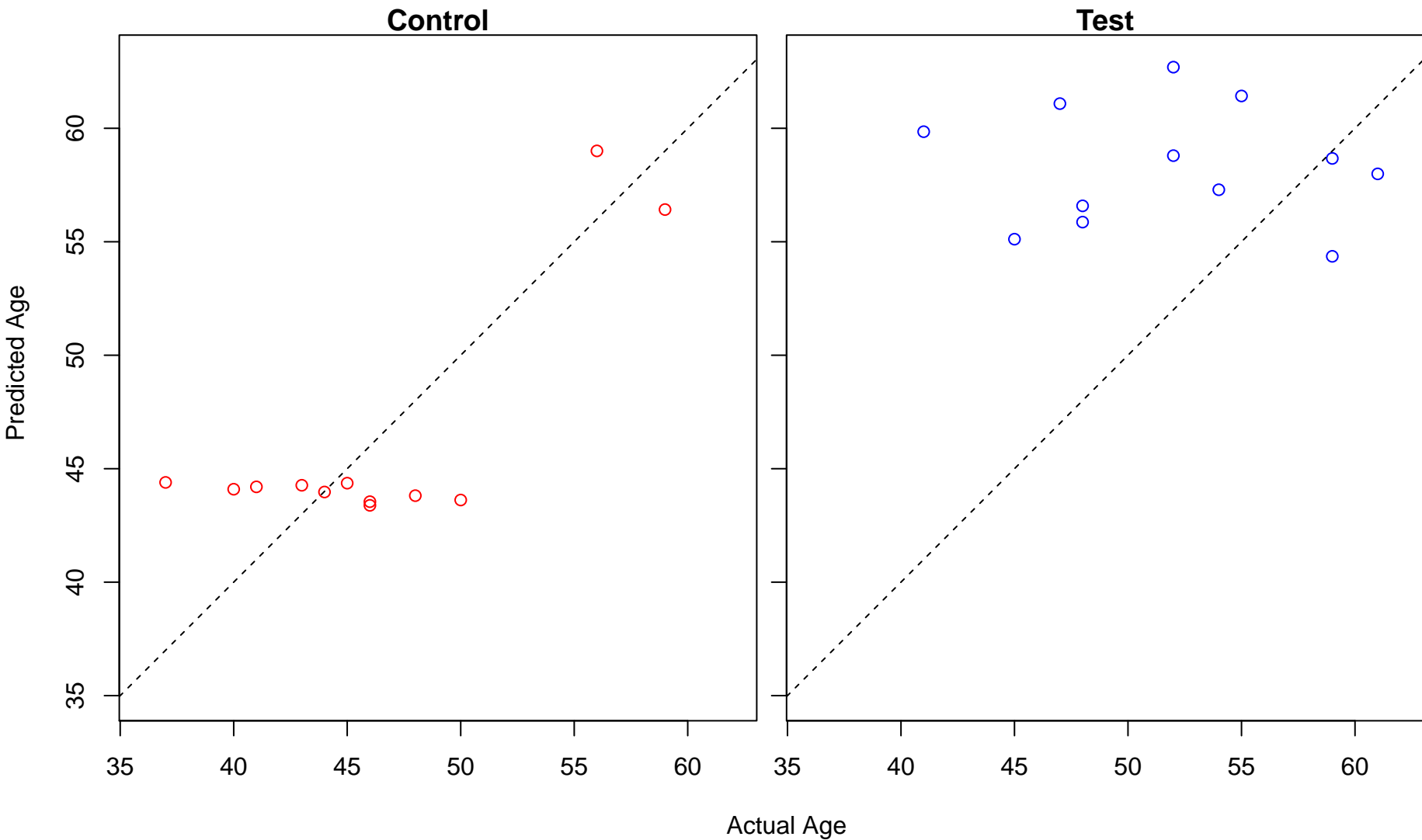
regulation of cholesterol storage (Score: 4.294702)



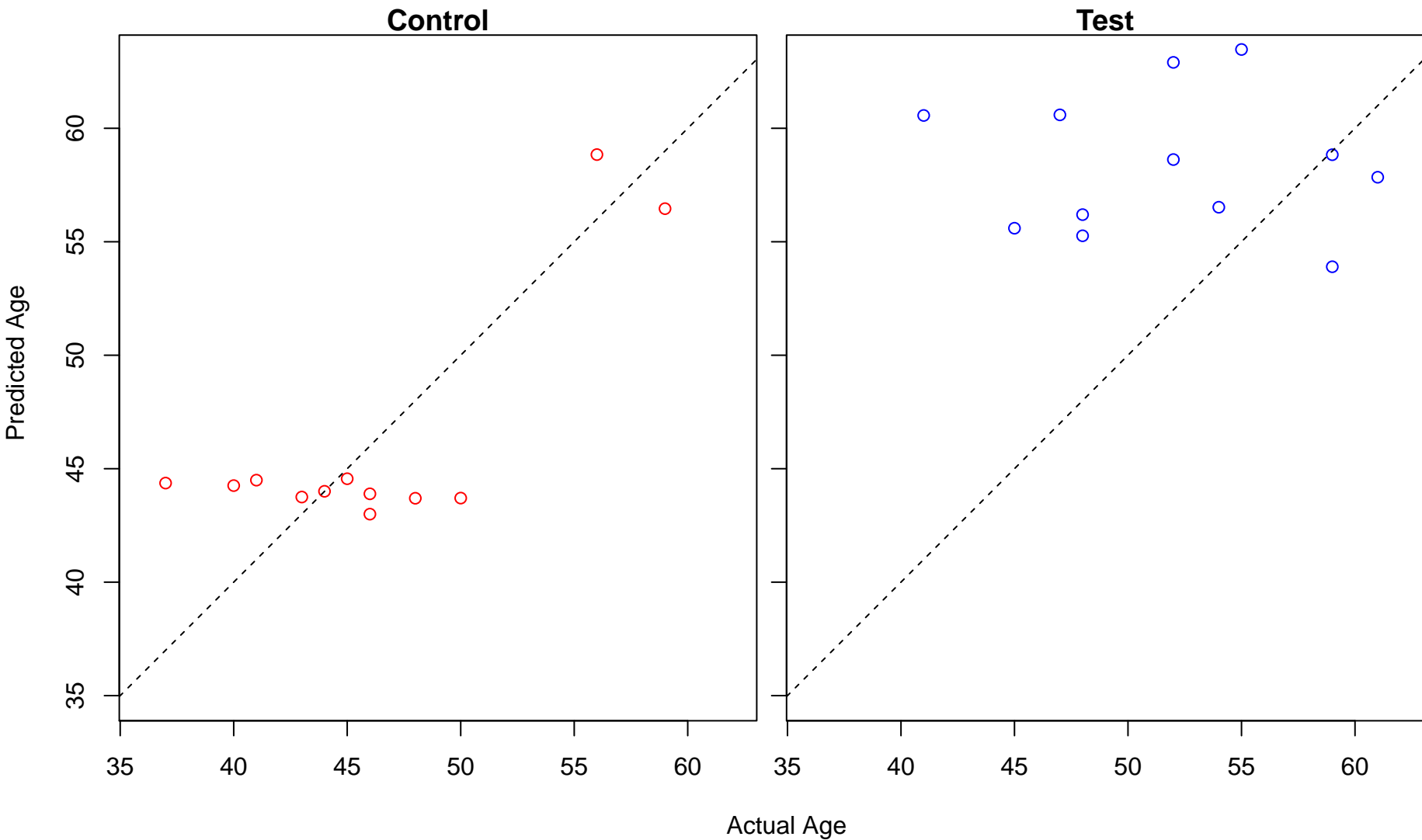
negative regulation of ERBB signaling pathway (Score: 4.294646)



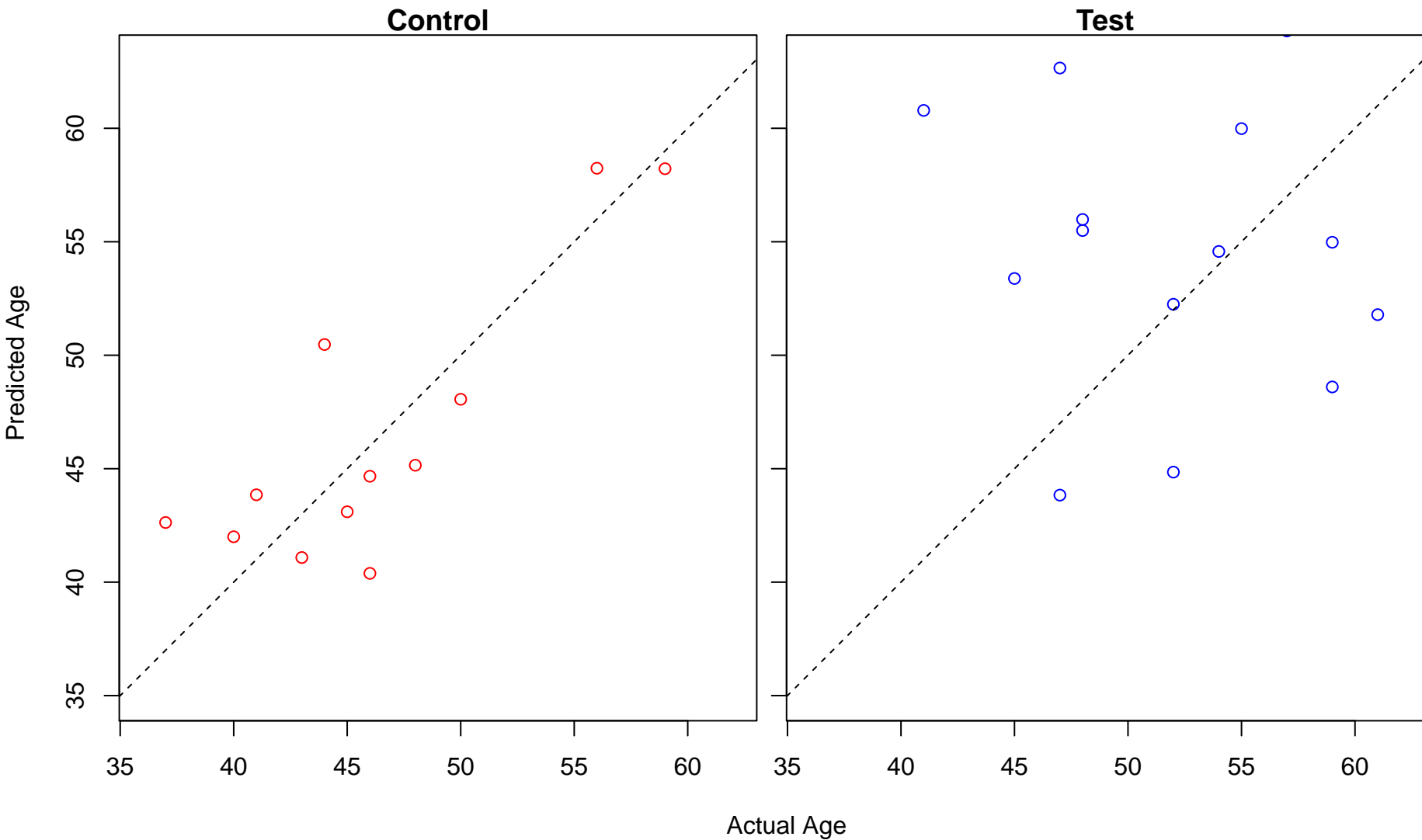
negative regulation of epidermal growth factor receptor signaling pathway (Score: 4.294515)



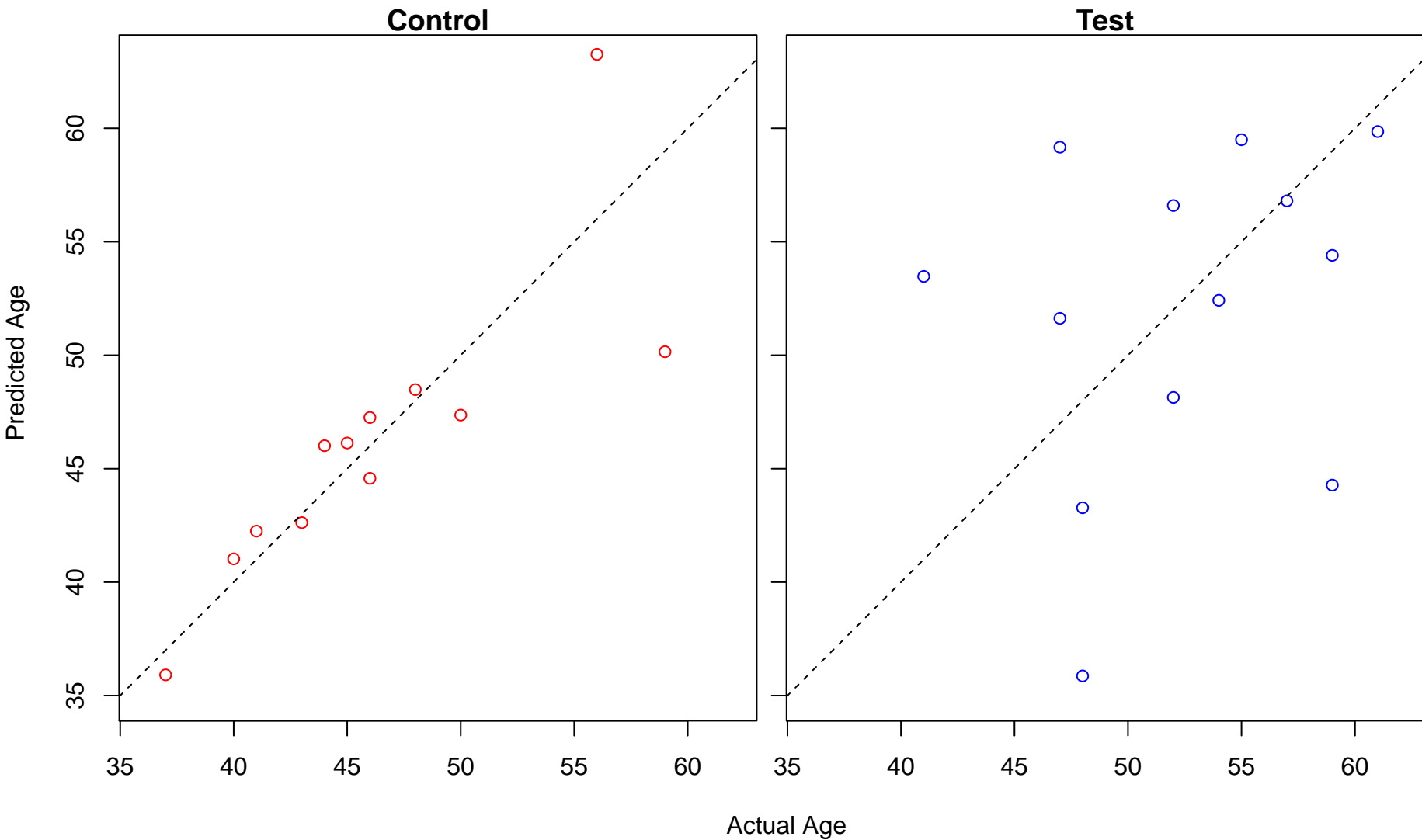
negative regulation of cell cycle G1/S phase transition (Score: 4.290057)



intracellular protein transmembrane import (Score: 4.279827)

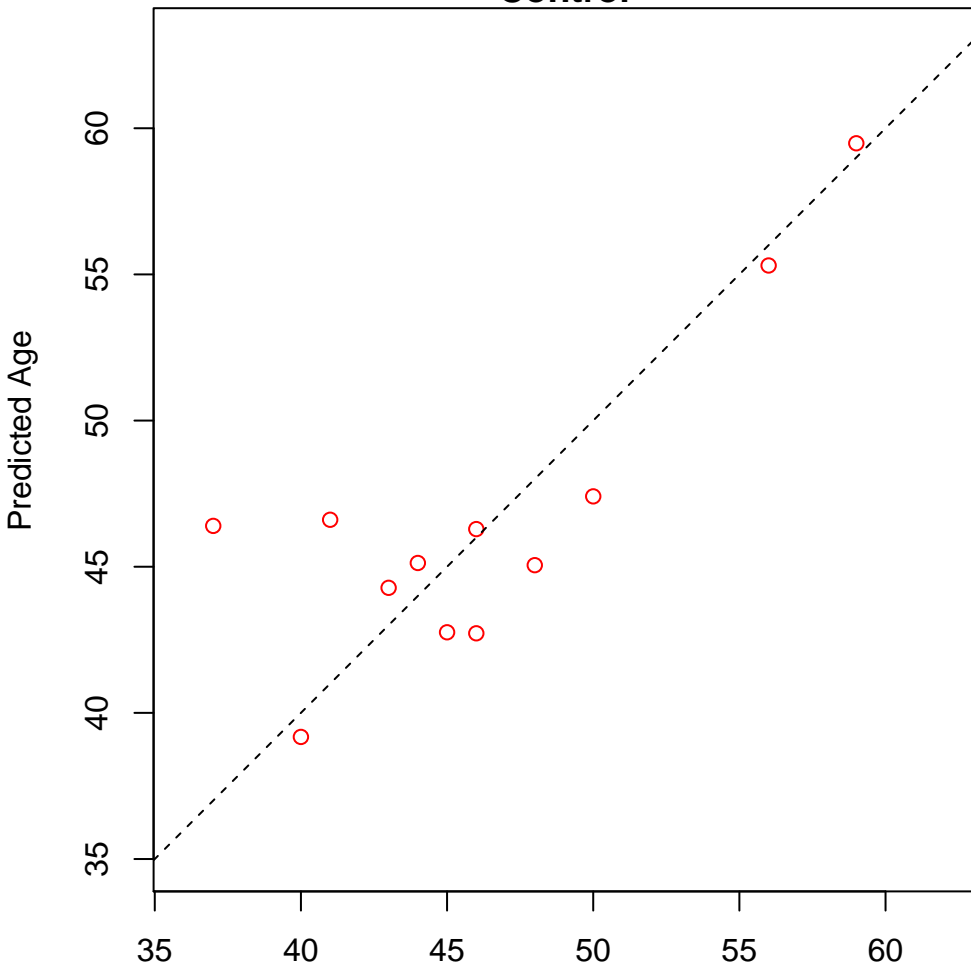


receptor clustering (Score: 4.279591)

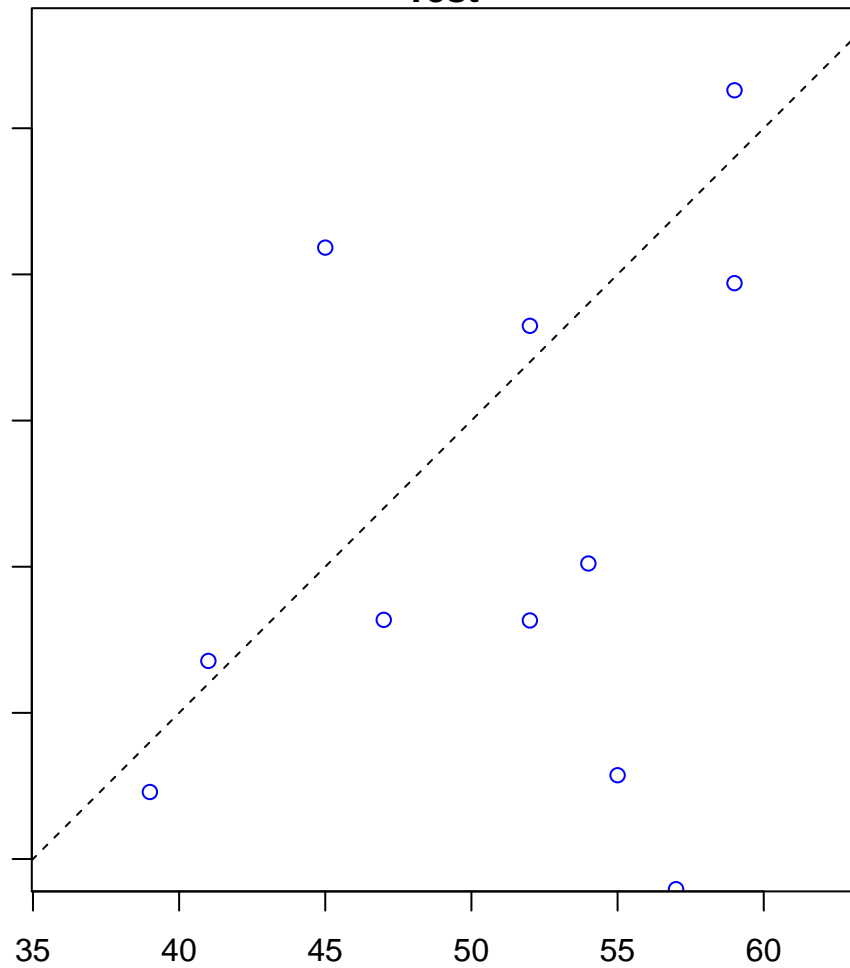


mucopolysaccharide metabolic process (Score: 4.276482)

Control

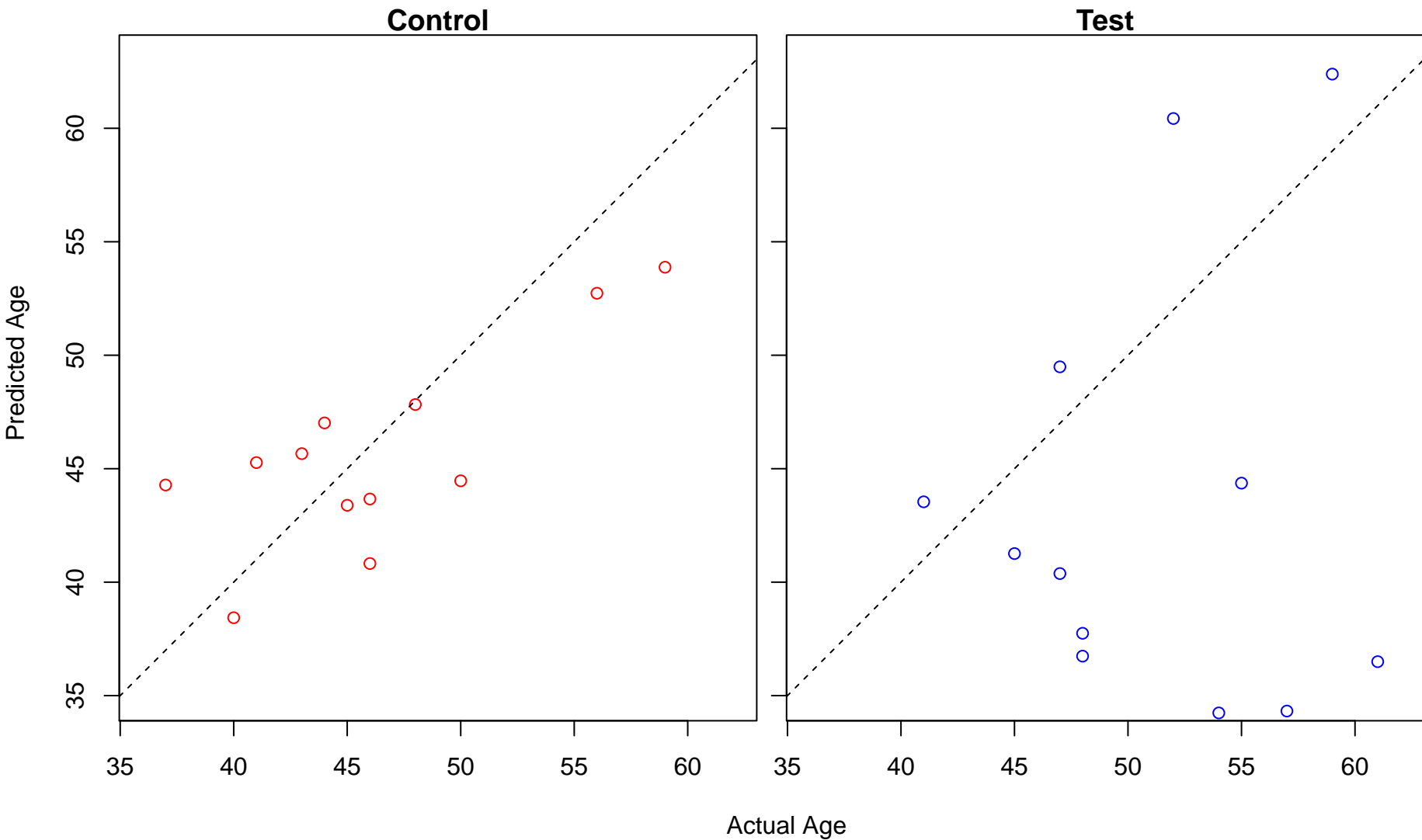


Test

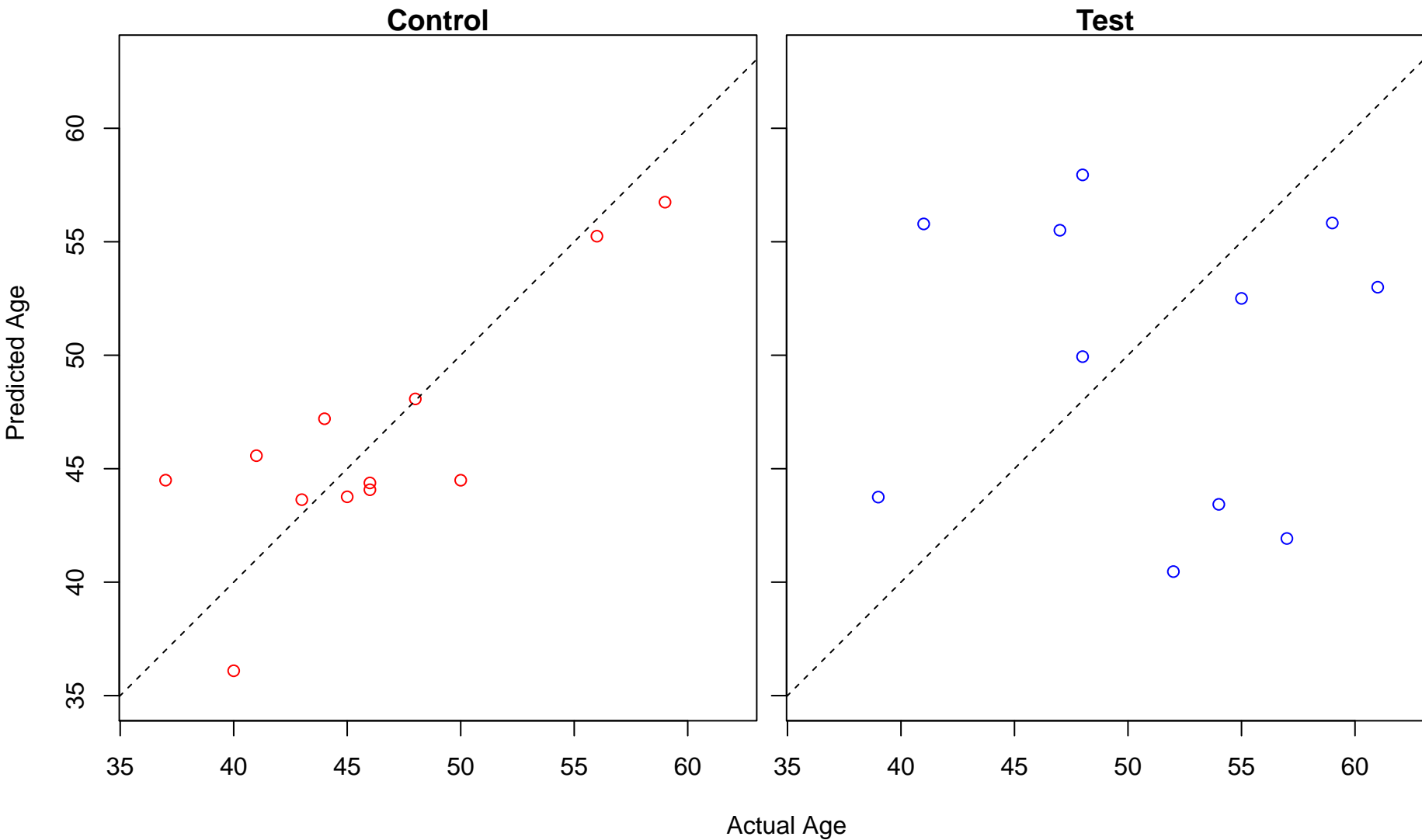


Actual Age

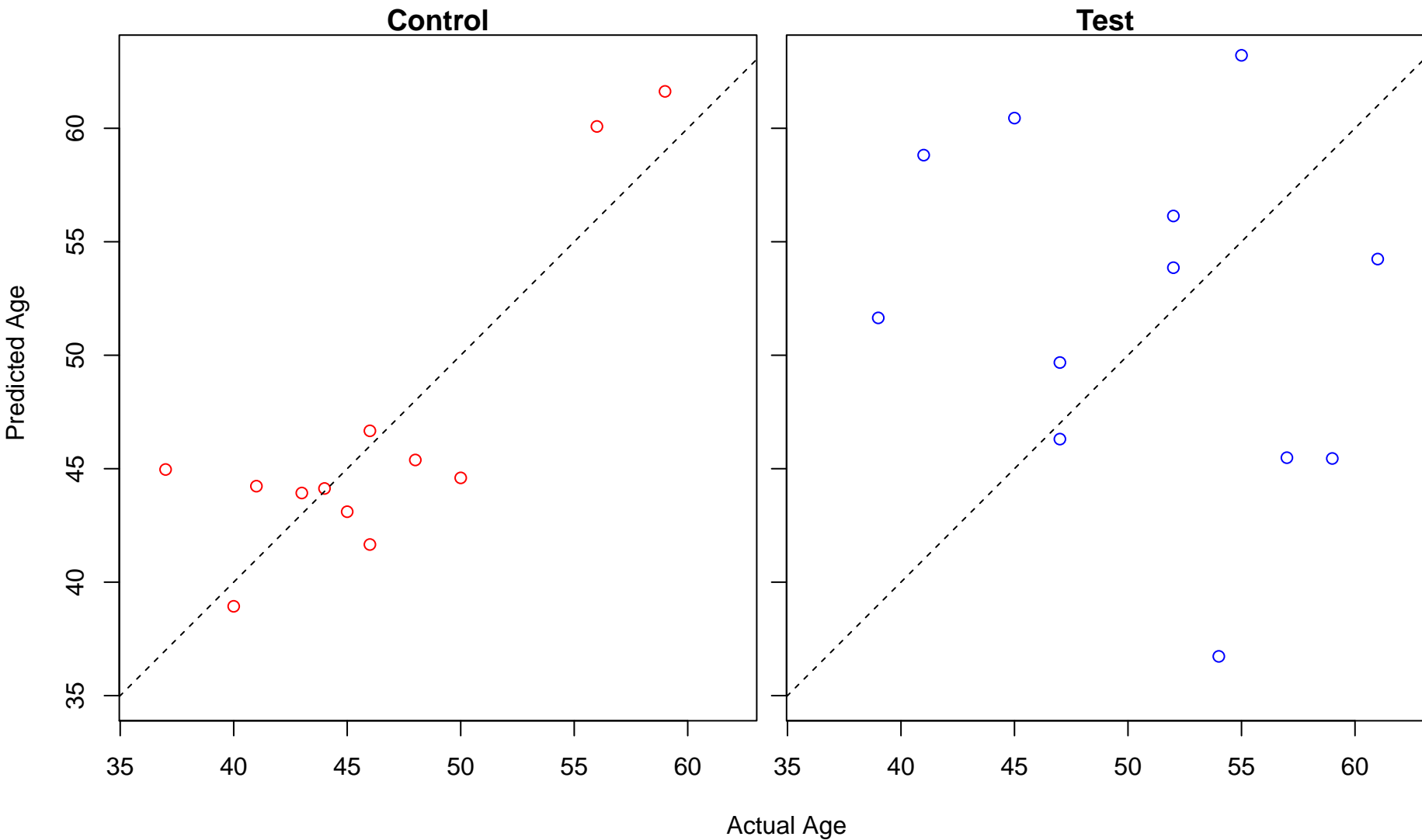
cellular amino acid metabolic process (Score: 4.276061)



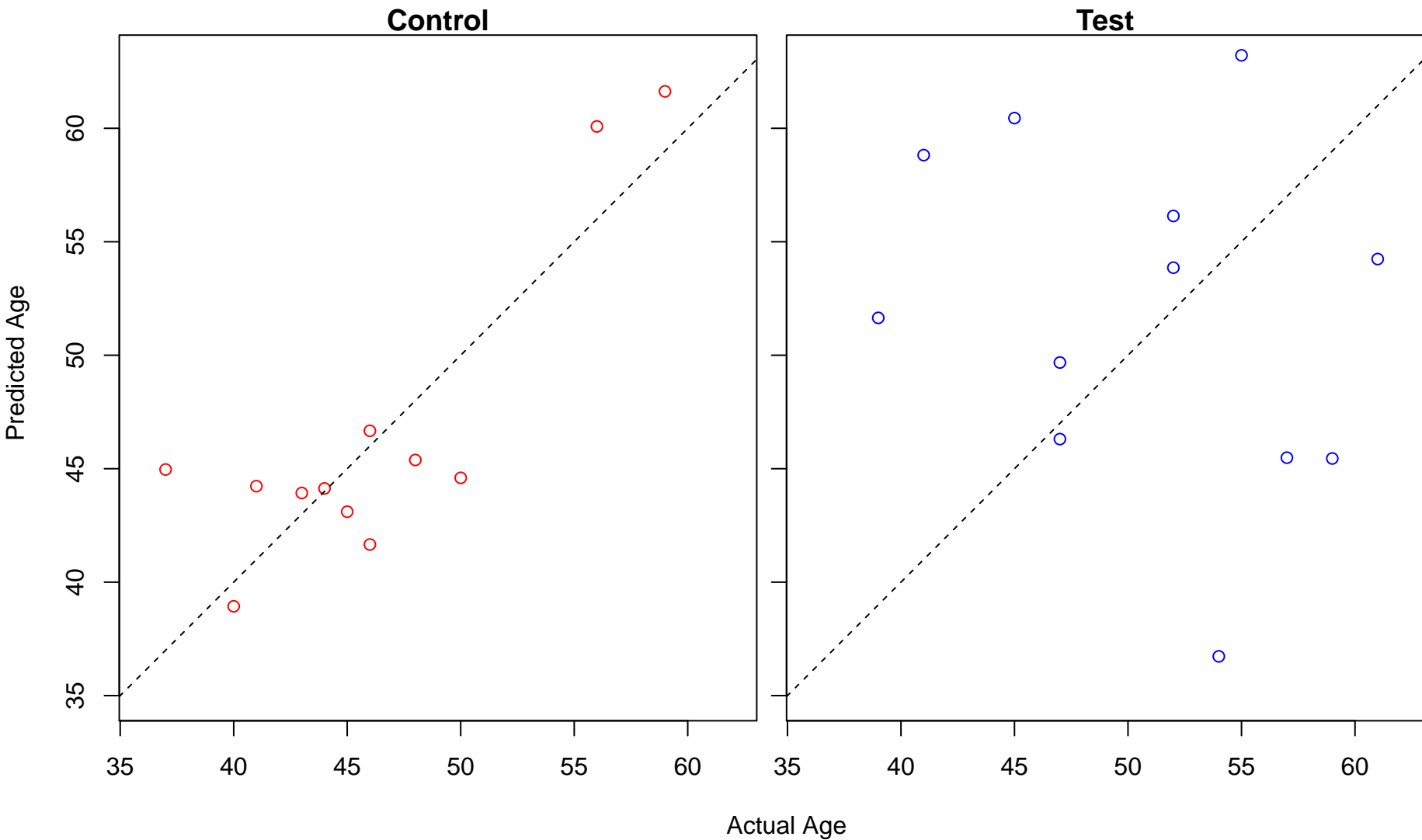
negative regulation of cell growth (Score: 4.274024)



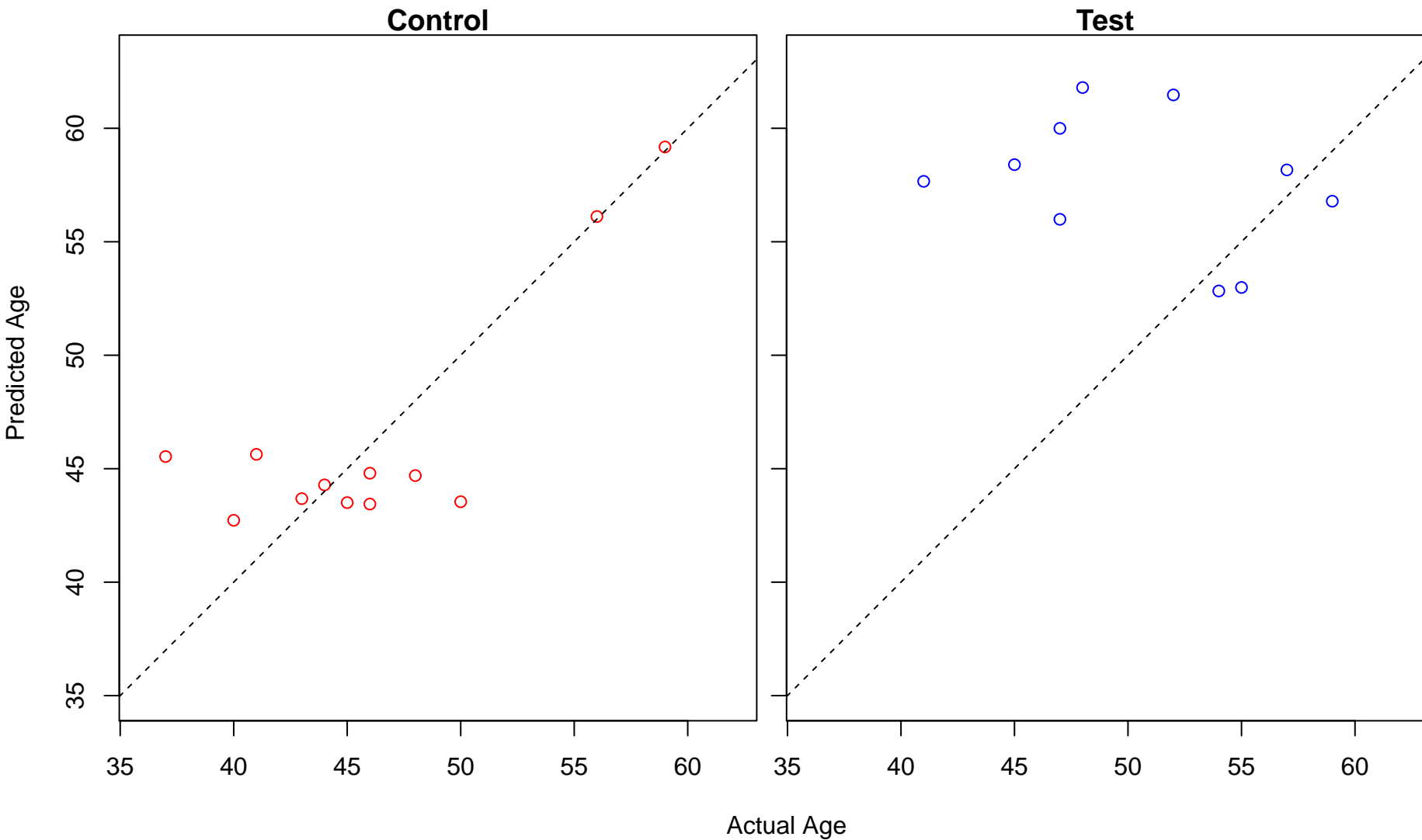
negative regulation of protein exit from endoplasmic reticulum (Score: 4.268774)



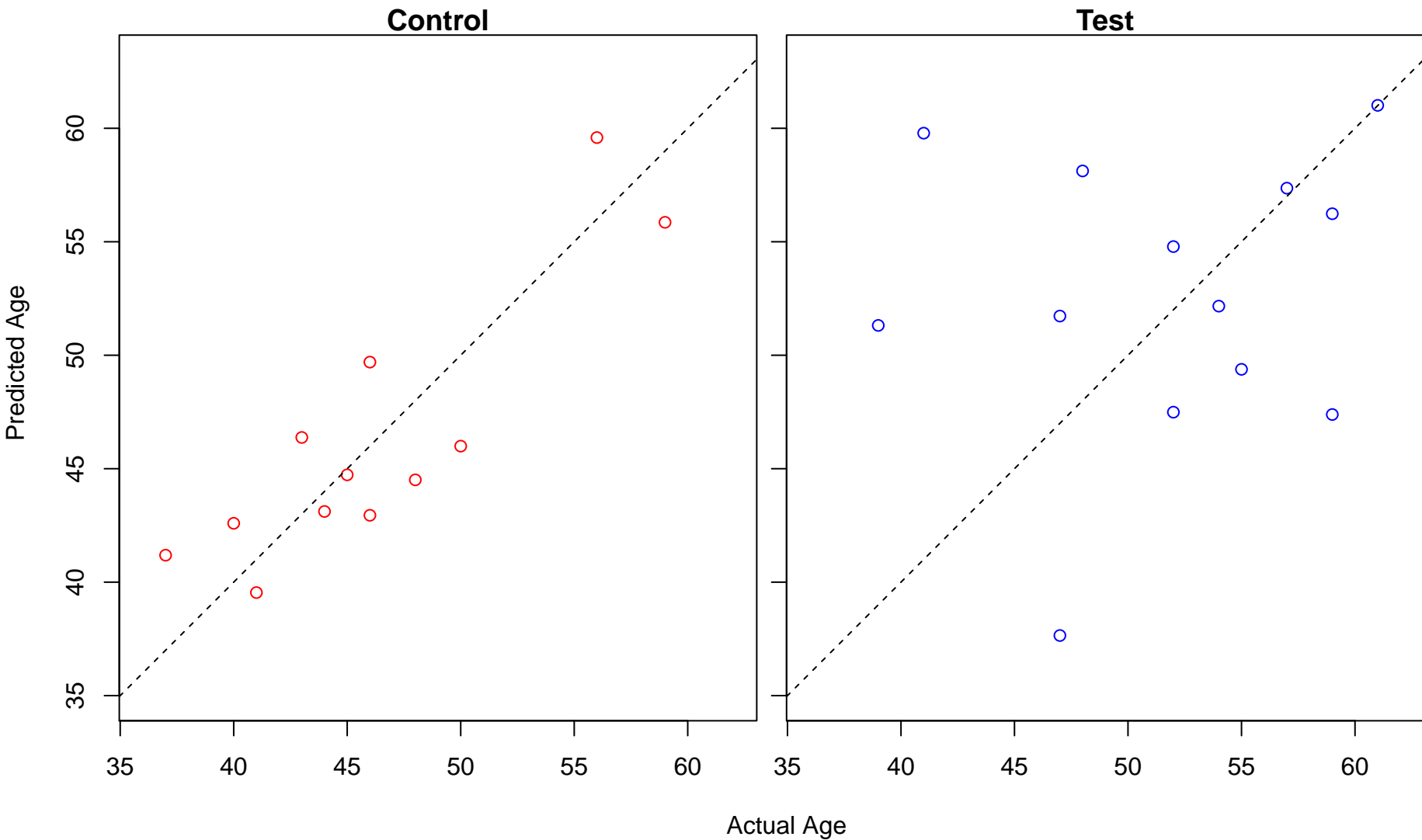
negative regulation of retrograde protein transport, ER to cytosol (Score: 4.268774)



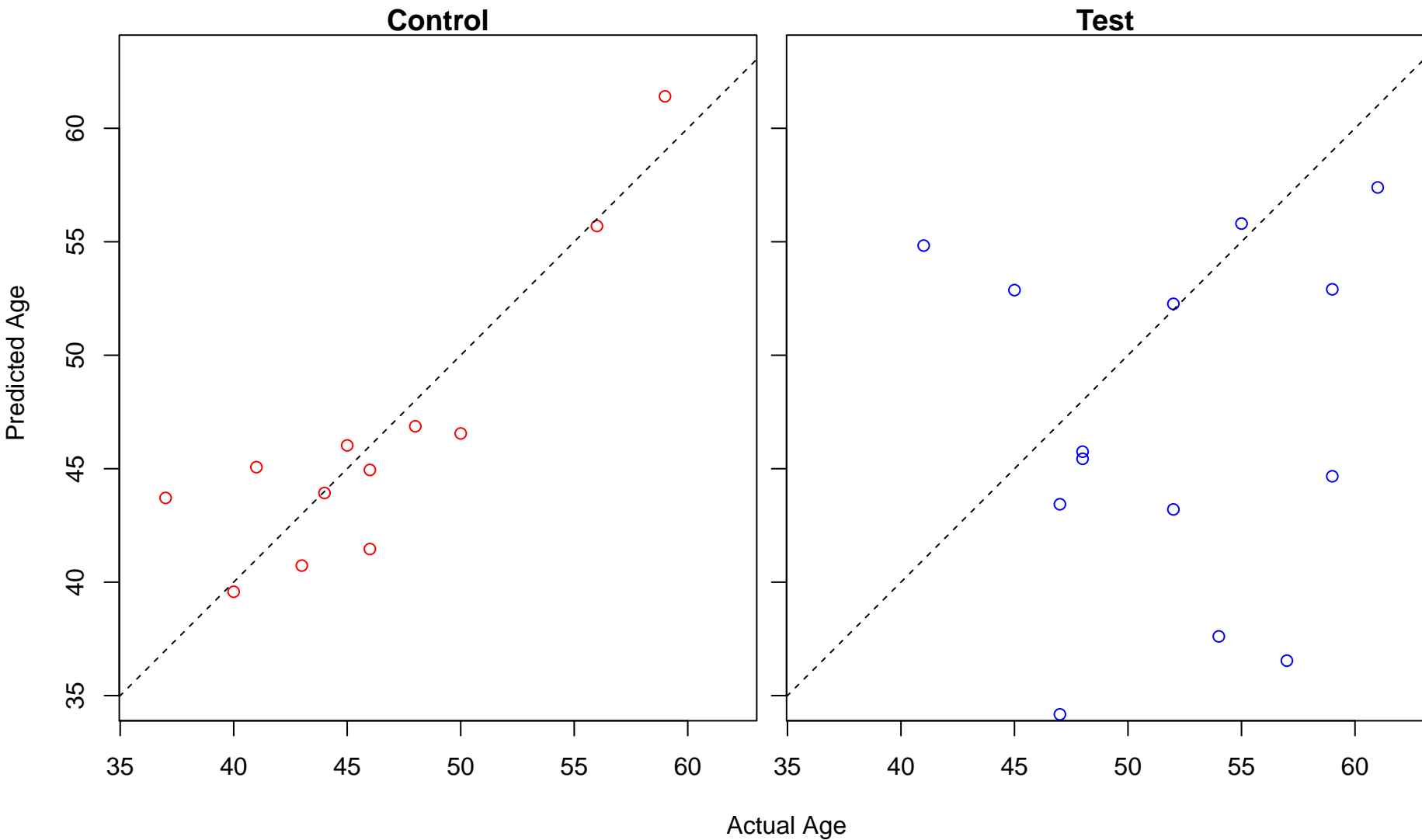
regulation of sulfur metabolic process (Score: 4.261619)



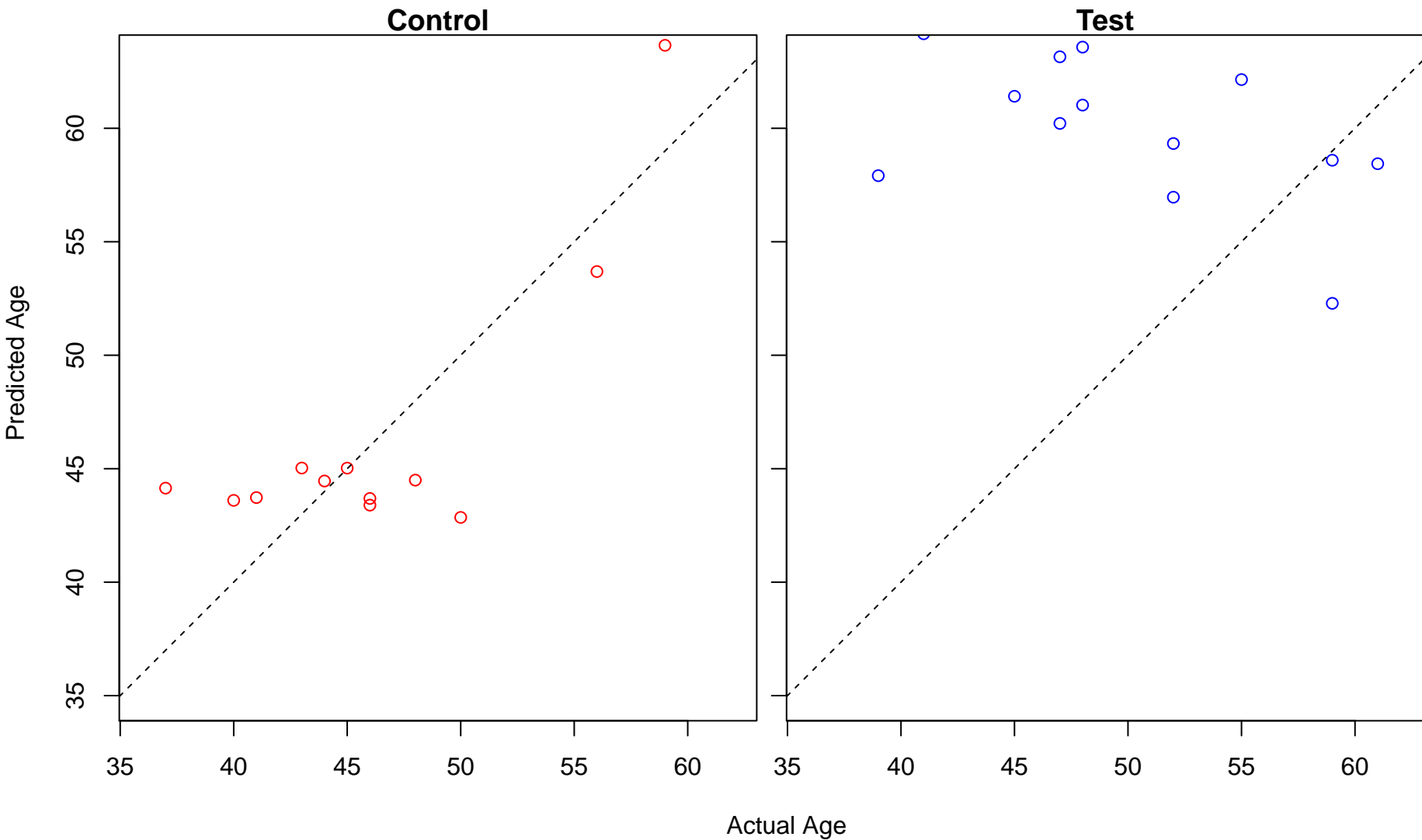
positive regulation of histone deacetylation (Score: 4.257120)



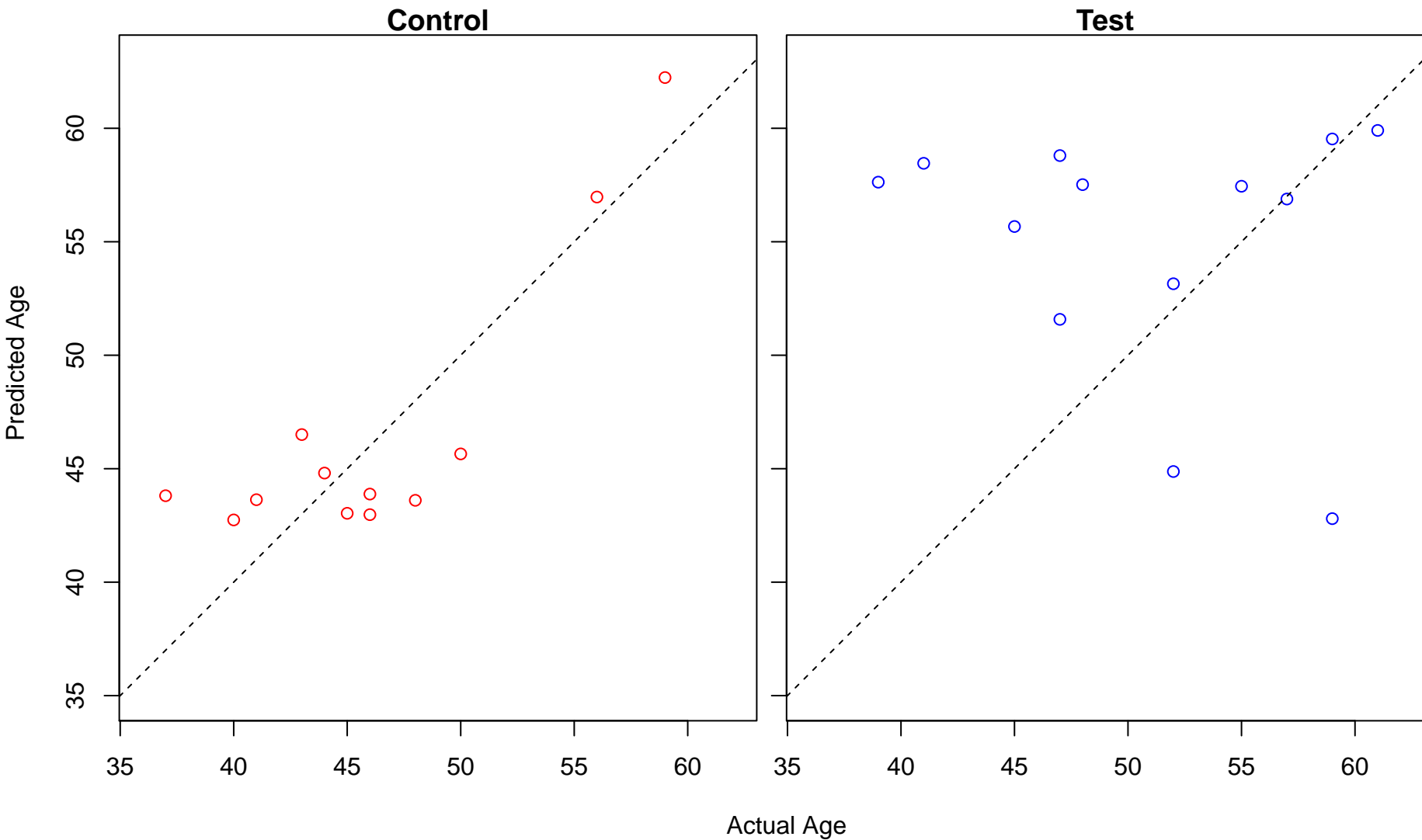
purine nucleobase metabolic process (Score: 4.250461)



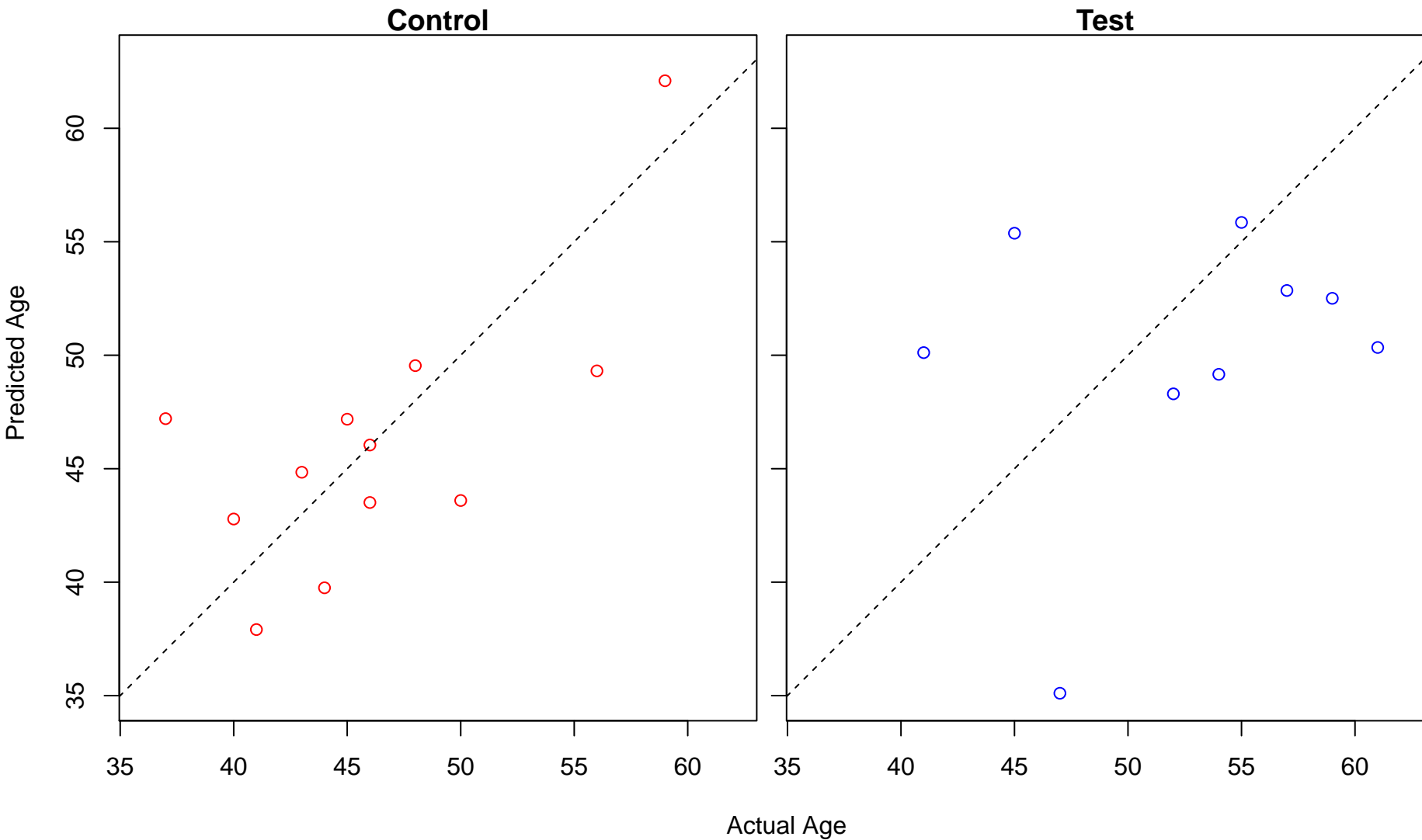
positive regulation of insulin receptor signaling pathway (Score: 4.249603)



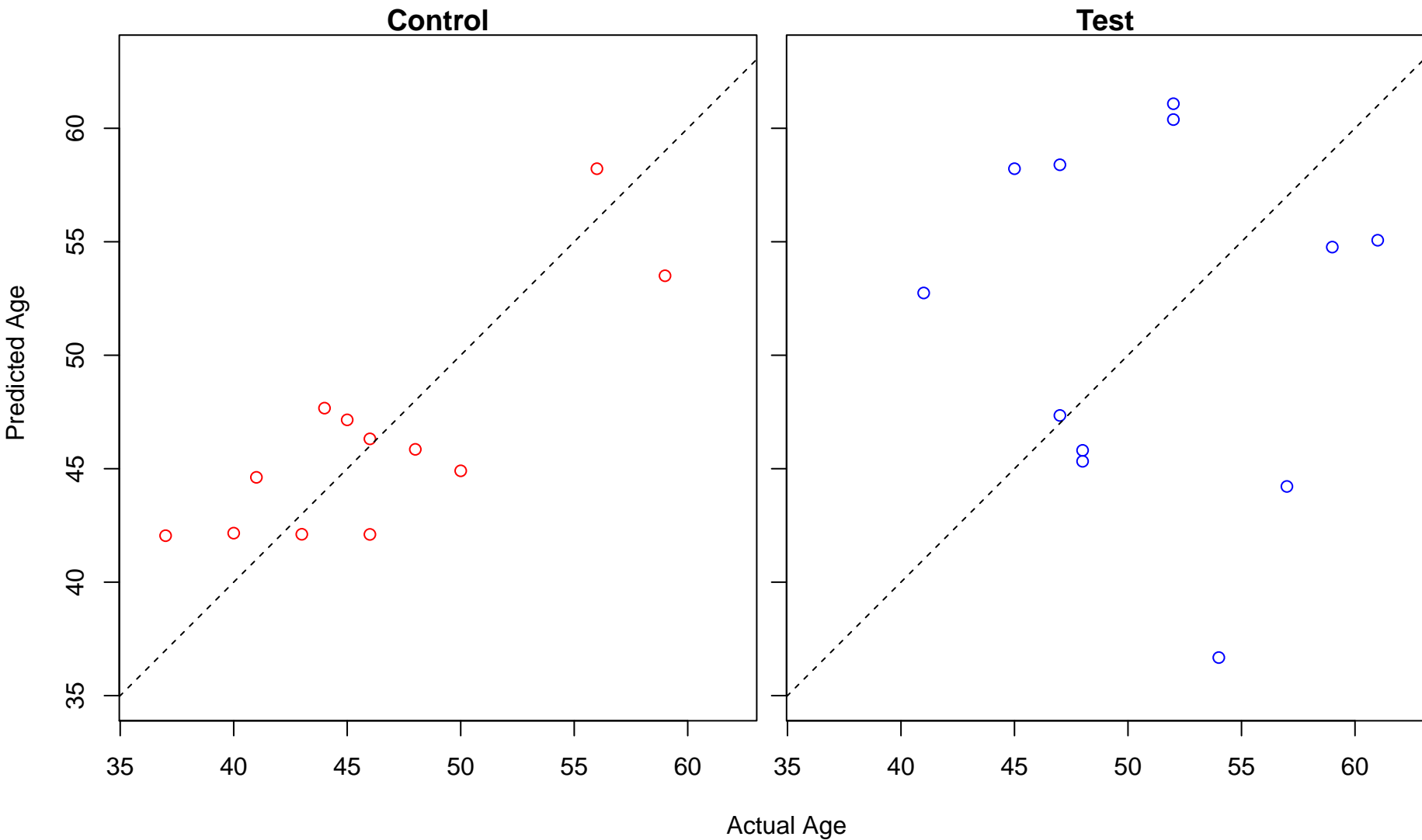
protein polyglutamylation (Score: 4.247268)



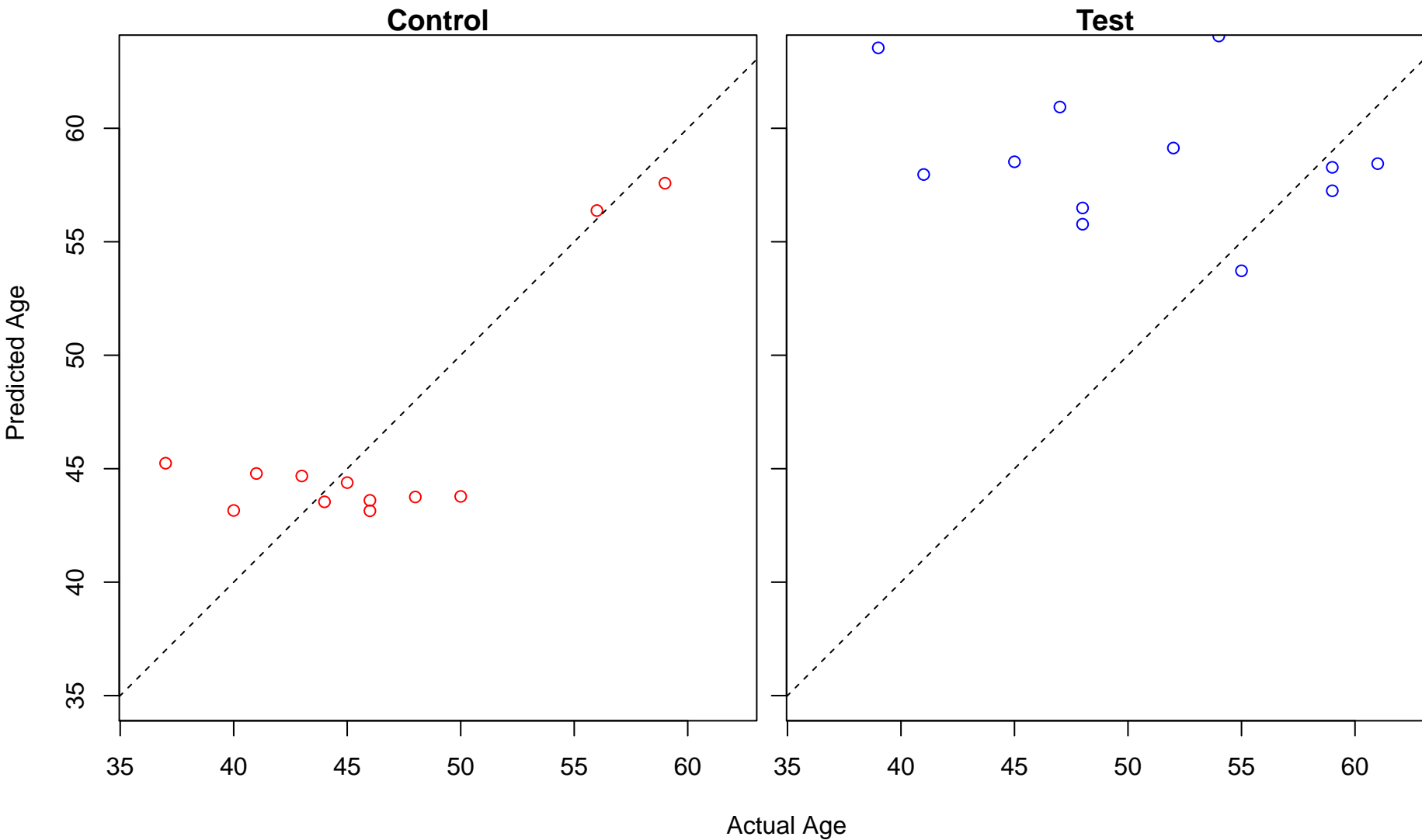
negative regulation of cellular extravasation (Score: 4.242484)



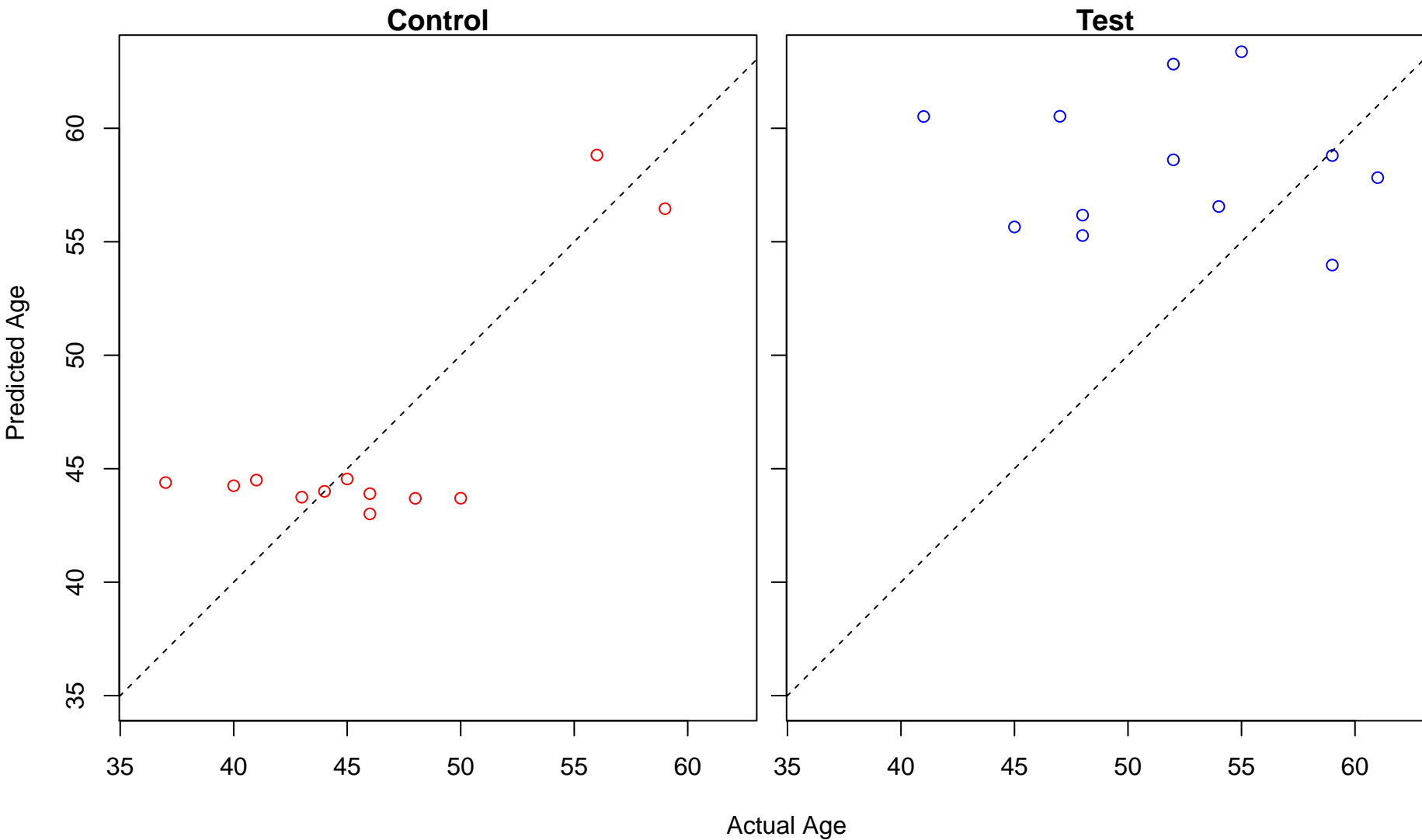
interferon-gamma-mediated signaling pathway (Score: 4.241715)



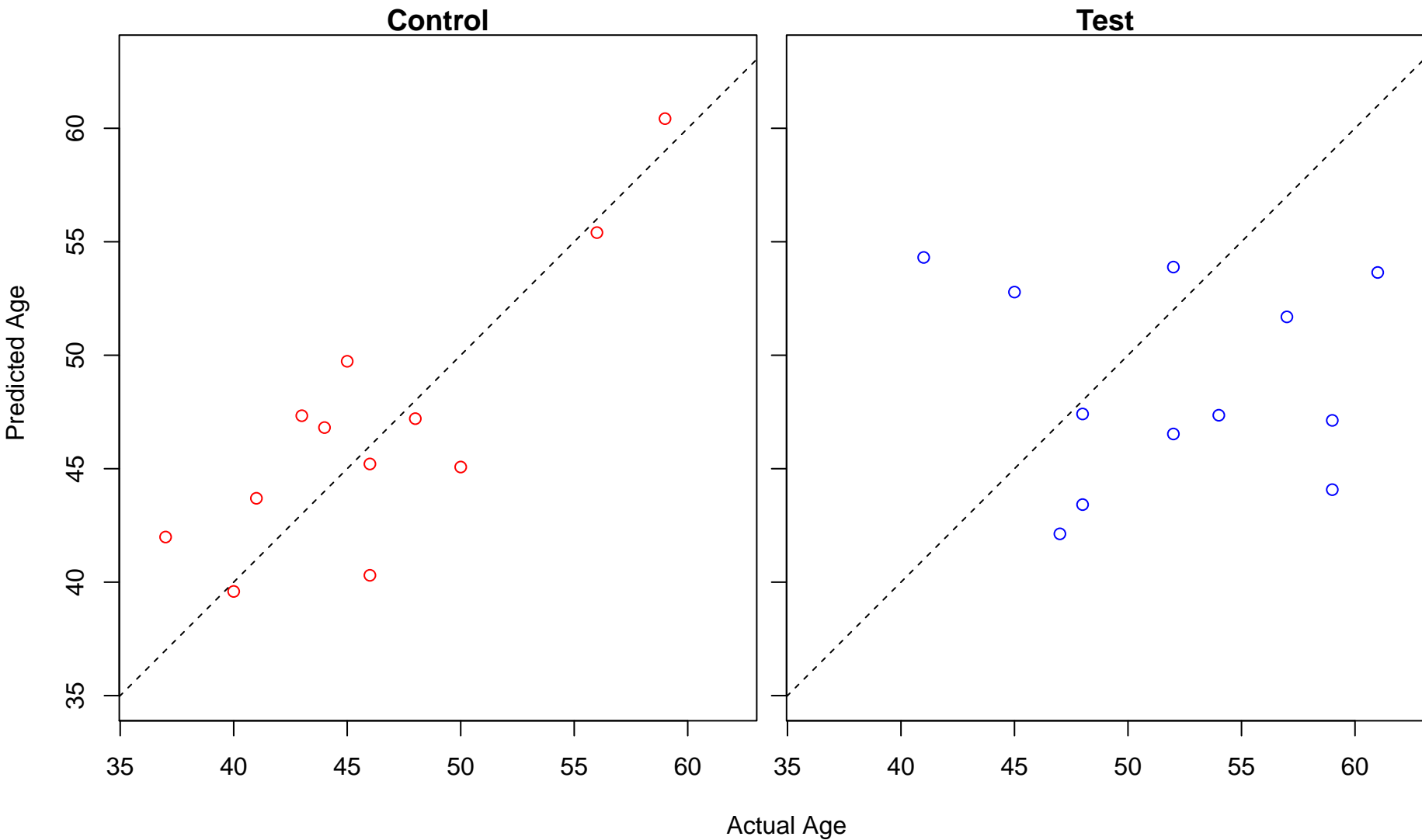
response to retinoic acid (Score: 4.241626)



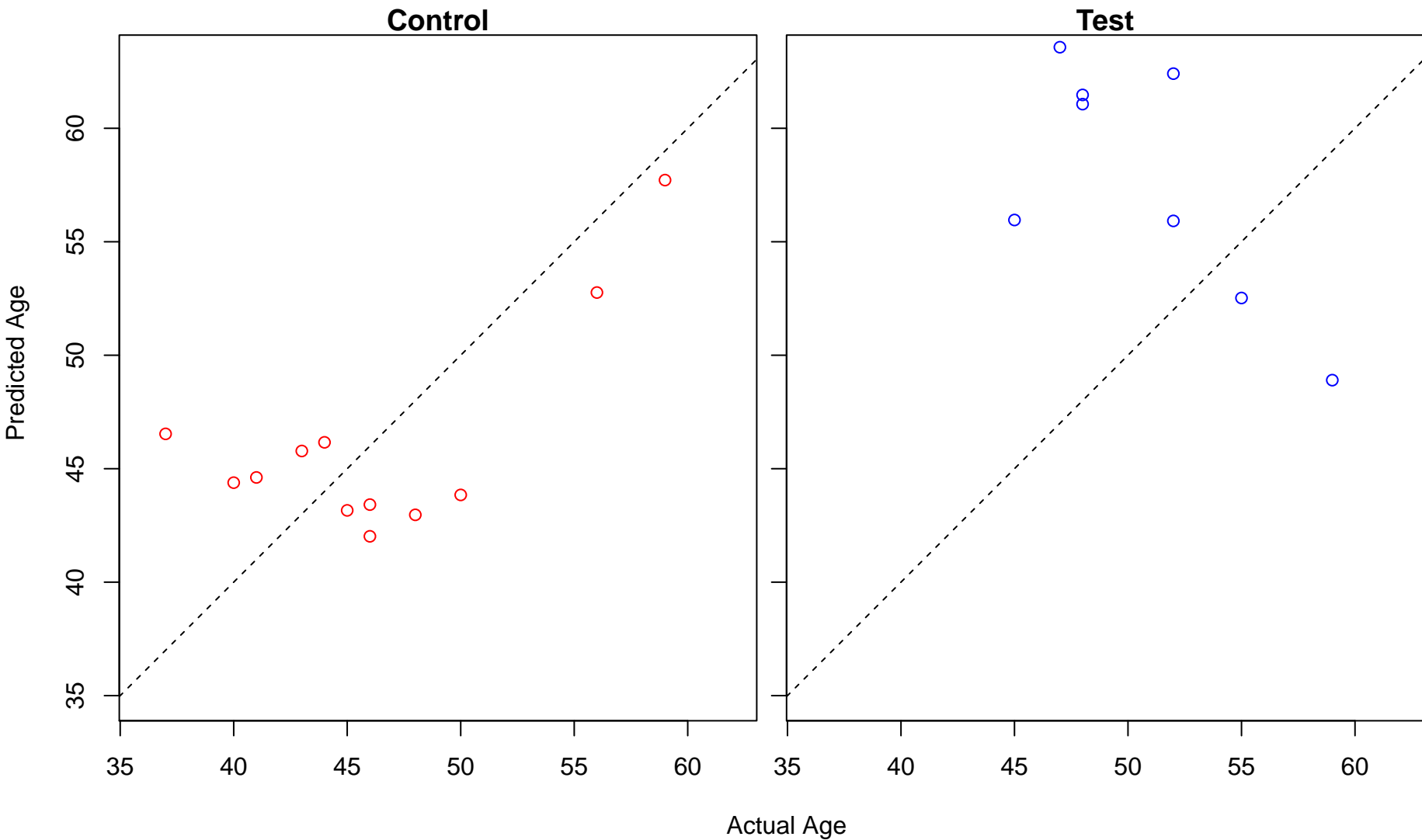
regulation of cell cycle G1/S phase transition (Score: 4.241373)



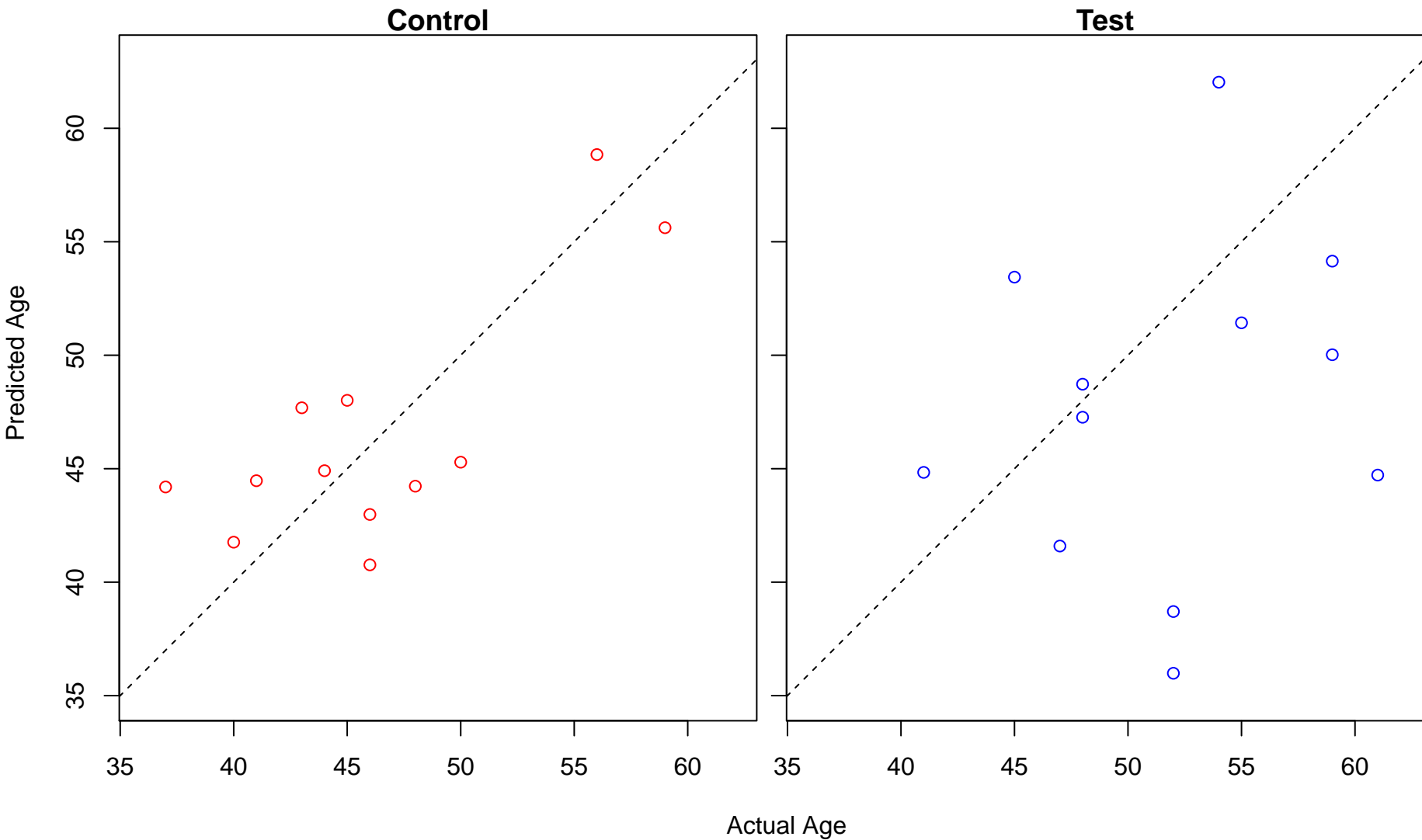
regulation of response to interferon- γ (Score: 4.239188)



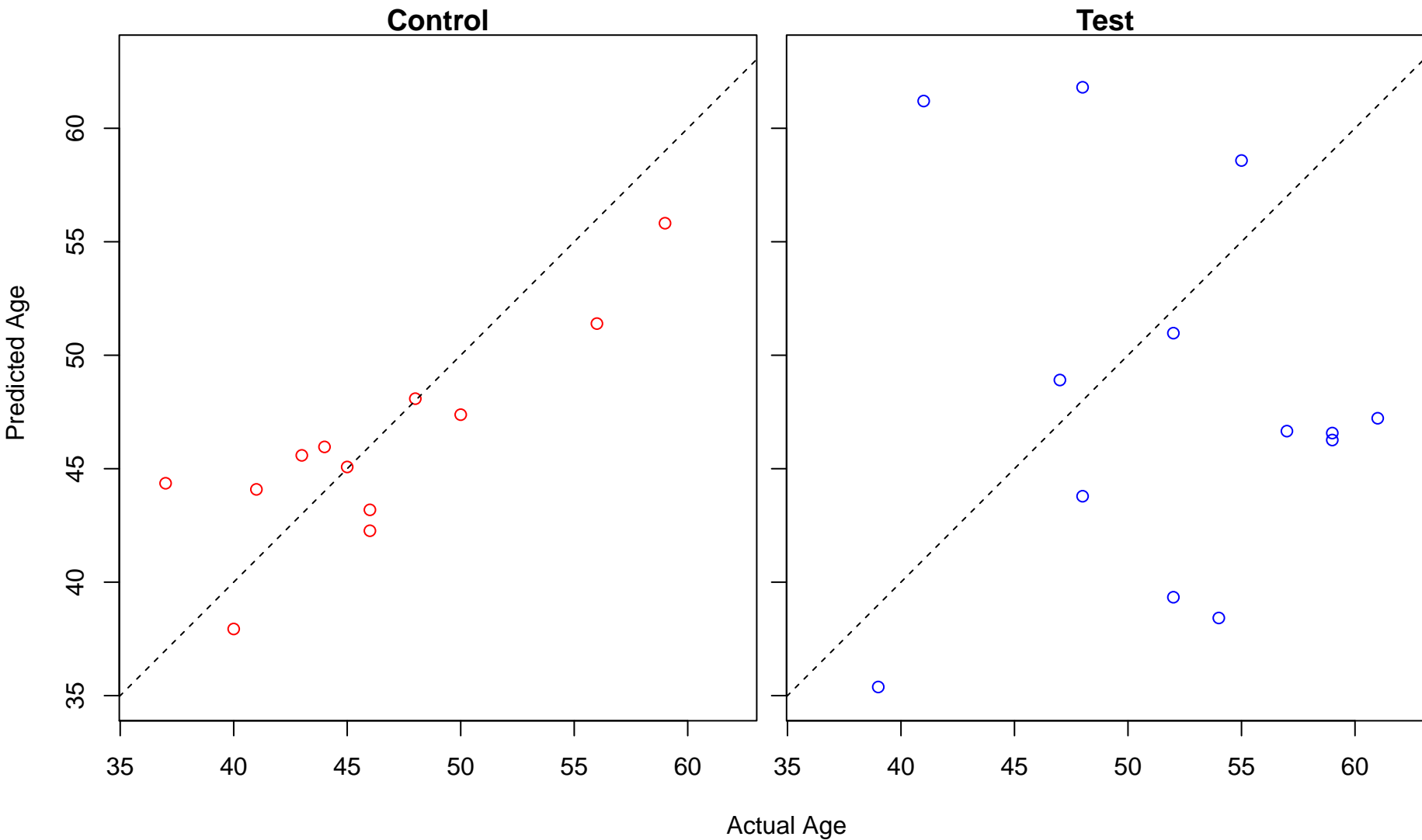
vascular endothelial growth factor signaling pathway (Score: 4.238411)



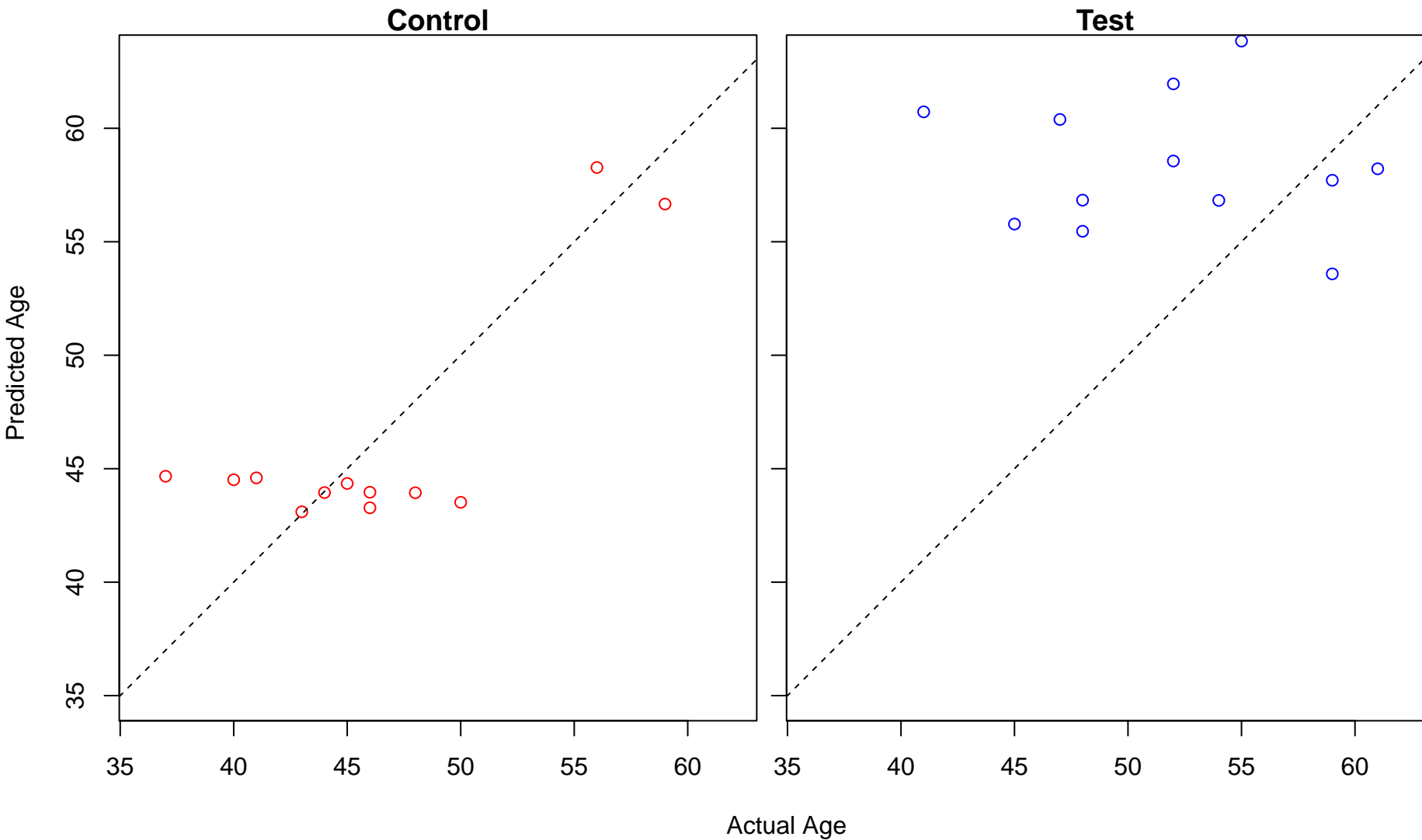
regulation of mitophagy (Score: 4.236840)



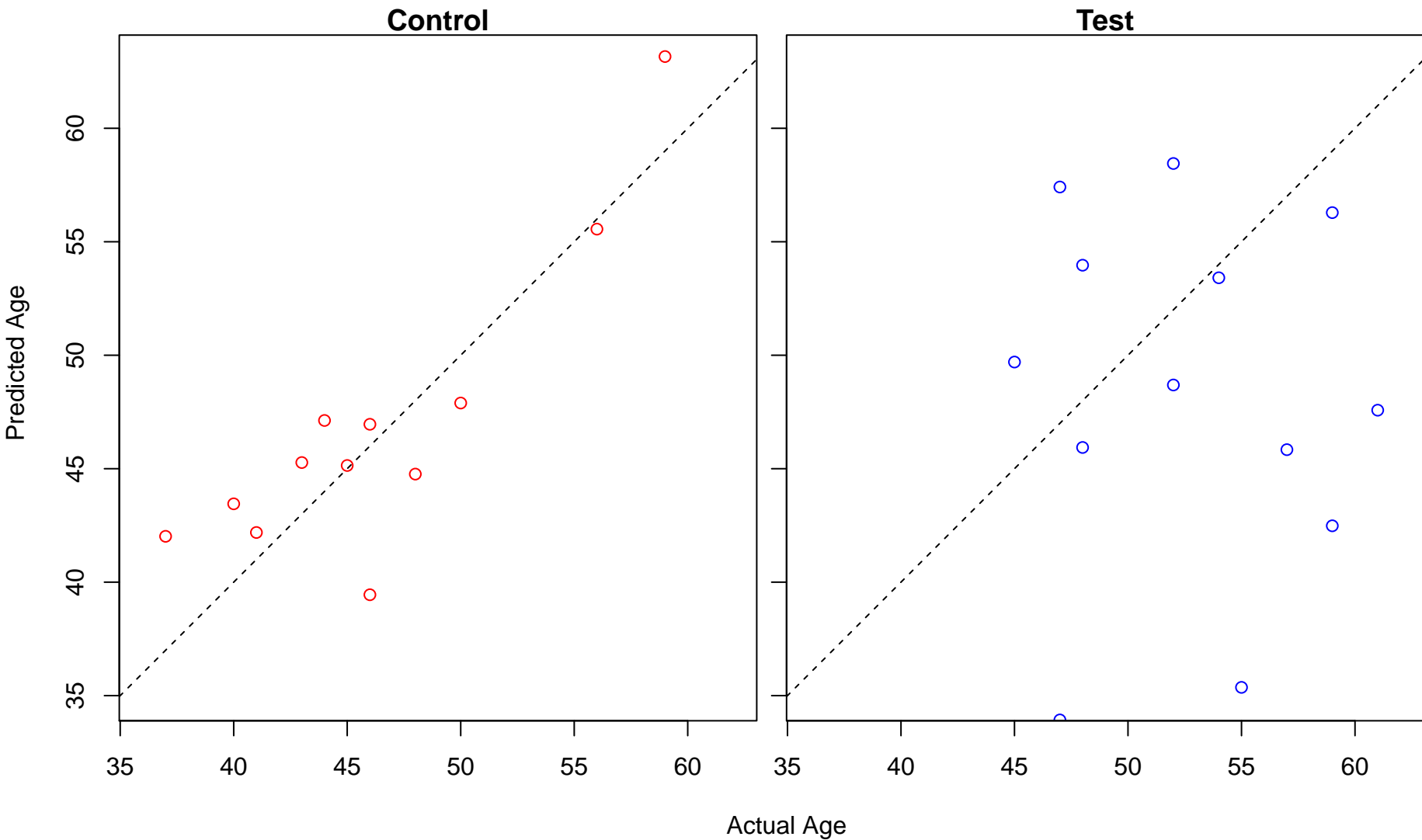
mesenchymal cell differentiation (Score: 4.232082)



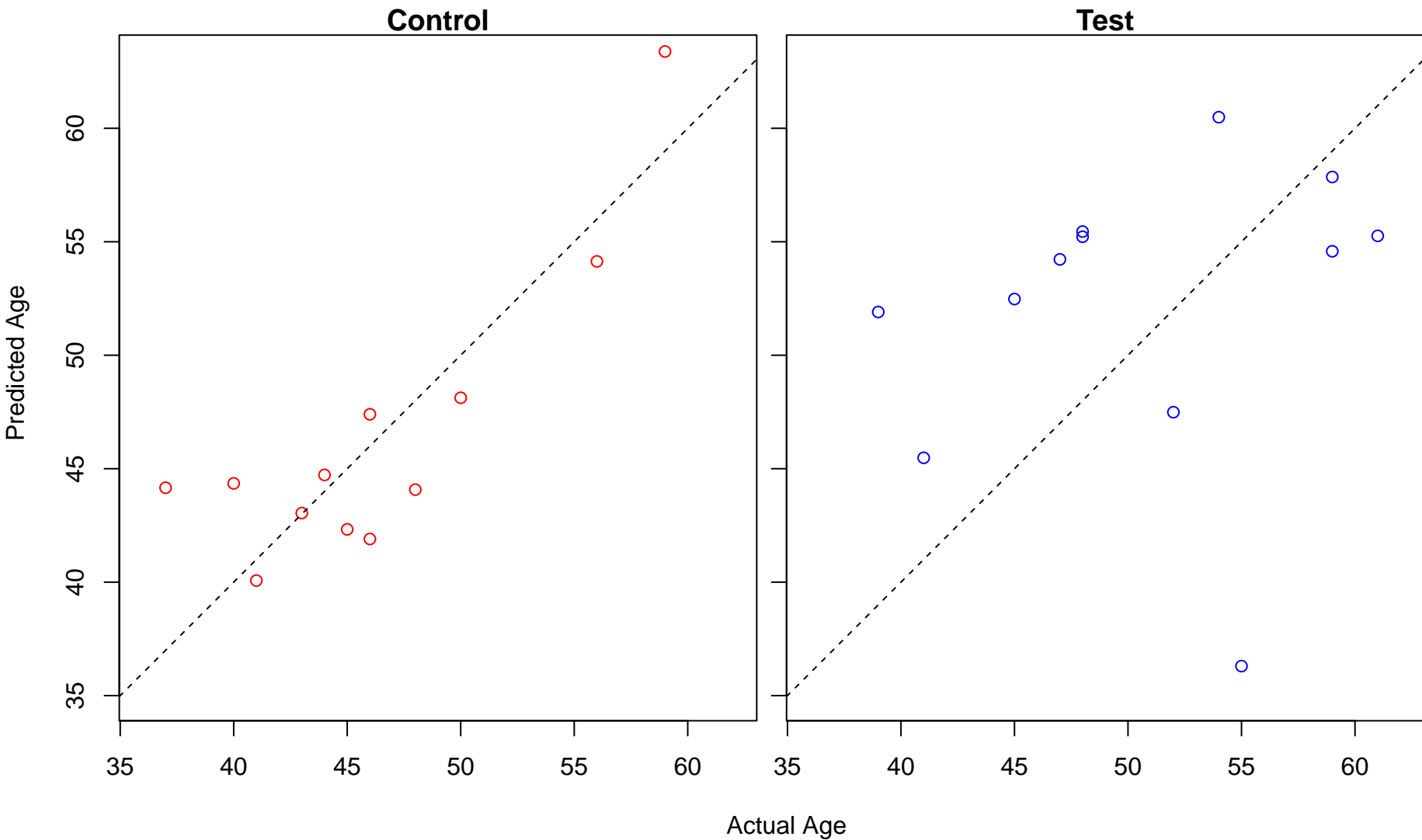
Notch signaling pathway (Score: 4.228227)



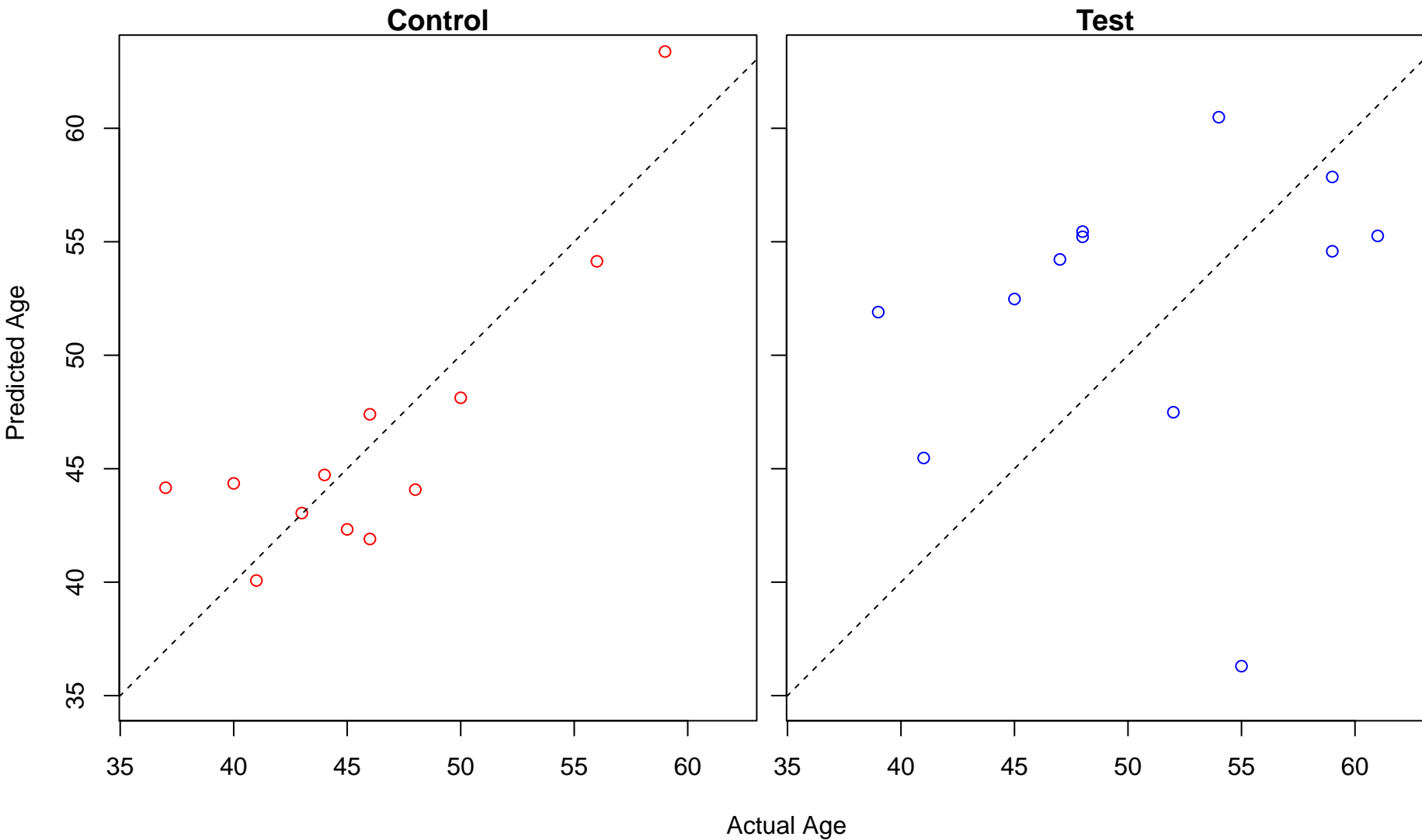
dendrite development (Score: 4.221403)



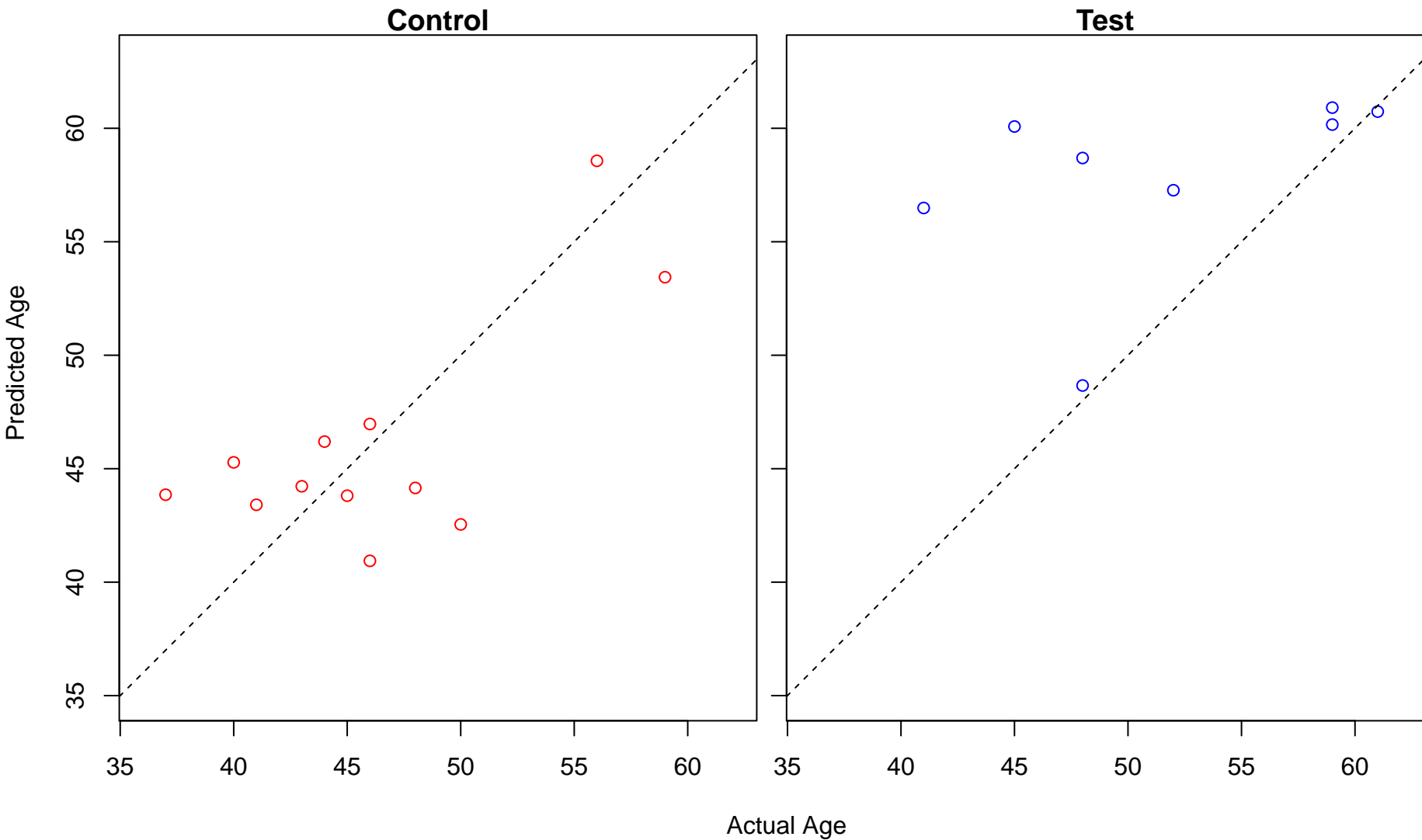
establishment of spindle localization (Score: 4.219922)



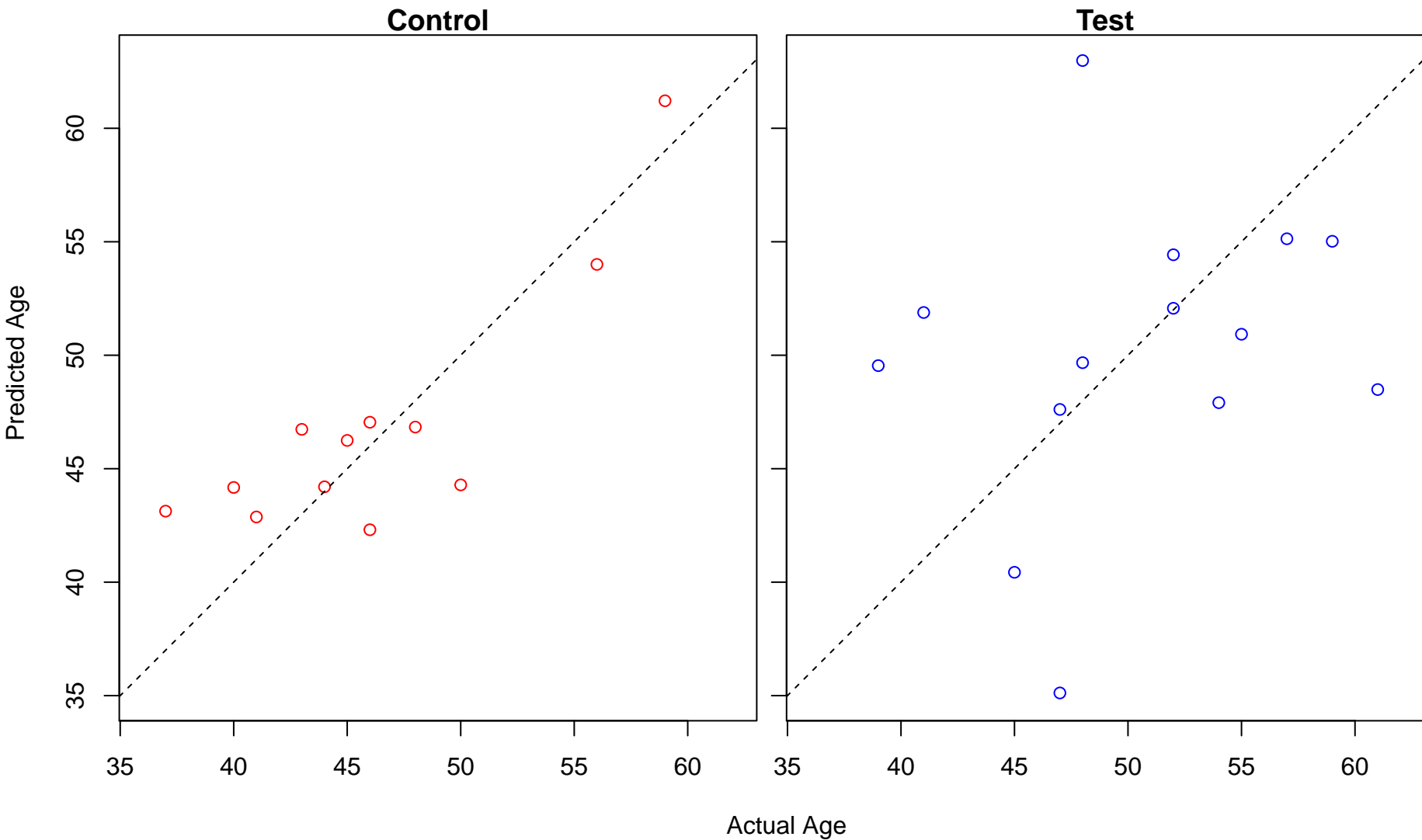
spindle localization (Score: 4.219829)



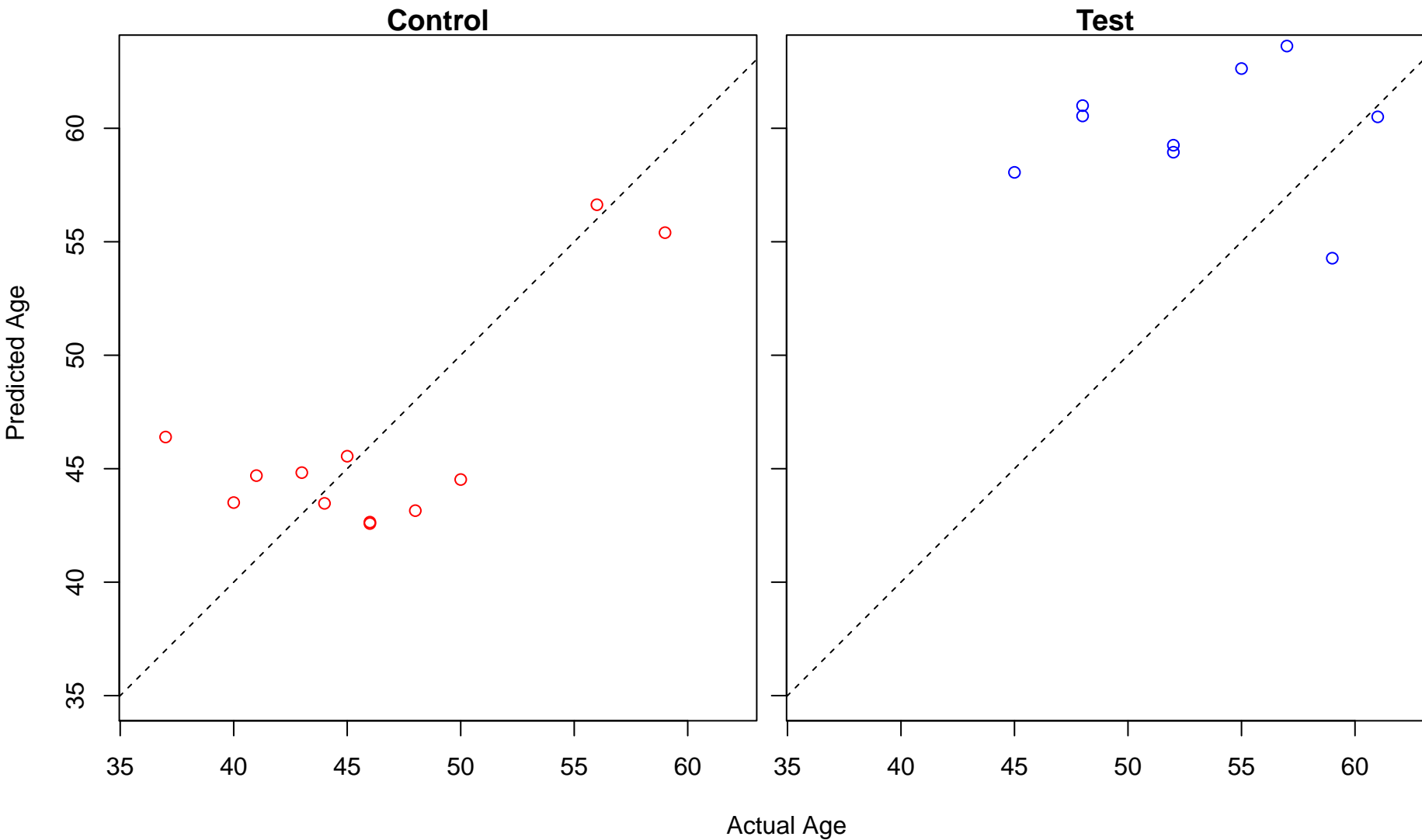
bile acid signaling pathway (Score: 4.218595)



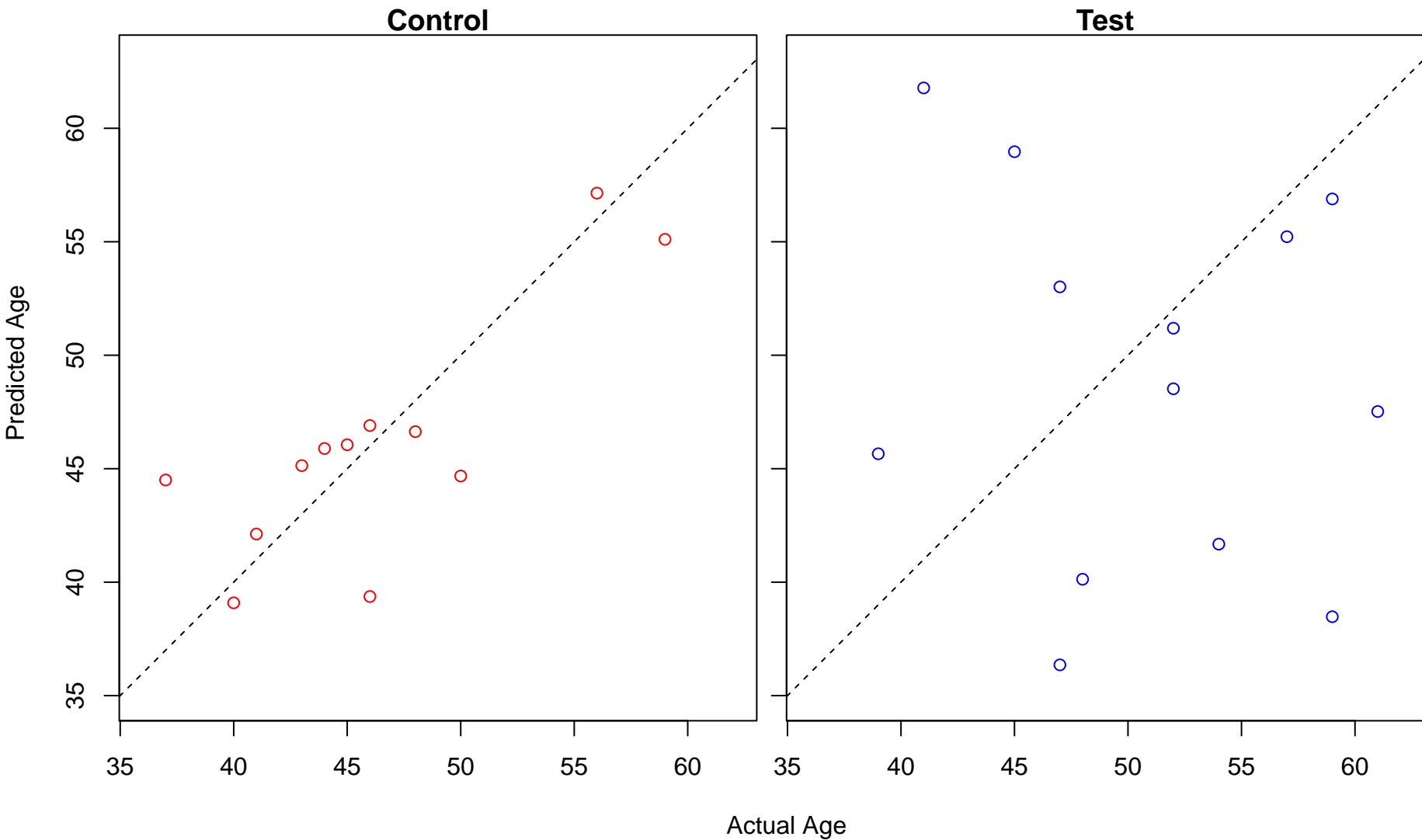
cellular response to topologically incorrect protein (Score: 4.217989)



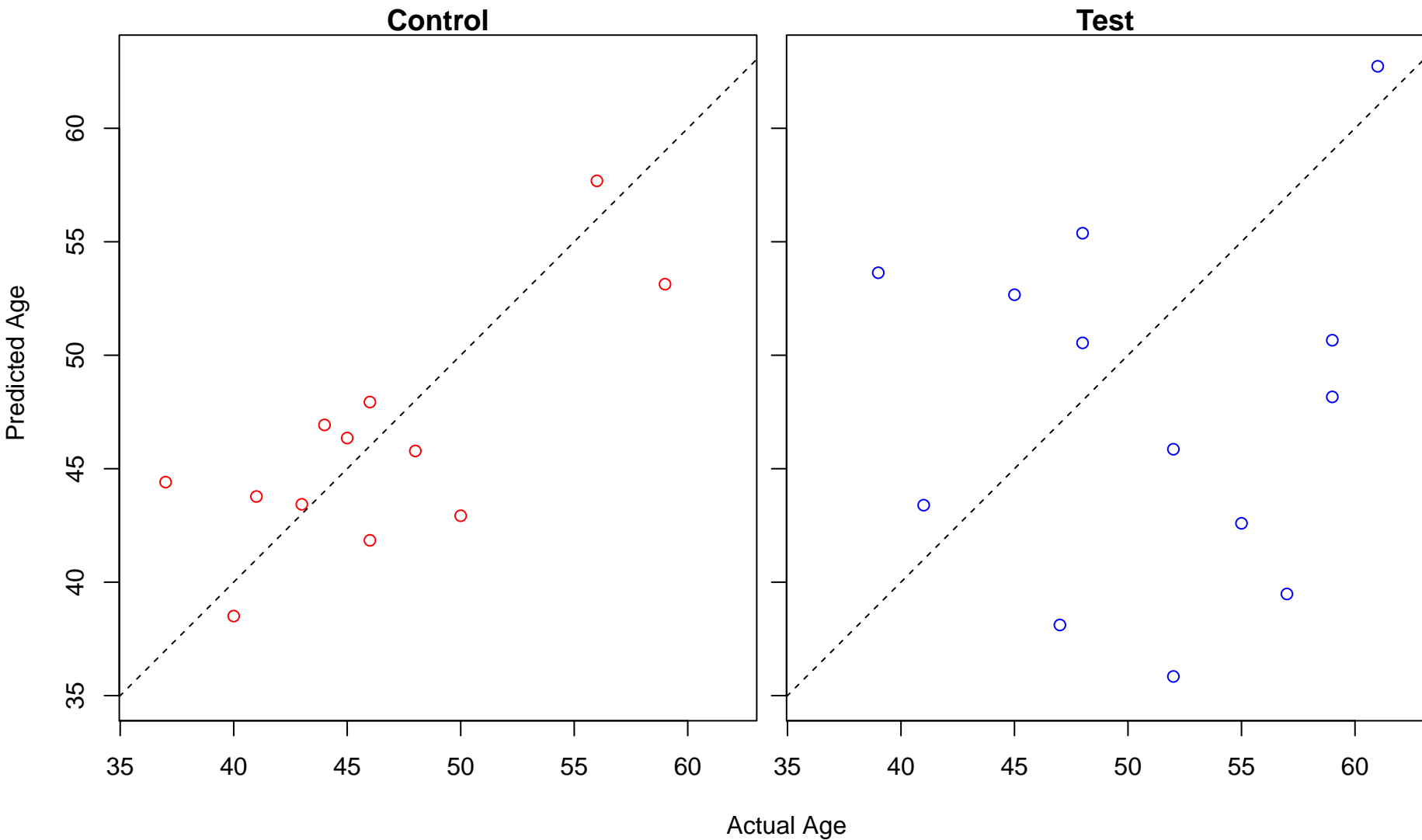
binding of sperm to zona pellucida (Score: 4.217216)



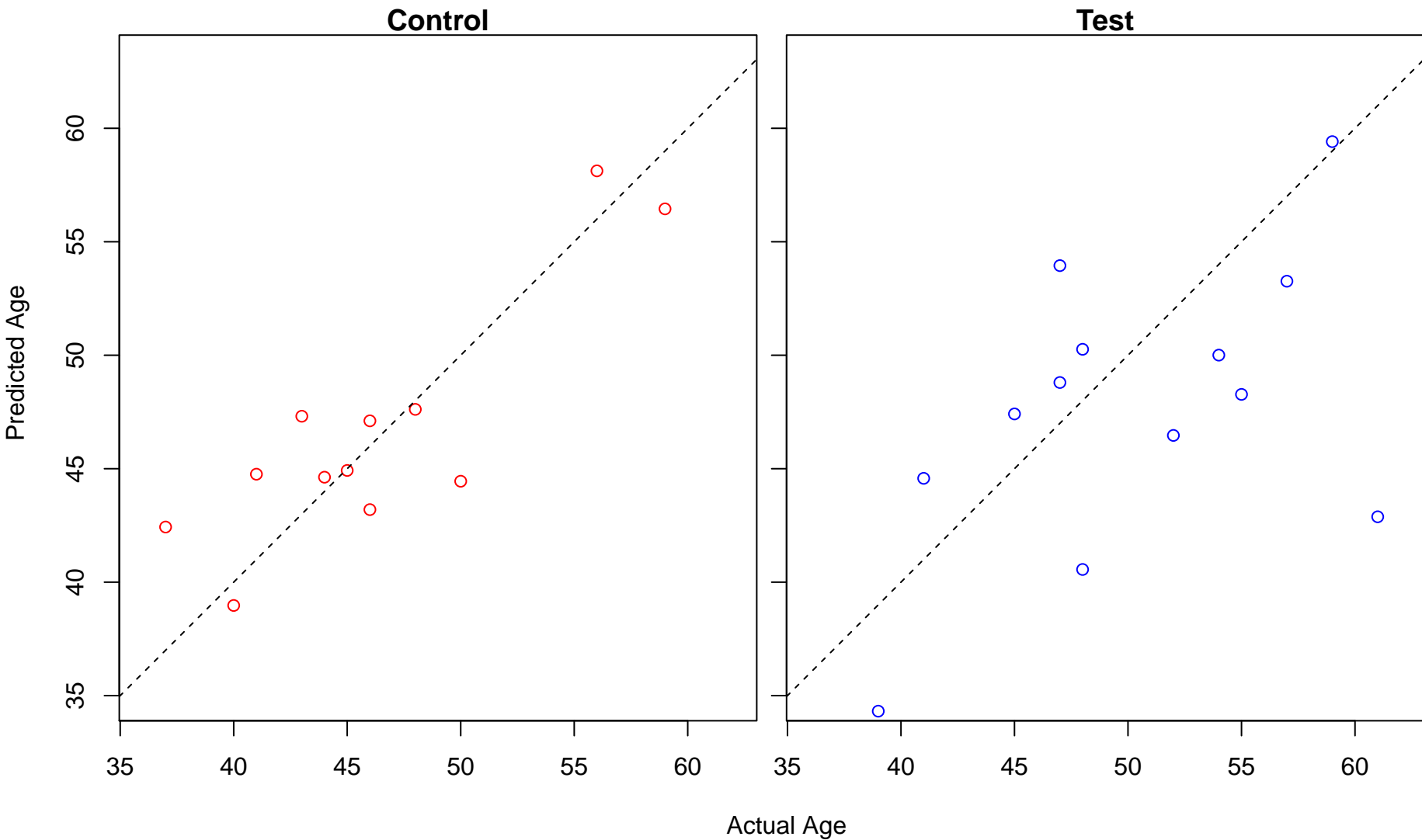
embryo development (Score: 4.214628)



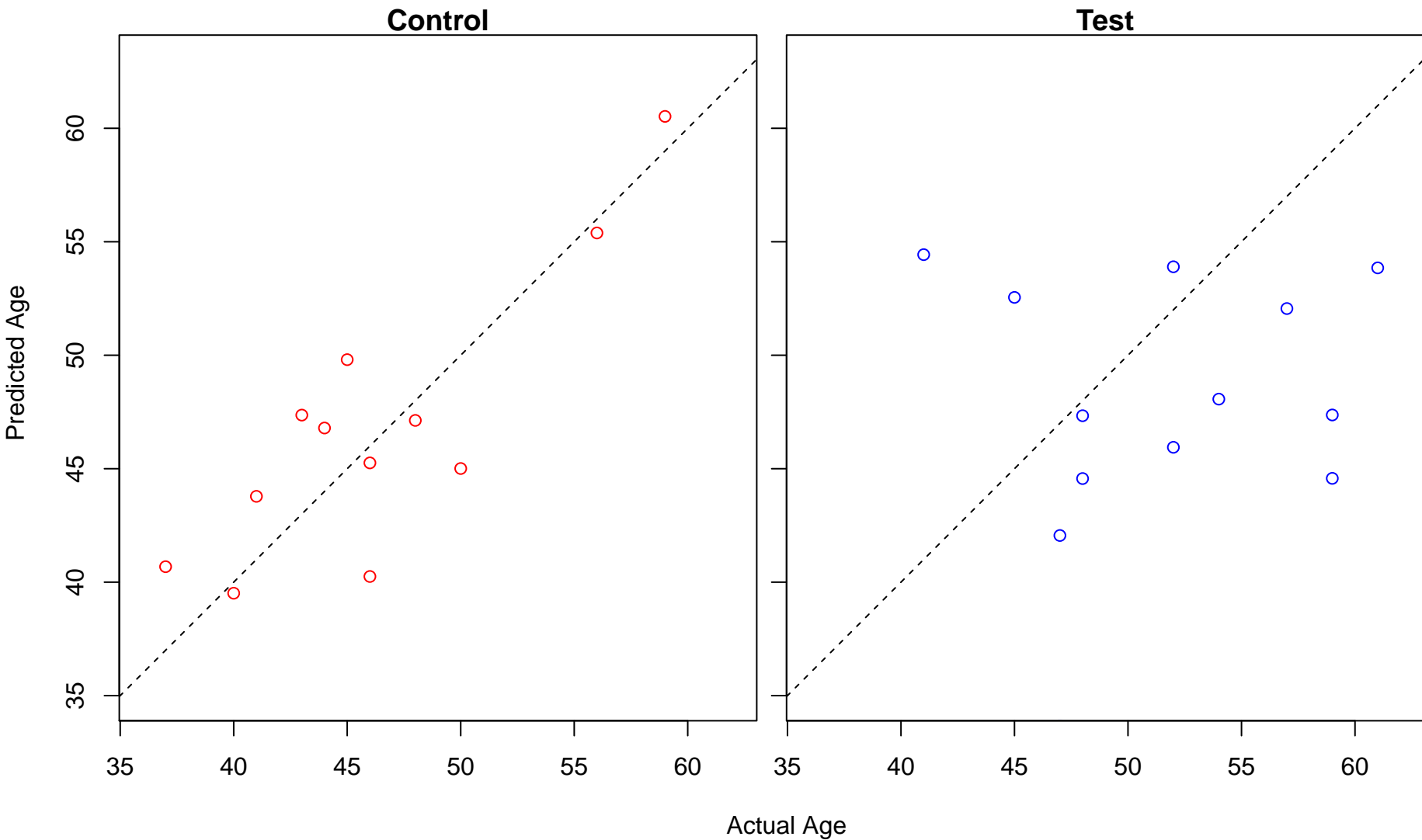
collagen metabolic process (Score: 4.211404)



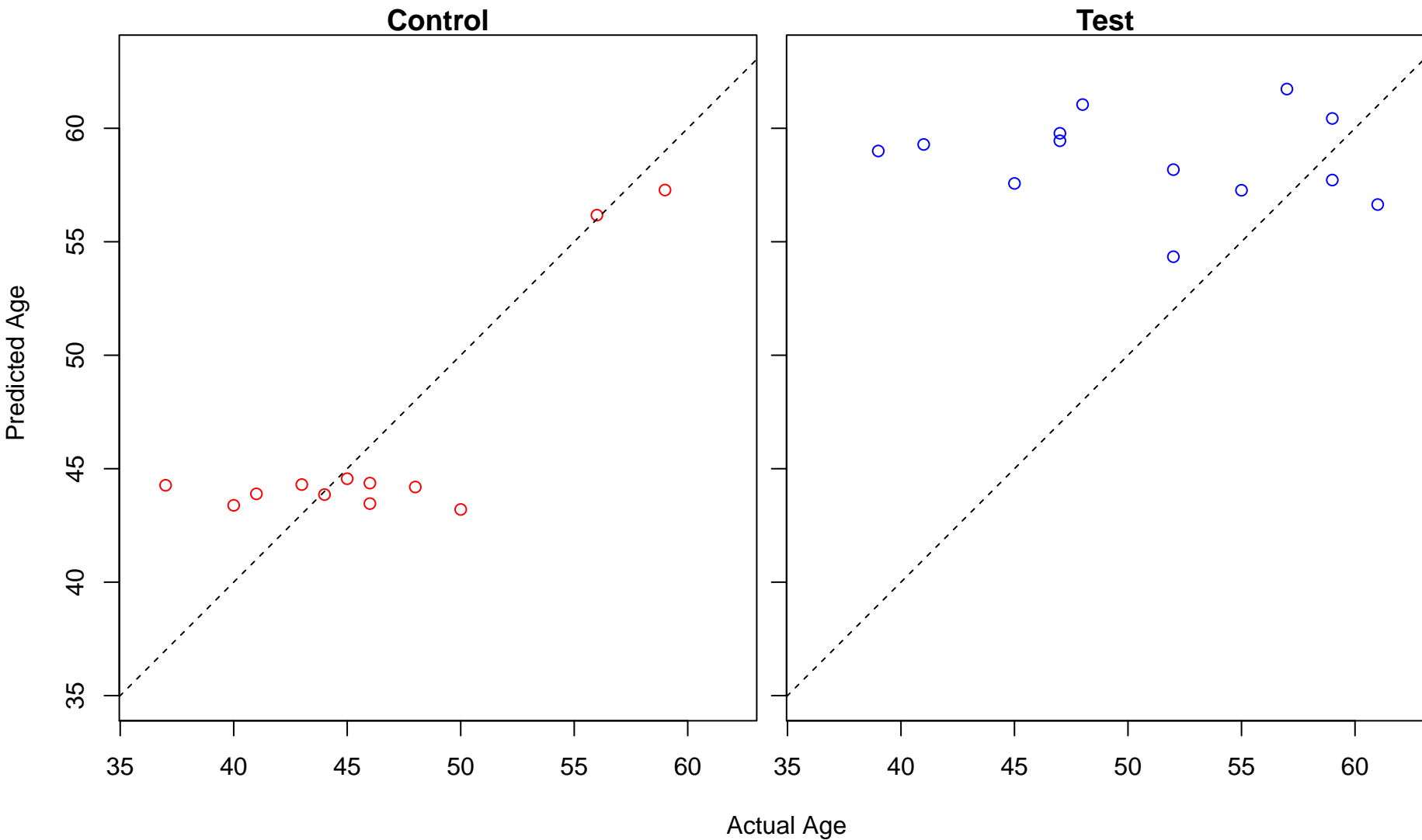
hematopoietic or lymphoid organ development (Score: 4.210996)



regulation of interferon-gamma-mediated signaling pathway (Score: 4.210015)

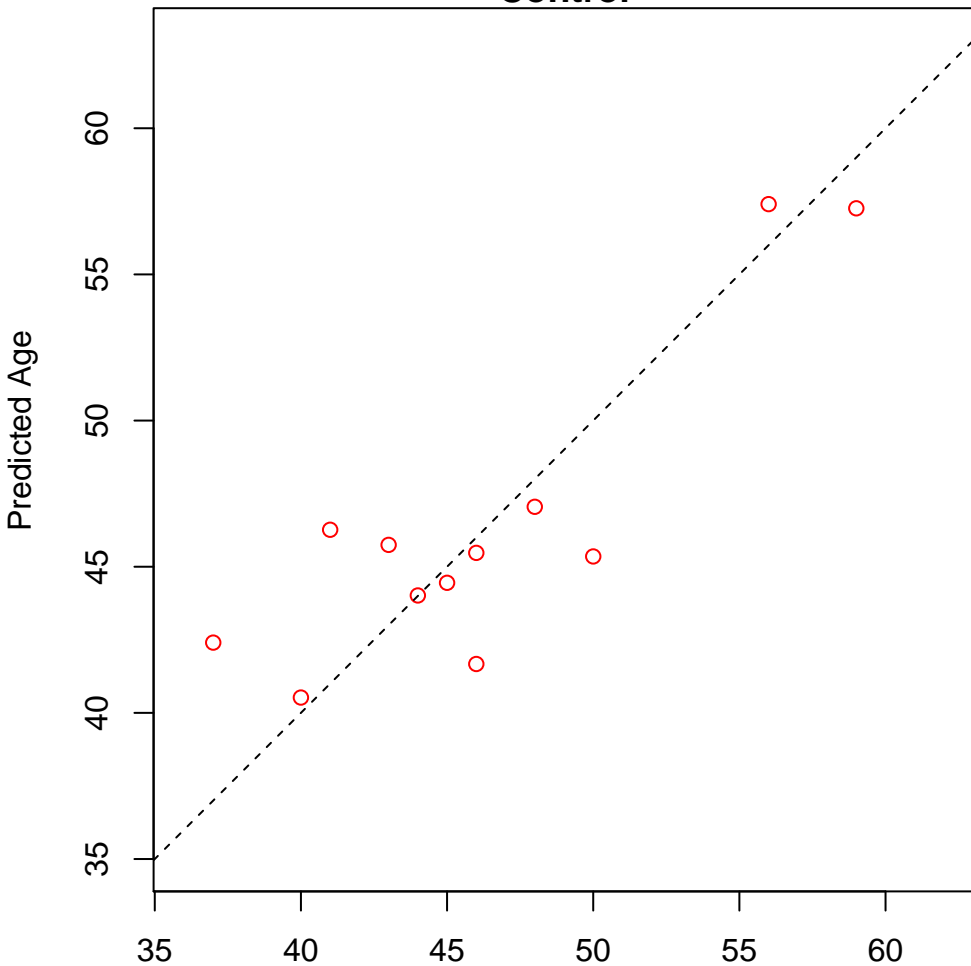


positive regulation of type 2 immune response (Score: 4.208762)

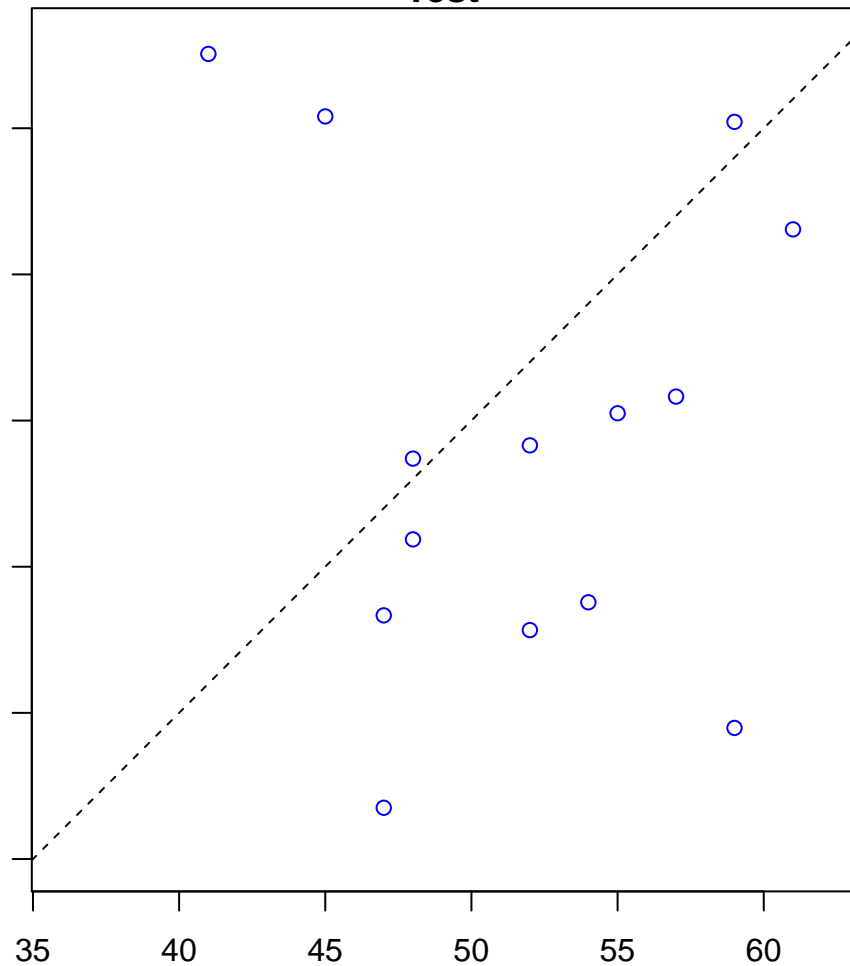


positive regulation of cell proliferation (Score: 4.207585)

Control

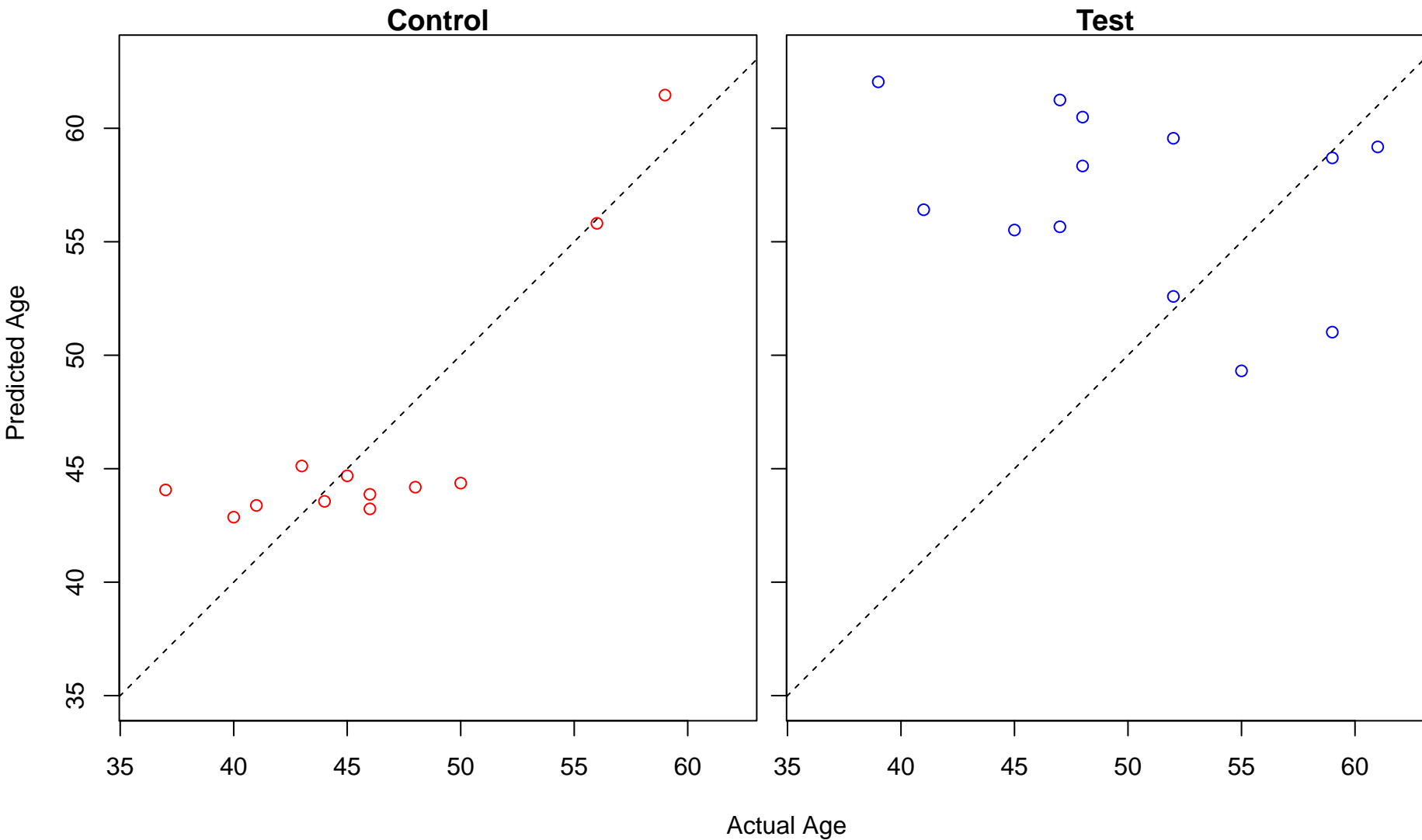


Test

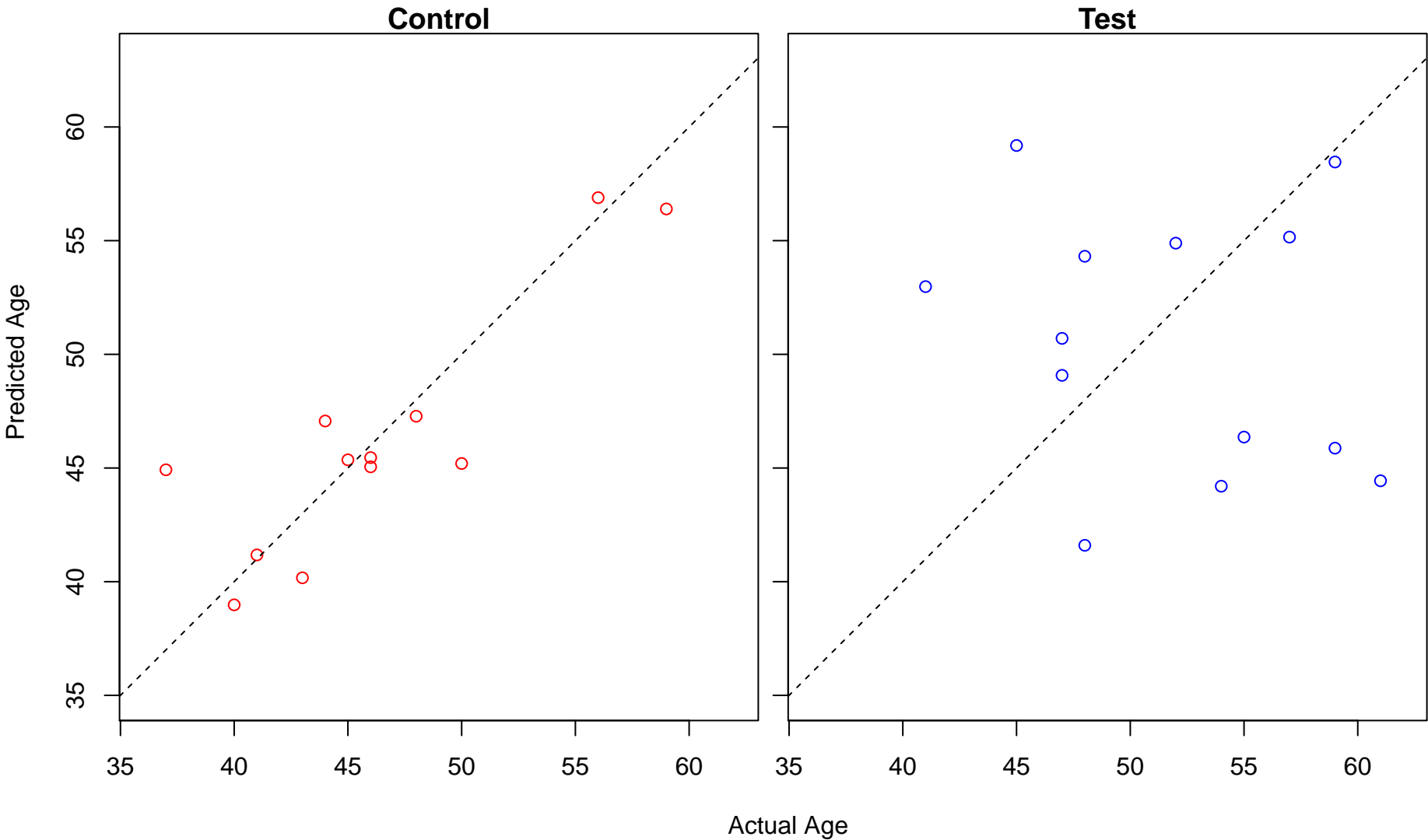


Actual Age

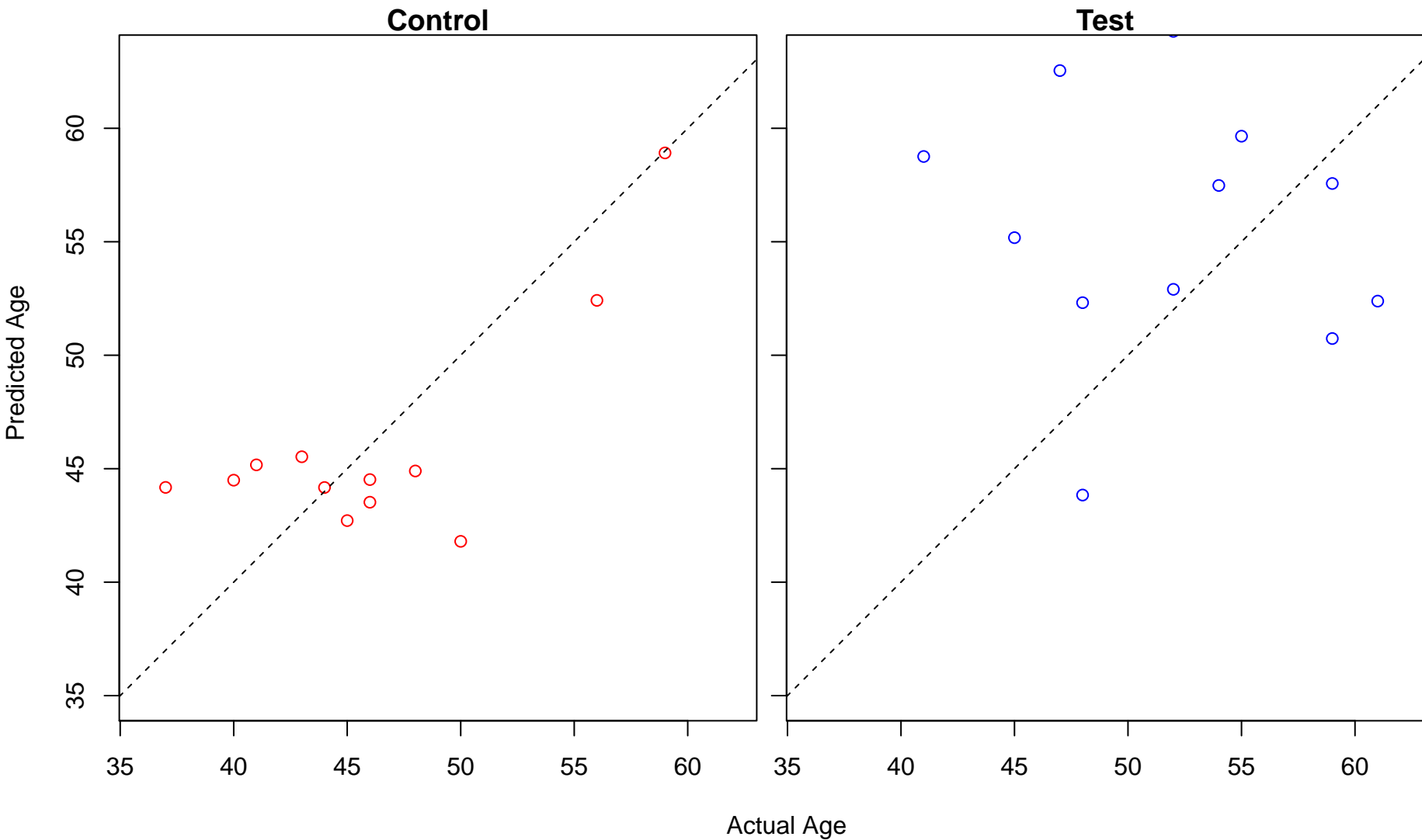
regulation of transcription from RNA polymerase III promoter (Score: 4.205377)



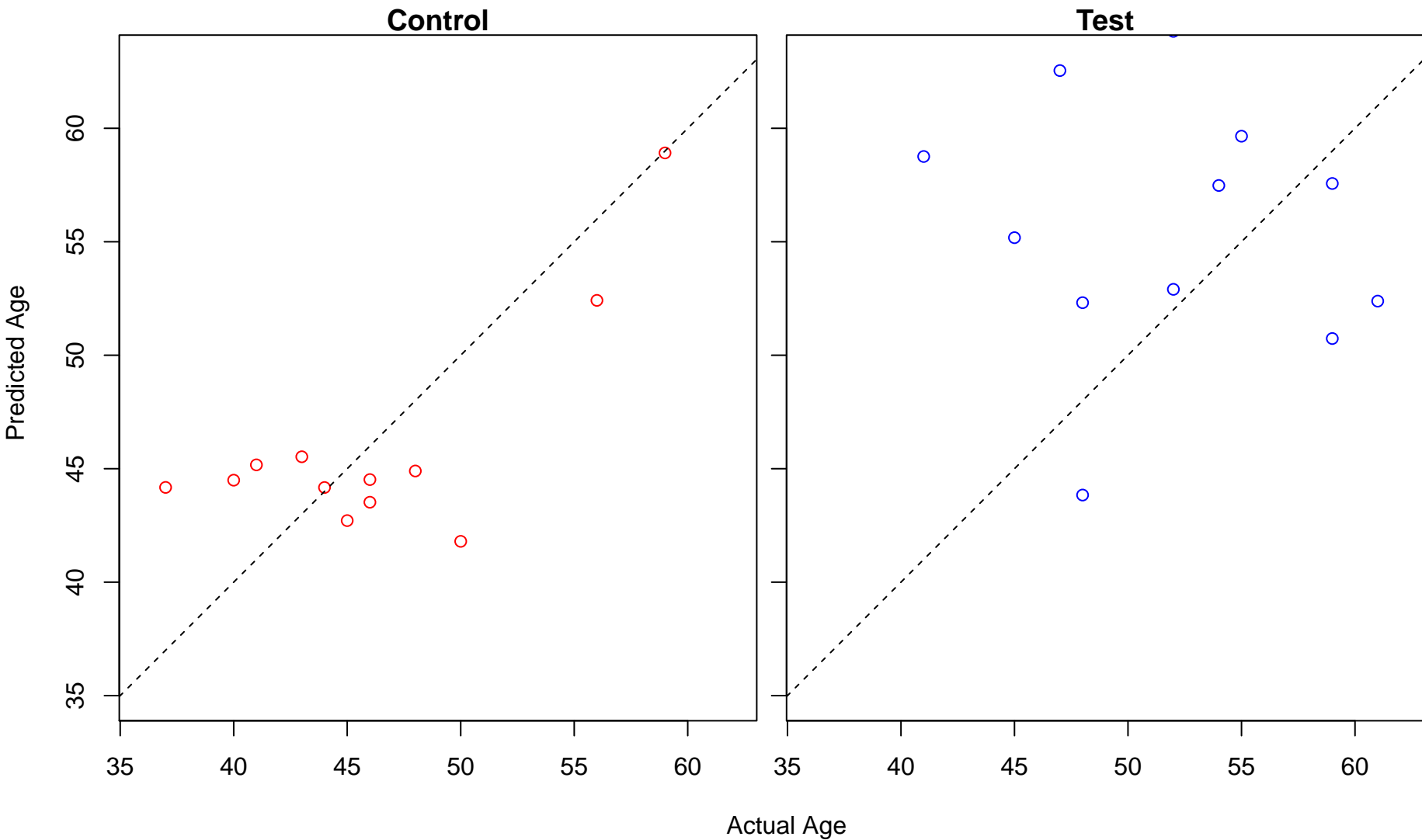
regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis (Score: 4.20)



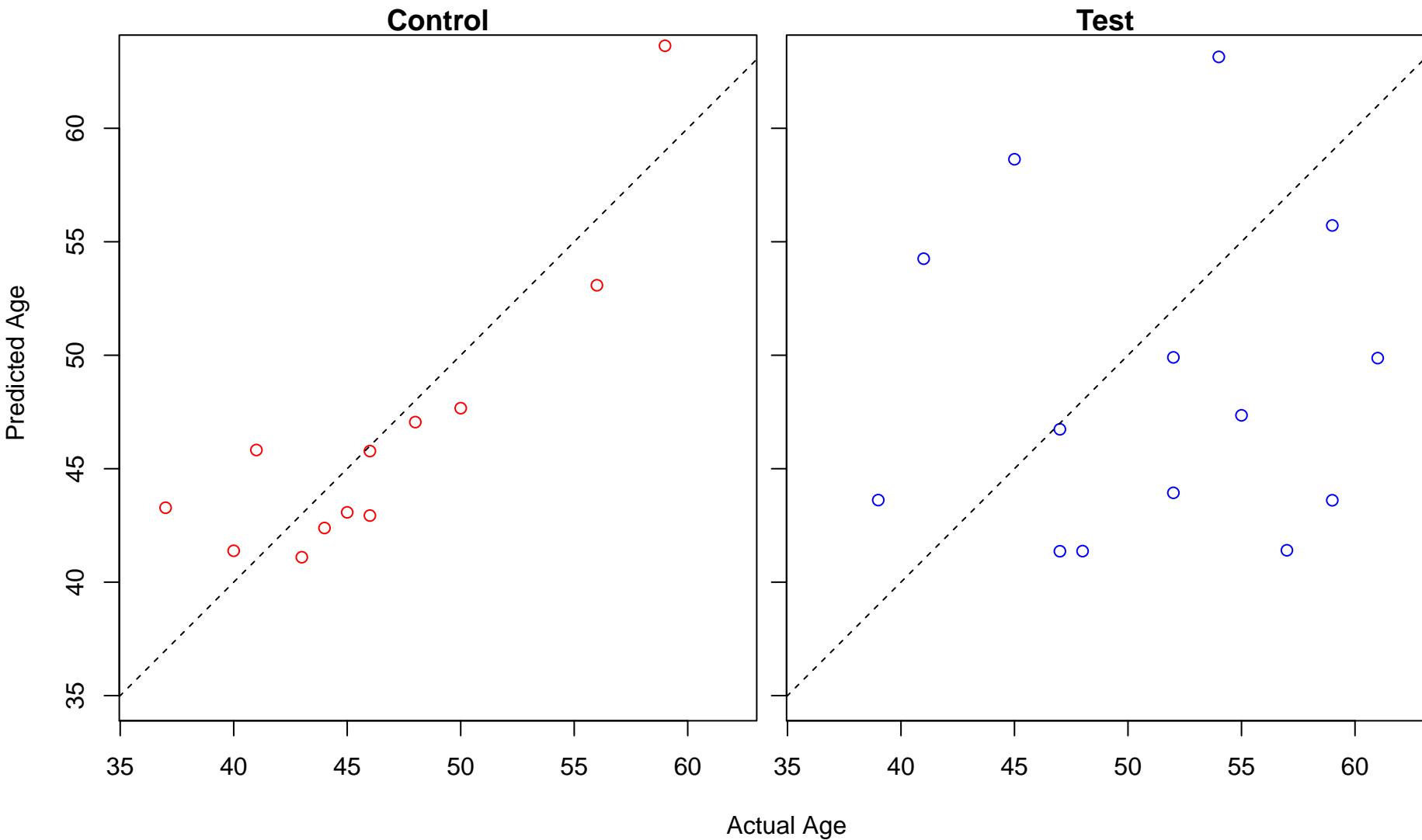
negative regulation of natural killer cell mediated immunity (Score: 4.203858)



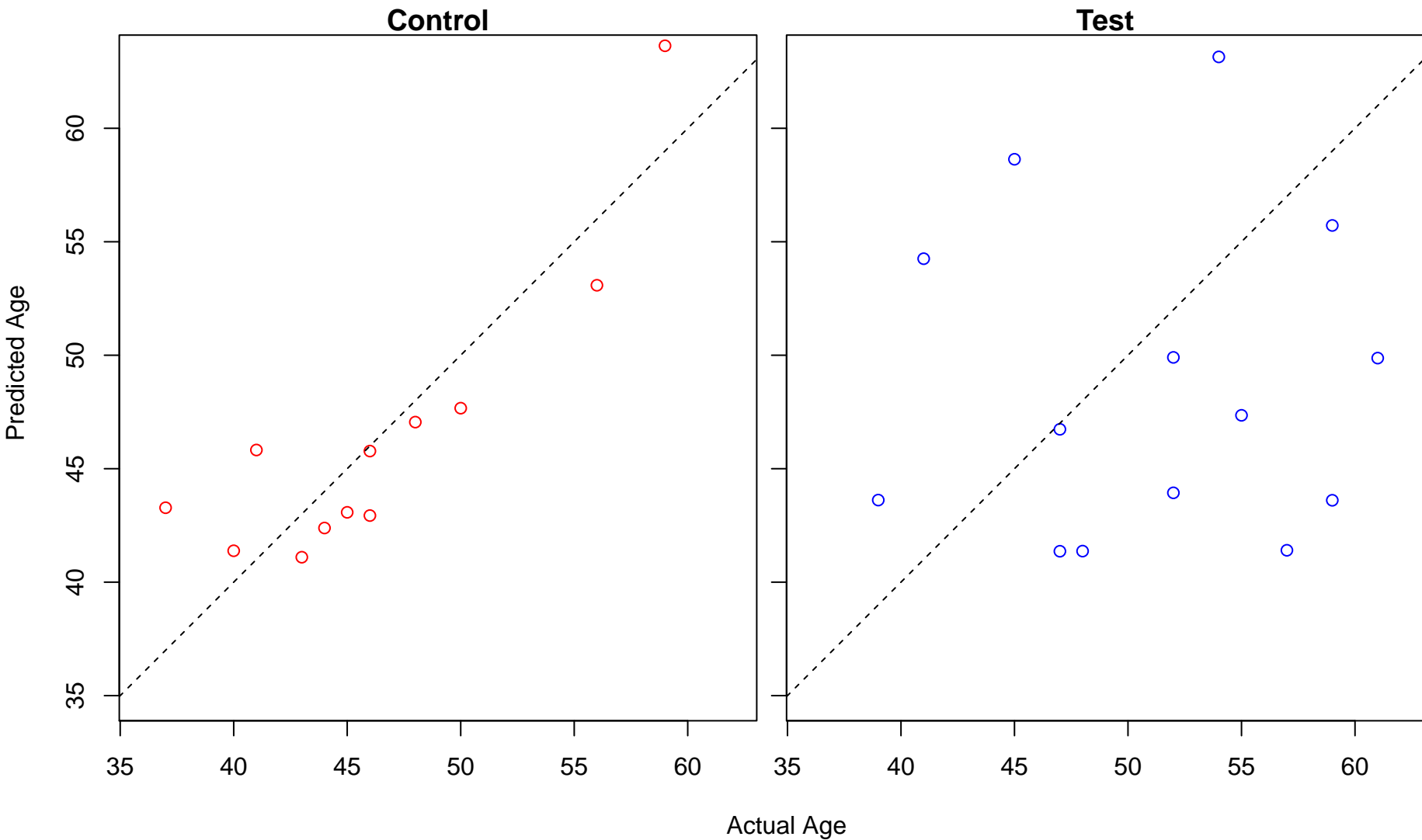
negative regulation of natural killer cell mediated cytotoxicity (Score: 4.203858)



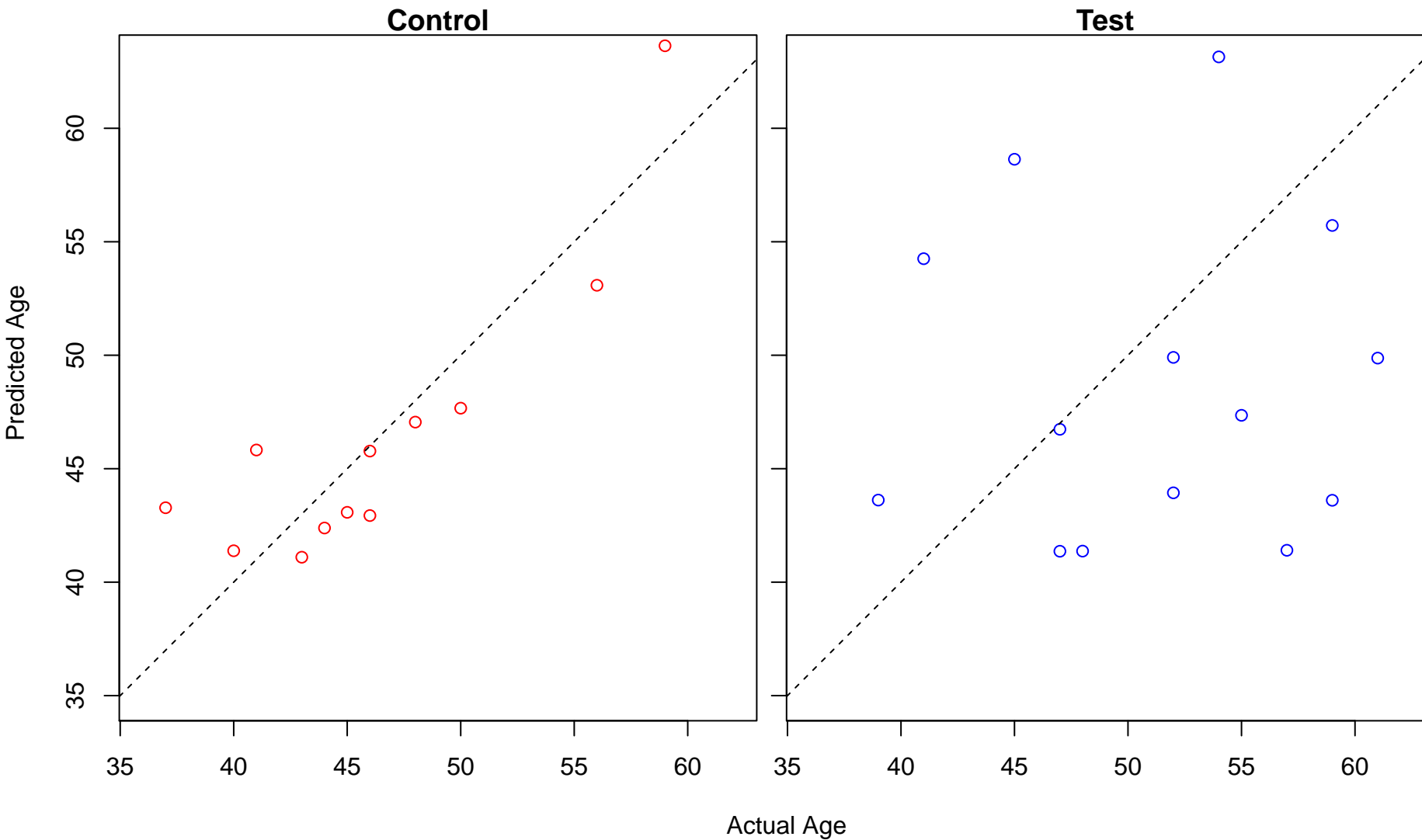
response to caffeine (Score: 4.203647)



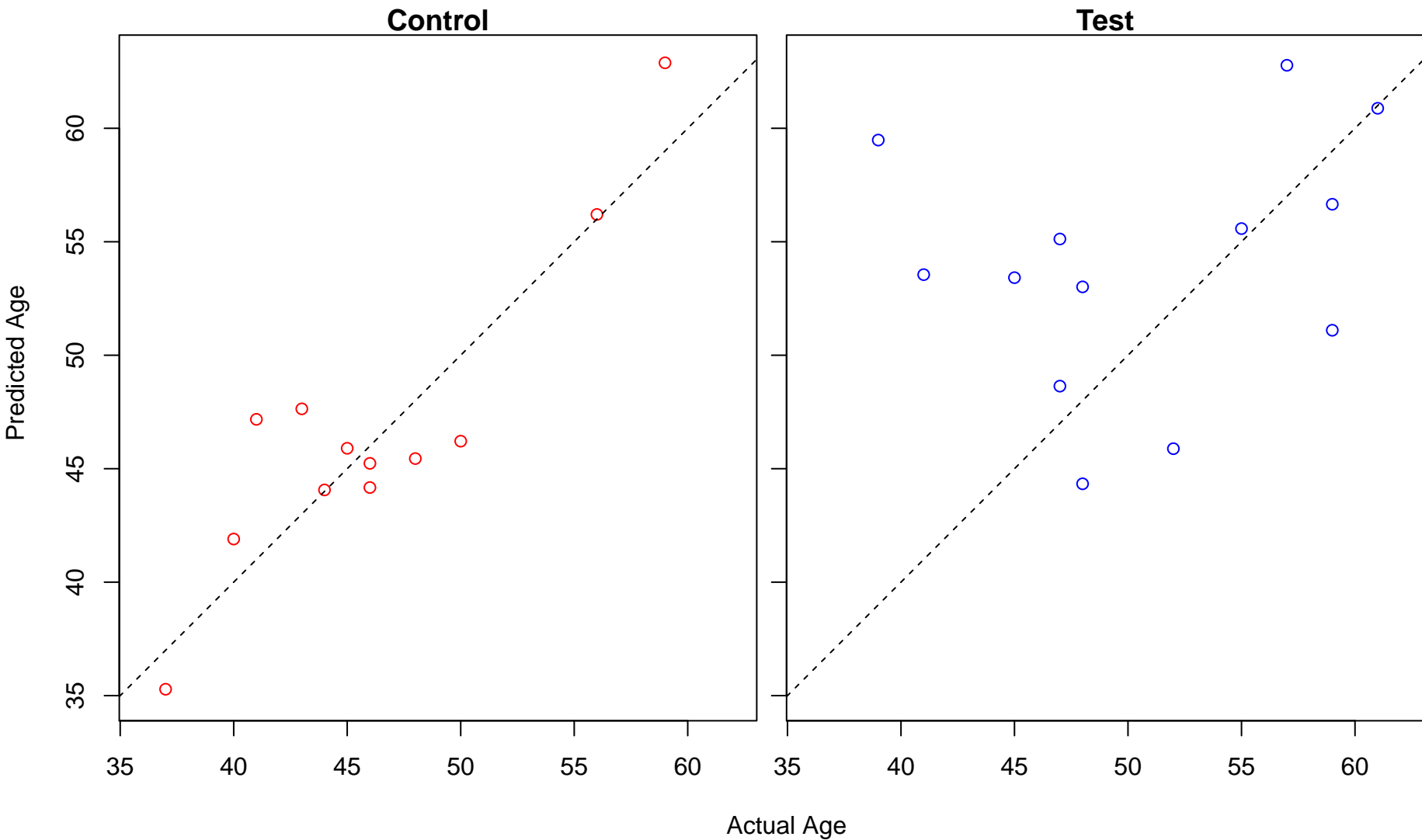
cellular response to caffeine (Score: 4.203647)



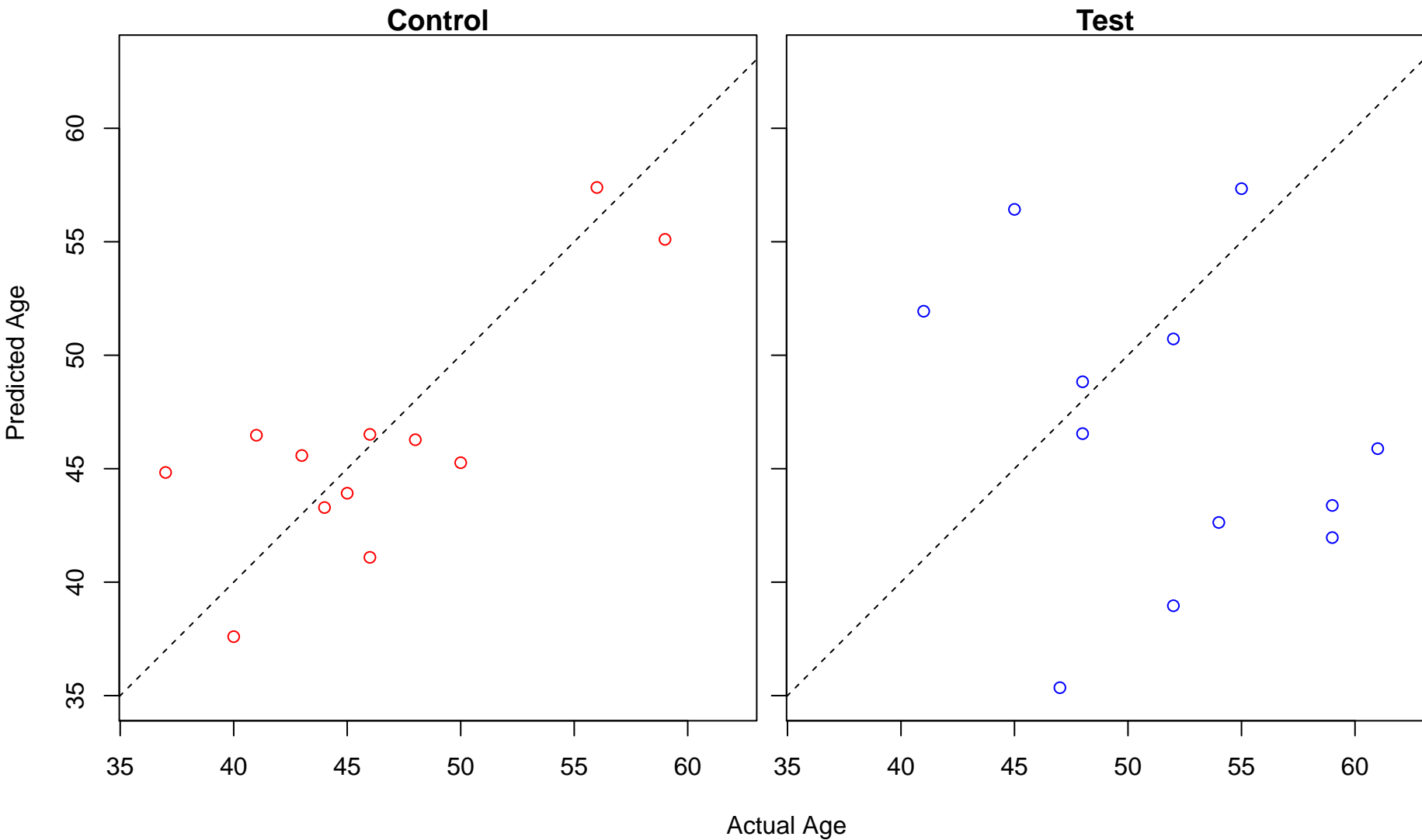
cellular response to purine-containing compound (Score: 4.203647)



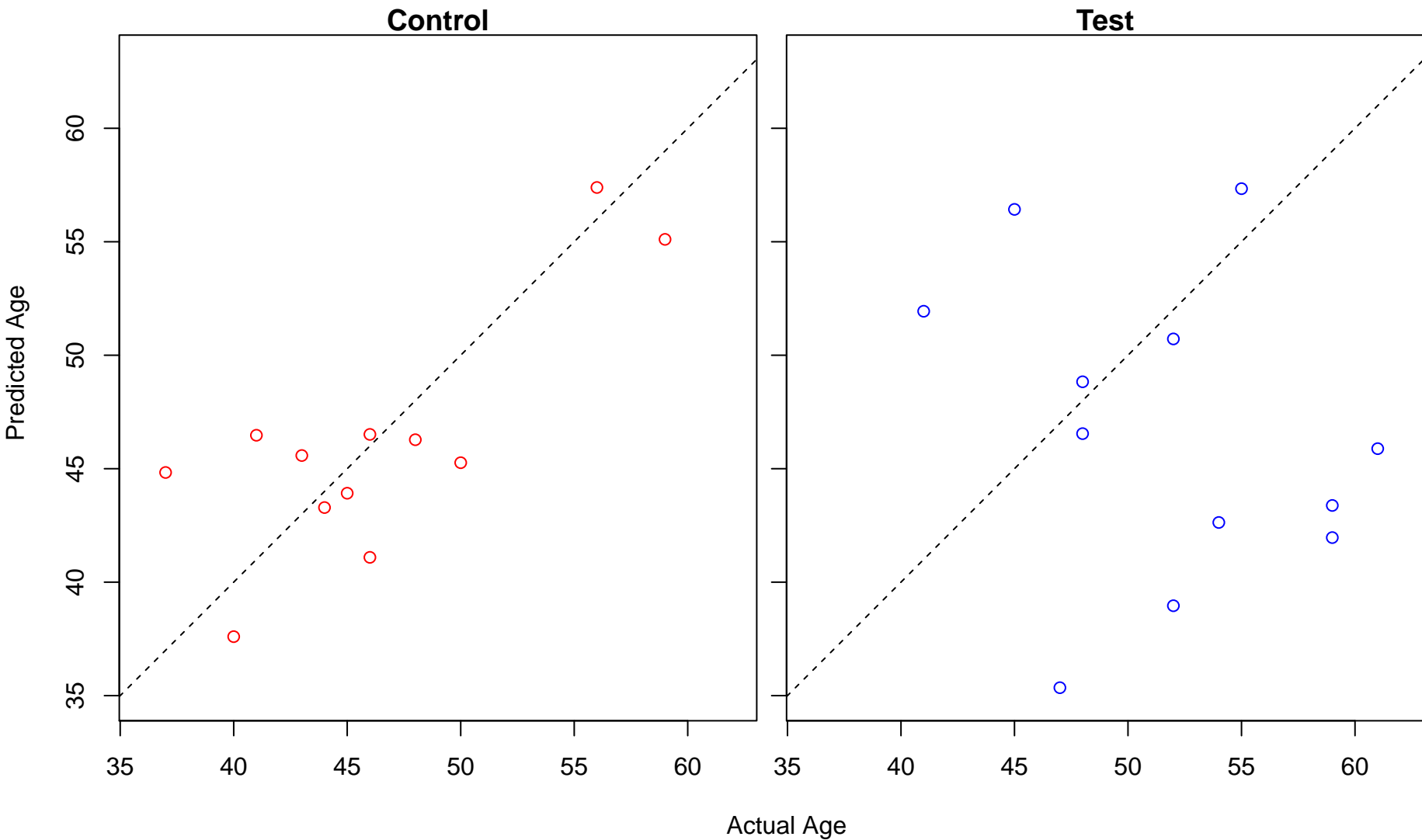
positive regulation of nitric-oxide synthase activity (Score: 4.199997)



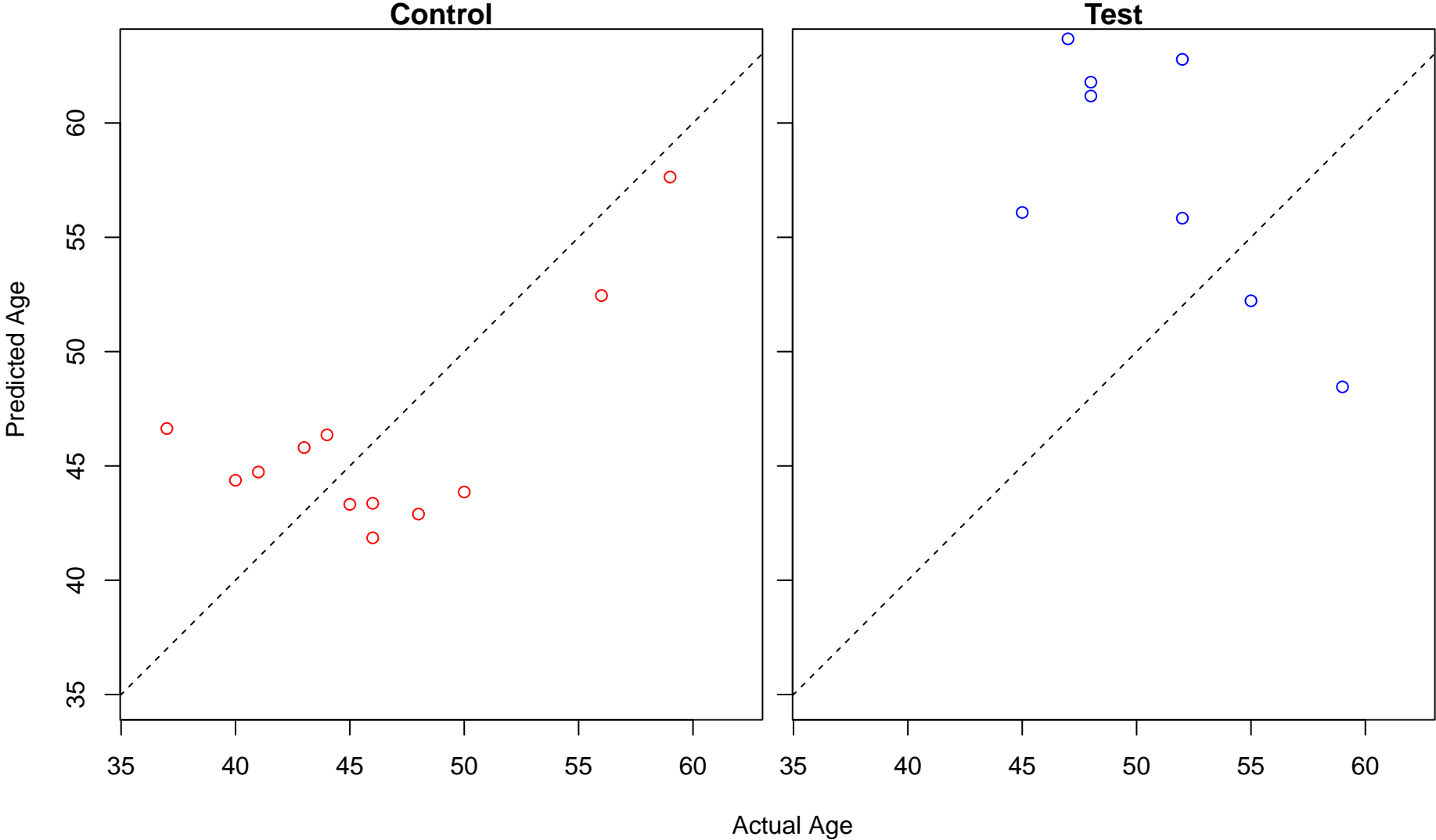
neutral lipid biosynthetic process (Score: 4.185908)



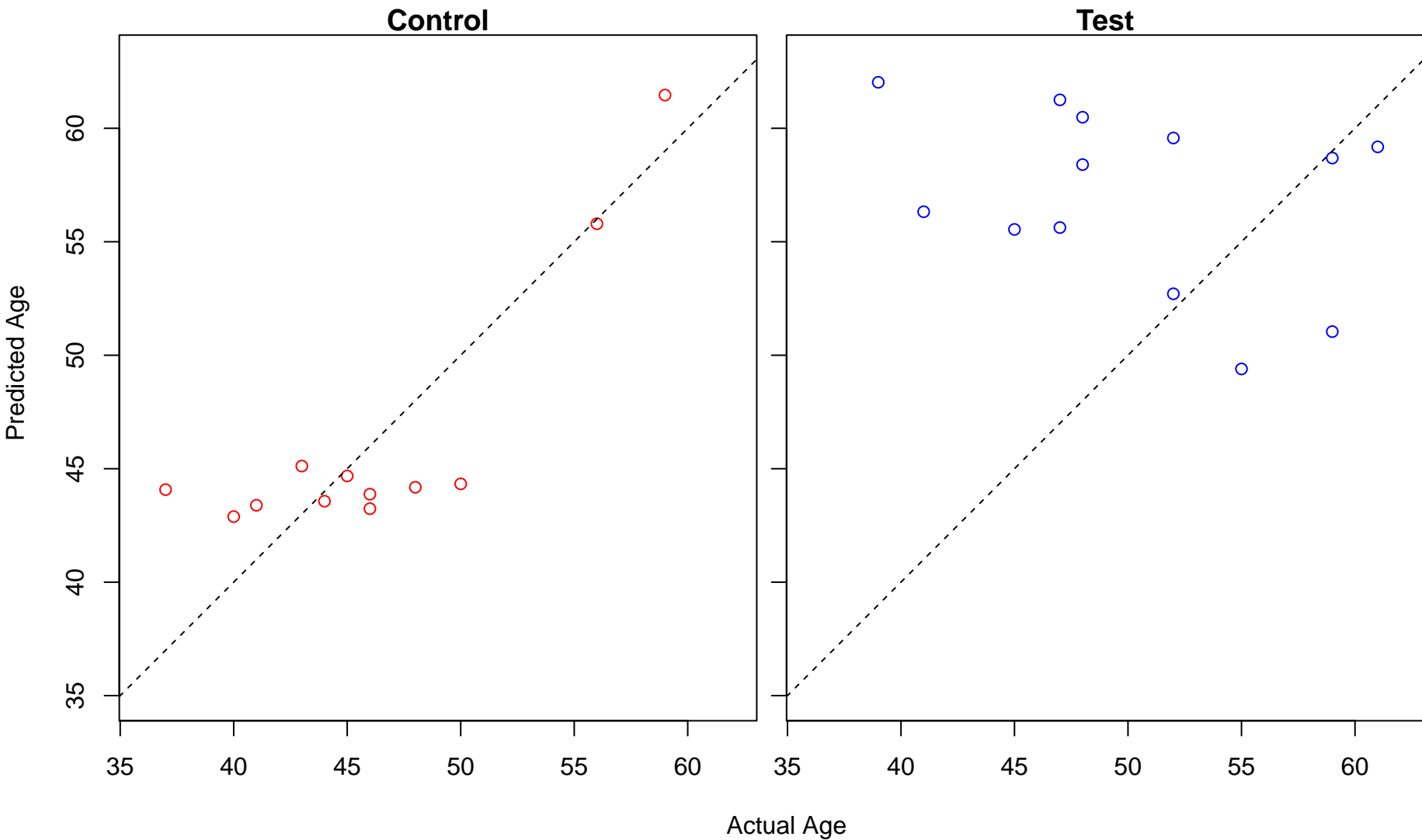
acylglycerol biosynthetic process (Score: 4.185908)



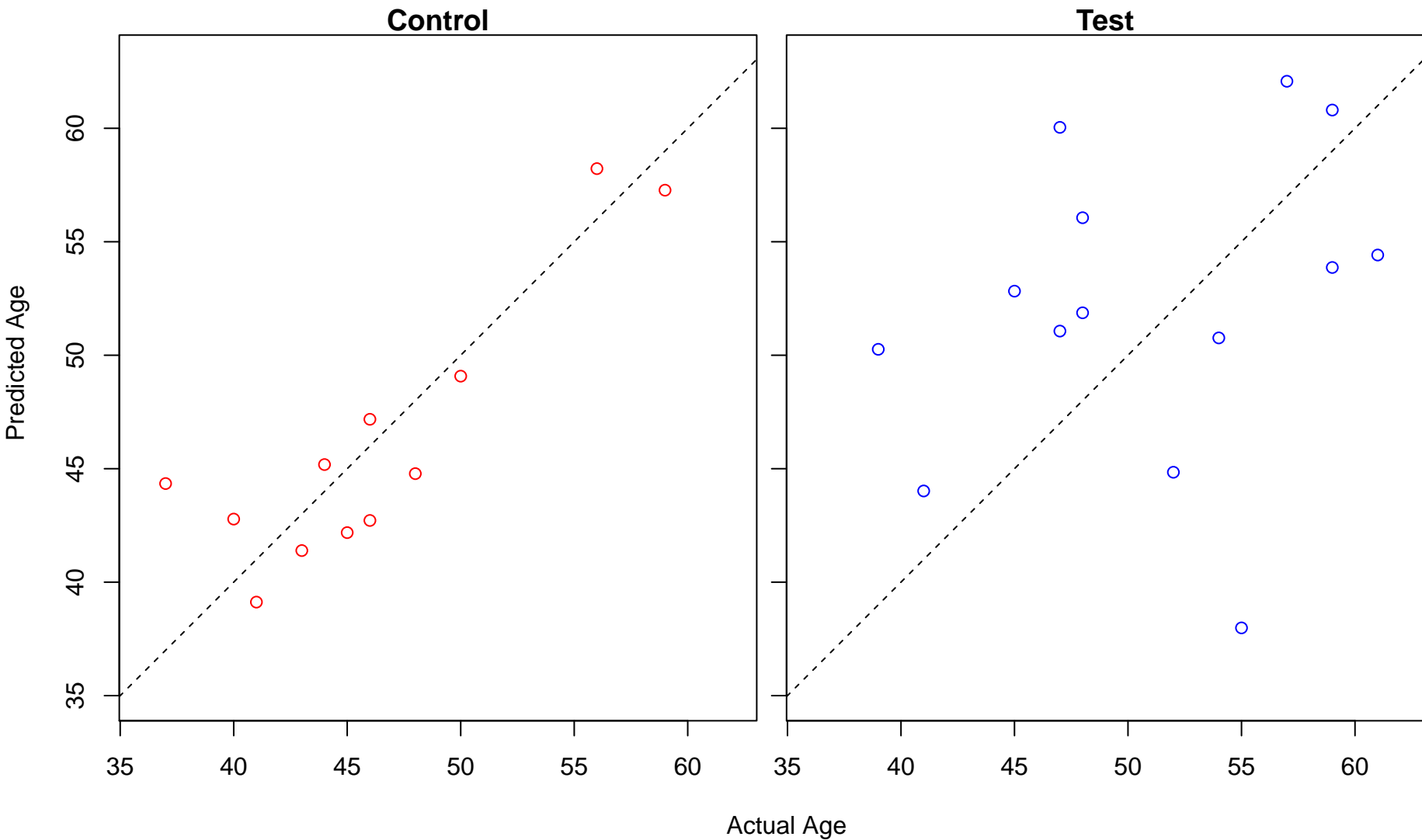
positive regulation of cell migration by vascular endothelial growth factor signaling pathway (Score: 4.1)



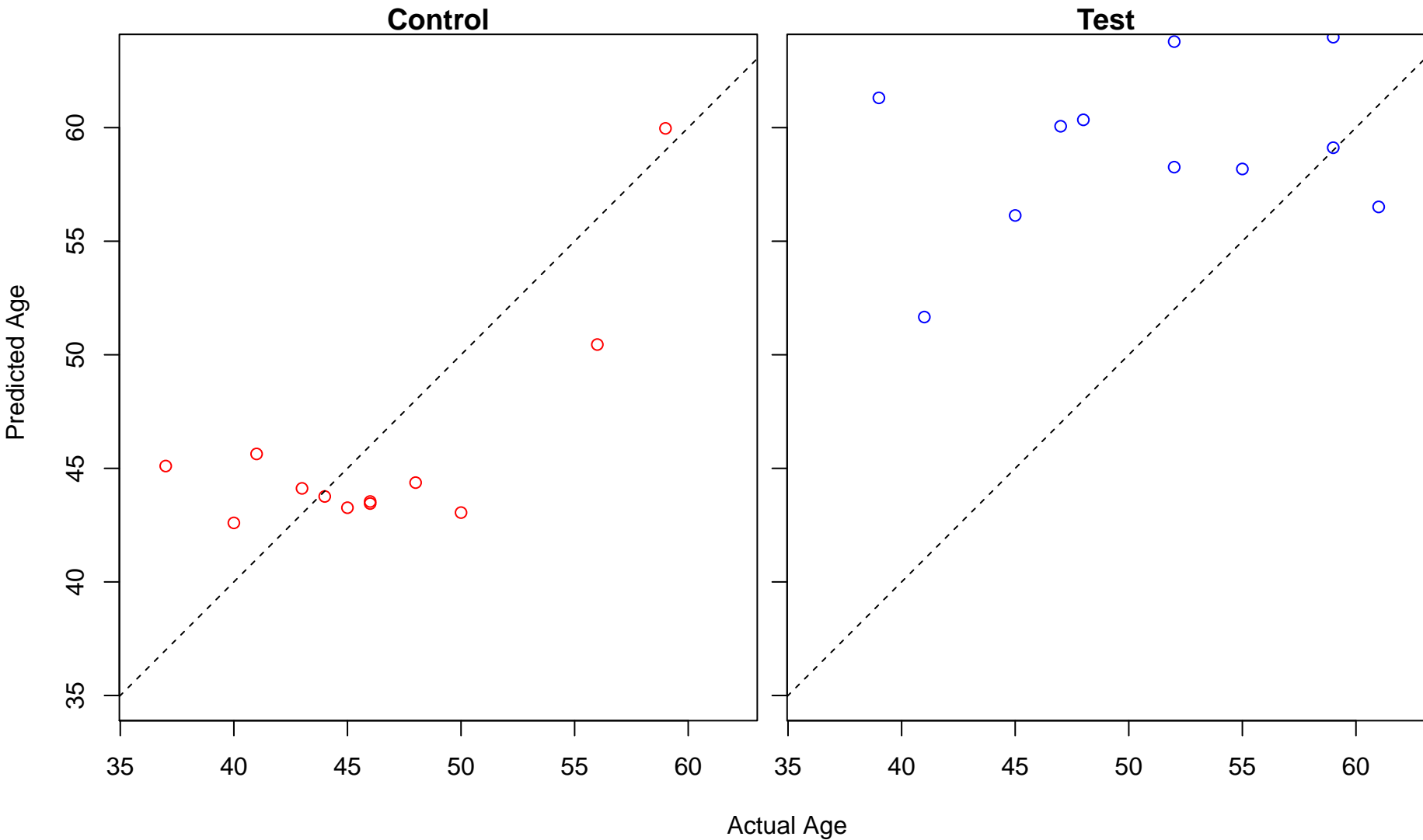
negative regulation of oxidoreductase activity (Score: 4.180646)



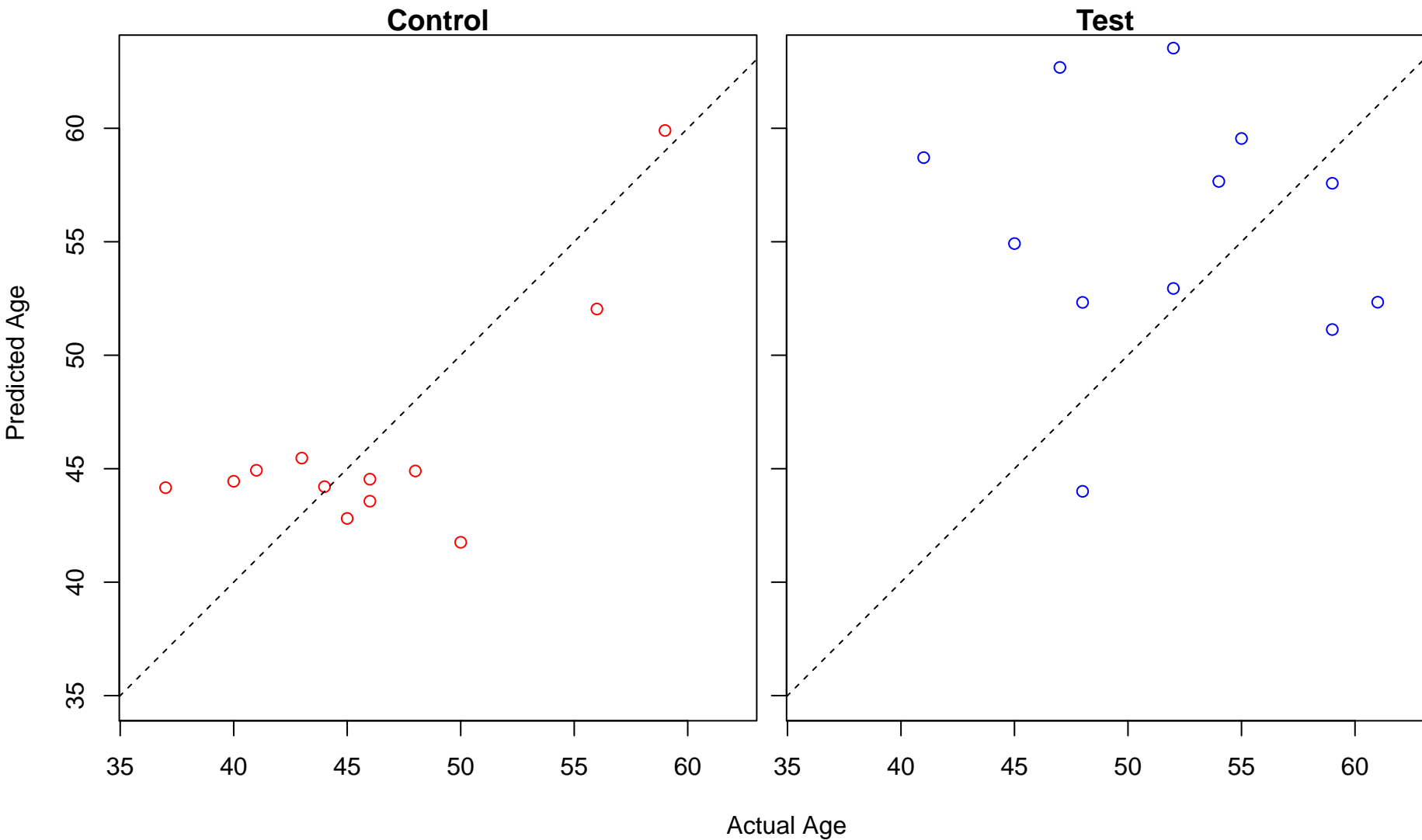
establishment of mitotic spindle localization (Score: 4.180273)



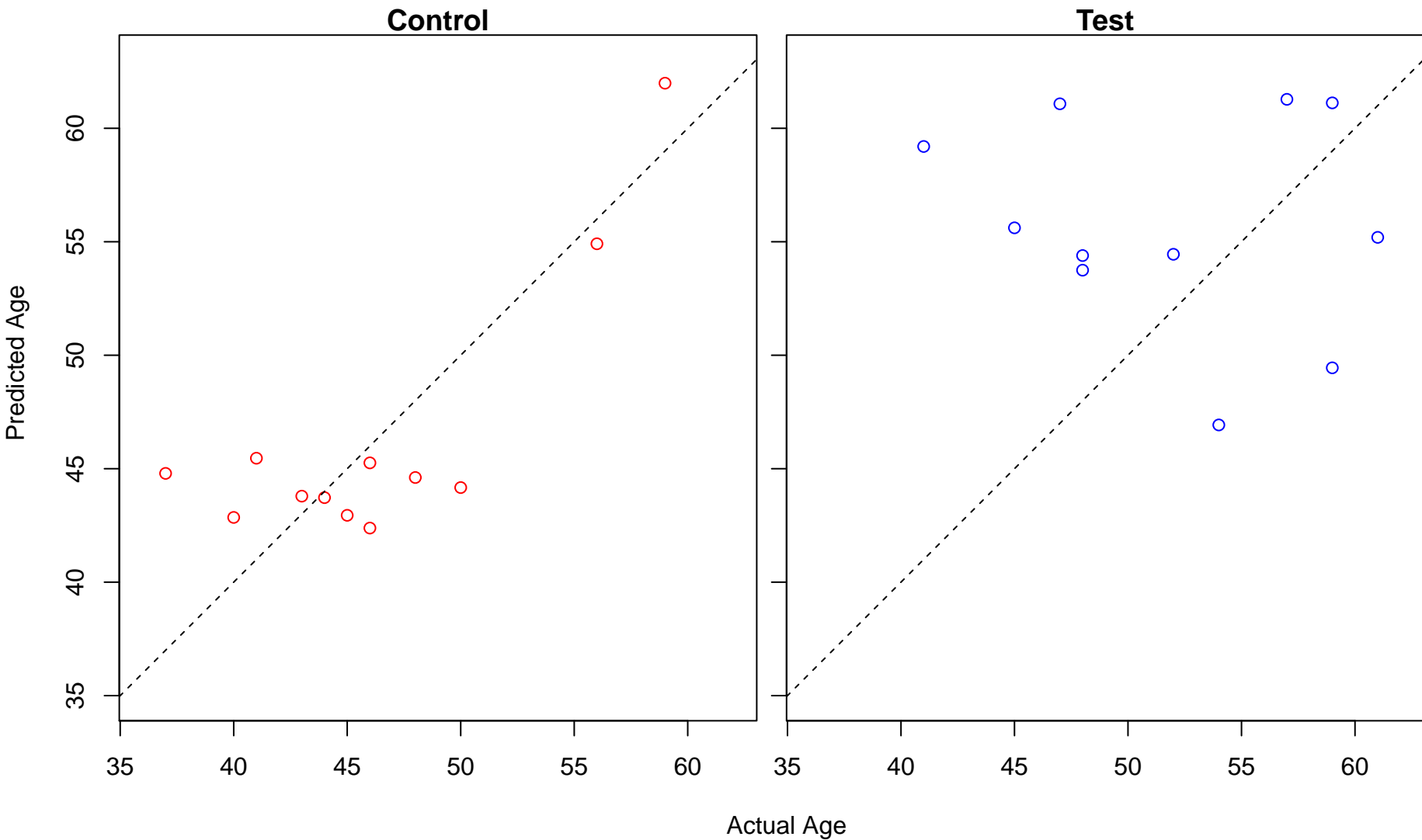
cell differentiation involved in embryonic placenta development (Score: 4.167765)



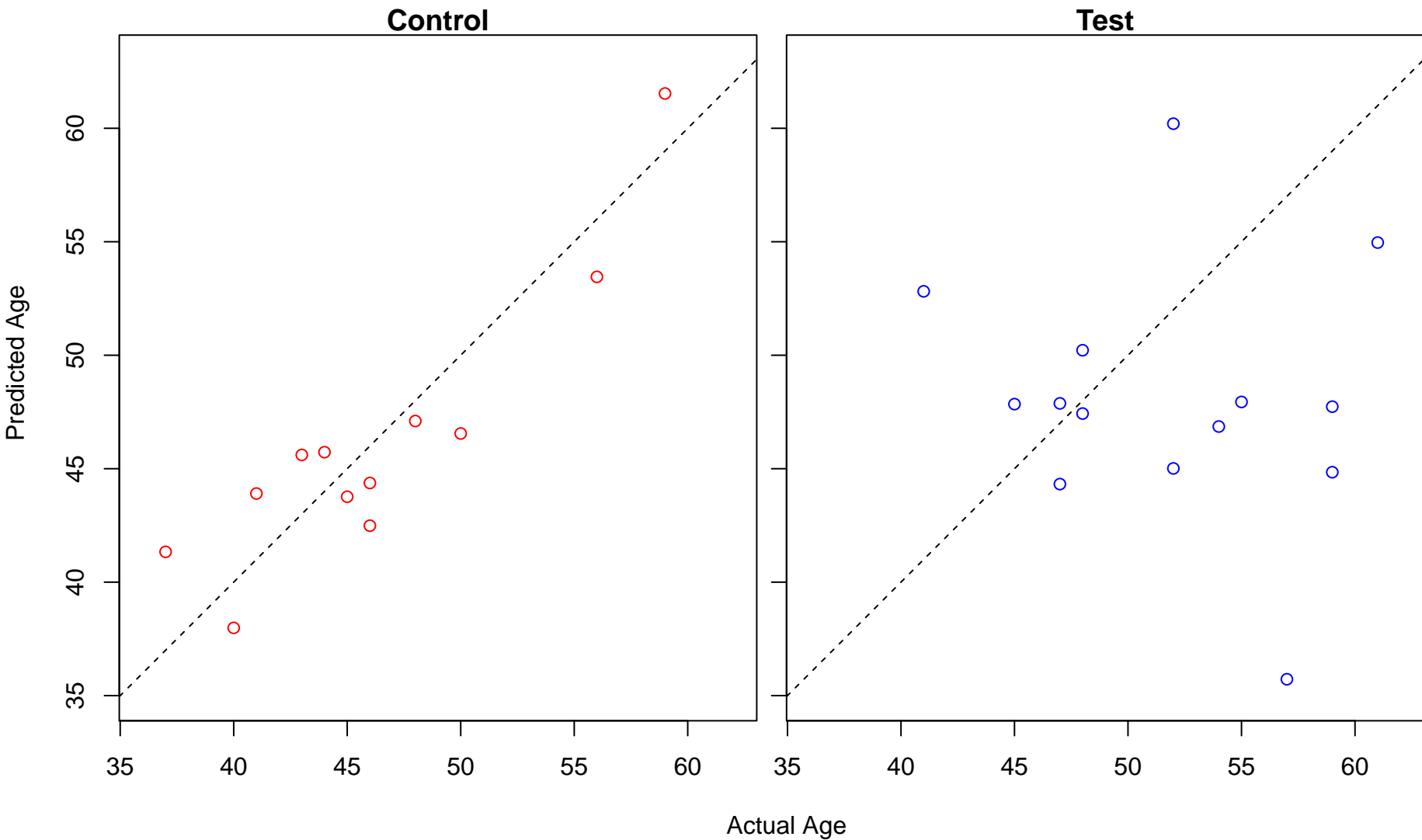
positive regulation of T cell mediated cytotoxicity (Score: 4.160813)



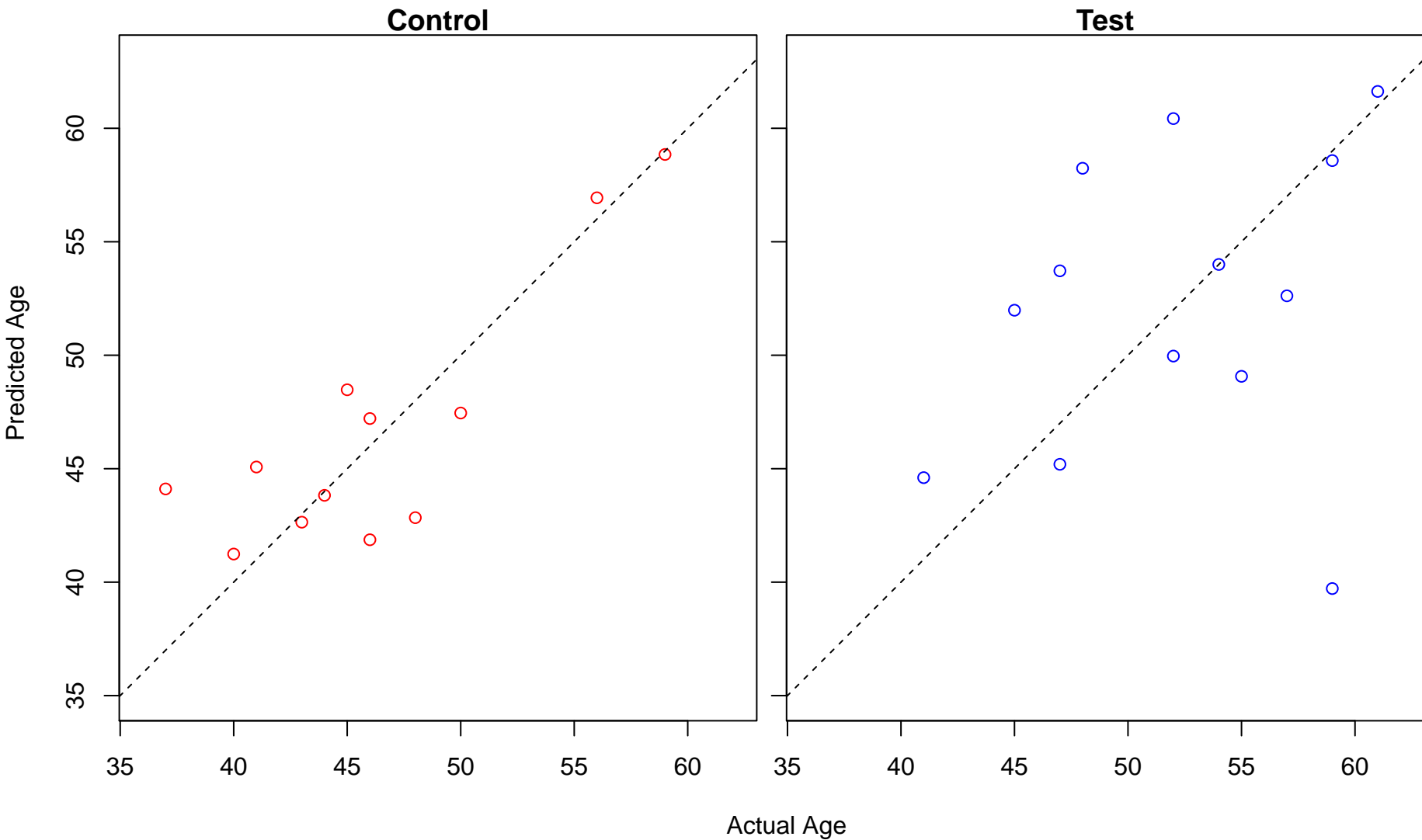
mitochondrion localization (Score: 4.154547)



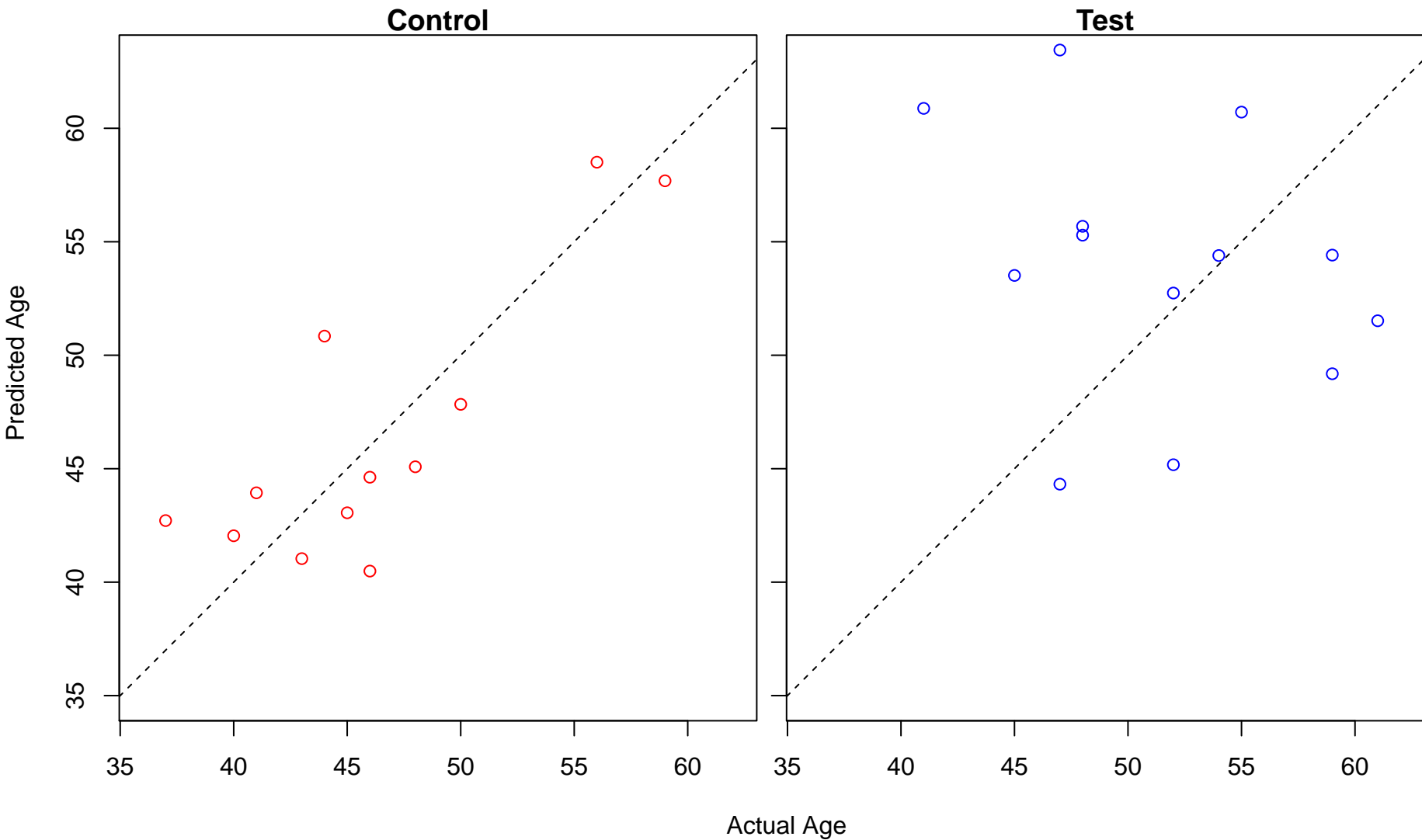
negative regulation of epithelial cell proliferation (Score: 4.154333)



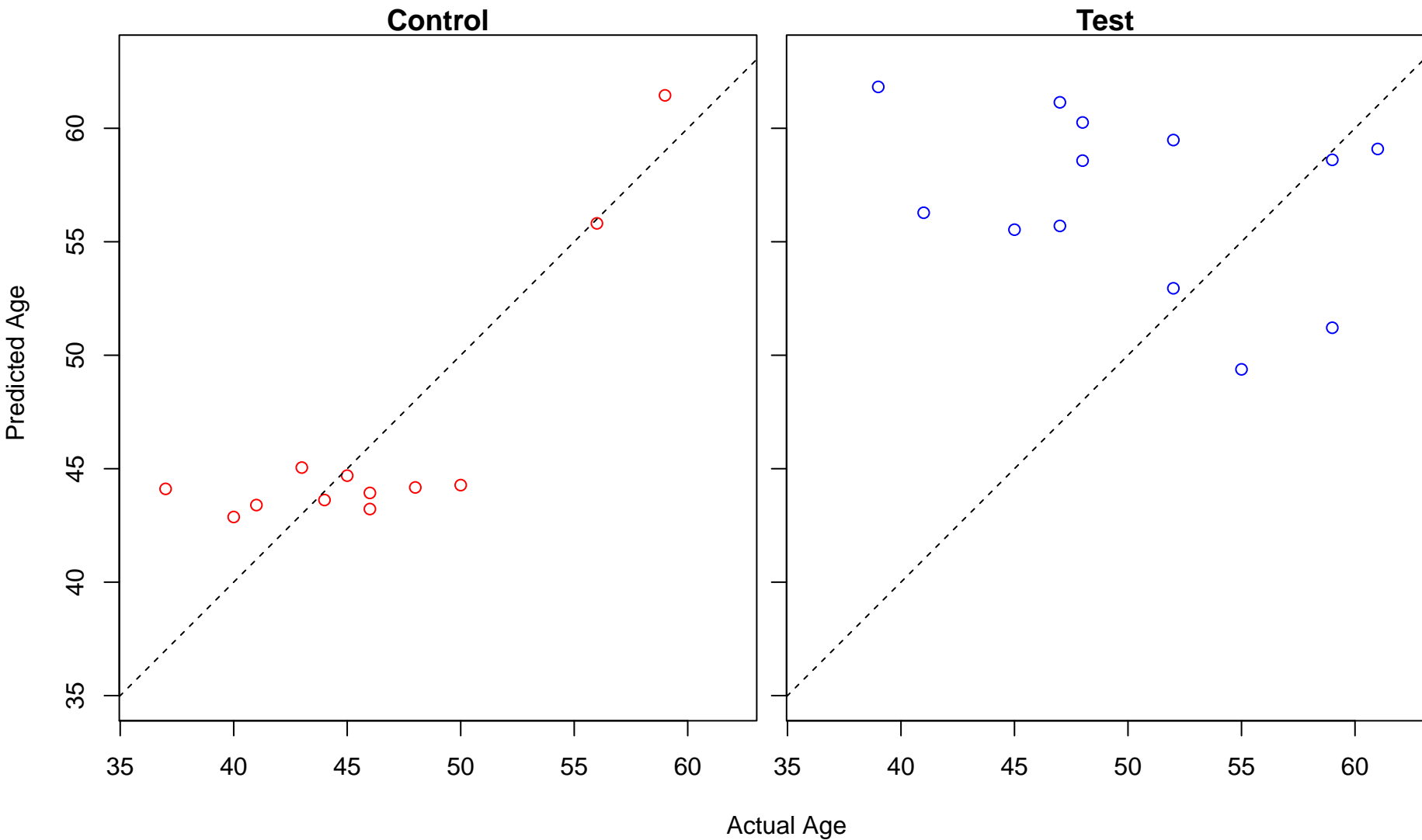
peptide catabolic process (Score: 4.153890)



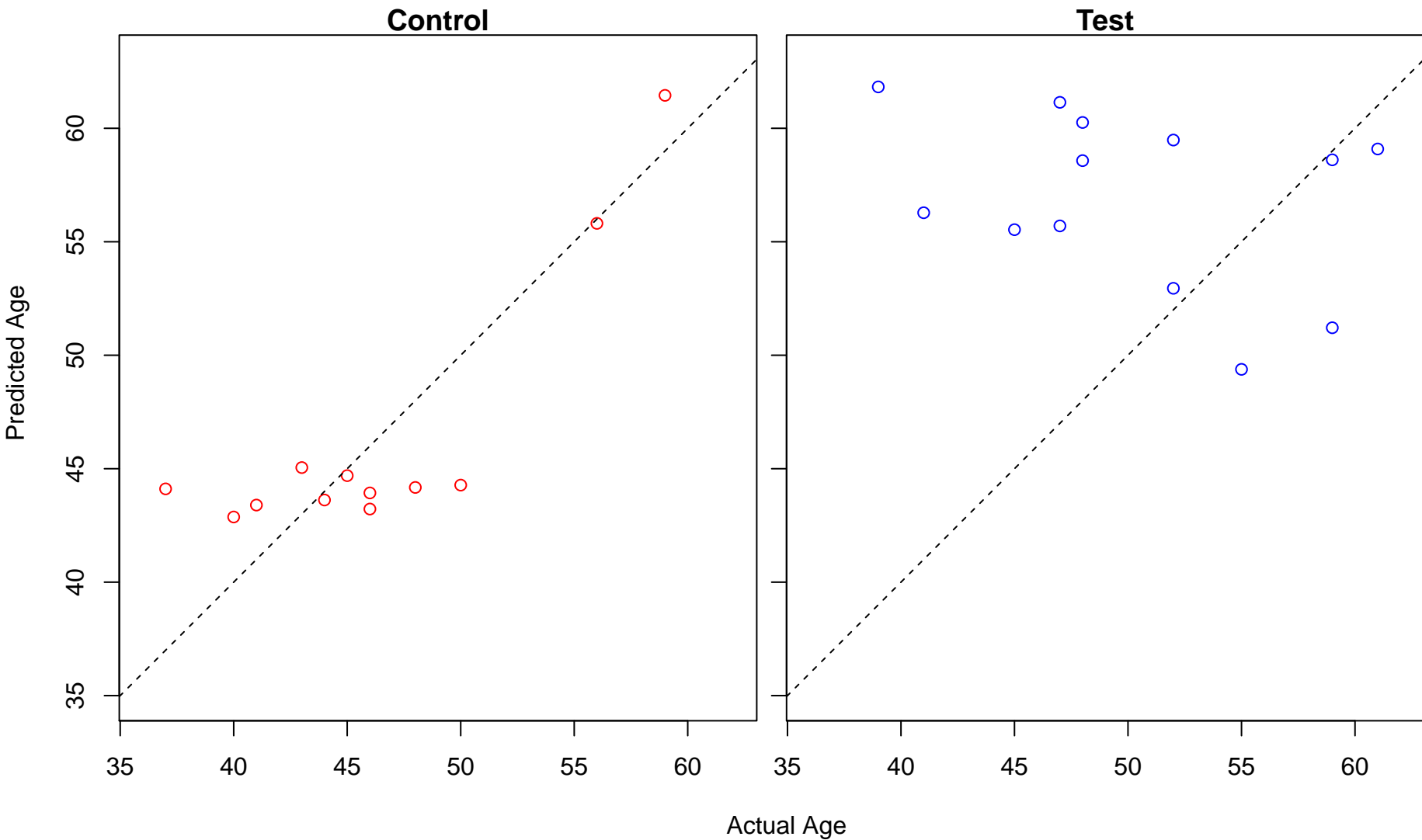
establishment of protein localization to mitochondrial membrane (Score: 4.150443)



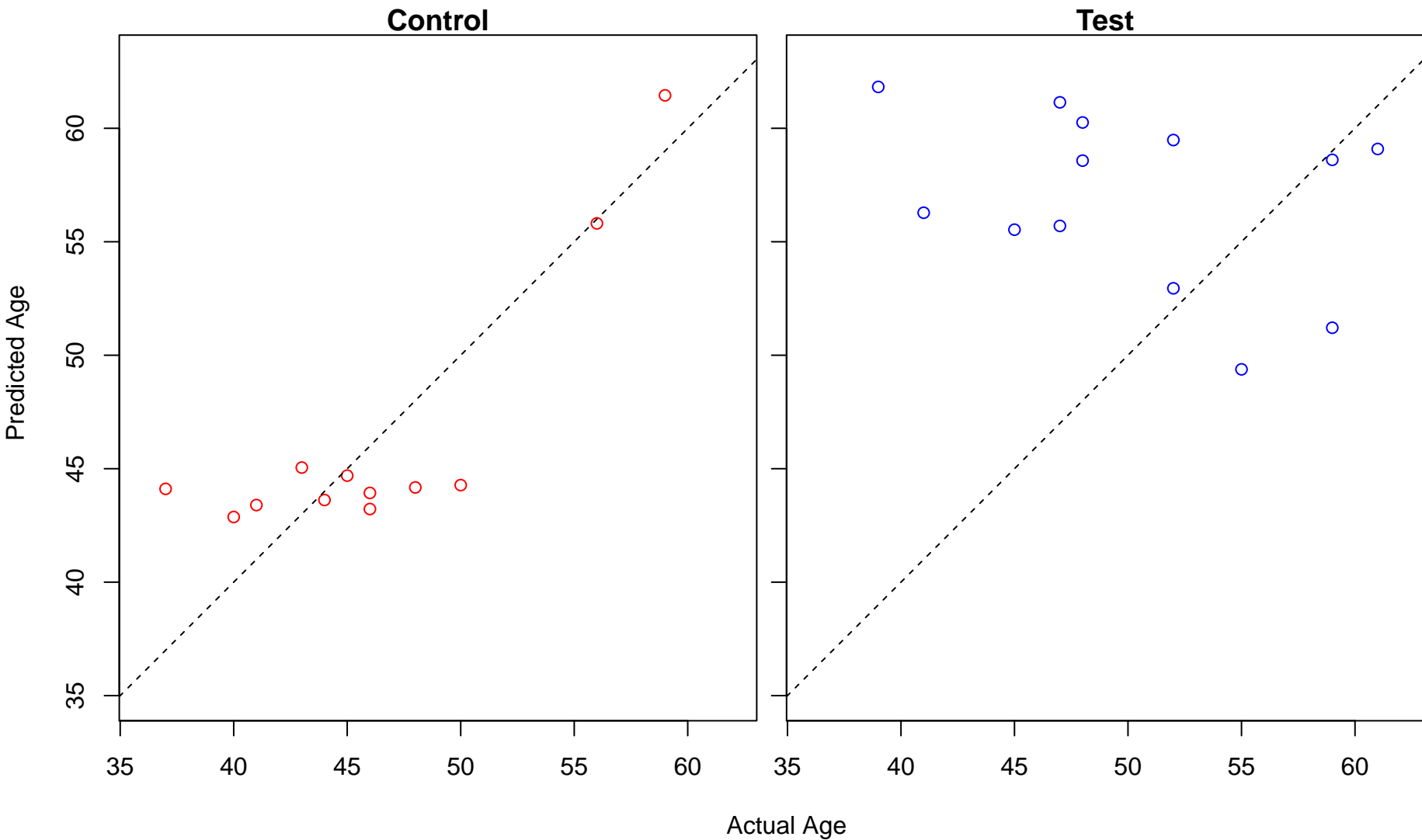
positive regulation of collagen metabolic process (Score: 4.143544)



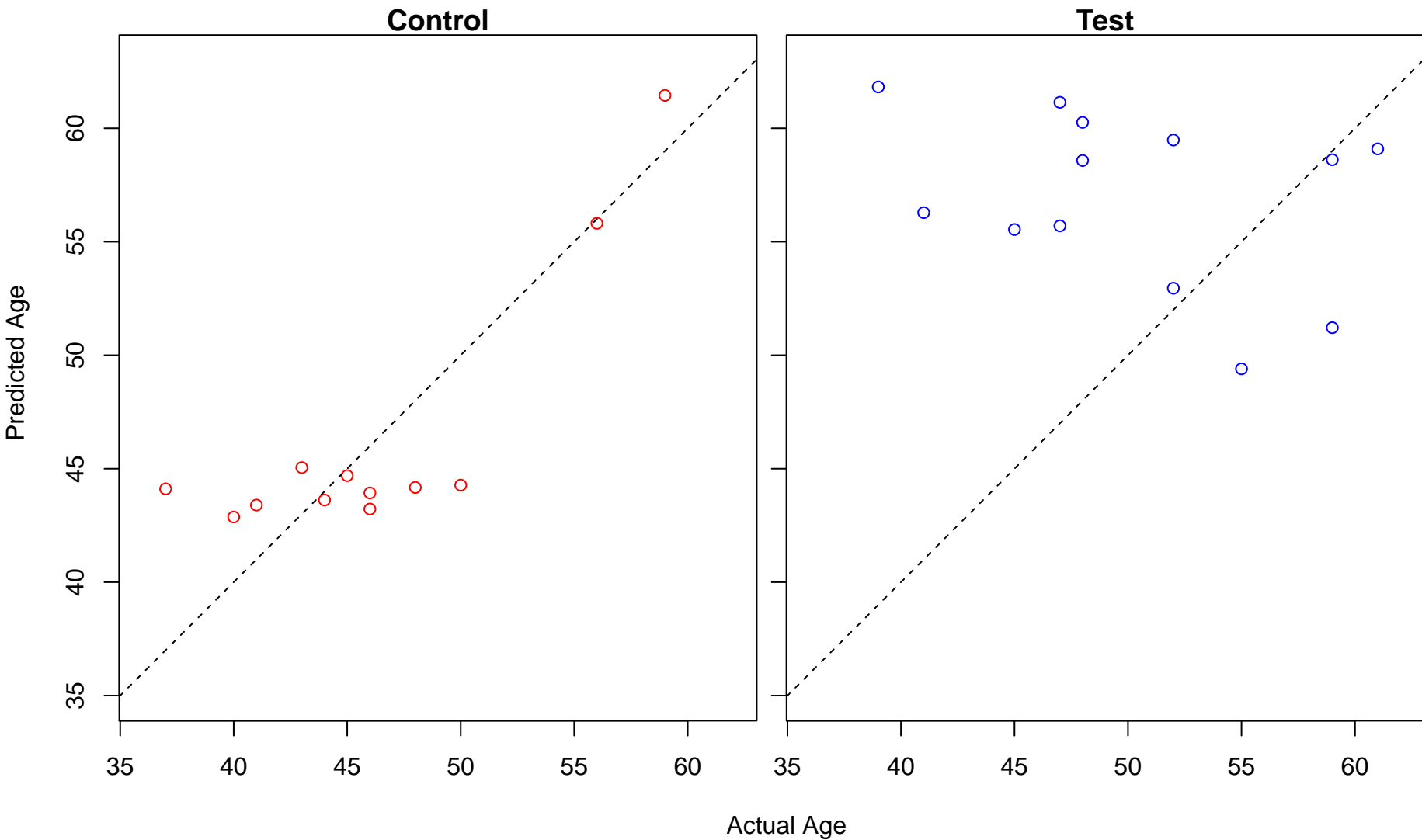
positive regulation of collagen biosynthetic process (Score: 4.143544)



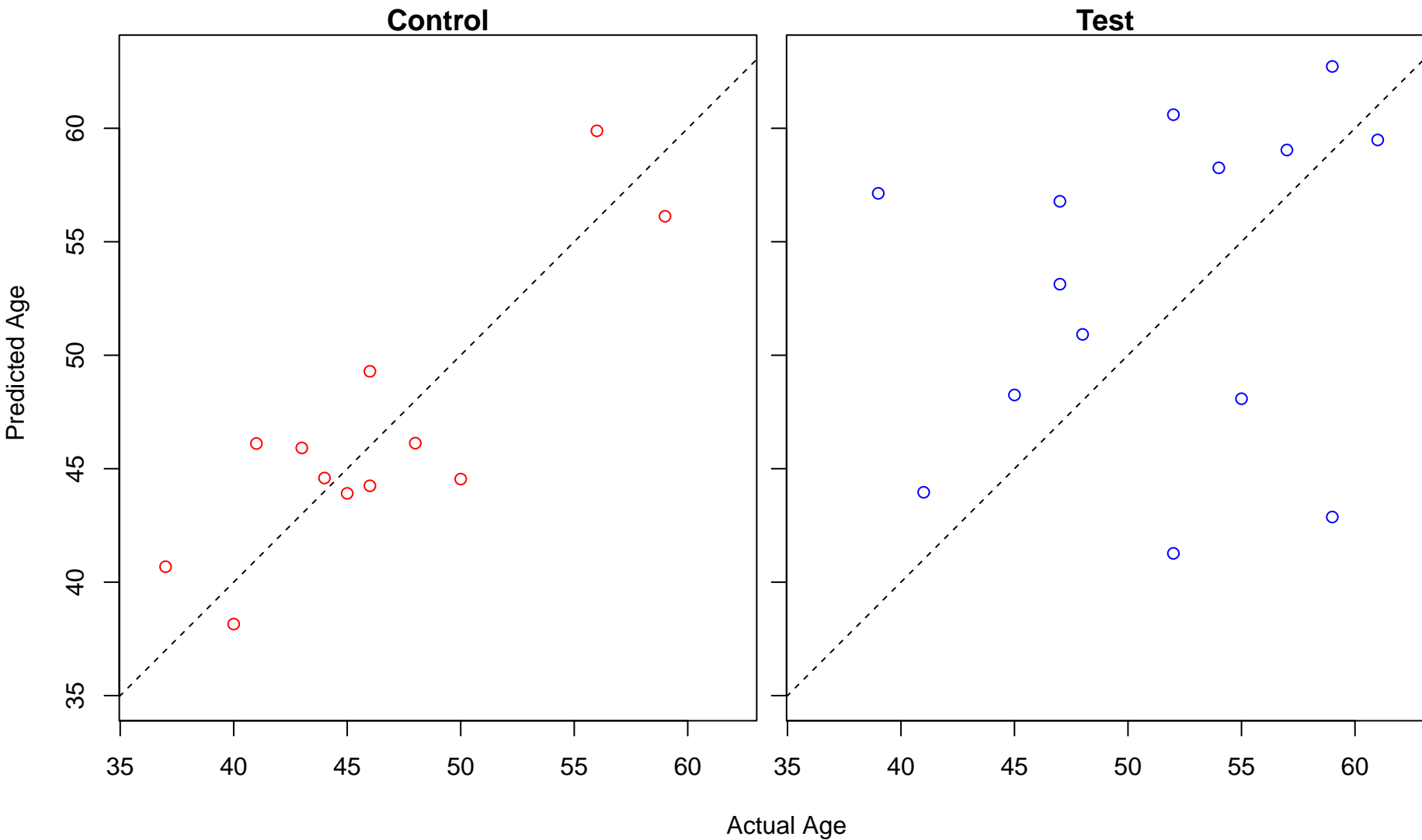
positive regulation of multicellular organismal metabolic process (Score: 4.143544)



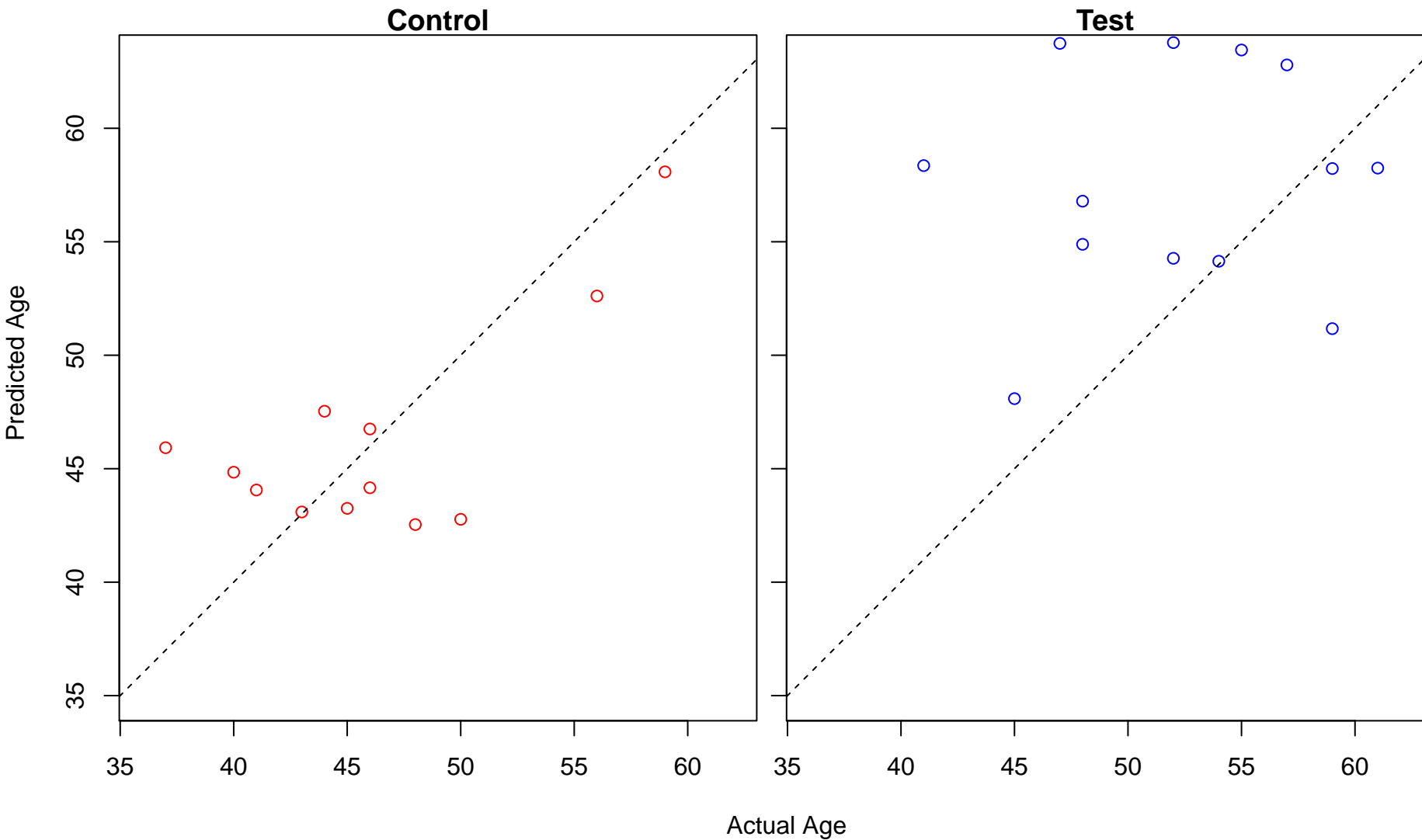
regulation of collagen biosynthetic process (Score: 4.143477)



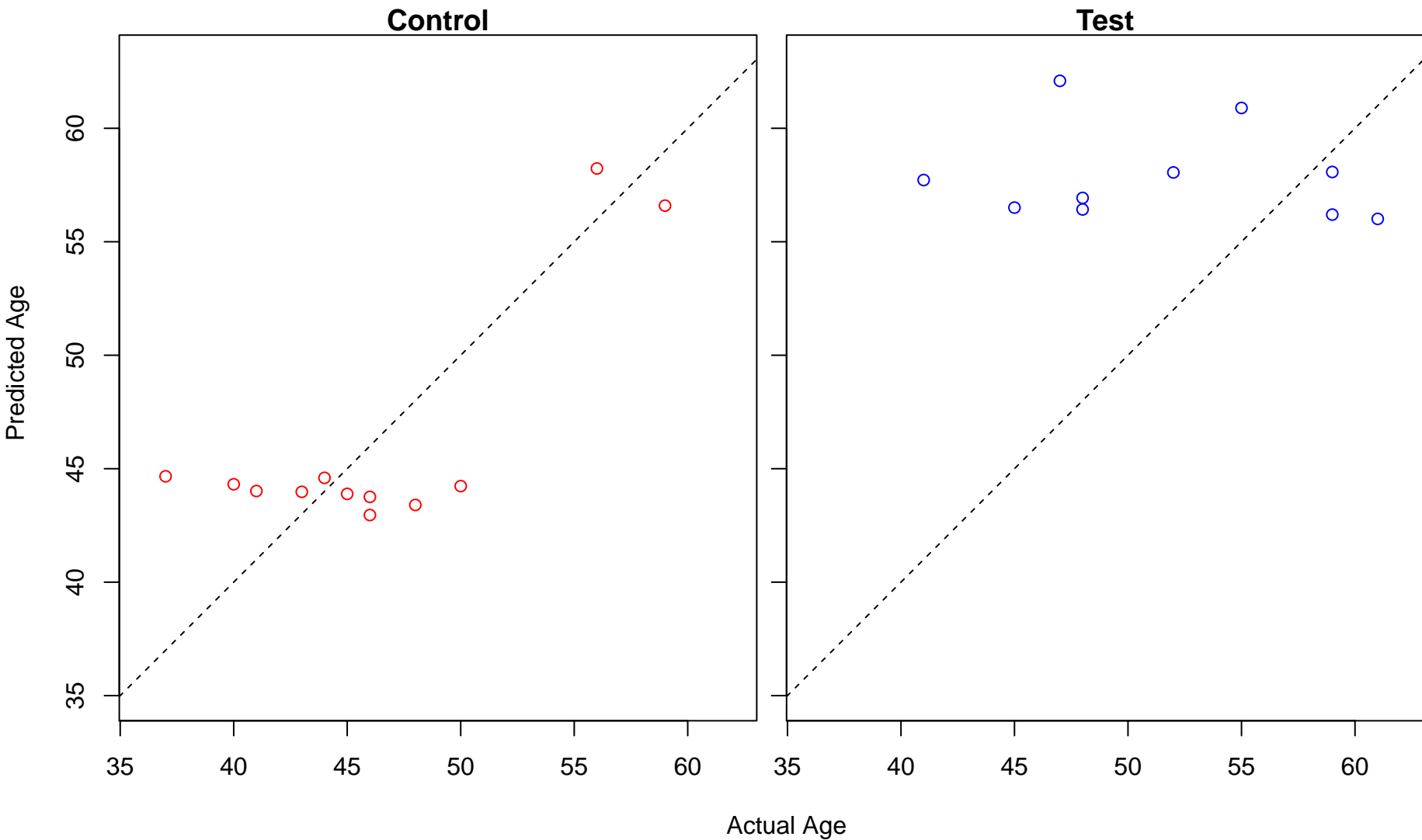
positive regulation of dendritic spine development (Score: 4.141369)



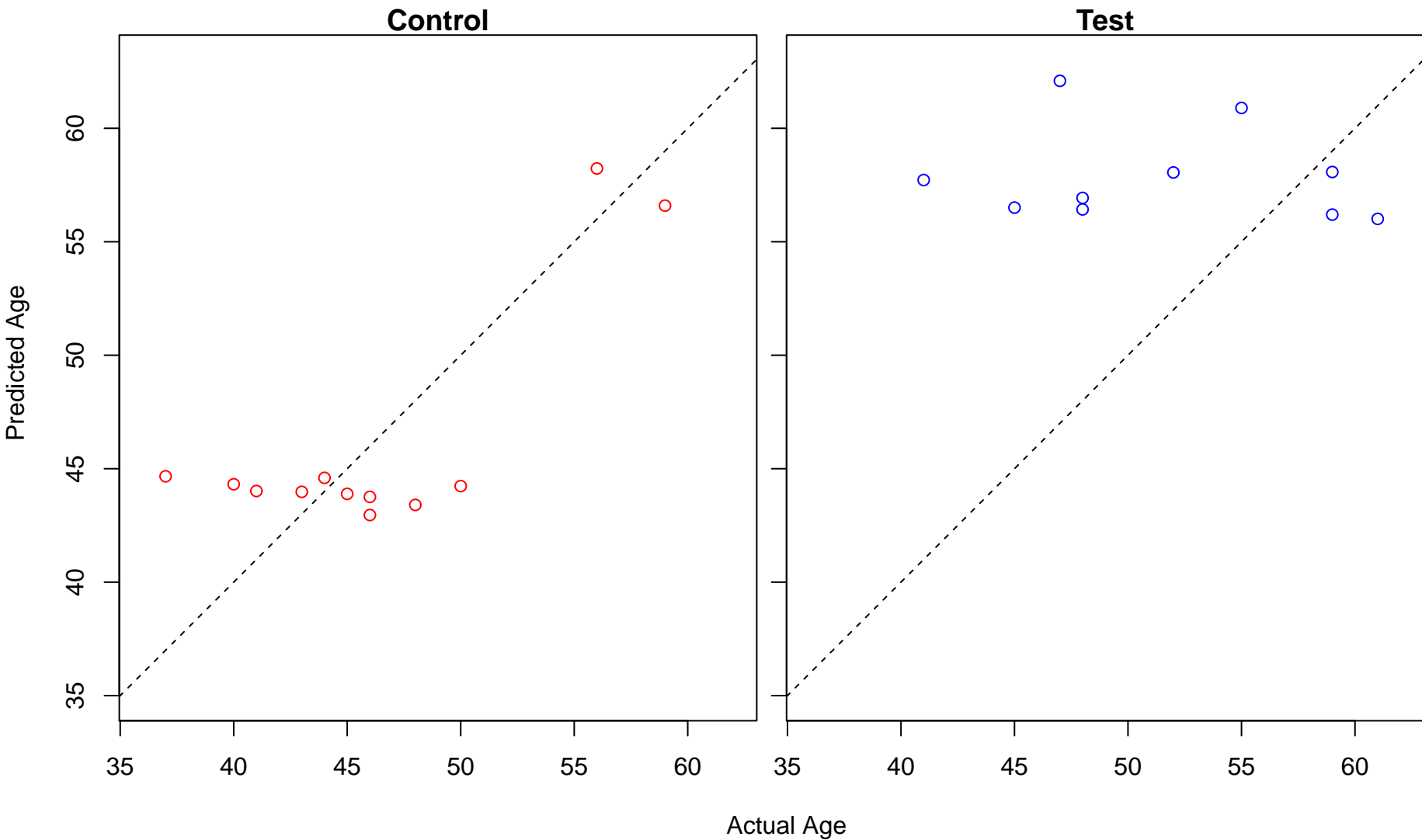
endochondral bone growth (Score: 4.140714)



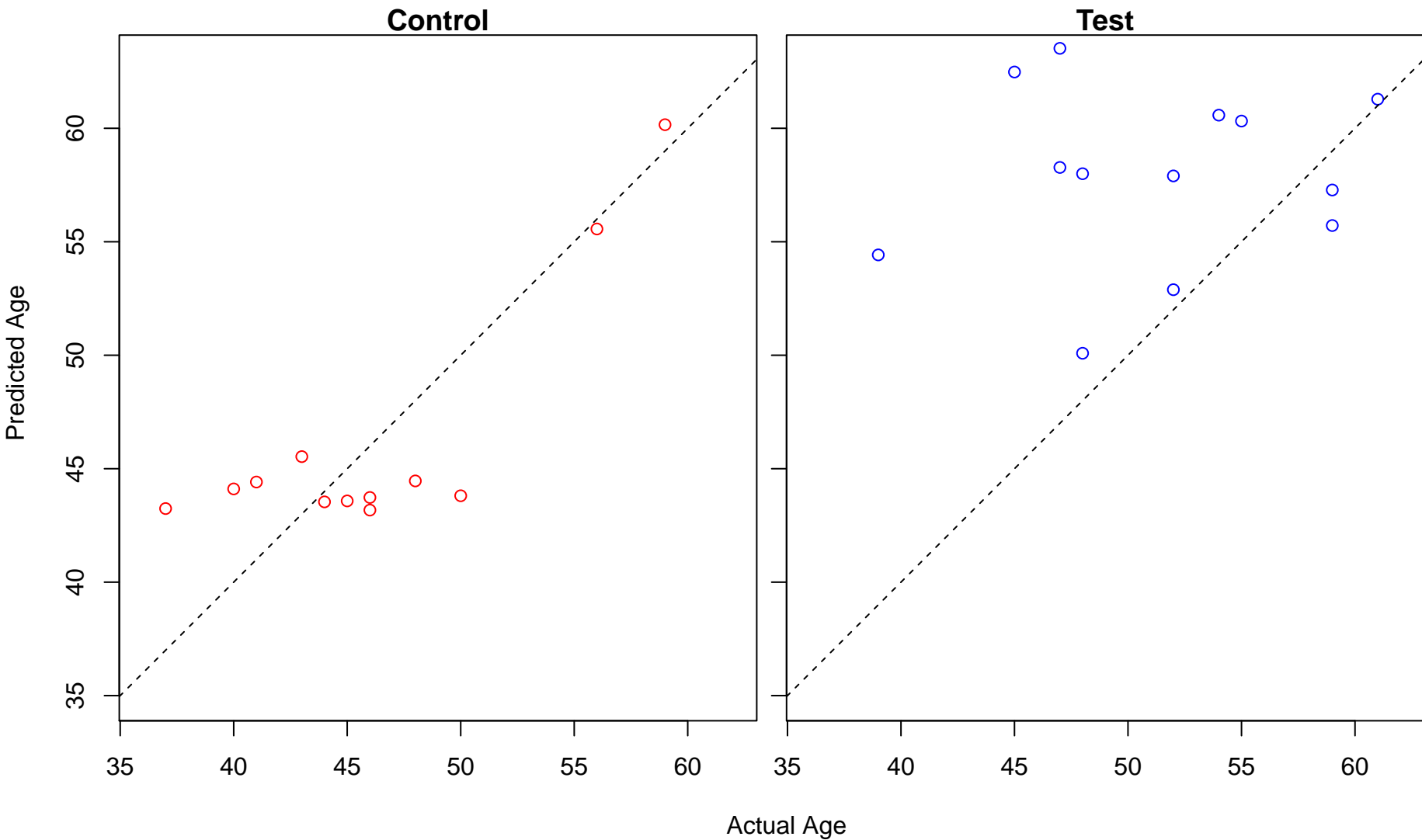
corticosteroid receptor signaling pathway (Score: 4.138013)



glucocorticoid receptor signaling pathway (Score: 4.138013)

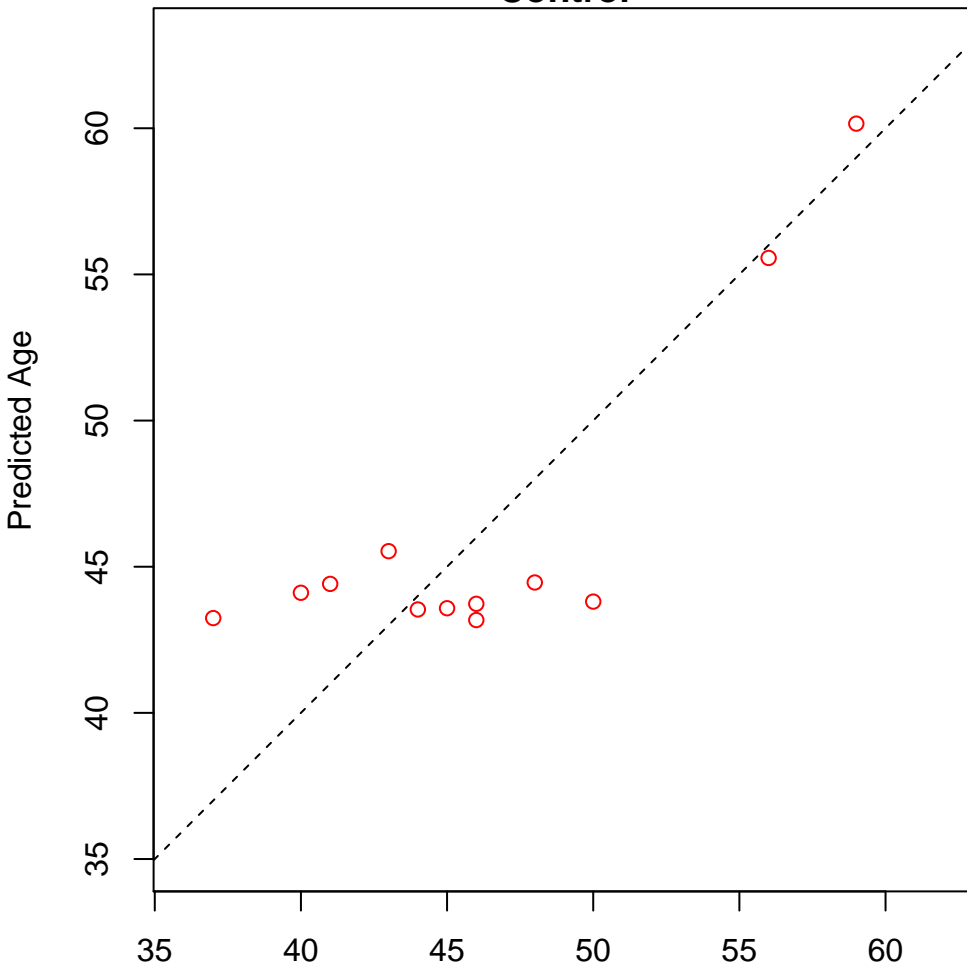


pentose-phosphate shunt (Score: 4.134445)

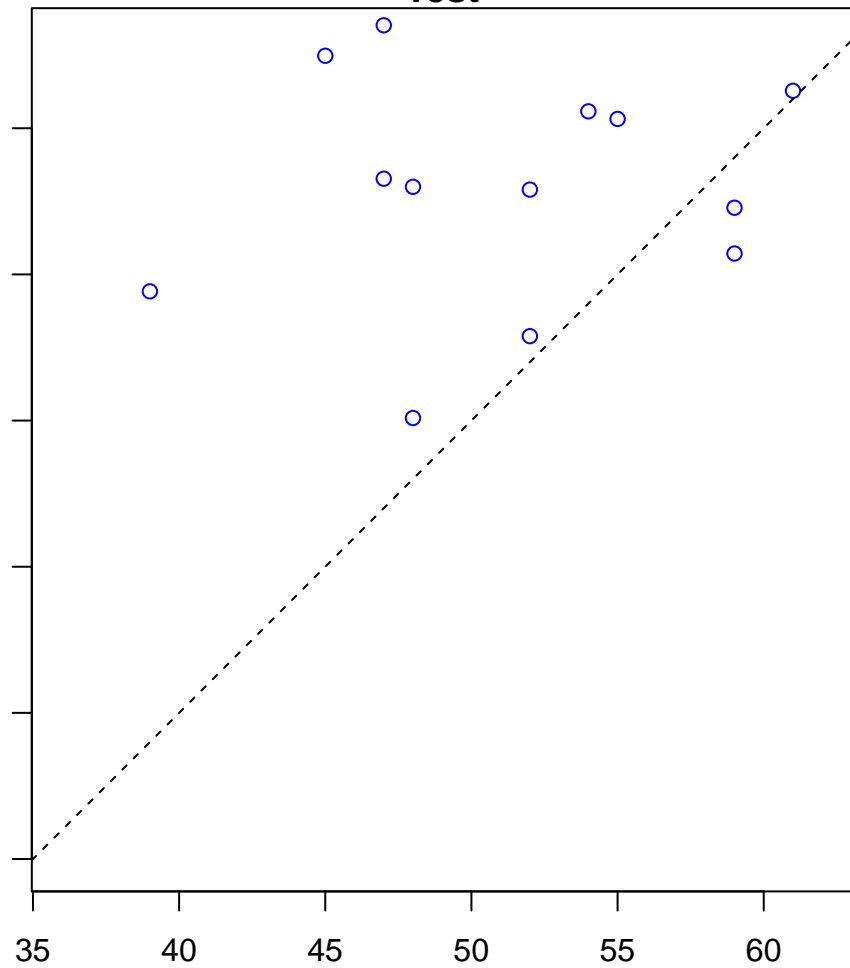


glucose 6-phosphate metabolic process (Score: 4.134437)

Control

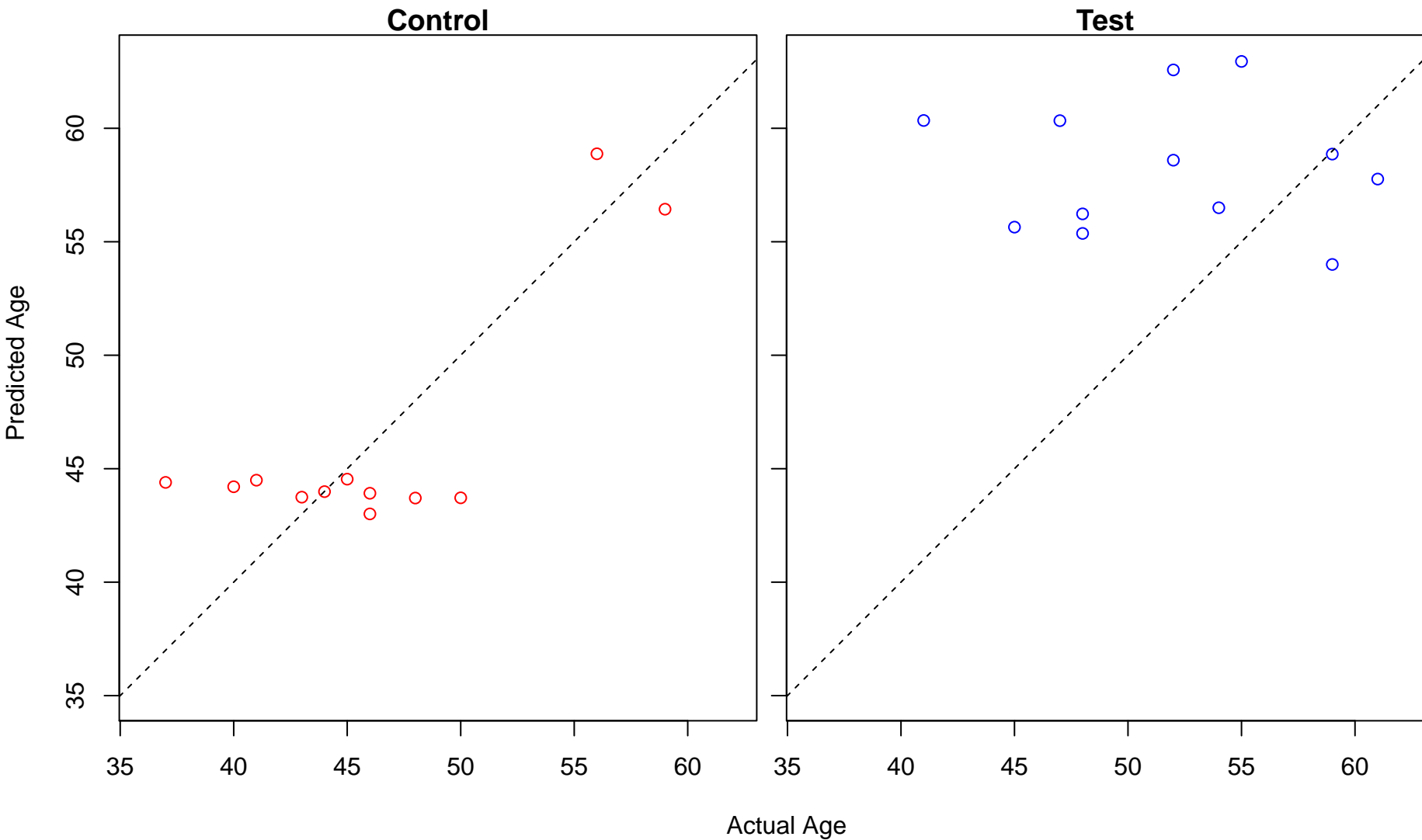


Test

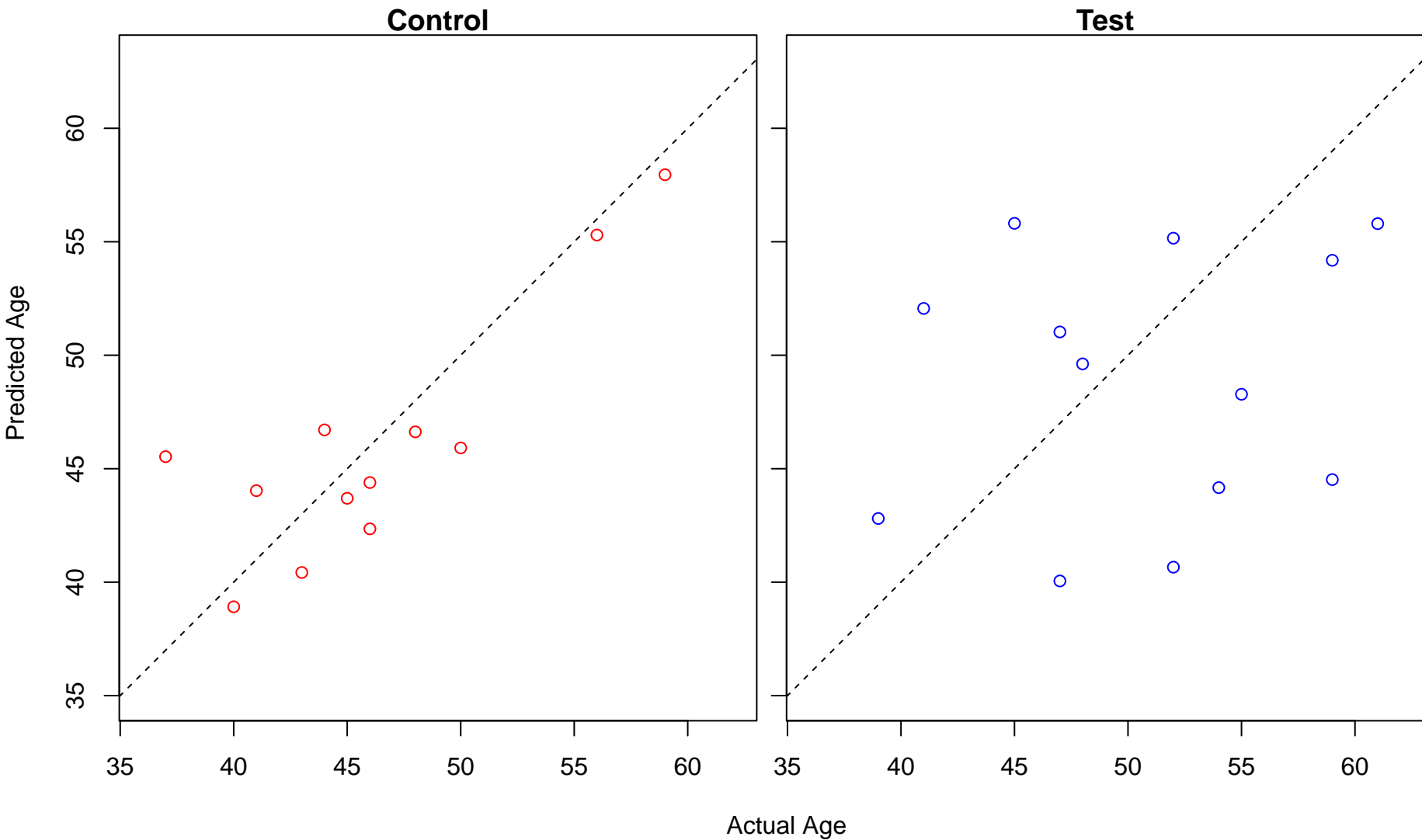


Actual Age

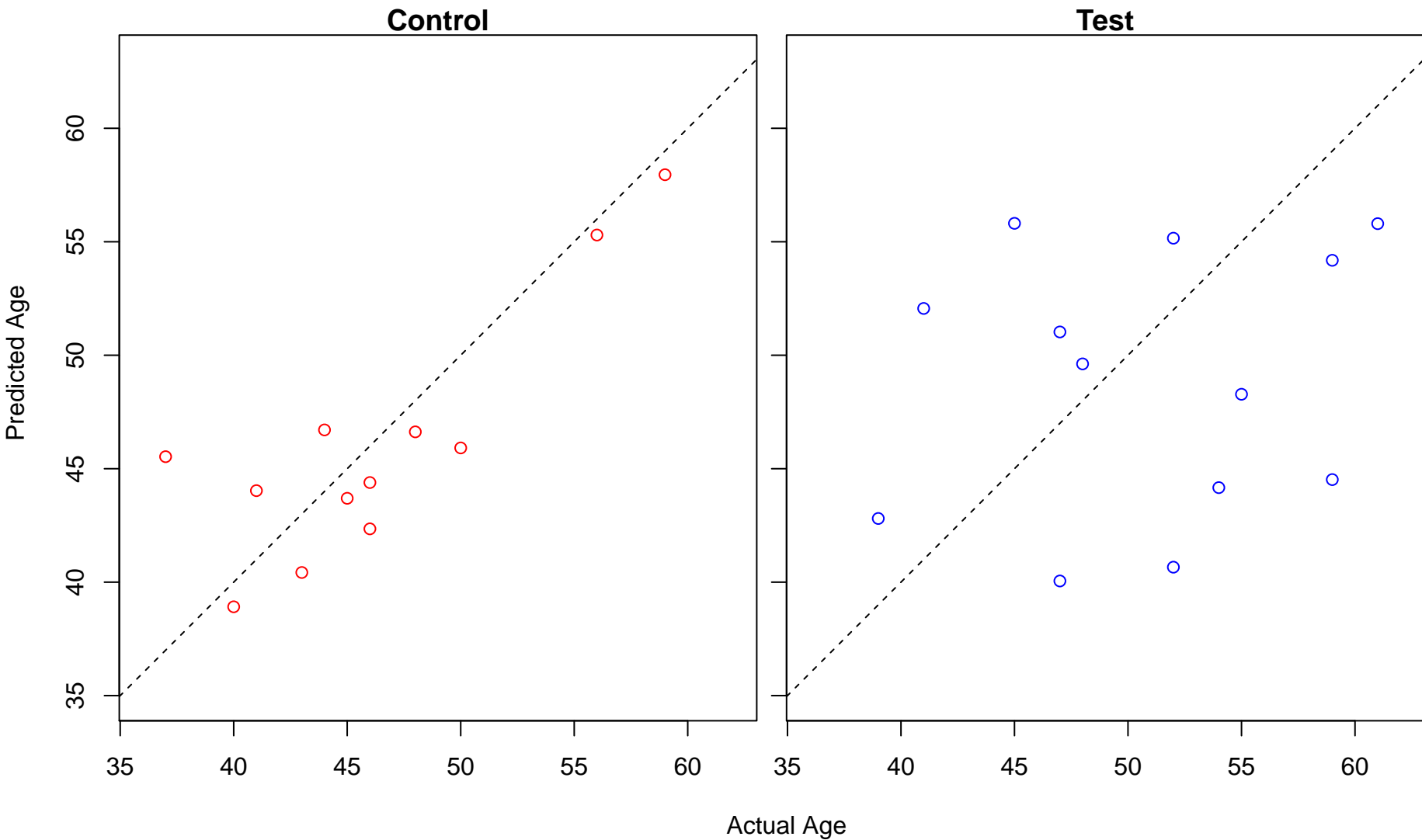
negative regulation of cell cycle phase transition (Score: 4.134349)



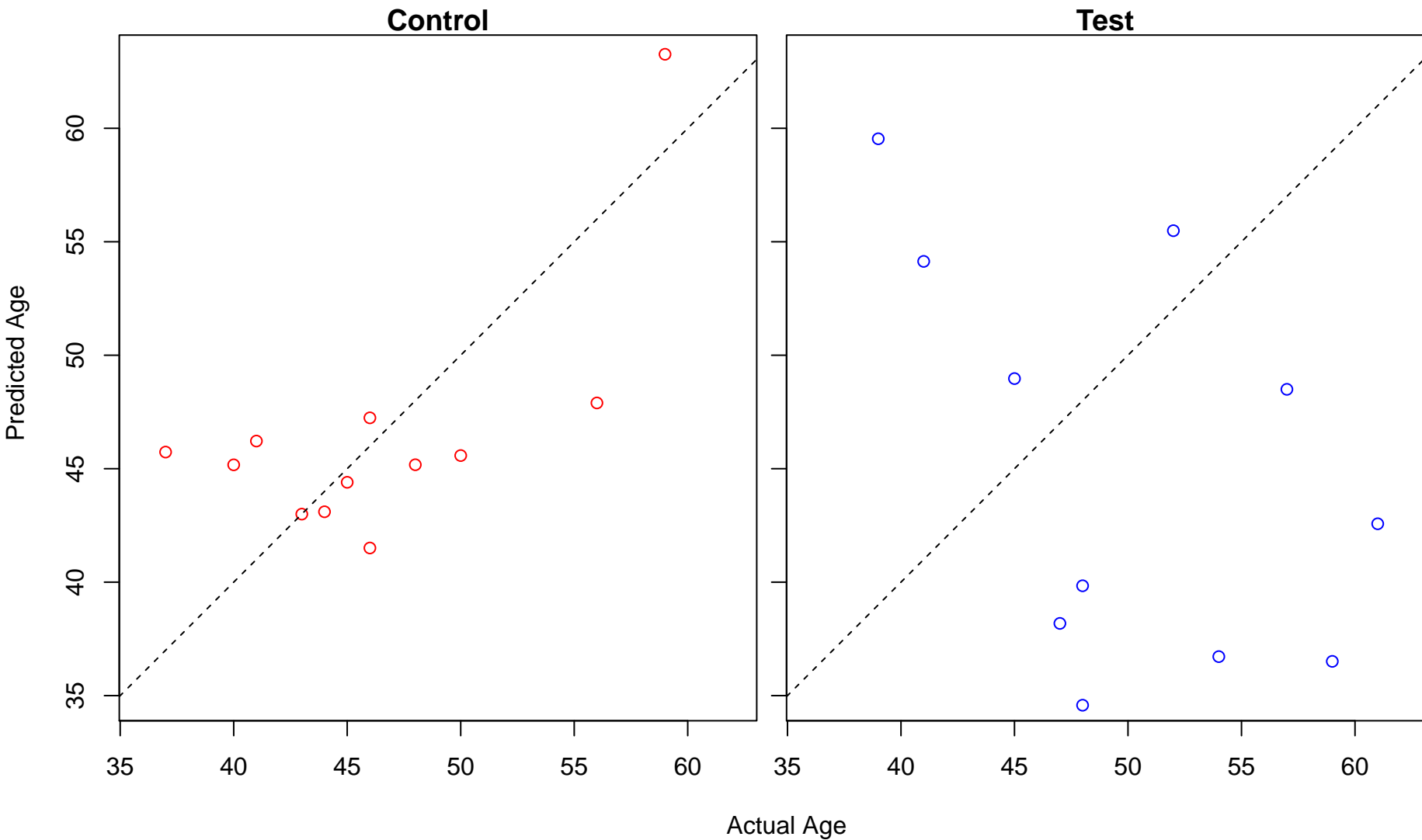
digestive tract development (Score: 4.13335)



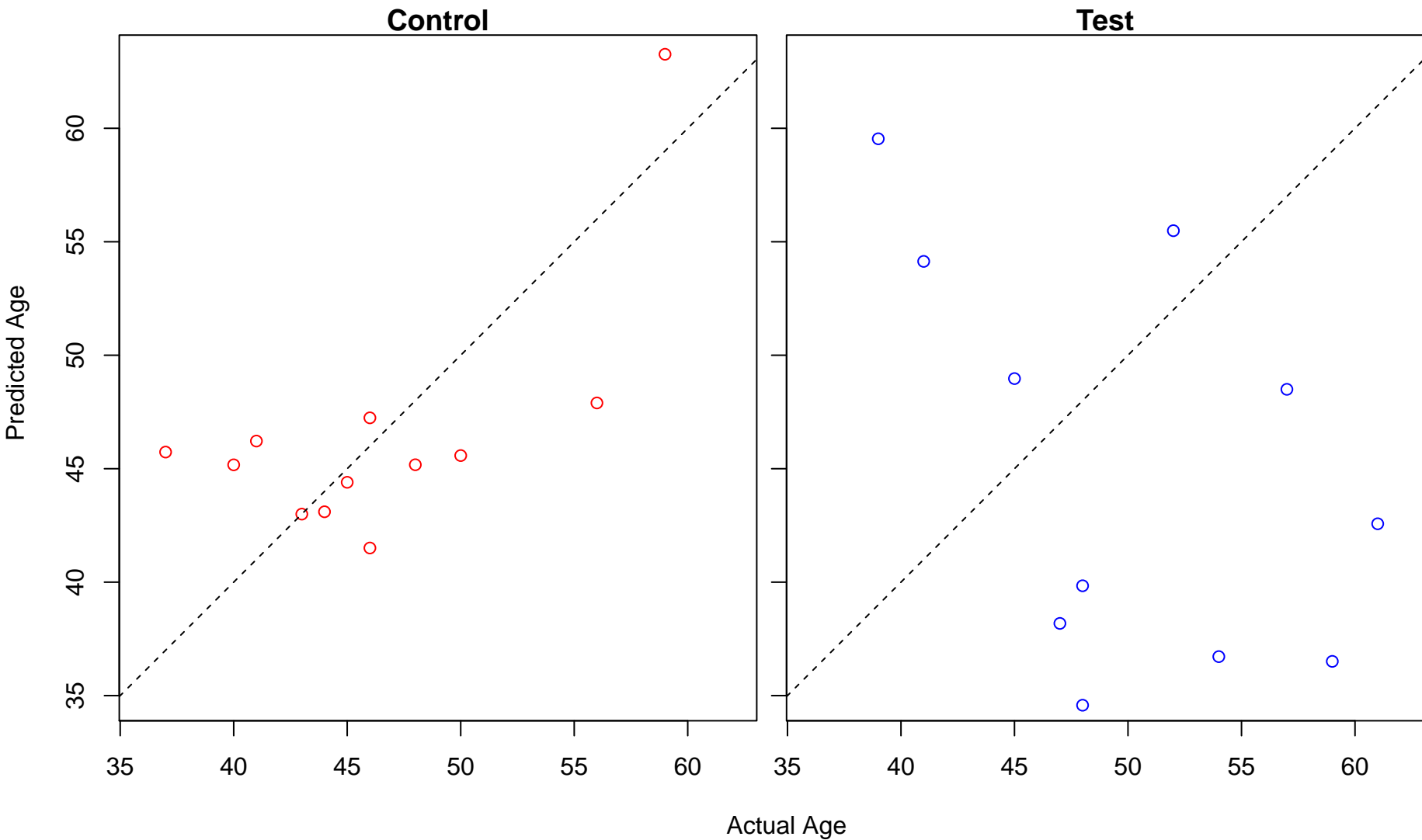
digestive system development (Score: 4.133335)



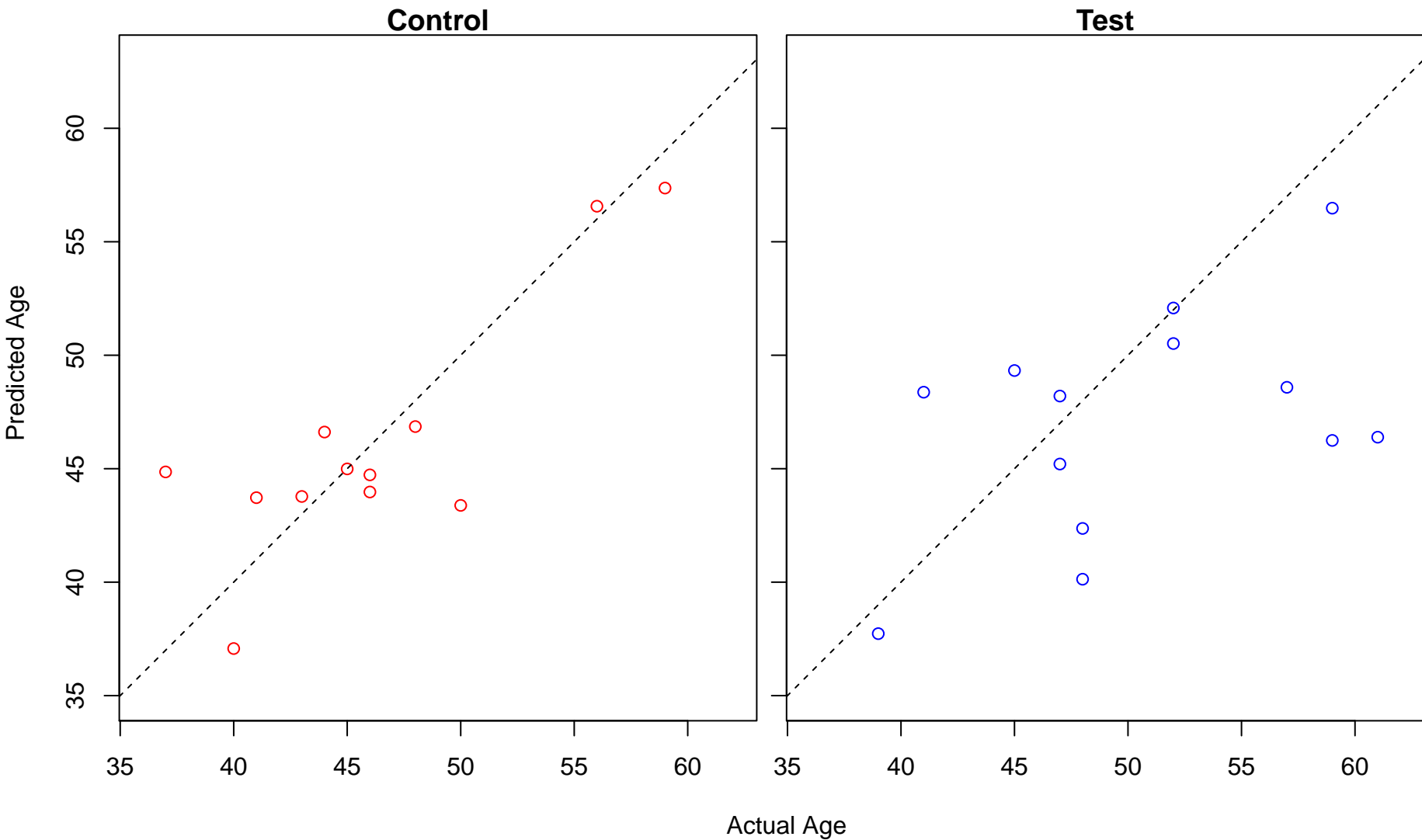
diol biosynthetic process (Score: 4.131756)



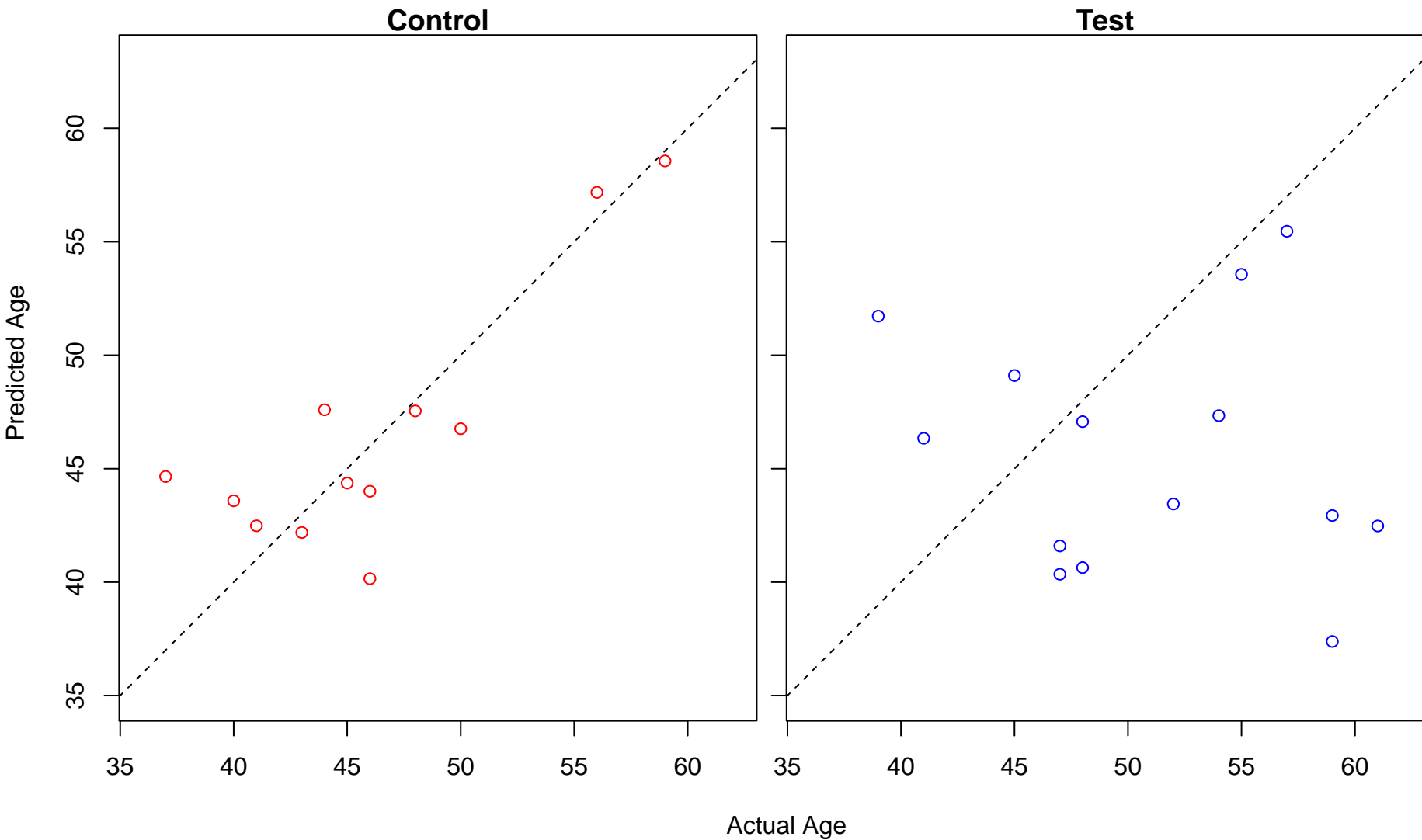
sphingosine biosynthetic process (Score: 4.131756)



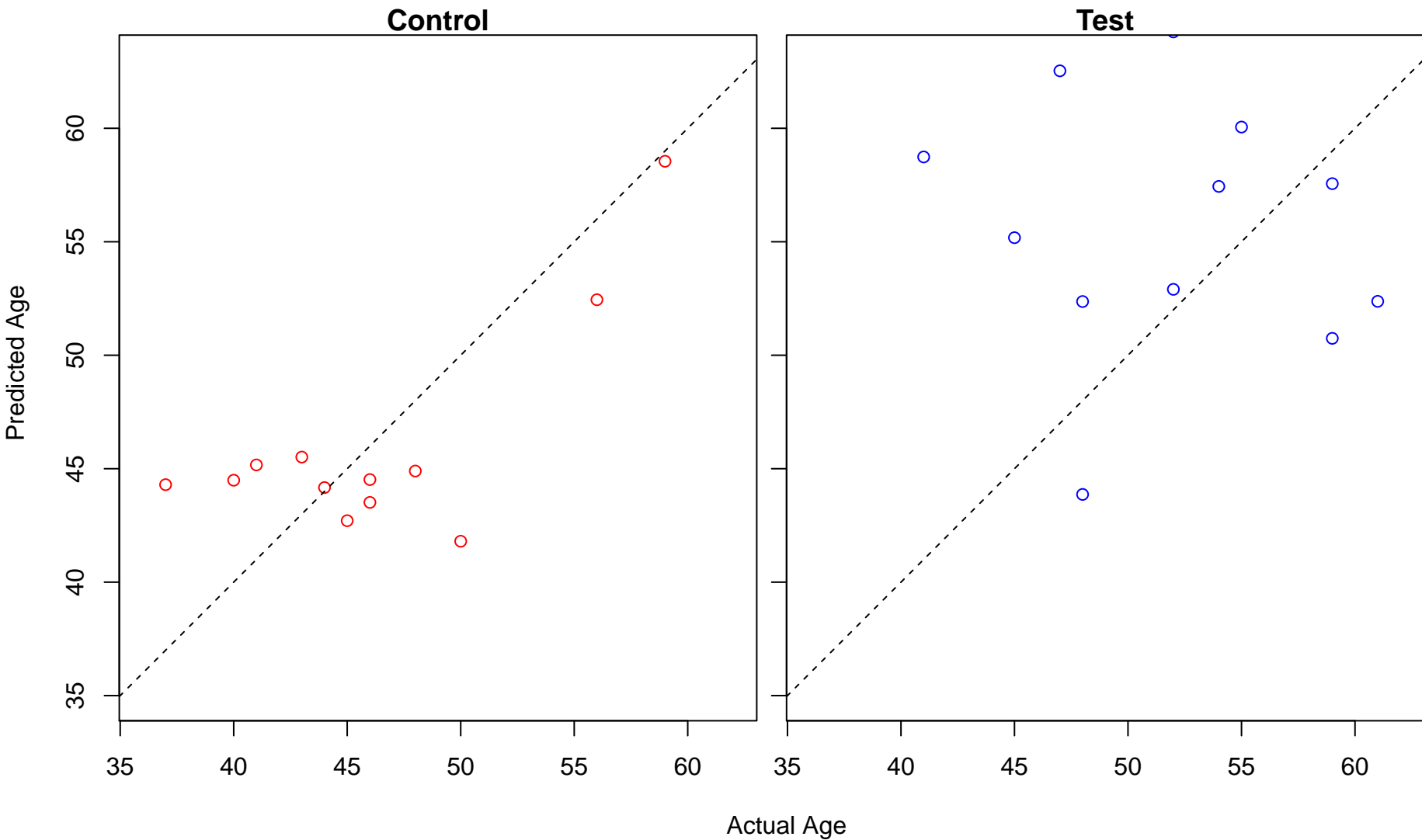
regulation of viral genome replication (Score: 4.131308)



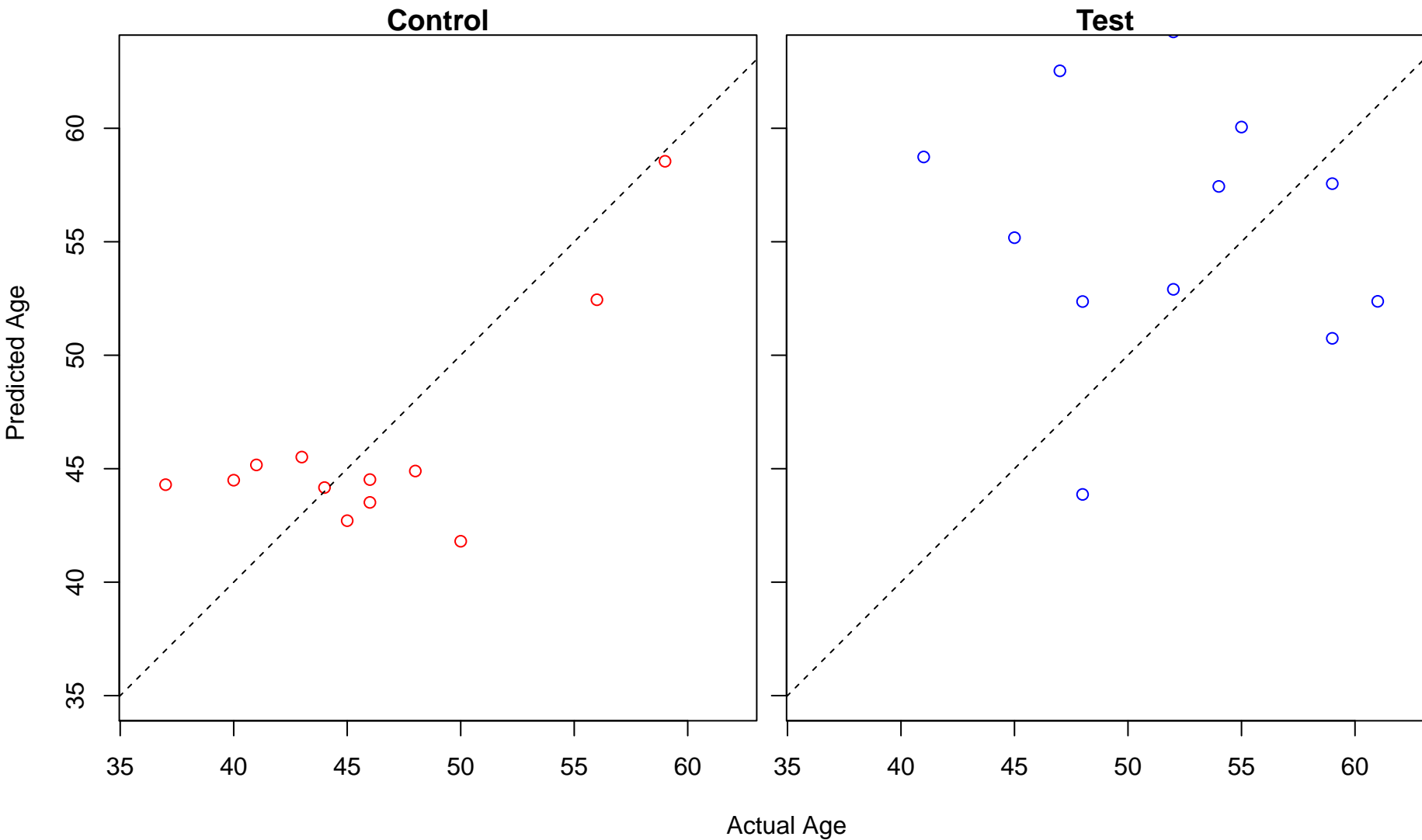
negative regulation of intracellular steroid hormone receptor signaling pathway (Score: 4.129416)



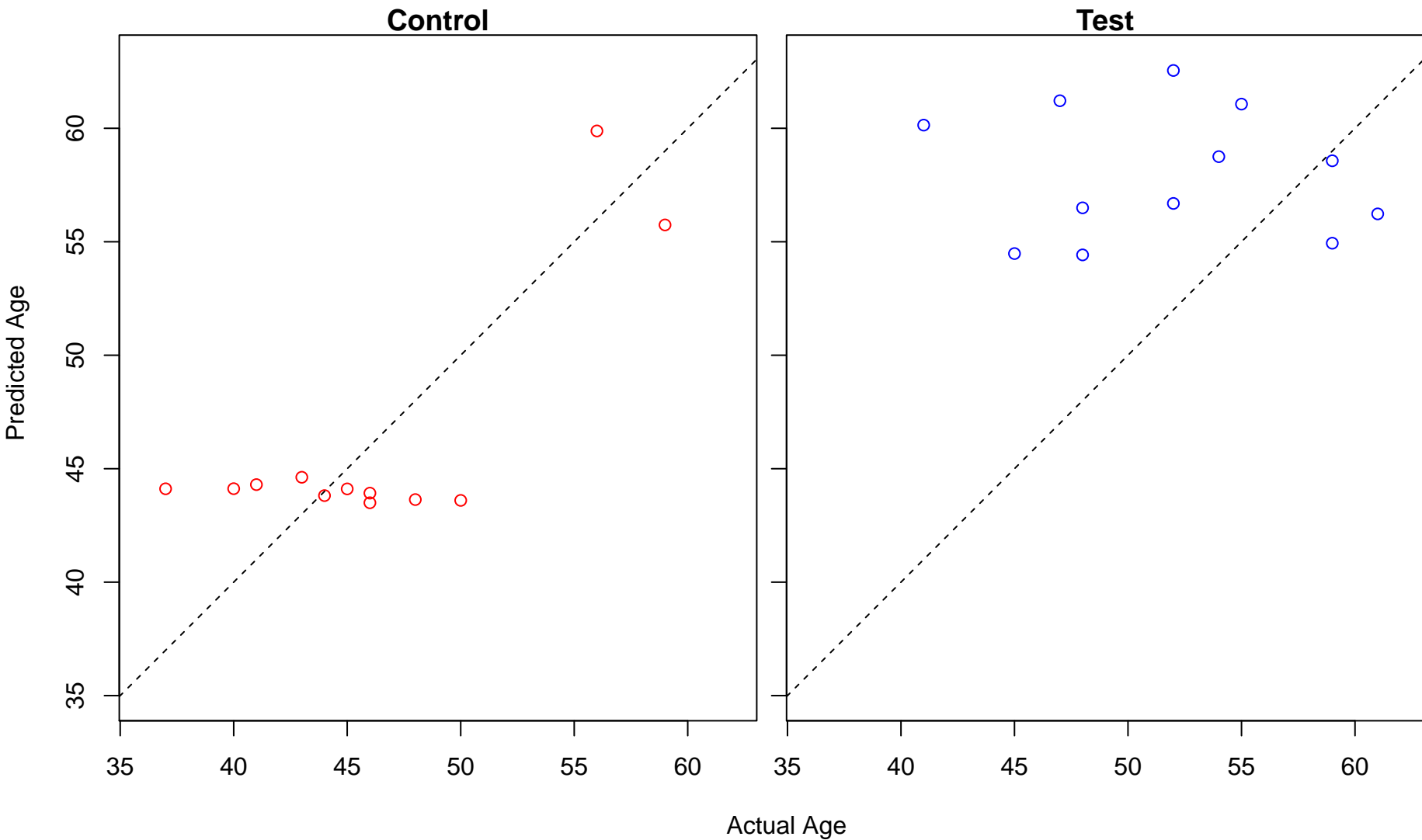
negative regulation of leukocyte mediated cytotoxicity (Score: 4.126694)



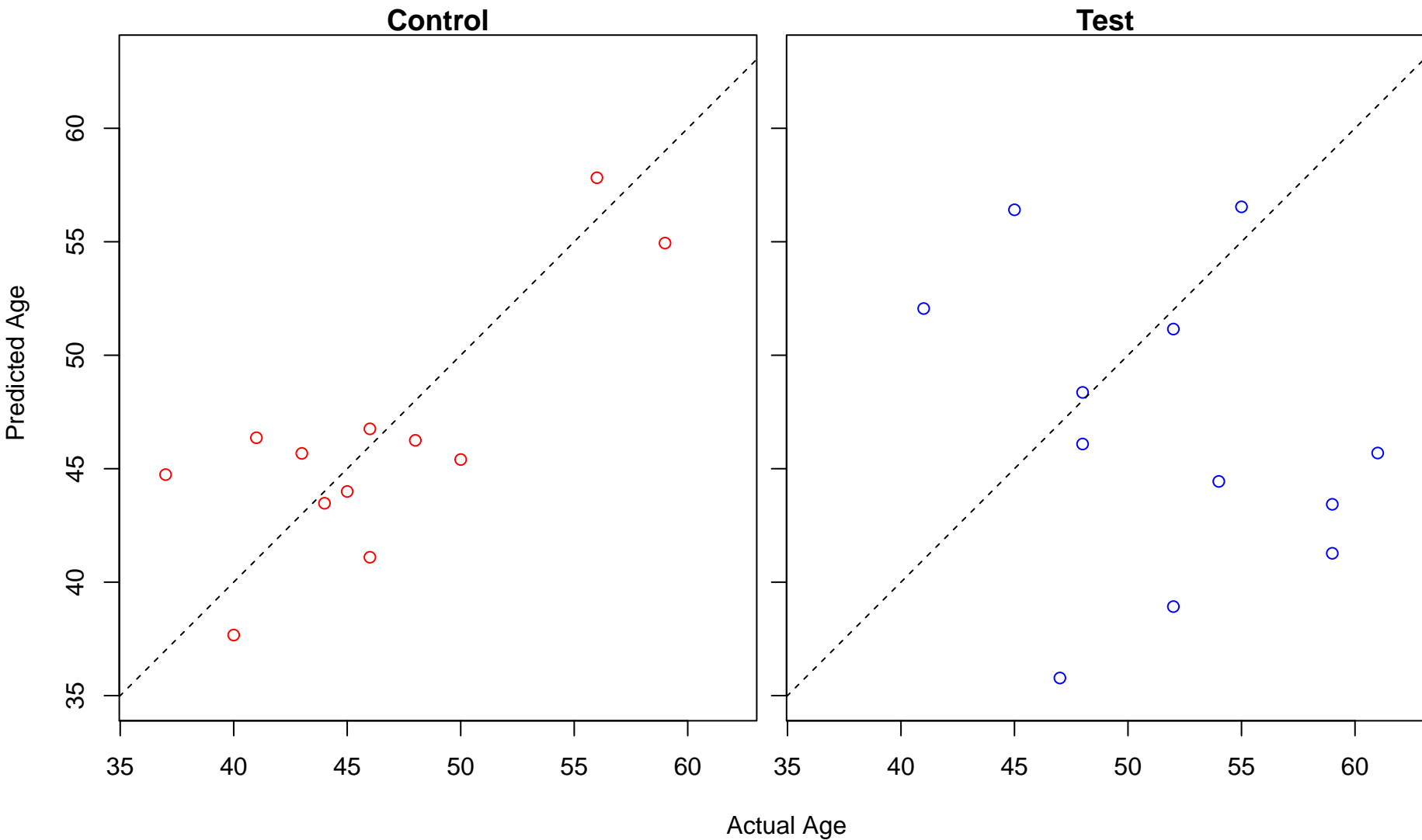
negative regulation of cell killing (Score: 4.126577)



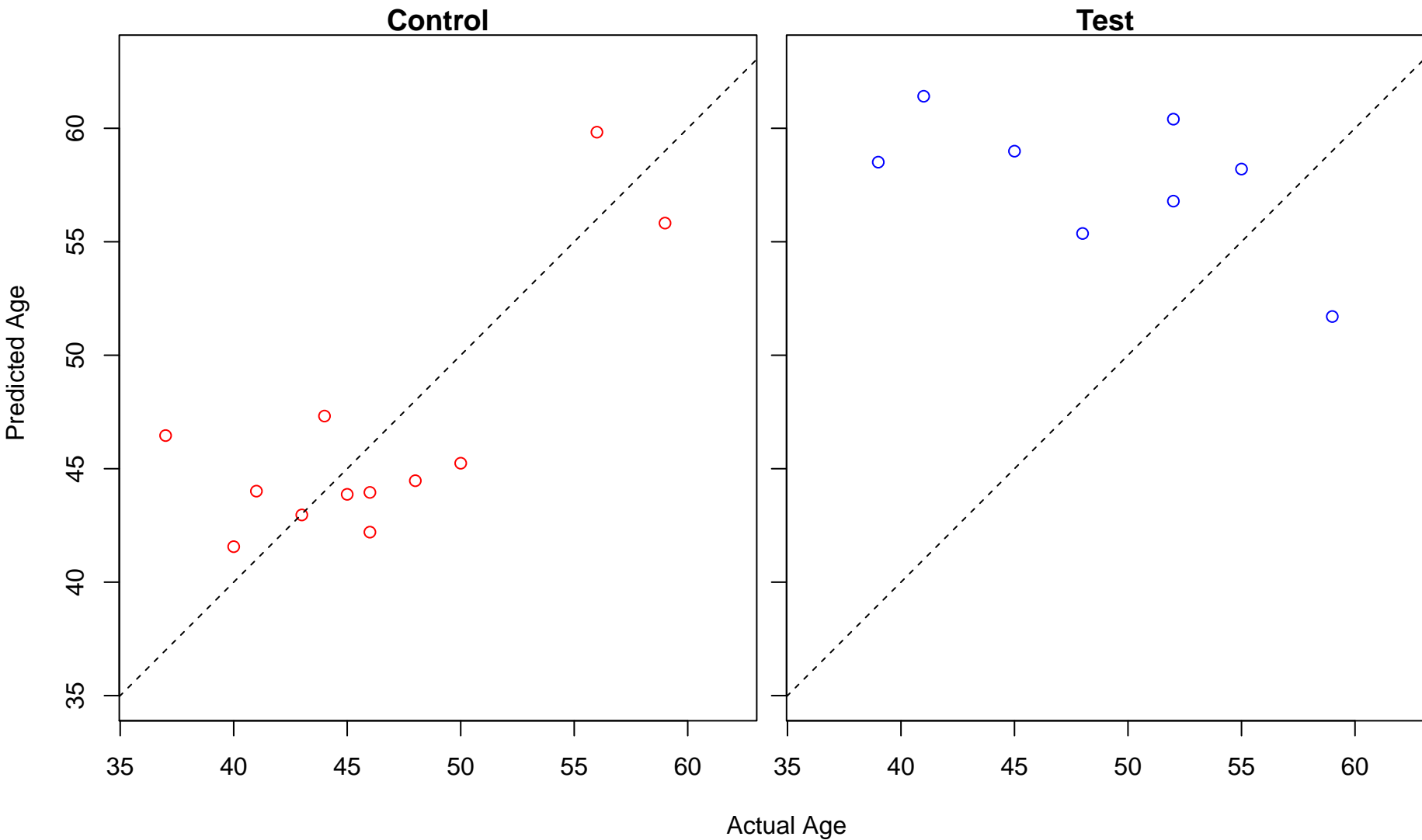
regulation of intrinsic apoptotic signaling pathway by p53 class mediator (Score: 4.125146)



triglyceride biosynthetic process (Score: 4.123683)

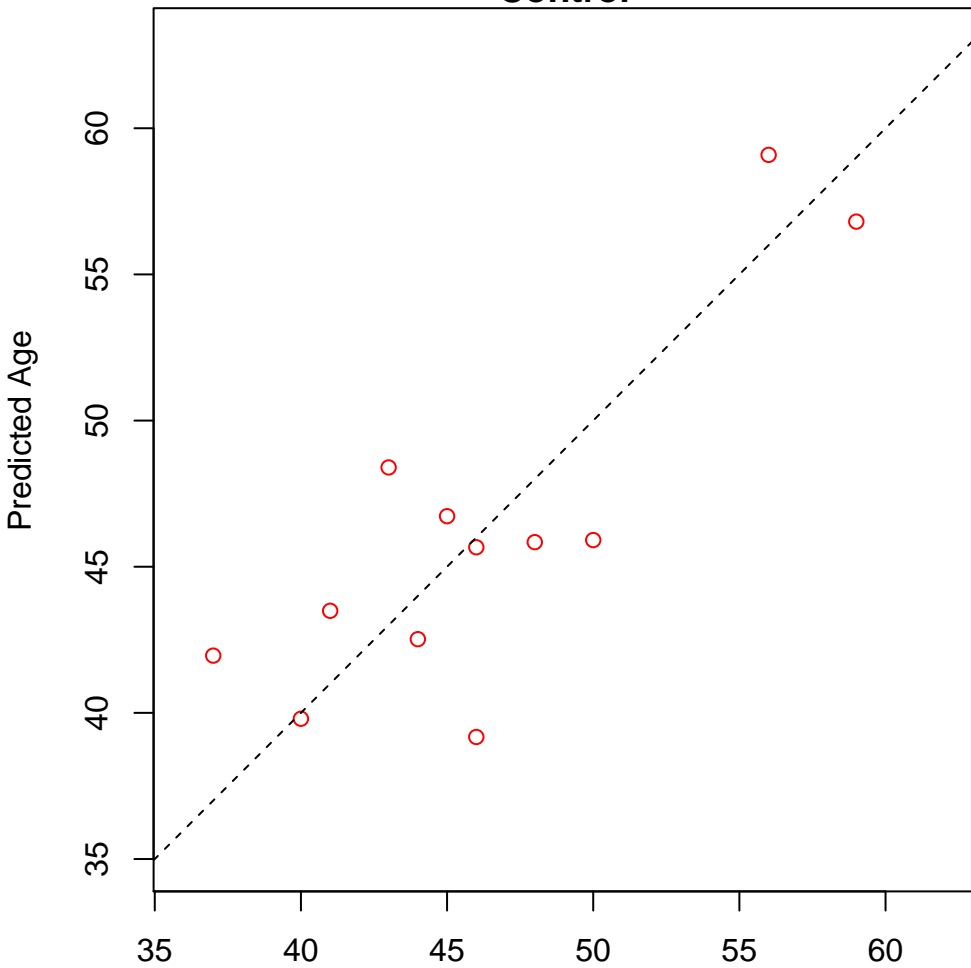


creatinine metabolic process (Score: 4.116950)

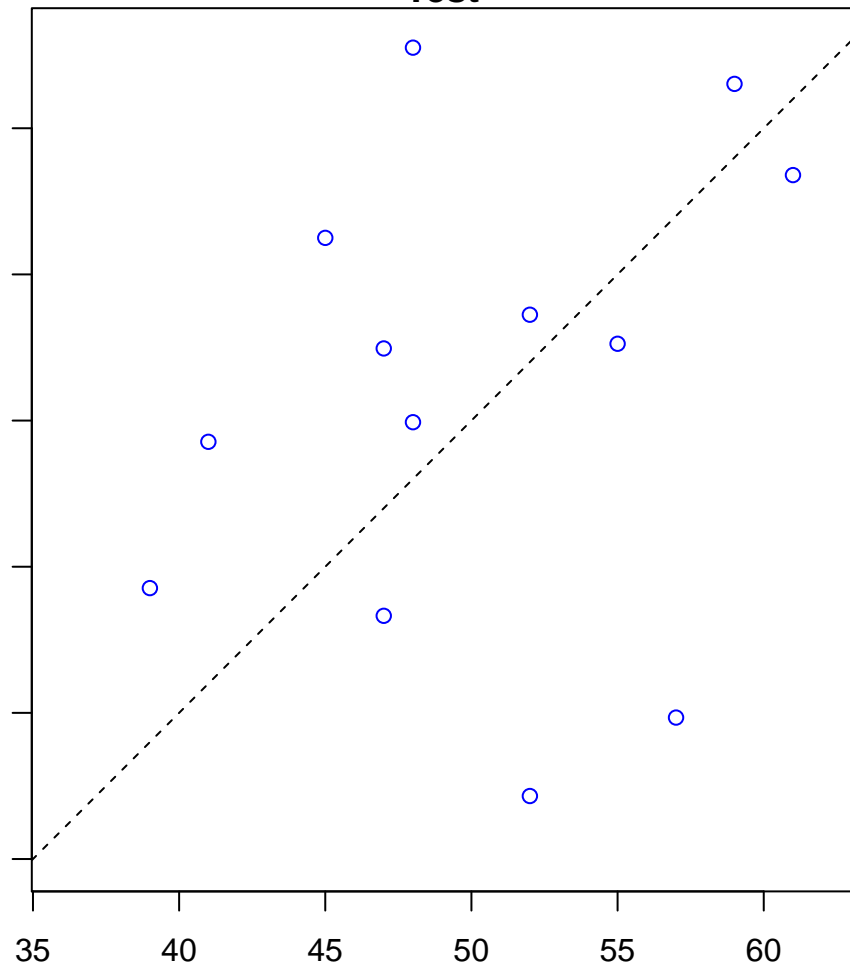


neurotransmitter biosynthetic process (Score: 4.113994)

Control

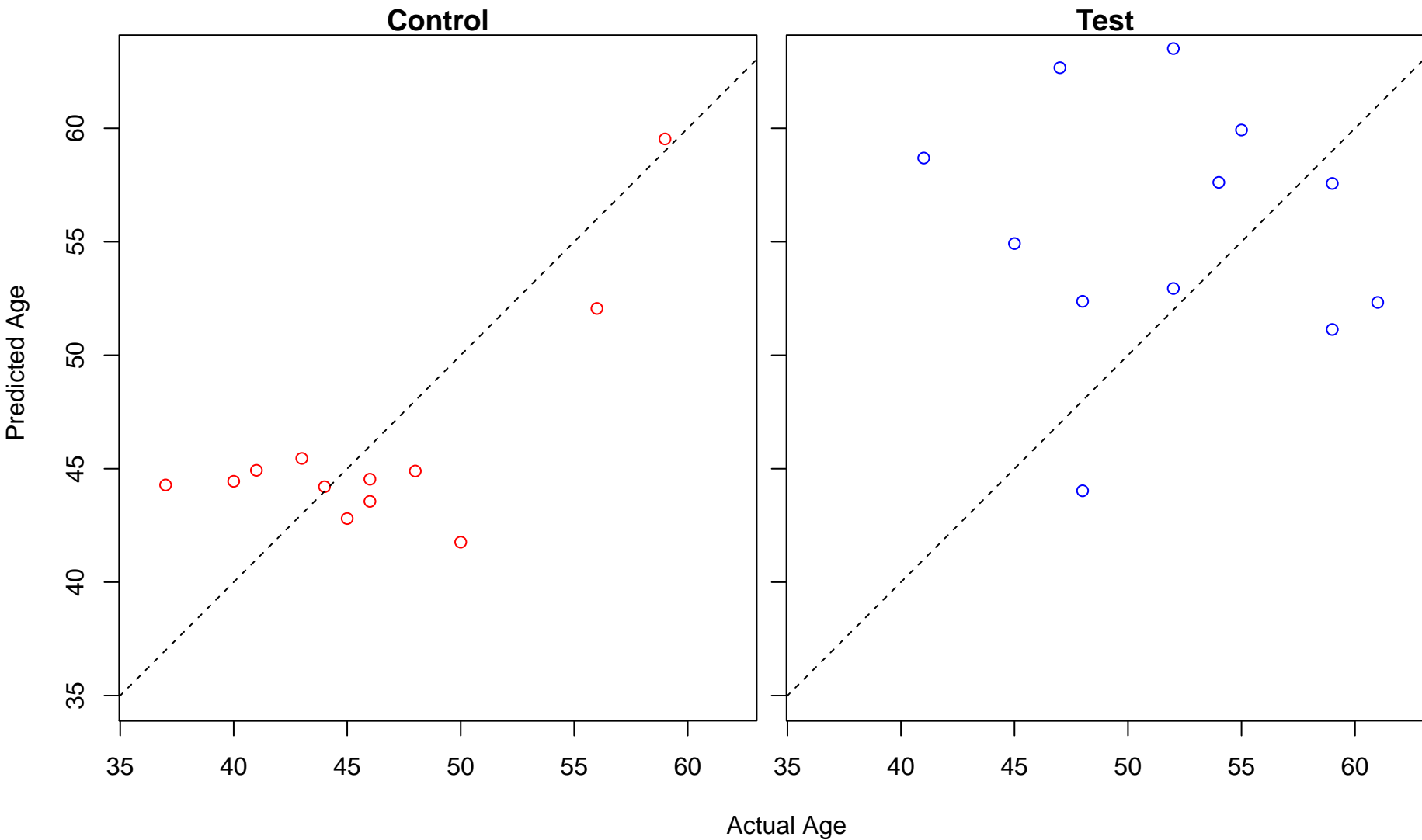


Test

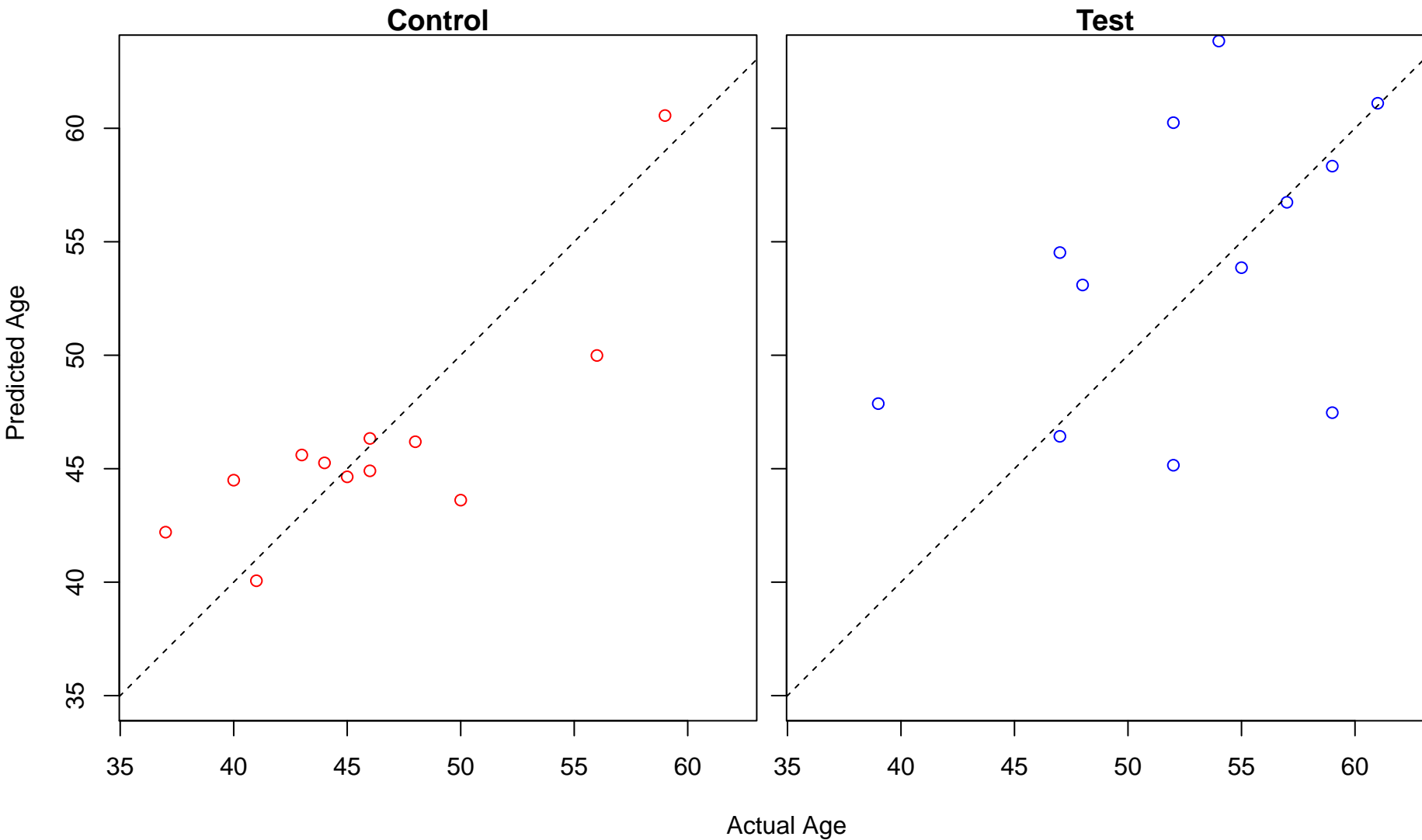


Actual Age

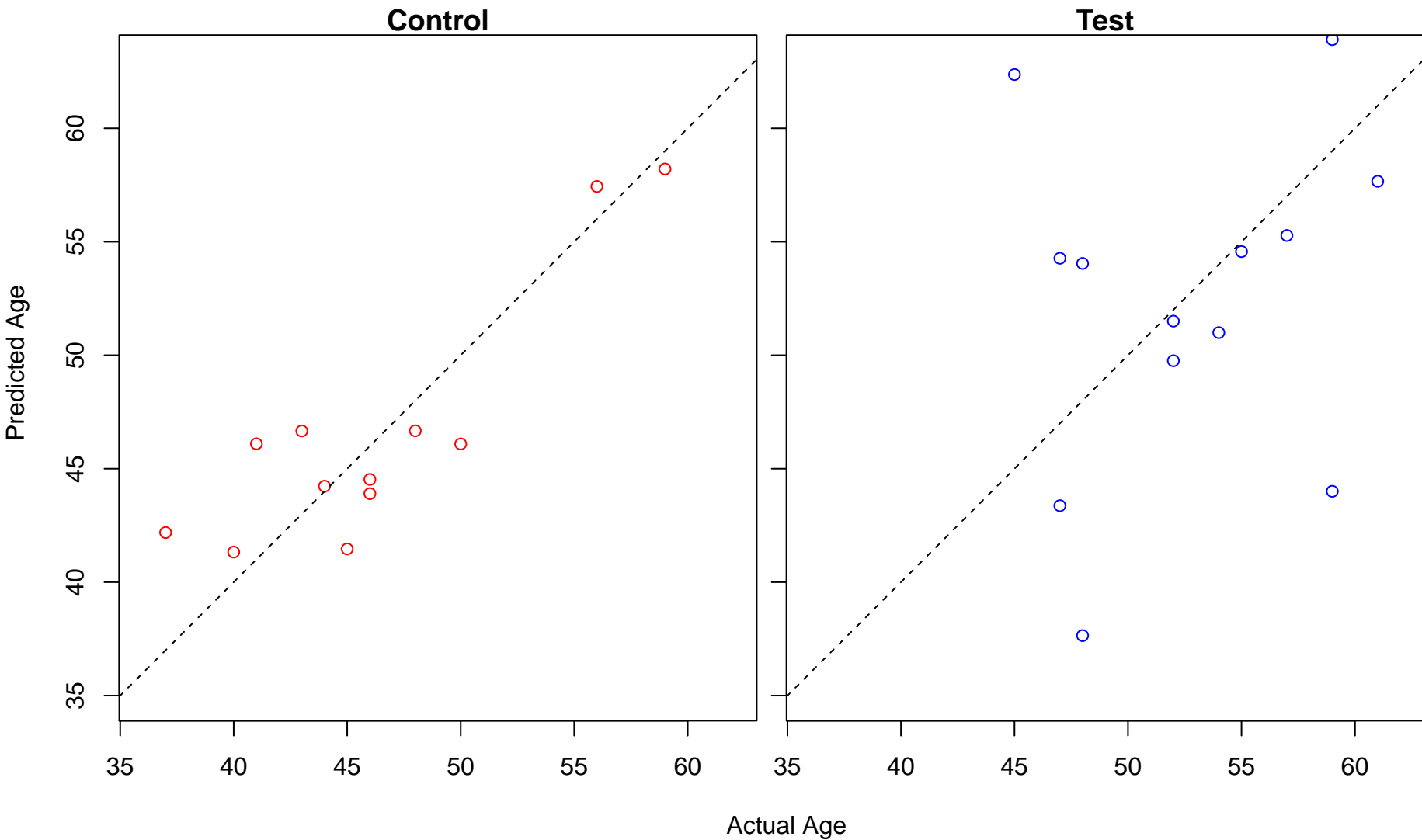
regulation of T cell mediated cytotoxicity (Score: 4.113771)



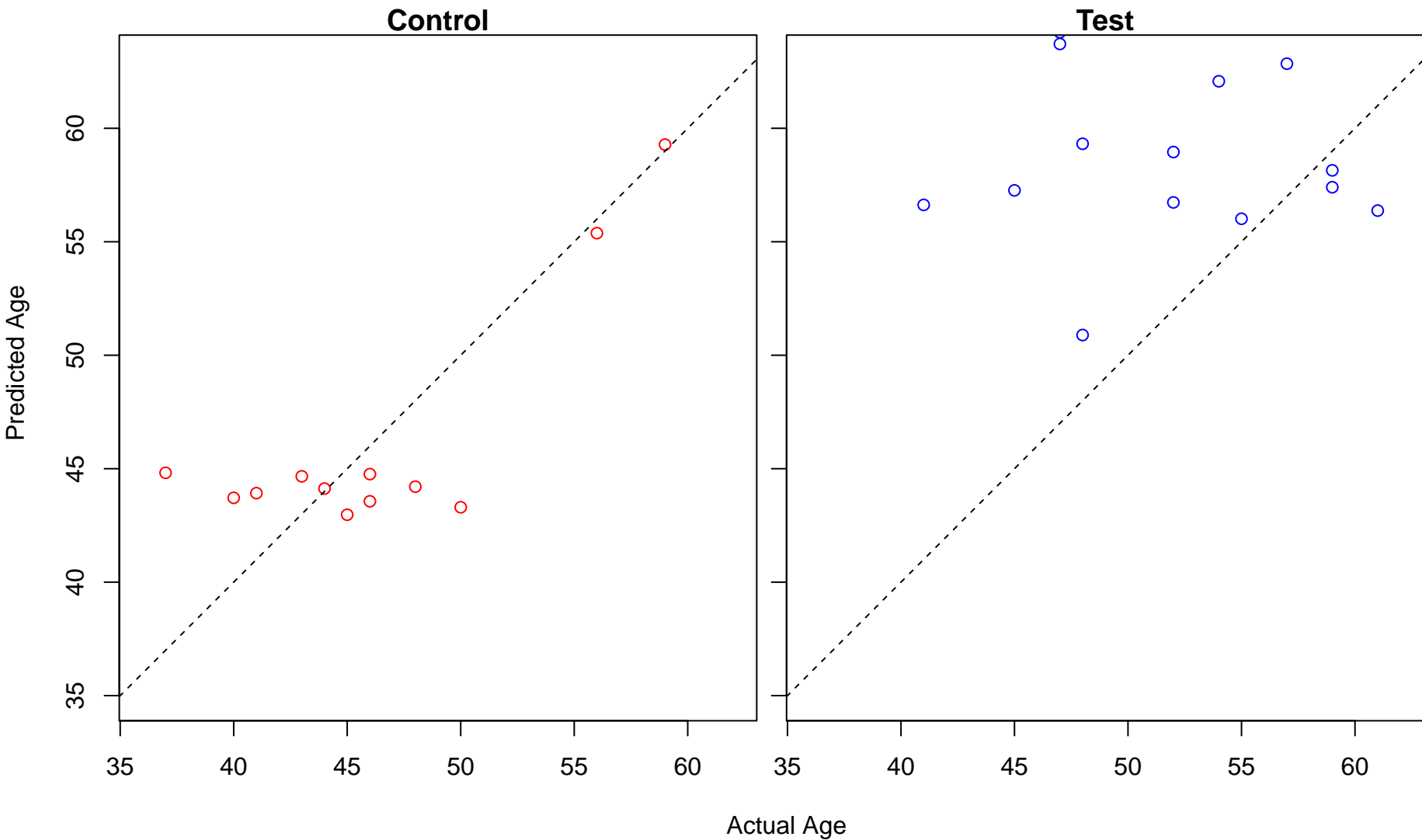
aromatic amino acid family catabolic process (Score: 4.113106)



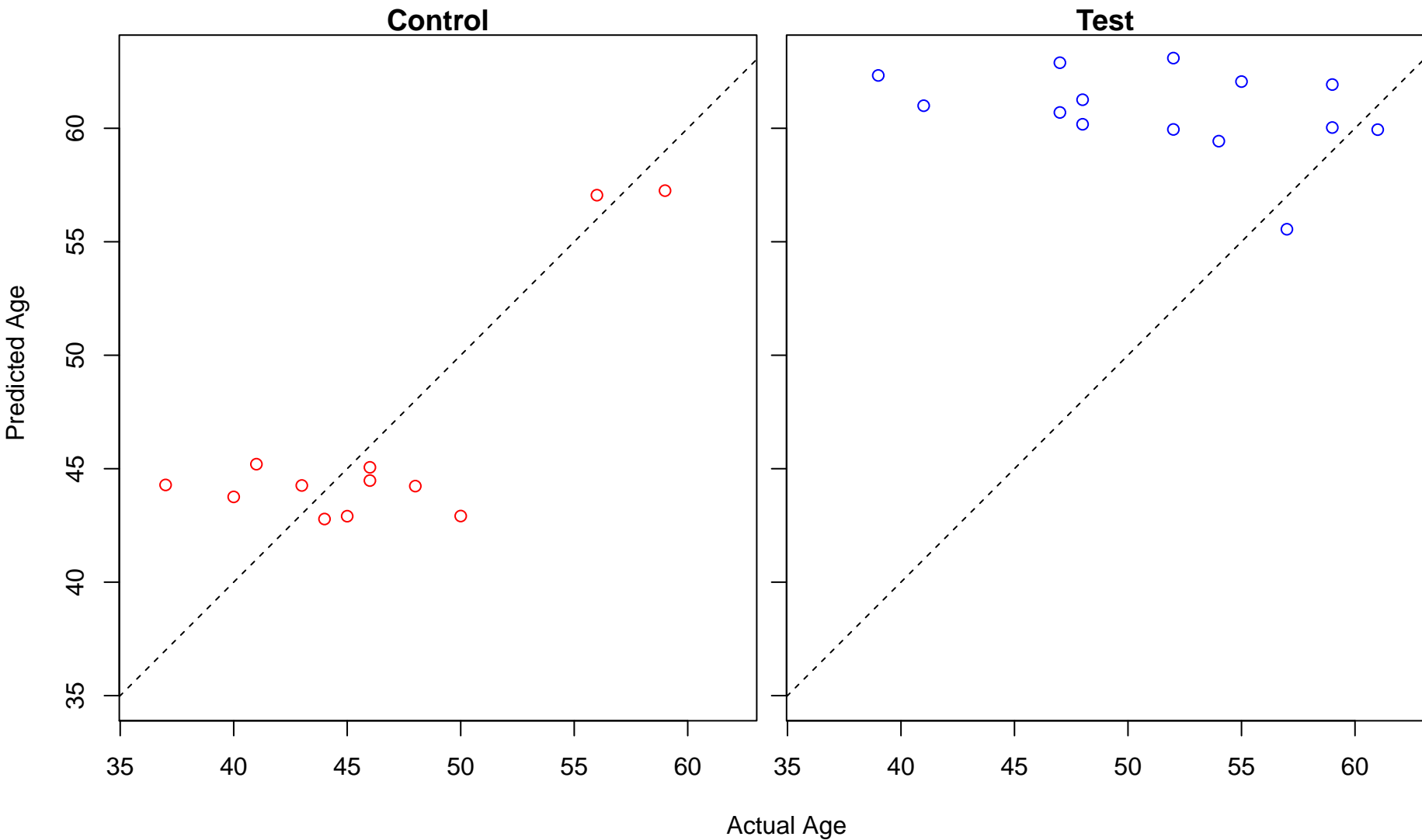
regulation of hormone levels (Score: 4.110125)



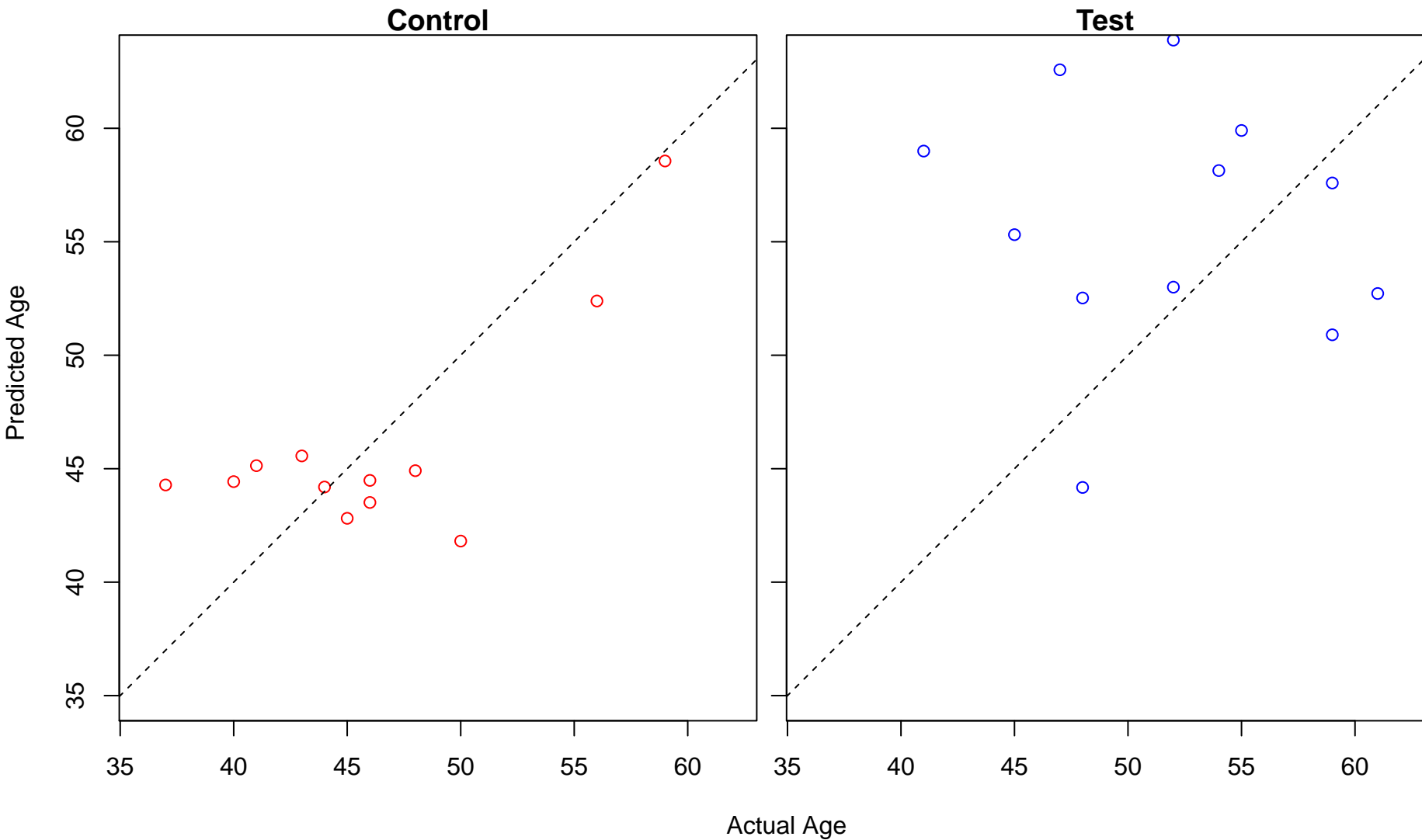
chemical synaptic transmission, postsynaptic (Score: 4.107910)



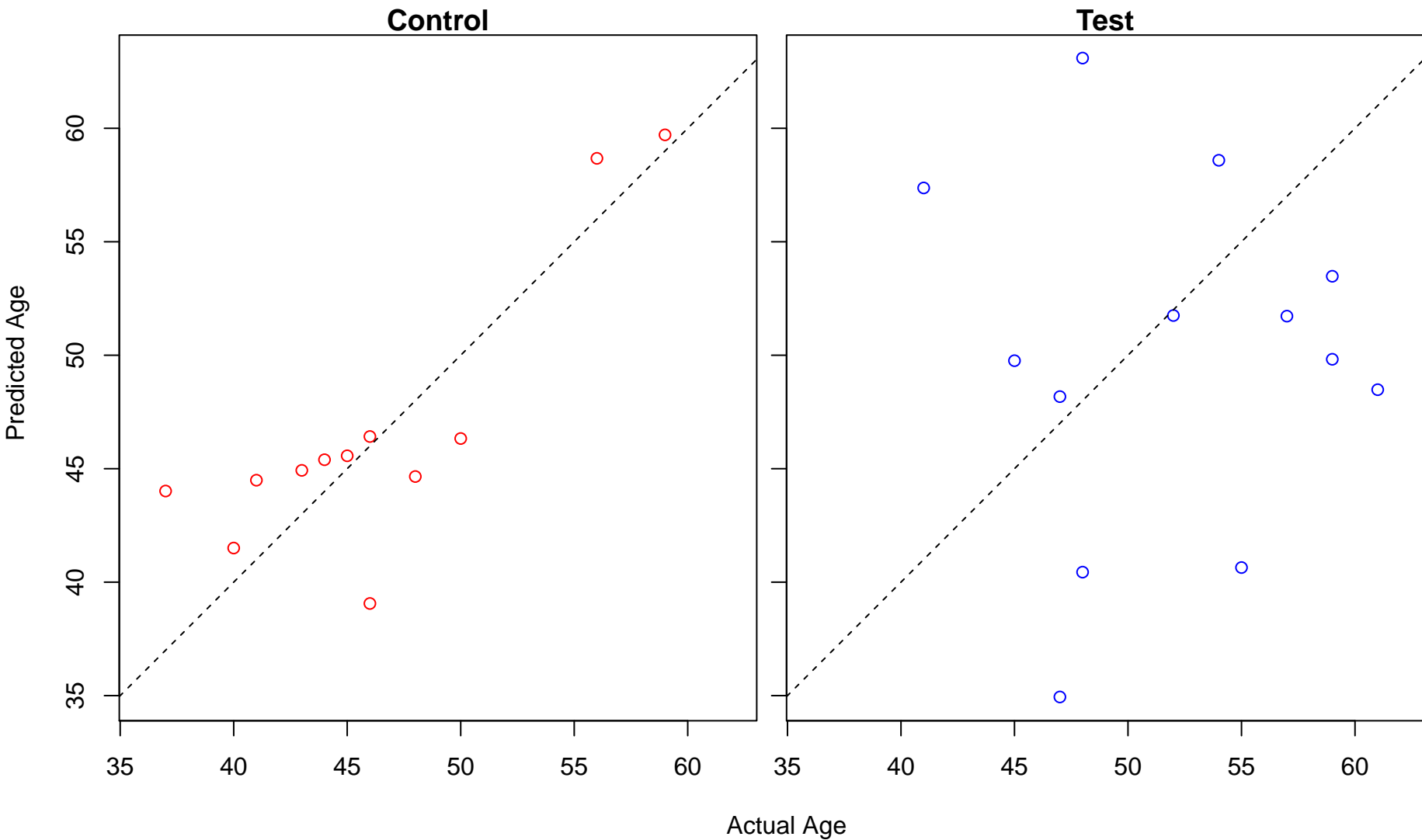
pre-miRNA processing (Score: 4.105599)



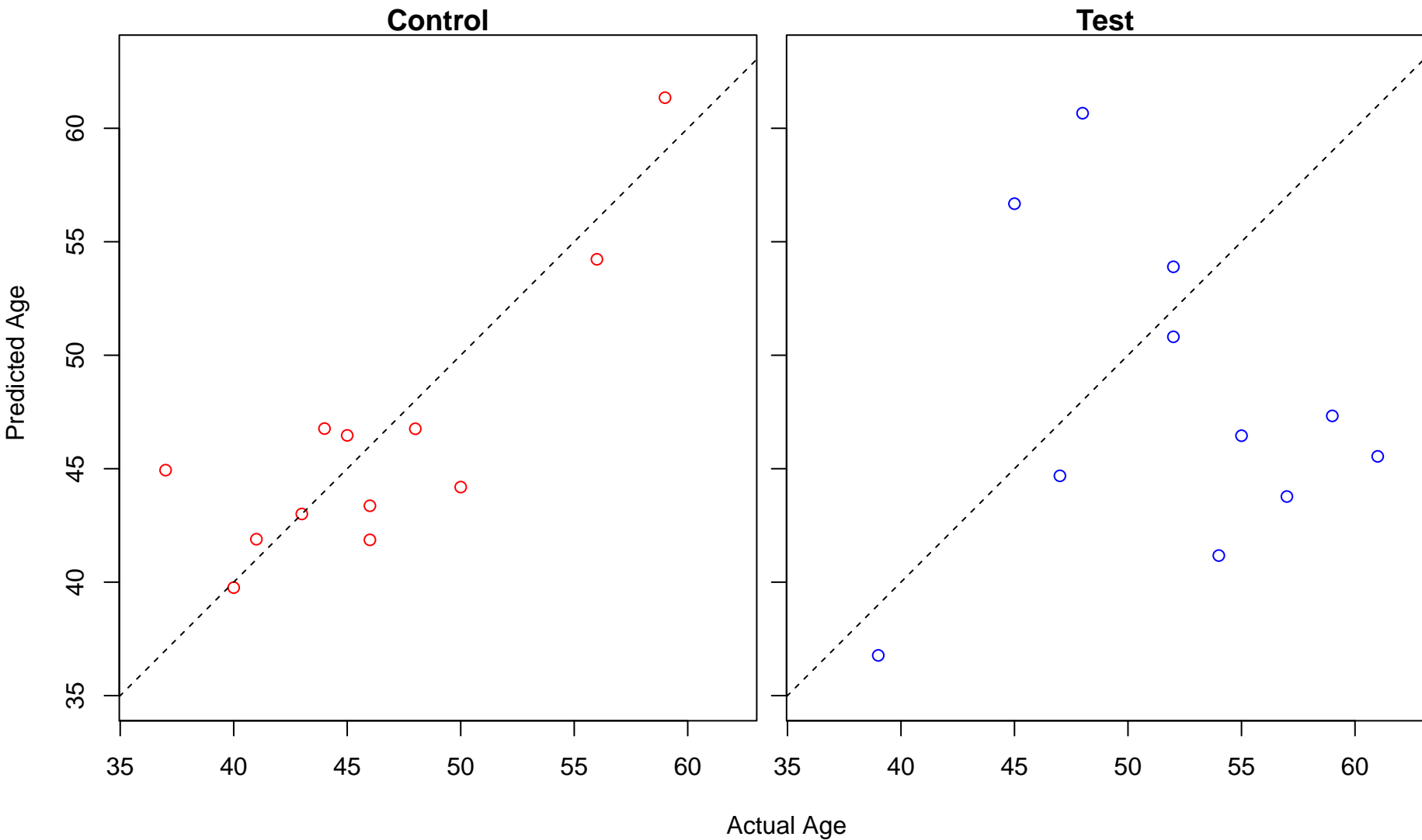
negative regulation of lymphocyte mediated immunity (Score: 4.095051)



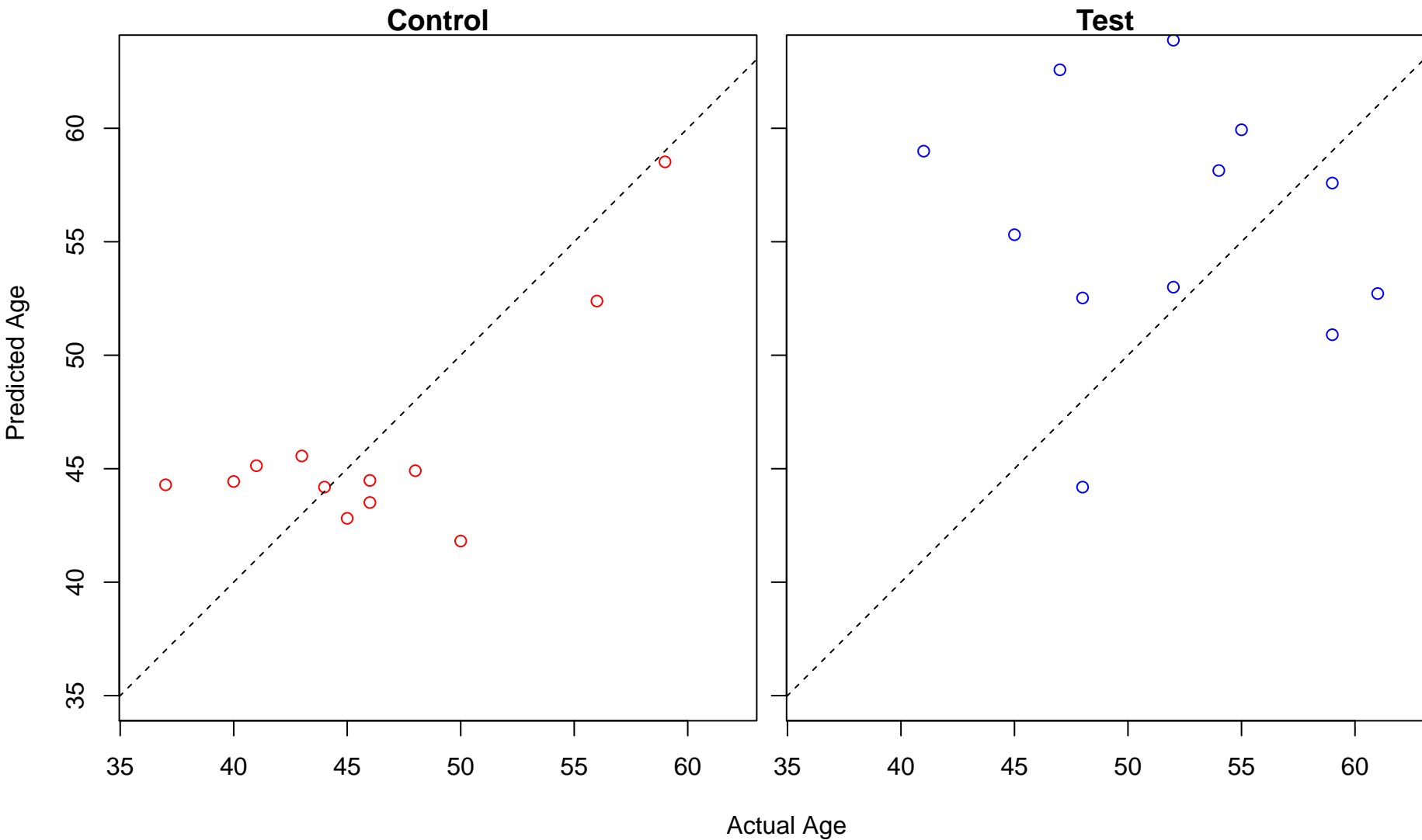
regulation of protein polymerization (Score: 4.094660)



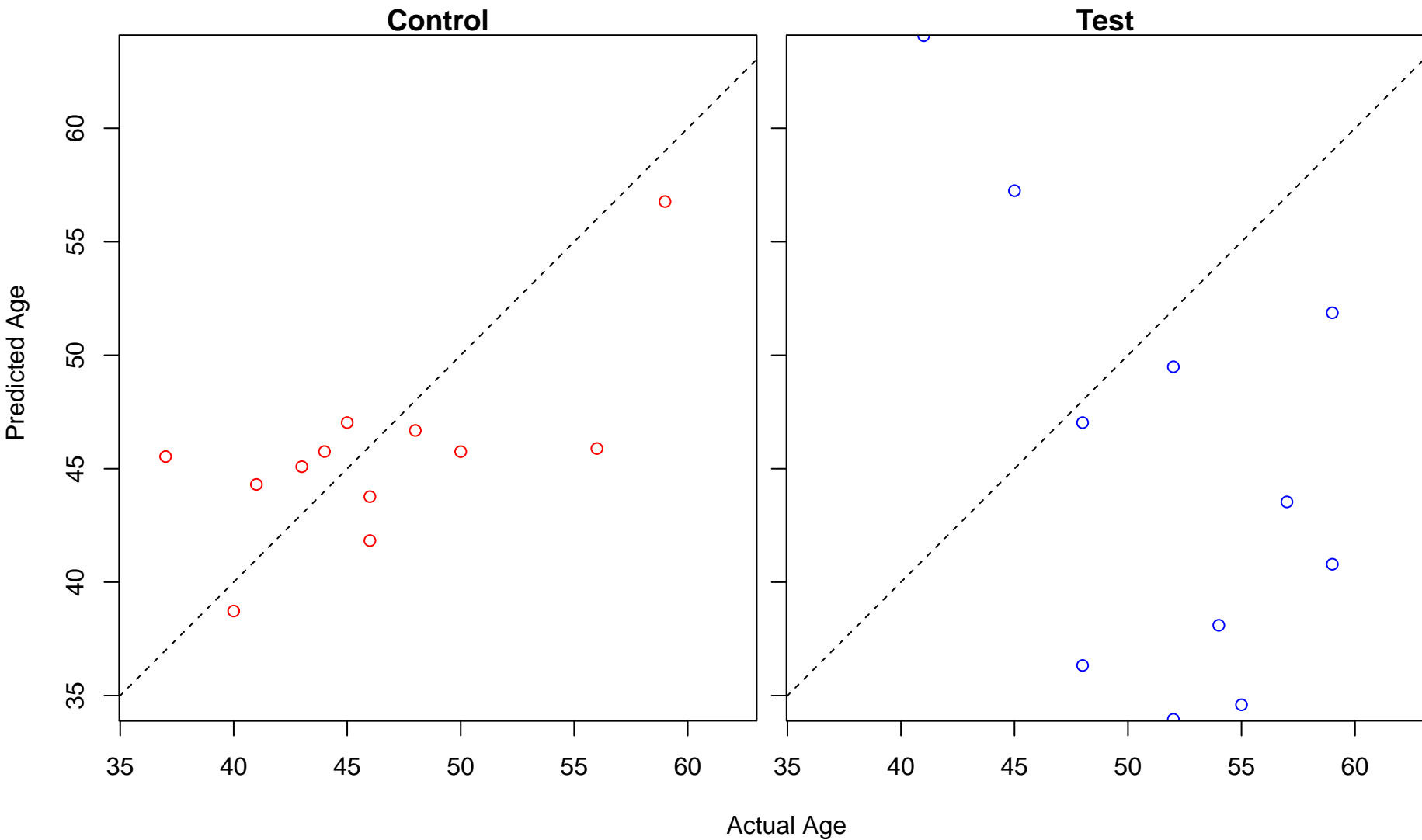
regulation of cell aging (Score: 4.086492)



negative regulation of leukocyte mediated immunity (Score: 4.085290)

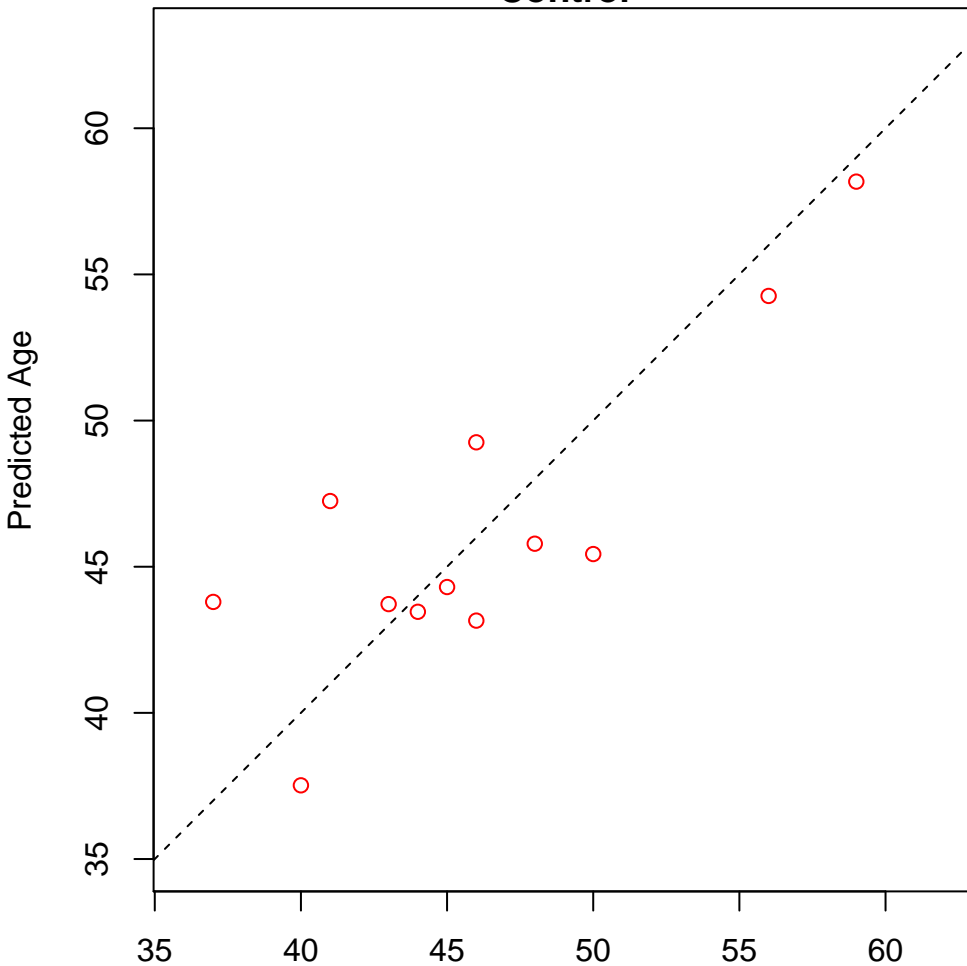


regulation of autophagosome maturation (Score: 4.081897)

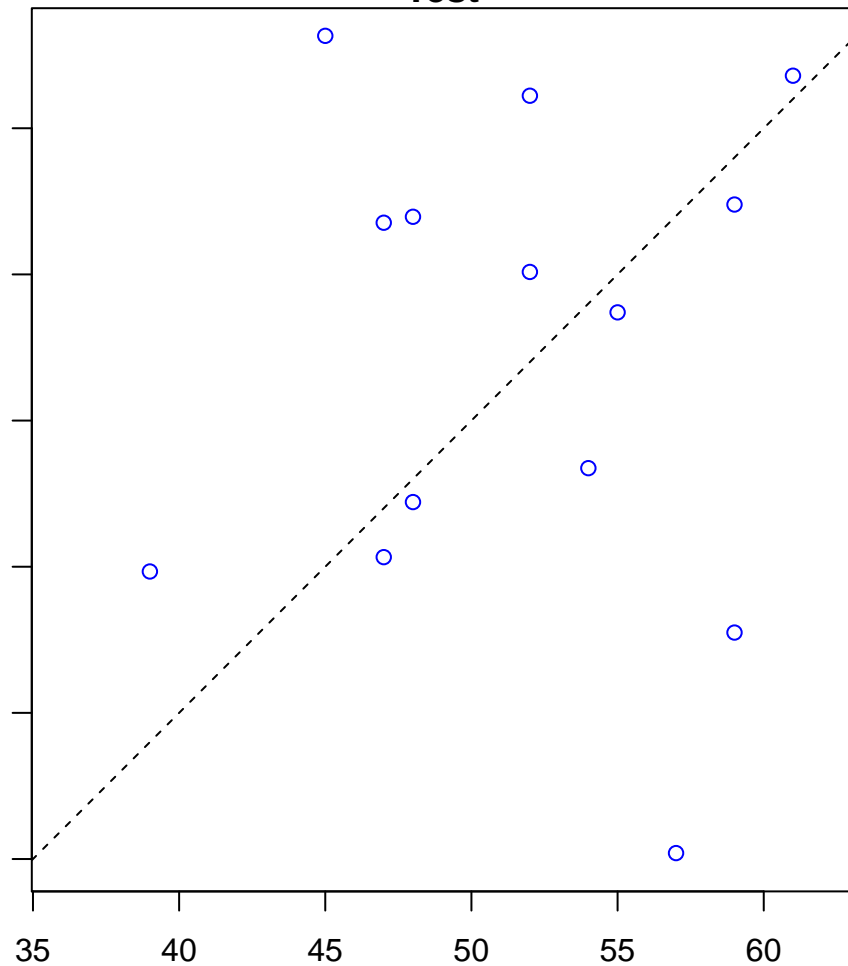


T-helper 1 type immune response (Score: 4.078319)

Control



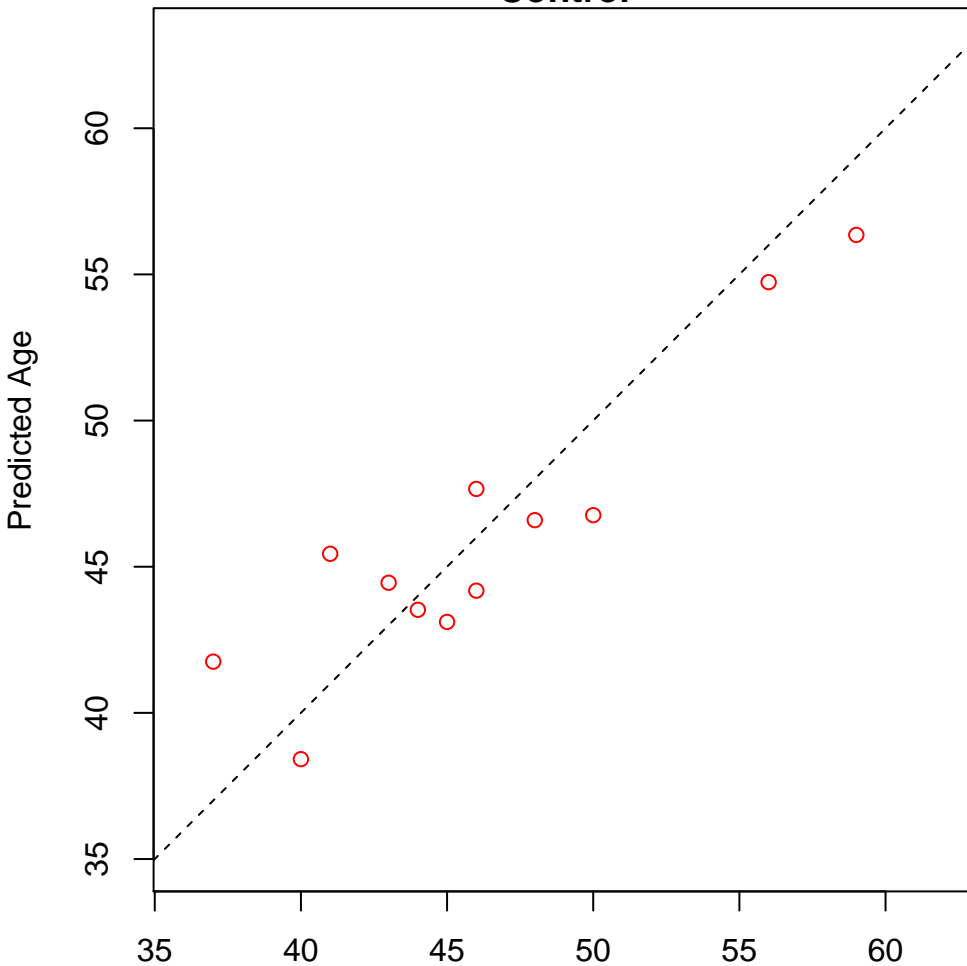
Test



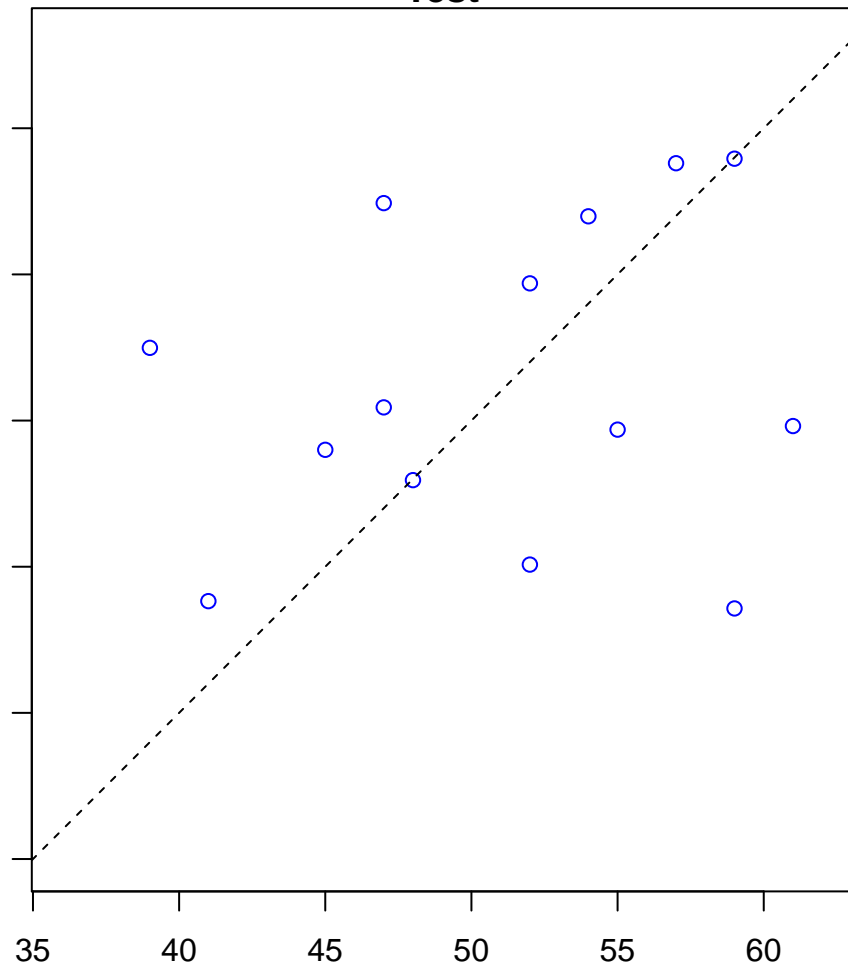
Actual Age

plasma lipoprotein particle clearance (Score: 4.076967)

Control

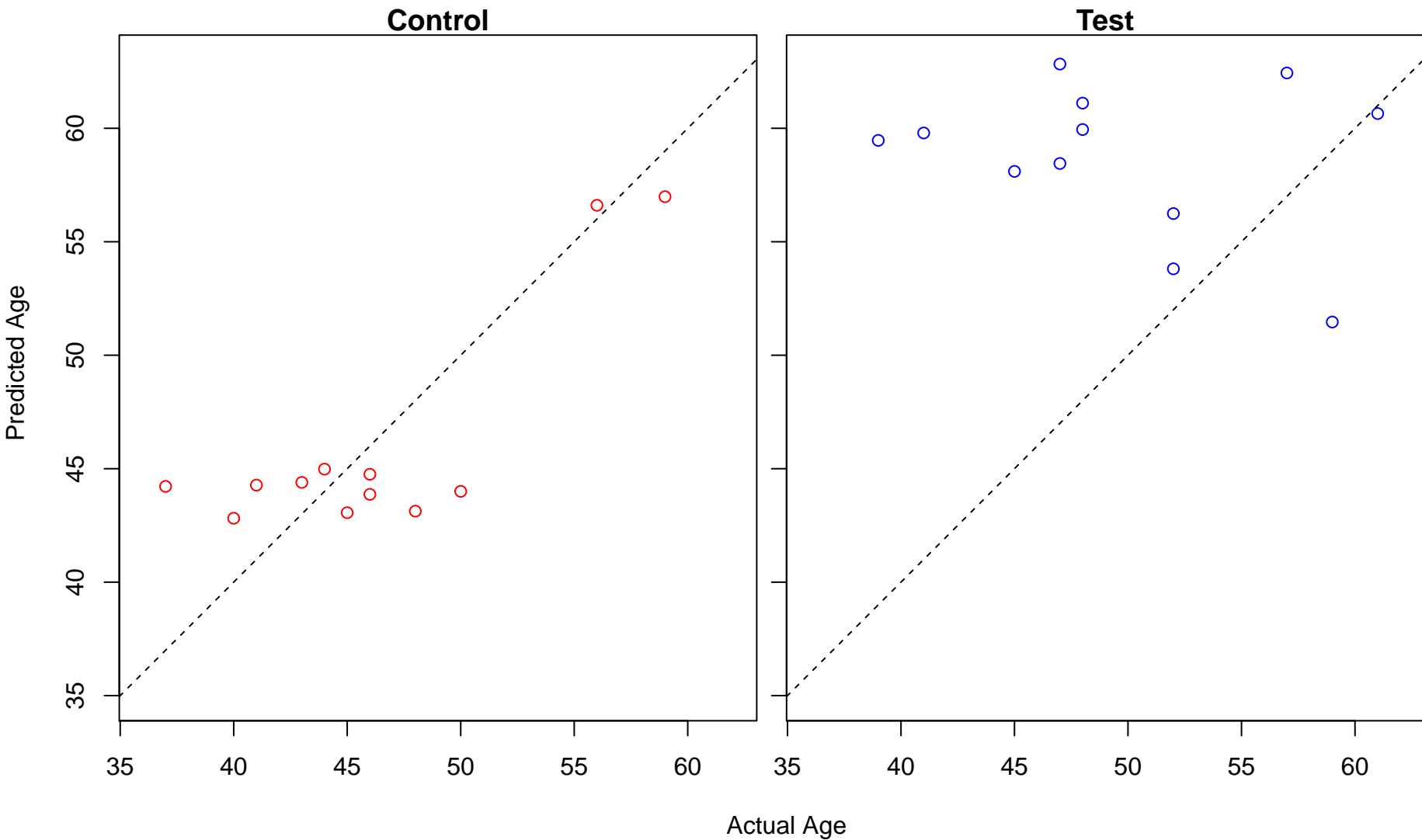


Test

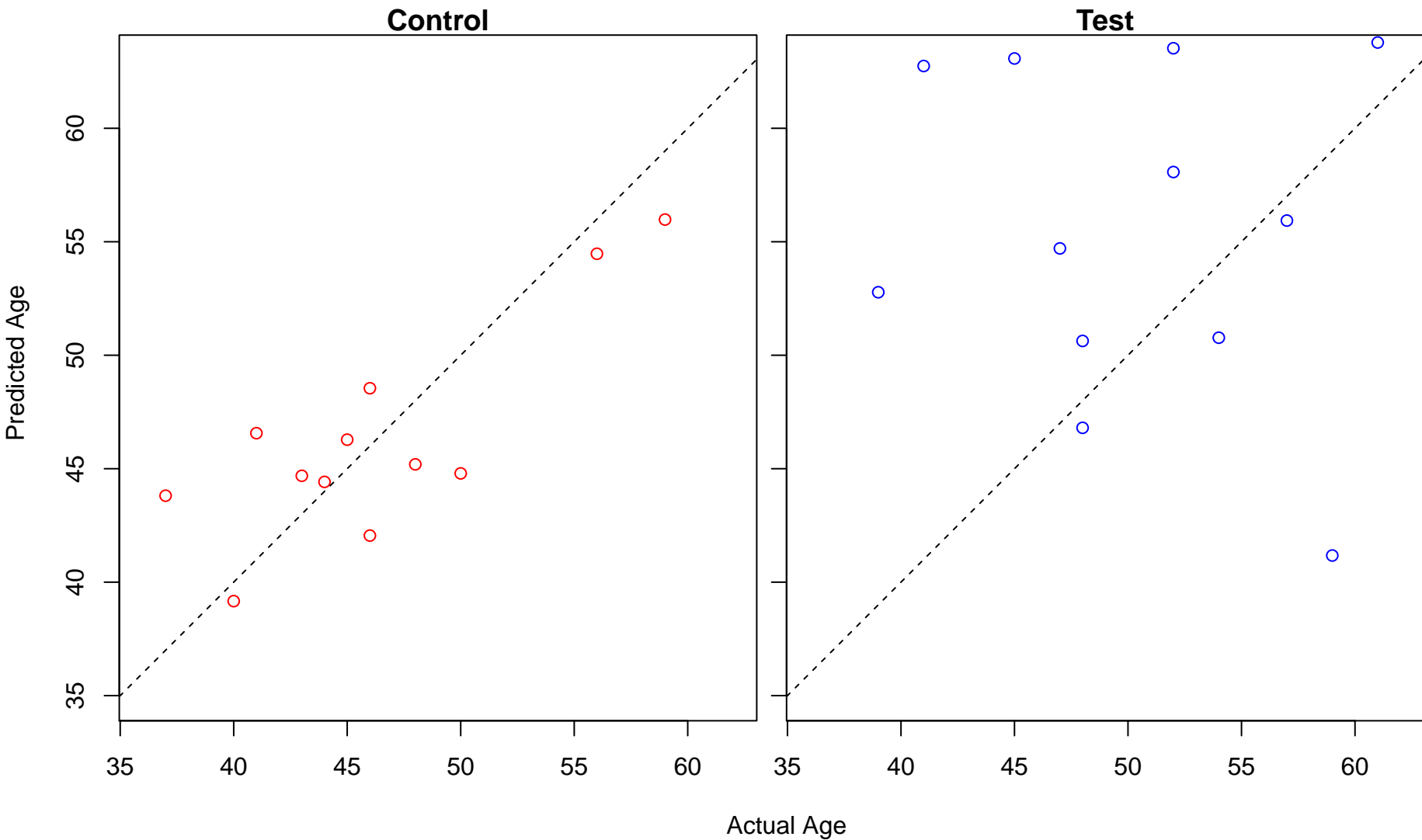


Actual Age

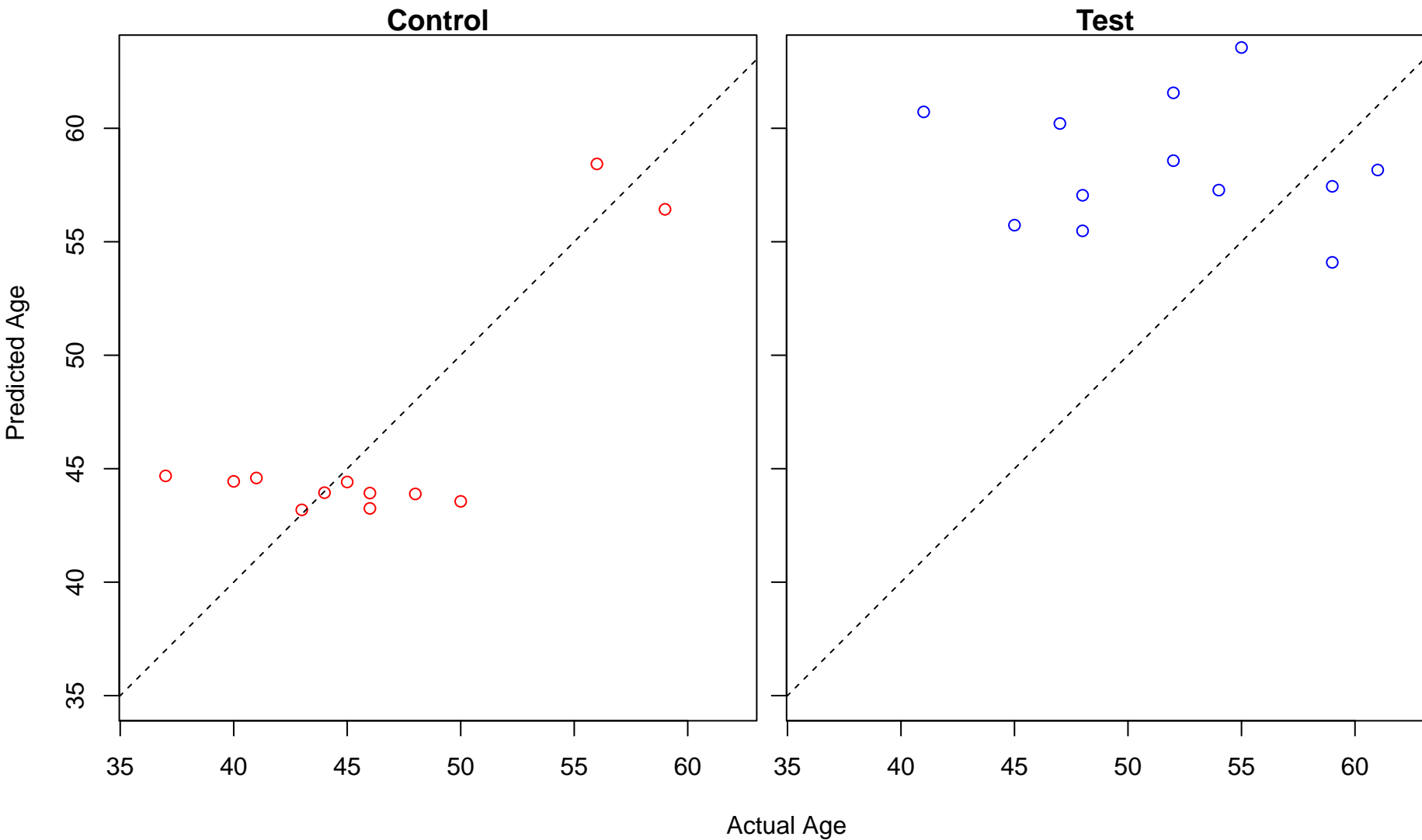
striated muscle adaptation (Score: 4.062541)



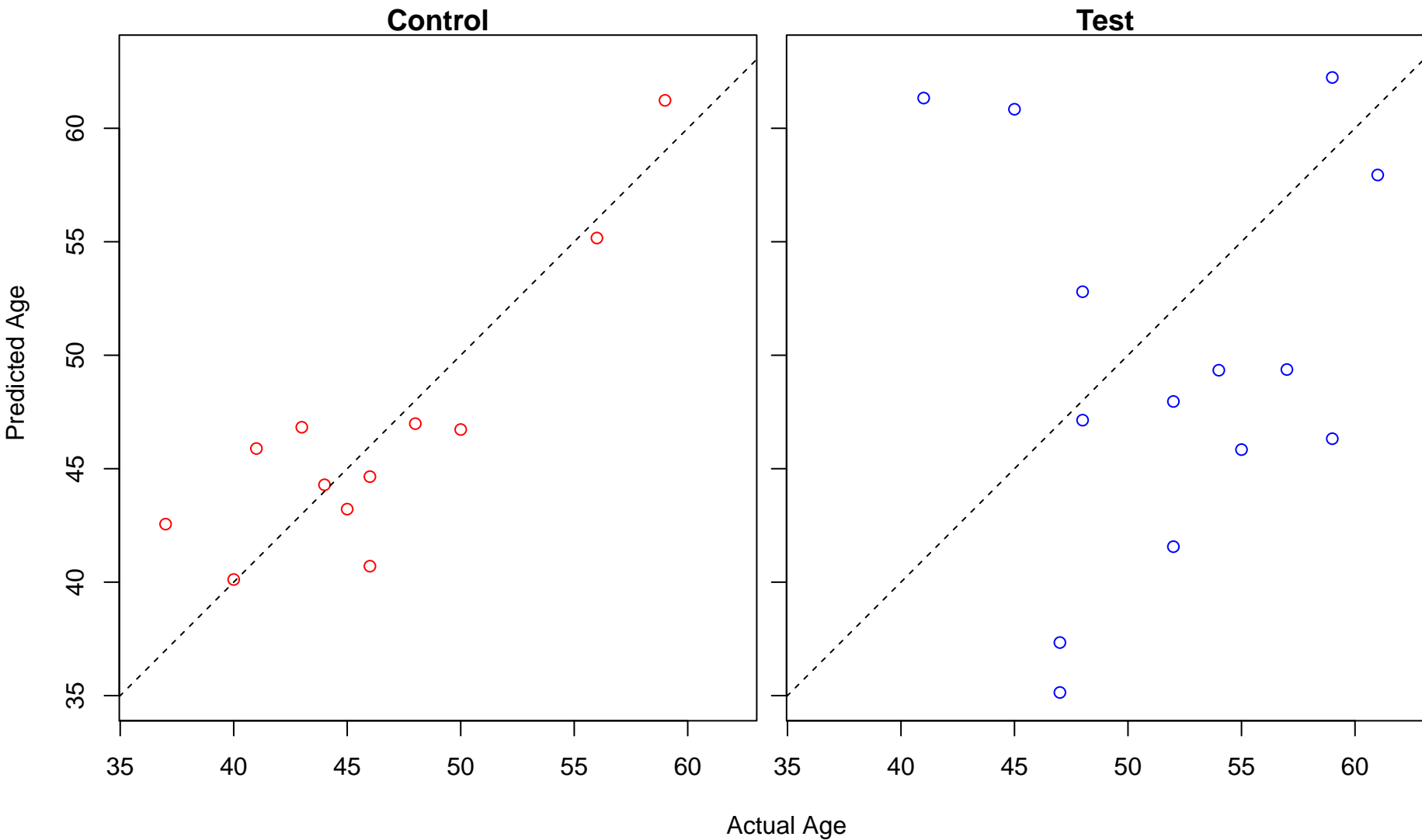
humoral immune response (Score: 4.061494)



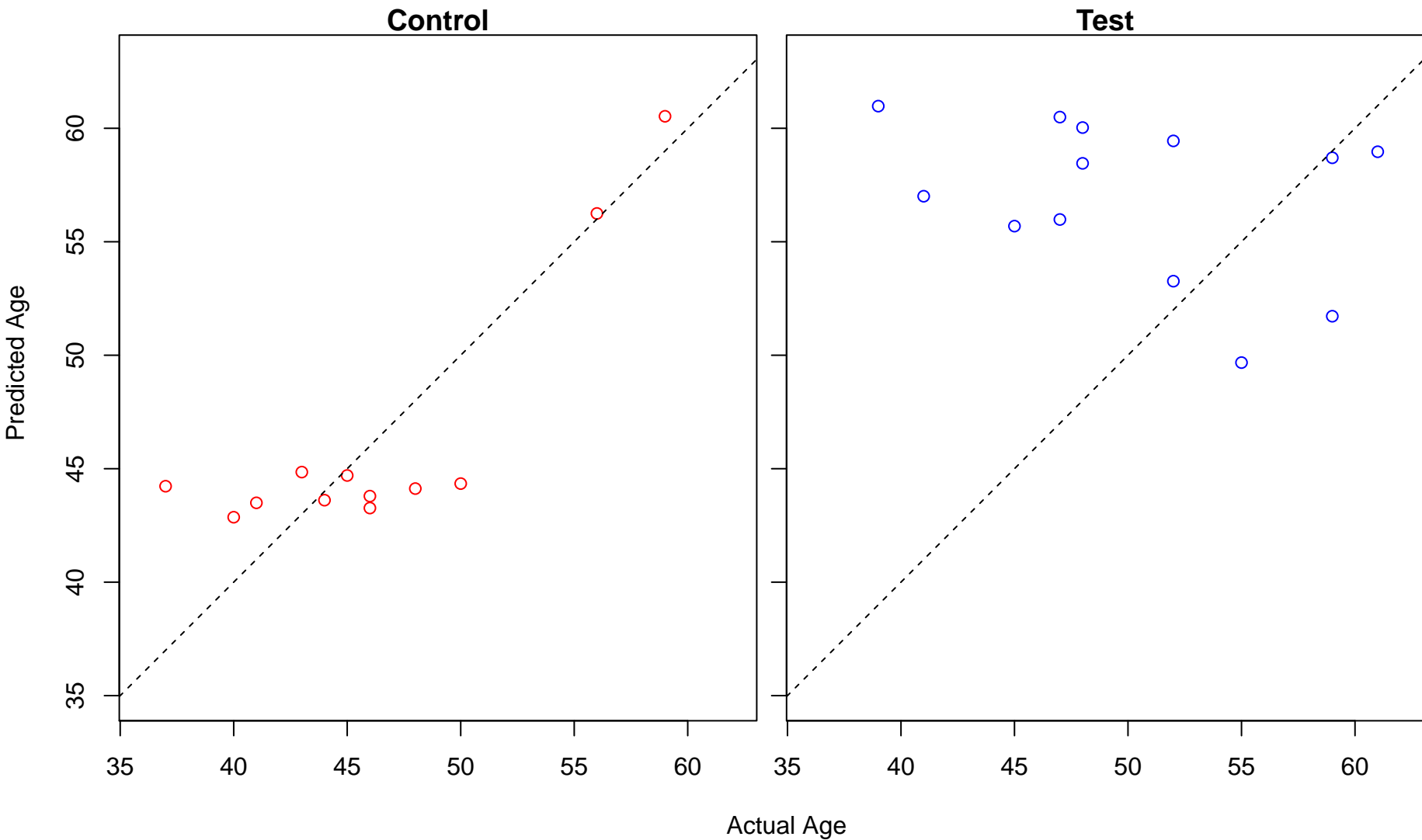
regulation of I-kappaB kinase/NF-kappaB signaling (Score: 4.060648)



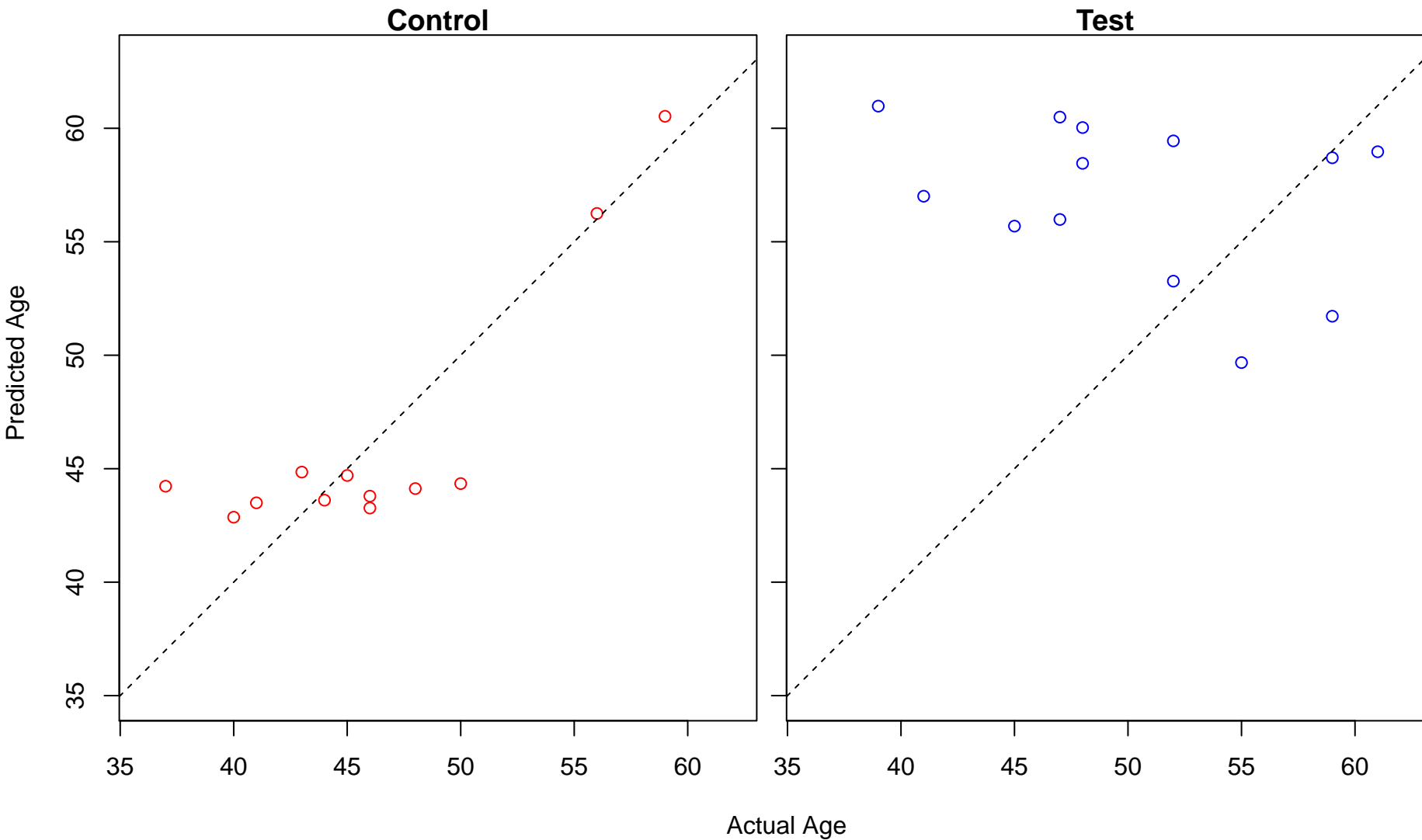
lipid biosynthetic process (Score: 4.057725)



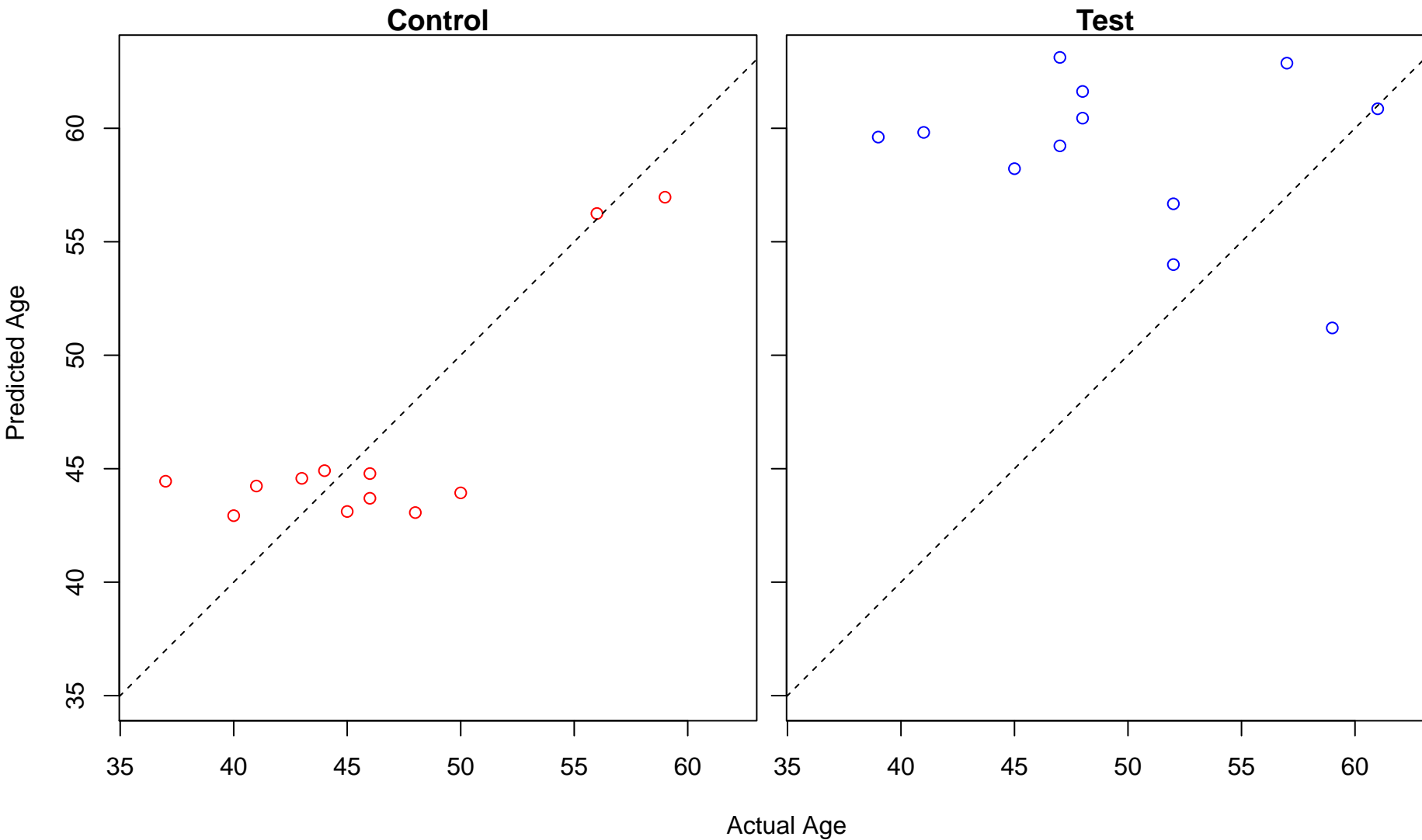
regulation of collagen metabolic process (Score: 4.054901)



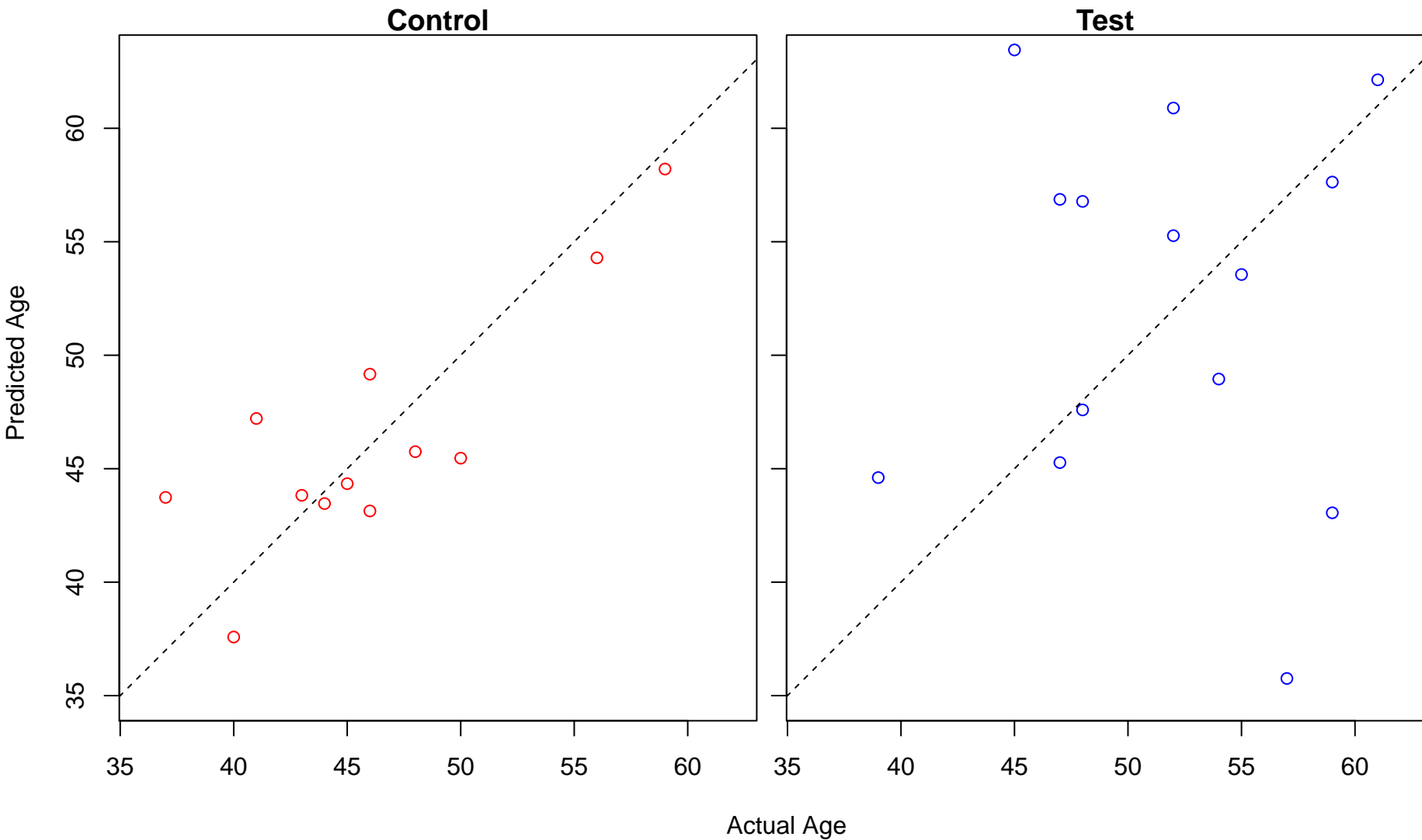
regulation of multicellular organismal metabolic process (Score: 4.054901)



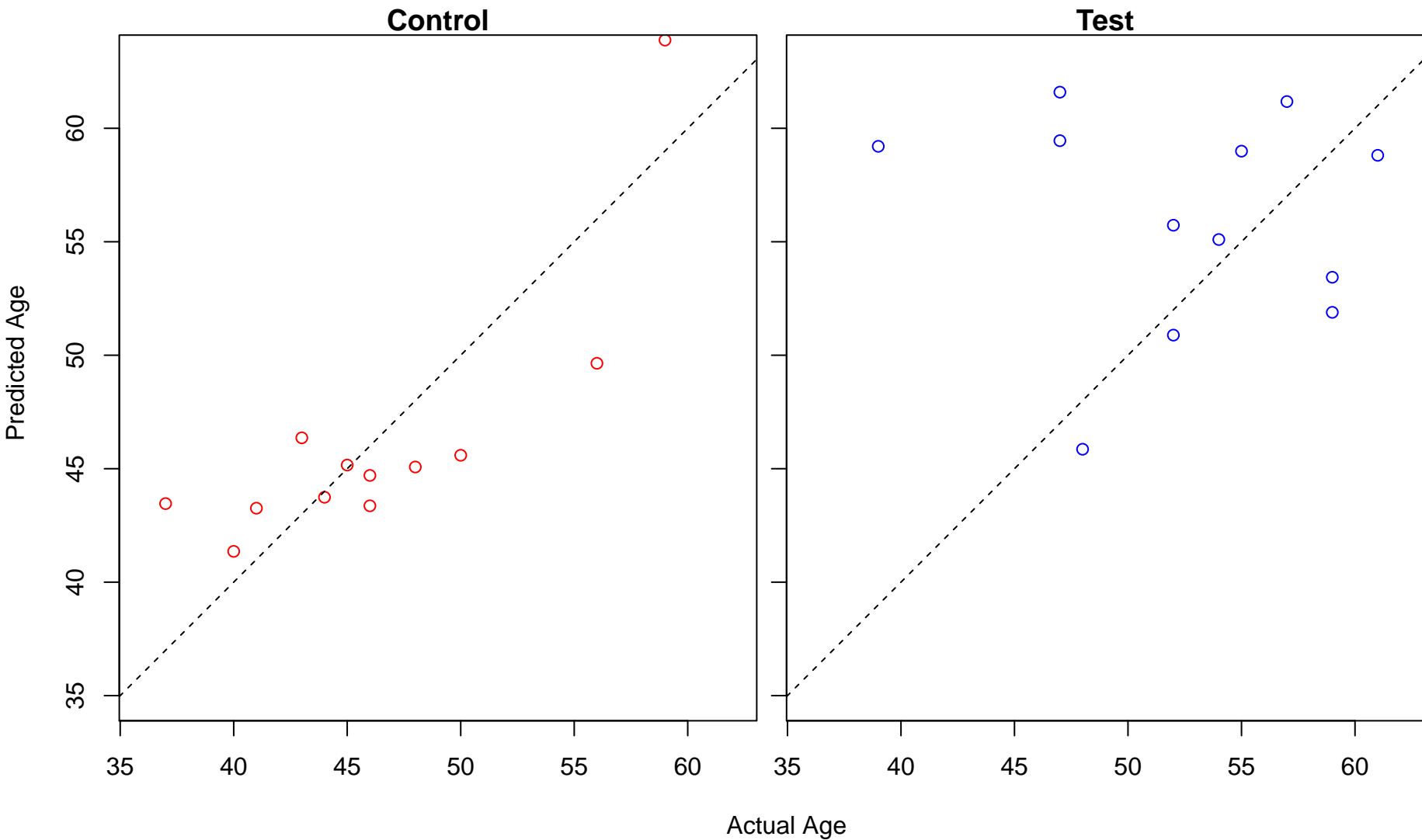
muscle adaptation (Score: 4.054683)



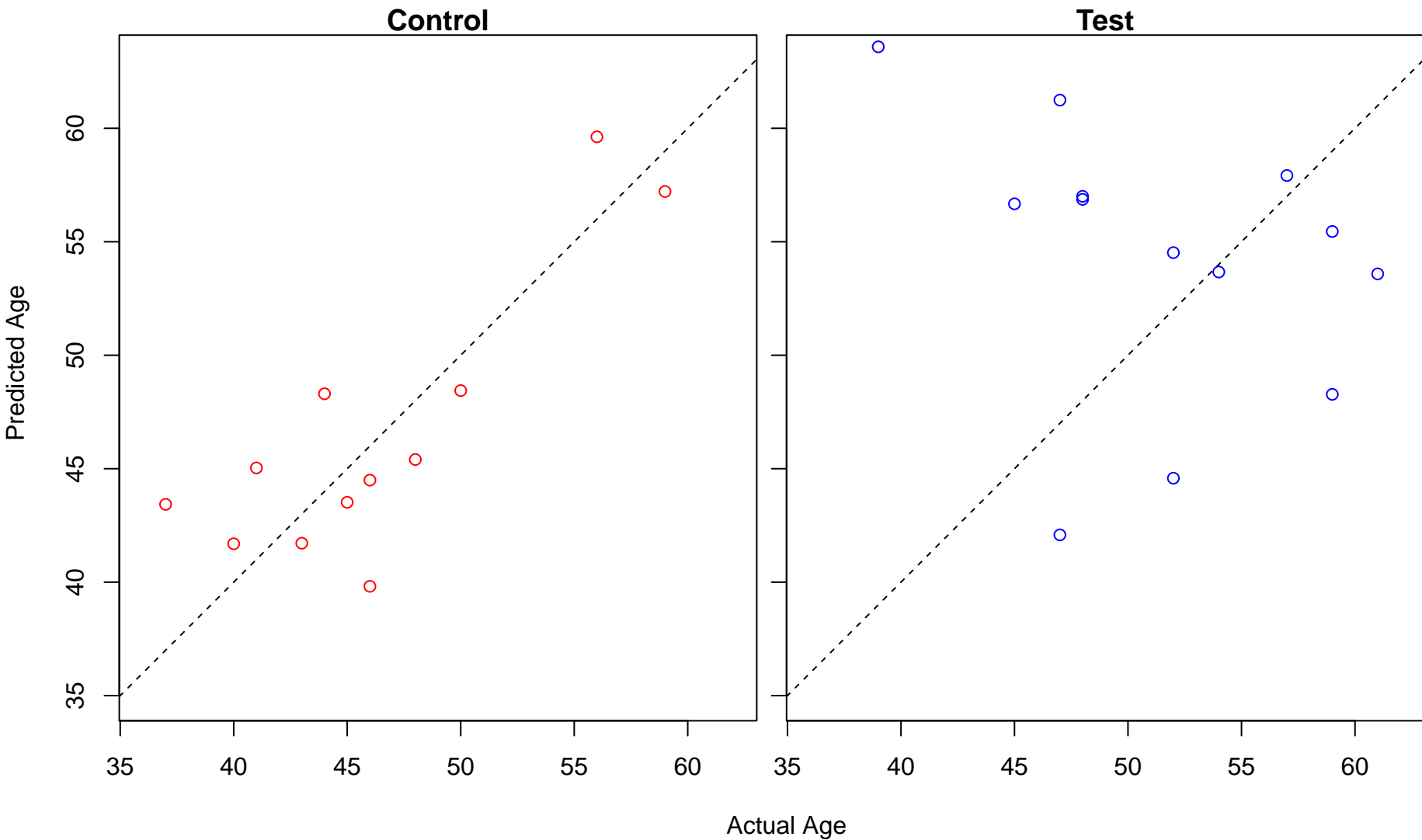
negative regulation of interferon-gamma production (Score: 4.054221)



tube formation (Score: 4.054041)

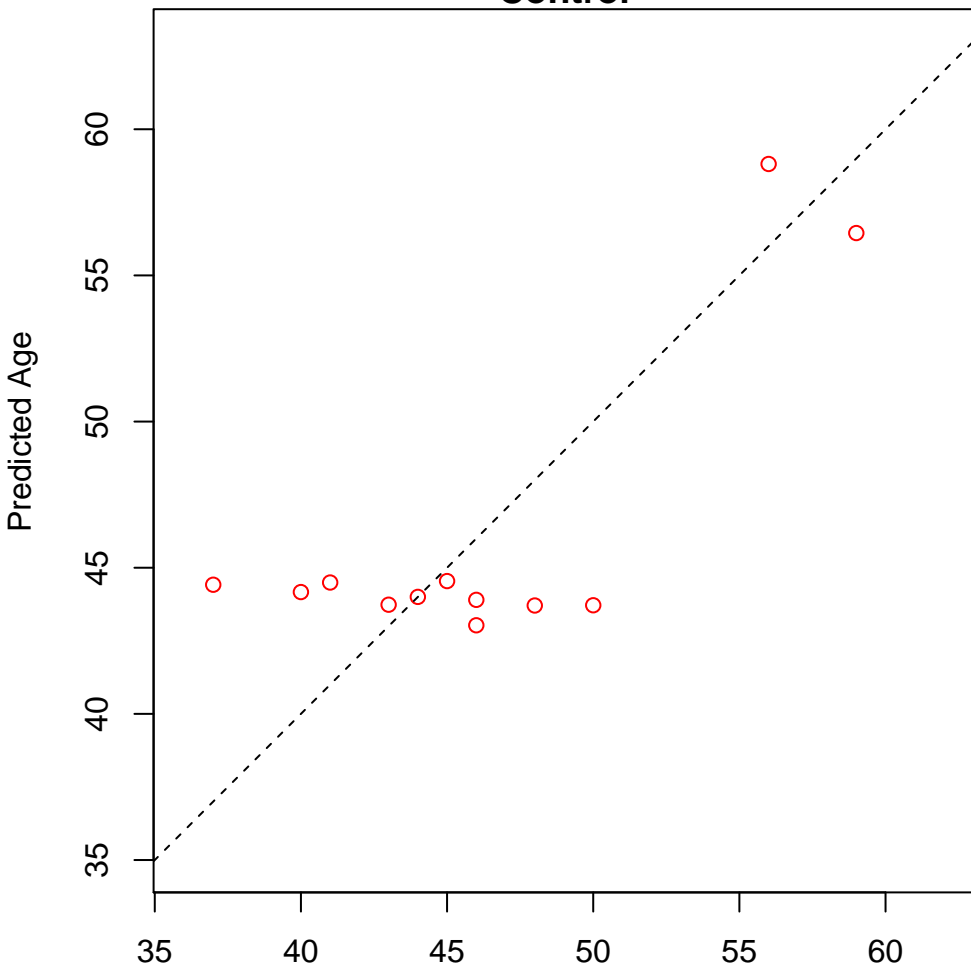


establishment of protein localization to mitochondrion (Score: 4.050847)

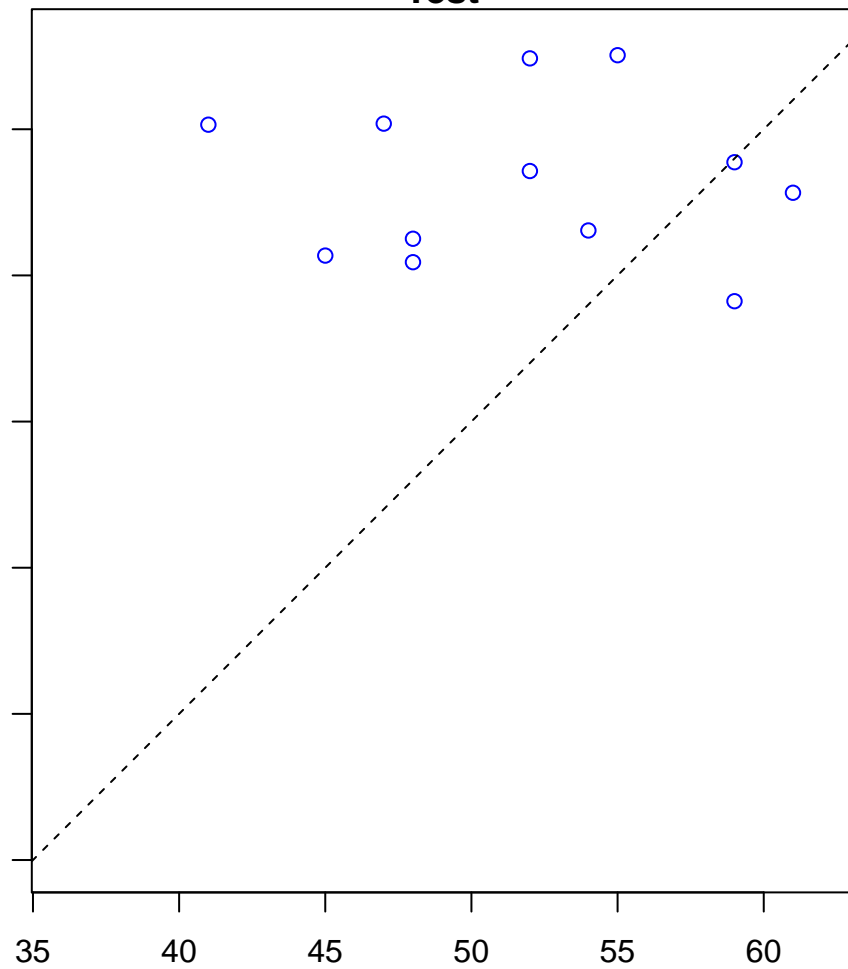


negative regulation of cell cycle process (Score: 4.049571)

Control



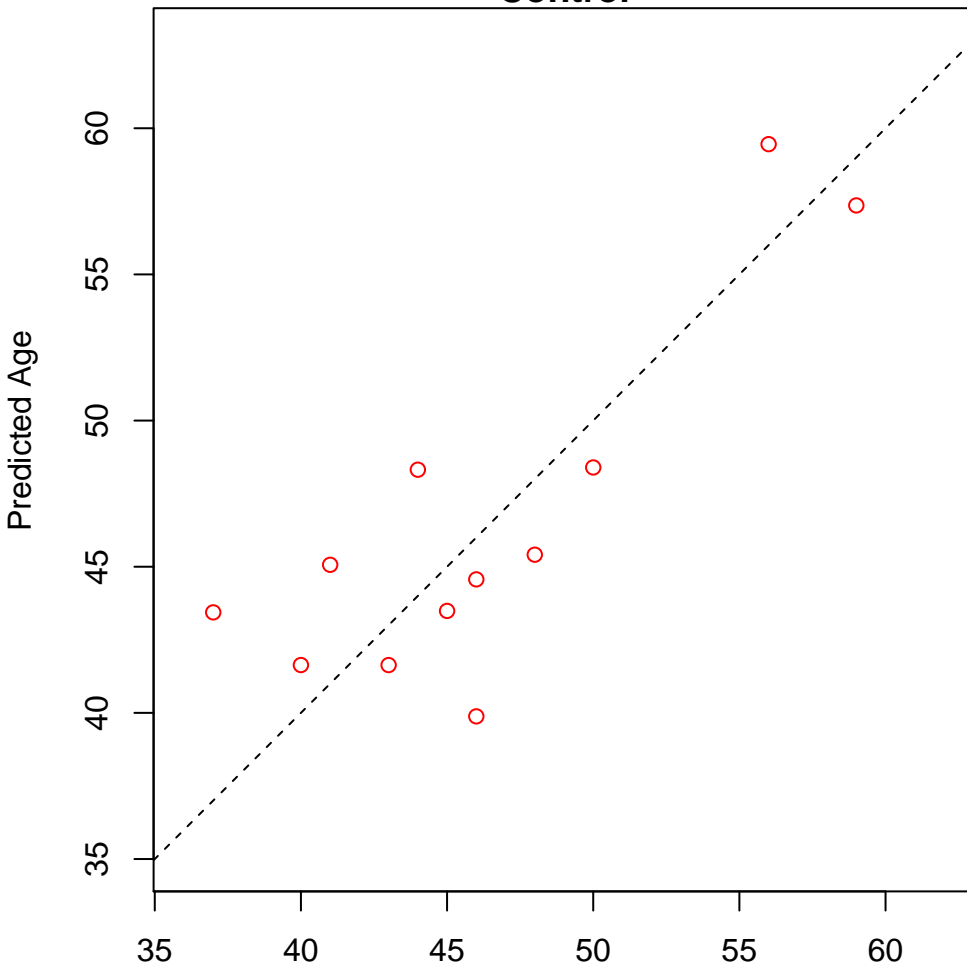
Test



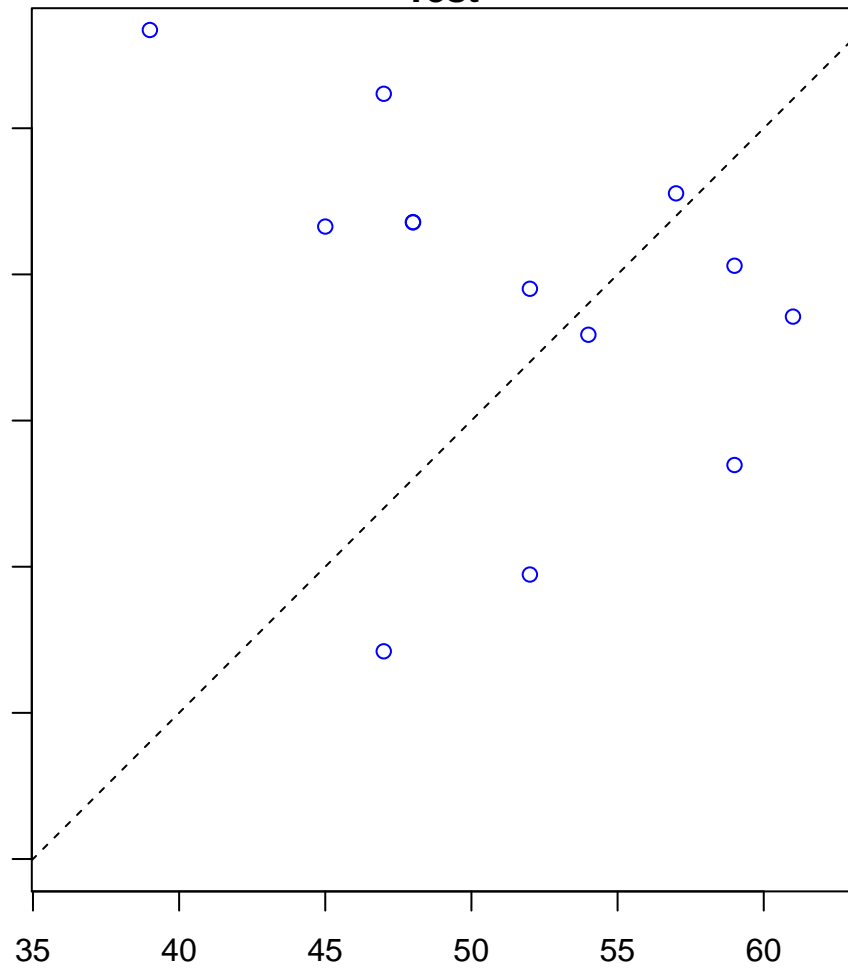
Actual Age

protein targeting to mitochondrion (Score: 4.044400)

Control

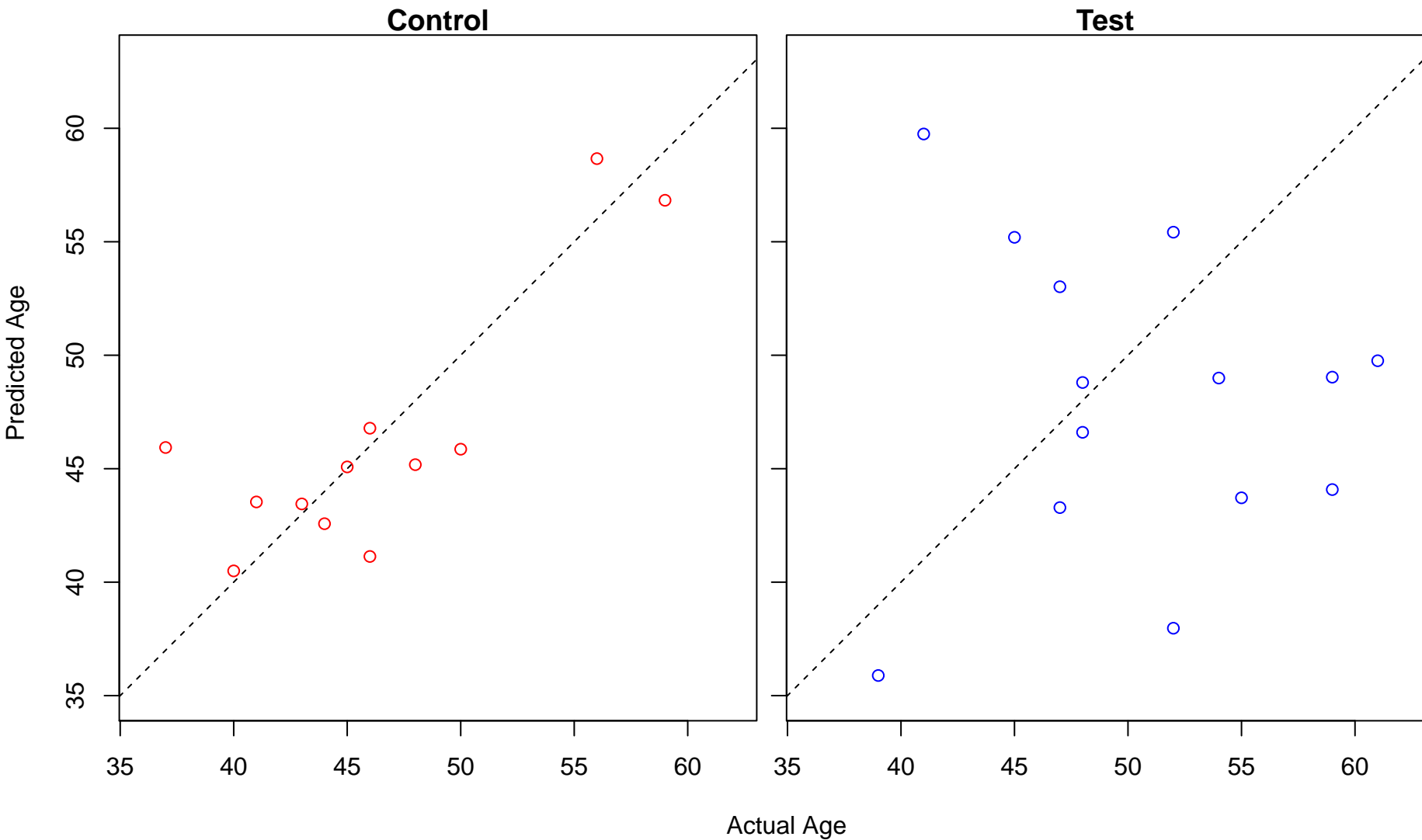


Test

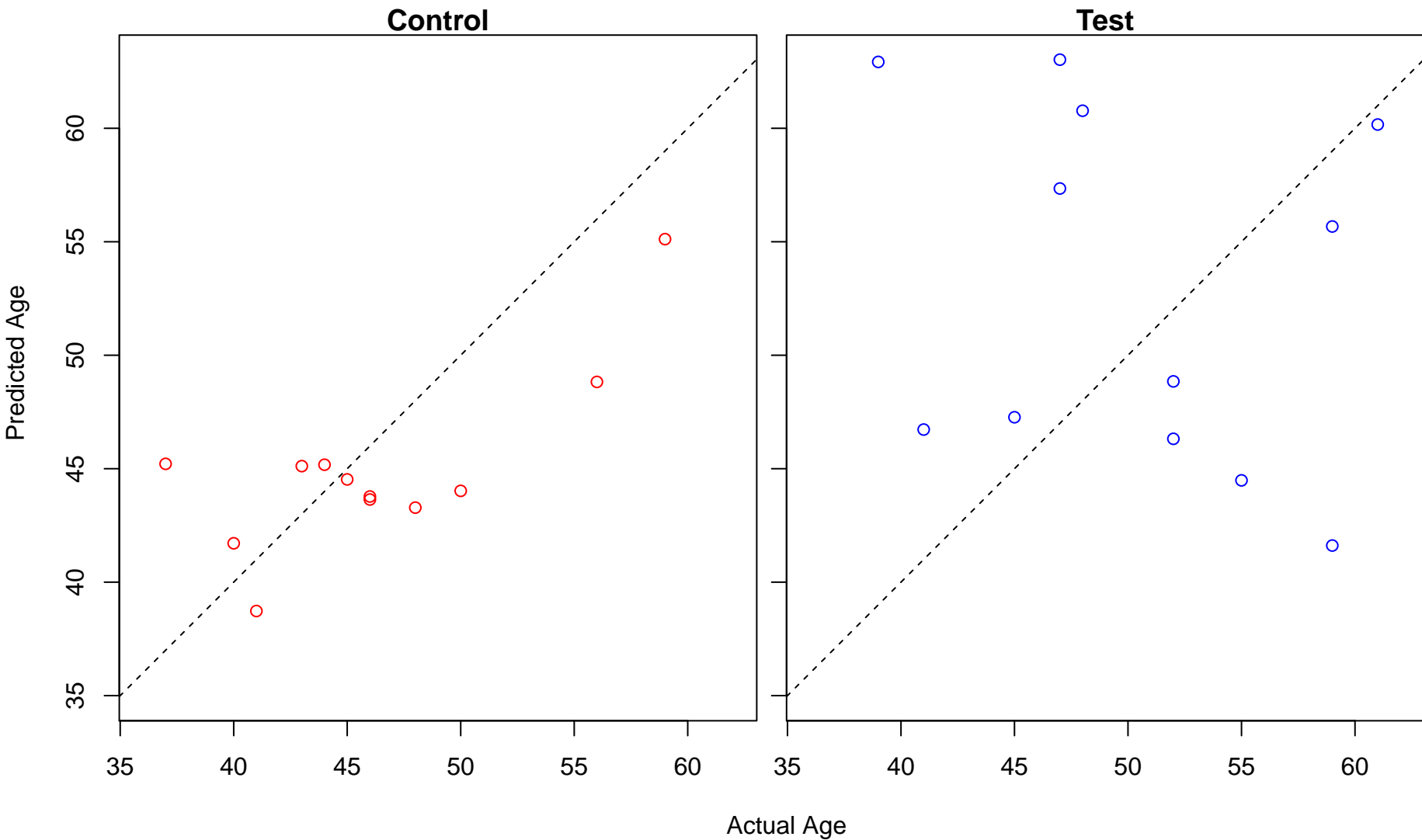


Actual Age

copper ion homeostasis (Score: 4.043103)

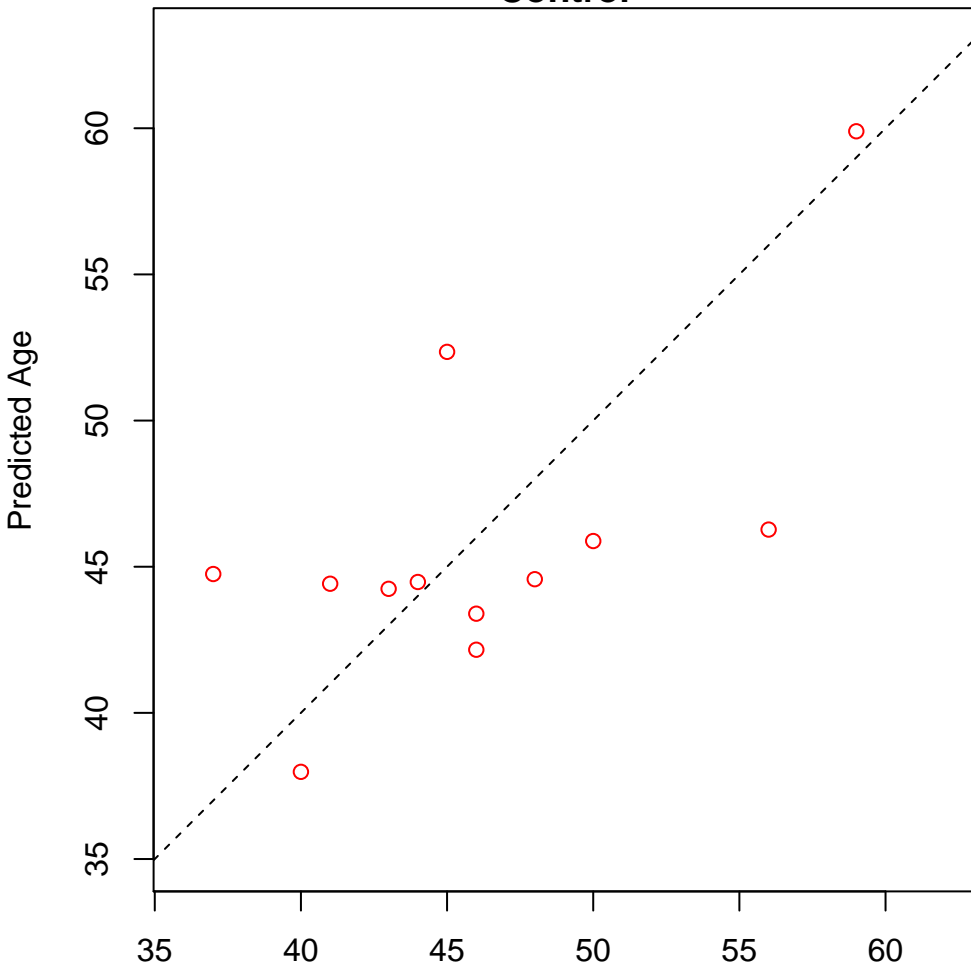


motor neuron axon guidance (Score: 4.041886)

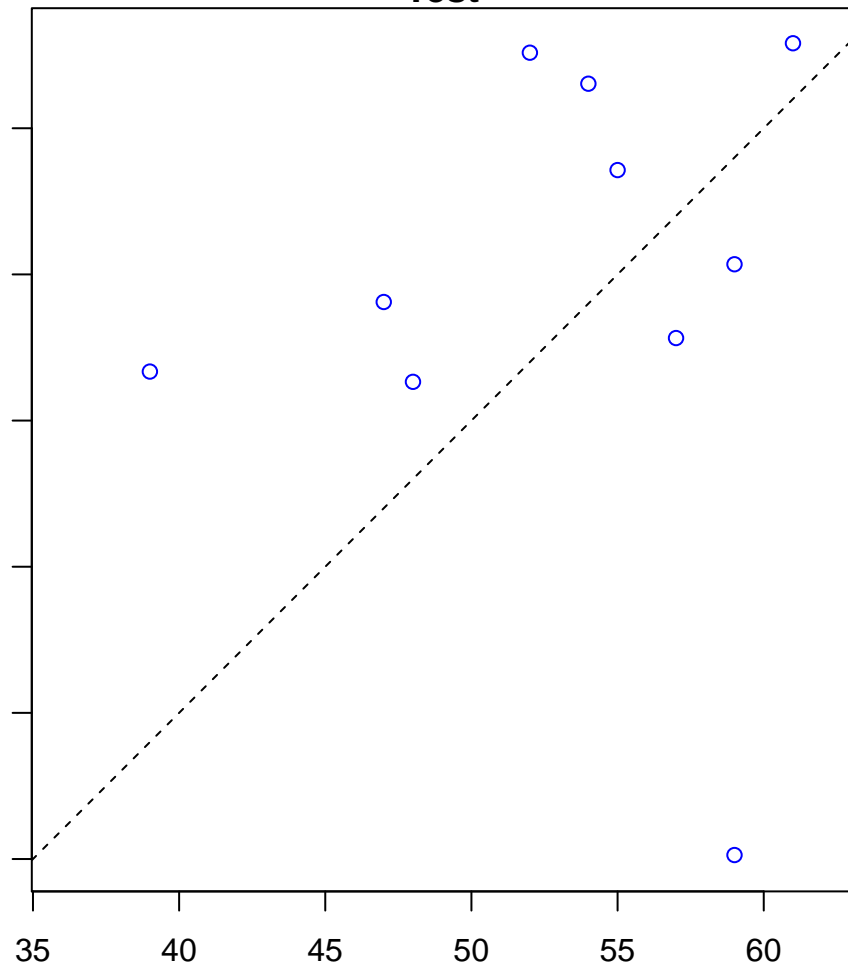


glandular epithelial cell differentiation (Score: 4.036590)

Control

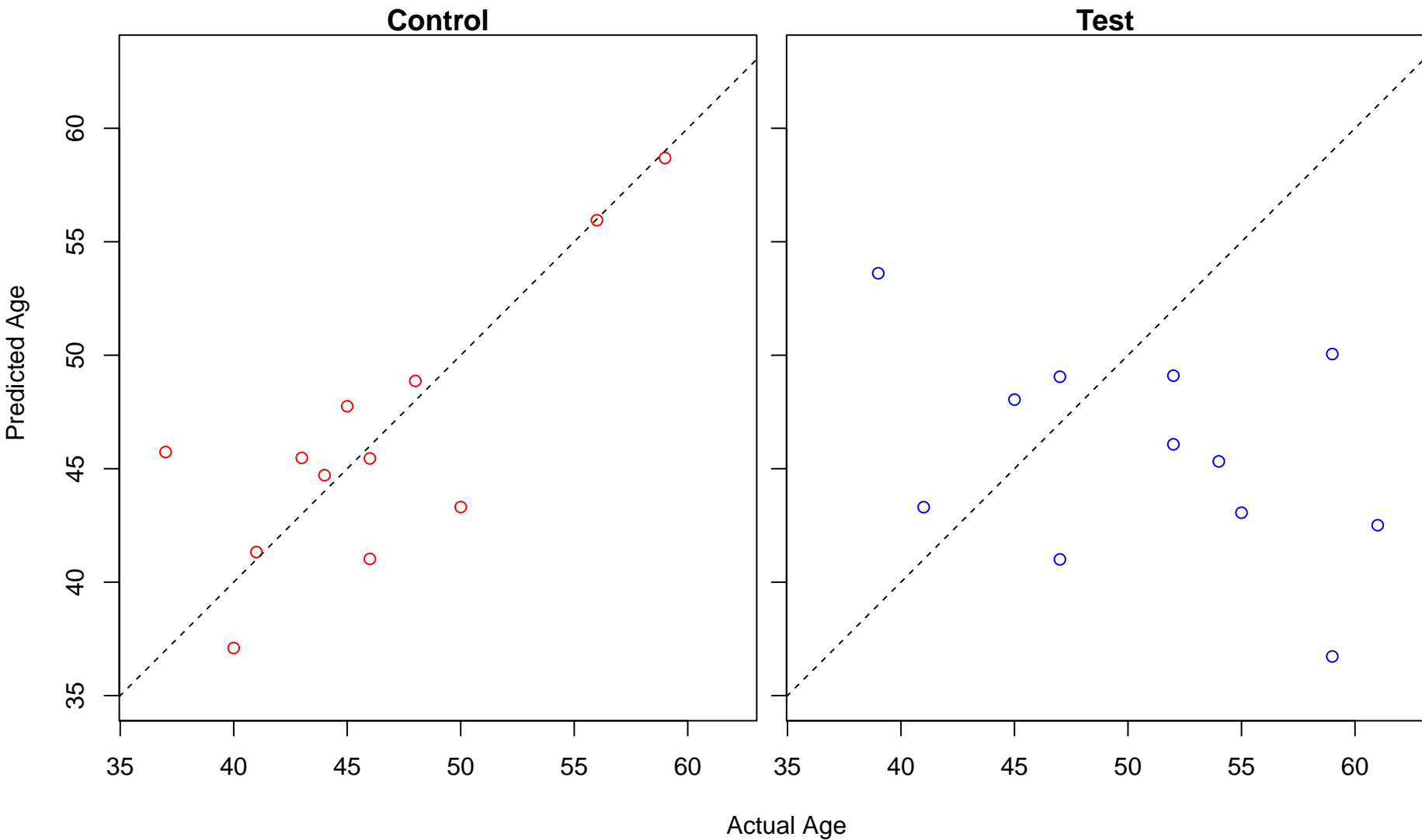


Test

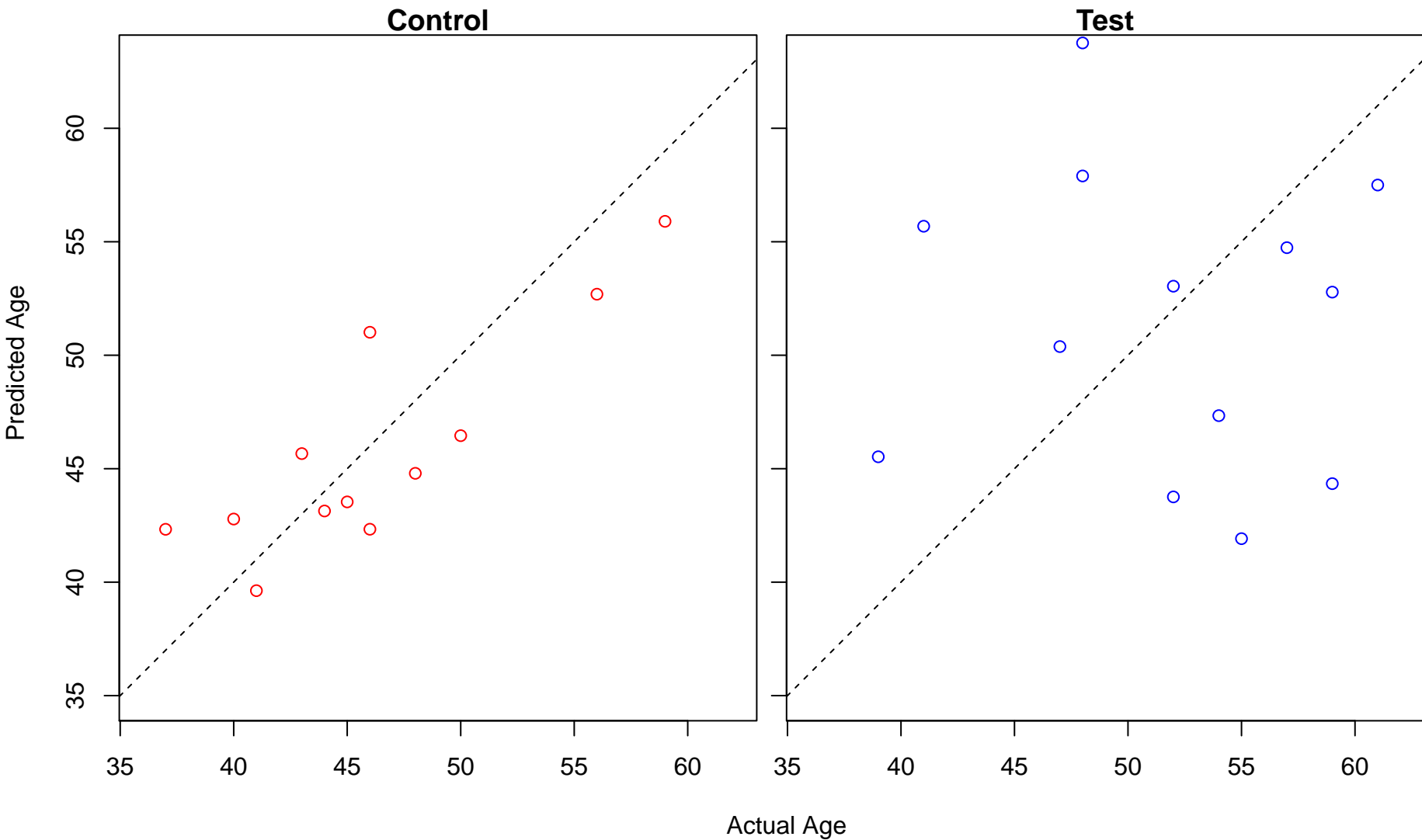


Actual Age

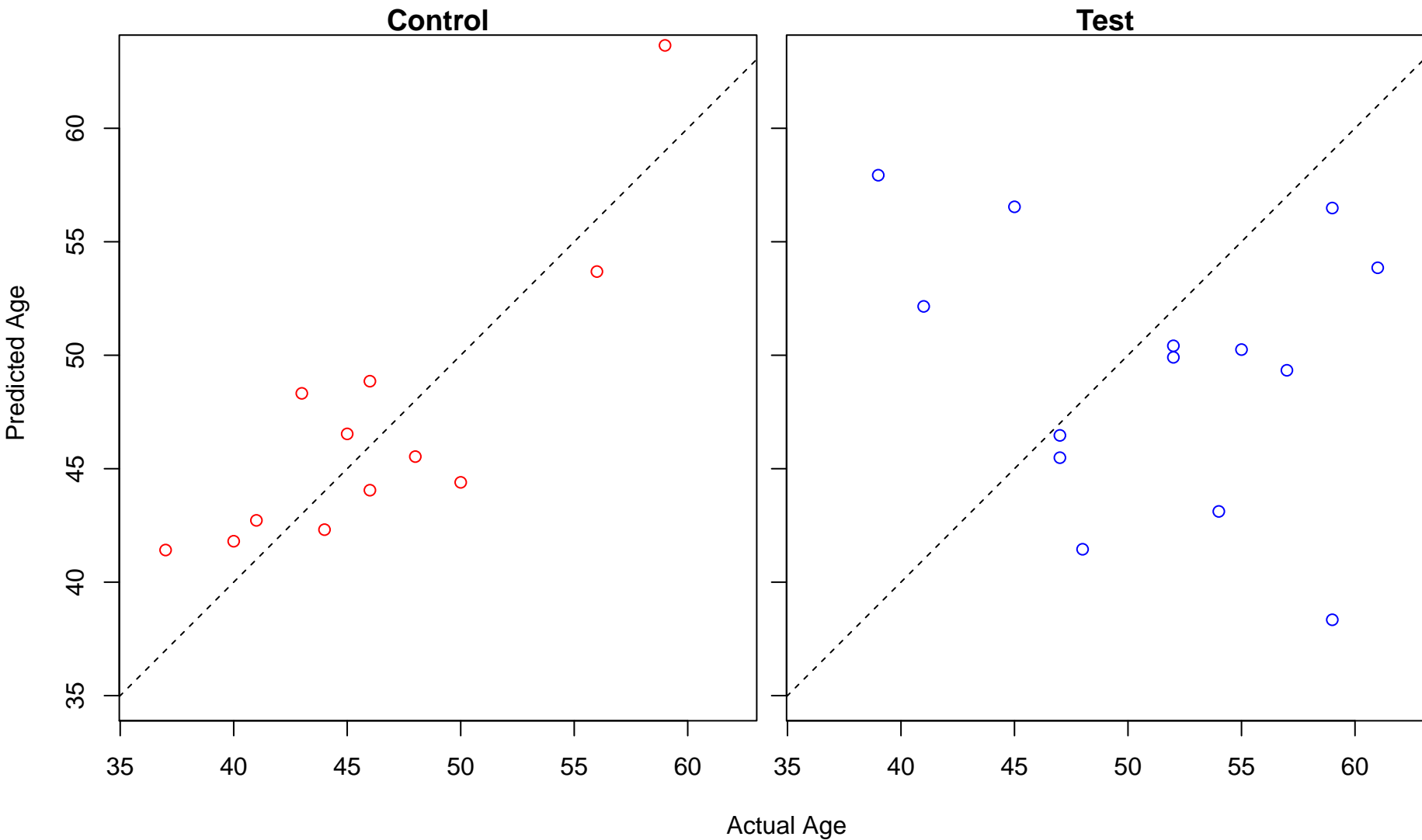
COPII-coated vesicle budding (Score: 4.036491)



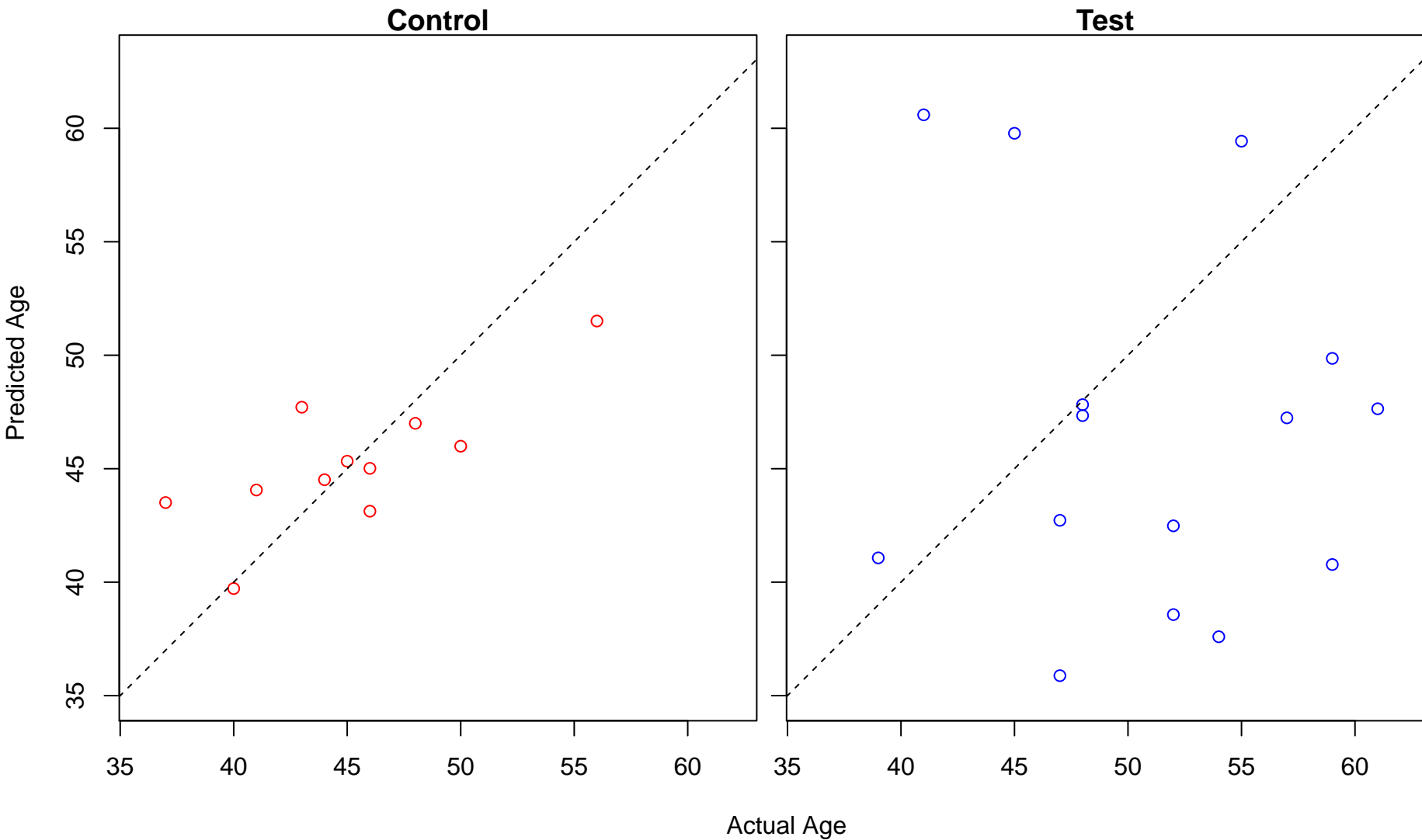
regulation of histone deacetylation (Score: 4.028541)



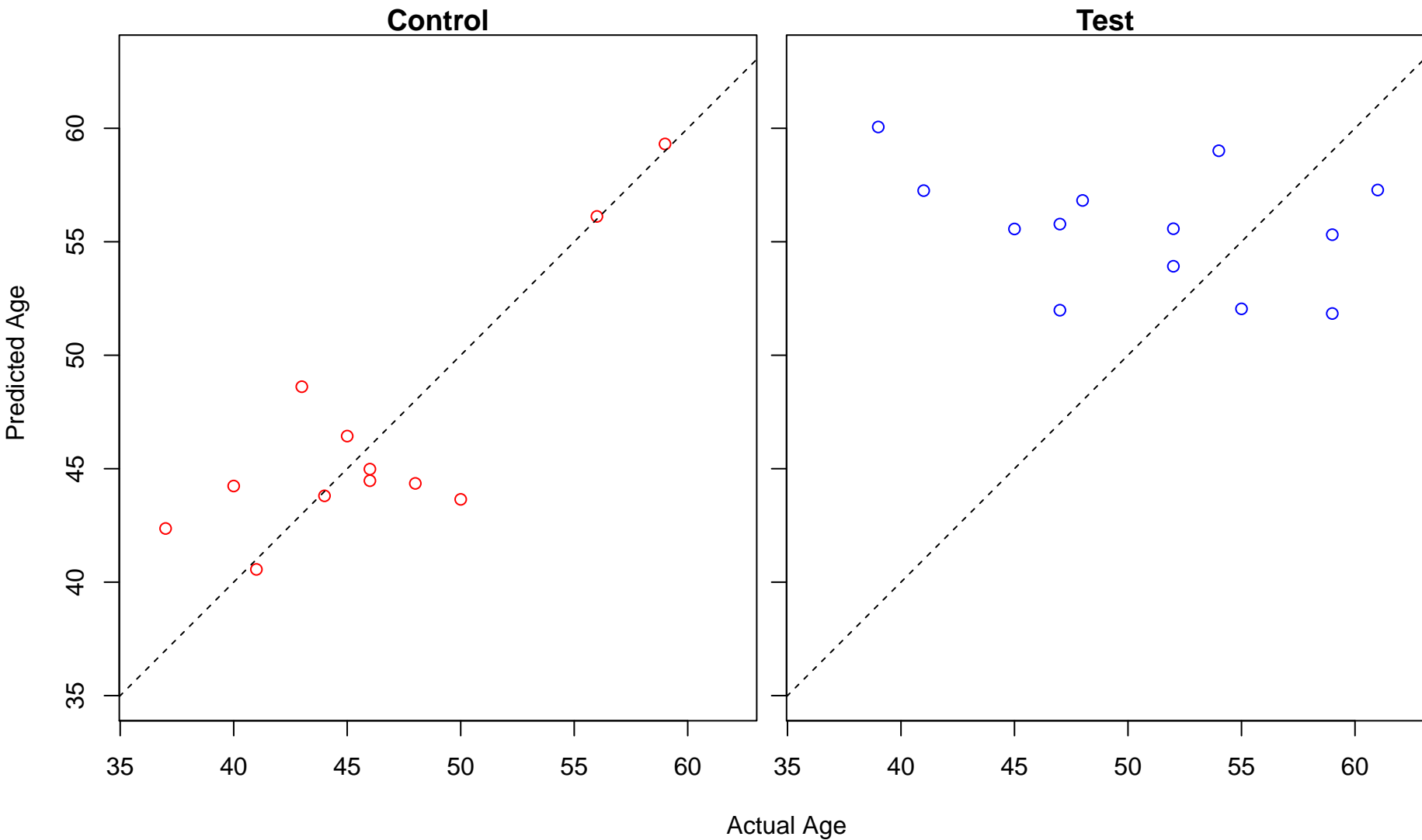
regulation of blood vessel endothelial cell migration (Score: 4.027289)



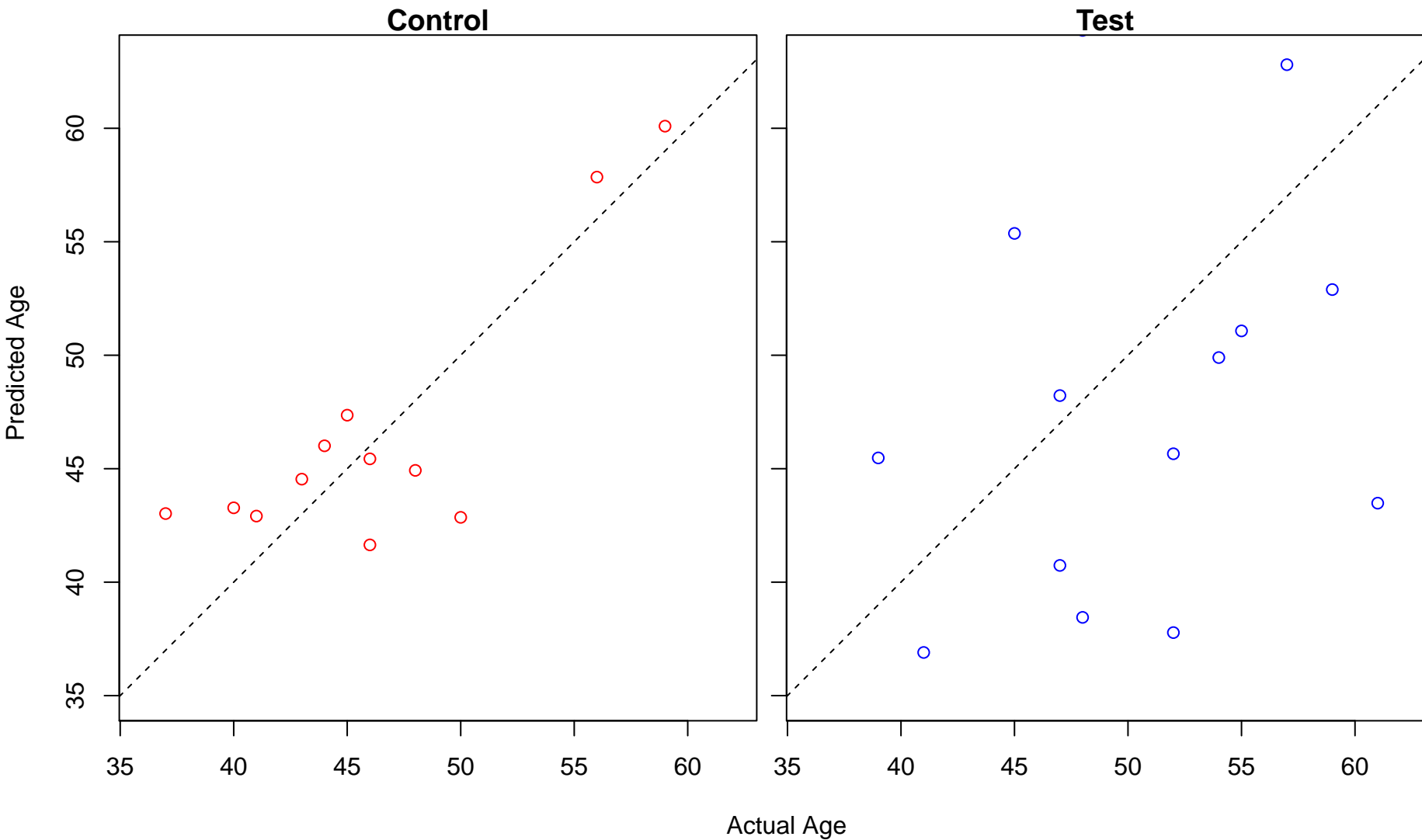
transcription initiation from RNA polymerase II promoter (Score: 4.026055)



regulation of cell migration involved in sprouting angiogenesis (Score: 4.017651)

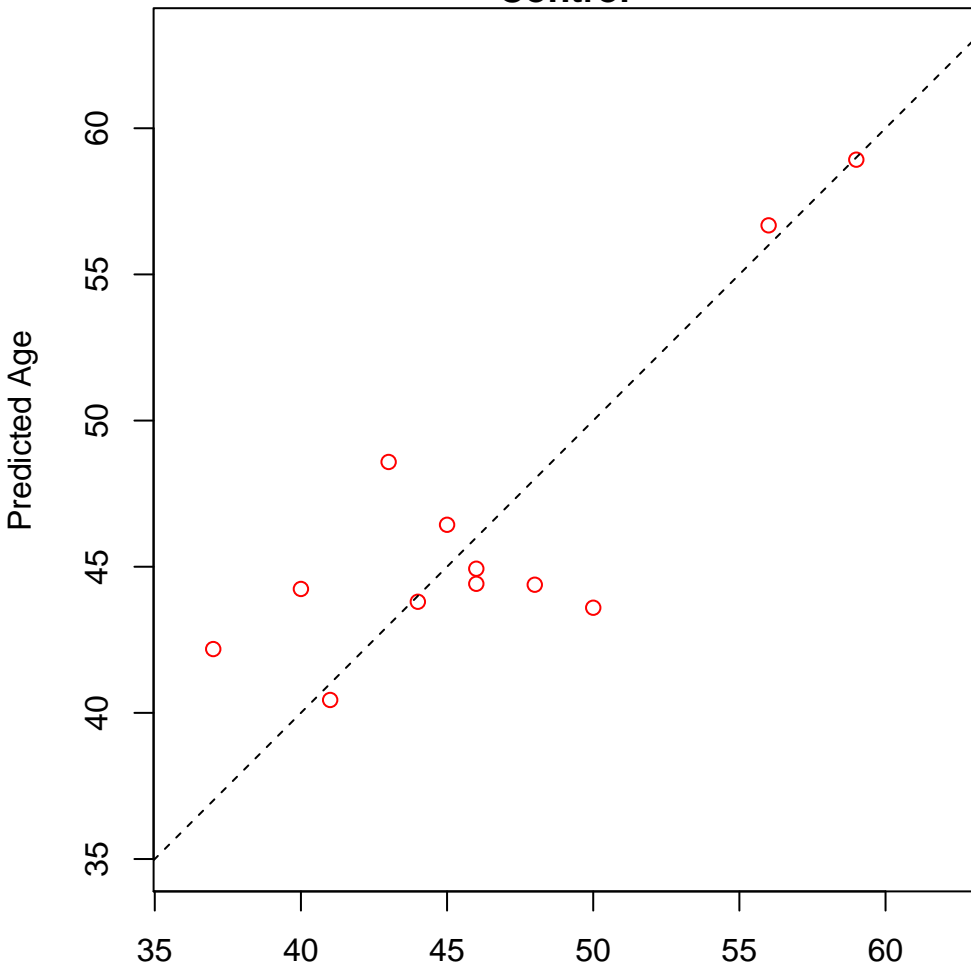


bone mineralization (Score: 4.017324)

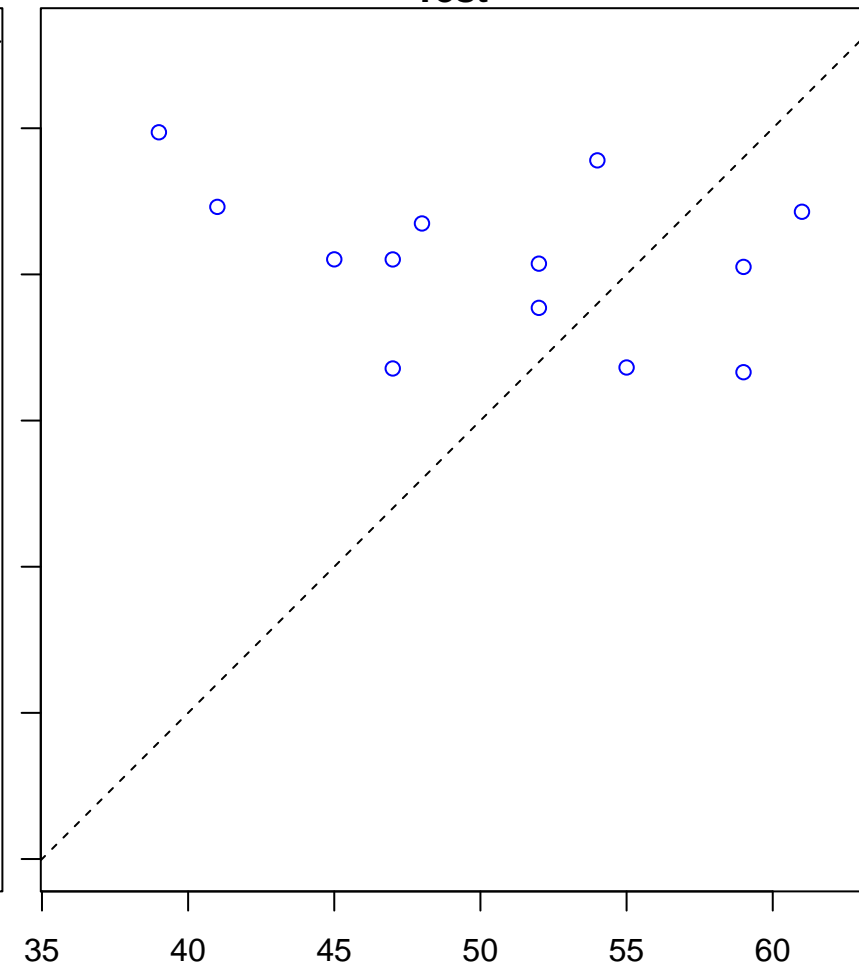


regulation of sprouting angiogenesis (Score: 4.009600)

Control

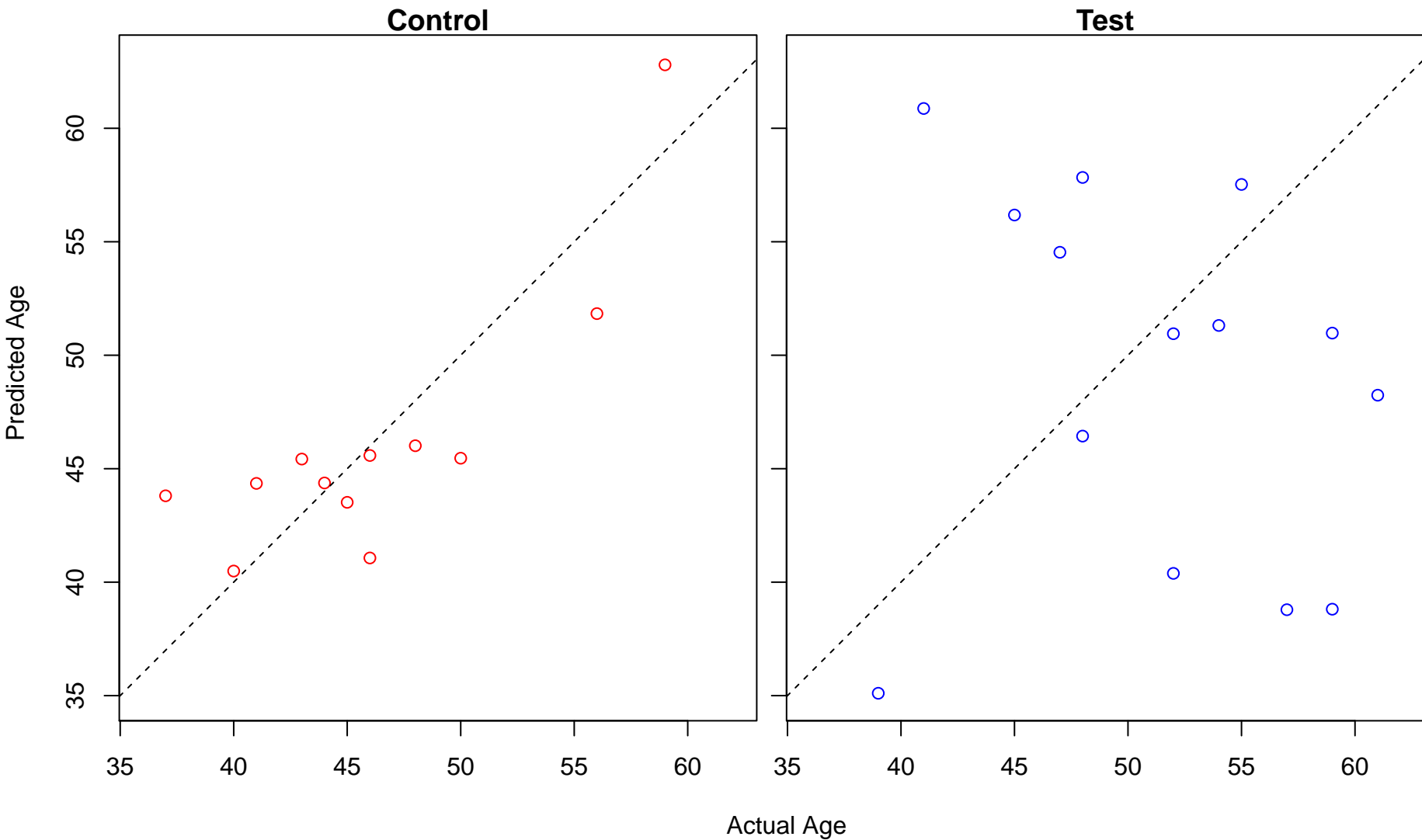


Test

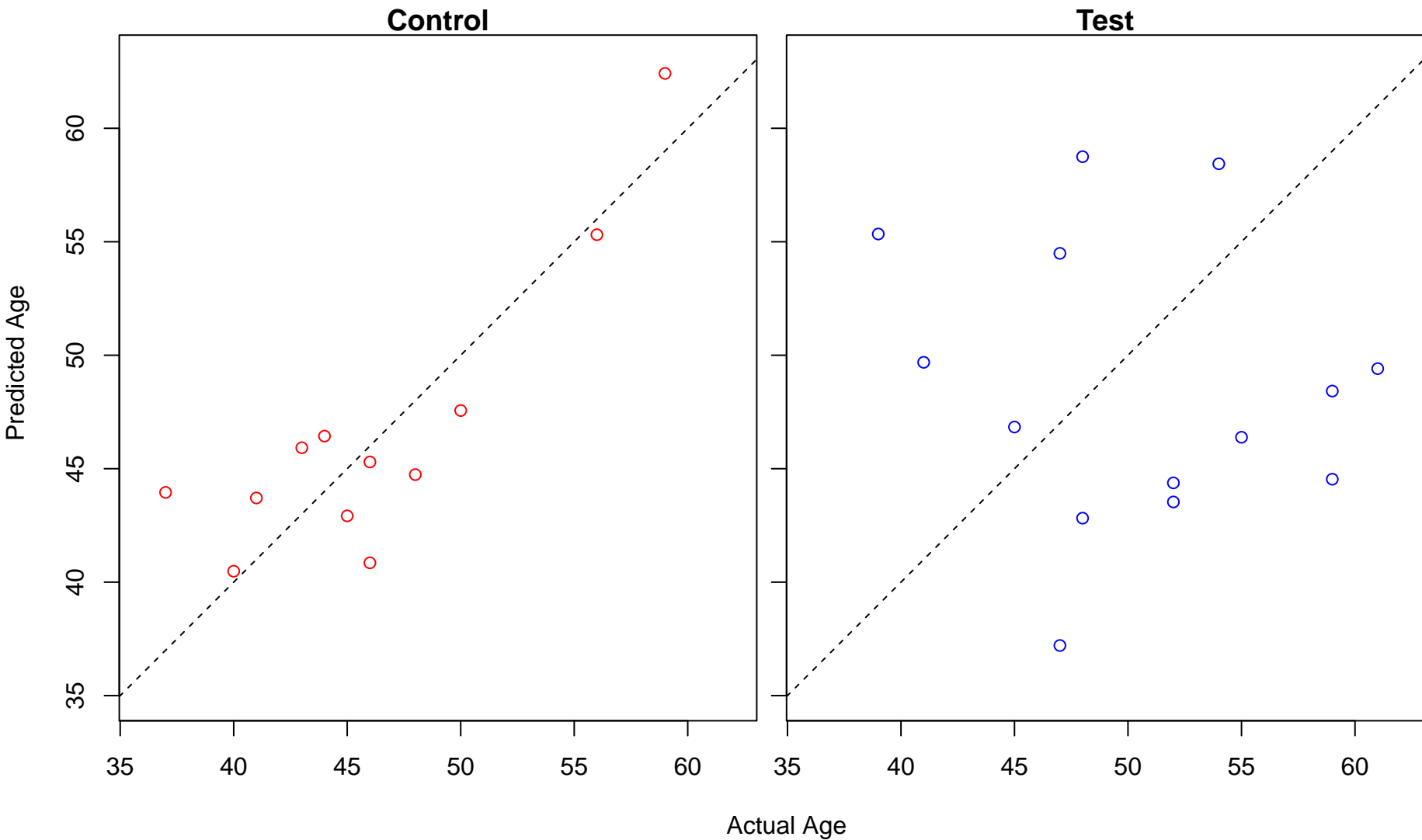


Actual Age

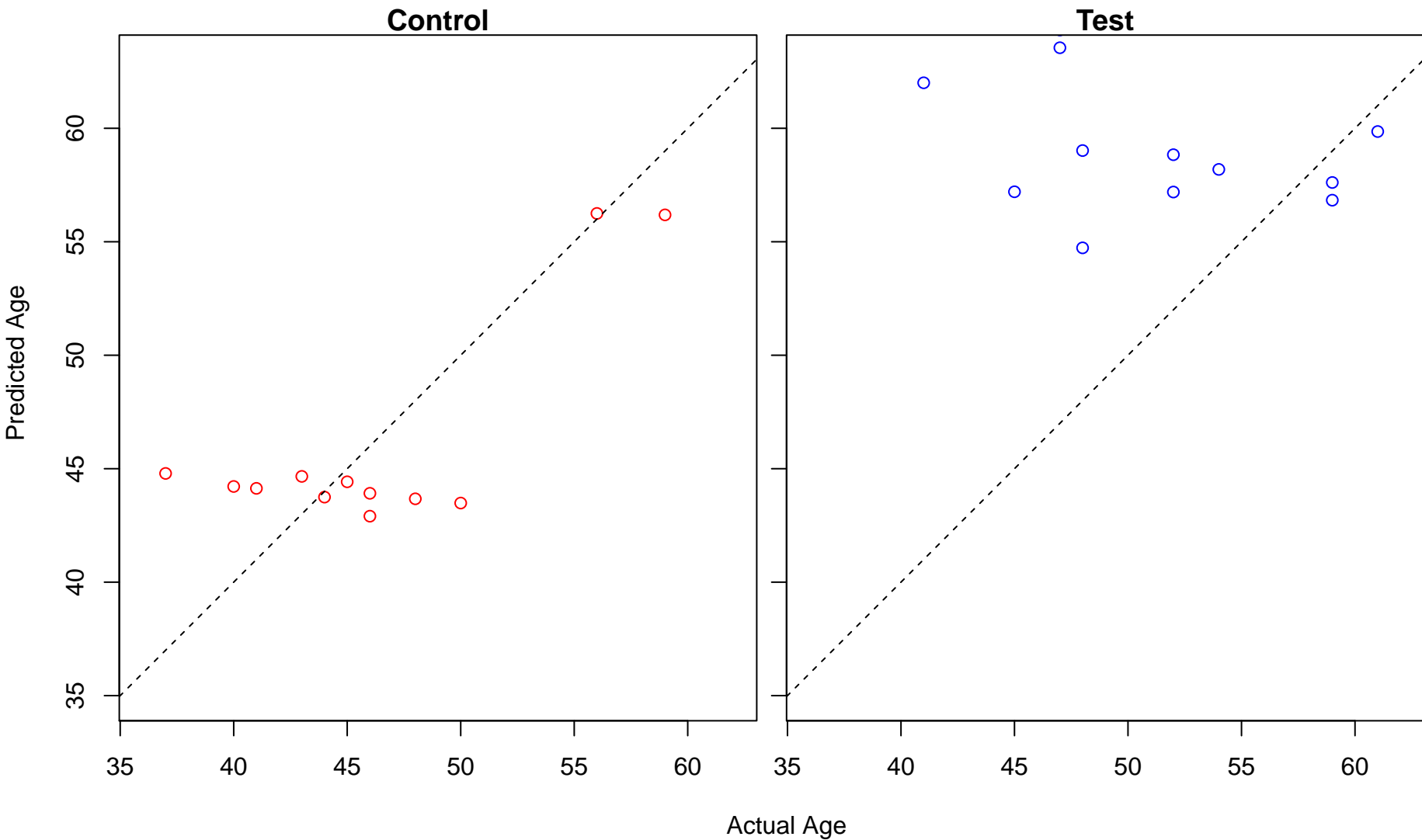
negative regulation of RNA splicing (Score: 3.999439)



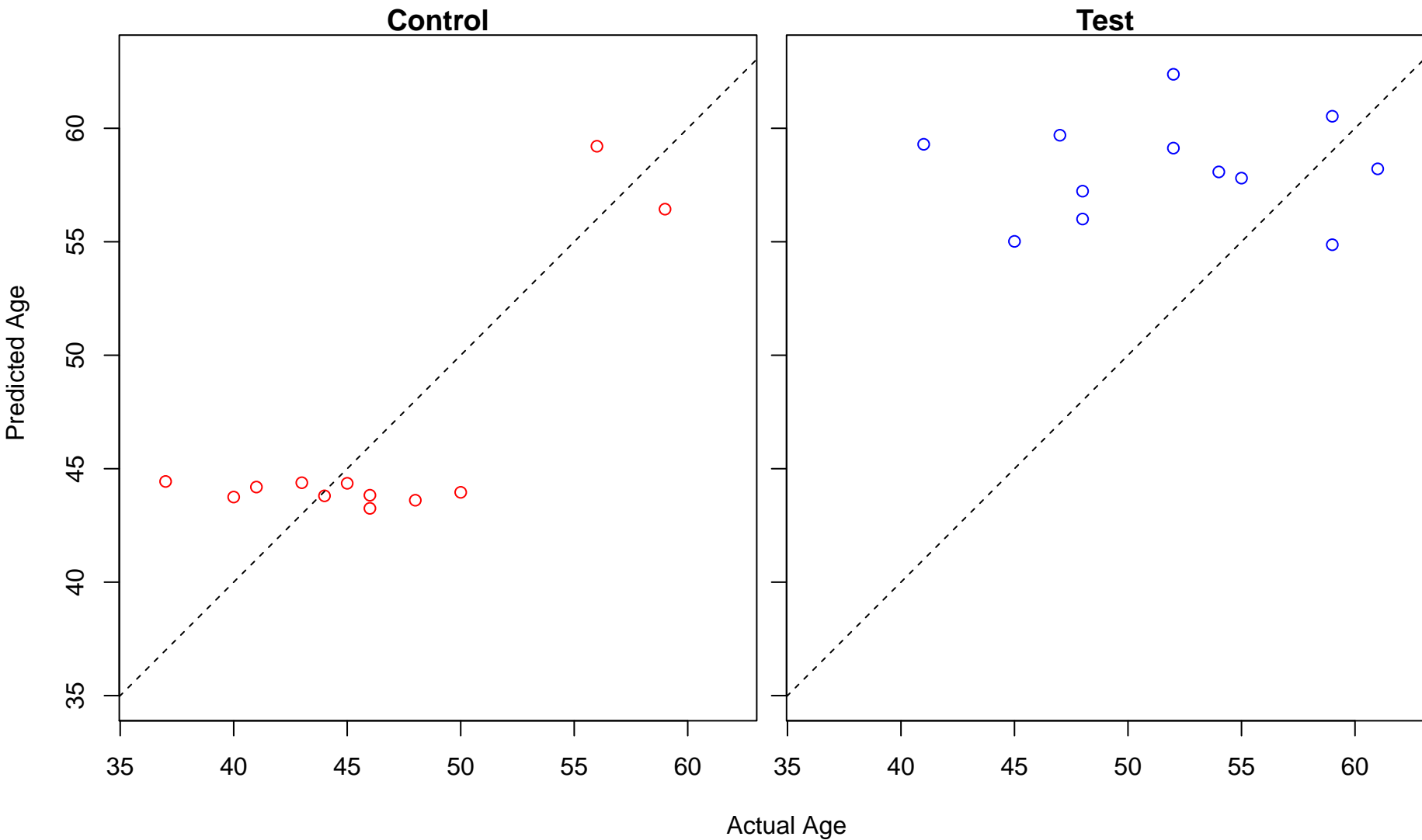
regulation of cation transmembrane transport (Score: 3.995363)



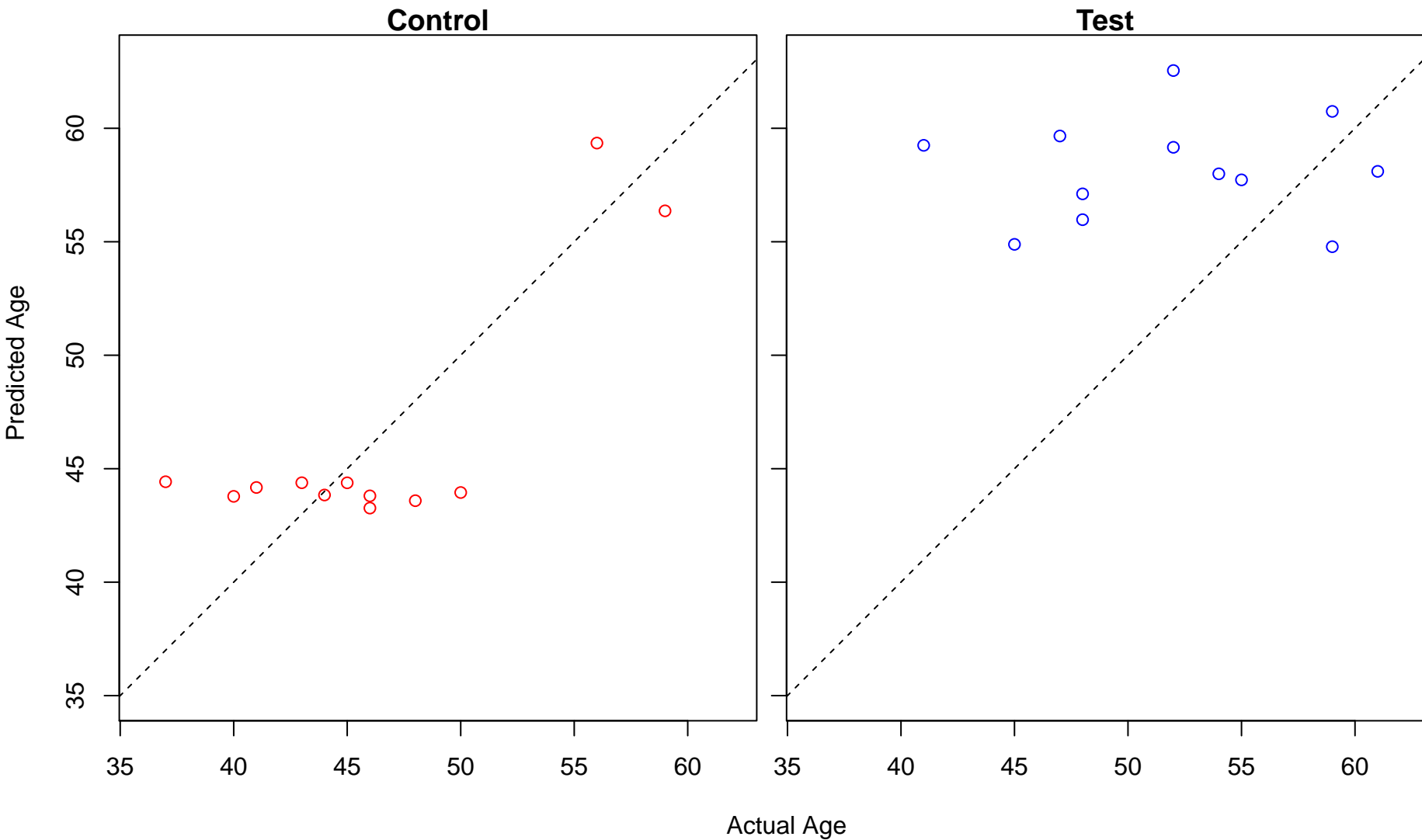
cellular iron ion homeostasis (Score: 3.991791)



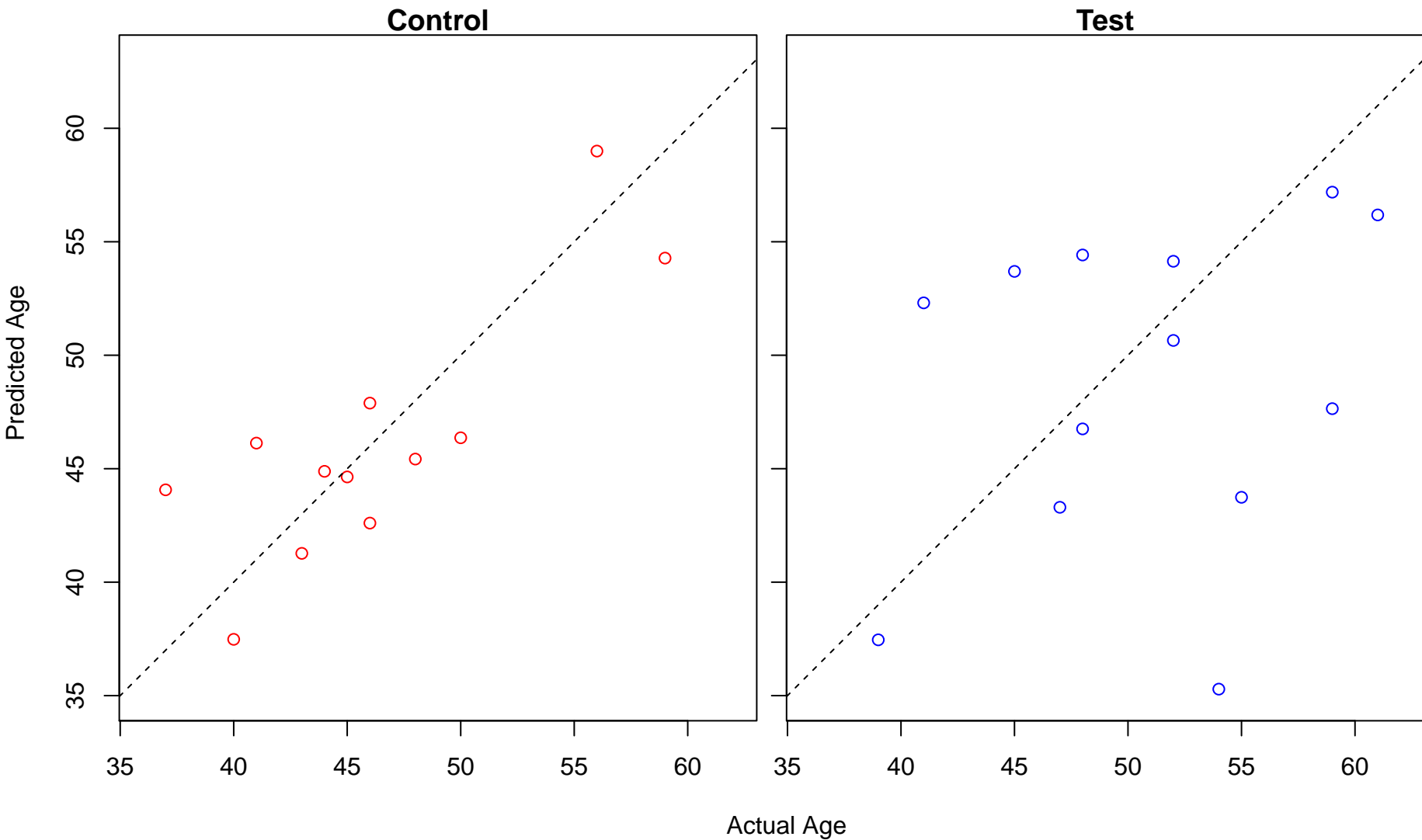
Notch receptor processing (Score: 3.983625)



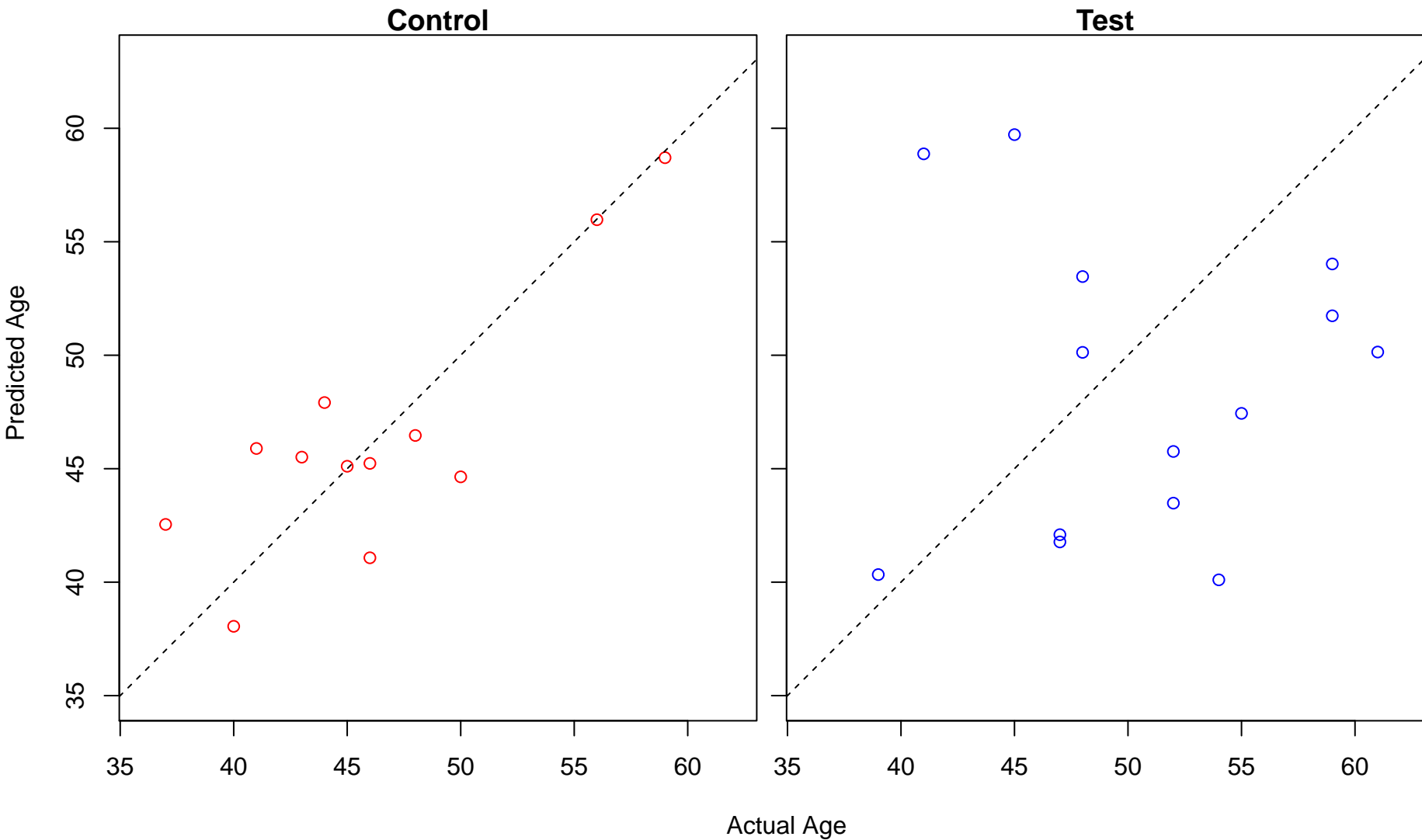
viral protein processing (Score: 3.983556)



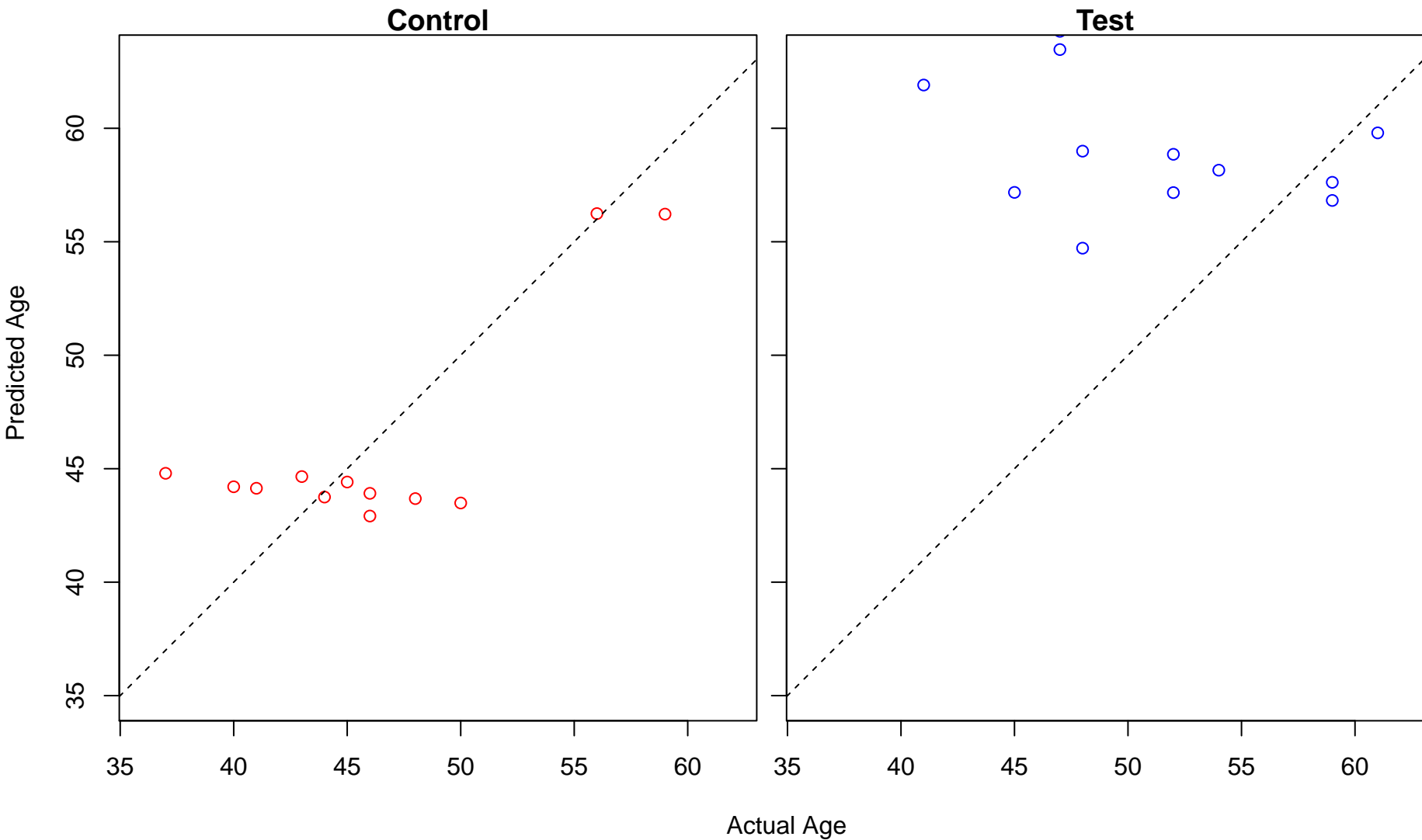
neuromuscular process (Score: 3.979952)



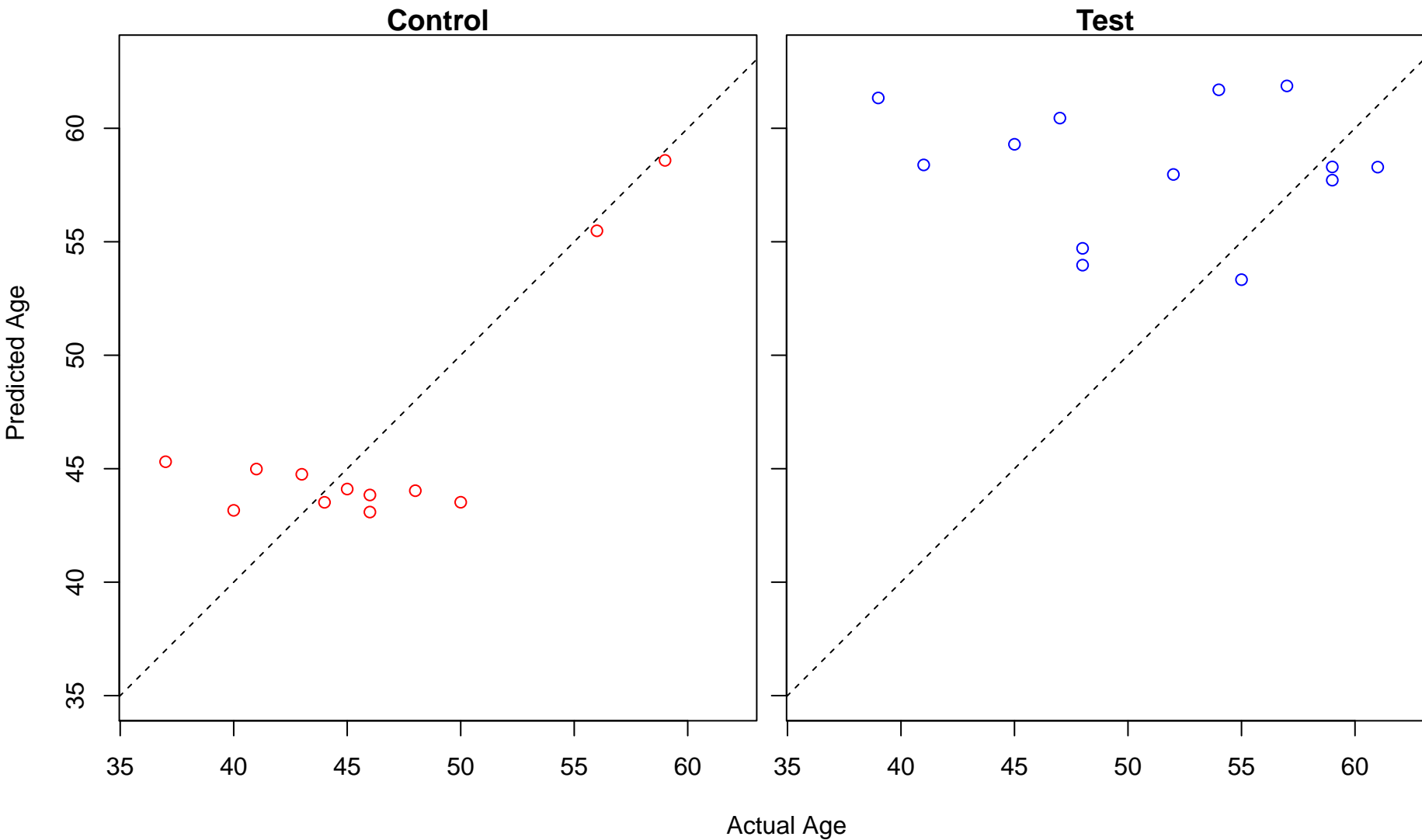
regulation of cell motility (Score: 3.976950)



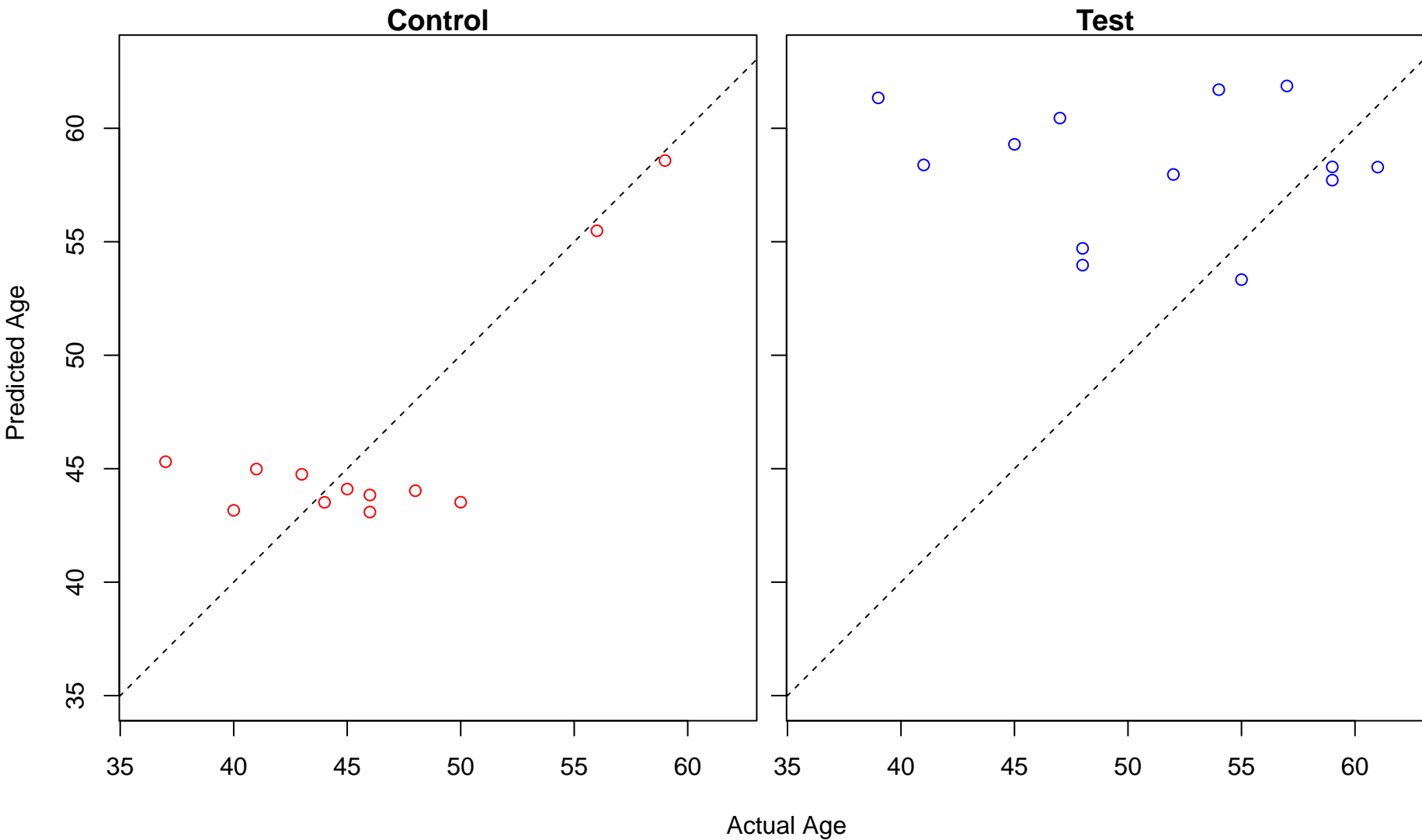
iron ion homeostasis (Score: 3.976031)



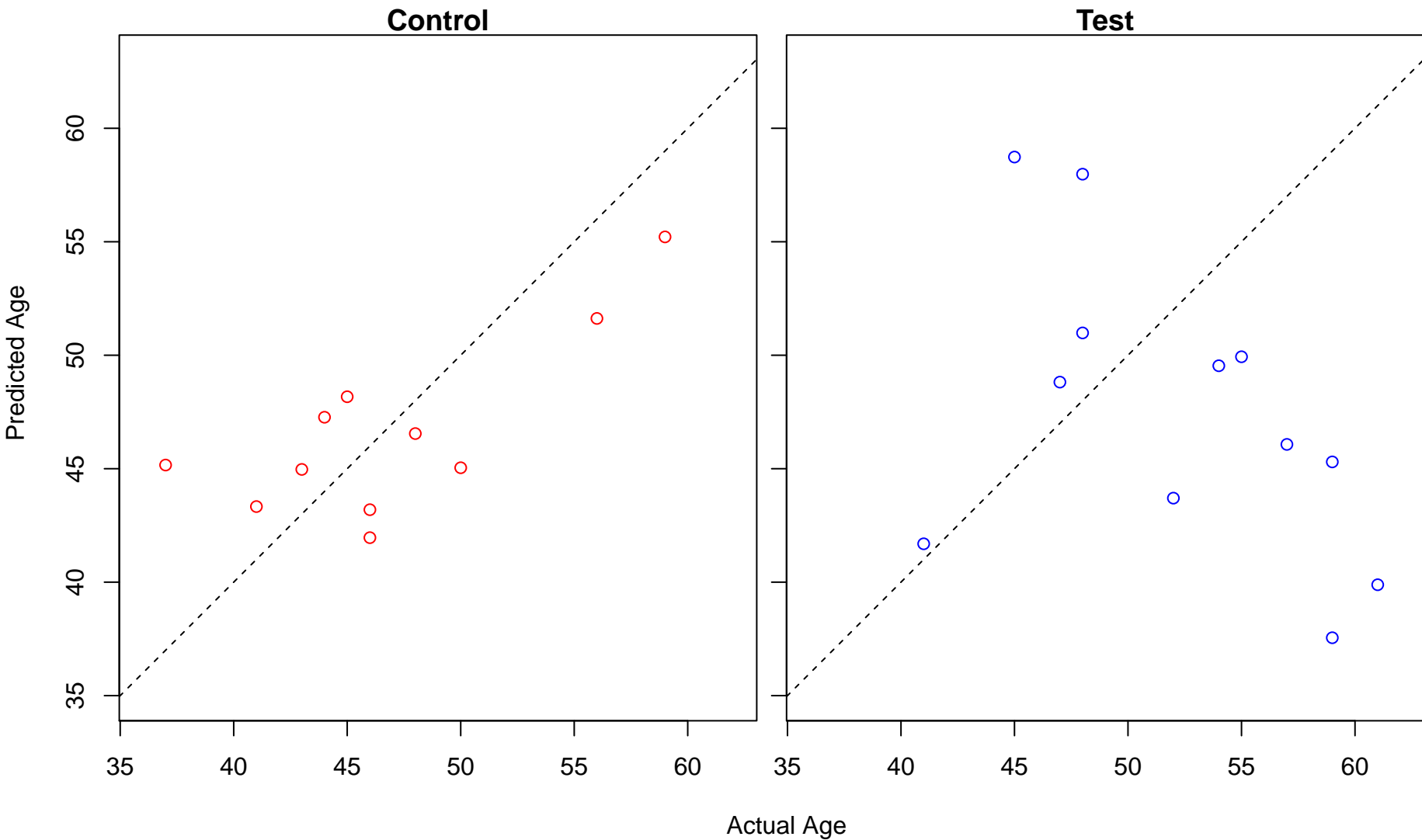
regulation of epidermal cell differentiation (Score: 3.974263)



regulation of epidermis development (Score: 3.973021)

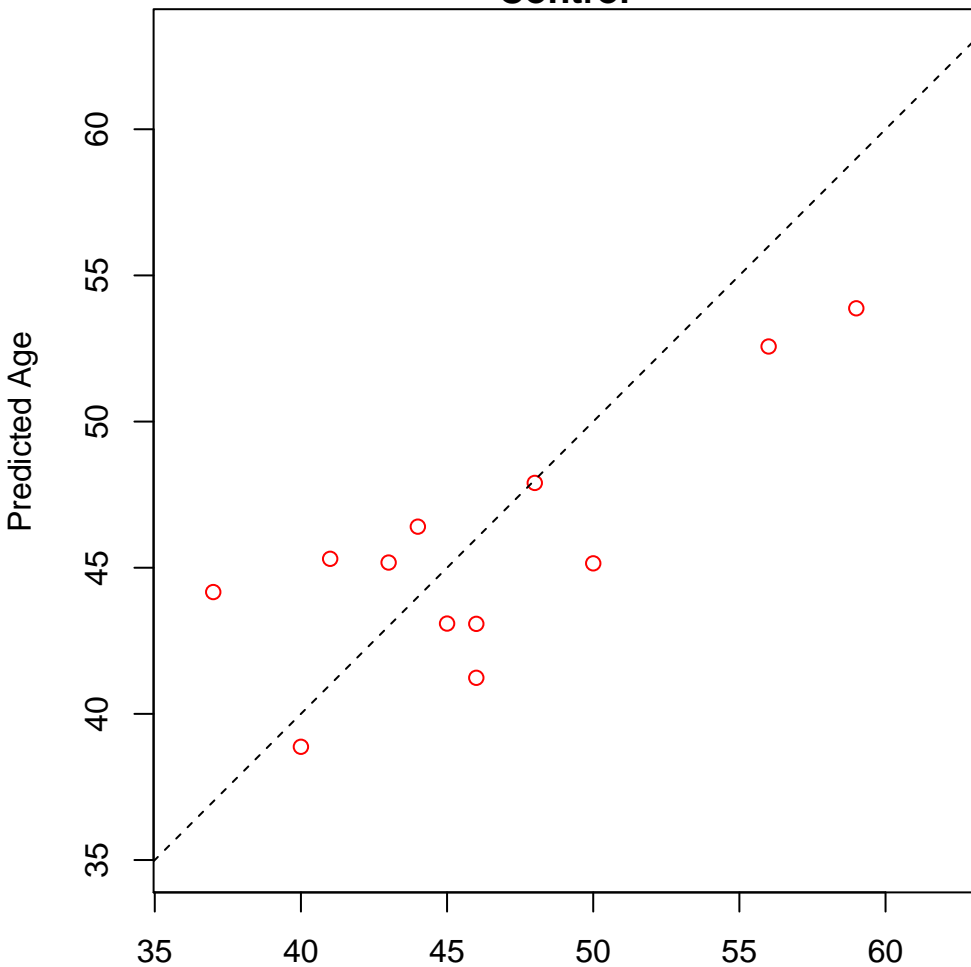


embryonic placenta development (Score: 3.970374)

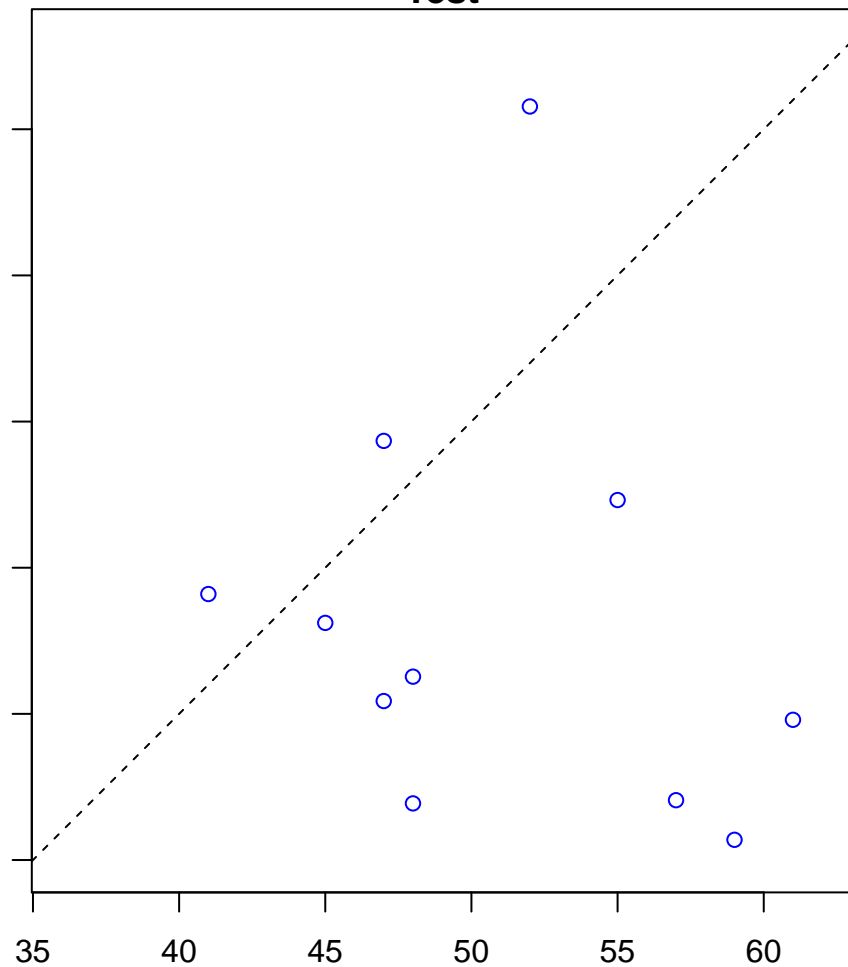


selenium compound metabolic process (Score: 3.969513)

Control

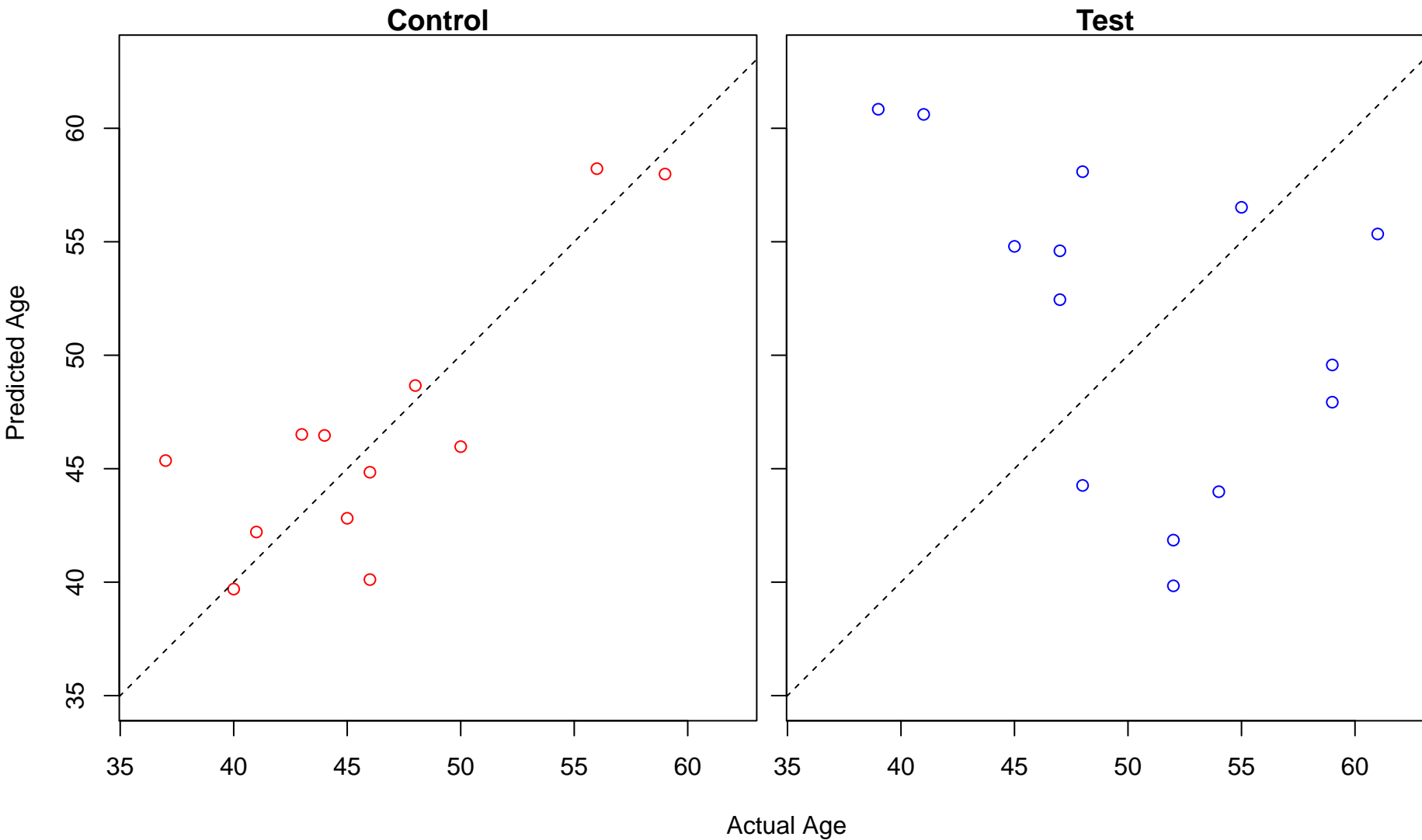


Test

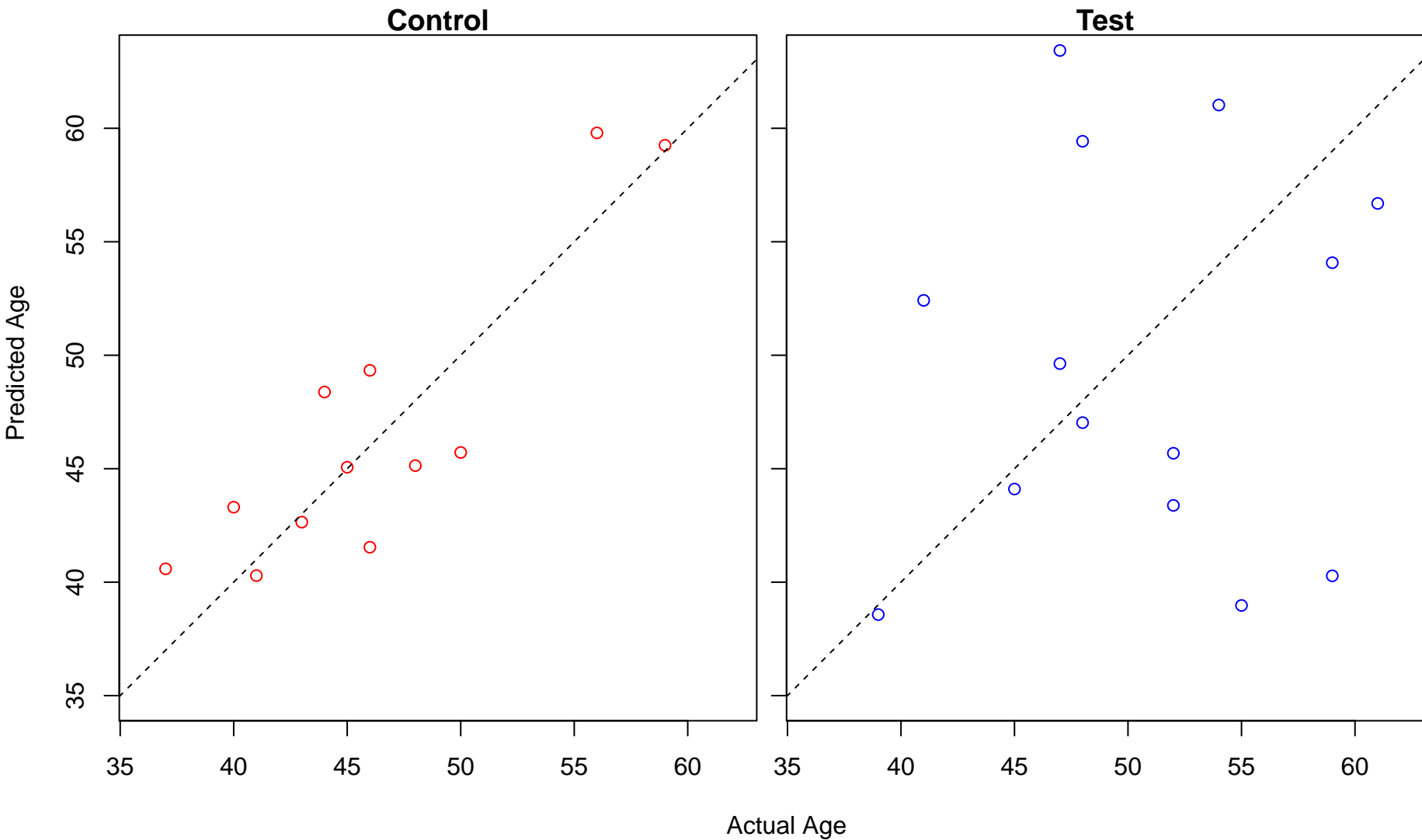


Actual Age

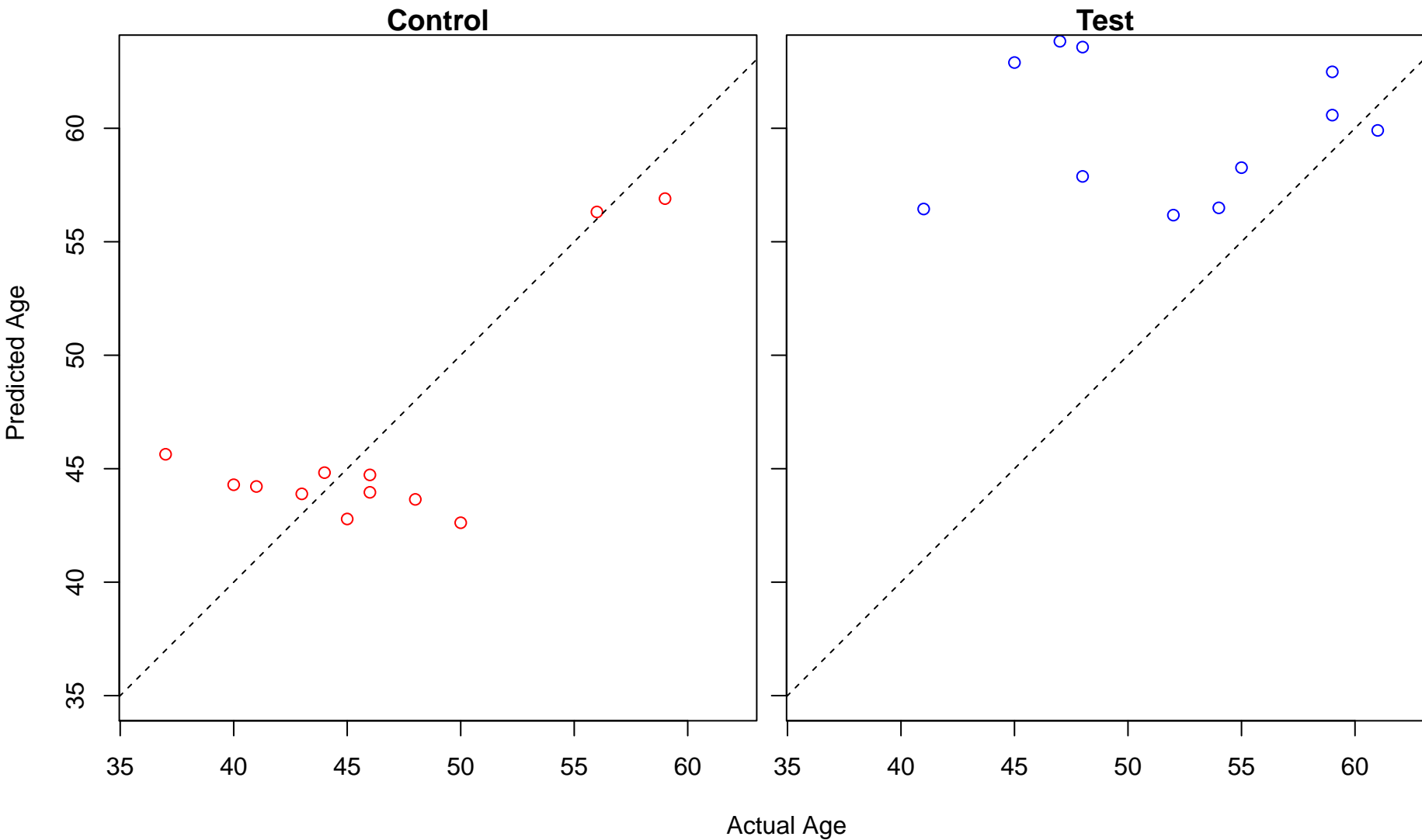
negative regulation of transport (Score: 3.966232)



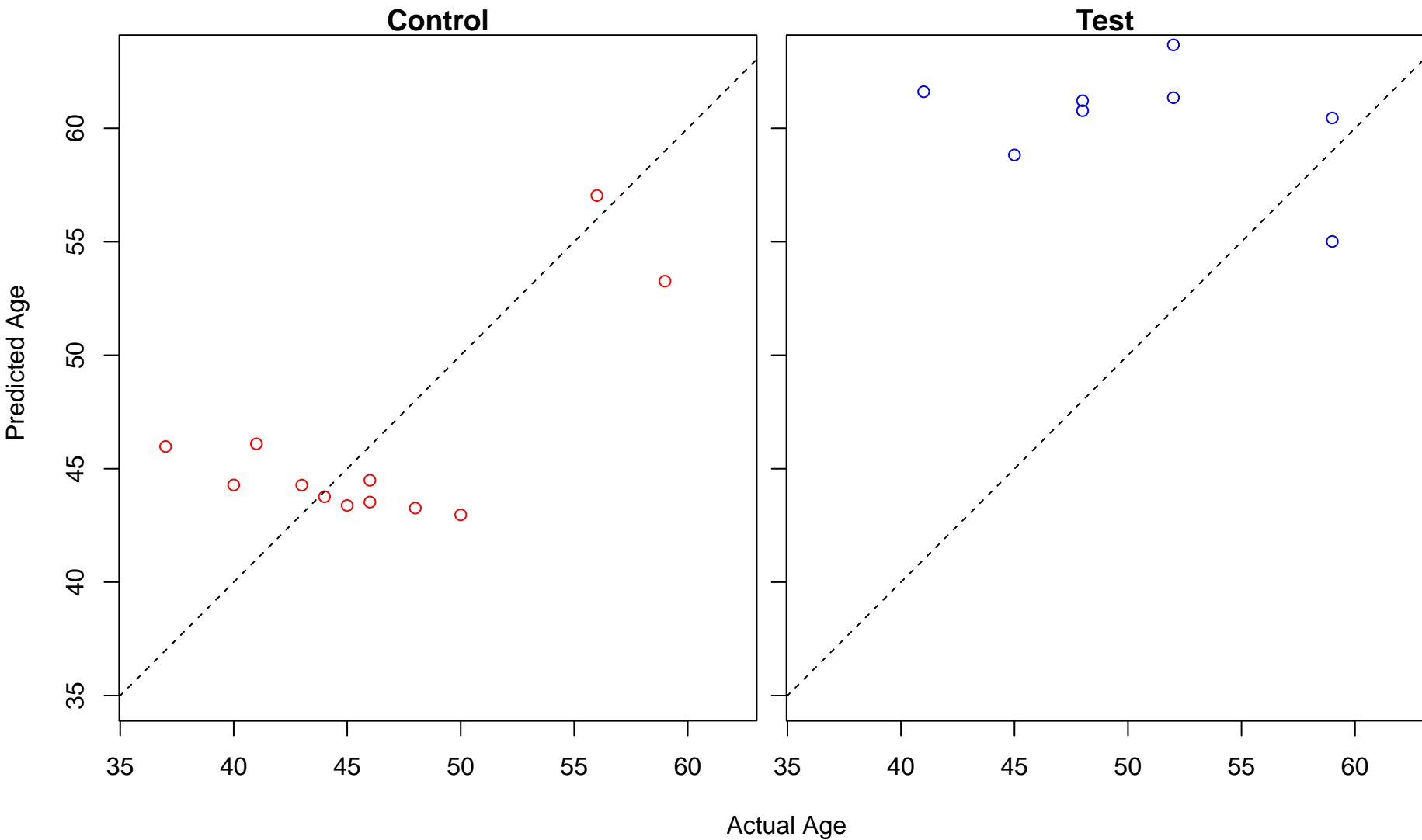
negative regulation of protein polymerization (Score: 3.965285)



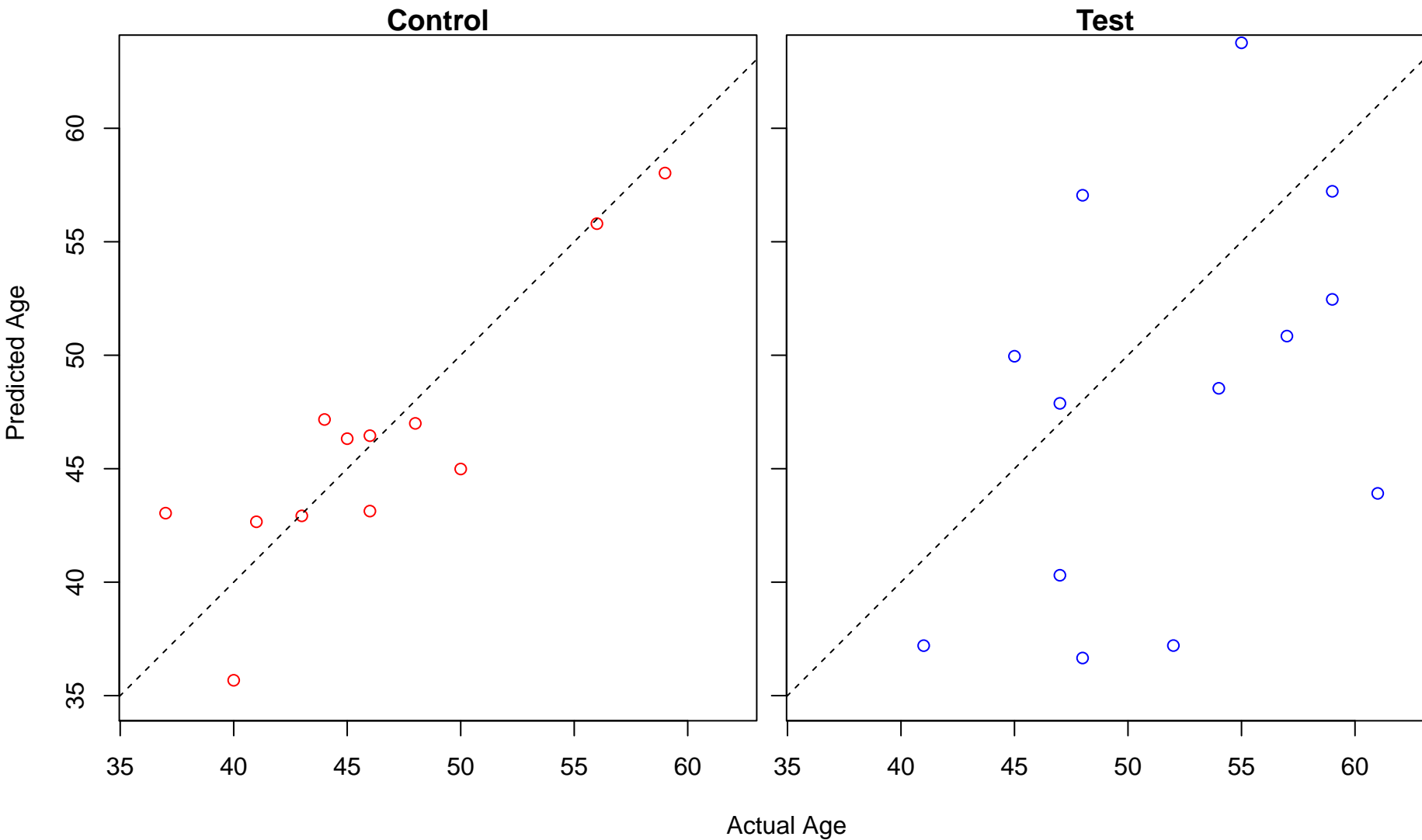
regulation of developmental pigmentation (Score: 3.963810)



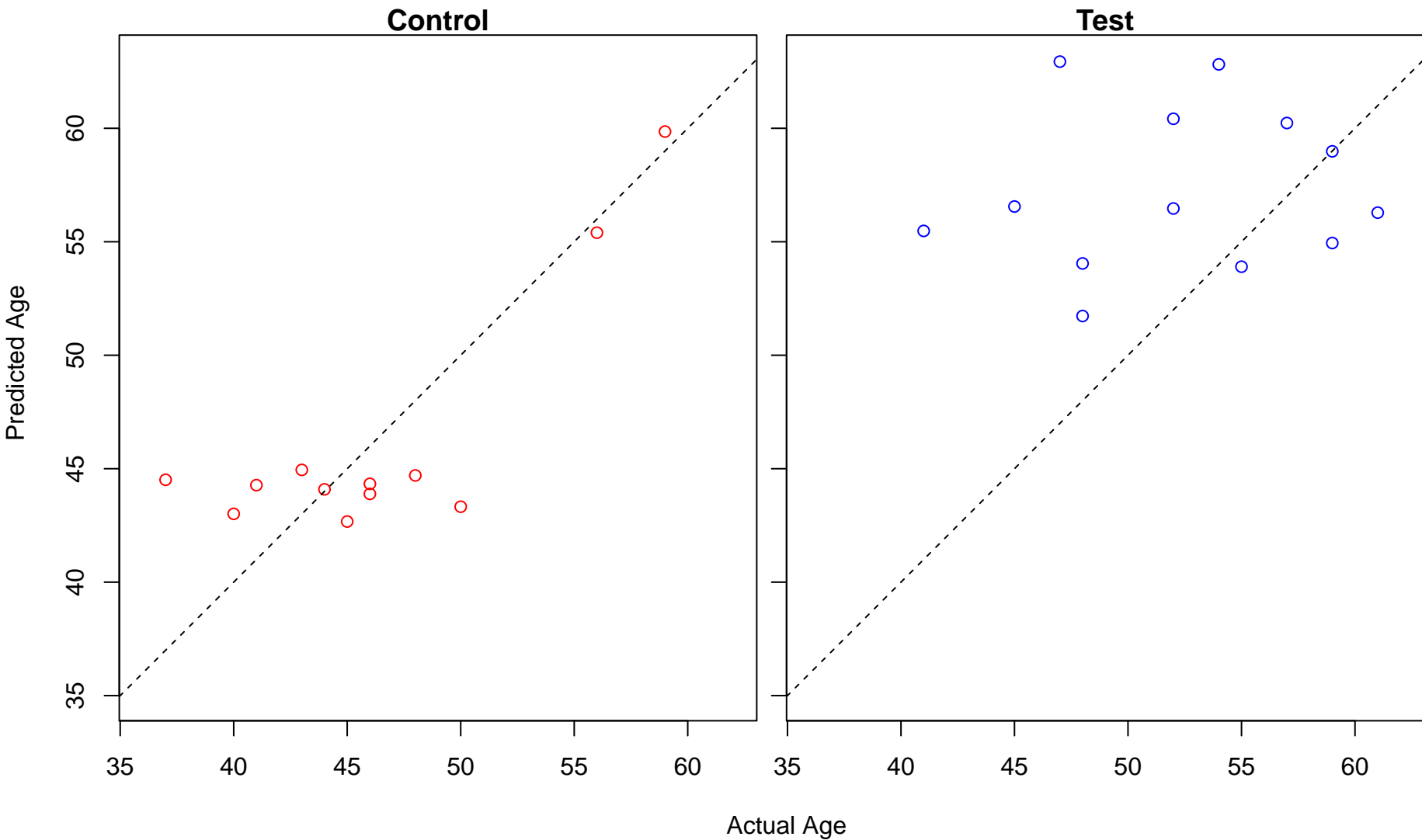
oxalate transport (Score: 3.963714)



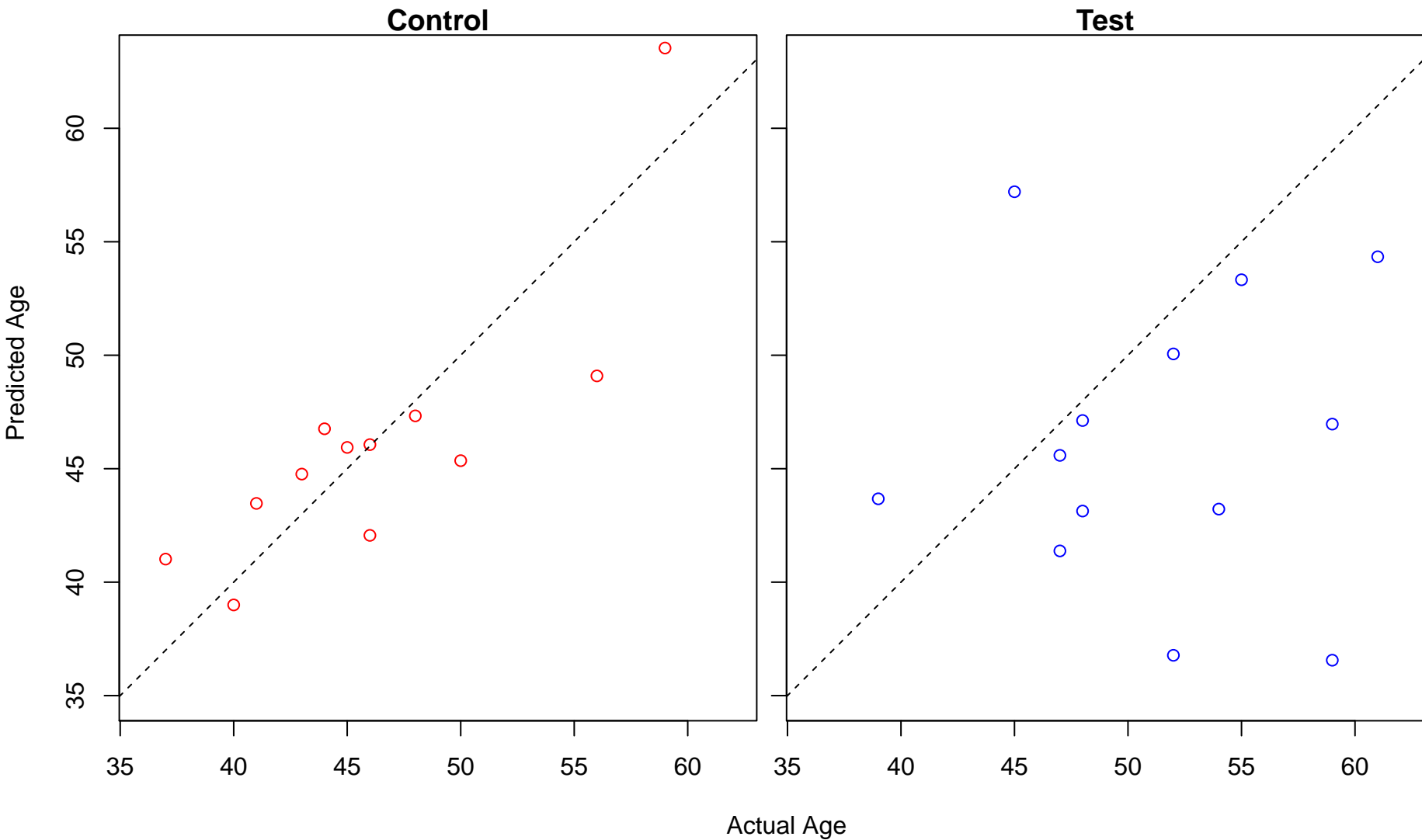
positive regulation of cyclic nucleotide metabolic process (Score: 3.959824)



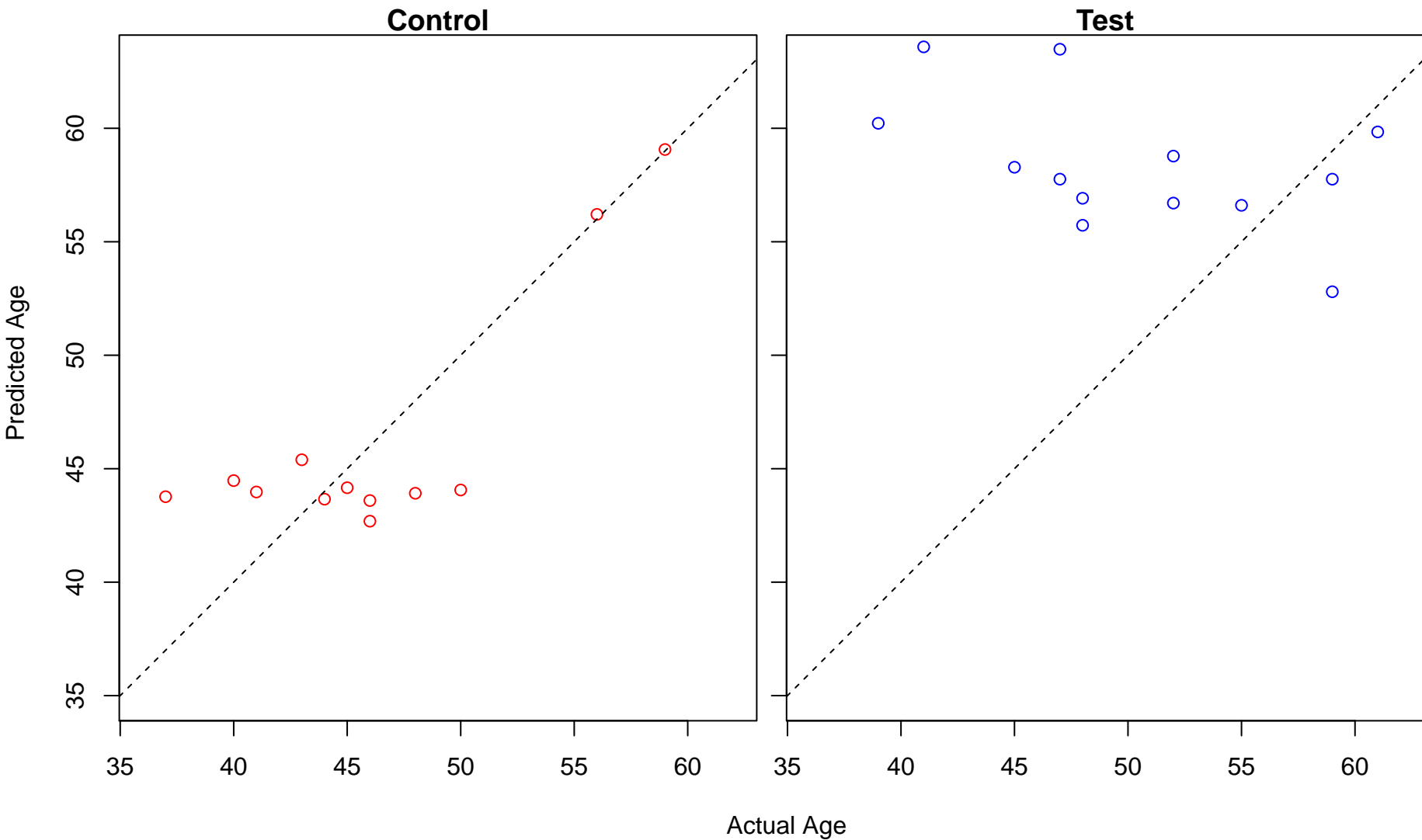
positive regulation of neurotransmitter transport (Score: 3.959574)



positive regulation of autophagy (Score: 3.958377)

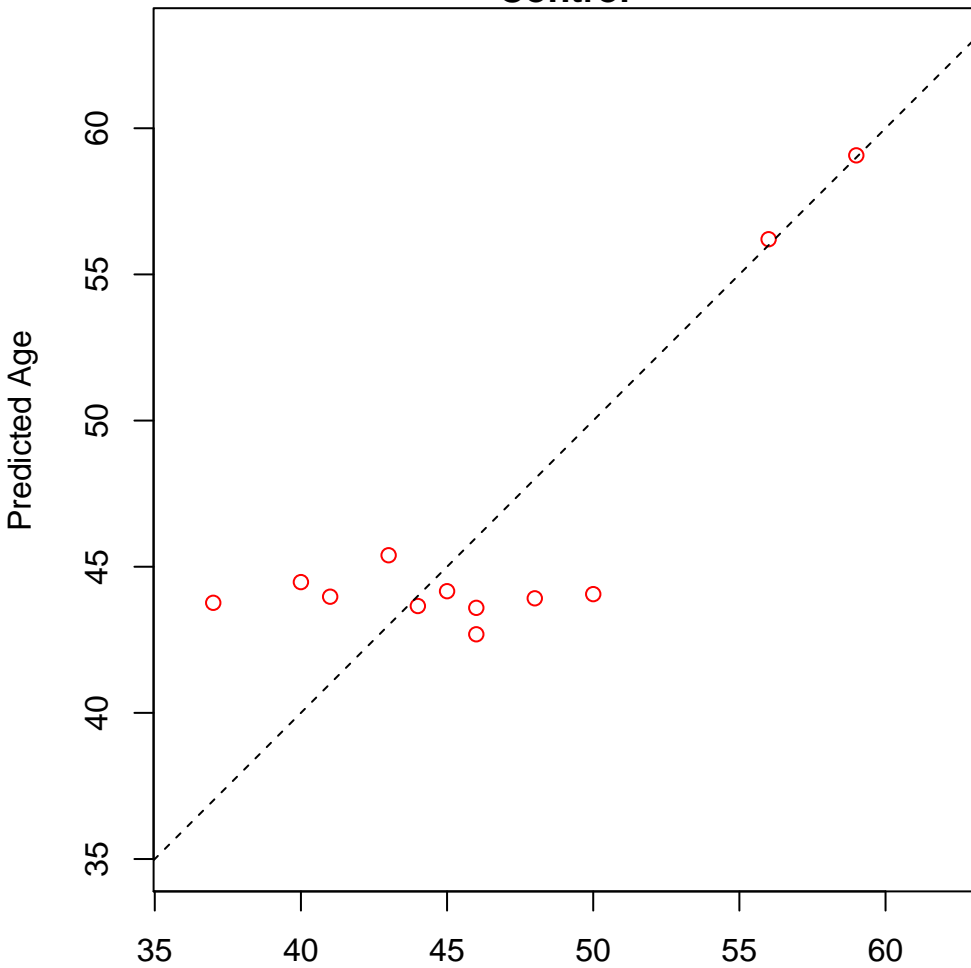


pyridine-containing compound metabolic process (Score: 3.957517)

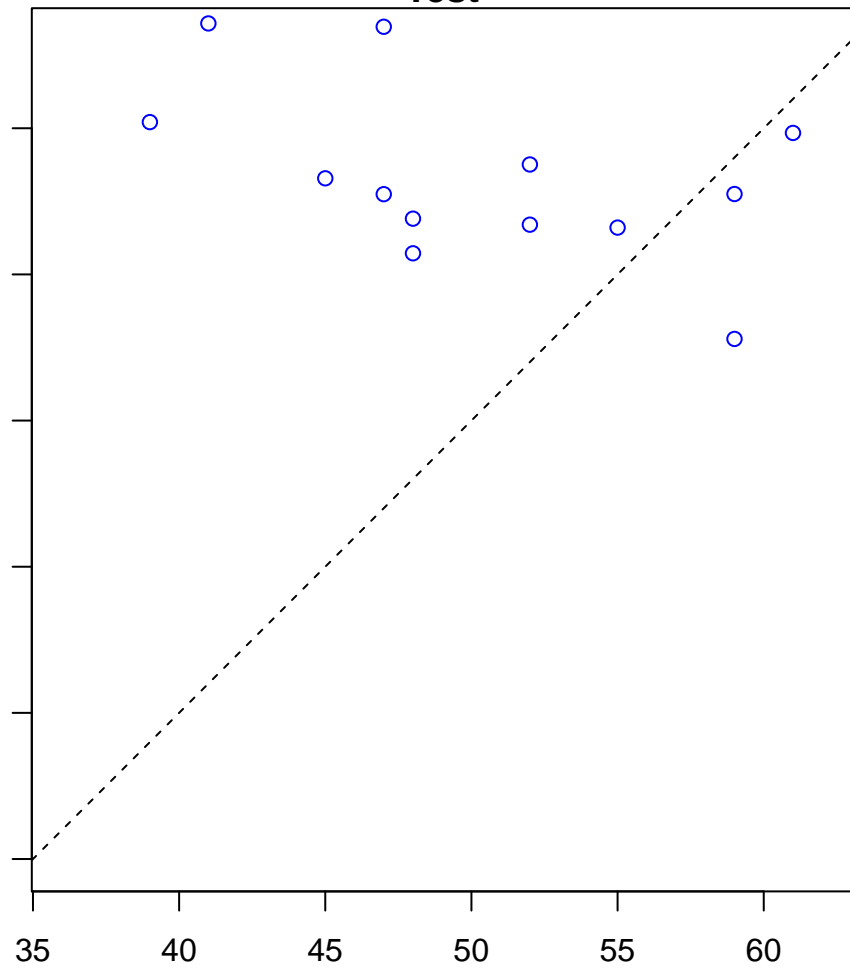


pyridine nucleotide metabolic process (Score: 3.955531)

Control

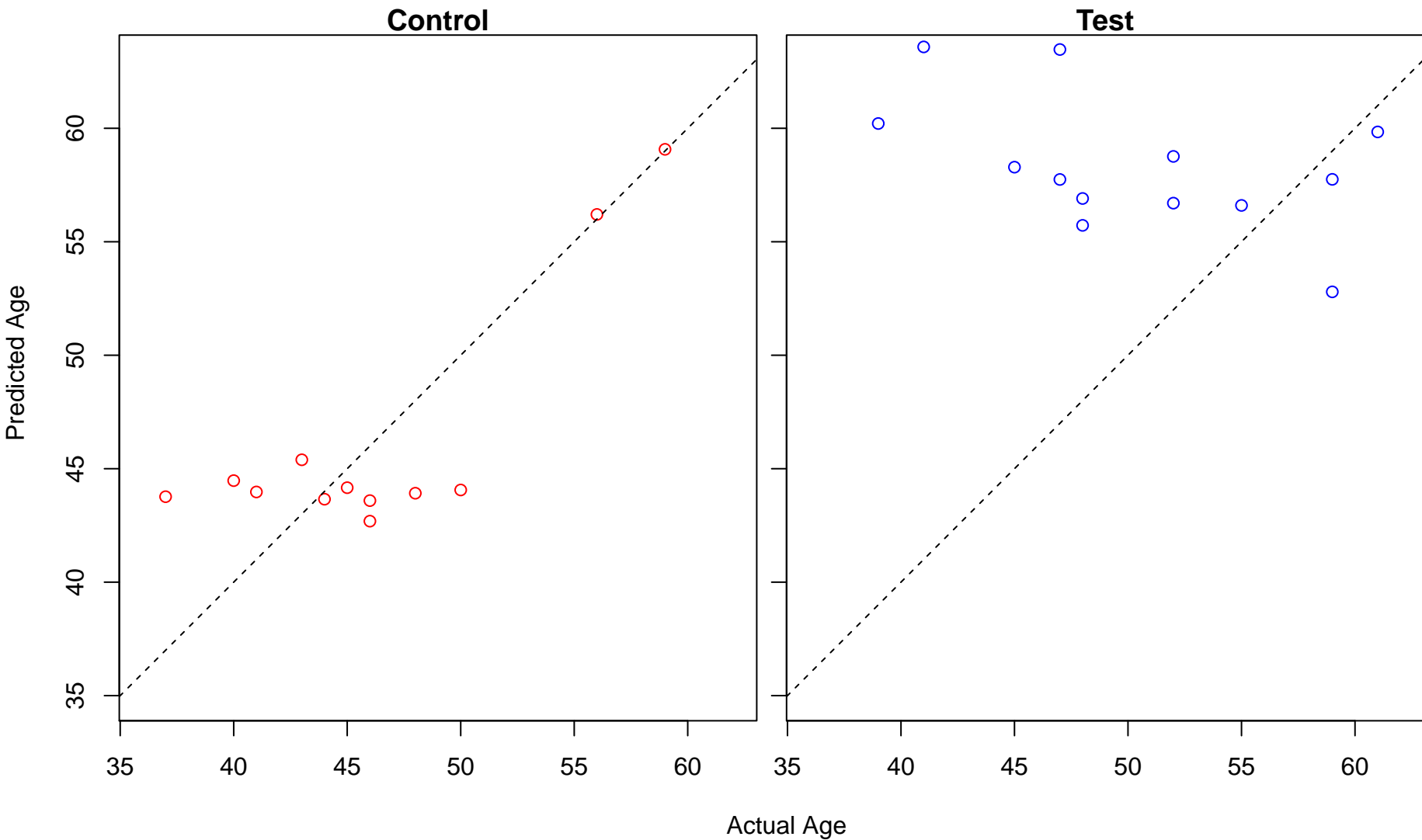


Test

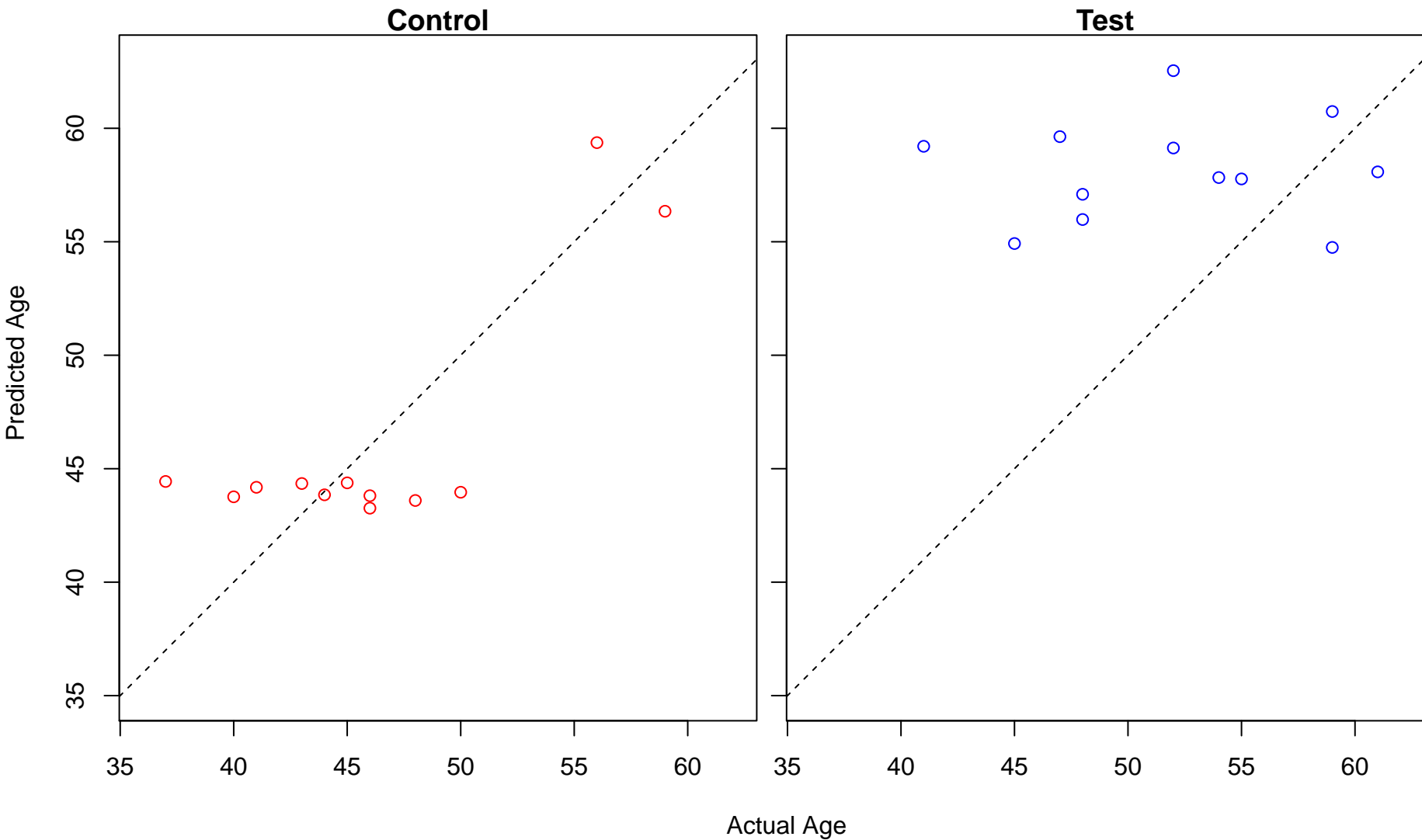


Actual Age

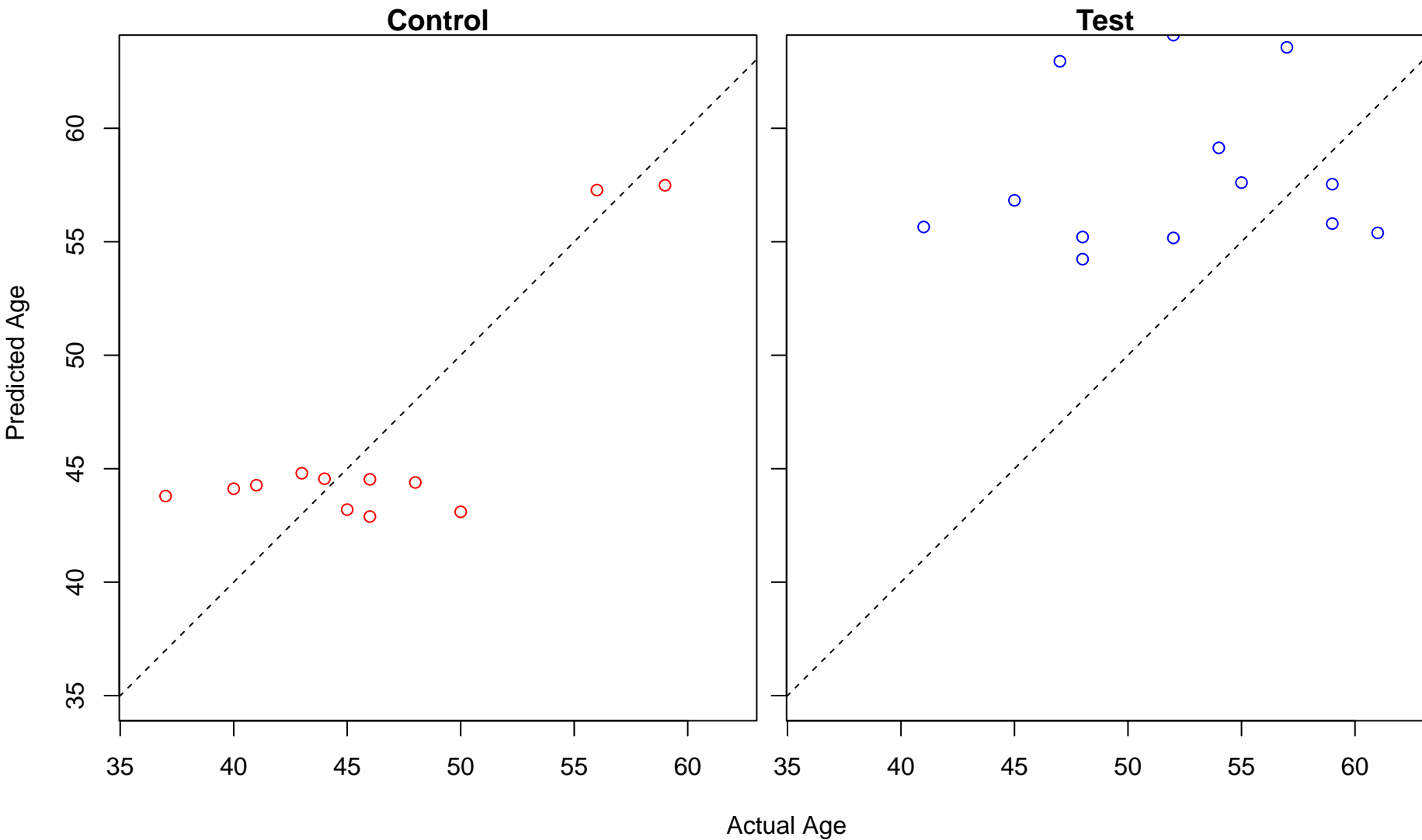
nicotinamide nucleotide metabolic process (Score: 3.955531)



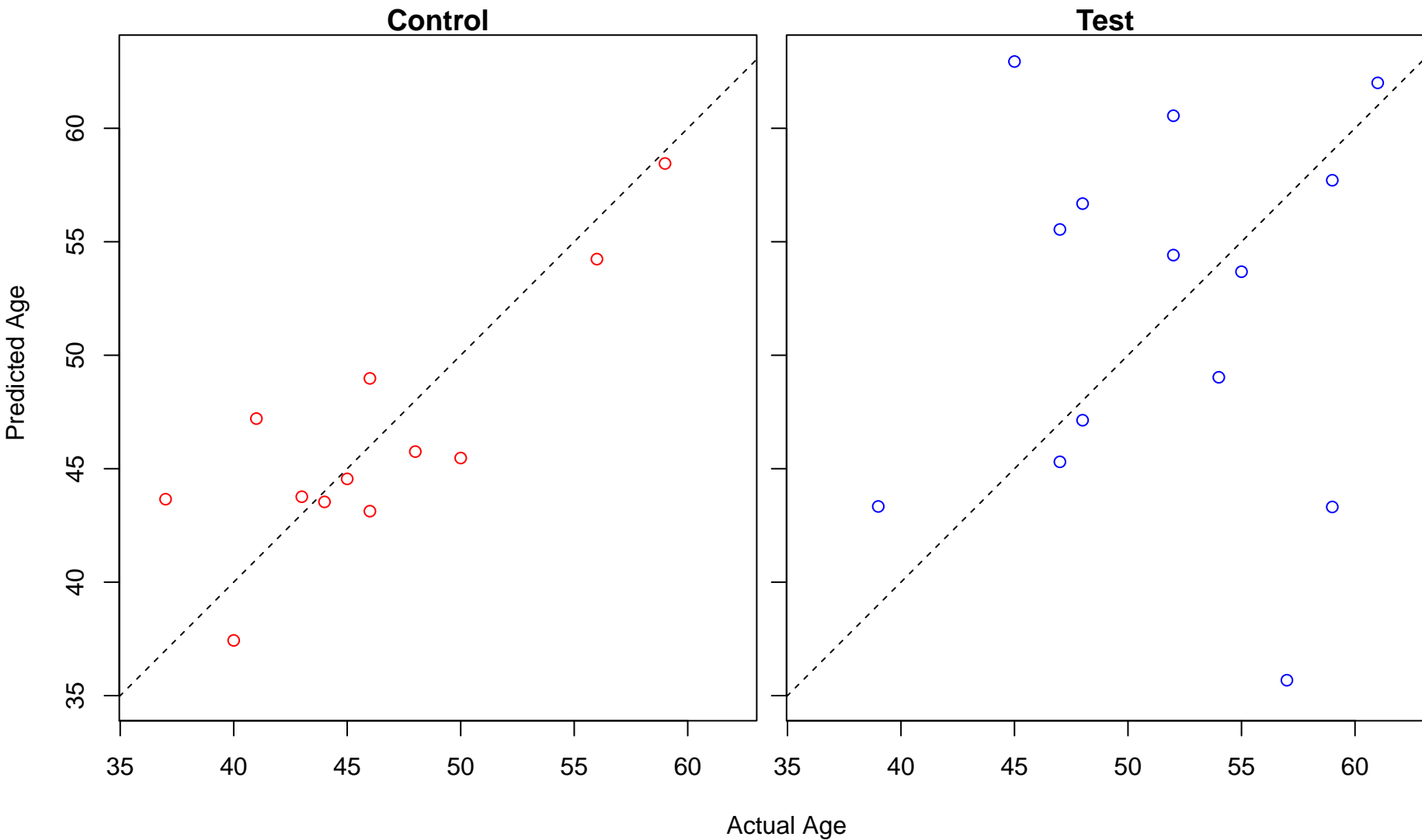
I-kappaB kinase/NF-kappaB signaling (Score: 3.950438)



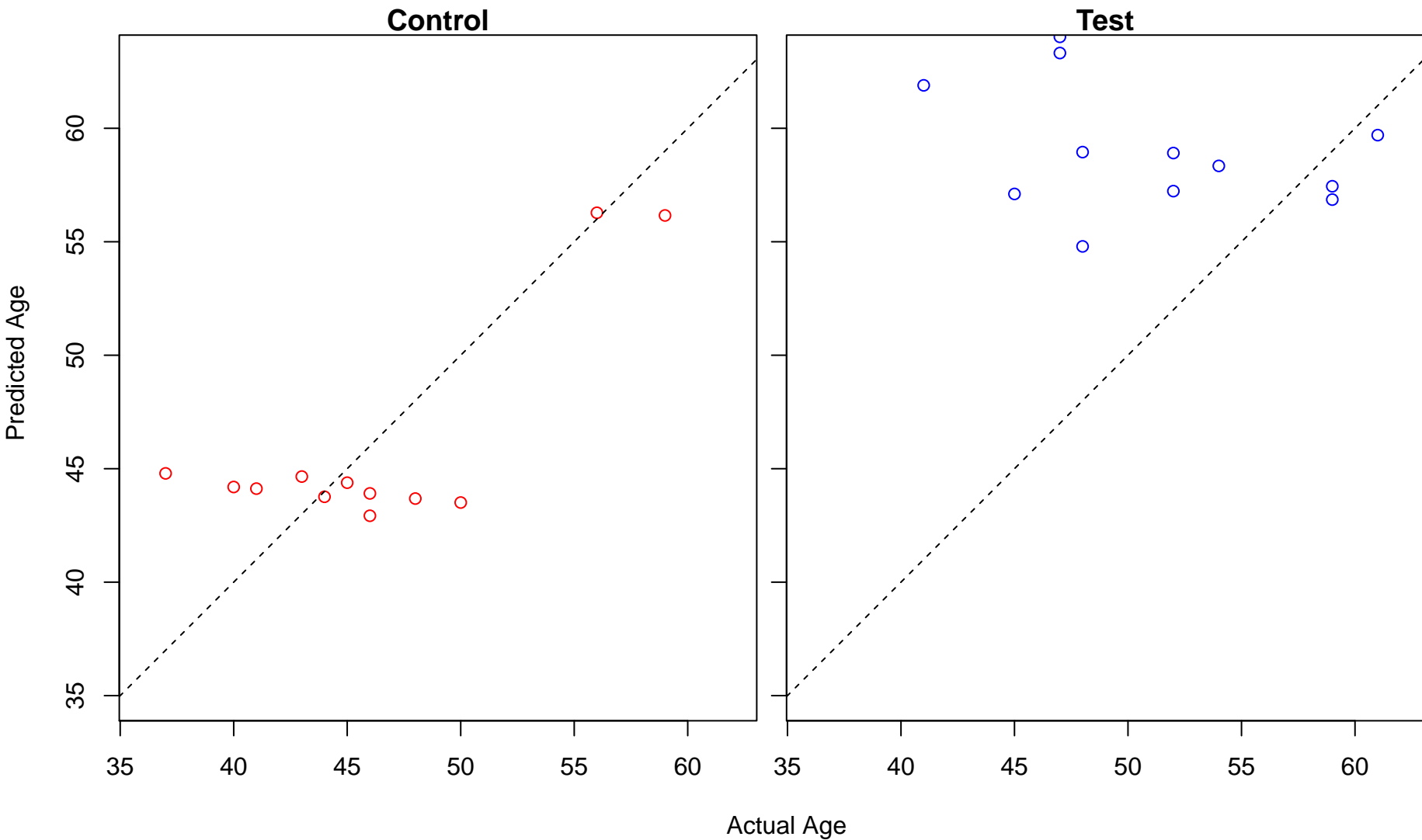
viral genome replication (Score: 3.950290)



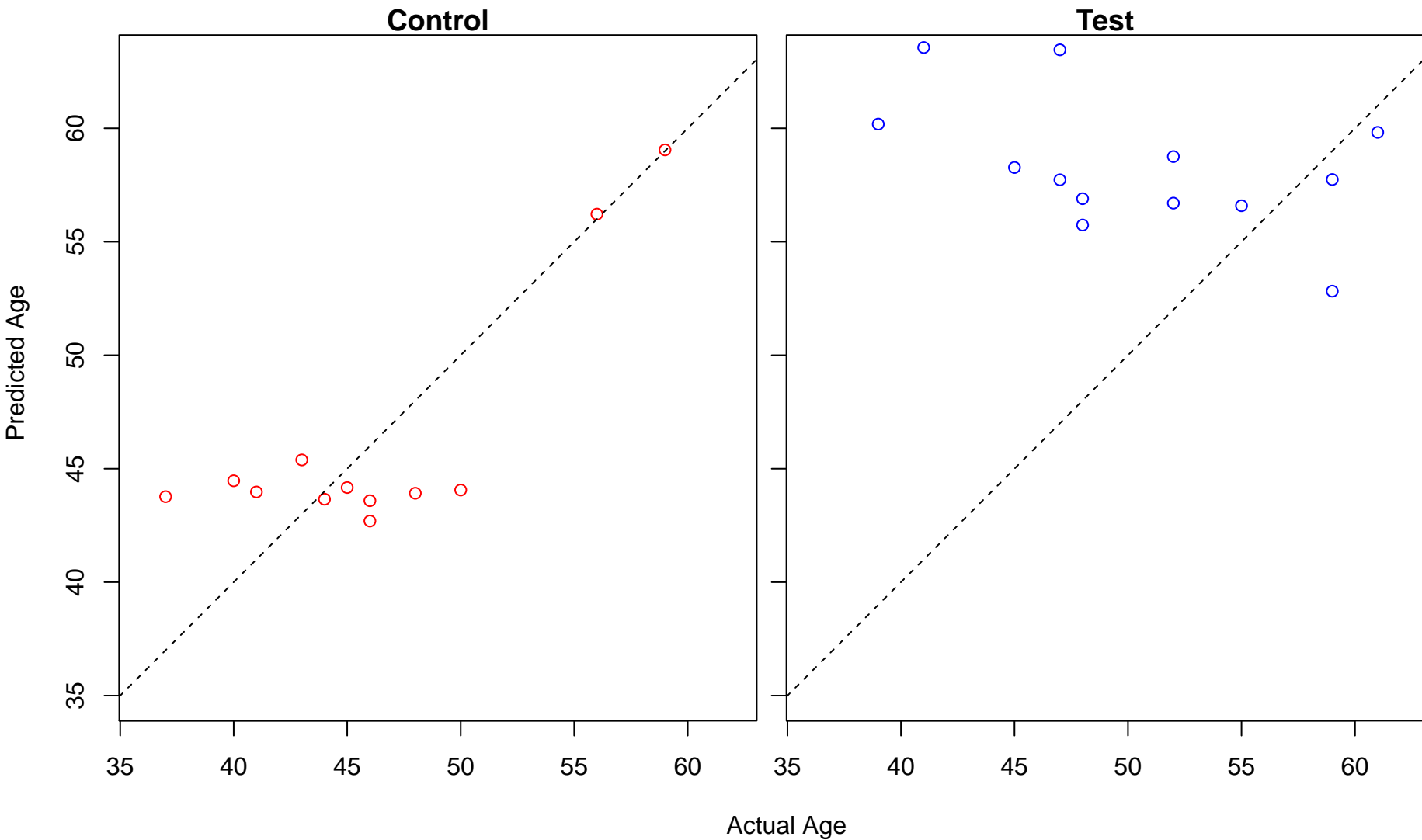
inflammatory response to antigenic stimulus (Score: 3.950172)



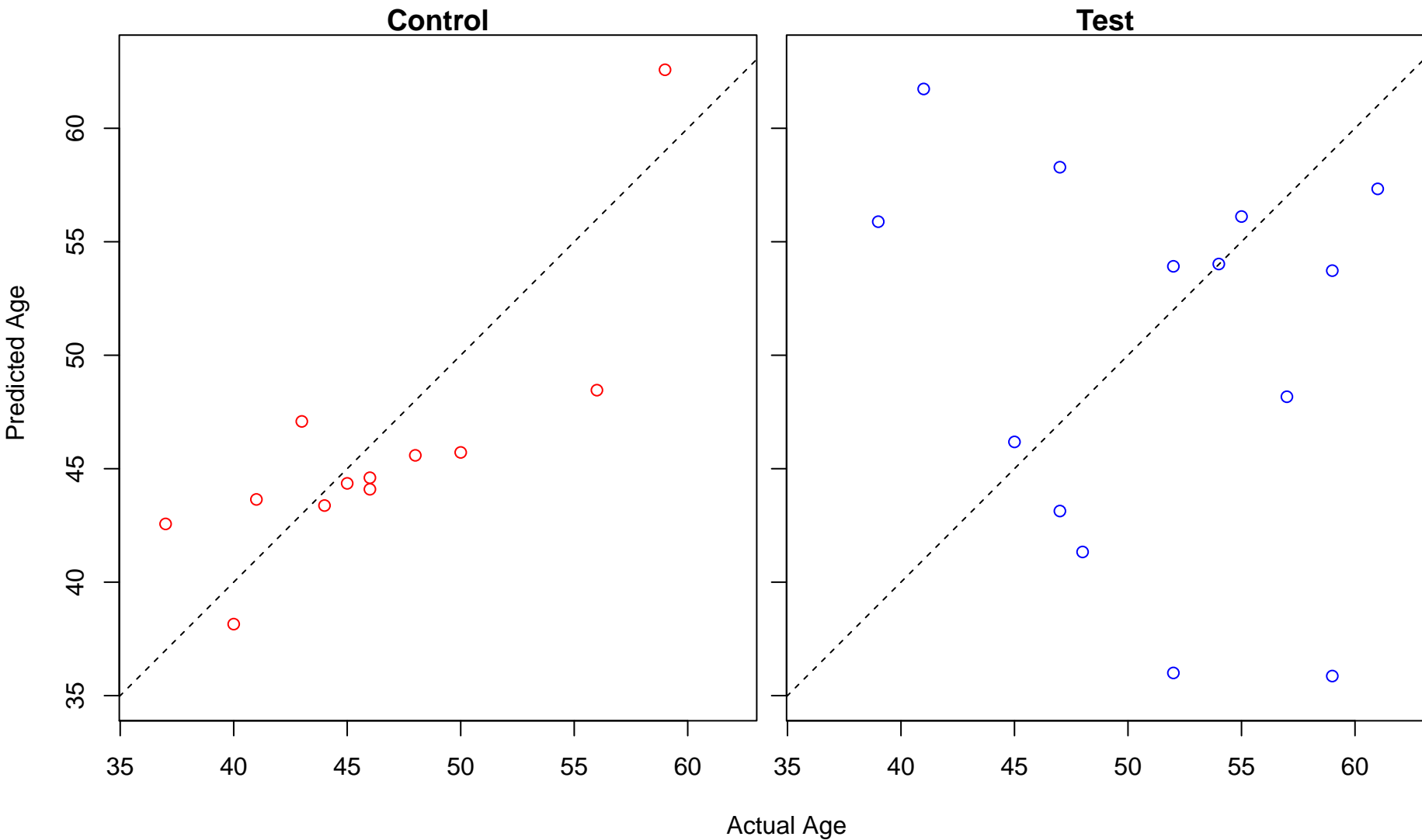
cellular transition metal ion homeostasis (Score: 3.949509)



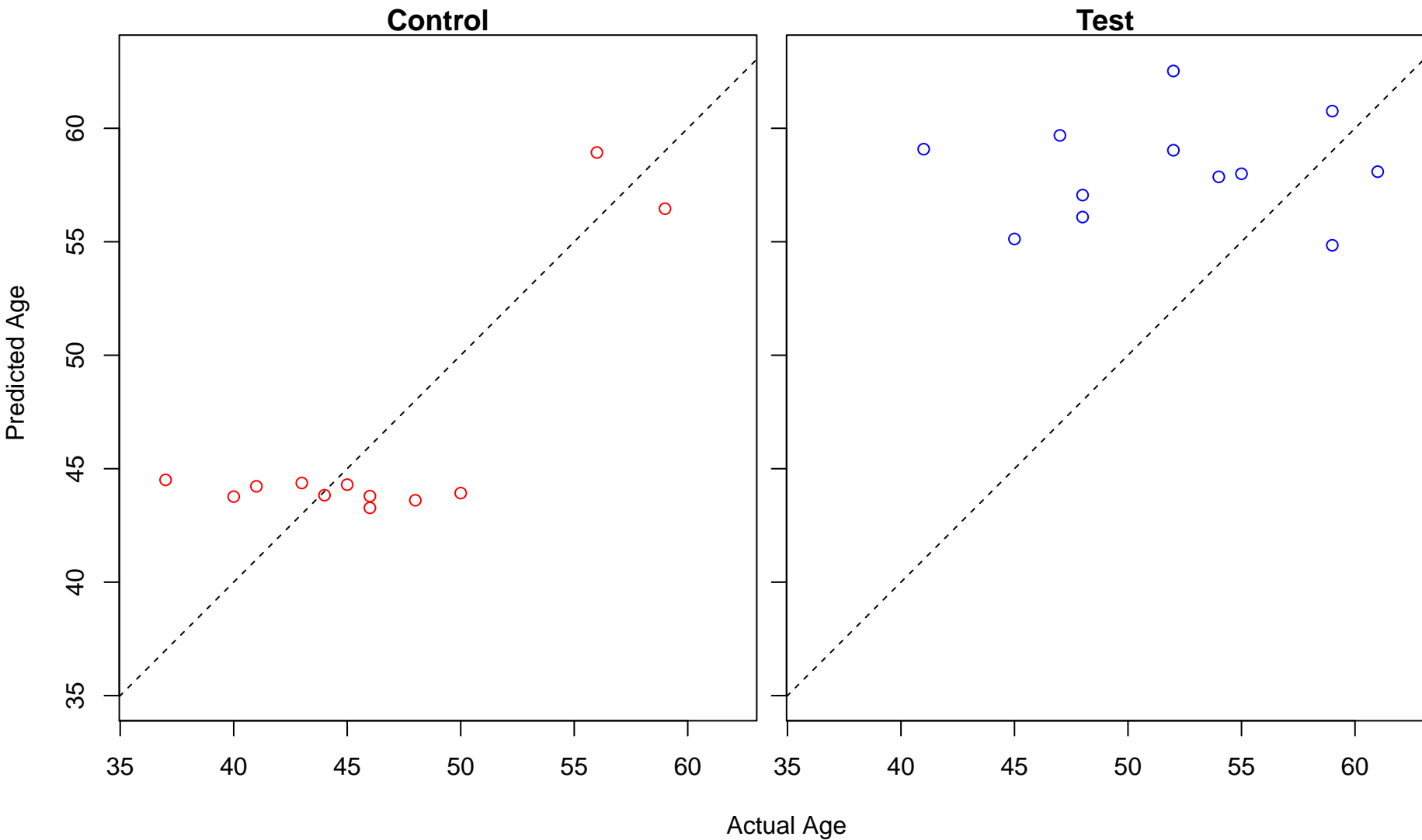
oxidoreduction coenzyme metabolic process (Score: 3.948662)



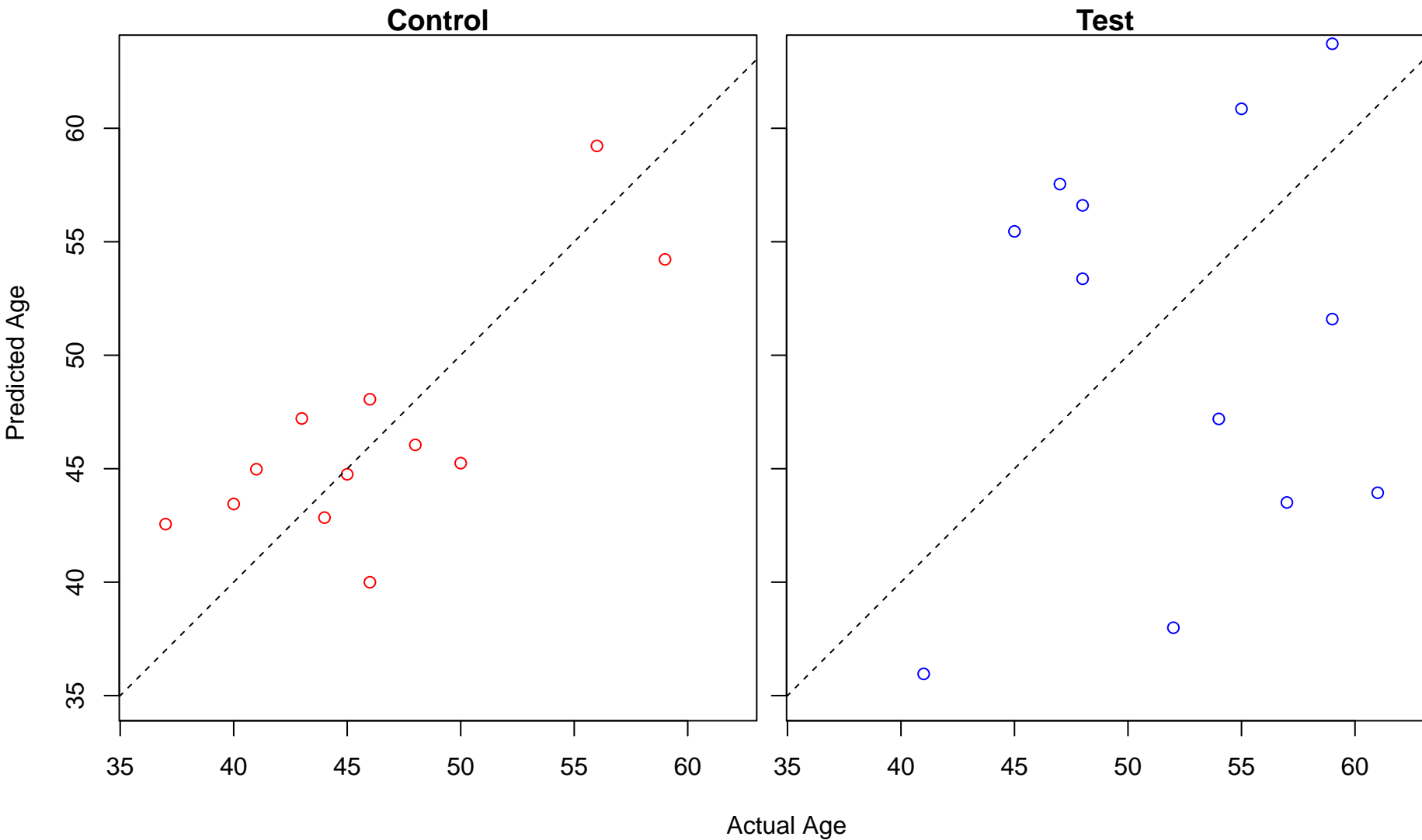
positive regulation of erythrocyte differentiation (Score: 3.945707)



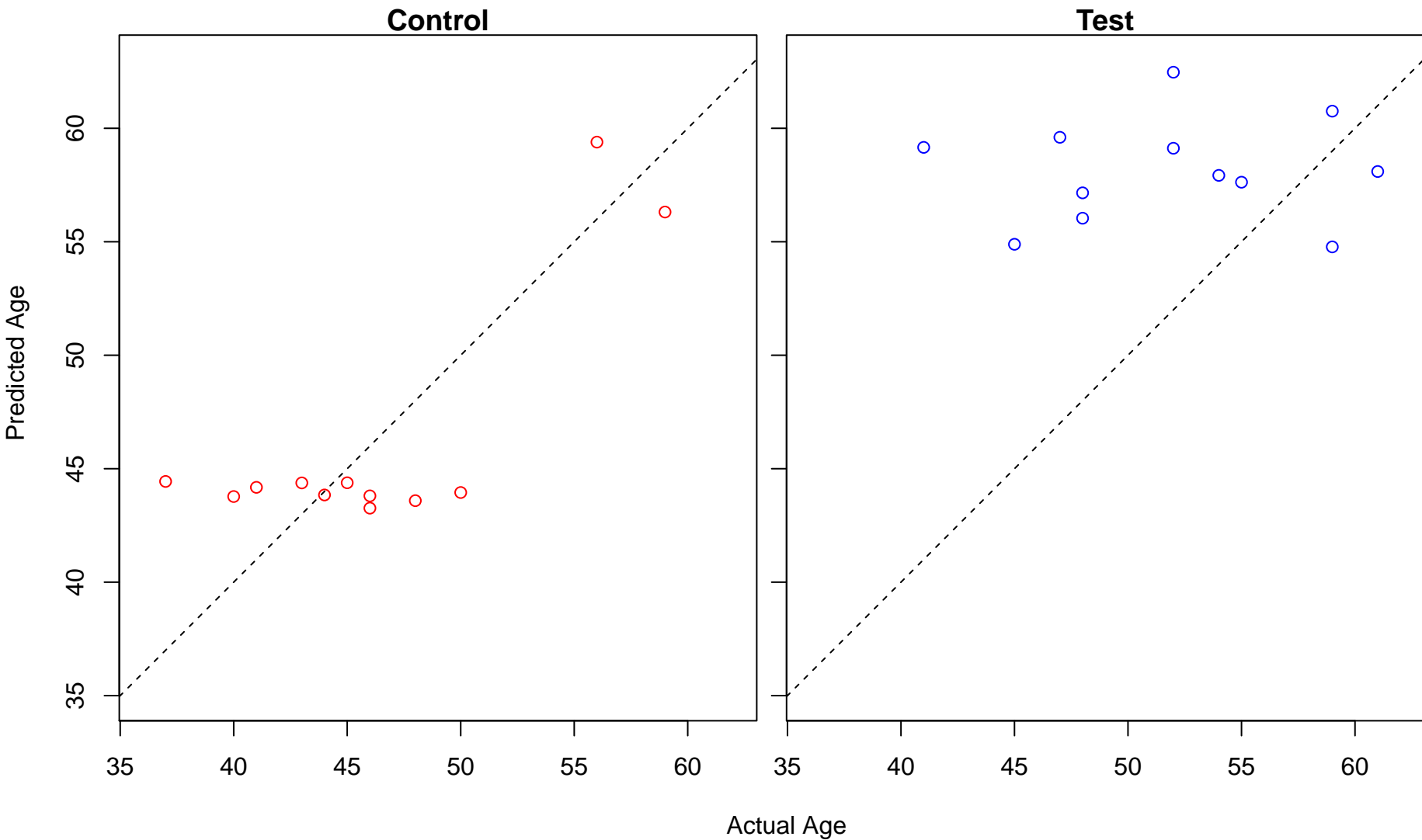
regulation of necrotic cell death (Score: 3.945545)



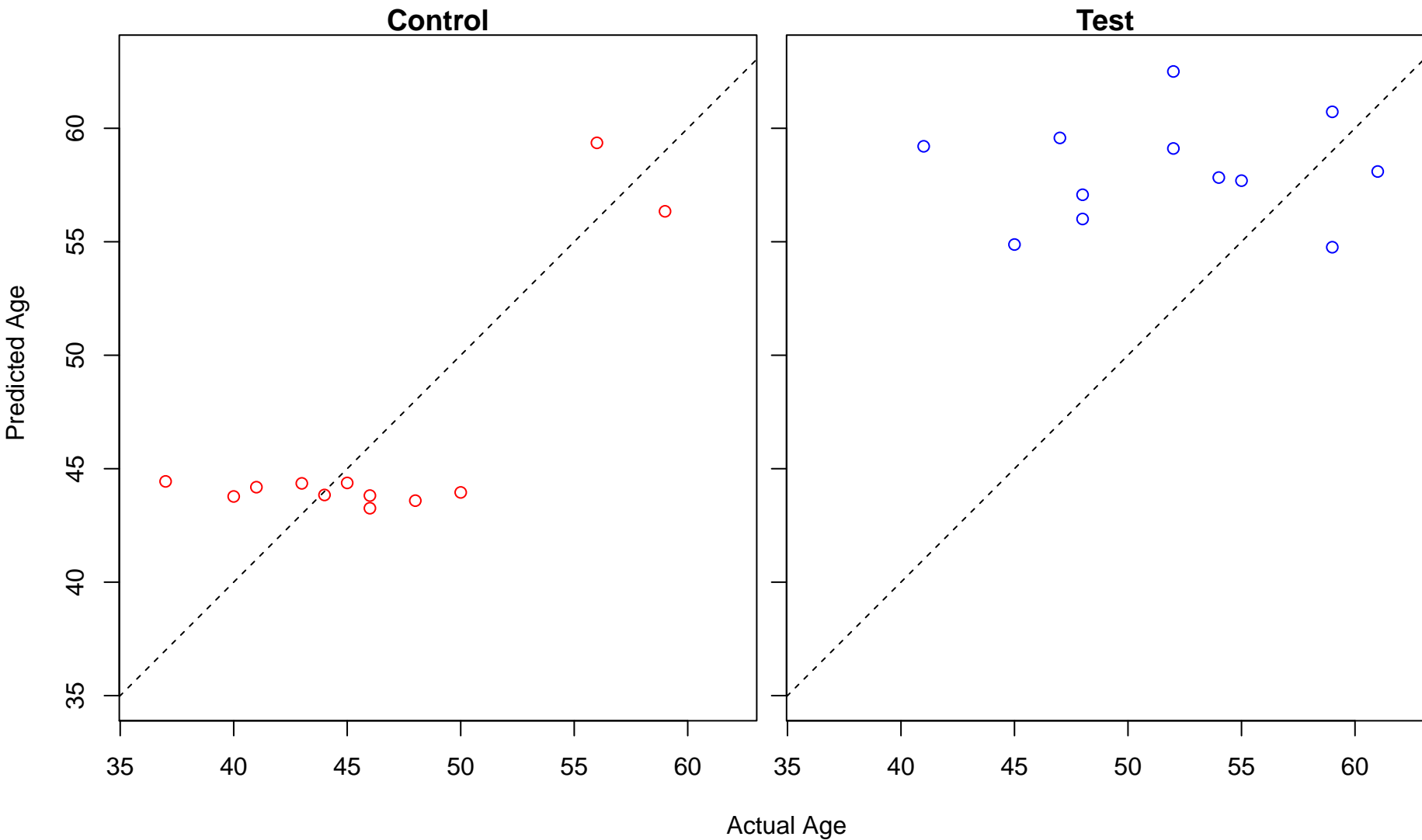
positive regulation of respiratory burst (Score: 3.943787)



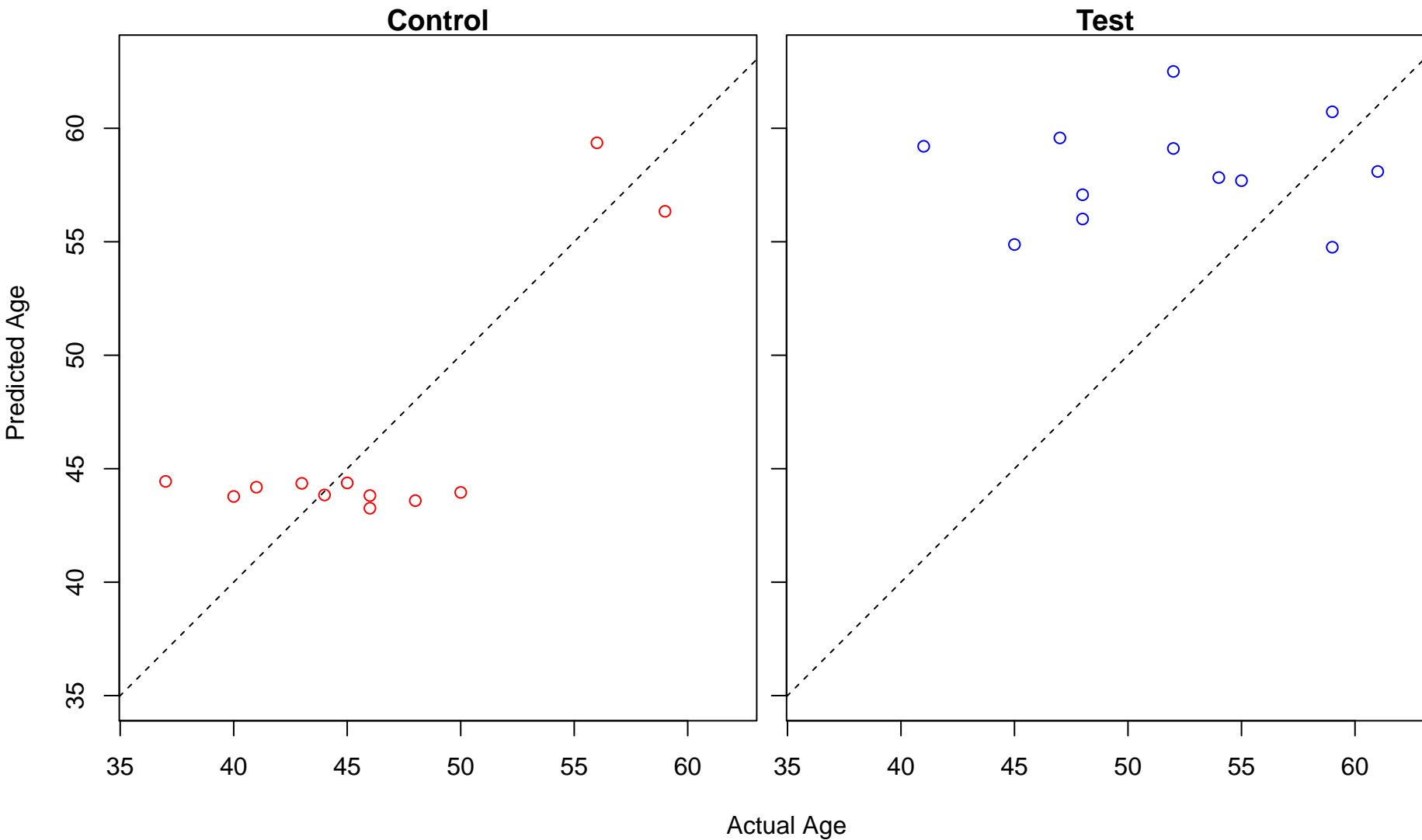
nucleotide-excision repair, DNA gap filling (Score: 3.943761)



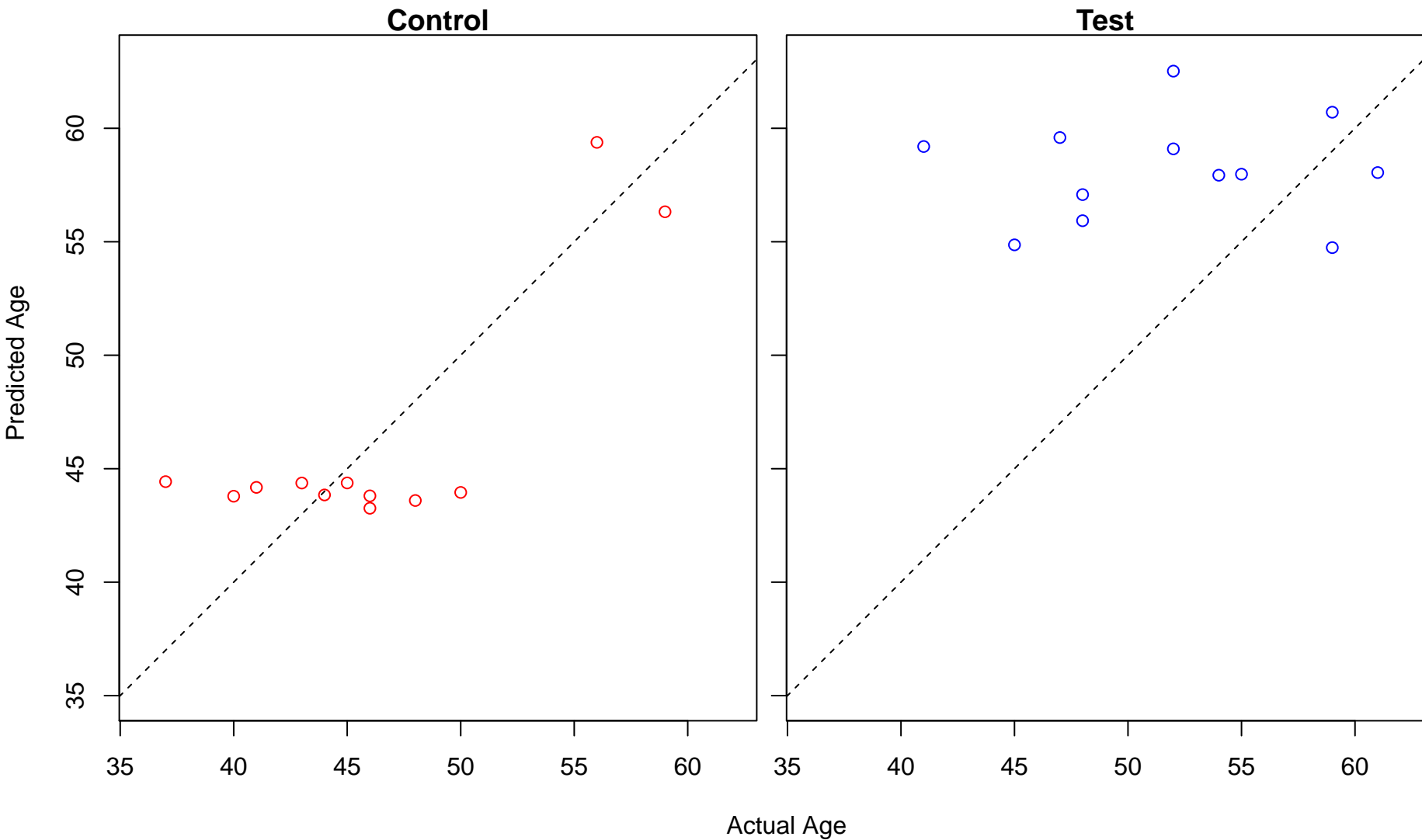
glycogen biosynthetic process (Score: 3.941358)



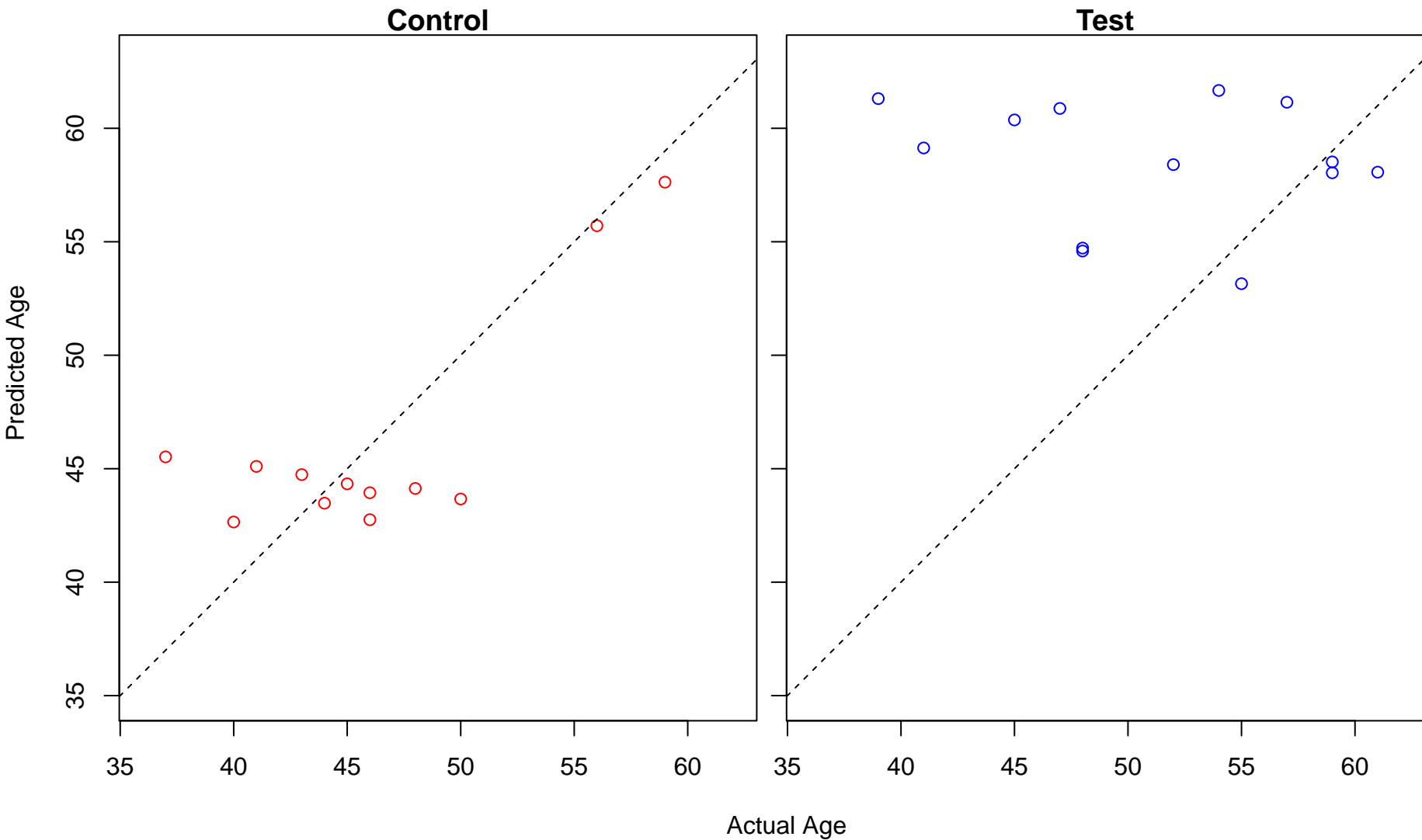
glucan biosynthetic process (Score: 3.941358)



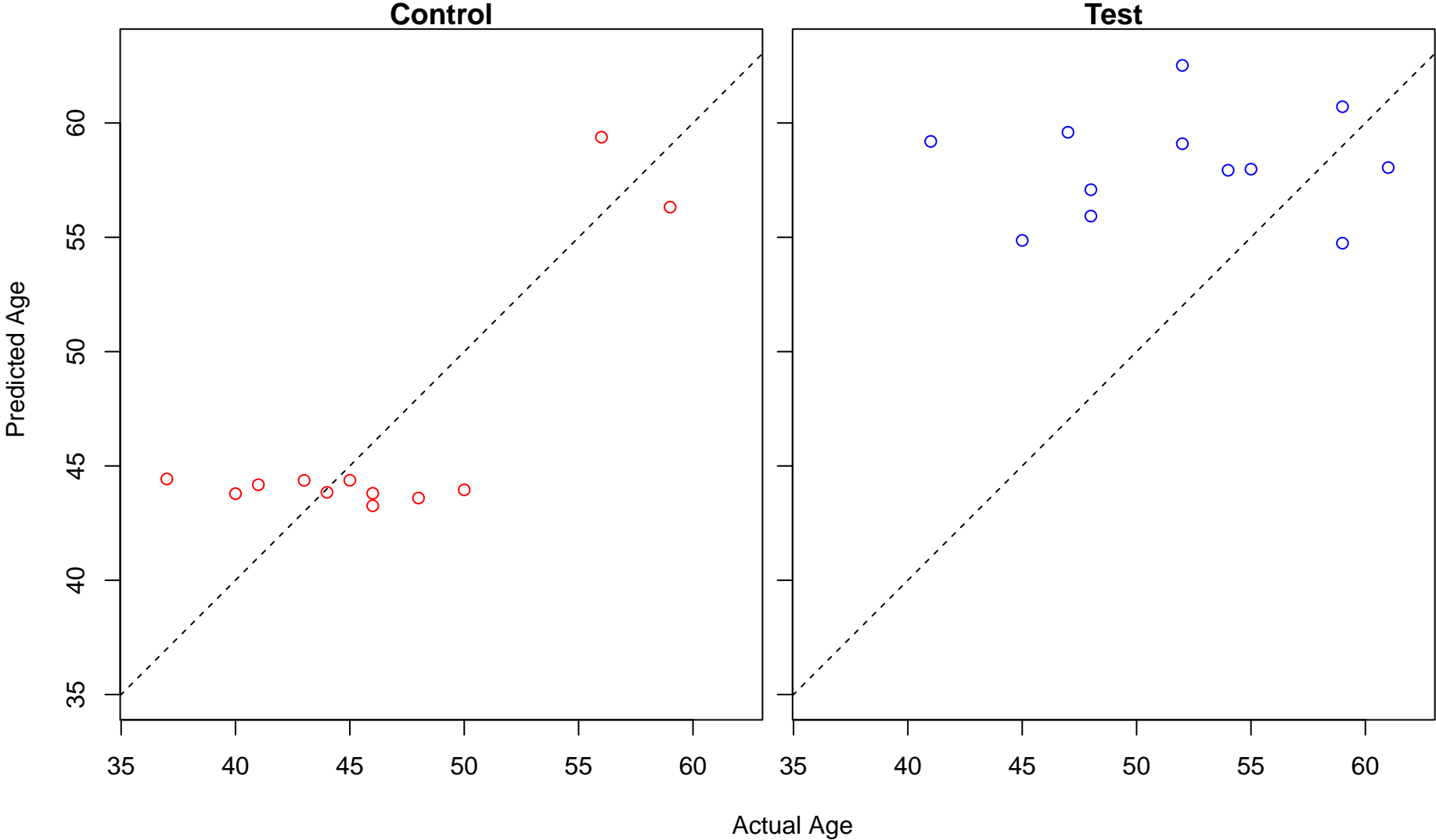
nucleotide-binding oligomerization domain containing signaling pathway (Score: 3.940314)



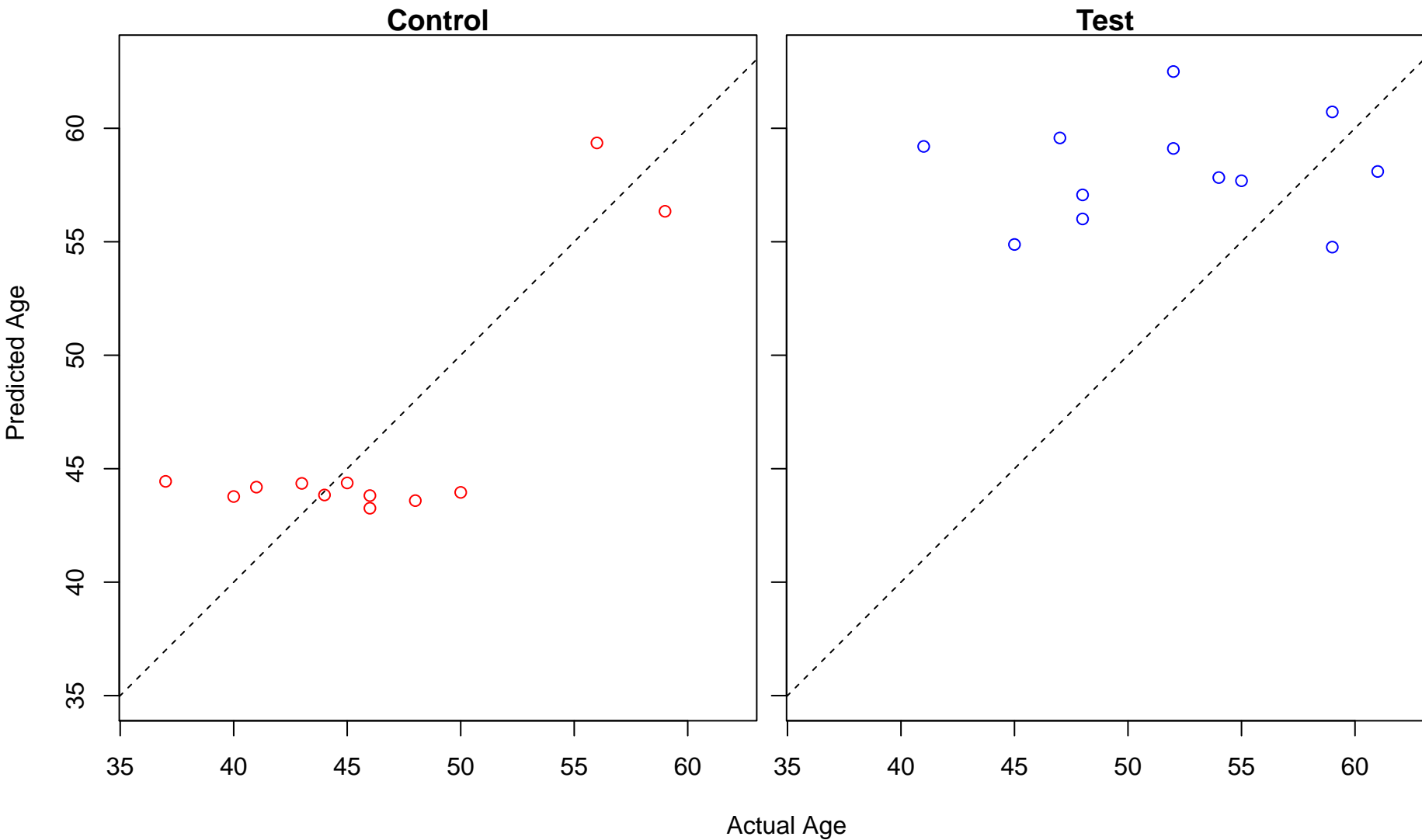
carbohydrate transport (Score: 3.940044)



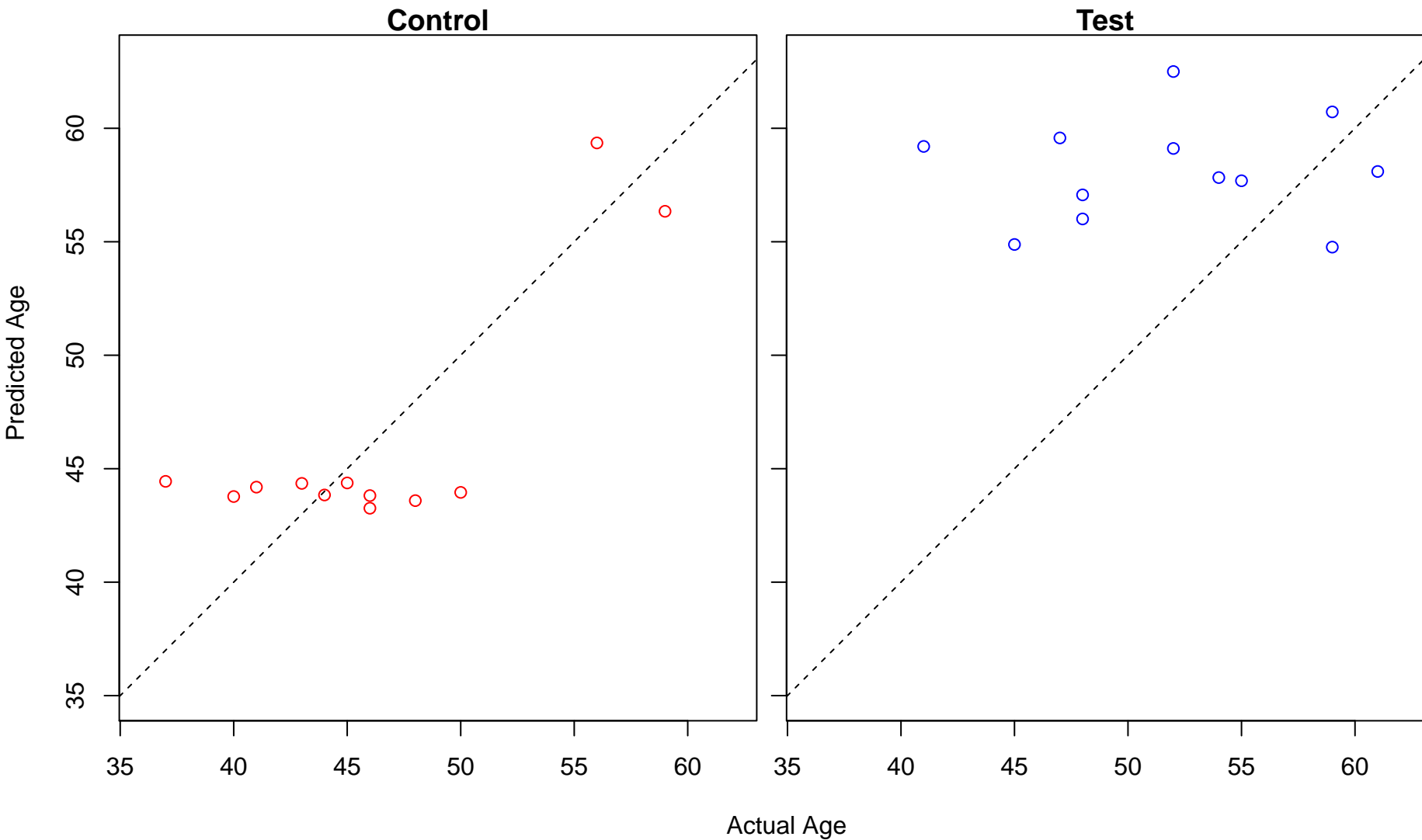
cytoplasmic pattern recognition receptor signaling pathway (Score: 3.939657)



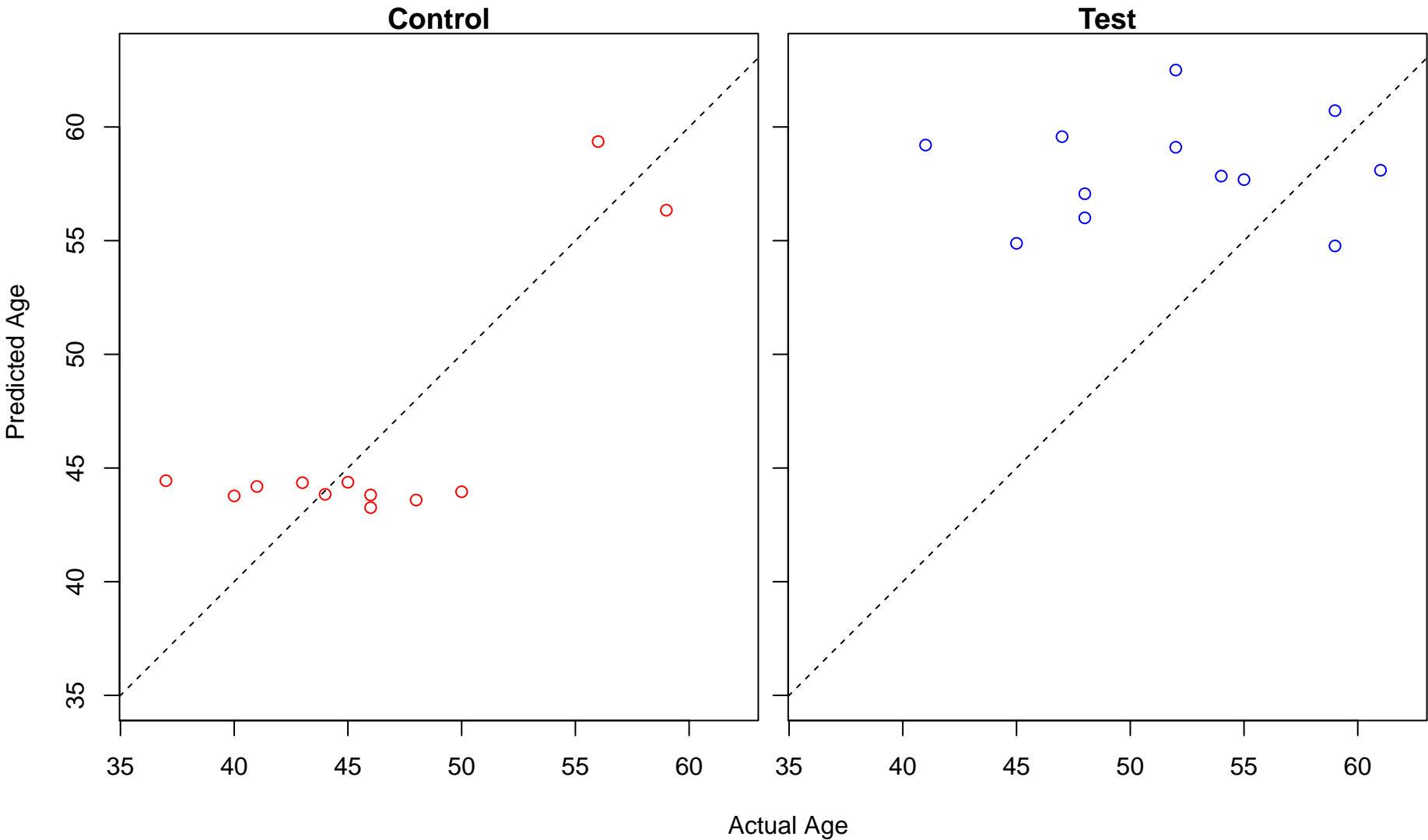
polysaccharide biosynthetic process (Score: 3.938591)



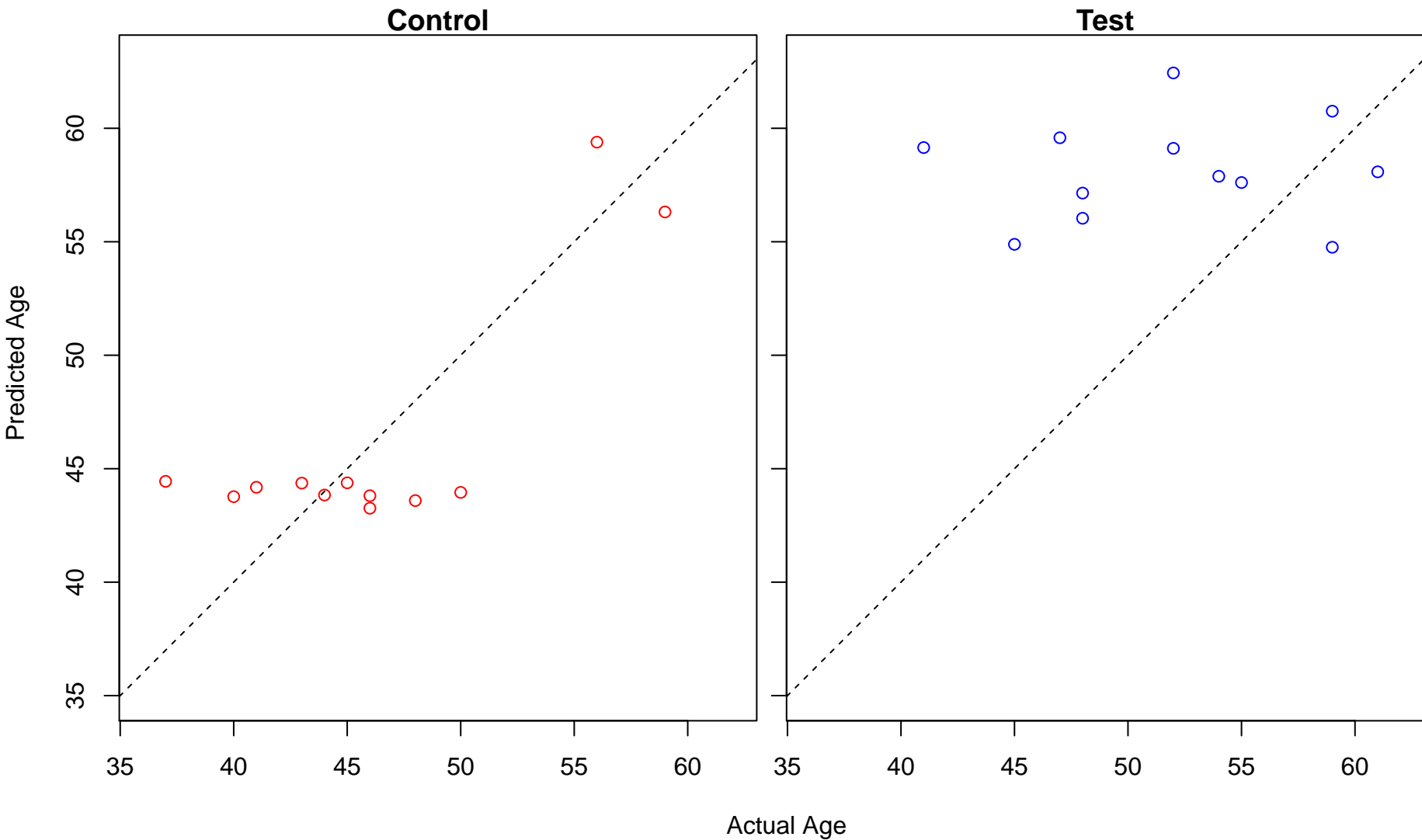
cellular polysaccharide biosynthetic process (Score: 3.938591)



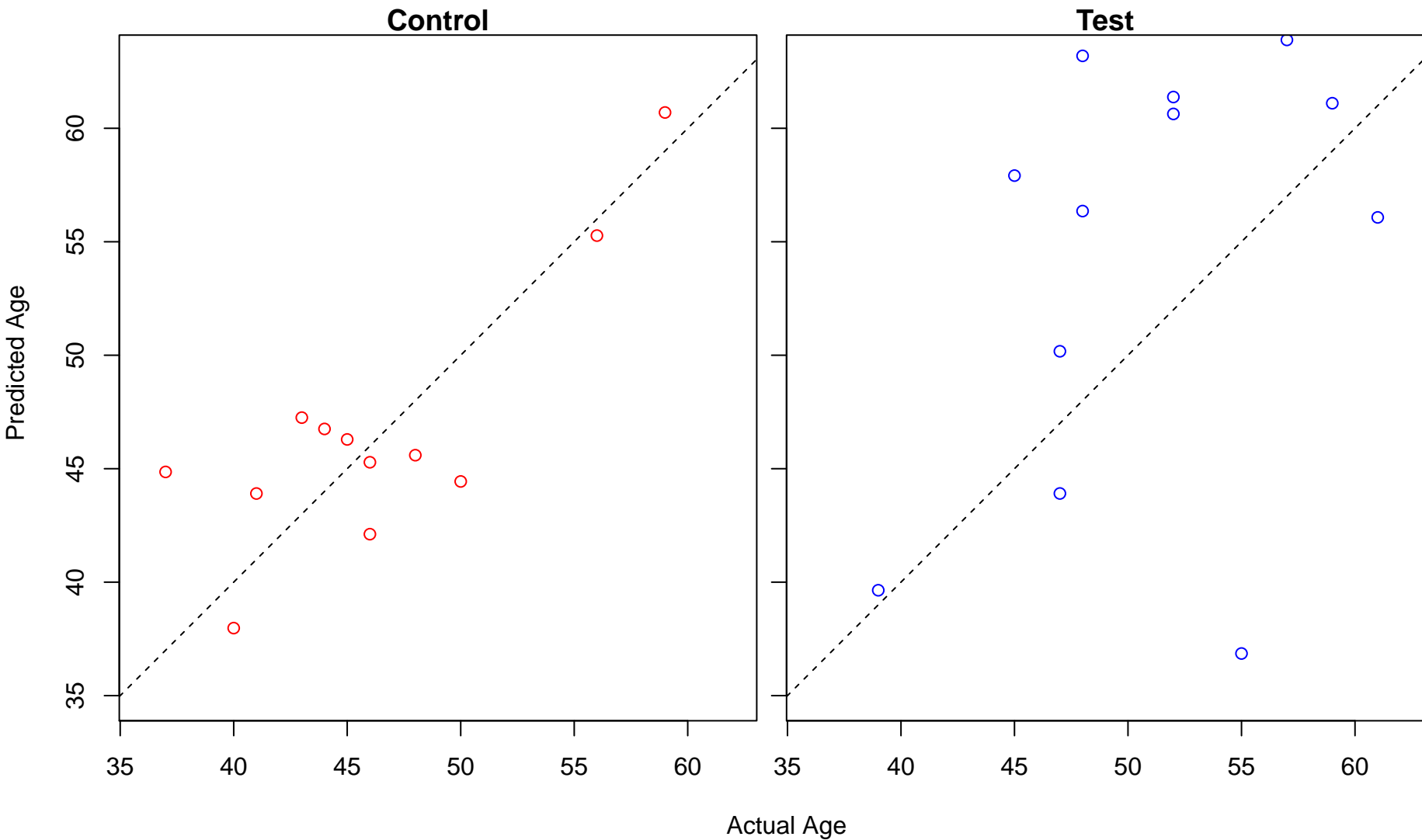
cellular carbohydrate biosynthetic process (Score: 3.936741)



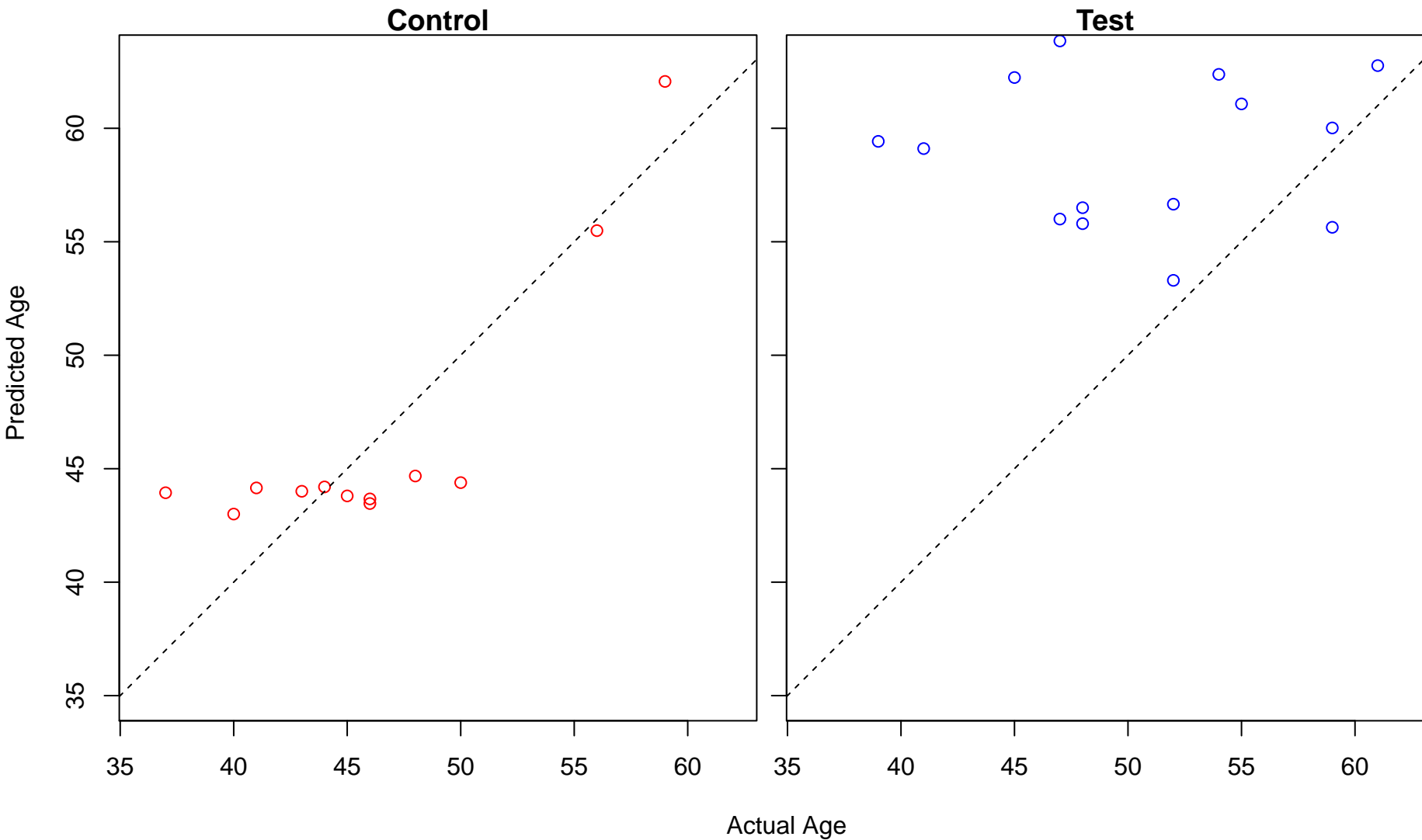
error-prone translesion synthesis (Score: 3.934588)



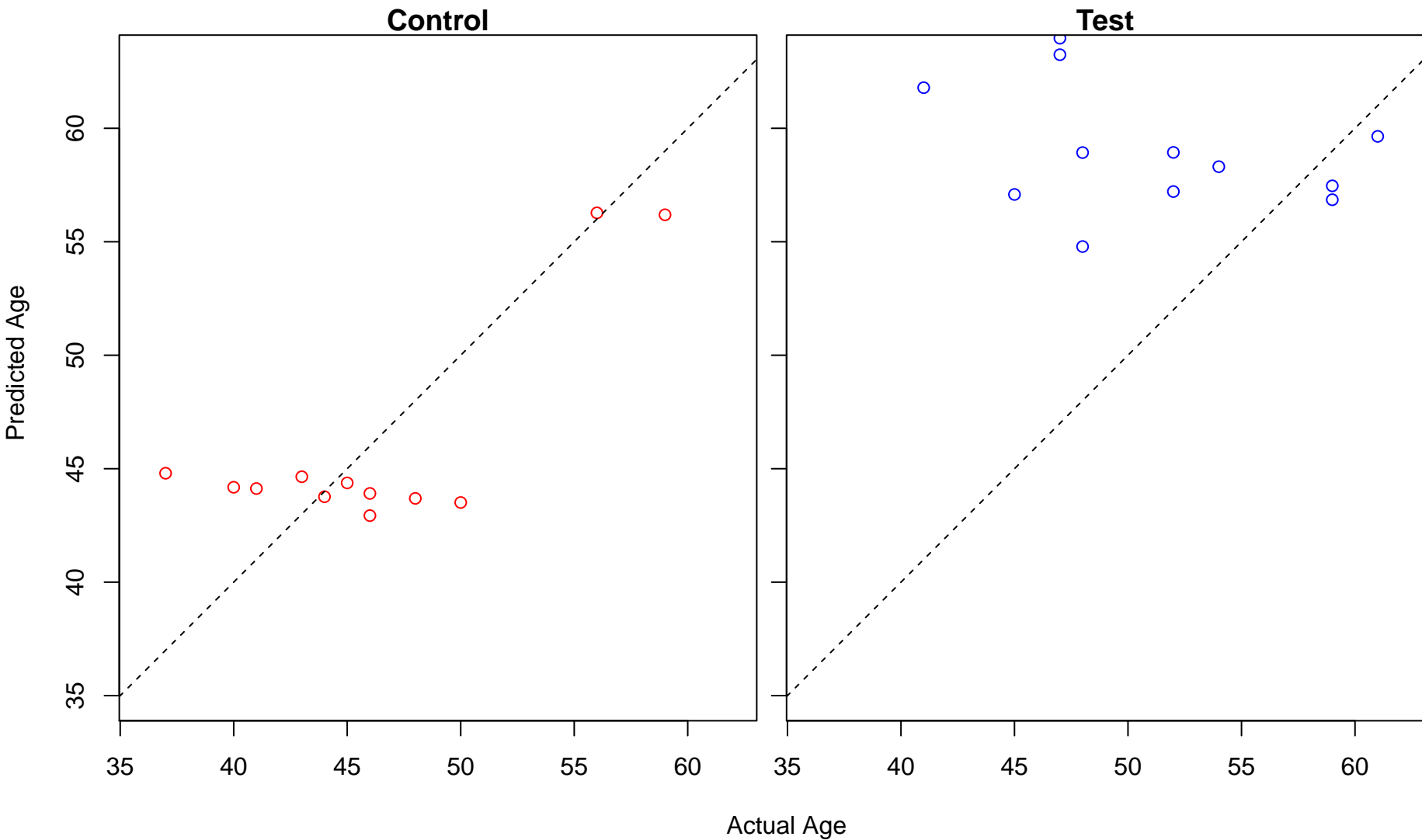
regulation of microtubule depolymerization (Score: 3.933271)



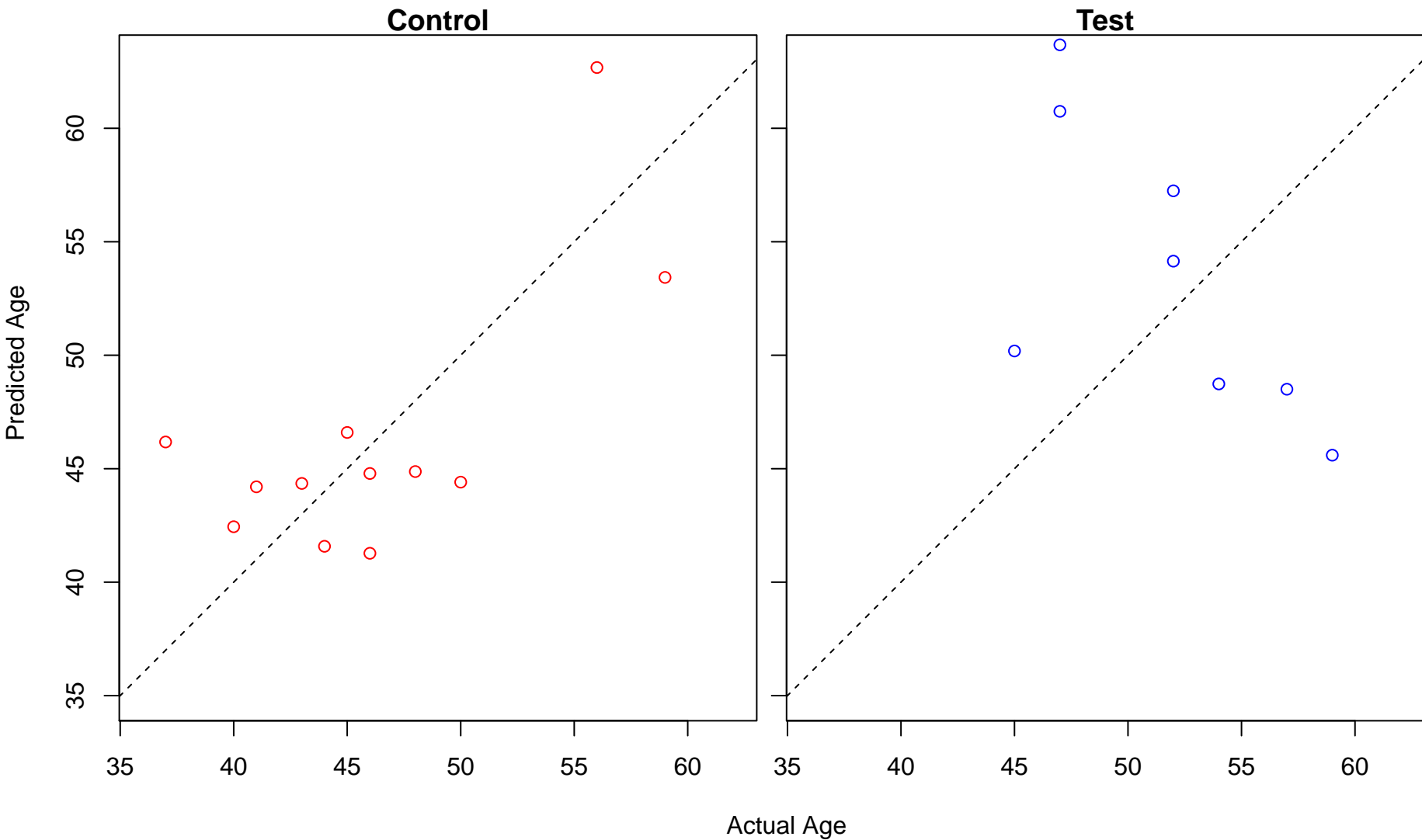
negative regulation of mitochondrion organization (Score: 3.933012)



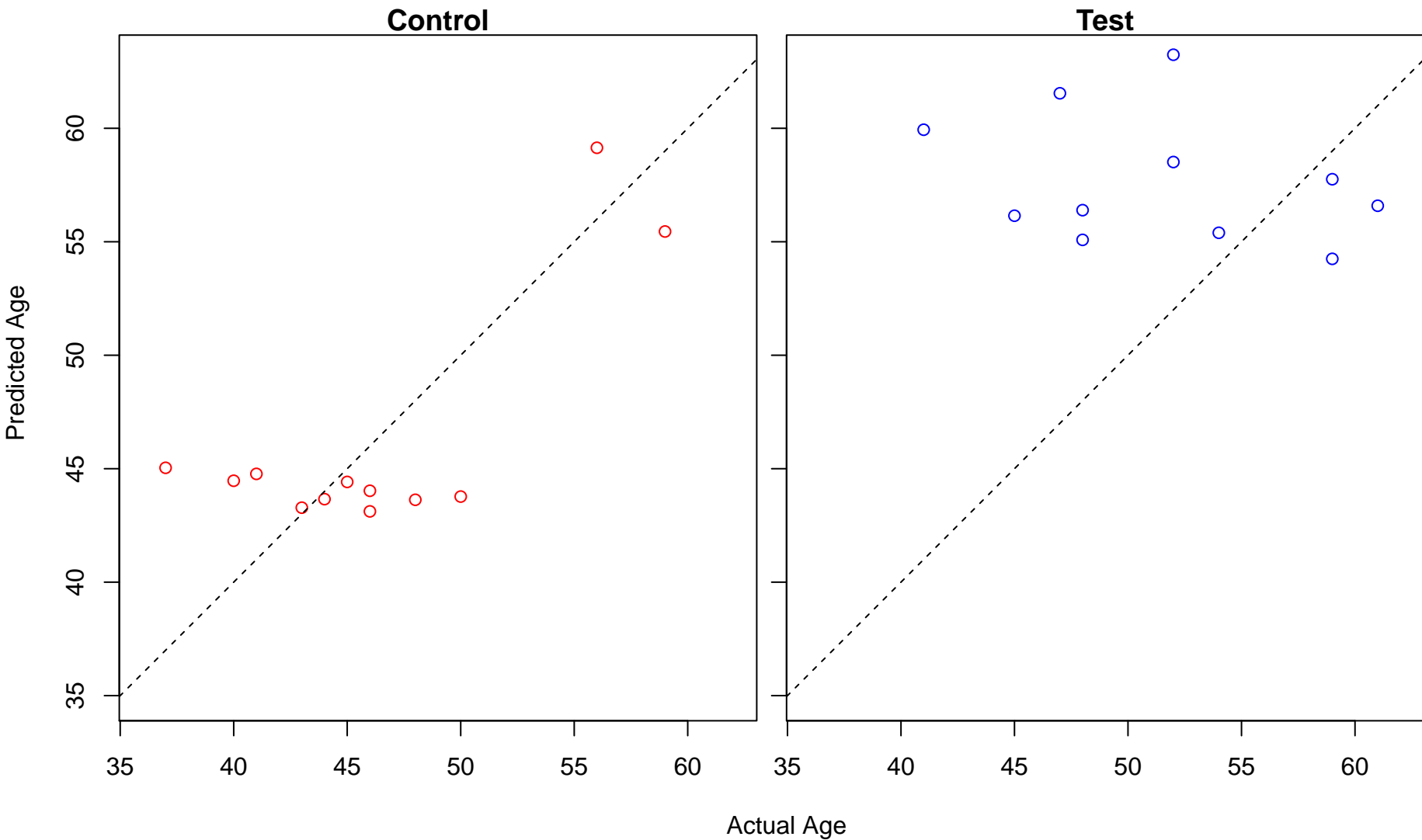
transition metal ion homeostasis (Score: 3.931361)



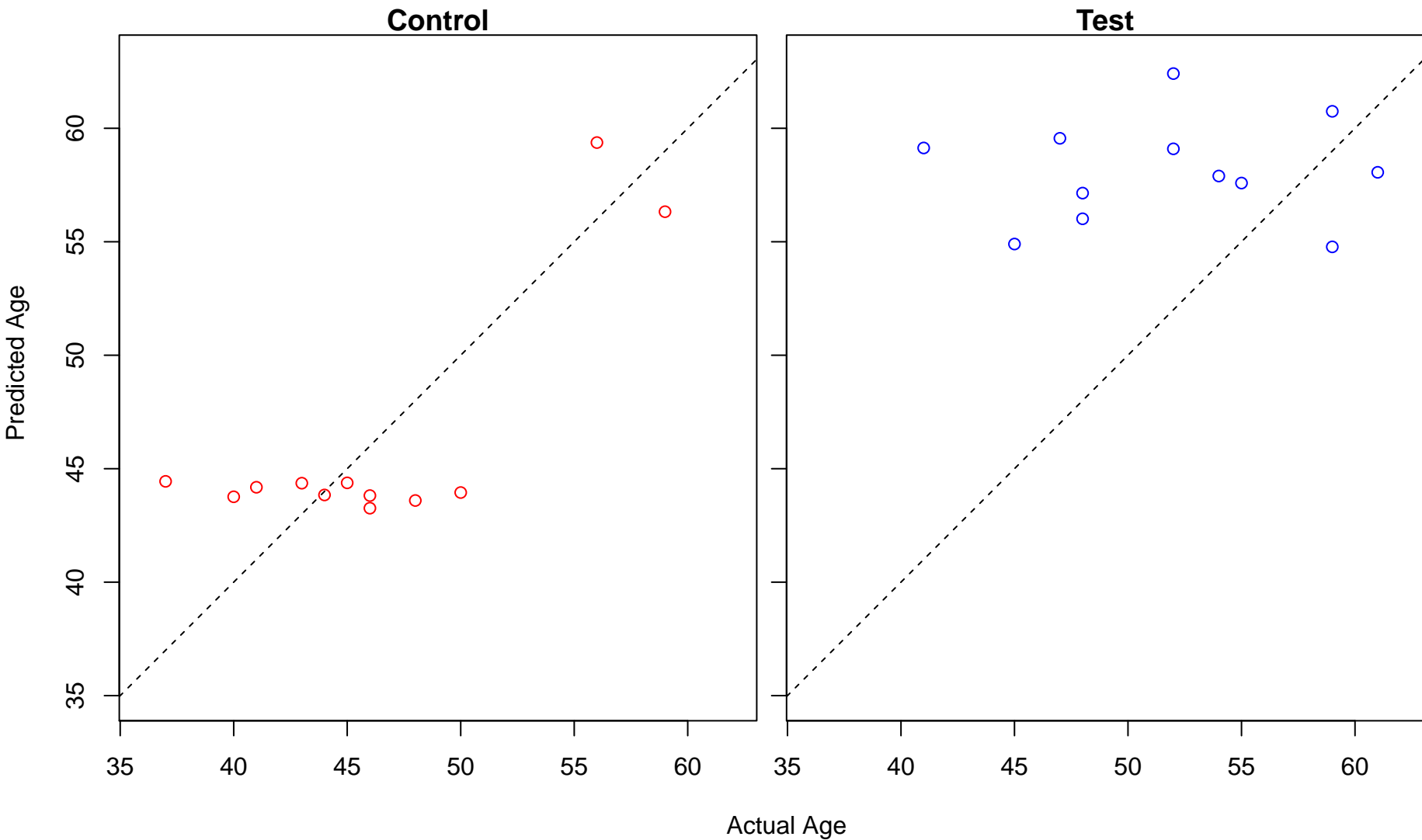
plasma membrane to endosome transport (Score: 3.928917)



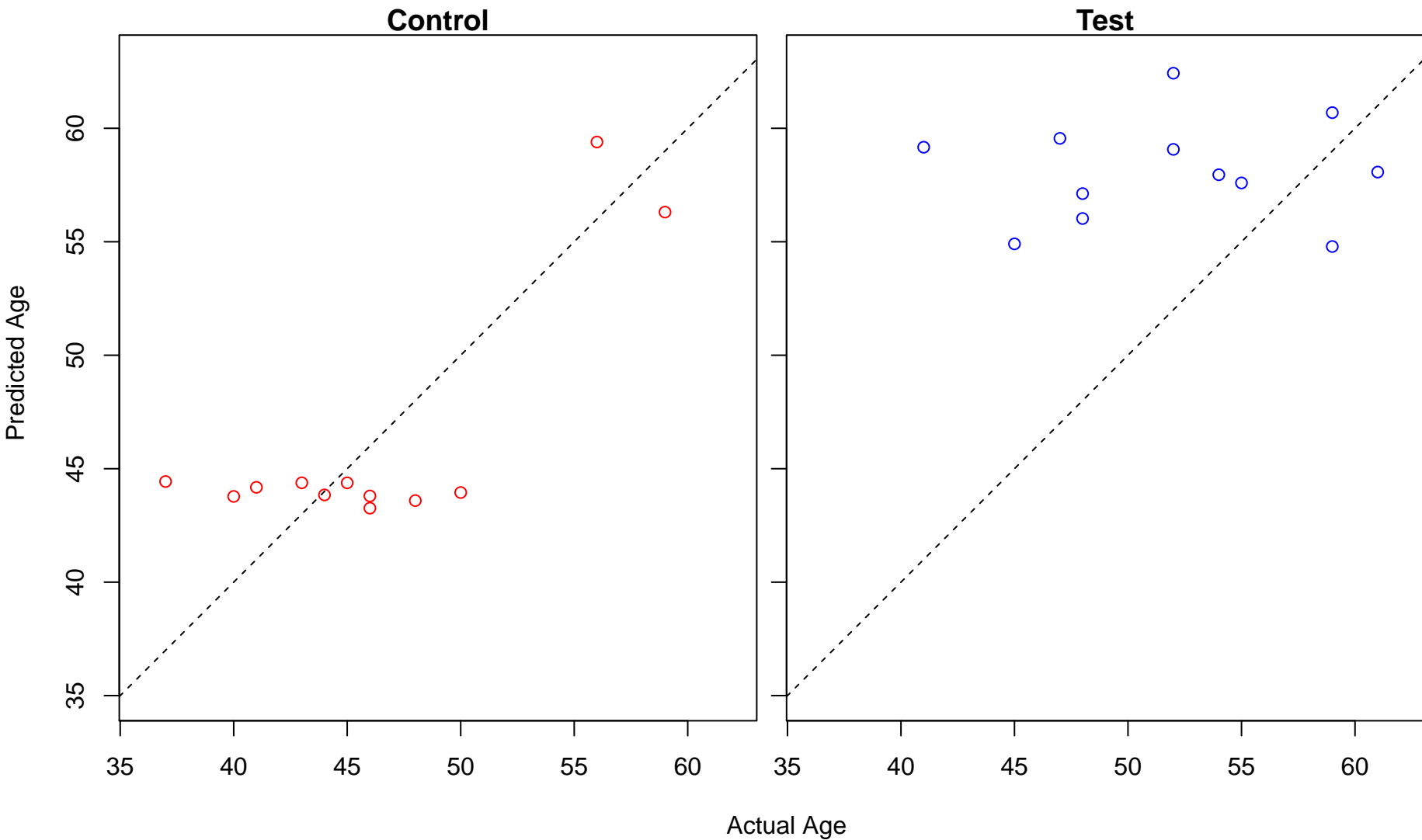
defense response to Gram-positive bacterium (Score: 3.928581)



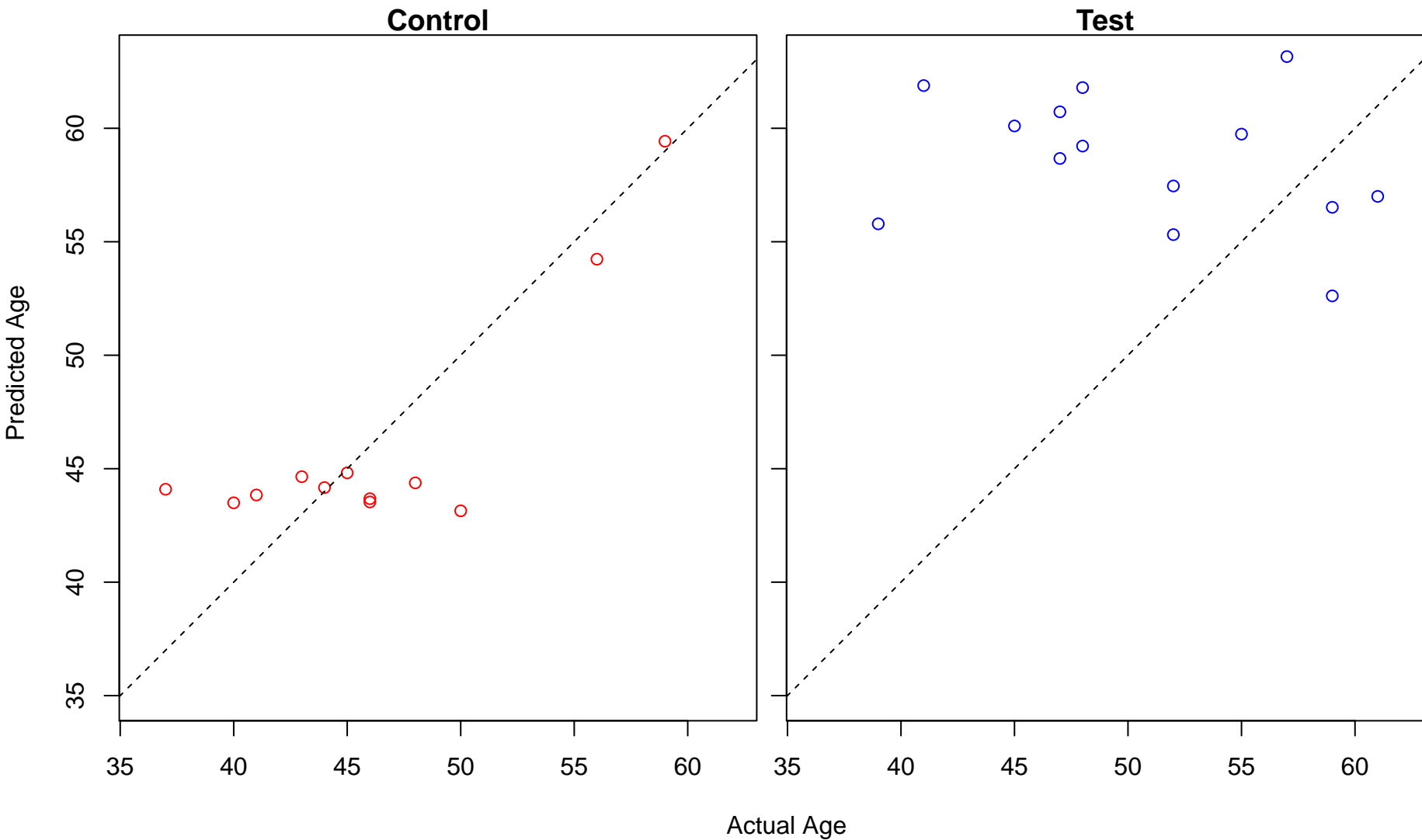
interstrand cross-link repair (Score: 3.925538)



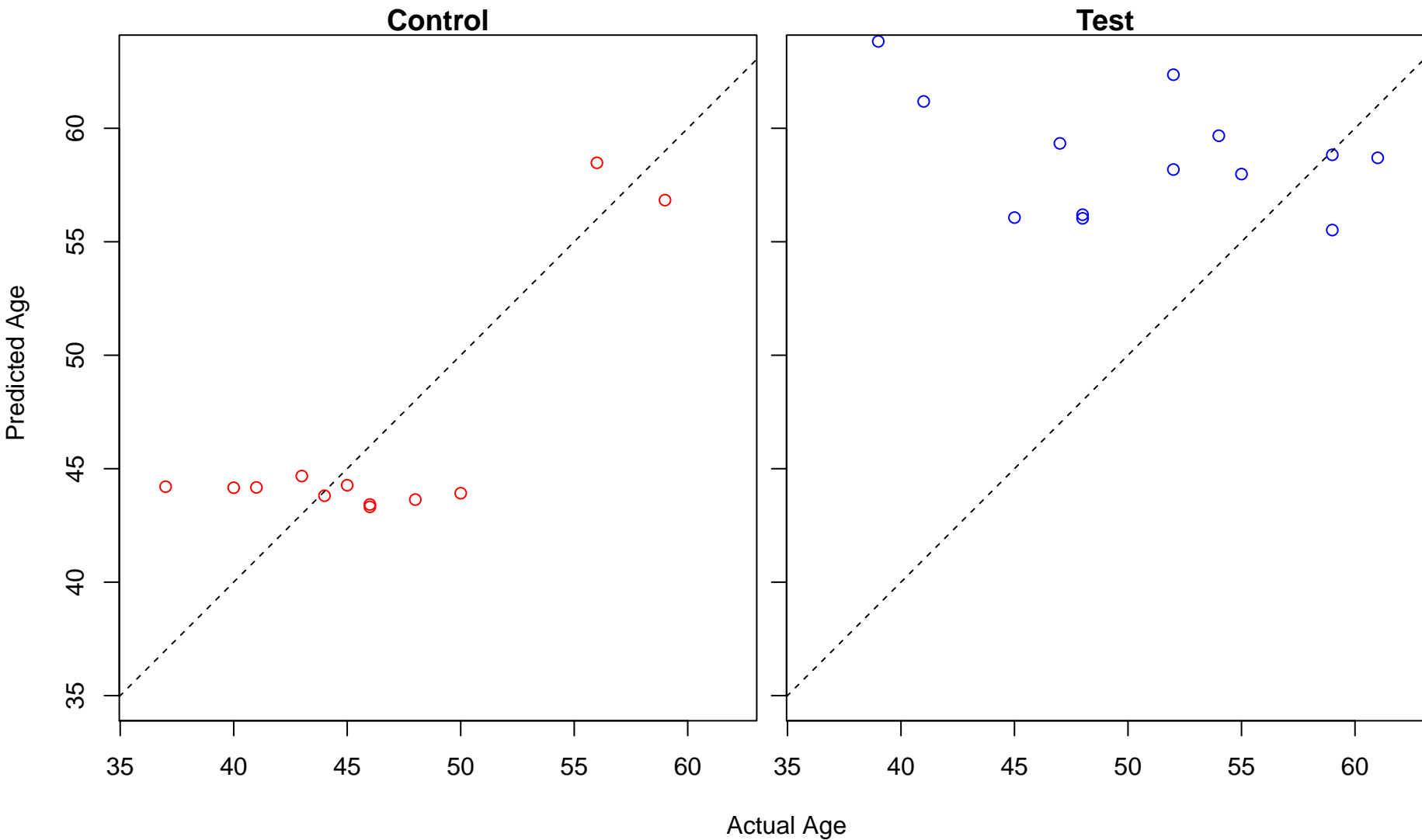
error-free translesion synthesis (Score: 3.922163)



positive regulation of interleukin-5 production (Score: 3.921176)

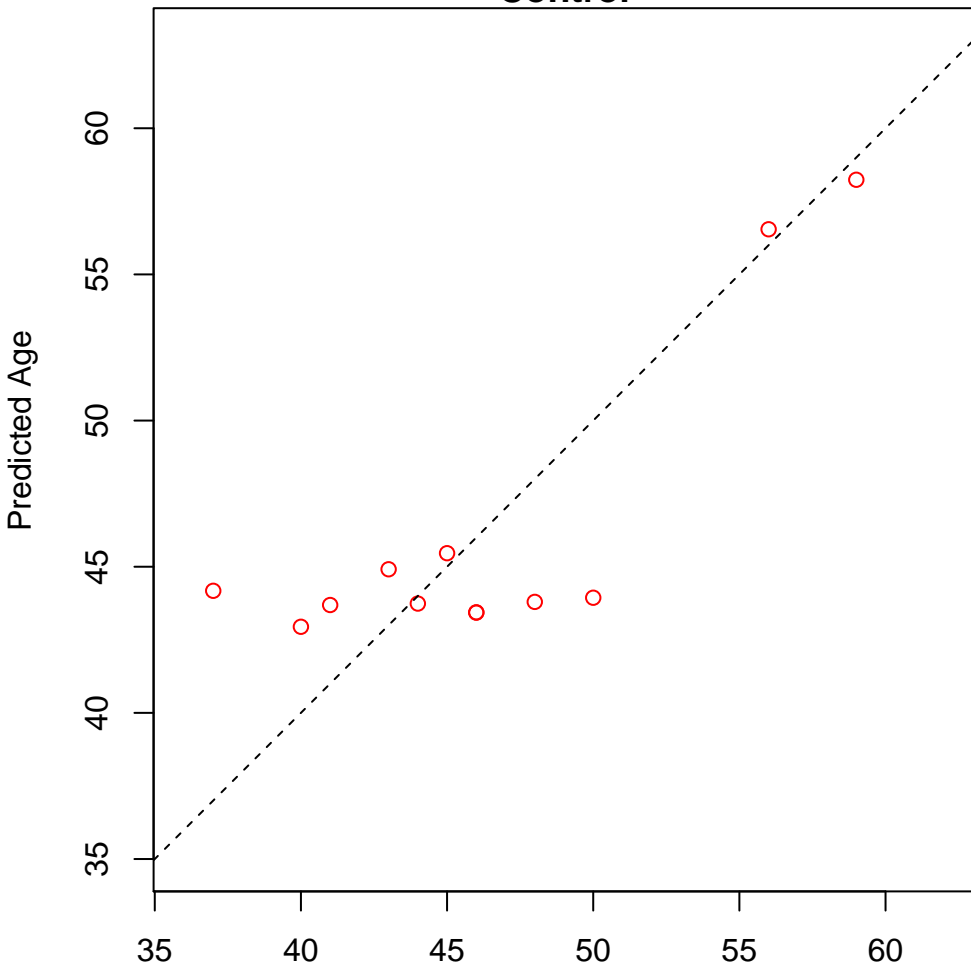


carbohydrate biosynthetic process (Score: 3.920201)

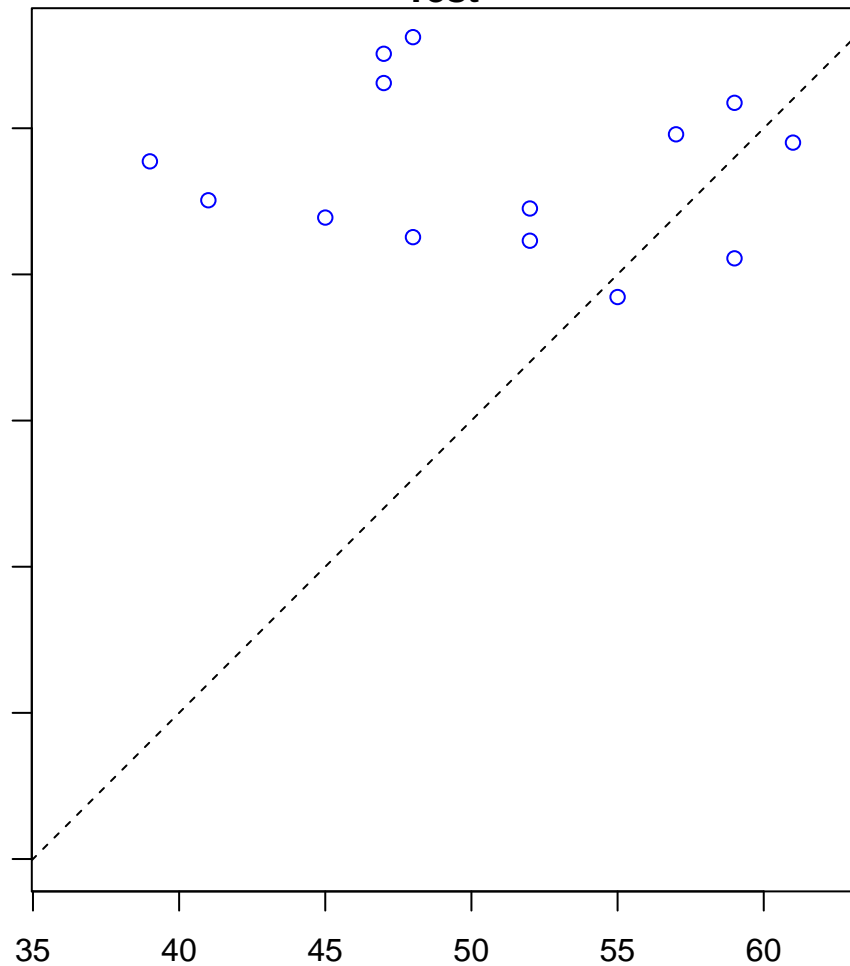


attachment of GPI anchor to protein (Score: 3.914708)

Control

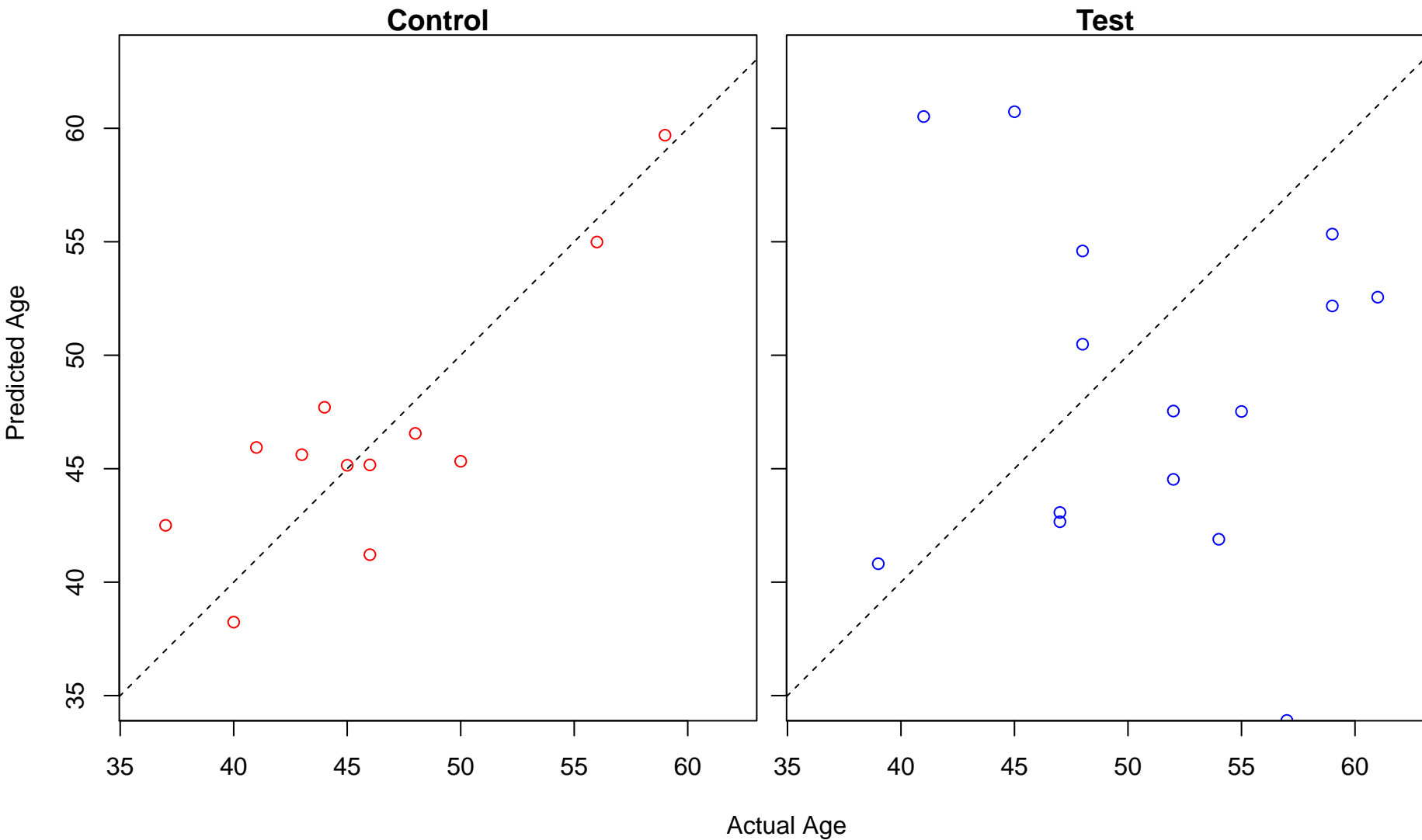


Test

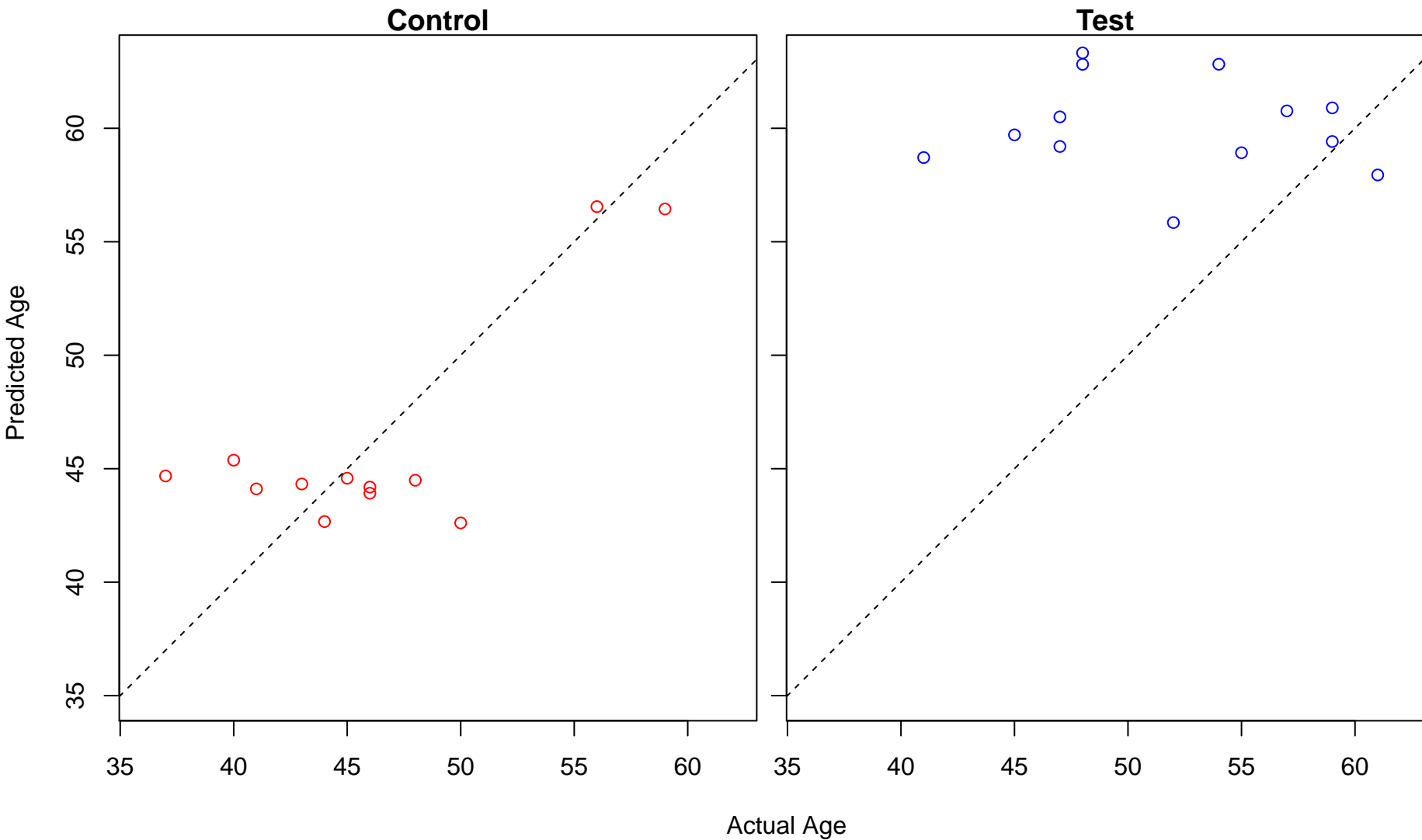


Actual Age

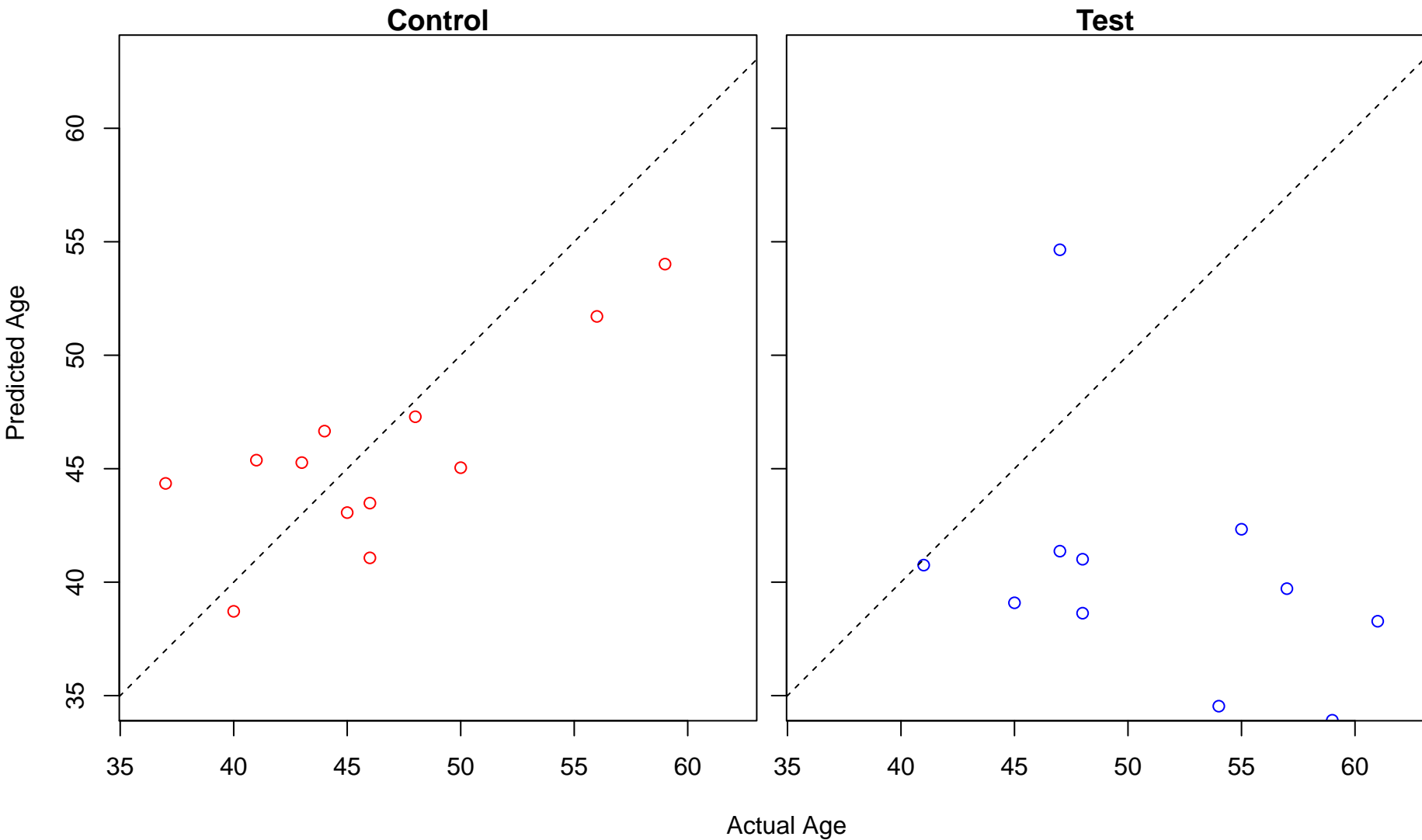
regulation of cell migration (Score: 3.914543)



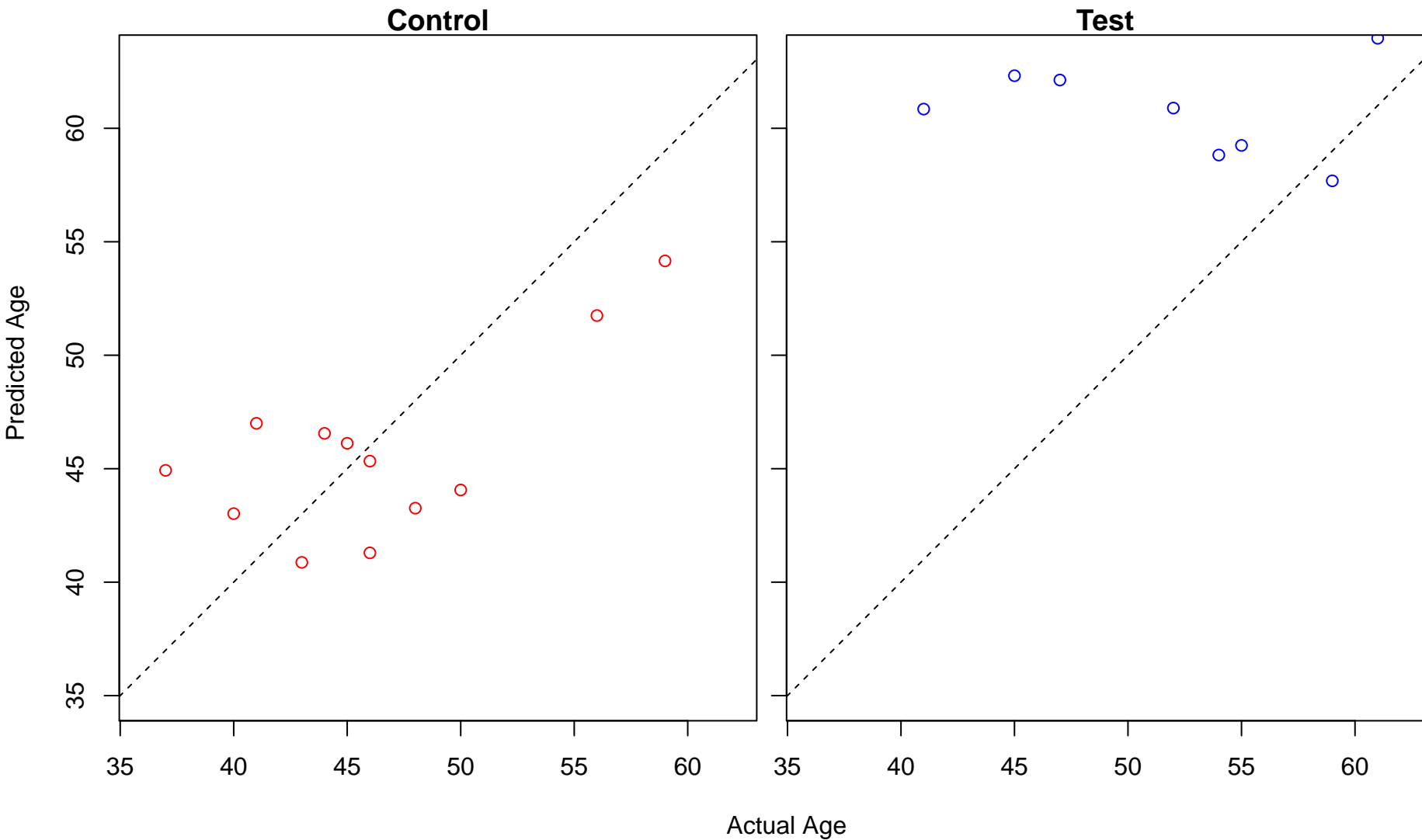
regulation of meiotic nuclear division (Score: 3.913395)



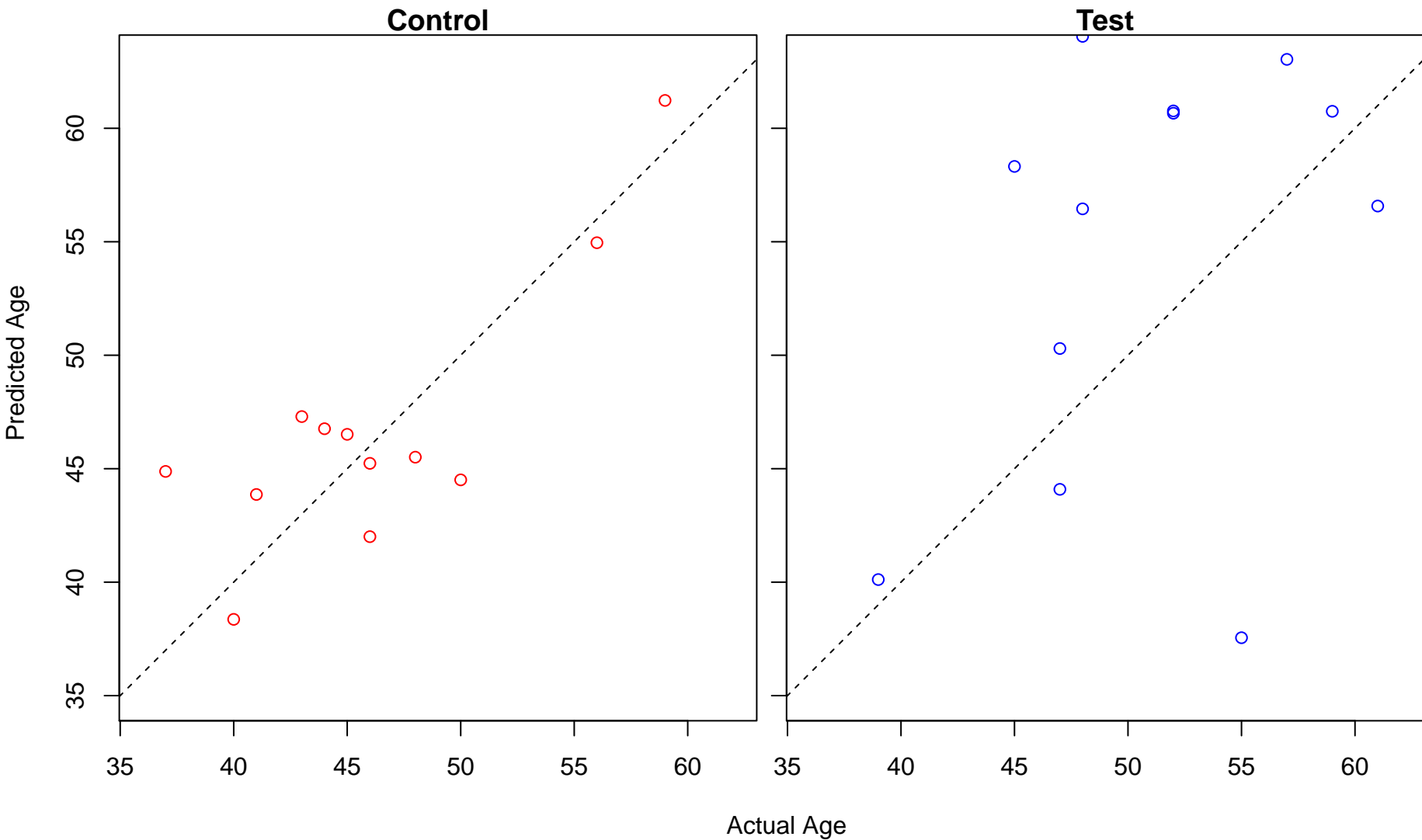
serine family amino acid metabolic process (Score: 3.909628)



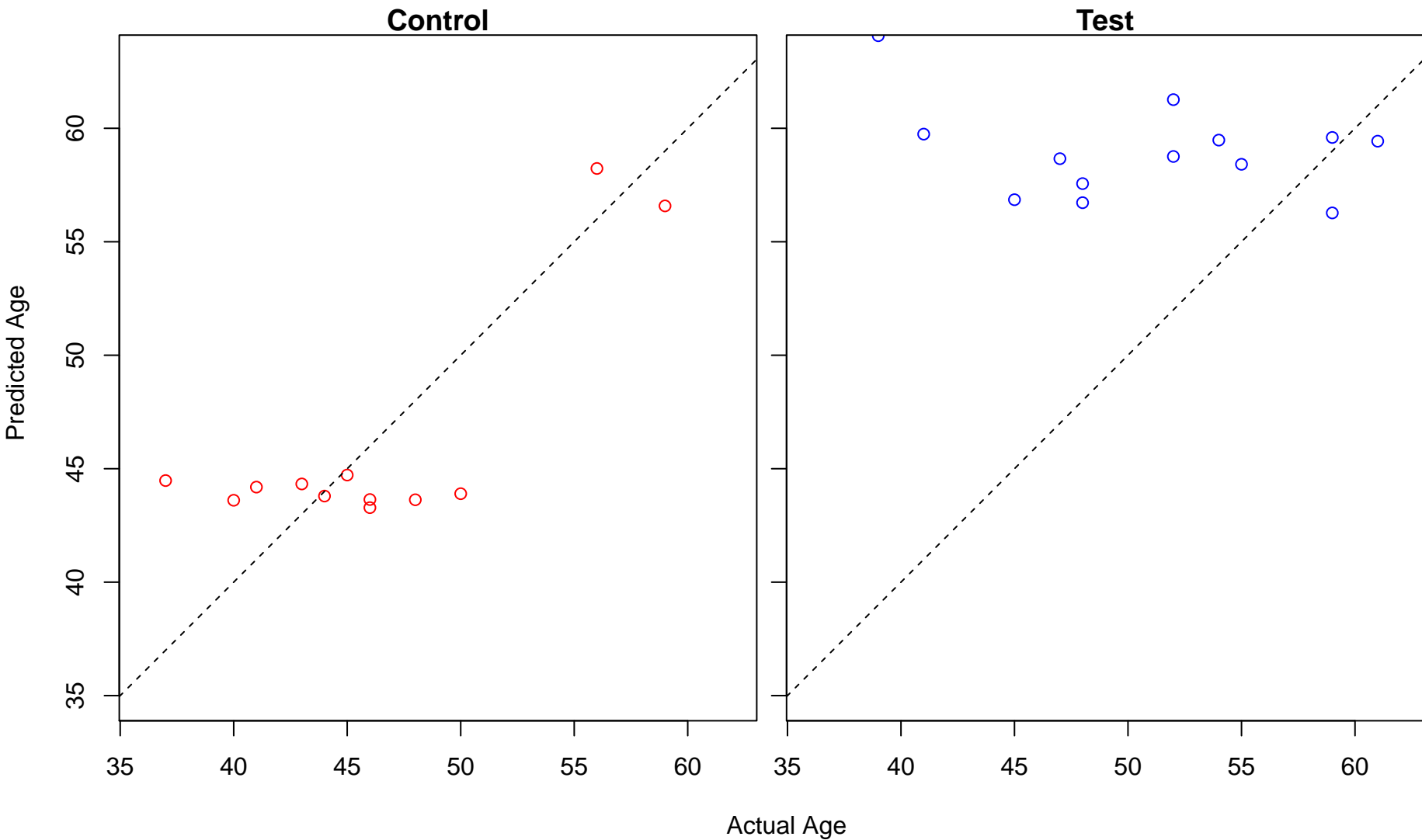
xenobiotic catabolic process (Score: 3.908638)



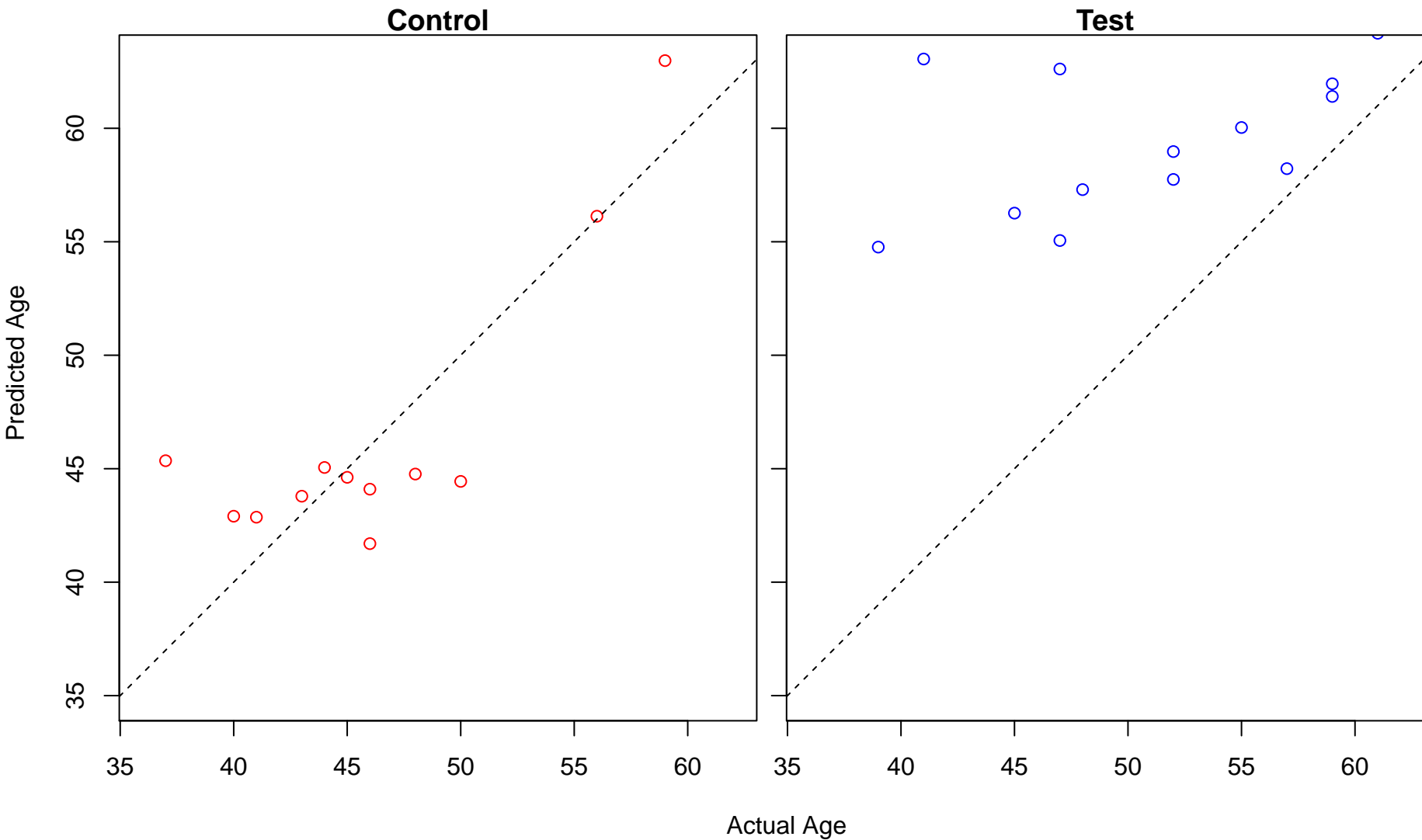
negative regulation of microtubule depolymerization (Score: 3.906942)



positive regulation of NF-kappaB transcription factor activity (Score: 3.905269)

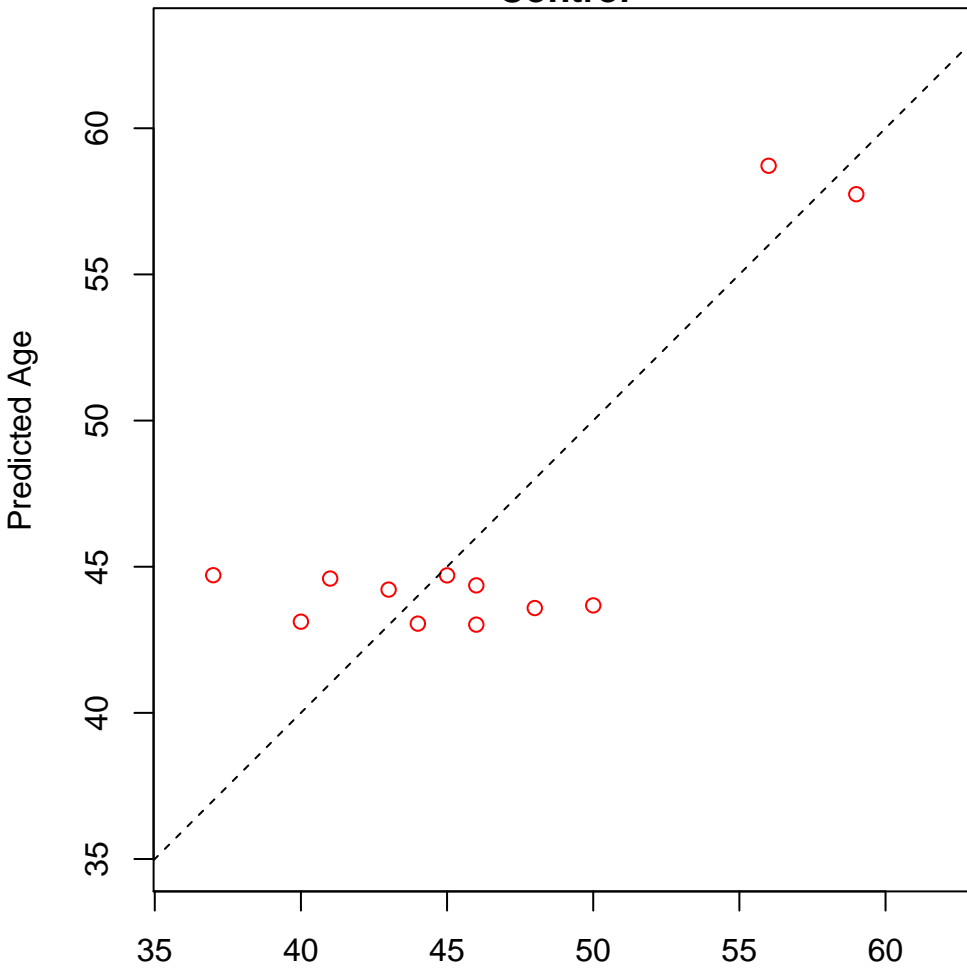


female meiotic division (Score: 3.904421)

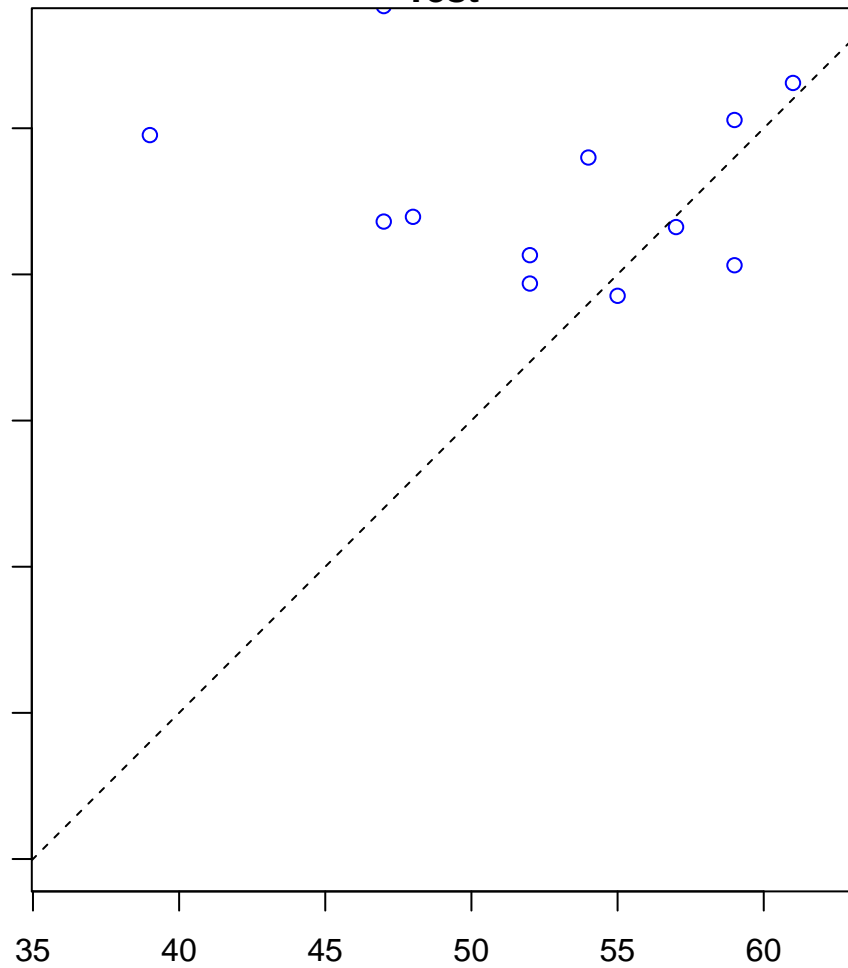


peptidyl-tyrosine autophosphorylation (Score: 3.902941)

Control

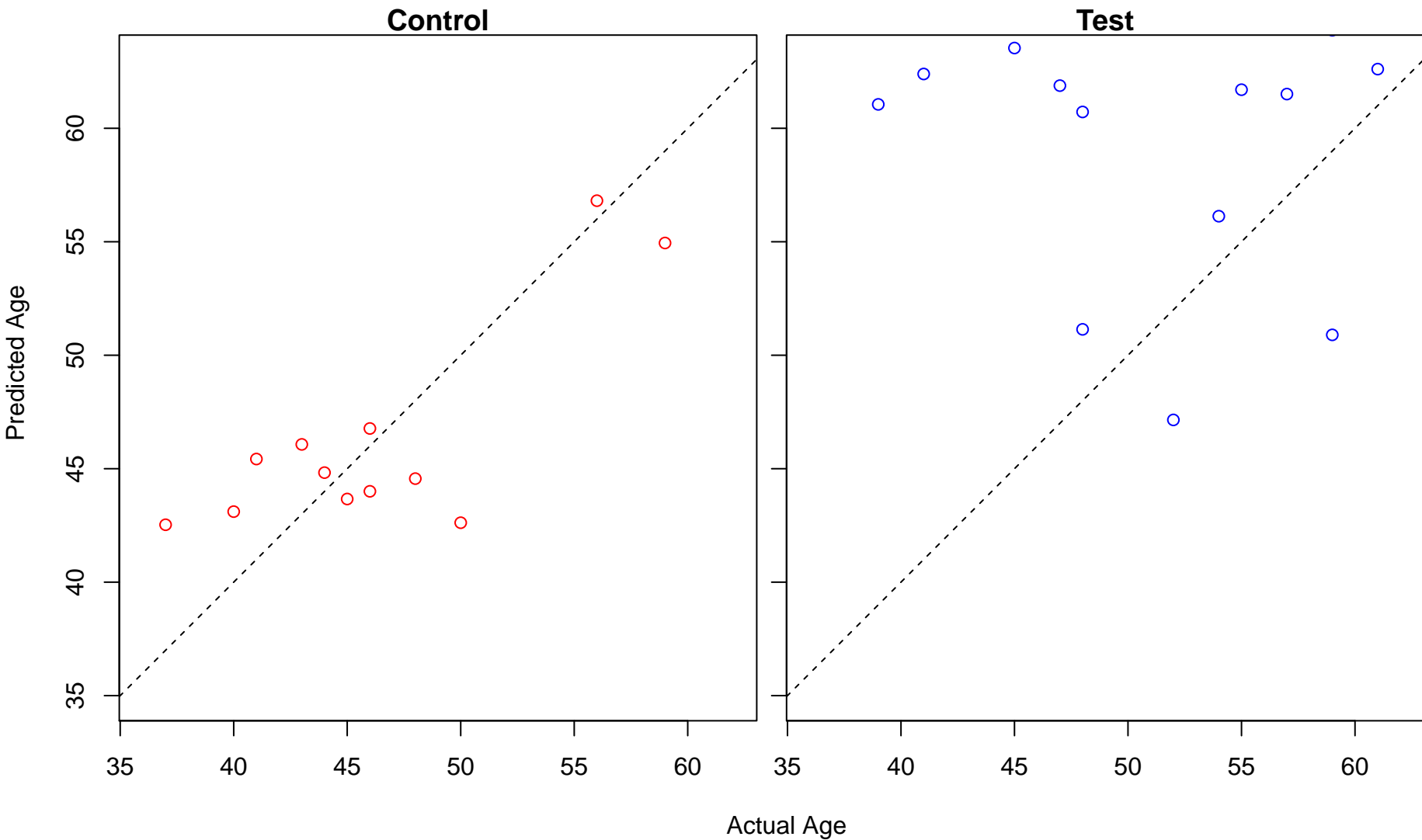


Test

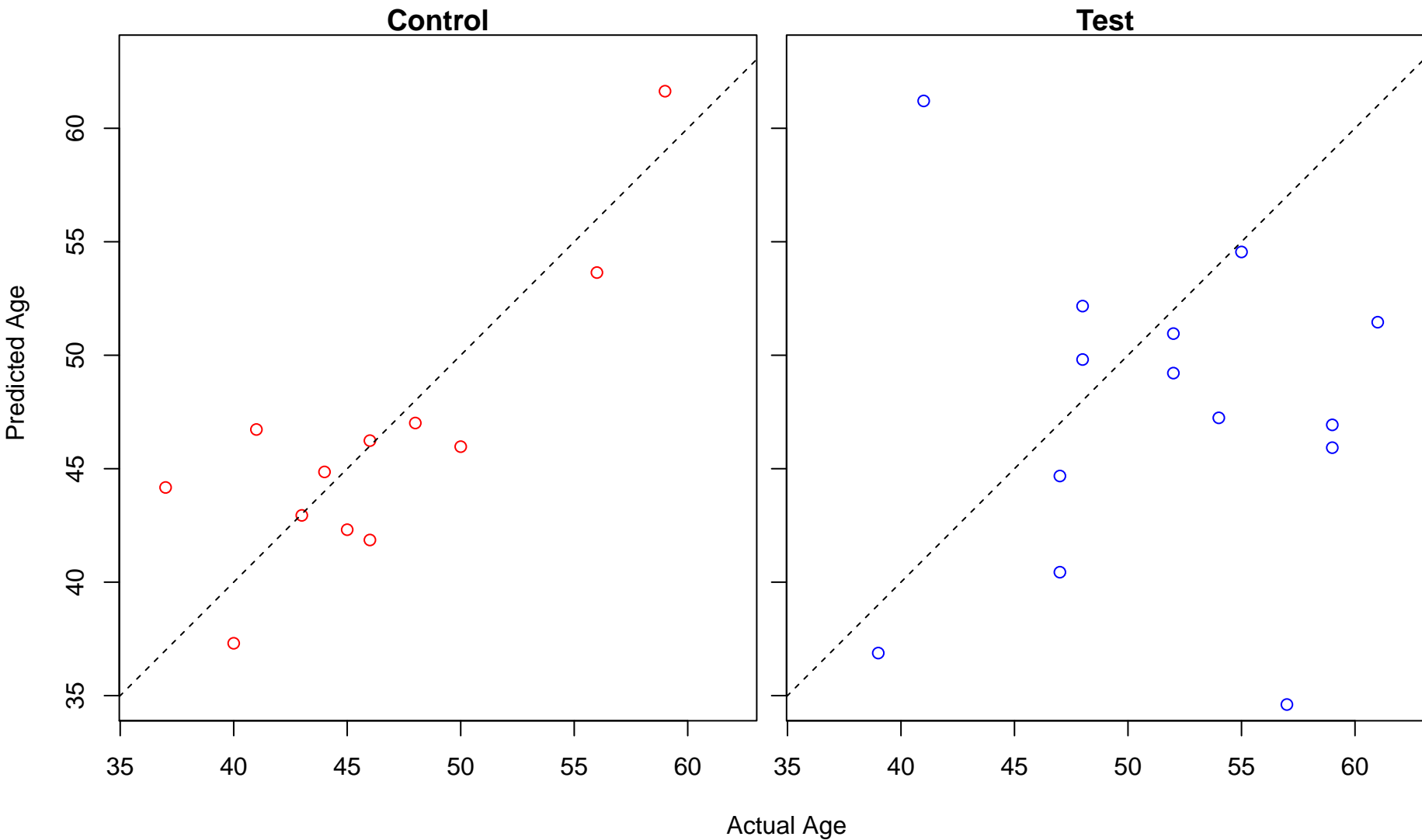


Actual Age

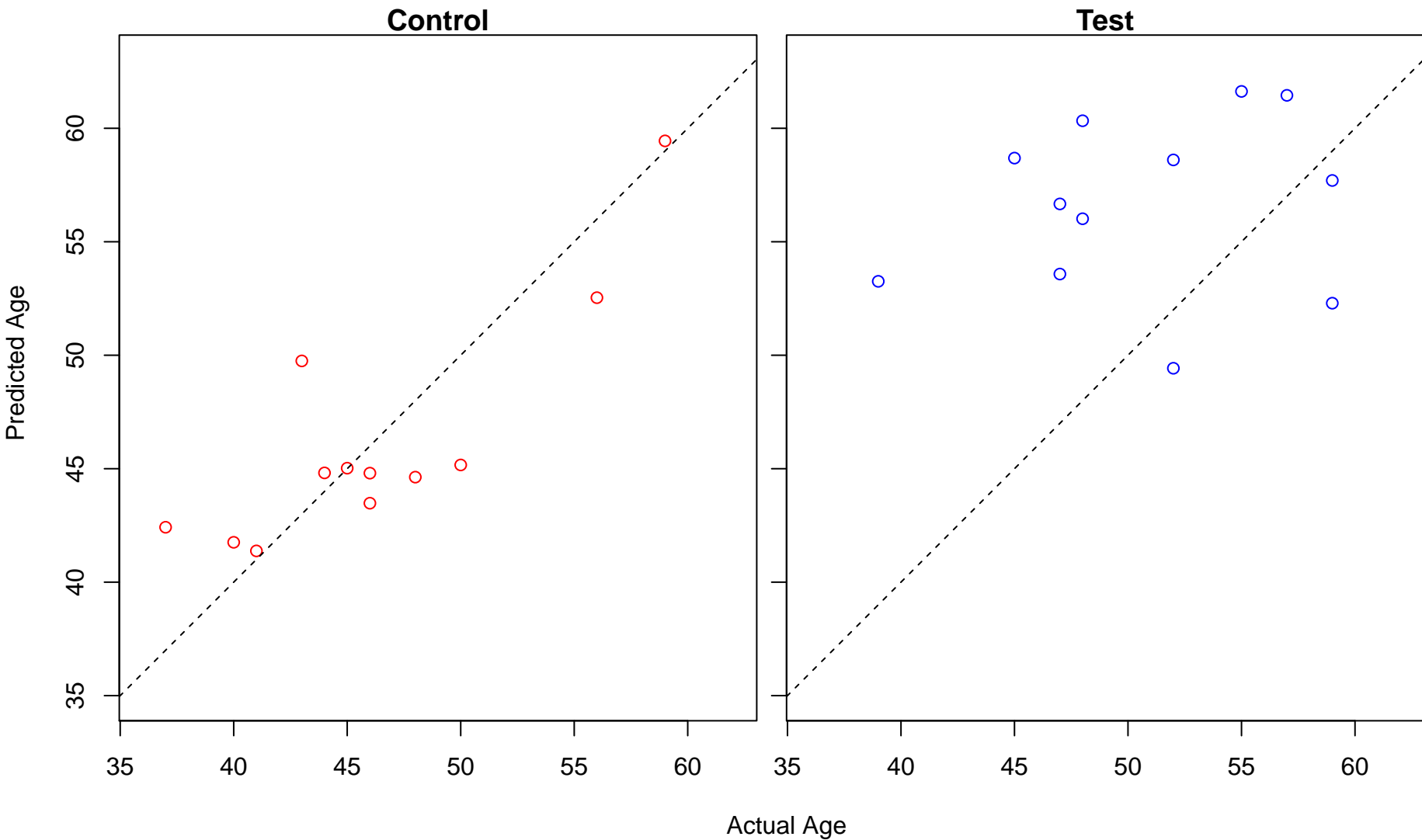
regulation of pri-miRNA transcription from RNA polymerase II promoter (Score: 3.901210)



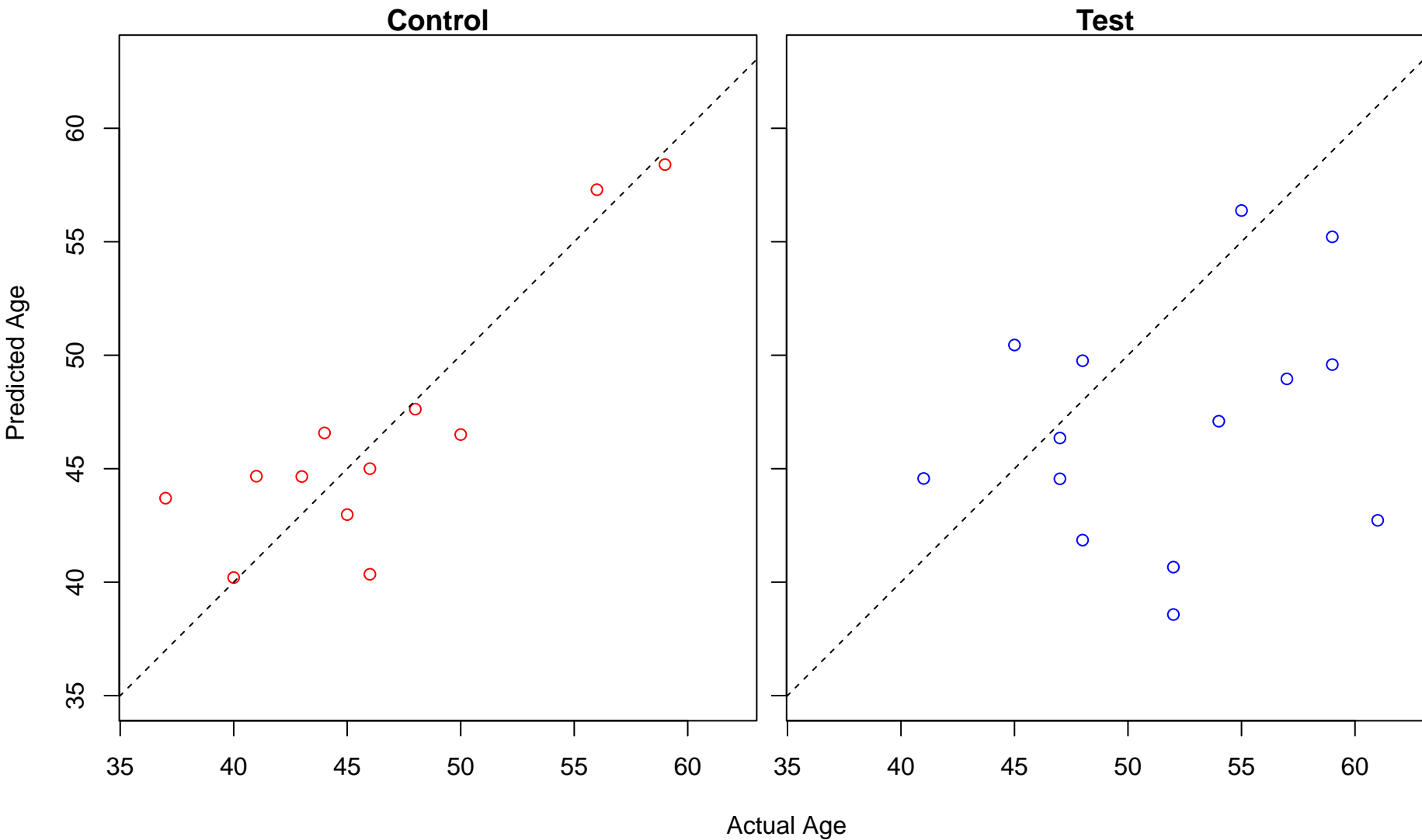
cofactor transport (Score: 3.899693)



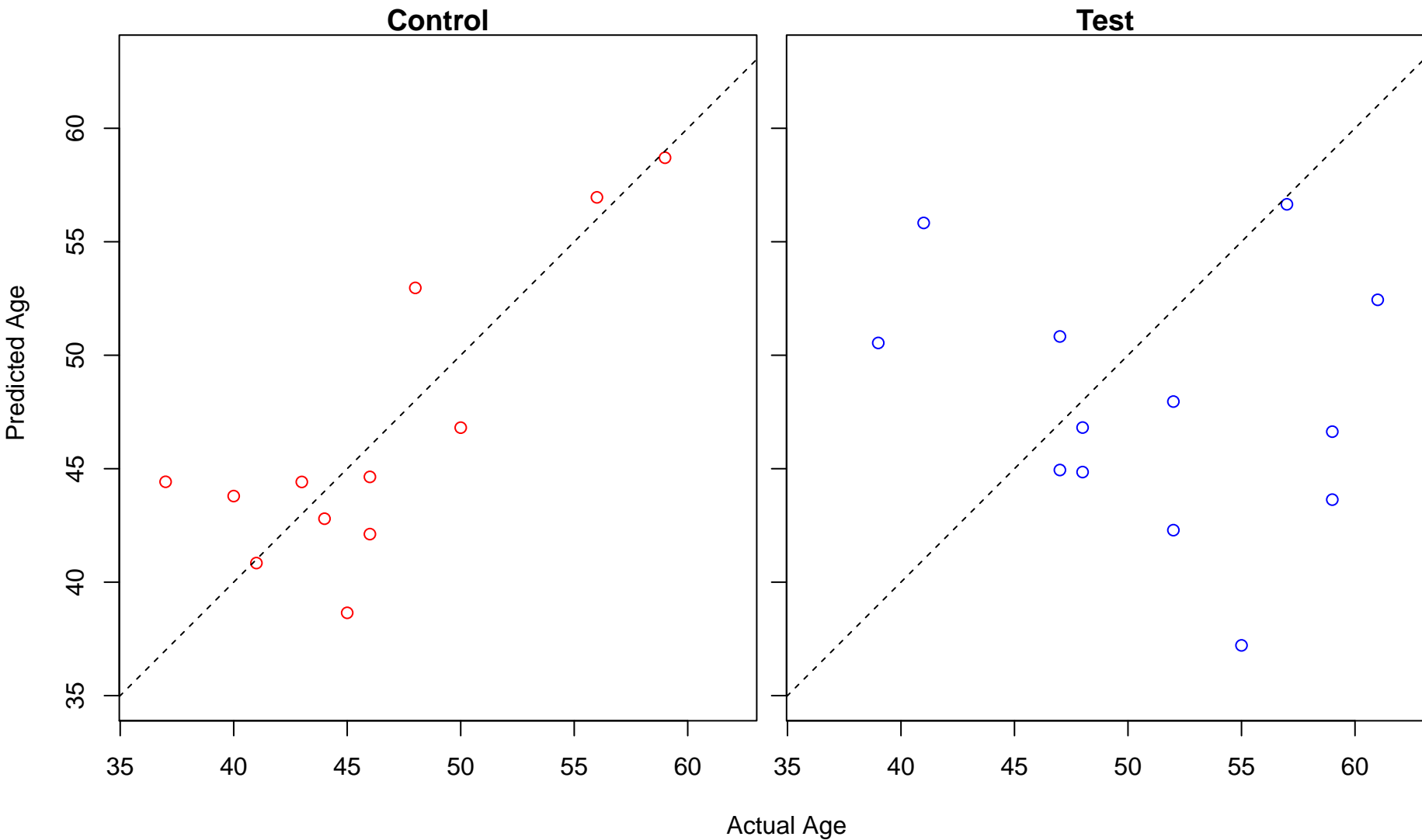
response to growth hormone (Score: 3.898880)



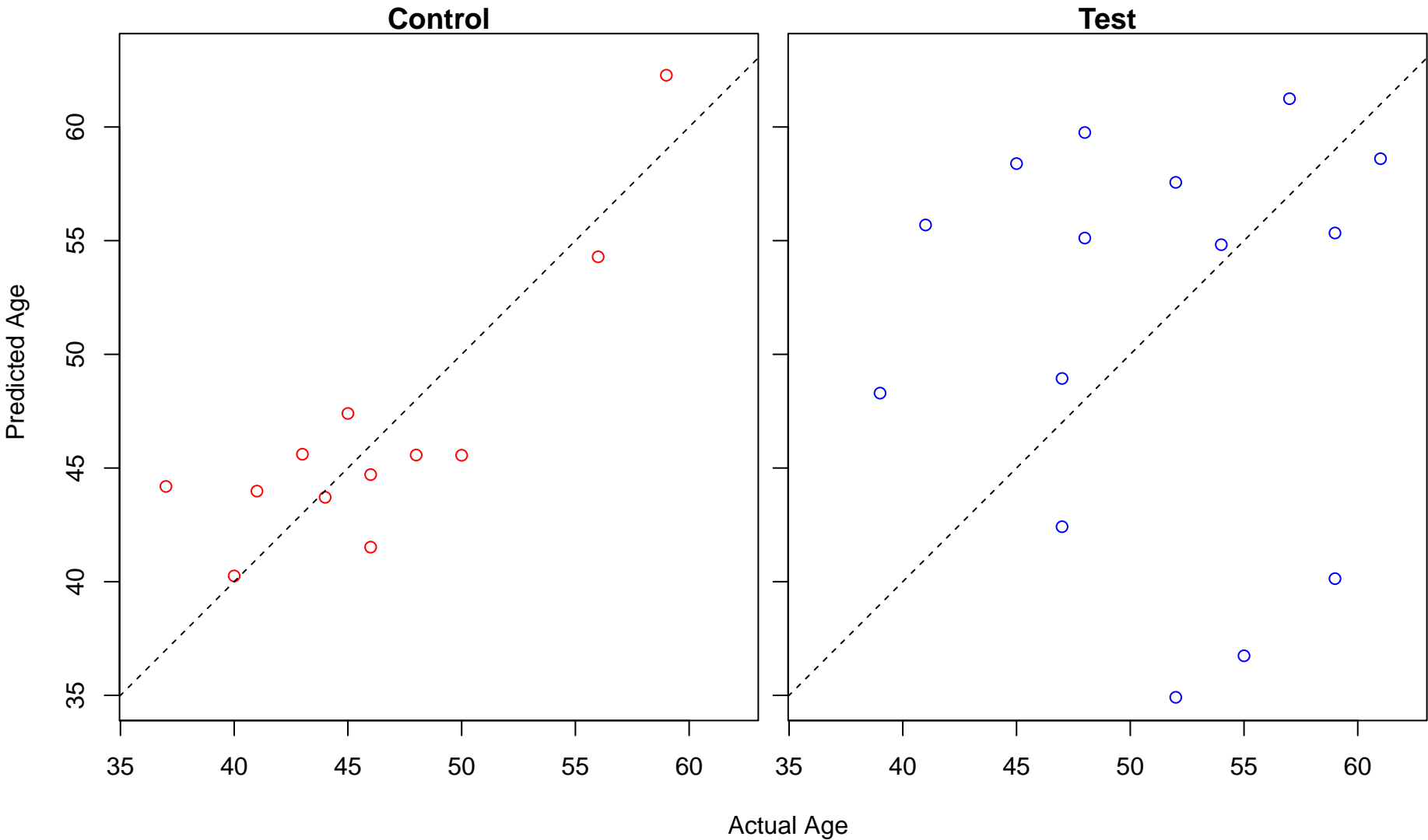
negative regulation of cellular component organization (Score: 3.898175)



membrane depolarization during action potential (Score: 3.895881)

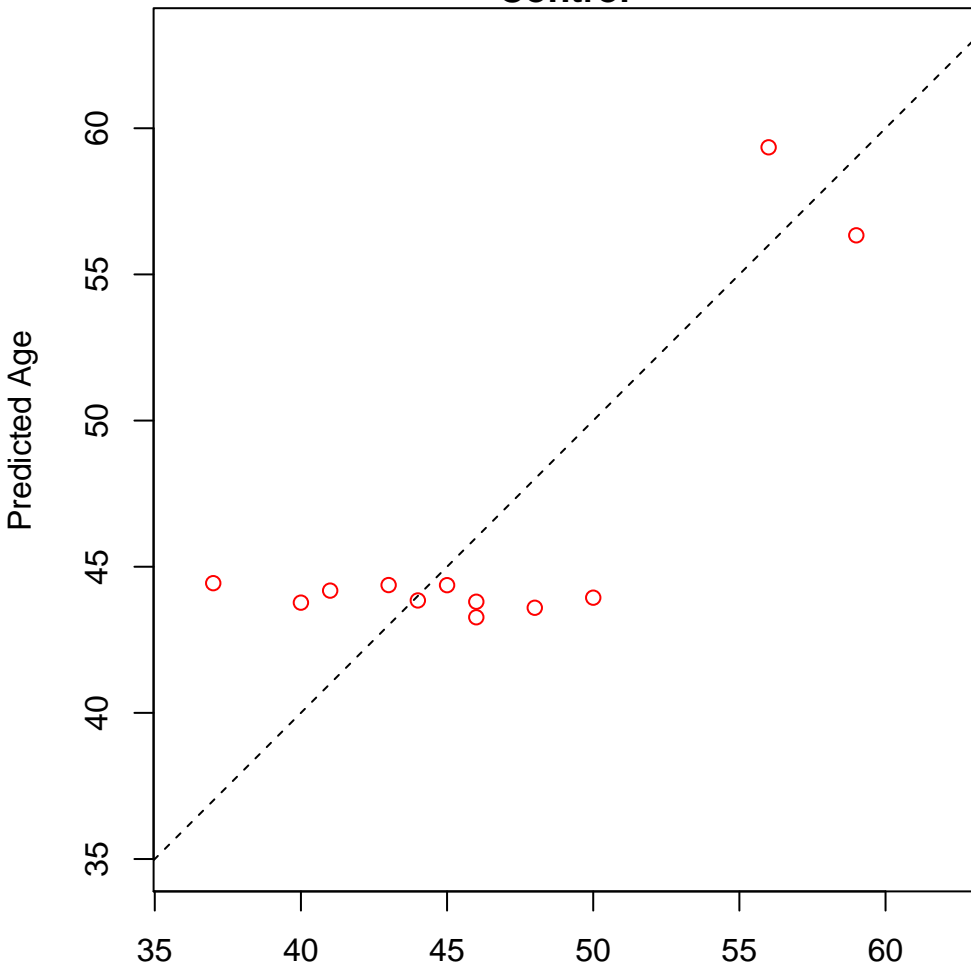


regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 3.893673)

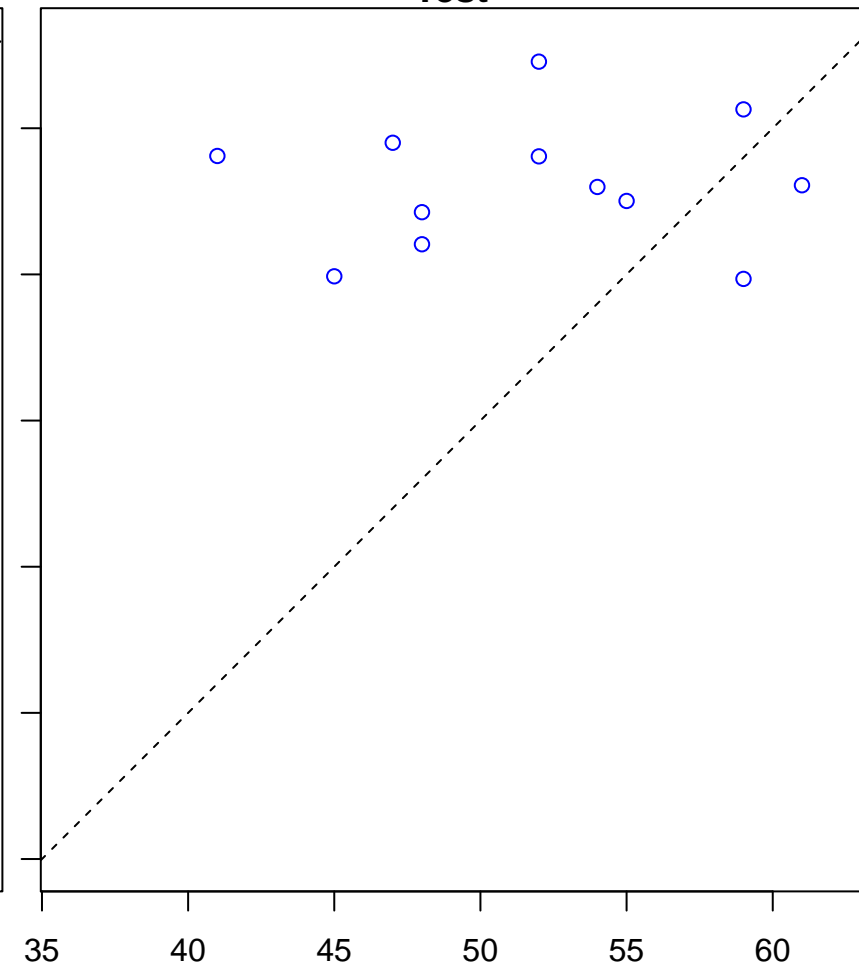


nucleotide–excision repair, DNA incision (Score: 3.892739)

Control

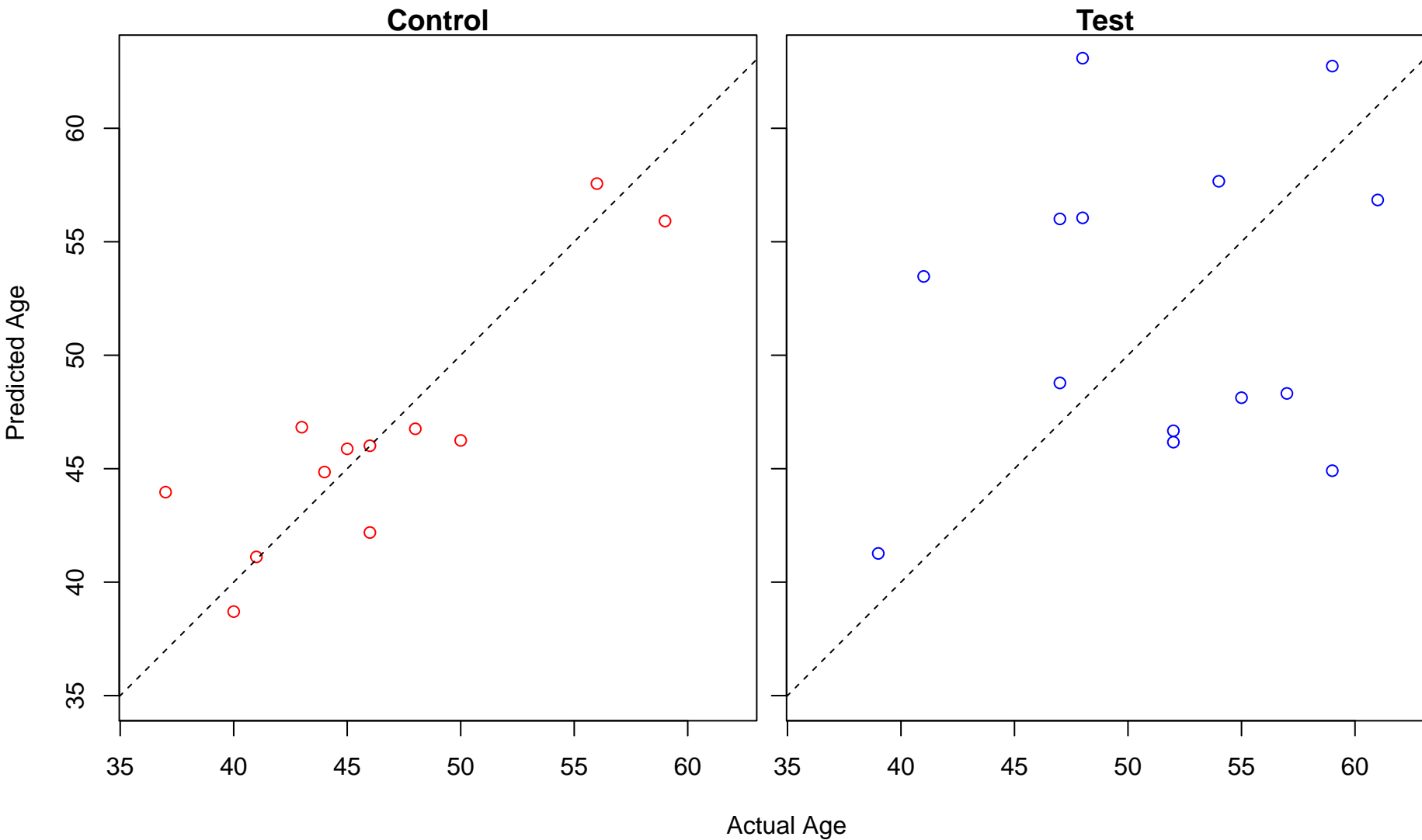


Test

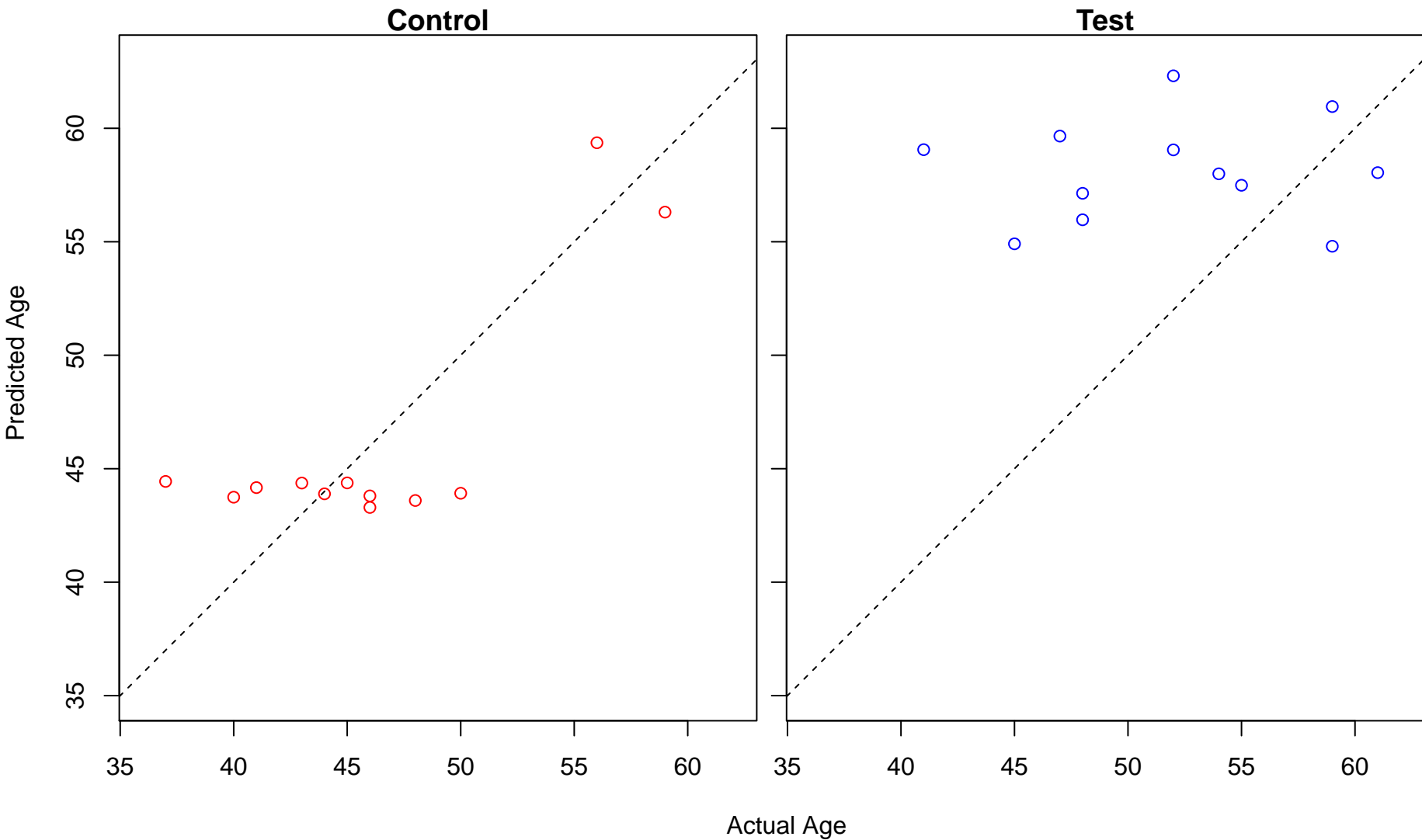


Actual Age

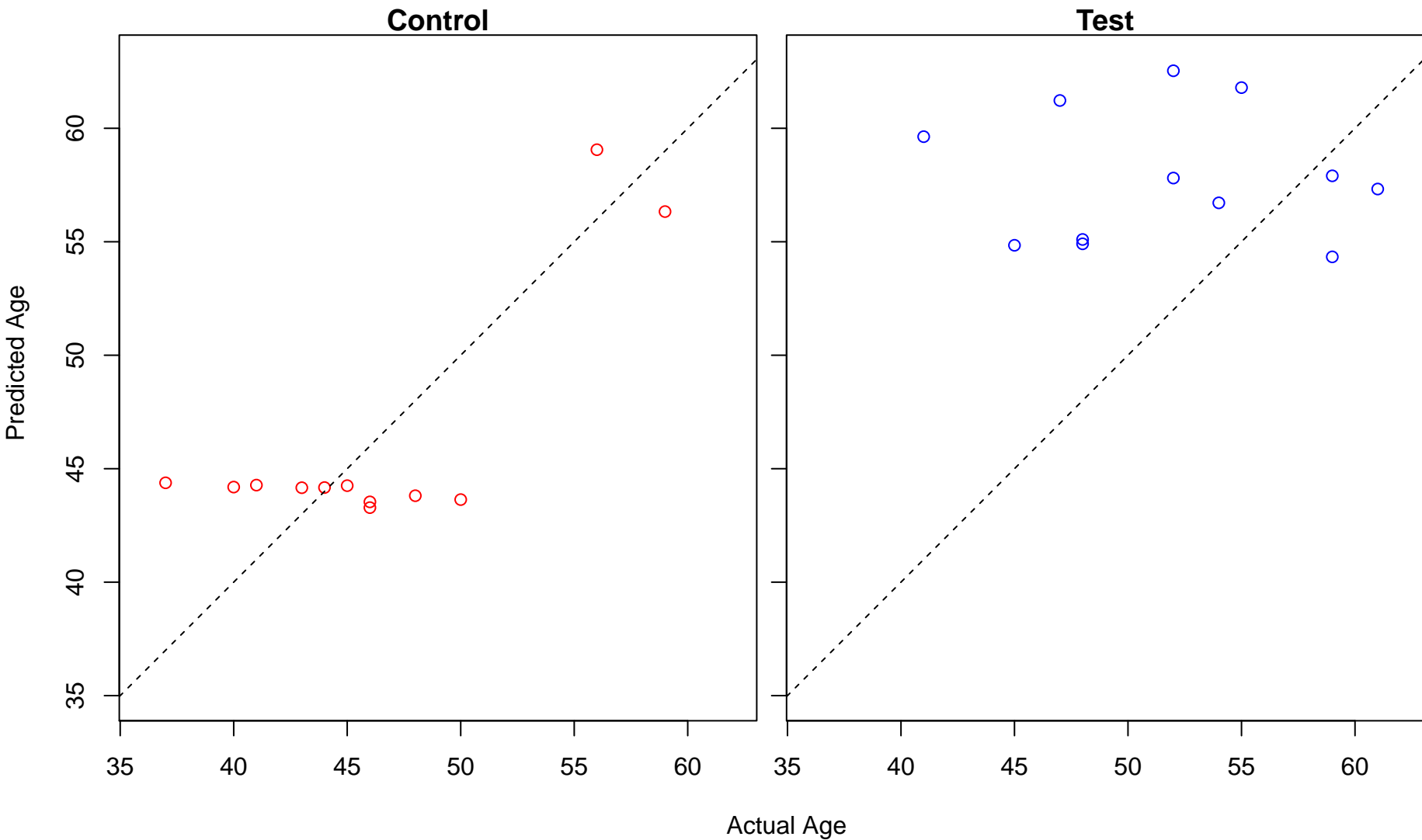
regulation of cell growth (Score: 3.890895)



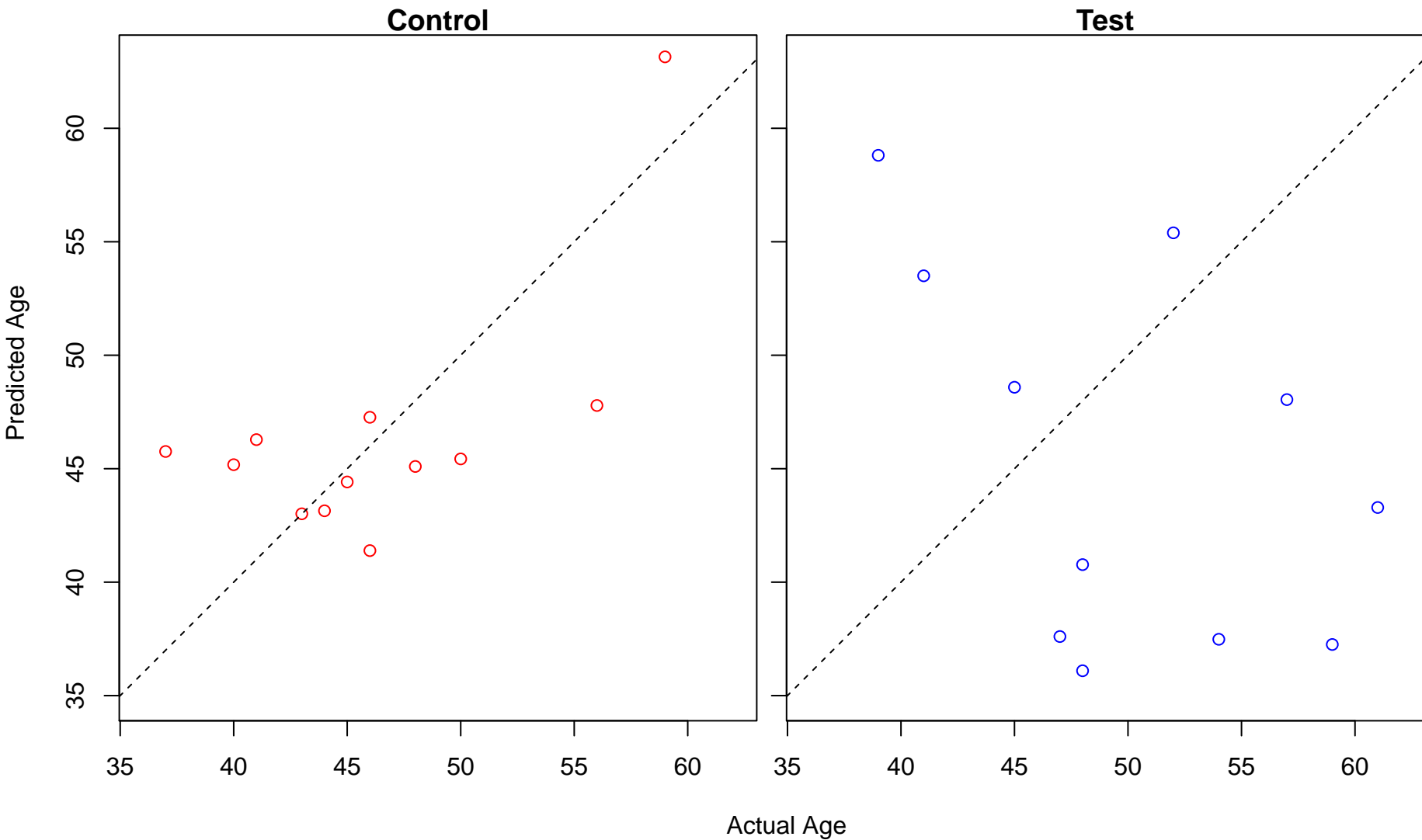
JNK cascade (Score: 3.889562)



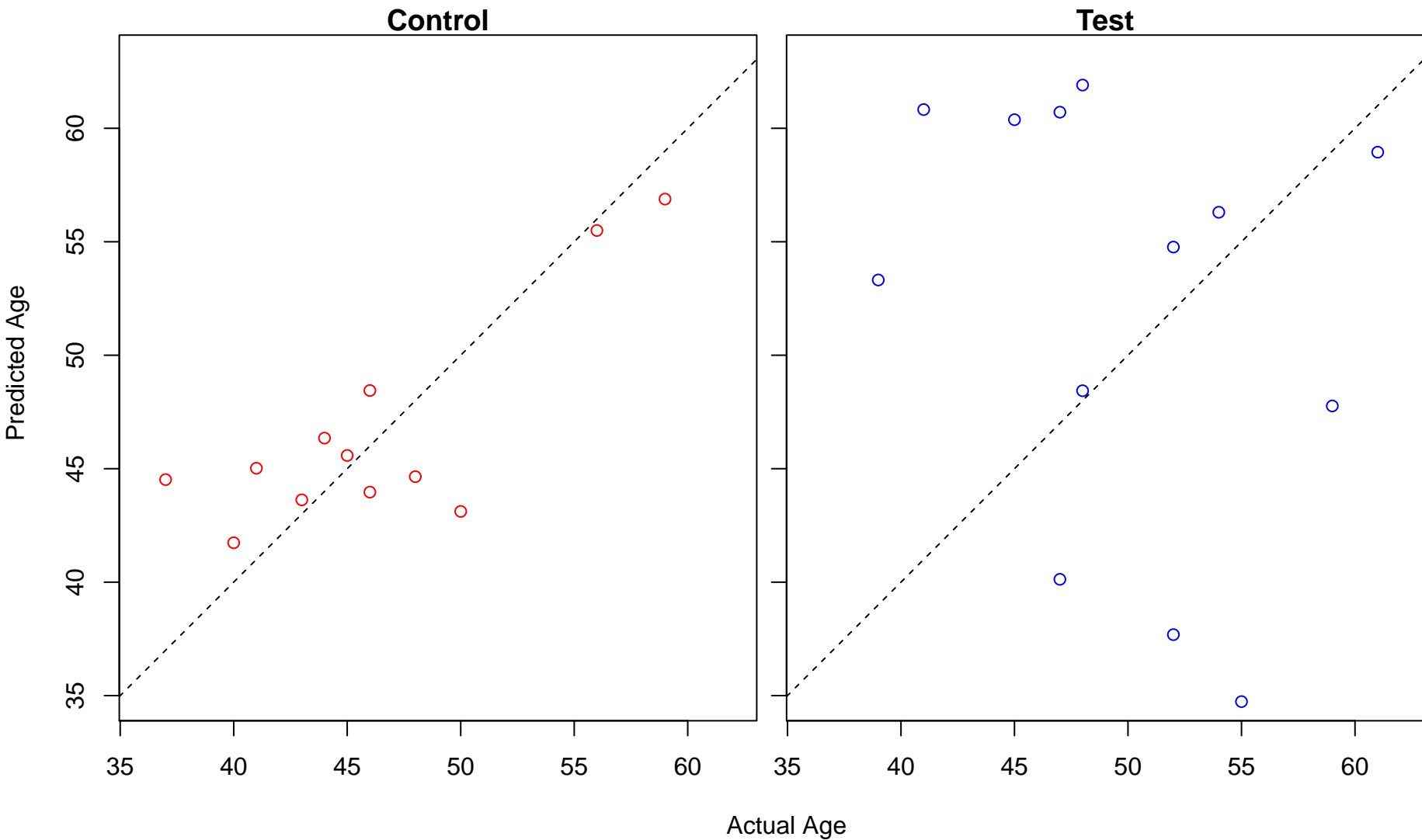
regulation of epidermal growth factor receptor signaling pathway (Score: 3.885596)



sphingoid biosynthetic process (Score: 3.881805)

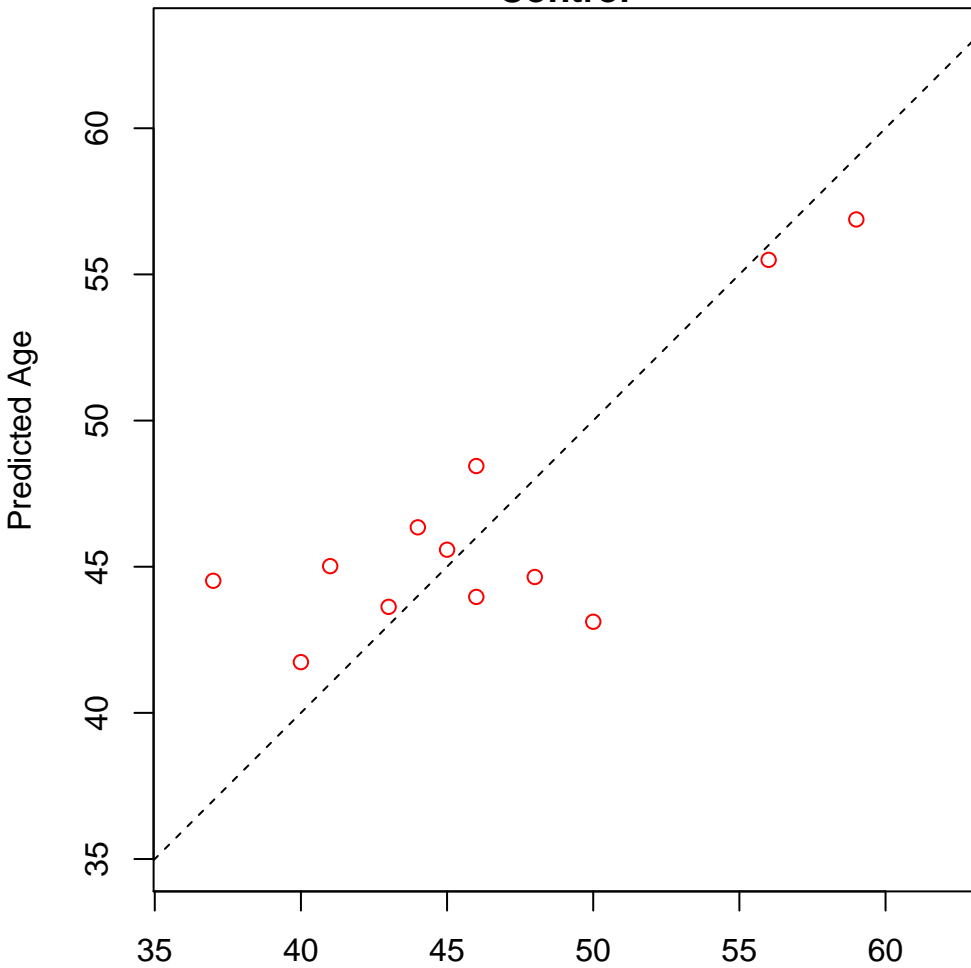


regulation of mitotic cell cycle spindle assembly checkpoint (Score: 3.880949)

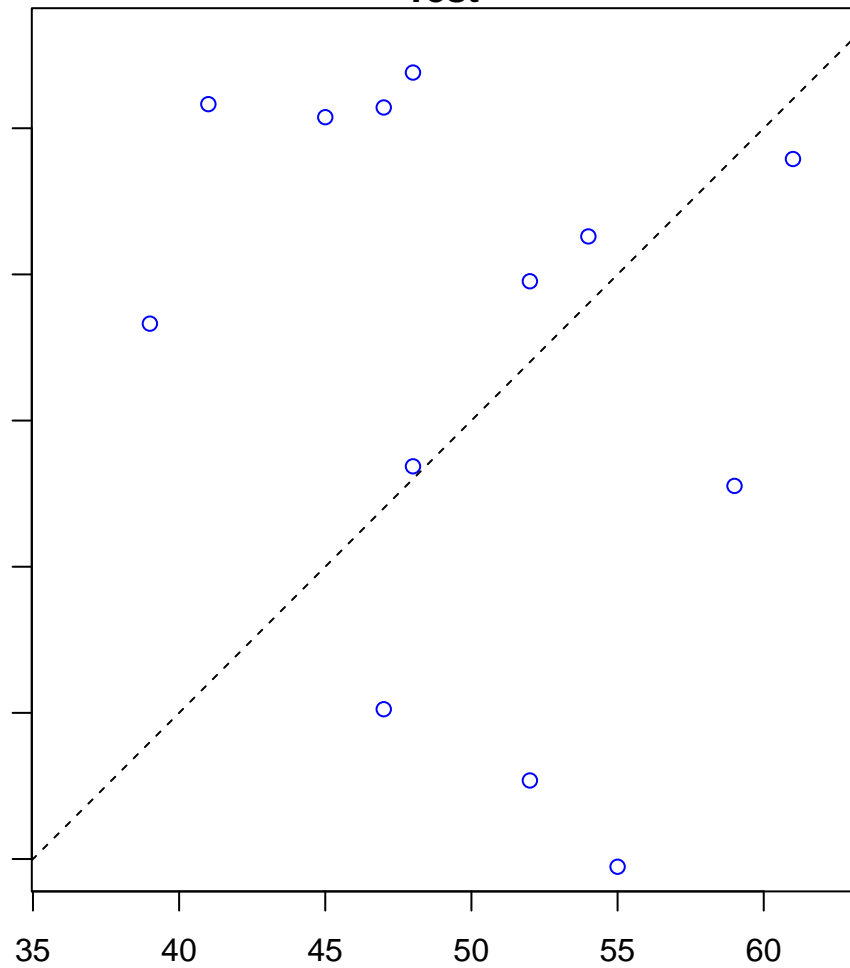


regulation of mitotic spindle checkpoint (Score: 3.880949)

Control

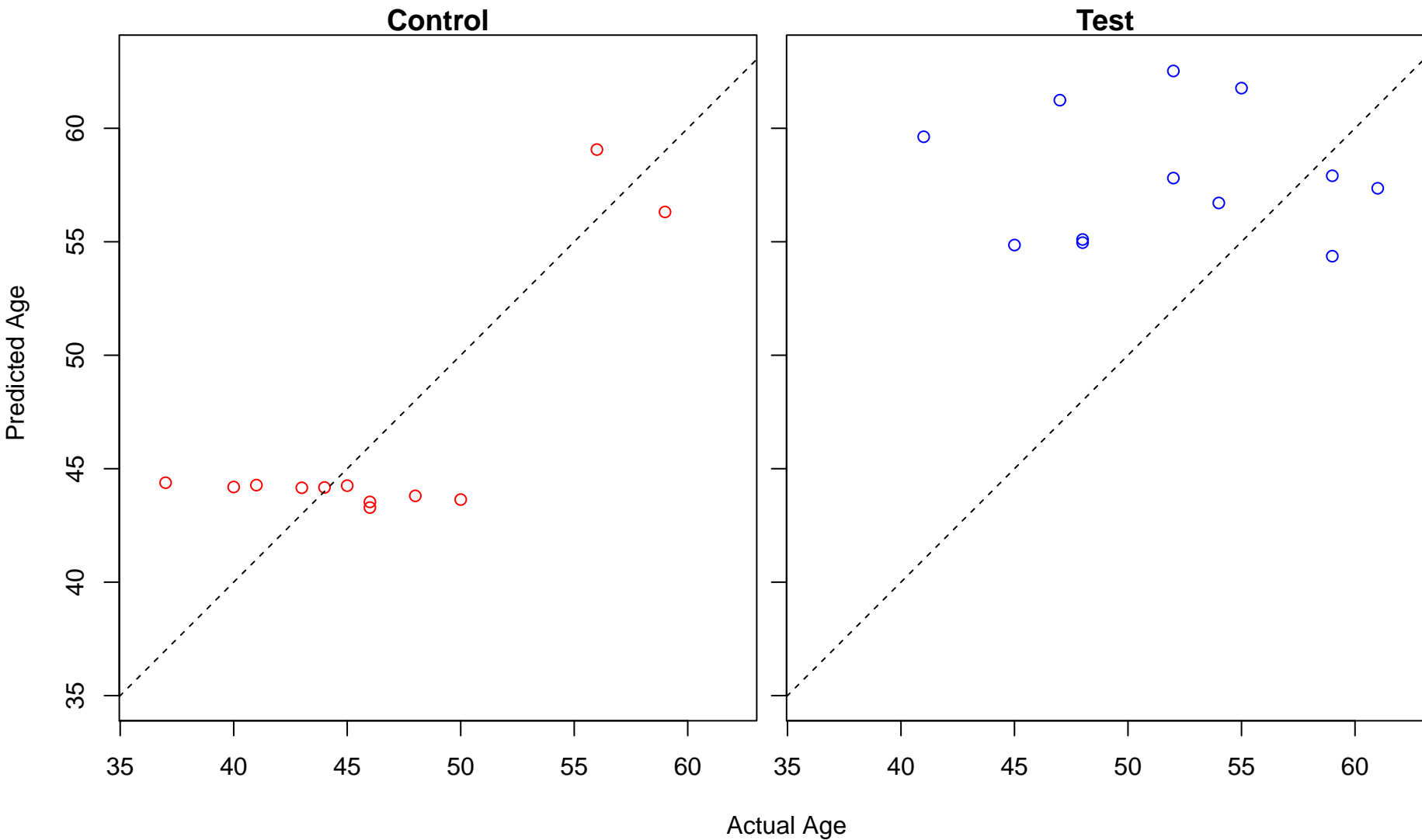


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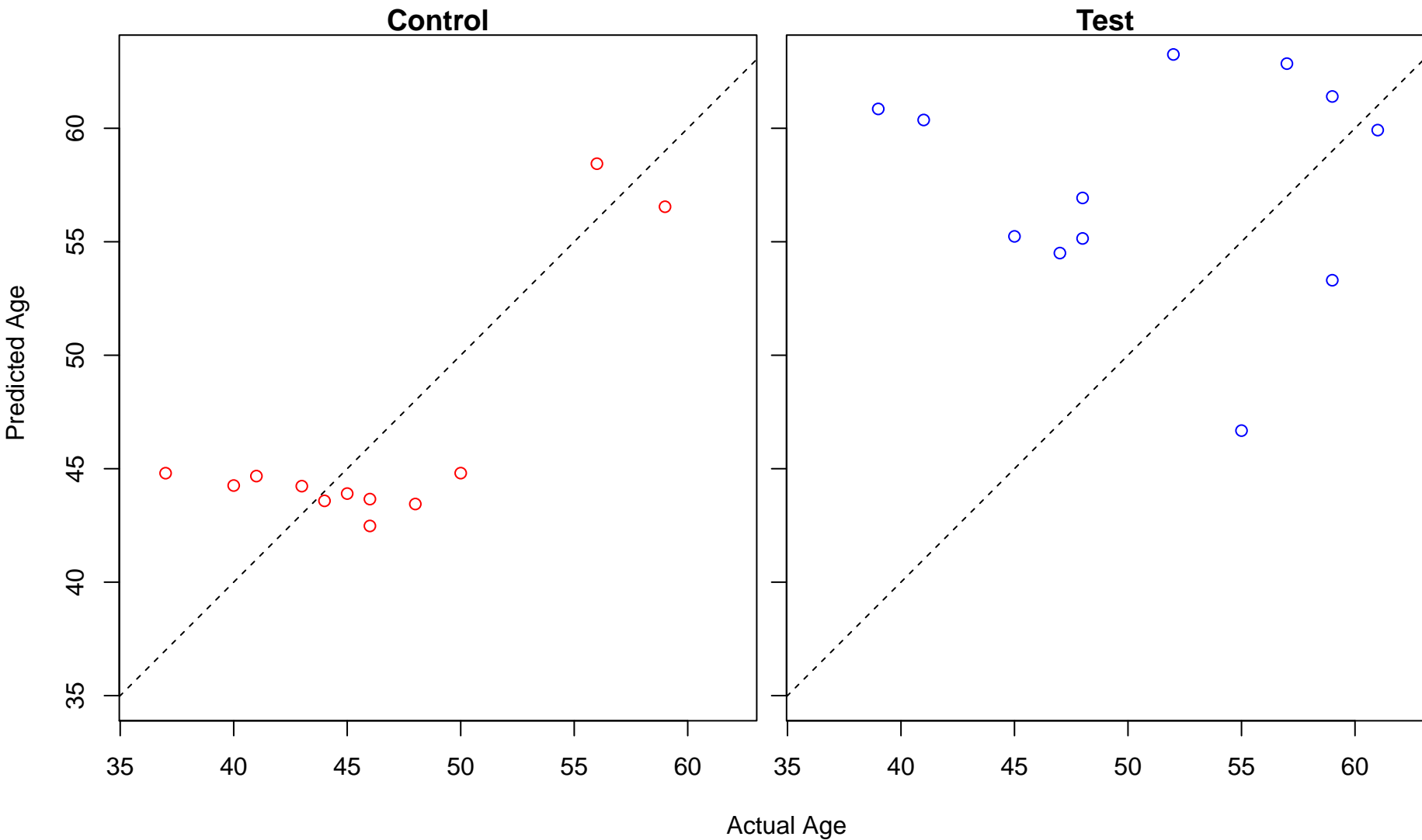


Actual Age

regulation of ERBB signaling pathway (Score: 3.879440)

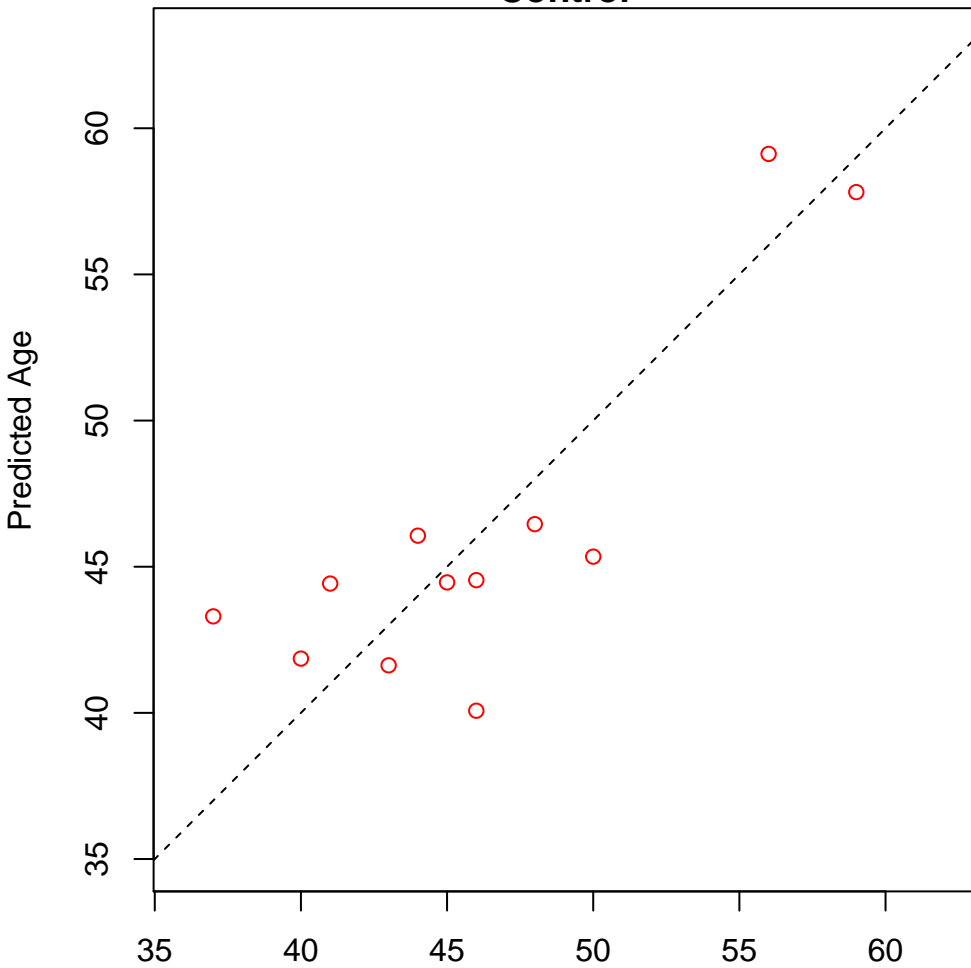


sarcomere organization (Score: 3.879071)

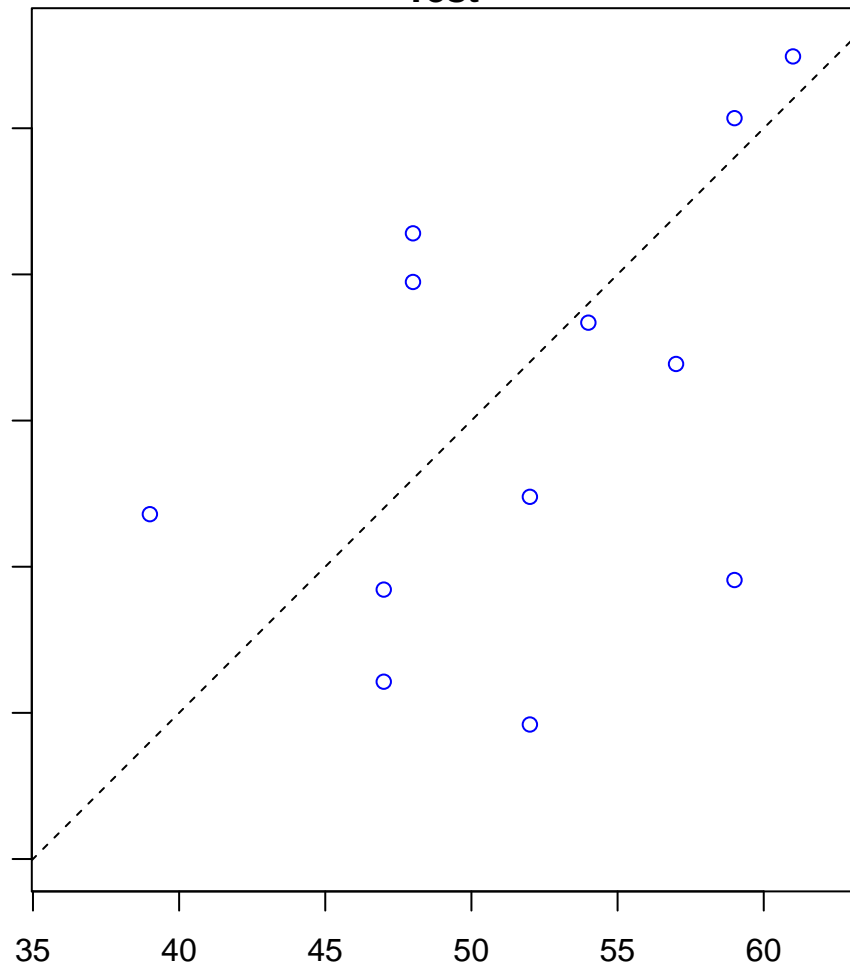


mitochondrial membrane organization (Score: 3.877724)

Control

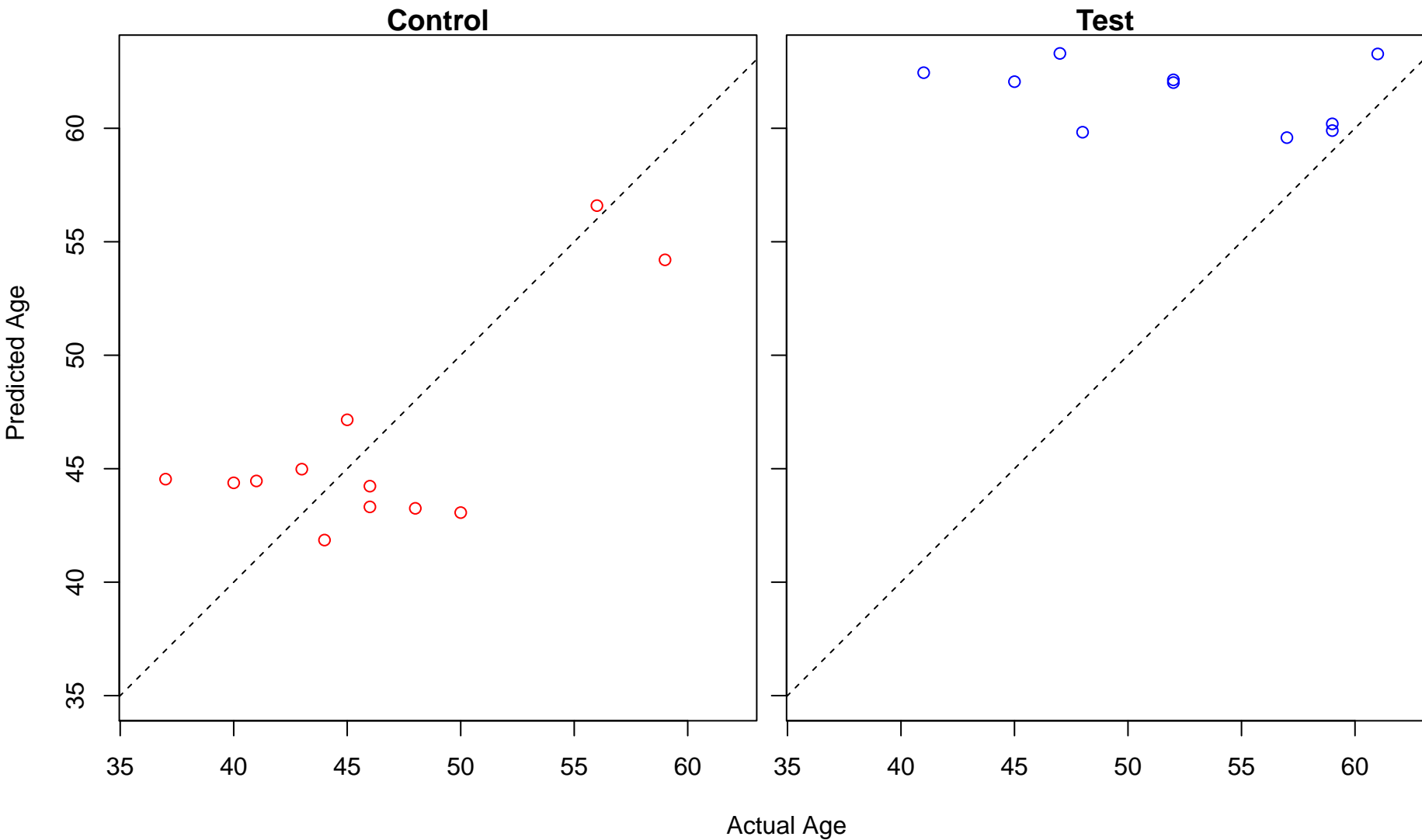


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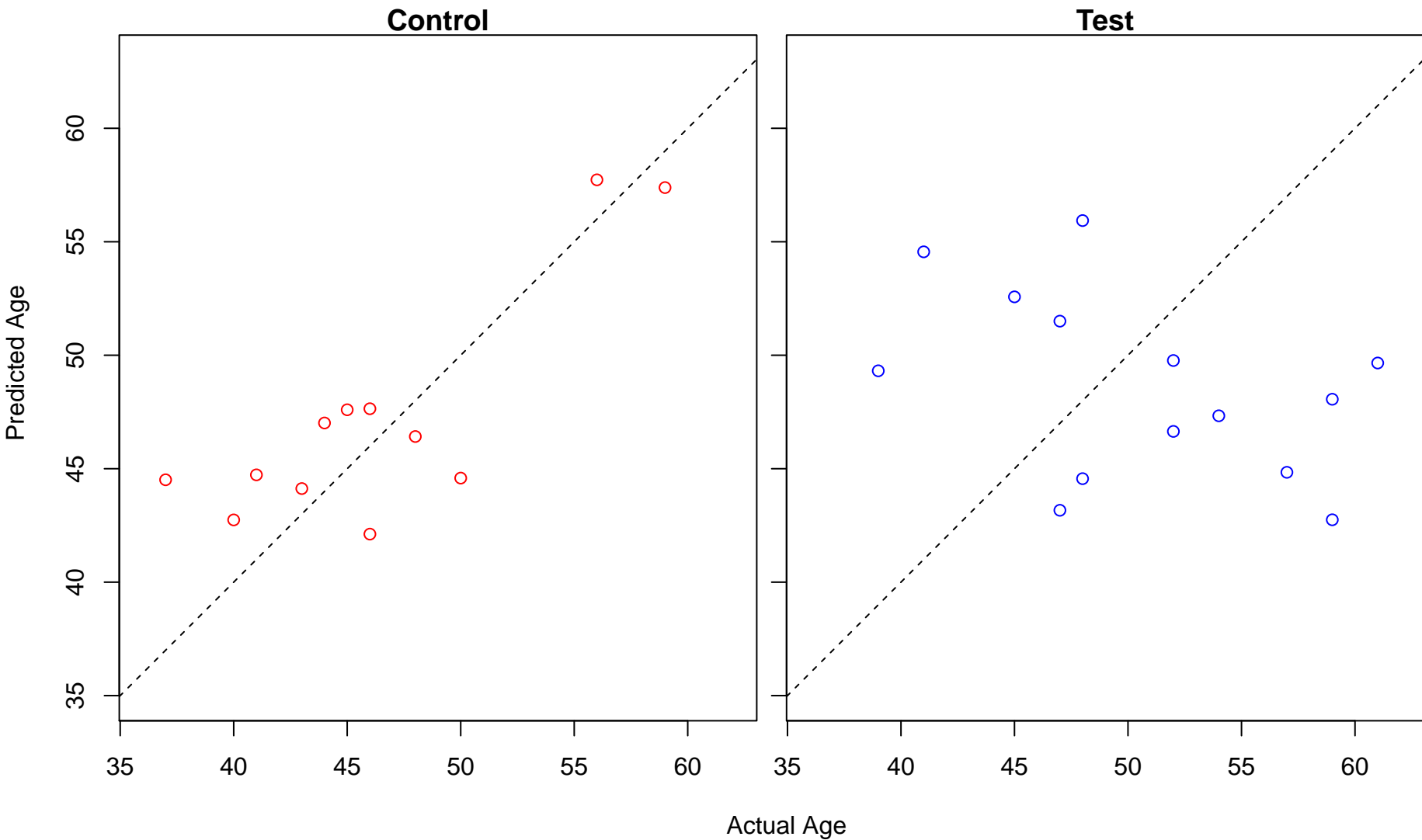


Actual Age

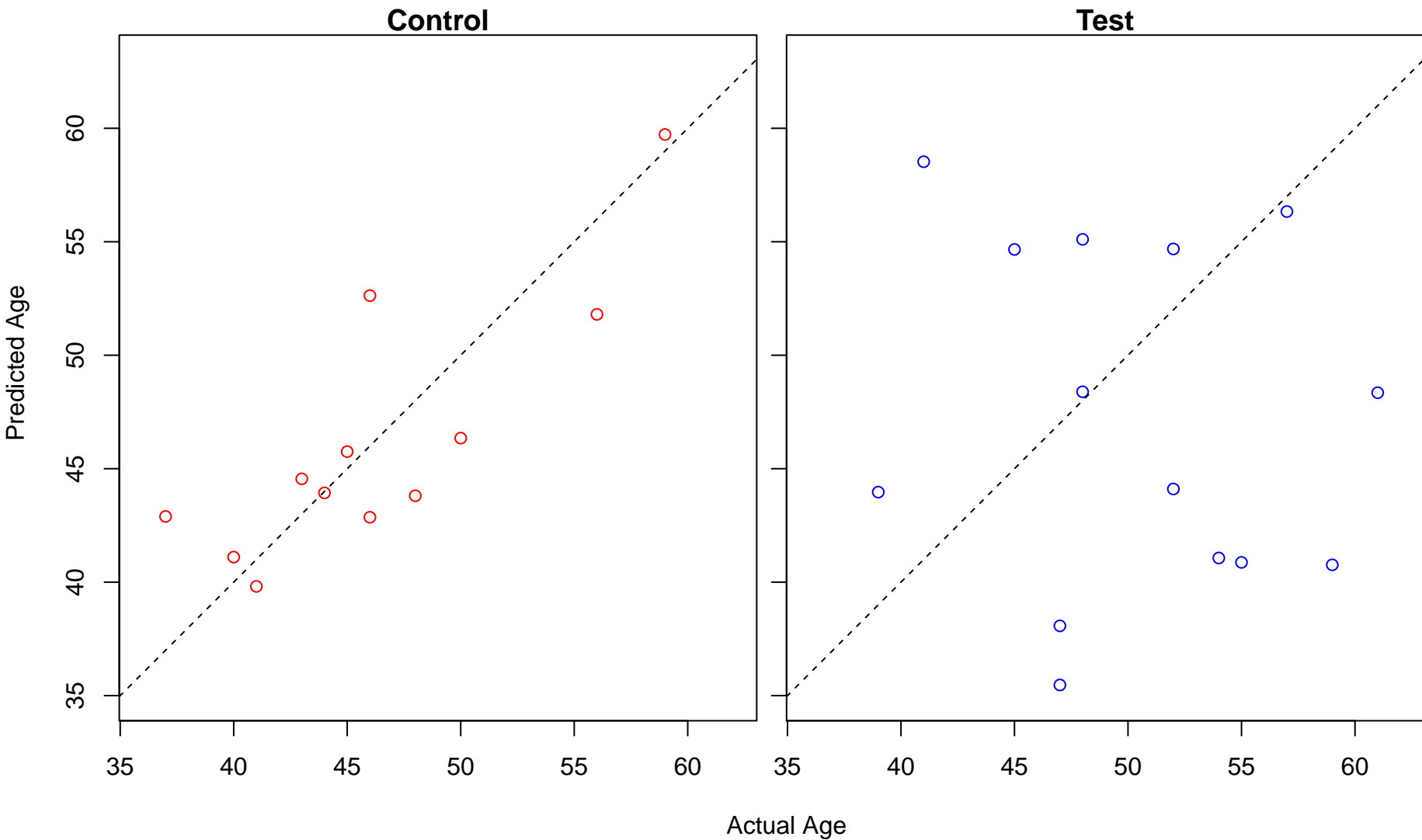
regulation of respiratory system process (Score: 3.872051)



positive regulation of leukocyte activation (Score: 3.869585)

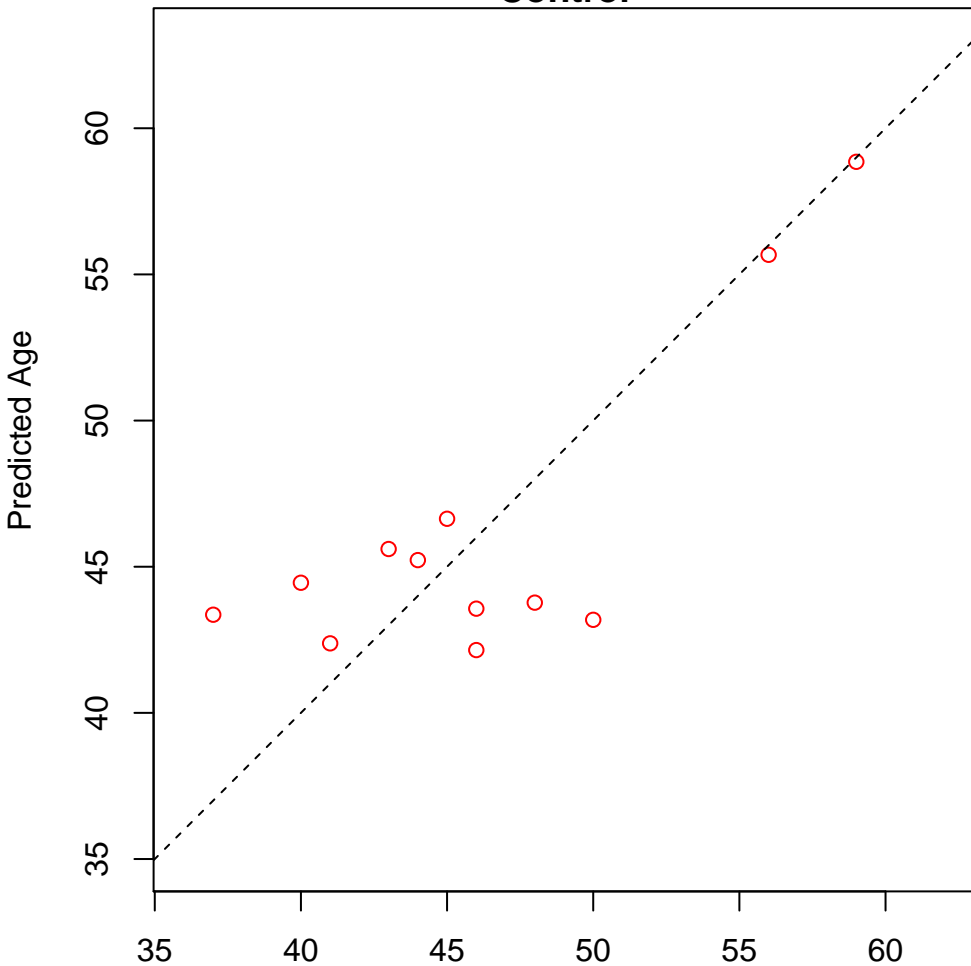


cardiac muscle fiber development (Score: 3.869202)

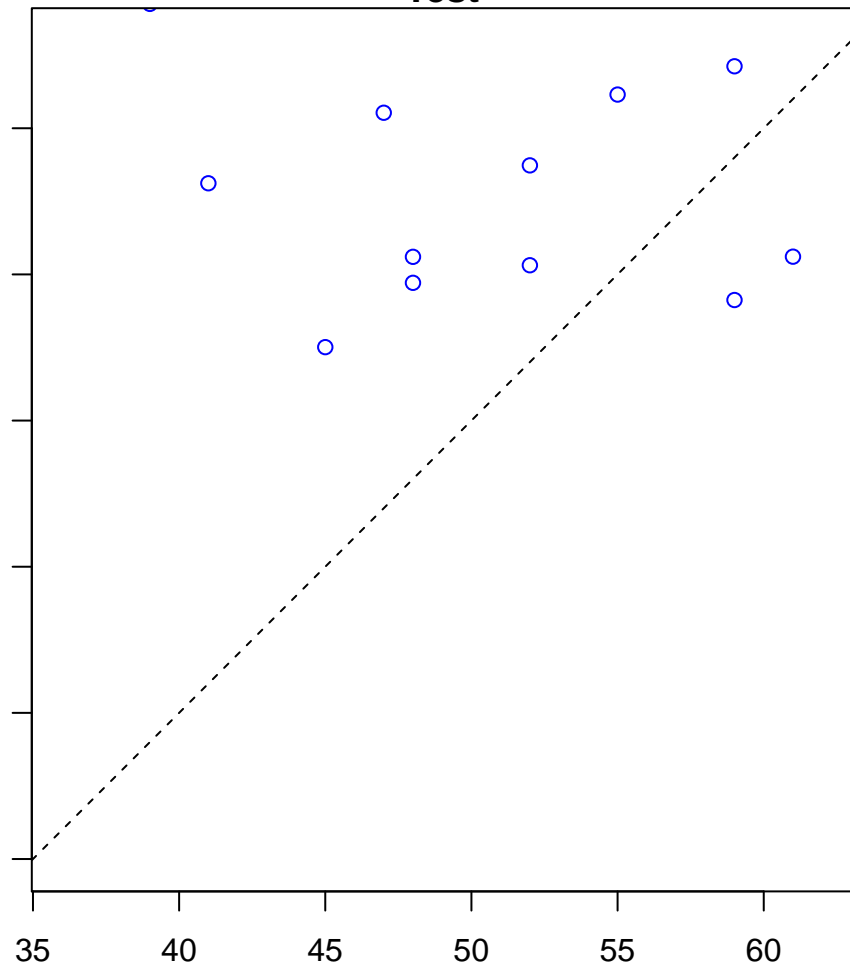


anterior/posterior axis specification (Score: 3.868268)

Control

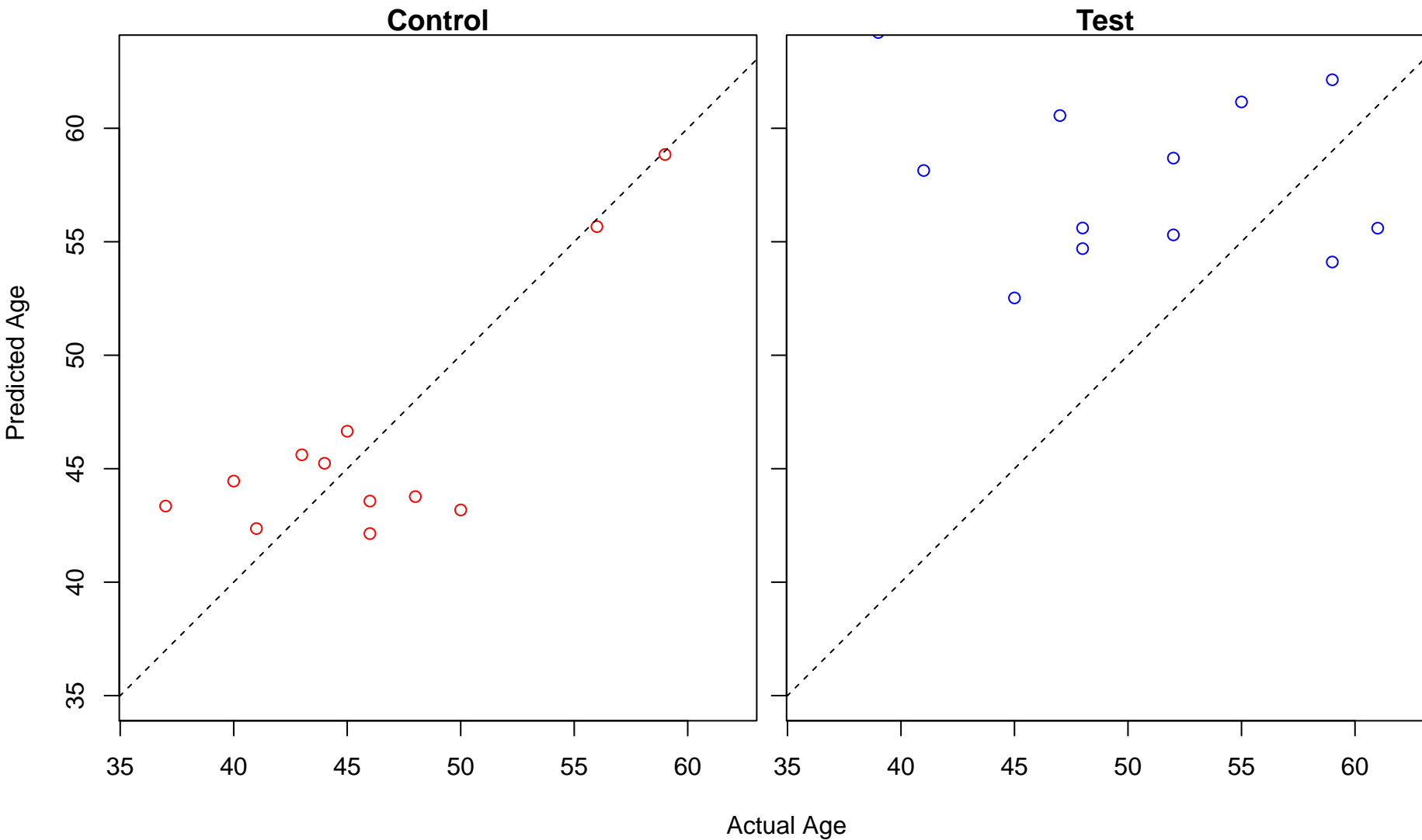


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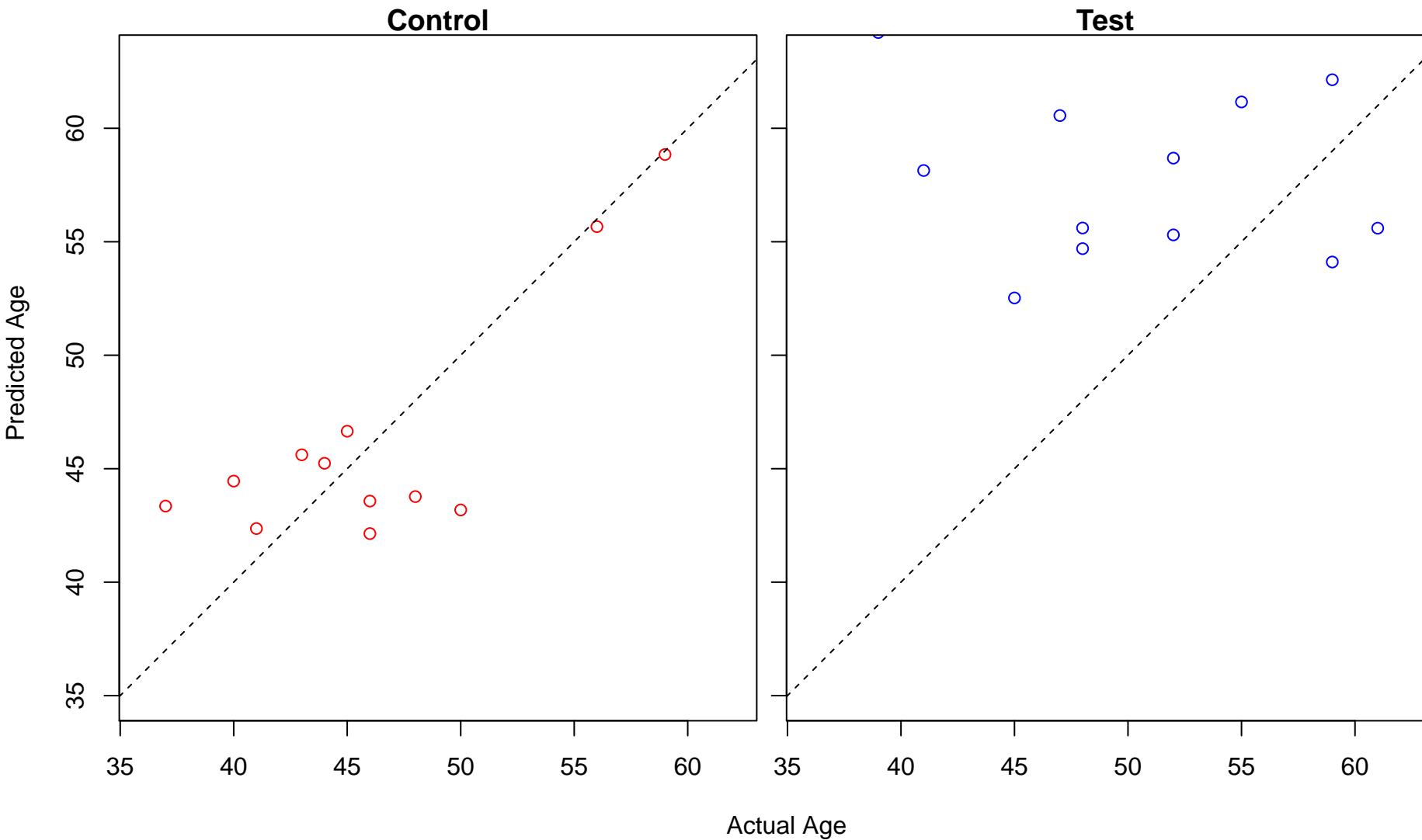


Actual Age

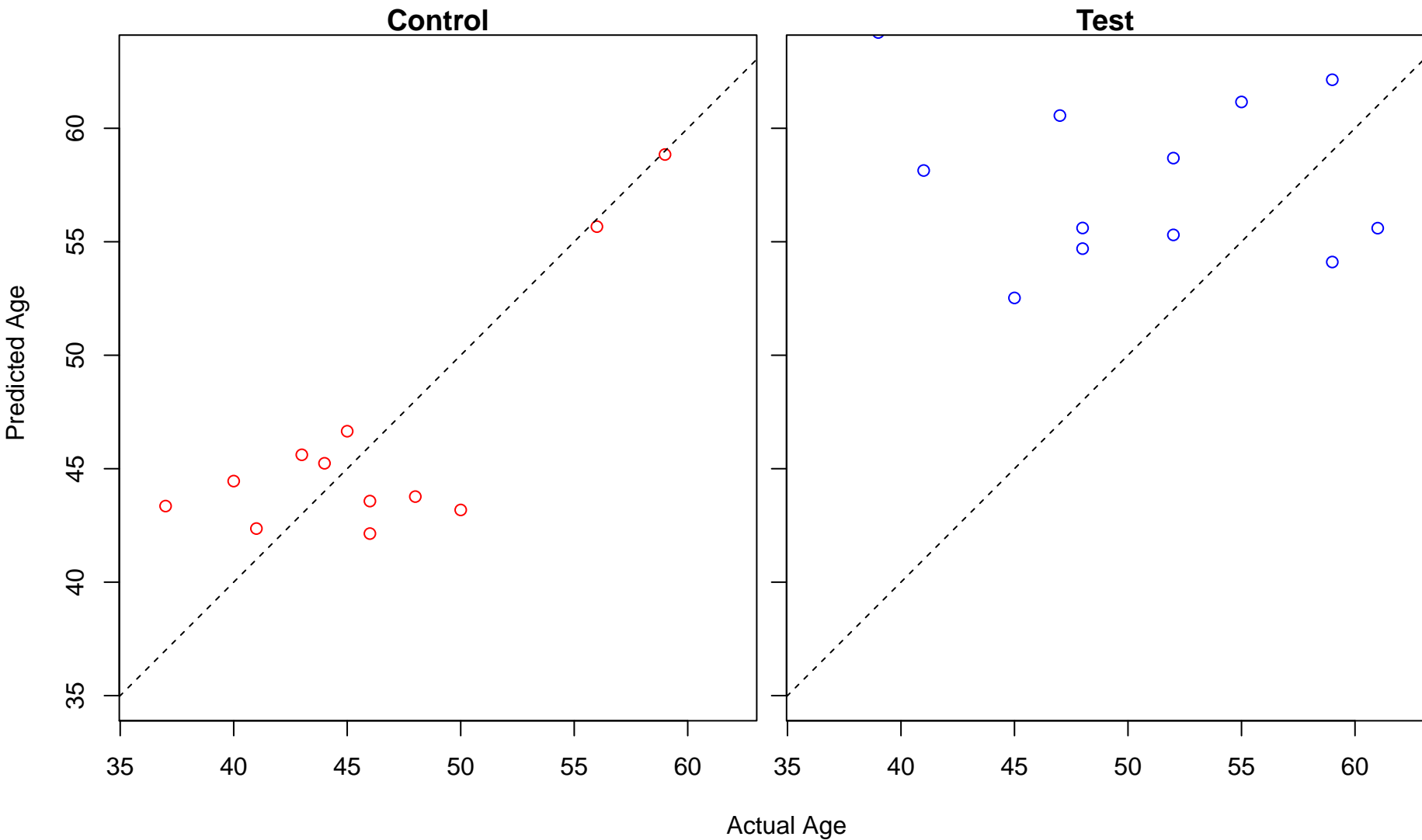
blastoderm segmentation (Score: 3.866665)



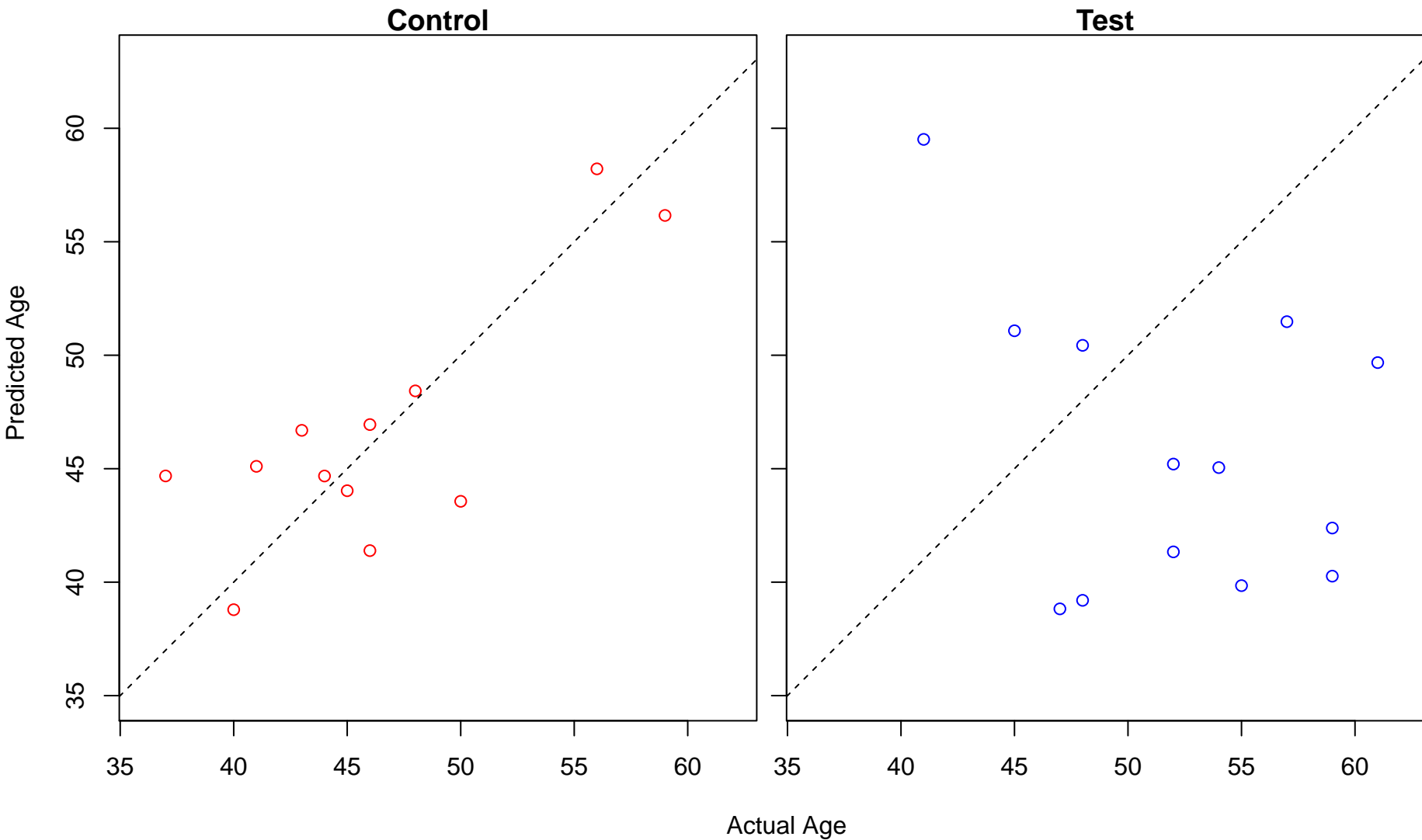
tripartite regional subdivision (Score: 3.86665)



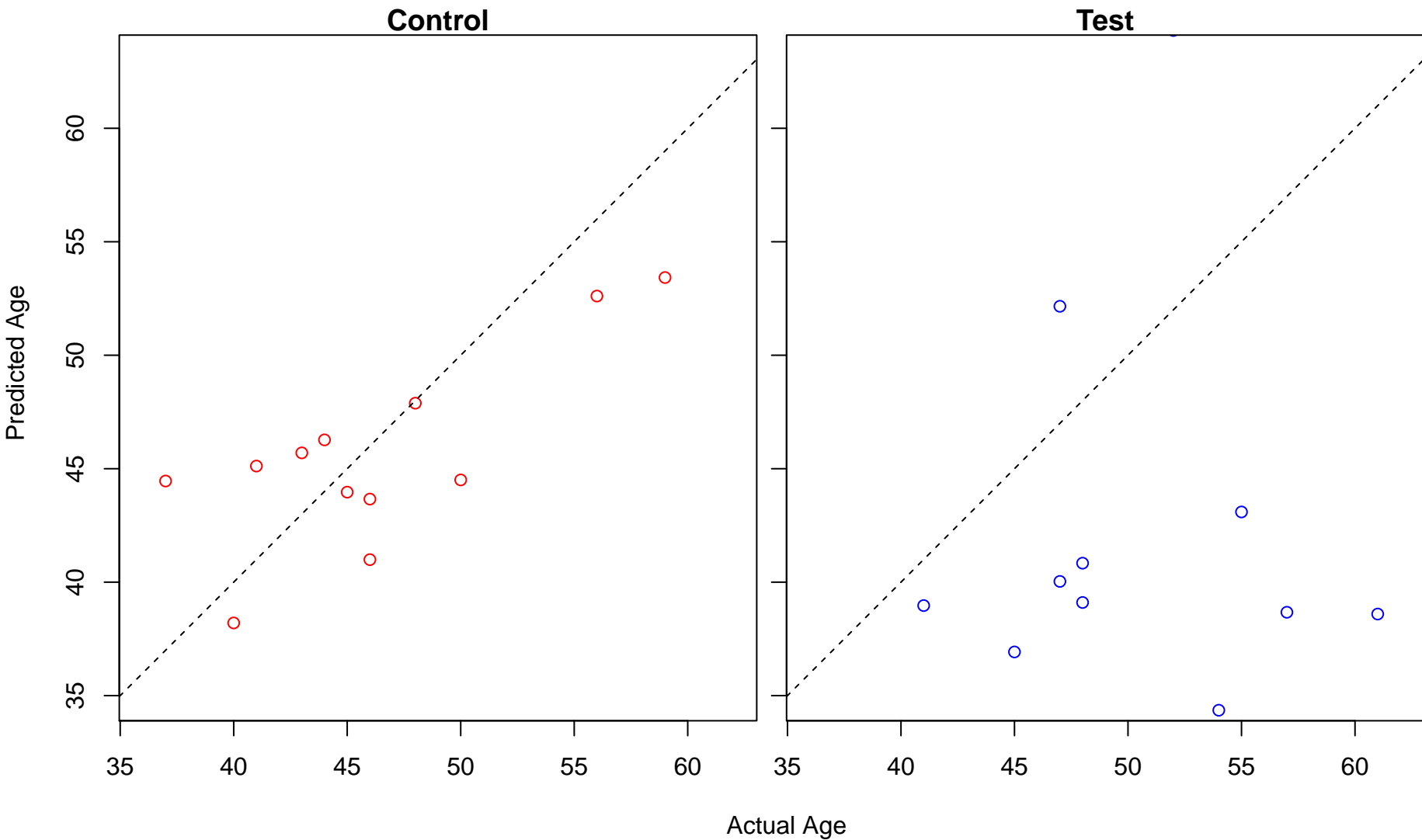
anterior/posterior axis specification, embryo (Score: 3.866665)



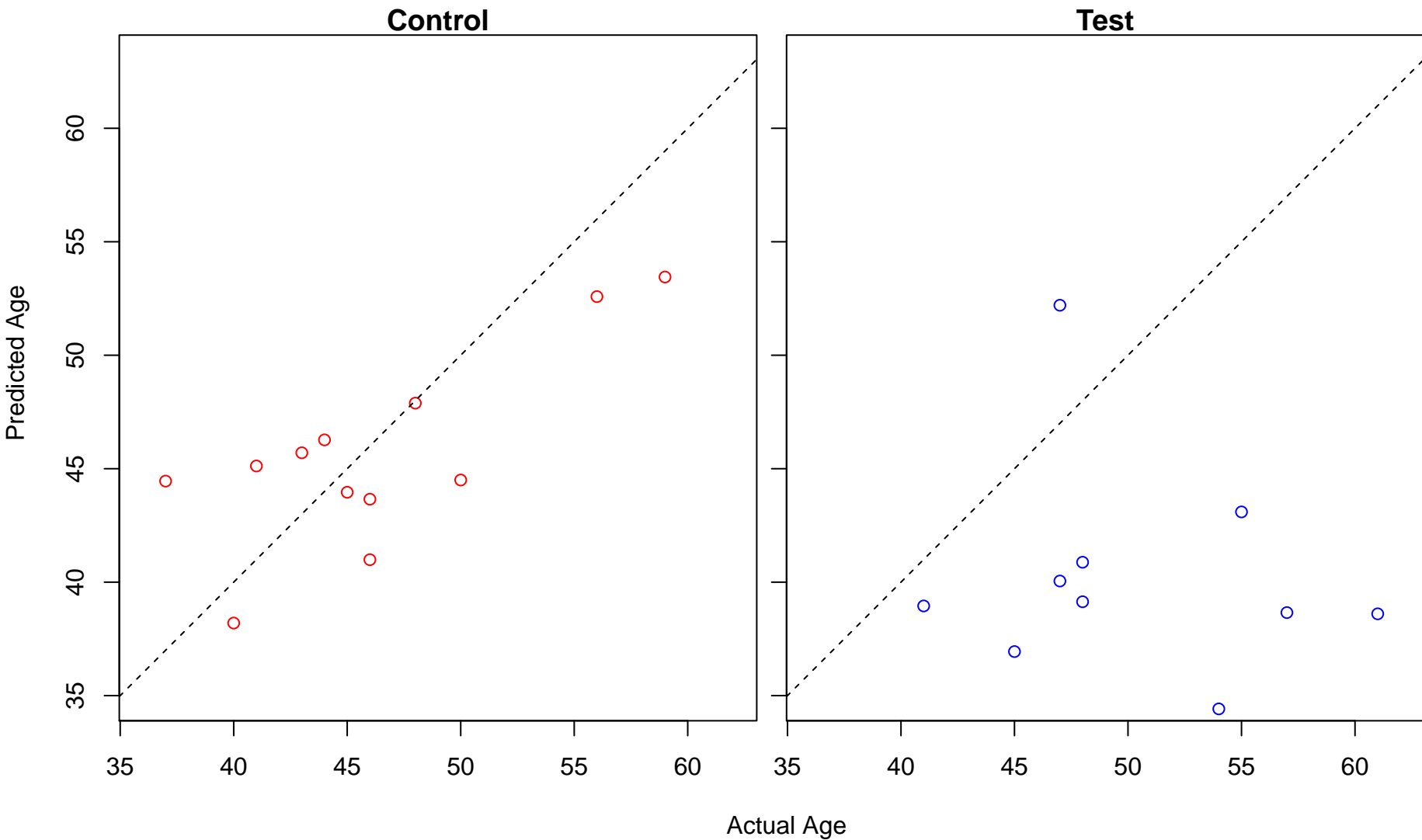
regulation of vesicle-mediated transport (Score: 3.862563)



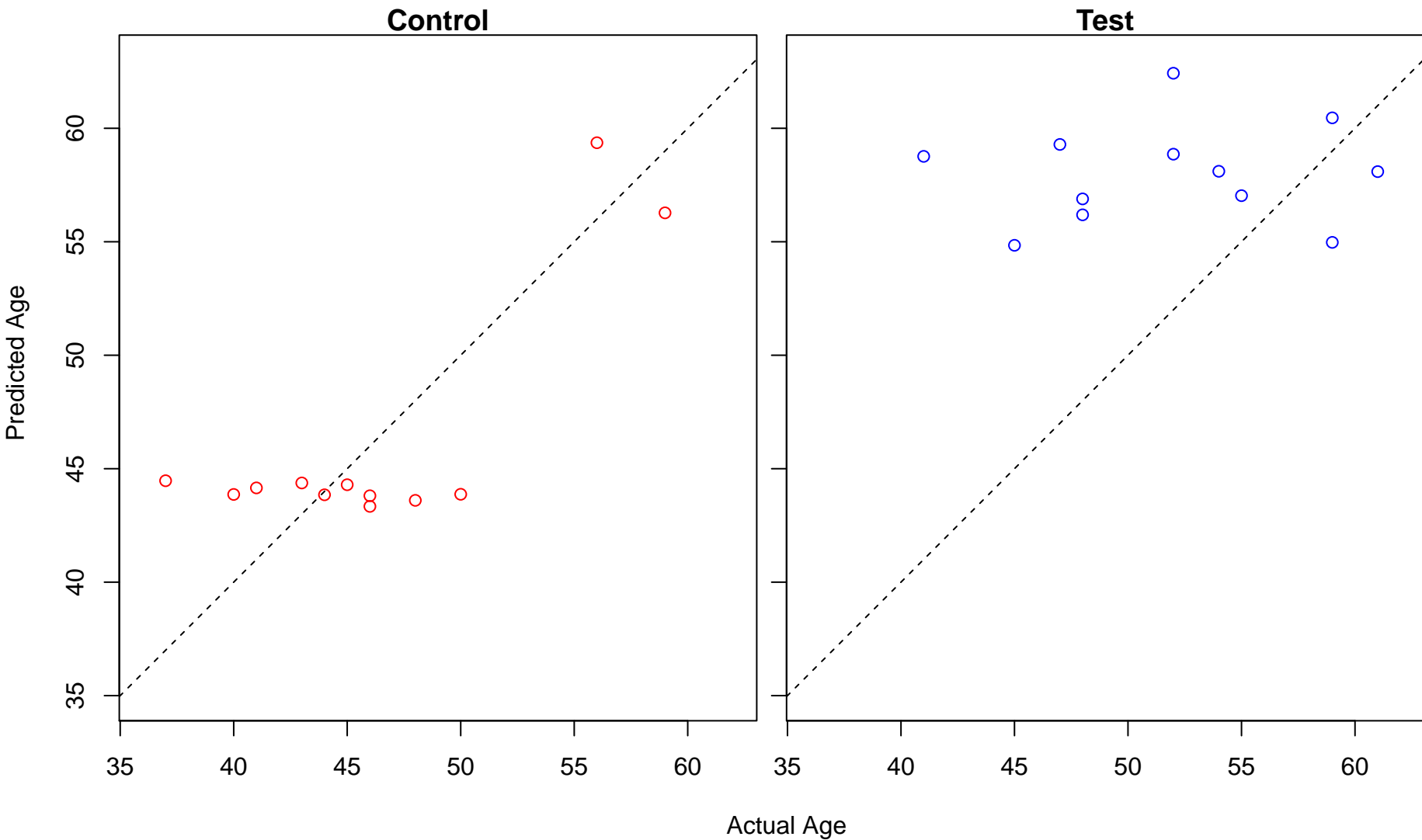
cellular protein complex disassembly (Score: 3.860928)



translational termination (Score: 3.860255)

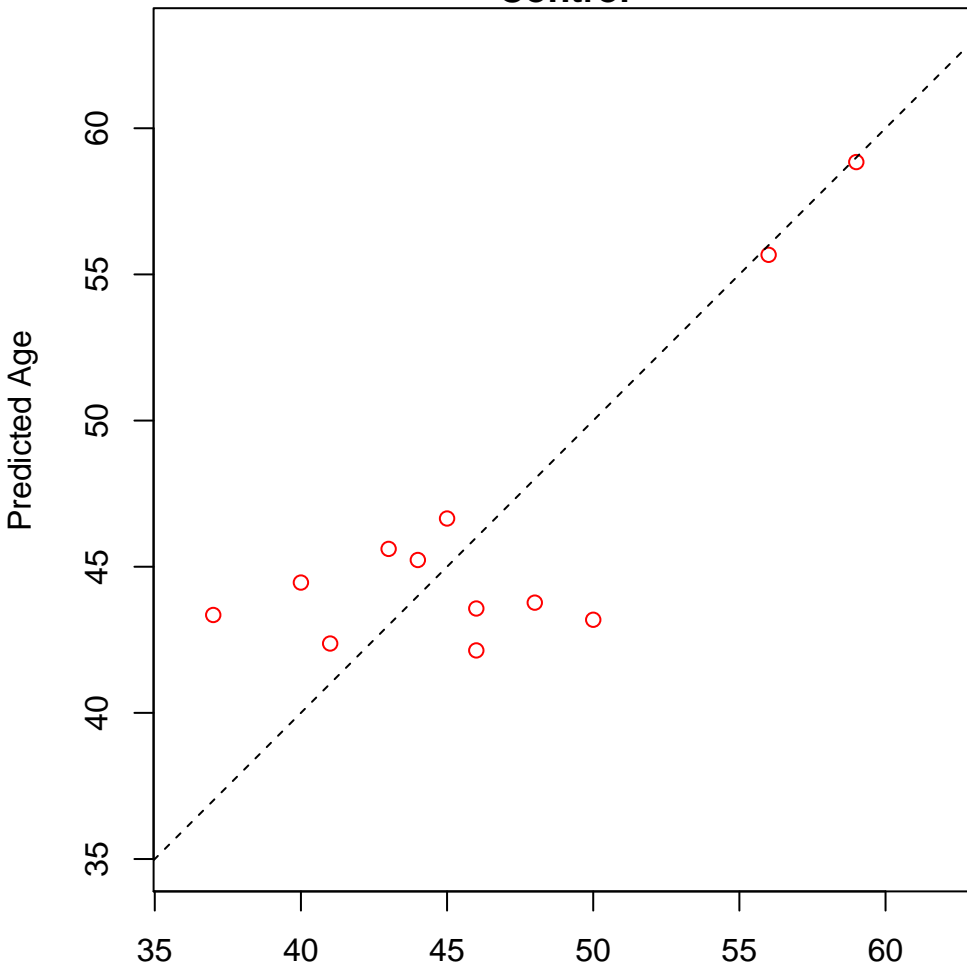


DNA damage response, detection of DNA damage (Score: 3.859965)

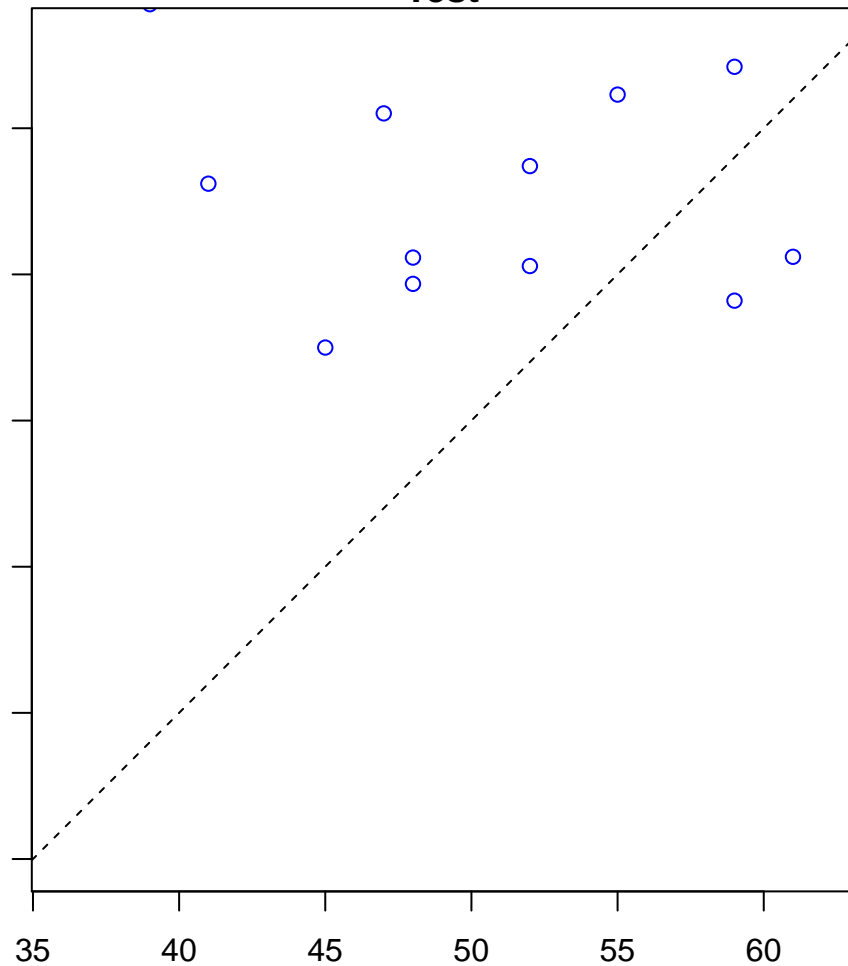


mesenchymal to epithelial transition (Score: 3.858807)

Control



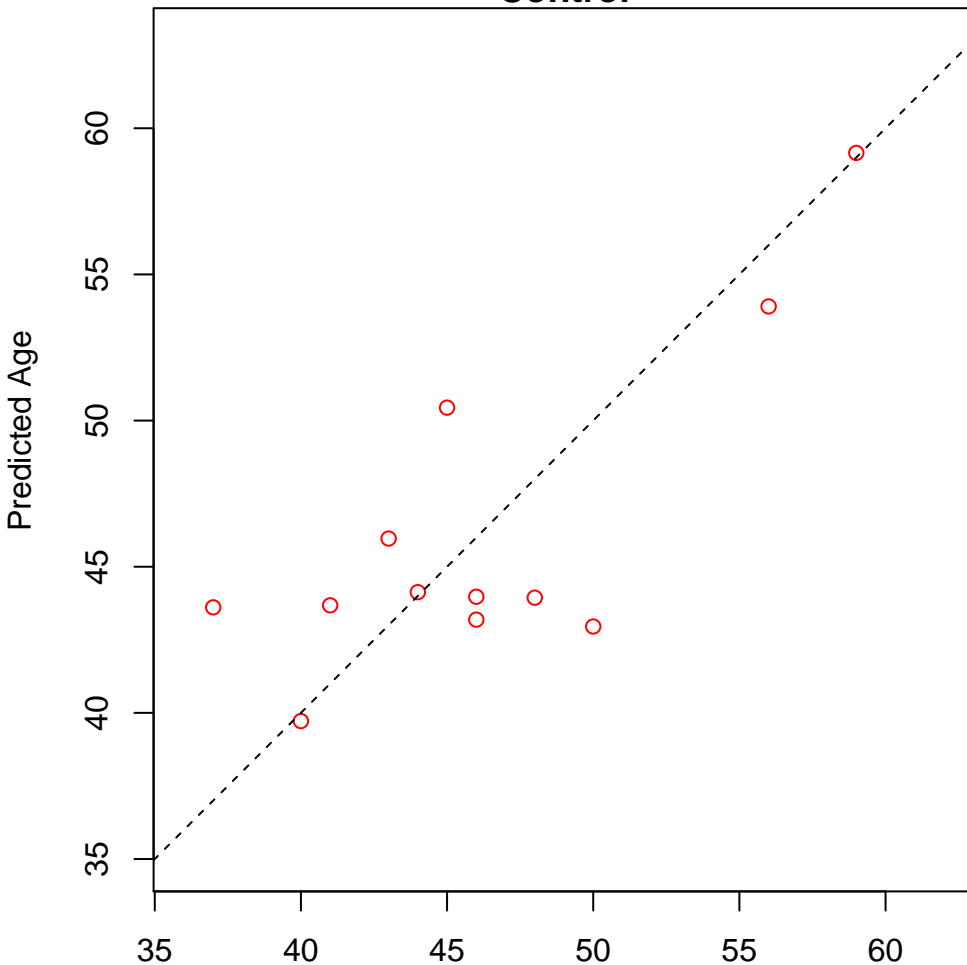
Test



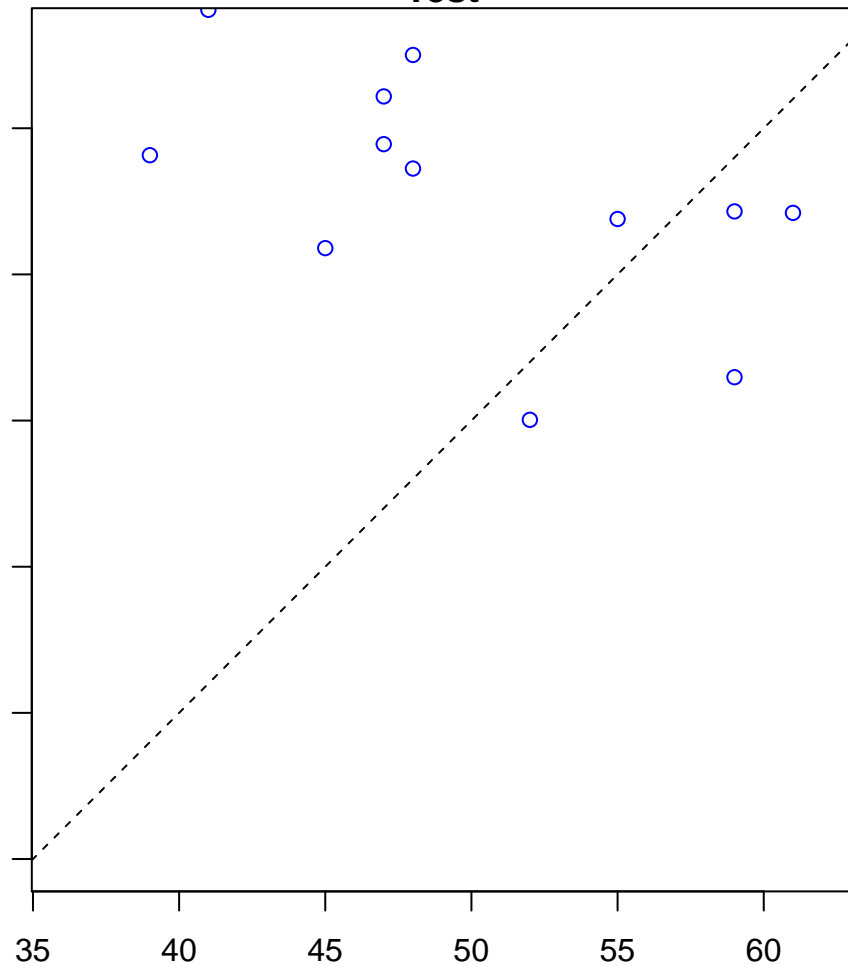
Actual Age

GDP-mannose biosynthetic process (Score: 3.858549)

Control

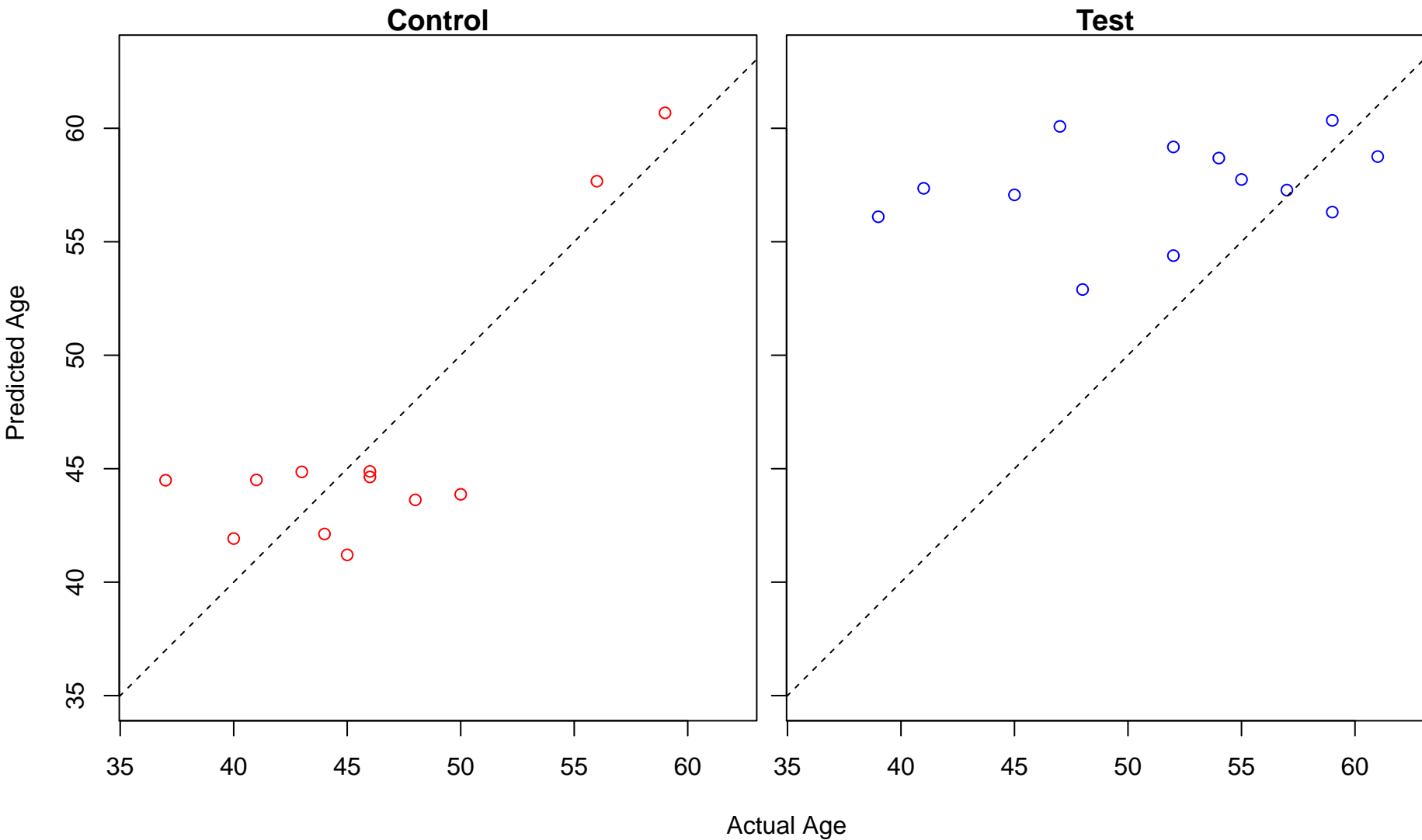


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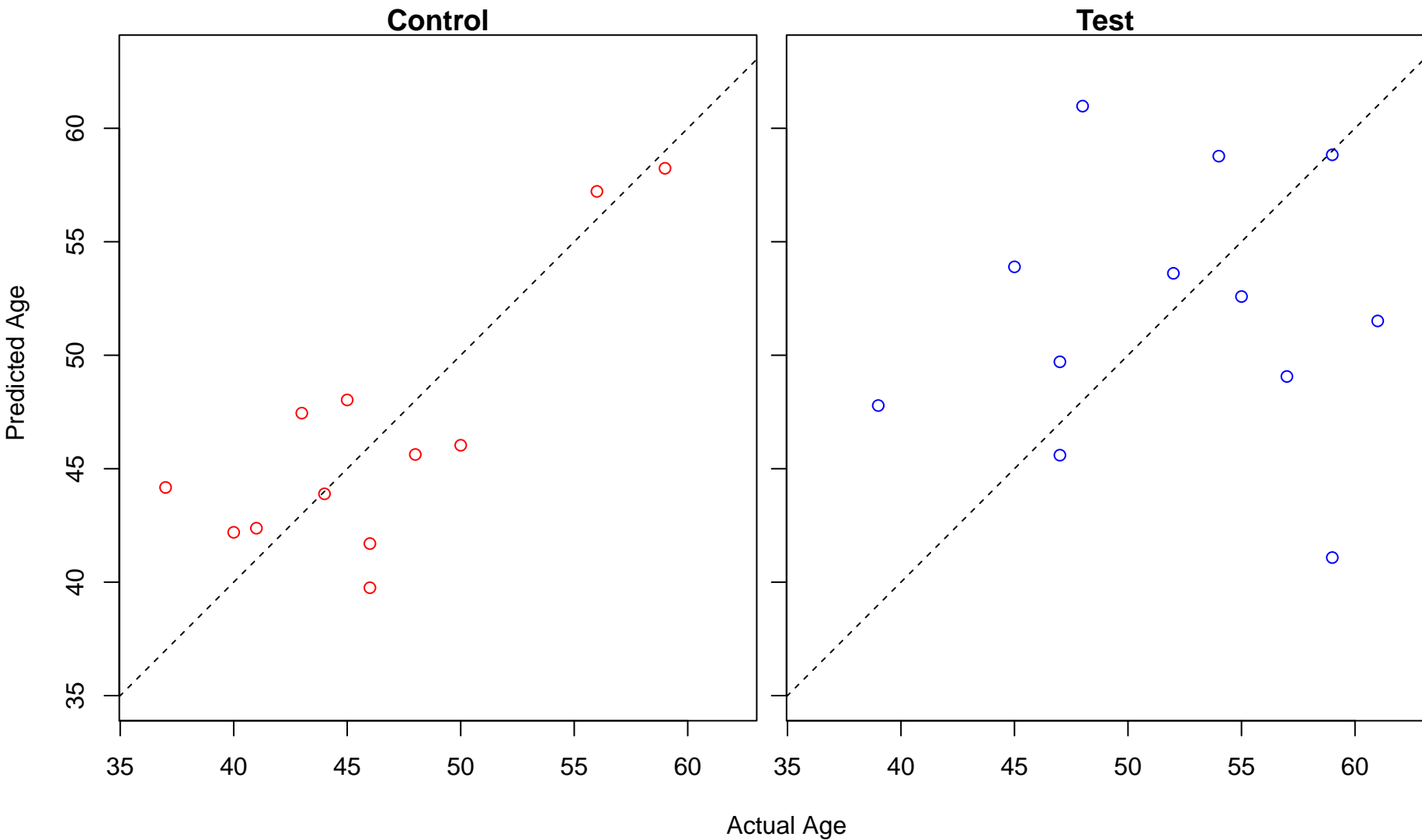


Actual Age

positive regulation of metalloenzyme activity (Score: 3.858387)

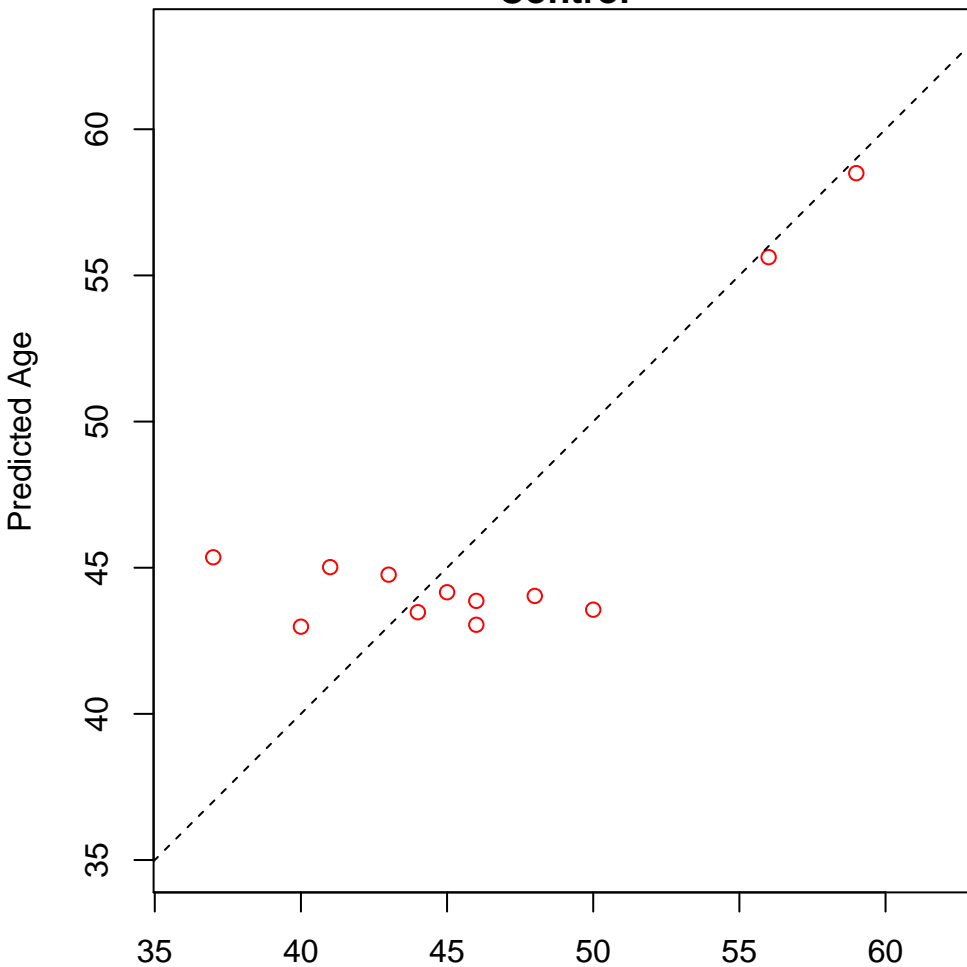


positive regulation of transcription from RNA polymerase III promoter (Score: 3.856863)

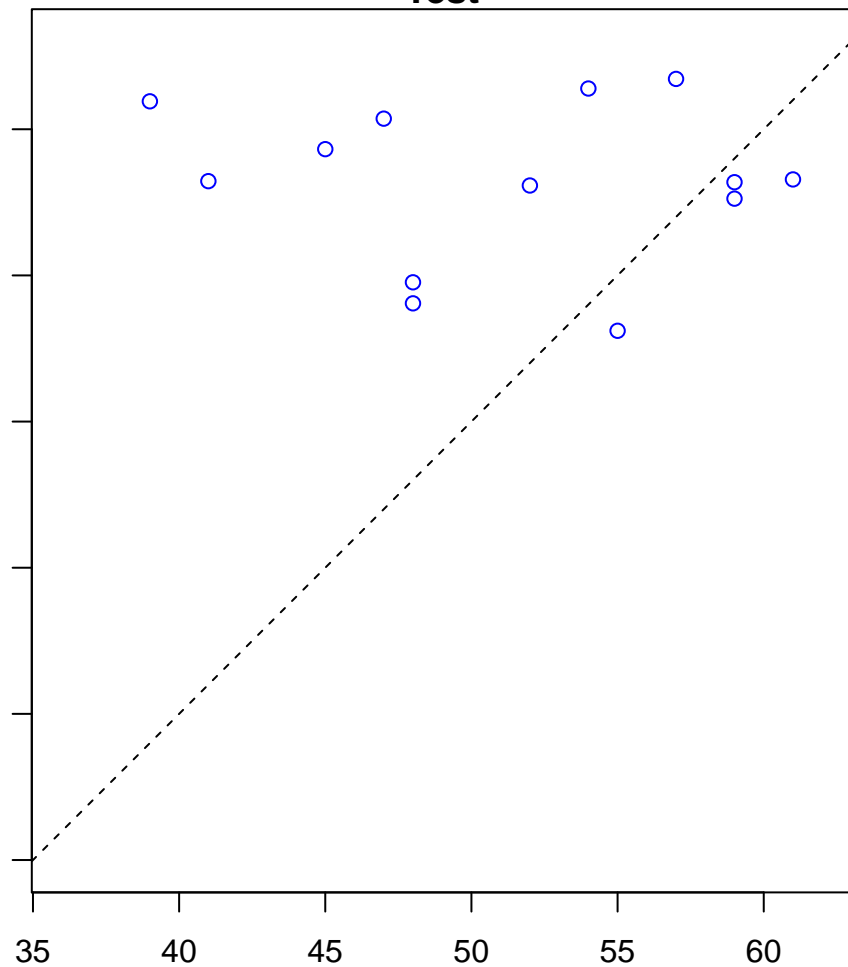


regulation of keratinocyte differentiation (Score: 3.855446)

Control

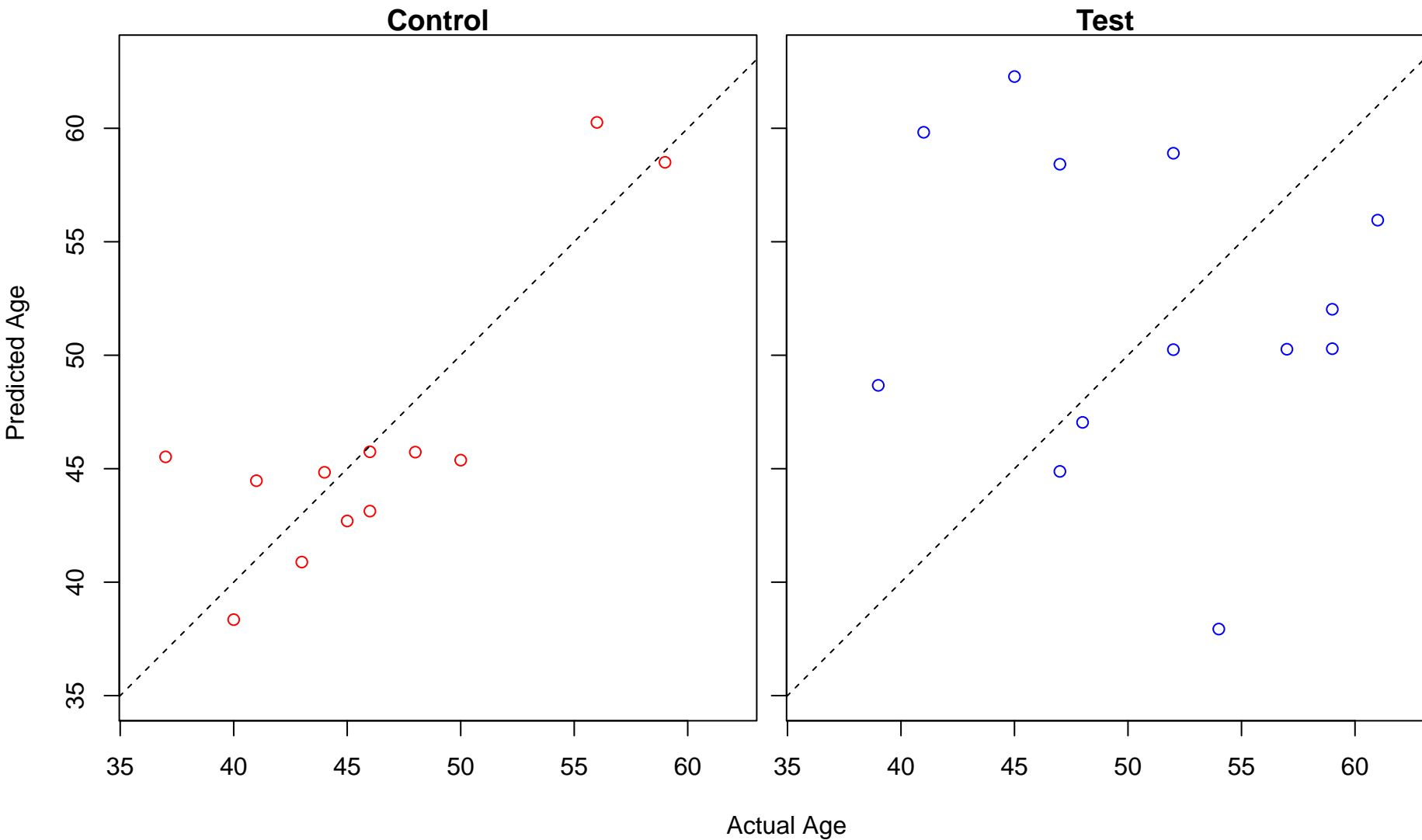


Test

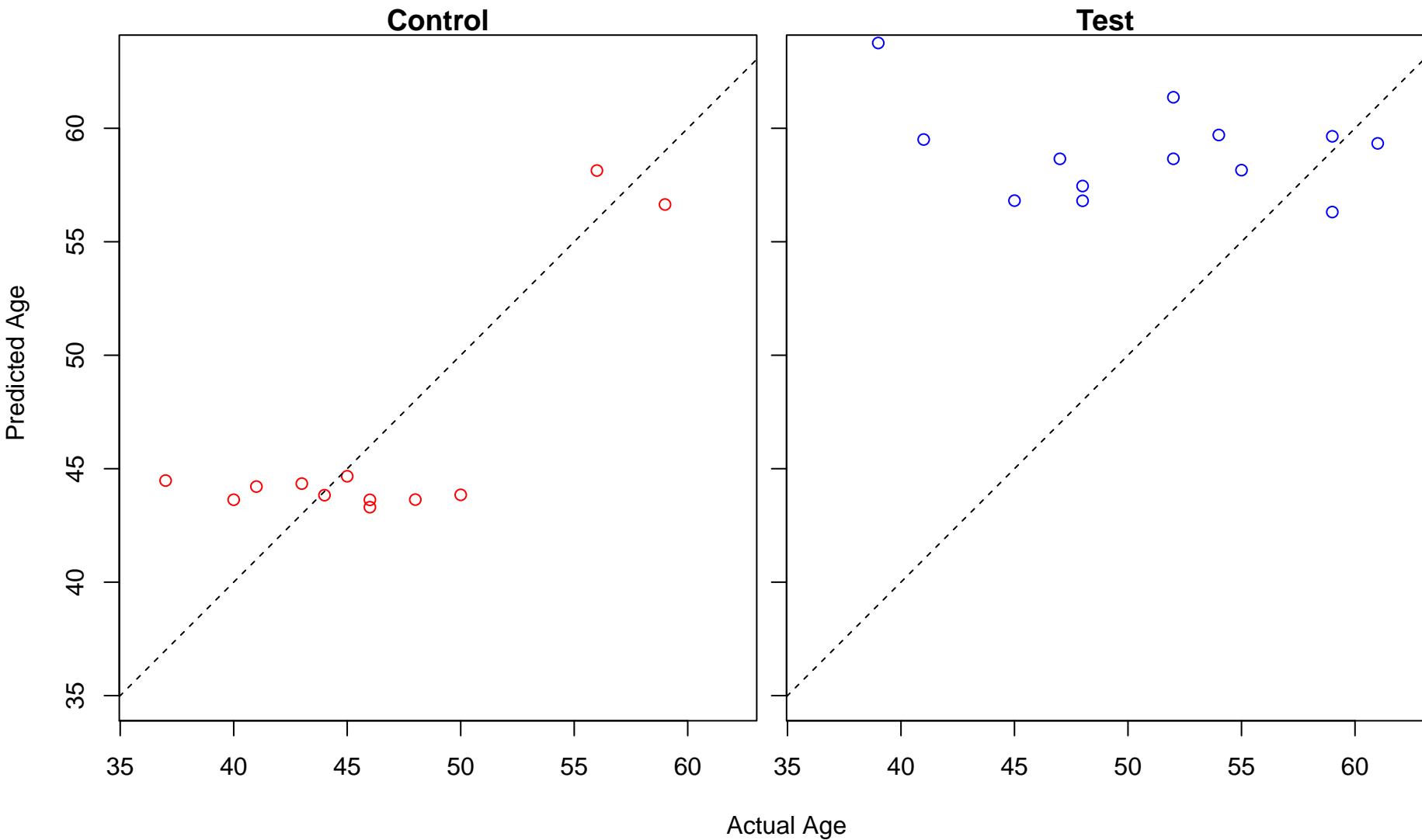


Actual Age

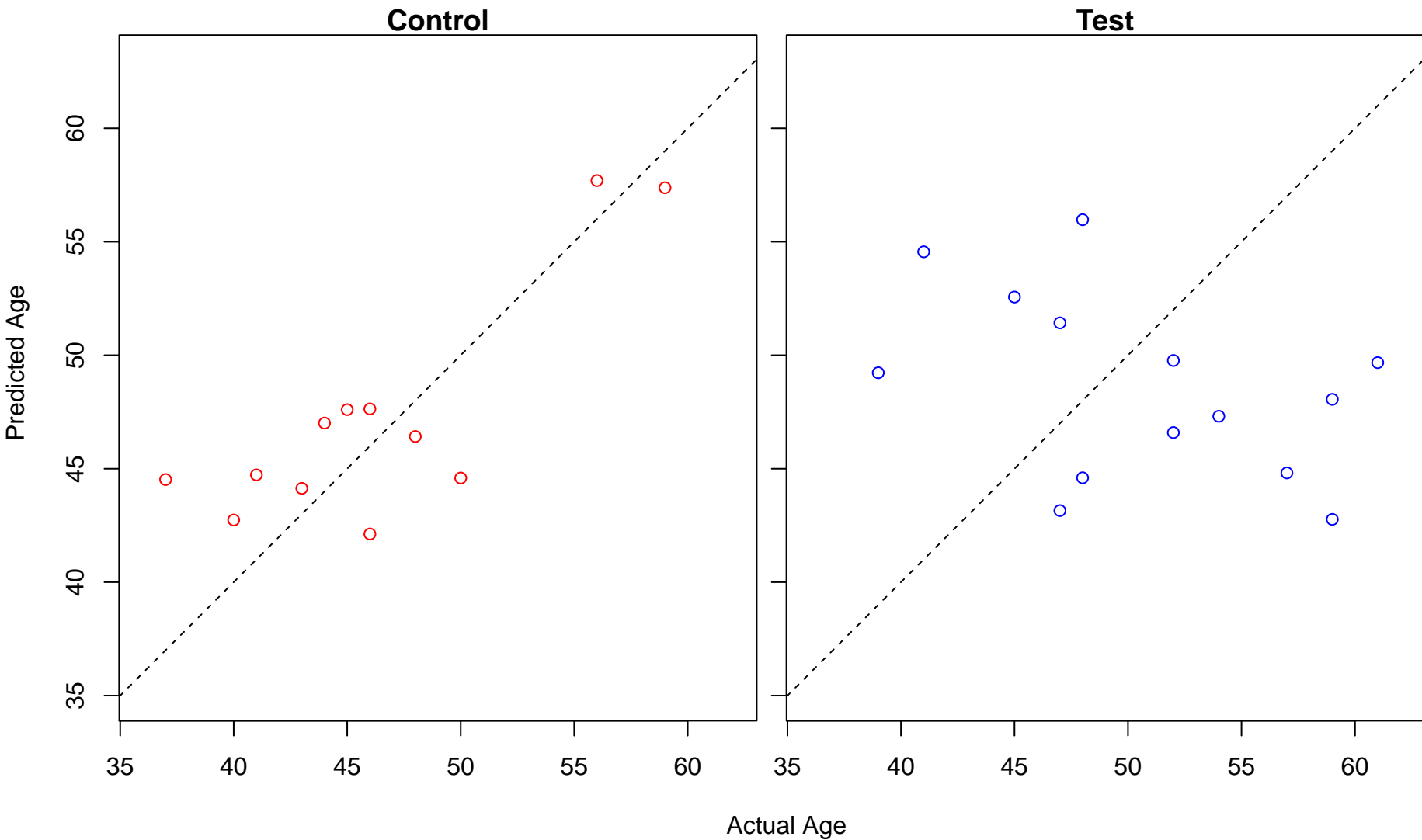
embryonic organ morphogenesis (Score: 3.853465)



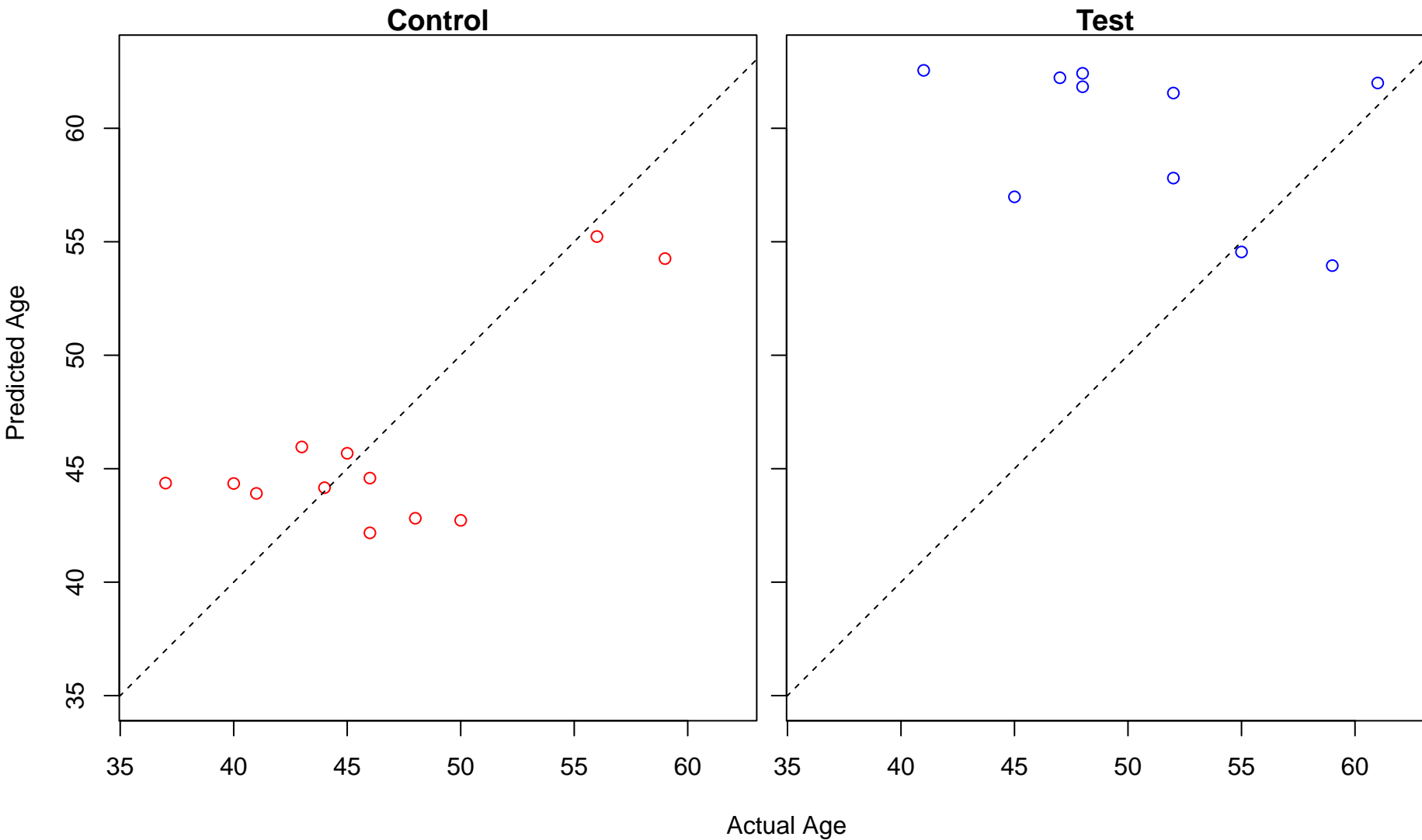
positive regulation of sequence-specific DNA binding transcription factor activity (Score: 3.852789)



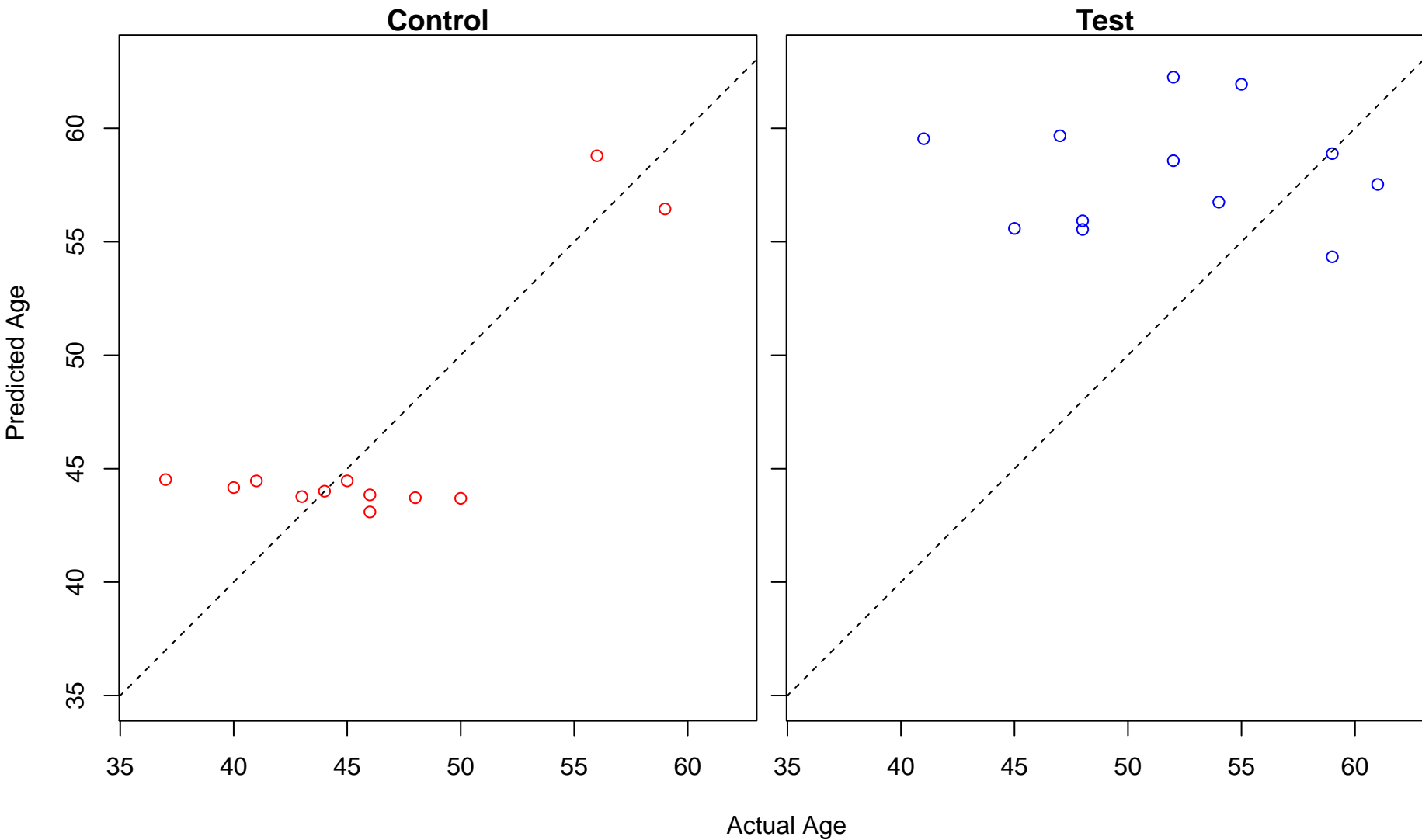
positive regulation of cell activation (Score: 3.850803)



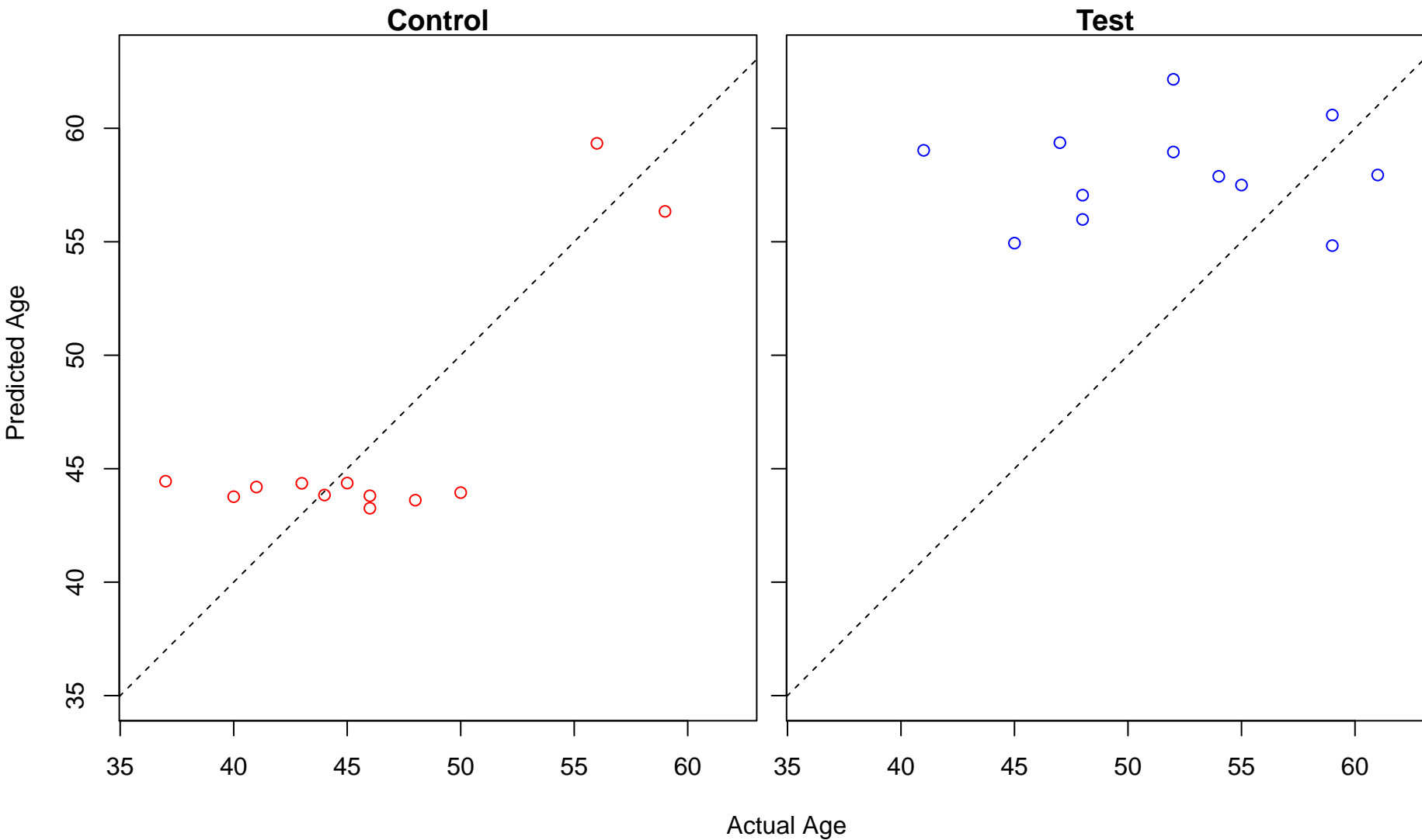
negative regulation of endoplasmic reticulum calcium ion concentration (Score: 3.842182)



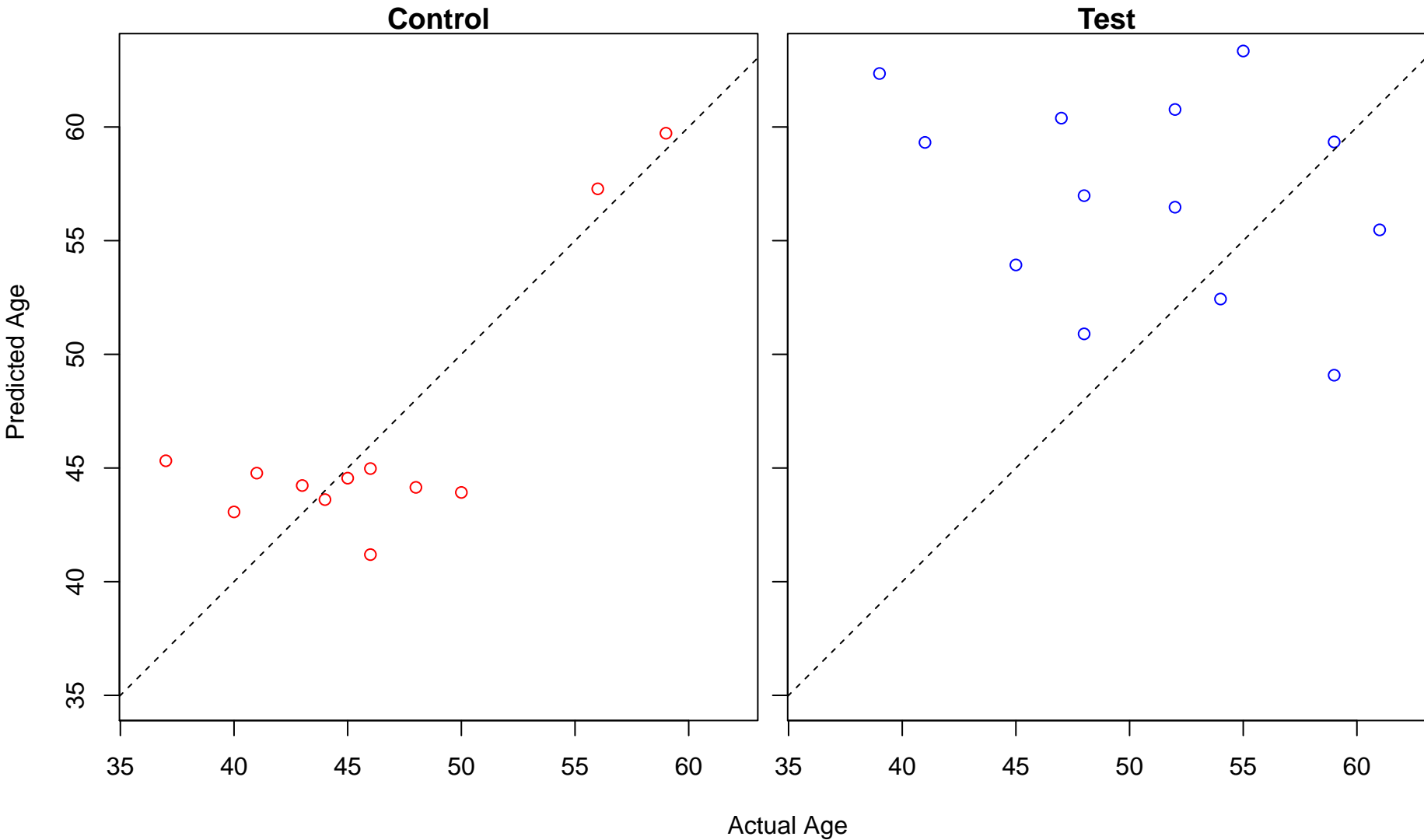
regulation of cell cycle phase transition (Score: 3.839719)



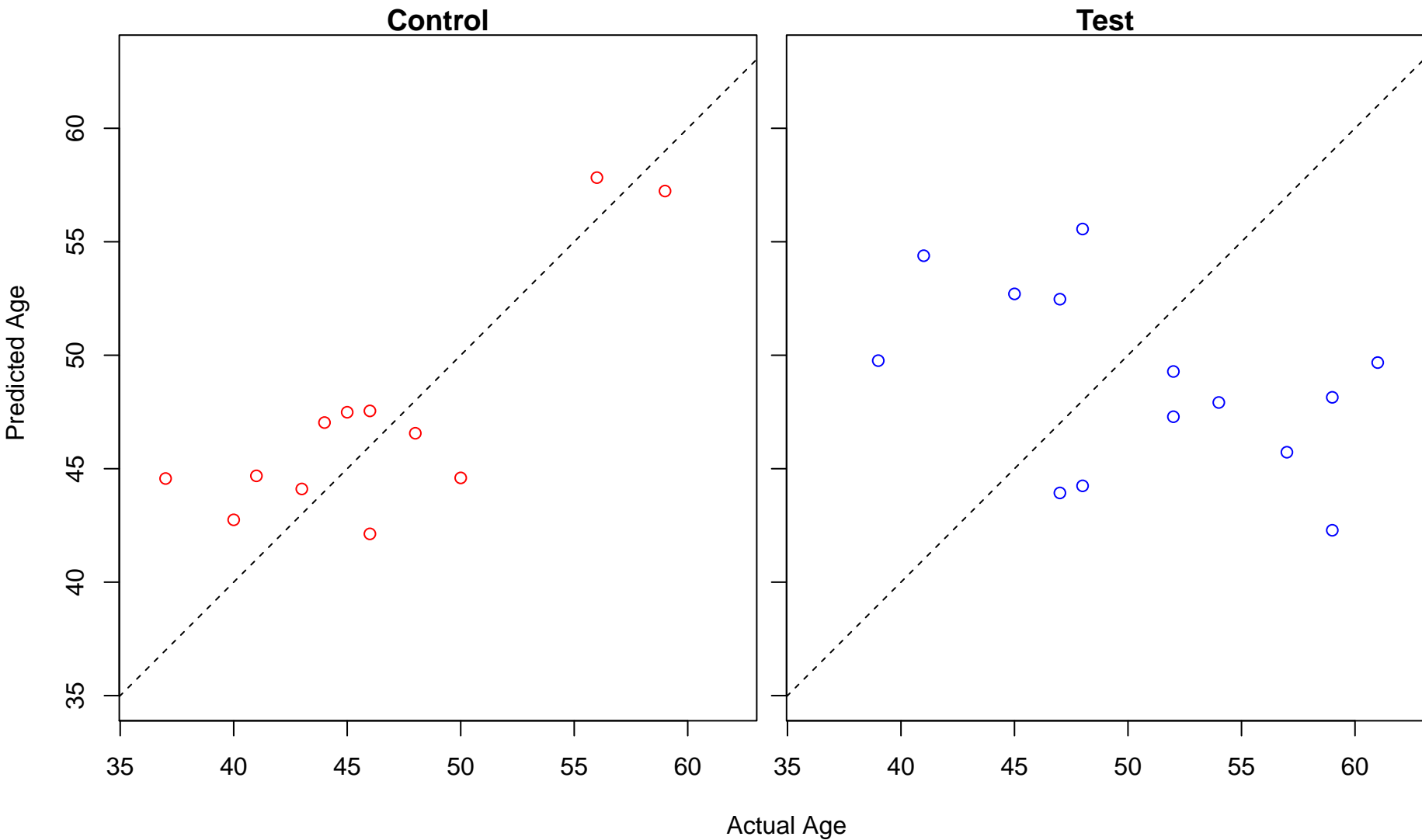
translesion synthesis (Score: 3.837861)



signal transduction by p53 class mediator (Score: 3.835193)

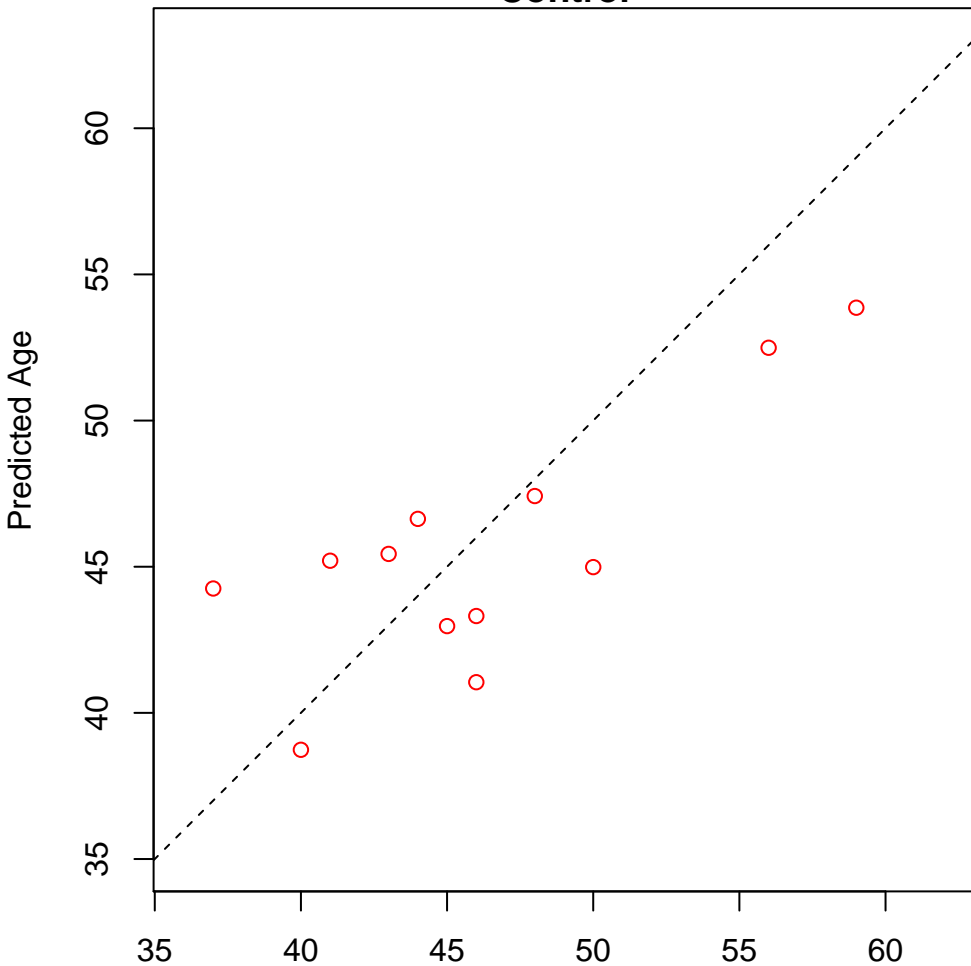


positive regulation of lymphocyte activation (Score: 3.833557)

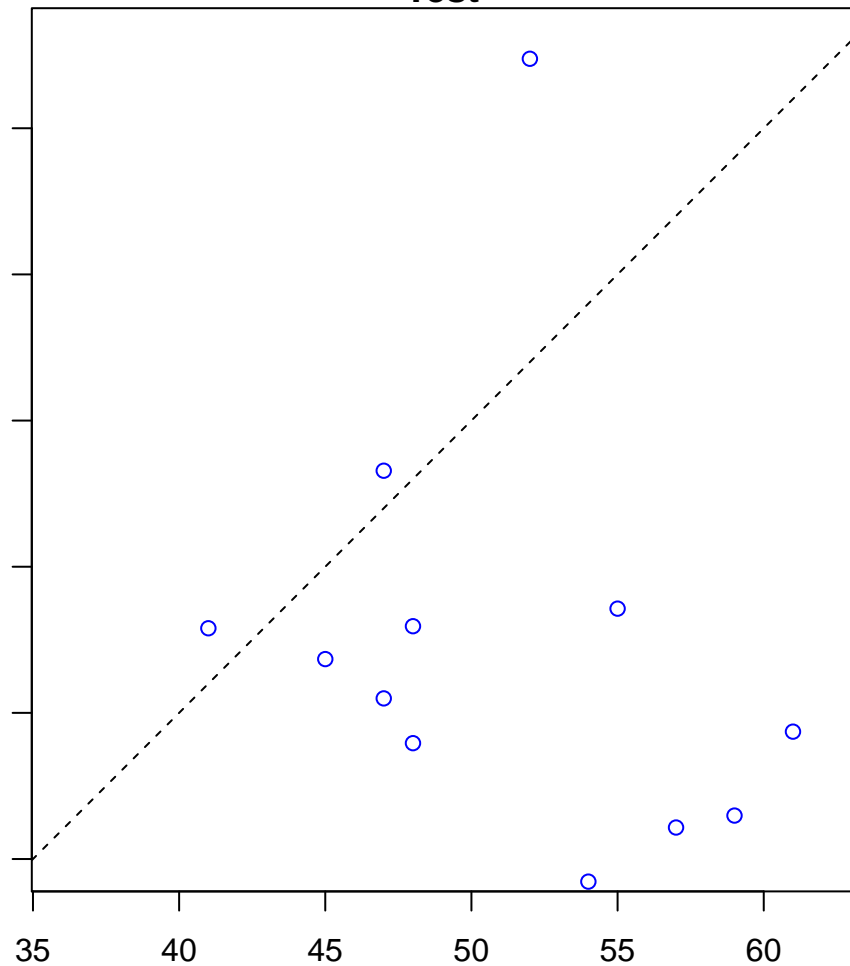


alpha-amino acid metabolic process (Score: 3.832993)

Control

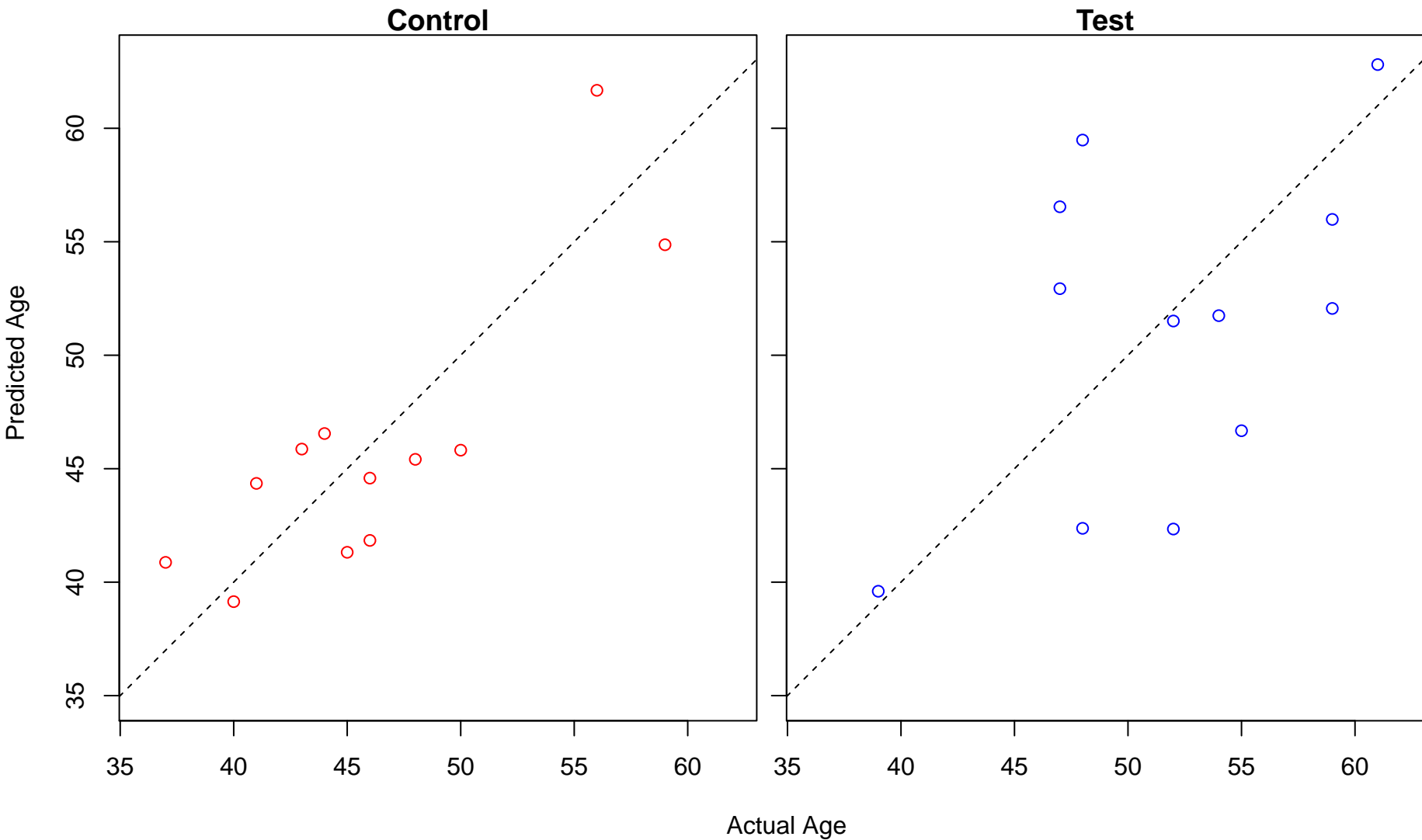


Test

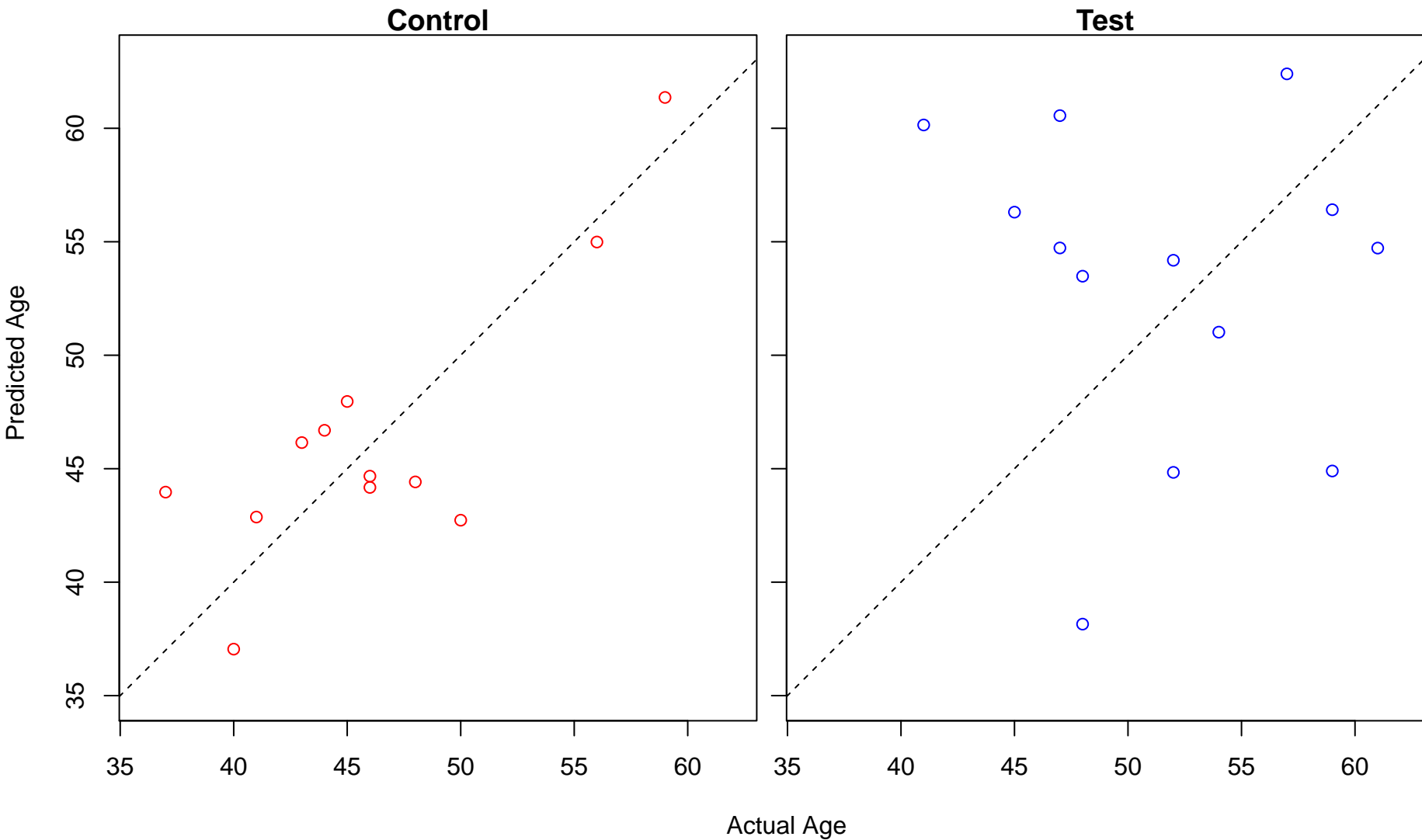


Actual Age

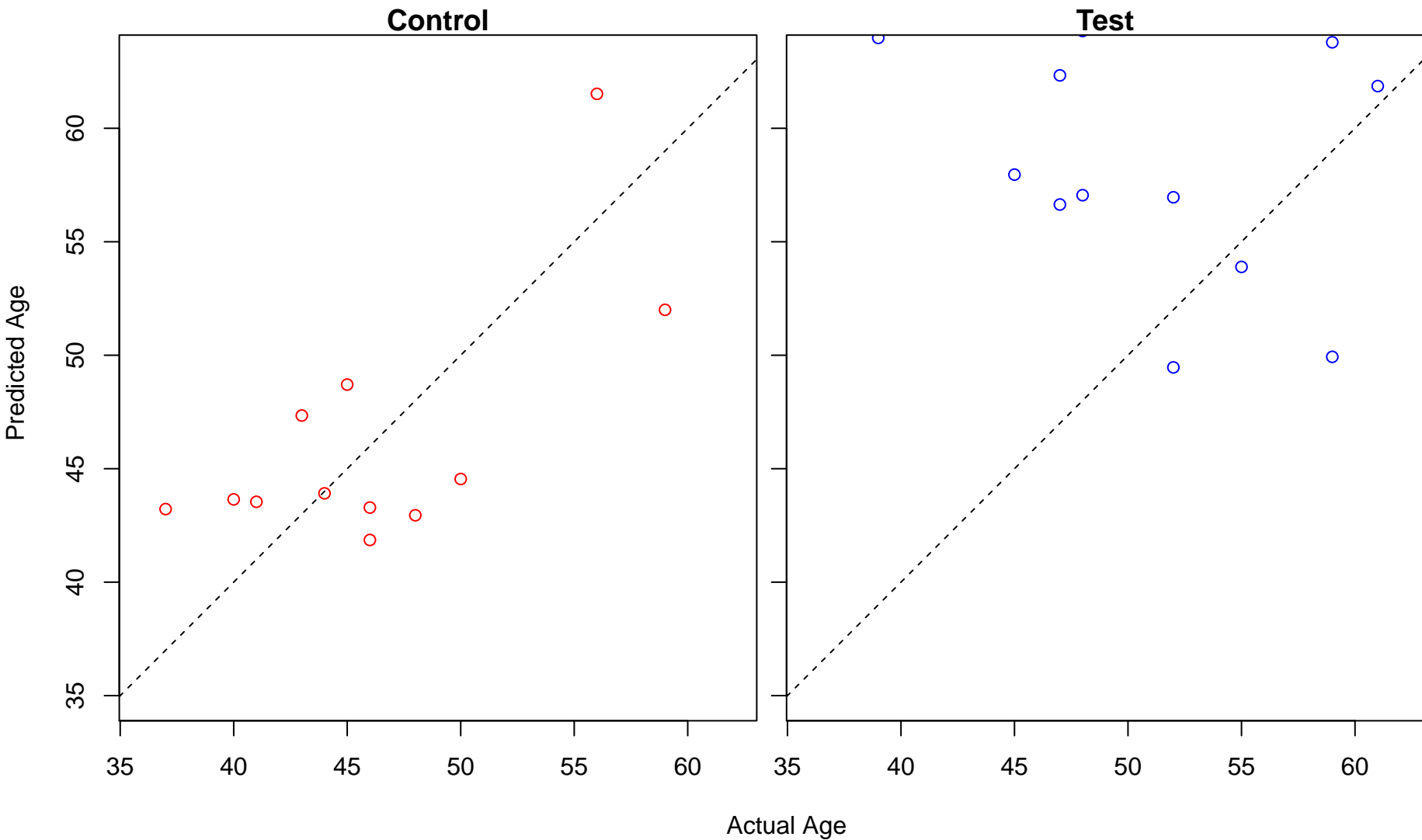
regulation of sequence-specific DNA binding transcription factor activity (Score: 3.828421)



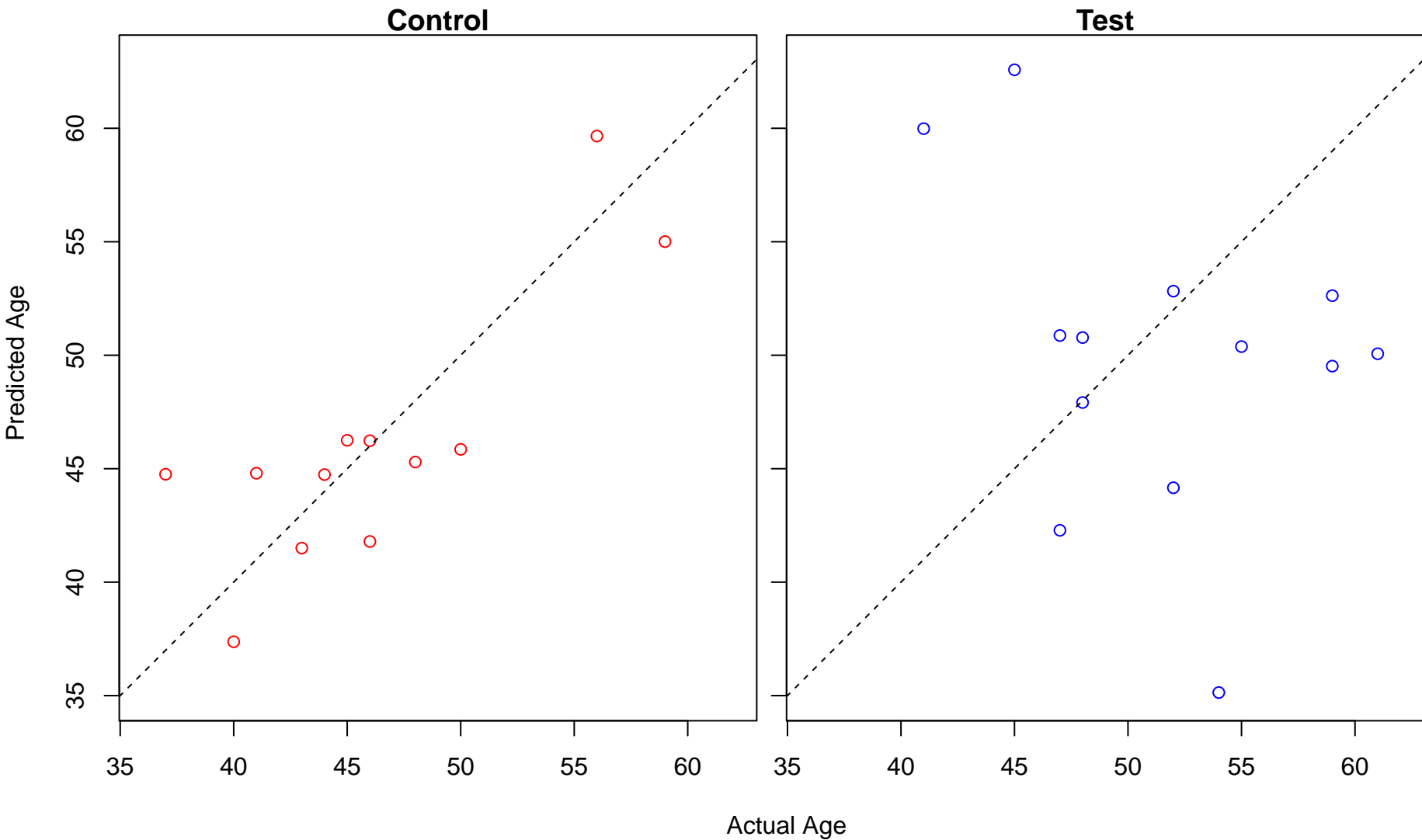
positive regulation of osteoblast differentiation (Score: 3.827482)



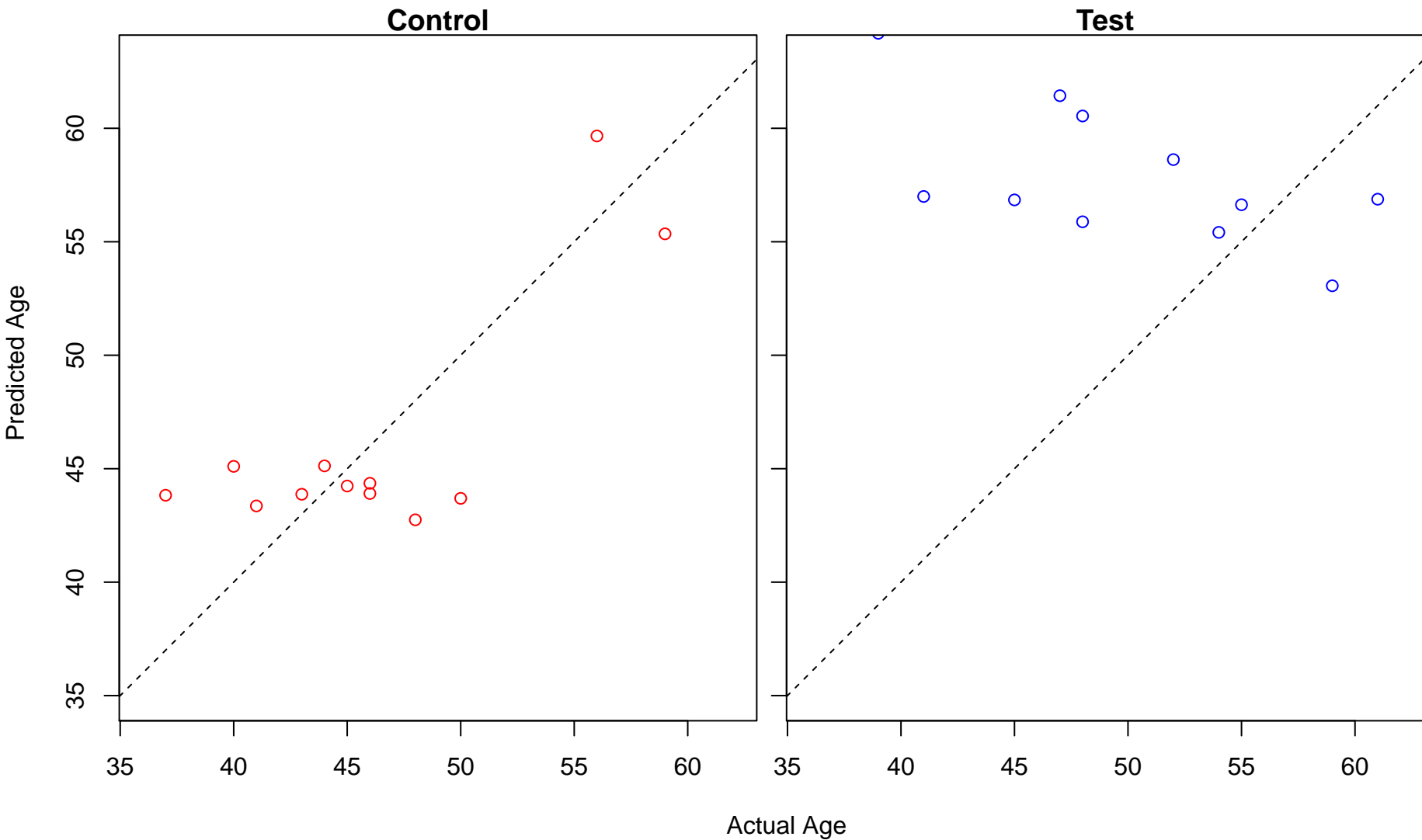
regulation of interleukin-6 biosynthetic process (Score: 3.825055)



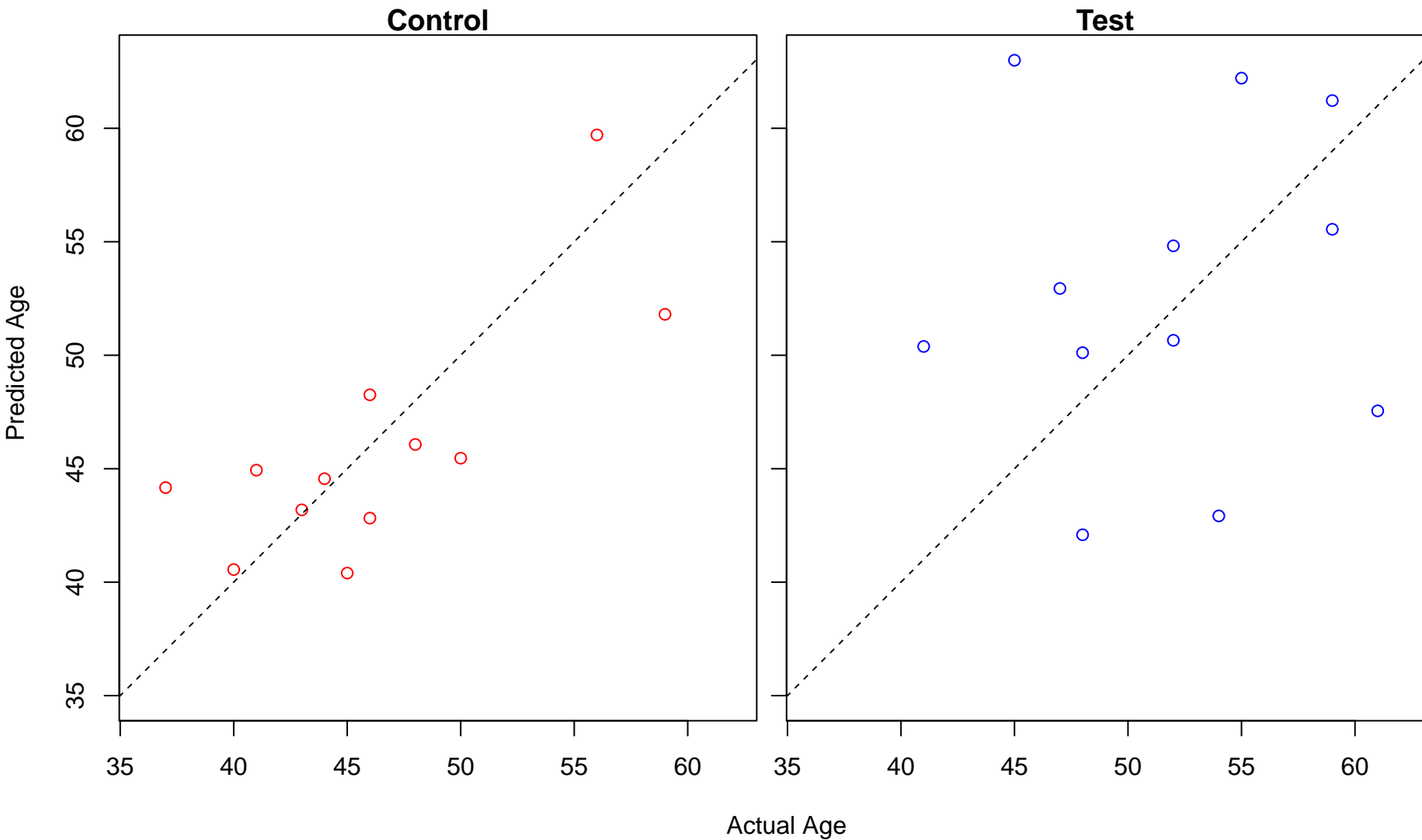
response to zinc ion (Score: 3.821975)



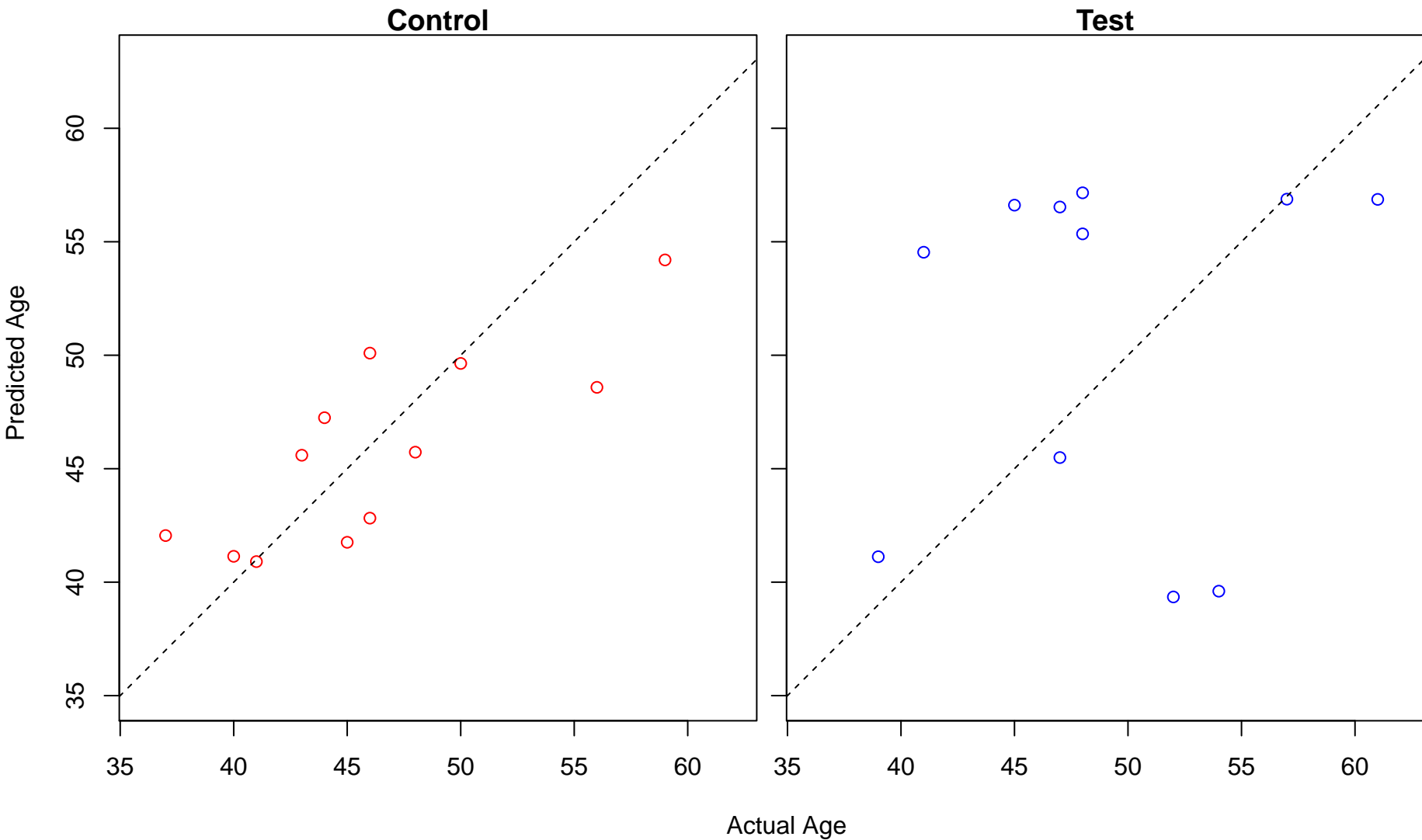
substrate-dependent cell migration, cell extension (Score: 3.821639)



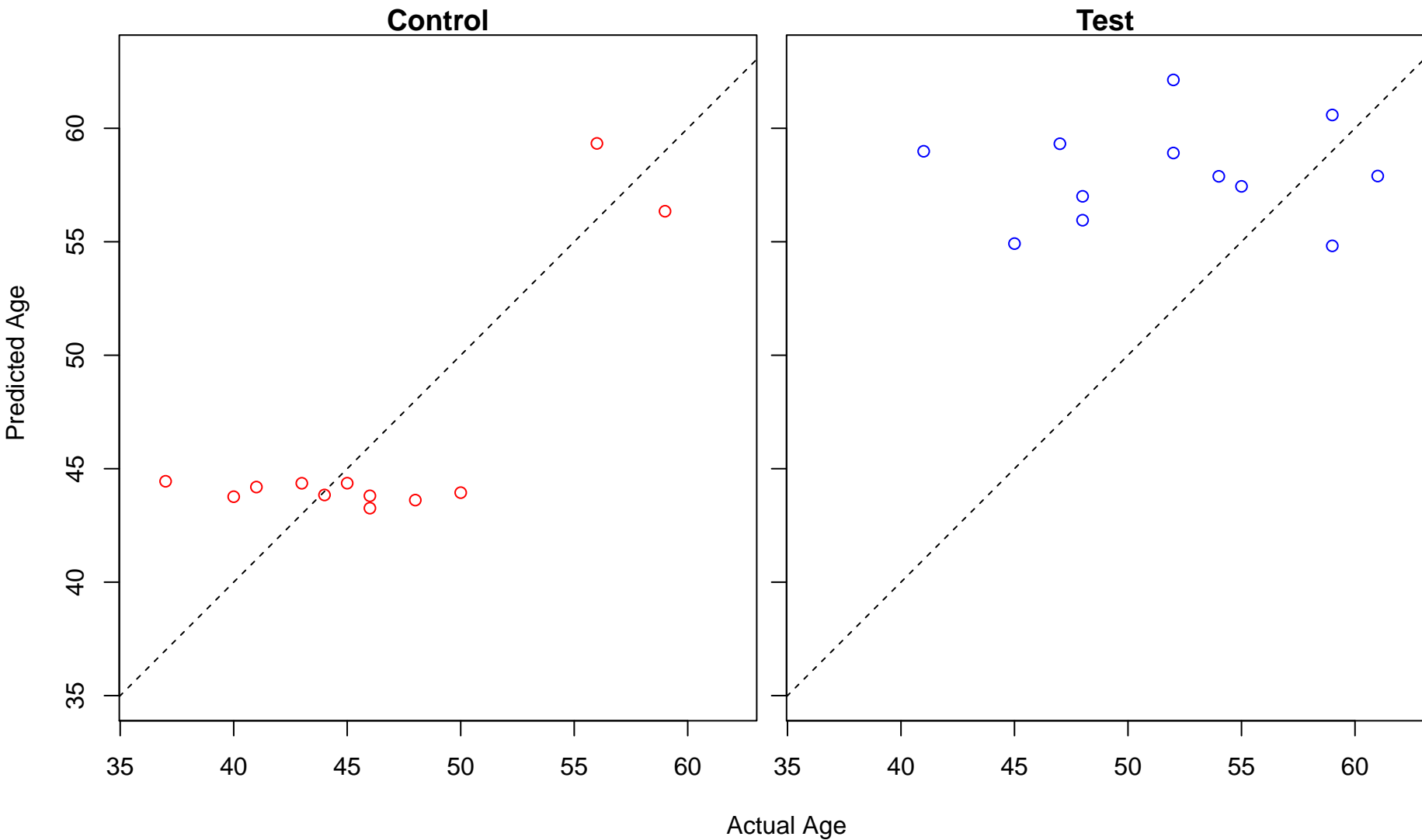
positive regulation of nucleotide catabolic process (Score: 3.821313)



sprouting angiogenesis (Score: 3.821202)

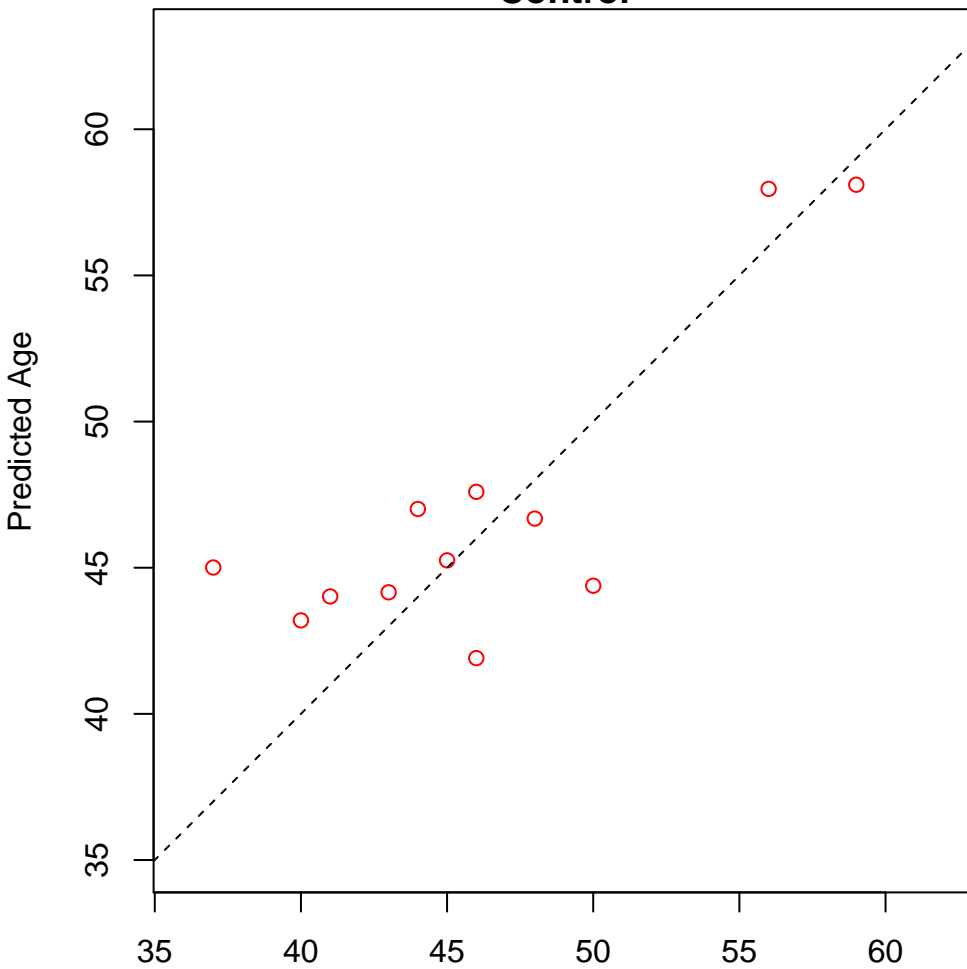


postreplication repair (Score: 3.819491)

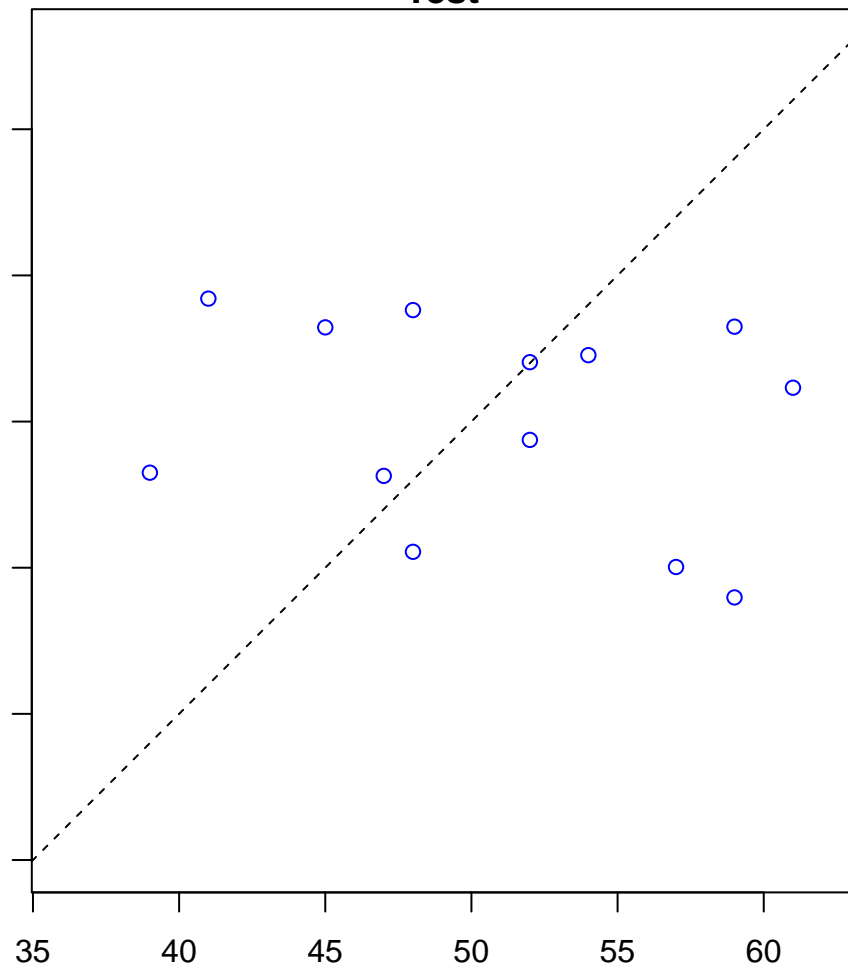


positive regulation of cell-cell adhesion (Score: 3.819278)

Control

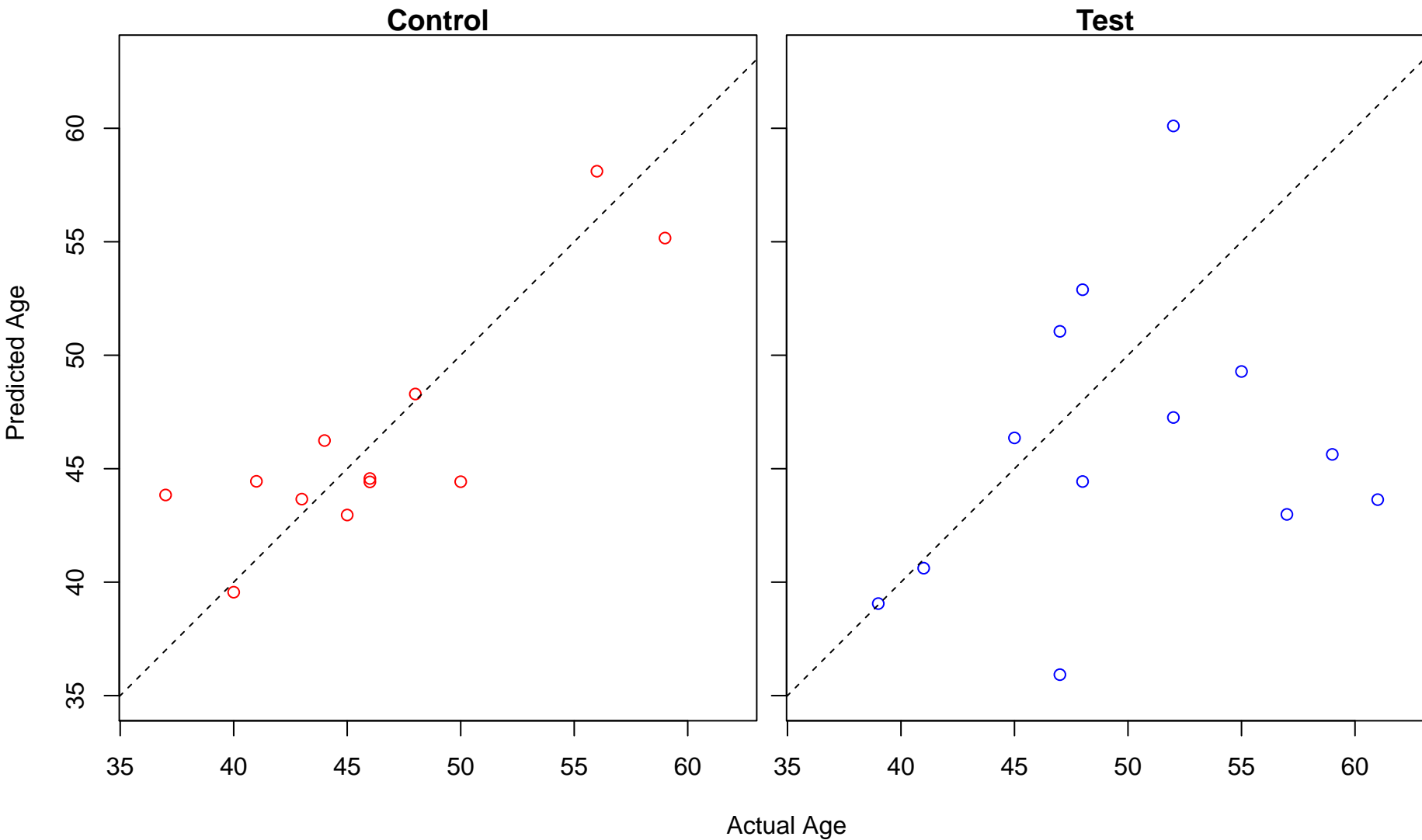


Test

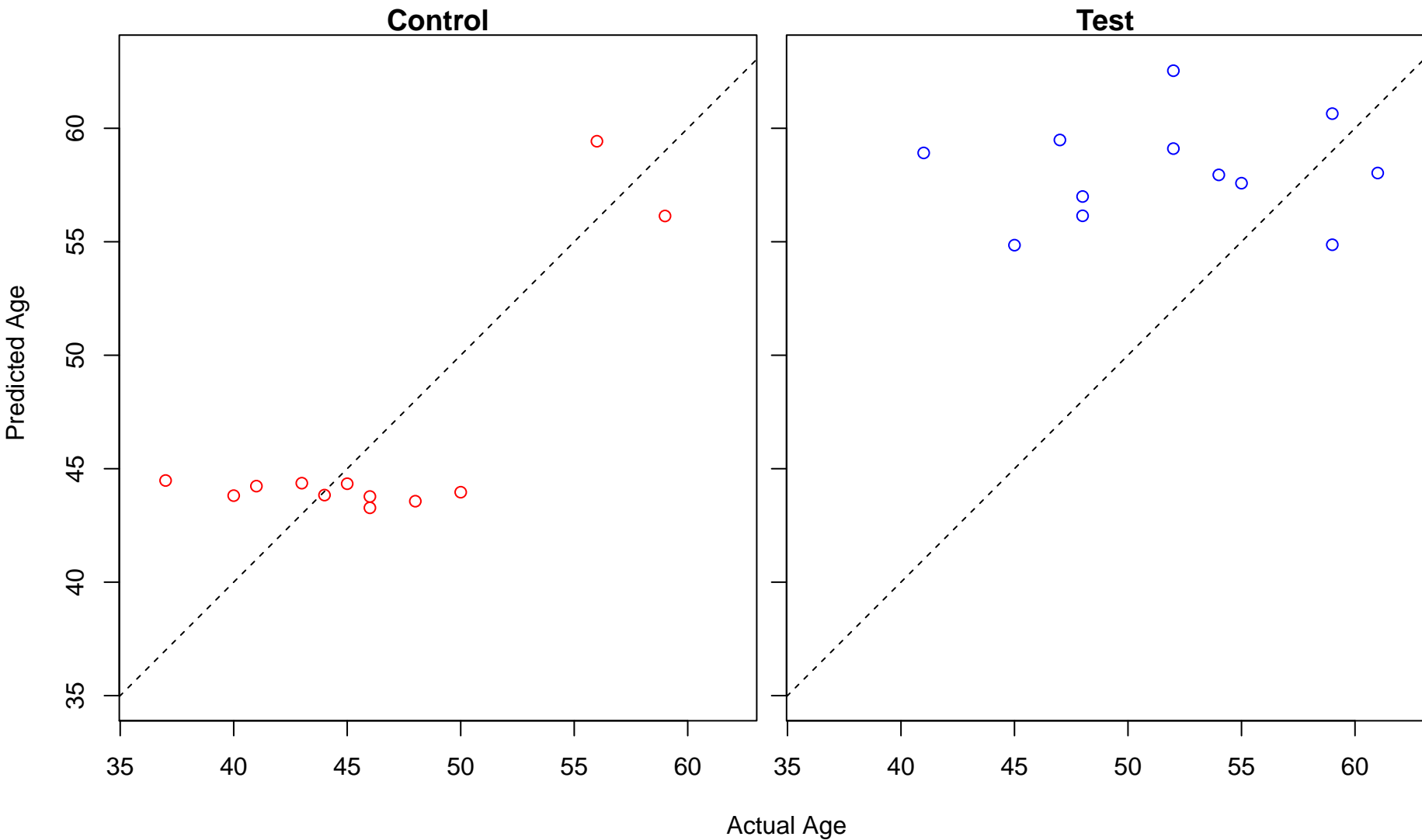


Actual Age

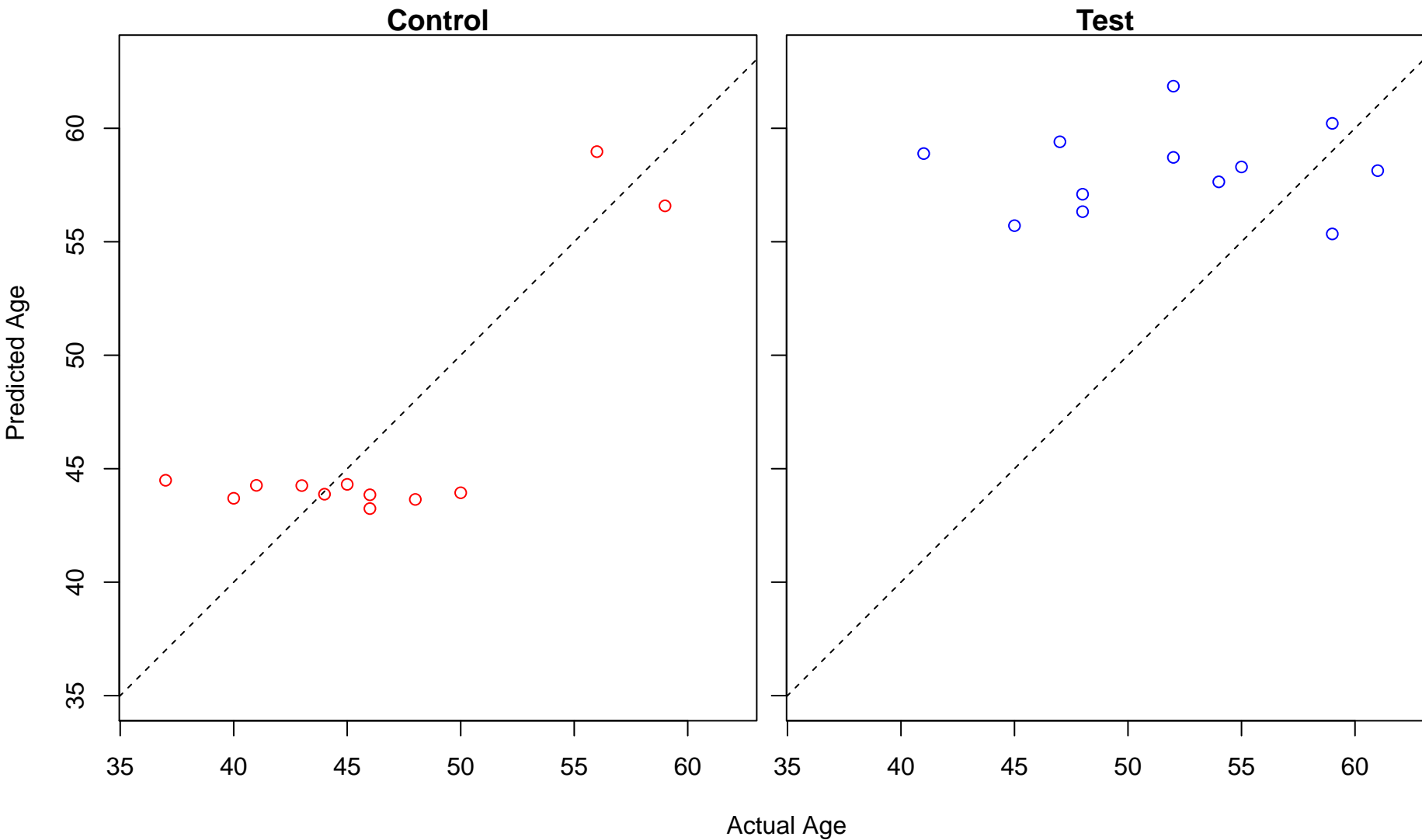
positive regulation of viral genome replication (Score: 3.817157)



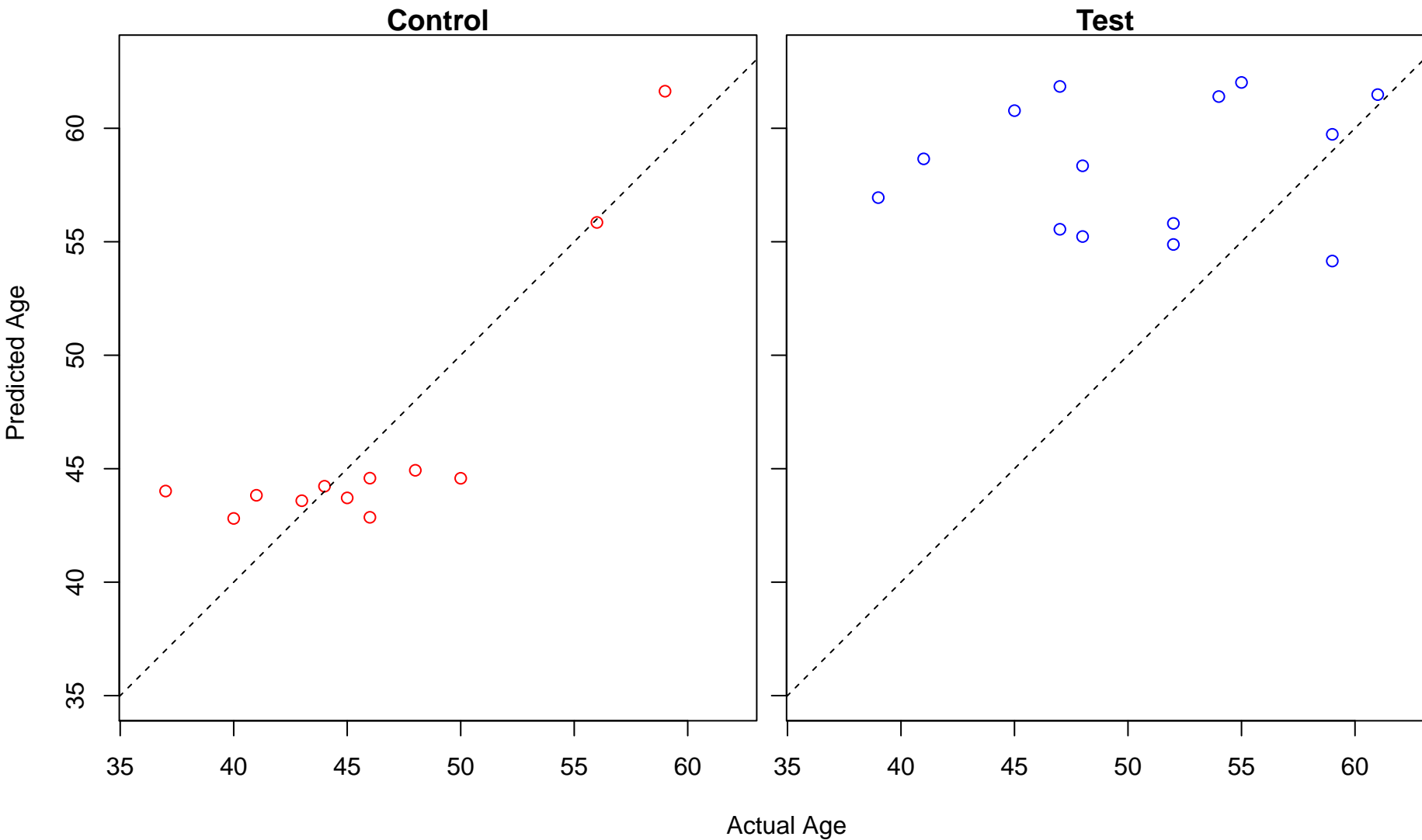
regulation of transcription from RNA polymerase II promoter in response to hypoxia (Score: 3.81006)



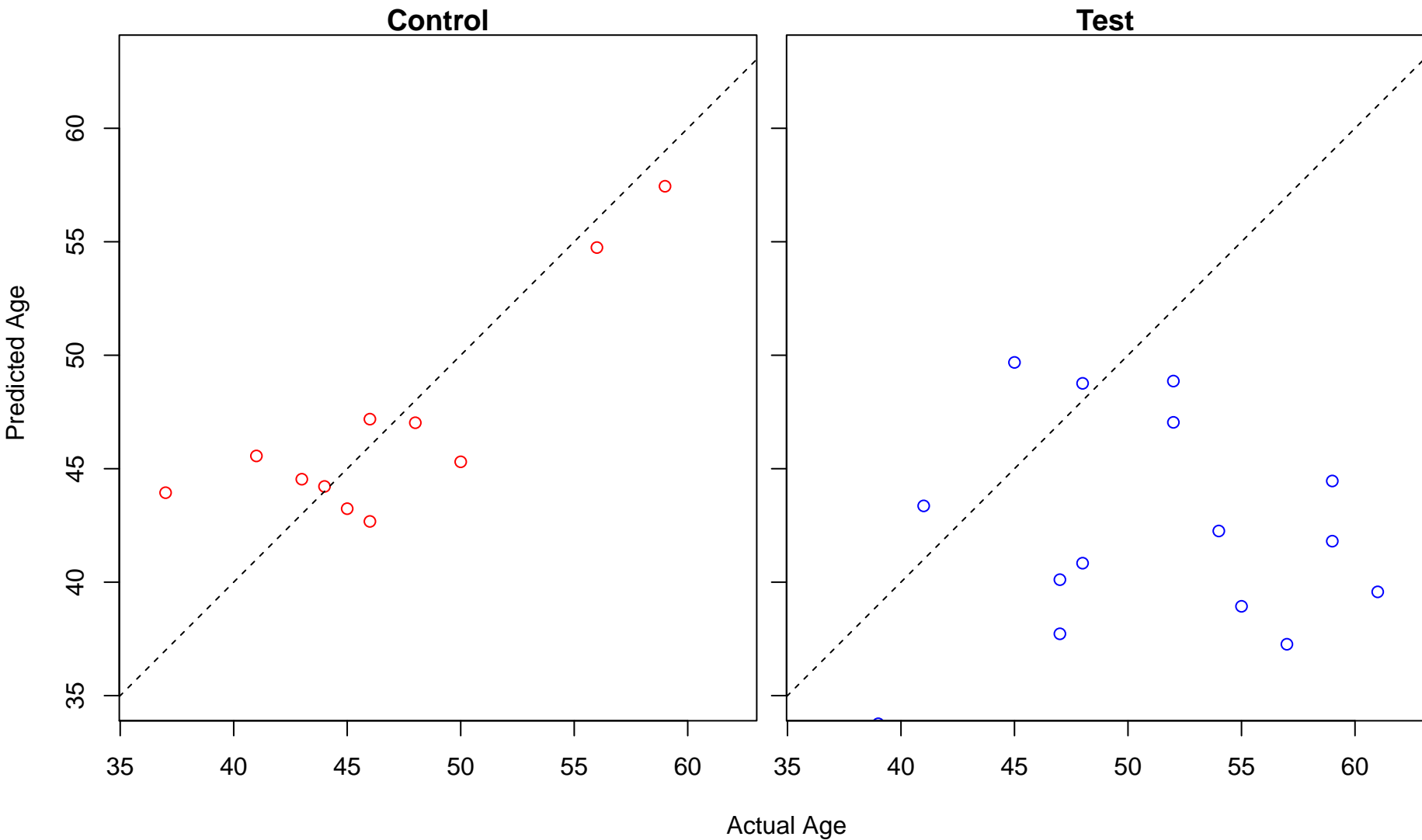
positive regulation of type I interferon production (Score: 3.808897)



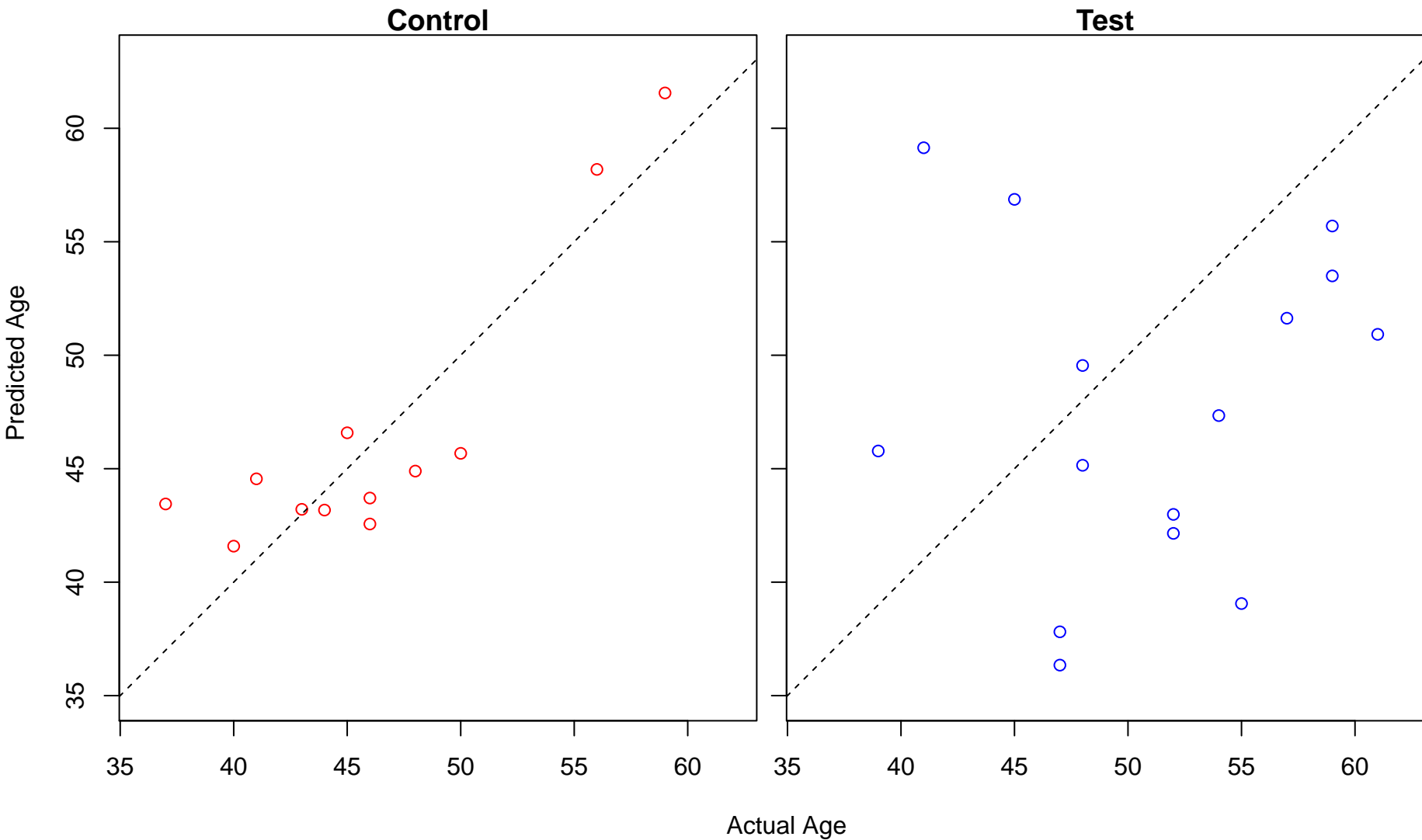
negative regulation of inclusion body assembly (Score: 3.805470)



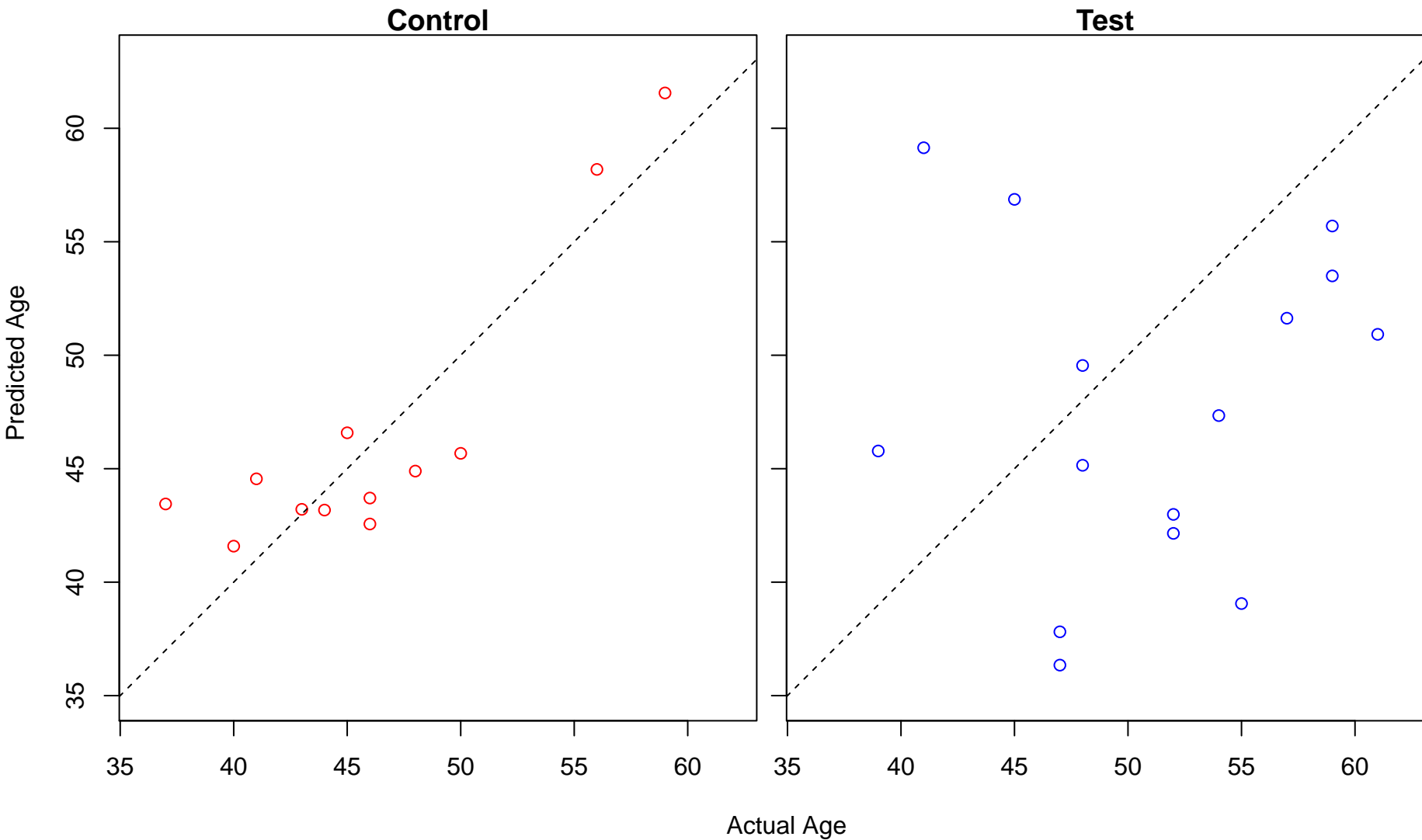
regulation of lysosomal lumen pH (Score: 3.800602)



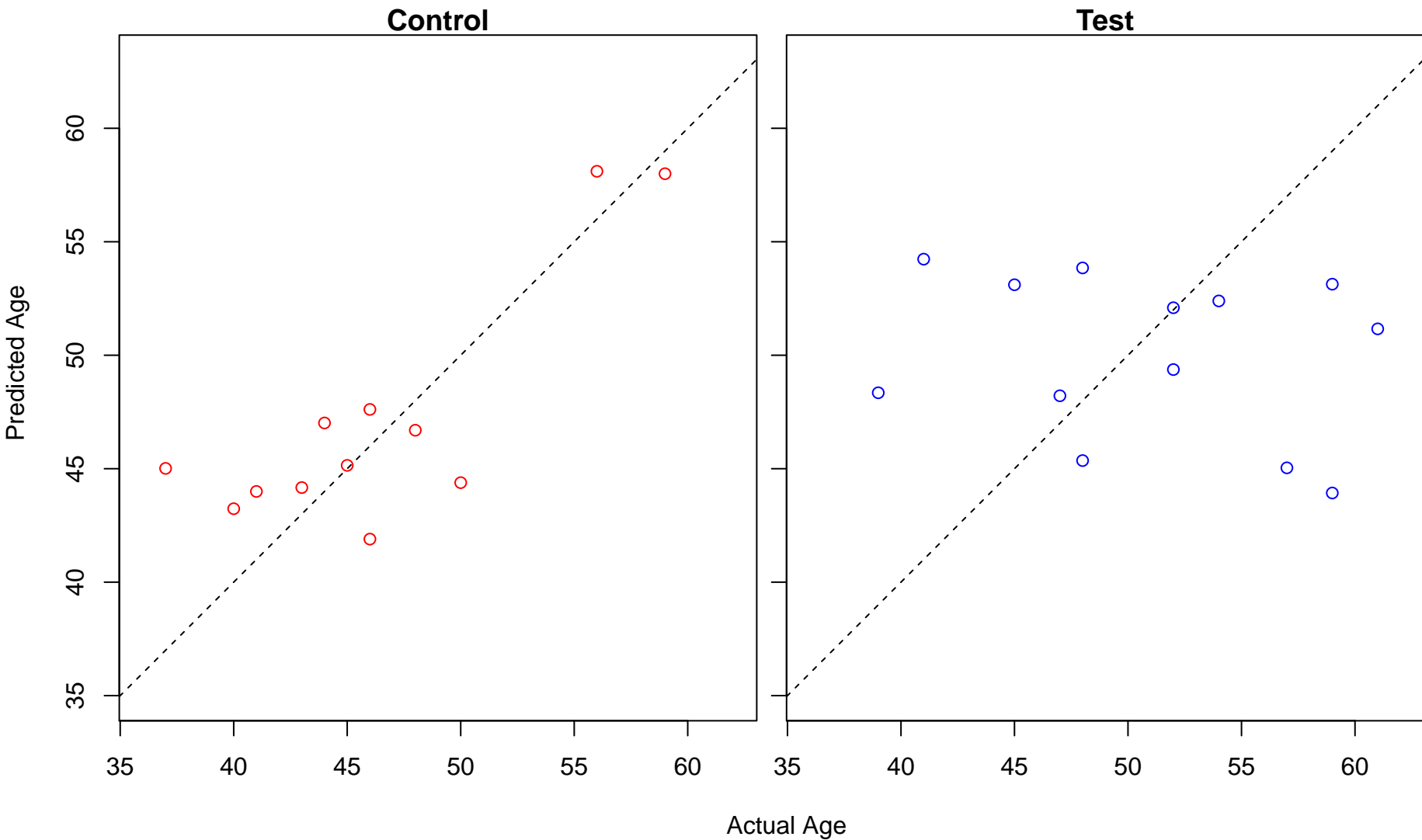
regulation of gene expression by genetic imprinting (Score: 3.799909)



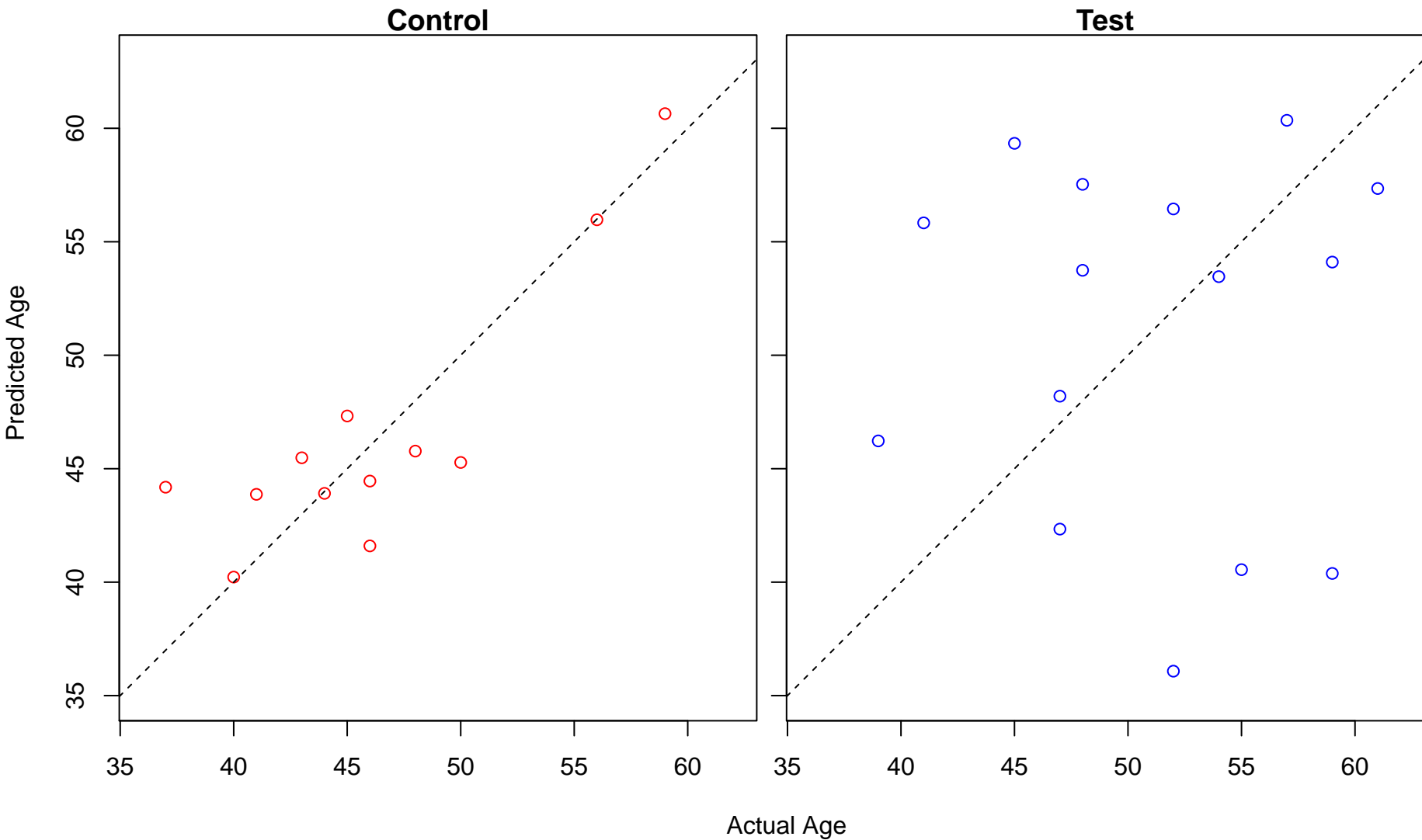
genetic imprinting (Score: 3.799909)



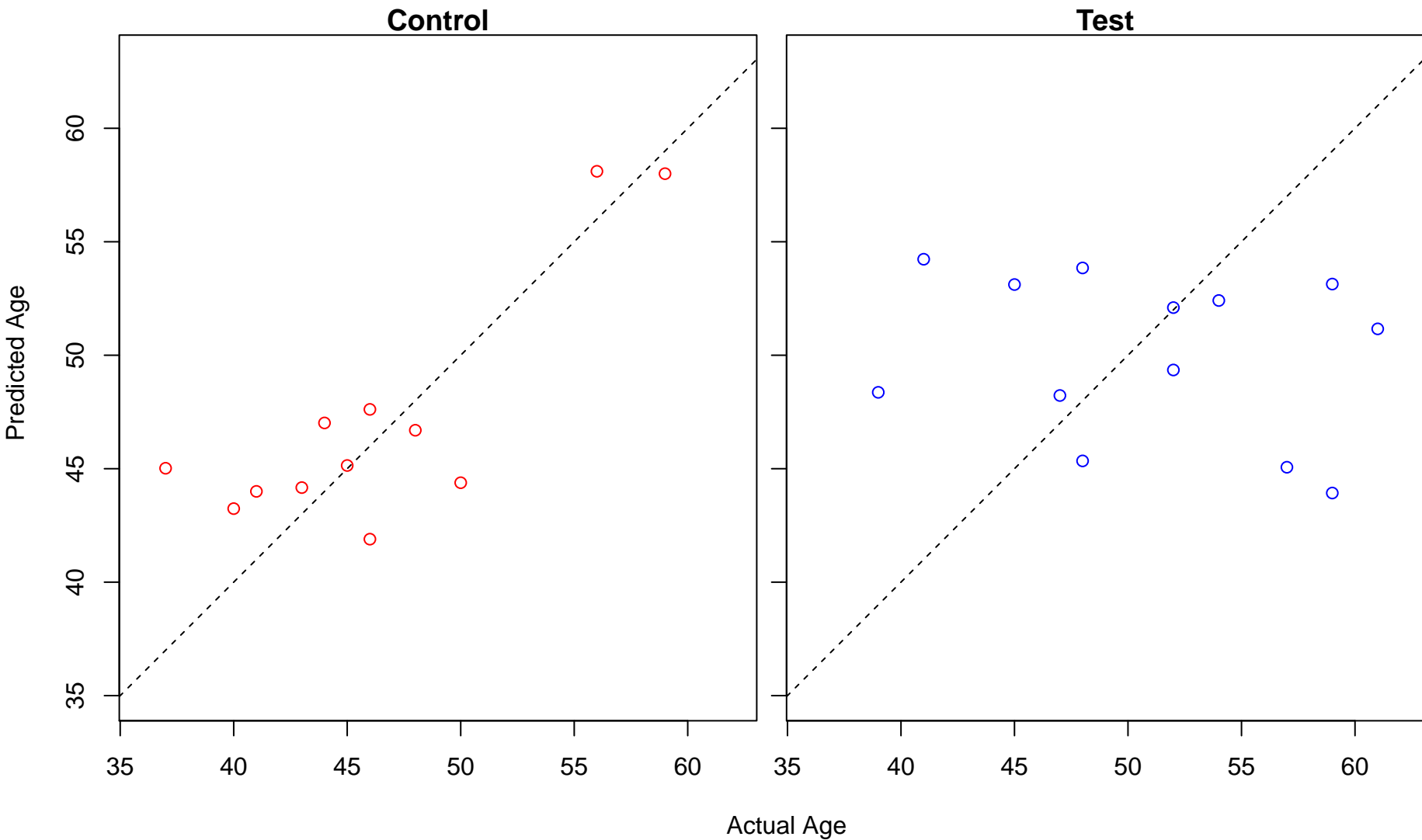
positive regulation of homotypic cell-cell adhesion (Score: 3.797214)



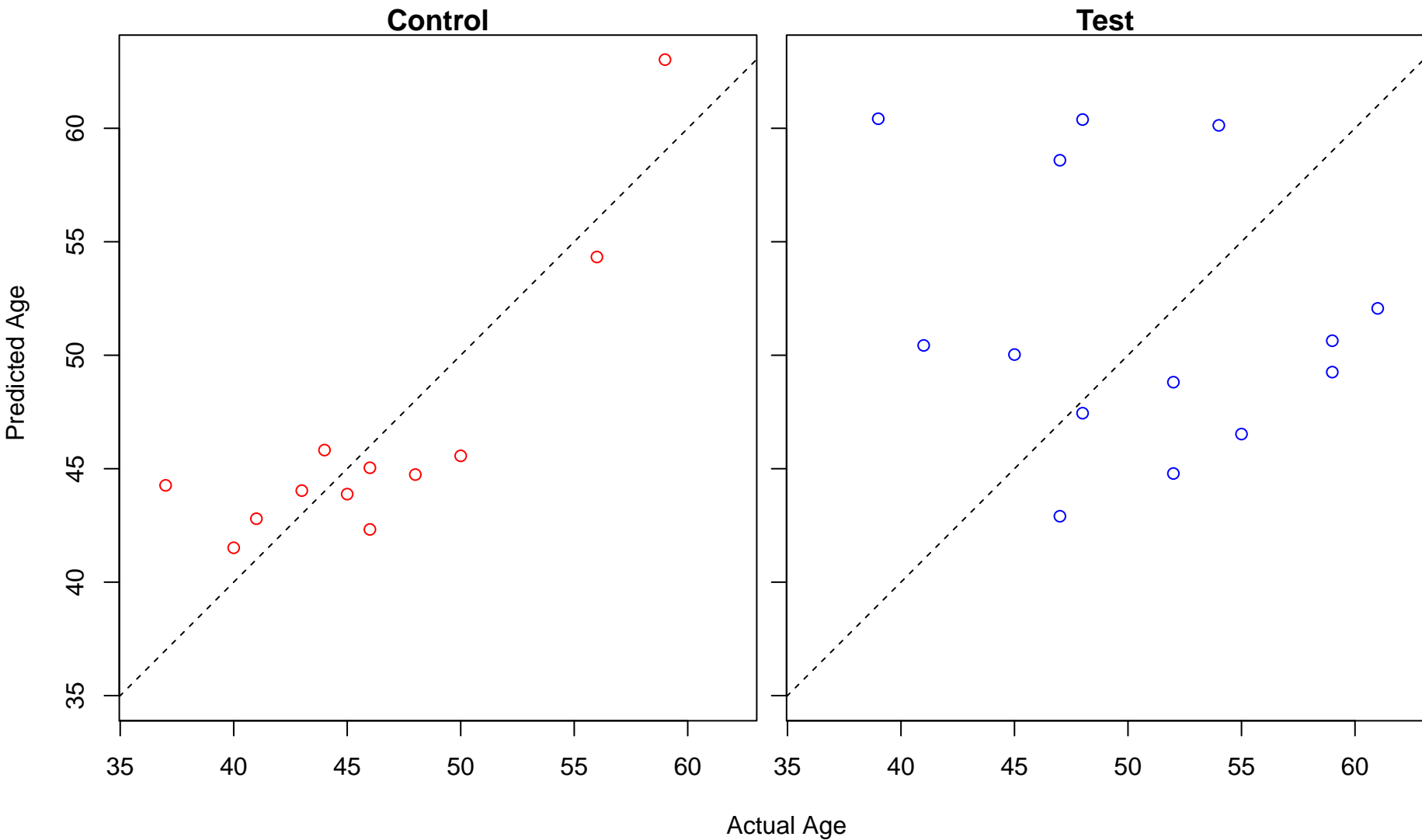
regulation of cysteine-type endopeptidase activity (Score: 3.796460)



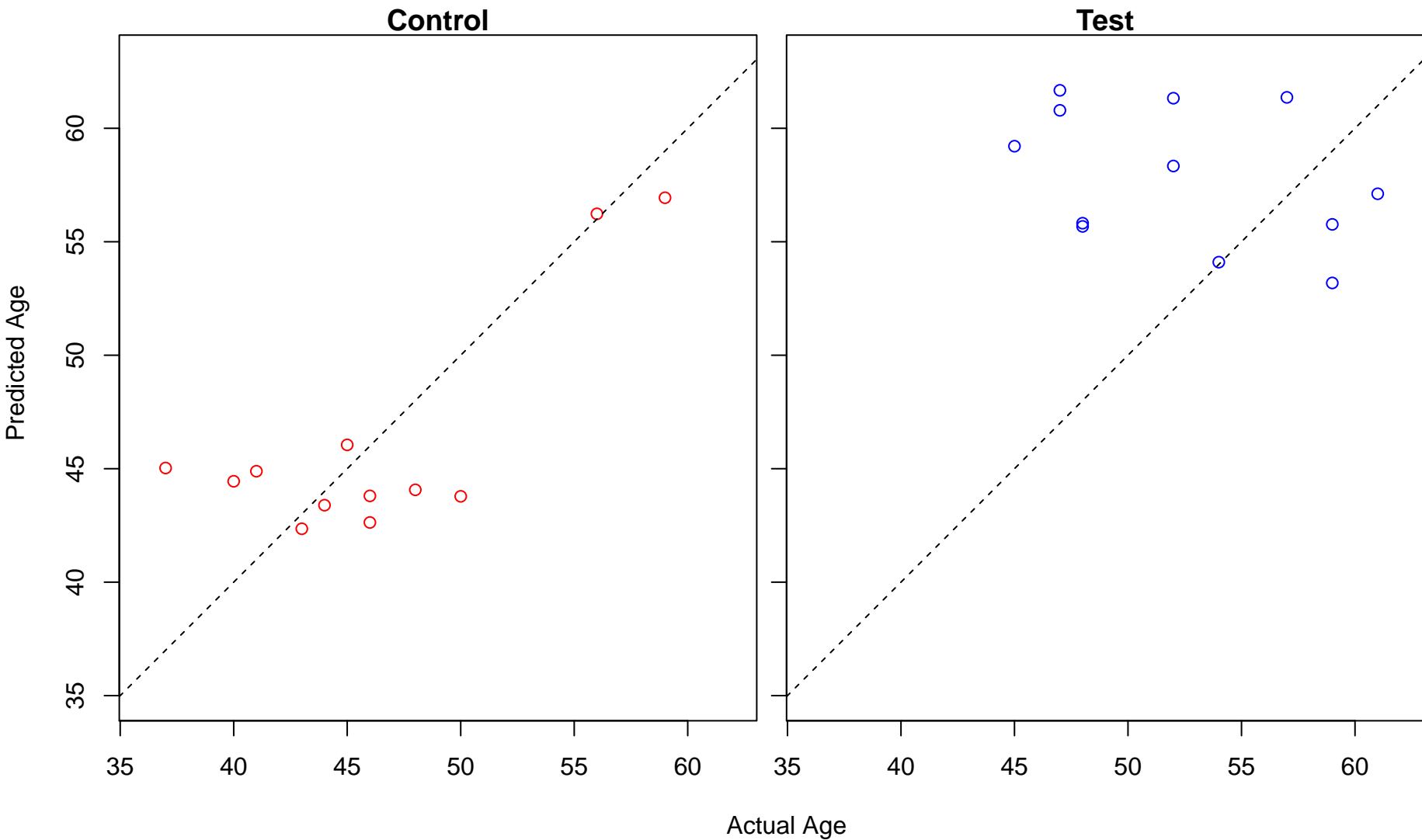
positive regulation of leukocyte cell-cell adhesion (Score: 3.795877)



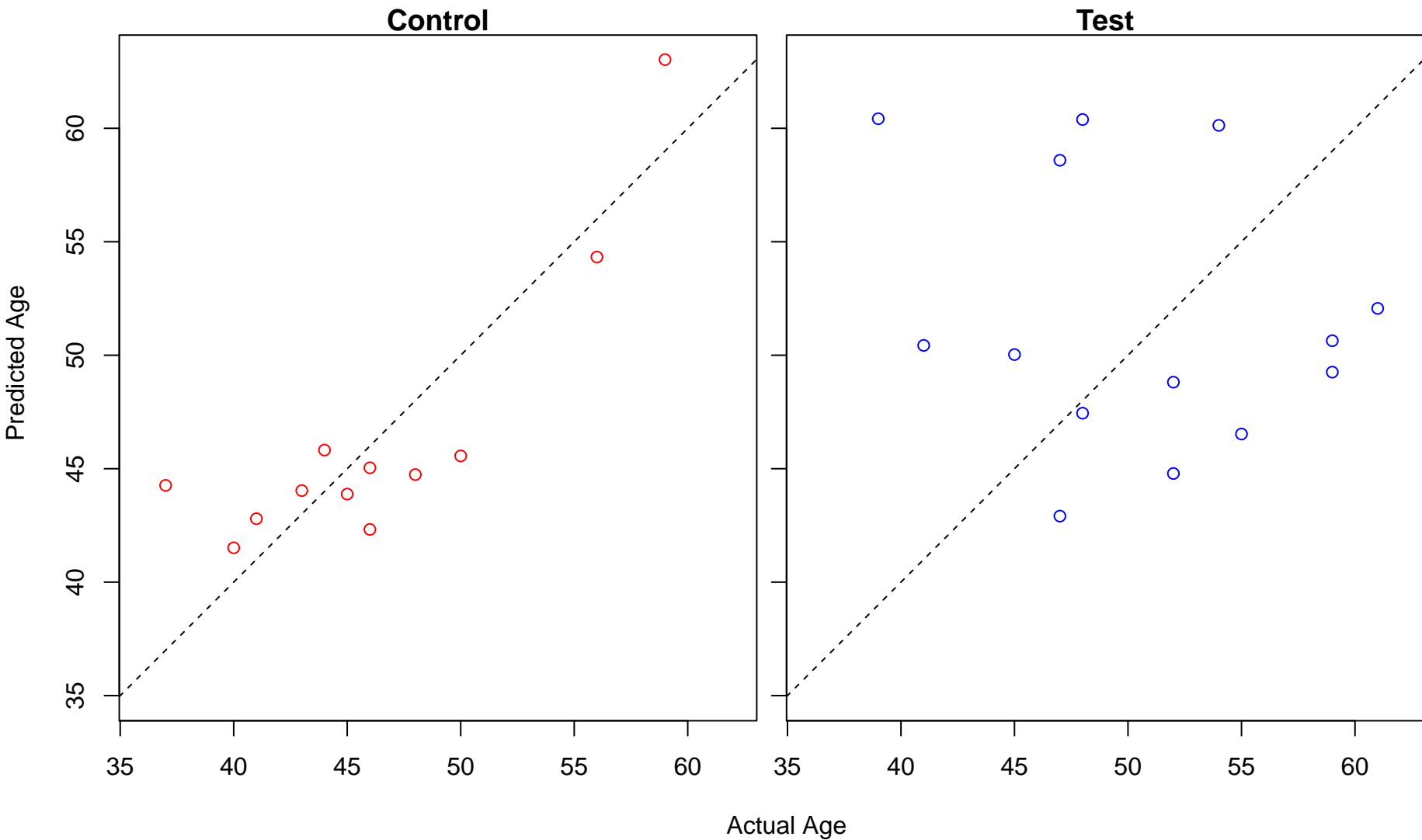
regulation of ion transmembrane transporter activity (Score: 3.794899)



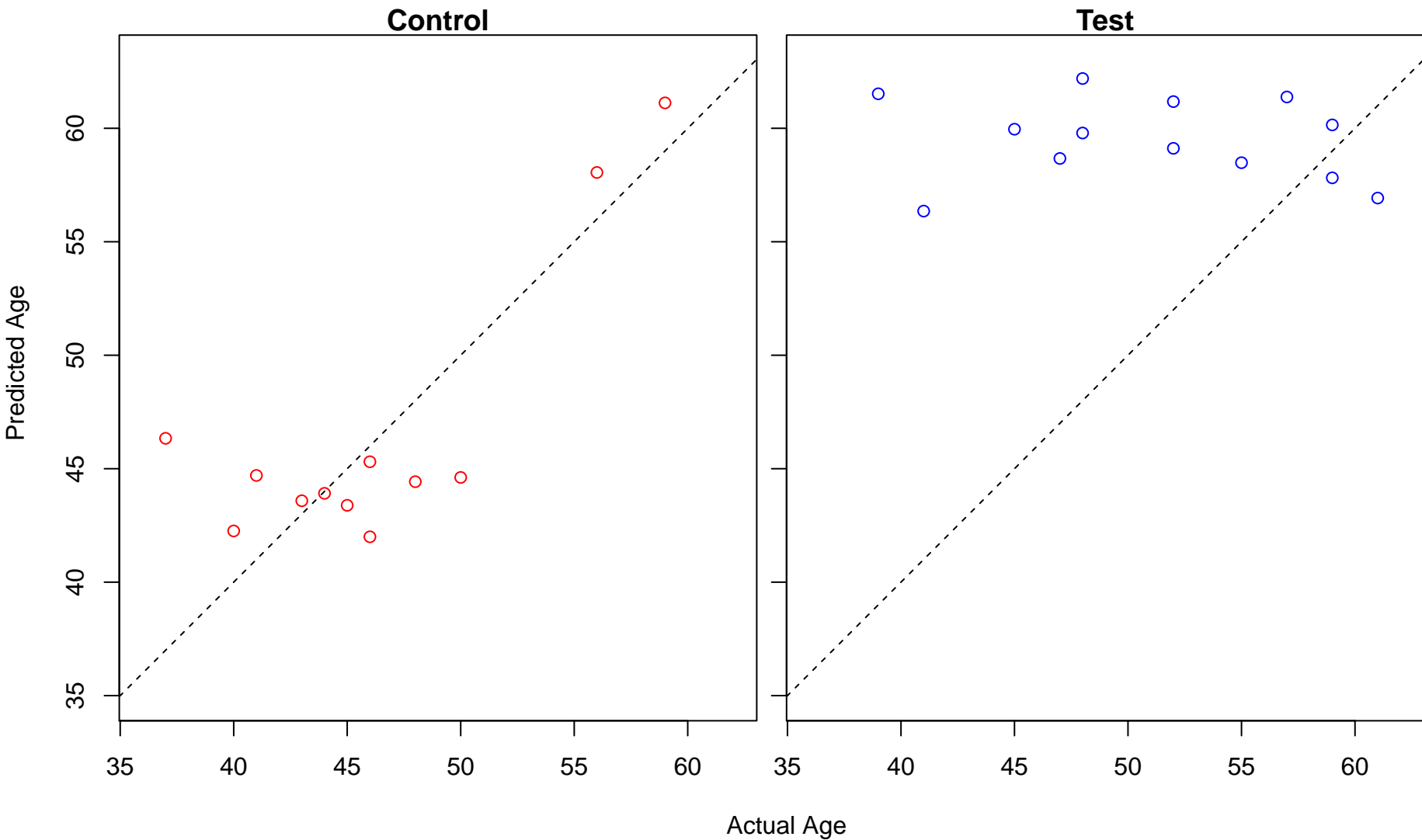
regulation of chemotaxis (Score: 3.794853)



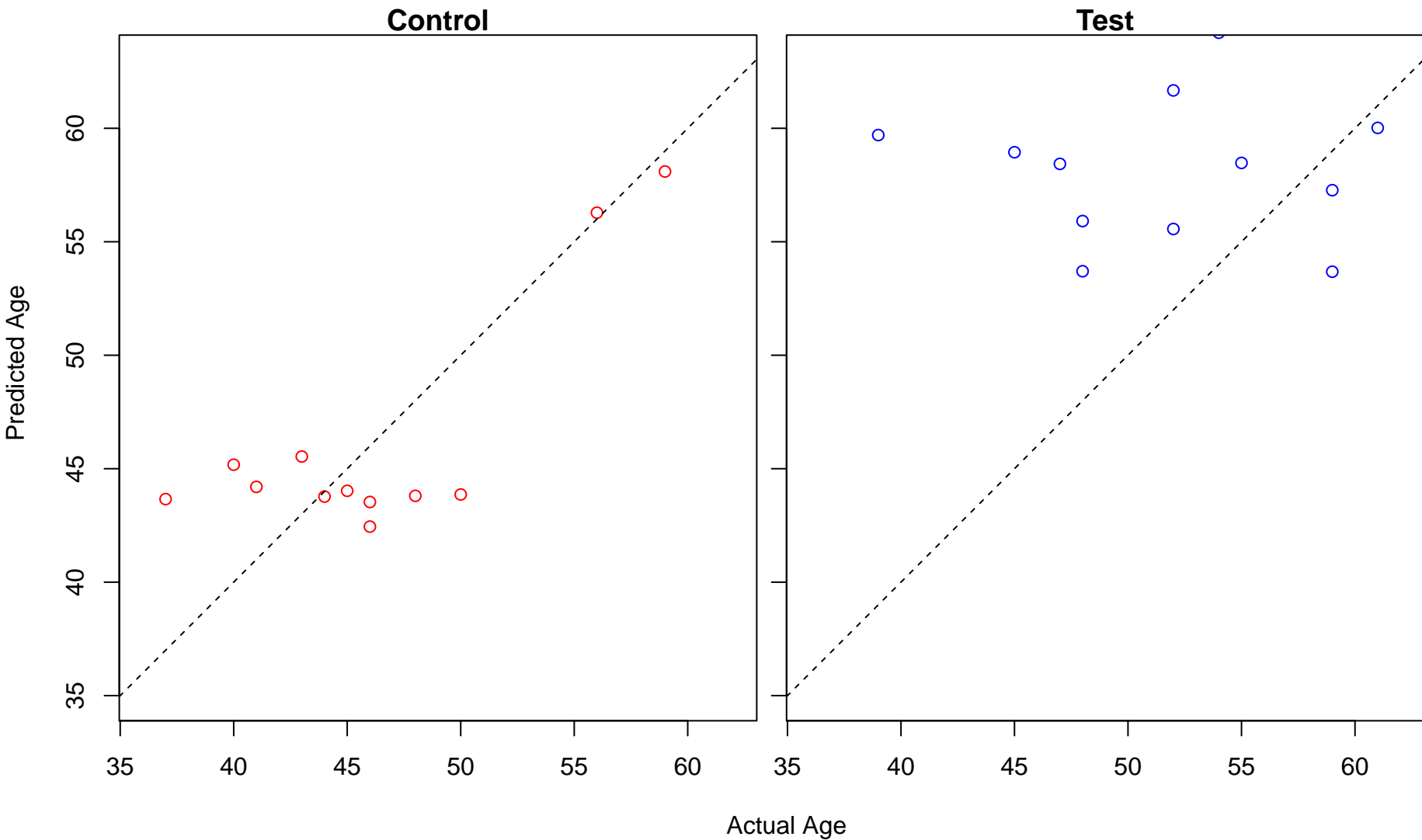
regulation of transmembrane transporter activity (Score: 3.794409)



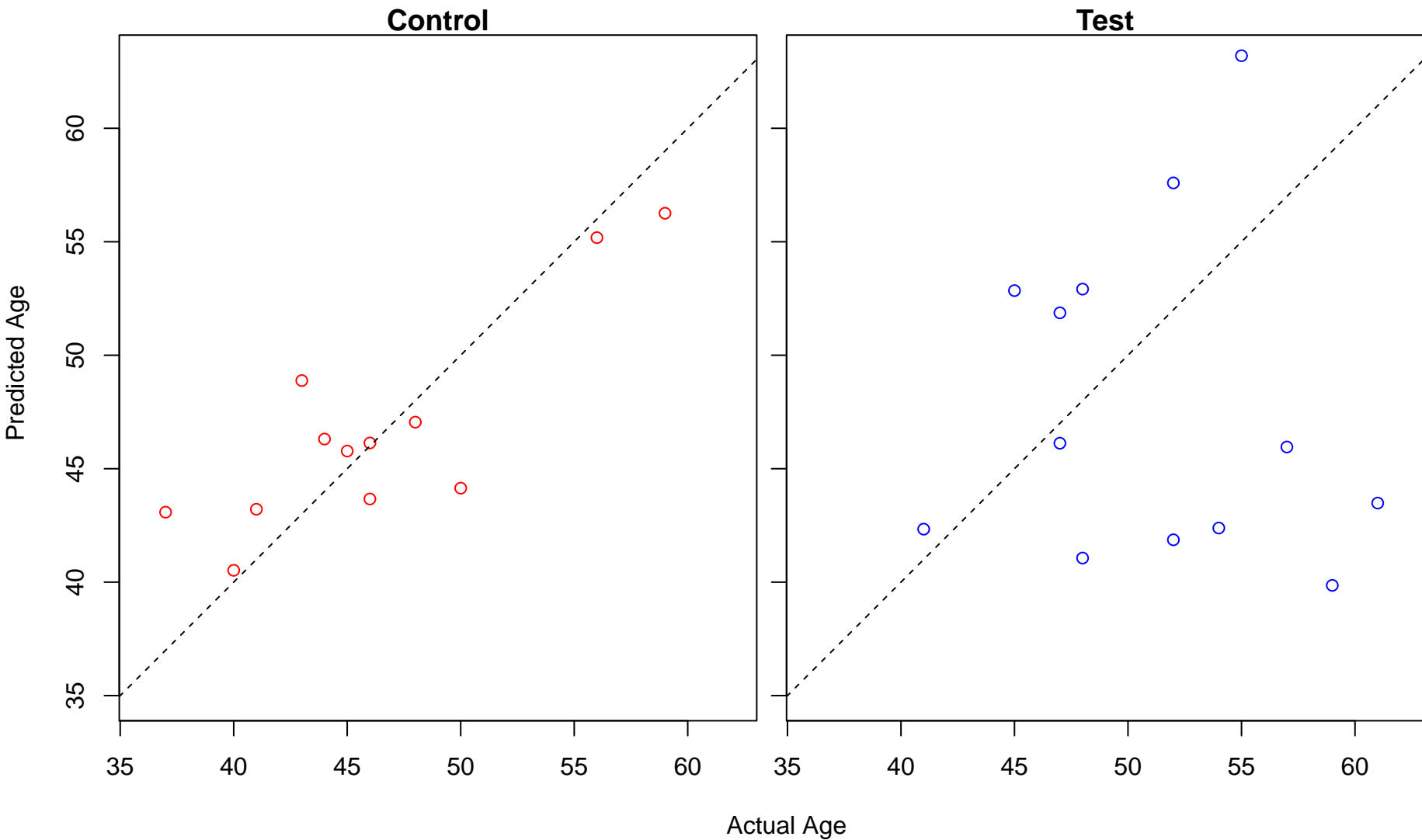
oocyte development (Score: 3.792775)



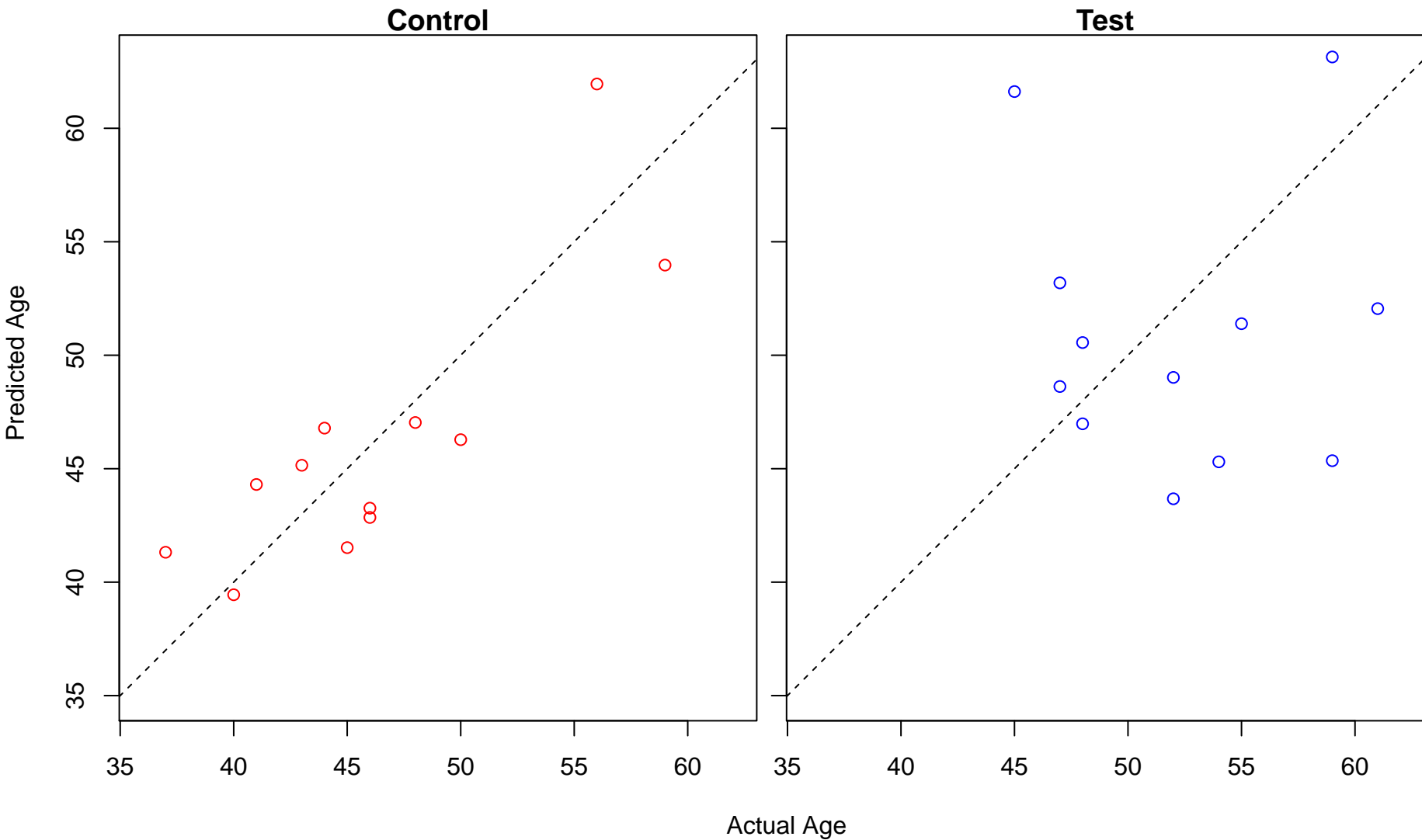
monosaccharide biosynthetic process (Score: 3.792751)



regulation of developmental growth (Score: 3.792391)

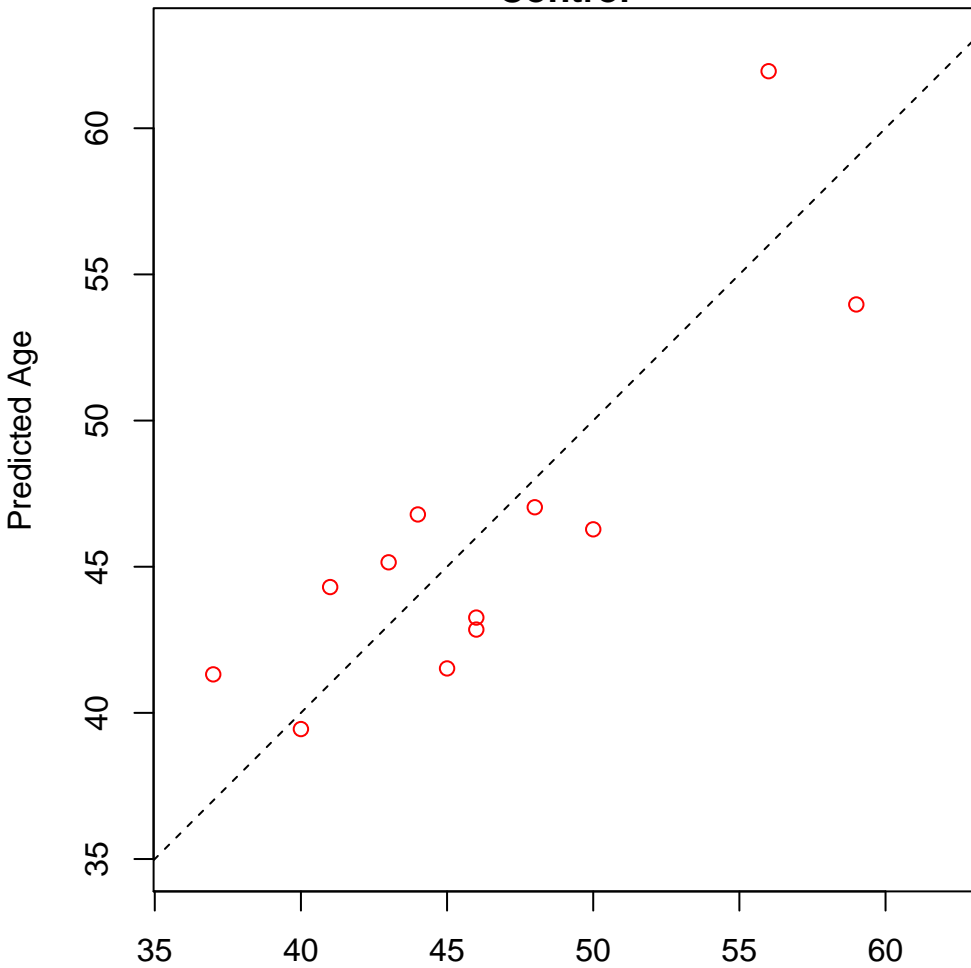


positive regulation of programmed cell death (Score: 3.786807)

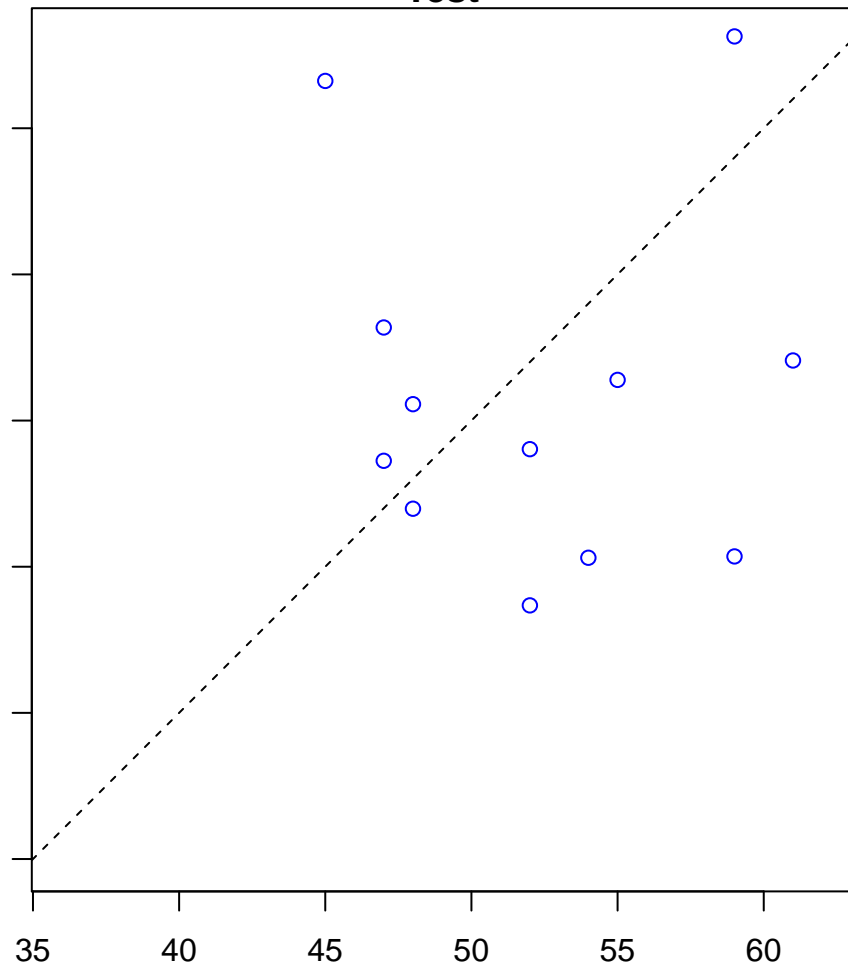


positive regulation of apoptotic process (Score: 3.786302)

Control

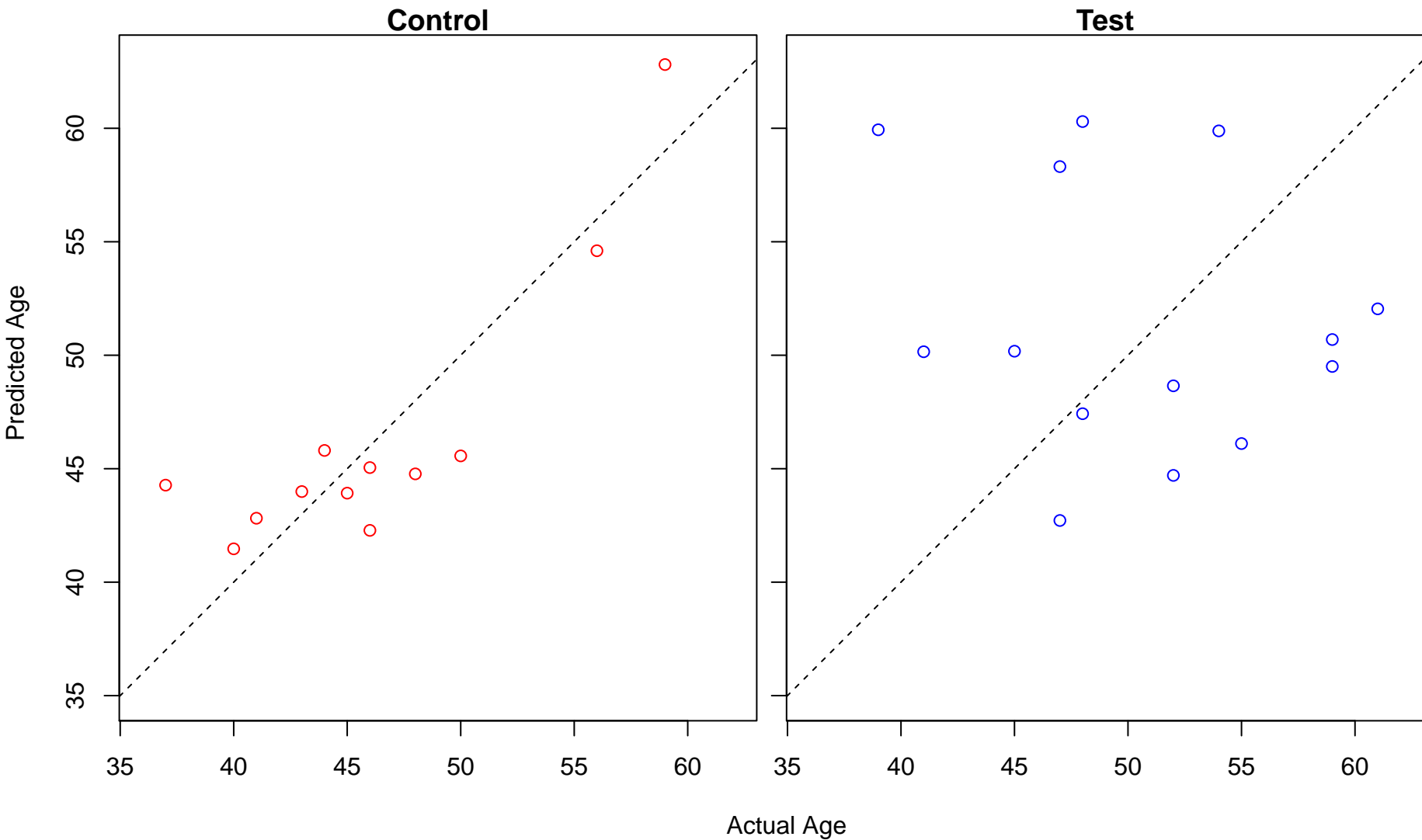


Test



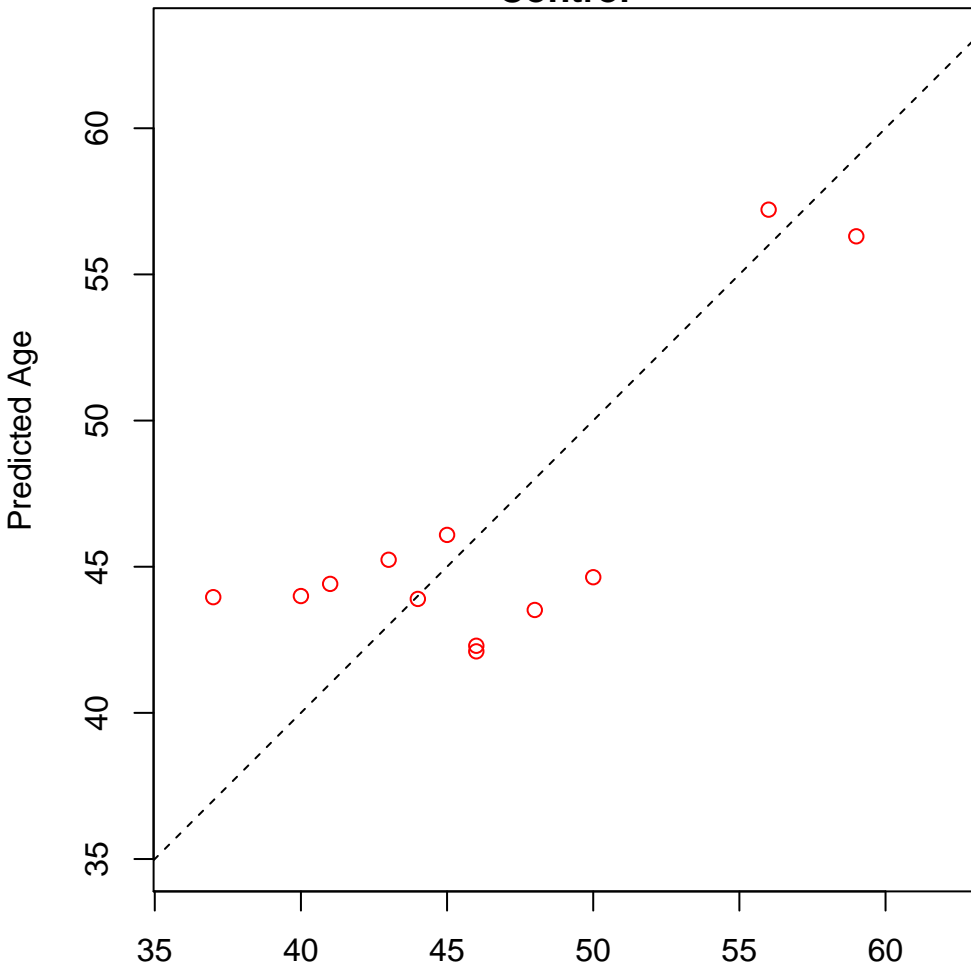
Actual Age

regulation of transporter activity (Score: 3.786202)

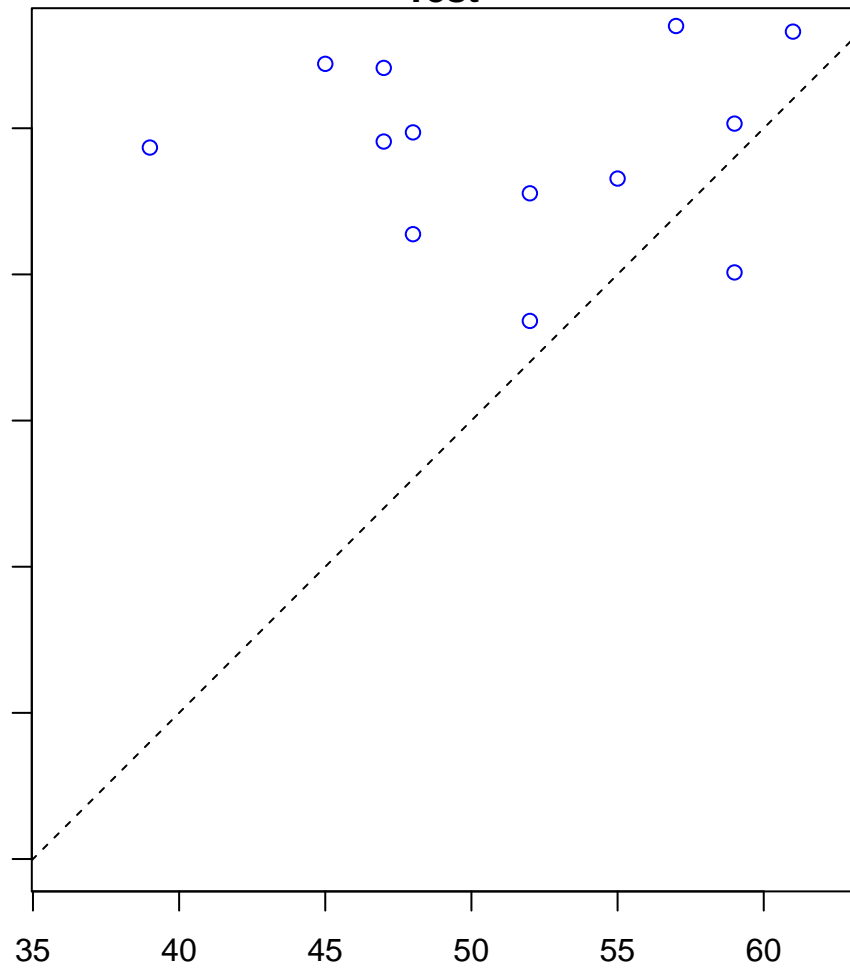


protein insertion into membrane (Score: 3.781726)

Control

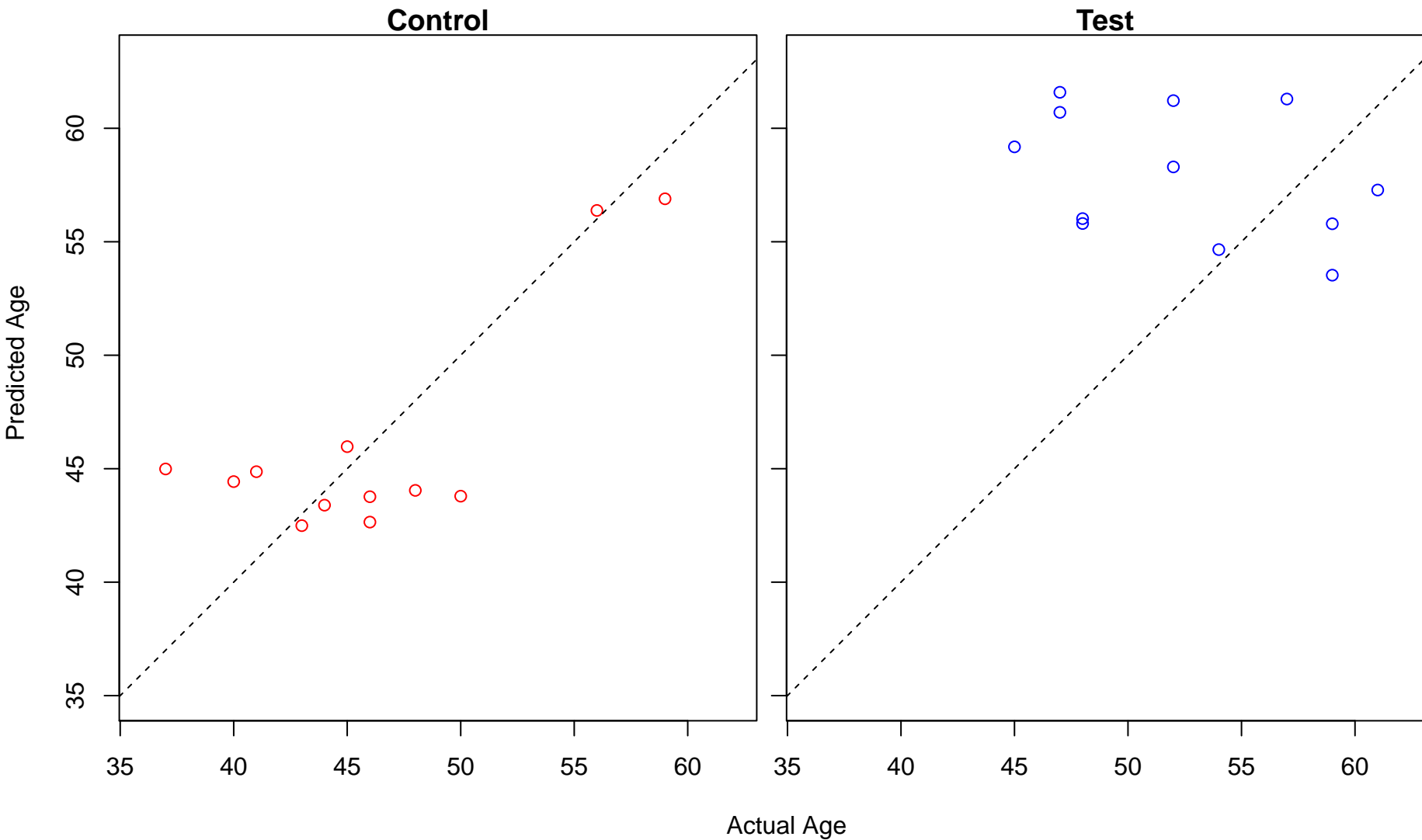


Test

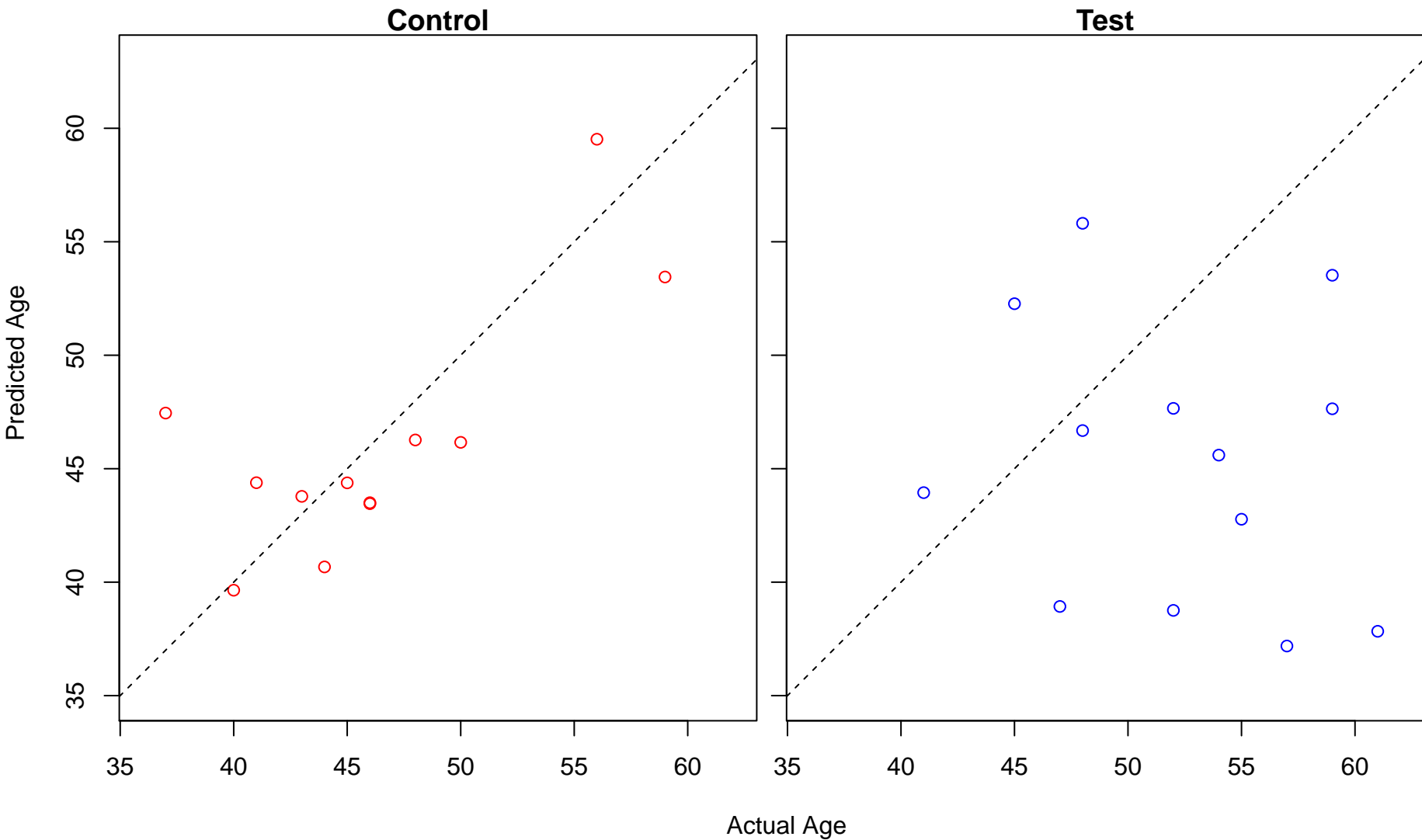


Actual Age

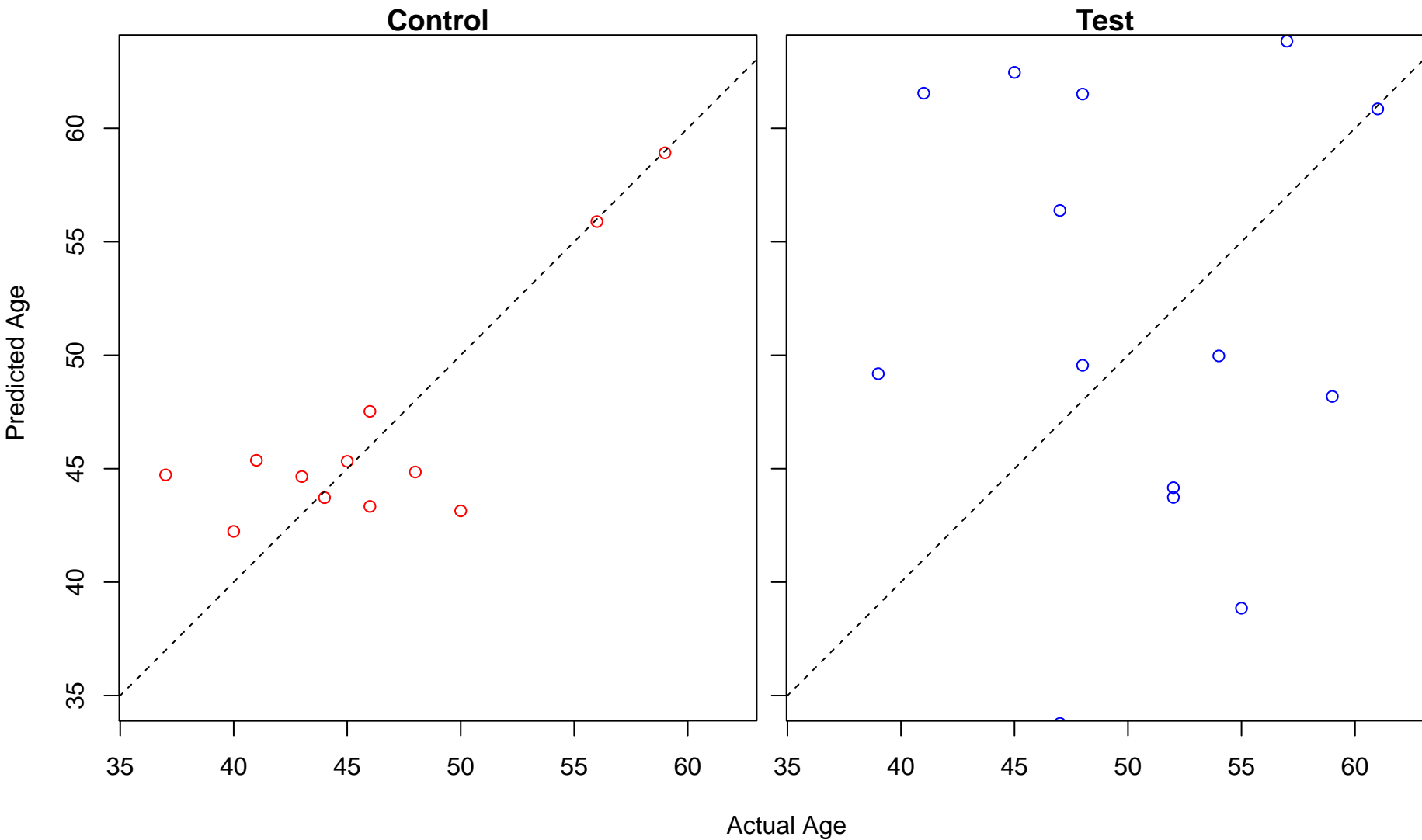
regulation of behavior (Score: 3.778029)



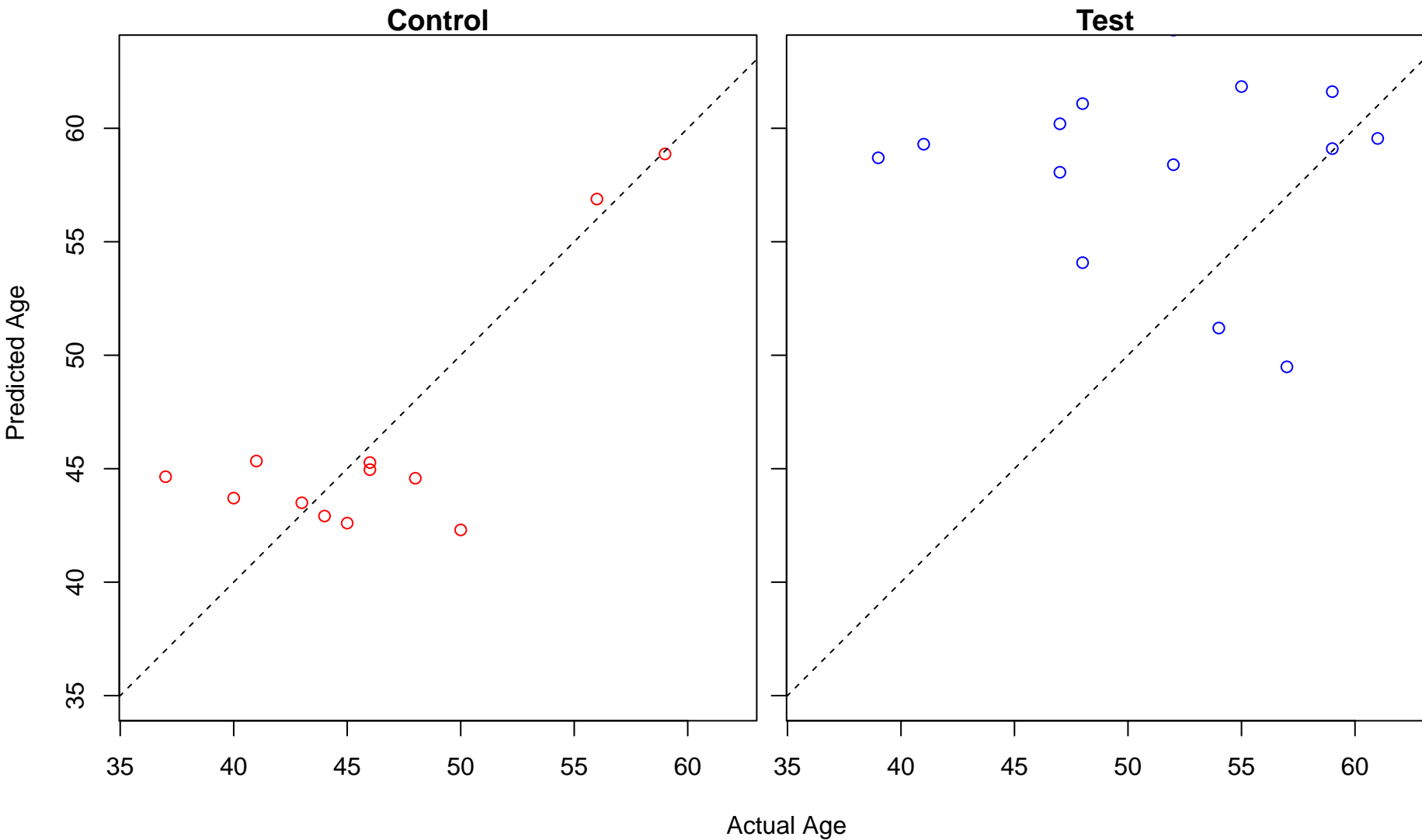
cardiac left ventricle morphogenesis (Score: 3.777260)



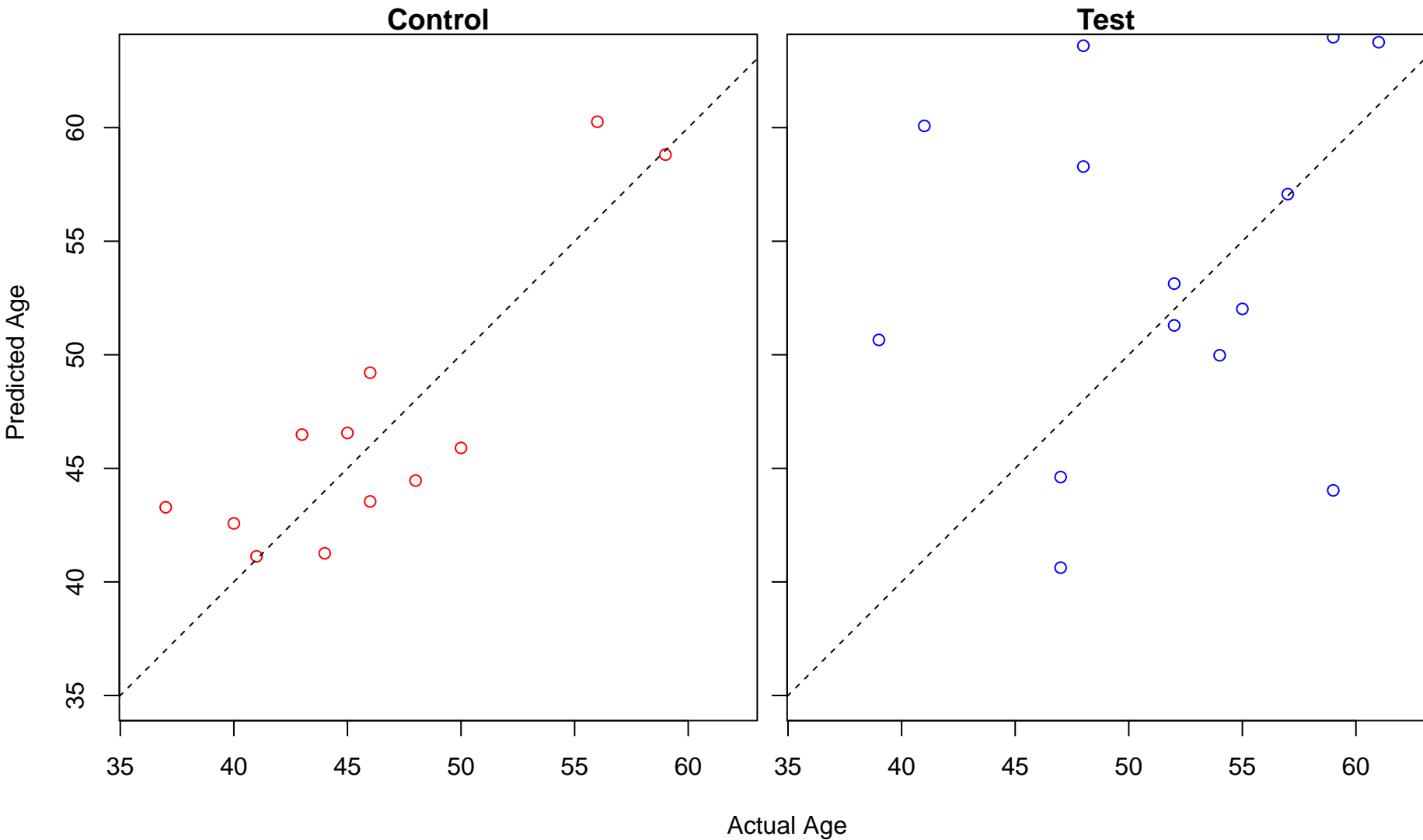
regulation of chromosome organization (Score: 3.776835)



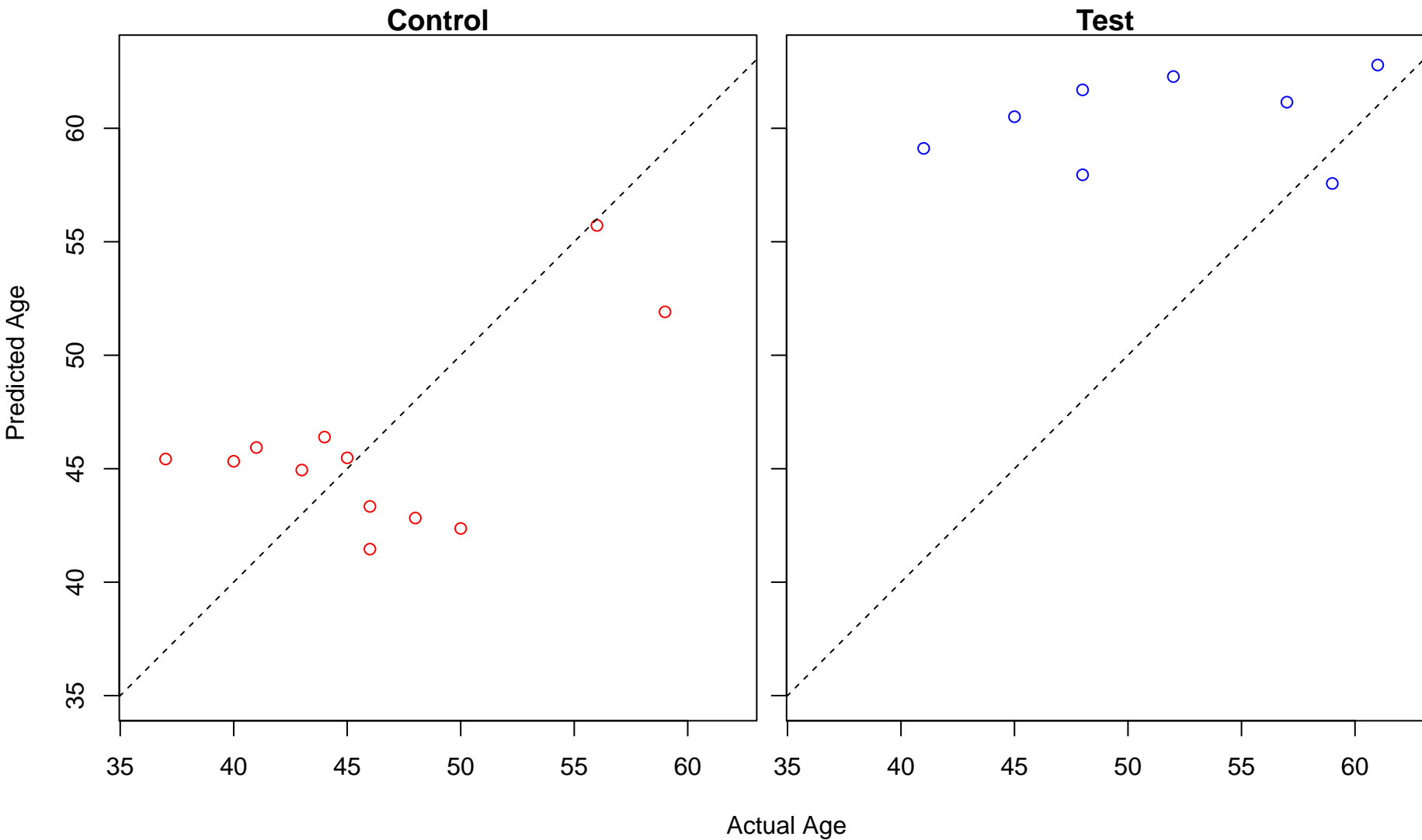
regulation of neurological system process (Score: 3.774935)



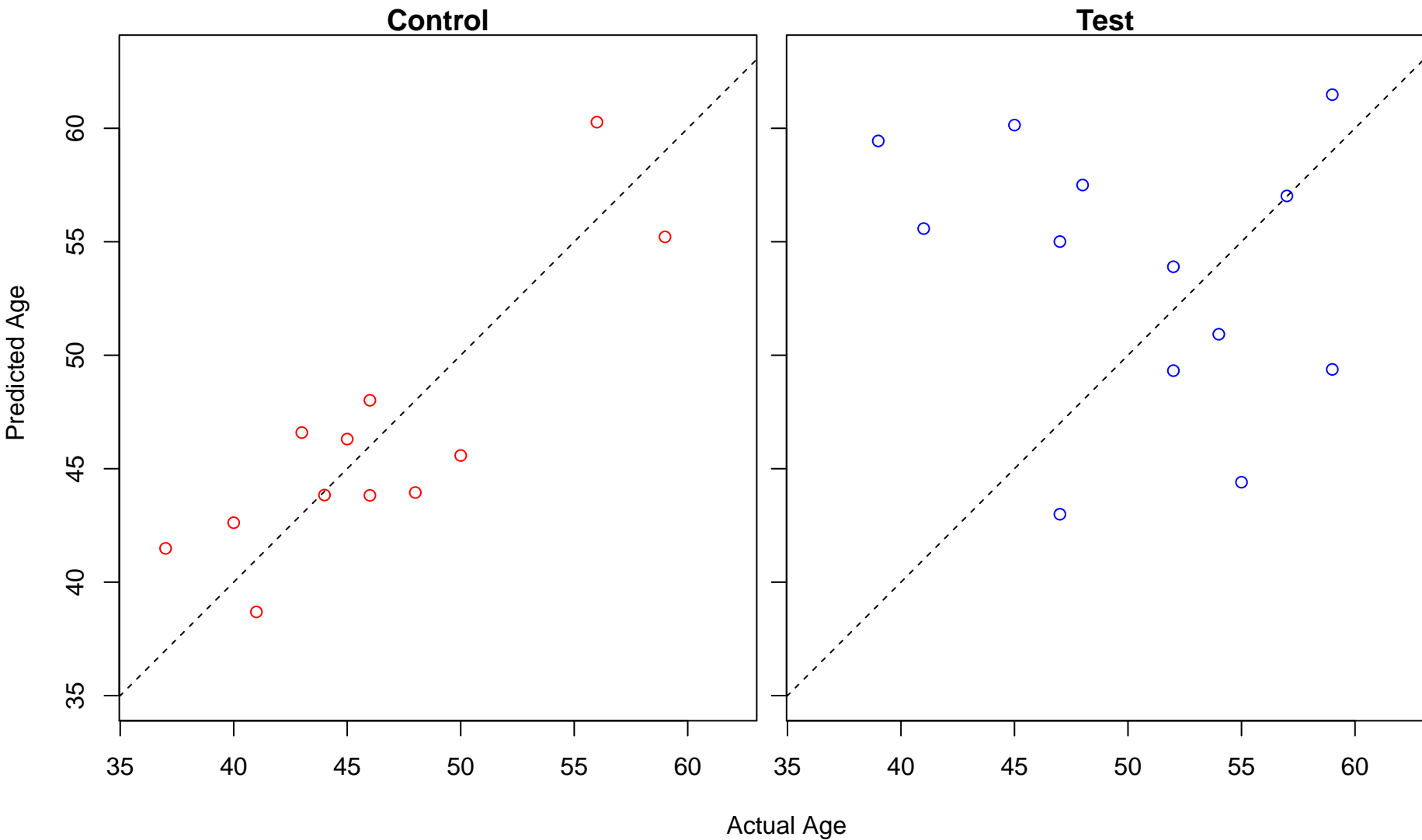
dopaminergic neuron differentiation (Score: 3.773253)



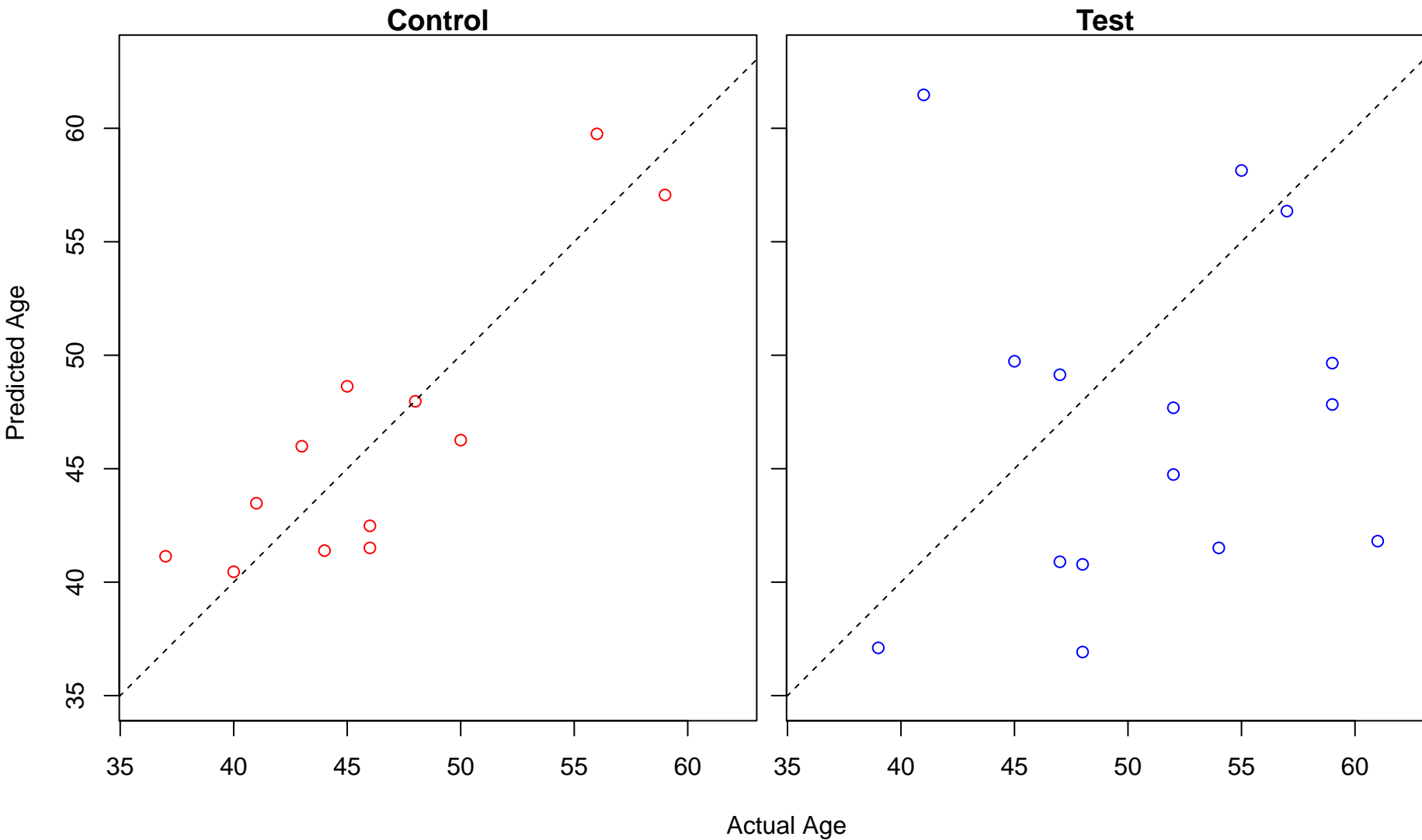
tooth mineralization (Score: 3.772532)



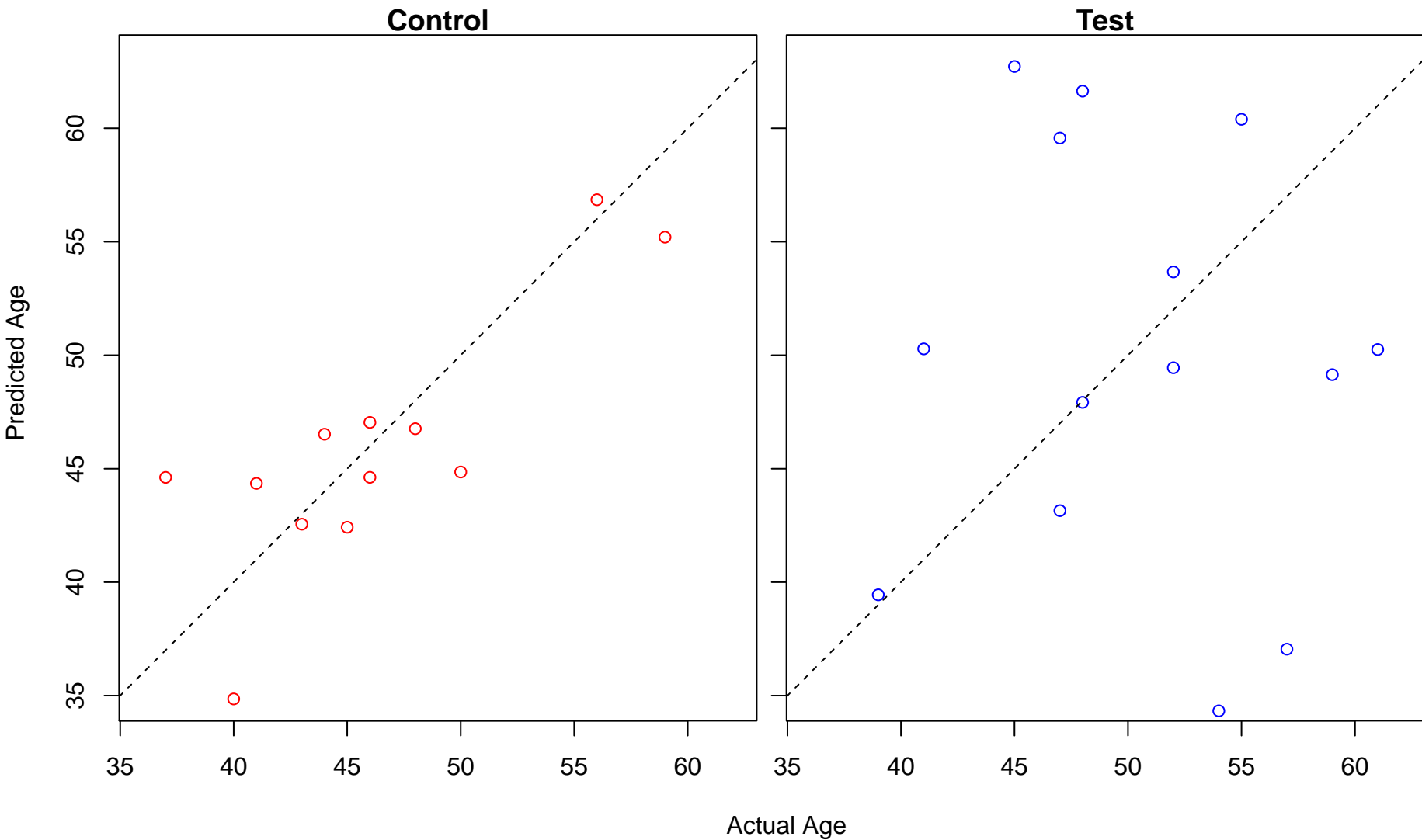
commissural neuron axon guidance (Score: 3.772407)



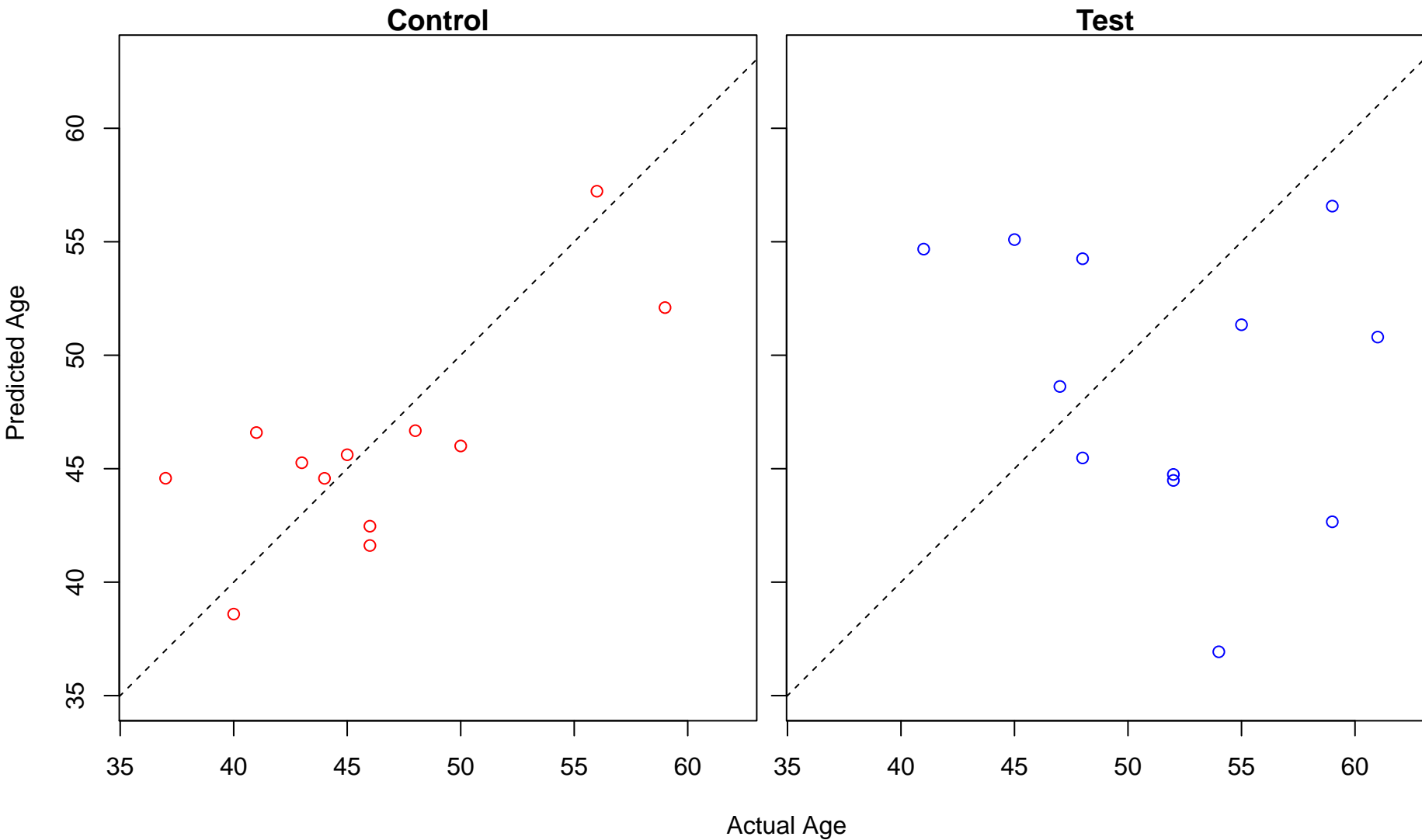
retrograde transport, endosome to plasma membrane (Score: 3.769863)



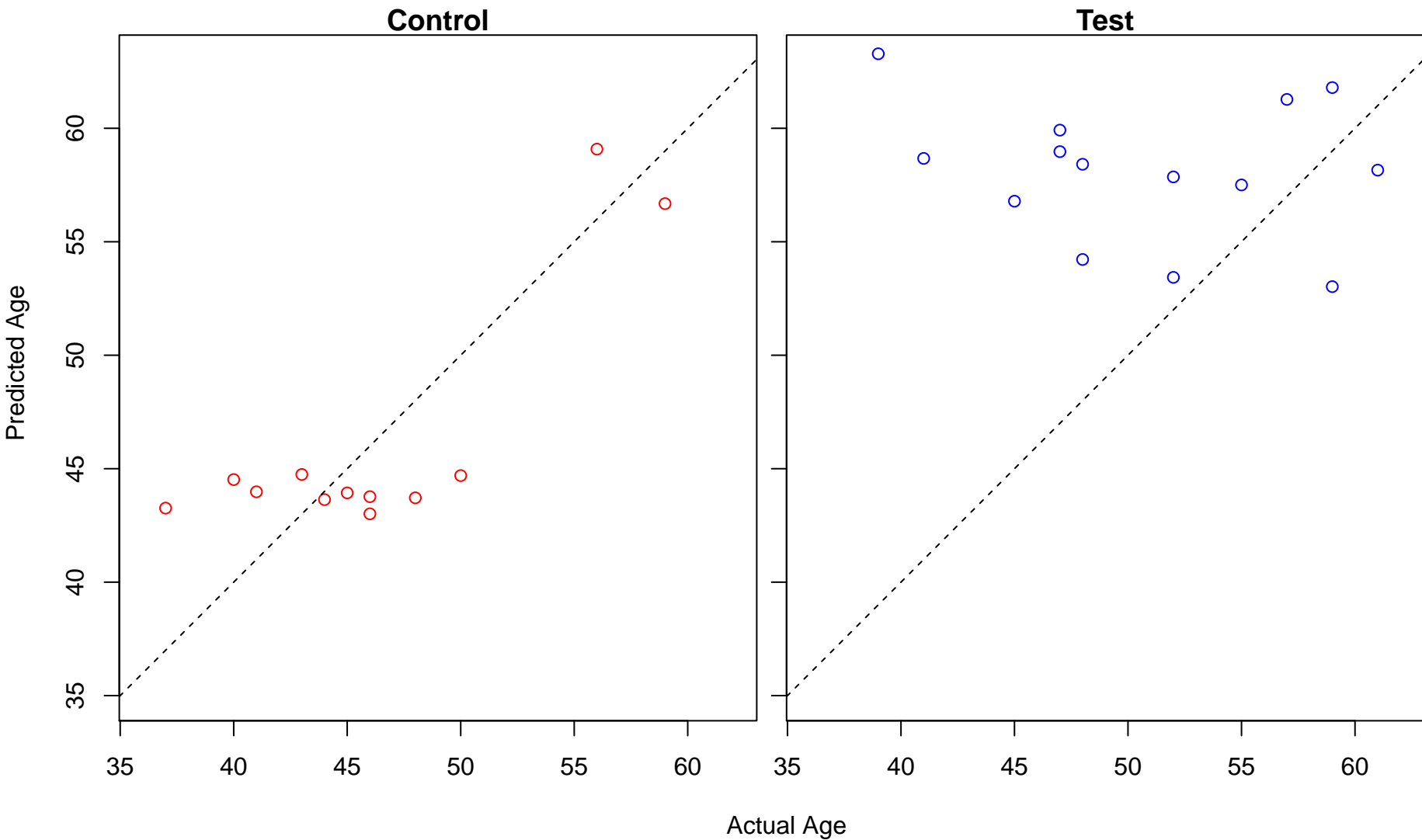
regulation of embryonic development (Score: 3.769799)



regulation of translation (Score: 3.767814)

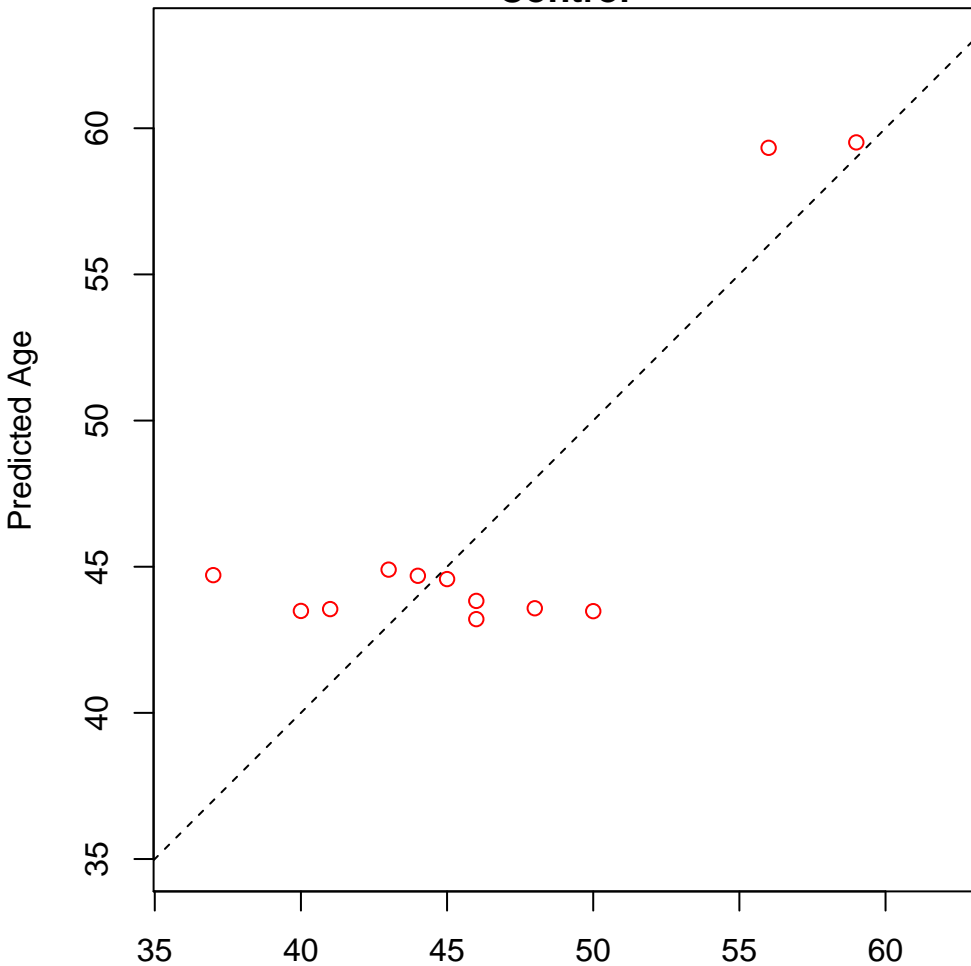


sulfur amino acid transport (Score: 3.767749)

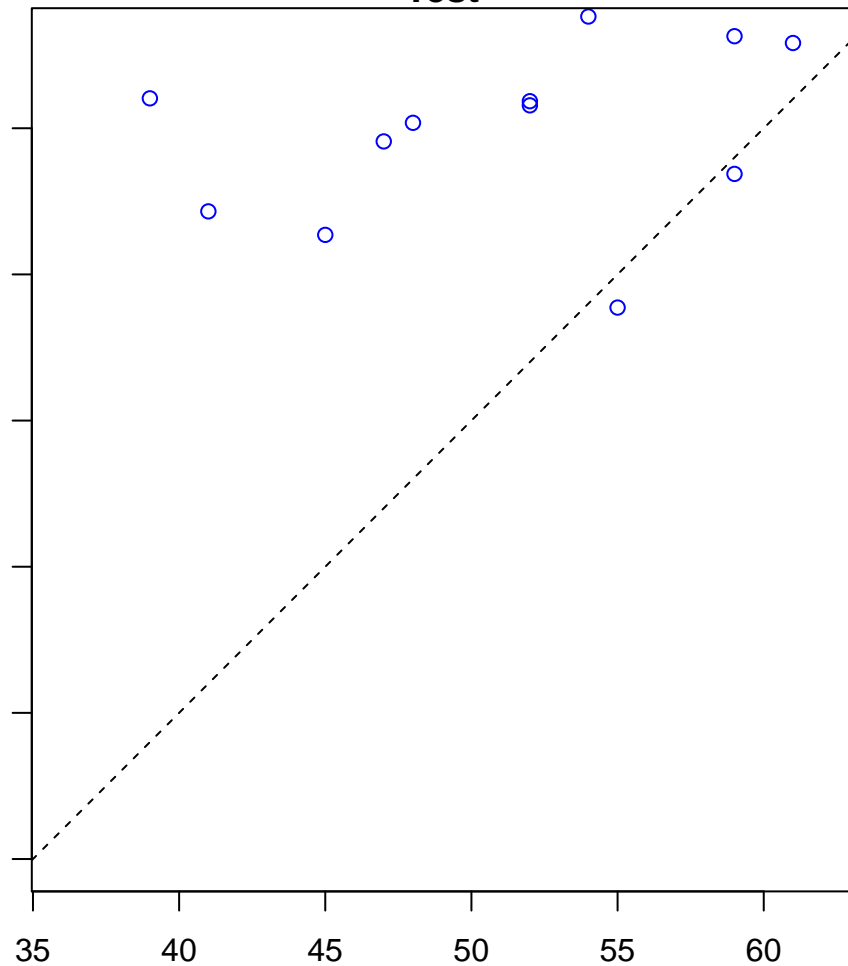


mitotic nuclear envelope disassembly (Score: 3.763855)

Control

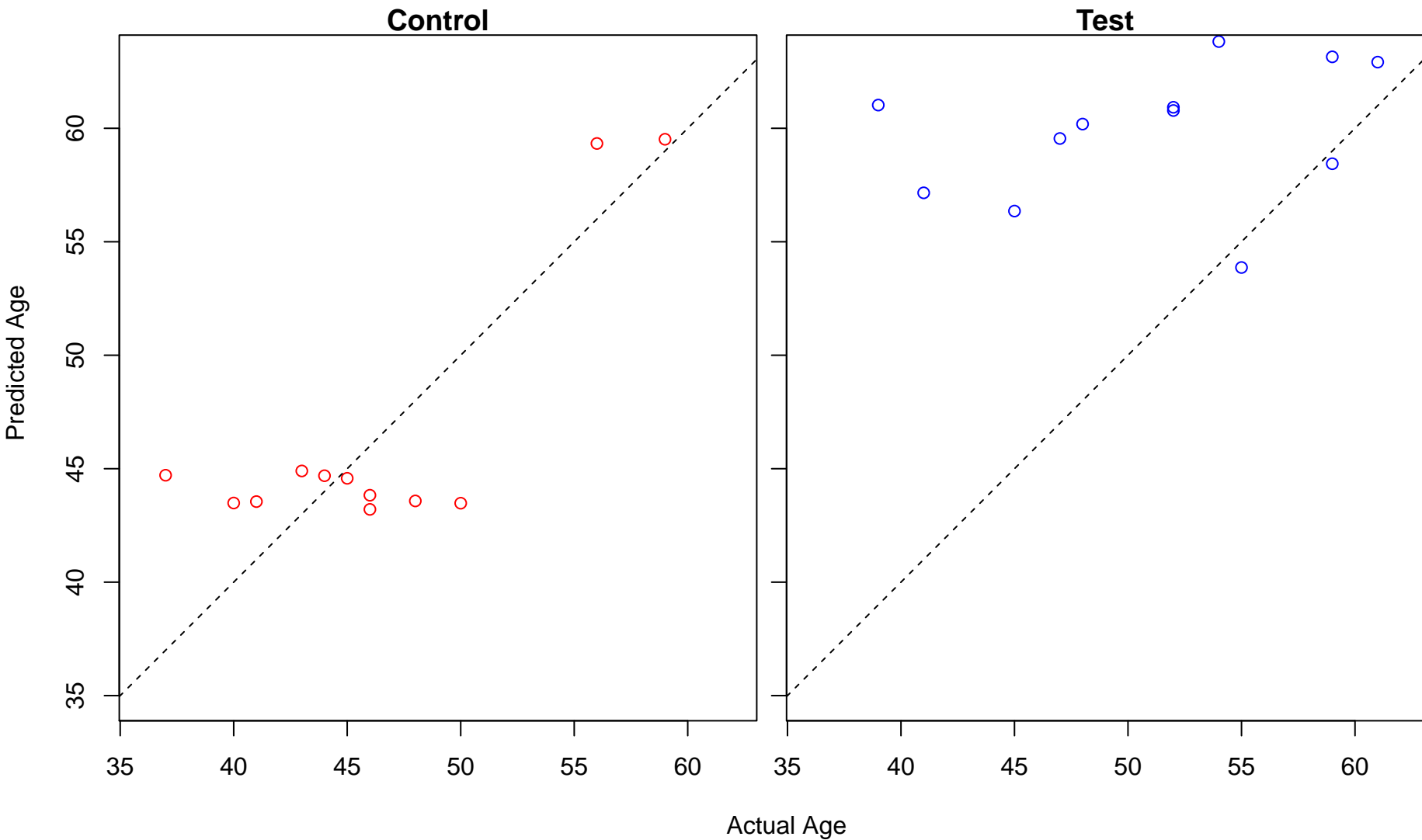


Test

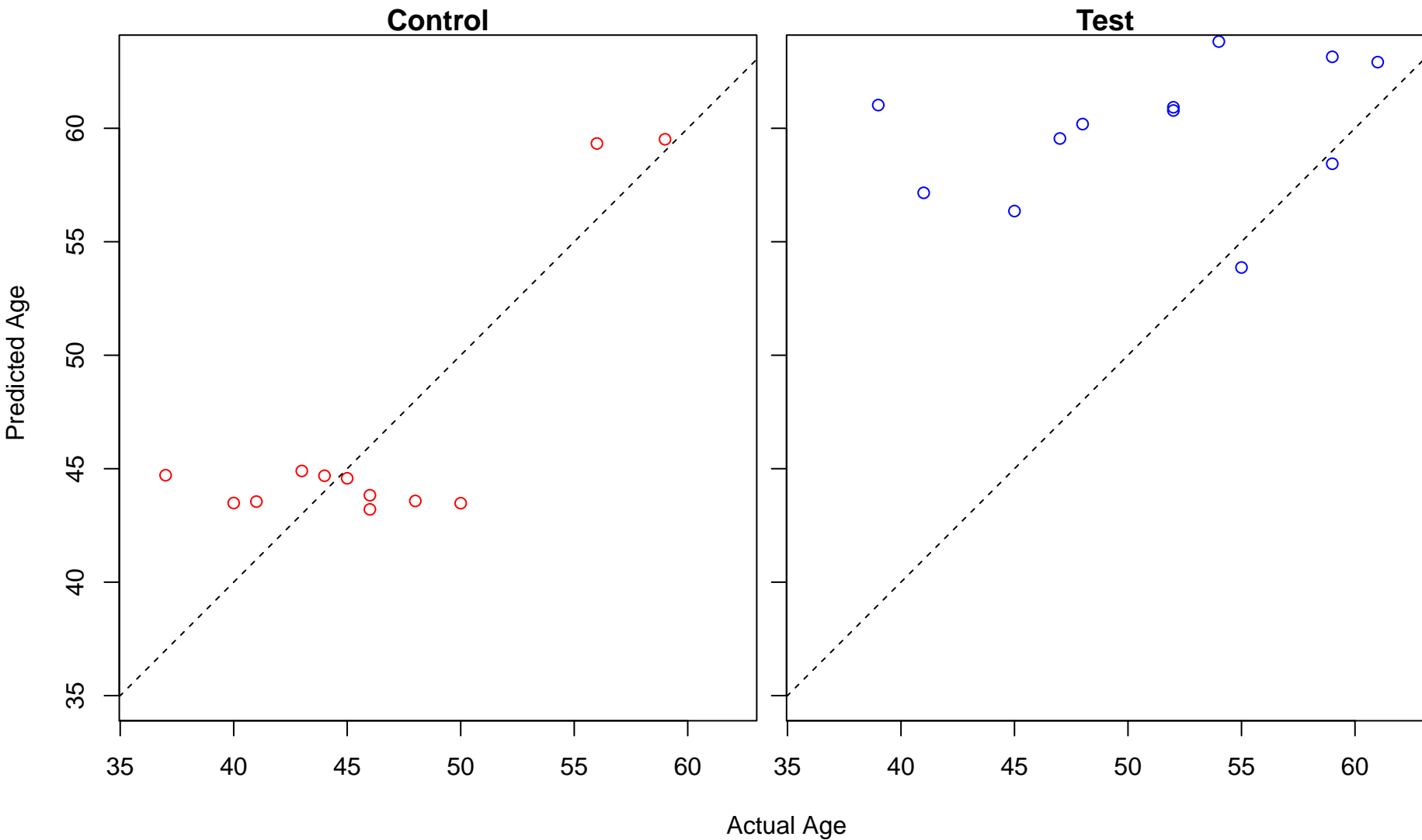


Actual Age

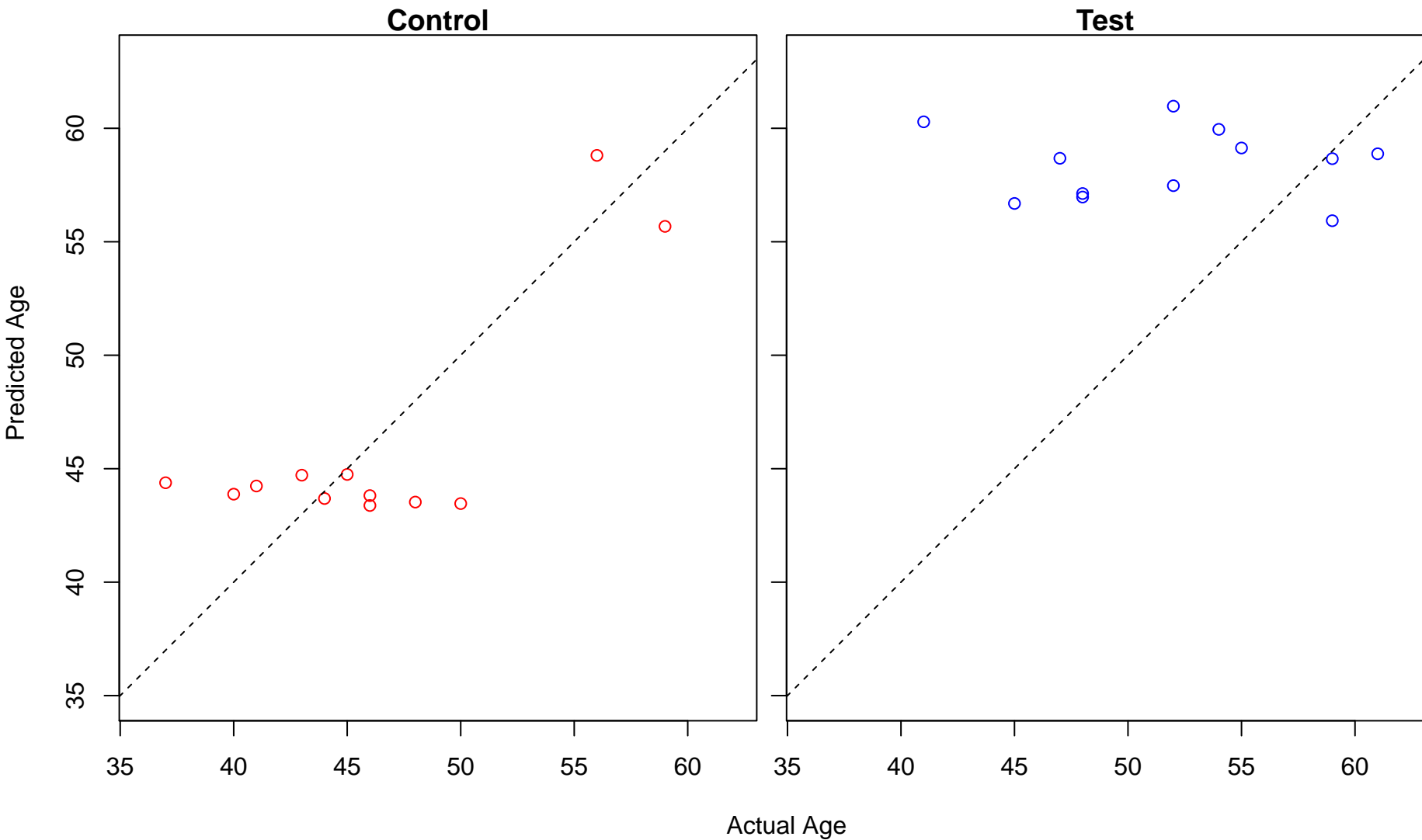
membrane disassembly (Score: 3.763855)



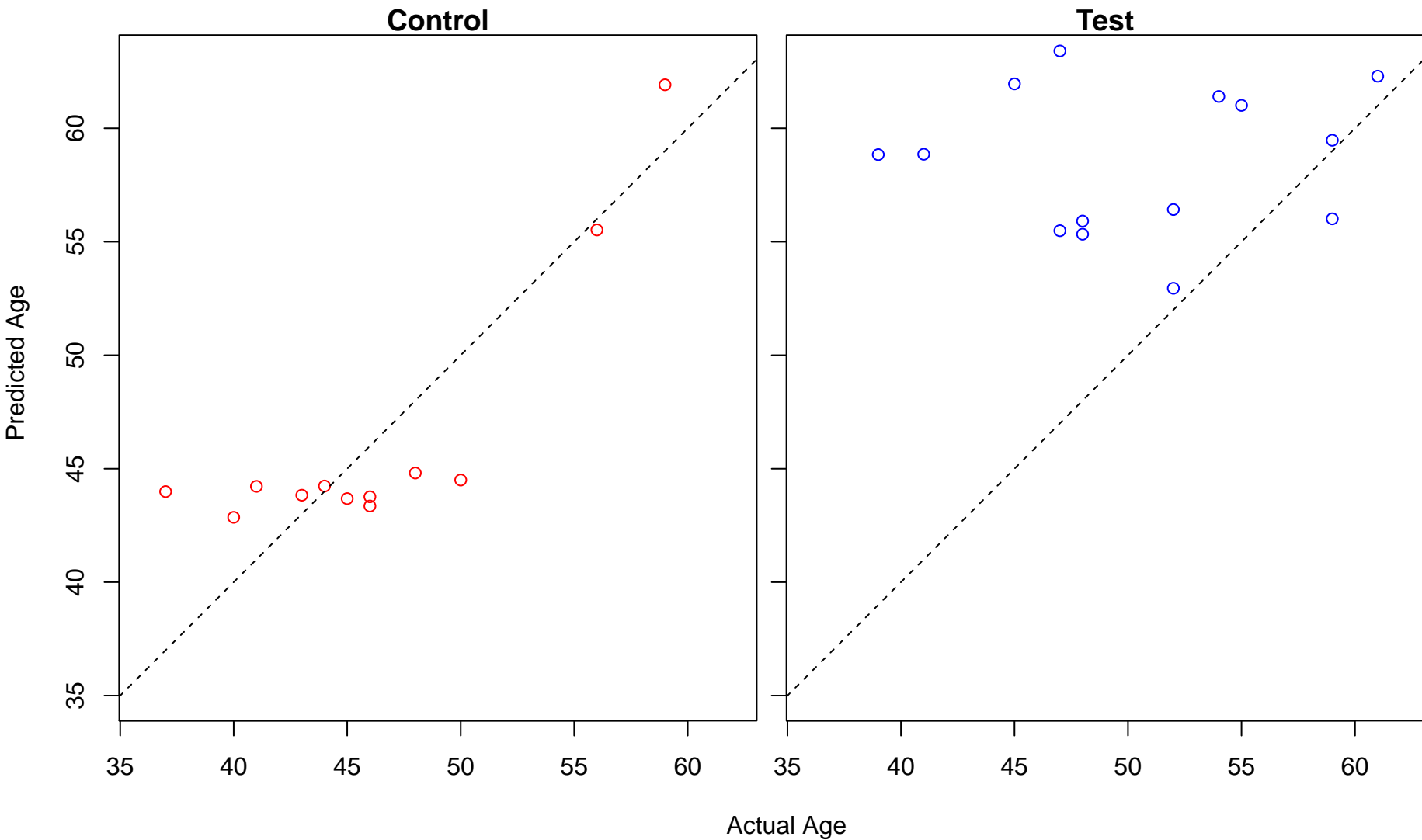
nuclear envelope disassembly (Score: 3.763855)



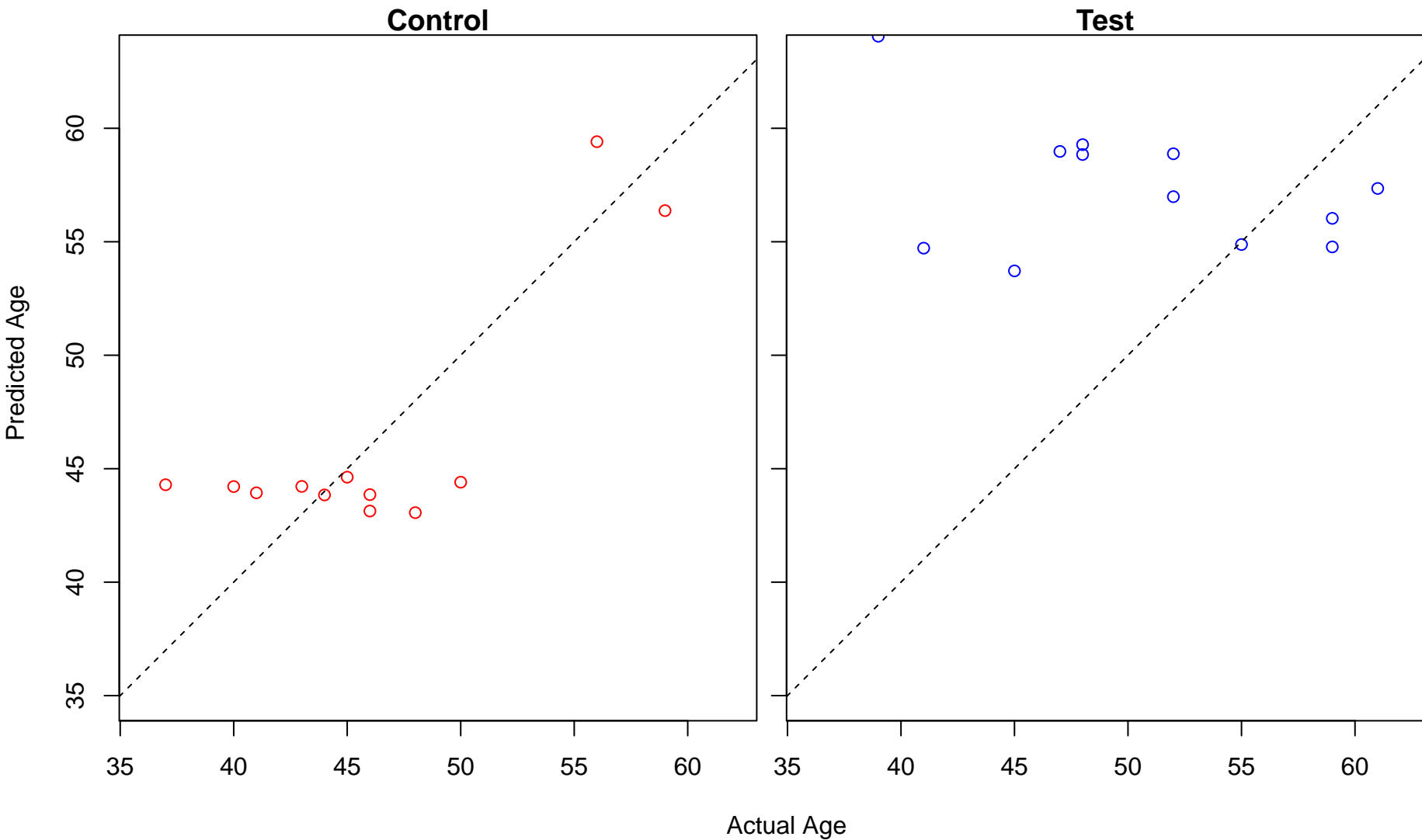
positive regulation of intrinsic apoptotic signaling pathway (Score: 3.762751)



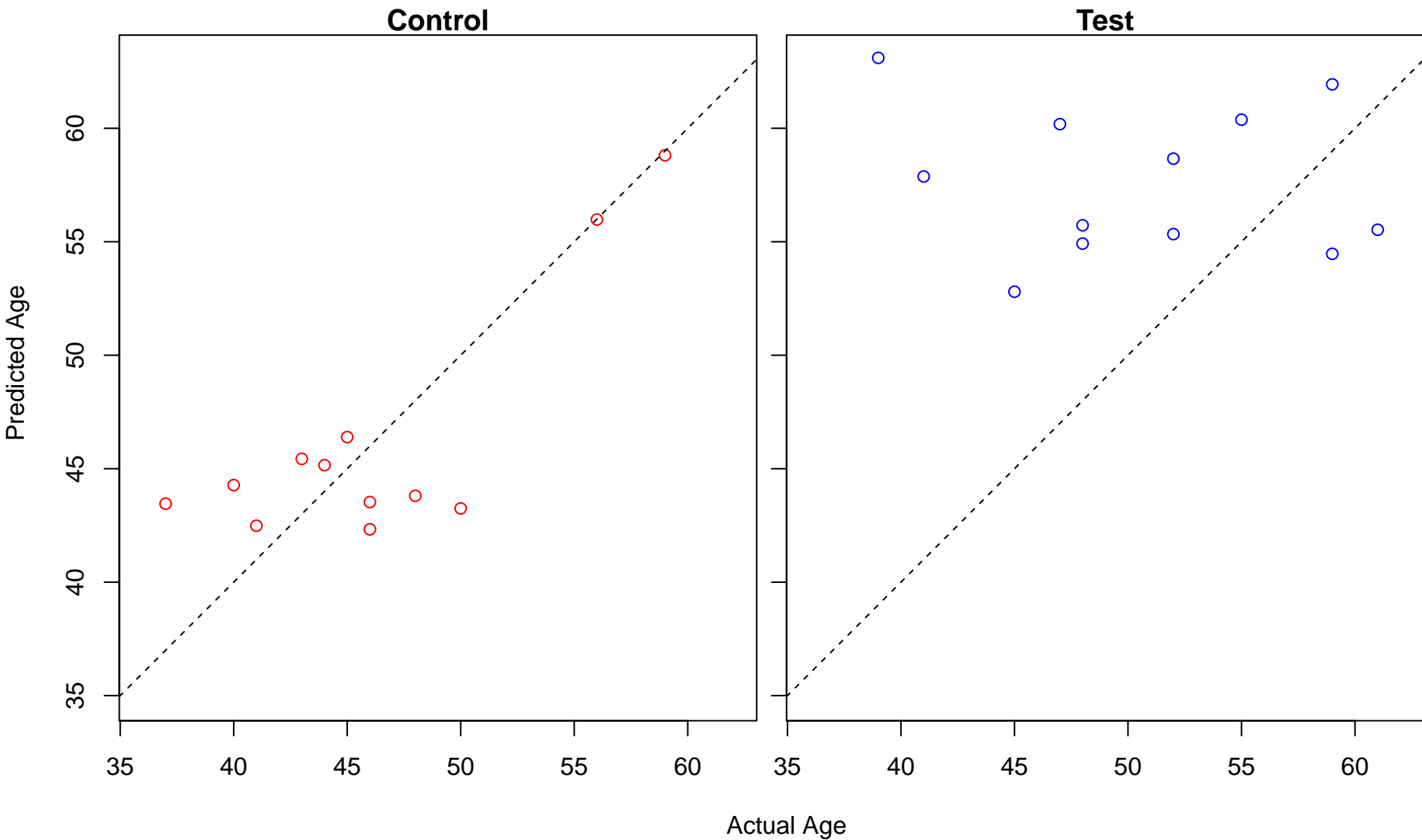
positive regulation of RNA splicing (Score: 3.762239)



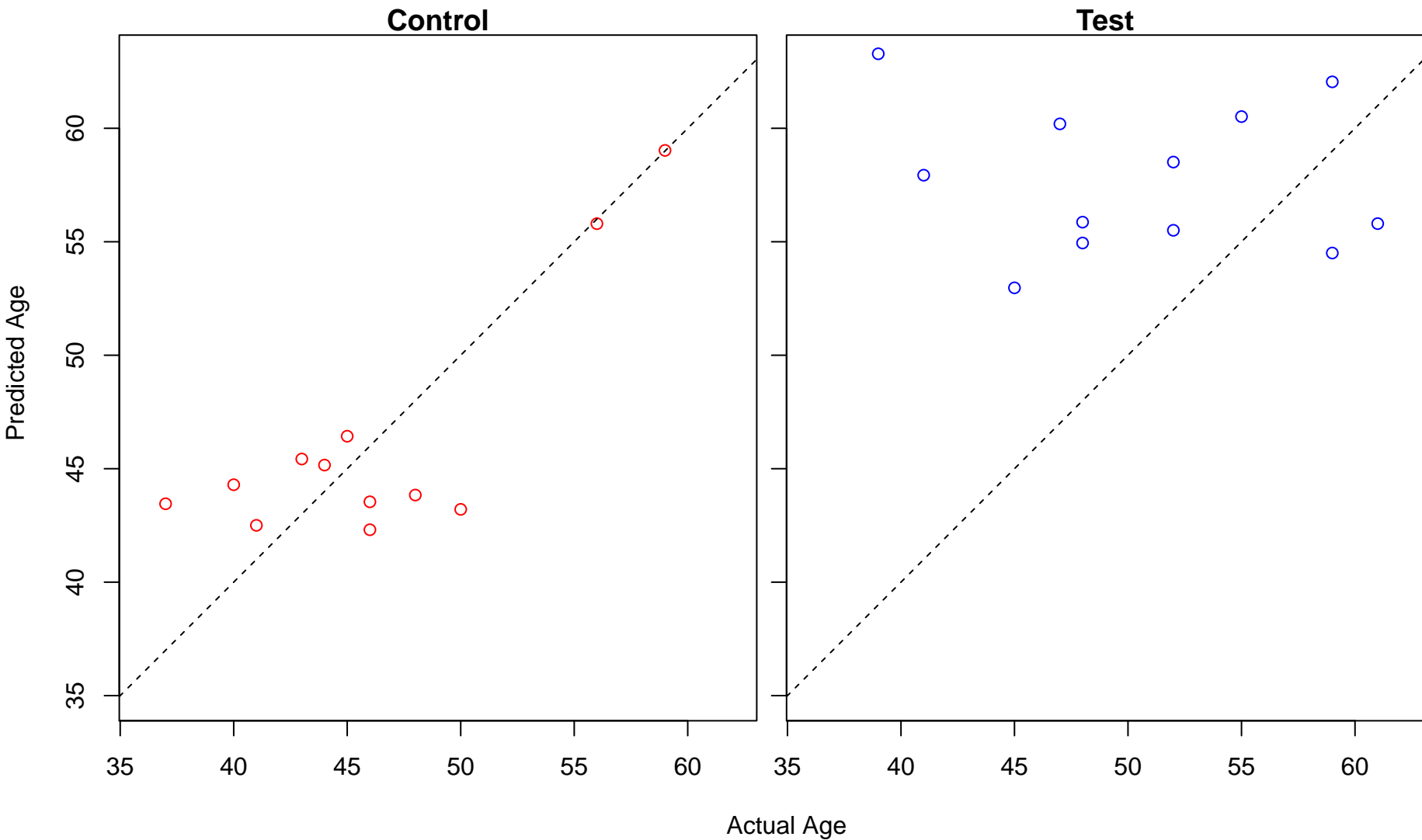
leukocyte mediated cytotoxicity (Score: 3.762090)



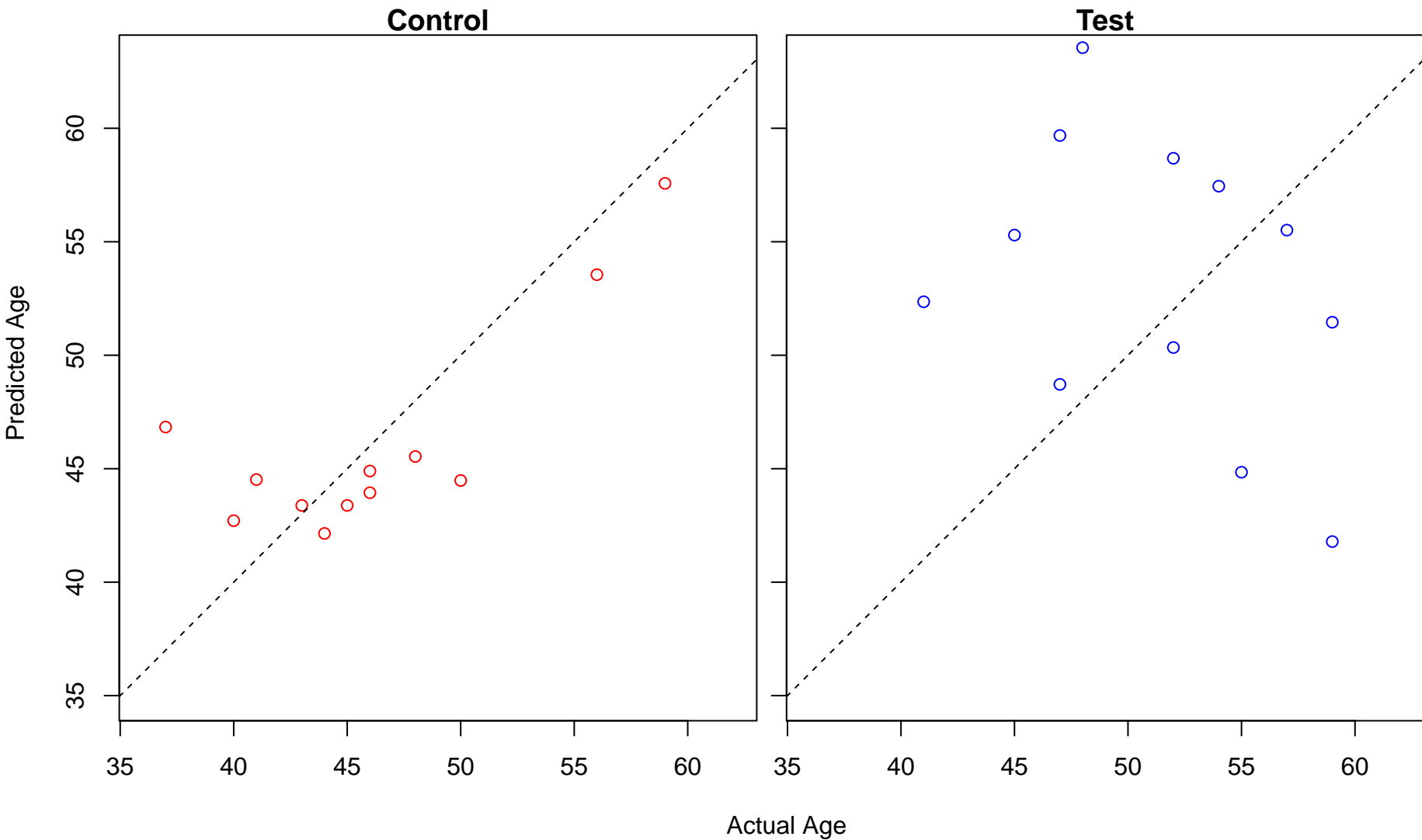
embryonic axis specification (Score: 3.762046)



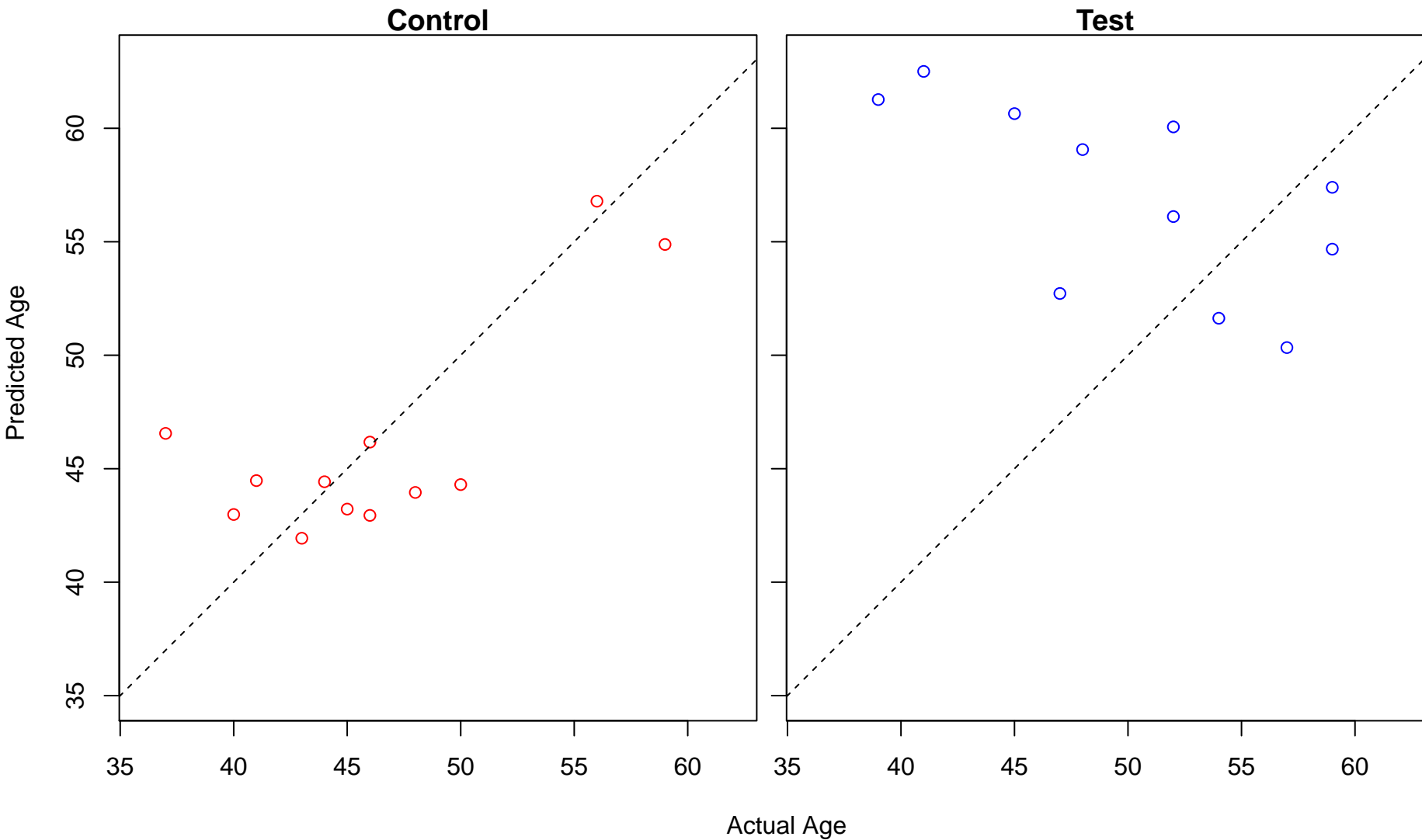
segmentation (Score: 3.752234)



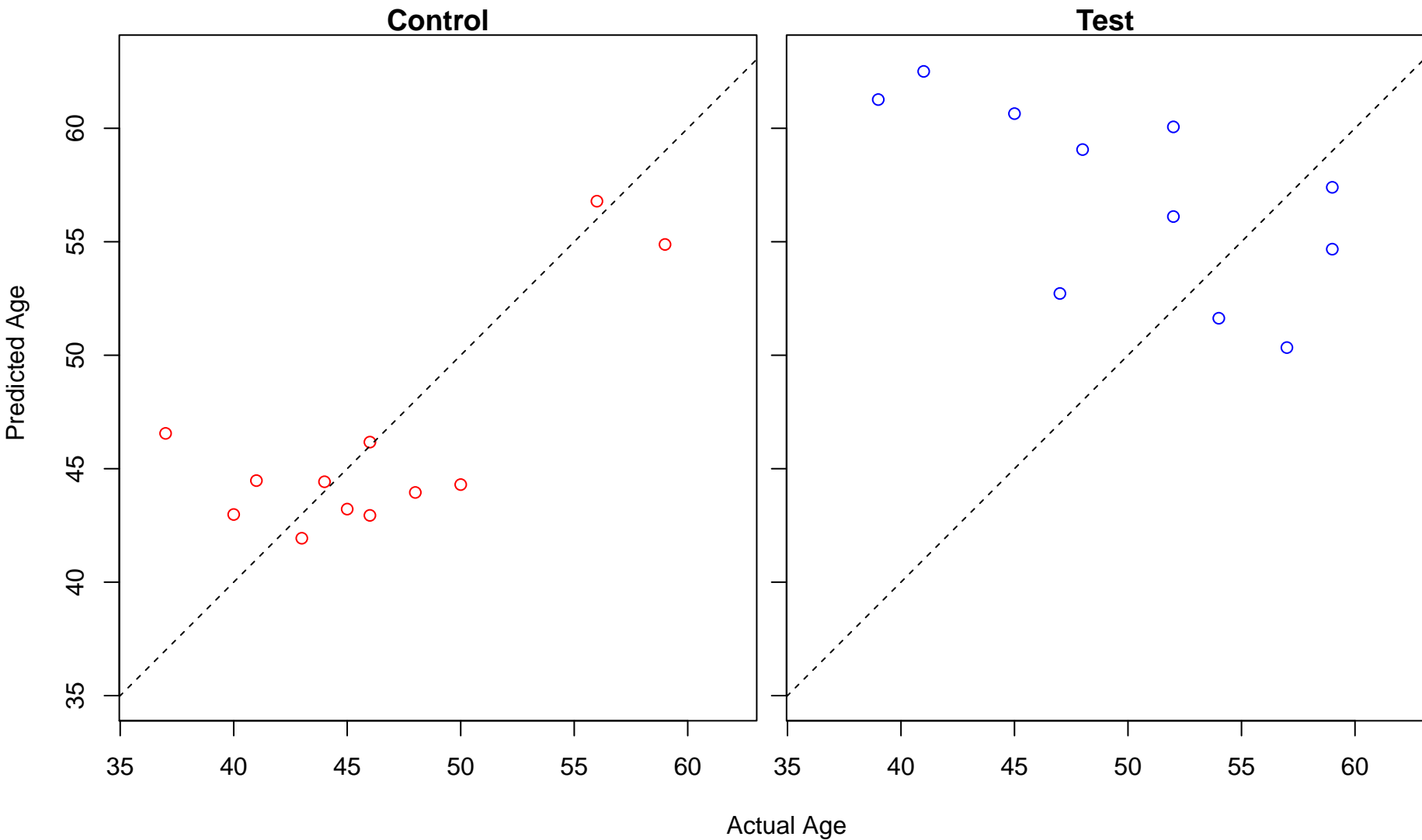
adult heart development (Score: 3.743737)



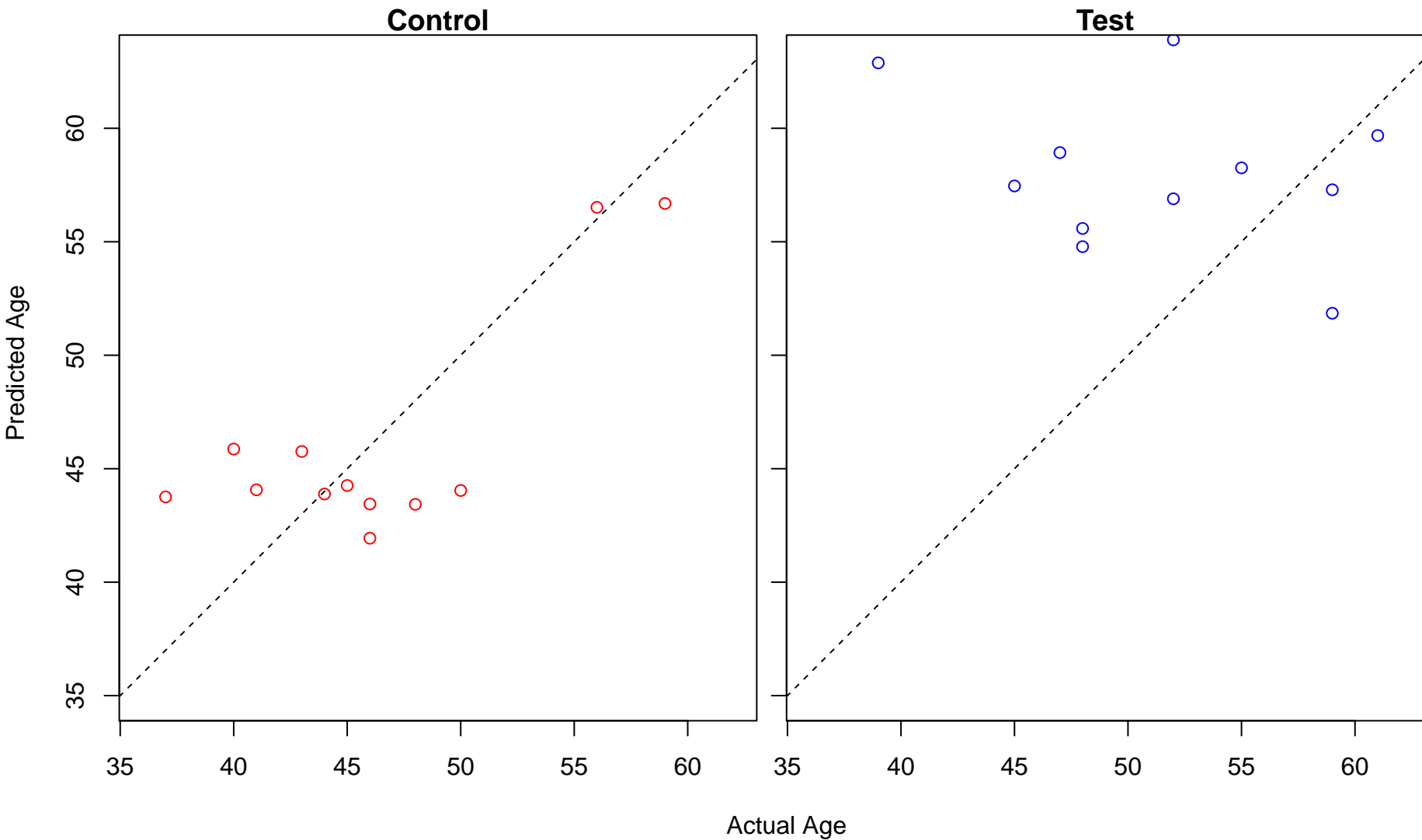
response to activity (Score: 3.738780)



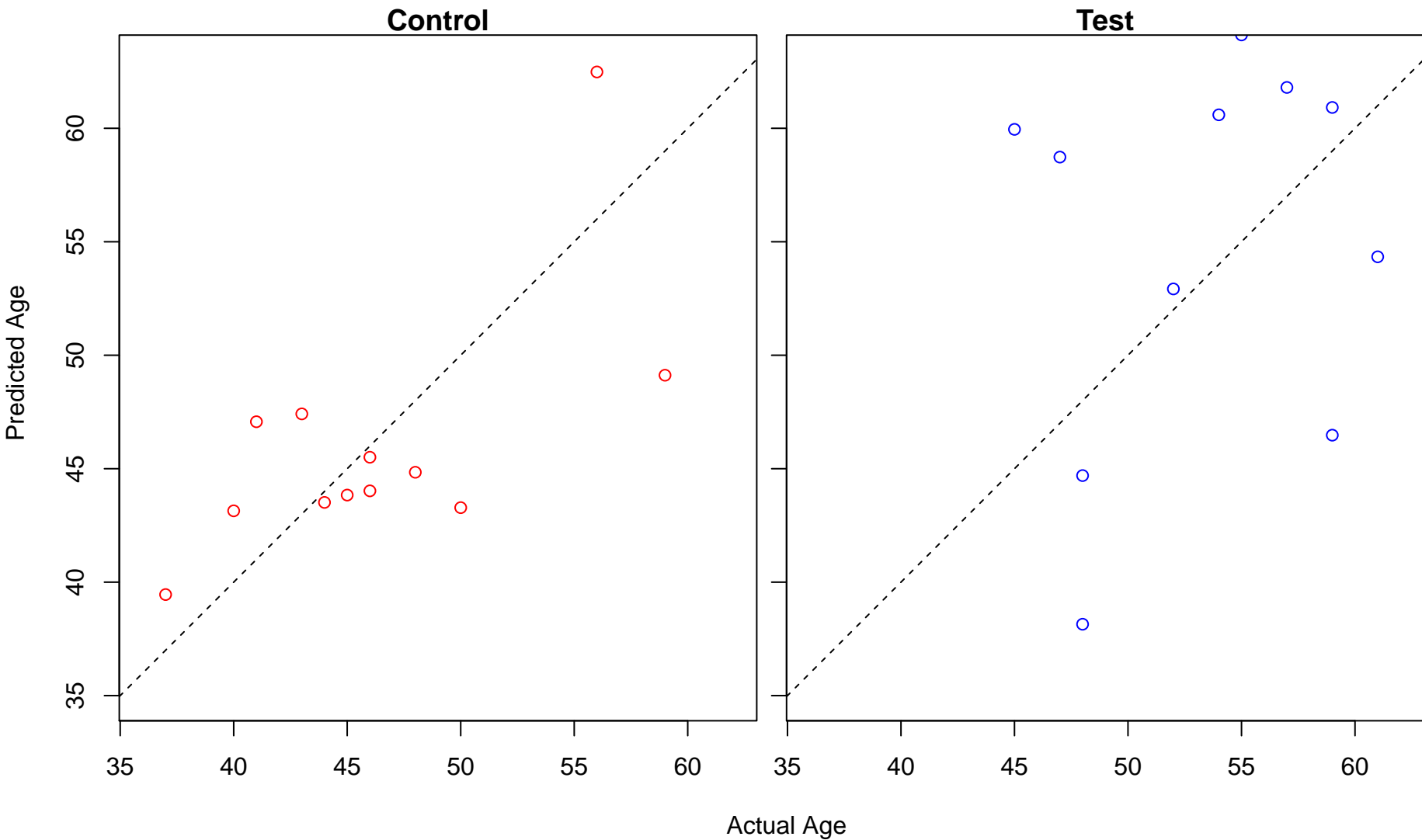
response to muscle activity (Score: 3.738780)



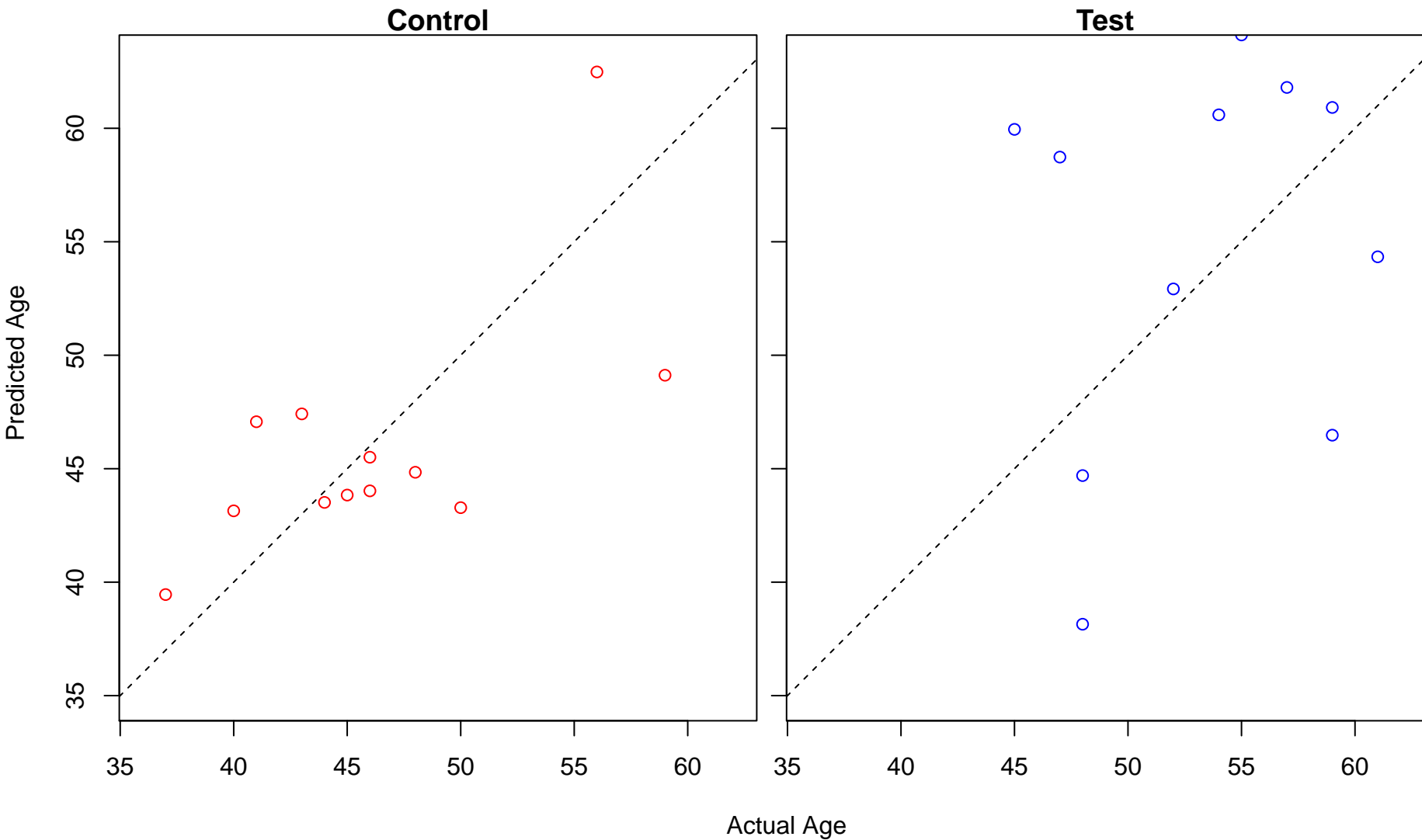
monosaccharide catabolic process (Score: 3.738225)



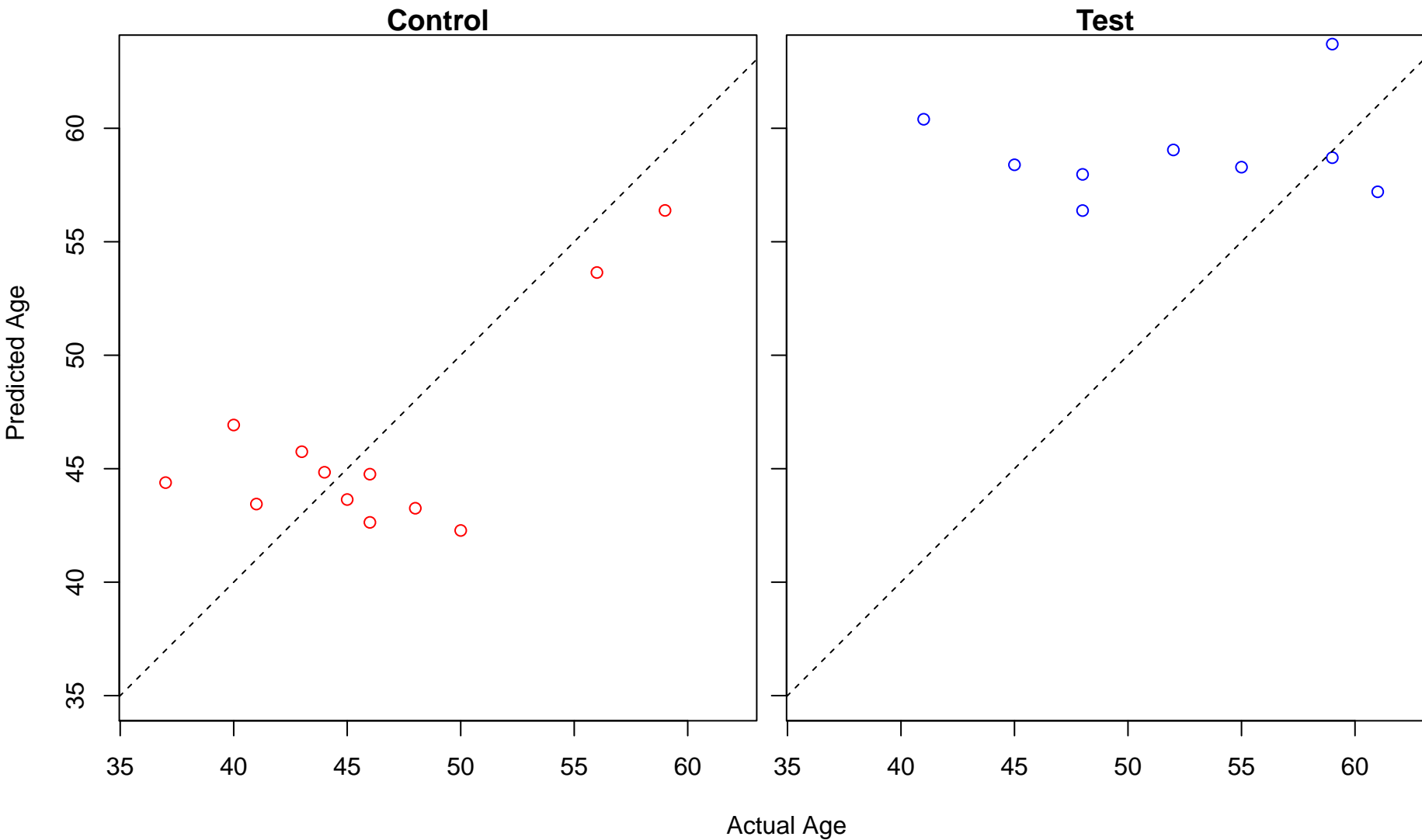
detection of bacterium (Score: 3.737982)



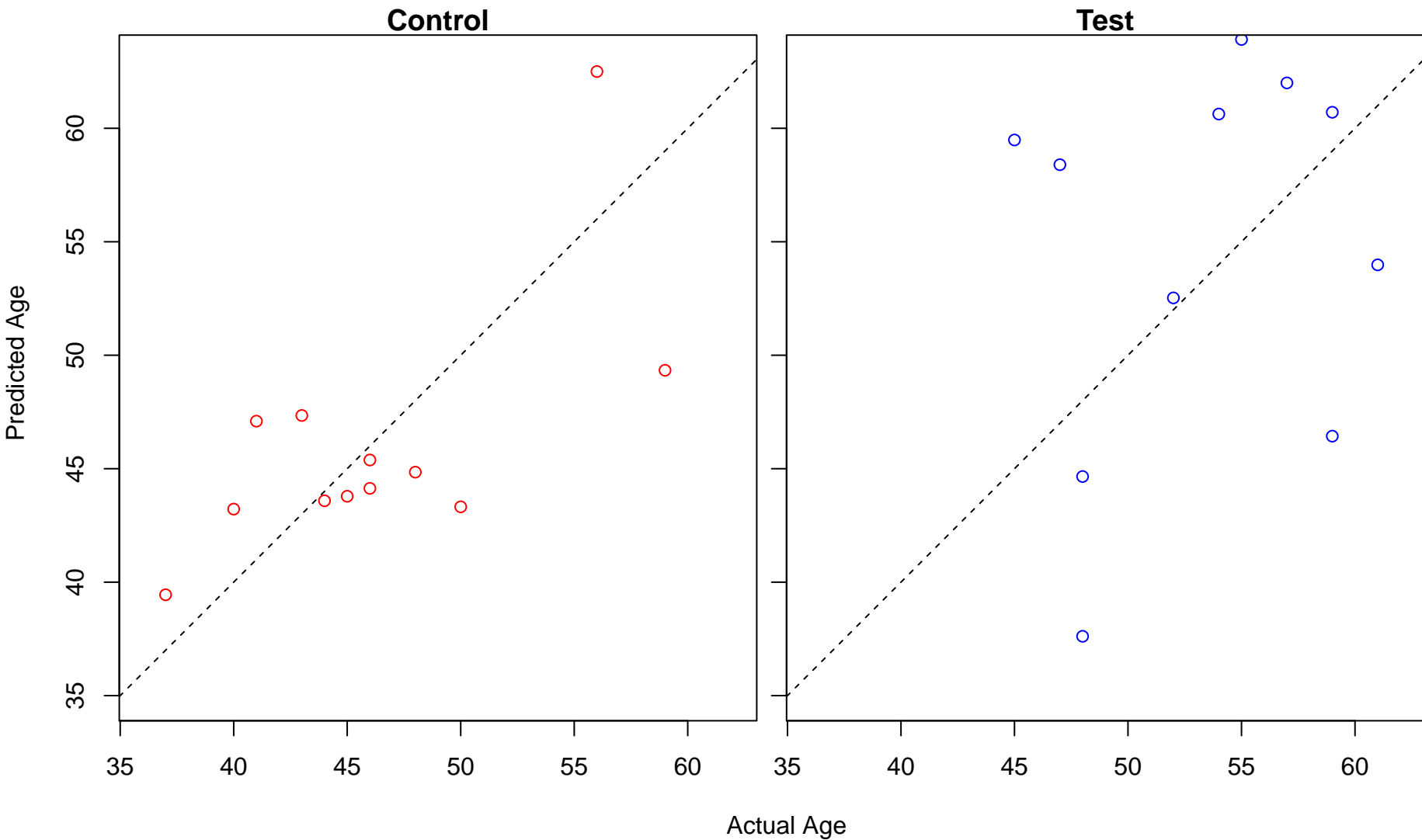
detection of other organism (Score: 3.737982)



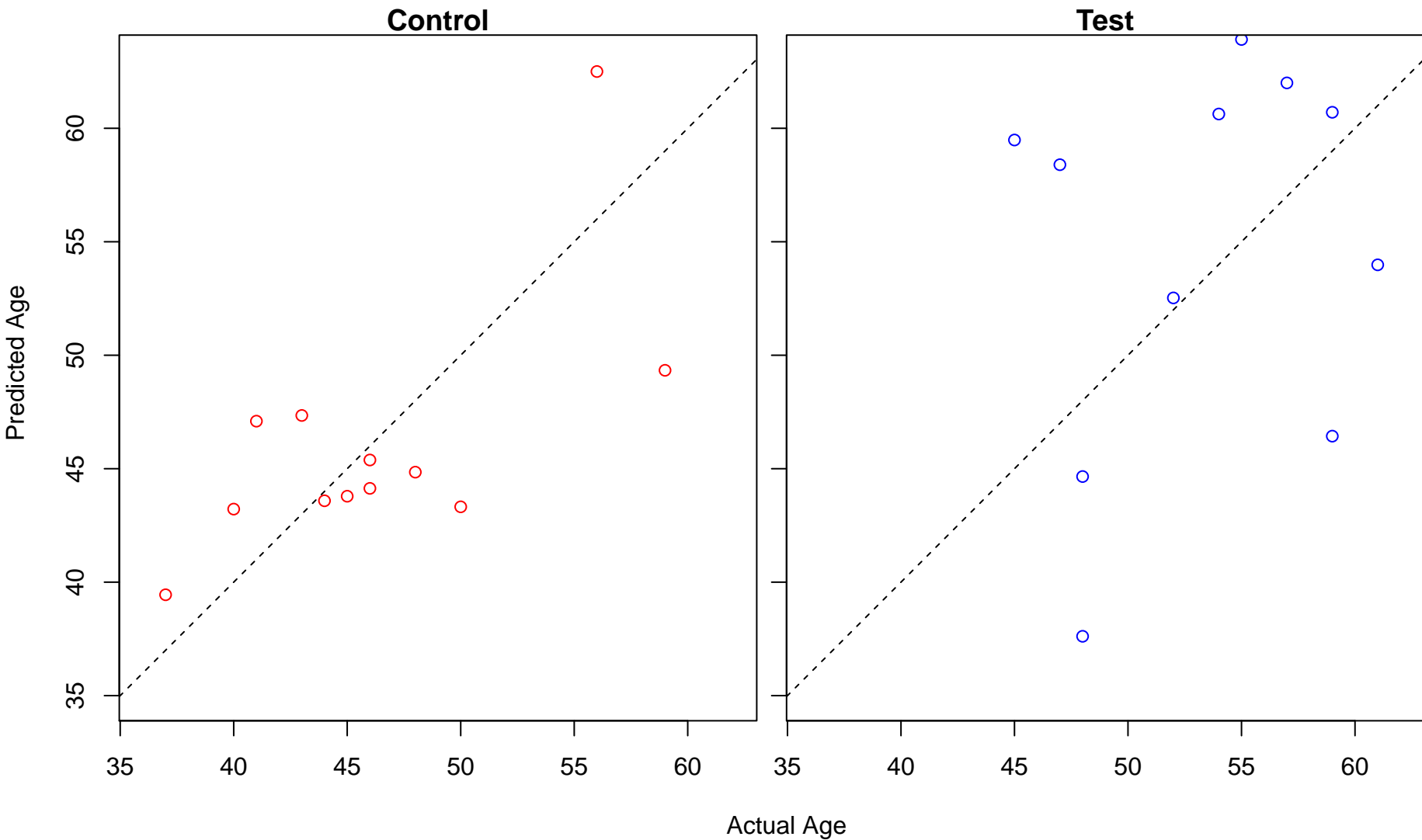
one-carbon metabolic process (Score: 3.736751)



detection of biotic stimulus (Score: 3.736461)

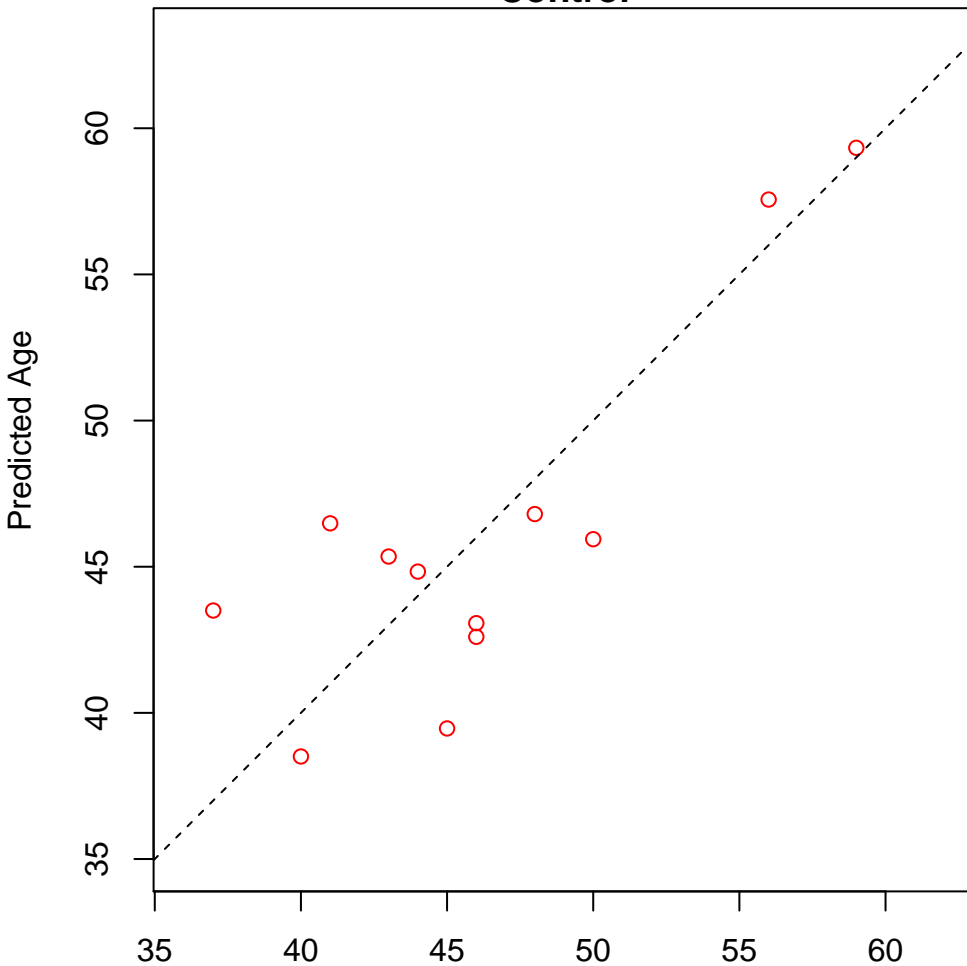


detection of external biotic stimulus (Score: 3.736316)

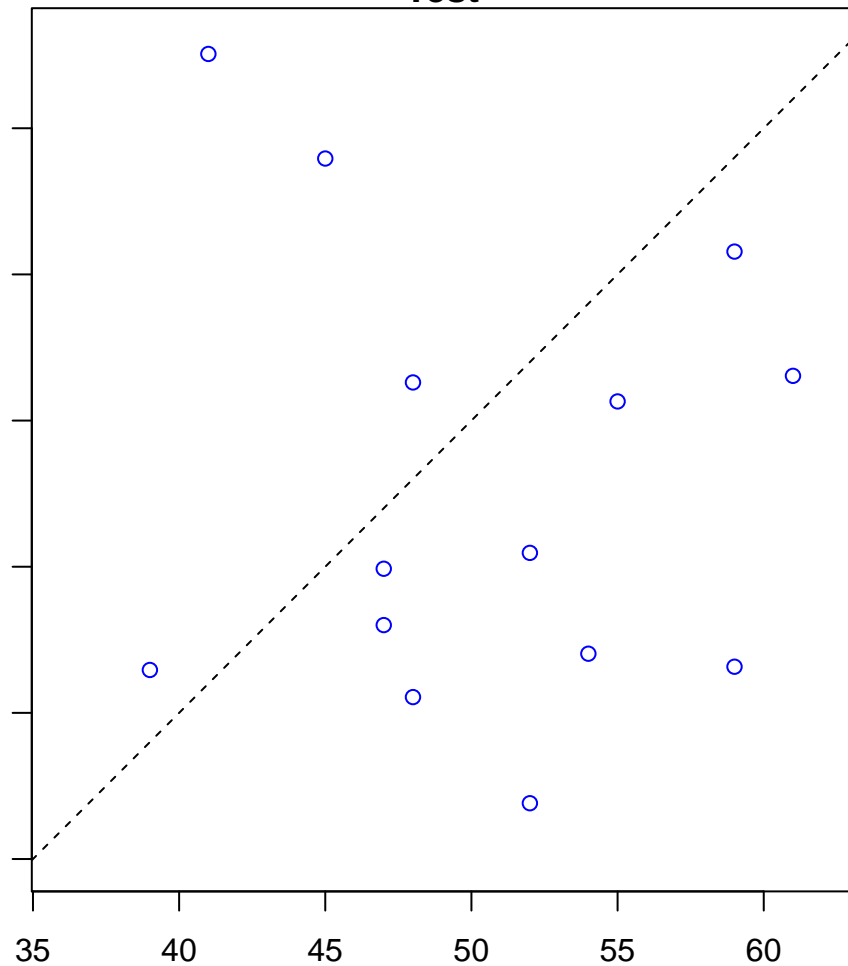


response to reactive oxygen species (Score: 3.736234)

Control

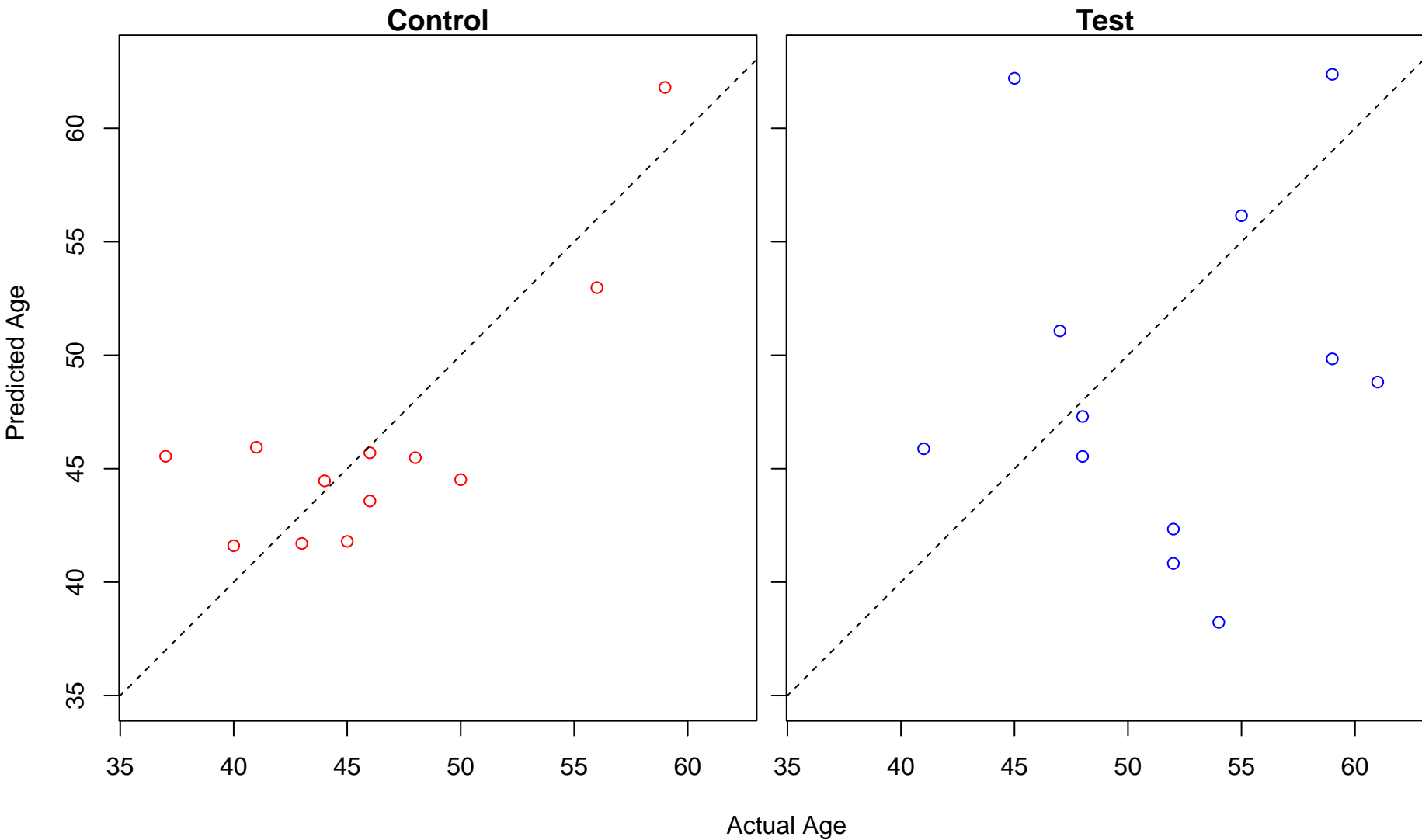


Test

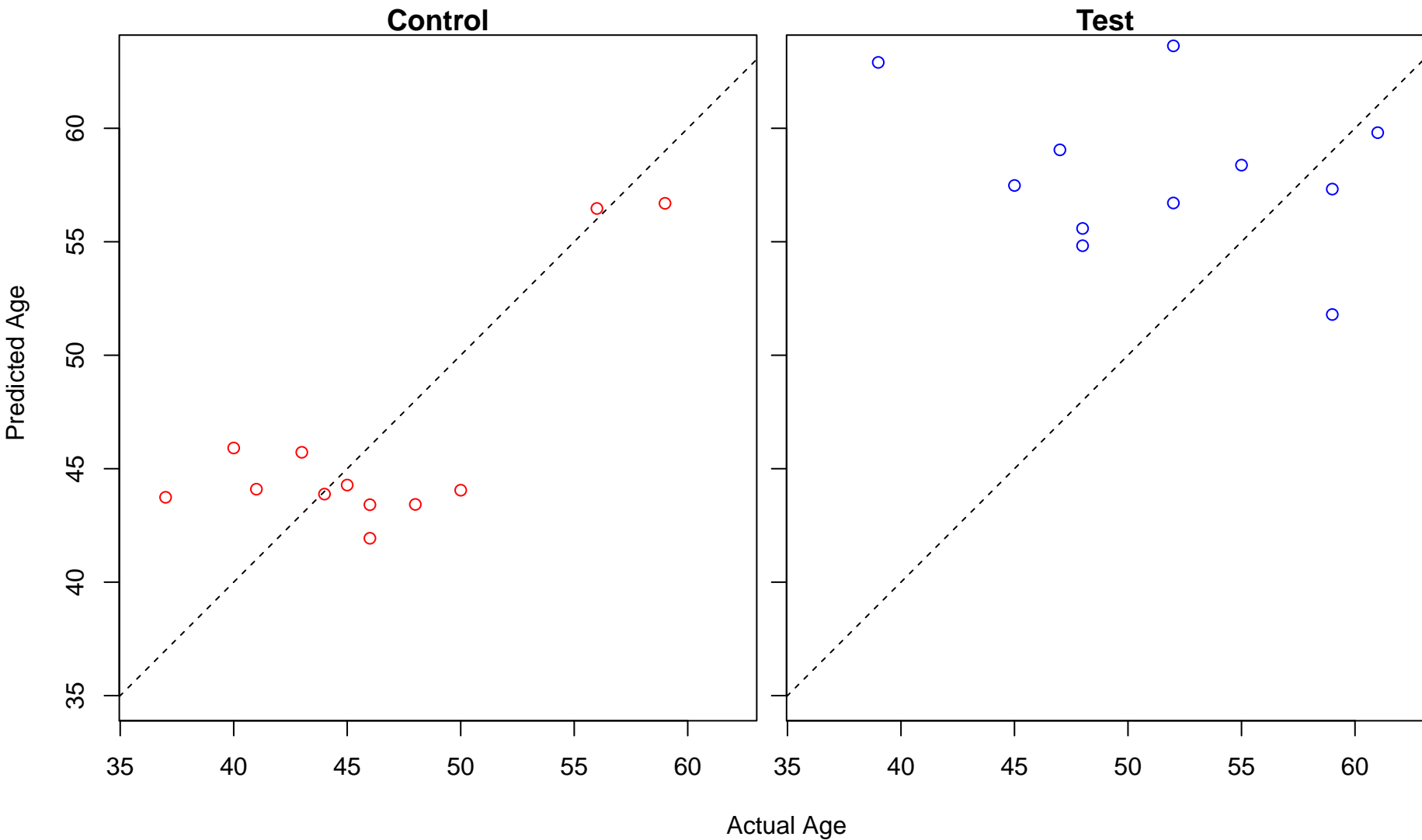


Actual Age

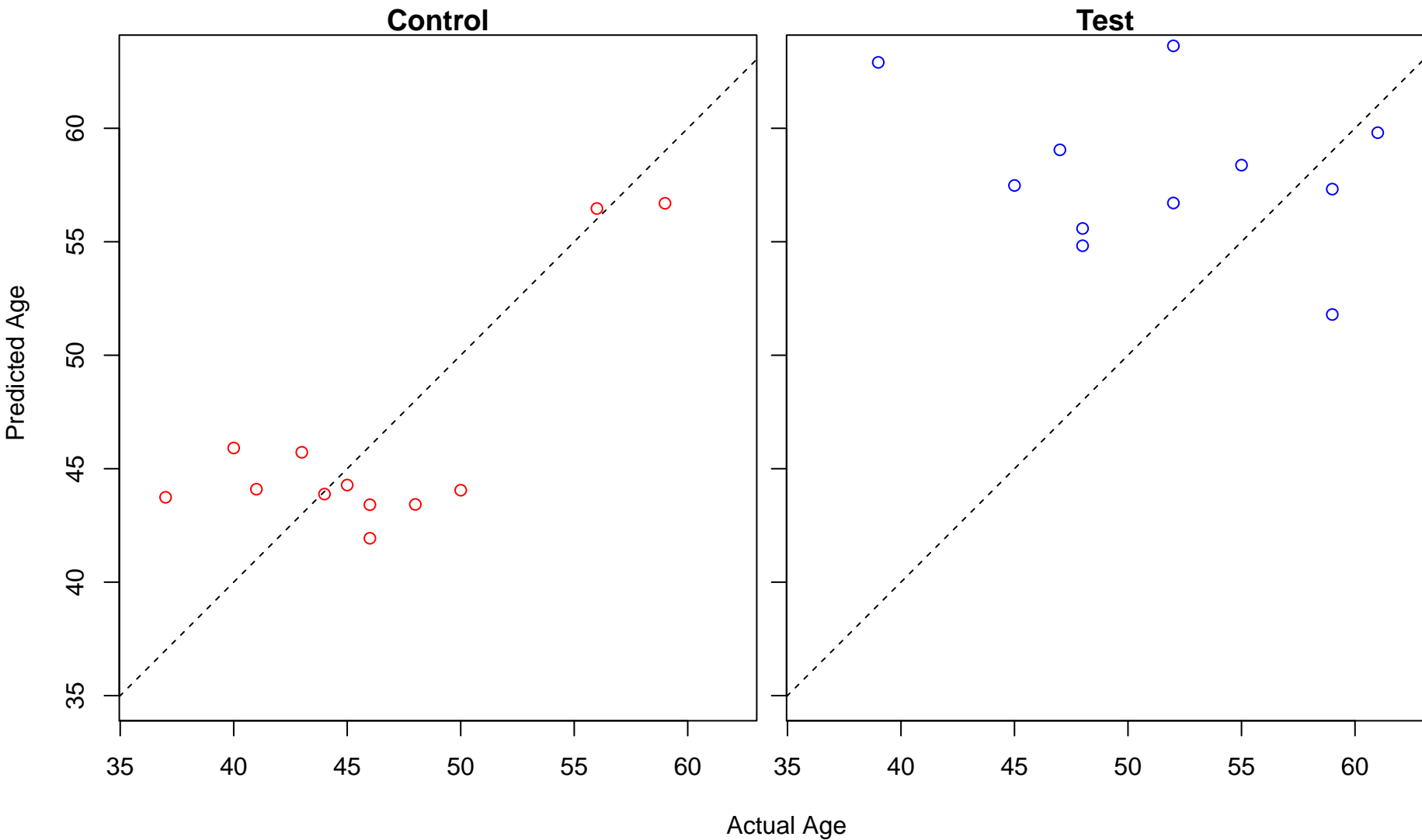
rRNA-containing ribonucleoprotein complex export from nucleus (Score: 3.735428)



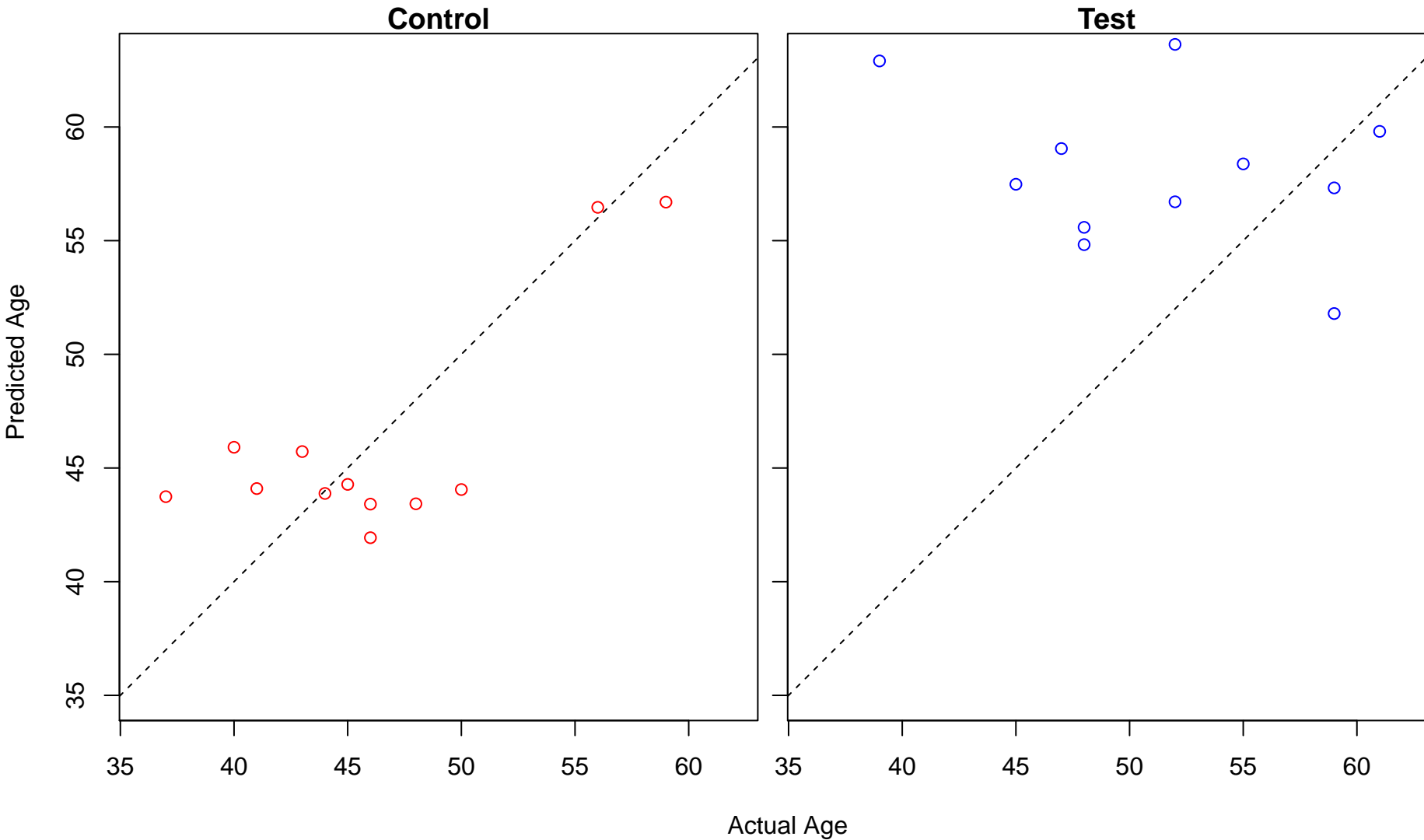
glucose catabolic process (Score: 3.733967)



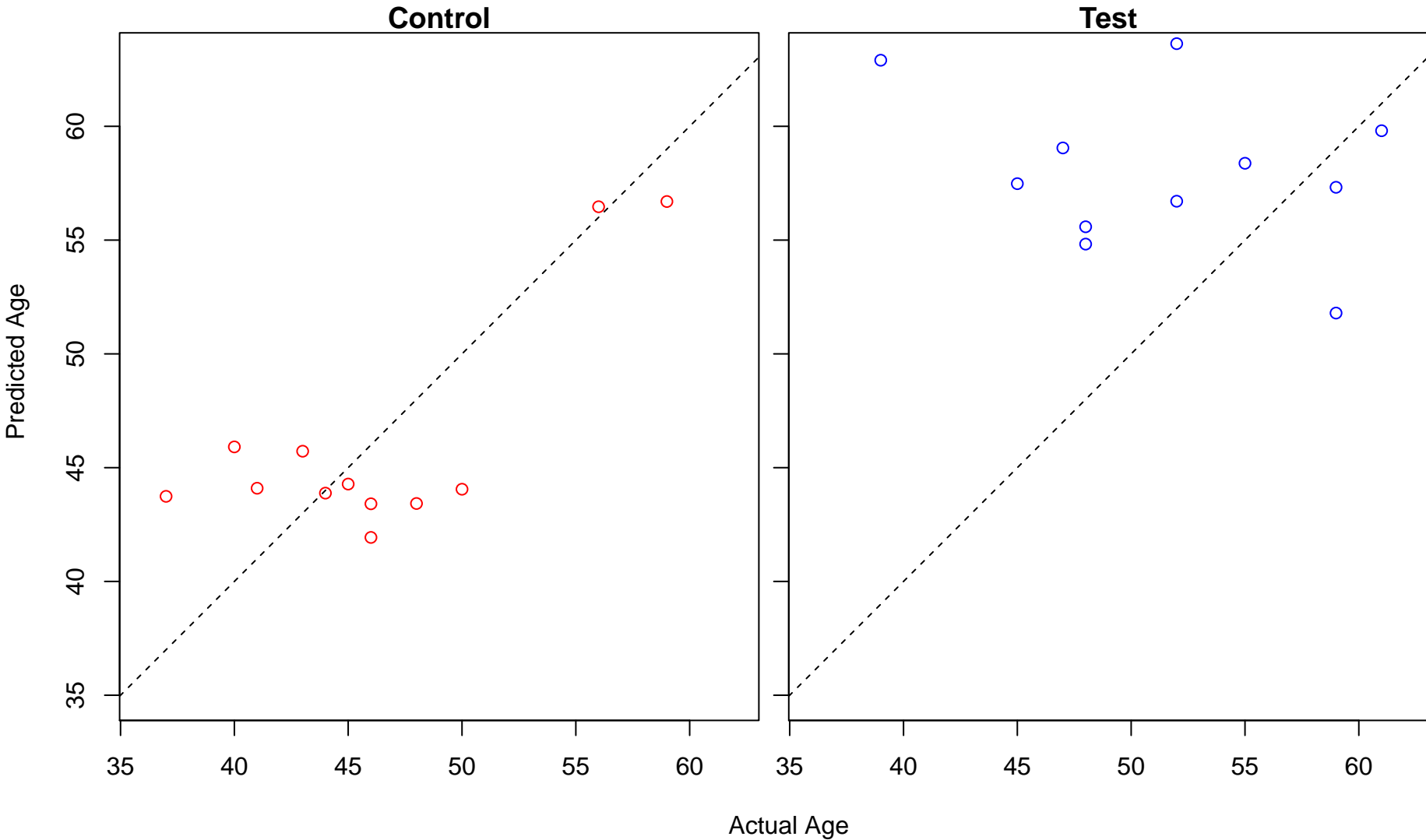
NADH regeneration (Score: 3.733942)



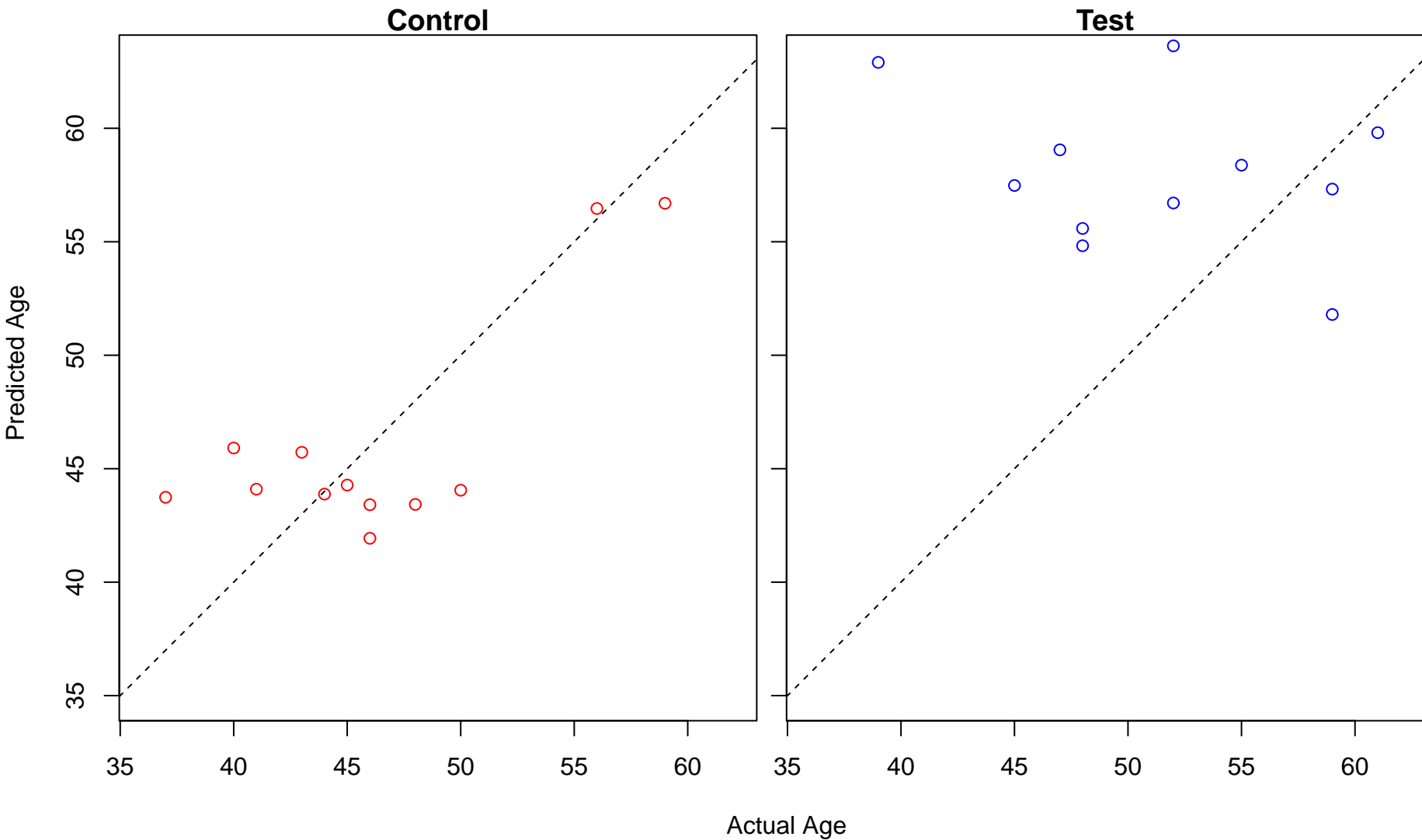
glycolytic process through fructose-6-phosphate (Score: 3.733942)



glycolytic process through glucose-6-phosphate (Score: 3.733942)

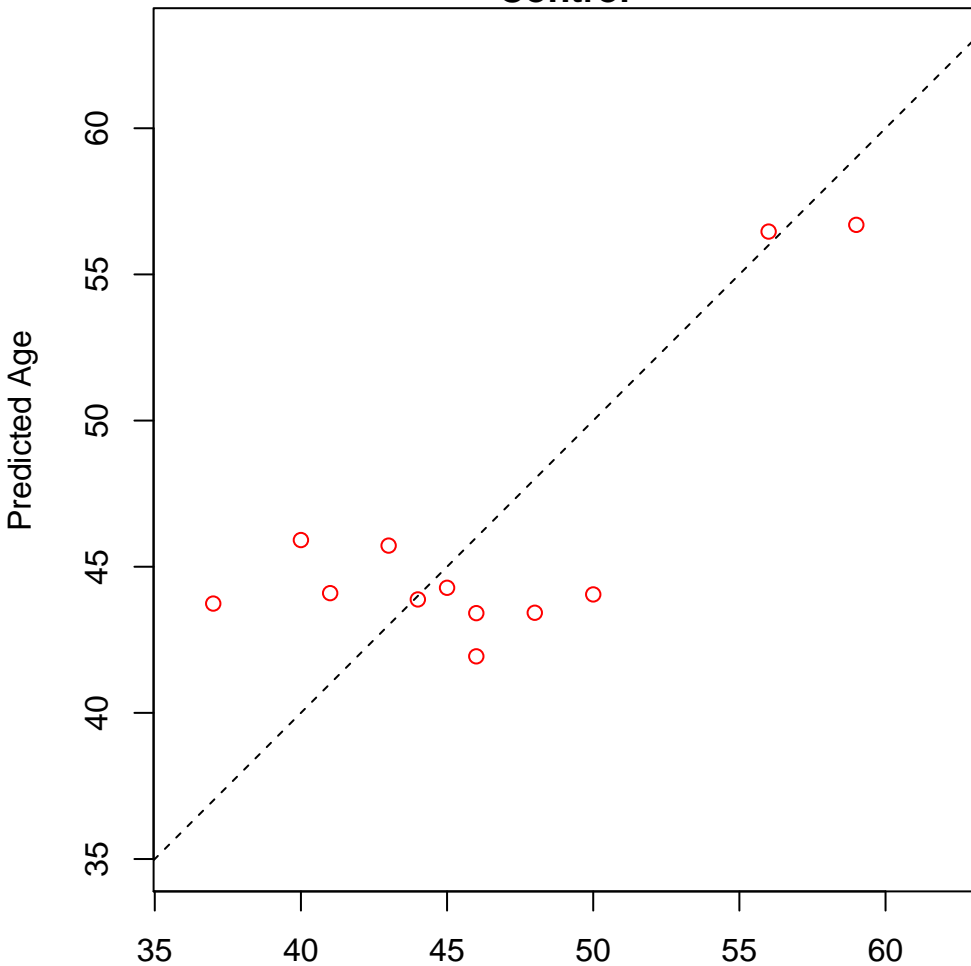


canonical glycolysis (Score: 3.733942)

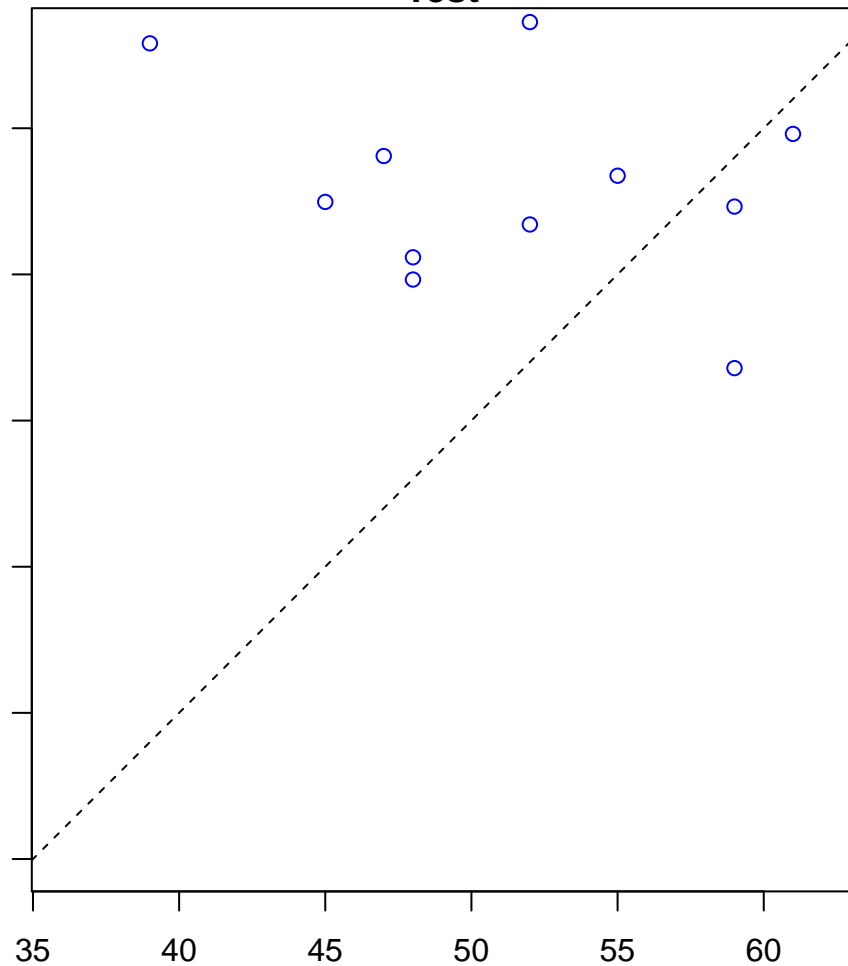


glucose catabolic process to pyruvate (Score: 3.733942)

Control

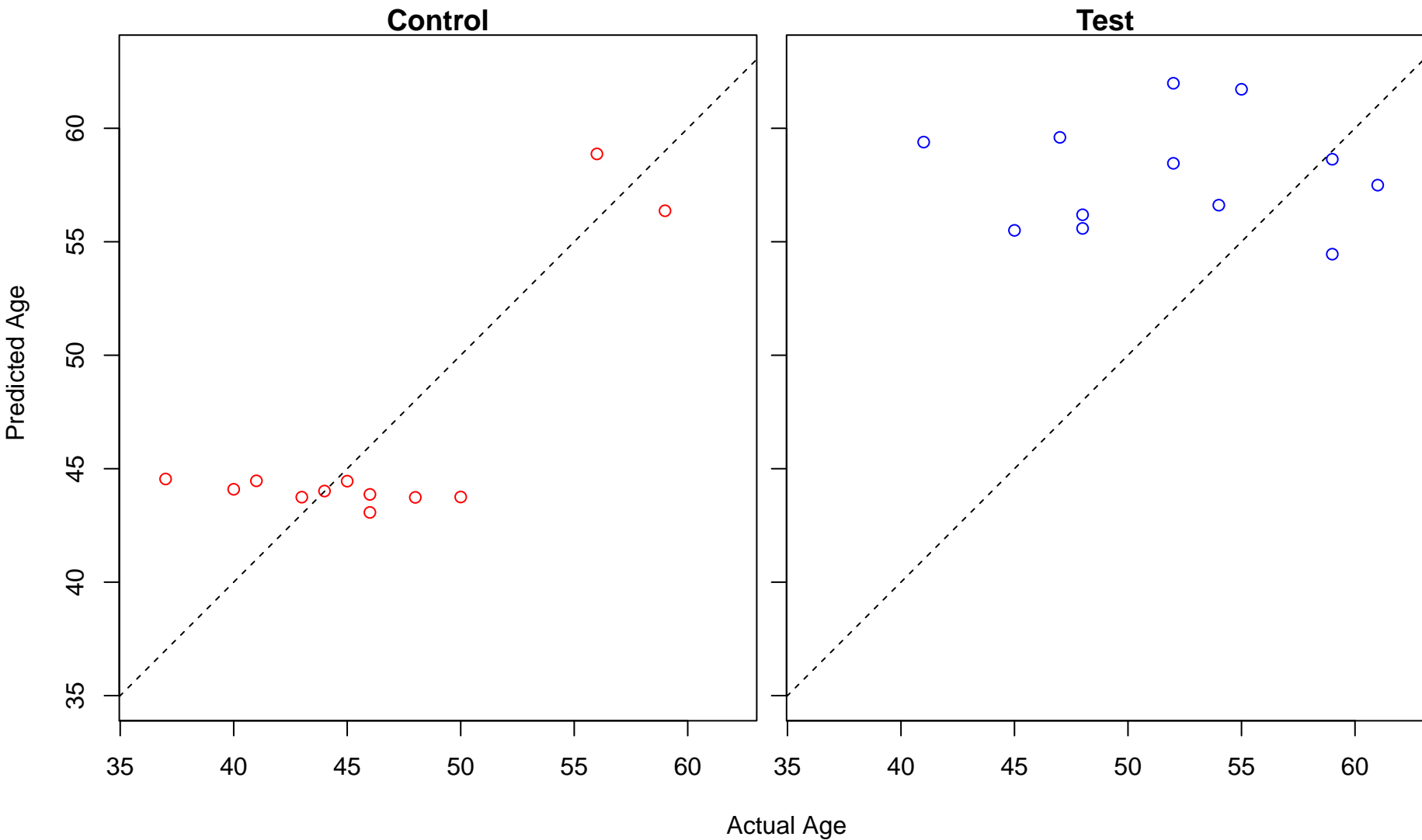


Test

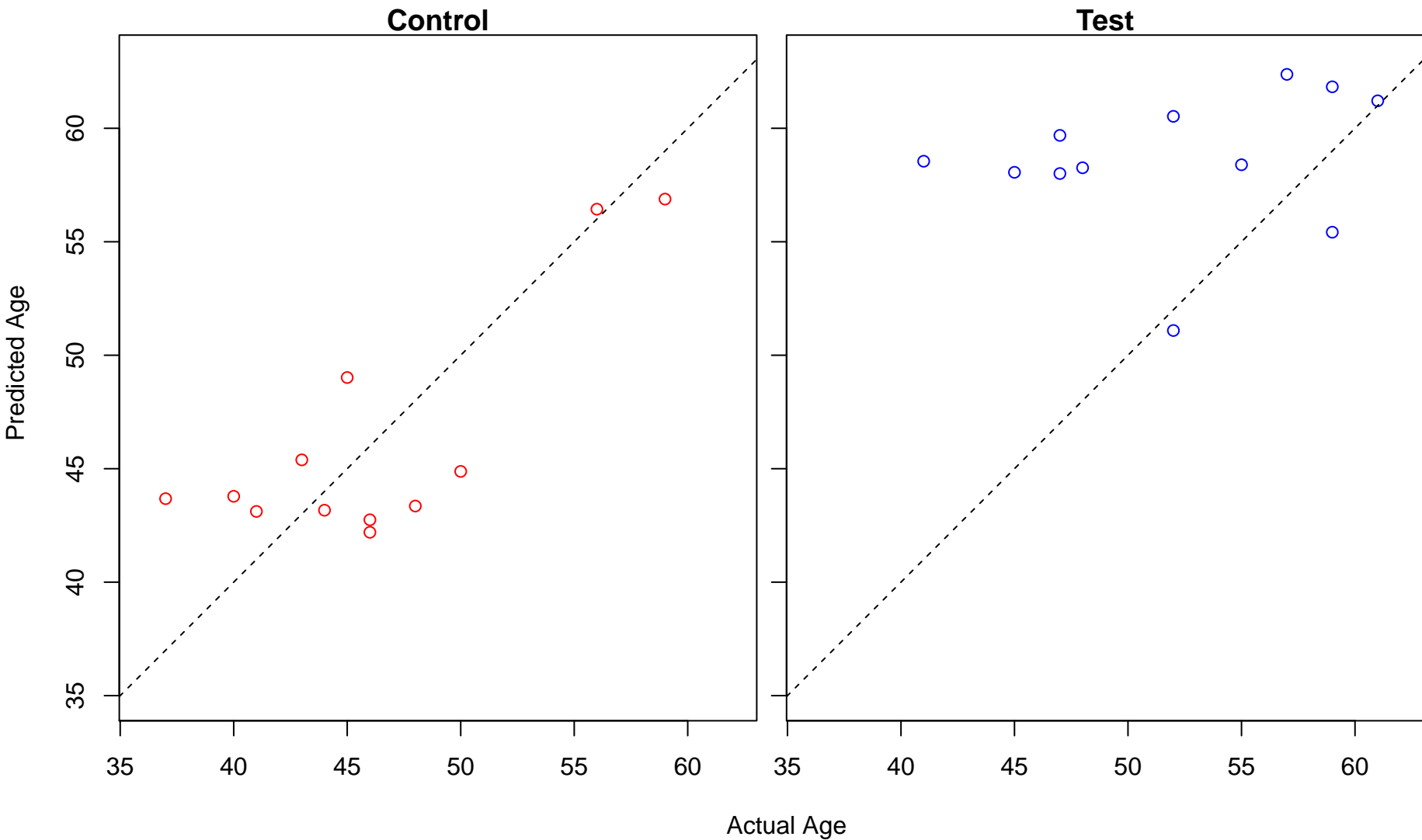


Actual Age

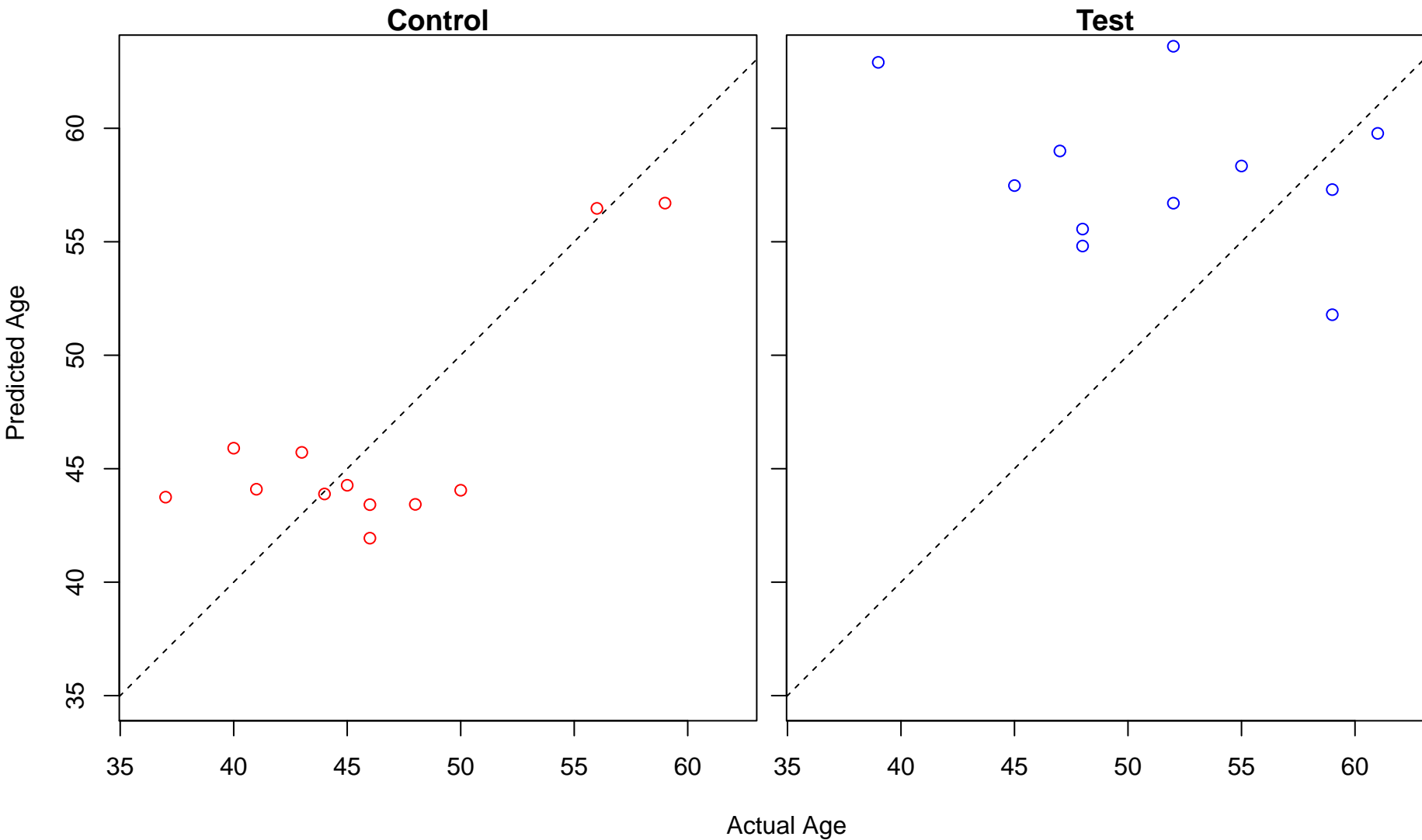
negative regulation of cell cycle (Score: 3.732937)



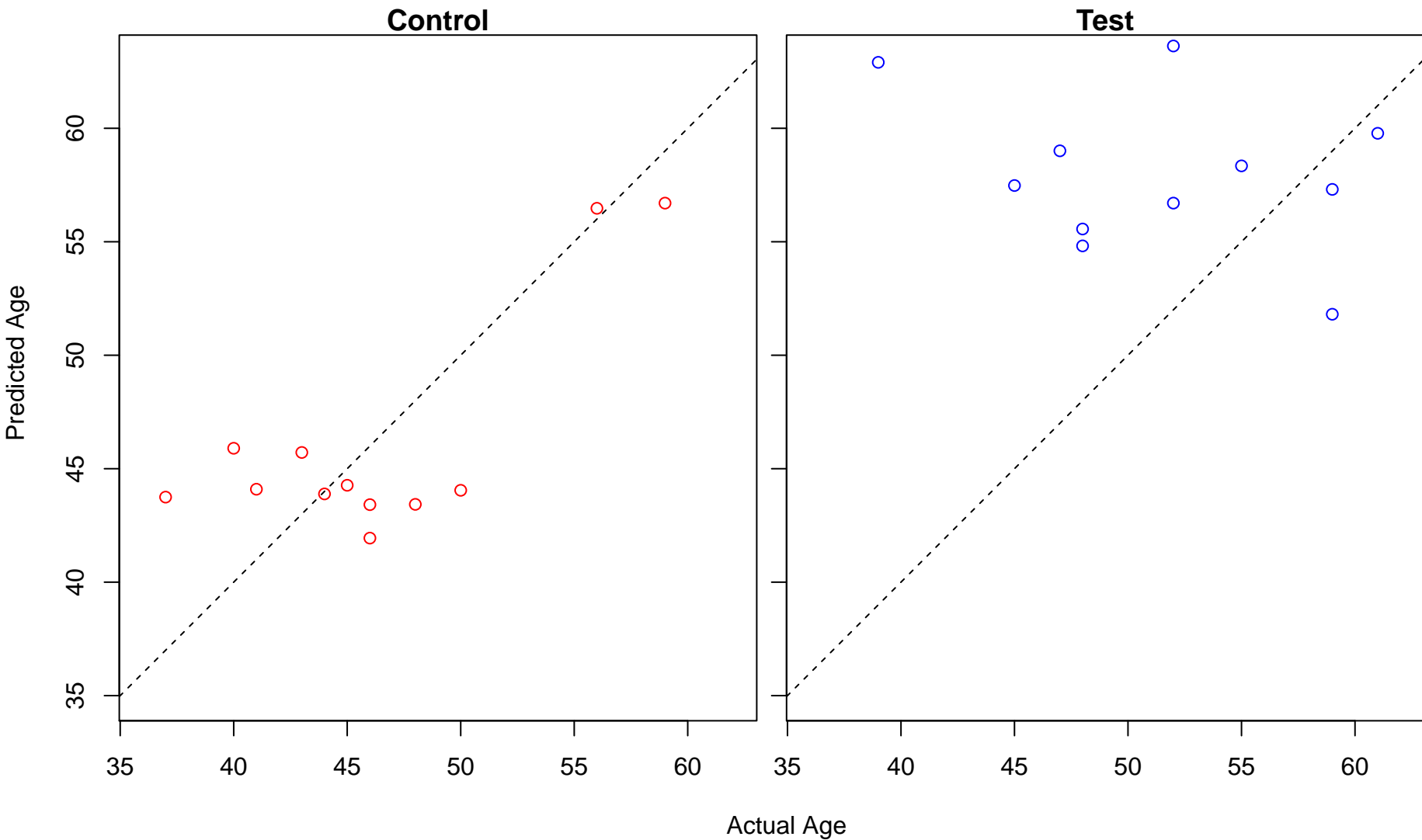
negative regulation of heart growth (Score: 3.732064)



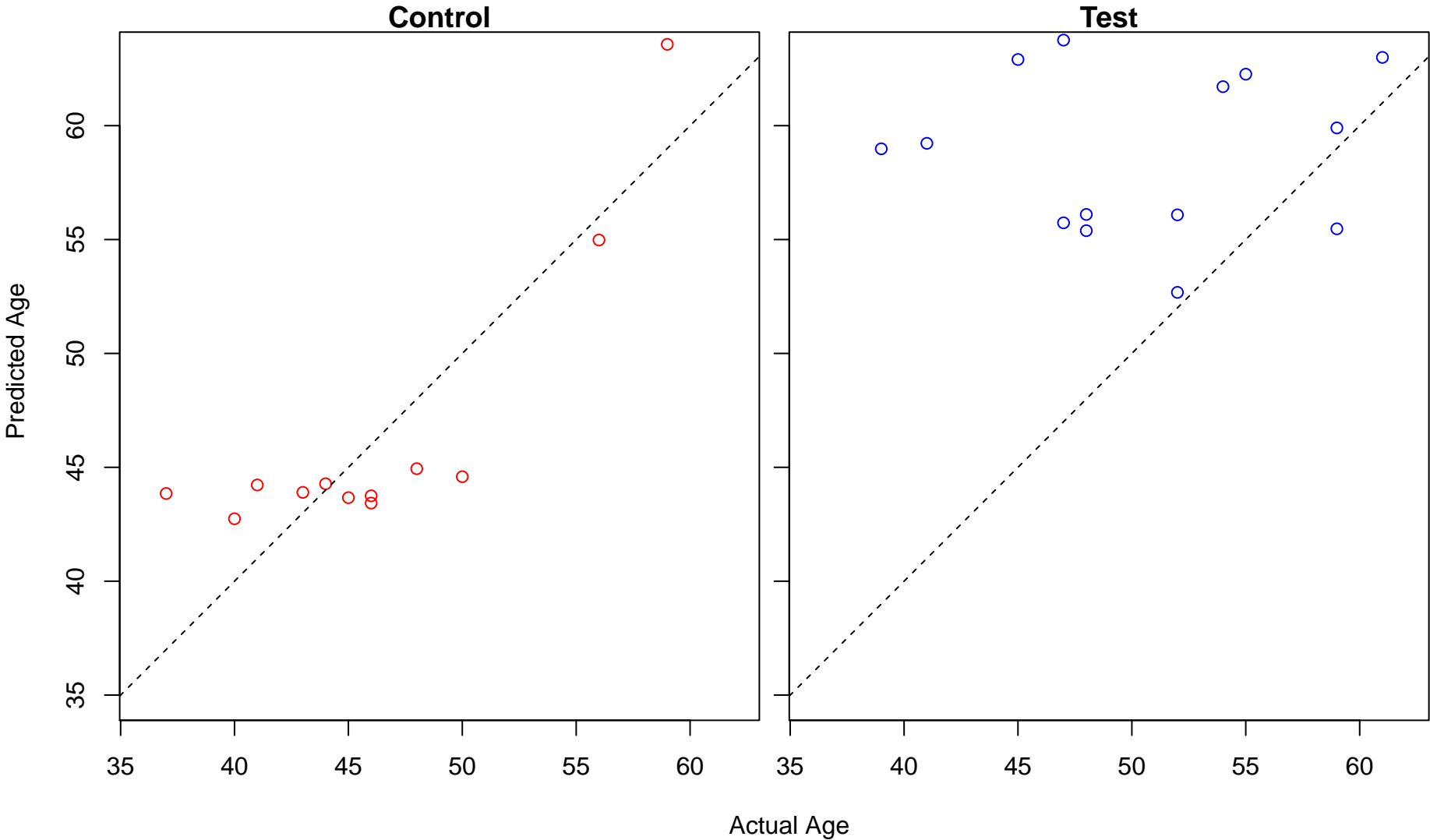
glycolytic process (Score: 3.730969)



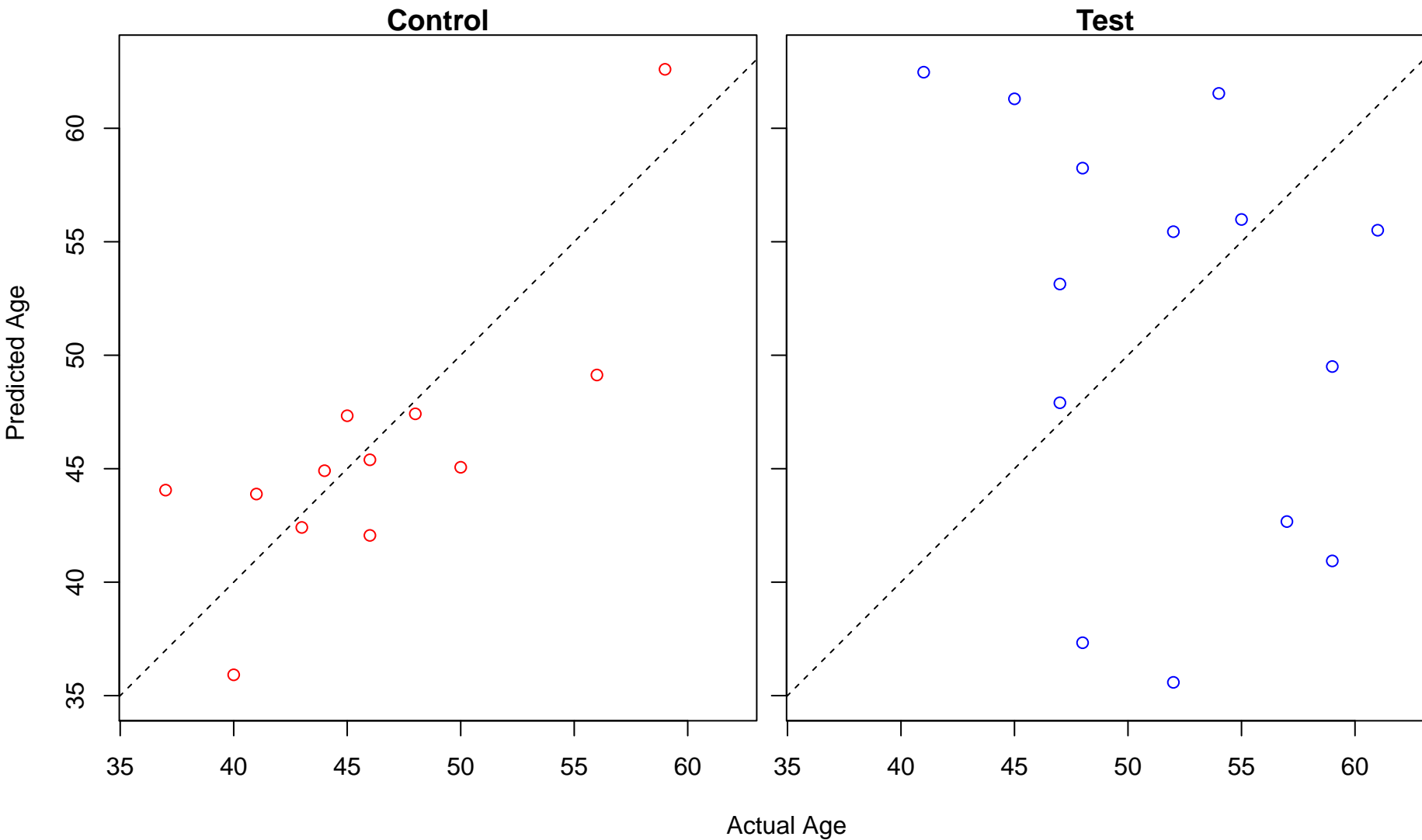
hexose catabolic process (Score: 3.730895)



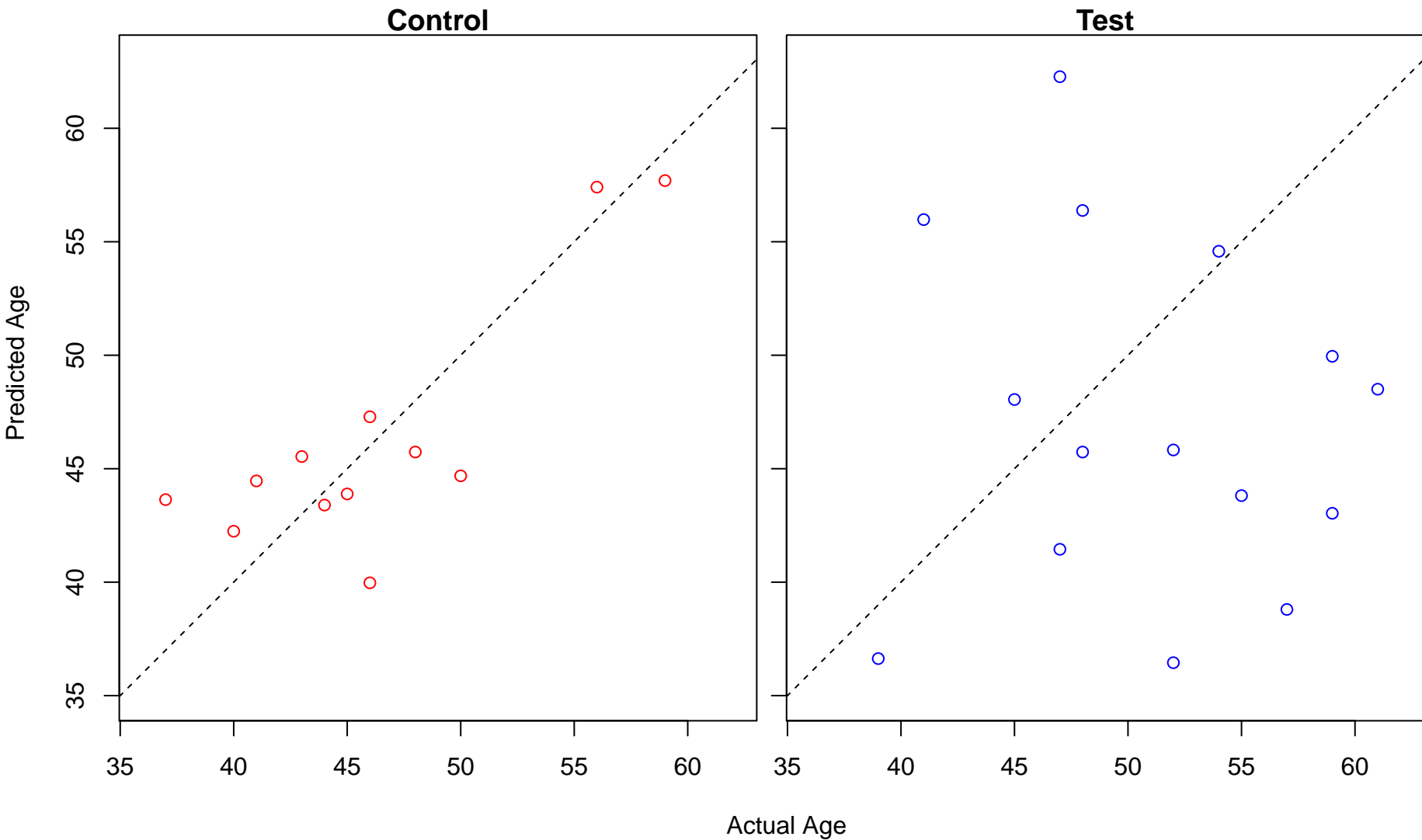
regulation of nucleotide-binding oligomerization domain containing signaling pathway (Score: 3.730)



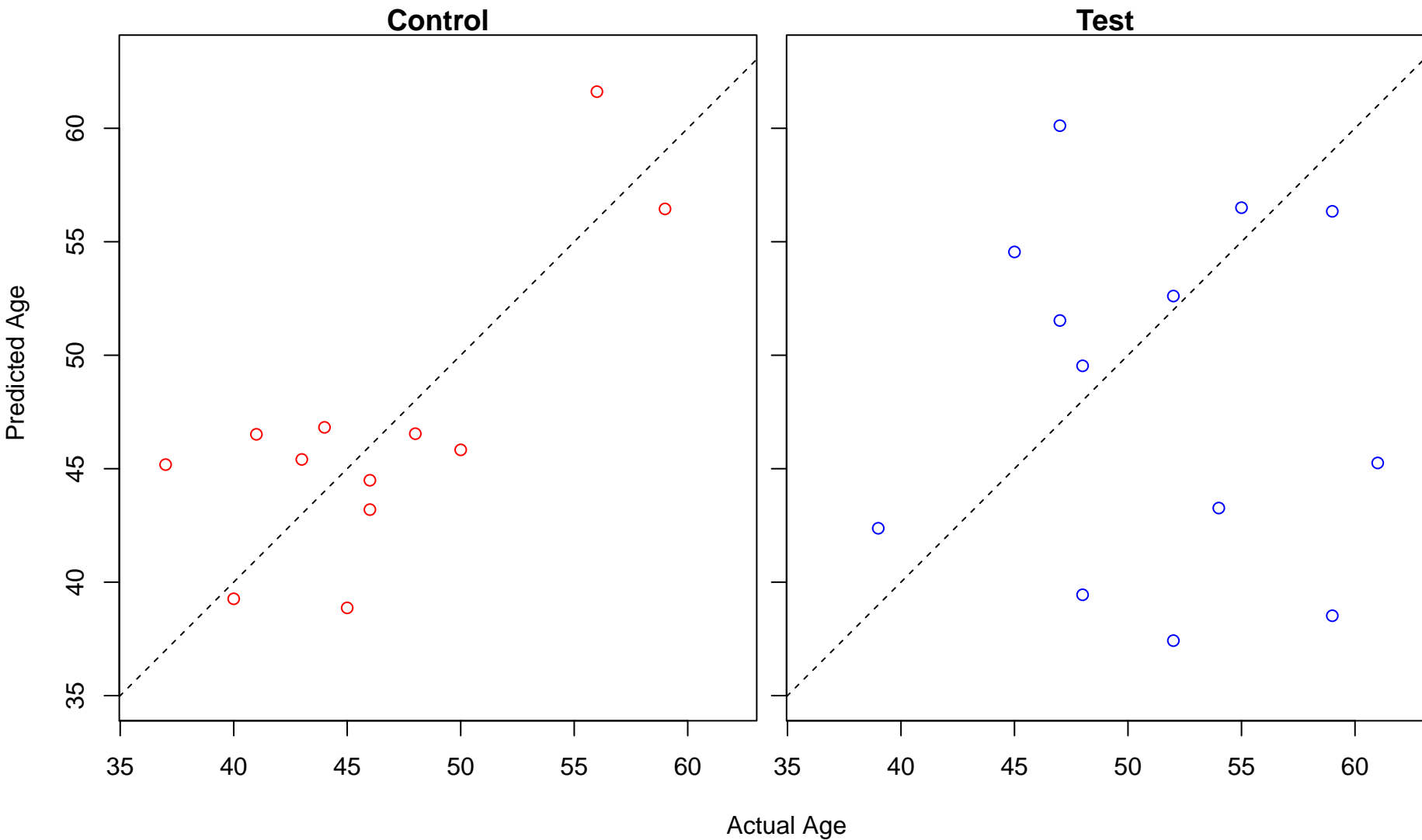
endoplasmic reticulum calcium ion homeostasis (Score: 3.726459)



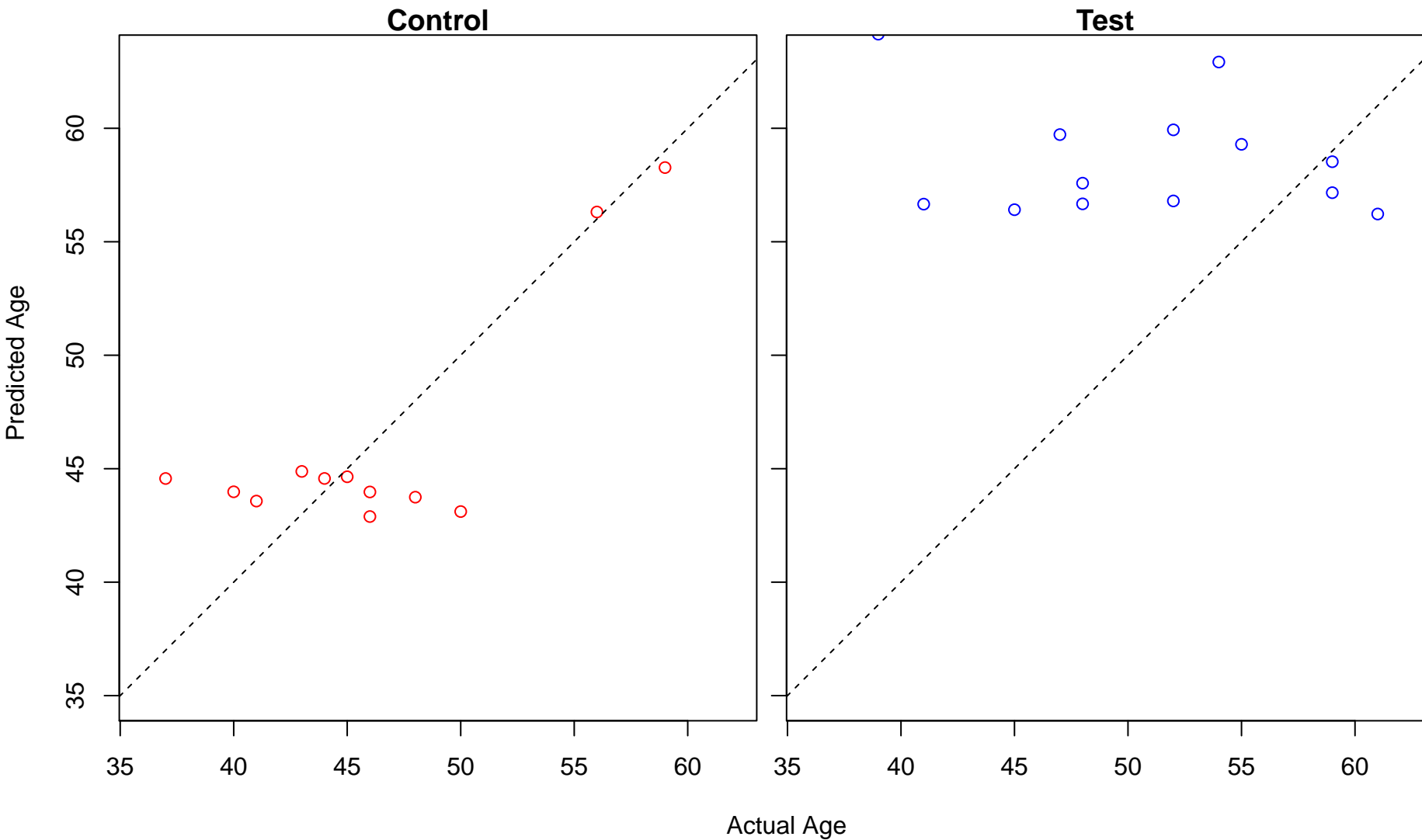
RNA splicing, via endonucleolytic cleavage and ligation (Score: 3.725112)



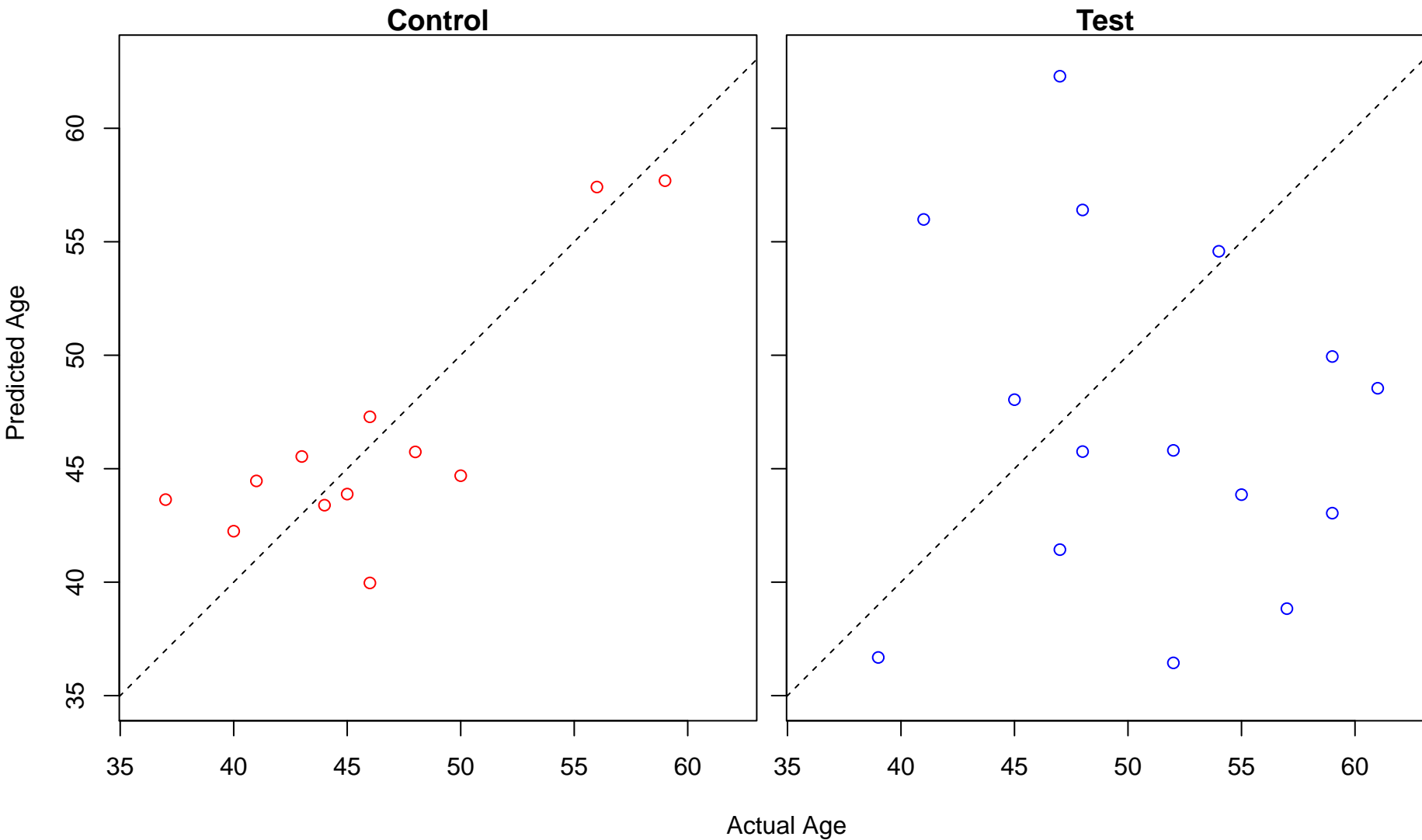
positive regulation of cell death (Score: 3.724998)



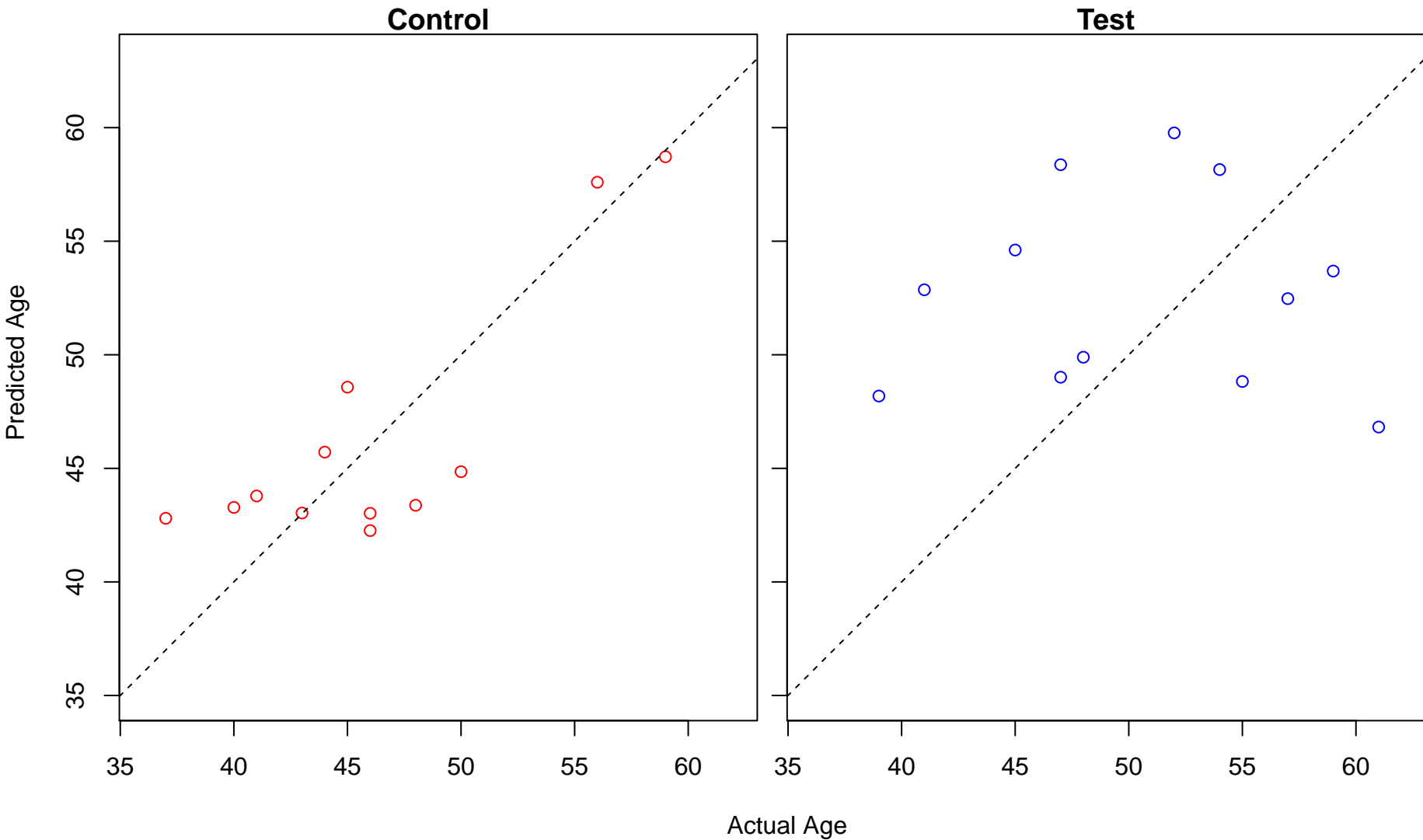
skeletal muscle organ development (Score: 3.723740)



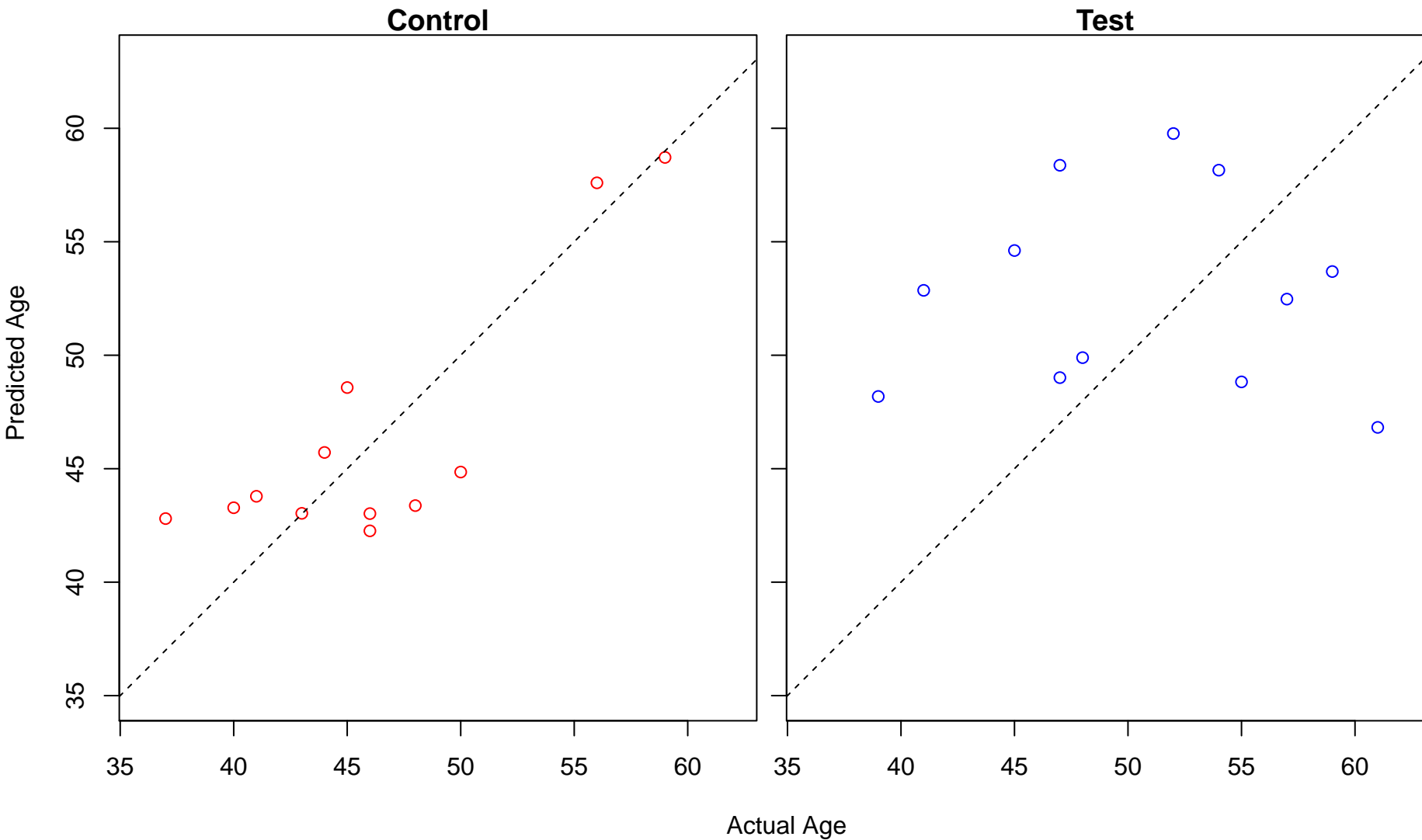
tRNA splicing, via endonucleolytic cleavage and ligation (Score: 3.720747)



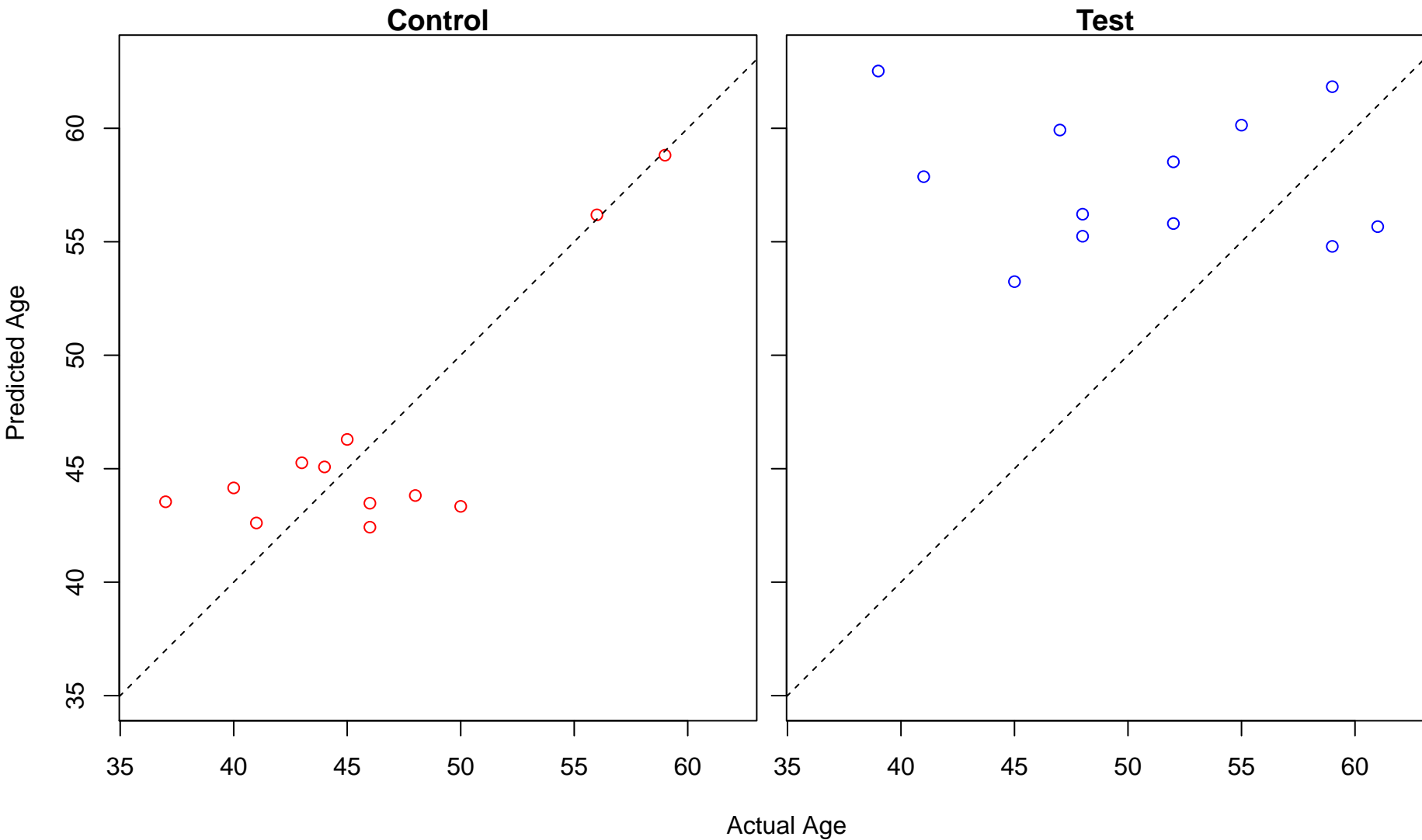
pyrimidine nucleoside biosynthetic process (Score: 3.720383)



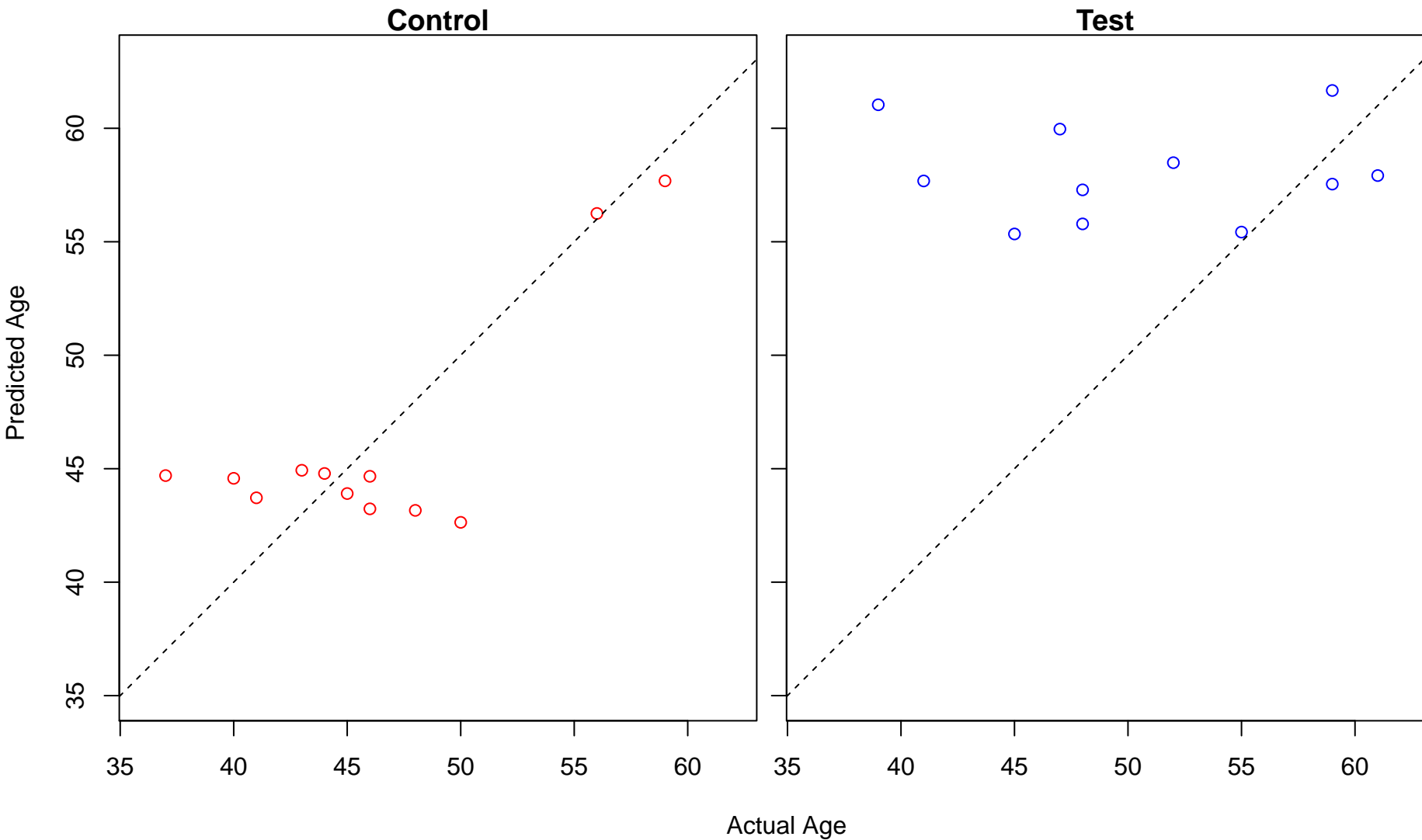
pyrimidine-containing compound biosynthetic process (Score: 3.720375)



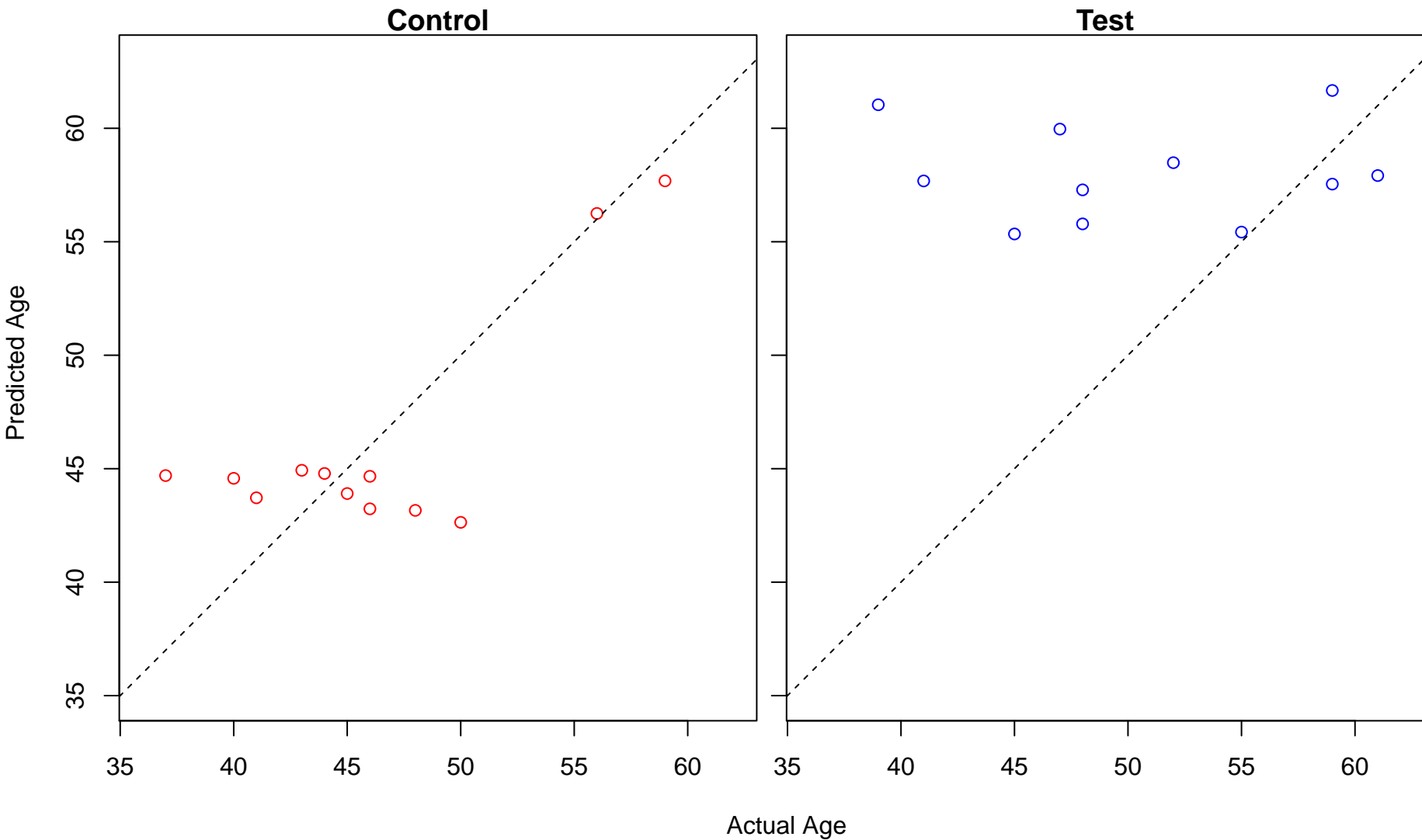
axis specification (Score: 3.719423)



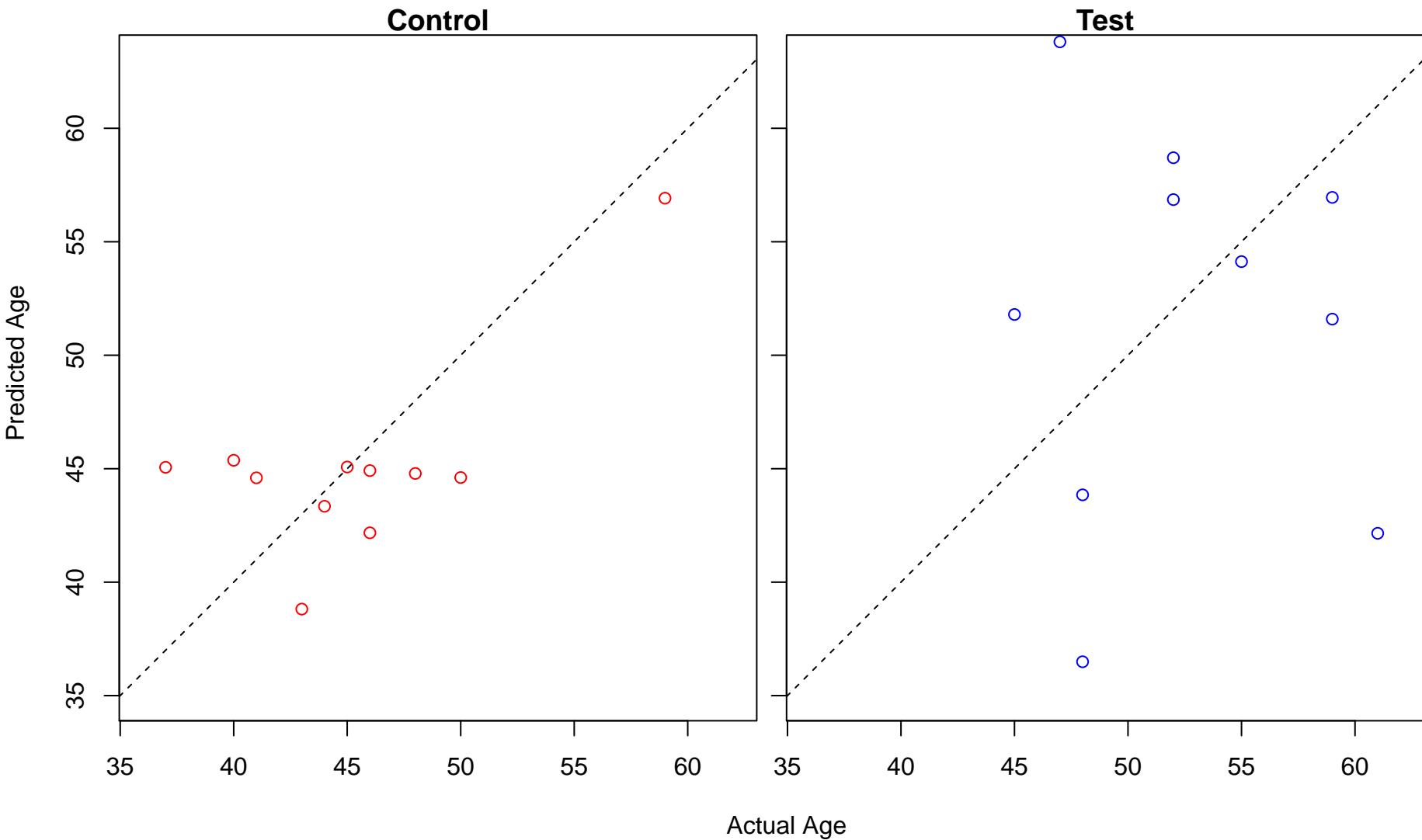
autophagosome maturation (Score: 3.717830)



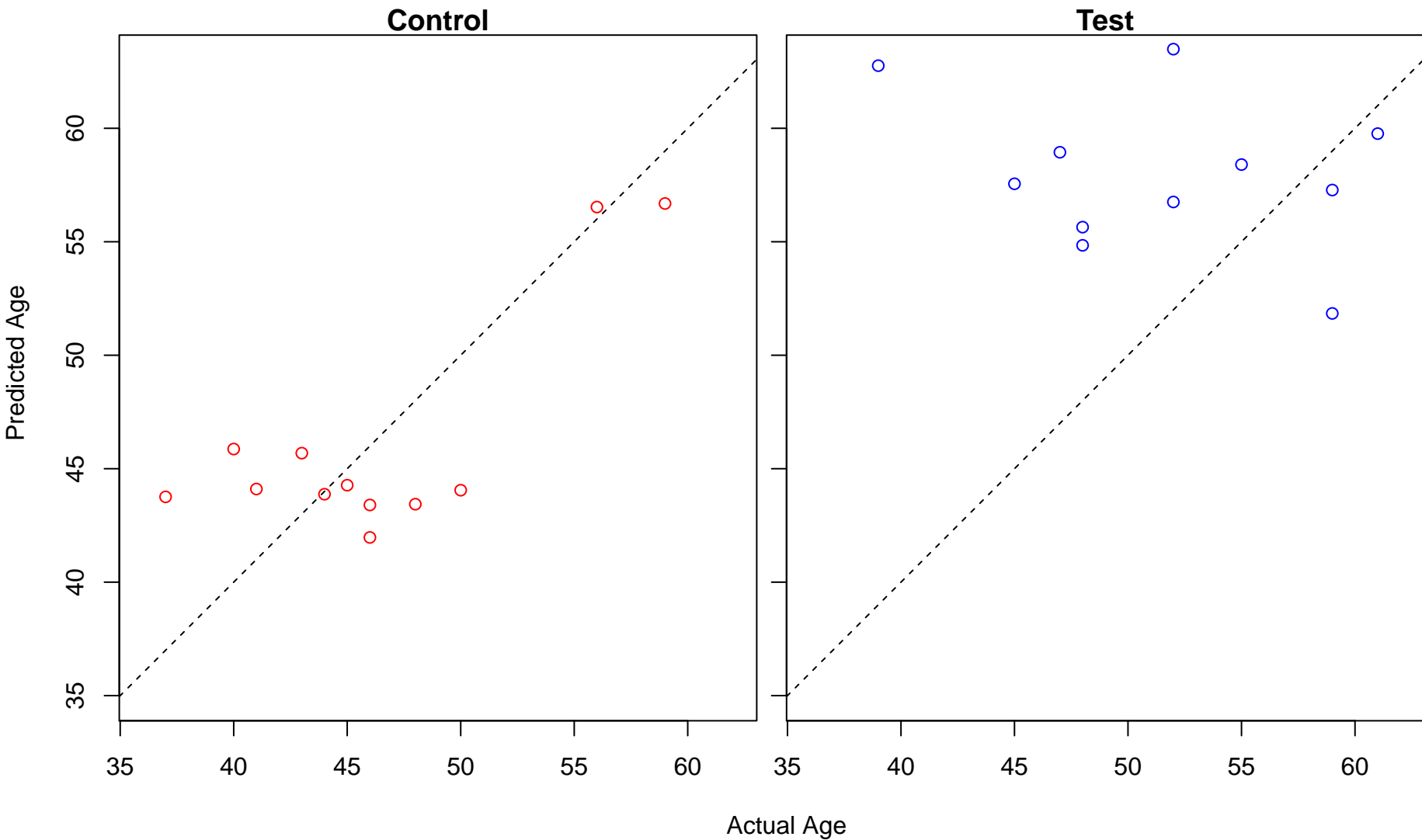
vacuole fusion (Score: 3.717830)



cellular response to platelet-derived growth factor stimulus (Score: 3.717663)

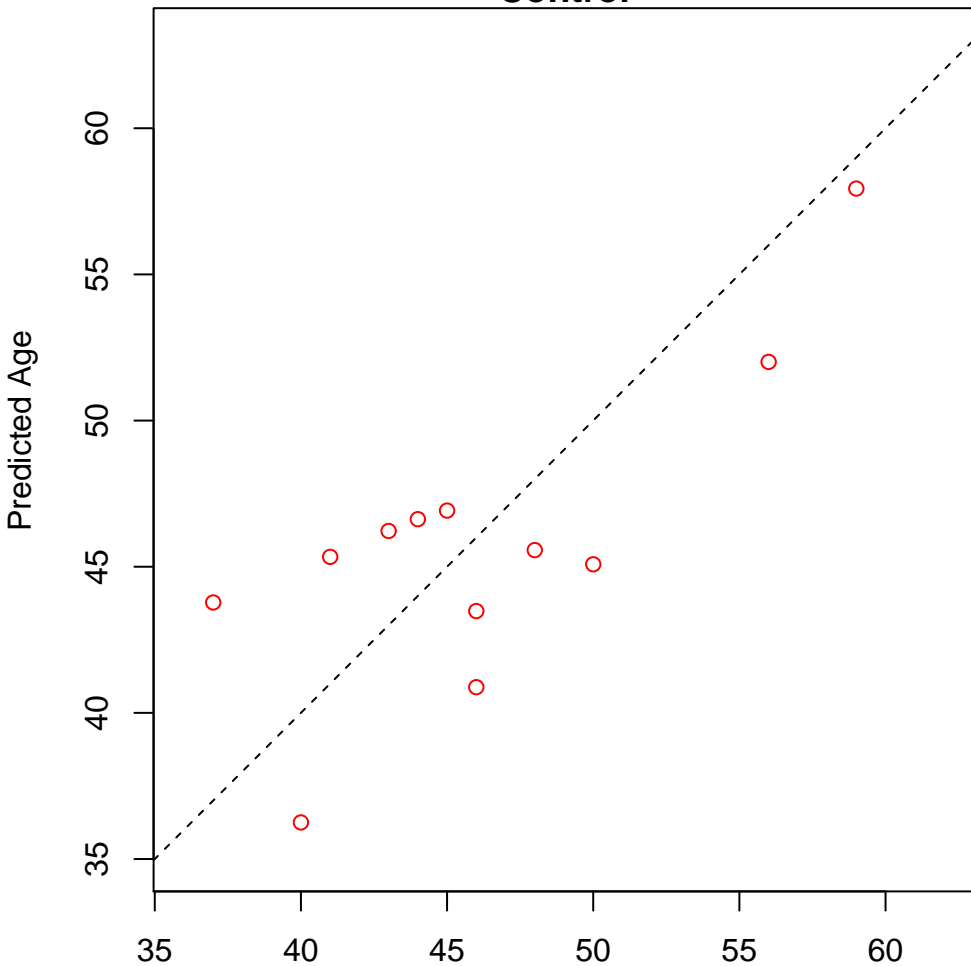


ADP metabolic process (Score: 3.714958)

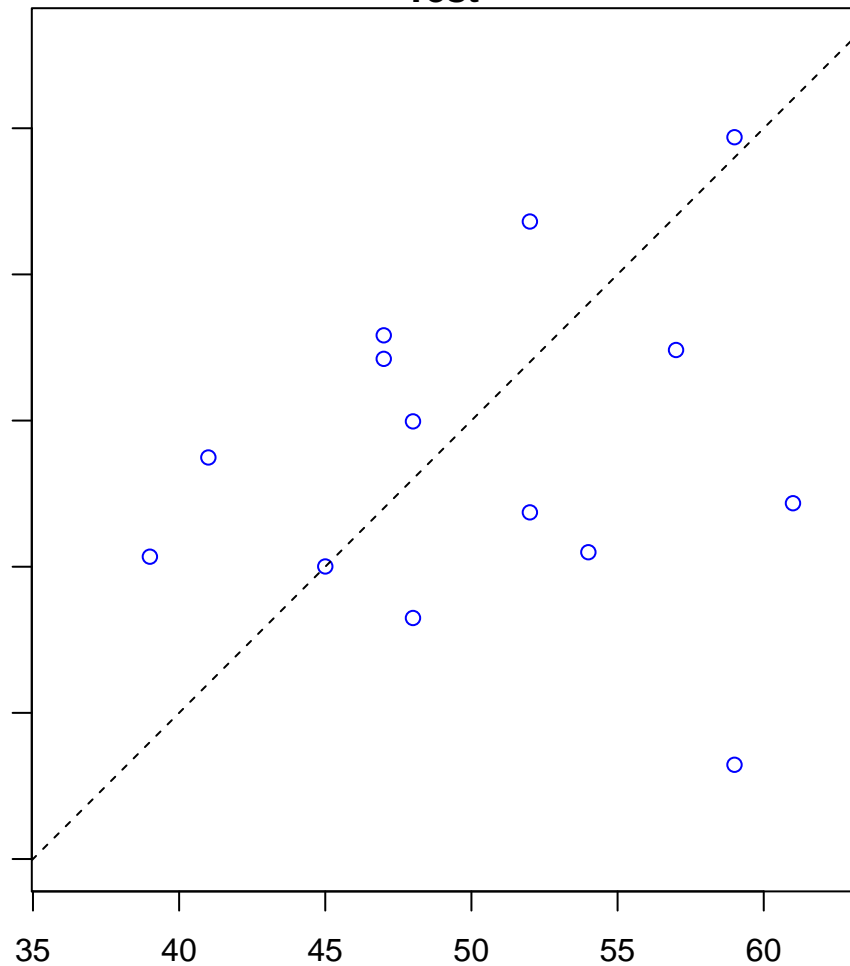


regulation of interferon-beta production (Score: 3.714879)

Control

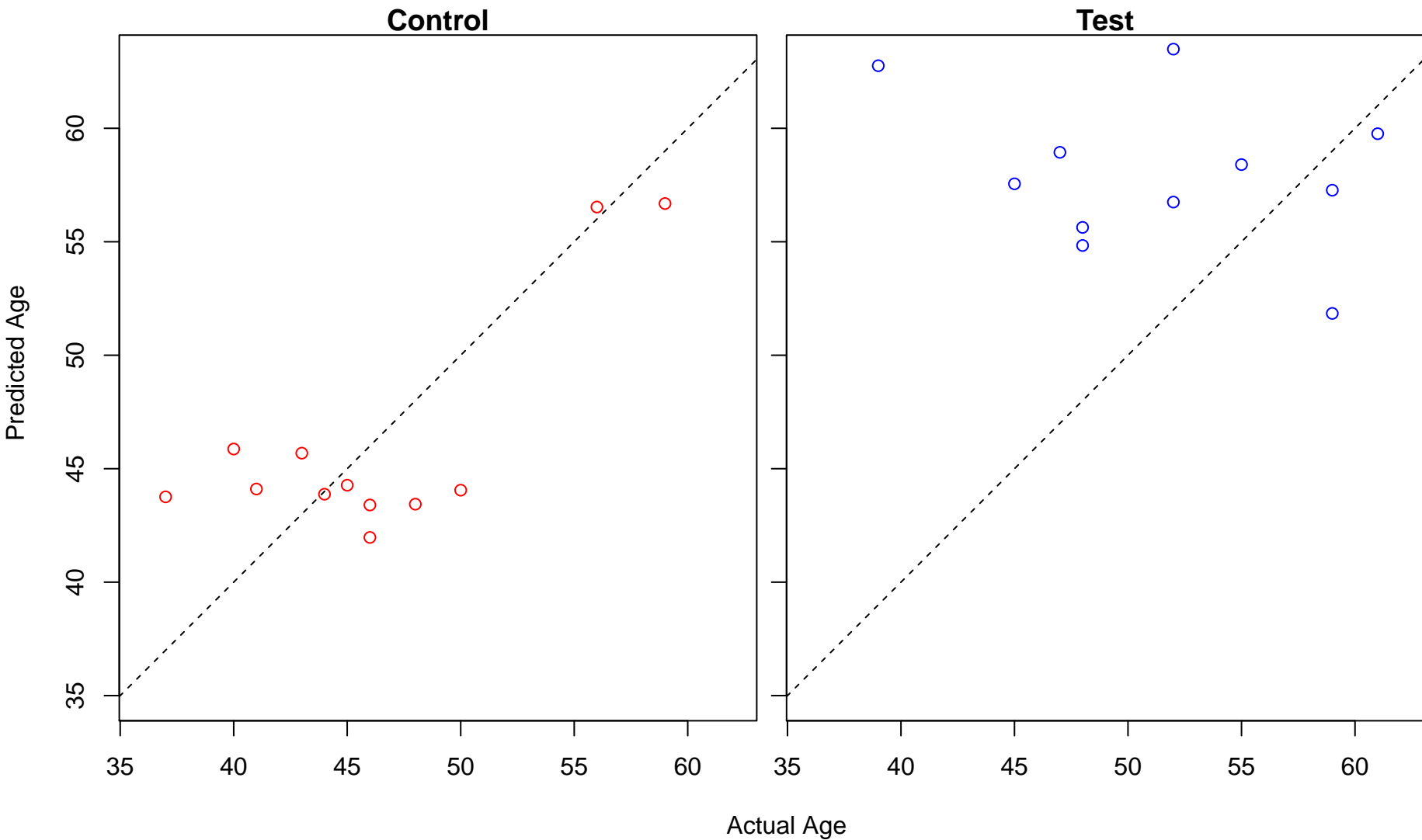


Test

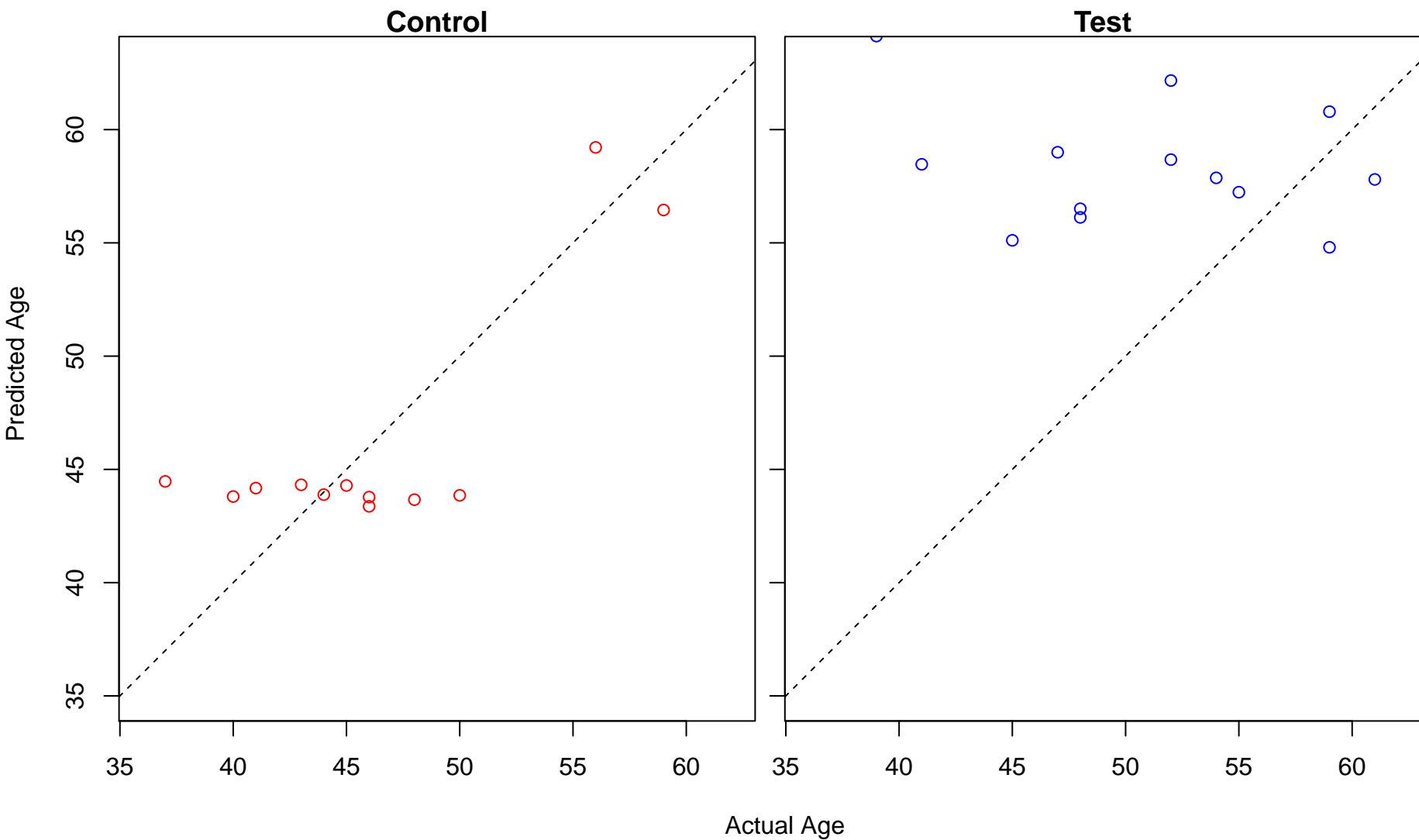


Actual Age

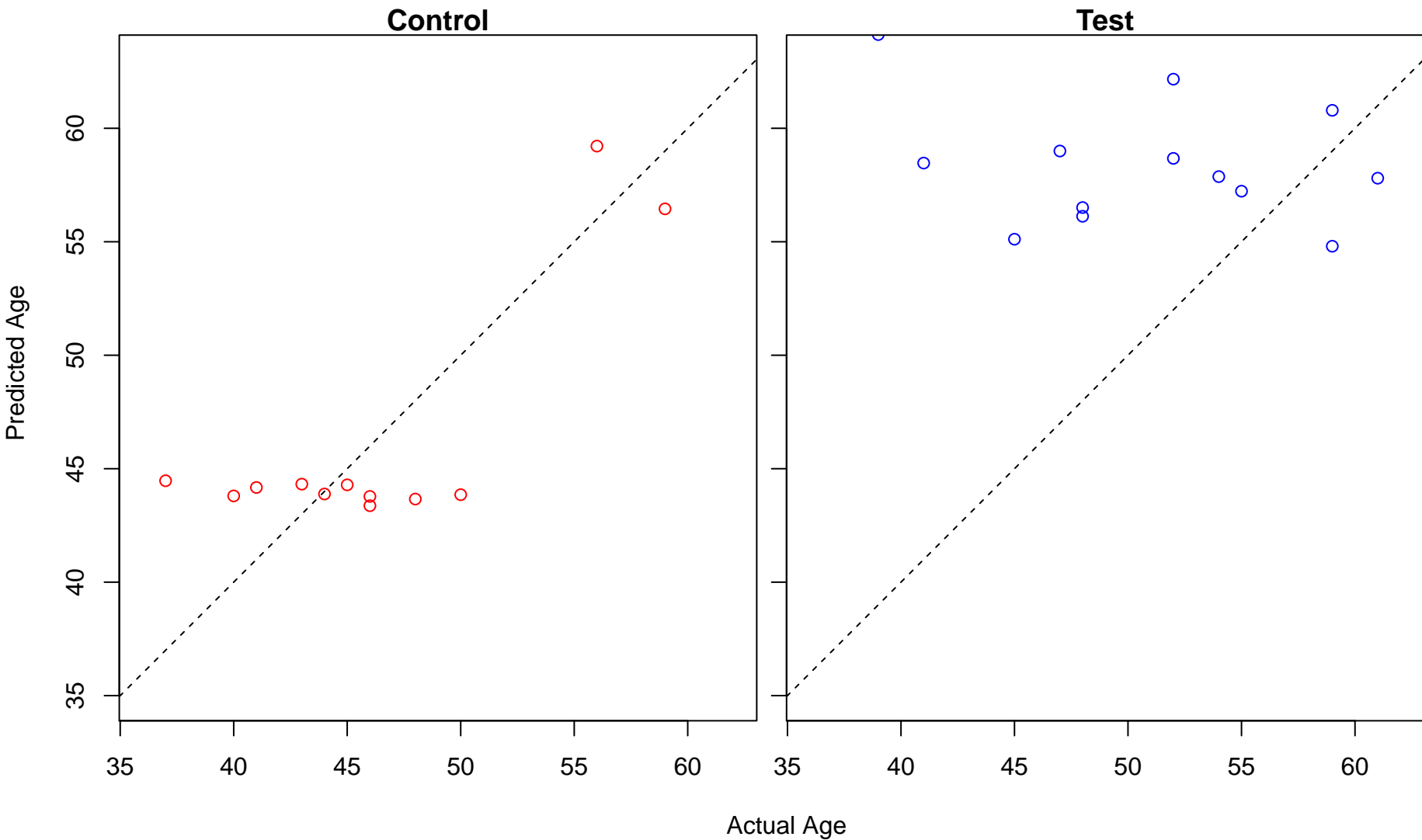
ATP generation from ADP (Score: 3.713628)



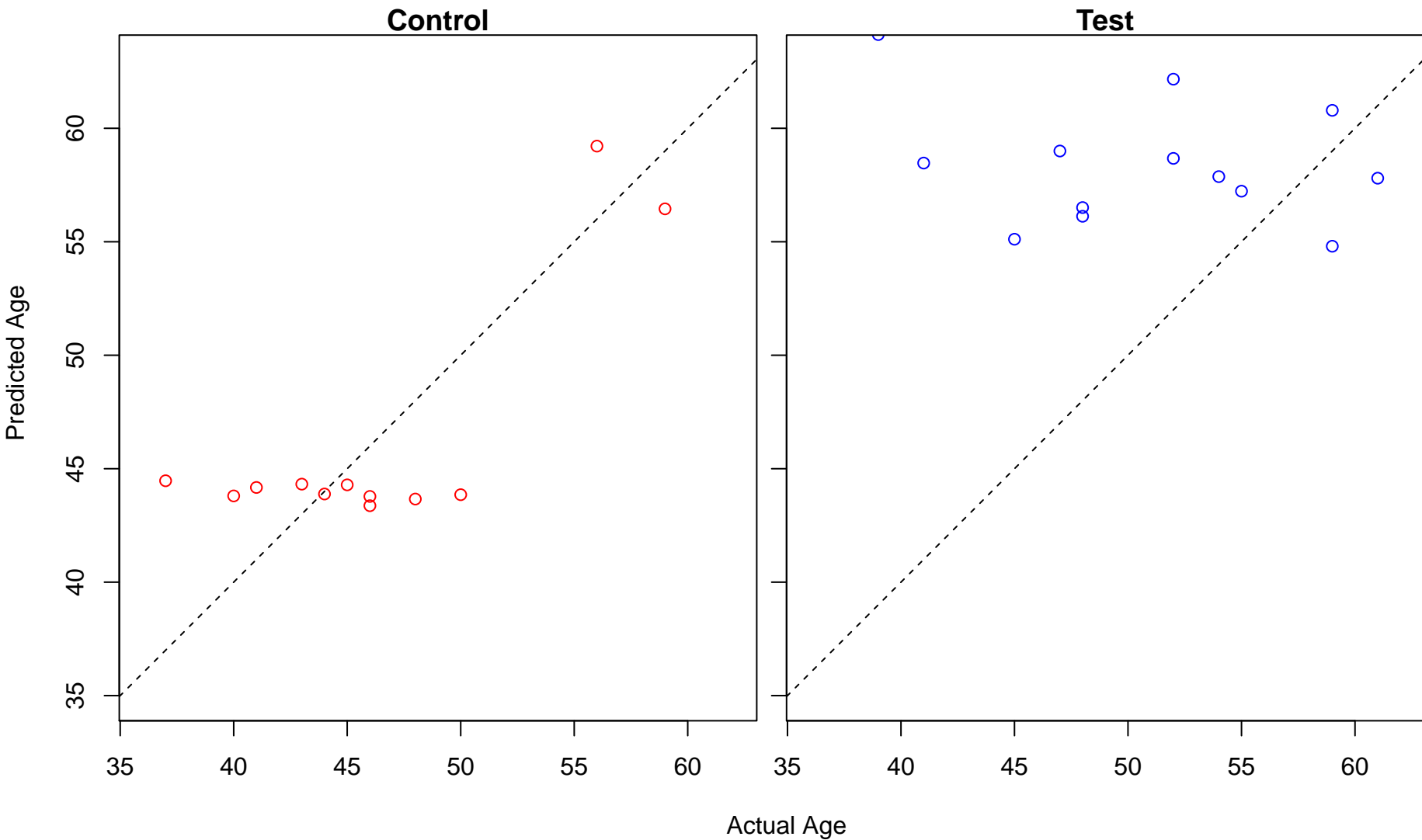
toll-like receptor 2 signaling pathway (Score: 3.712632)



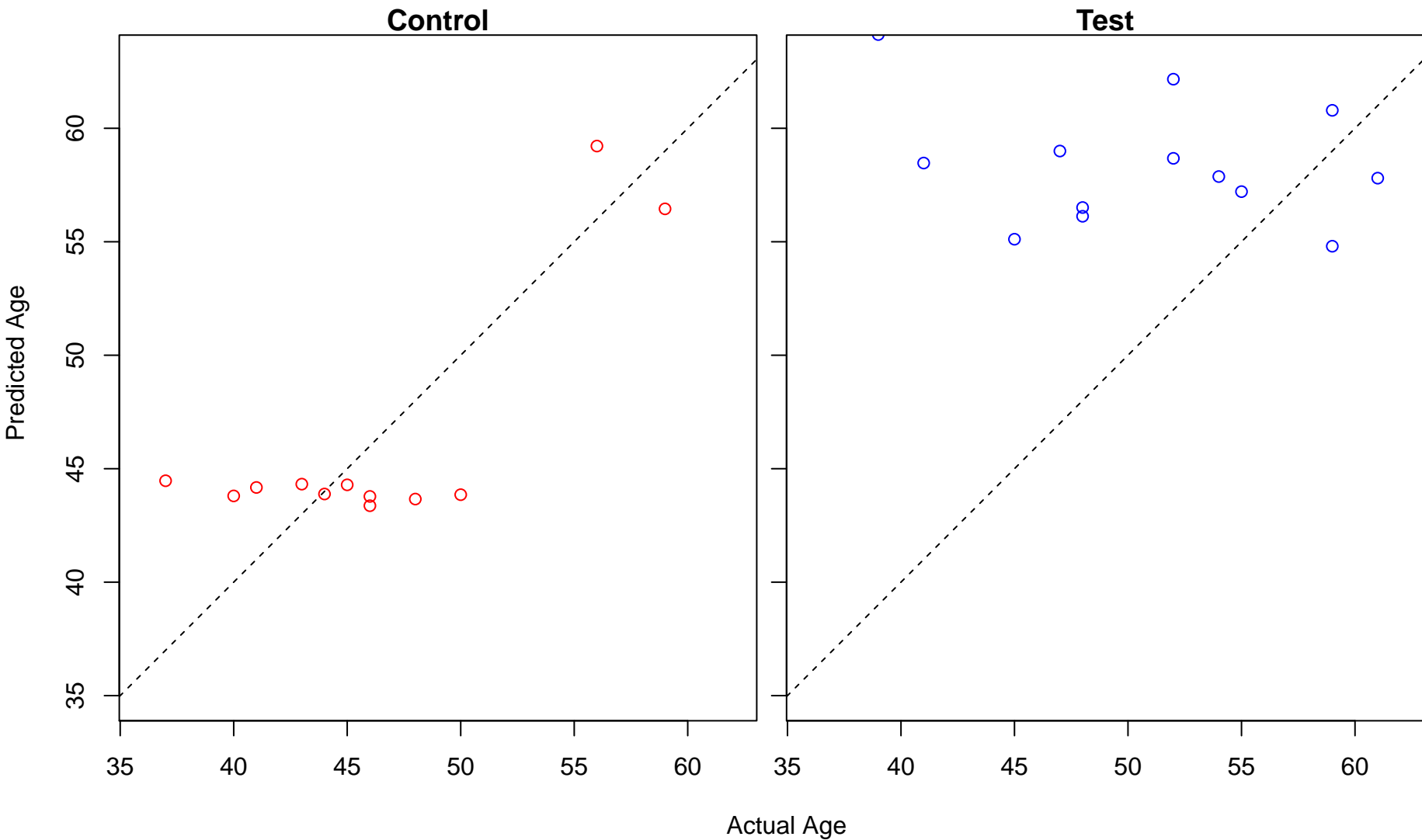
toll-like receptor TLR1:TLR2 signaling pathway (Score: 3.712523)



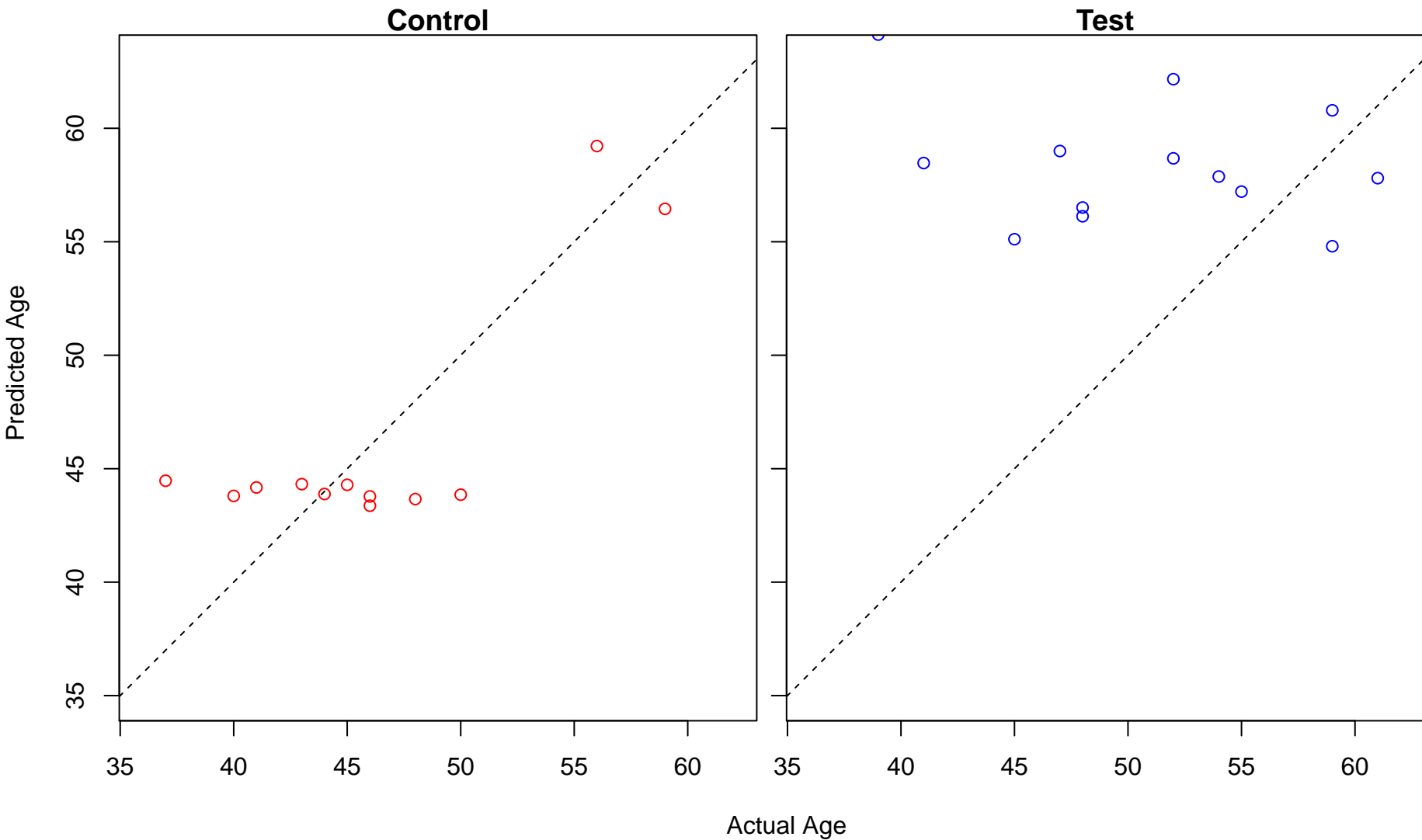
toll-like receptor TLR6:TLR2 signaling pathway (Score: 3.712523)



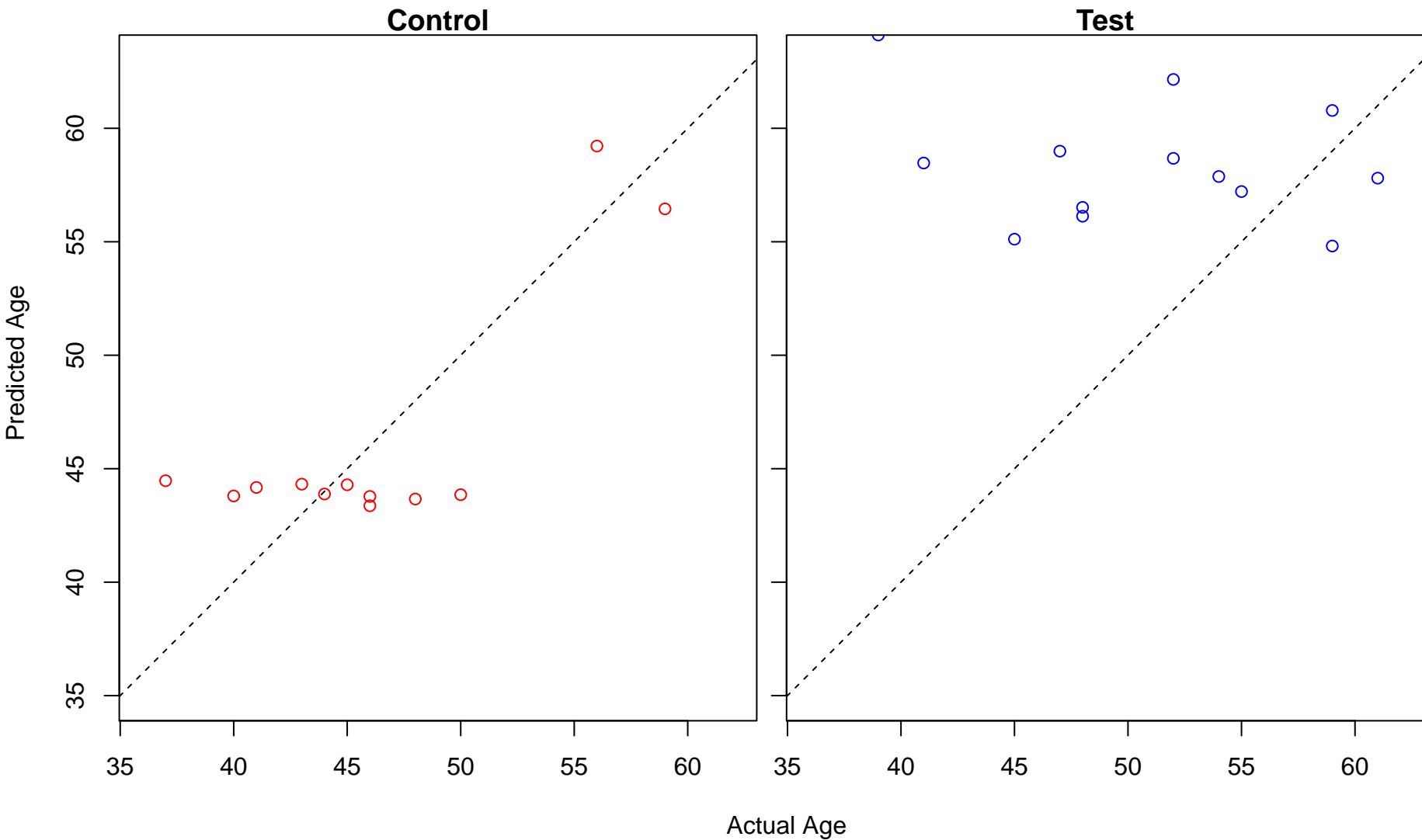
toll-like receptor 5 signaling pathway (Score: 3.712198)



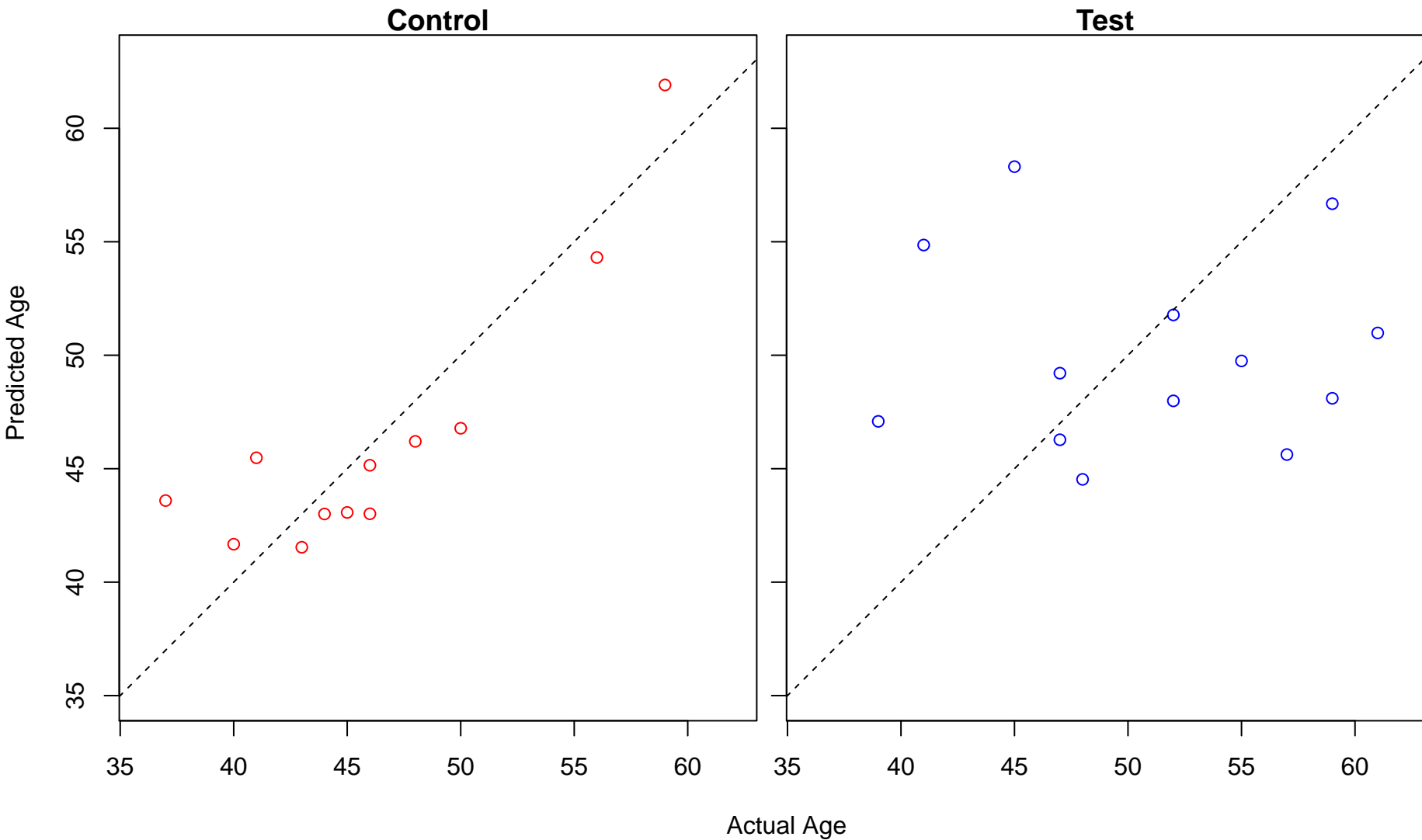
toll-like receptor 10 signaling pathway (Score: 3.712198)



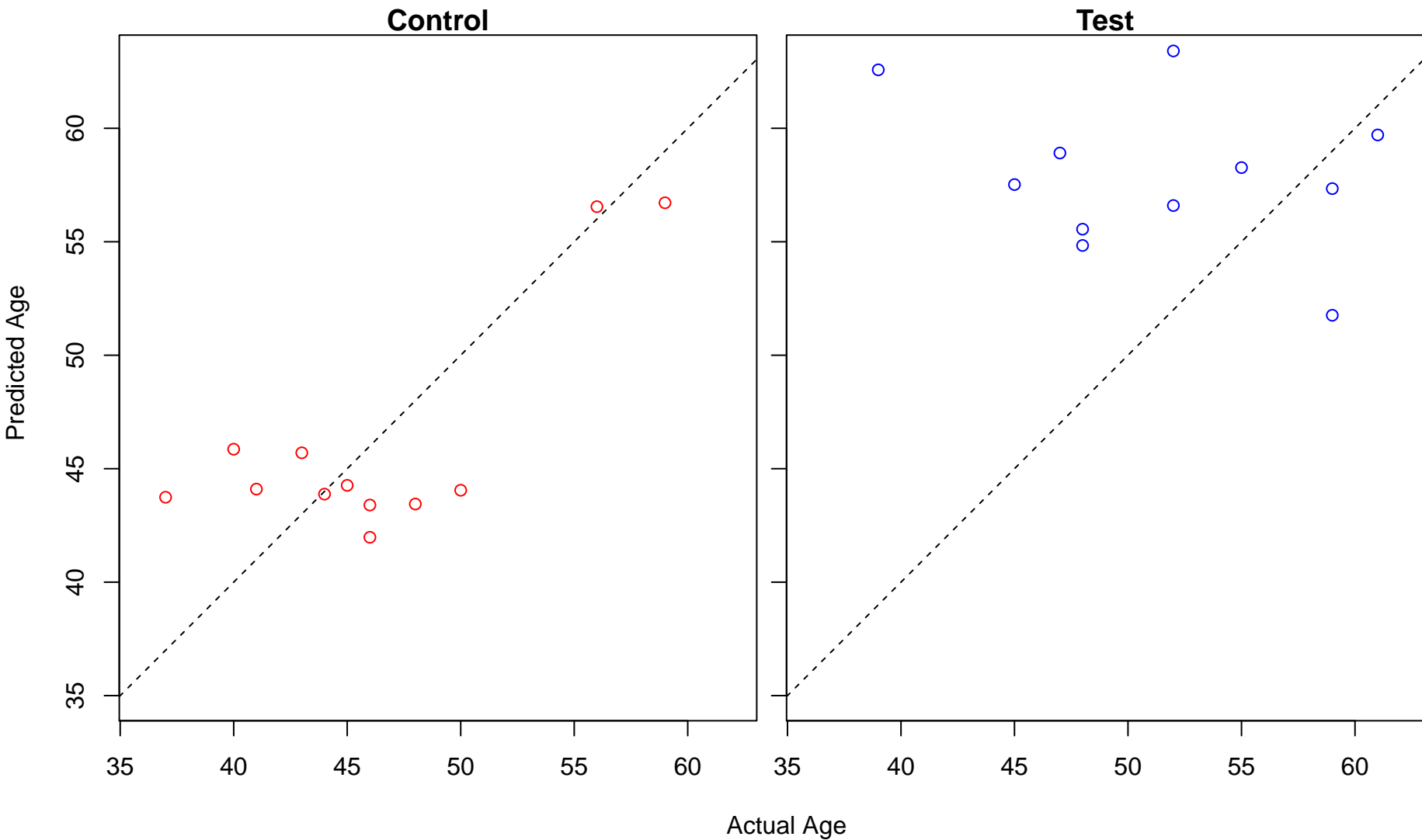
toll-like receptor 9 signaling pathway (Score: 3.708923)



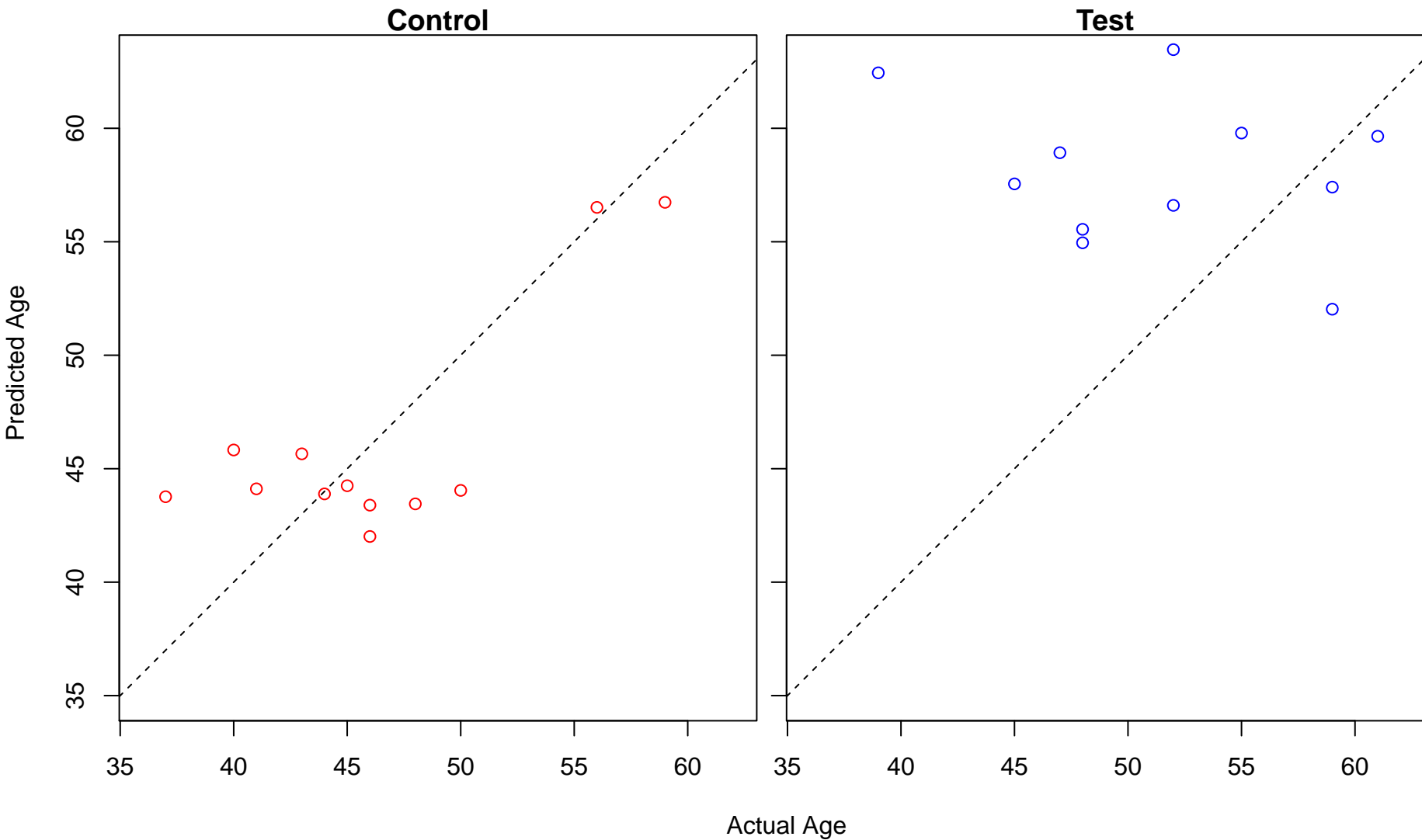
response to alkaloid (Score: 3.698354)



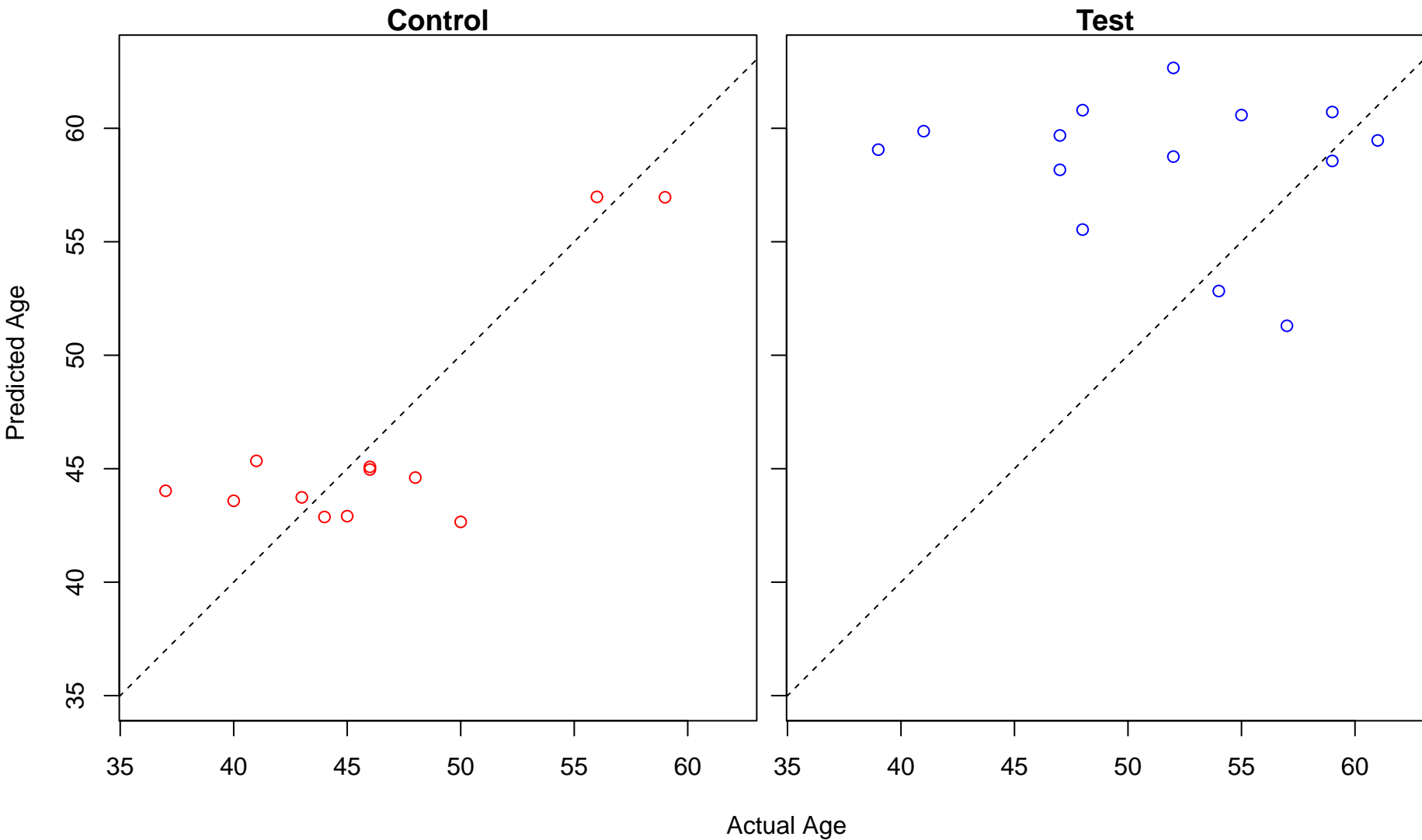
NADH metabolic process (Score: 3.696736)



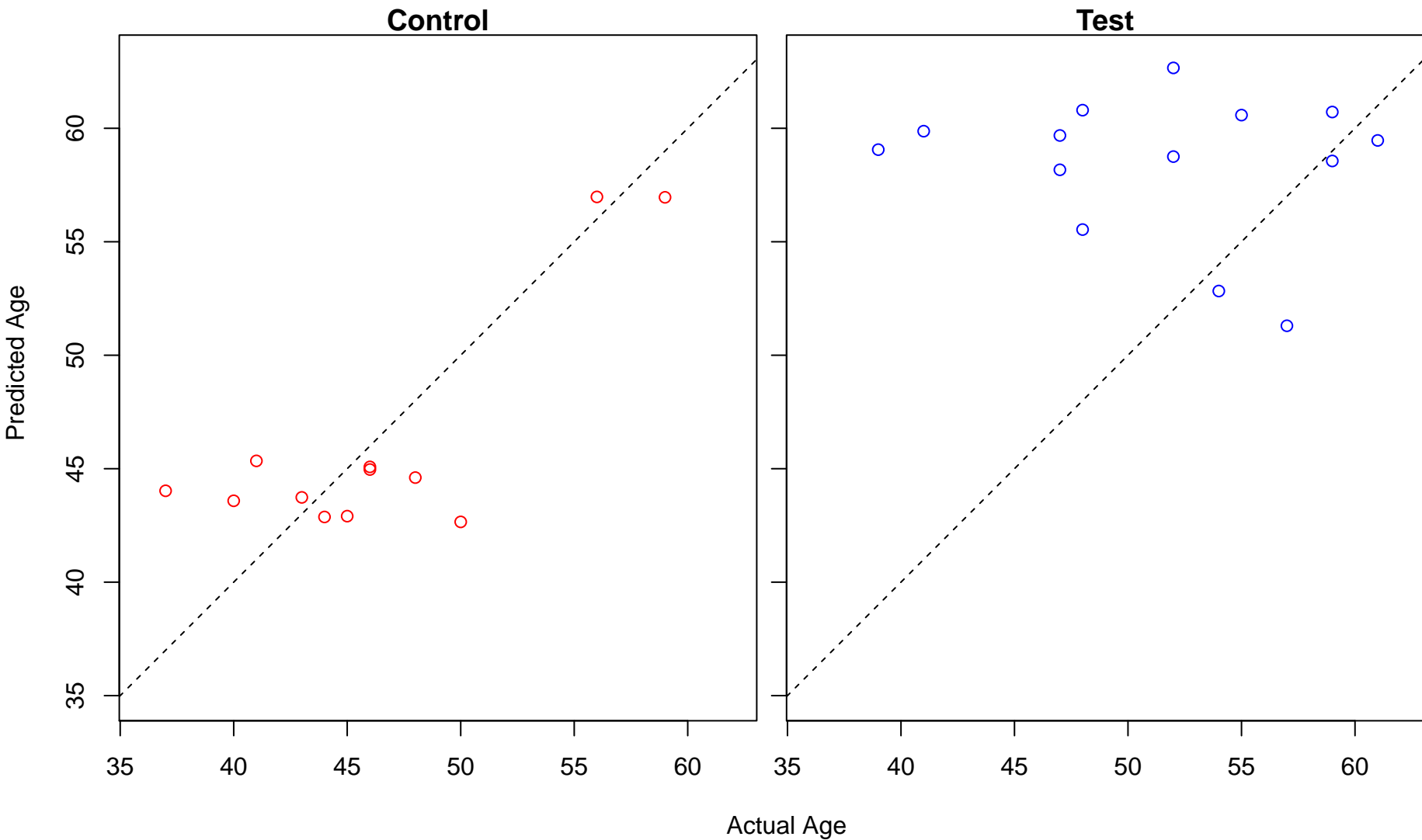
NAD metabolic process (Score: 3.696472)



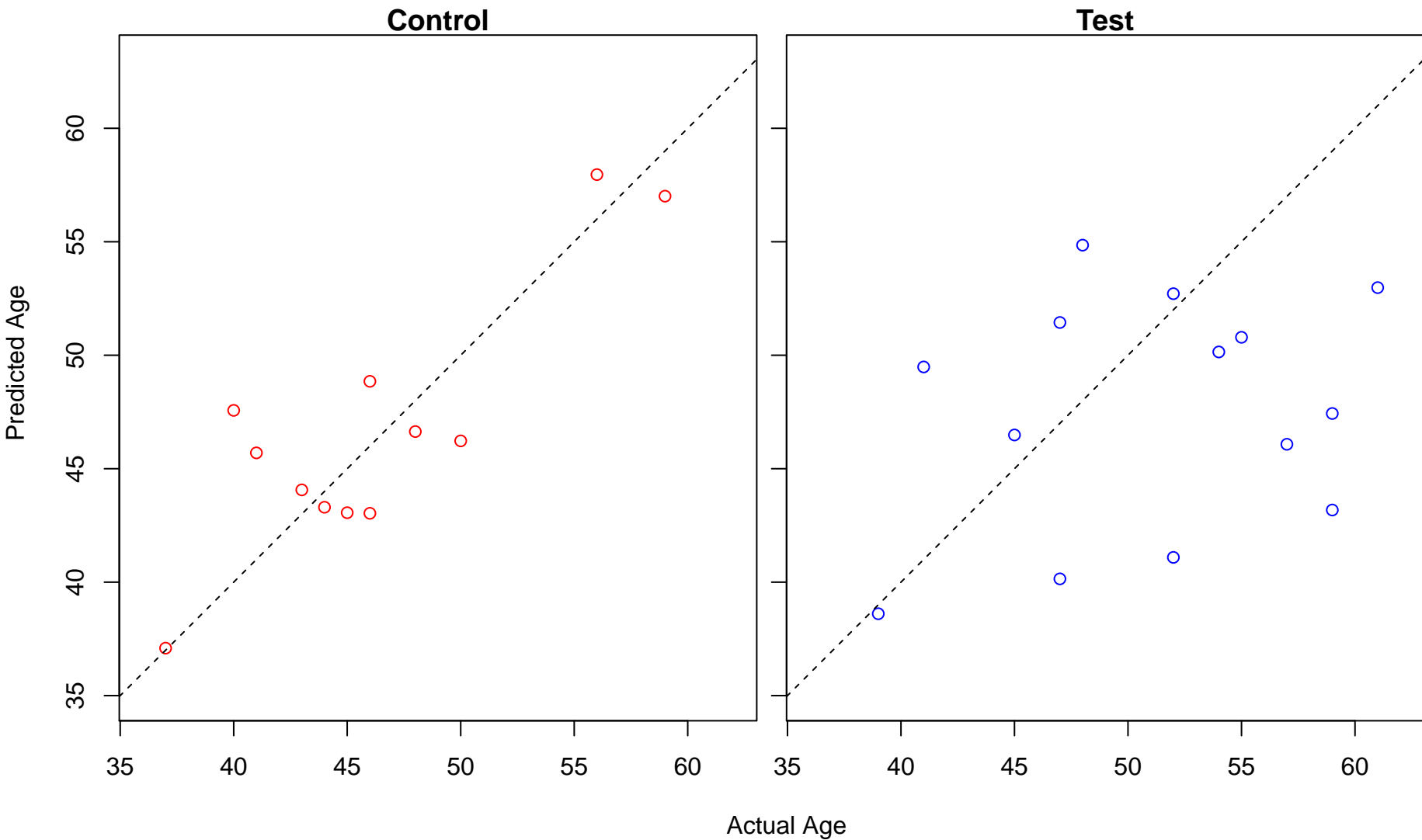
positive regulation of myelination (Score: 3.692871)



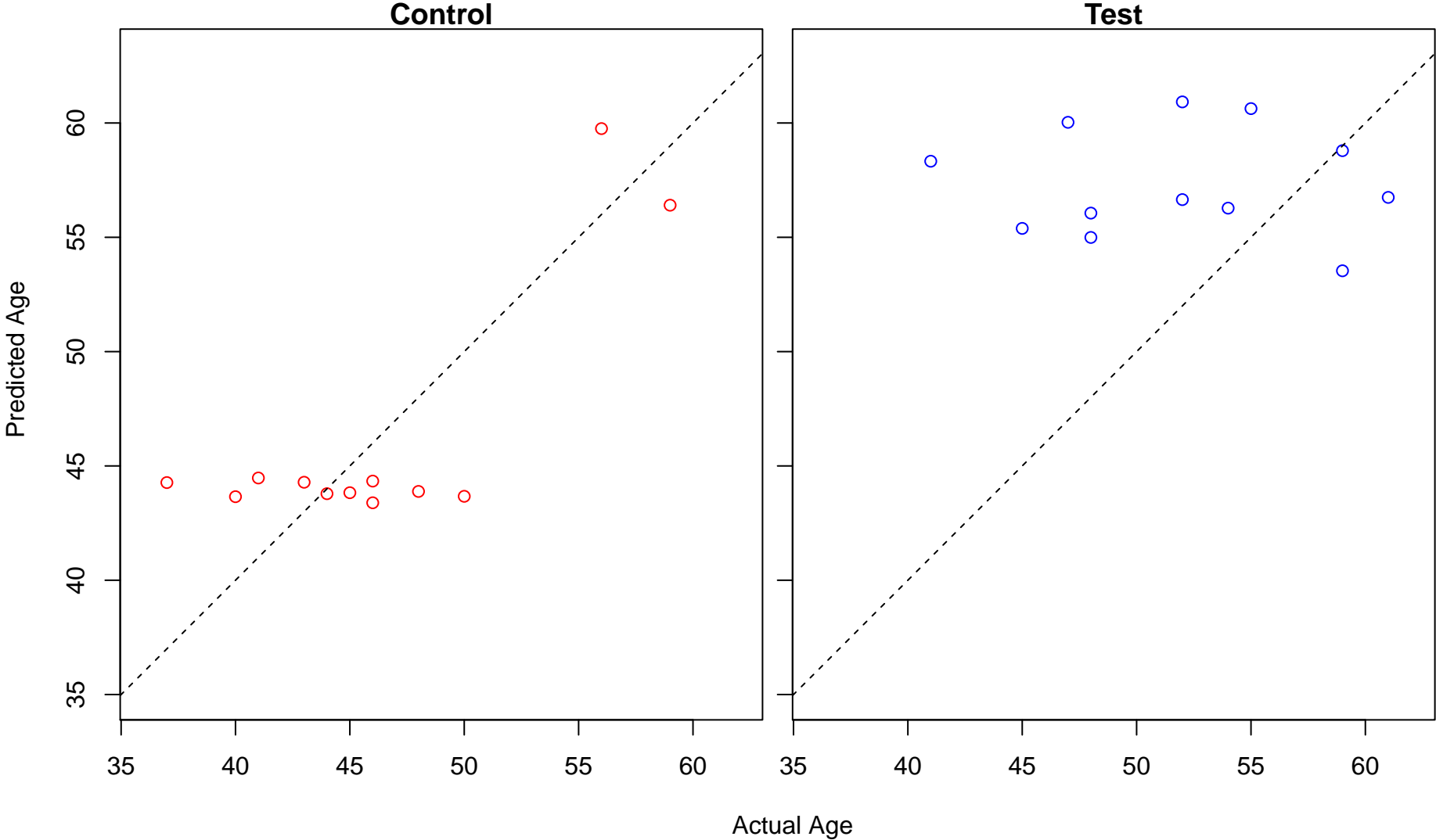
positive regulation of neurological system process (Score: 3.692748)



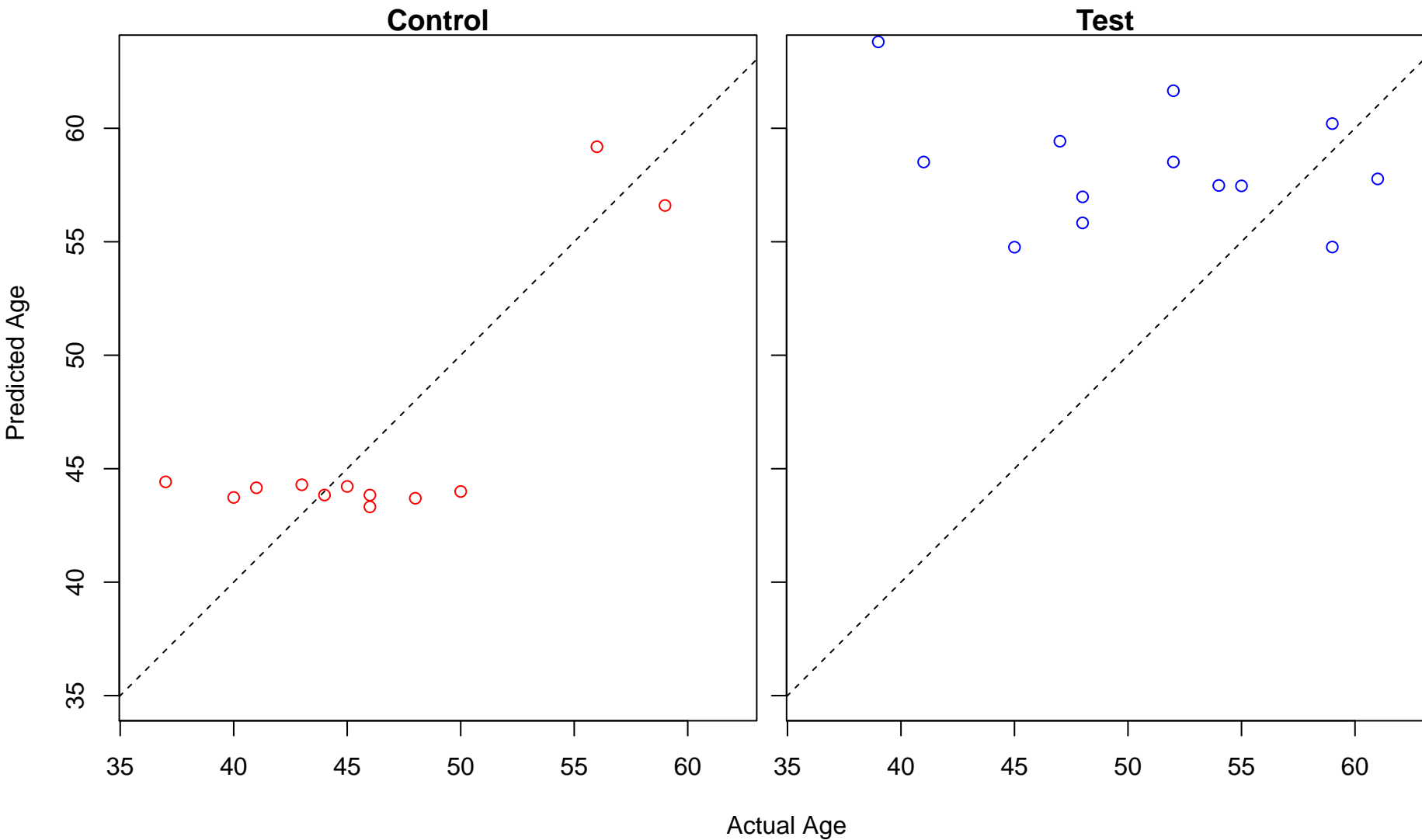
regulation of neuronal synaptic plasticity (Score: 3.691467)



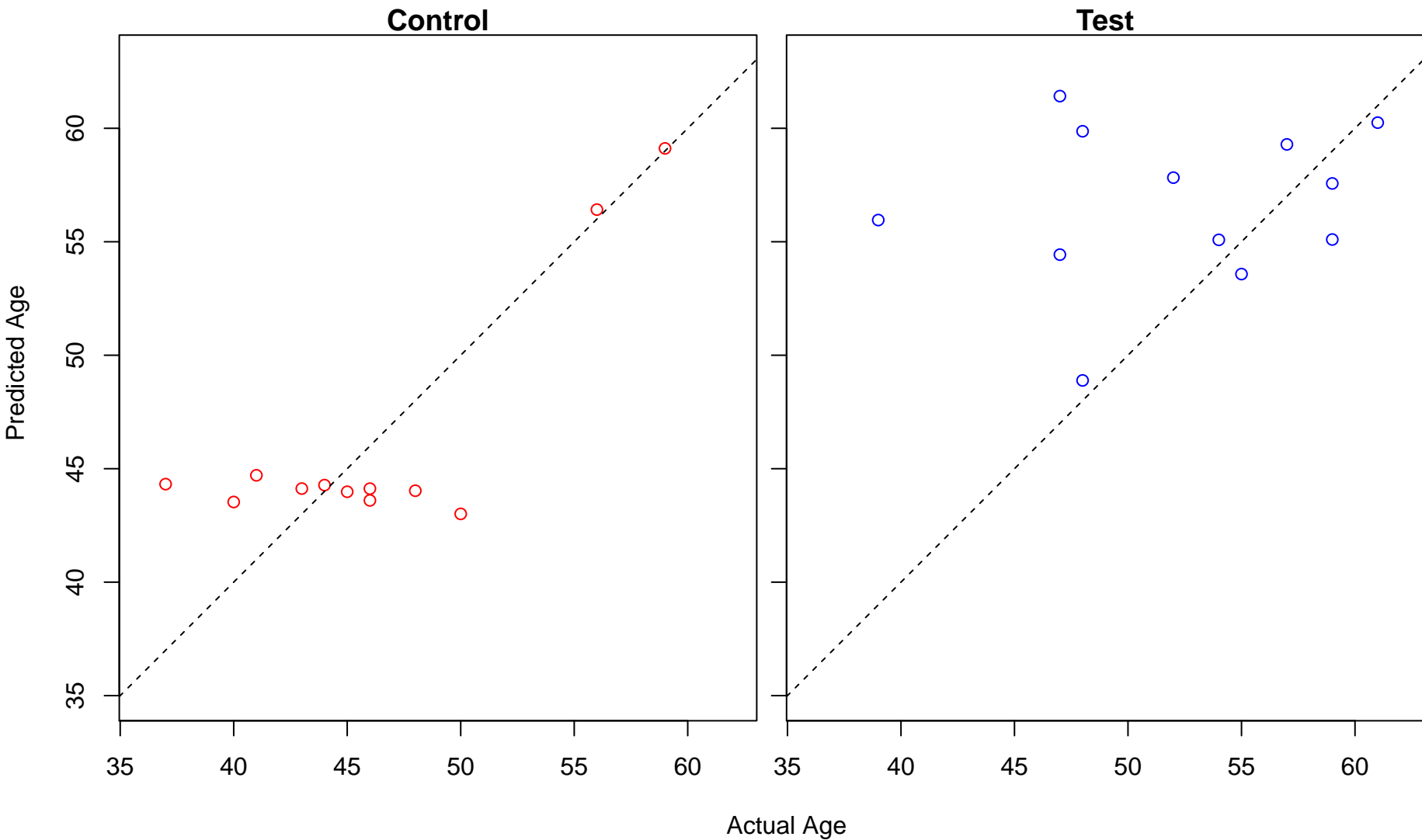
positive regulation of signal transduction by p53 class mediator (Score: 3.690056)



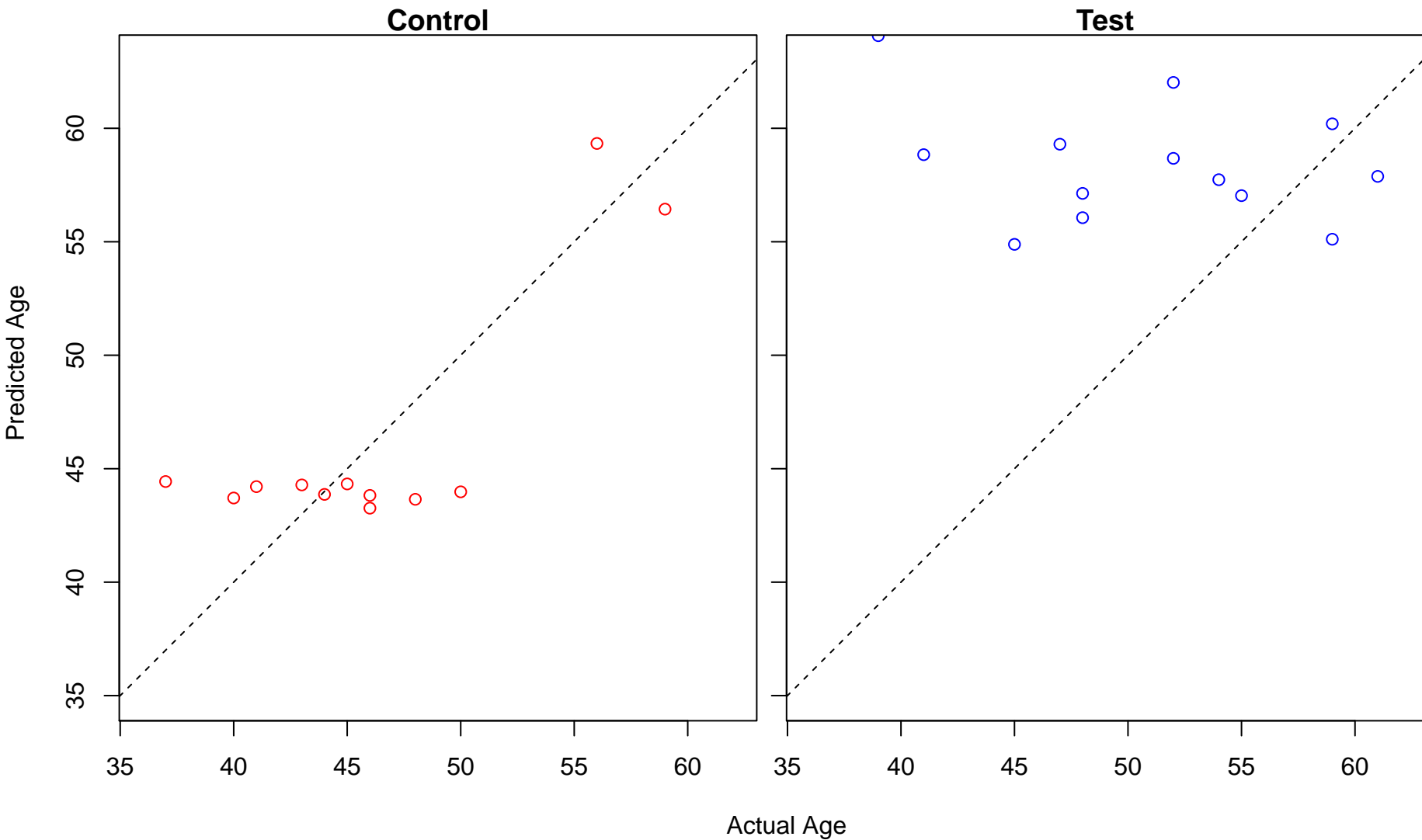
negative regulation of type I interferon production (Score: 3.688582)



protein repair (Score: 3.685793)

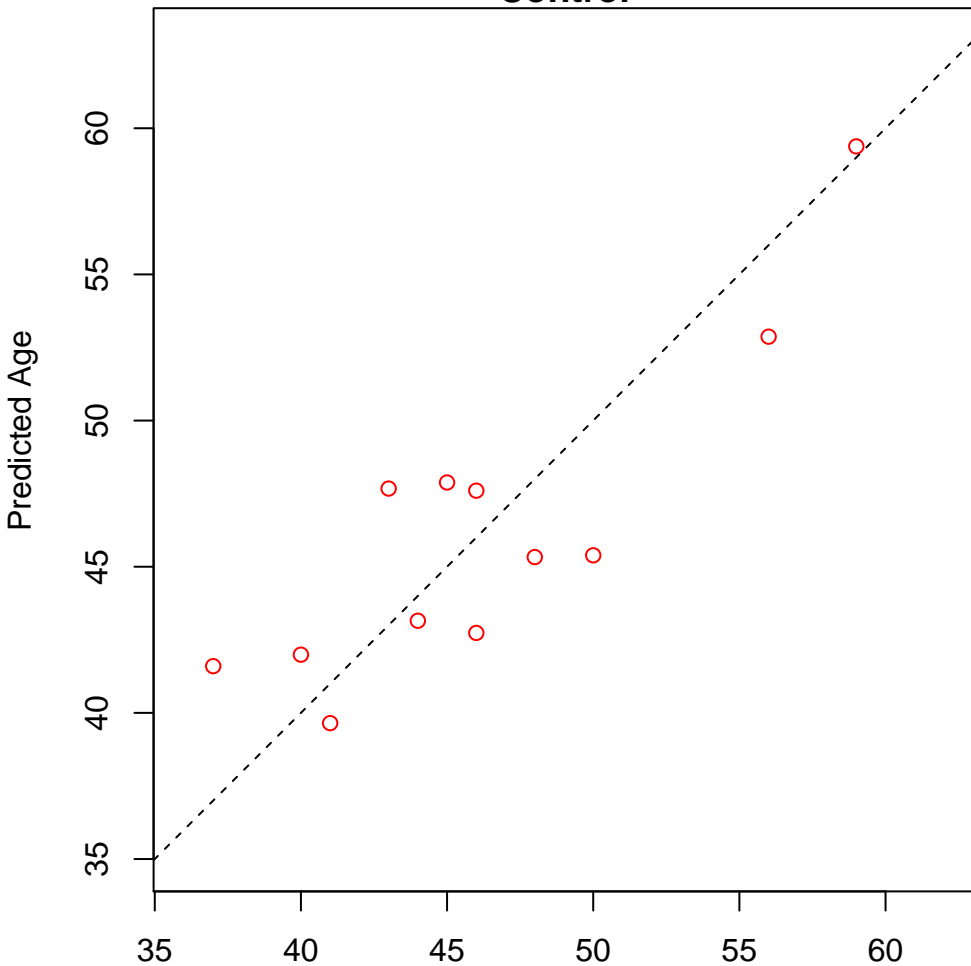


DNA biosynthetic process (Score: 3.682233)

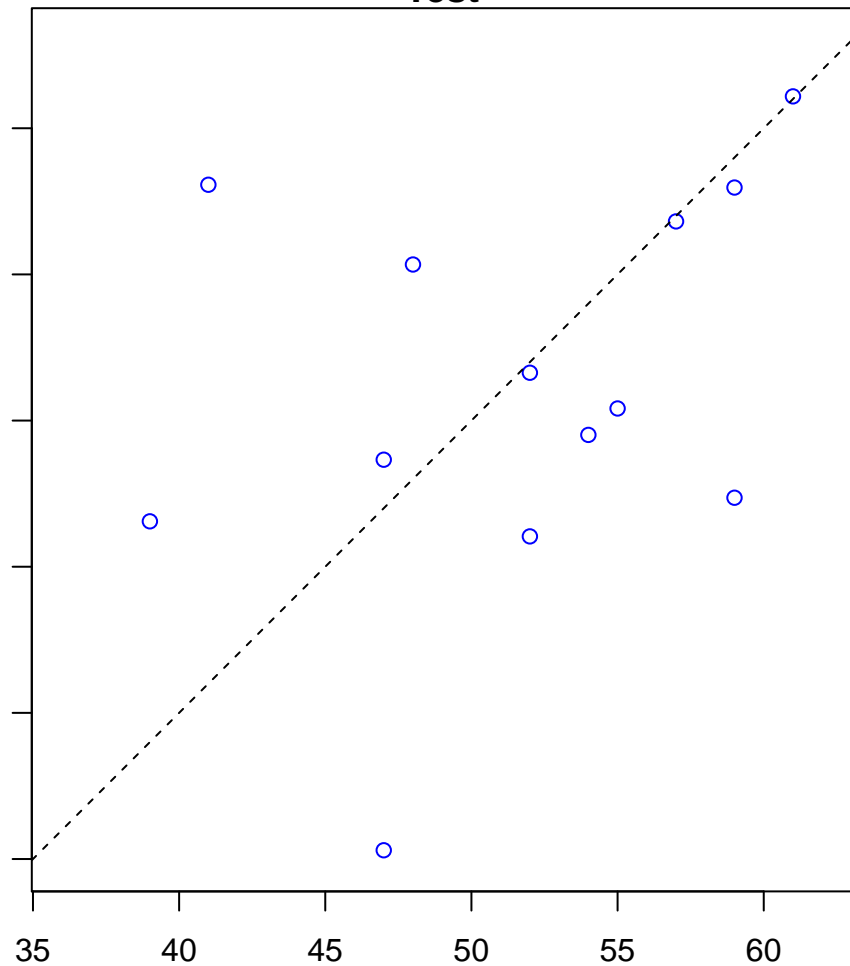


eye photoreceptor cell differentiation (Score: 3.678585)

Control

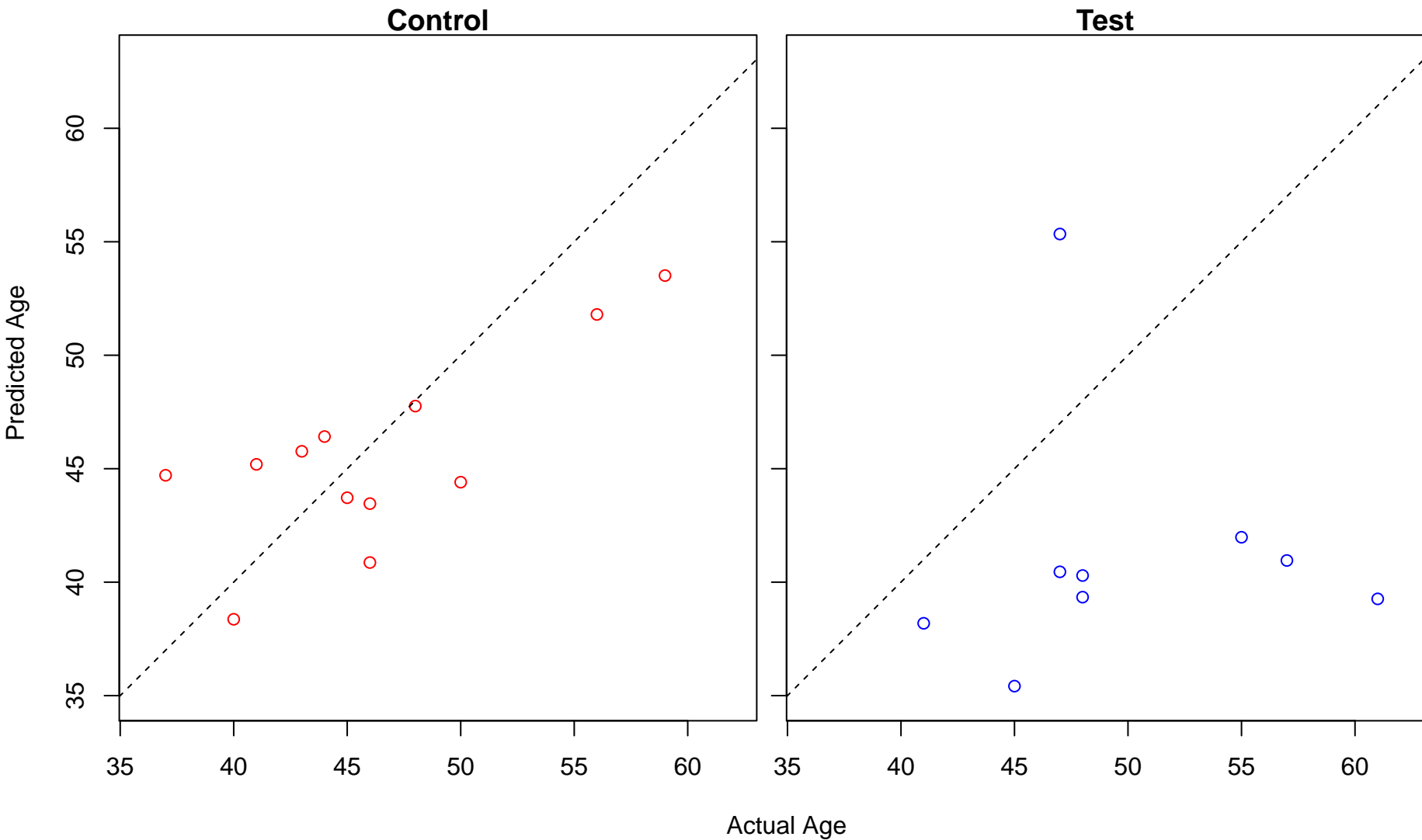


Test

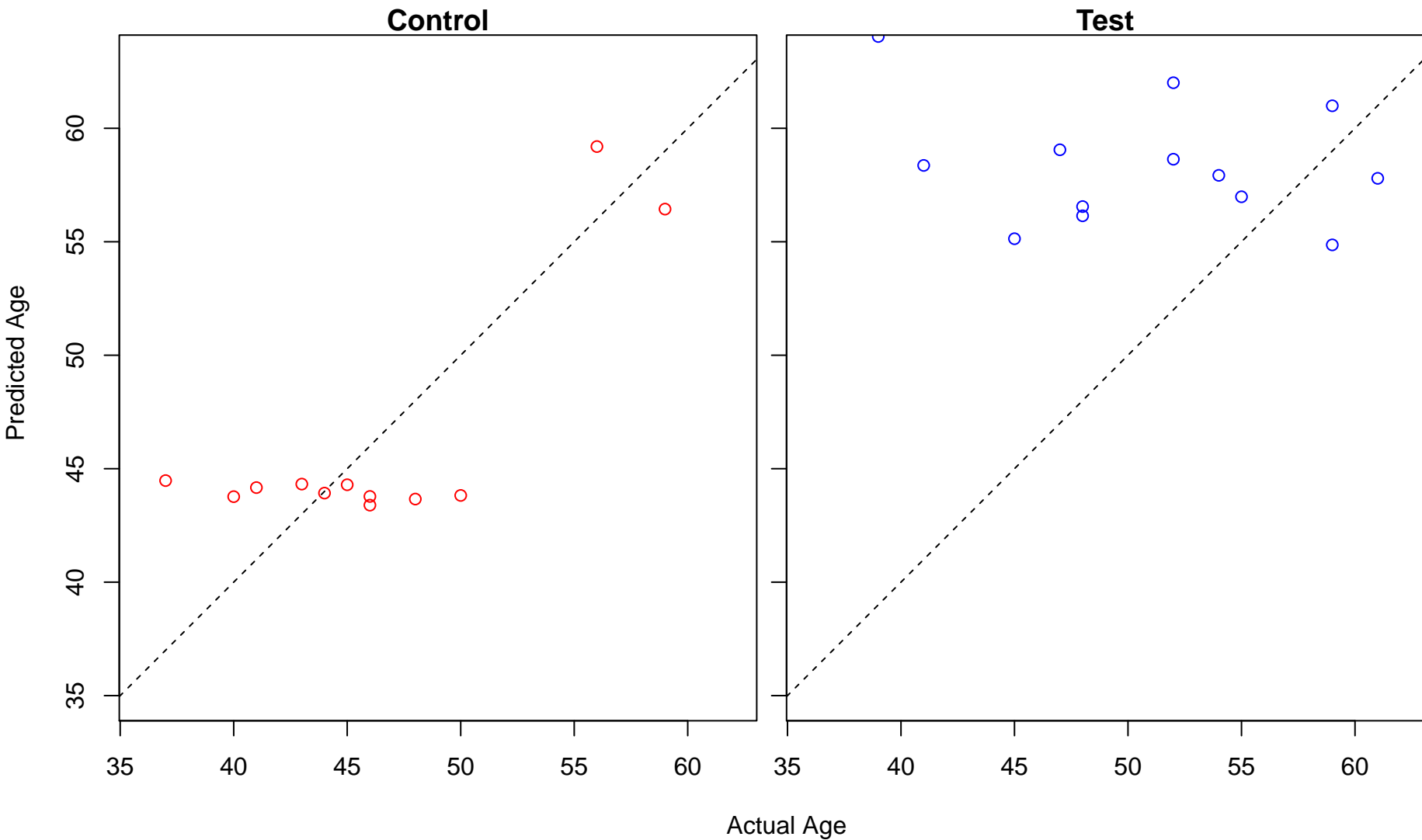


Actual Age

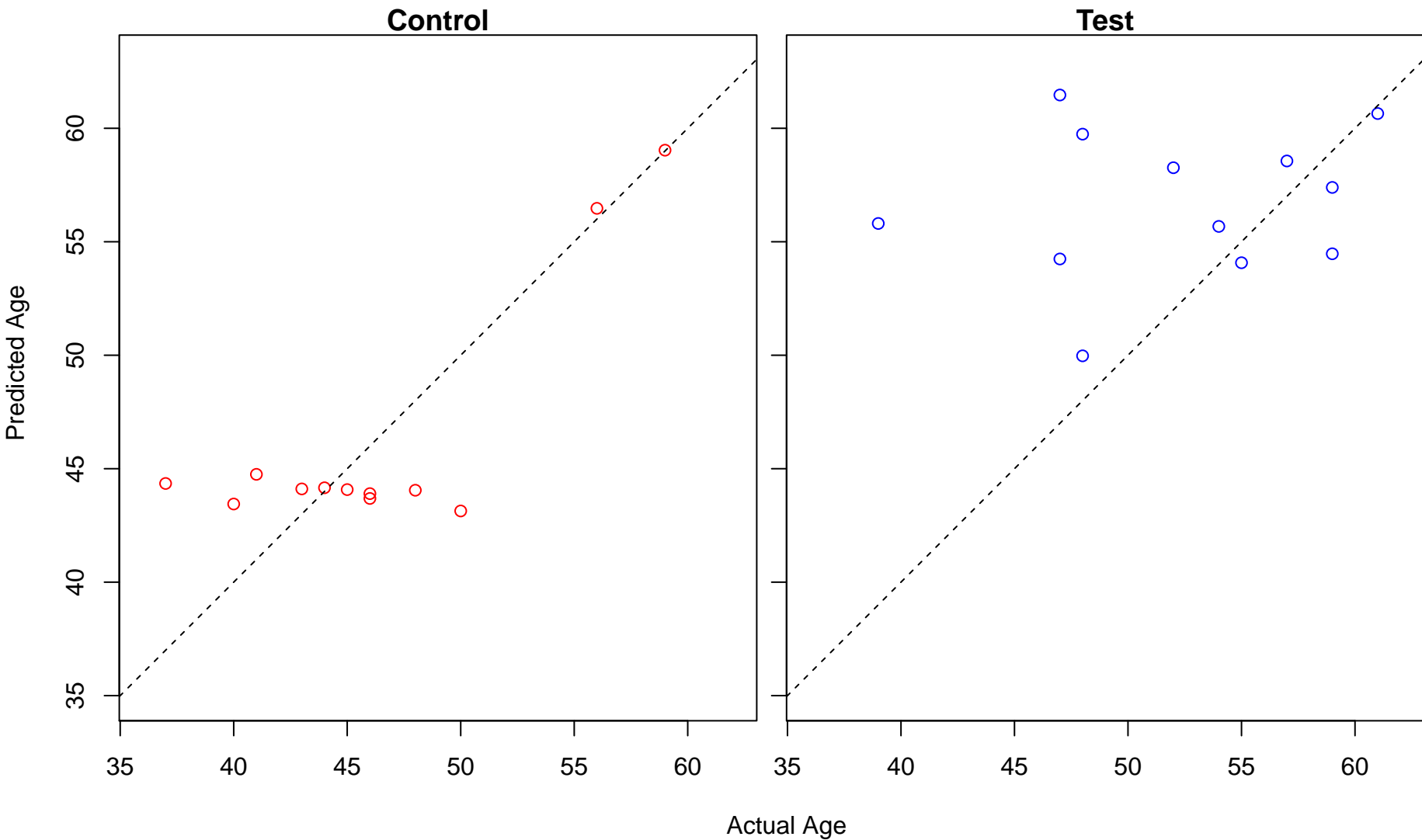
SRP-dependent cotranslational protein targeting to membrane (Score: 3.677788)



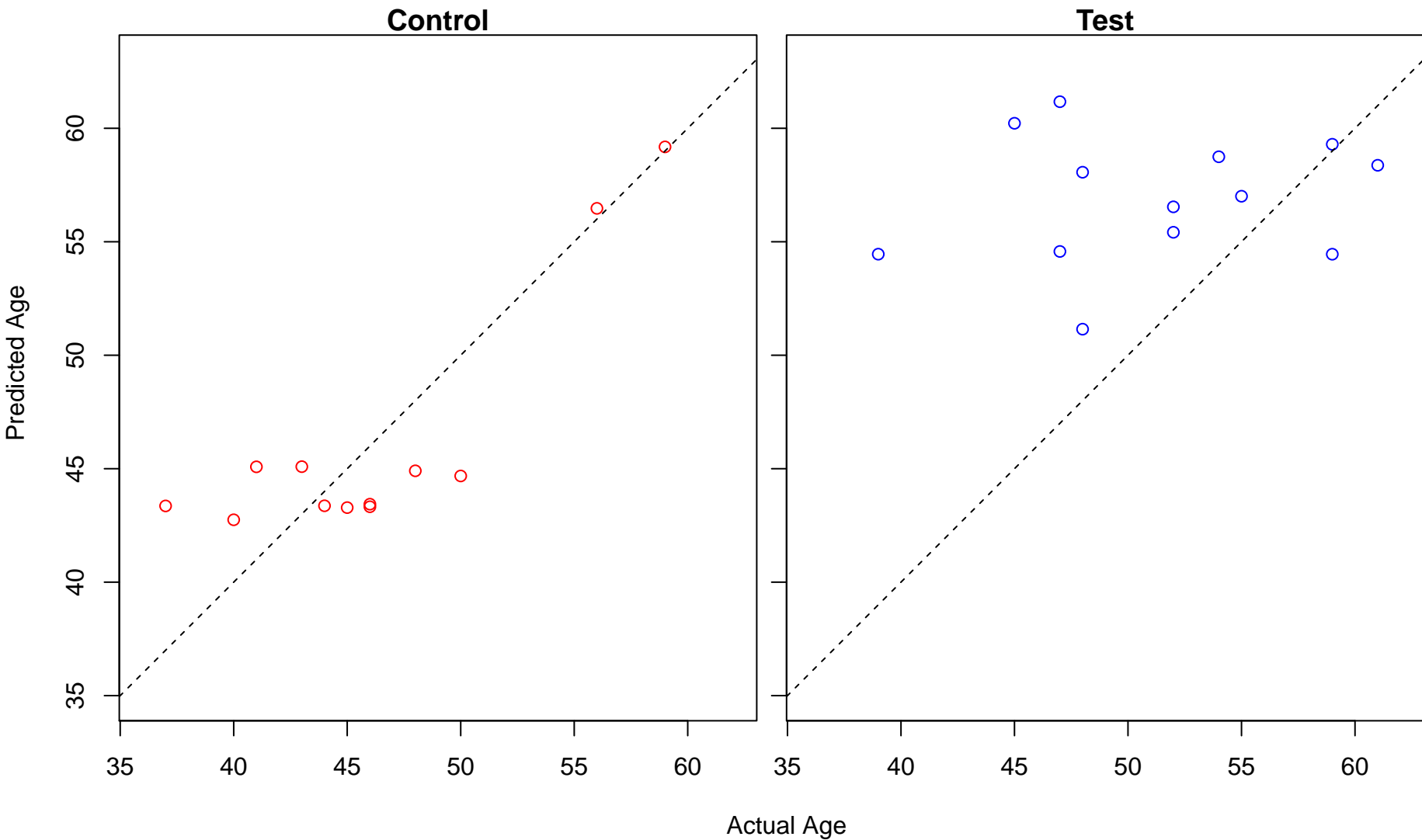
stress-activated MAPK cascade (Score: 3.677003)



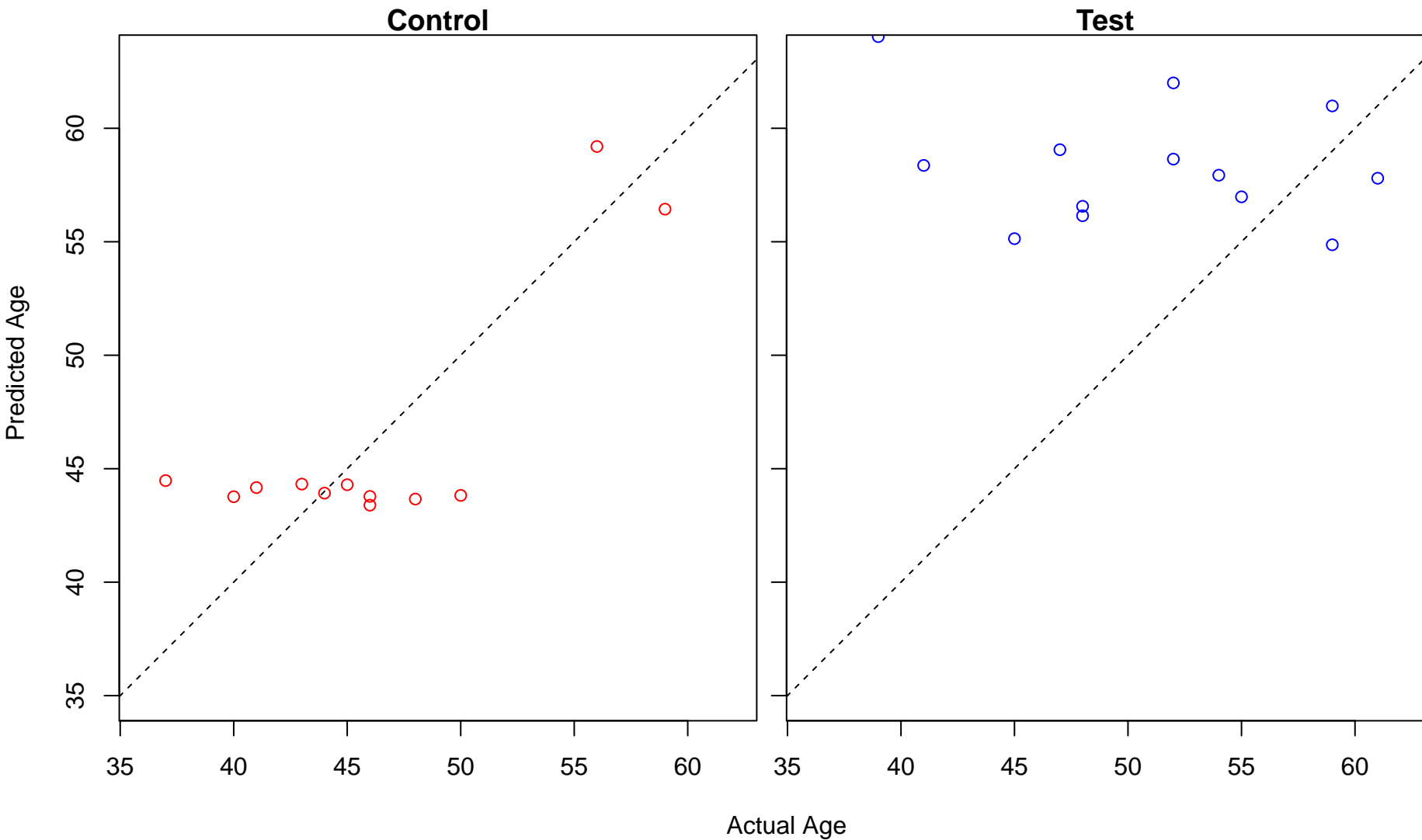
regulation of protein import into nucleus, translocation (Score: 3.676988)



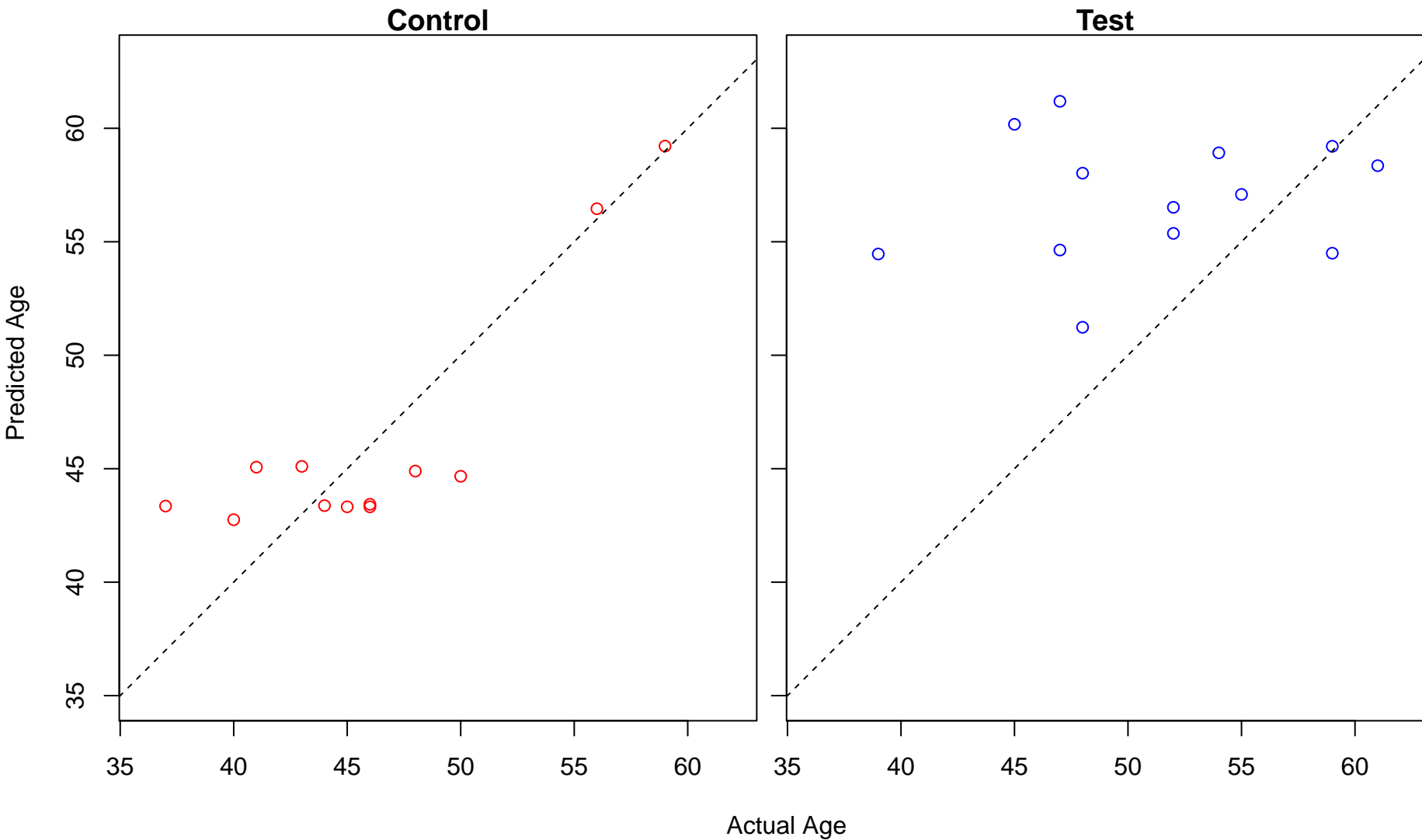
lipid transport (Score: 3.676234)



stress-activated protein kinase signaling cascade (Score: 3.676165)

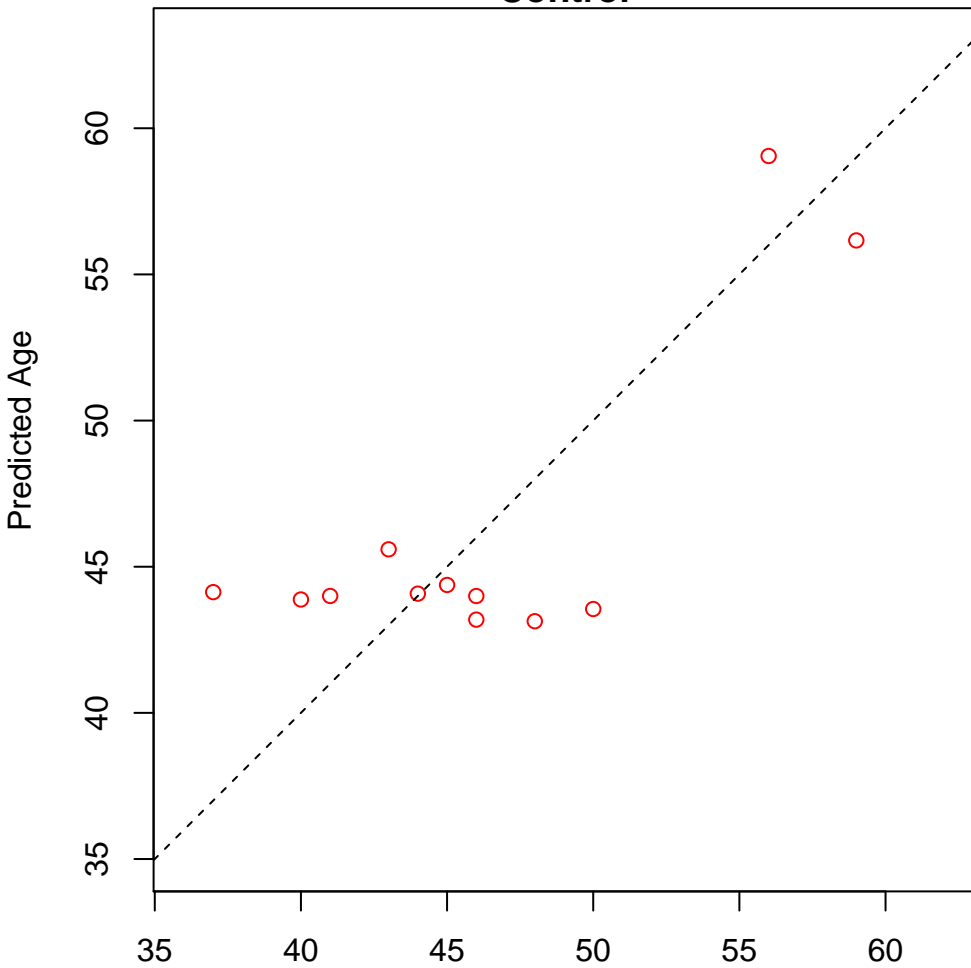


lipid localization (Score: 3.675691)

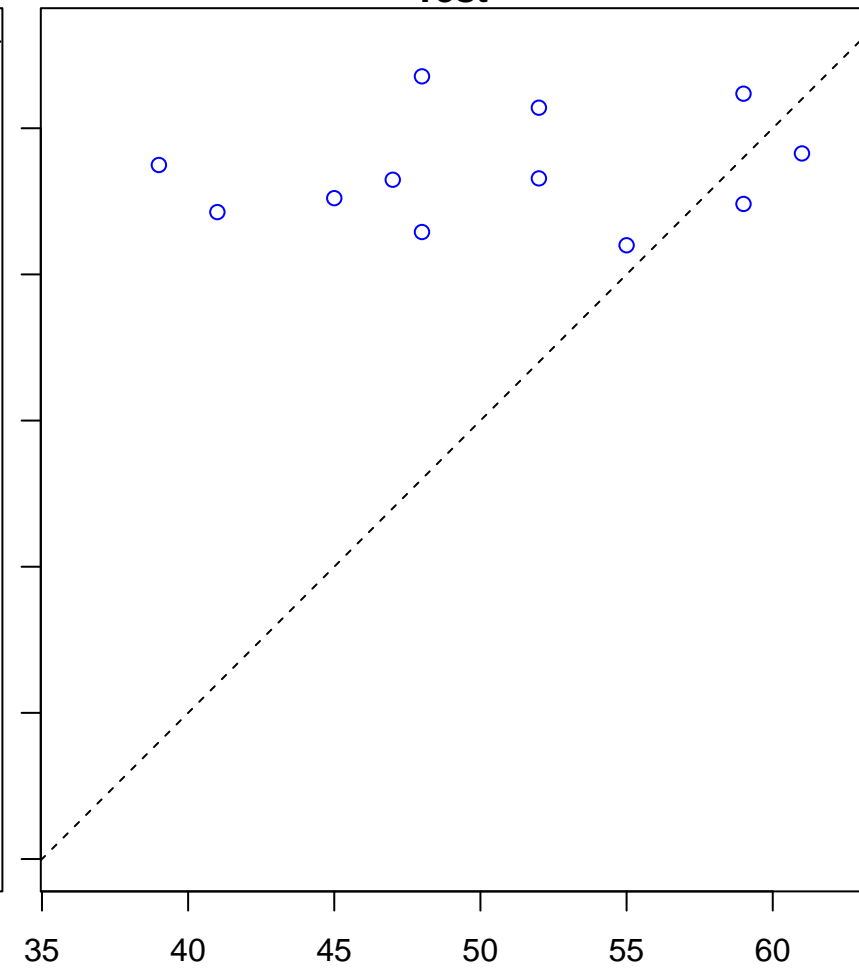


cellular response to estradiol stimulus (Score: 3.672603)

Control

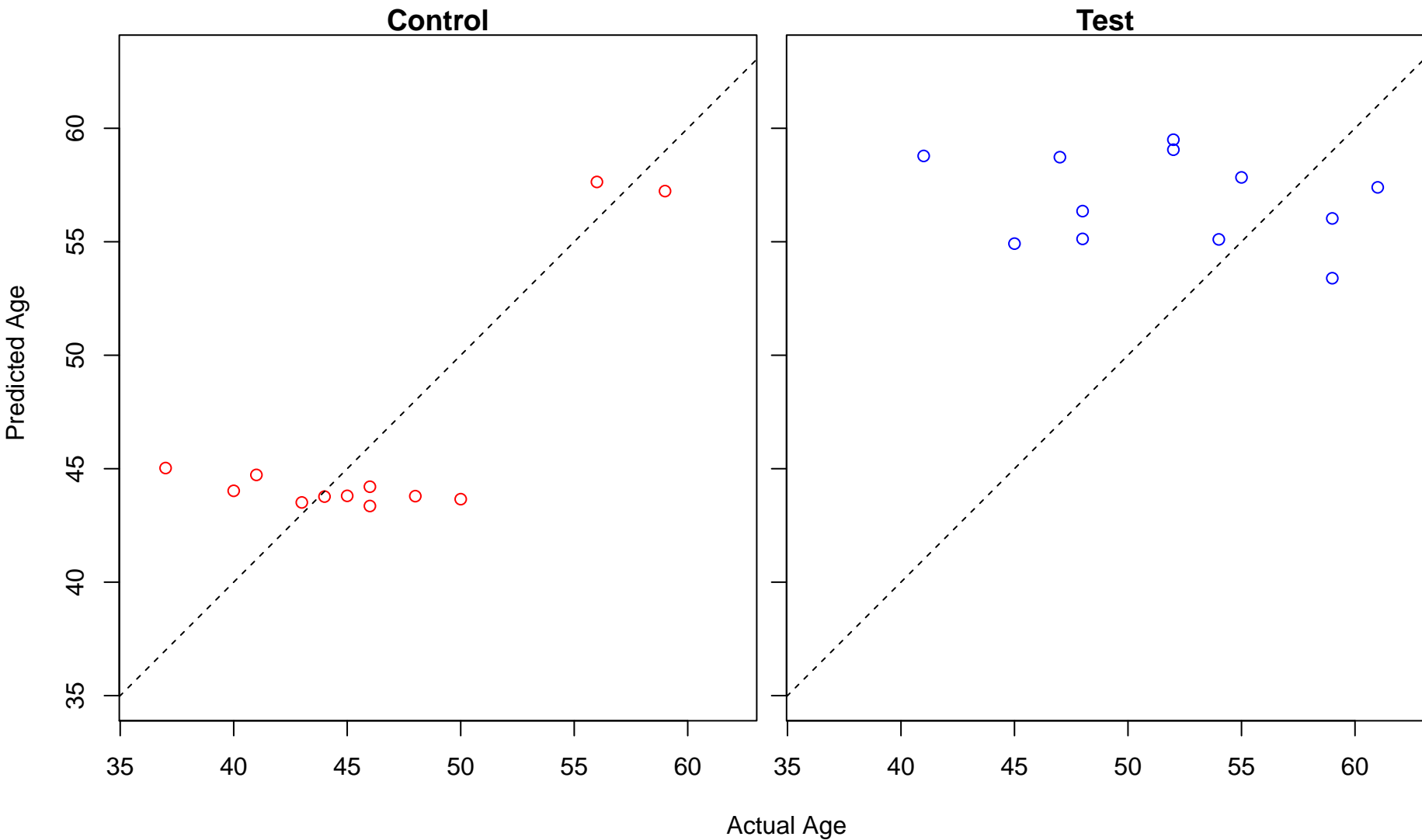


Test

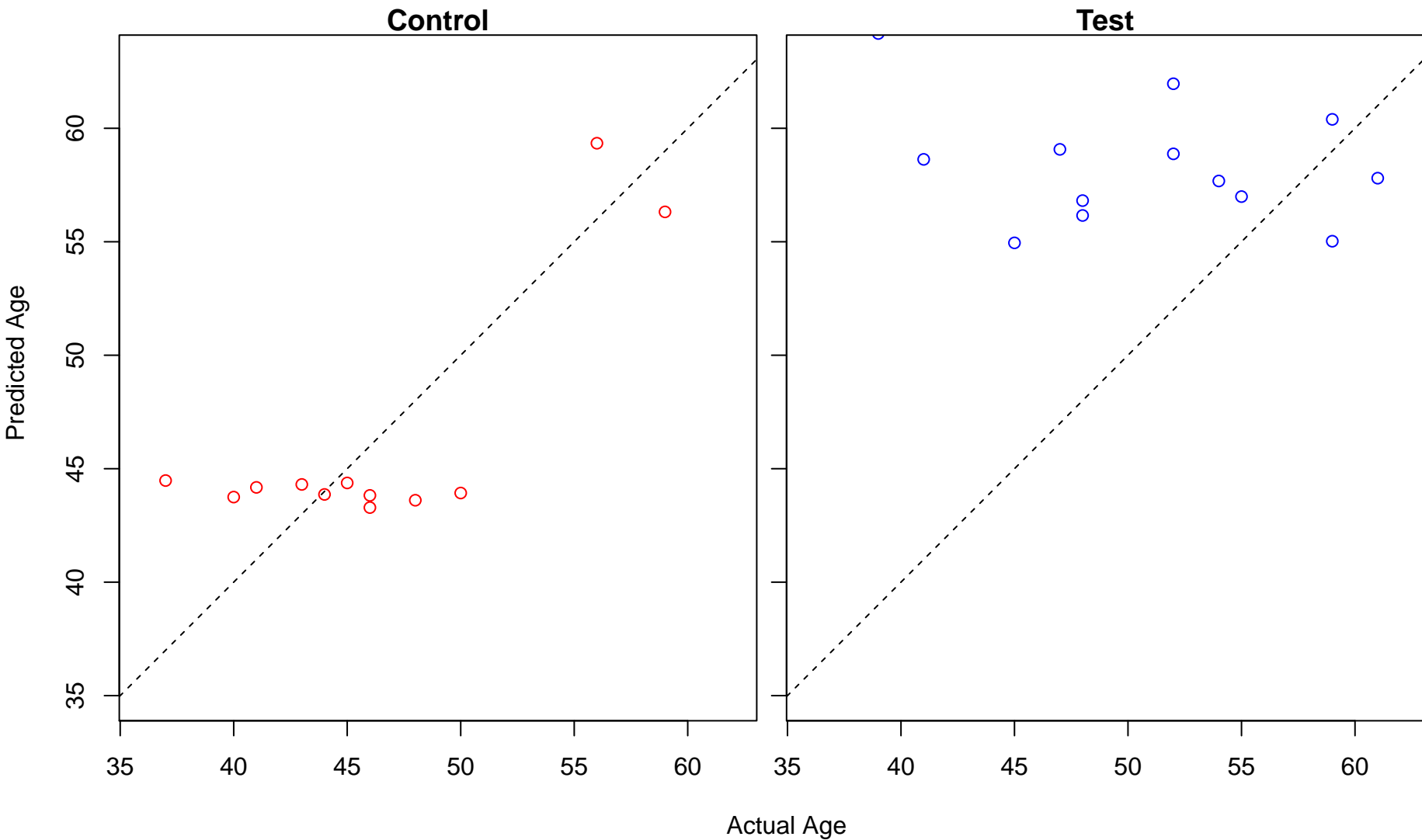


Actual Age

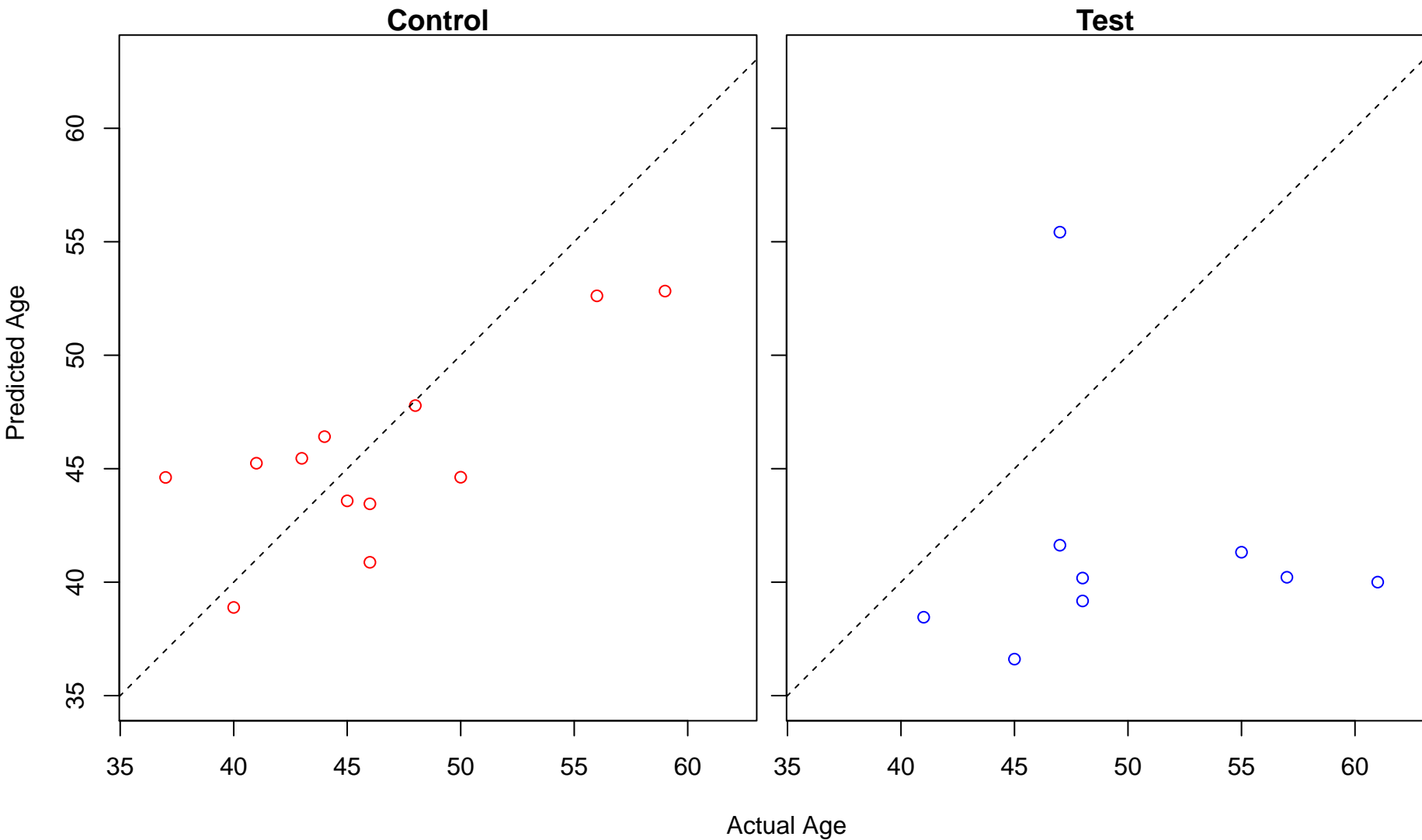
cellular response to epidermal growth factor stimulus (Score: 3.669512)



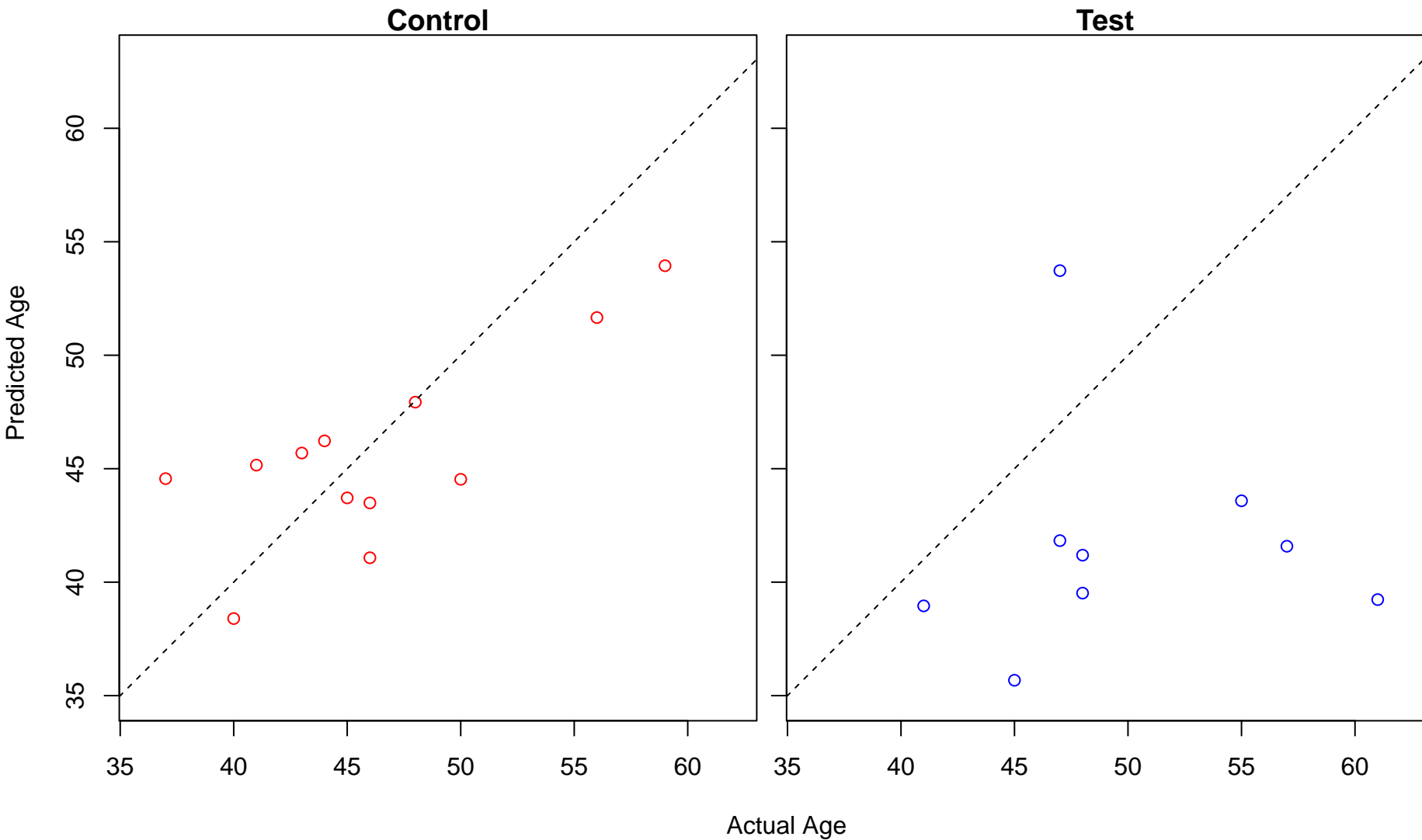
transcription-coupled nucleotide-excision repair (Score: 3.667846)



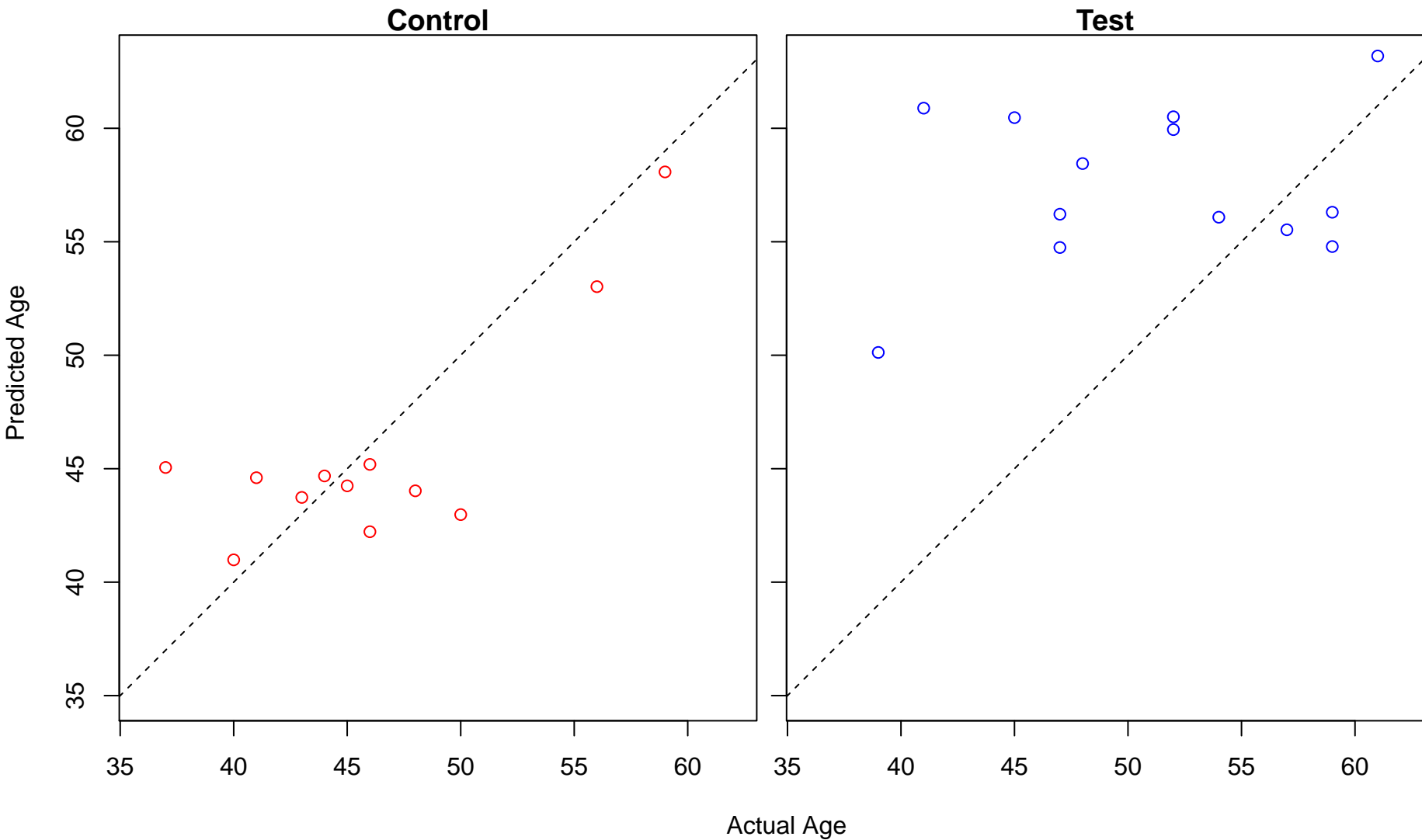
mRNA catabolic process (Score: 3.667818)



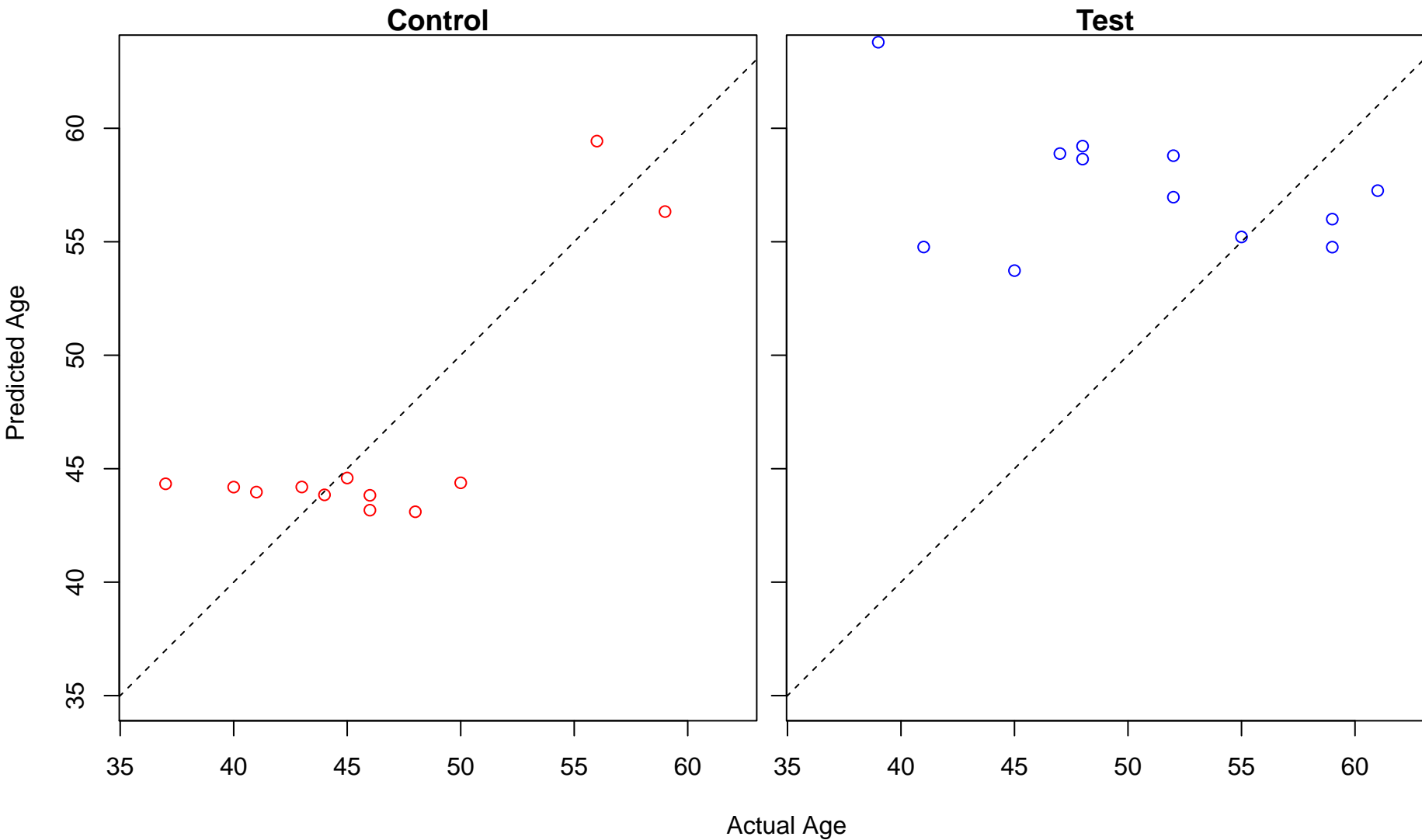
protein localization to endoplasmic reticulum (Score: 3.666420)



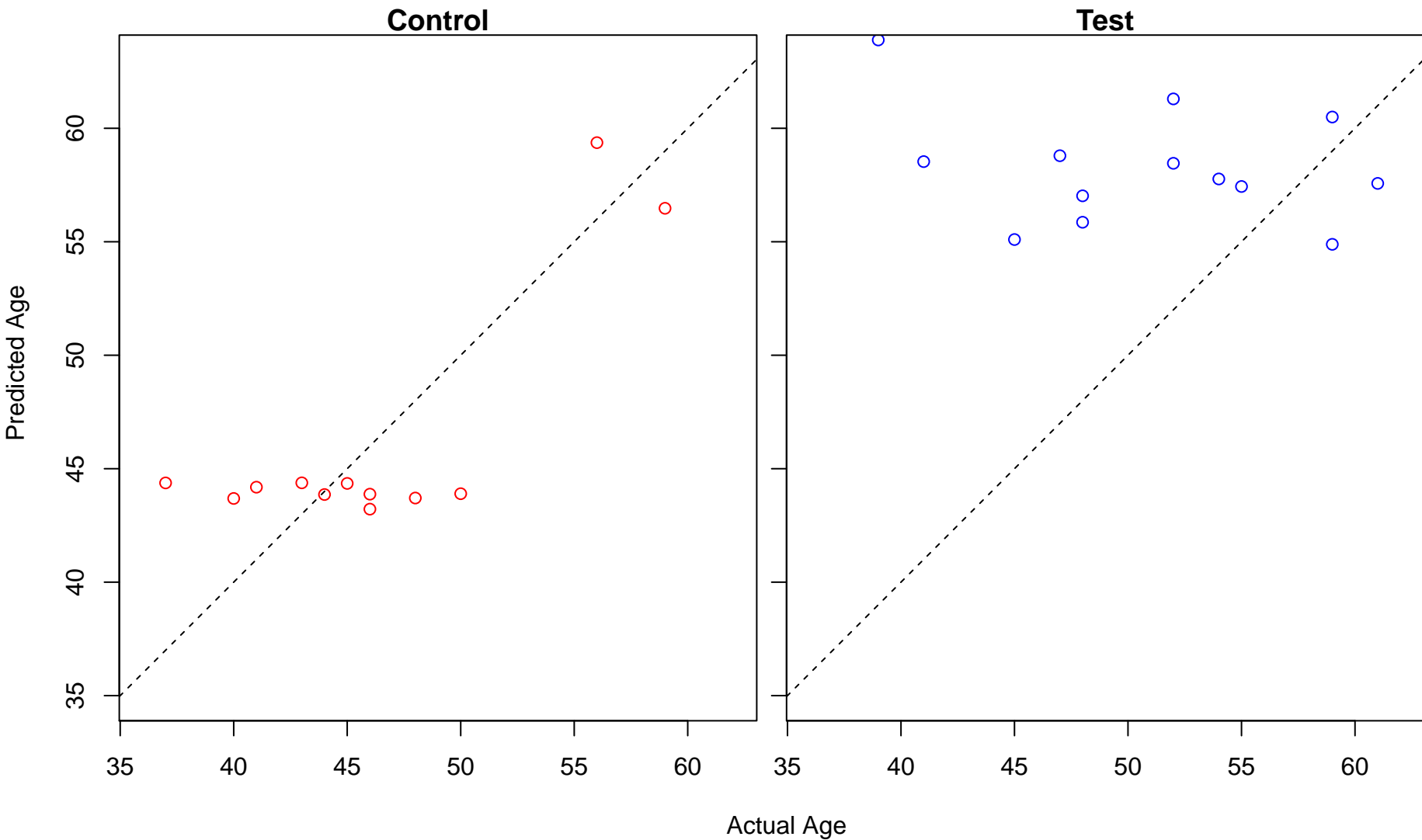
diacylglycerol metabolic process (Score: 3.665675)



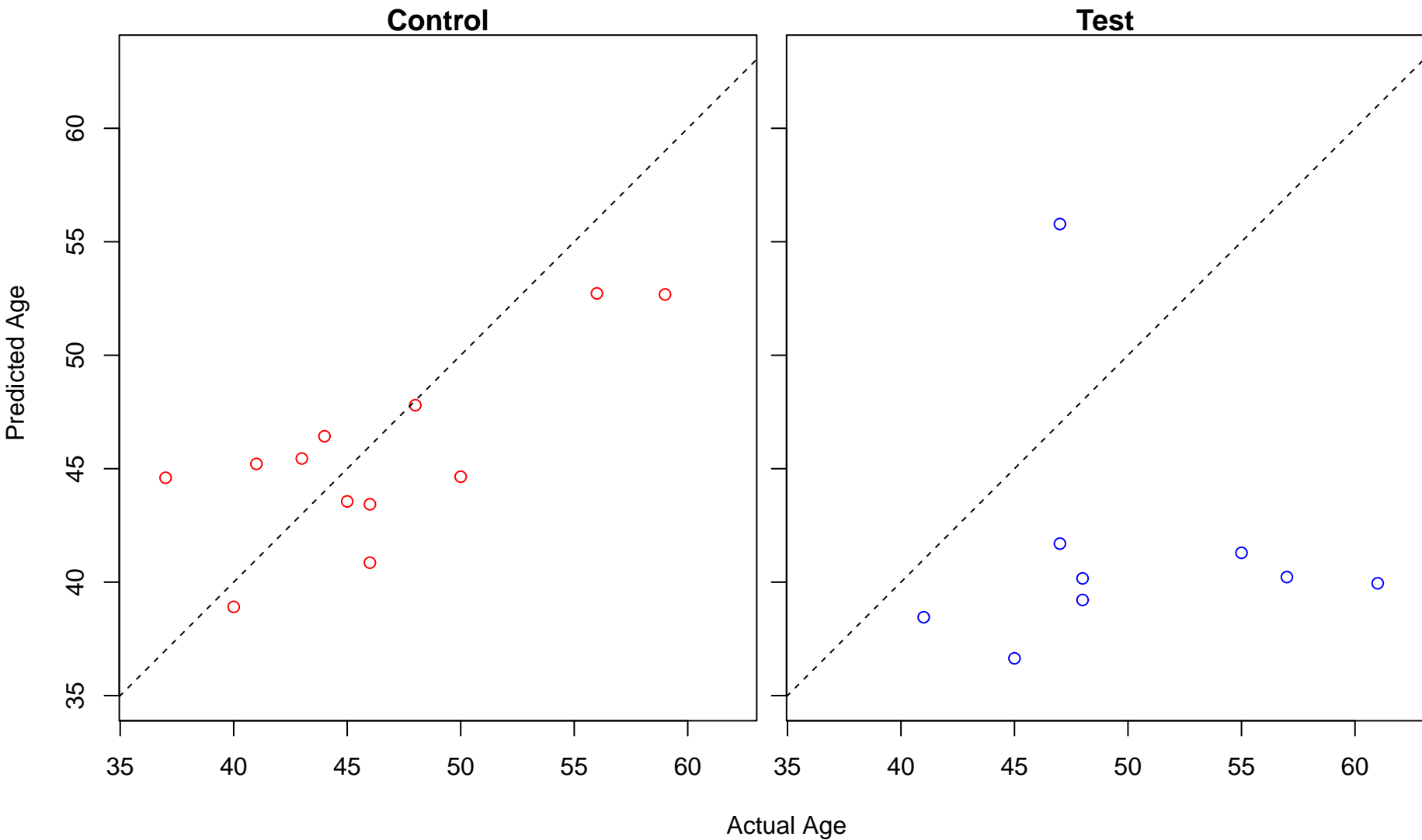
cell killing (Score: 3.664771)



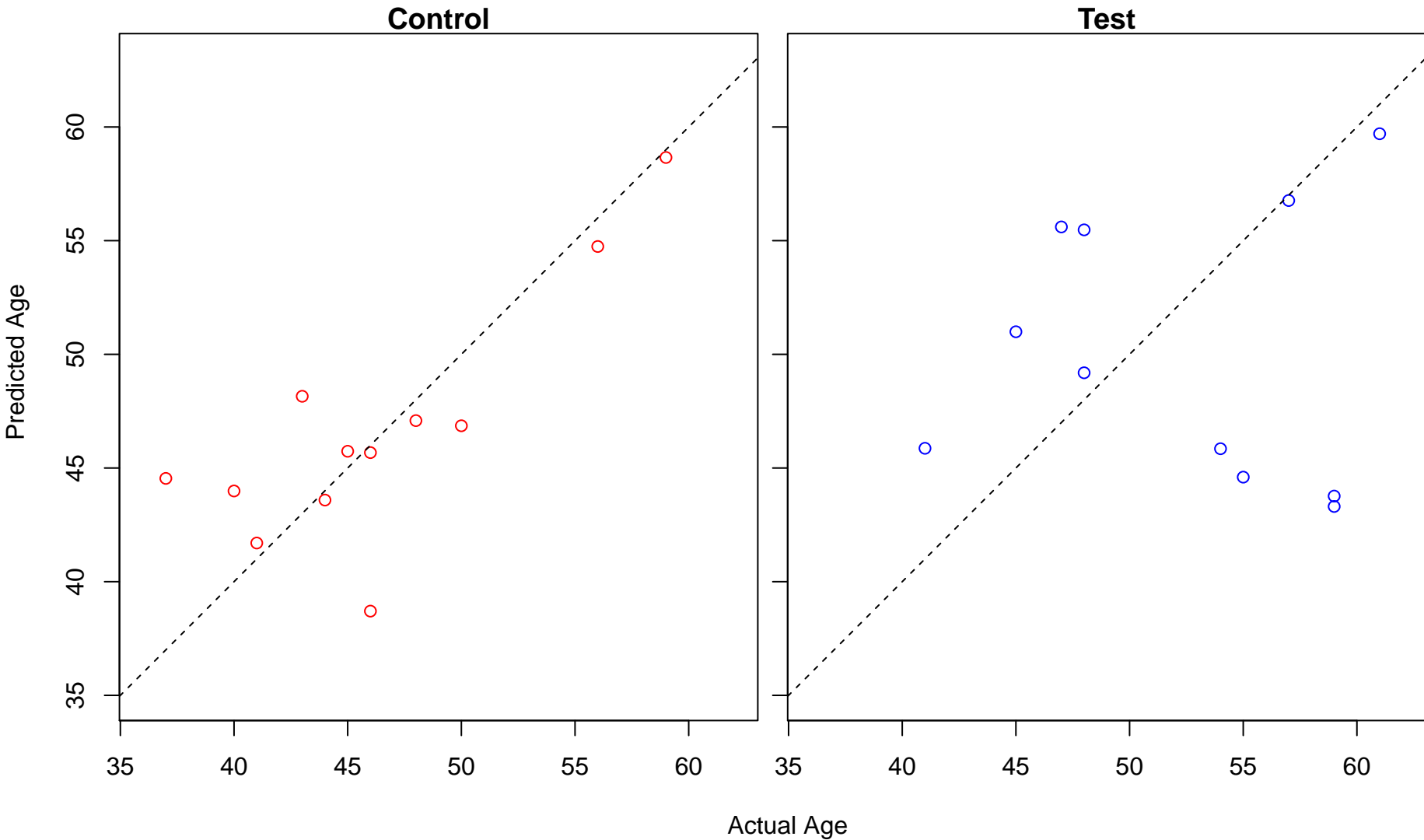
nucleotide-excision repair, DNA damage recognition (Score: 3.664680)



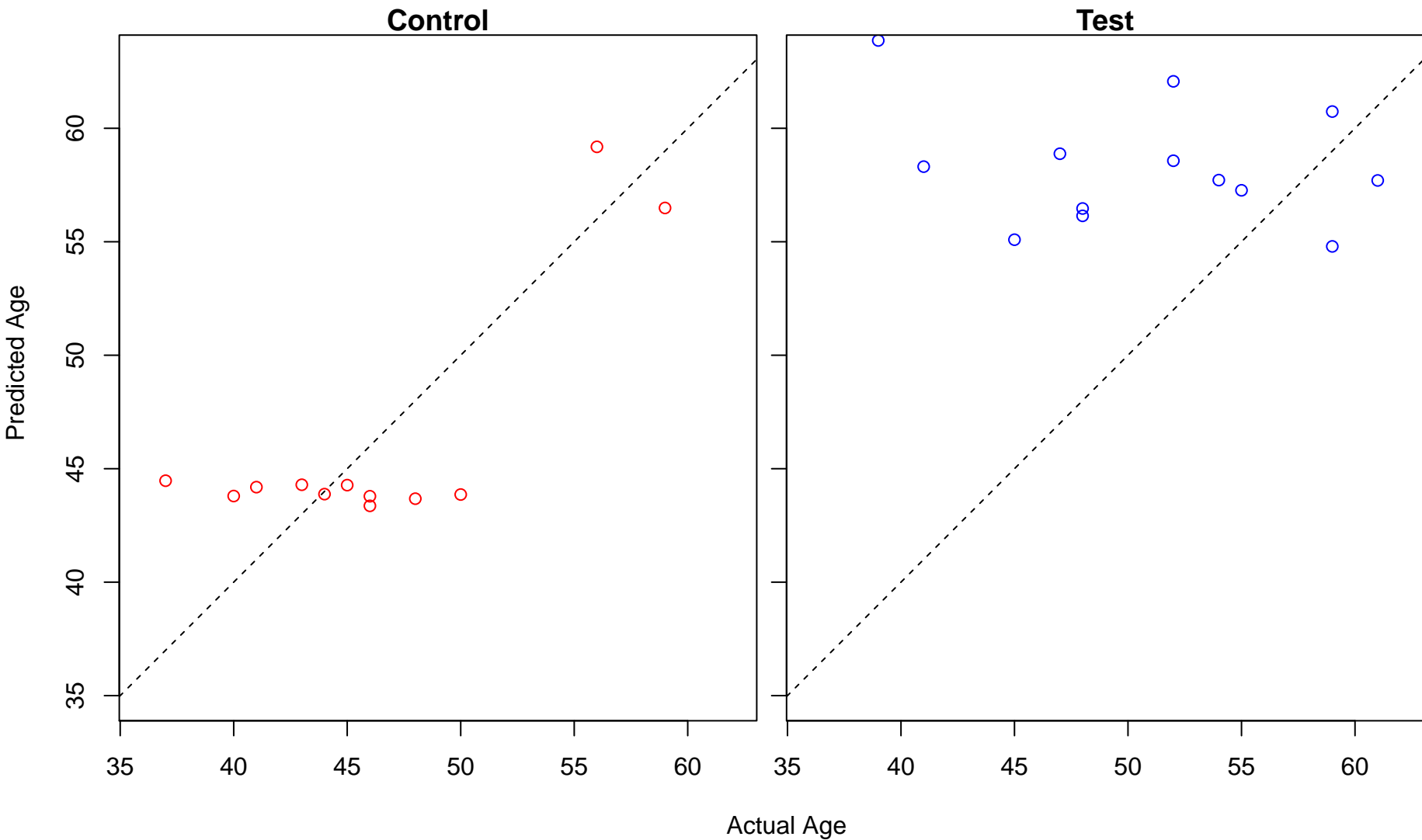
nuclear-transcribed mRNA catabolic process (Score: 3.663001)



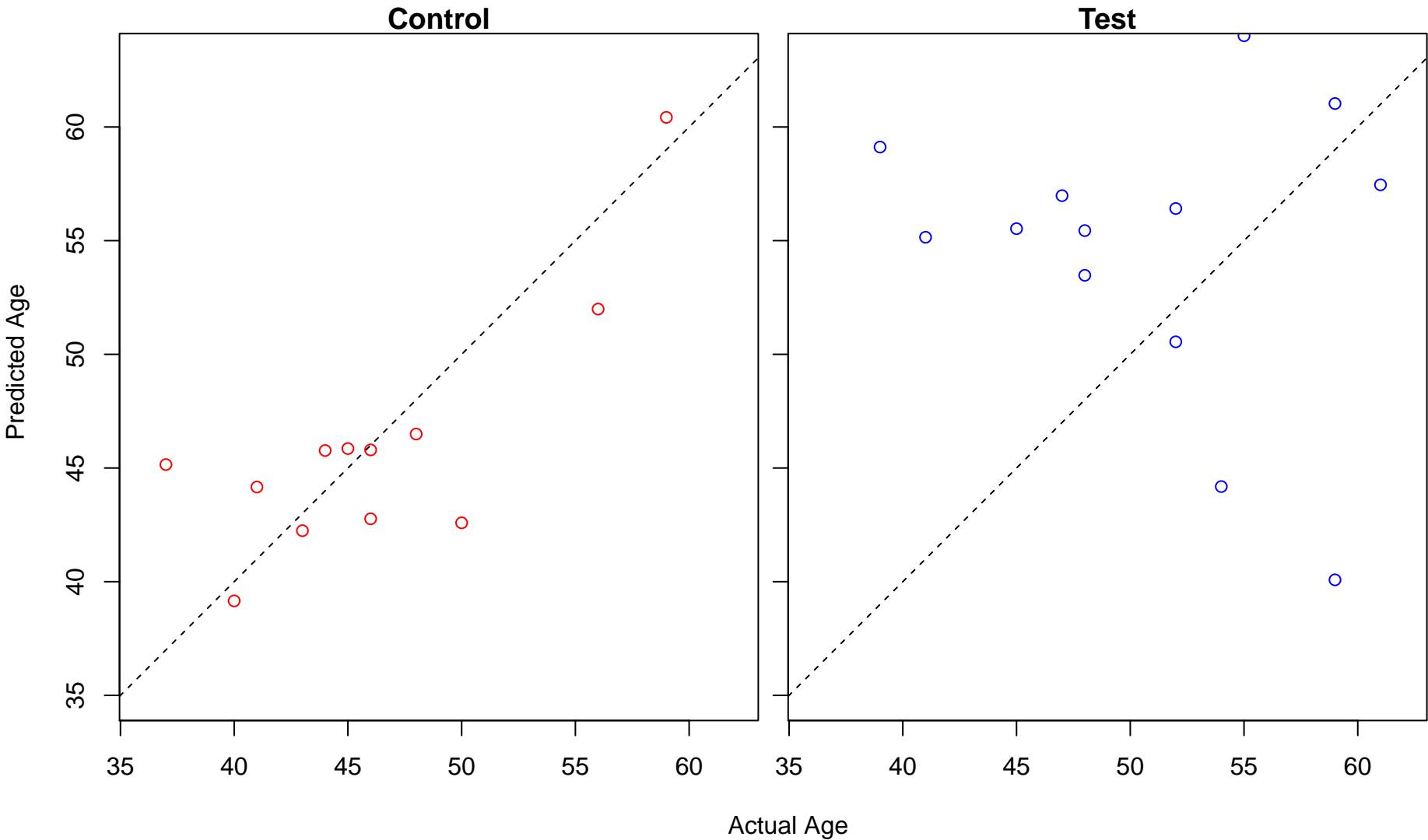
endoplasmic reticulum to cytosol transport (Score: 3.660742)



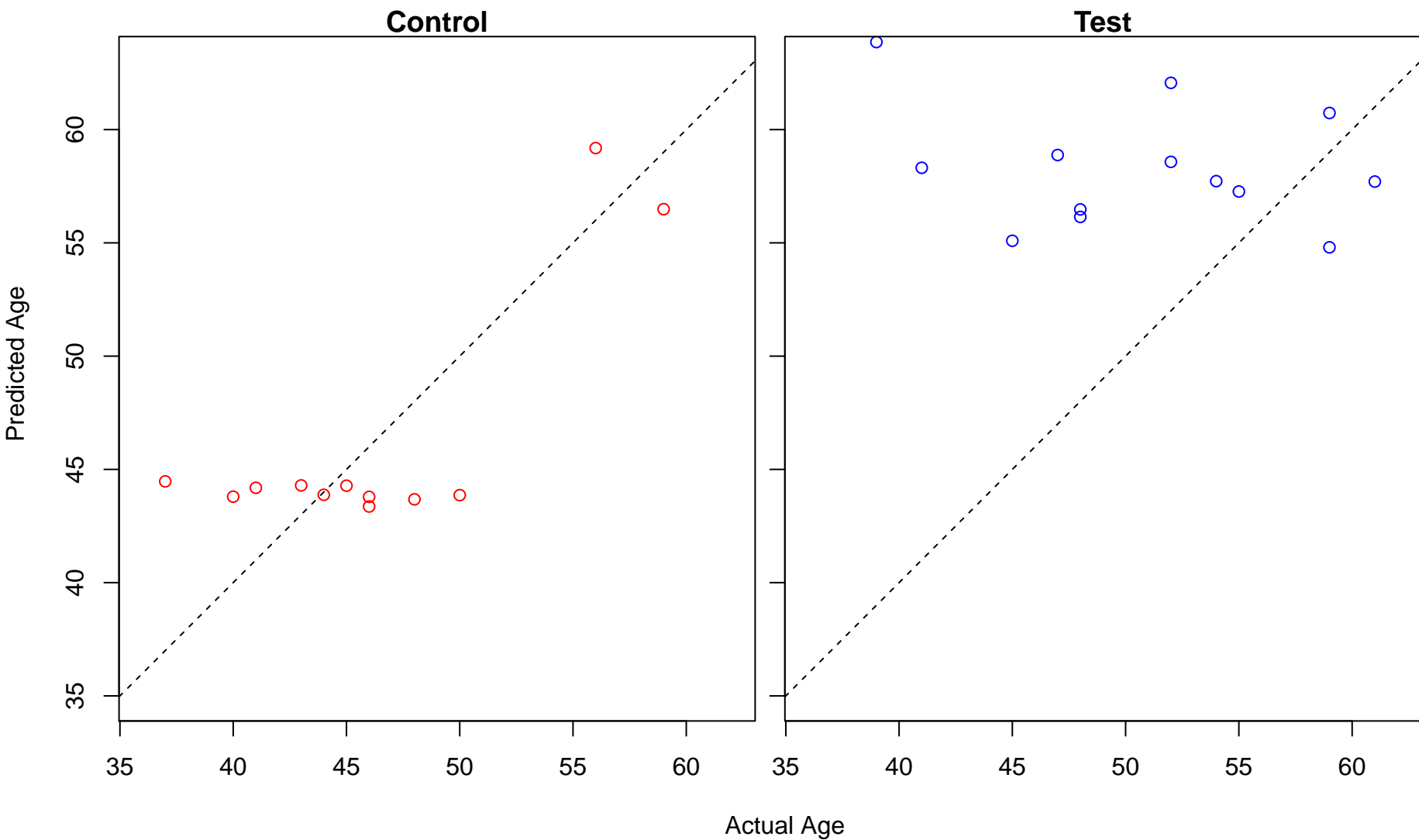
TRIF-dependent toll-like receptor signaling pathway (Score: 3.659845)



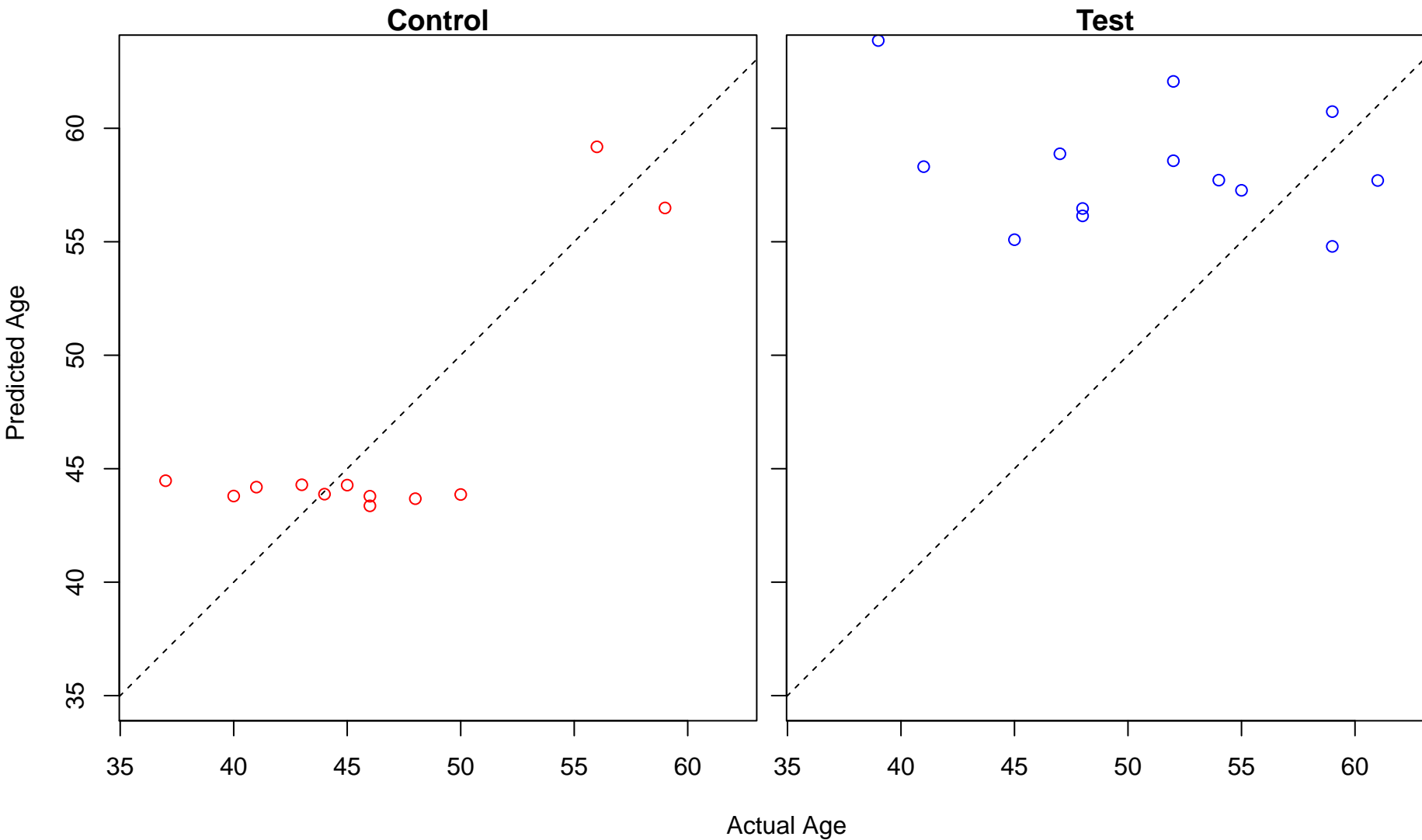
positive regulation of production of molecular mediator of immune response (Score: 3.659804)



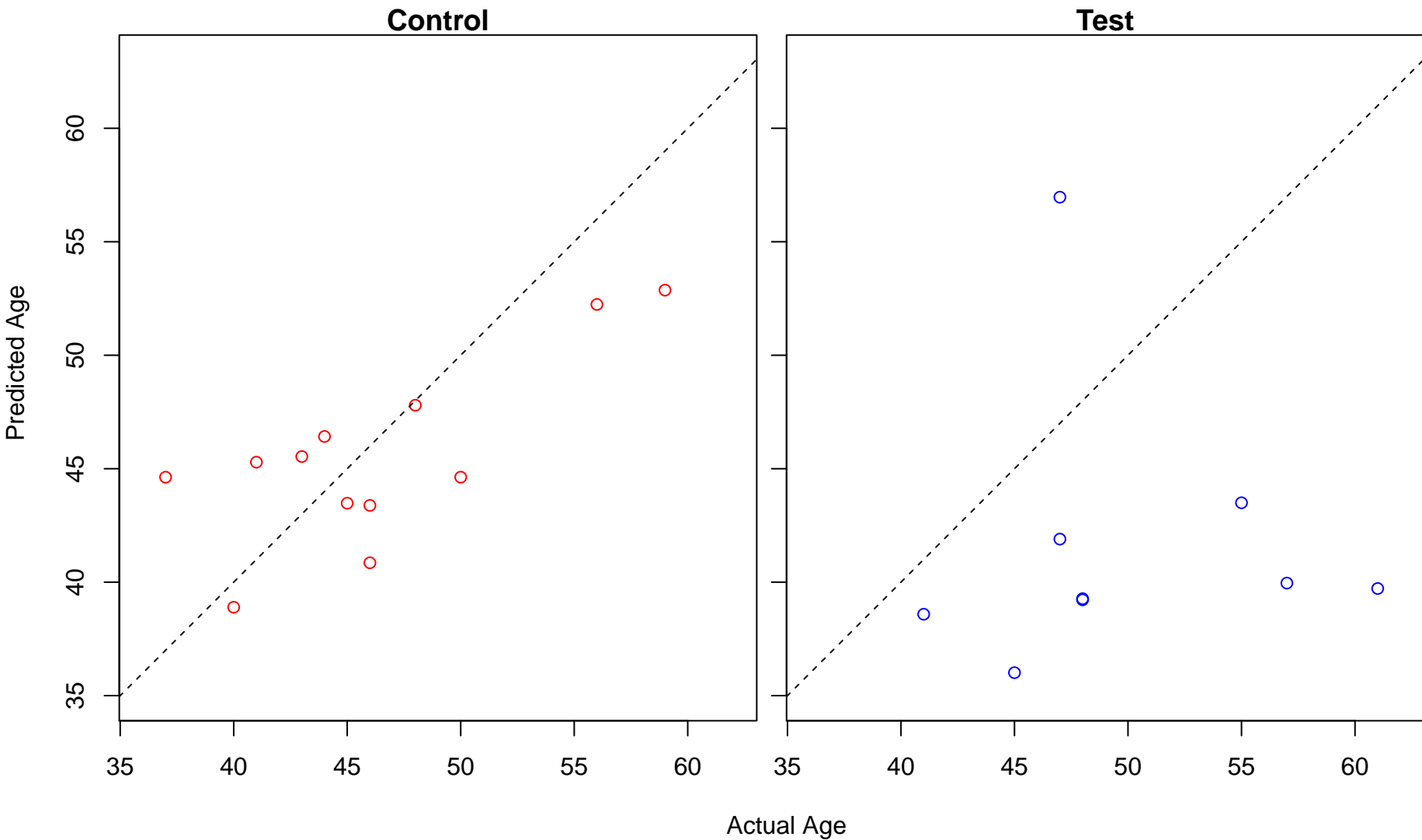
toll-like receptor 3 signaling pathway (Score: 3.659363)



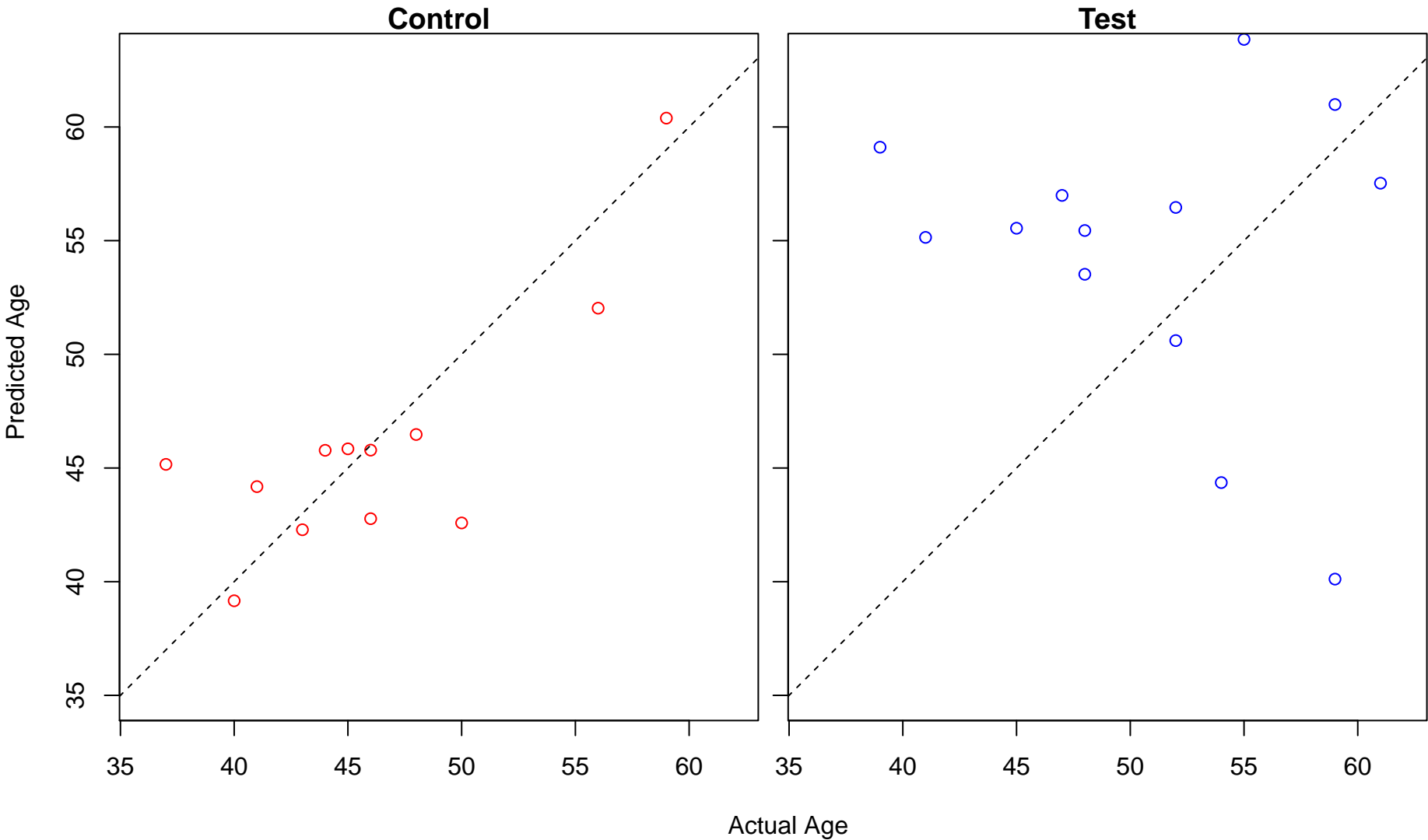
MyD88-independent toll-like receptor signaling pathway (Score: 3.659232)



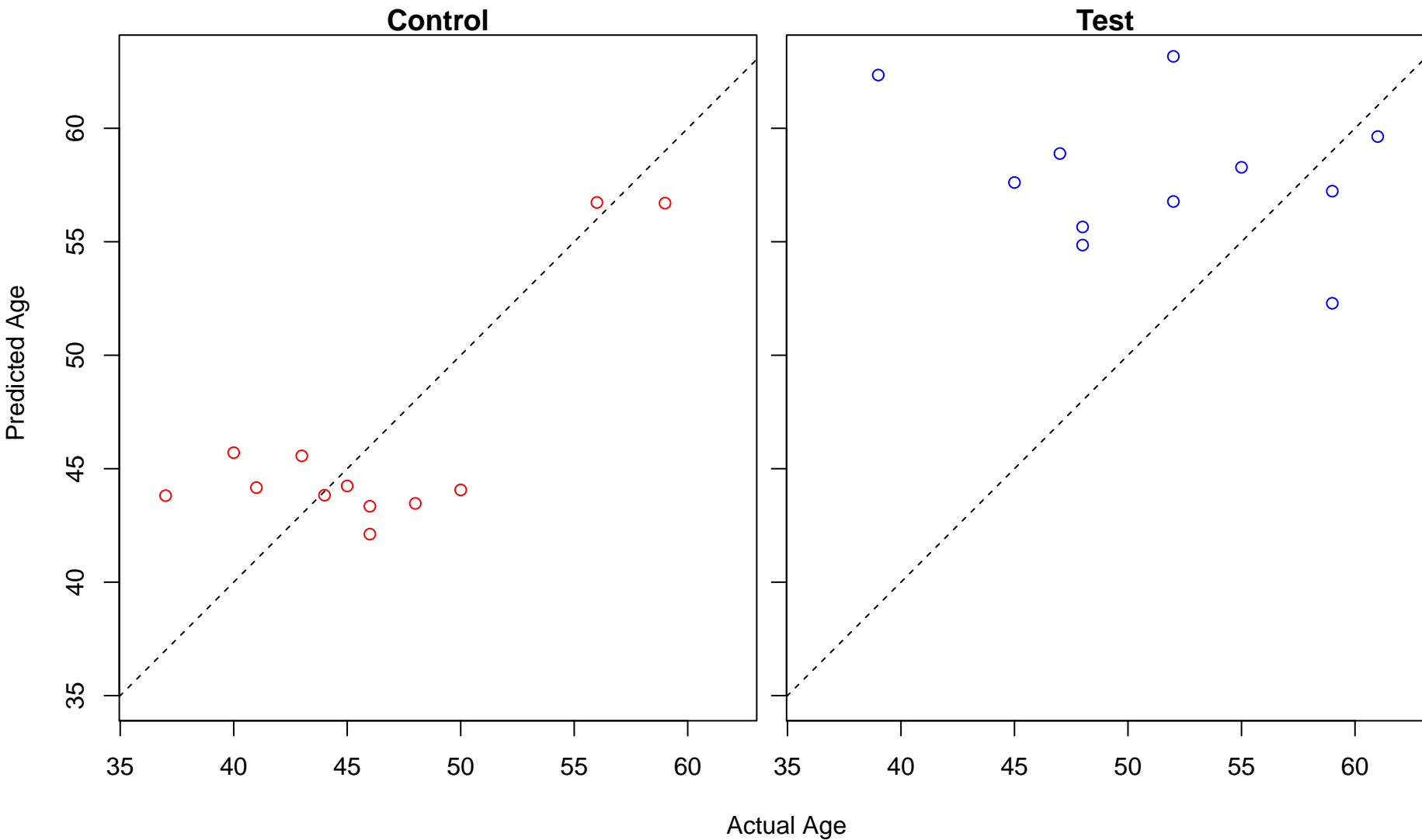
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (Score: 3.658736)



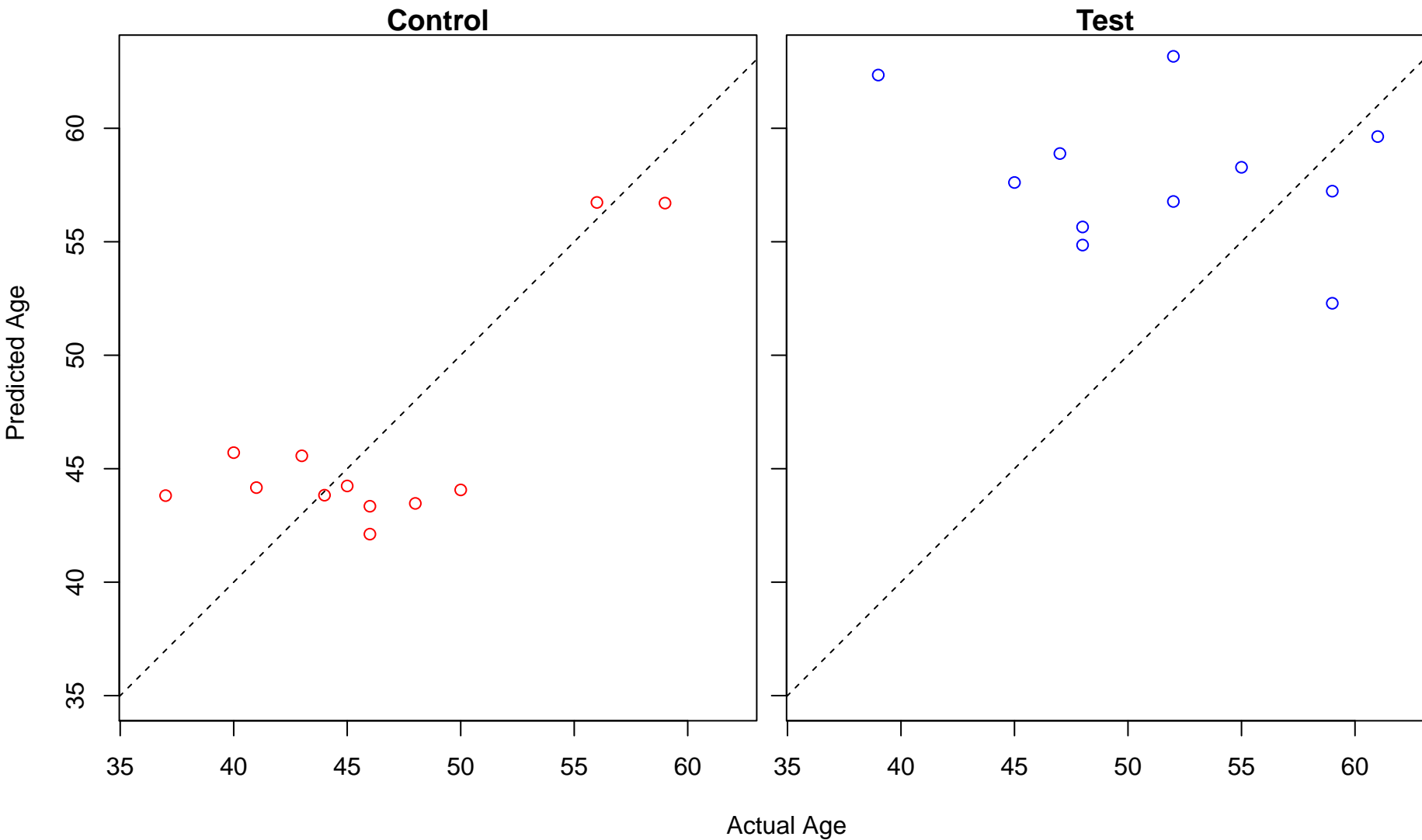
regulation of production of molecular mediator of immune response (Score: 3.658687)



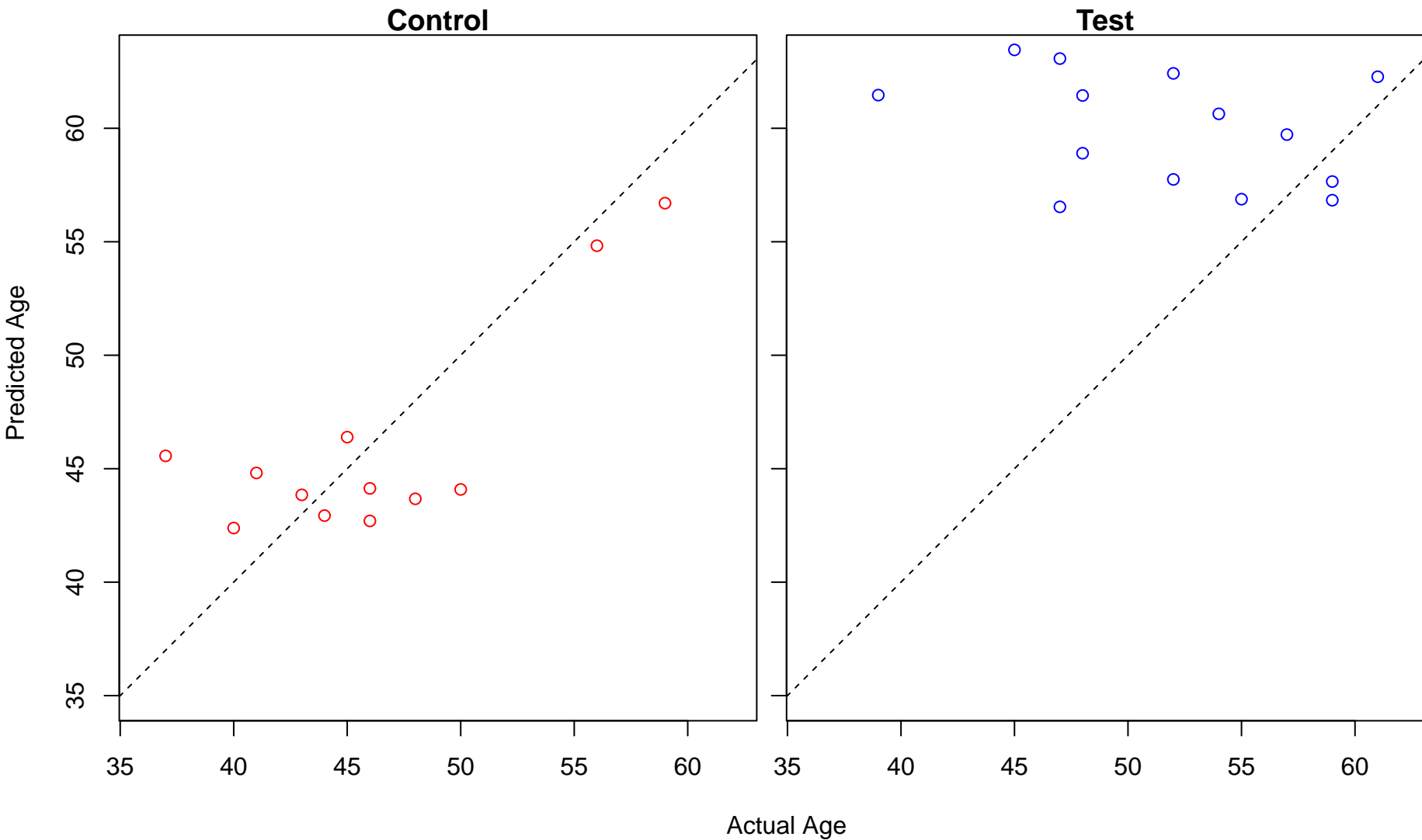
purine nucleoside diphosphate metabolic process (Score: 3.657559)



purine ribonucleoside diphosphate metabolic process (Score: 3.657559)

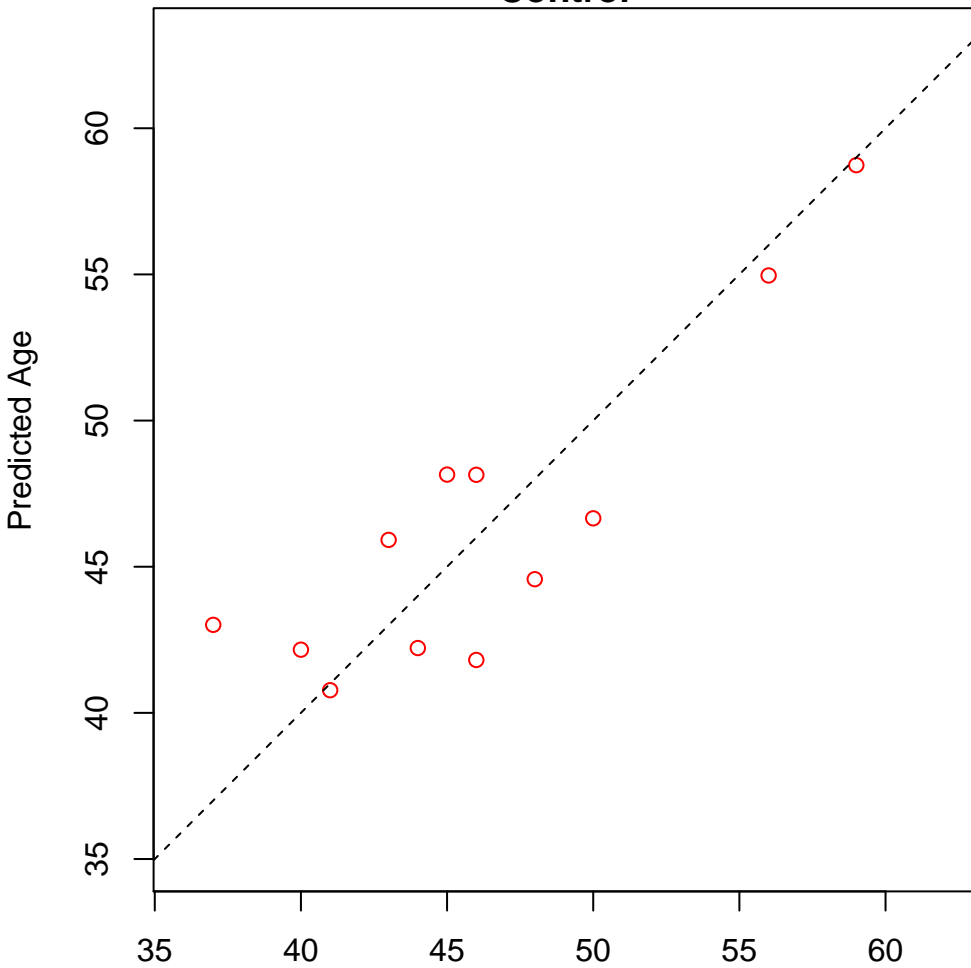


myeloid leukocyte activation (Score: 3.657243)

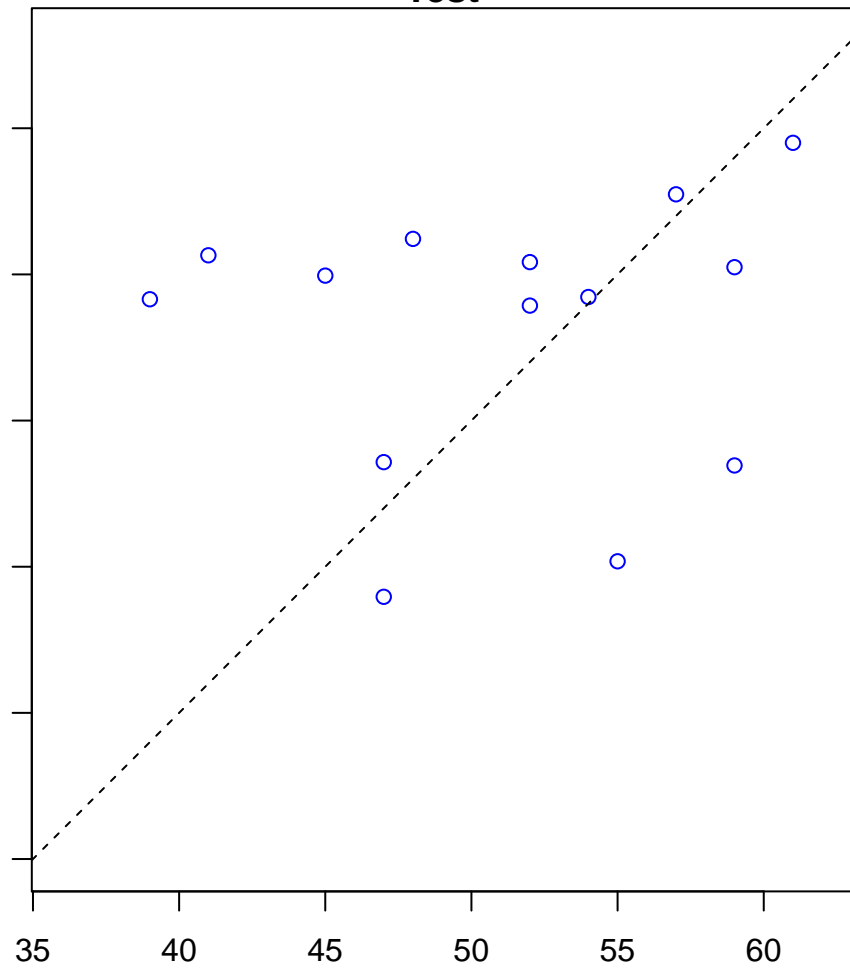


positive regulation of p38MAPK cascade (Score: 3.653403)

Control



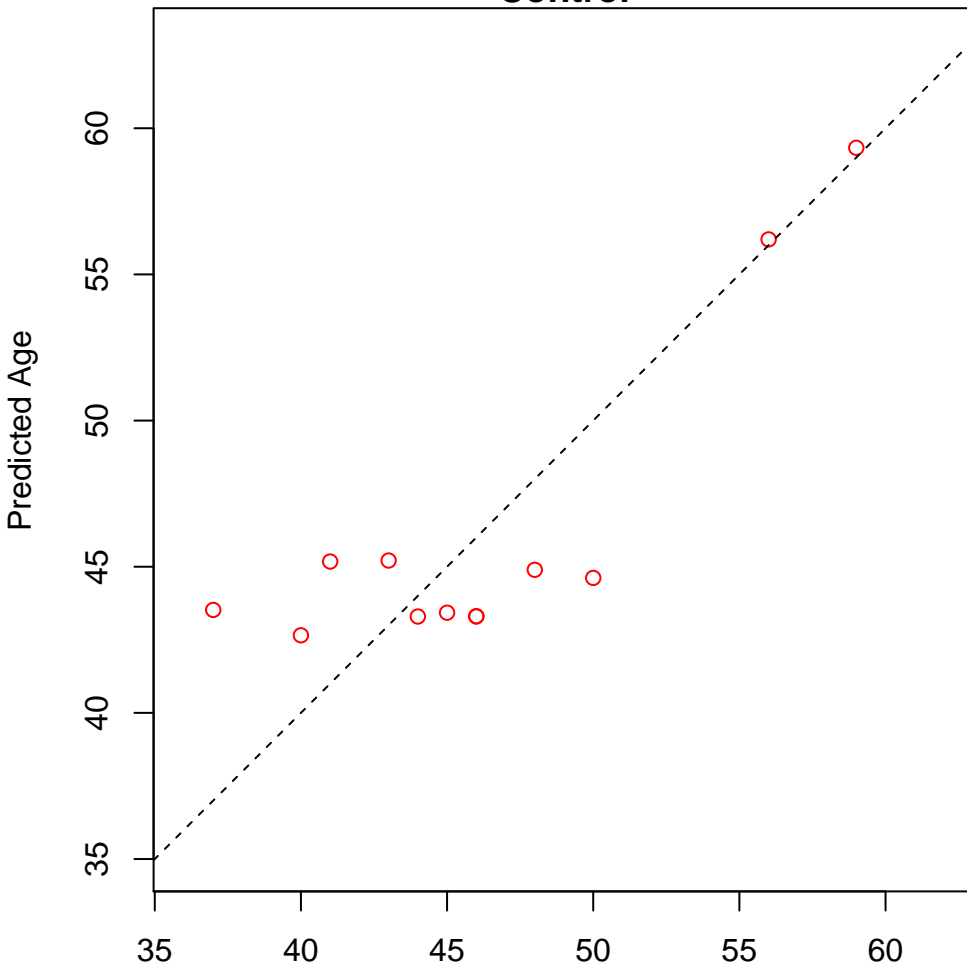
Test



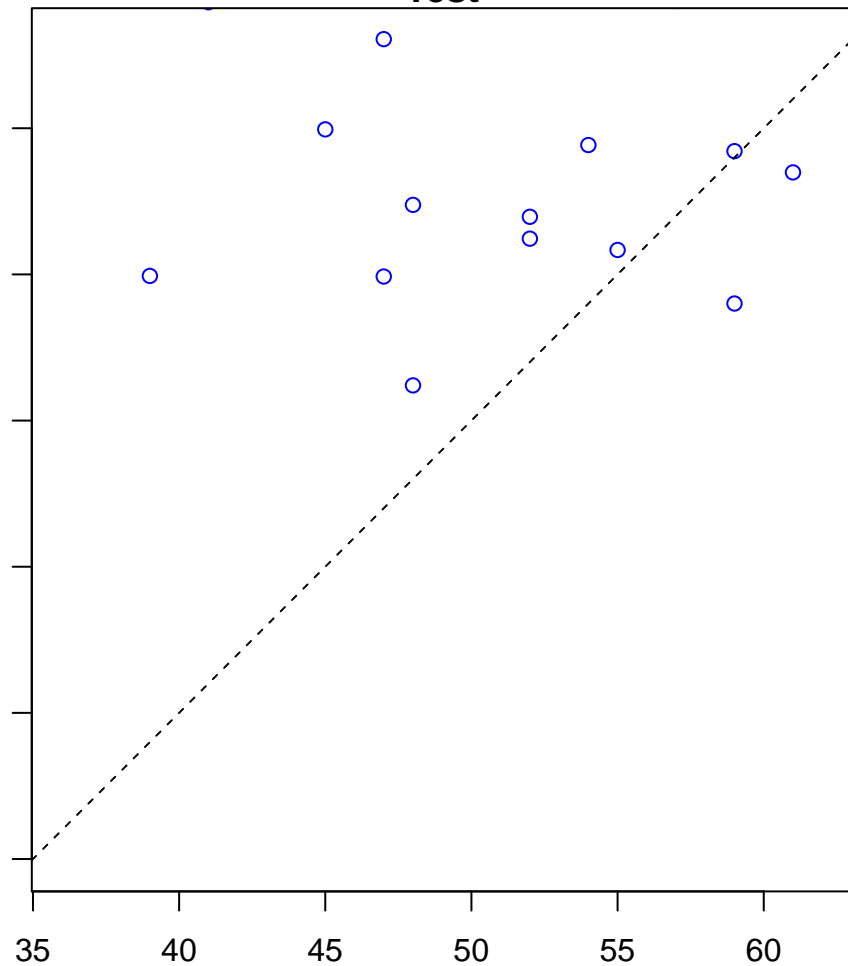
Actual Age

organic hydroxy compound transport (Score: 3.651953)

Control

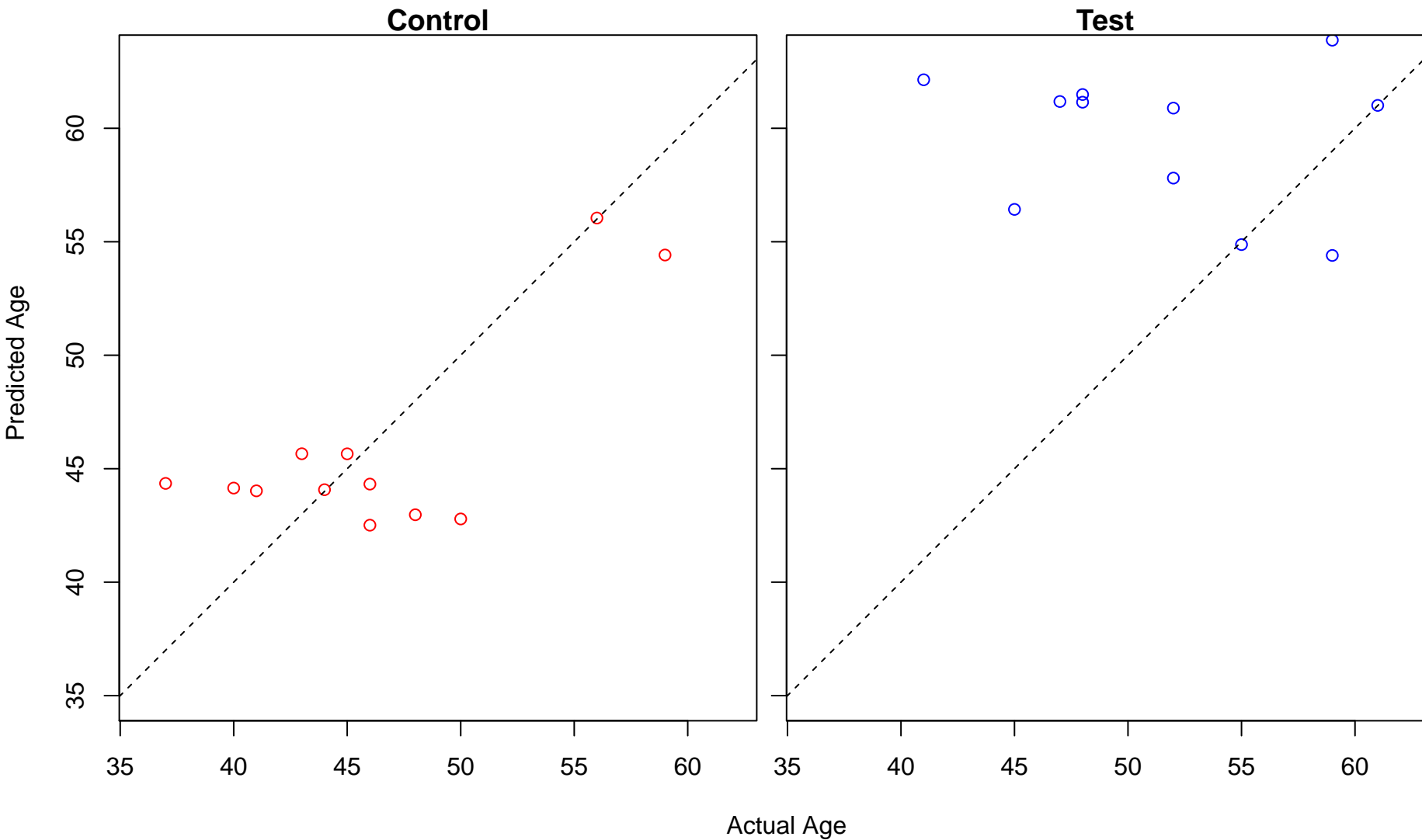


Test

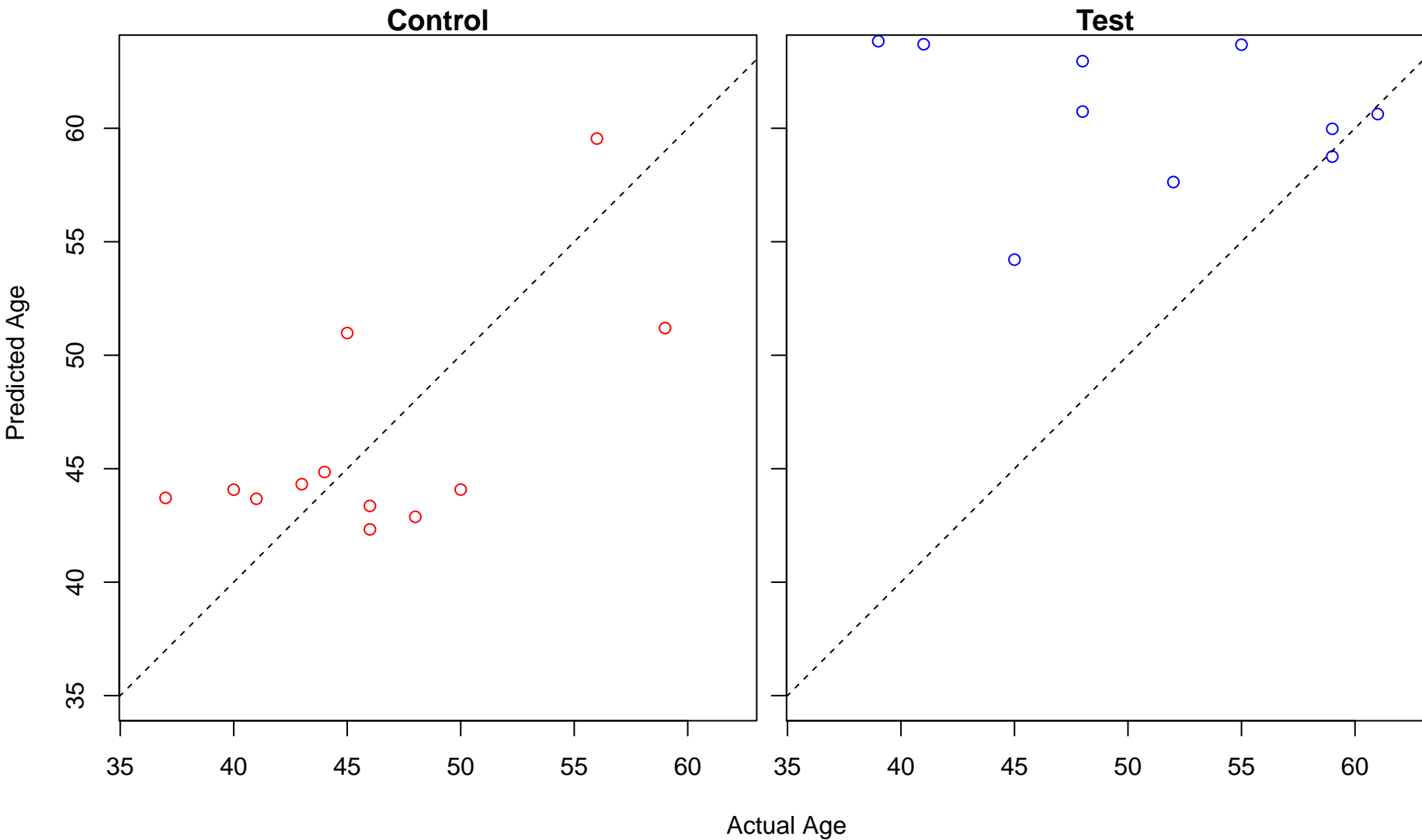


Actual Age

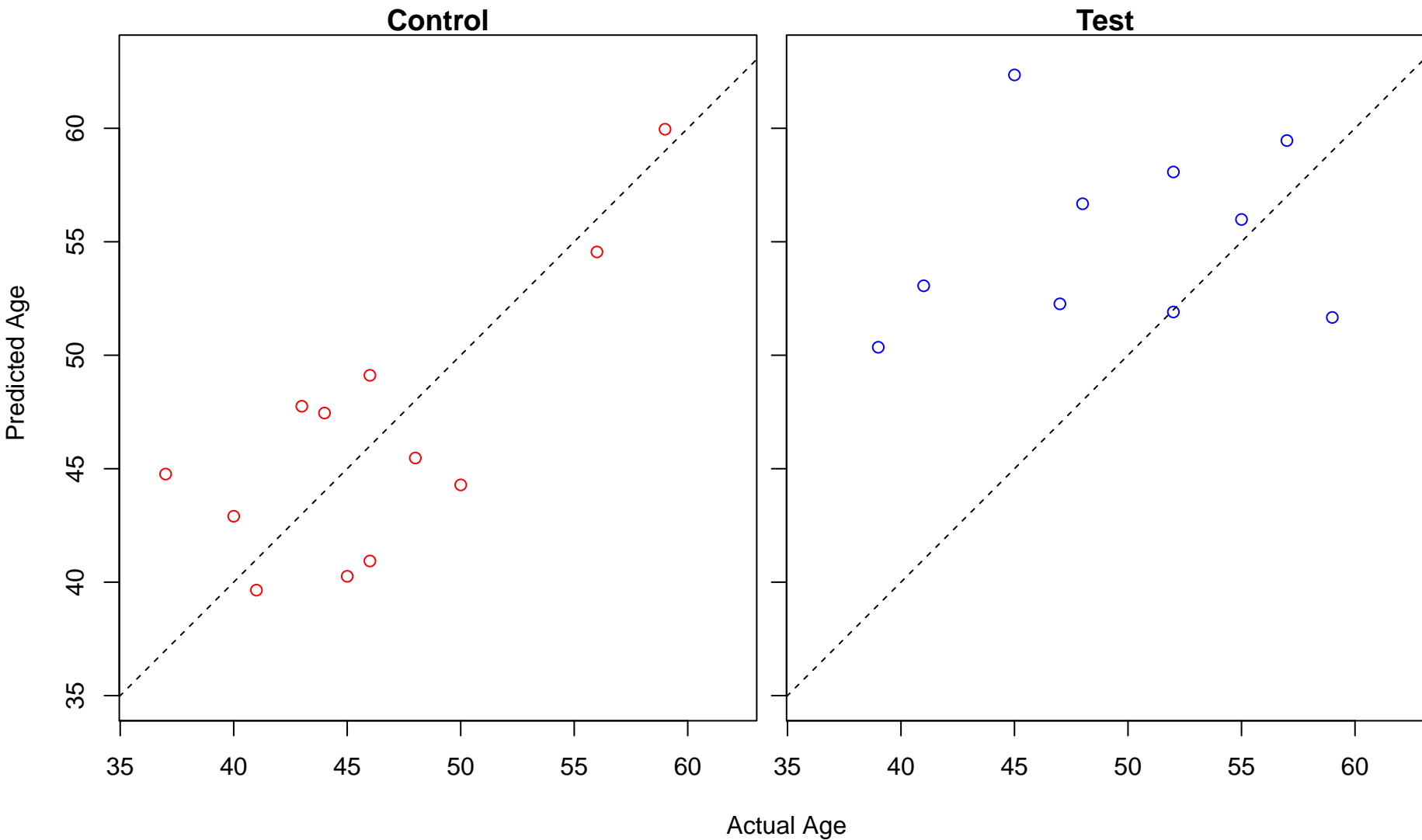
positive regulation of mitochondrial calcium ion concentration (Score: 3.650982)



positive regulation of fatty acid biosynthetic process (Score: 3.647206)

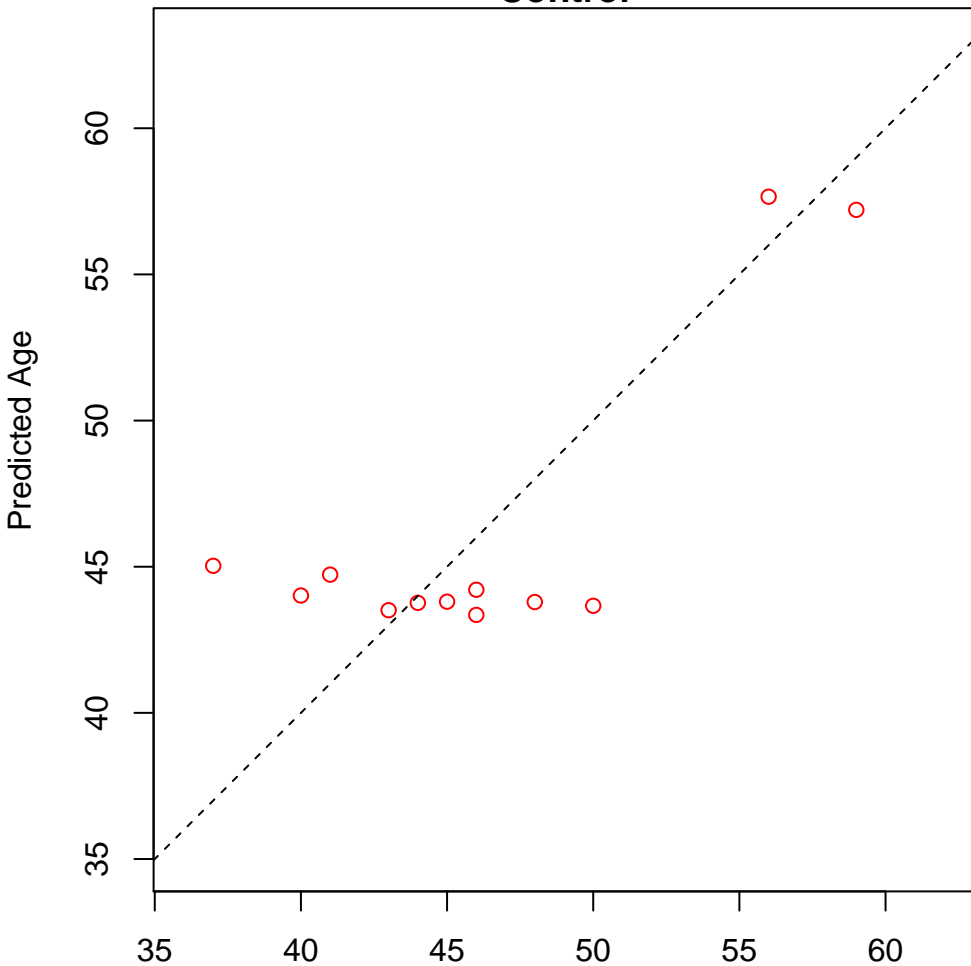


monosaccharide transport (Score: 3.647072)

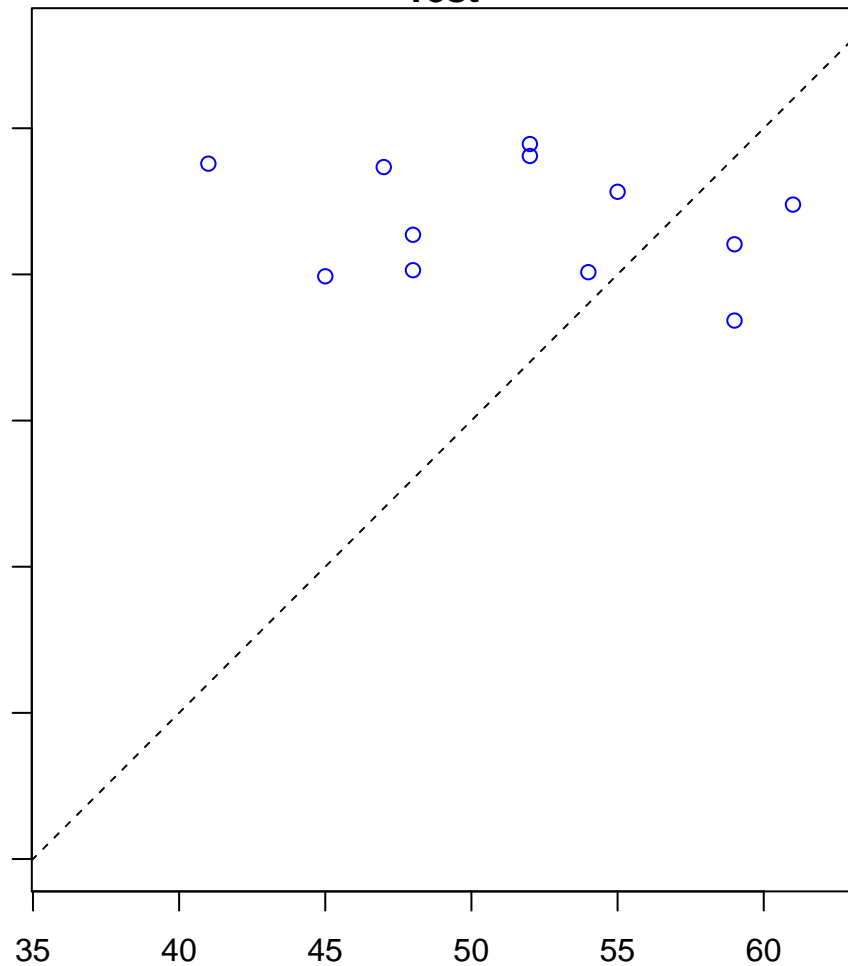


response to epidermal growth factor (Score: 3.646602)

Control

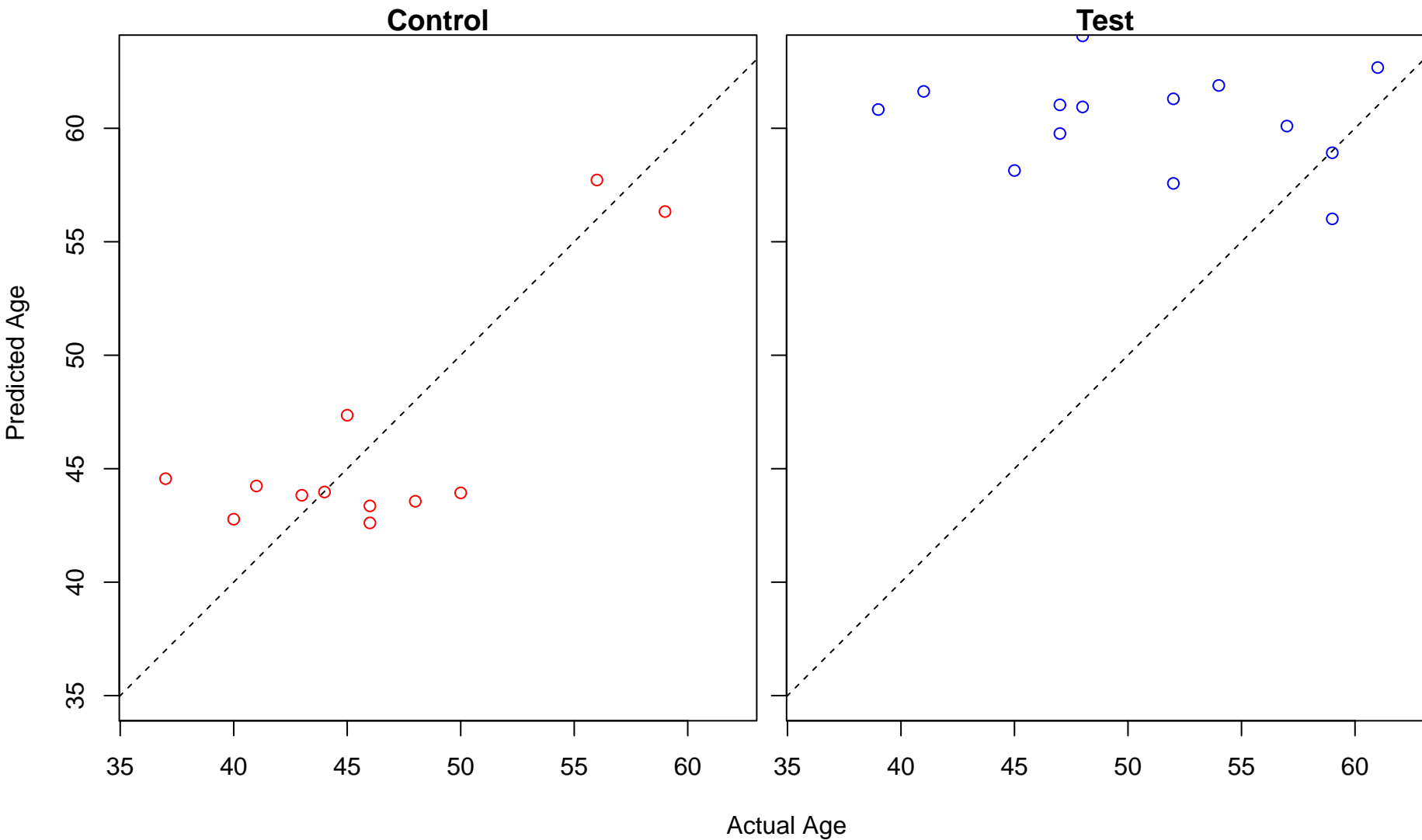


Test

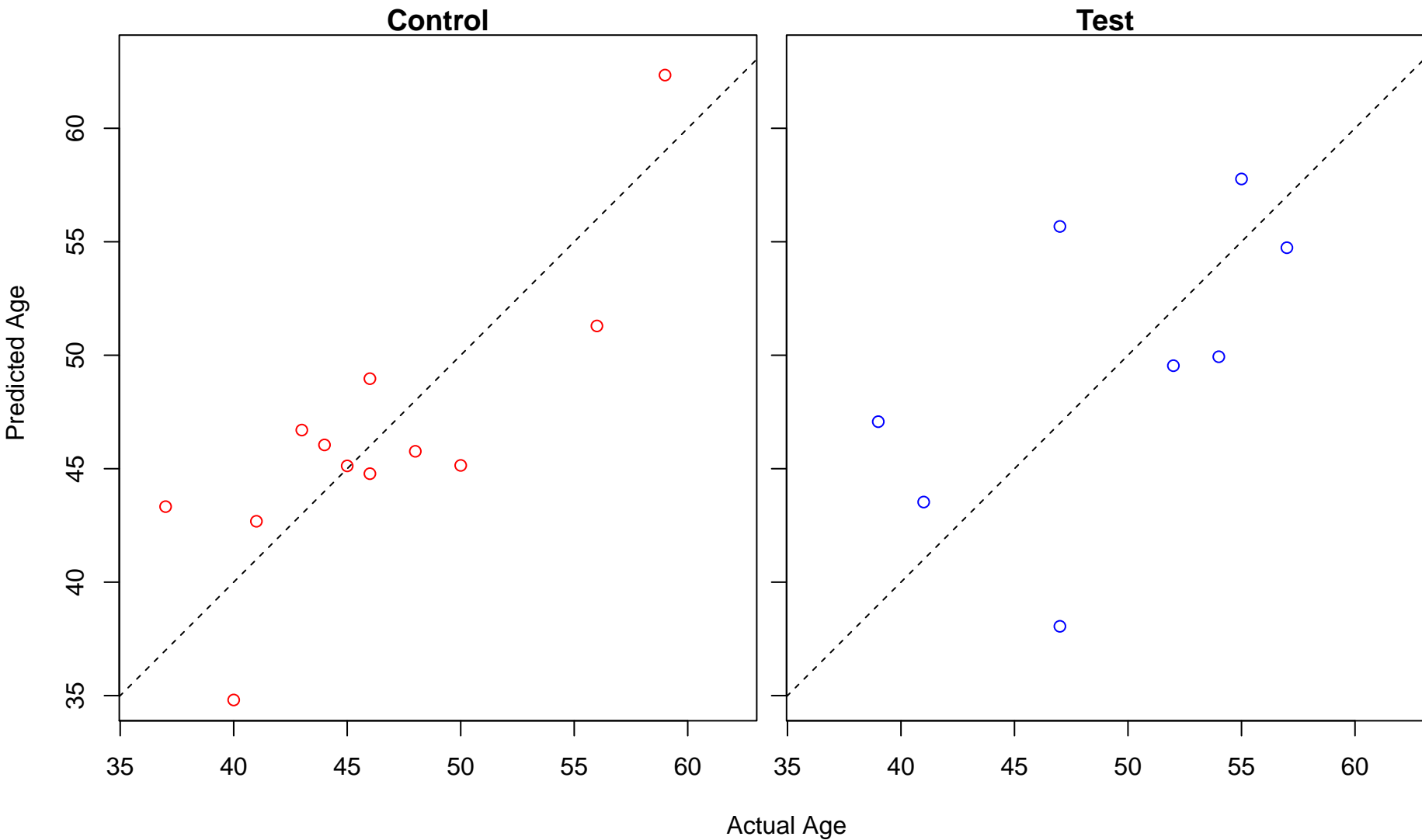


Actual Age

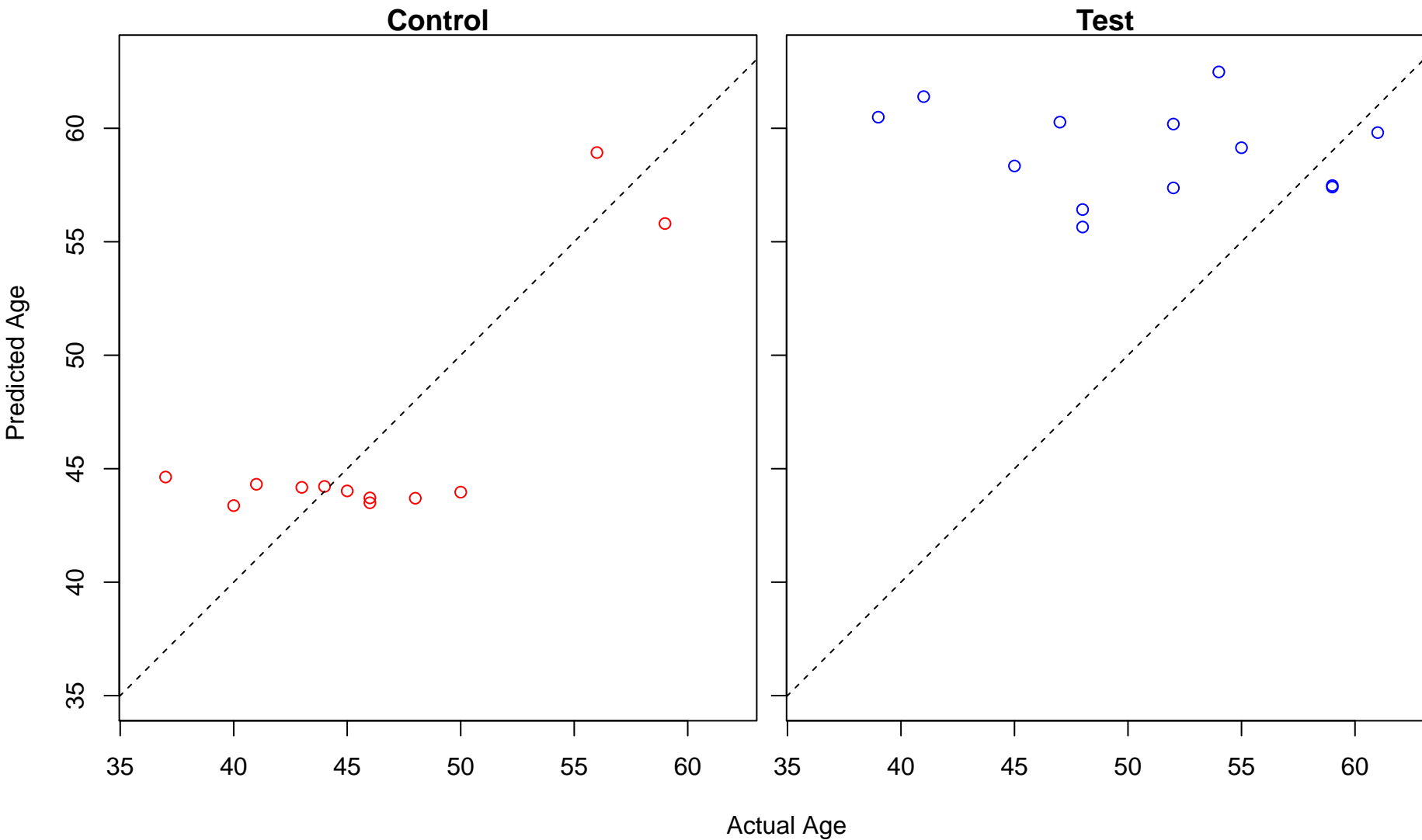
viral mRNA export from host cell nucleus (Score: 3.645738)



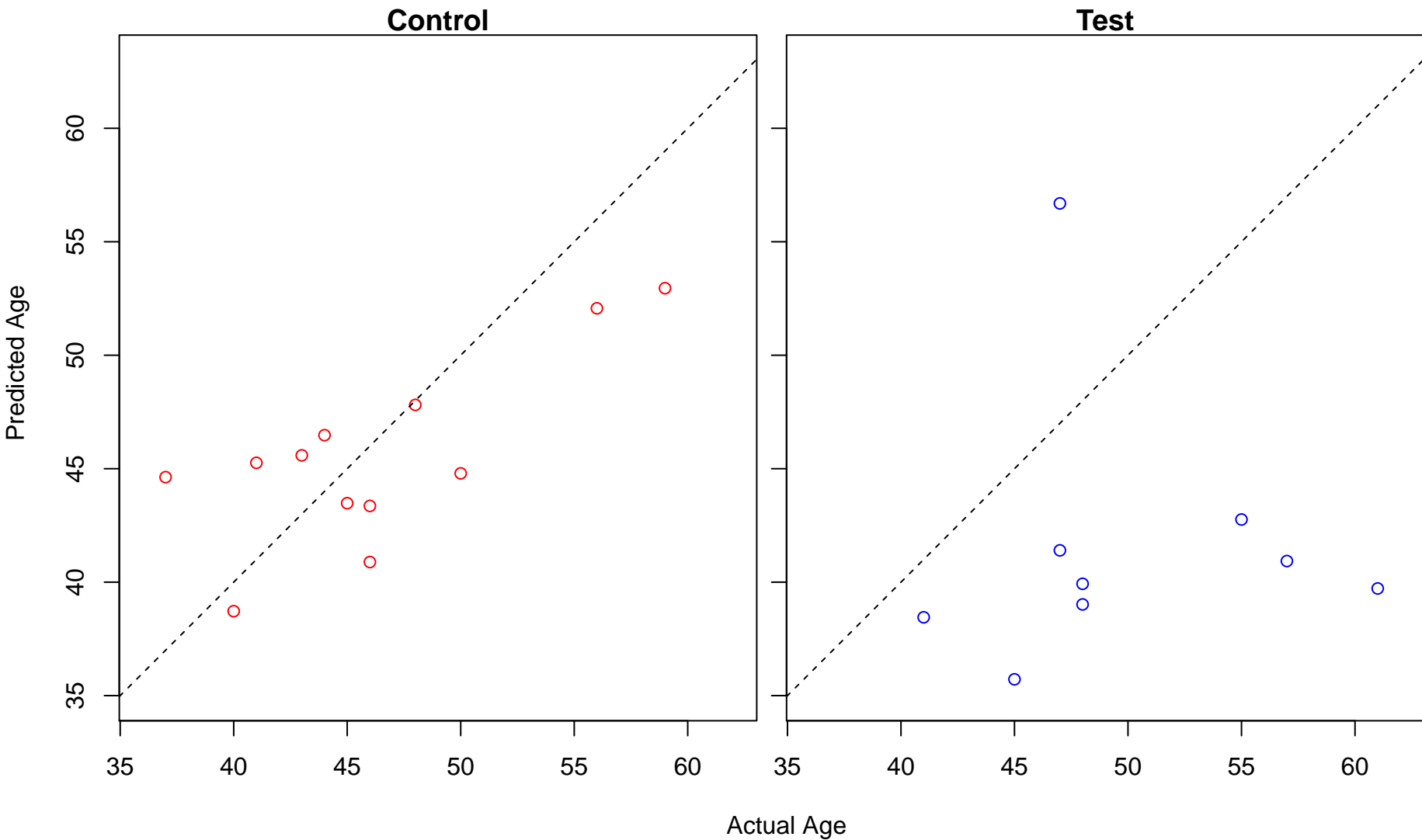
negative regulation of exocytosis (Score: 3.645388)



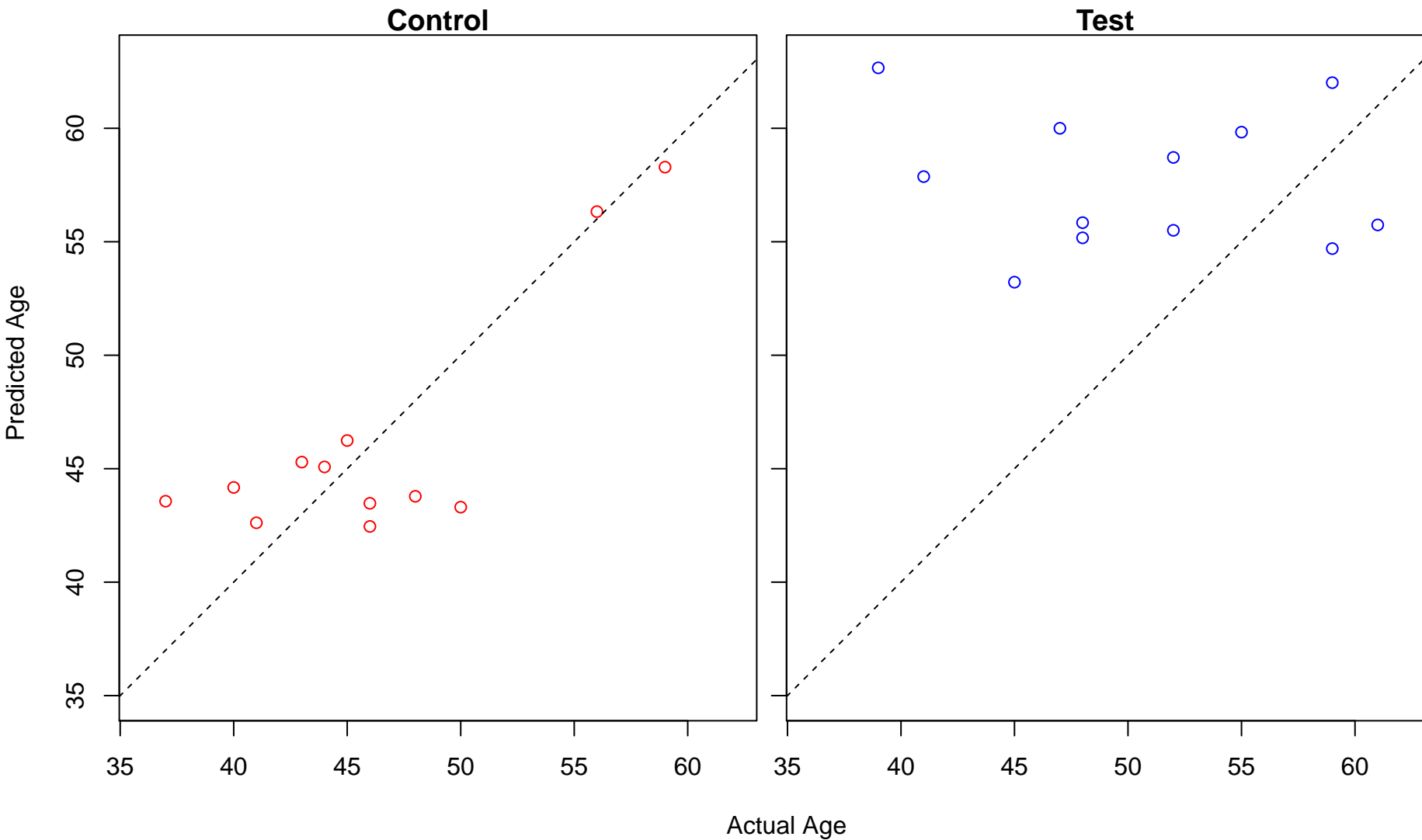
negative regulation of extrinsic apoptotic signaling pathway (Score: 3.641733)



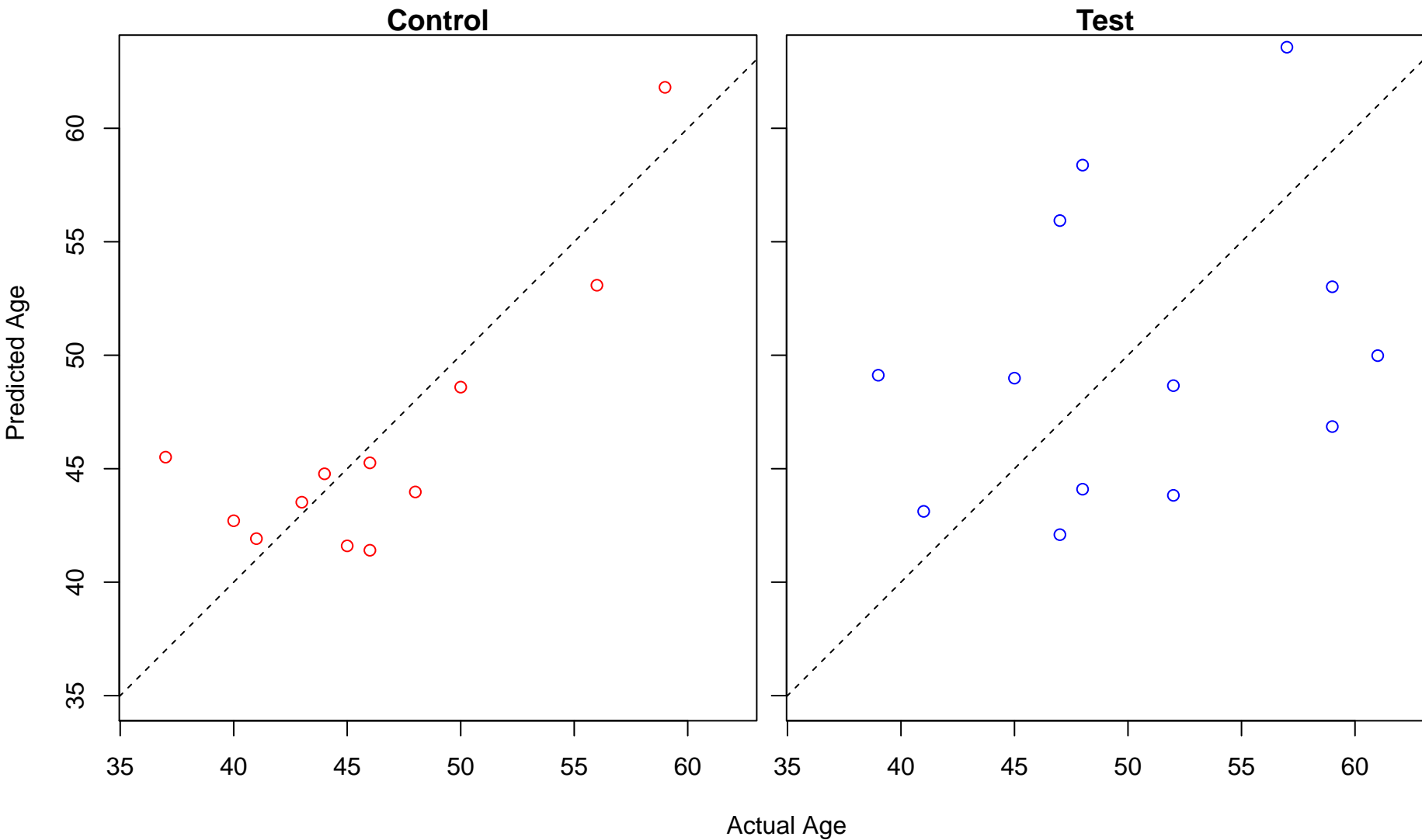
selenocysteine metabolic process (Score: 3.640985)



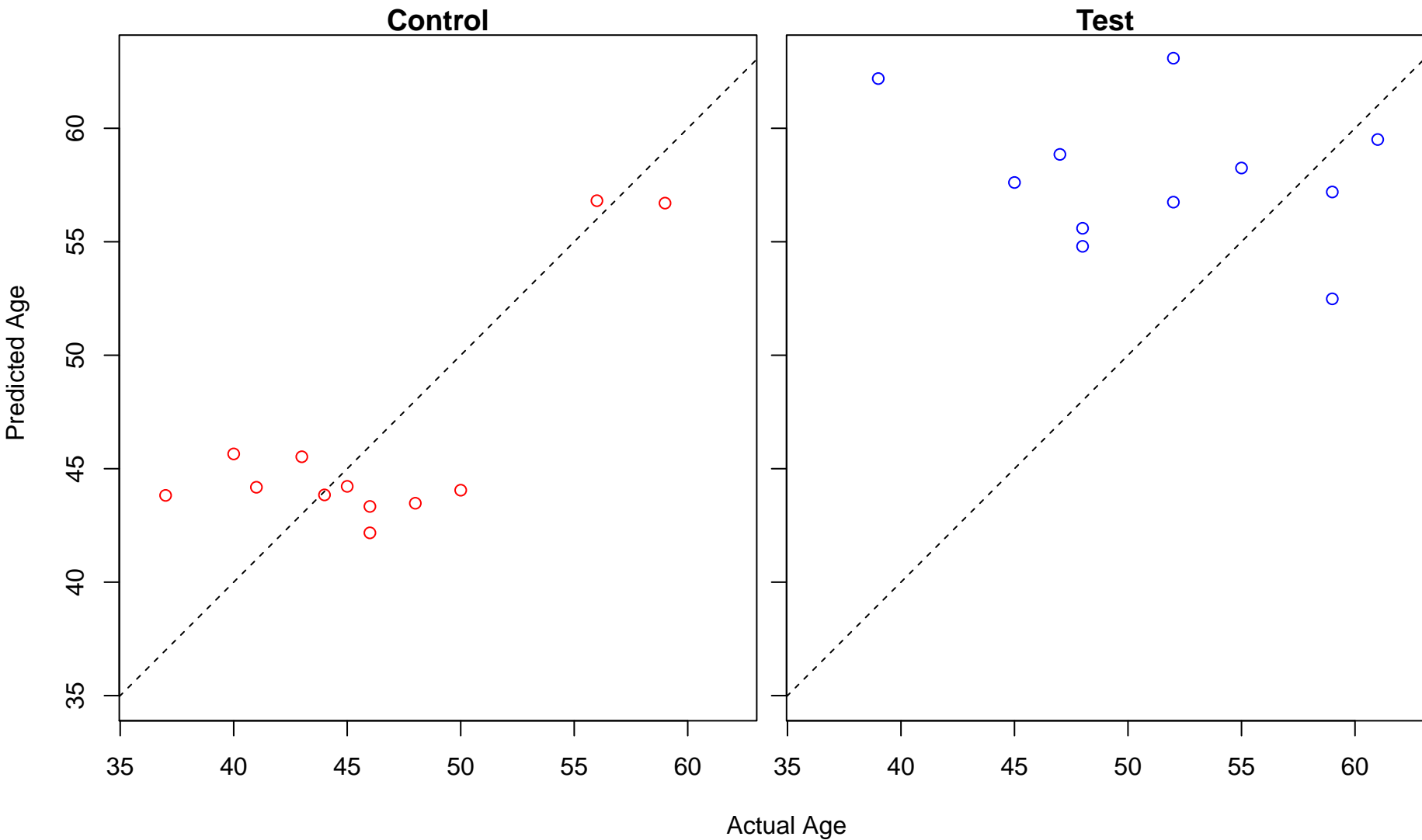
embryonic pattern specification (Score: 3.638767)



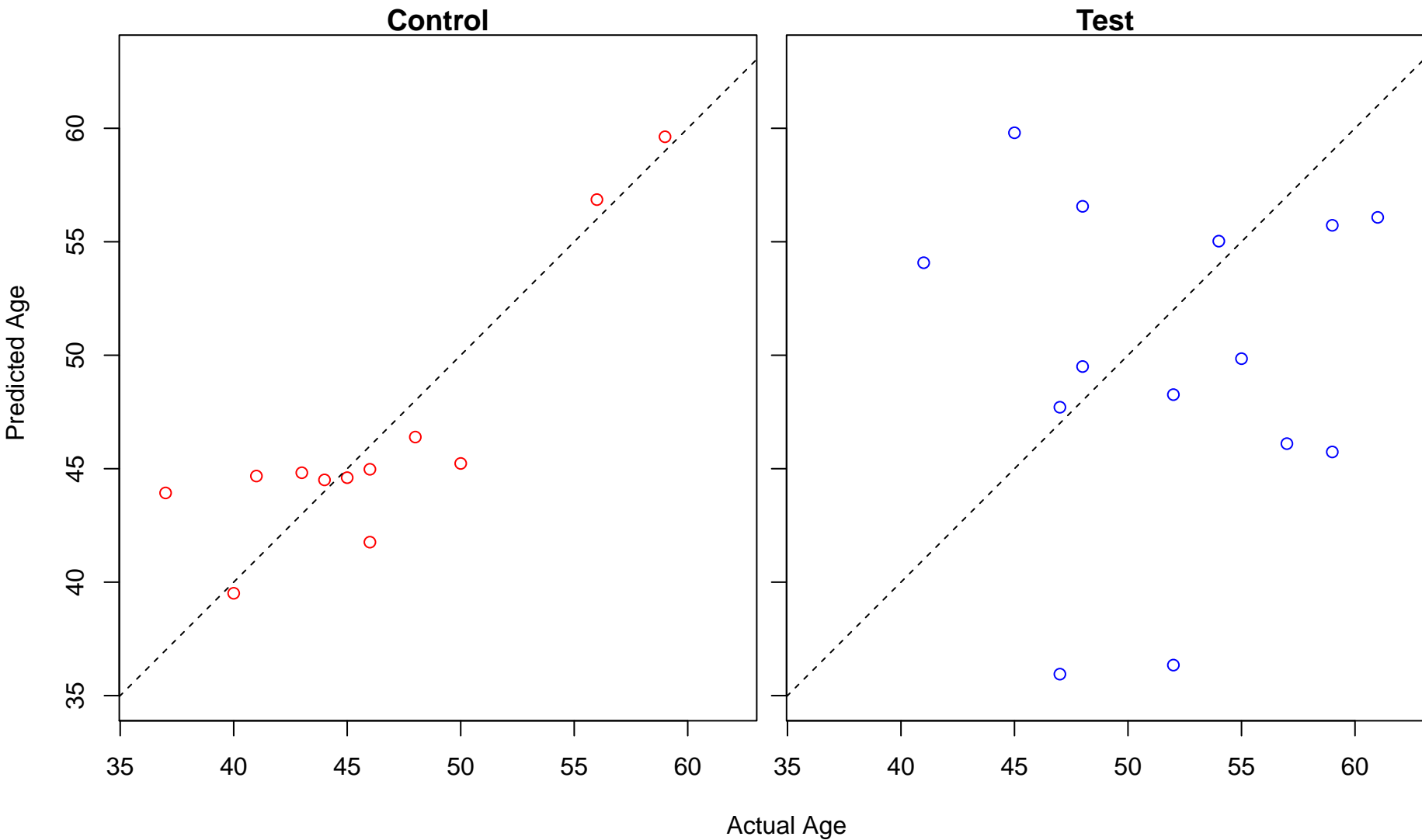
cell communication involved in cardiac conduction (Score: 3.629535)



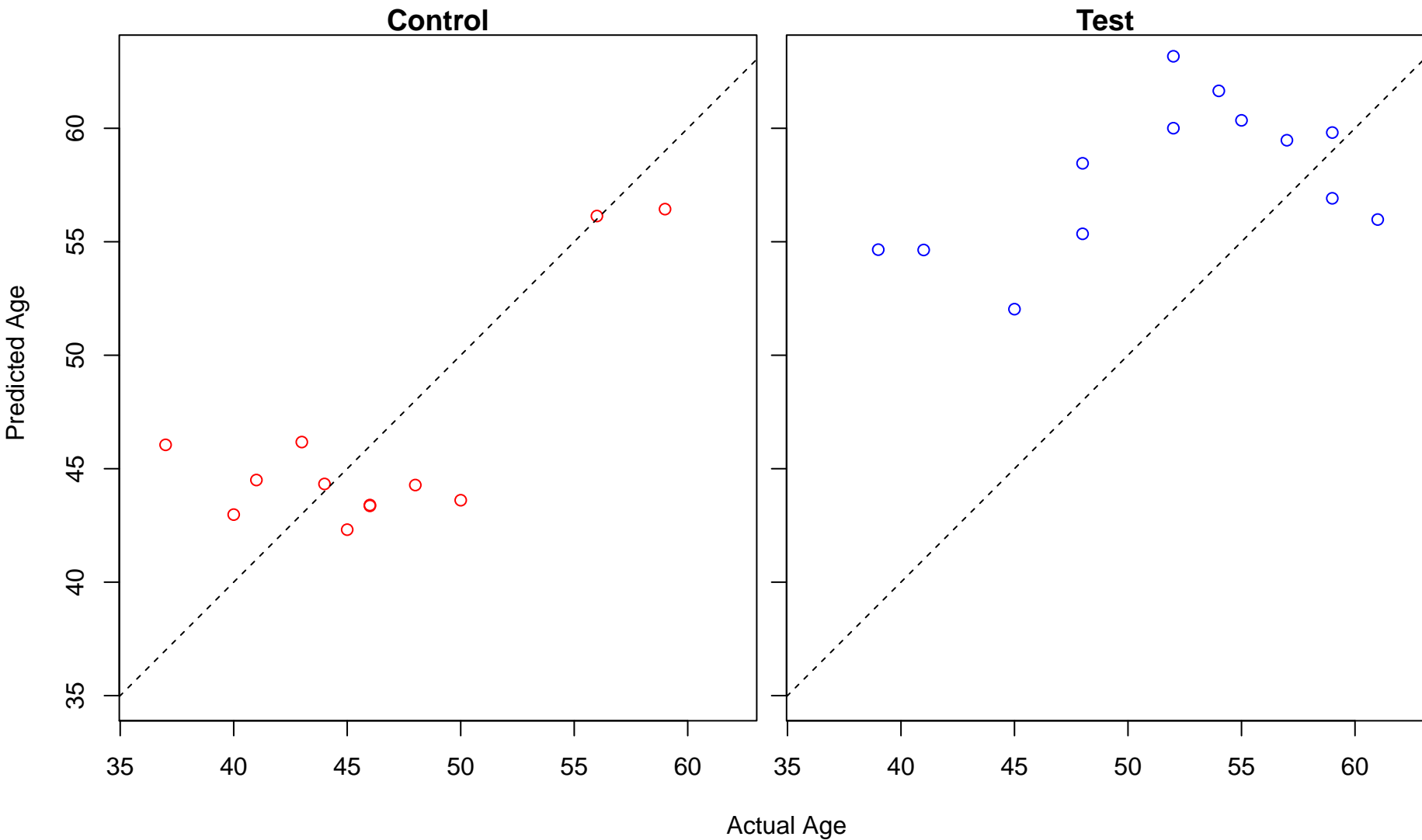
ribonucleoside diphosphate metabolic process (Score: 3.628372)



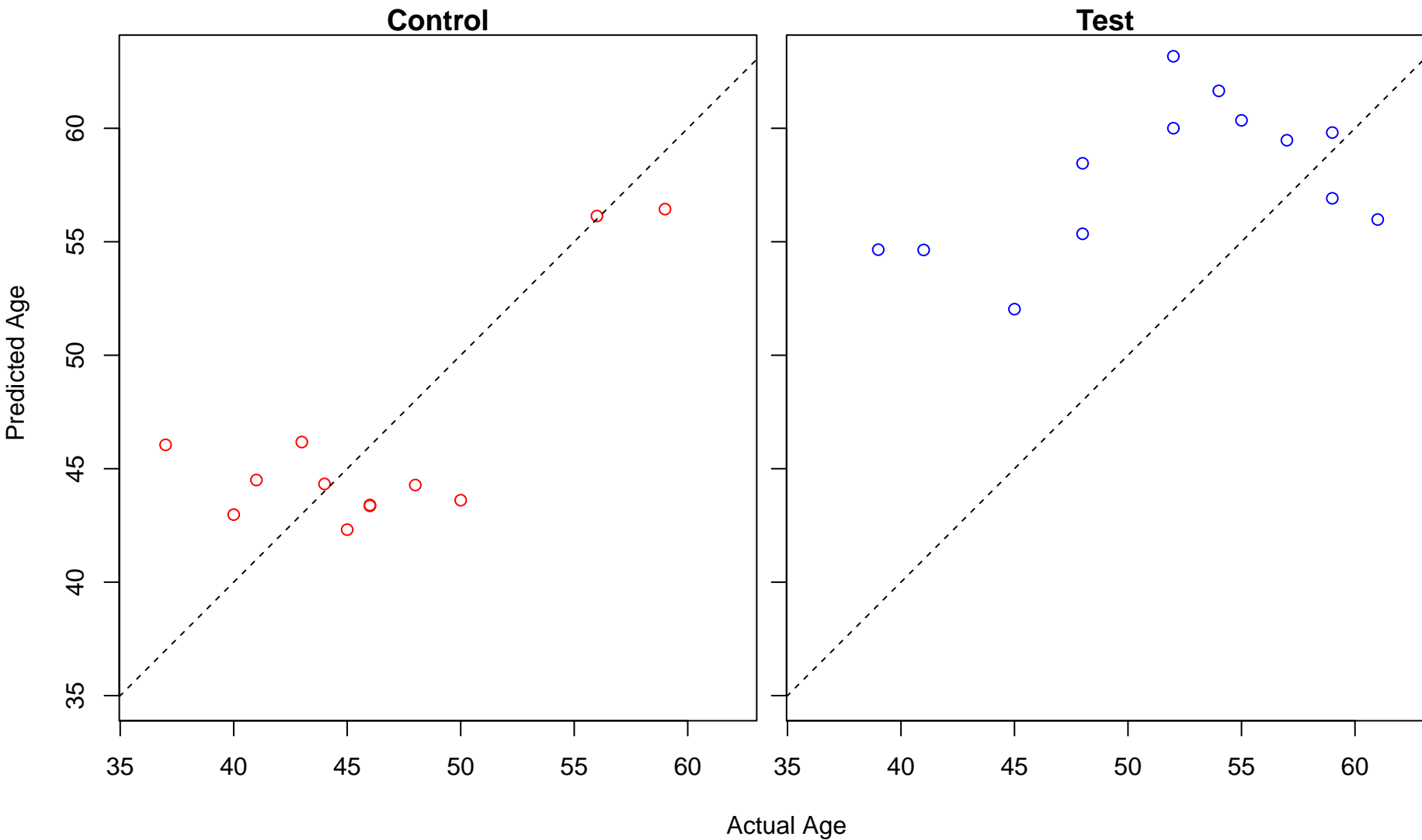
regulation of intracellular transport (Score: 3.624124)



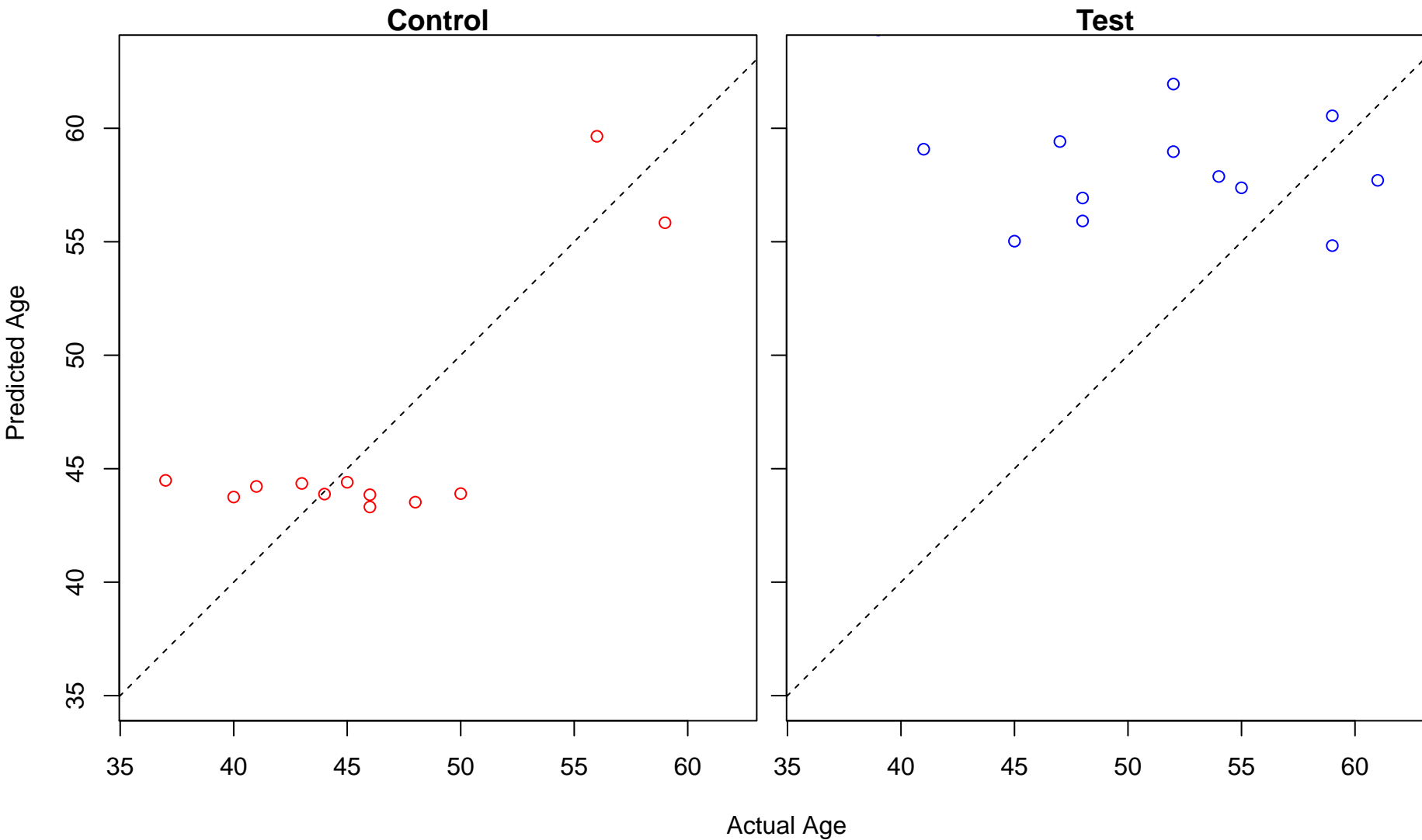
aortic valve development (Score: 3.623322)



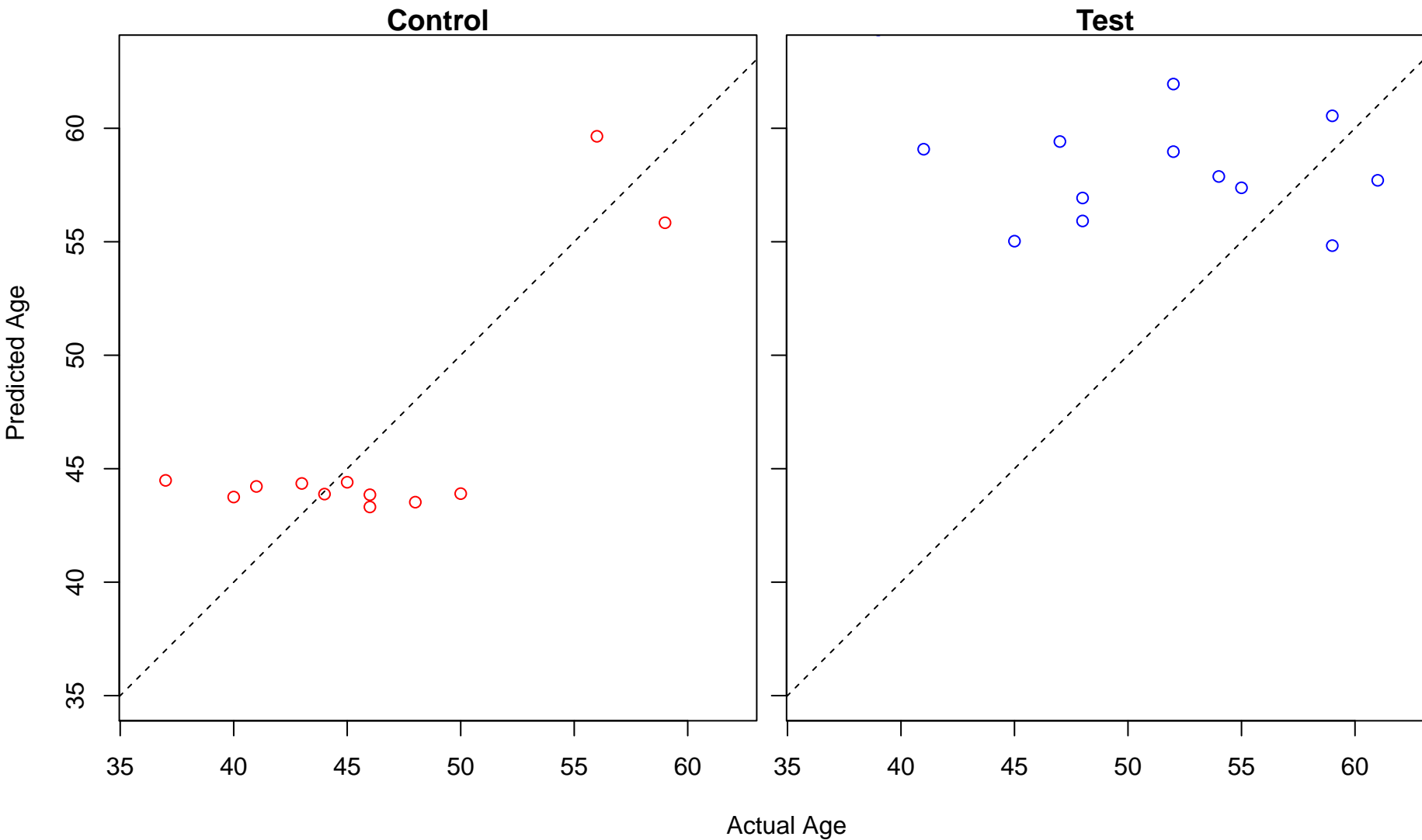
aortic valve morphogenesis (Score: 3.623322)



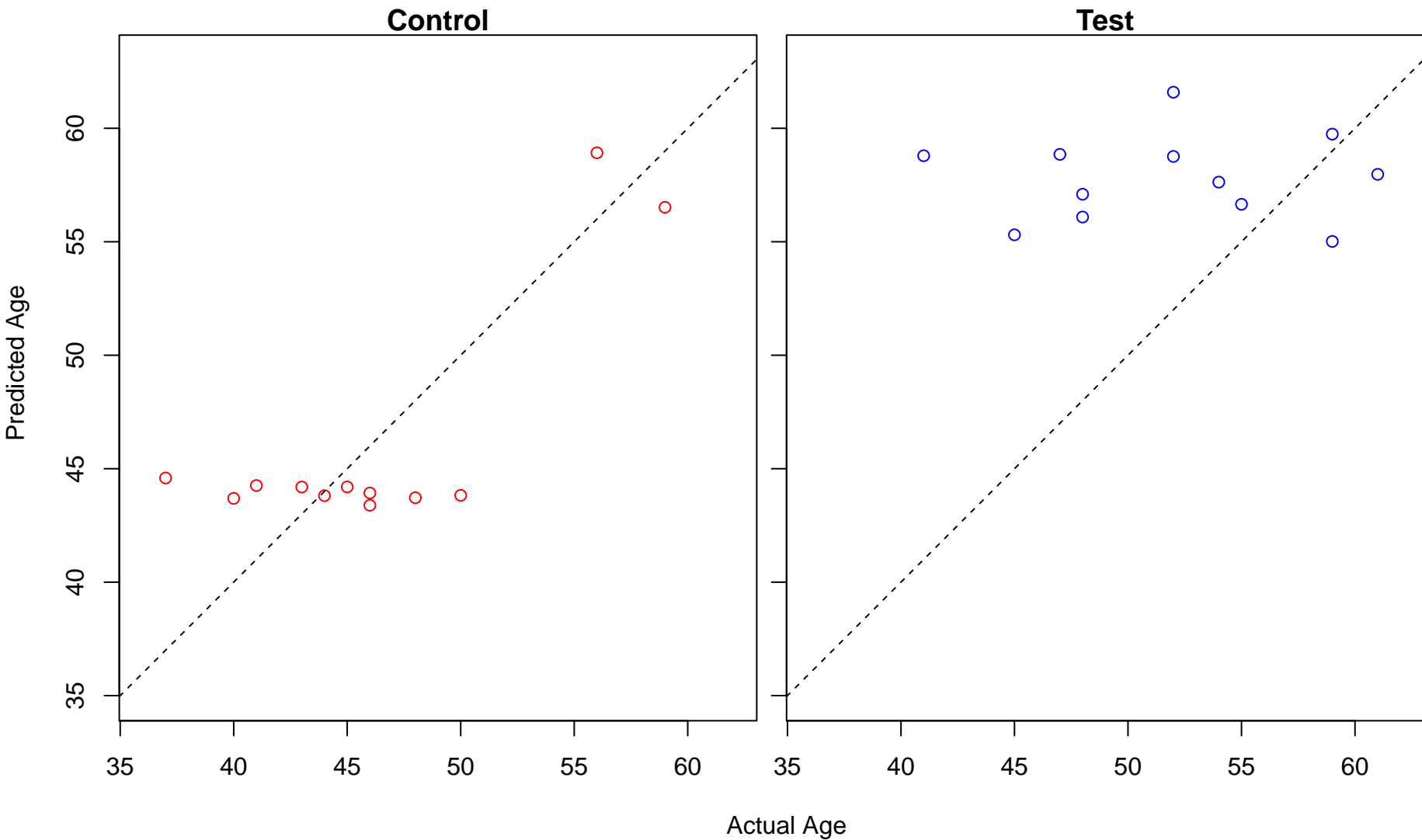
intracellular transport of virus (Score: 3.623218)



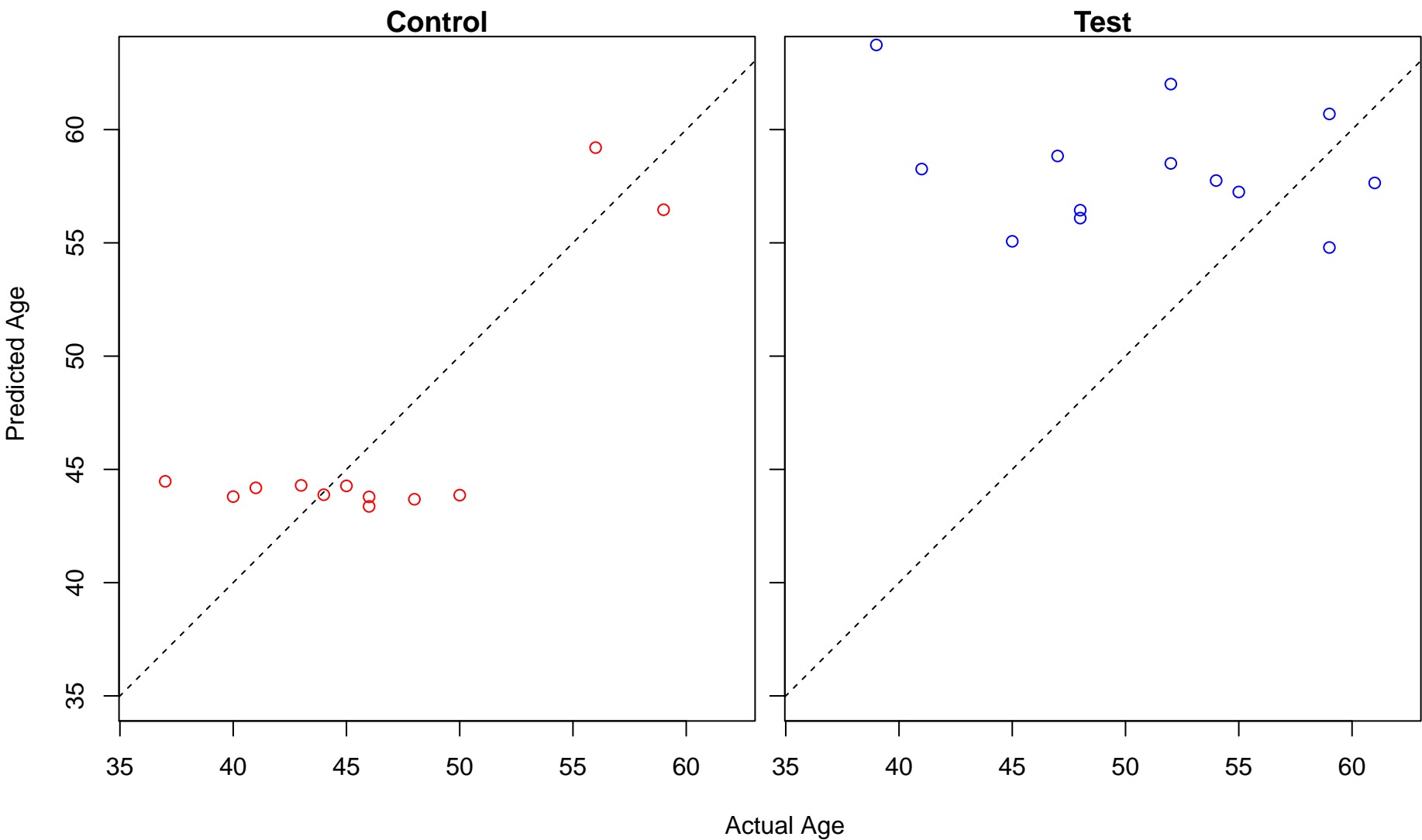
multi-organism intracellular transport (Score: 3.623218)



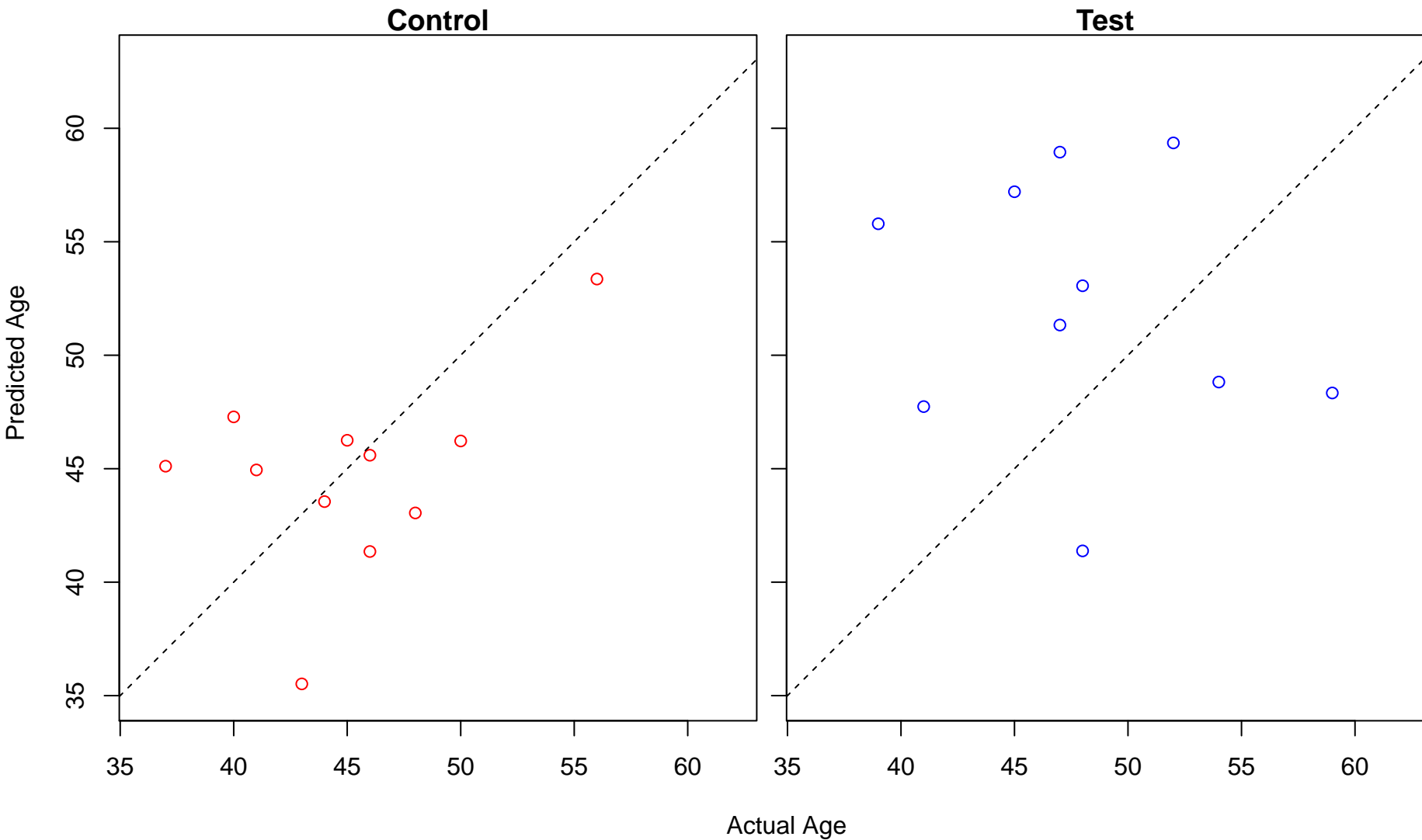
nucleic acid phosphodiester bond hydrolysis (Score: 3.623197)



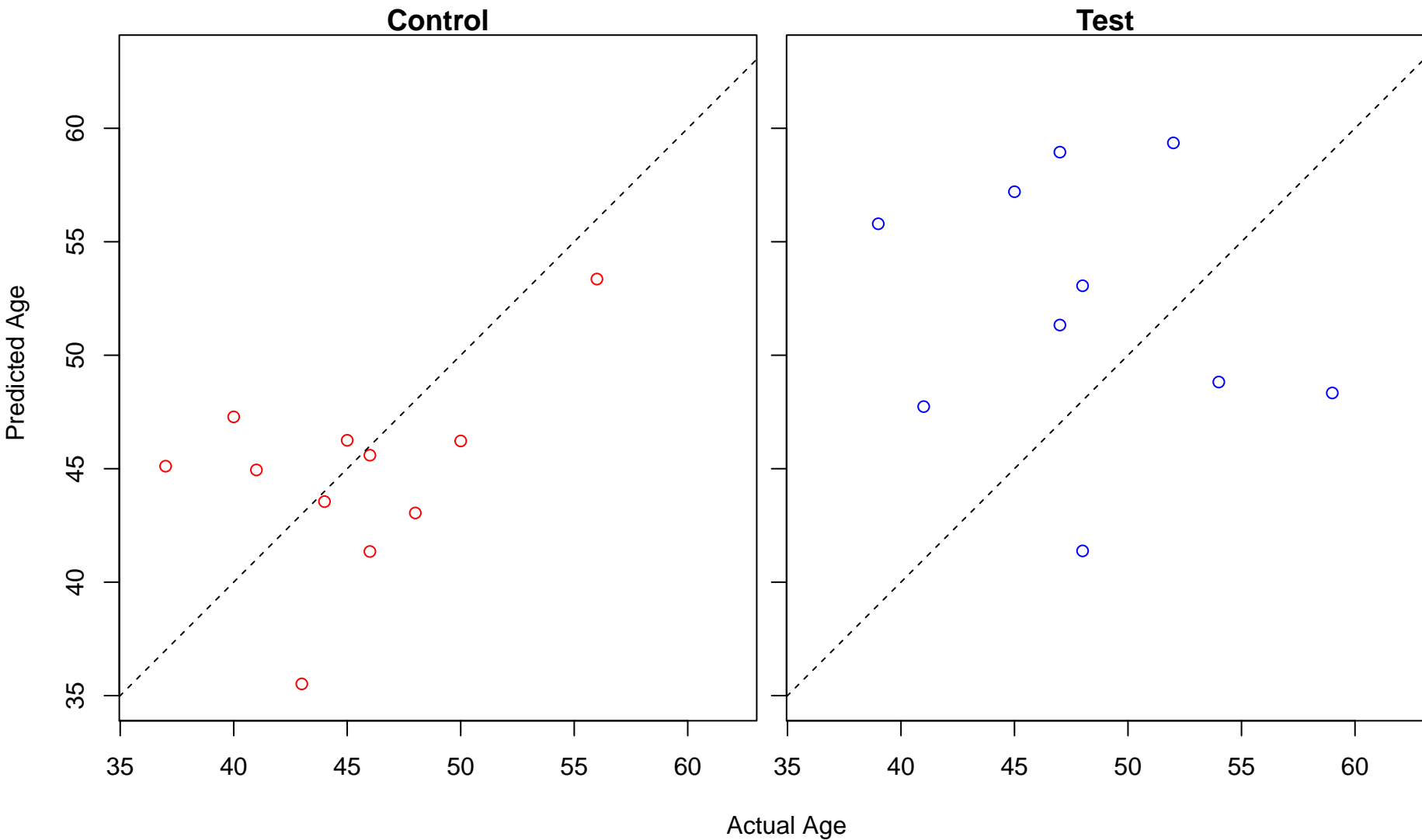
toll-like receptor 4 signaling pathway (Score: 3.623052)



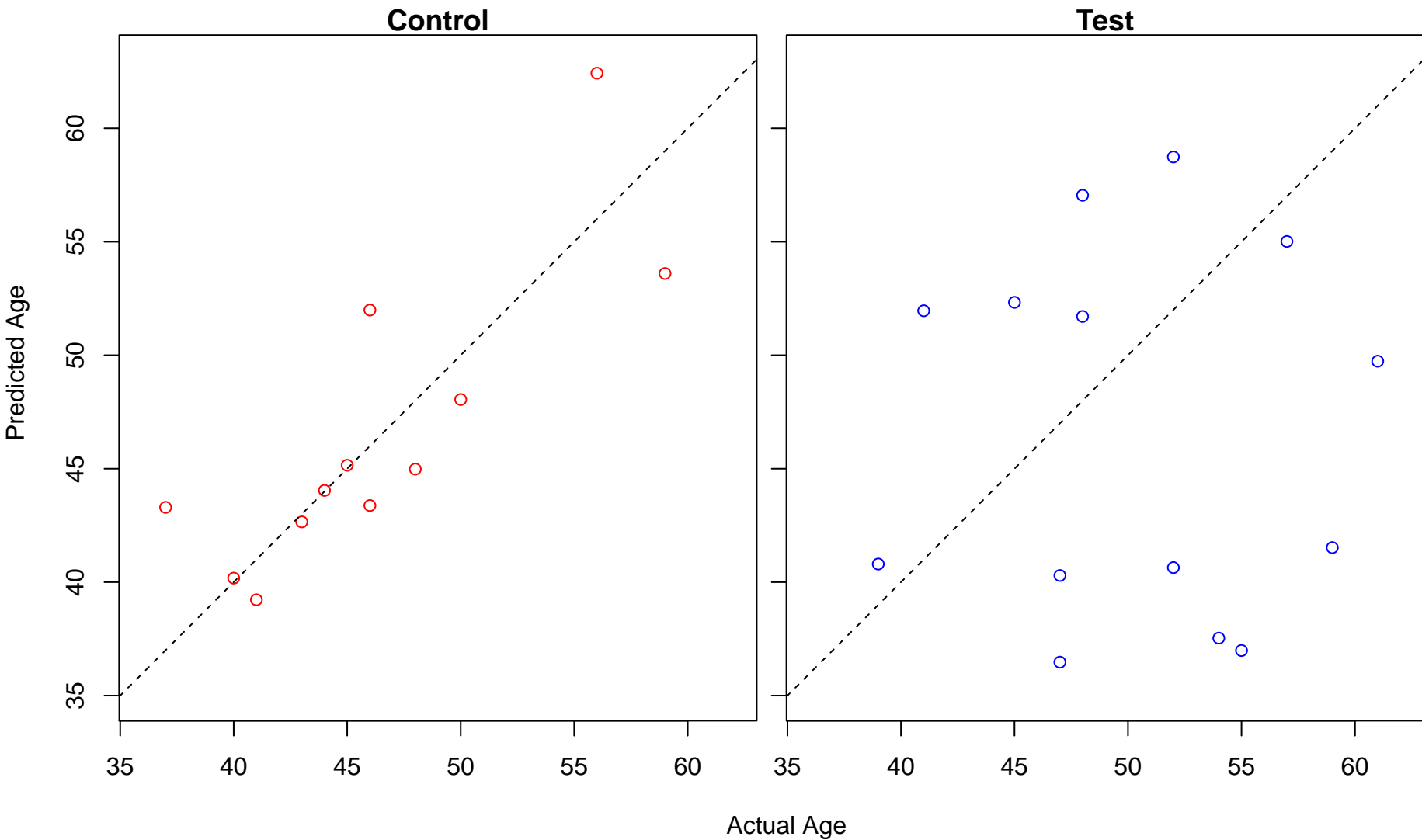
hepoxilin metabolic process (Score: 3.621542)



hepoxilin biosynthetic process (Score: 3.621542)

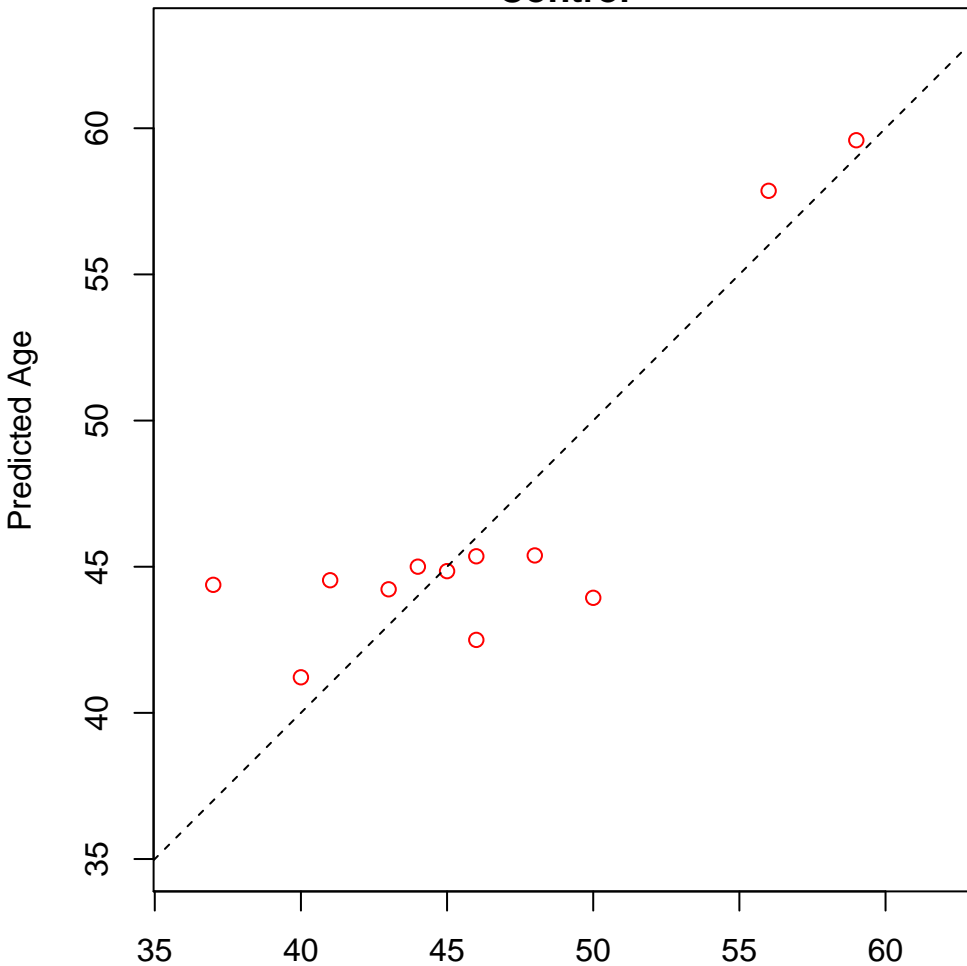


muscle fiber development (Score: 3.620972)

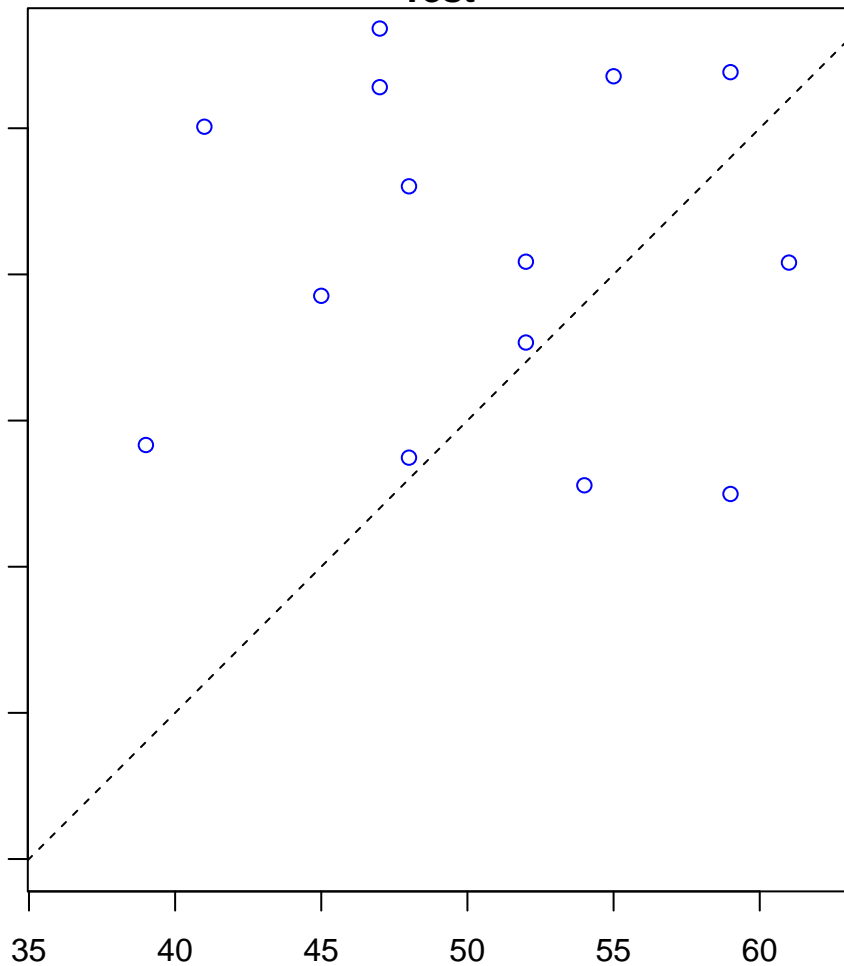


response to tumor necrosis factor (Score: 3.620839)

Control

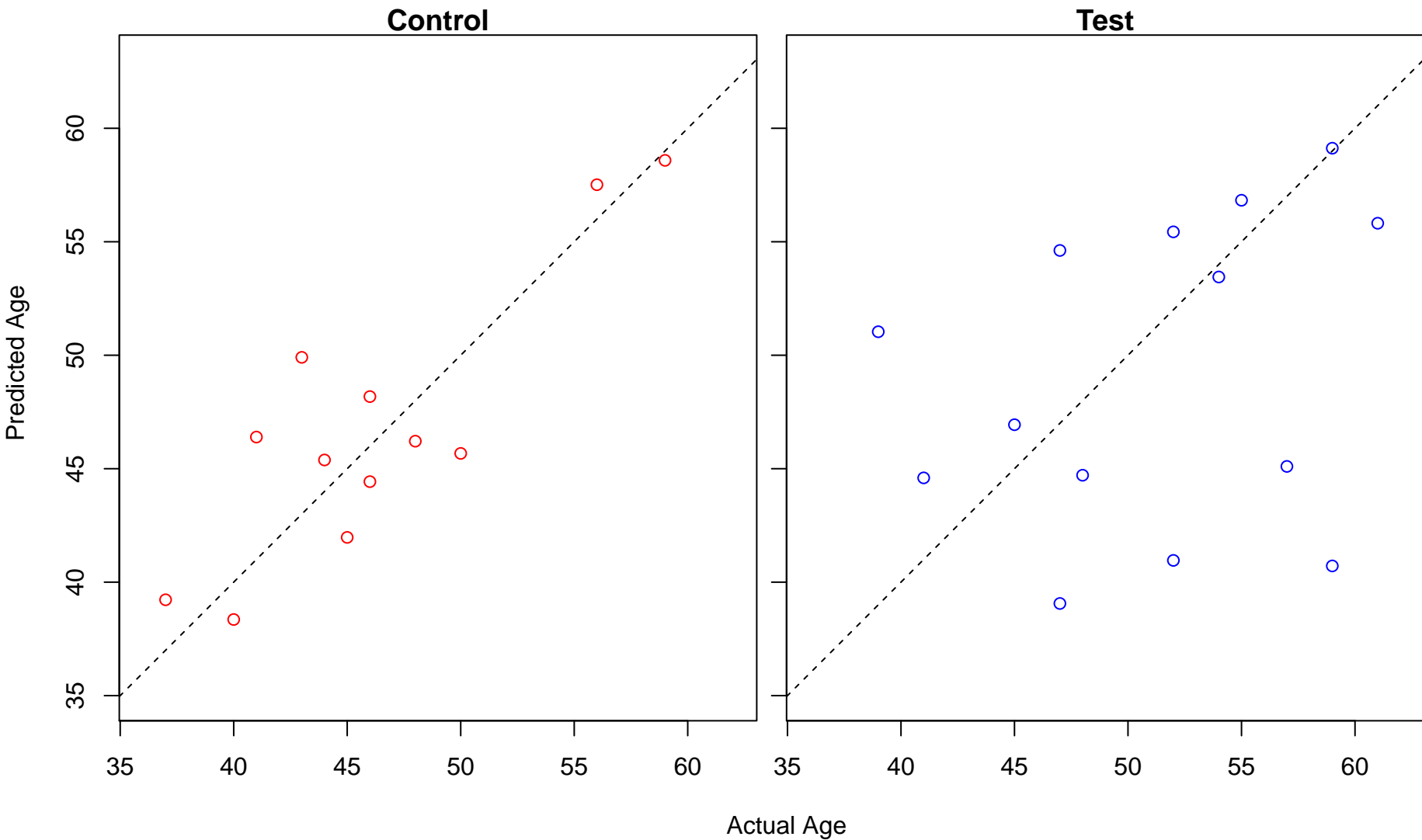


Test

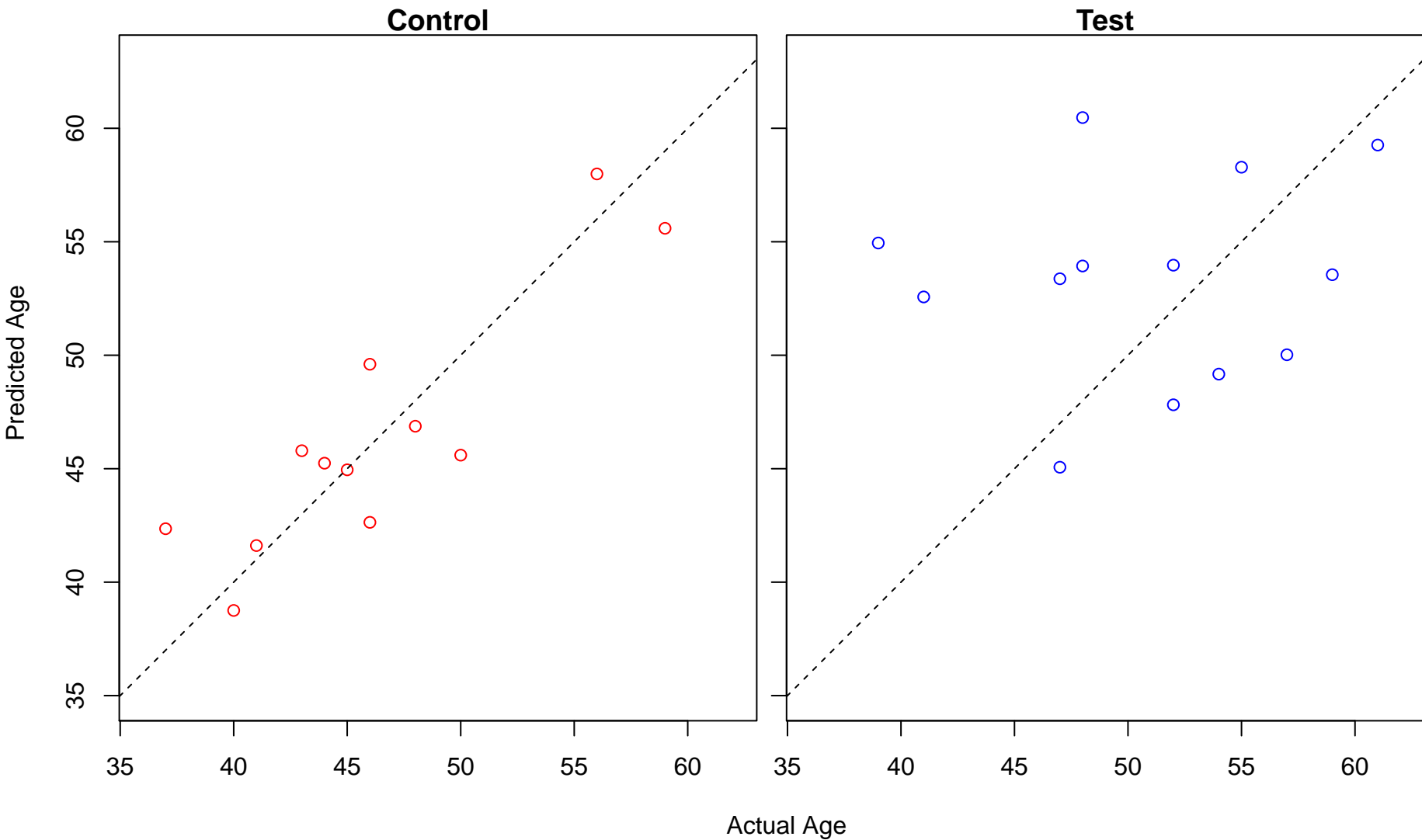


Actual Age

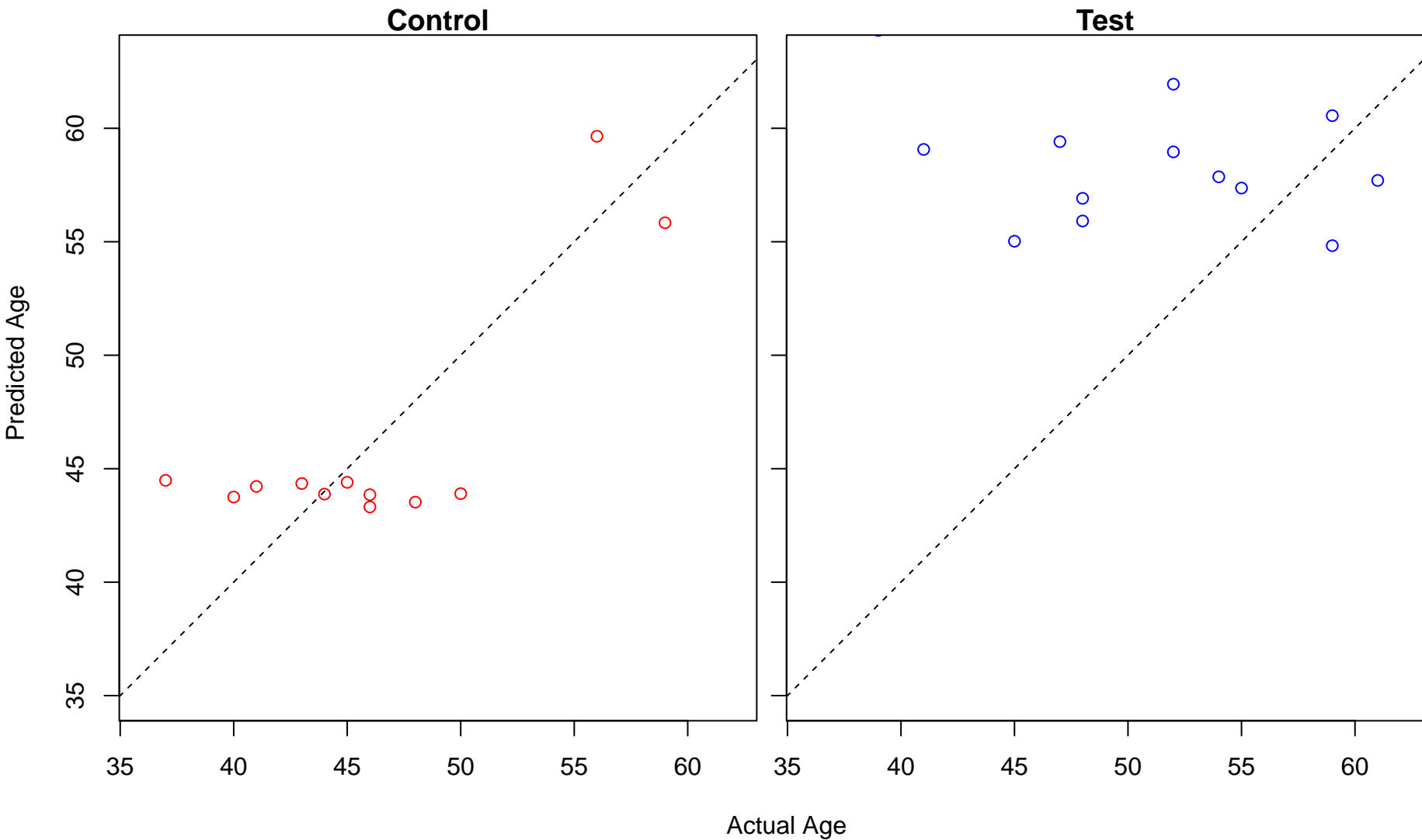
synapse organization (Score: 3.620746)



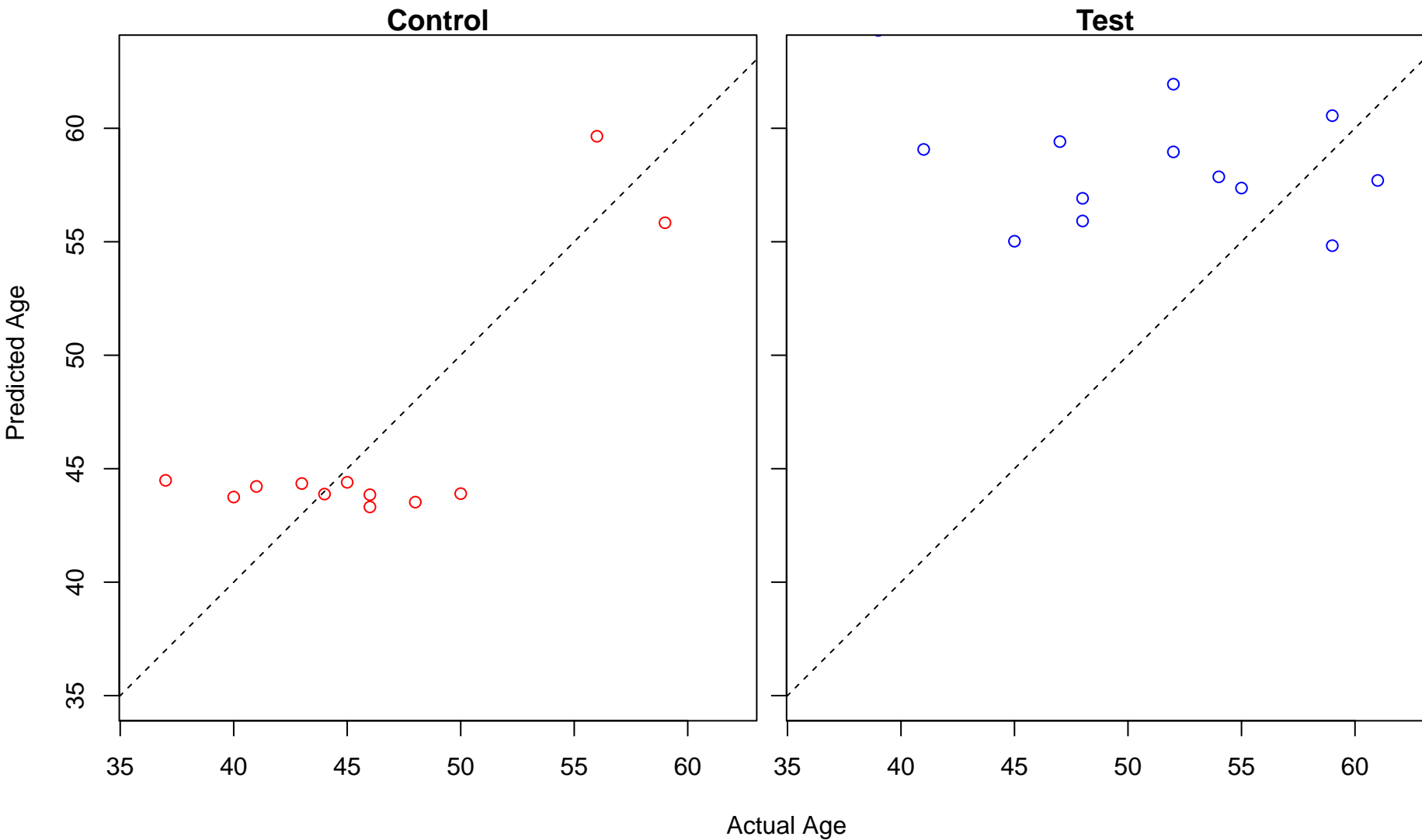
positive regulation of lipid metabolic process (Score: 3.619475)



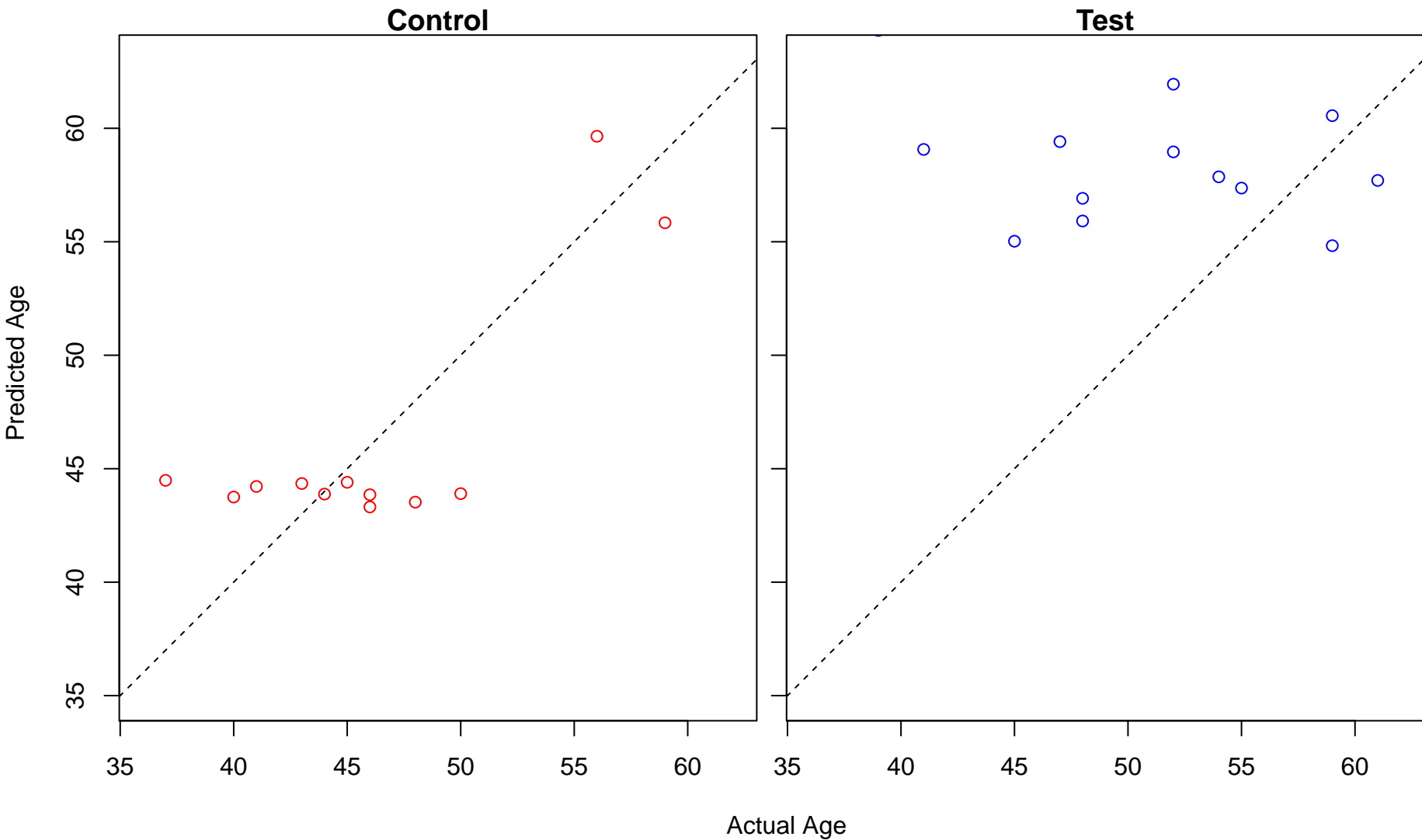
multi-organism transport (Score: 3.617036)



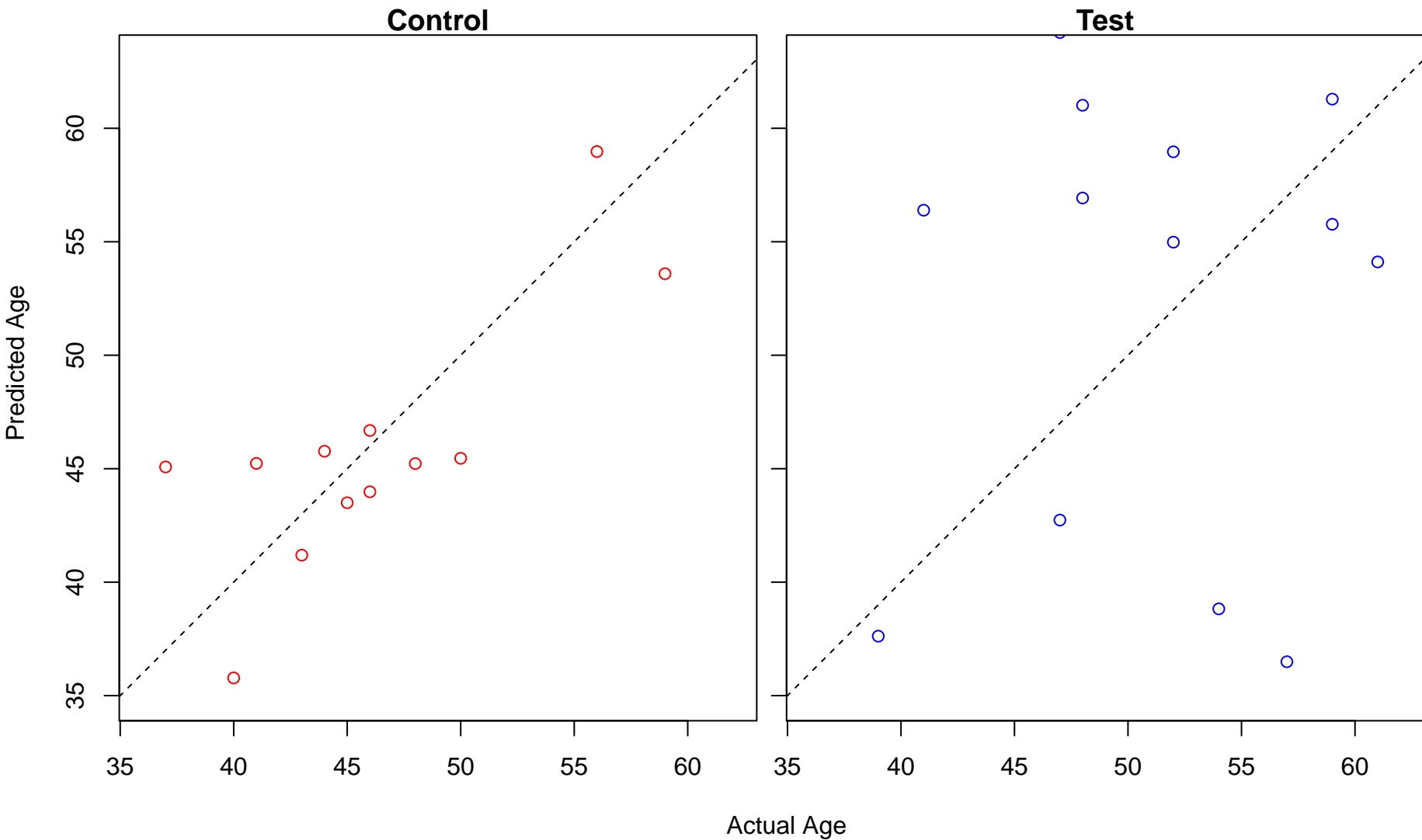
transport of virus (Score: 3.617036)



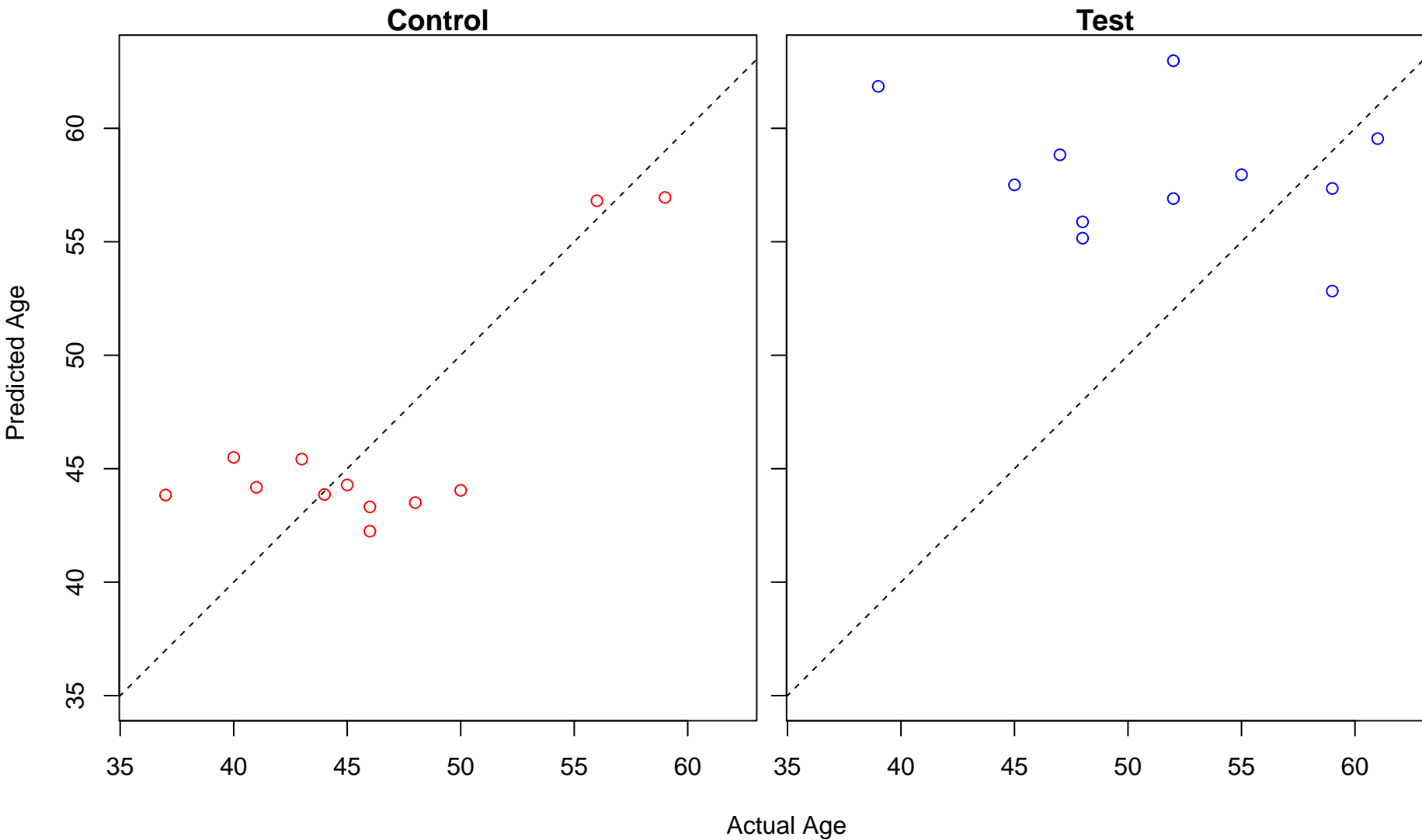
multi-organism localization (Score: 3.617036)



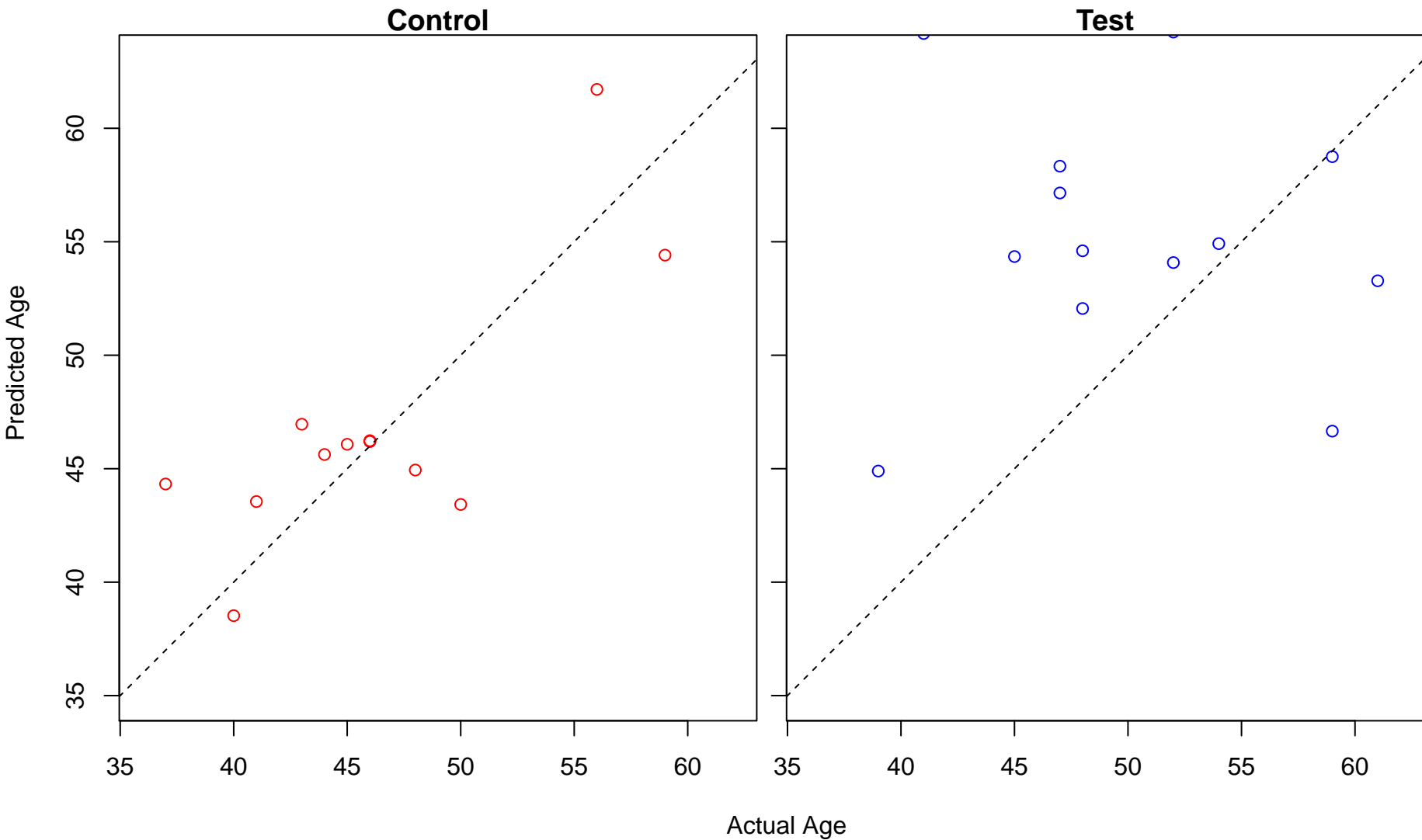
negative regulation of protein tyrosine kinase activity (Score: 3.614306)



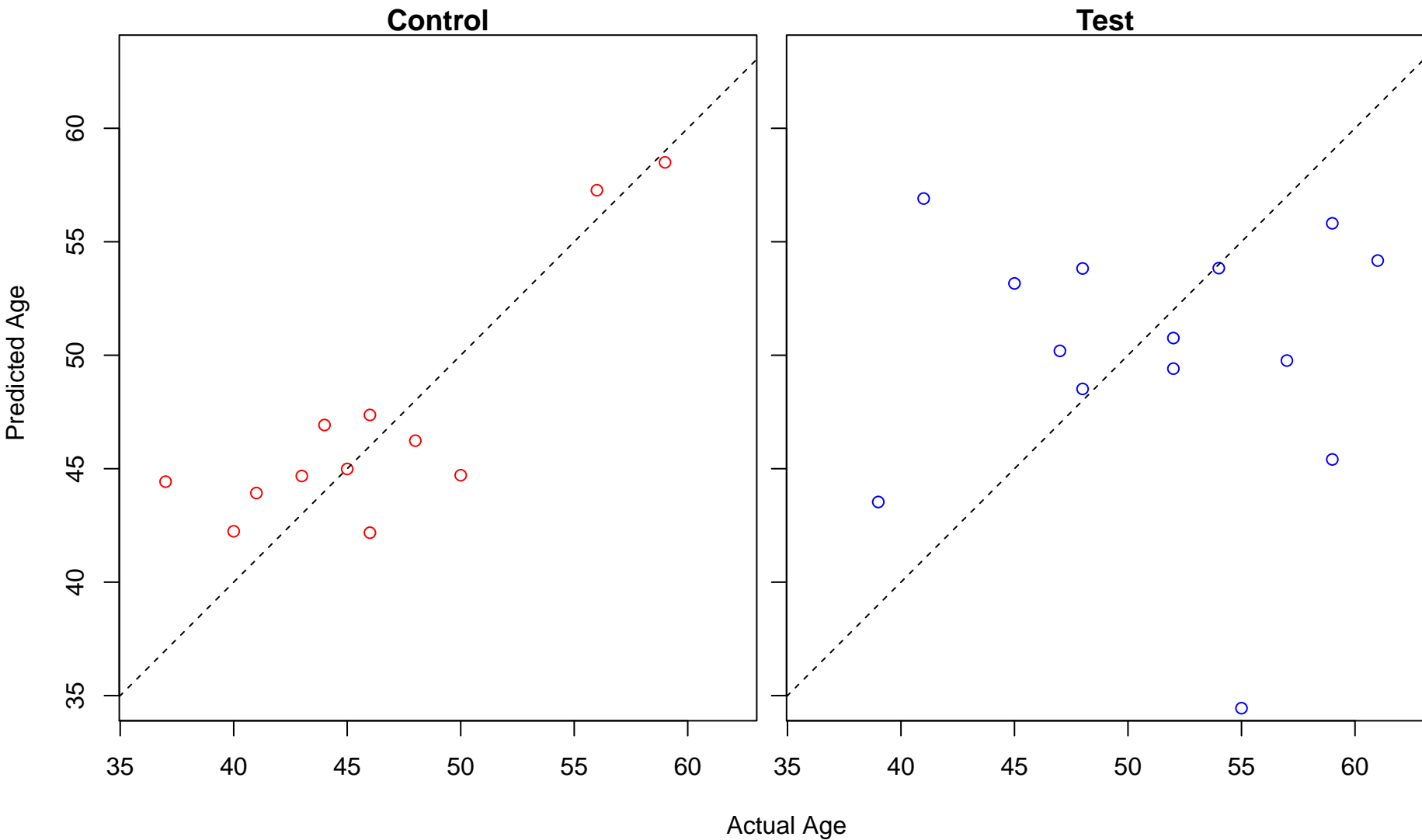
nucleotide phosphorylation (Score: 3.612951)



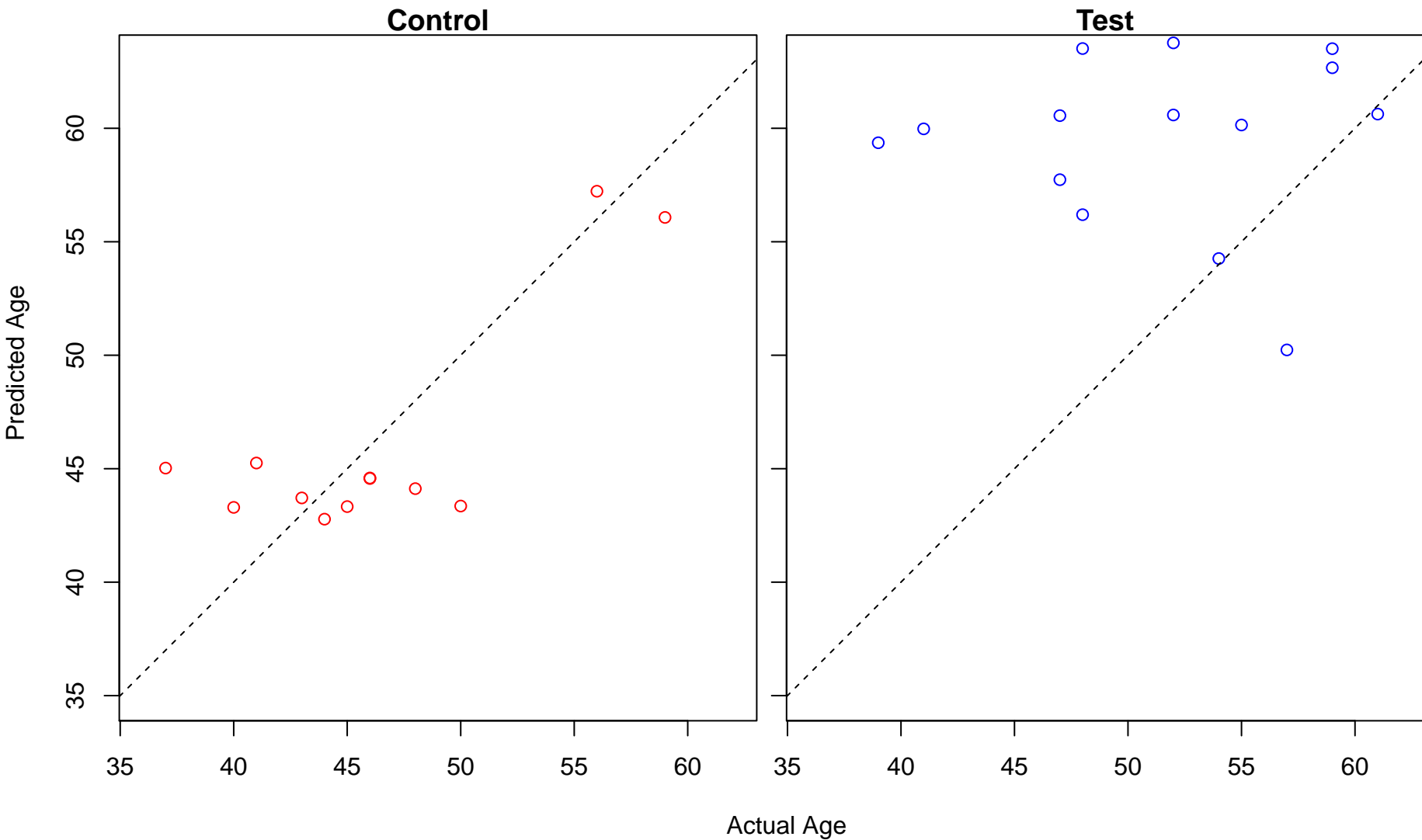
granulocyte migration (Score: 3.612756)



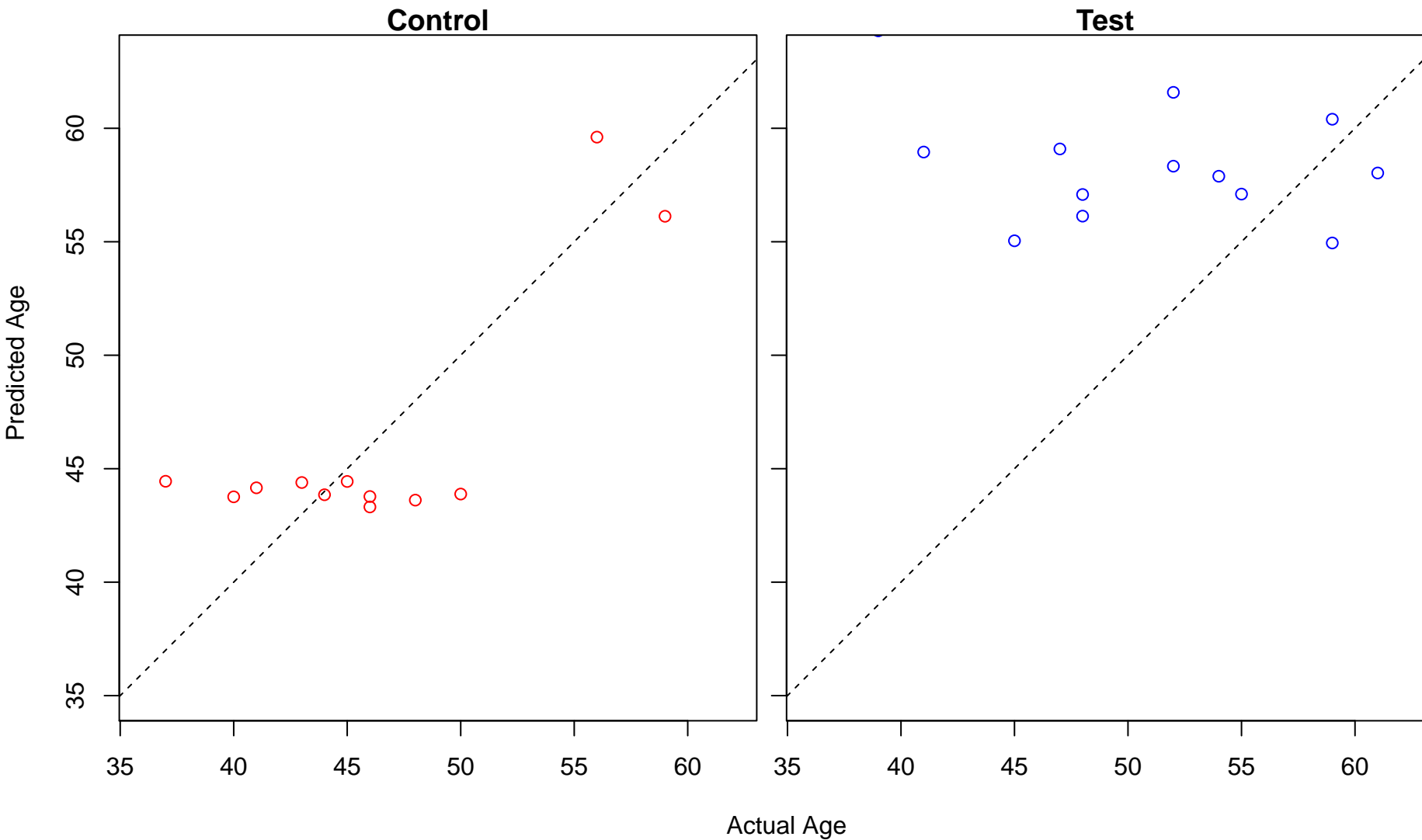
regulation of T cell activation (Score: 3.612406)



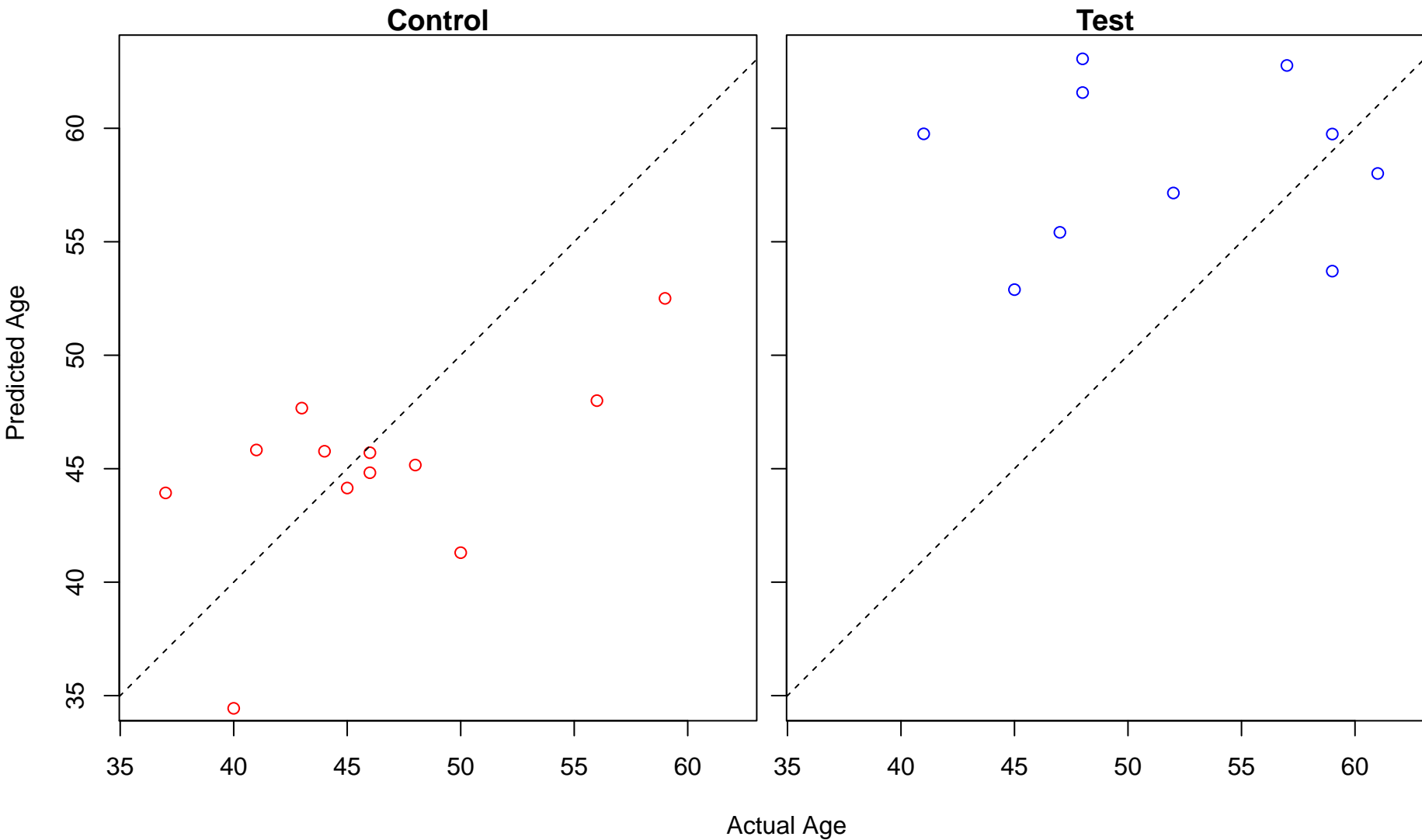
positive regulation of gliogenesis (Score: 3.609589)



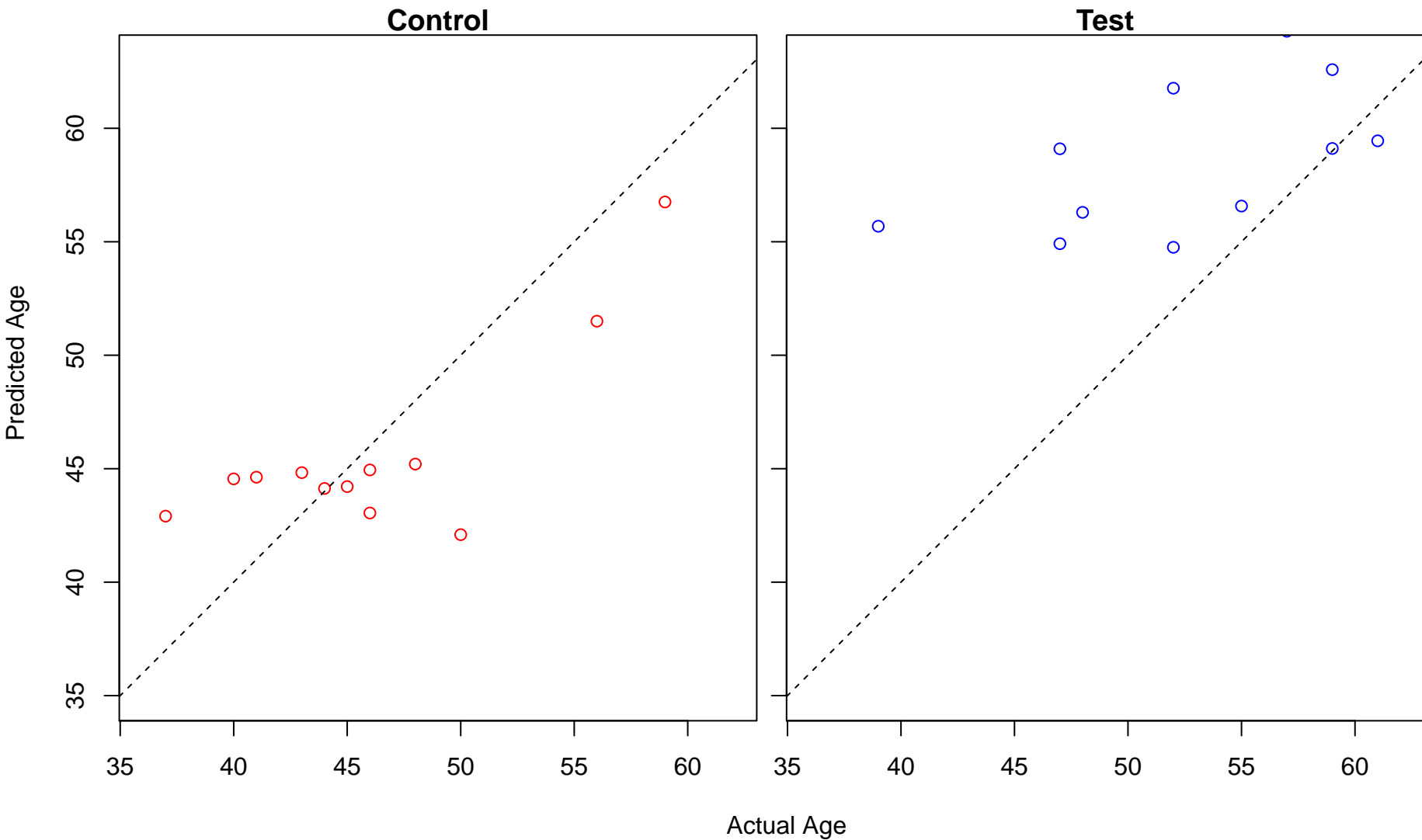
activation of MAPK activity (Score: 3.608125)



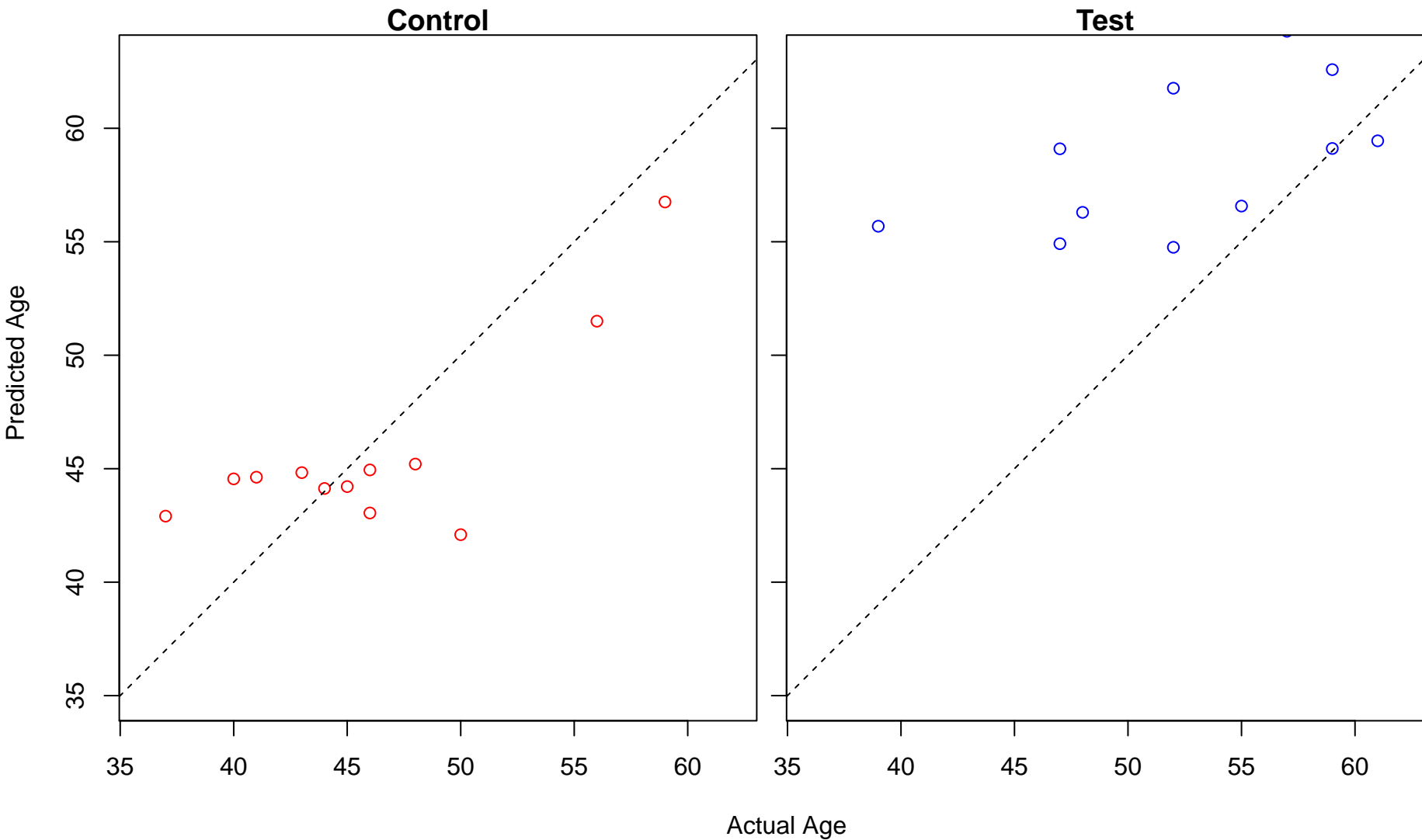
positive T cell selection (Score: 3.599344)



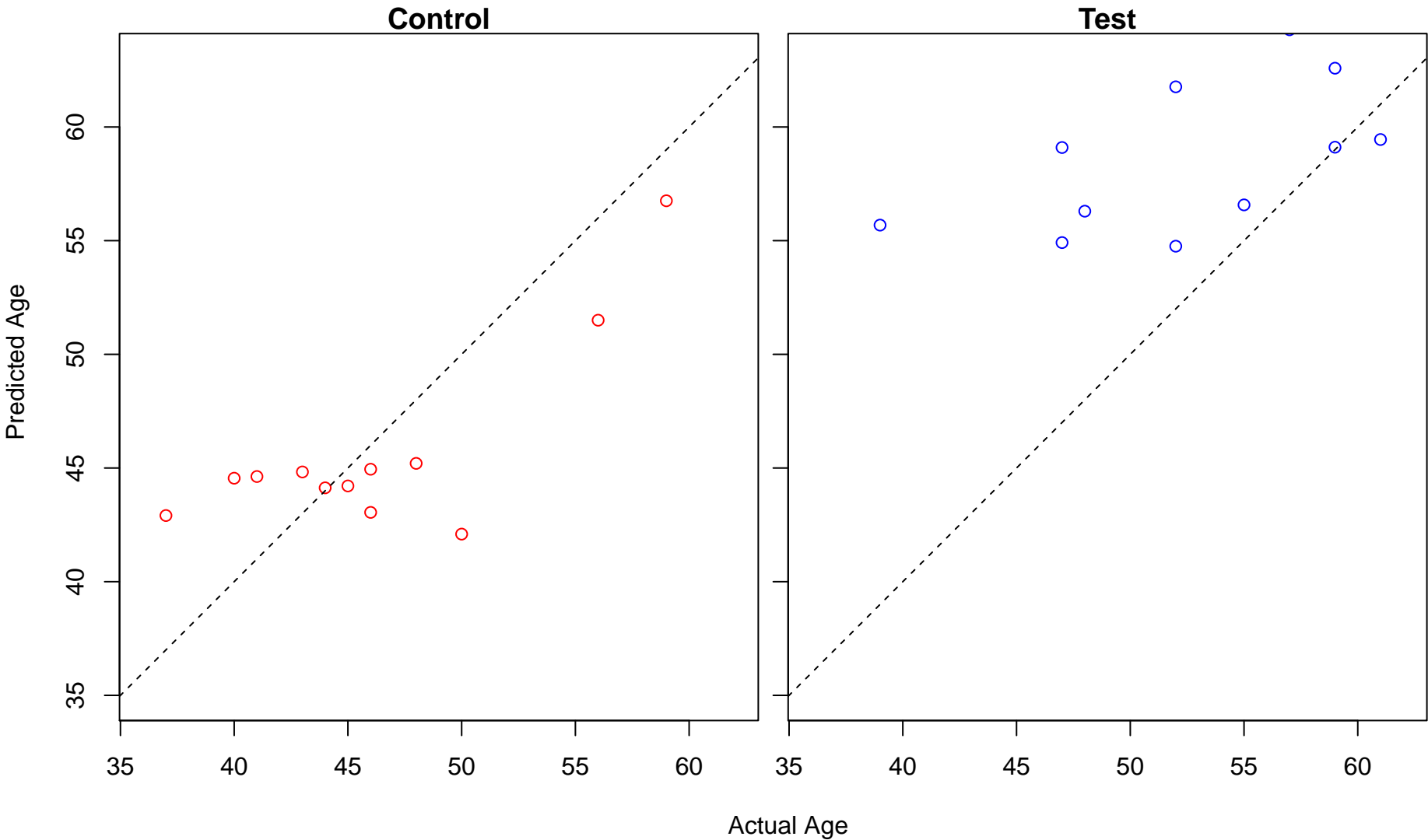
L-phenylalanine metabolic process (Score: 3.599292)



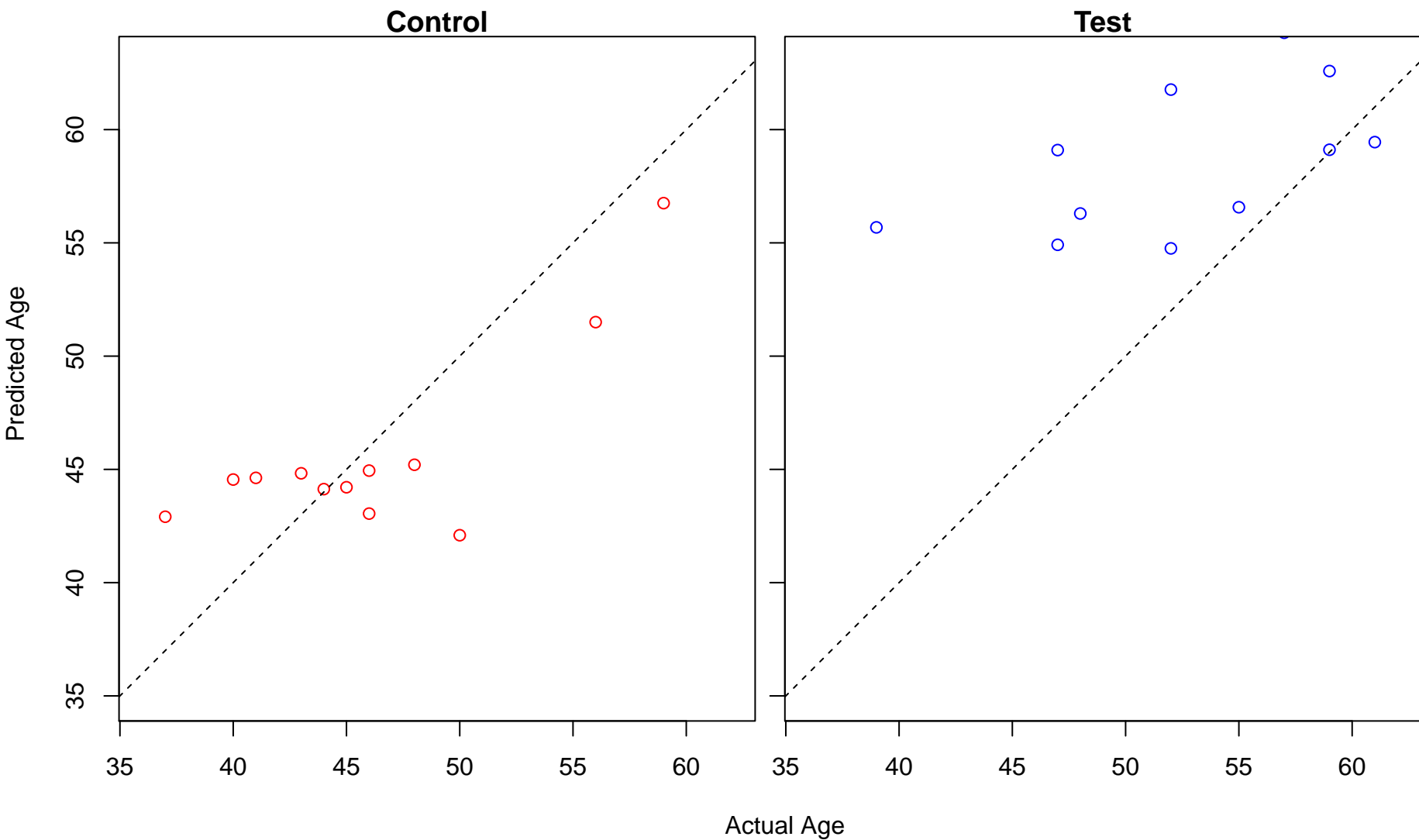
L-phenylalanine catabolic process (Score: 3.599292)



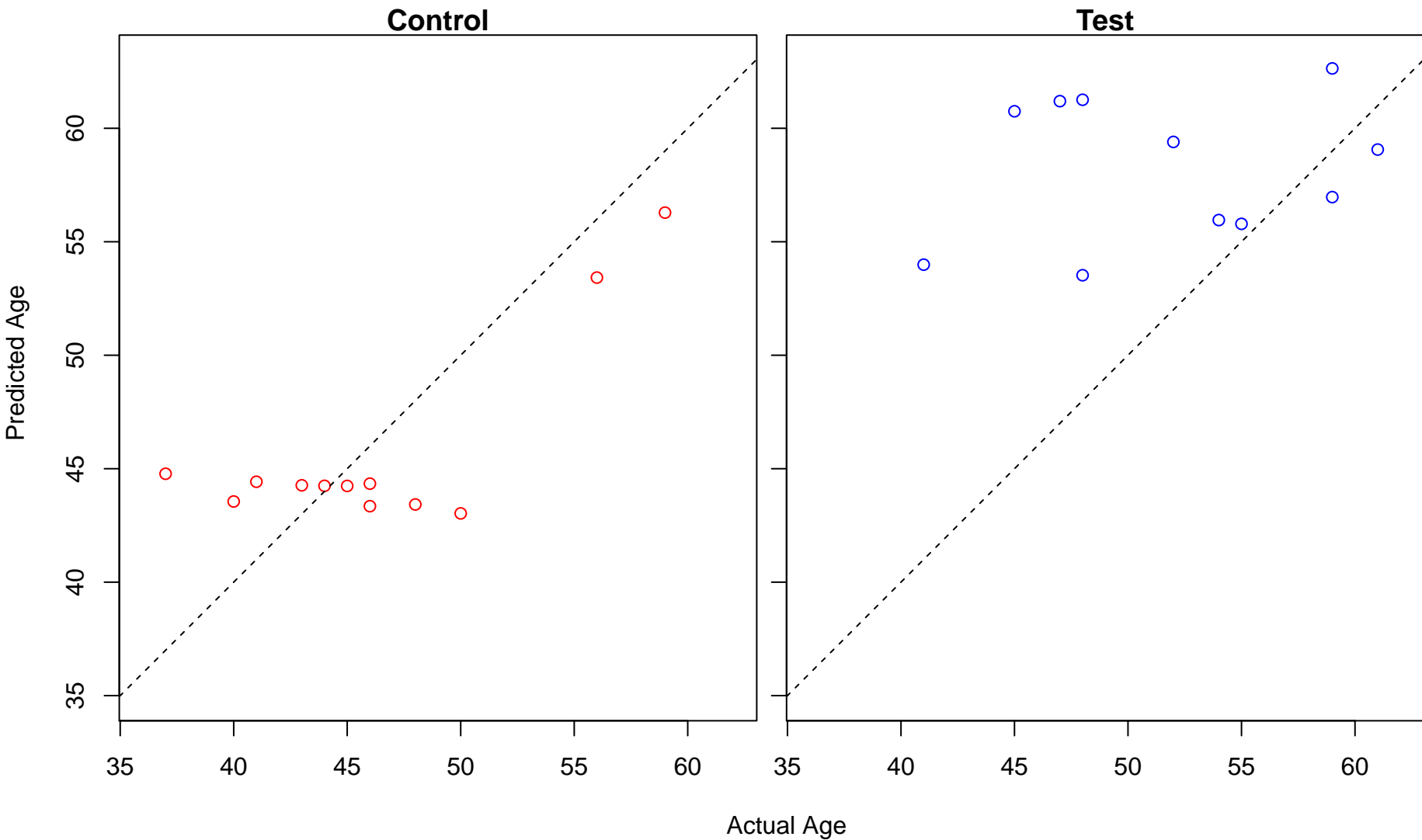
erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process (Score: 3.59929)



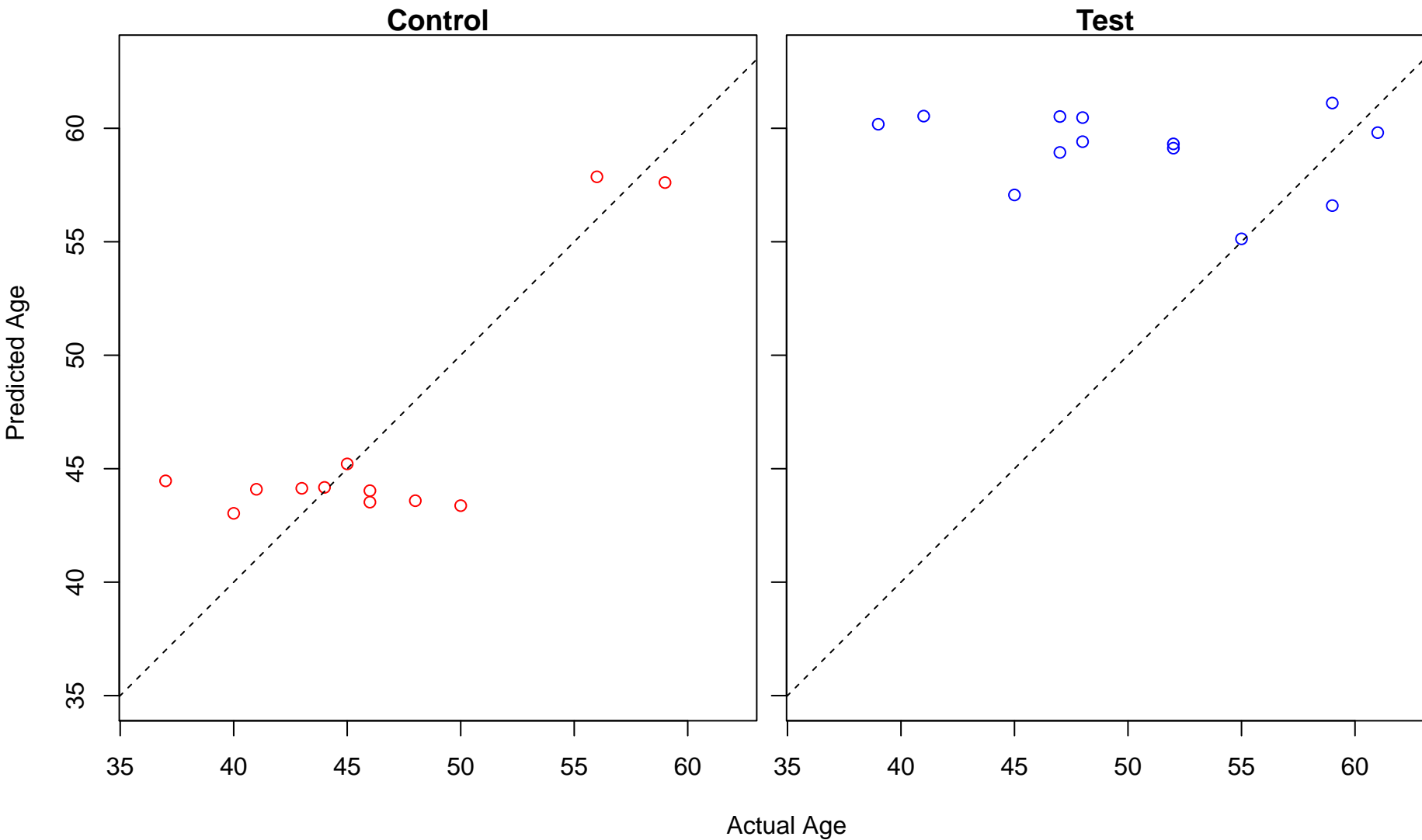
erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process (Score: 3.59929)



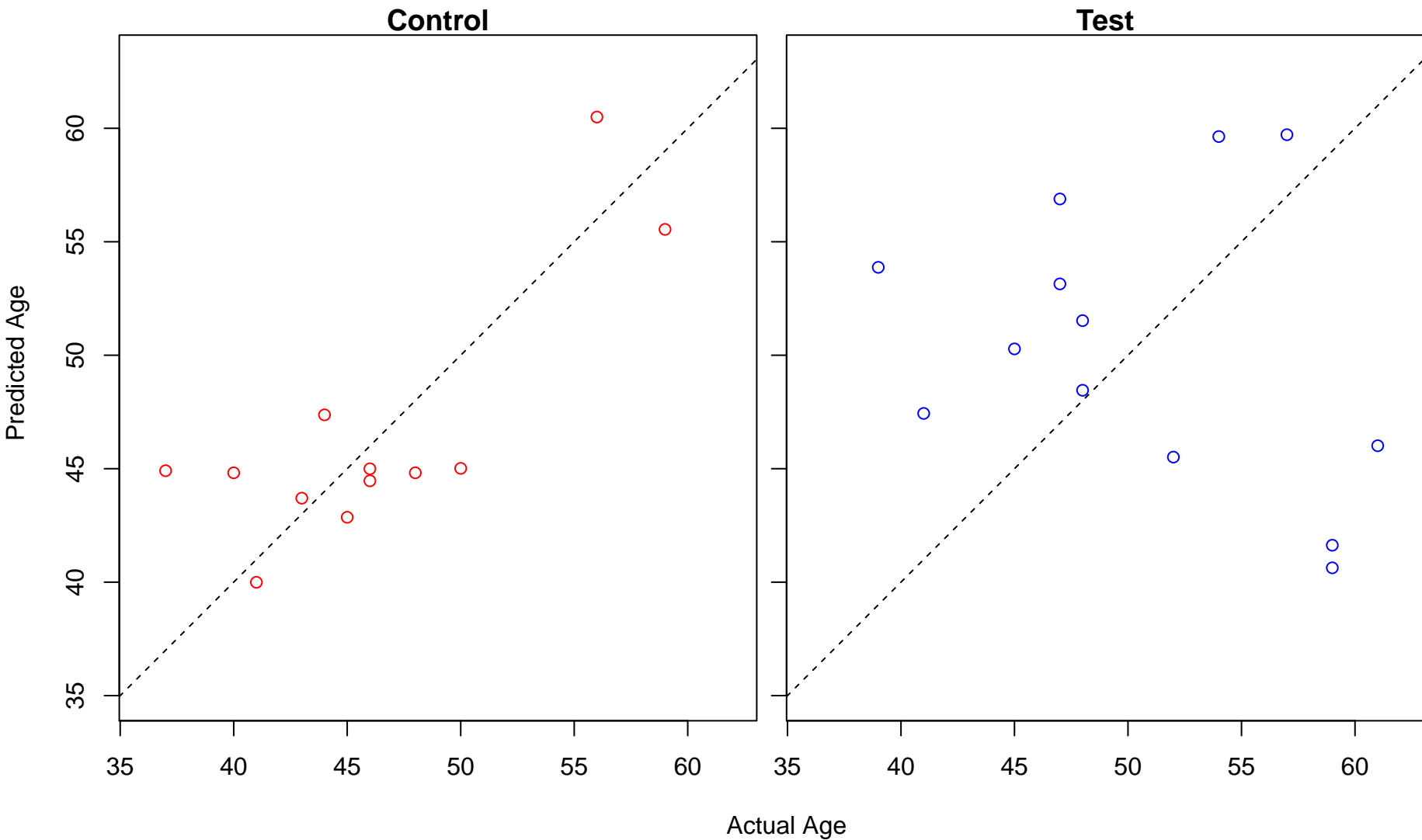
ribonucleotide catabolic process (Score: 3.598595)



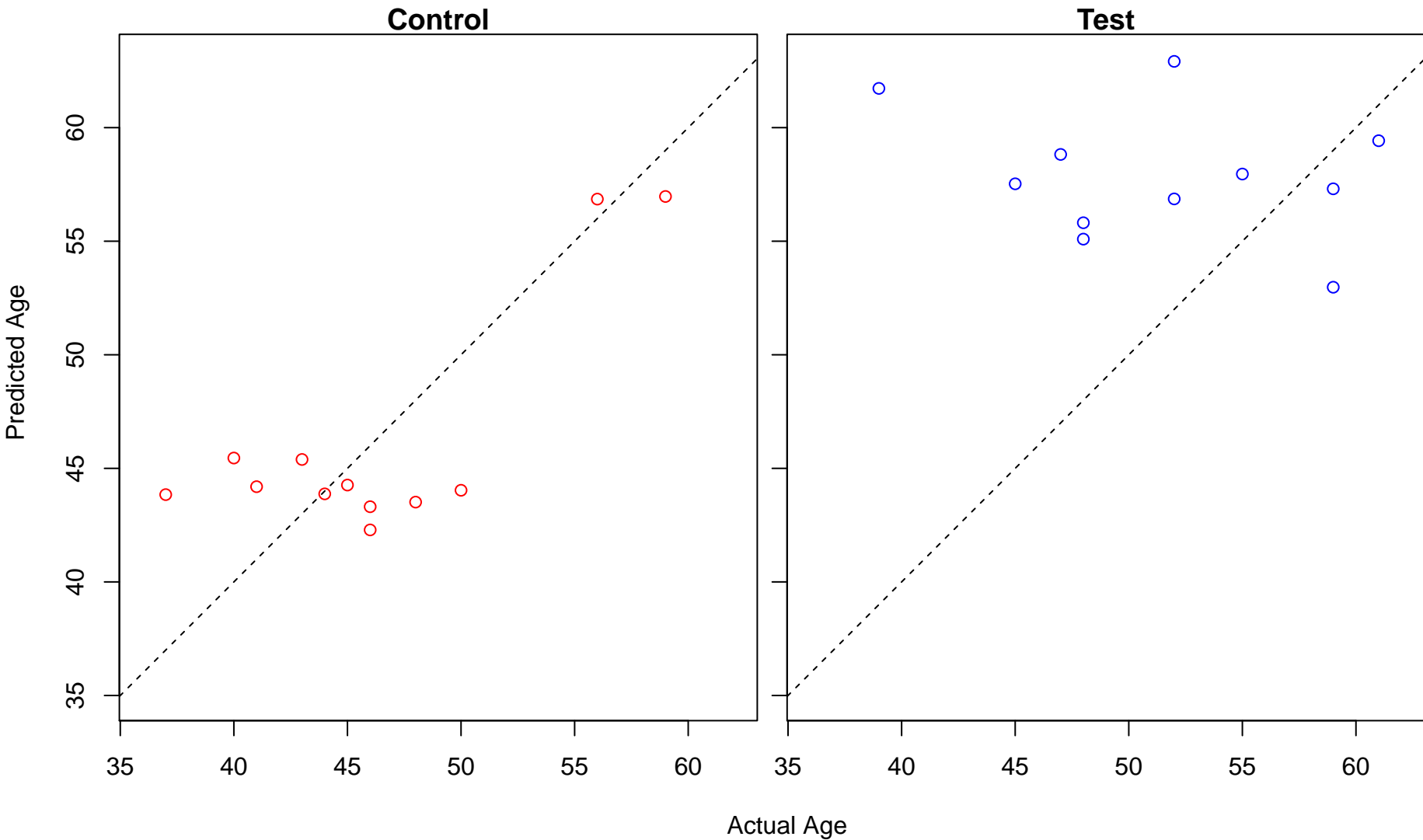
mitochondrion morphogenesis (Score: 3.598342)



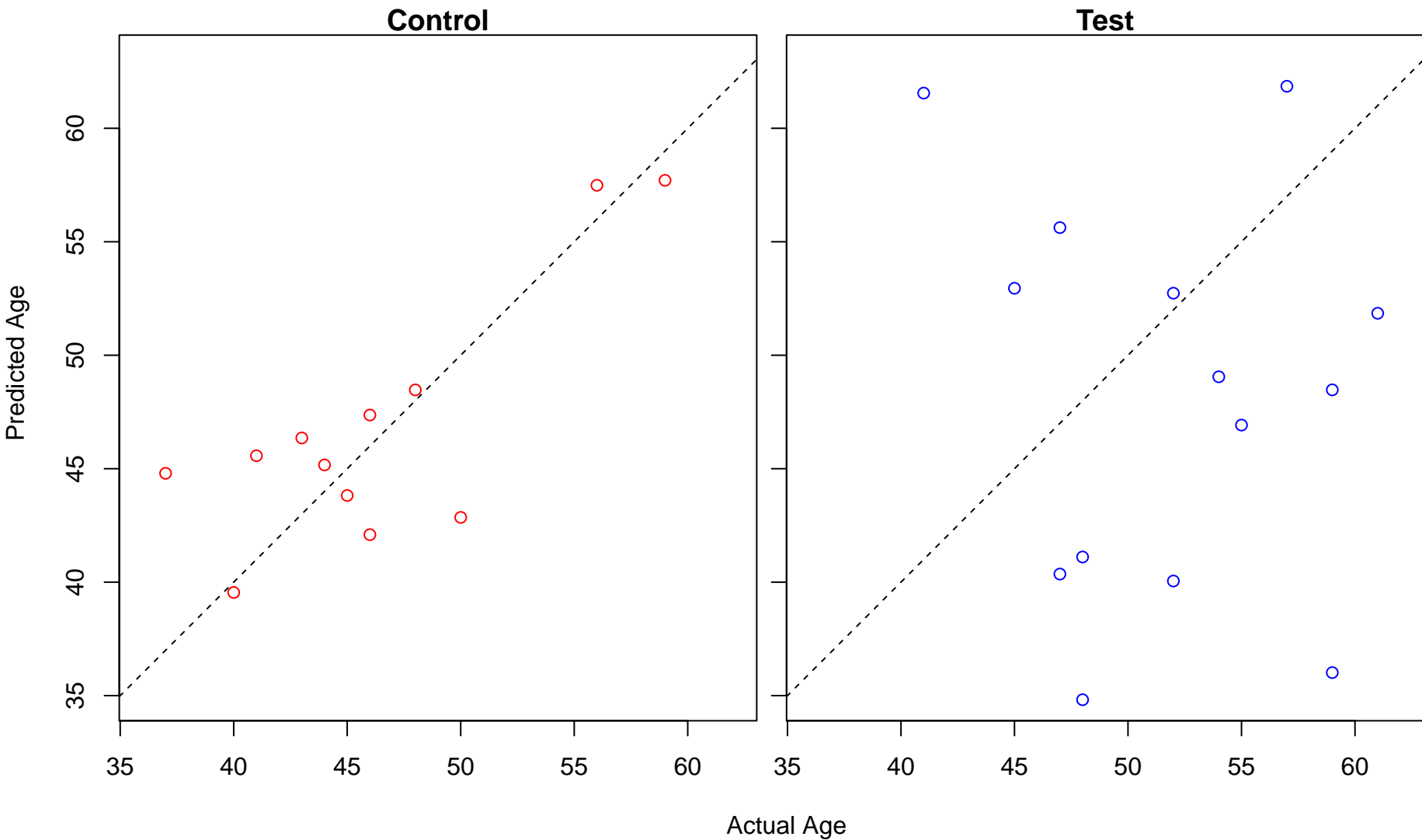
sulfate transmembrane transport (Score: 3.597095)



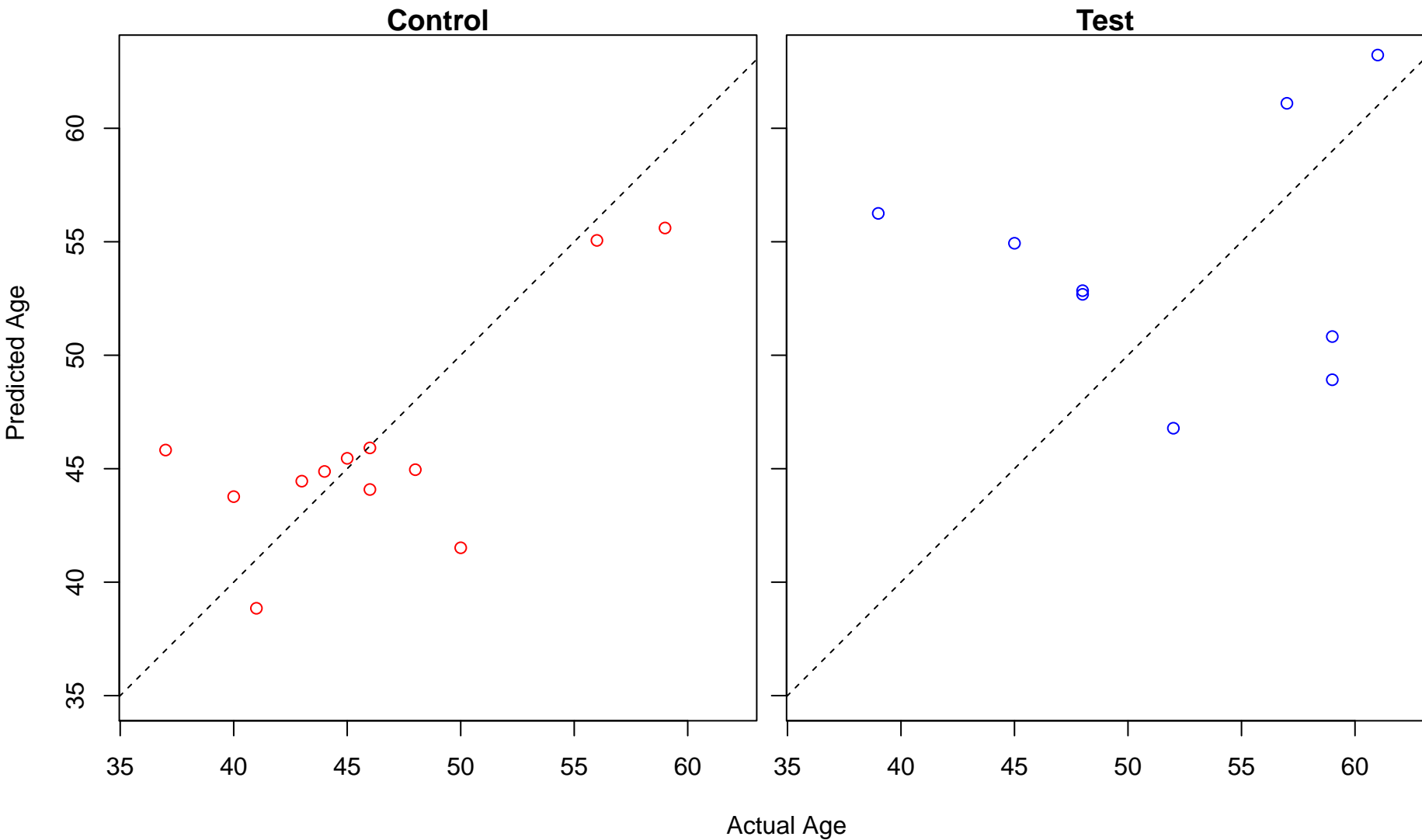
nucleoside diphosphate metabolic process (Score: 3.595450)



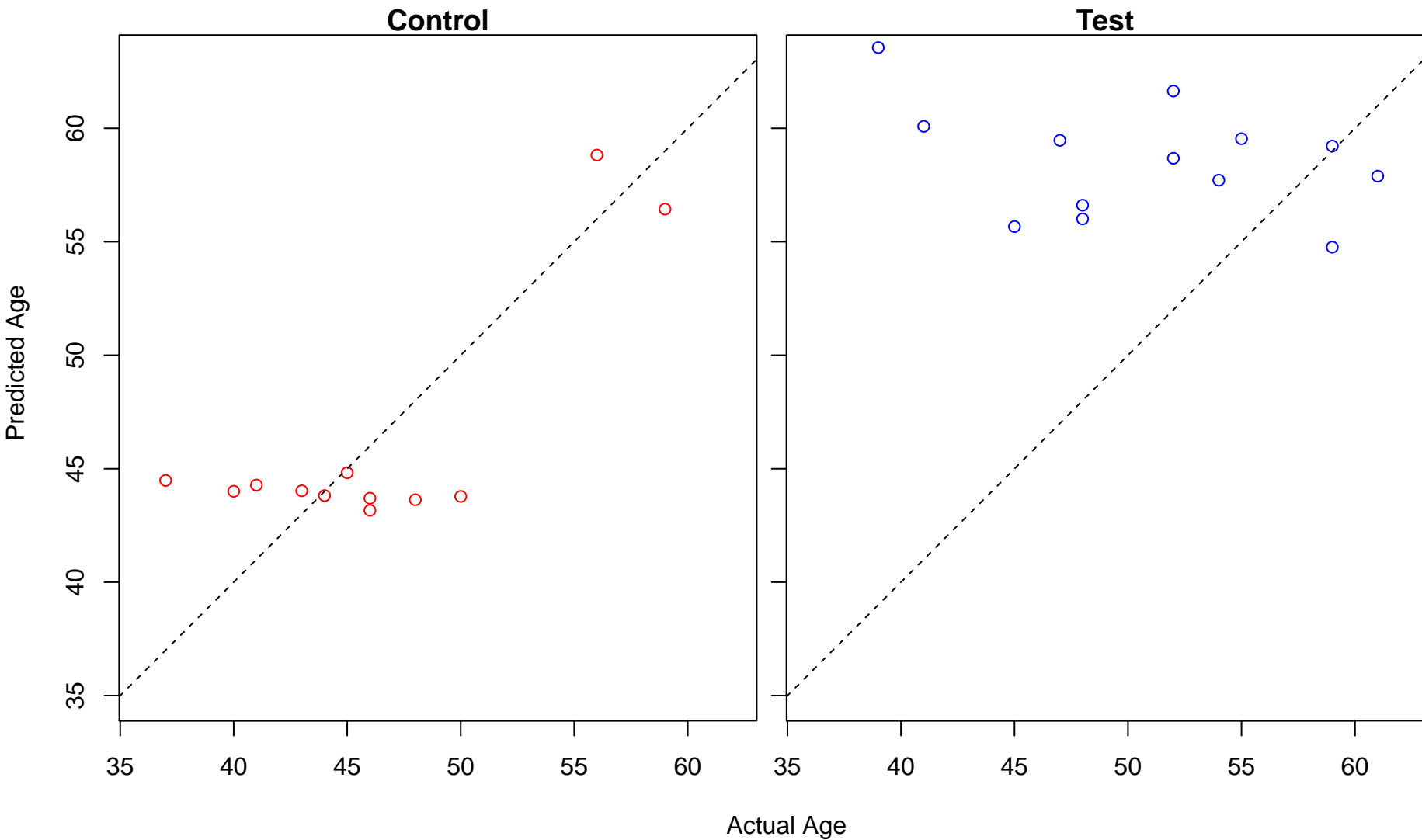
regulation of endocytosis (Score: 3.593031)



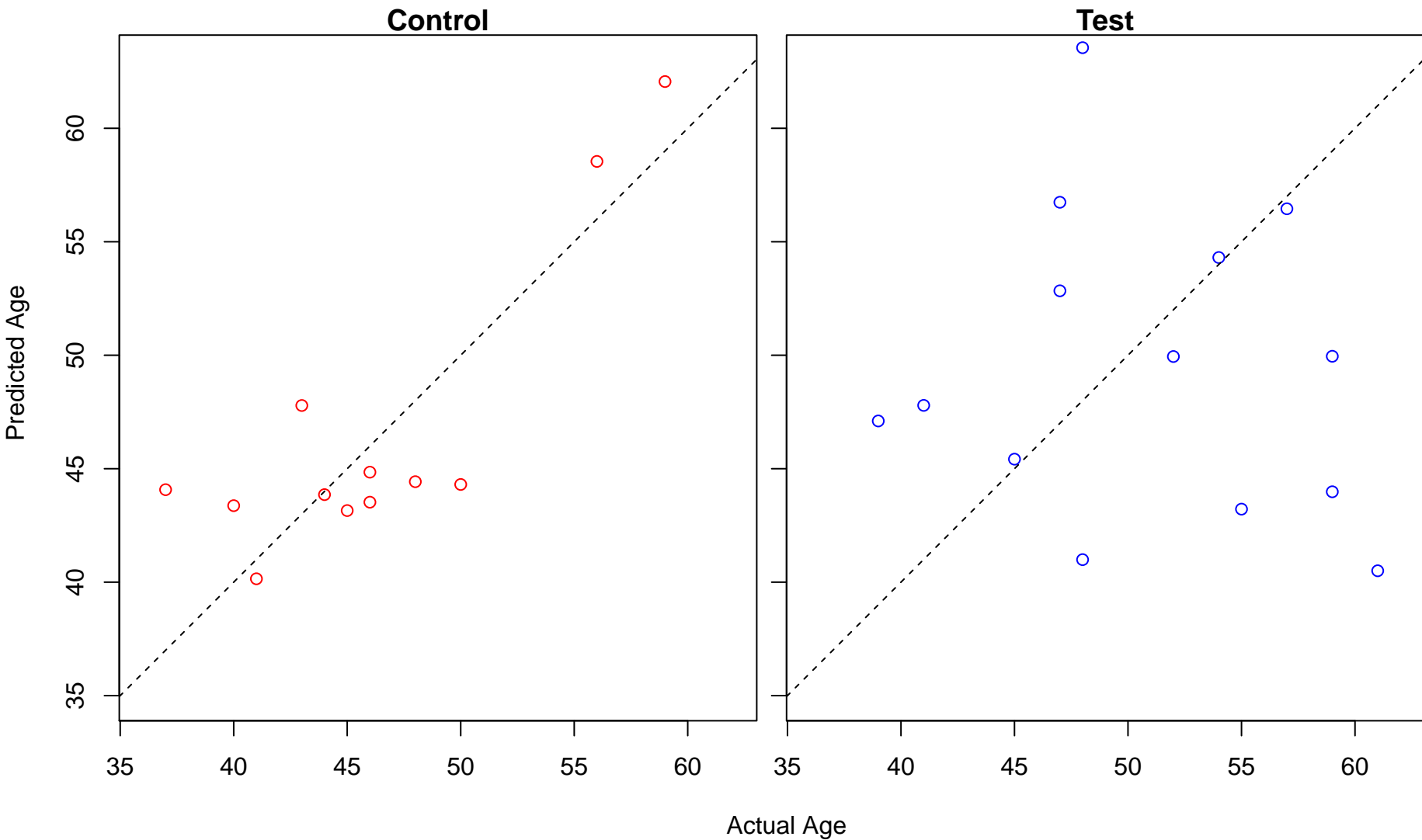
regulation of triglyceride biosynthetic process (Score: 3.592846)



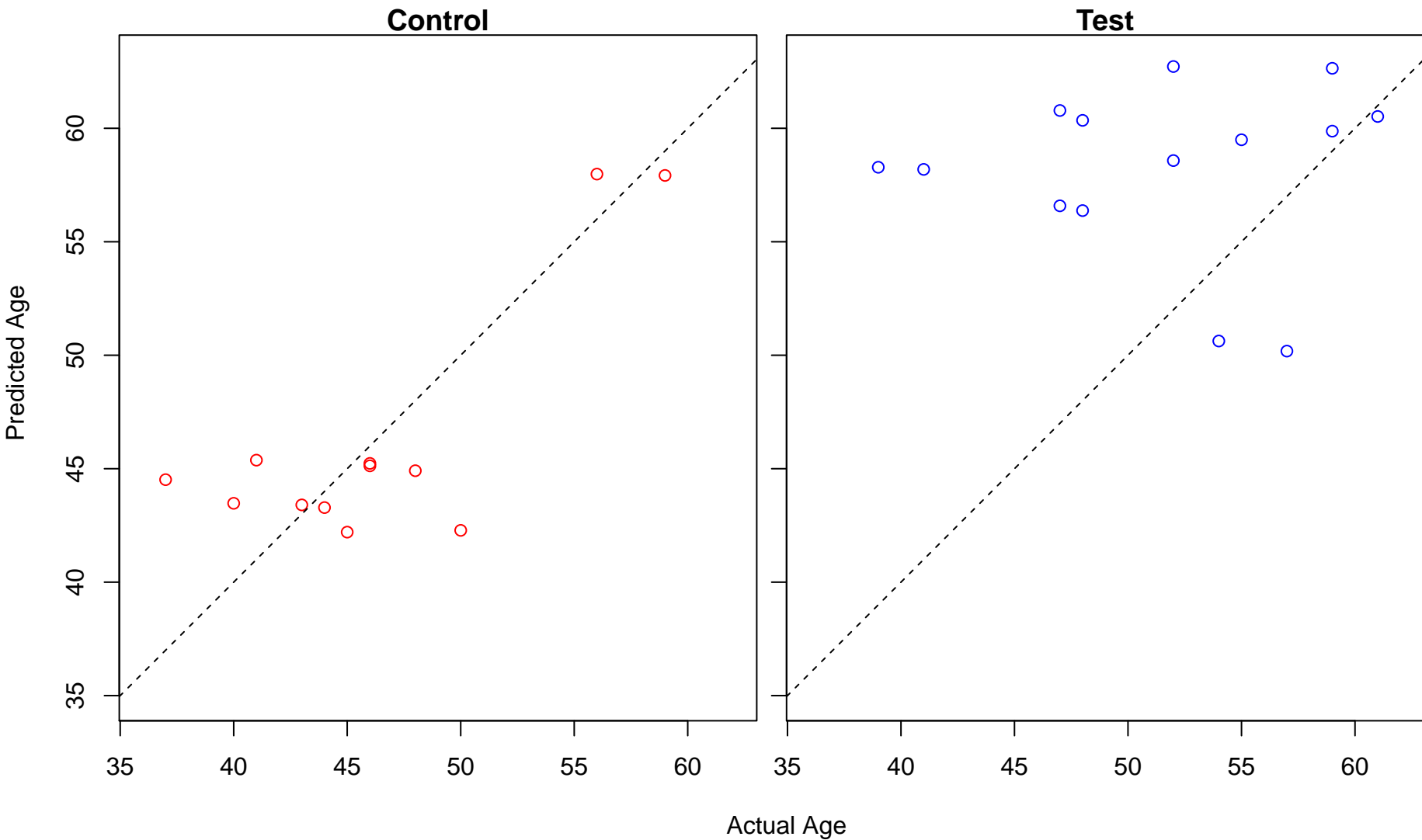
negative regulation of canonical Wnt signaling pathway (Score: 3.591955)



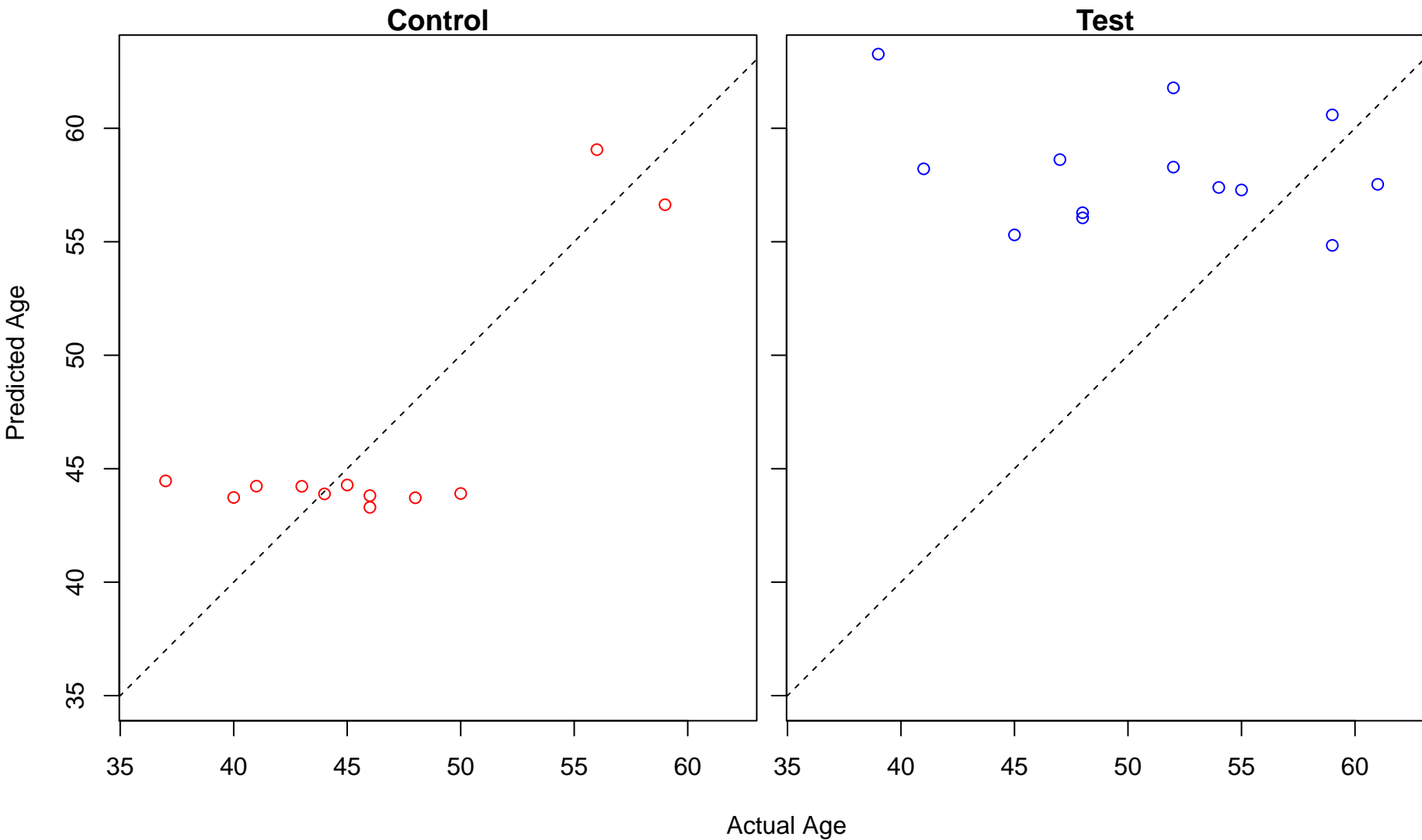
peptidyl-lysine dimethylation (Score: 3.591000)



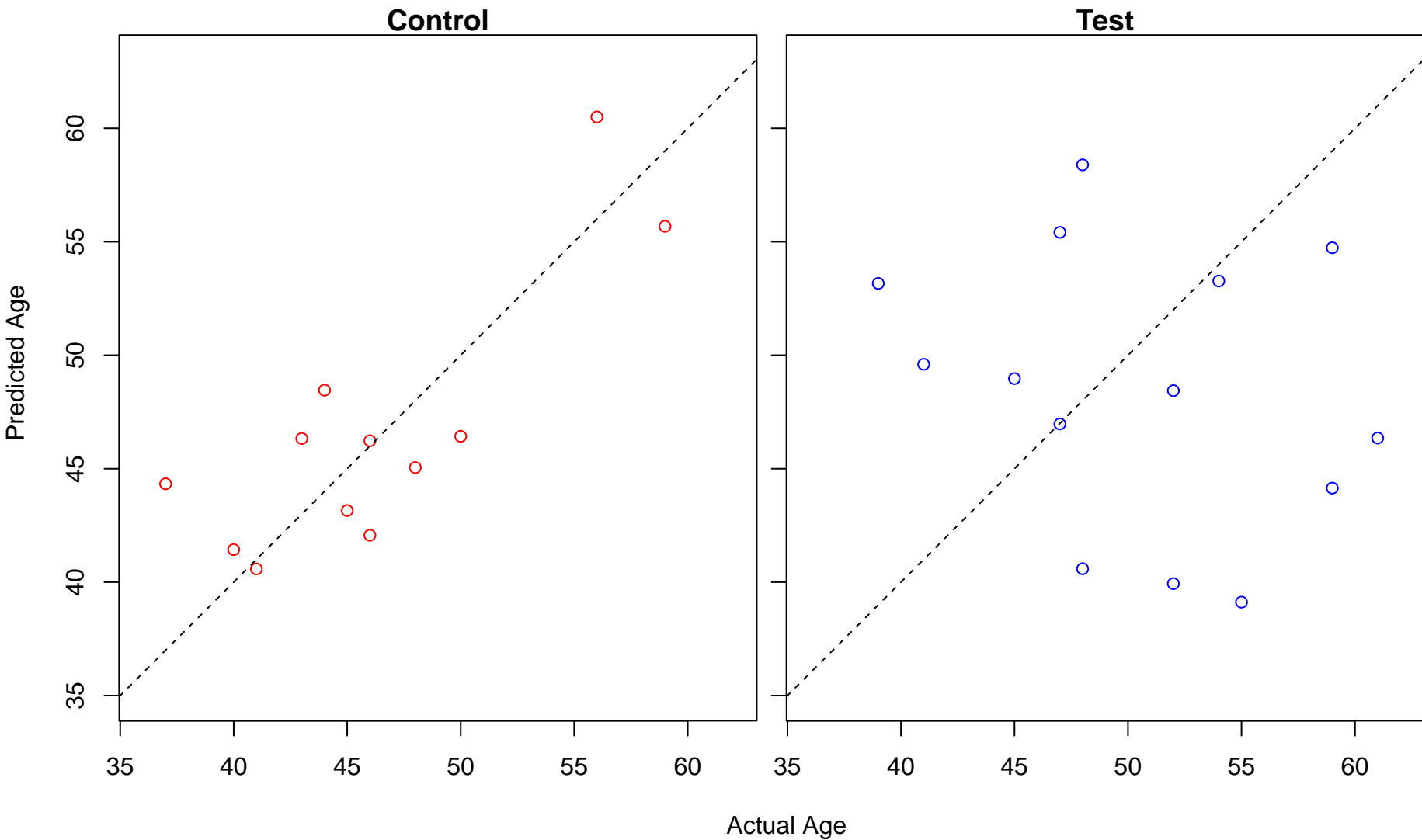
RNA phosphodiester bond hydrolysis, endonucleolytic (Score: 3.586618)



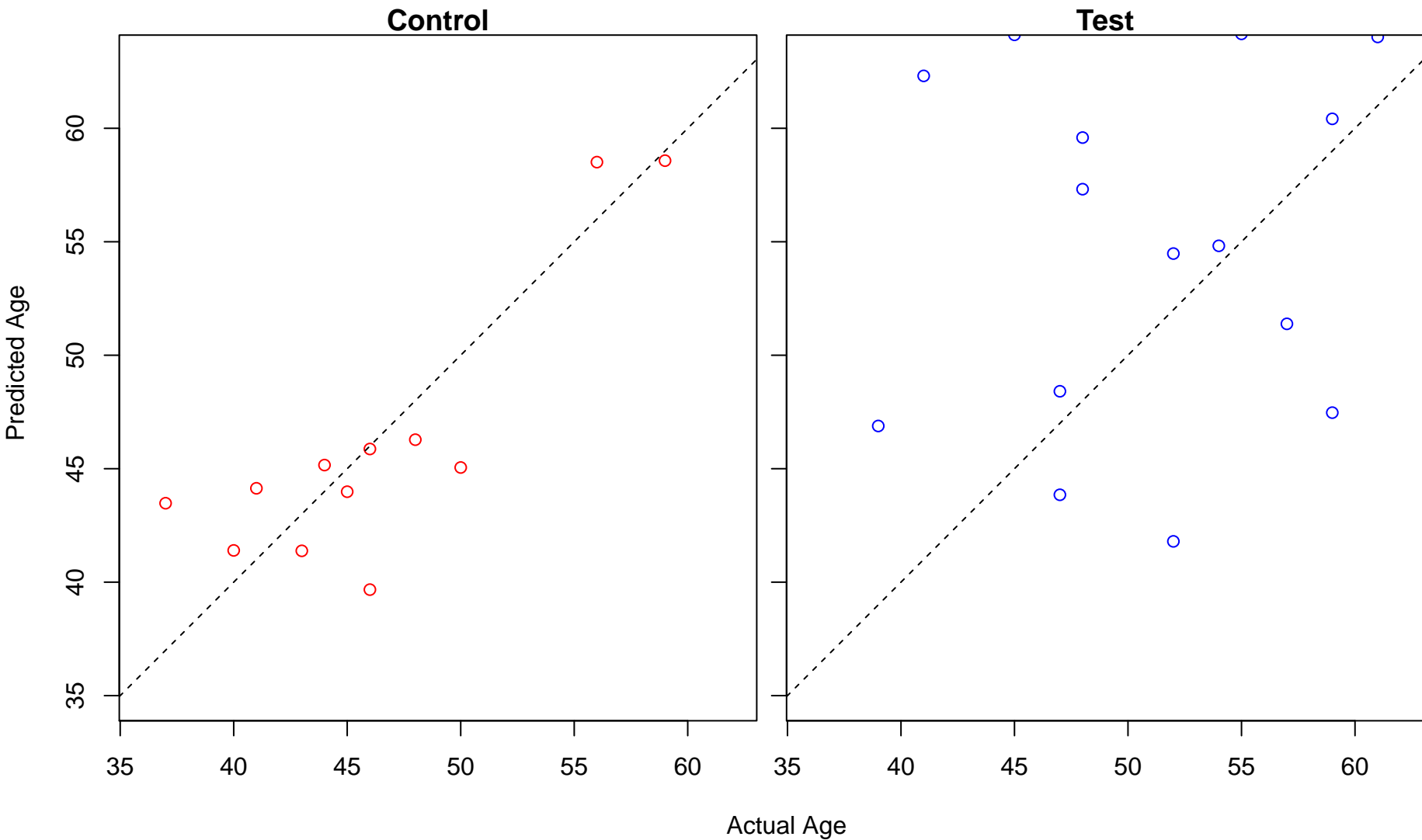
MyD88-dependent toll-like receptor signaling pathway (Score: 3.583551)



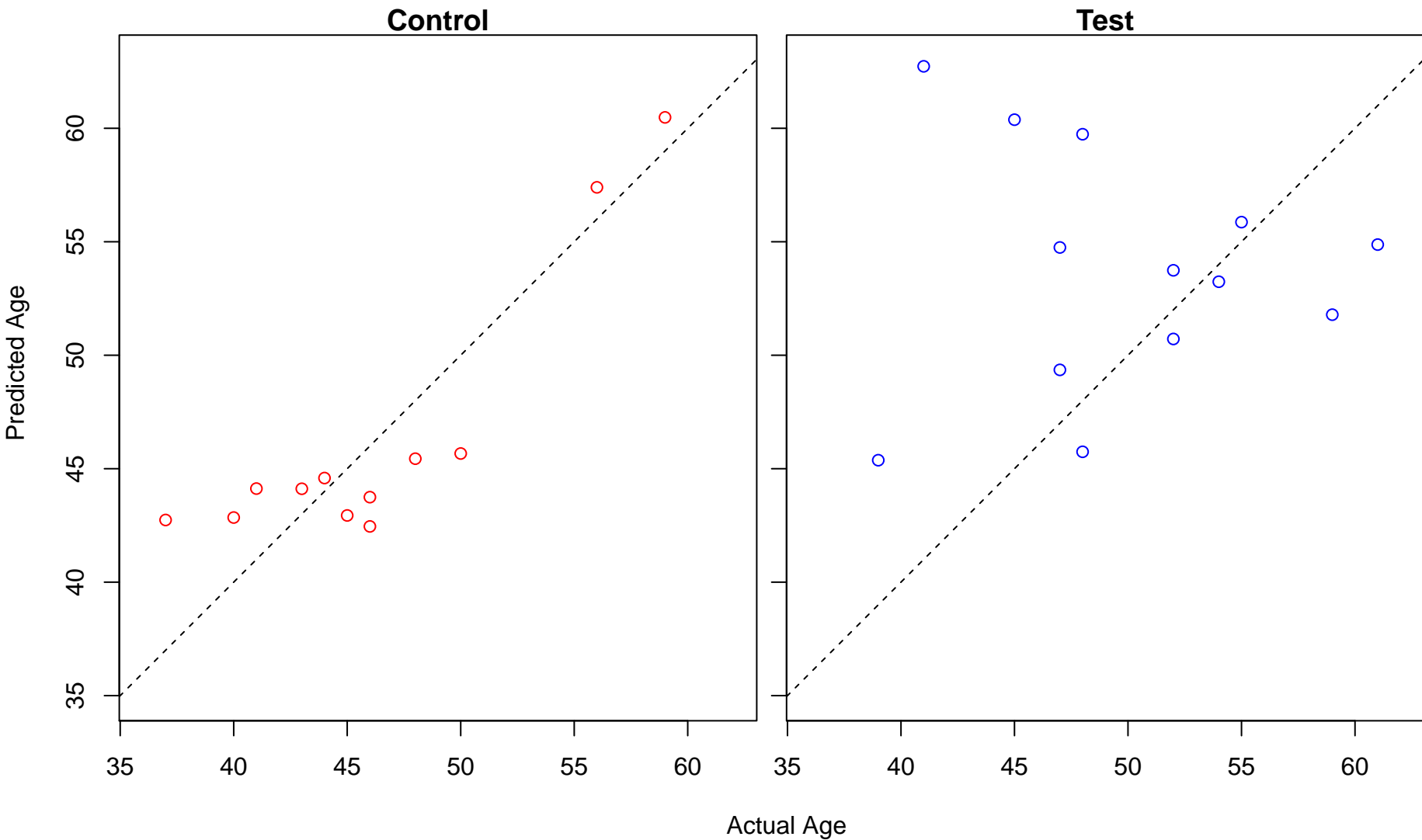
regulation of membrane potential (Score: 3.578767)



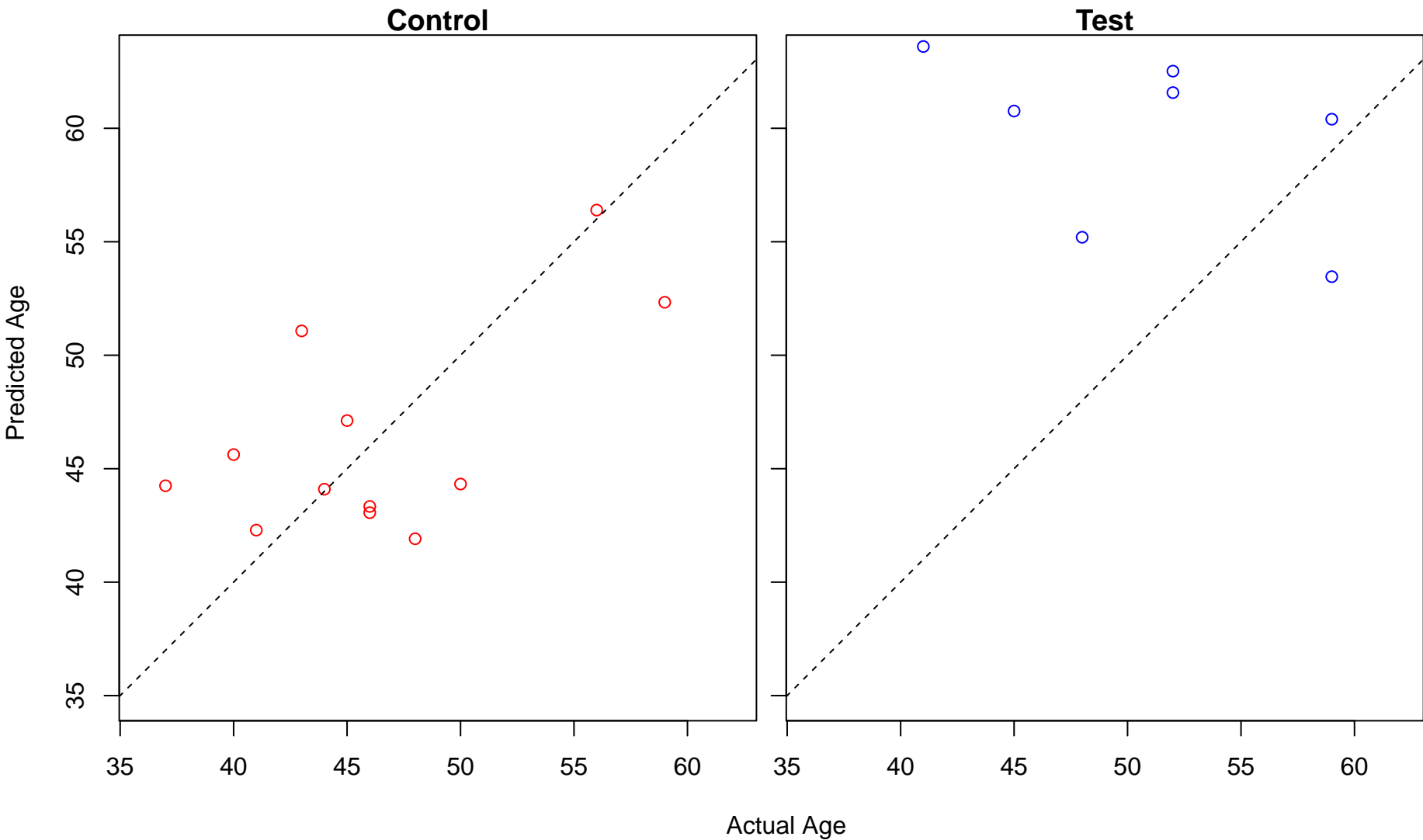
protein refolding (Score: 3.577636)



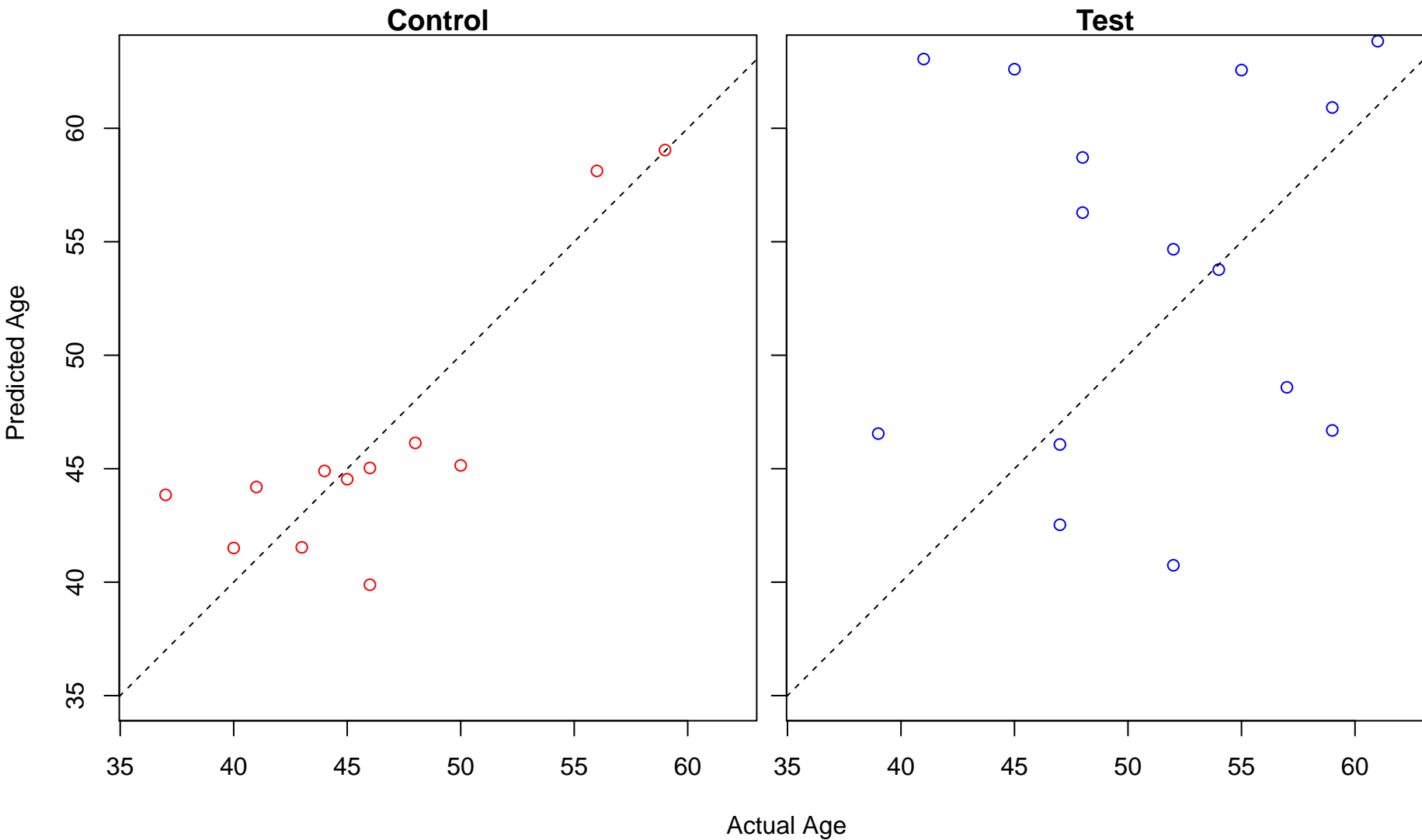
negative regulation of vitamin metabolic process (Score: 3.575703)



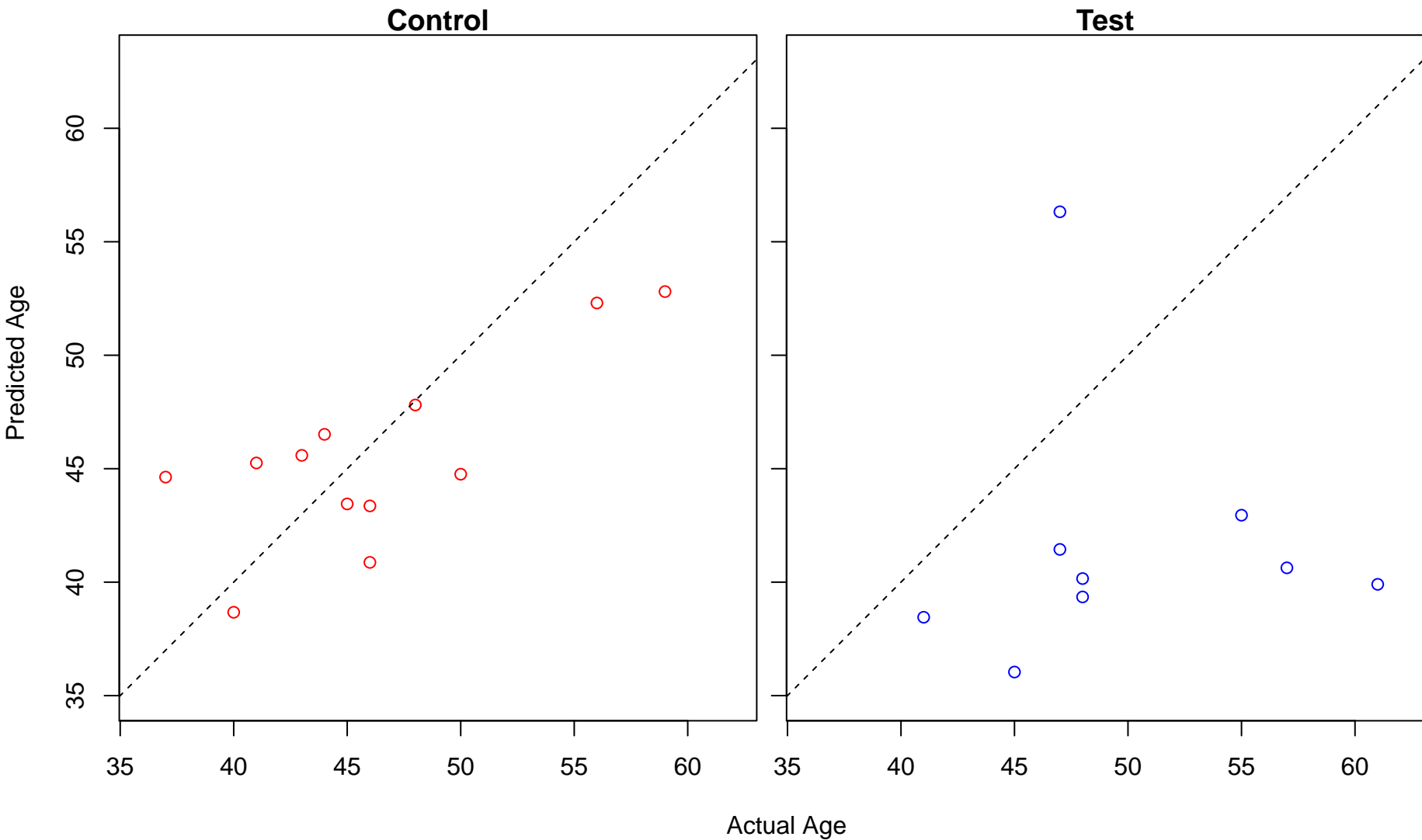
positive regulation of vascular endothelial growth factor receptor signaling pathway (Score: 3.57335)



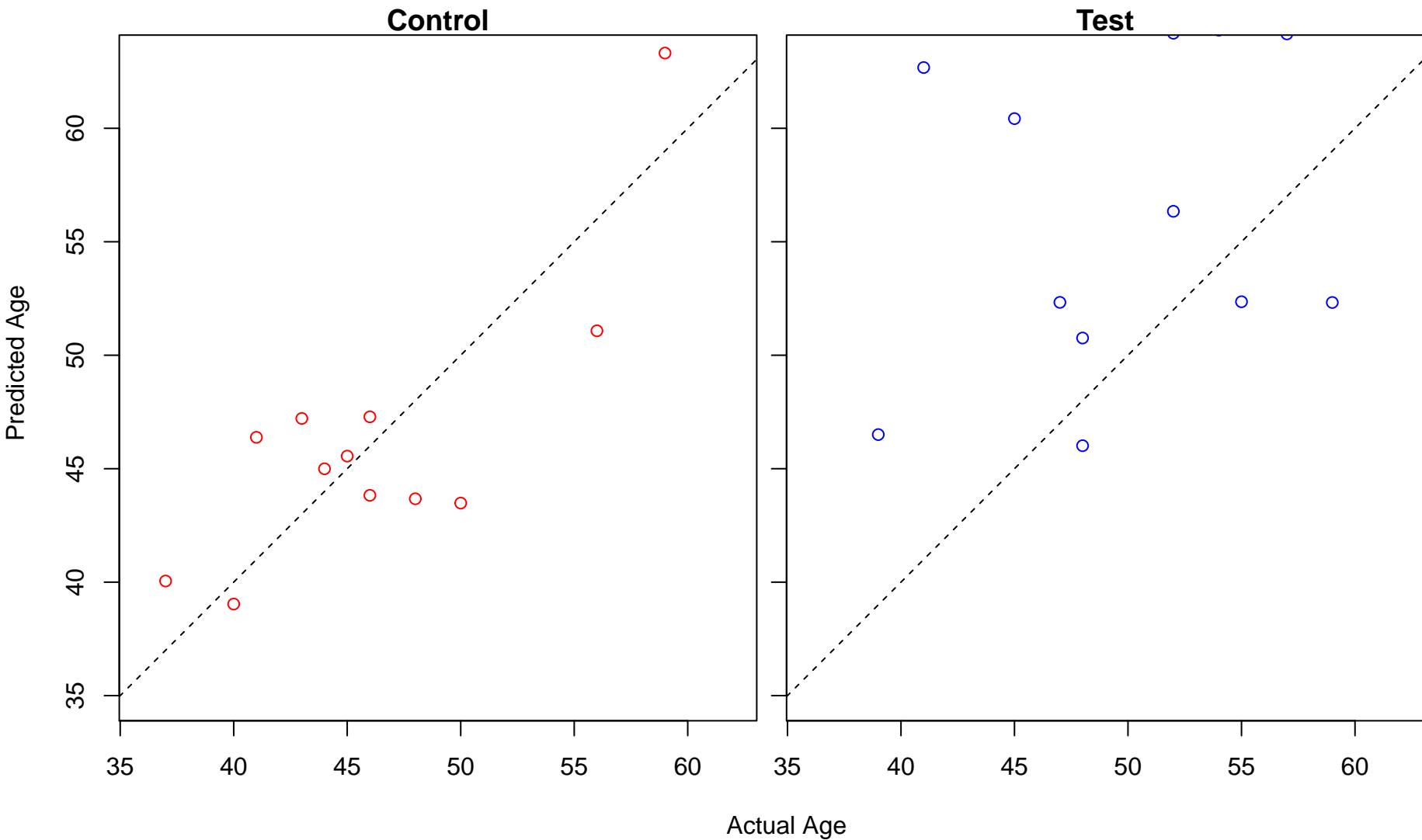
regulation of cellular response to heat (Score: 3.572718)



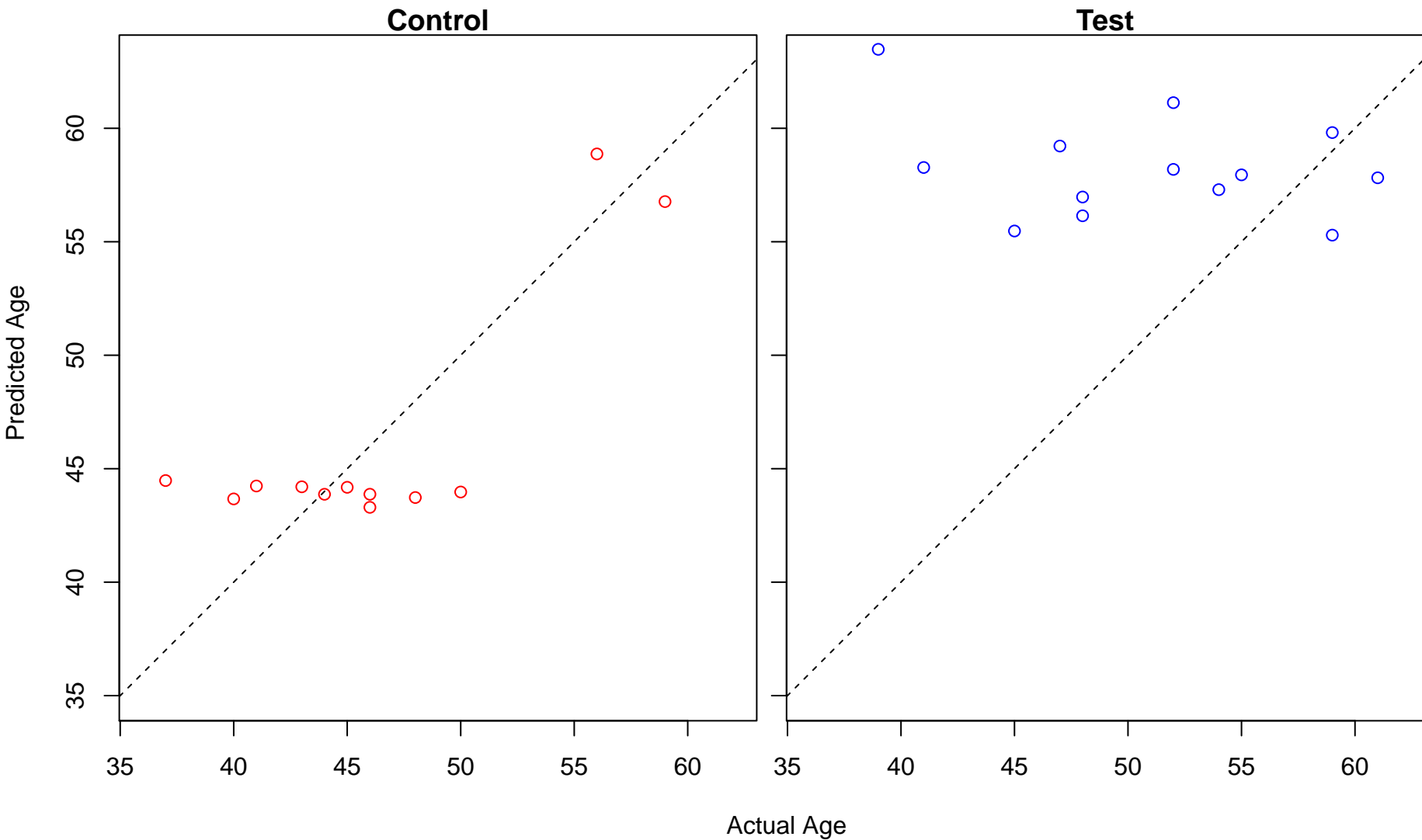
viral transcription (Score: 3.571673)



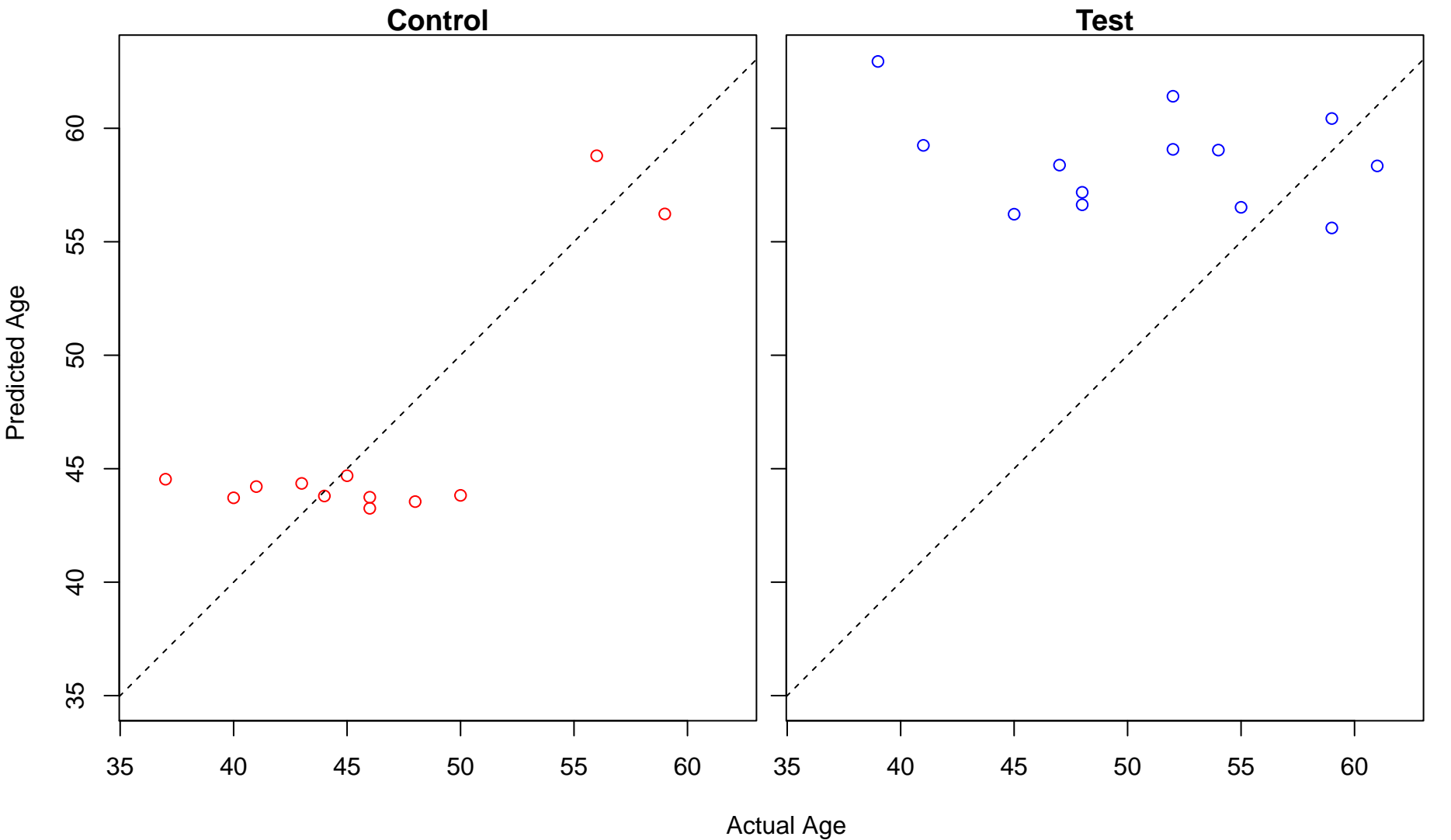
positive regulation of hormone secretion (Score: 3.570447)



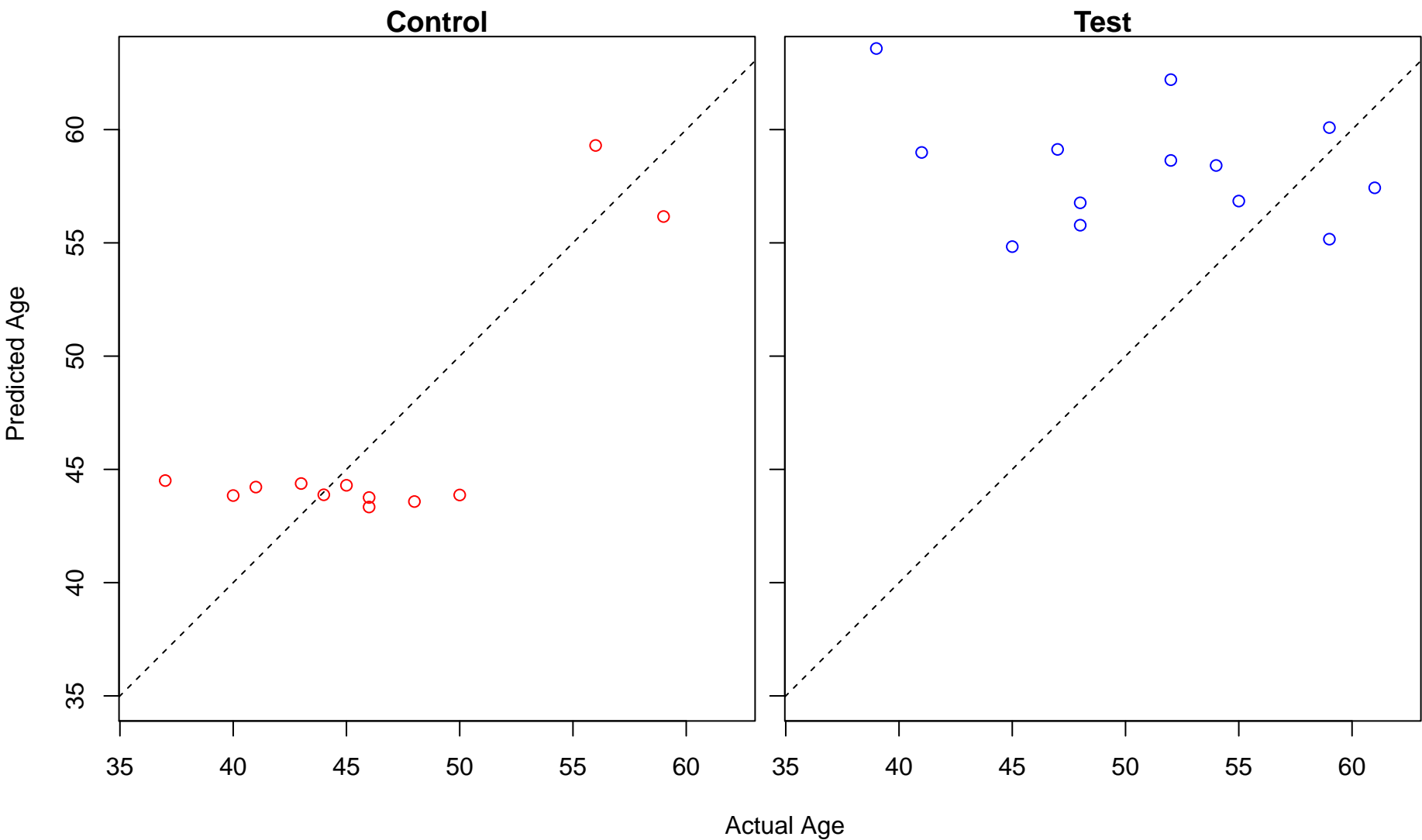
regulation of type I interferon production (Score: 3.567506)



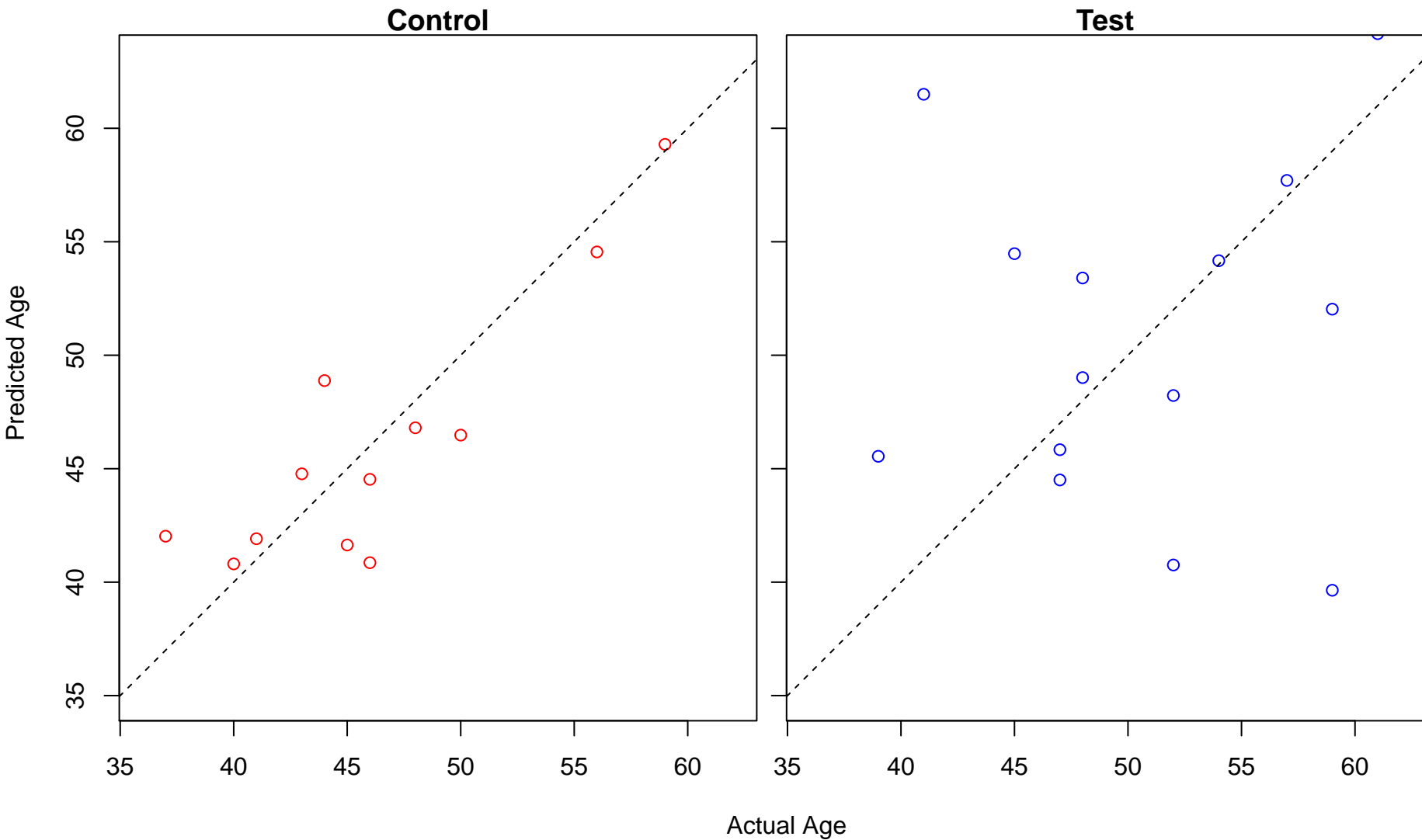
Positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score



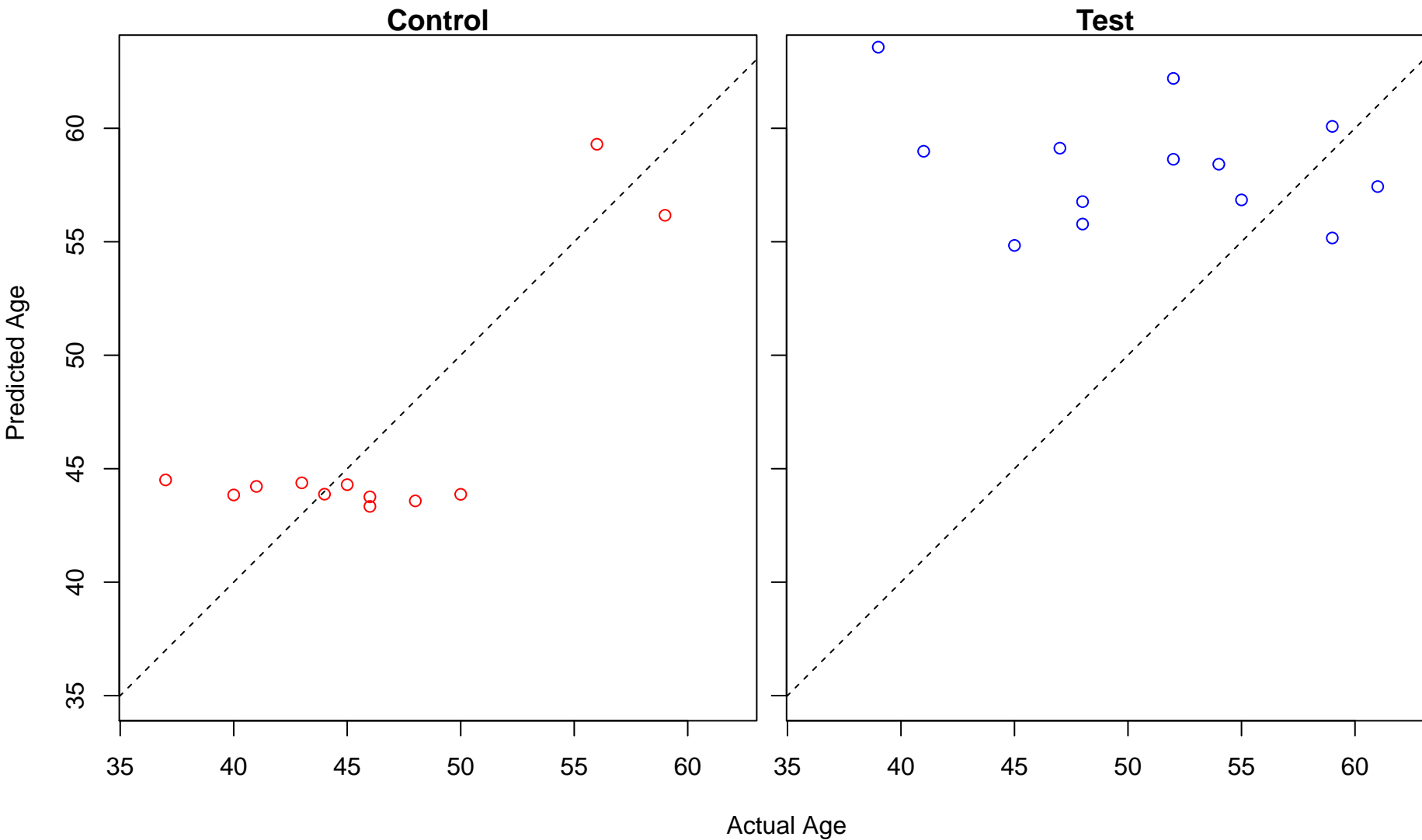
DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (Score: 3.



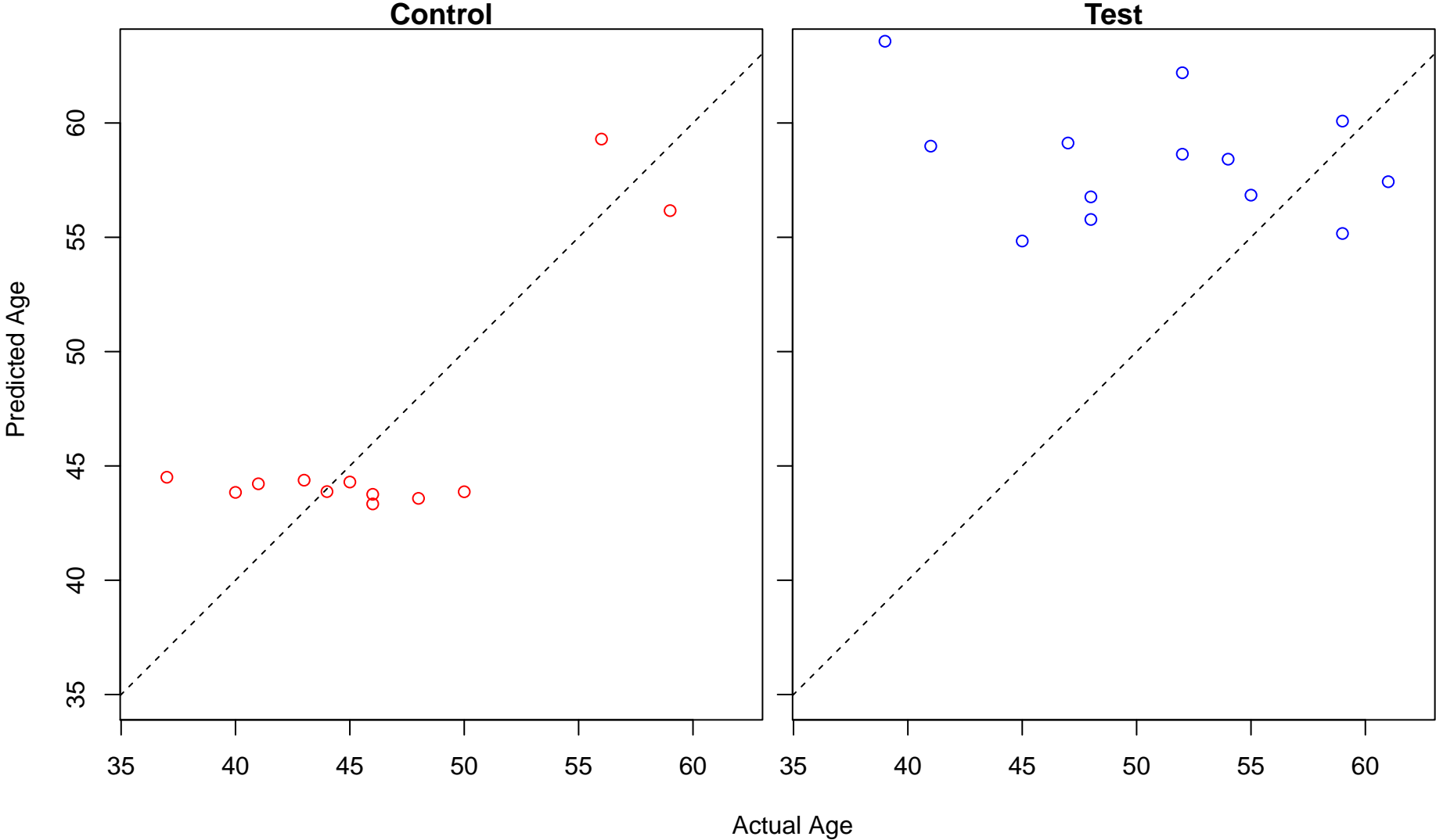
regulation of protein stability (Score: 3.563374)



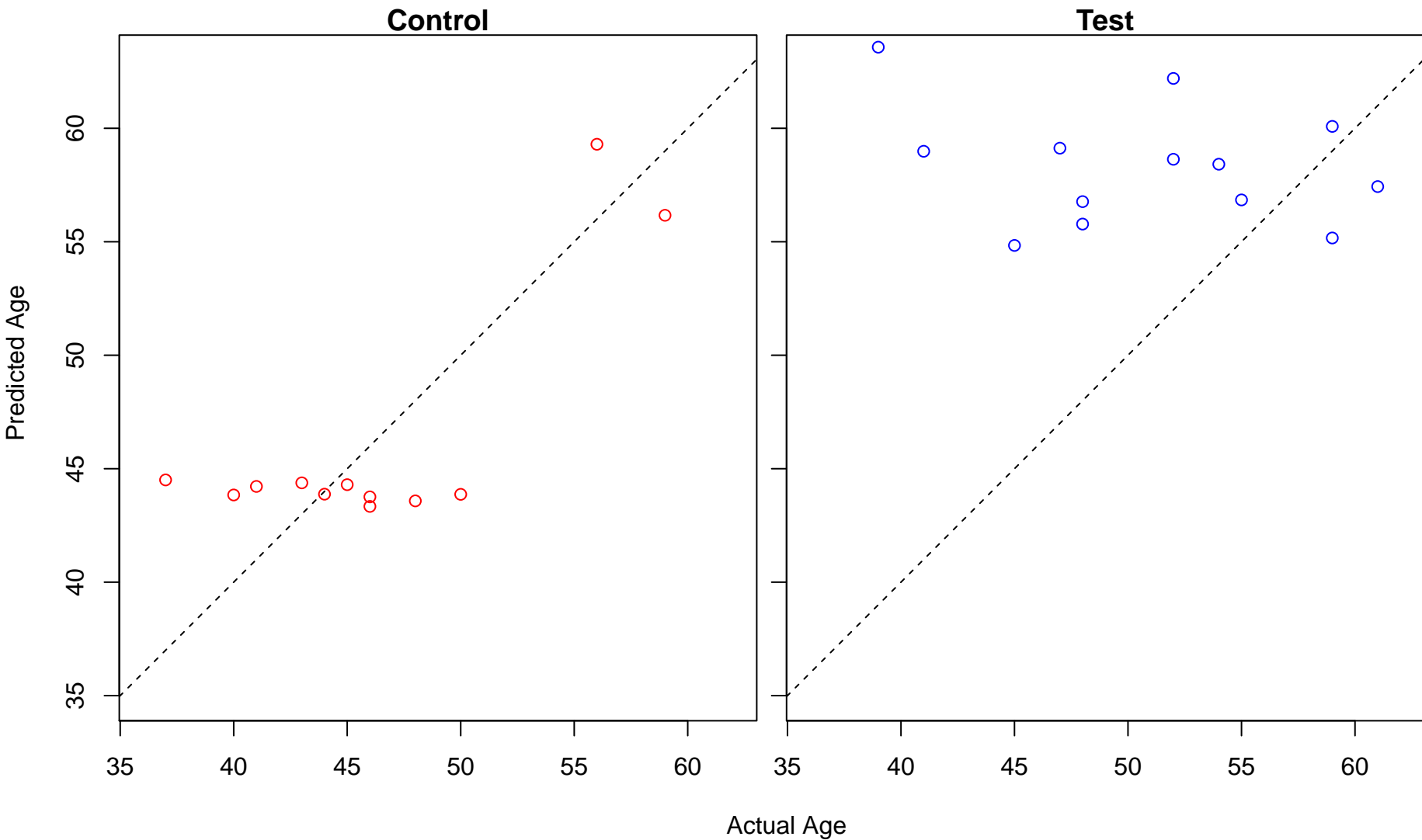
signal transduction involved in mitotic G1 DNA damage checkpoint (Score: 3.563070)



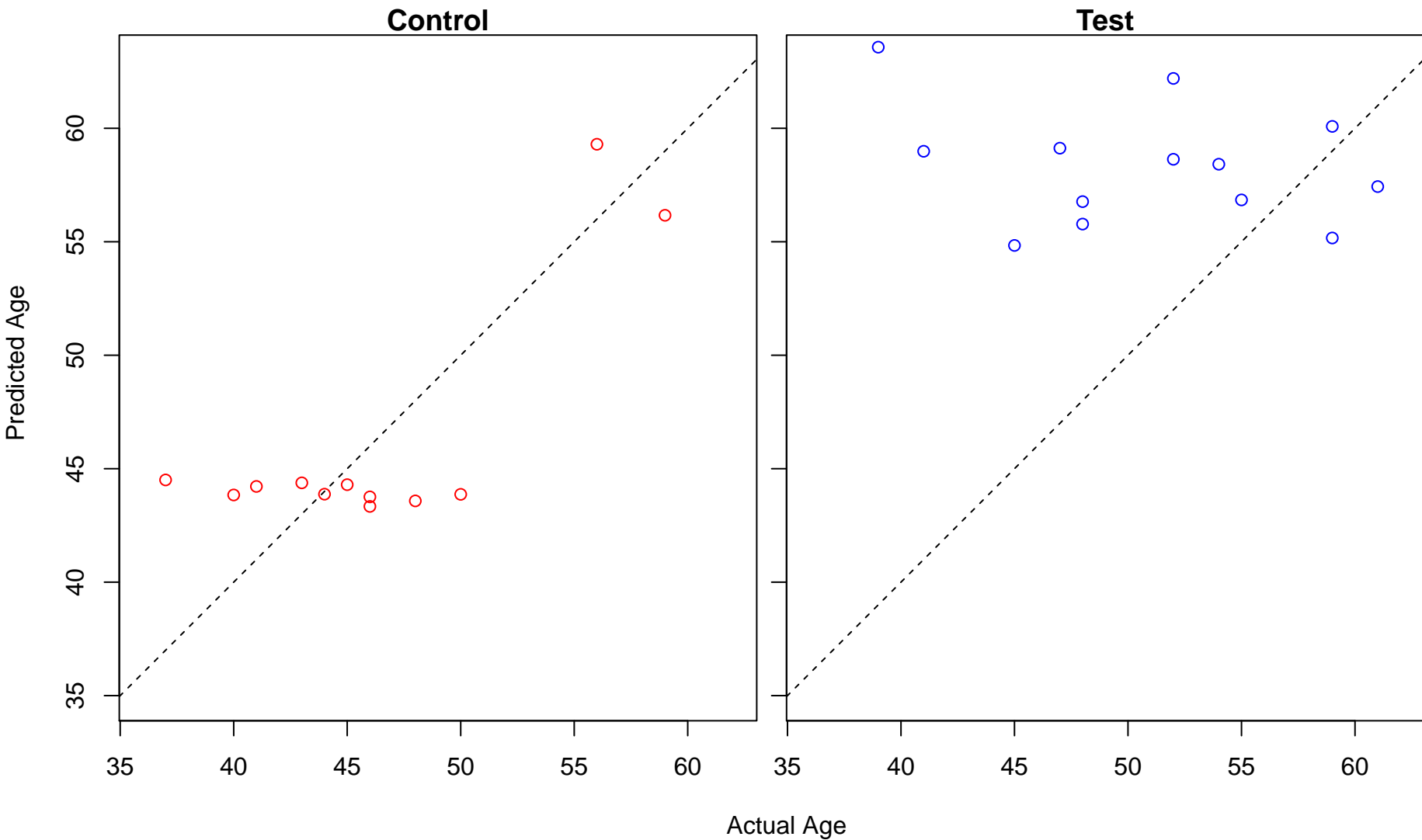
intracellular signal transduction involved in G1 DNA damage checkpoint (Score: 3.563070)



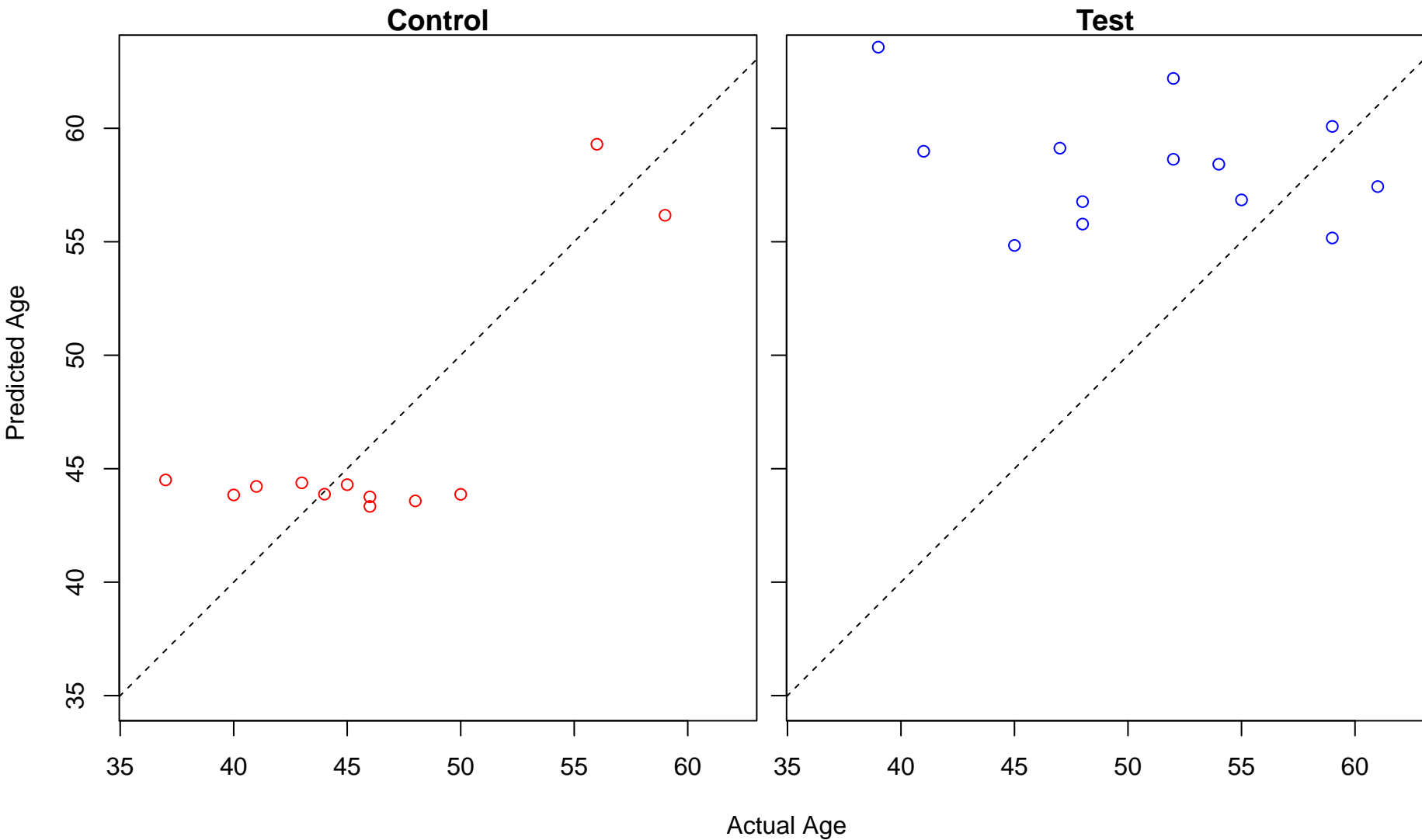
signal transduction involved in mitotic cell cycle checkpoint (Score: 3.563068)



signal transduction involved in mitotic DNA damage checkpoint (Score: 3.563068)

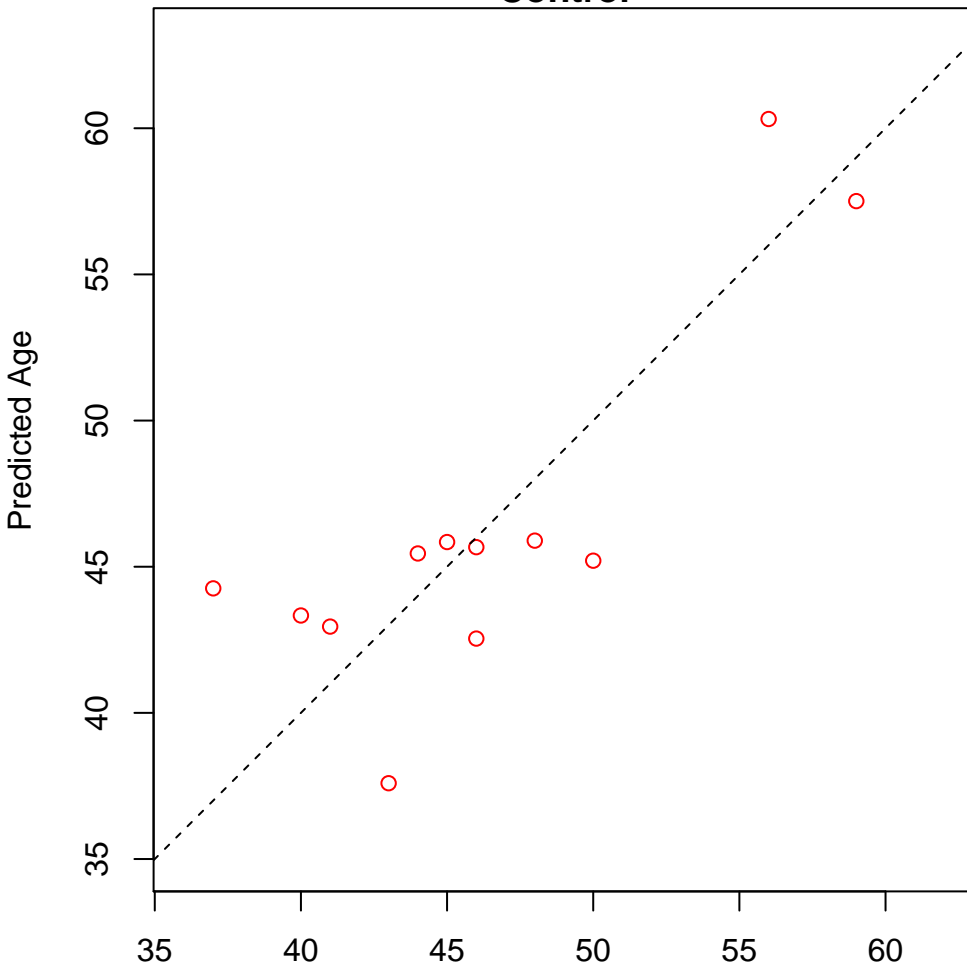


signal transduction involved in mitotic DNA integrity checkpoint (Score: 3.563068)

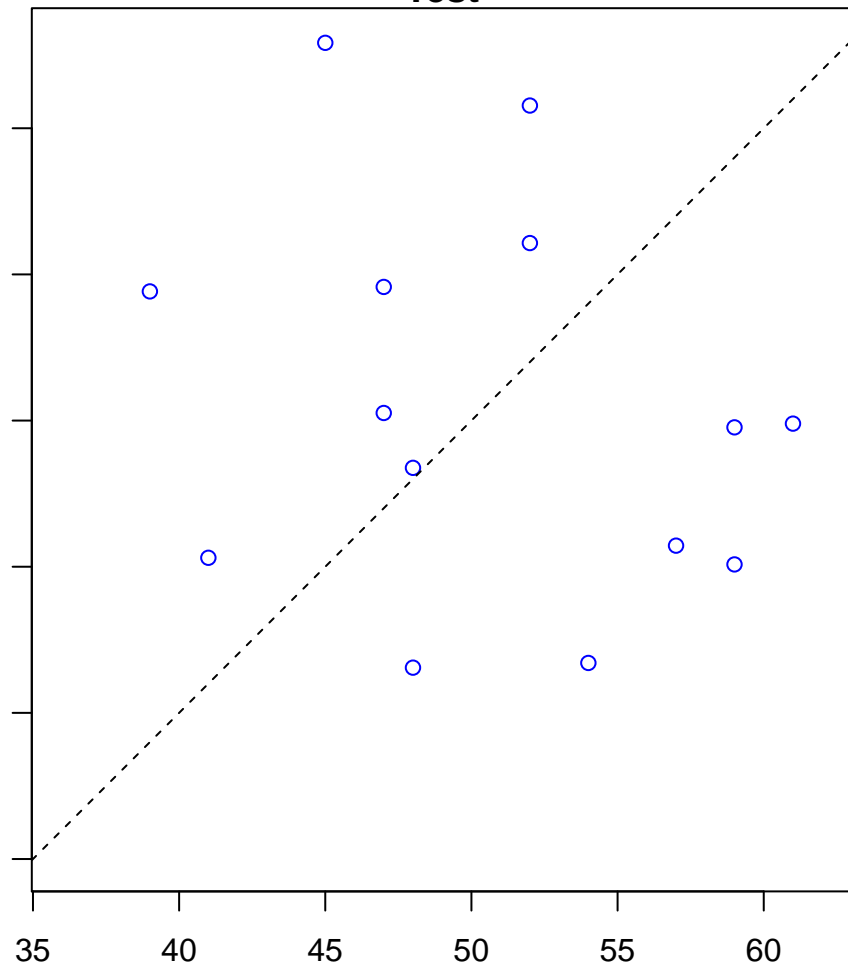


protein maturation by protein folding (Score: 3.561566)

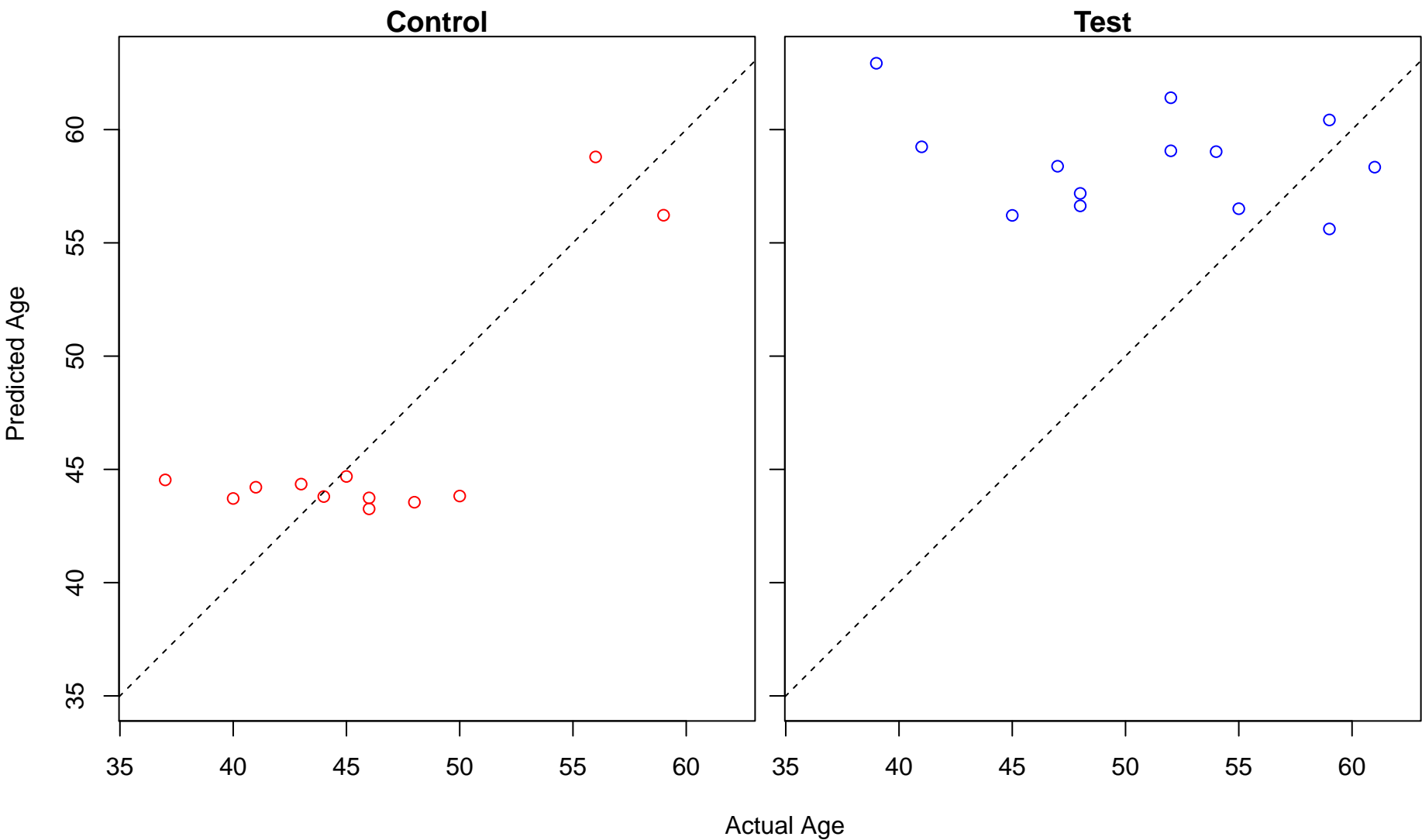
Control



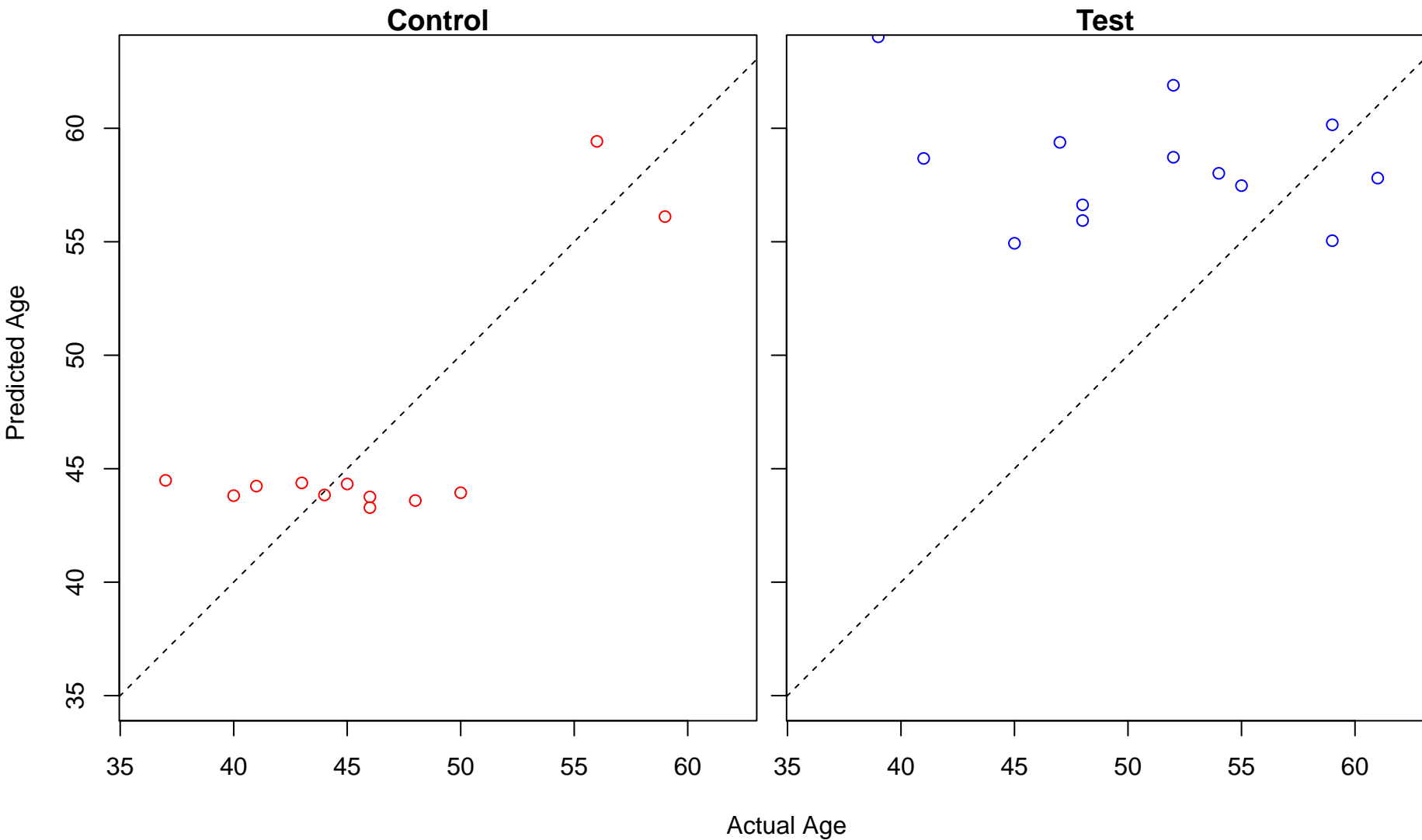
Test



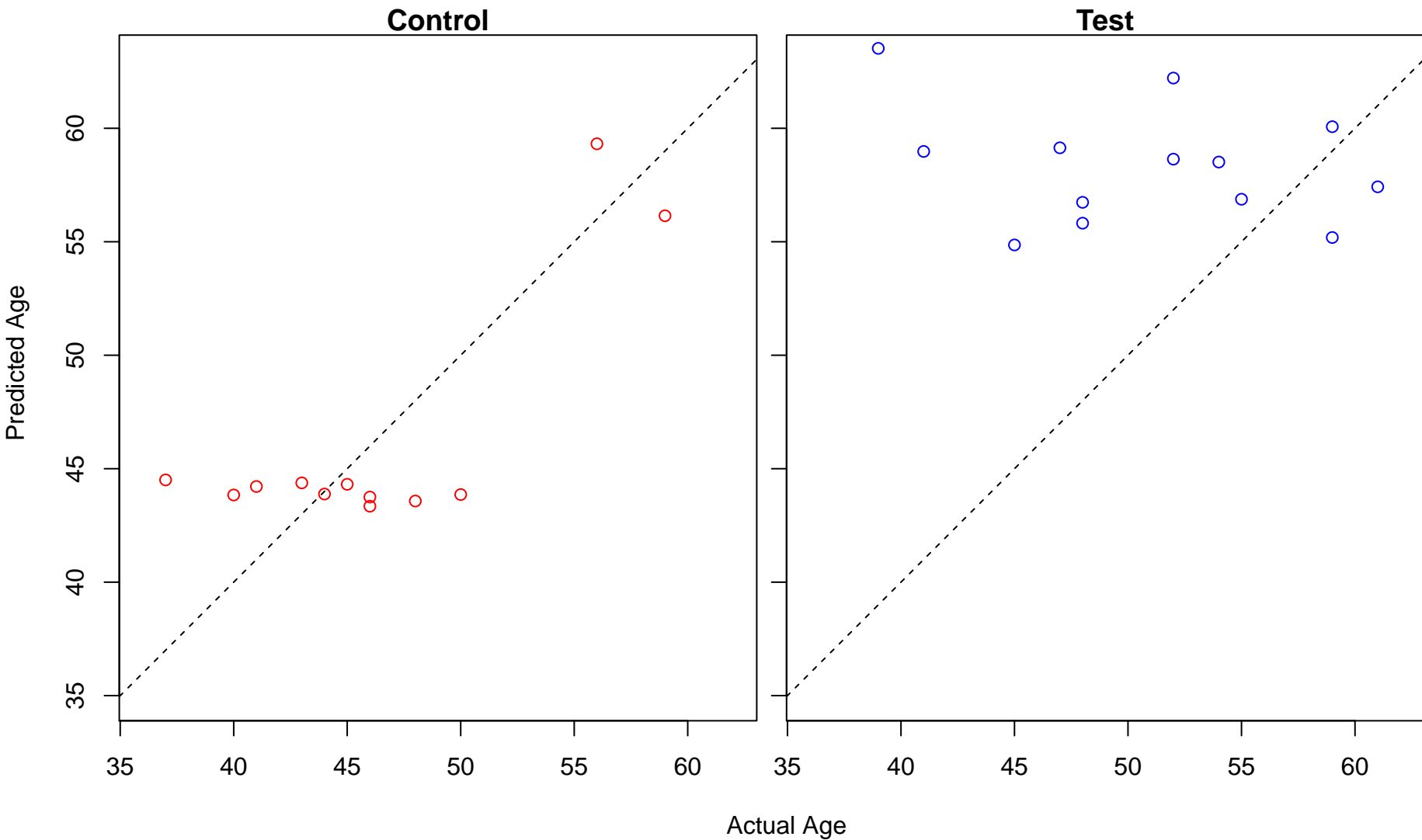
Actual Age



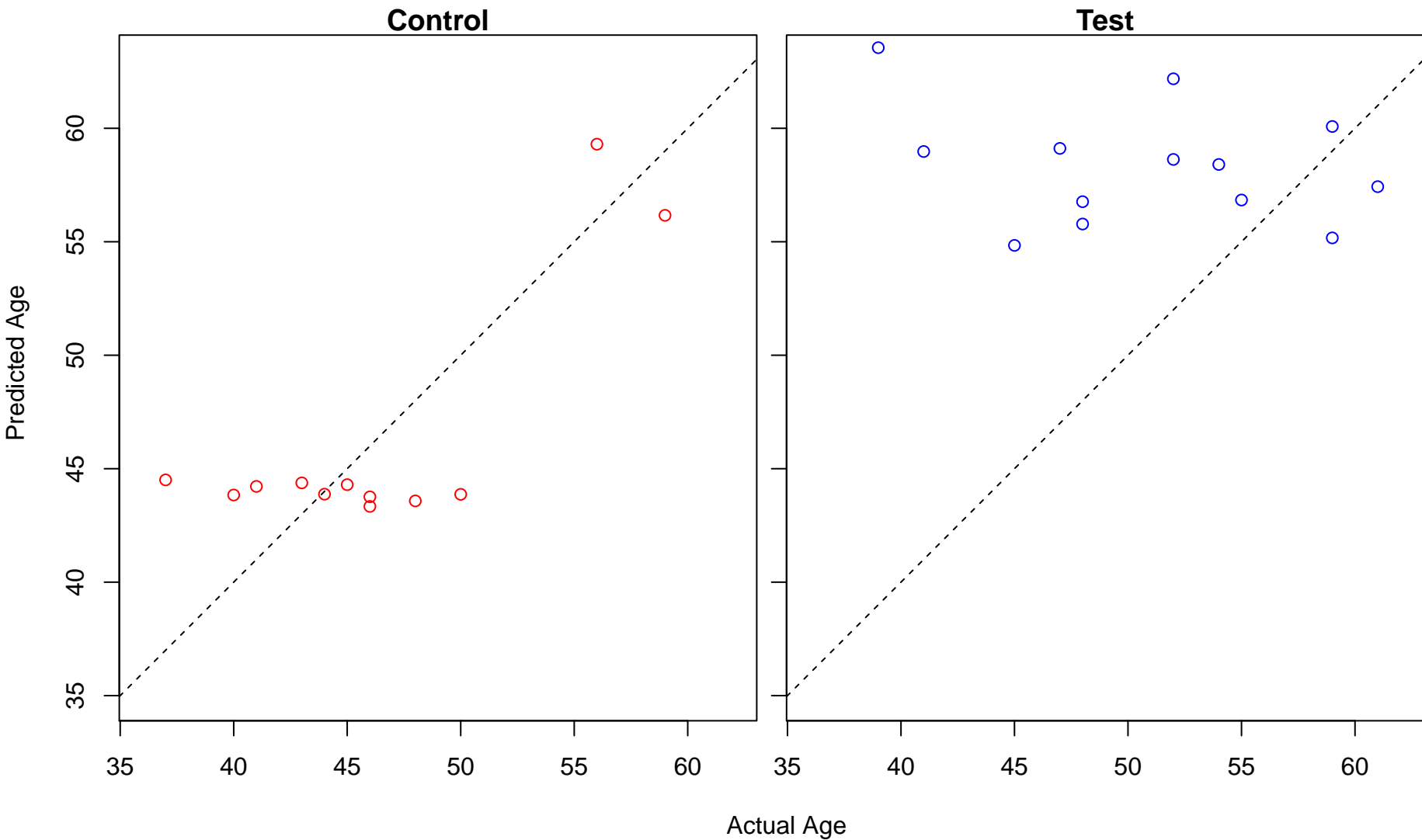
cellular response to hypoxia (Score: 3.560527)



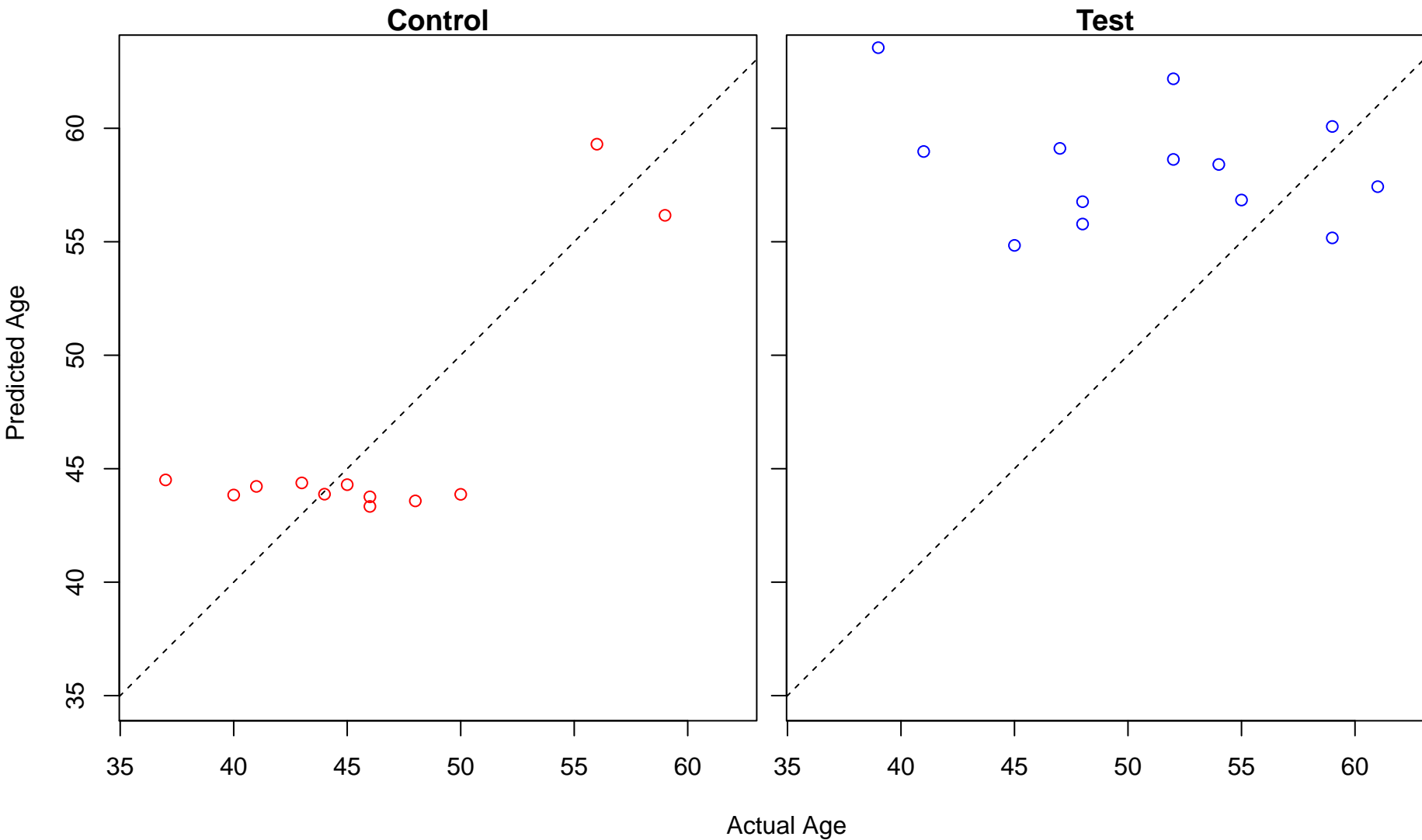
positive regulation of cell cycle arrest (Score: 3.557658)



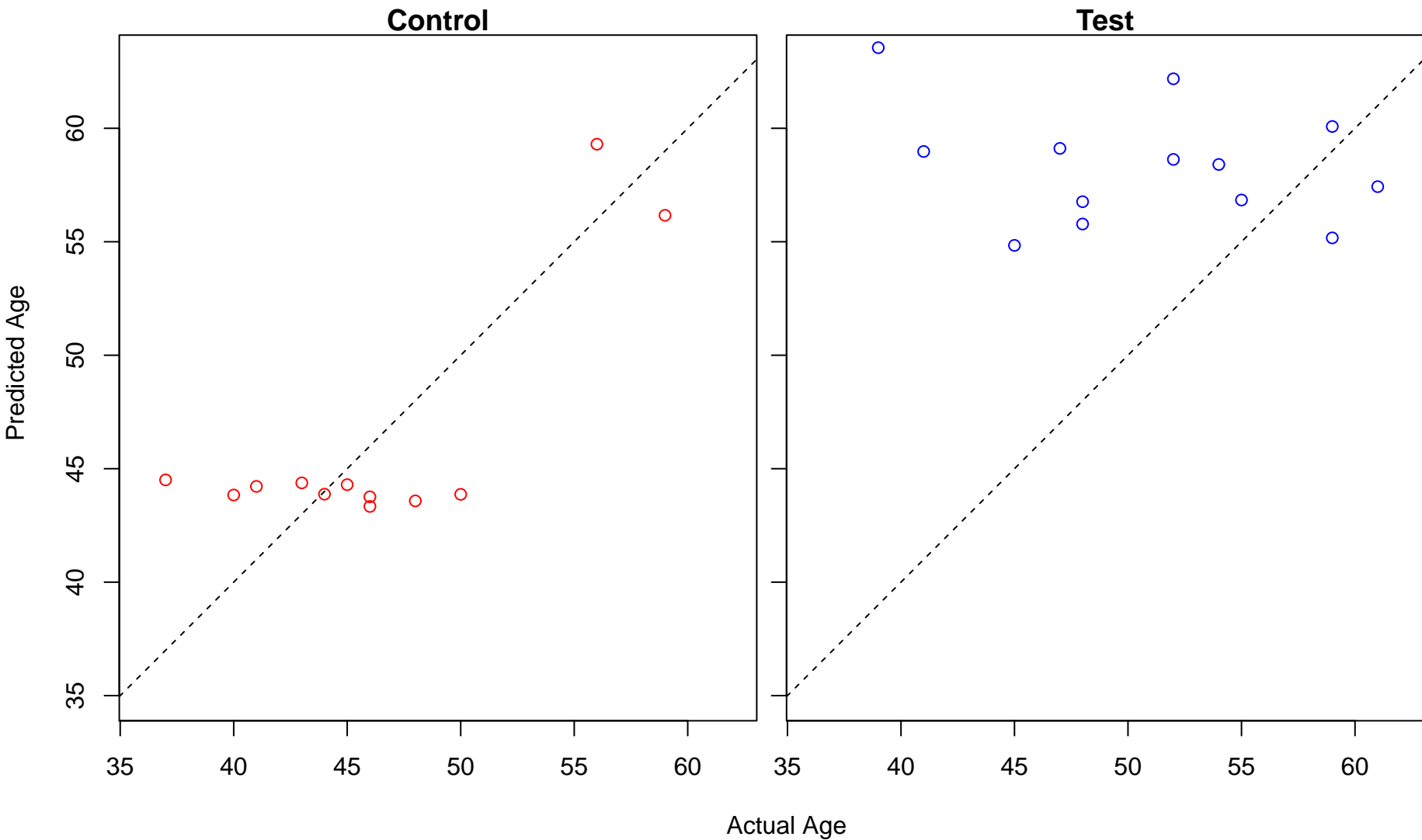
signal transduction involved in DNA integrity checkpoint (Score: 3.557384)



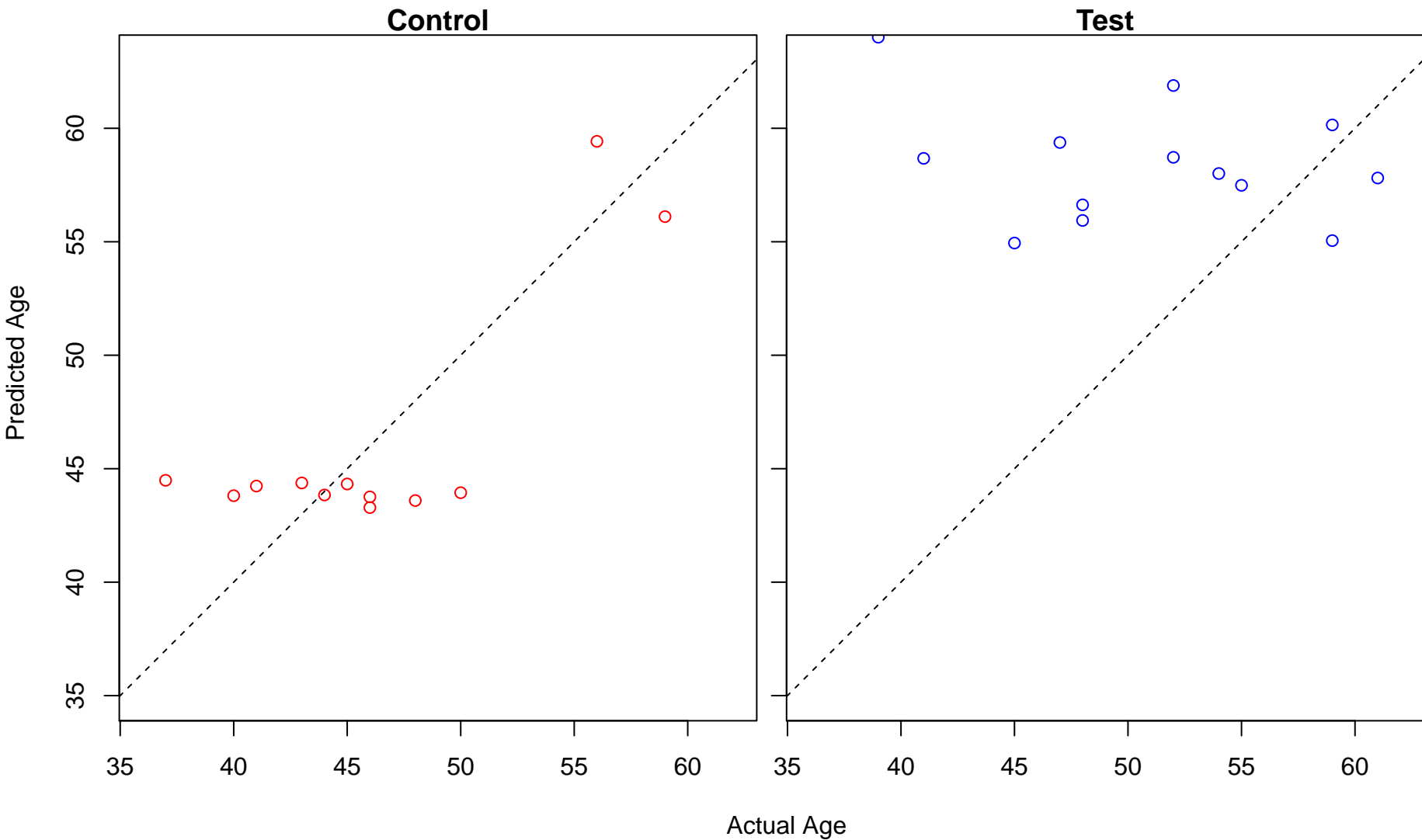
signal transduction involved in DNA damage checkpoint (Score: 3.557384)



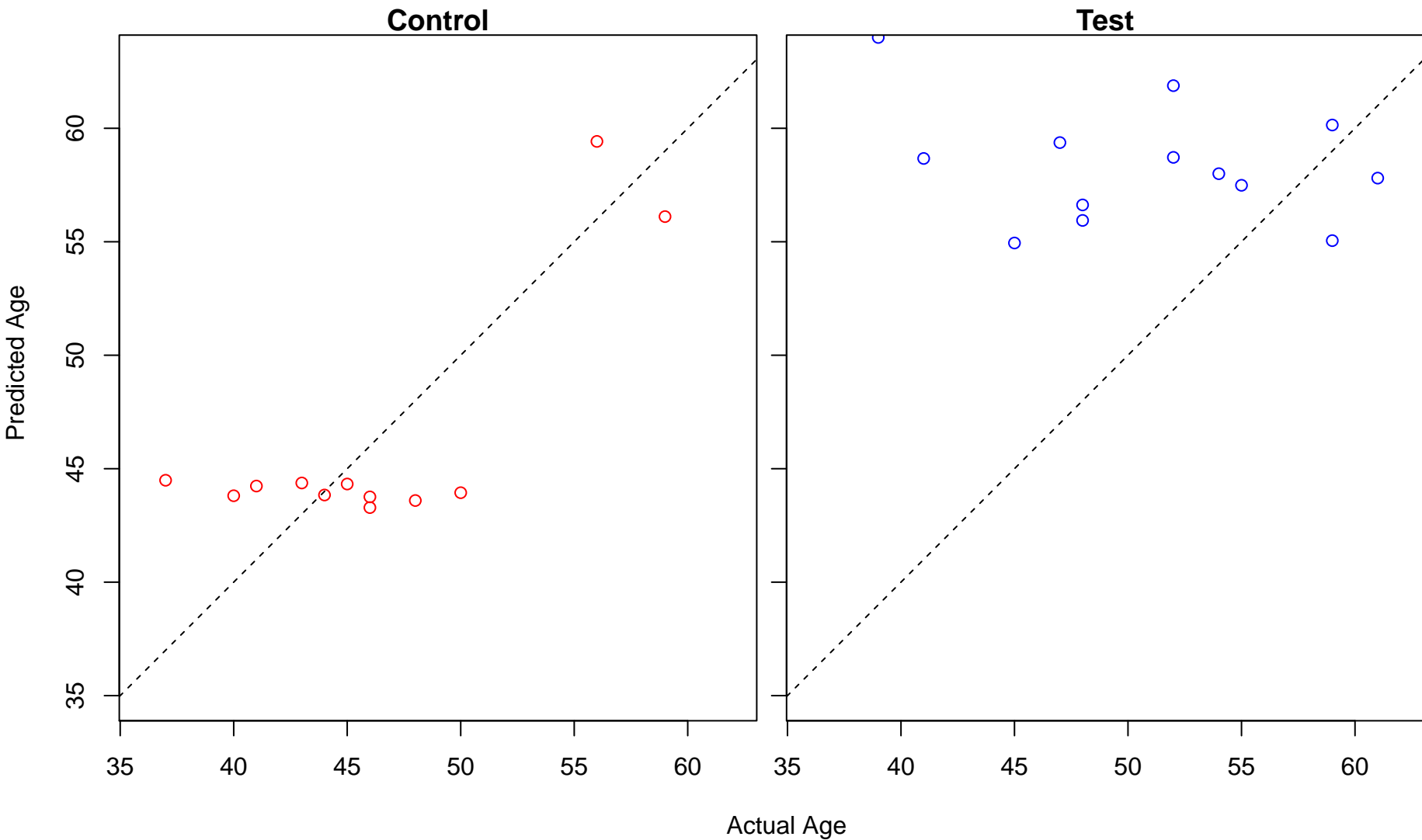
signal transduction involved in cell cycle checkpoint (Score: 3.557383)



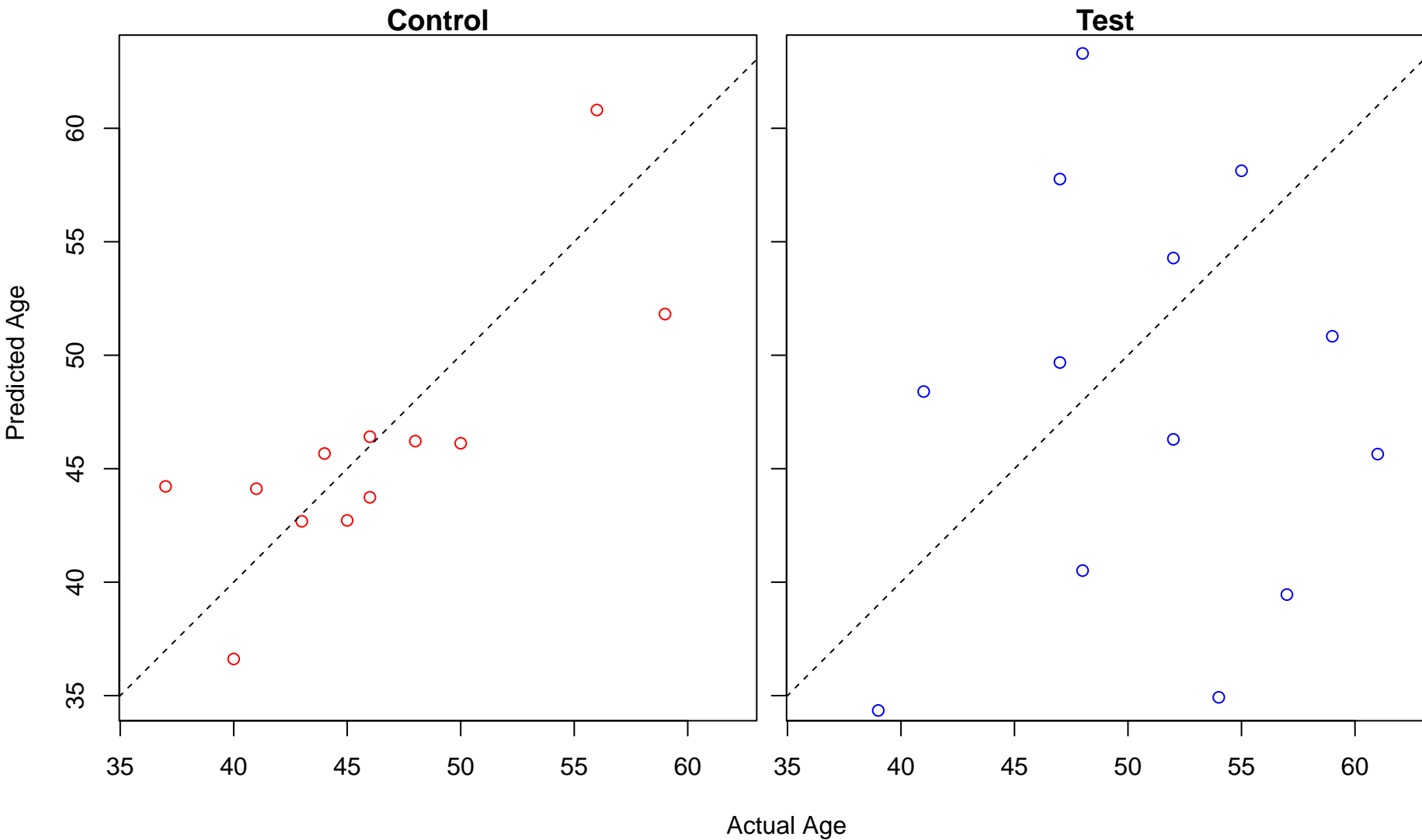
cellular response to decreased oxygen levels (Score: 3.557290)



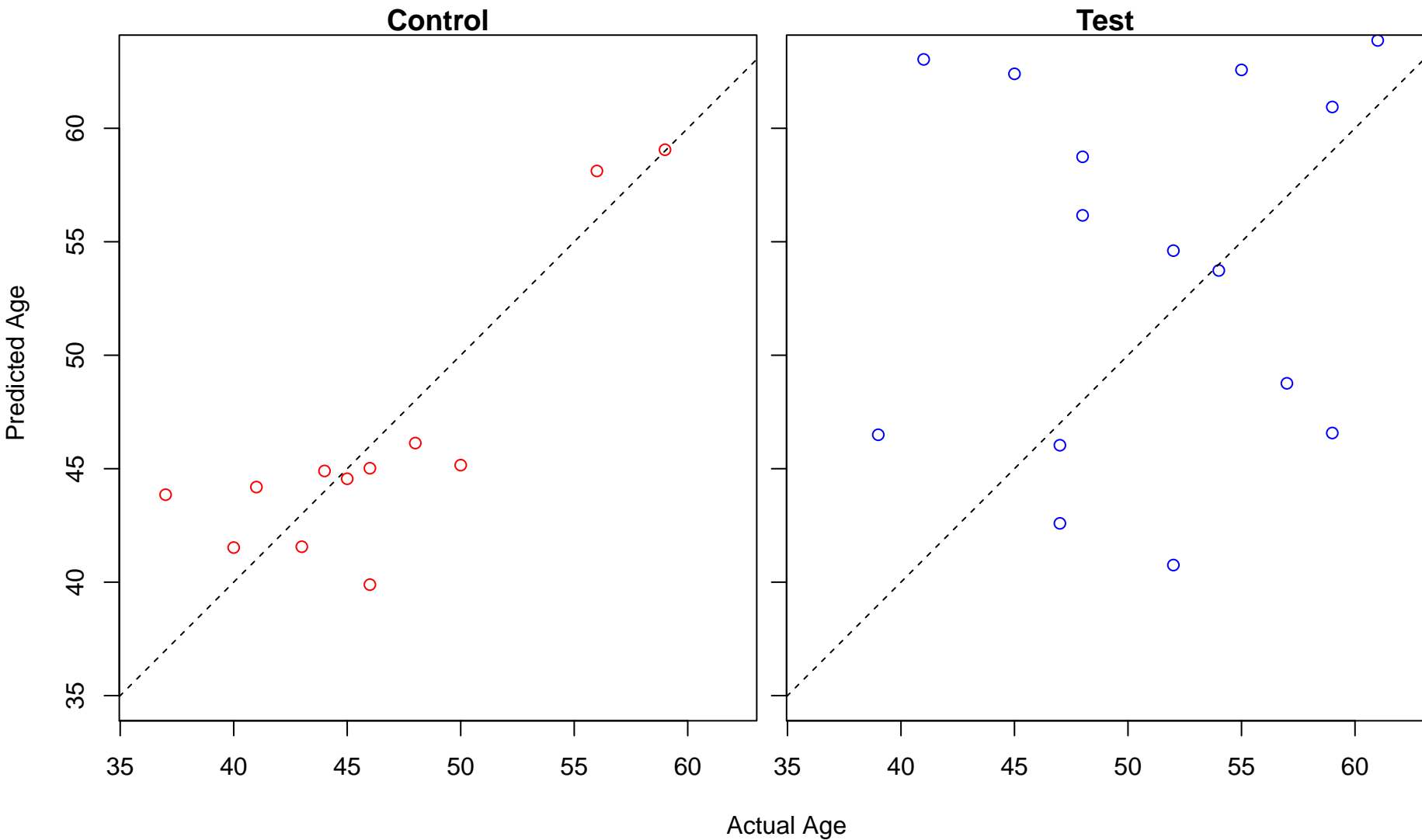
cellular response to oxygen levels (Score: 3.554877)



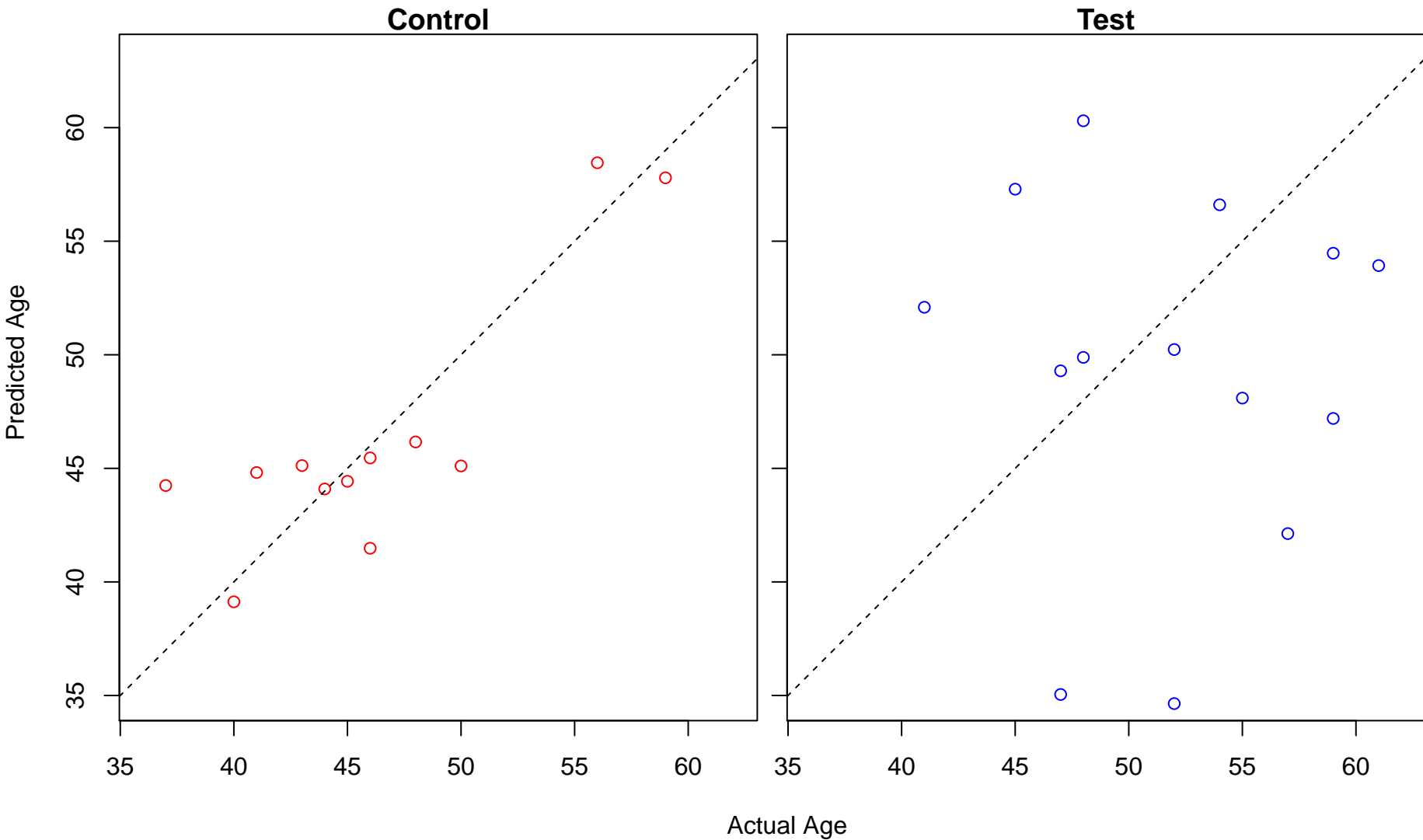
positive regulation of embryonic development (Score: 3.554635)



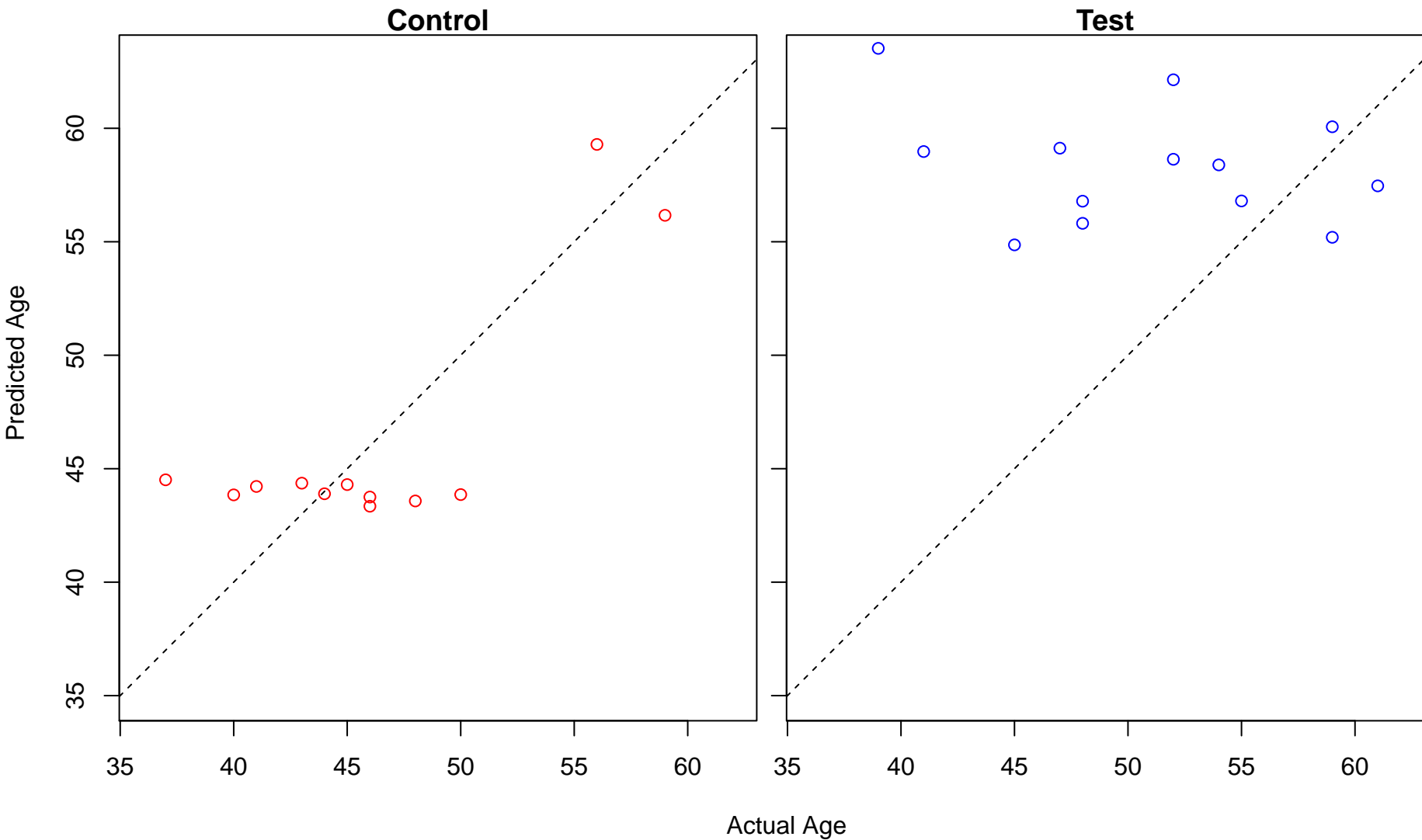
cellular response to heat (Score: 3.553458)



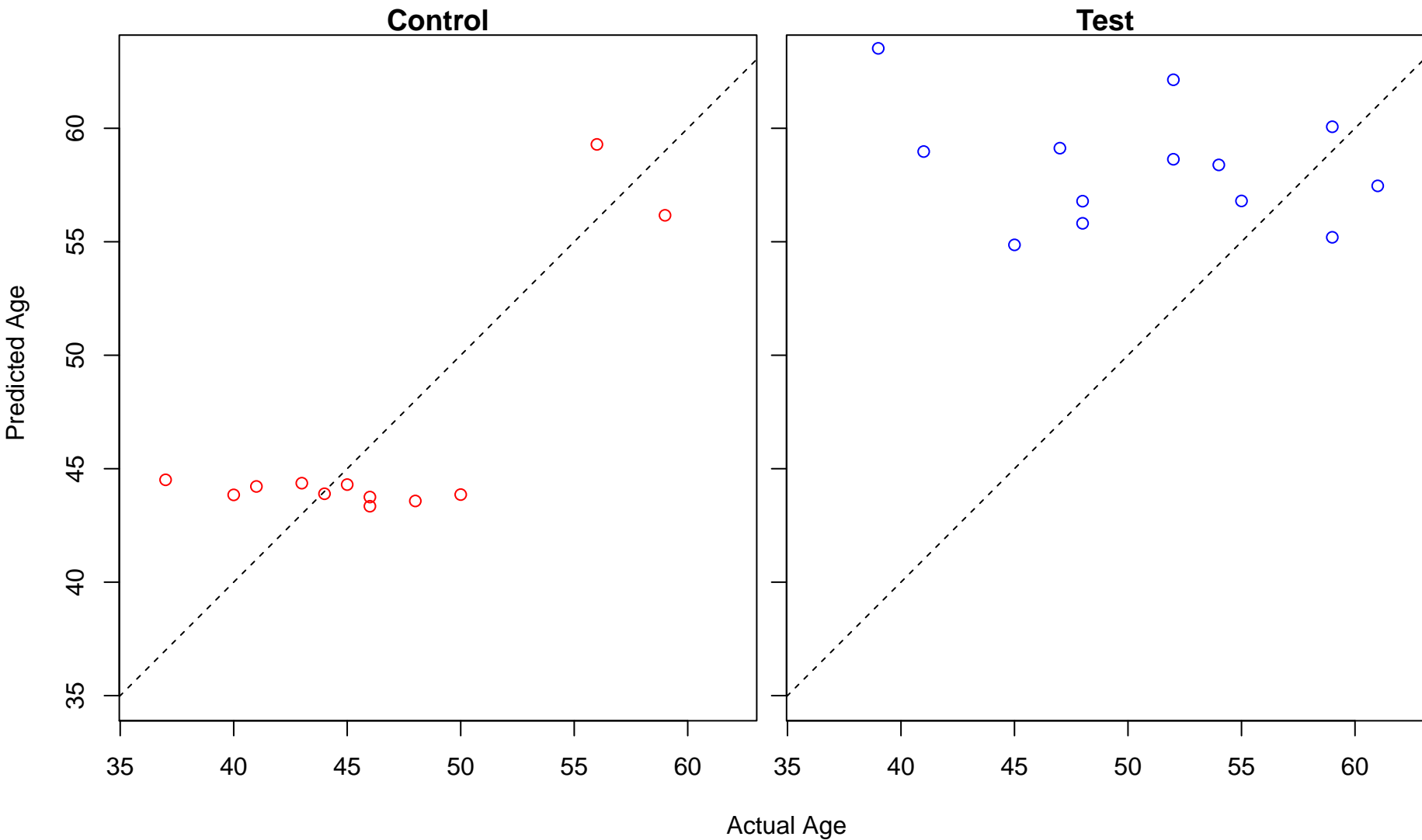
positive regulation of intracellular transport (Score: 3.553141)



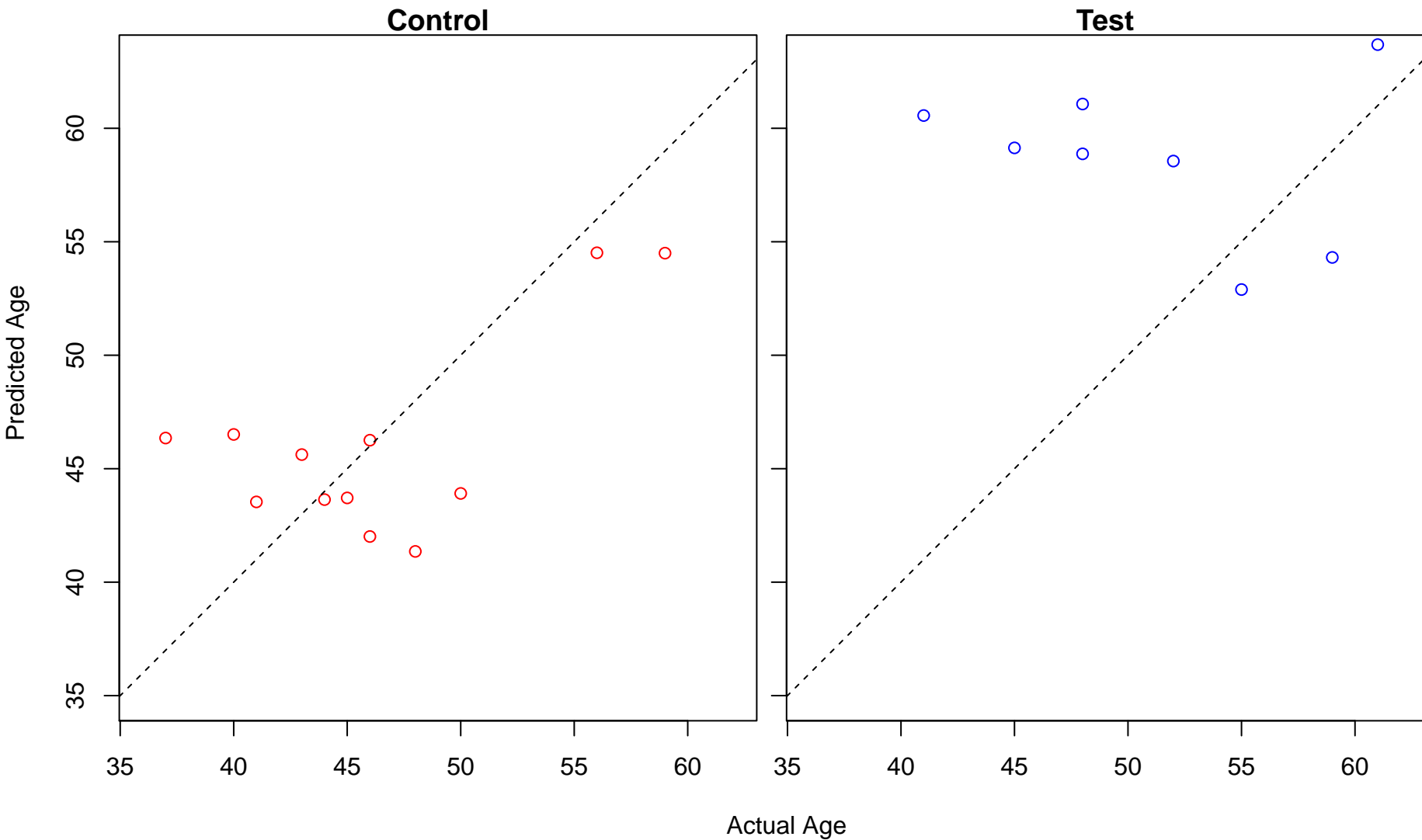
mitotic G1/S transition checkpoint (Score: 3.546302)



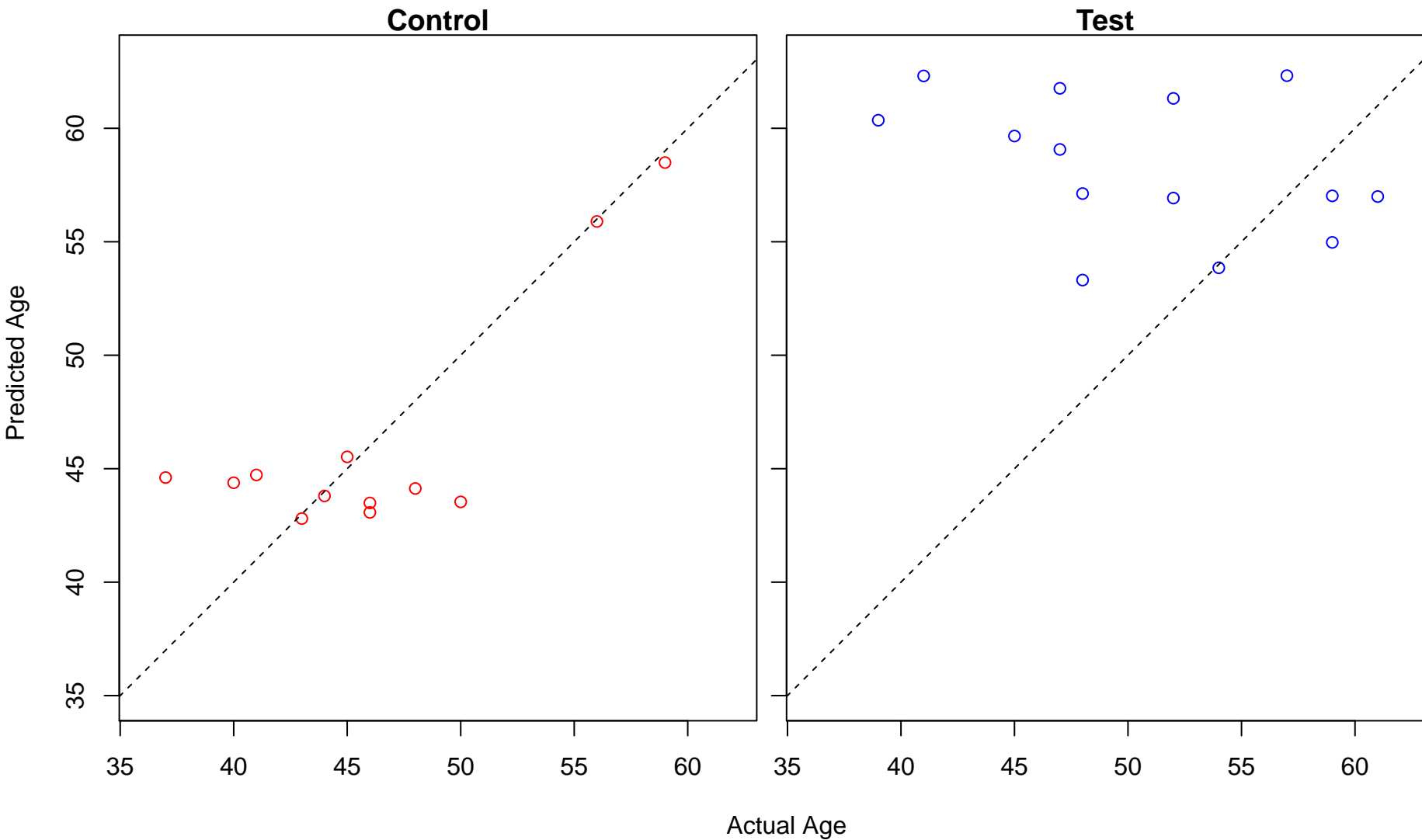
mitotic G1 DNA damage checkpoint (Score: 3.546291)



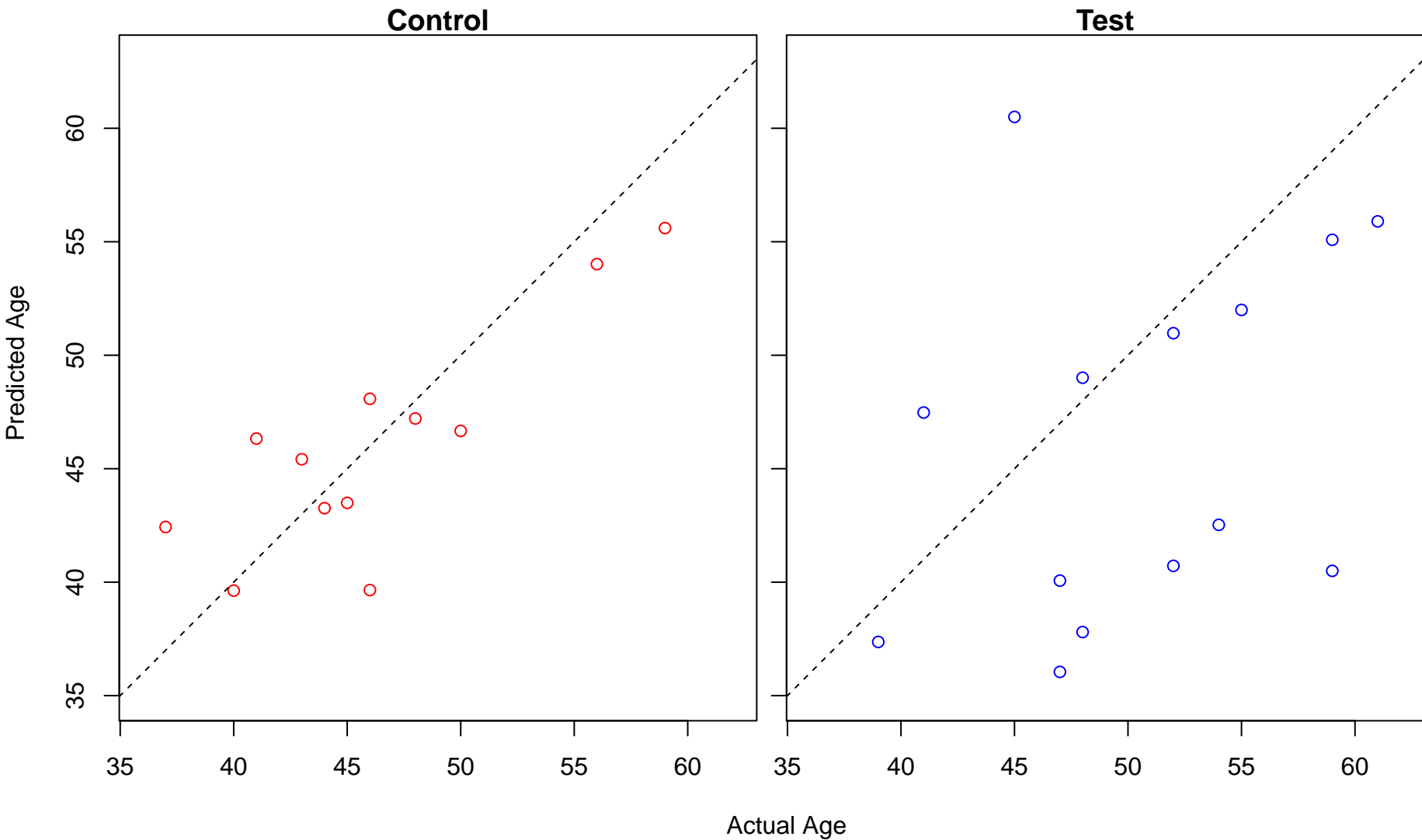
regulation of mammary gland epithelial cell proliferation (Score: 3.545894)



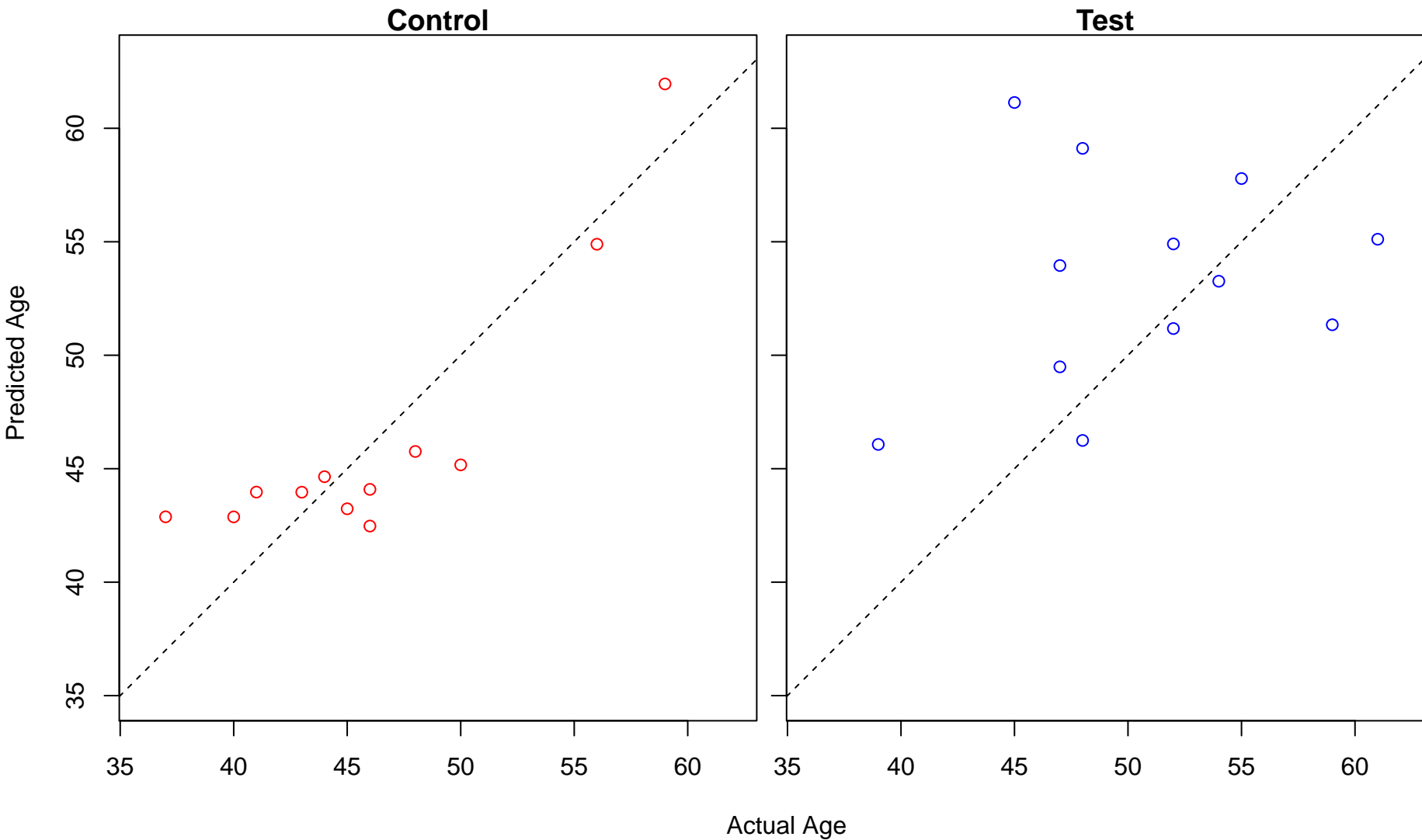
negative regulation of axonogenesis (Score: 3.544619)



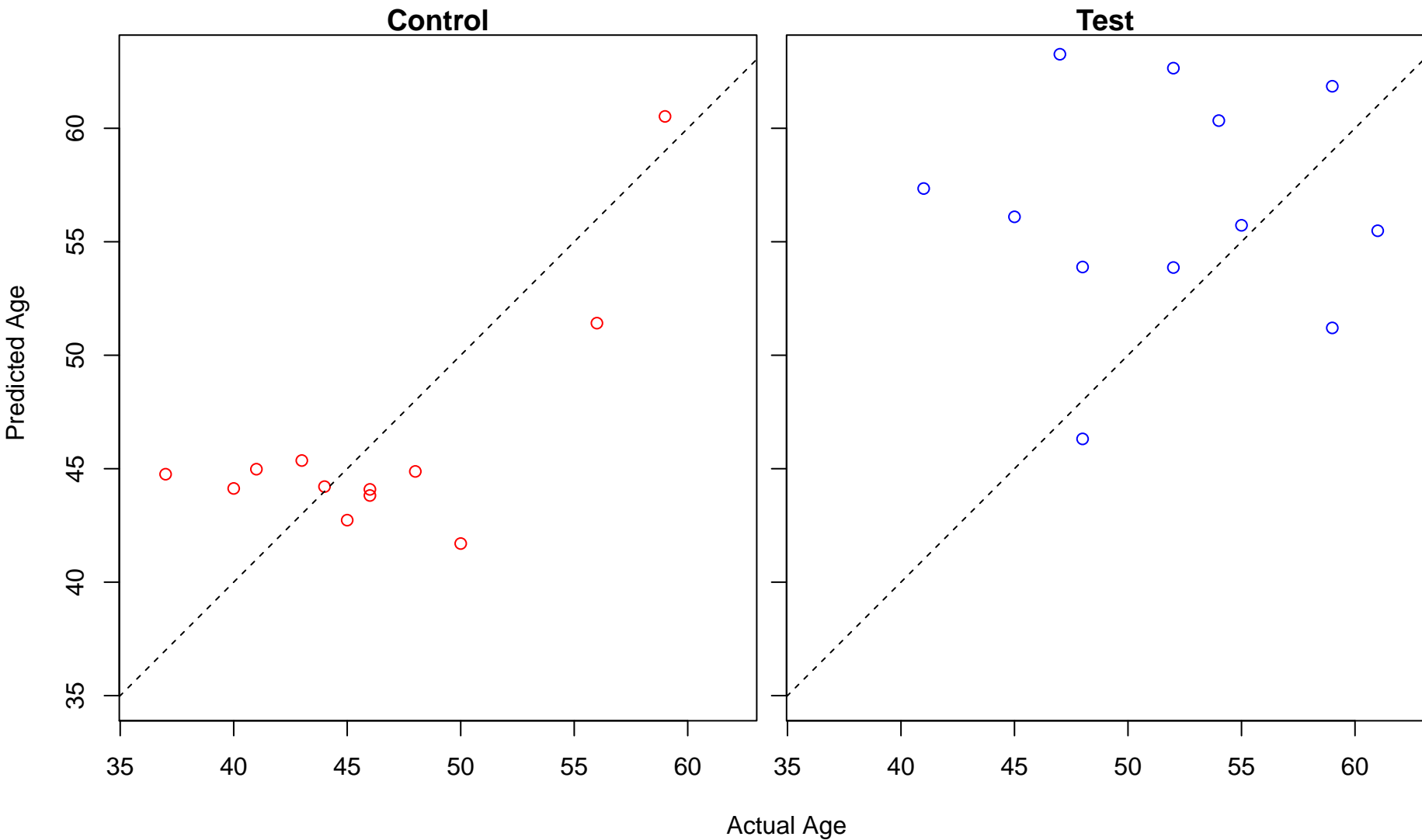
negative regulation of lipid transport (Score: 3.544618)



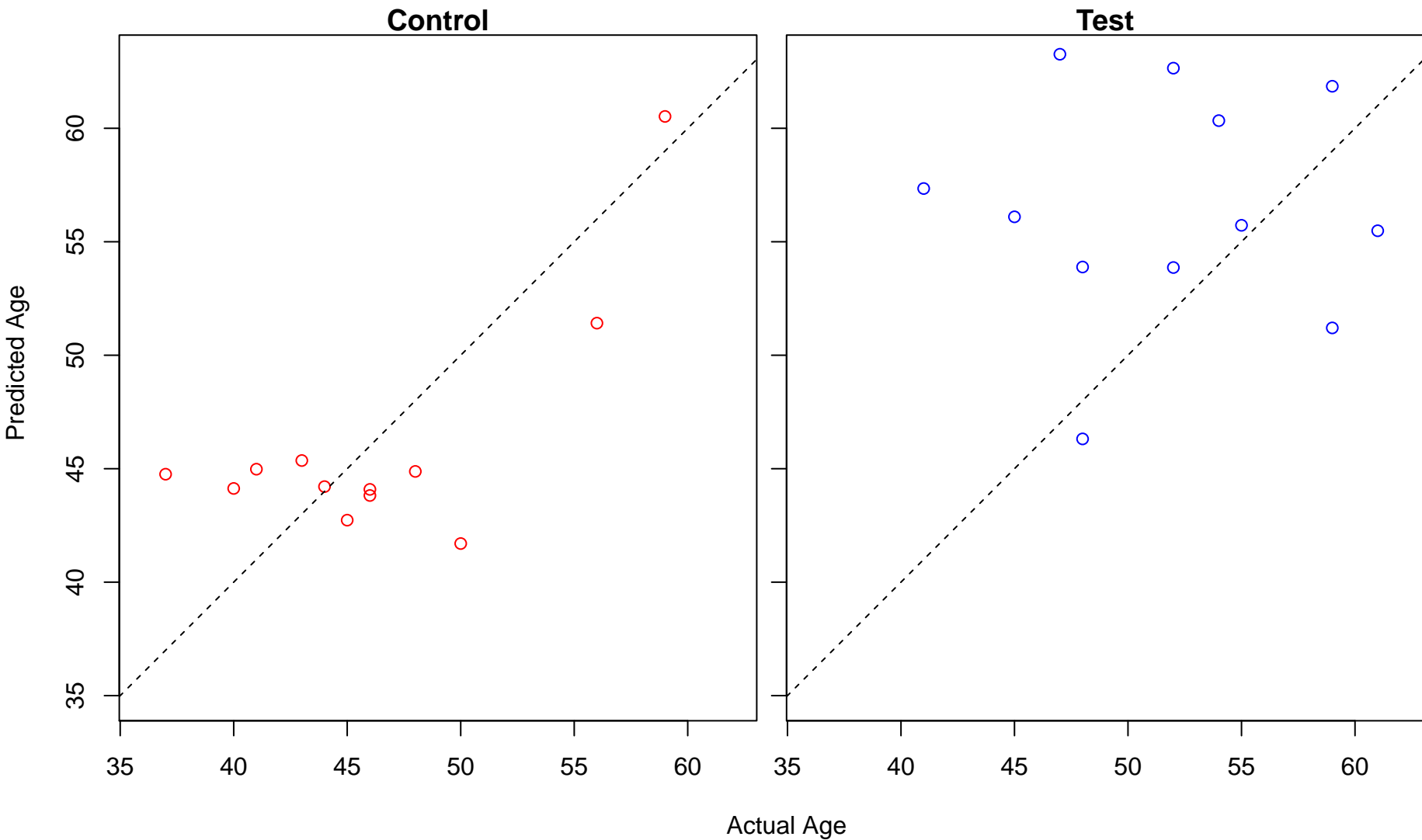
alcohol catabolic process (Score: 3.544038)



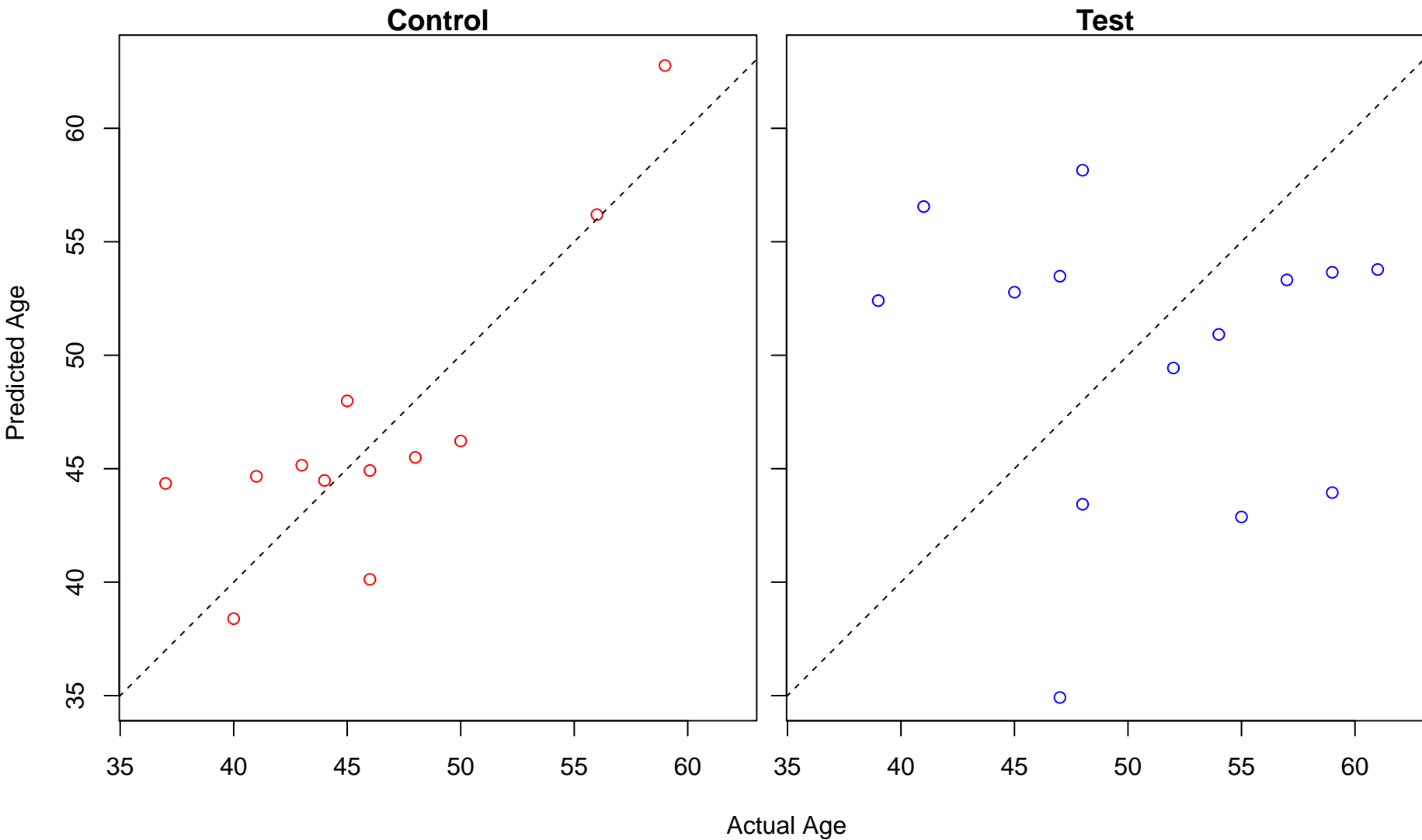
regulation of natural killer cell mediated cytotoxicity (Score: 3.540352)



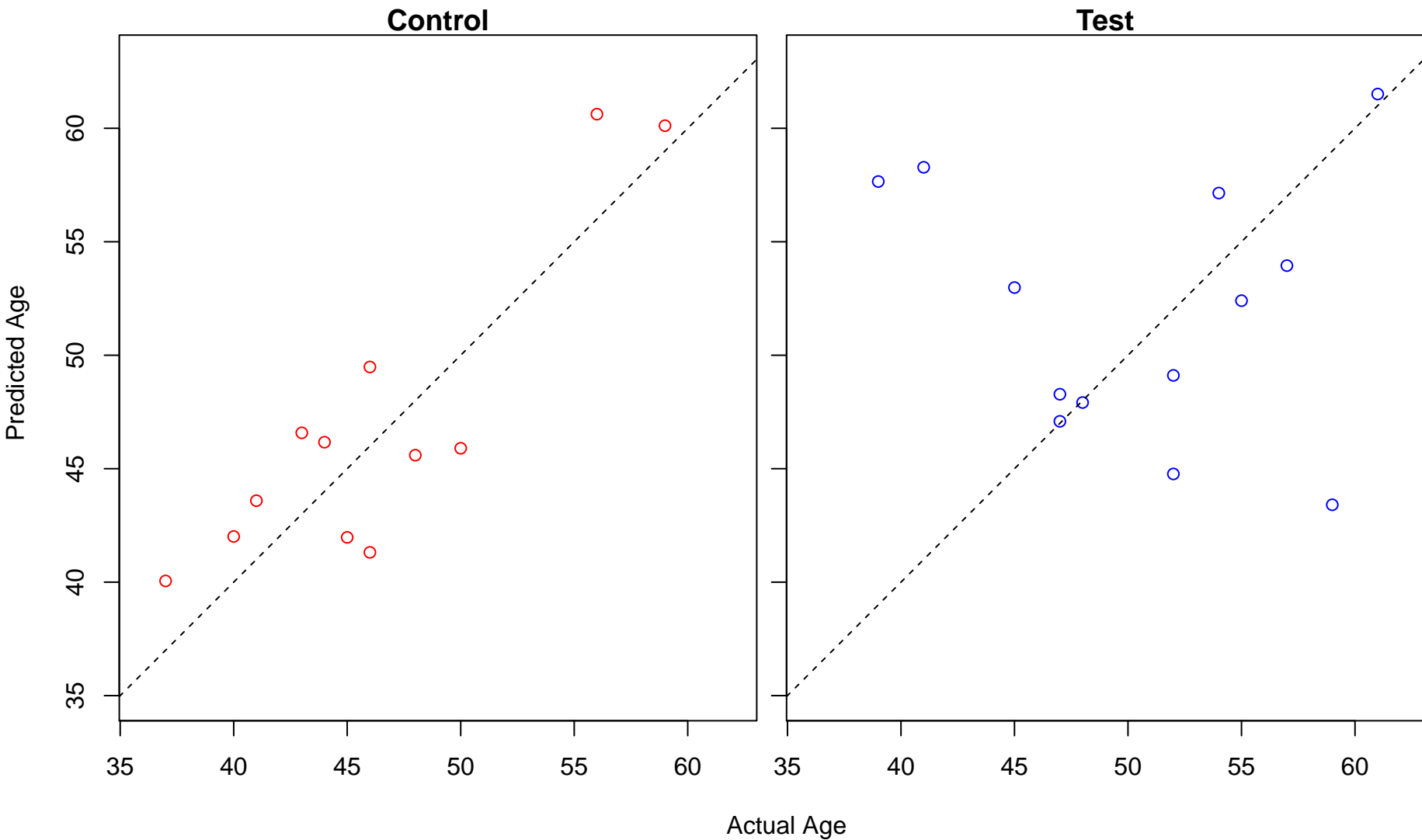
regulation of natural killer cell mediated immunity (Score: 3.540341)



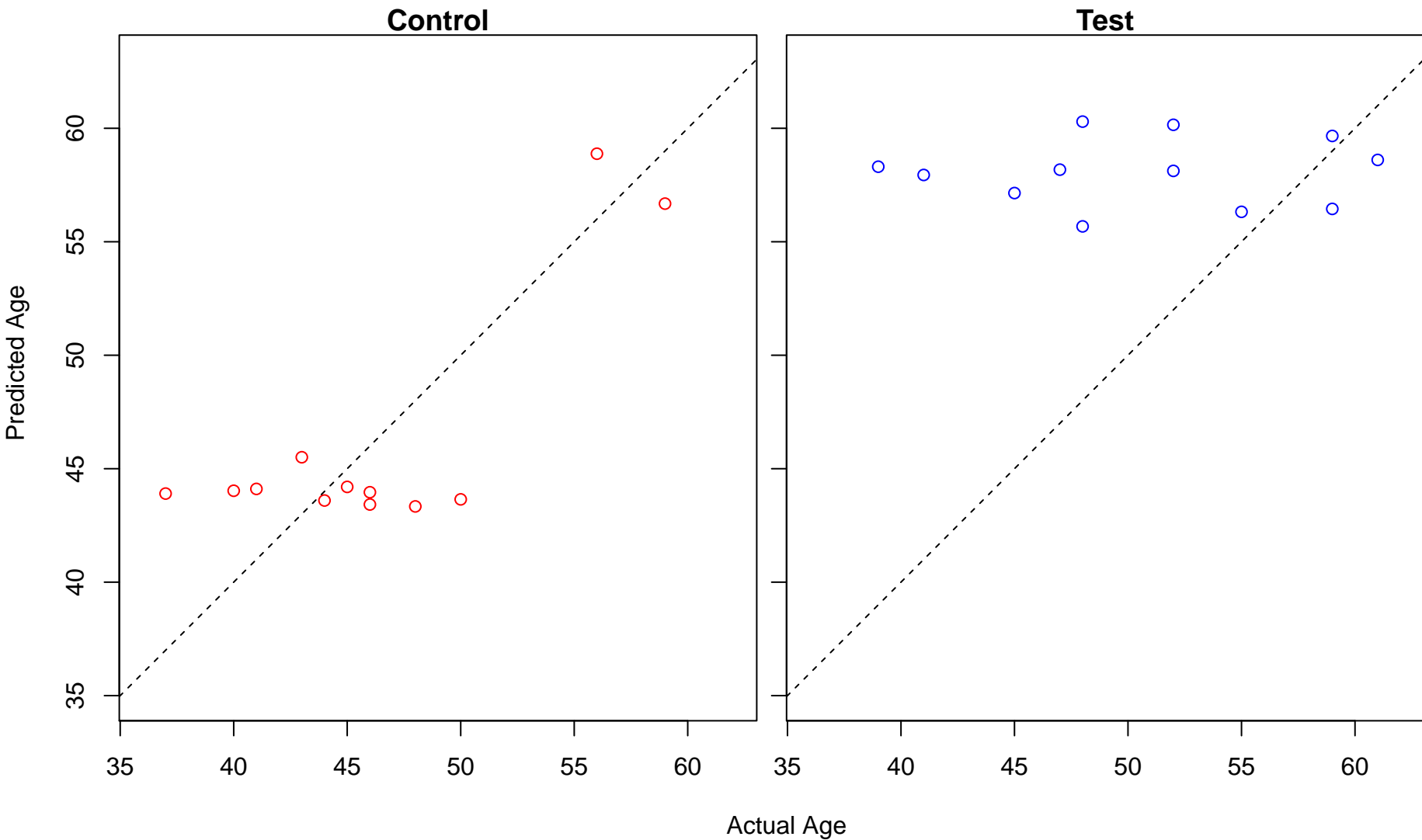
negative regulation of cytoplasmic transport (Score: 3.539424)



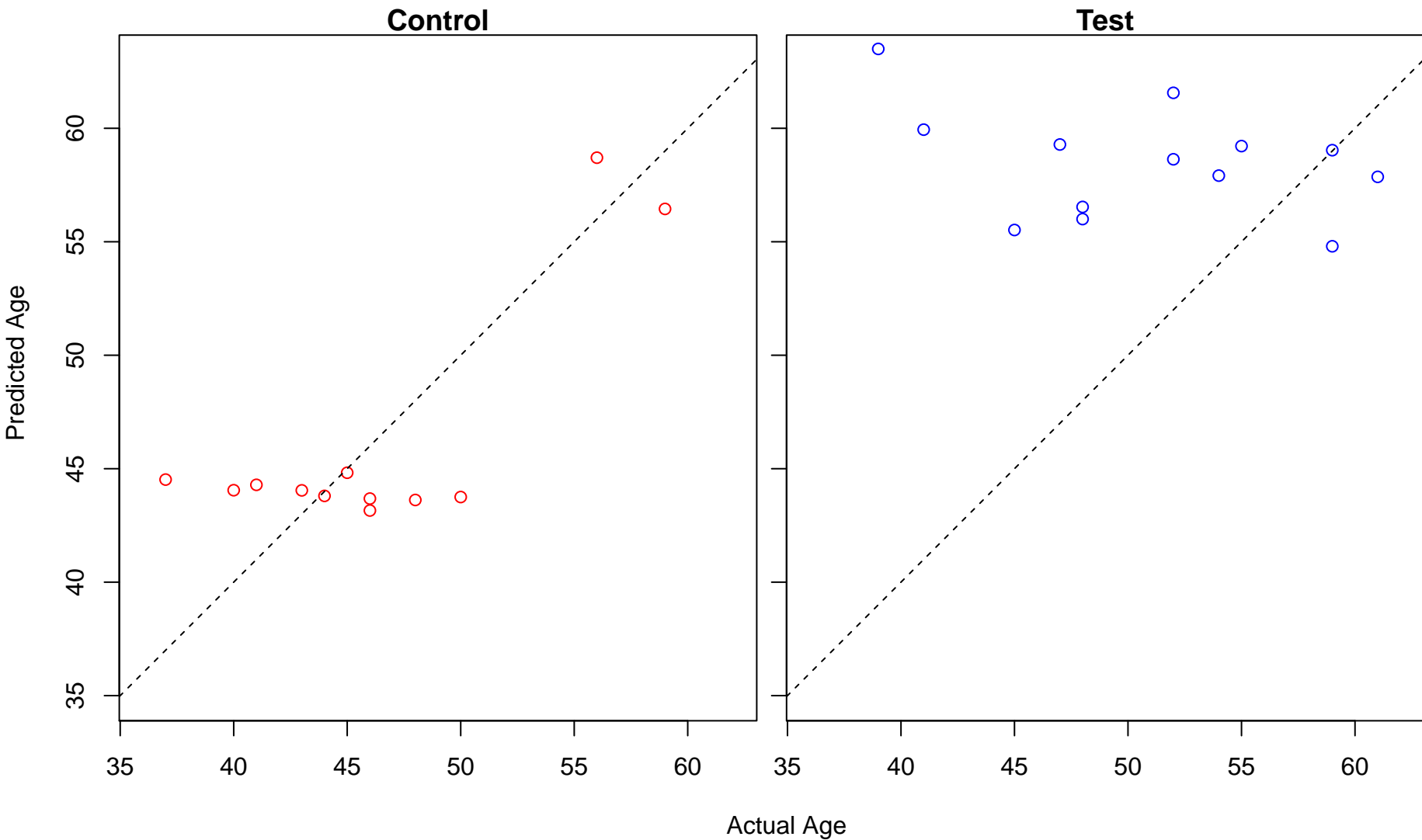
negative regulation of epithelial cell migration (Score: 3.536573)



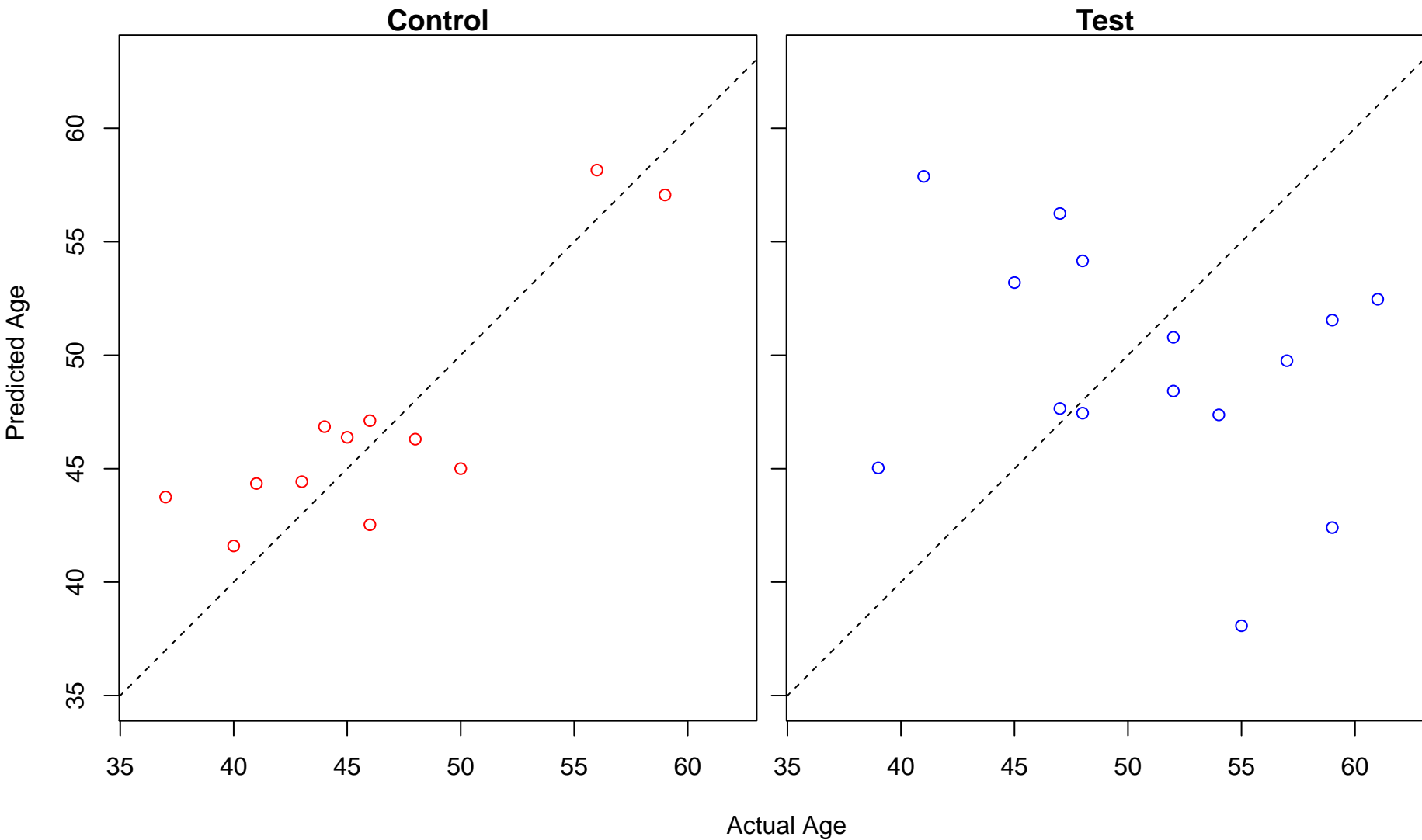
establishment of protein localization to chromosome (Score: 3.535991)



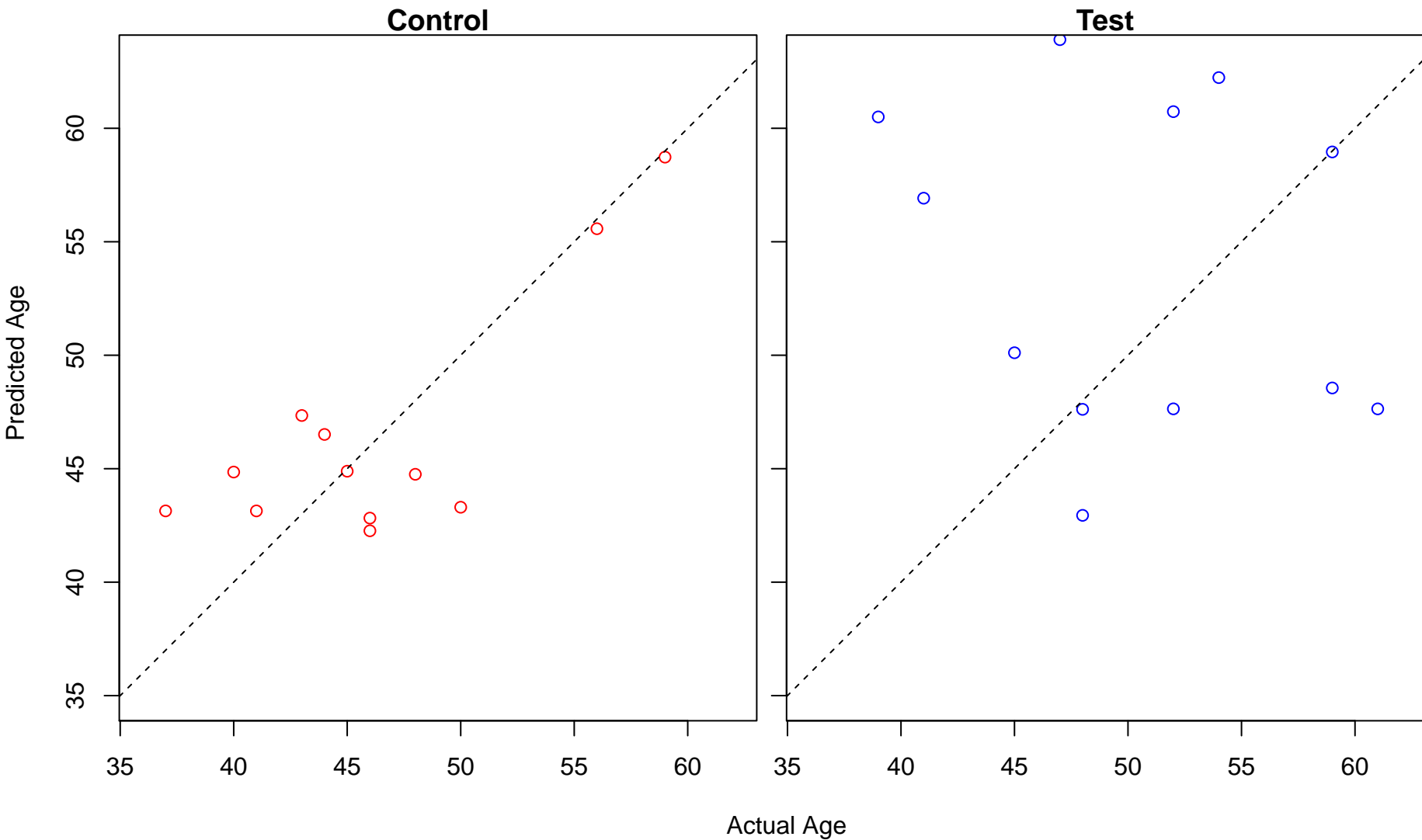
negative regulation of Wnt signaling pathway (Score: 3.533853)



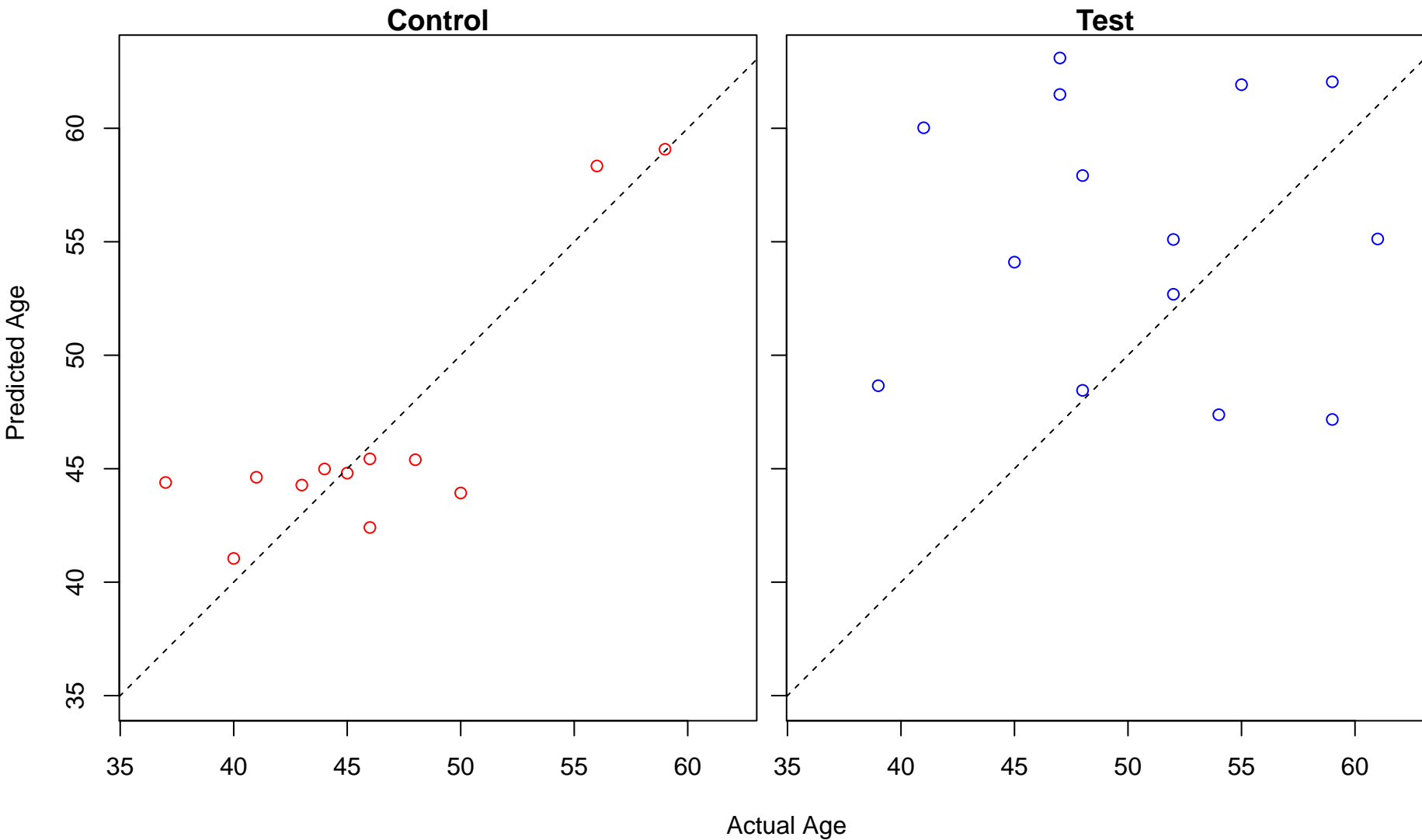
regulation of leukocyte activation (Score: 3.533269)



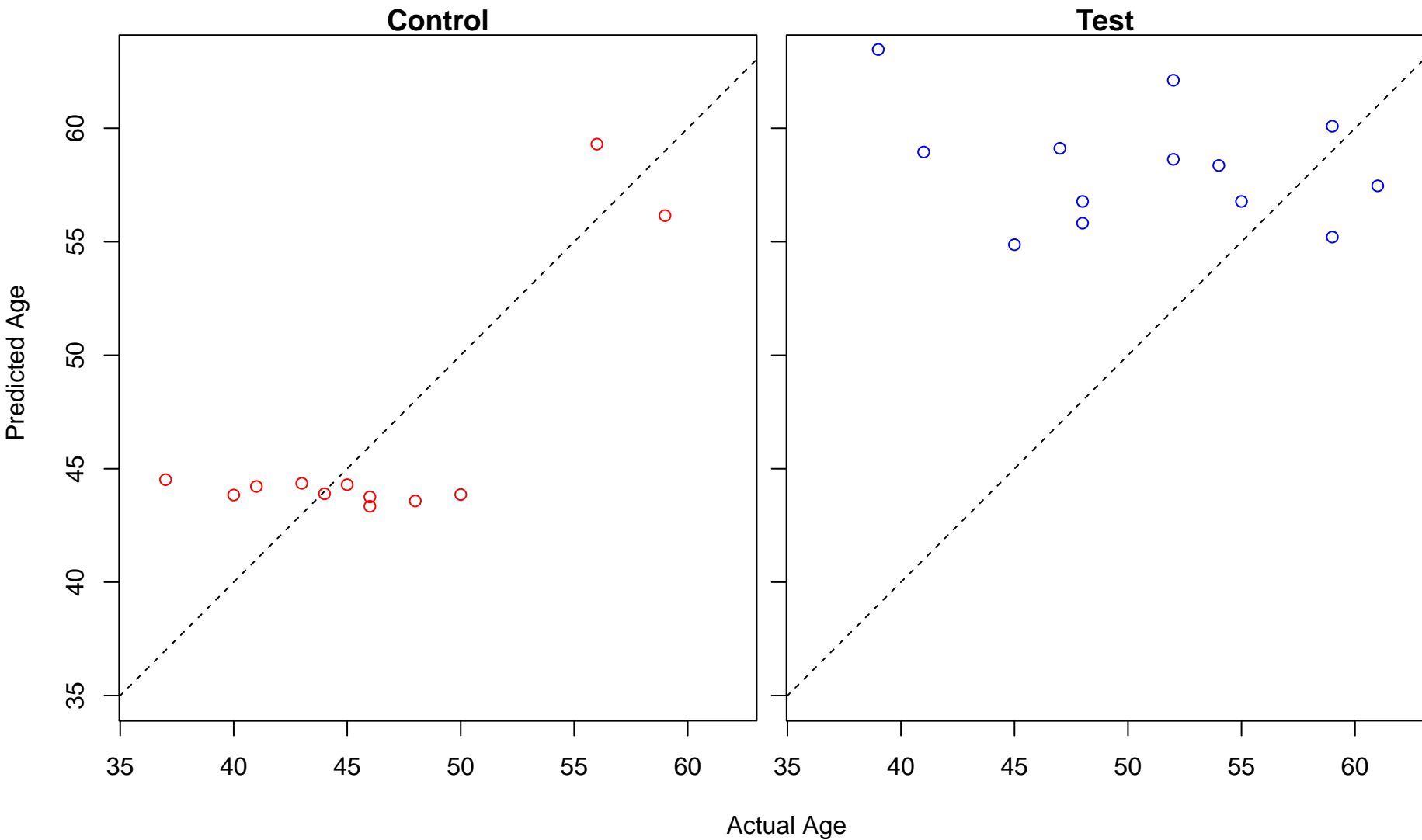
positive regulation of developmental growth (Score: 3.532307)



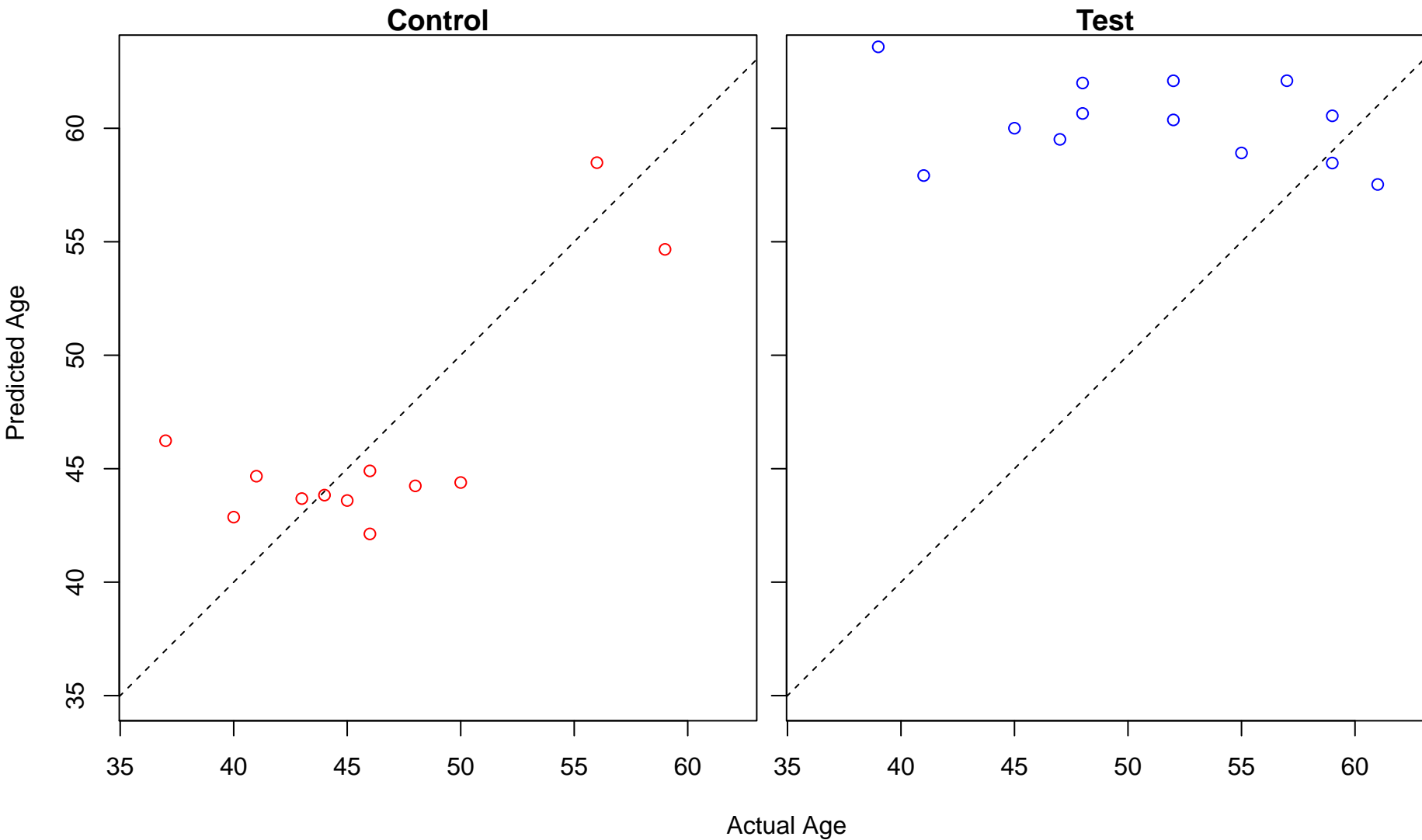
cellular response to tumor necrosis factor (Score: 3.531309)



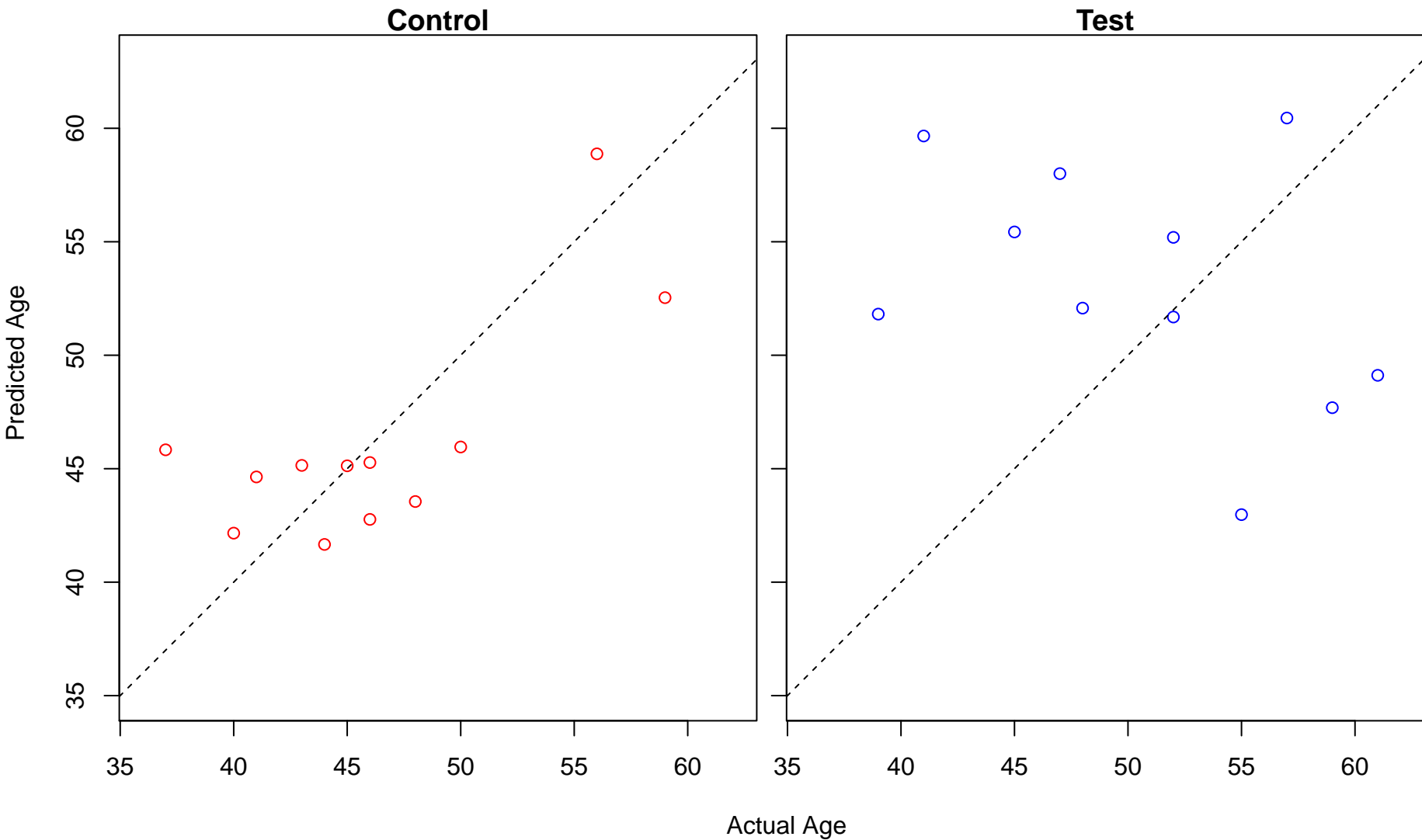
G1 DNA damage checkpoint (Score: 3.531041)



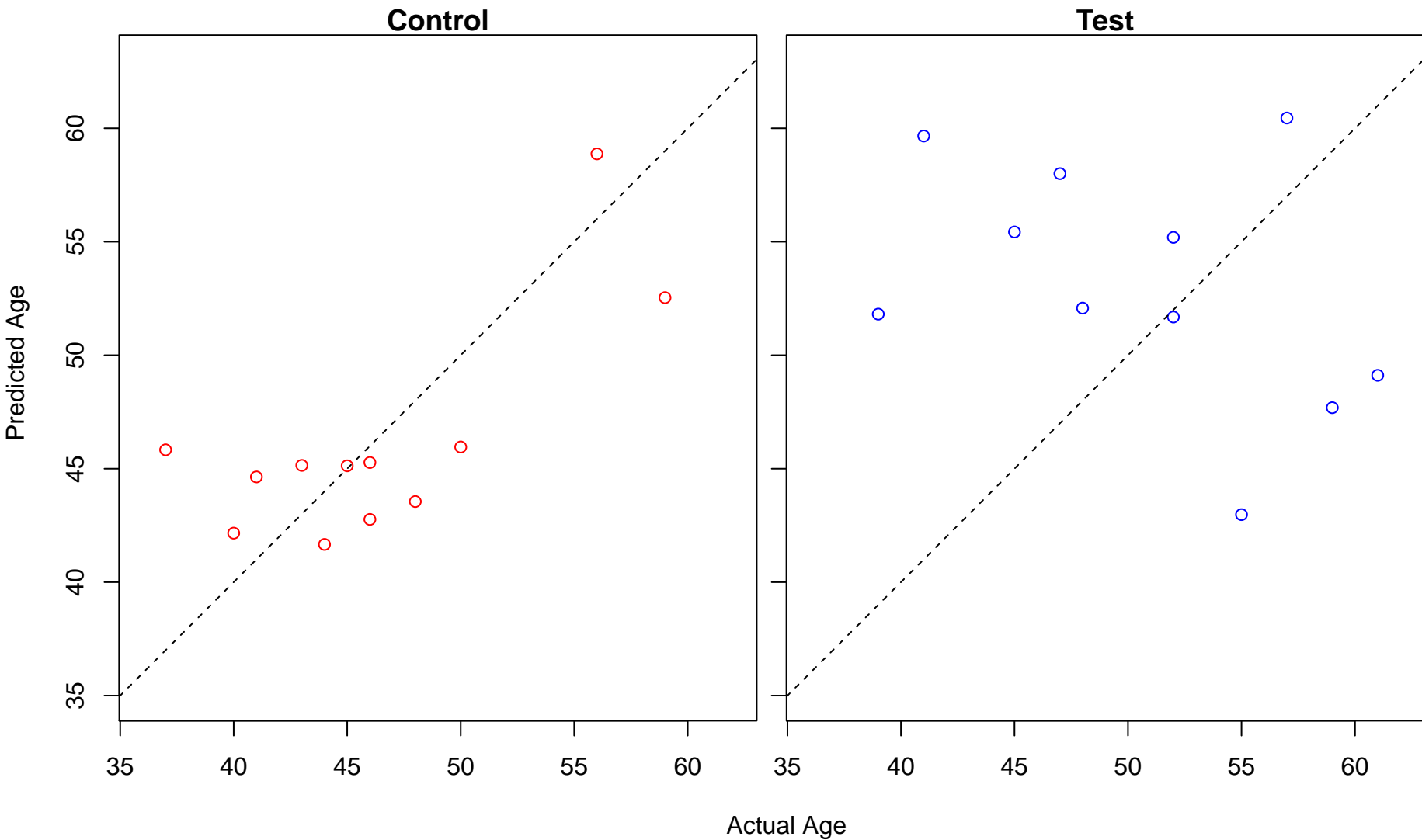
oocyte differentiation (Score: 3.530636)



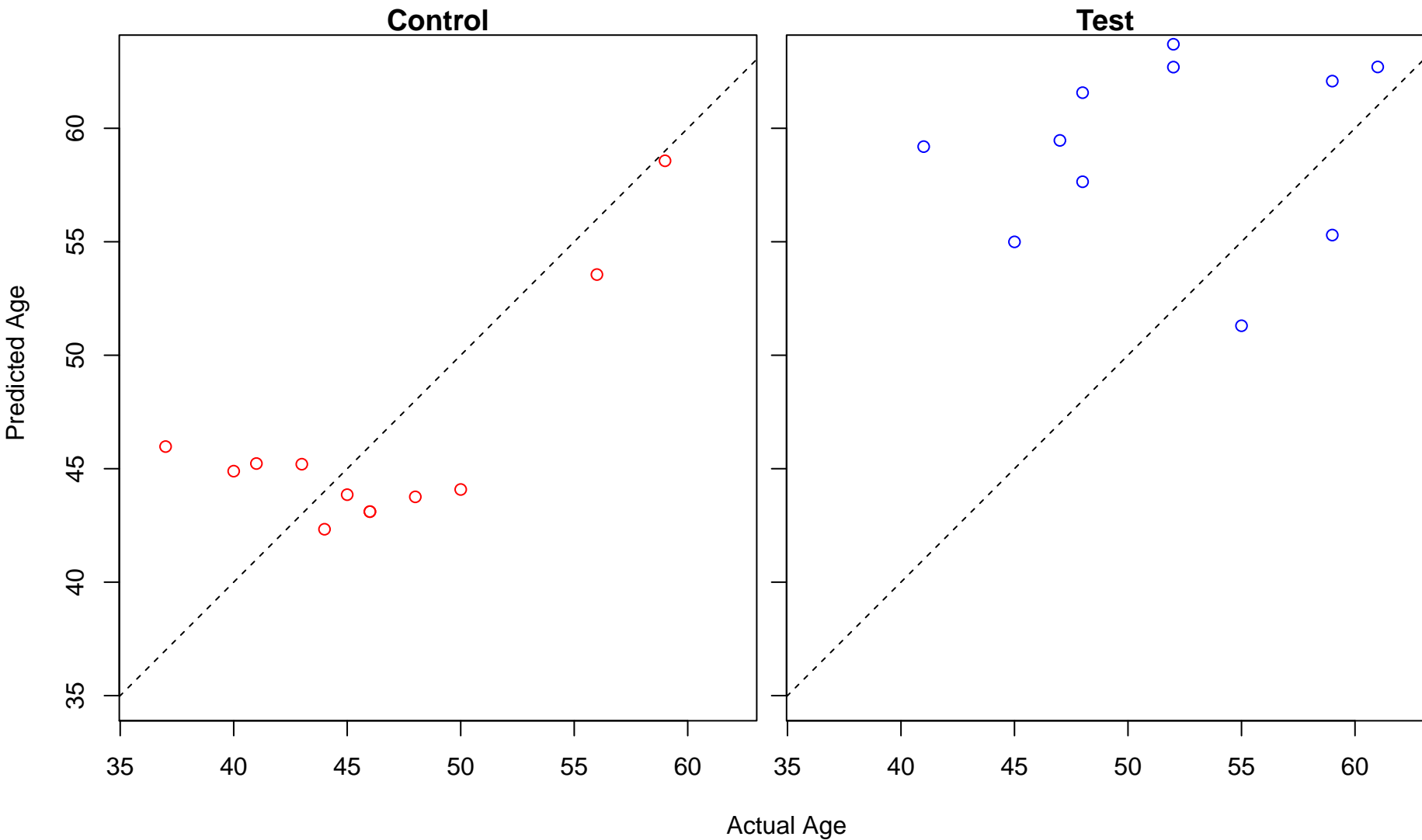
vitamin biosynthetic process (Score: 3.528559)



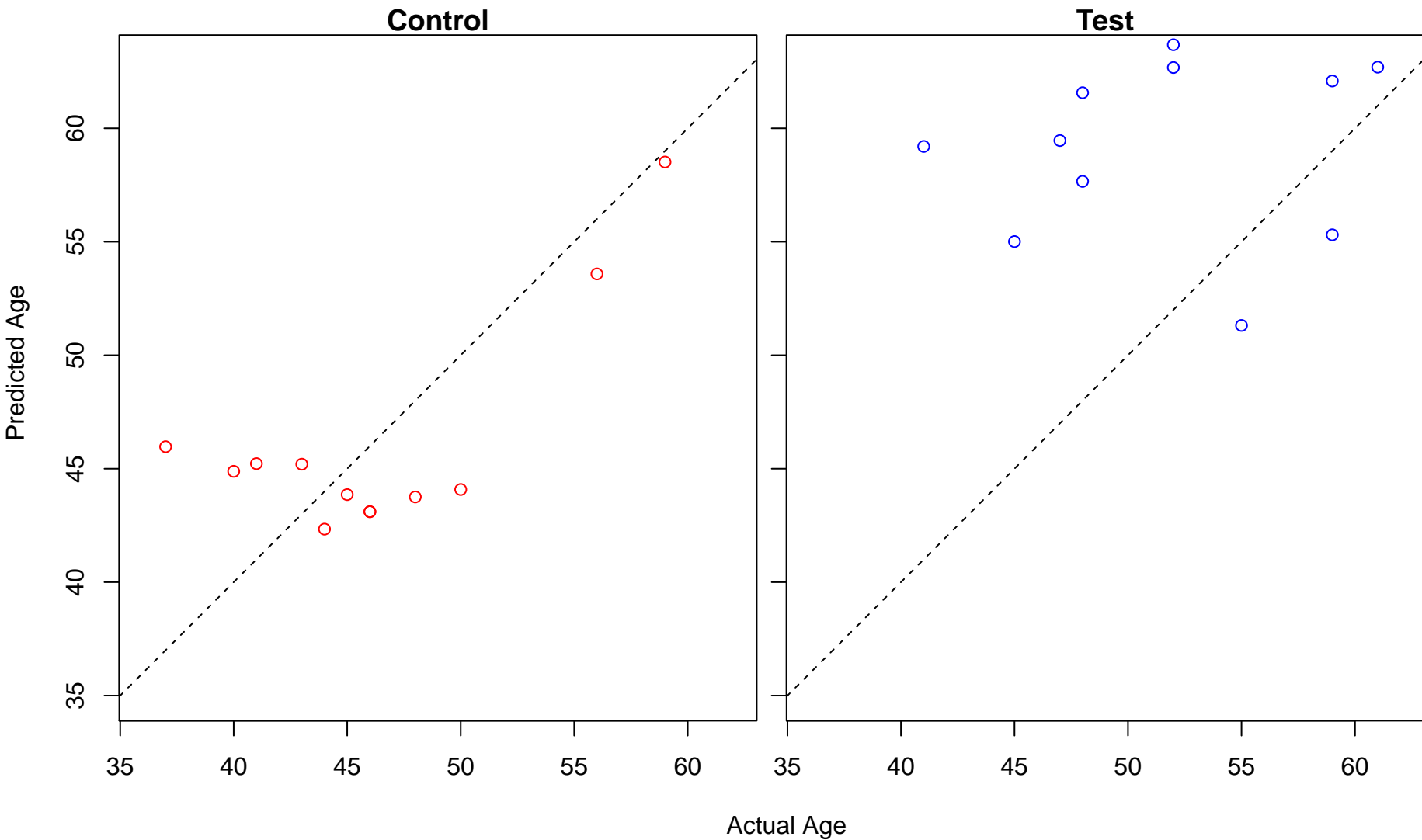
fat-soluble vitamin biosynthetic process (Score: 3.528559)



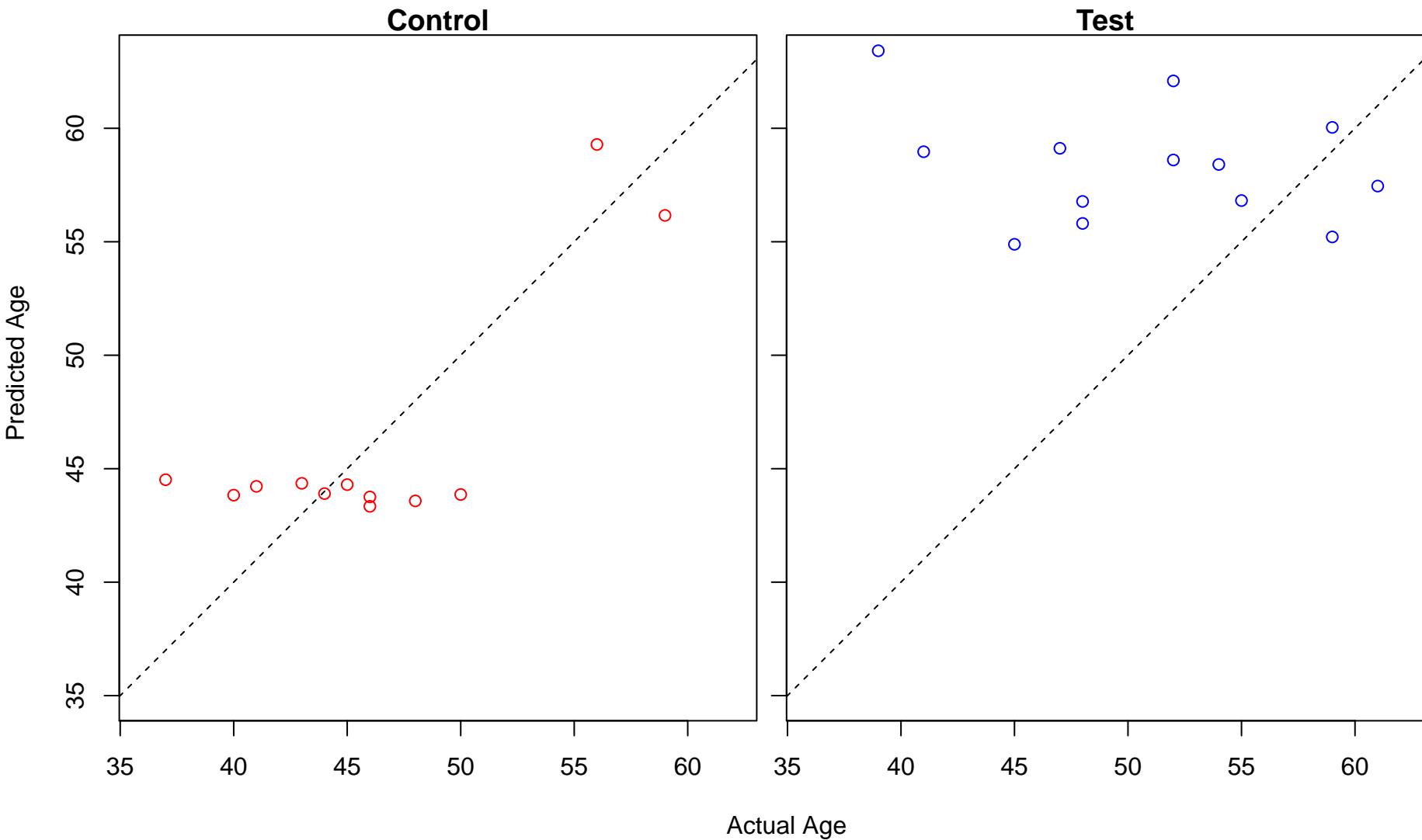
peptidyl-diphthamide biosynthetic process from peptidyl-histidine (Score: 3.527675)



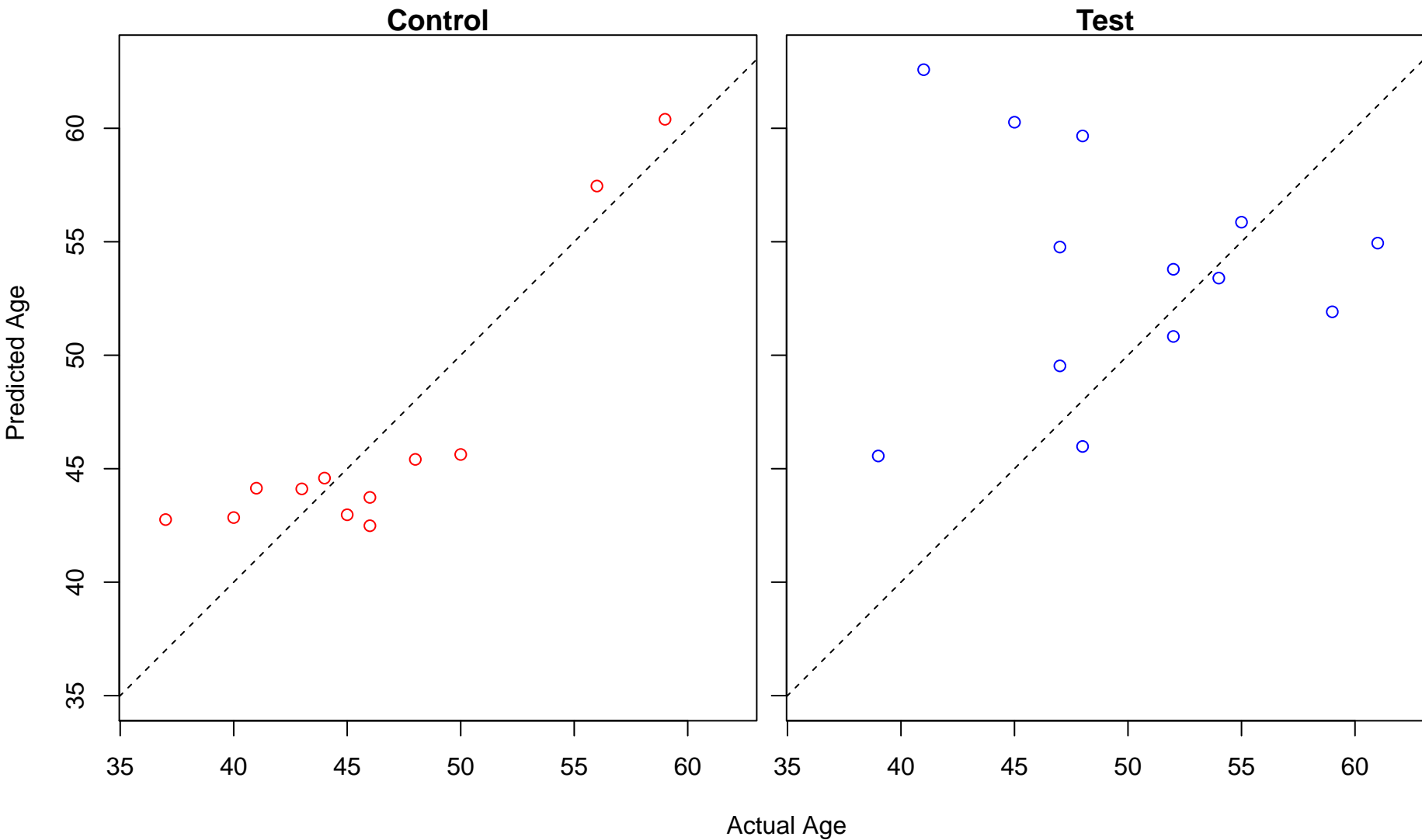
peptidyl-histidine modification (Score: 3.527430)



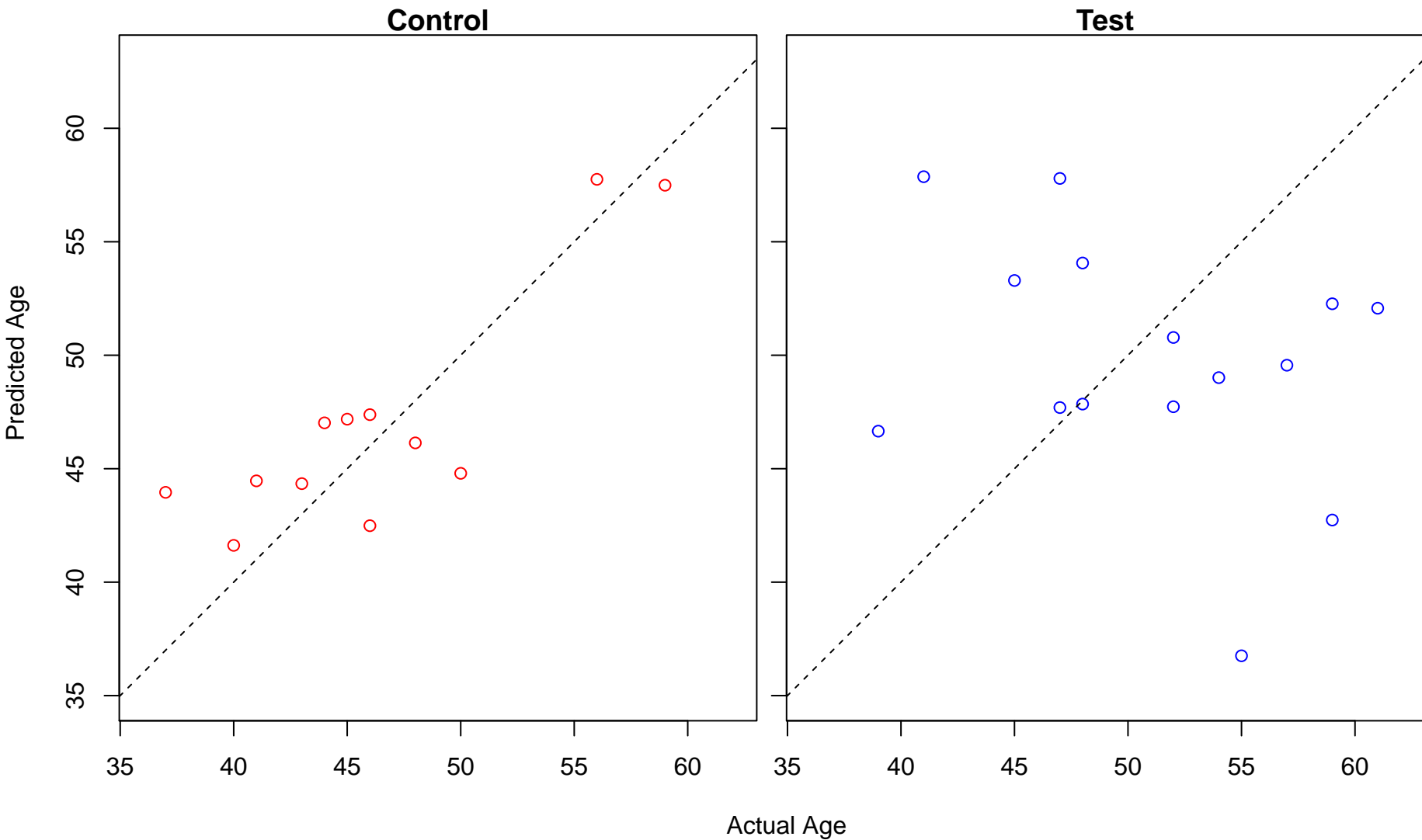
negative regulation of G1/S transition of mitotic cell cycle (Score: 3.526980)



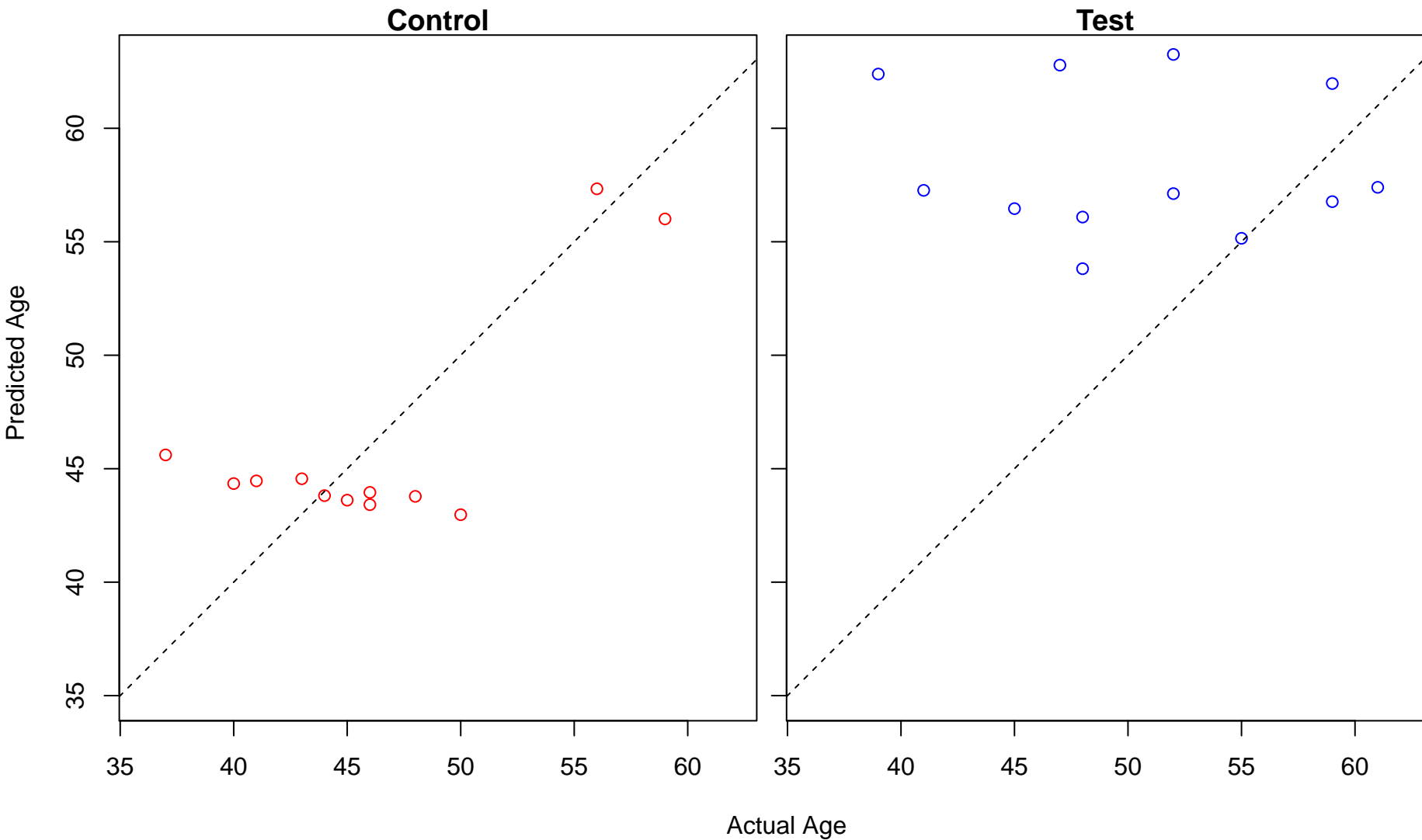
androgen biosynthetic process (Score: 3.524275)



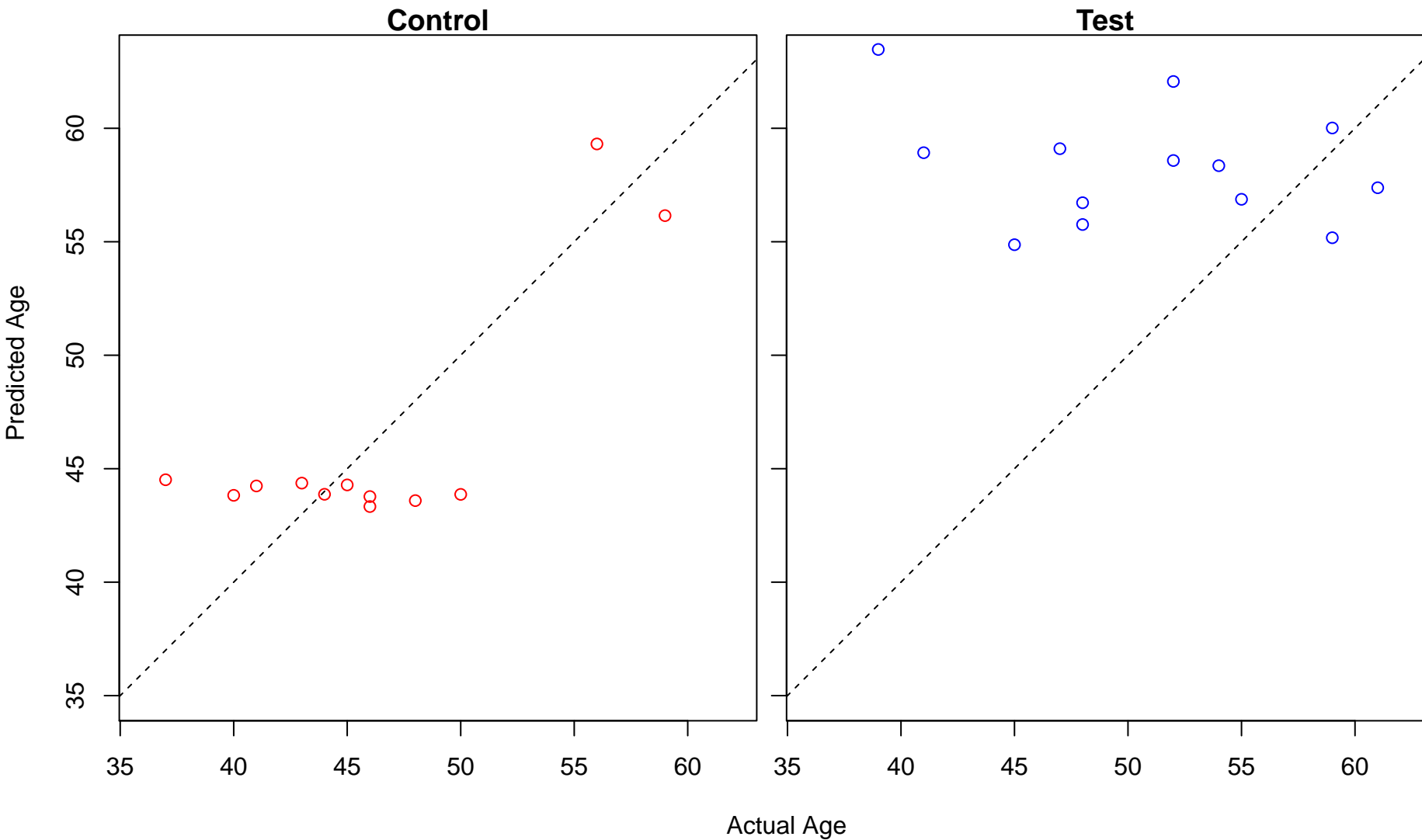
regulation of lymphocyte activation (Score: 3.524180)



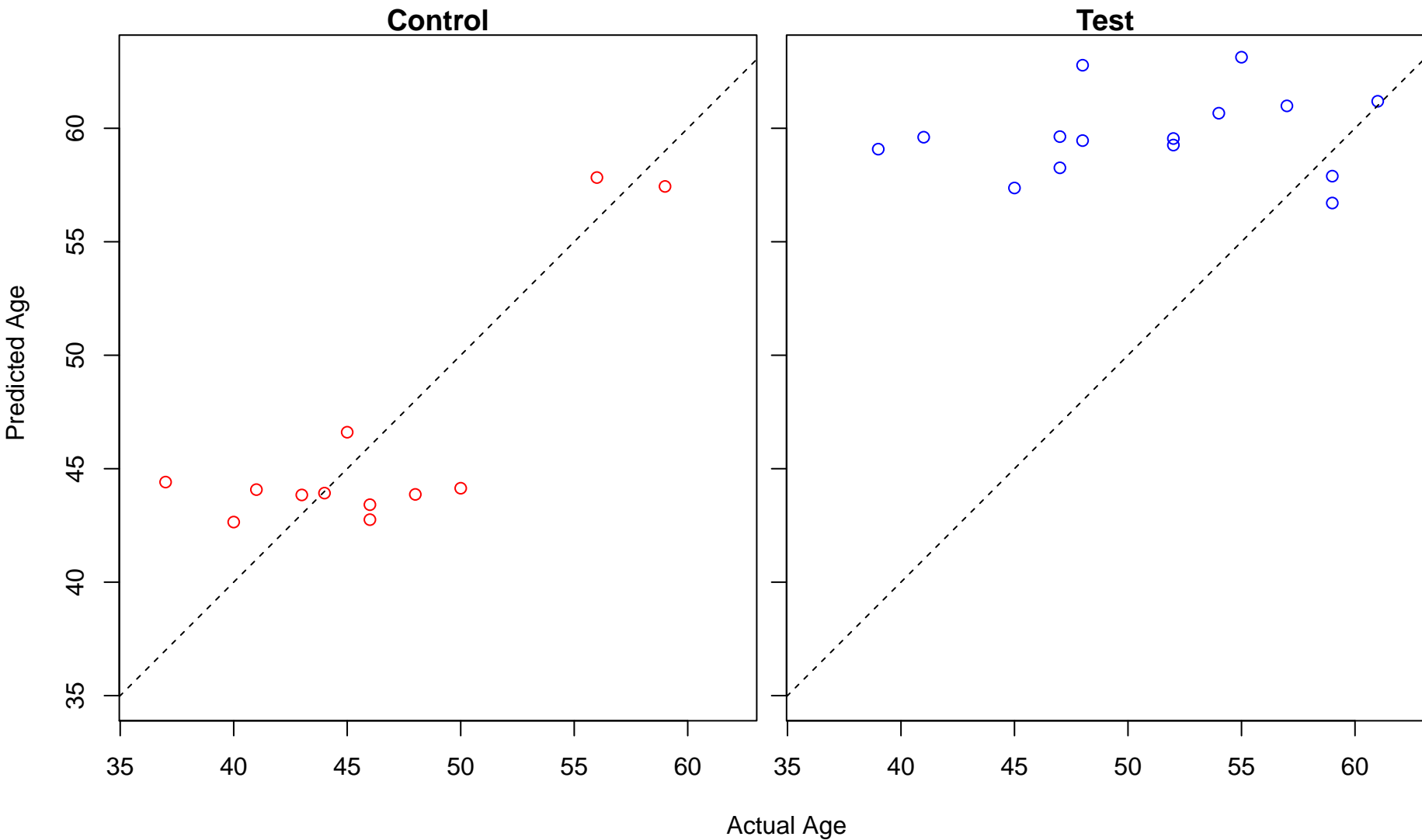
positive regulation of regulated secretory pathway (Score: 3.523020)



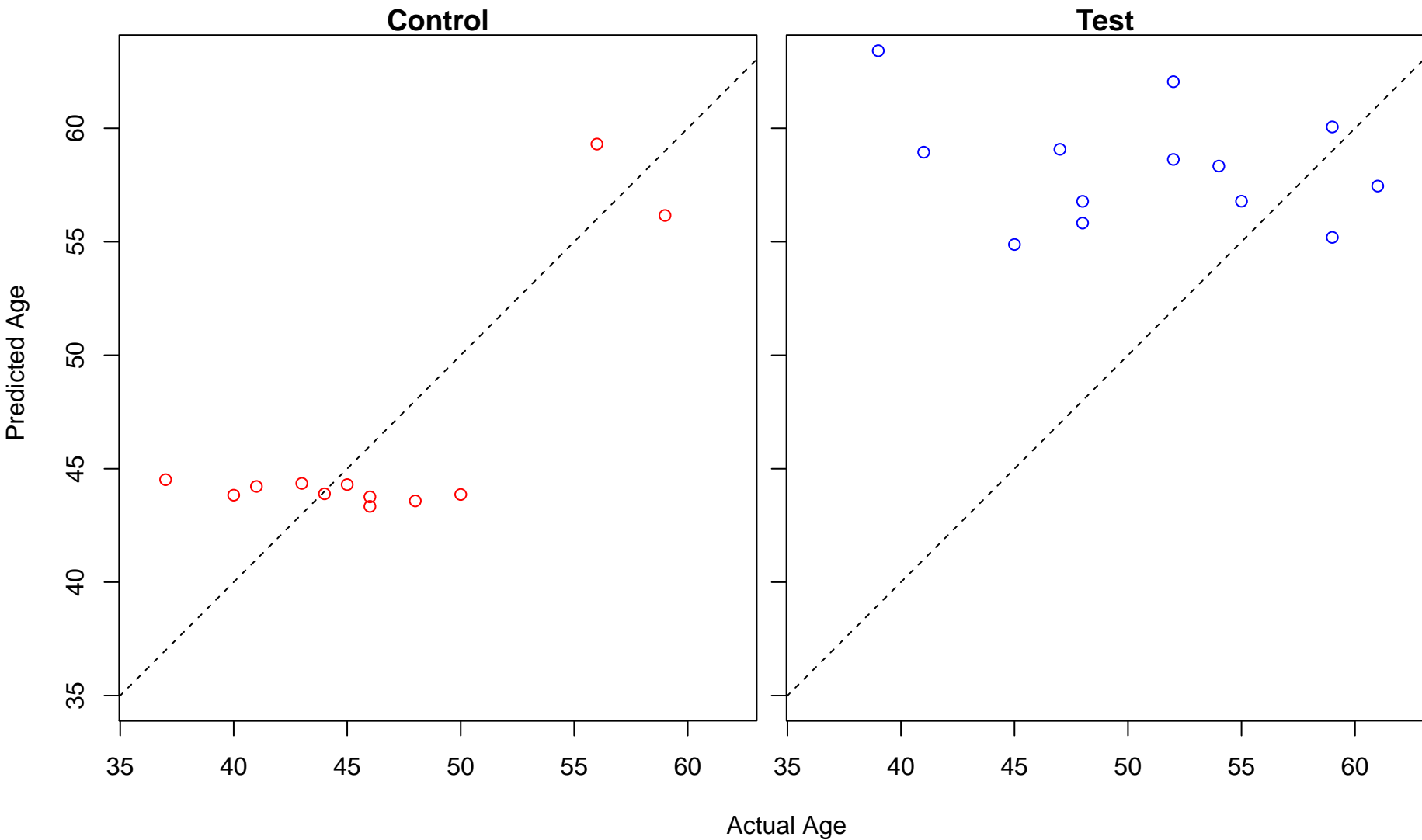
DNA damage response, signal transduction by p53 class mediator (Score: 3.522765)



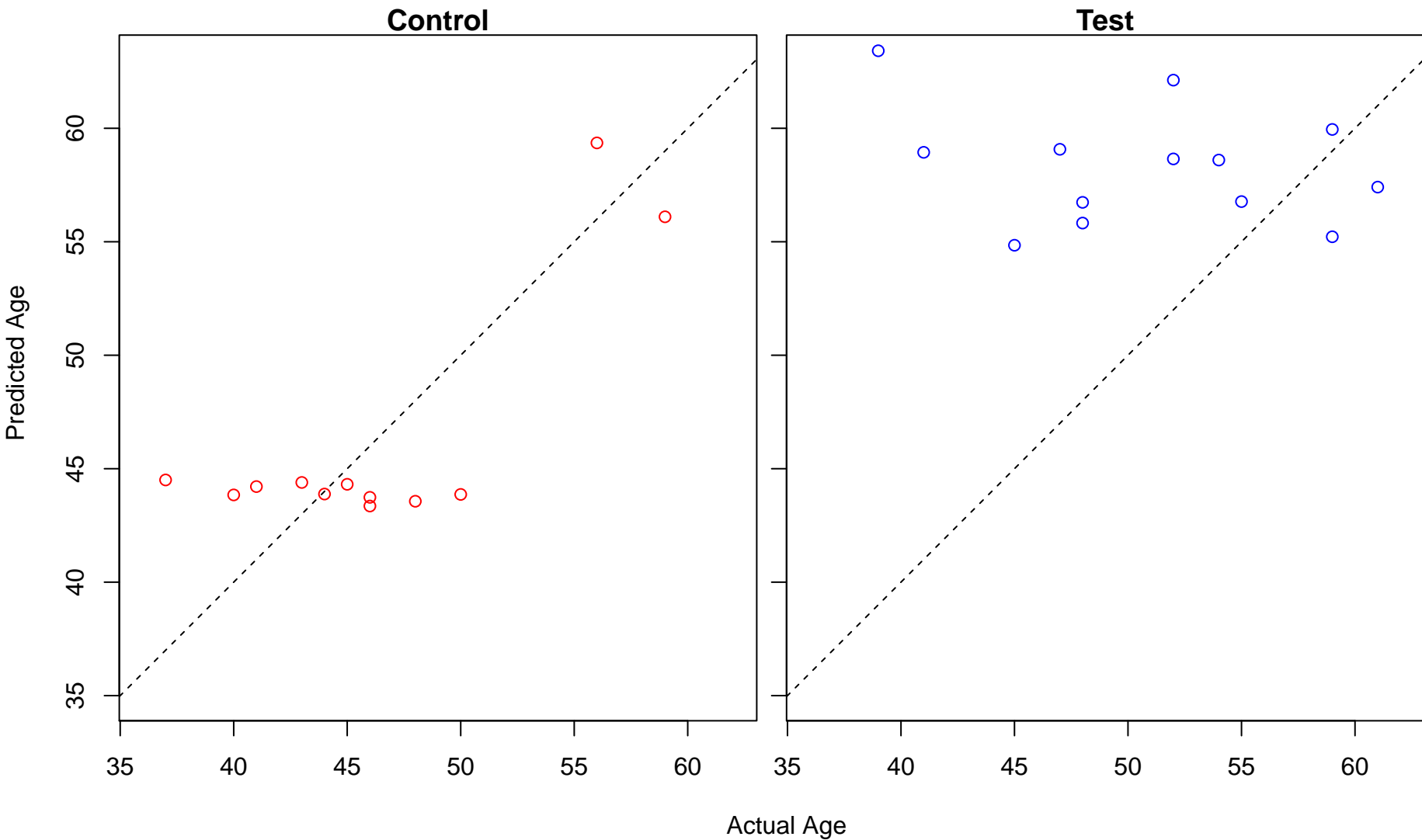
regulation of DNA damage checkpoint (Score: 3.522181)



mitotic DNA damage checkpoint (Score: 3.521910)

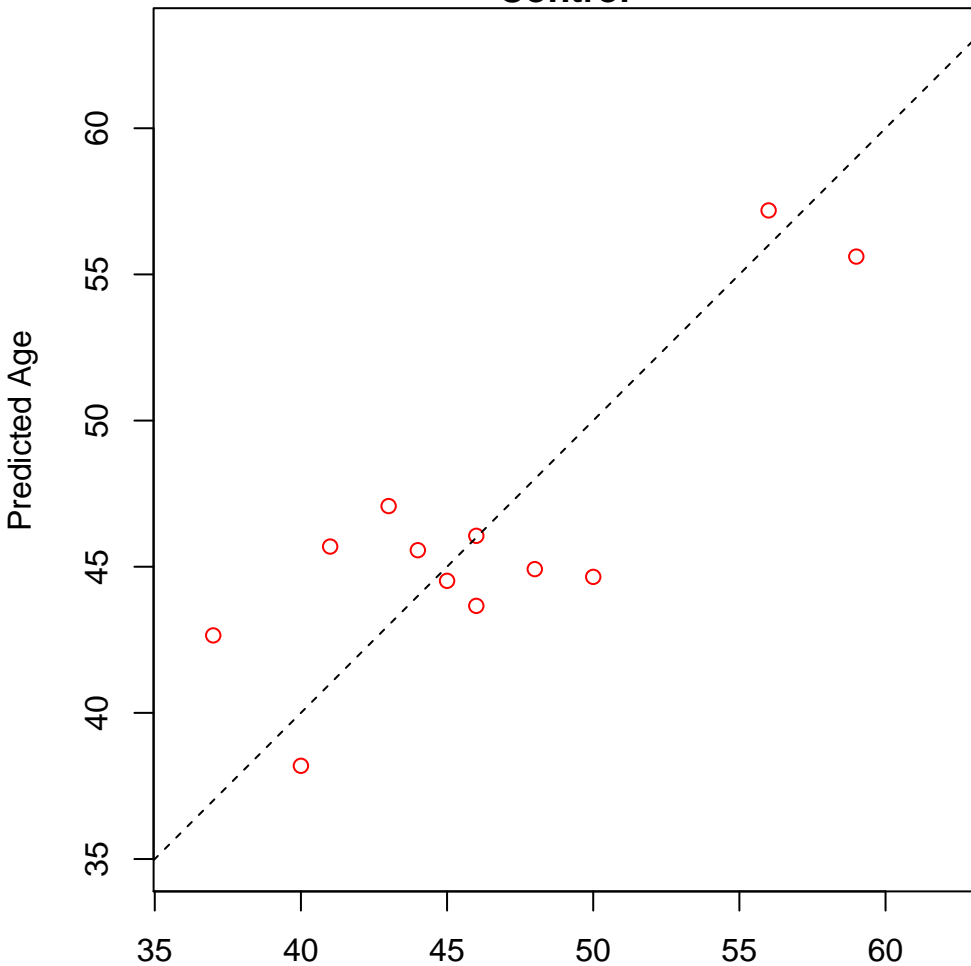


regulation of cell cycle arrest (Score: 3.521682)

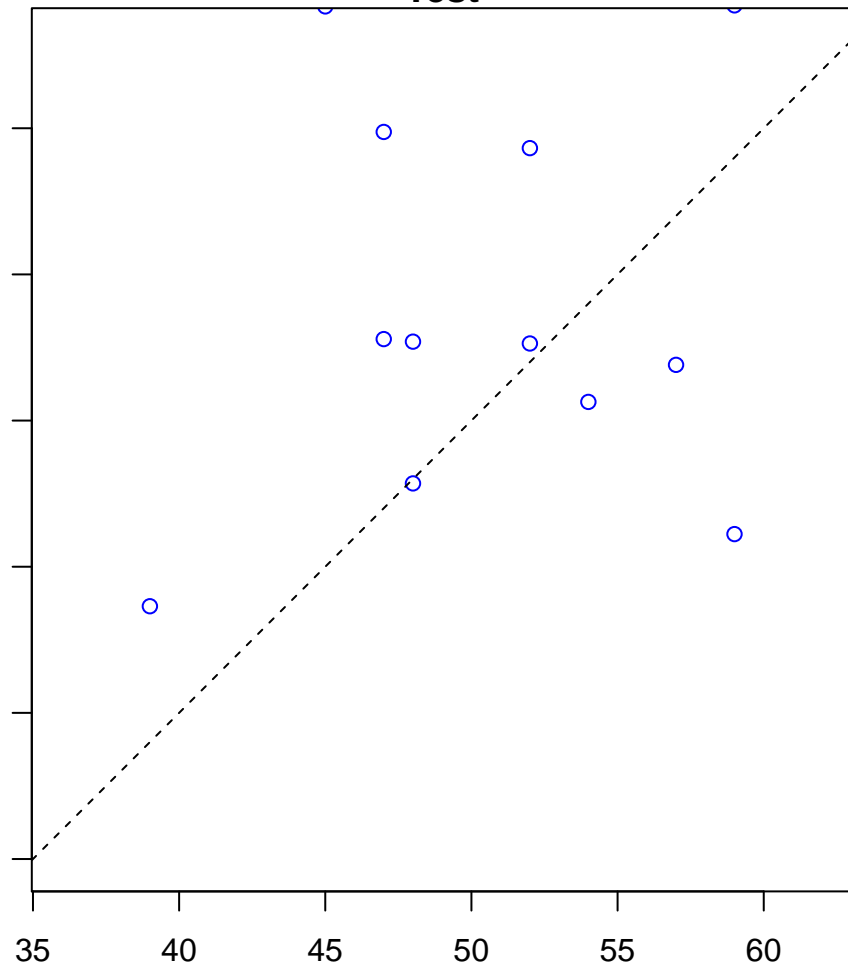


negative regulation of cell proliferation (Score: 3.519722)

Control

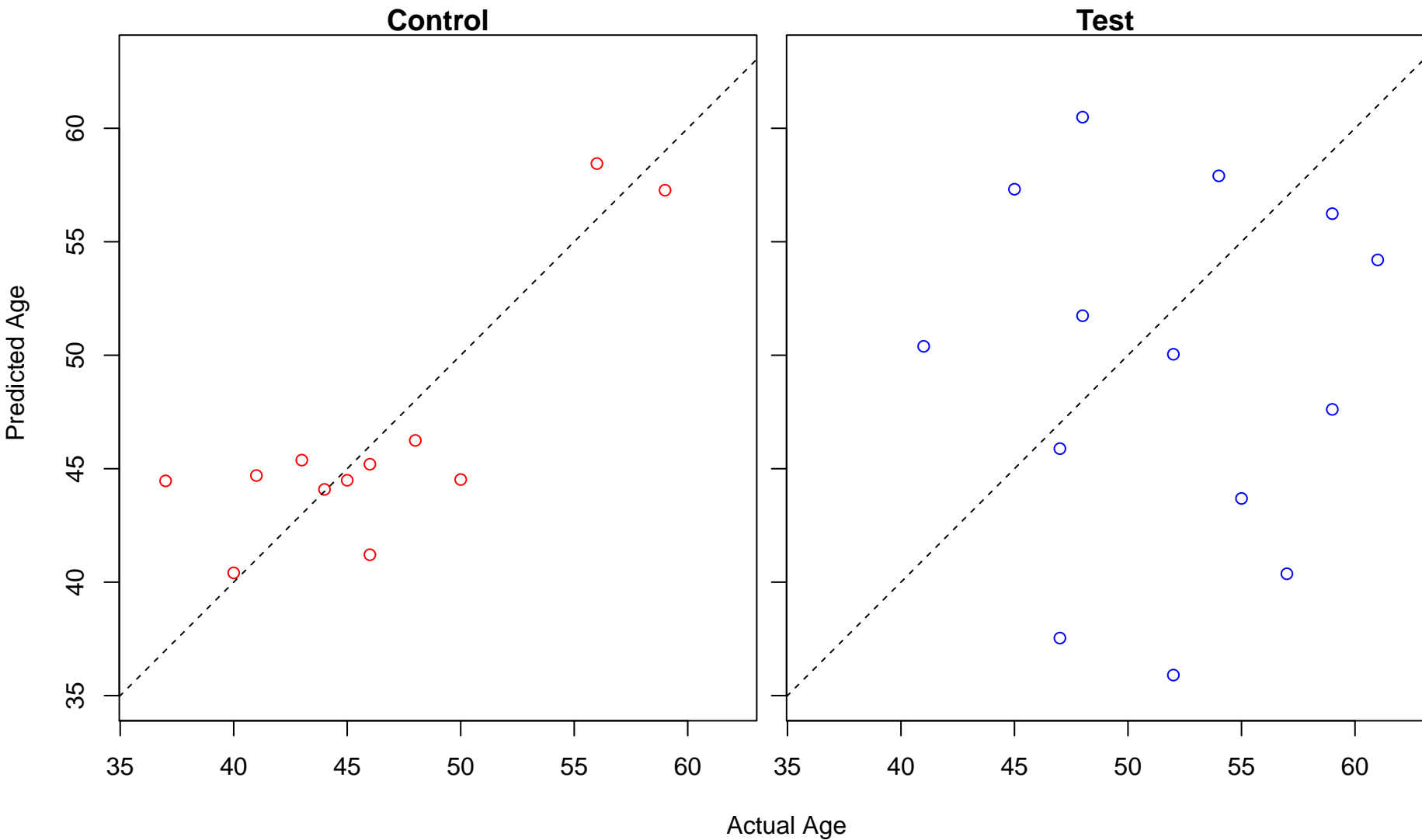


Test

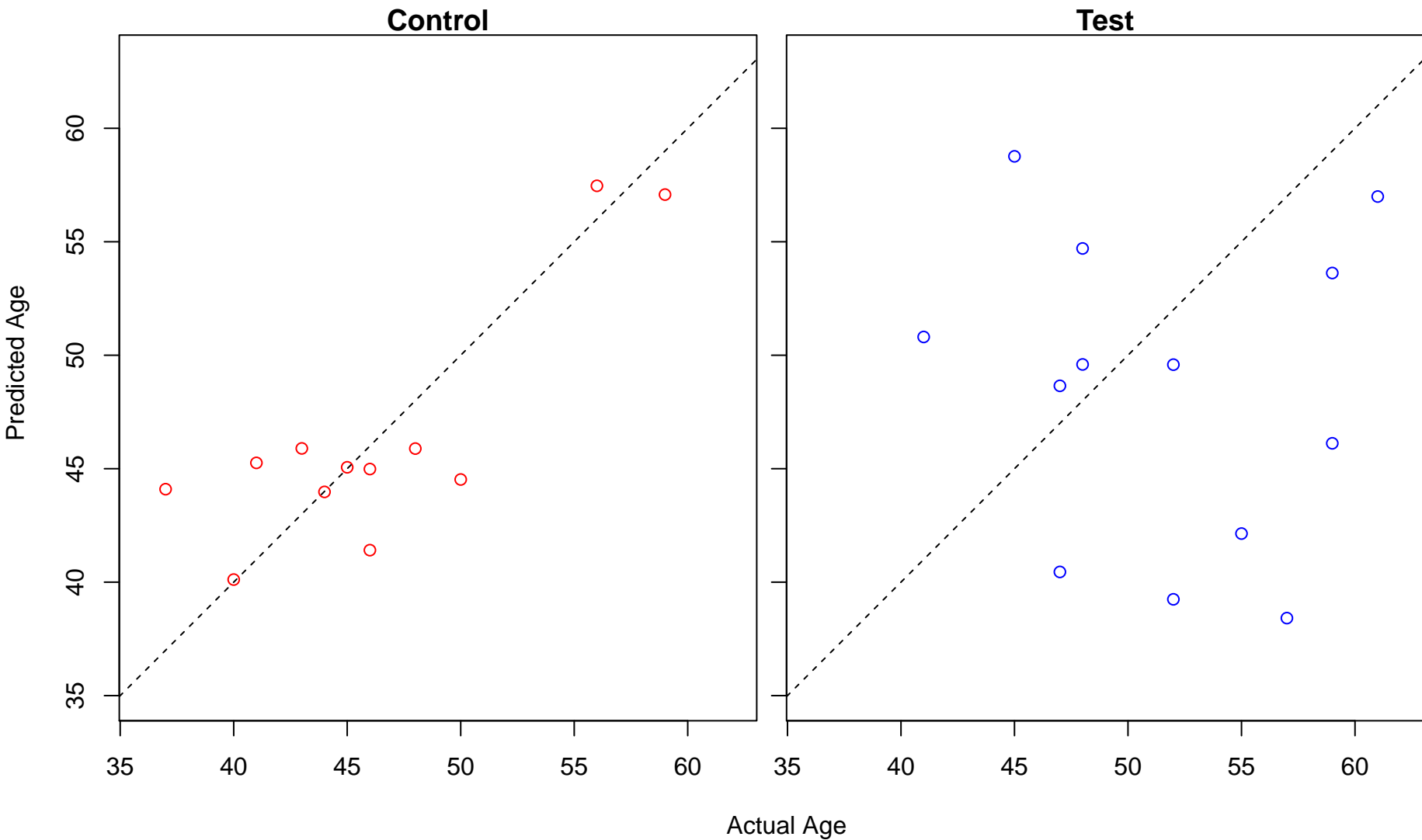


Actual Age

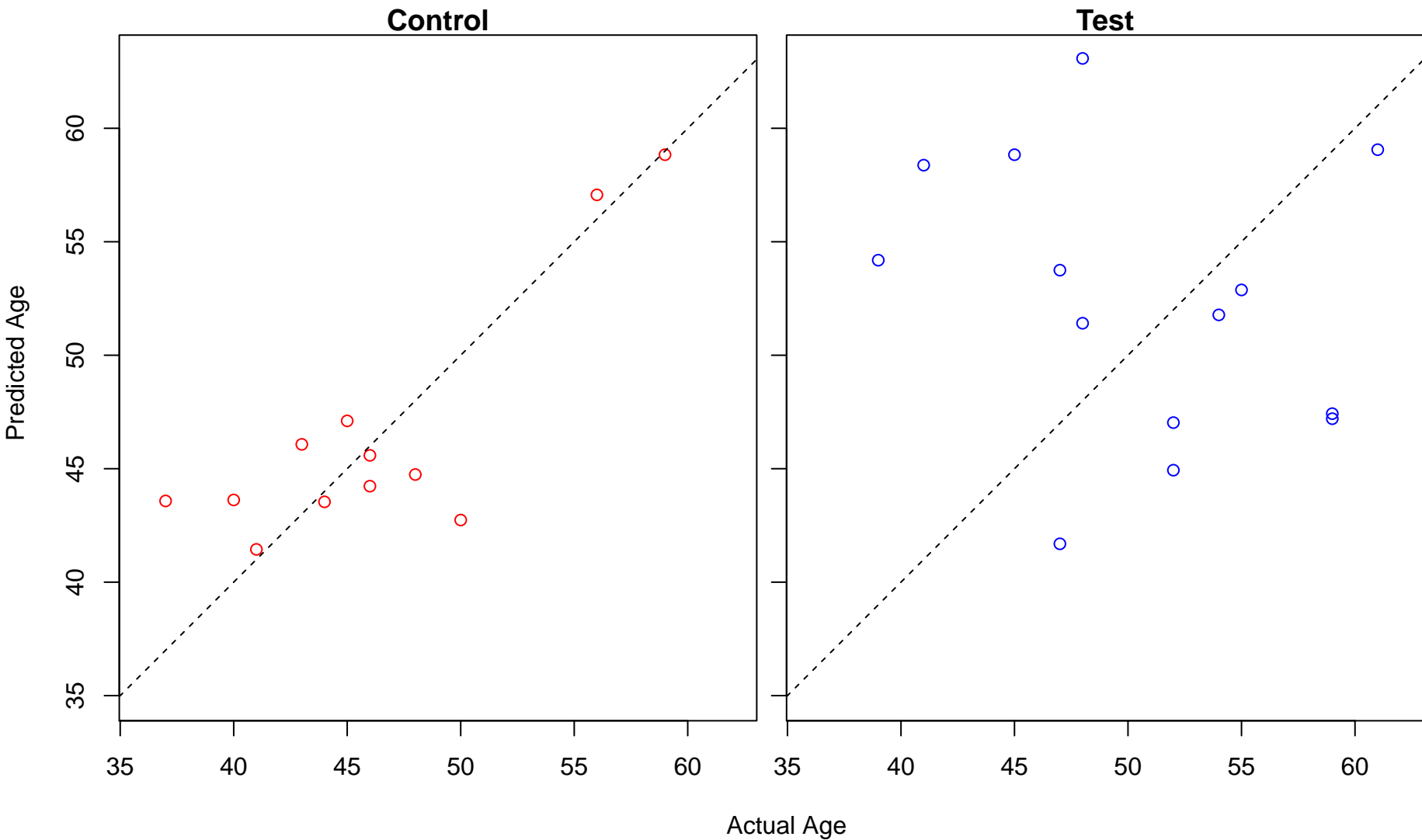
positive regulation of cellular protein localization (Score: 3.519524)



regulation of protein targeting (Score: 3.519372)

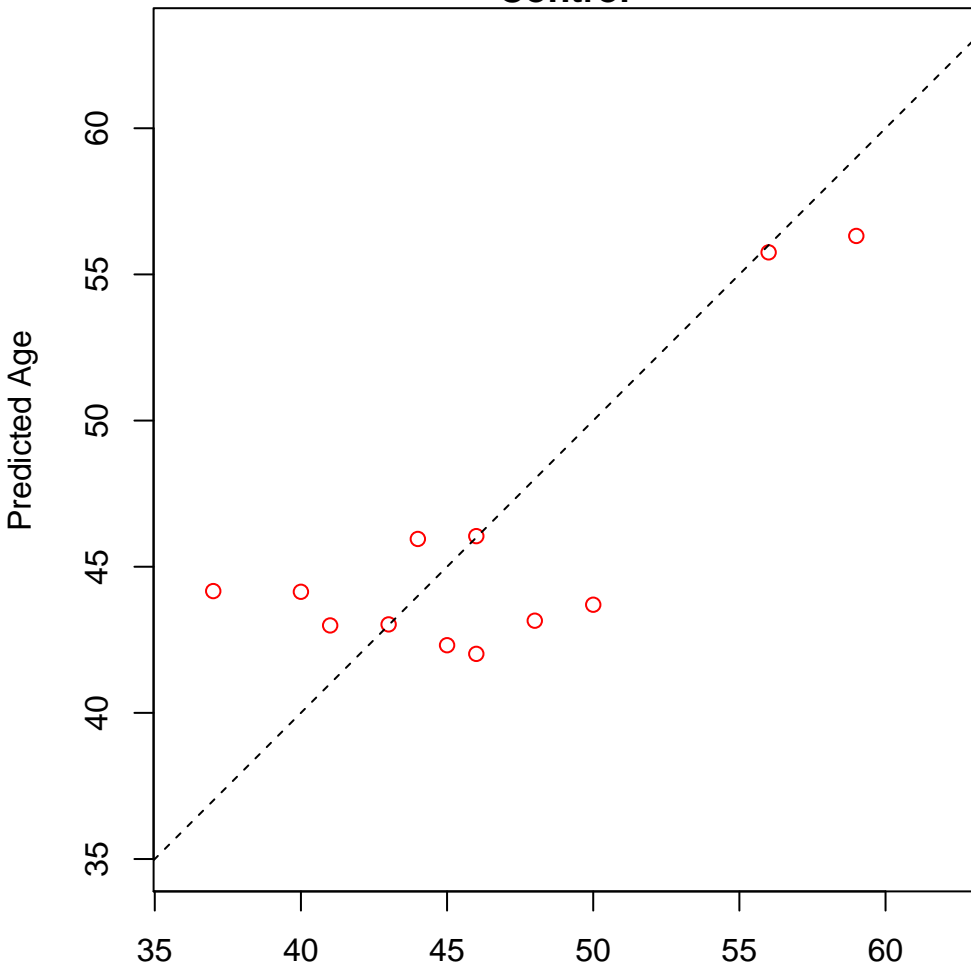


positive regulation of endothelial cell migration (Score: 3.515472)

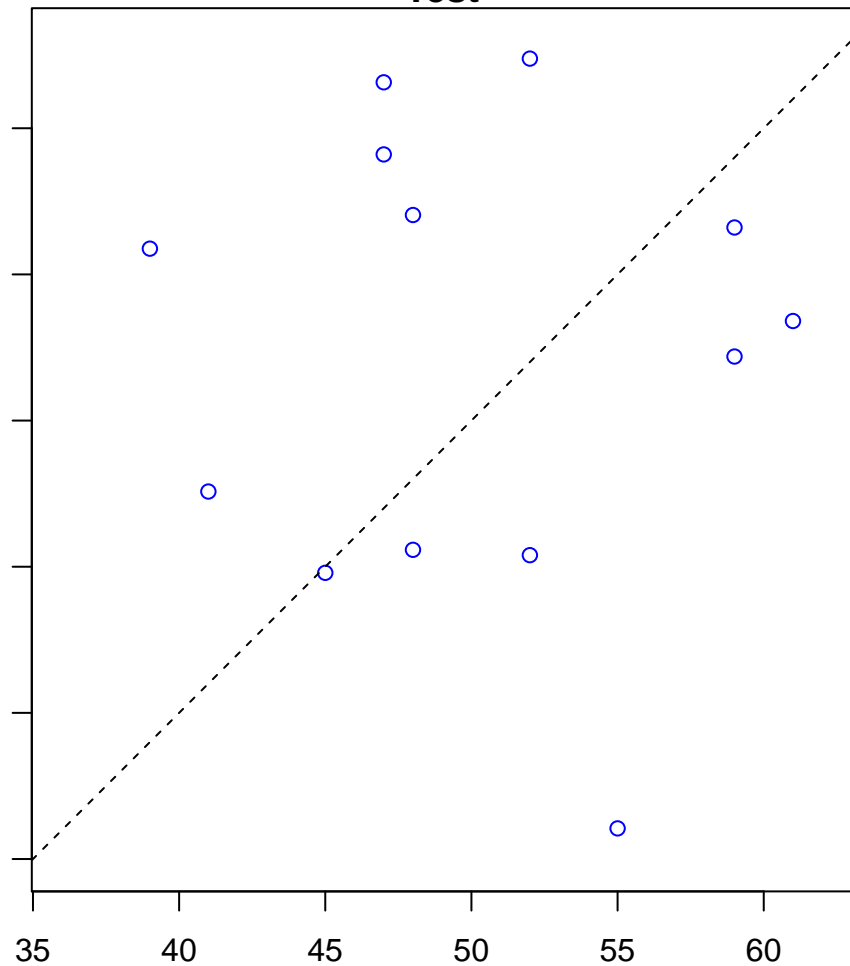


sodium ion transmembrane transport (Score: 3.515160)

Control

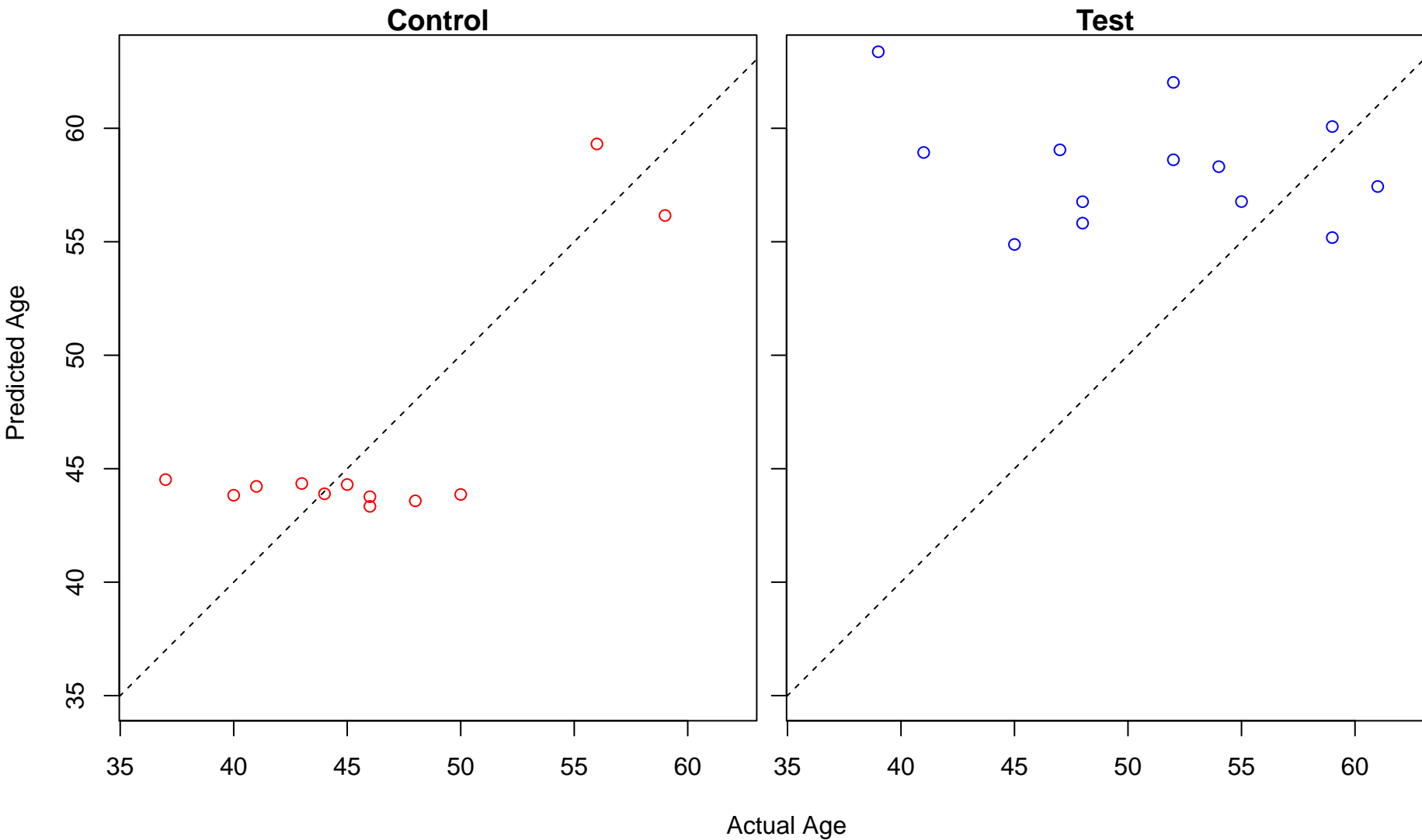


Test

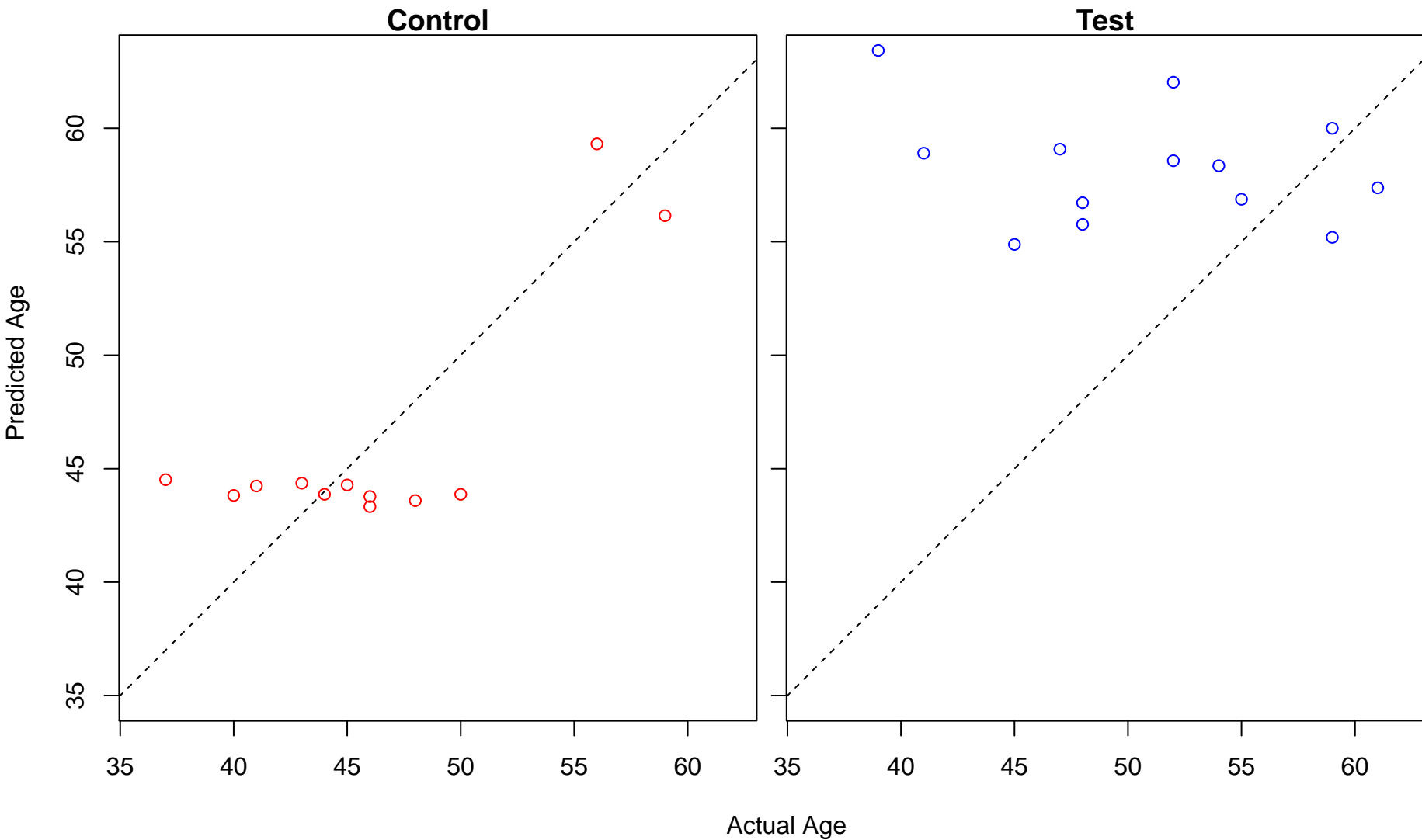


Actual Age

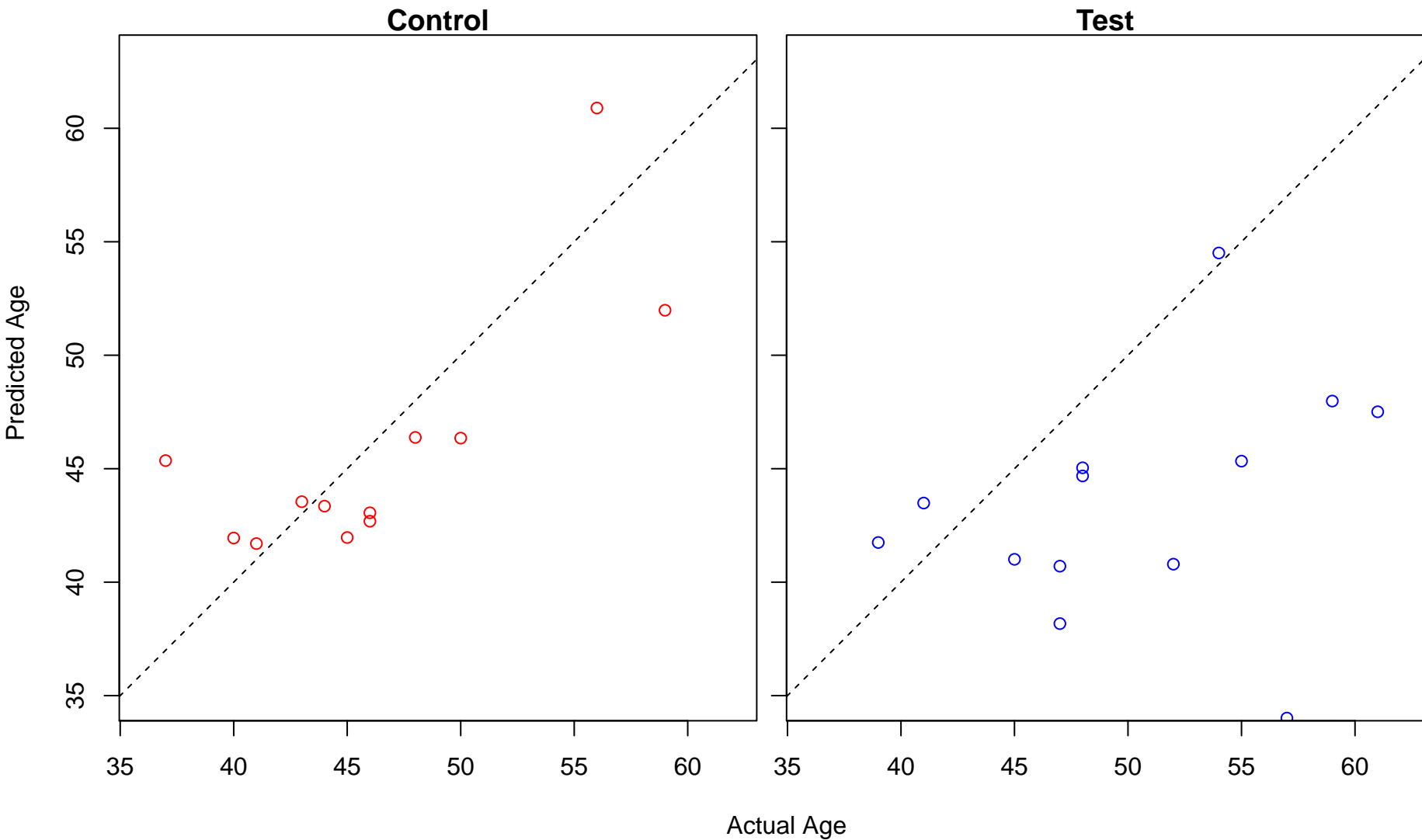
mitotic DNA integrity checkpoint (Score: 3.512398)



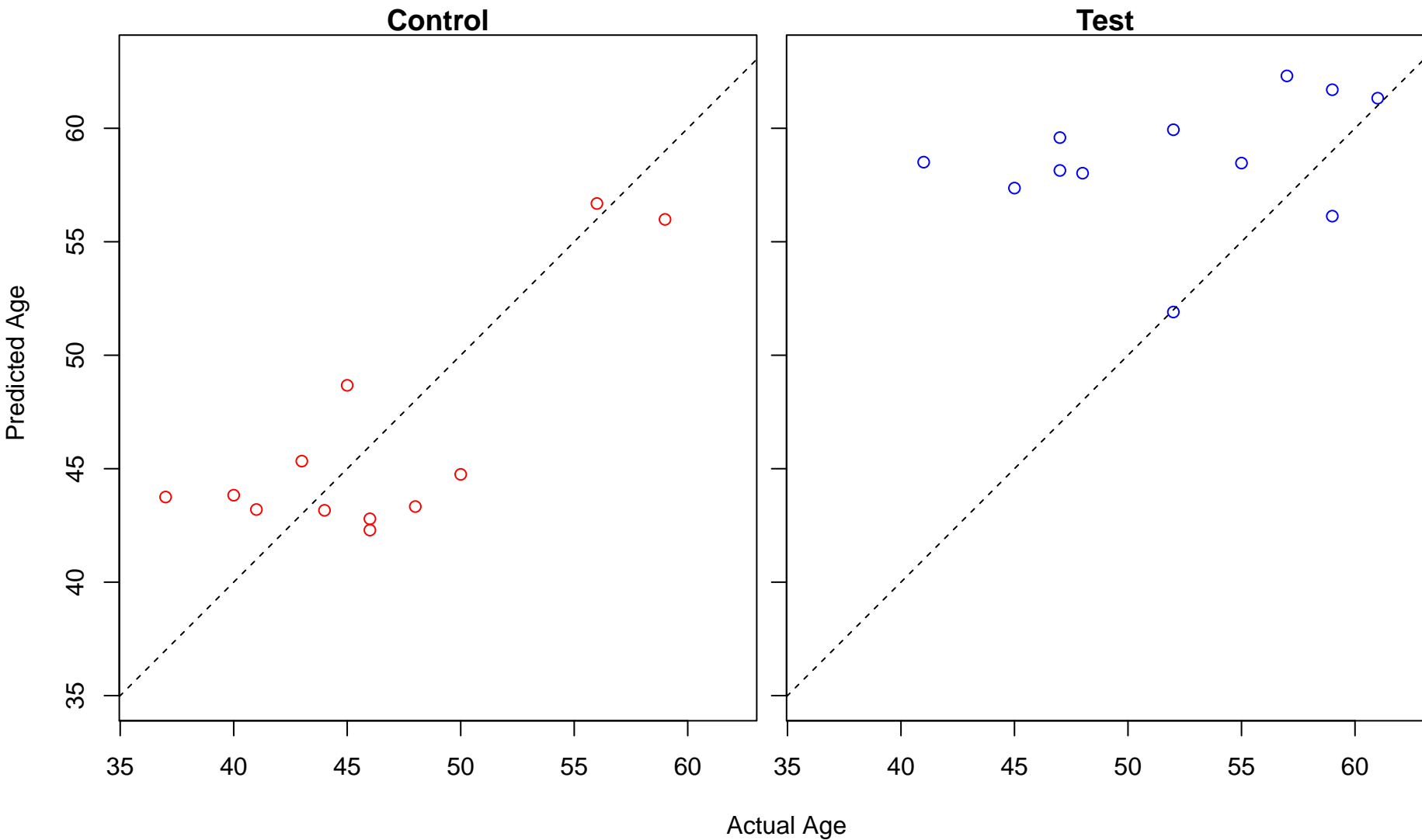
signal transduction in response to DNA damage (Score: 3.511706)



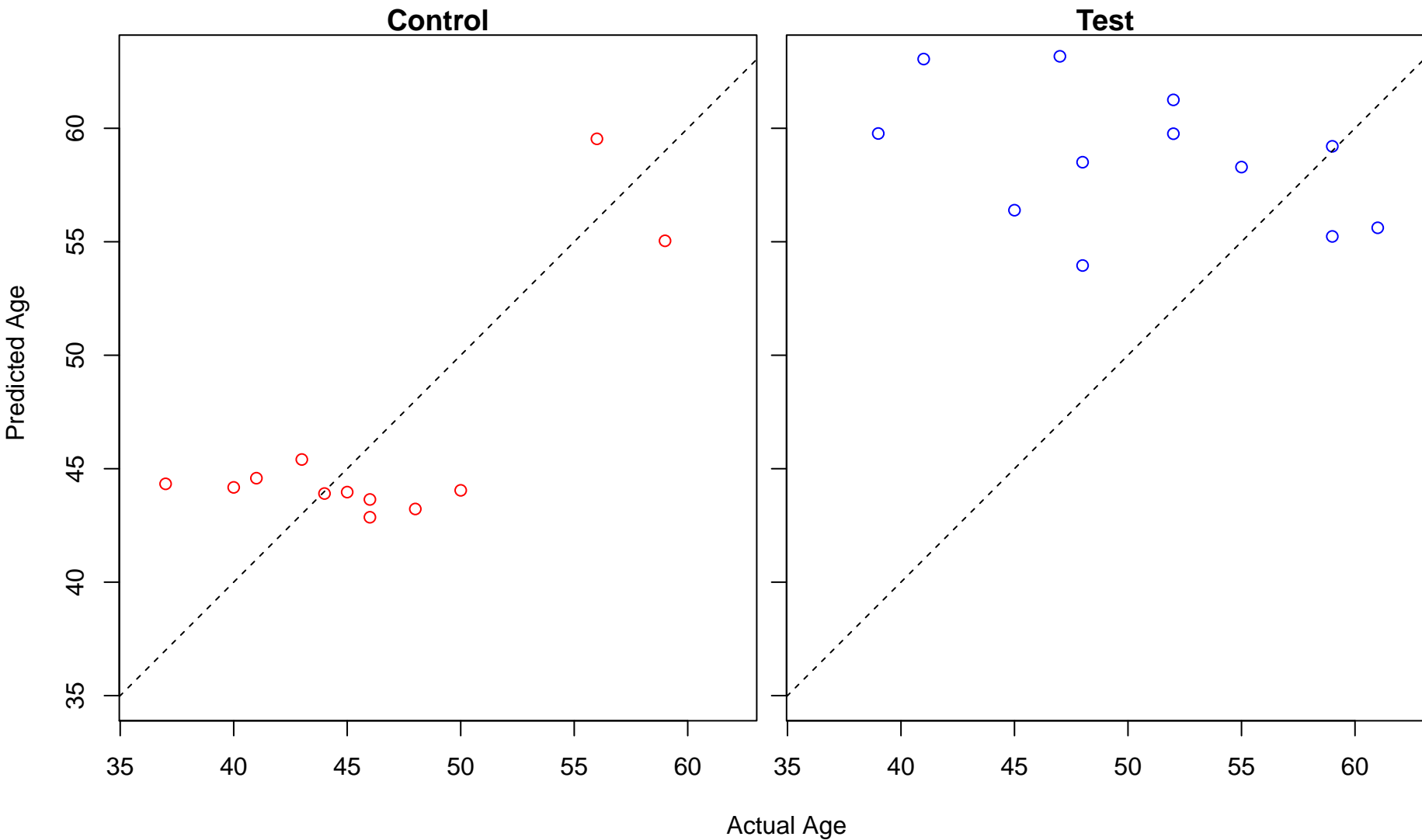
apoptotic process involved in development (Score: 3.509335)



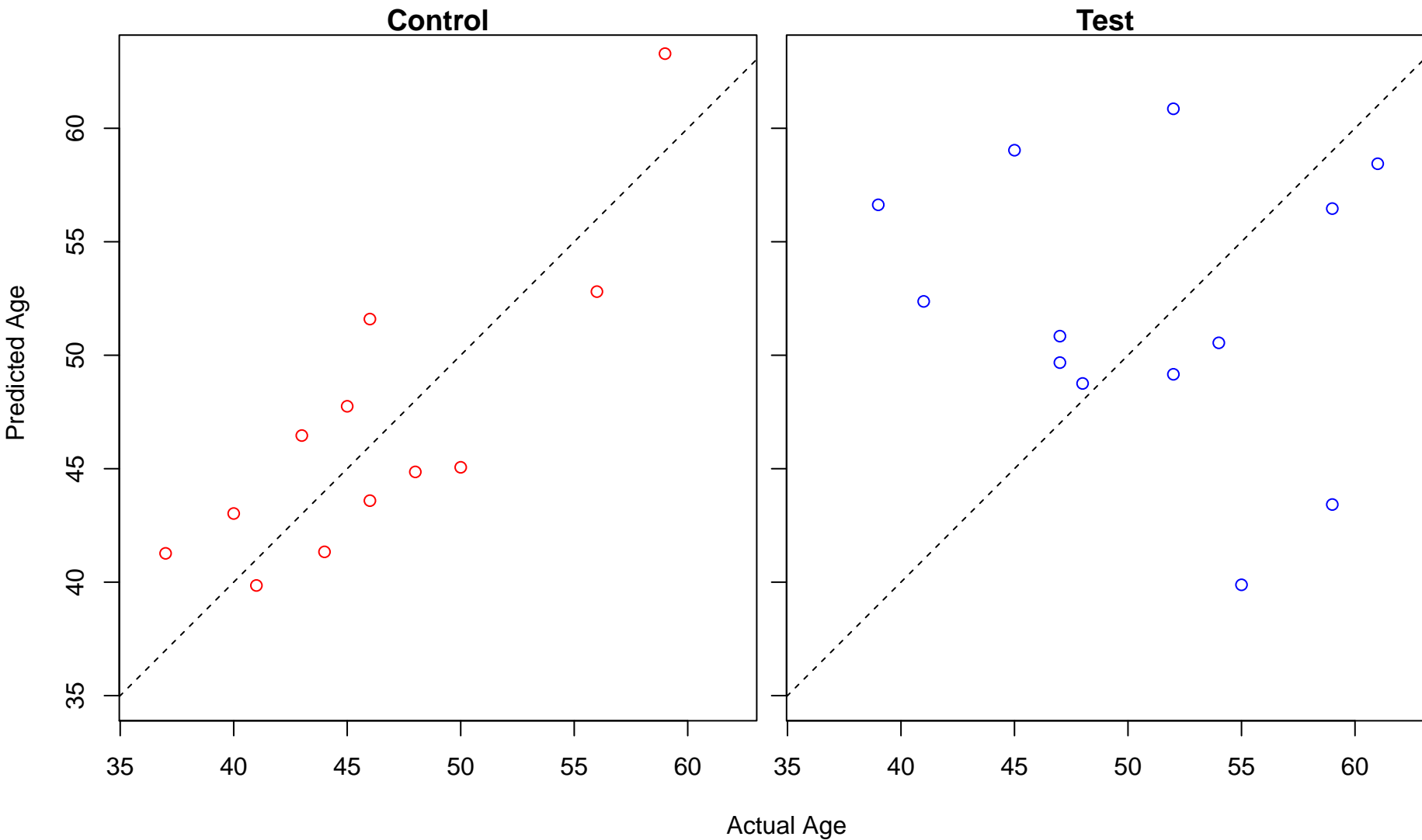
negative regulation of cardiac muscle tissue development (Score: 3.508951)



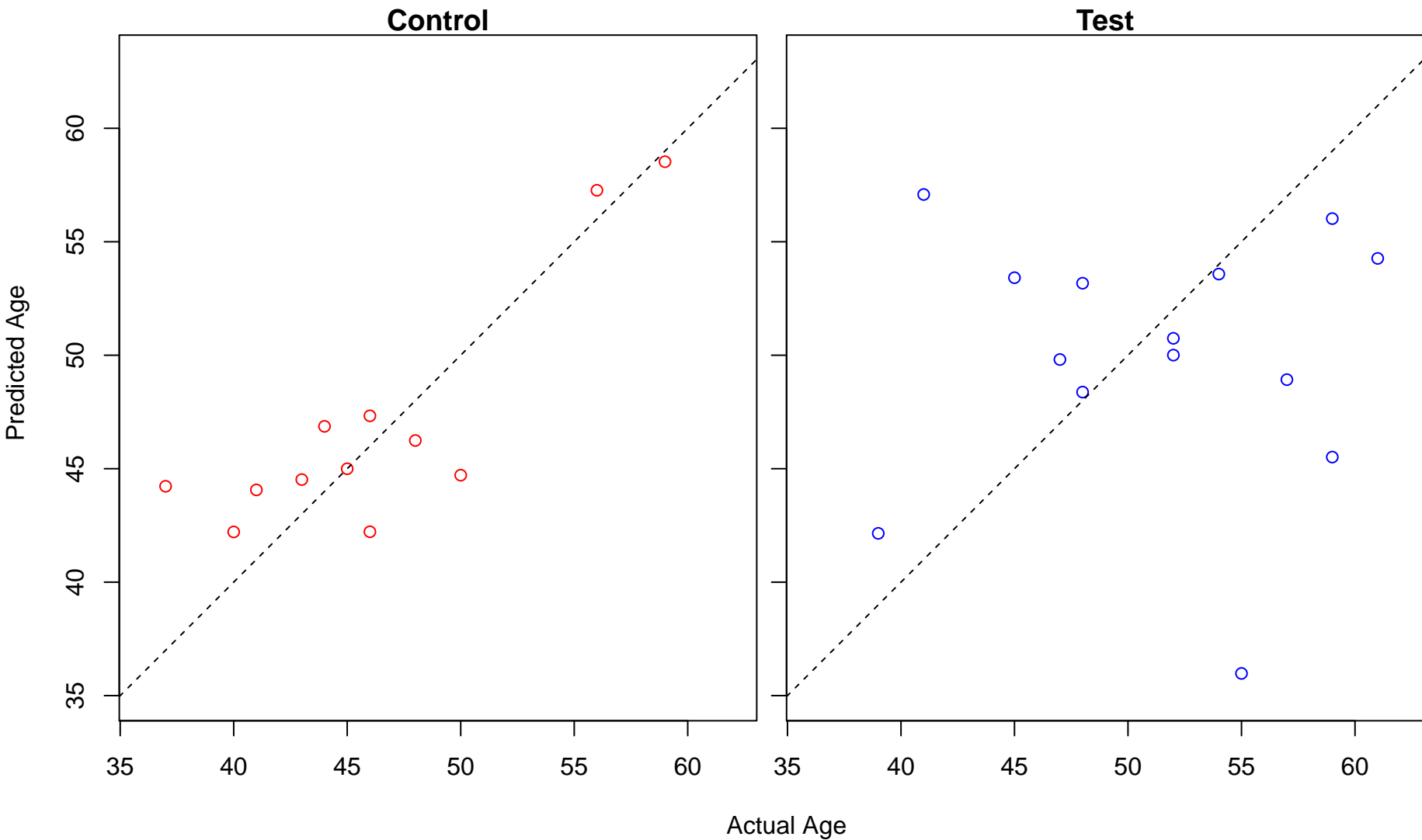
positive regulation of histone acetylation (Score: 3.508437)



regulation of mesonephros development (Score: 3.505387)

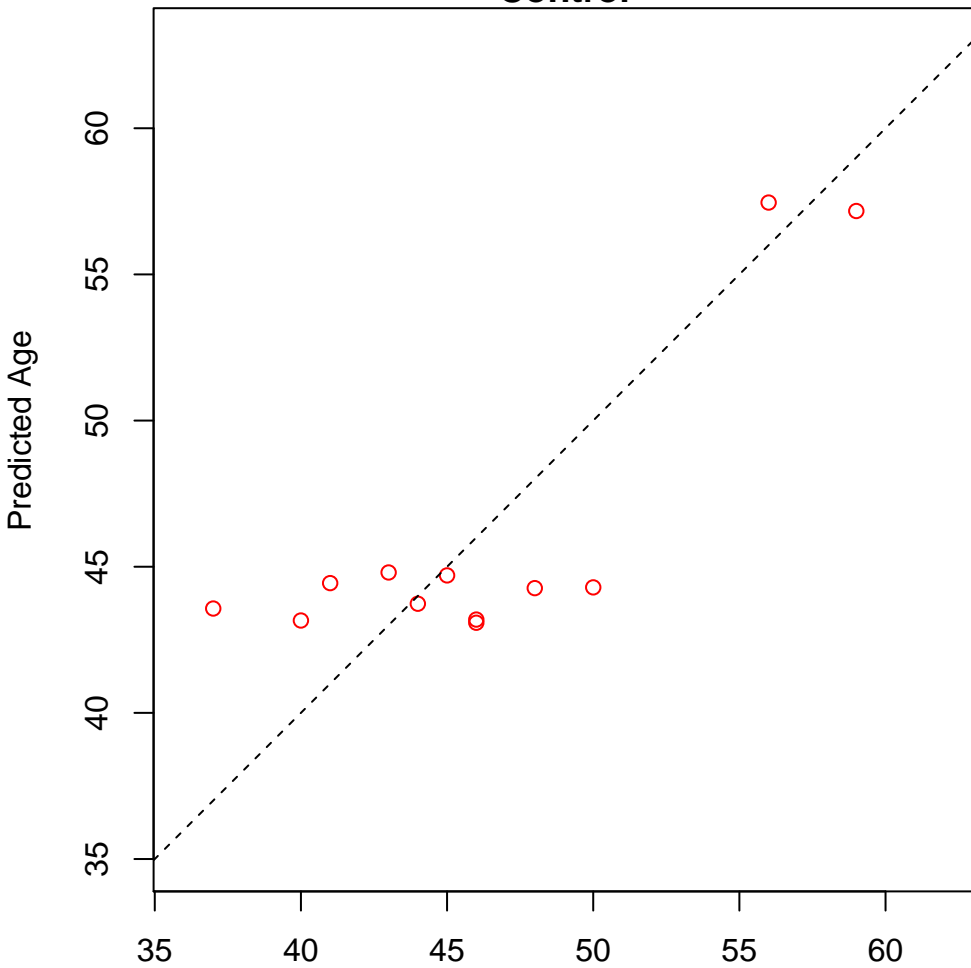


regulation of homotypic cell-cell adhesion (Score: 3.503989)

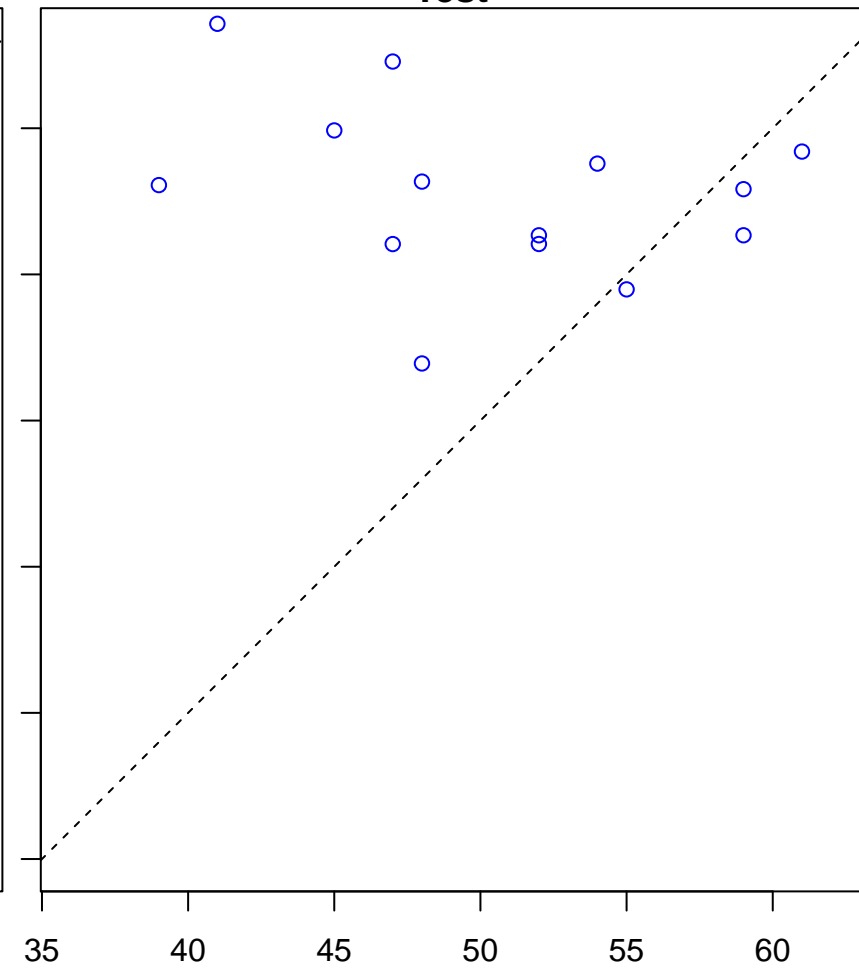


response to xenobiotic stimulus (Score: 3.503298)

Control

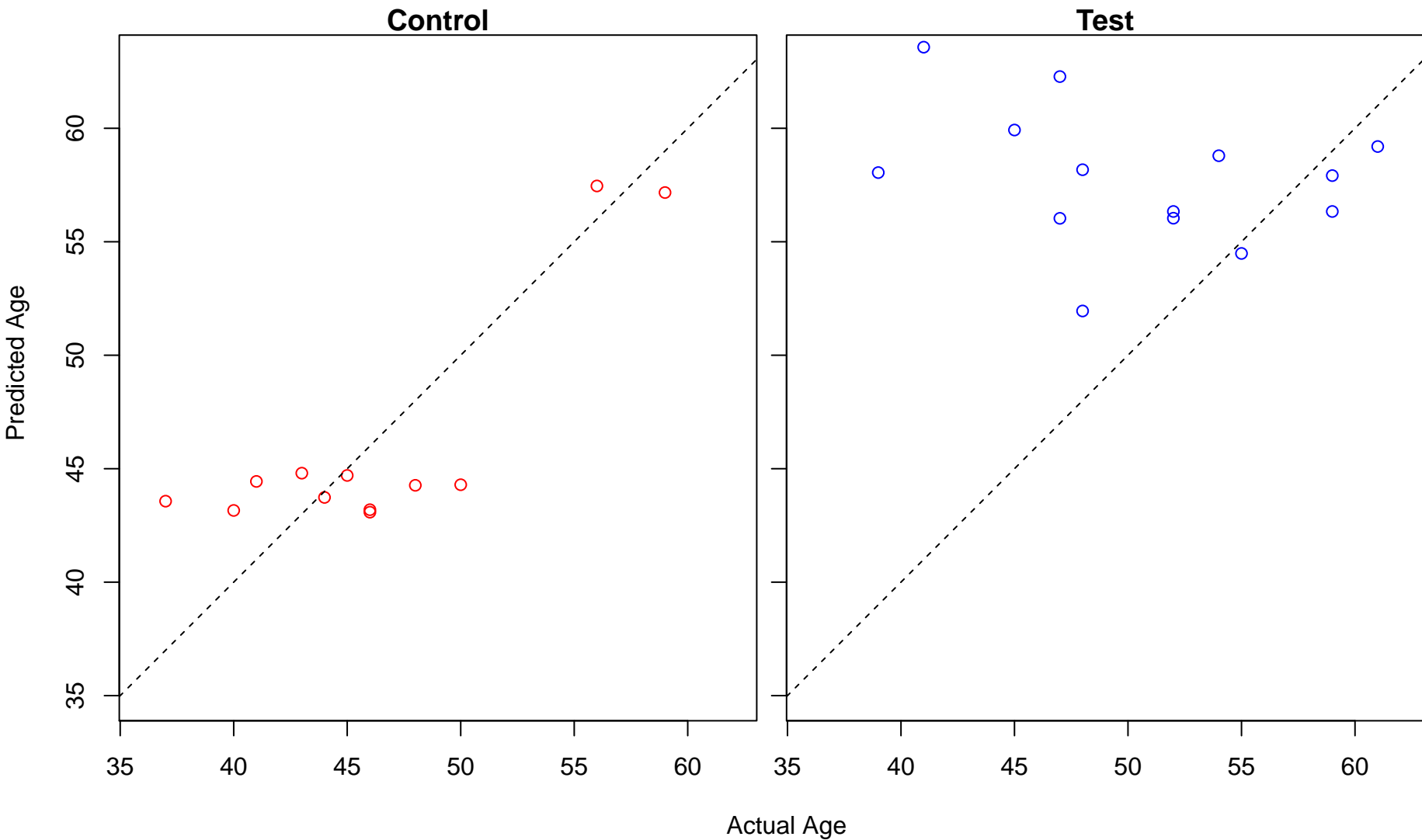


Test

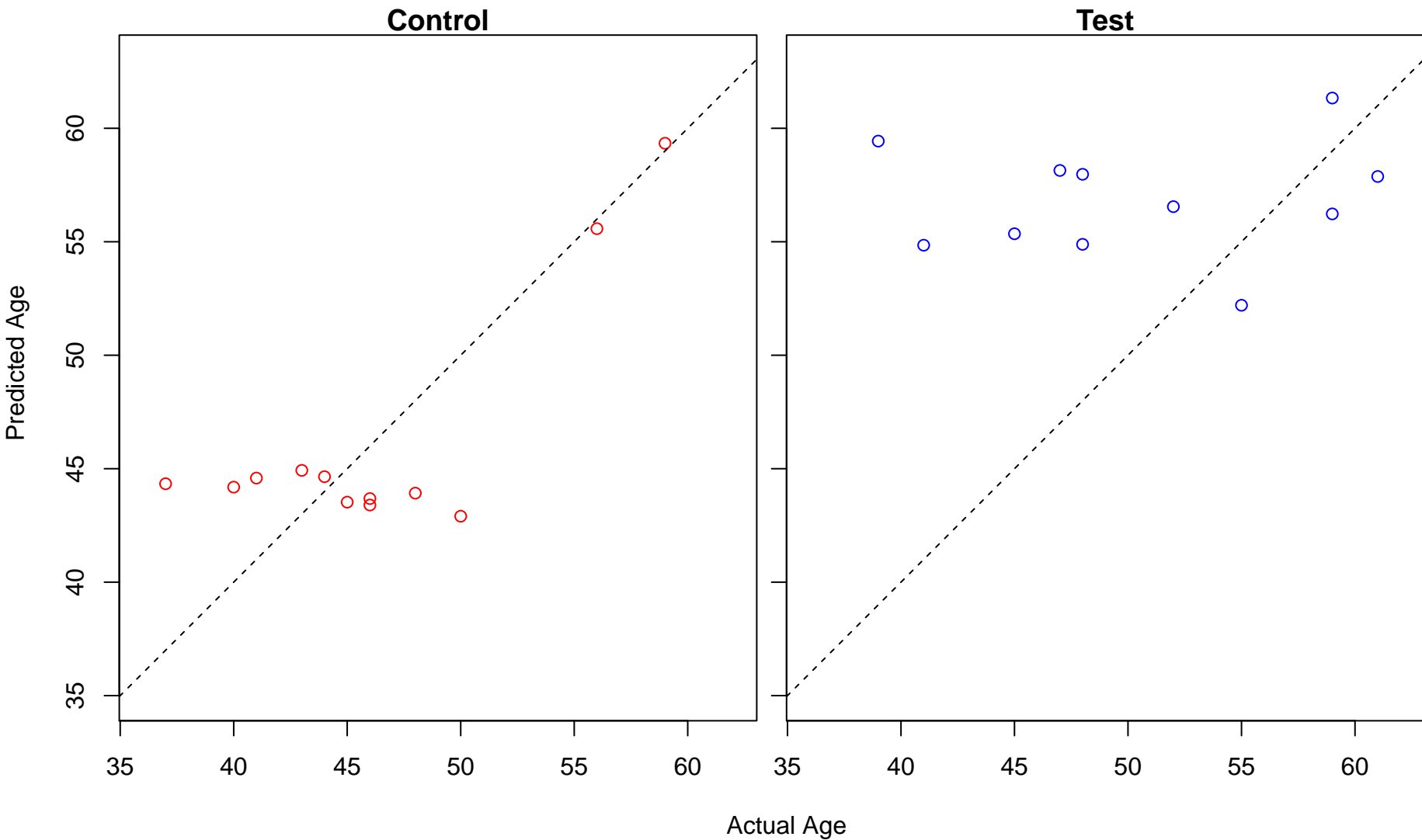


Actual Age

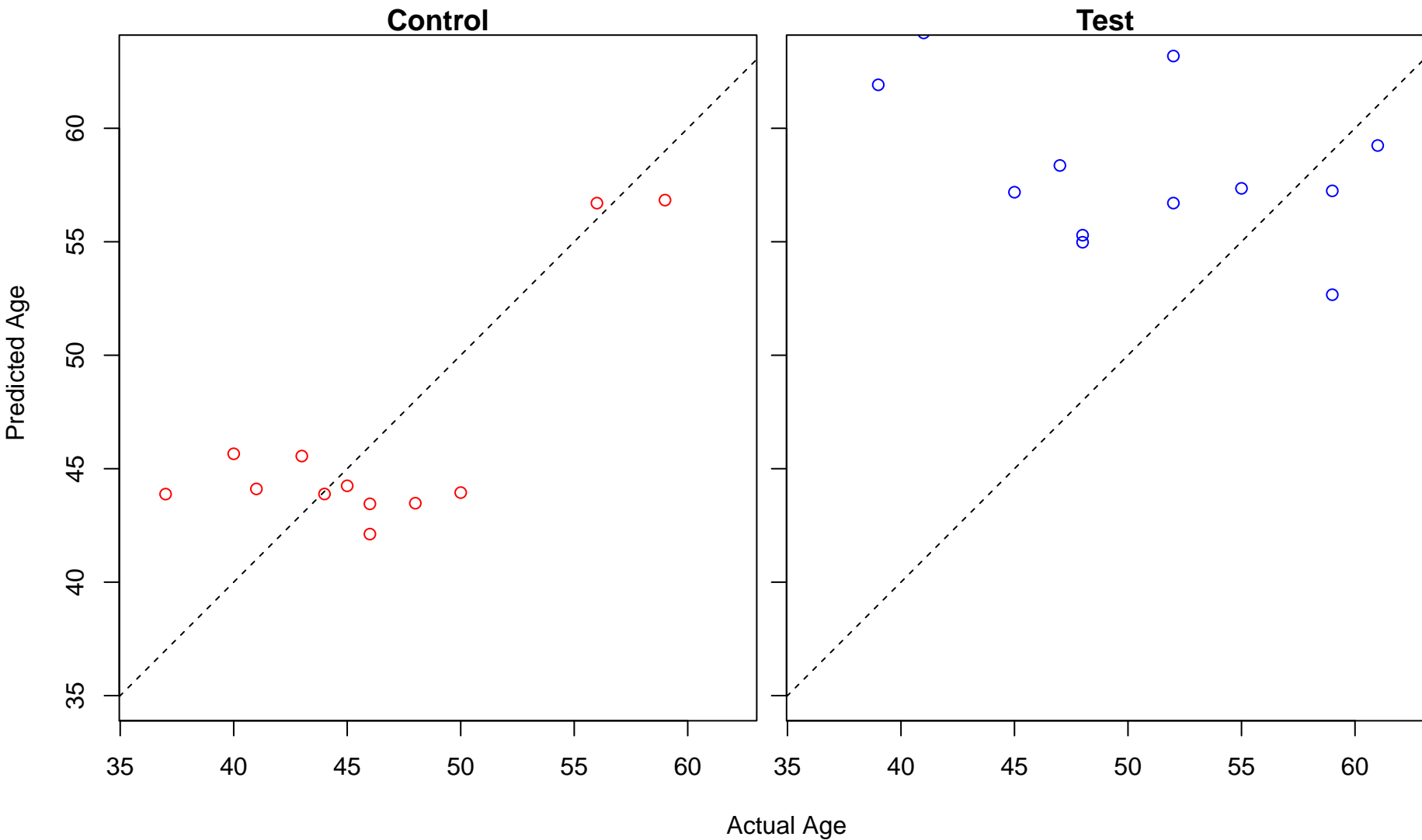
xenobiotic metabolic process (Score: 3.502639)



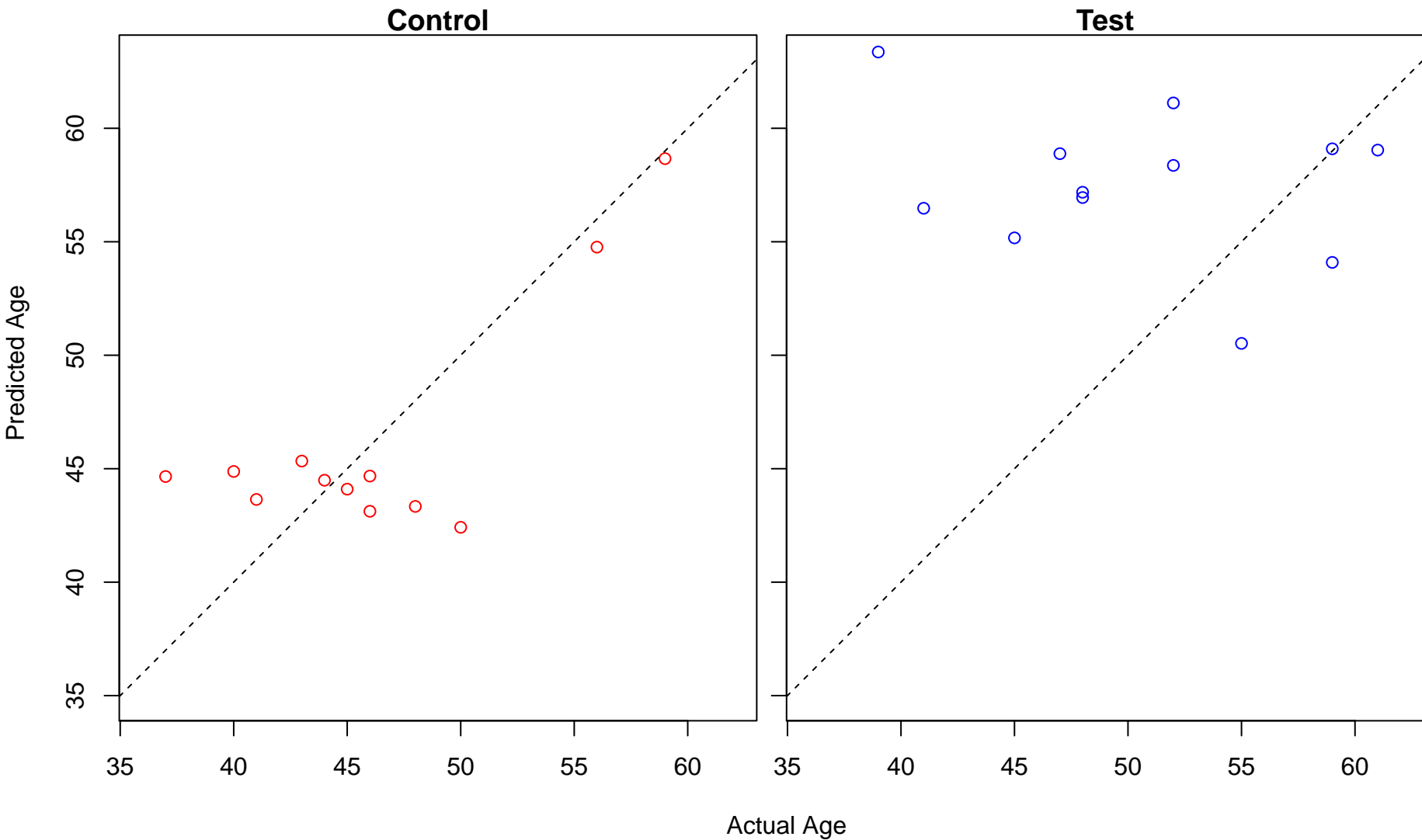
positive regulation of protein homodimerization activity (Score: 3.501449)



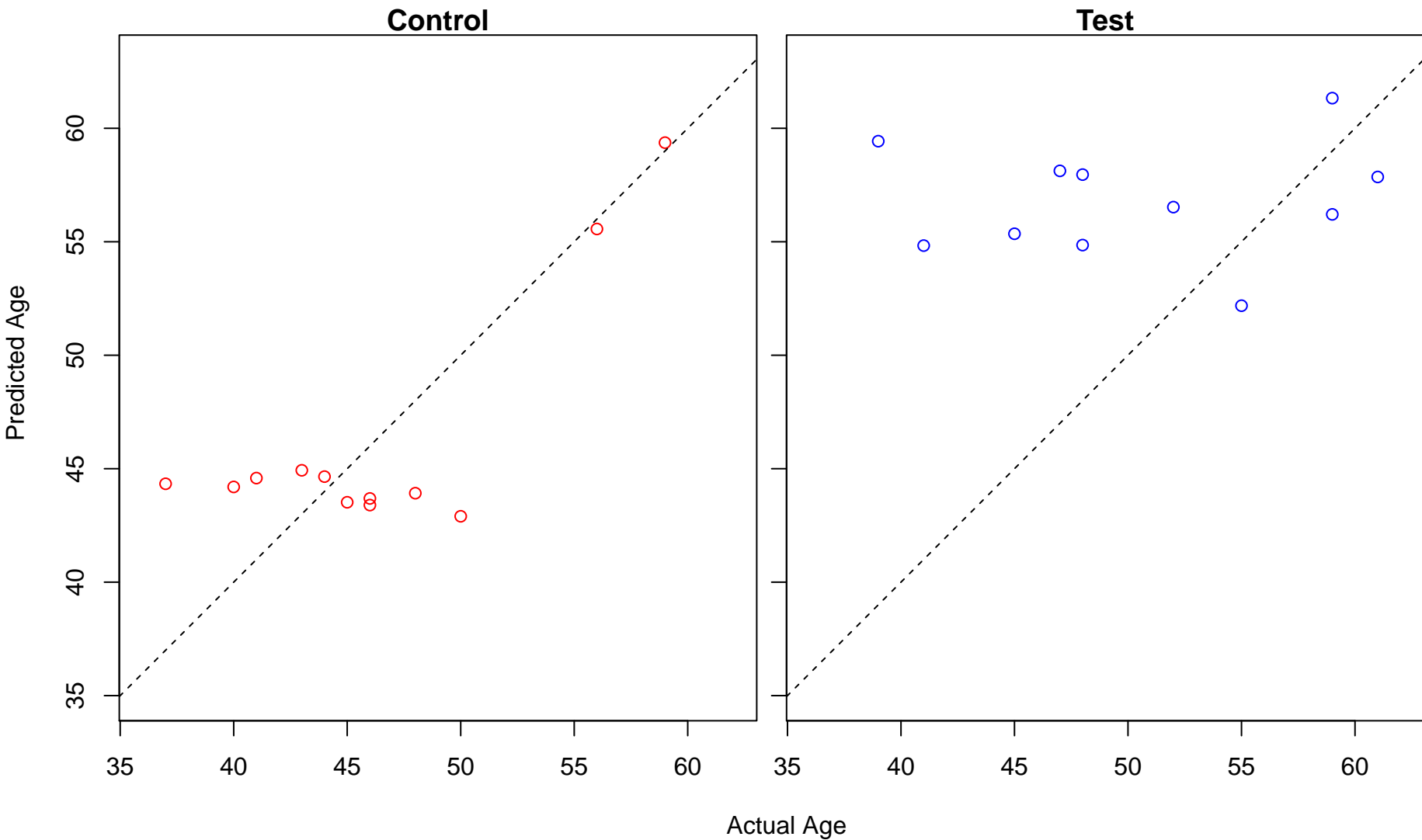
hexose biosynthetic process (Score: 3.500810)



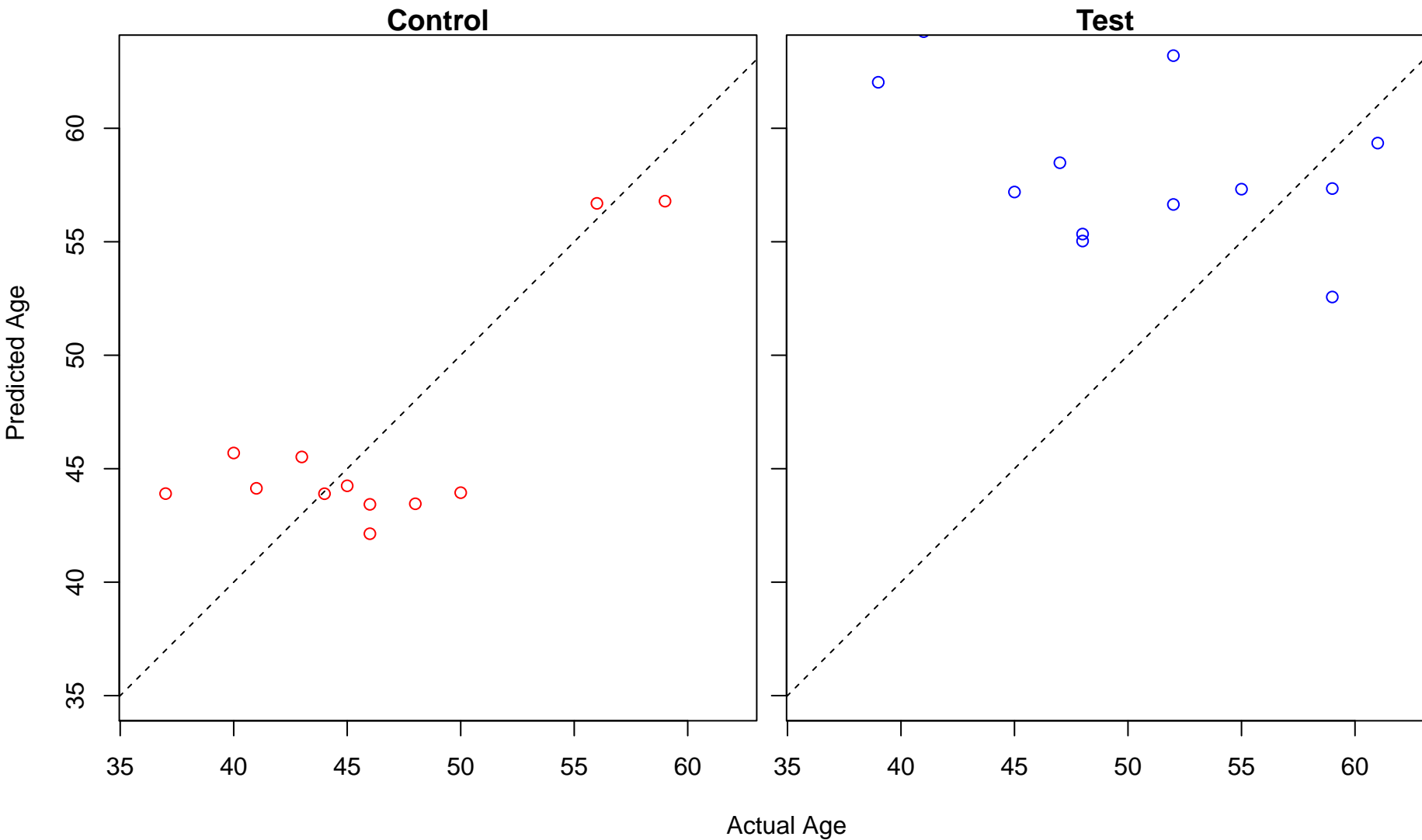
respiratory chain complex IV assembly (Score: 3.499602)



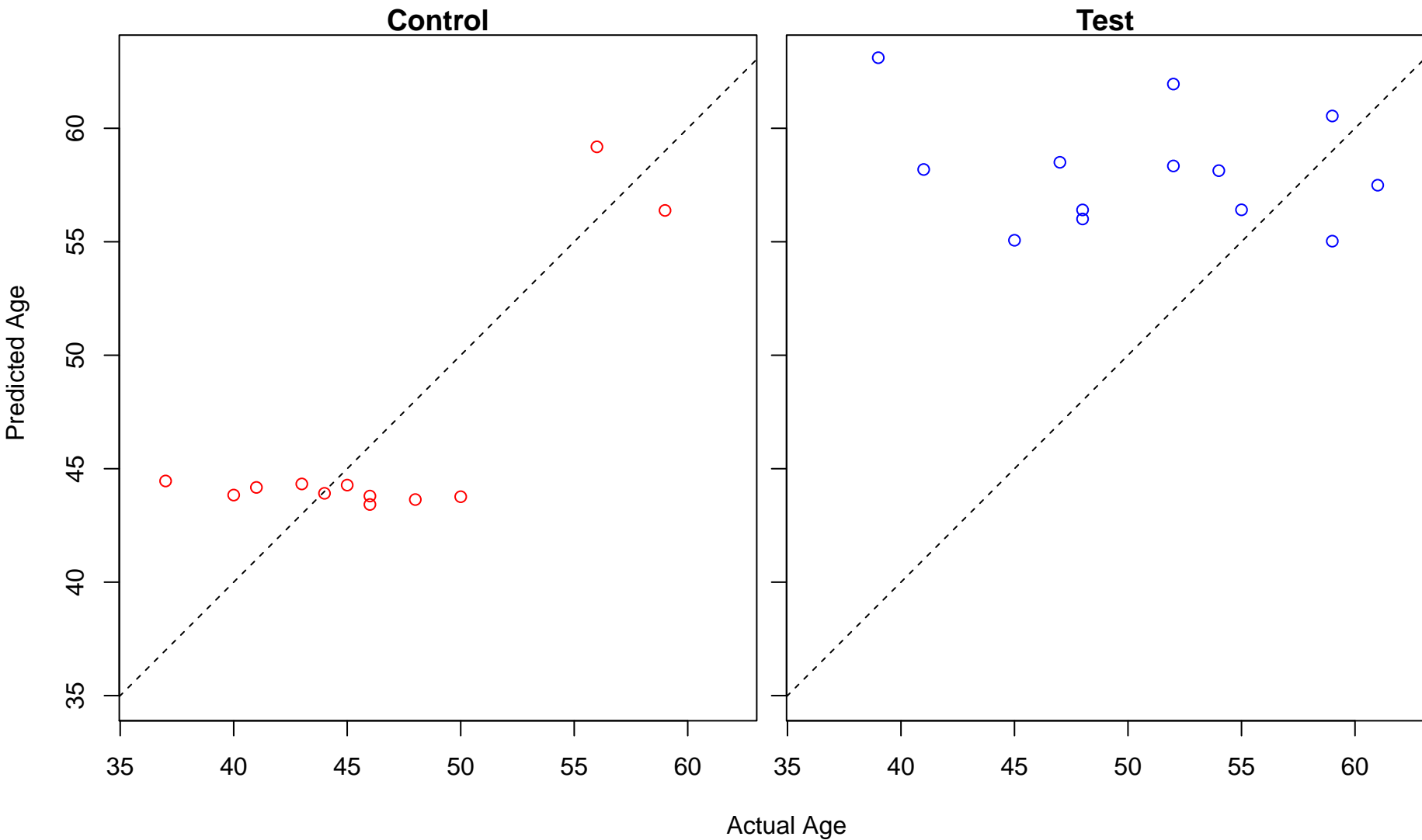
positive regulation of transcription regulatory region DNA binding (Score: 3.498140)



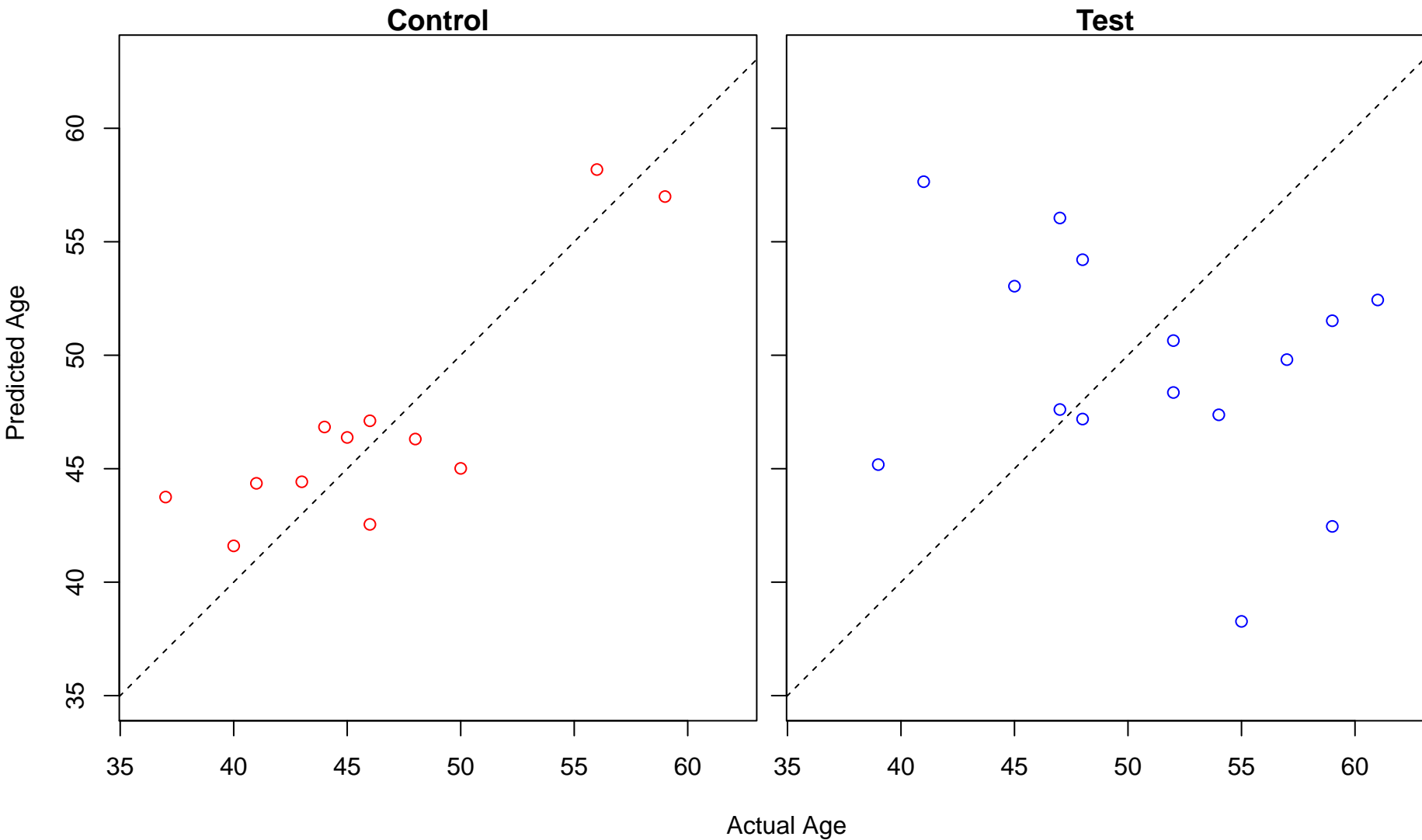
gluconeogenesis (Score: 3.496761)



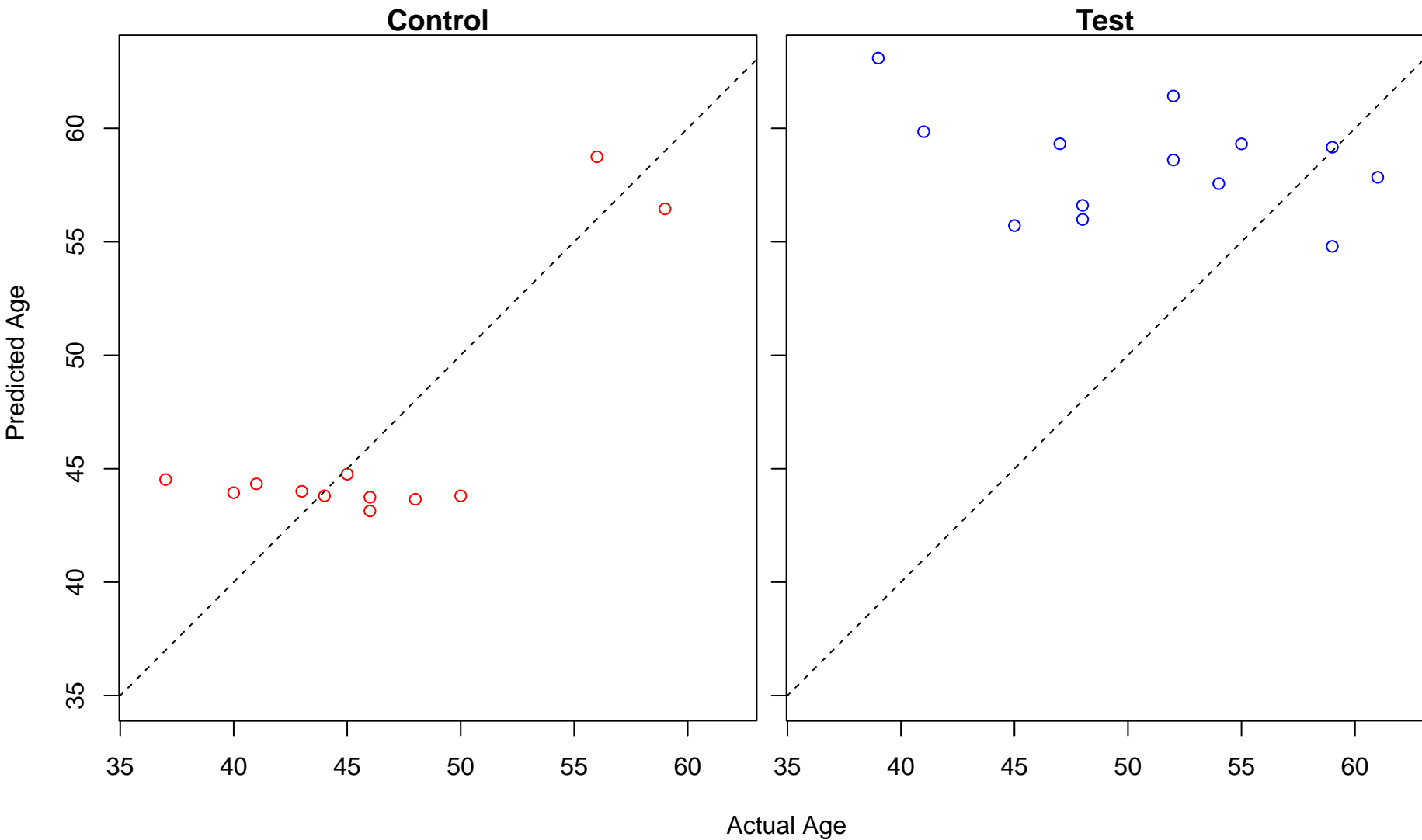
NIK/NF-kappaB signaling (Score: 3.496258)



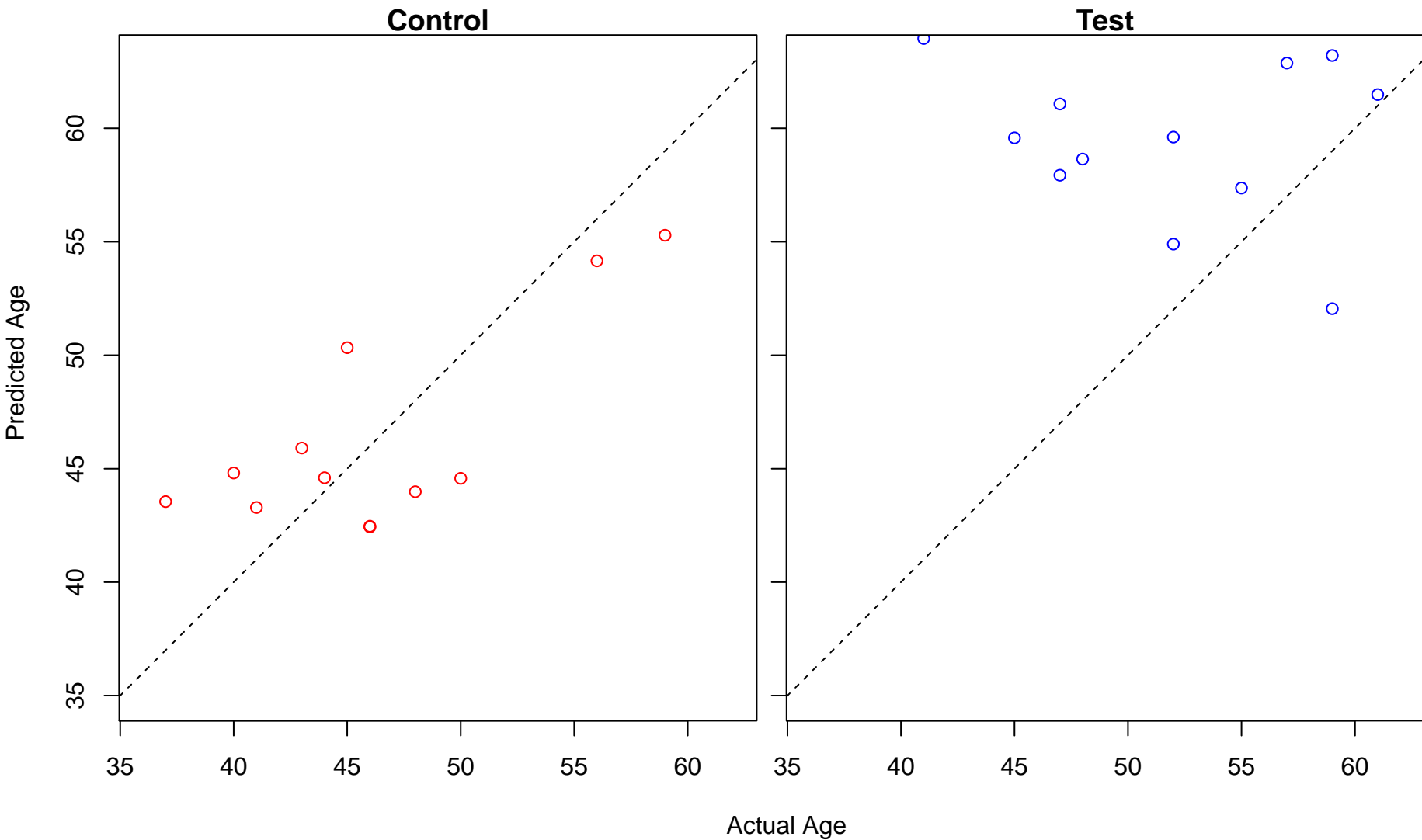
regulation of cell activation (Score: 3.495234)



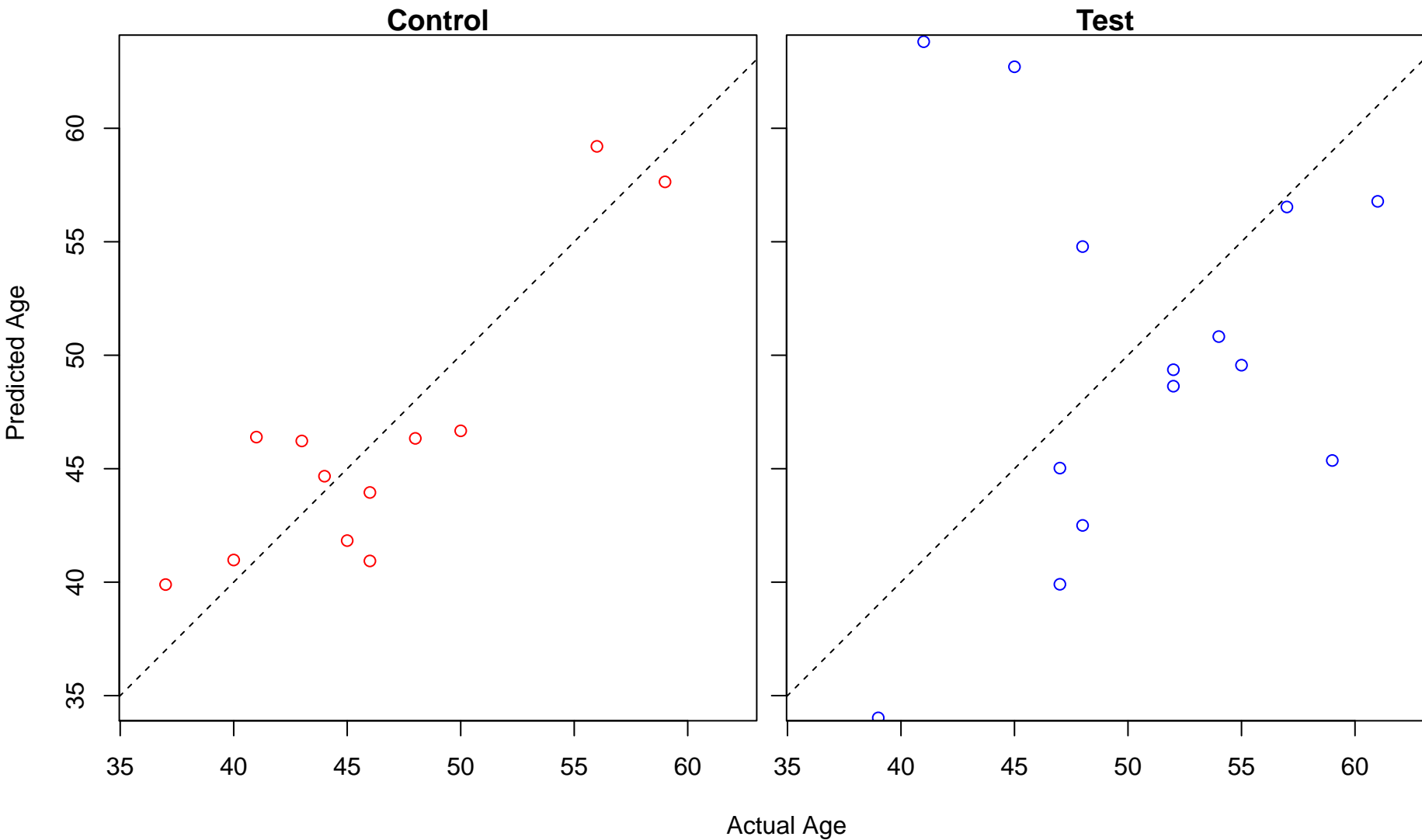
regulation of canonical Wnt signaling pathway (Score: 3.494848)



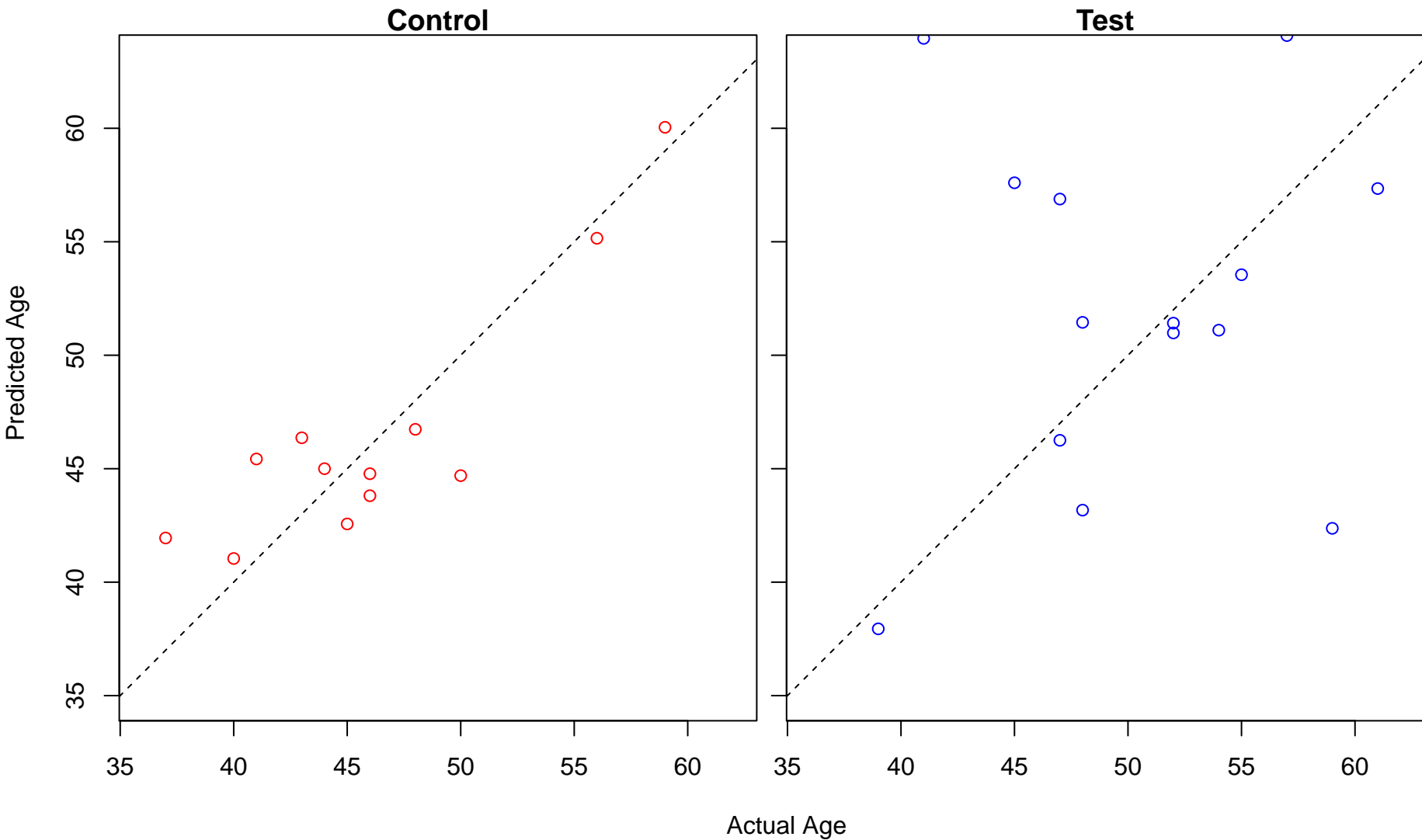
T cell selection (Score: 3.494729)



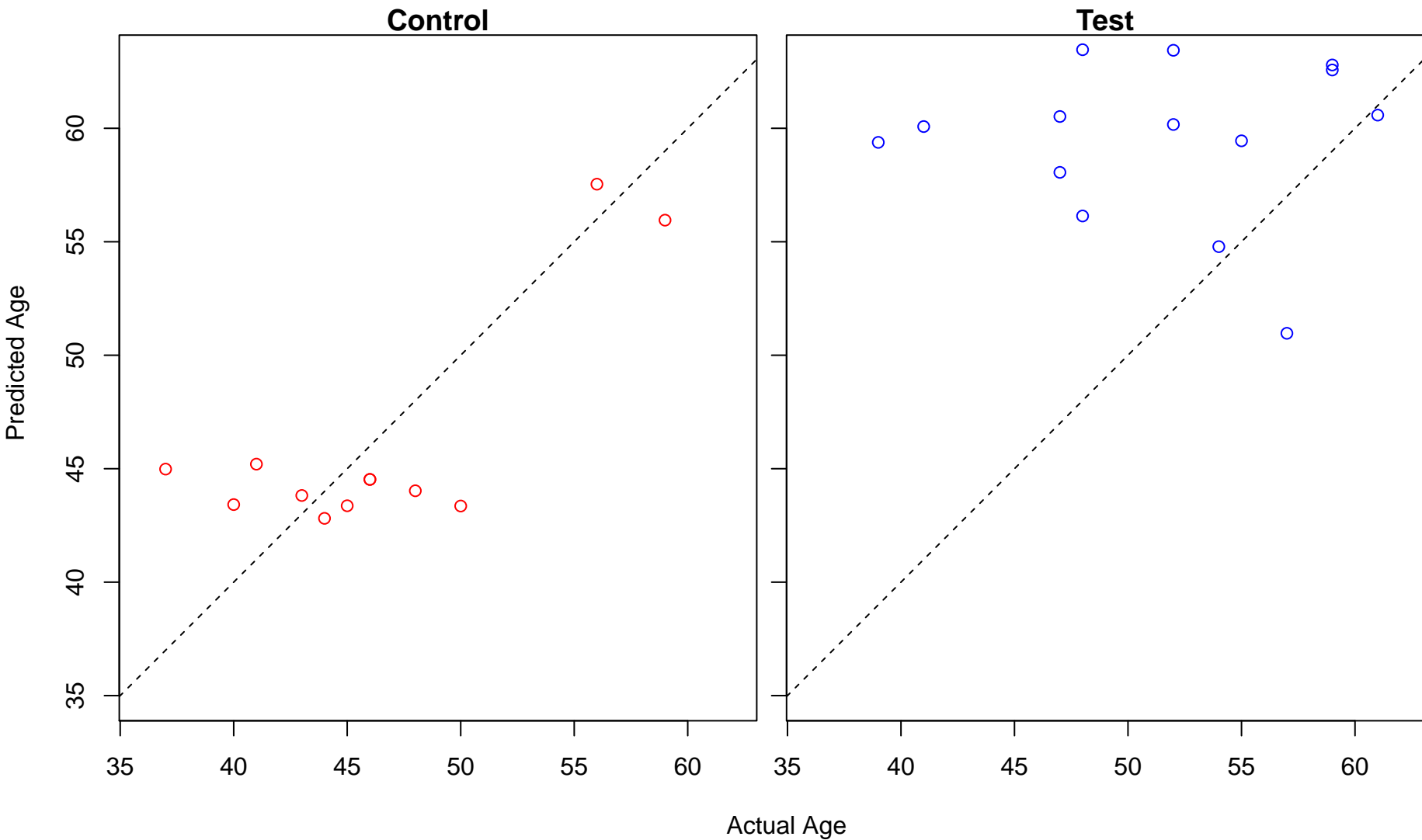
fatty acid derivative biosynthetic process (Score: 3.494572)



detection of stimulus (Score: 3.493965)

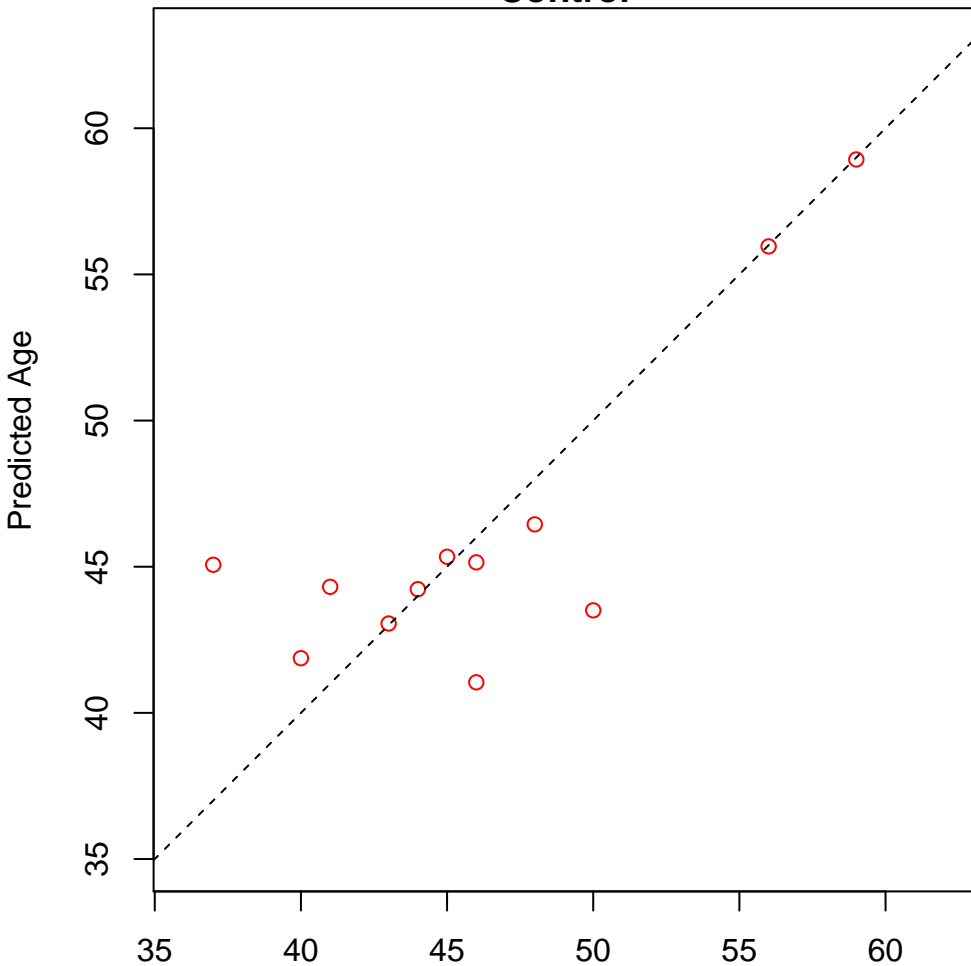


regulation of glial cell proliferation (Score: 3.493884)

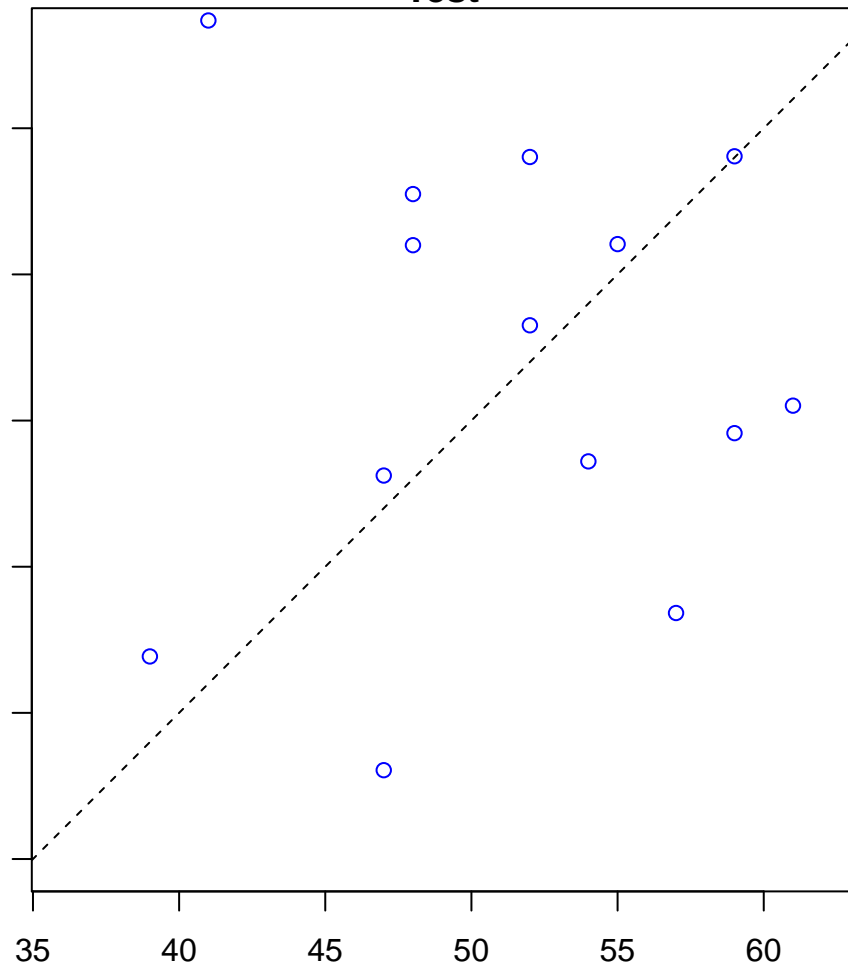


nucleotide-sugar biosynthetic process (Score: 3.493376)

Control

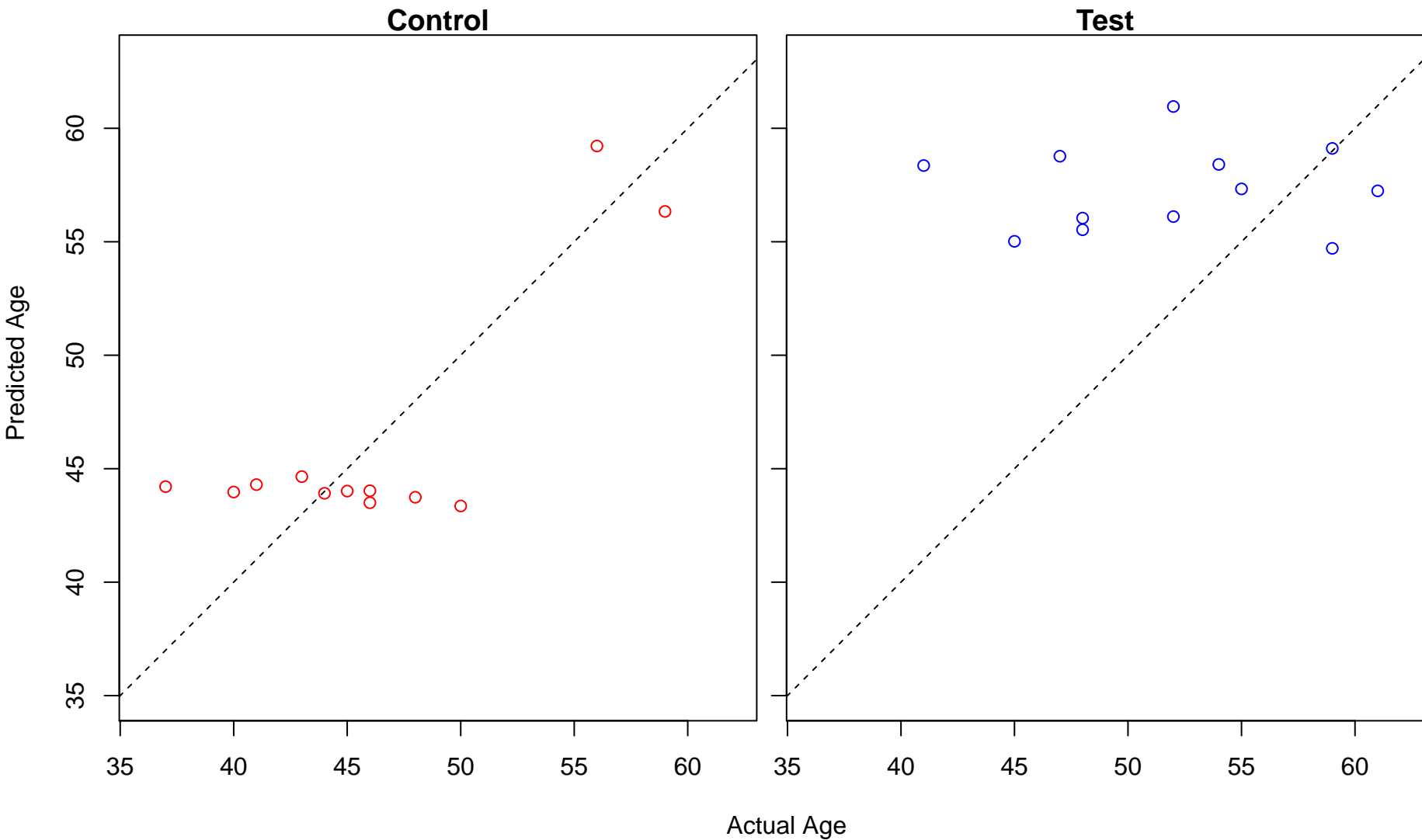


Test

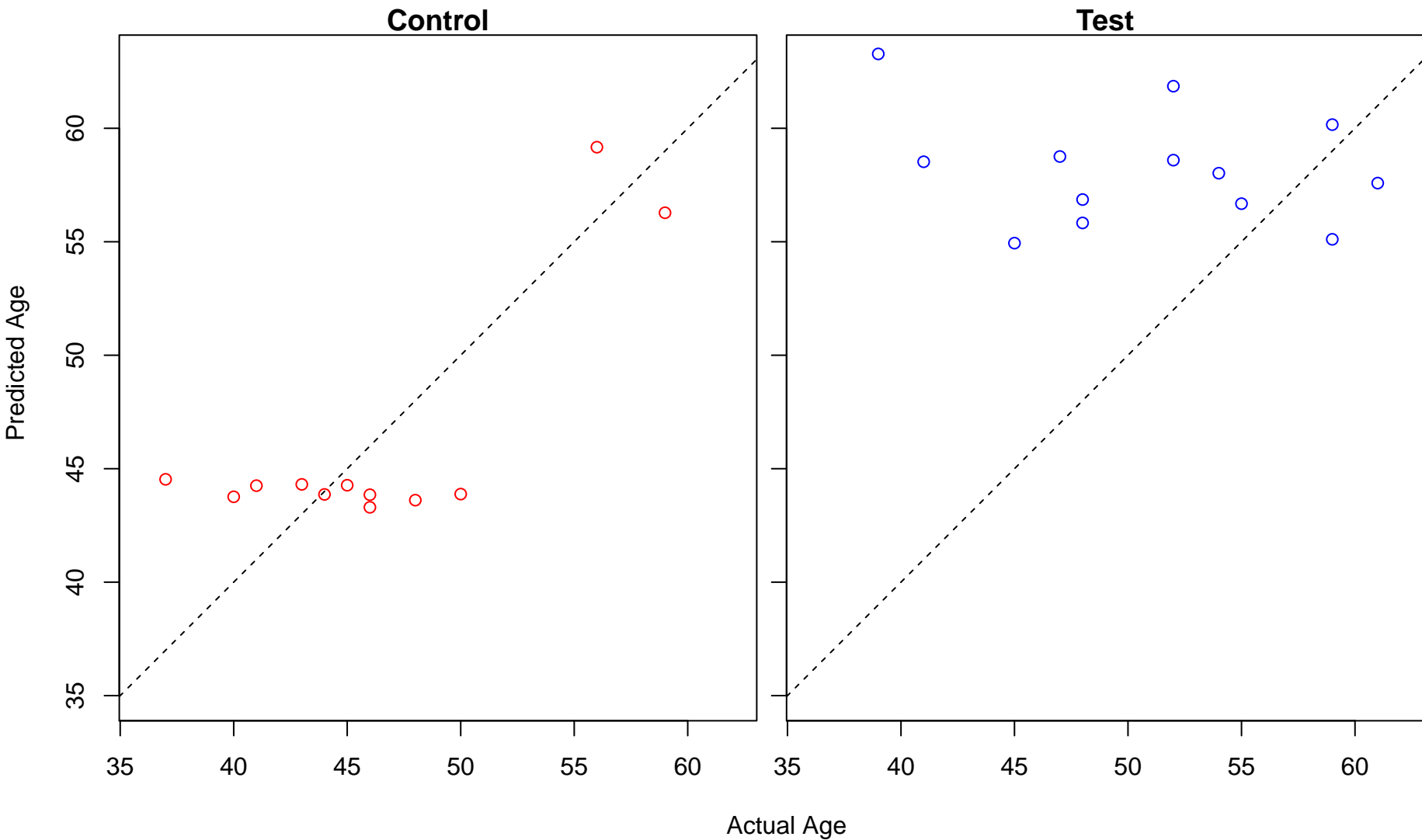


Actual Age

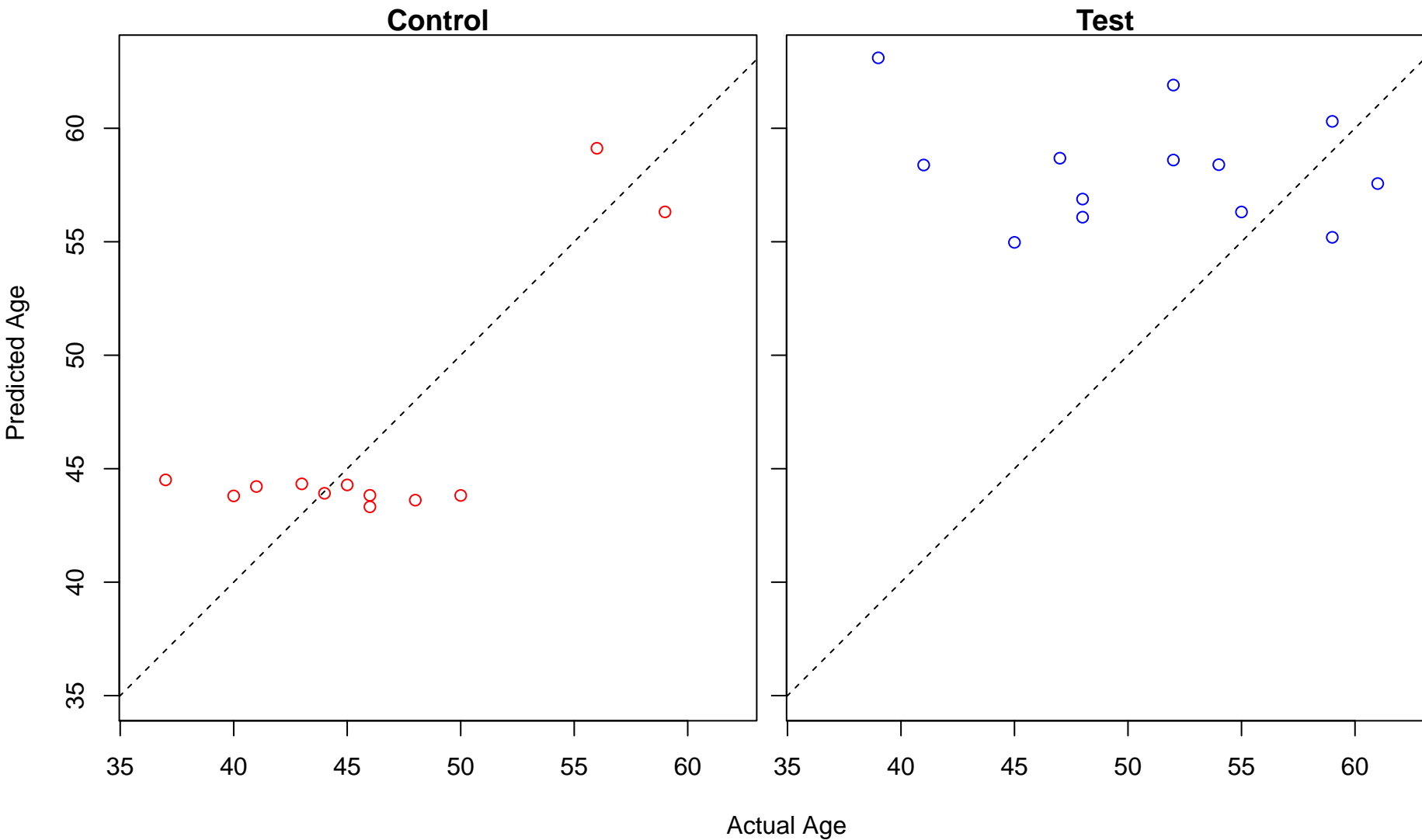
regulation of mitochondrial membrane potential (Score: 3.490534)



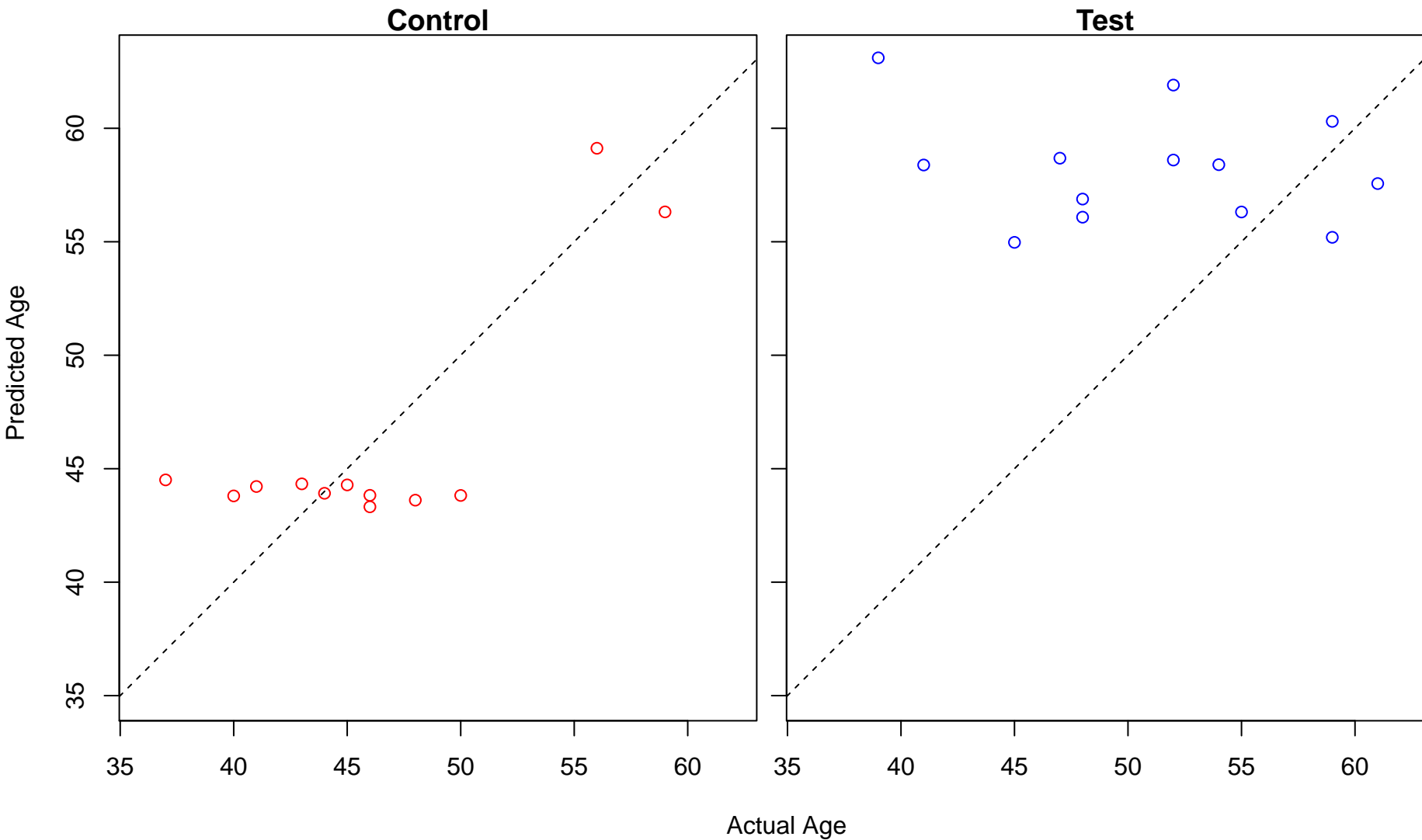
positive regulation of canonical Wnt signaling pathway (Score: 3.490201)



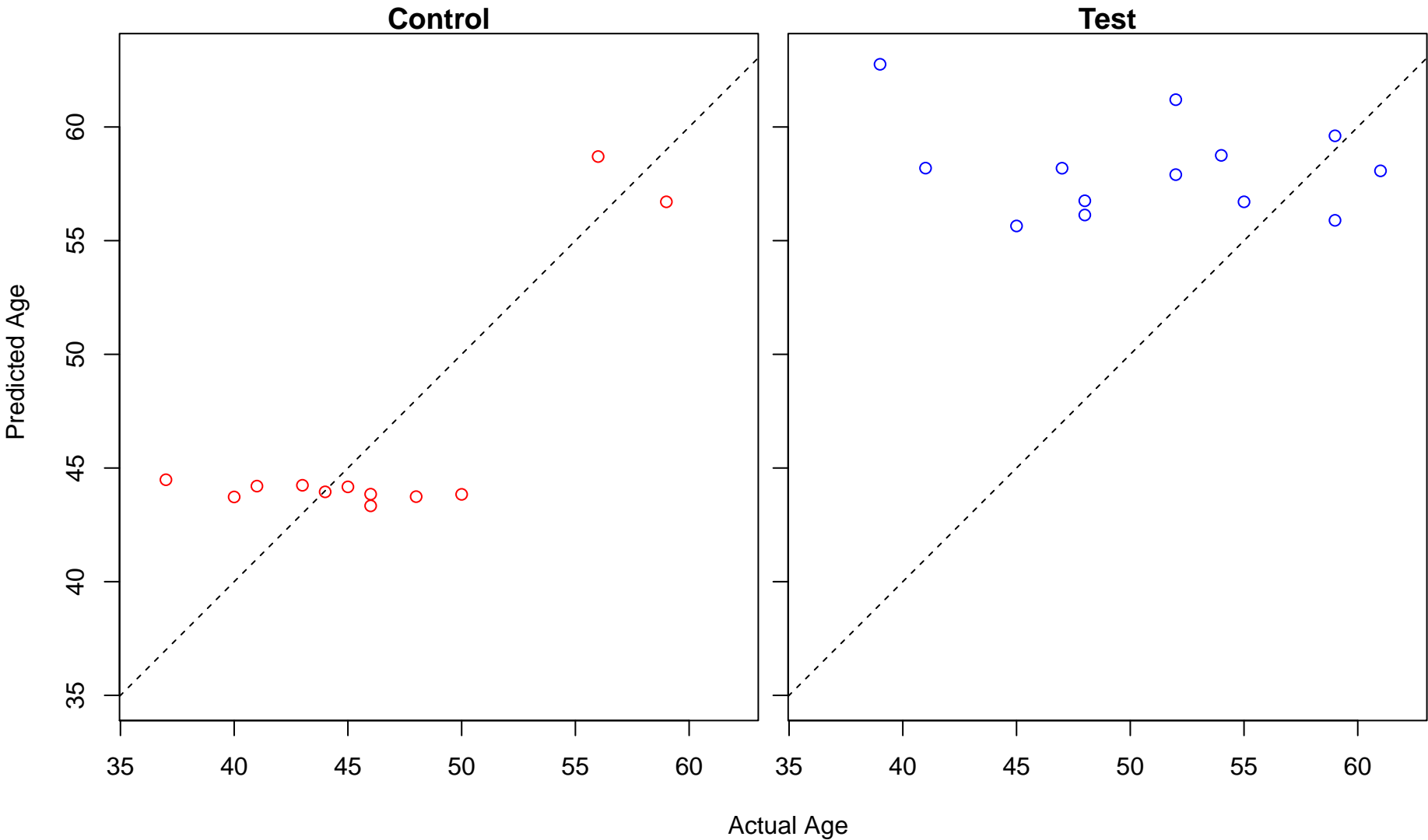
negative regulation of ligase activity (Score: 3.485472)



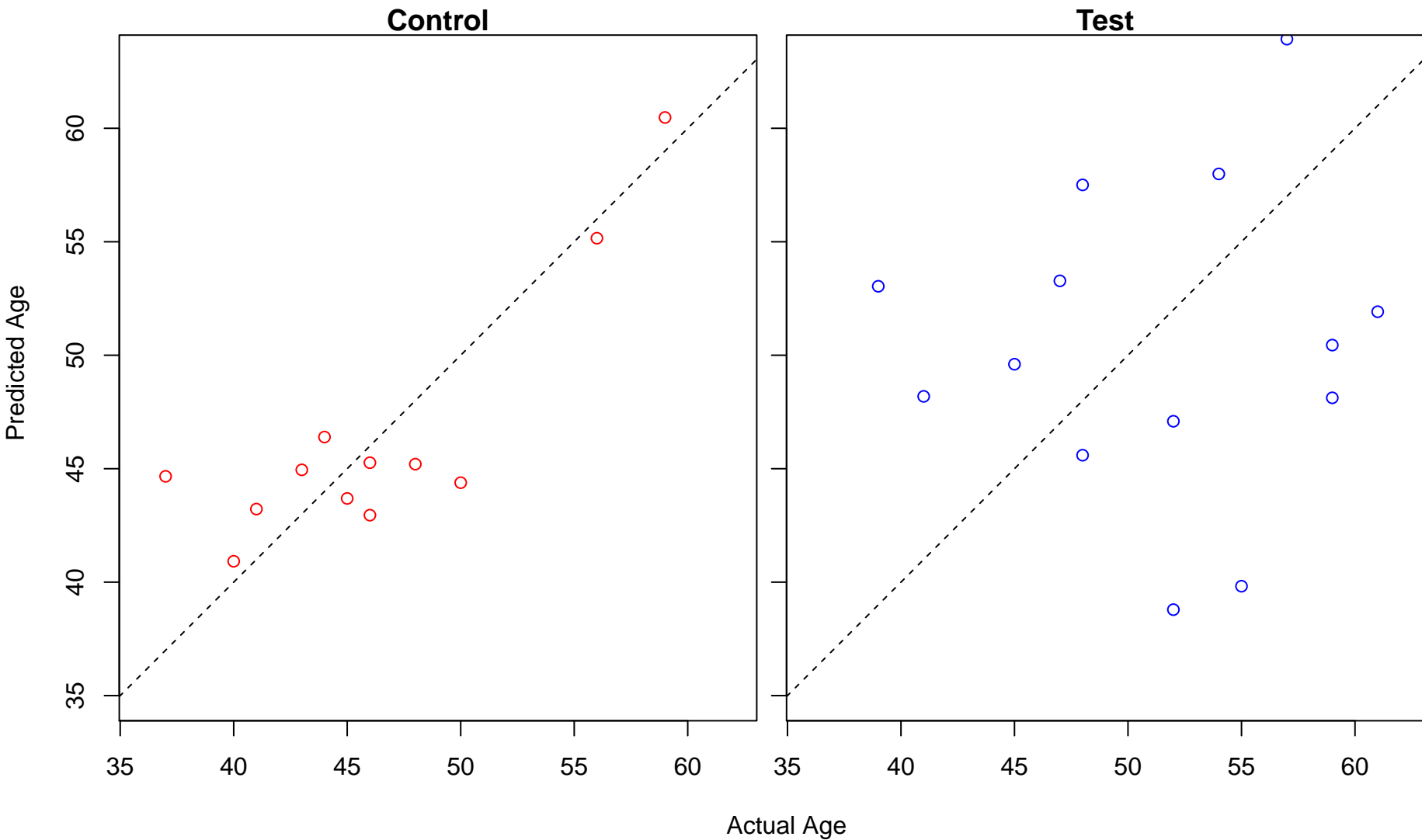
negative regulation of ubiquitin–protein transferase activity (Score: 3.485472)



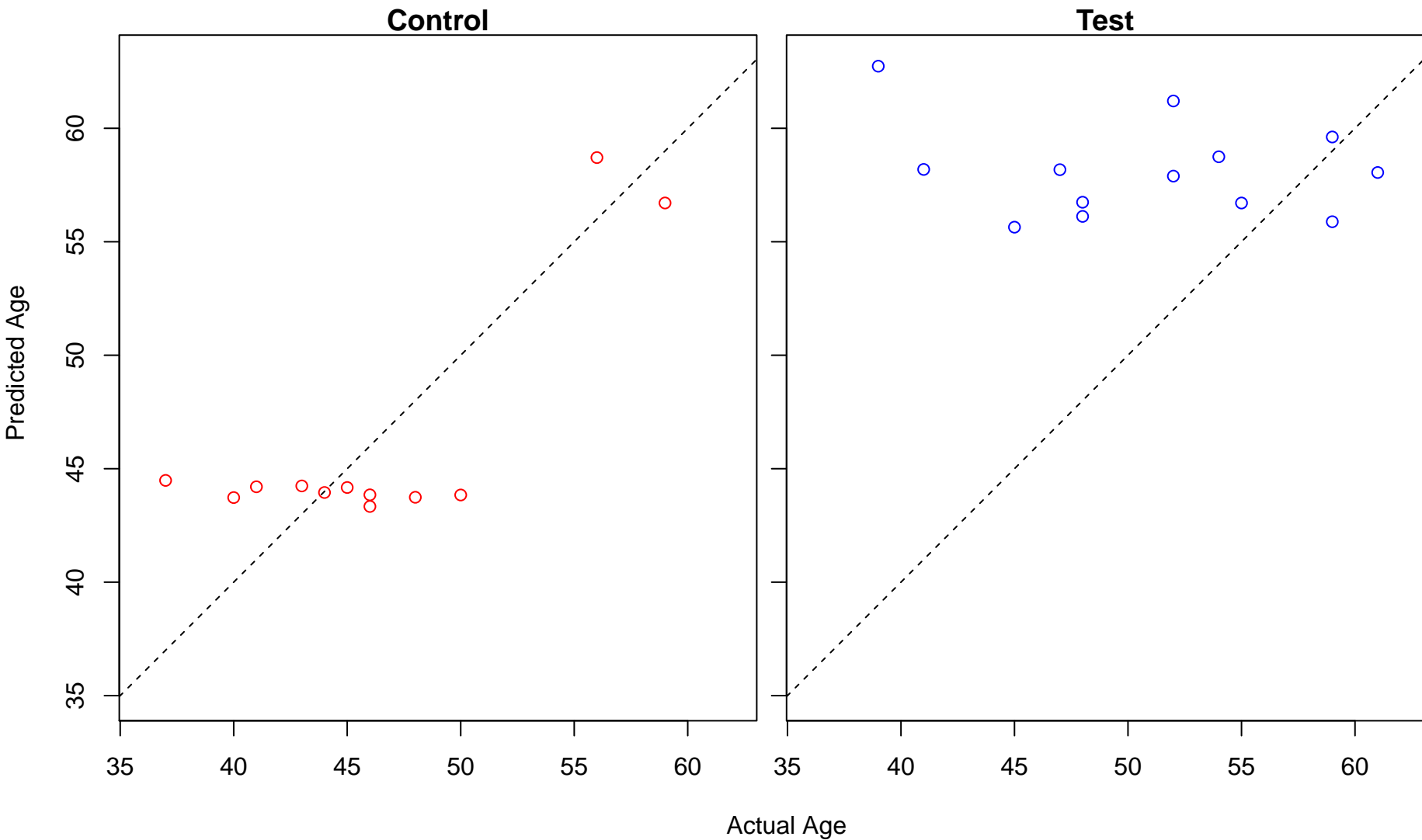
negative regulation of protein modification by small protein conjugation or removal (Score: 3.48530)



positive regulation of ion transport (Score: 3.483387)

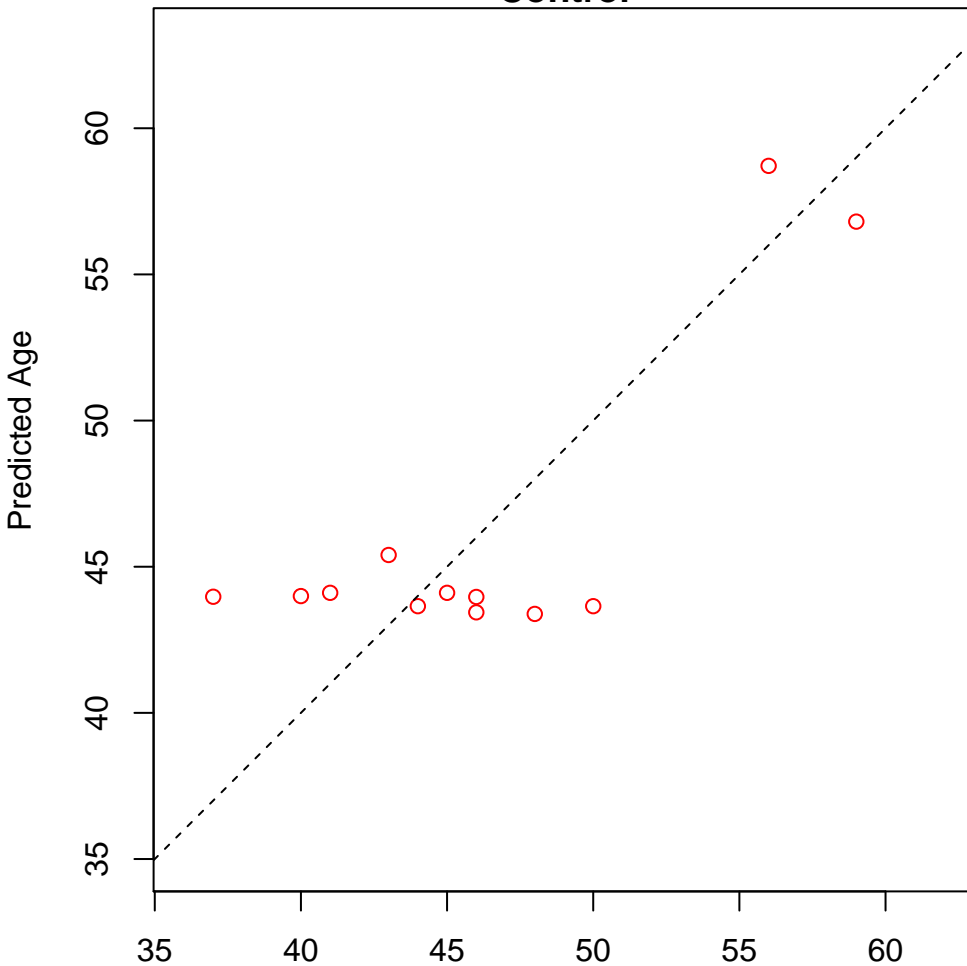


negative regulation of protein ubiquitination (Score: 3.482464)

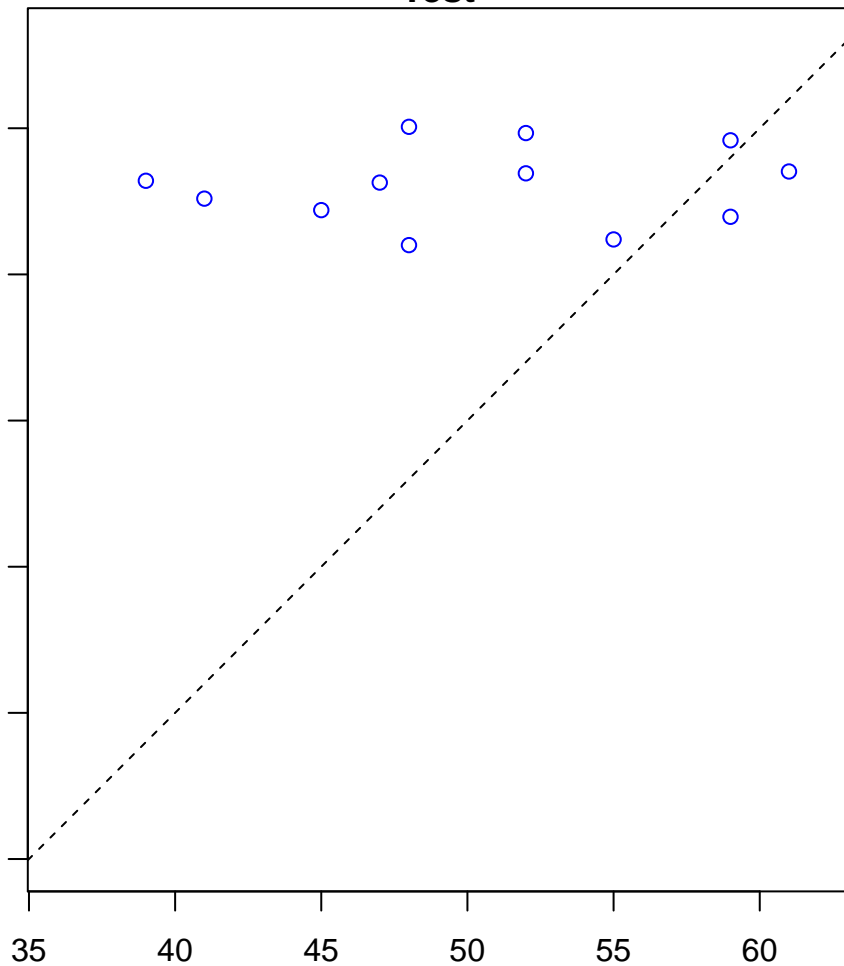


protein localization to chromatin (Score: 3.481966)

Control

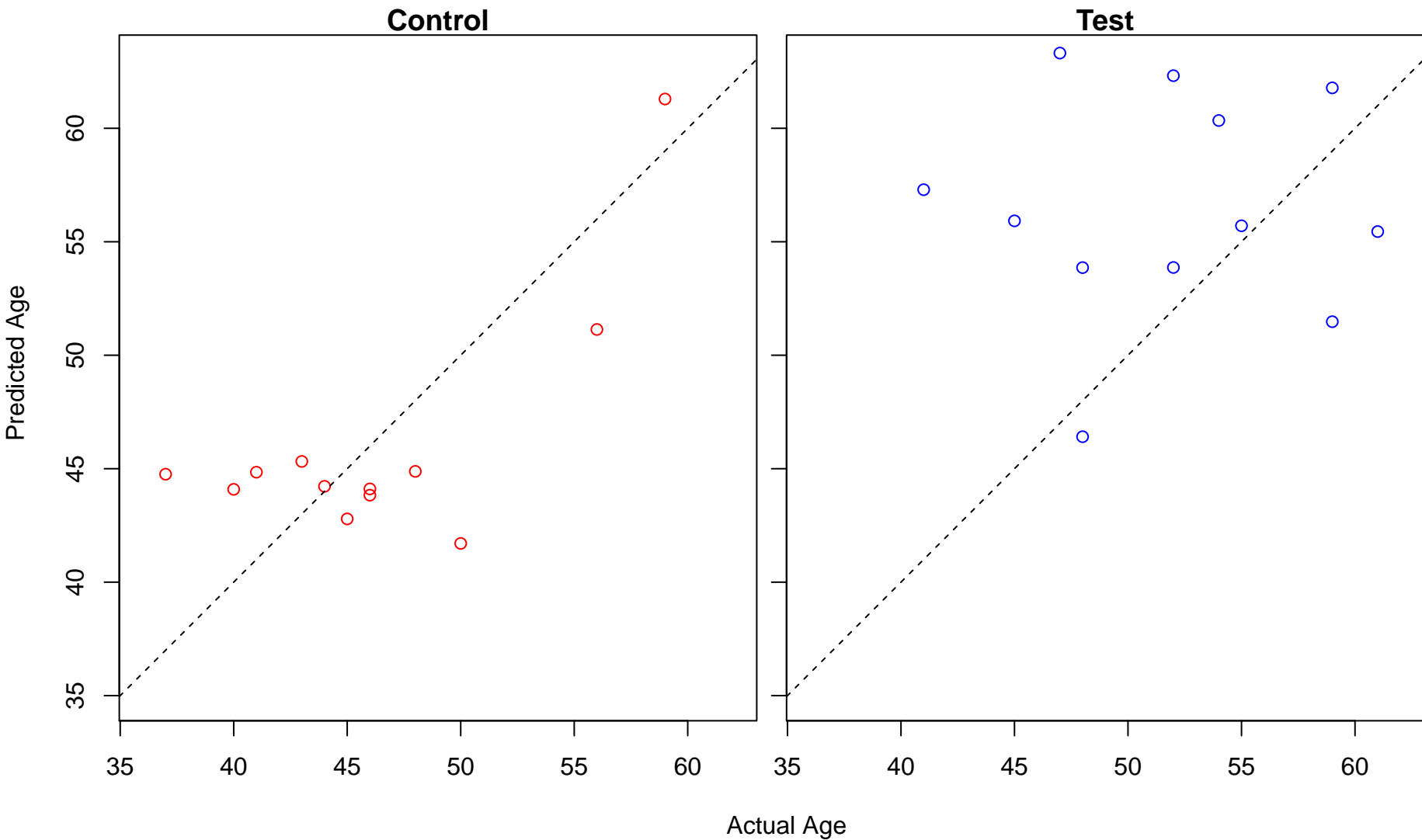


Test

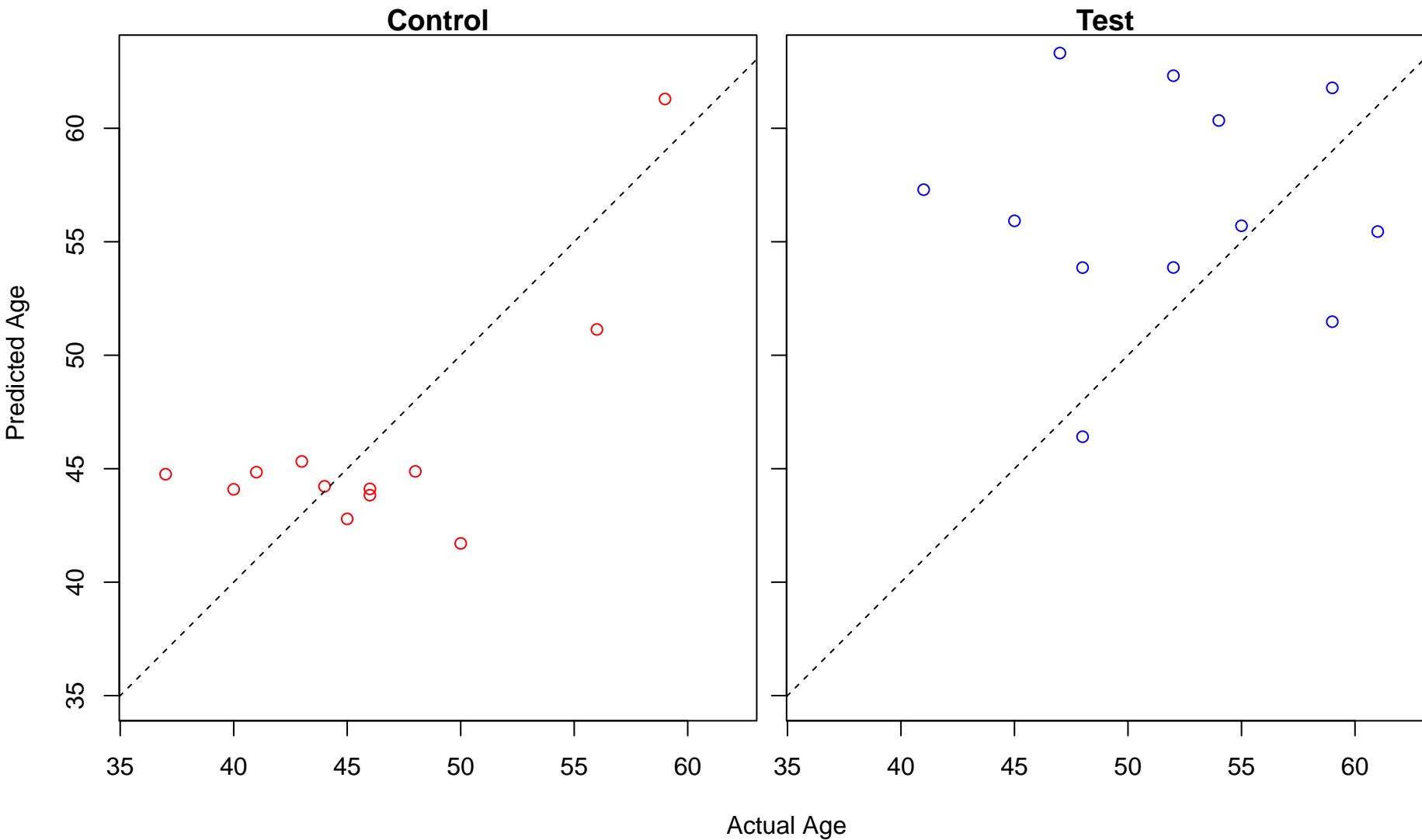


Actual Age

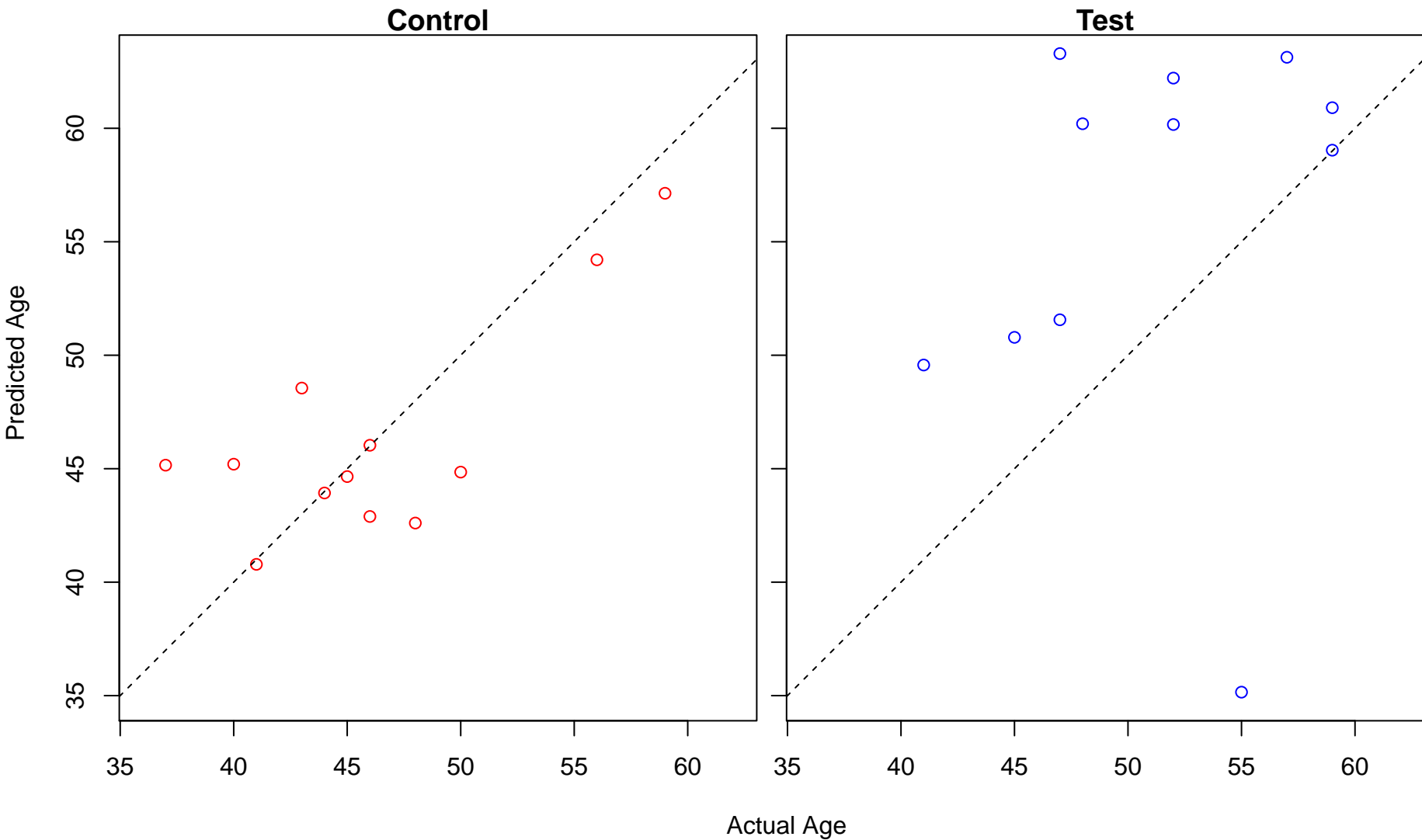
positive regulation of leukocyte mediated cytotoxicity (Score: 3.478779)



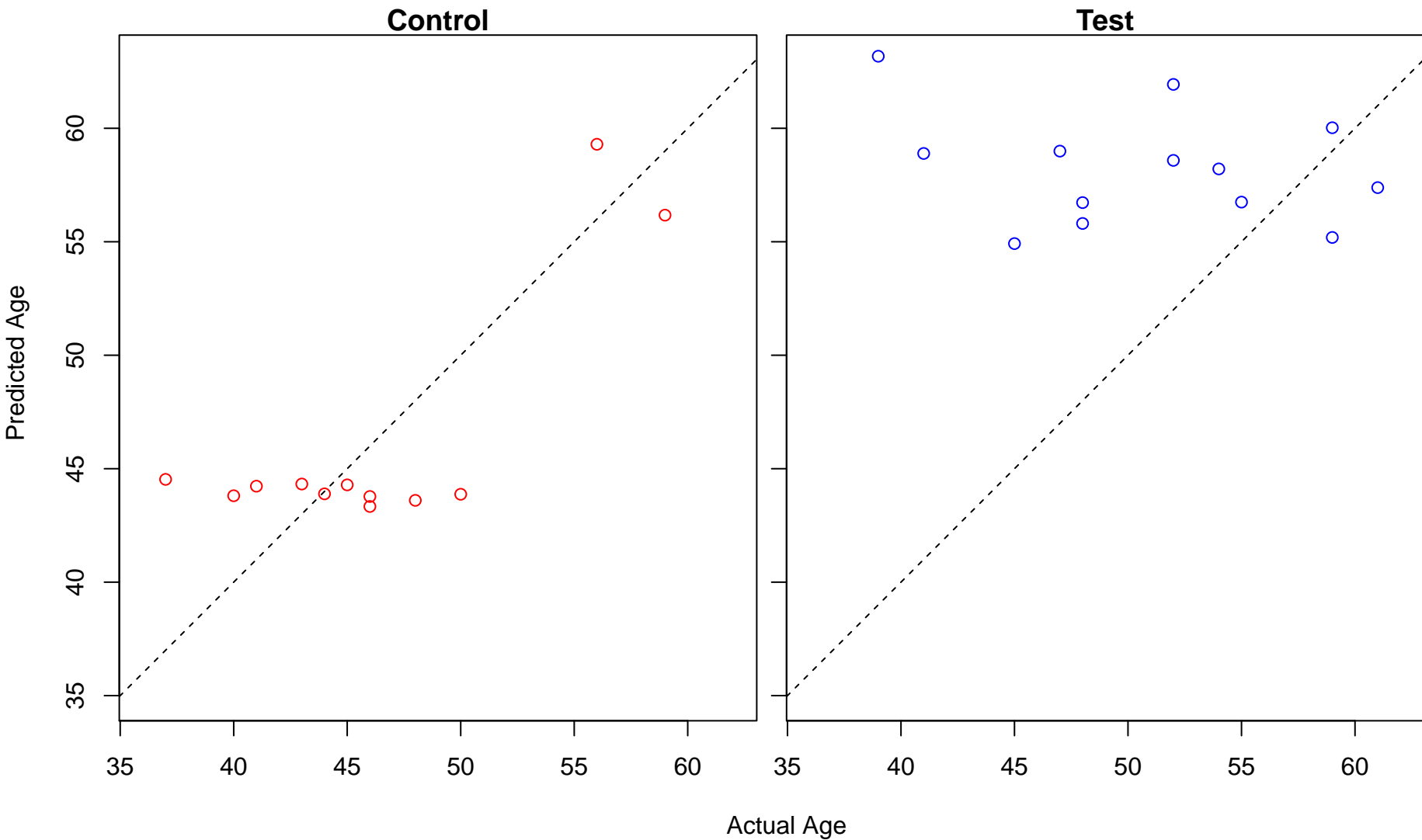
positive regulation of cell killing (Score: 3.478741)



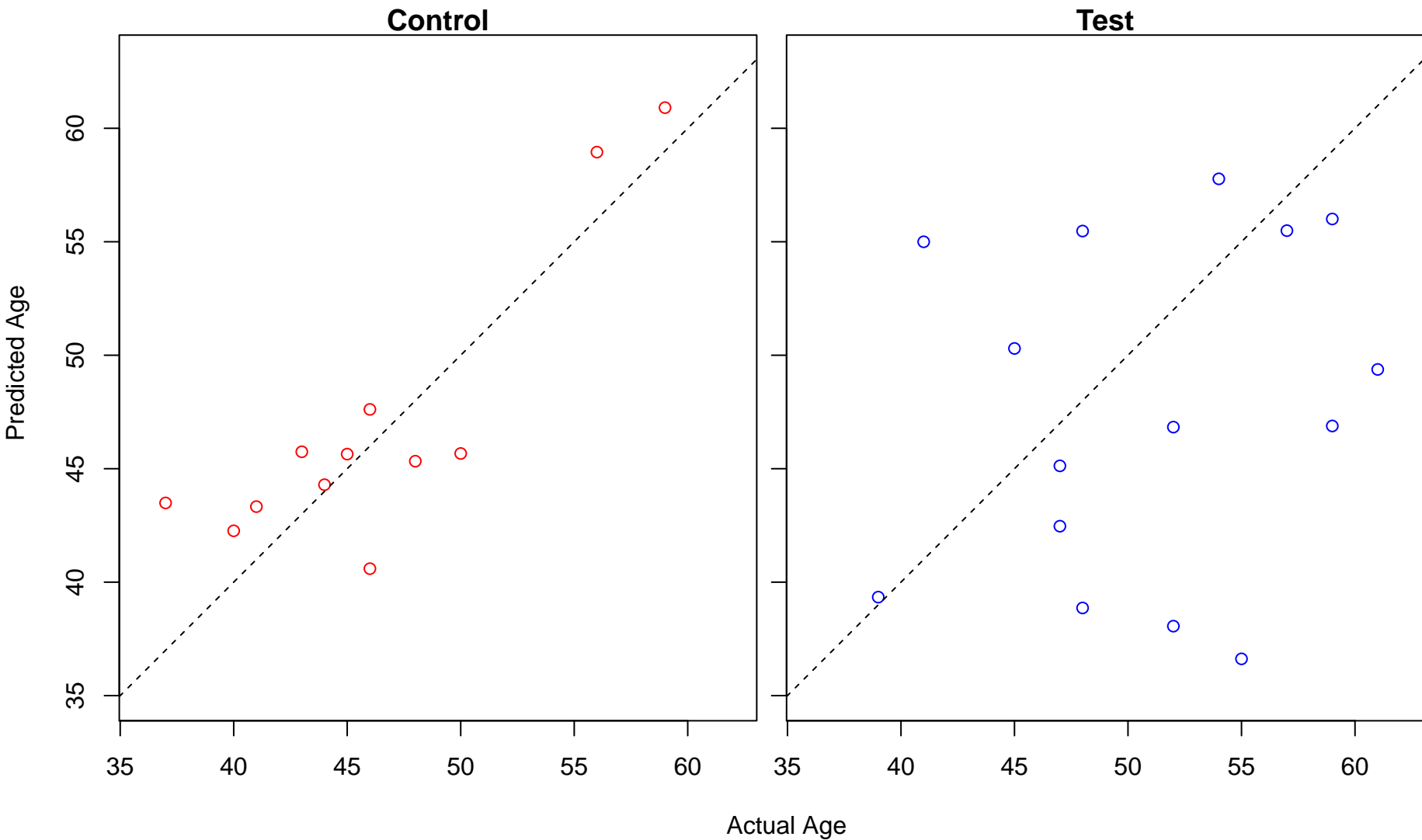
smooth muscle cell differentiation (Score: 3.478437)



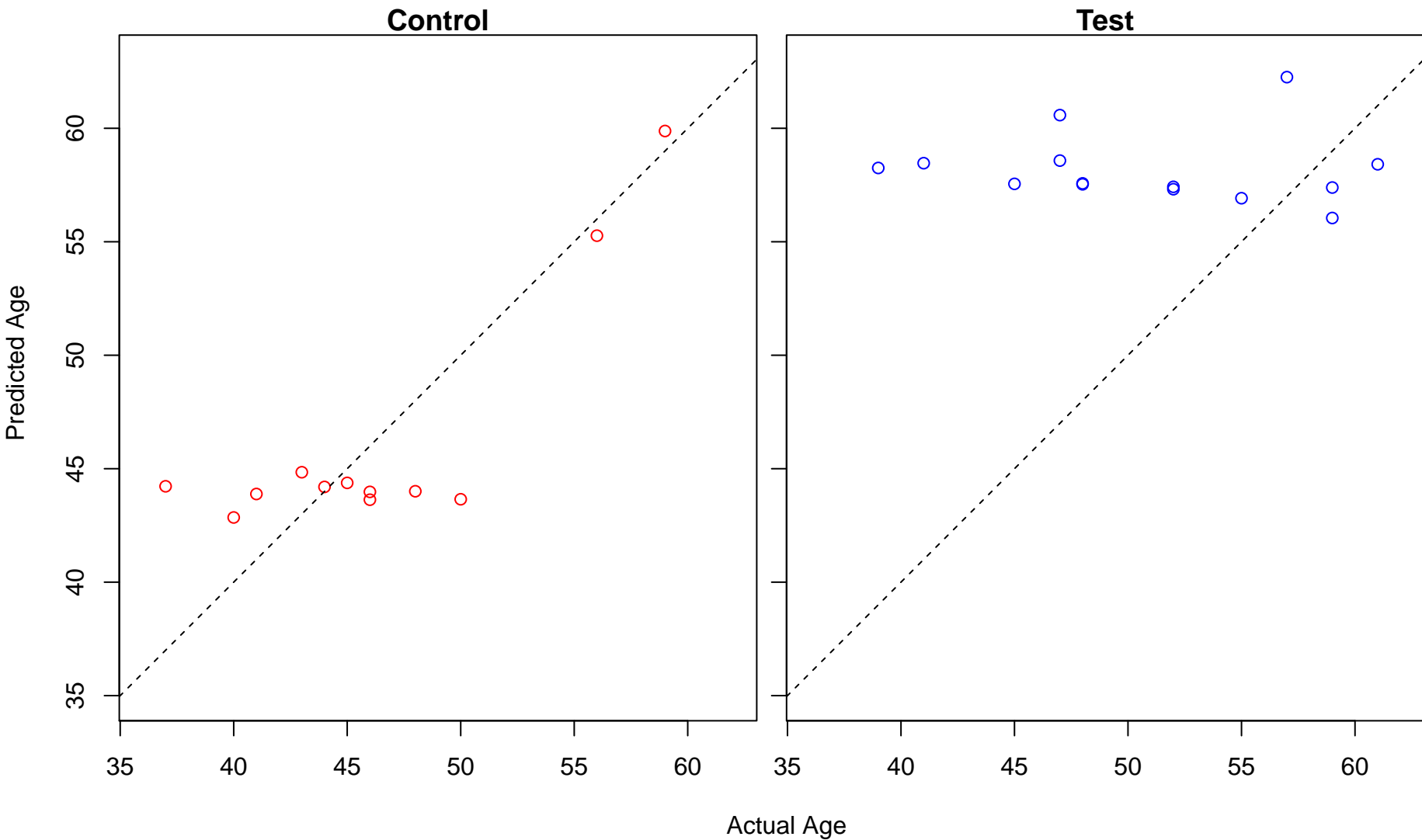
DNA damage checkpoint (Score: 3.477710)



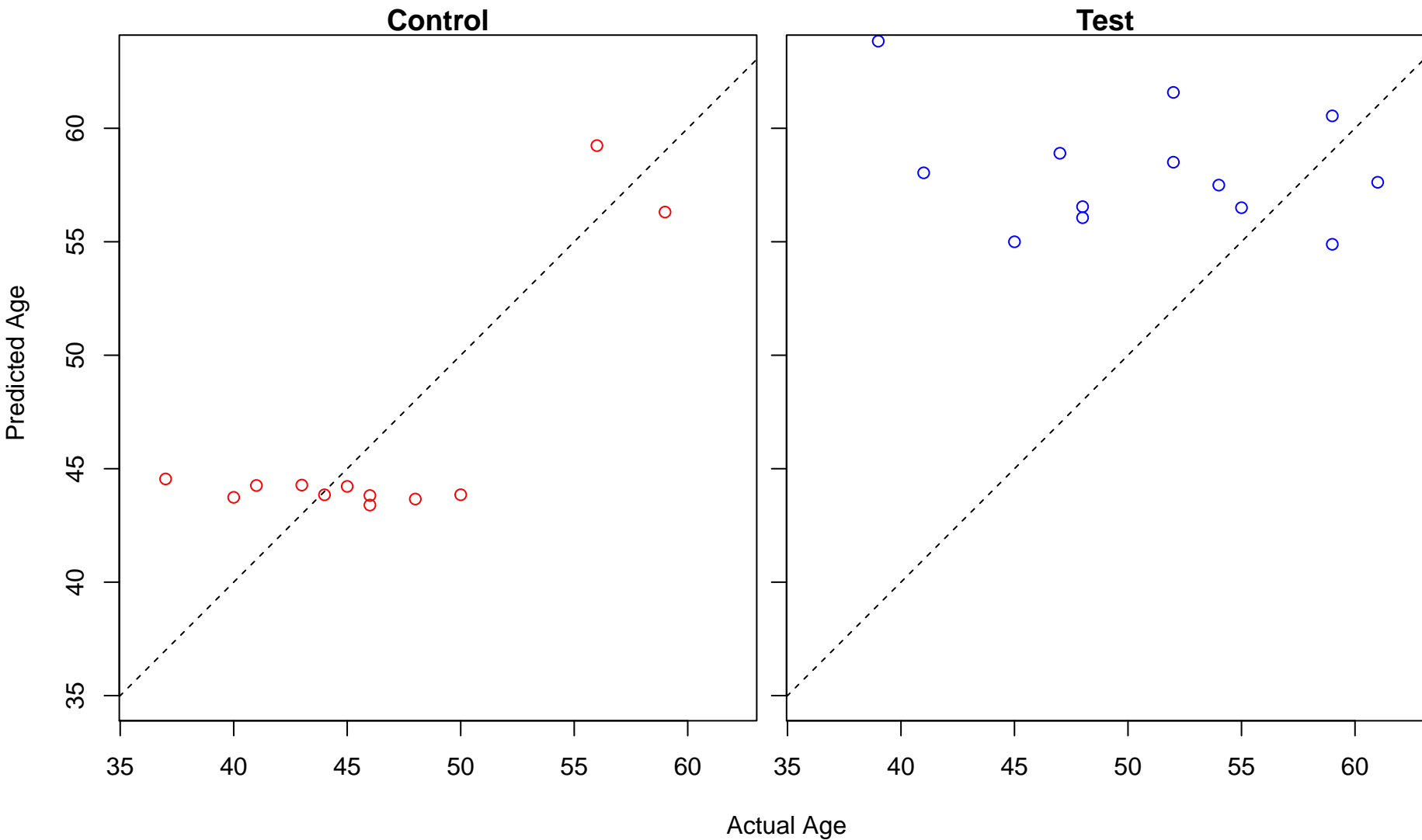
regulation of cellular component size (Score: 3.477157)



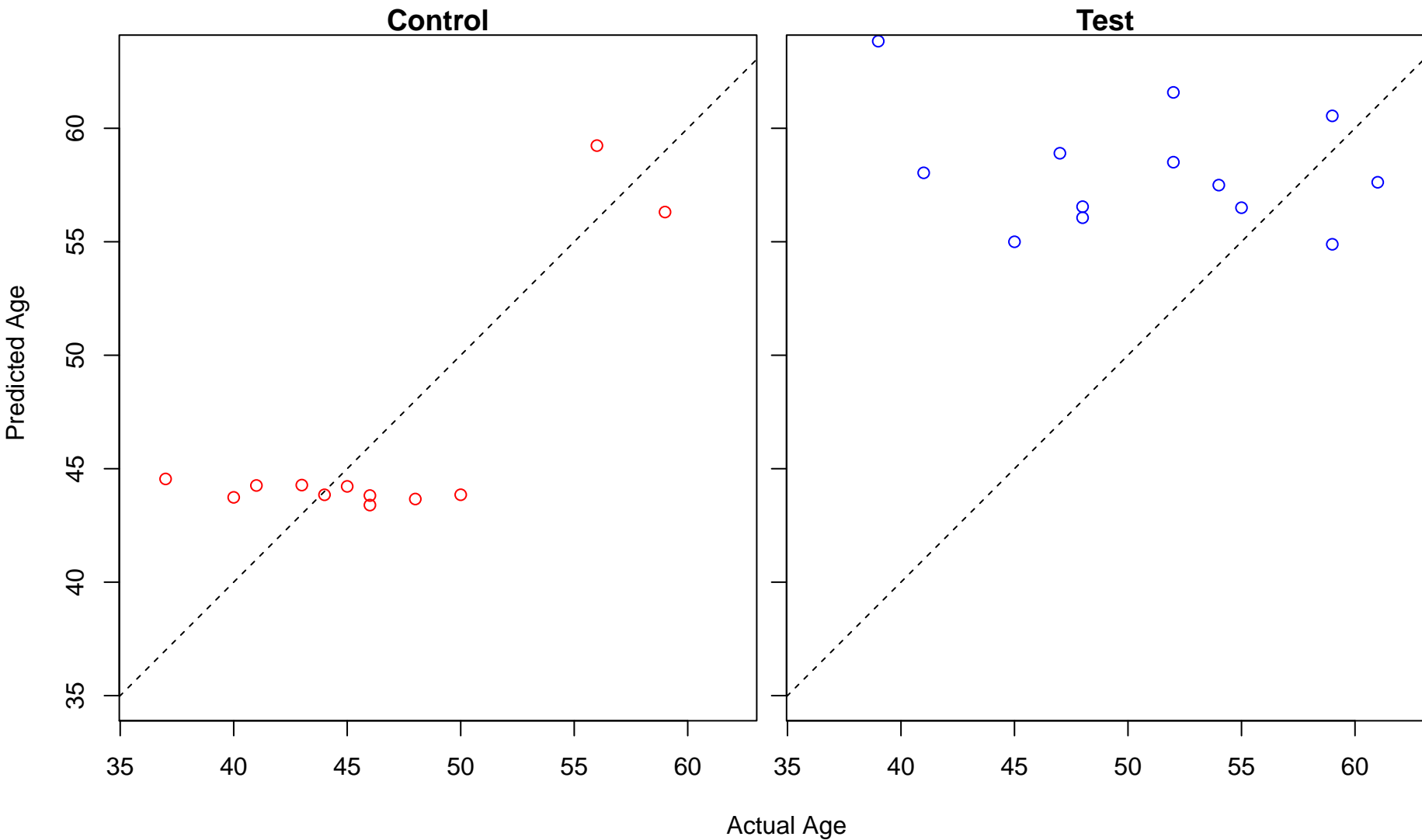
phosphatidylglycerol biosynthetic process (Score: 3.475806)



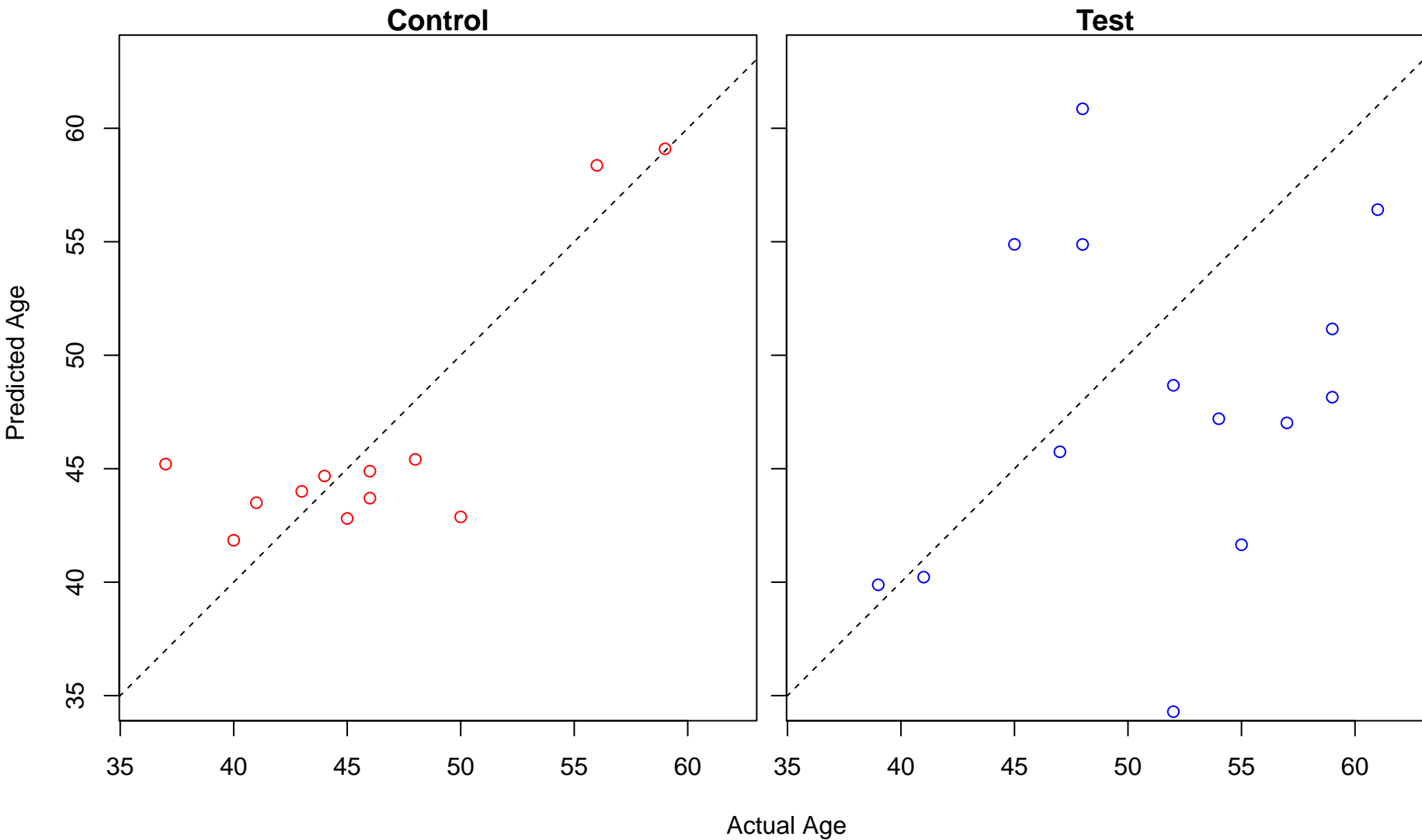
double-strand break repair via homologous recombination (Score: 3.474571)



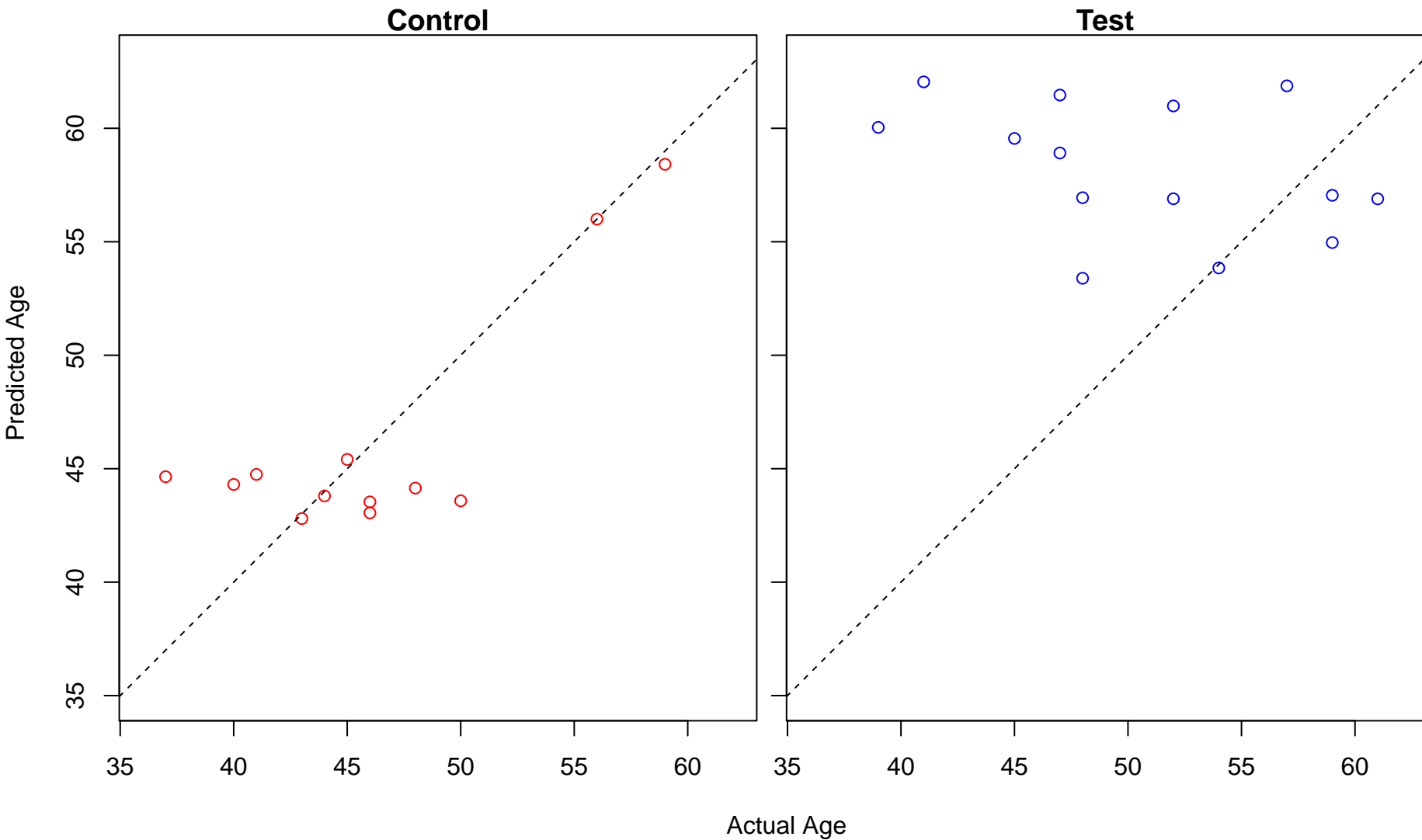
recombinational repair (Score: 3.474571)



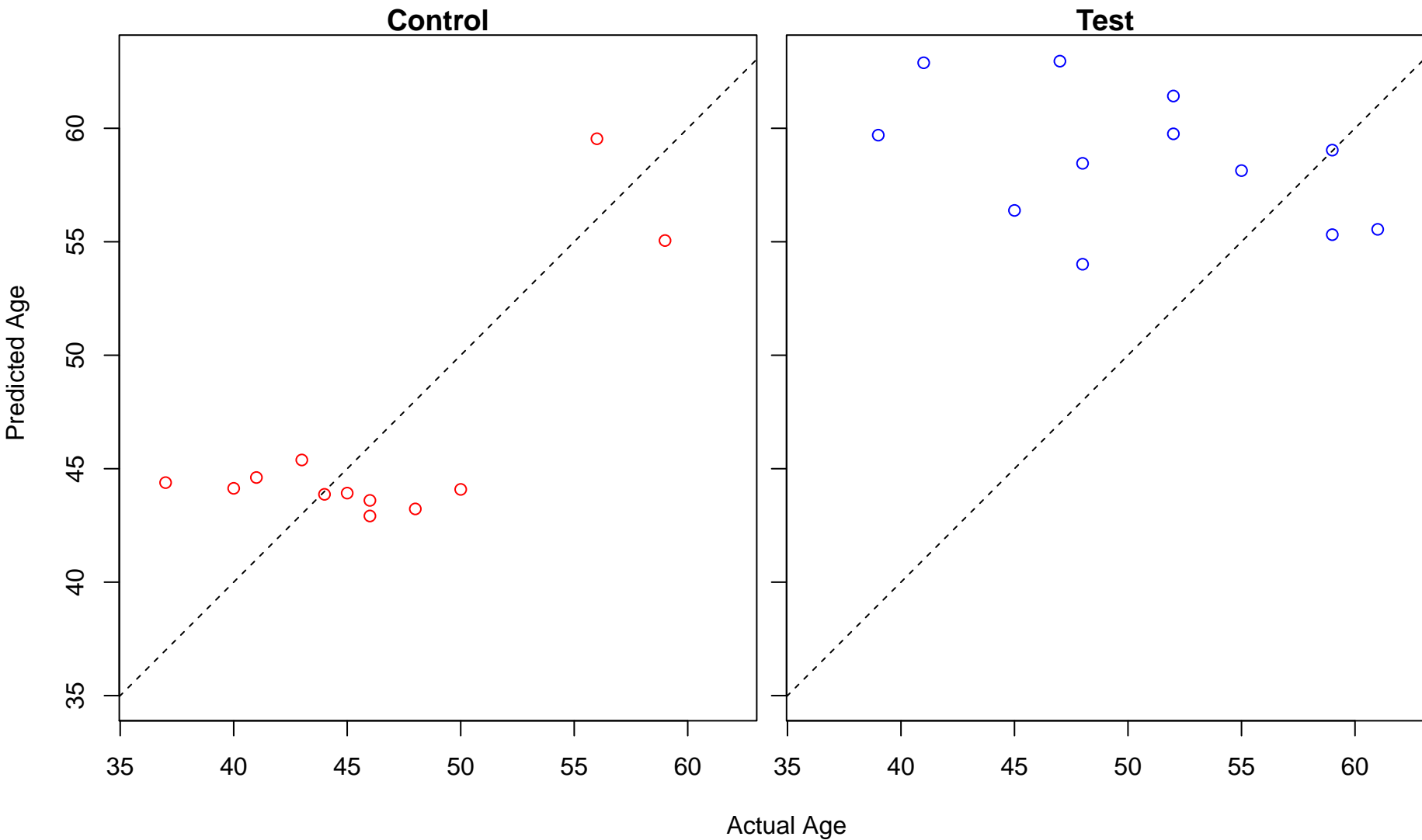
multicellular organism reproduction (Score: 3.474241)



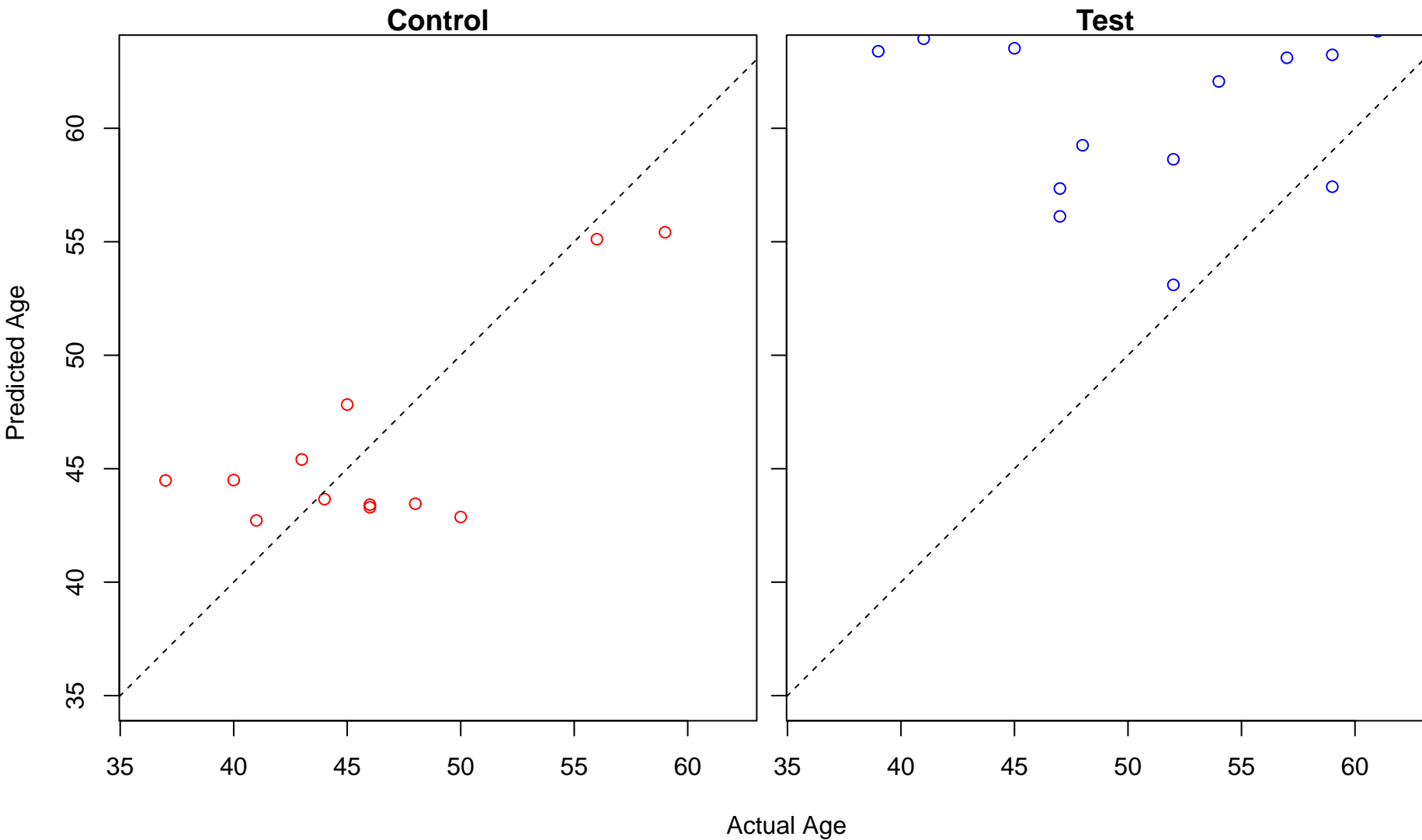
regulation of axonogenesis (Score: 3.473021)



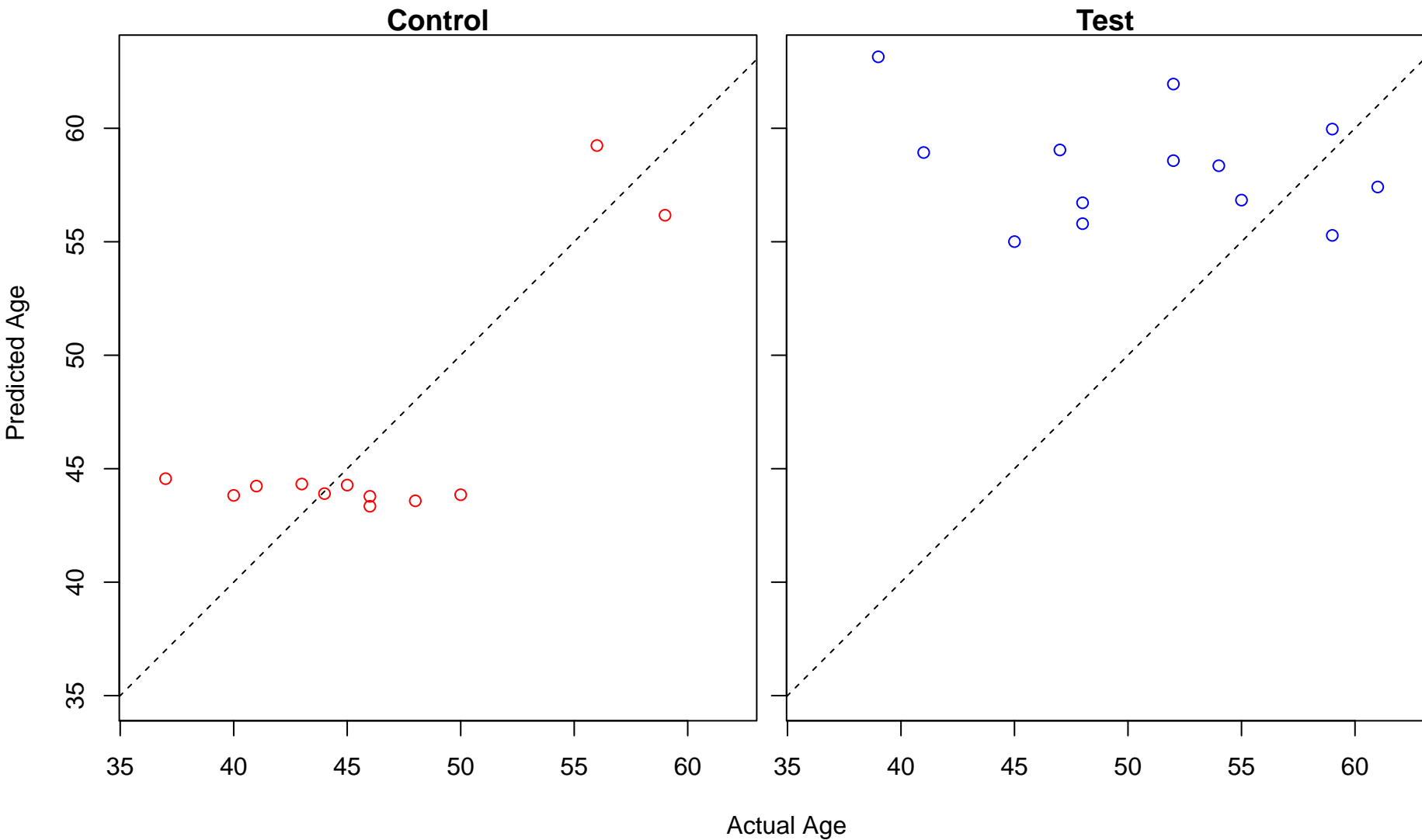
positive regulation of peptidyl-lysine acetylation (Score: 3.472495)



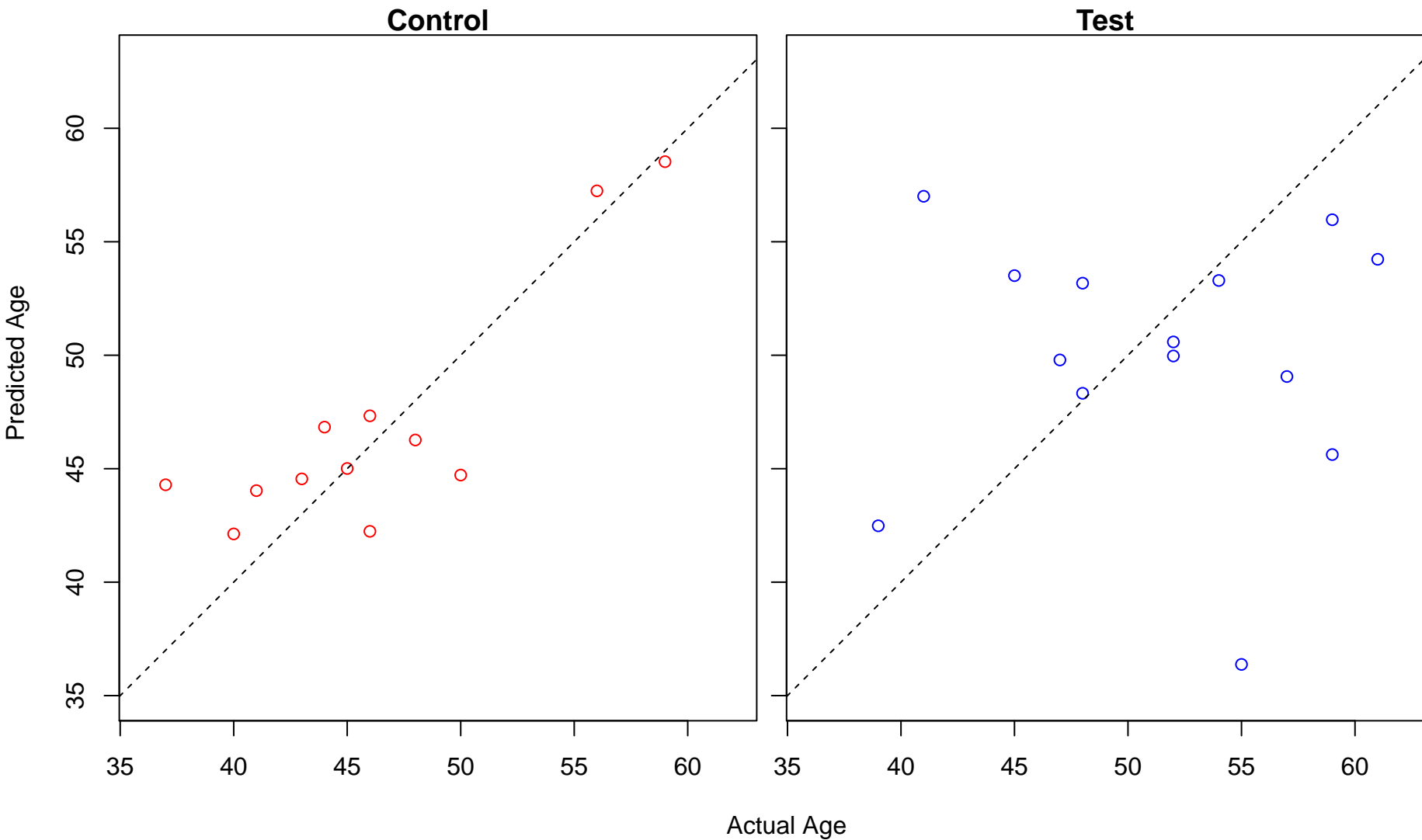
positive regulation of triglyceride biosynthetic process (Score: 3.470855)



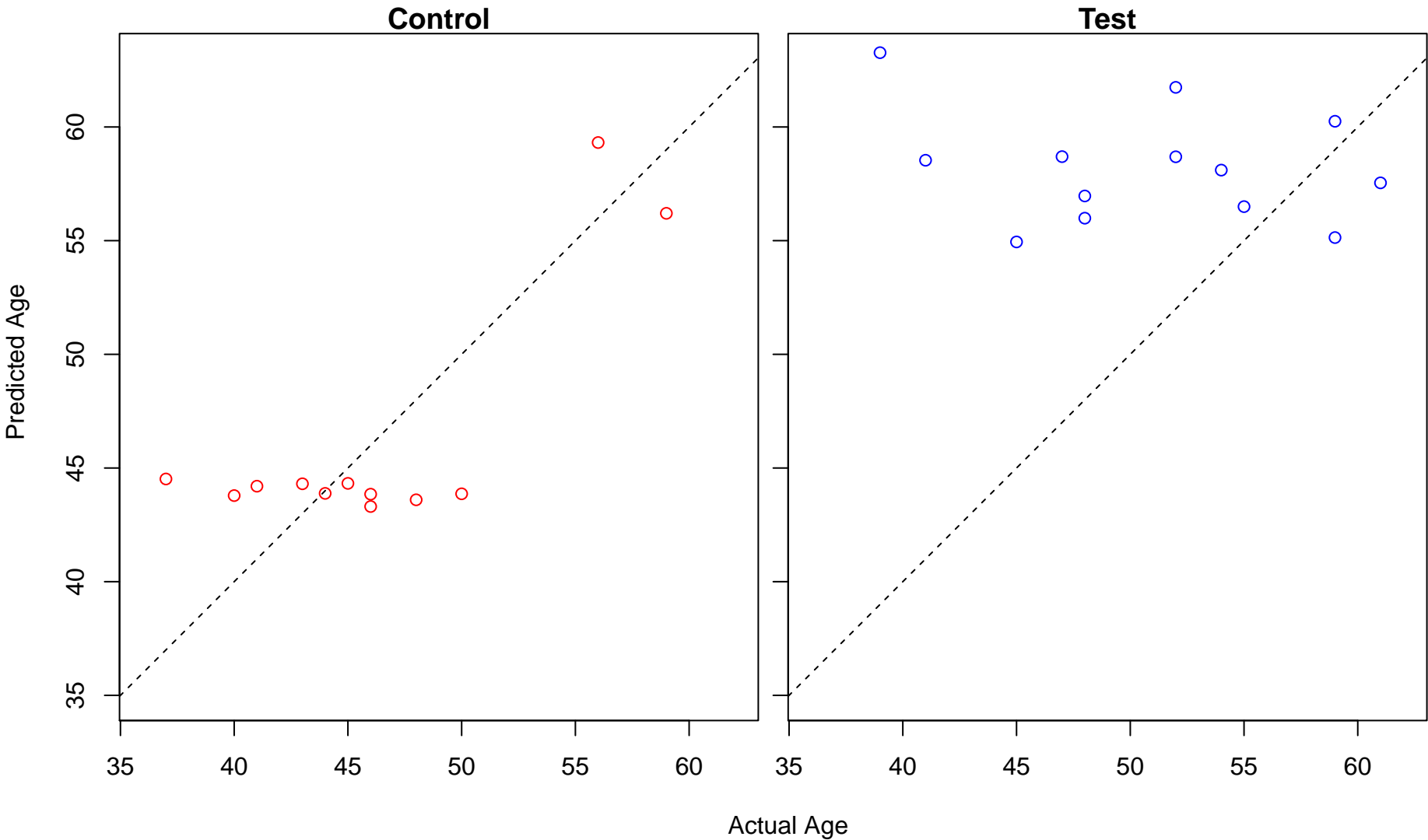
regulation of G1/S transition of mitotic cell cycle (Score: 3.470413)



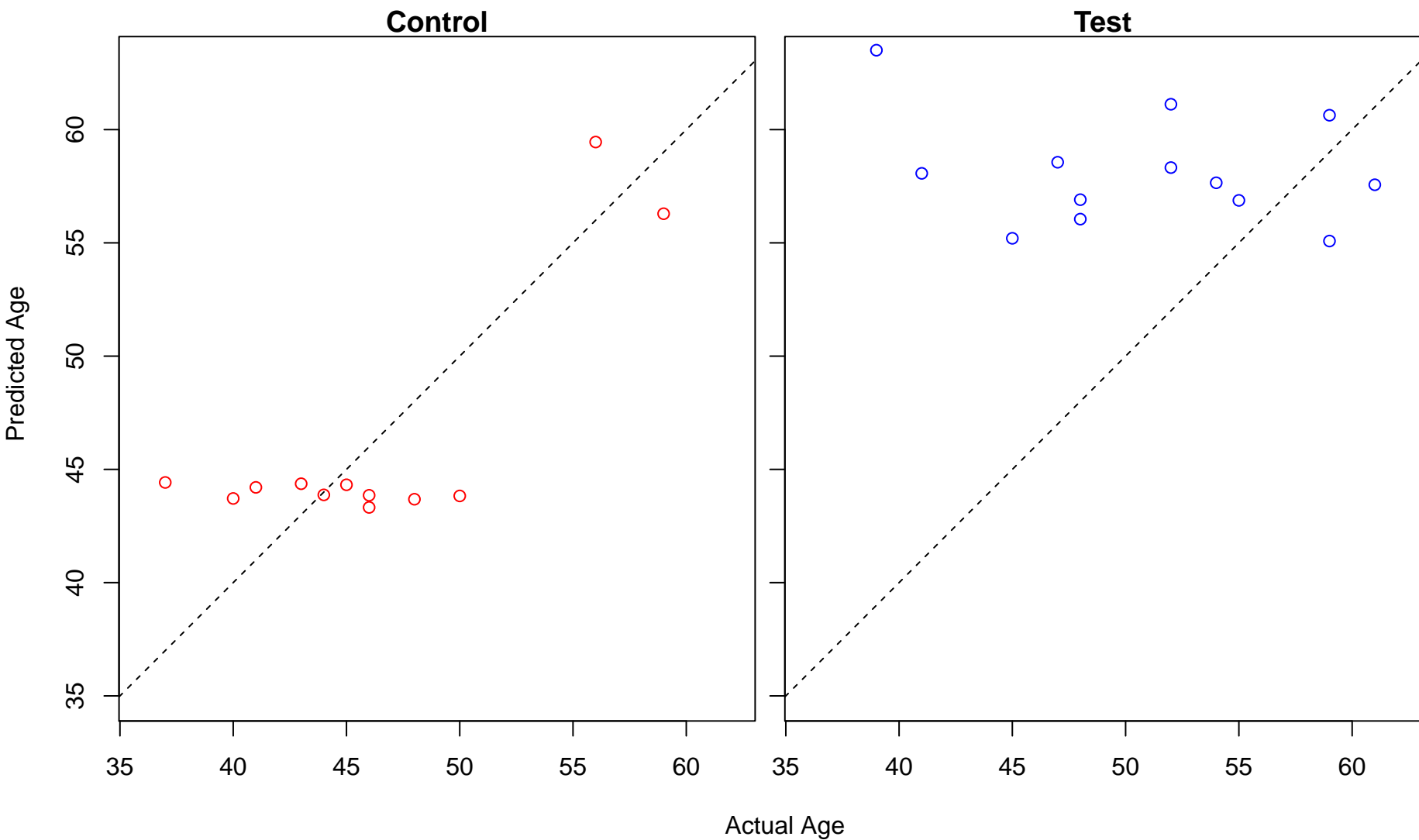
regulation of leukocyte cell-cell adhesion (Score: 3.469087)



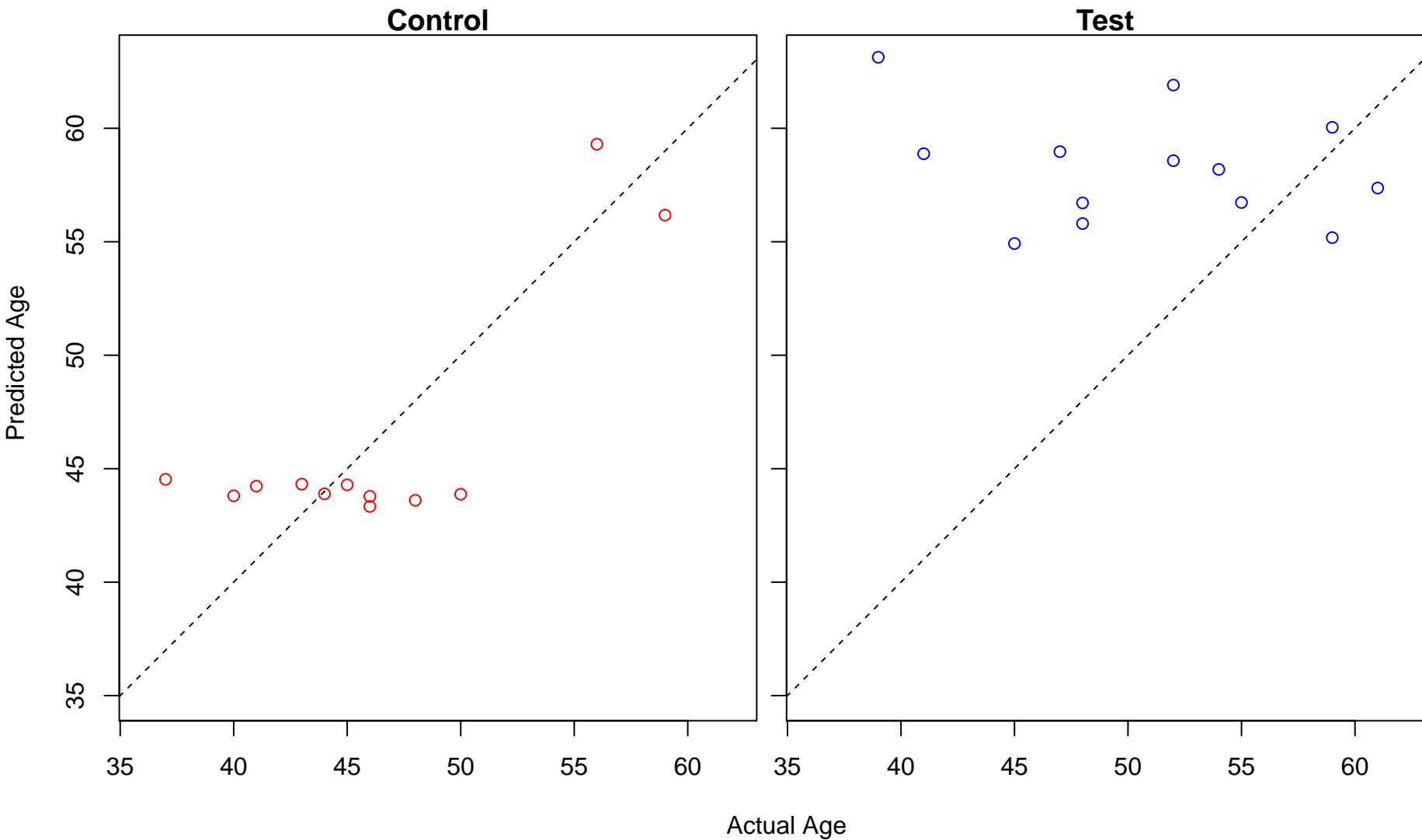
negative regulation of ubiquitin–protein ligase activity involved in mitotic cell cycle (Score: 3.46902)



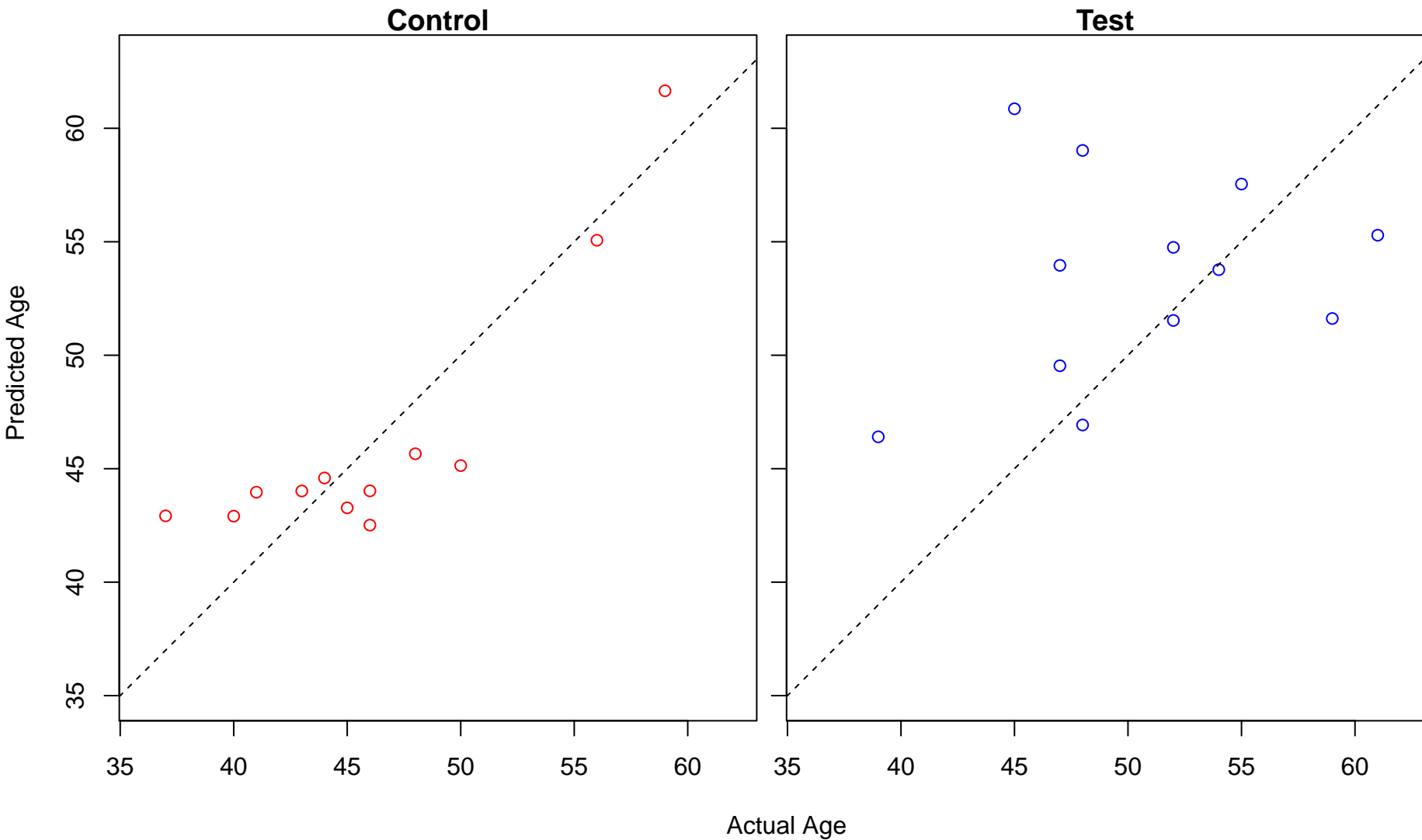
global genome nucleotide–excision repair (Score: 3.468895)



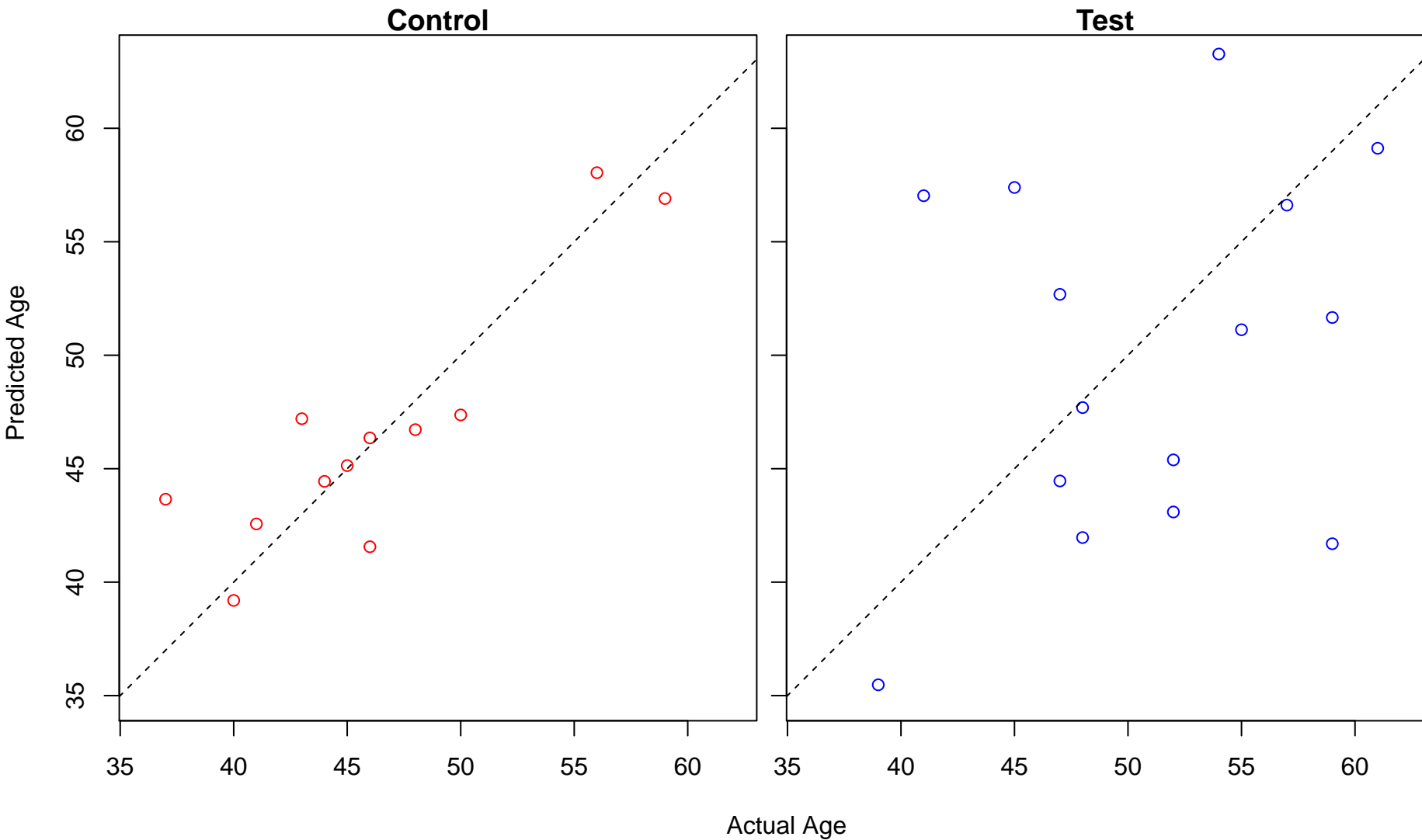
DNA integrity checkpoint (Score: 3.468597)



organic hydroxy compound catabolic process (Score: 3.468429)

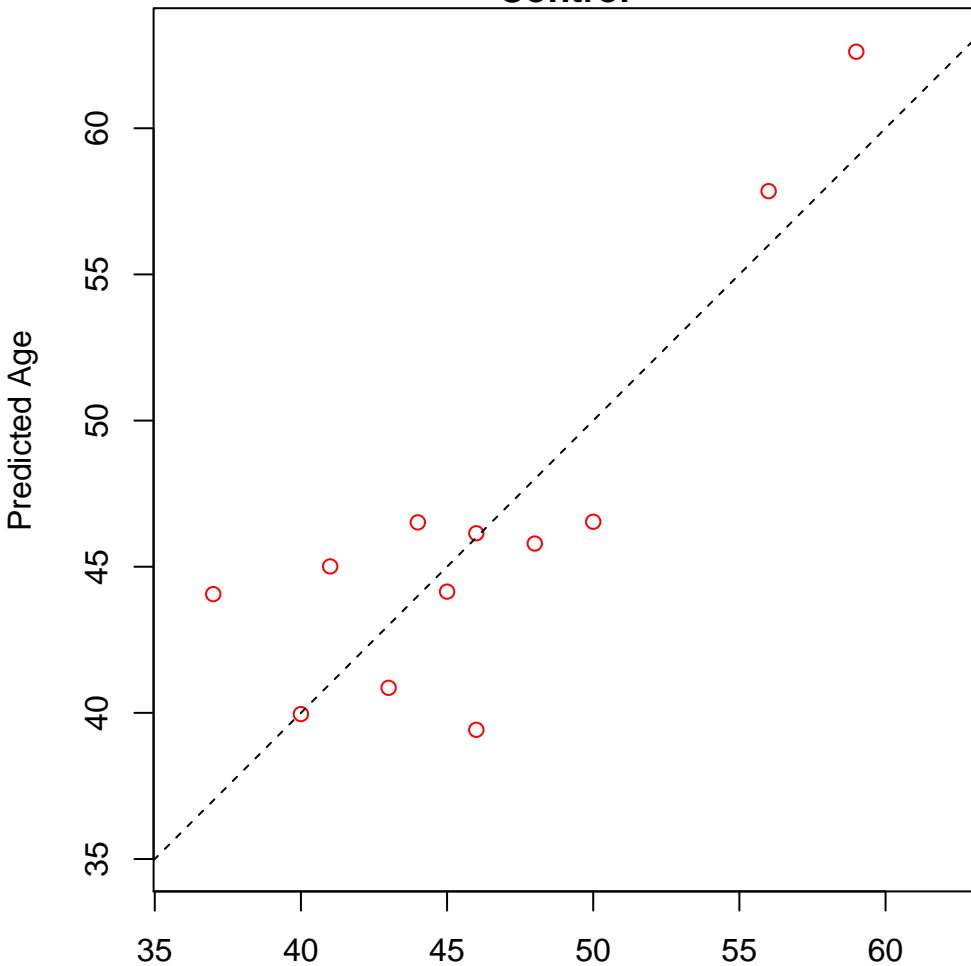


phospholipid metabolic process (Score: 3.467812)

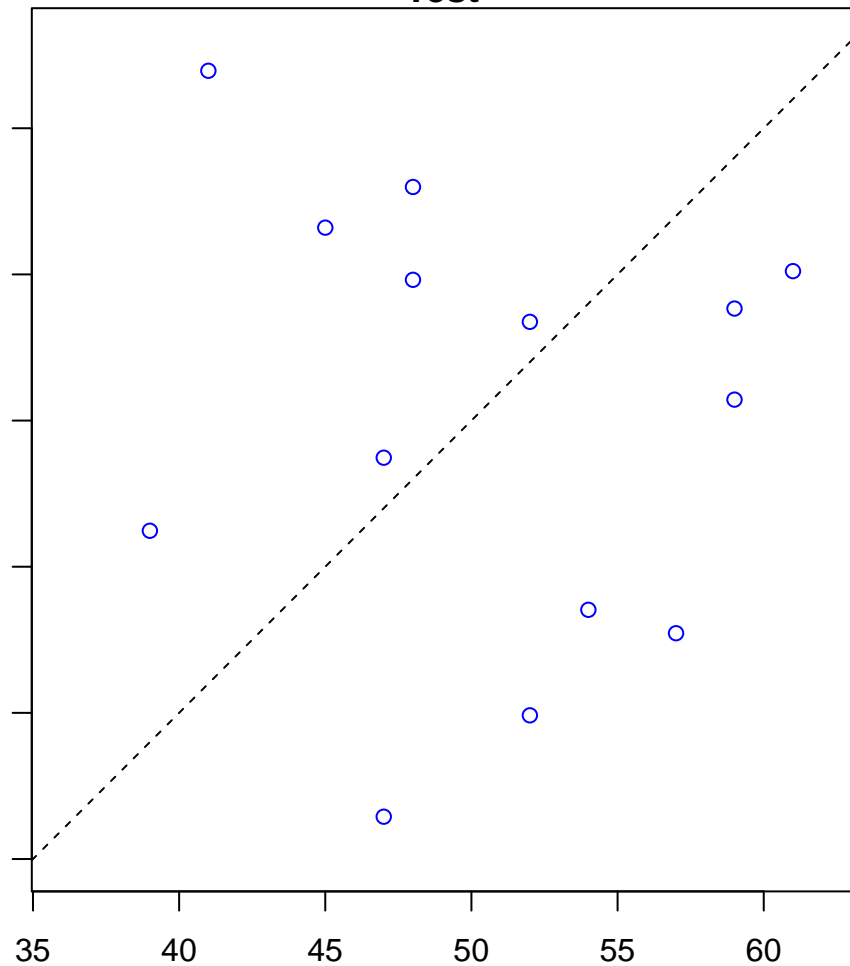


mitochondrial transmembrane transport (Score: 3.467412)

Control

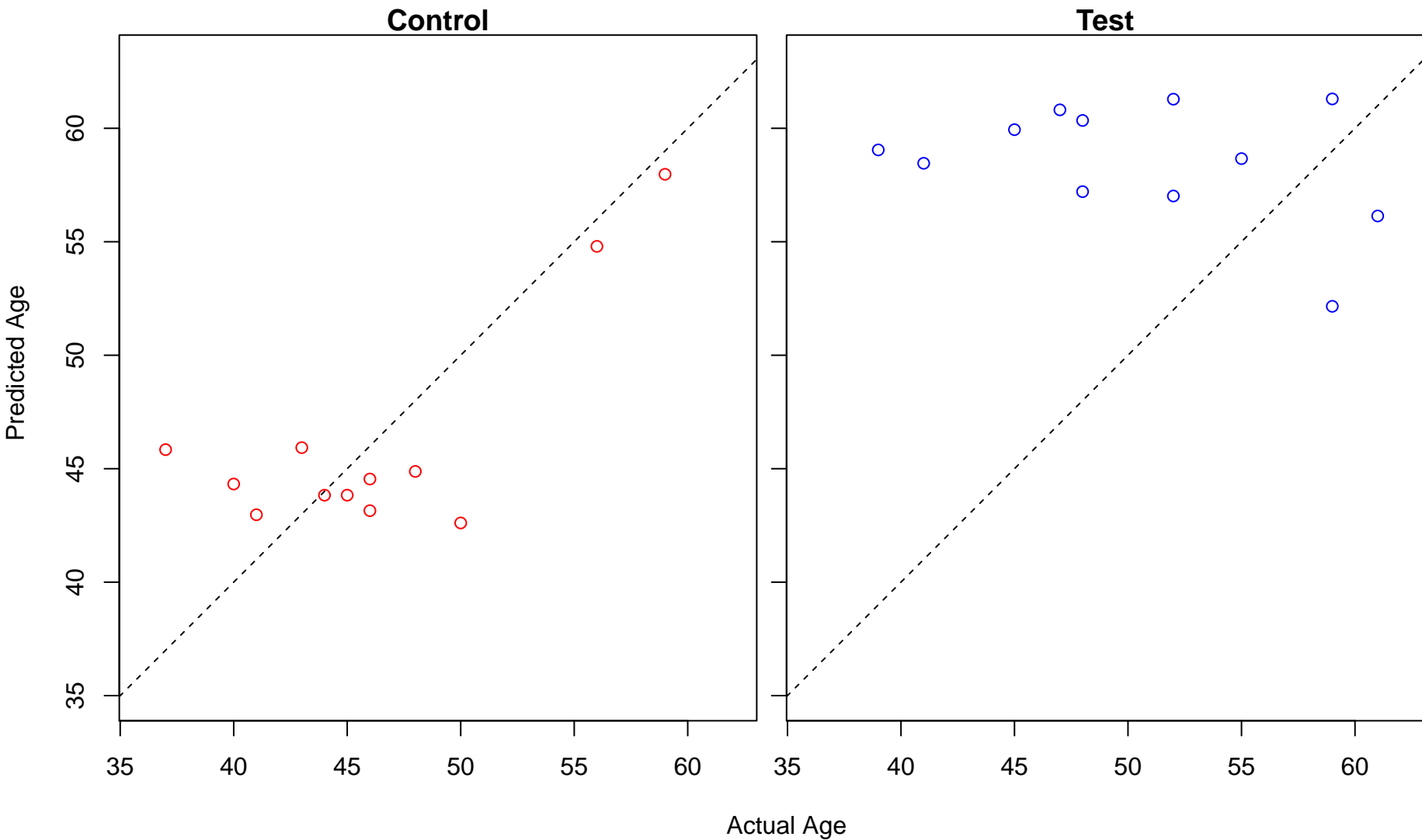


Test

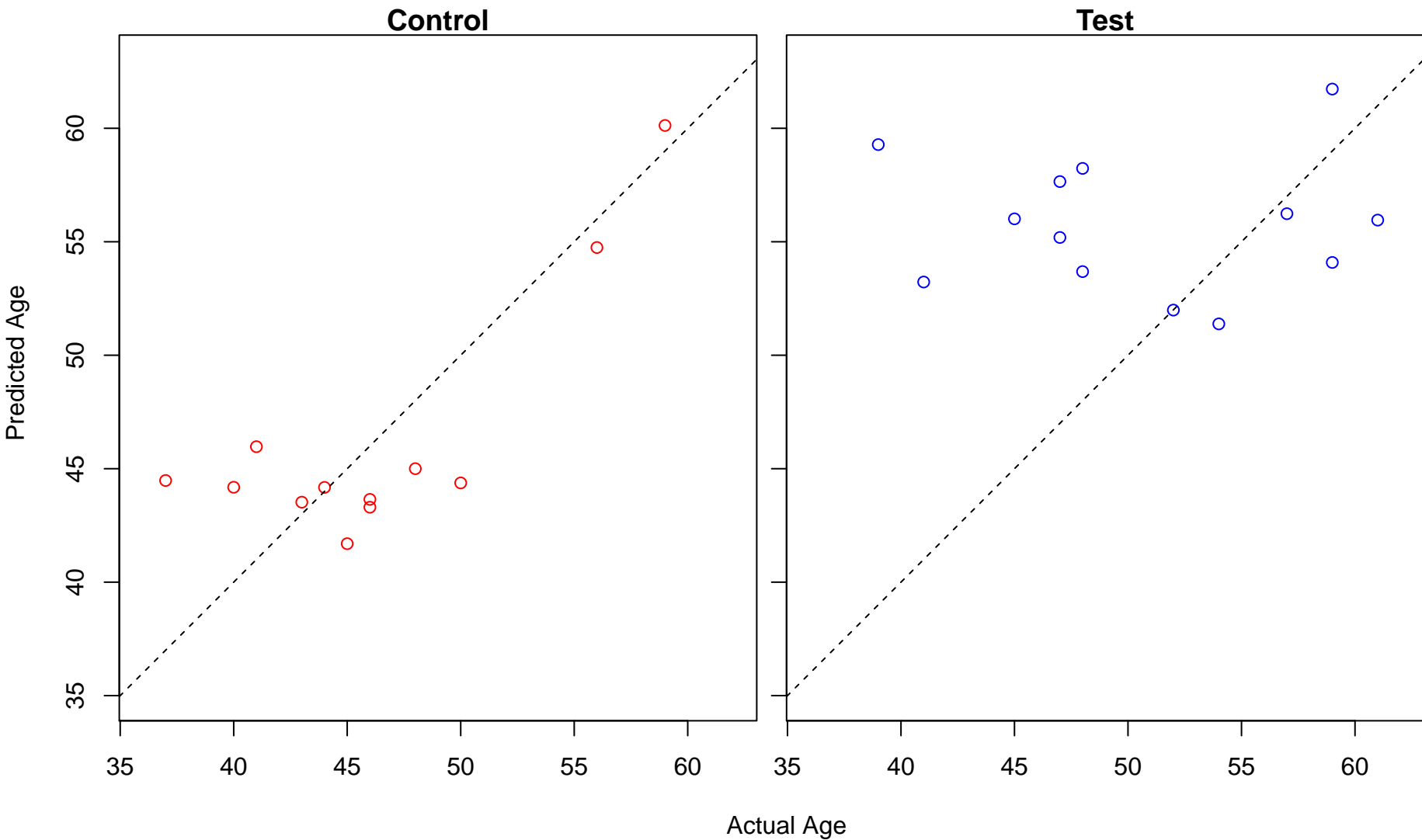


Actual Age

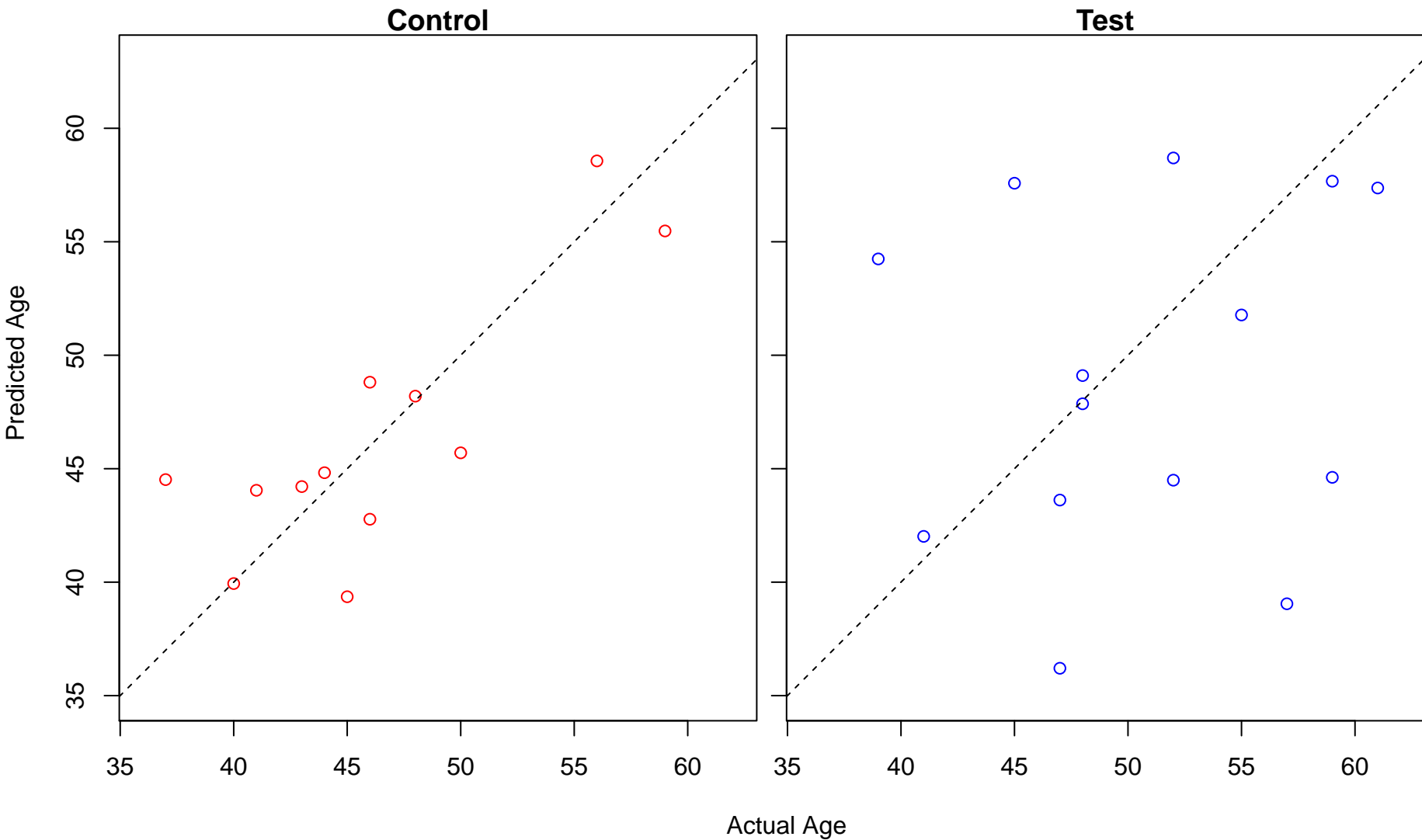
glutamate secretion (Score: 3.467208)



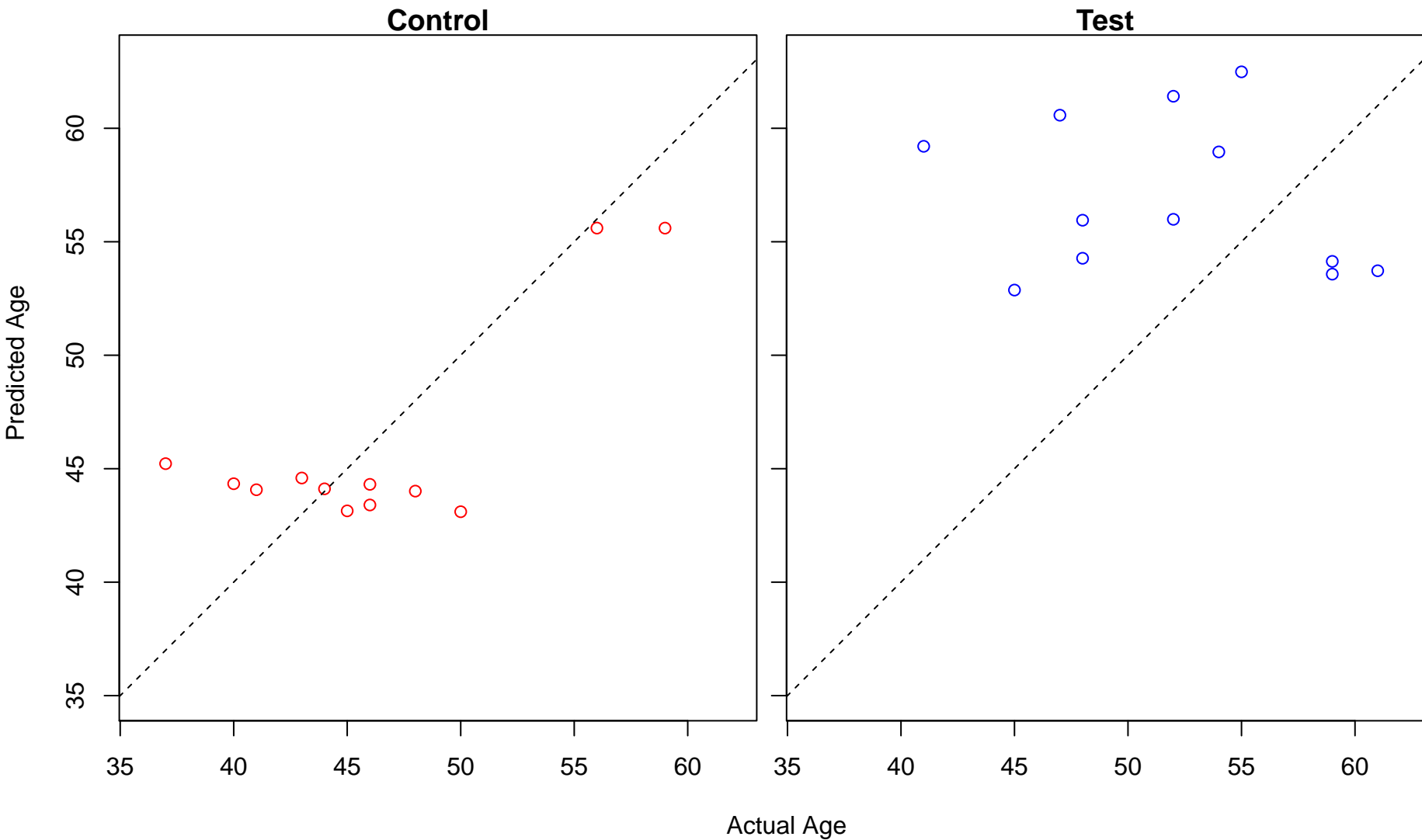
positive regulation of hormone metabolic process (Score: 3.466658)



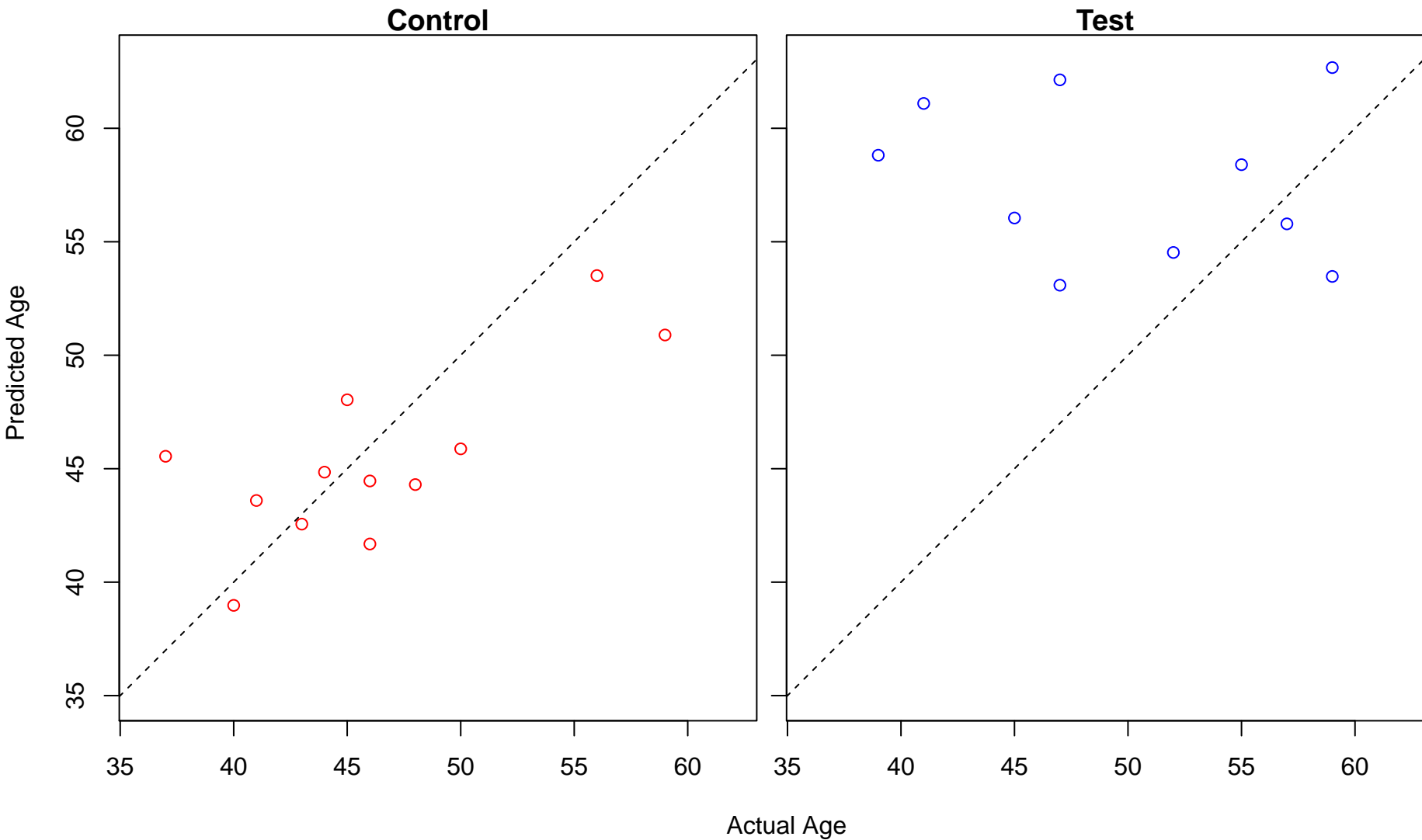
phospholipid transport (Score: 3.464260)



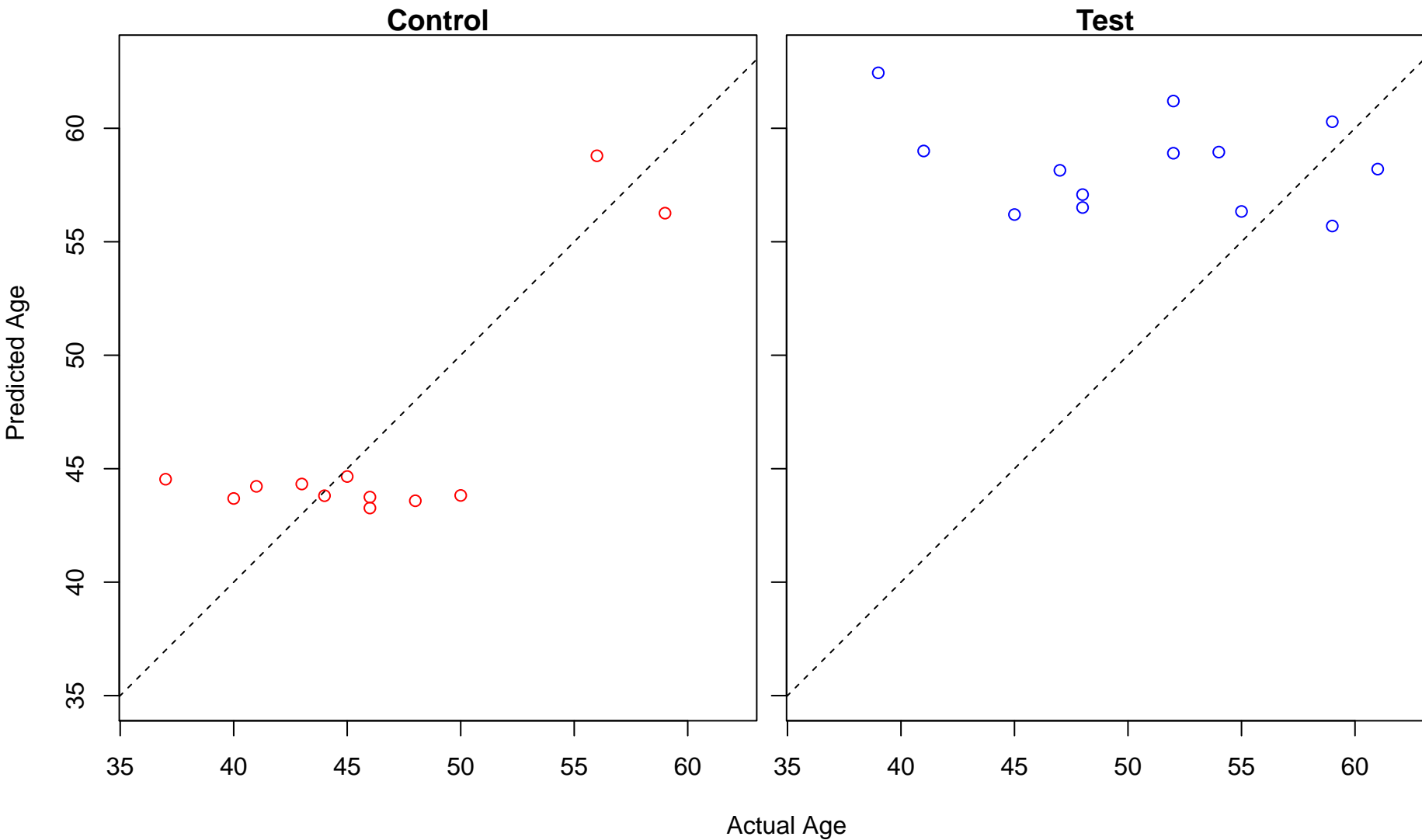
platelet activation (Score: 3.462512)



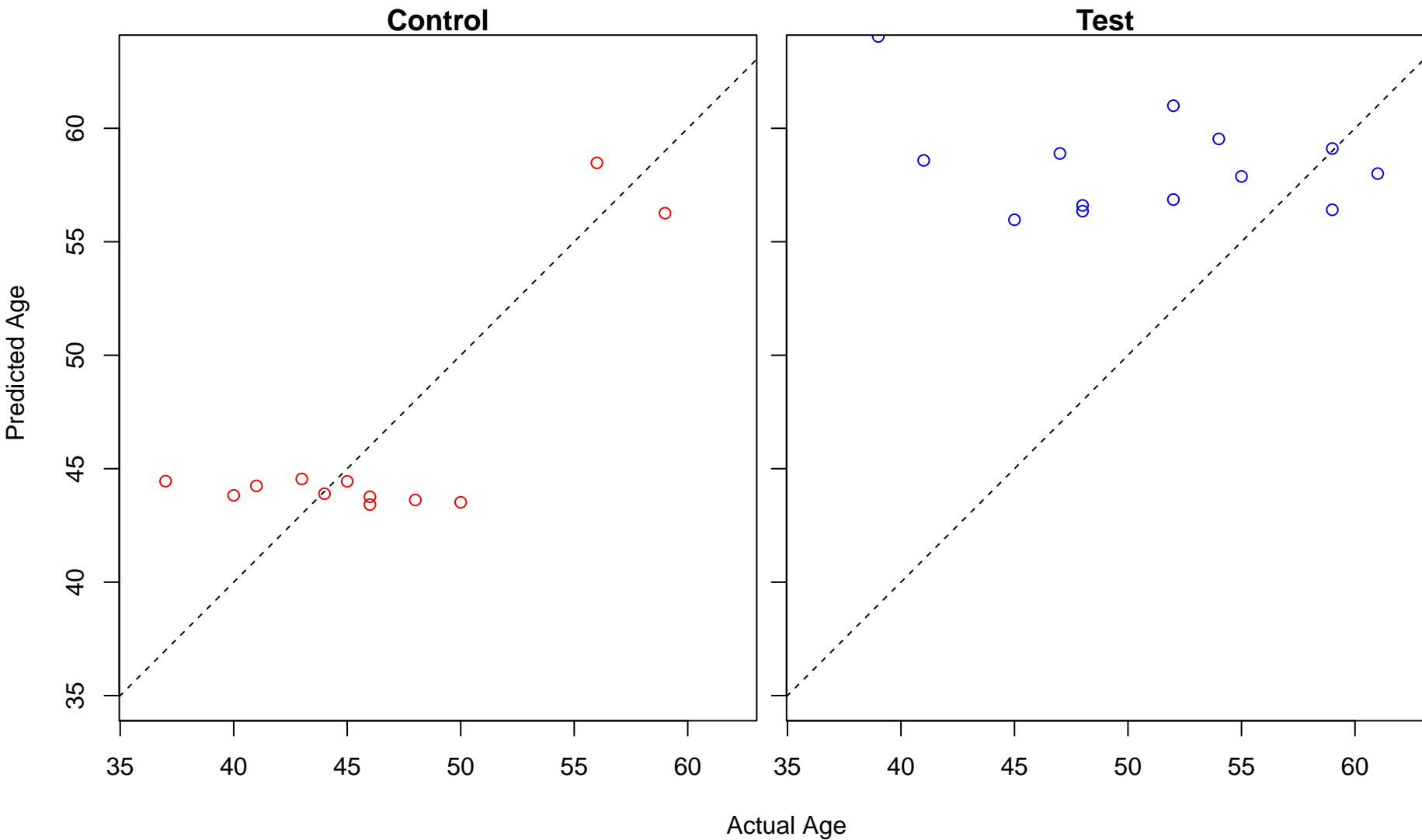
regulation of synapse maturation (Score: 3.461739)



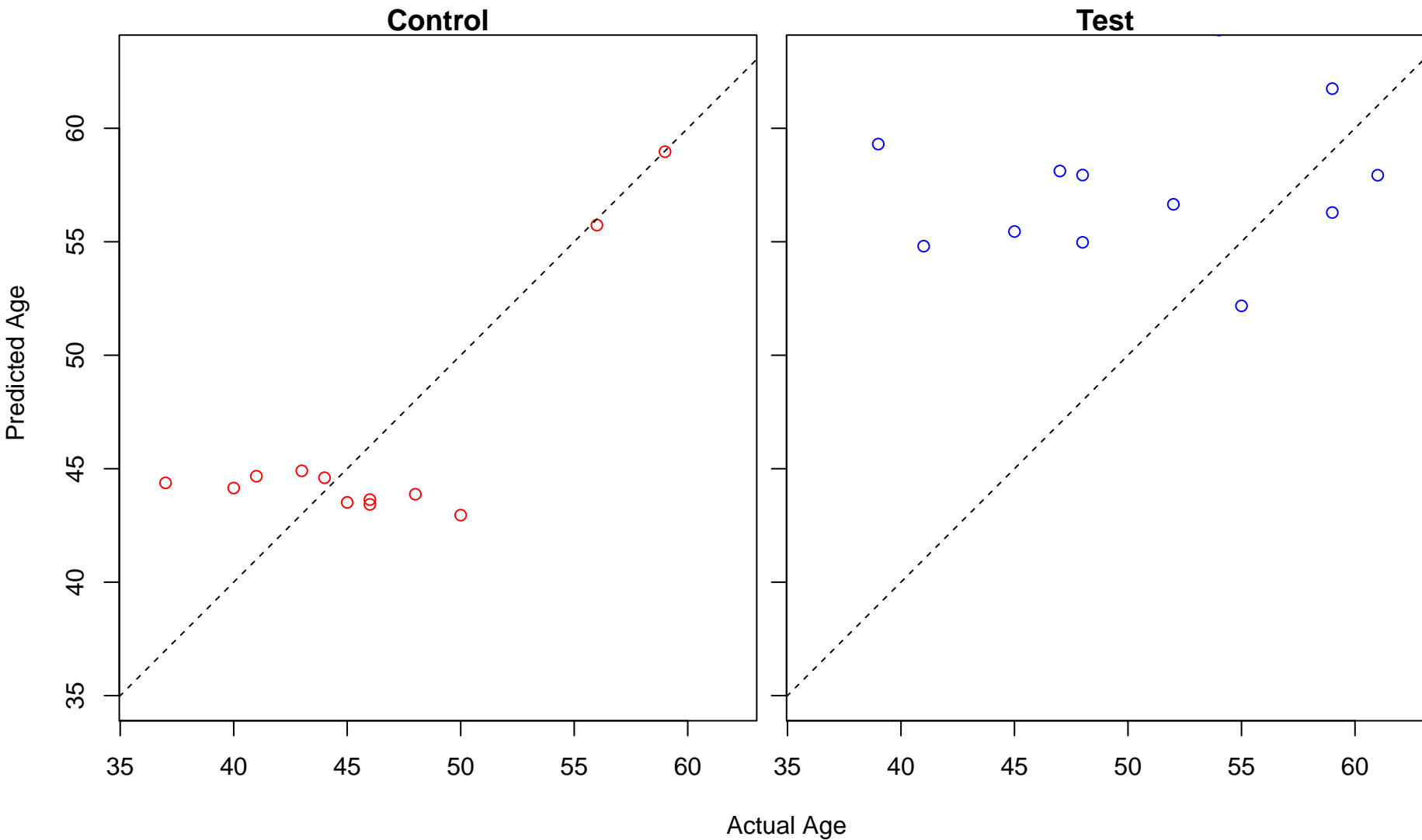
positive regulation of protein ubiquitination (Score: 3.461418)



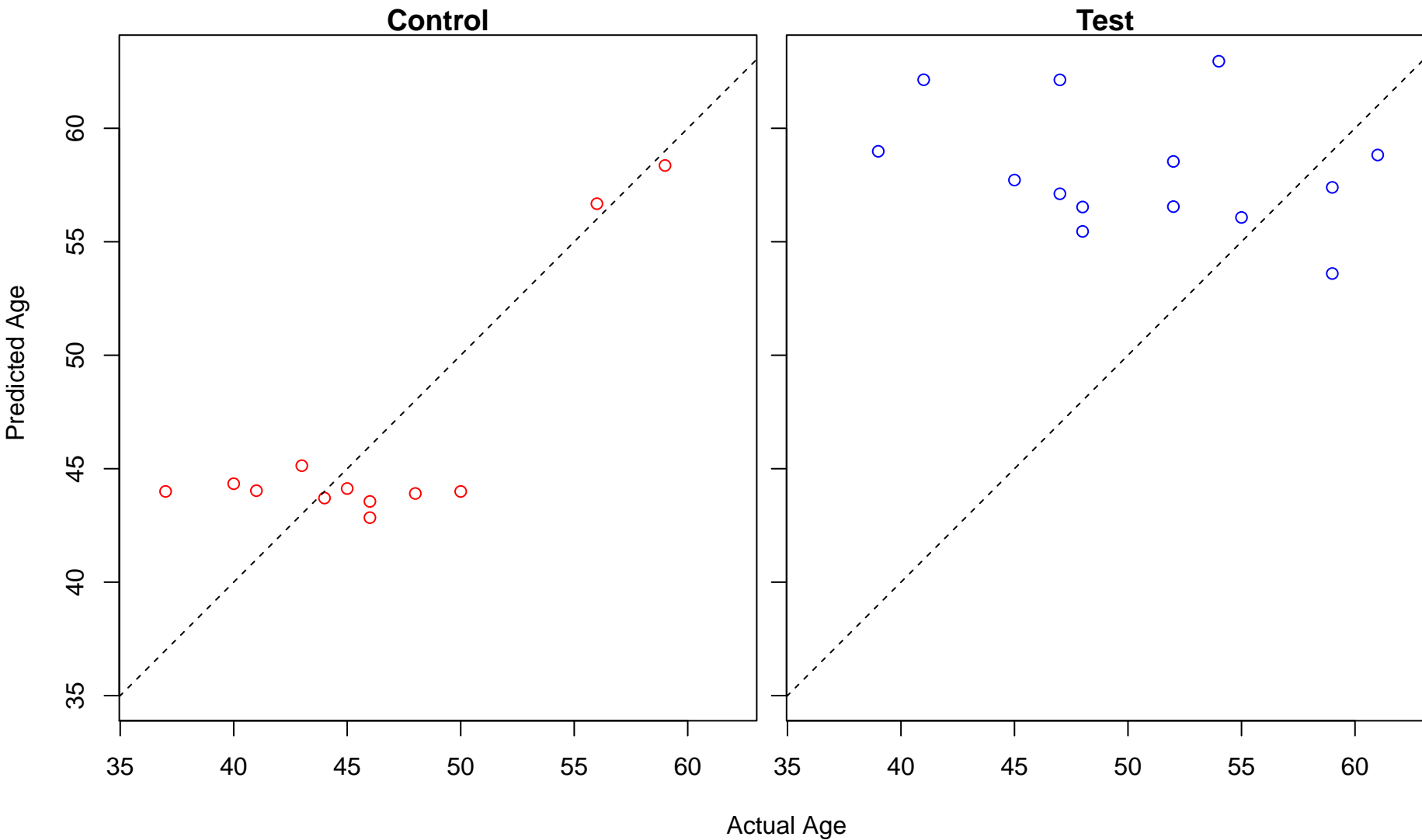
positive regulation of apoptotic signaling pathway (Score: 3.459664)



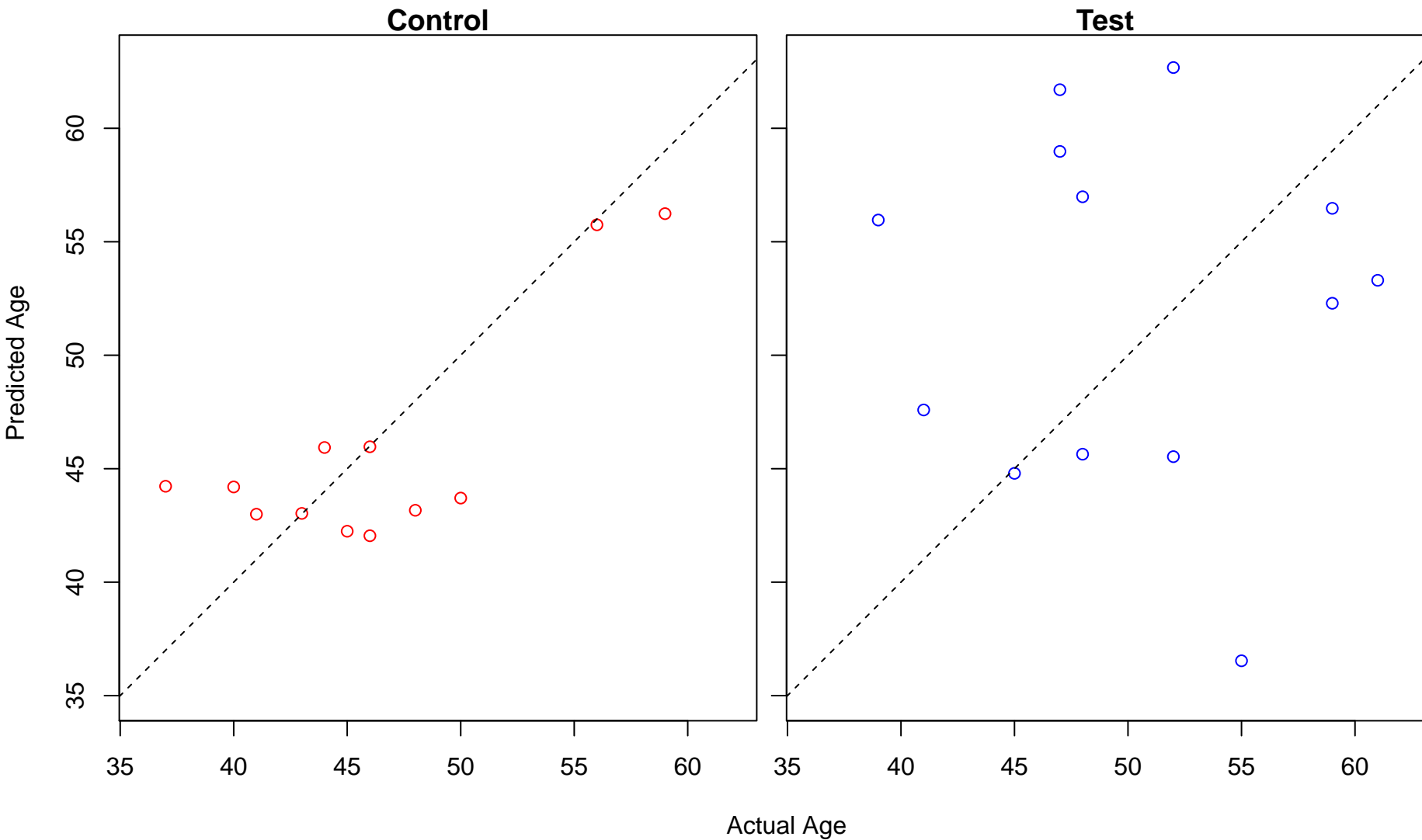
regulation of hydrogen peroxide-mediated programmed cell death (Score: 3.458764)



coenzyme metabolic process (Score: 3.457558)

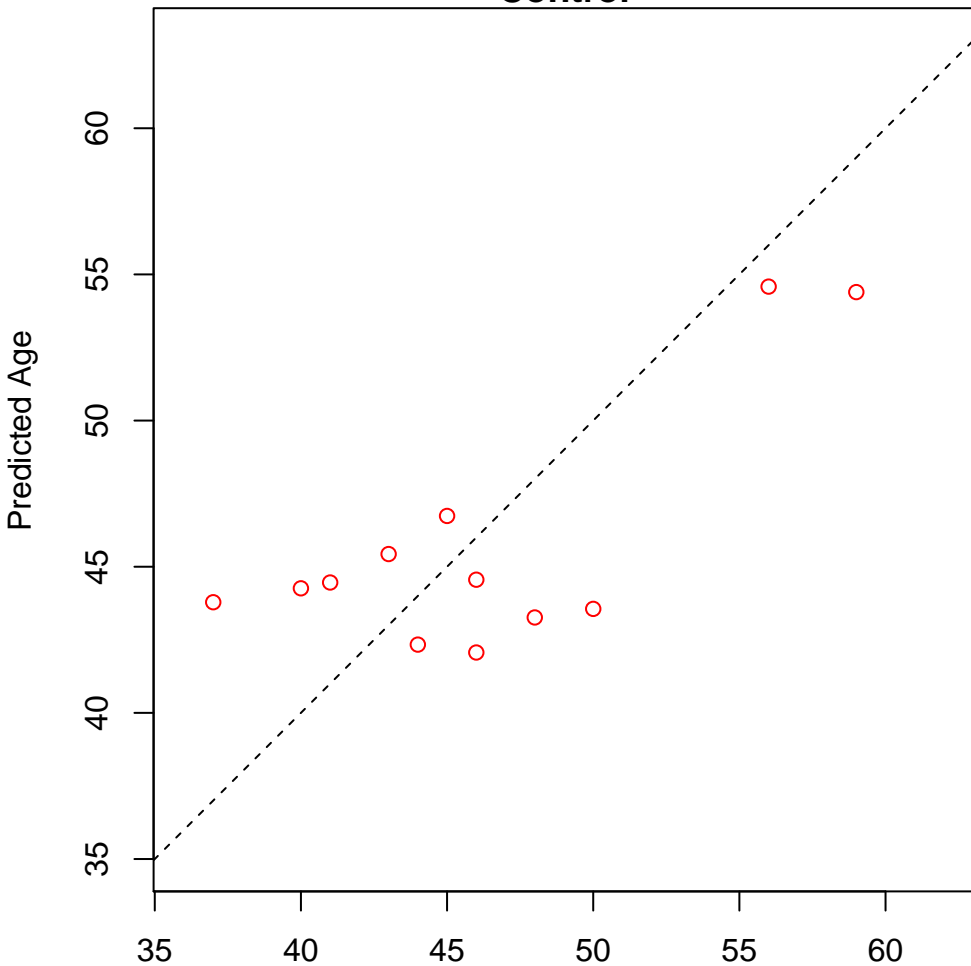


sodium ion transport (Score: 3.457550)

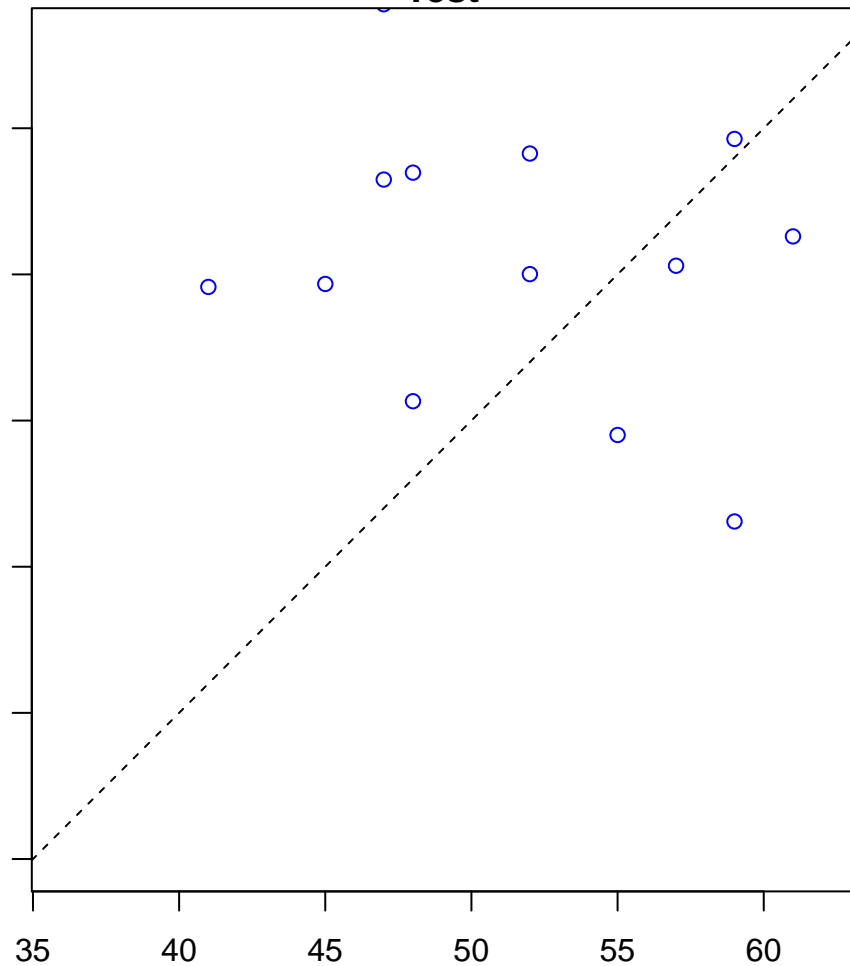


sensory perception of sour taste (Score: 3.456855)

Control

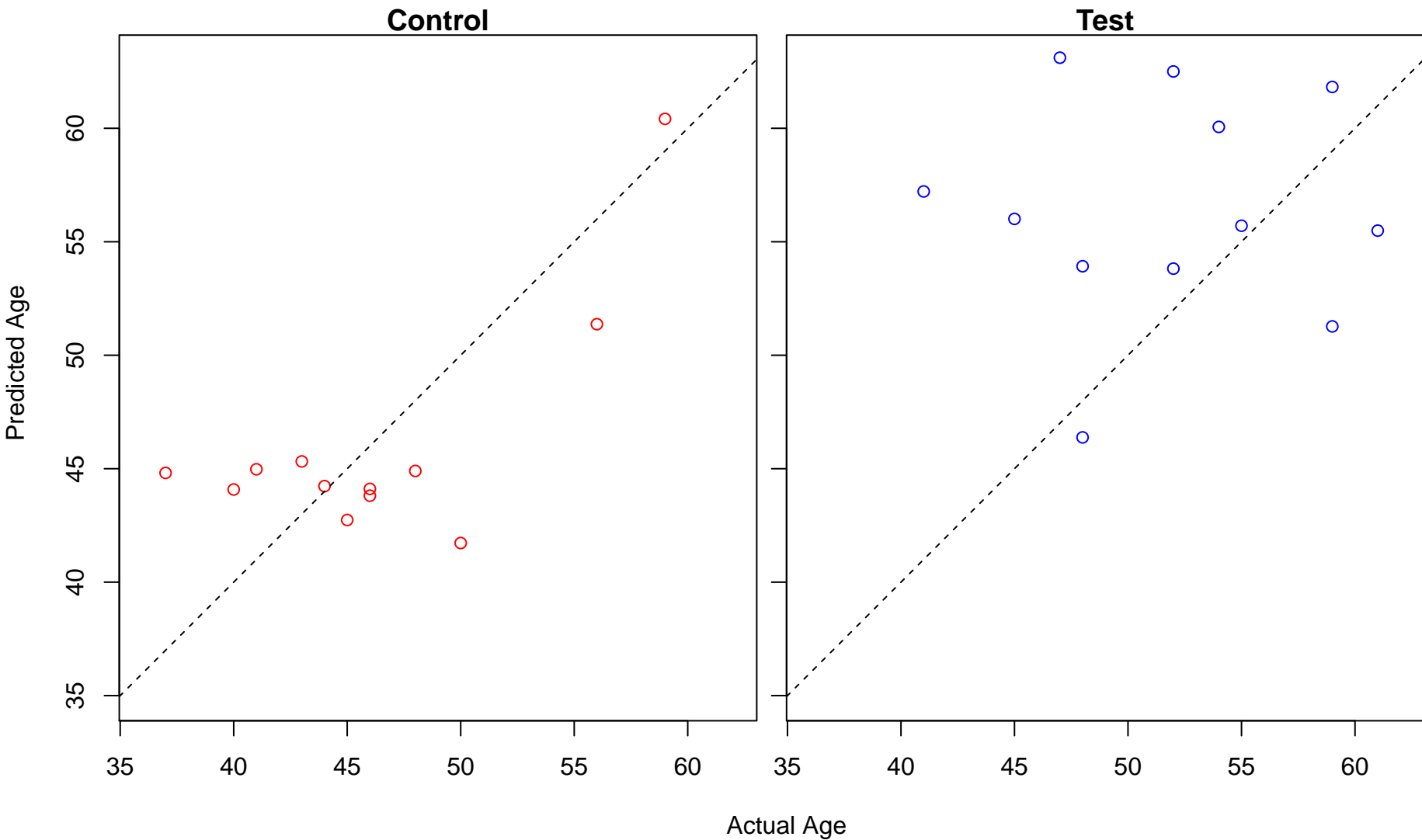


Test

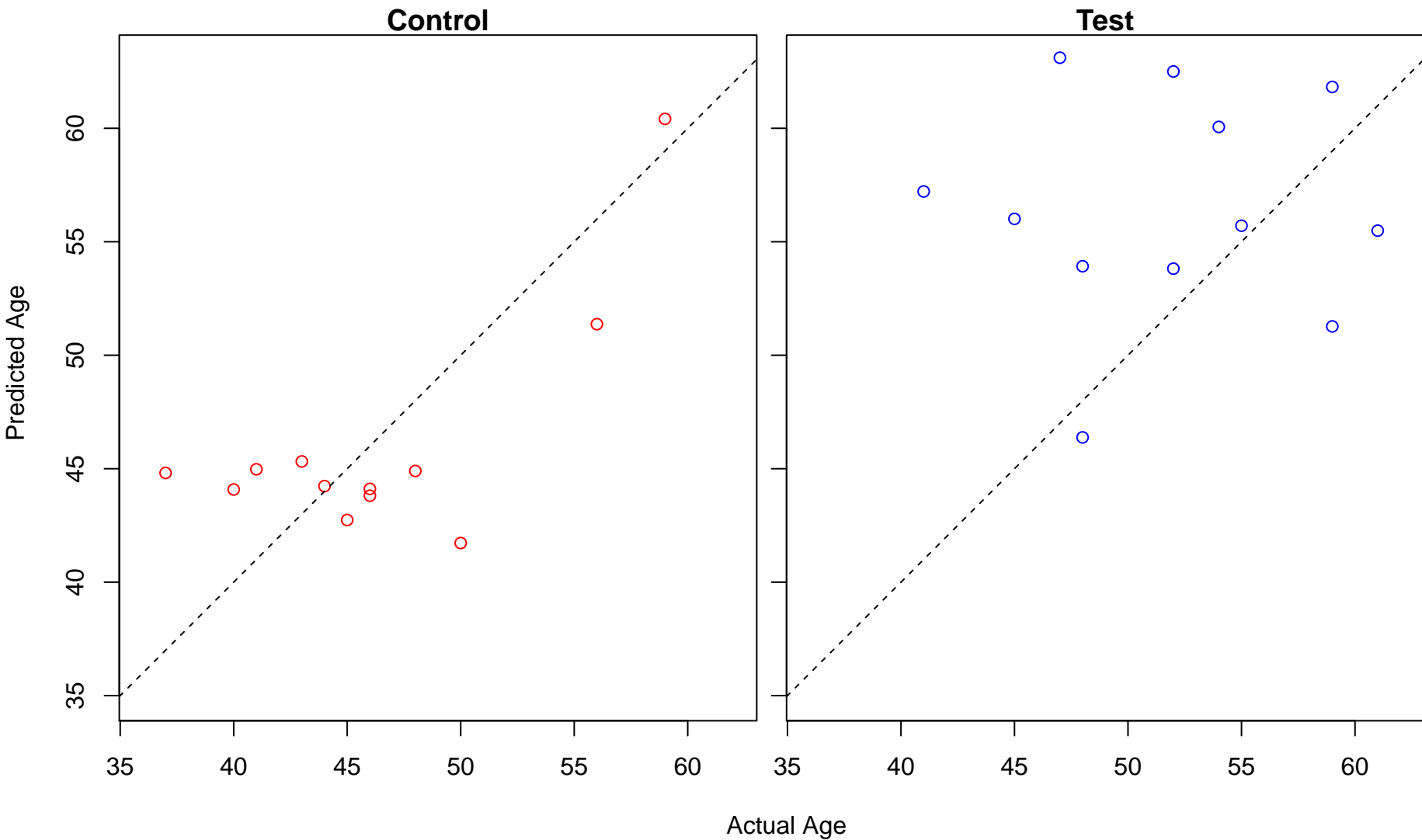


Actual Age

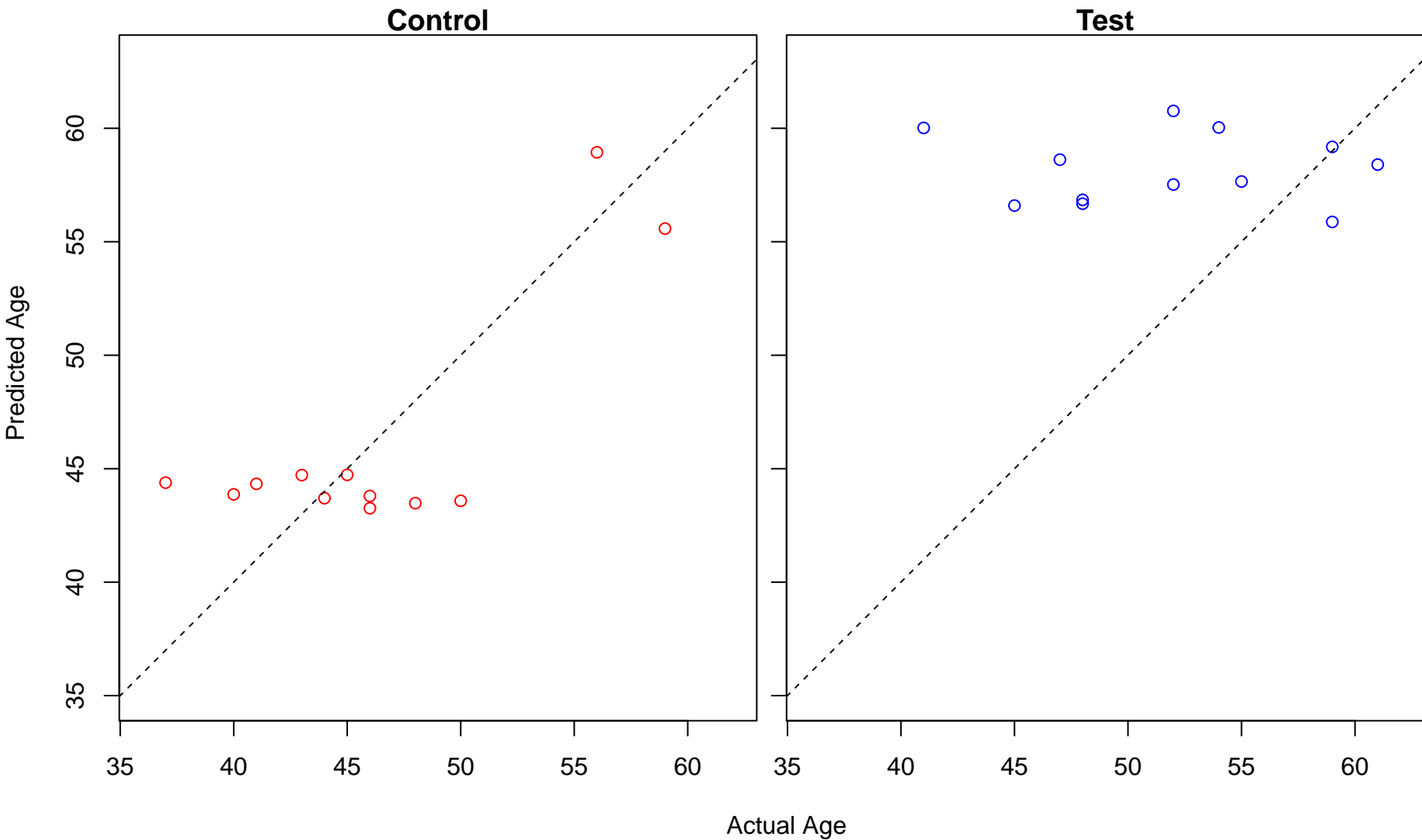
regulation of leukocyte mediated cytotoxicity (Score: 3.454168)



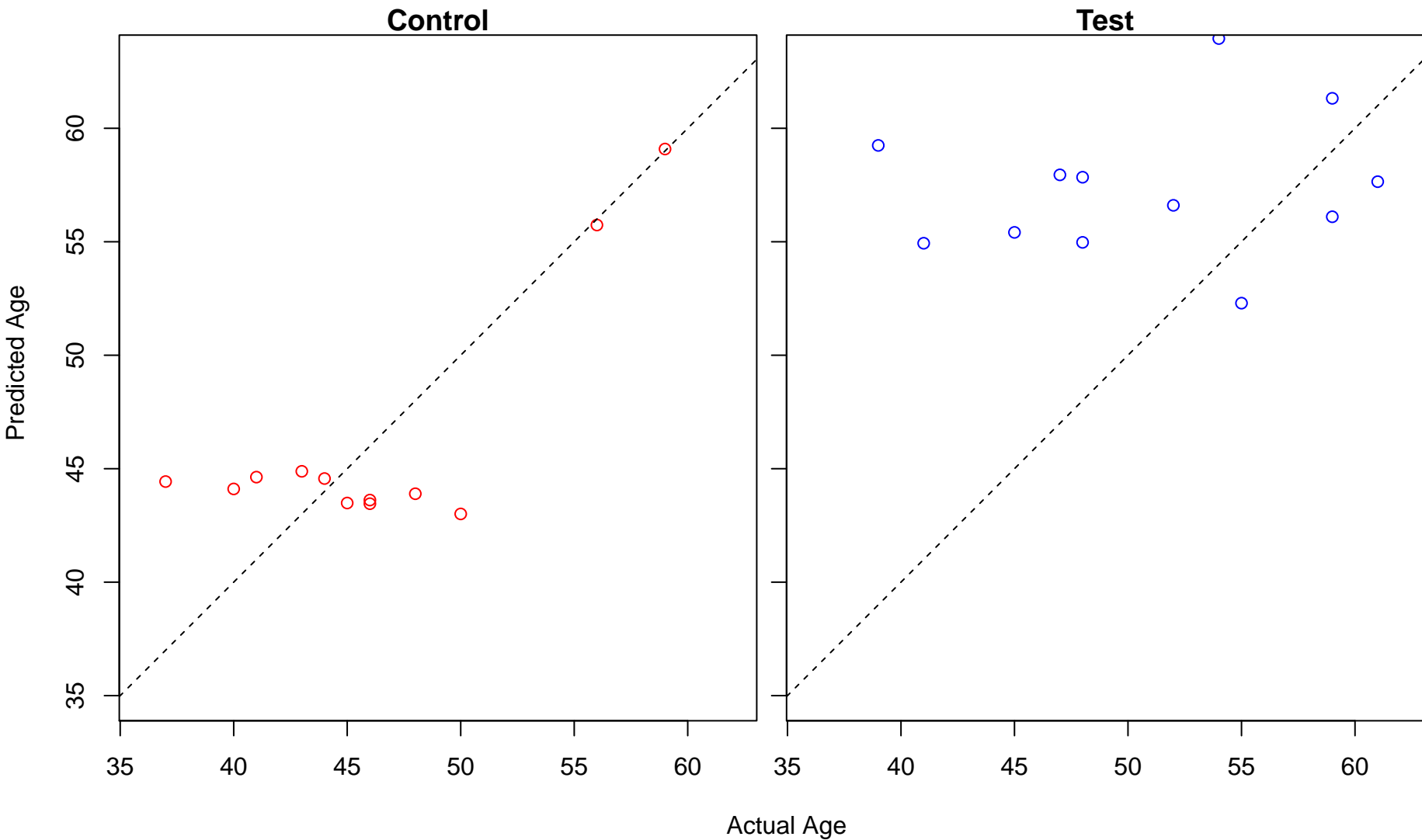
regulation of cell killing (Score: 3.454096)



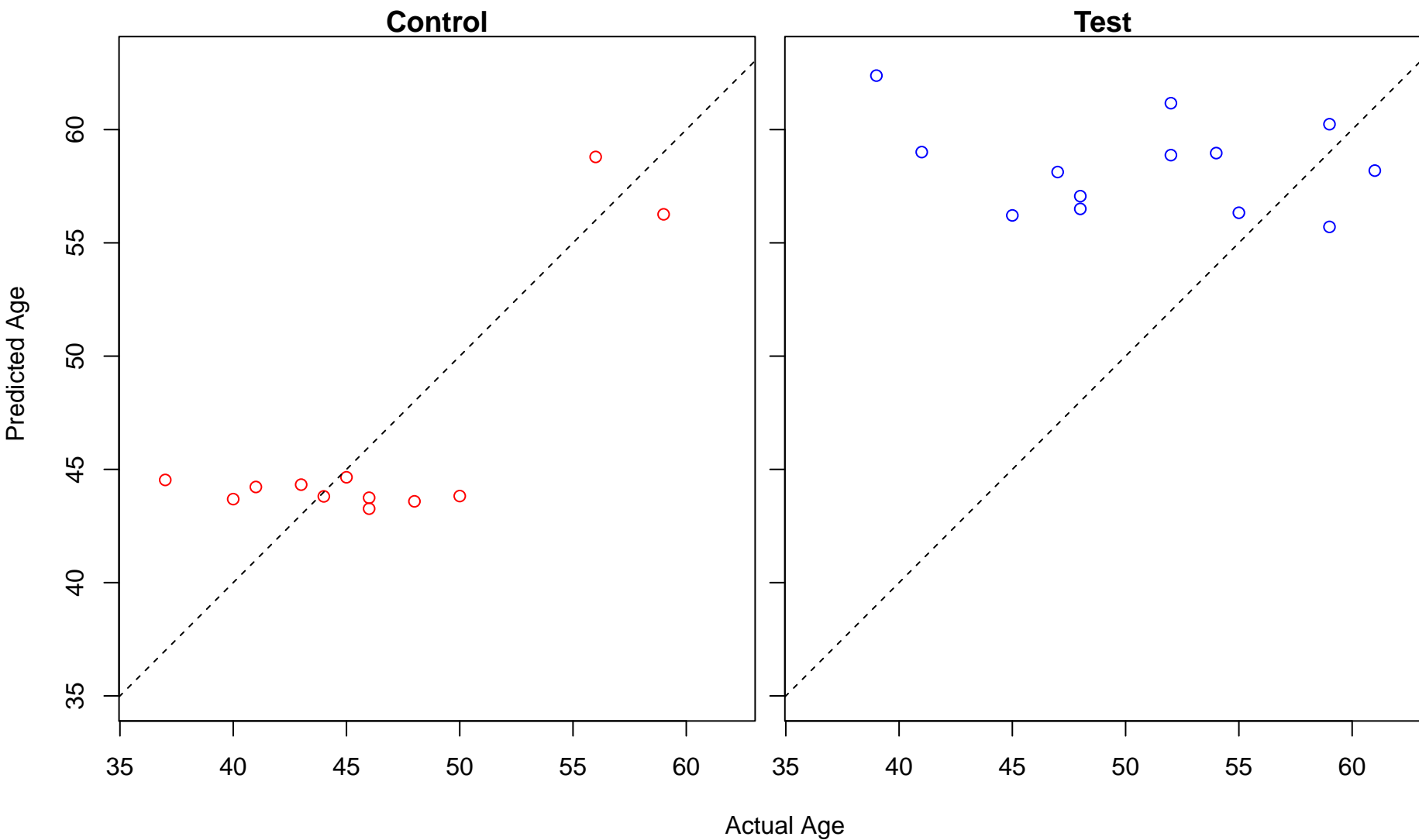
regulation of neuron death (Score: 3.453459)



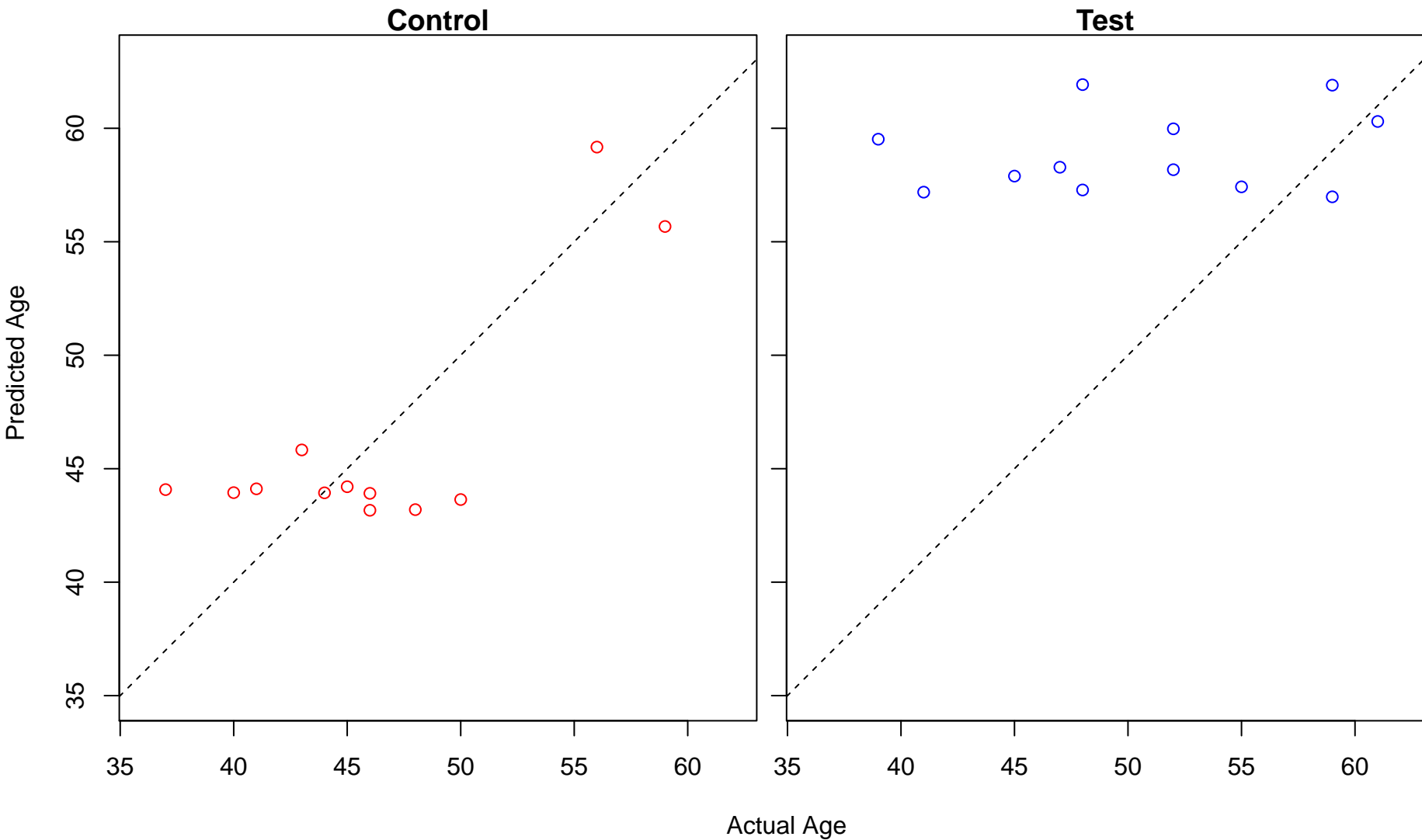
negative regulation of protein export from nucleus (Score: 3.451424)



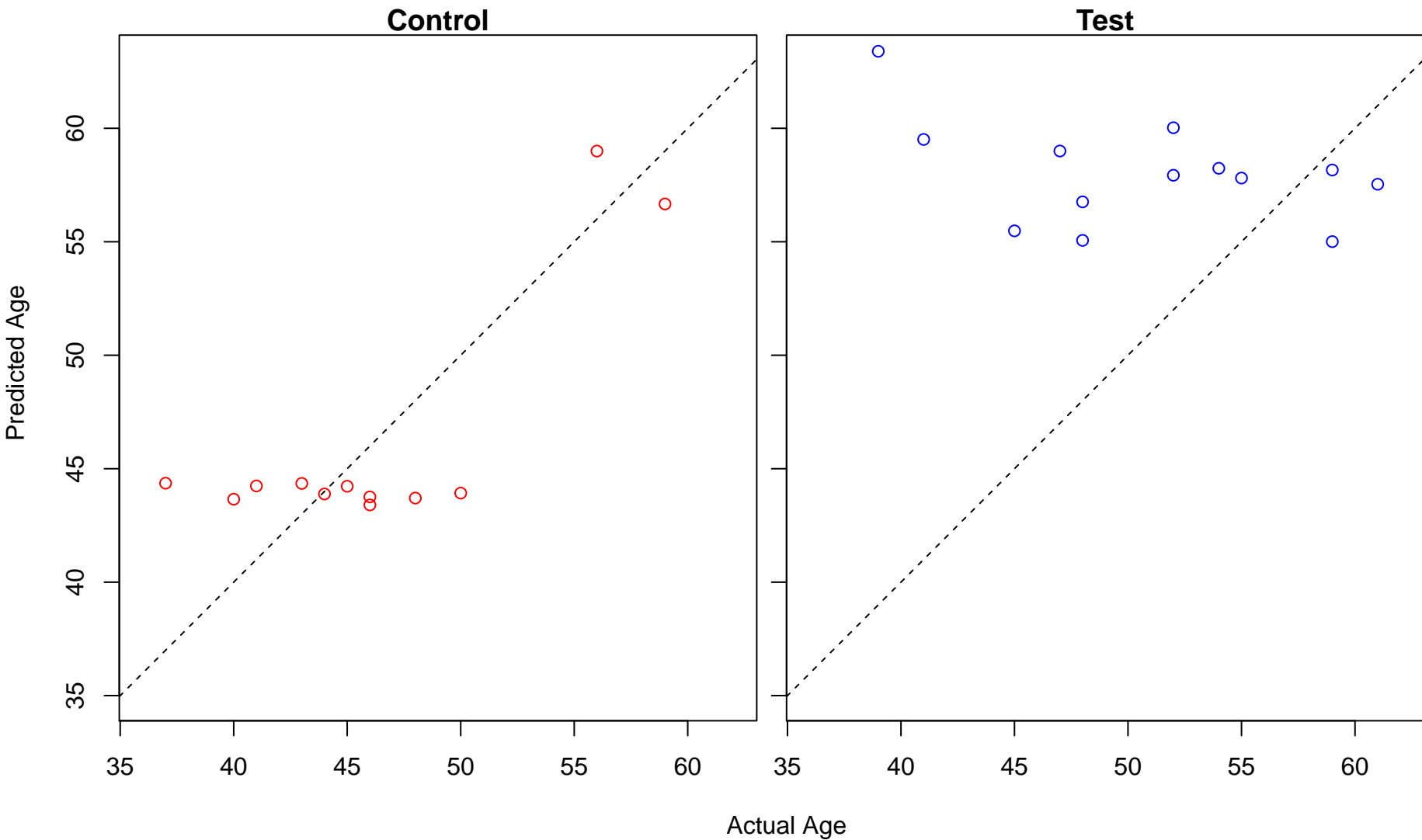
positive regulation of protein modification by small protein conjugation or removal (Score: 3.45011)

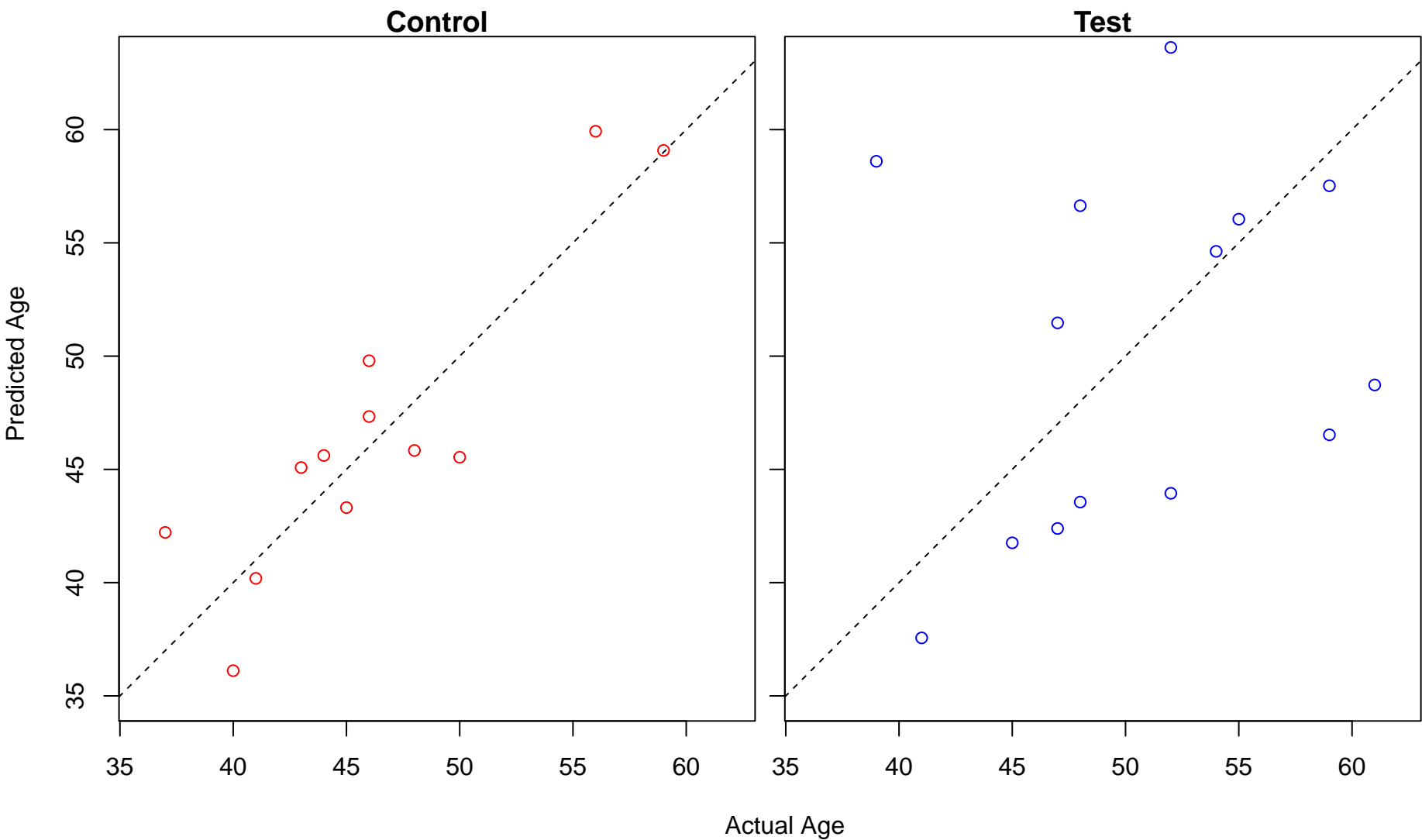


response to estradiol (Score: 3.448039)

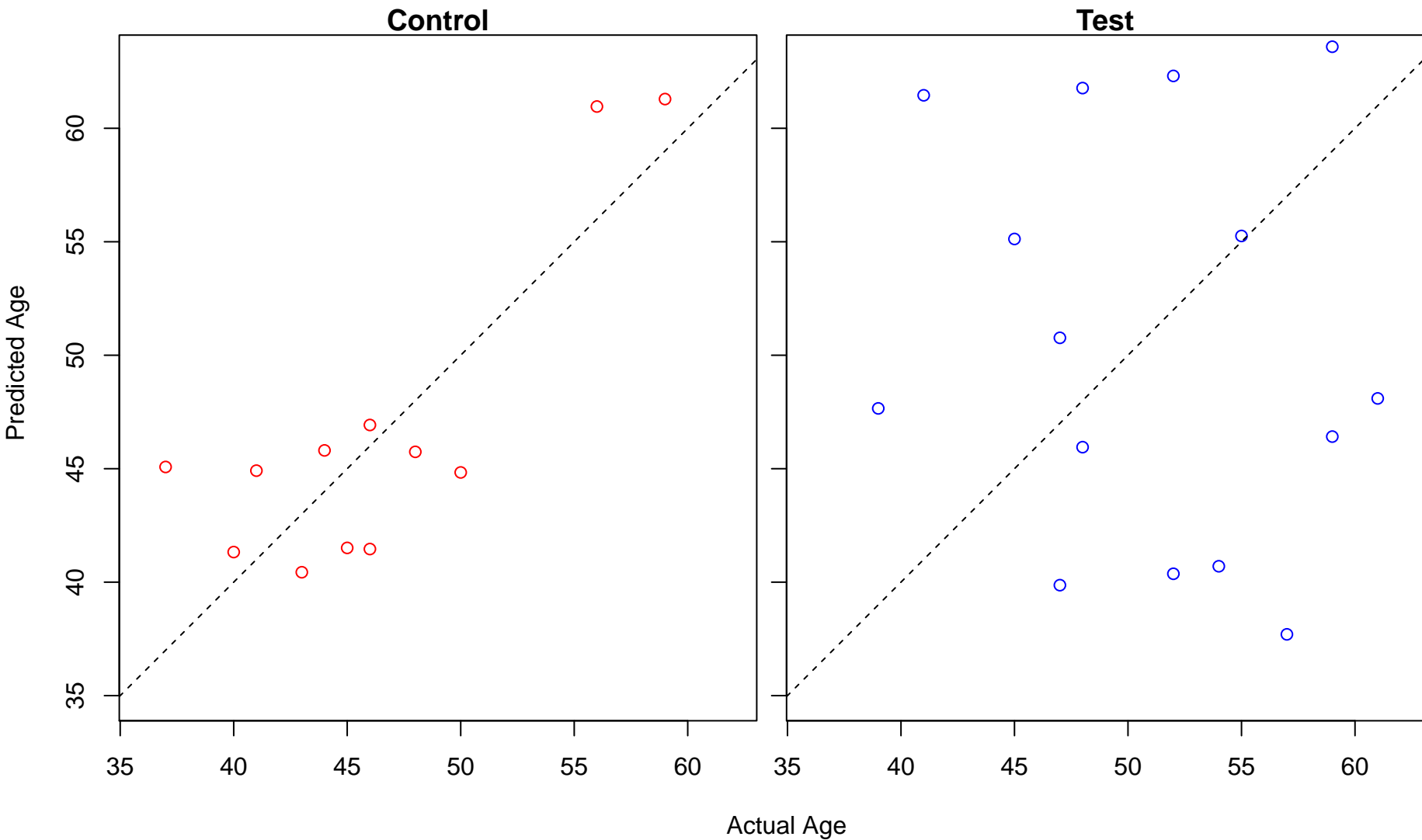


glucose metabolic process (Score: 3.446225)

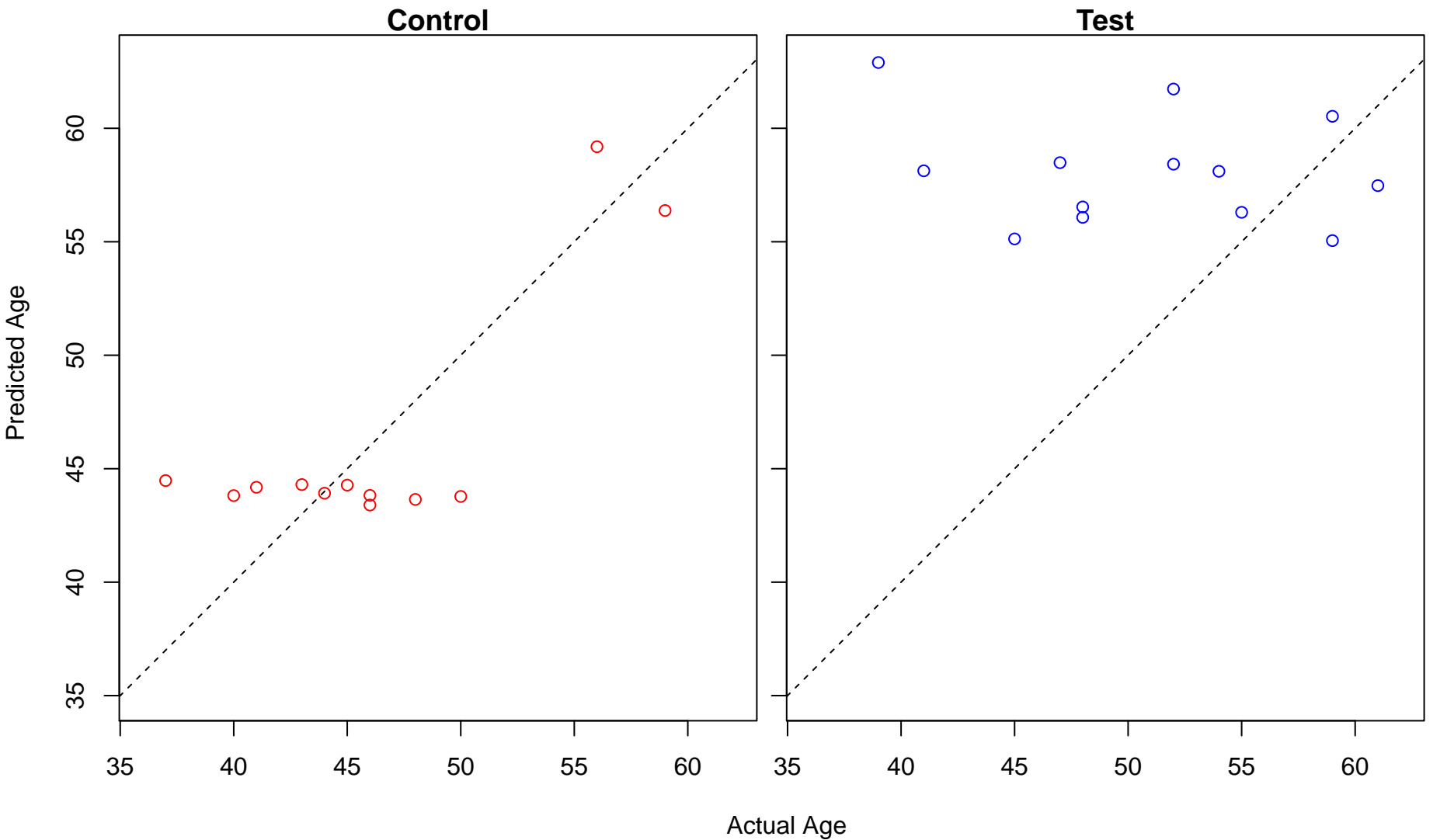




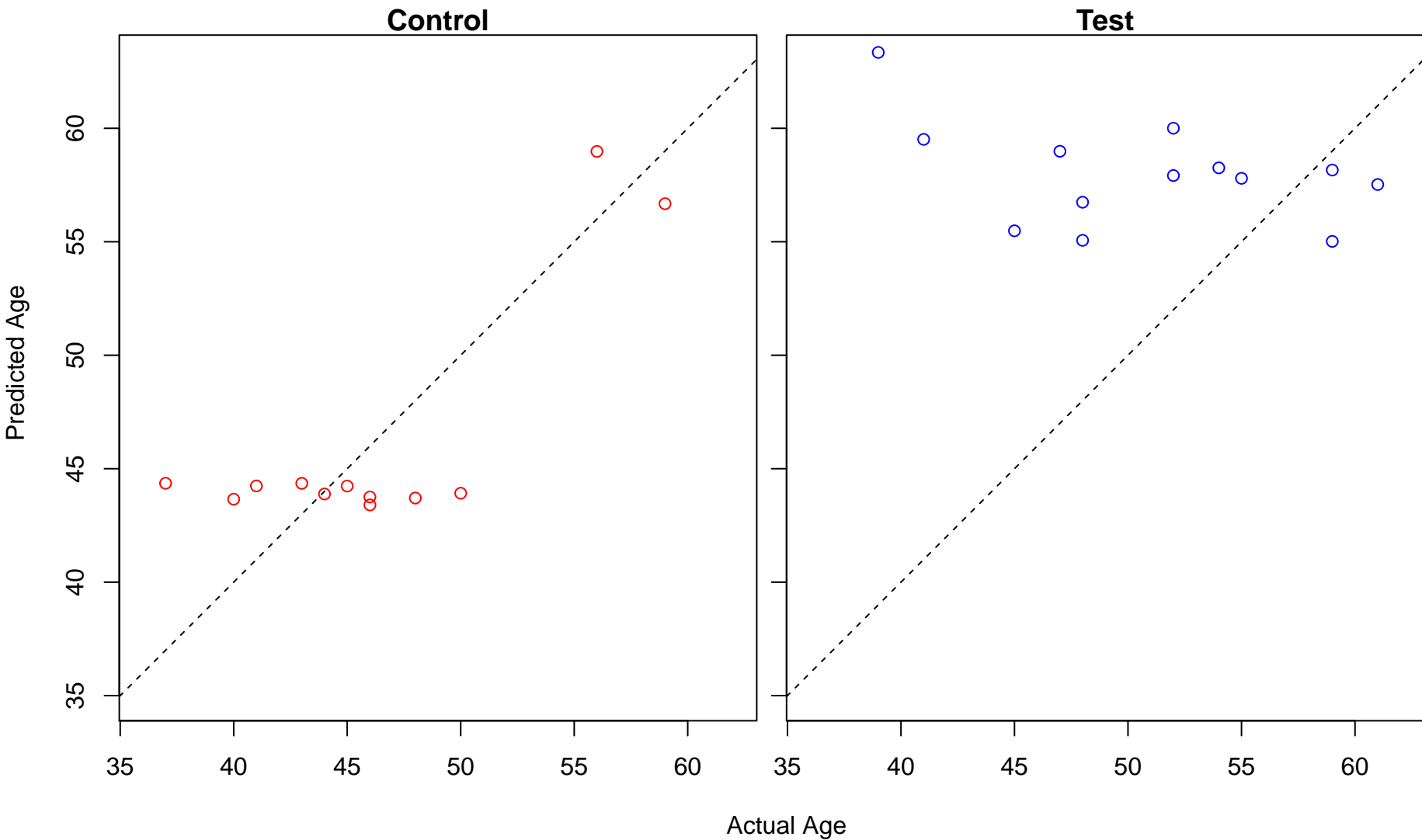
left/right pattern formation (Score: 3.445612)



Positive regulation of ubiquitin–protein ligase activity involved in regulation of mitotic cell cycle transition (Score)

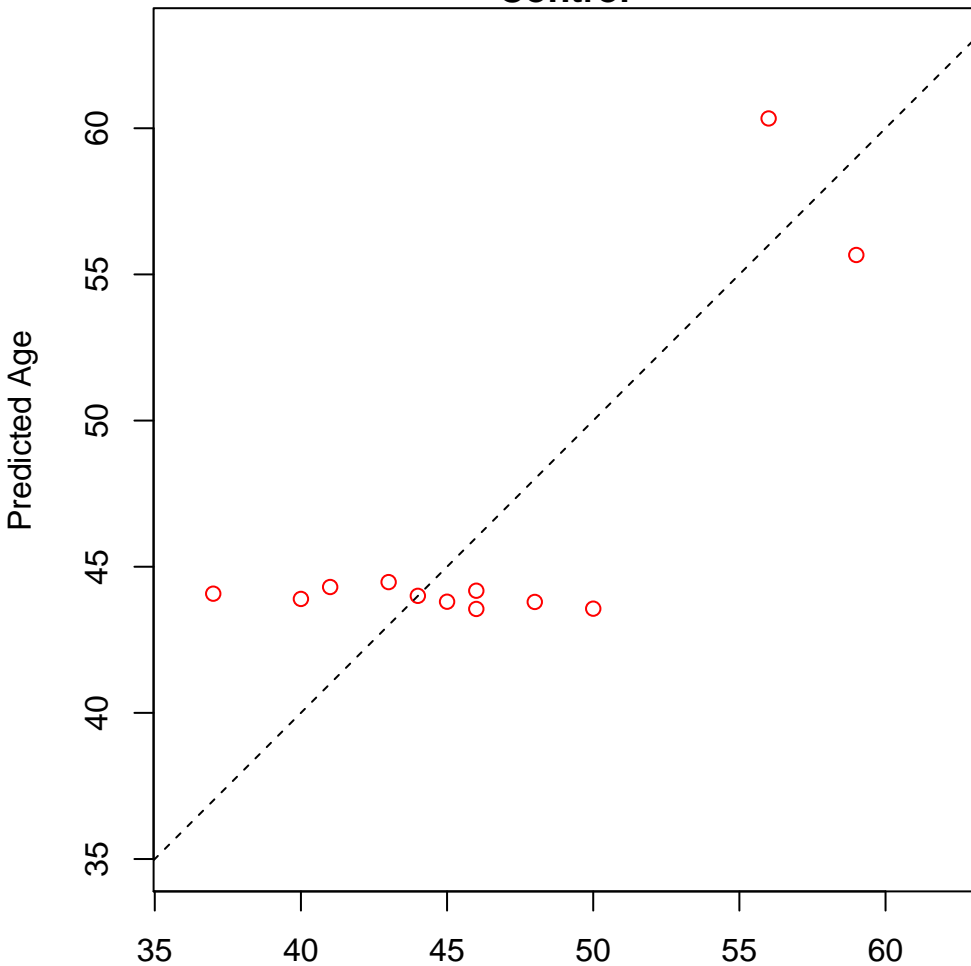


hexose metabolic process (Score: 3.442830)

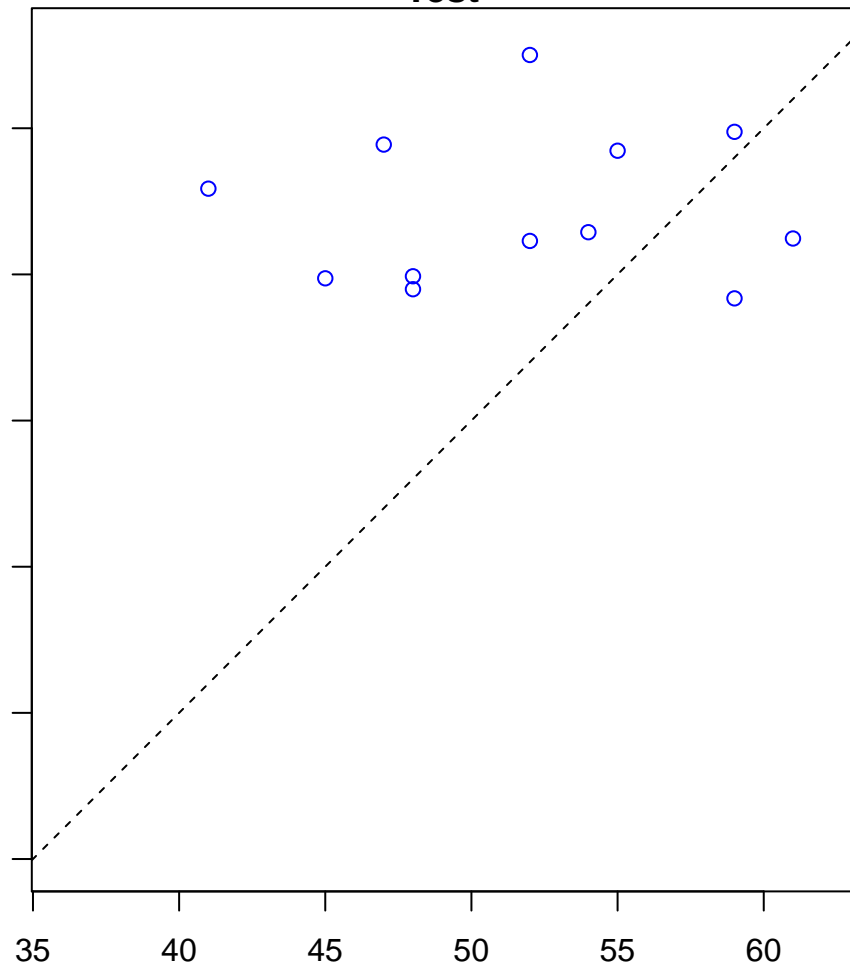


organelle transport along microtubule (Score: 3.441378)

Control

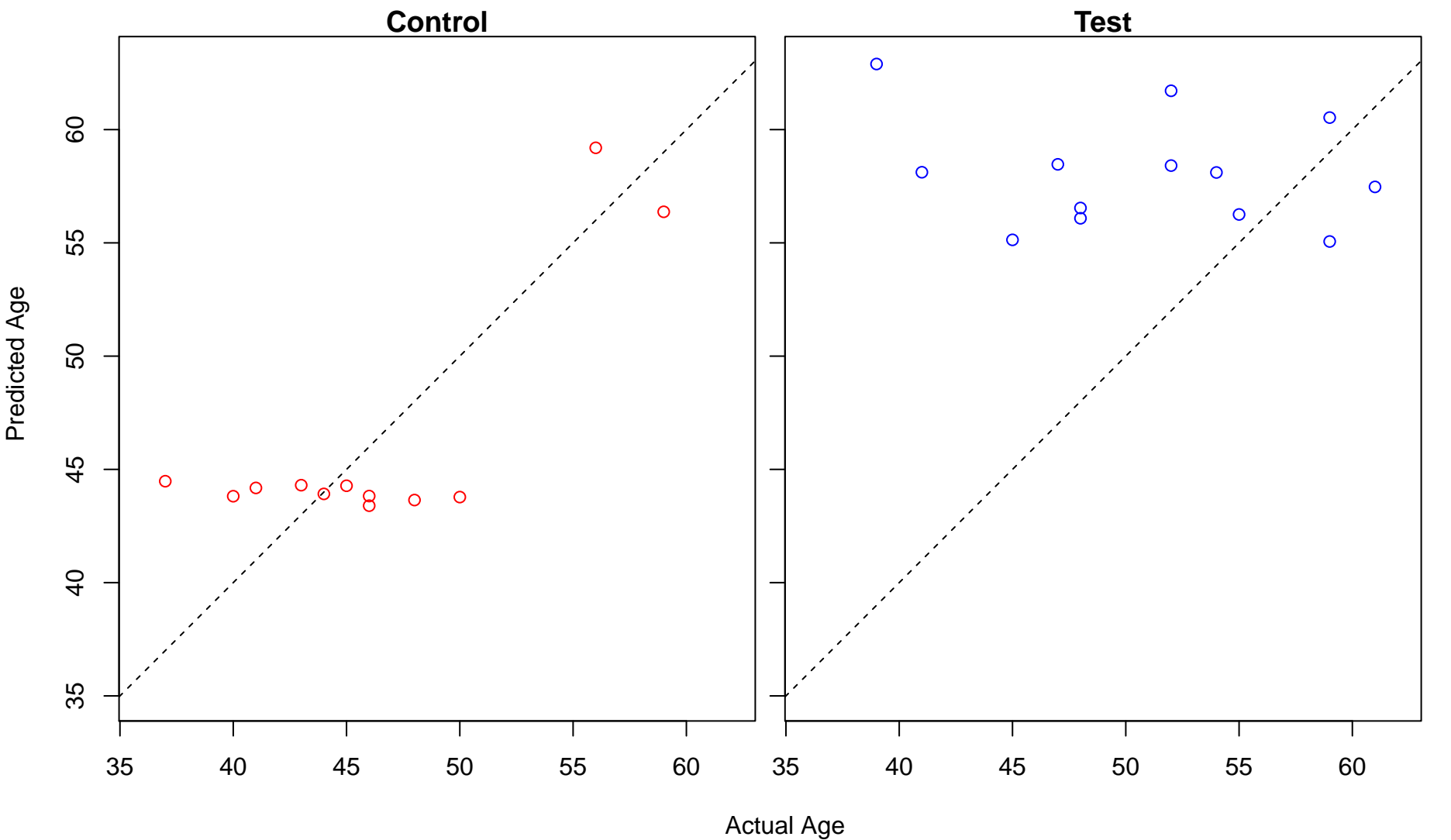


Test



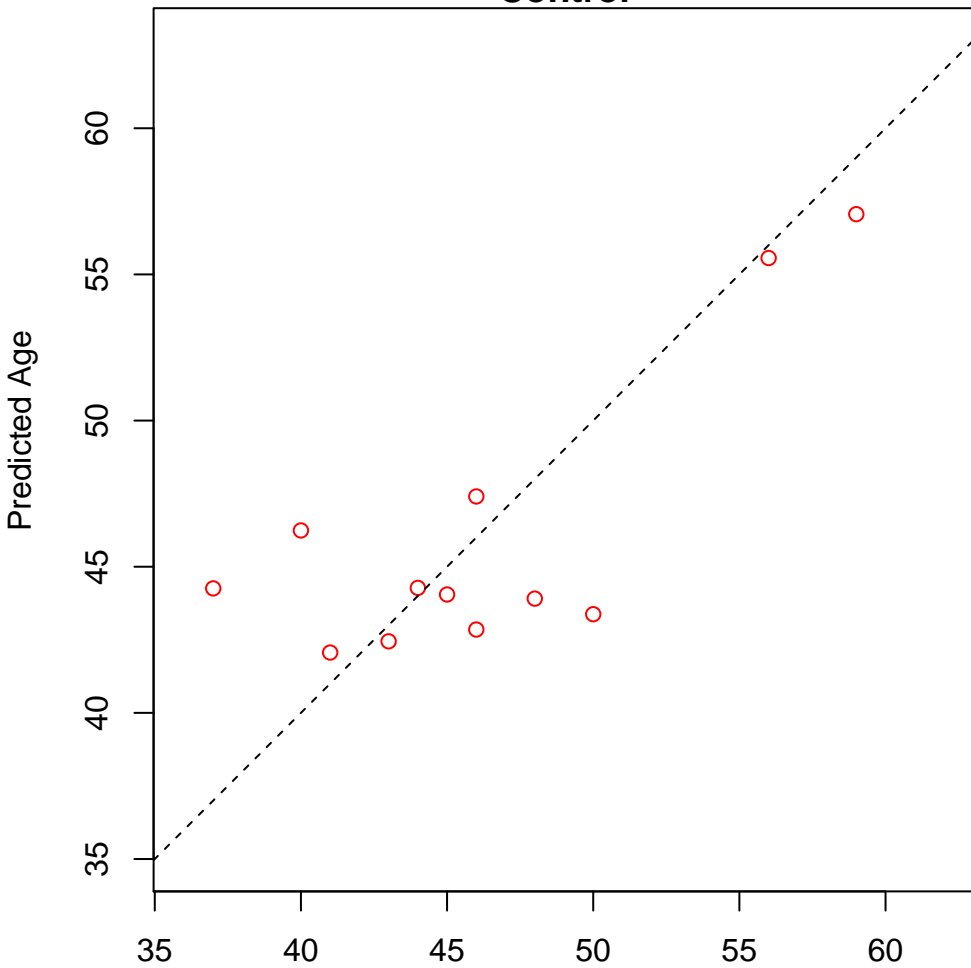
Actual Age

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

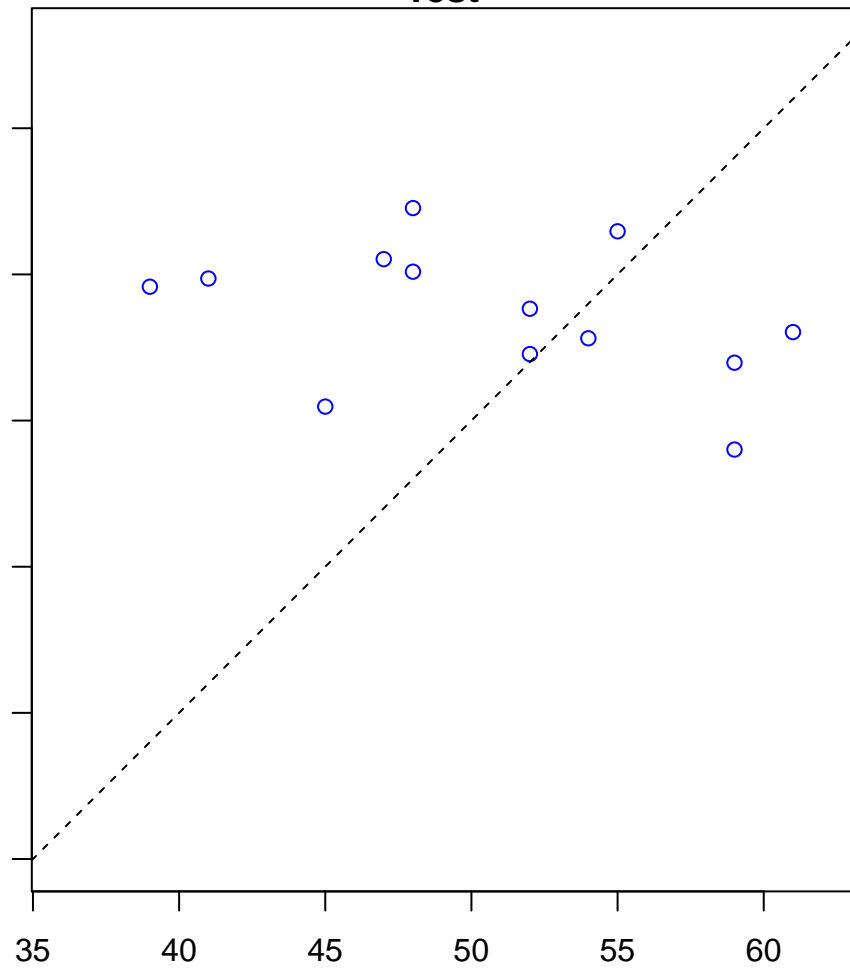


complement activation, lectin pathway (Score: 3.440044)

Control

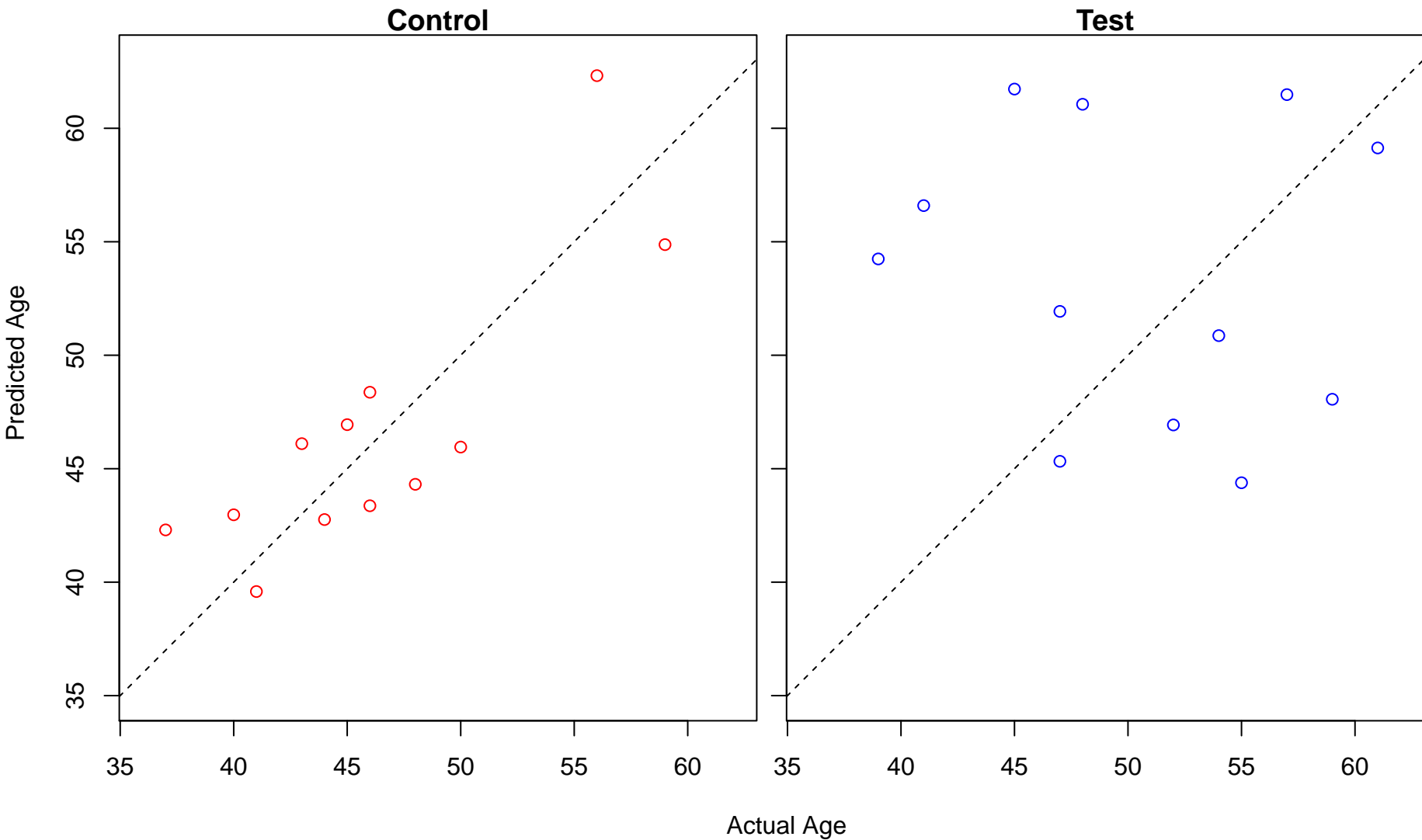


Test

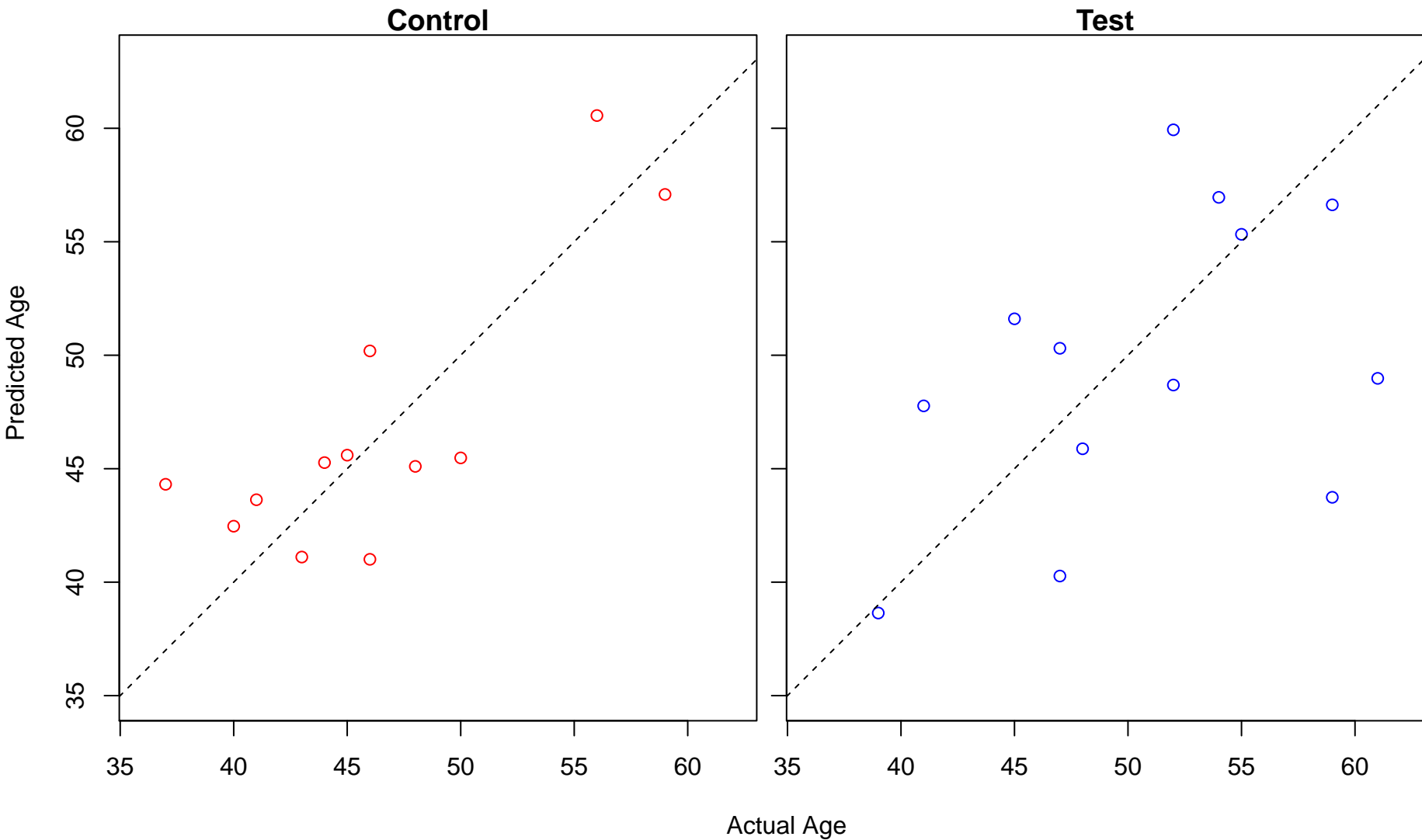


Actual Age

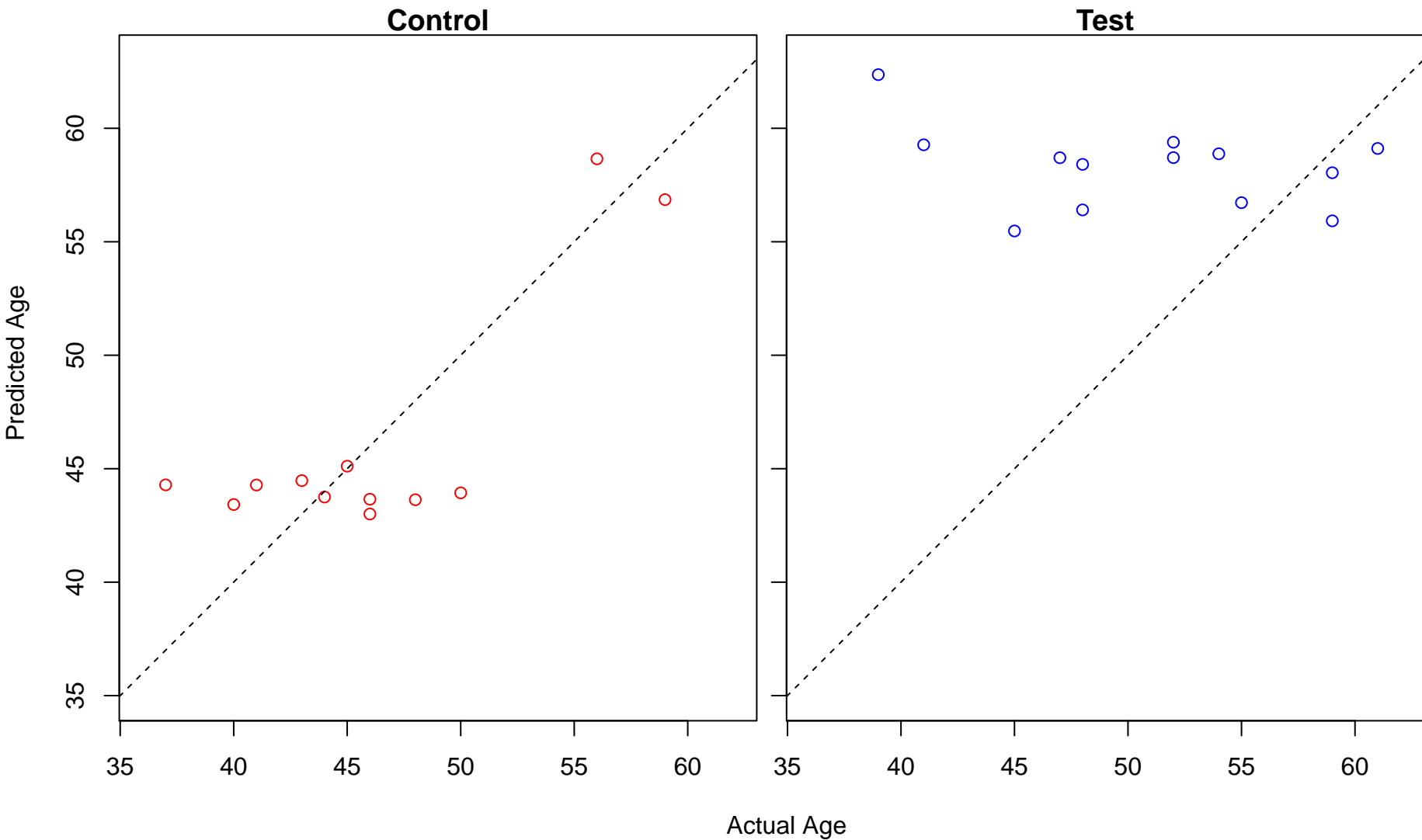
lymph vessel development (Score: 3.439703)



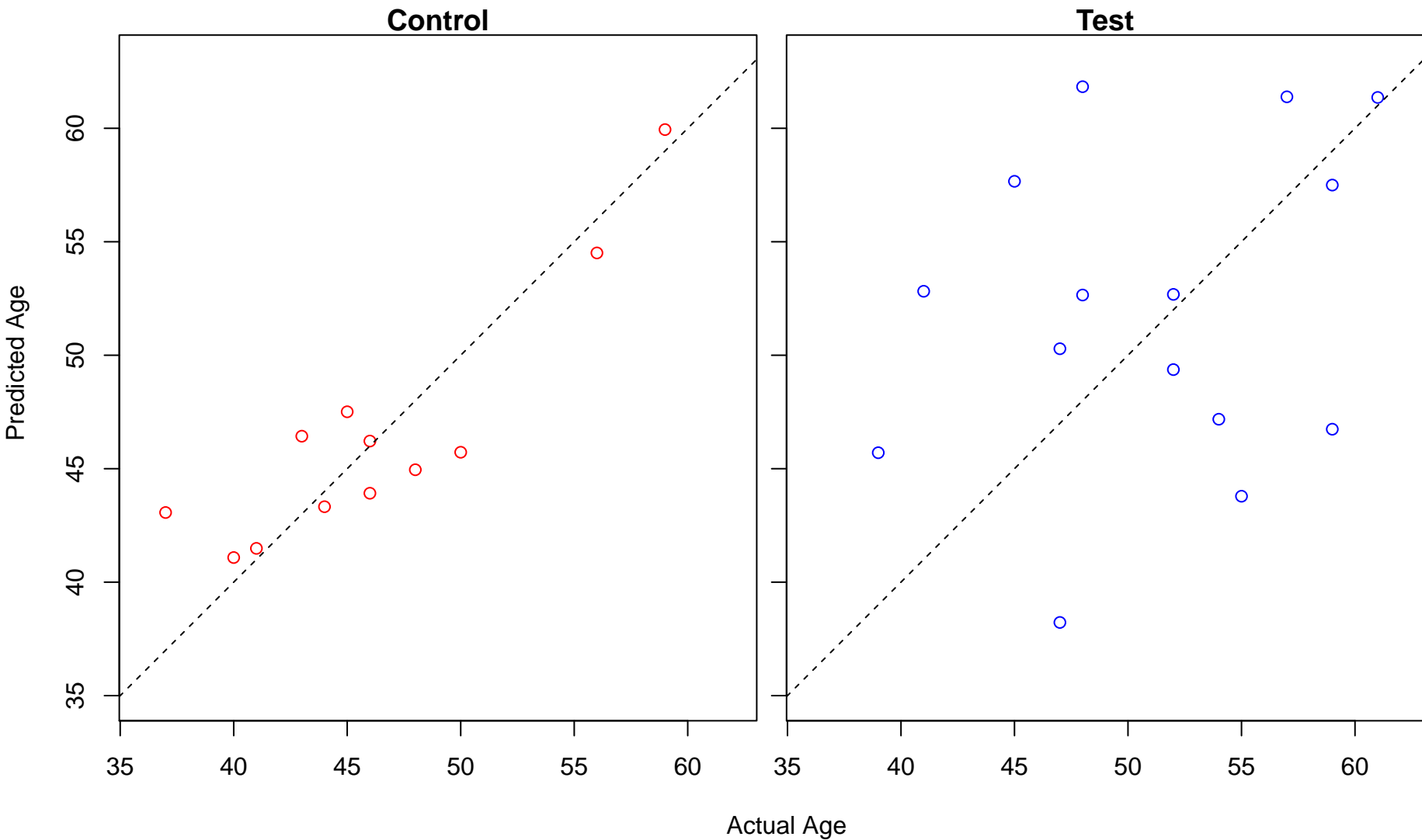
ectoderm development (Score: 3.436212)



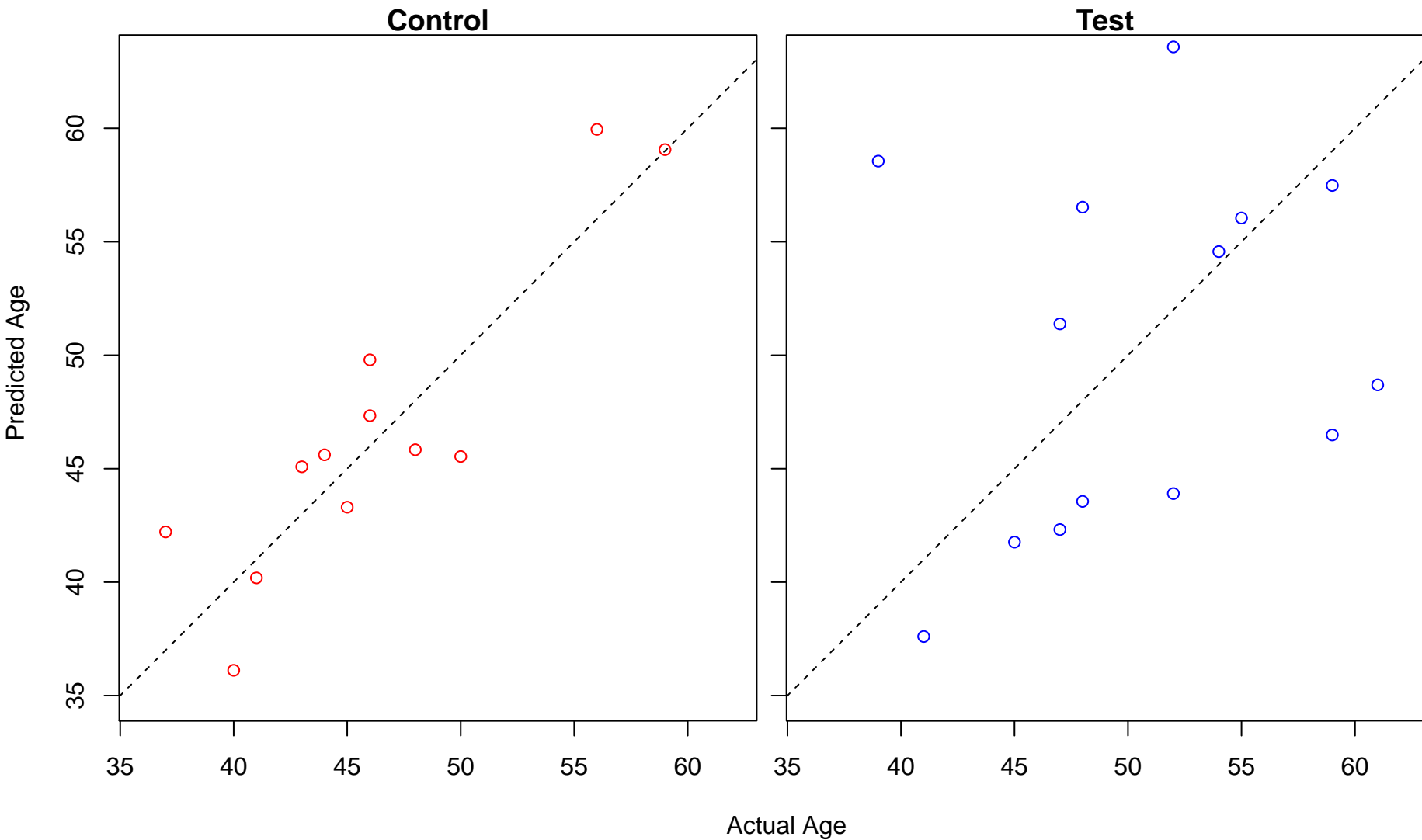
macromitophagy (Score: 3.435103)



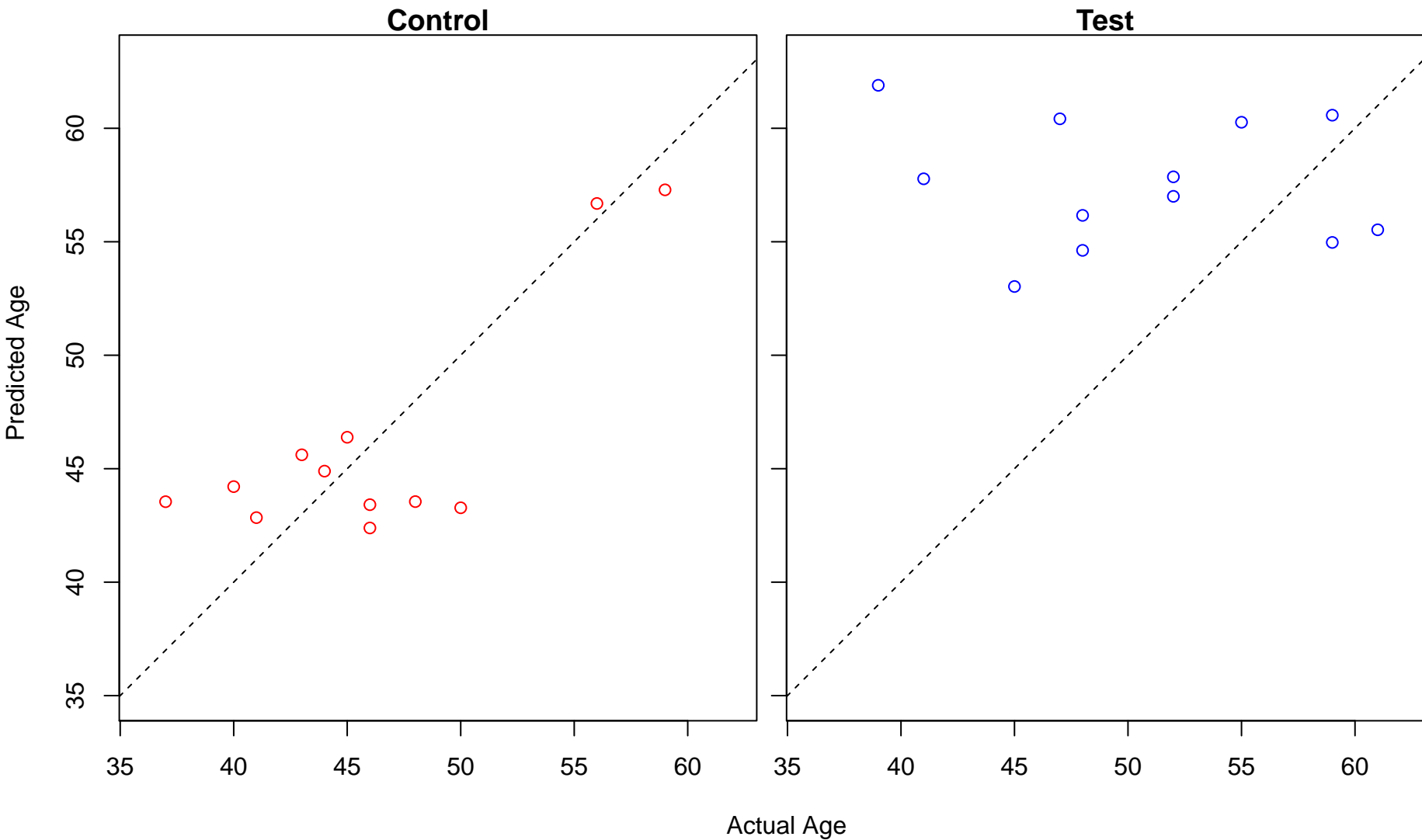
positive regulation of endothelial cell proliferation (Score: 3.433935)



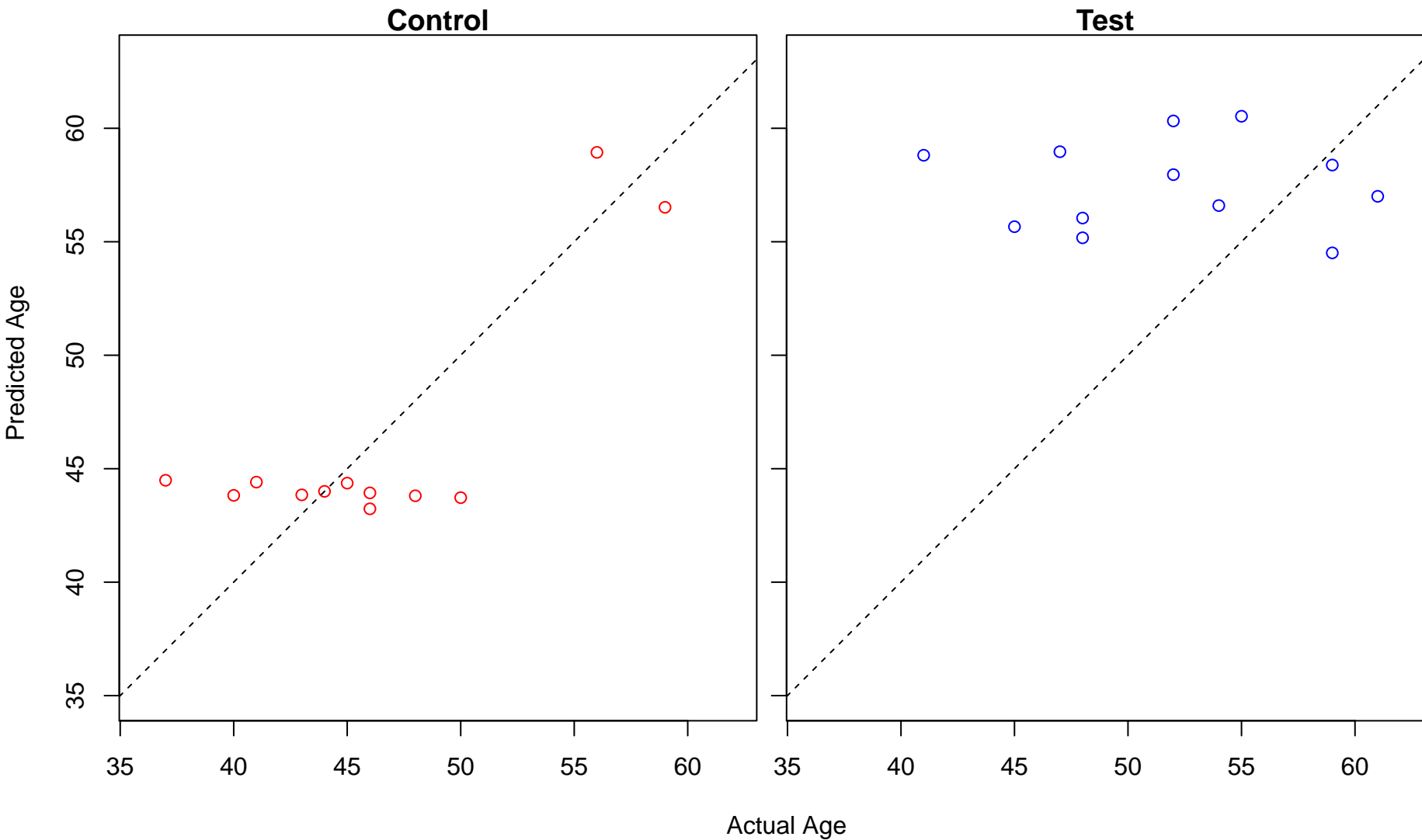
modification of morphology or physiology of other organism (Score: 3.433656)



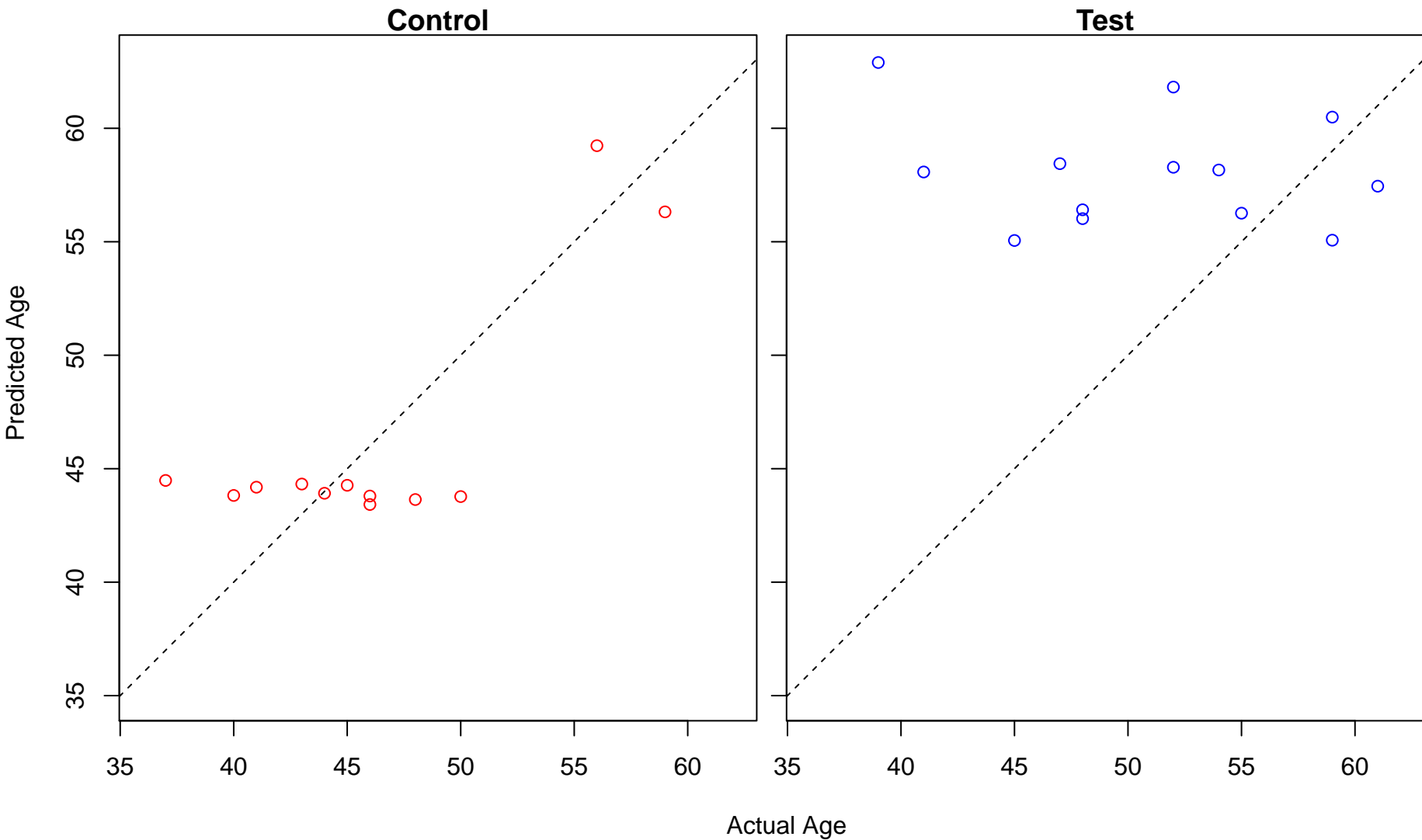
epithelial cell morphogenesis (Score: 3.432897)



regulation of cell cycle process (Score: 3.432888)

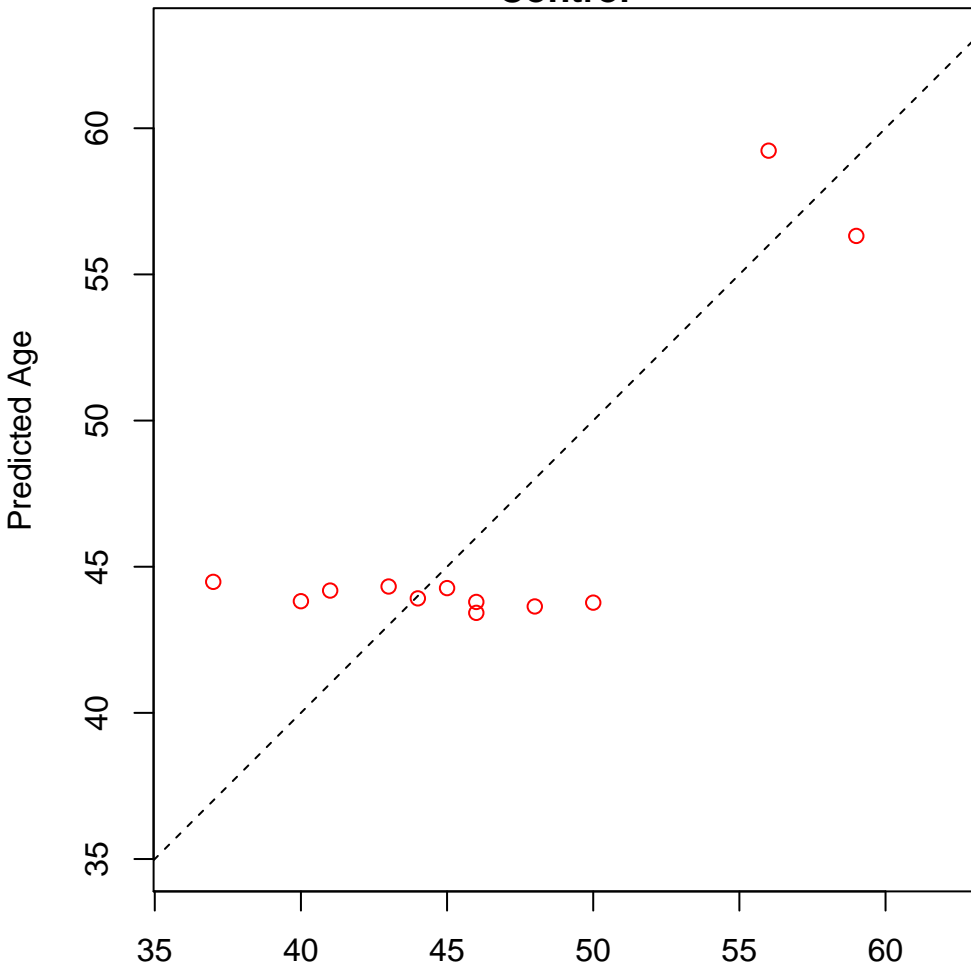


G1/S transition of mitotic cell cycle (Score: 3.432364)

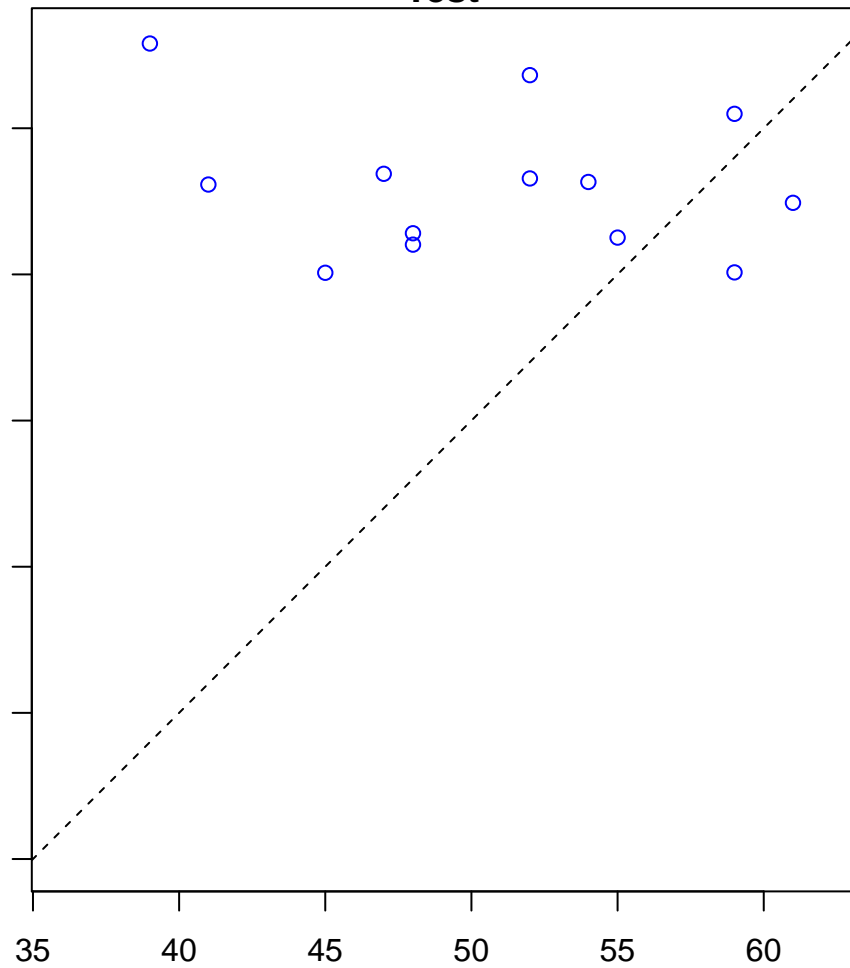


cell cycle G1/S phase transition (Score: 3.432364)

Control

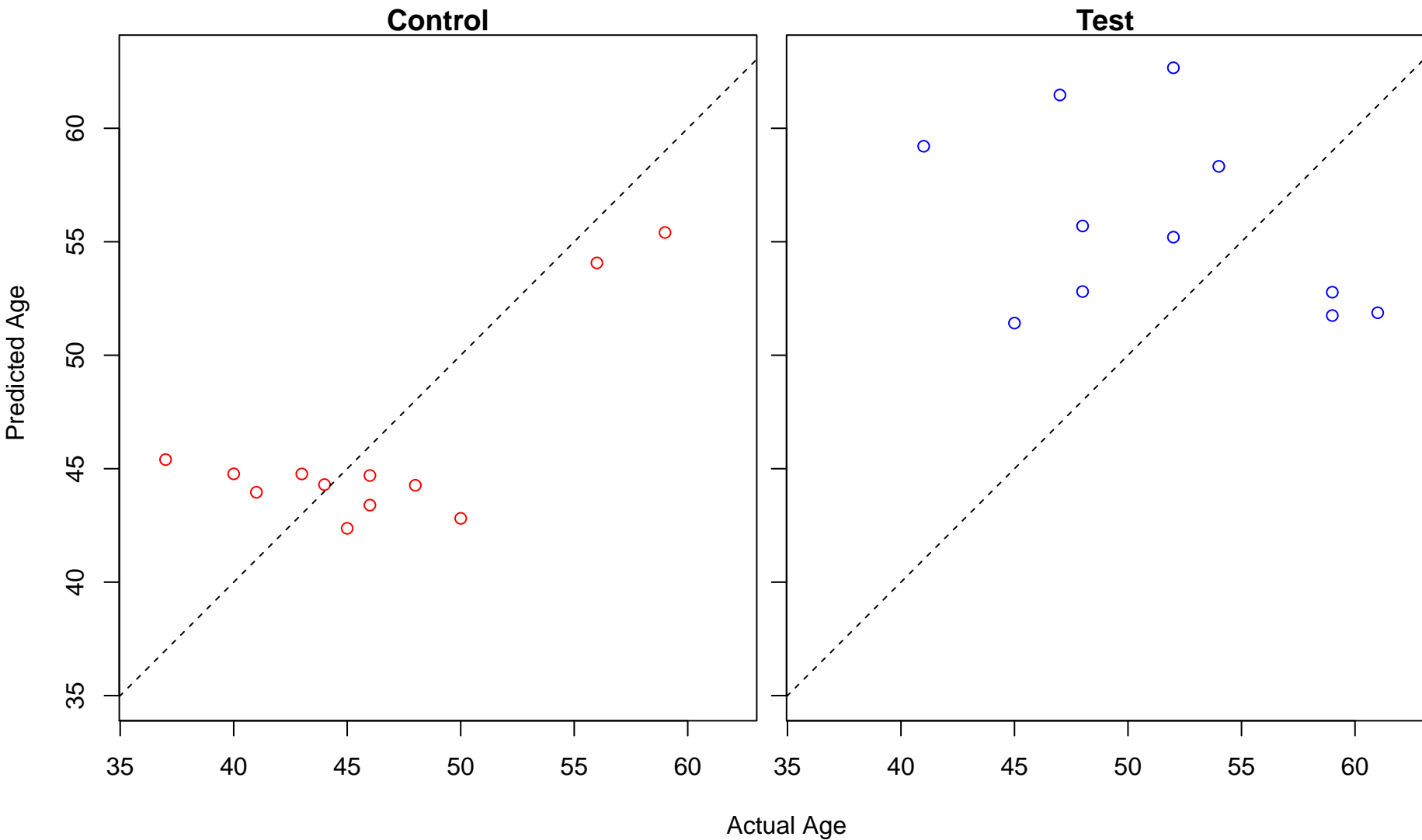


Test

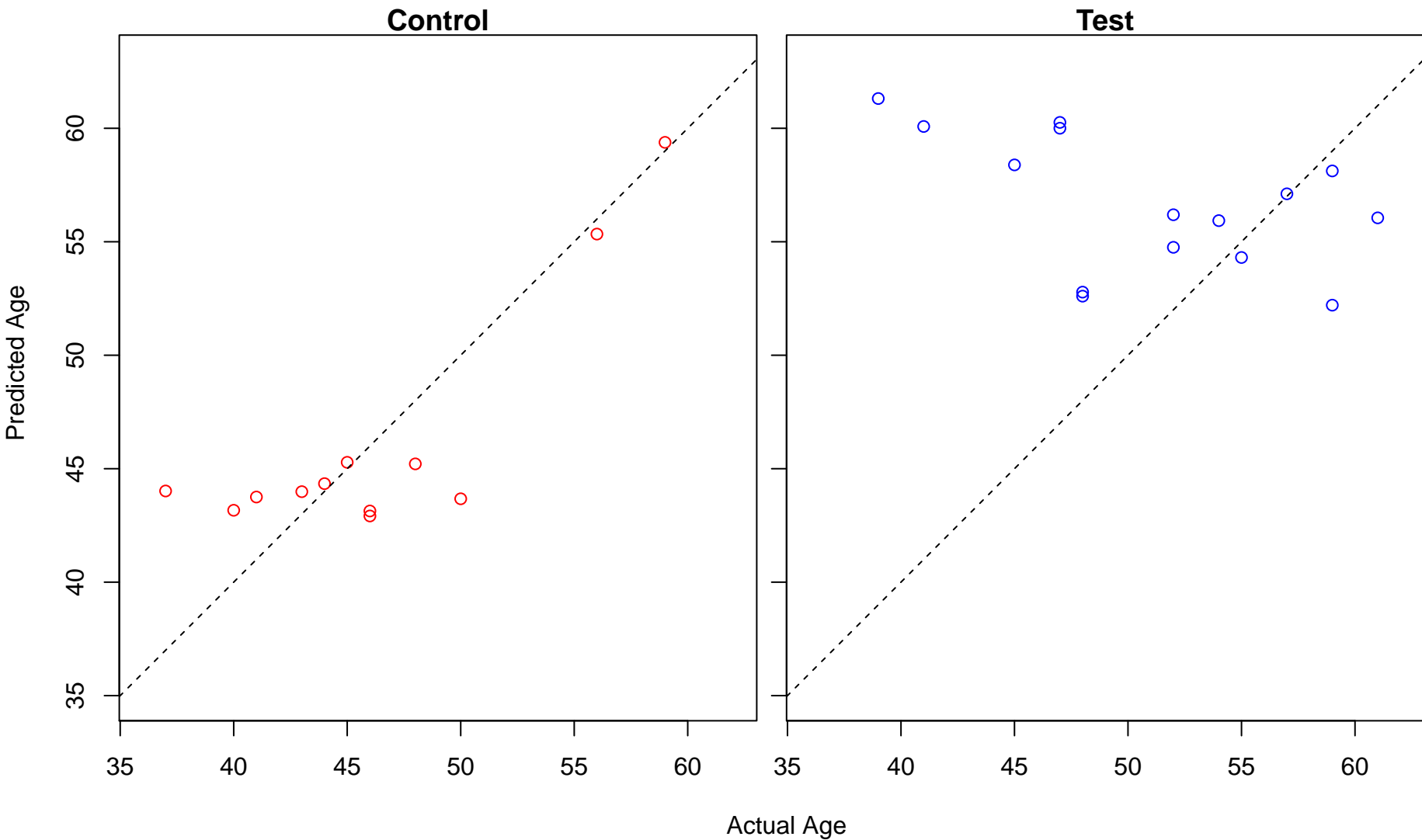


Actual Age

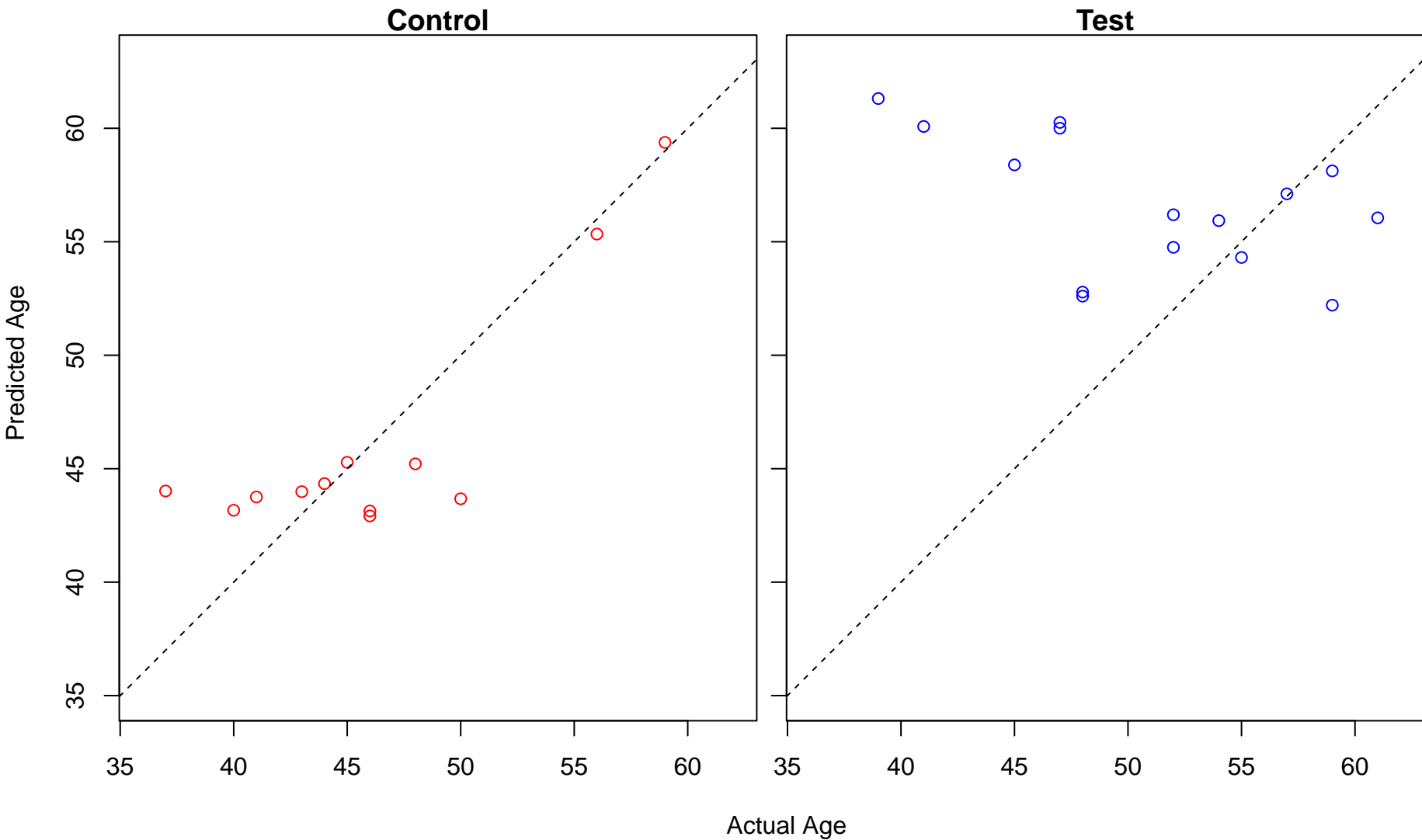
platelet aggregation (Score: 3.430628)



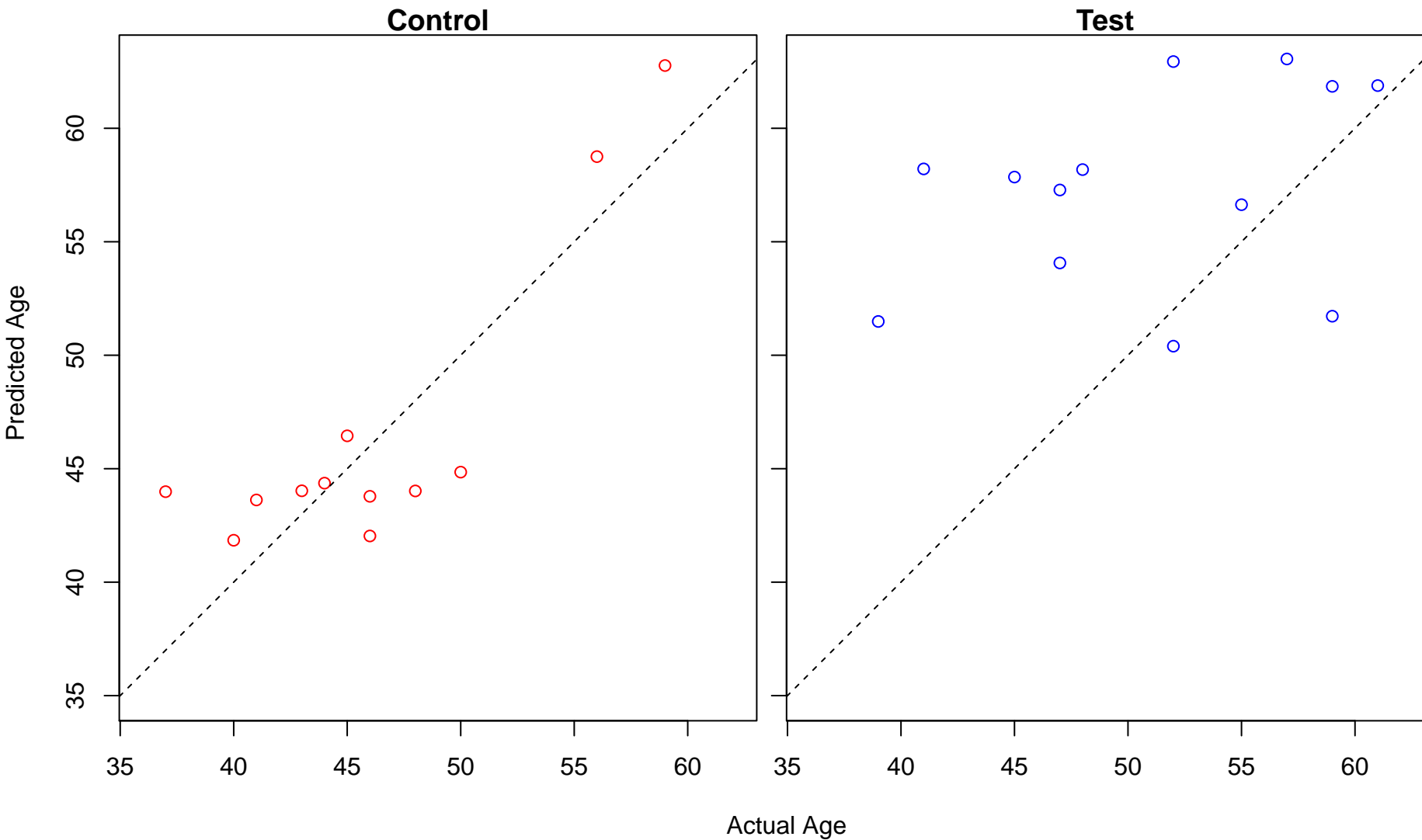
phosphatidylinositol-mediated signaling (Score: 3.429547)



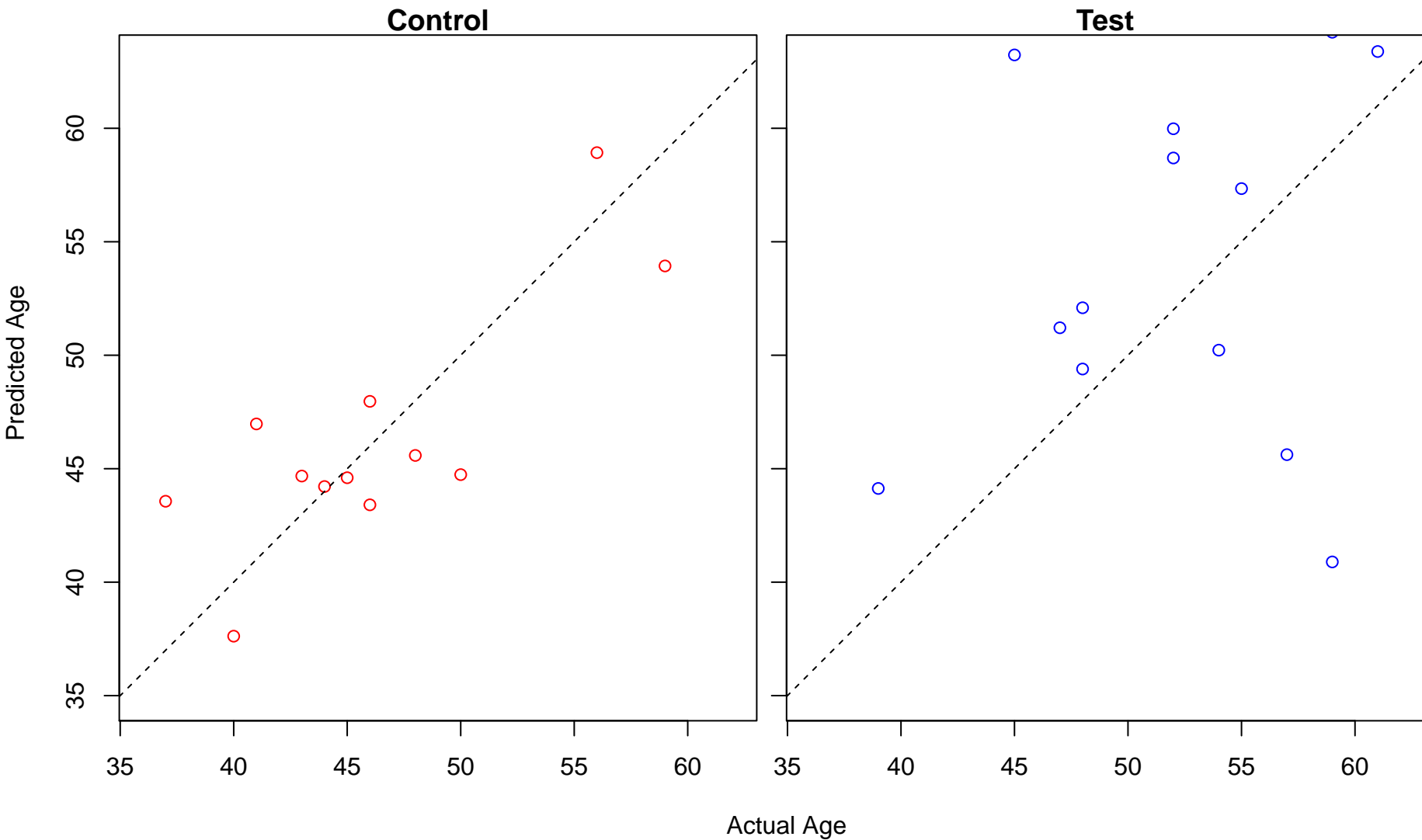
inositol lipid-mediated signaling (Score: 3.429547)



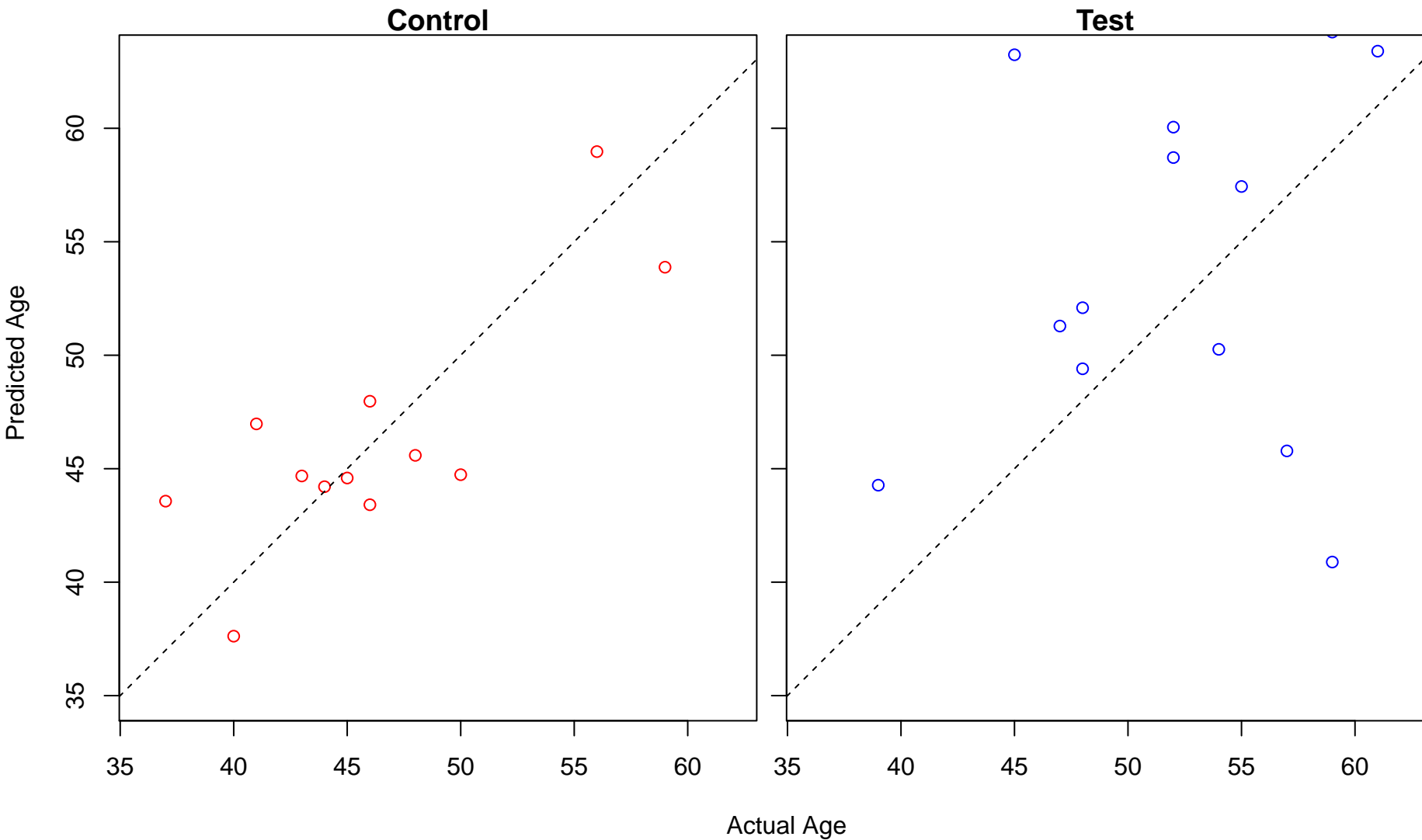
motile cilium assembly (Score: 3.428277)



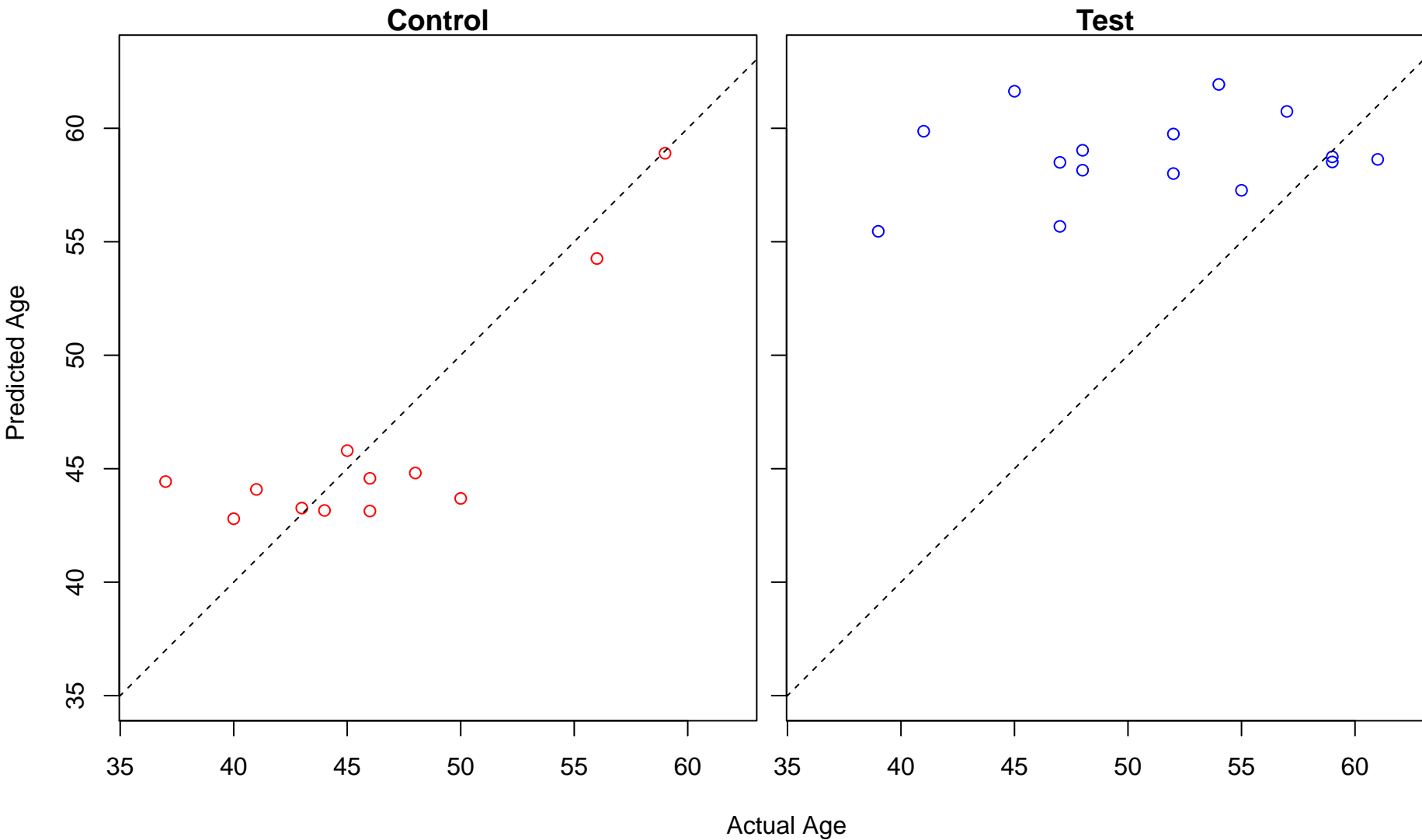
negative regulation of homotypic cell–cell adhesion (Score: 3.426495)



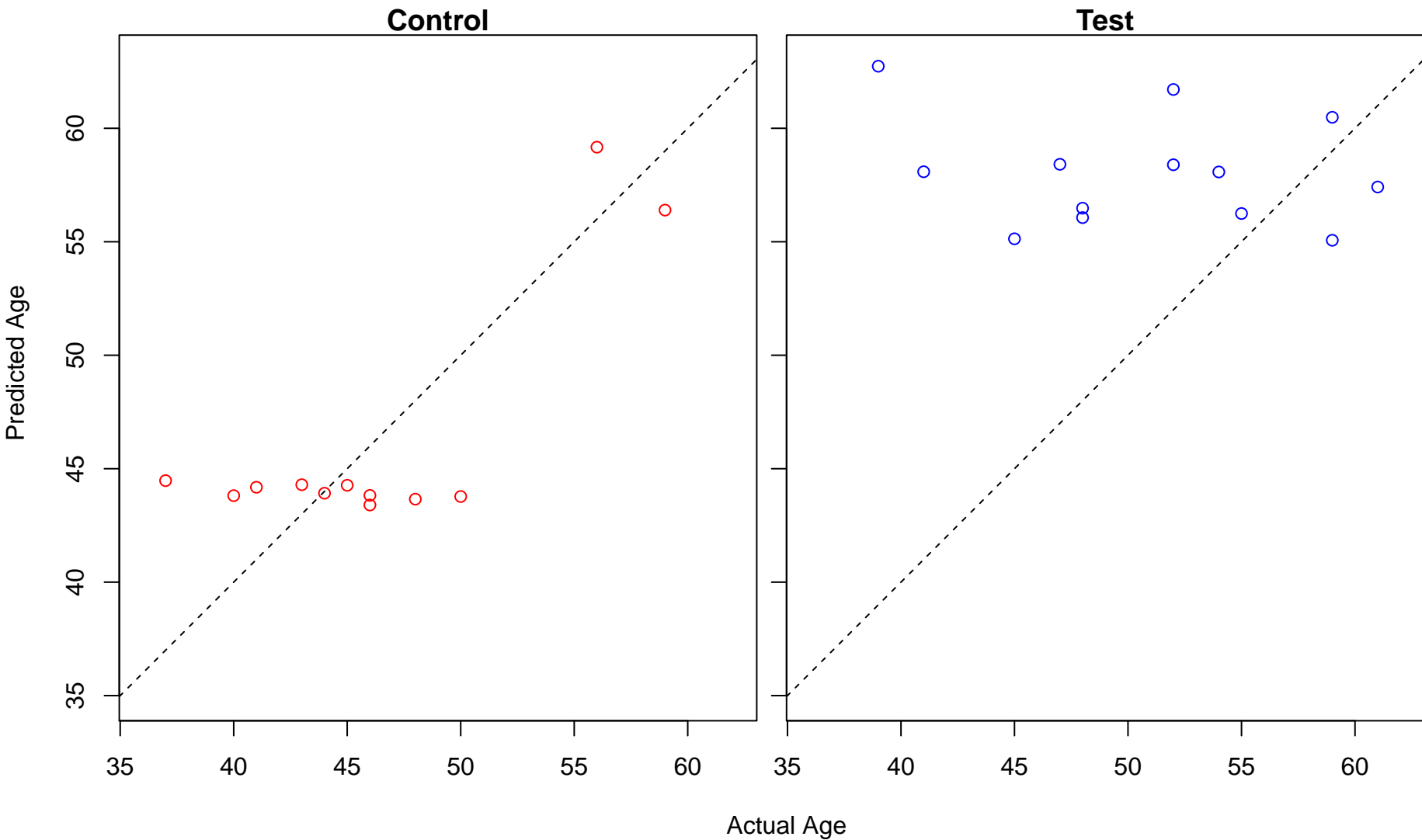
negative regulation of T cell activation (Score: 3.423572)



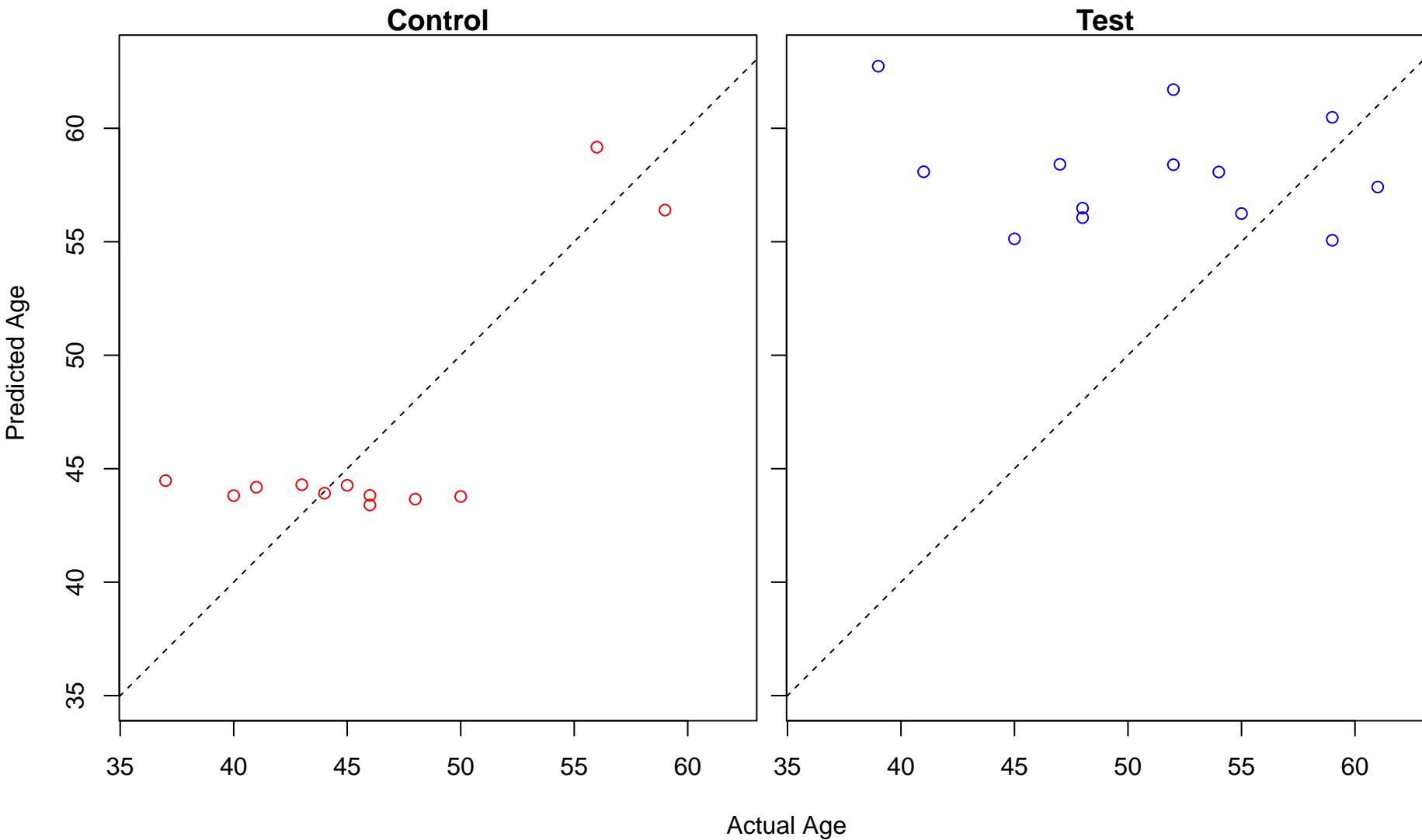
C4-dicarboxylate transport (Score: 3.423569)



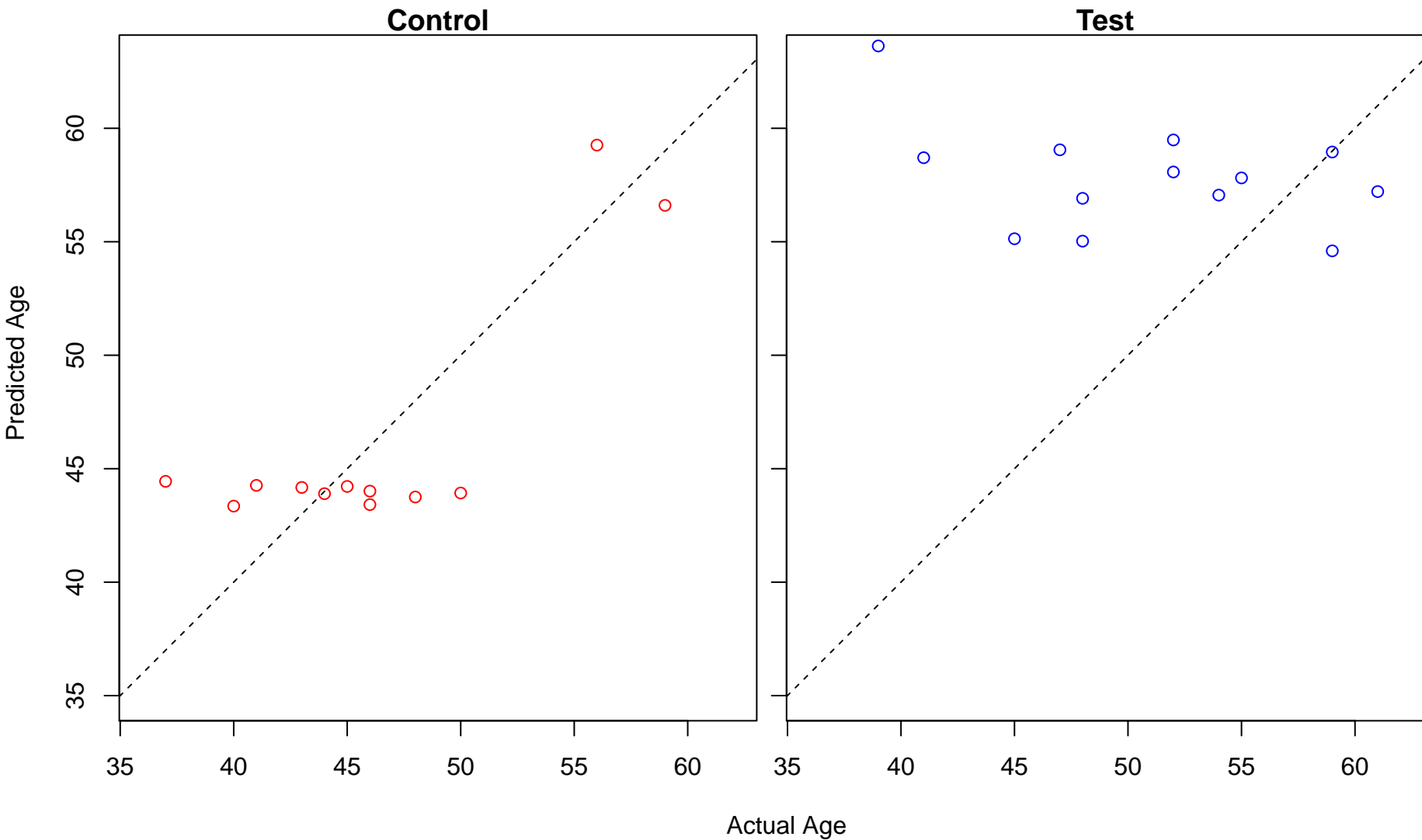
positive regulation of ligase activity (Score: 3.420079)



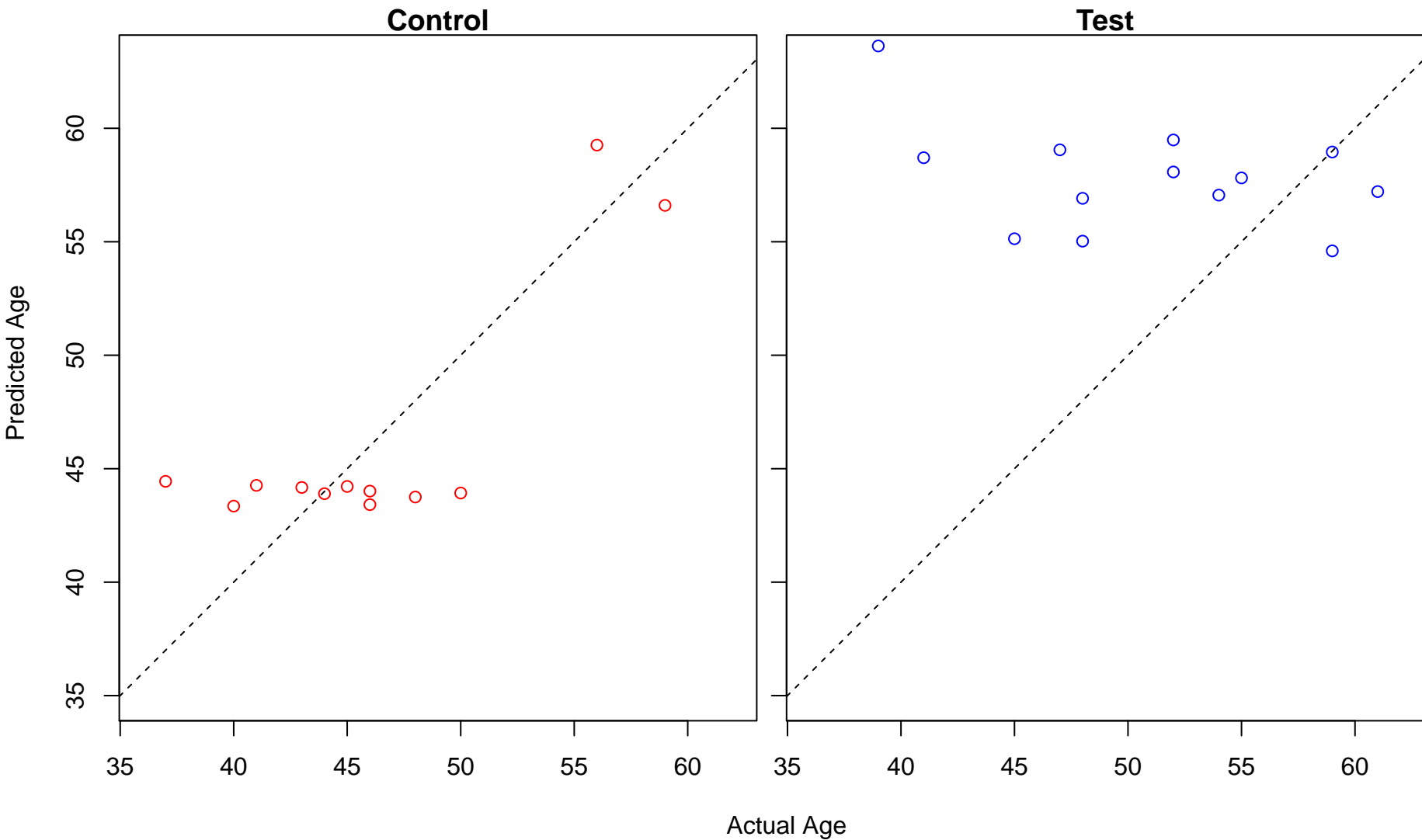
positive regulation of ubiquitin–protein transferase activity (Score: 3.419849)



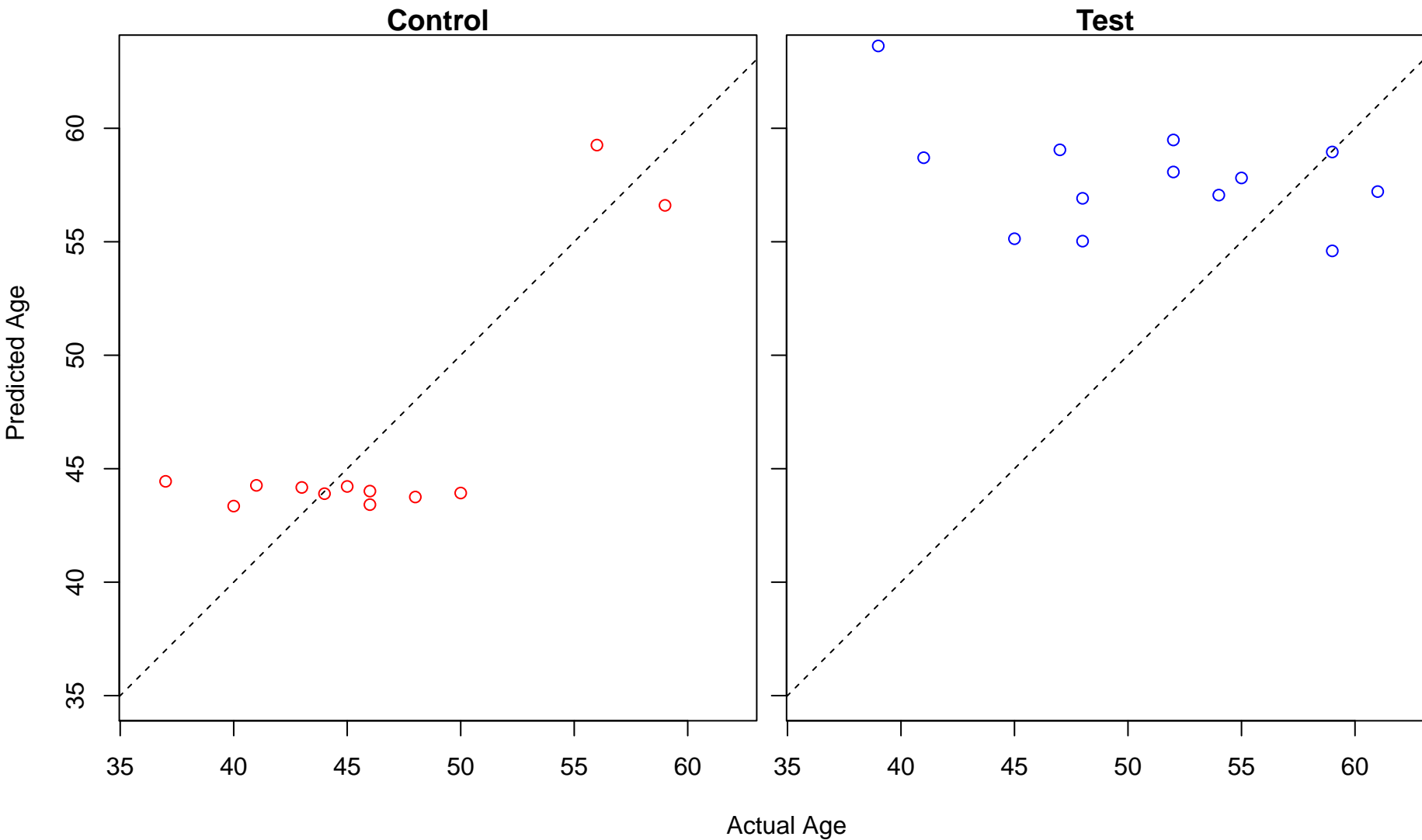
cellular glucan metabolic process (Score: 3.418232)



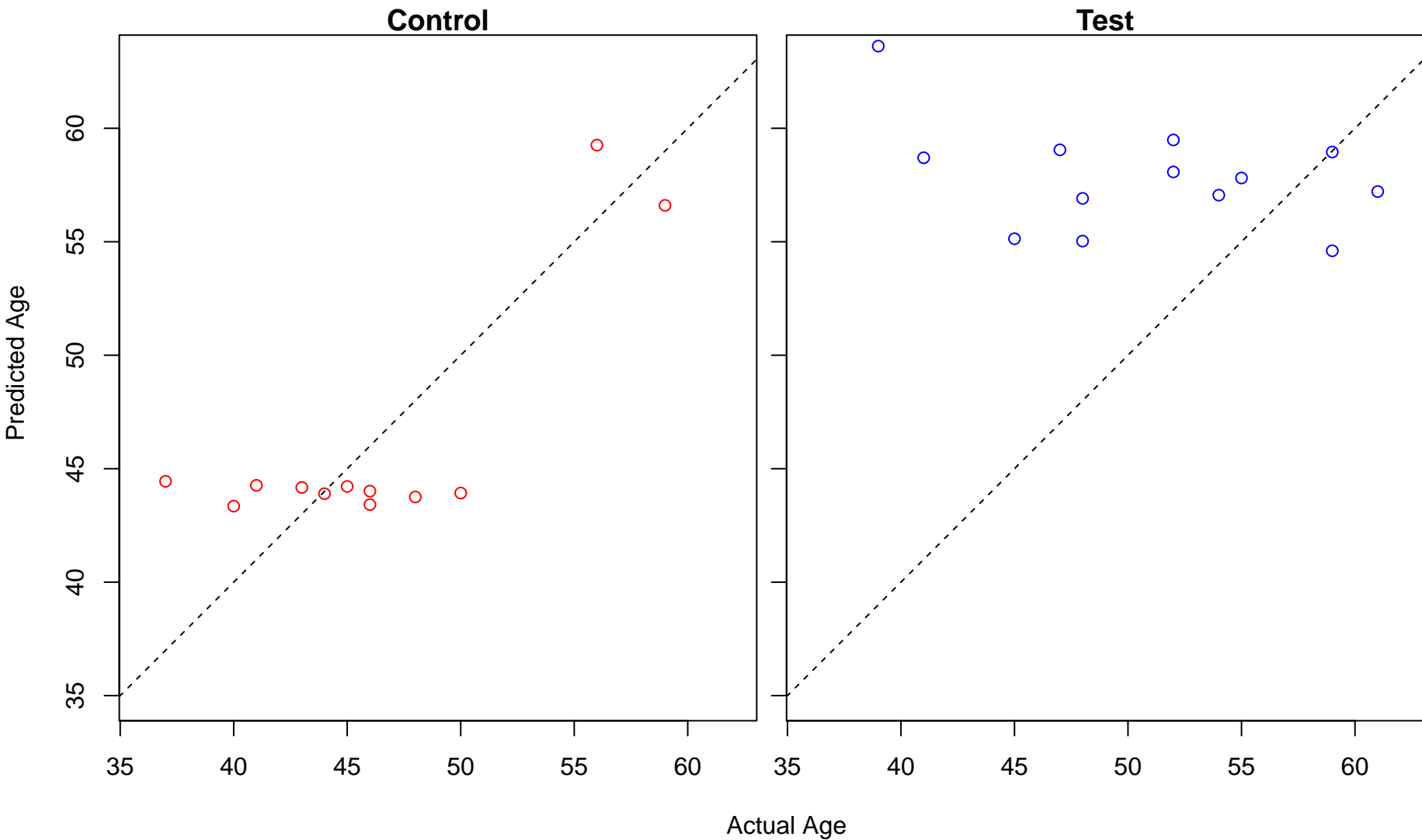
glucan metabolic process (Score: 3.418232)



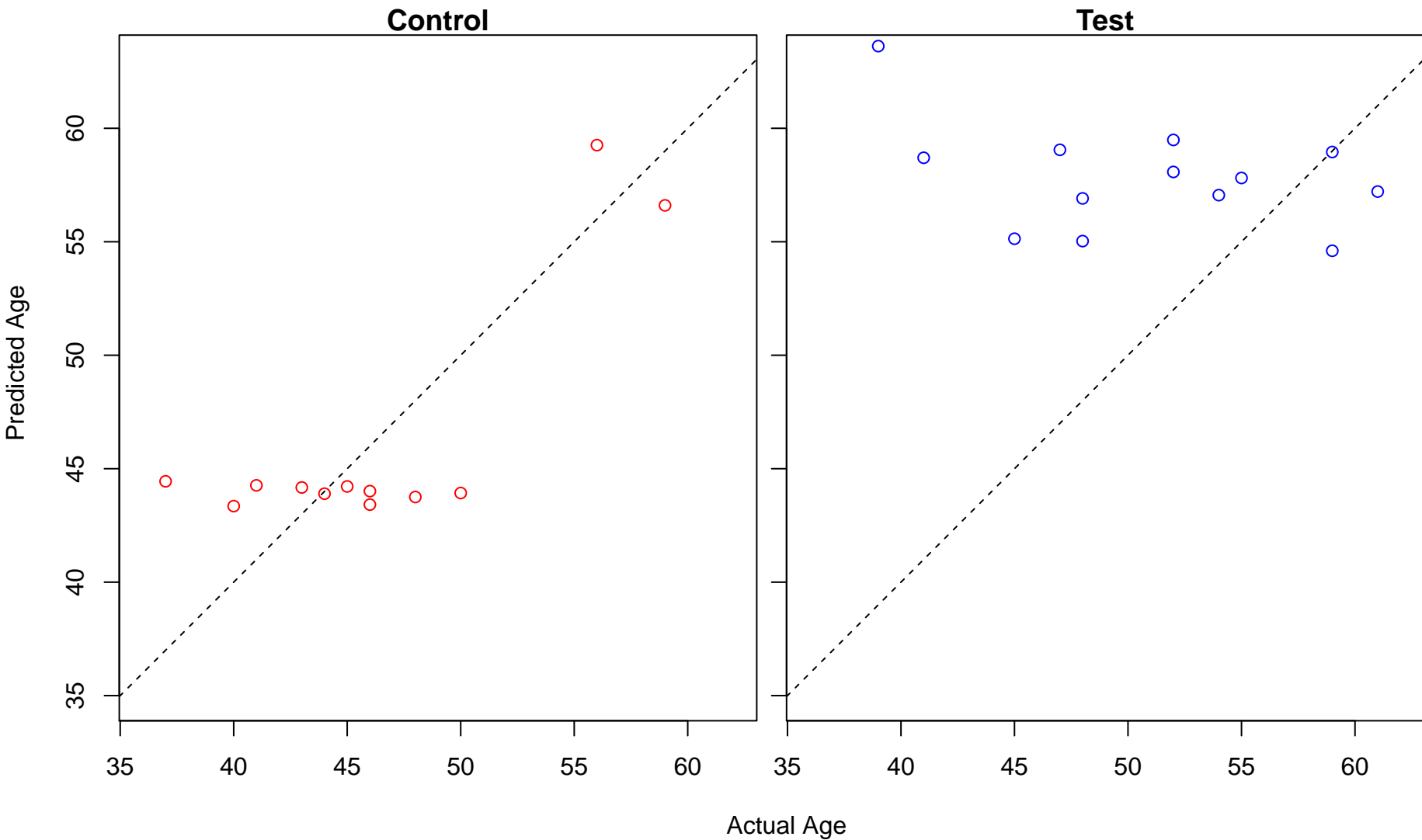
glycogen metabolic process (Score: 3.418222)



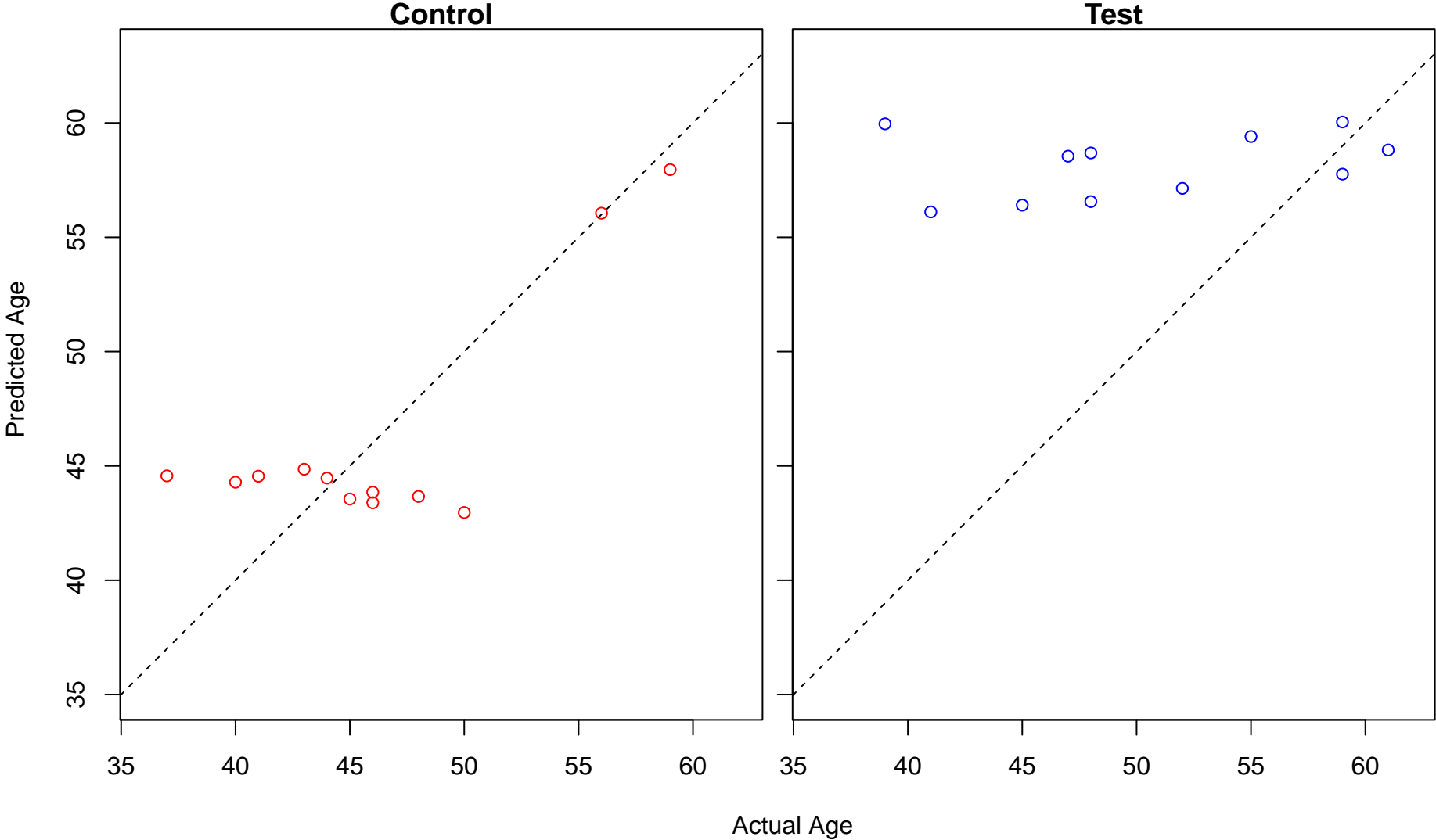
cellular polysaccharide metabolic process (Score: 3.417201)



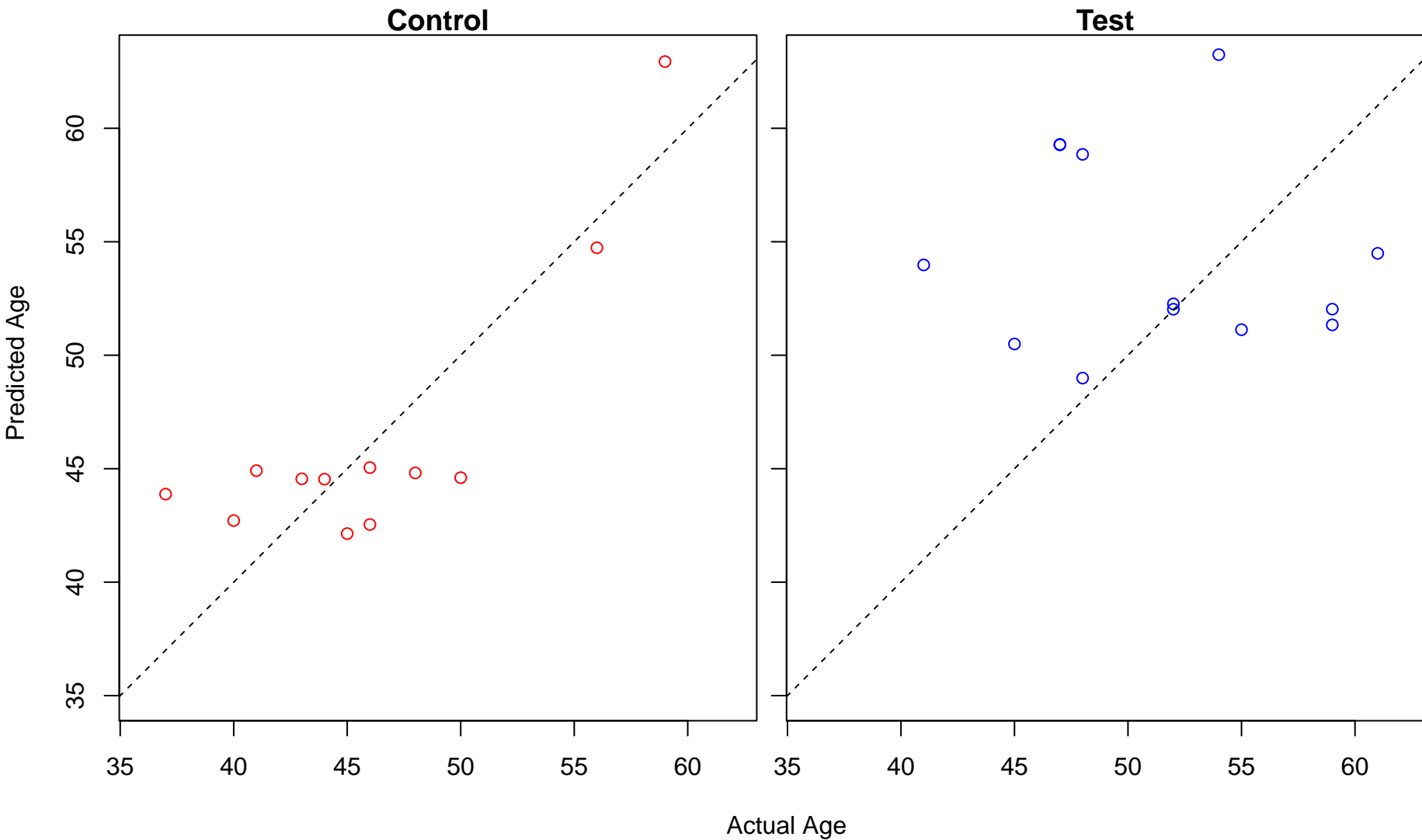
polysaccharide metabolic process (Score: 3.417175)



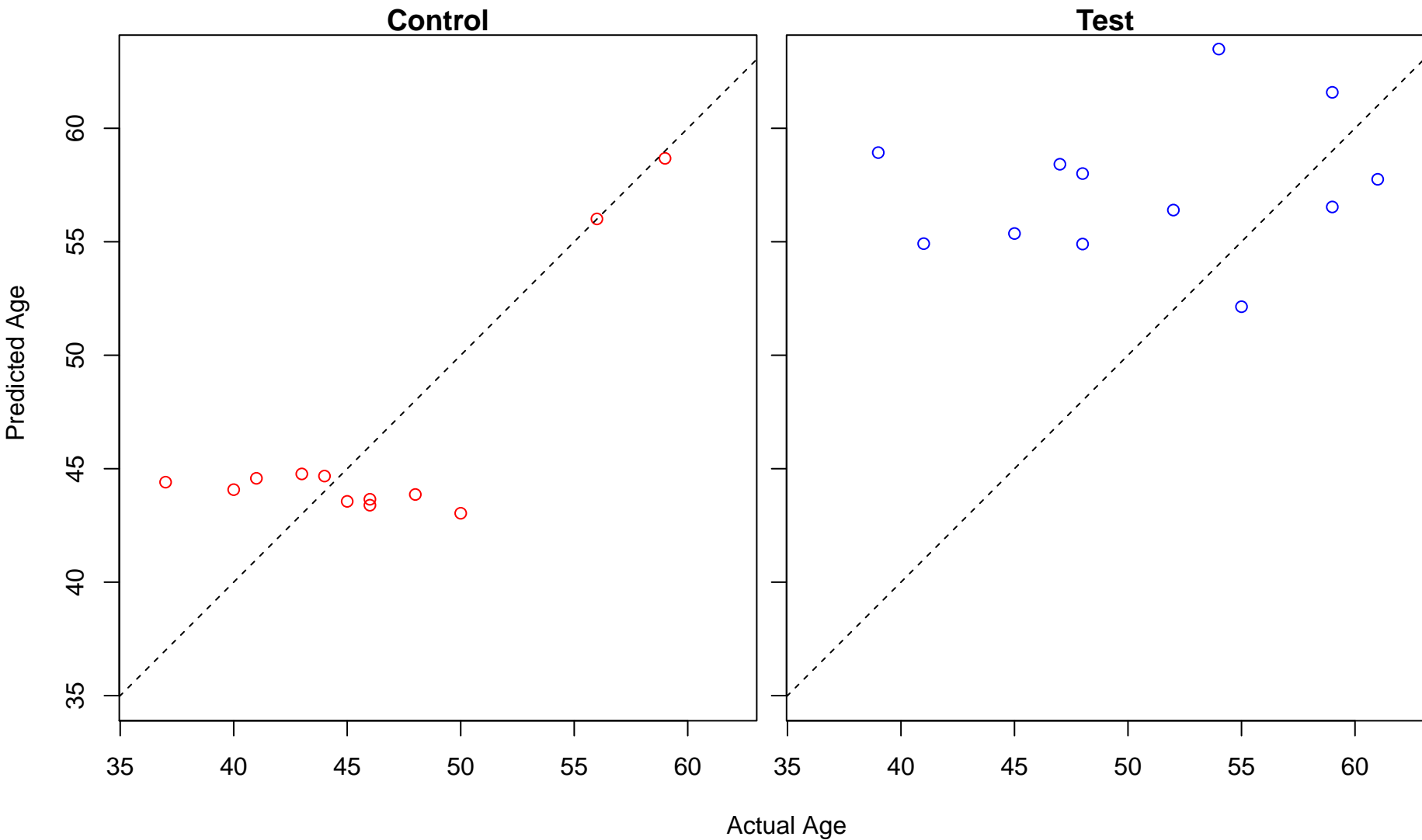
negative regulation of extrinsic apoptotic signaling pathway via death domain receptors (Score: 3.417)



muscle contraction (Score: 3.416067)

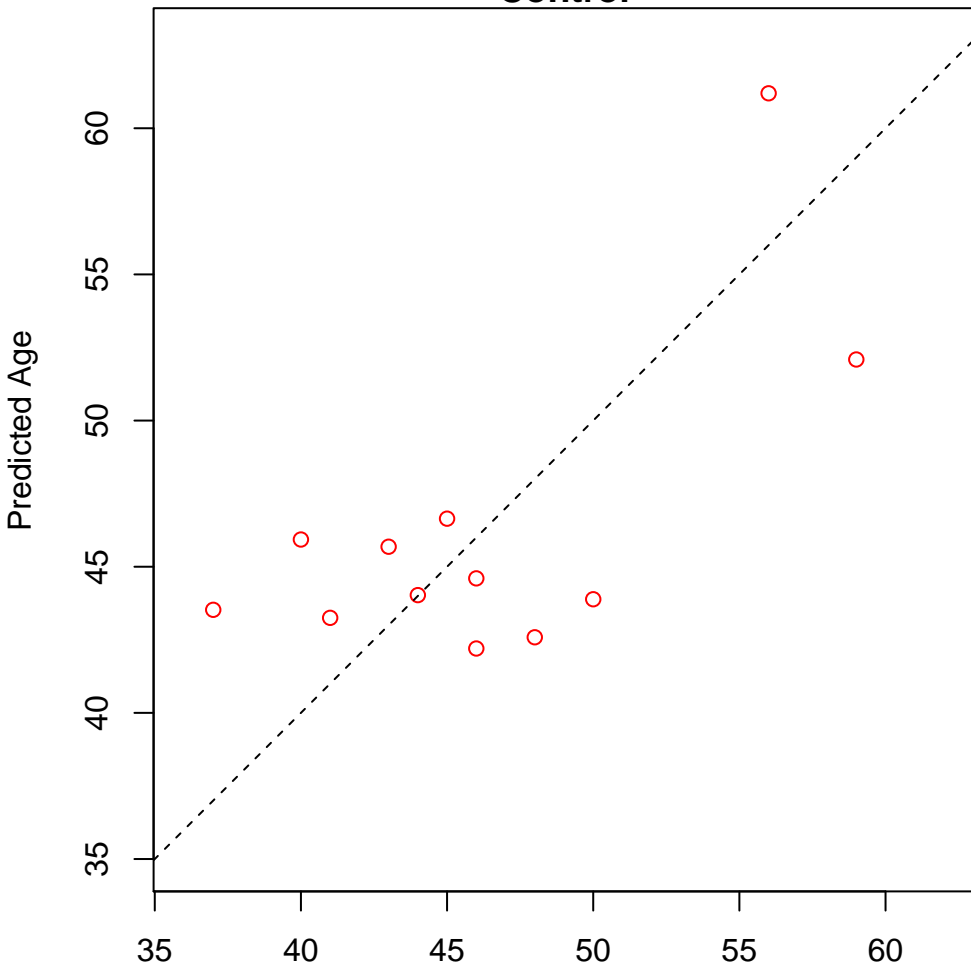


positive regulation of cellular amine metabolic process (Score: 3.415052)

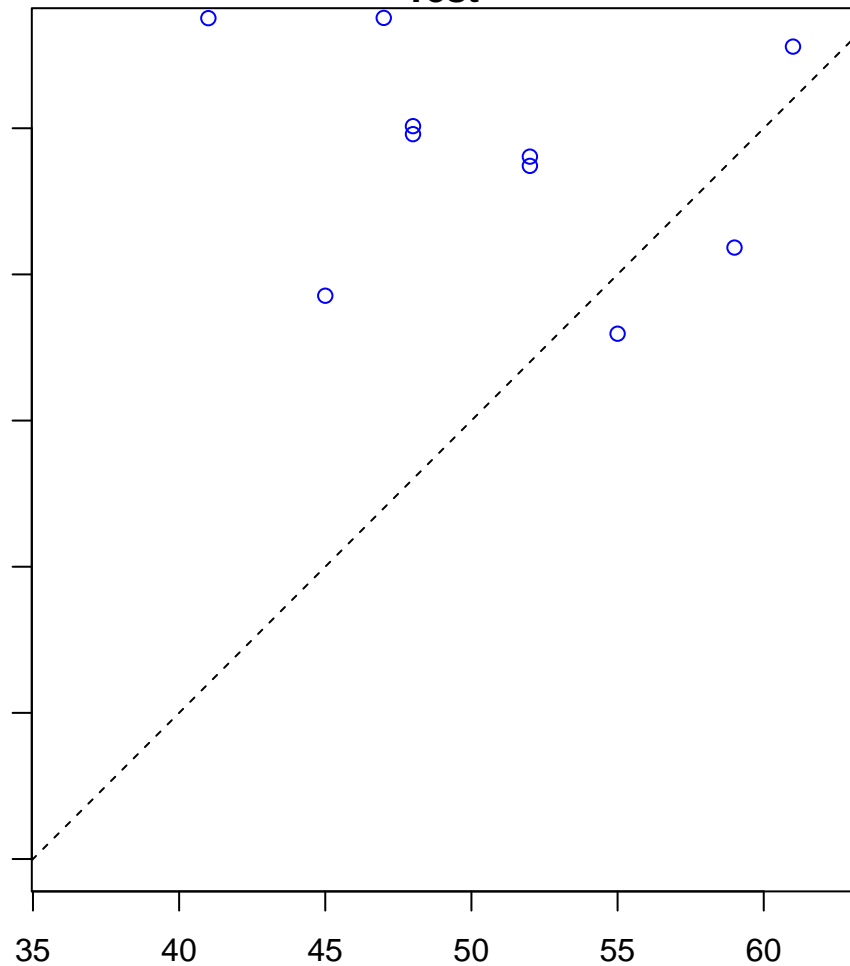


response to platelet-derived growth factor (Score: 3.414385)

Control

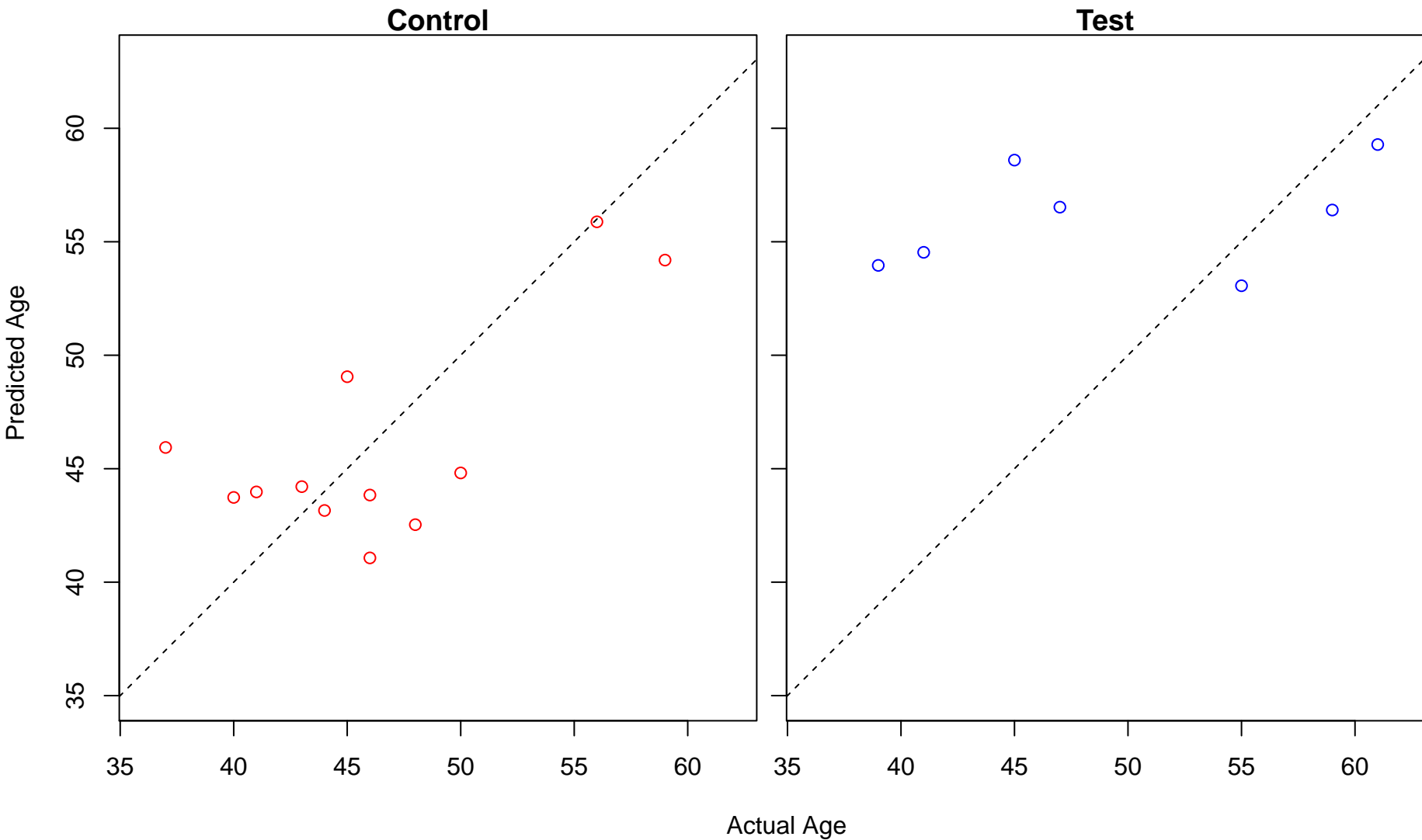


Test



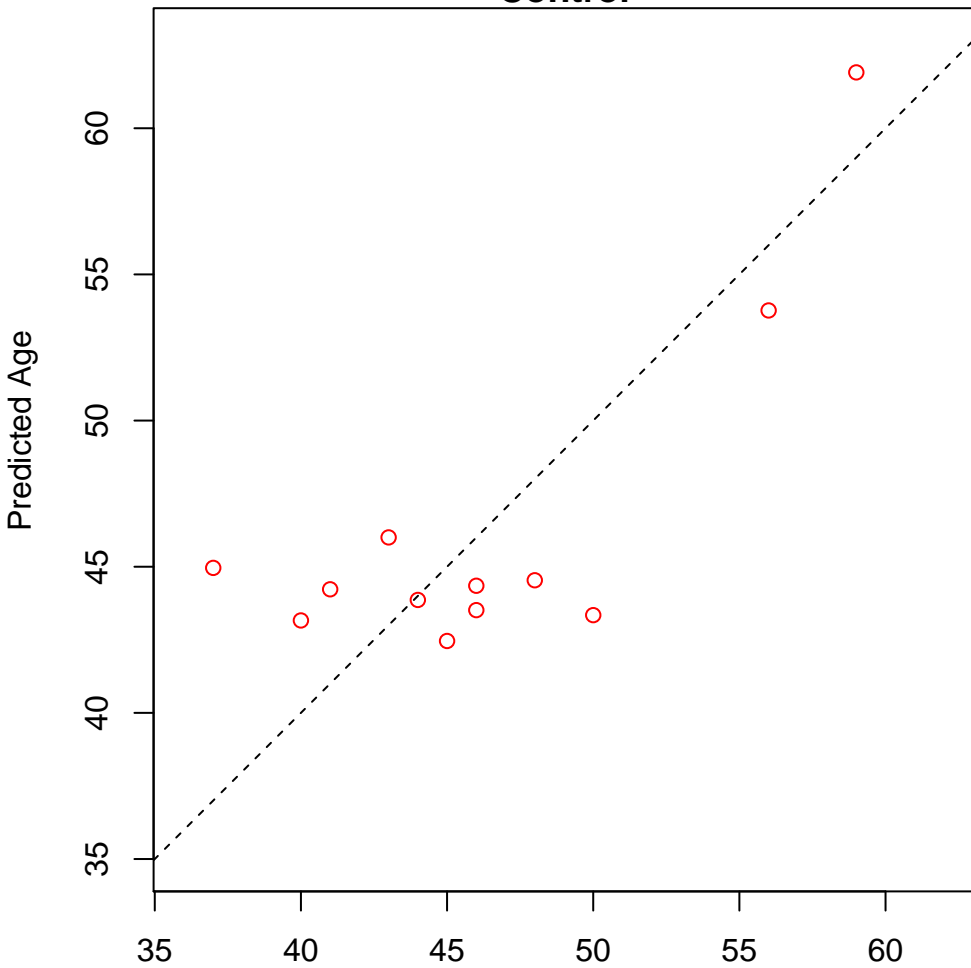
Actual Age

lateral mesoderm development (Score: 3.412811)

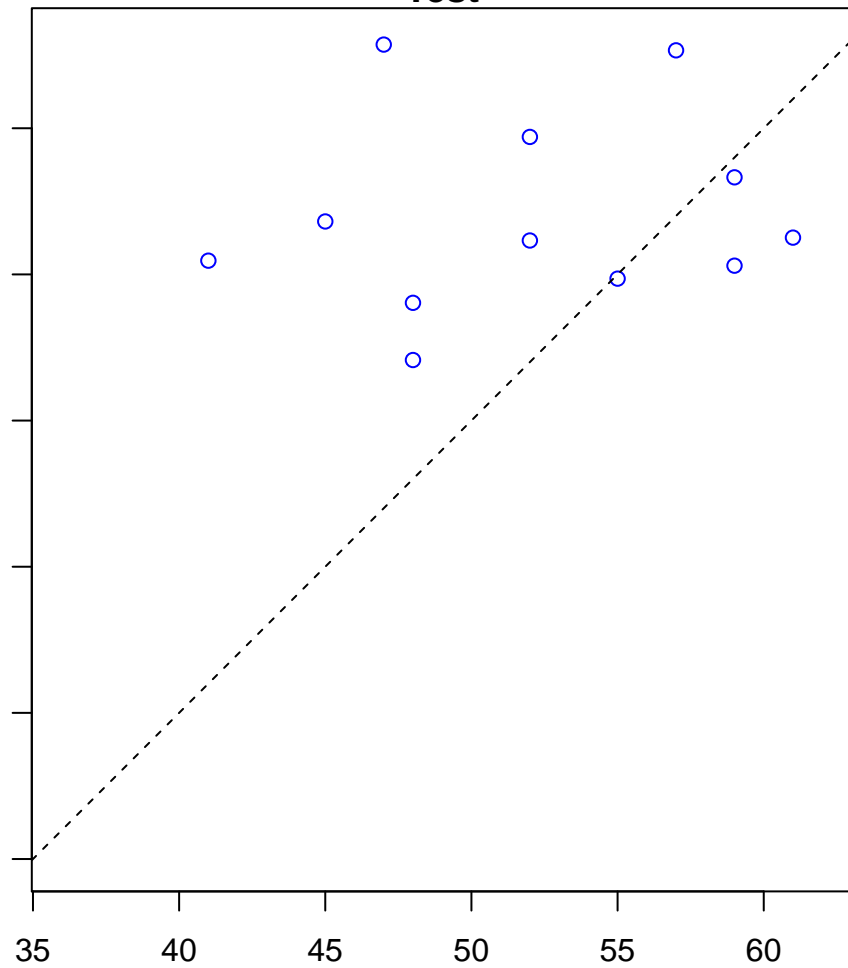


regulation of synaptic vesicle transport (Score: 3.412705)

Control

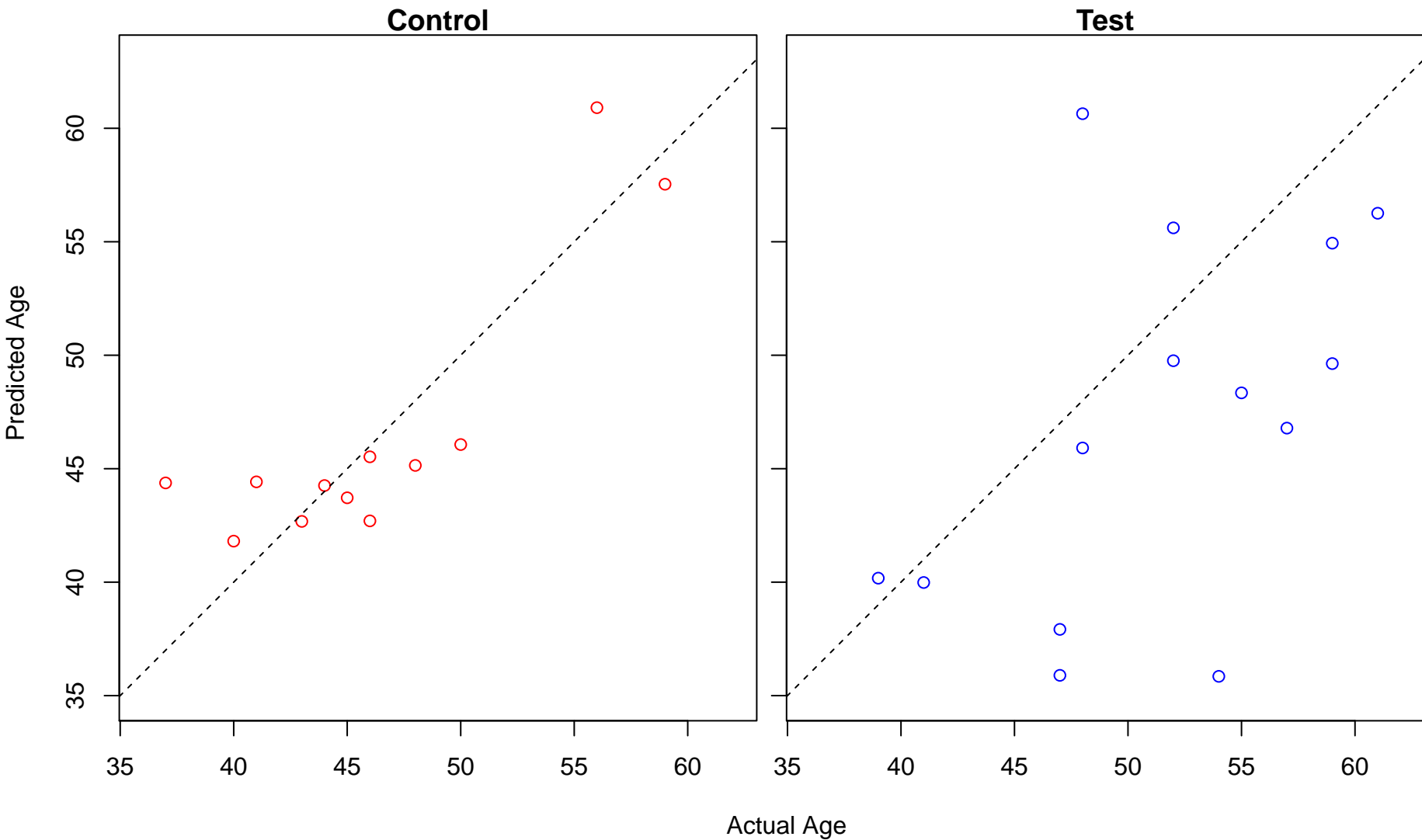


Test

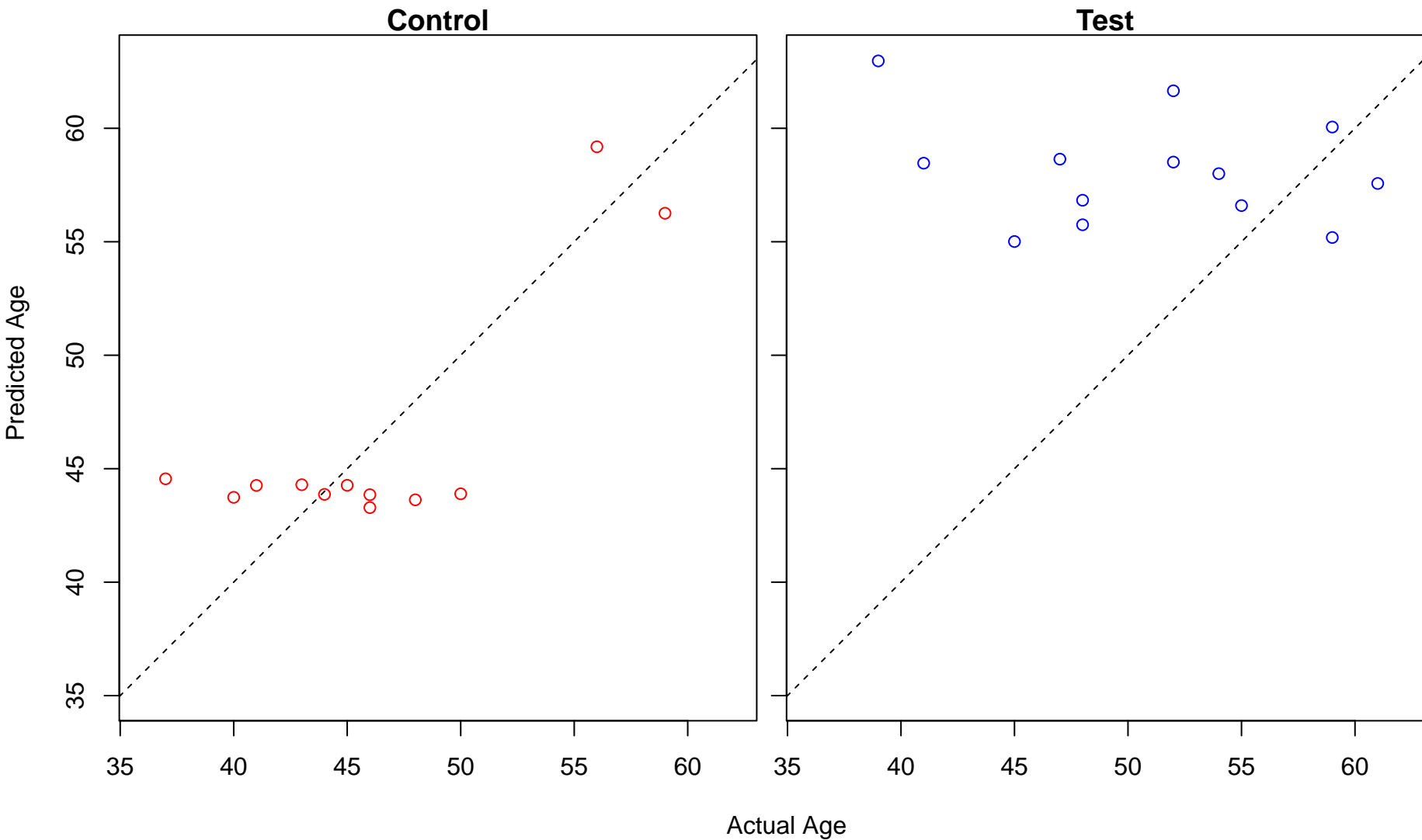


Actual Age

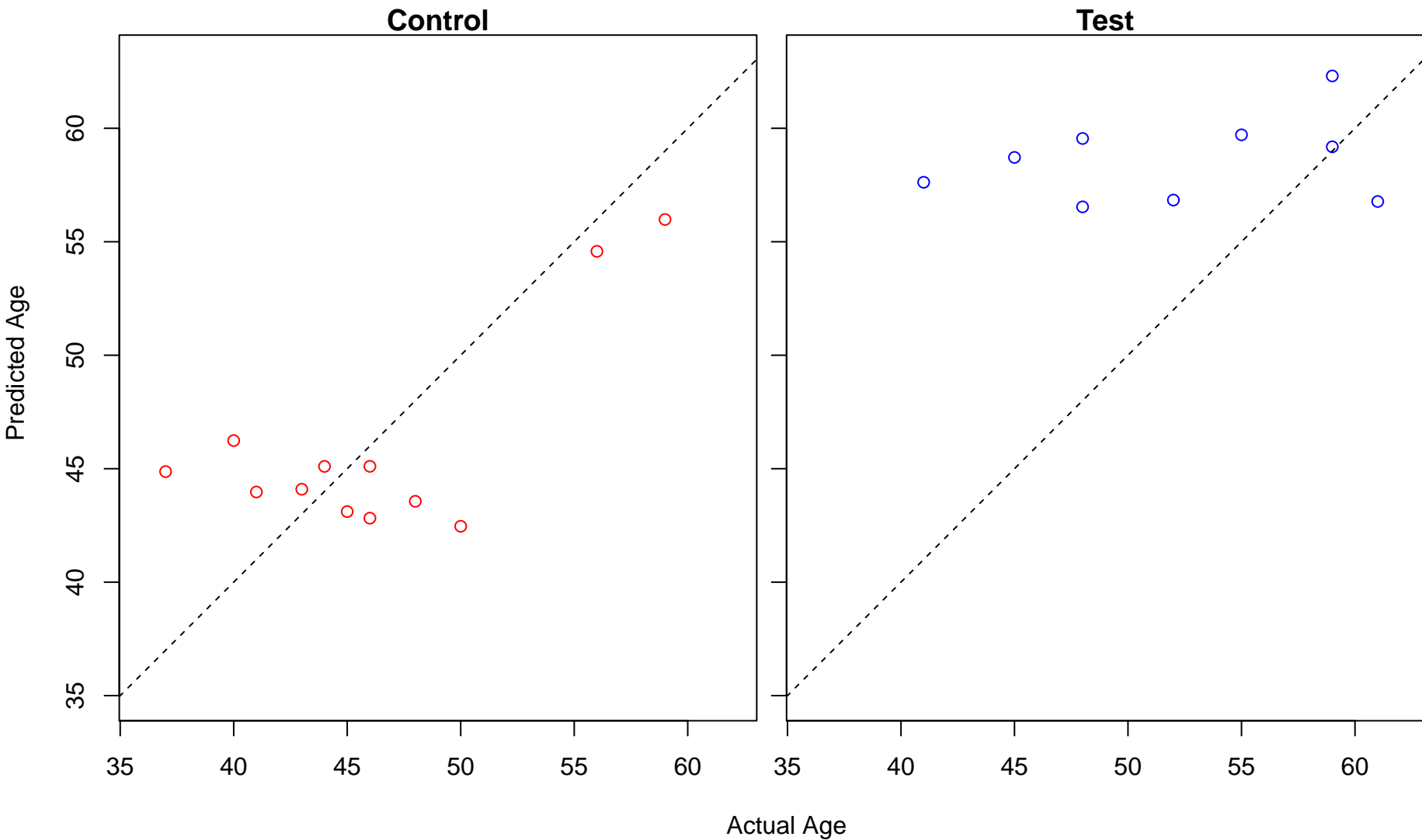
positive regulation of dendritic cell chemotaxis (Score: 3.412373)



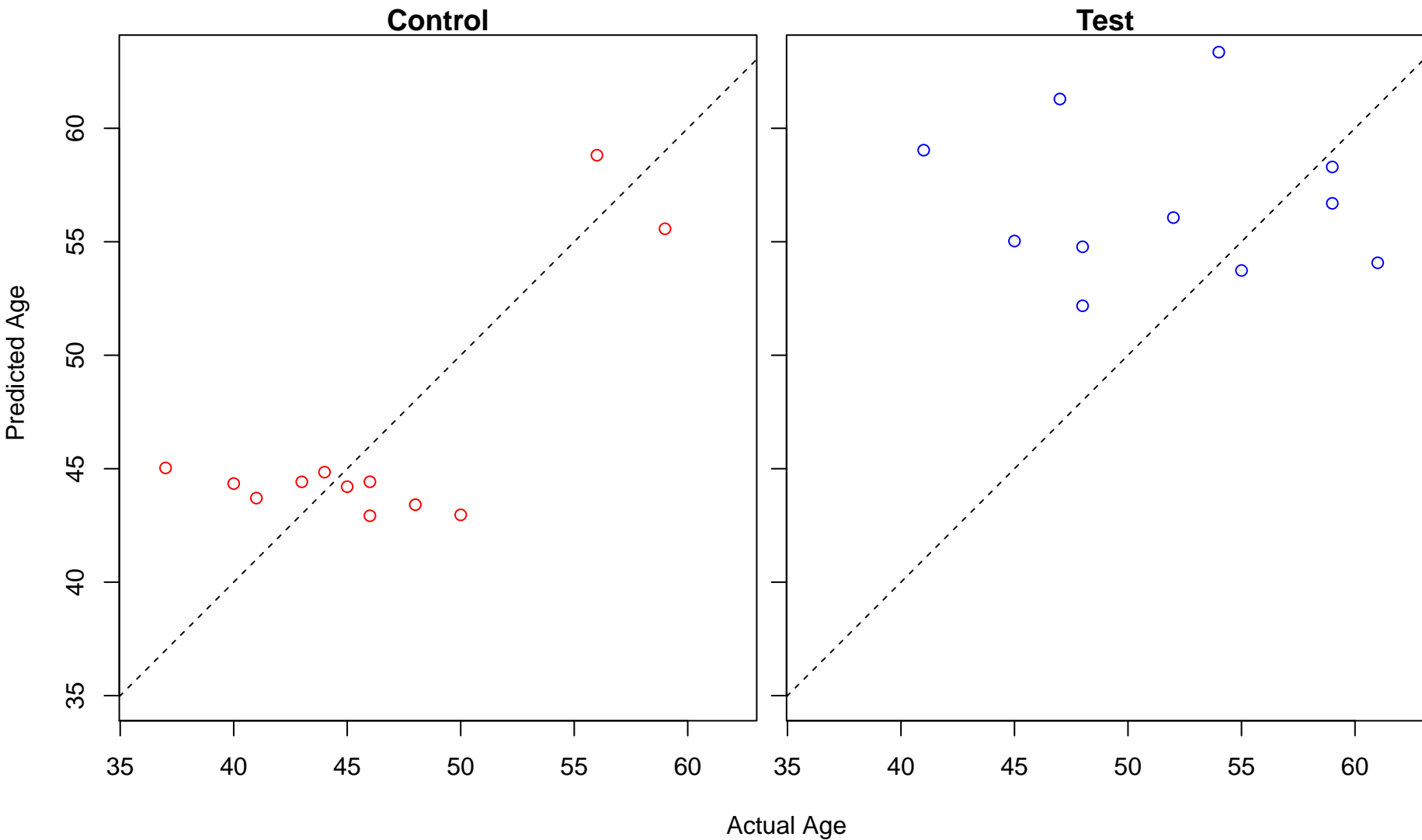
positive regulation of Wnt signaling pathway (Score: 3.412321)



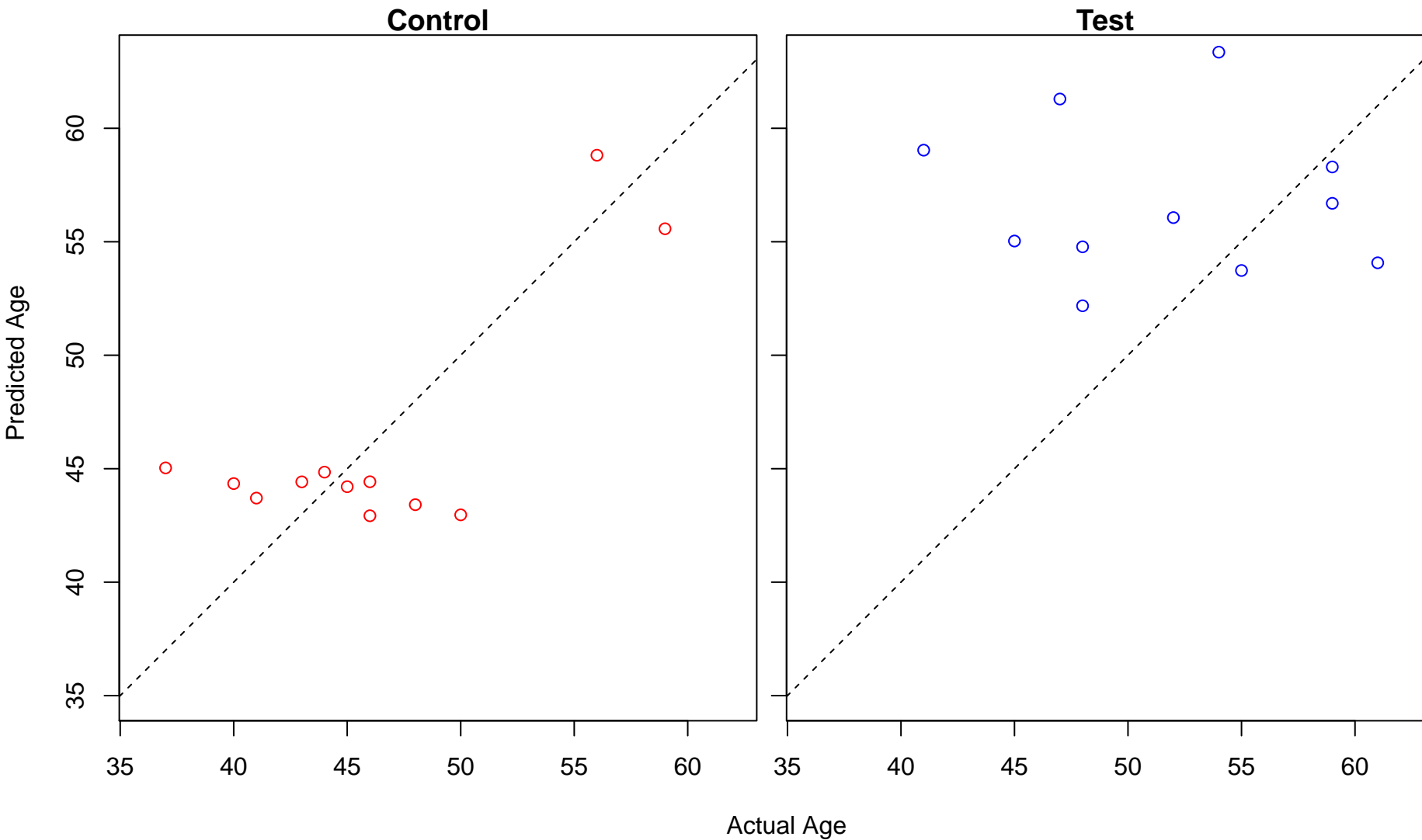
tetrahydrofolate metabolic process (Score: 3.409395)



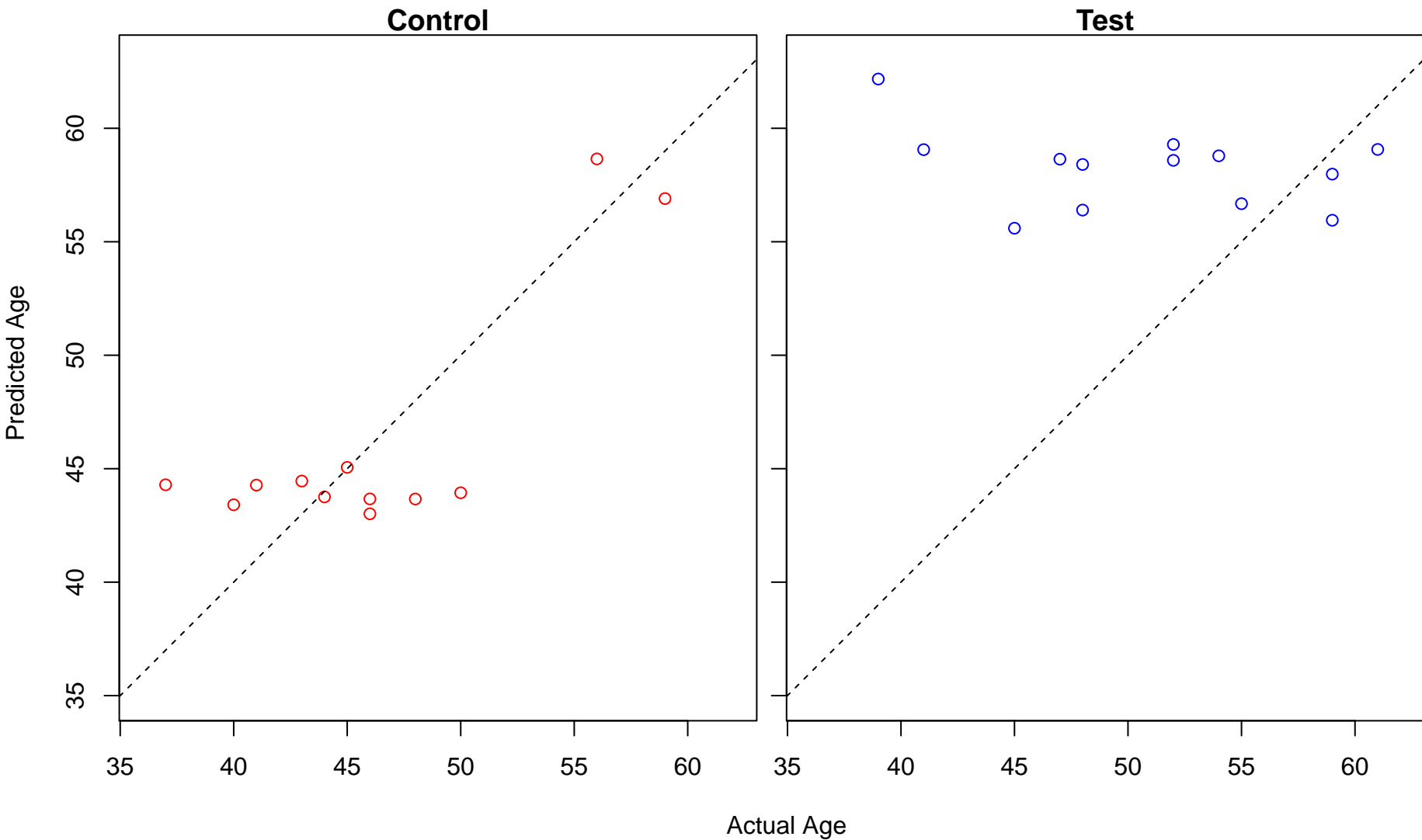
regulation of cellular response to vascular endothelial growth factor stimulus (Score: 3.409189)



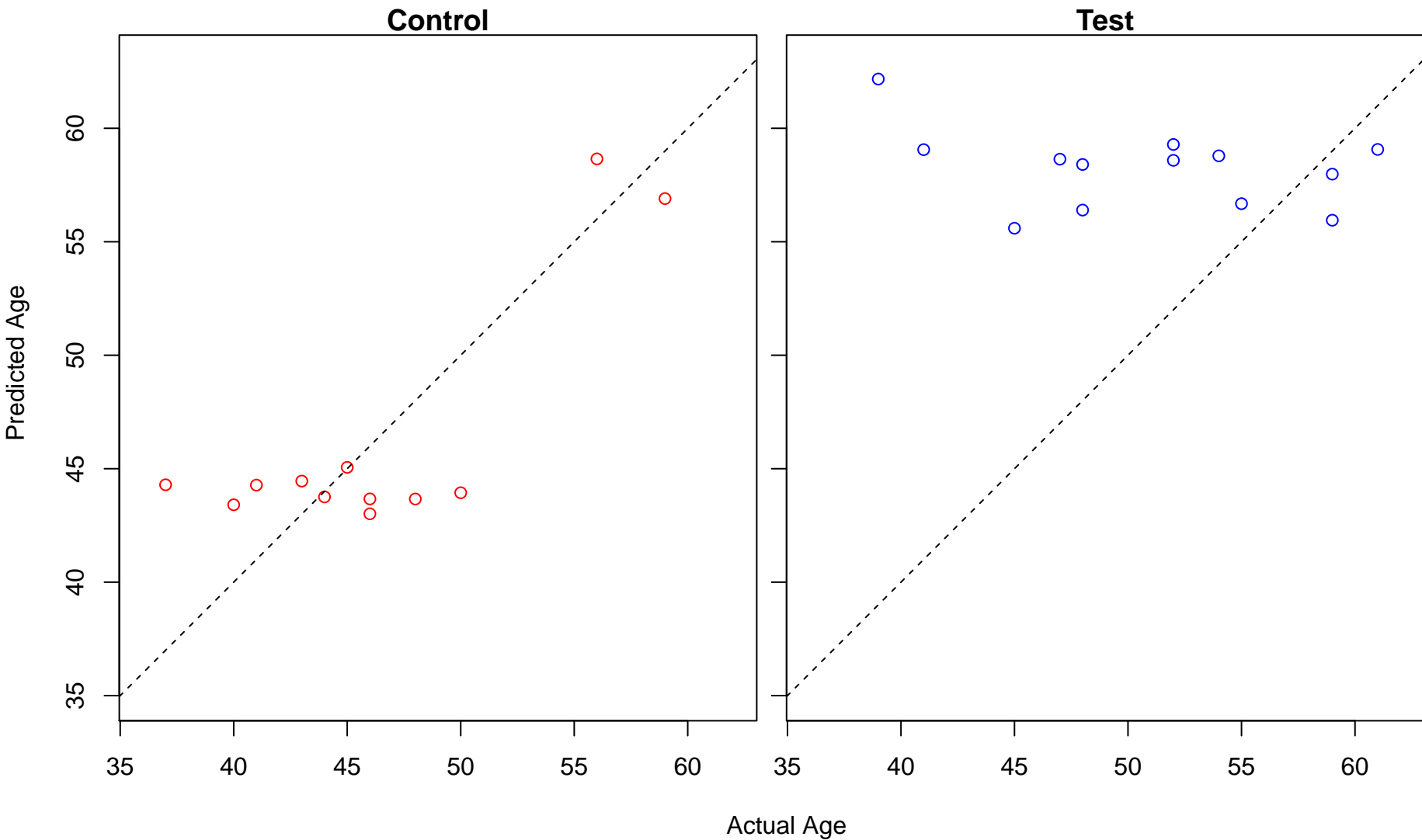
regulation of vascular endothelial growth factor signaling pathway (Score: 3.409169)



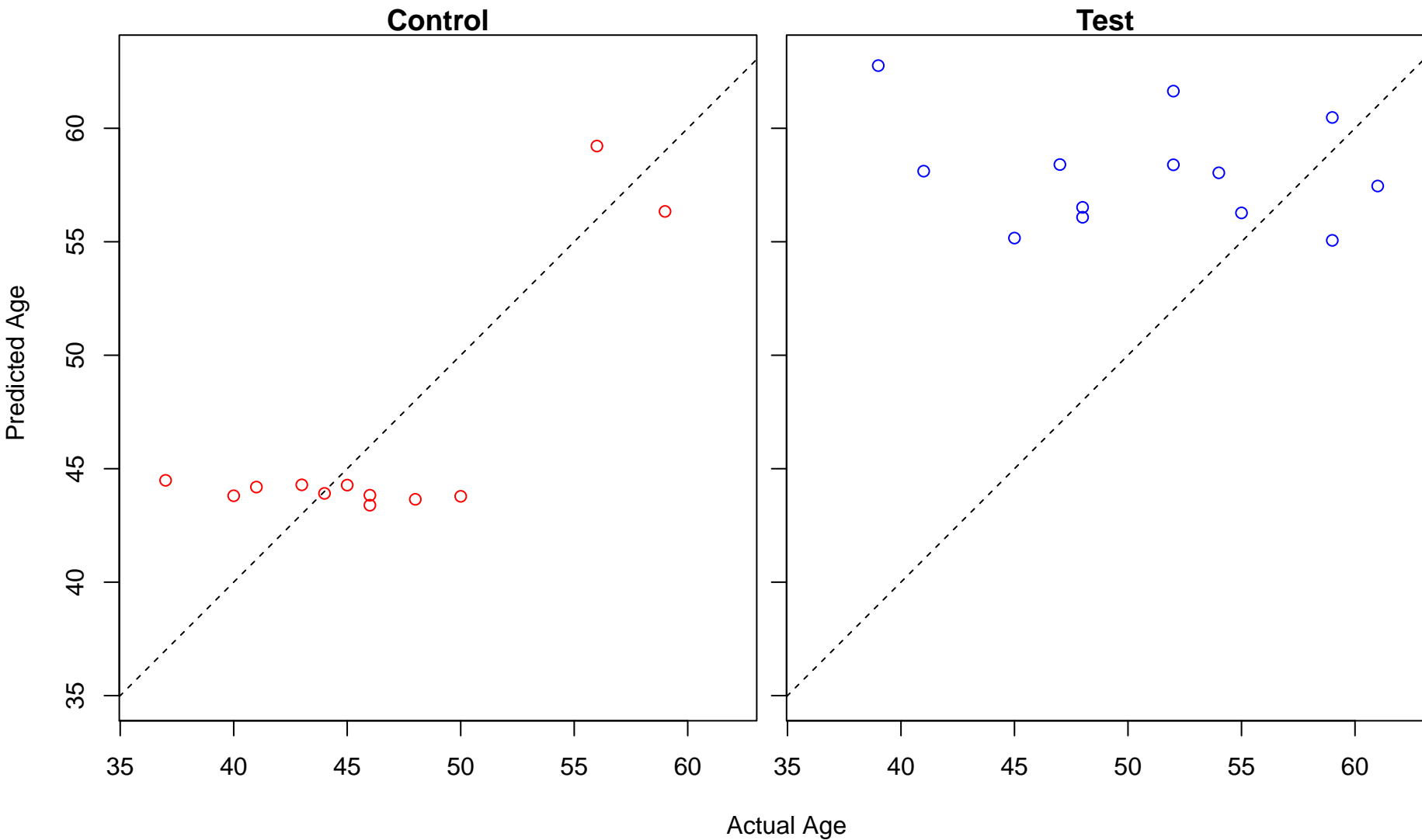
mitophagy (Score: 3.405542)



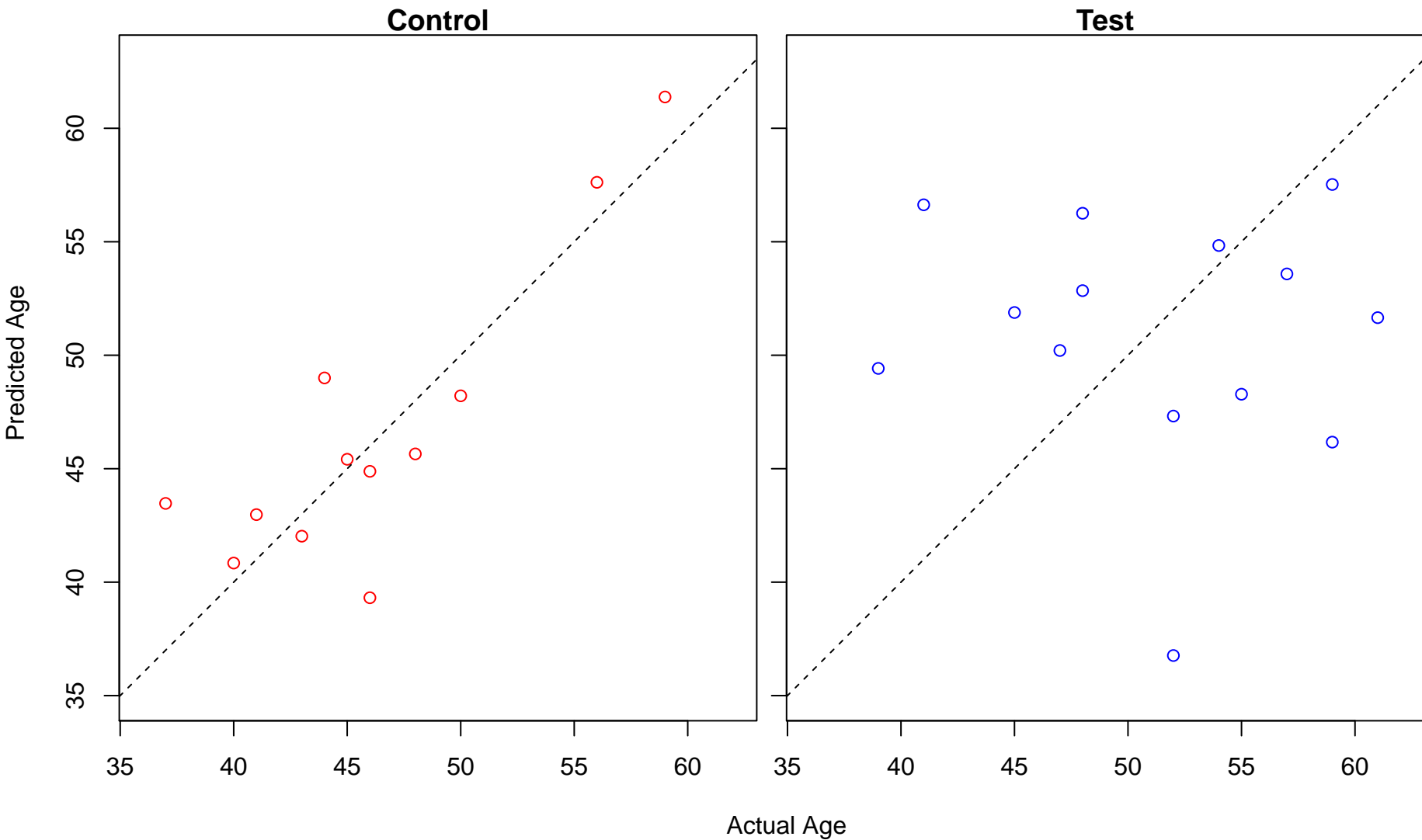
mitochondrion disassembly (Score: 3.405542)



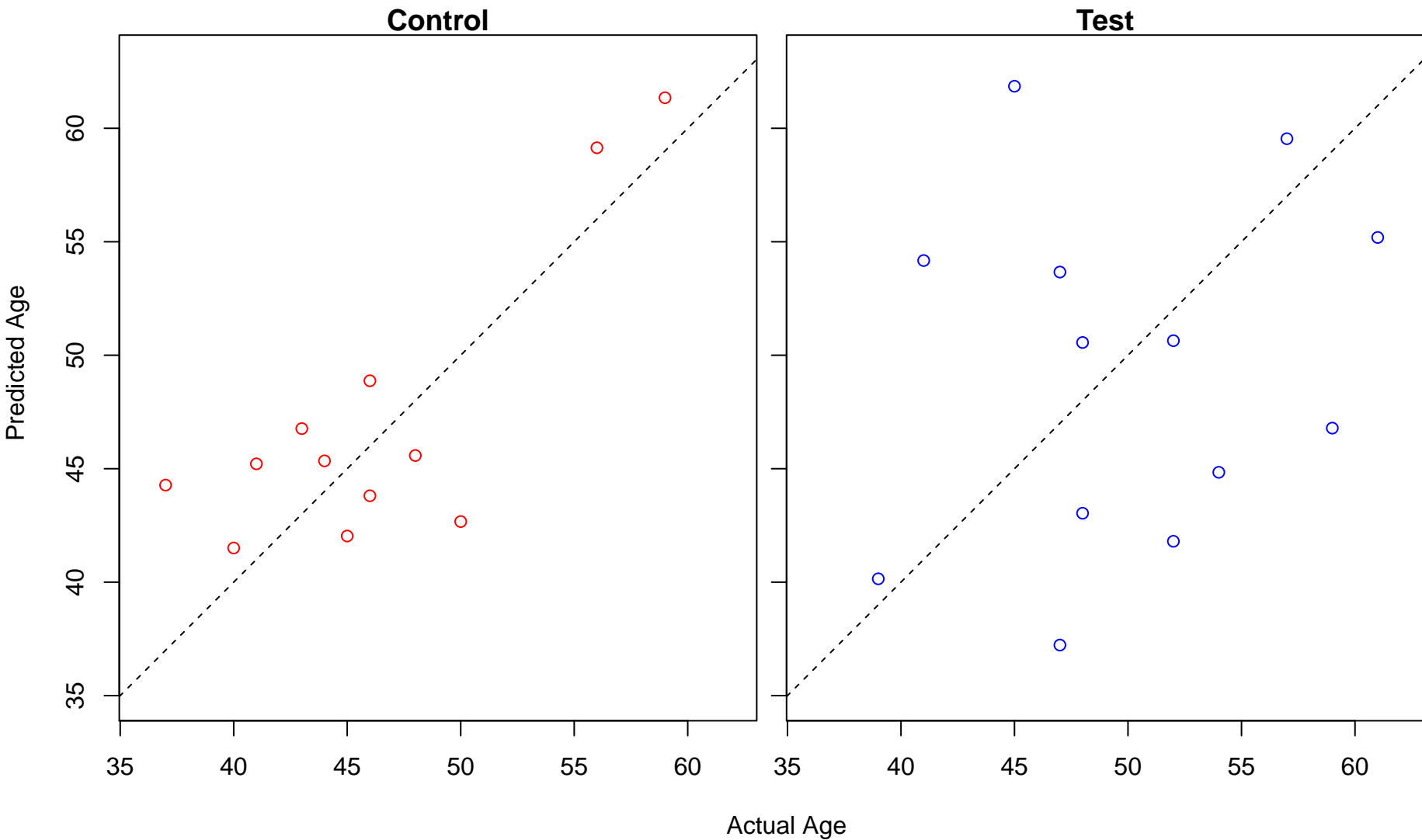
regulation of ubiquitin–protein ligase activity involved in mitotic cell cycle (Score: 3.404273)



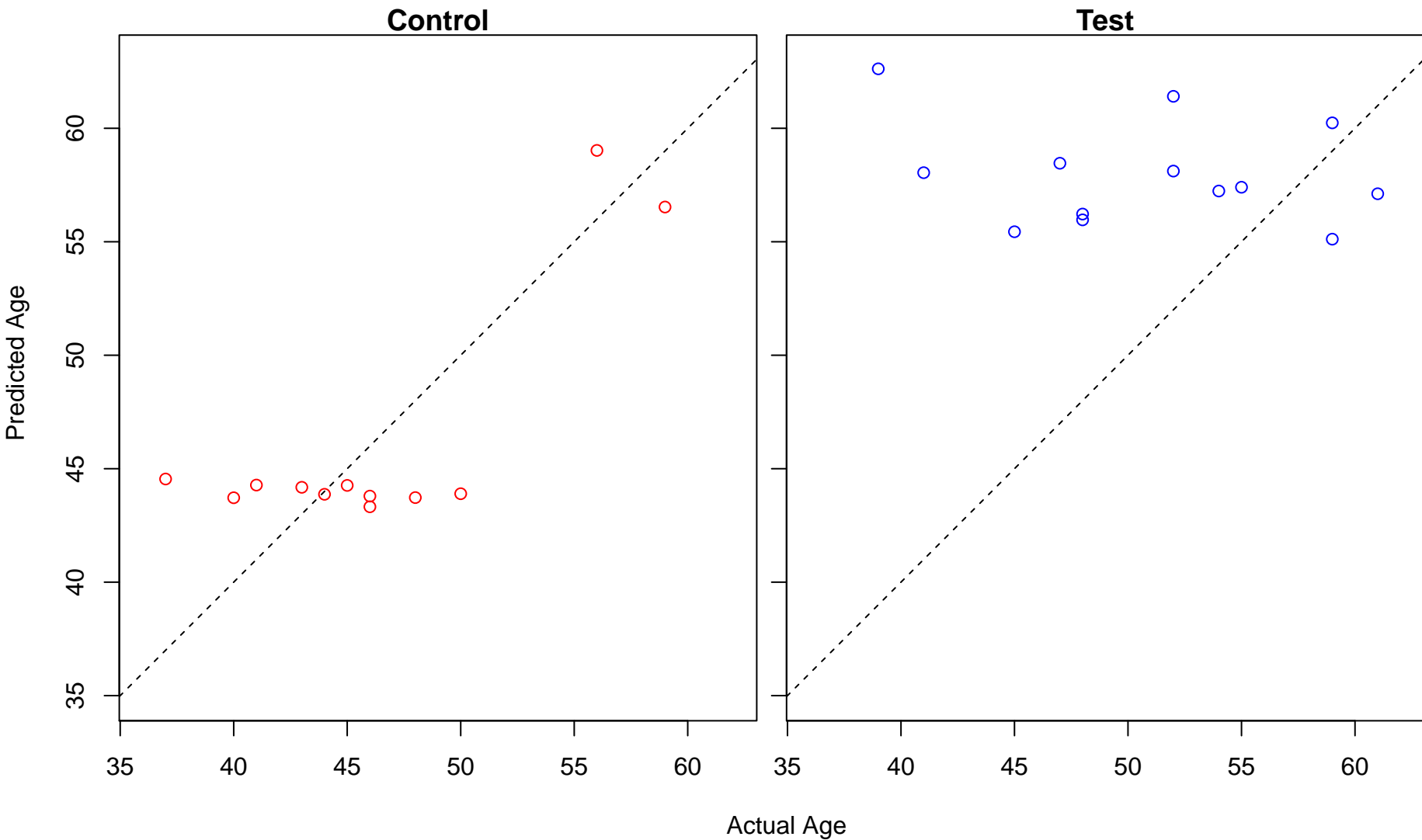
regulation of nitric-oxide synthase activity (Score: 3.404088)



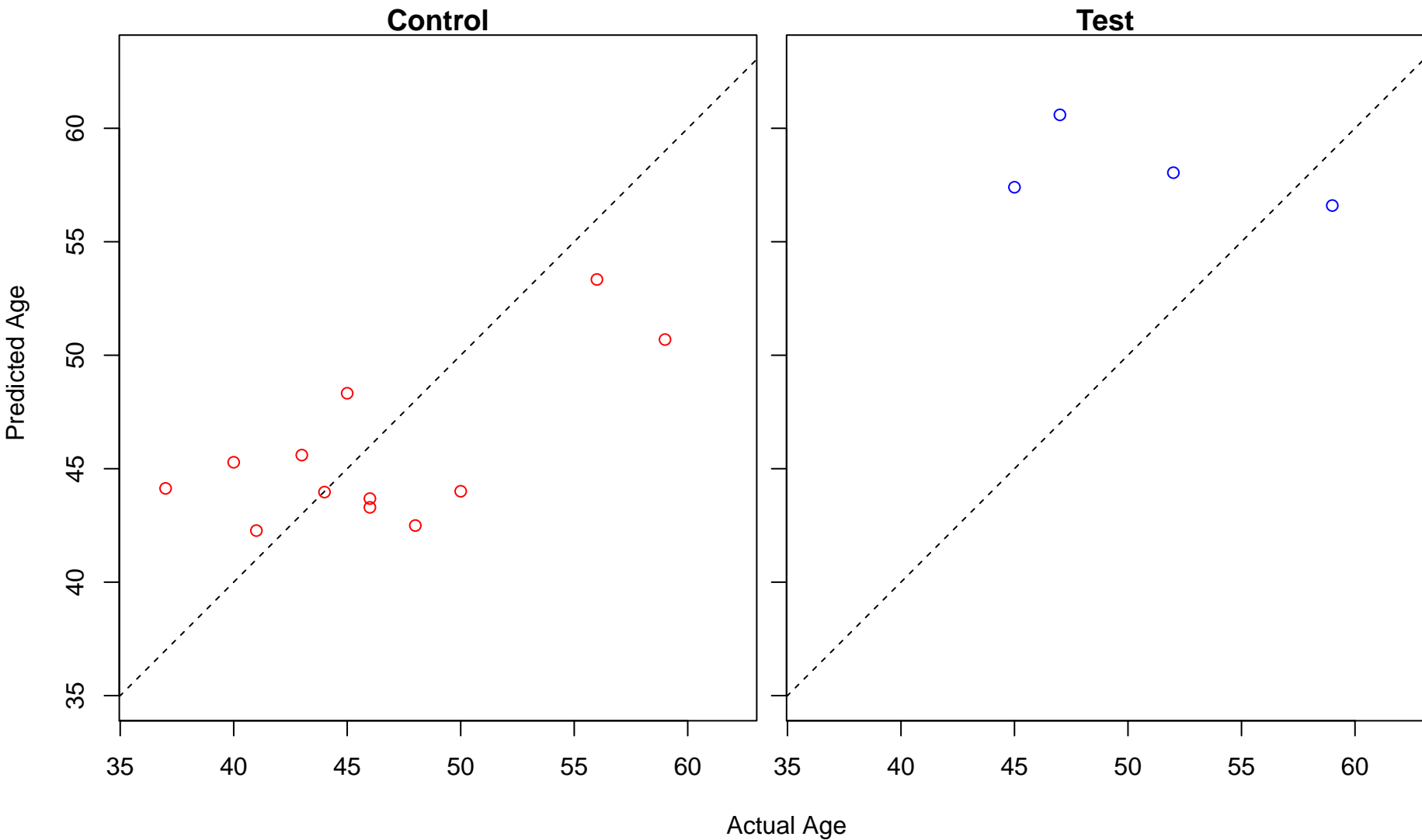
dephosphorylation (Score: 3.399578)



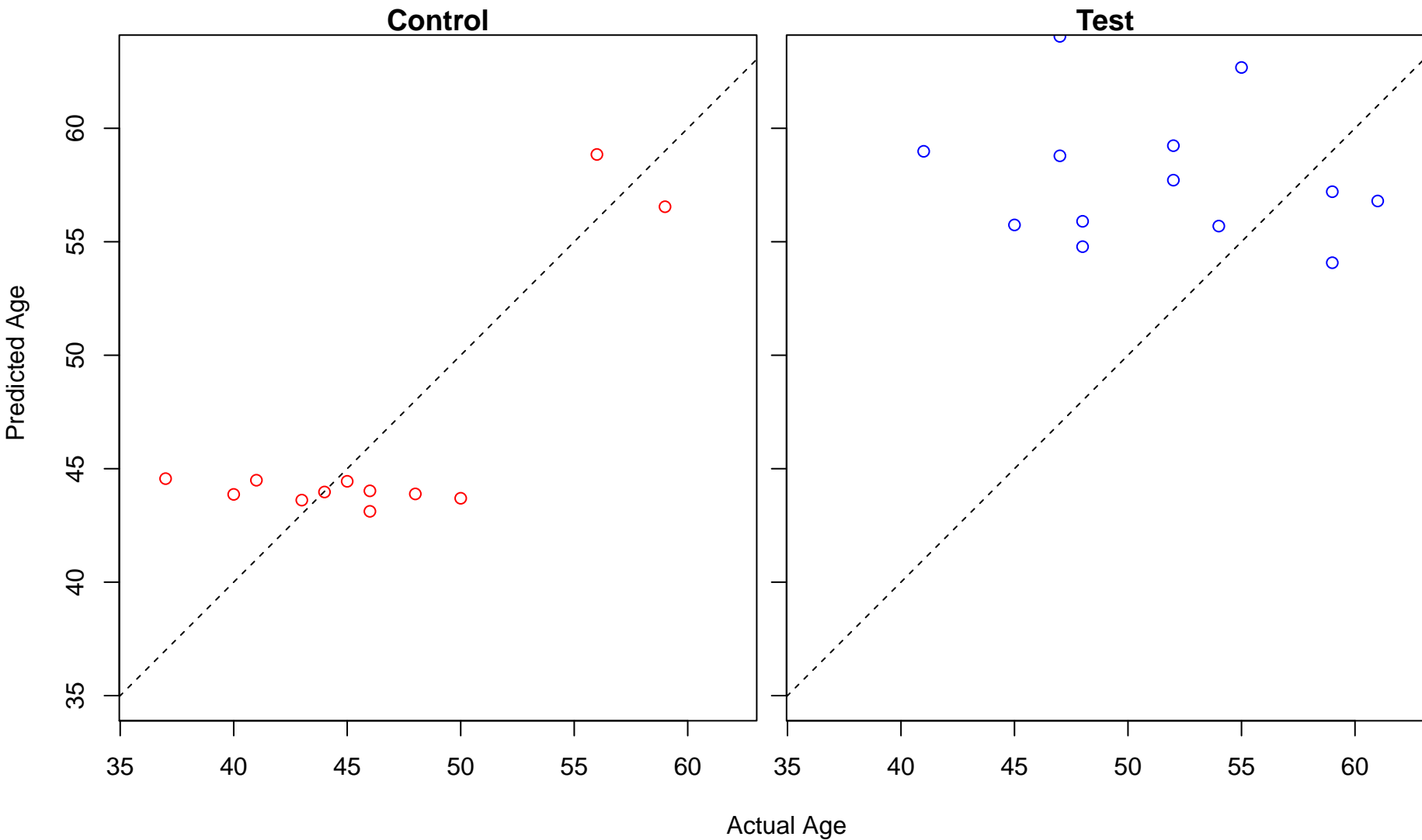
toll-like receptor signaling pathway (Score: 3.399547)



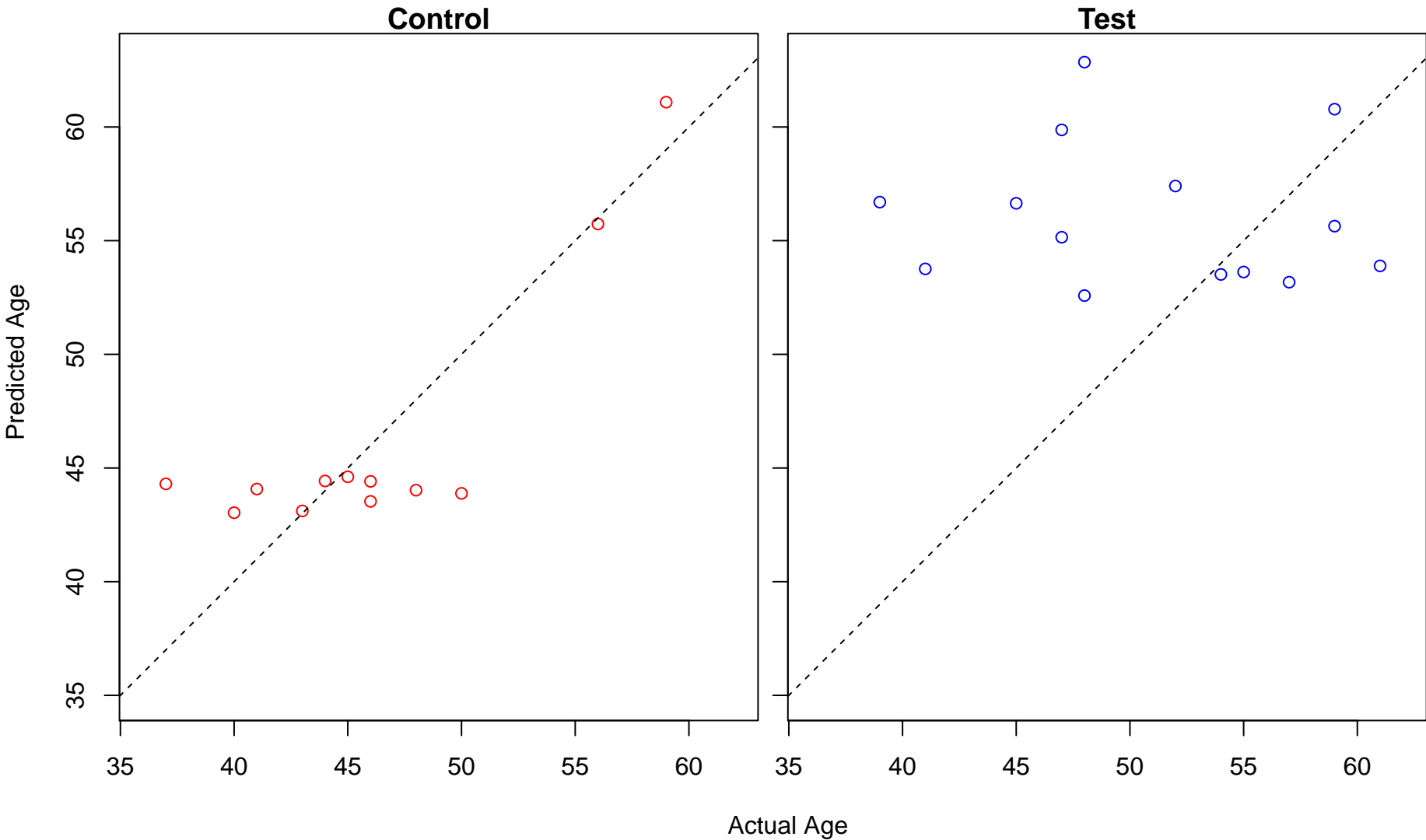
positive regulation of triglyceride lipase activity (Score: 3.399307)



regulation of cell division (Score: 3.397180)

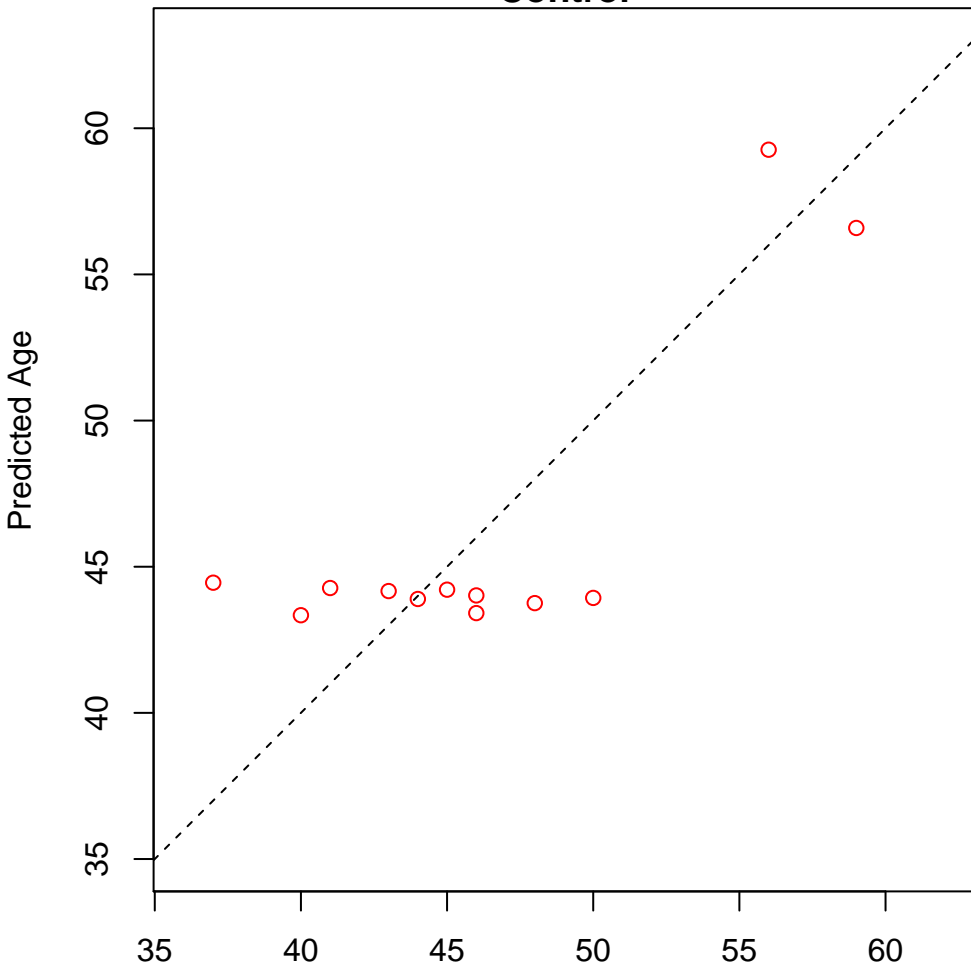


pyrimidine nucleotide biosynthetic process (Score: 3.395713)

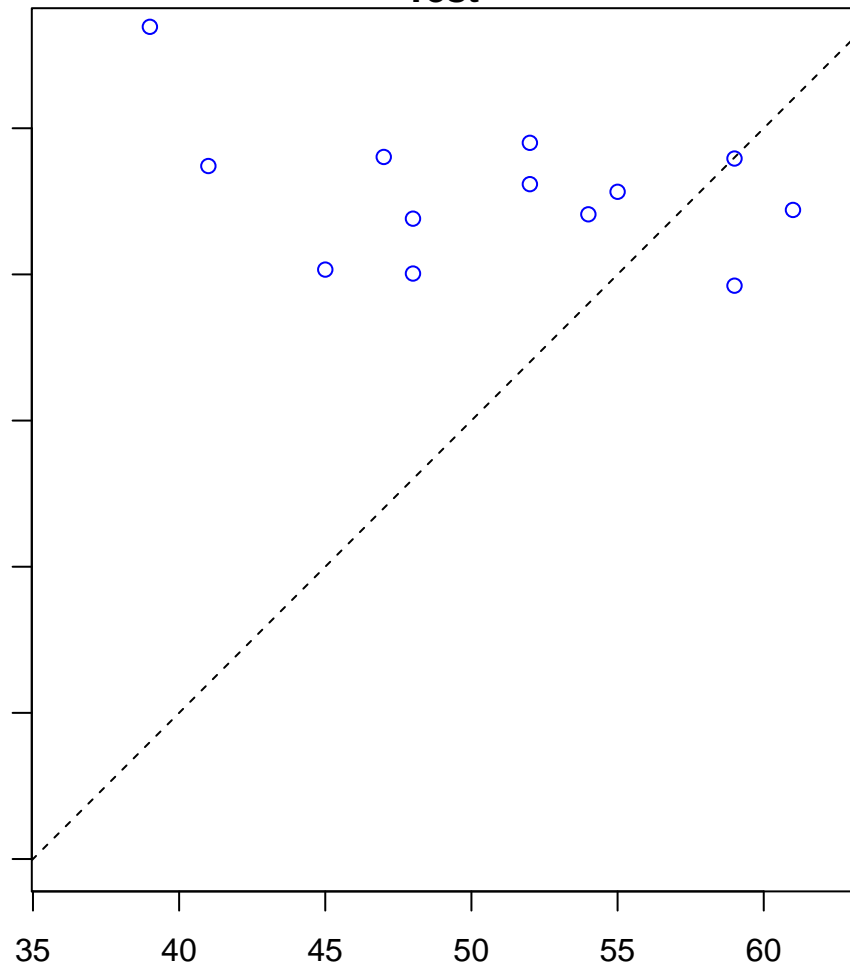


cellular carbohydrate metabolic process (Score: 3.393220)

Control

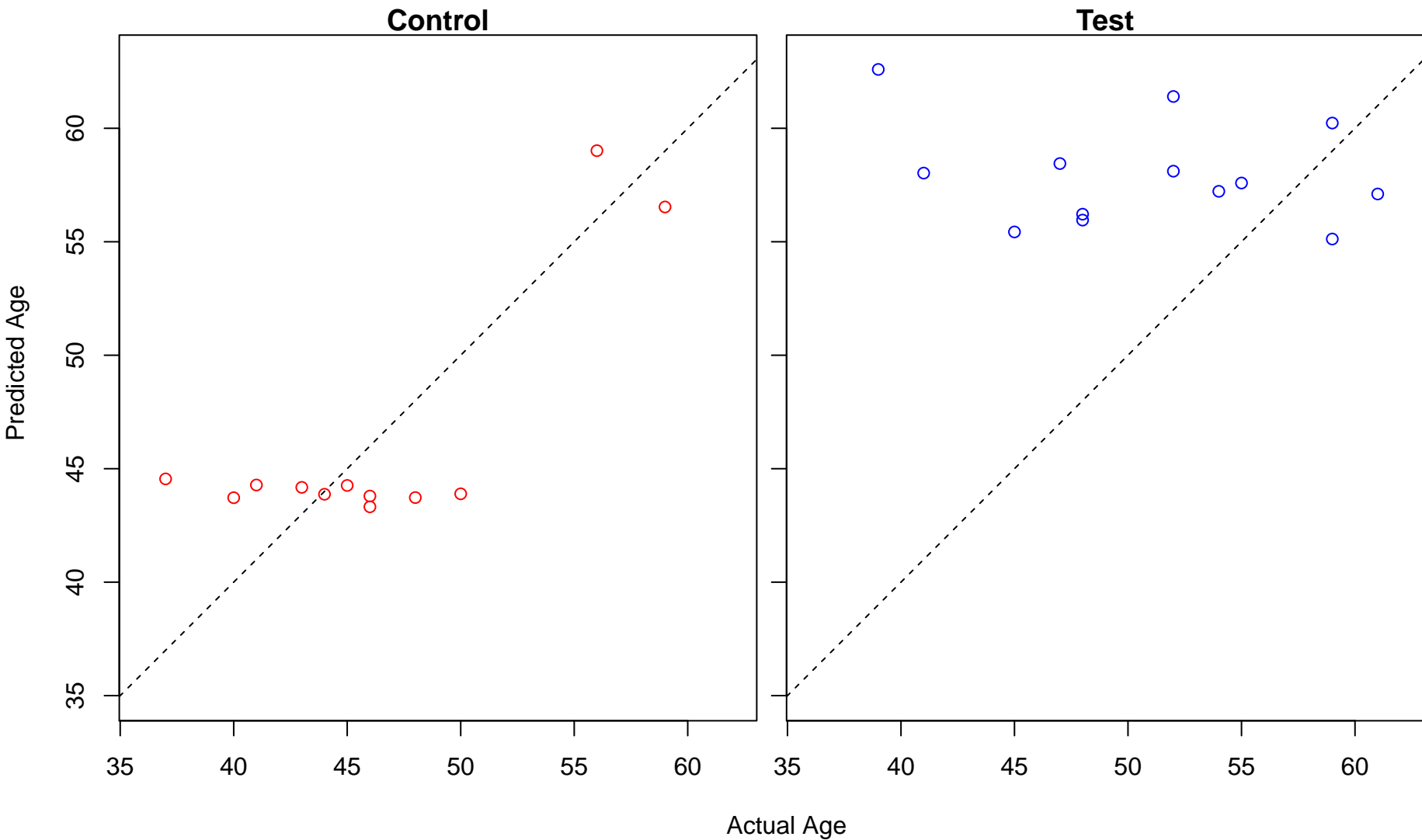


Test

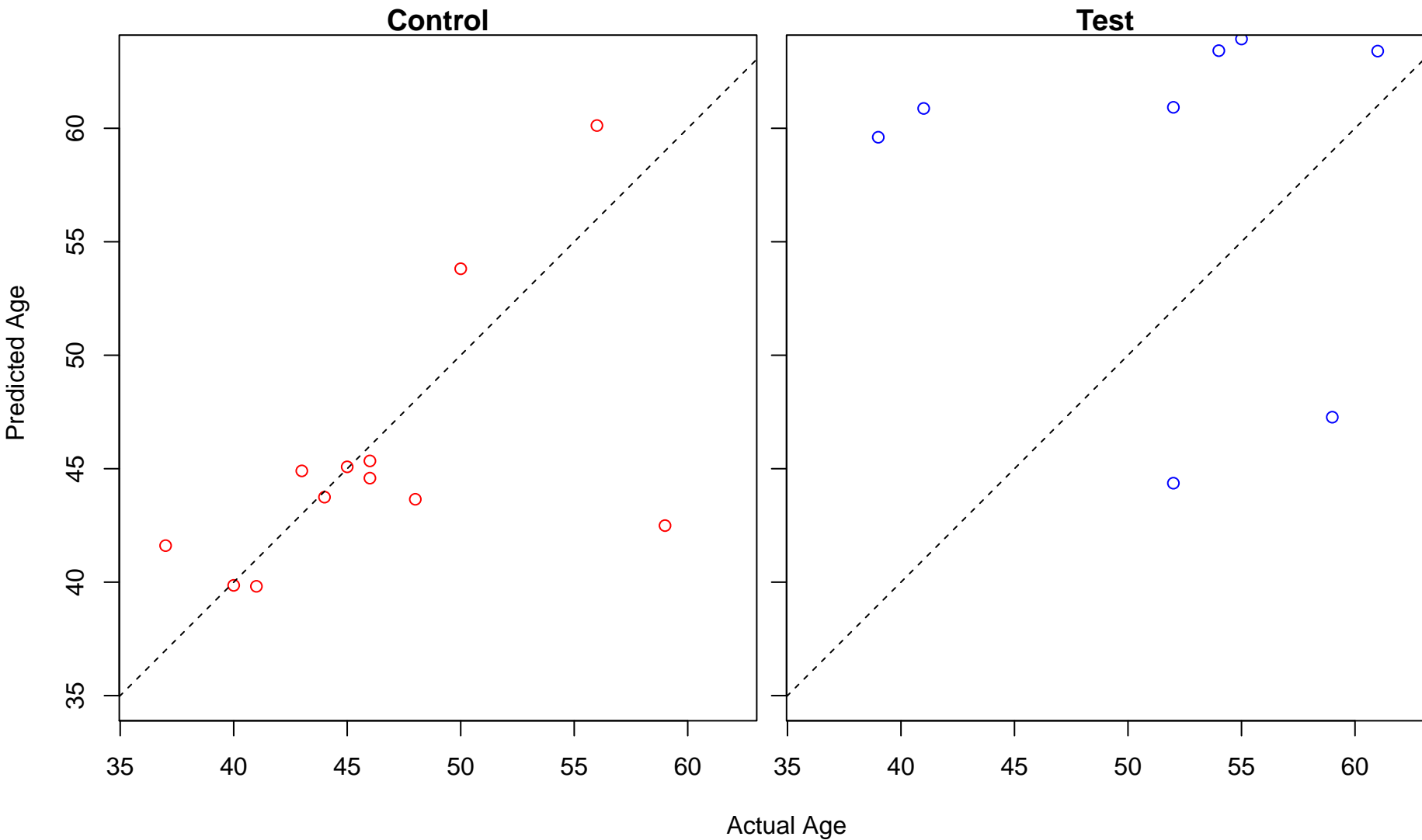


Actual Age

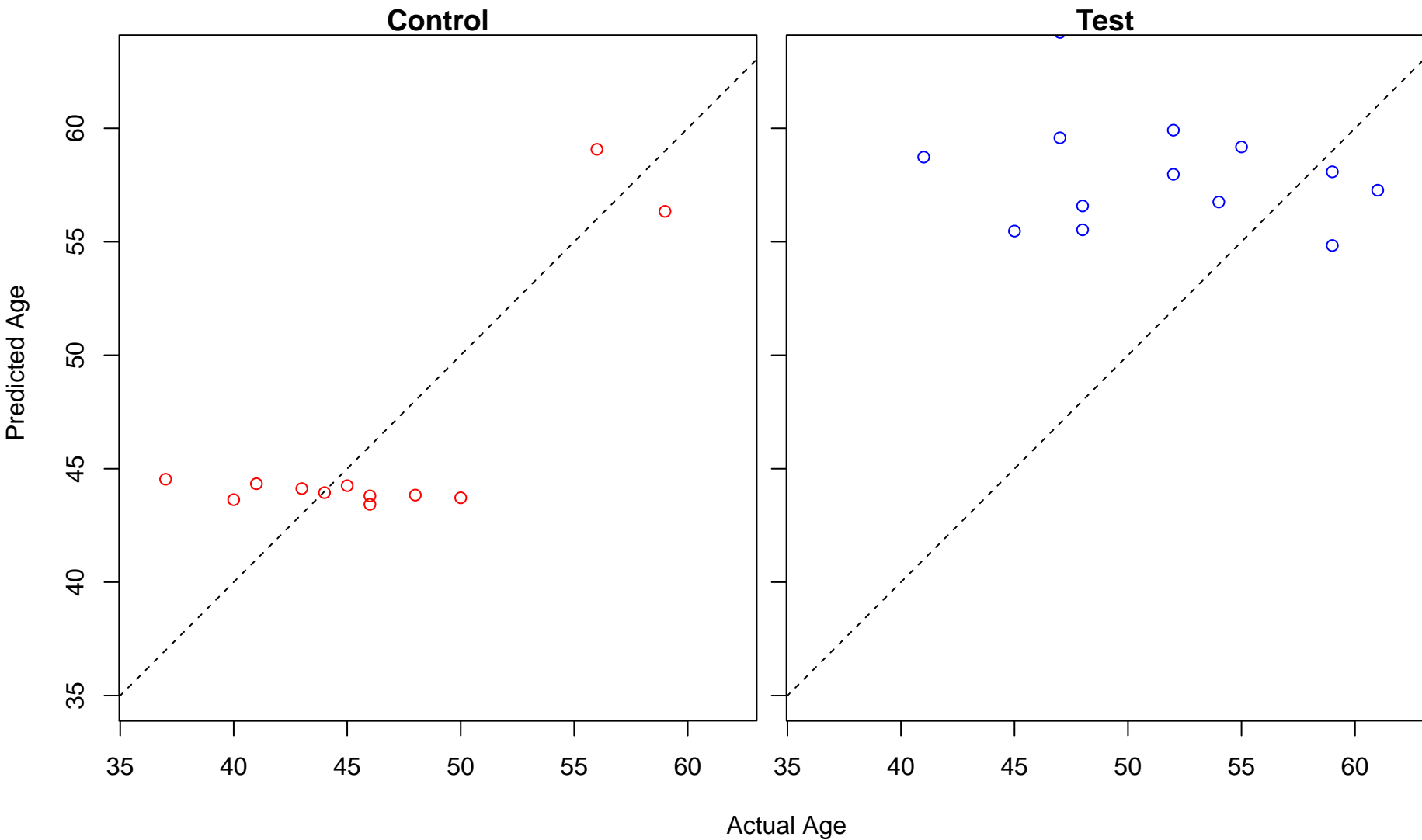
pattern recognition receptor signaling pathway (Score: 3.393079)



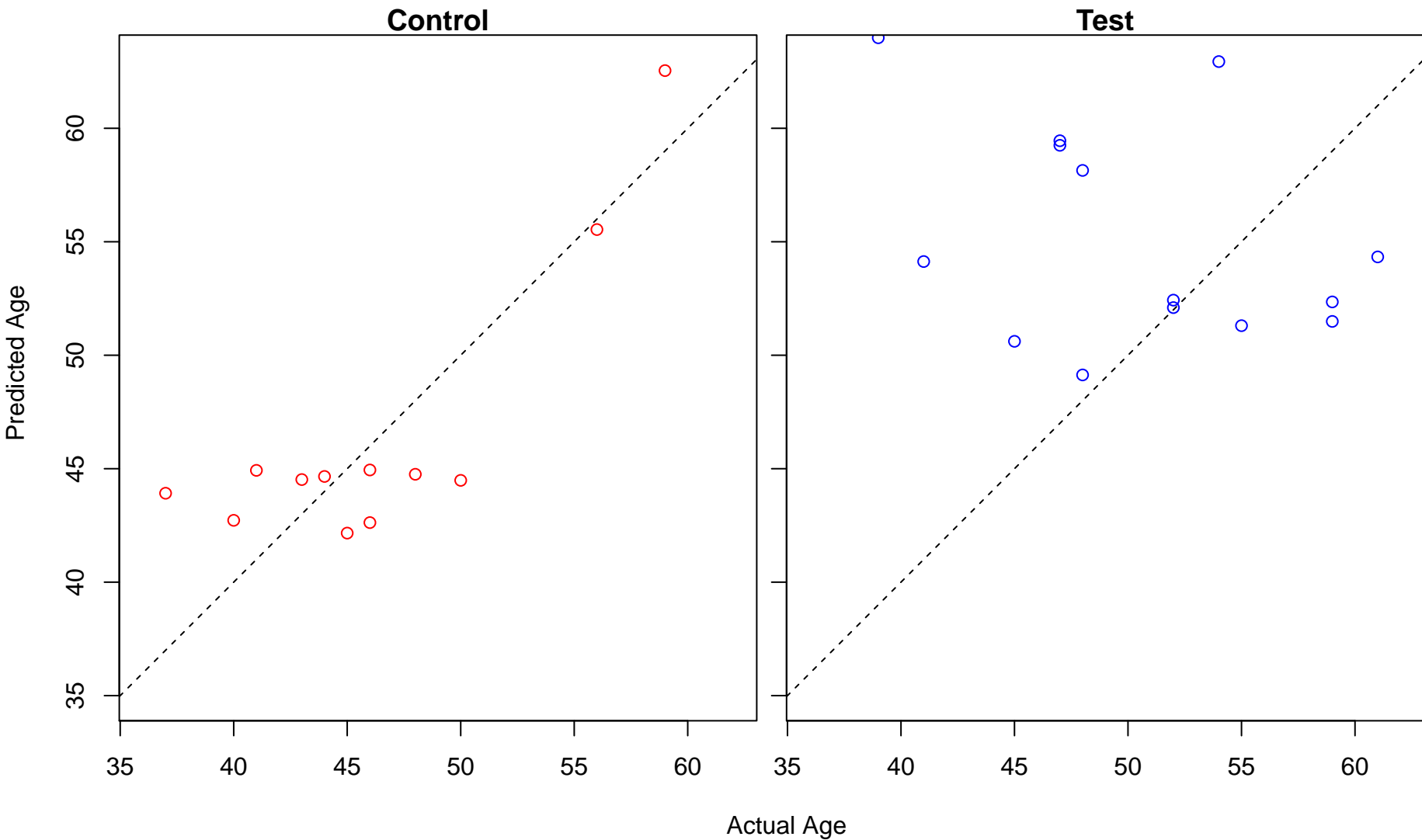
patterning of blood vessels (Score: 3.390225)



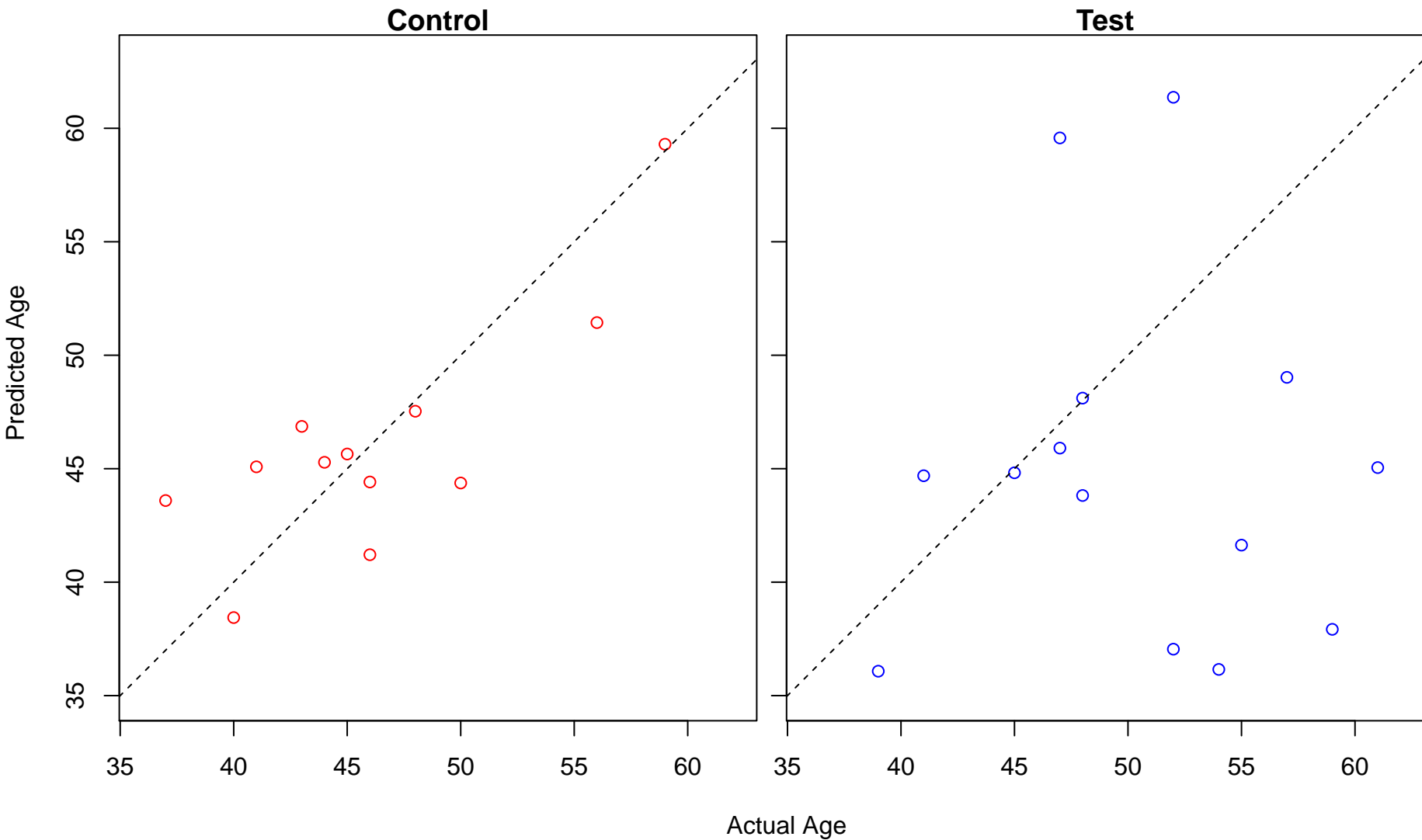
epidermal growth factor receptor signaling pathway (Score: 3.389099)



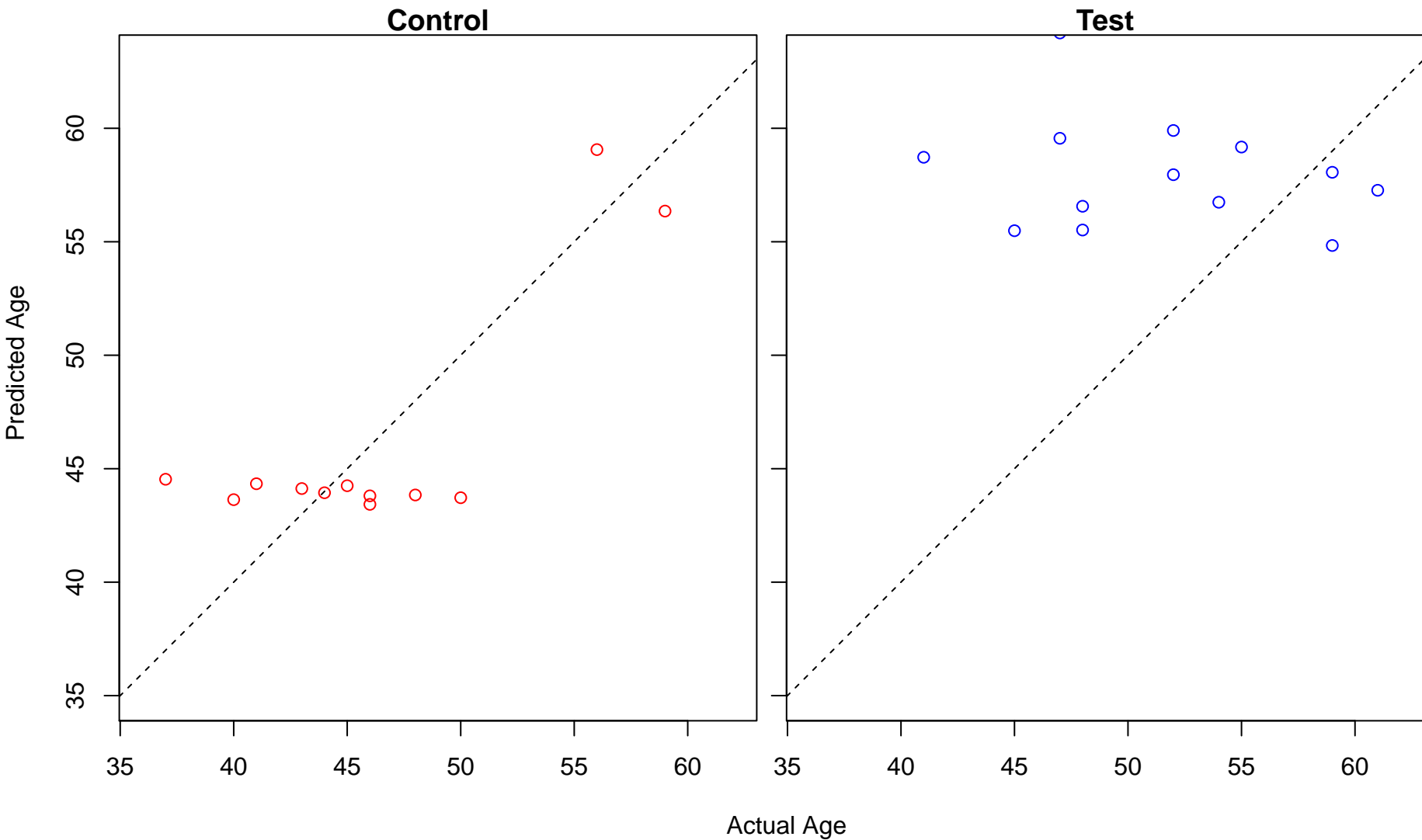
muscle system process (Score: 3.388363)



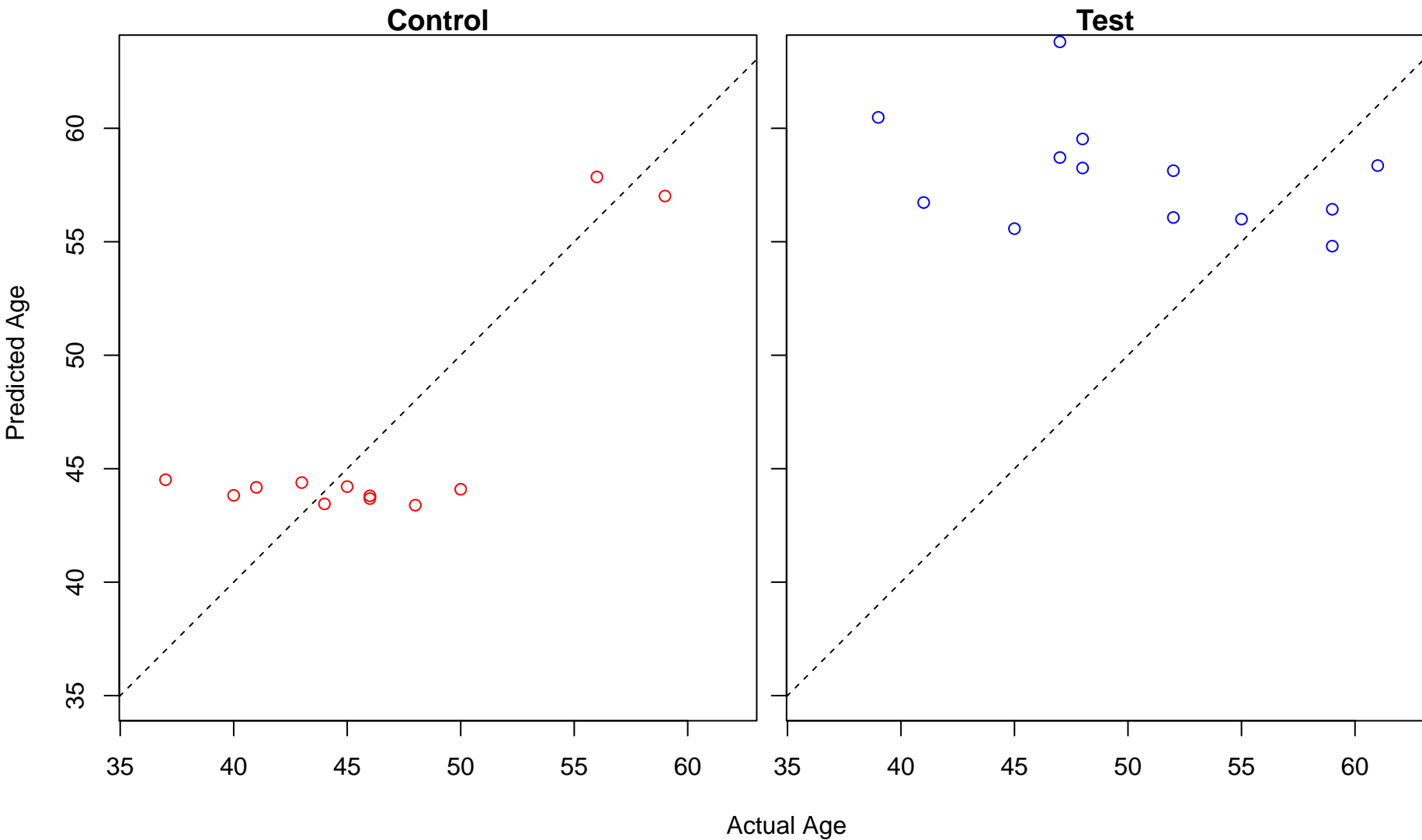
viral life cycle (Score: 3.387676)



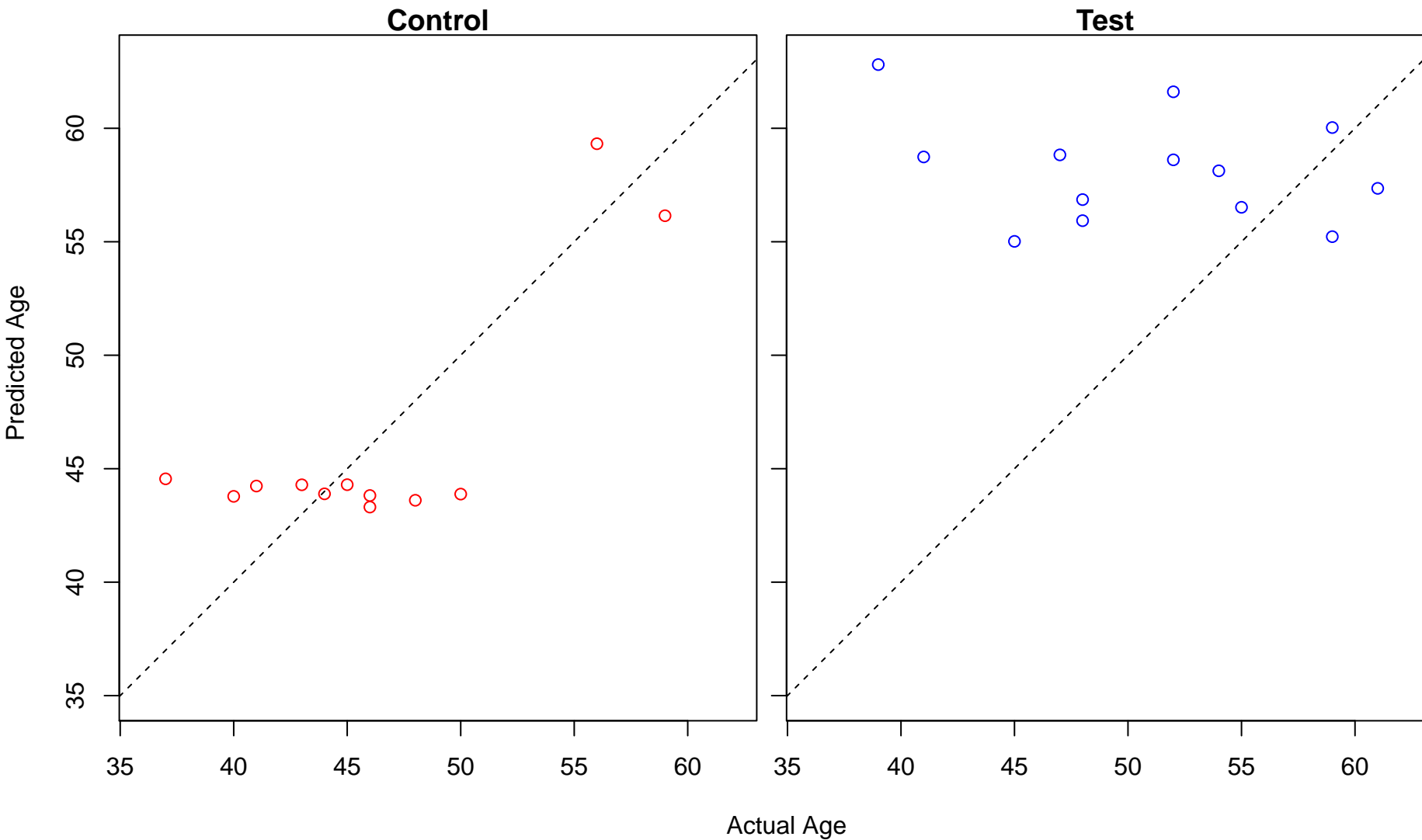
ERBB signaling pathway (Score: 3.385174)



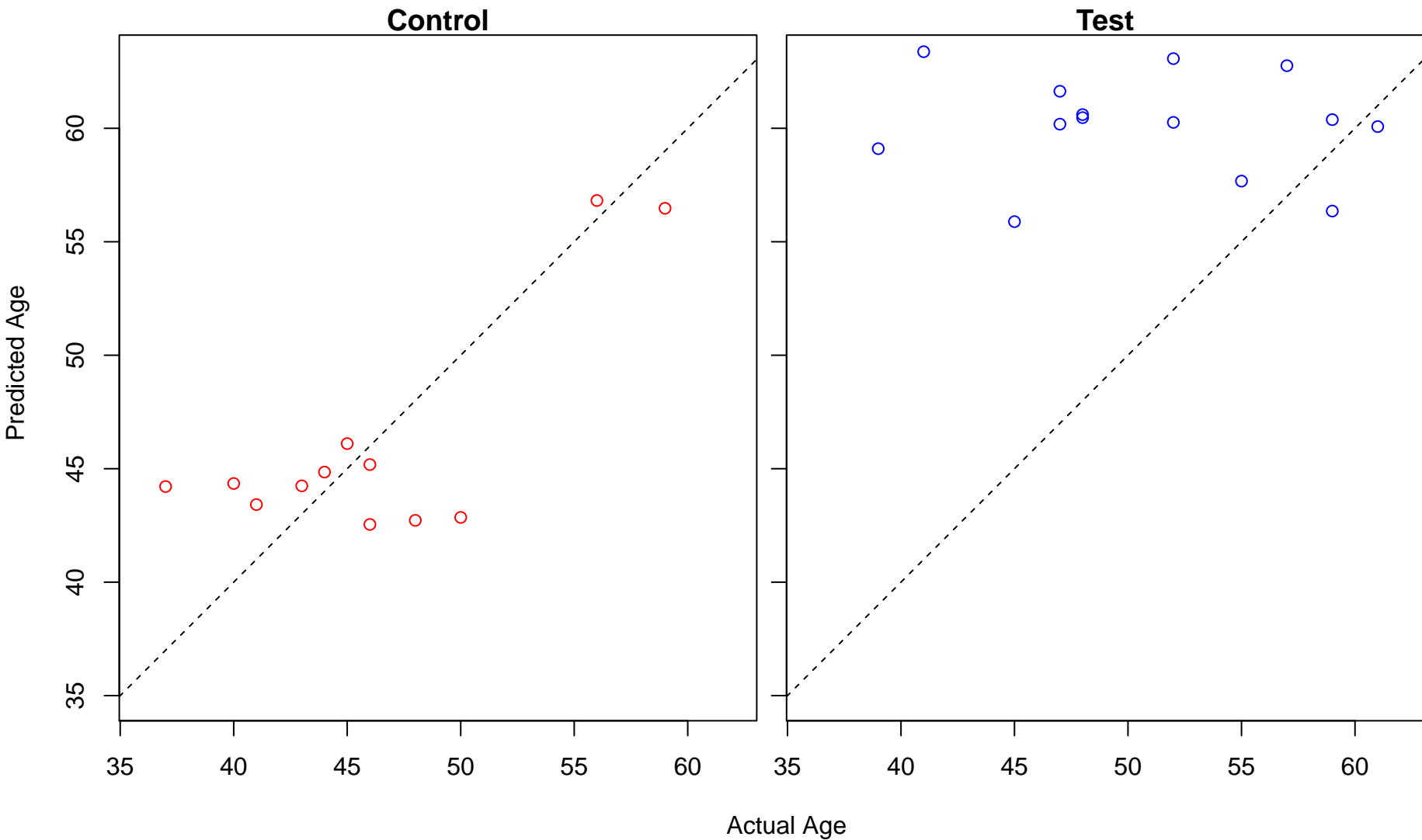
membrane protein proteolysis (Score: 3.385022)



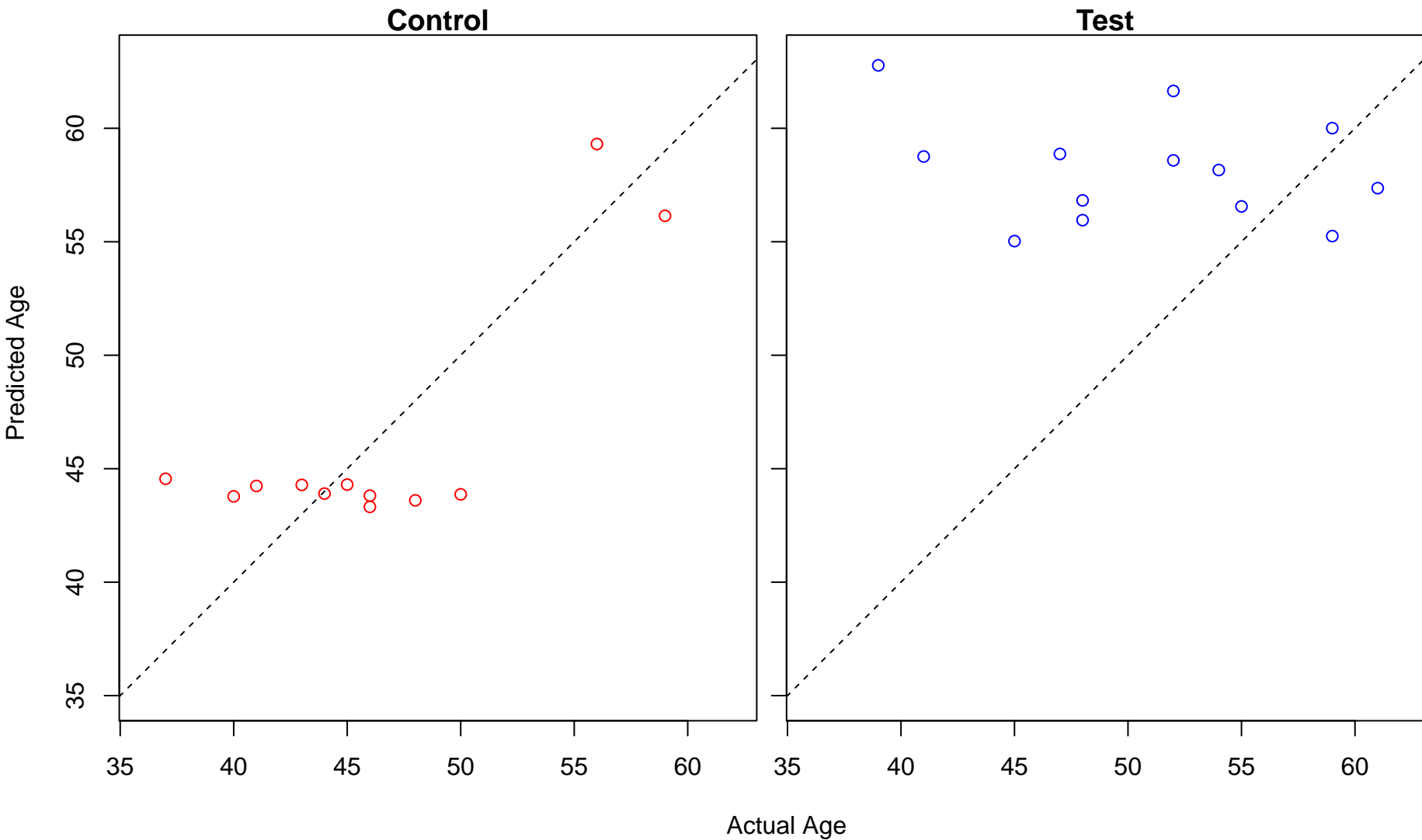
mitotic cell cycle checkpoint (Score: 3.384278)



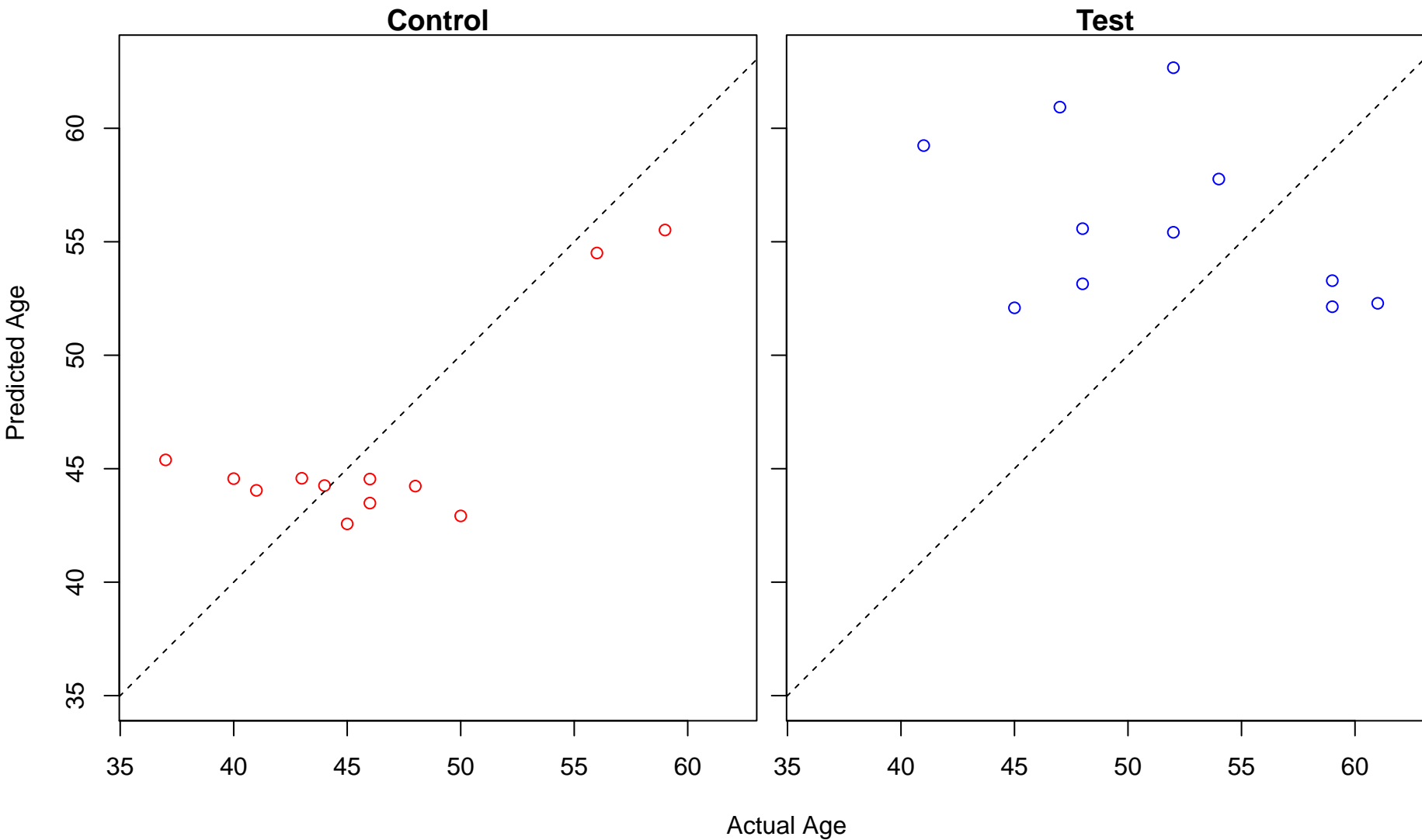
positive regulation of cell aging (Score: 3.383872)



negative regulation of mitotic cell cycle phase transition (Score: 3.381266)

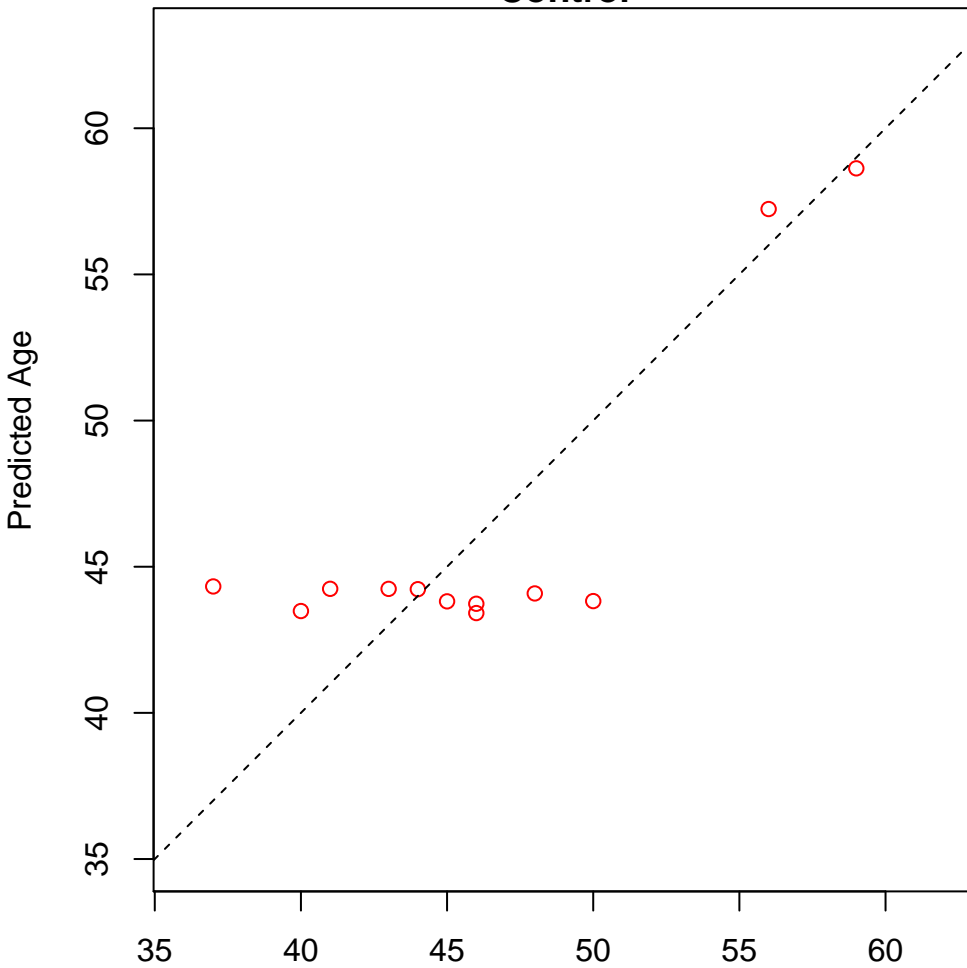


homotypic cell-cell adhesion (Score: 3.379998)

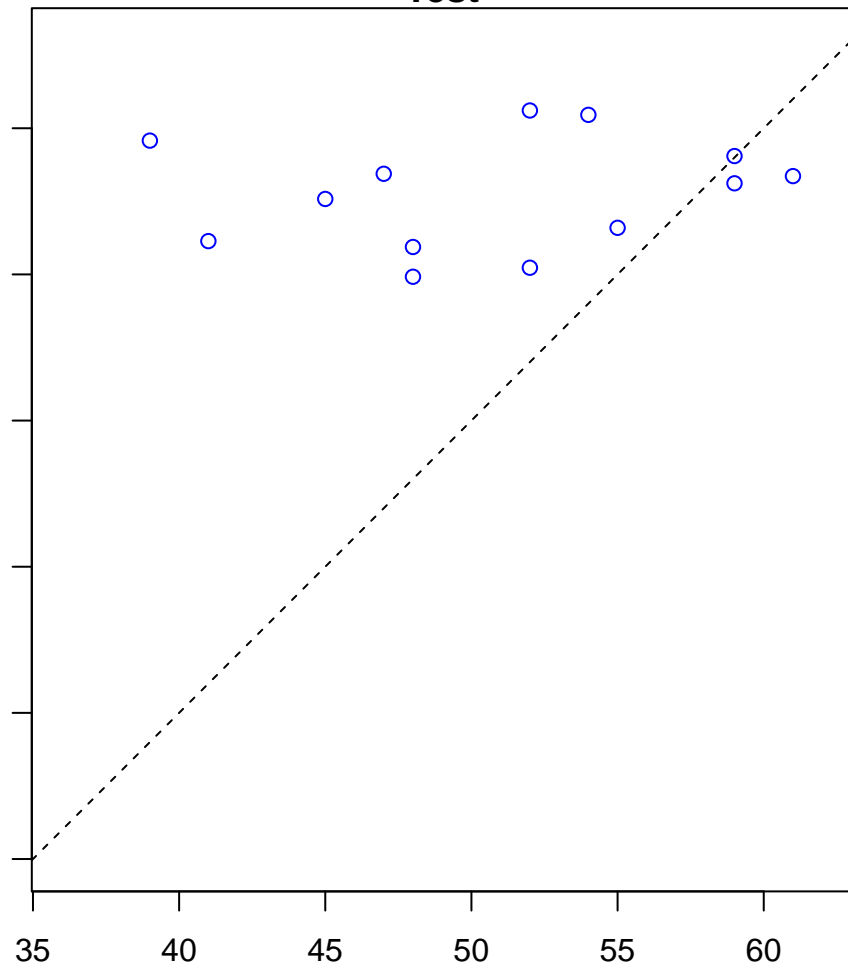


regulation of membrane permeability (Score: 3.378695)

Control



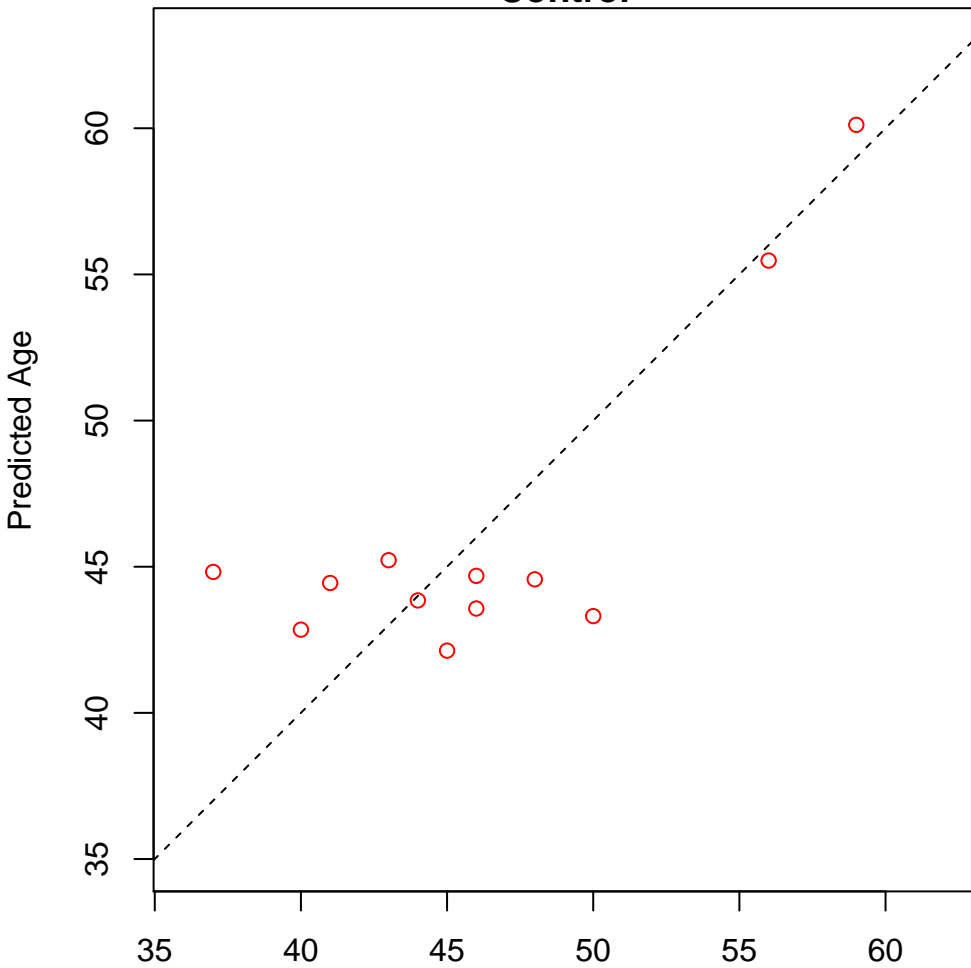
Test



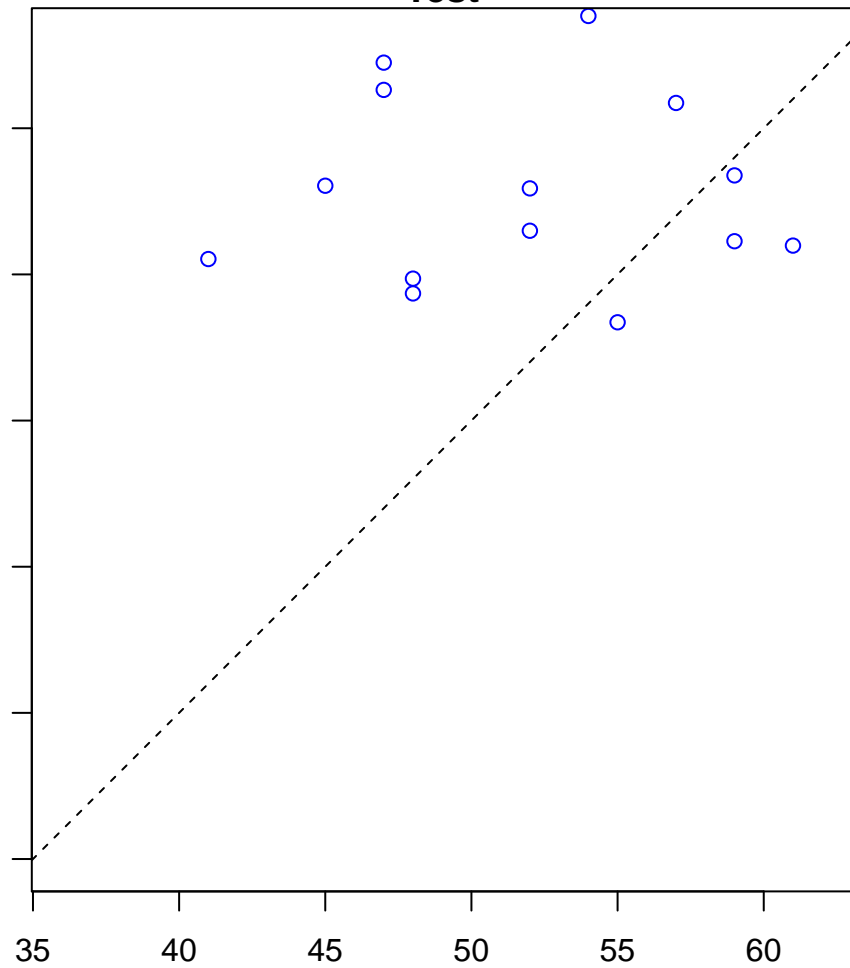
Actual Age

regulation of neurotransmitter secretion (Score: 3.378515)

Control

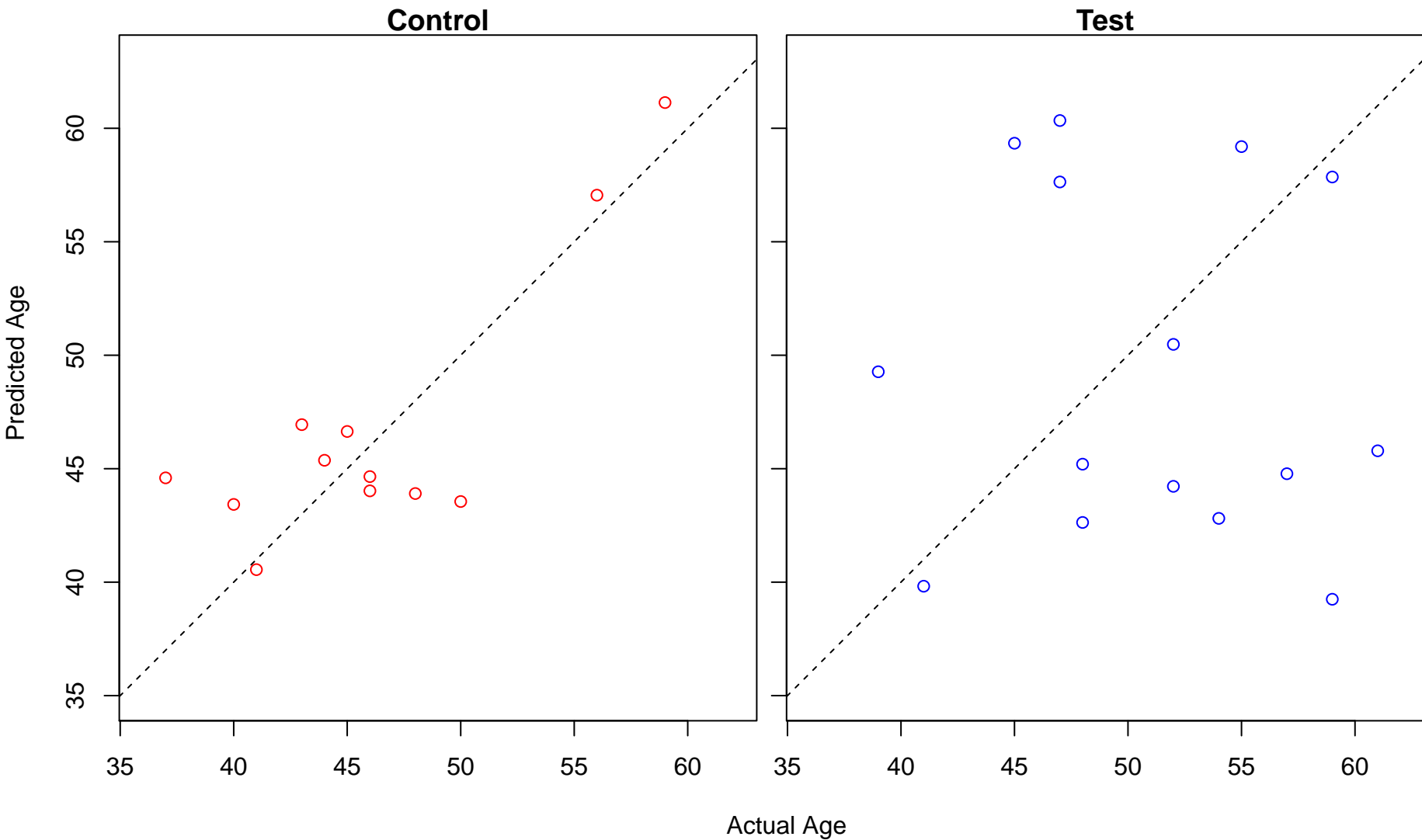


Test

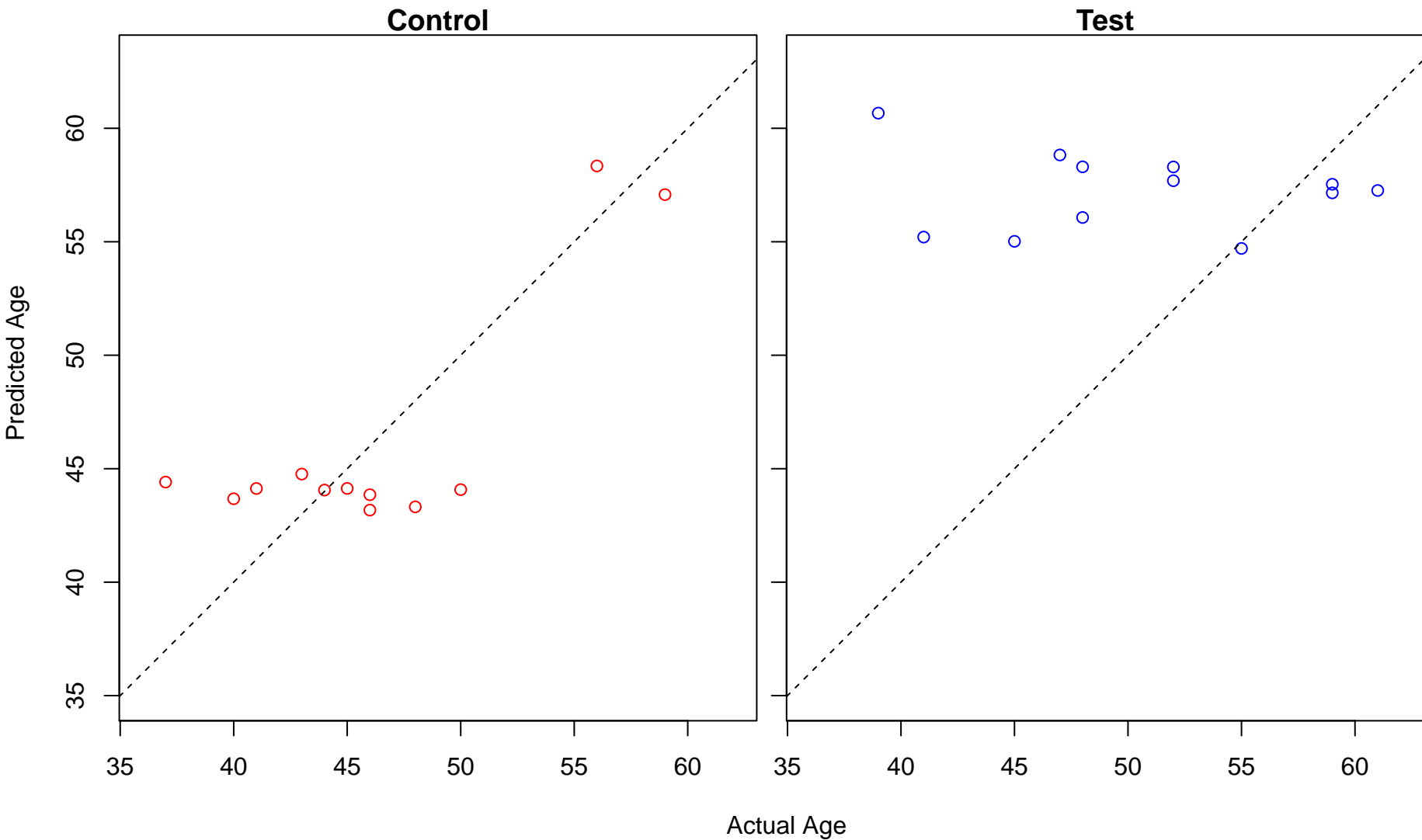


Actual Age

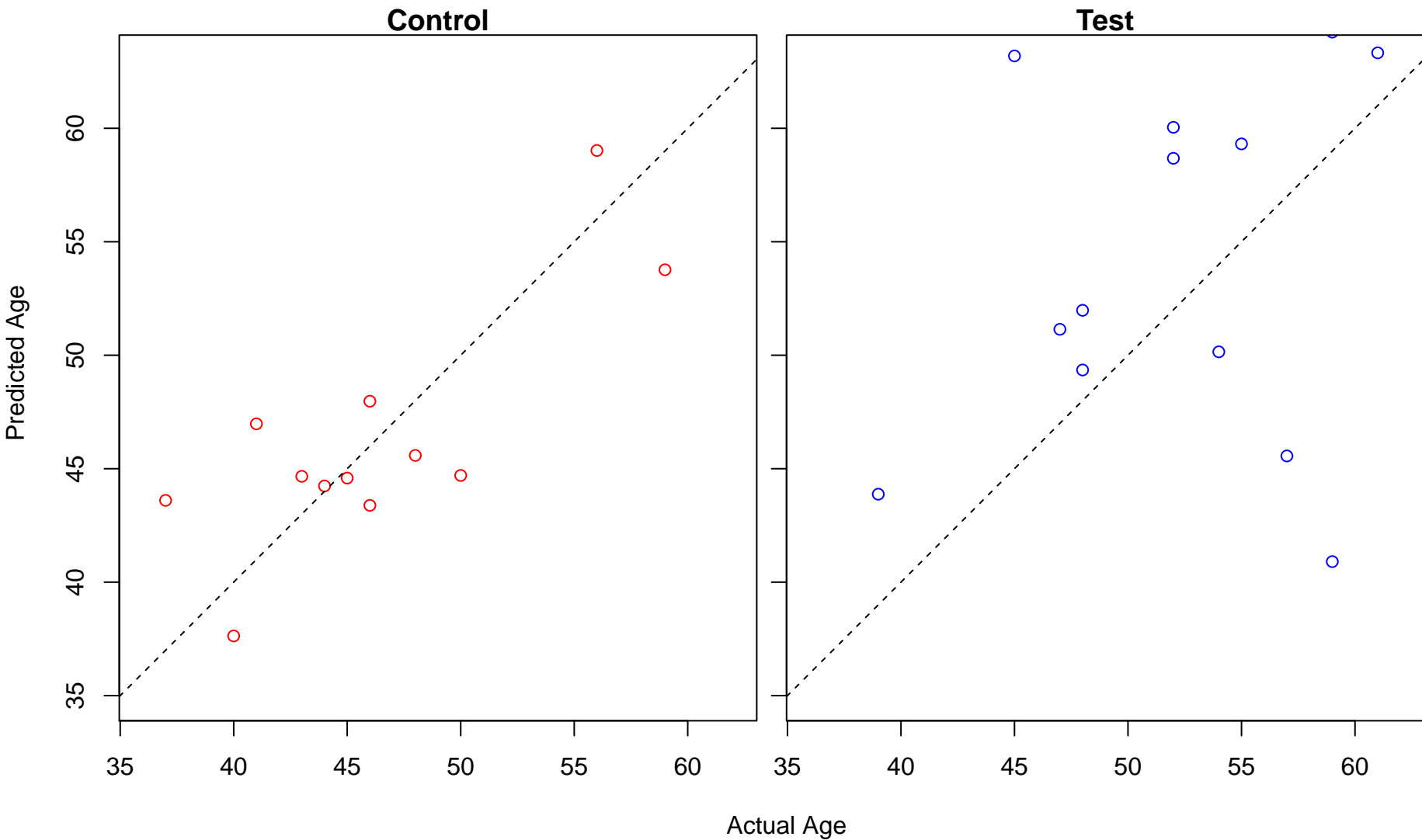
positive regulation of DNA-templated transcription, elongation (Score: 3.378346)



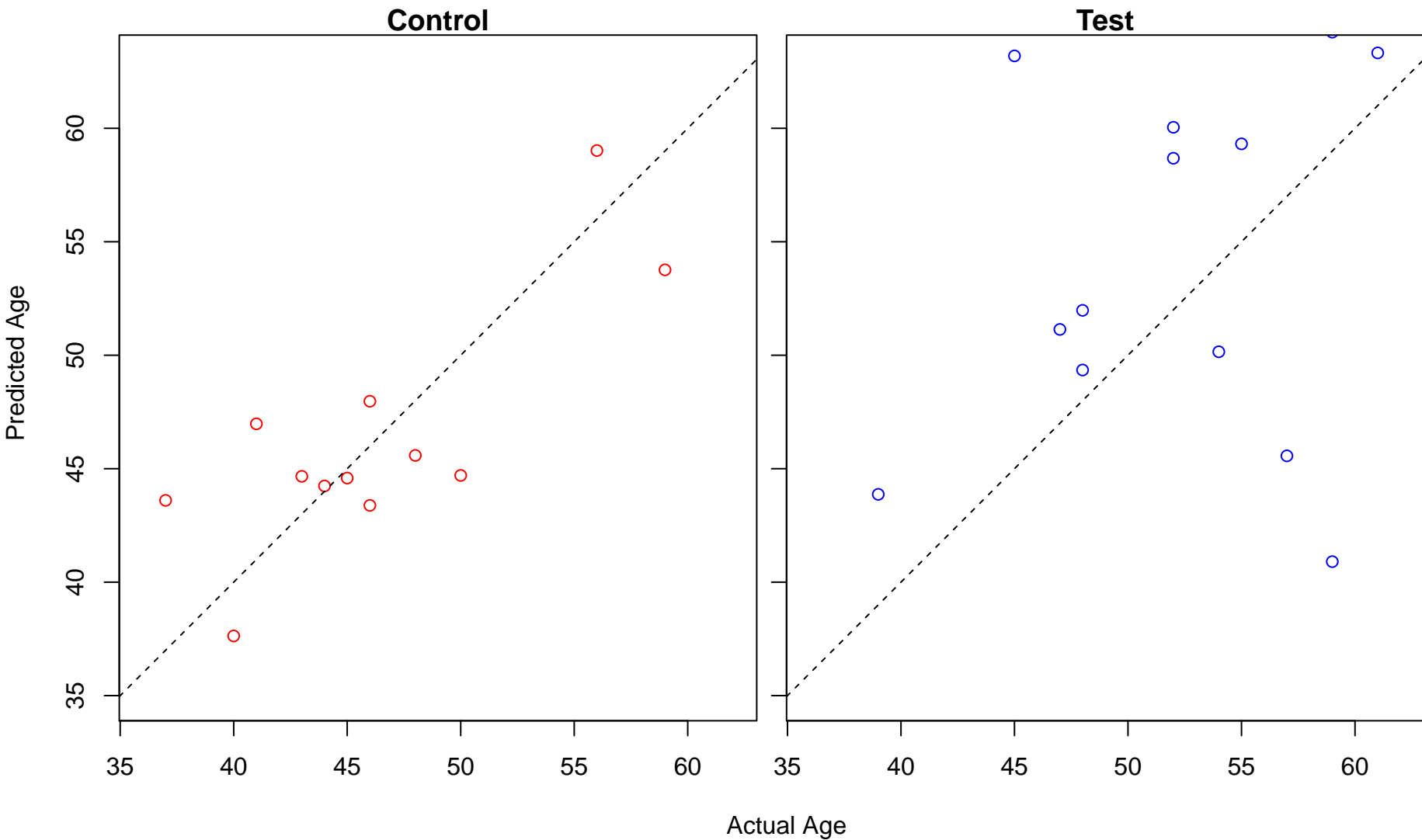
protein destabilization (Score: 3.378273)



negative regulation of lymphocyte activation (Score: 3.377719)

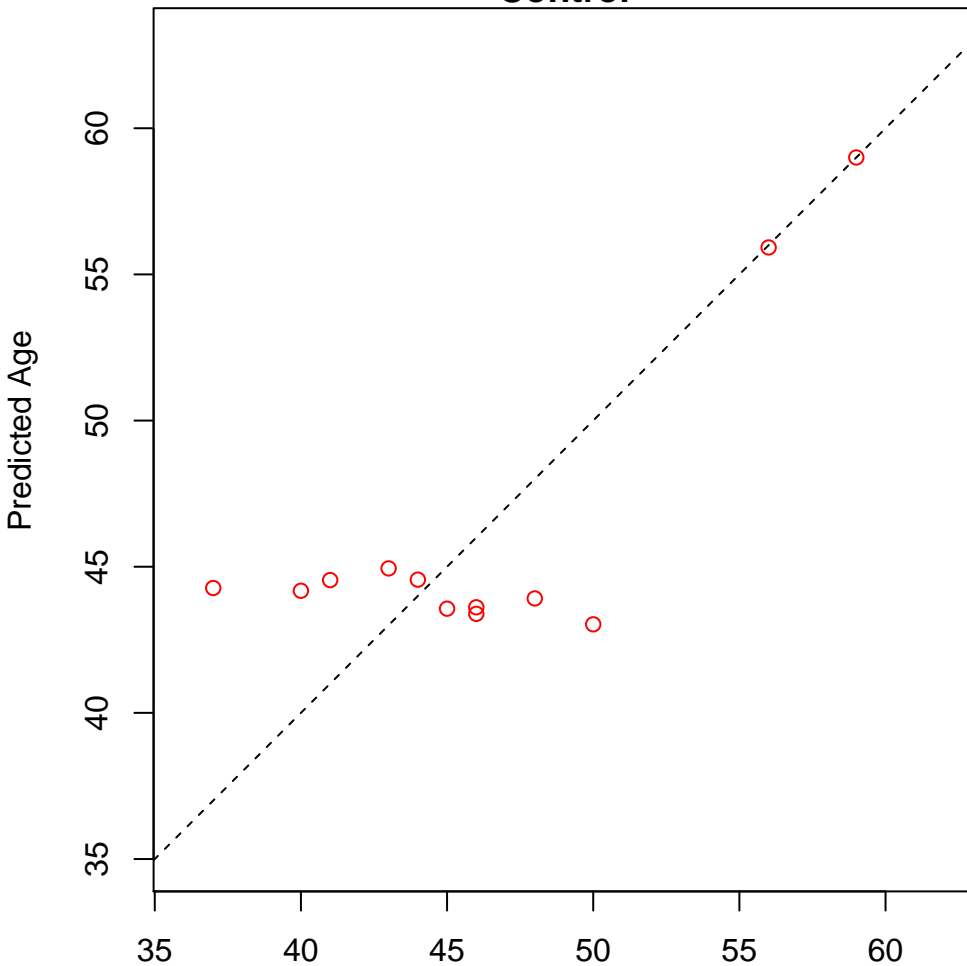


negative regulation of leukocyte activation (Score: 3.377387)

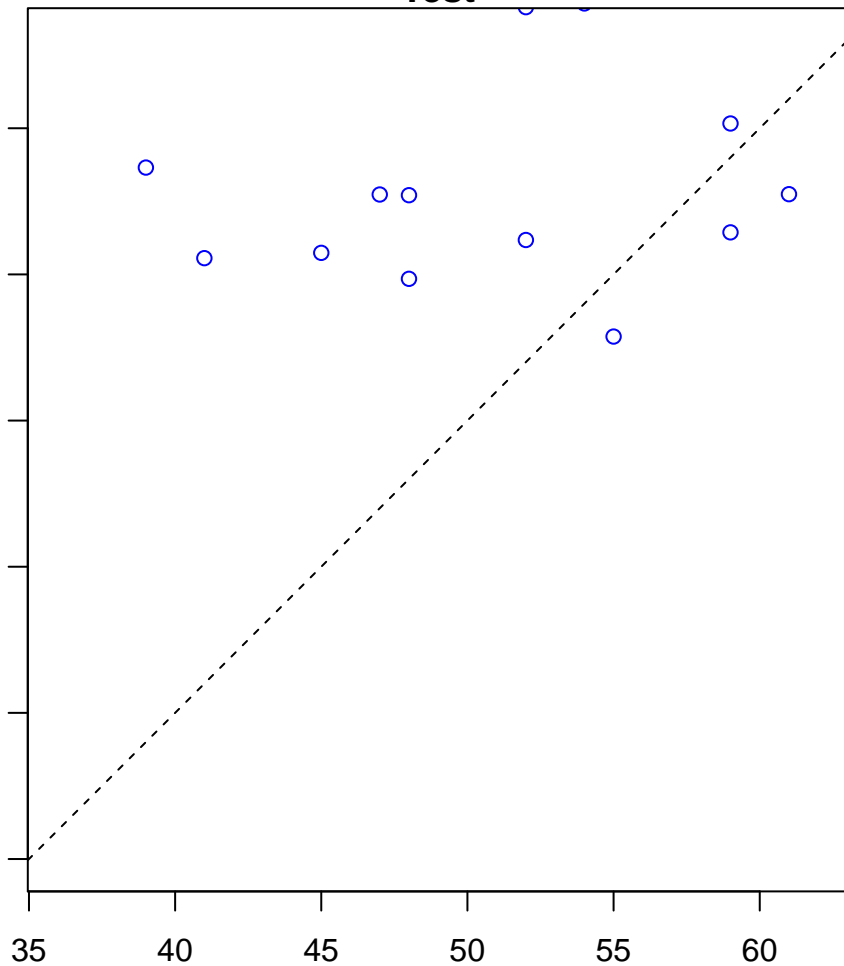


regulation of oxidative phosphorylation (Score: 3.372592)

Control

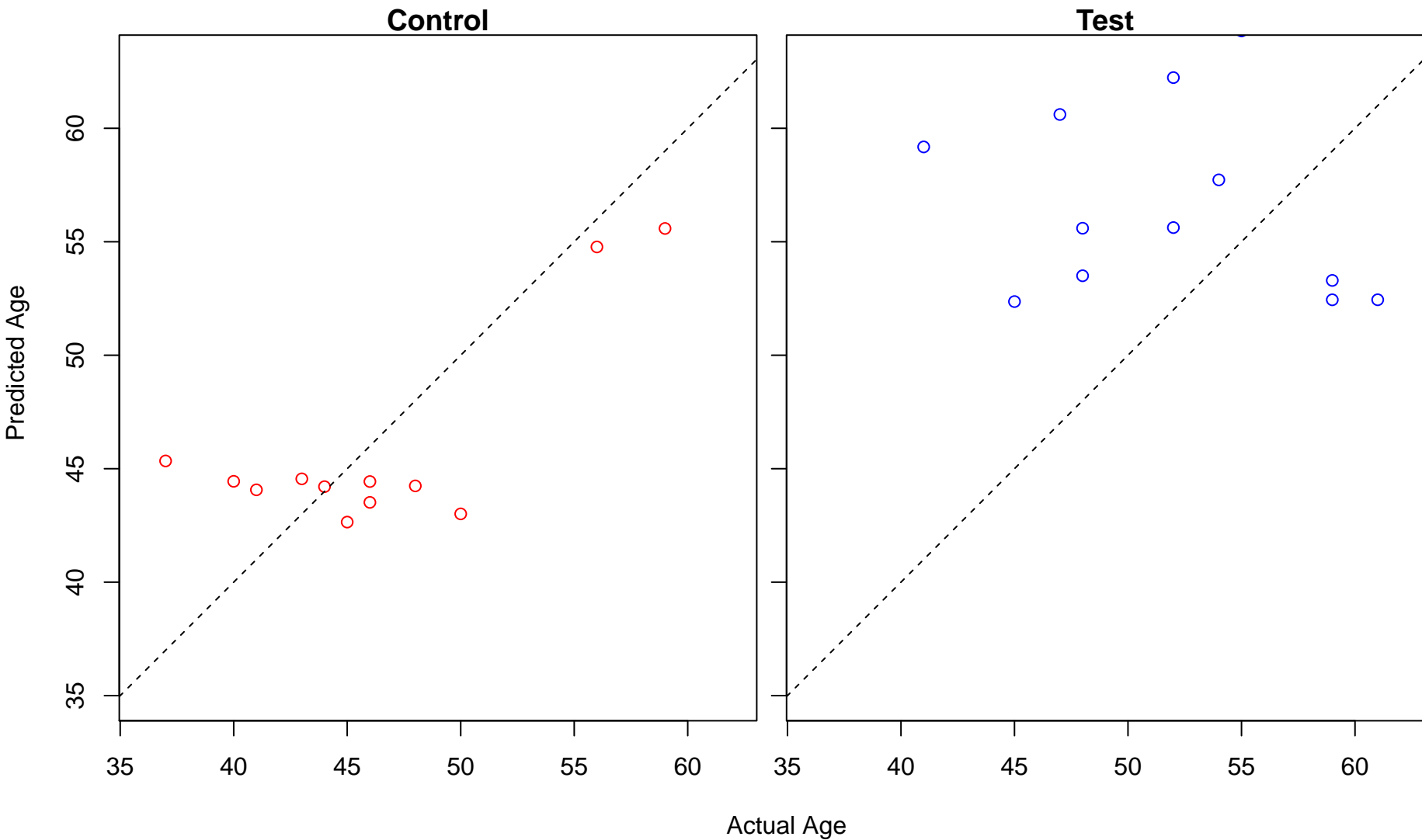


Test

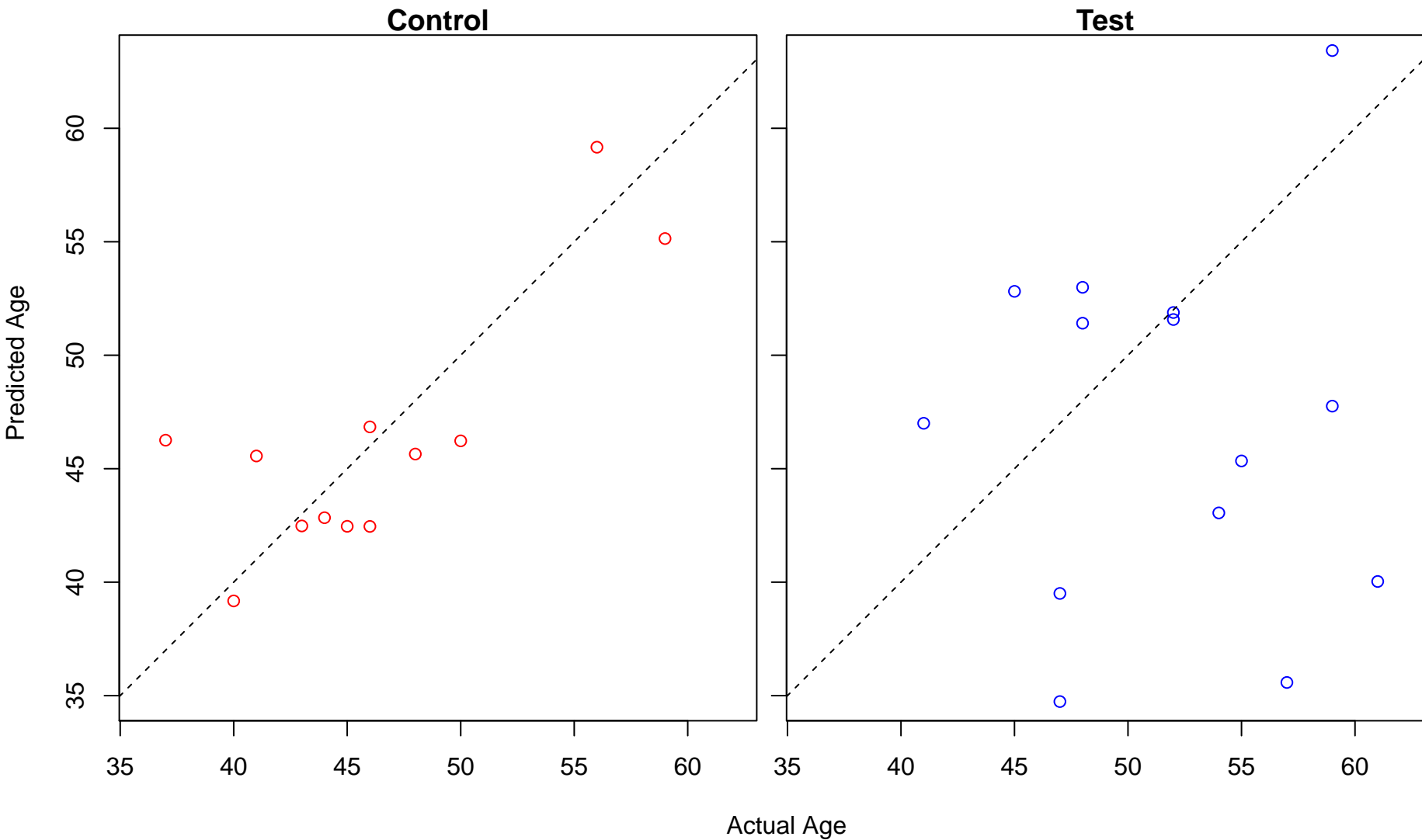


Actual Age

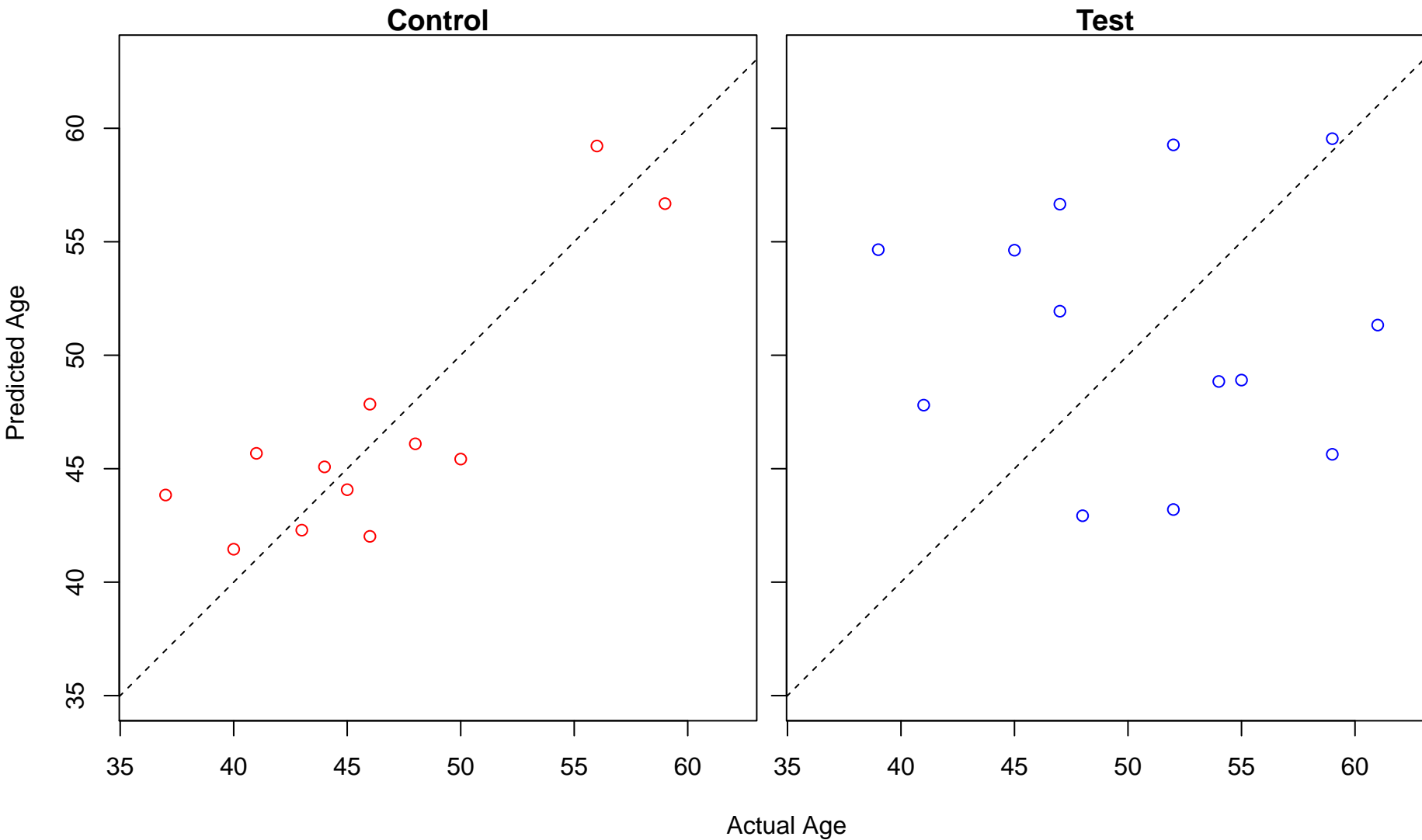
single organismal cell-cell adhesion (Score: 3.369245)



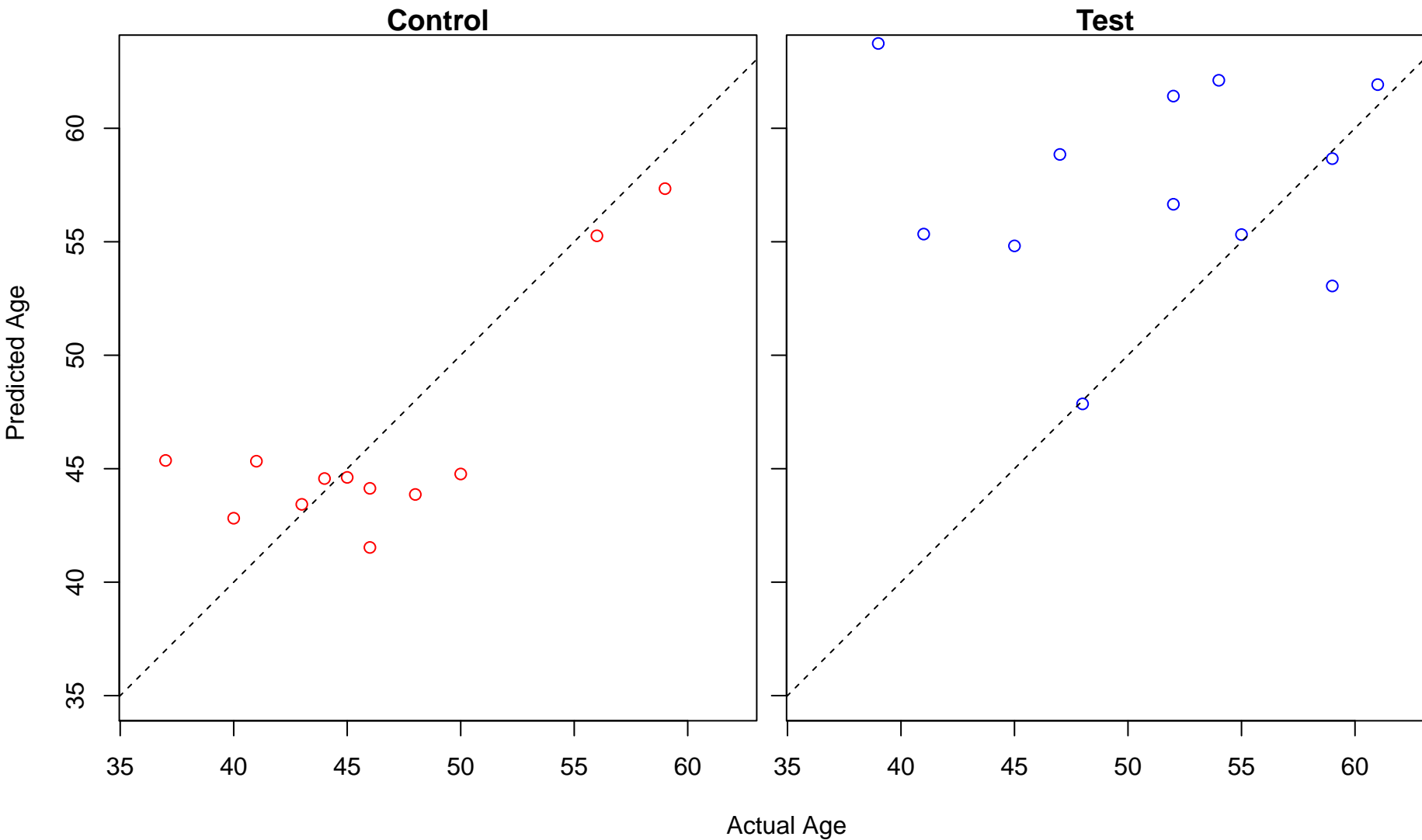
atrioventricular canal development (Score: 3.366438)



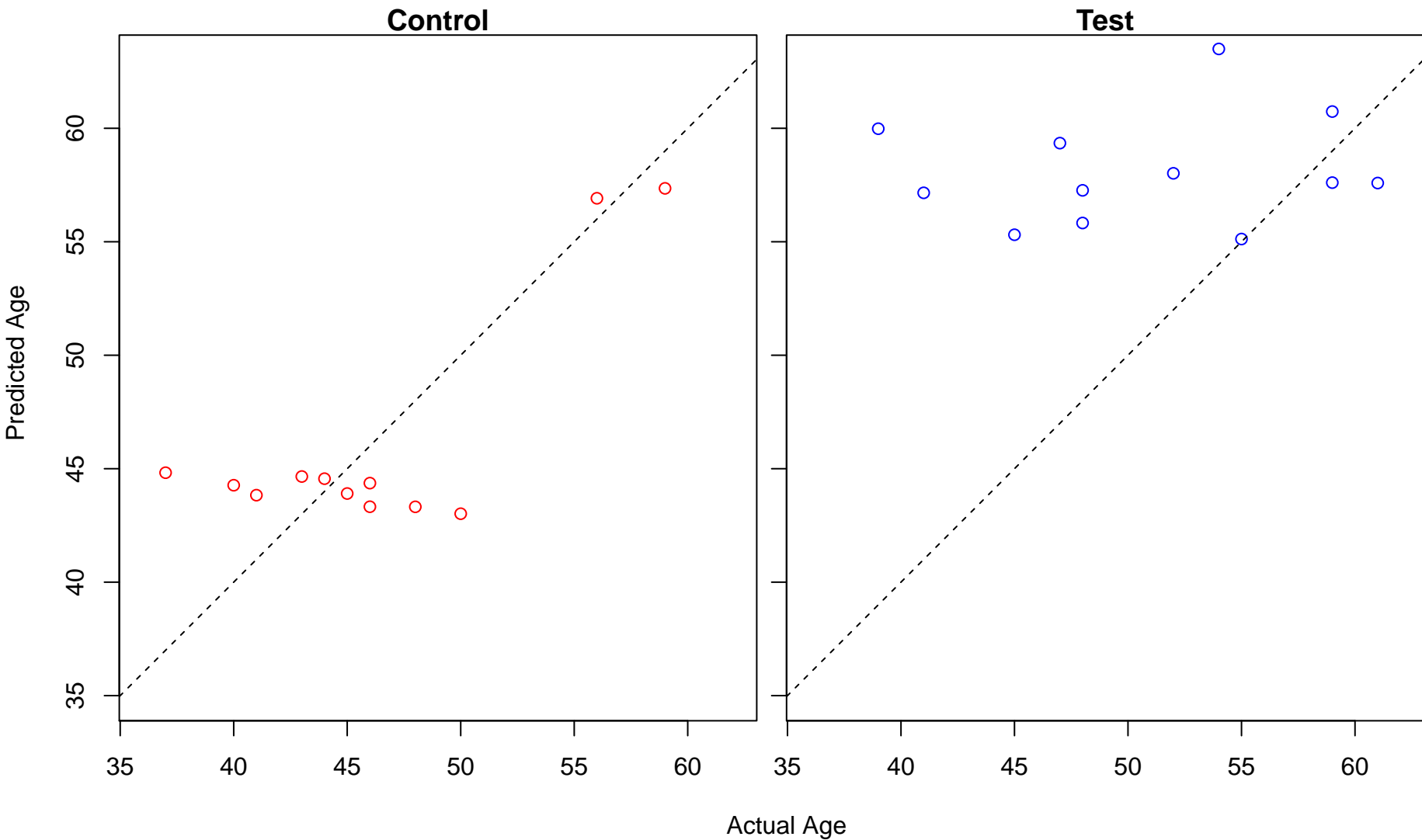
protein-lipid complex assembly (Score: 3.362434)



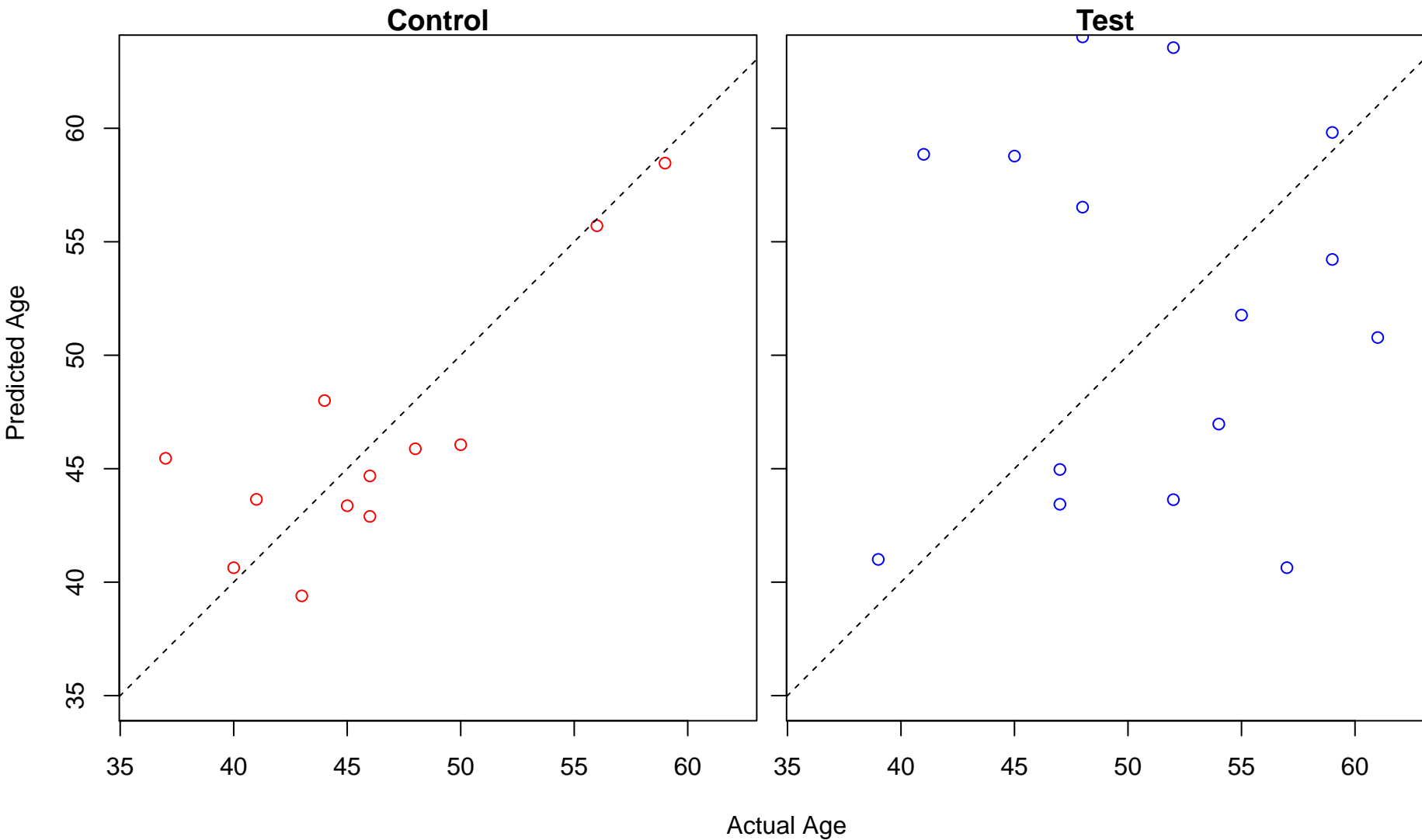
histone H4-K20 demethylation (Score: 3.362246)



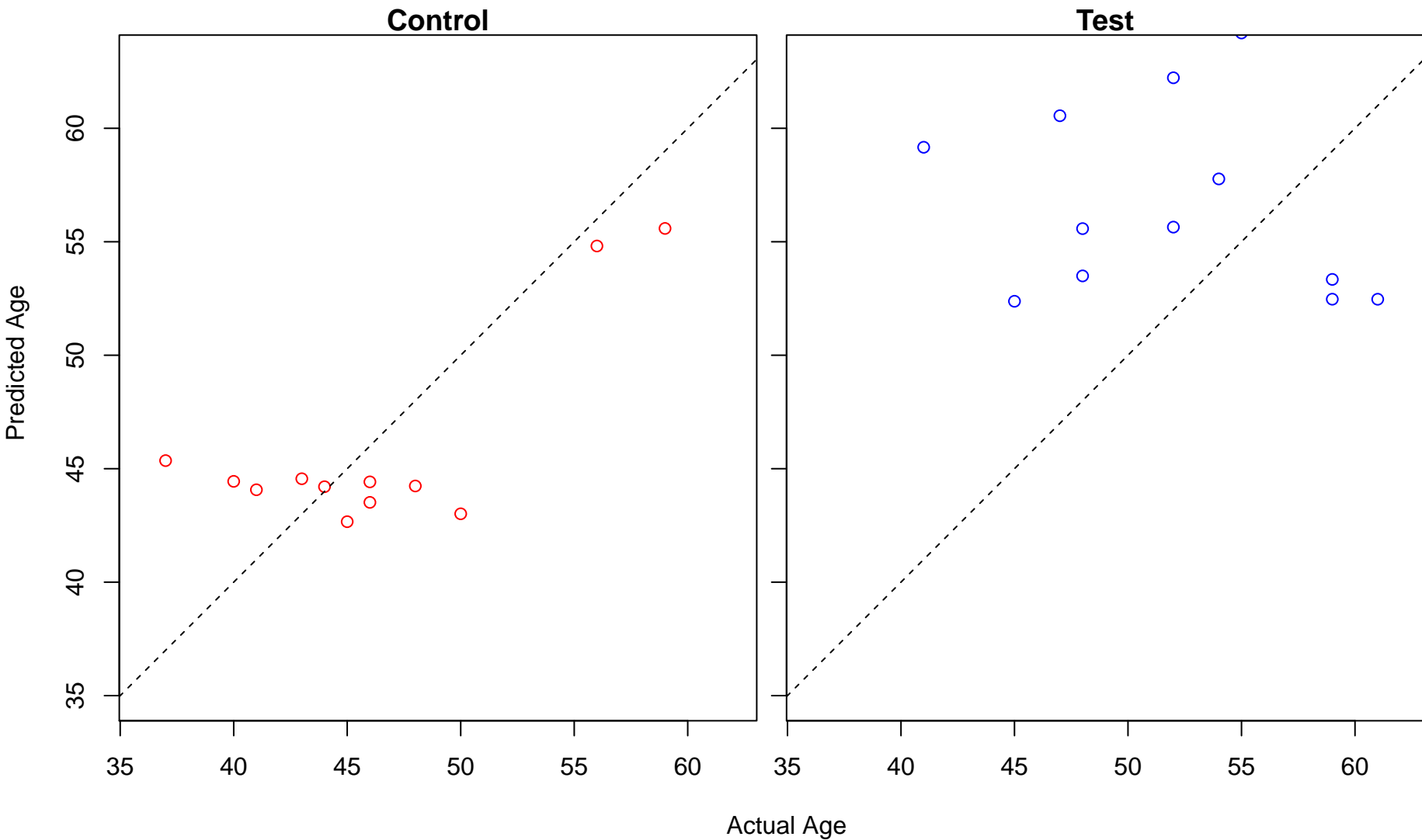
organelle membrane fusion (Score: 3.357306)



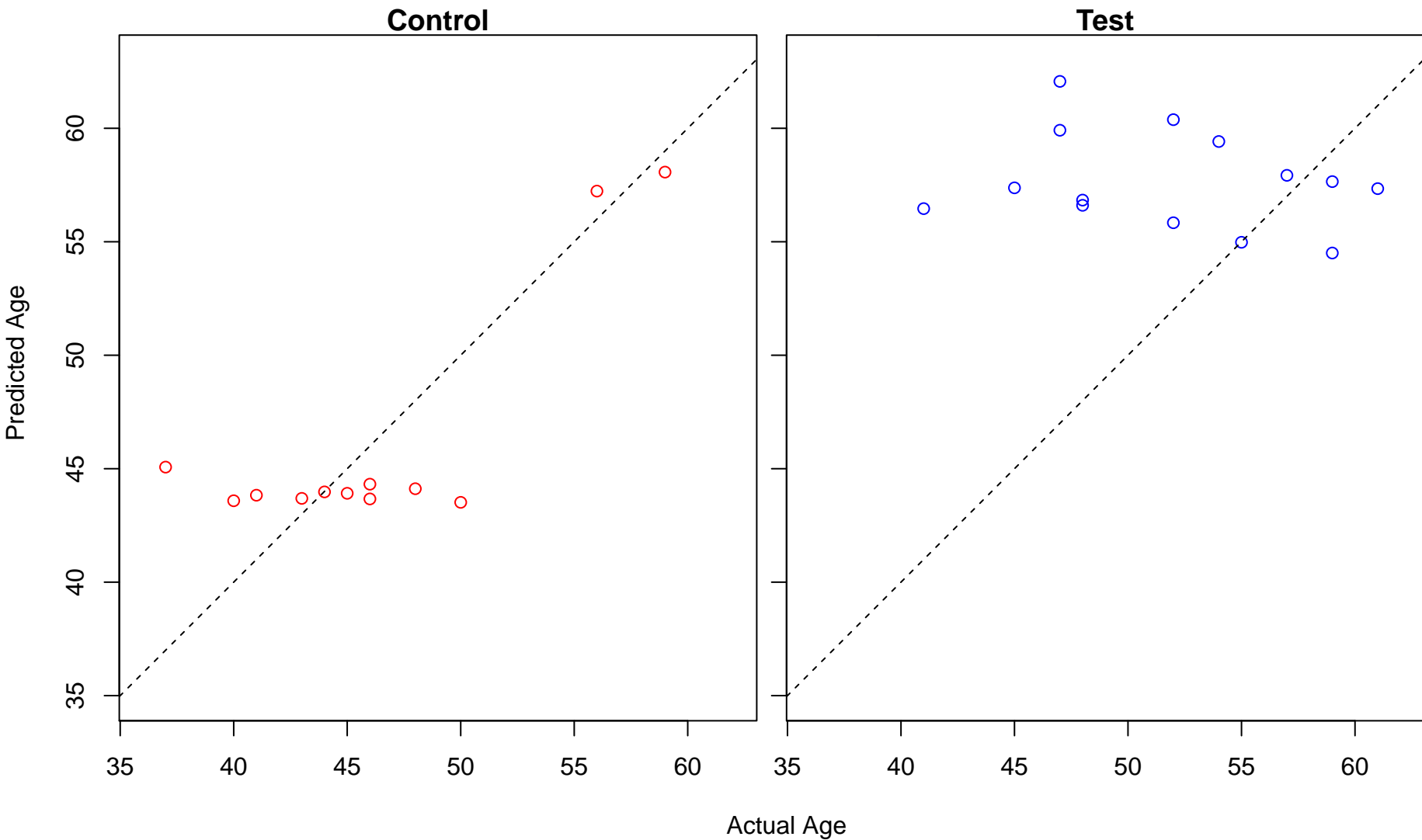
retina layer formation (Score: 3.354748)



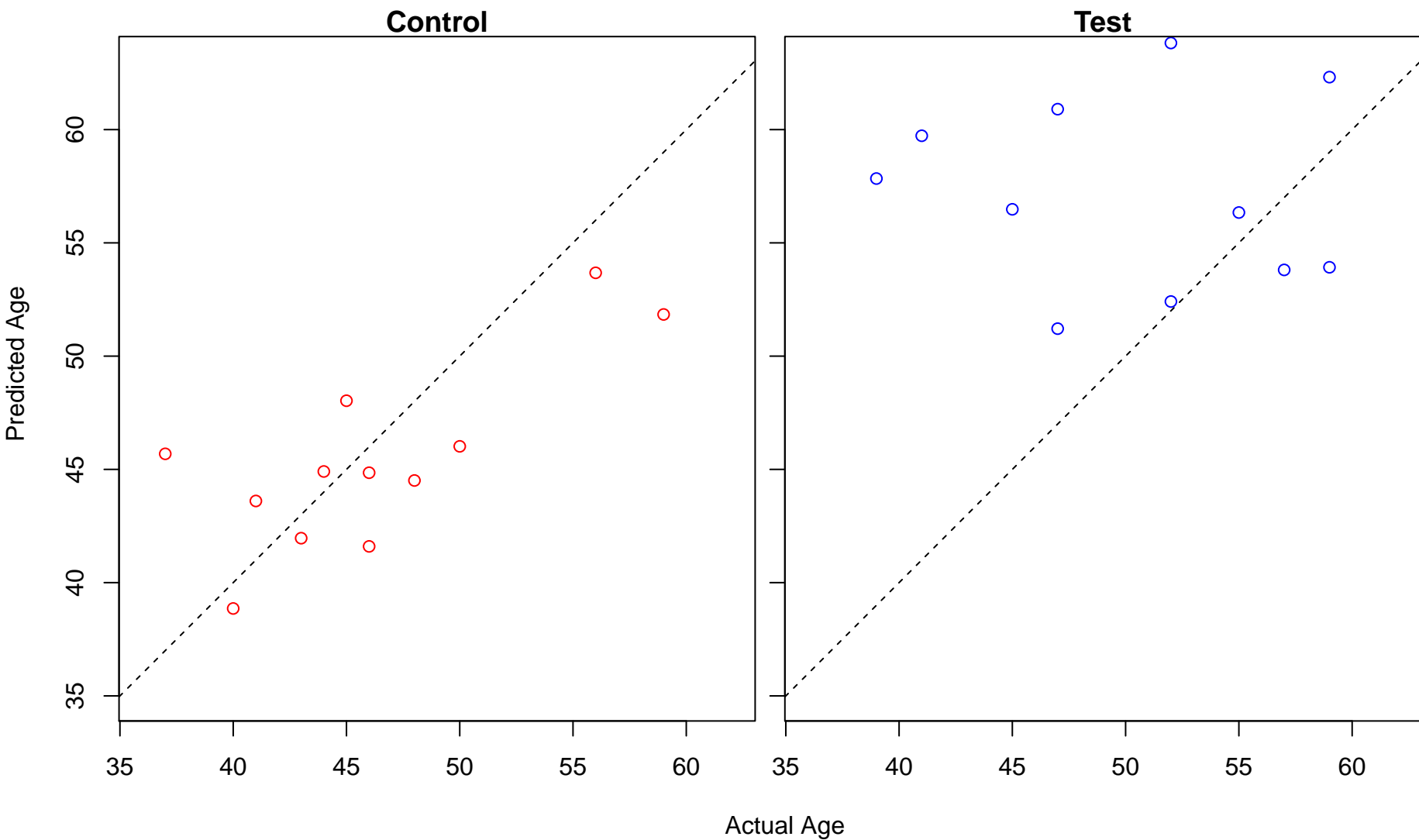
single organism cell adhesion (Score: 3.354676)



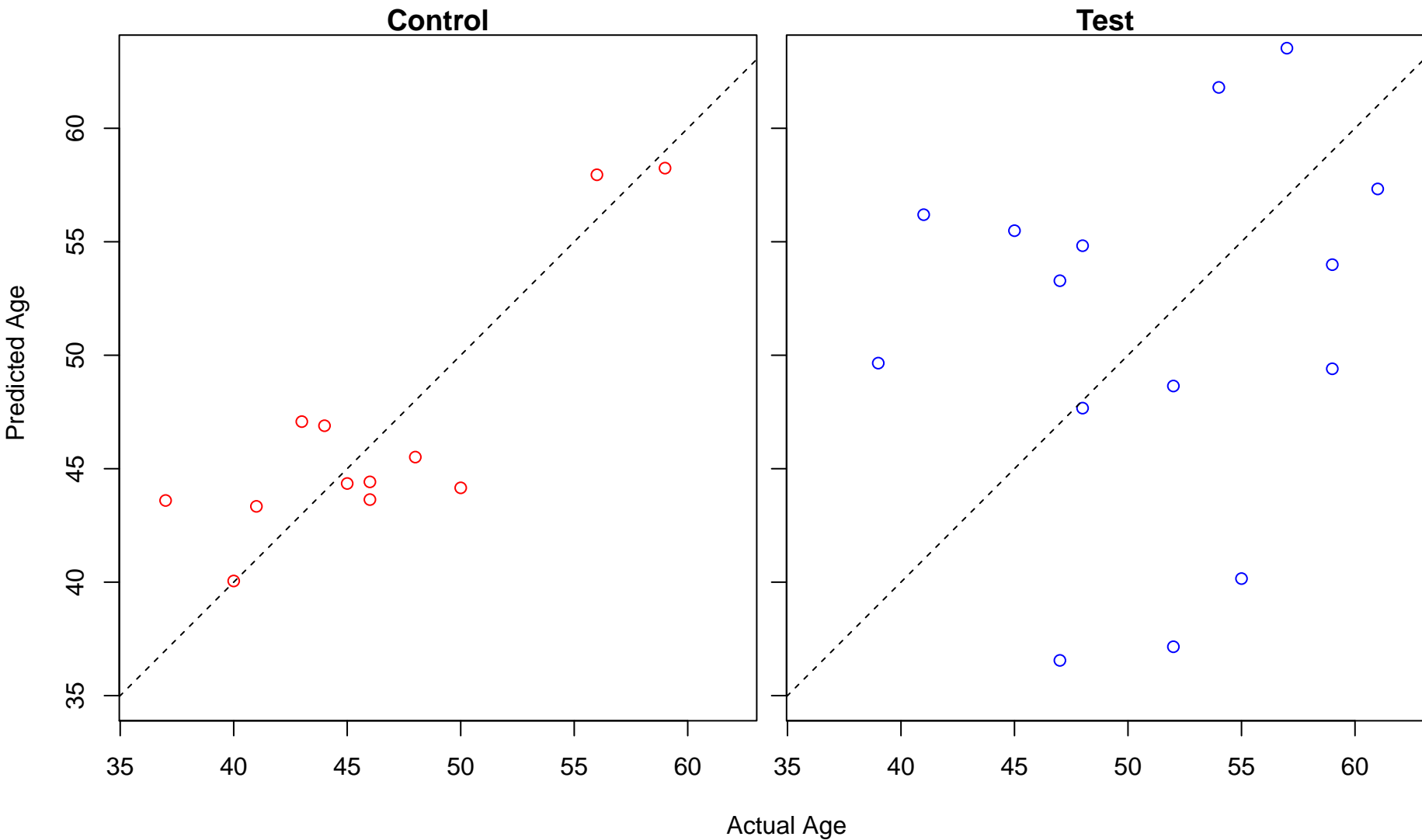
regulation of defense response to bacterium (Score: 3.353516)



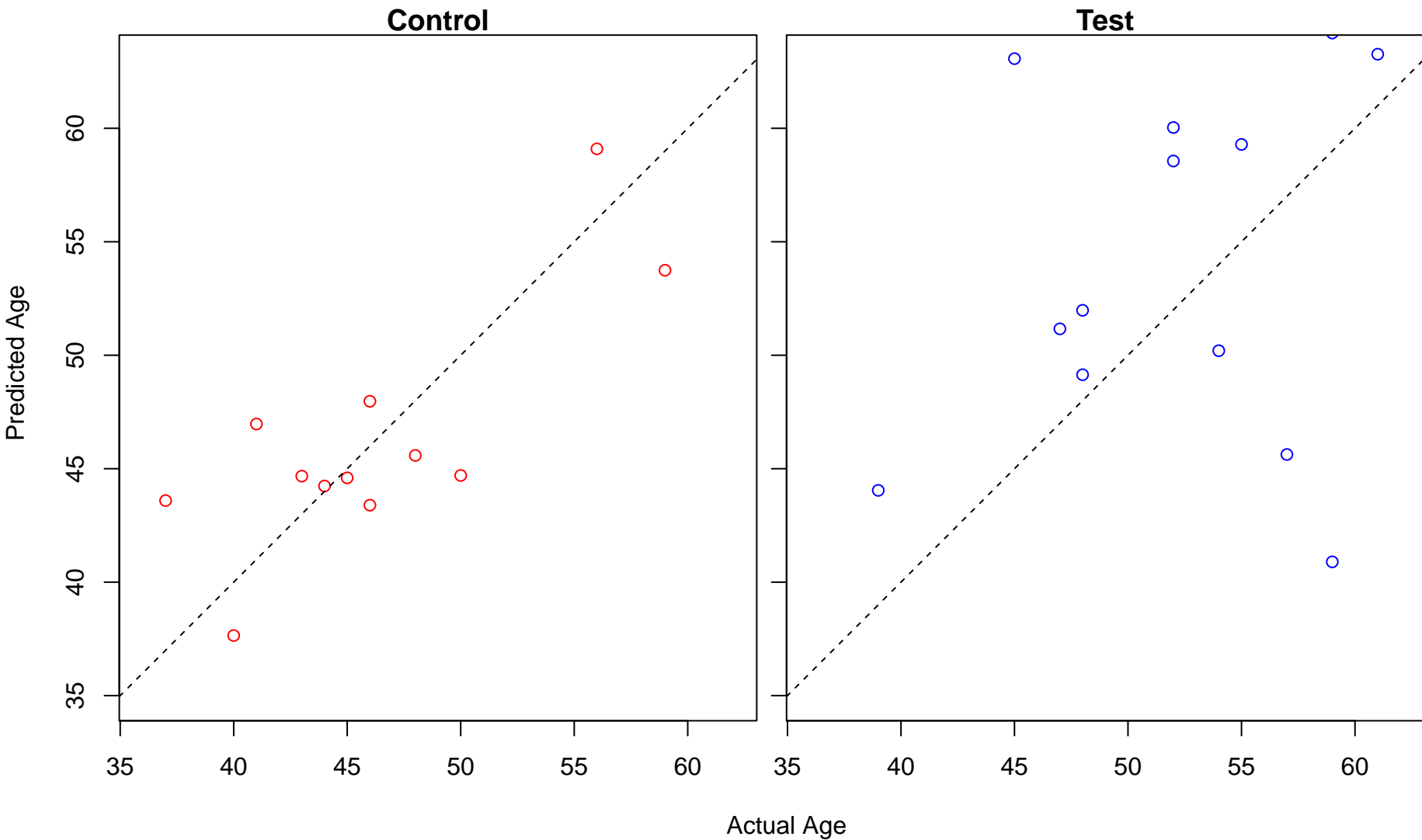
positive regulation of synapse maturation (Score: 3.352796)



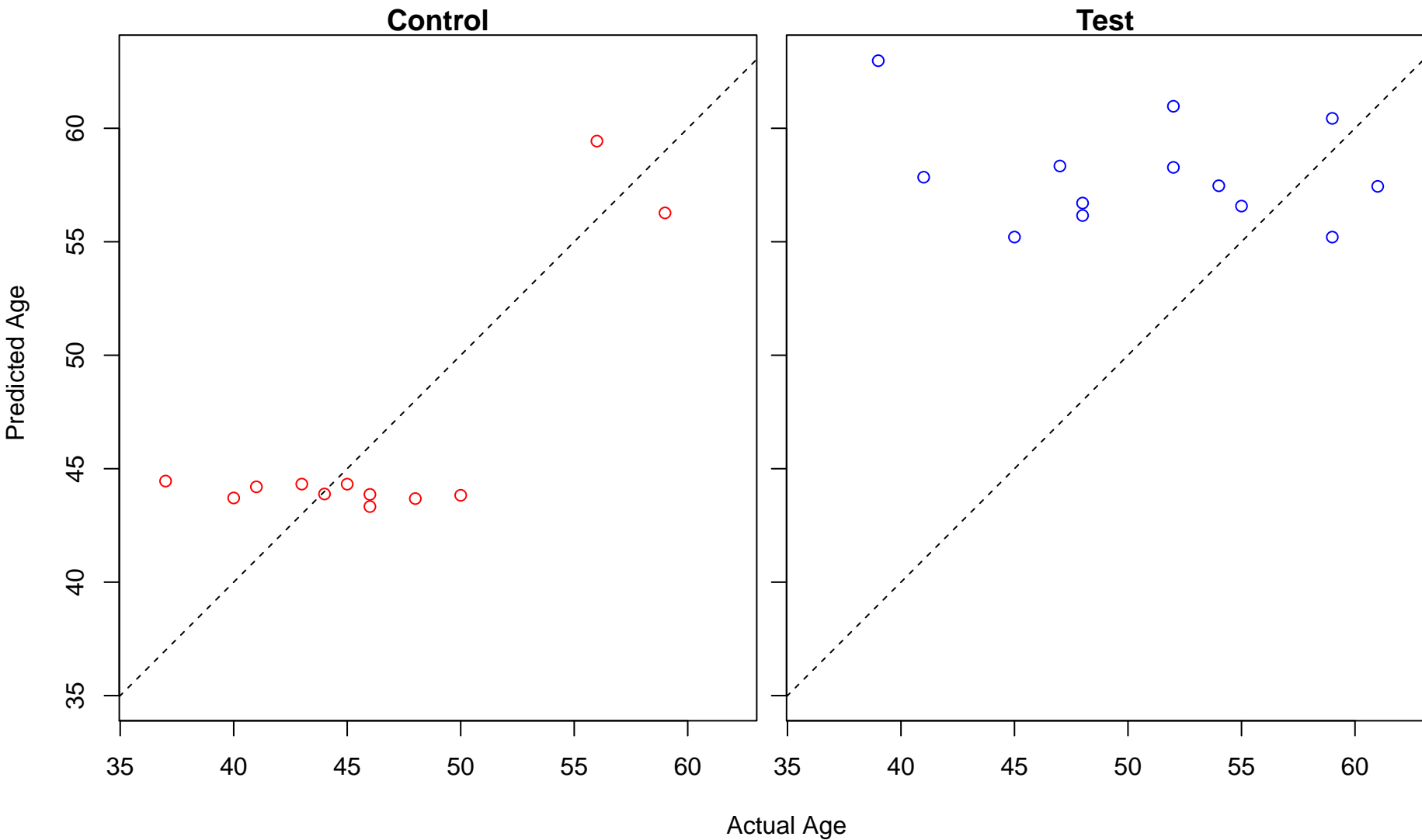
regulation of ion homeostasis (Score: 3.352126)



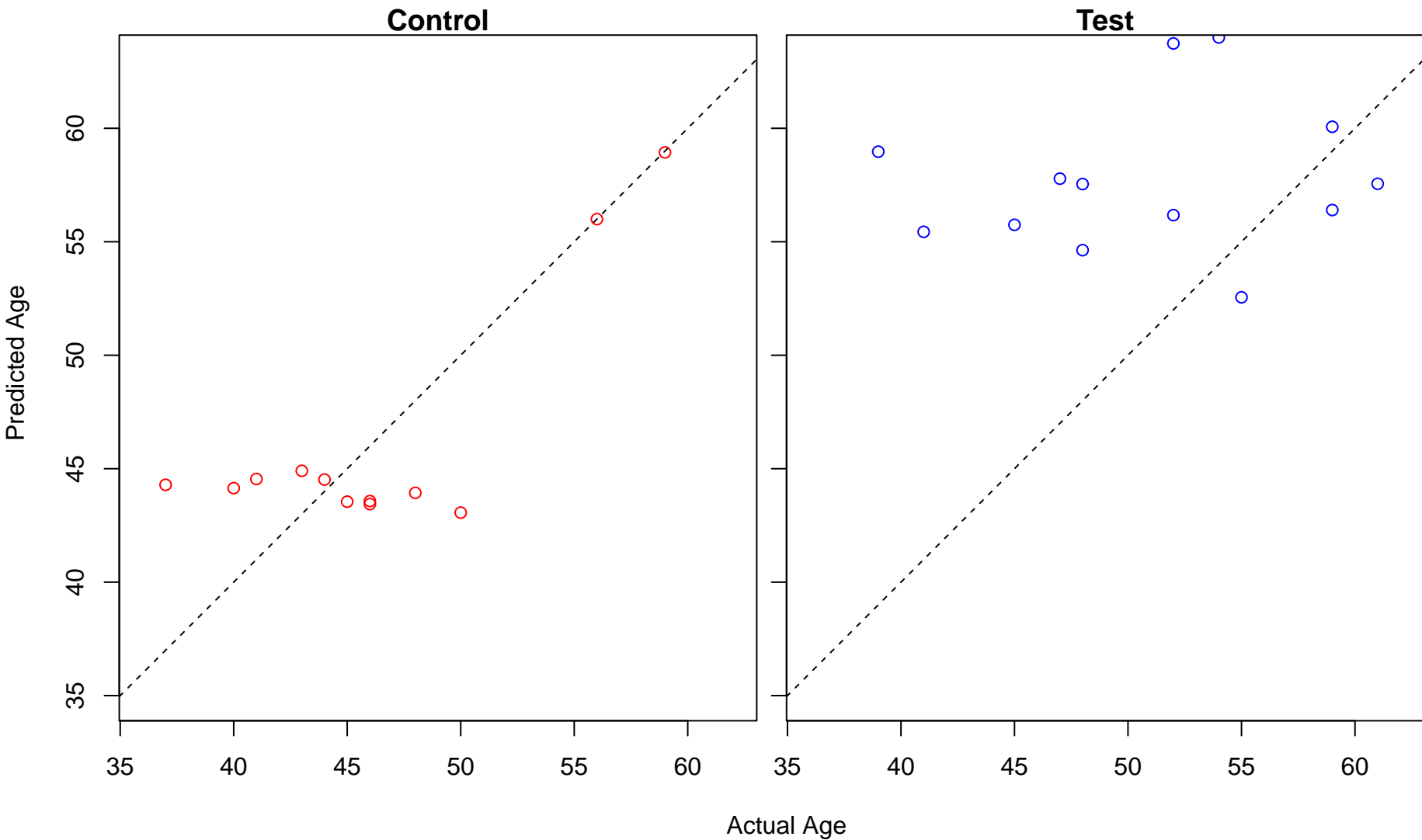
negative regulation of cell activation (Score: 3.350747)



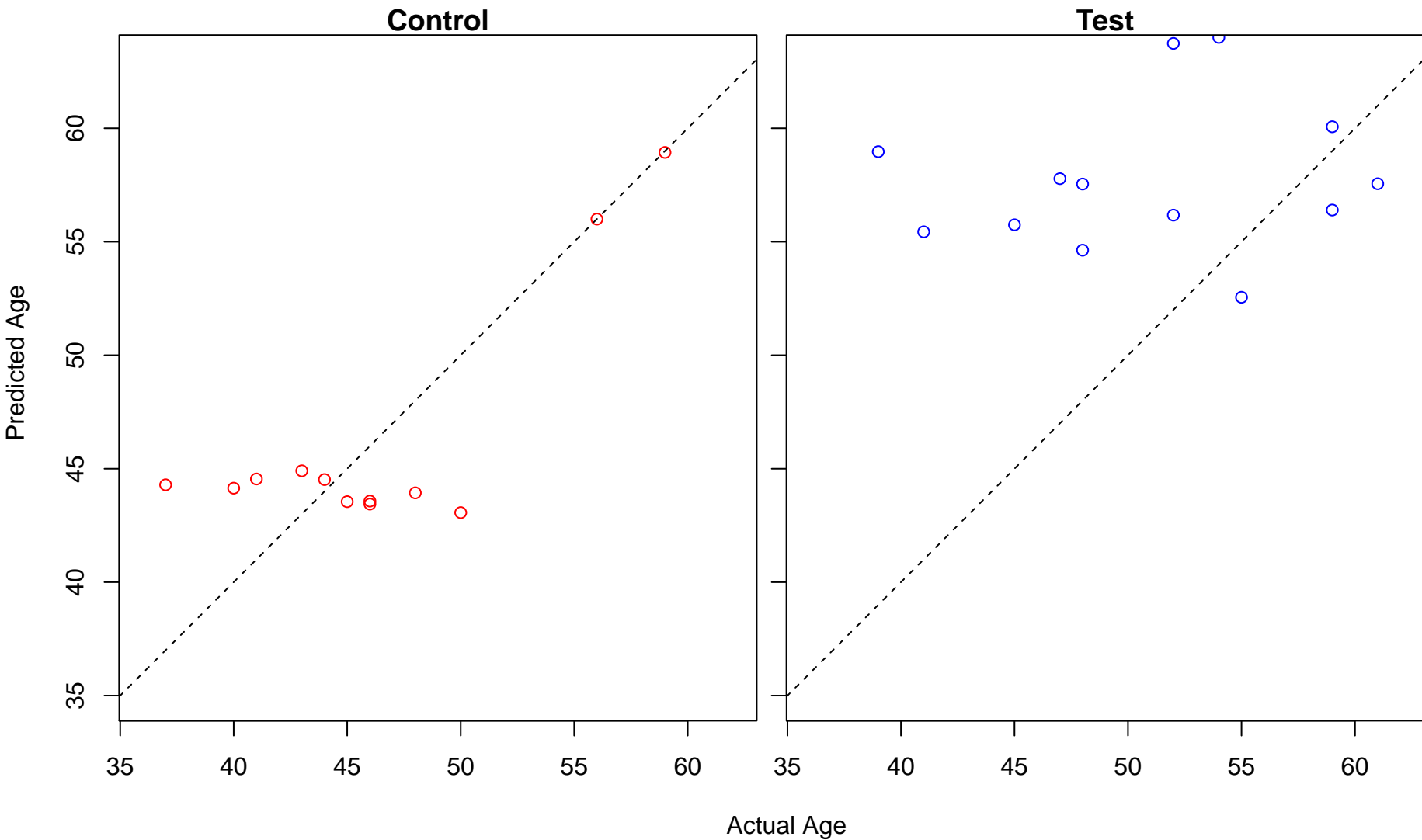
nucleotide-excision repair (Score: 3.350606)



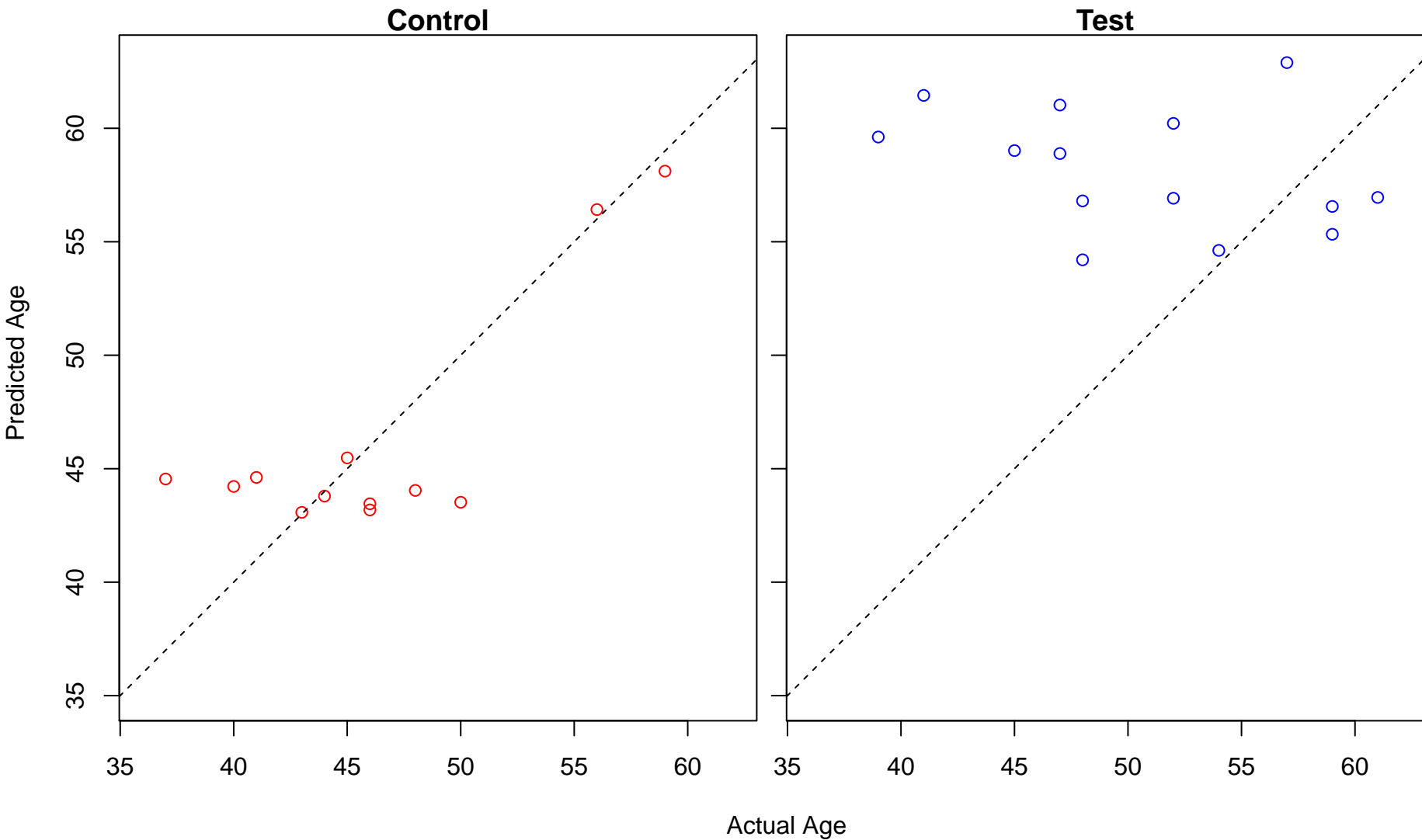
positive regulation of nucleoside metabolic process (Score: 3.349560)



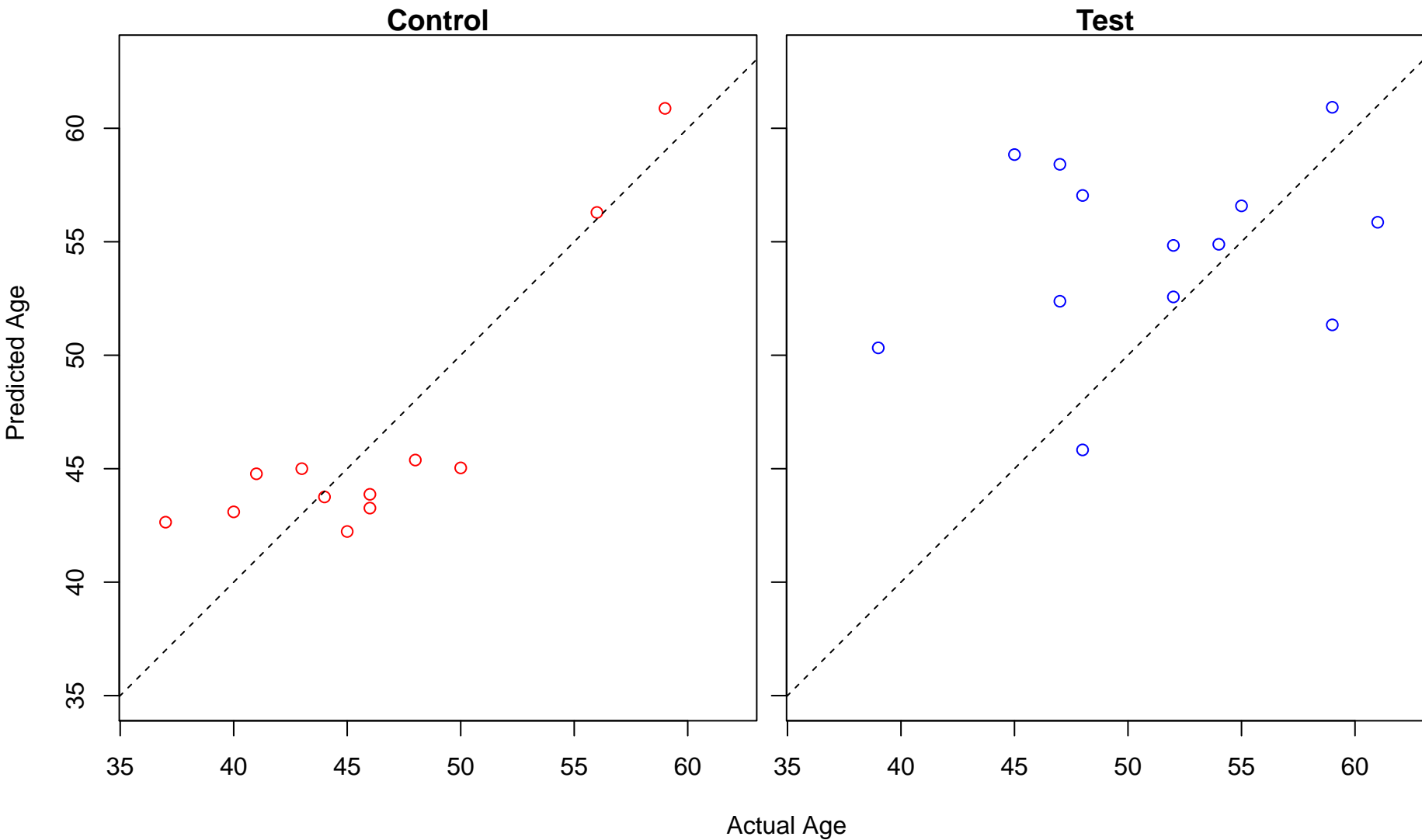
positive regulation of ATP metabolic process (Score: 3.349560)



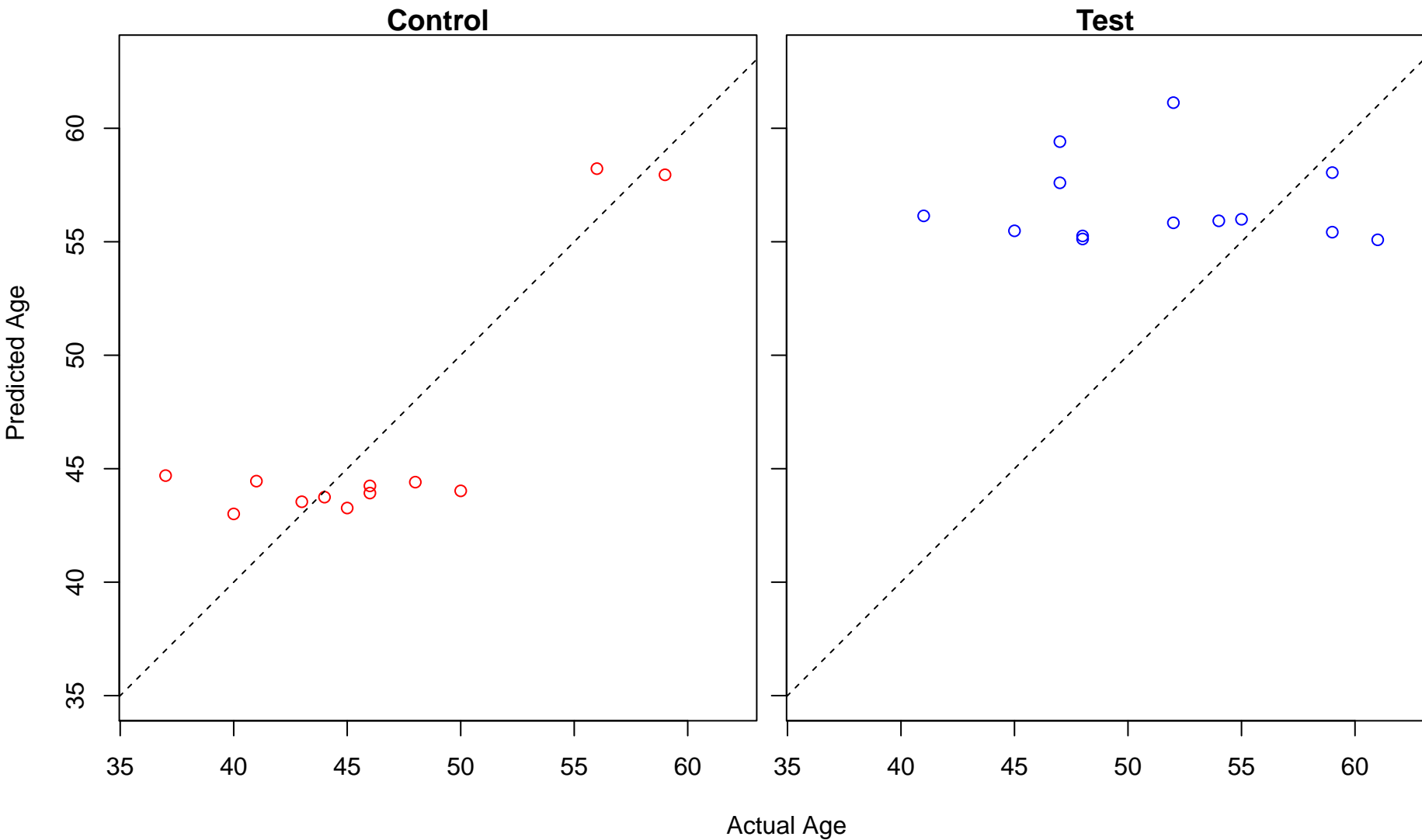
negative regulation of neuron projection development (Score: 3.348699)



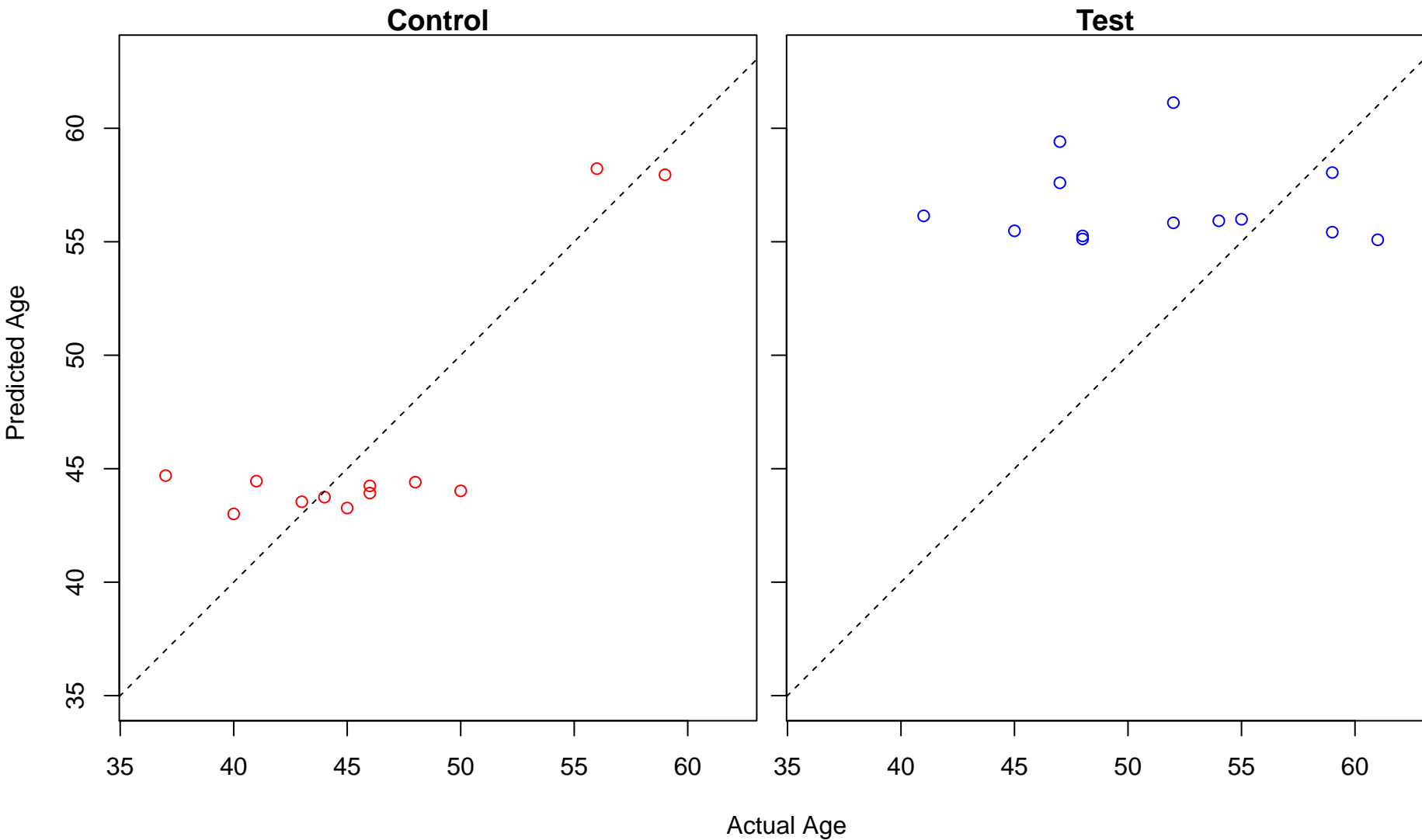
quinone metabolic process (Score: 3.348643)



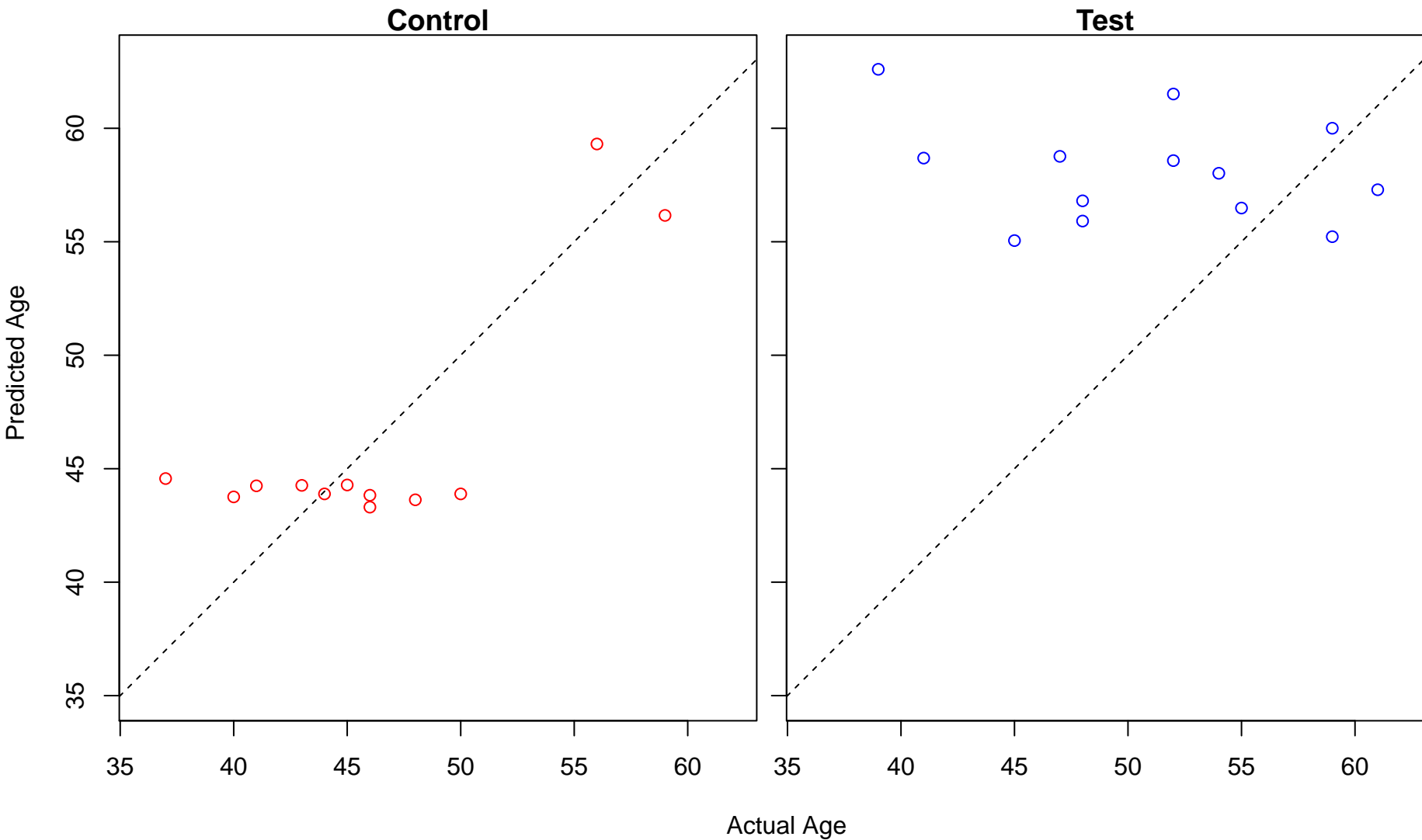
modulation by host of viral release from host cell (Score: 3.348401)



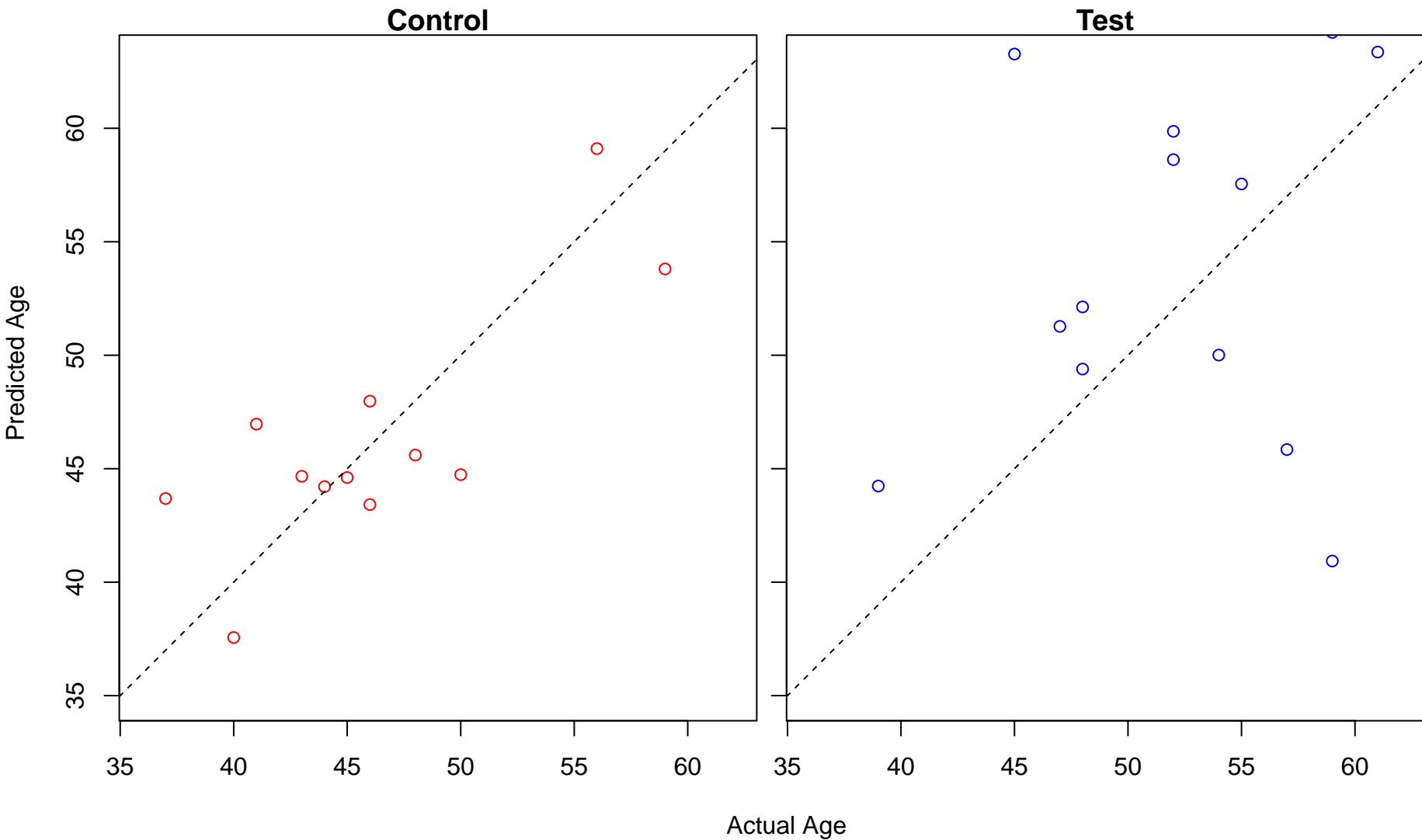
positive regulation by host of viral release from host cell (Score: 3.348401)



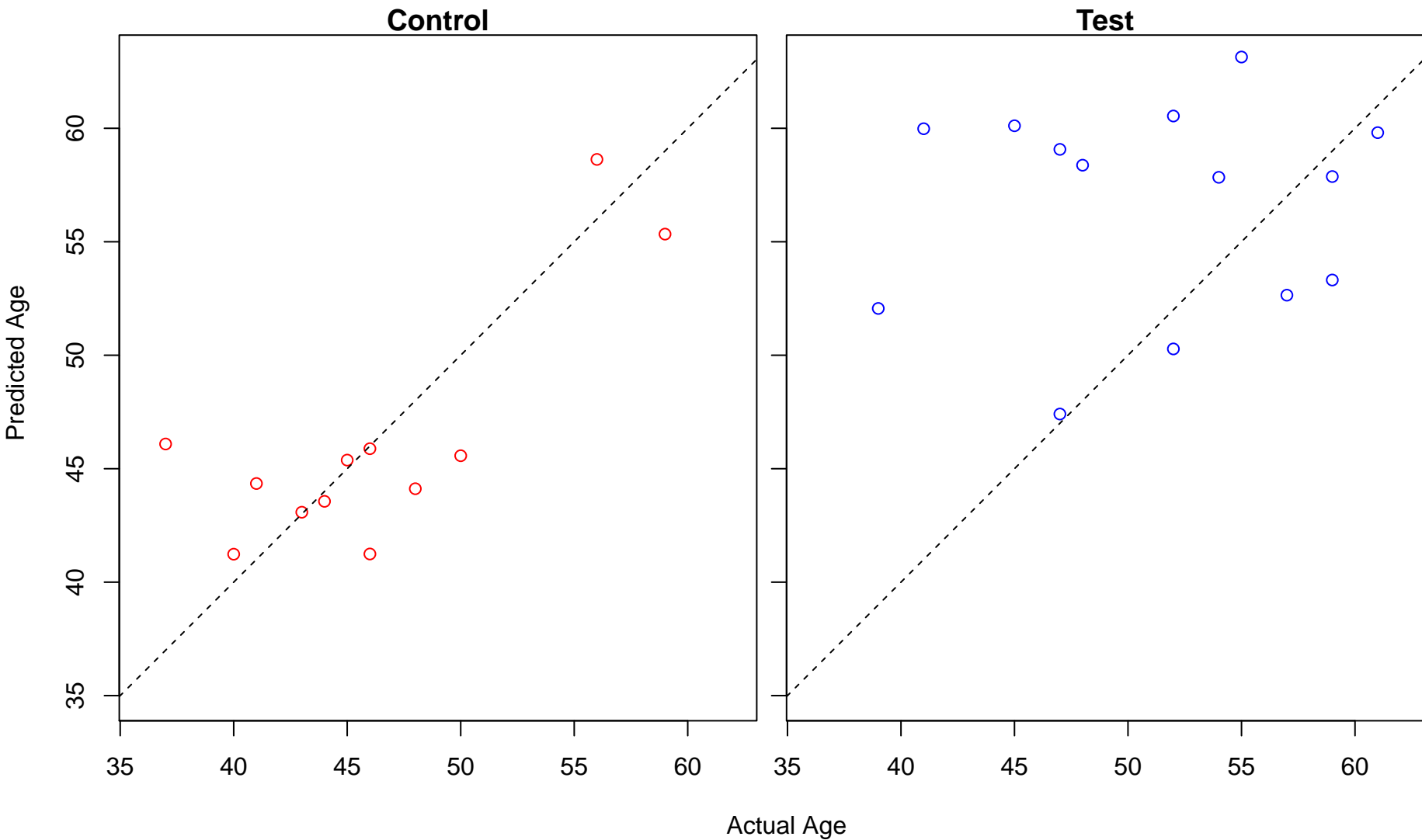
cell cycle checkpoint (Score: 3.347902)



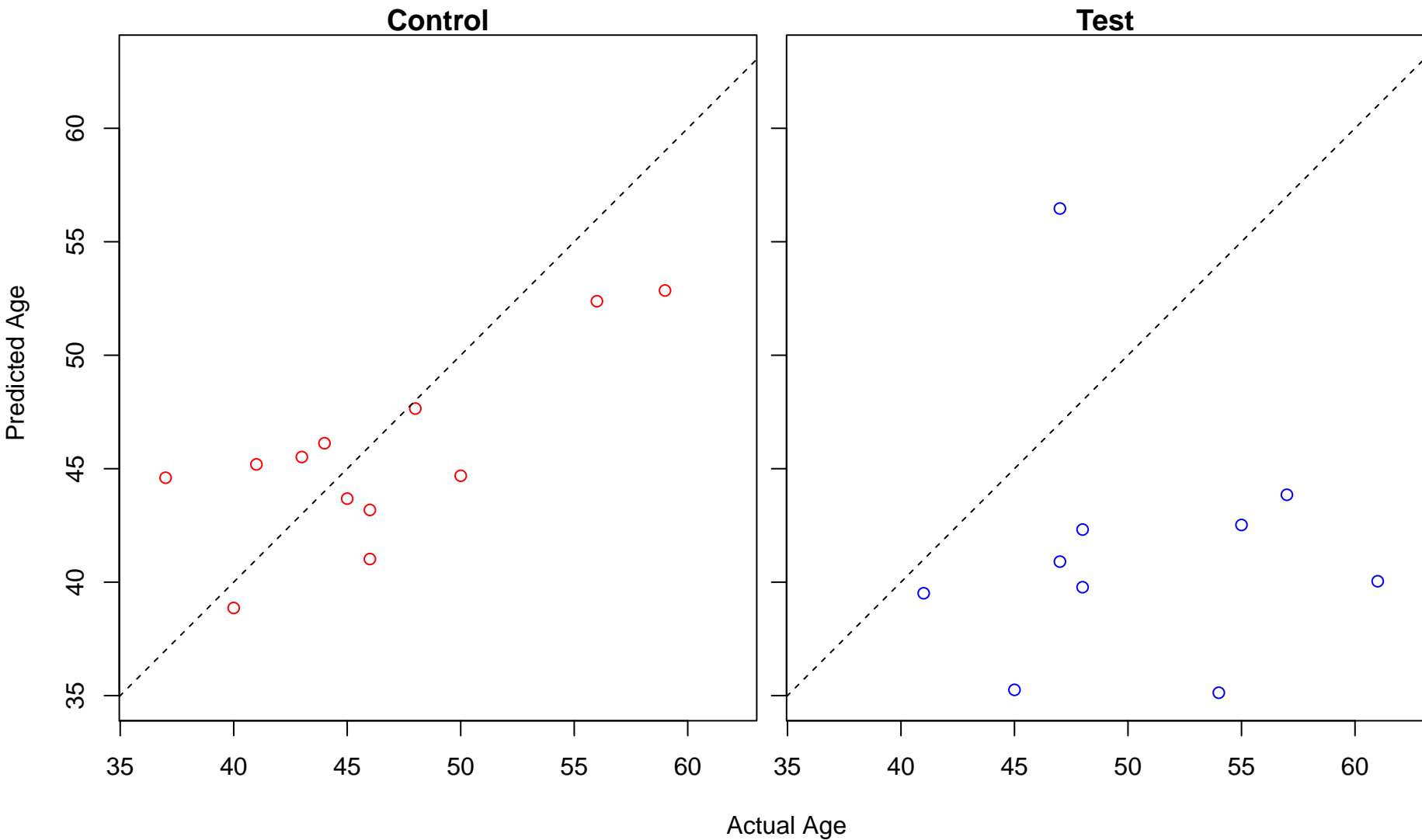
negative regulation of leukocyte cell-cell adhesion (Score: 3.347769)



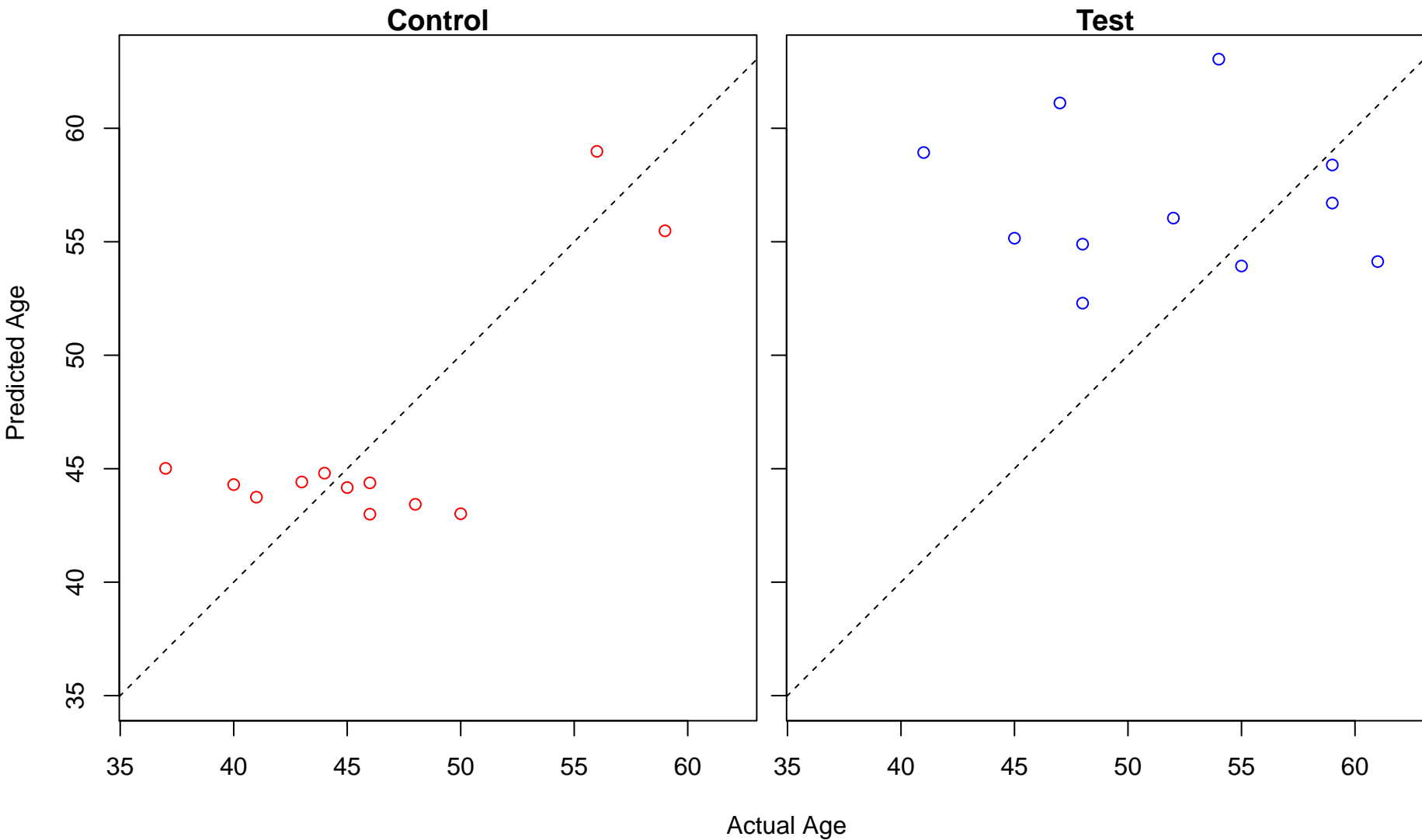
positive regulation of smoothened signaling pathway (Score: 3.346781)



protein targeting to ER (Score: 3.346736)

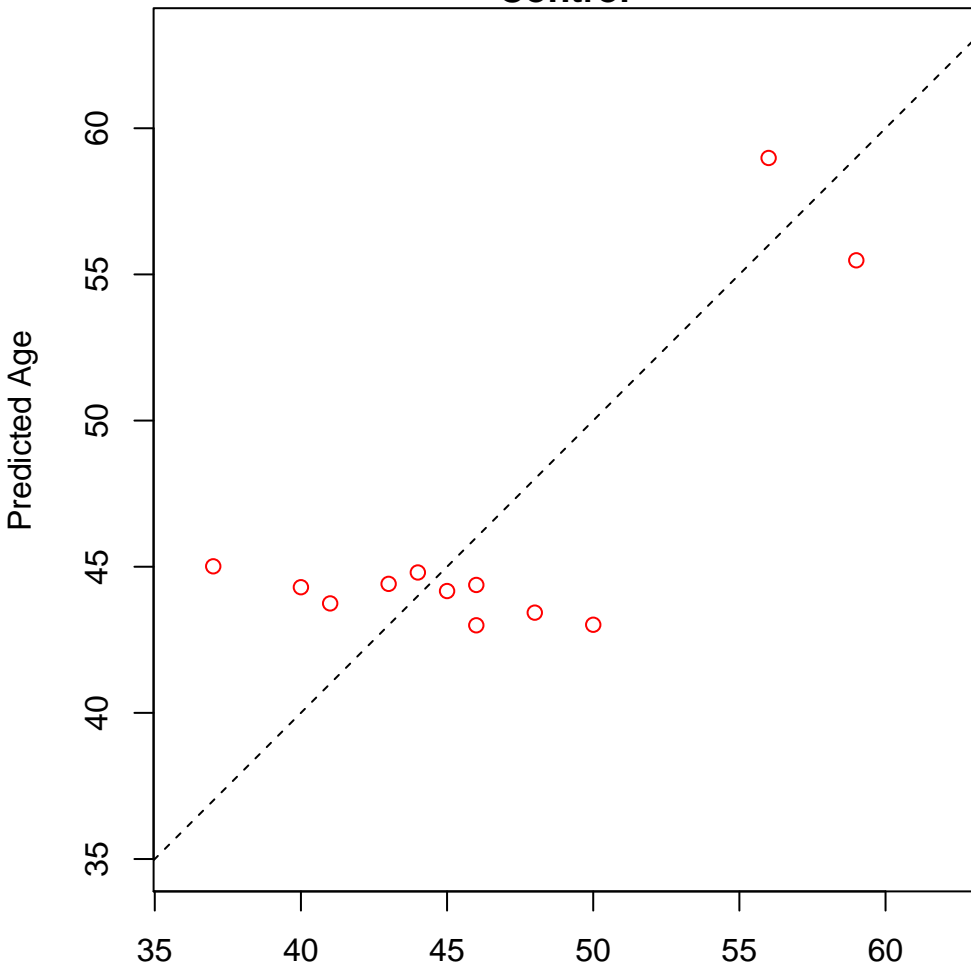


endosome to melanosome transport (Score: 3.345752)

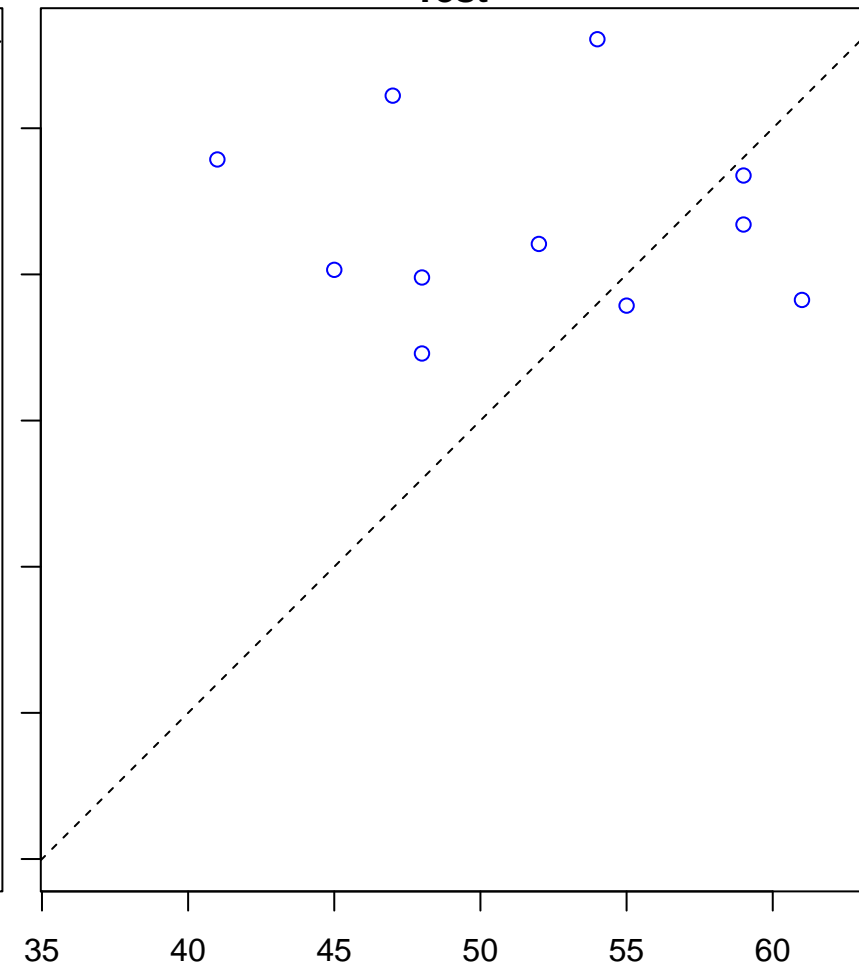


endosome to pigment granule transport (Score: 3.345752)

Control

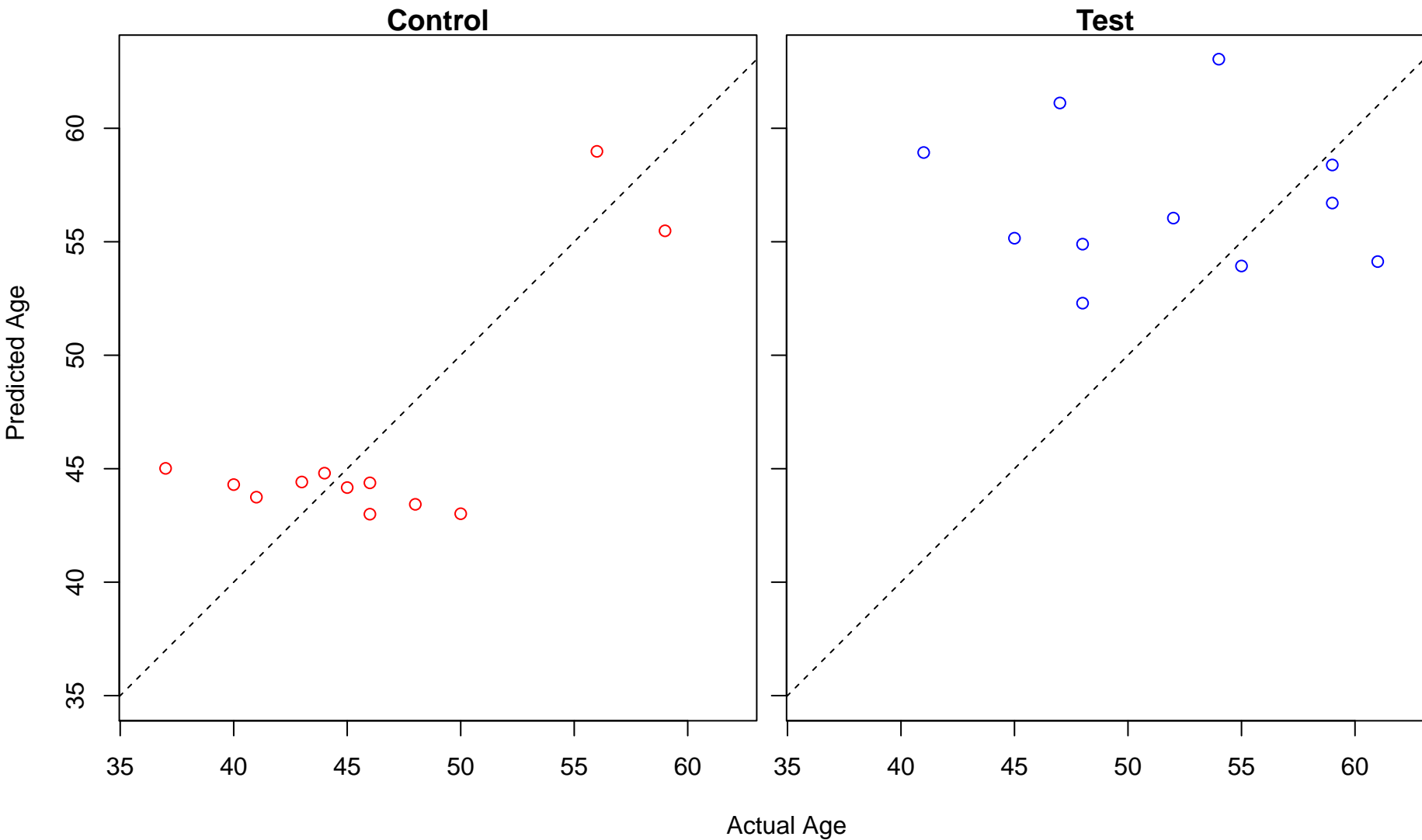


Test



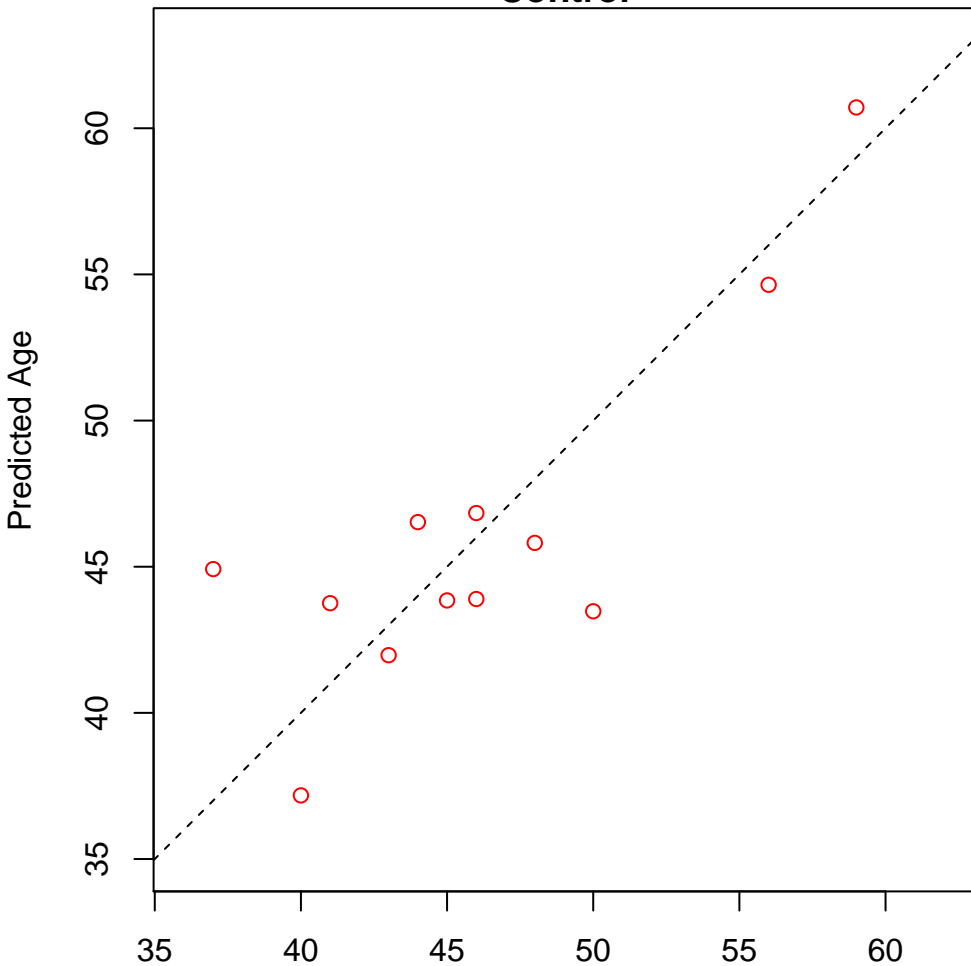
Actual Age

pigment granule maturation (Score: 3.345752)

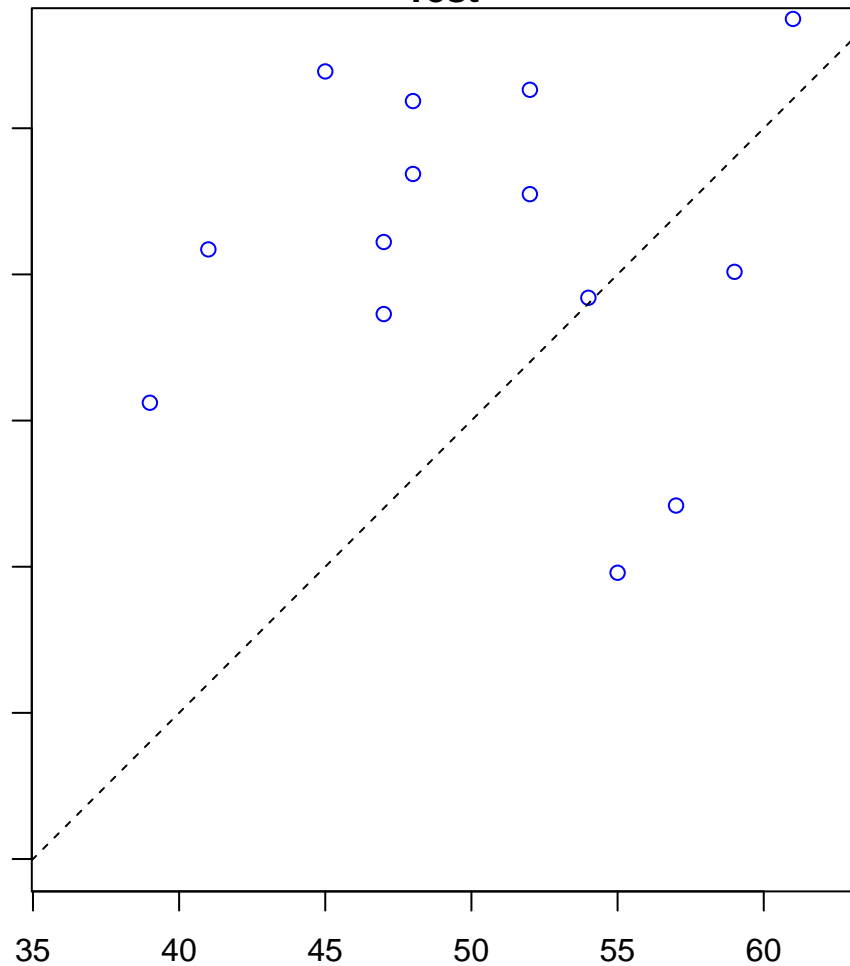


protein localization to microtubule (Score: 3.345712)

Control



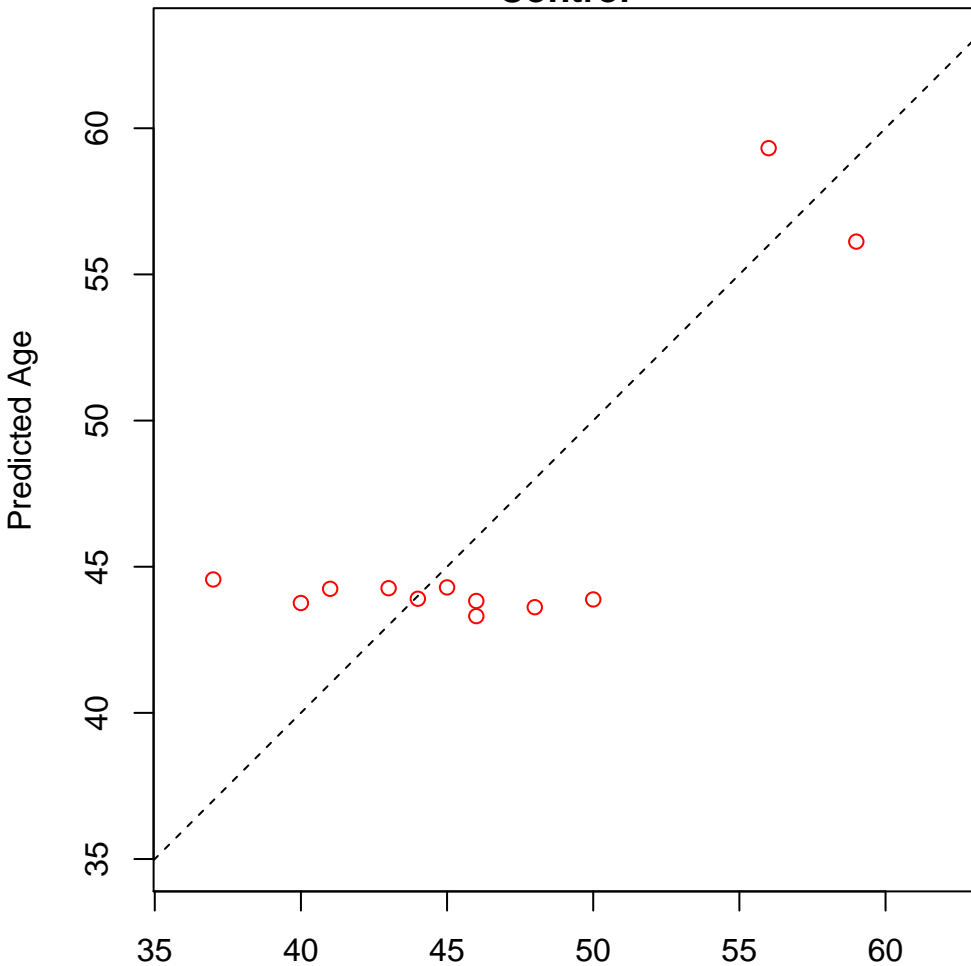
Test



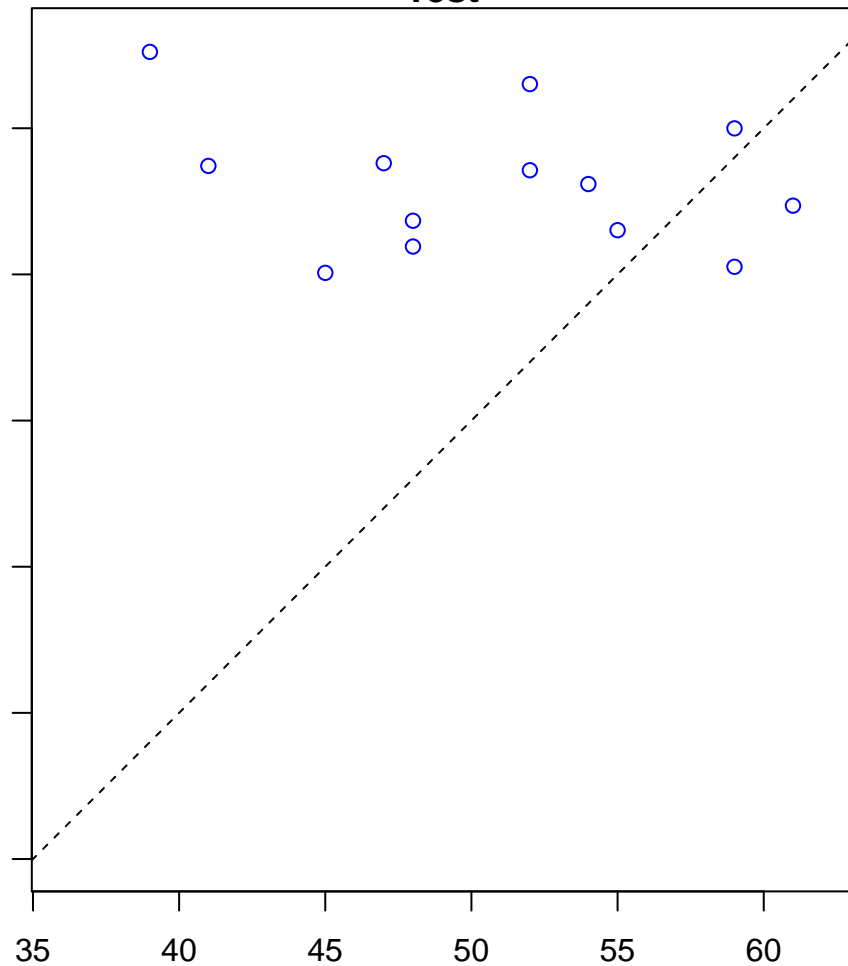
Actual Age

negative regulation of mitotic cell cycle (Score: 3.345646)

Control

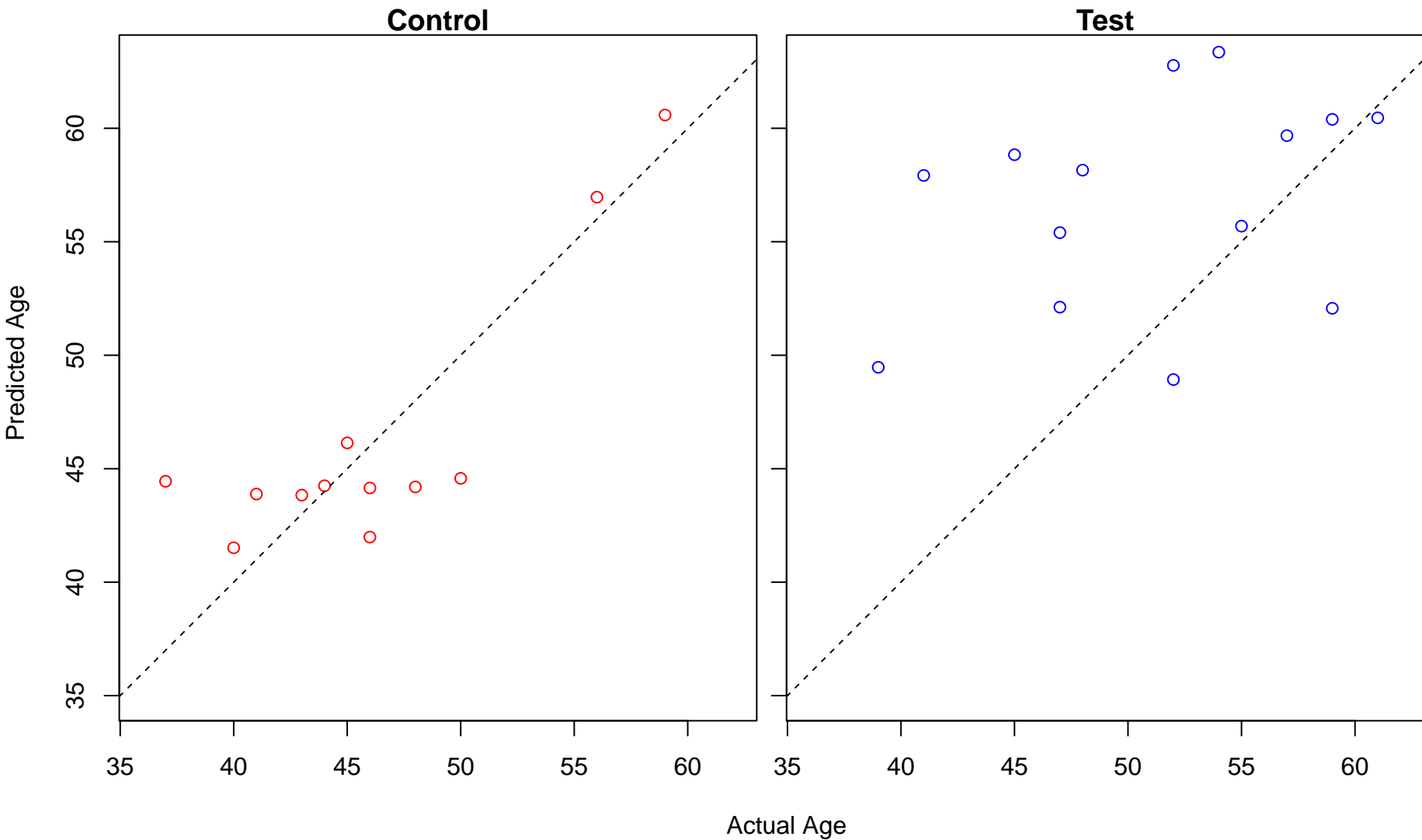


Test

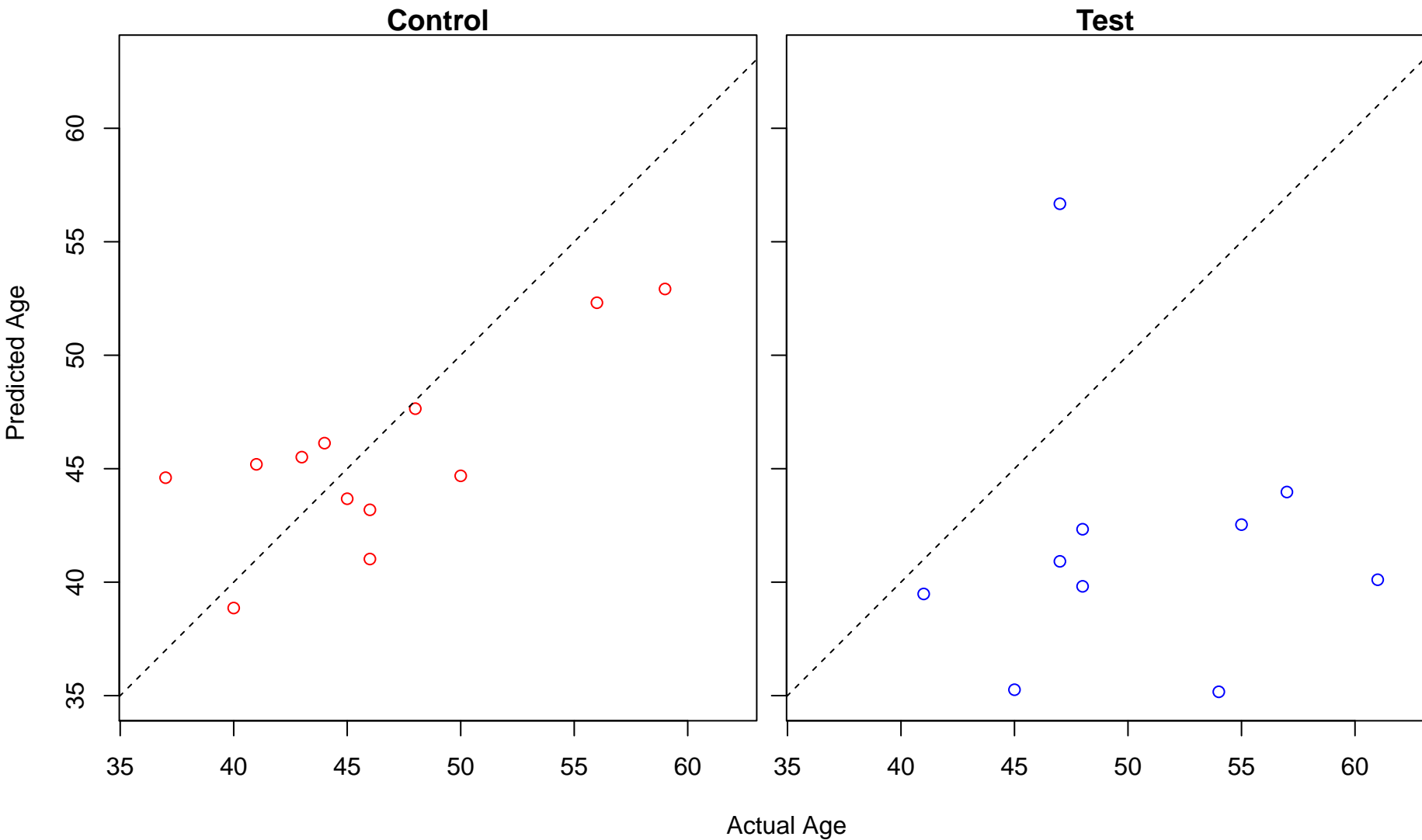


Actual Age

inner dynein arm assembly (Score: 3.345428)

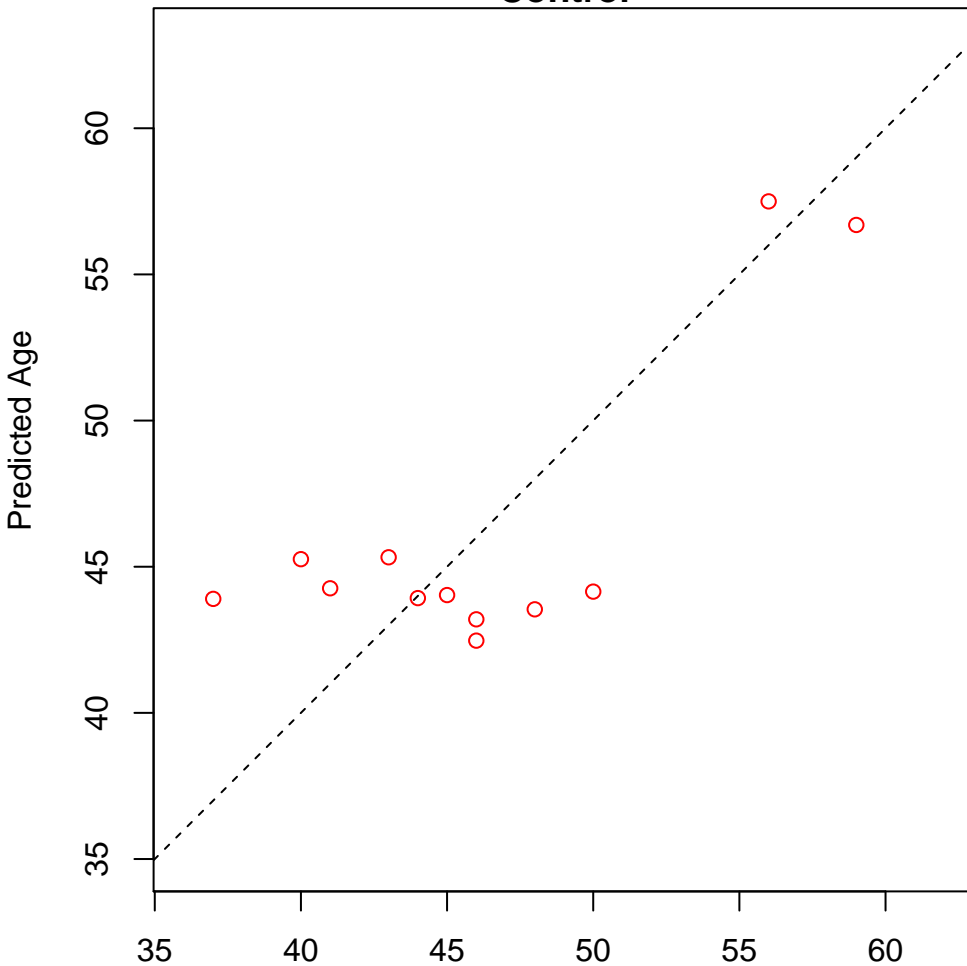


cotranslational protein targeting to membrane (Score: 3.34710)

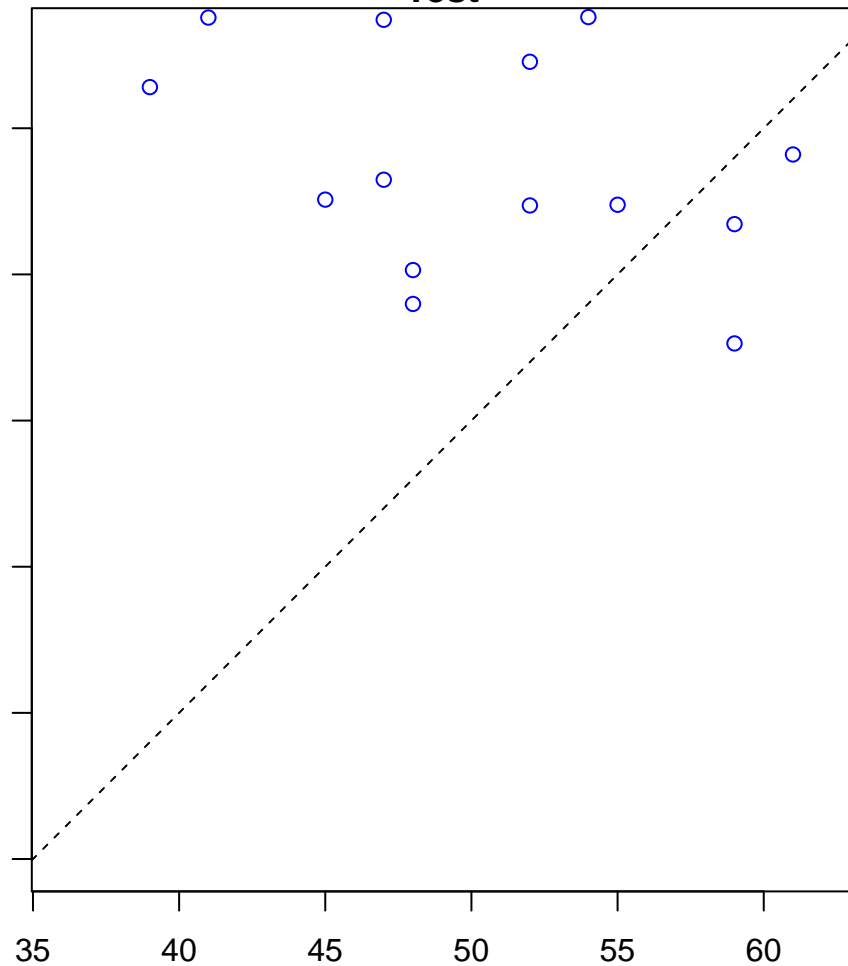


cell-type specific apoptotic process (Score: 3.343673)

Control

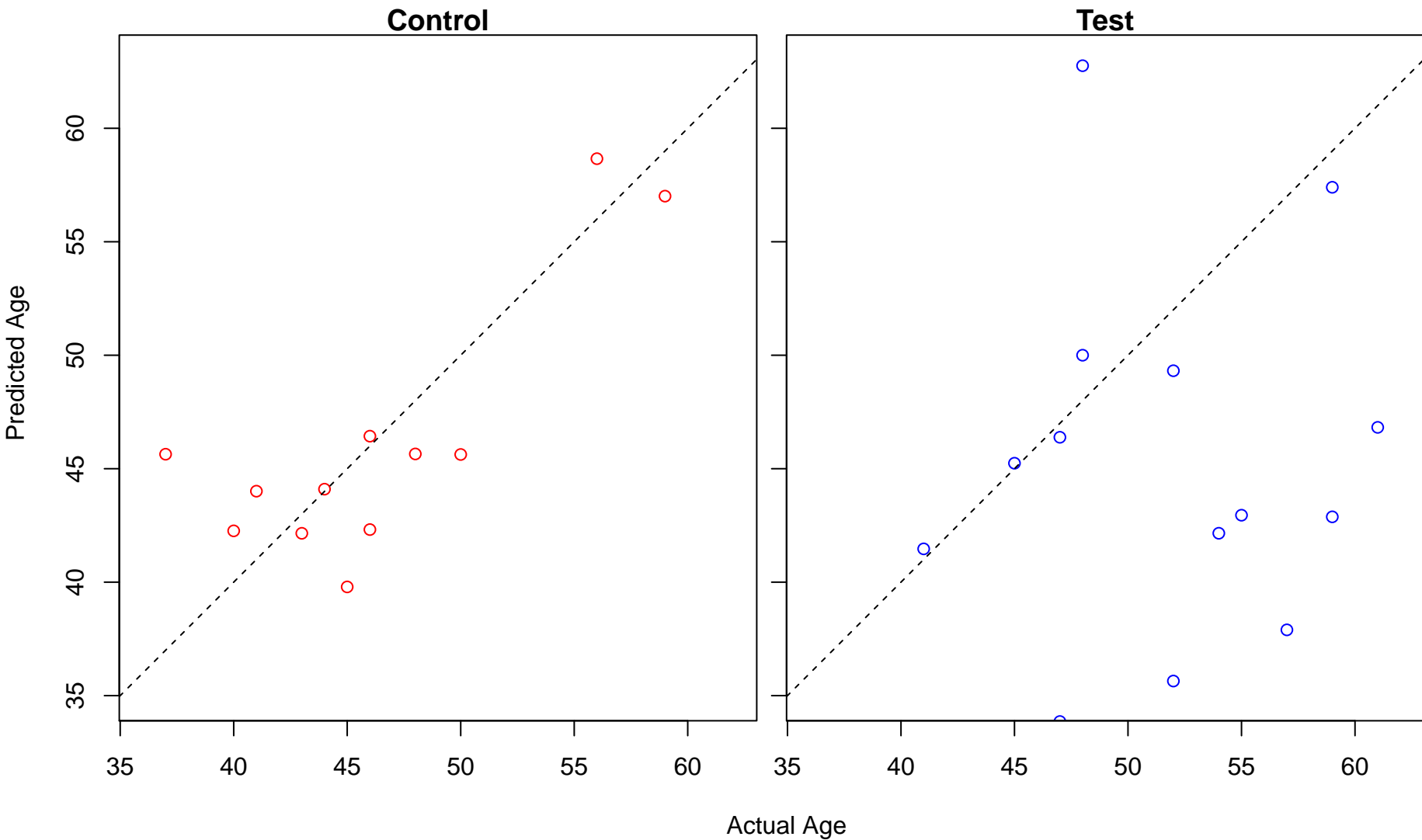


Test

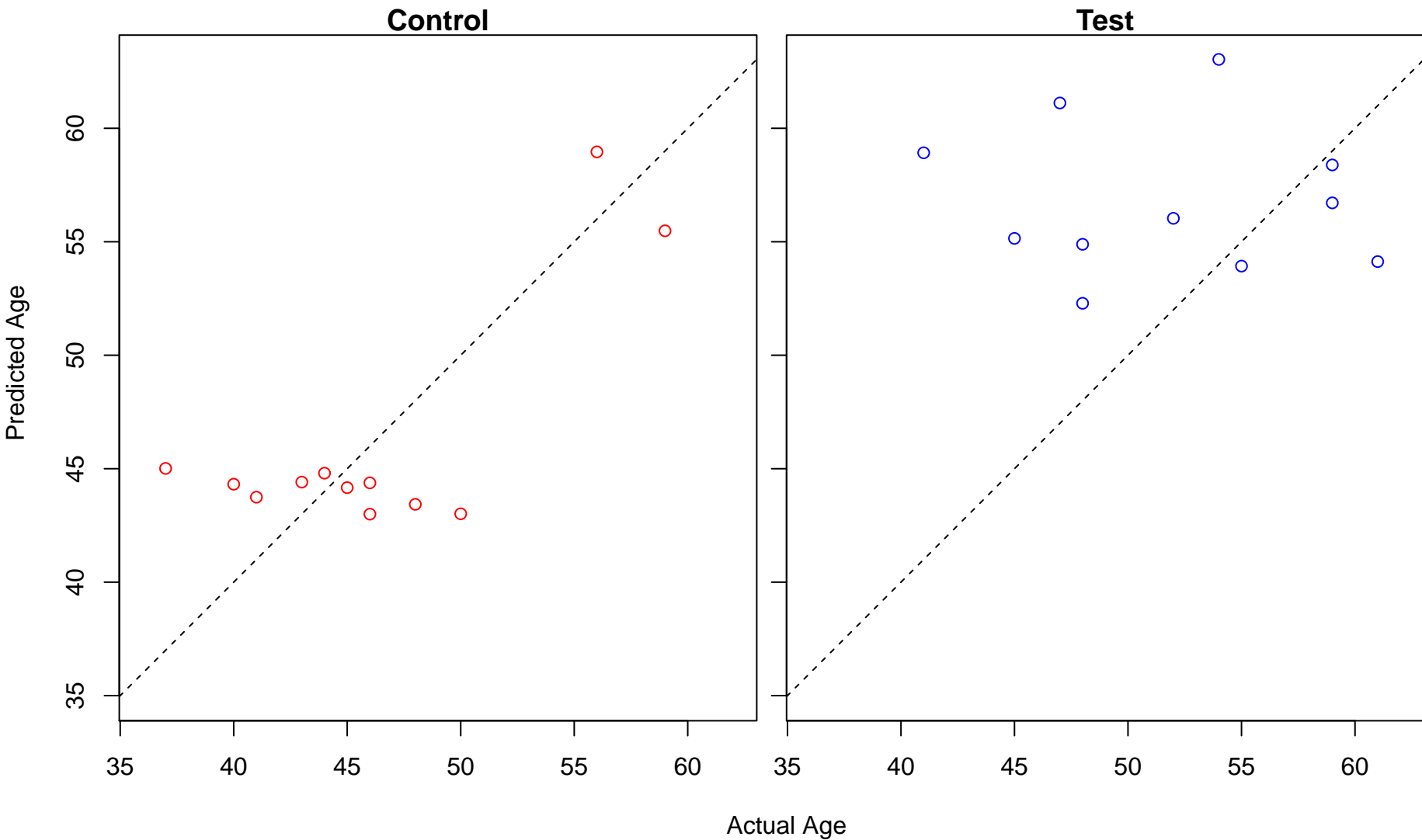


Actual Age

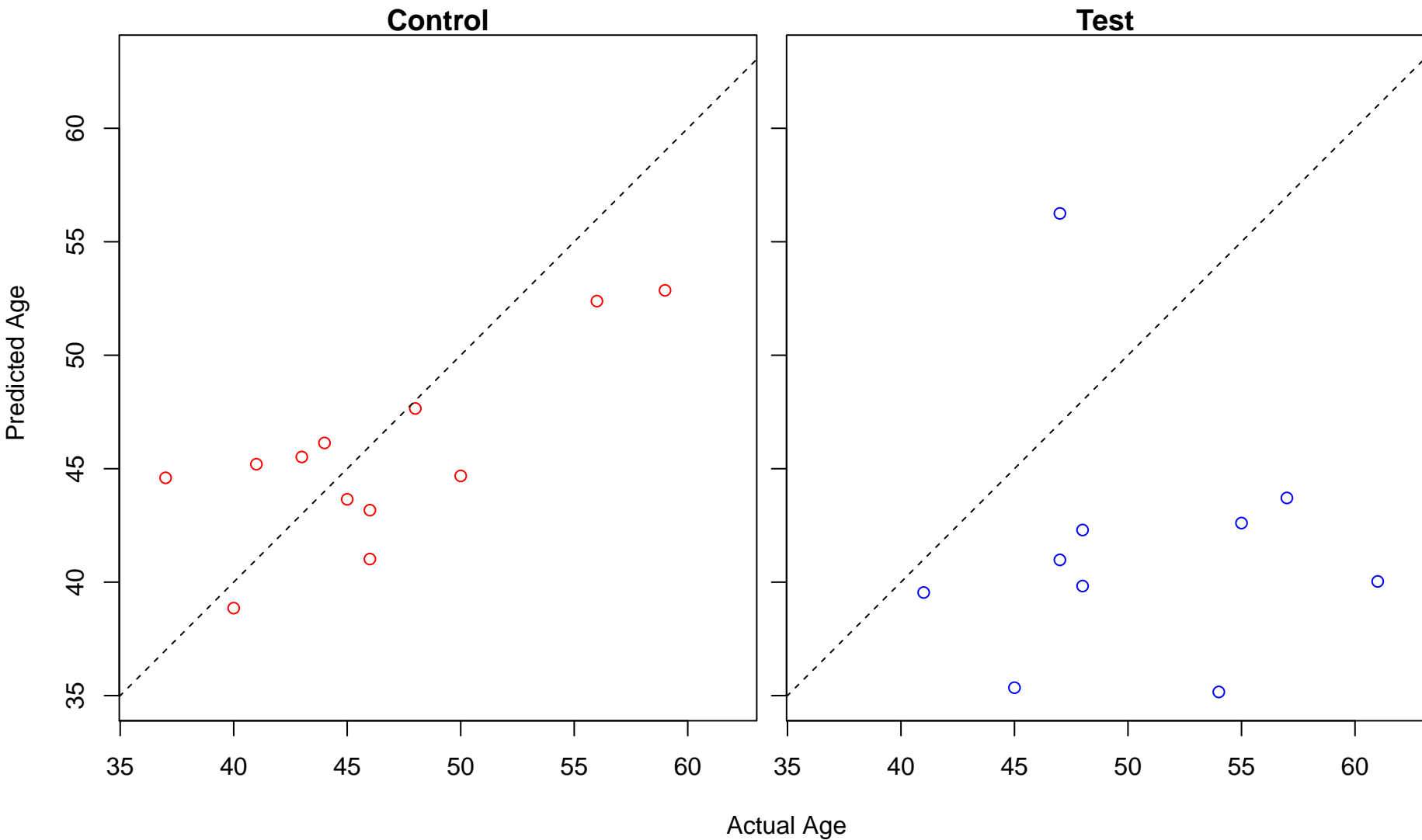
proteasome assembly (Score: 3.342363)



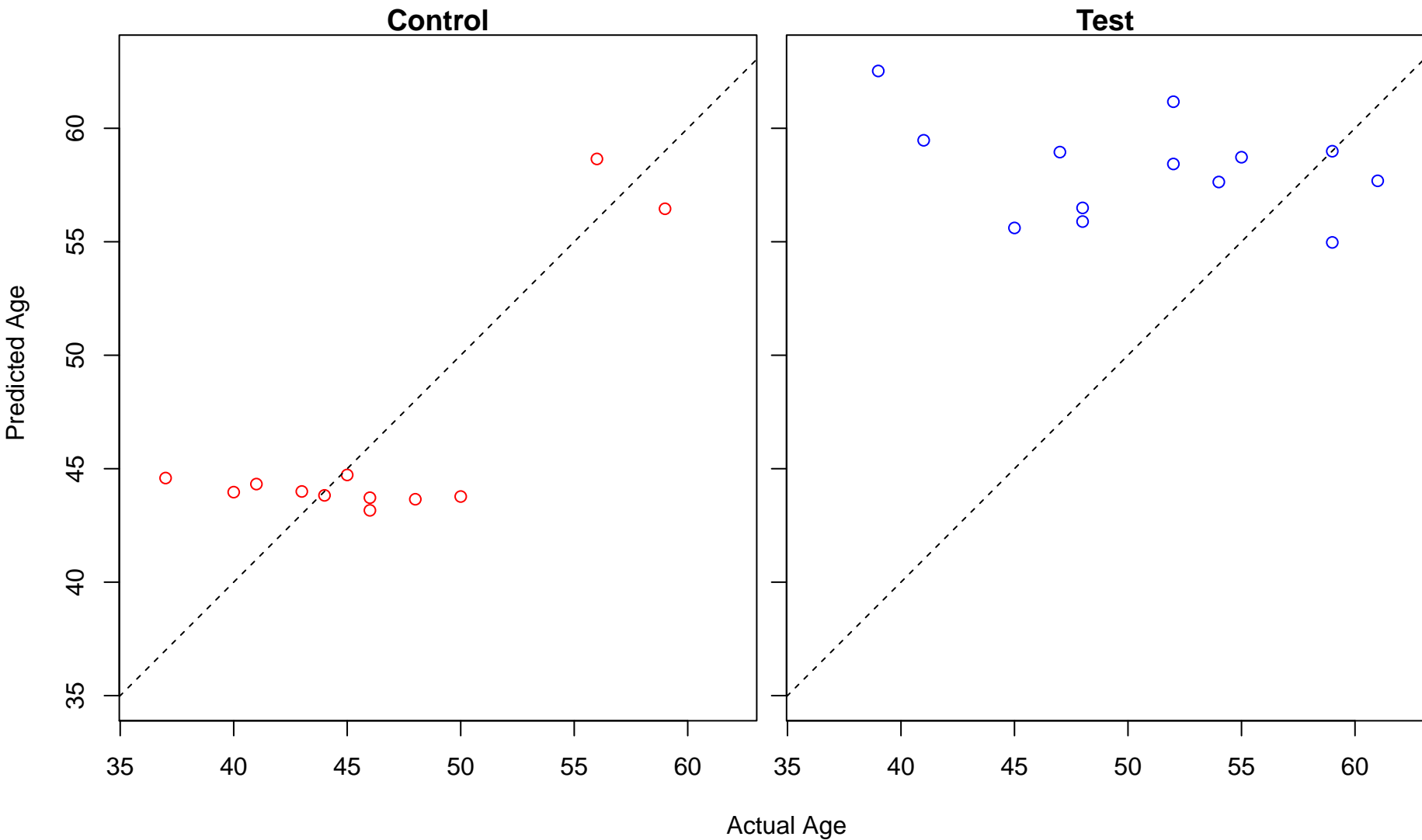
pigment cell differentiation (Score: 3.342279)



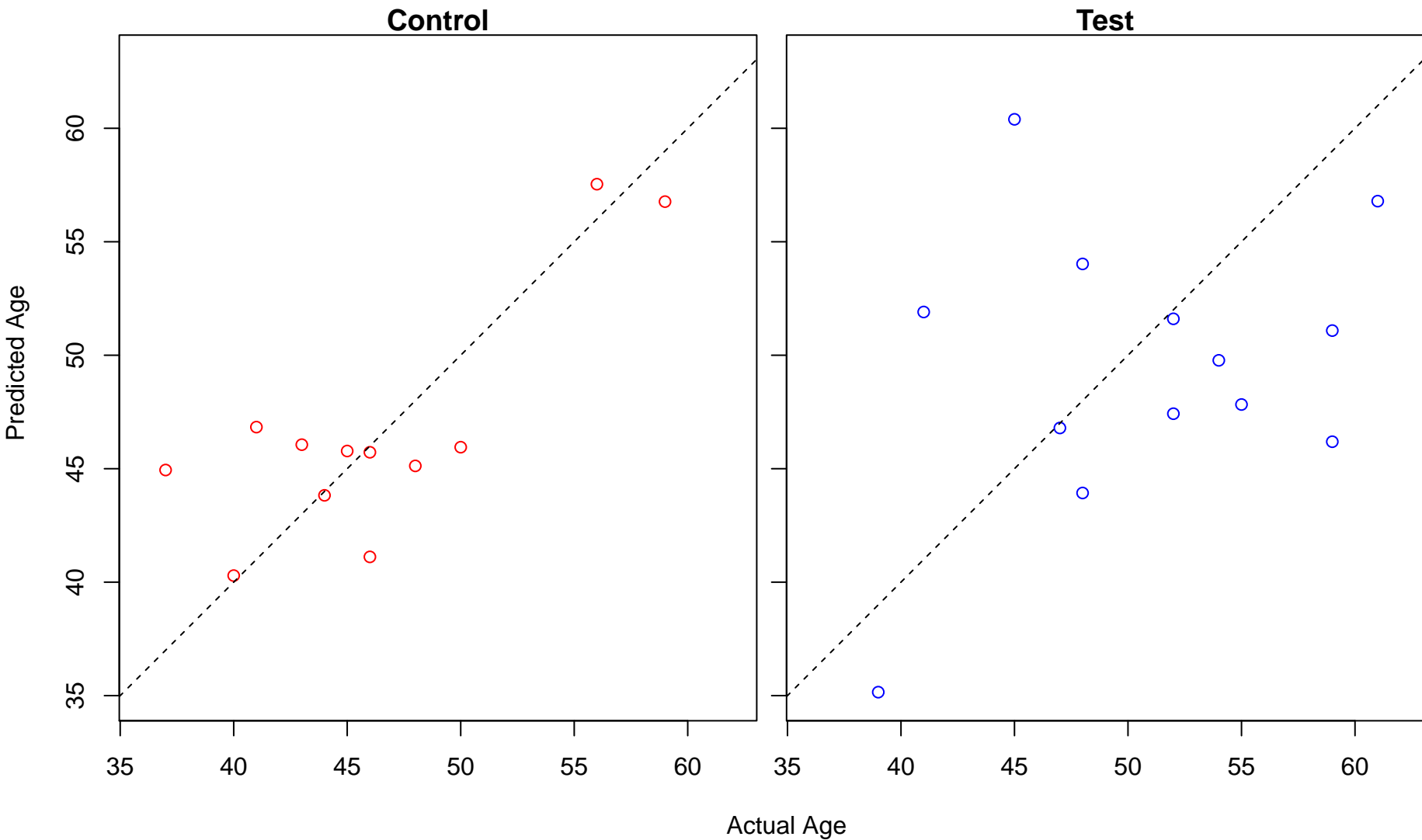
establishment of protein localization to endoplasmic reticulum (Score: 3.337637)



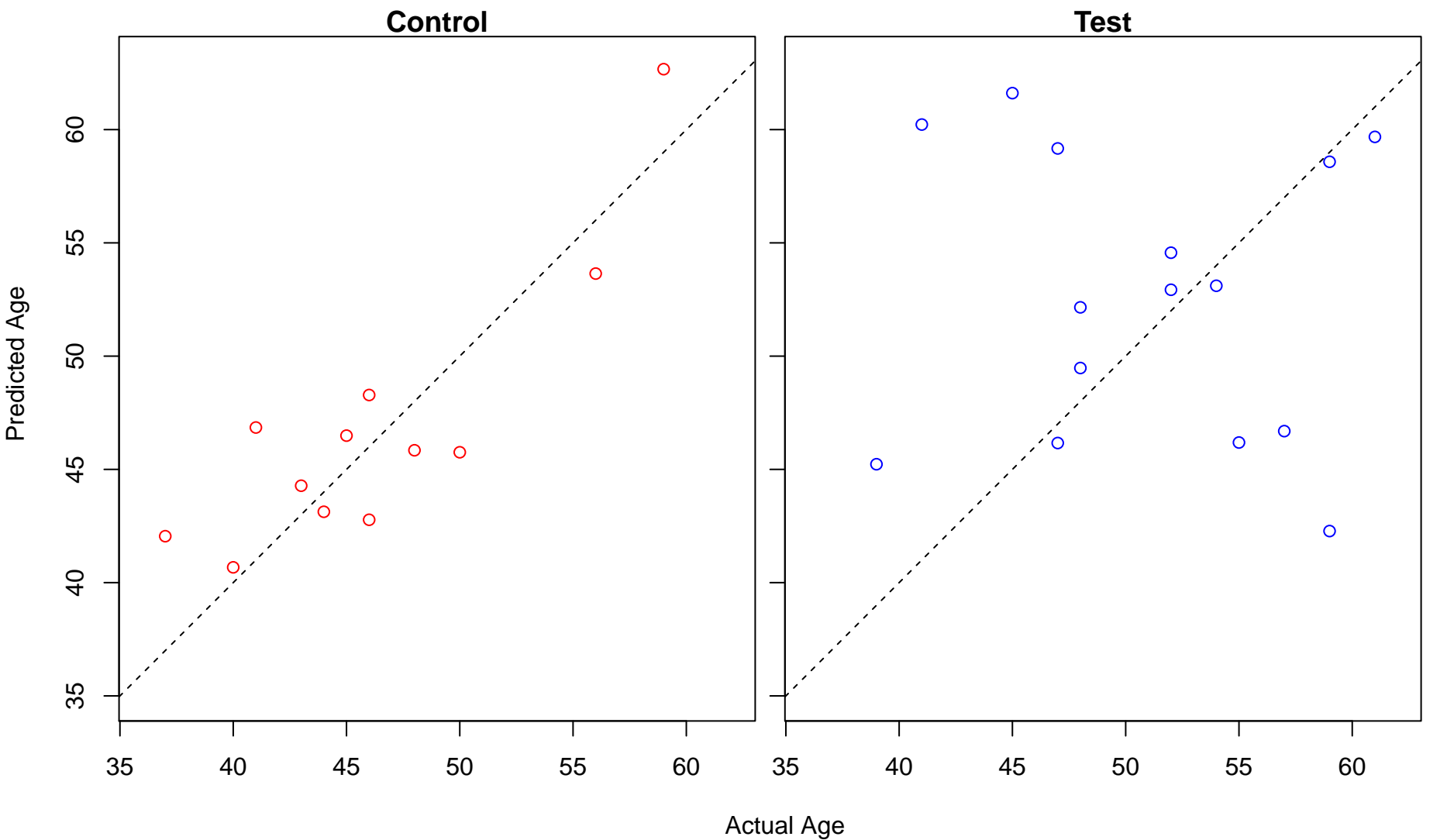
regulation of Wnt signaling pathway (Score: 3.337627)



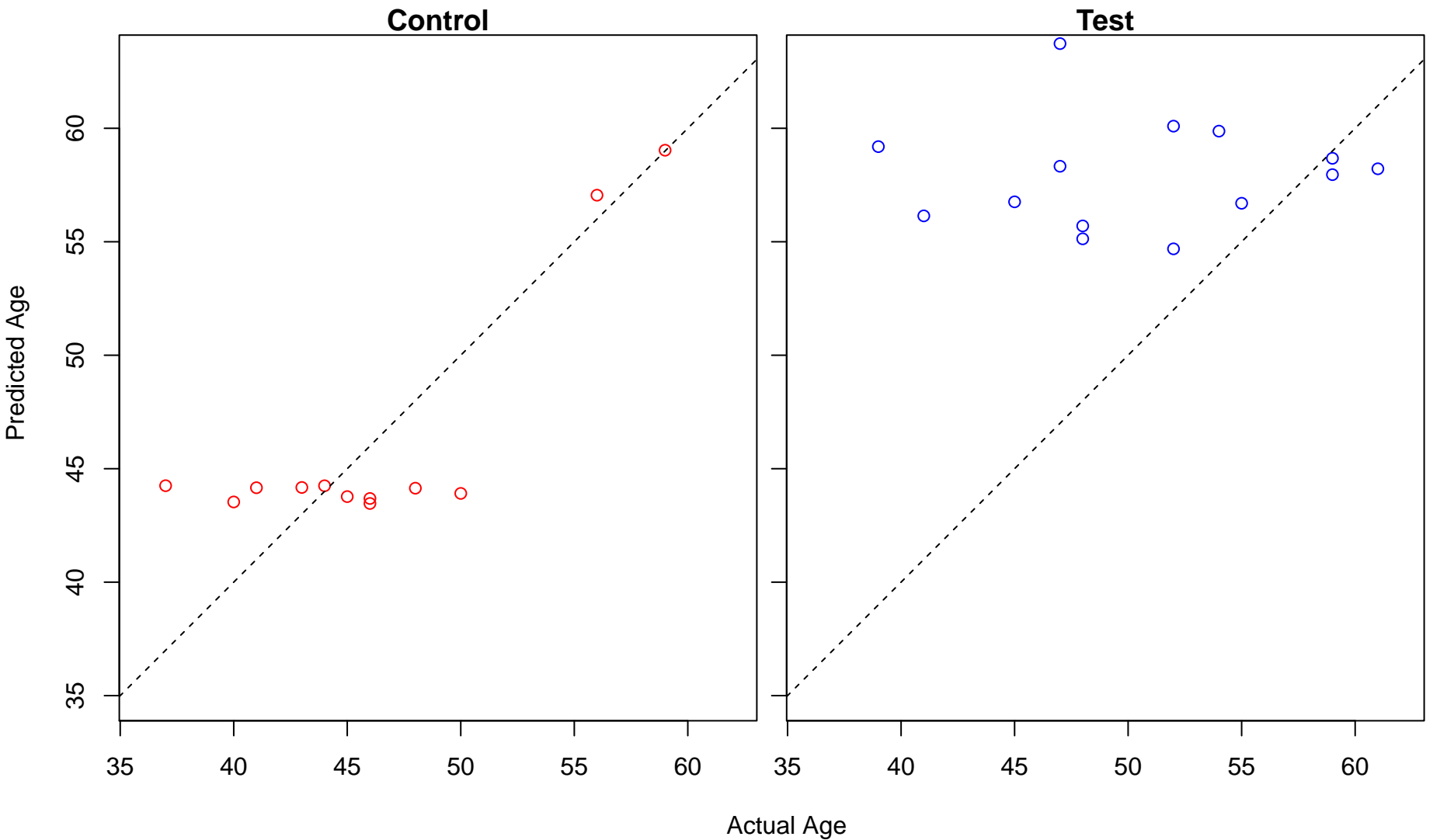
lipoprotein metabolic process (Score: 3.337437)



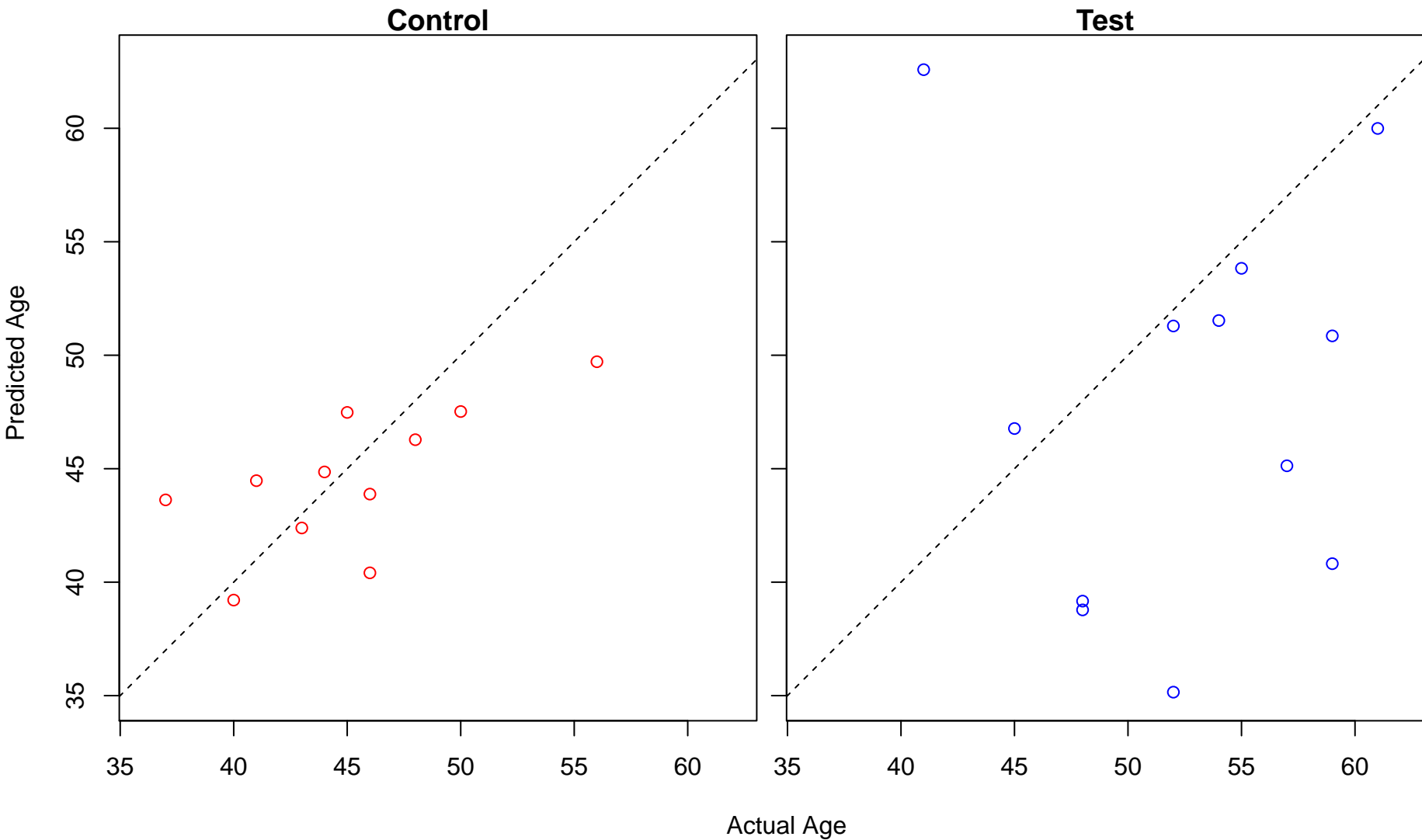
response based on somatic recombination of immune receptors built from immunoglobulin superfamily c



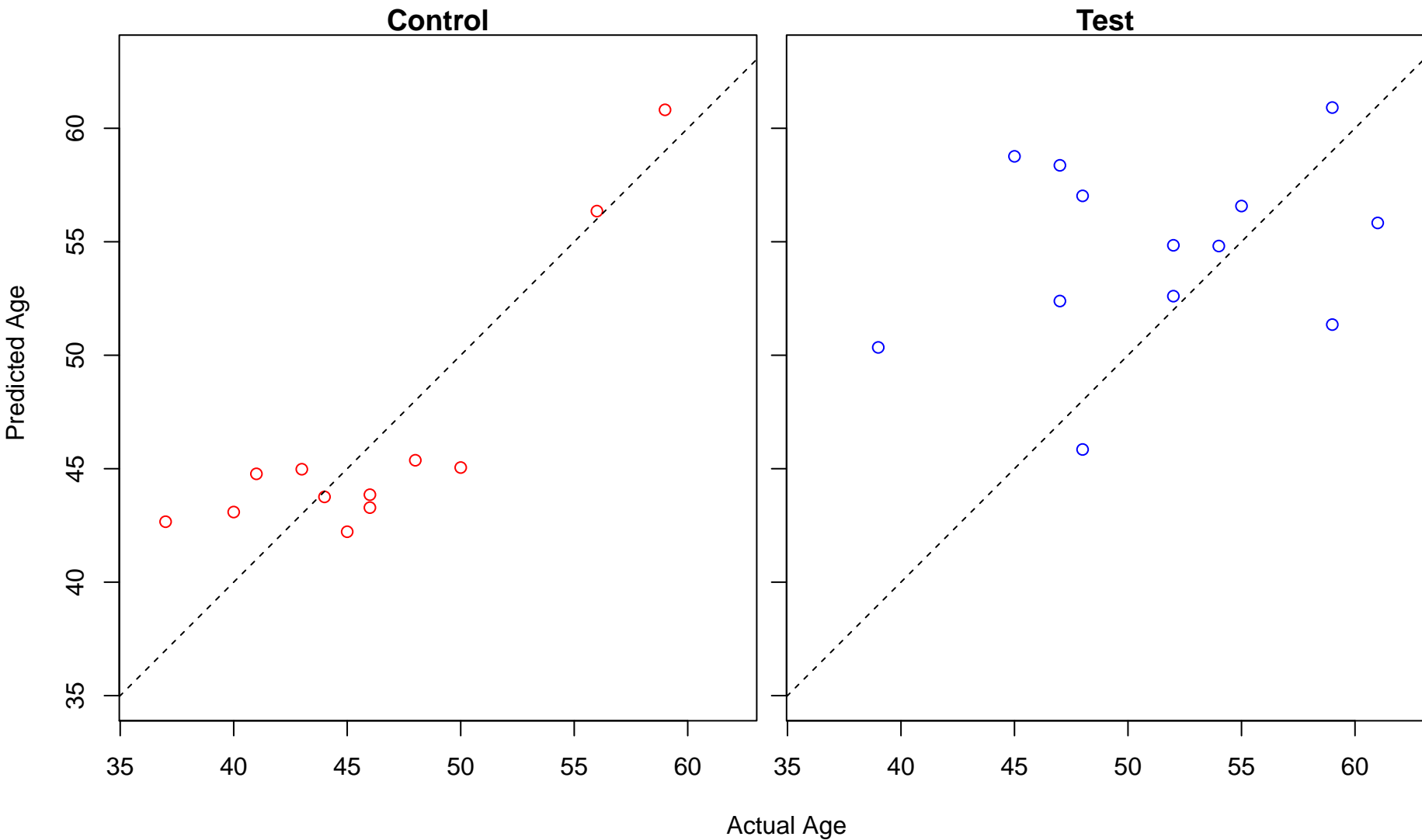
Regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (Score



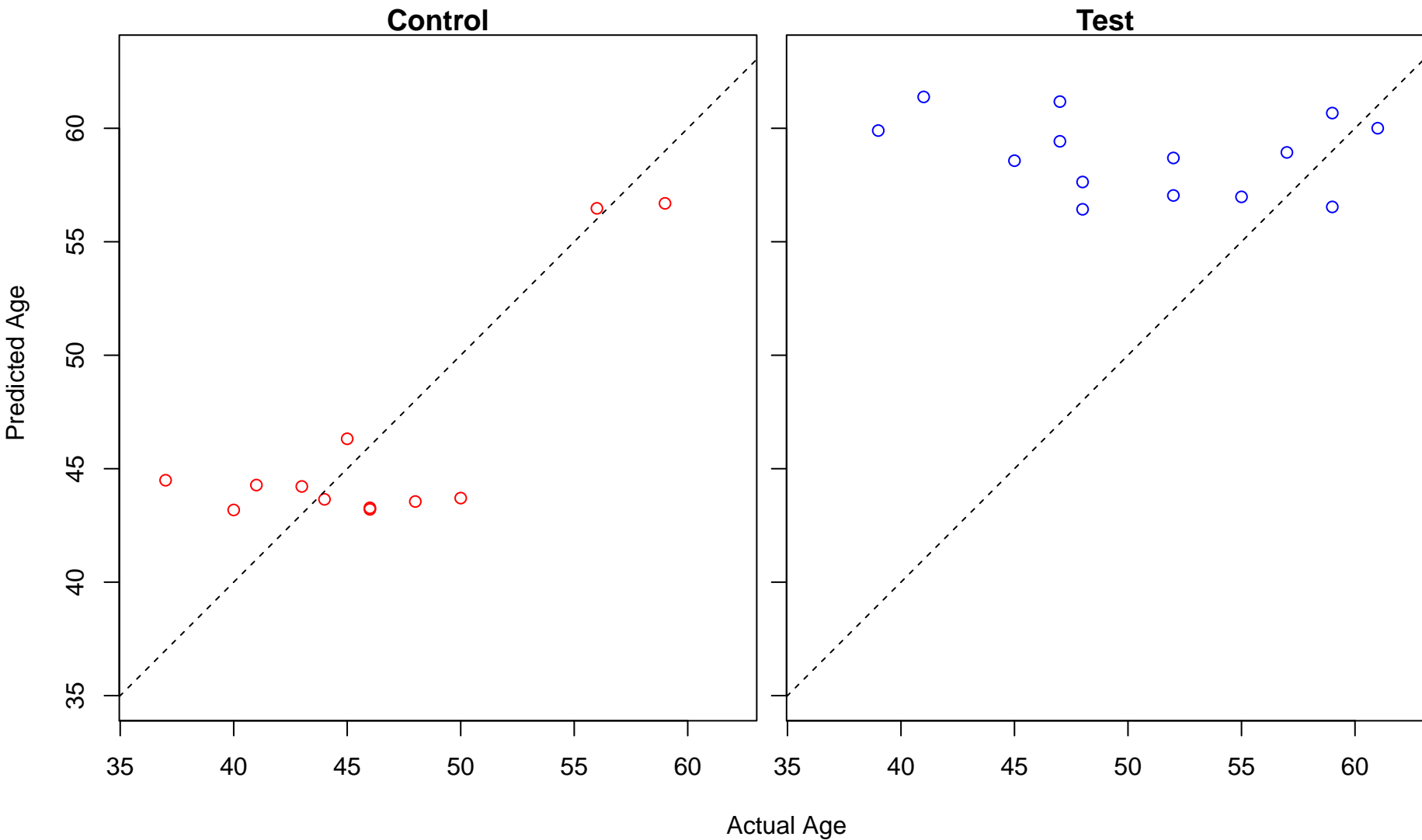
nucleotide catabolic process (Score: 3.332066)



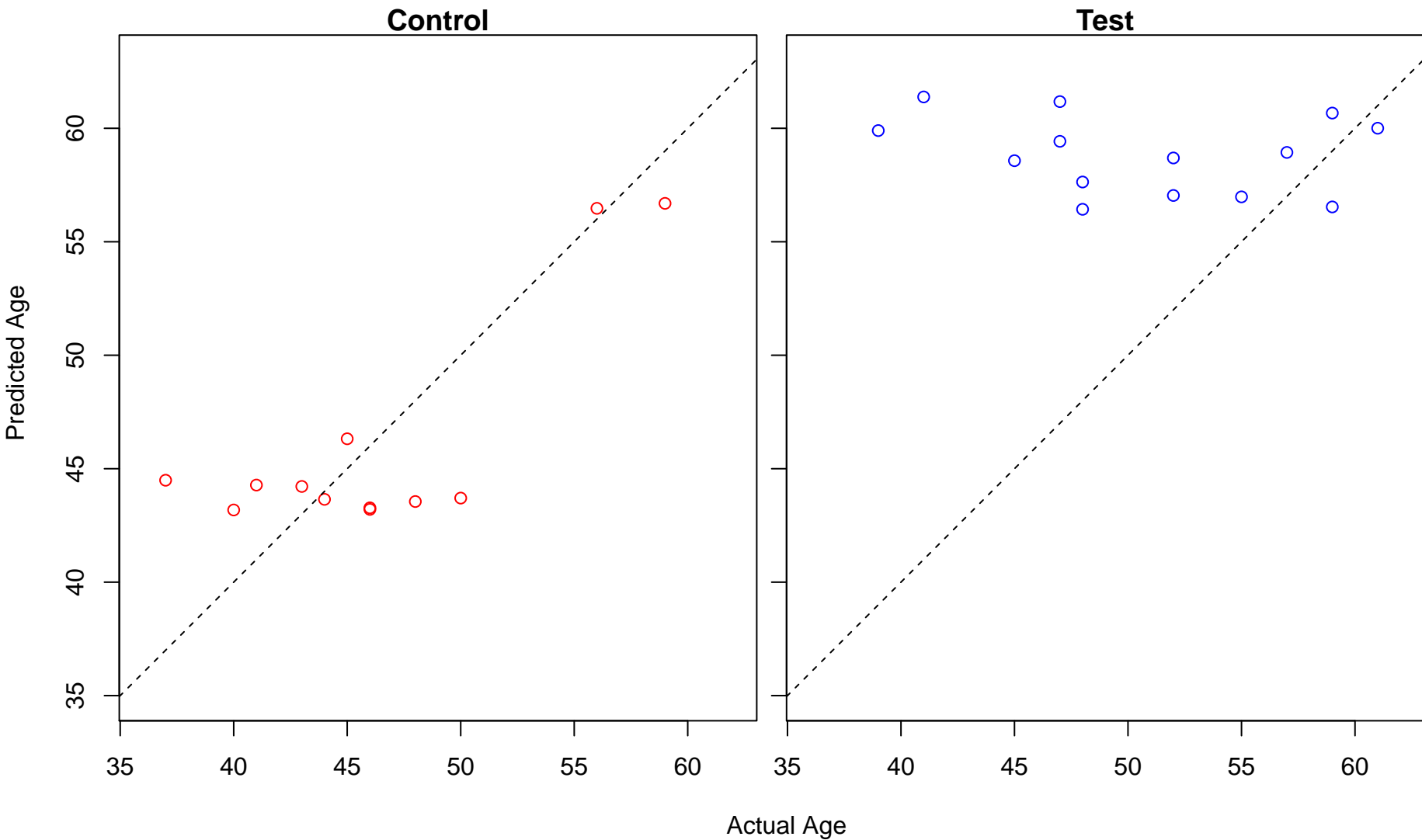
secondary metabolic process (Score: 3.331633)



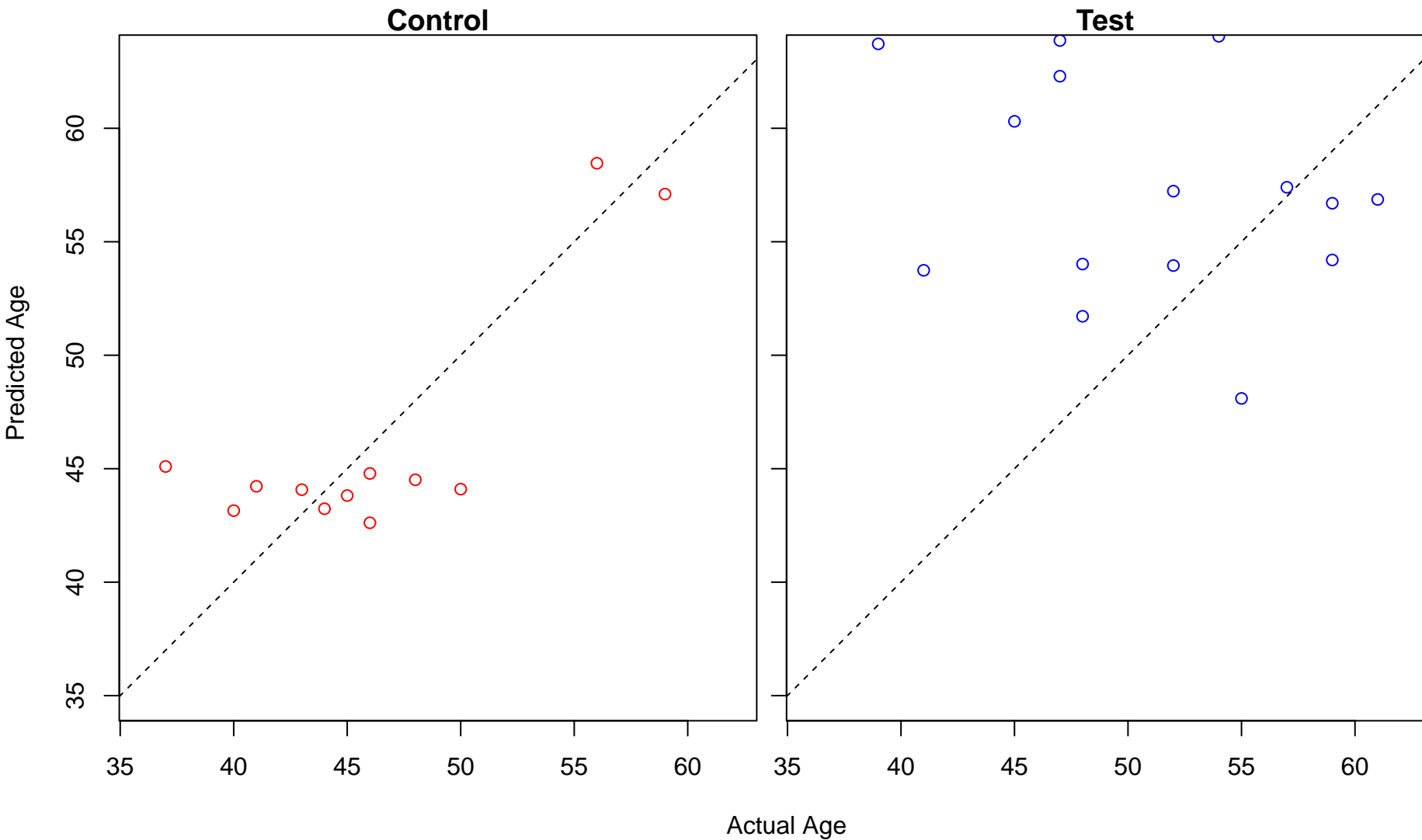
cerebellum development (Score: 3.331571)



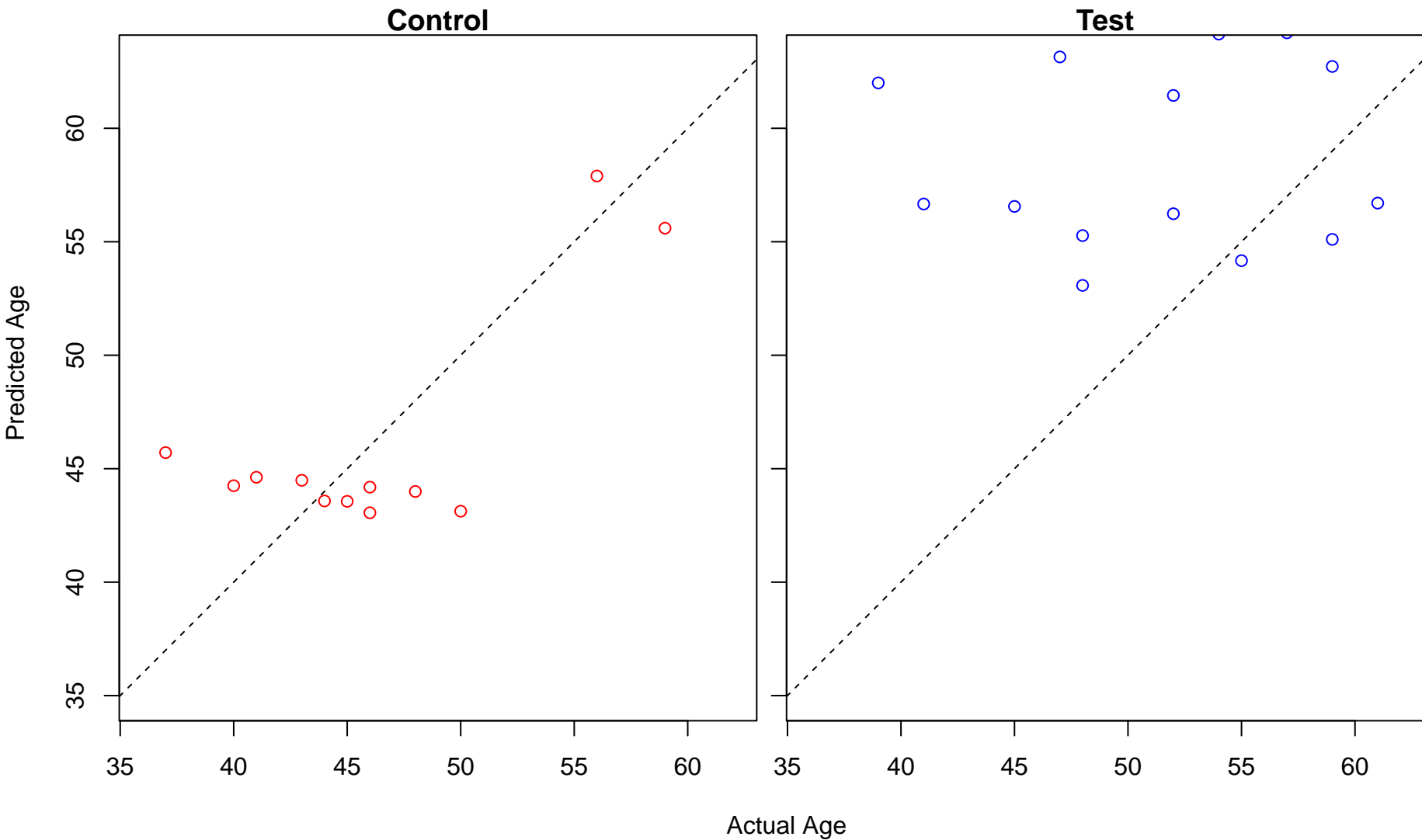
metencephalon development (Score: 3.331571)



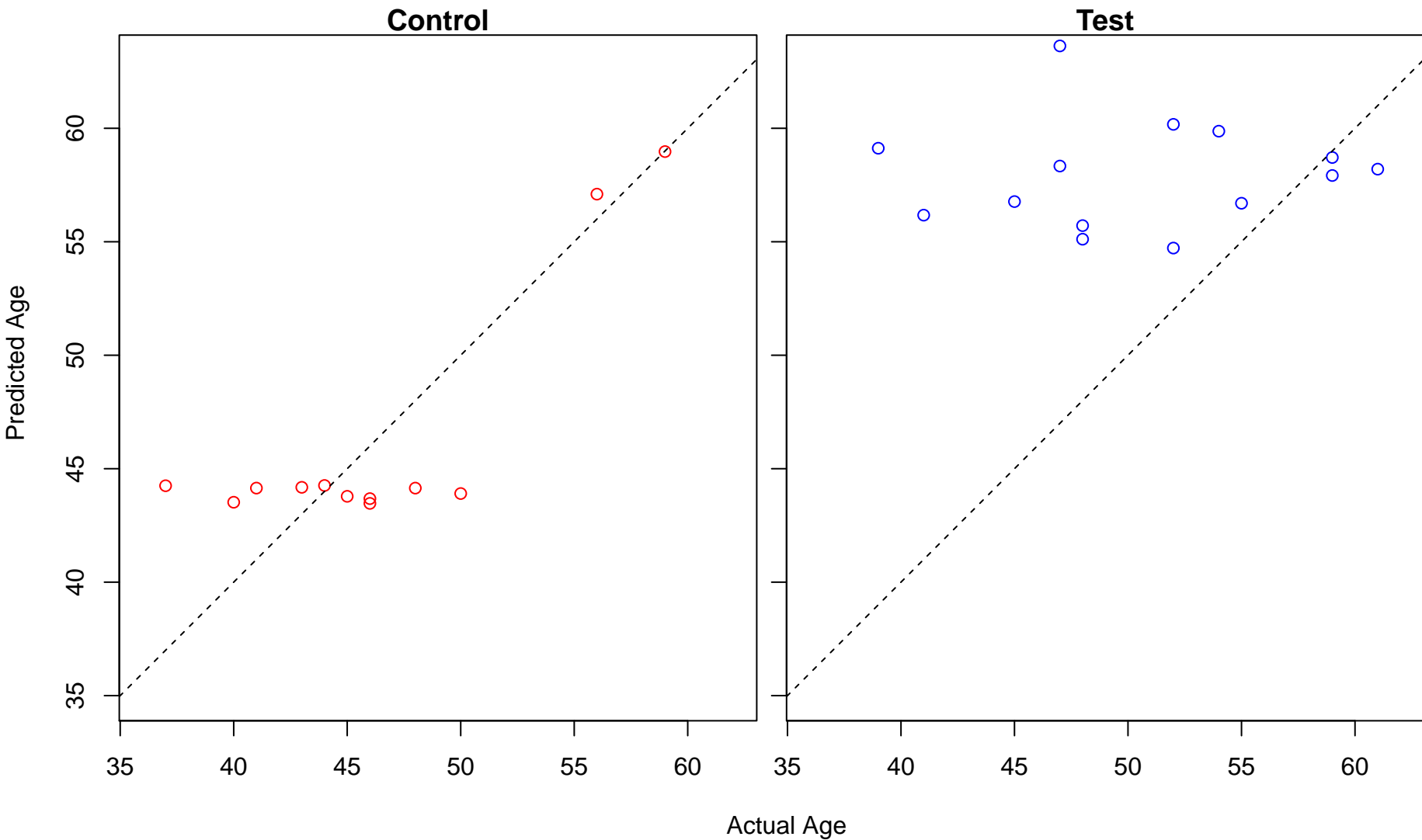
dating (Score: 3.330014)



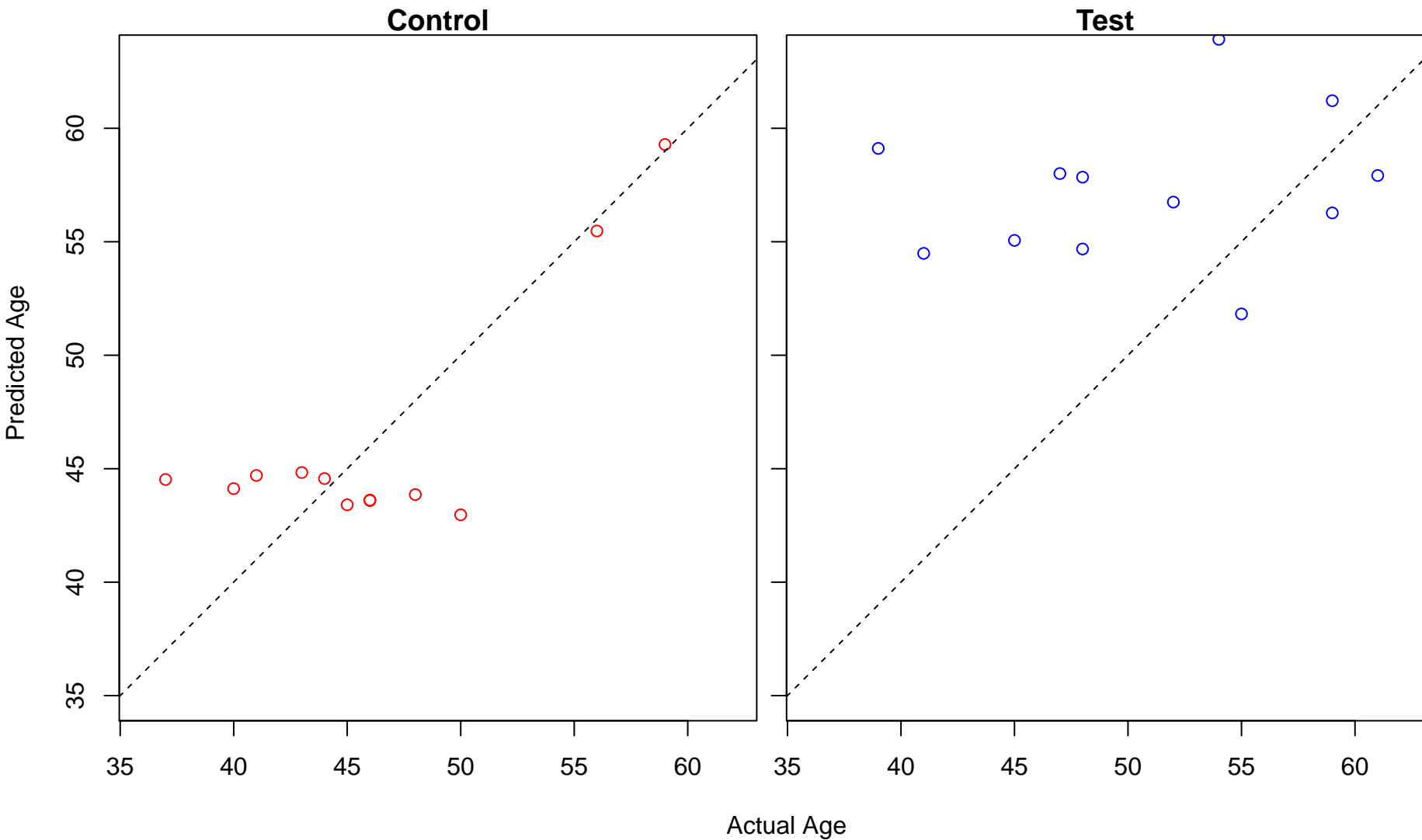
positive regulation of natural killer cell mediated cytotoxicity (Score: 3.327267)



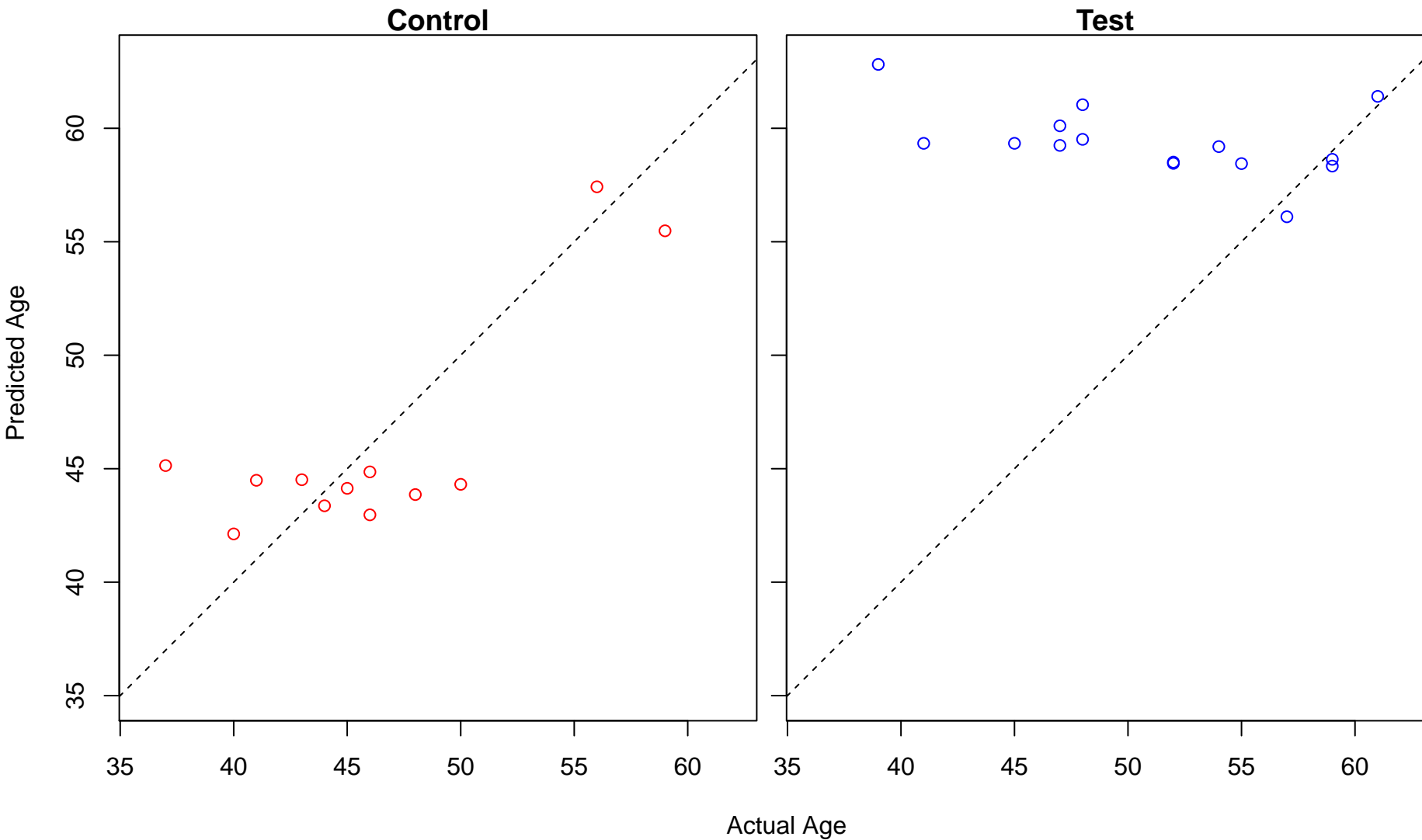
regulation of mitochondrial membrane permeability (Score: 3.326188)



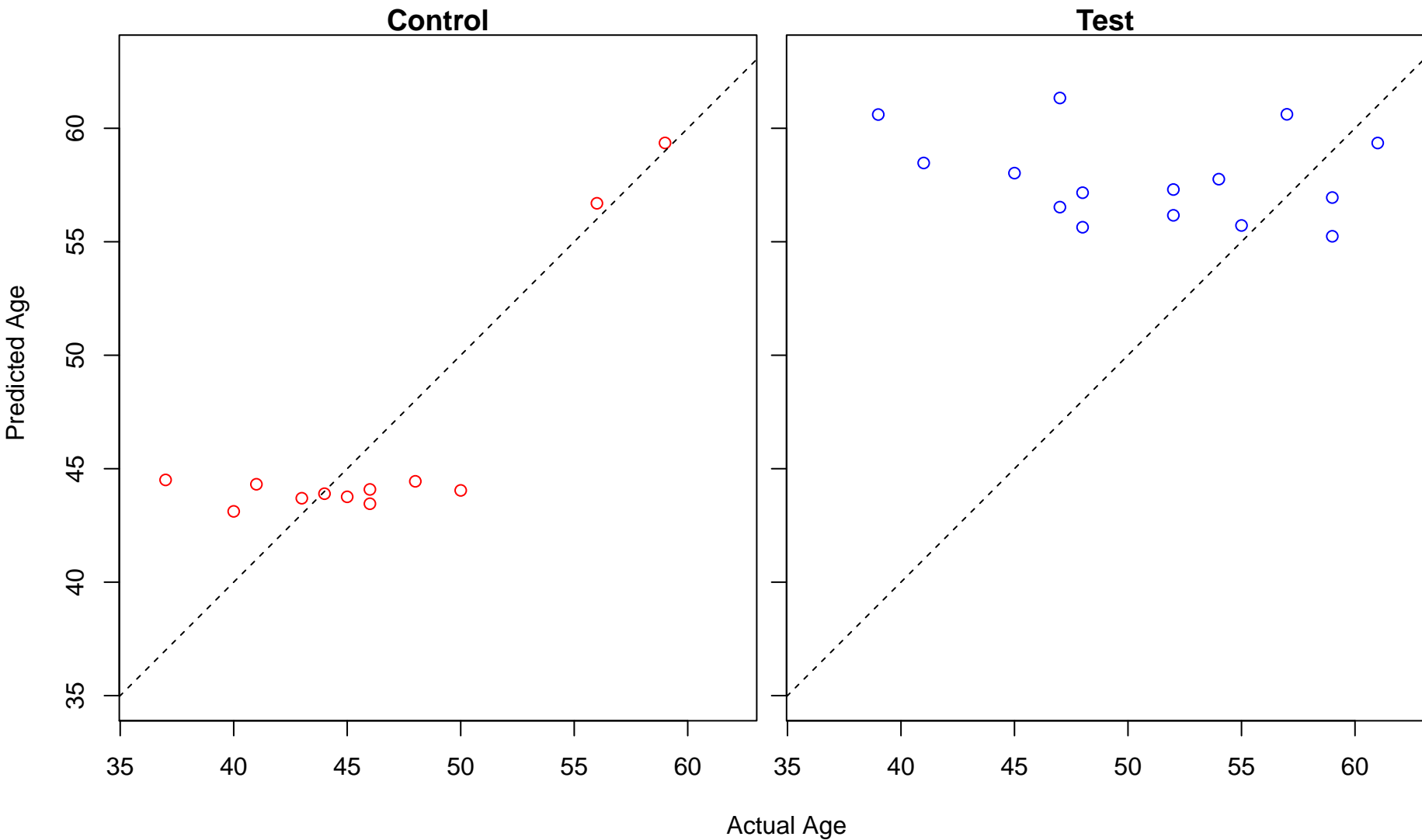
regulation of transcription regulatory region DNA binding (Score: 3.325447)



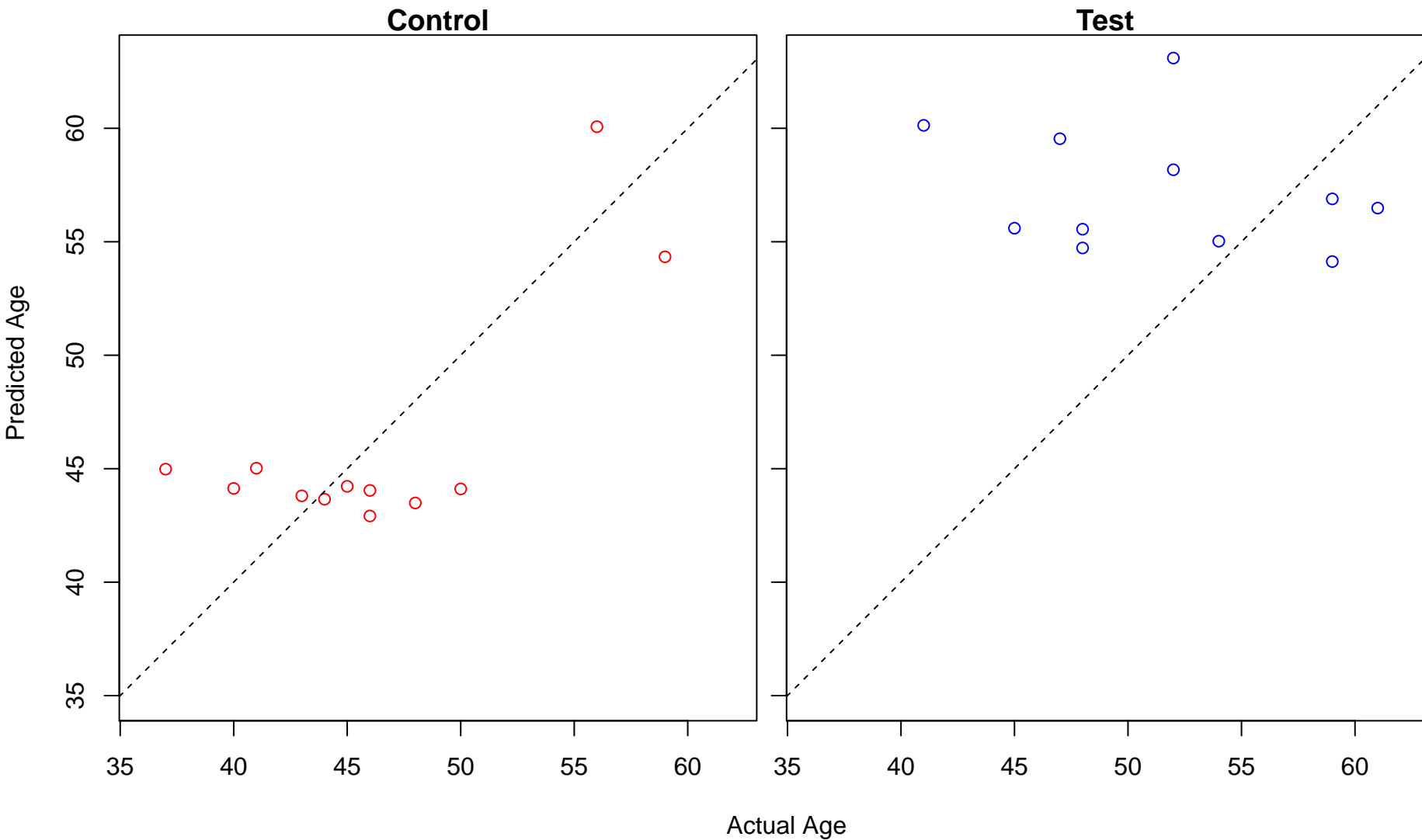
negative regulation of myoblast differentiation (Score: 3.321210)



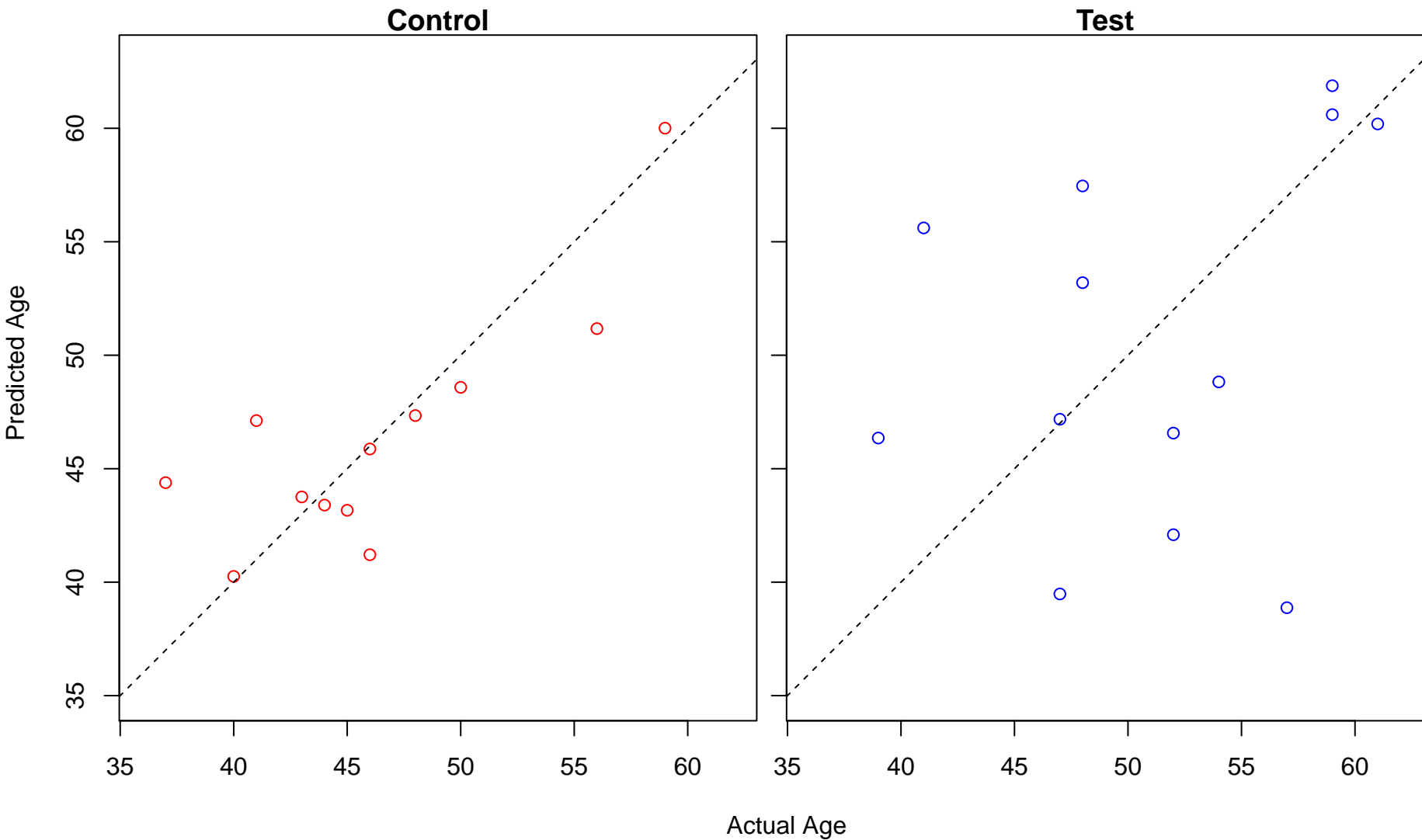
regulation of nuclease activity (Score: 3.319819)



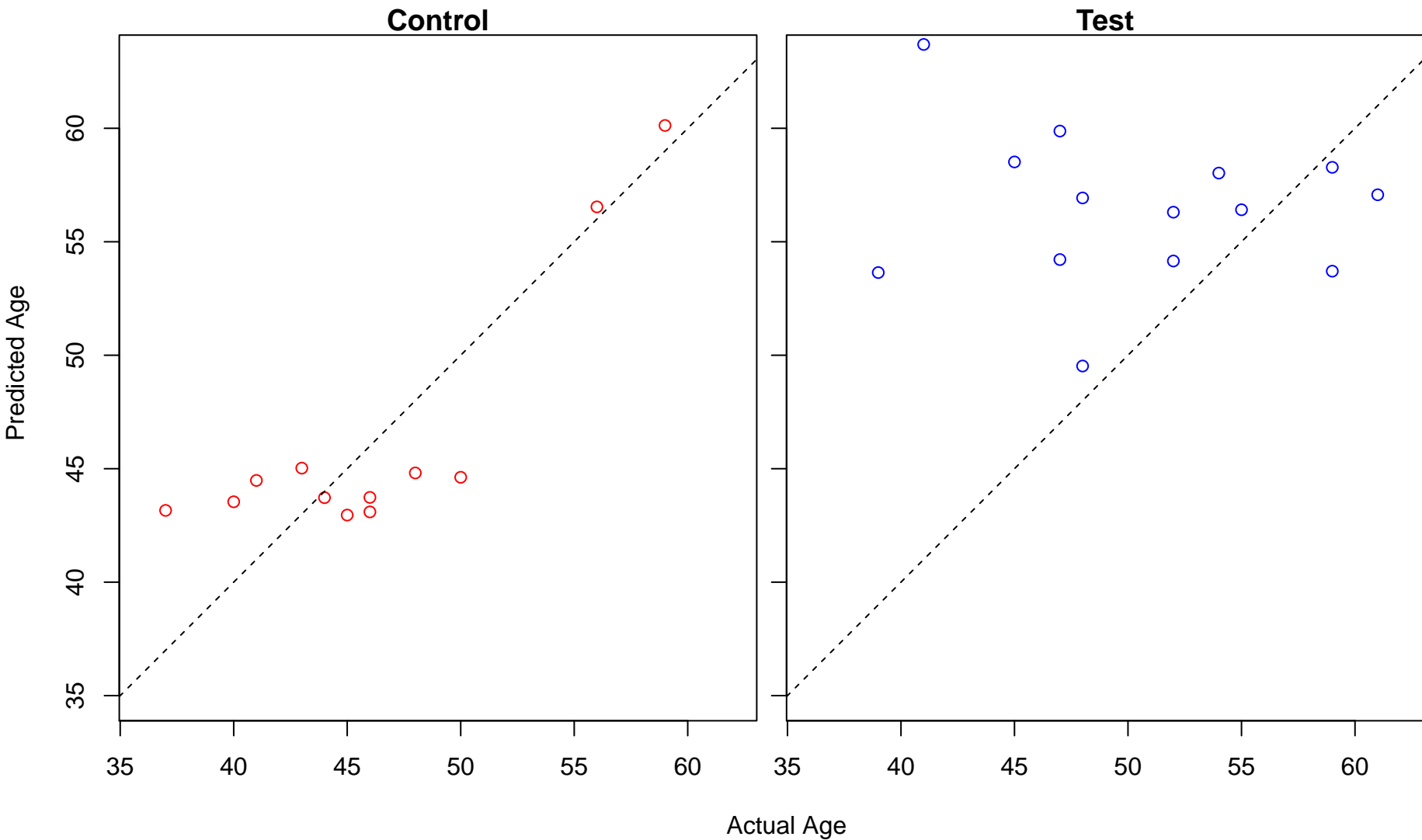
defense response to bacterium (Score: 3.315877)



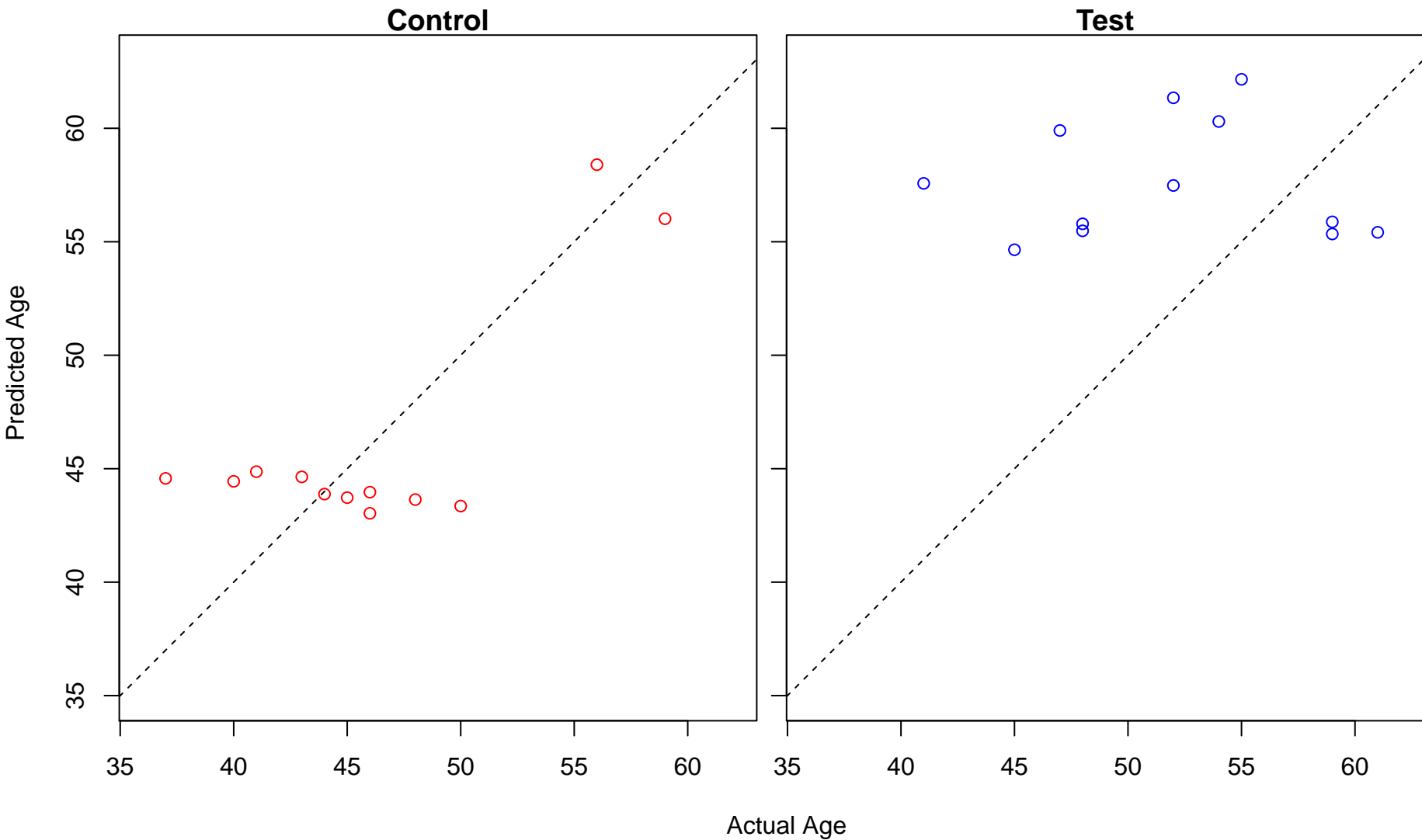
sulfur compound catabolic process (Score: 3.314904)



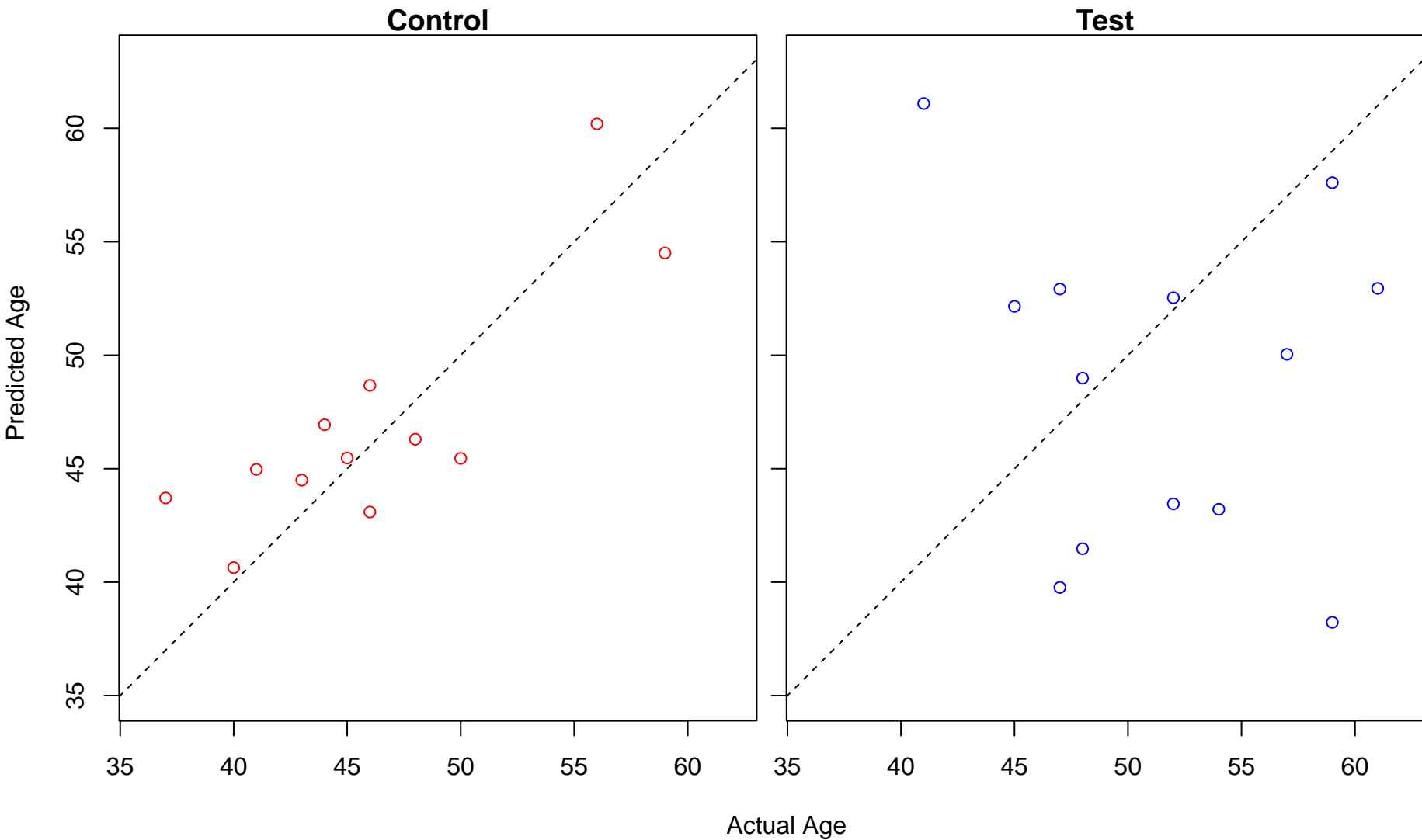
cofactor metabolic process (Score: 3.314903)



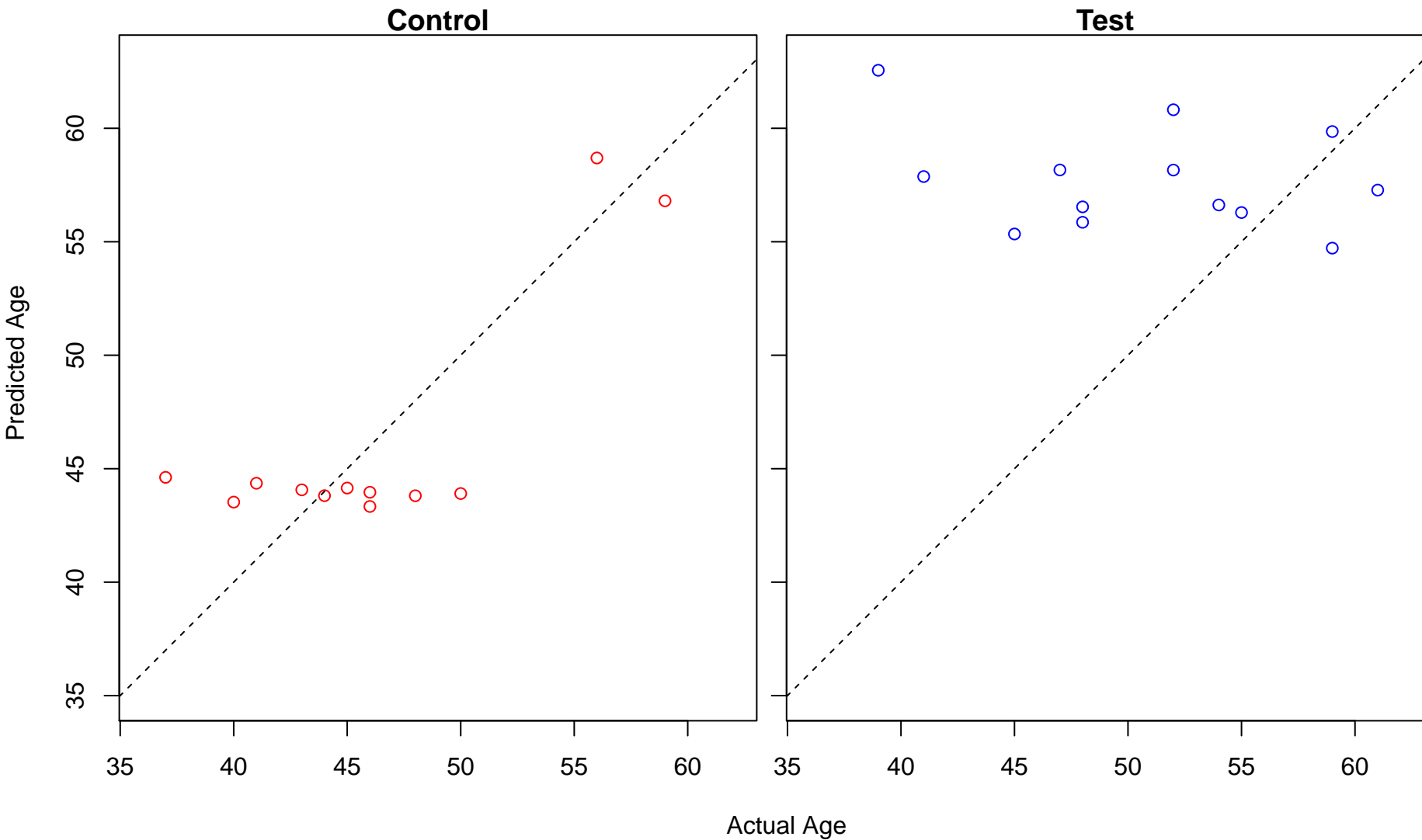
ephrin receptor signaling pathway (Score: 3.314796)



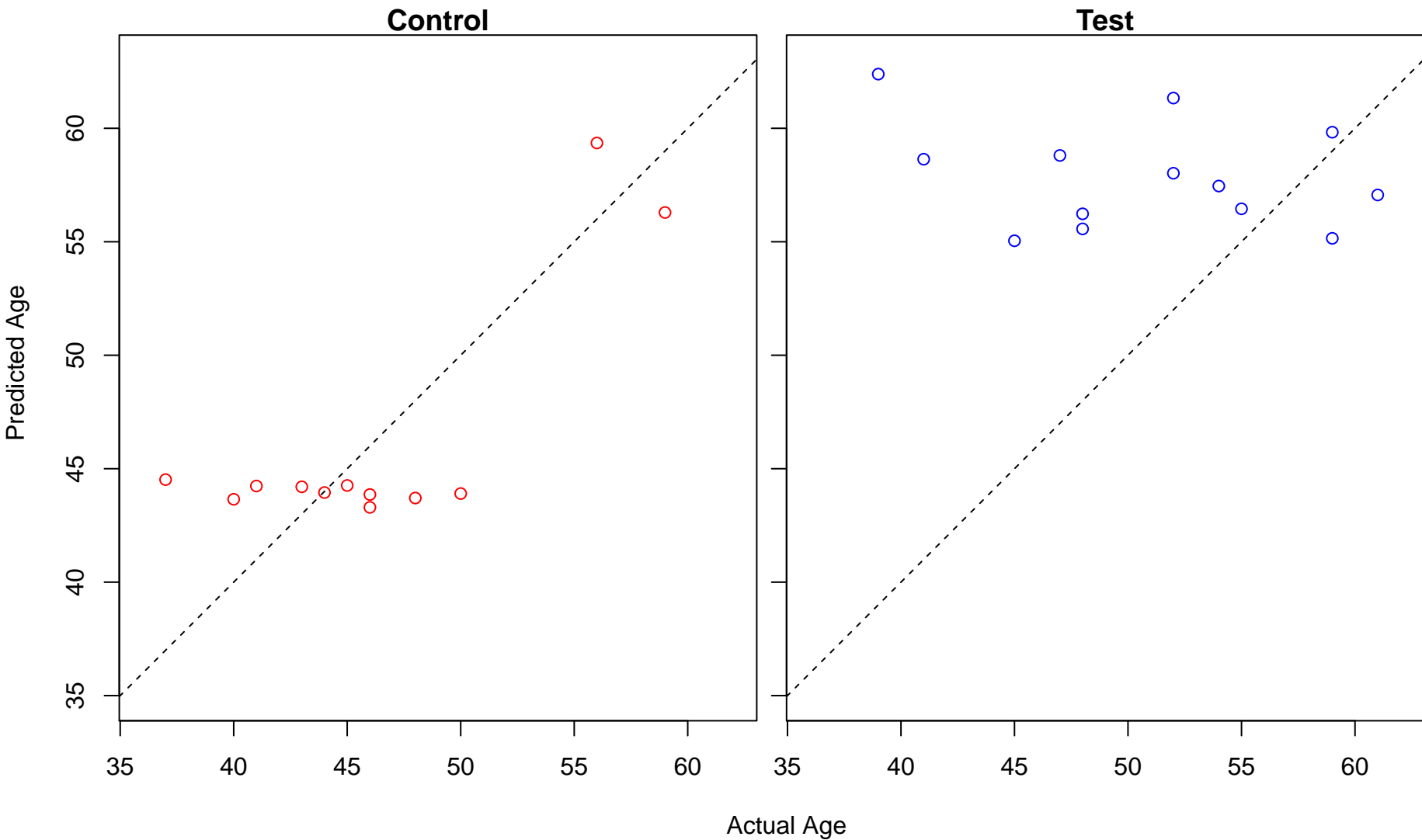
immune effector process (Score: 3.314186)



DNA recombination (Score: 3.313583)

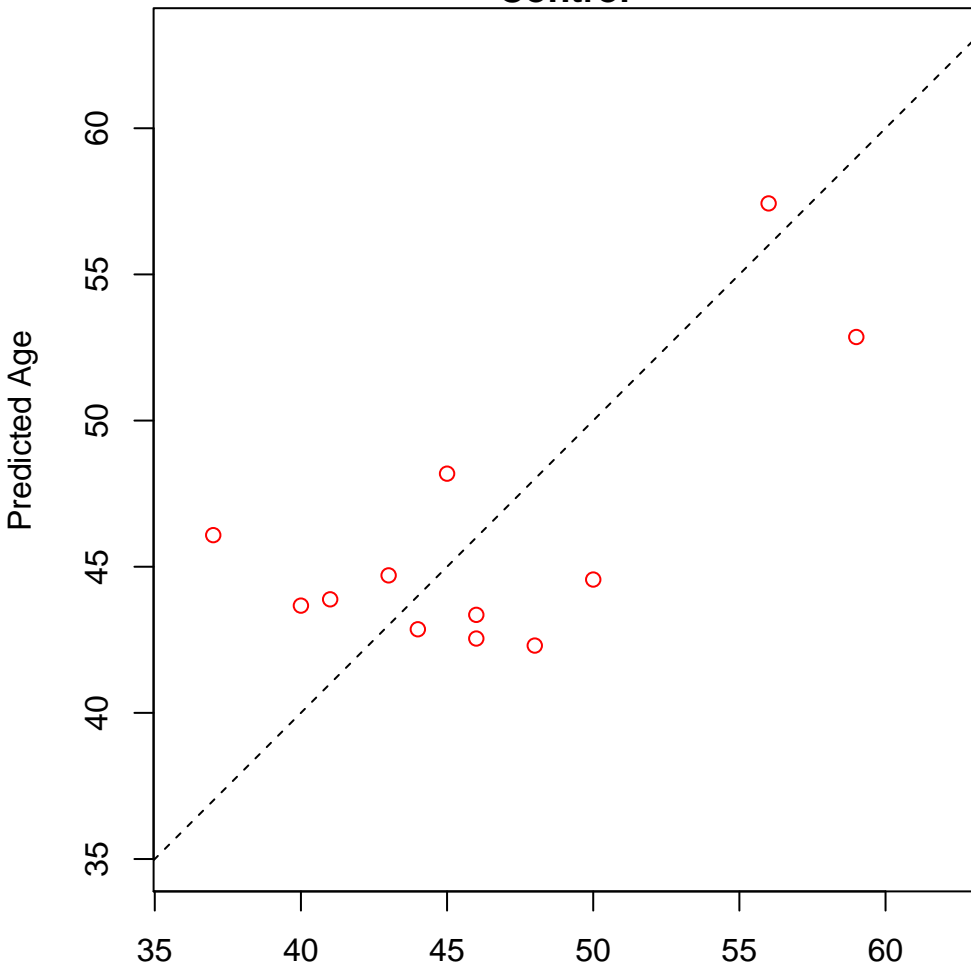


endosomal transport (Score: 3.313093)

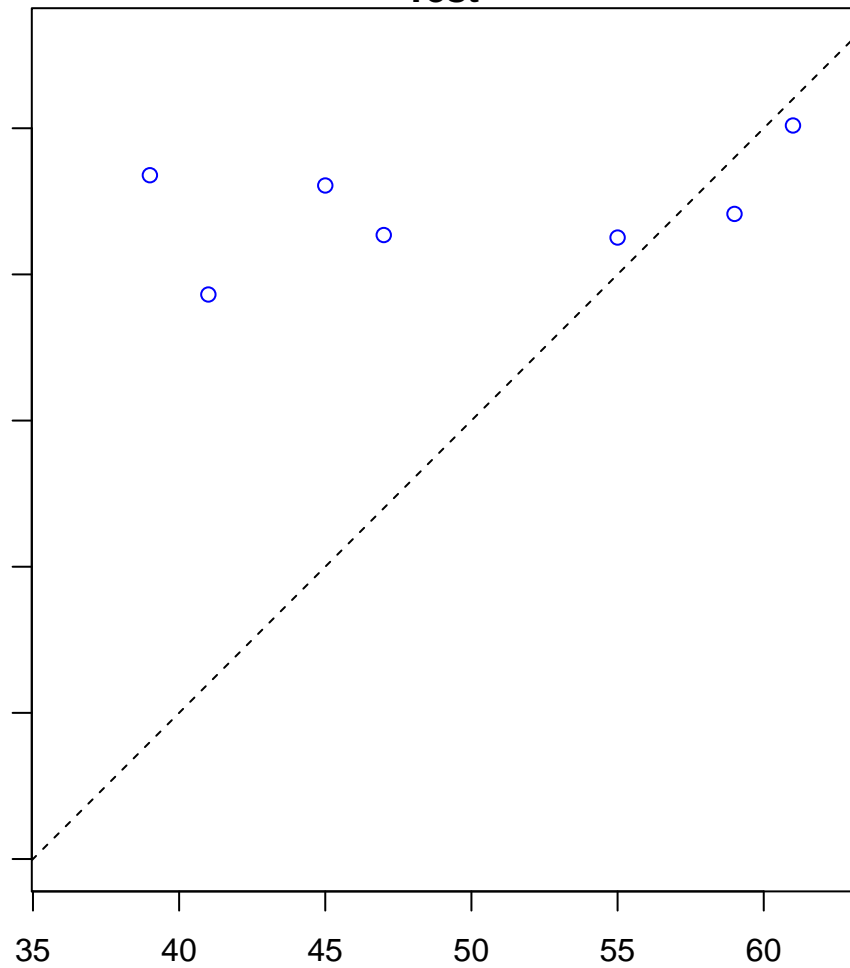


regulation of male gonad development (Score: 3.312744)

Control

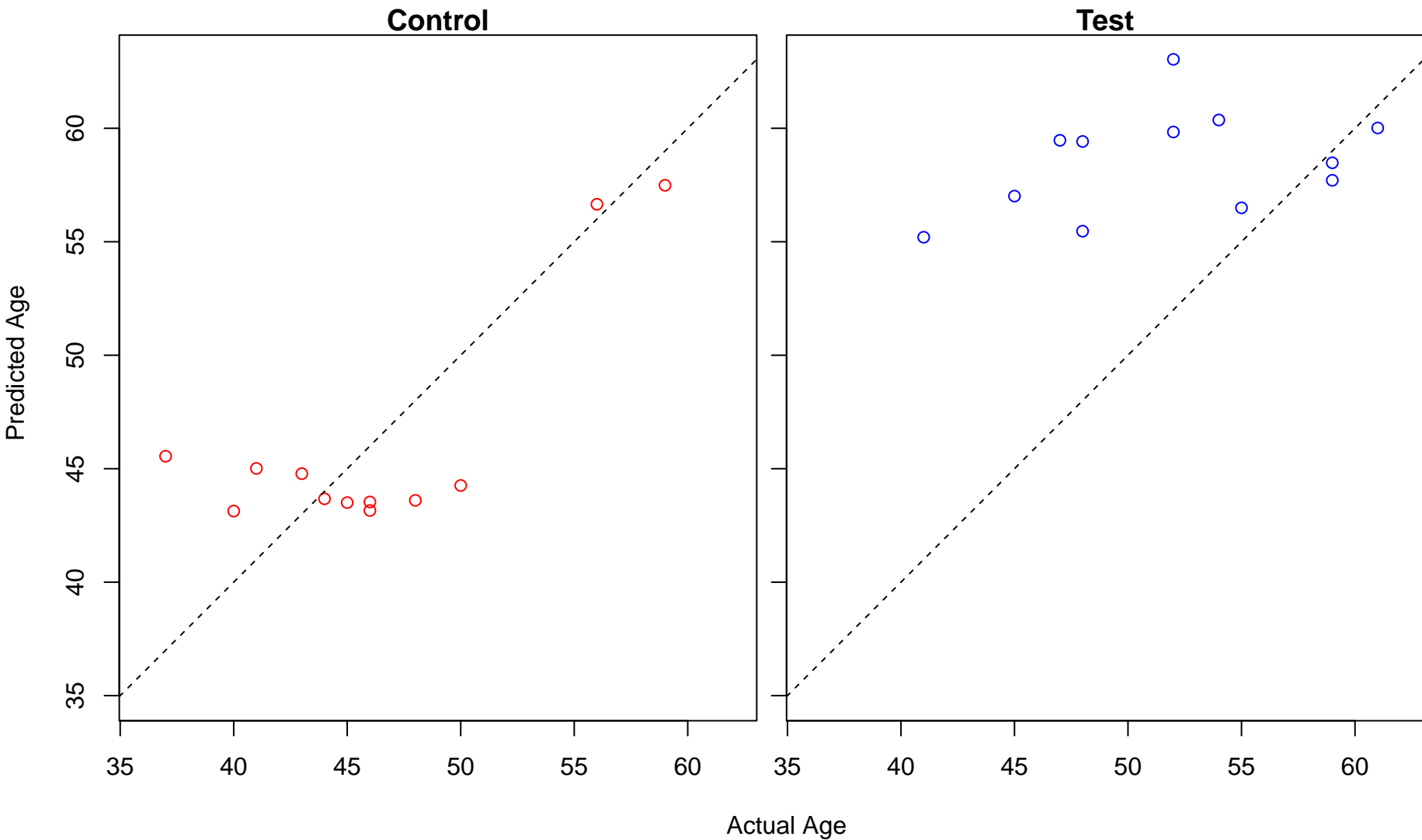


Test

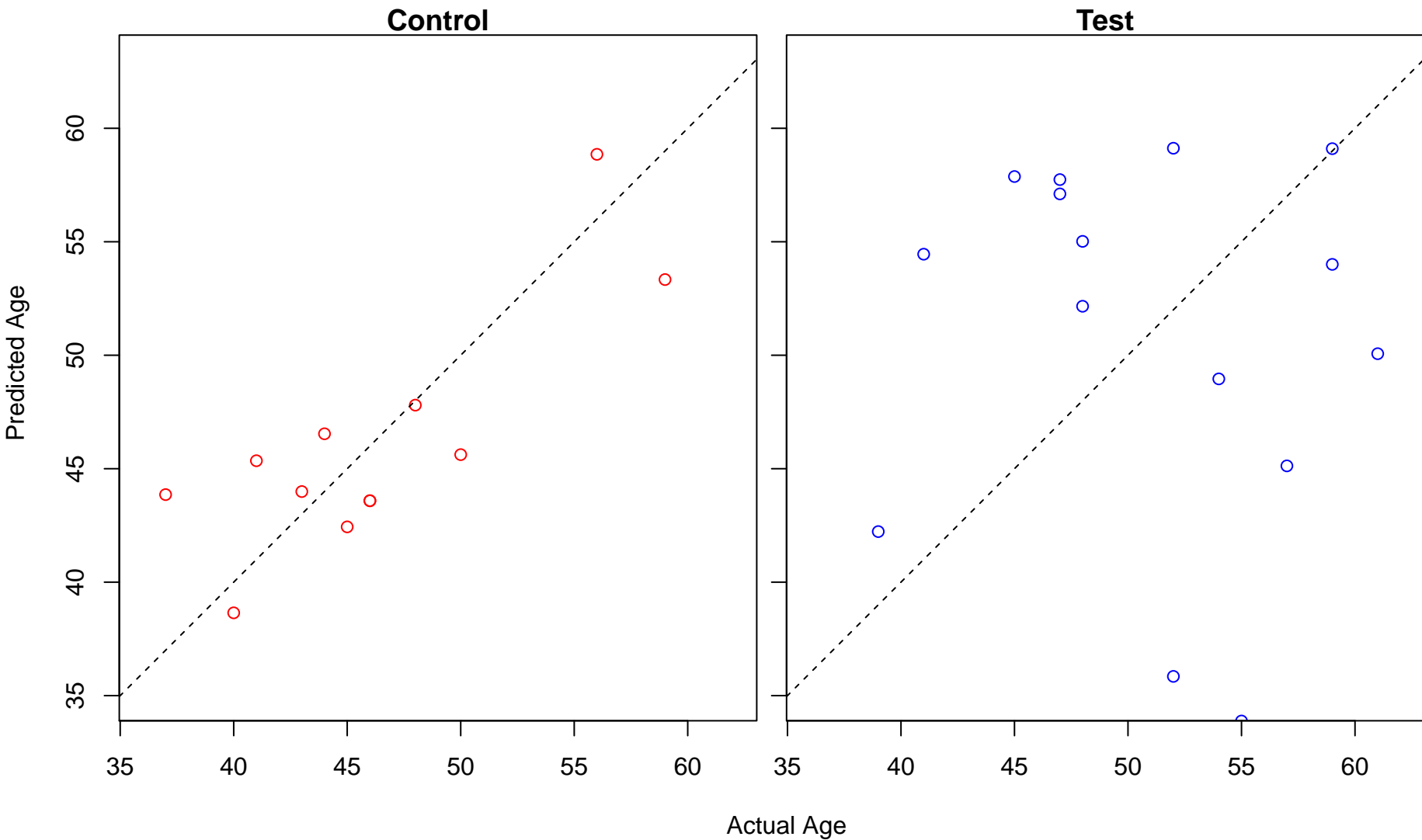


Actual Age

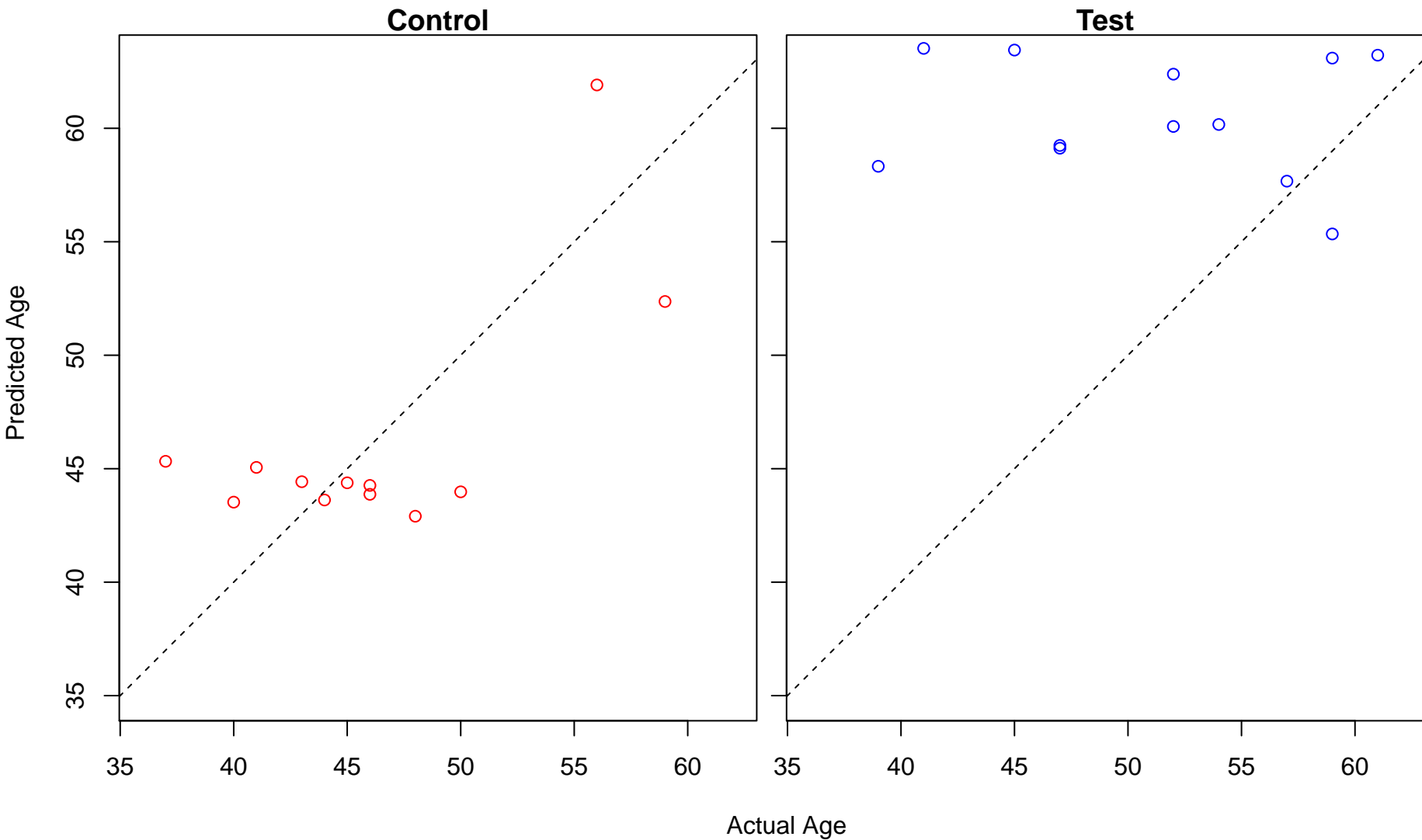
dicarboxylic acid catabolic process (Score: 3.312704)



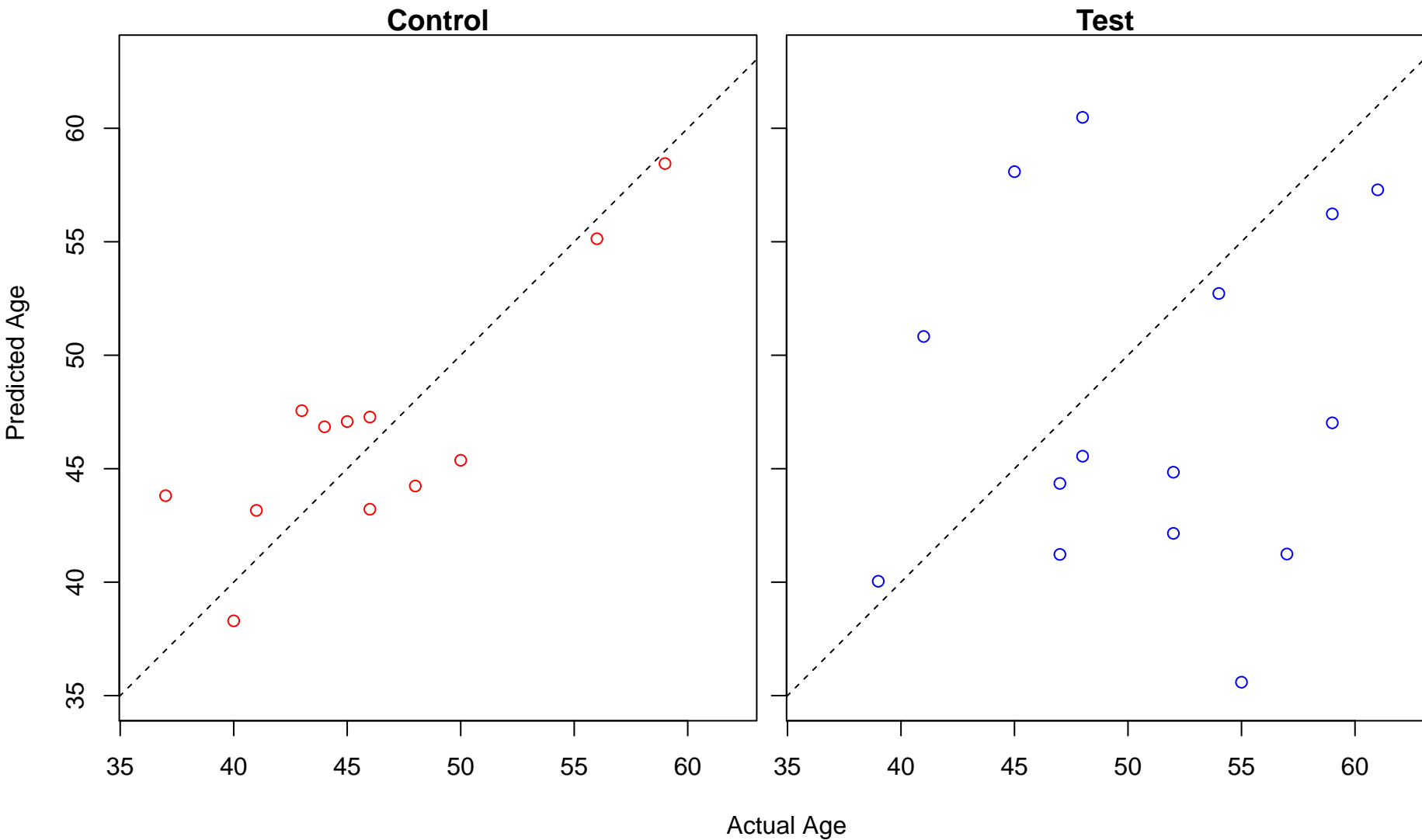
negative regulation of growth (Score: 3.312006)



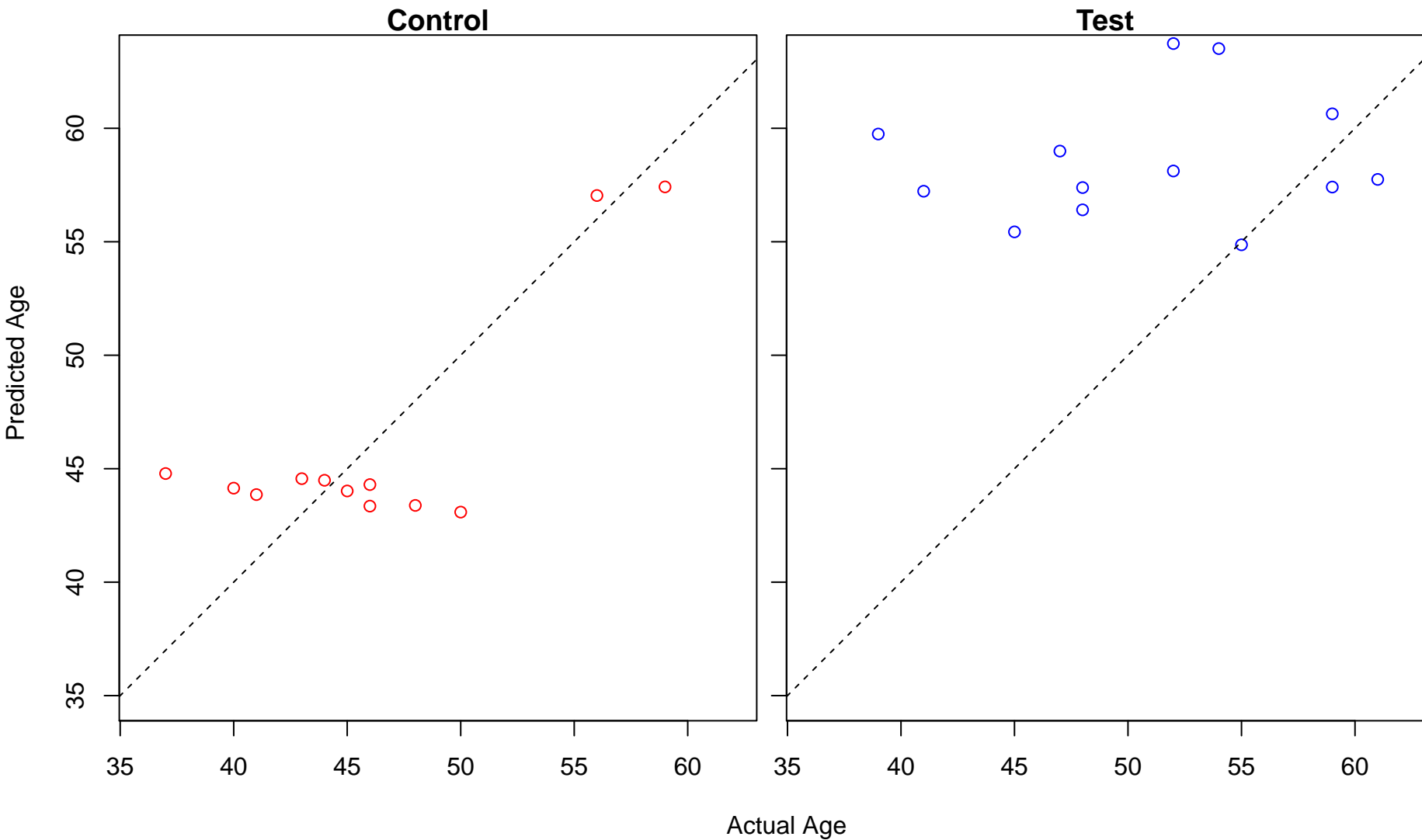
regulation of syncytium formation by plasma membrane fusion (Score: 3.311592)



regulation of autophagy (Score: 3.311209)

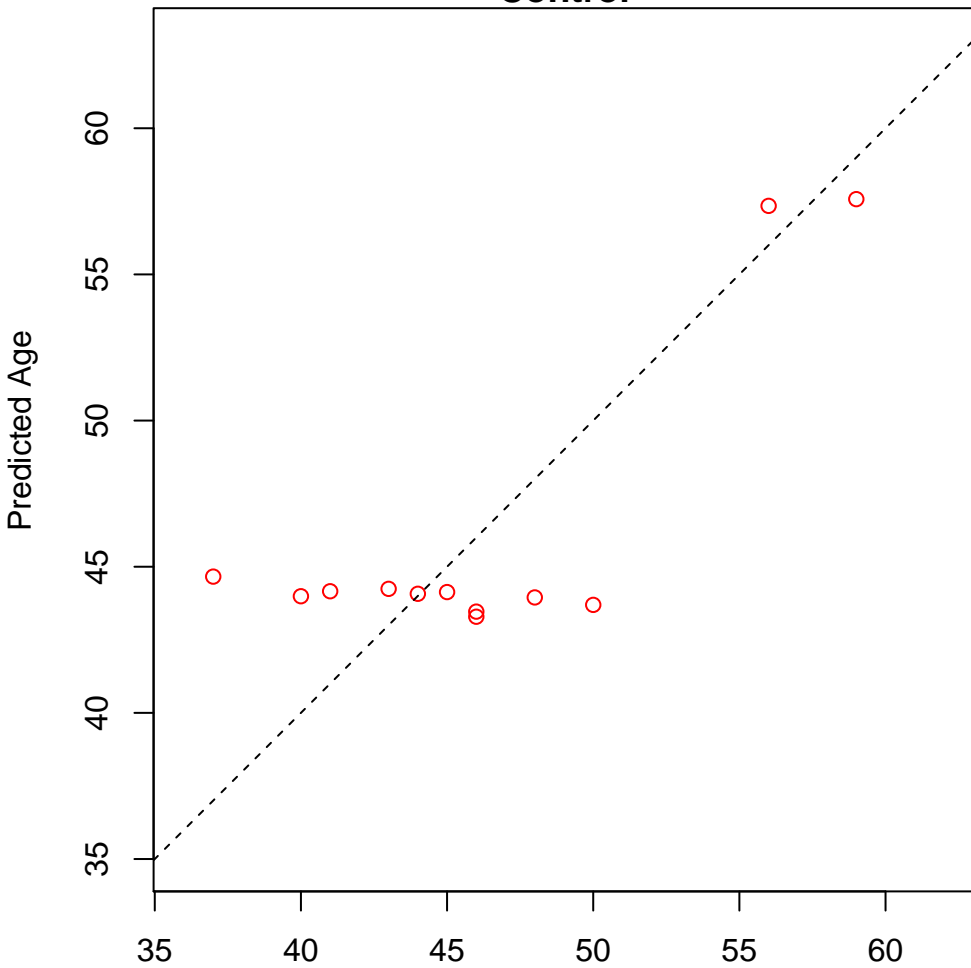


organelle fusion (Score: 3.311190)

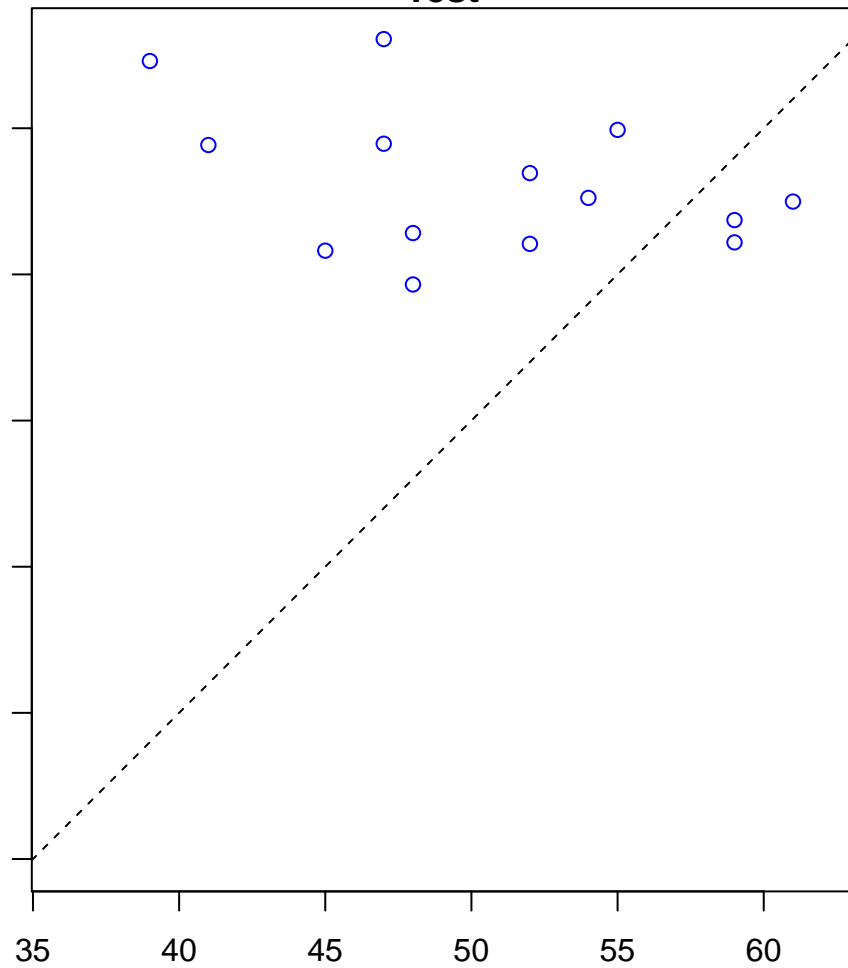


post-Golgi vesicle-mediated transport (Score: 3.309313)

Control

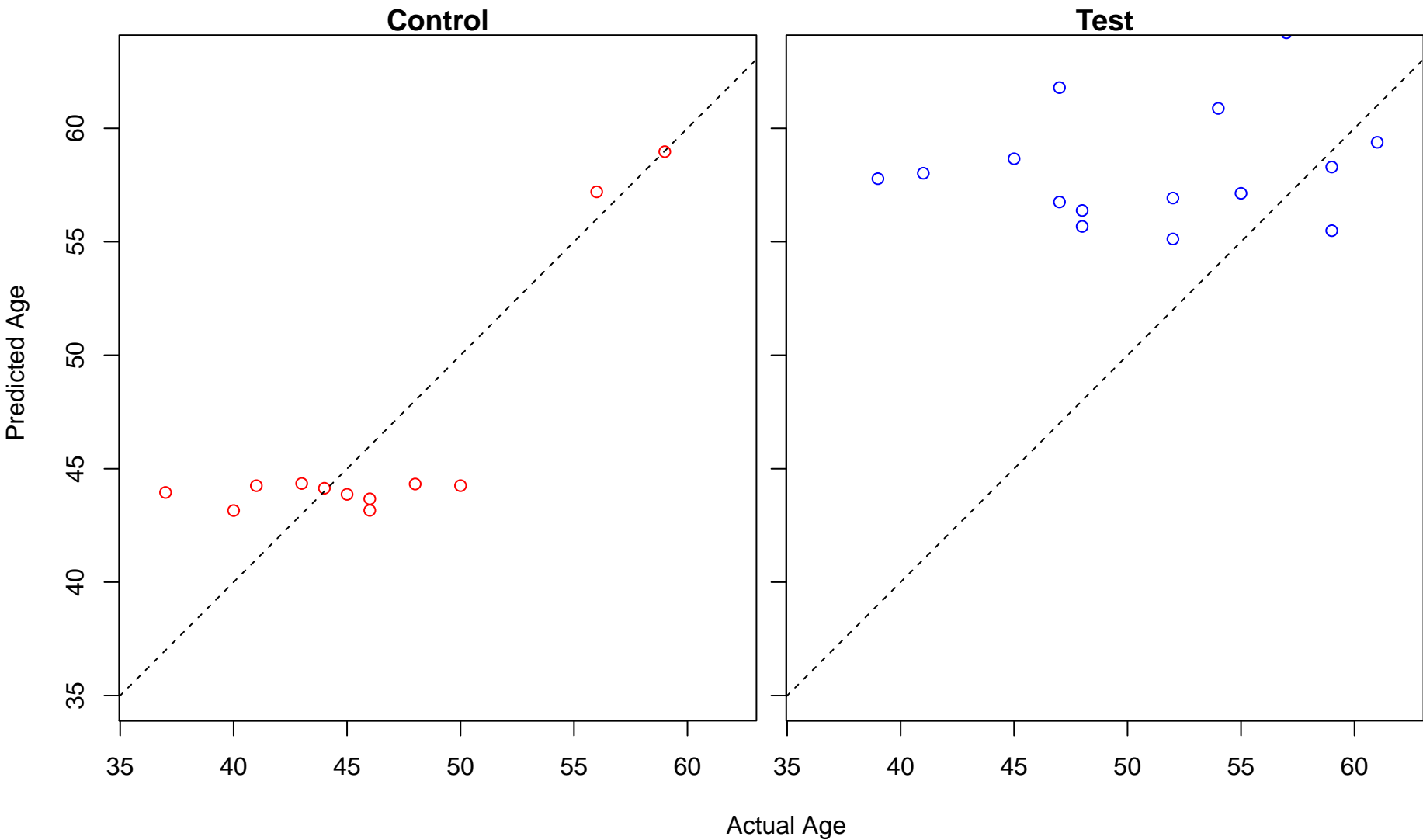


Test

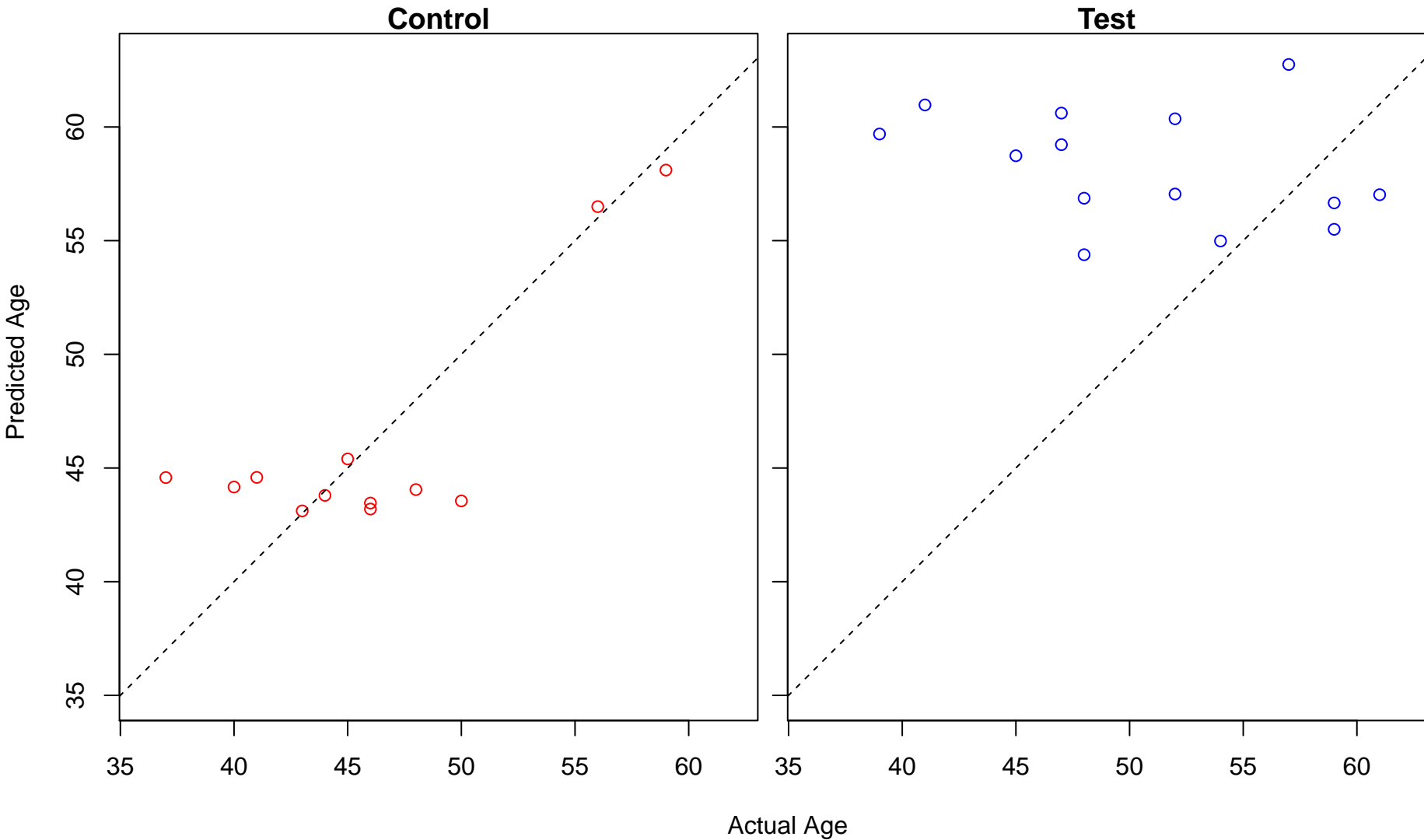


Actual Age

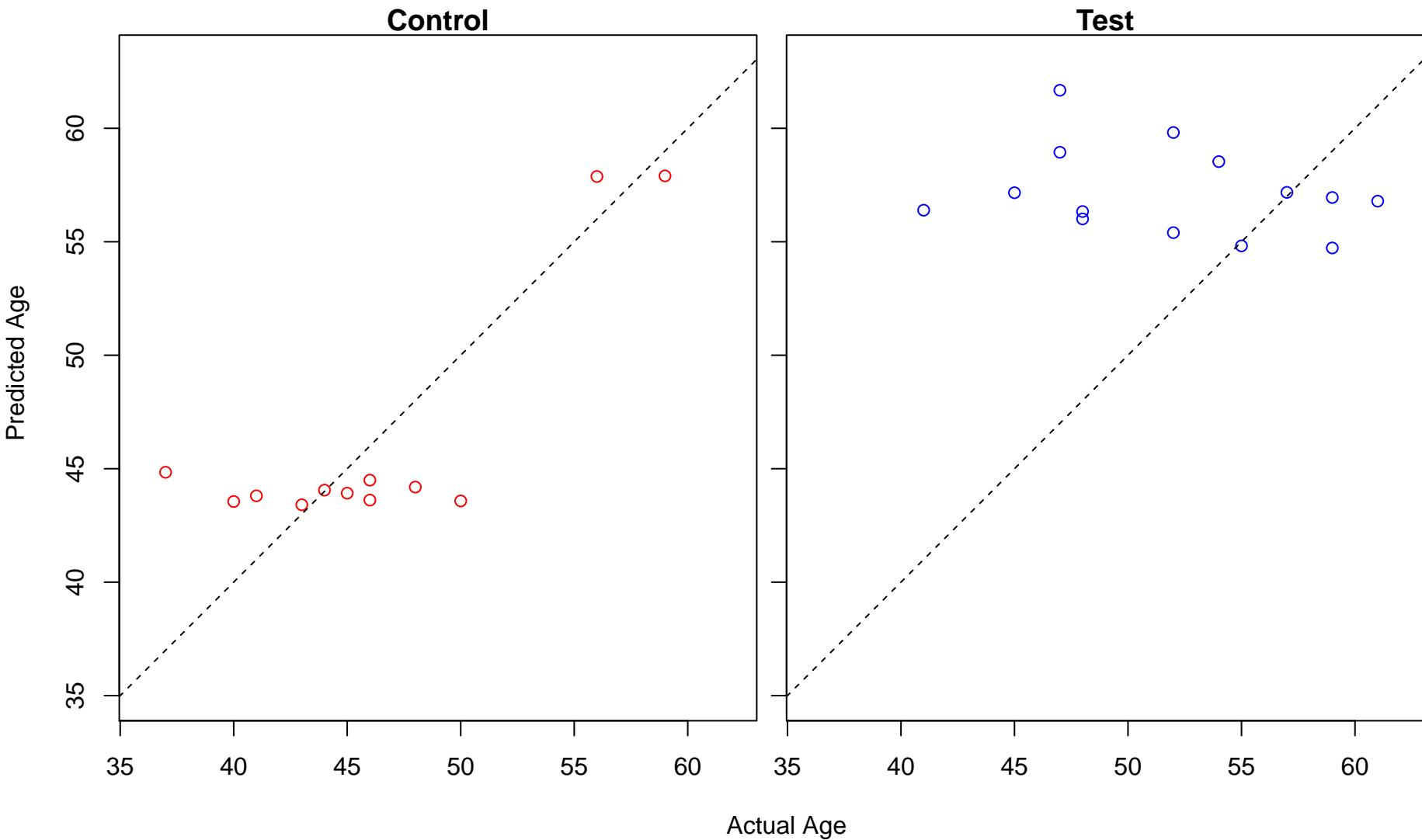
Negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway (Score: 1)



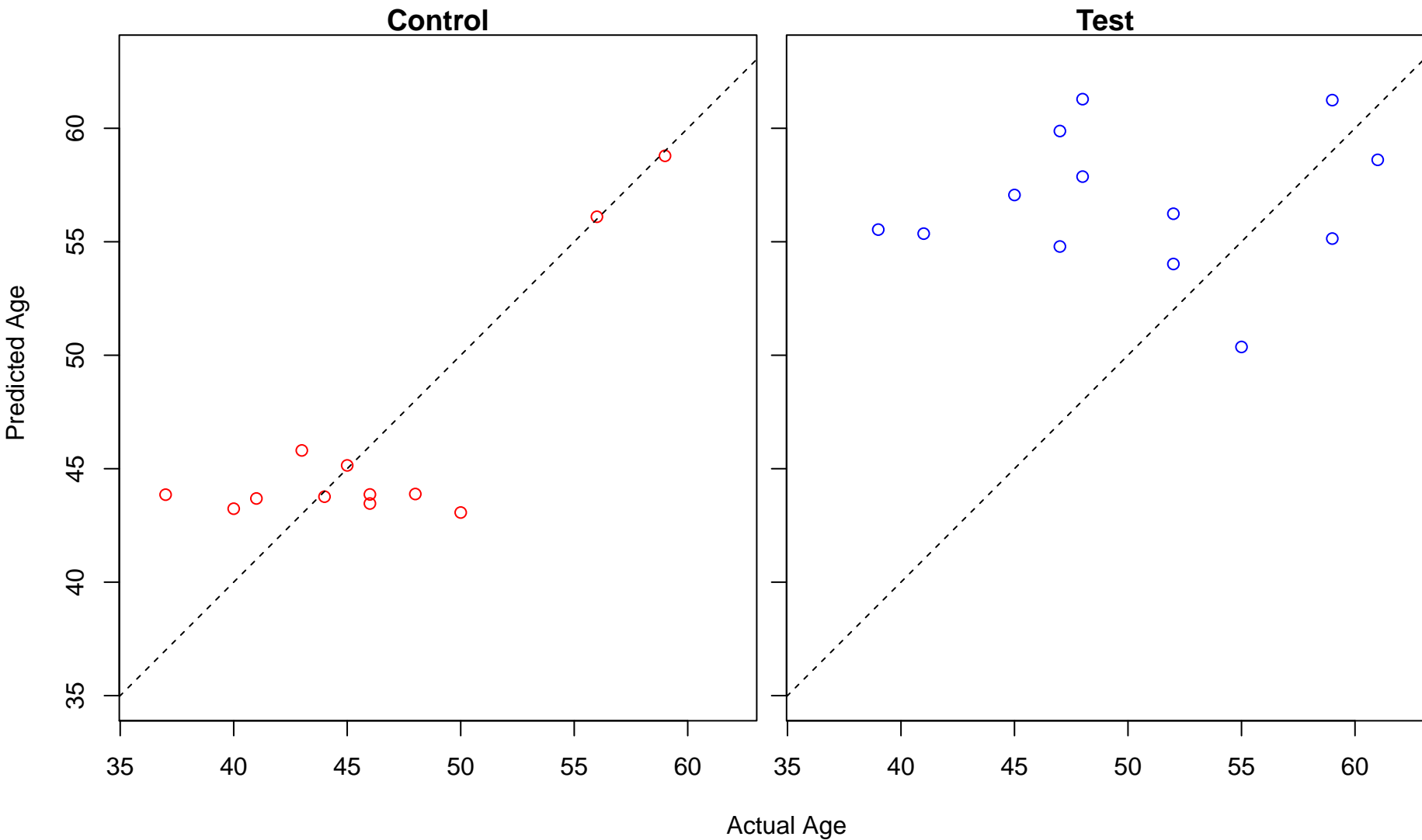
negative regulation of neuron differentiation (Score: 3.308255)



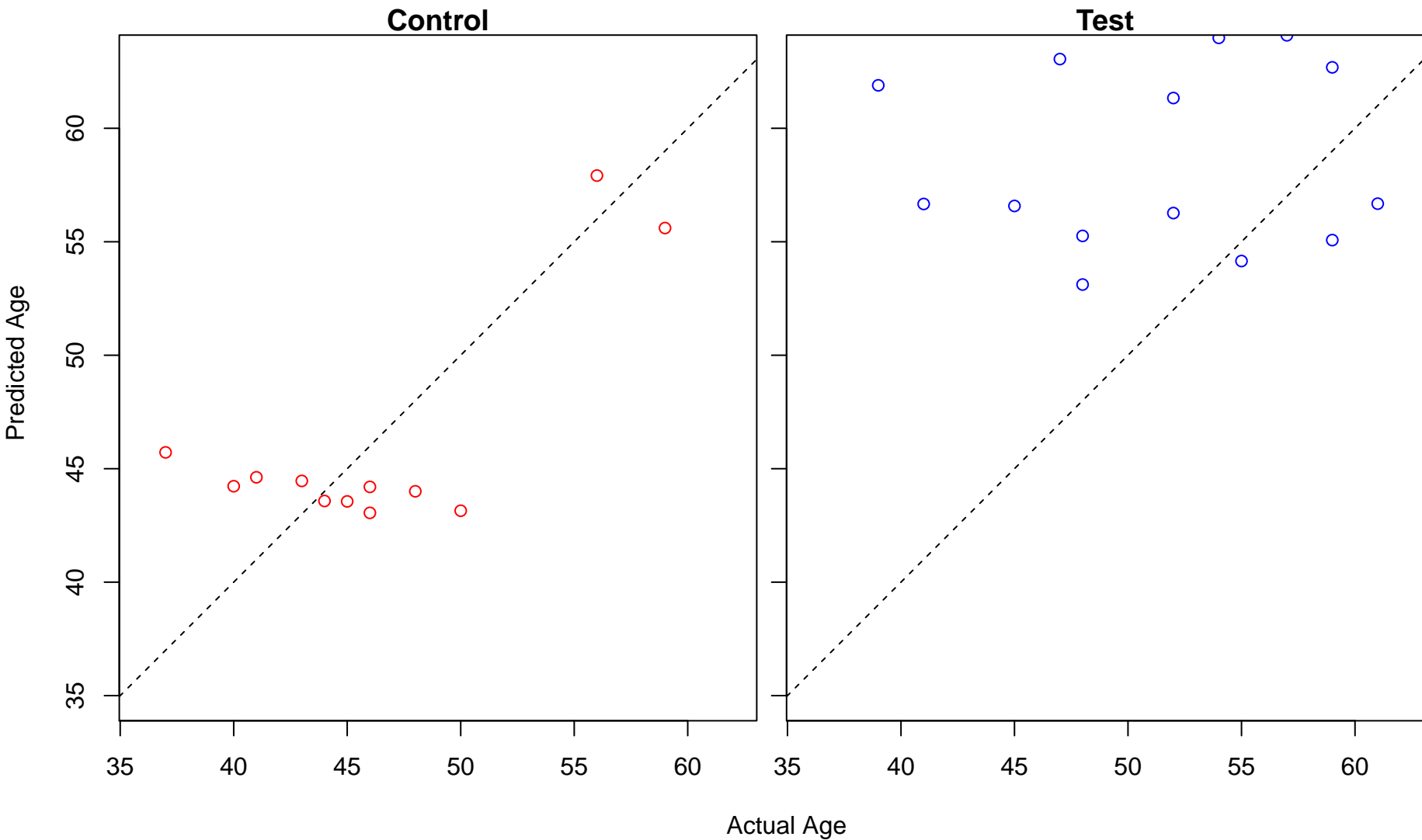
regulation of monocyte differentiation (Score: 3.308013)



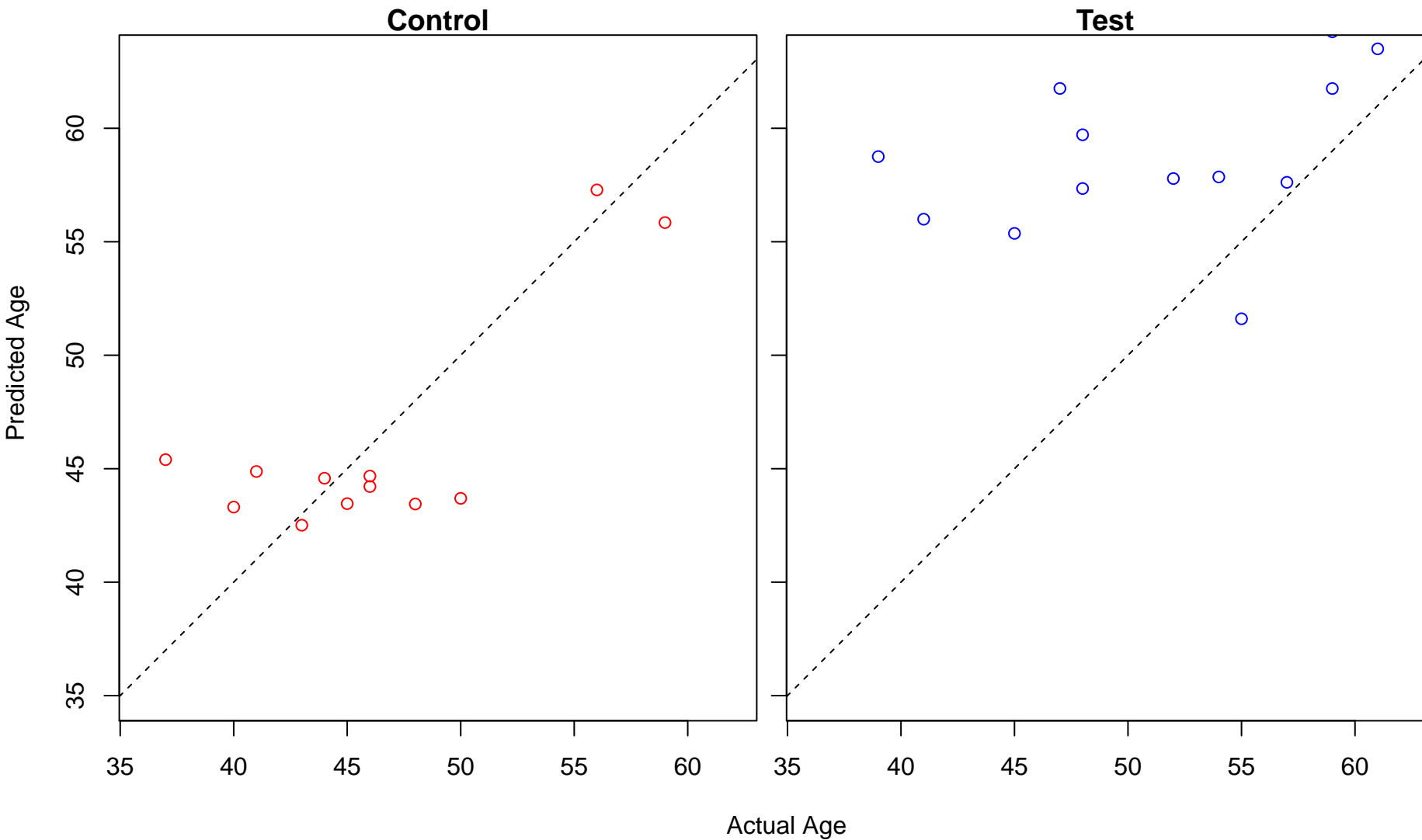
deoxyribonucleoside monophosphate metabolic process (Score: 3.307158)



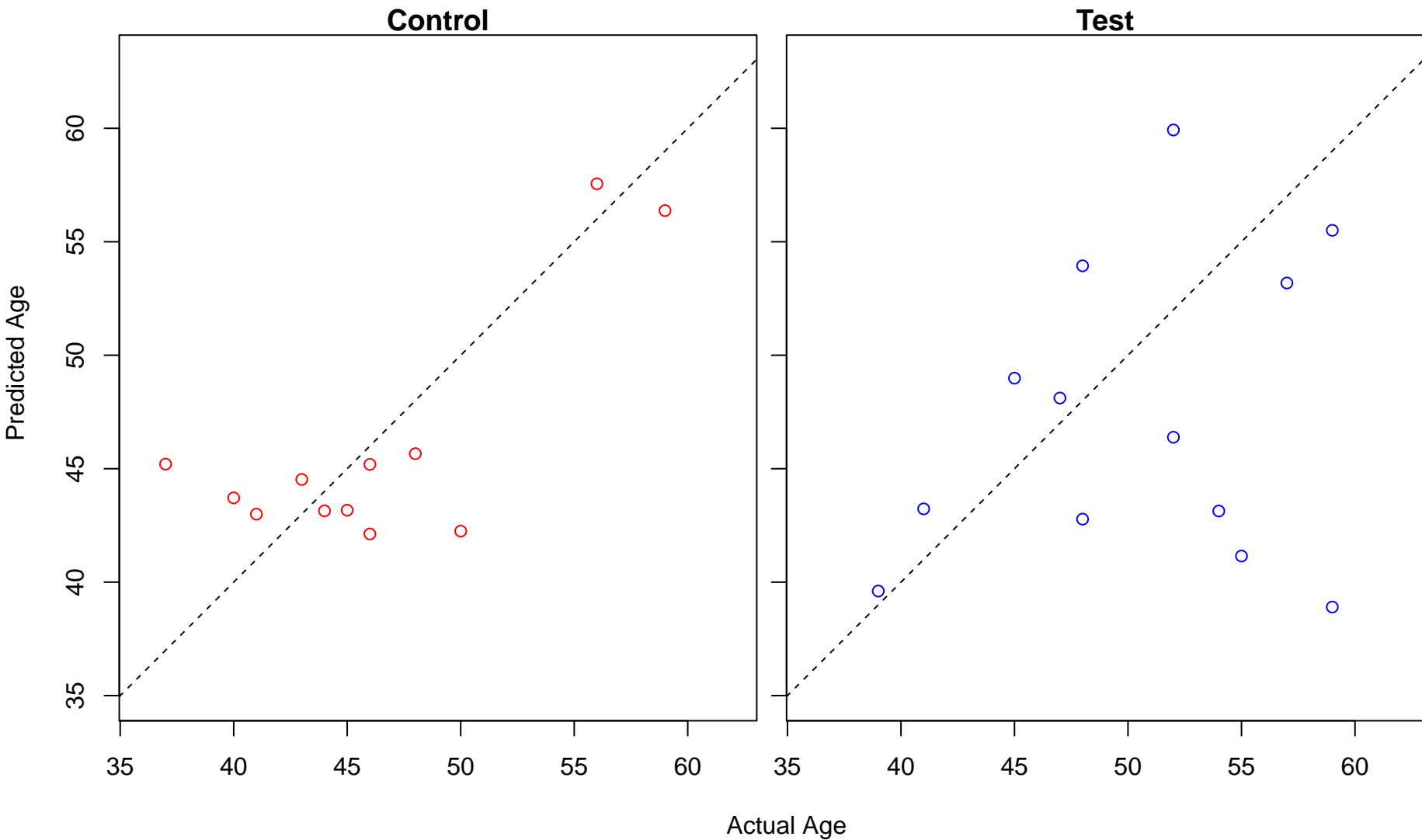
positive regulation of natural killer cell activation (Score: 3.305946)



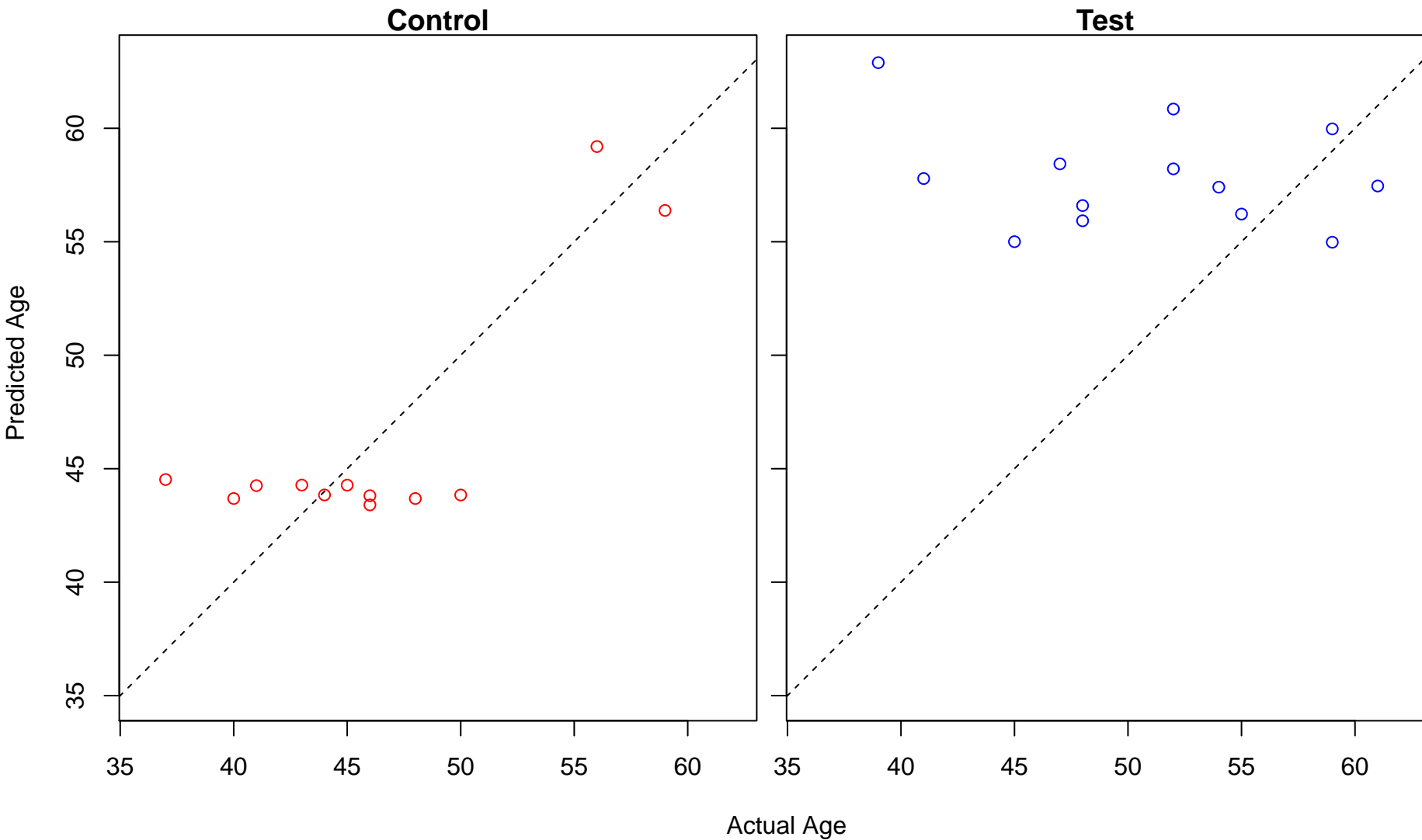
regulation of dopamine receptor signaling pathway (Score: 3.304800)



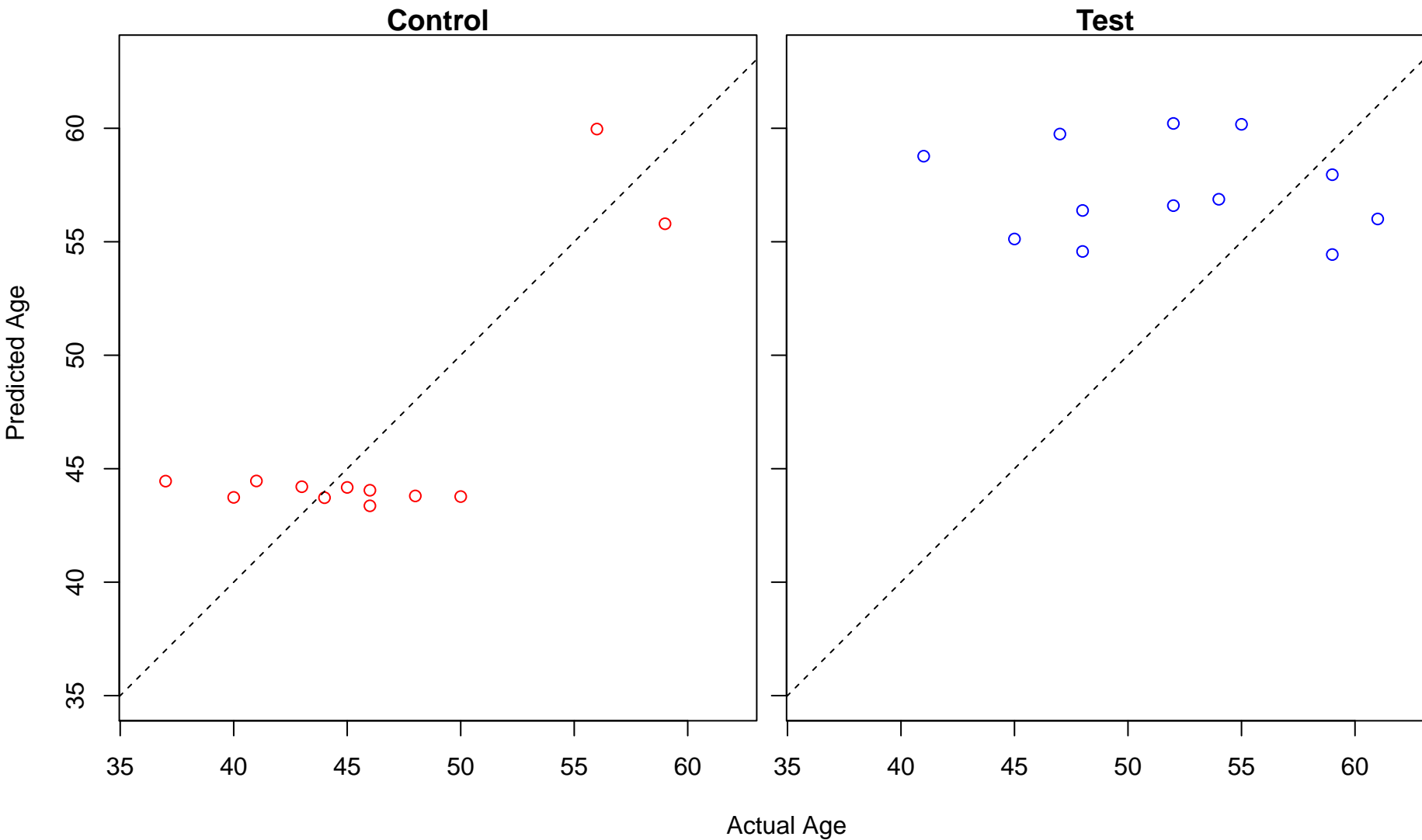
S-adenosylmethionine metabolic process (Score: 3.303930)



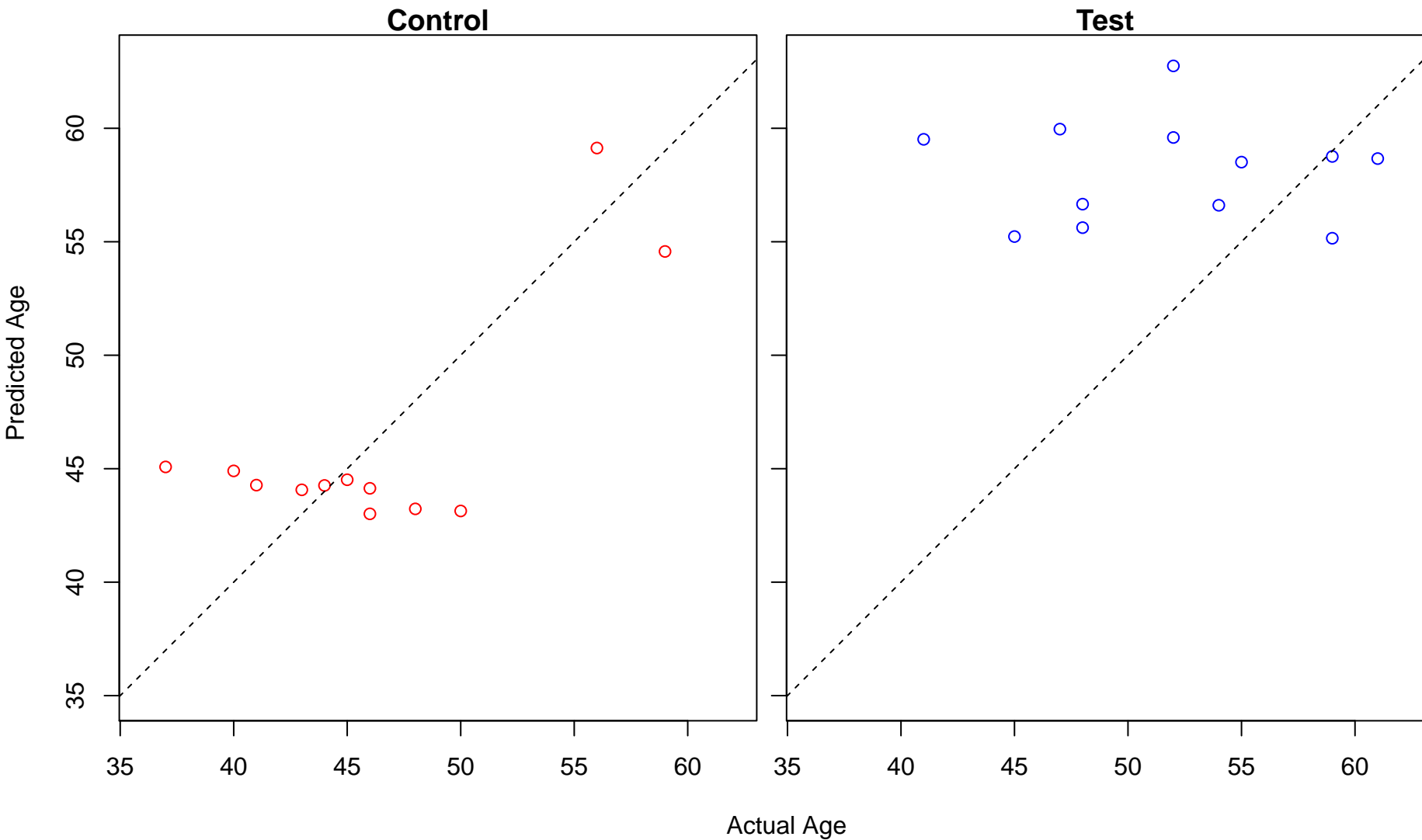
double-strand break repair (Score: 3.303468)



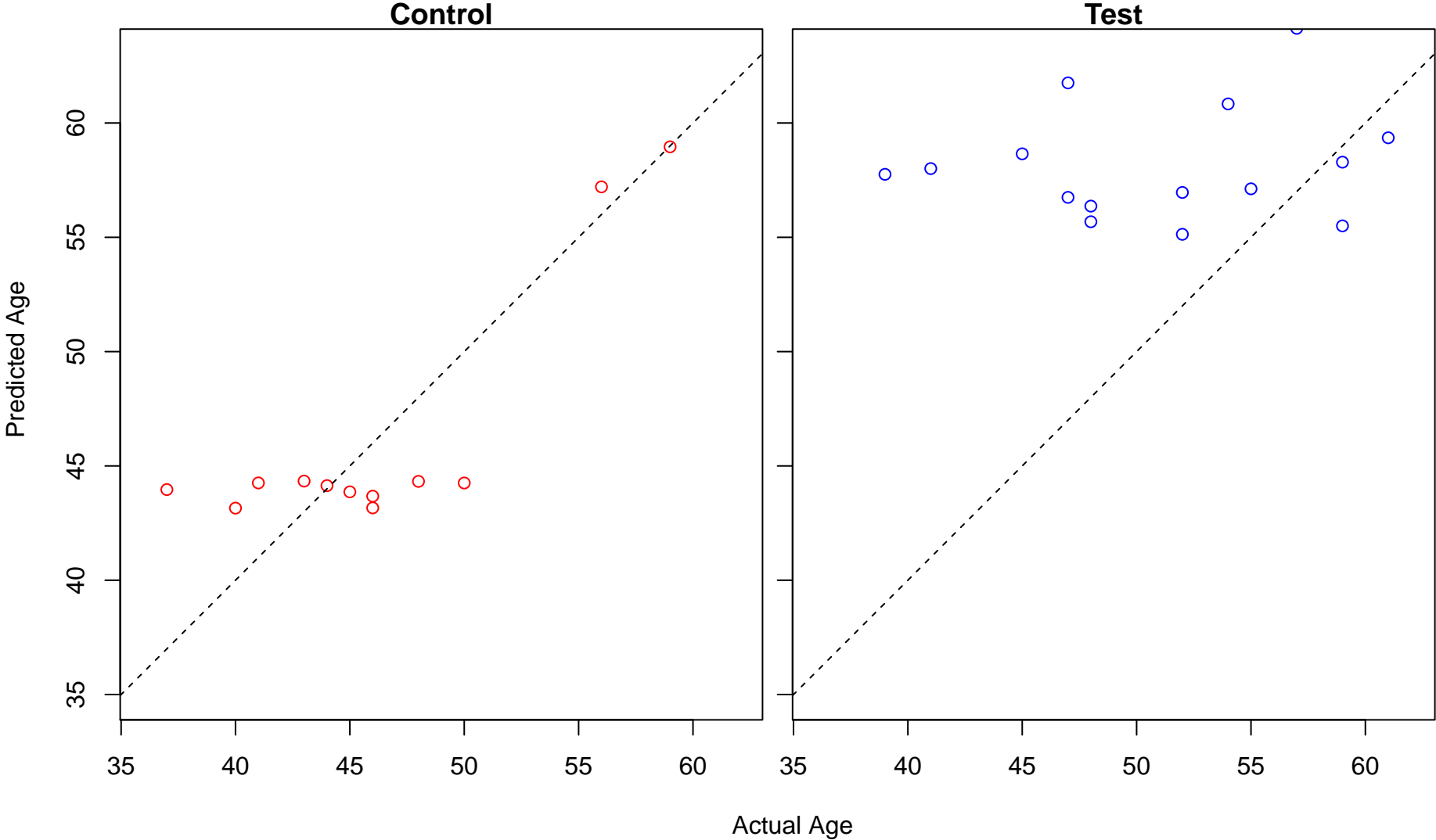
regulation of signal transduction by p53 class mediator (Score: 3.302184)



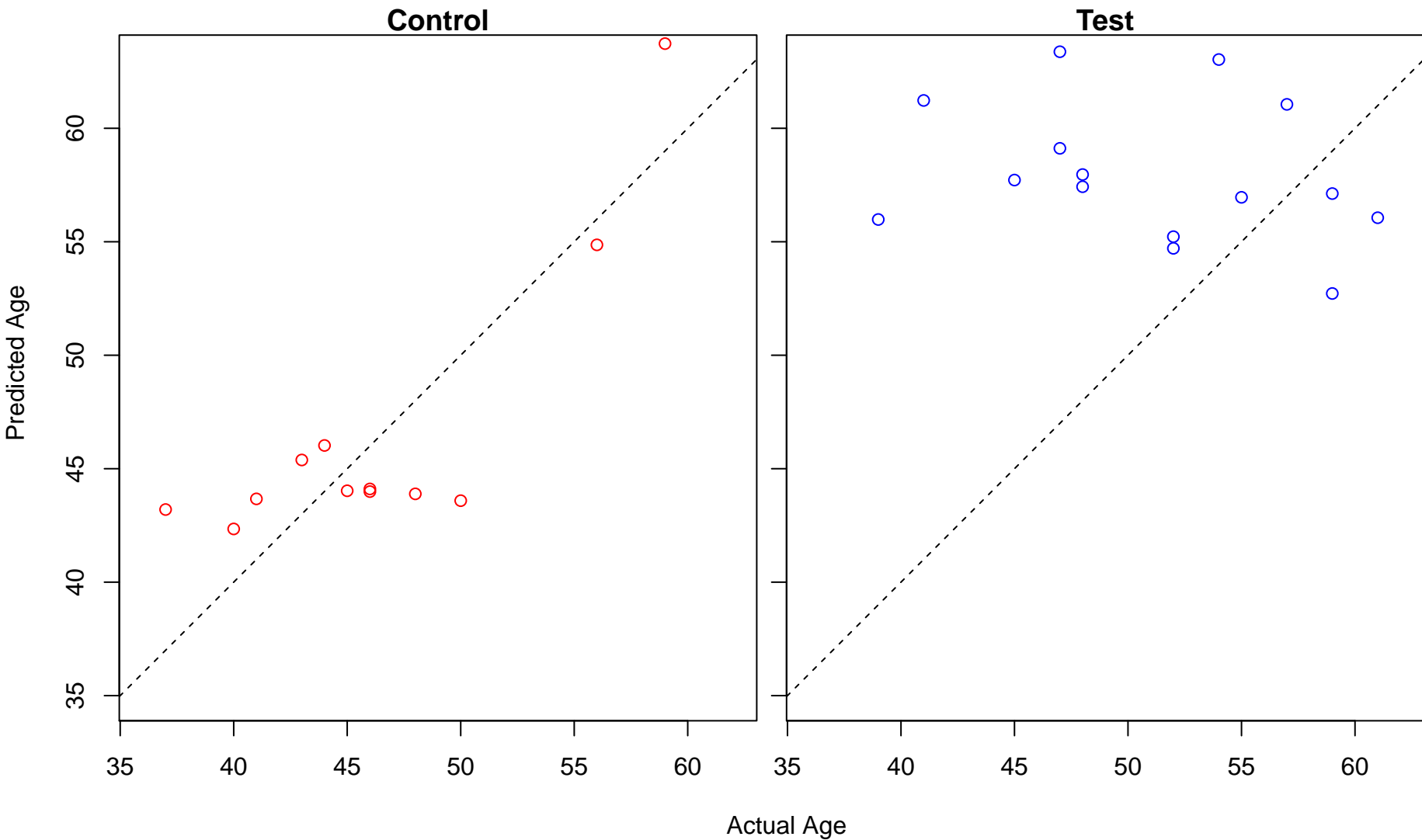
response to virus (Score: 3.297929)



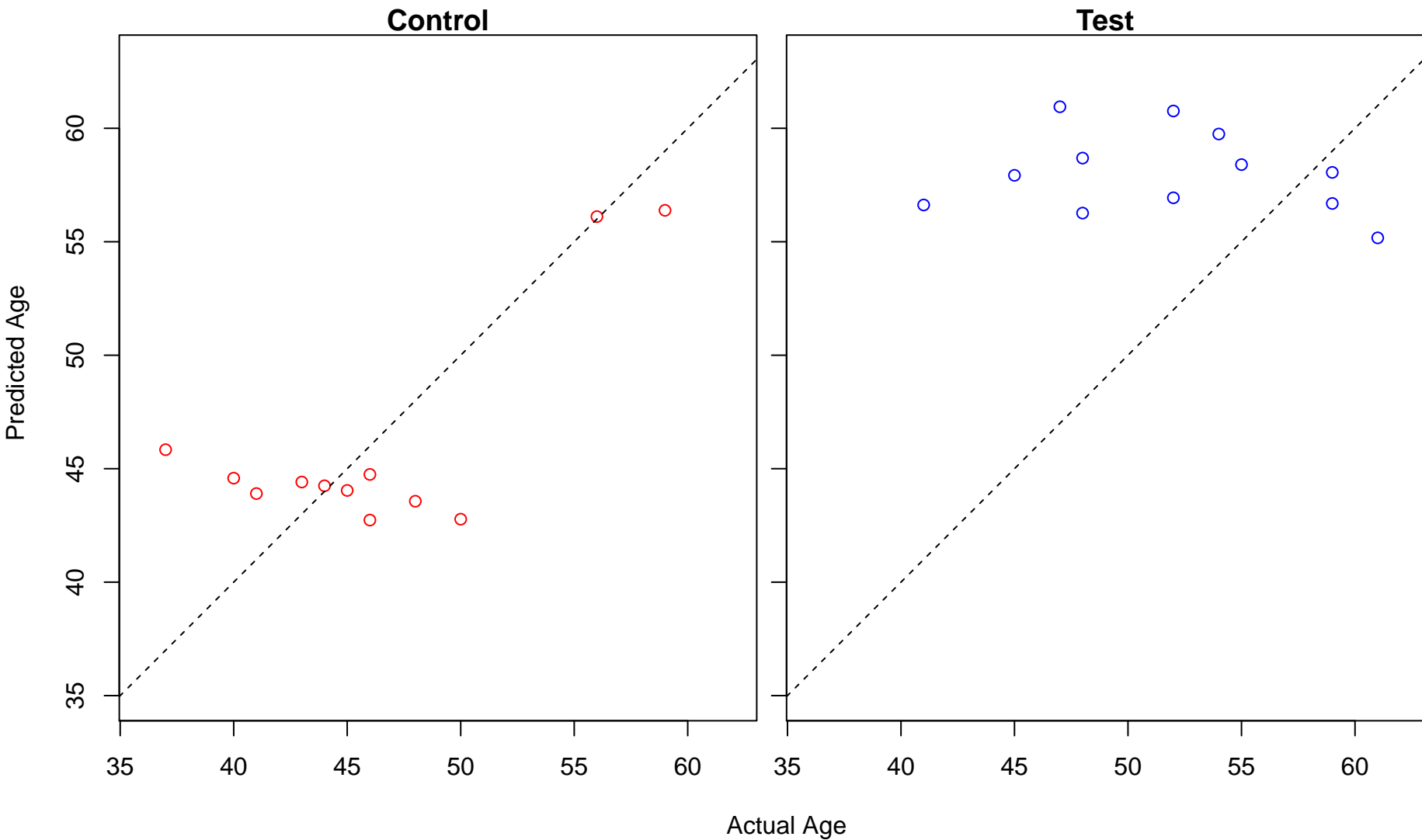
regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway (Score: 3.29)



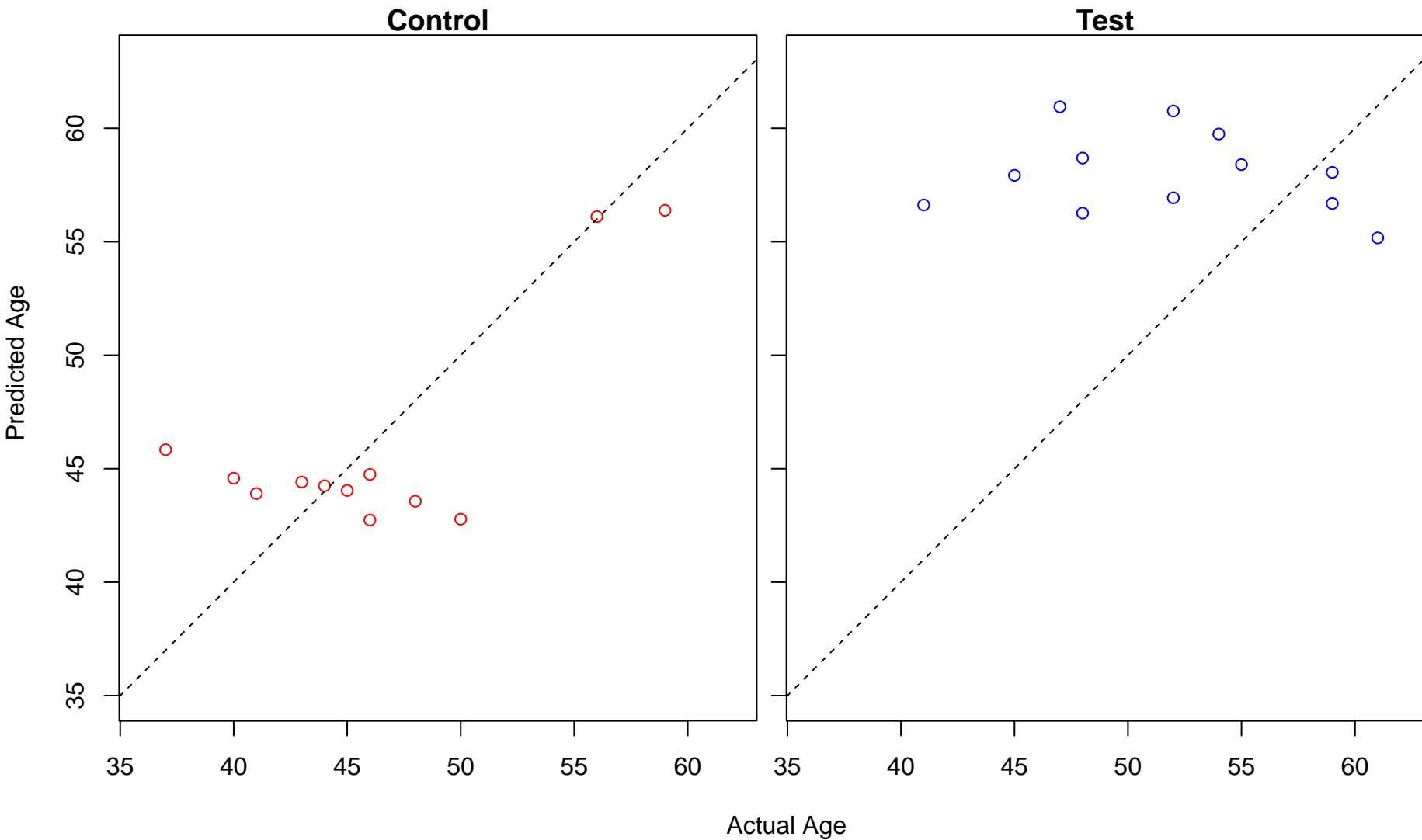
cardiac muscle hypertrophy (Score: 3.295134)



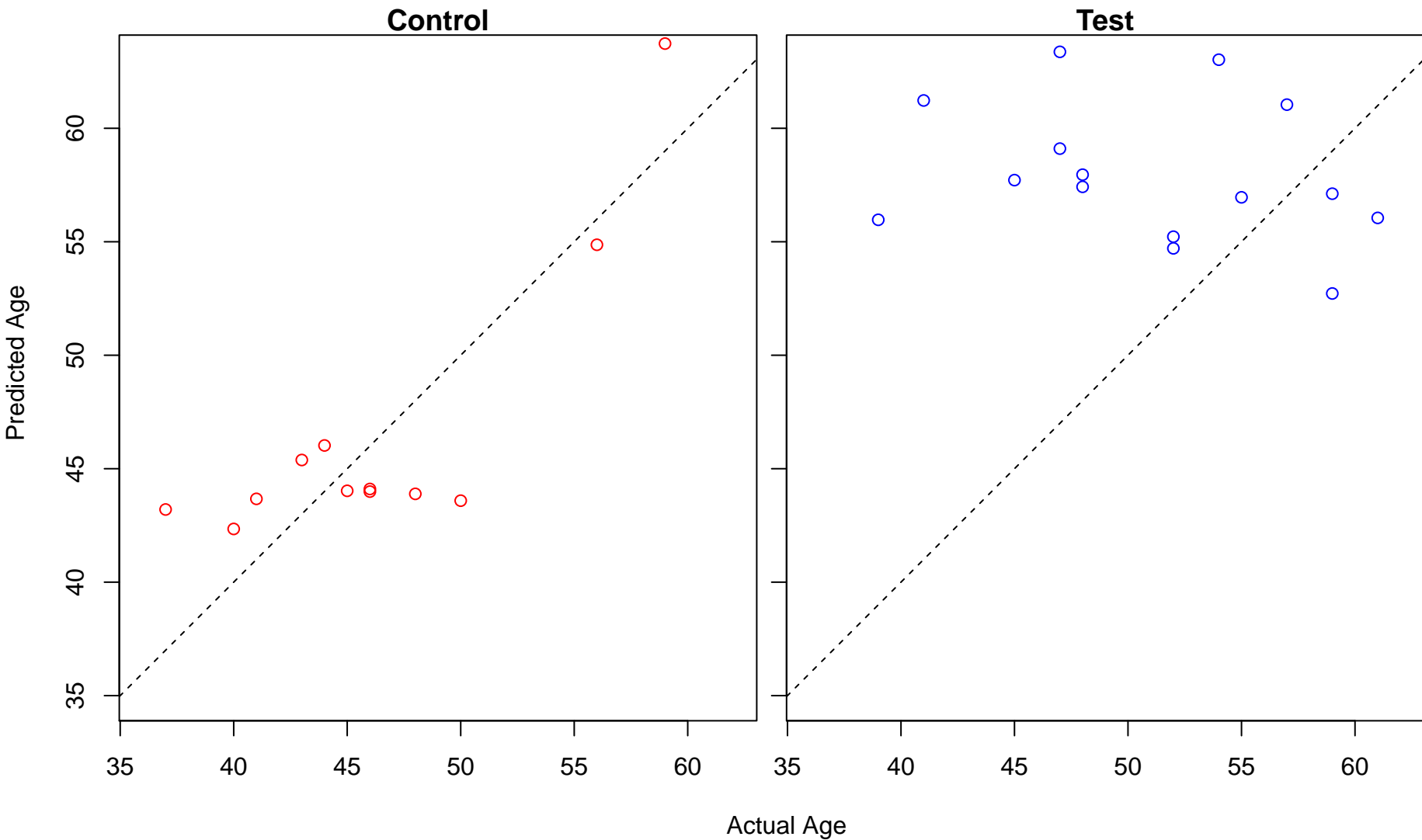
muscle filament sliding (Score: 3.294674)



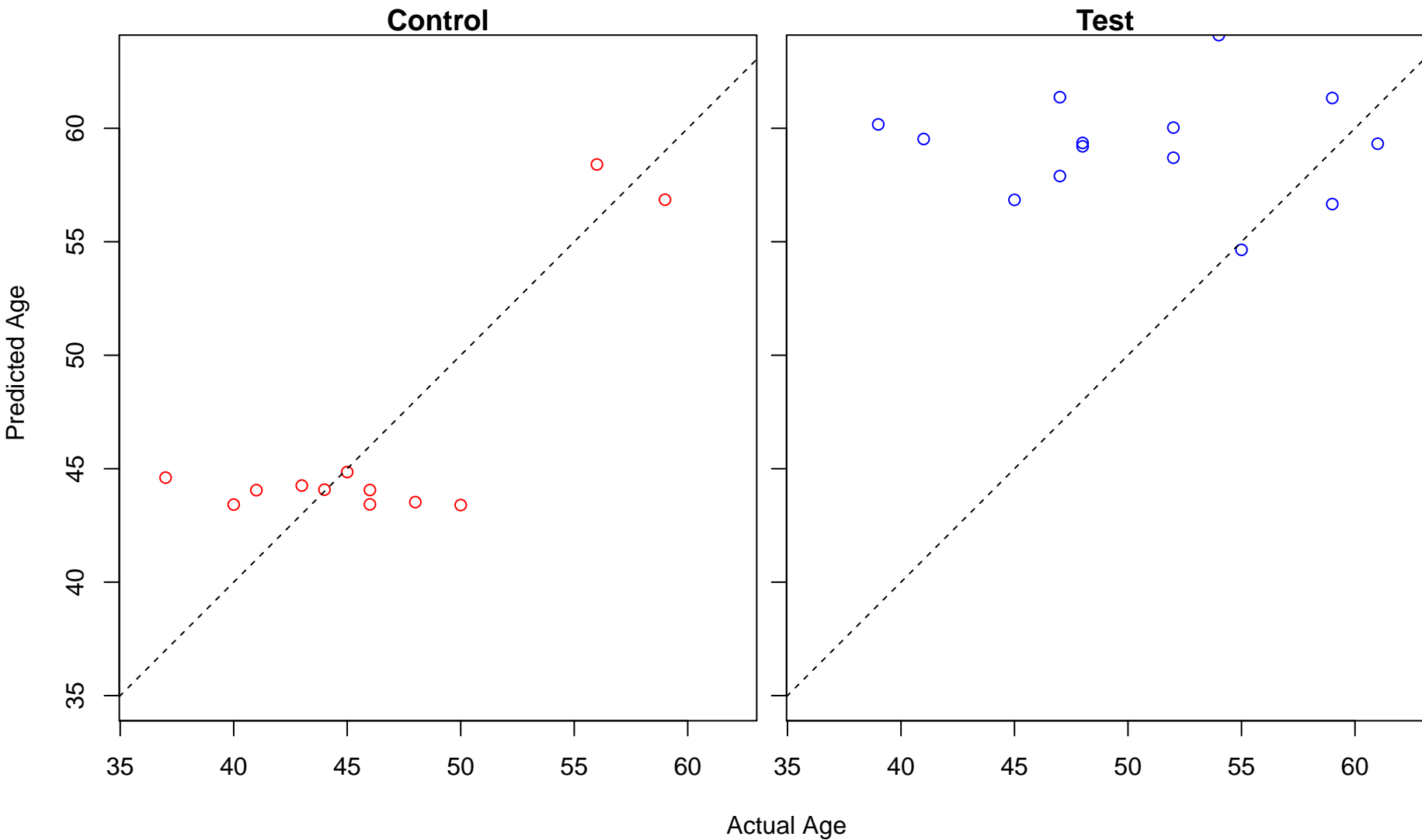
actin-myosin filament sliding (Score: 3.294674)



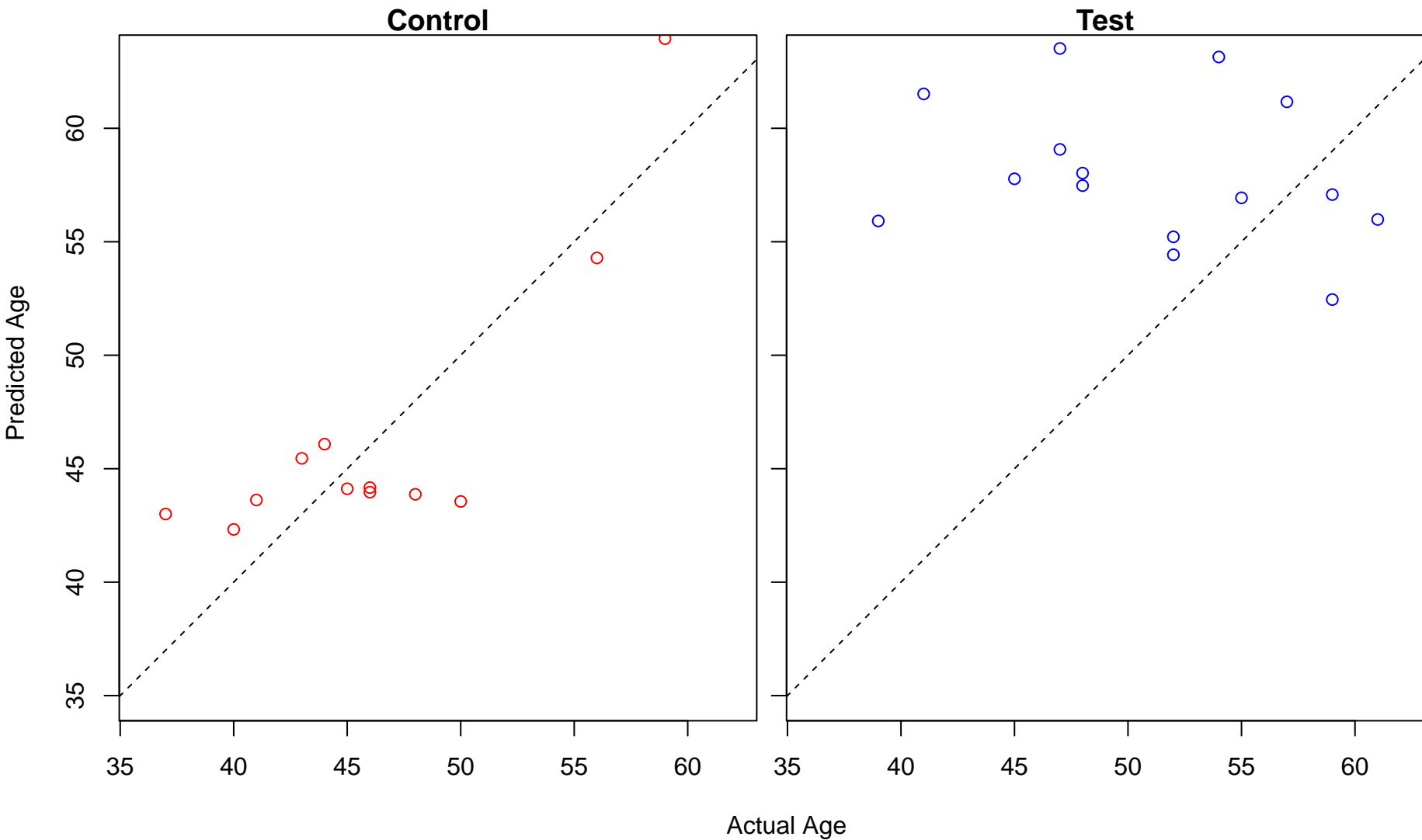
striated muscle hypertrophy (Score: 3.292823)



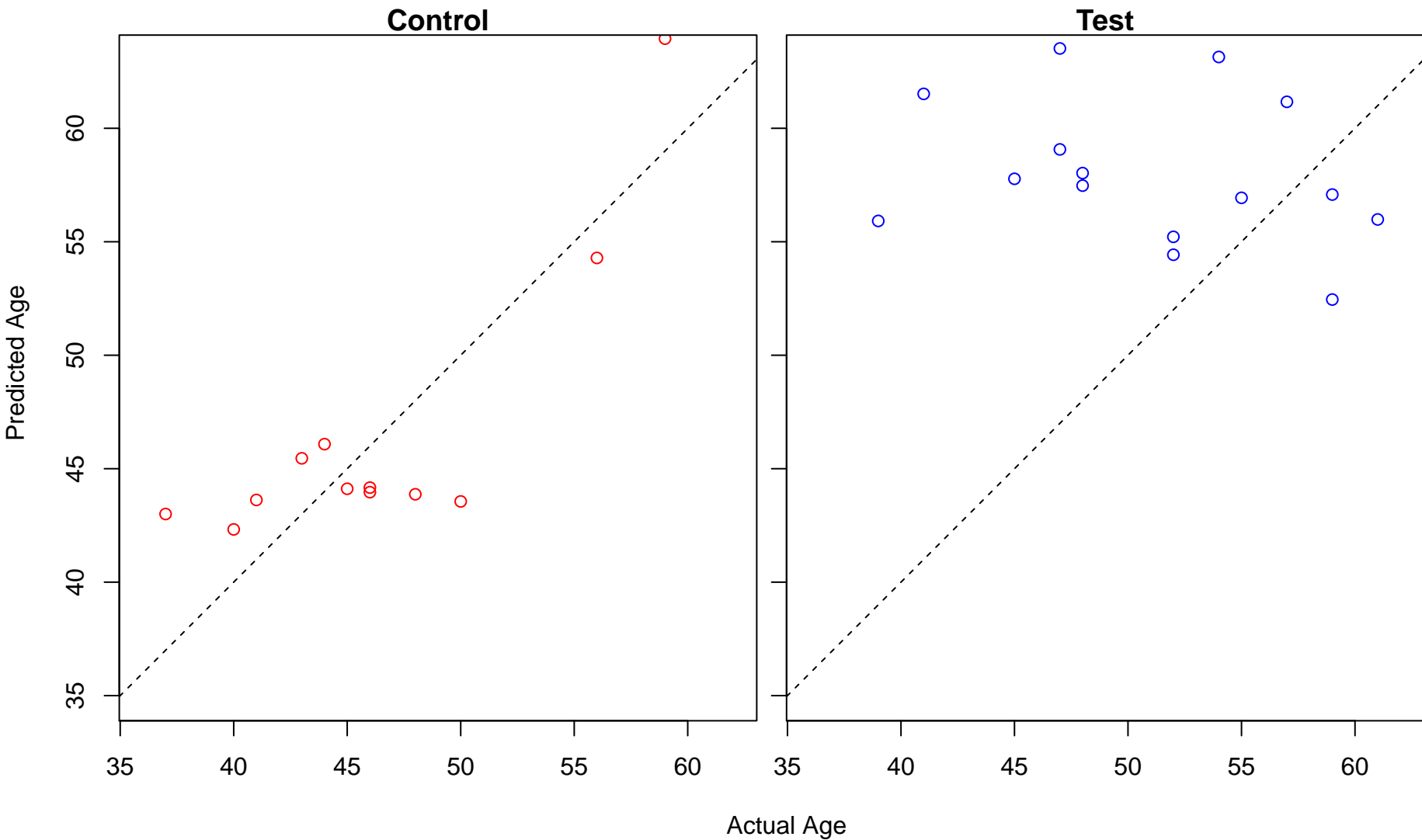
peroxisome fission (Score: 3.292639)



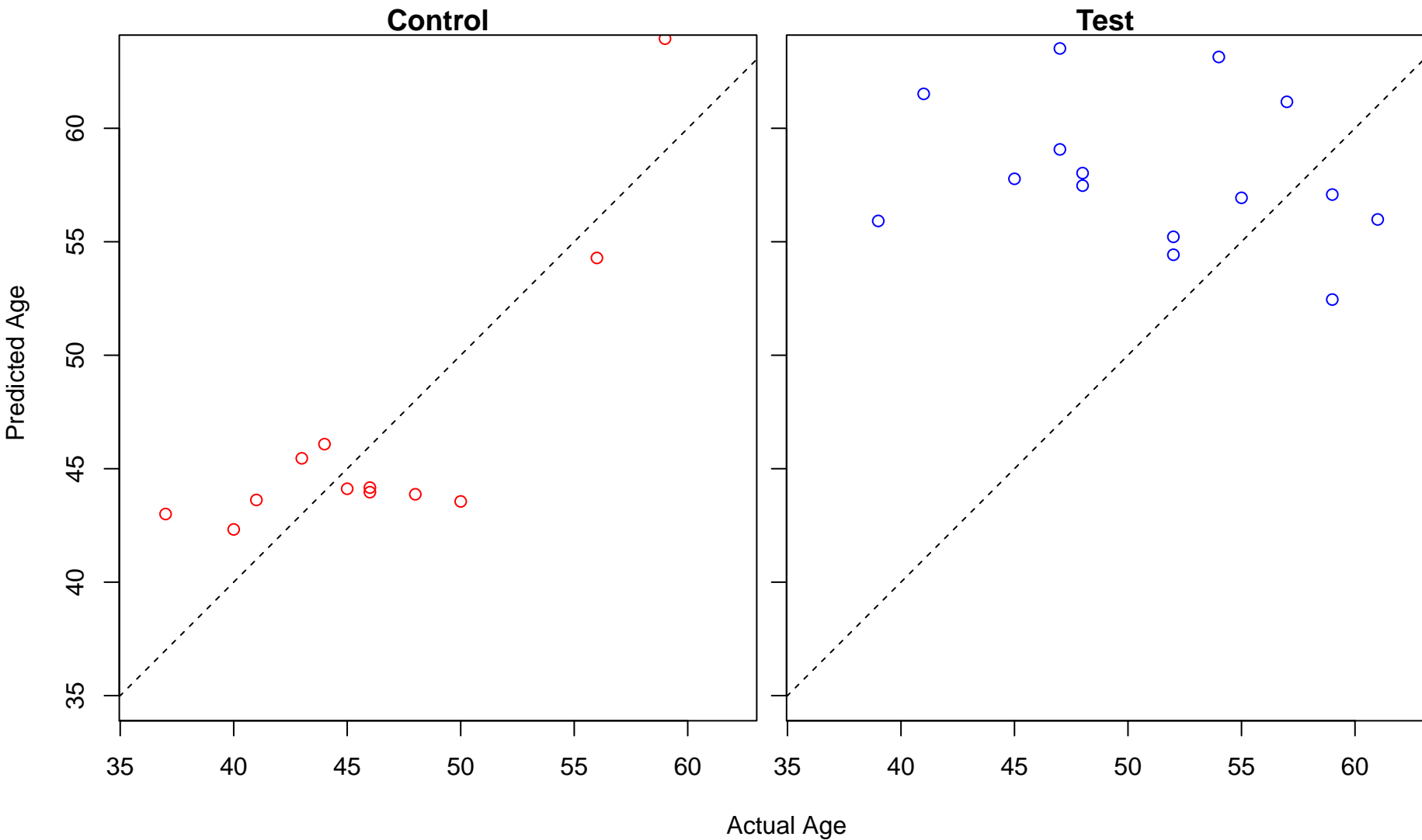
physiological muscle hypertrophy (Score: 3.292055)



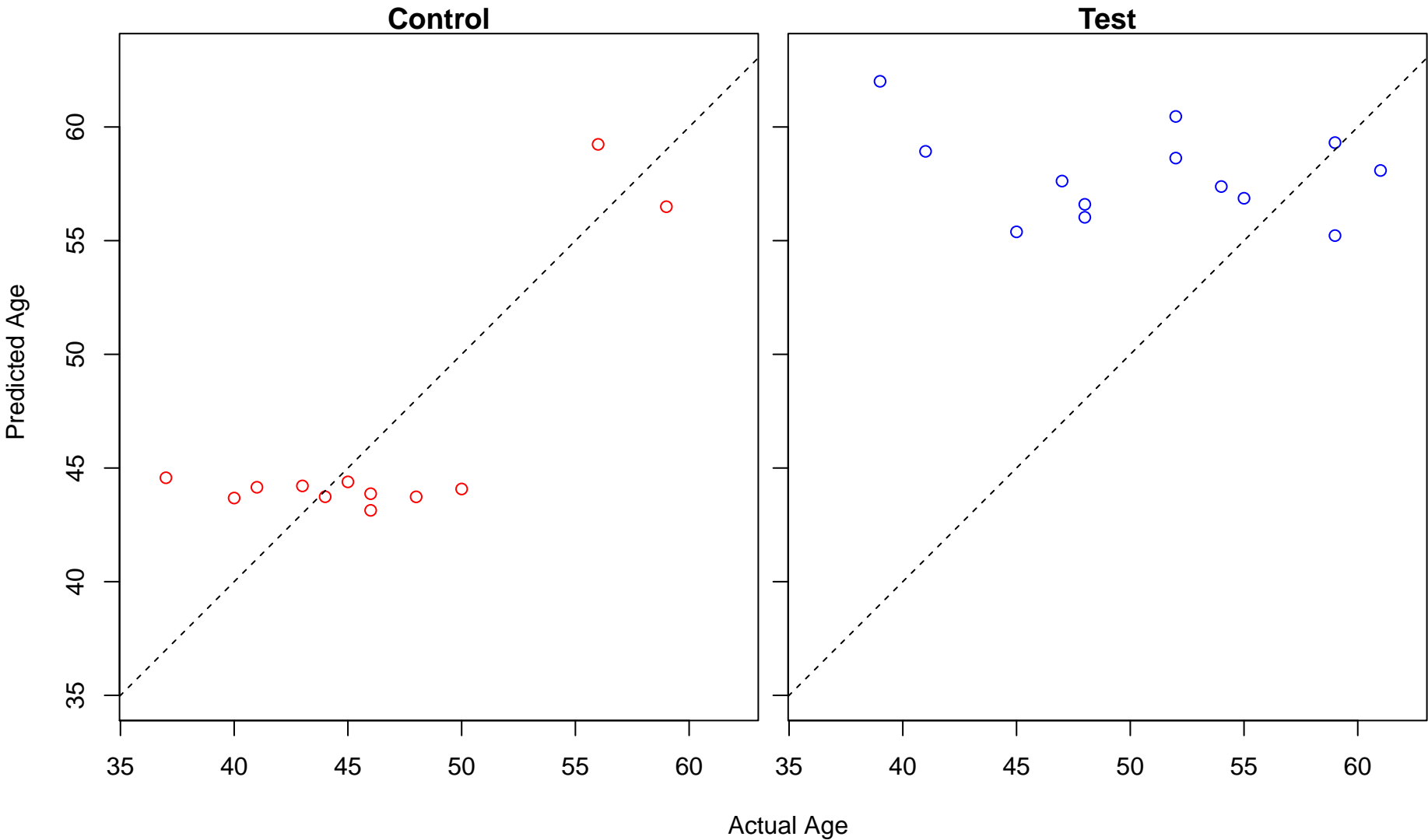
physiological cardiac muscle hypertrophy (Score: 3.292055)



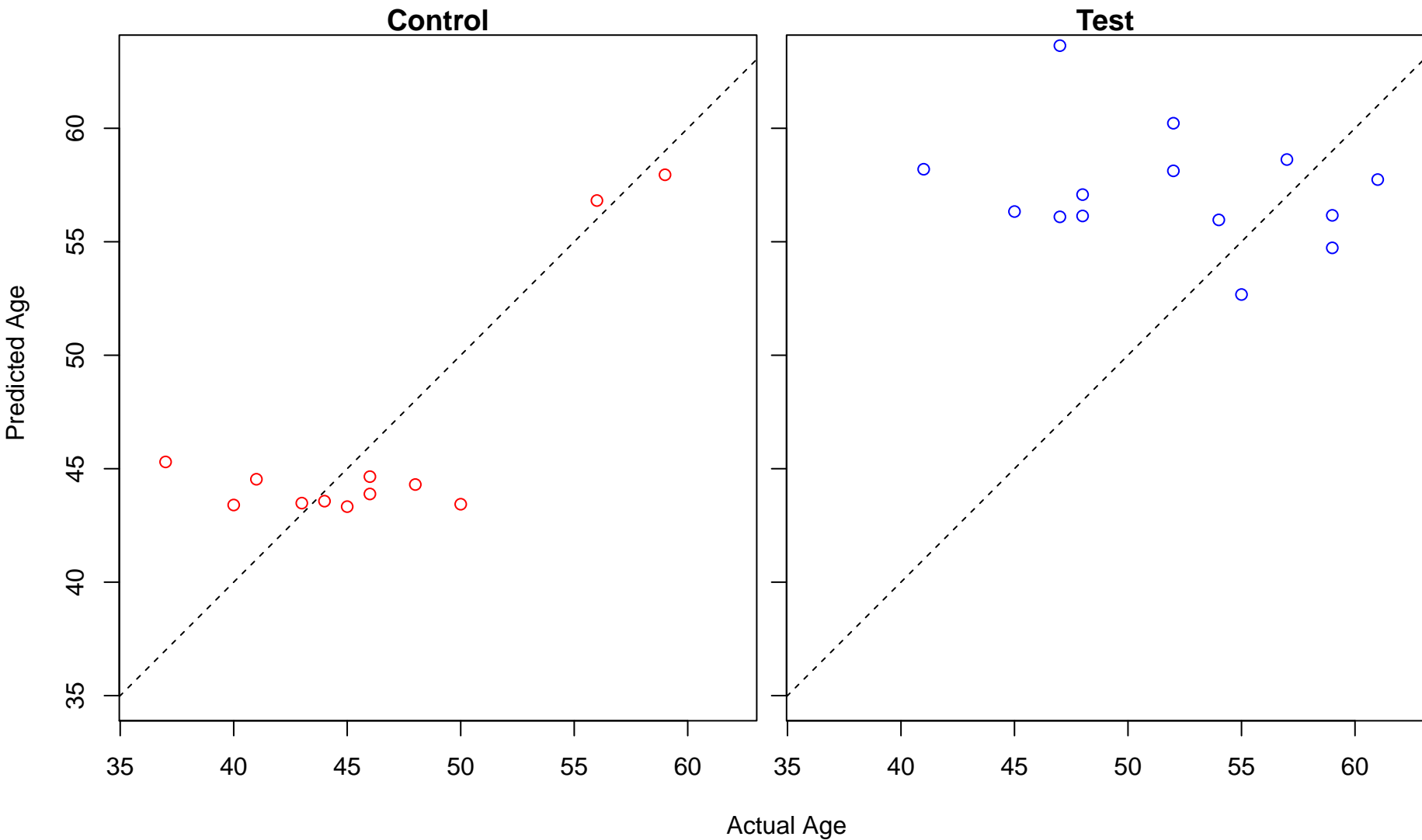
cell growth involved in cardiac muscle cell development (Score: 3.292055)



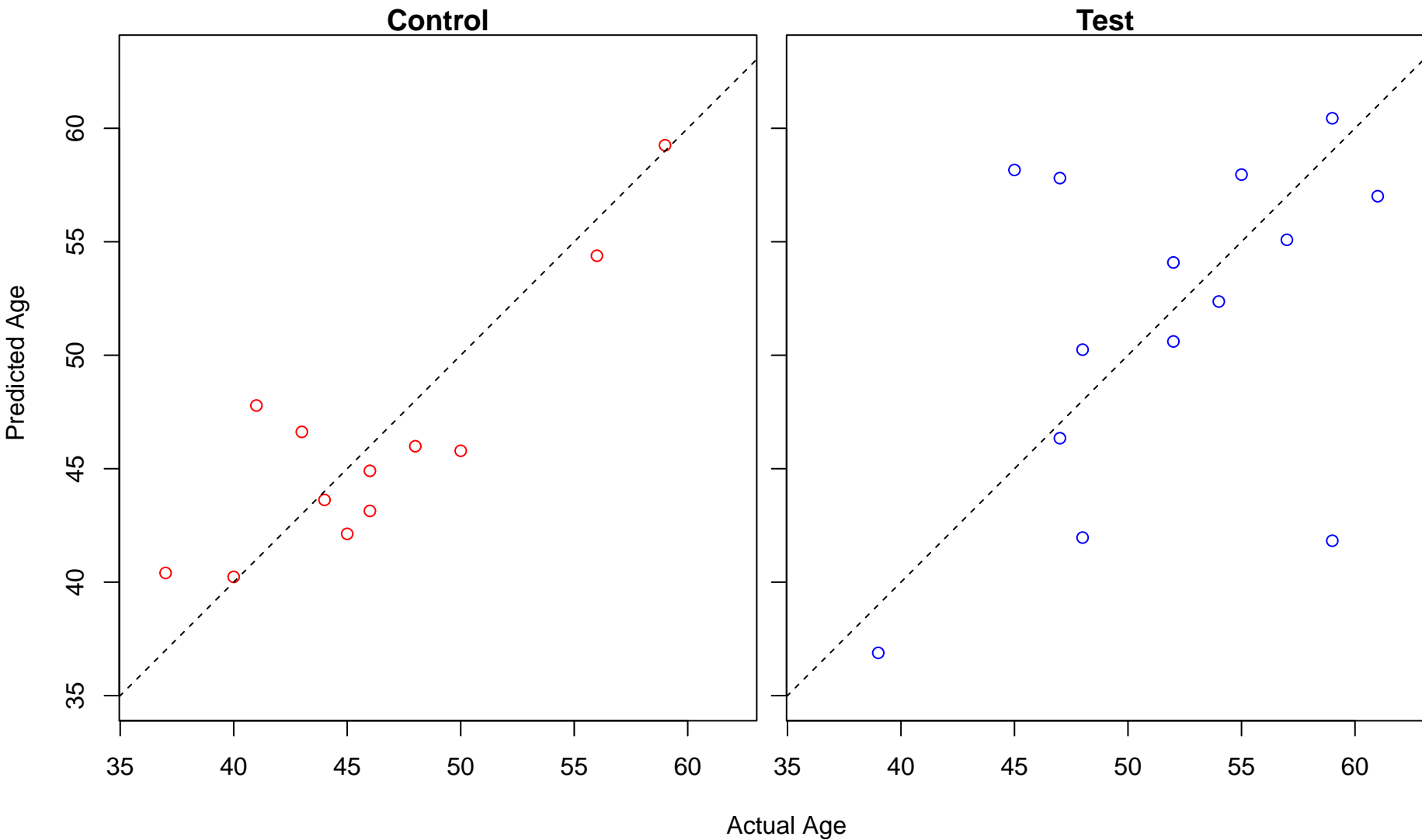
nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway (Score: 3.2900)



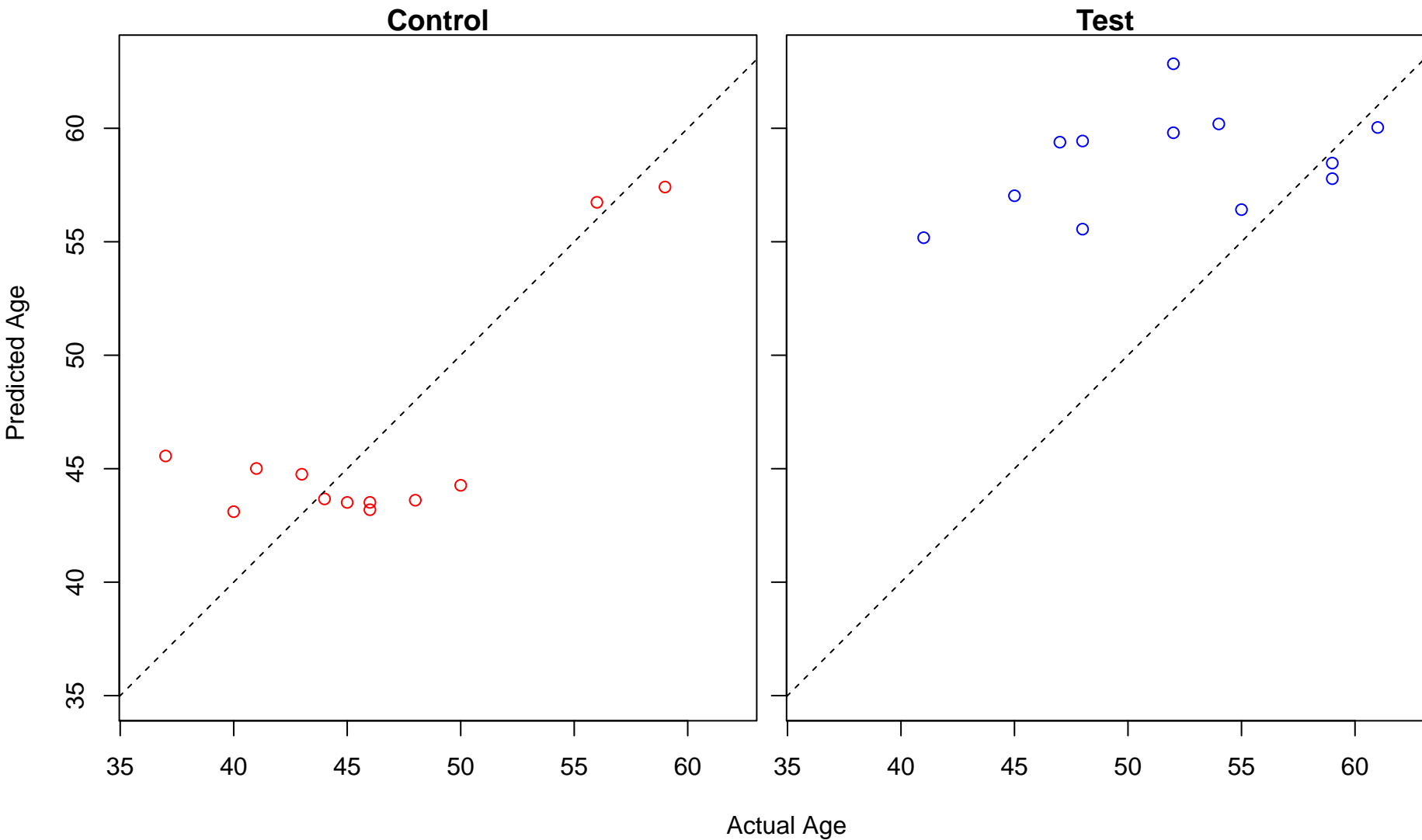
positive regulation of DNA repair (Score: 3.288085)



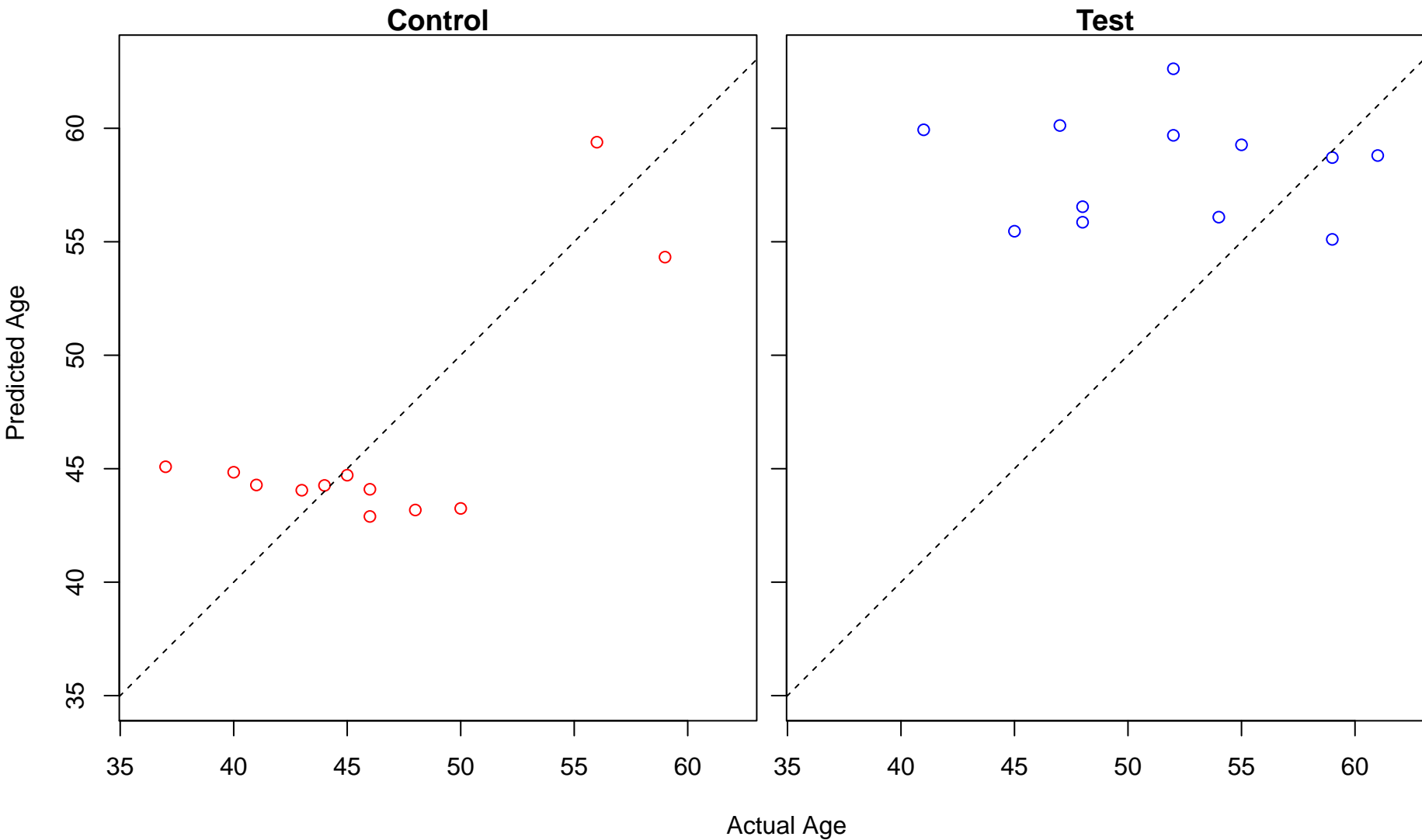
protein oligomerization (Score: 3.284274)



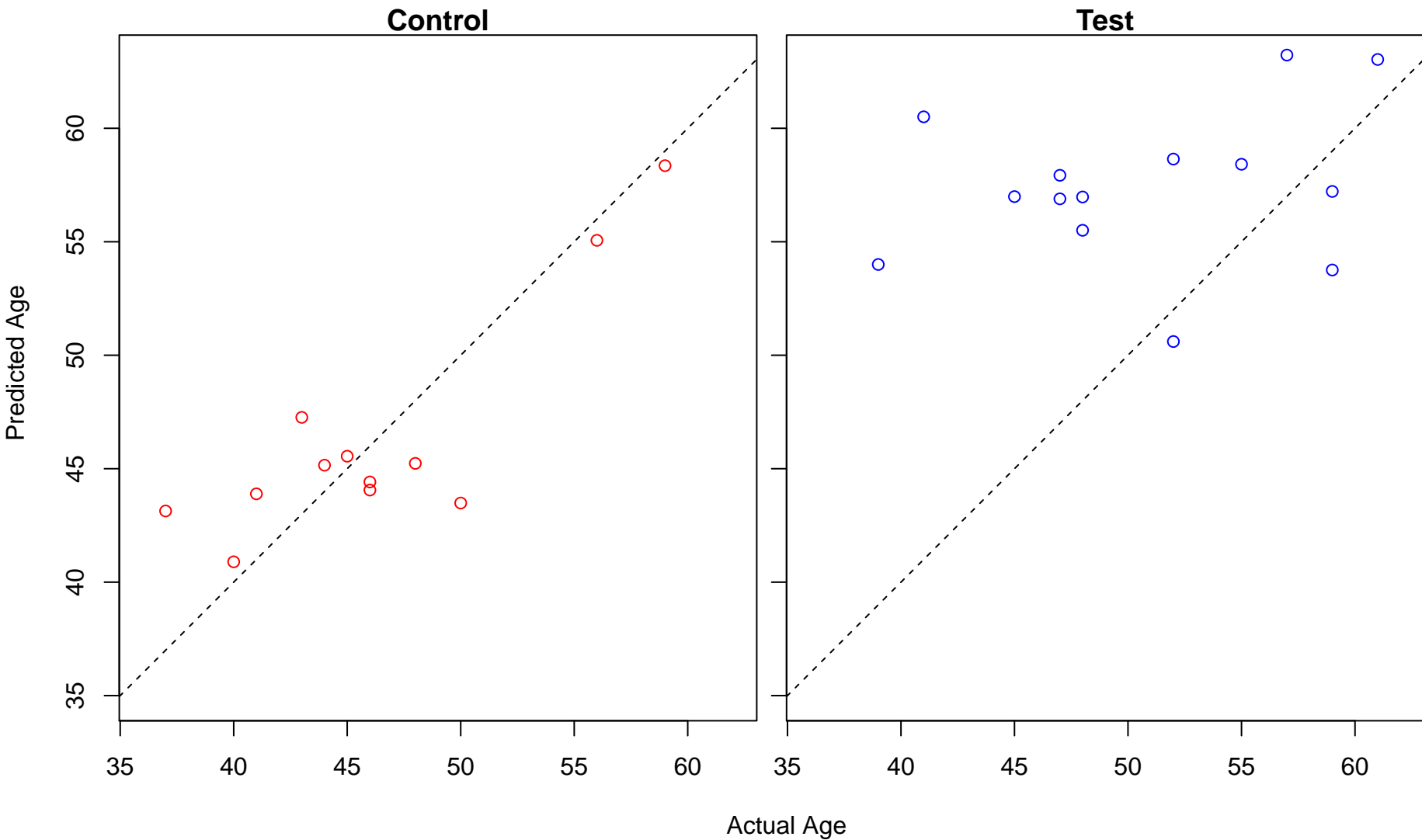
glutamine metabolic process (Score: 3.281173)



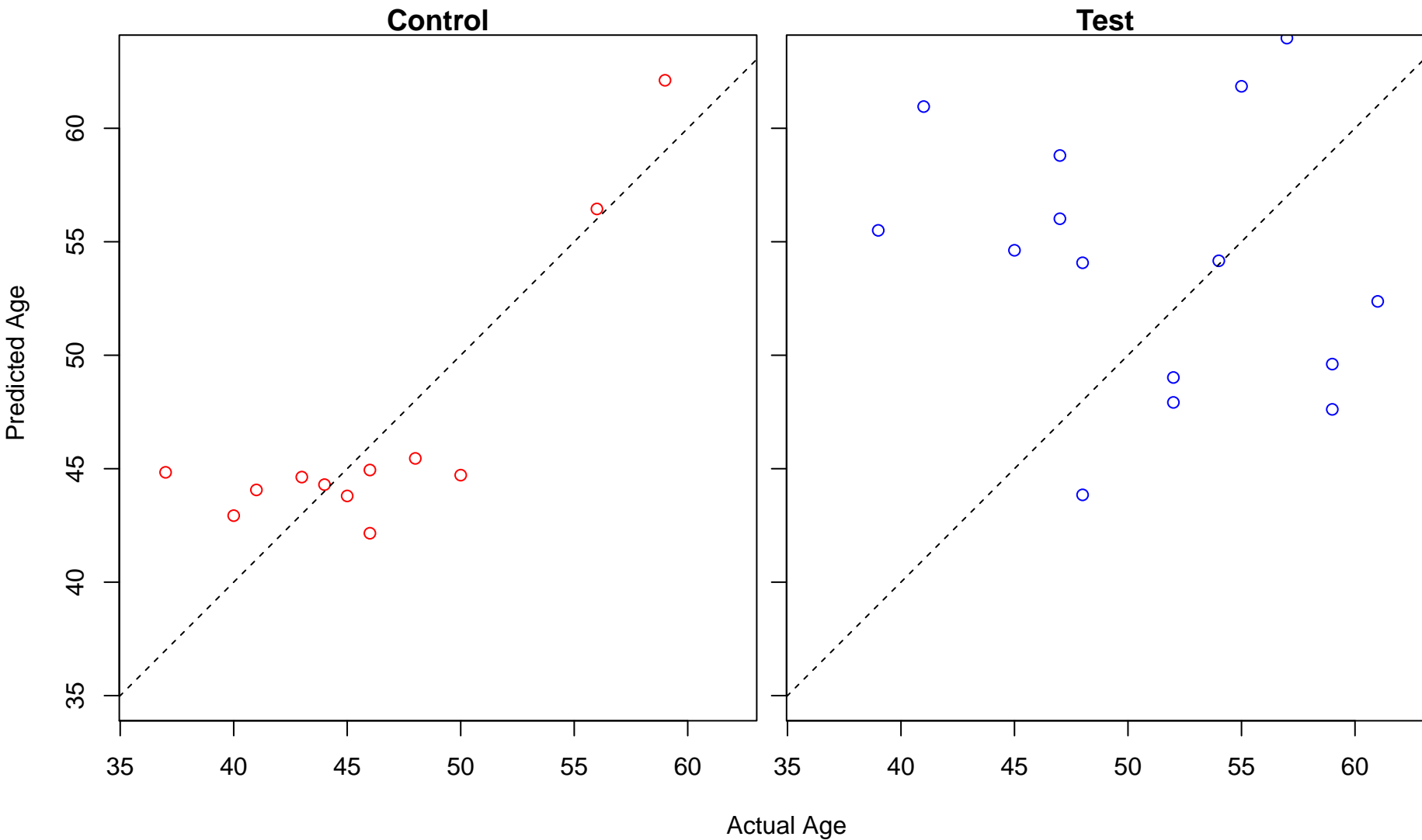
regulation of intrinsic apoptotic signaling pathway in response to DNA damage (Score: 3.279728)



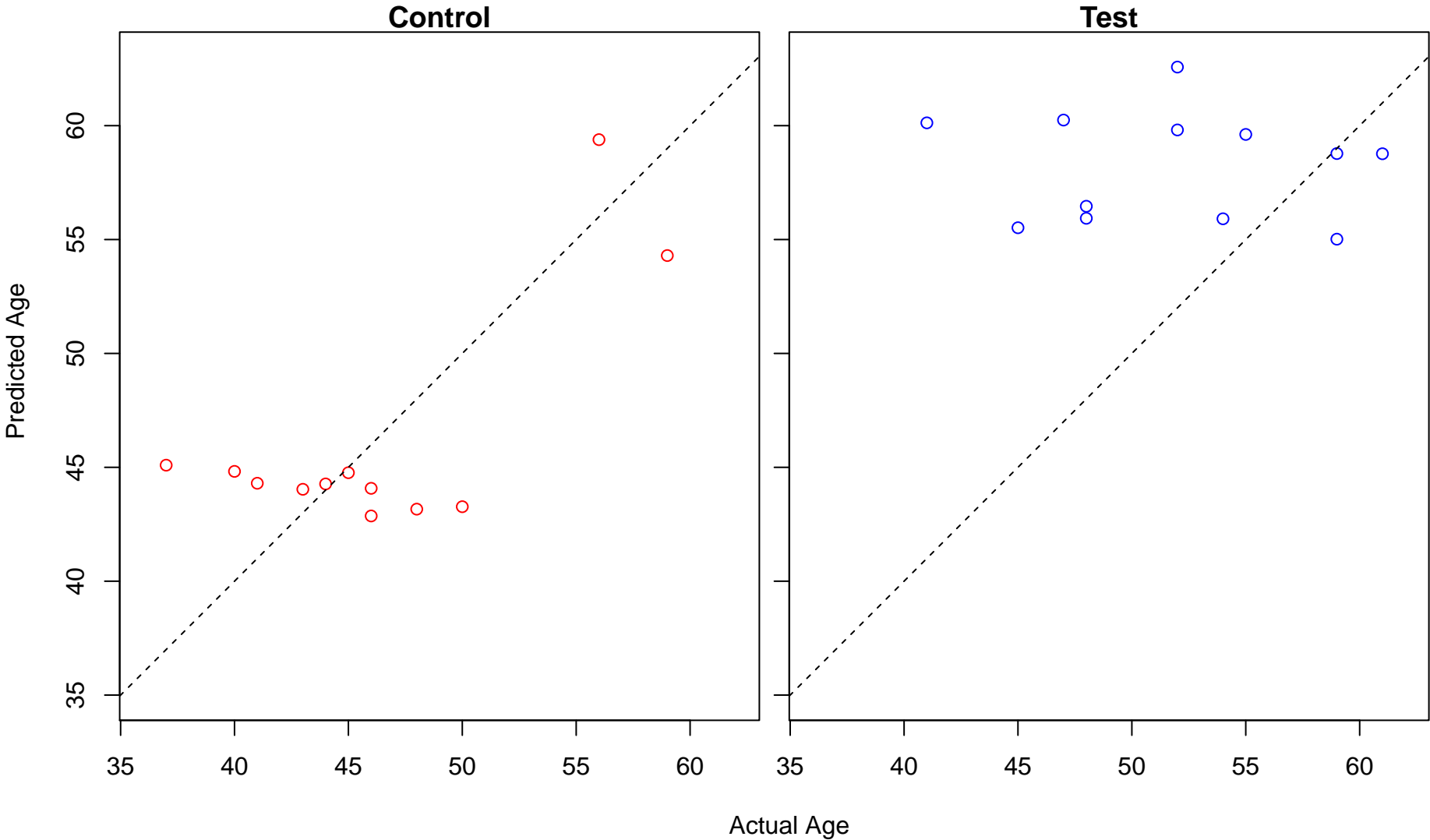
regulation of smooth muscle cell proliferation (Score: 3.279186)



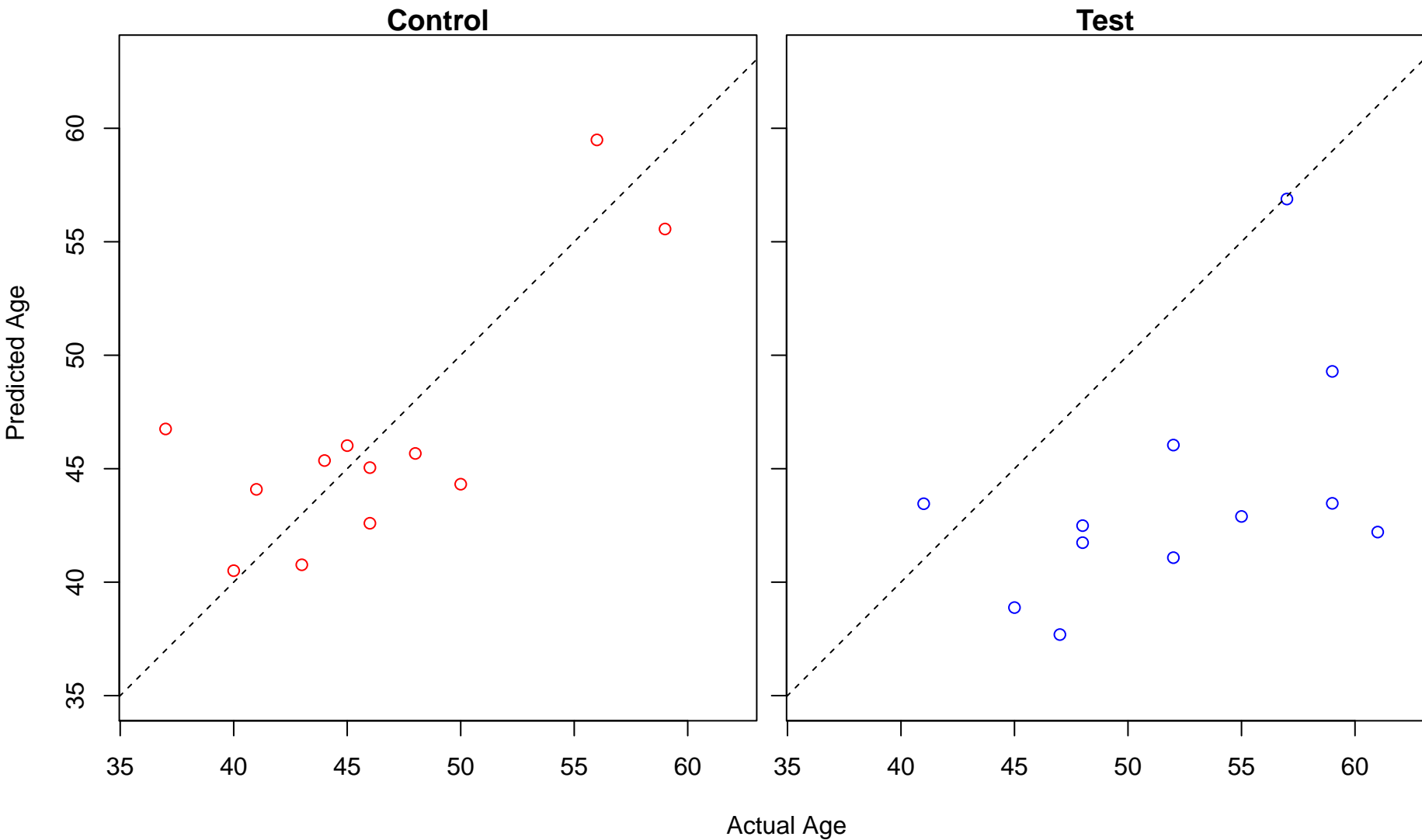
monosaccharide metabolic process (Score: 3.279081)



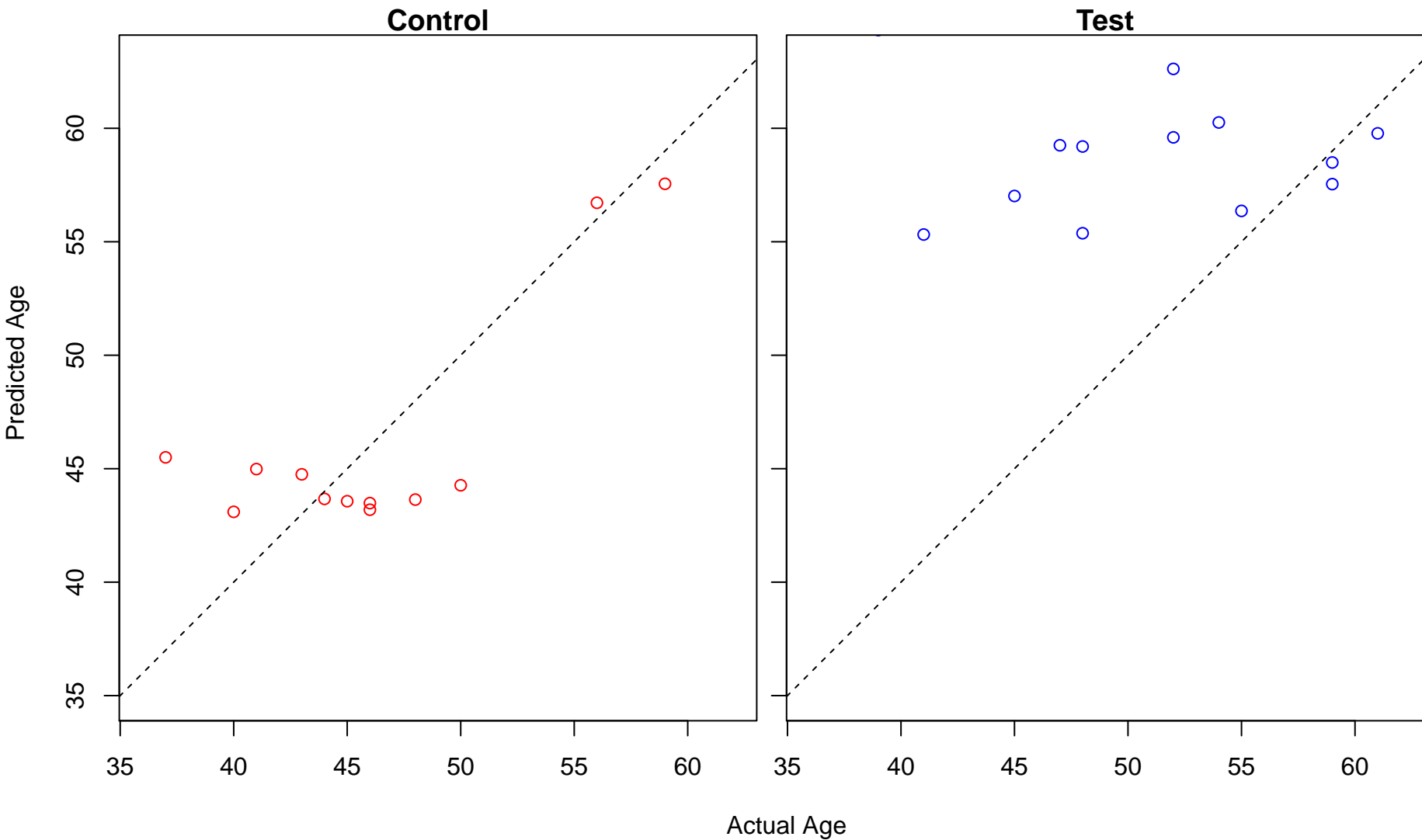
negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage (Score: 3.276)



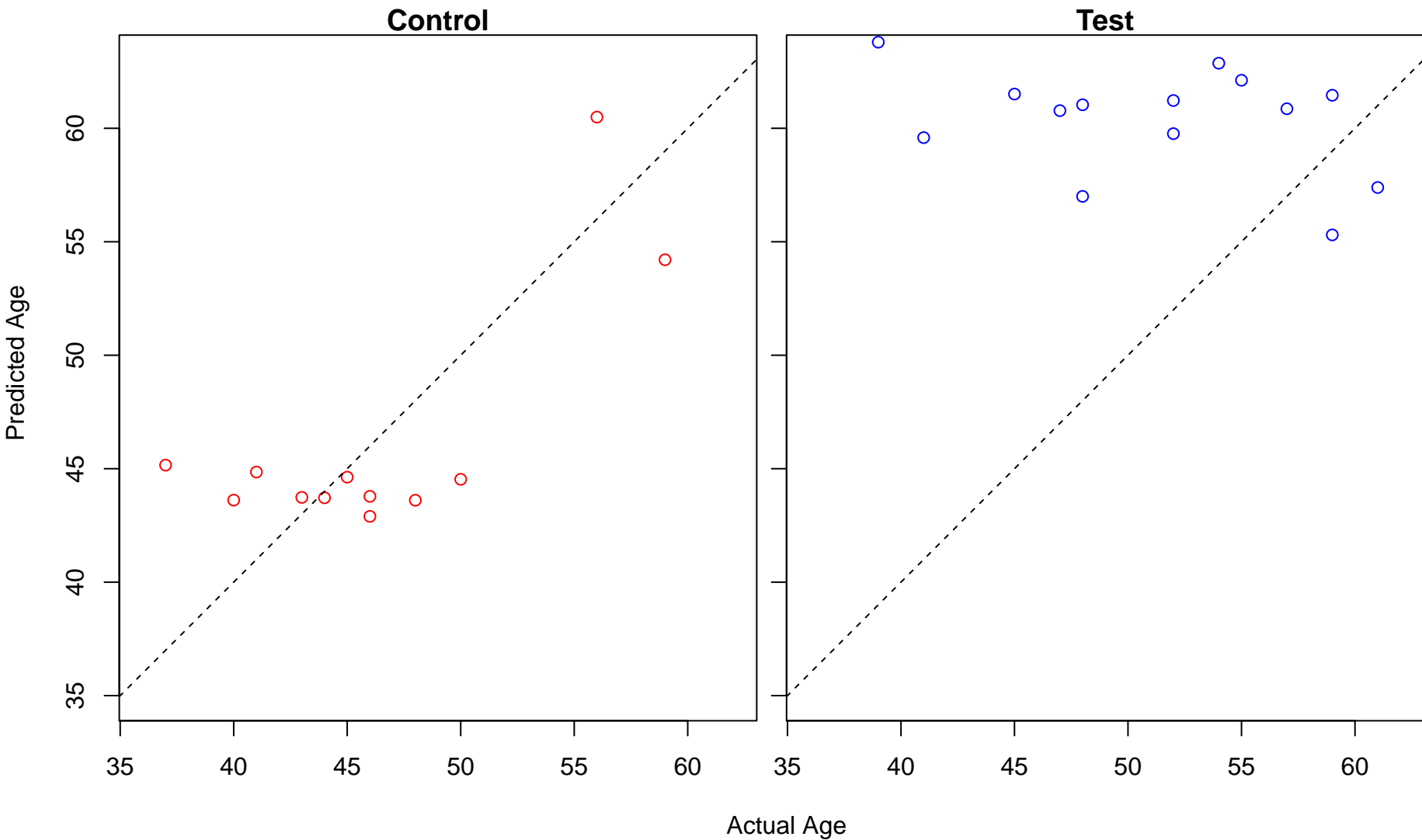
regulation of receptor recycling (Score: 3.275457)



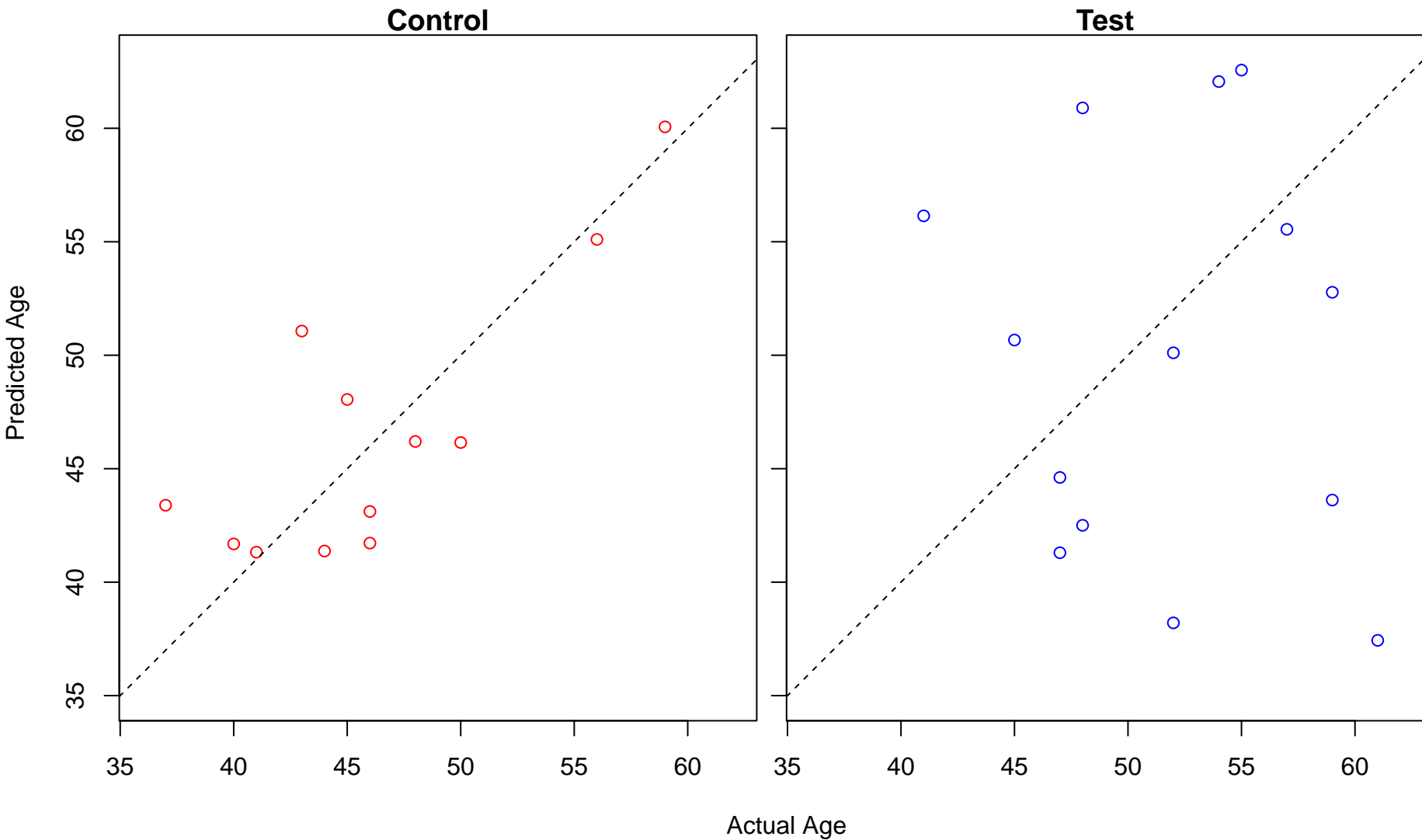
glutamine family amino acid biosynthetic process (Score: 3.274230)



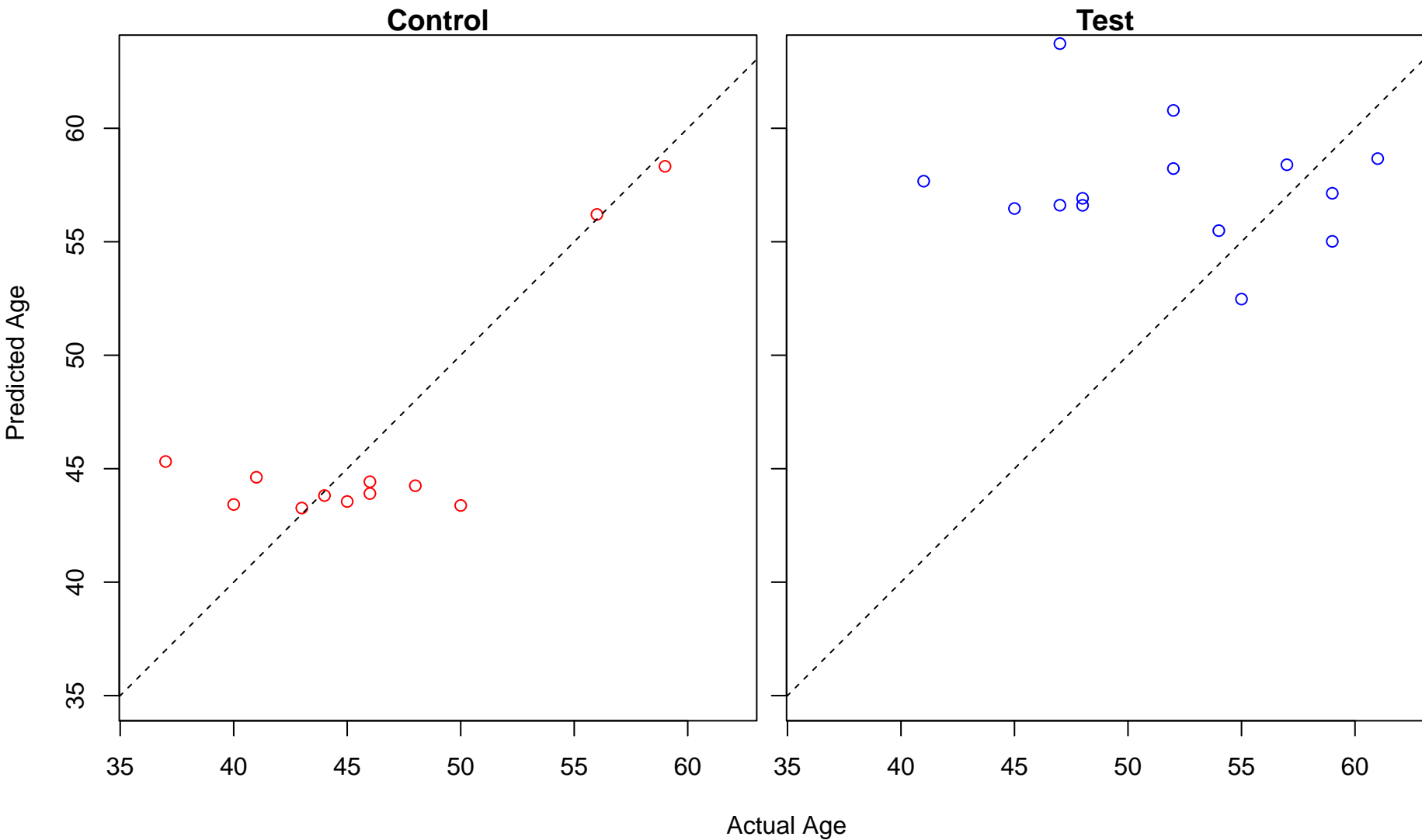
histone H3-K27 methylation (Score: 3.273852)



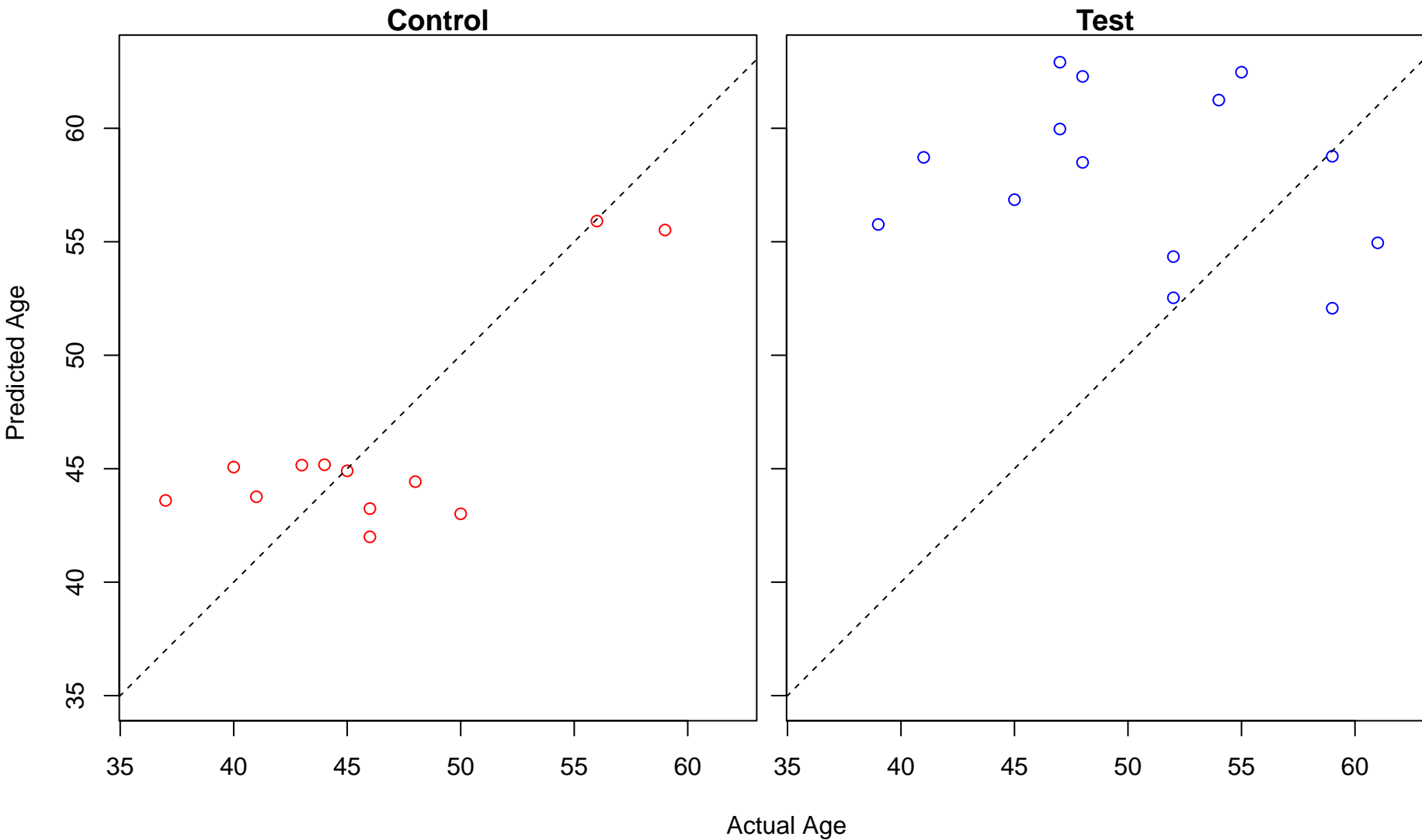
trabecula morphogenesis (Score: 3.273591)



regulation of endodeoxyribonuclease activity (Score: 3.270415)

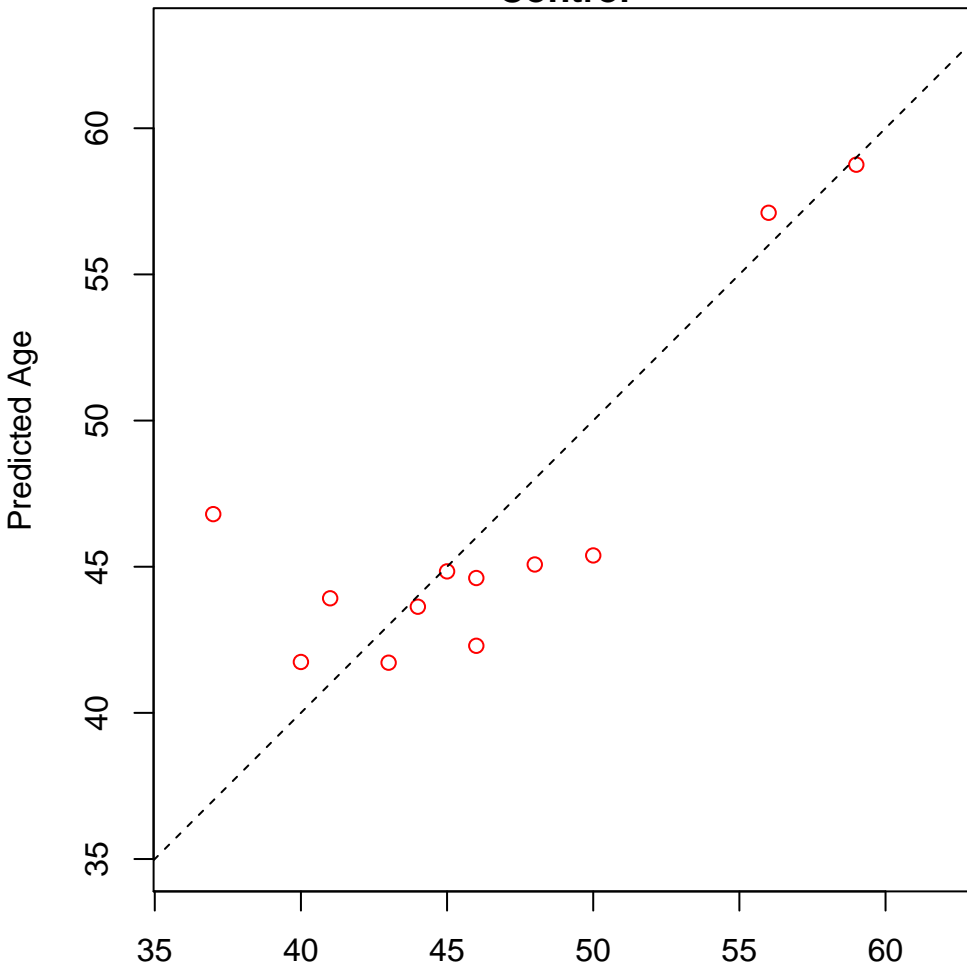


regulation of immature T cell proliferation (Score: 3.269312)

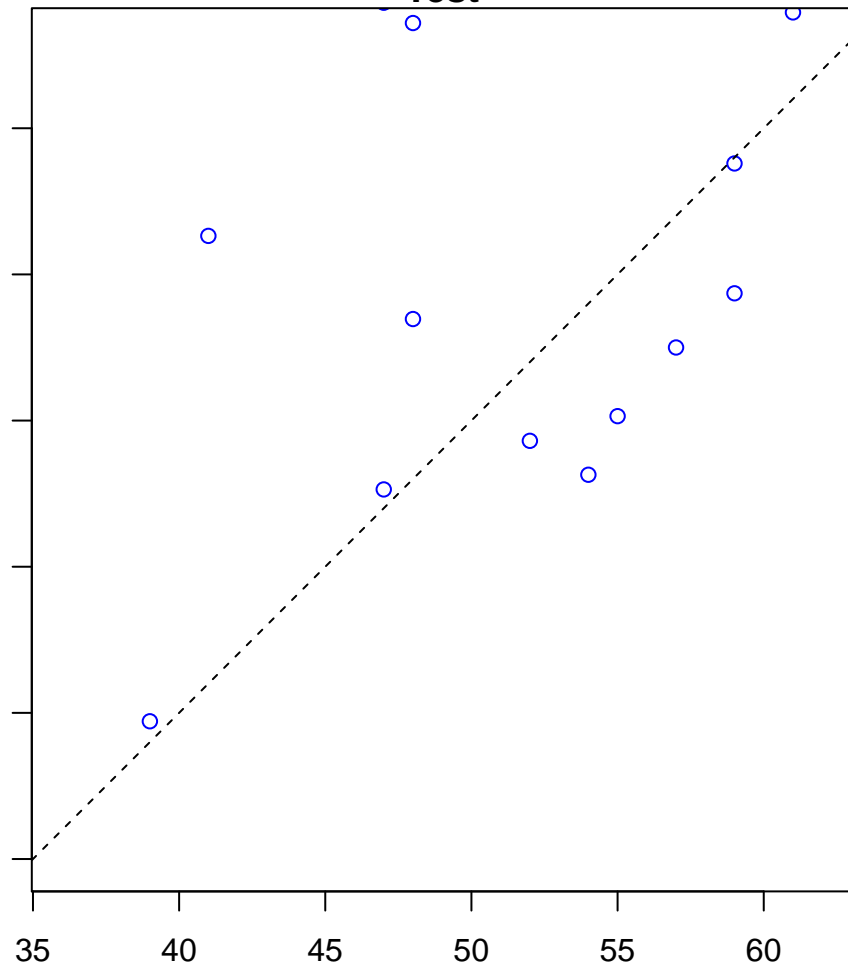


RNA (guanine-N7)-methylation (Score: 3.268851)

Control



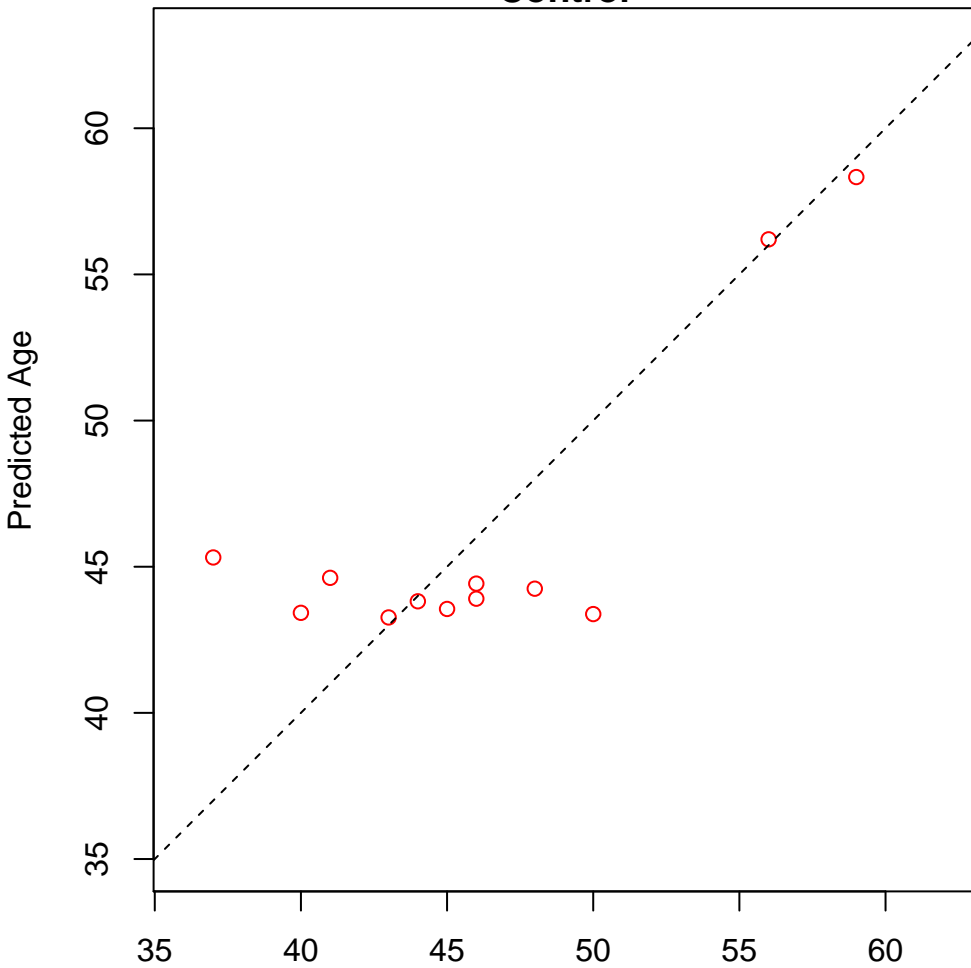
Test



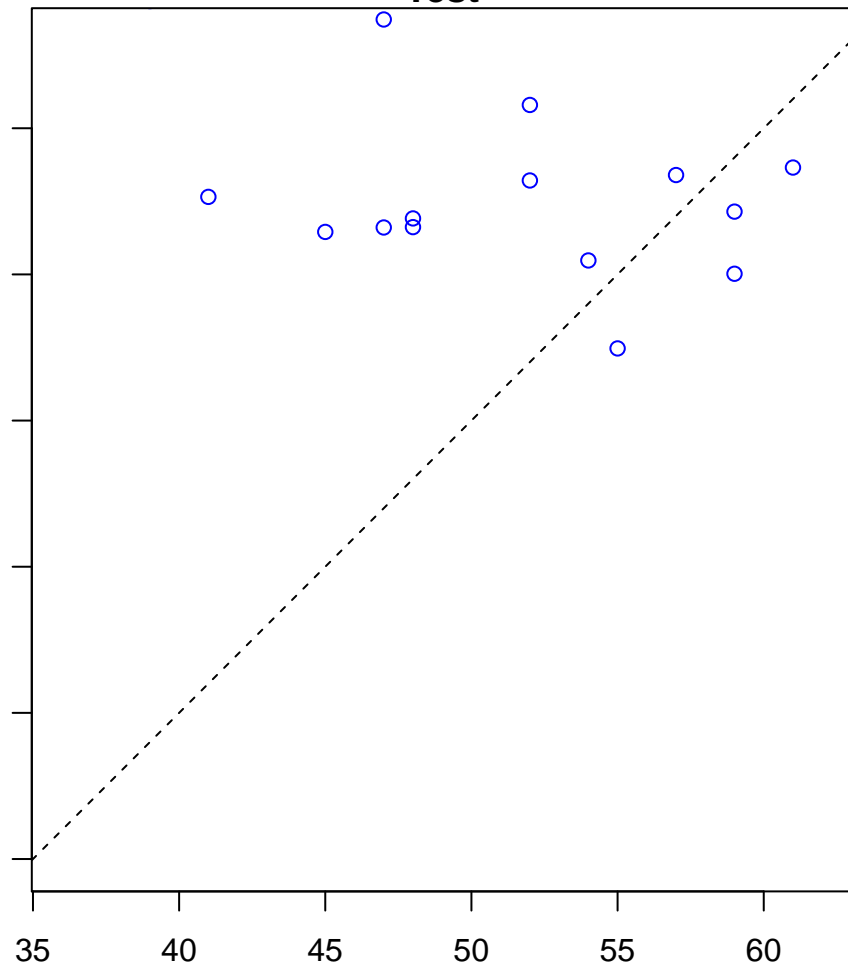
Actual Age

regulation of deoxyribonuclease activity (Score: 3.268558)

Control

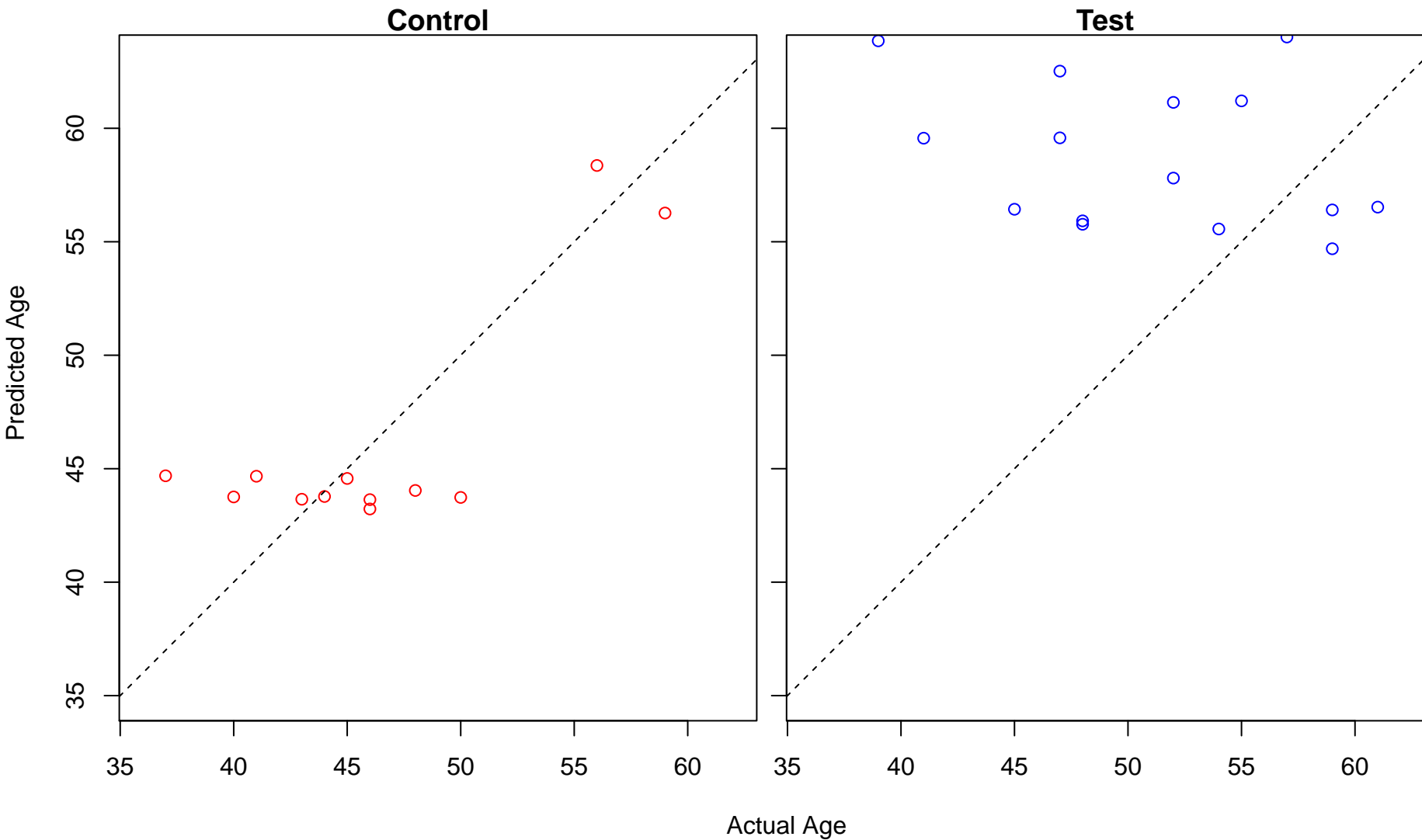


Test

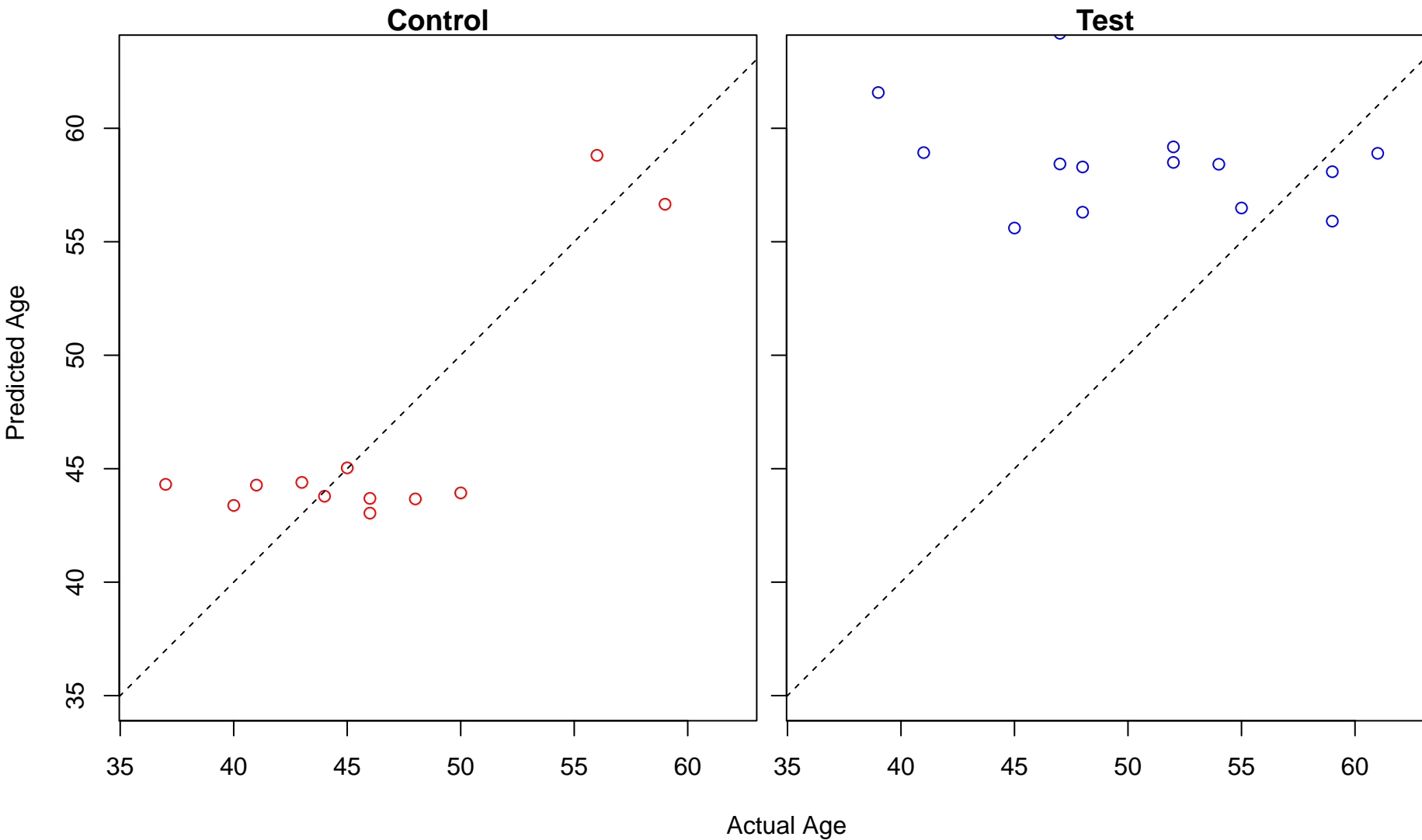


Actual Age

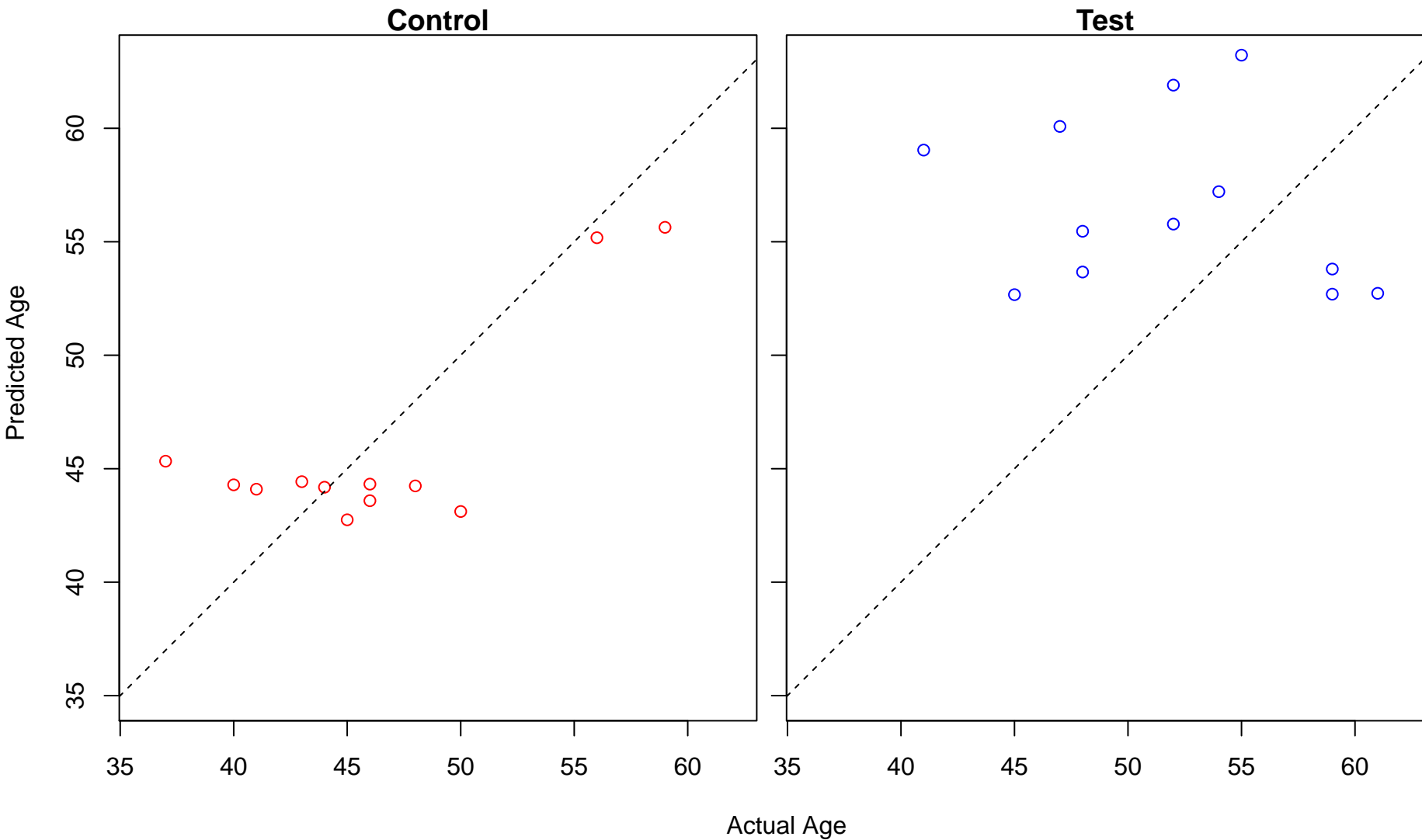
regulation of cell morphogenesis (Score: 3.267702)



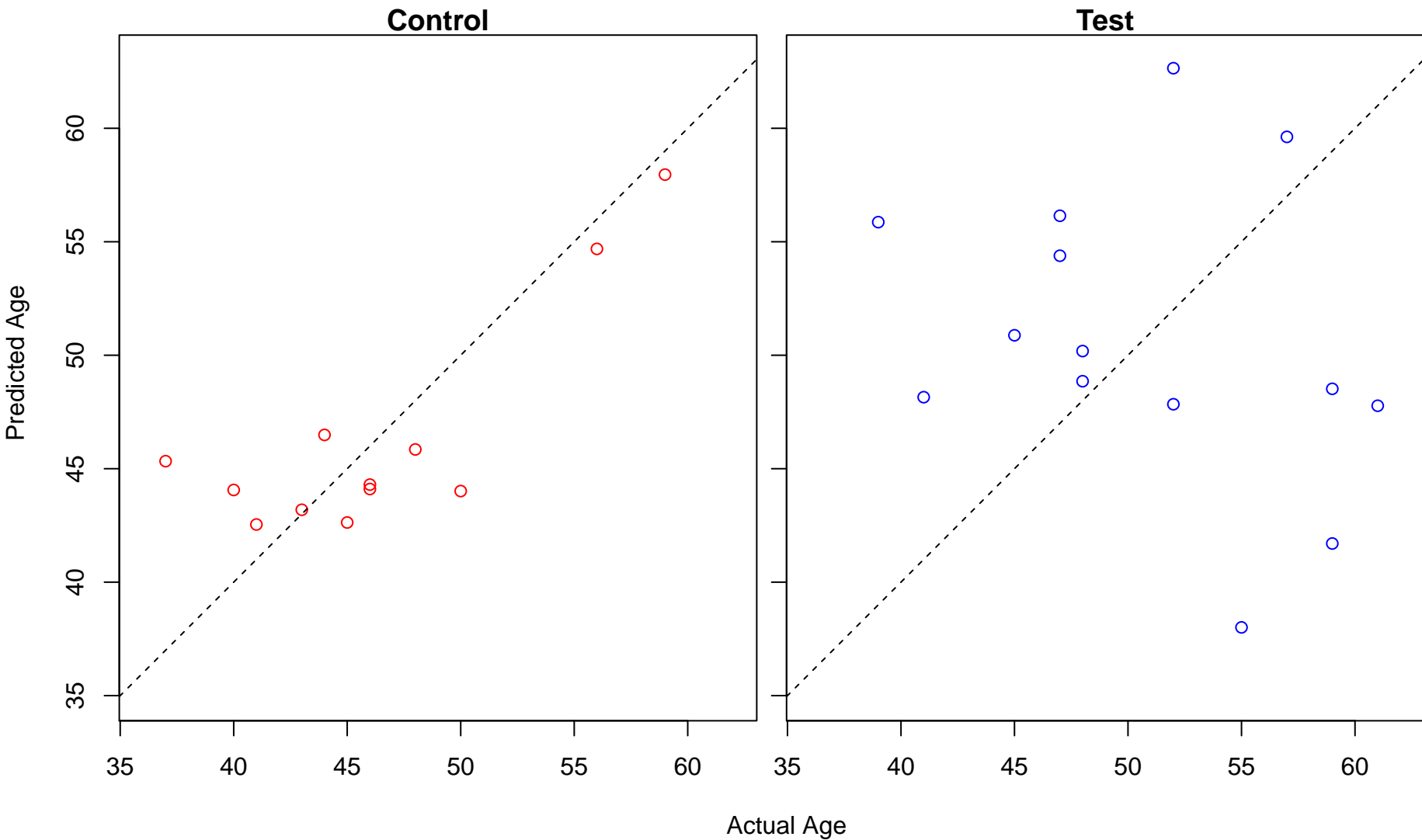
organelle disassembly (Score: 3.264281)



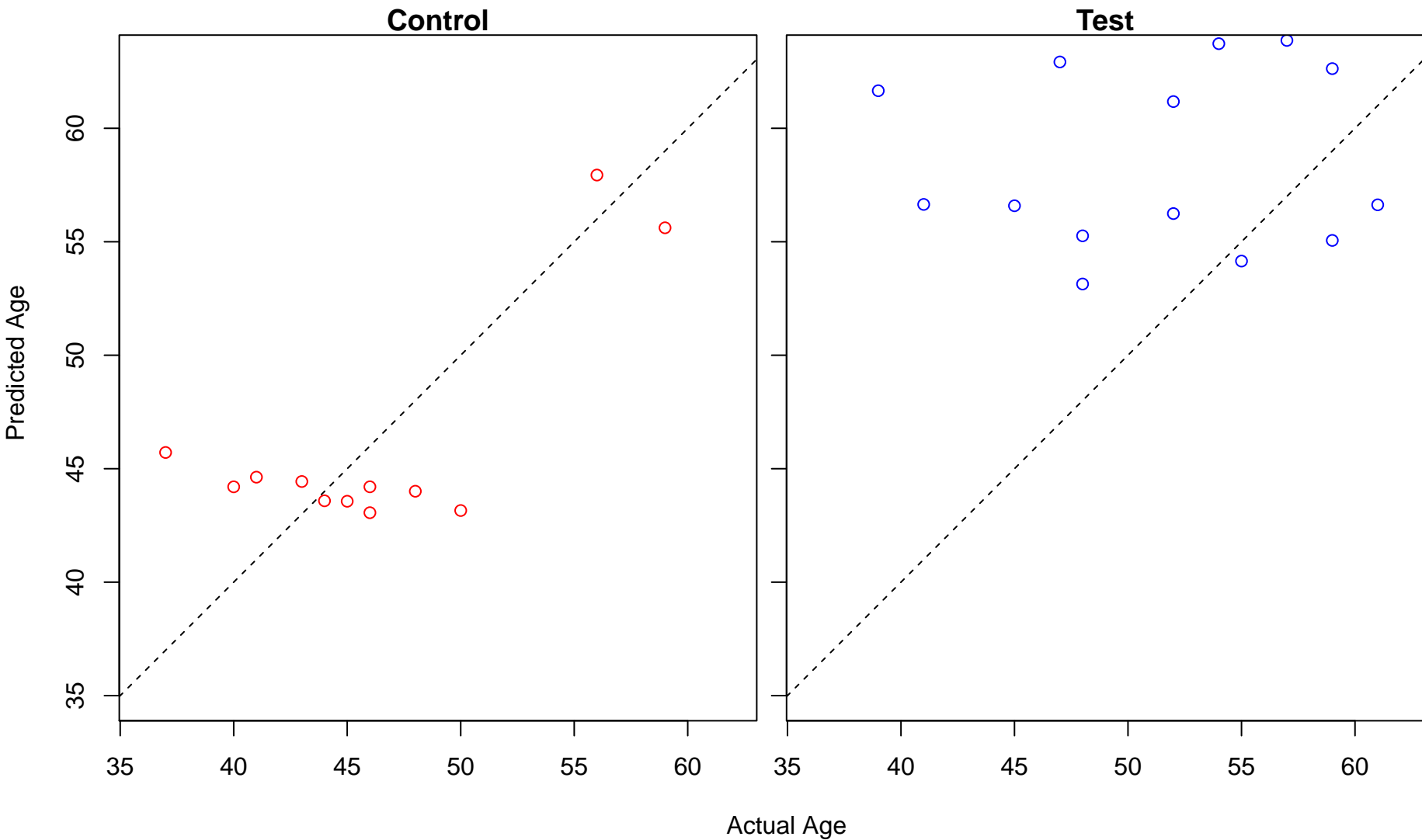
cell-cell adhesion (Score: 3.264256)



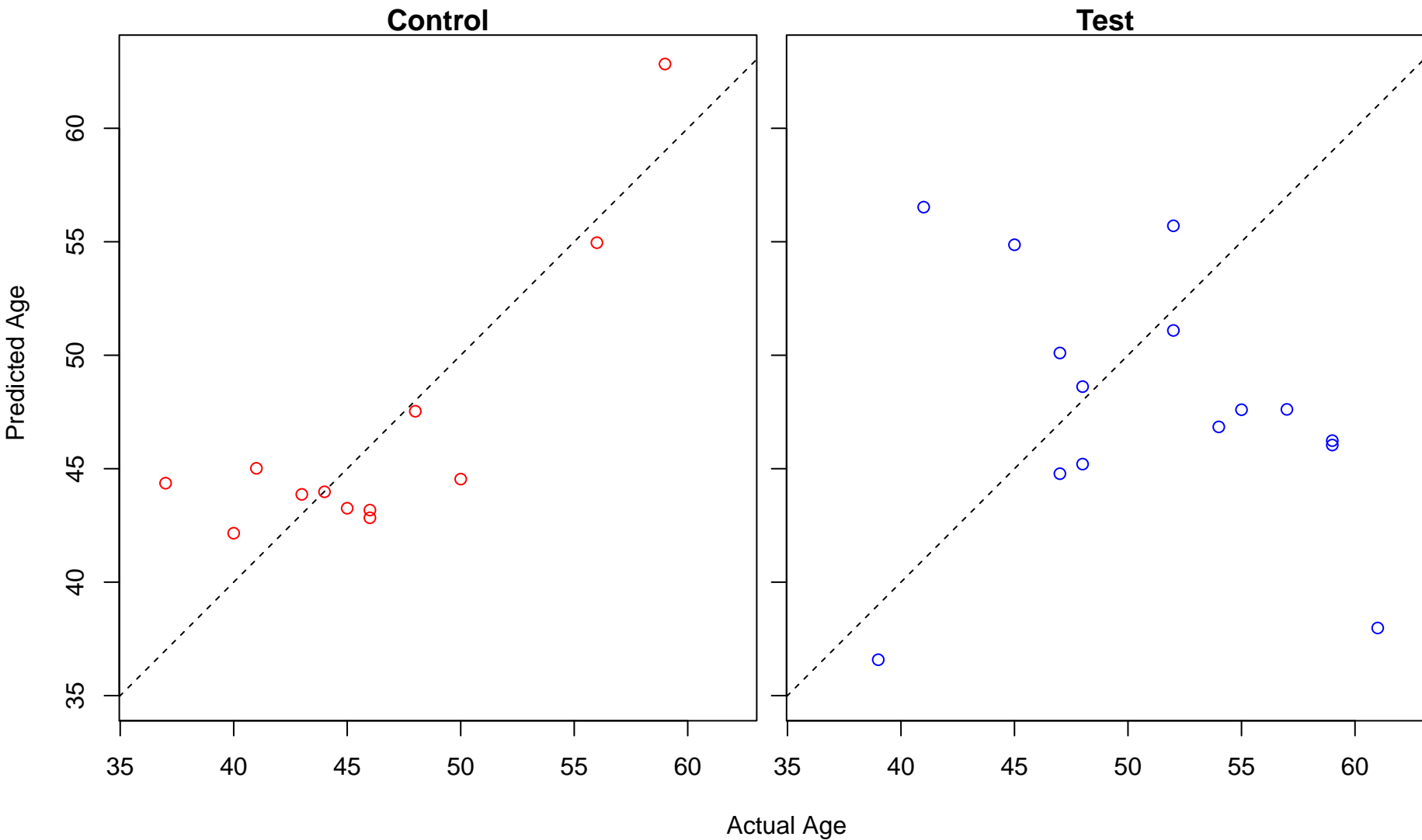
sulfate transport (Score: 3.263669)



regulation of natural killer cell activation (Score: 3.262188)

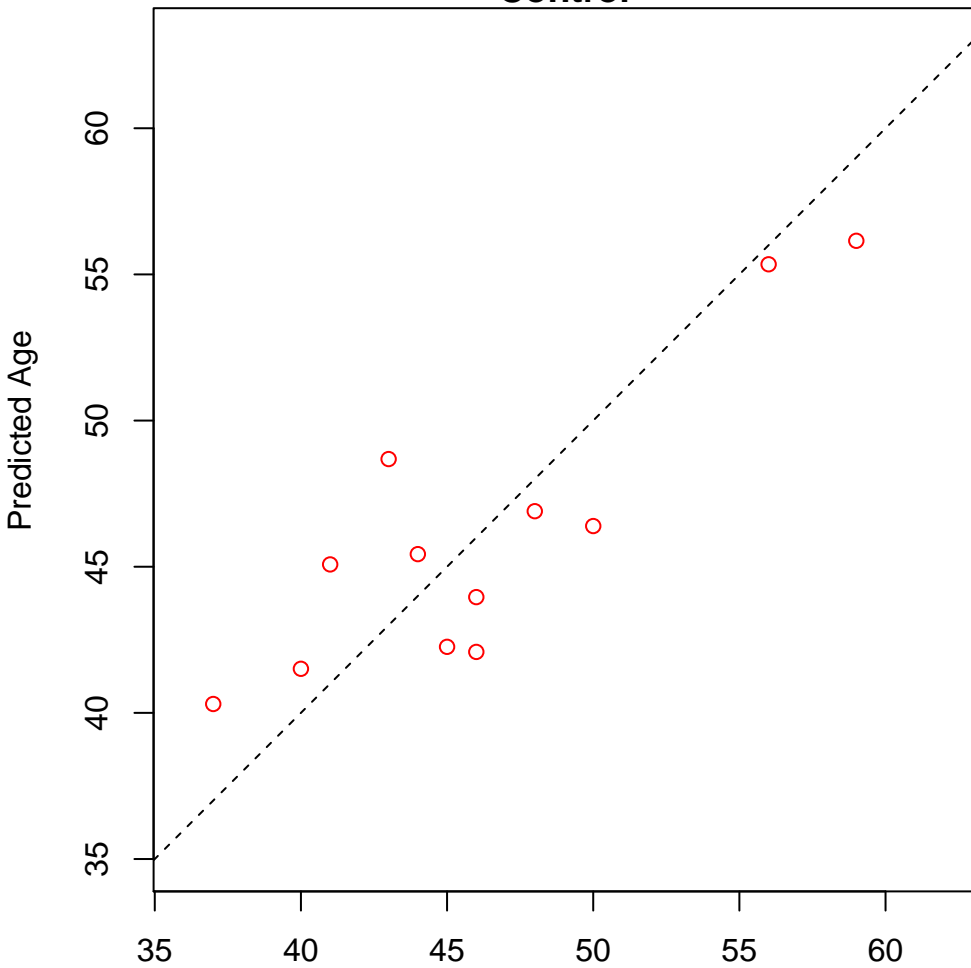


G2 DNA damage checkpoint (Score: 3.261798)

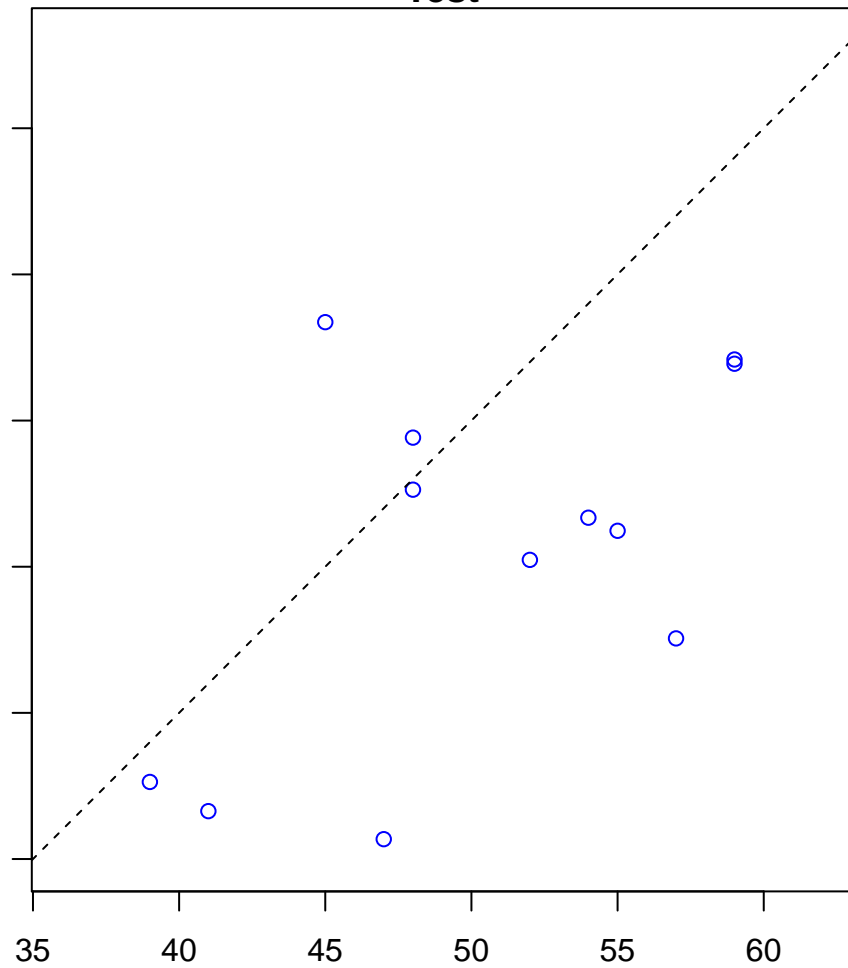


phosphatidylinositol 3-kinase signaling (Score: 3.260889)

Control



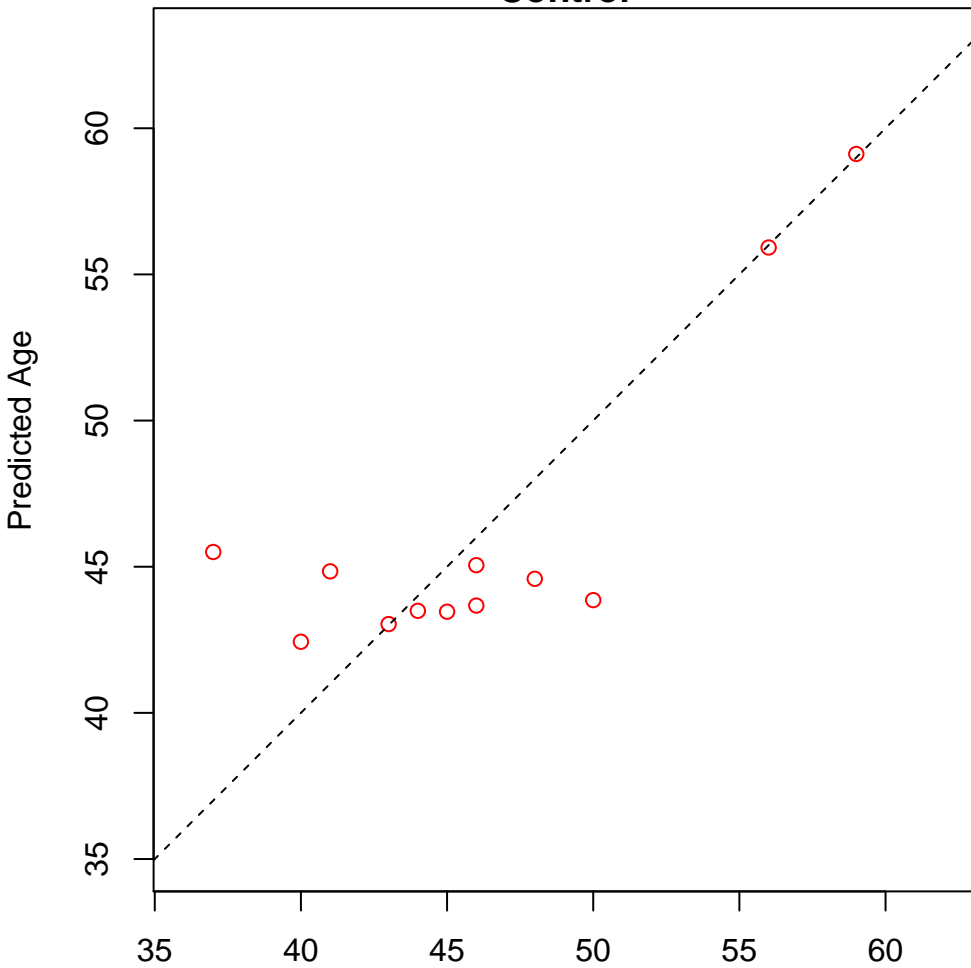
Test



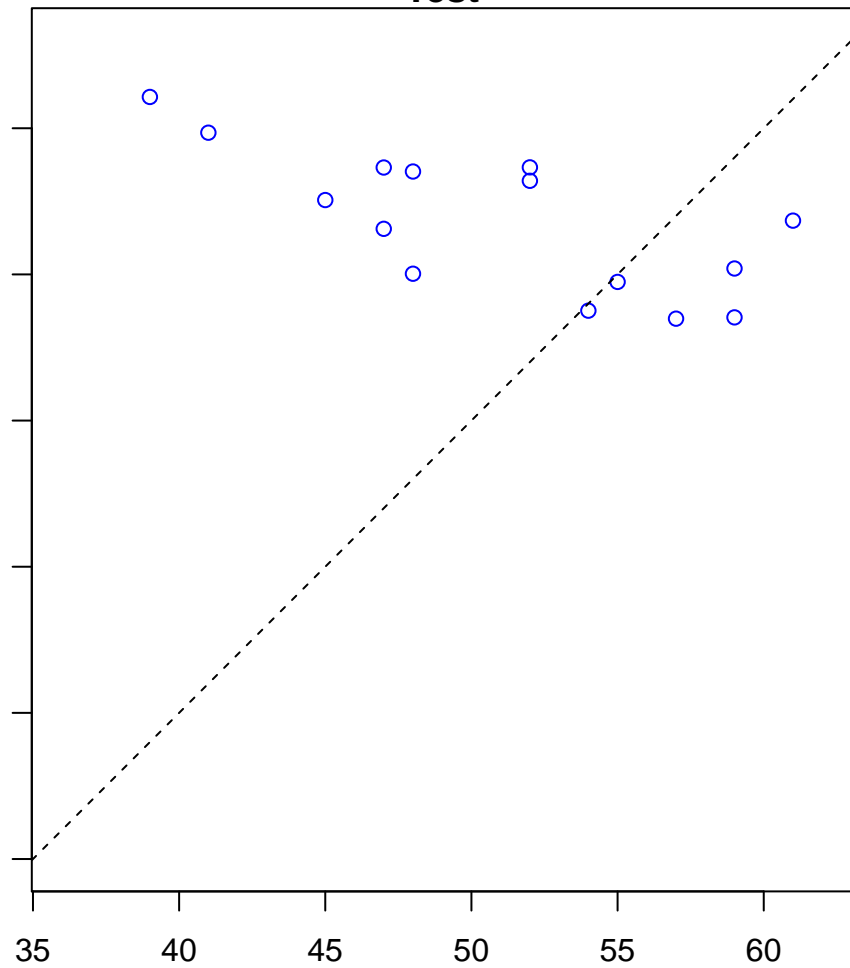
Actual Age

regulation of interleukin-1 secretion (Score: 3.260612)

Control

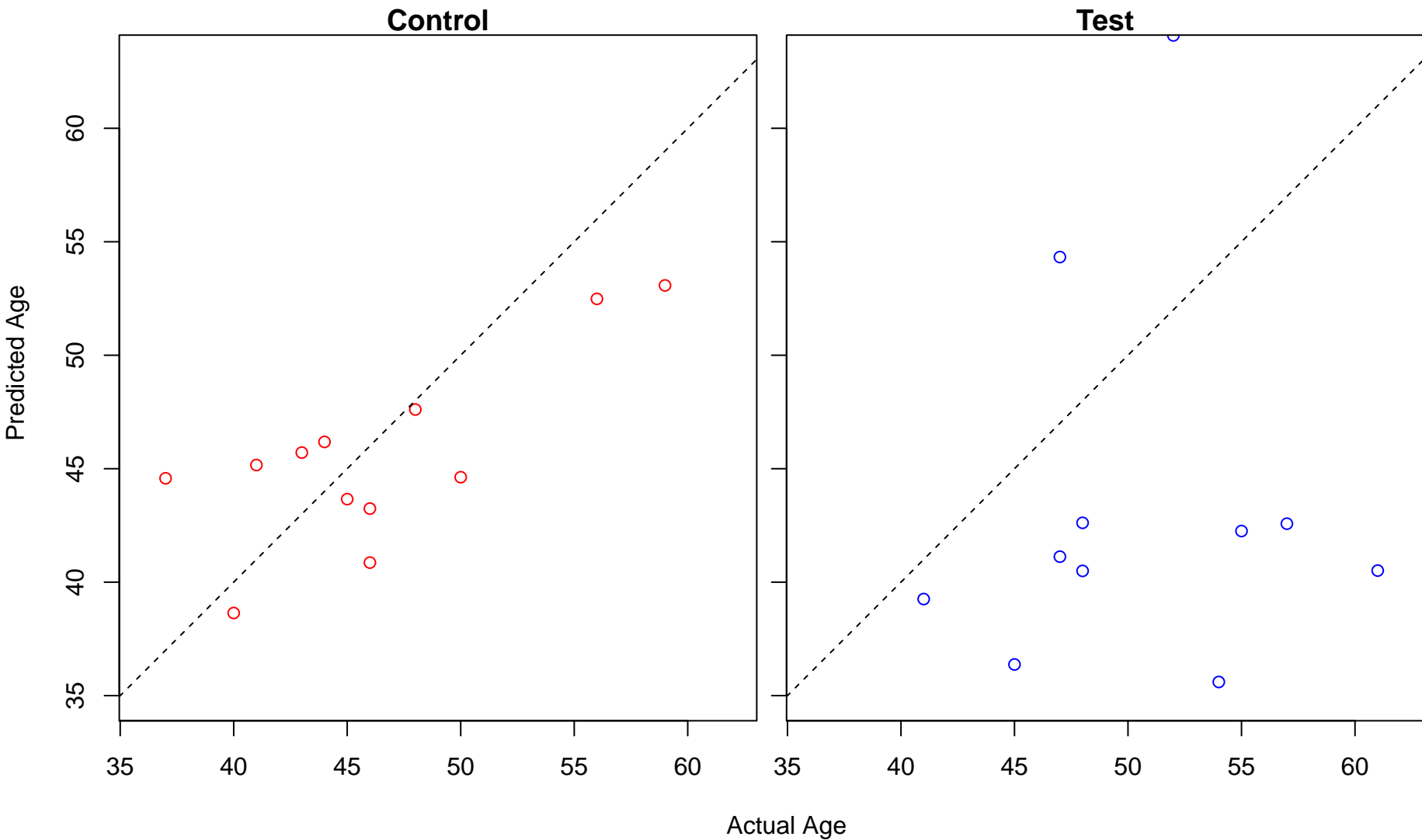


Test

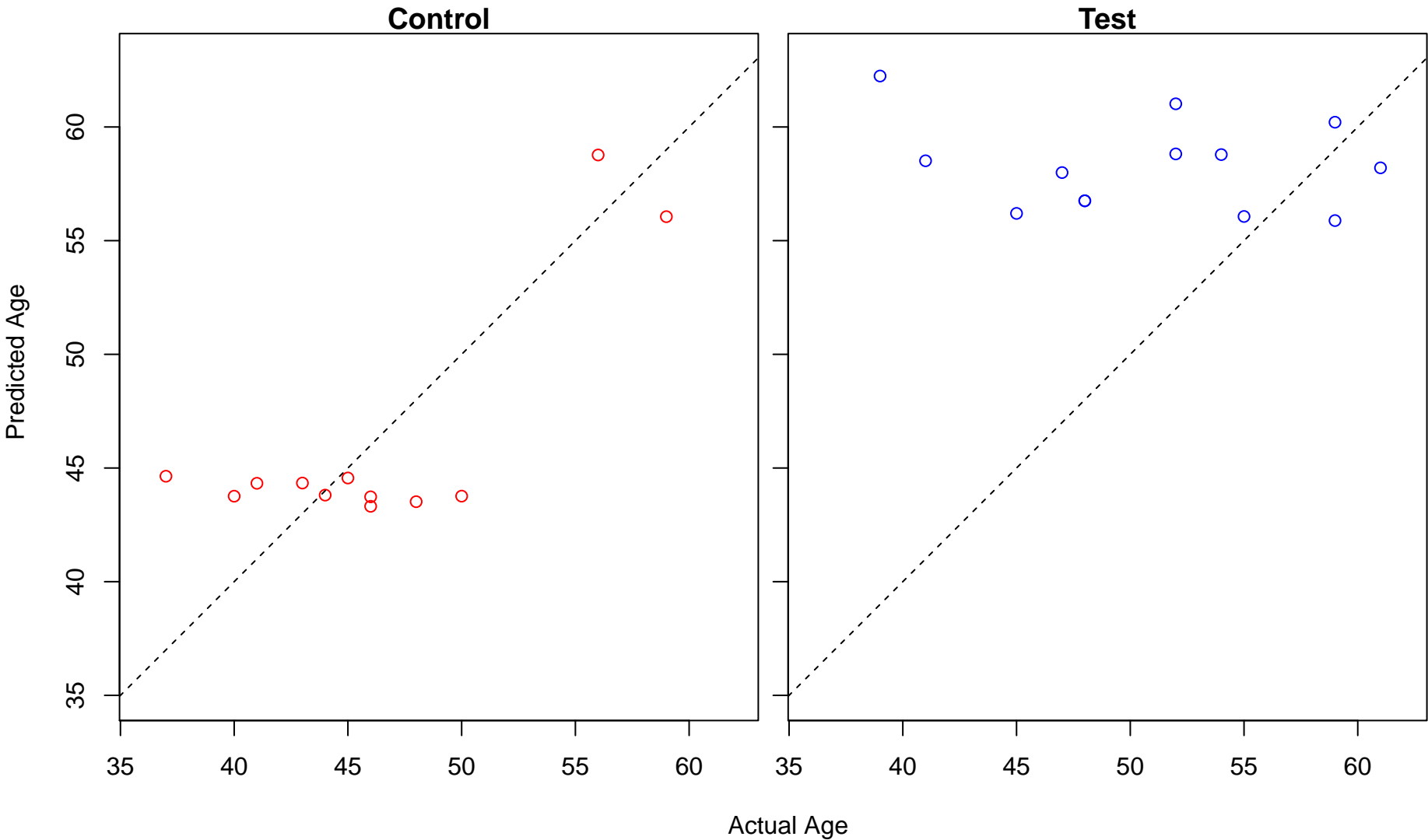


Actual Age

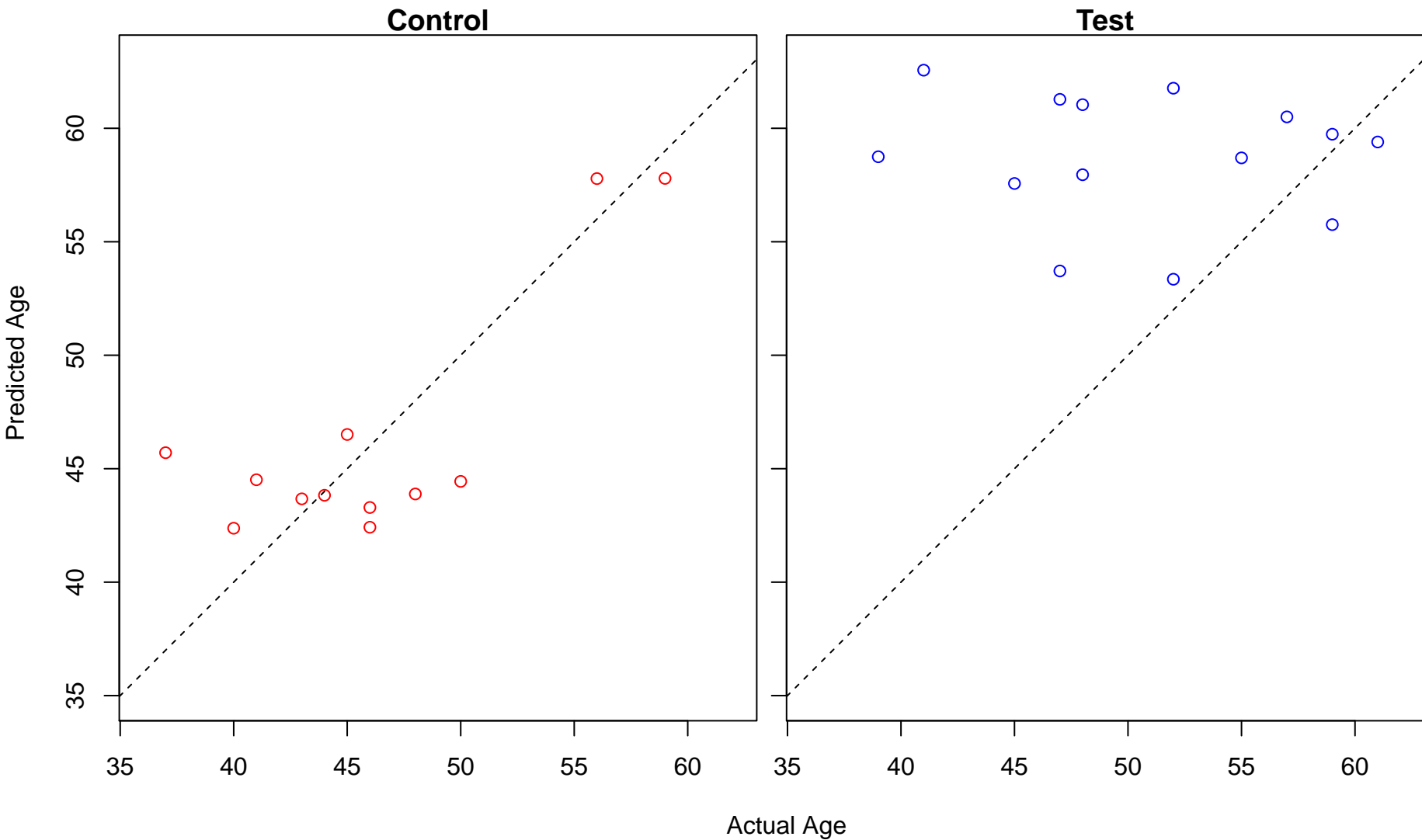
protein targeting to membrane (Score: 3.258905)



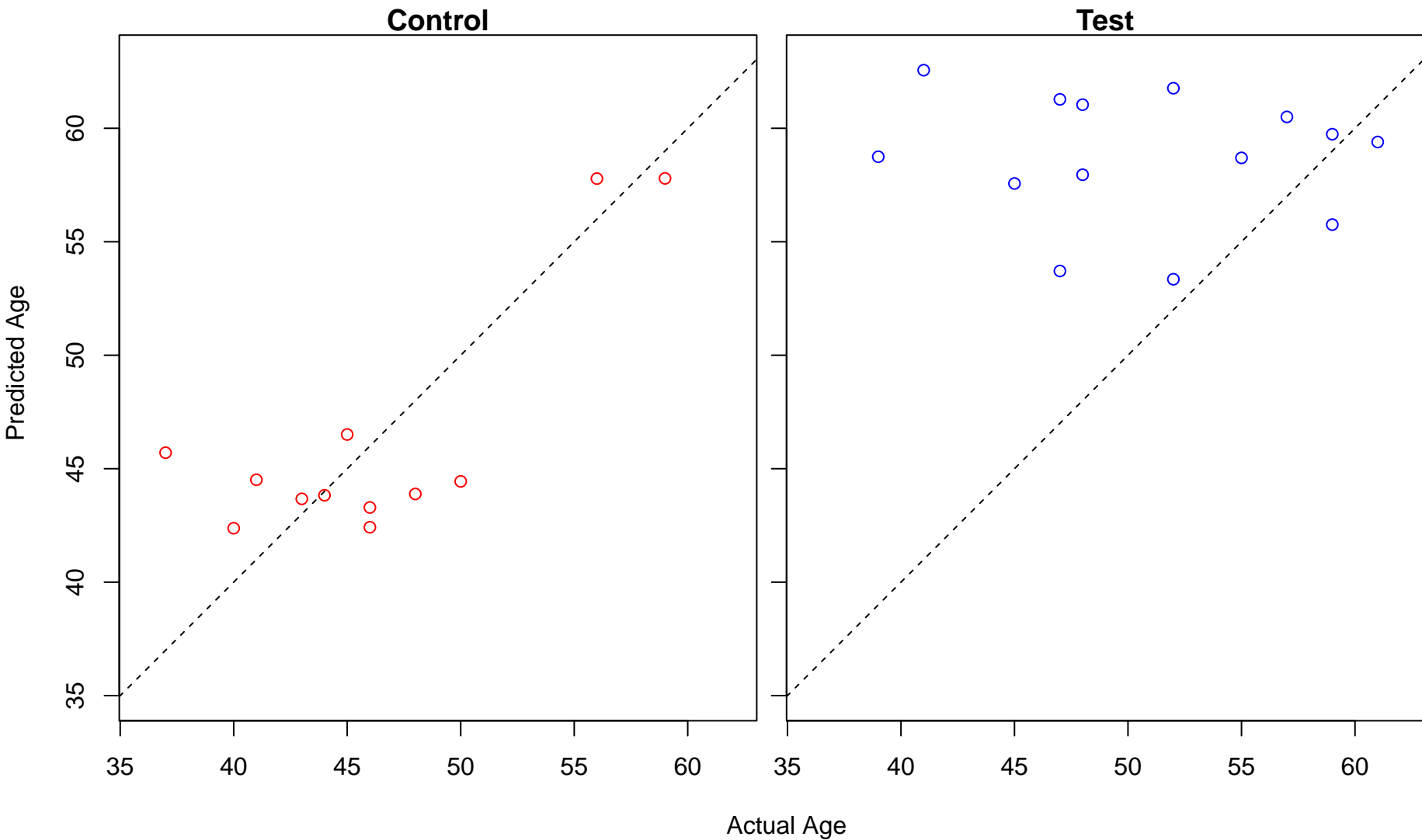
positive regulation of proteolysis involved in cellular protein catabolic process (Score: 3.258471)



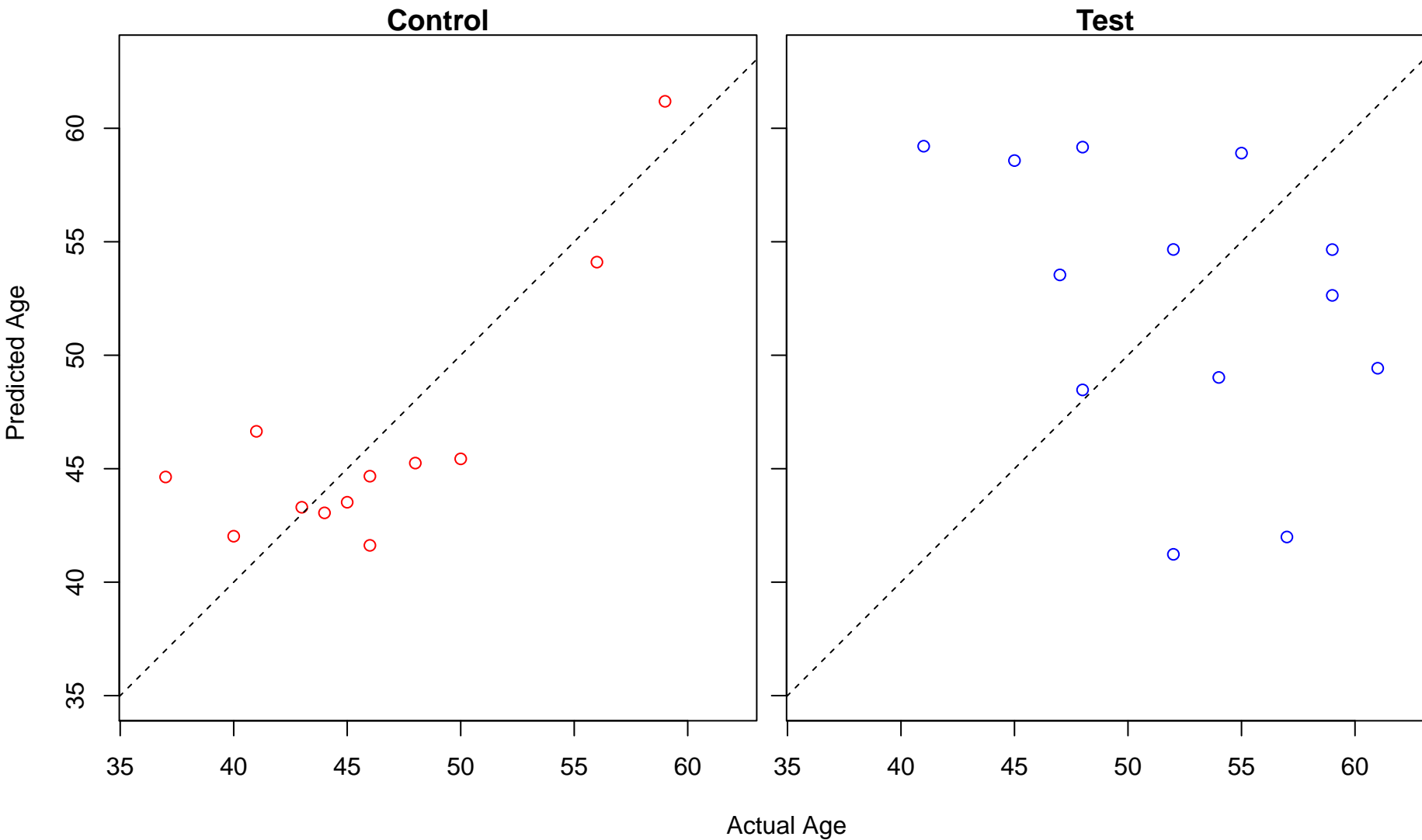
regulation of T cell differentiation in thymus (Score: 3.258024)



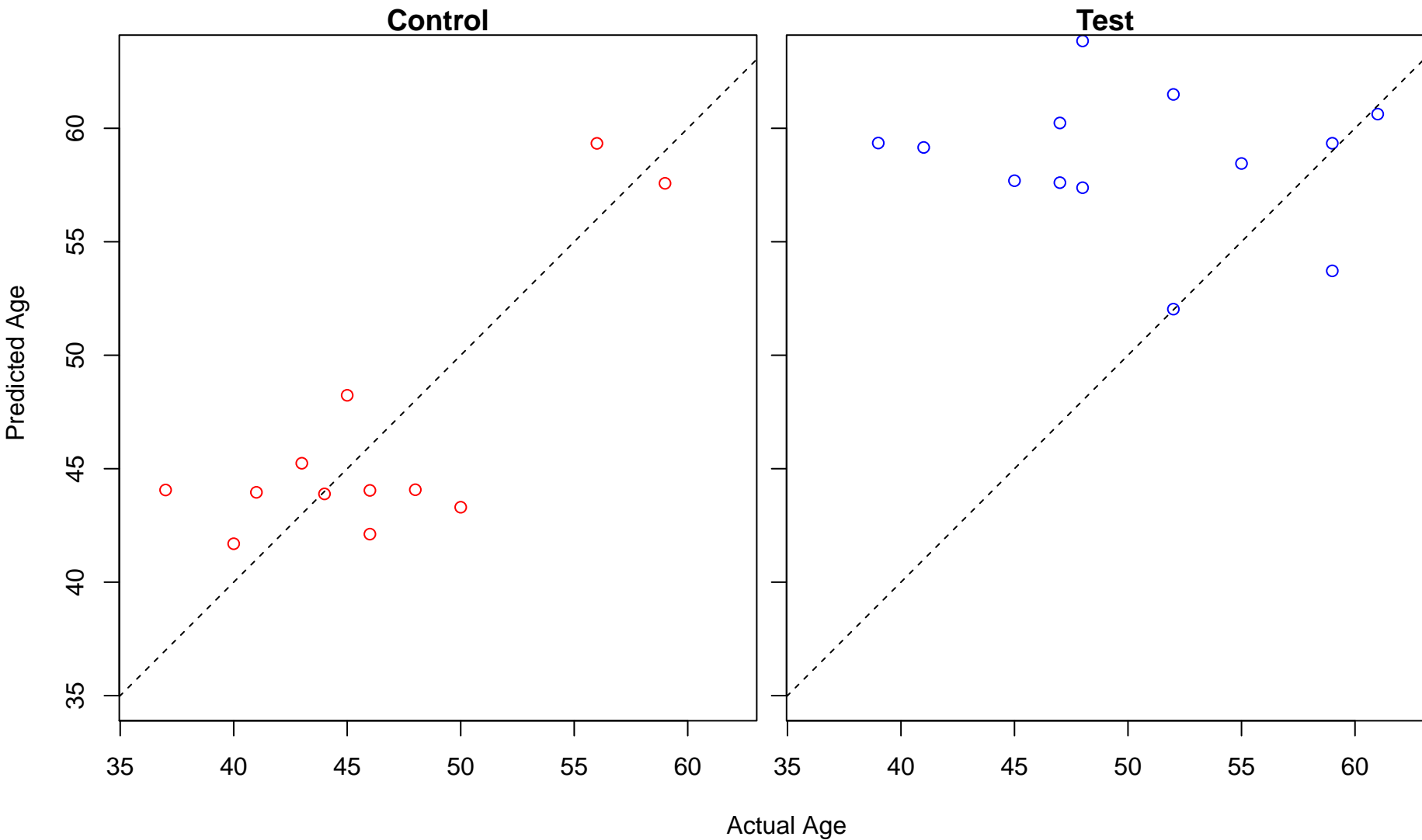
regulation of thymocyte aggregation (Score: 3.258024)



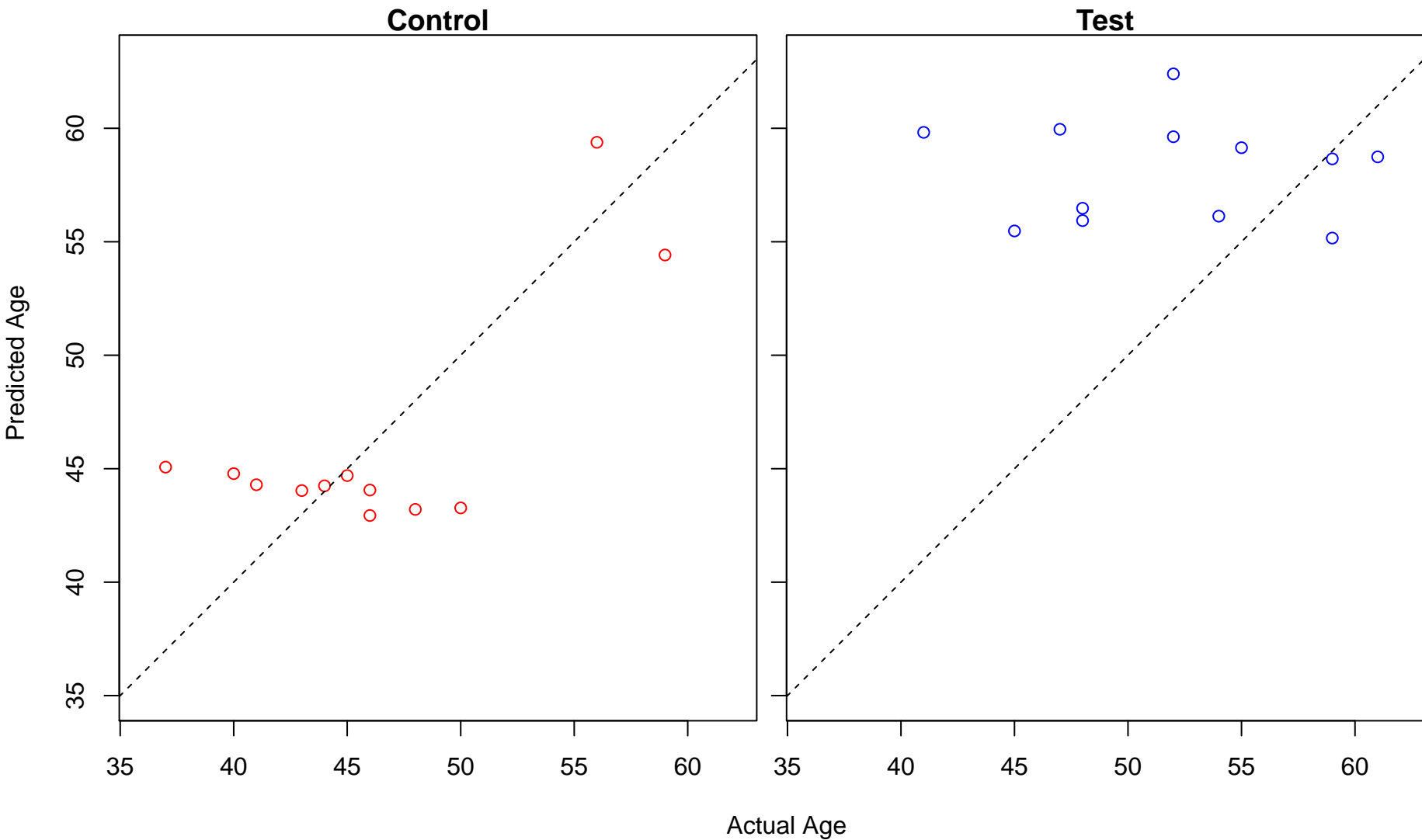
negative regulation of DNA repair (Score: 3.254511)



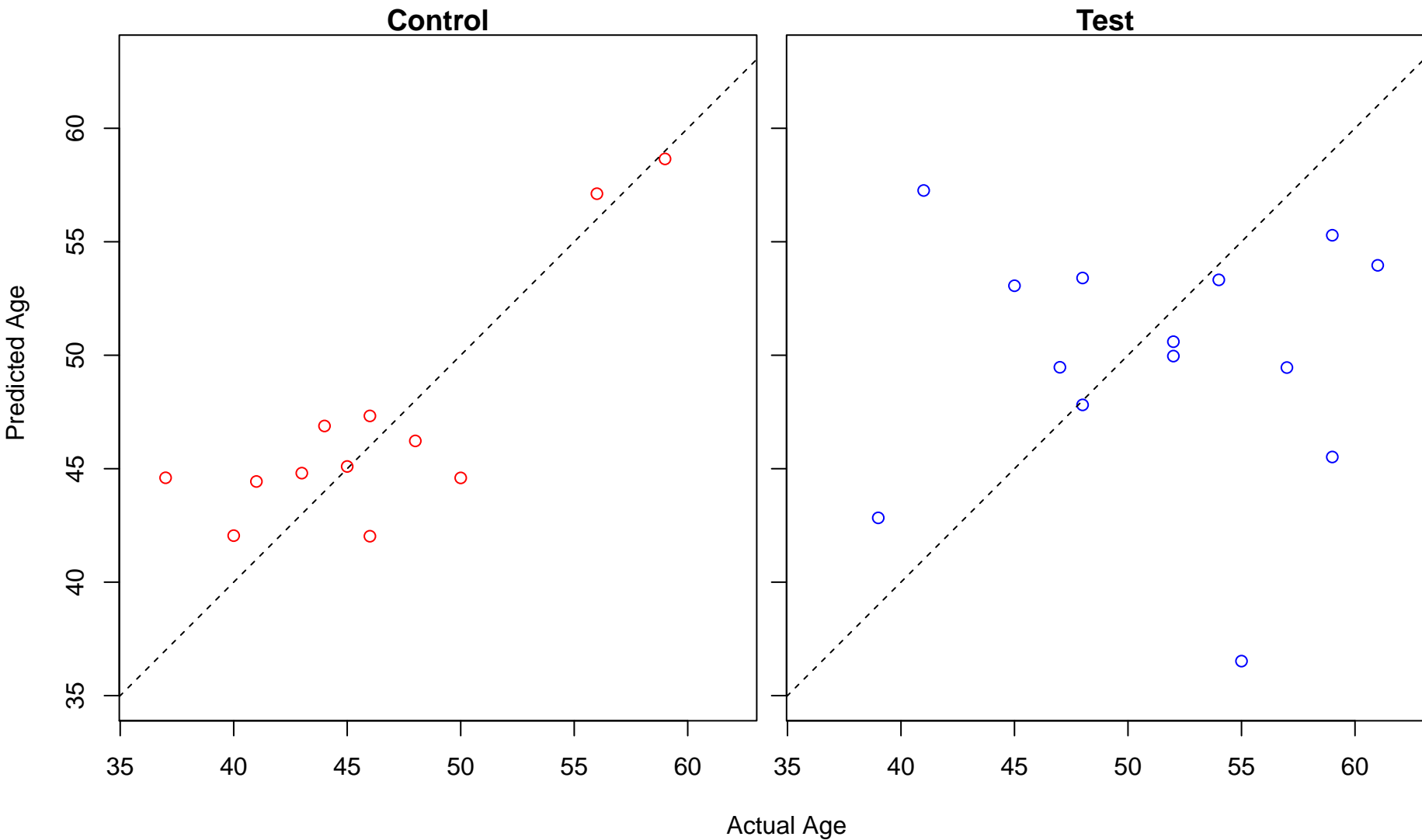
microtubule bundle formation (Score: 3.253022)



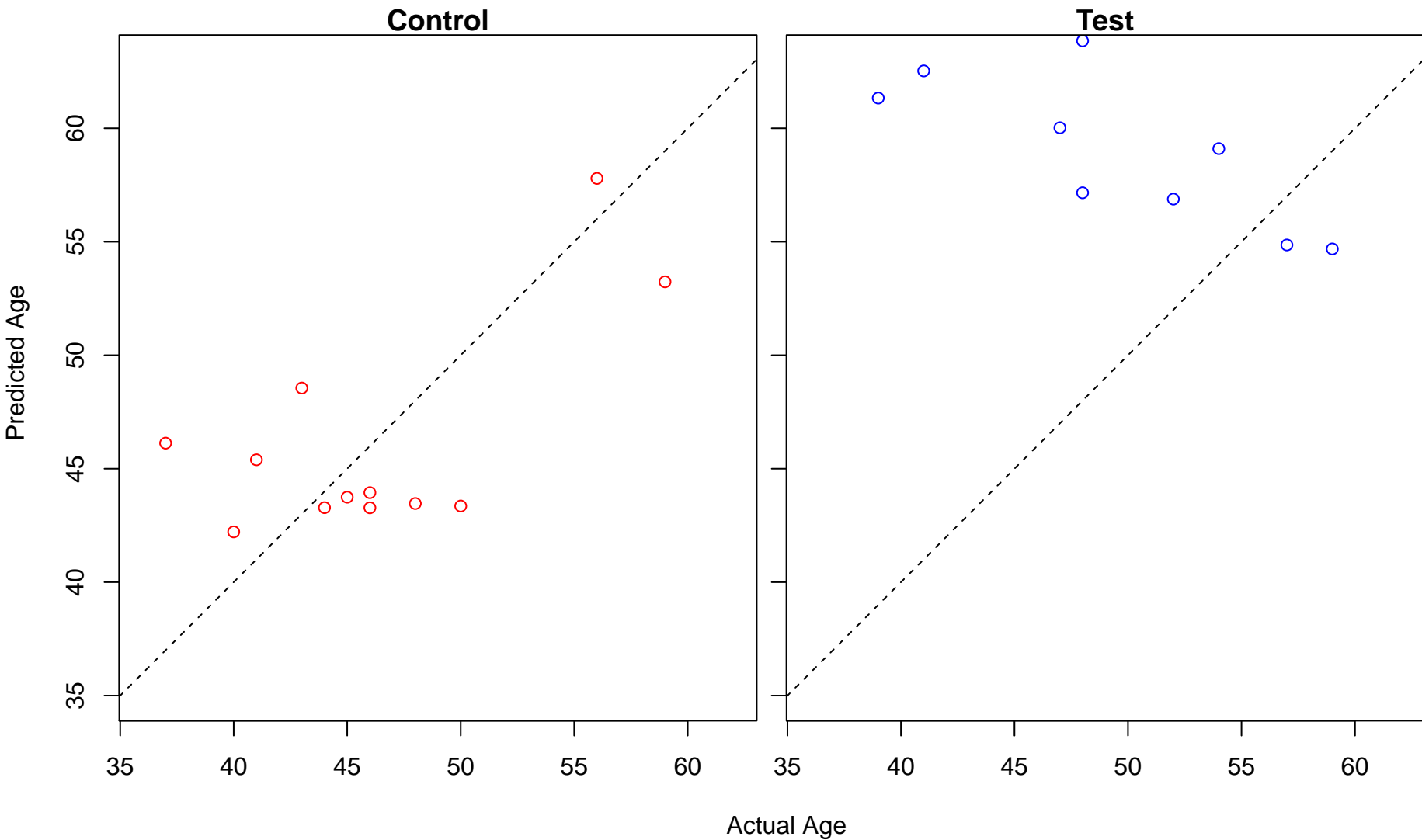
negative regulation of response to DNA damage stimulus (Score: 3.252784)



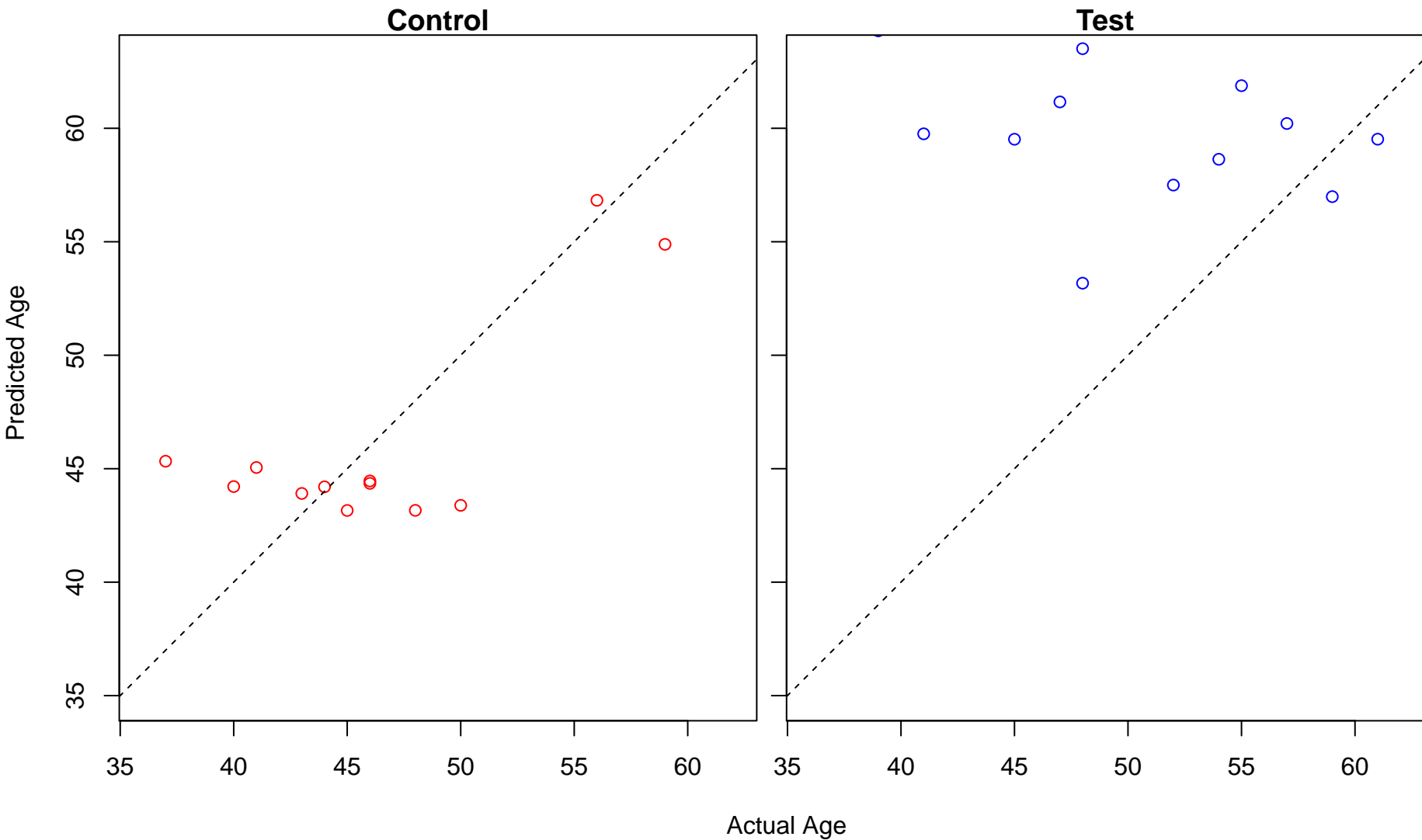
regulation of cell-cell adhesion (Score: 3.250820)



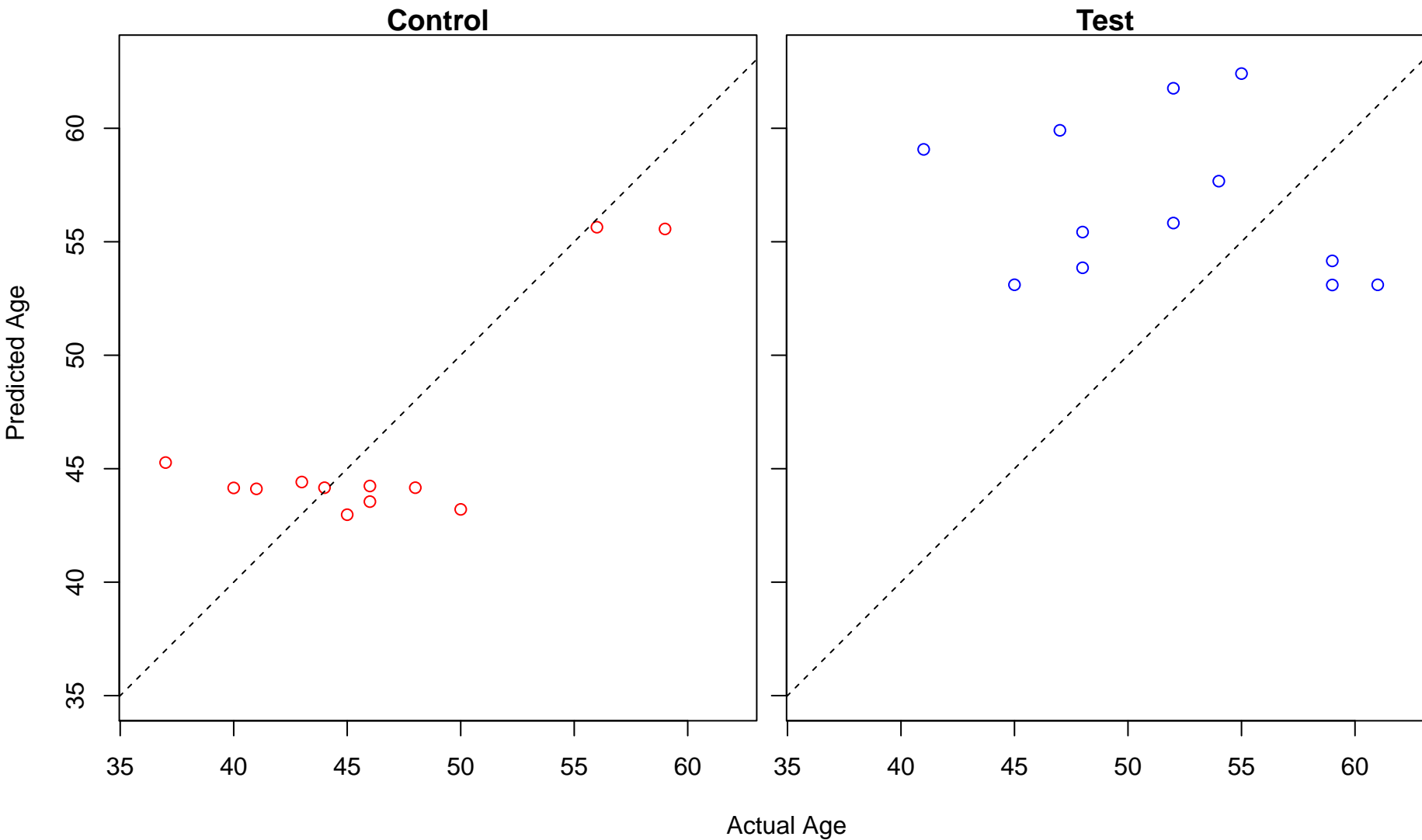
sphingoid metabolic process (Score: 3.250144)



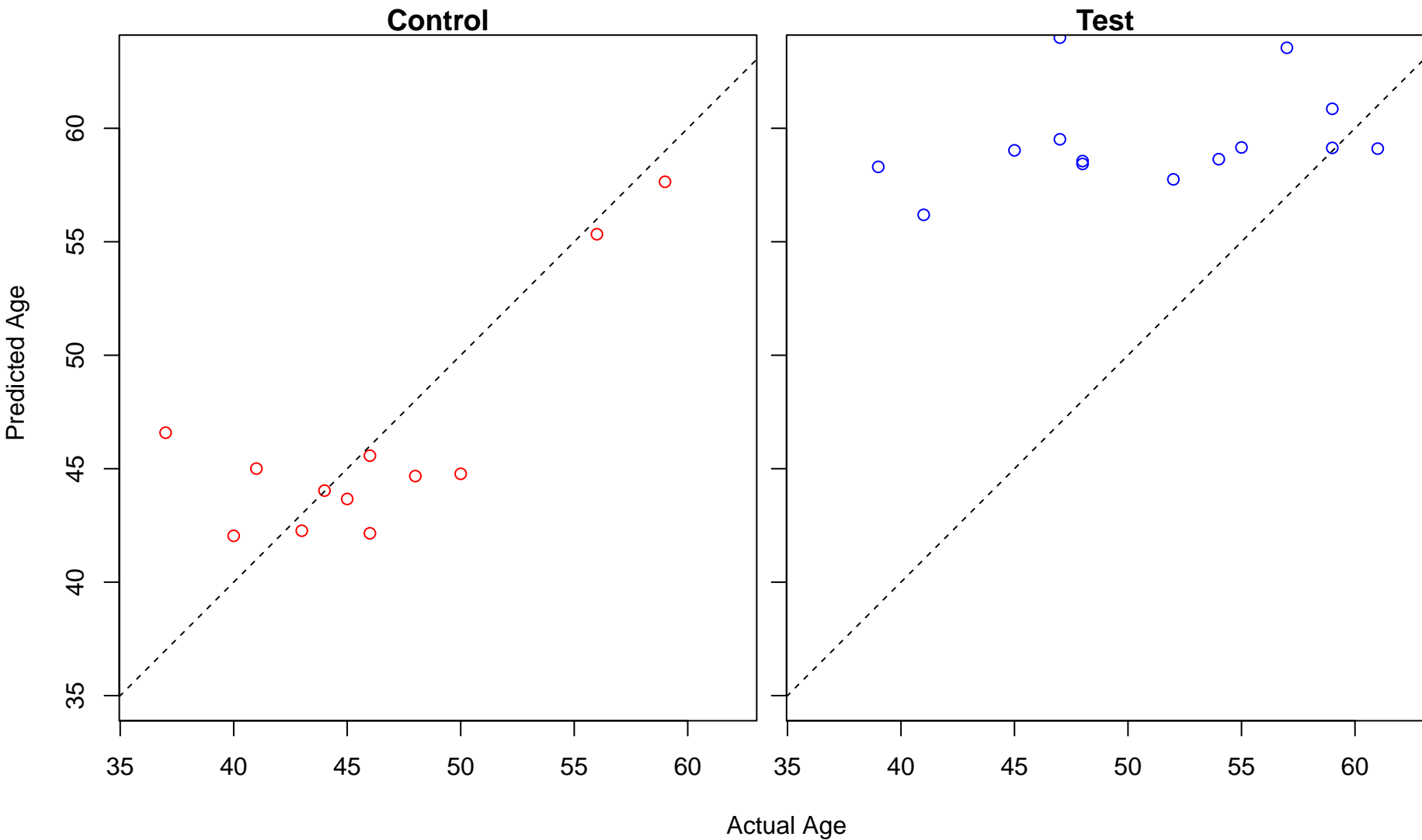
tryptophan metabolic process (Score: 3.249591)



cell adhesion (Score: 3.248932)

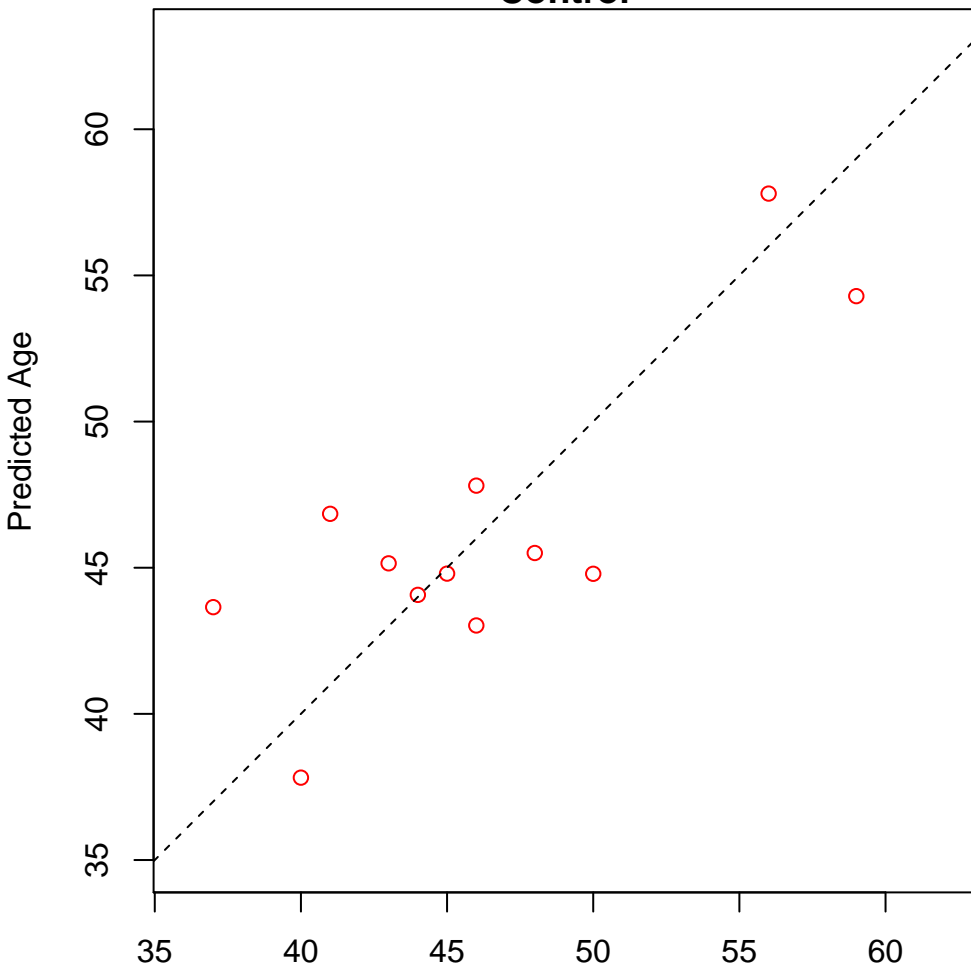


calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules (Score: 3.2488)

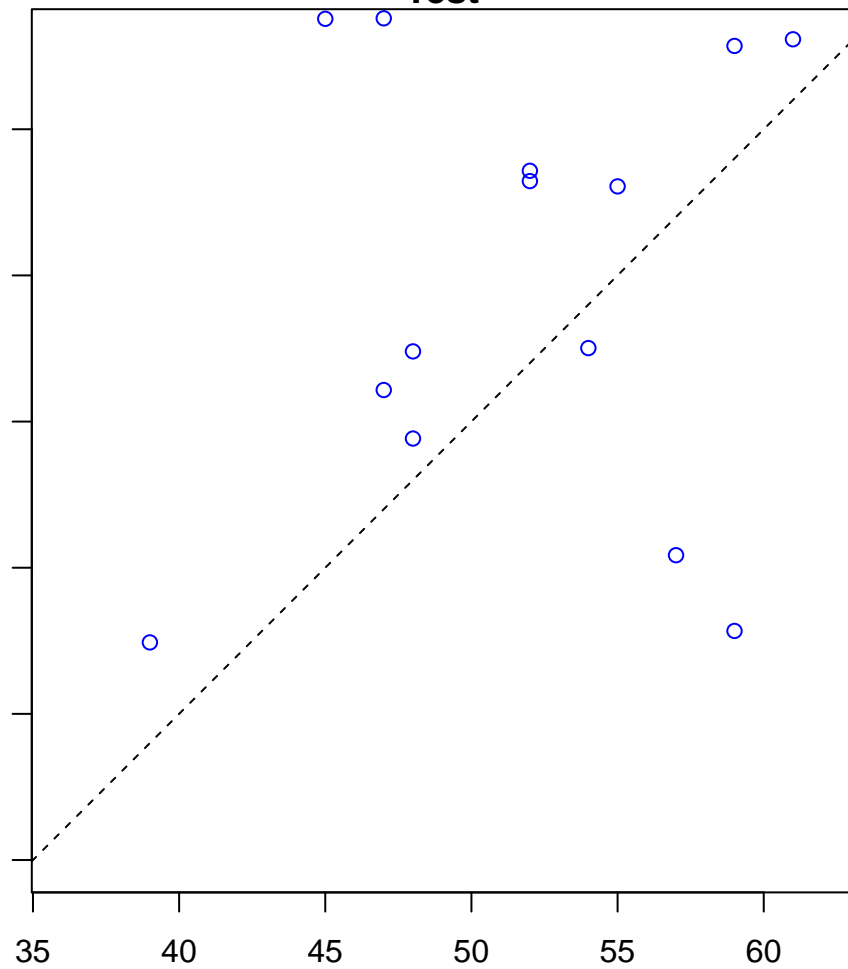


negative regulation of cell-cell adhesion (Score: 3.248376)

Control

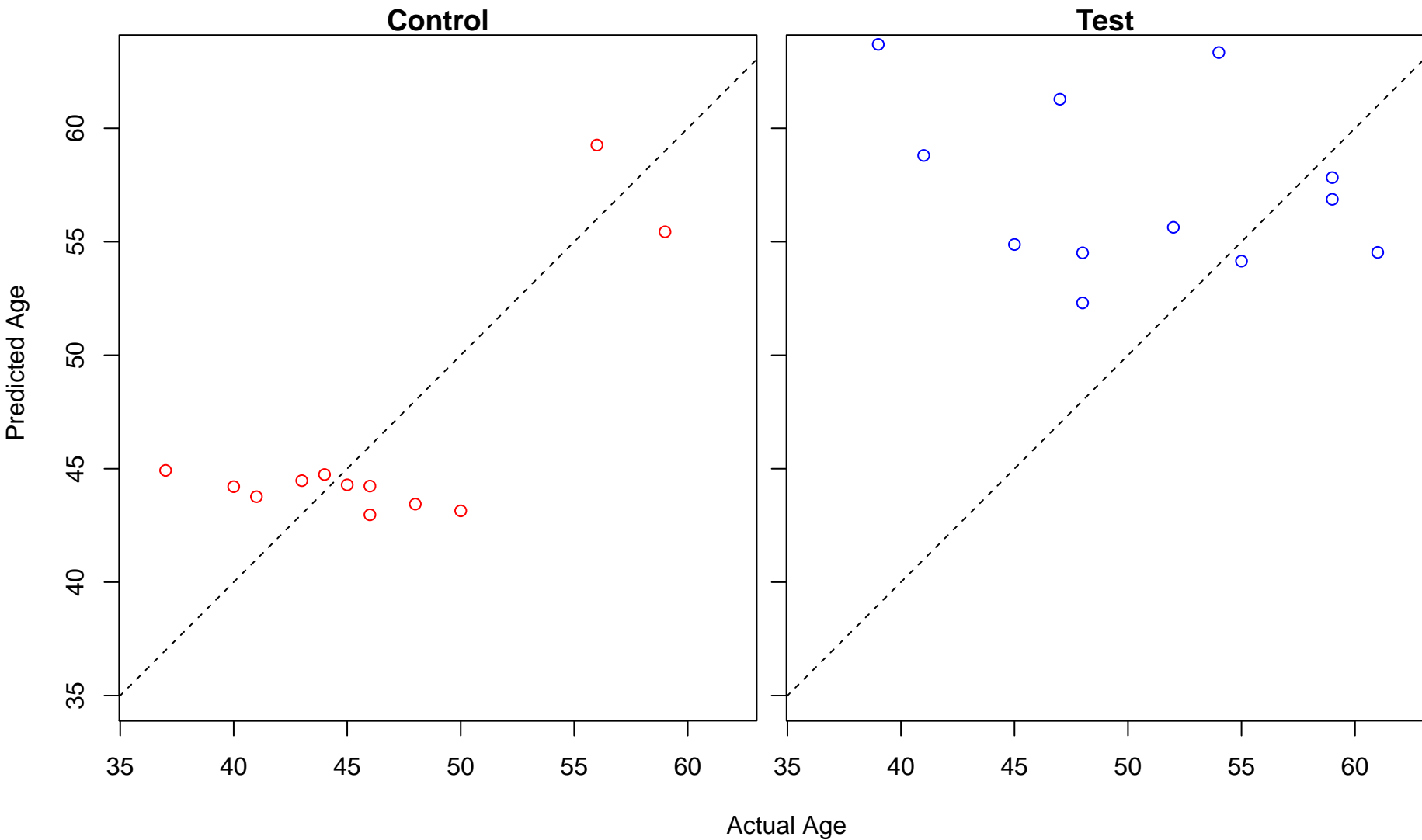


Test

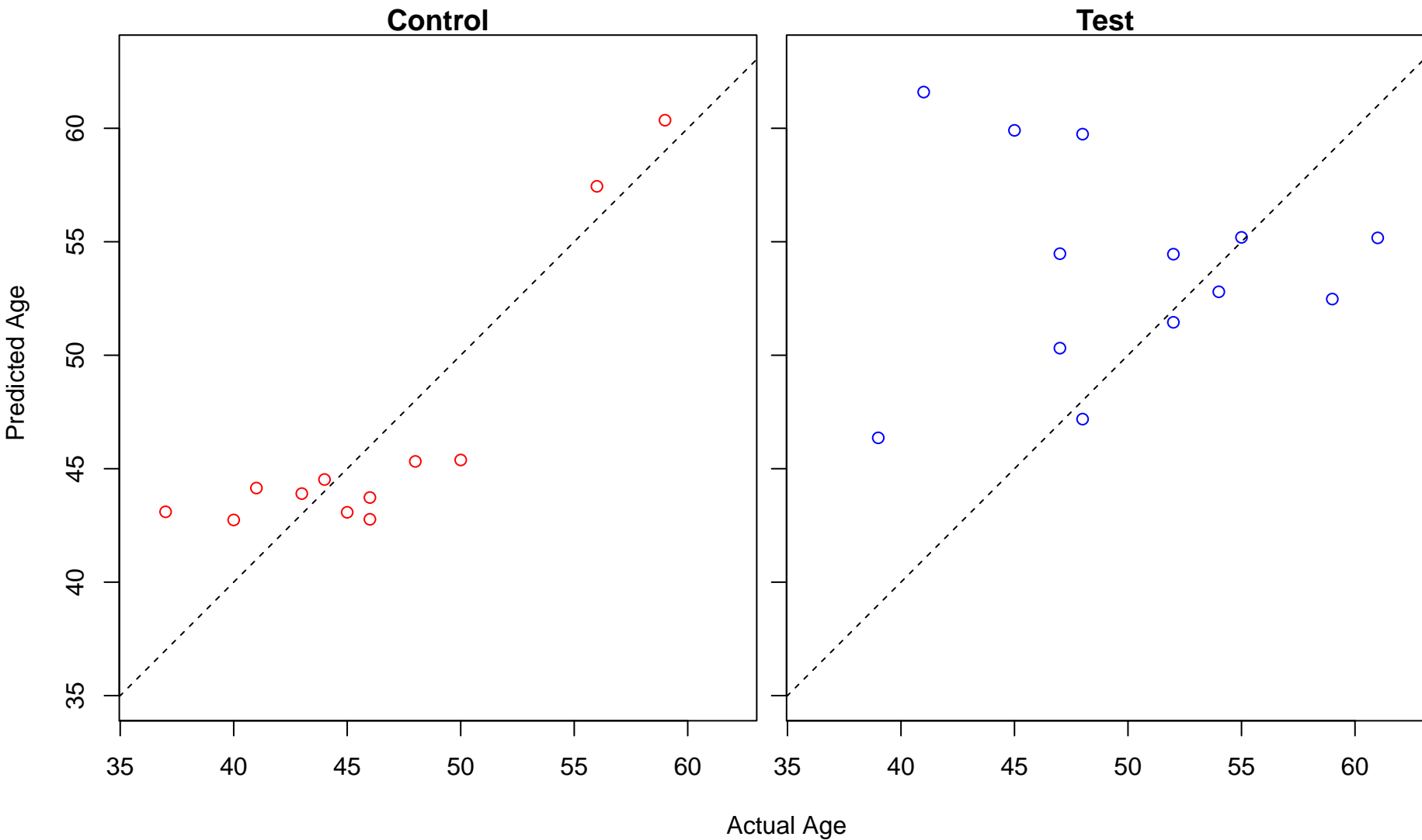


Actual Age

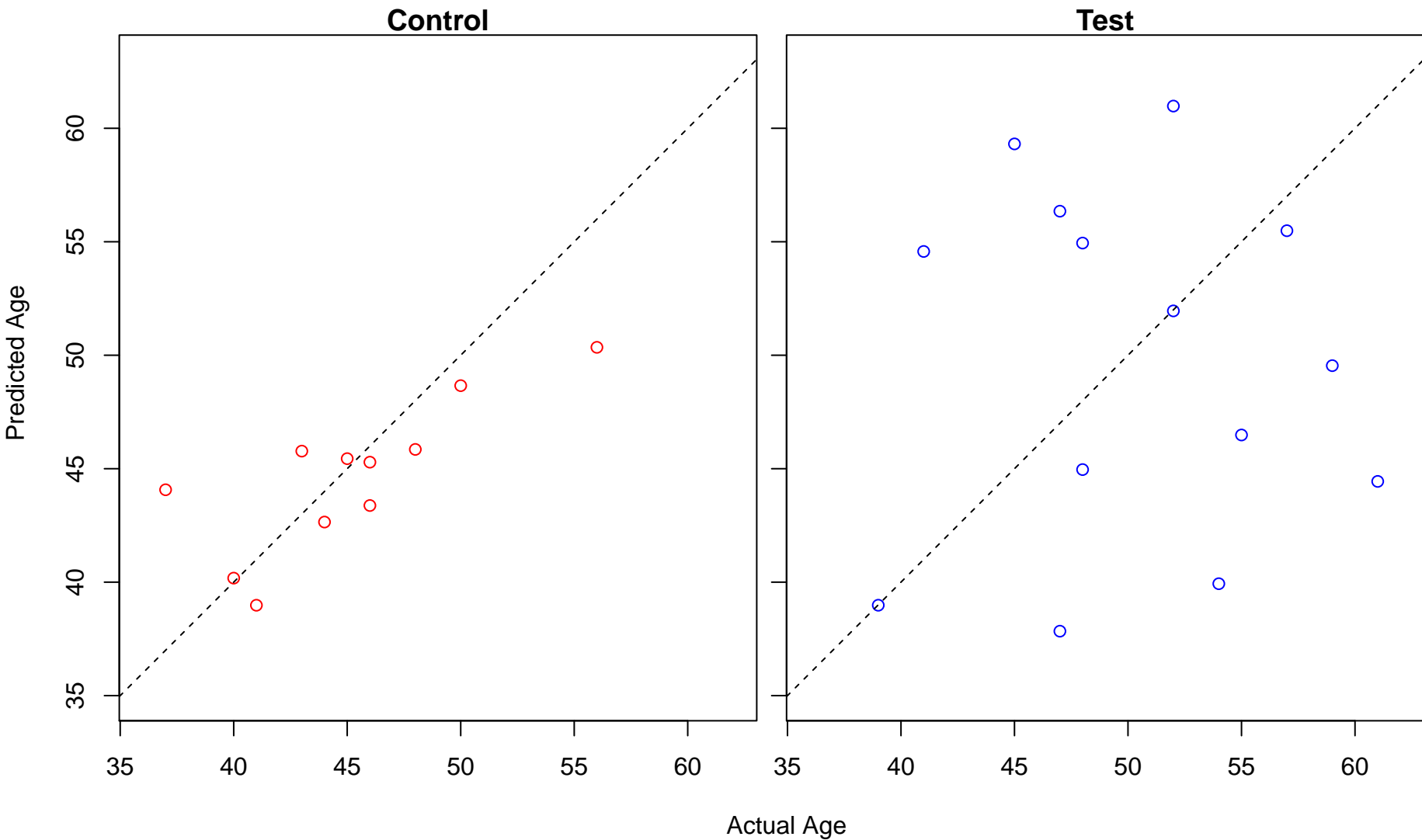
regulation of integrin-mediated signaling pathway (Score: 3.245940)



ketone biosynthetic process (Score: 3.240518)

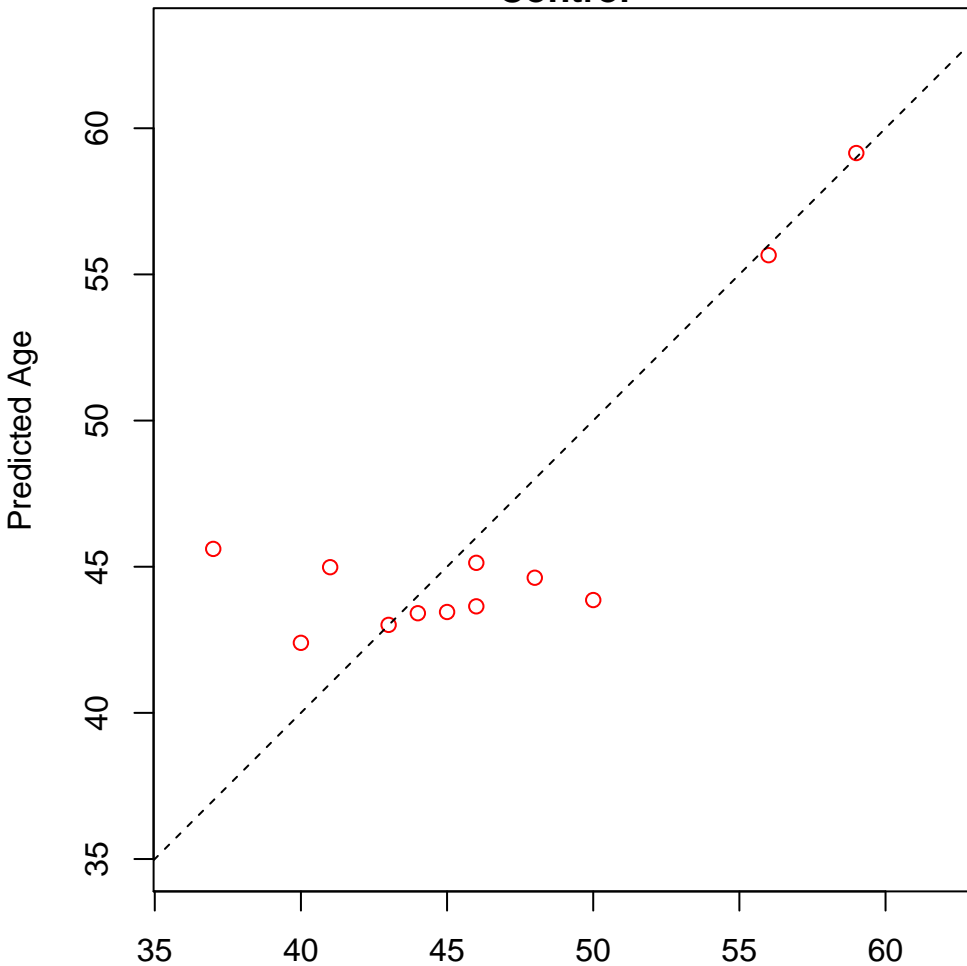


ammonium transport (Score: 3.238923)

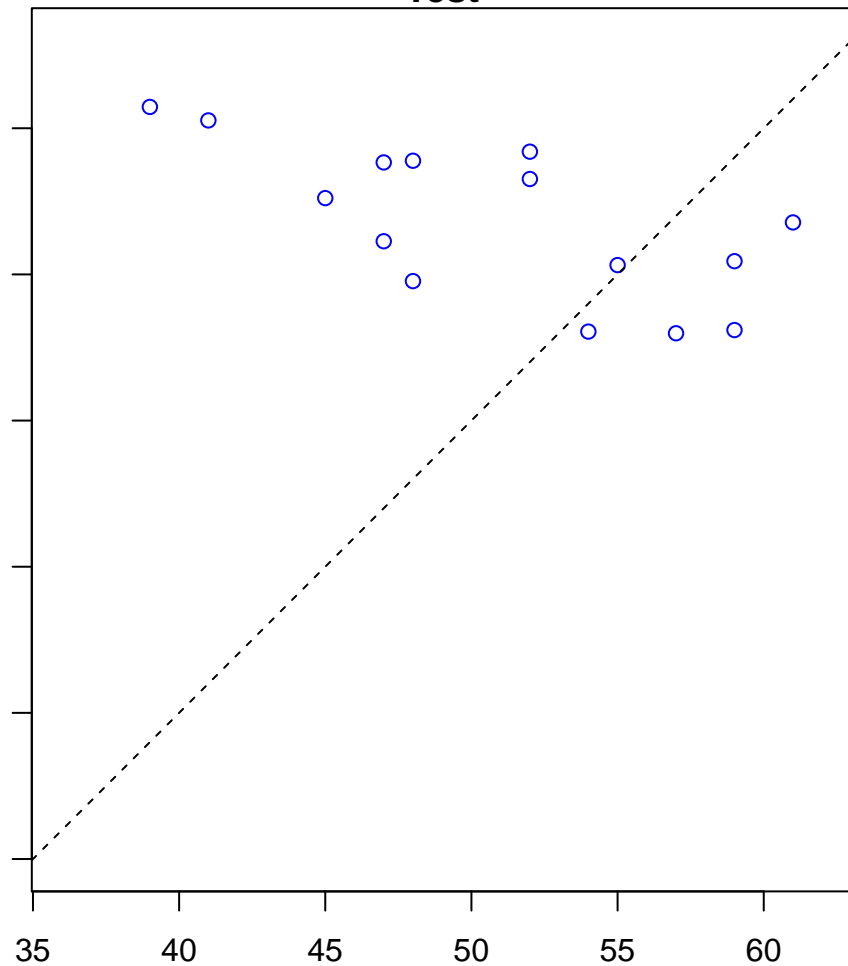


regulation of monocyte chemotaxis (Score: 3.238450)

Control

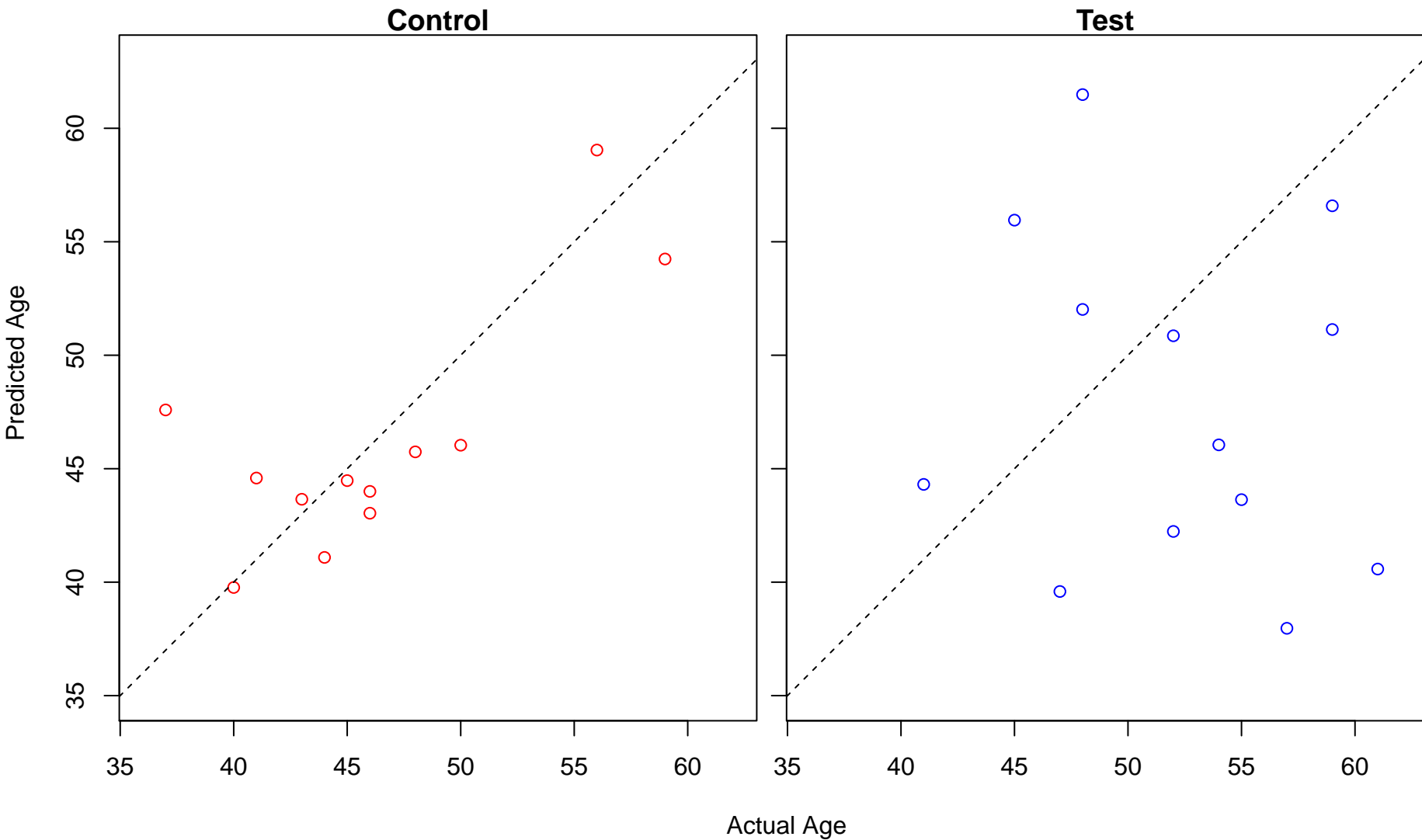


Test

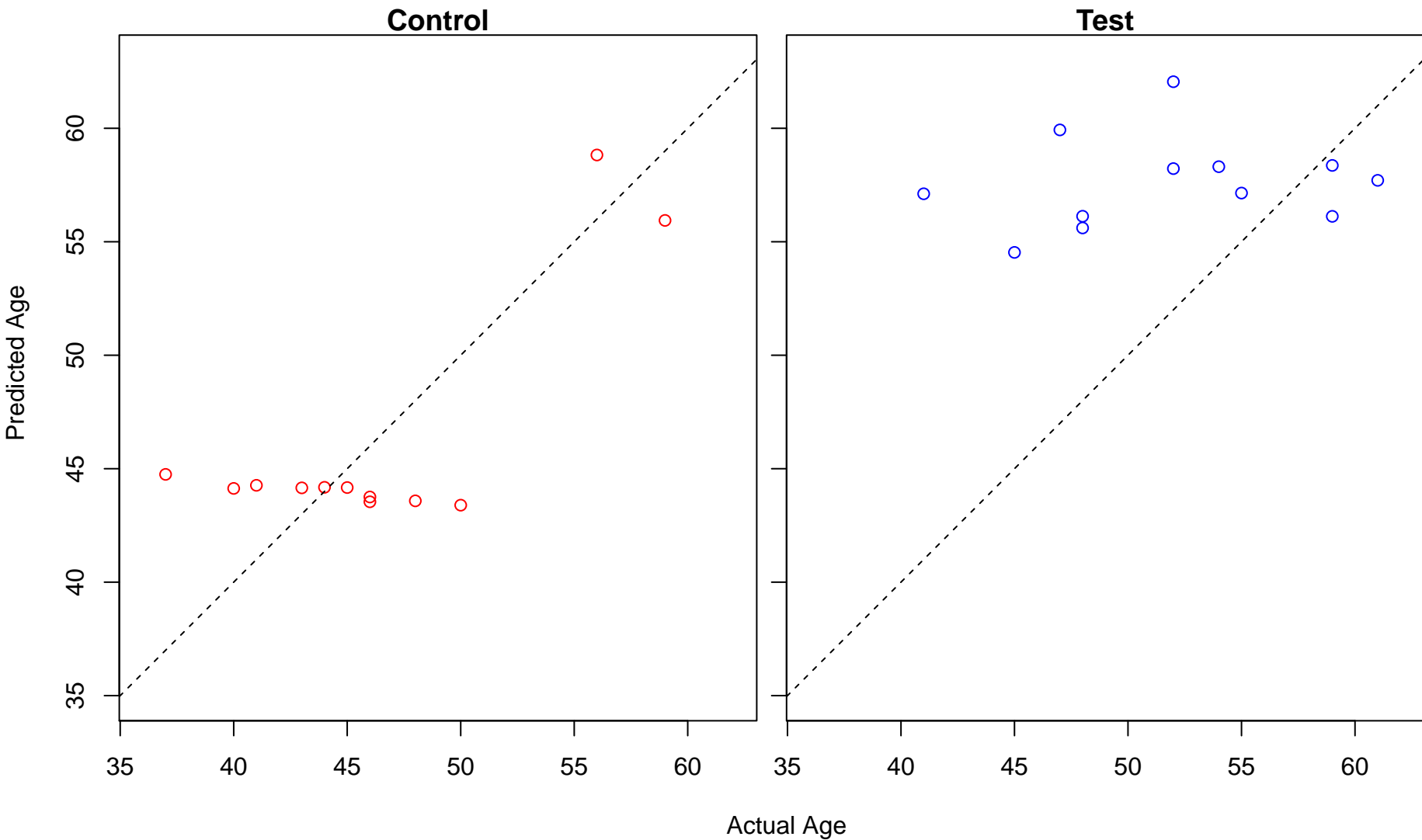


Actual Age

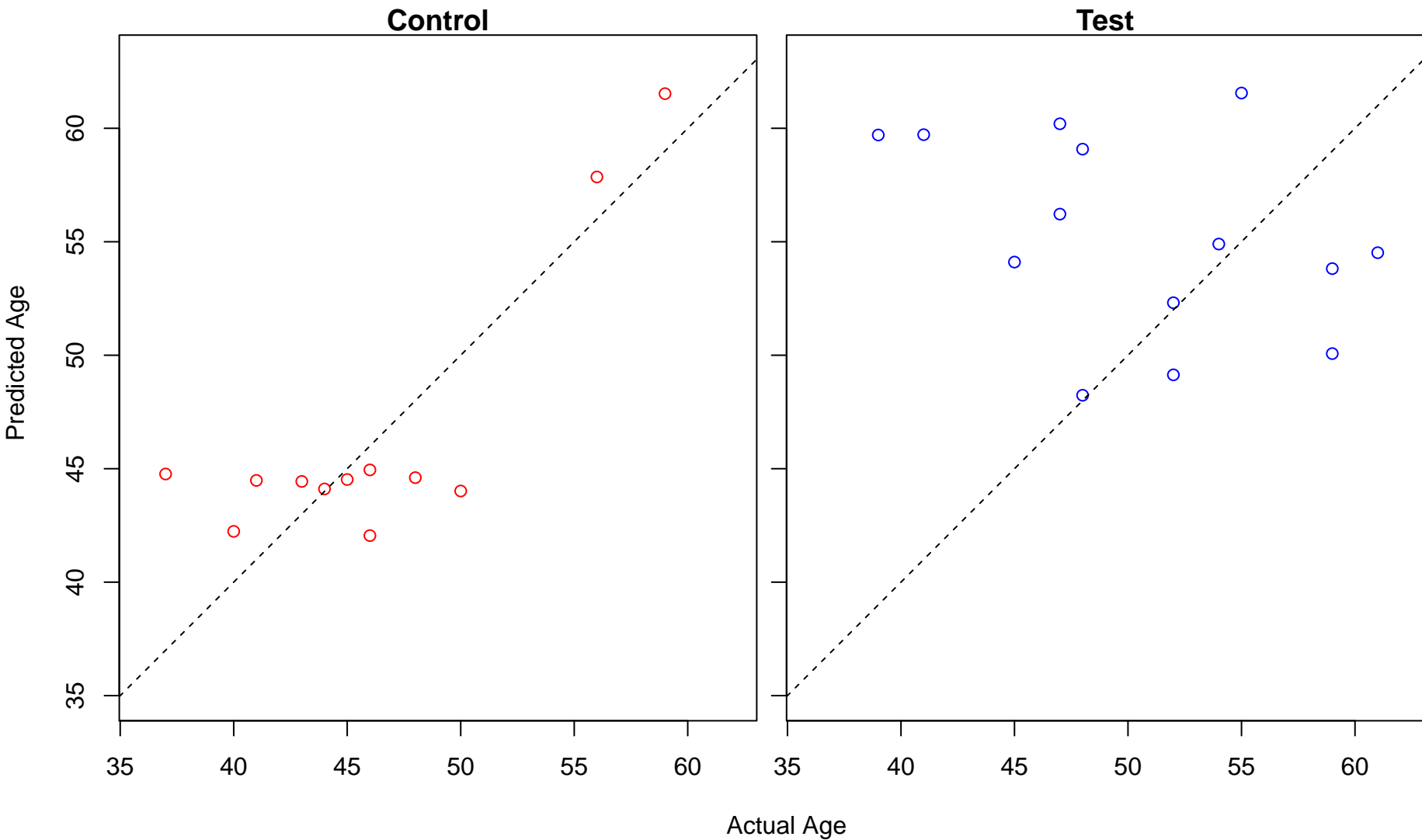
cardiac muscle cell myoblast differentiation (Score: 3.238062)



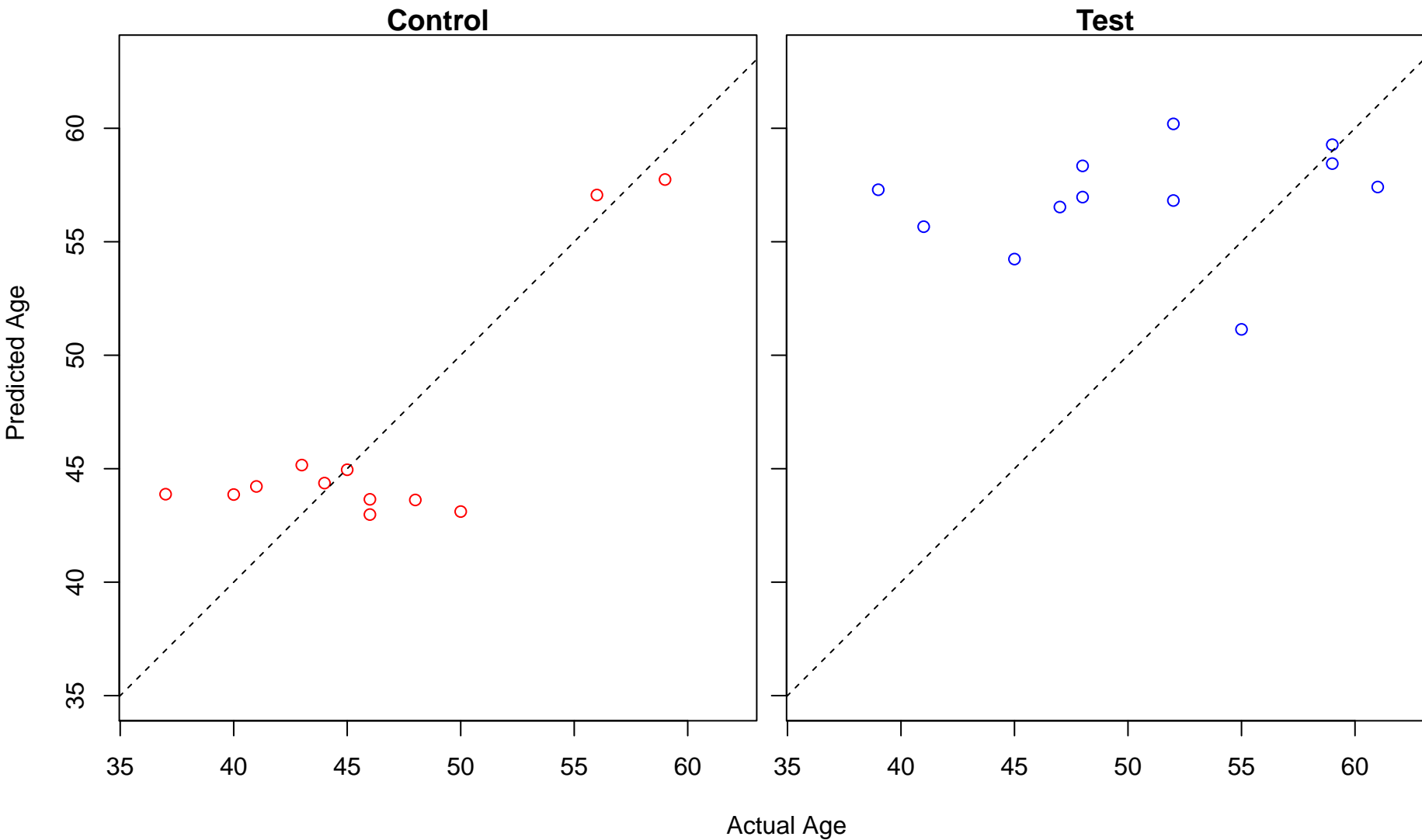
positive regulation of establishment of protein localization to mitochondrion (Score: 3.237313)



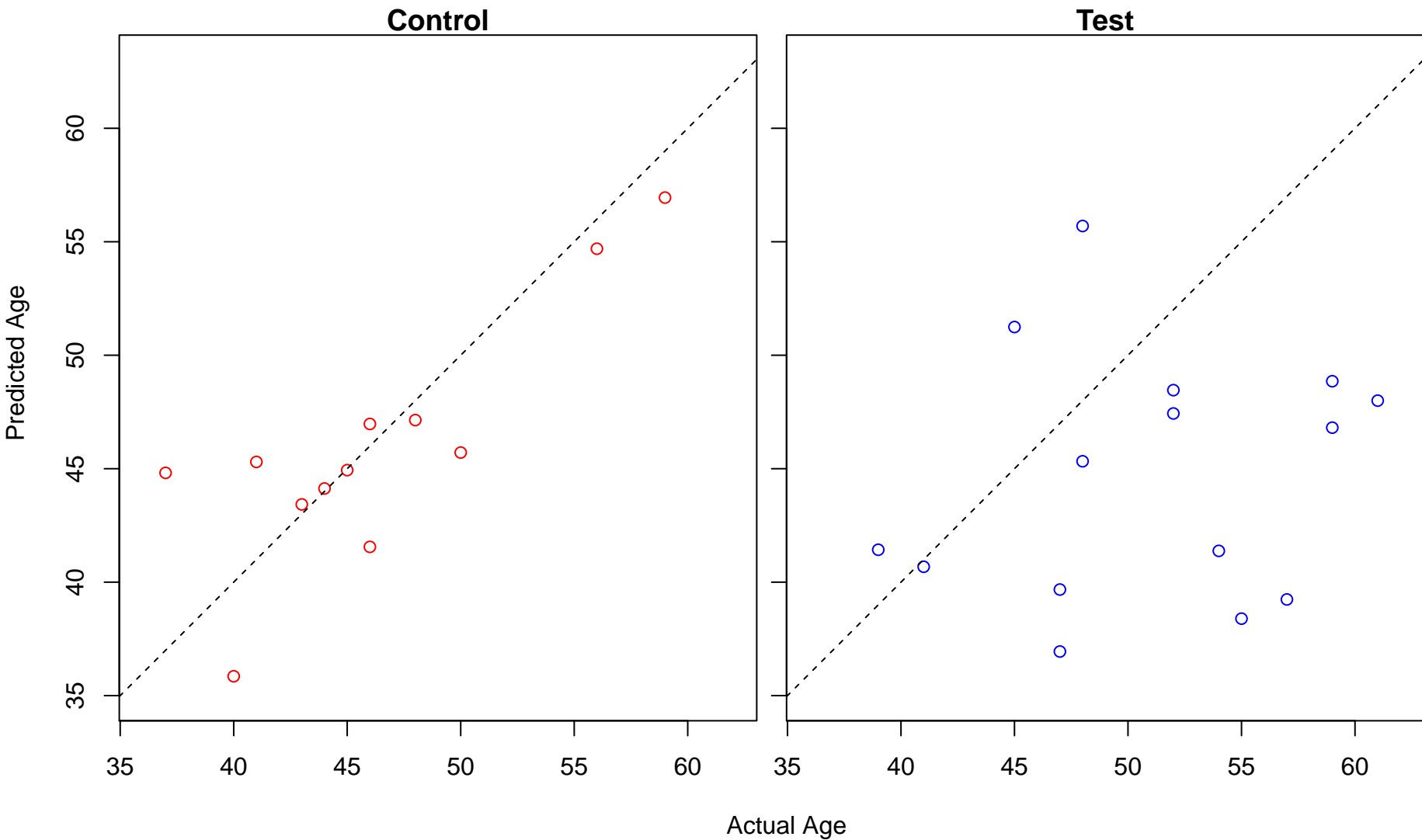
activation of MAPKK activity (Score: 3.237022)



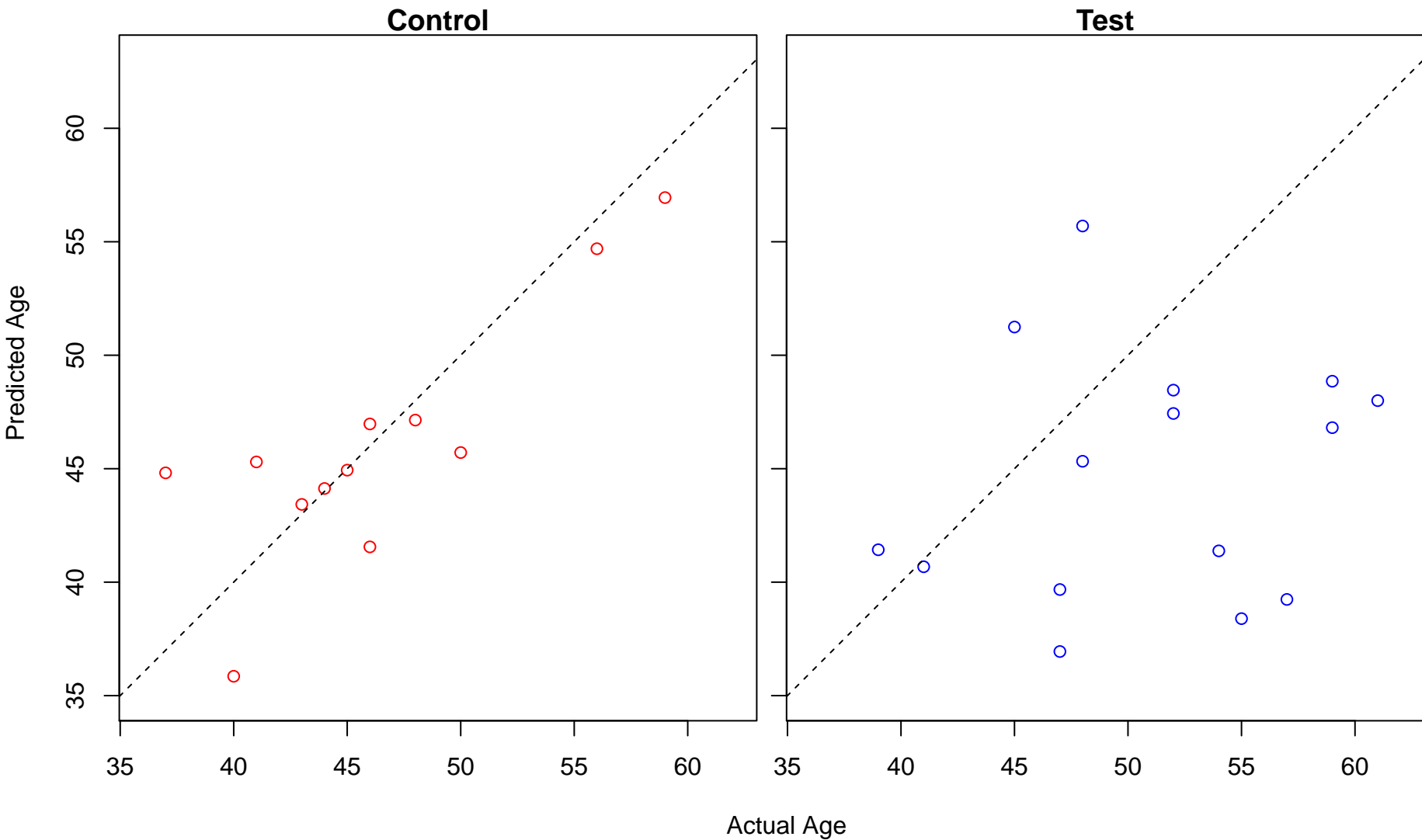
aldehyde catabolic process (Score: 3.235400)



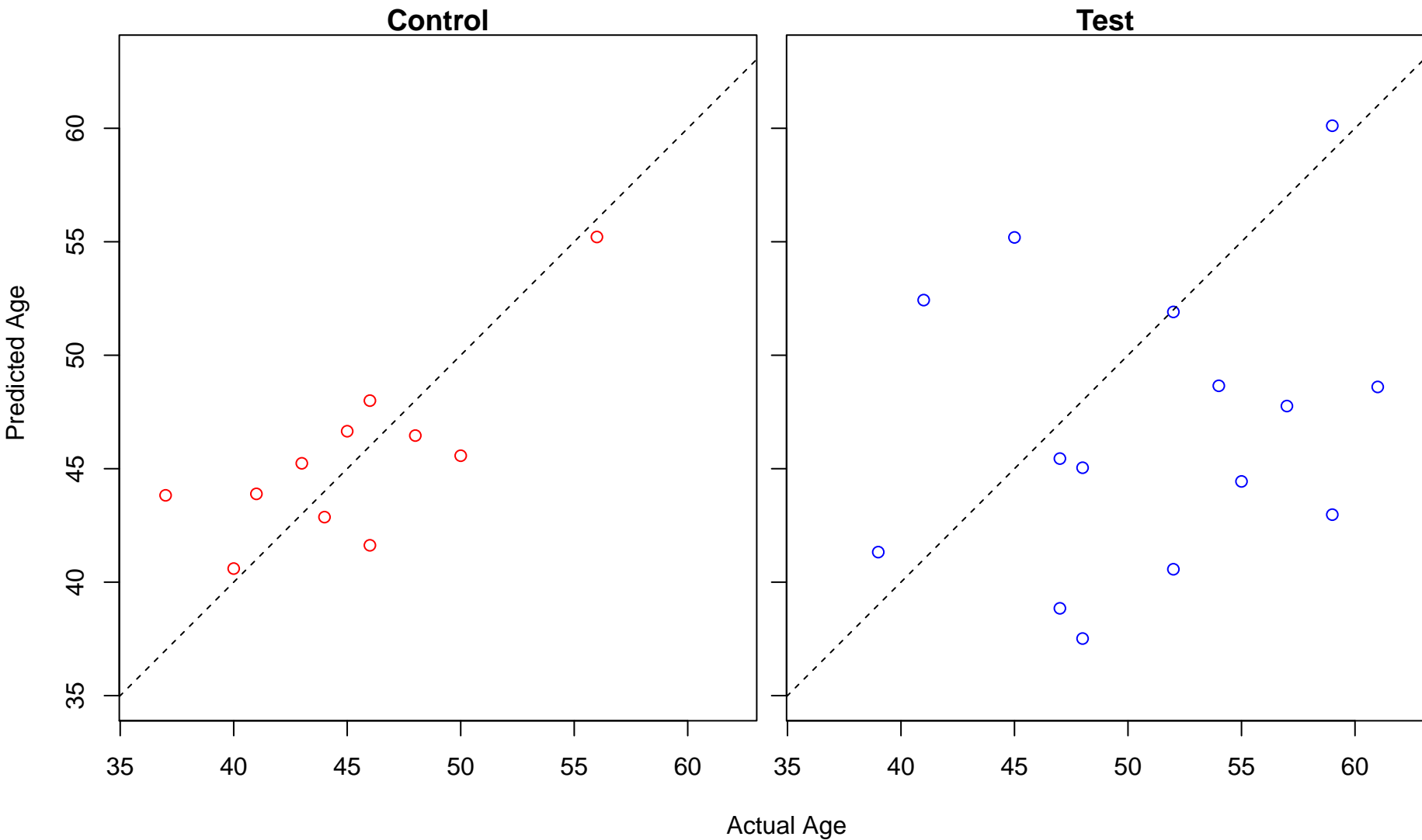
lysosome organization (Score: 3.234632)



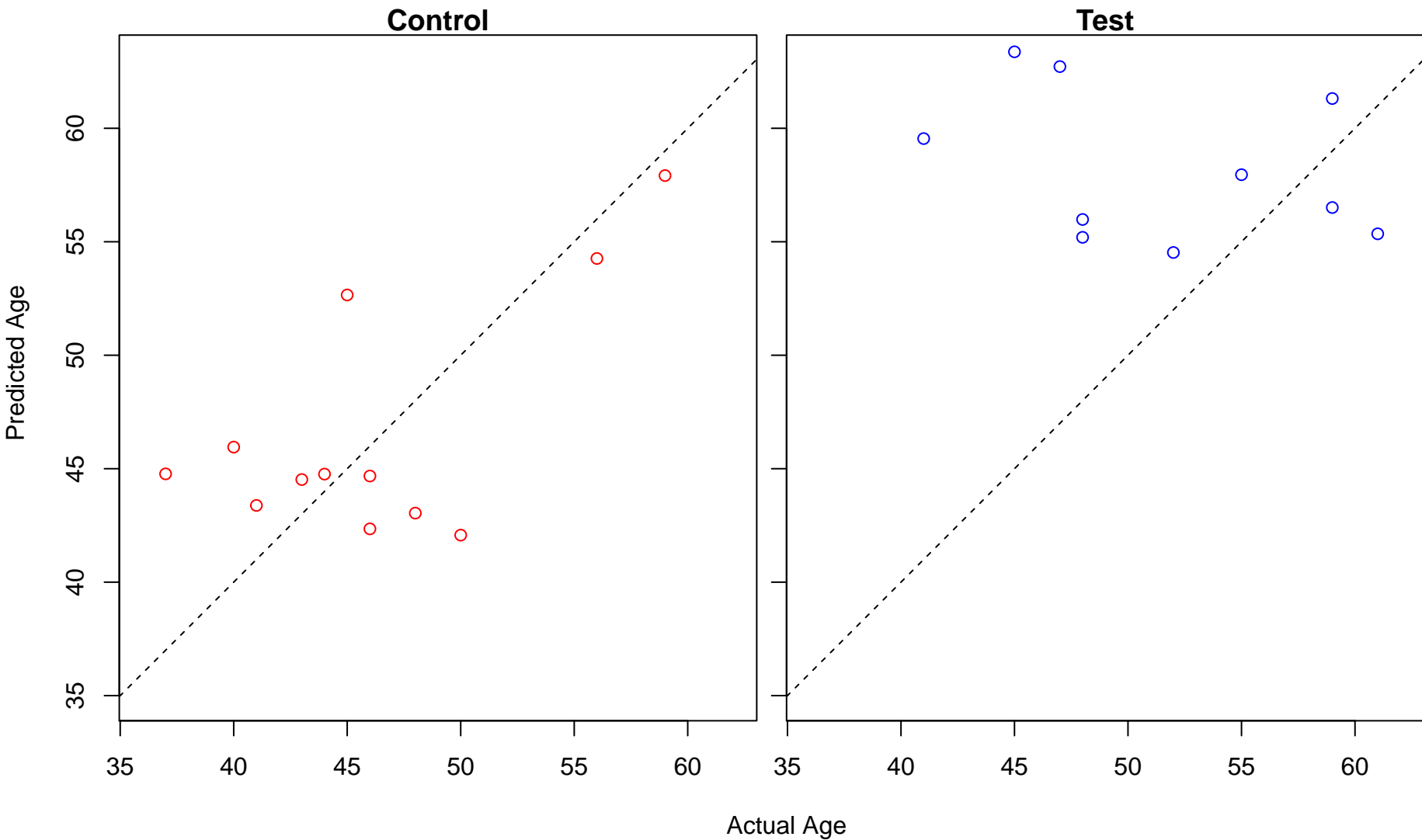
lytic vacuole organization (Score: 3.234632)



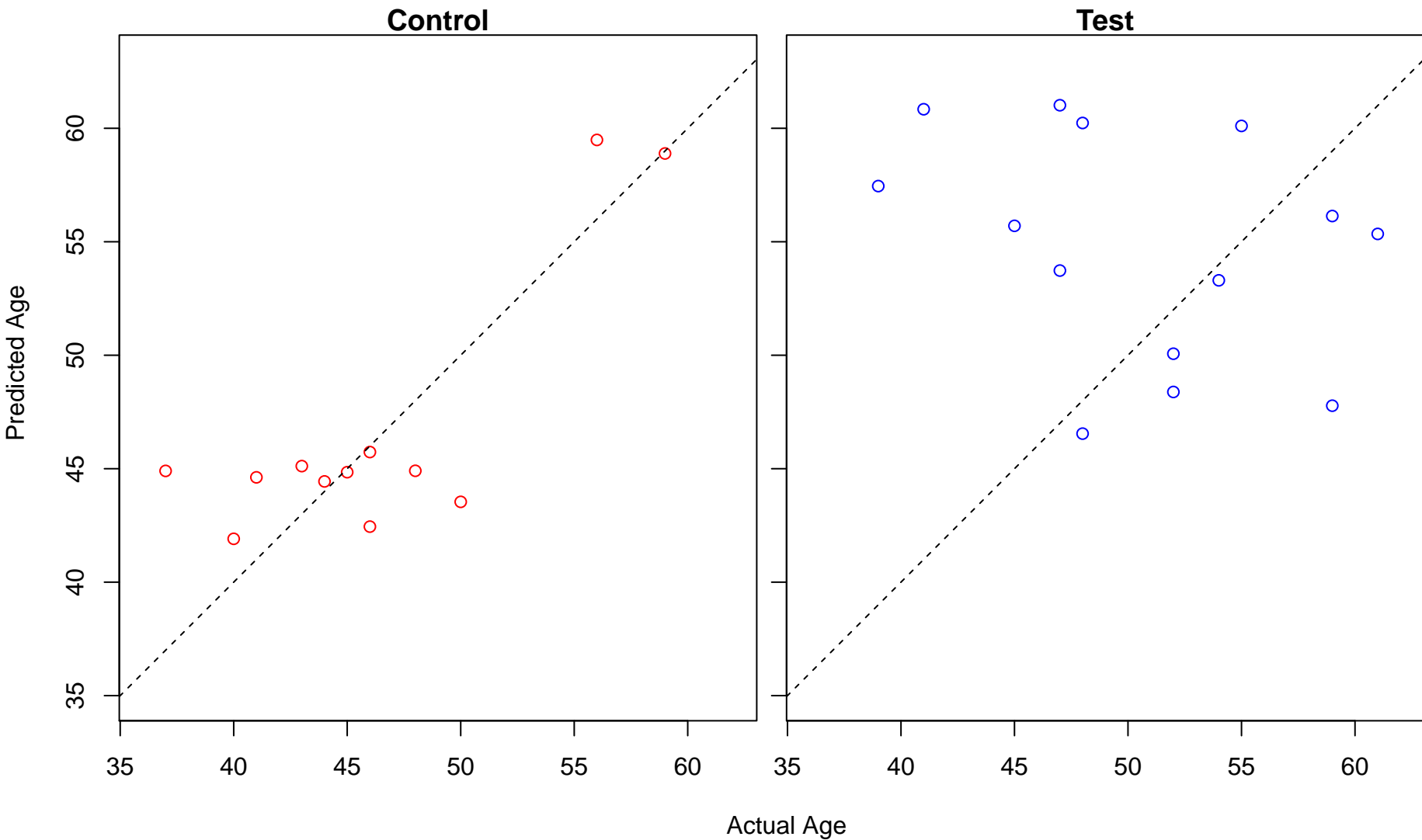
regulation of cell size (Score: 3.234473)



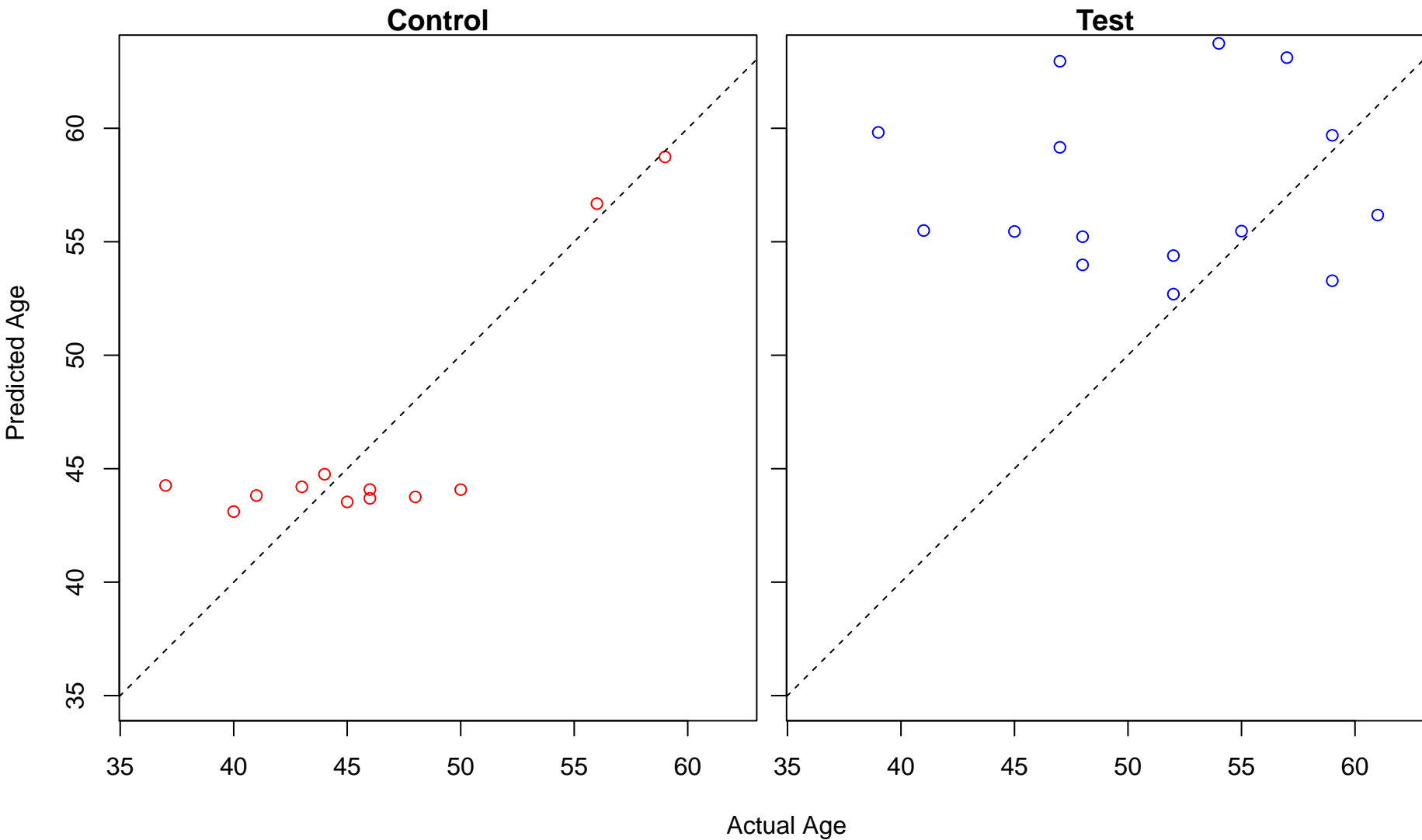
decidualization (Score: 3.234419)



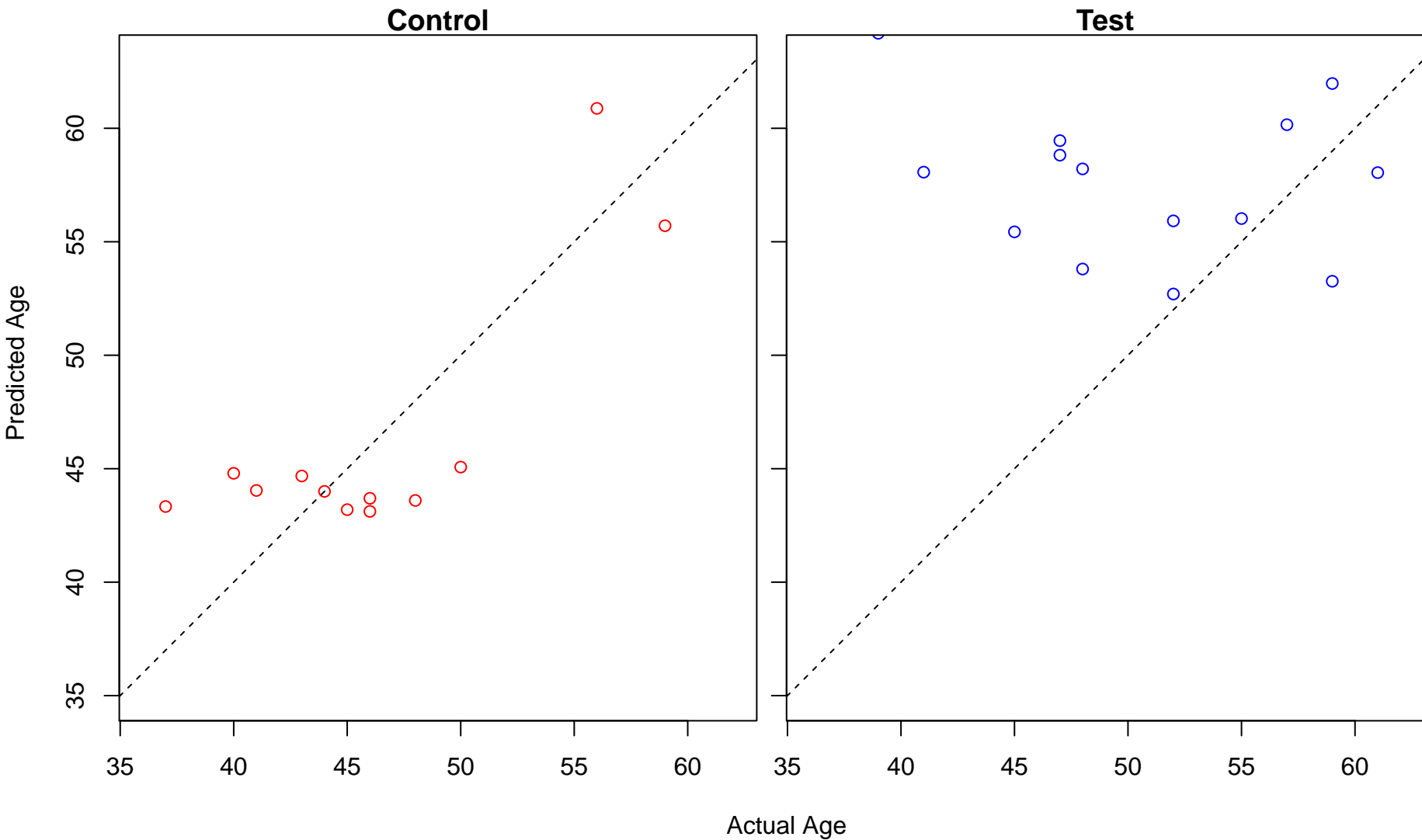
MAPK cascade (Score: 3.233460)



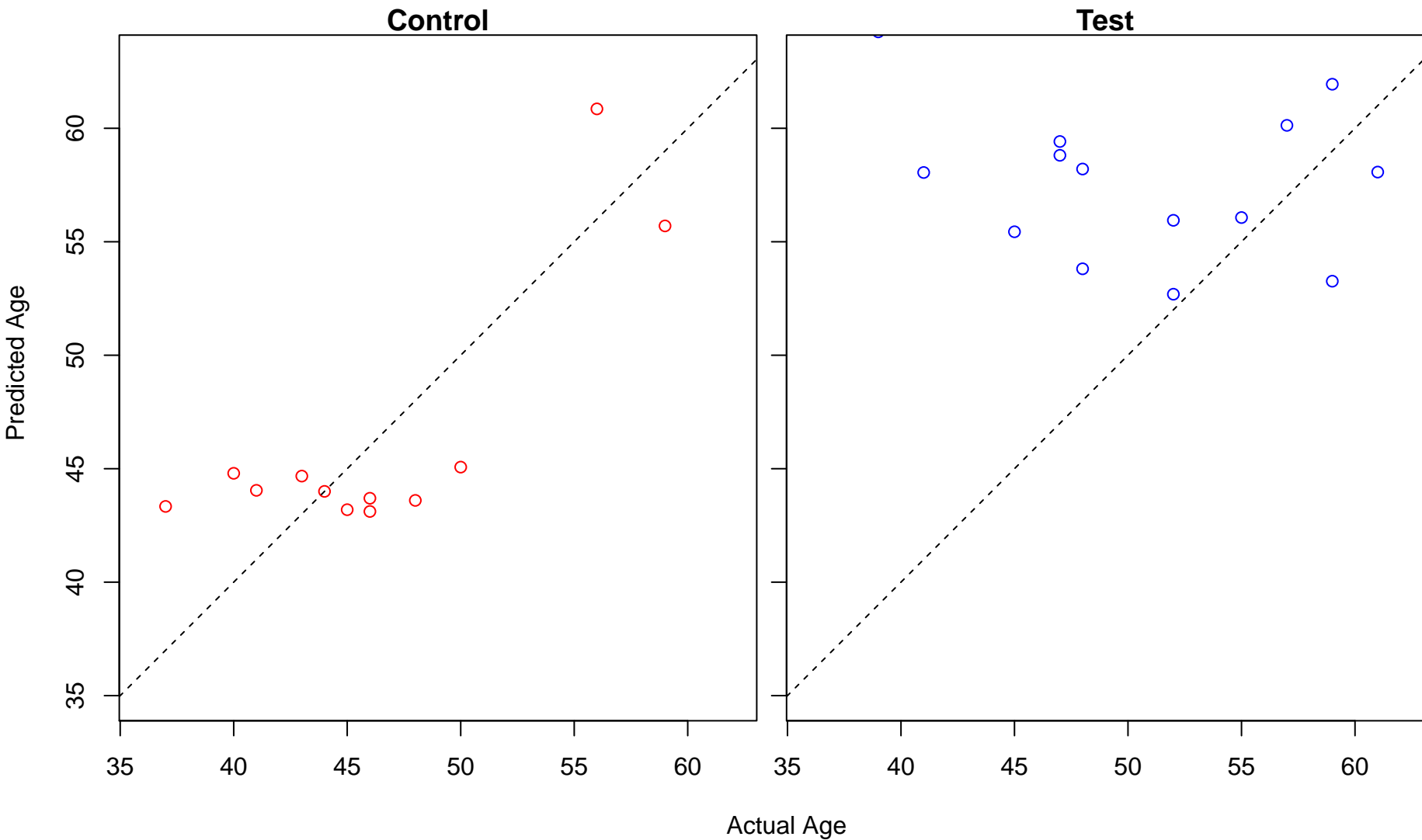
amyloid fibril formation (Score: 3.233334)



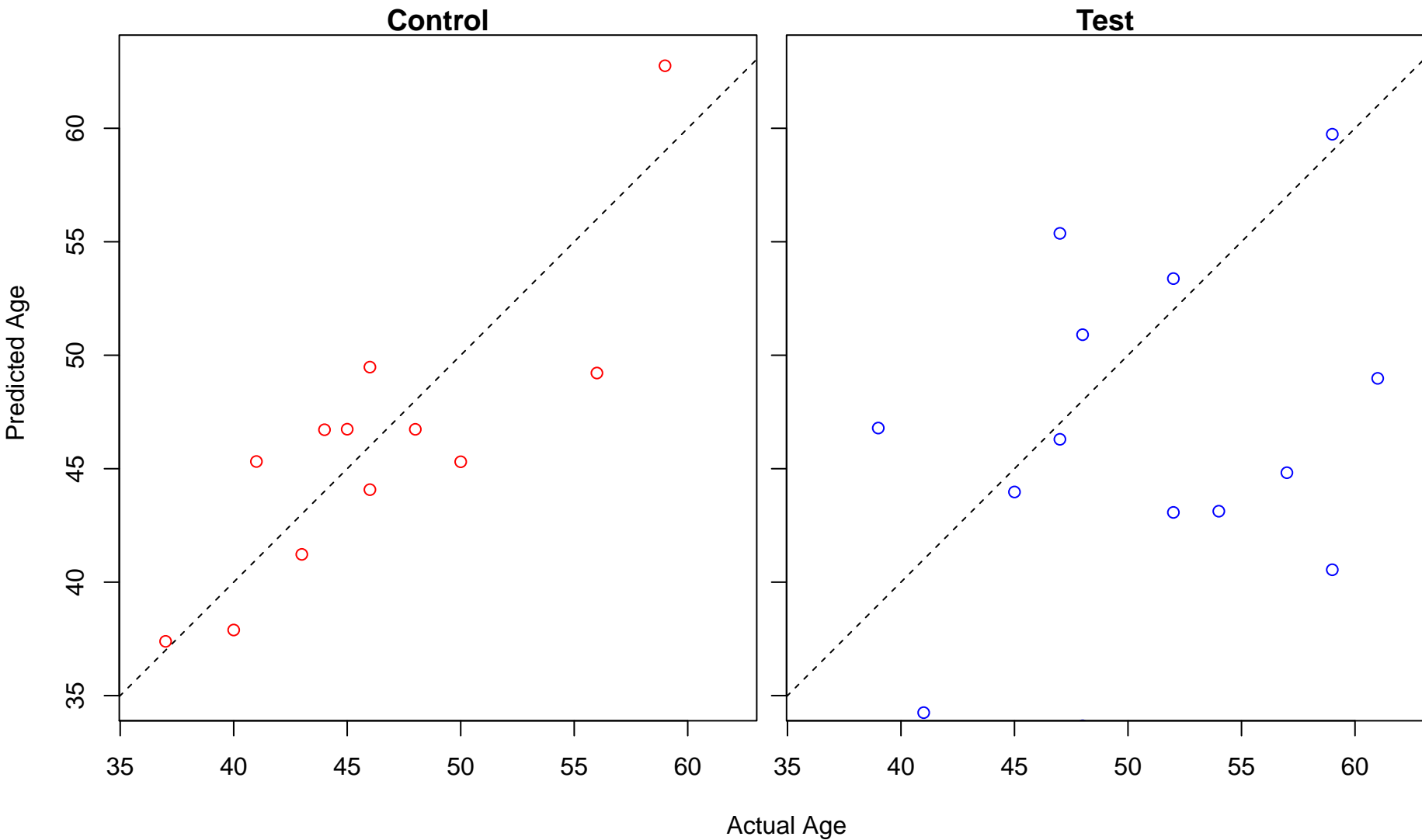
L-alanine transport (Score: 3.233093)



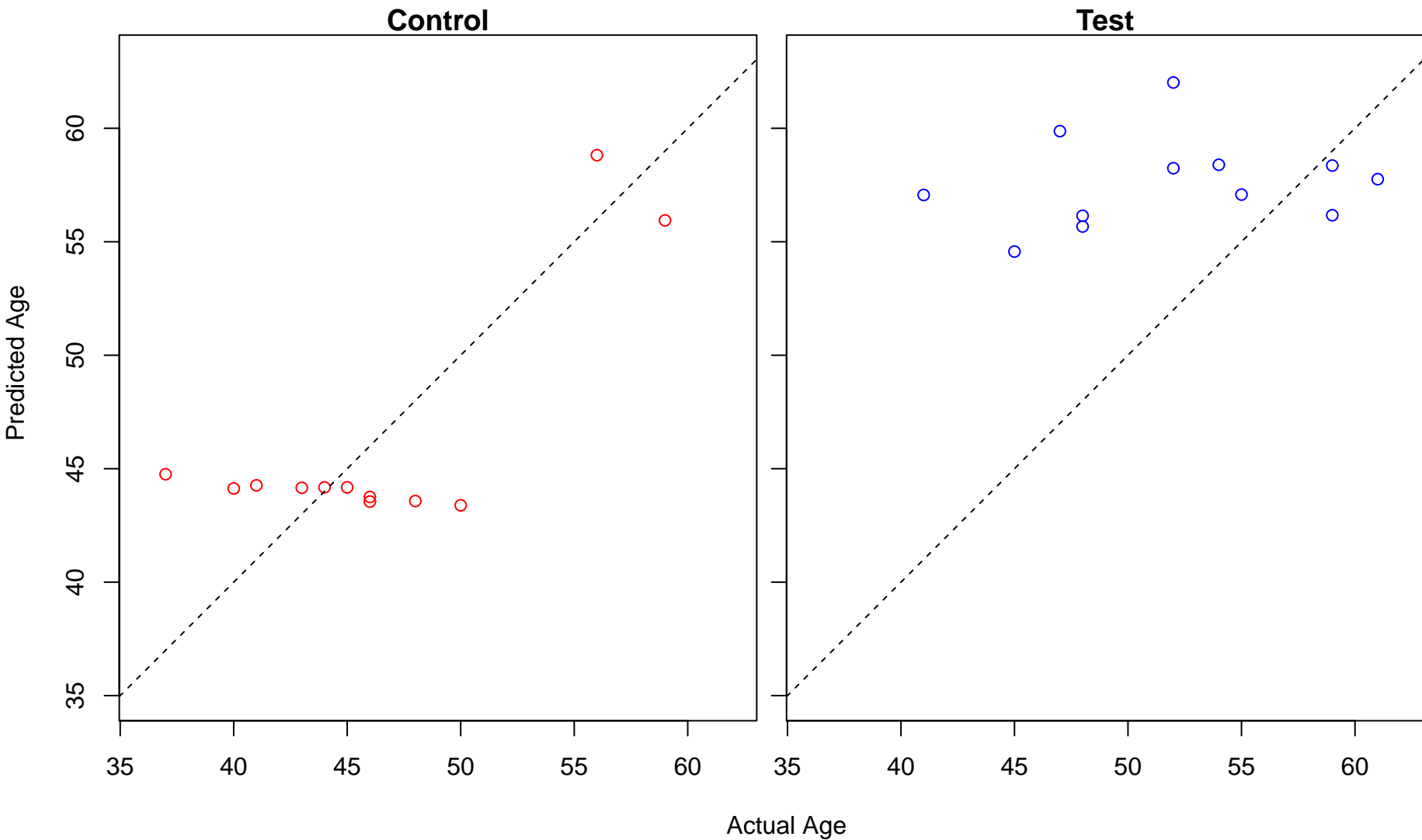
proline transport (Score: 3.233050)



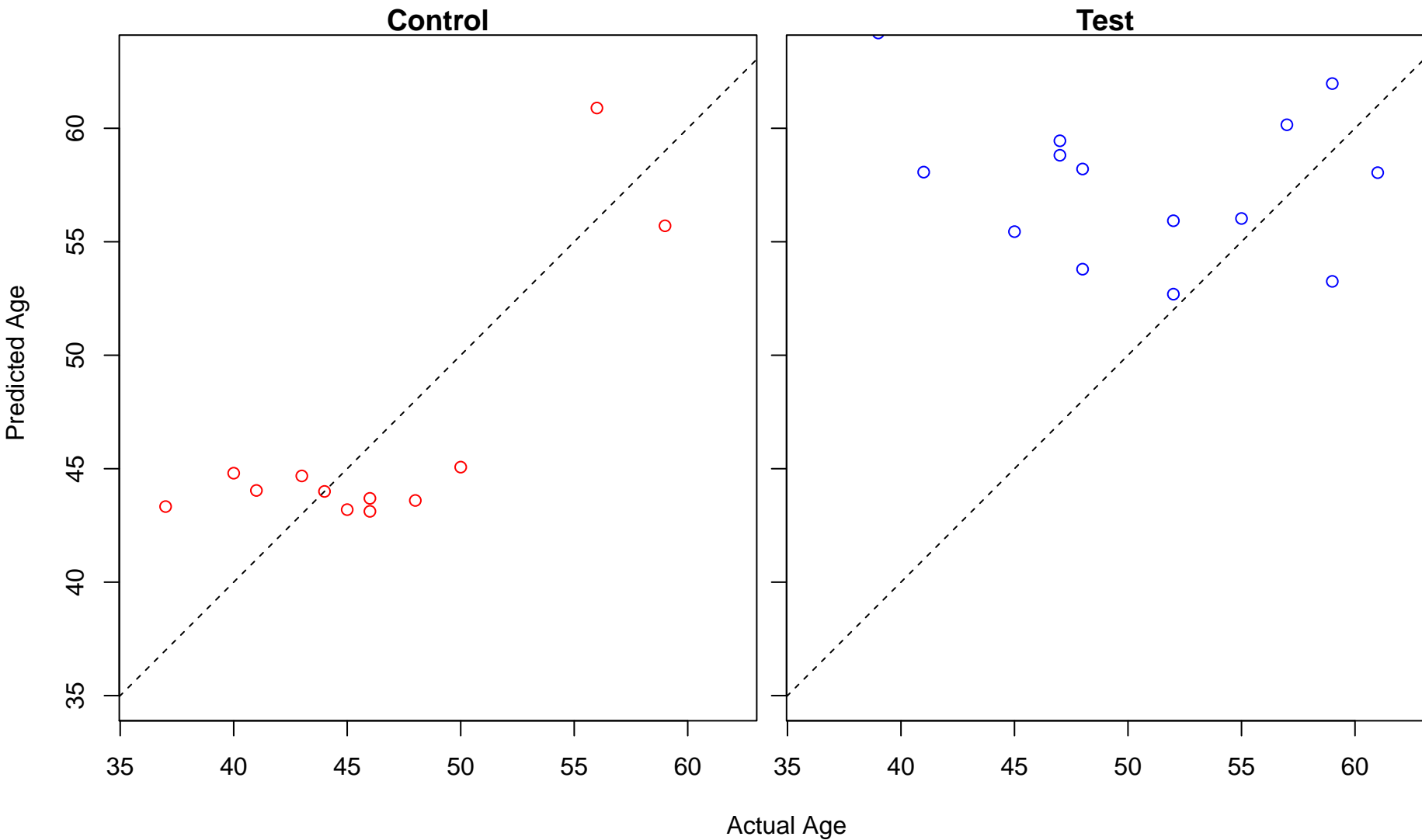
regulation of coagulation (Score: 3.232013)



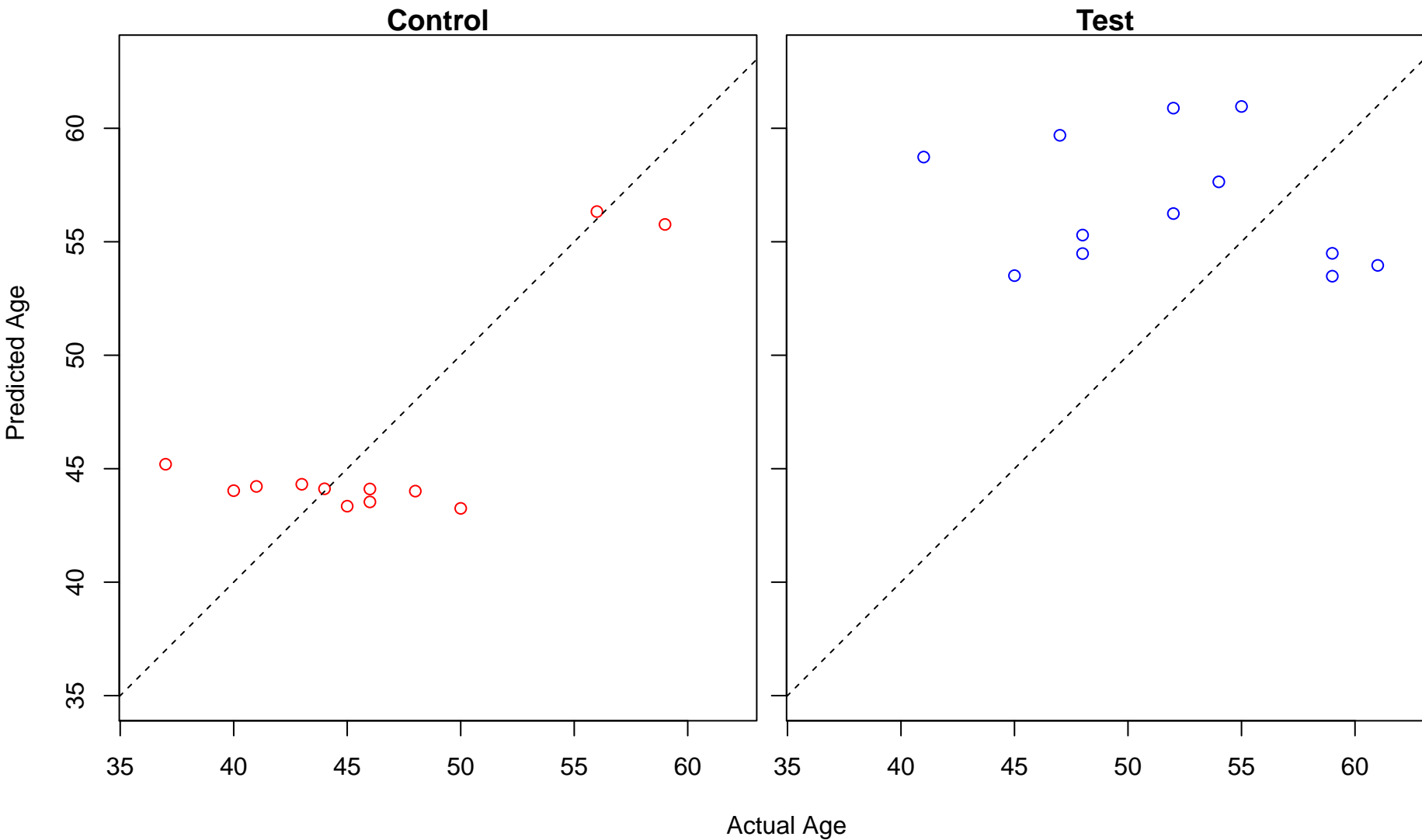
regulation of establishment of protein localization to mitochondrion (Score: 3.231408)



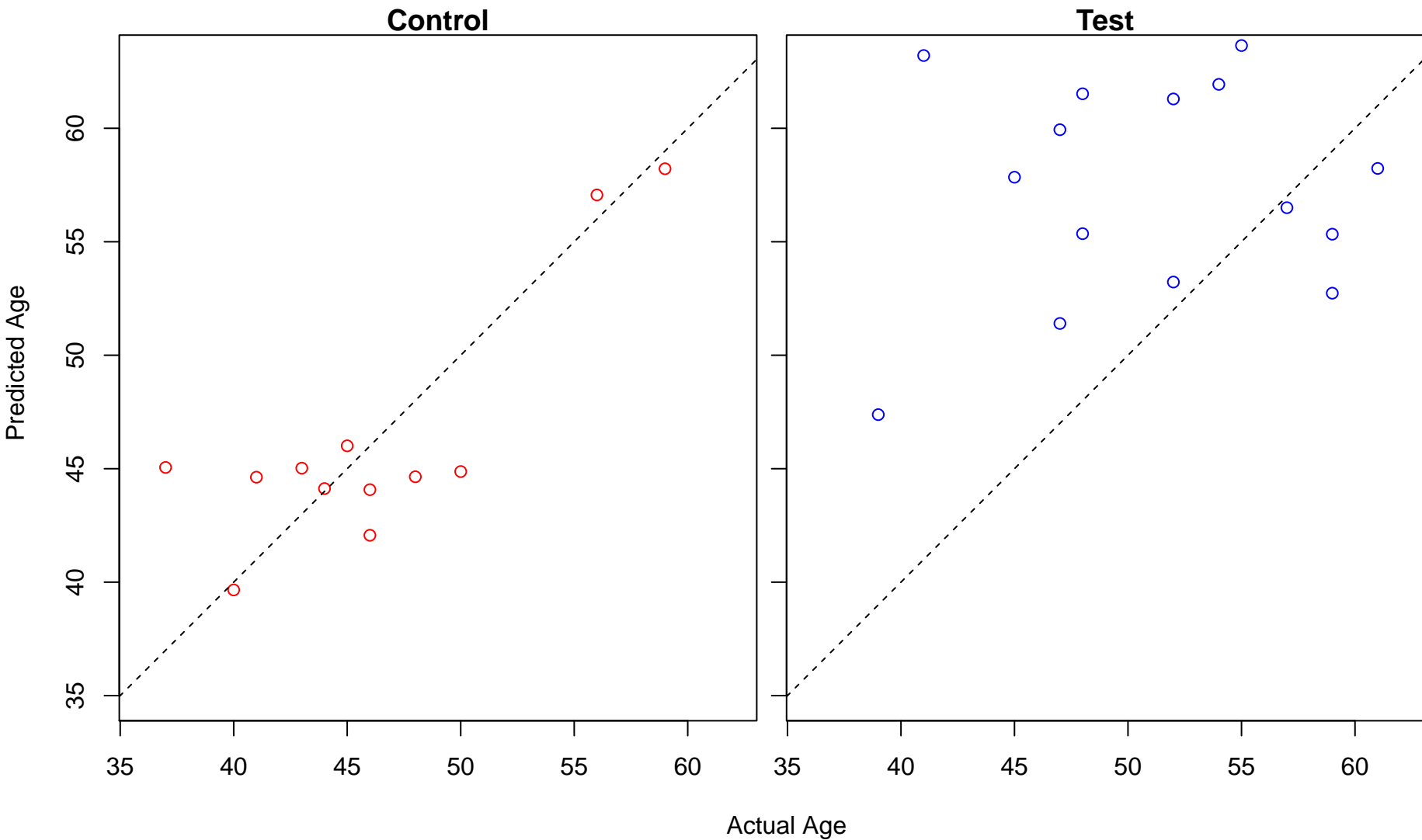
proline transmembrane transport (Score: 3.230229)



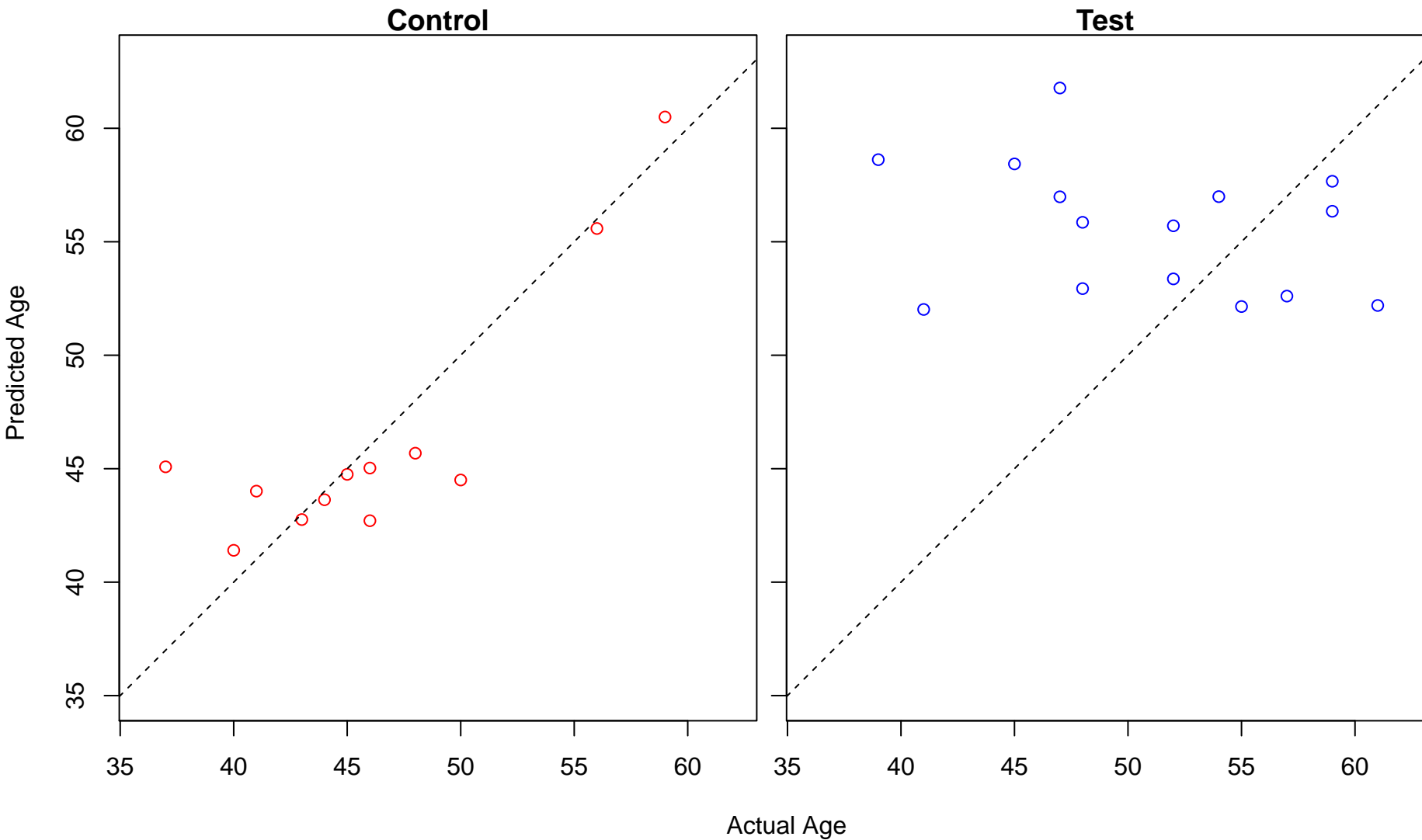
cell activation (Score: 3.229633)



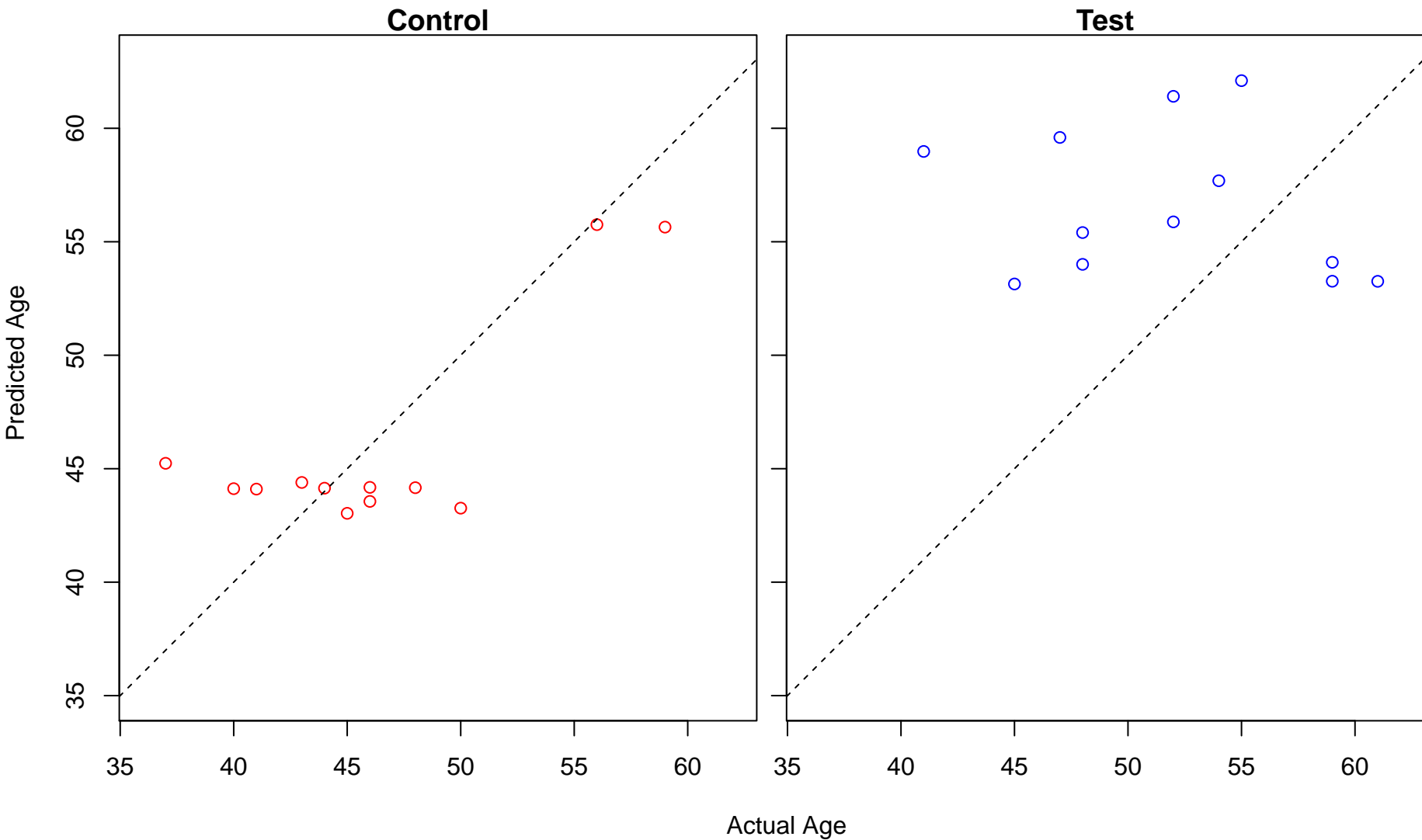
negative regulation of smoothened signaling pathway (Score: 3.229482)



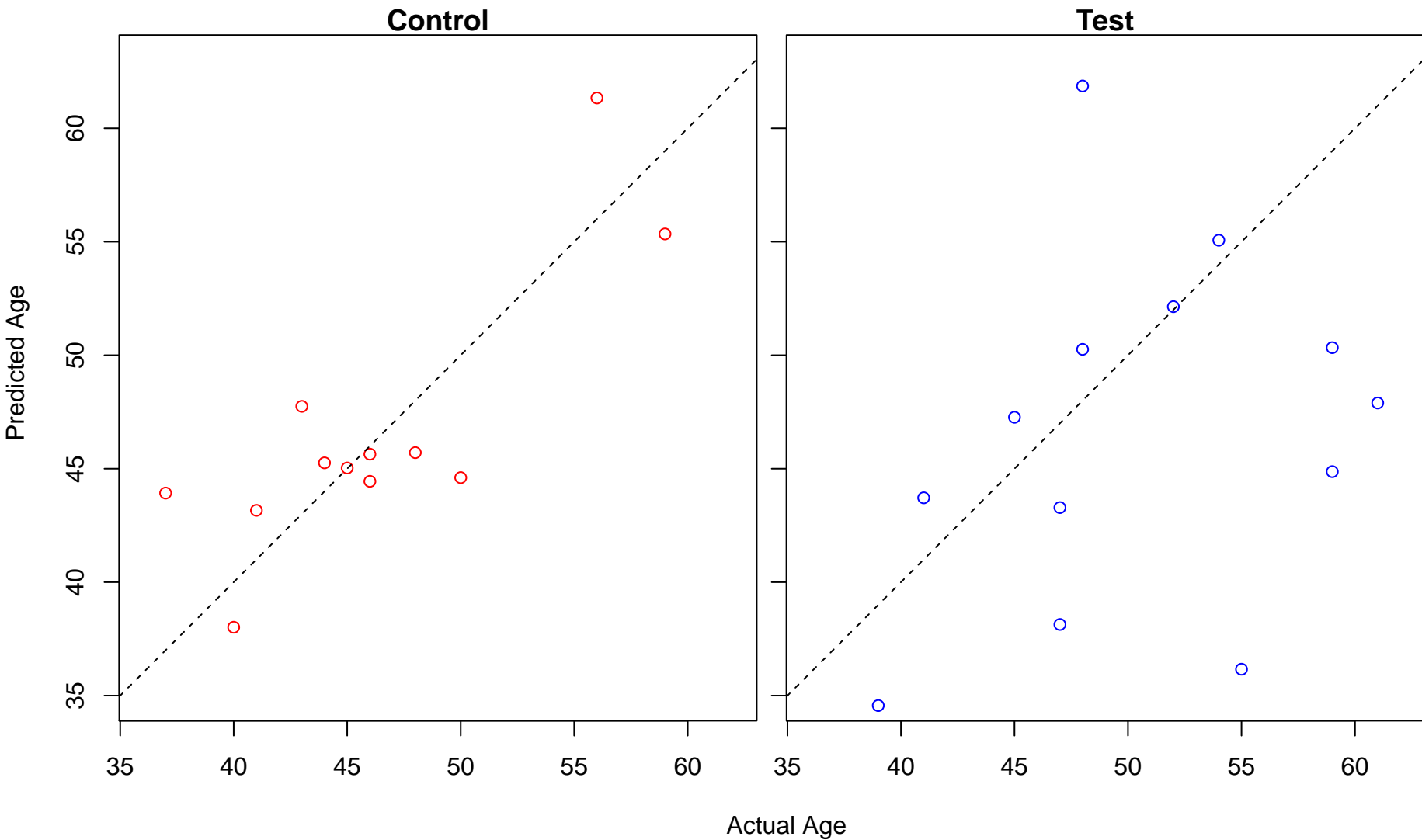
cytokine biosynthetic process (Score: 3.228070)



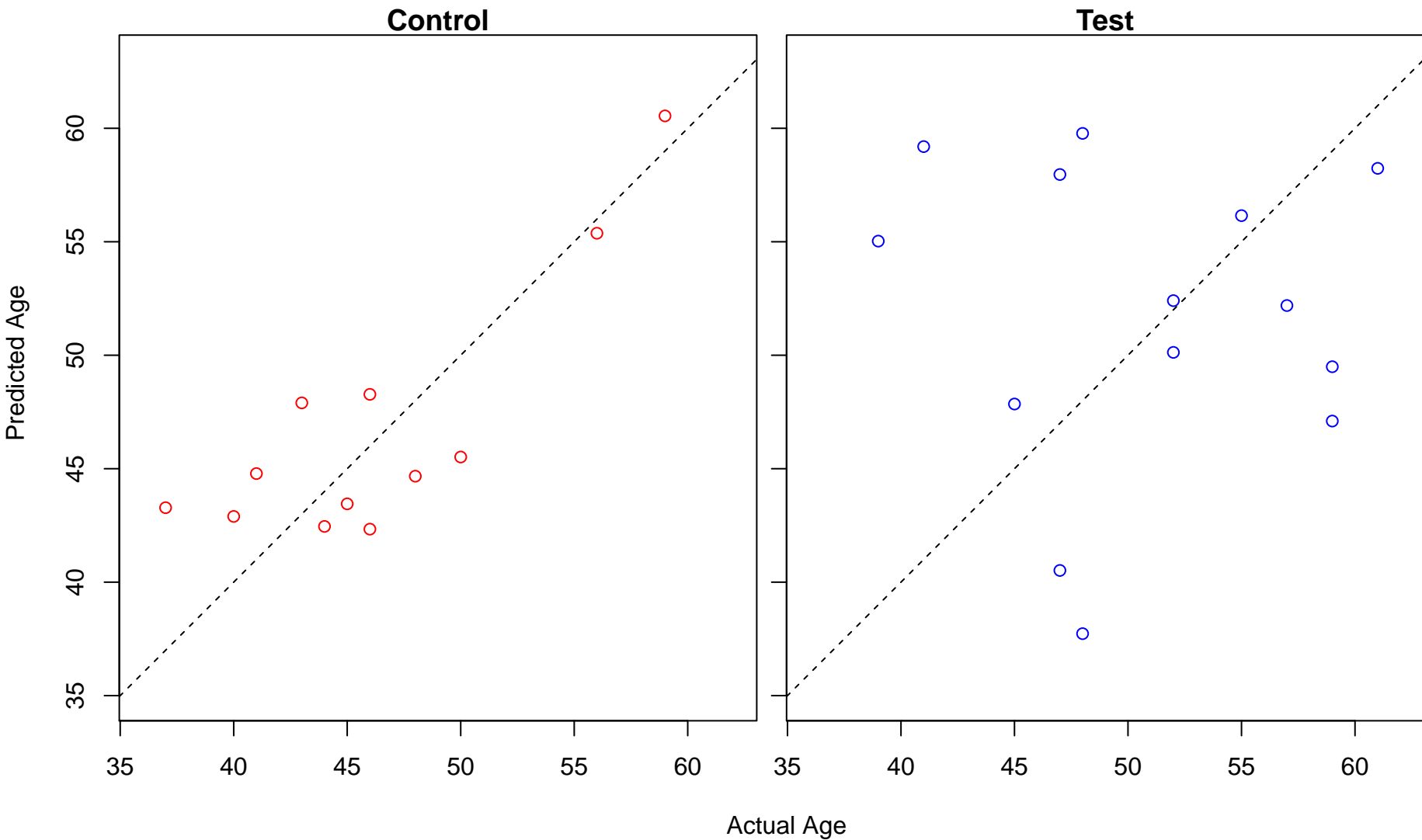
biological adhesion (Score: 3.226479)



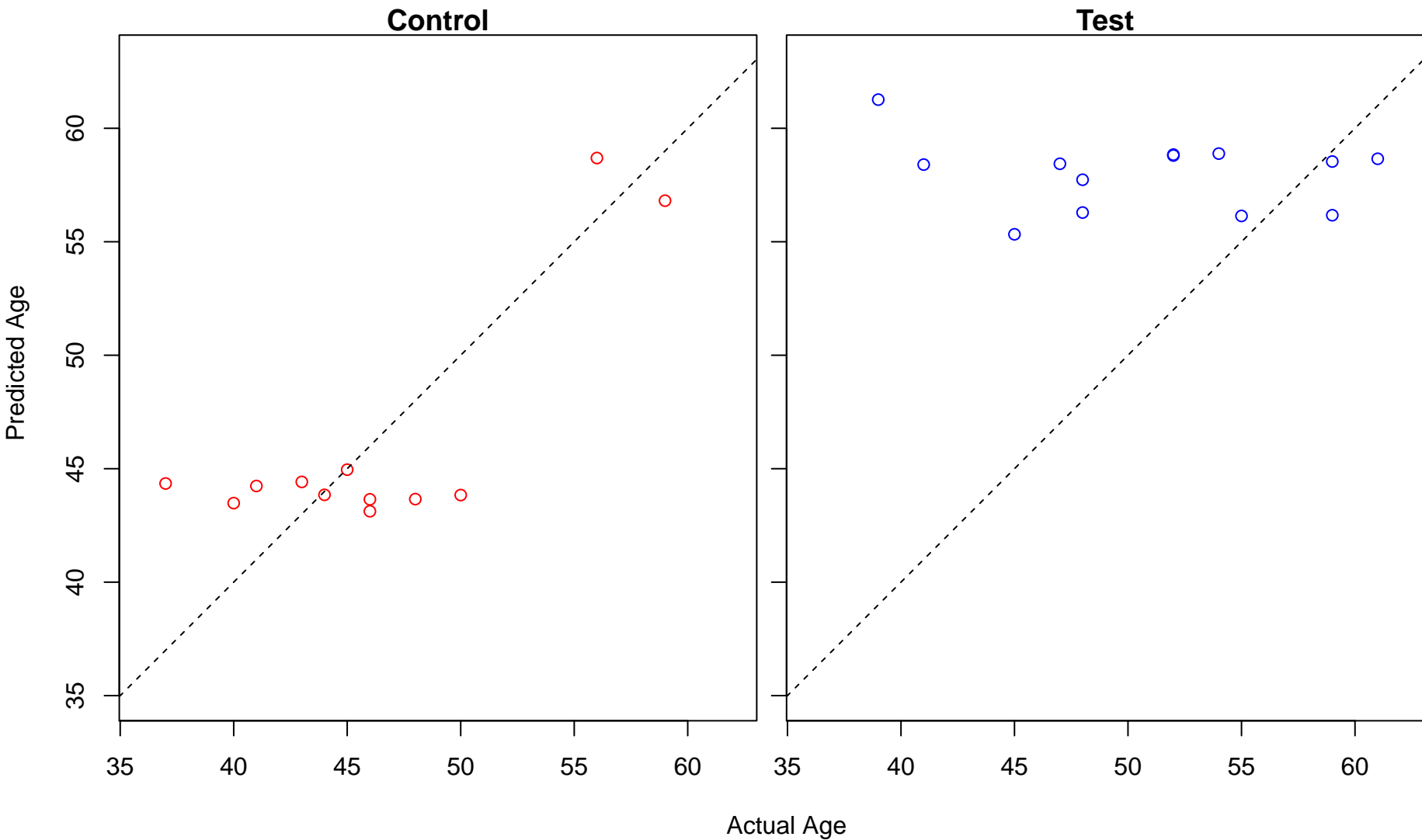
cell-cell recognition (Score: 3.226261)



regulation of synapse structure or activity (Score: 3.225443)

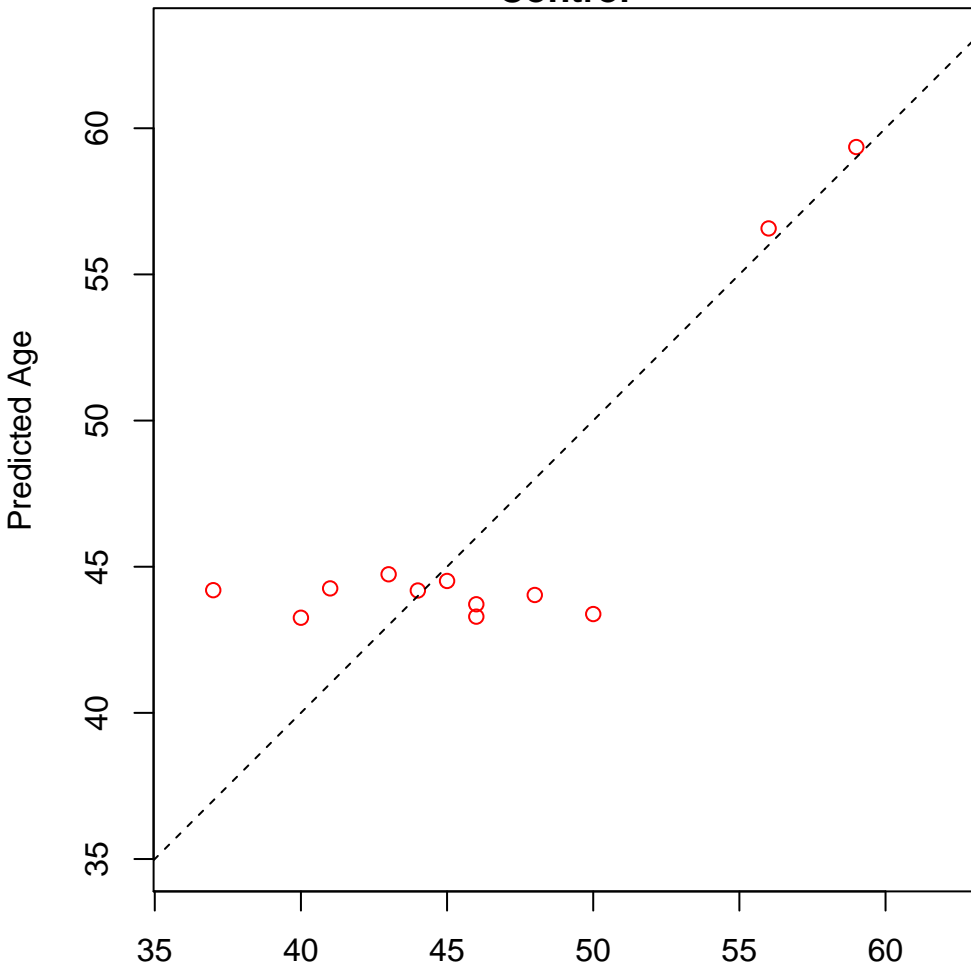


macroautophagy (Score: 3.222438)

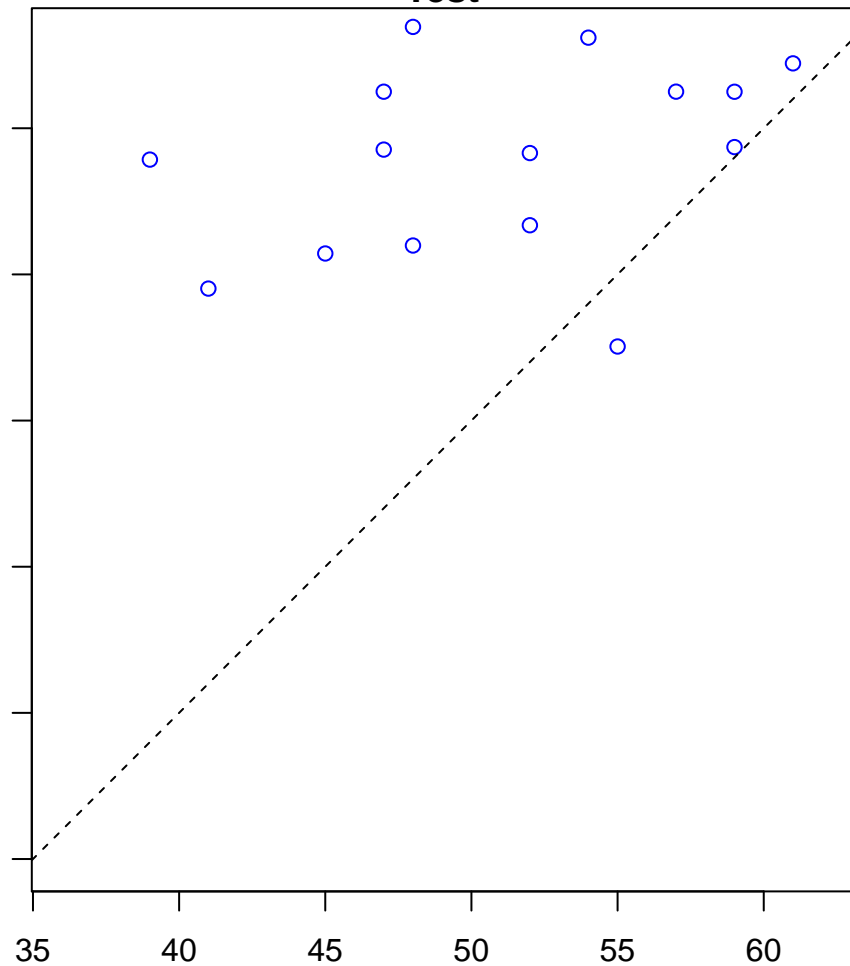


amino-acid betaine metabolic process (Score: 3.221745)

Control

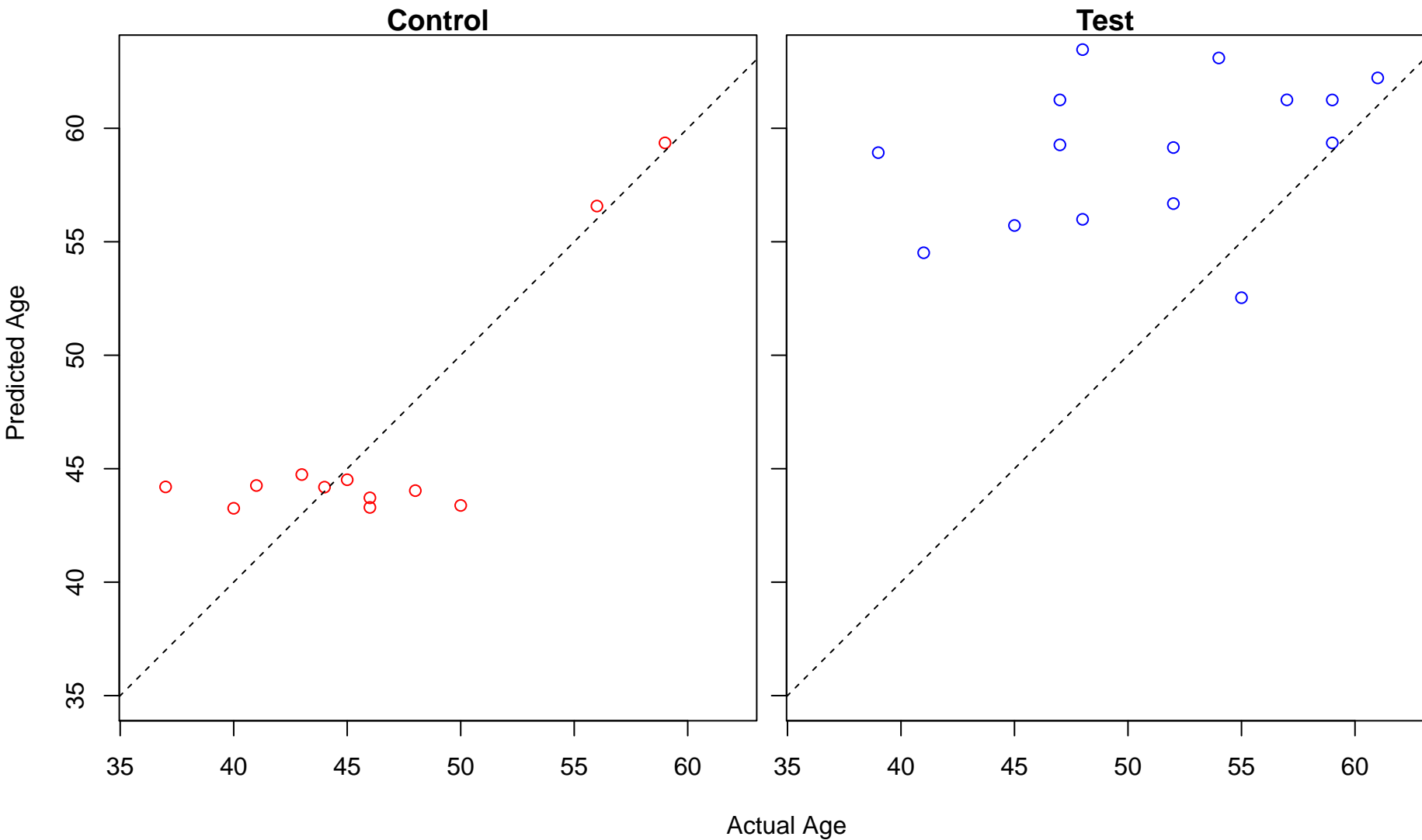


Test

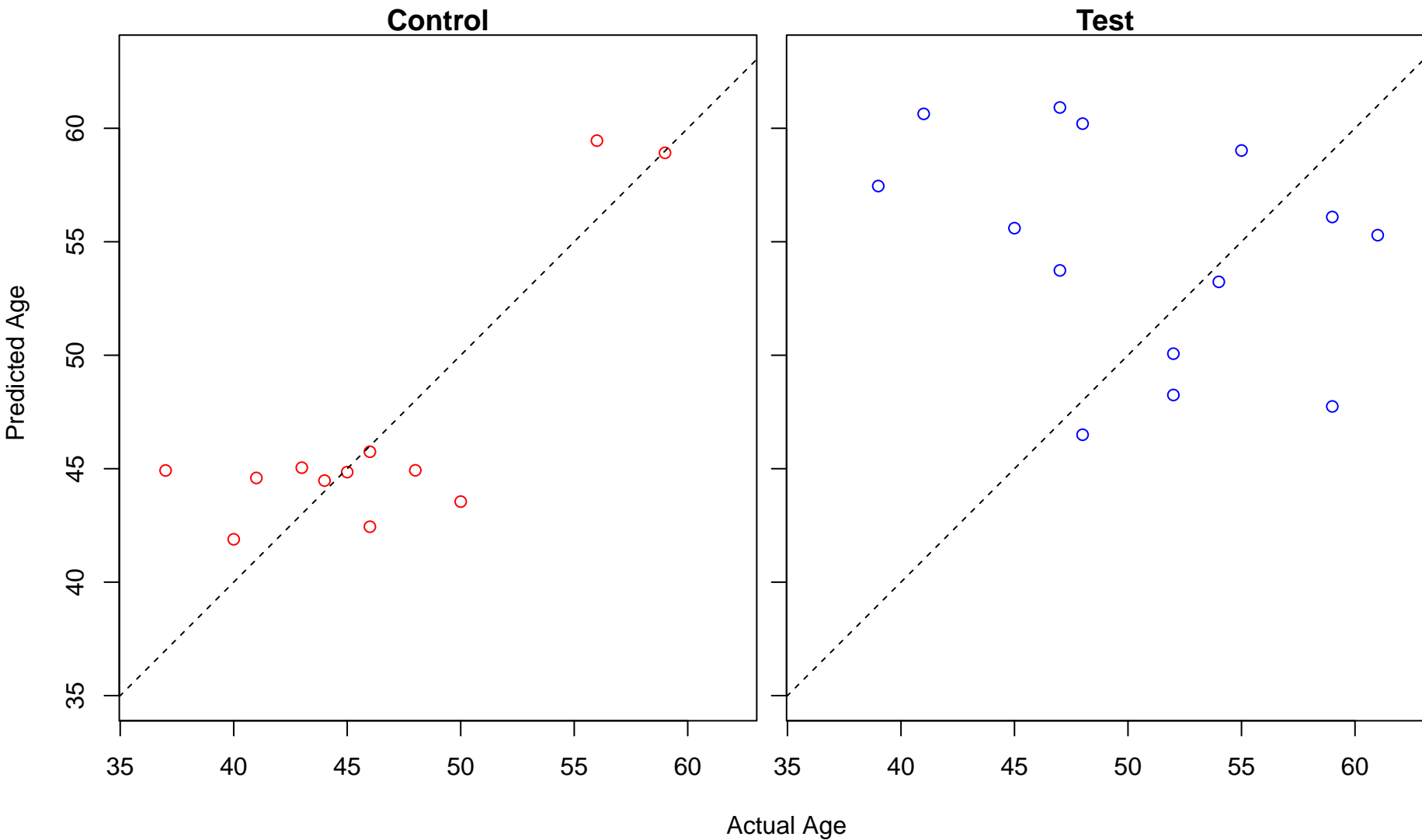


Actual Age

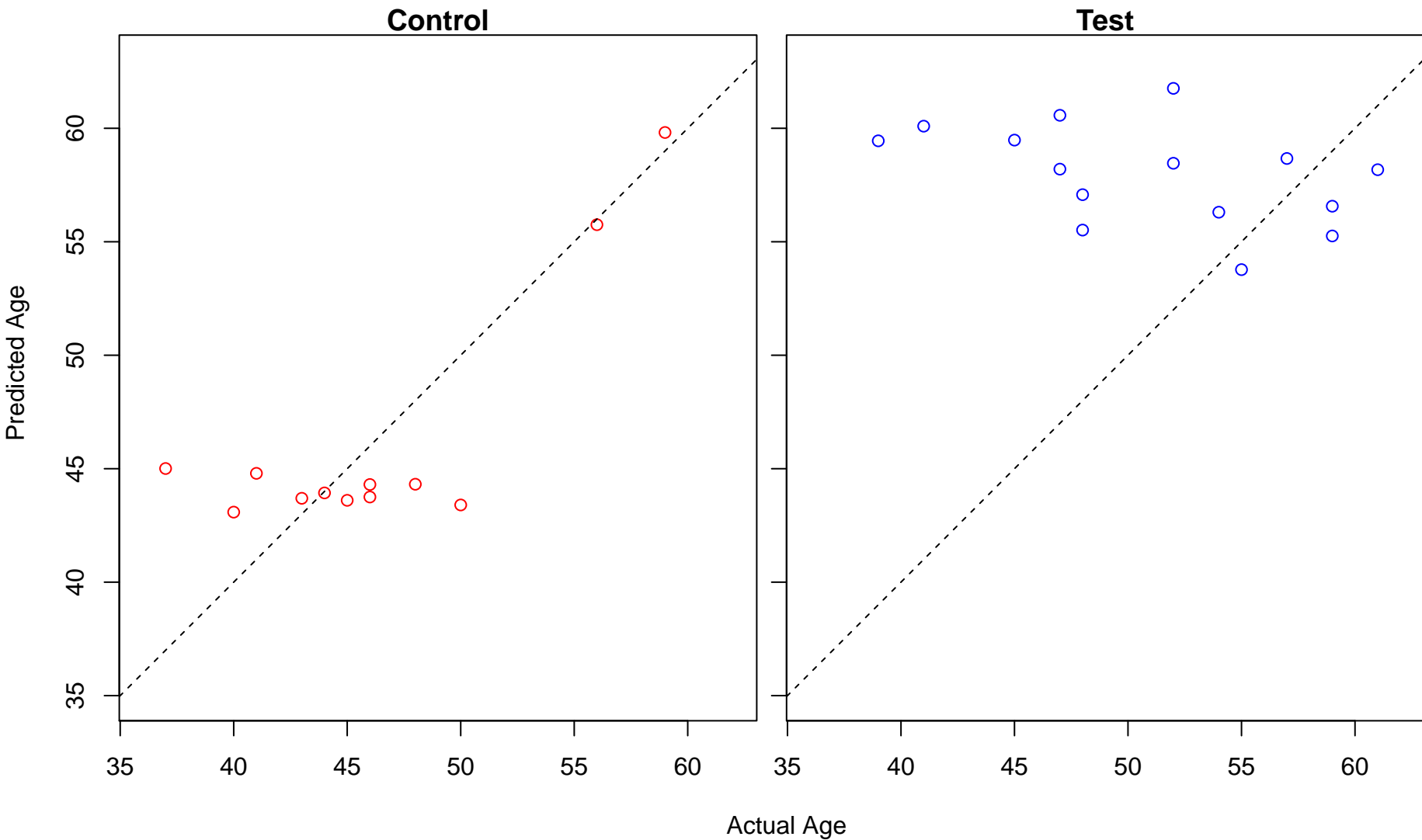
carnitine metabolic process (Score: 3.221685)



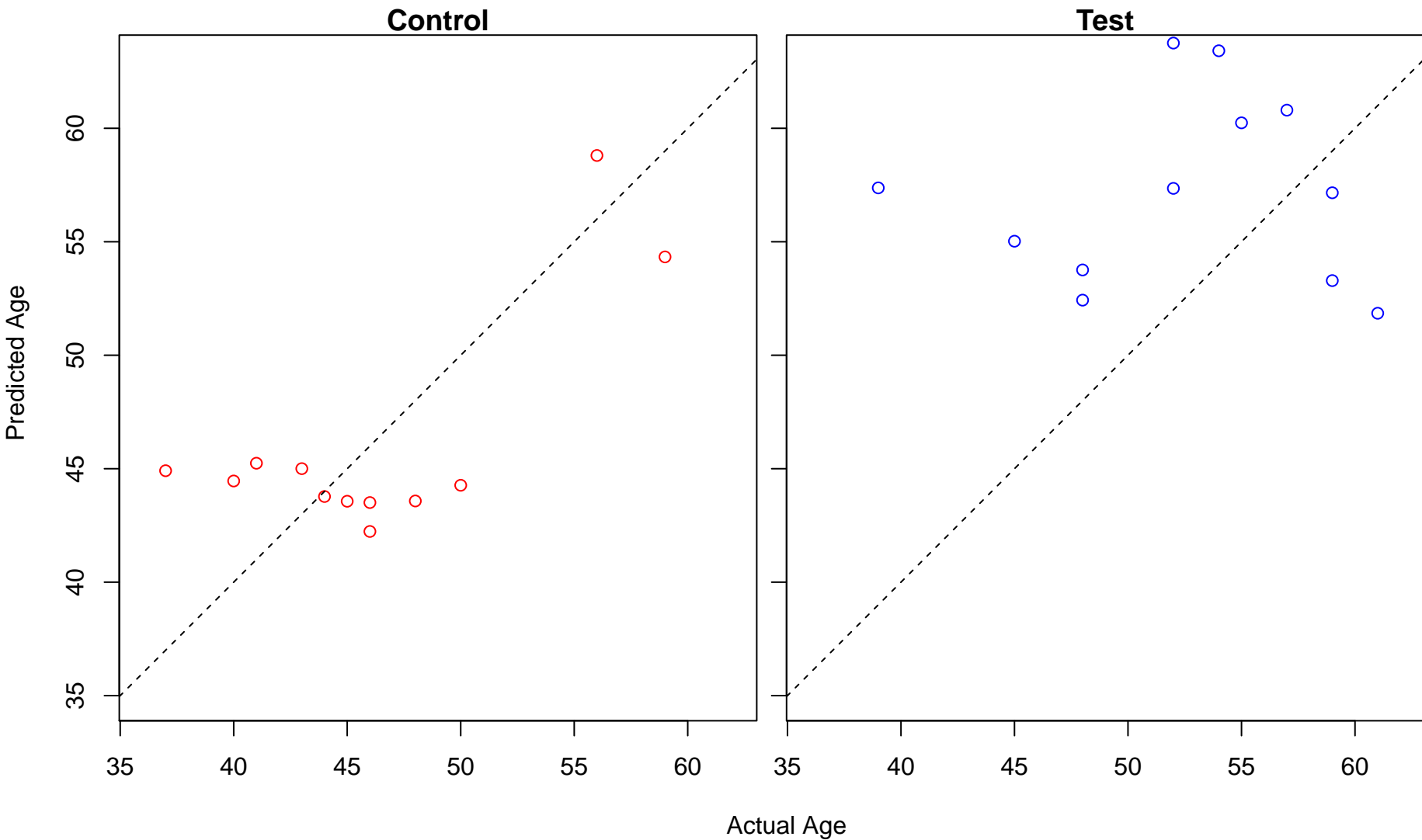
signal transduction by protein phosphorylation (Score: 3.221425)



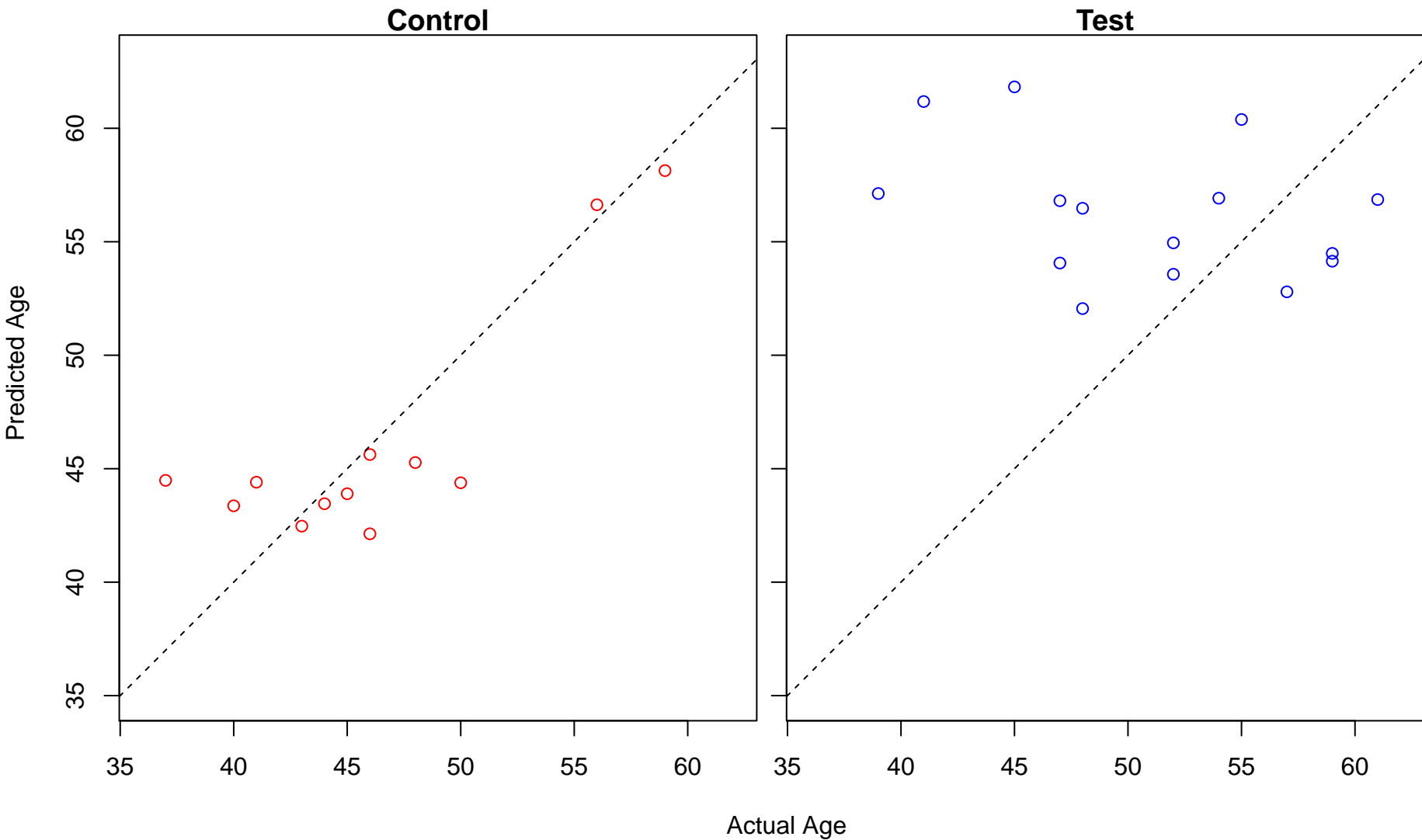
positive regulation of DNA binding (Score: 3.221249)



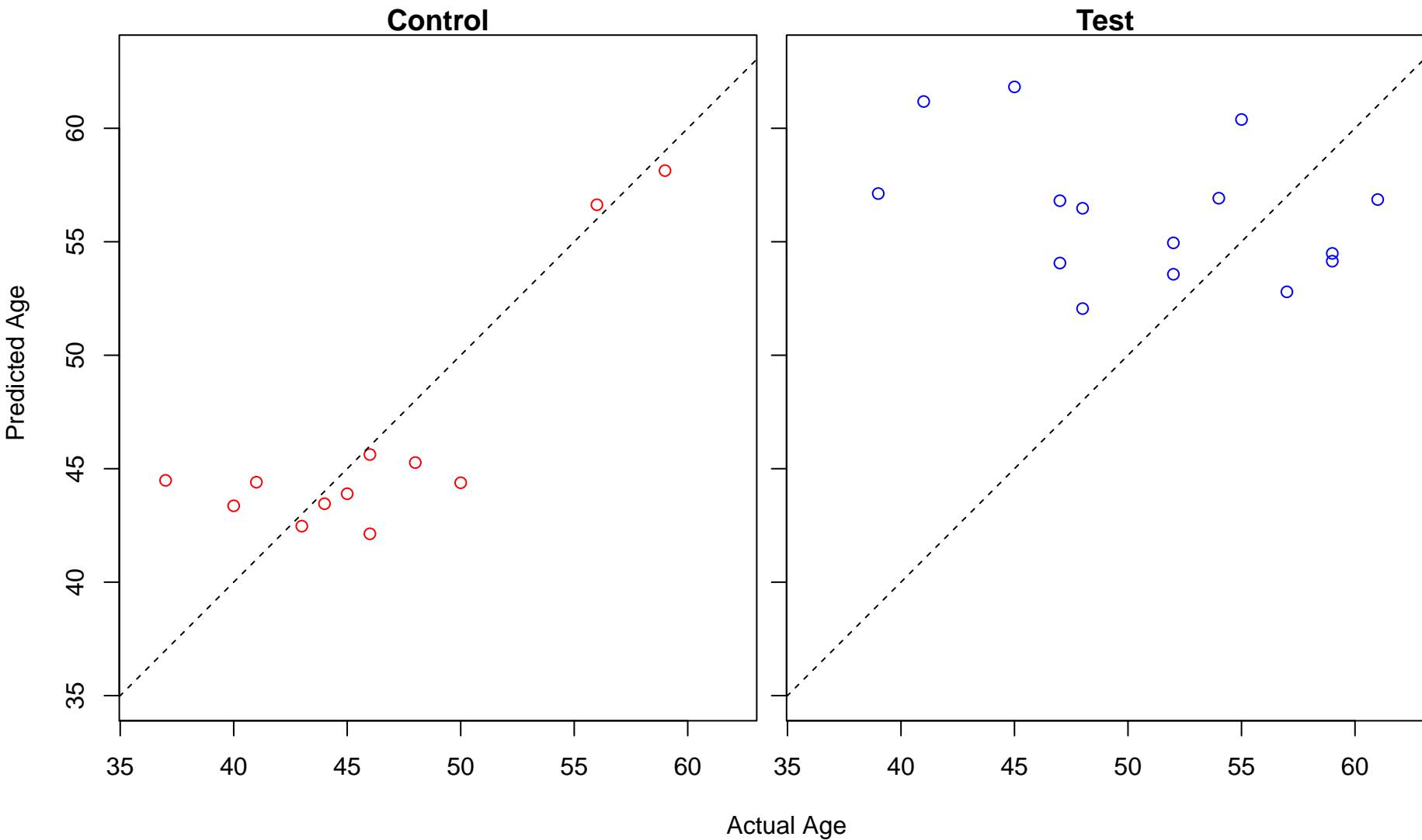
negative regulation of transcription by competitive promoter binding (Score: 3.220480)



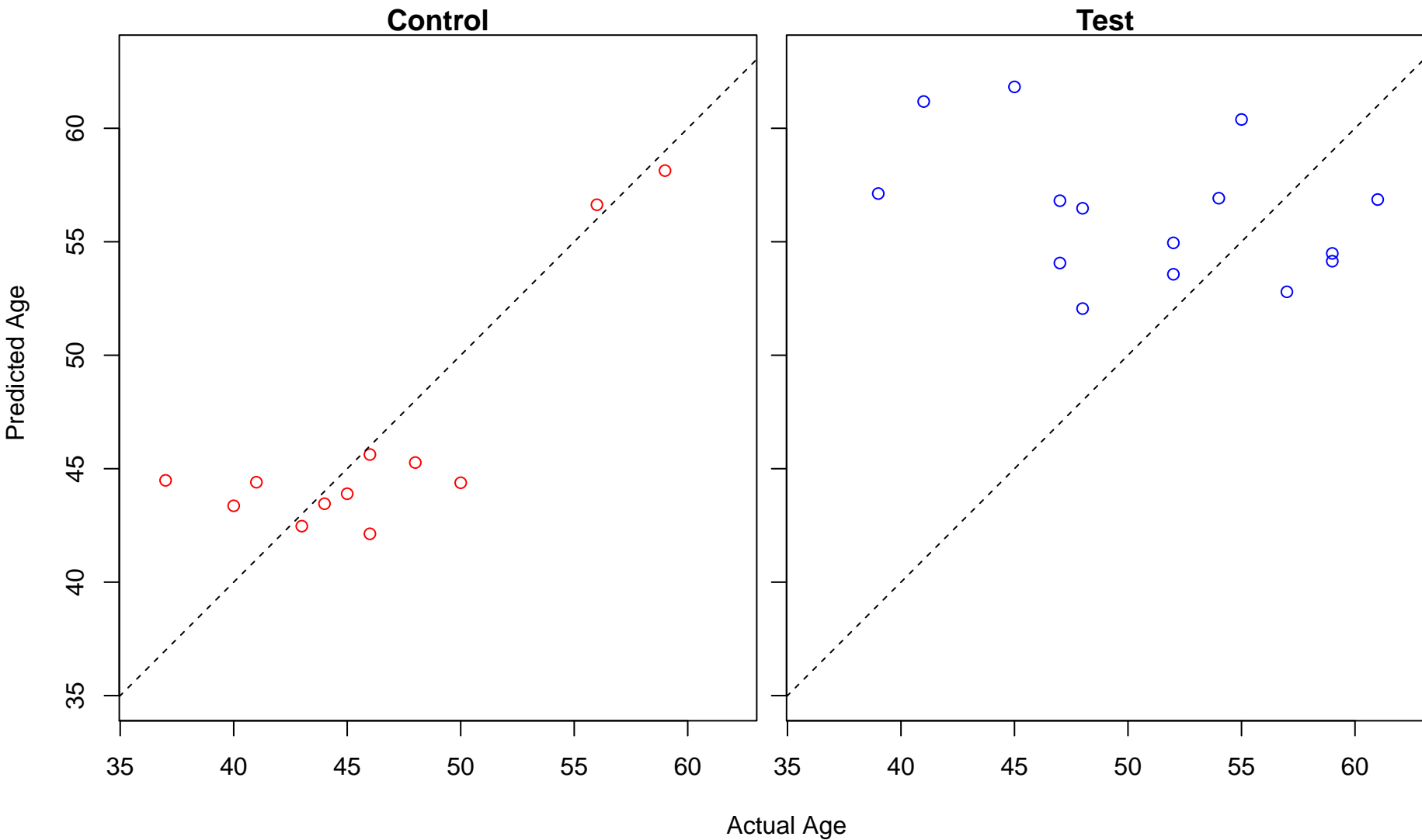
SA node cell action potential (Score: 3.219686)



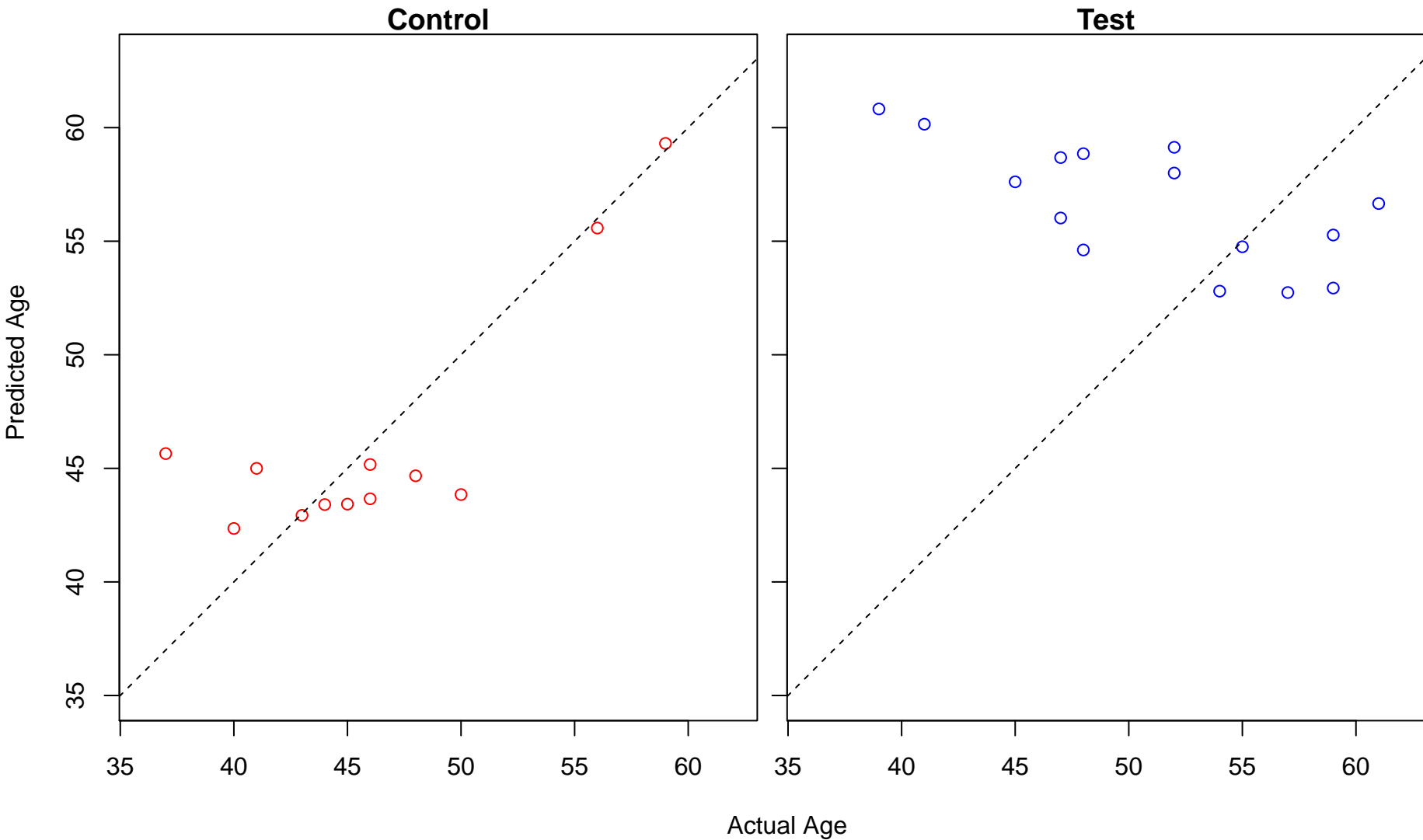
SA node cell to atrial cardiac muscle cell signalling (Score: 3.219686)



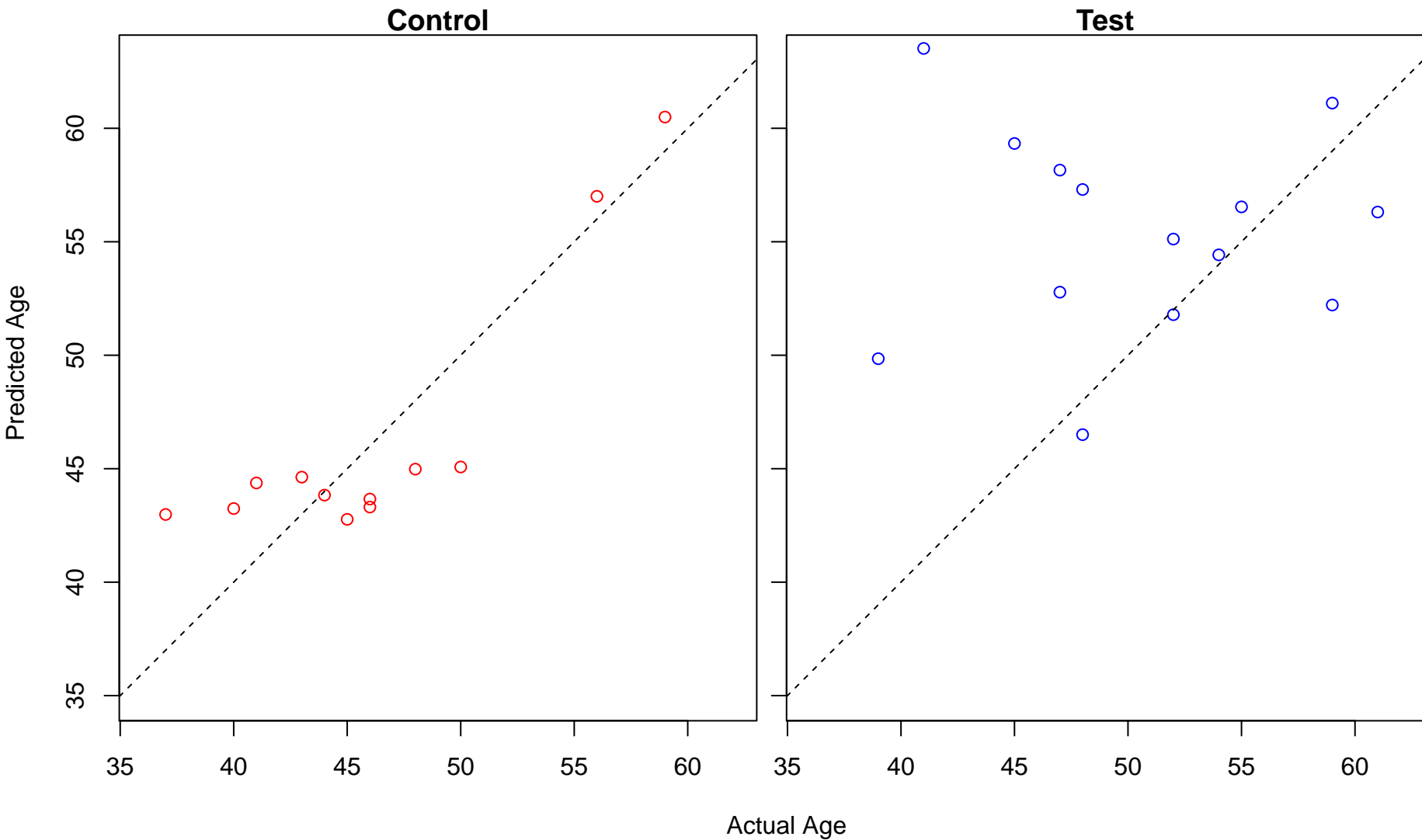
SA node cell to atrial cardiac muscle cell communication (Score: 3.219686)



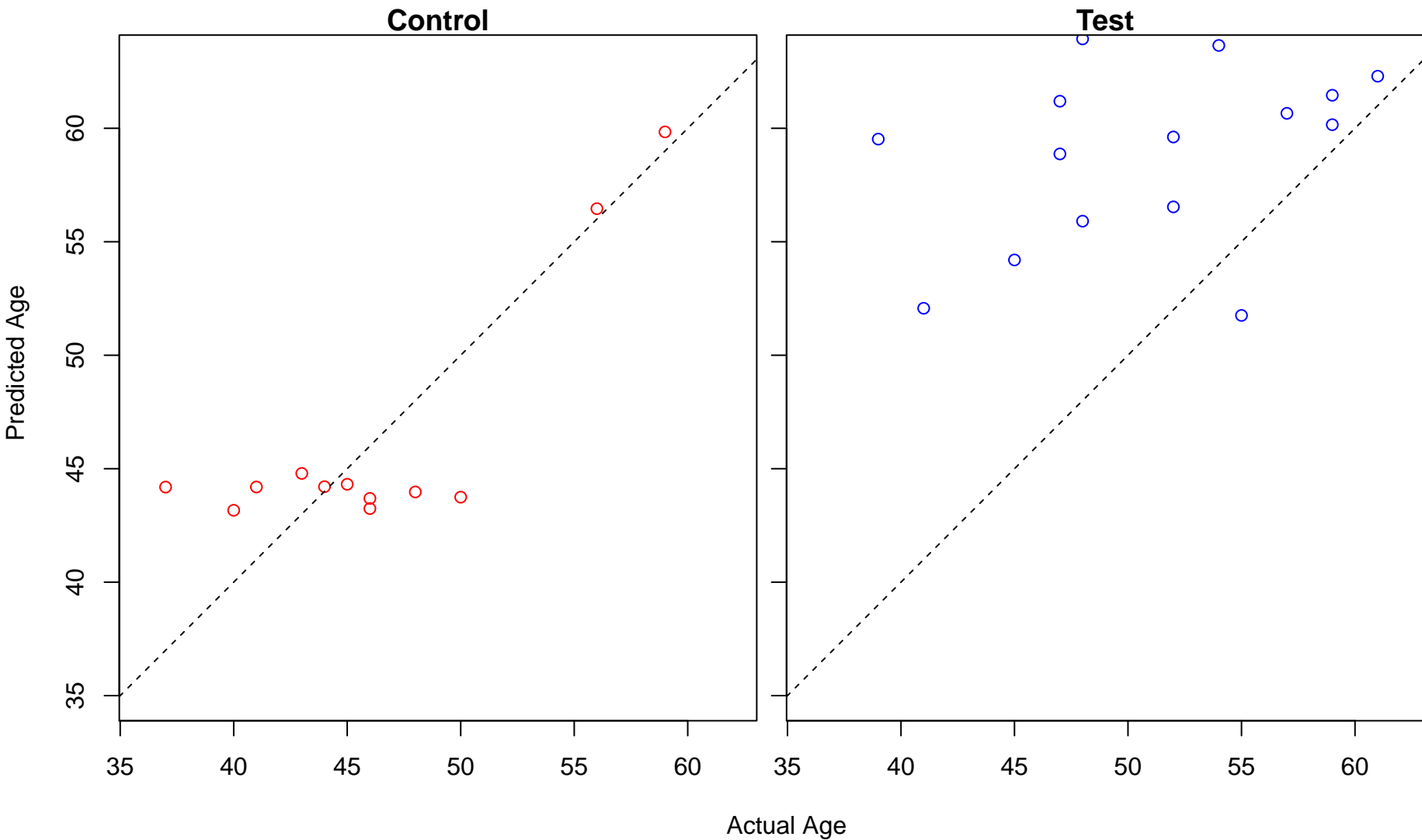
regulation of transcription initiation from RNA polymerase II promoter (Score: 3.218884)



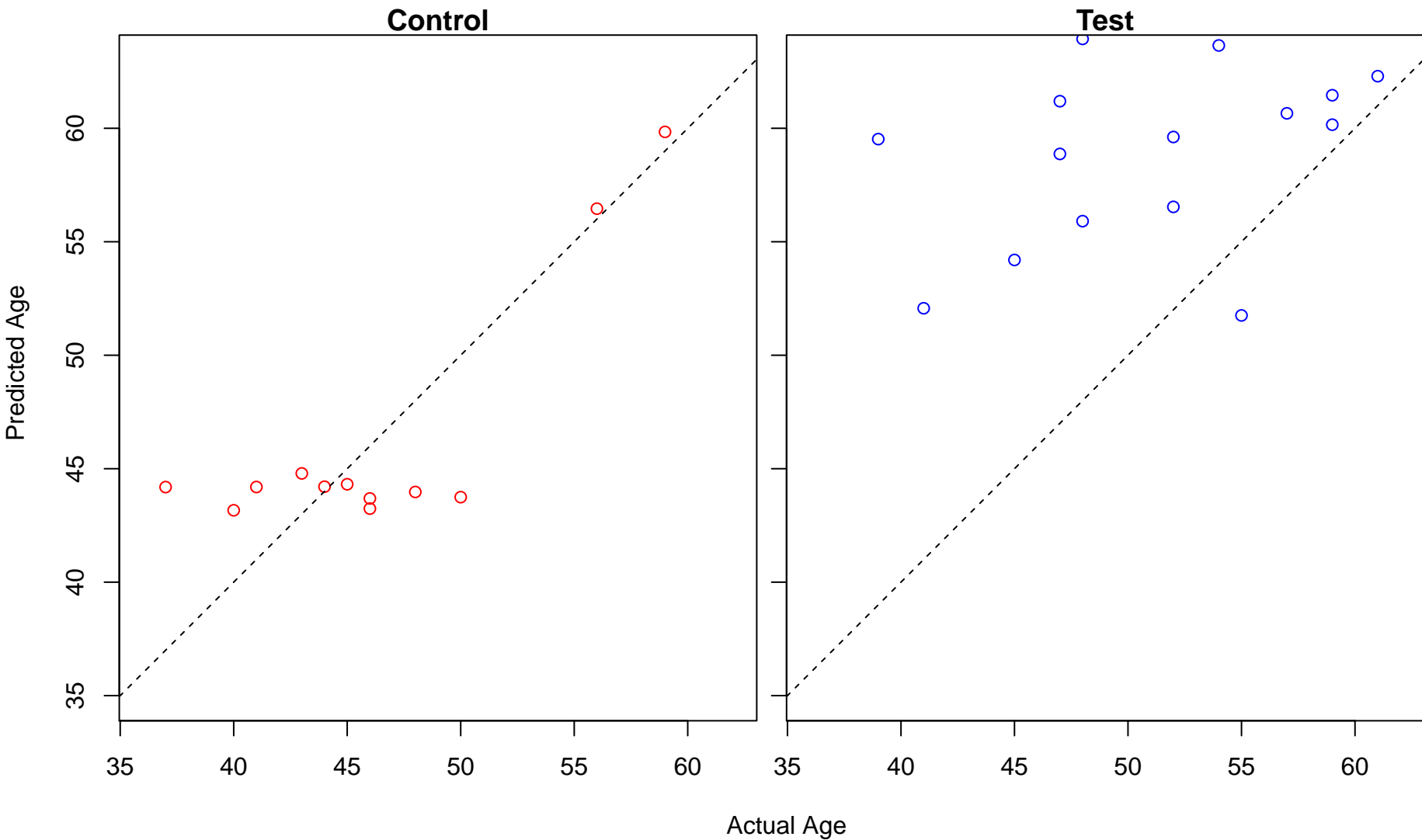
positive regulation of protein kinase B signaling (Score: 3.216105)



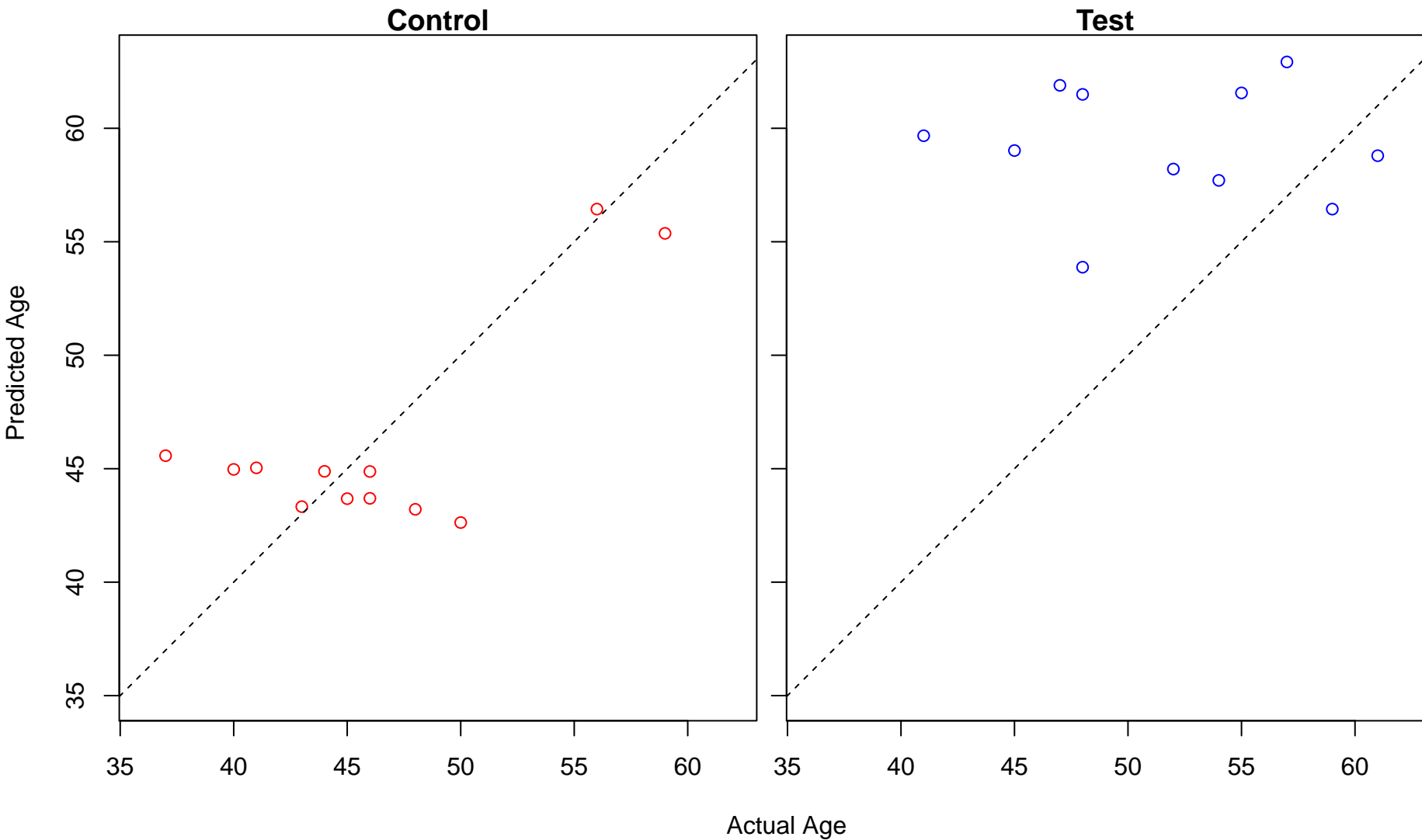
amino-acid betaine biosynthetic process (Score: 3.214597)



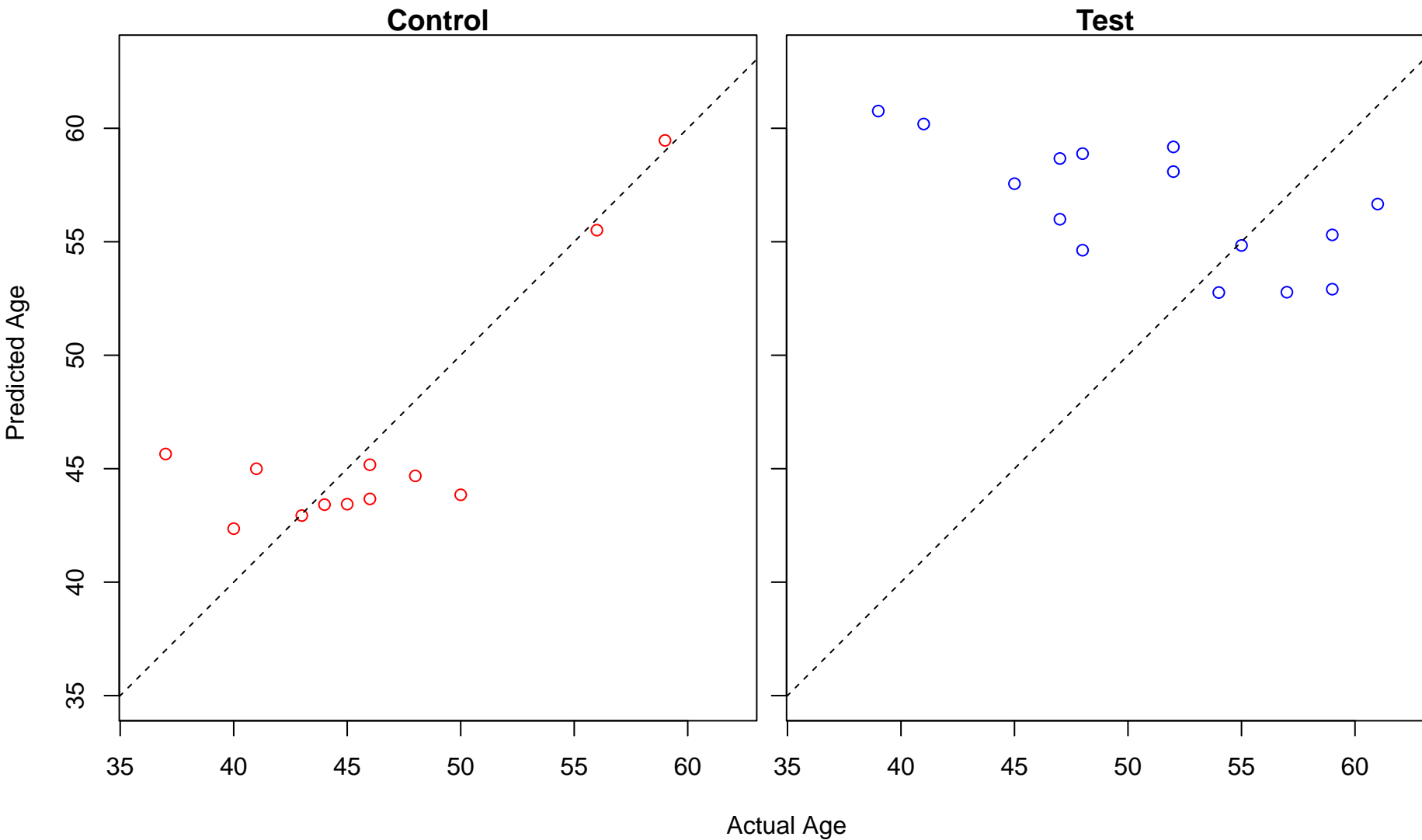
carnitine biosynthetic process (Score: 3.214597)



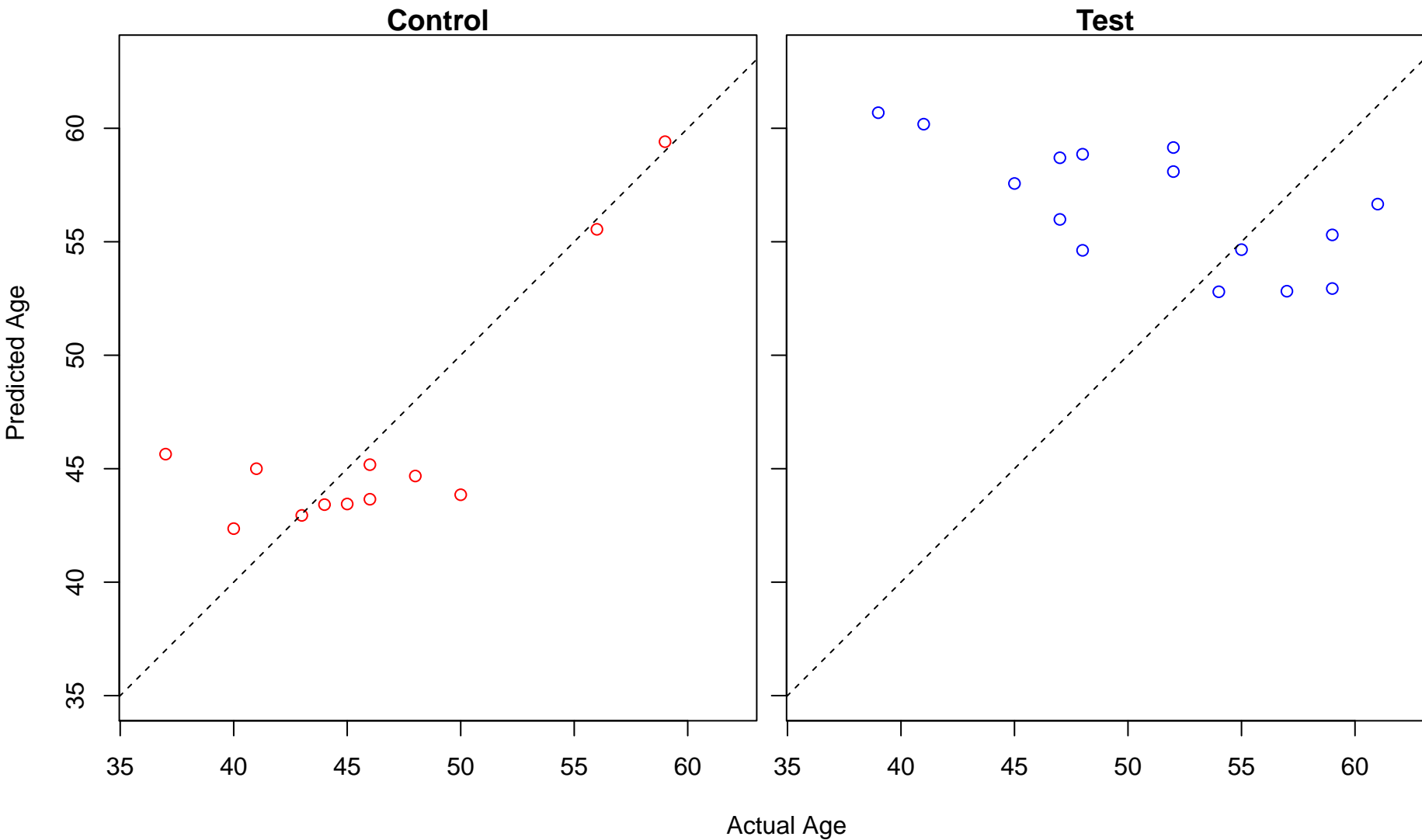
cellular biogenic amine catabolic process (Score: 3.214070)



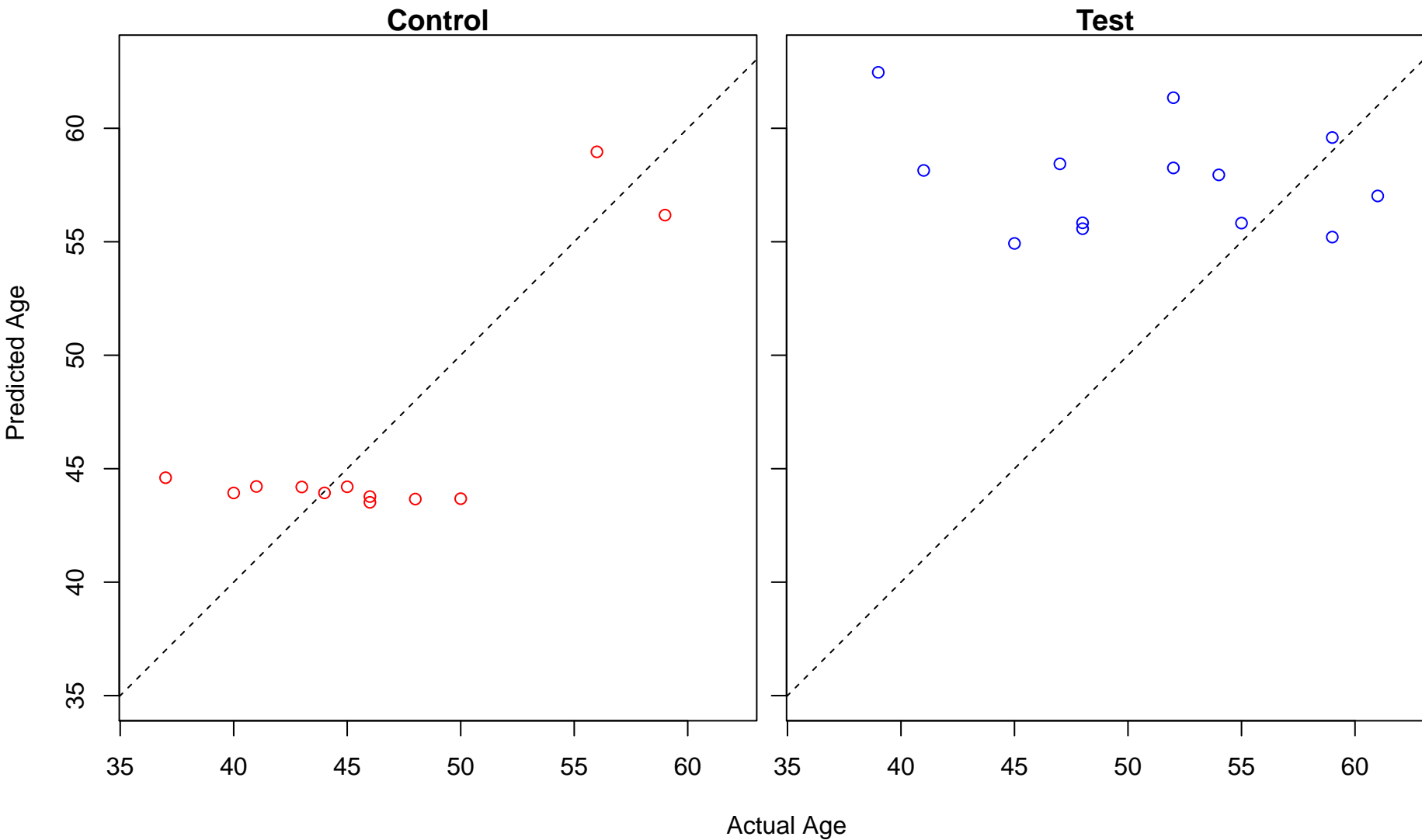
dendritic cell chemotaxis (Score: 3.213138)



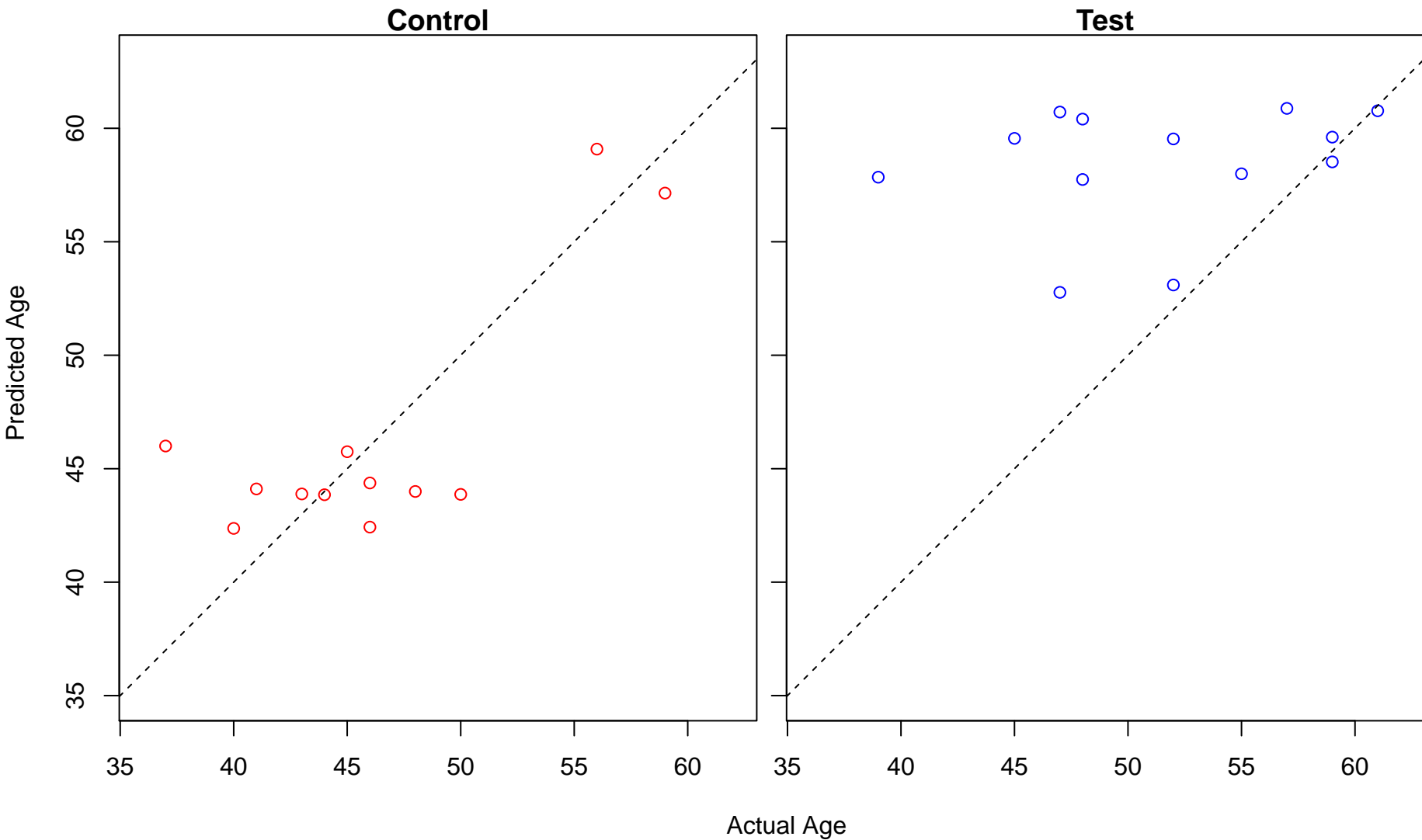
positive regulation of monocyte chemotaxis (Score: 3.211485)



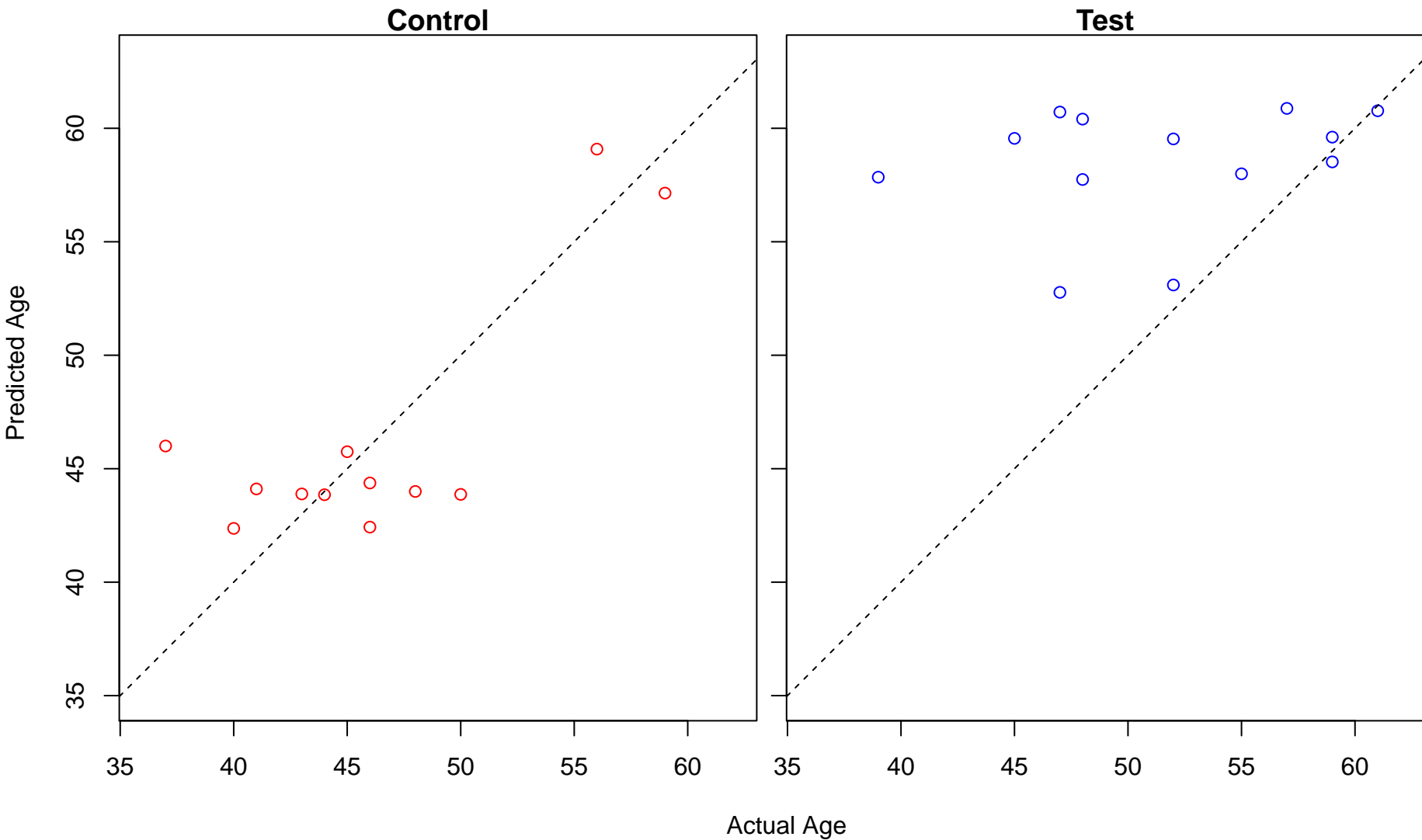
positive regulation of cell cycle (Score: 3.210180)



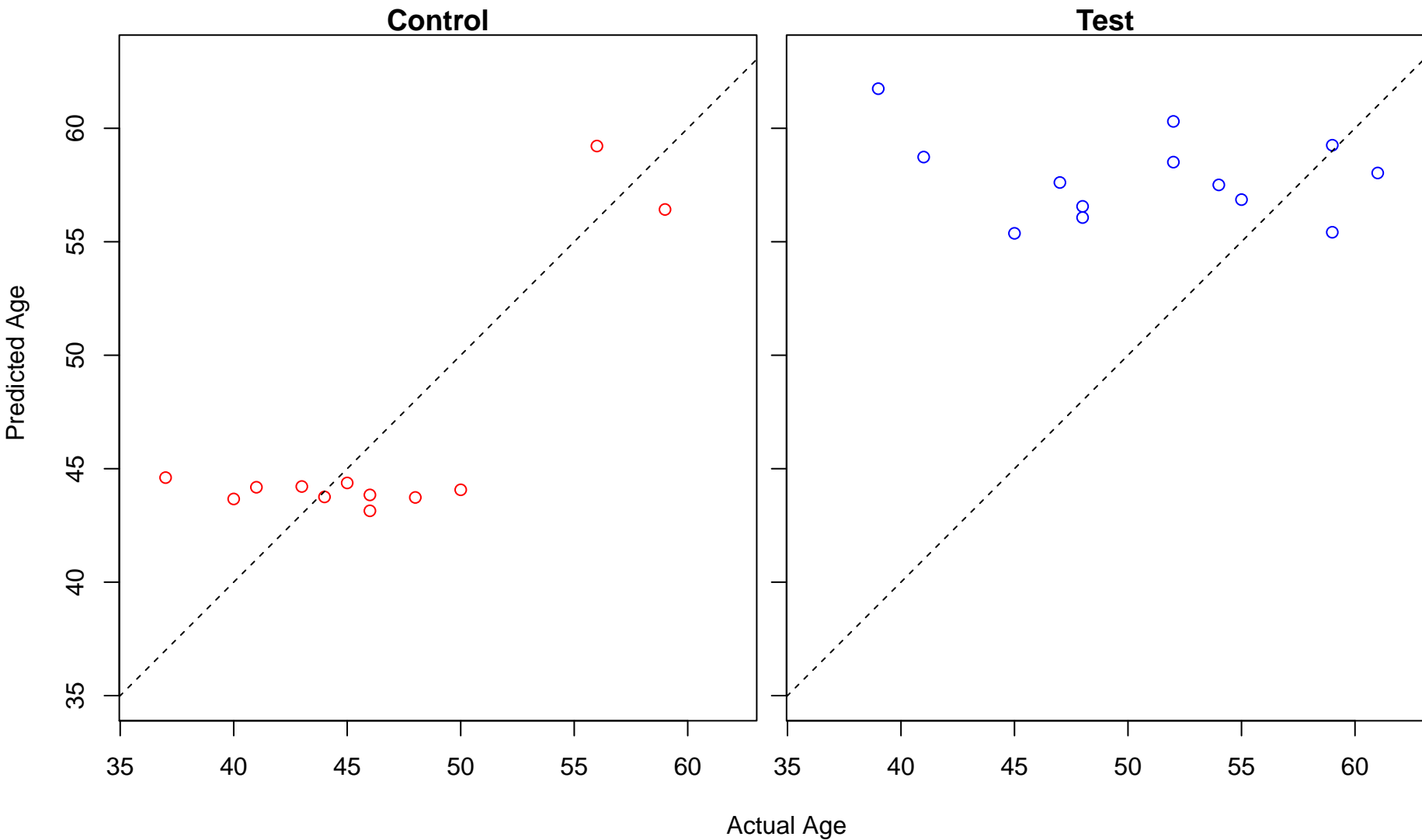
negative regulation of B cell mediated immunity (Score: 3.204367)



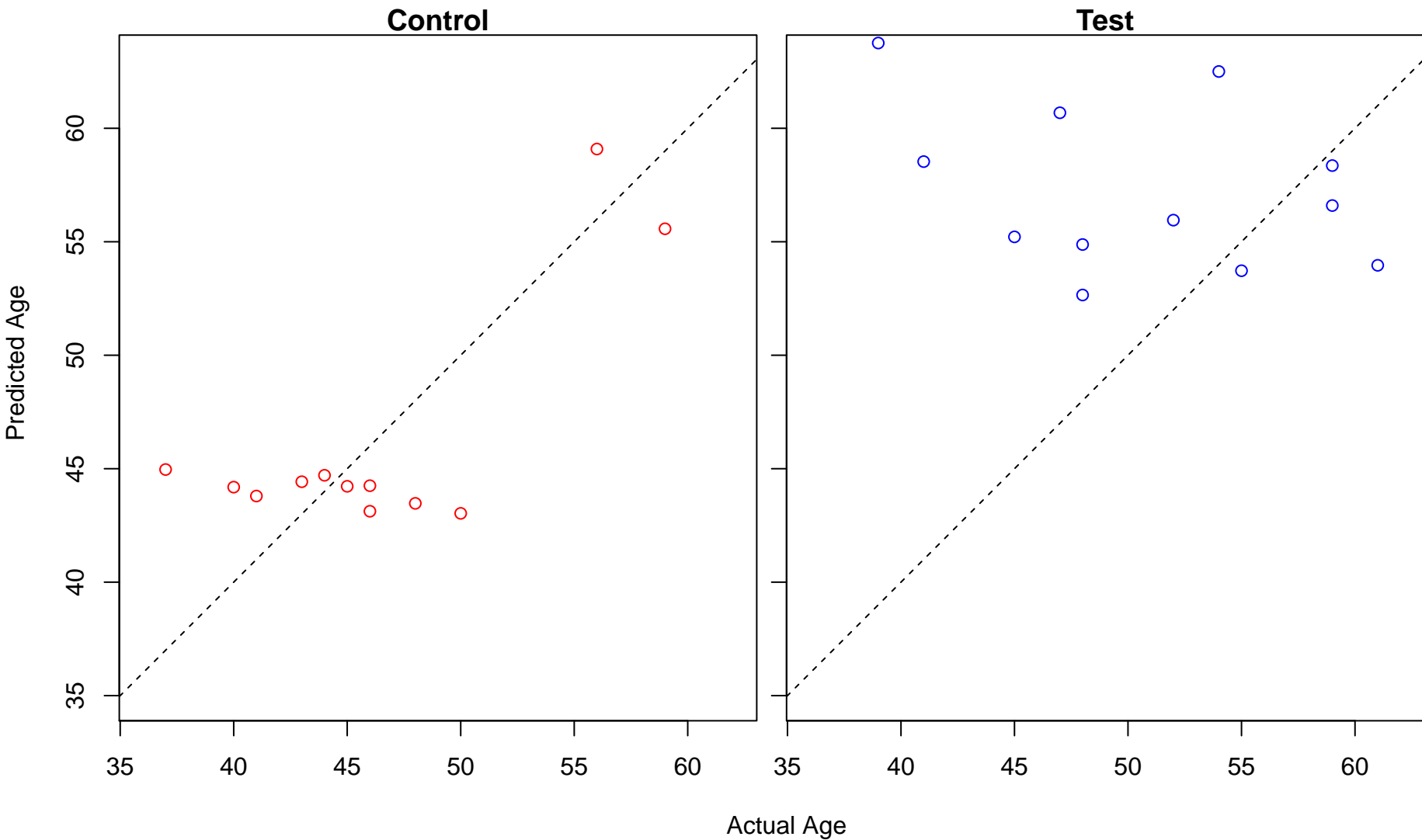
negative regulation of immunoglobulin mediated immune response (Score: 3.204367)



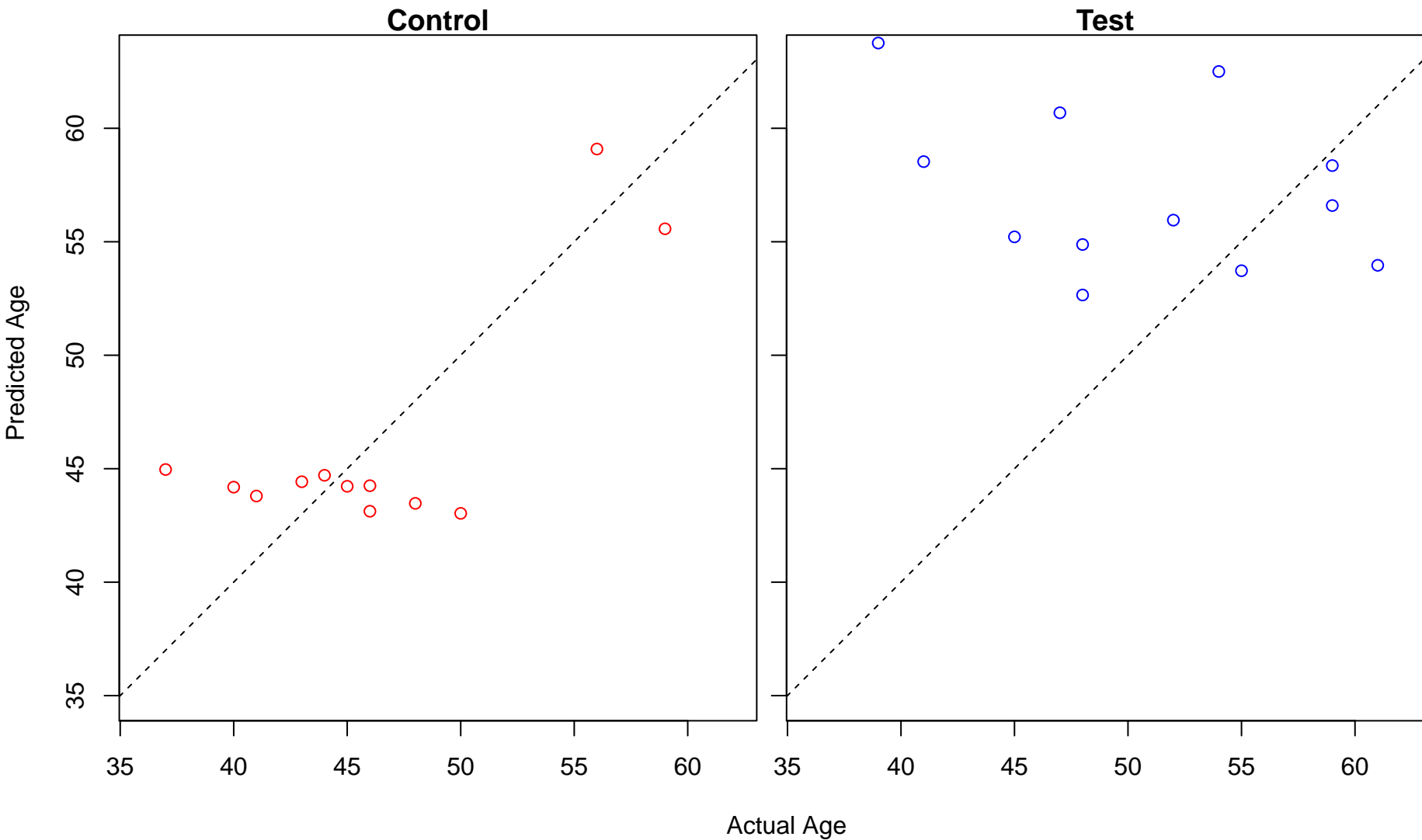
intracellular receptor signaling pathway (Score: 3.203333)



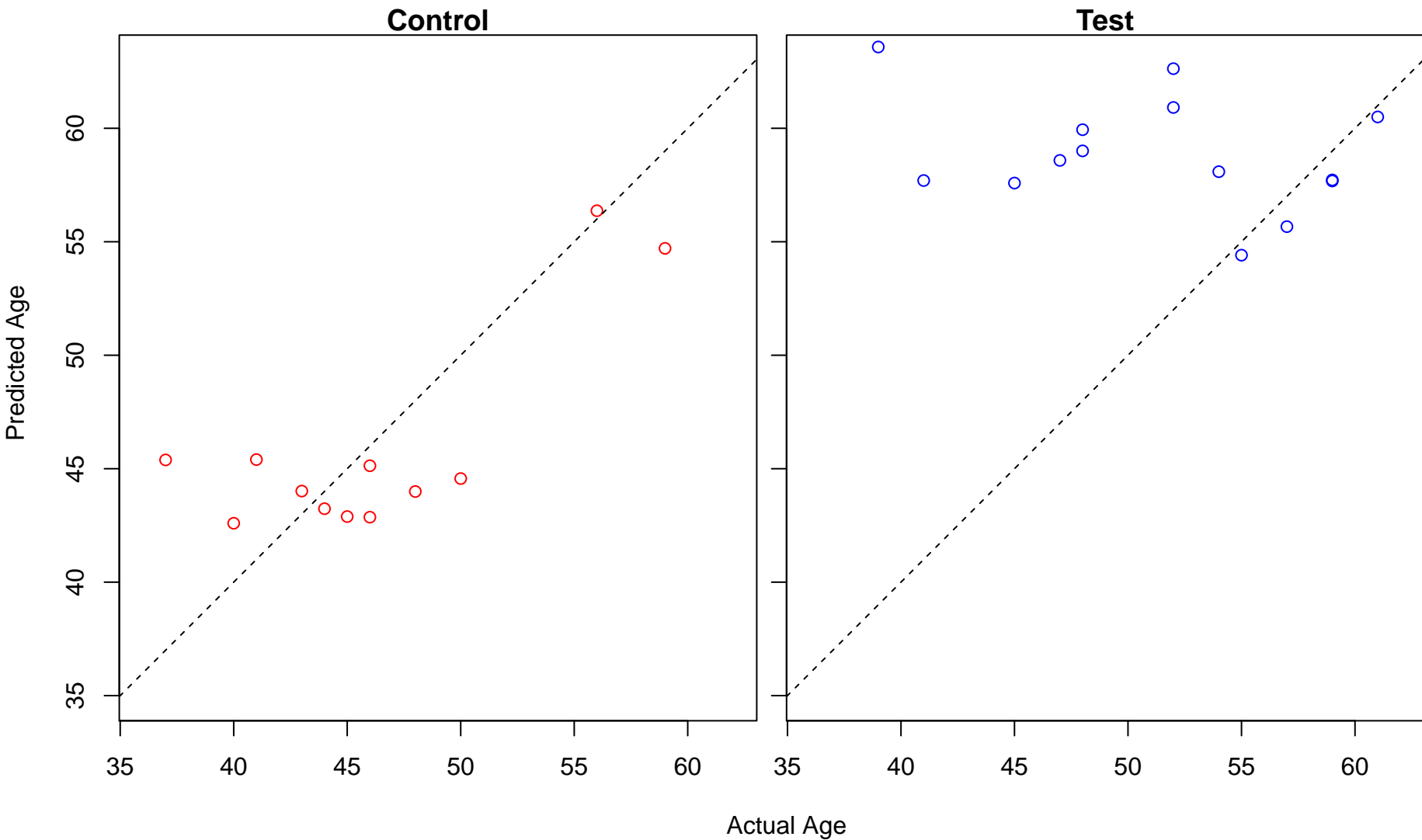
pigment accumulation (Score: 3.203136)



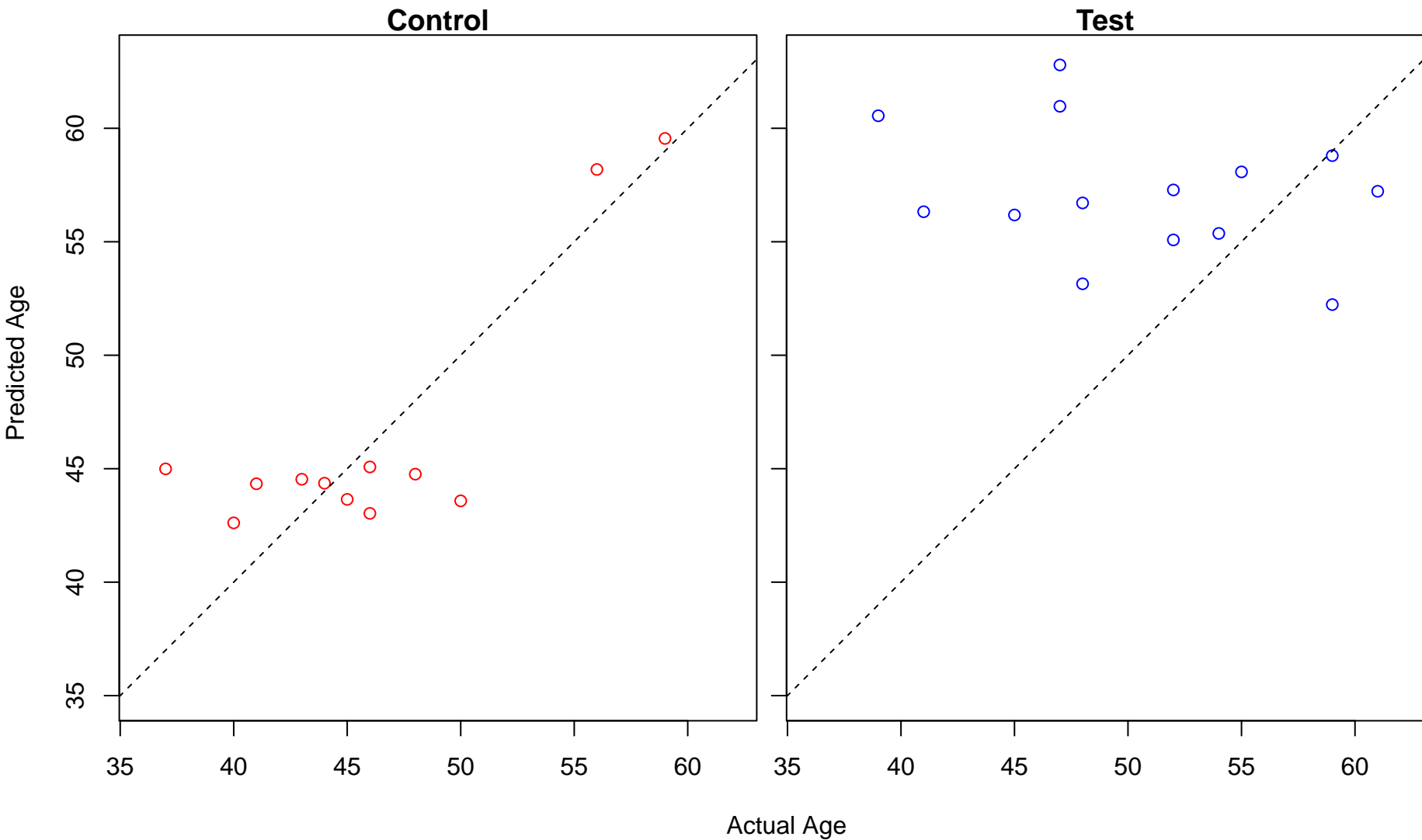
cellular pigment accumulation (Score: 3.203136)



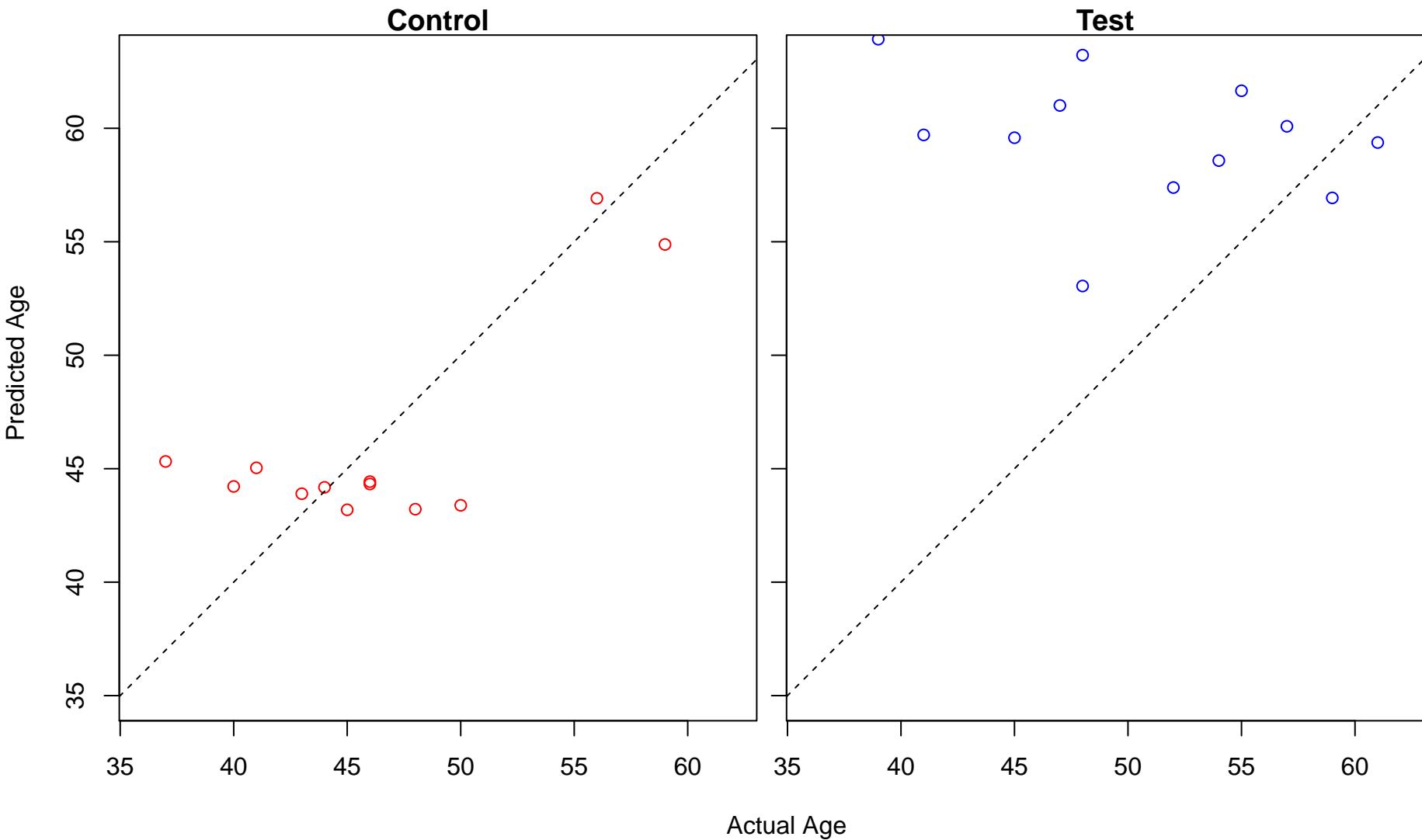
sympathetic nervous system development (Score: 3.203055)



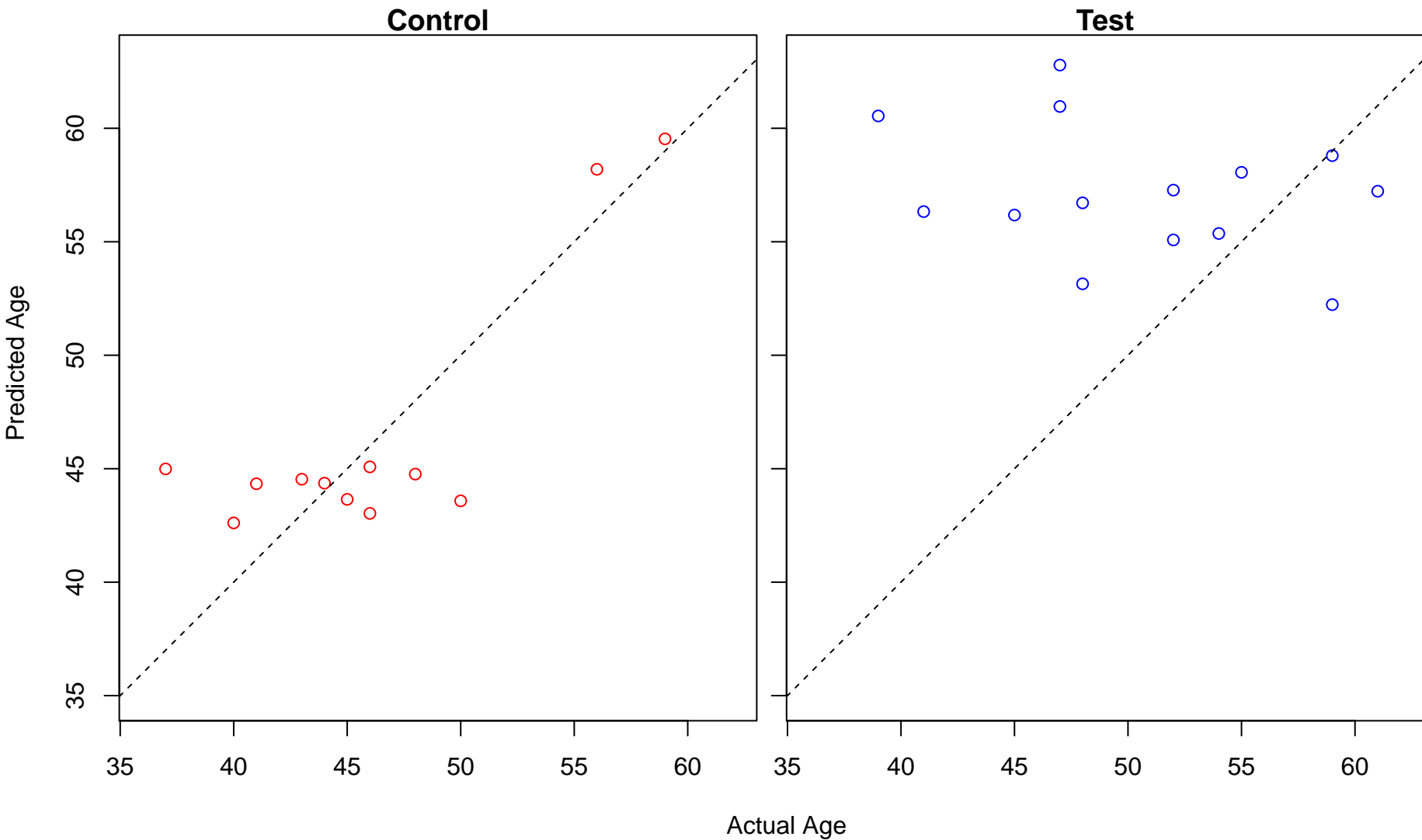
cellular response to peptide hormone stimulus (Score: 3.200579)



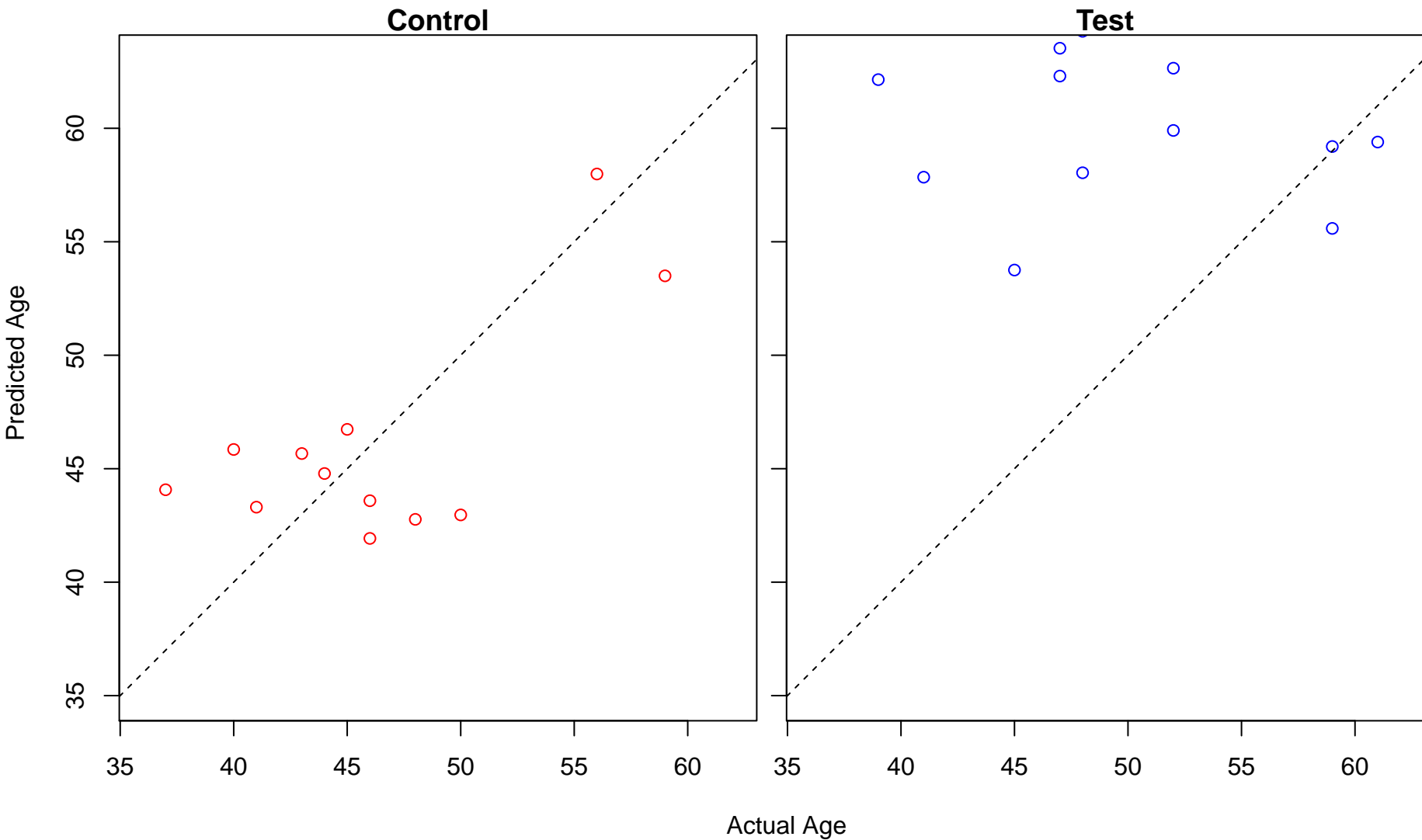
indolalkylamine metabolic process (Score: 3.200097)



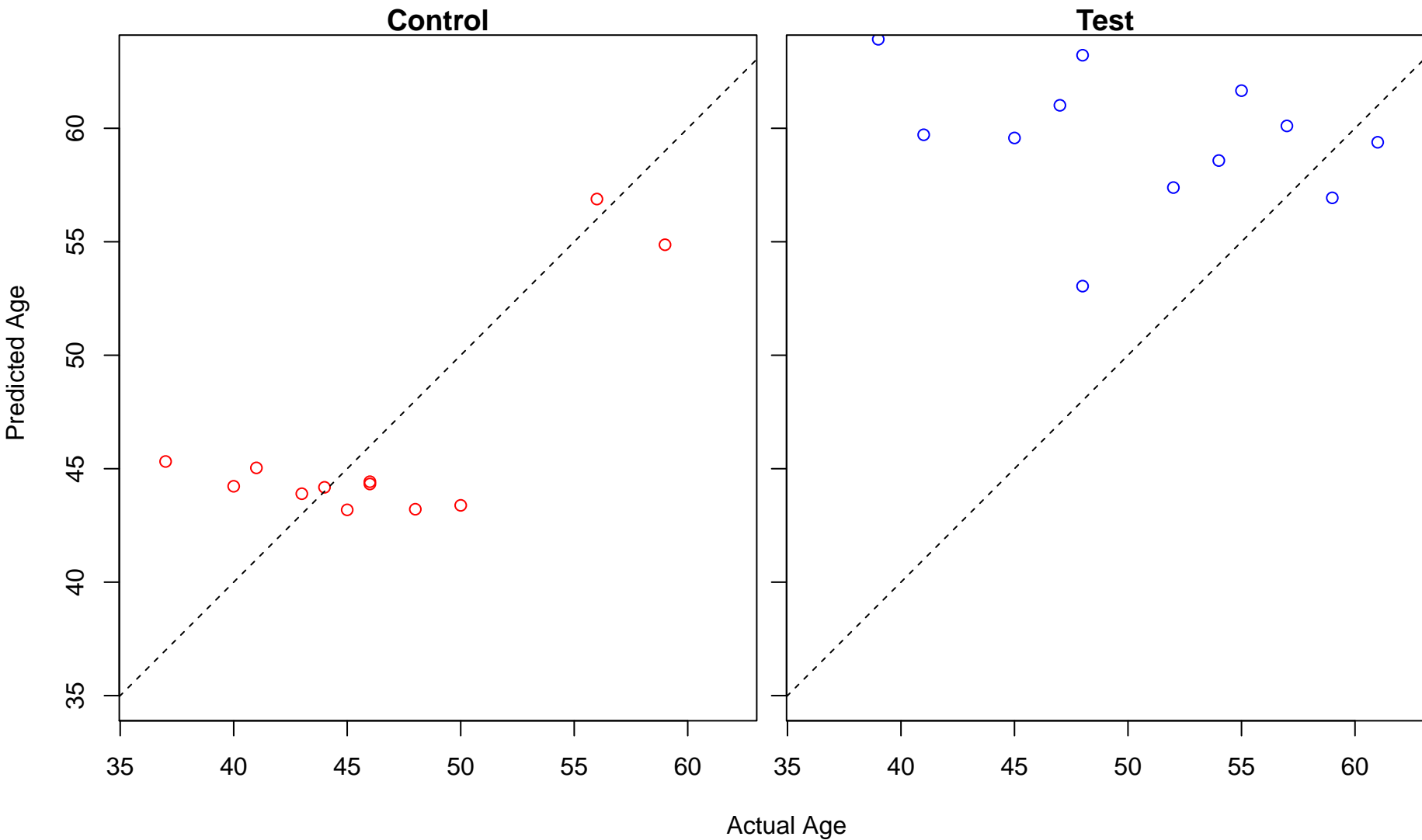
cellular response to peptide (Score: 3.199567)



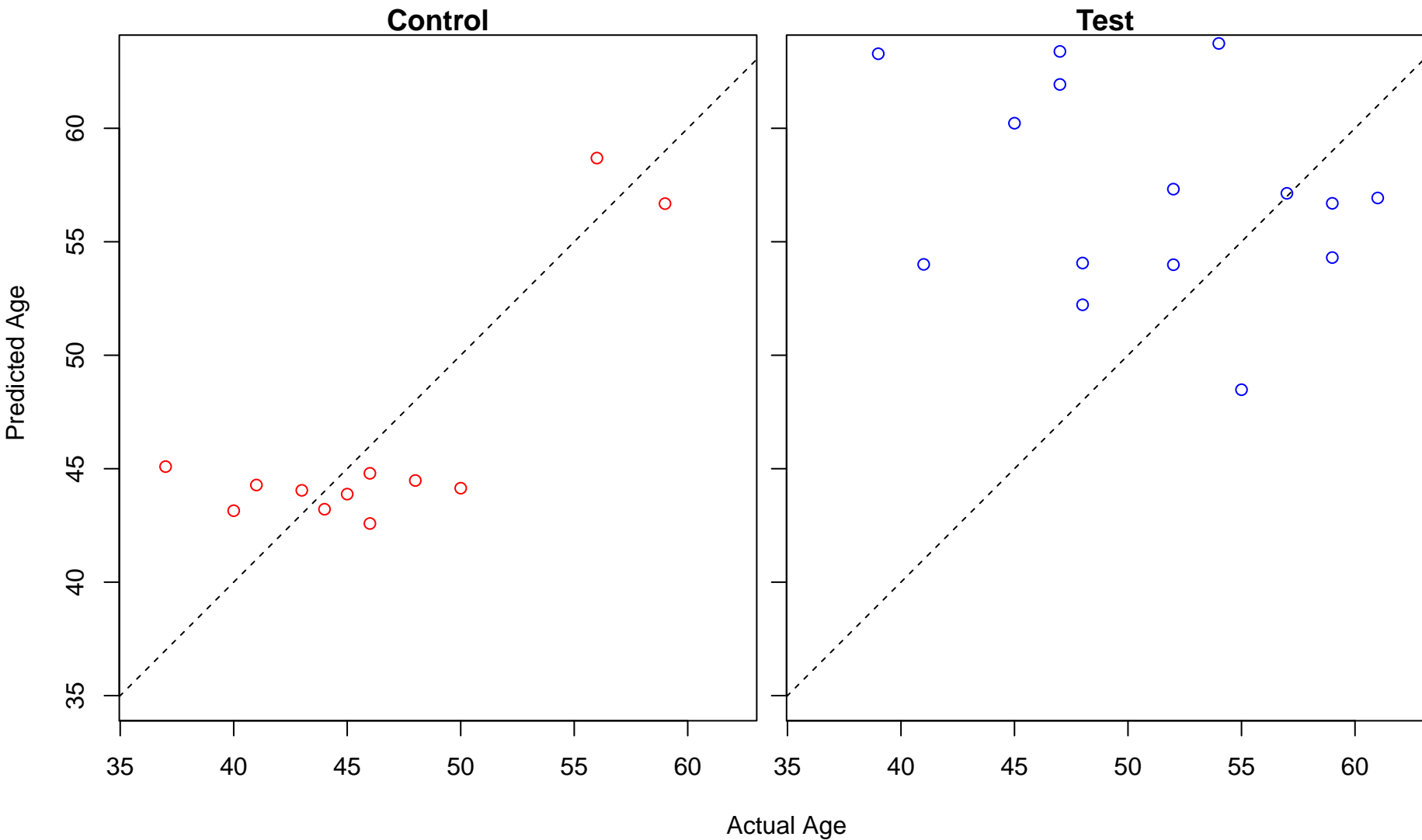
regulation of synaptic transmission, dopaminergic (Score: 3.197930)



indole-containing compound metabolic process (Score: 3.196638)

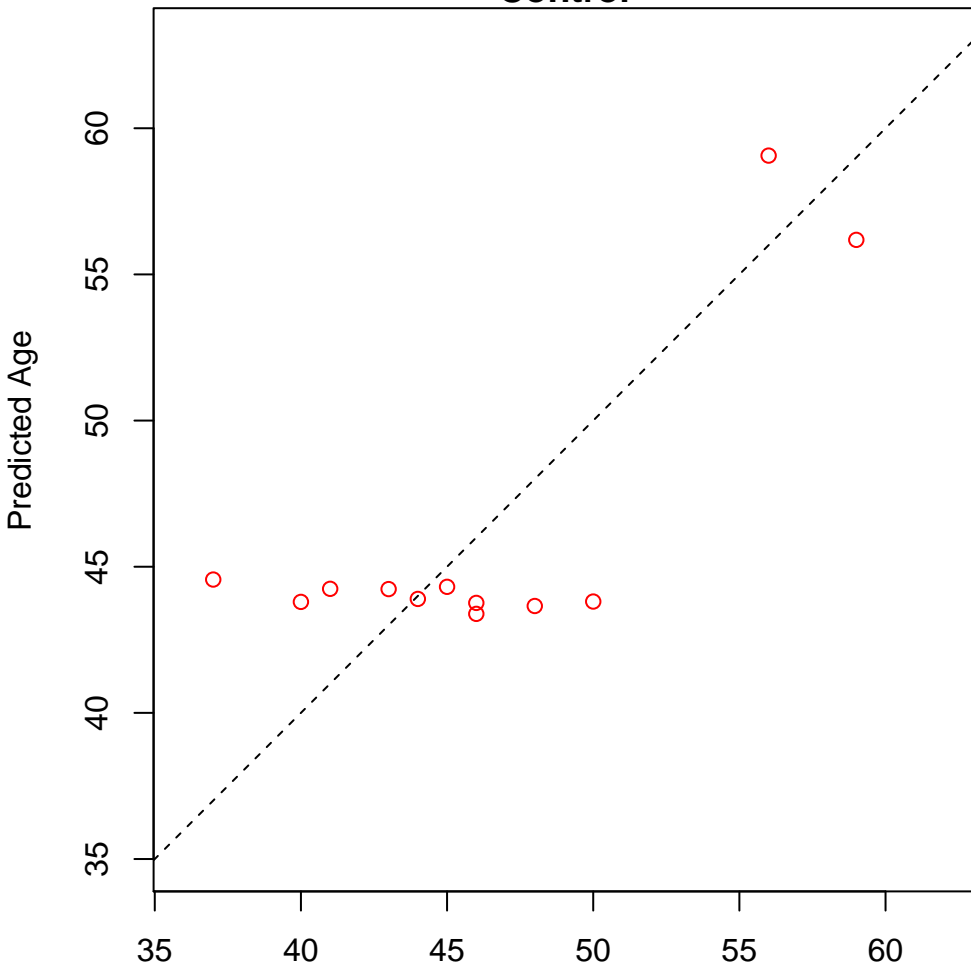


associative learning (Score: 3.195765)

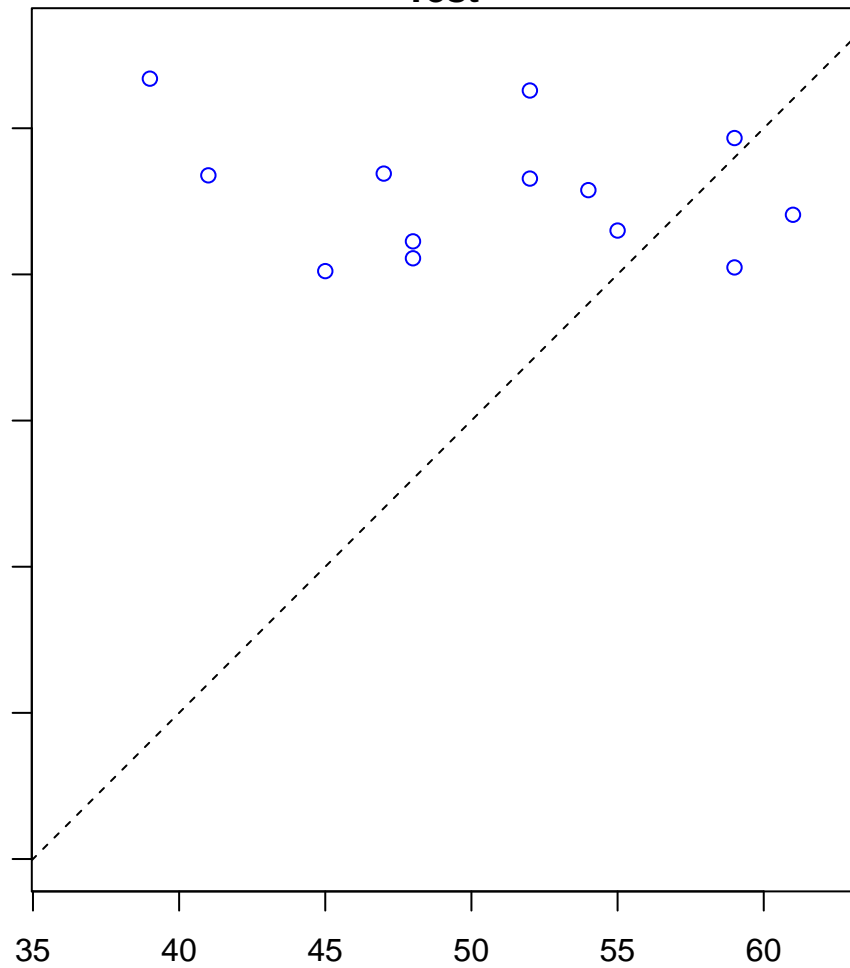


positive regulation of cell cycle process (Score: 3.195386)

Control



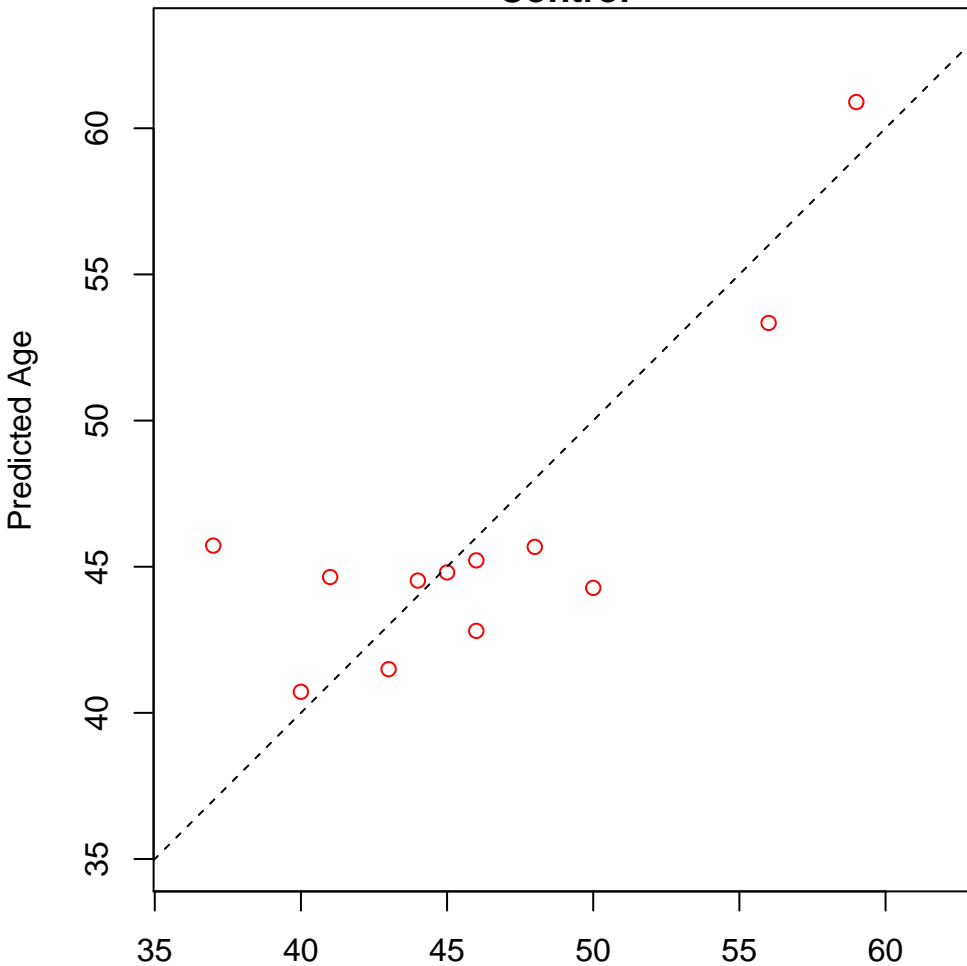
Test



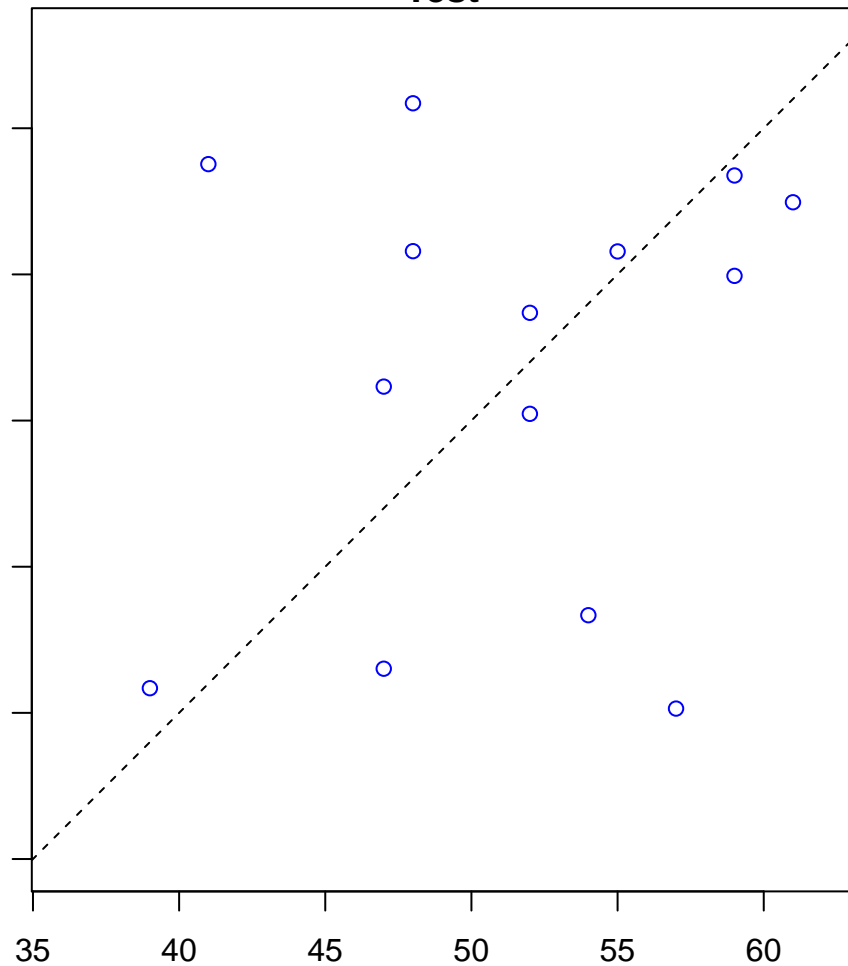
Actual Age

nucleotide-sugar metabolic process (Score: 3.195098)

Control

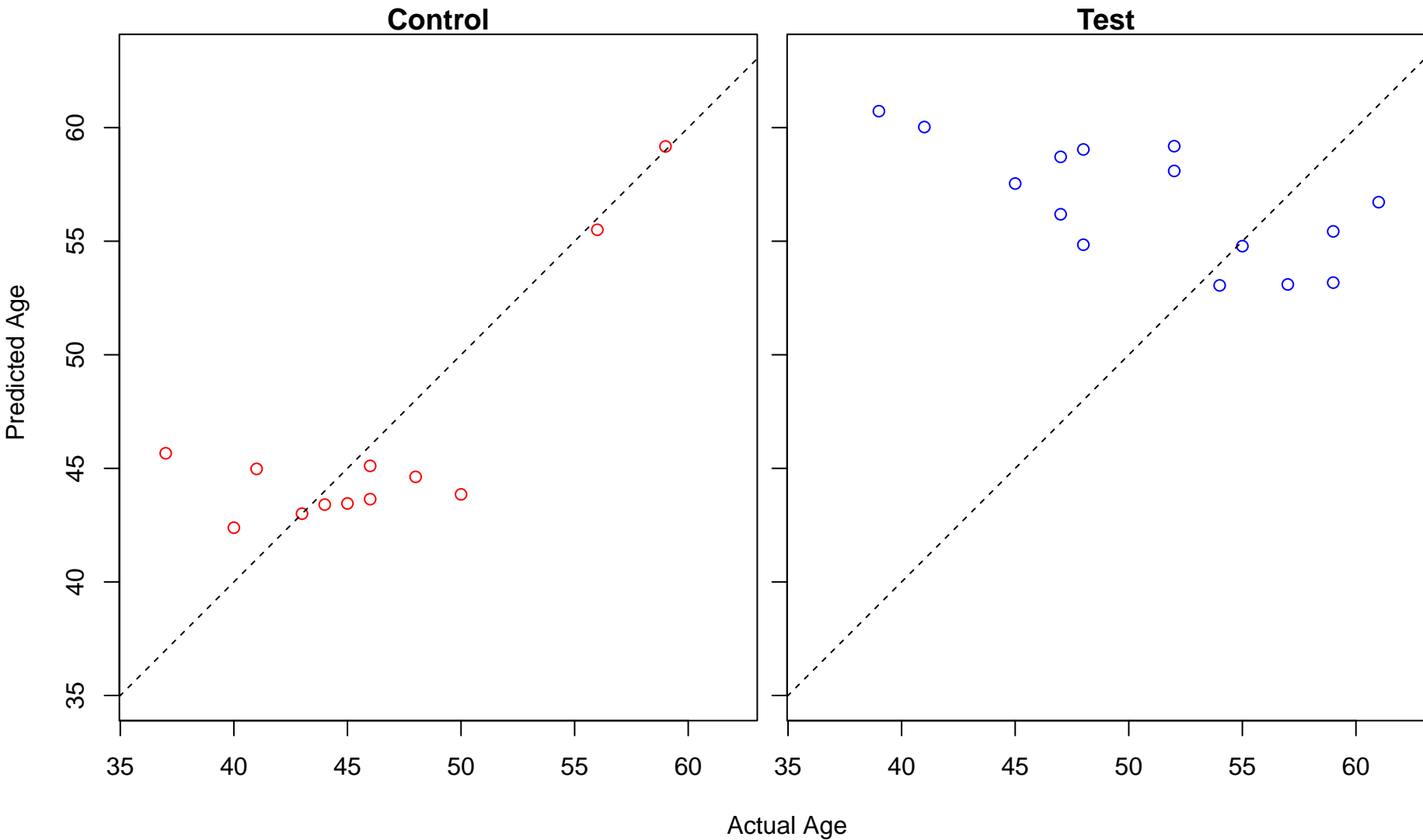


Test

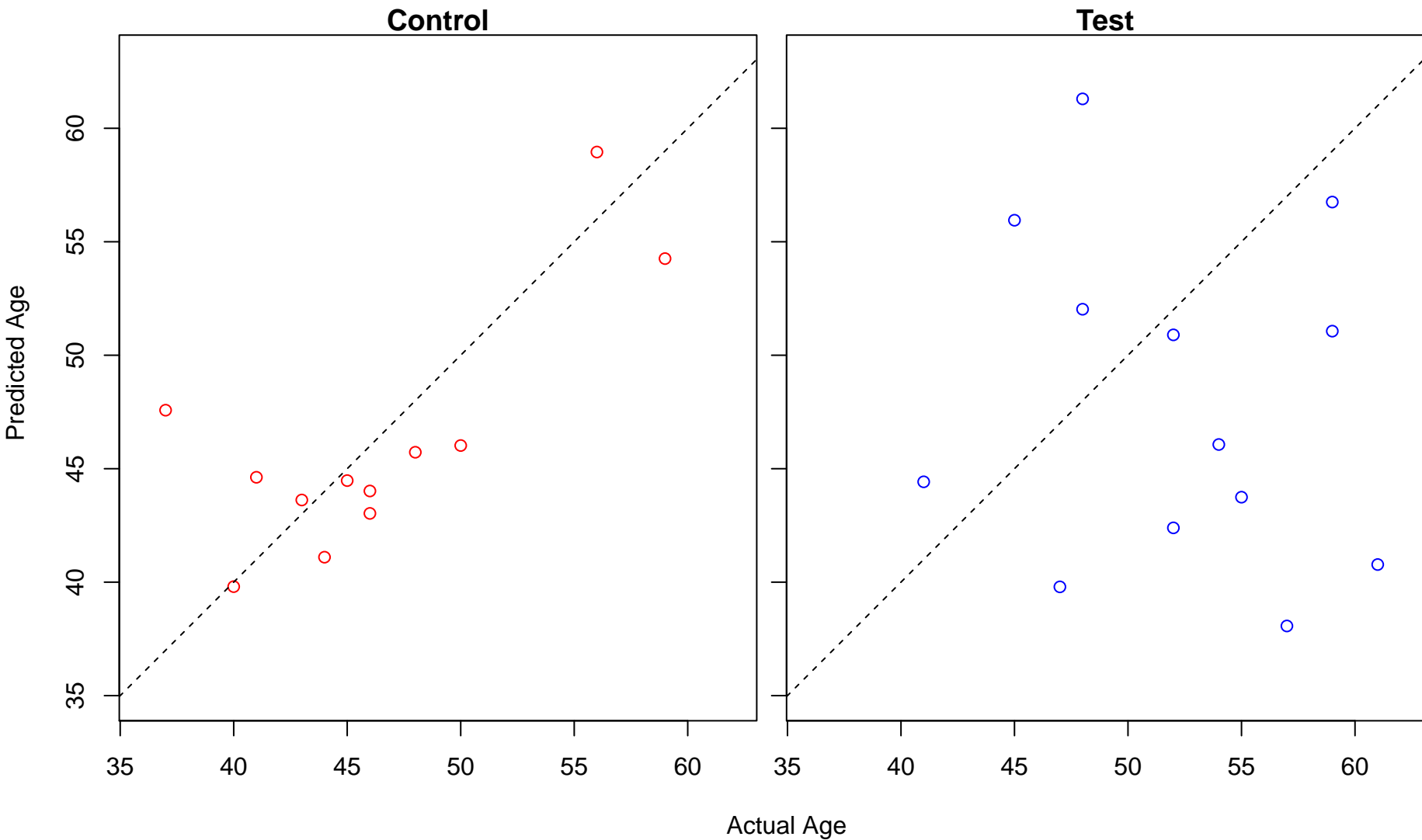


Actual Age

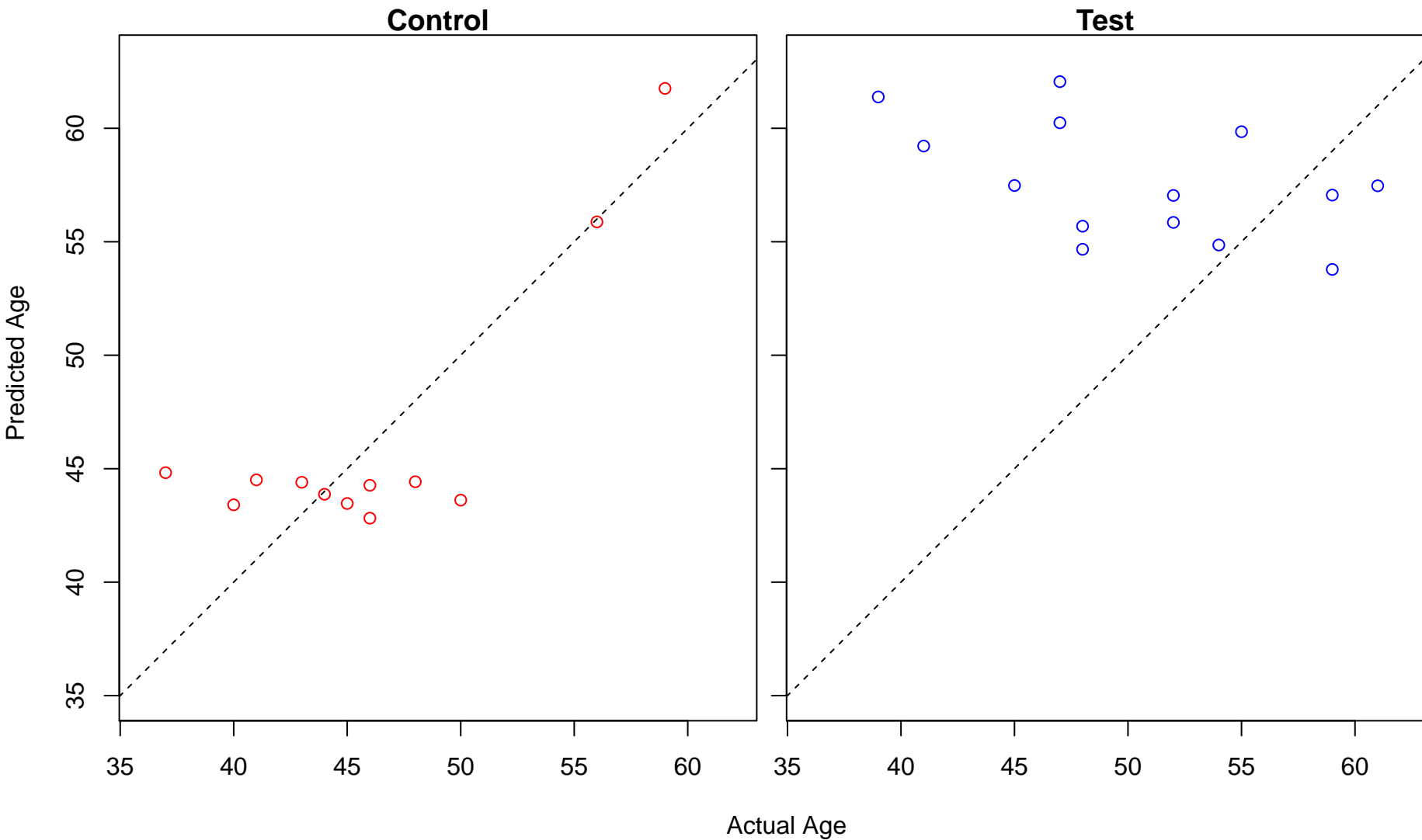
positive regulation of toll-like receptor signaling pathway (Score: 3.194356)



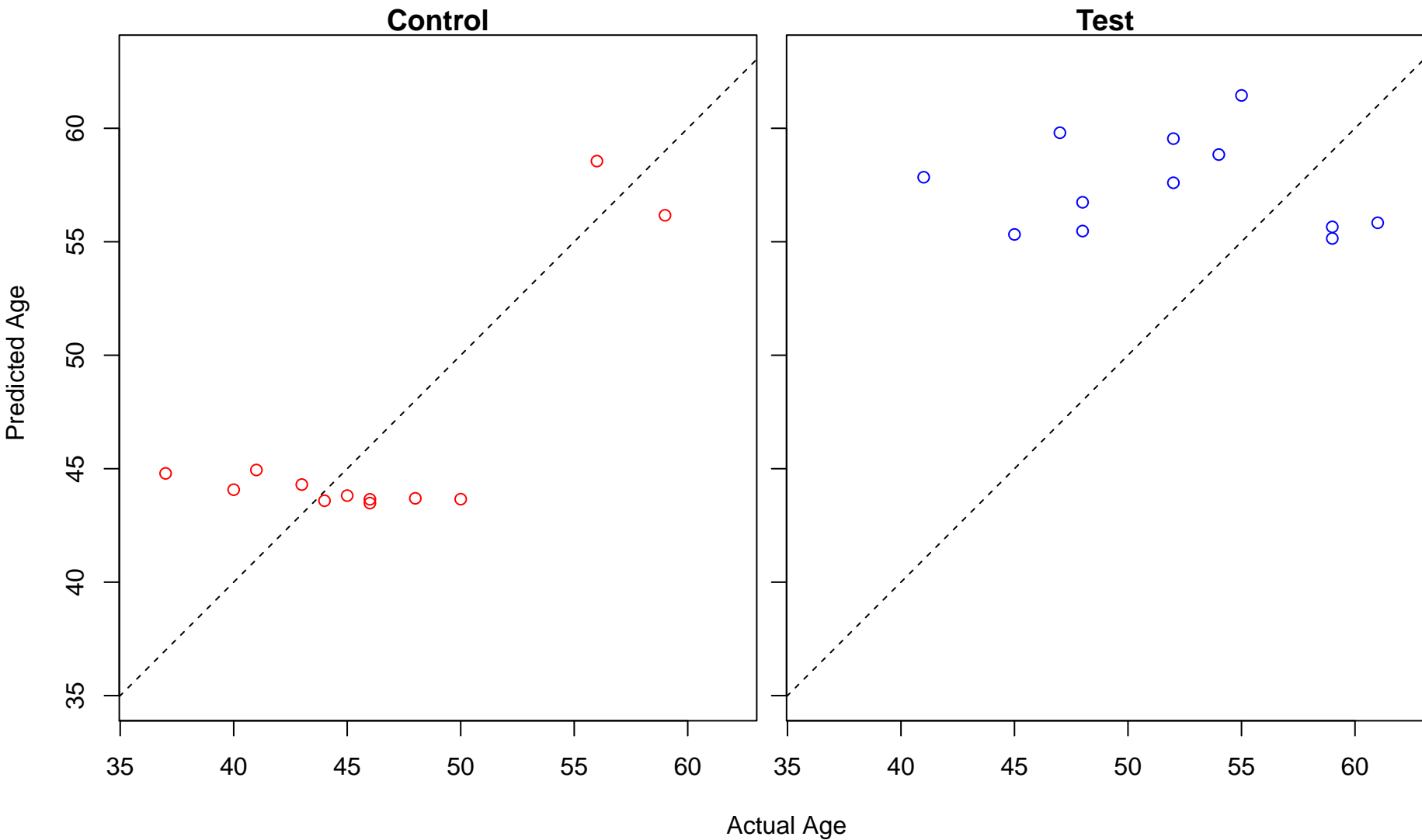
cardioblast differentiation (Score: 3.191508)



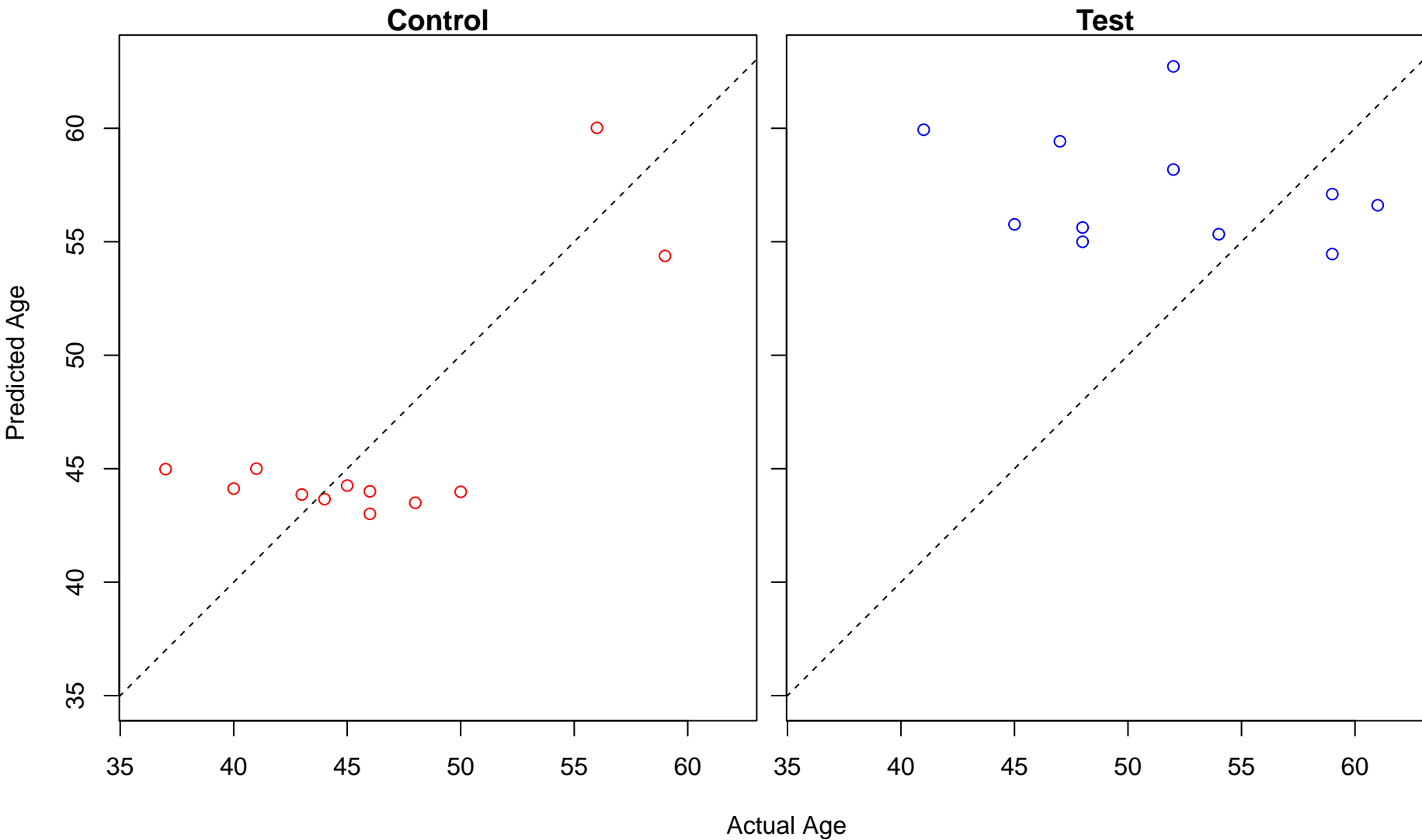
generation of precursor metabolites and energy (Score: 3.190845)



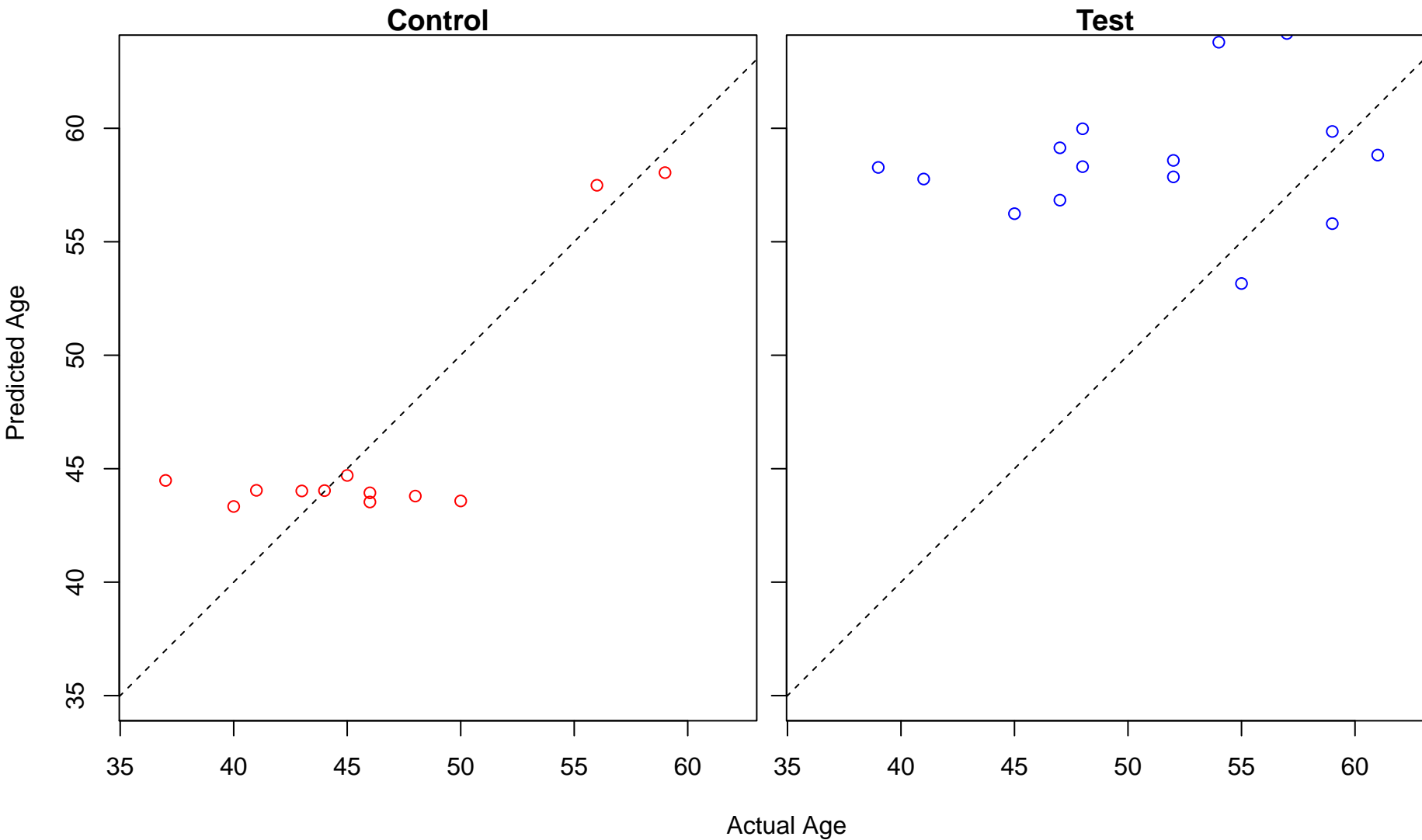
tissue homeostasis (Score: 3.189907)



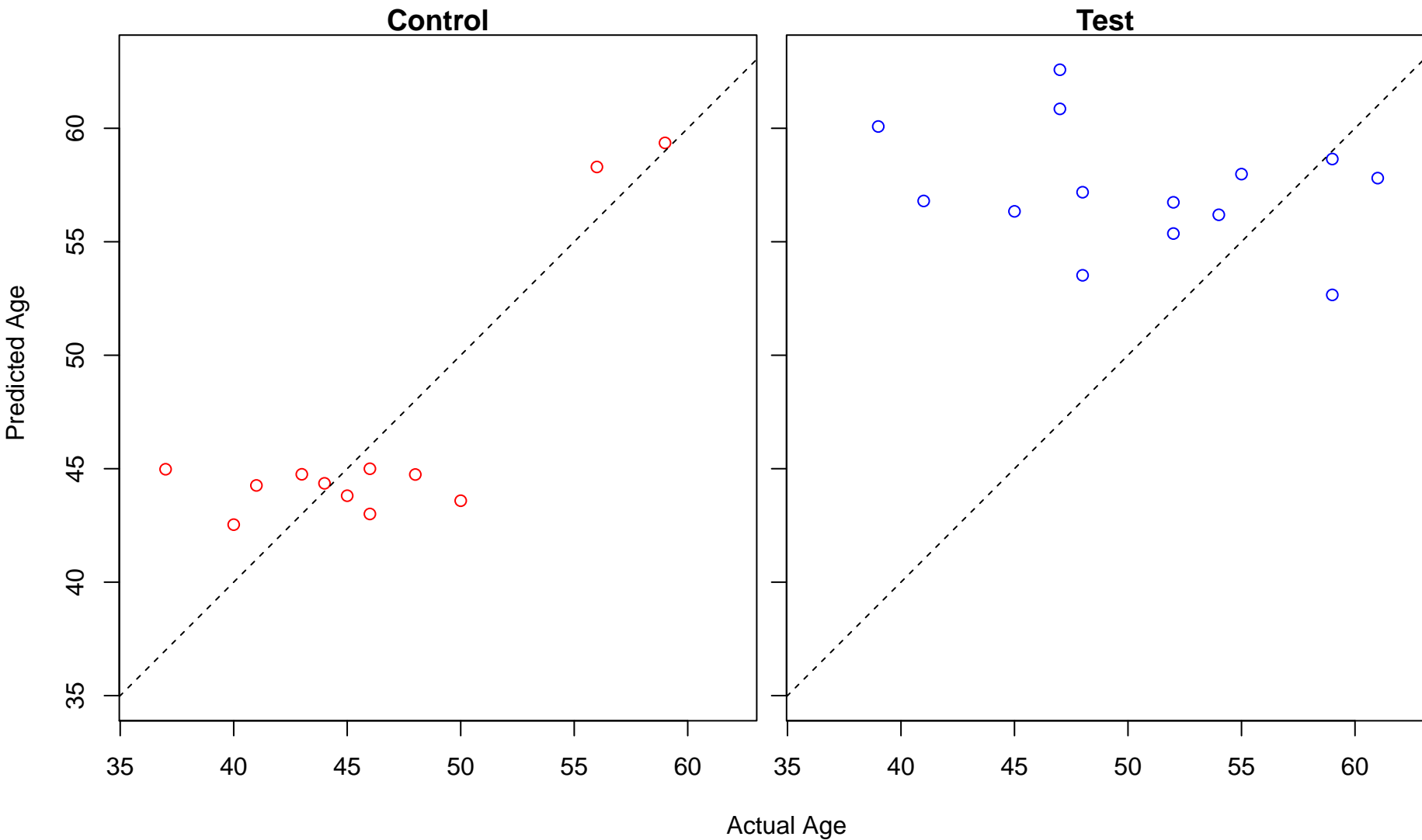
defense response to other organism (Score: 3.187999)



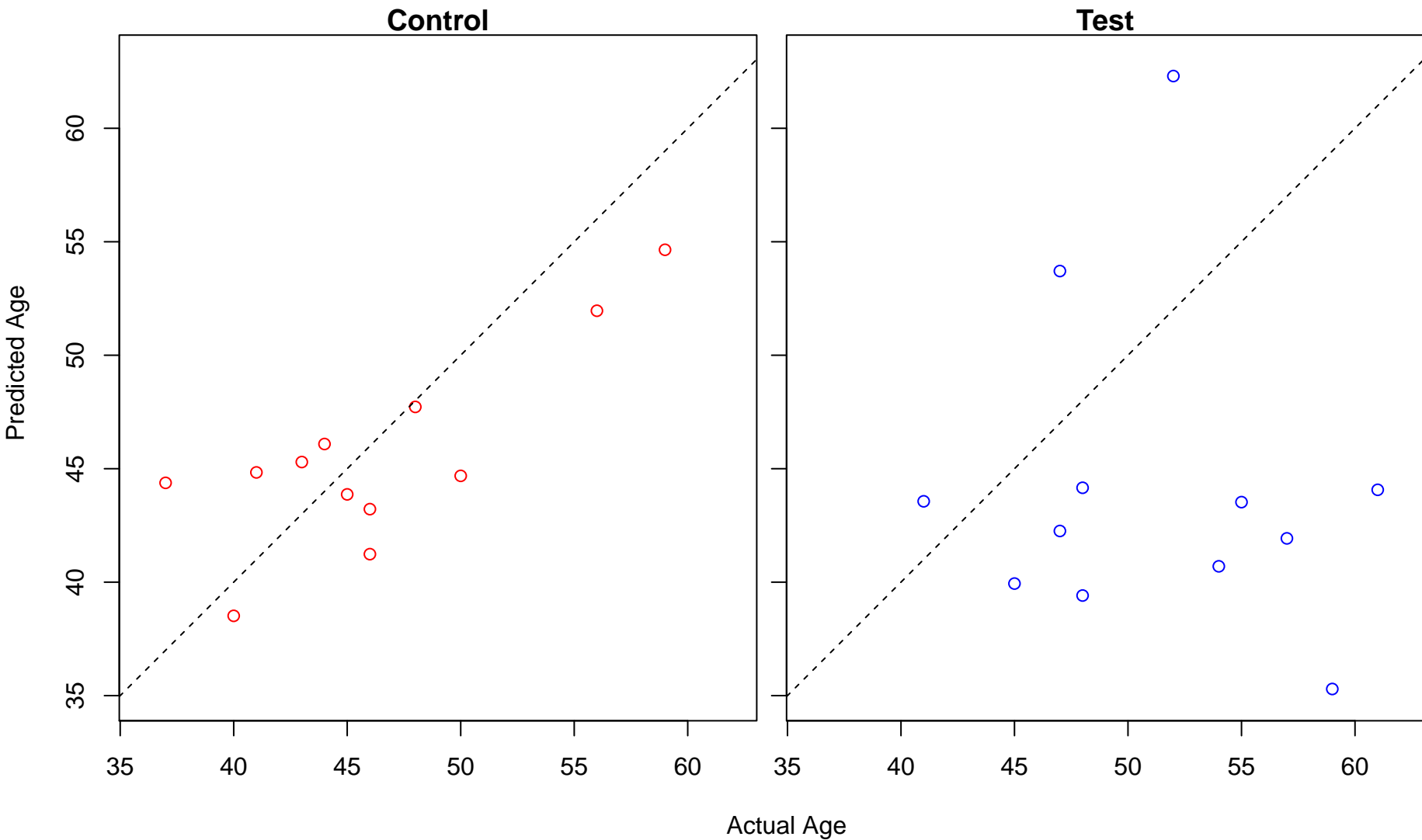
mitochondrial fusion (Score: 3.185140)



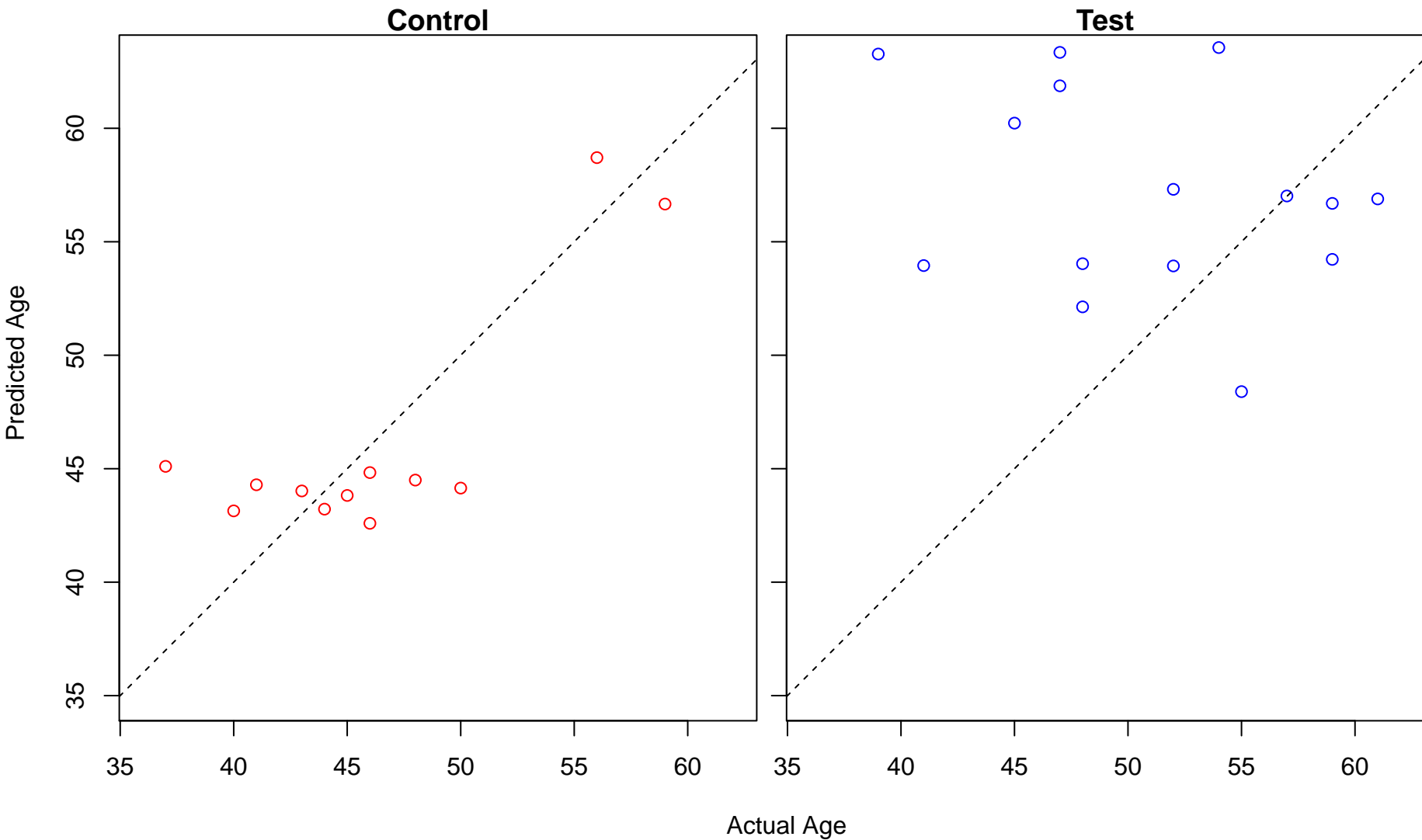
response to peptide hormone (Score: 3.184399)



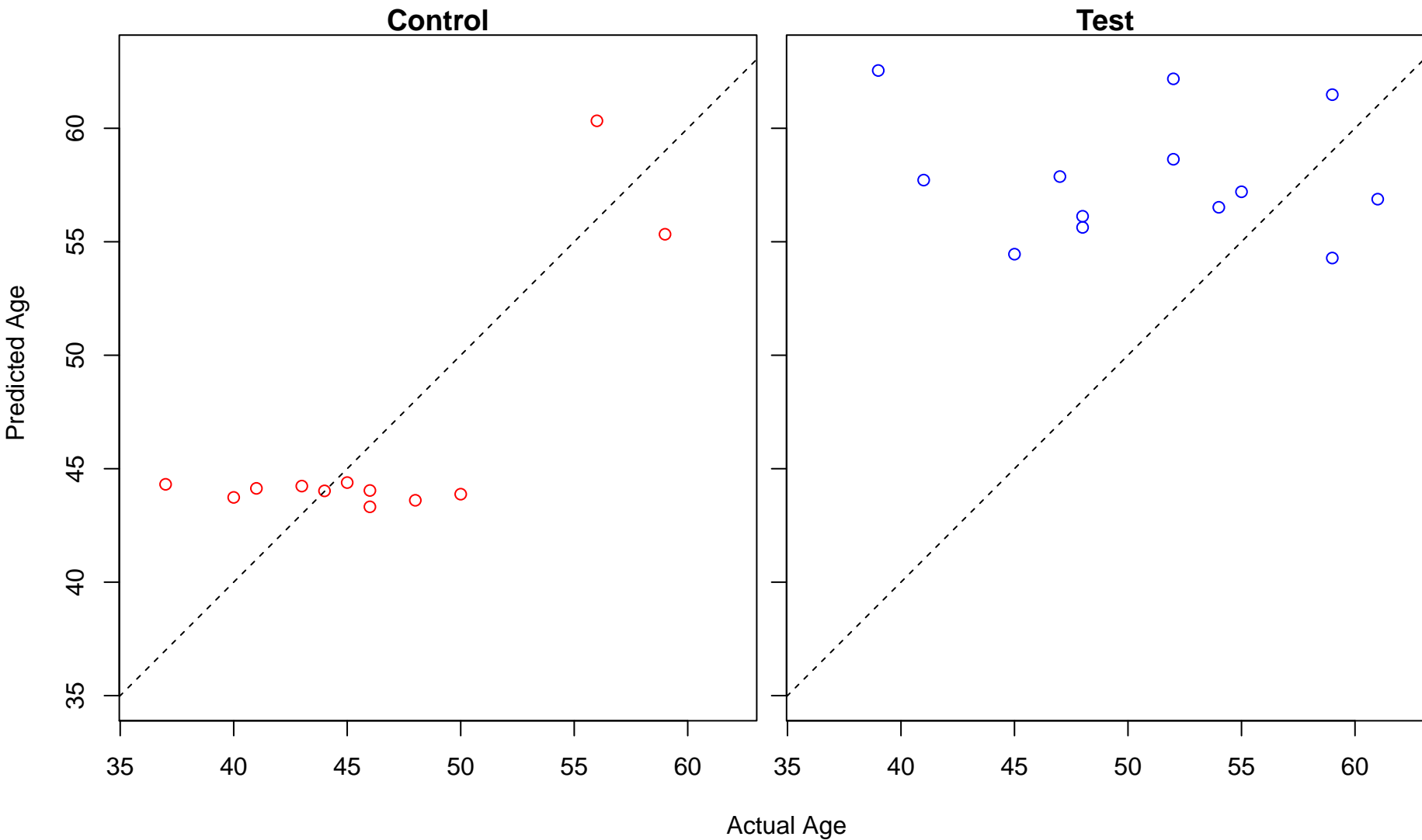
nucleobase-containing compound catabolic process (Score: 3.183164)



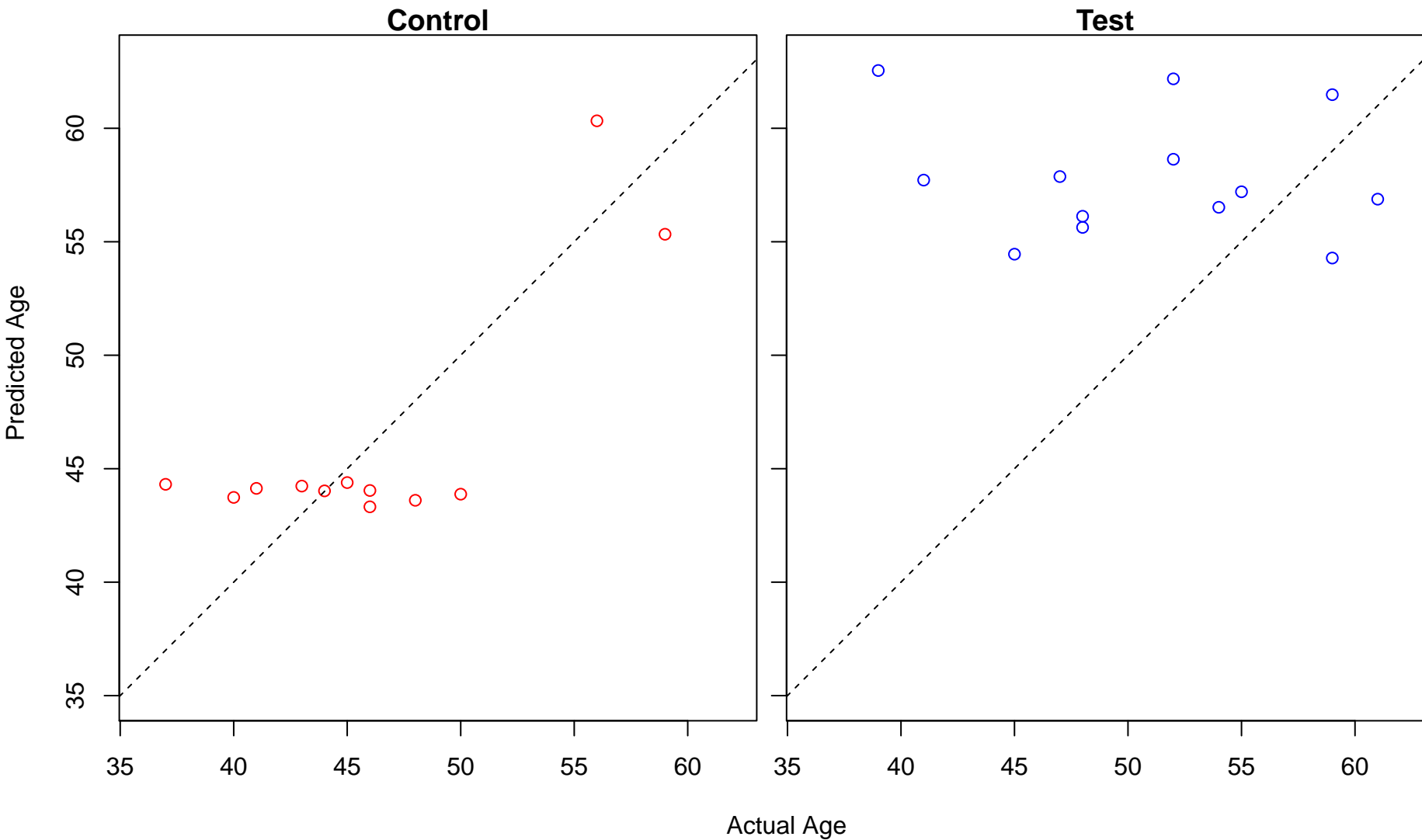
visual learning (Score: 3.182045)



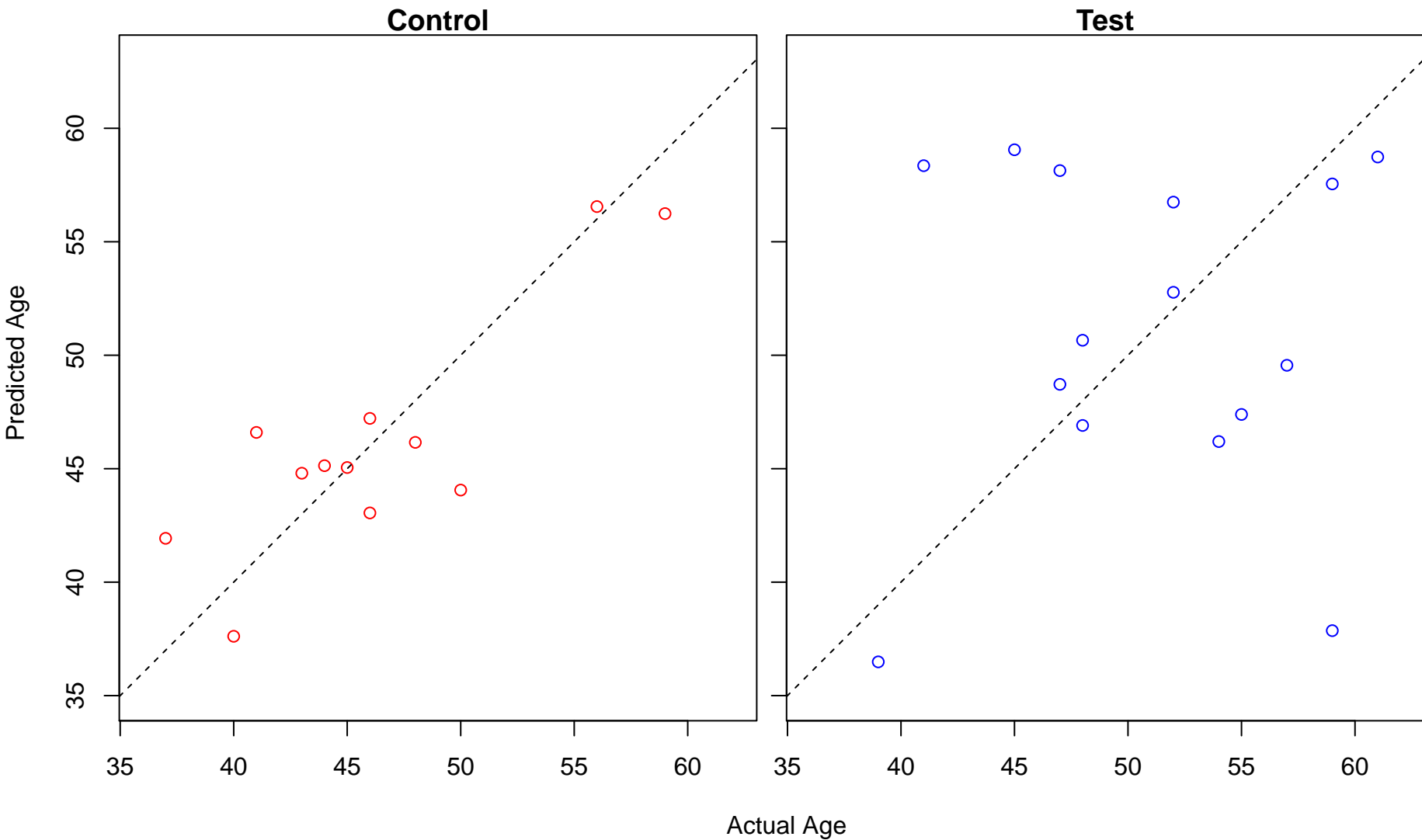
negative regulation of transforming growth factor beta receptor signaling pathway (Score: 3.17719)



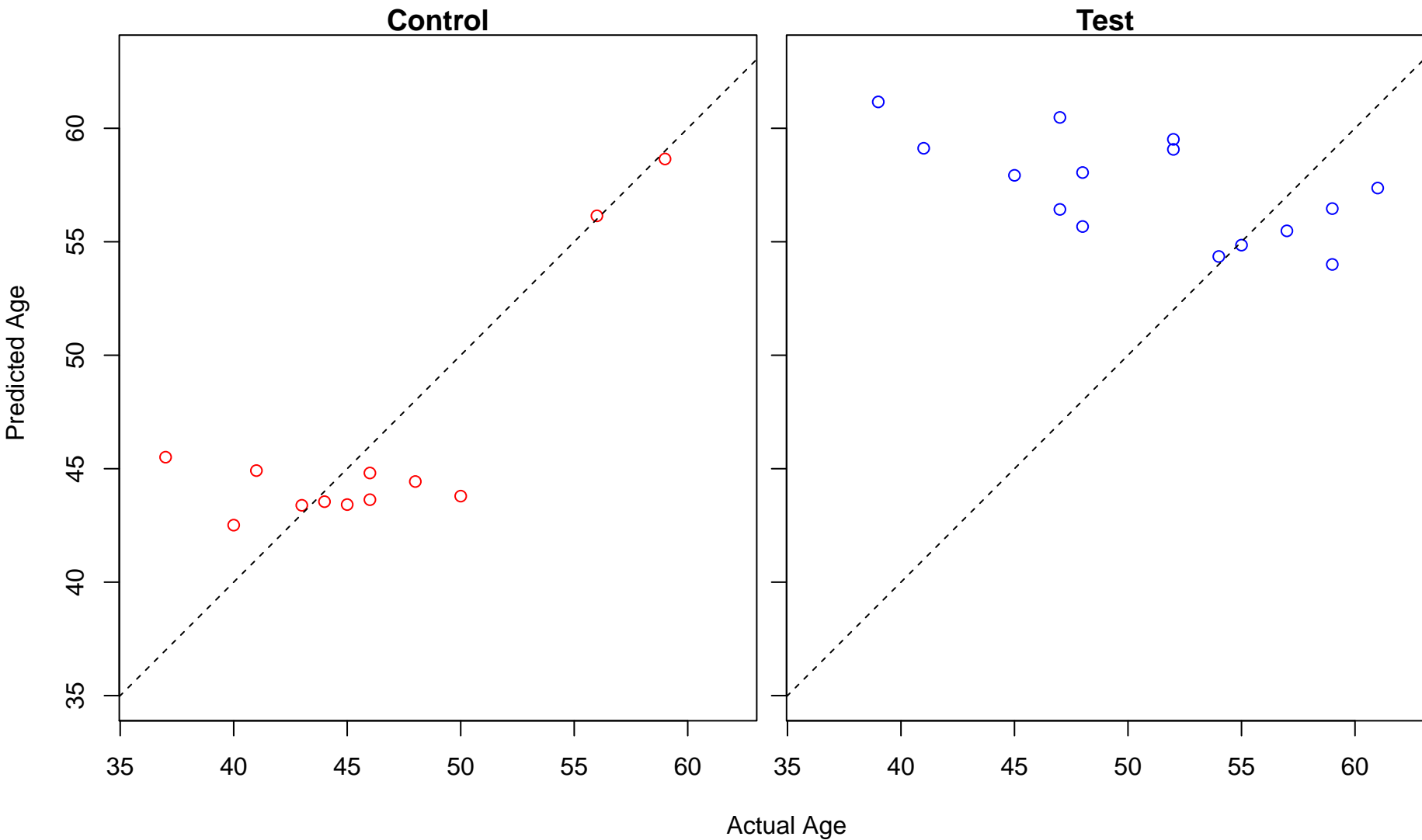
negative regulation of cellular response to transforming growth factor beta stimulus (Score: 3.17719)



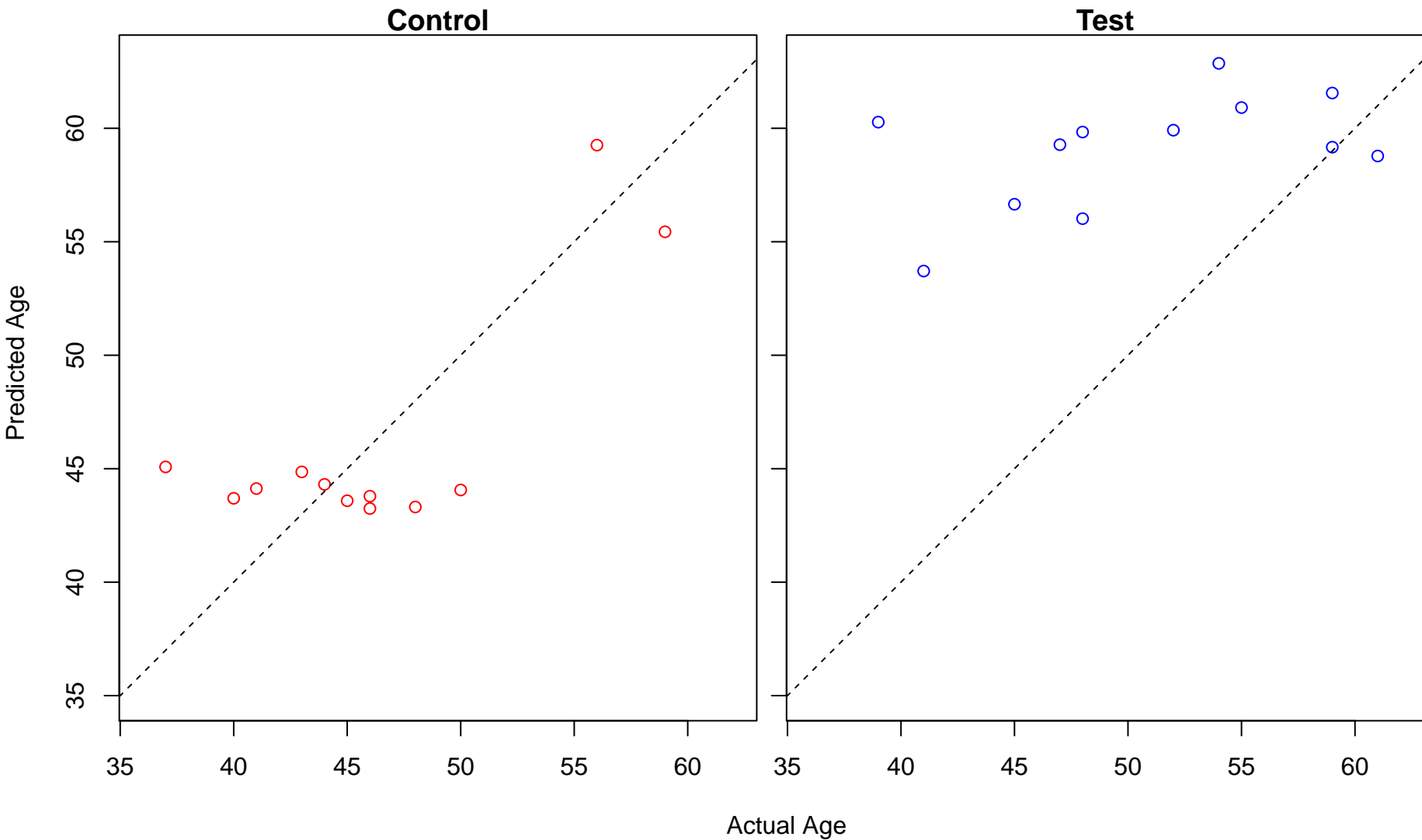
regulation of leukocyte proliferation (Score: 3.174445)



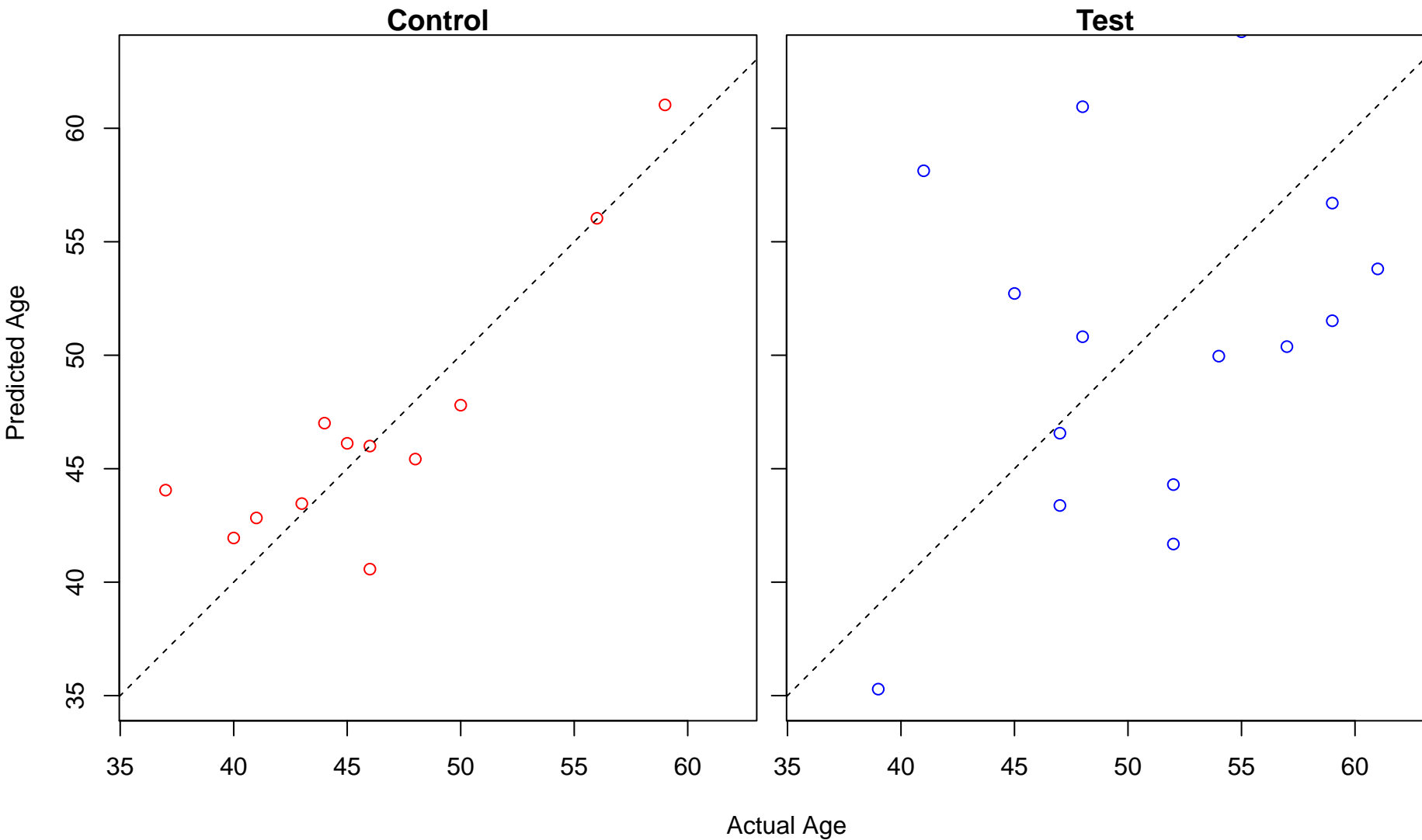
positive regulation of interleukin-6 secretion (Score: 3.173164)



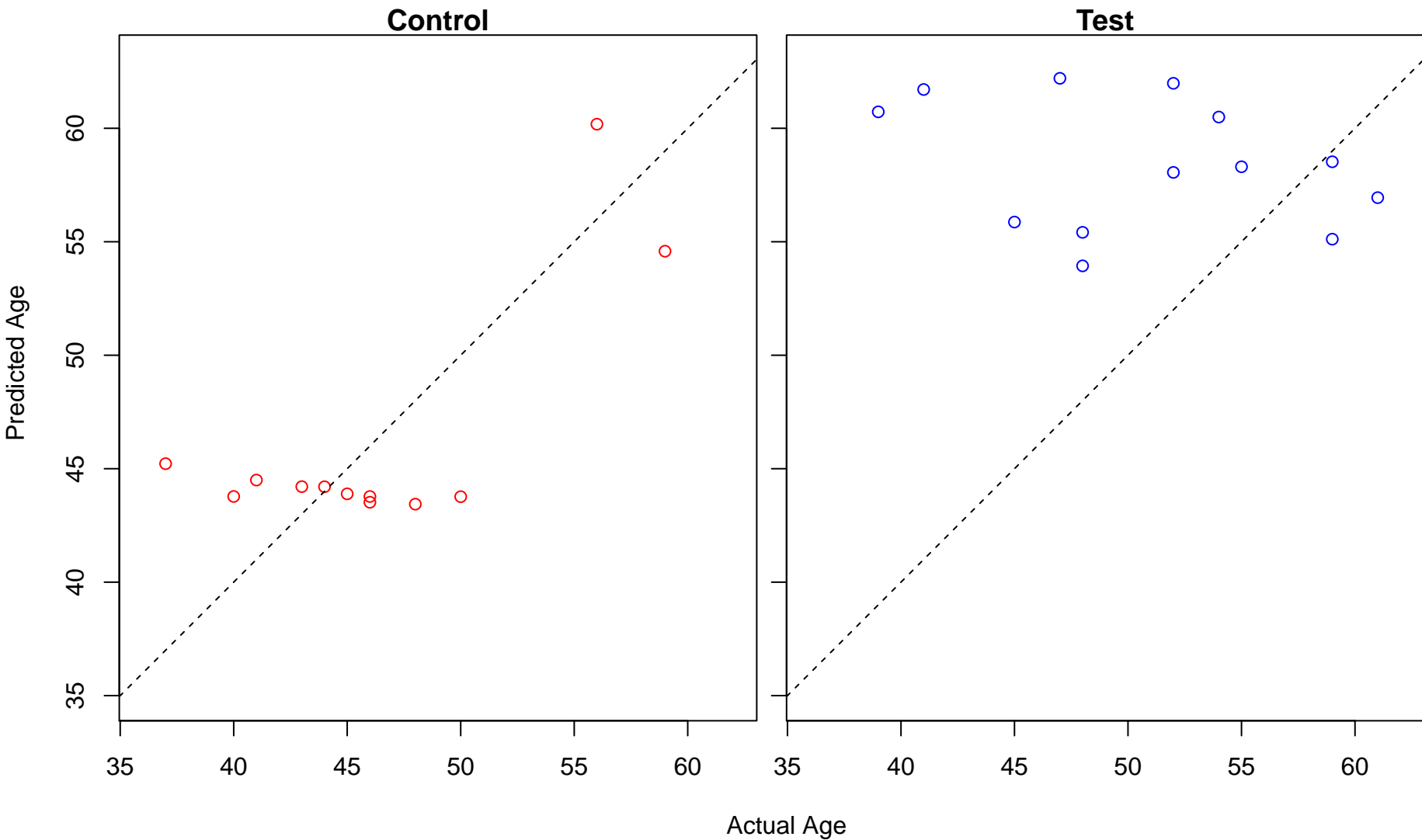
epithelial cell proliferation (Score: 3.172570)



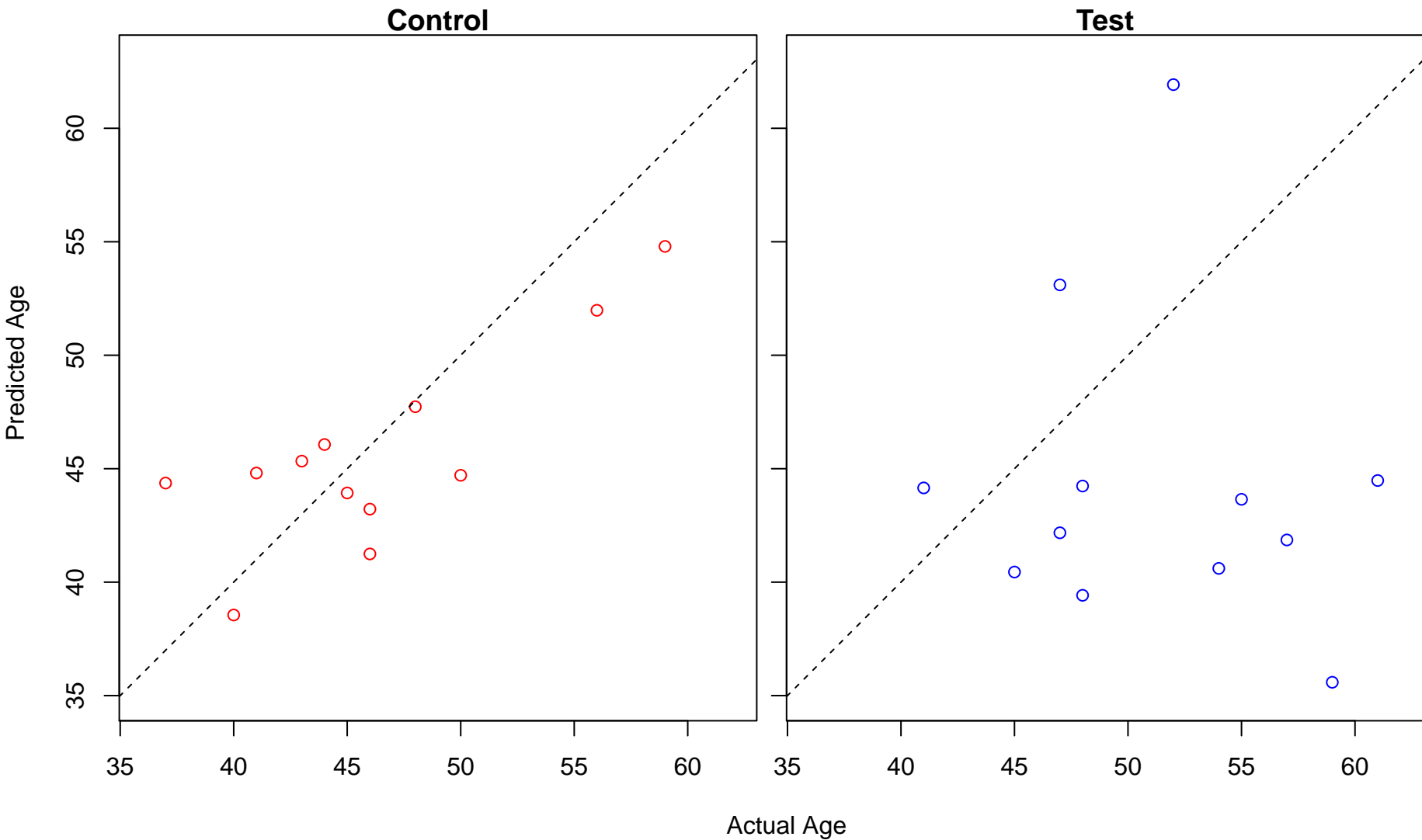
phagocytosis (Score: 3.168514)



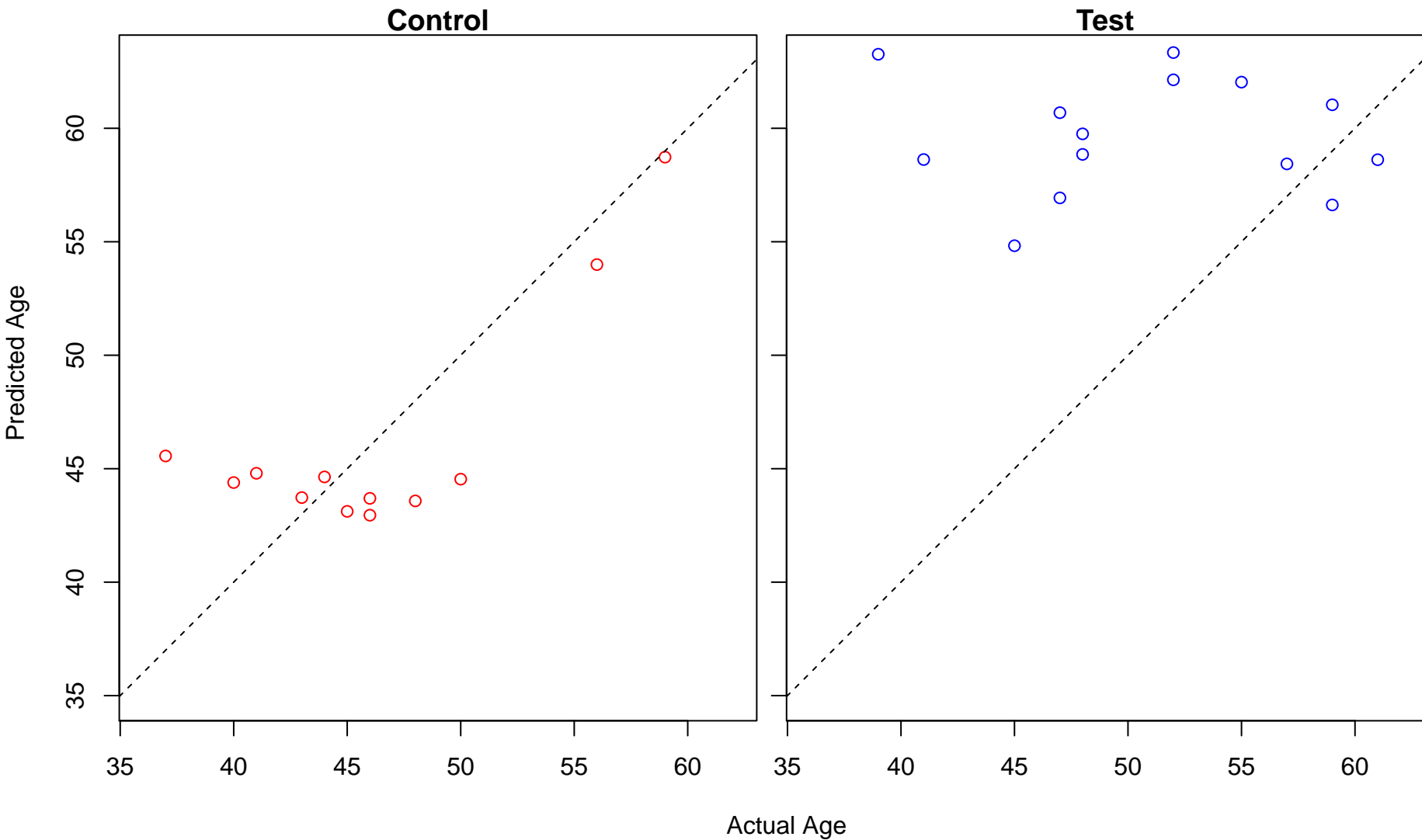
regulation of extrinsic apoptotic signaling pathway via death domain receptors (Score: 3.168073)



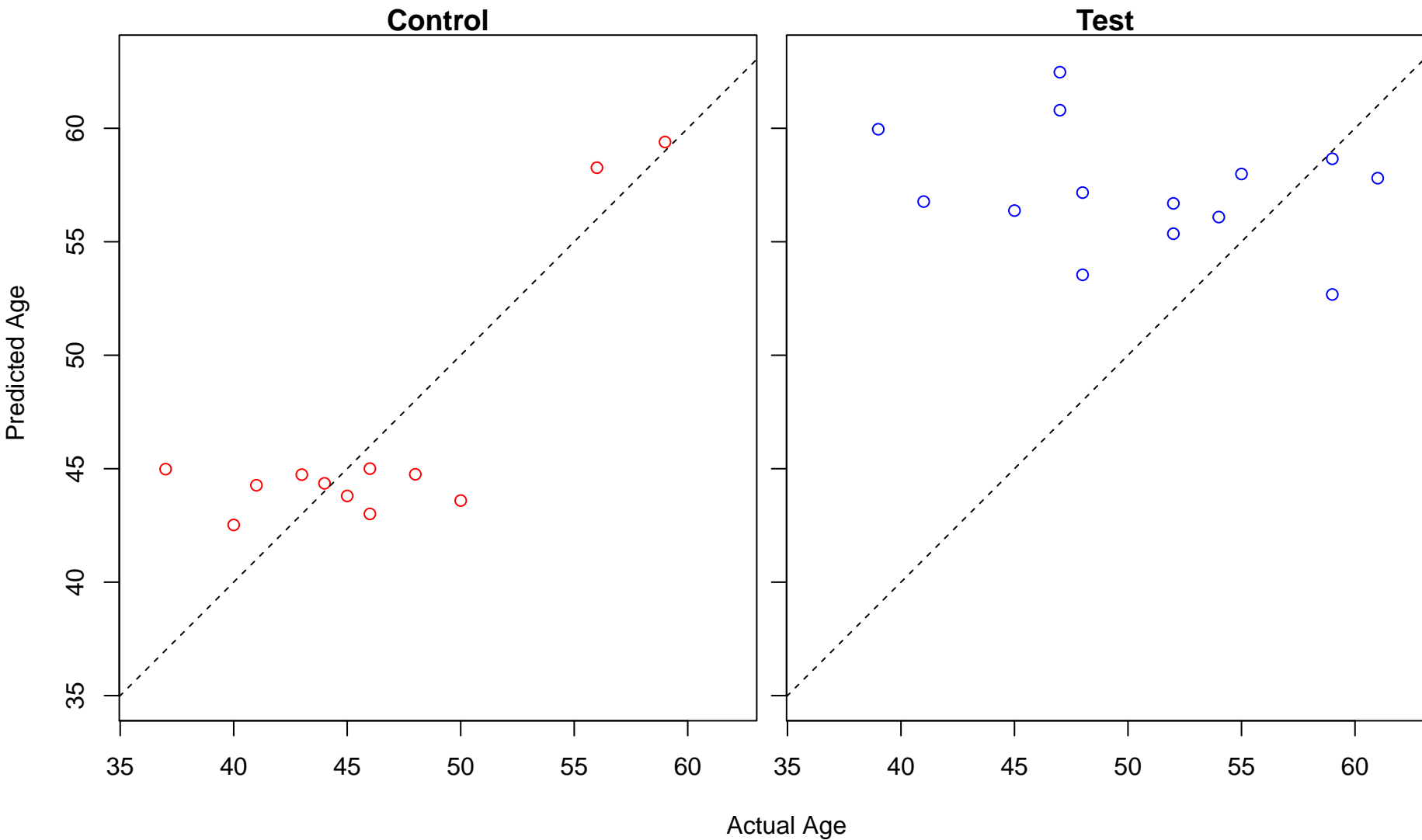
heterocycle catabolic process (Score: 3.167165)



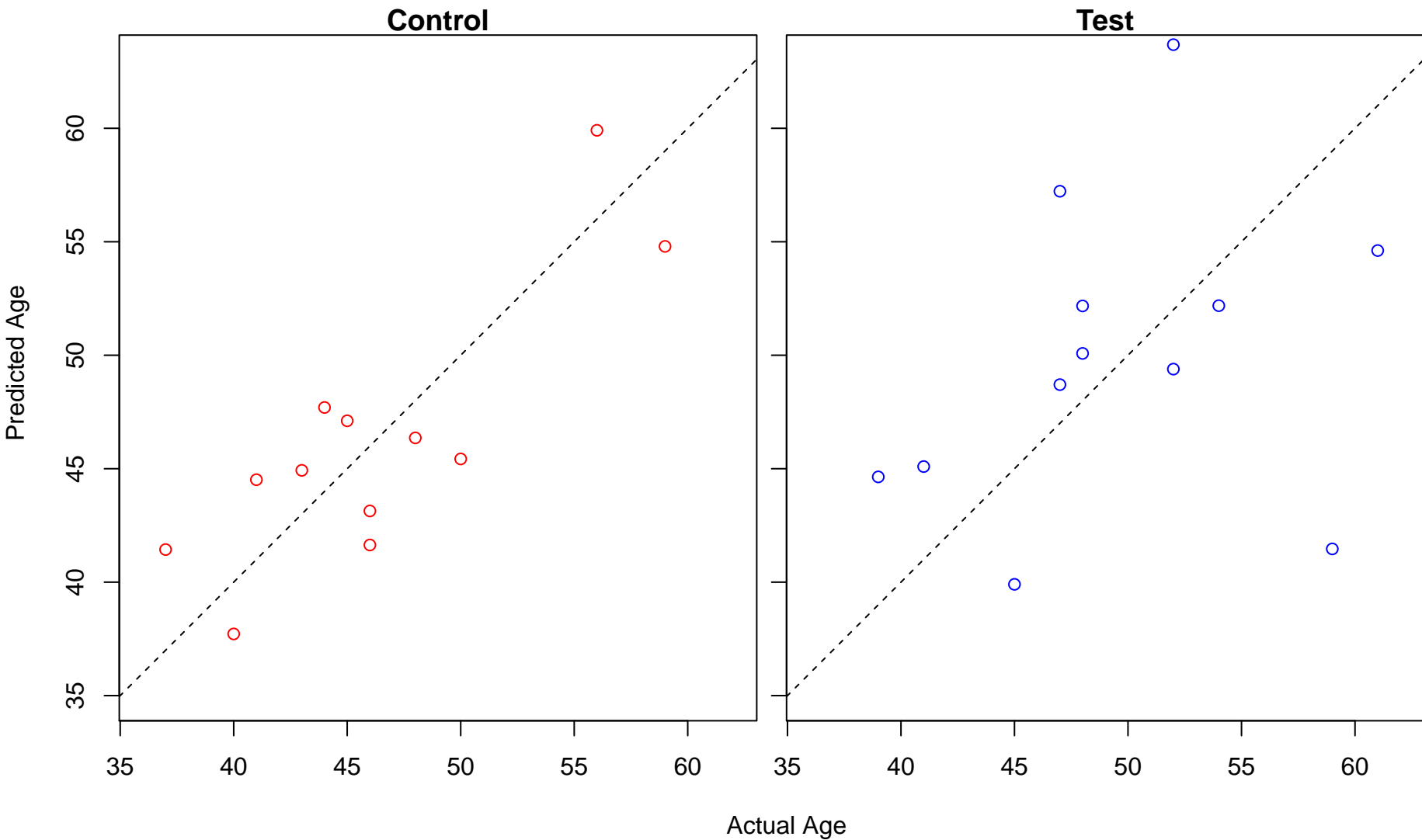
negative regulation of platelet-derived growth factor receptor signaling pathway (Score: 3.166104)



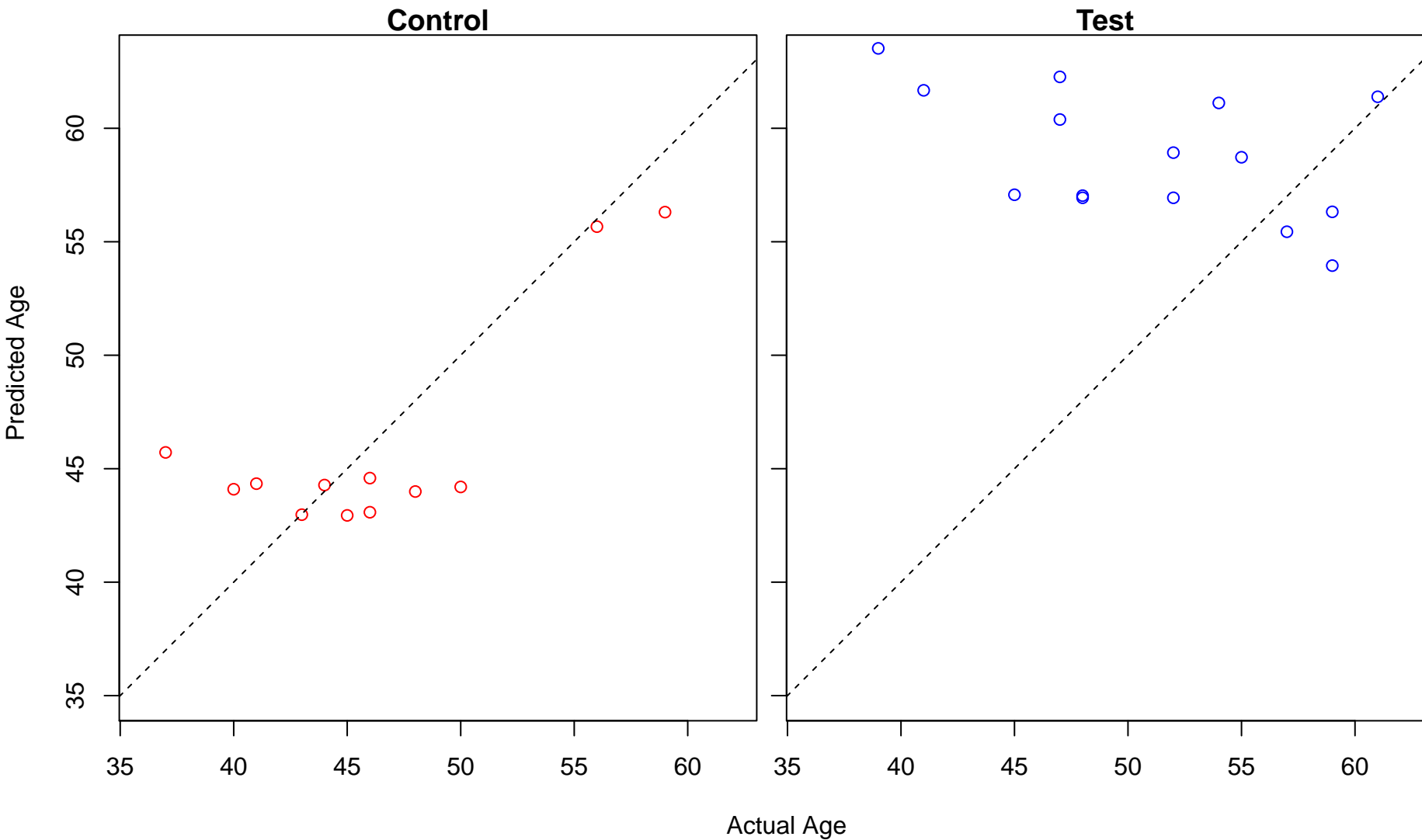
response to peptide (Score: 3.165540)



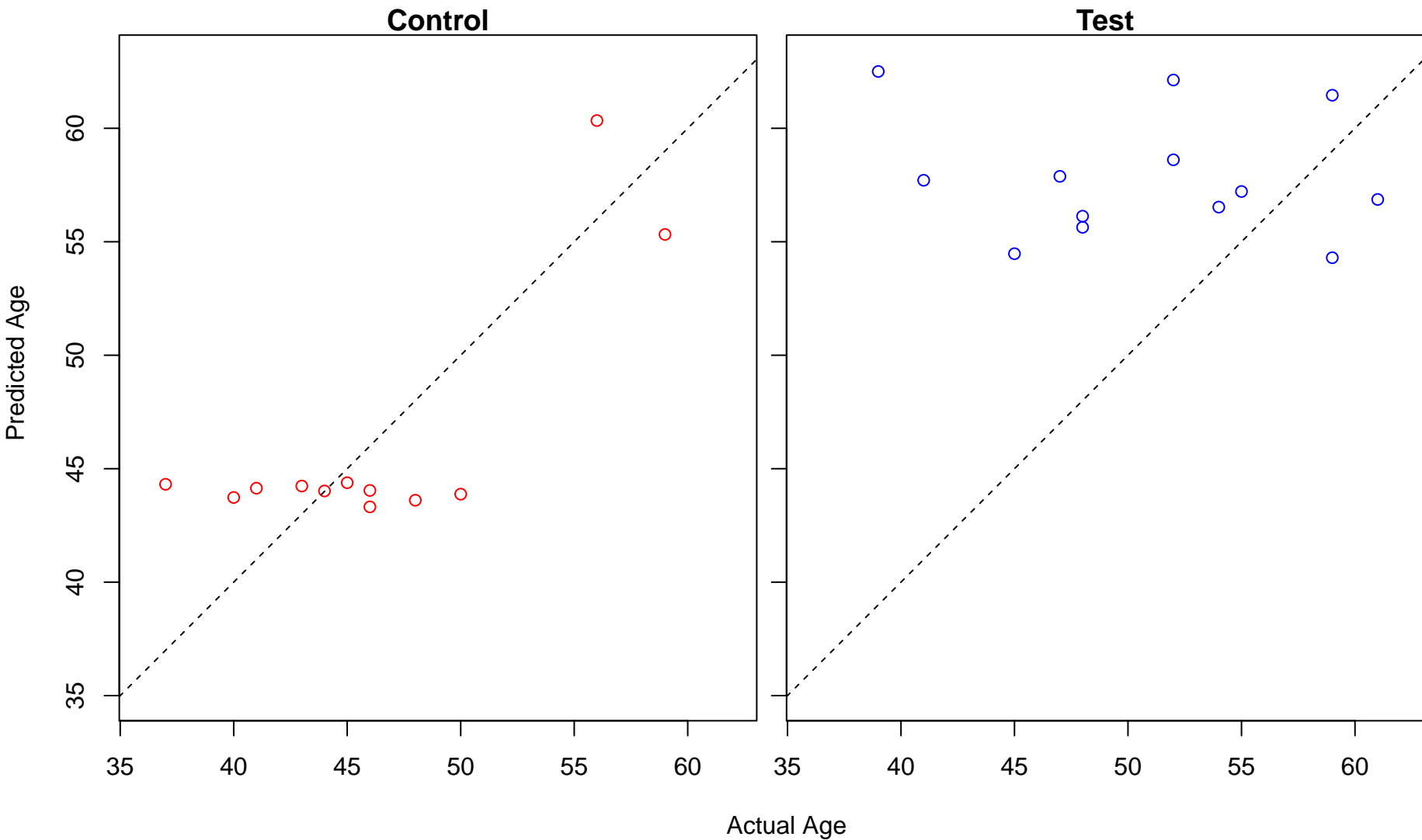
positive regulation of mitotic cell cycle phase transition (Score: 3.165096)



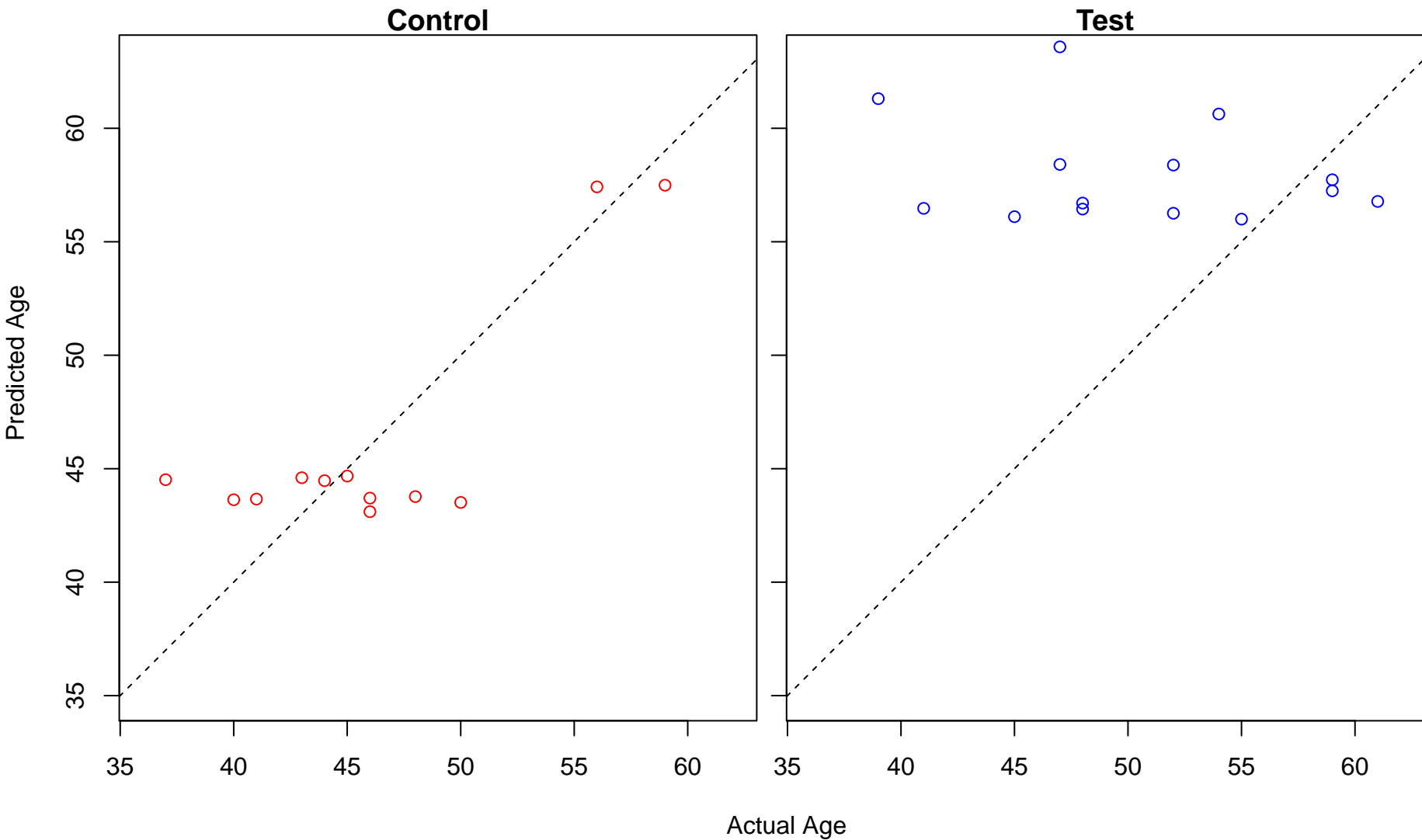
syncytium formation by plasma membrane fusion (Score: 3.164102)



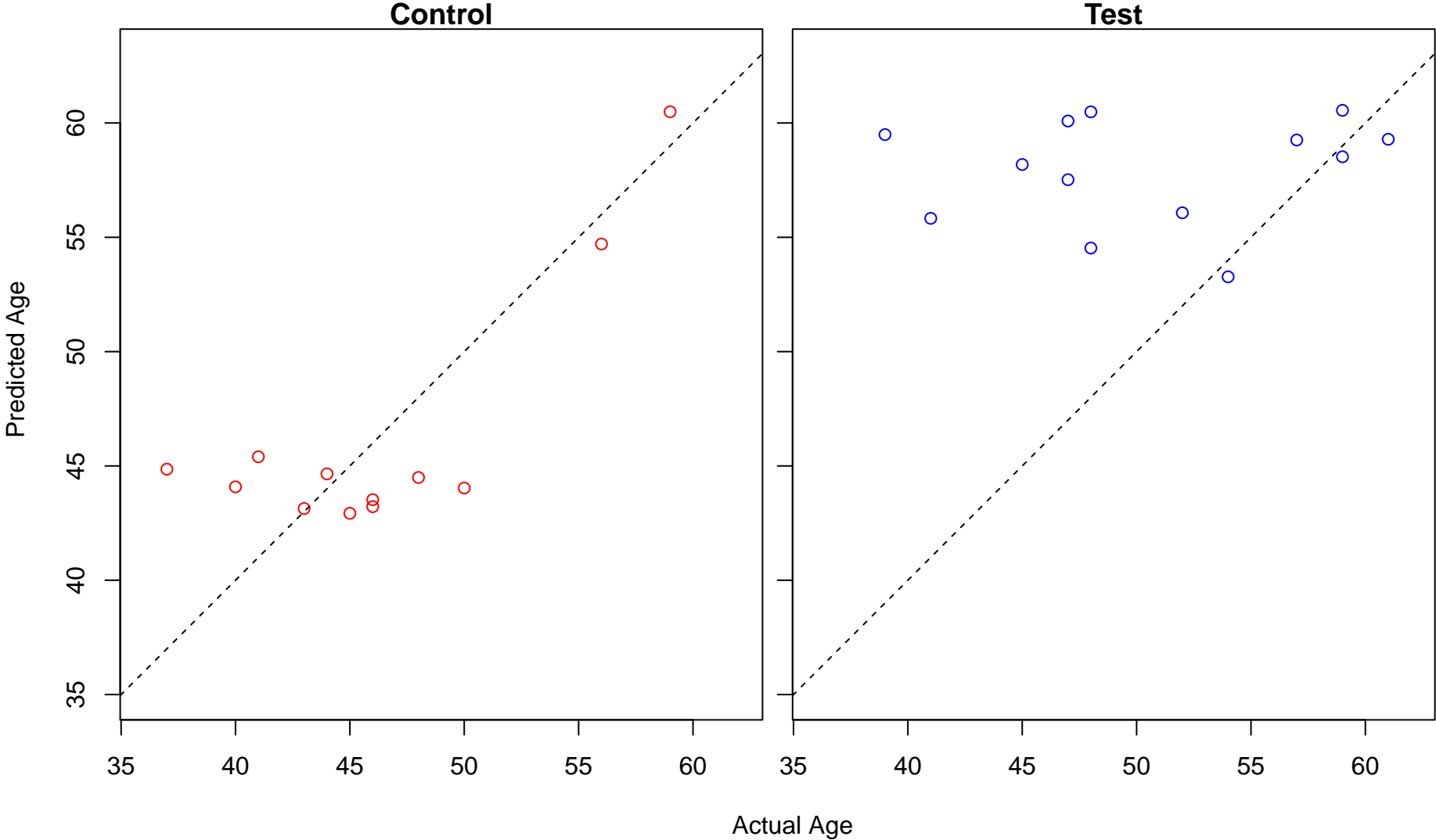
Negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 1)



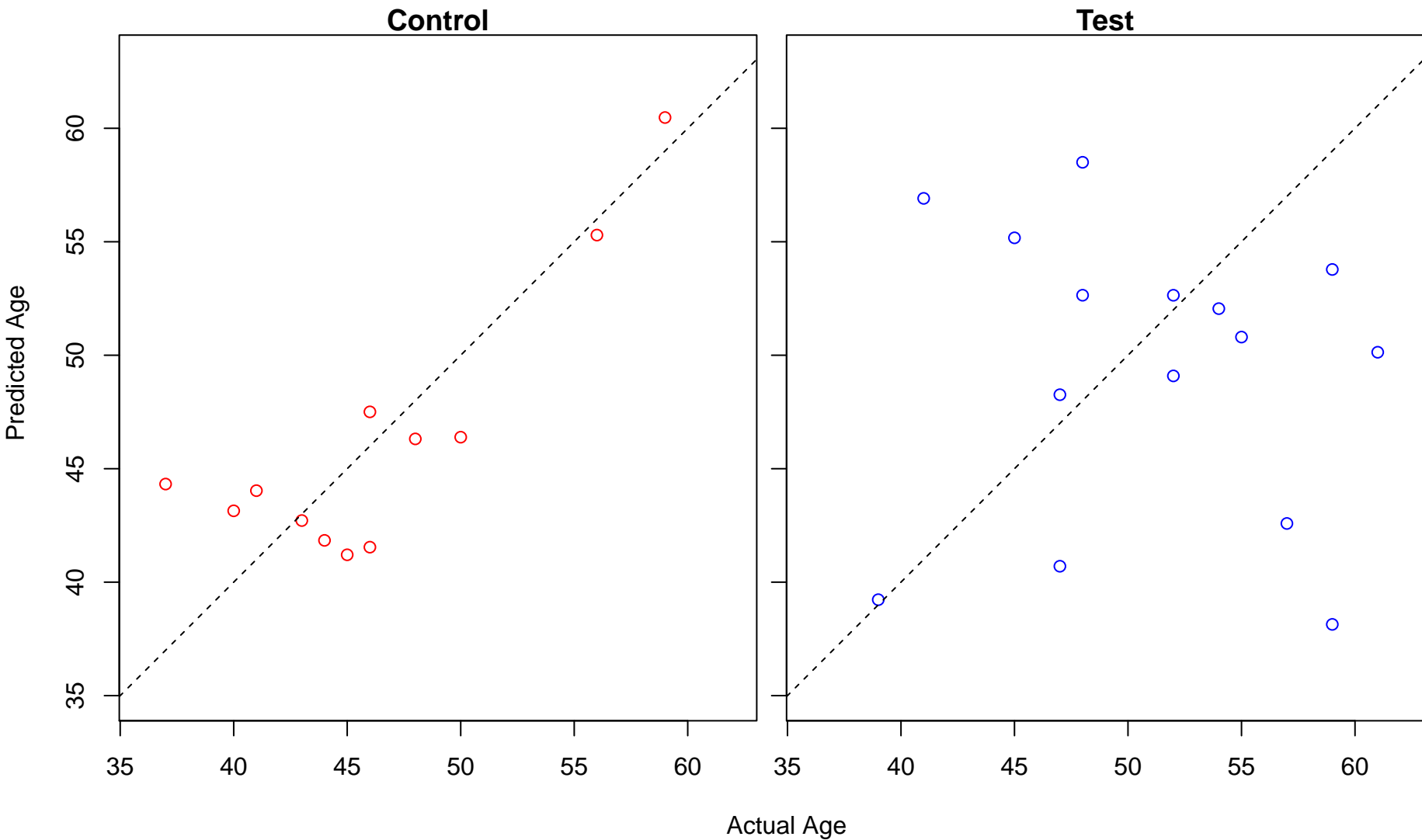
muscle organ development (Score: 3.161523)



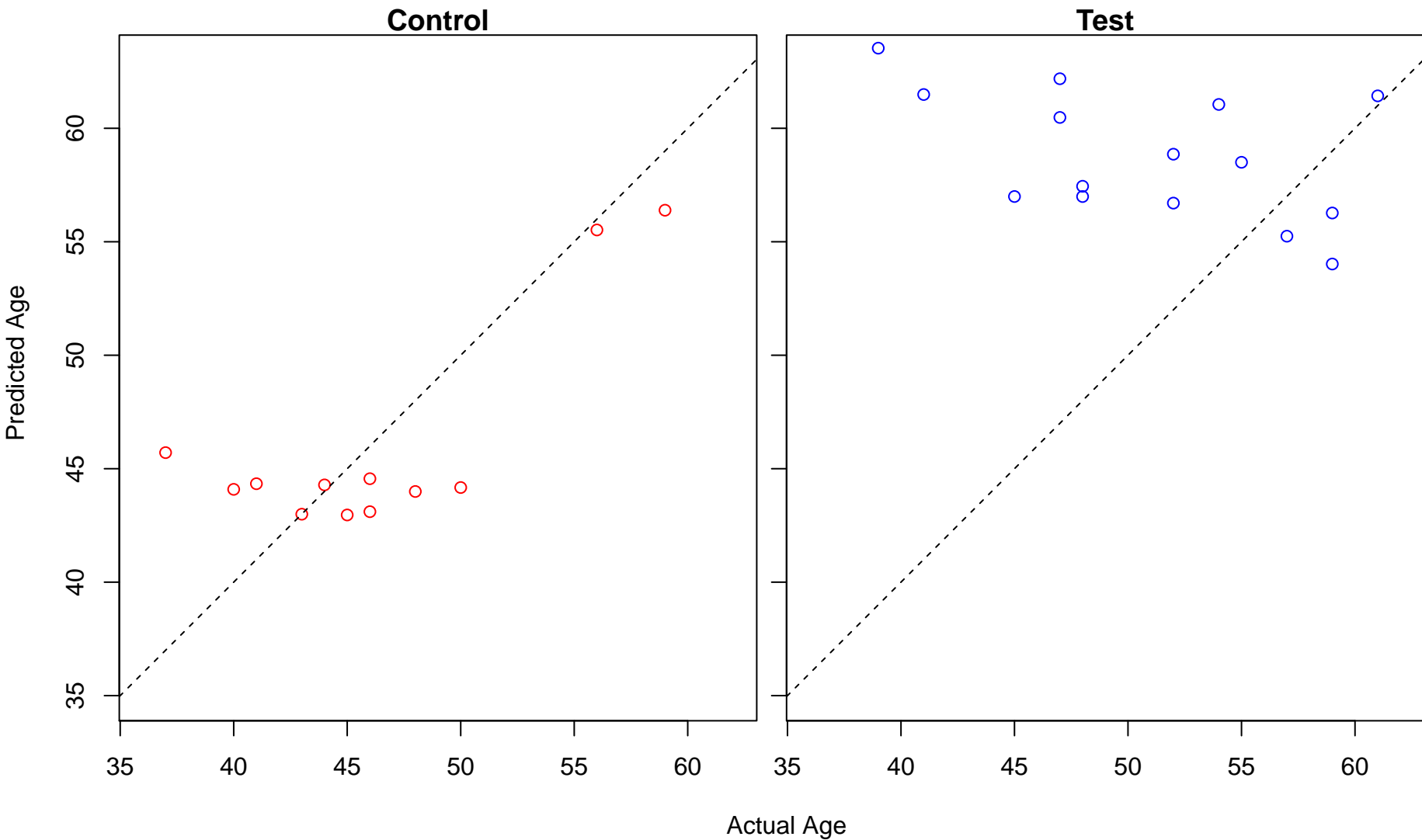
regulation of transcription from RNA polymerase II promoter in response to oxidative stress (Score: 3.1)



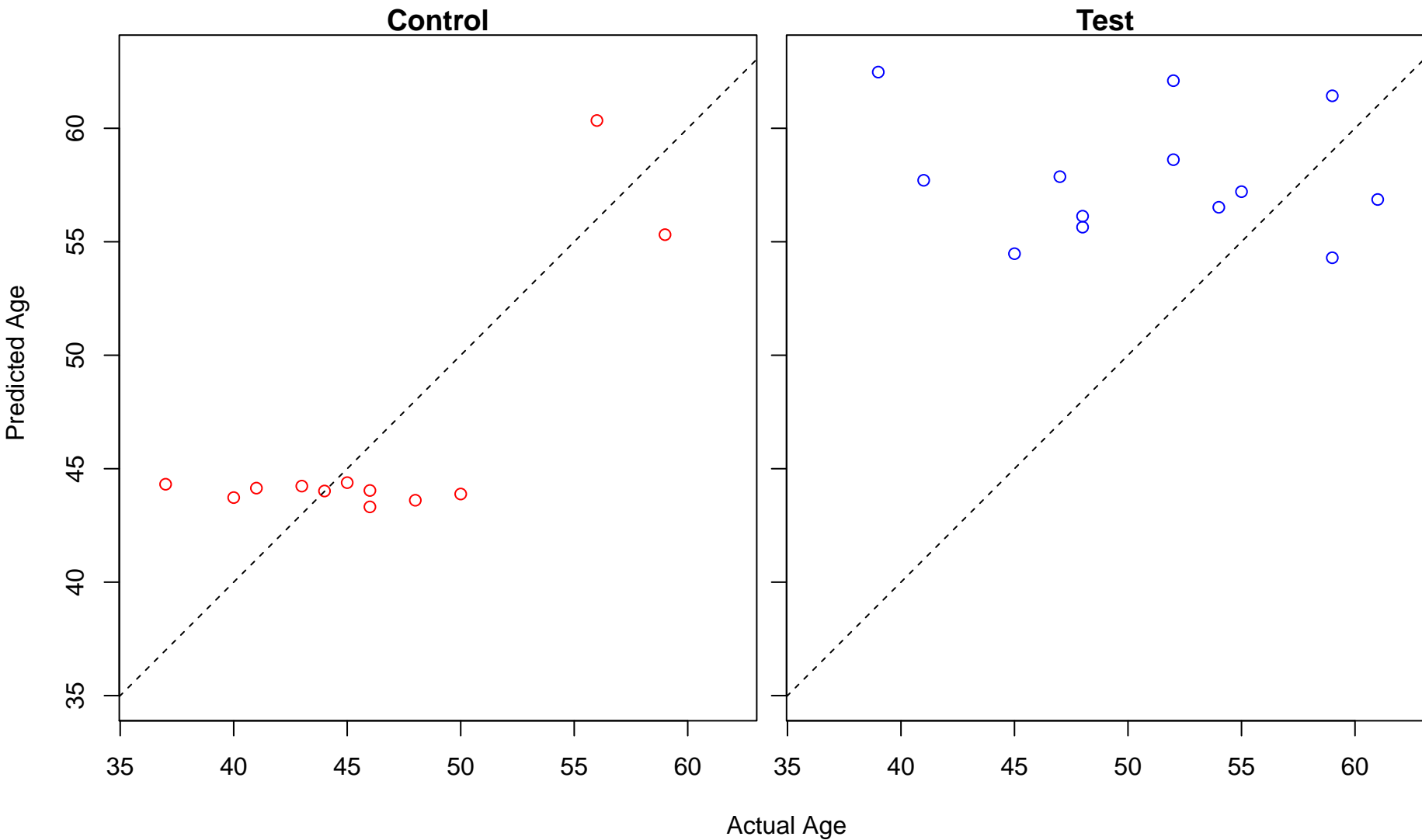
regulation of short-term neuronal synaptic plasticity (Score: 3.160038)



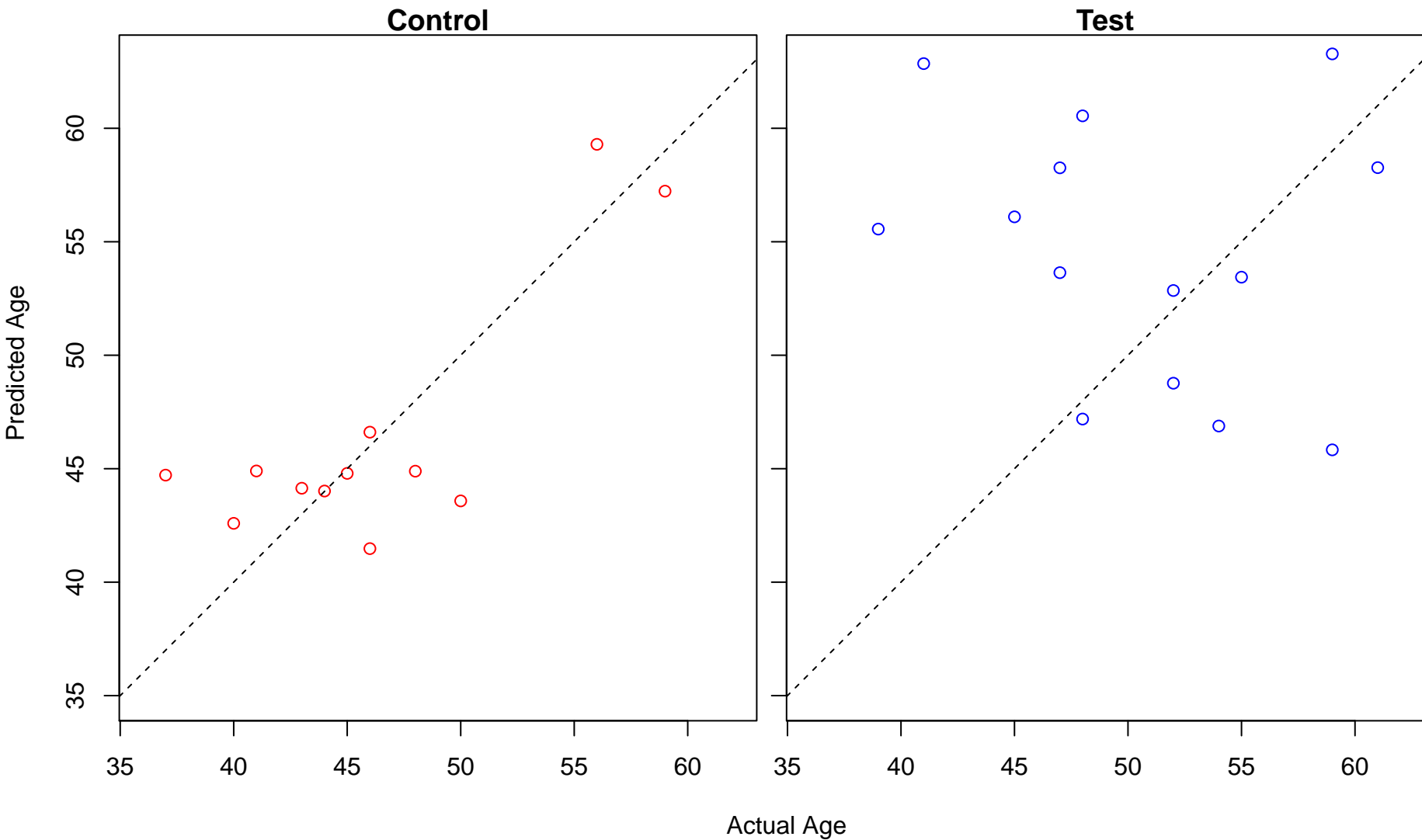
syncytium formation (Score: 3.157976)



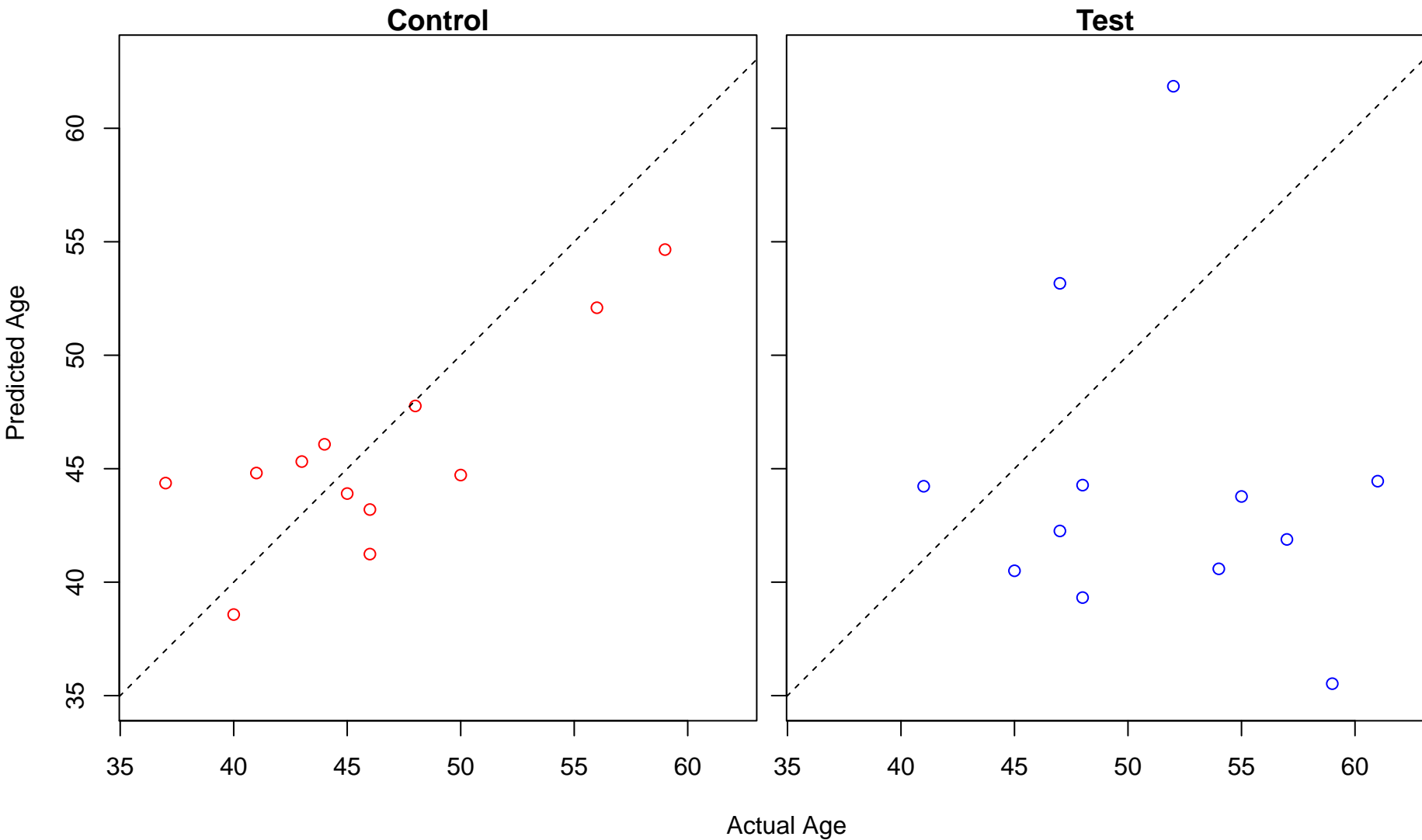
negative regulation of cellular response to growth factor stimulus (Score: 3.157212)



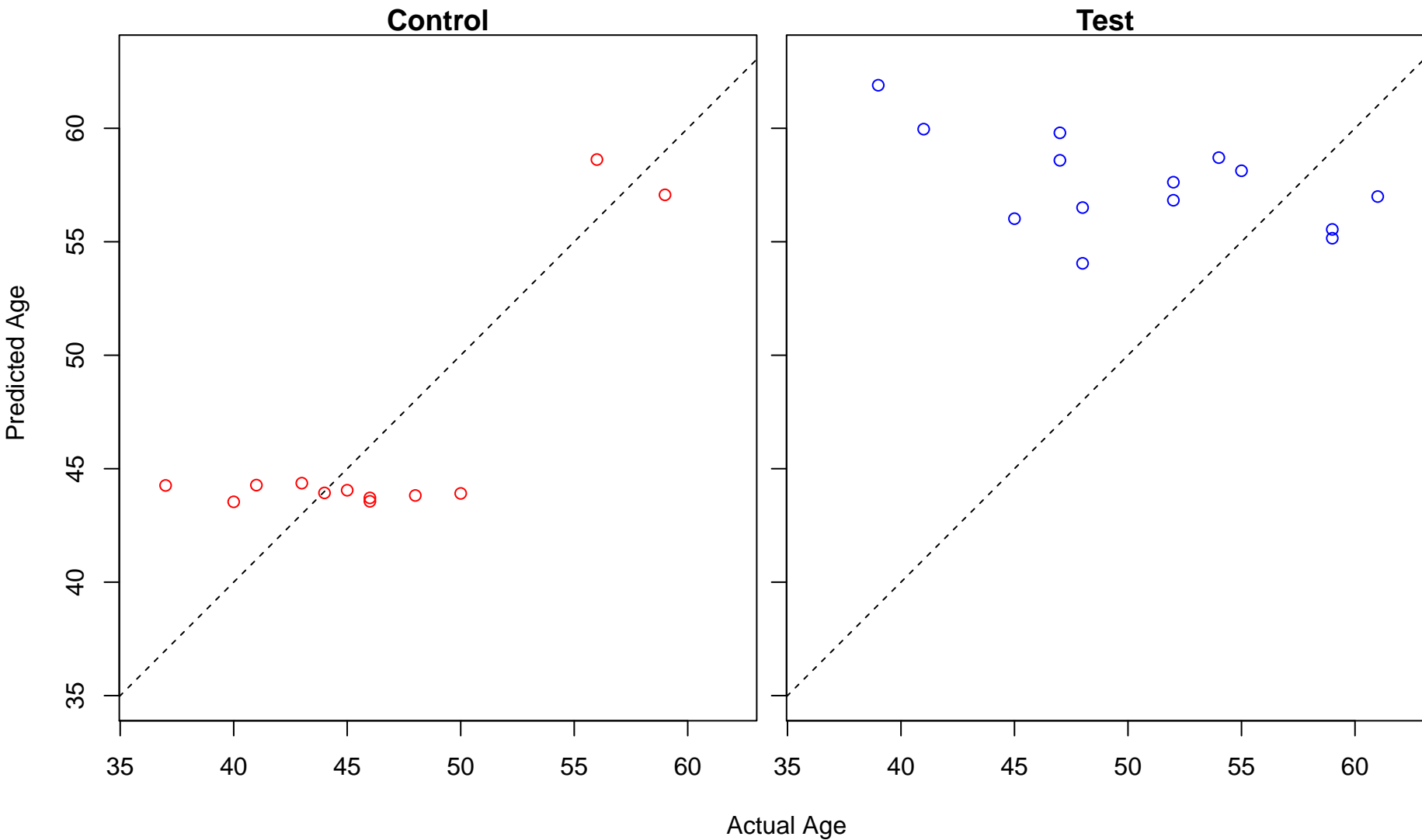
regulation of proteolysis involved in cellular protein catabolic process (Score: 3.156649)



cellular nitrogen compound catabolic process (Score: 3.155844)

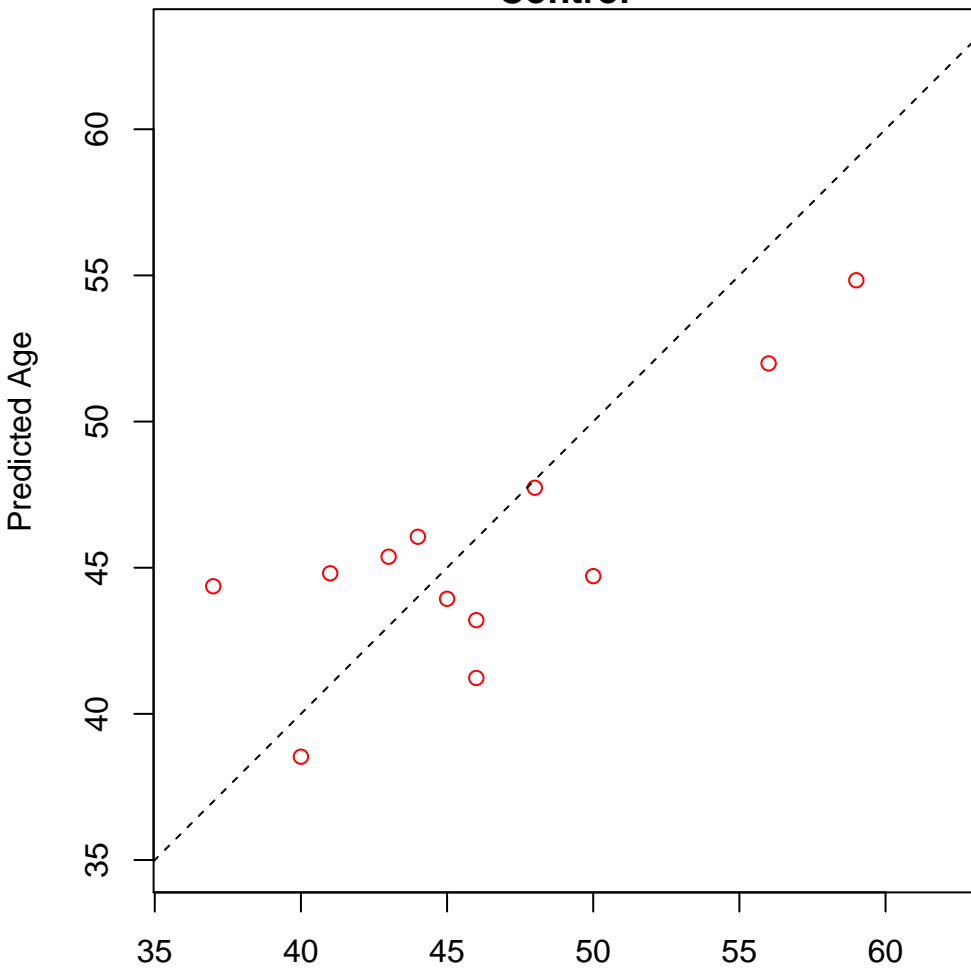


single-organism carbohydrate catabolic process (Score: 3.153879)

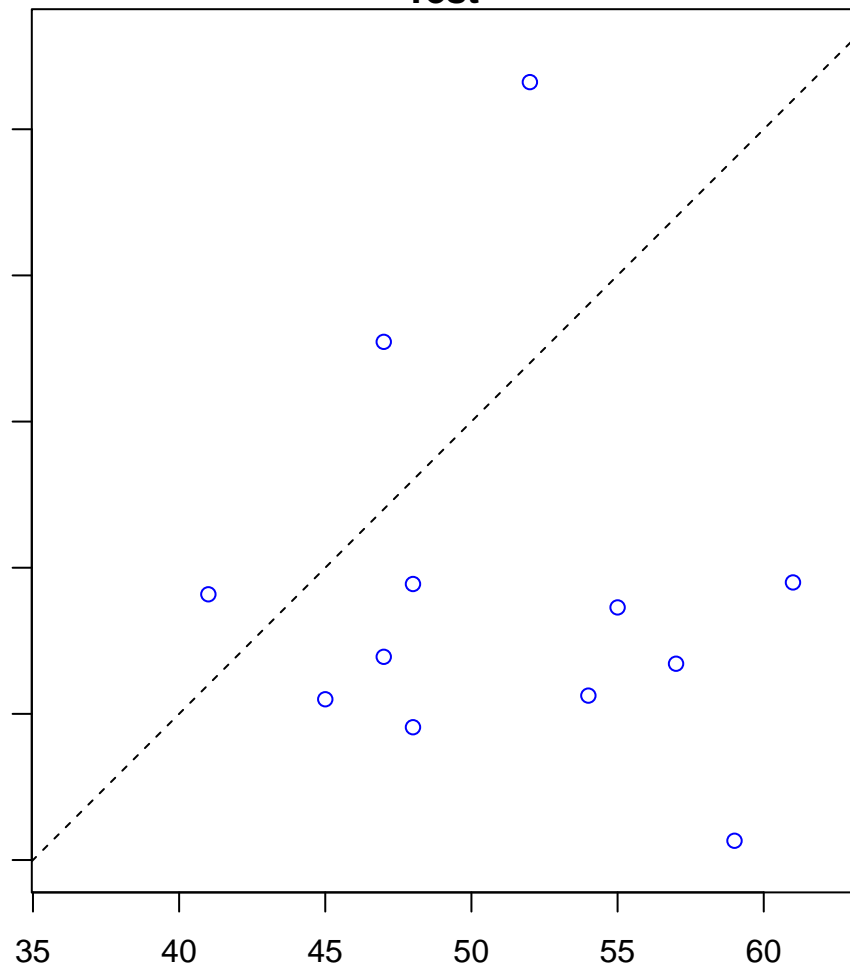


aromatic compound catabolic process (Score: 3.152943)

Control

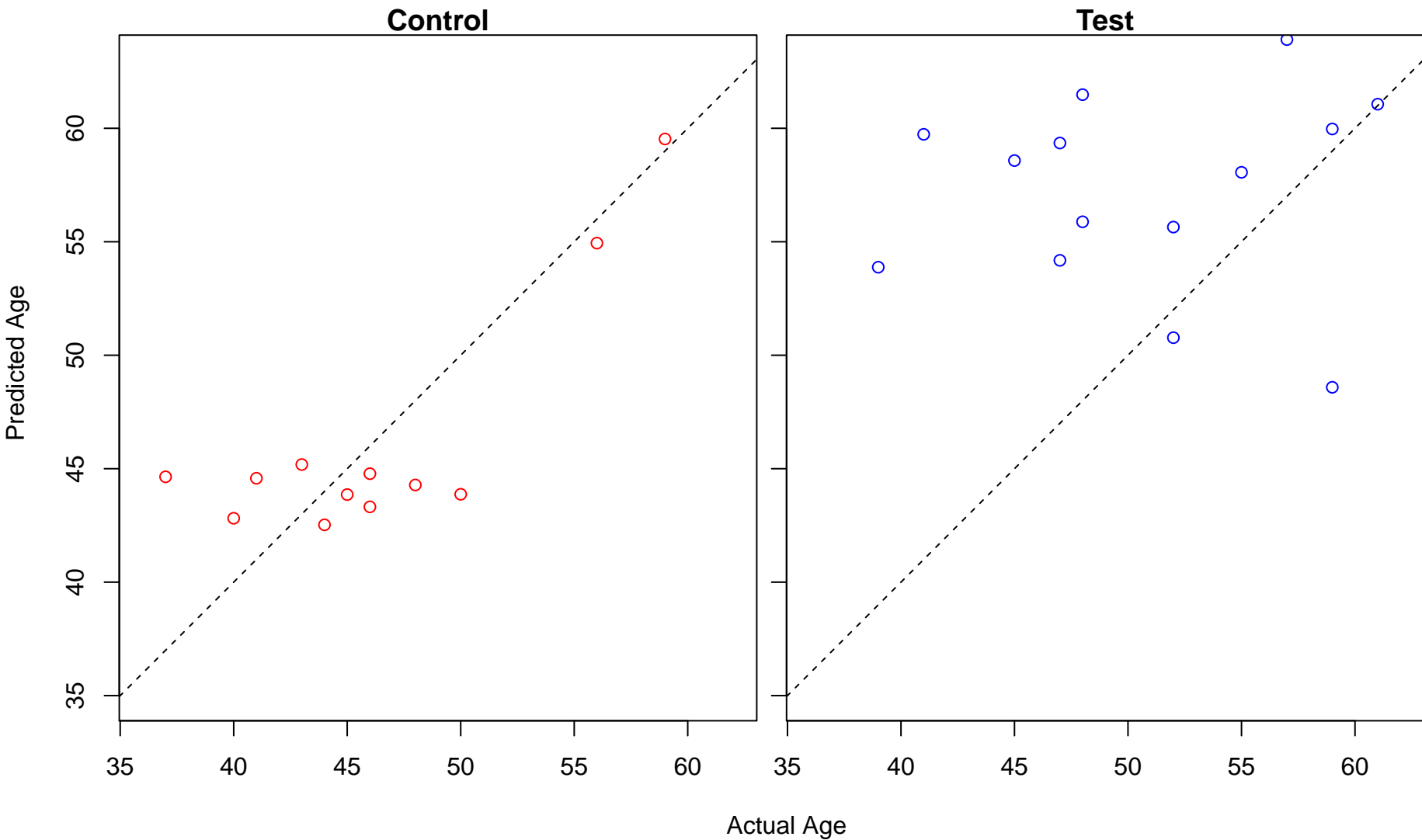


Test

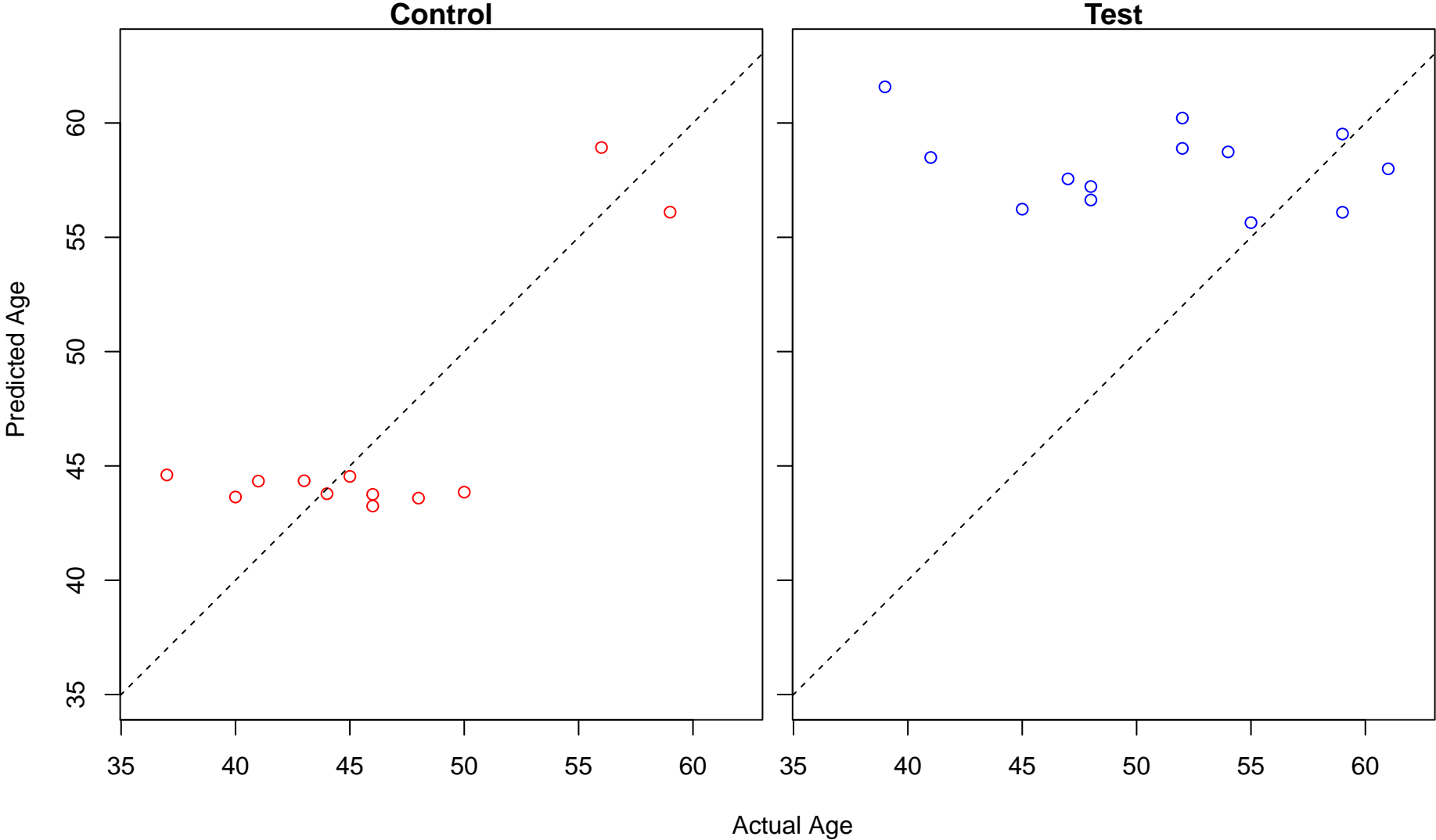


Actual Age

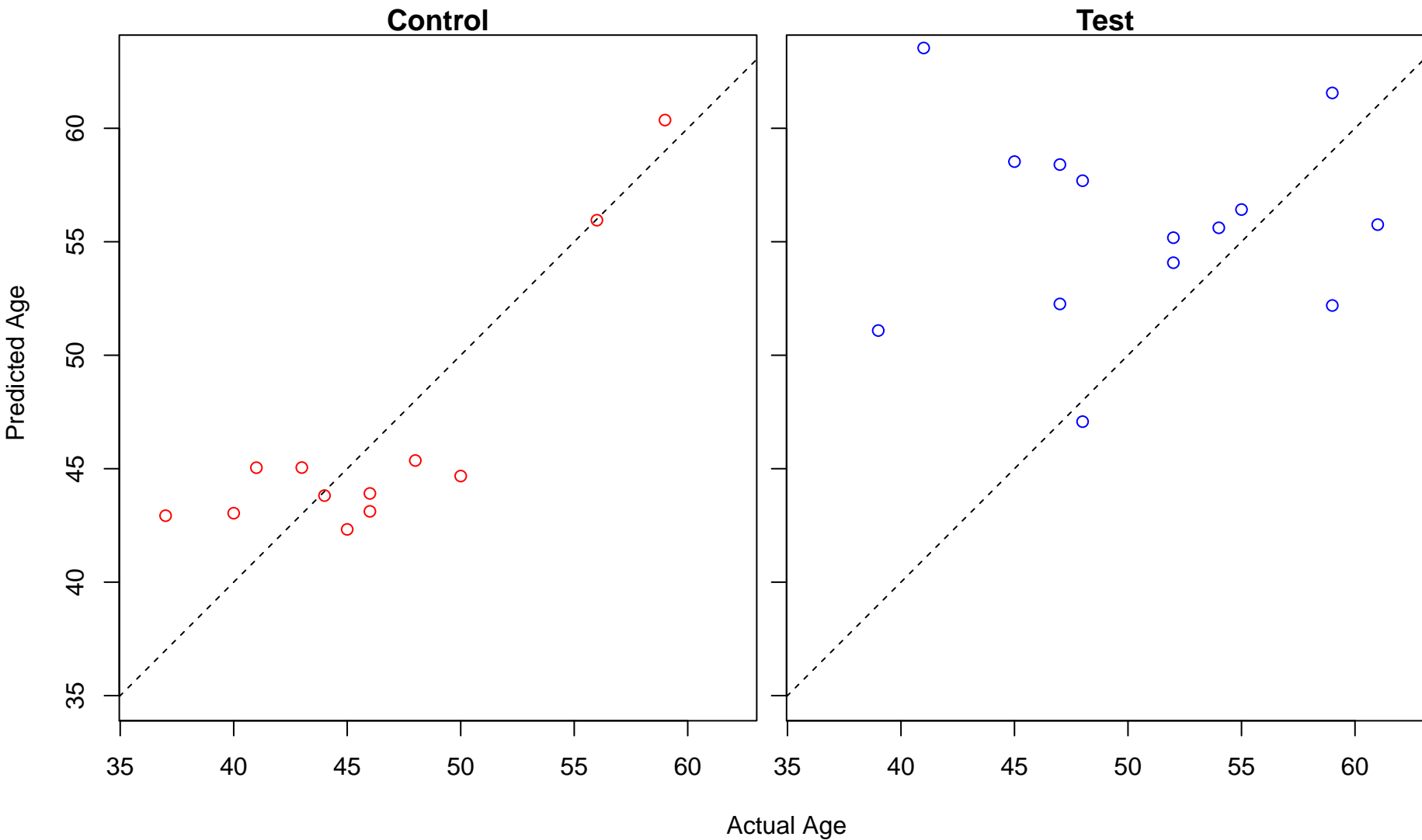
membrane protein intracellular domain proteolysis (Score: 3.152463)



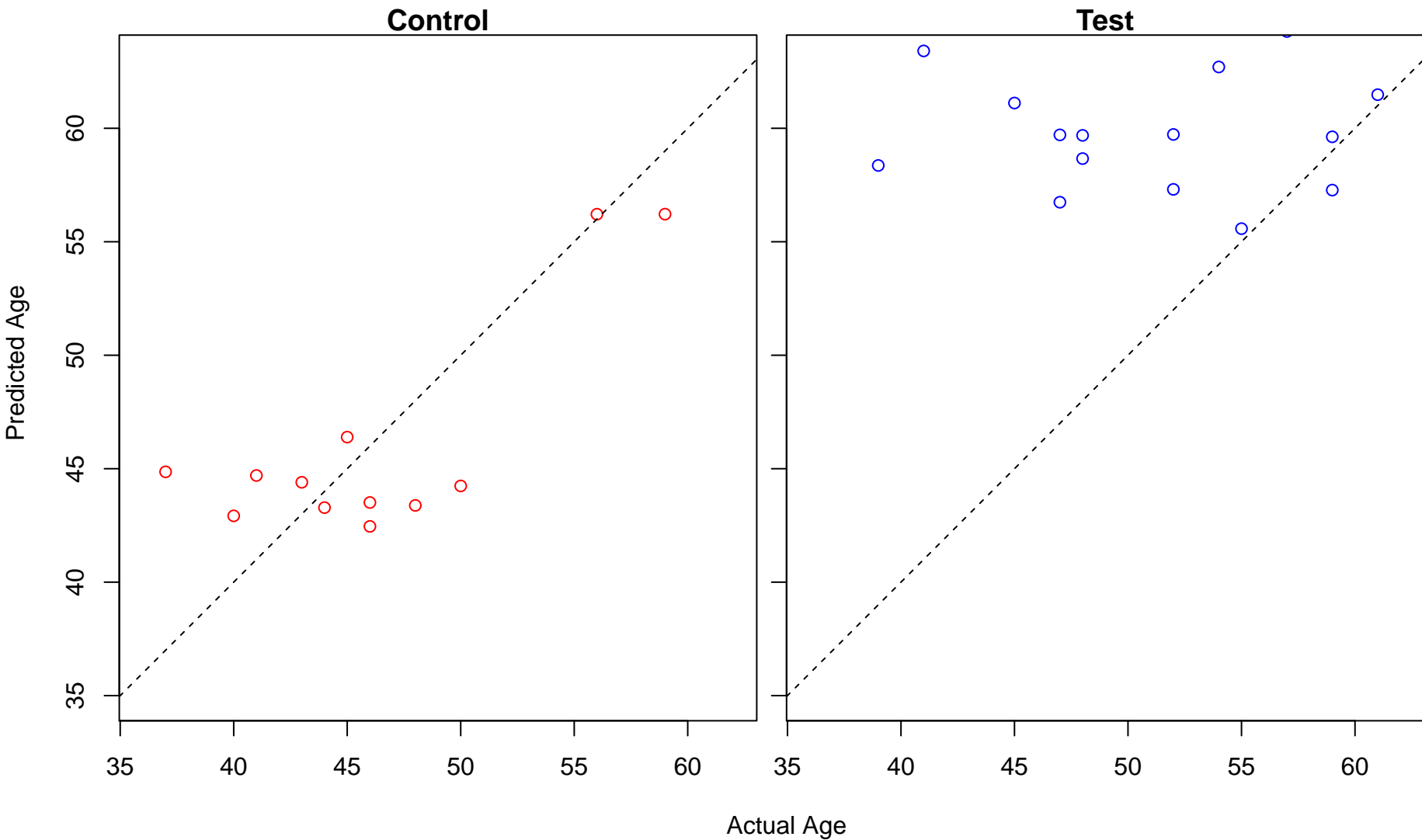
positive regulation of cellular protein catabolic process (Score: 3.151904)



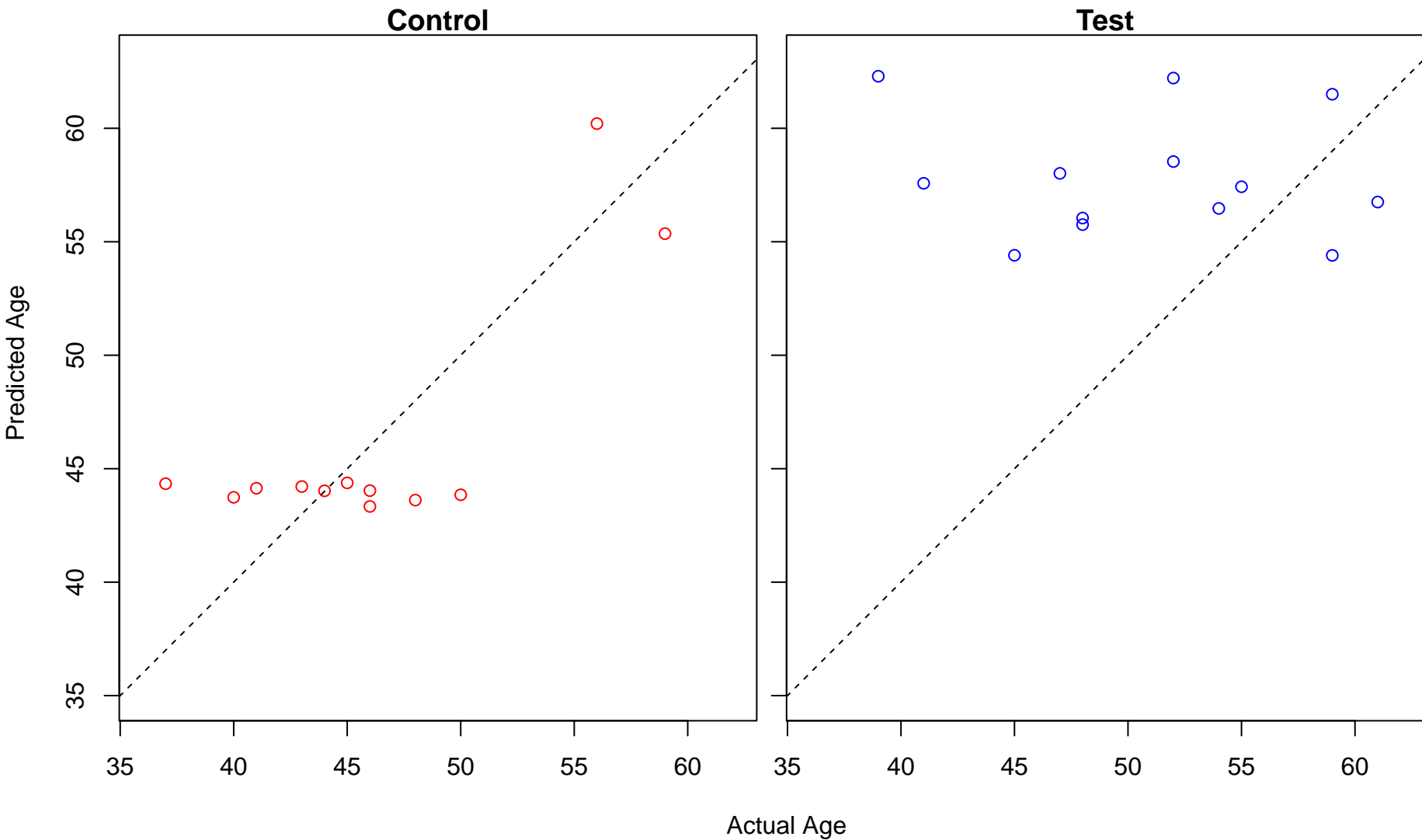
vitamin metabolic process (Score: 3.151463)



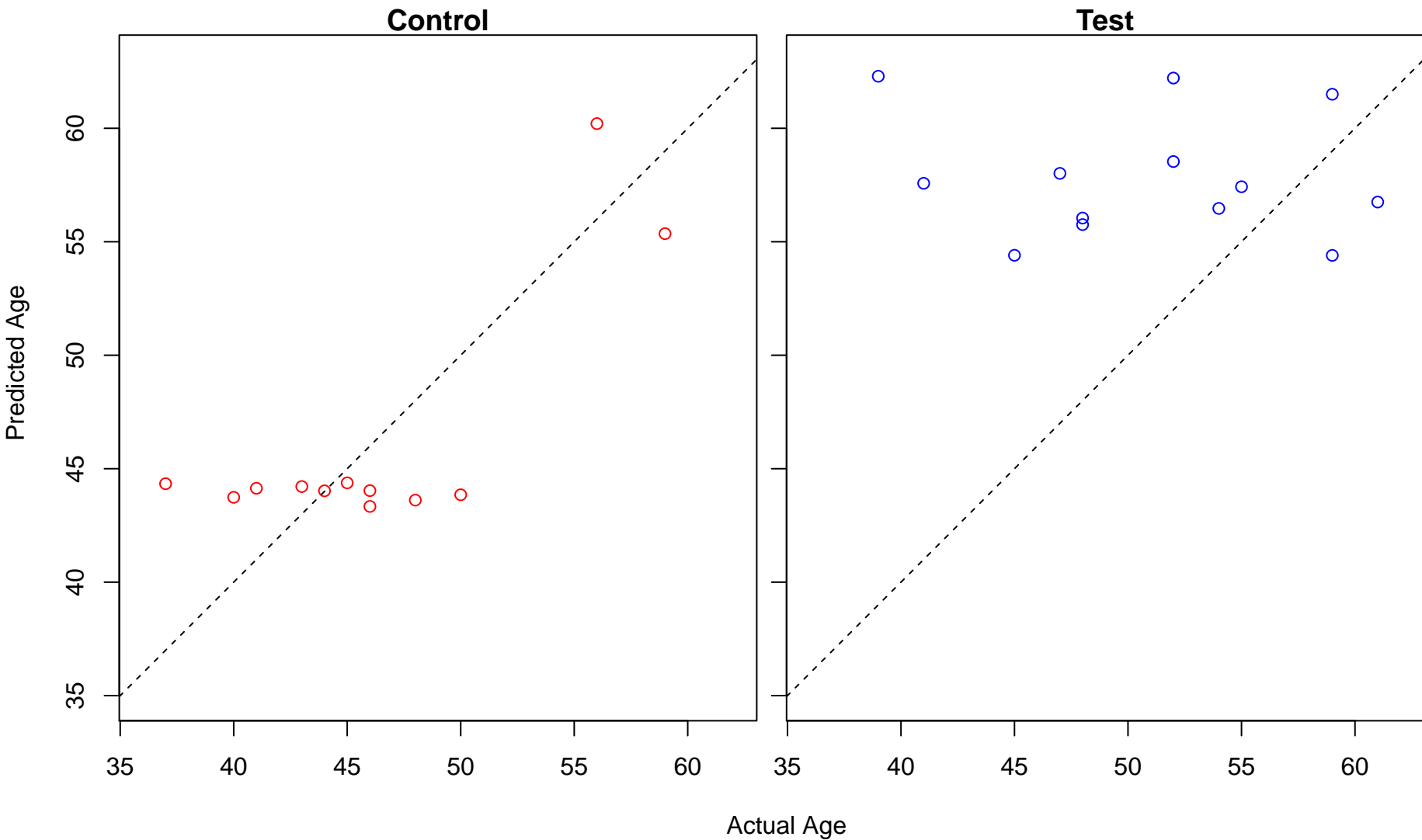
chaperone-mediated protein folding (Score: 3.151264)



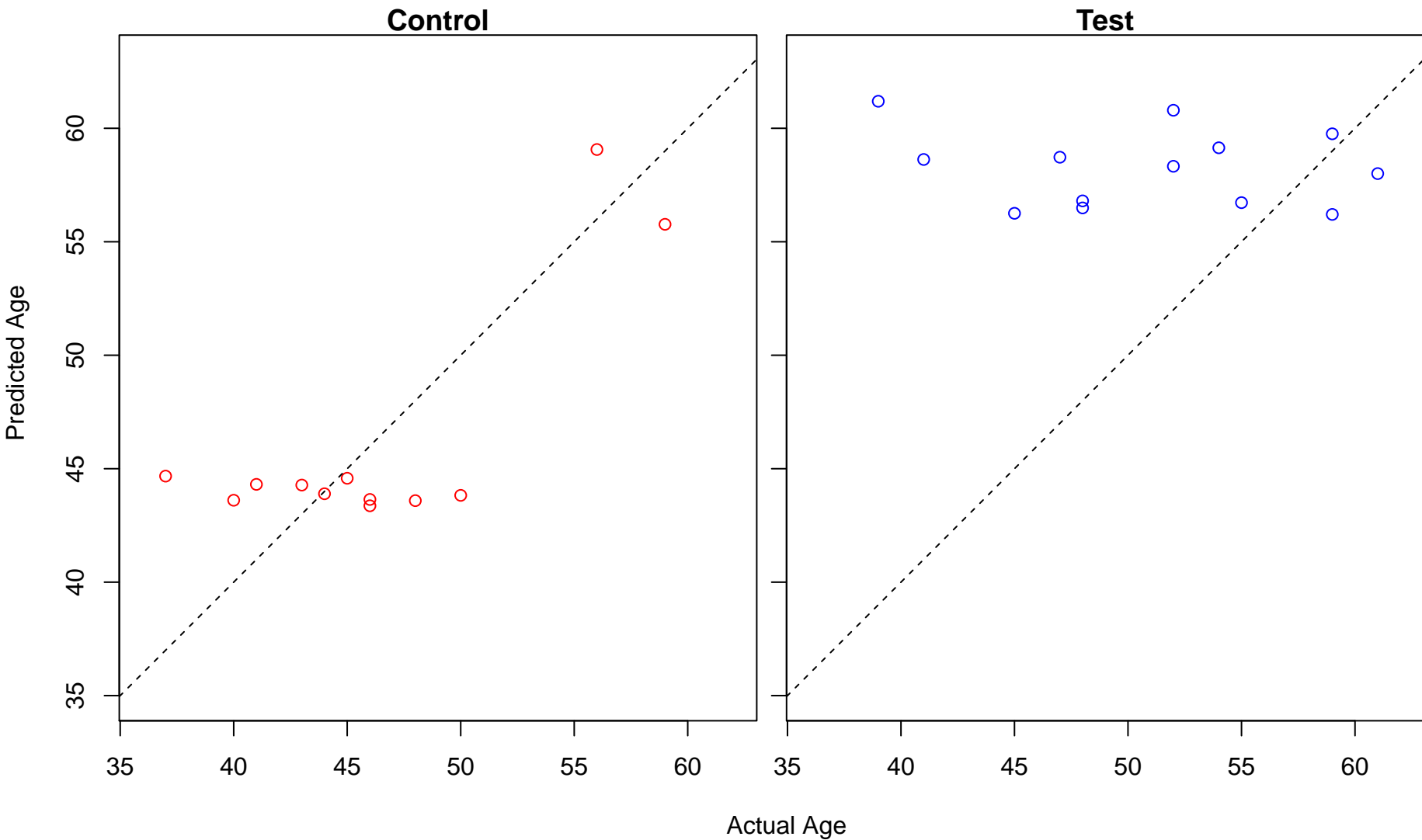
regulation of transforming growth factor beta receptor signaling pathway (Score: 3.148552)



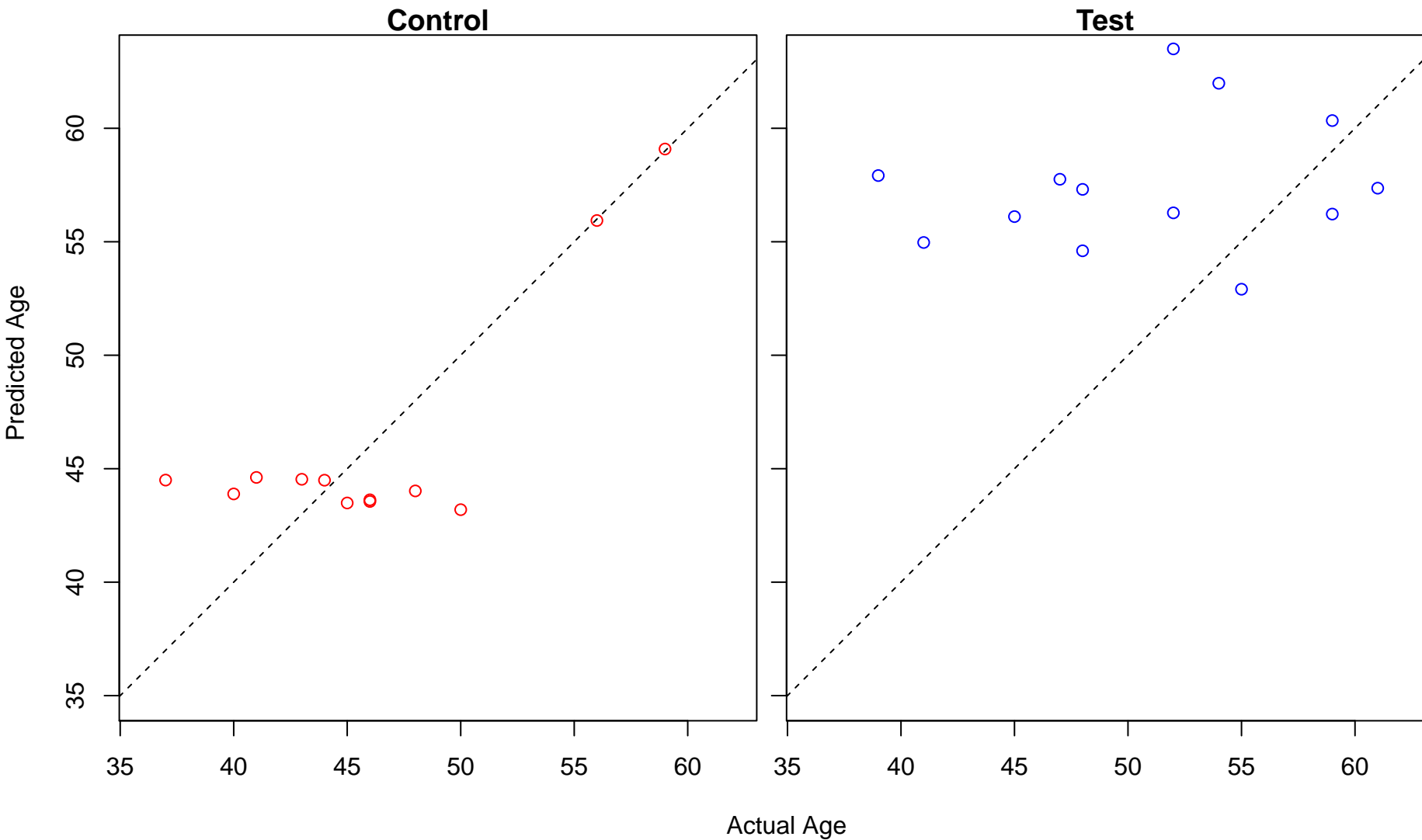
regulation of cellular response to transforming growth factor beta stimulus (Score: 3.148552)



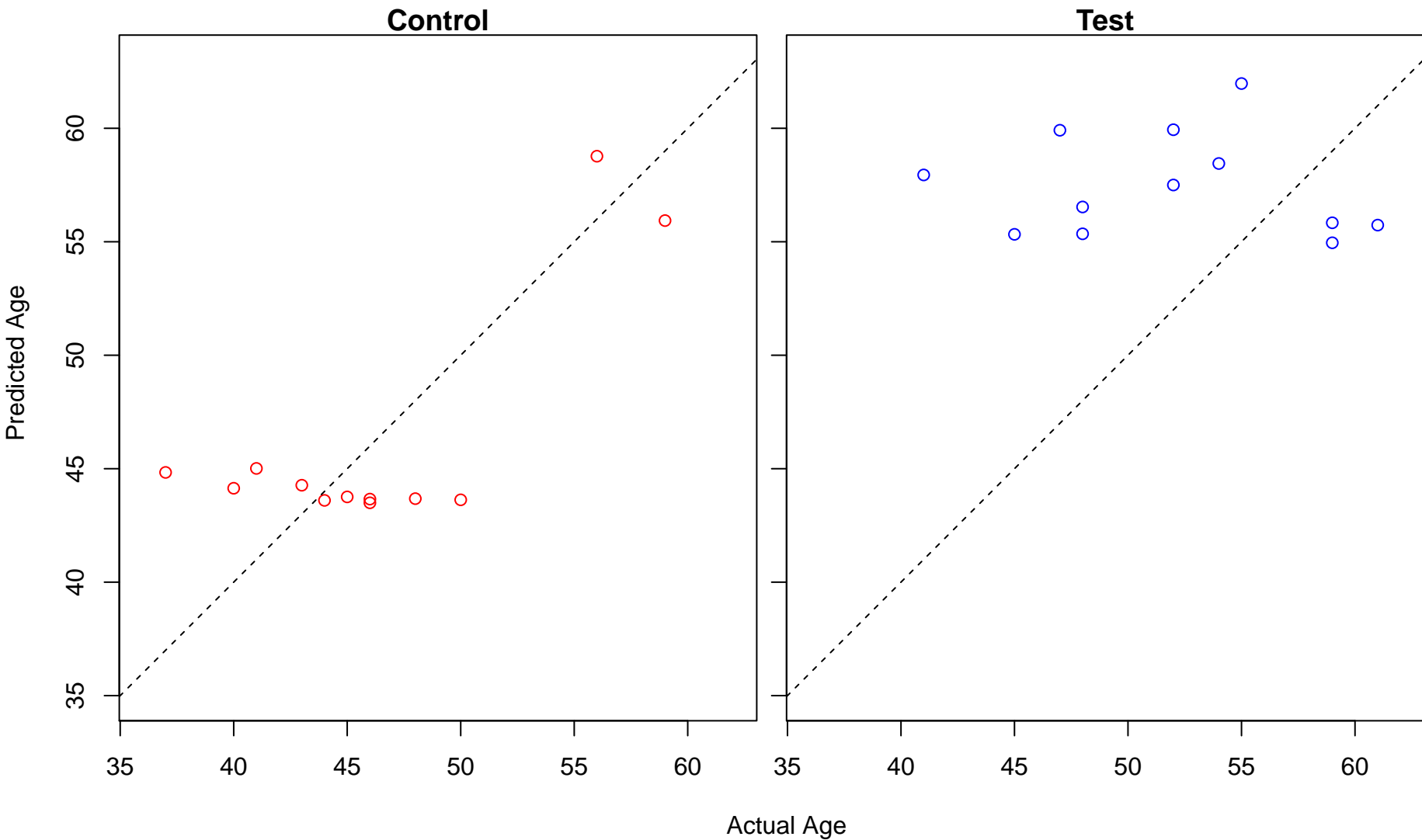
apoptotic signaling pathway (Score: 3.146179)



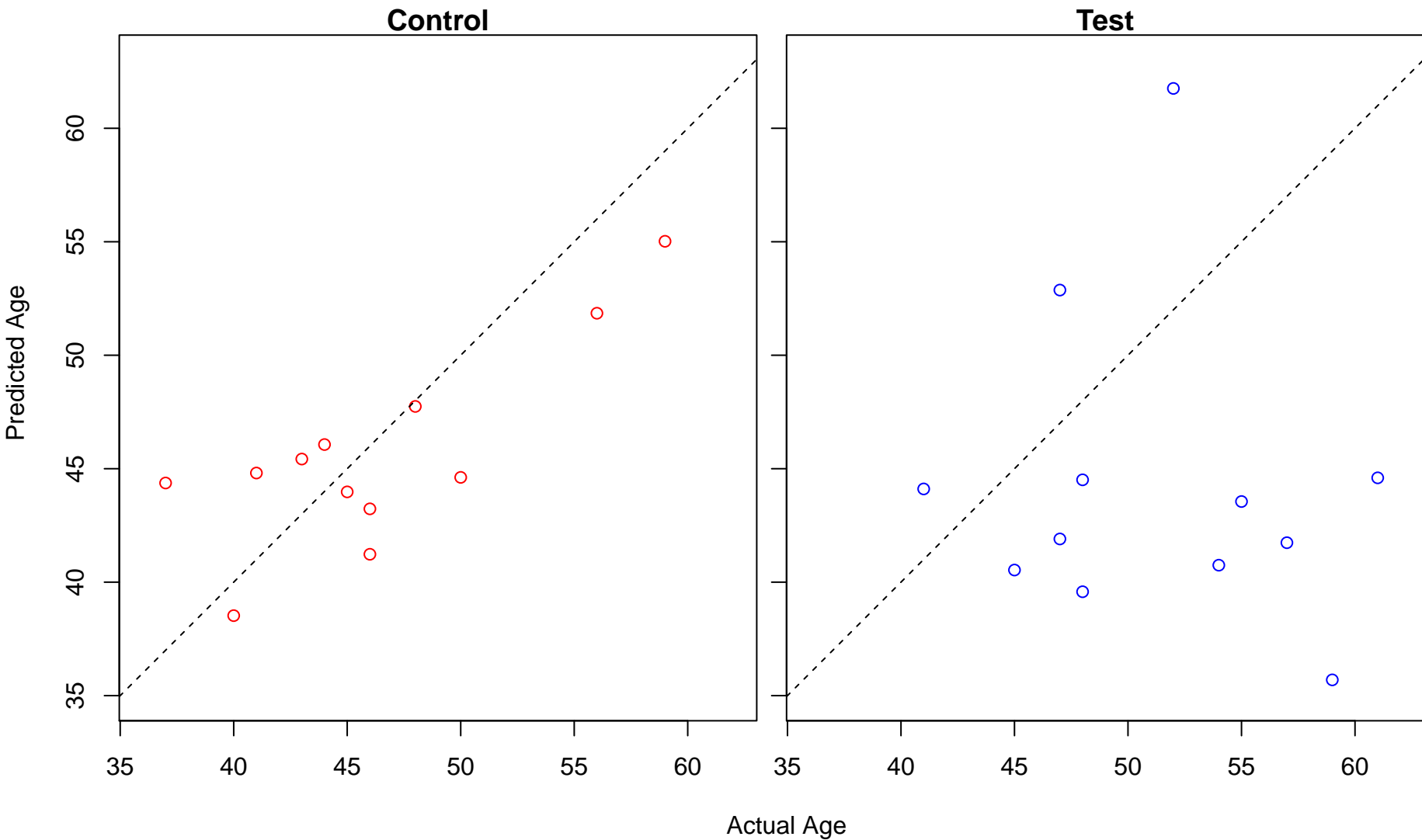
protein deglycosylation (Score: 3.145411)



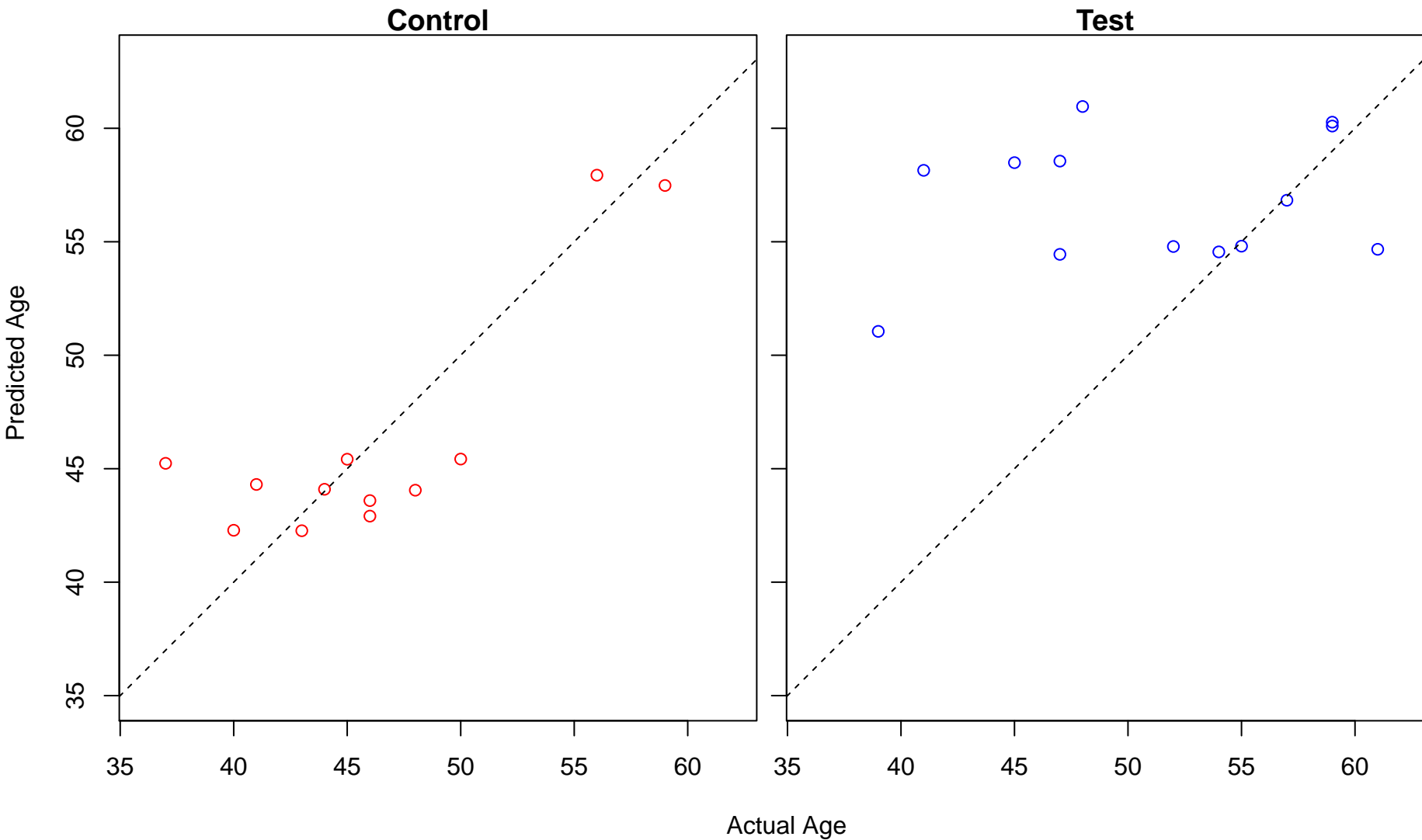
retina homeostasis (Score: 3.142906)



organic cyclic compound catabolic process (Score: 3.142476)

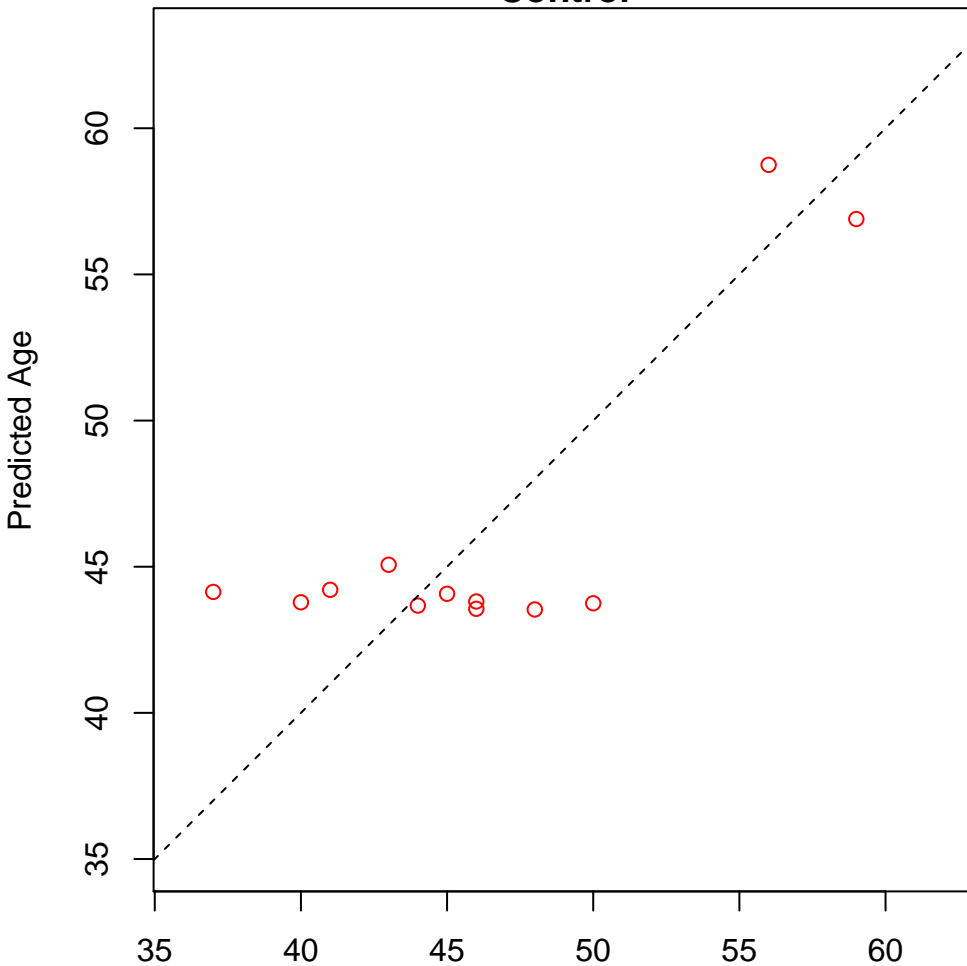


left/right axis specification (Score: 3.142388)

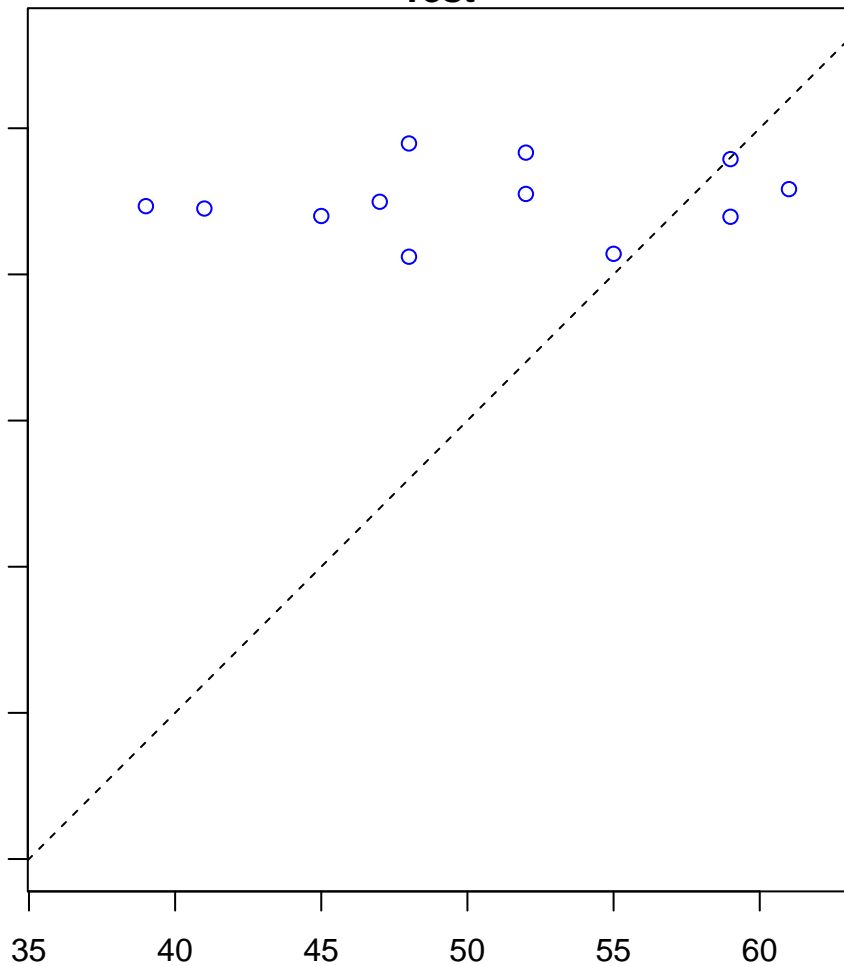


protein localization to chromosome (Score: 3.139918)

Control

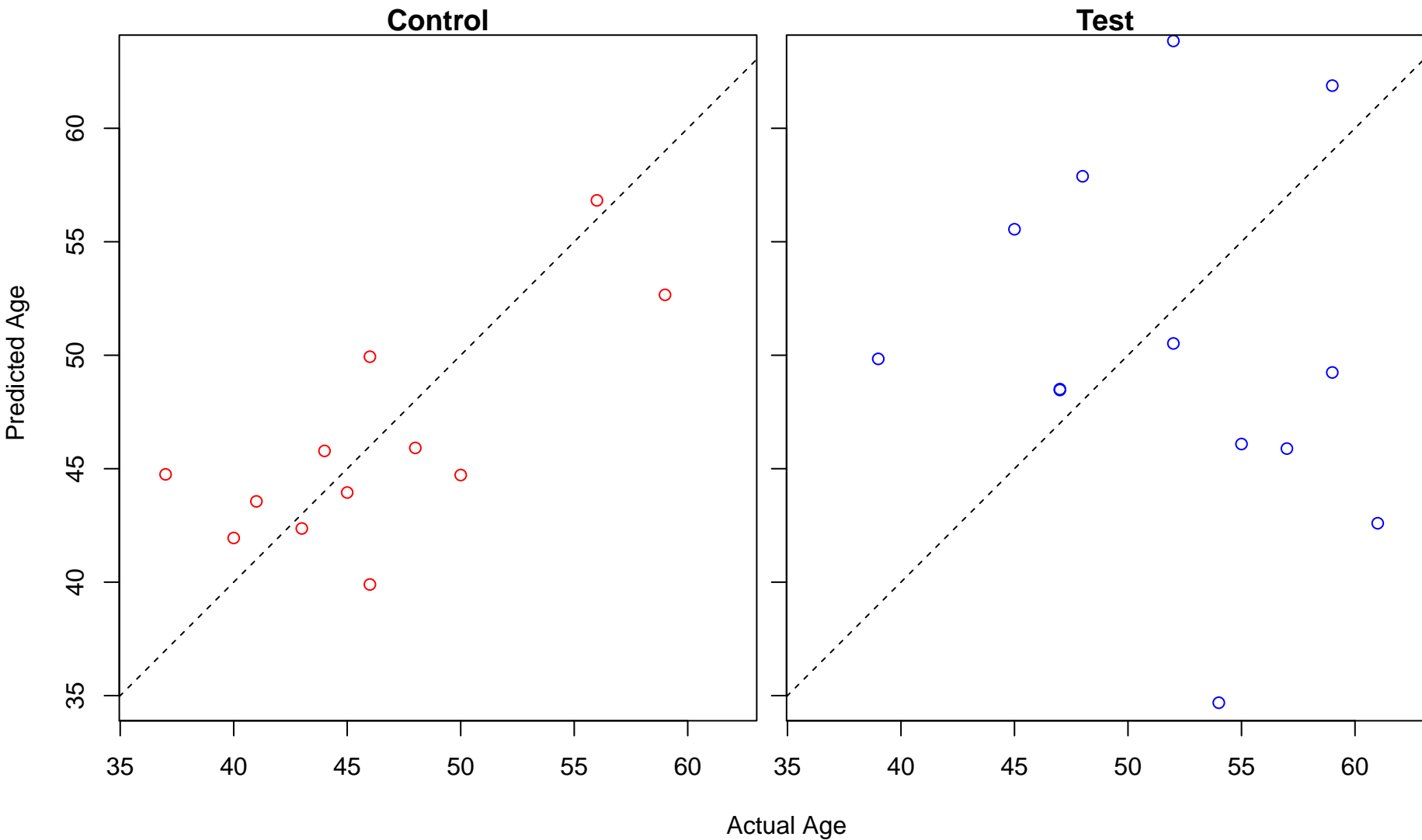


Test

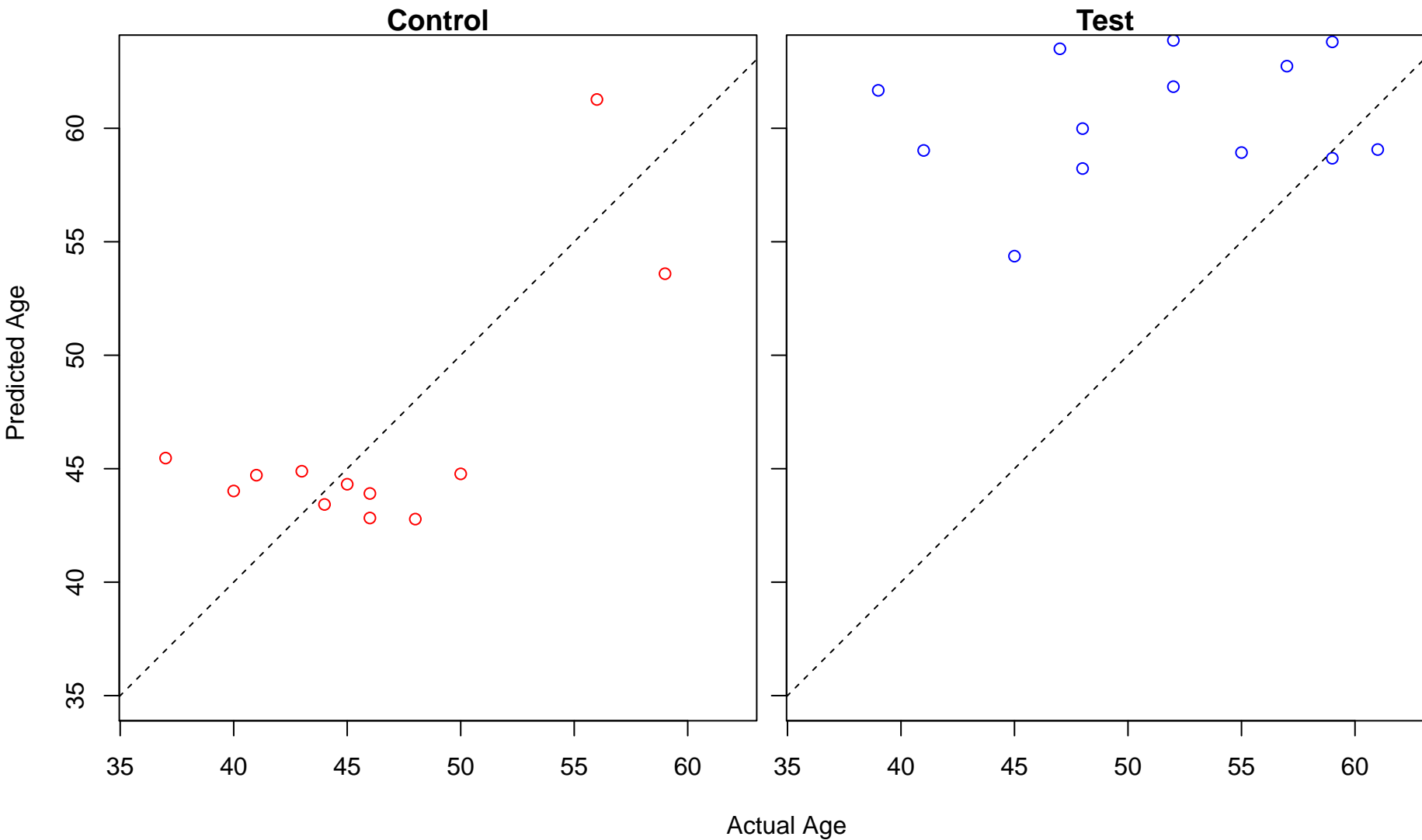


Actual Age

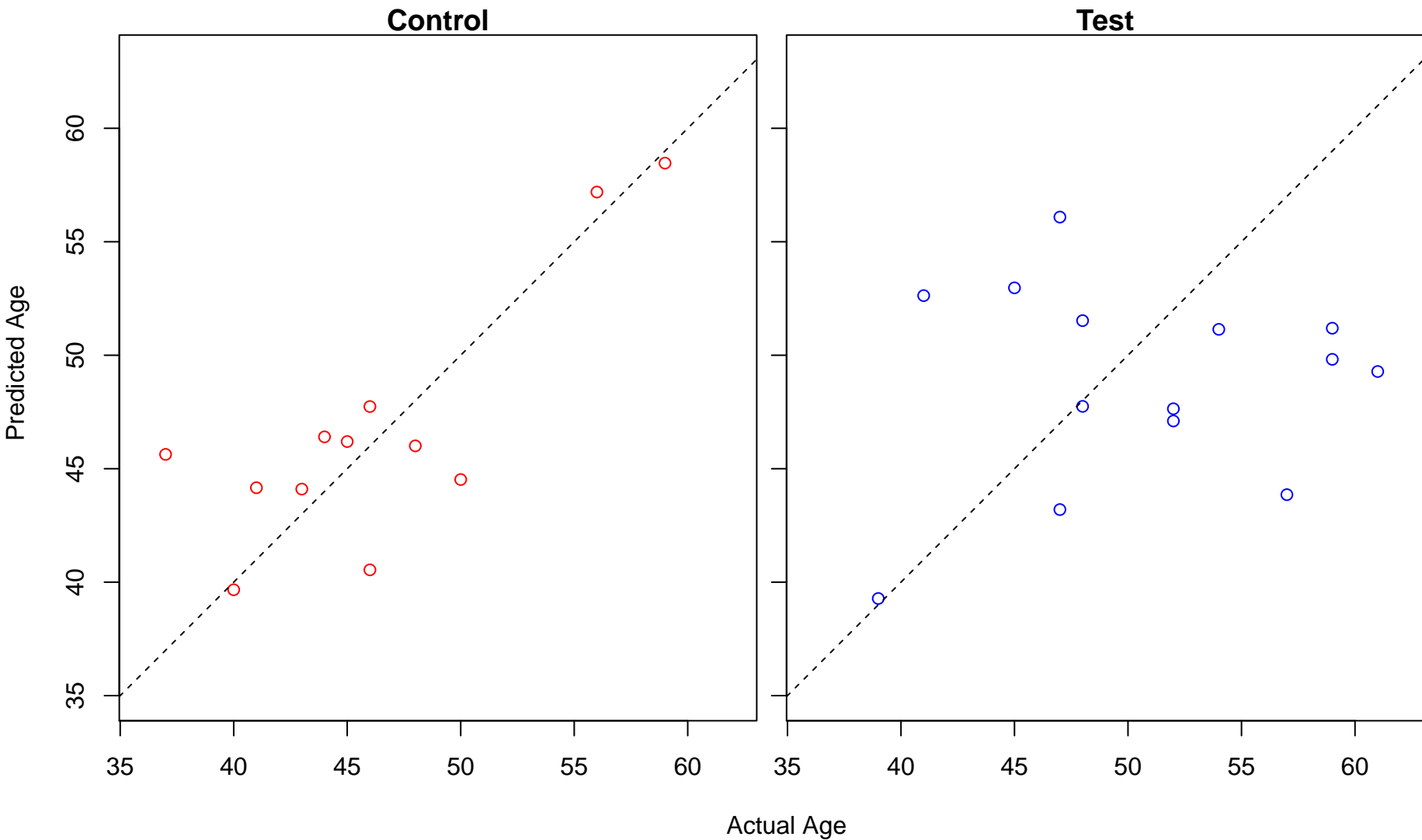
positive regulation of multicellular organism growth (Score: 3.138667)



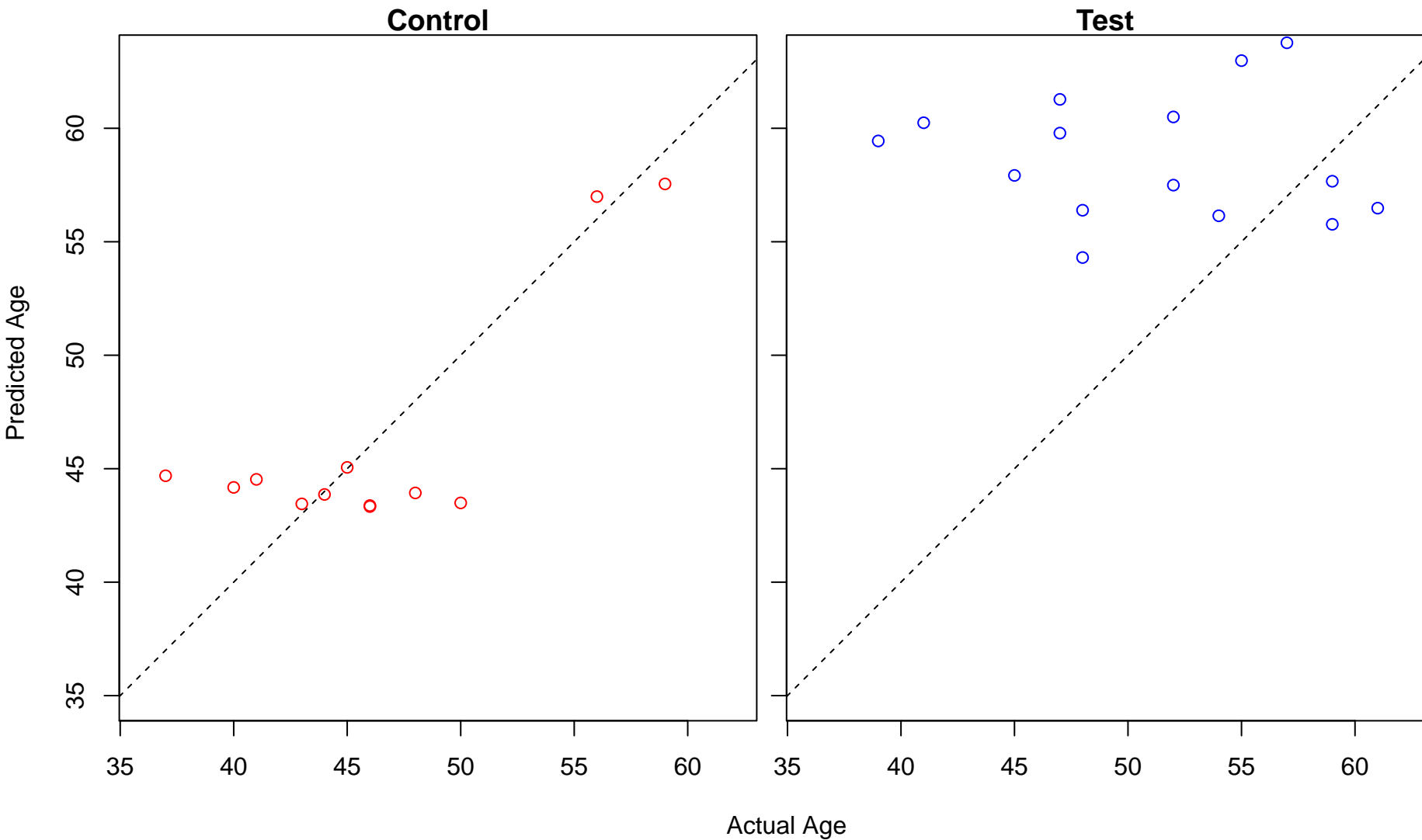
chromatin-mediated maintenance of transcription (Score: 3.137468)



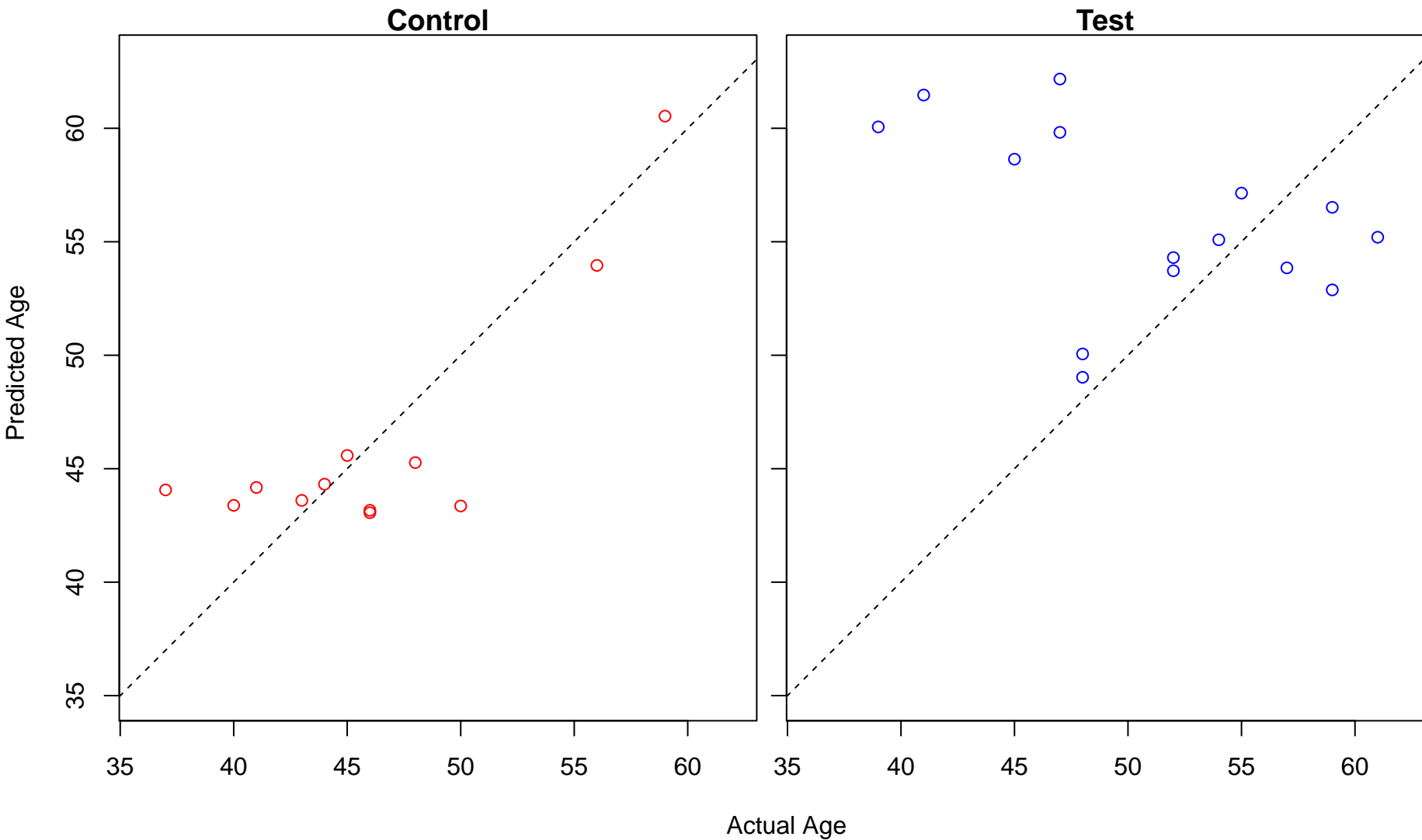
positive regulation of cell adhesion (Score: 3.136579)



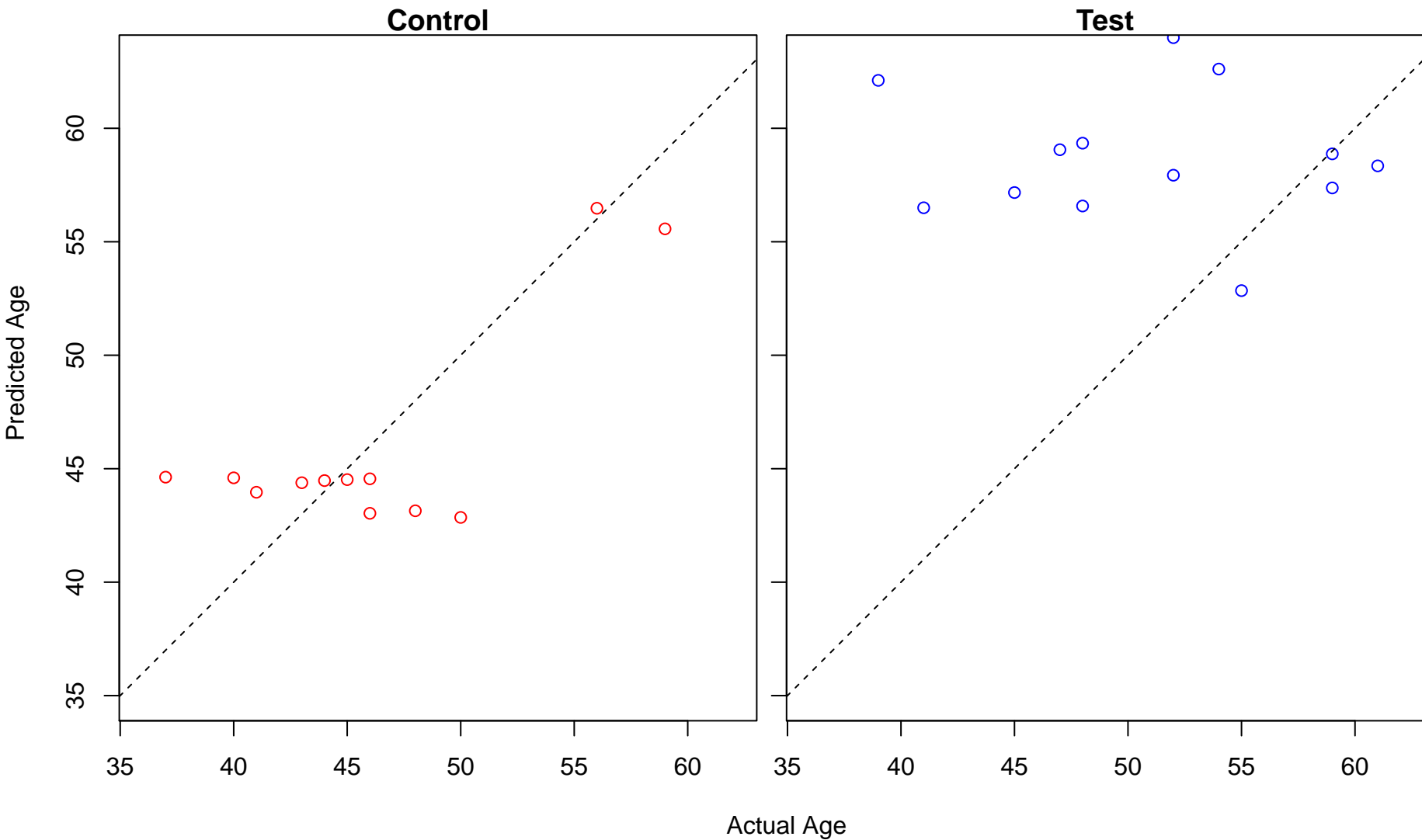
regulation of neuron projection development (Score: 3.136313)



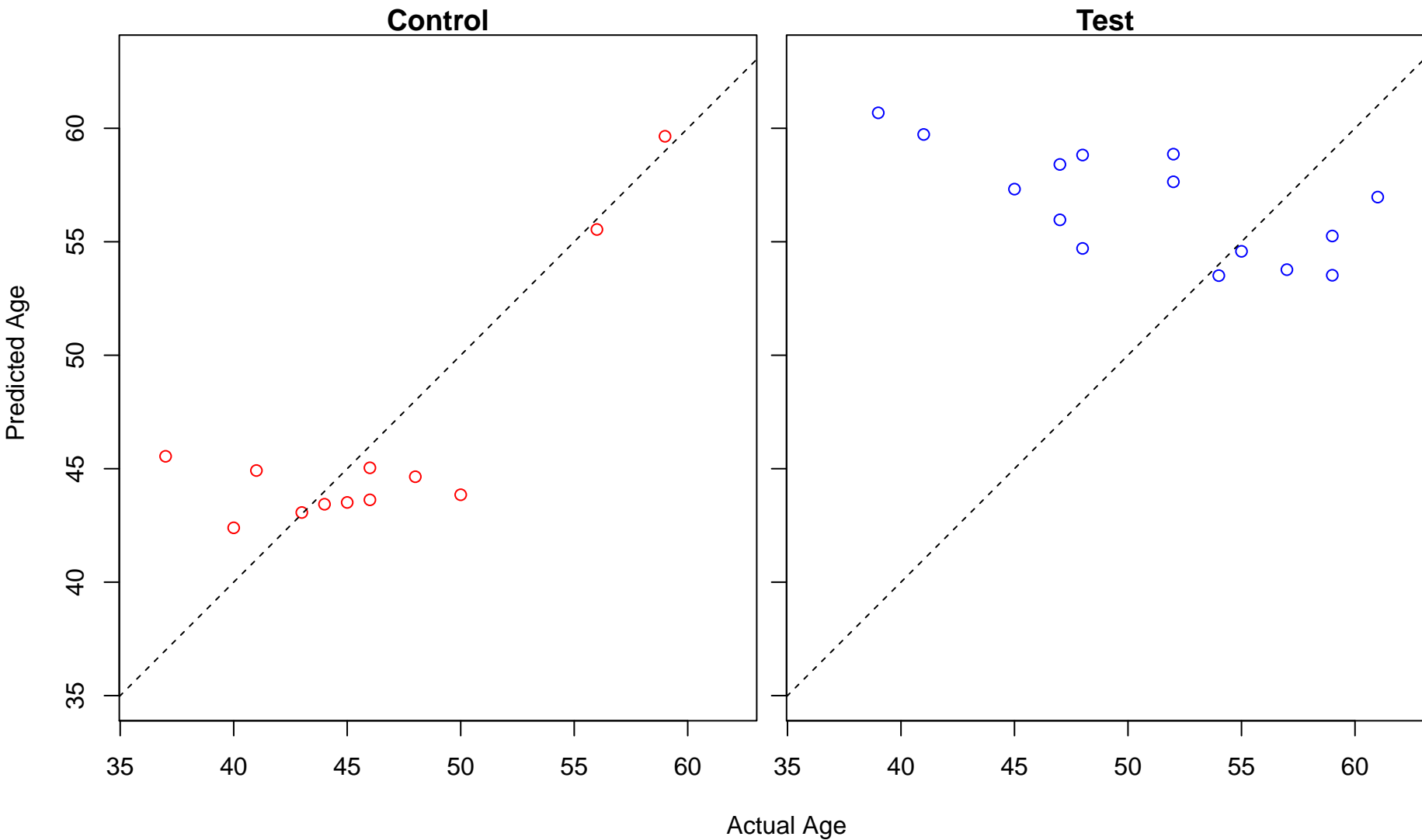
protein O-linked glycosylation (Score: 3.136096)



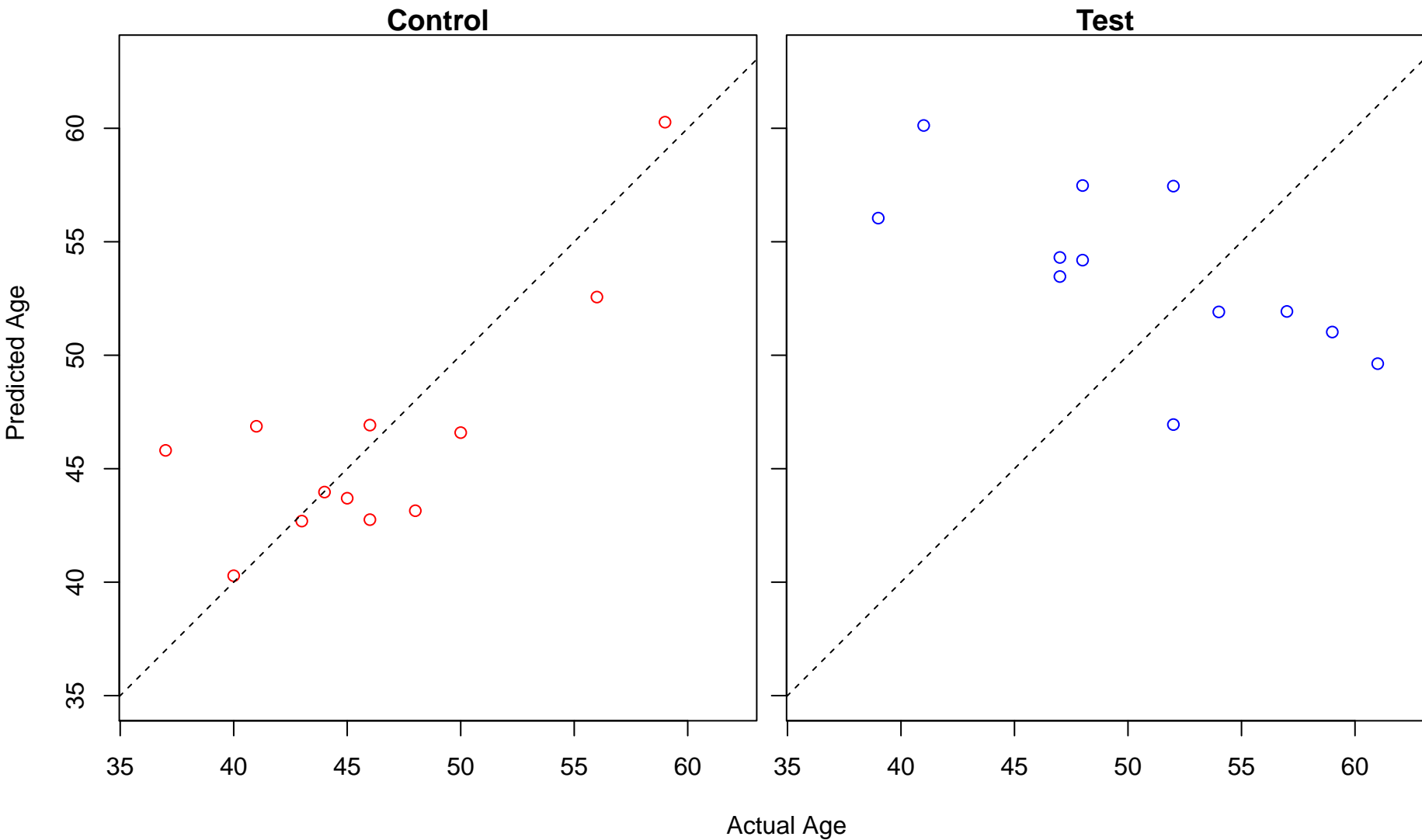
ribonucleoside monophosphate biosynthetic process (Score: 3.134942)



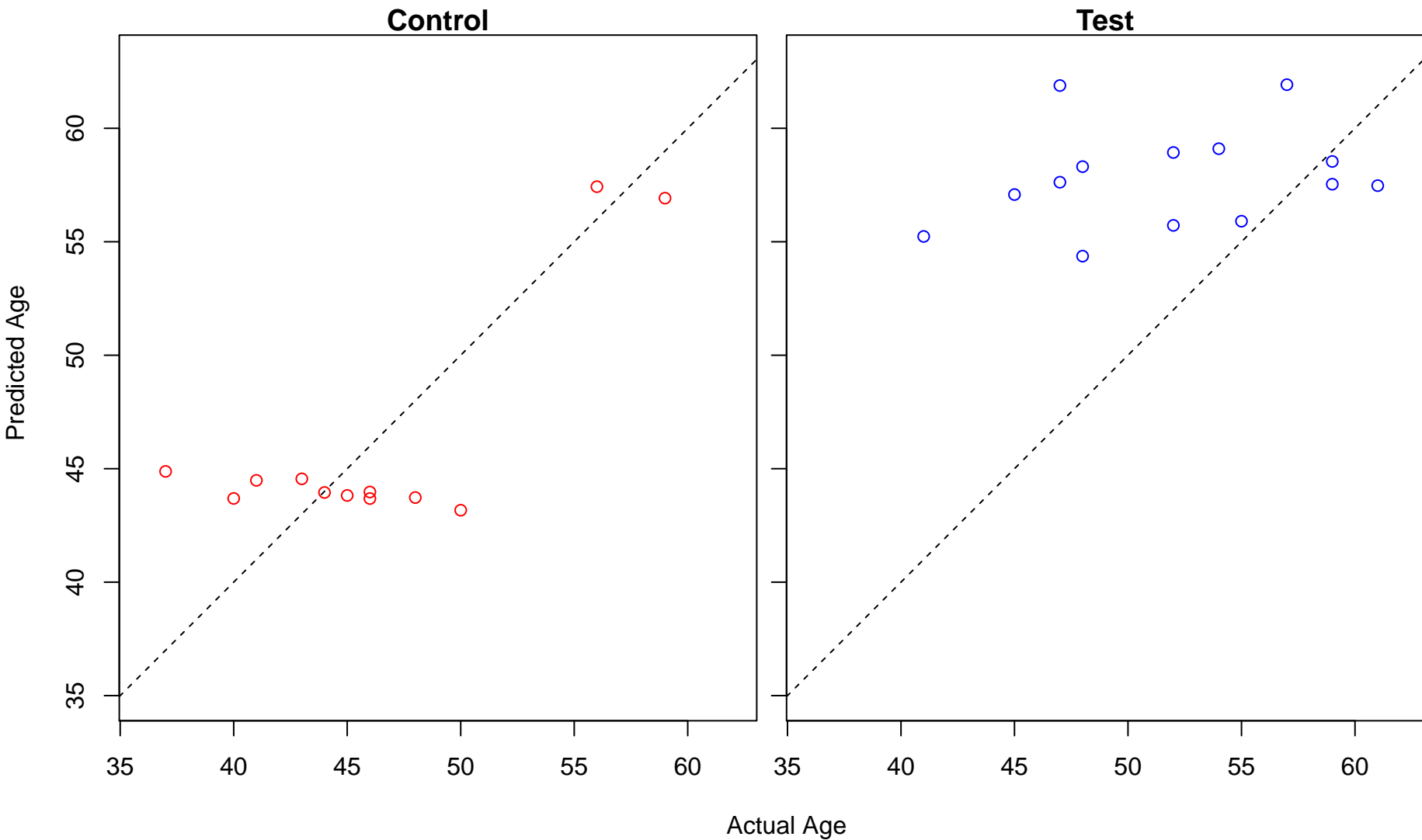
DNA ligation (Score: 3.132519)



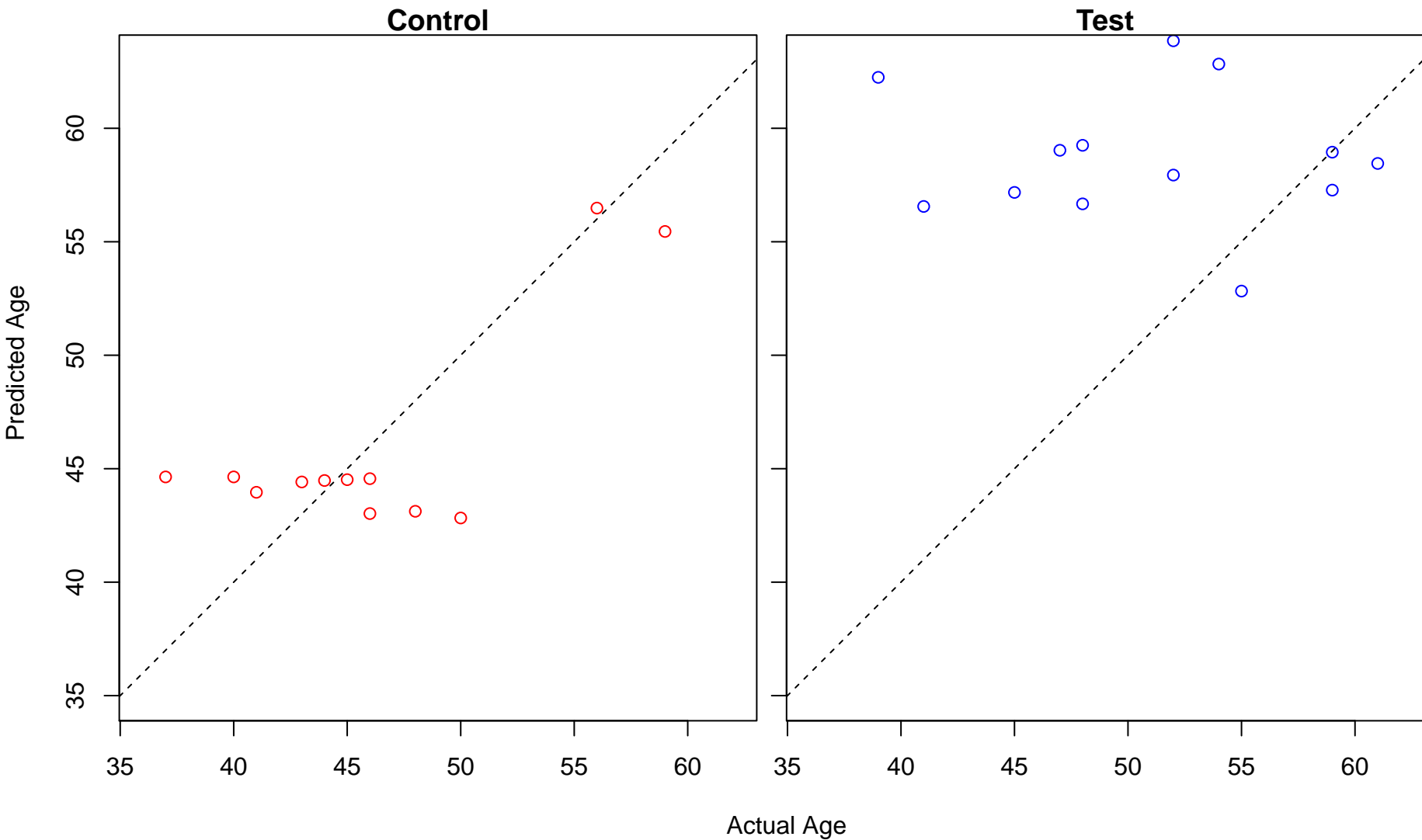
positive regulation of SMAD protein import into nucleus (Score: 3.130624)



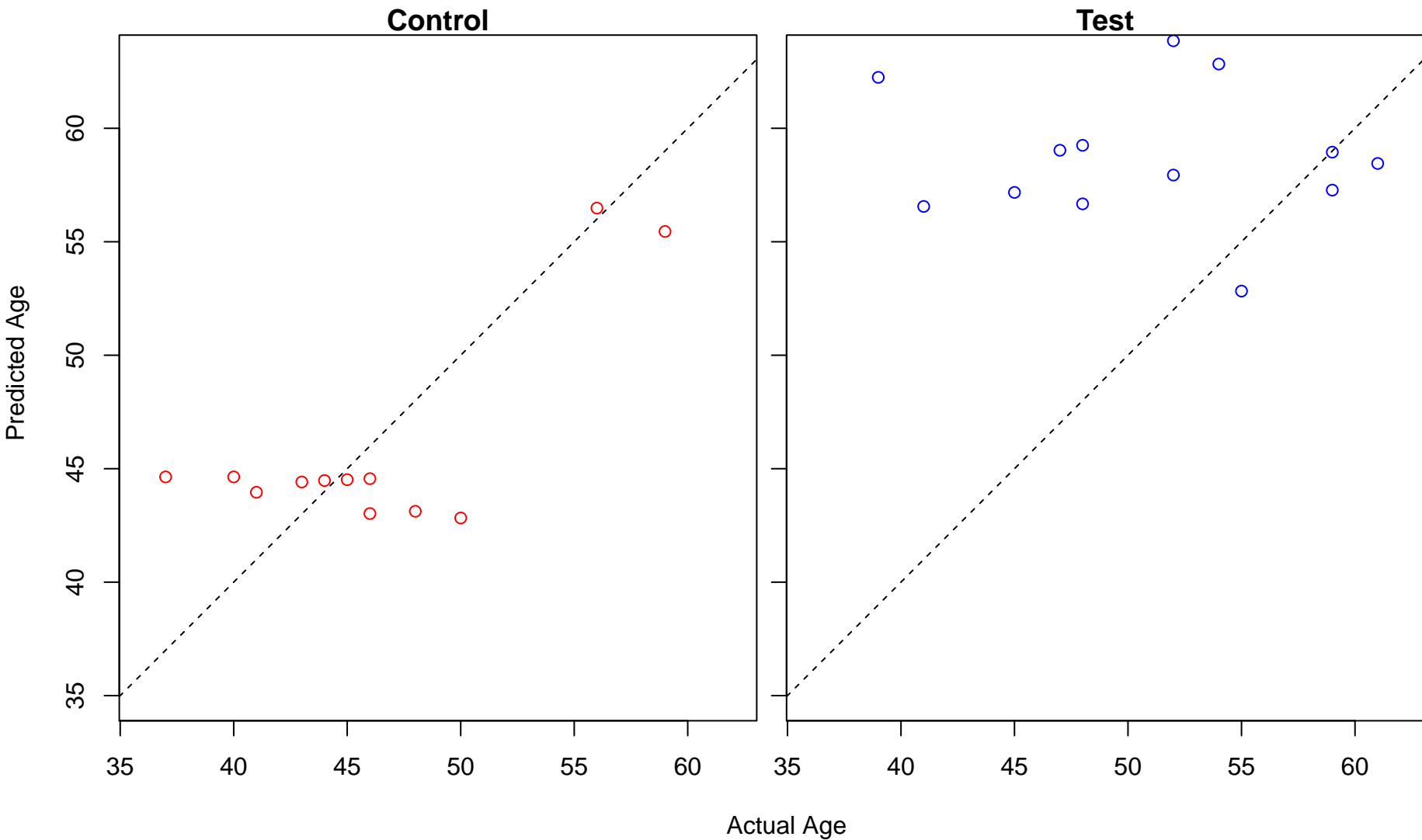
branched-chain amino acid metabolic process (Score: 3.129759)



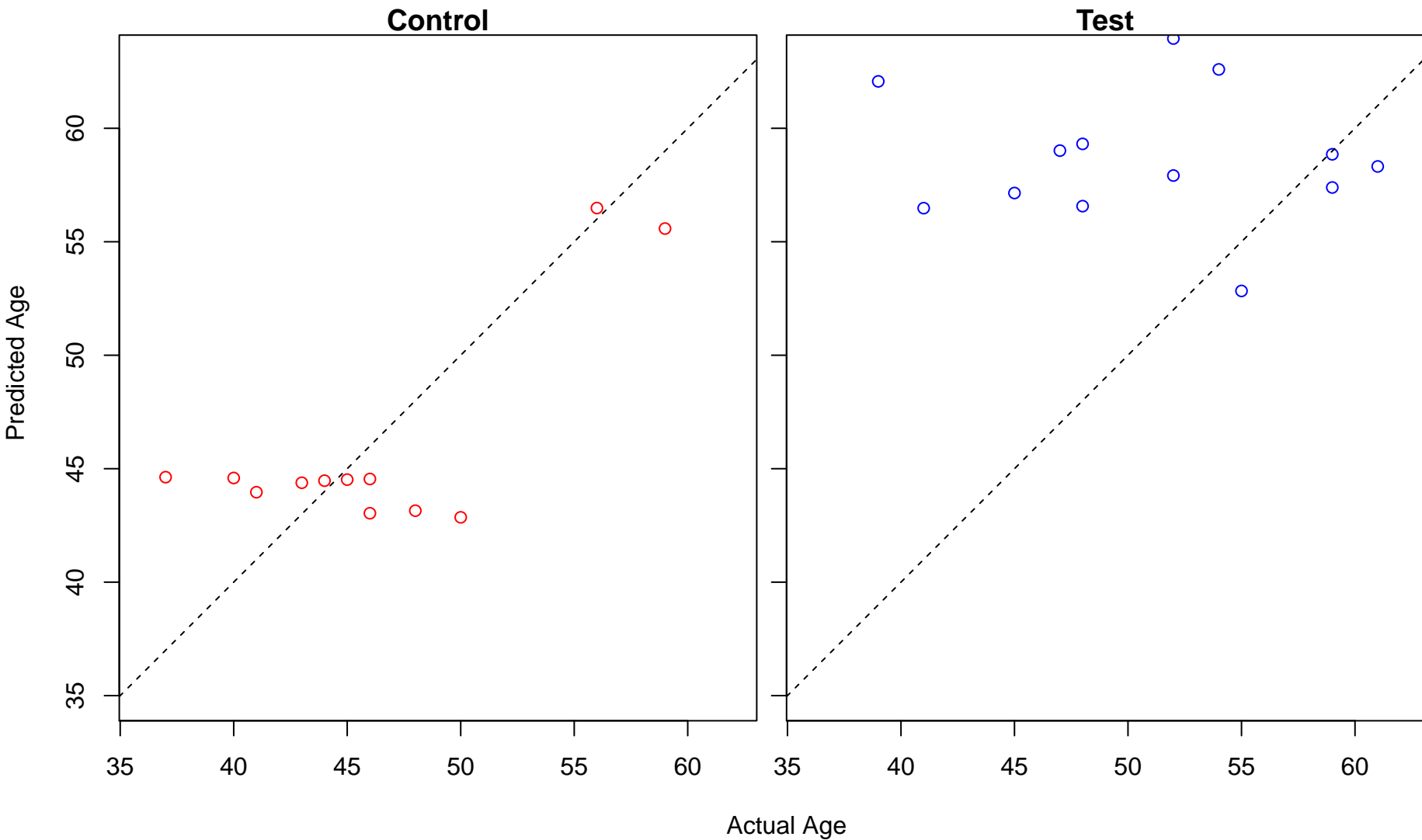
purine nucleoside monophosphate biosynthetic process (Score: 3.129600)



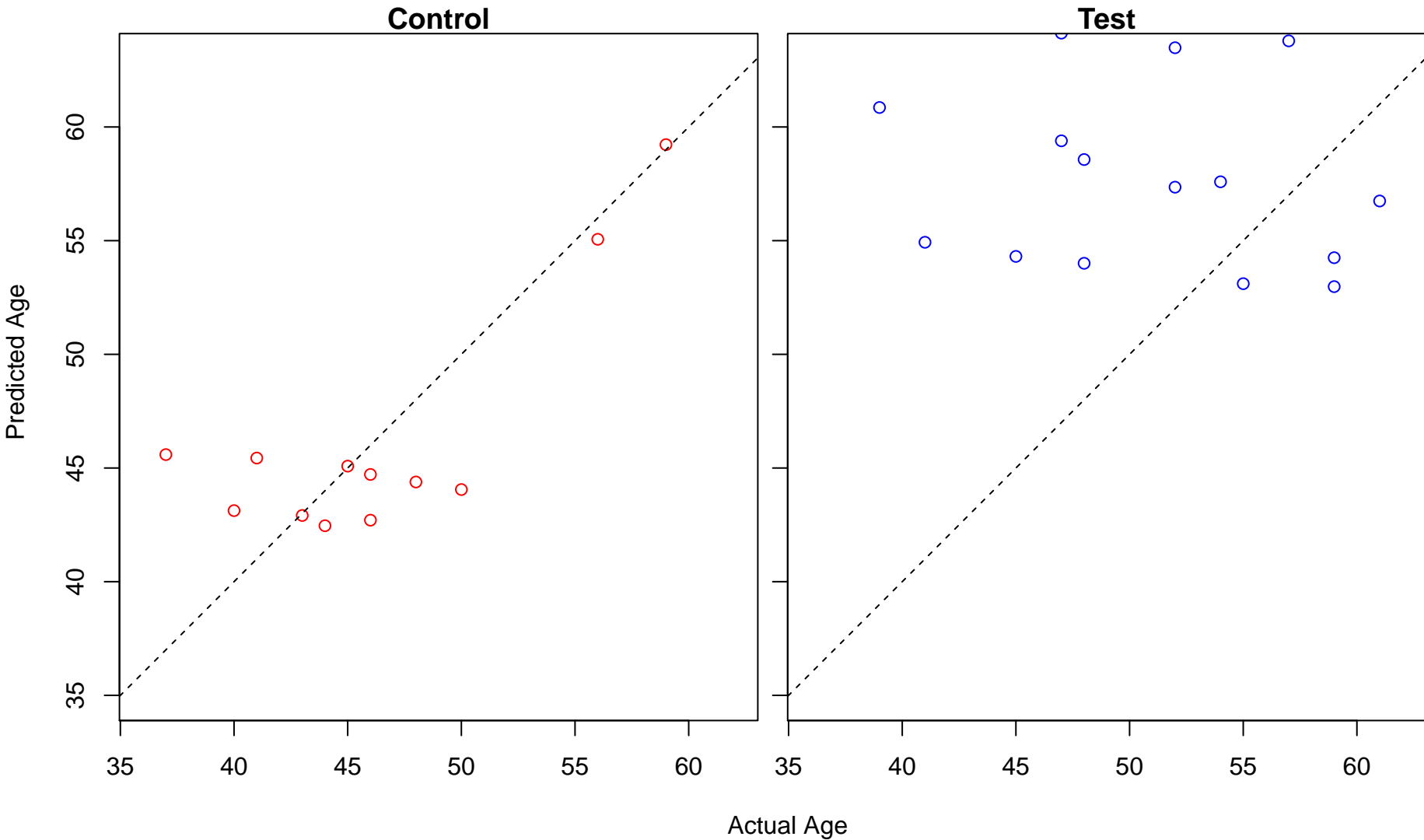
purine ribonucleoside monophosphate biosynthetic process (Score: 3.129600)



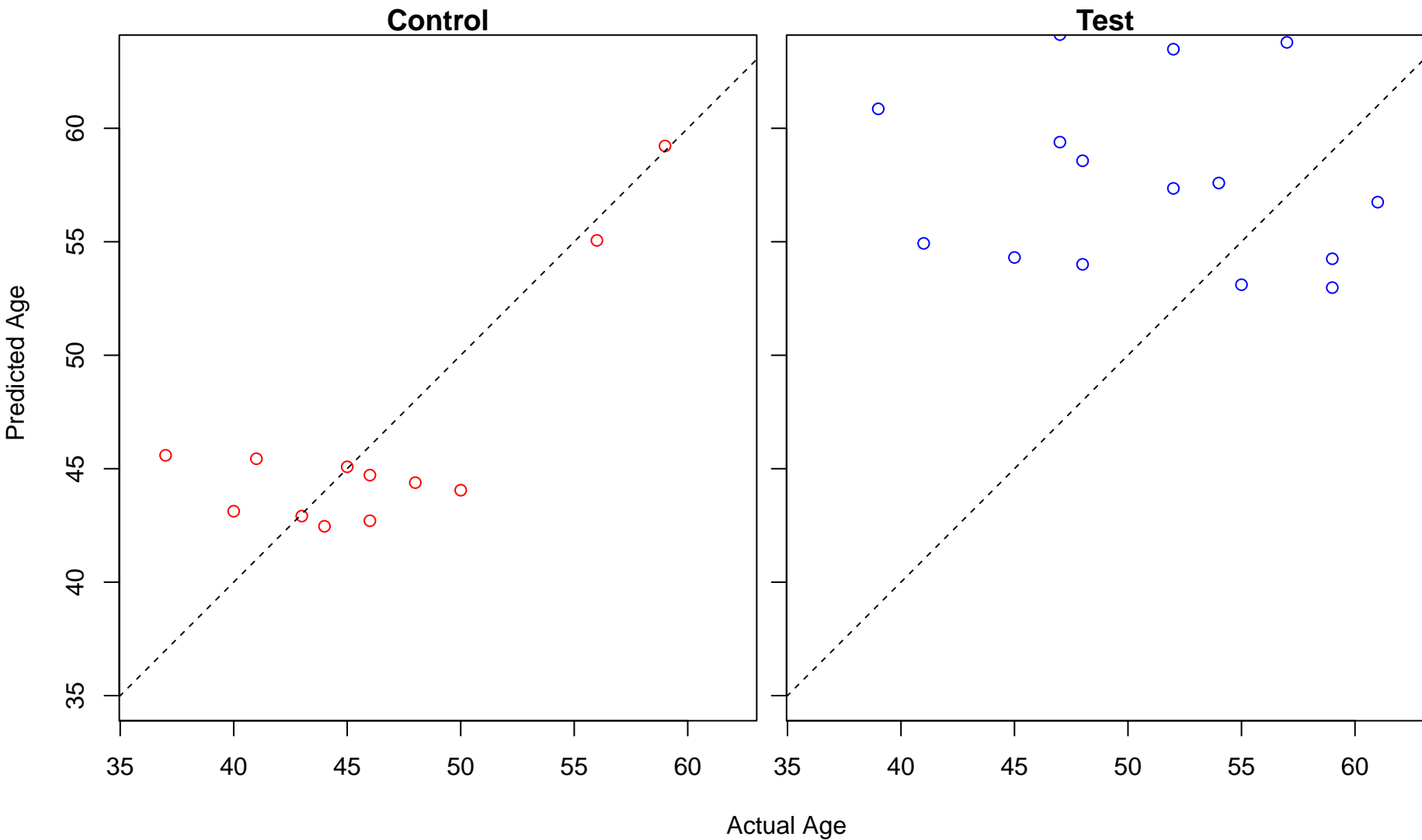
nucleoside monophosphate biosynthetic process (Score: 3.129151)



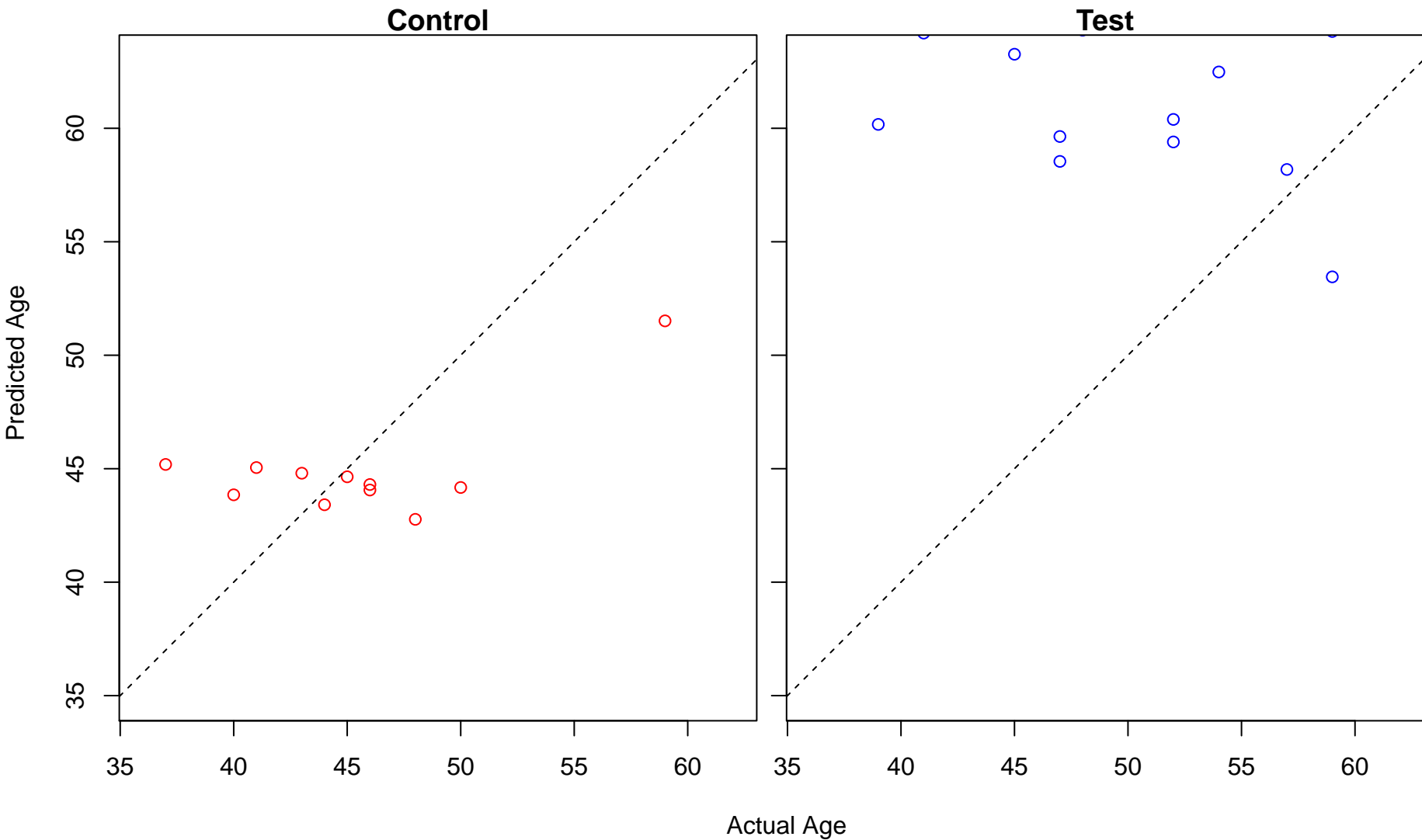
negative regulation of stress fiber assembly (Score: 3.129098)



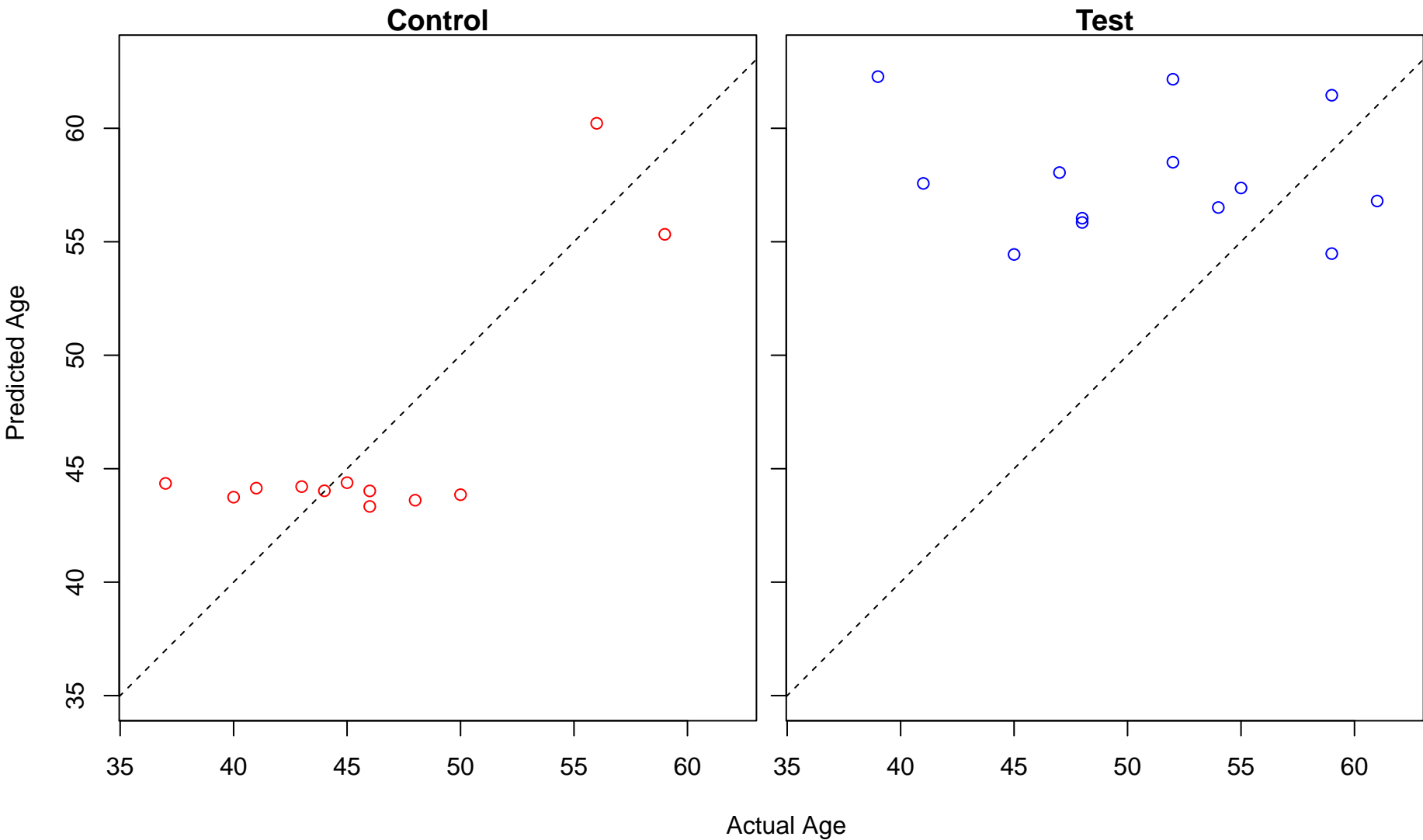
negative regulation of actin filament bundle assembly (Score: 3.129082)



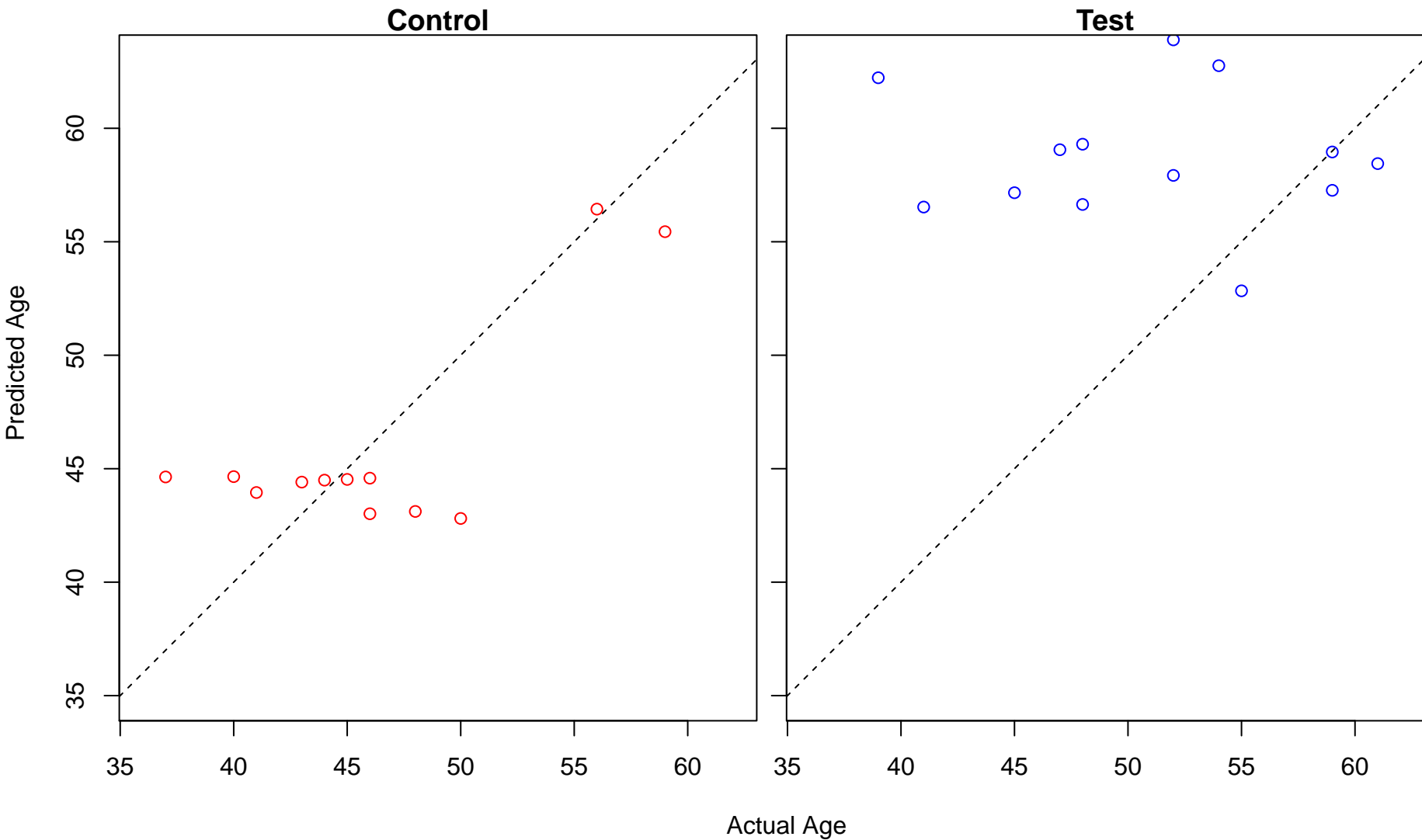
regulation of myoblast fusion (Score: 3.128492)



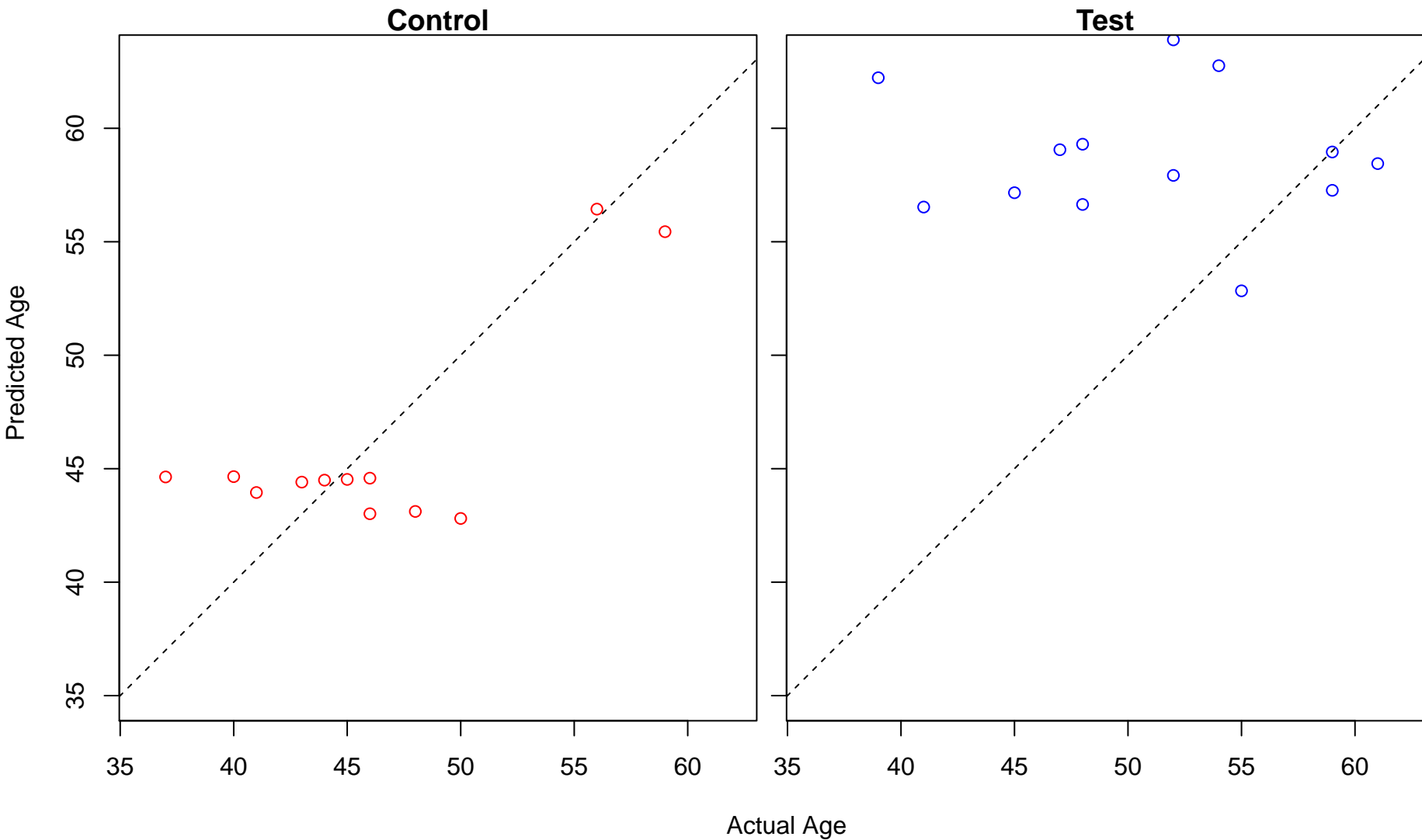
regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 3.127)



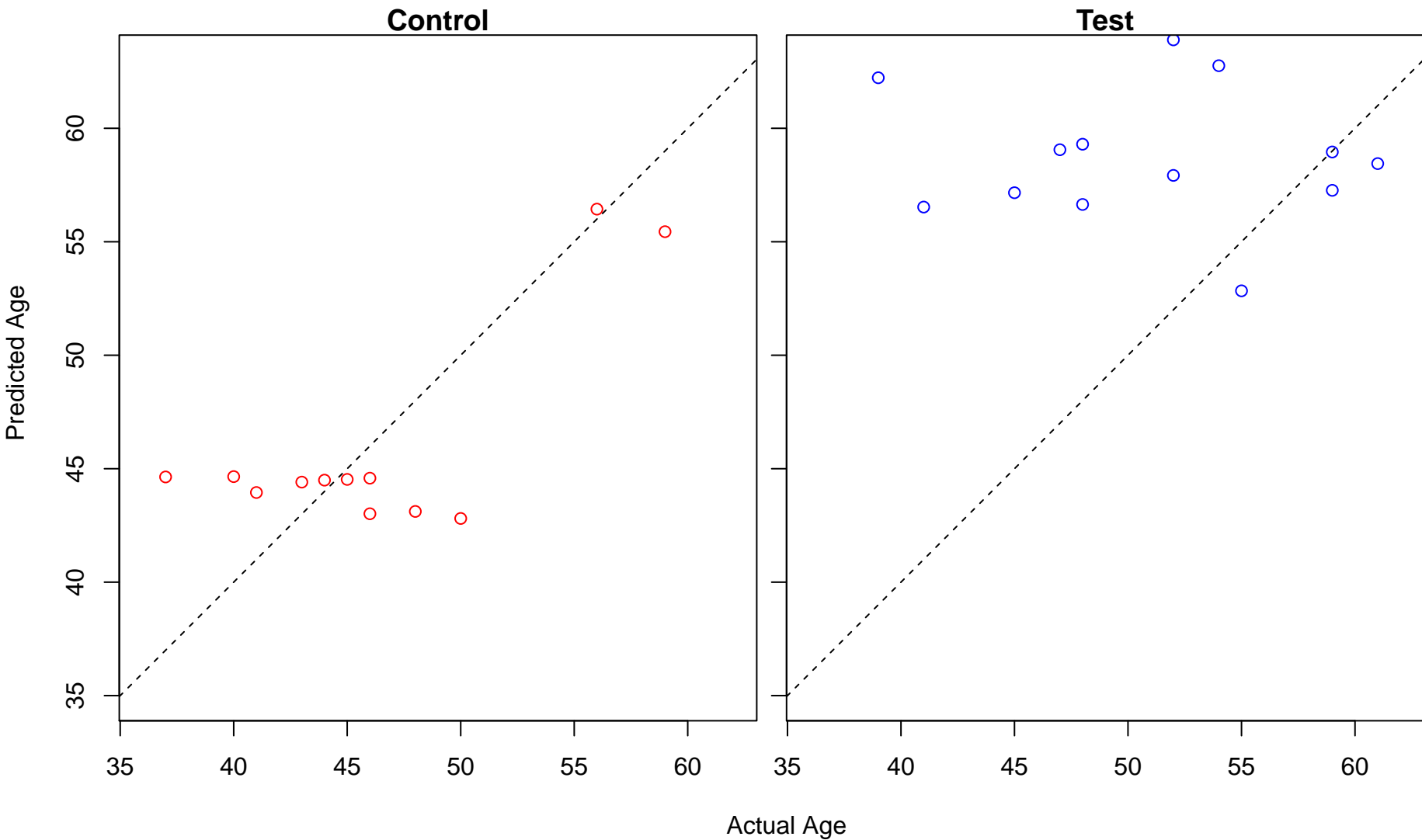
ATP biosynthetic process (Score: 3.127234)



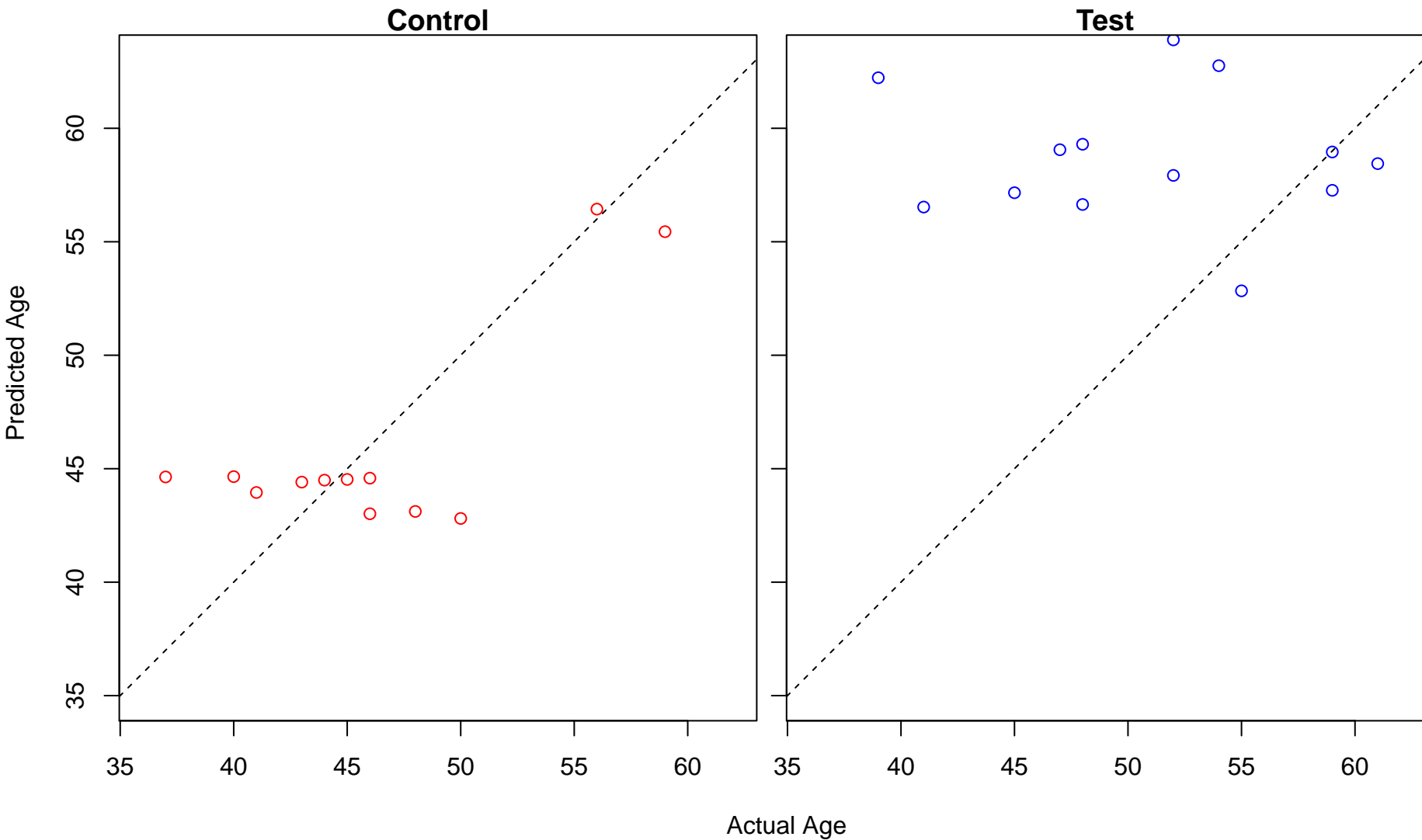
purine nucleoside triphosphate biosynthetic process (Score: 3.127234)



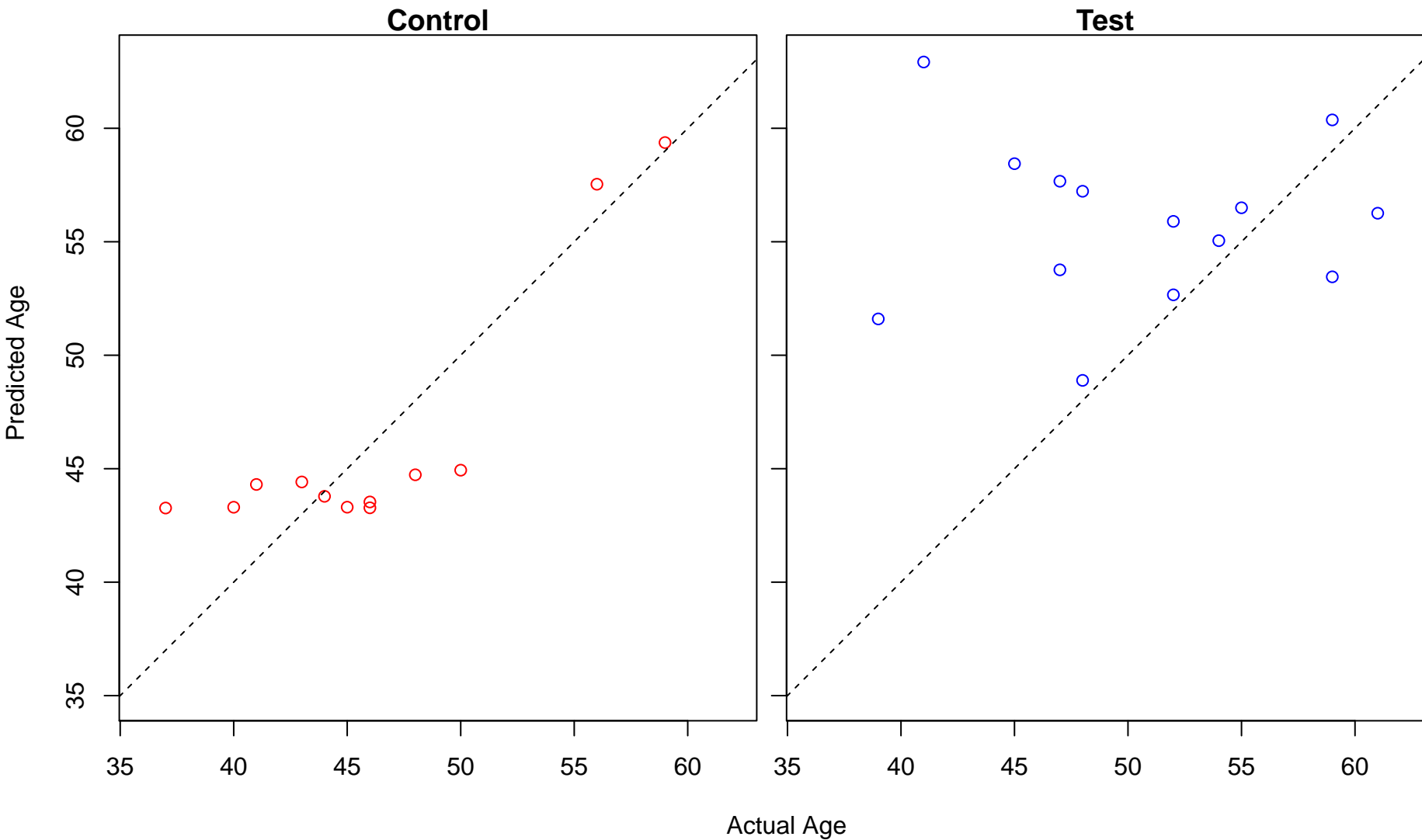
purine ribonucleoside triphosphate biosynthetic process (Score: 3.127234)



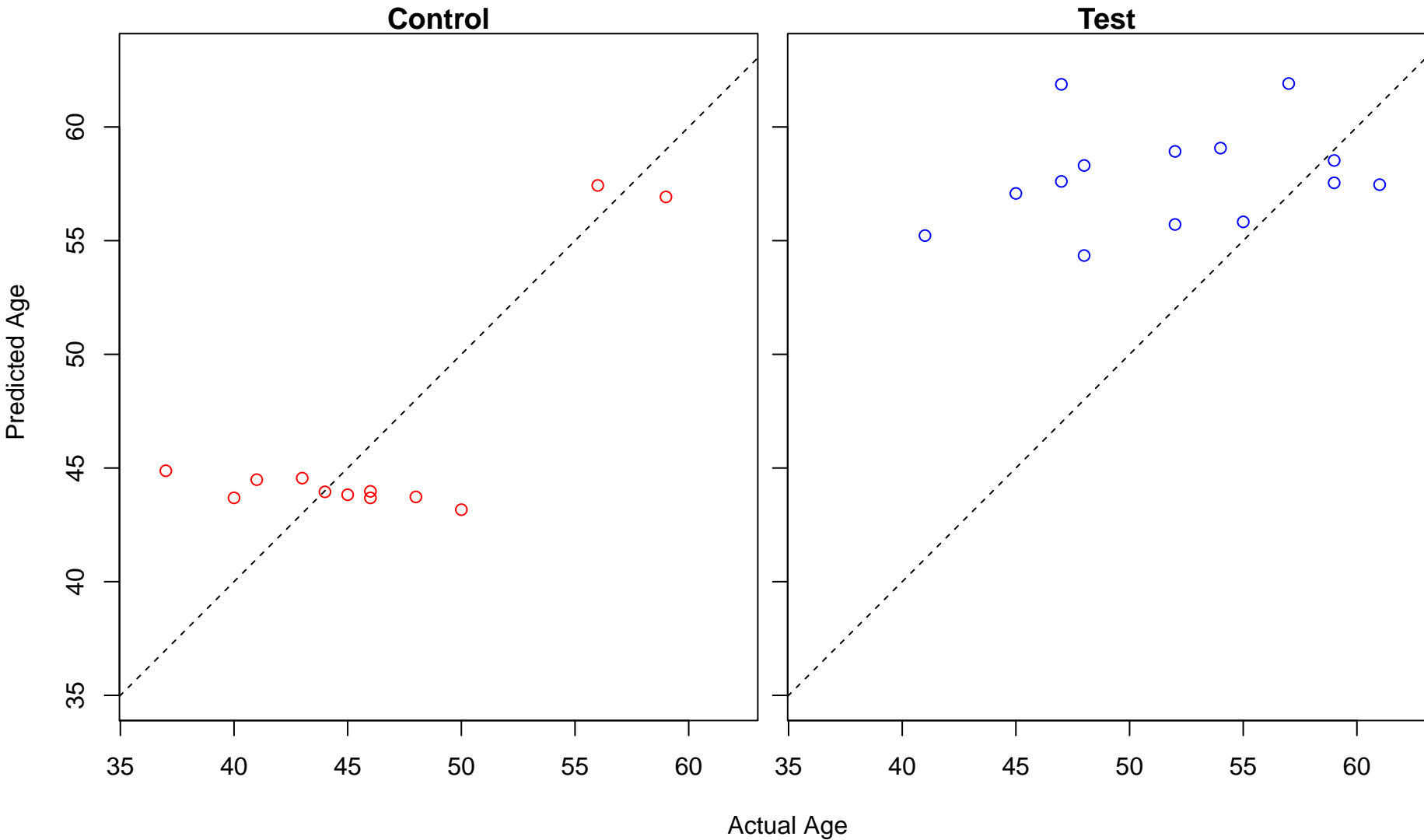
ribonucleoside triphosphate biosynthetic process (Score: 3.127135)



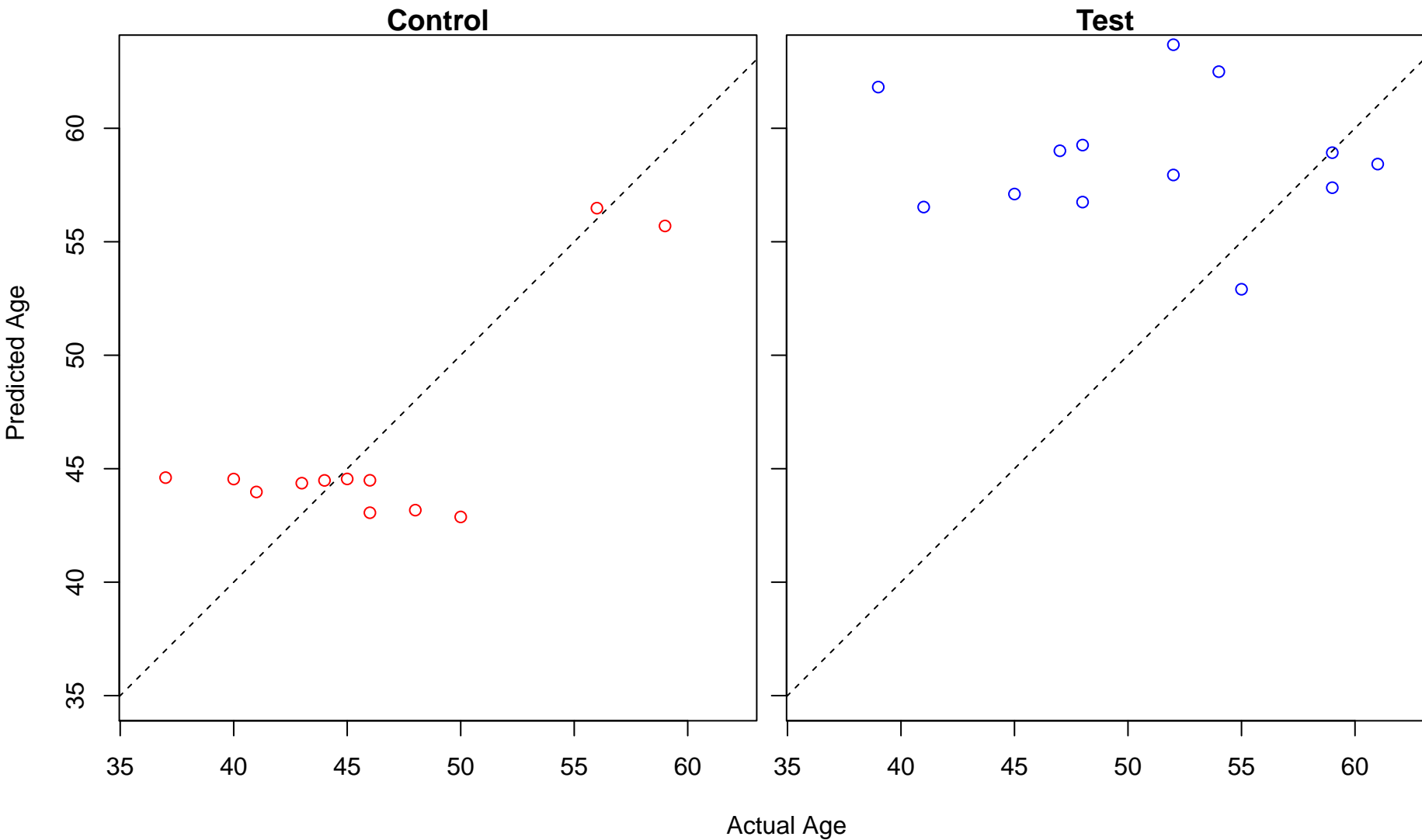
prostanoid metabolic process (Score: 3.126746)



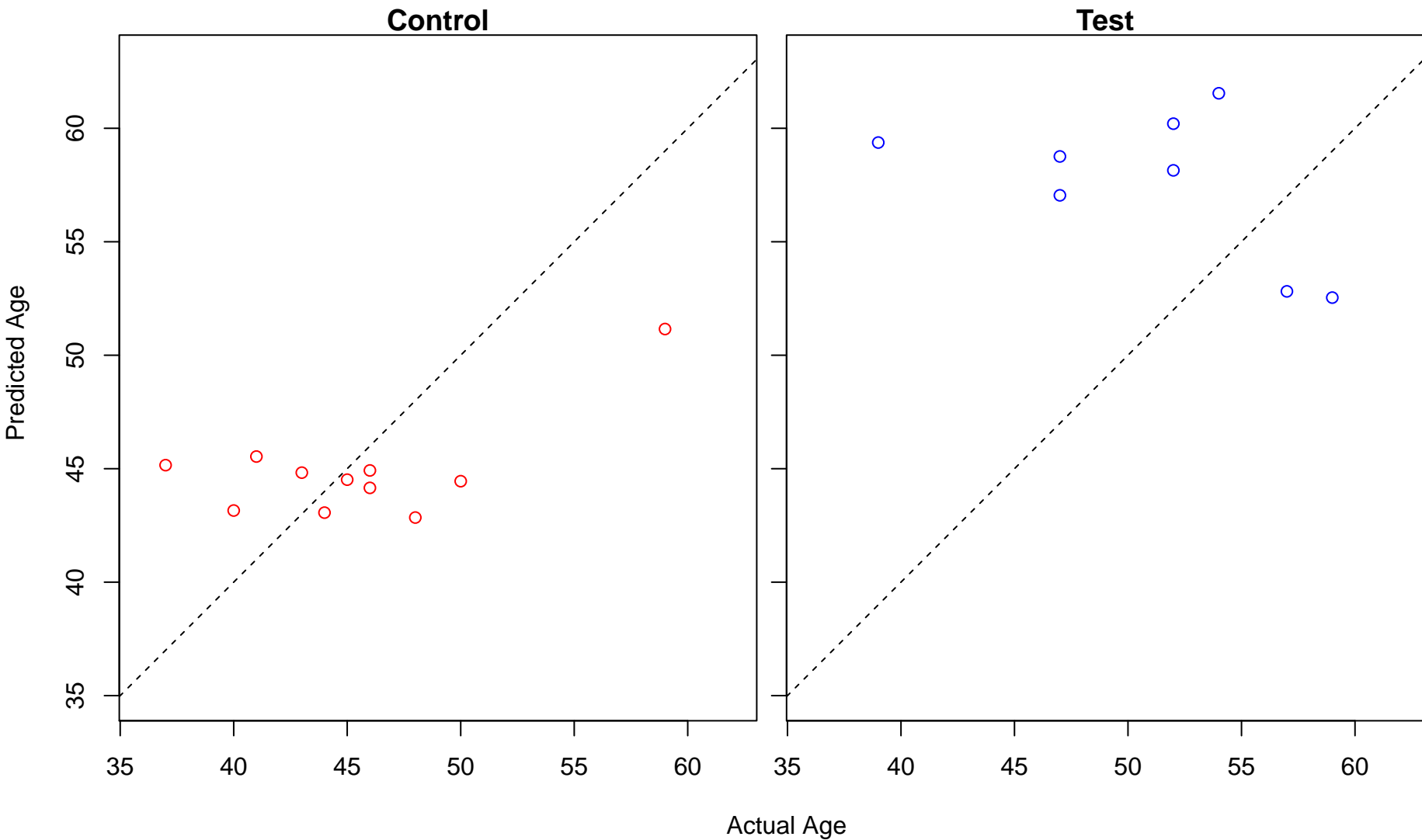
branched-chain amino acid catabolic process (Score: 3.126710)



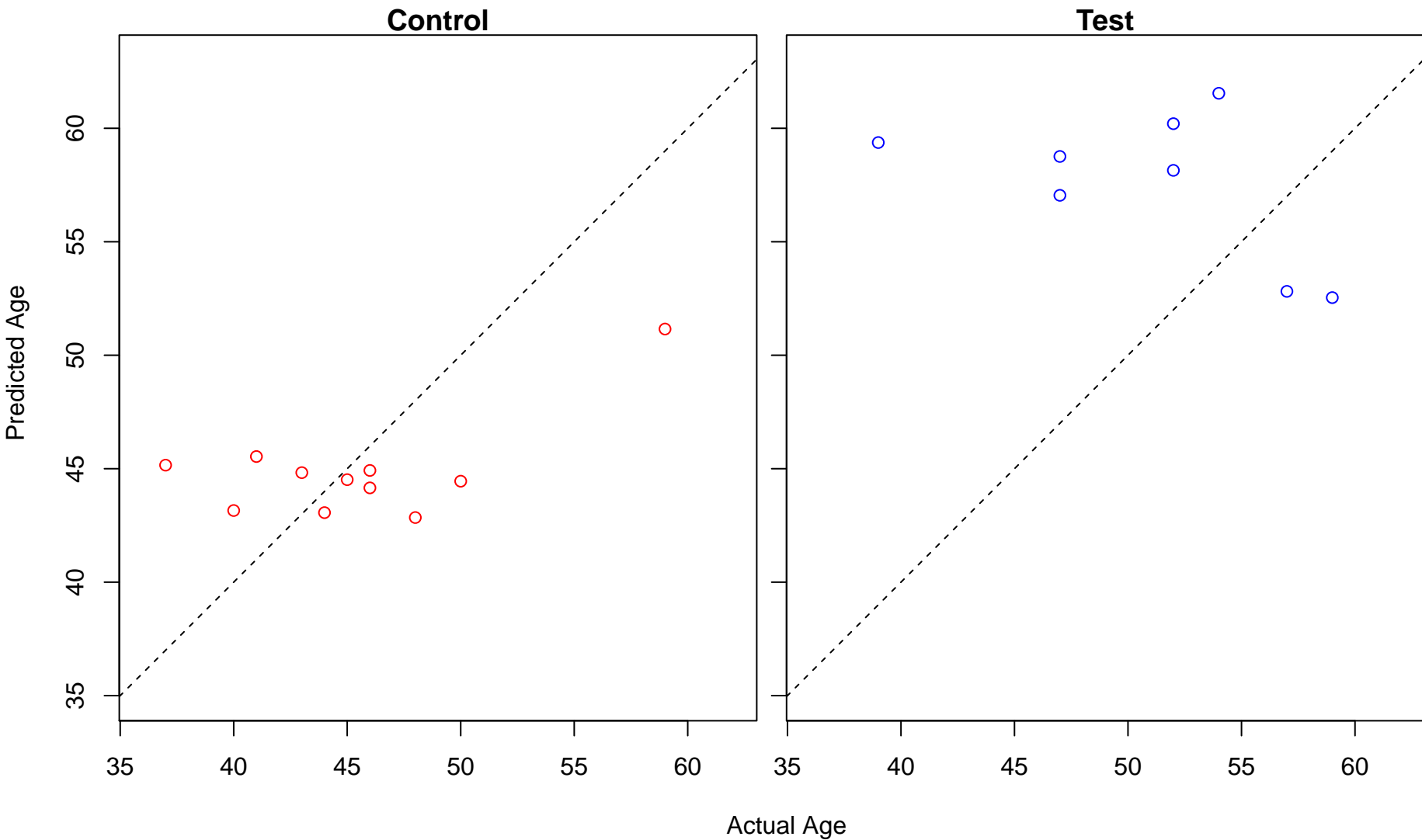
nucleoside triphosphate biosynthetic process (Score: 3.125532)



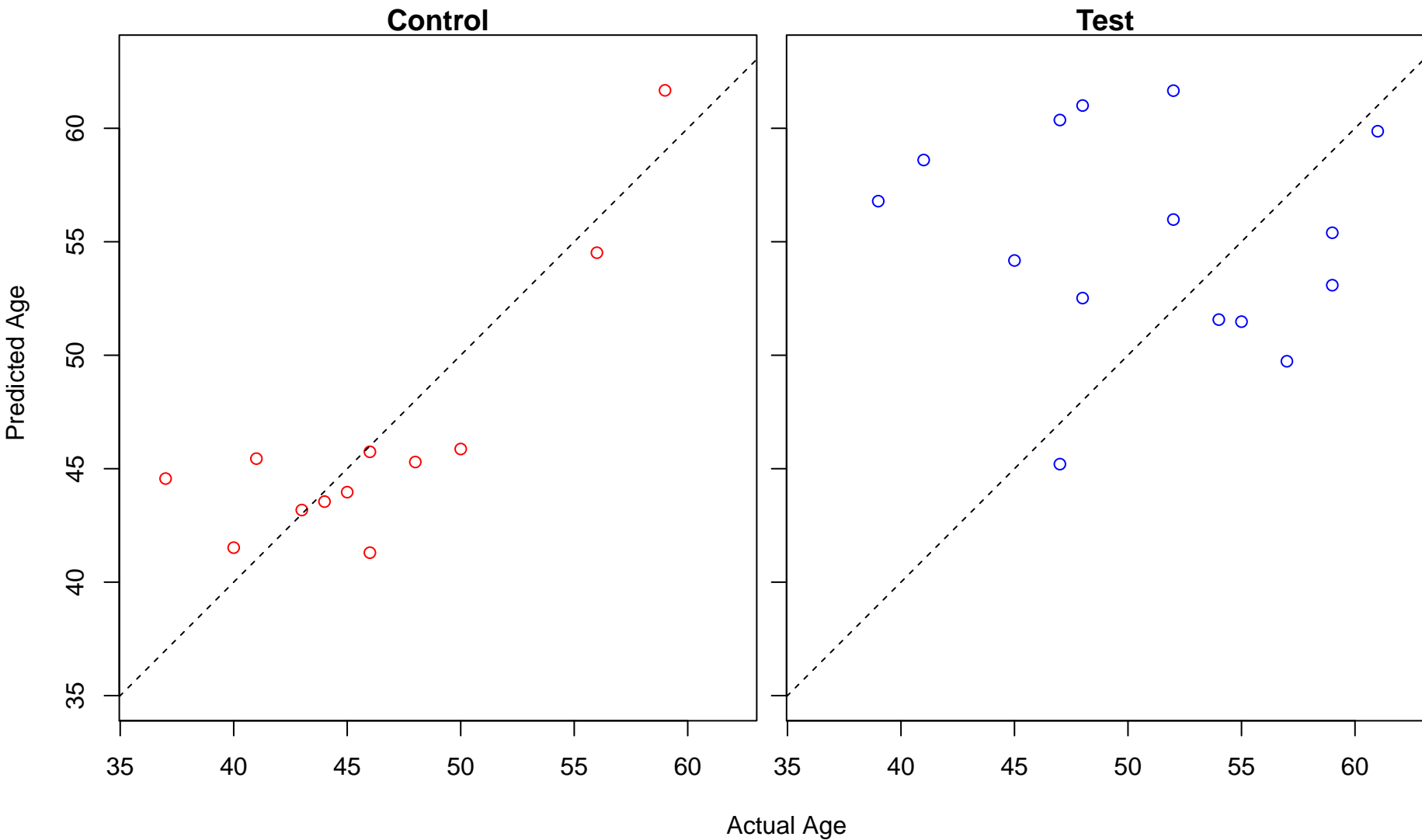
regulation of skeletal muscle satellite cell proliferation (Score: 3.124097)



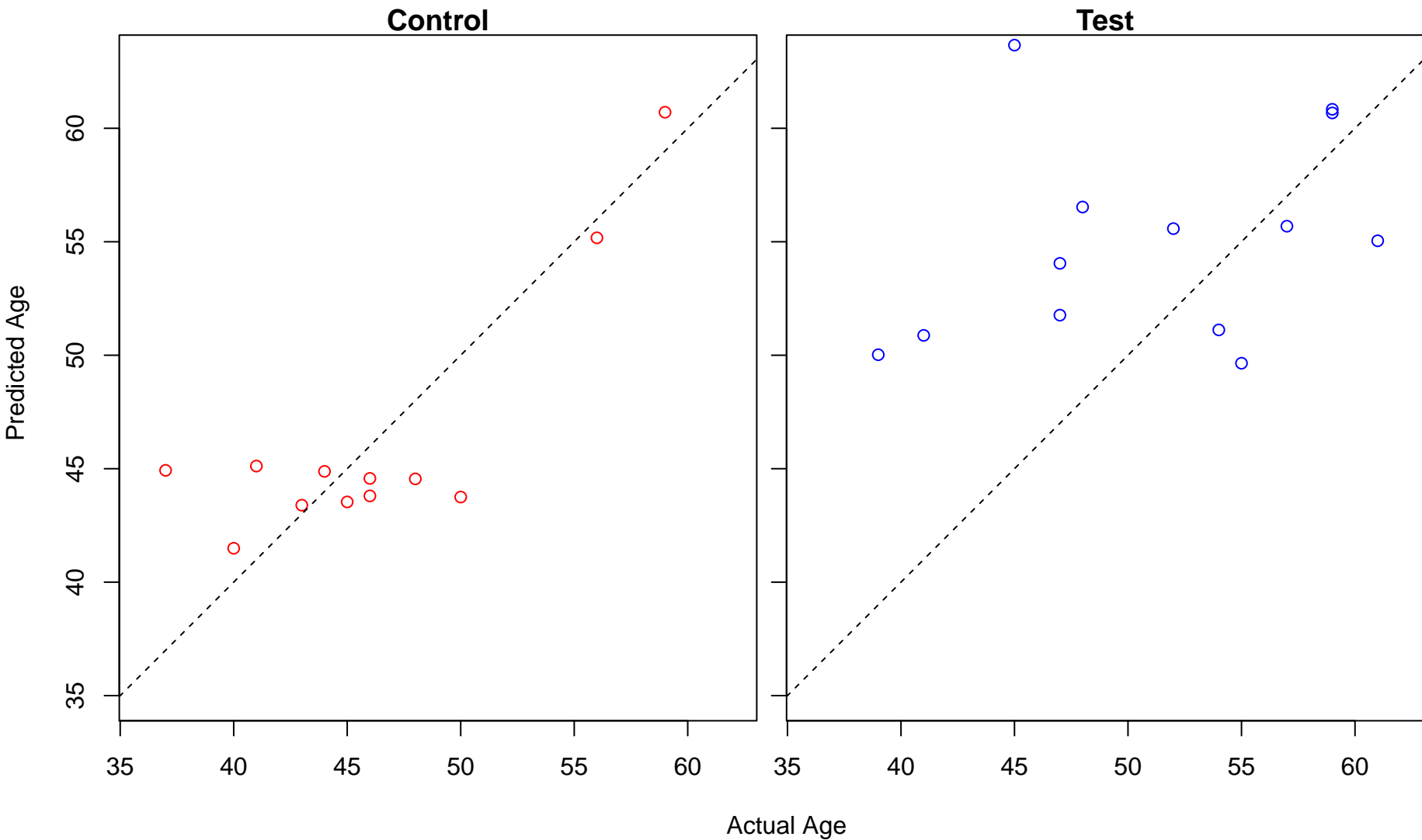
regulation of skeletal muscle cell proliferation (Score: 3.124097)



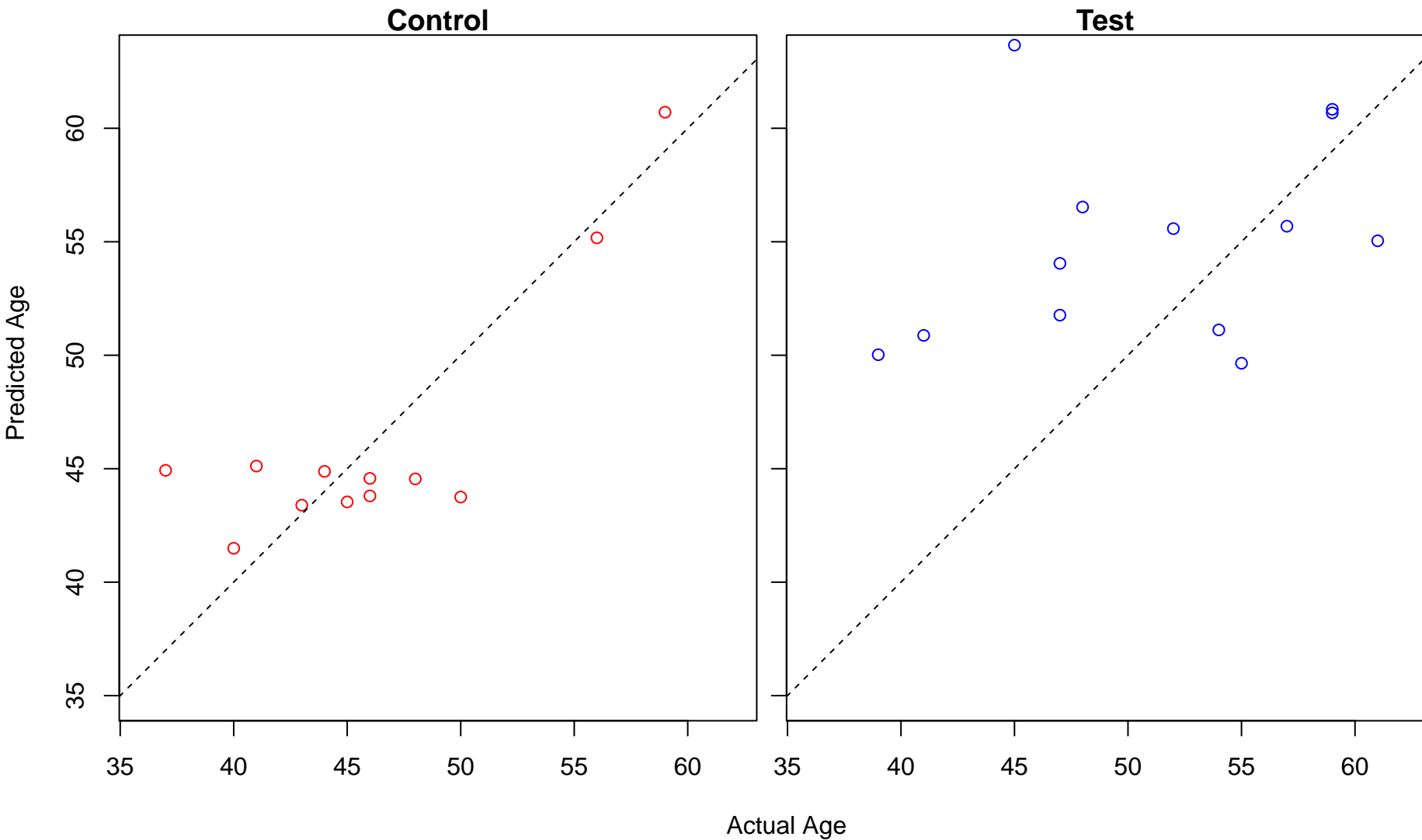
telomere maintenance (Score: 3.119119)



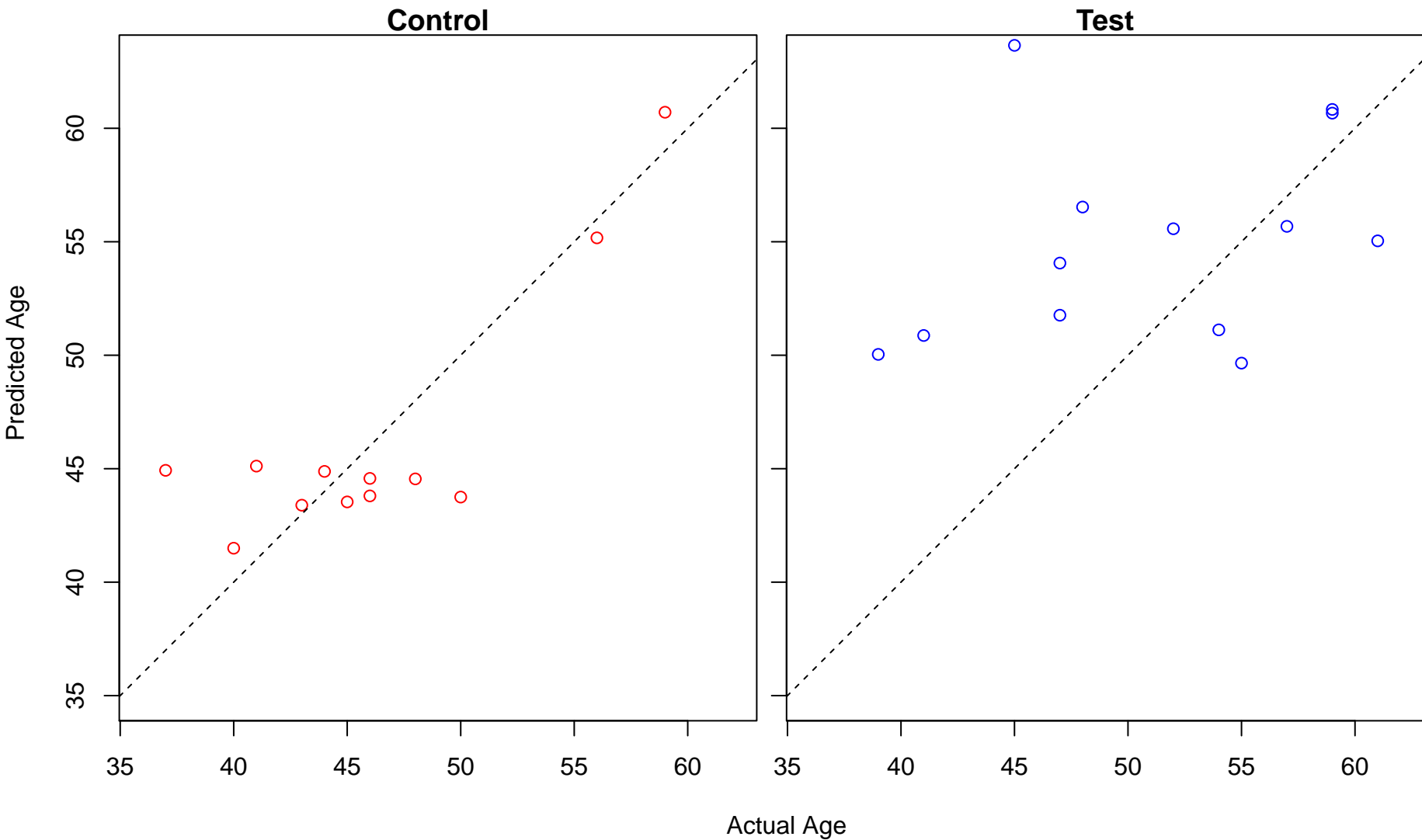
purine ribonucleotide transport (Score: 3.115834)



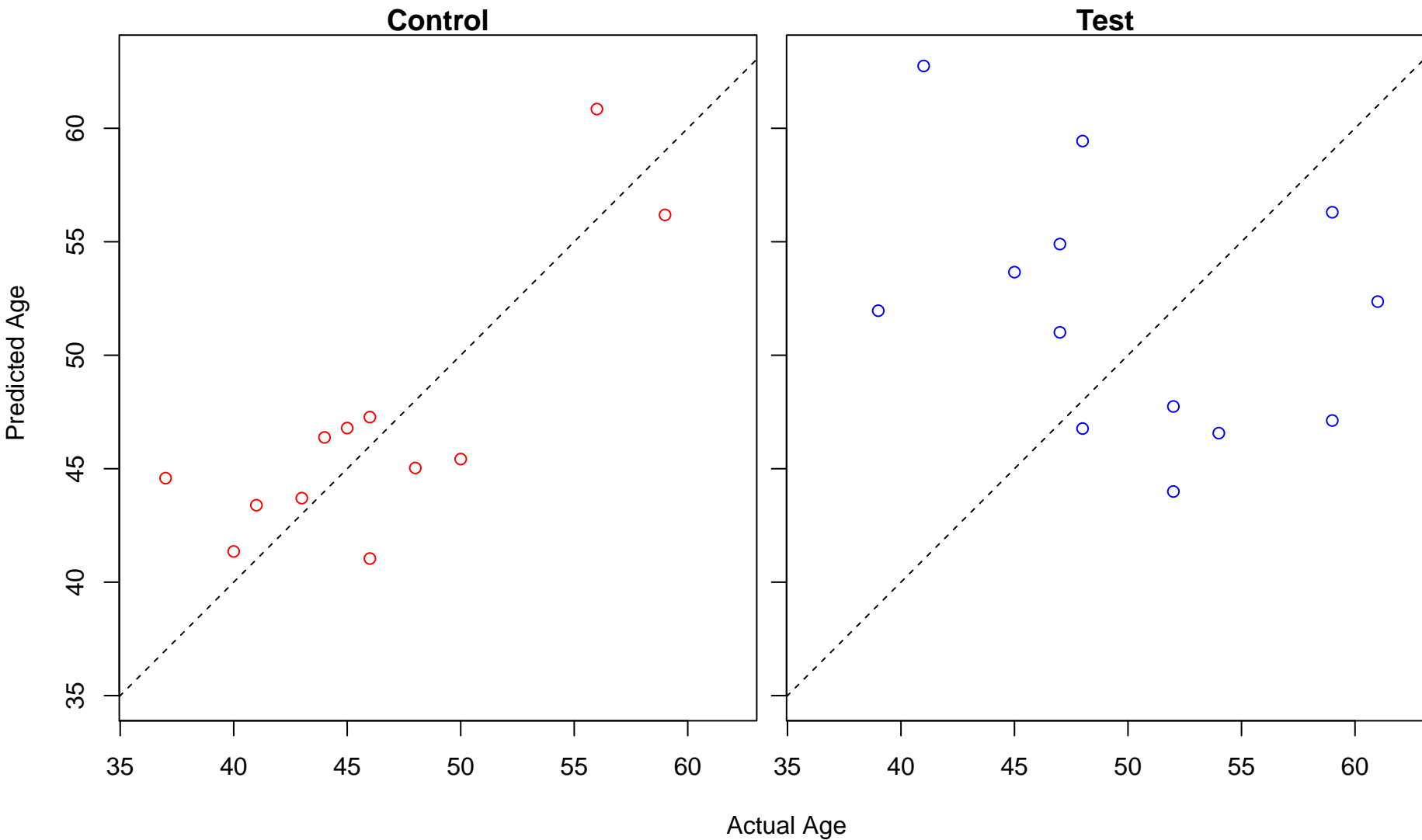
adenine nucleotide transport (Score: 3.115834)



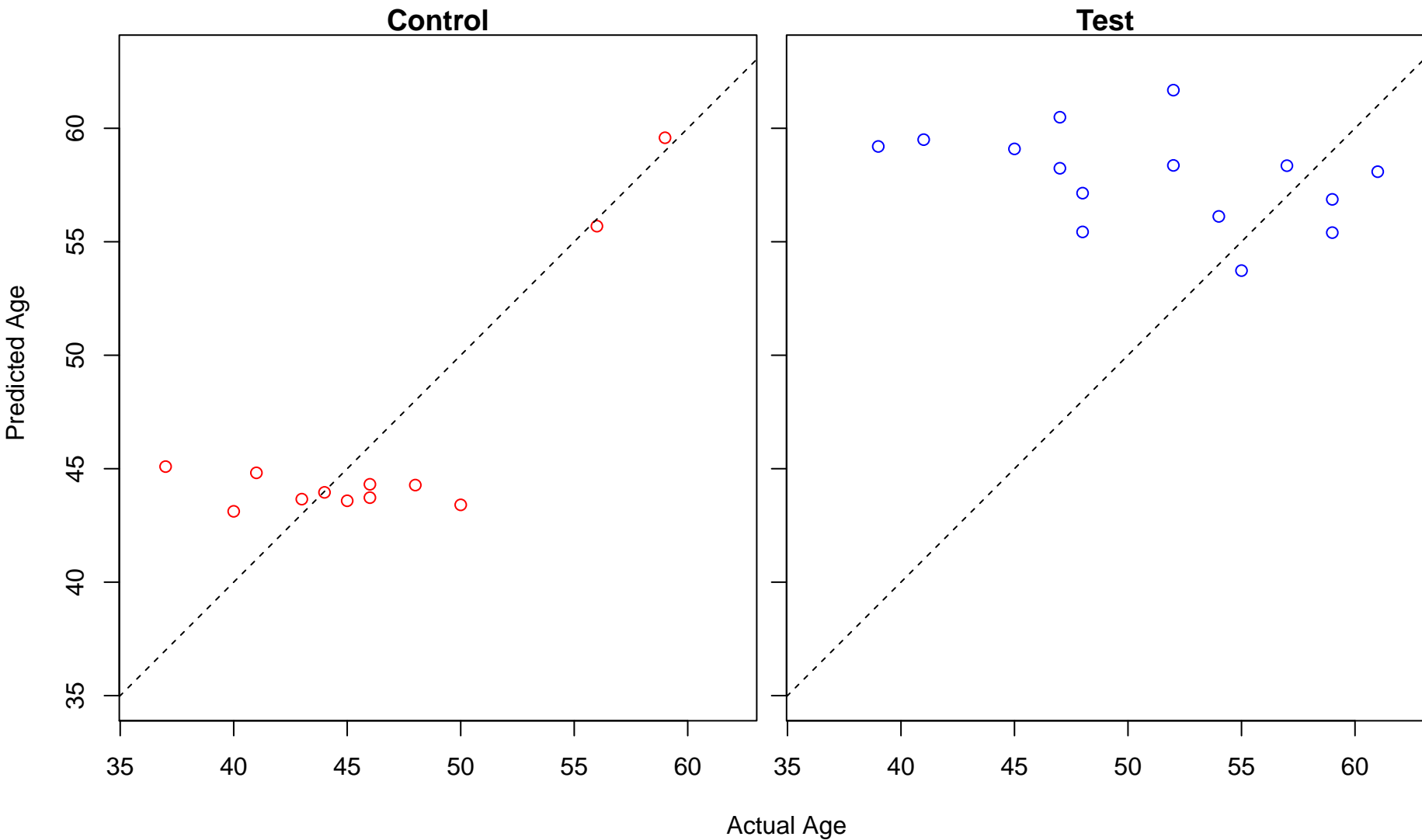
purine nucleotide transport (Score: 3.114619)



vascular endothelial growth factor receptor signaling pathway (Score: 3.112752)

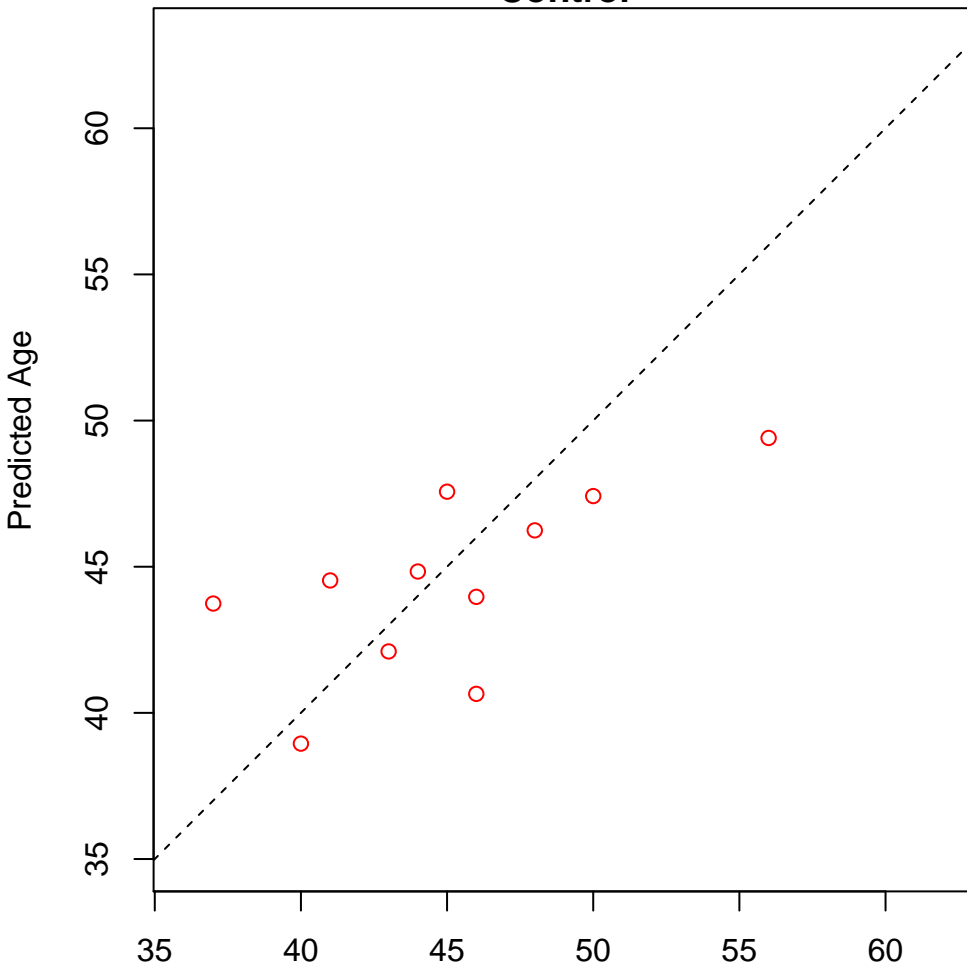


regulation of DNA binding (Score: 3.112548)

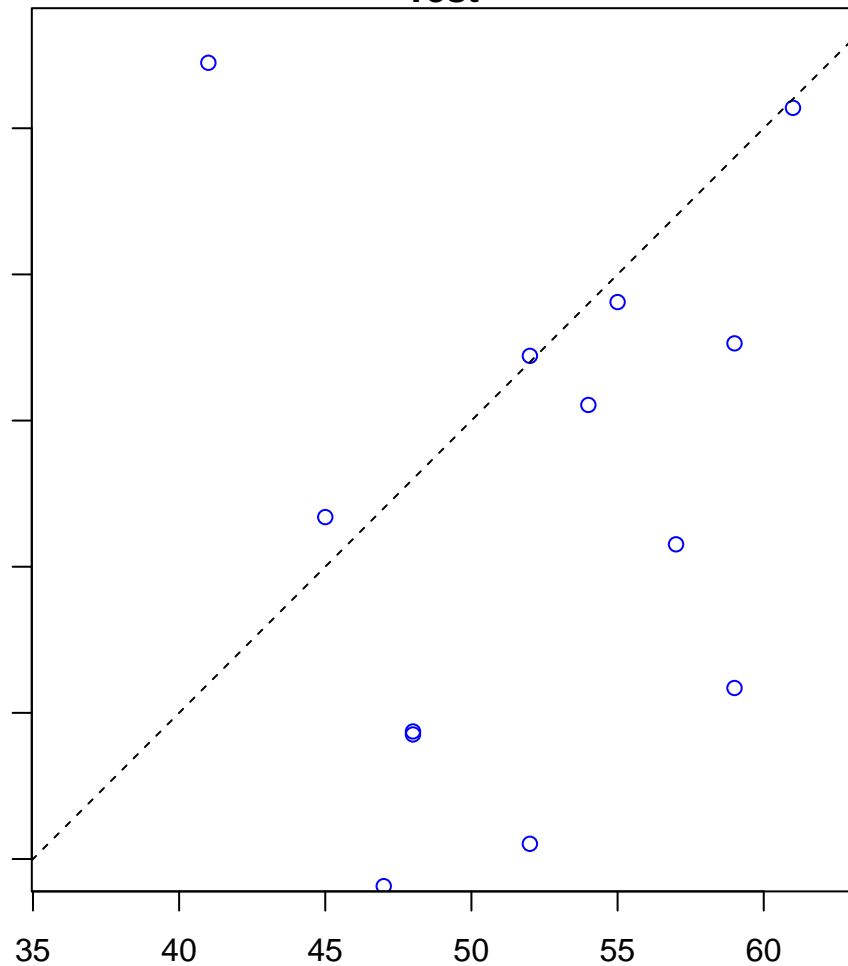


purine nucleotide catabolic process (Score: 3.112267)

Control

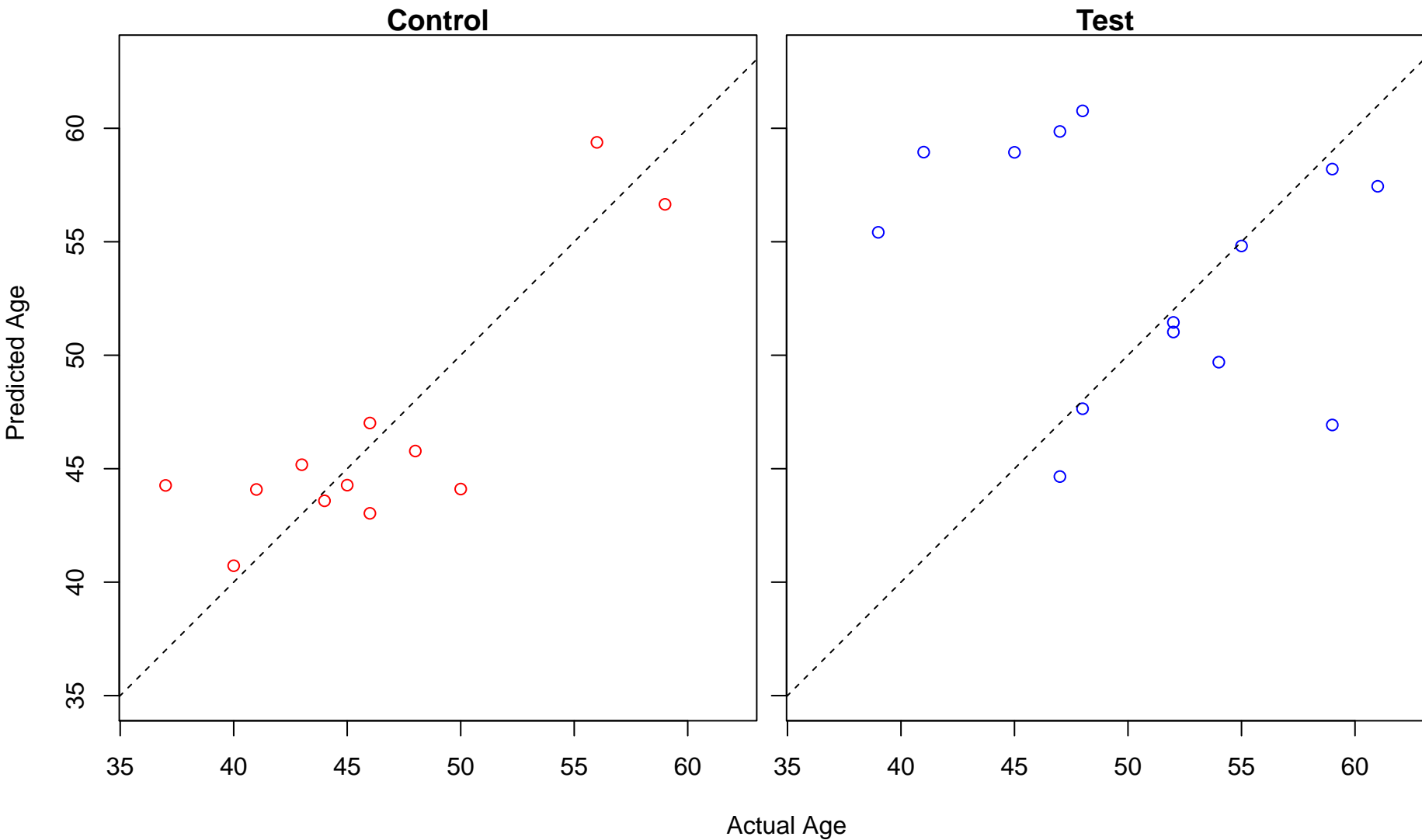


Test

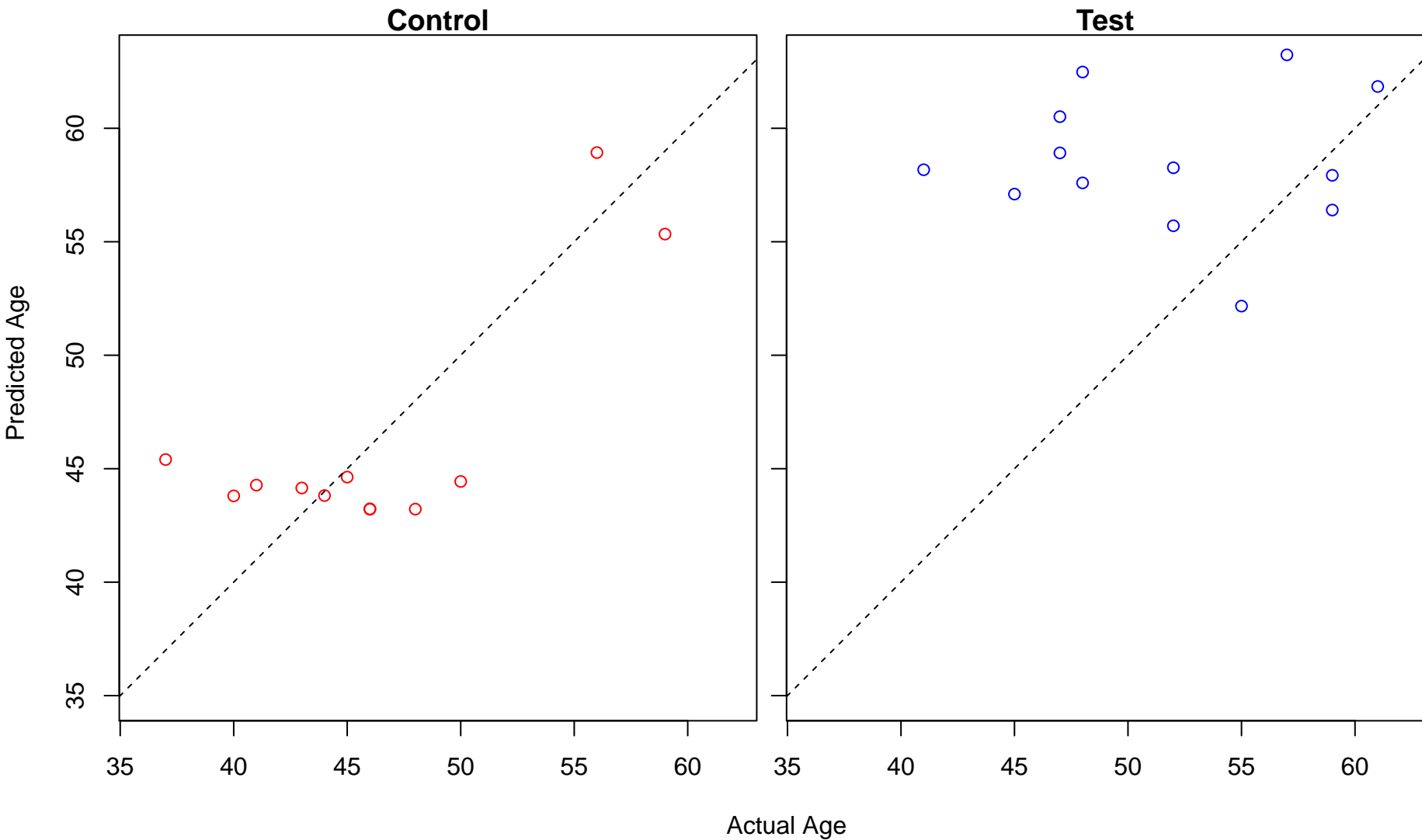


Actual Age

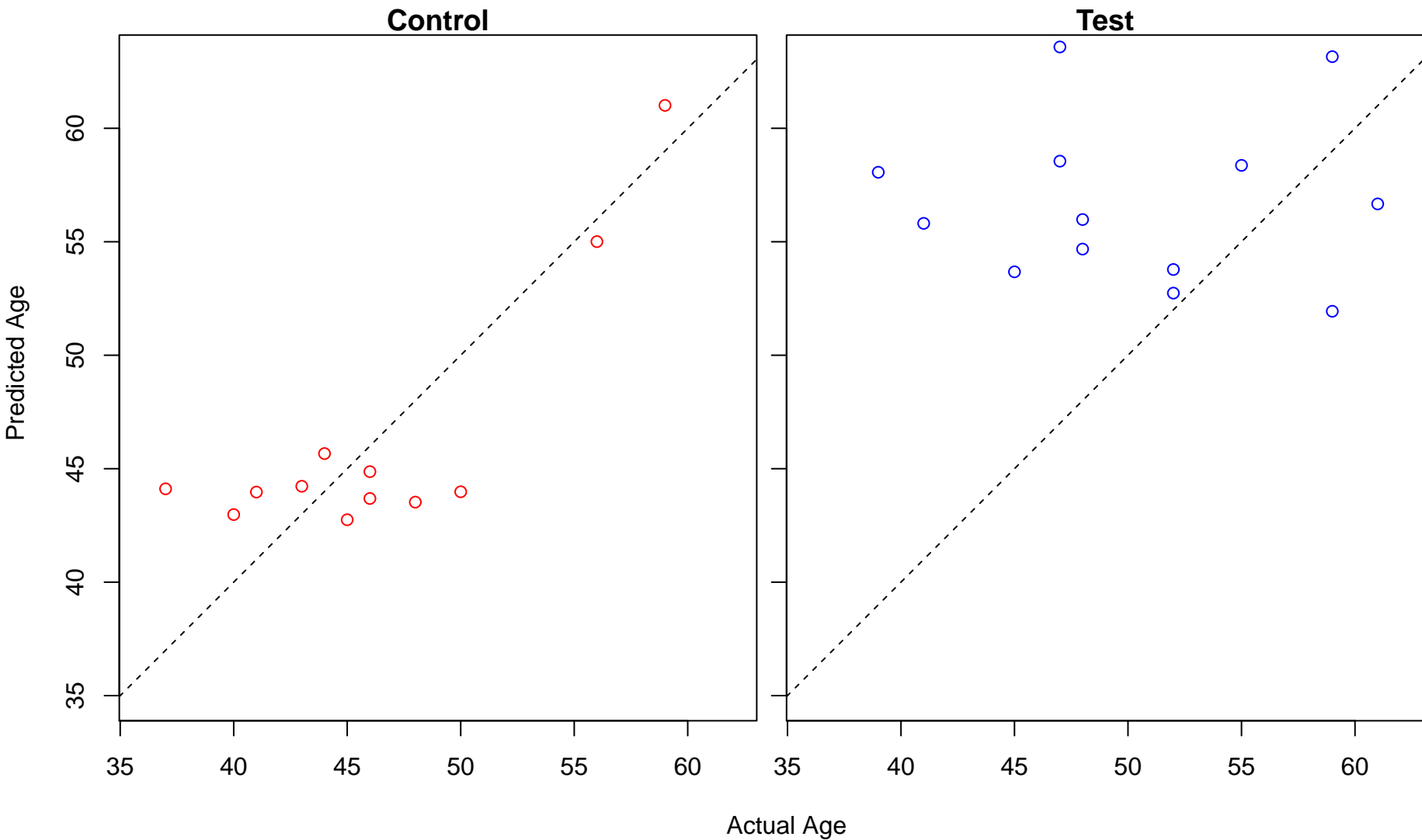
cellular response to organonitrogen compound (Score: 3.111255)



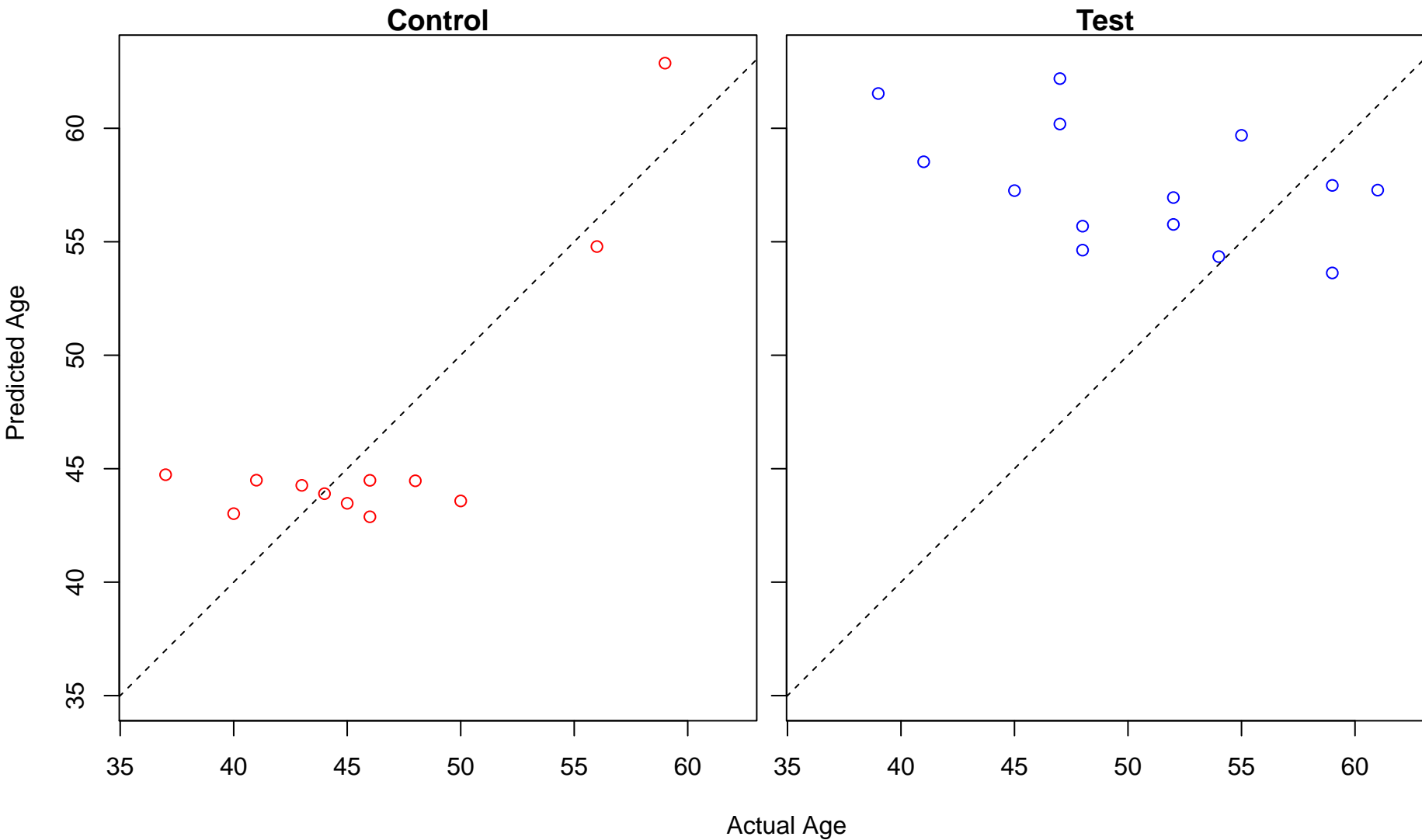
positive regulation of lipid kinase activity (Score: 3.107678)



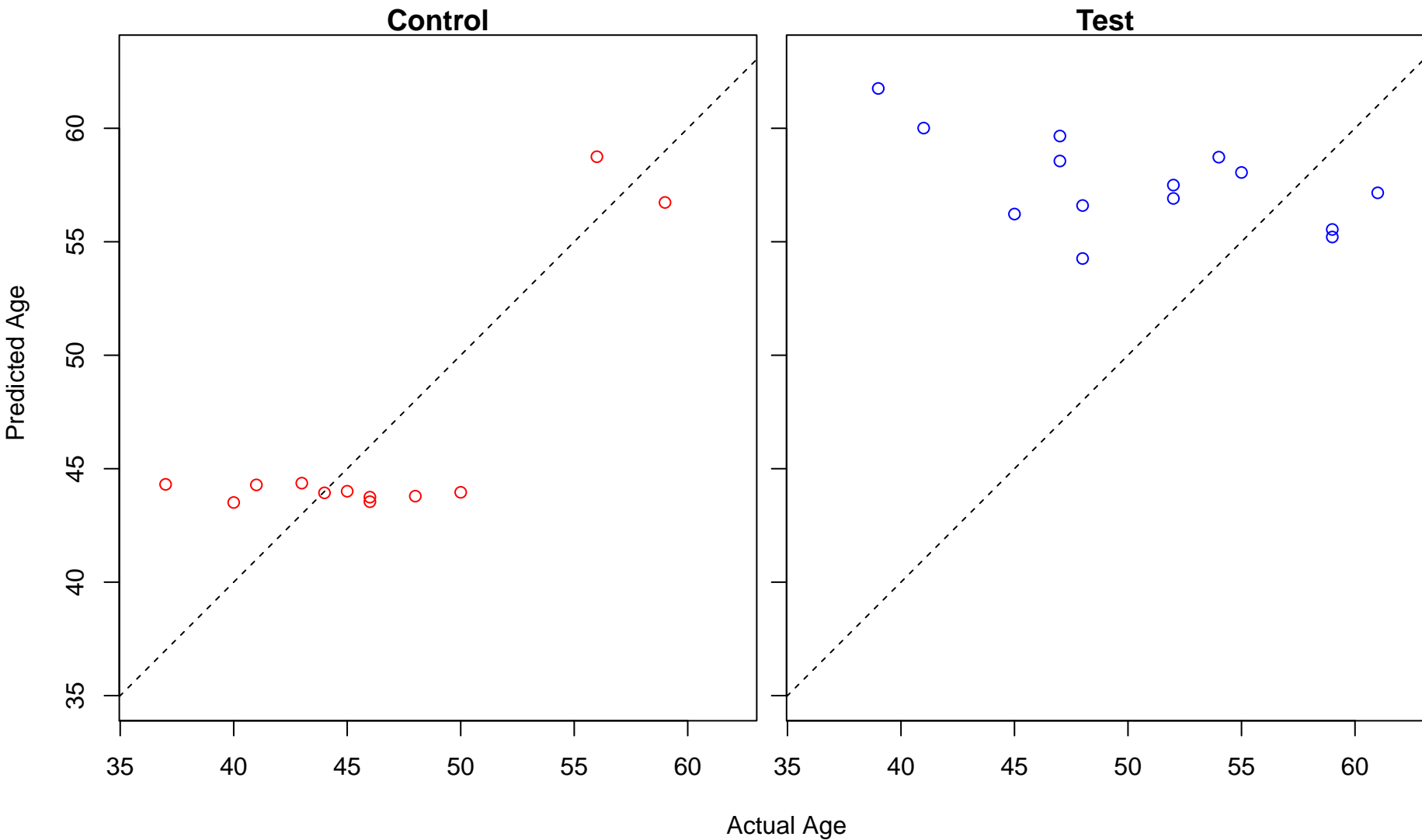
regulation of wound healing, spreading of epidermal cells (Score: 3.103491)



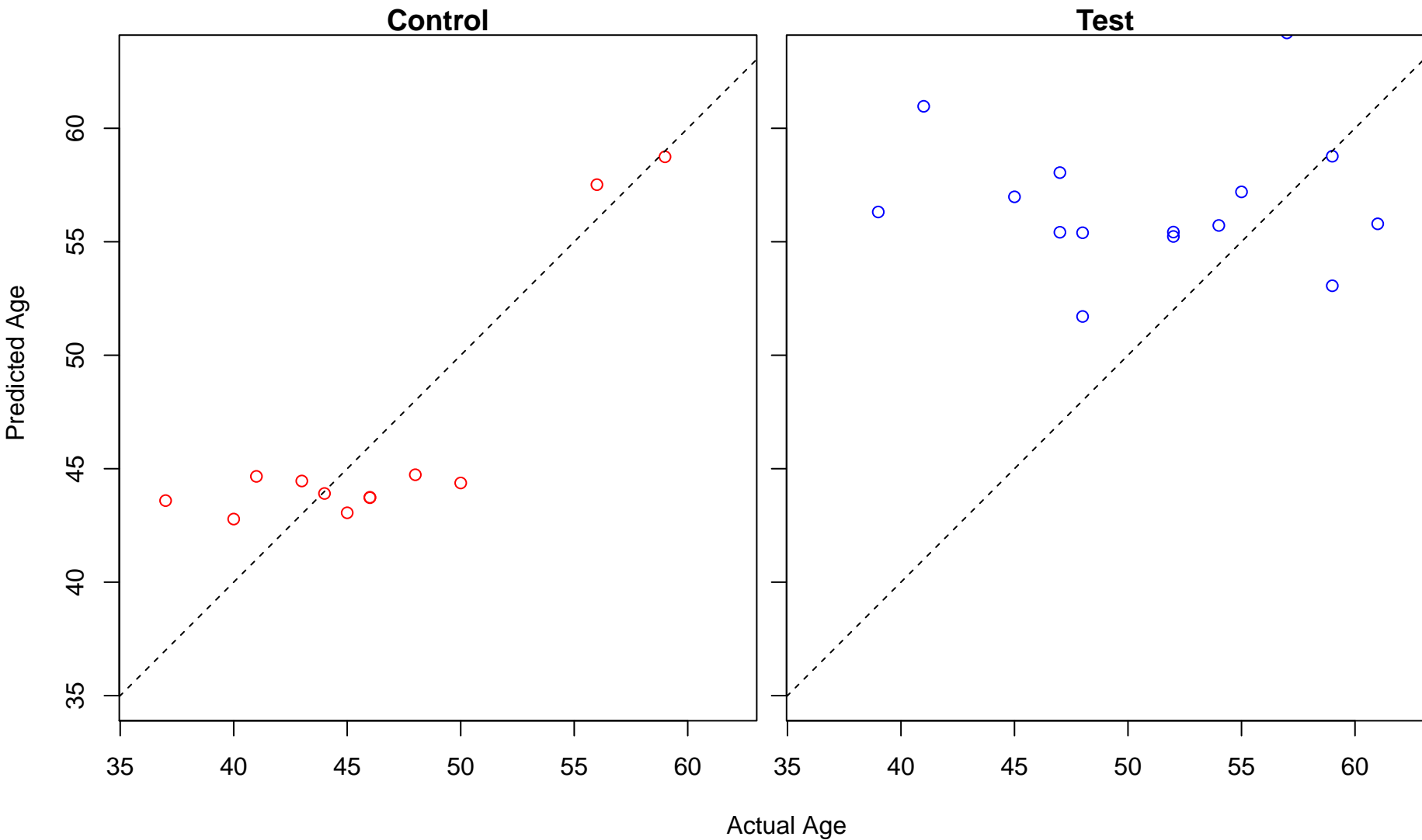
energy derivation by oxidation of organic compounds (Score: 3.103396)



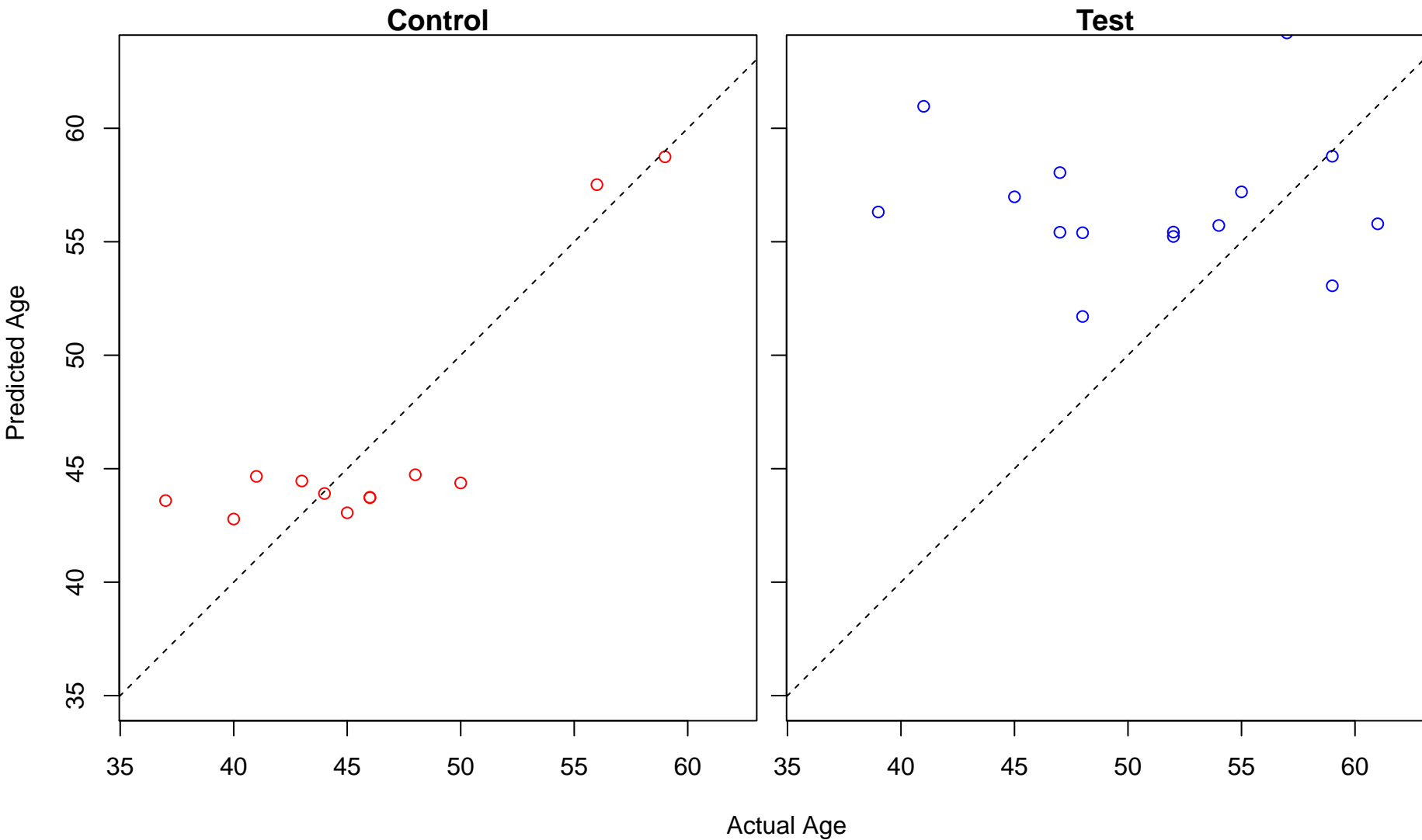
carbohydrate catabolic process (Score: 3.102901)



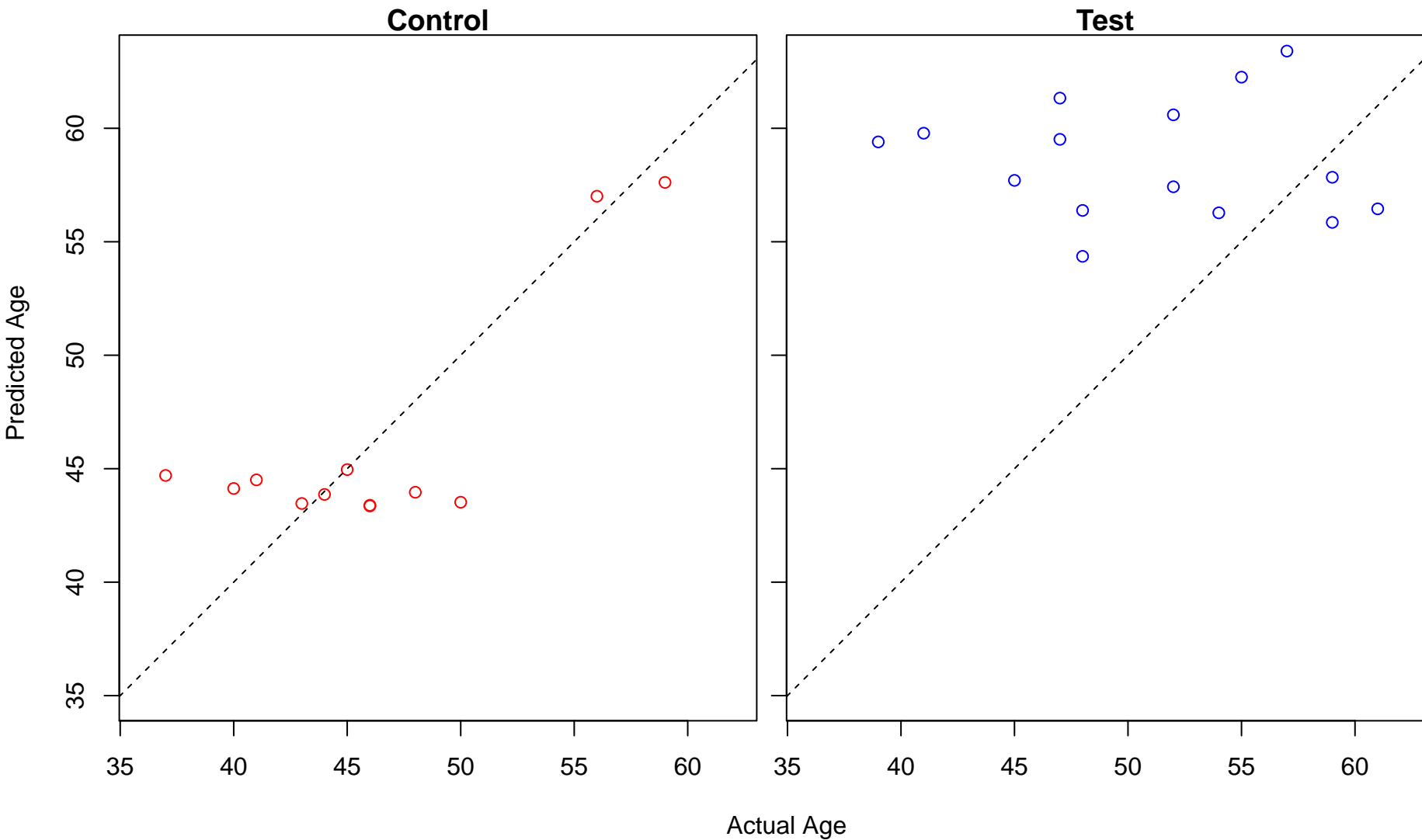
detection of light stimulus (Score: 3.101804)



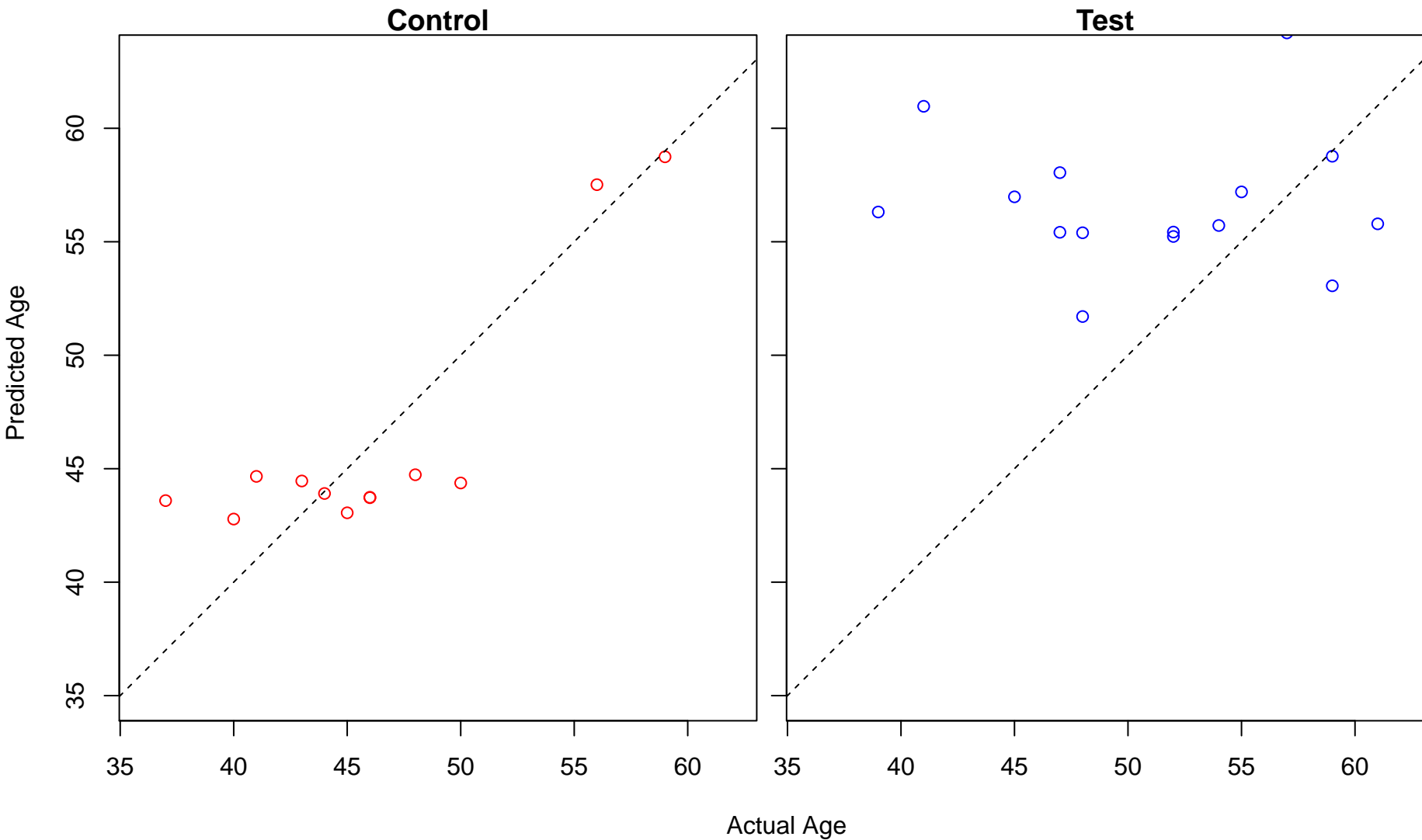
phototransduction (Score: 3.101802)



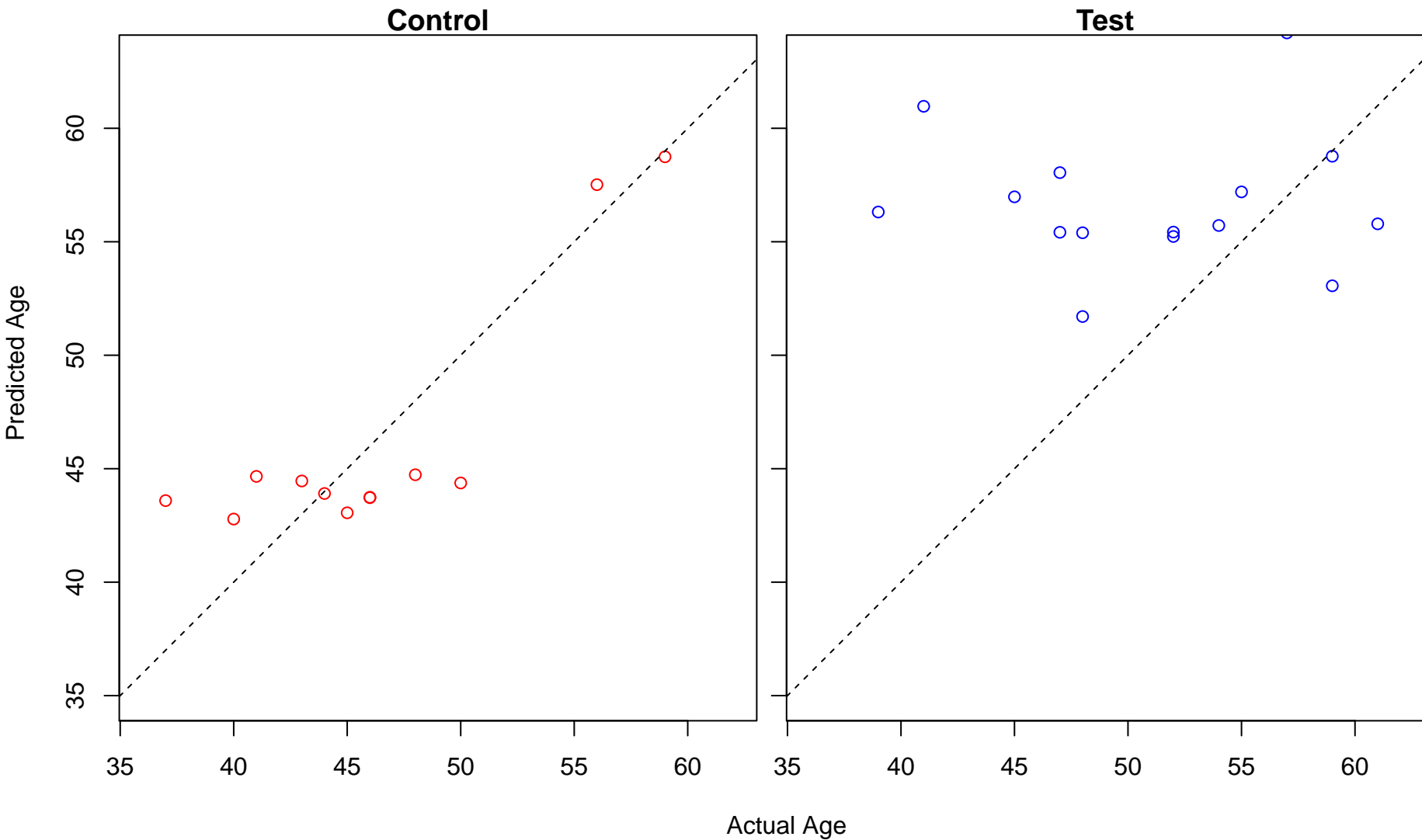
regulation of neuron differentiation (Score: 3.101673)



detection of visible light (Score: 3.101654)

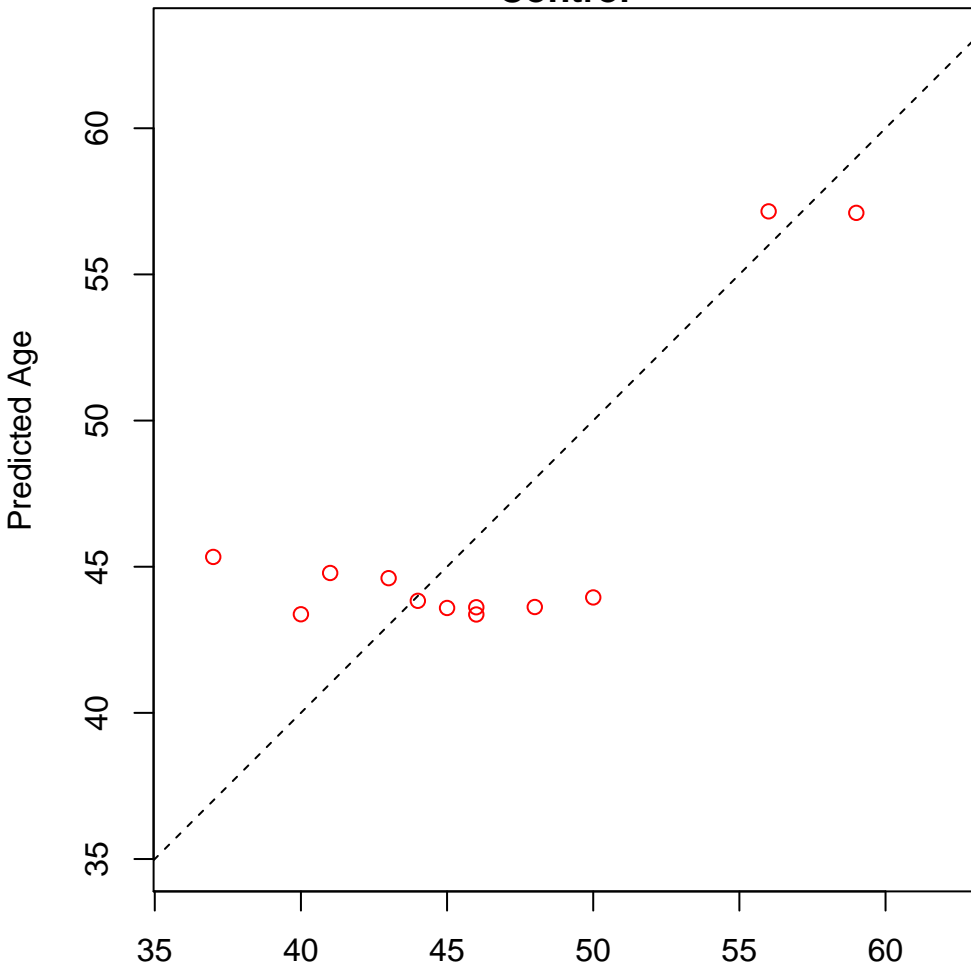


phototransduction, visible light (Score: 3.101653)

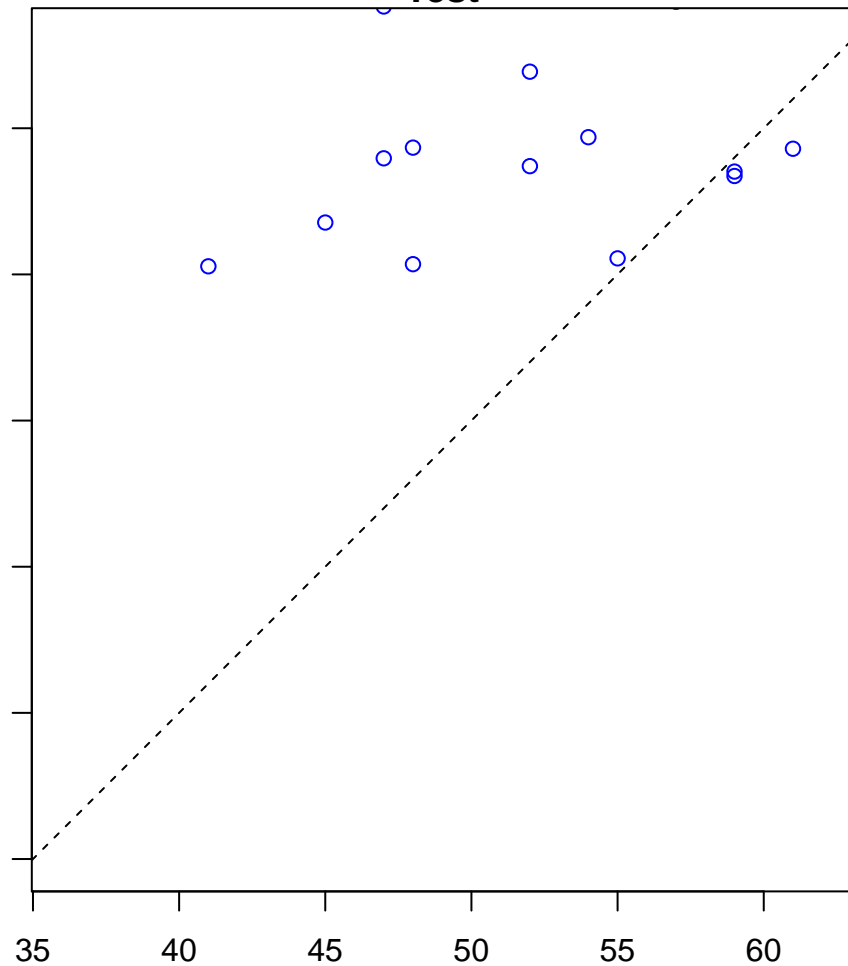


cellular amino acid catabolic process (Score: 3.101540)

Control

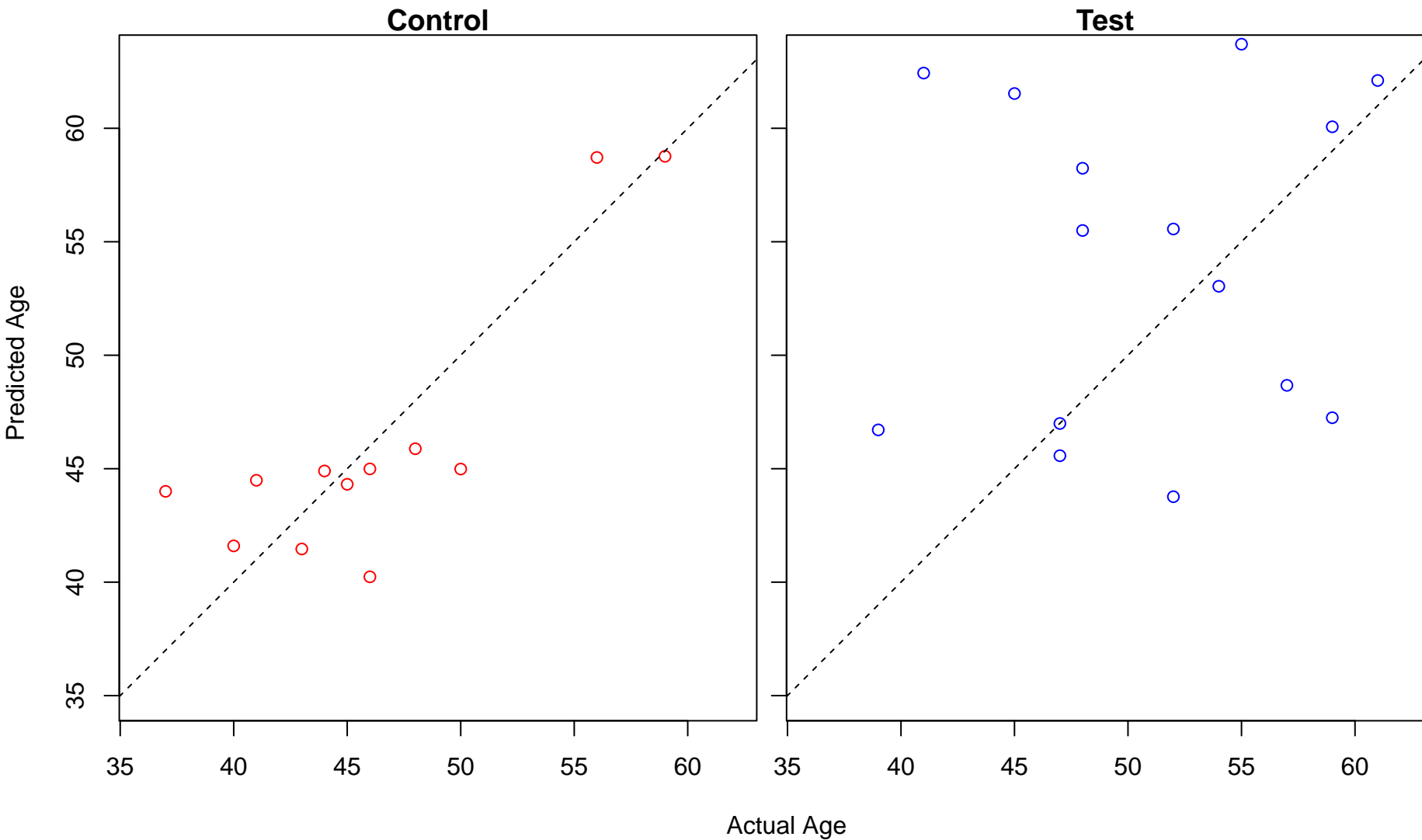


Test

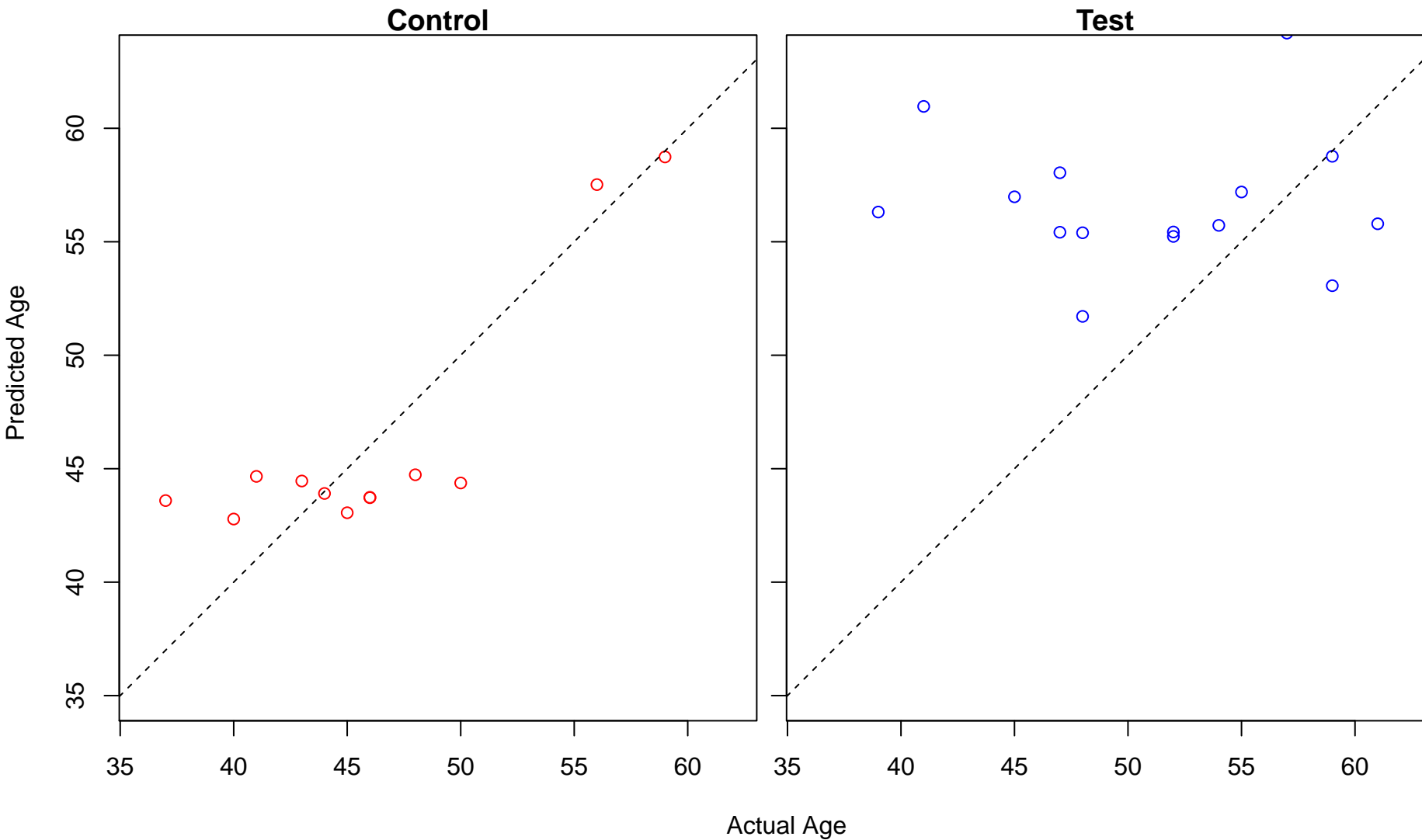


Actual Age

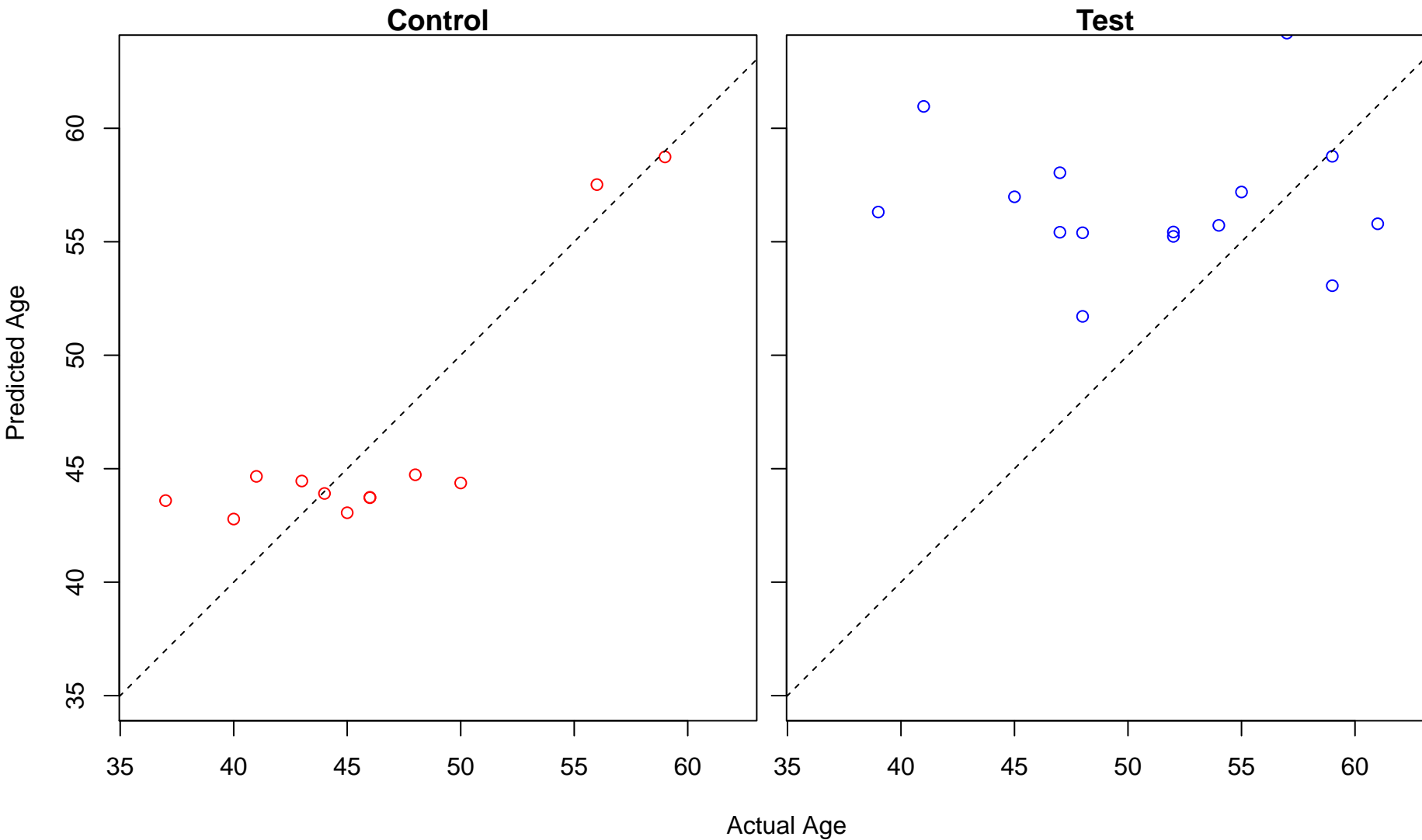
response to heat (Score: 3.101041)



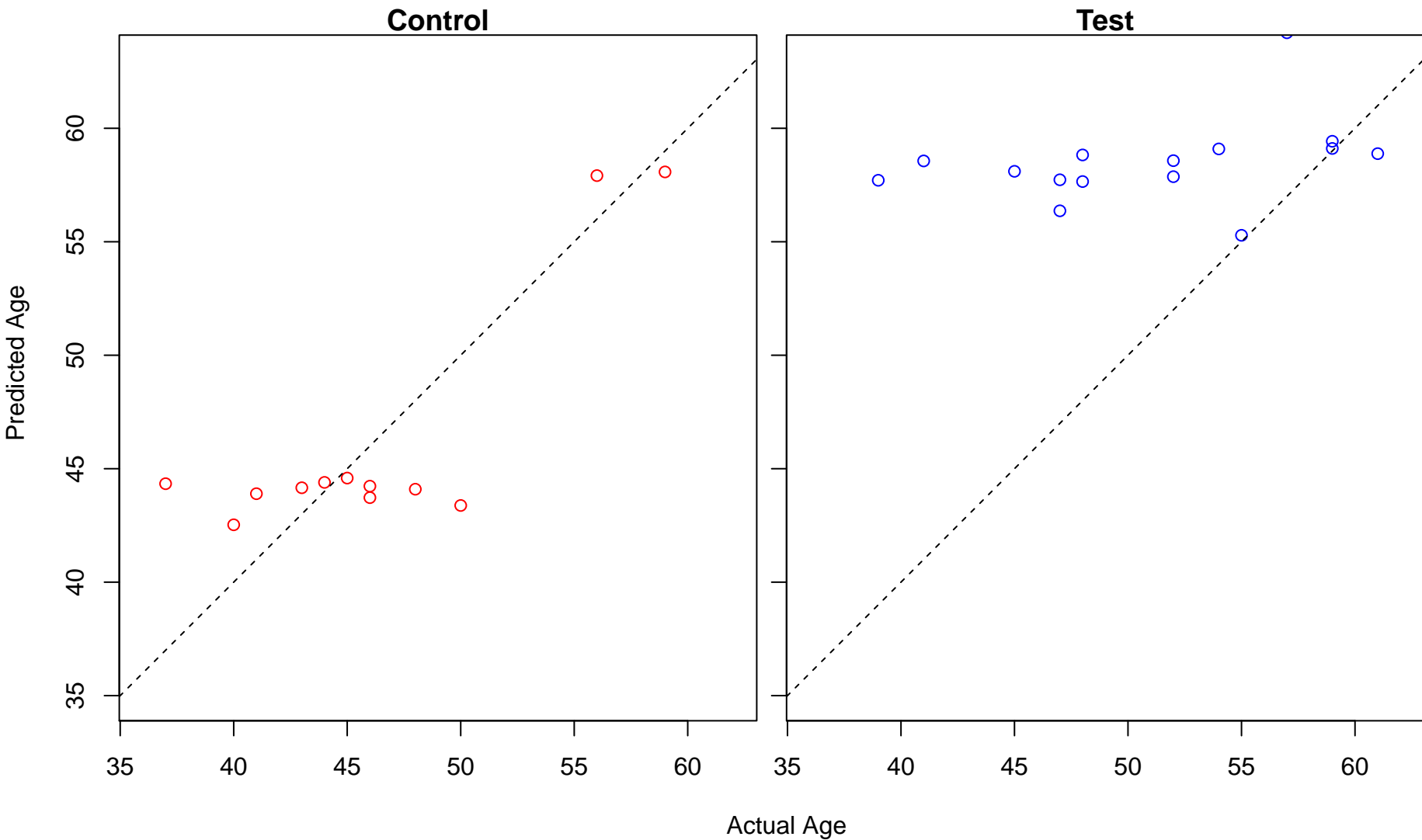
detection of abiotic stimulus (Score: 3.100307)



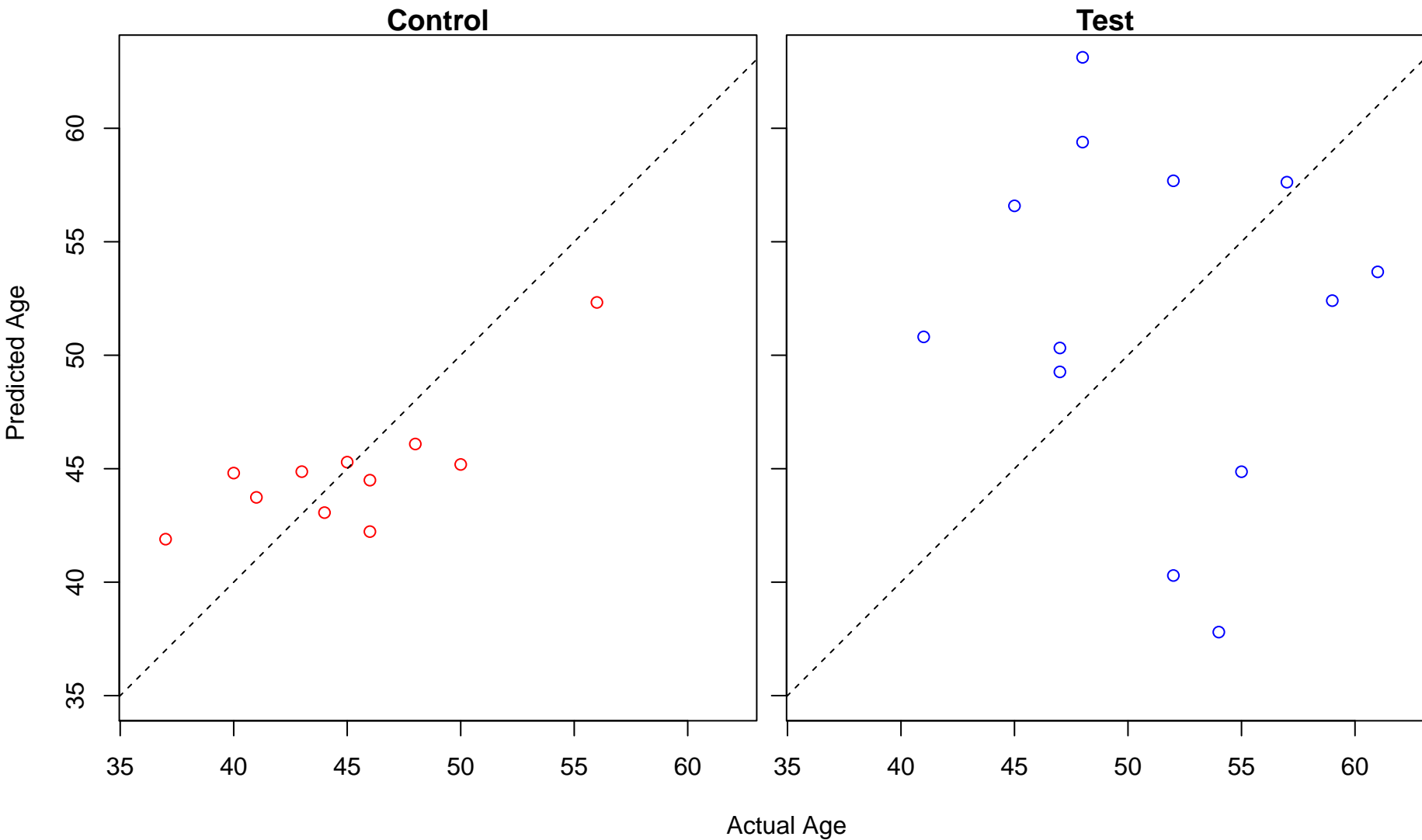
detection of external stimulus (Score: 3.100302)



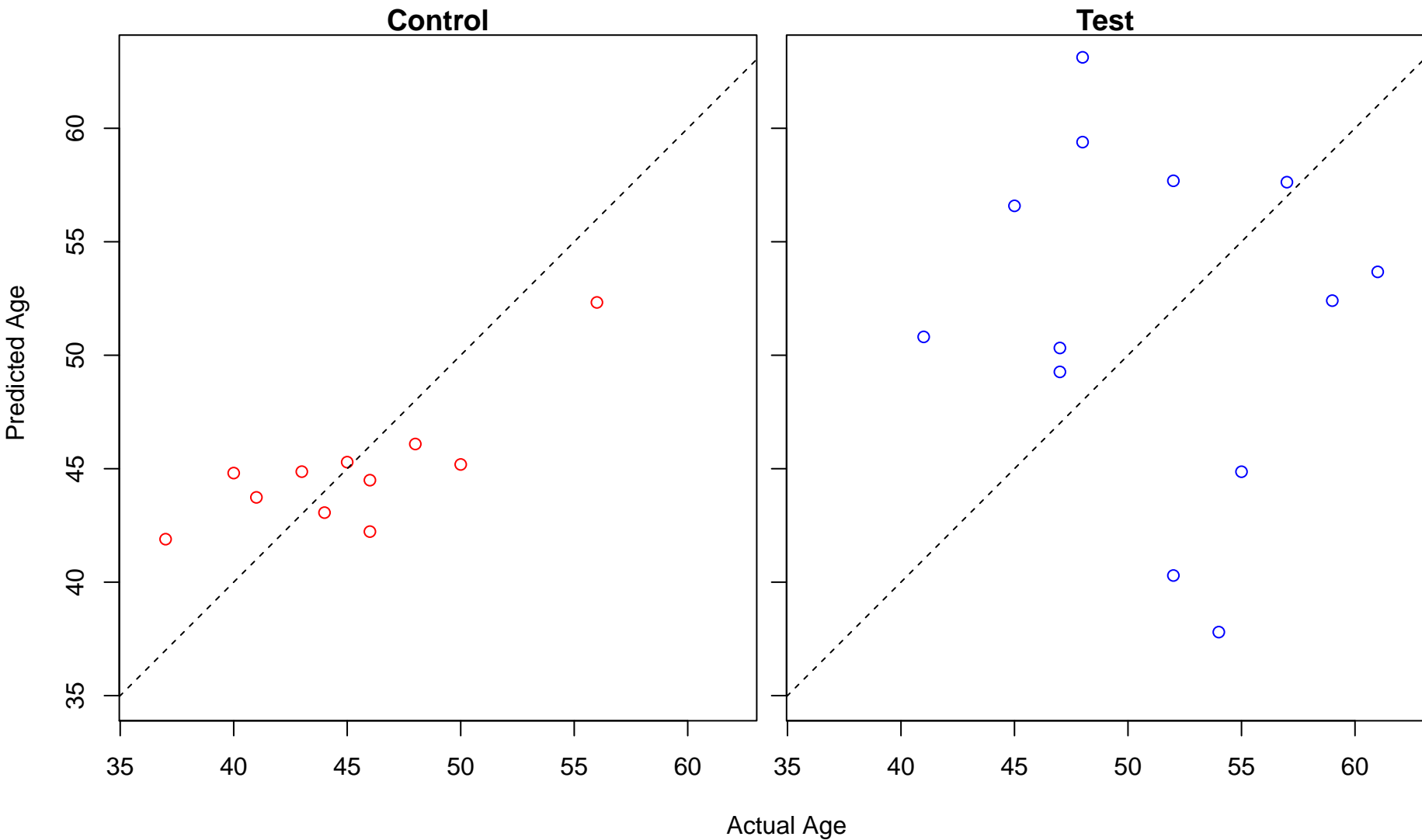
regulation of mitochondrial fission (Score: 3.098495)



response to forskolin (Score: 3.098032)

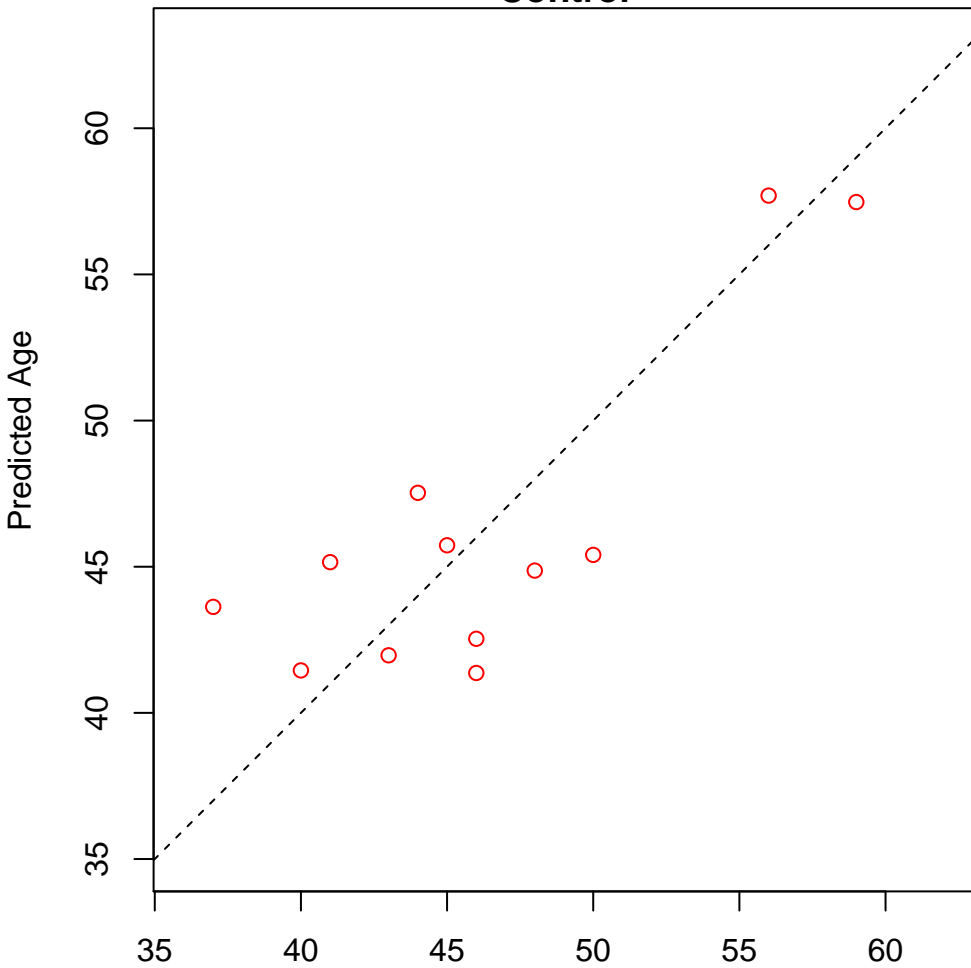


cellular response to forskolin (Score: 3.098032)

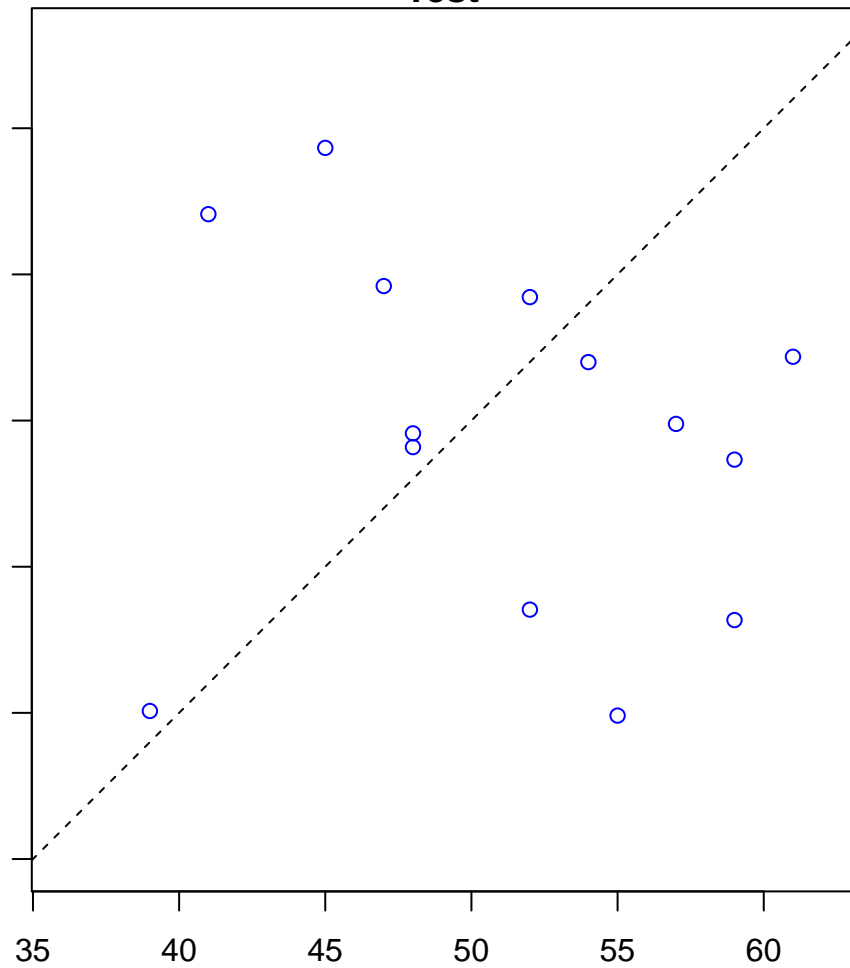


metanephric epithelium development (Score: 3.097824)

Control

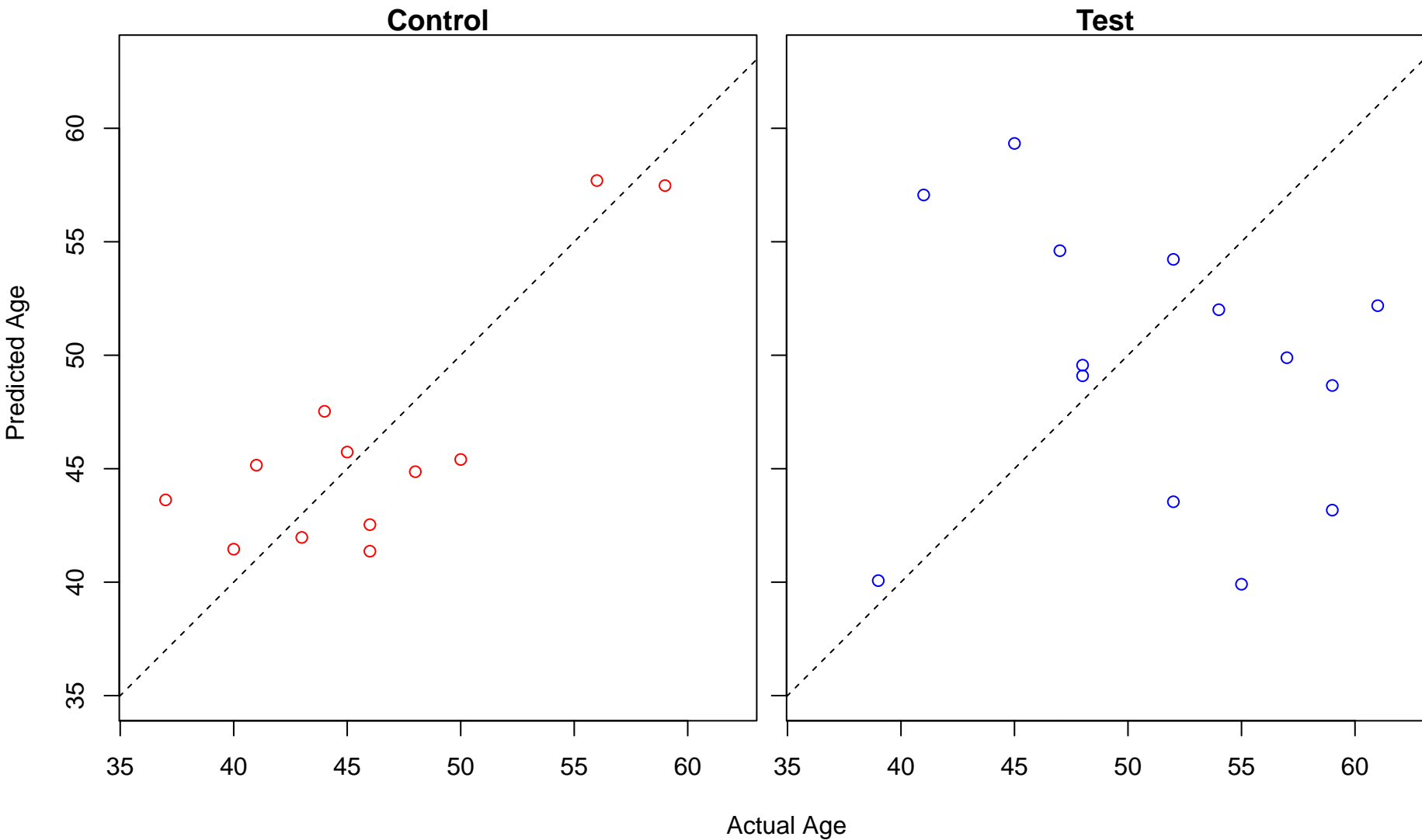


Test

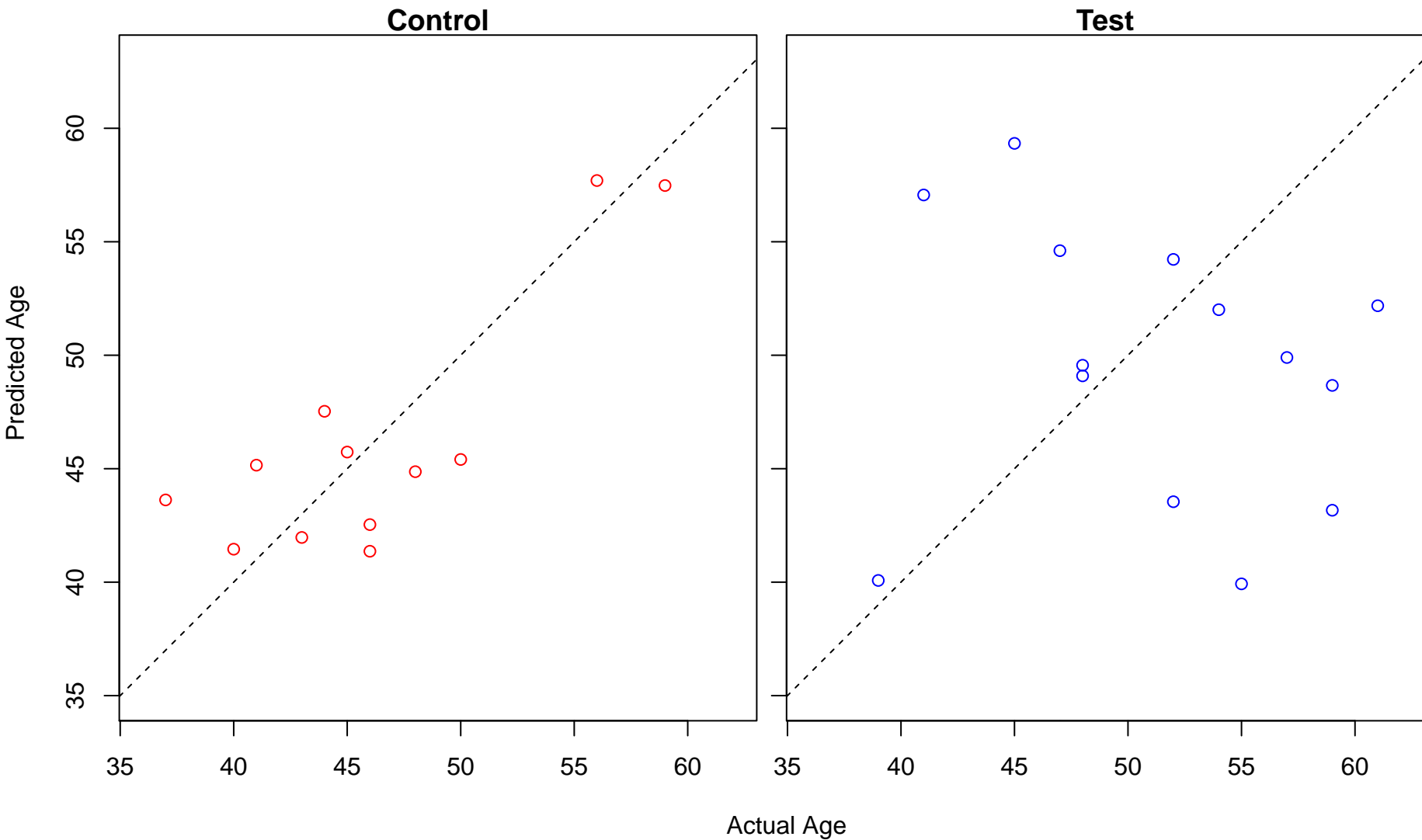


Actual Age

metanephric nephron epithelium development (Score: 3.097743)

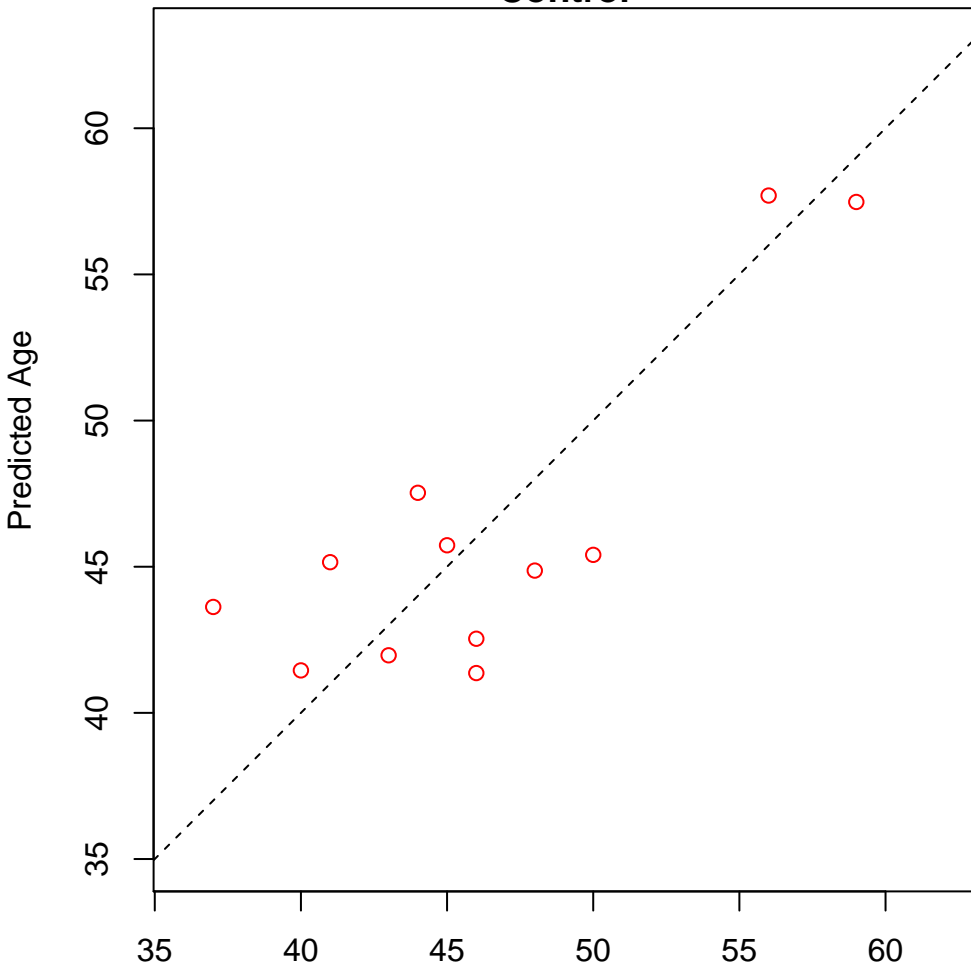


metanephric tubule development (Score: 3.097509)

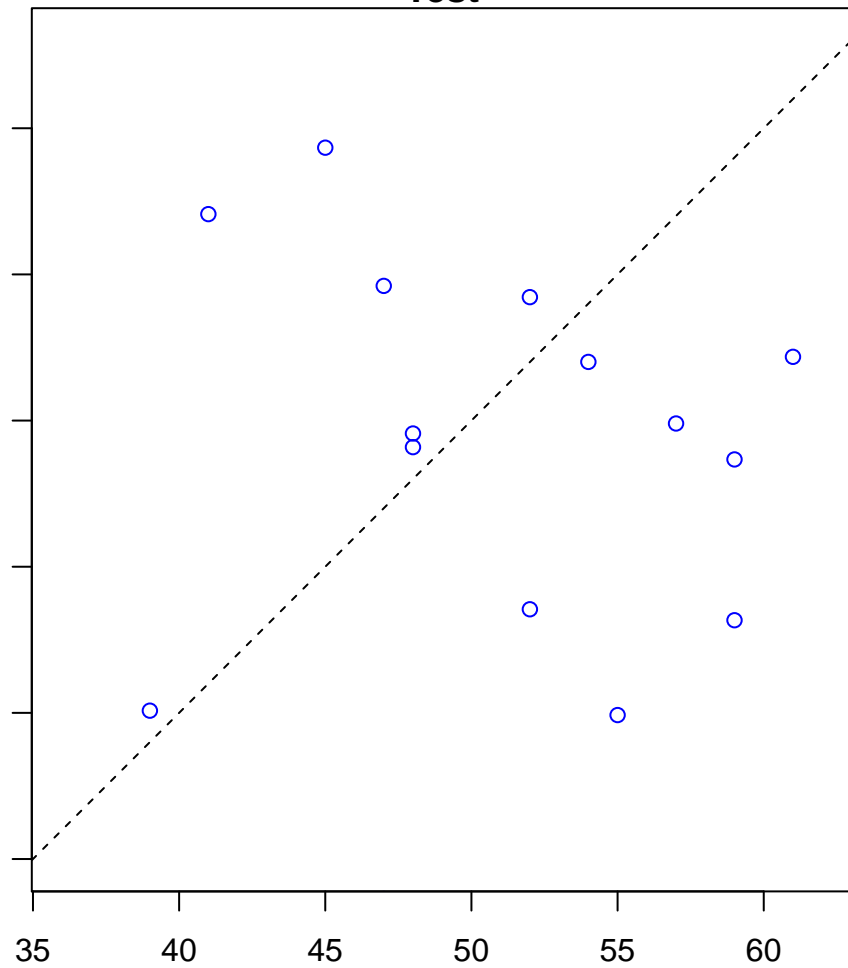


metanephric nephron tubule development (Score: 3.097509)

Control

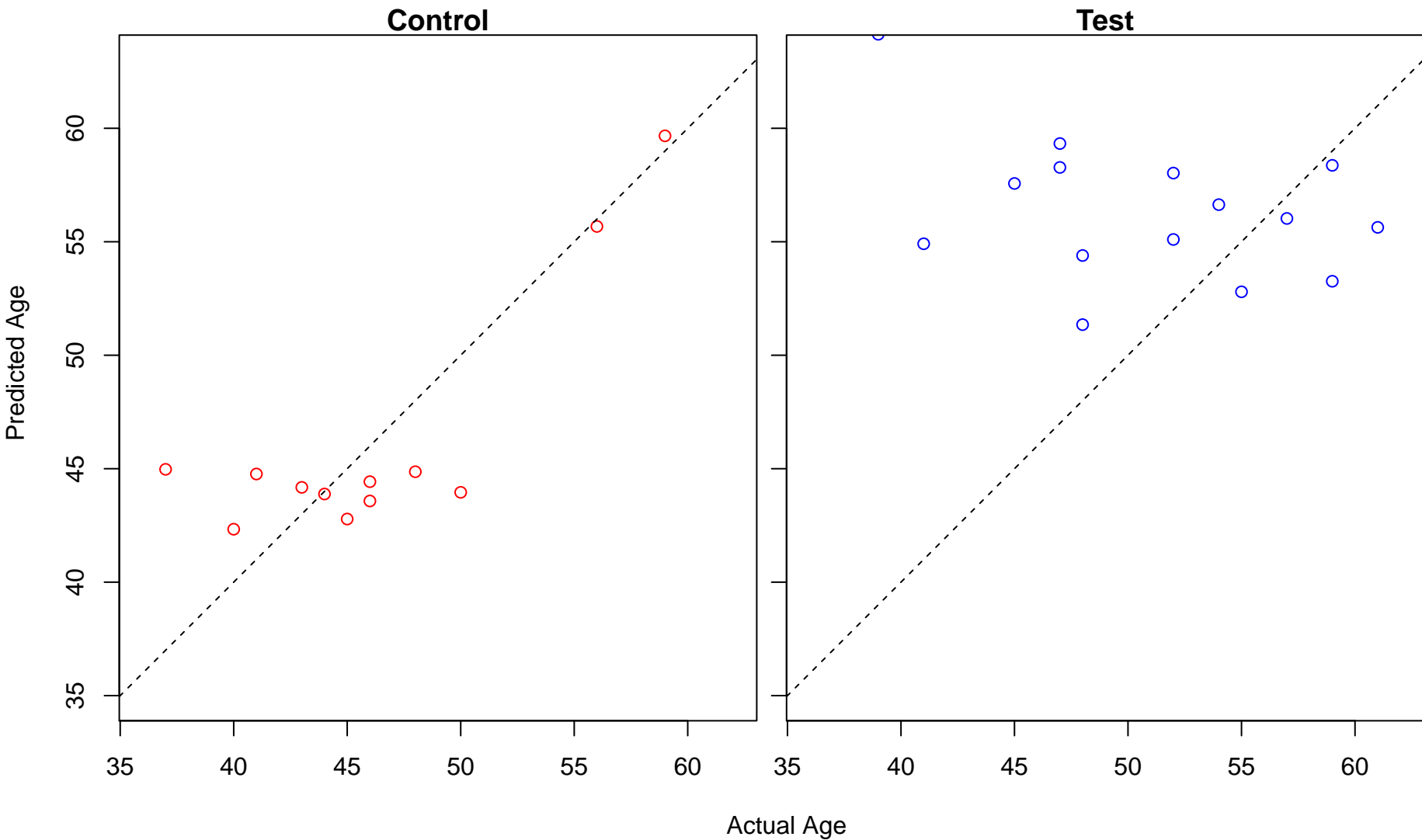


Test

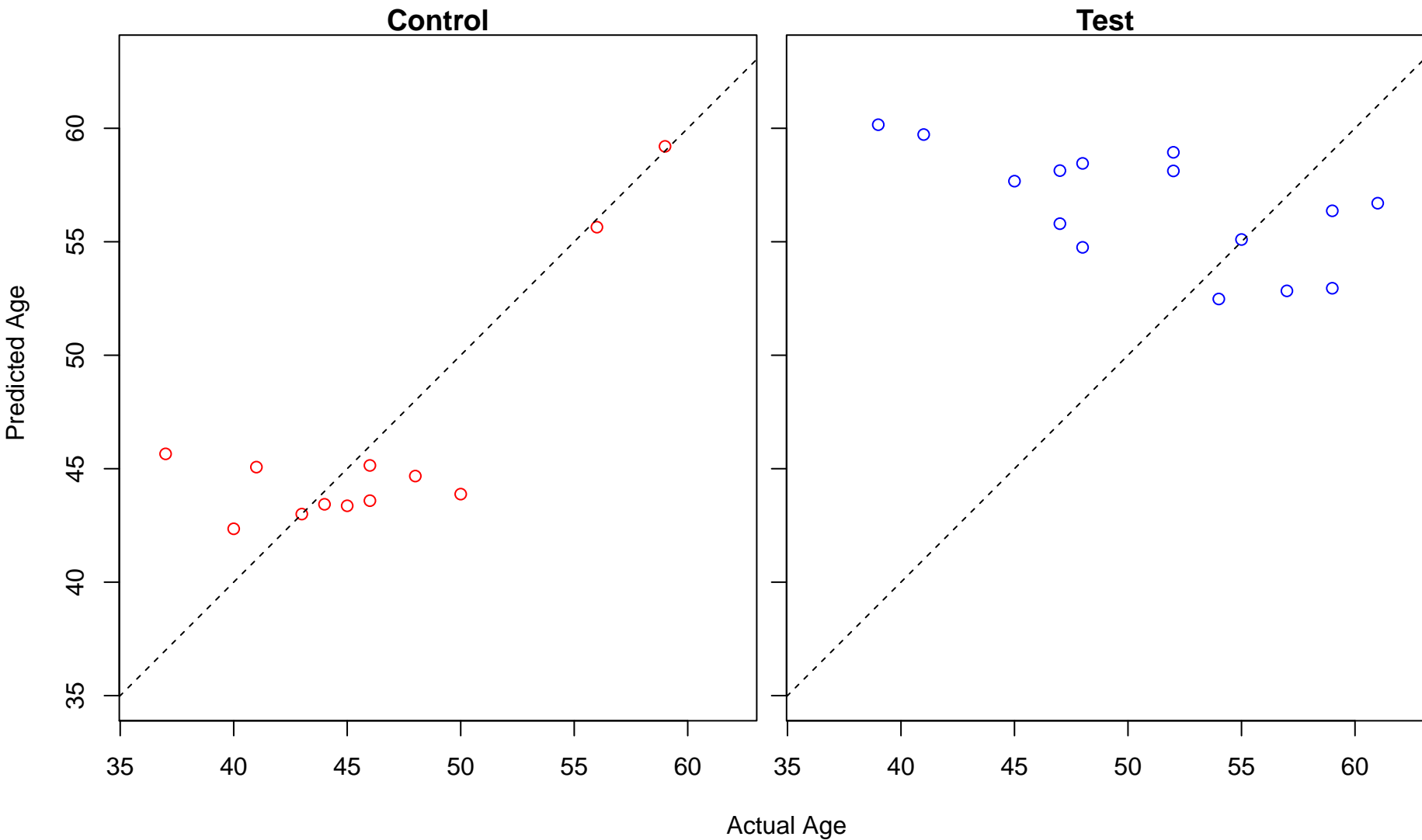


Actual Age

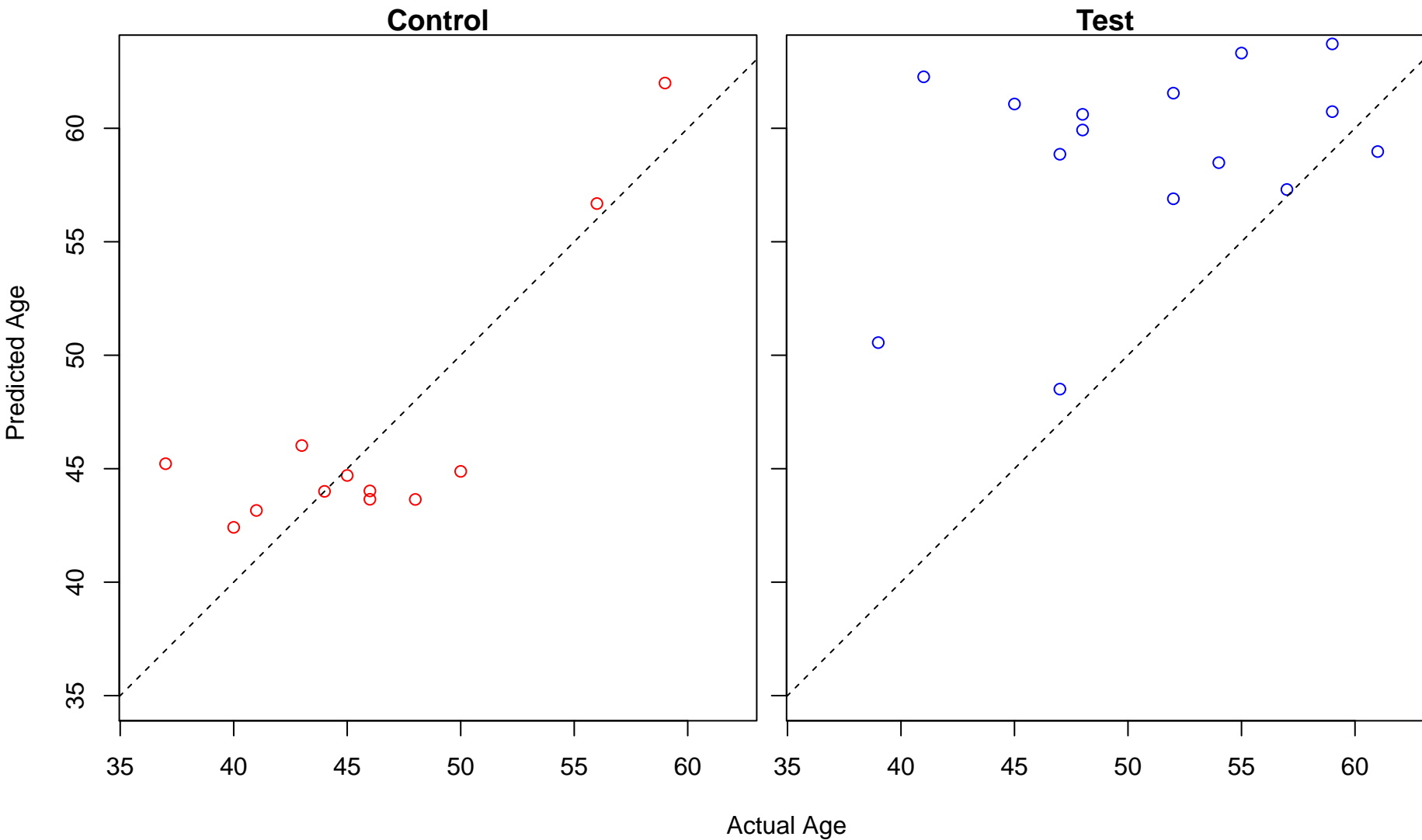
regulation of synaptic transmission, glutamatergic (Score: 3.096799)



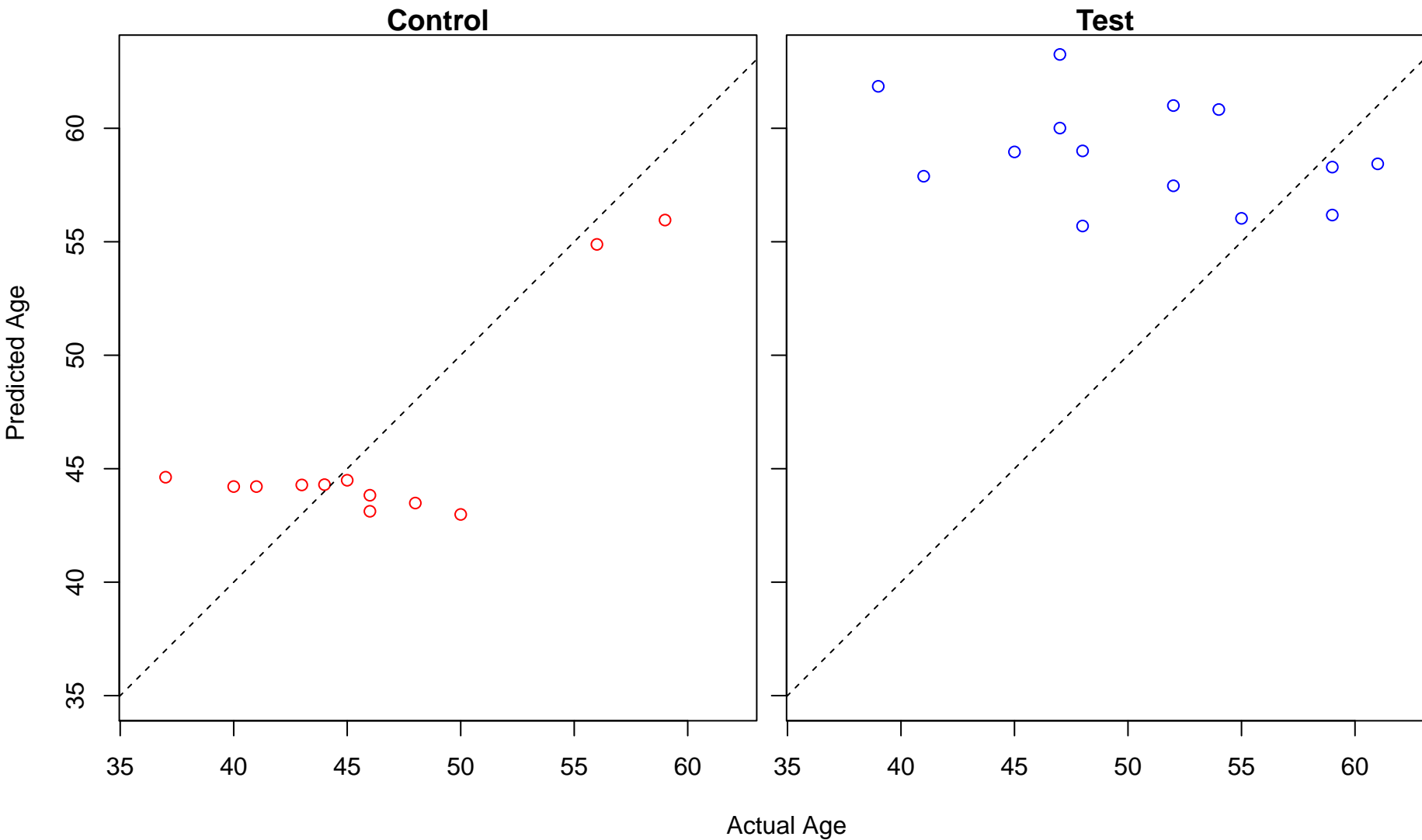
dendritic cell migration (Score: 3.093967)



protein deglutamylation (Score: 3.092401)

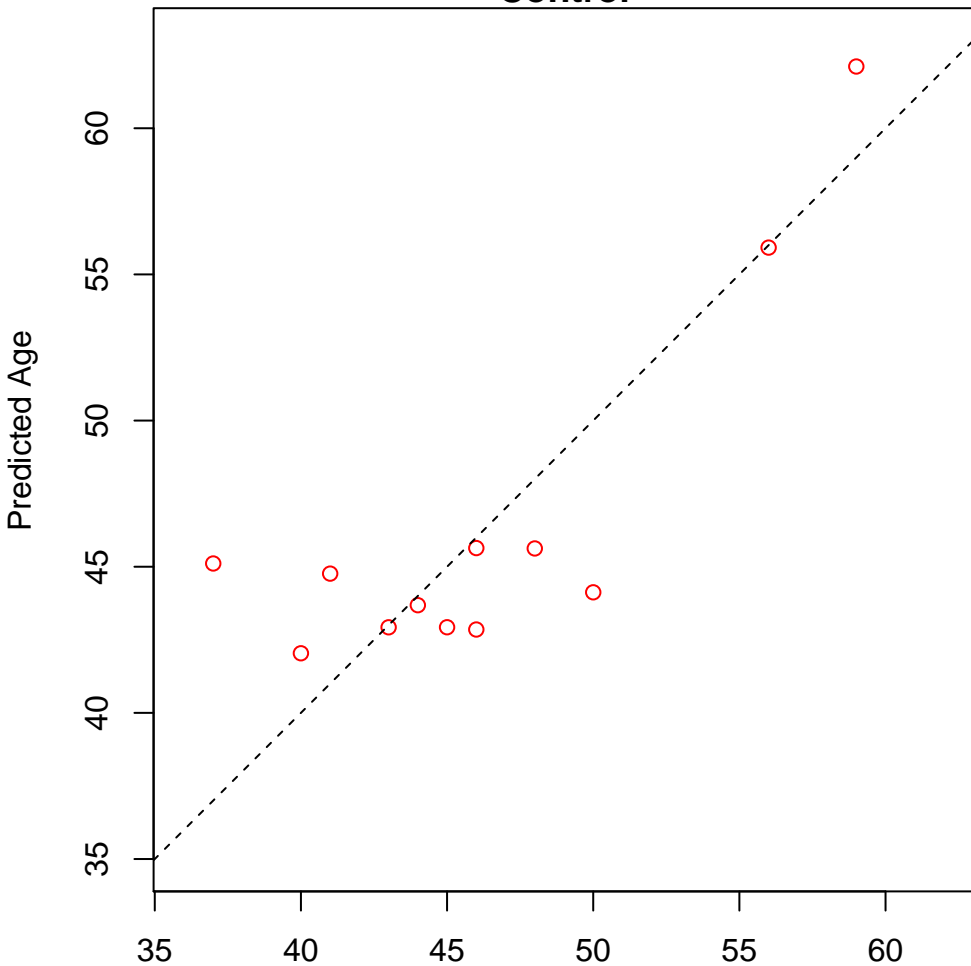


nucleotide biosynthetic process (Score: 3.090787)

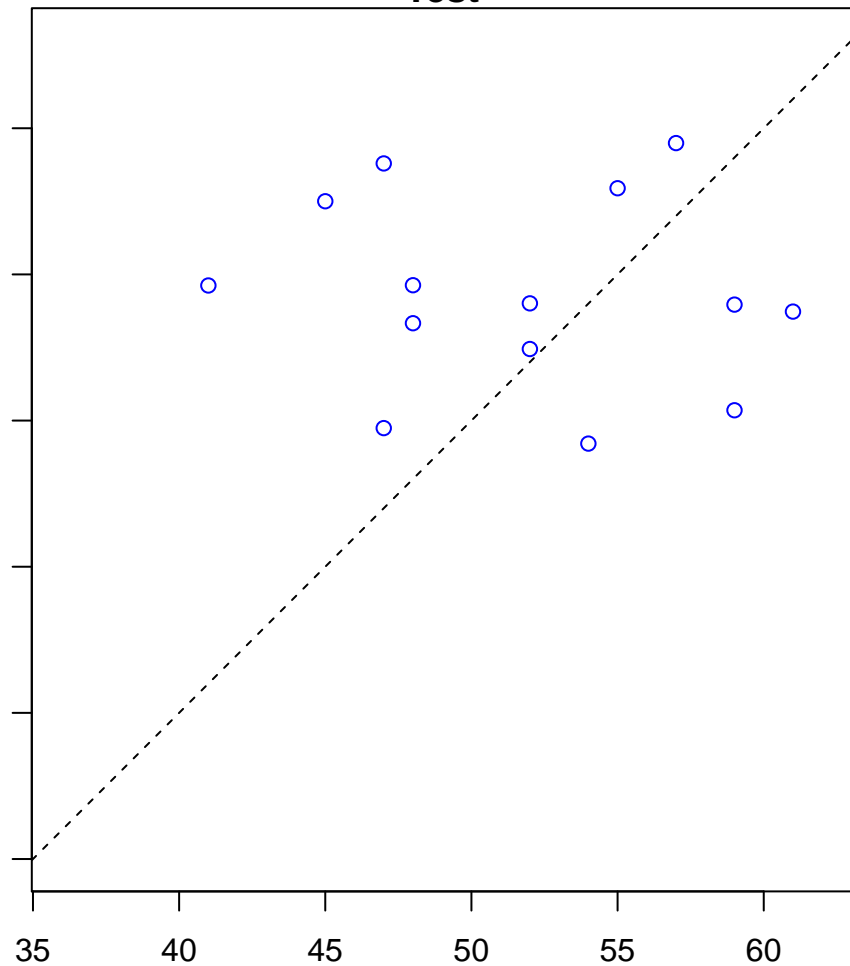


regulation of viral release from host cell (Score: 3.088415)

Control

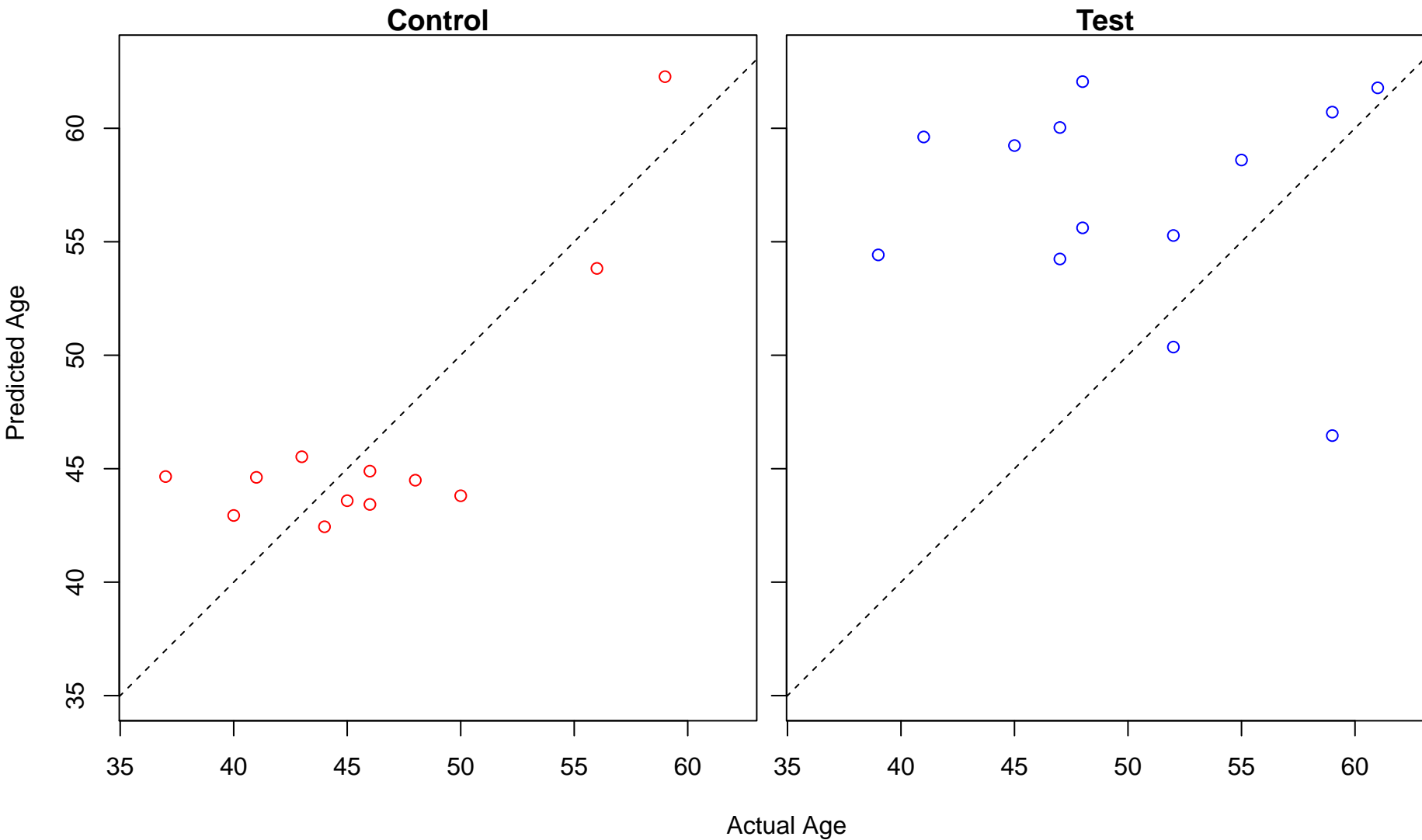


Test

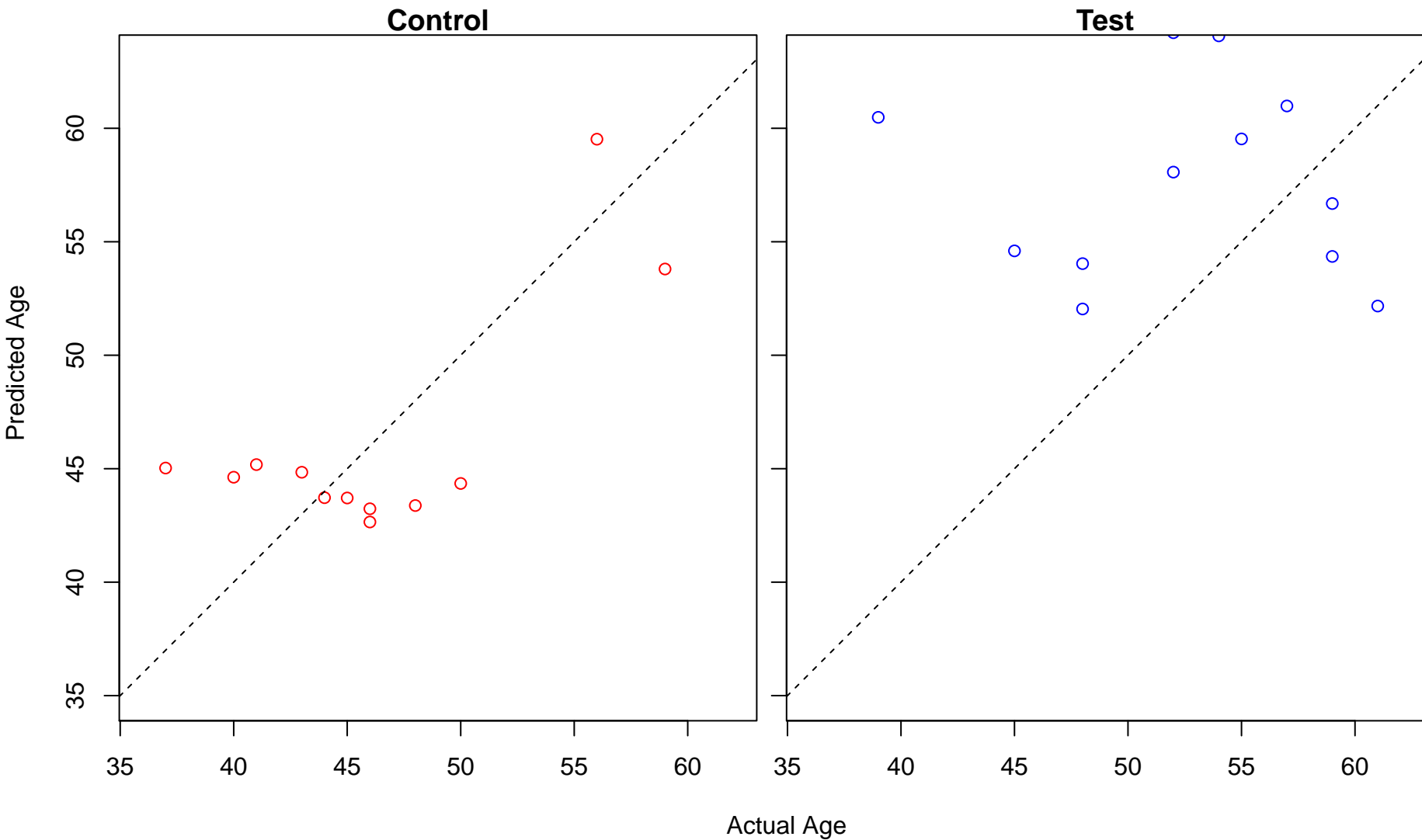


Actual Age

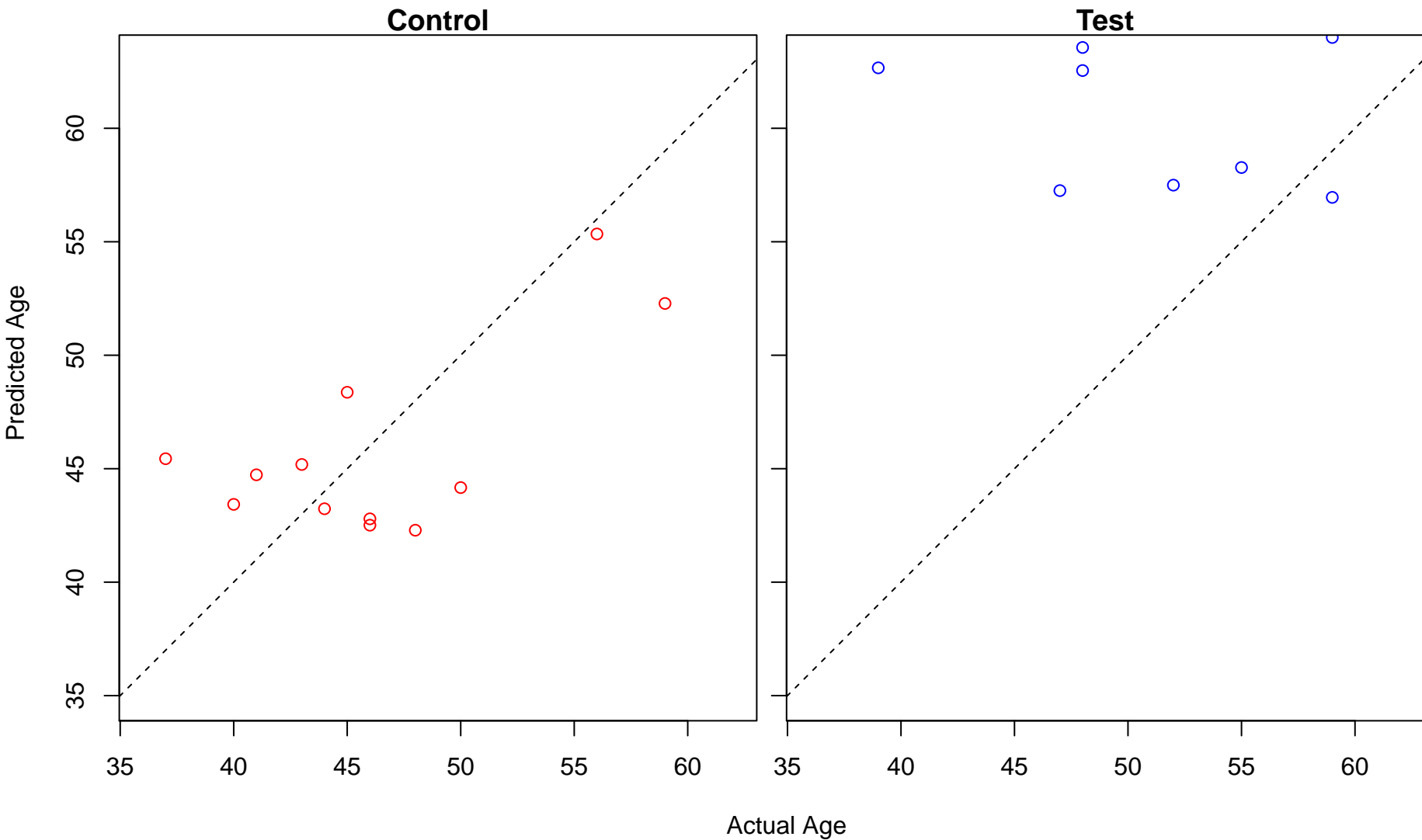
amyloid precursor protein metabolic process (Score: 3.087298)



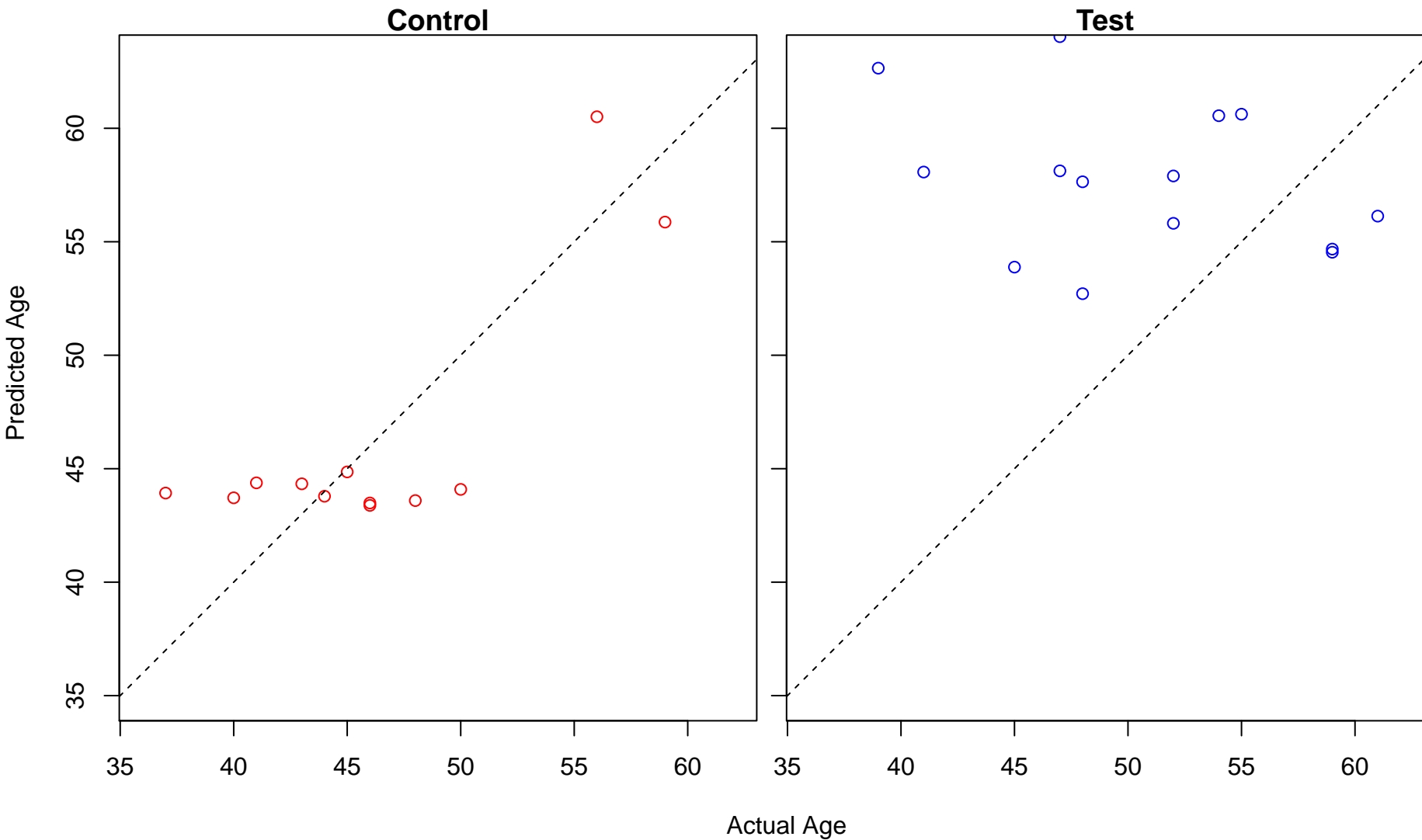
positive regulation of histone H4 acetylation (Score: 3.084891)



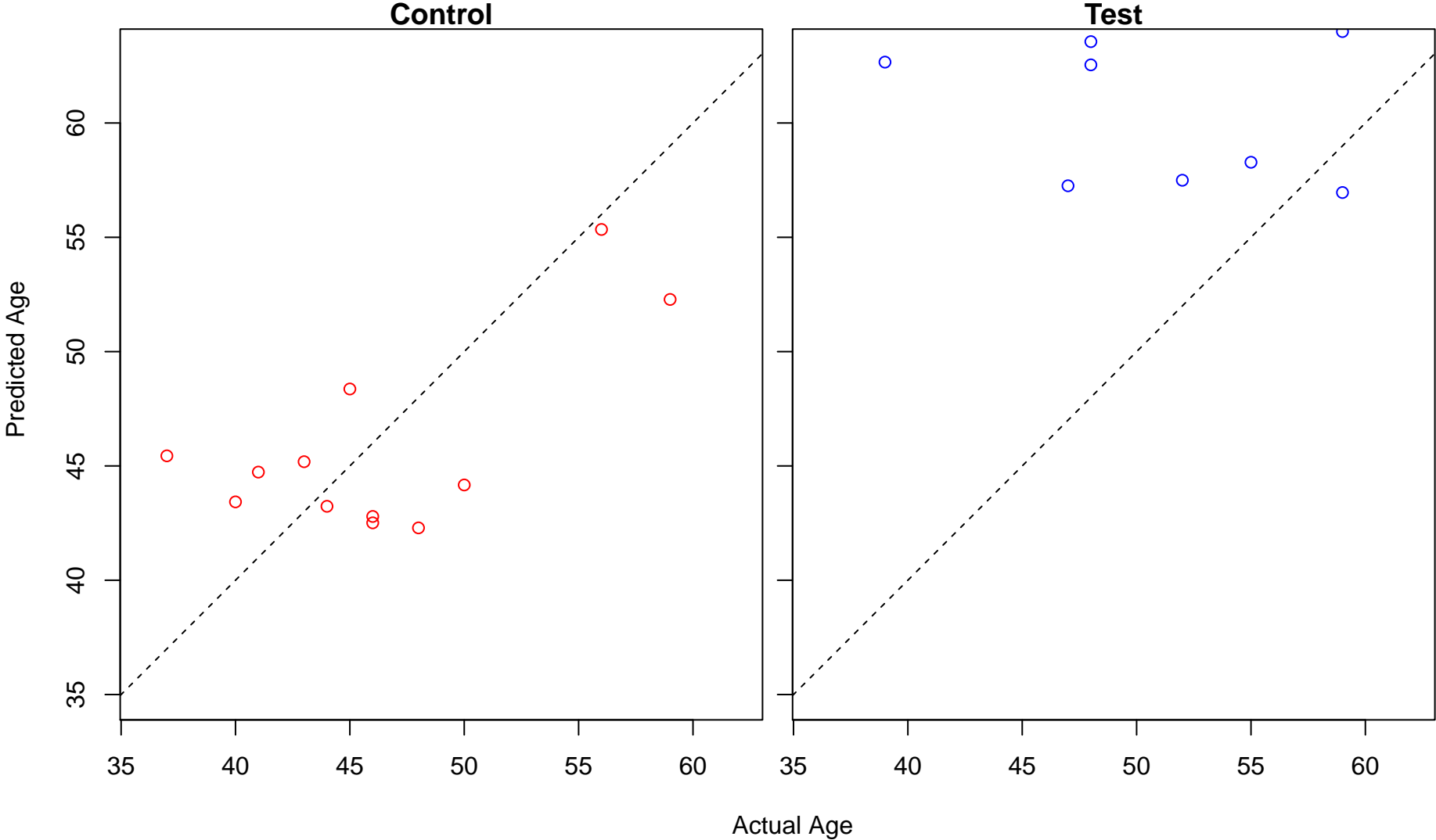
regulation of tumor necrosis factor production (Score: 3.083854)



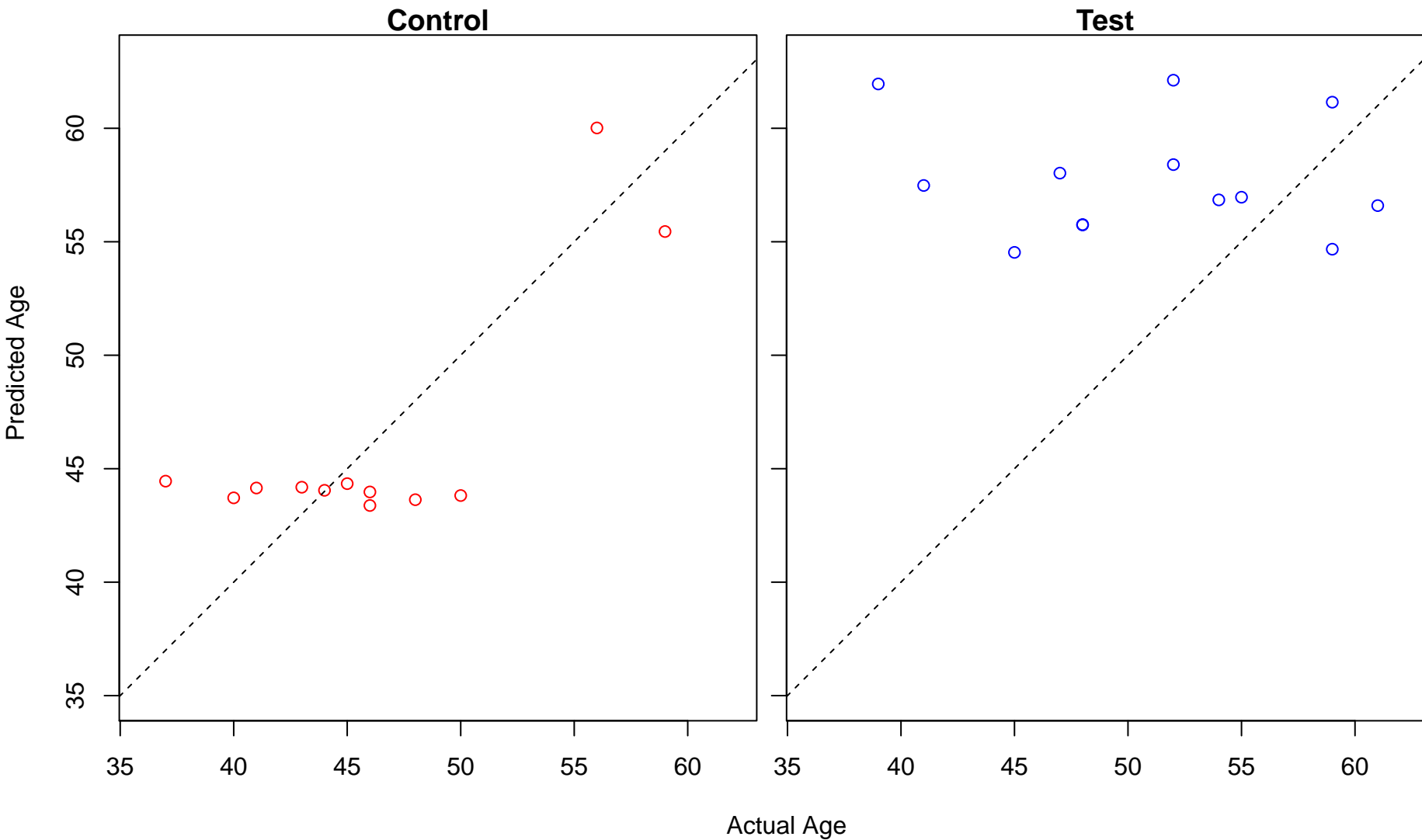
'de novo' protein folding (Score: 3.083765)



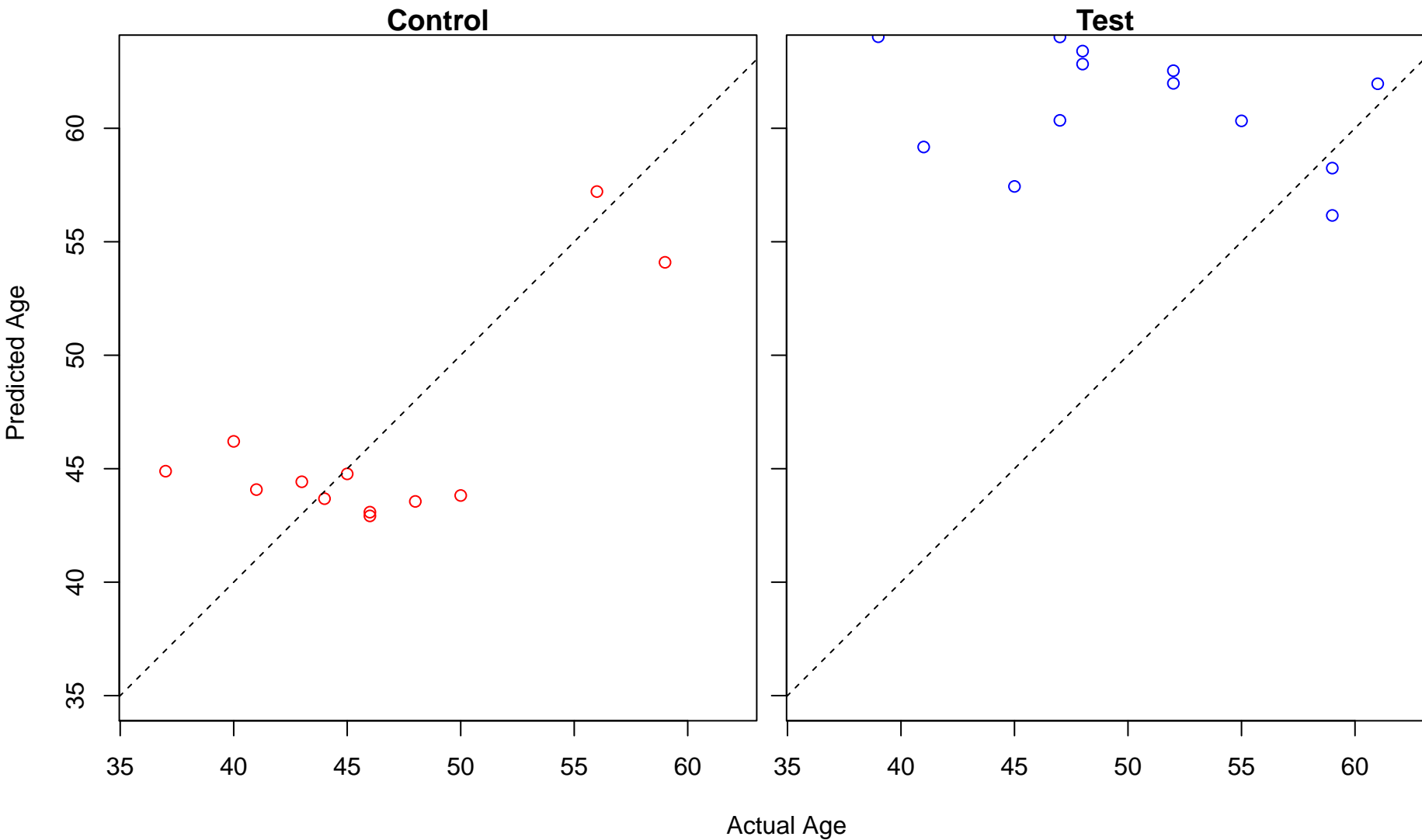
regulation of tumor necrosis factor superfamily cytokine production (Score: 3.083588)



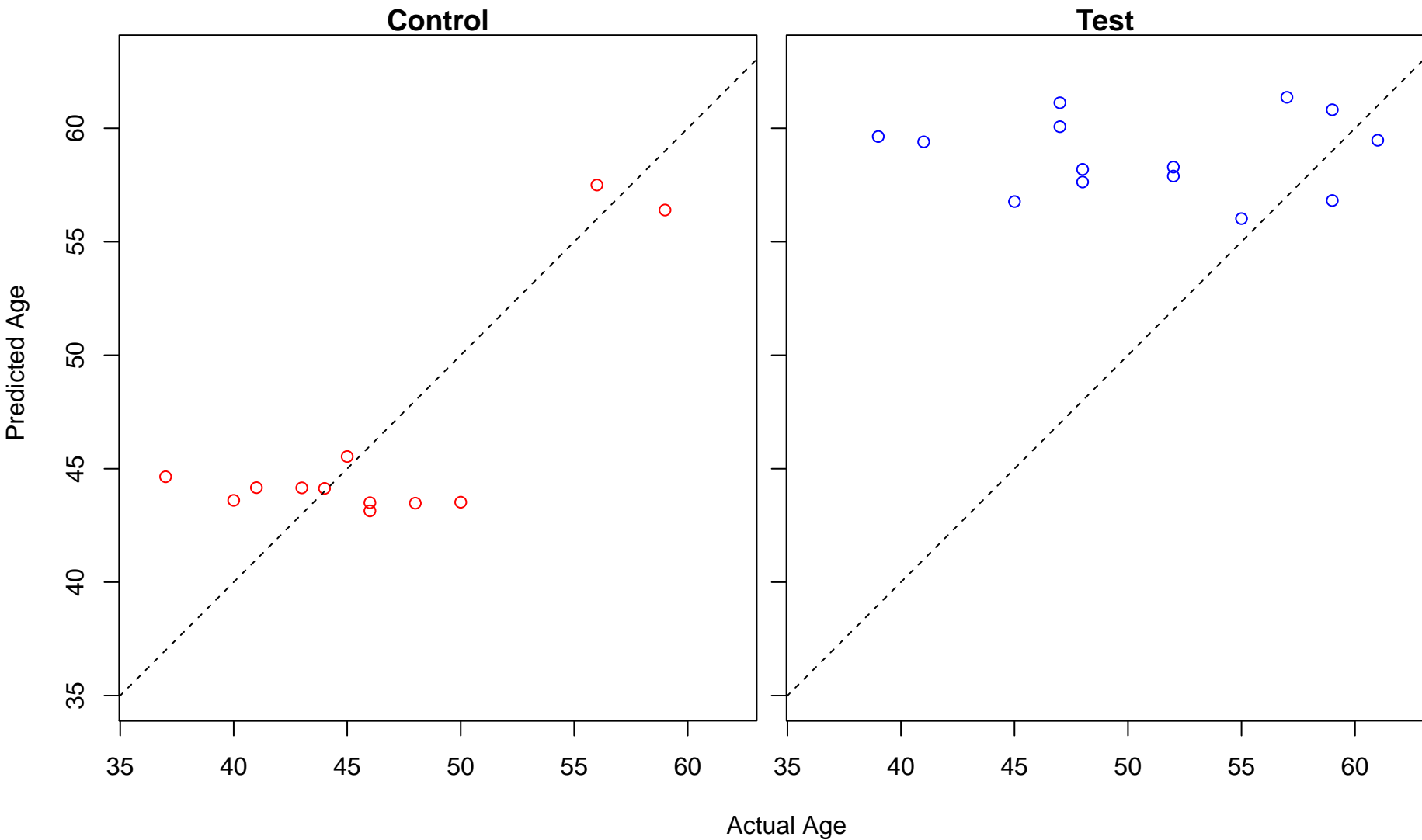
regulation of cellular response to growth factor stimulus (Score: 3.082875)



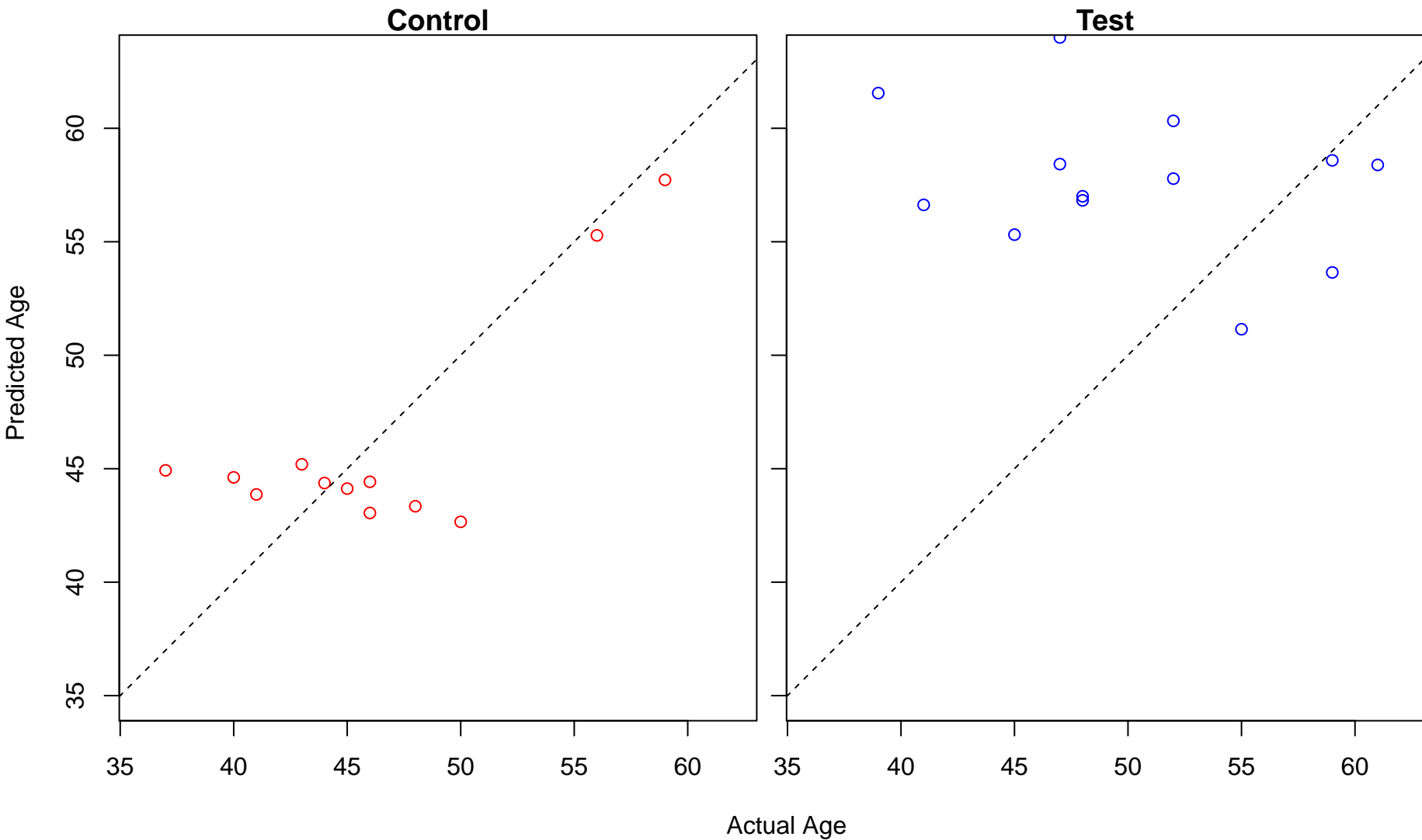
peptidyl-lysine deacetylation (Score: 3.082216)



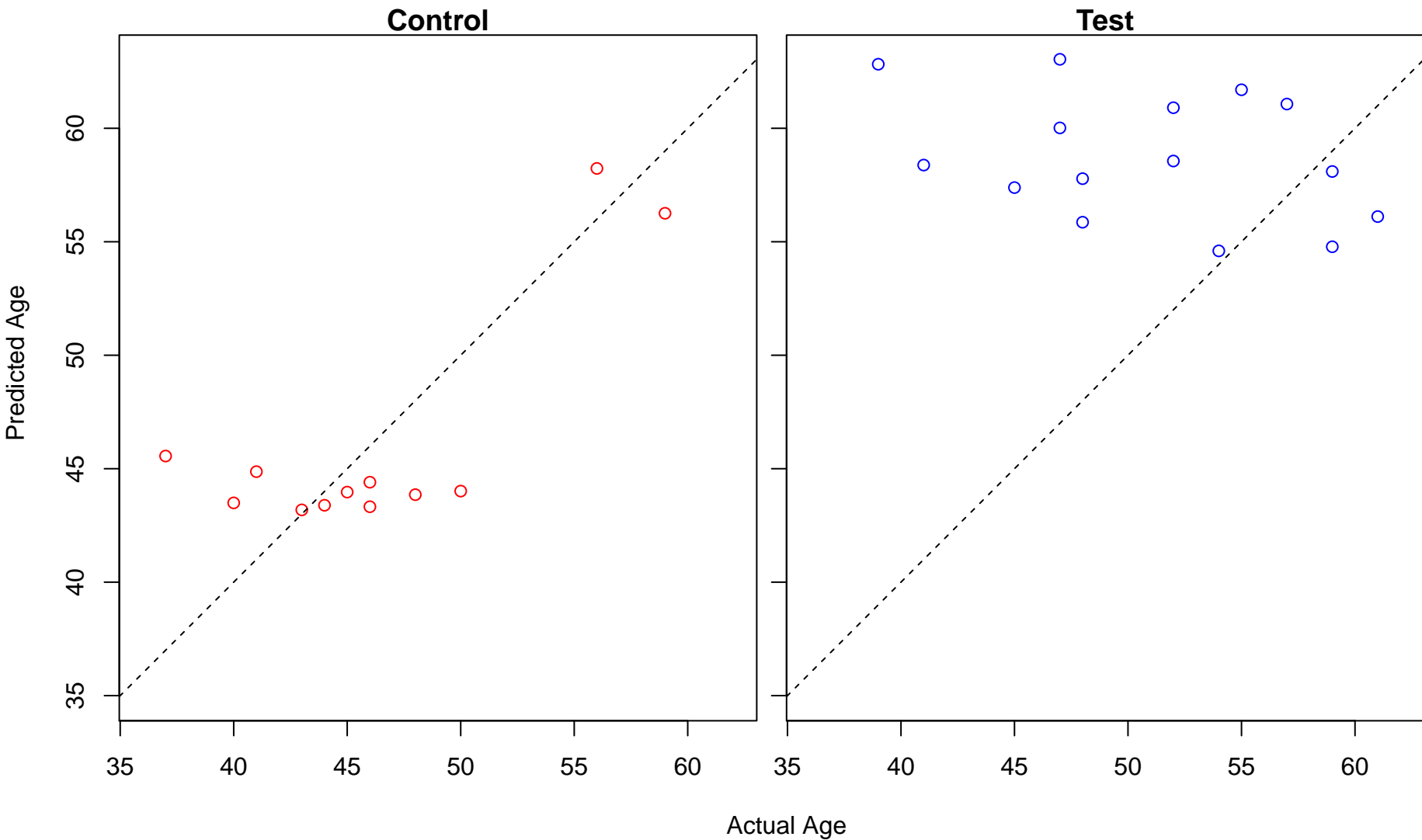
calcium ion regulated exocytosis (Score: 3.081693)



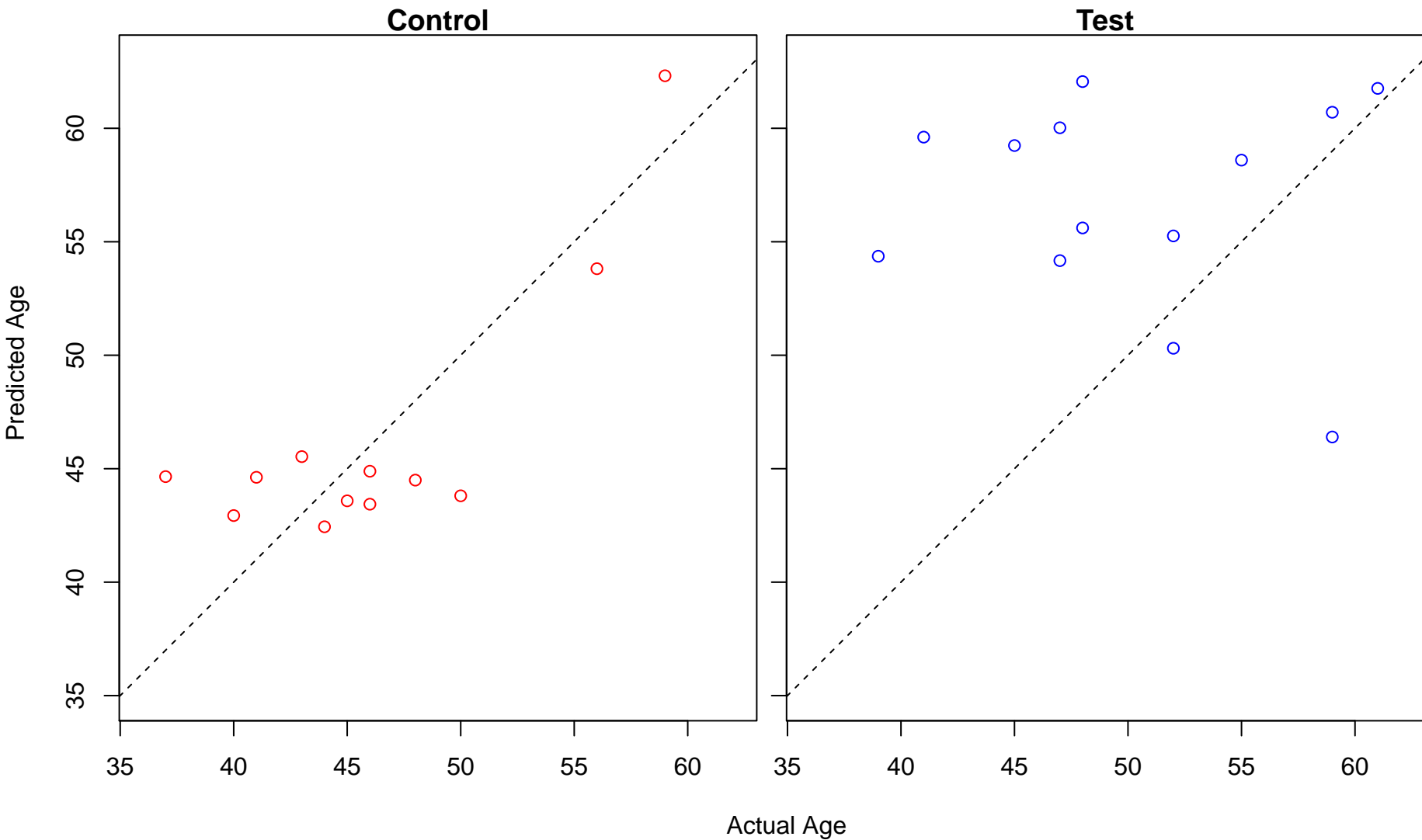
cytochrome complex assembly (Score: 3.080591)



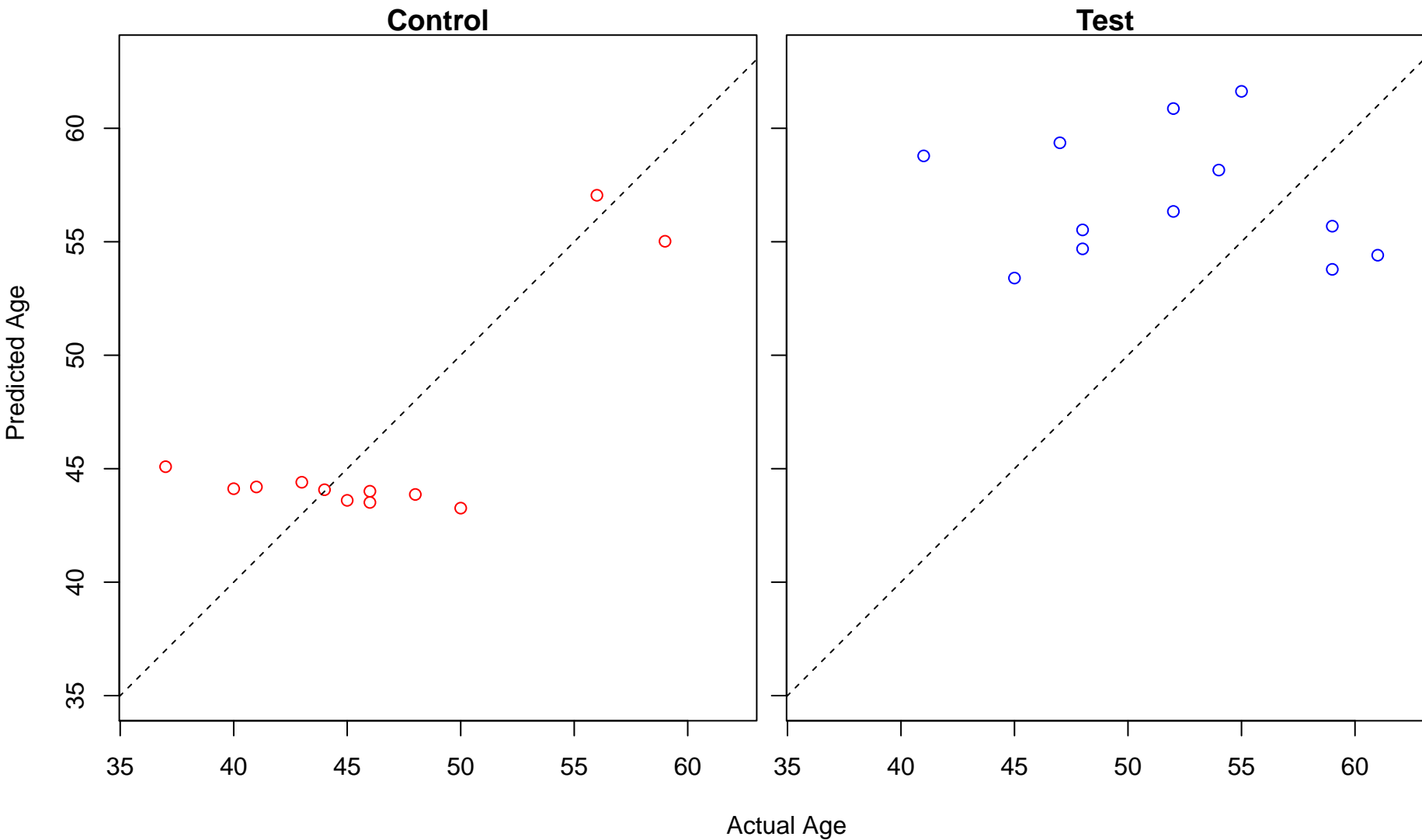
positive regulation of binding (Score: 3.080511)



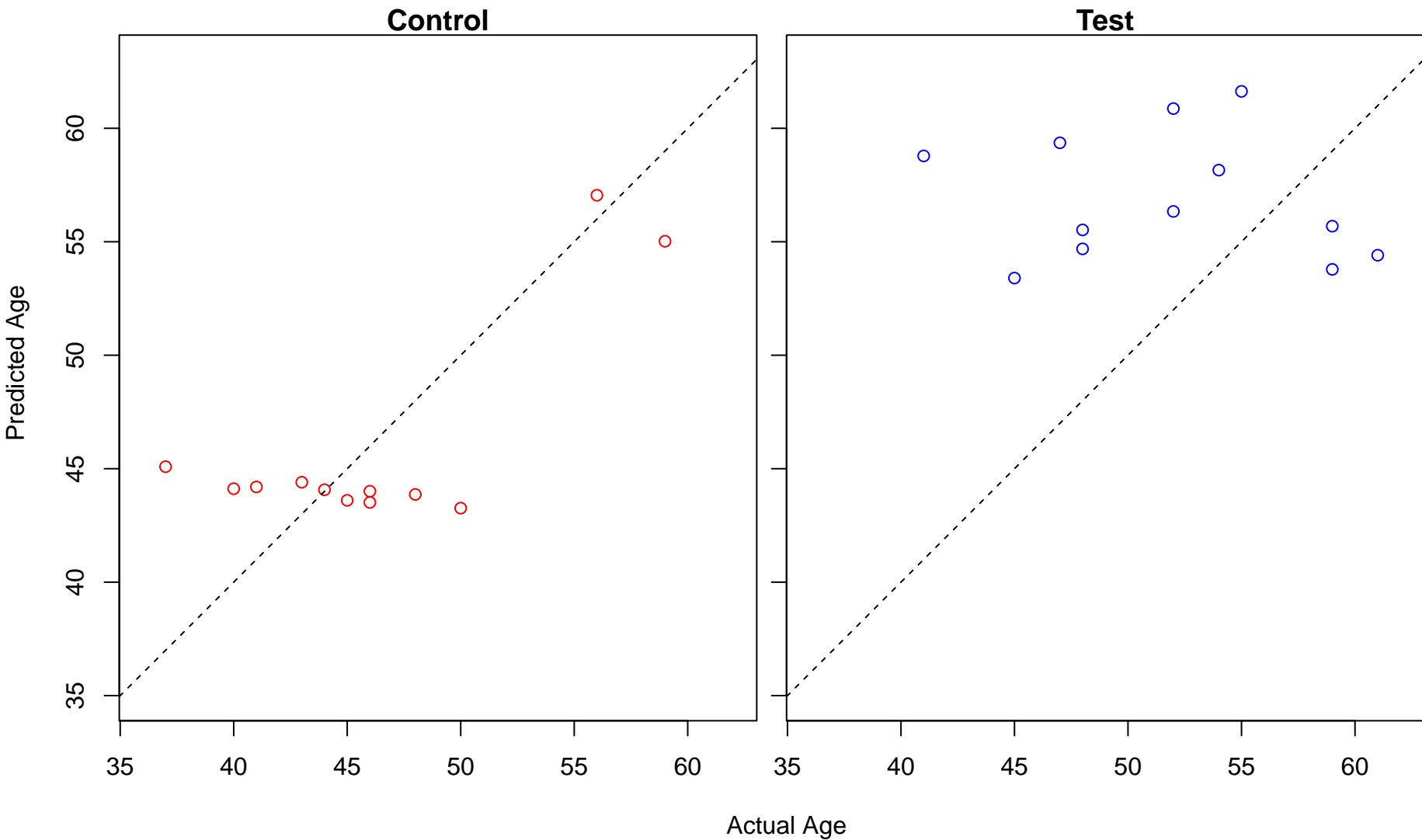
amyloid precursor protein catabolic process (Score: 3.080372)



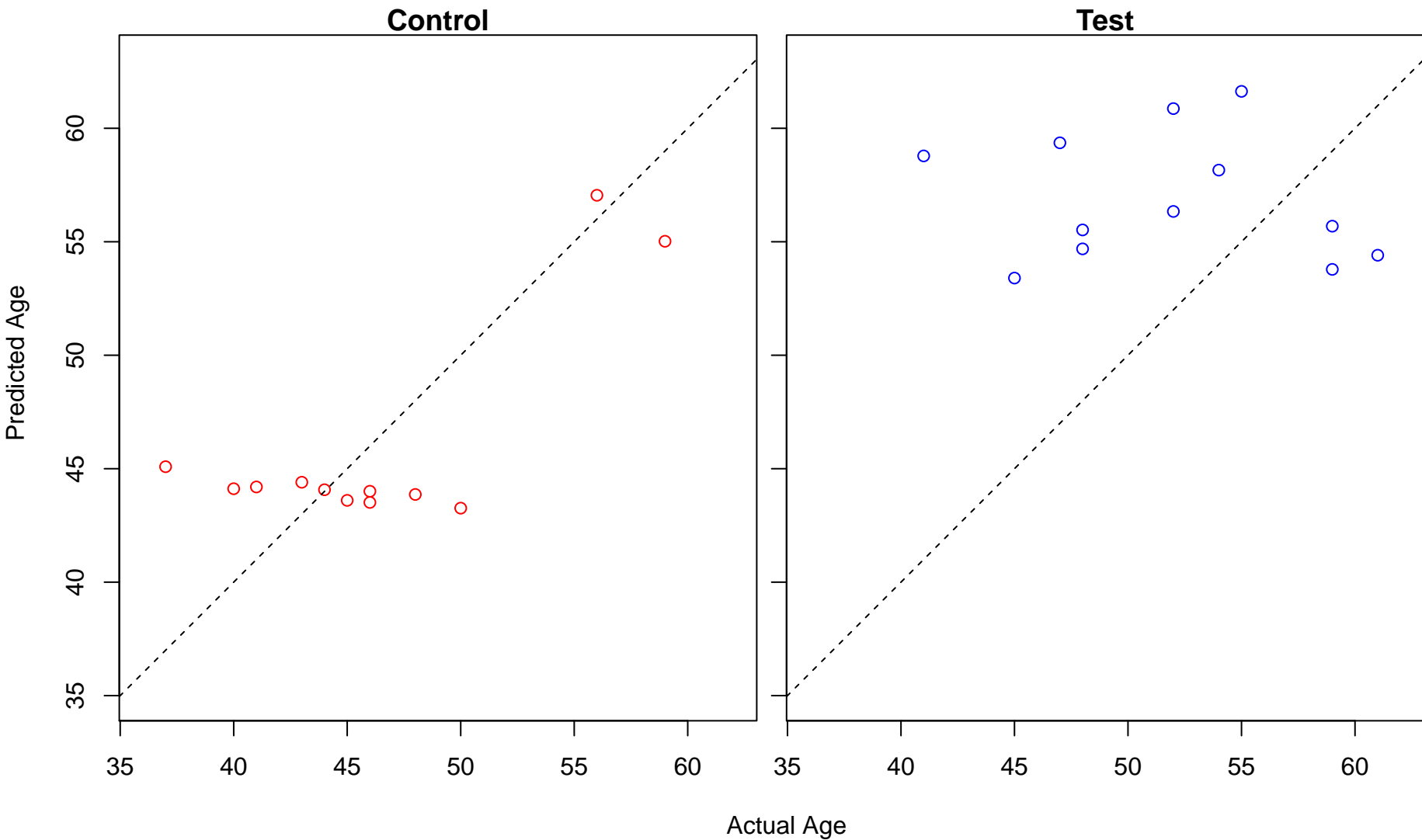
hemostasis (Score: 3.079700)



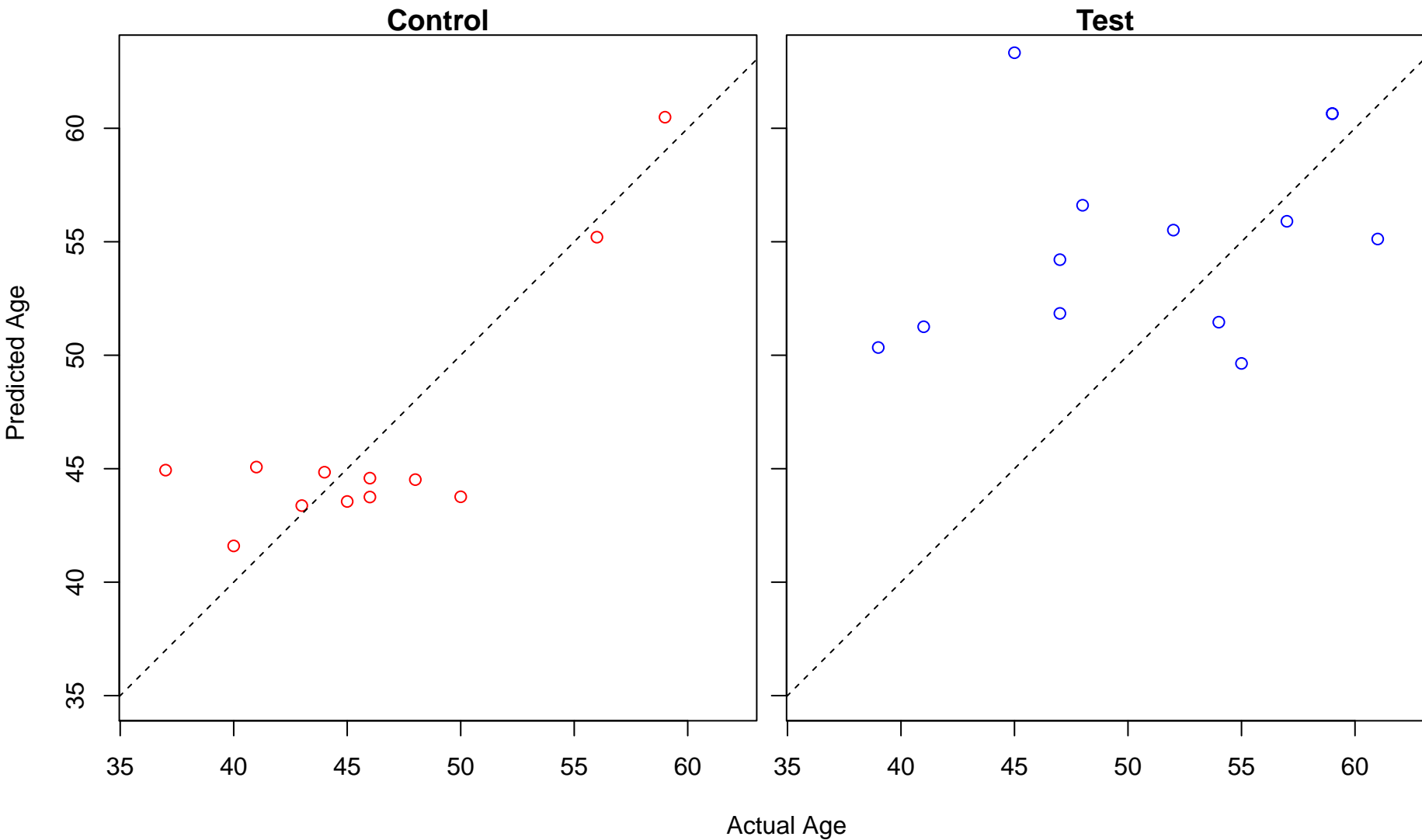
blood coagulation (Score: 3.079529)



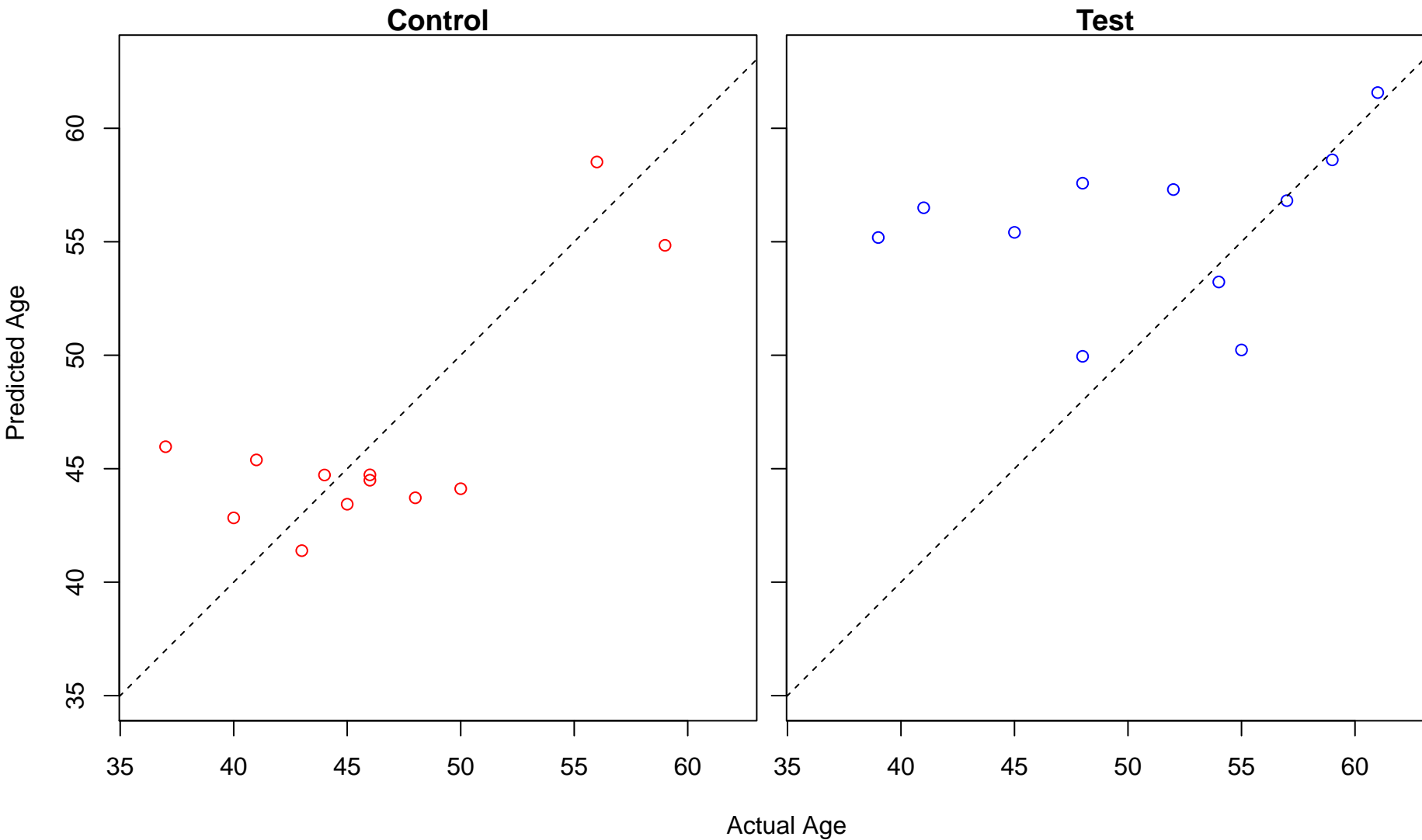
coagulation (Score: 3.079529)



nucleoside transport (Score: 3.078358)

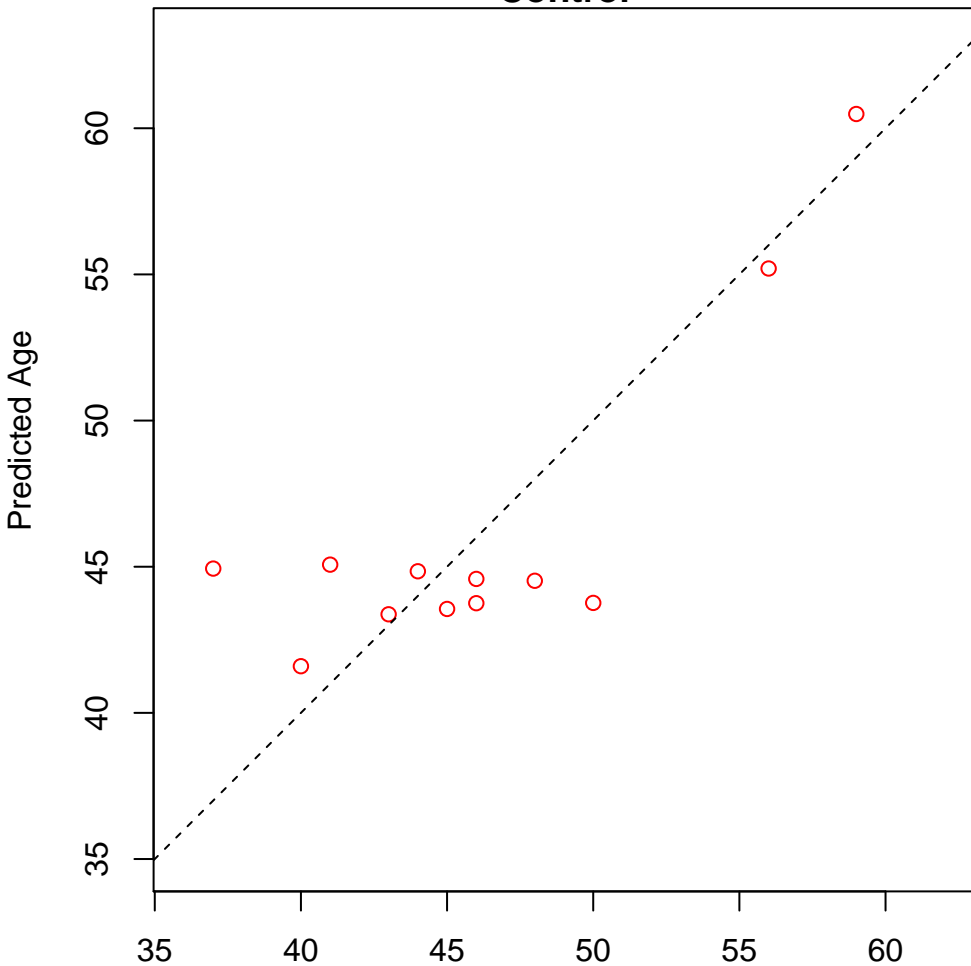


myotube cell development (Score: 3.077440)

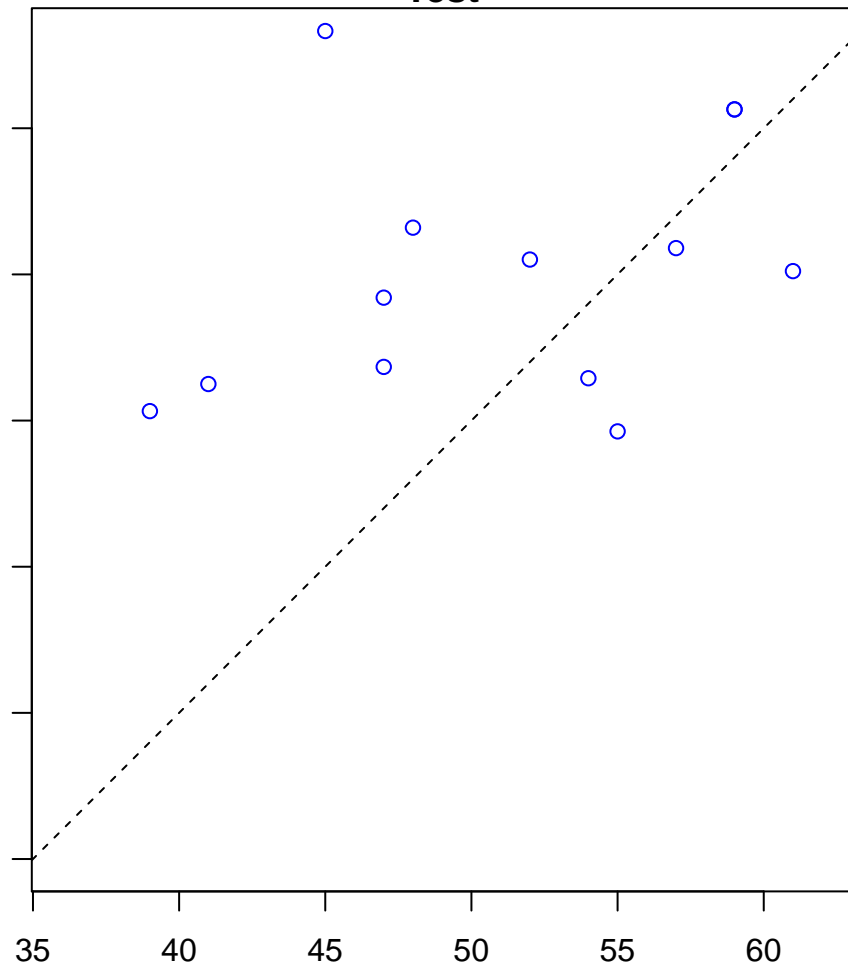


nucleoside transmembrane transport (Score: 3.076789)

Control

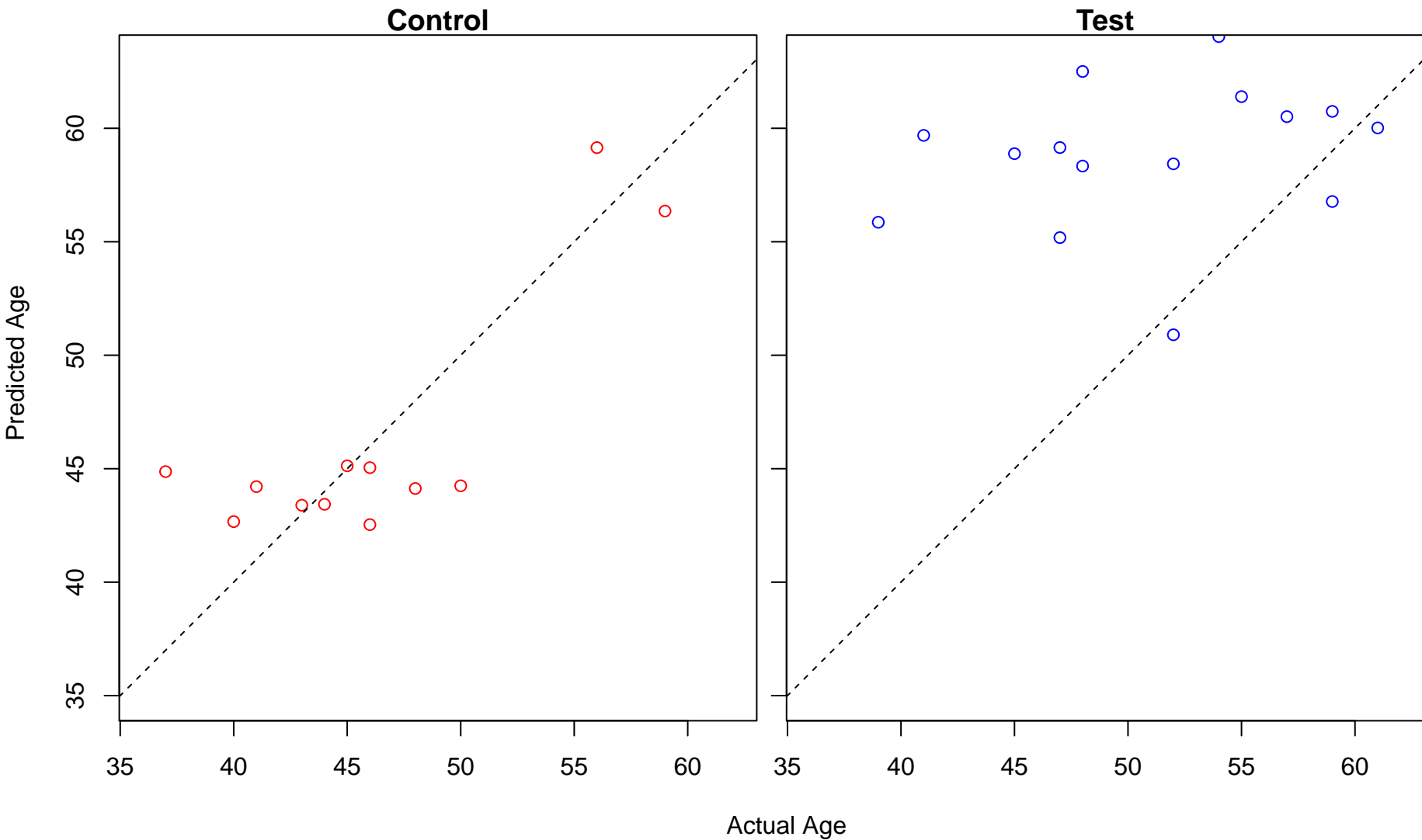


Test

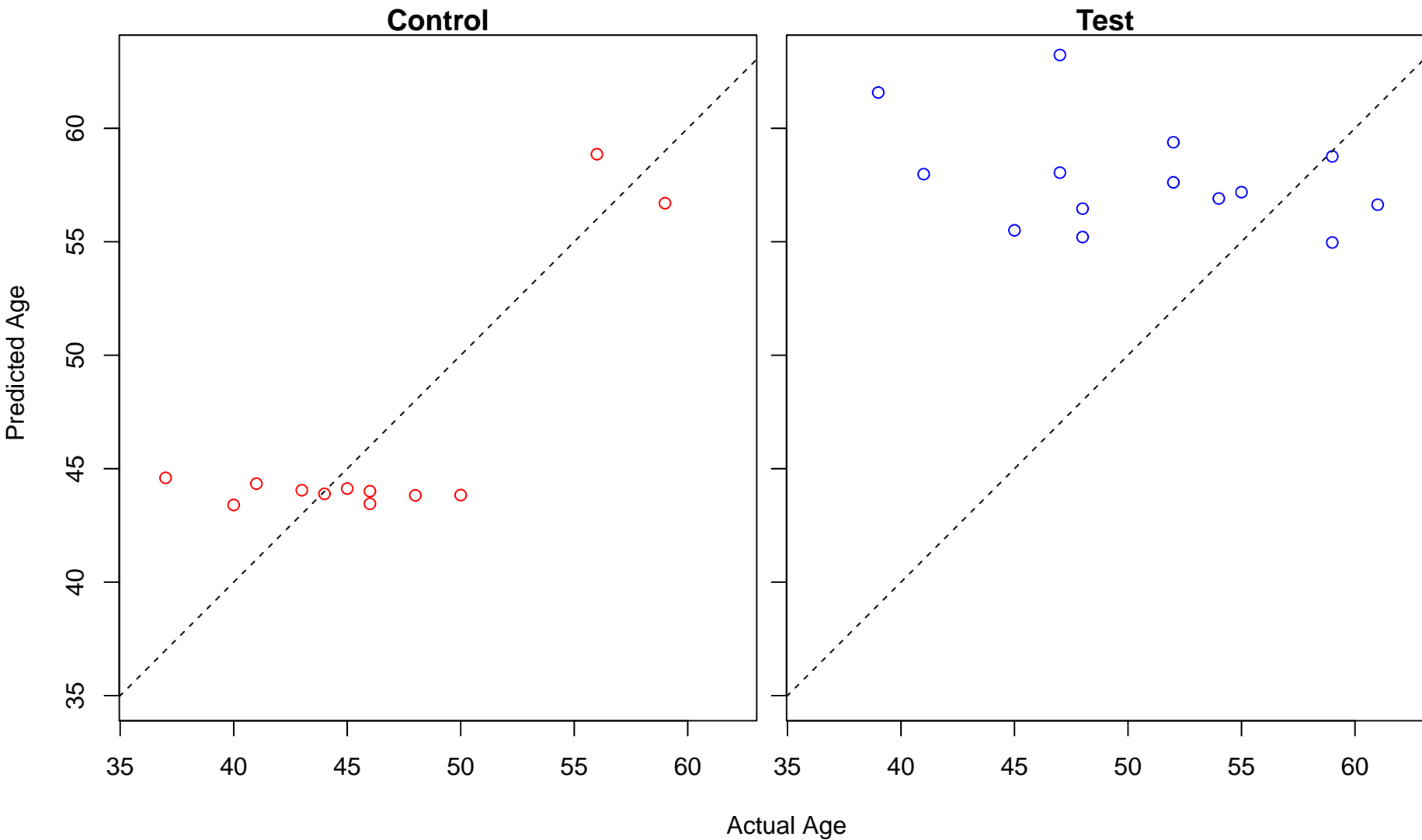


Actual Age

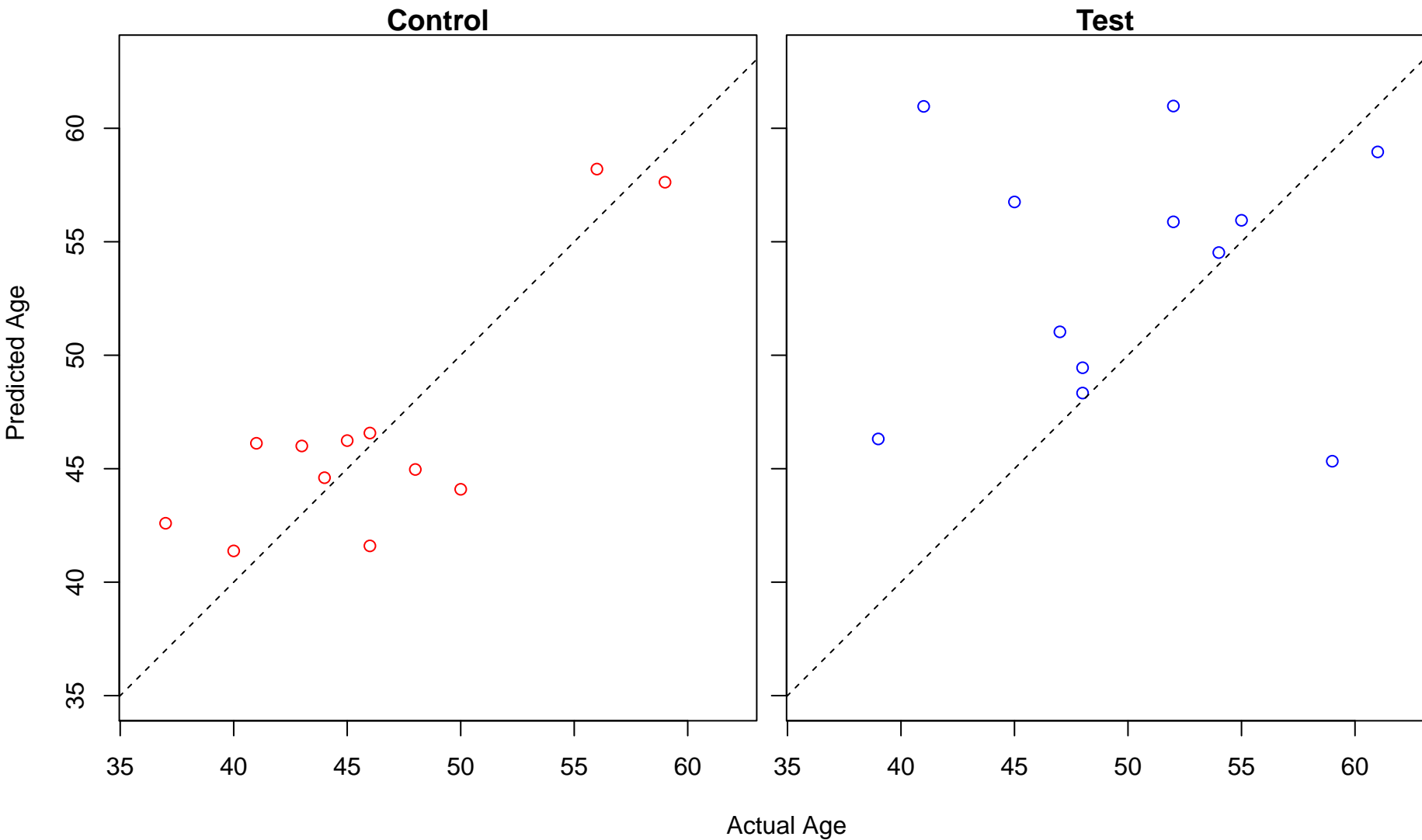
regulation of respiratory gaseous exchange (Score: 3.075201)



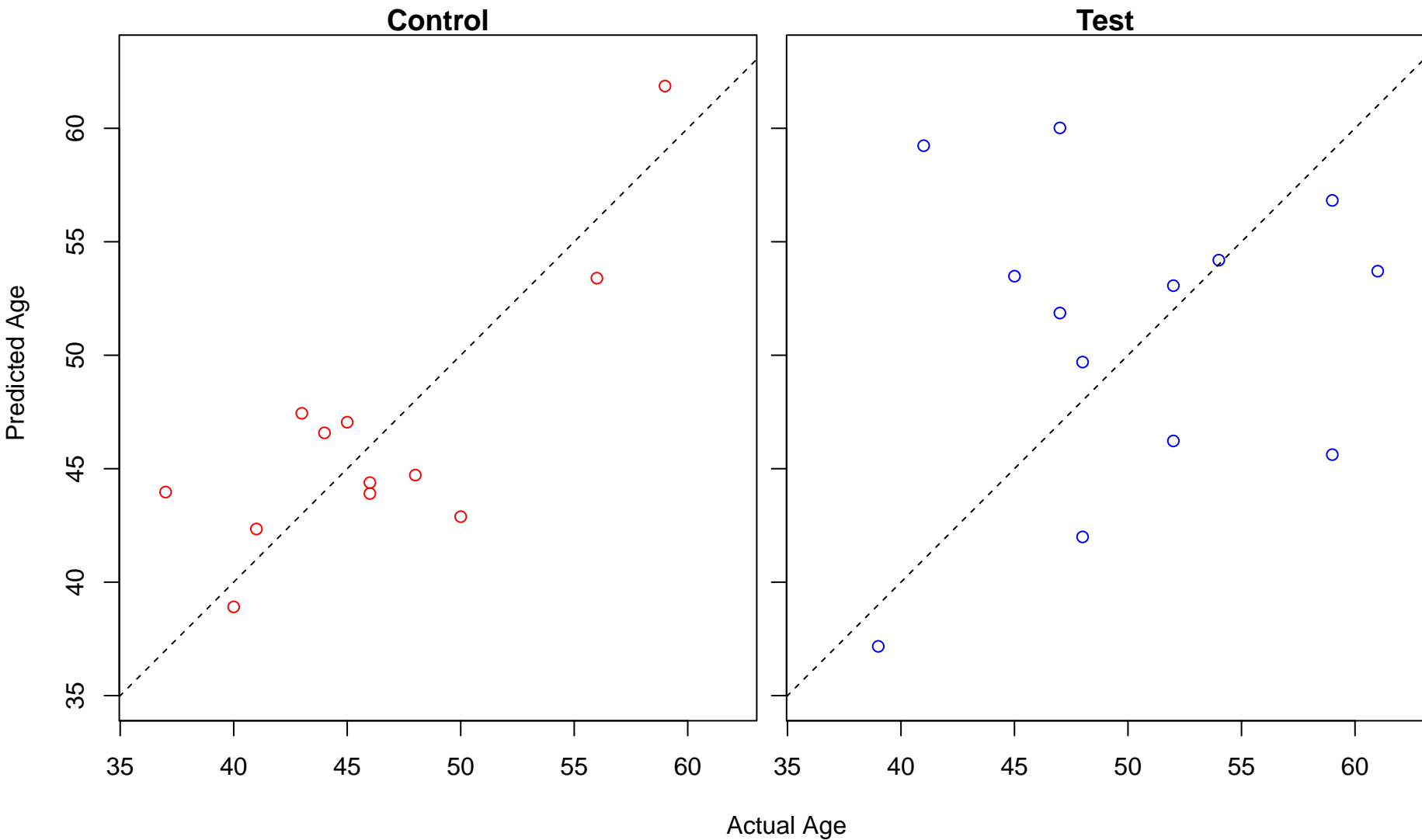
activation of innate immune response (Score: 3.073358)



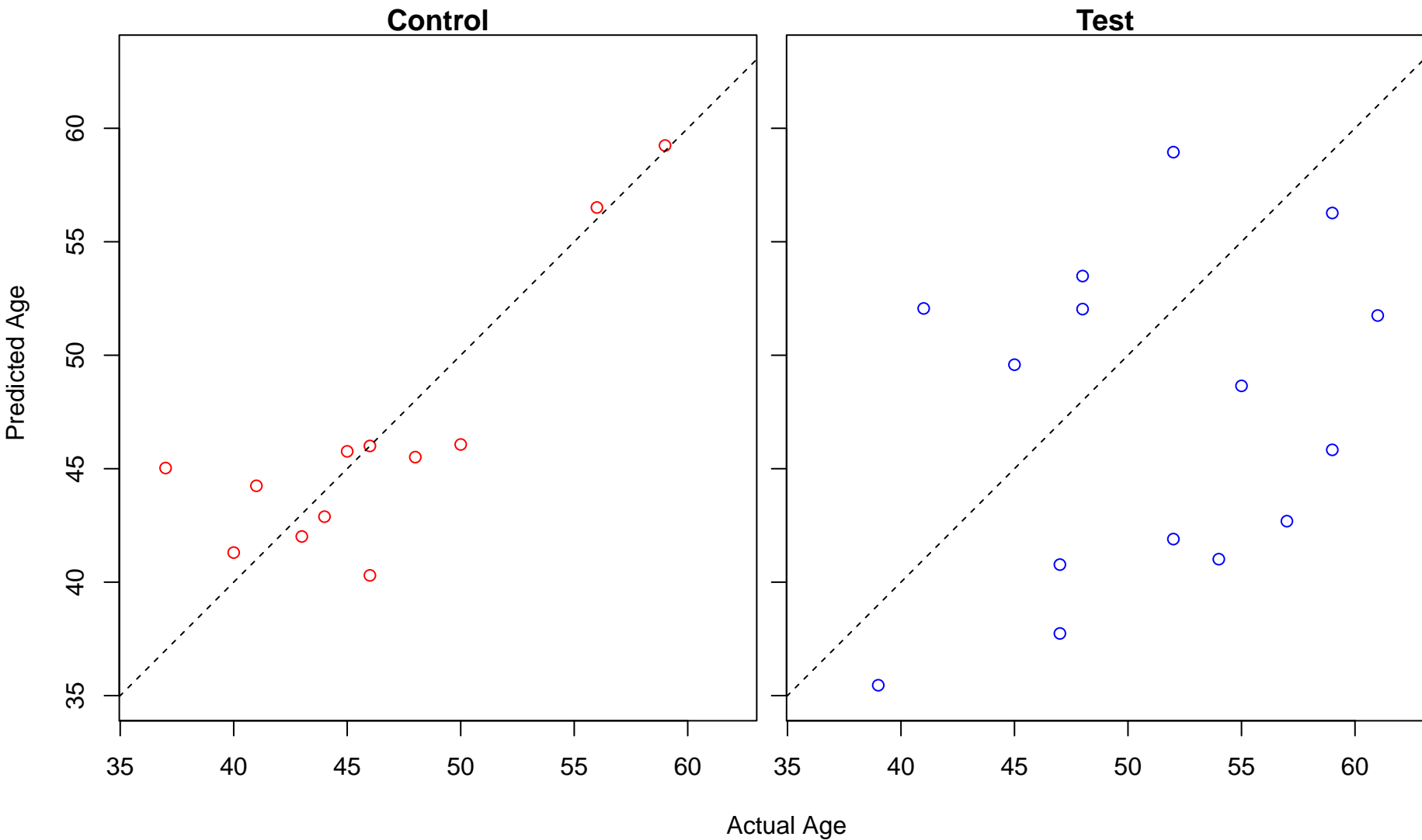
antigen receptor-mediated signaling pathway (Score: 3.072598)



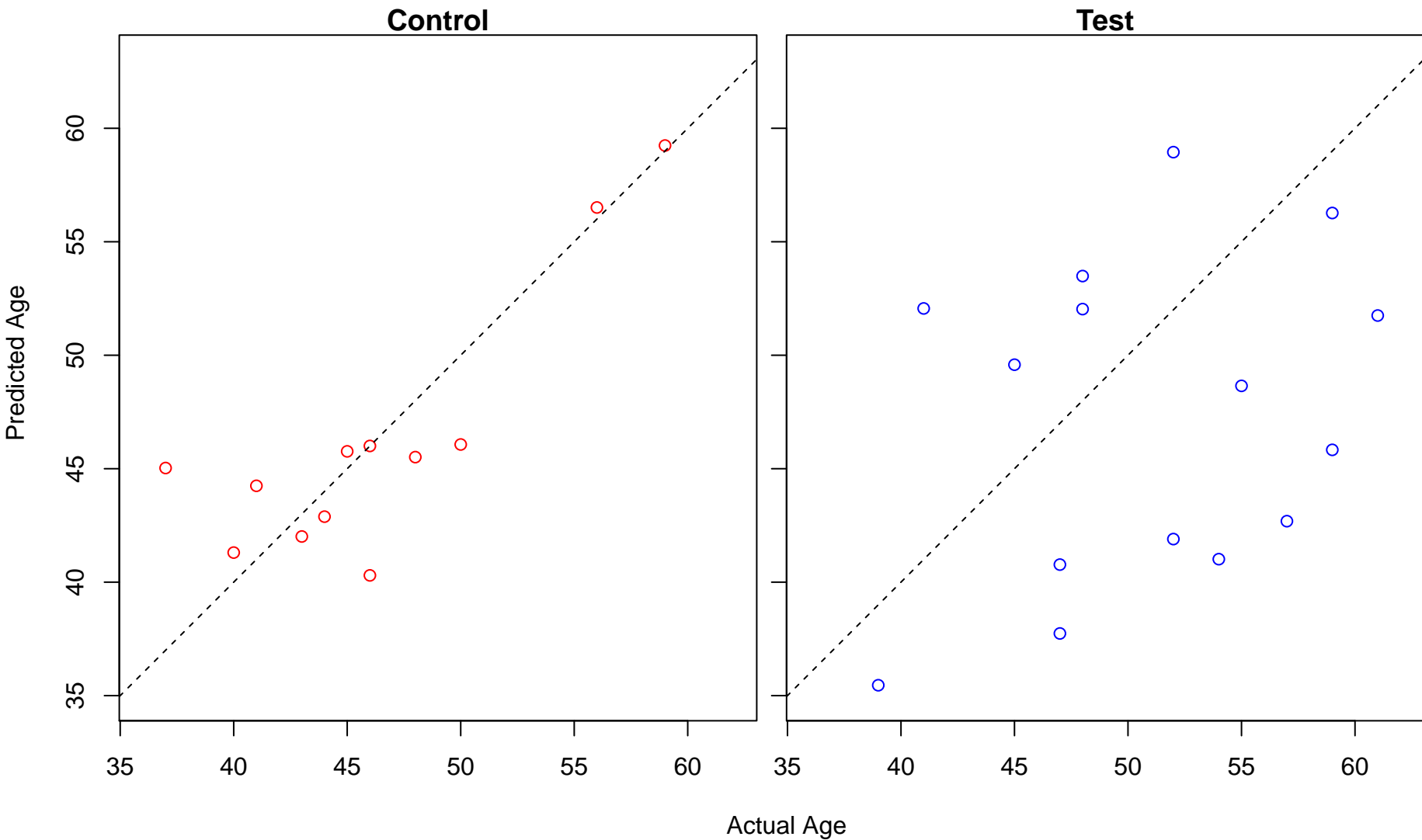
regulation of osteoblast differentiation (Score: 3.072233)



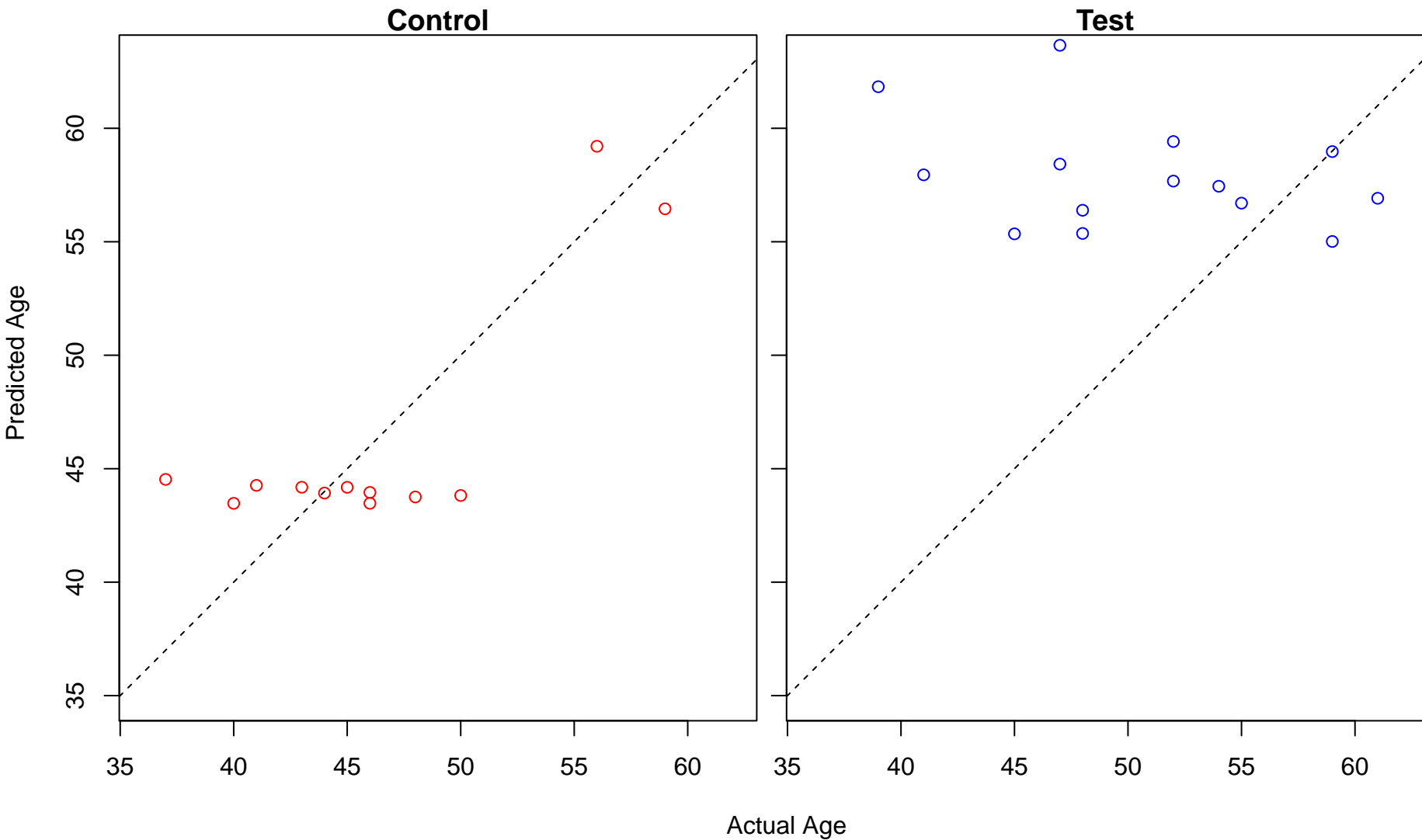
virion attachment to host cell (Score: 3.071637)



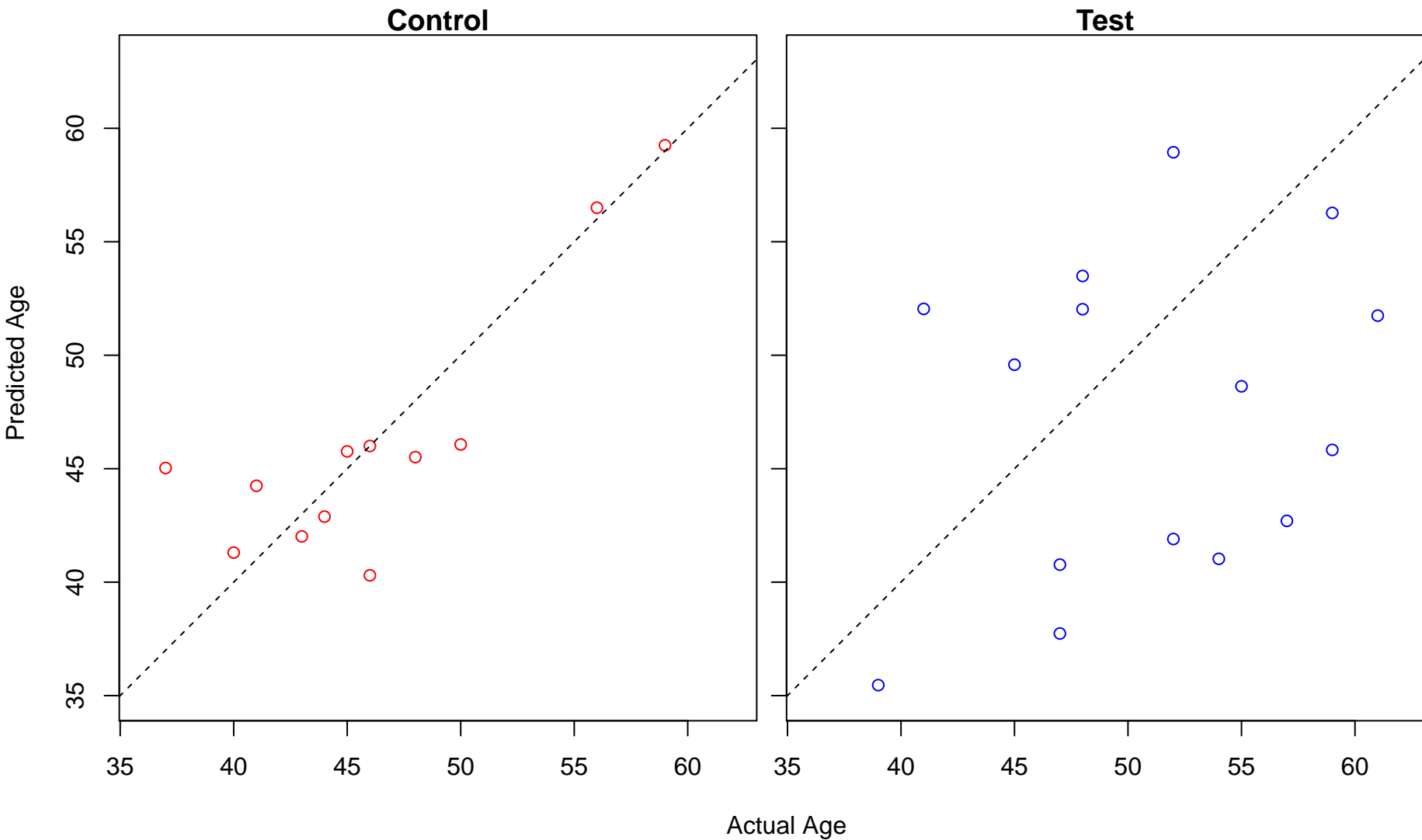
adhesion of symbiont to host cell (Score: 3.071637)



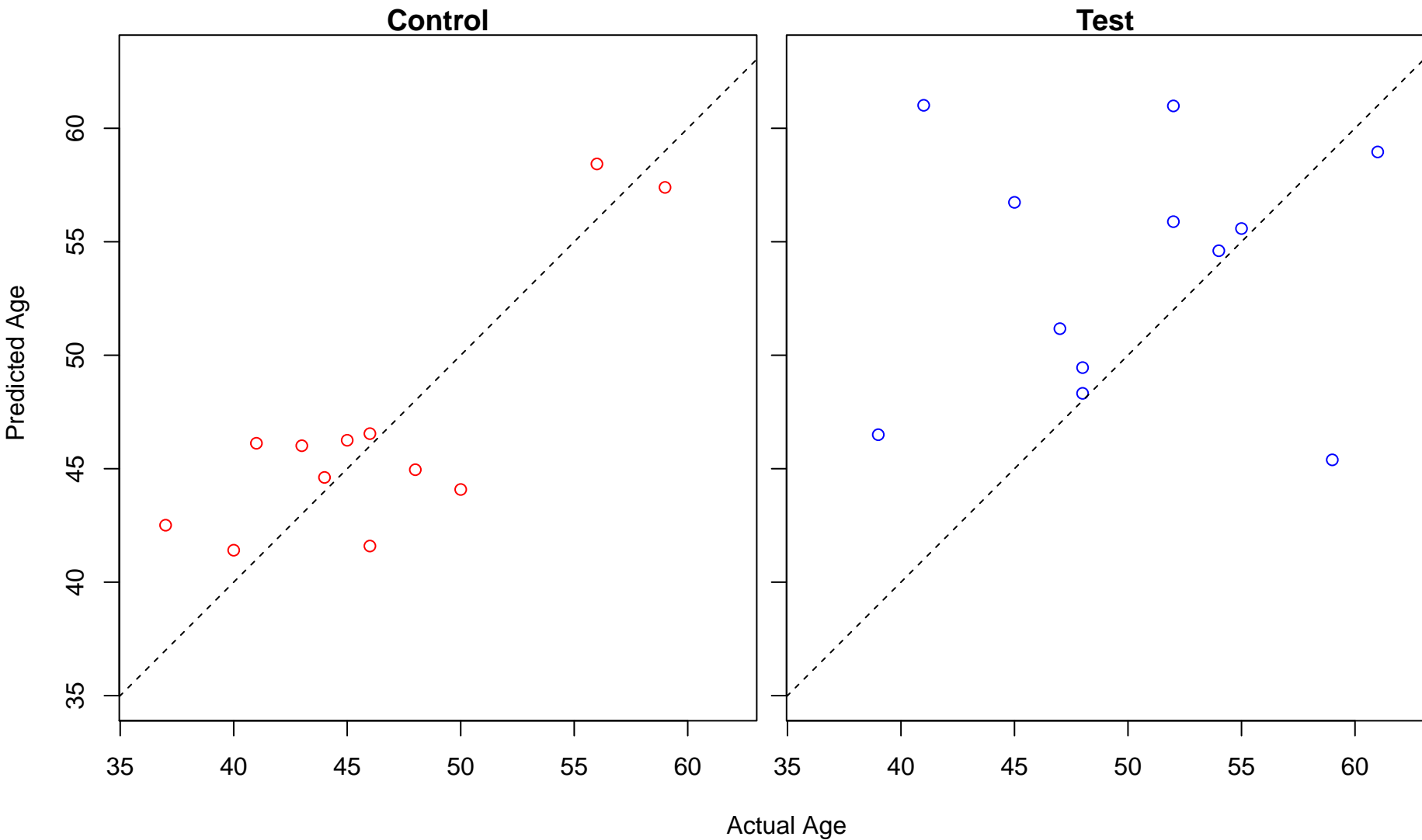
Fc-epsilon receptor signaling pathway (Score: 3.071151)



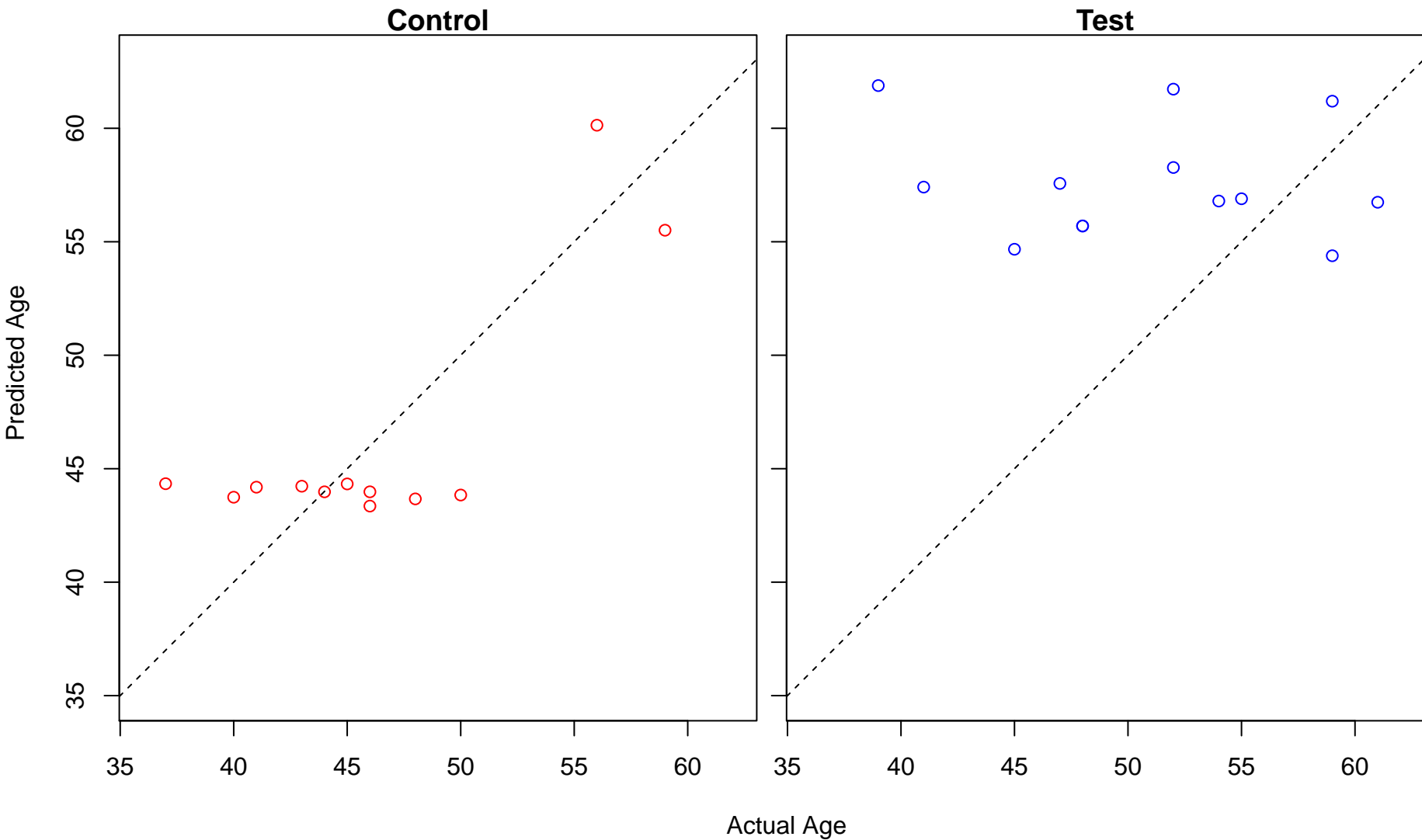
adhesion of symbiont to host (Score: 3.070829)



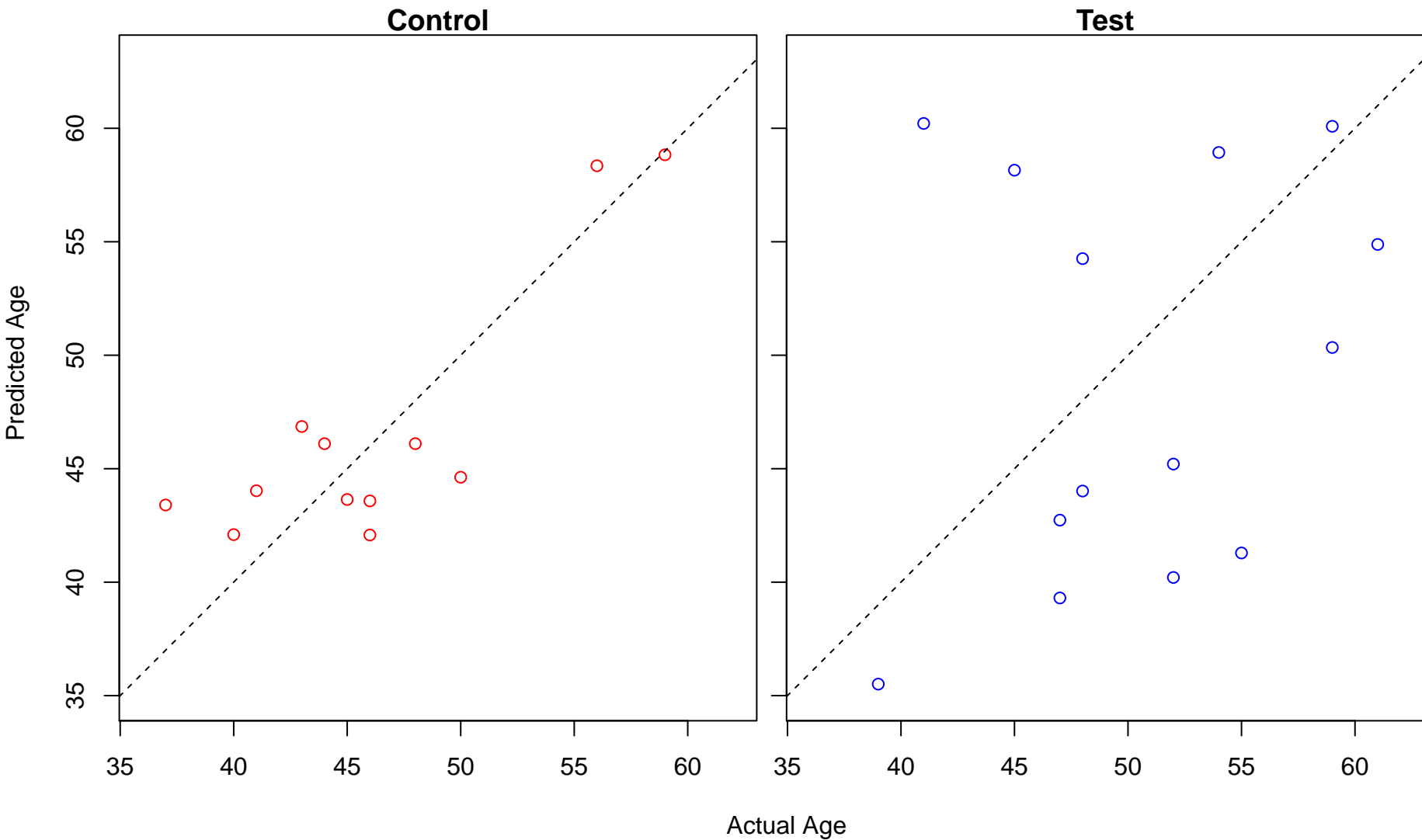
T cell receptor signaling pathway (Score: 3.068841)



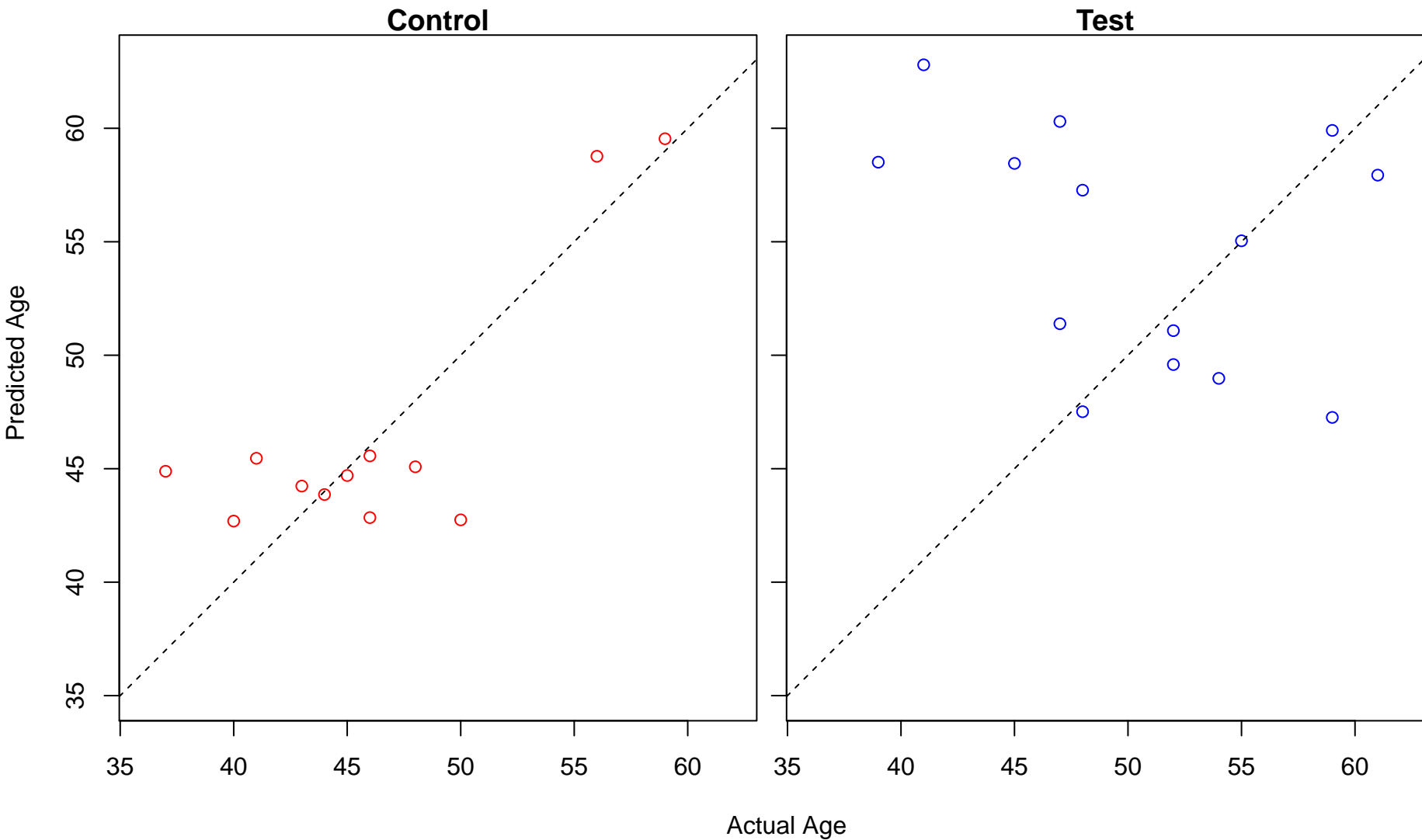
circadian rhythm (Score: 3.067716)



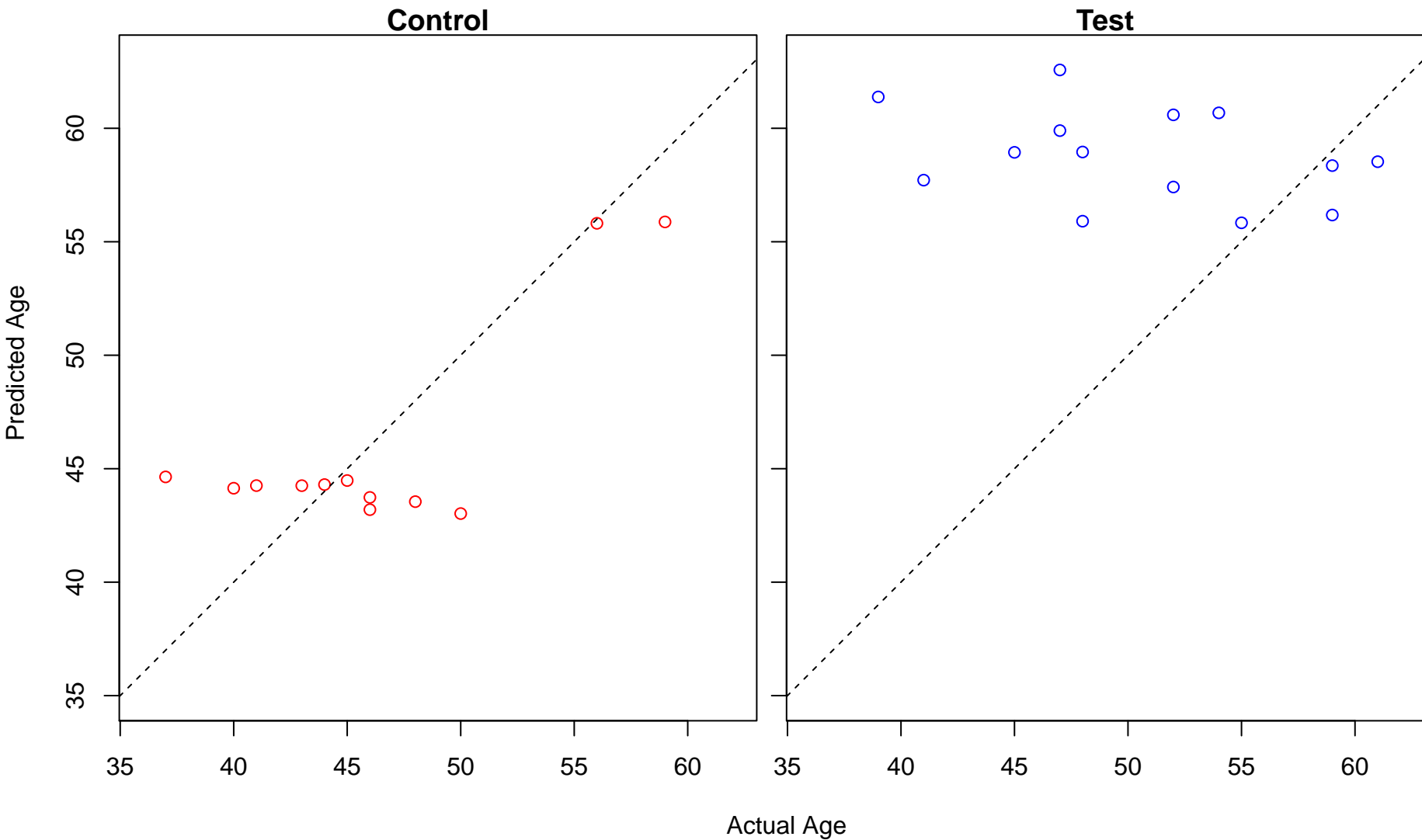
response to metal ion (Score: 3.067443)



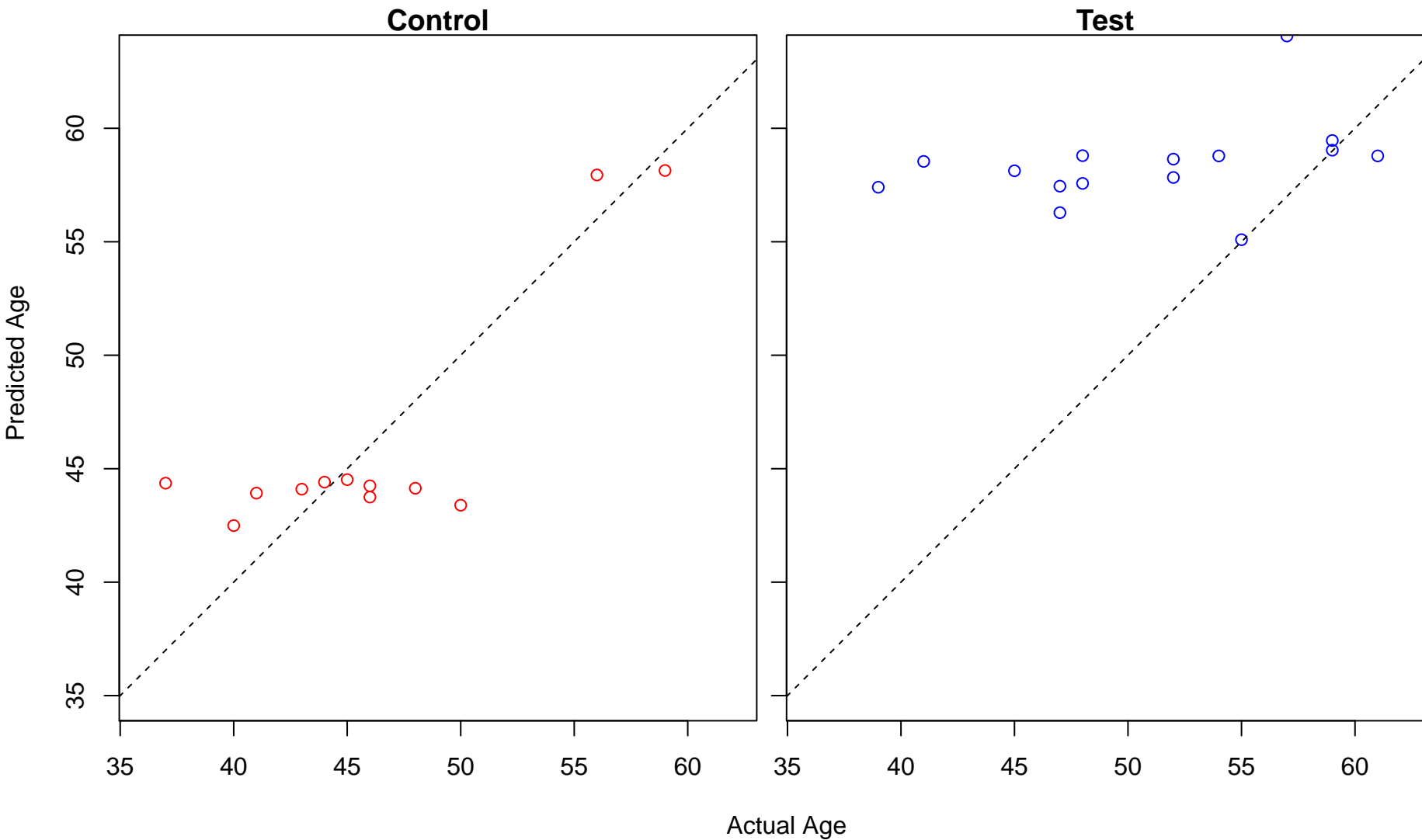
regulation of MAP kinase activity (Score: 3.065206)



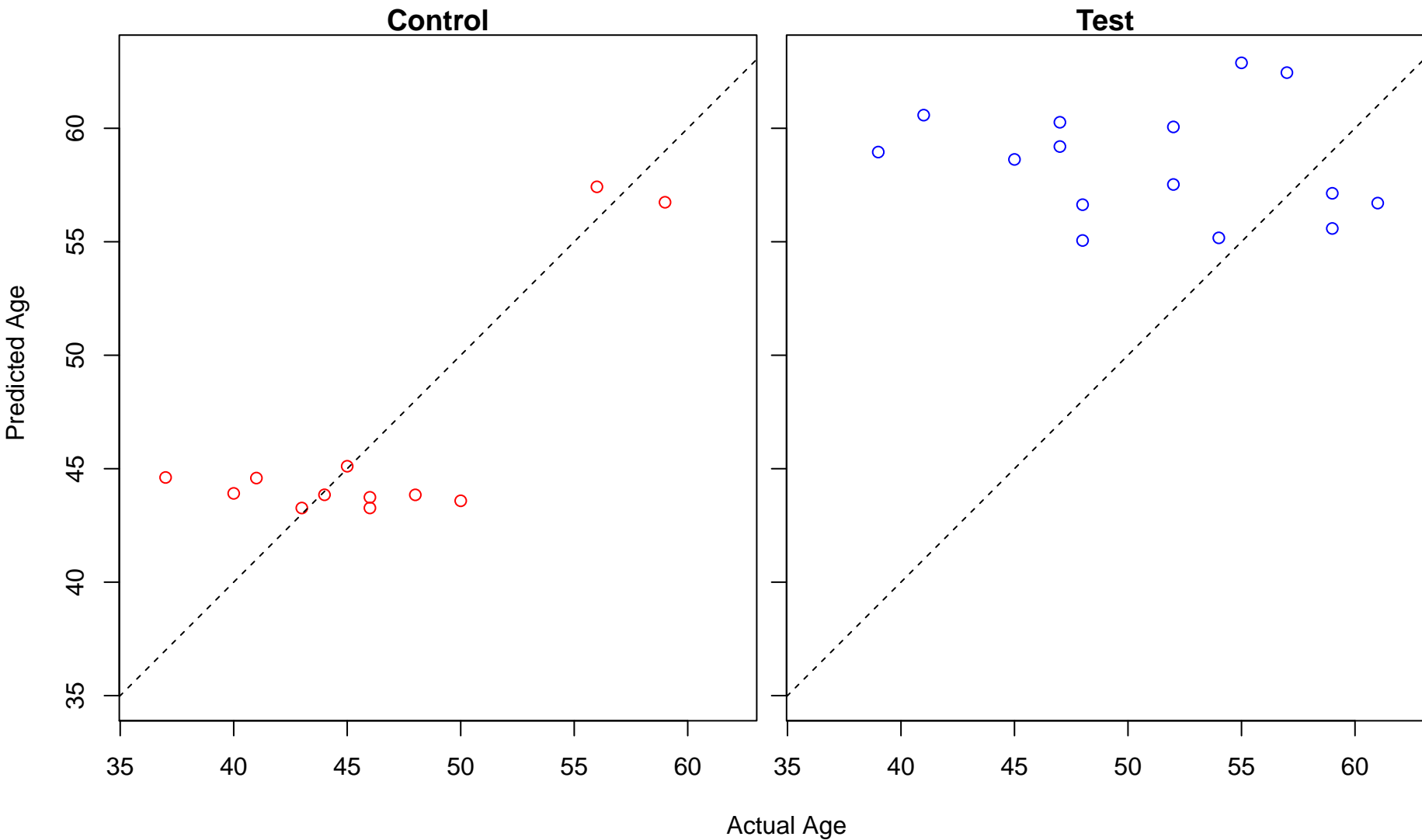
nucleoside phosphate biosynthetic process (Score: 3.064566)



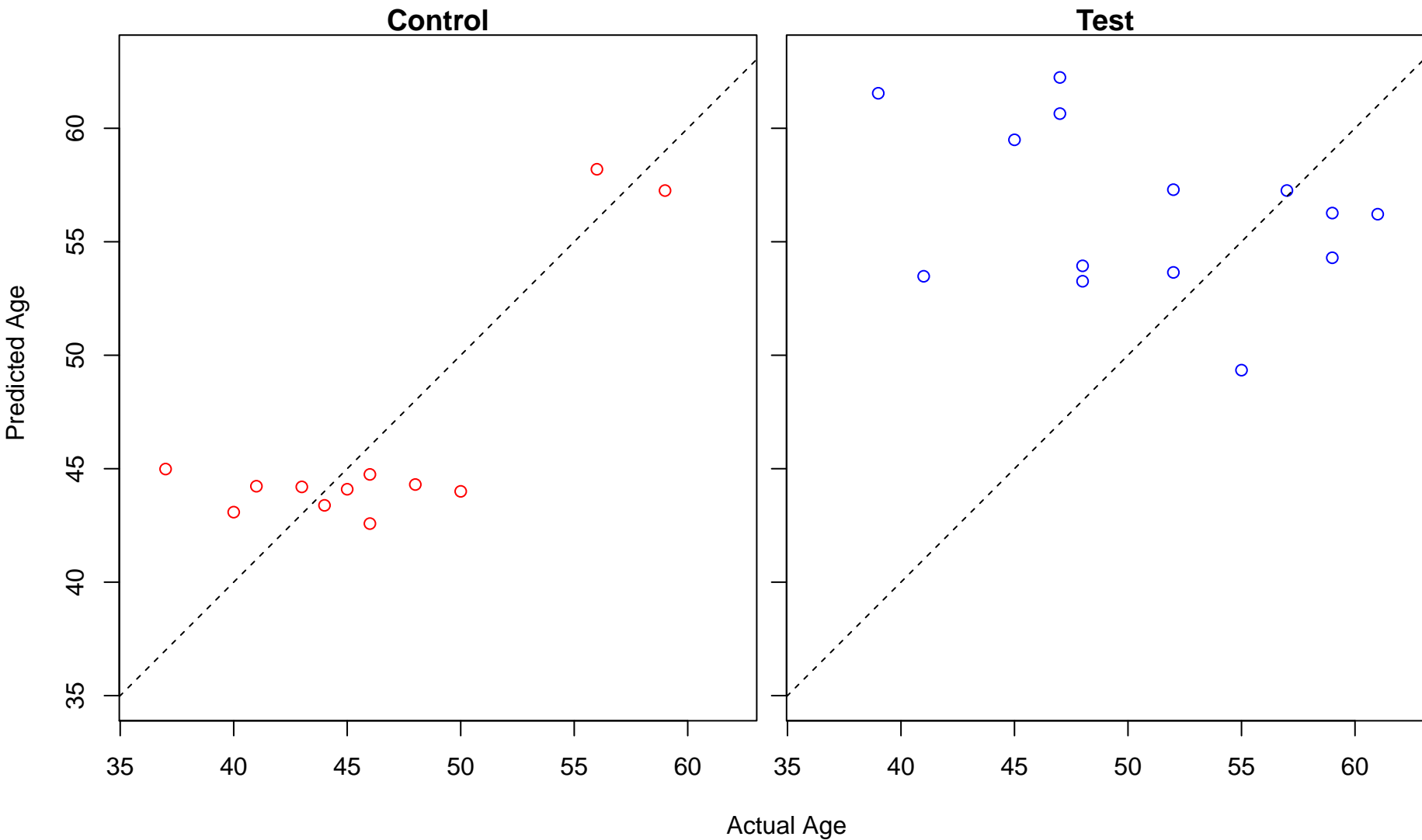
positive regulation of mitochondrial fission (Score: 3.064432)



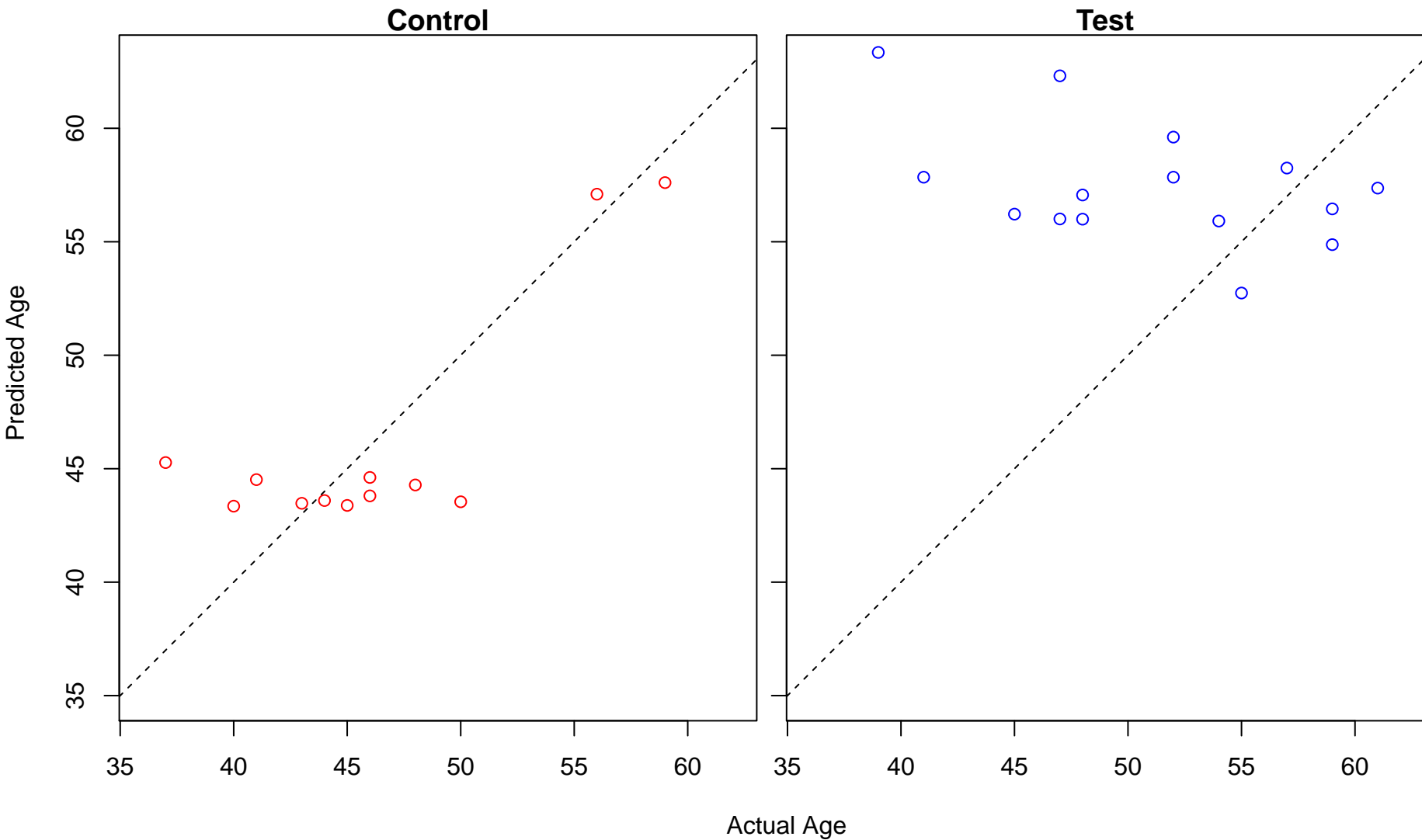
negative regulation of nervous system development (Score: 3.064203)



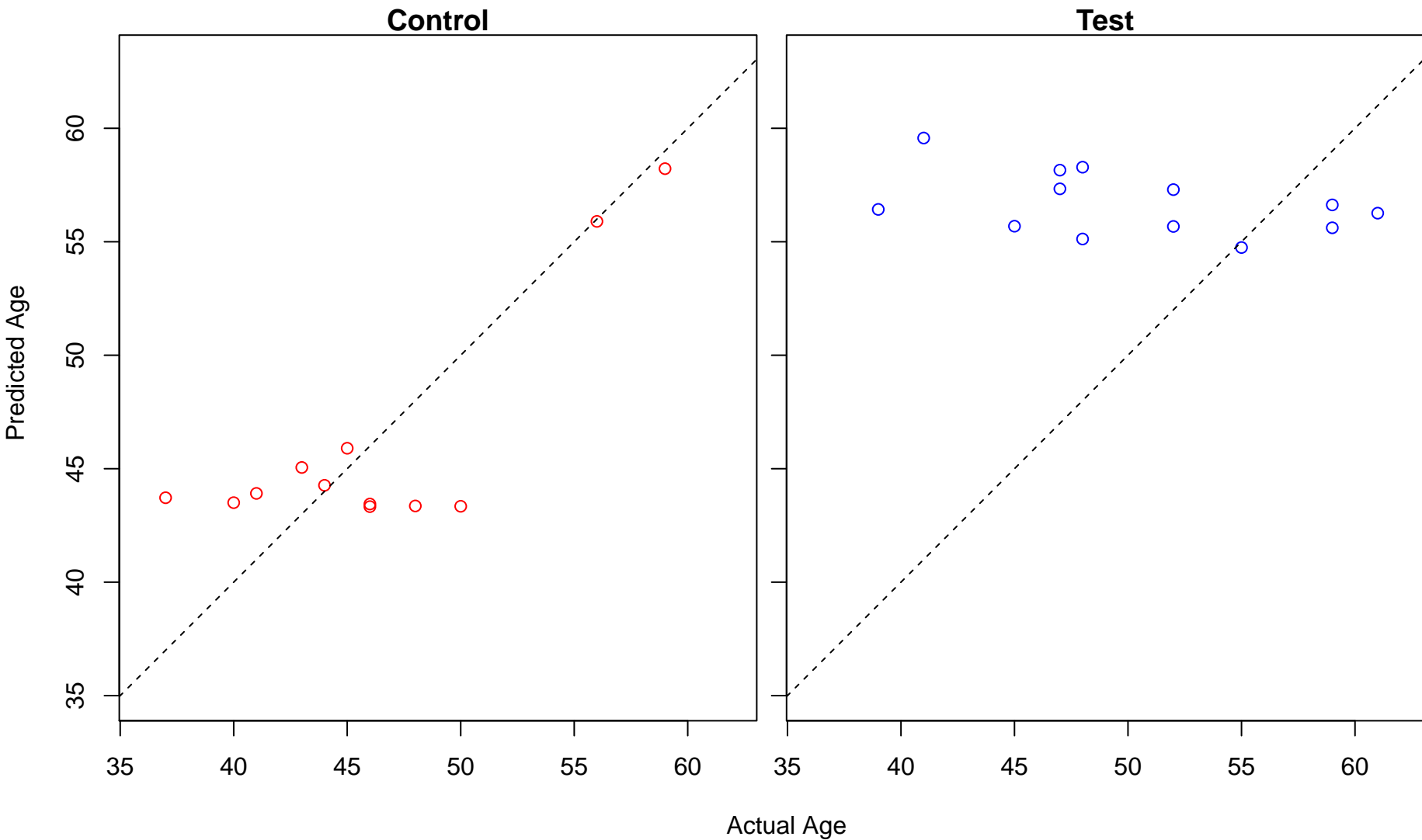
neuron maturation (Score: 3.063831)



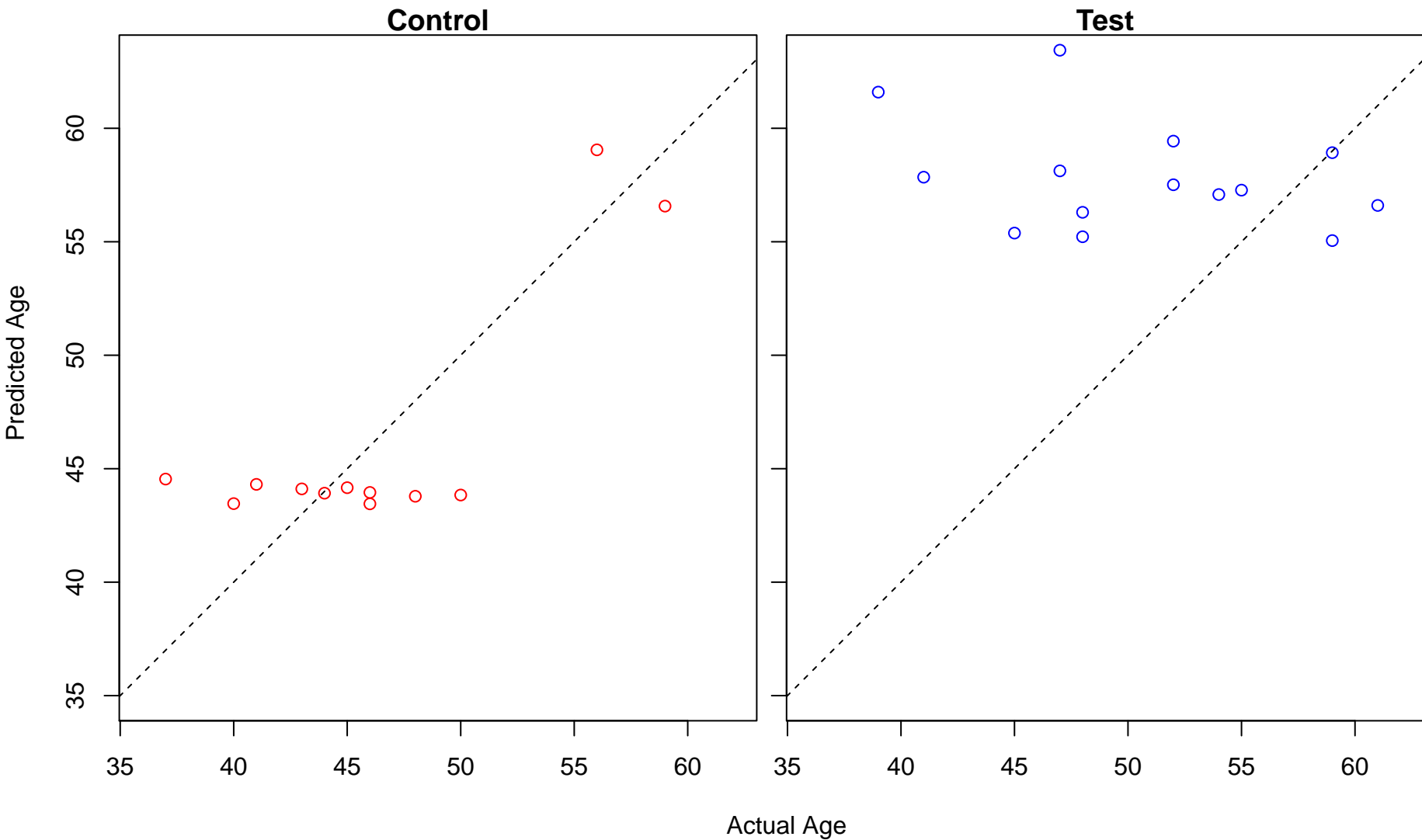
regulation of DNA repair (Score: 3.062550)



cristae formation (Score: 3.061840)

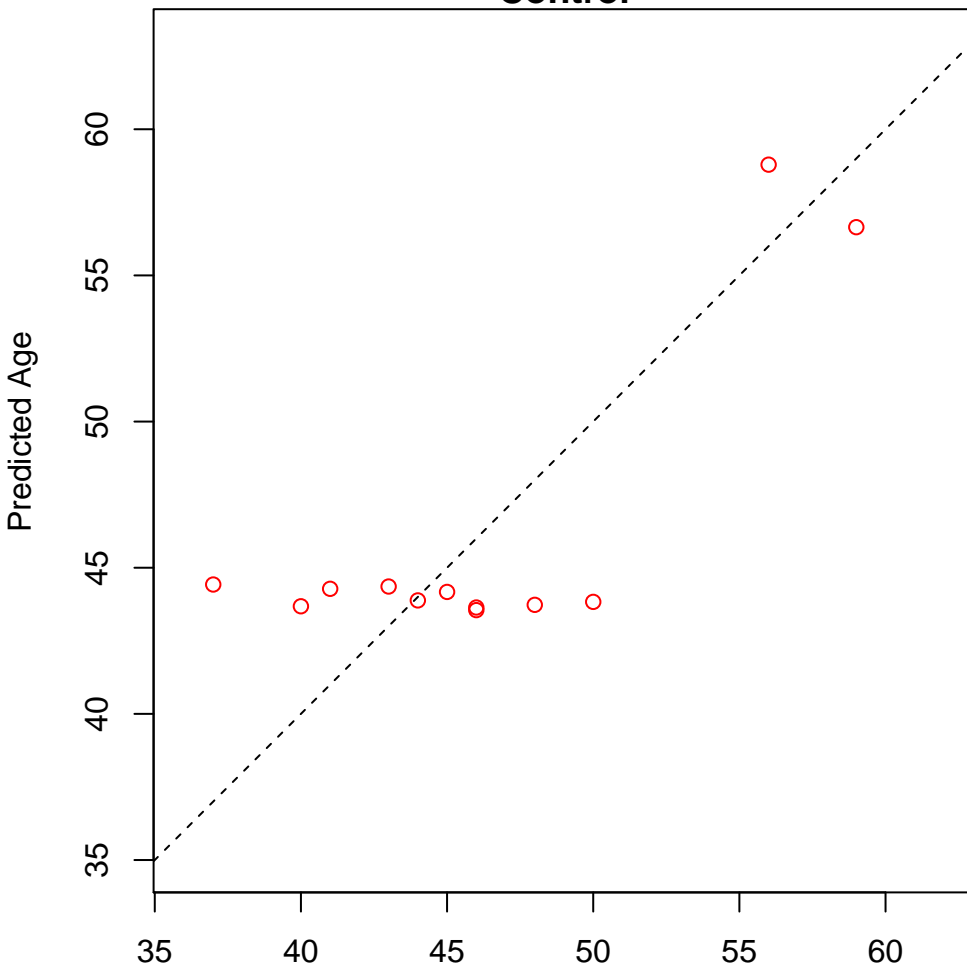


innate immune response-activating signal transduction (Score: 3.060897)

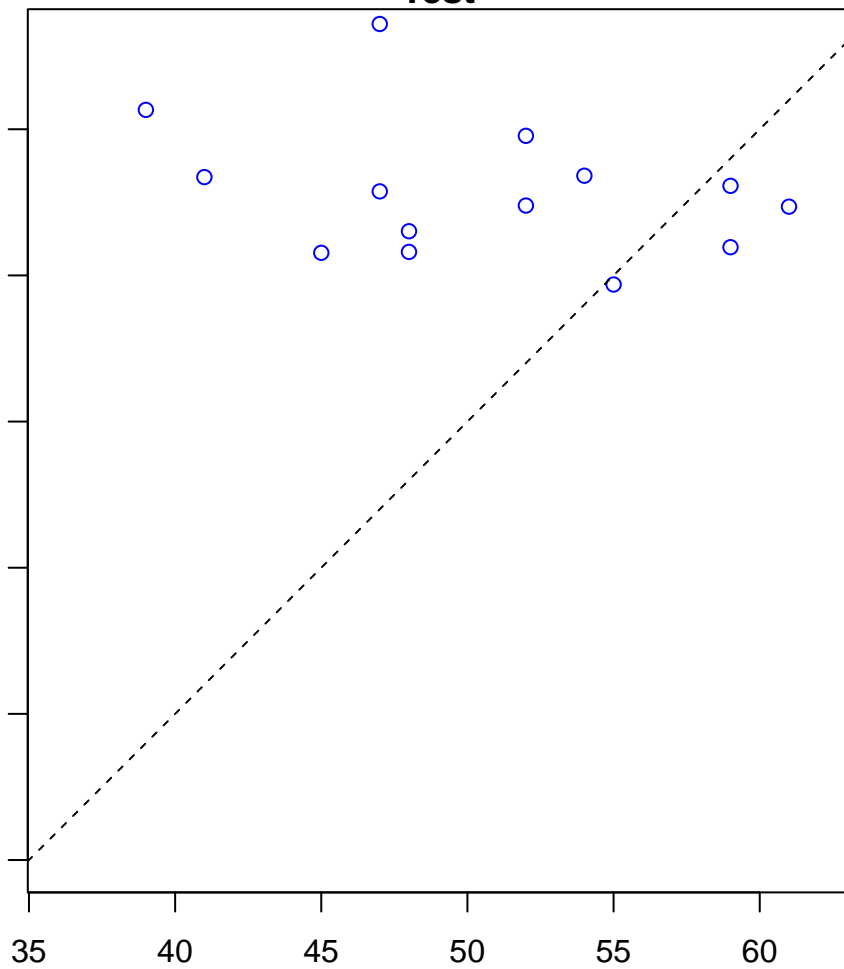


DNA-templated transcription, initiation (Score: 3.059071)

Control

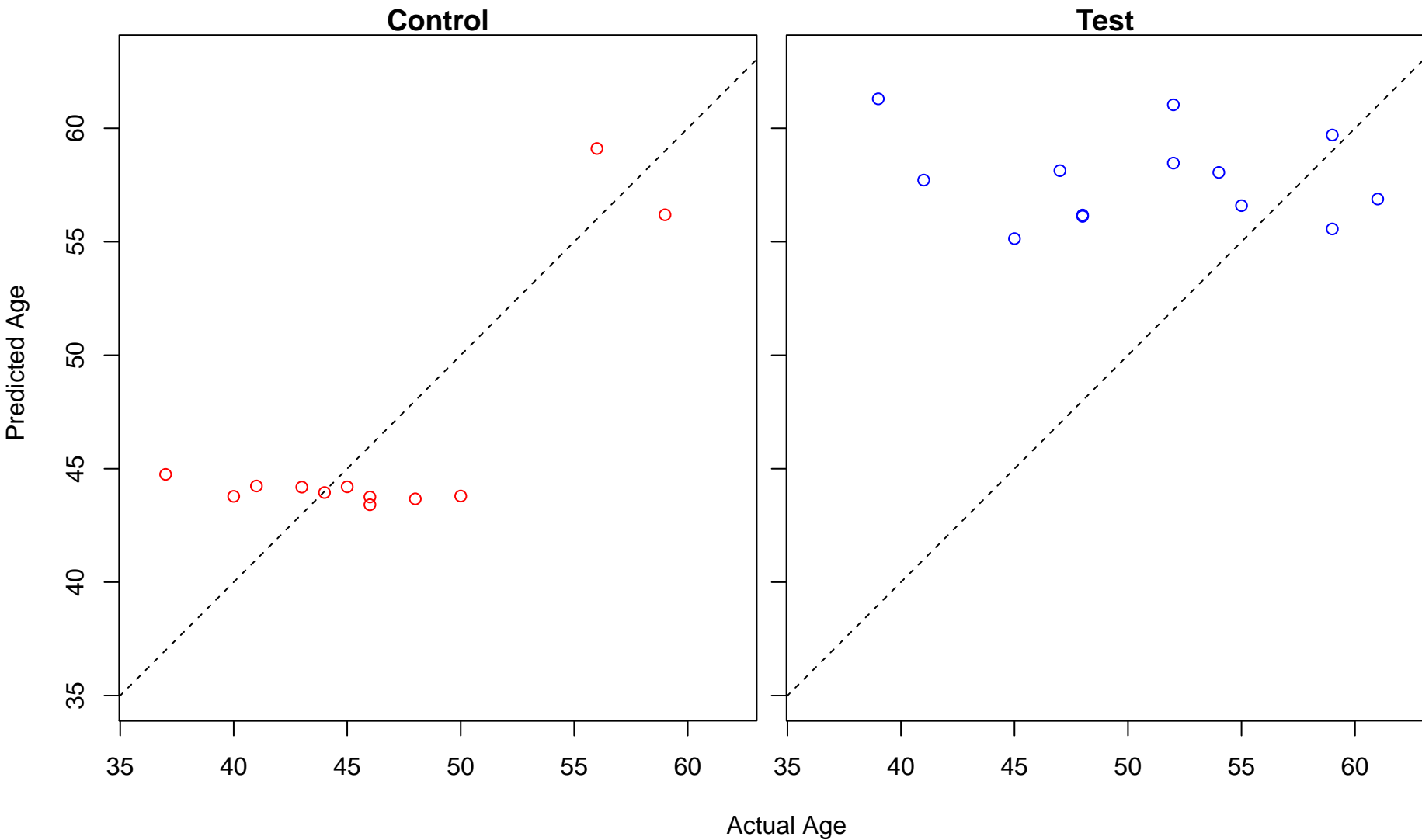


Test

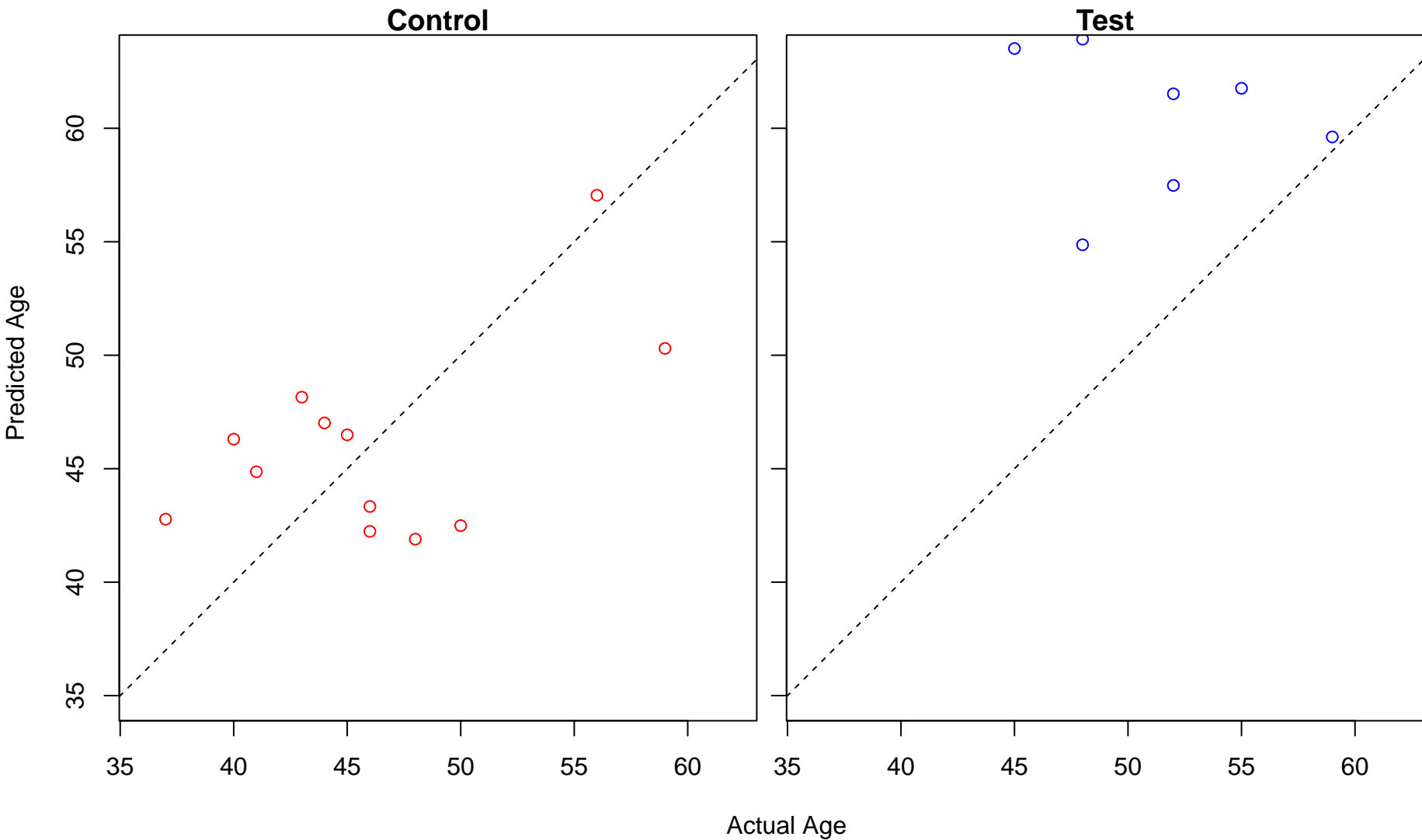


Actual Age

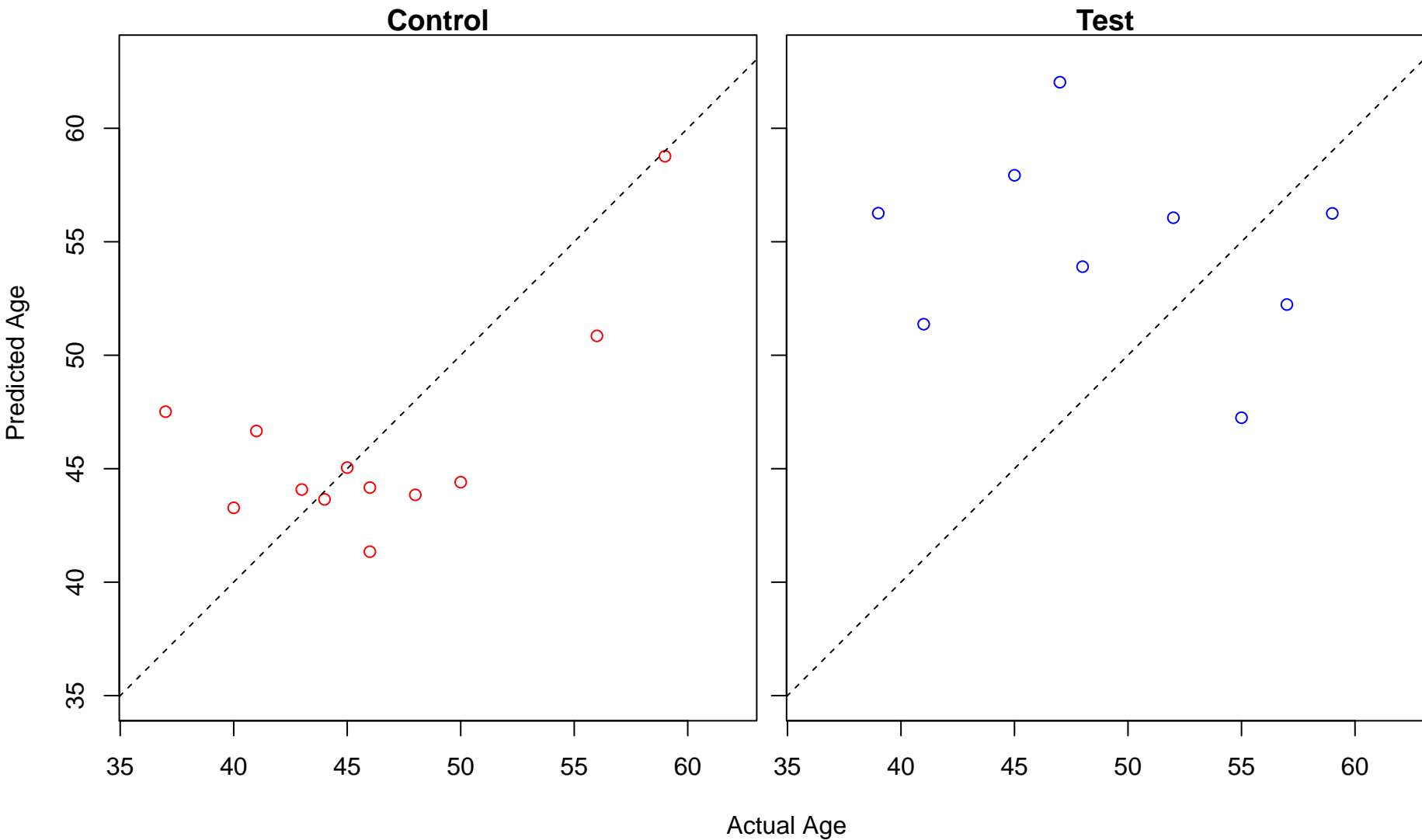
regulation of mitotic cell cycle (Score: 3.058830)



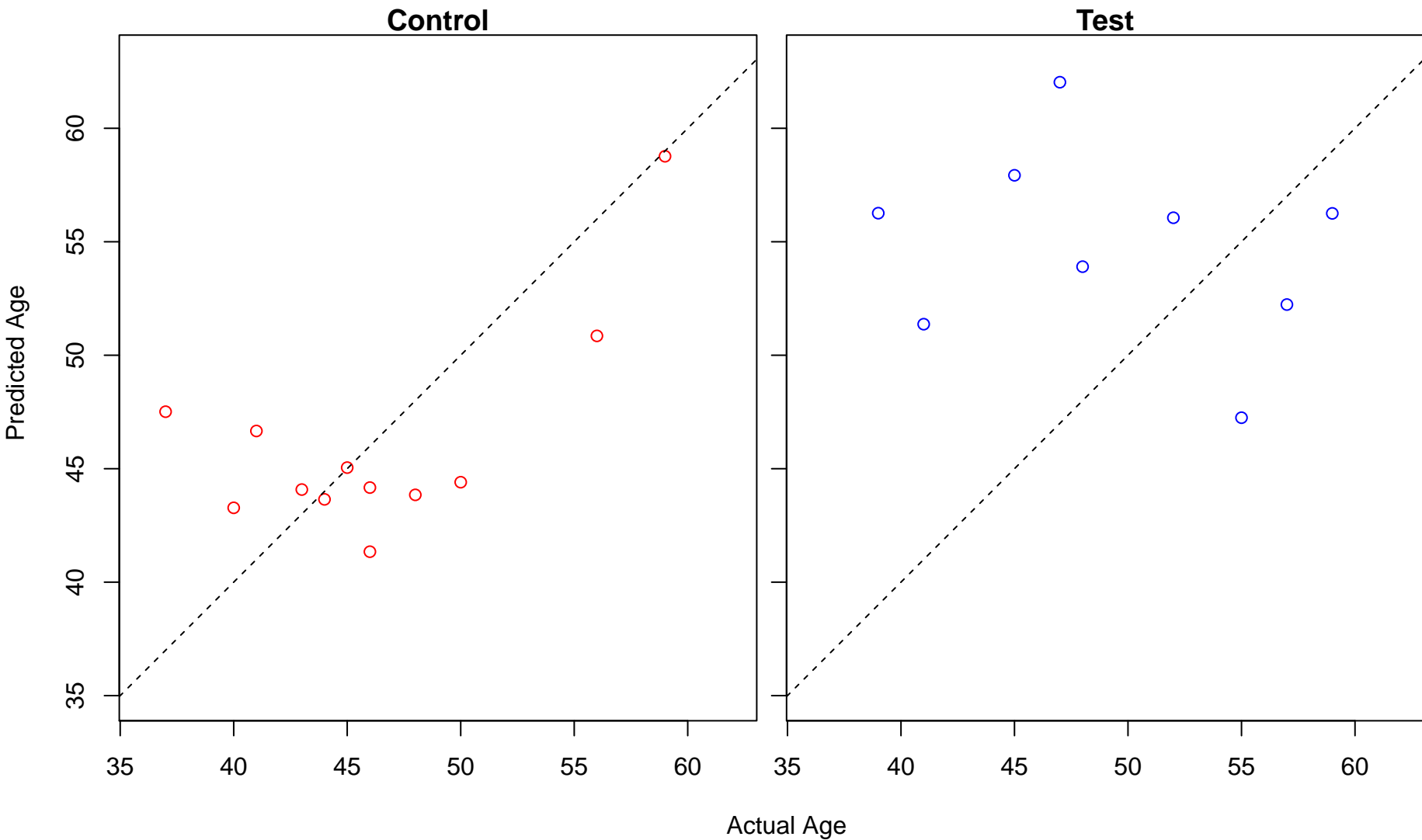
maintenance of protein location in extracellular region (Score: 3.055518)



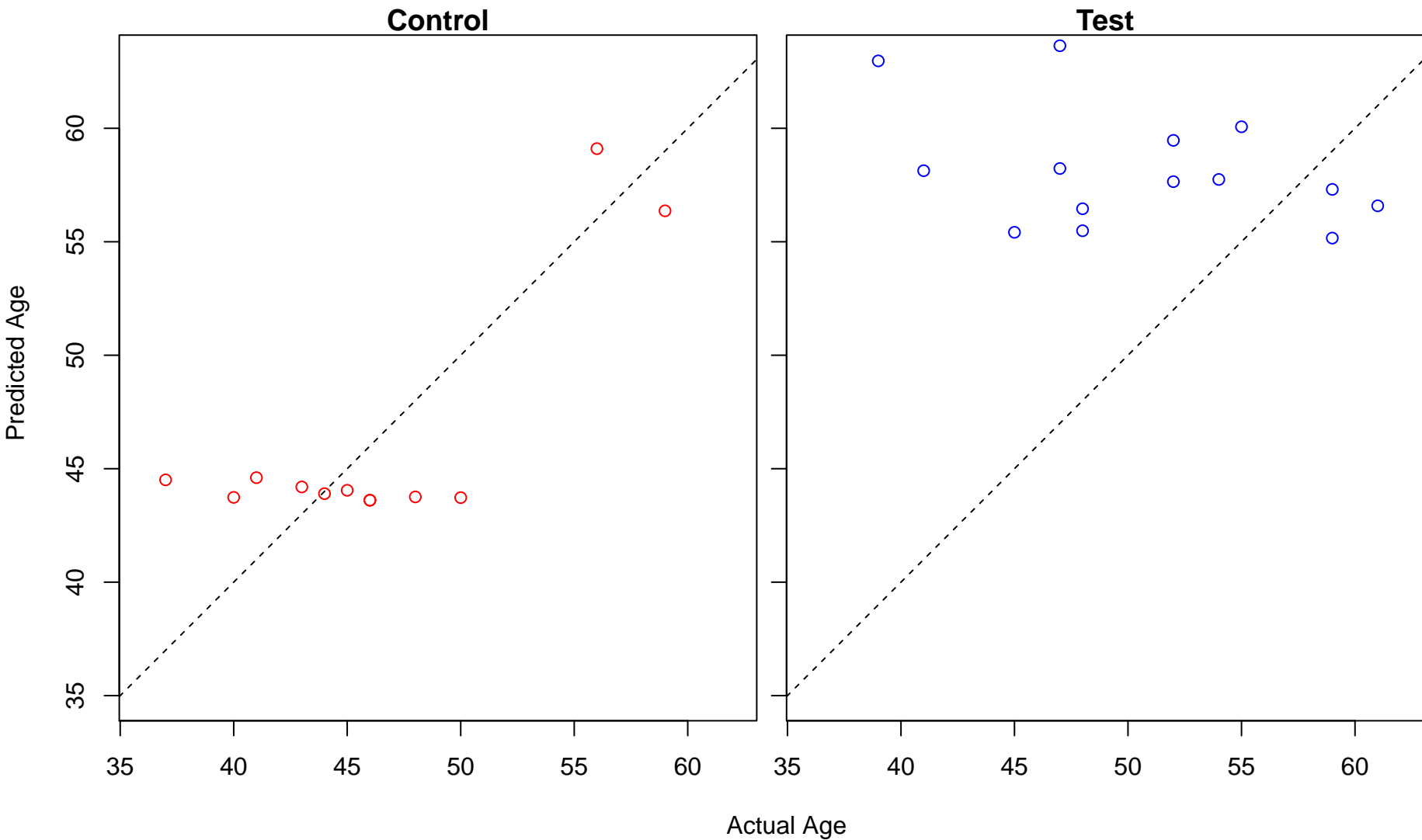
killing of cells of other organism (Score: 3.053603)



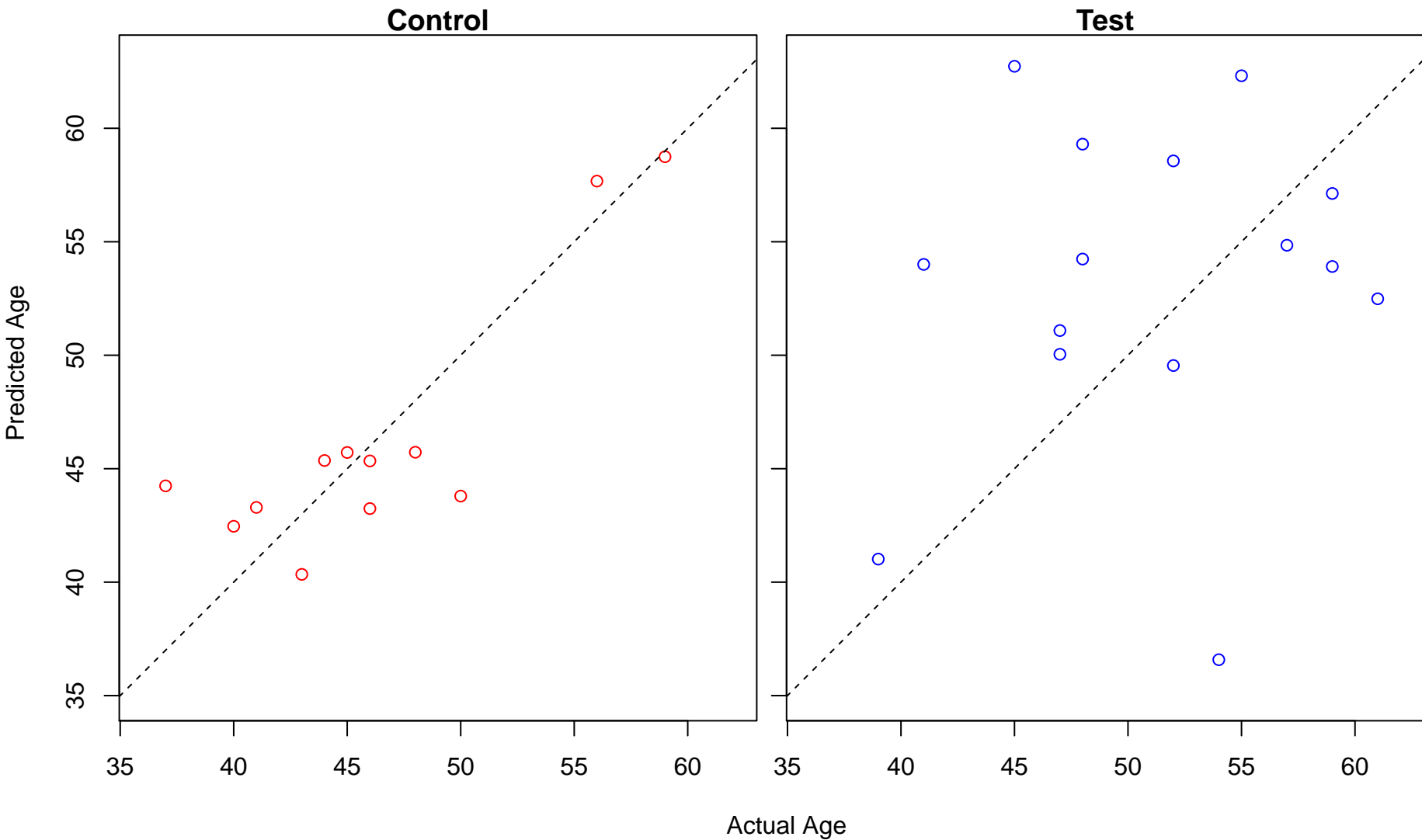
disruption of cells of other organism (Score: 3.053603)



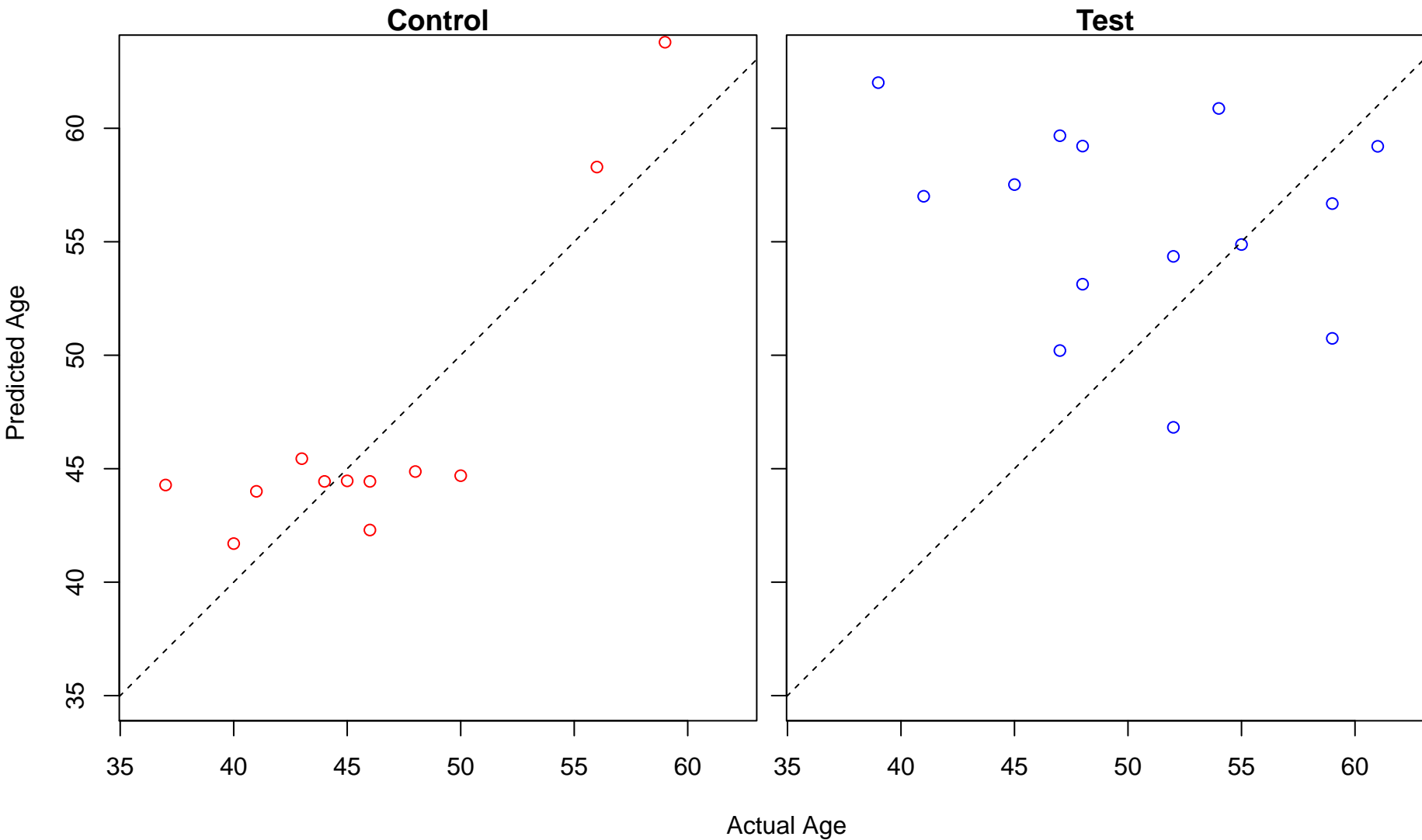
Fc receptor signaling pathway (Score: 3.05373)



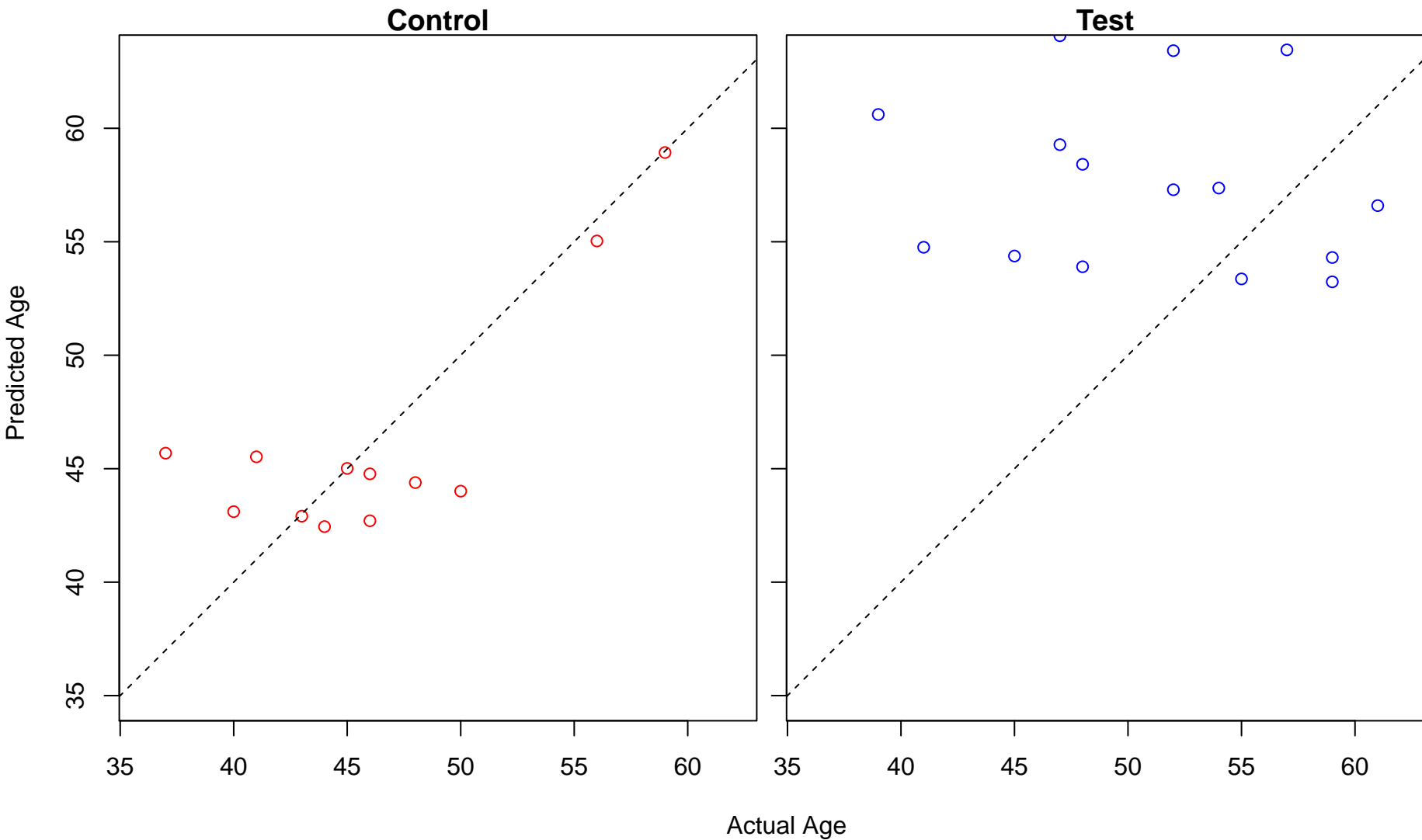
positive regulation of keratinocyte proliferation (Score: 3.049822)



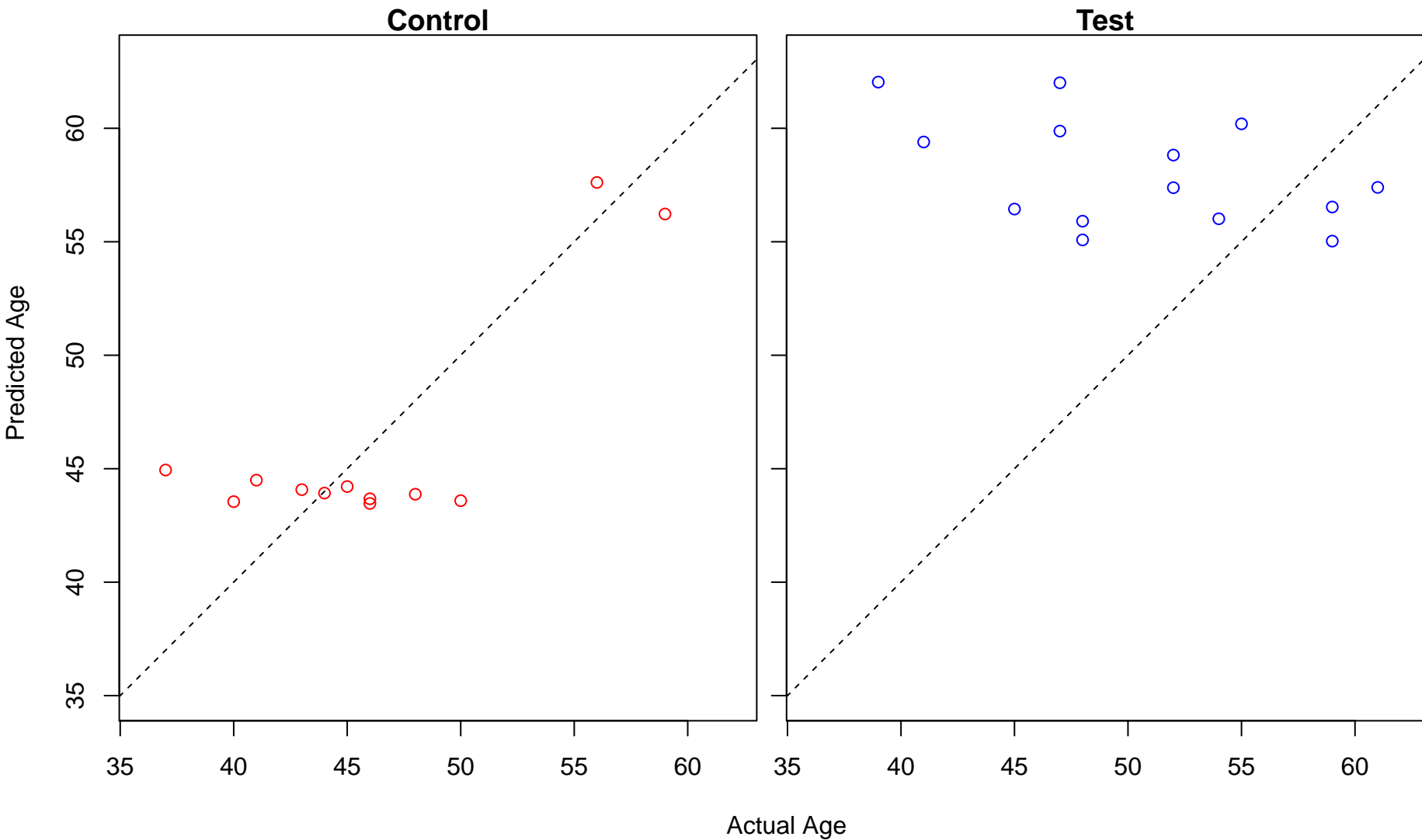
negative regulation of ion transport (Score: 3.045213)



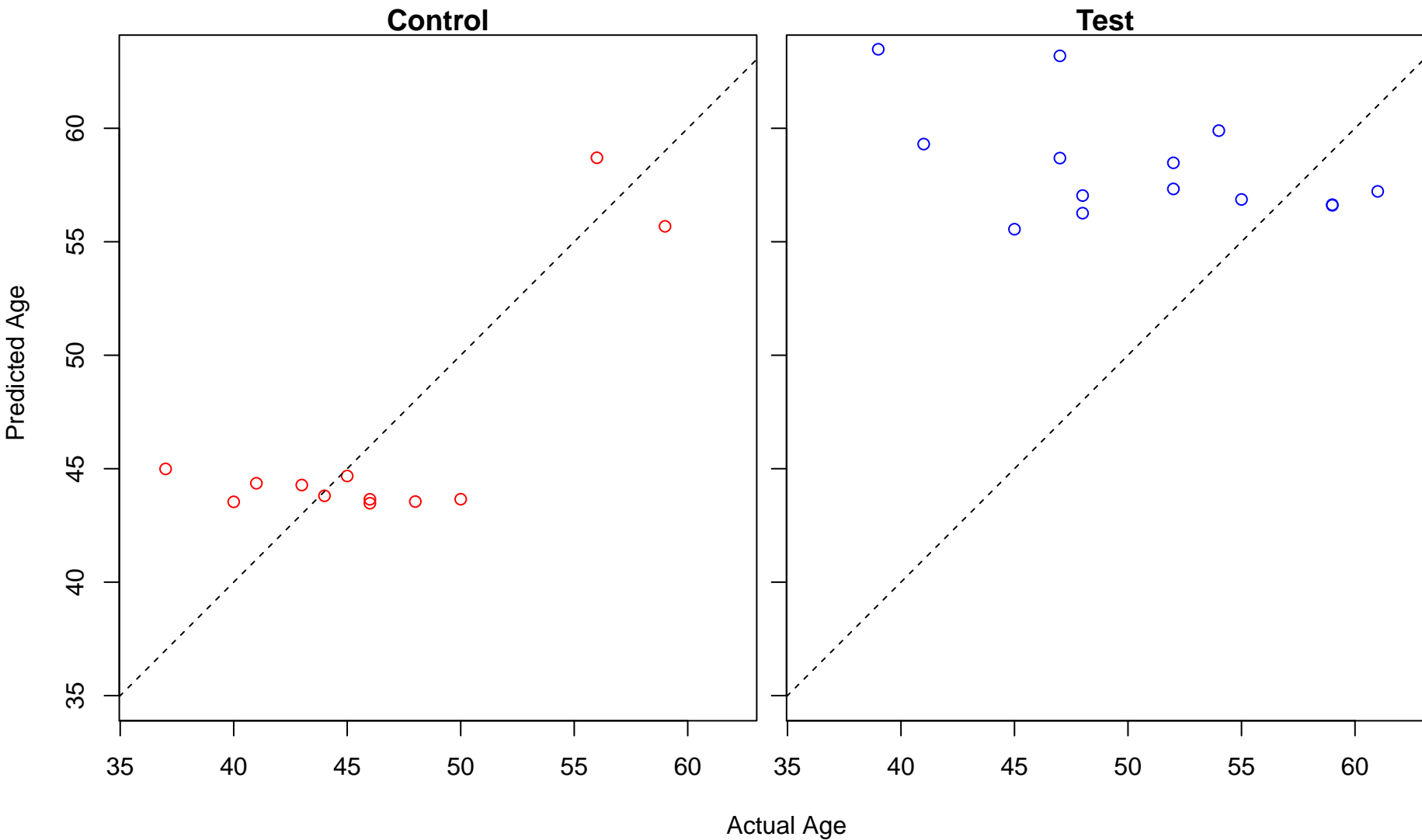
negative regulation of substrate adhesion-dependent cell spreading (Score: 3.038554)



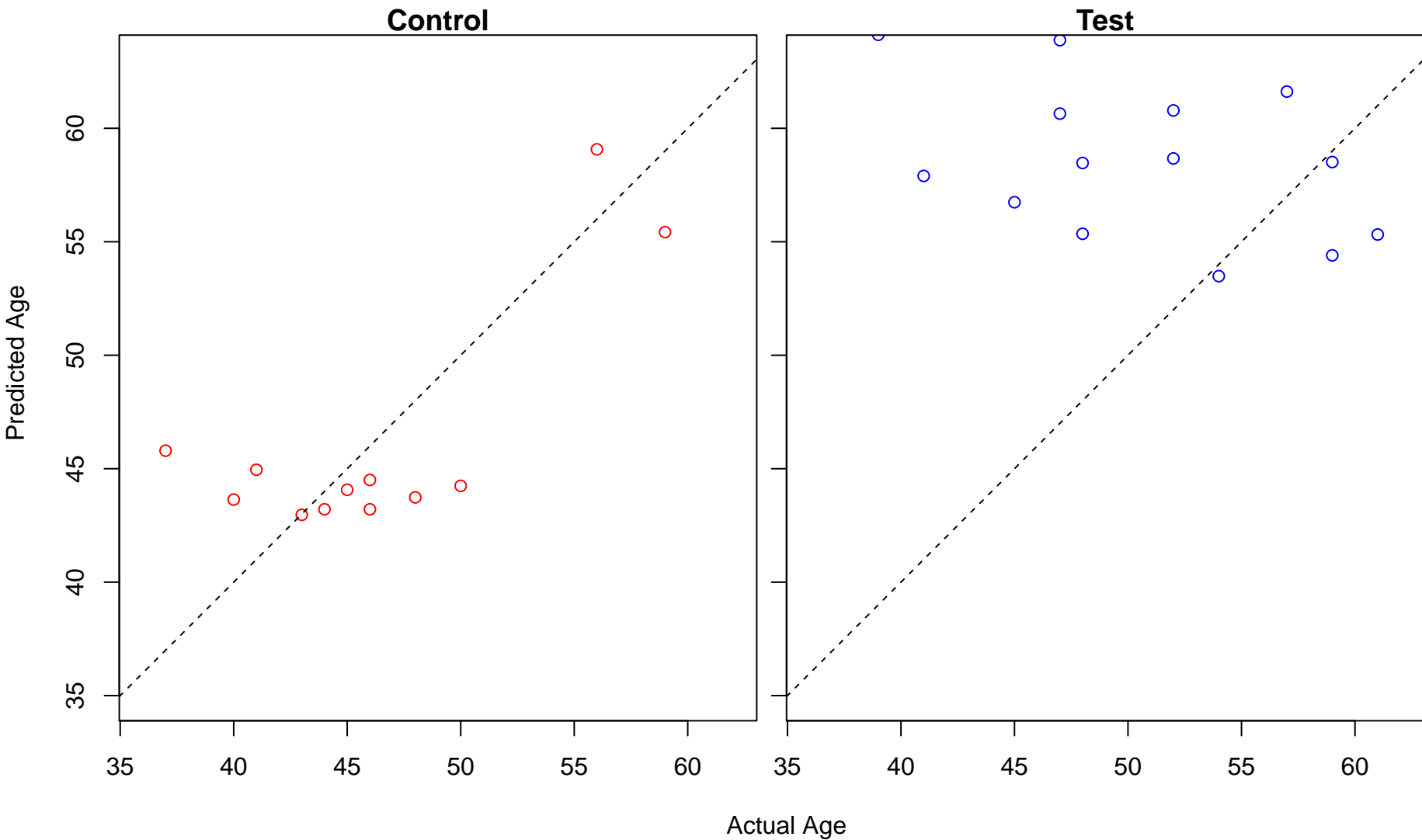
cellular metal ion homeostasis (Score: 3.037534)



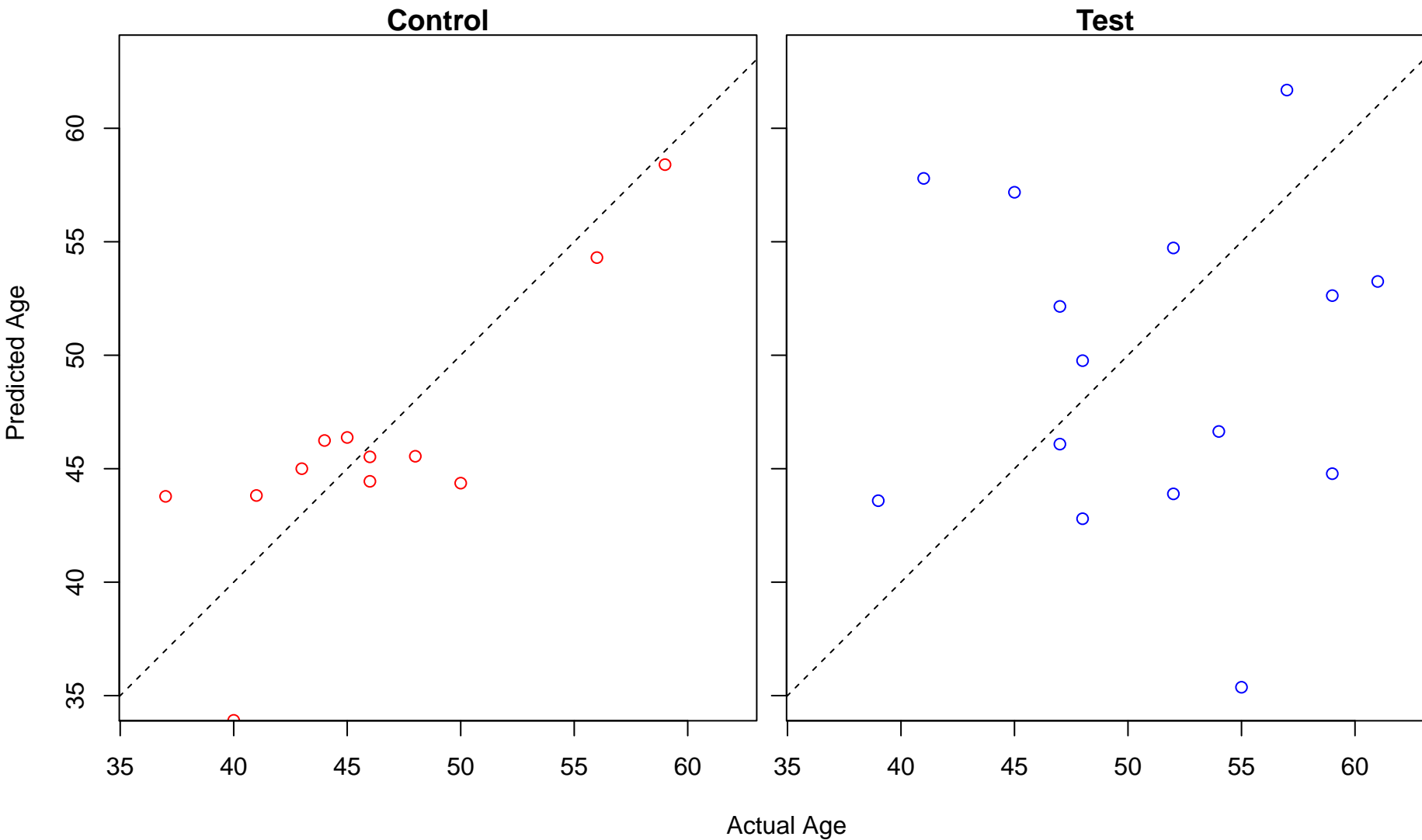
platelet degranulation (Score: 3.035403)



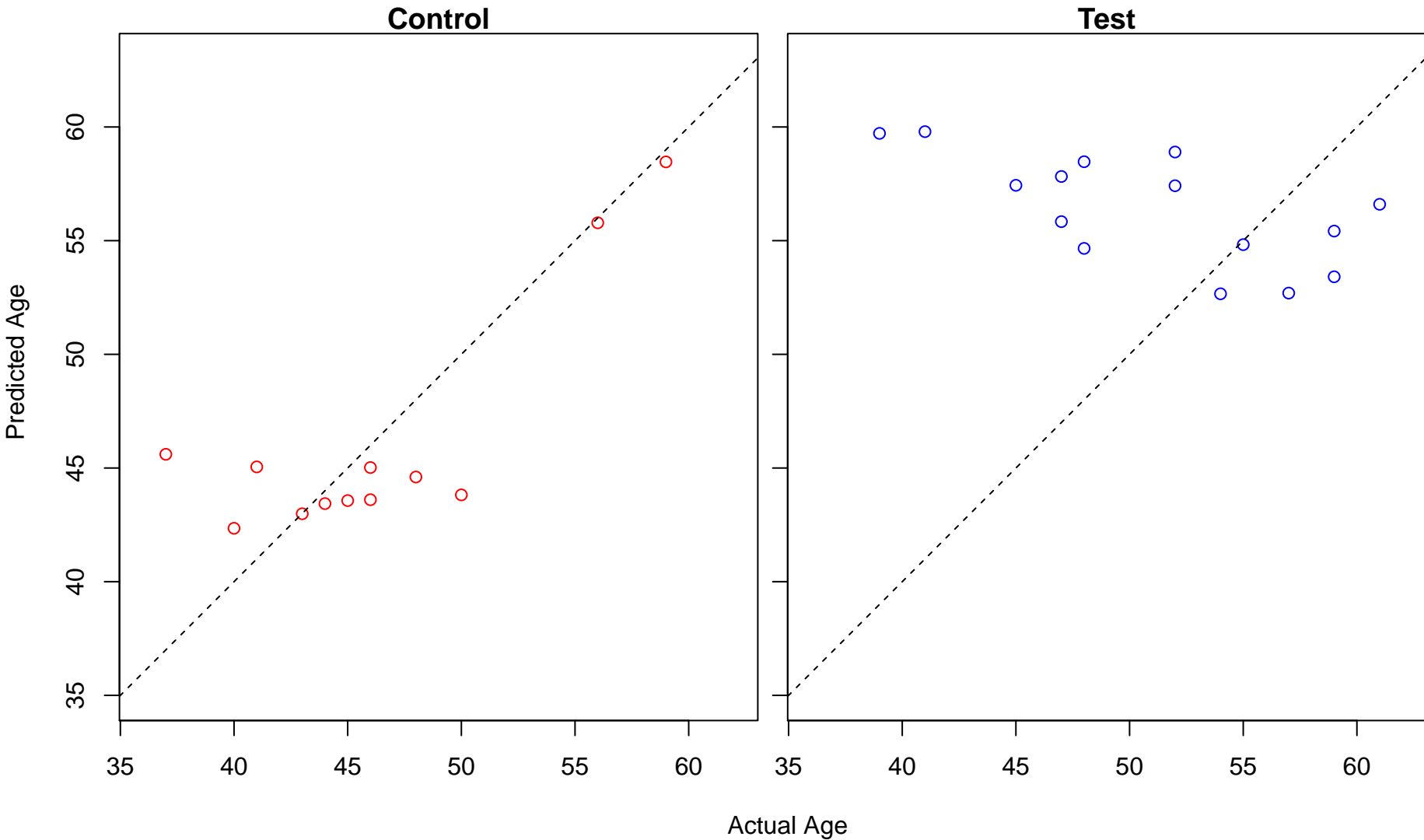
cellular response to iron ion (Score: 3.030987)



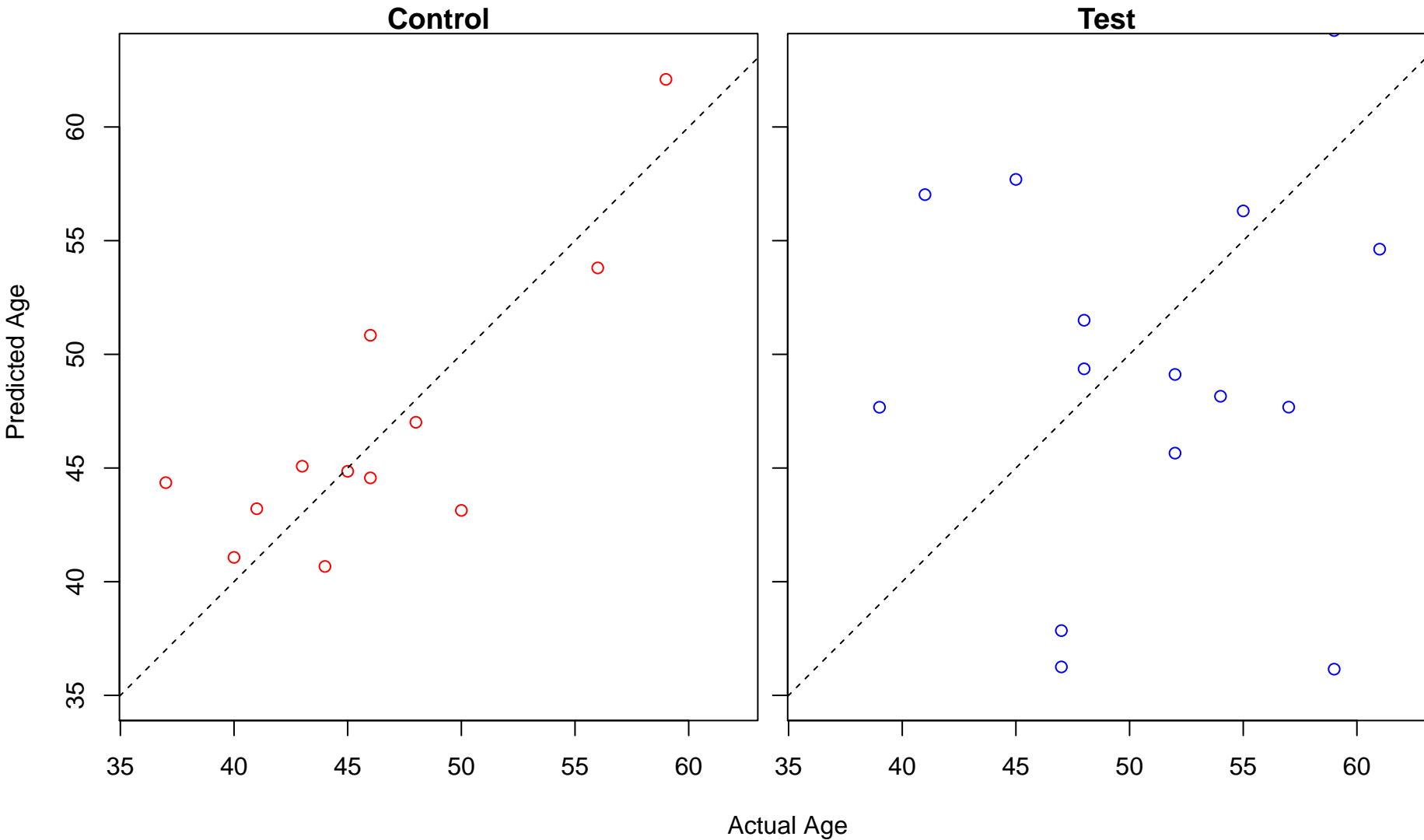
negative regulation of viral process (Score: 3.030534)



apoptotic DNA fragmentation (Score: 3.030231)

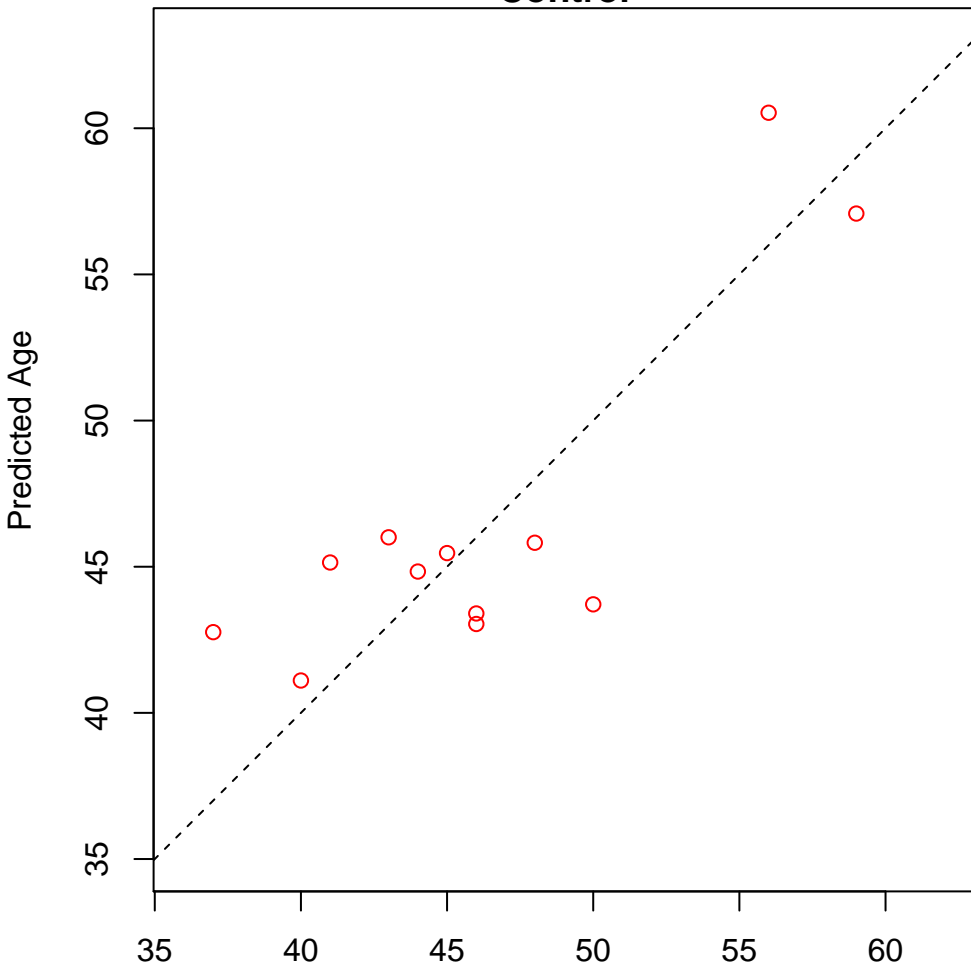


regulation of triglyceride metabolic process (Score: 3.029686)

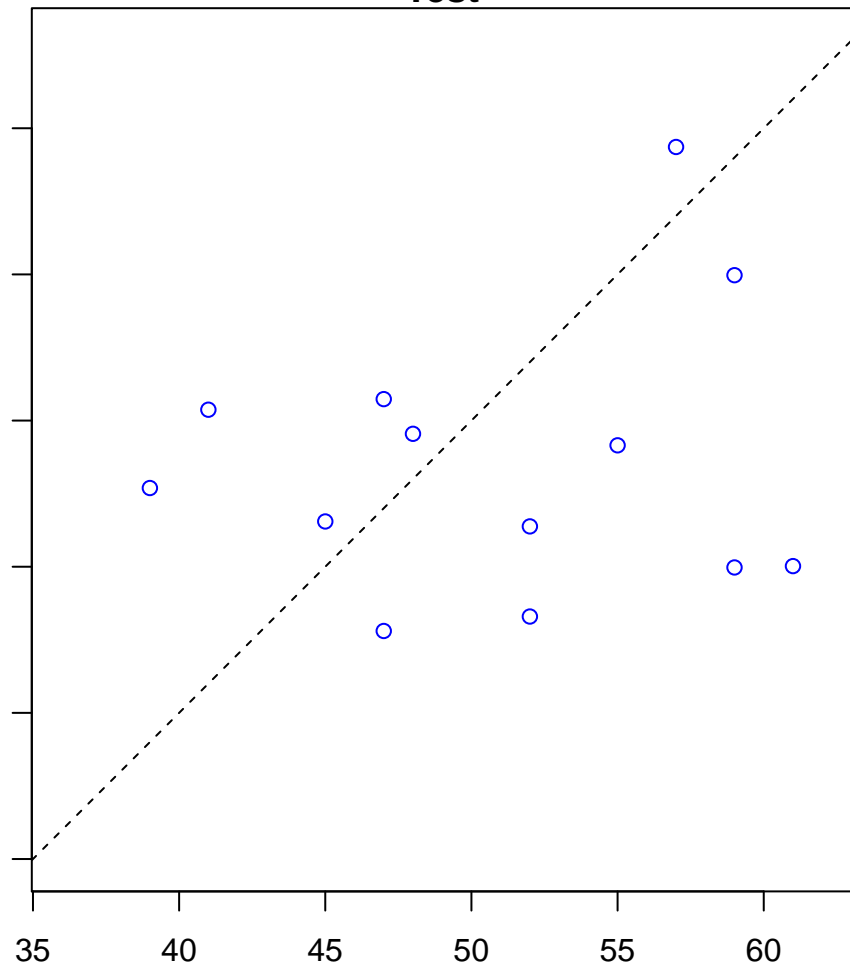


mammary gland epithelium development (Score: 3.026368)

Control

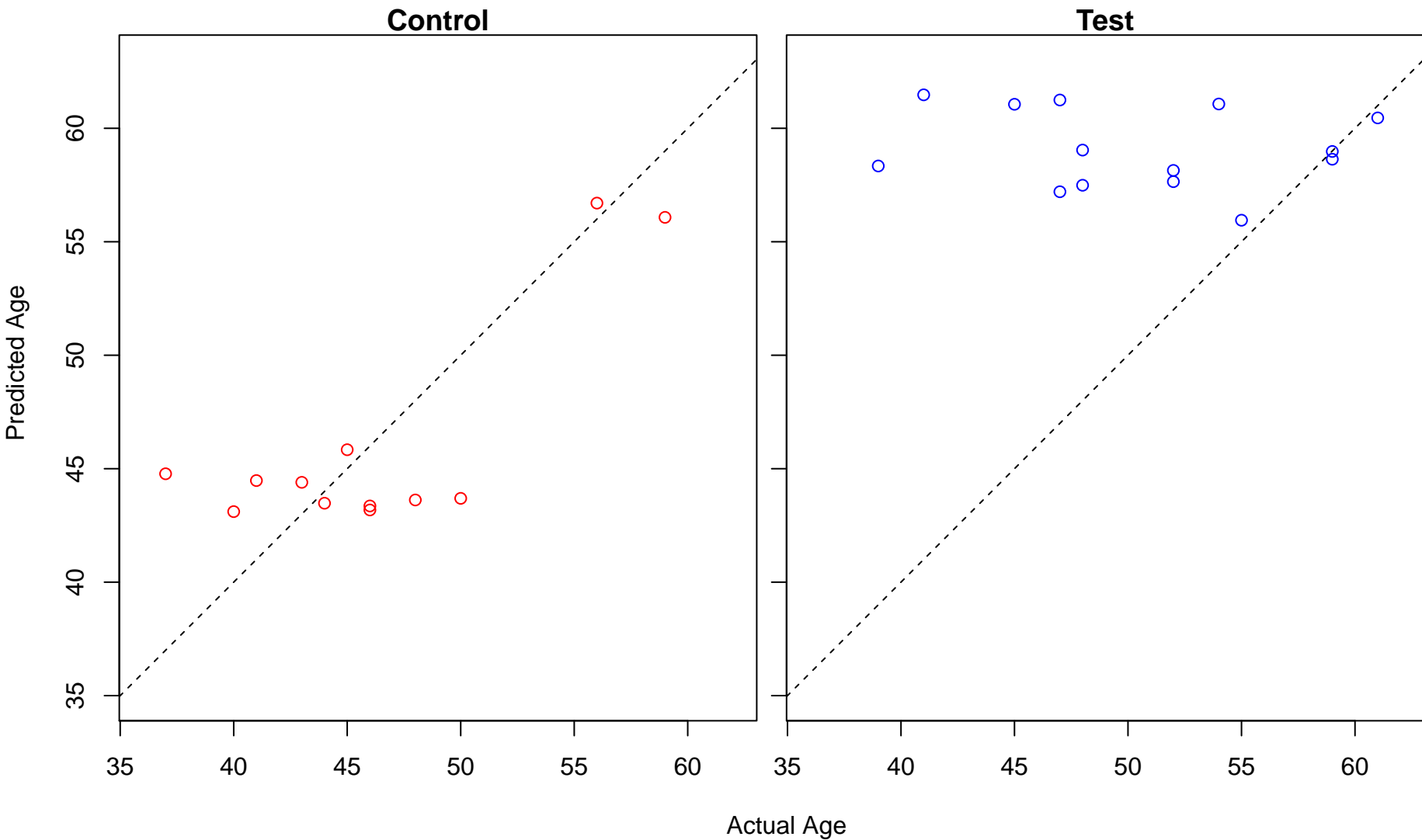


Test

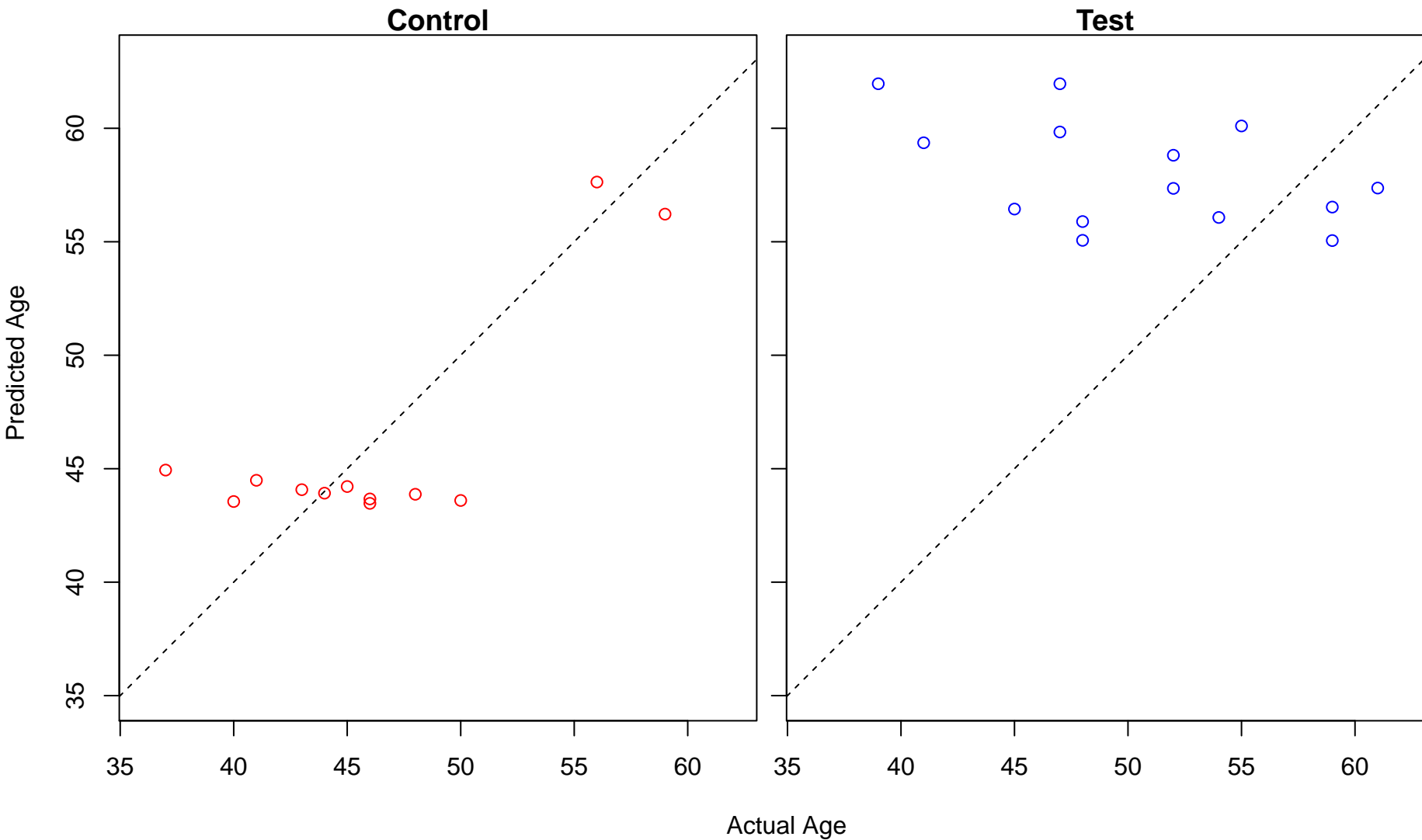


Actual Age

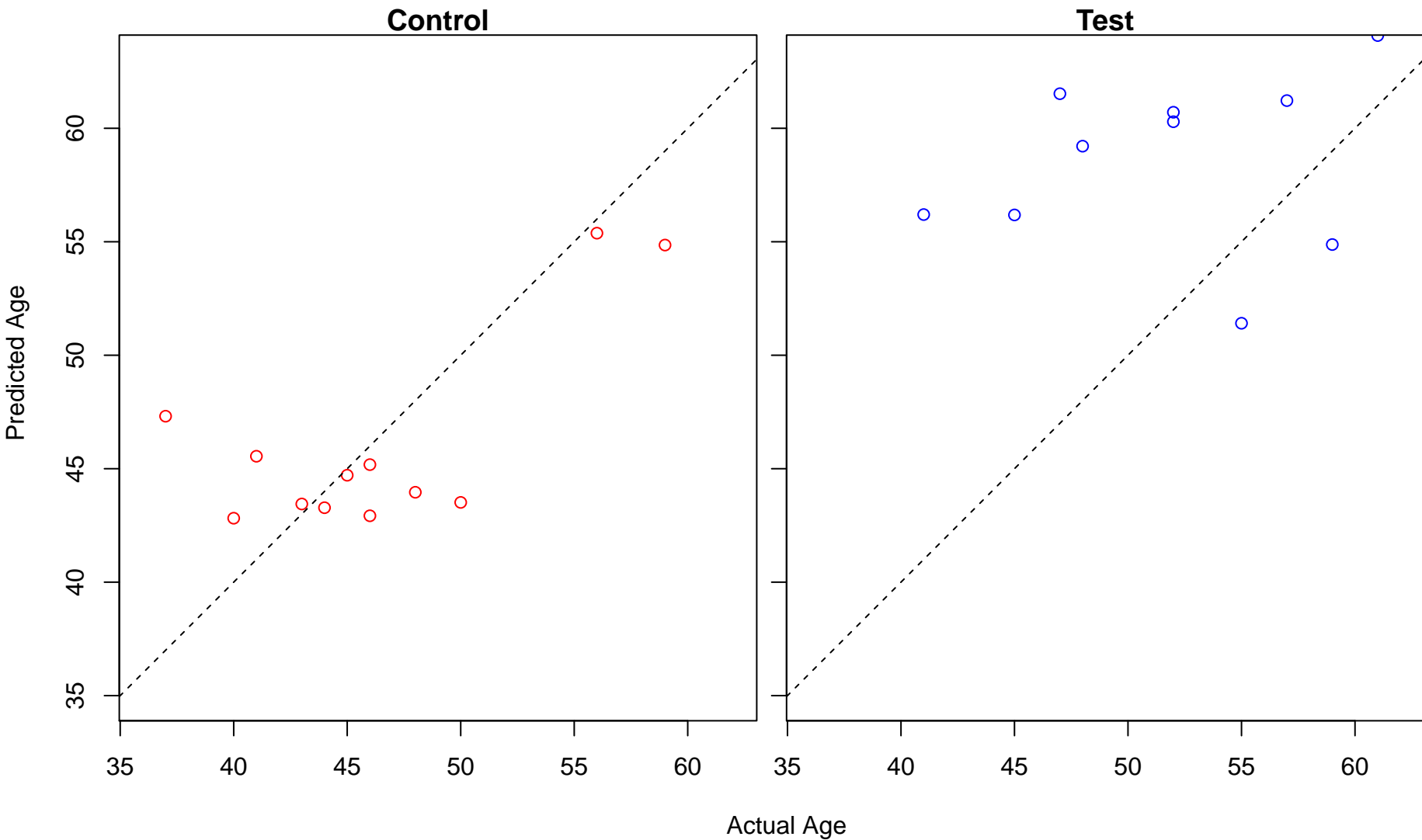
gliogenesis (Score: 3.026154)



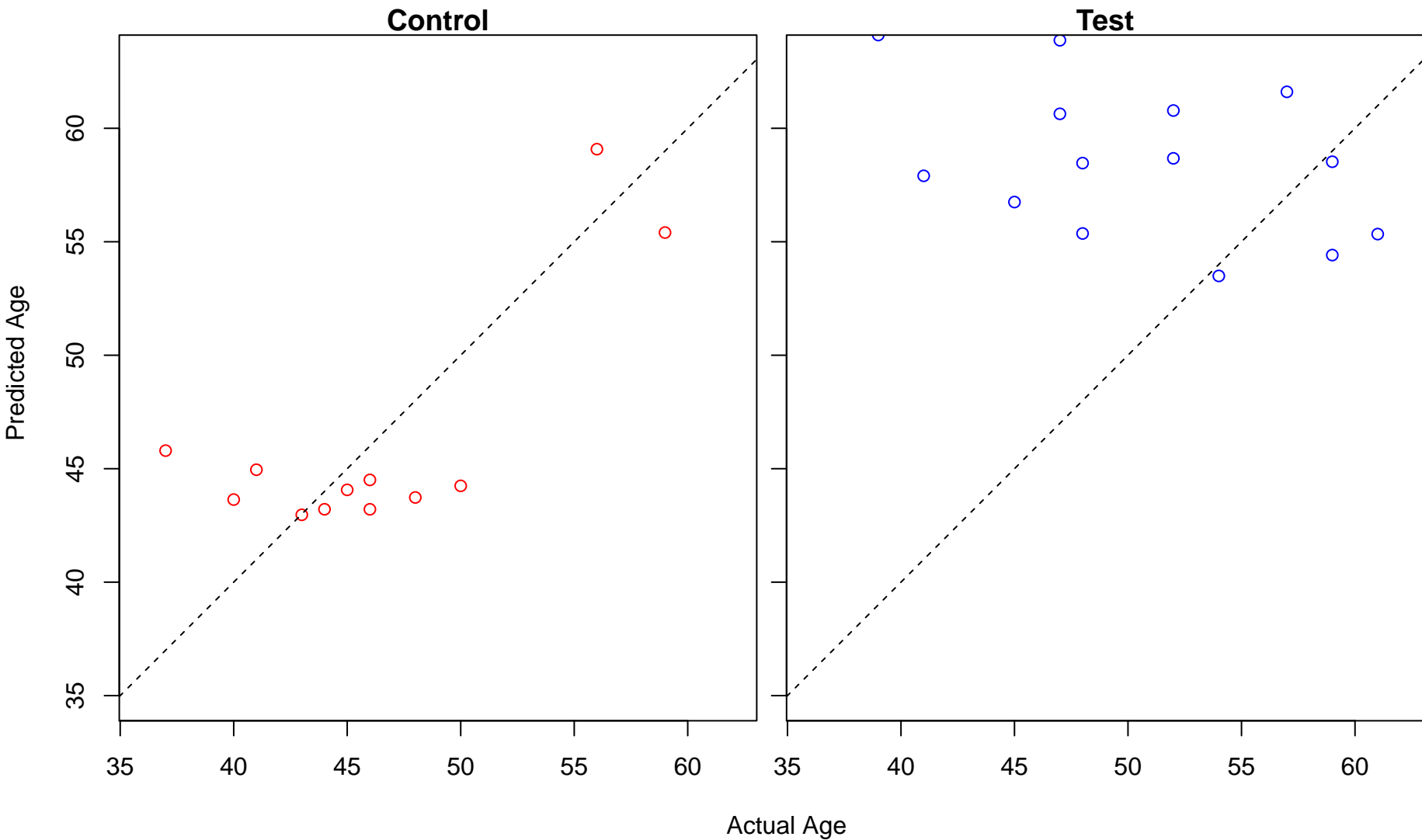
cellular cation homeostasis (Score: 3.026149)



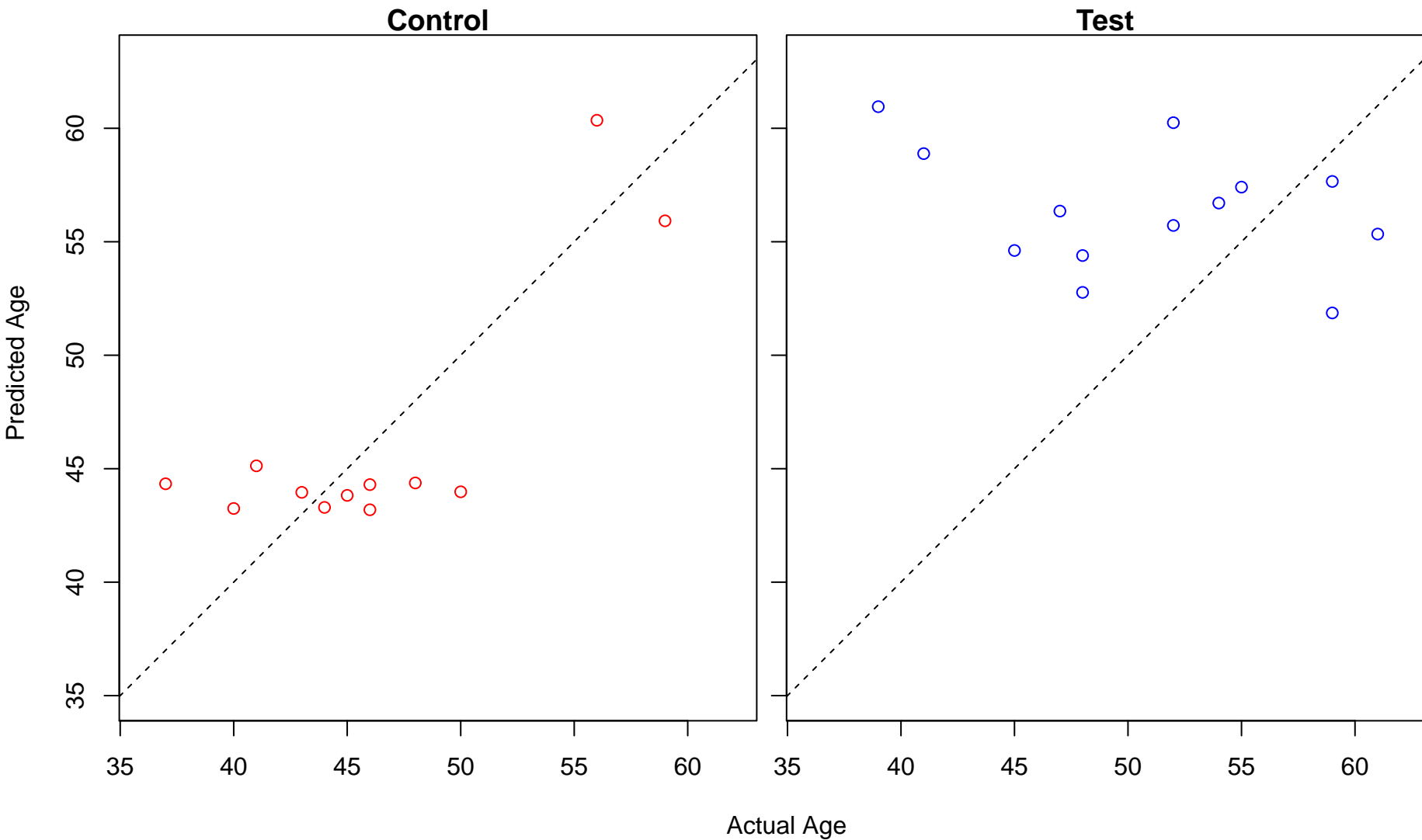
regulation of dopamine secretion (Score: 3.025711)



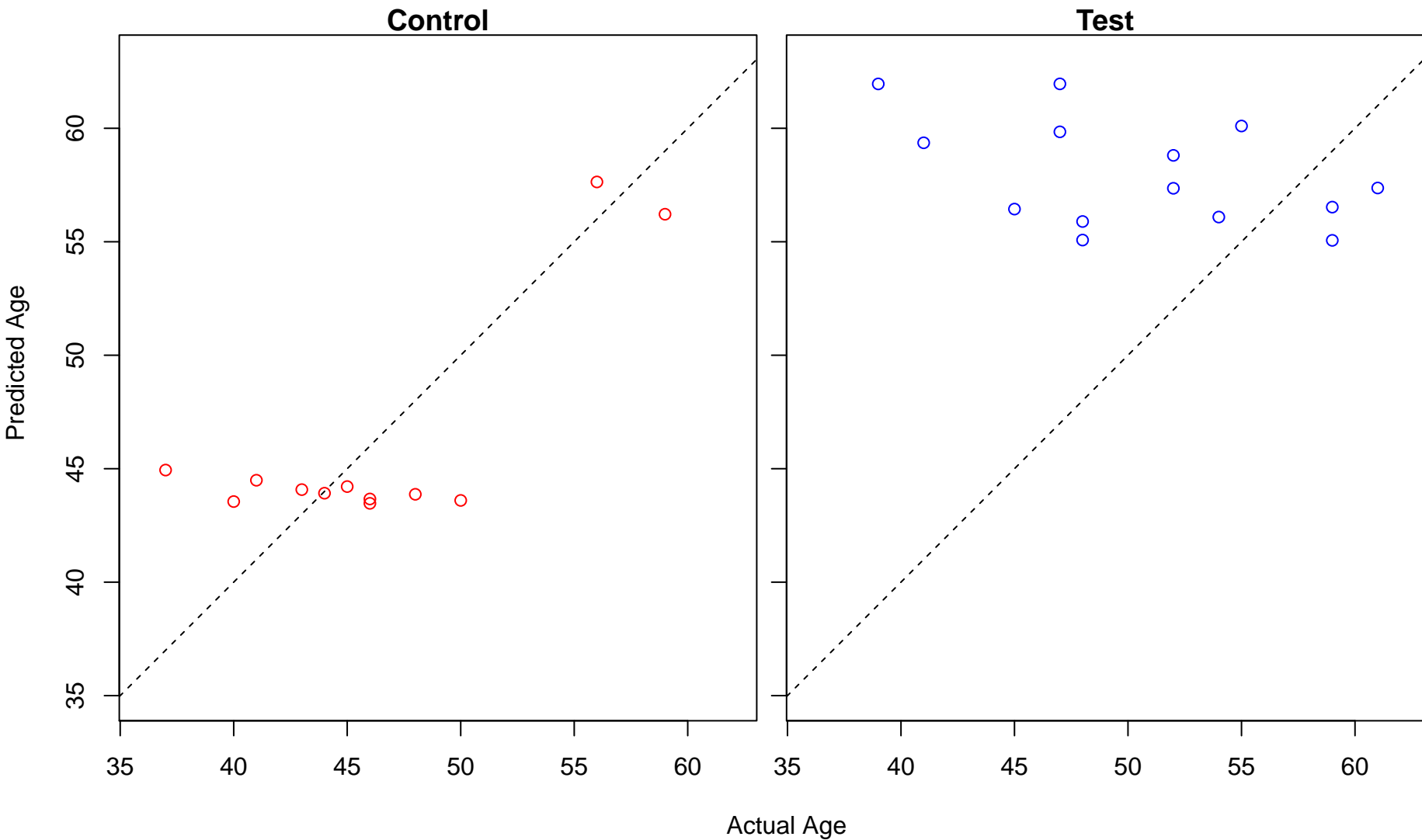
response to iron ion (Score: 3.025699)



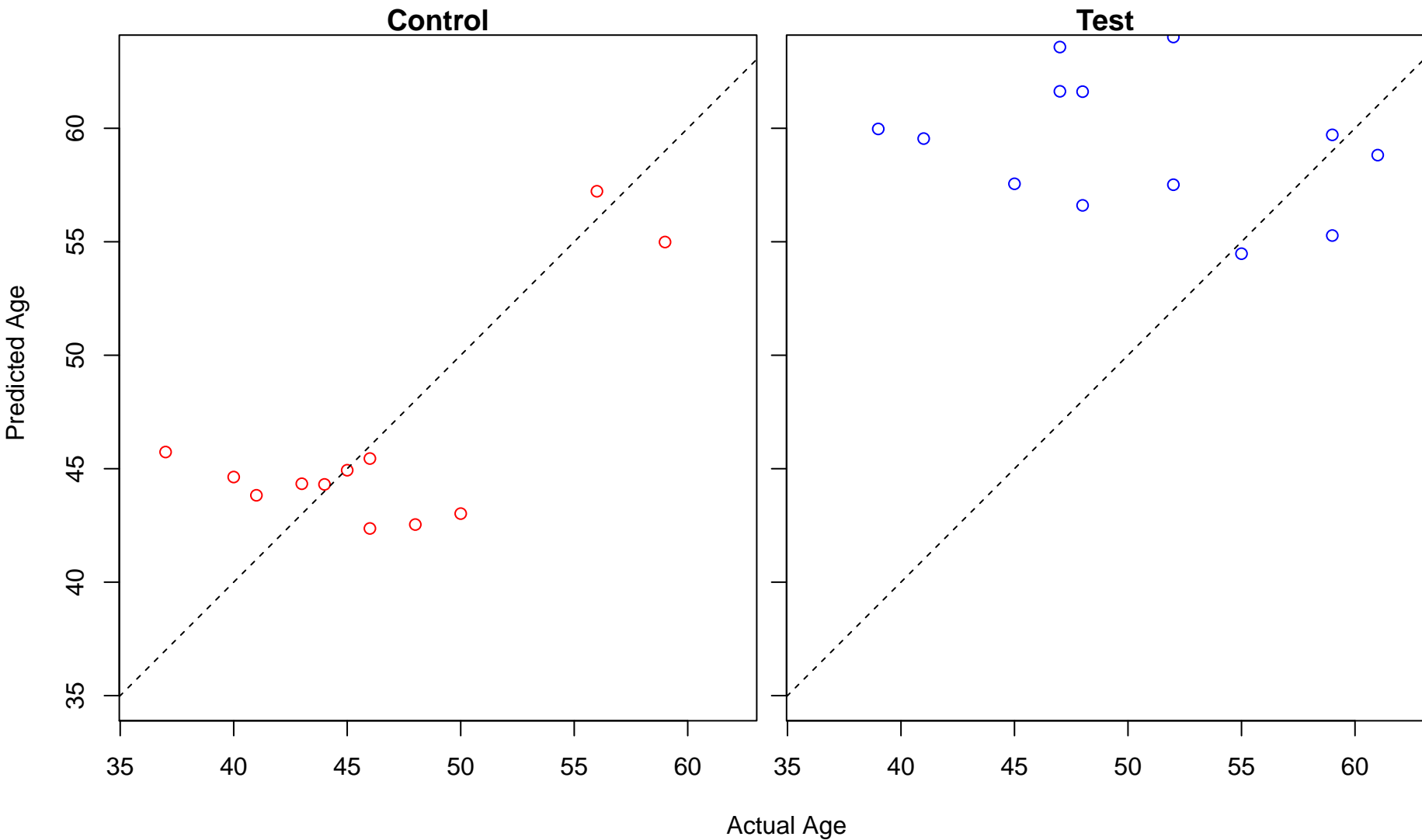
myeloid cell development (Score: 3.025090)



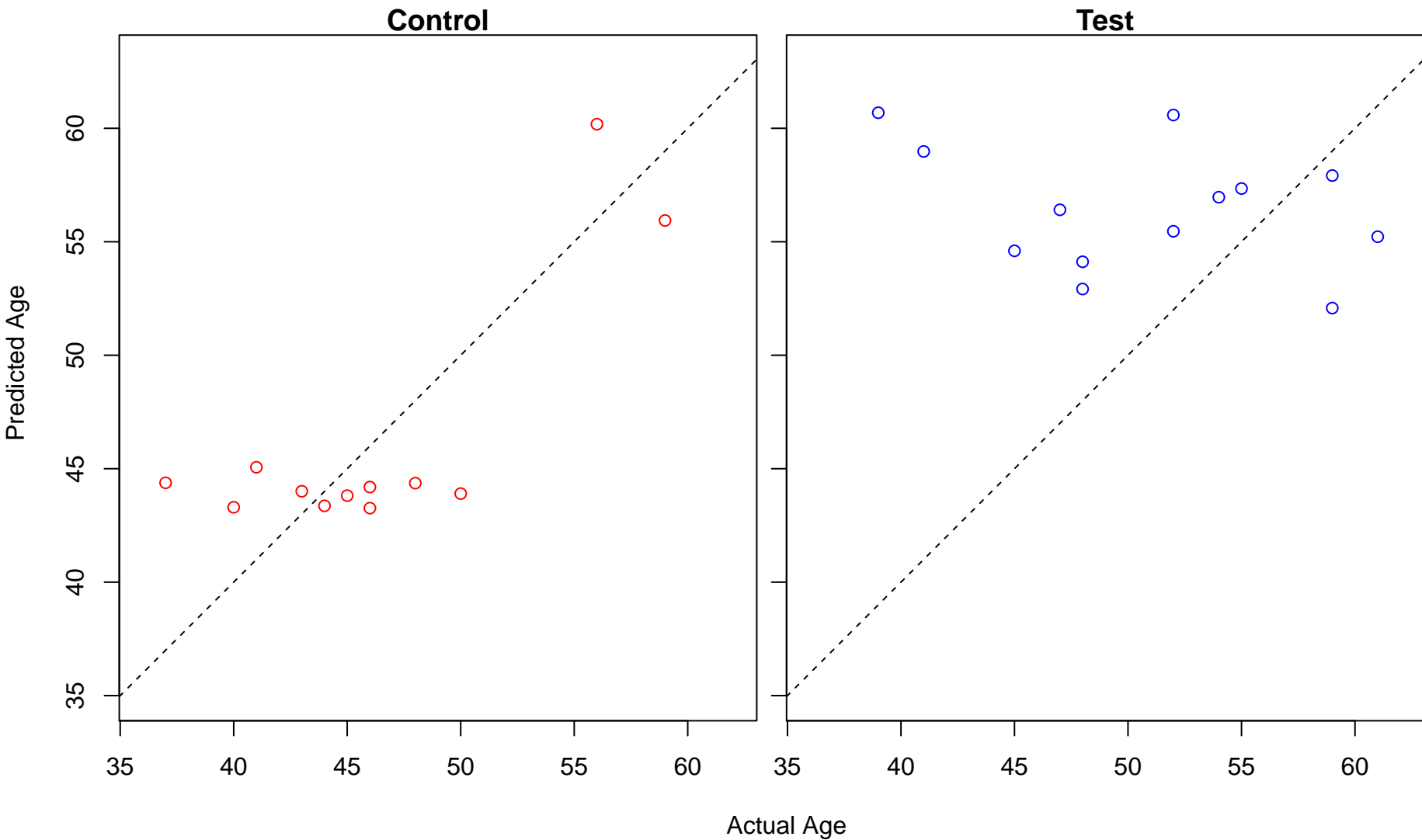
cellular ion homeostasis (Score: 3.024791)



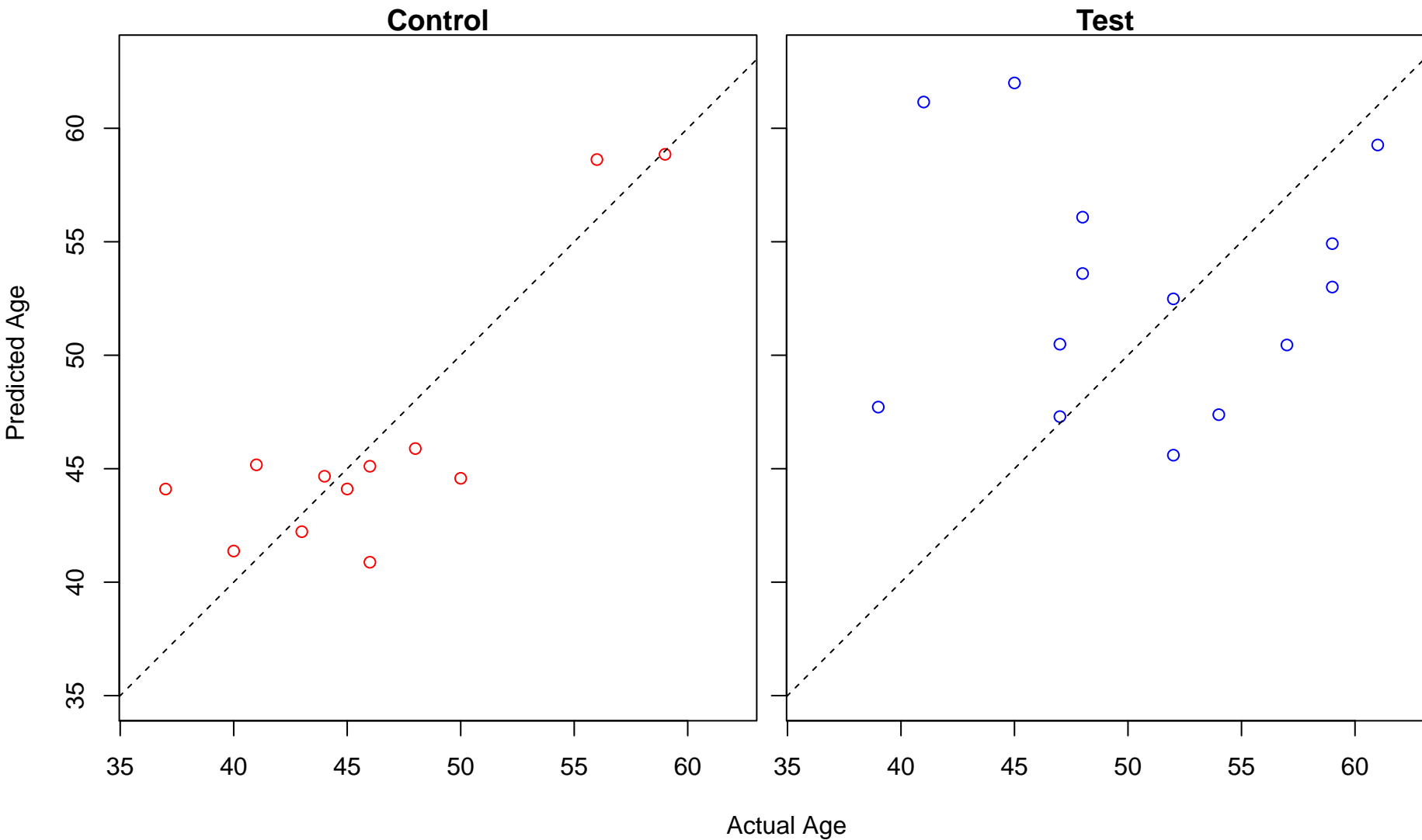
positive regulation of extracellular matrix organization (Score: 3.024335)



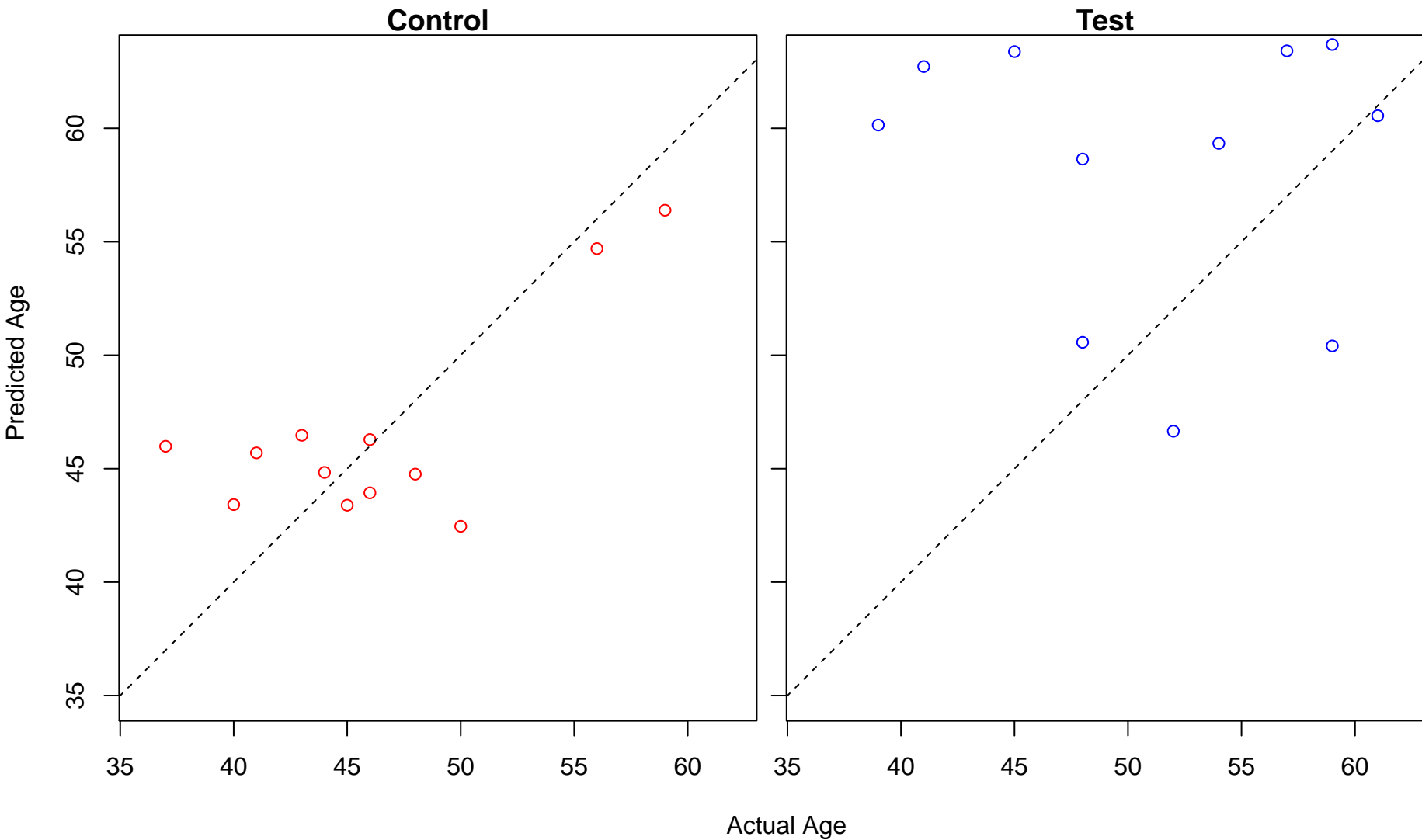
membrane raft organization (Score: 3.023629)



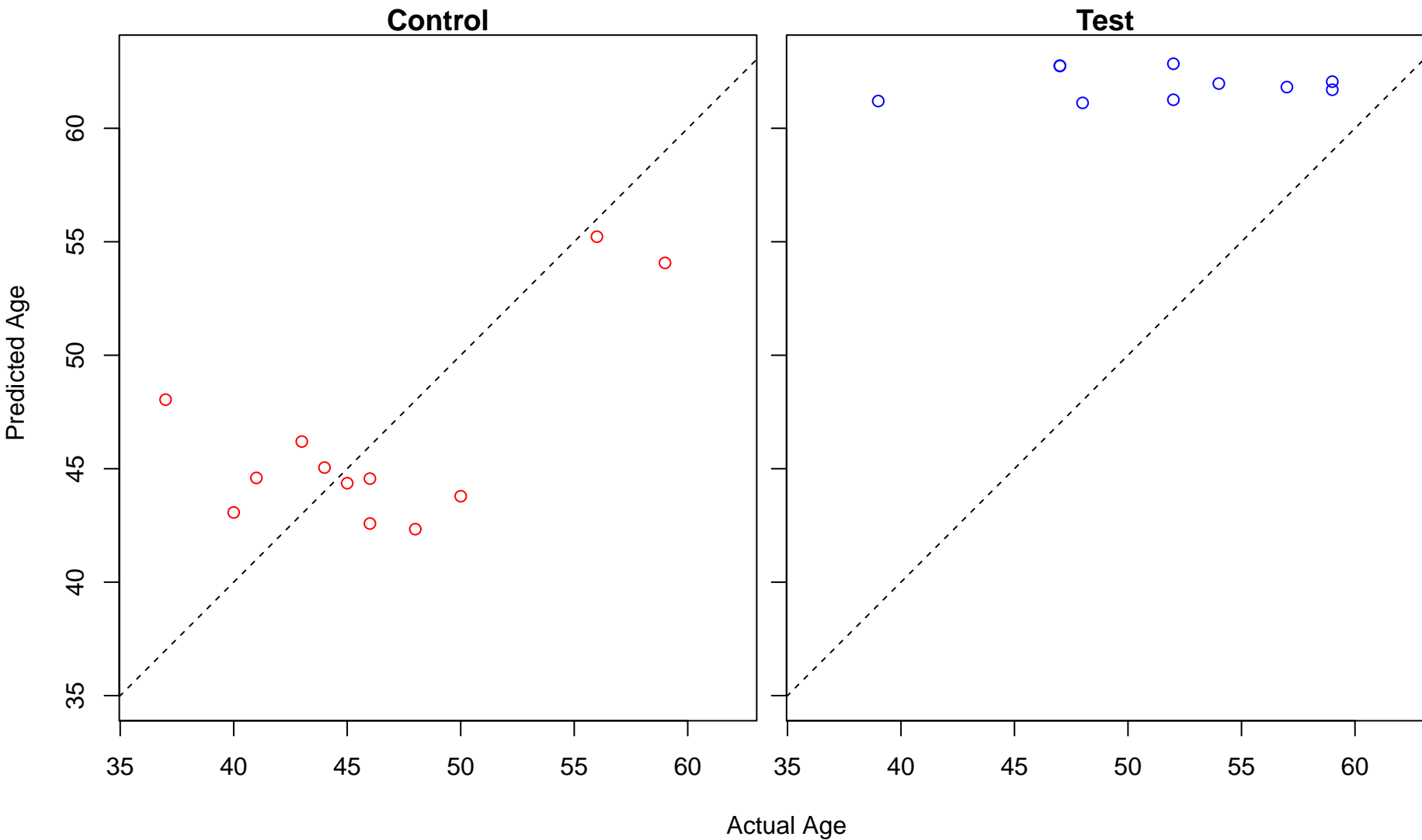
mitochondrial transport (Score: 3.023393)



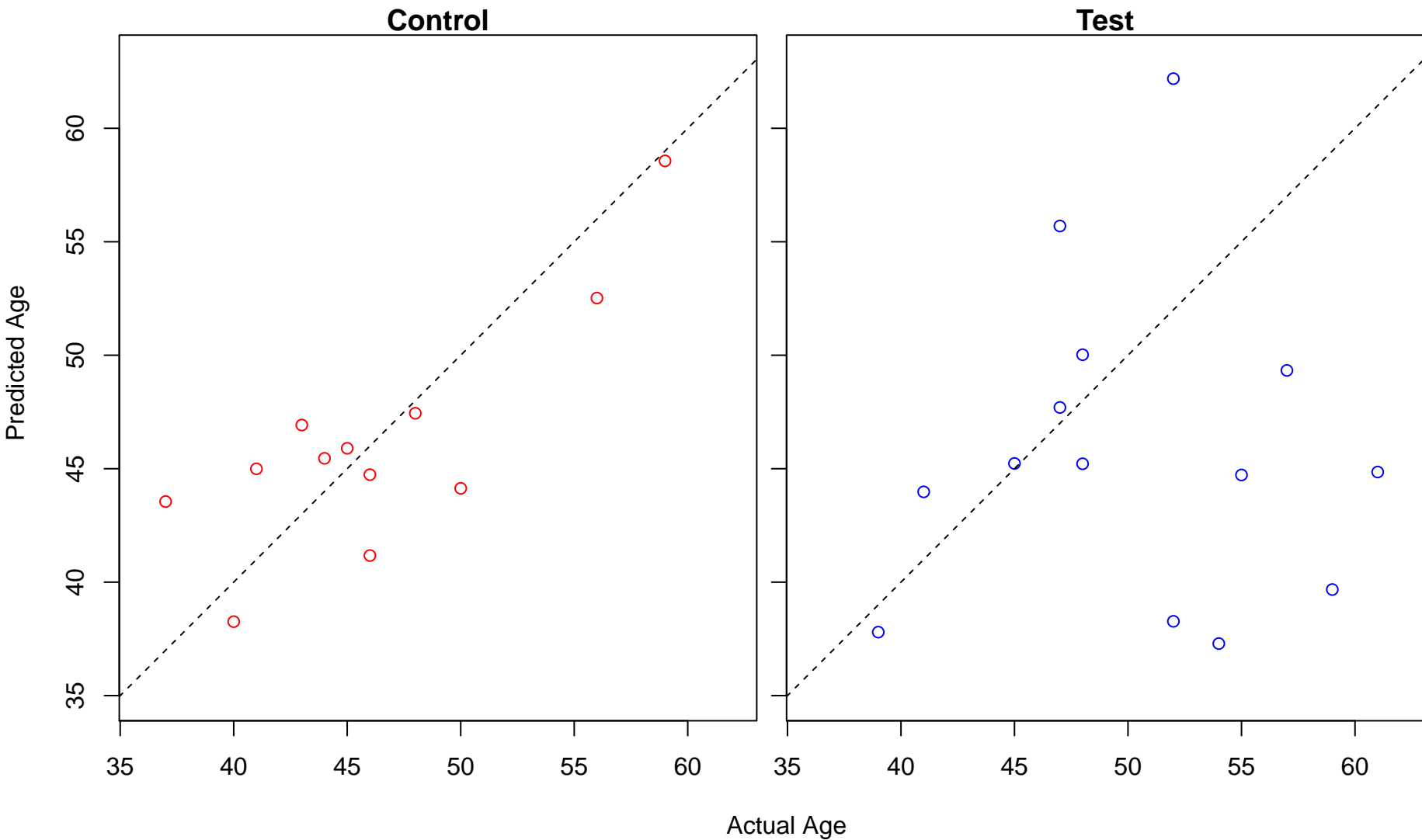
positive regulation of pri-miRNA transcription from RNA polymerase II promoter (Score: 3.023294)



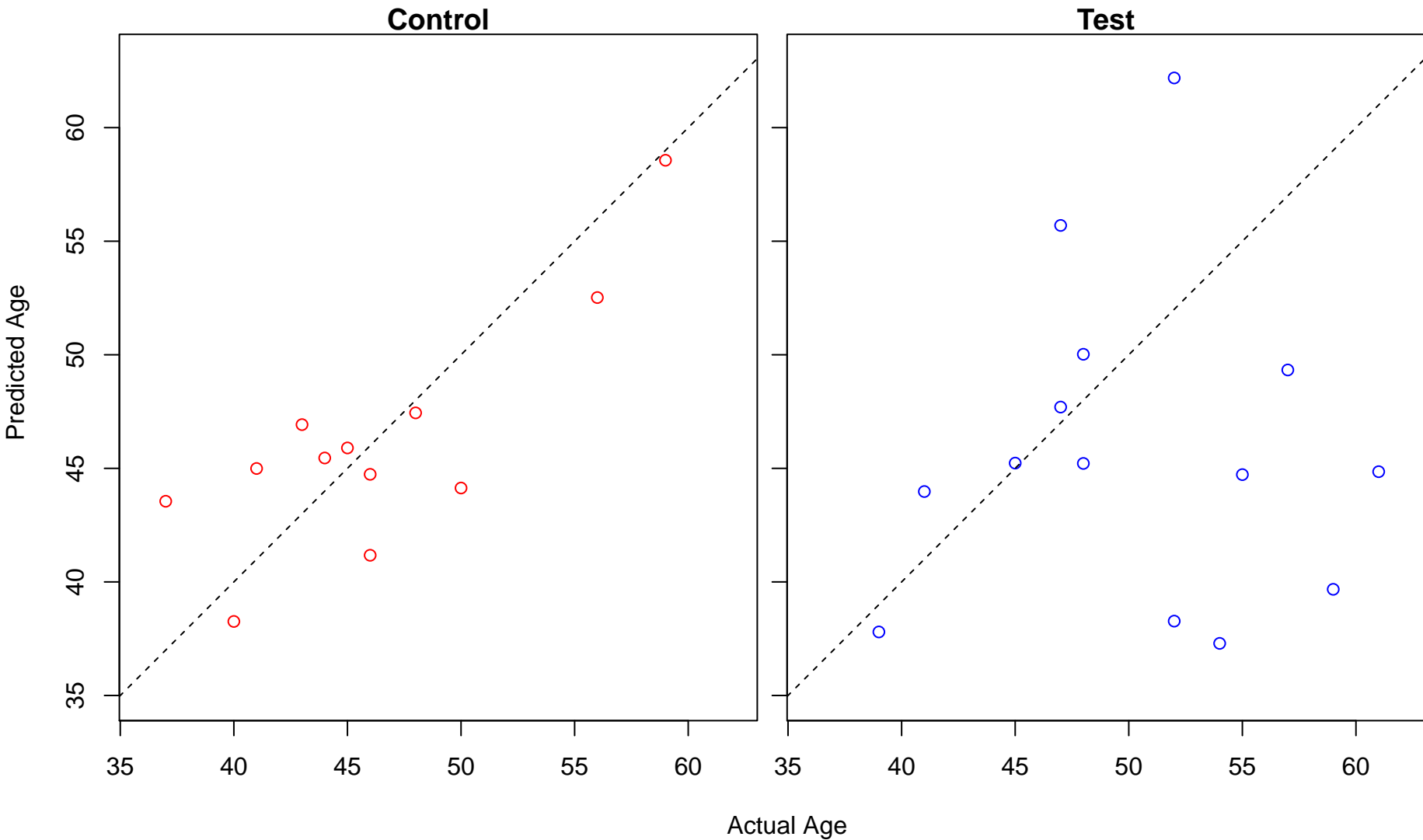
regulation of triglyceride catabolic process (Score: 3.023118)



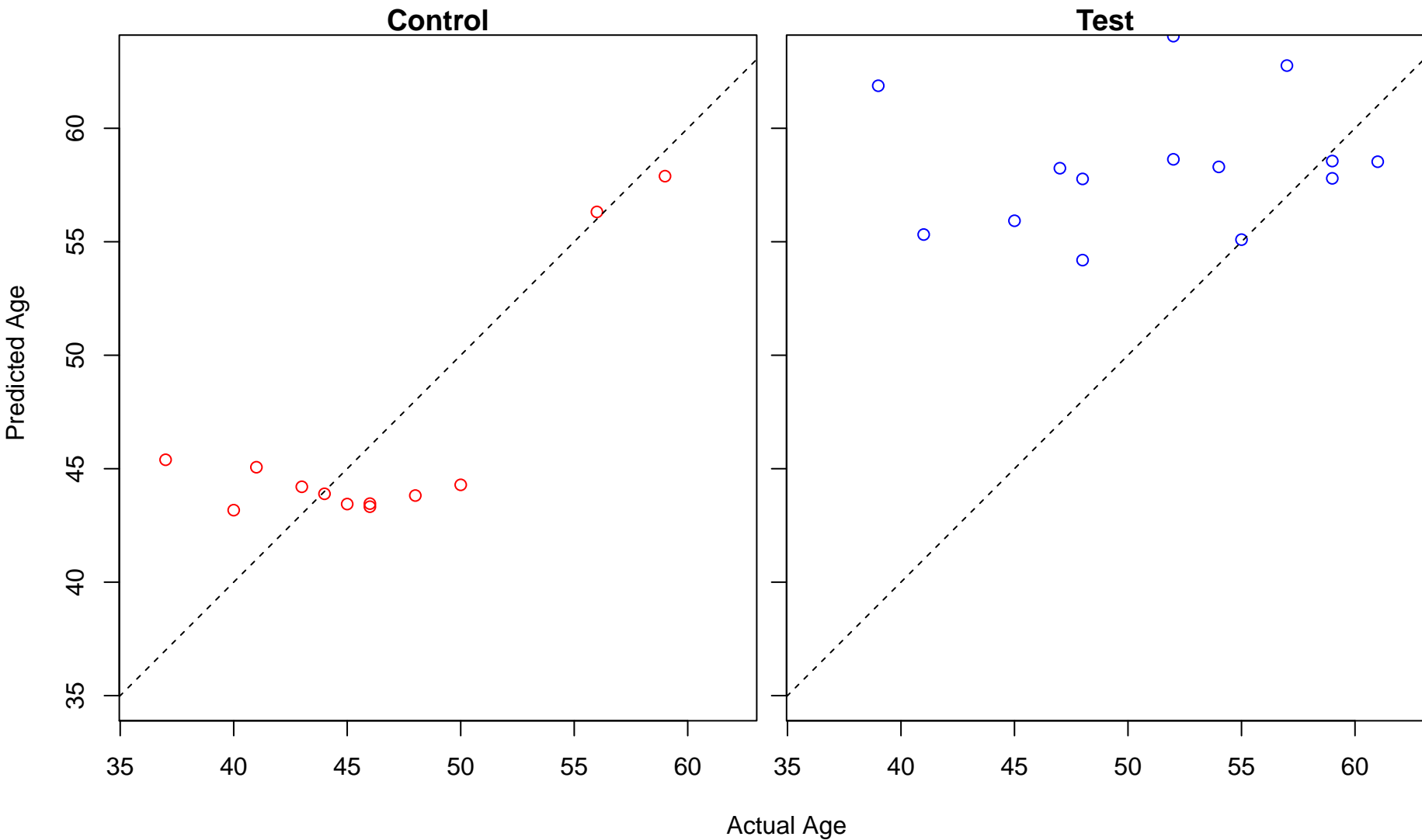
symbiosis, encompassing mutualism through parasitism (Score: 3.023016)



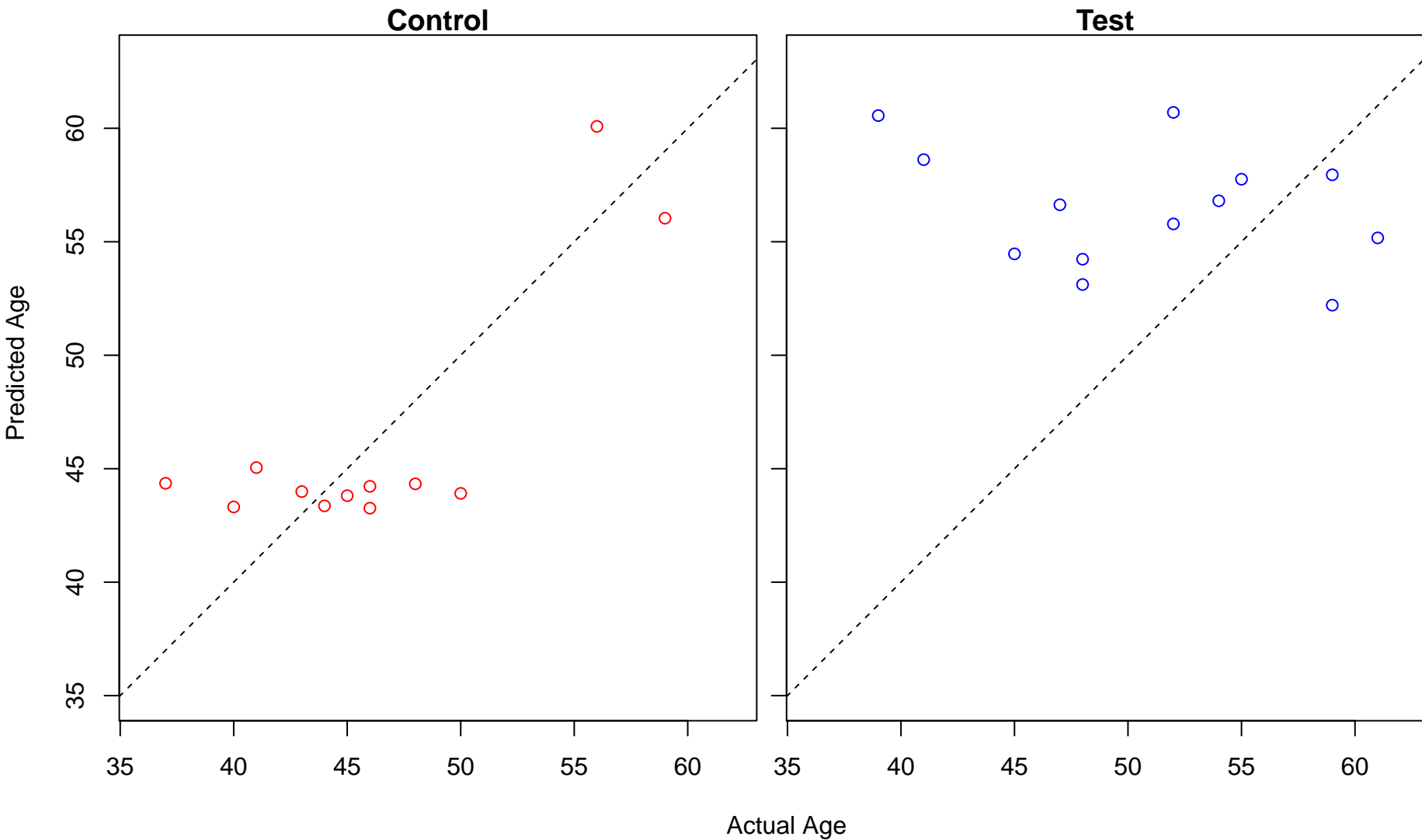
interspecies interaction between organisms (Score: 3.023016)



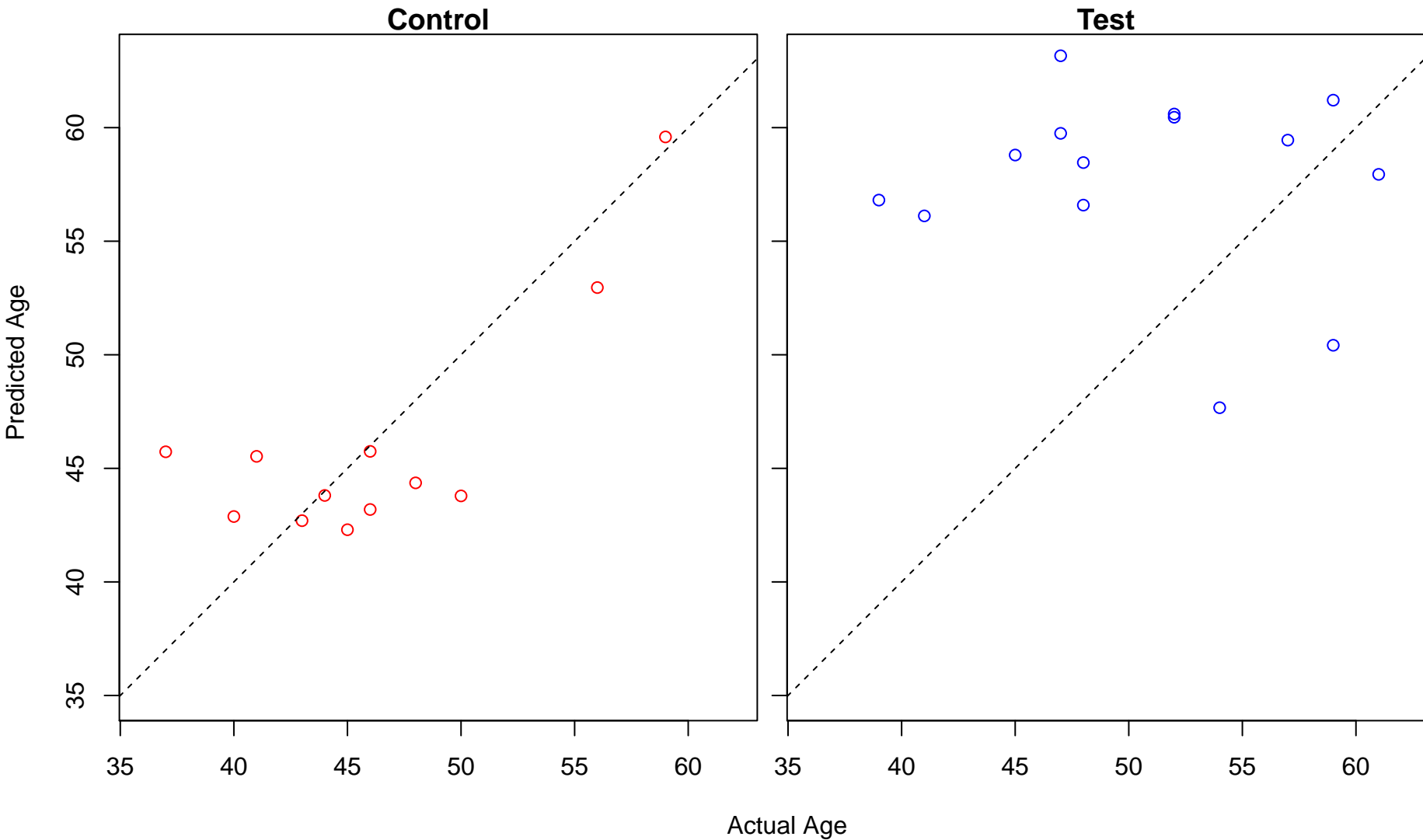
cellular amino acid biosynthetic process (Score: 3.021054)



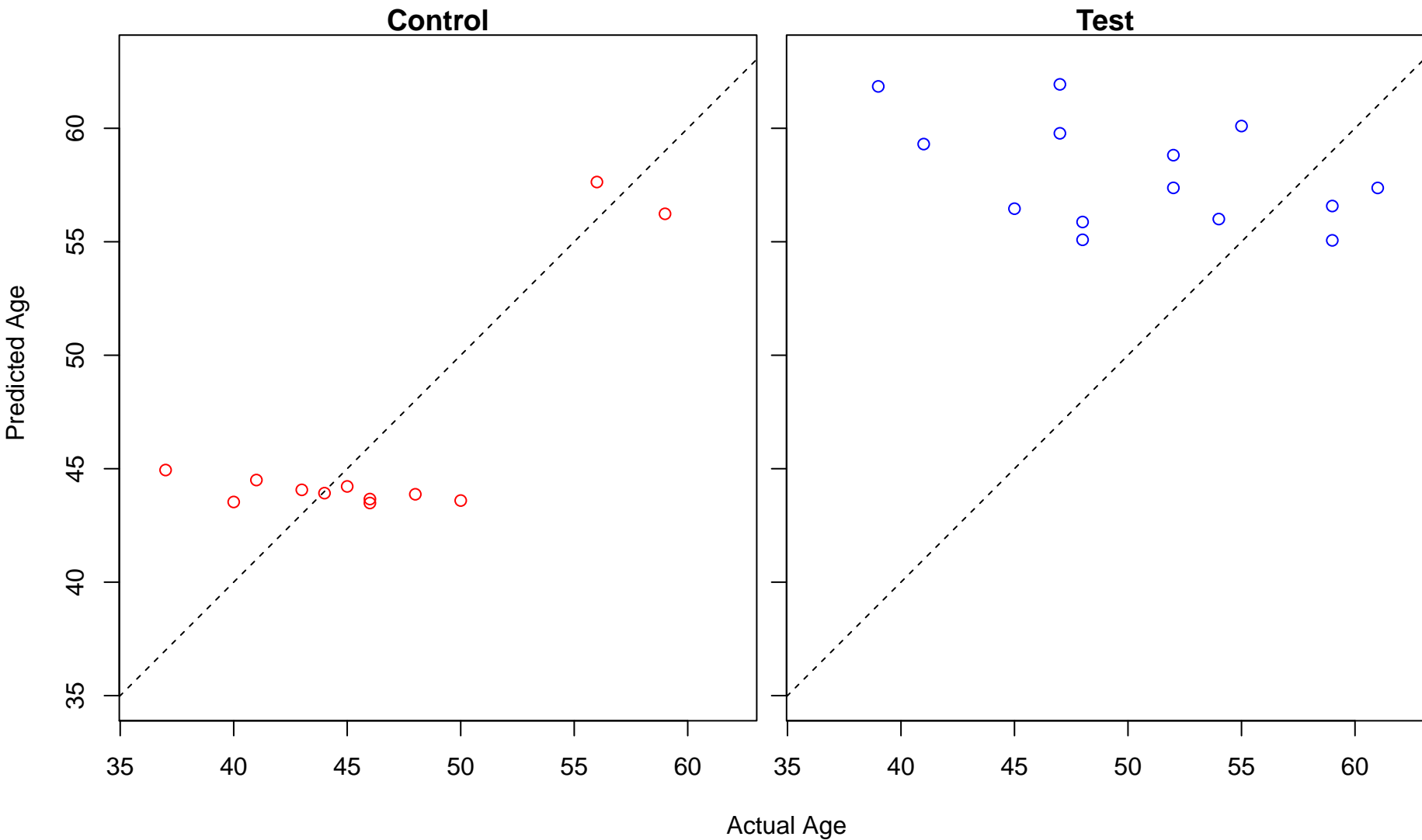
negative regulation of receptor-mediated endocytosis (Score: 3.018952)



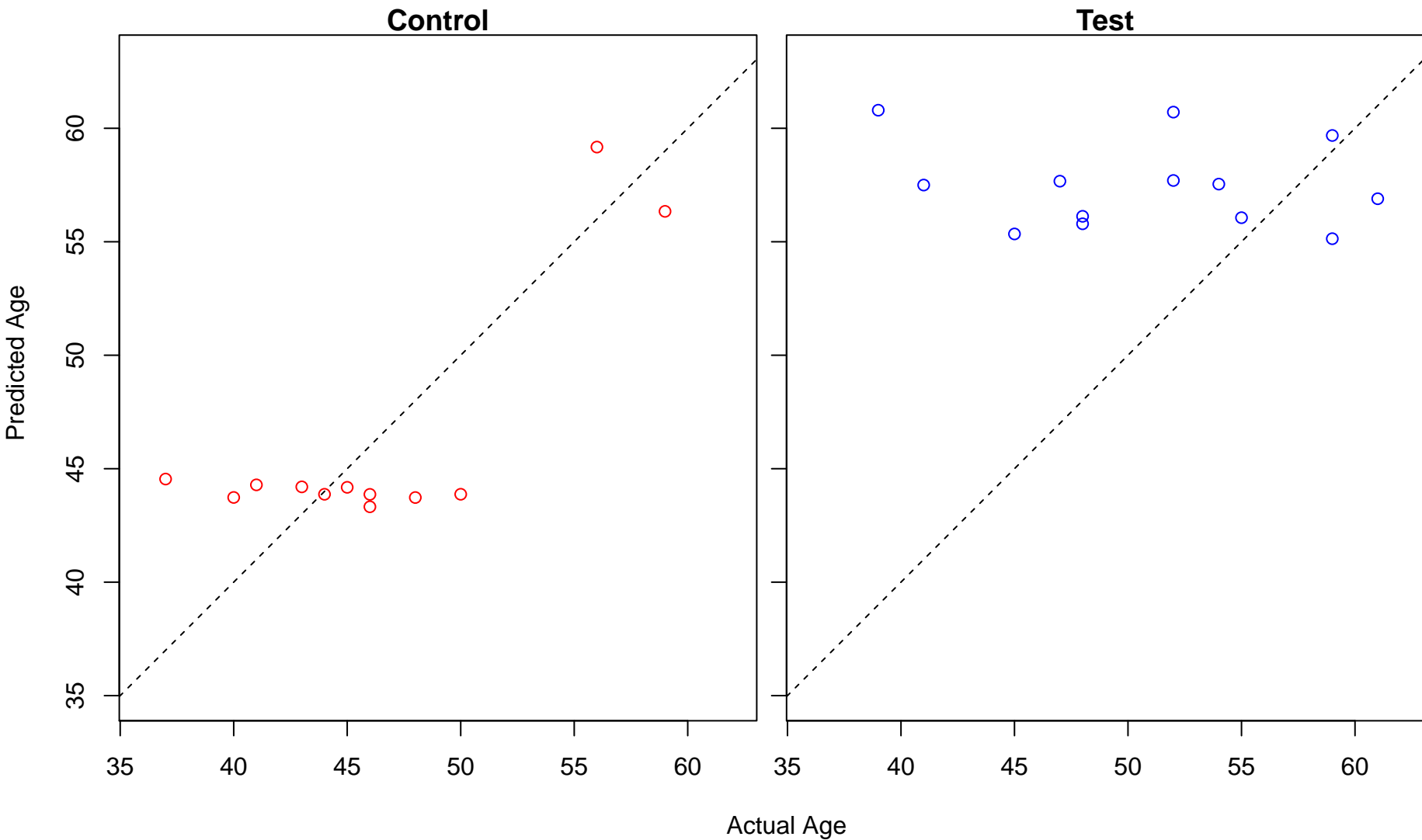
positive regulation of cytokine production involved in immune response (Score: 3.014386)



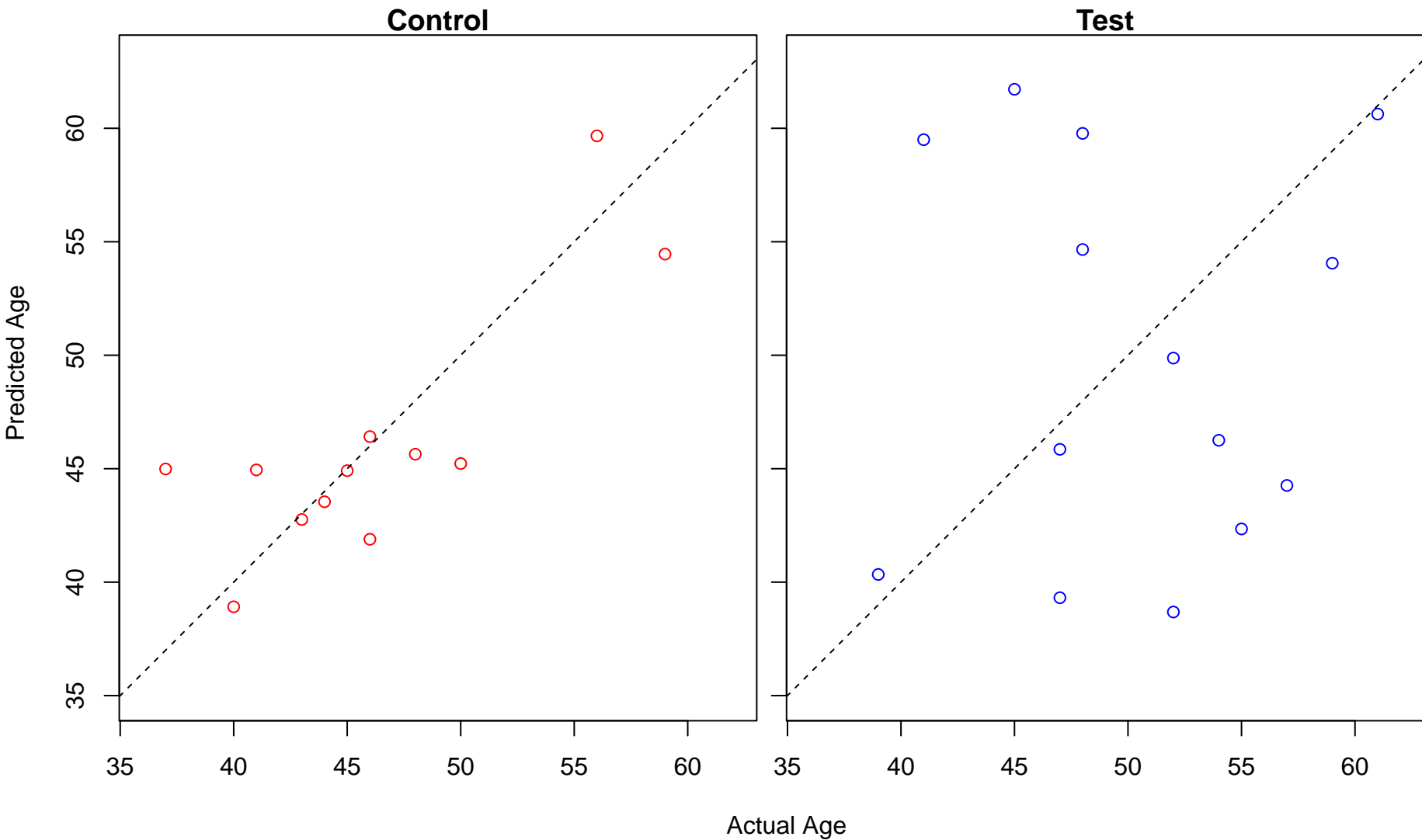
metal ion homeostasis (Score: 3.012950)



proteasome-mediated ubiquitin-dependent protein catabolic process (Score: 3.010822)

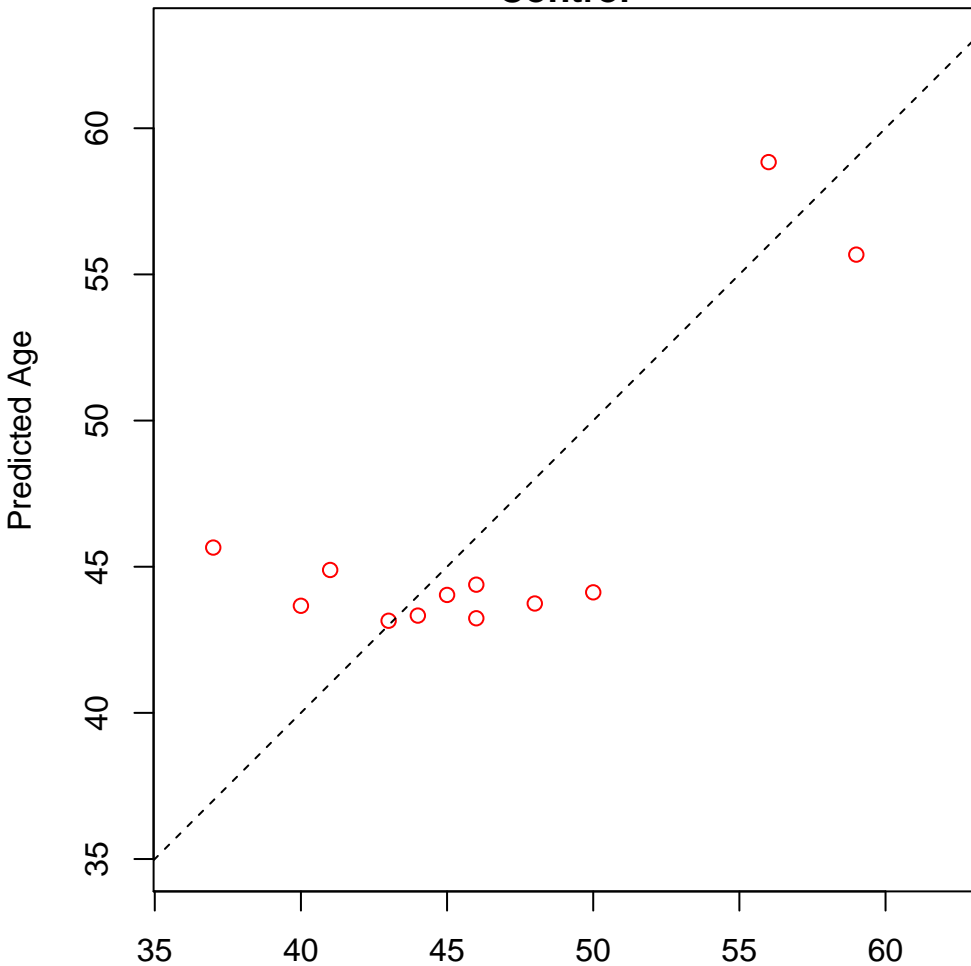


long-term memory (Score: 3.010423)

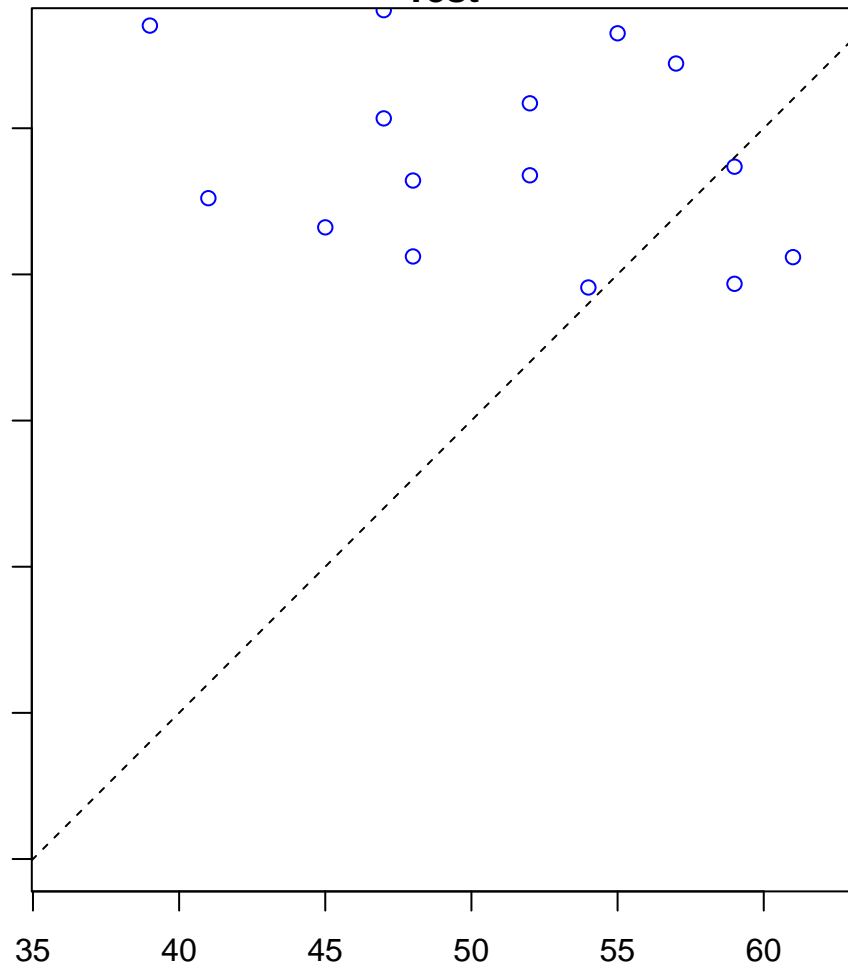


positive regulation of protein binding (Score: 3.010147)

Control

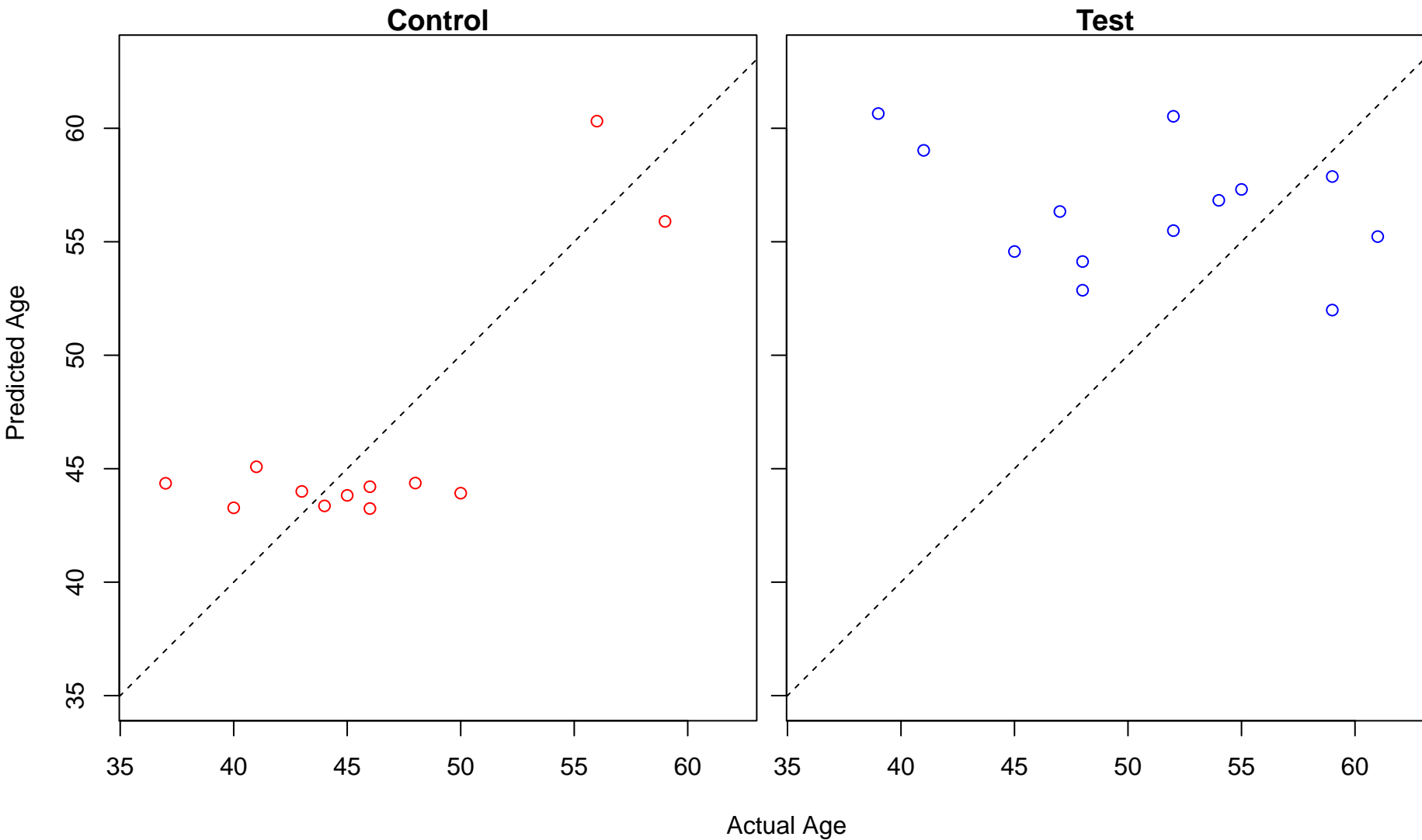


Test

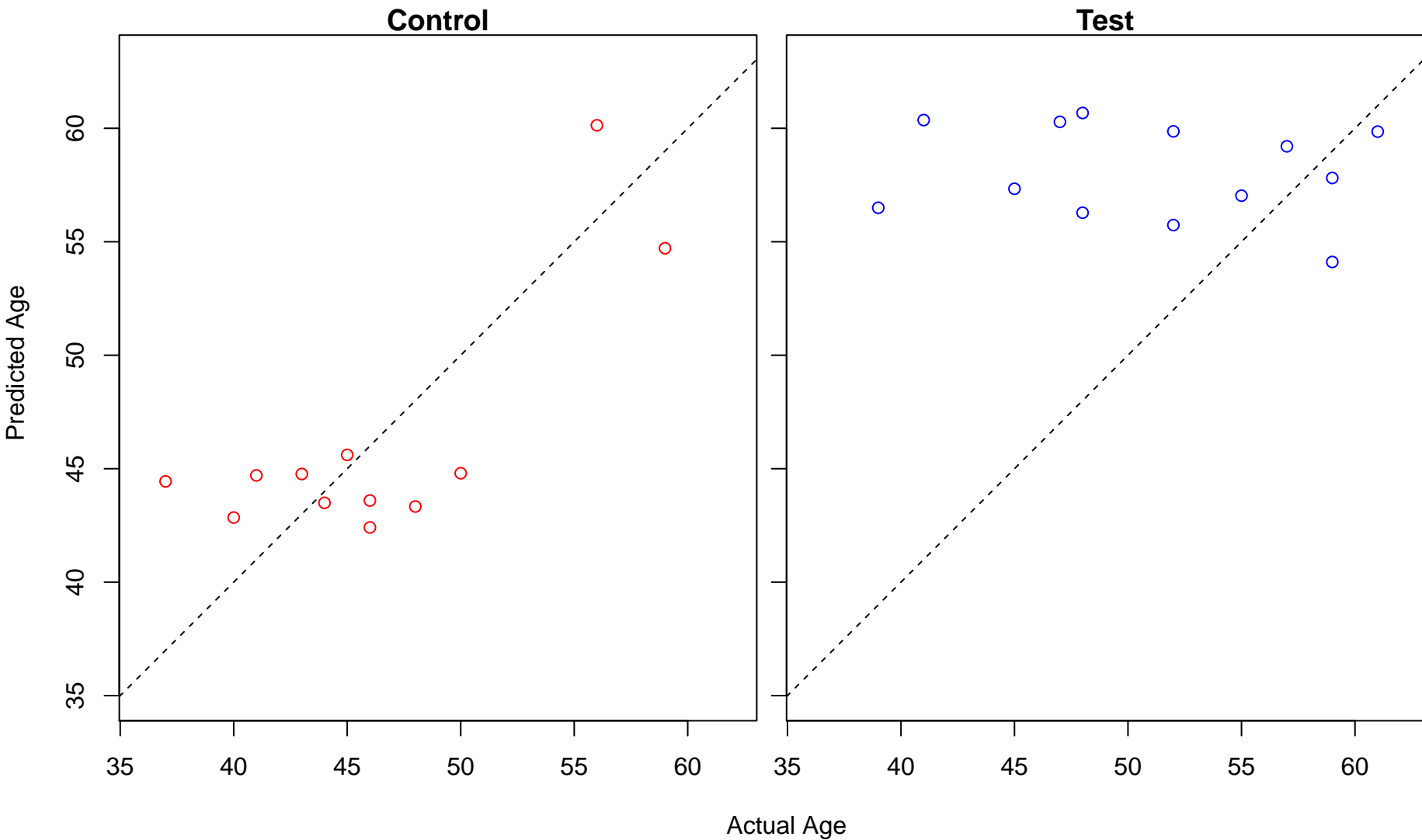


Actual Age

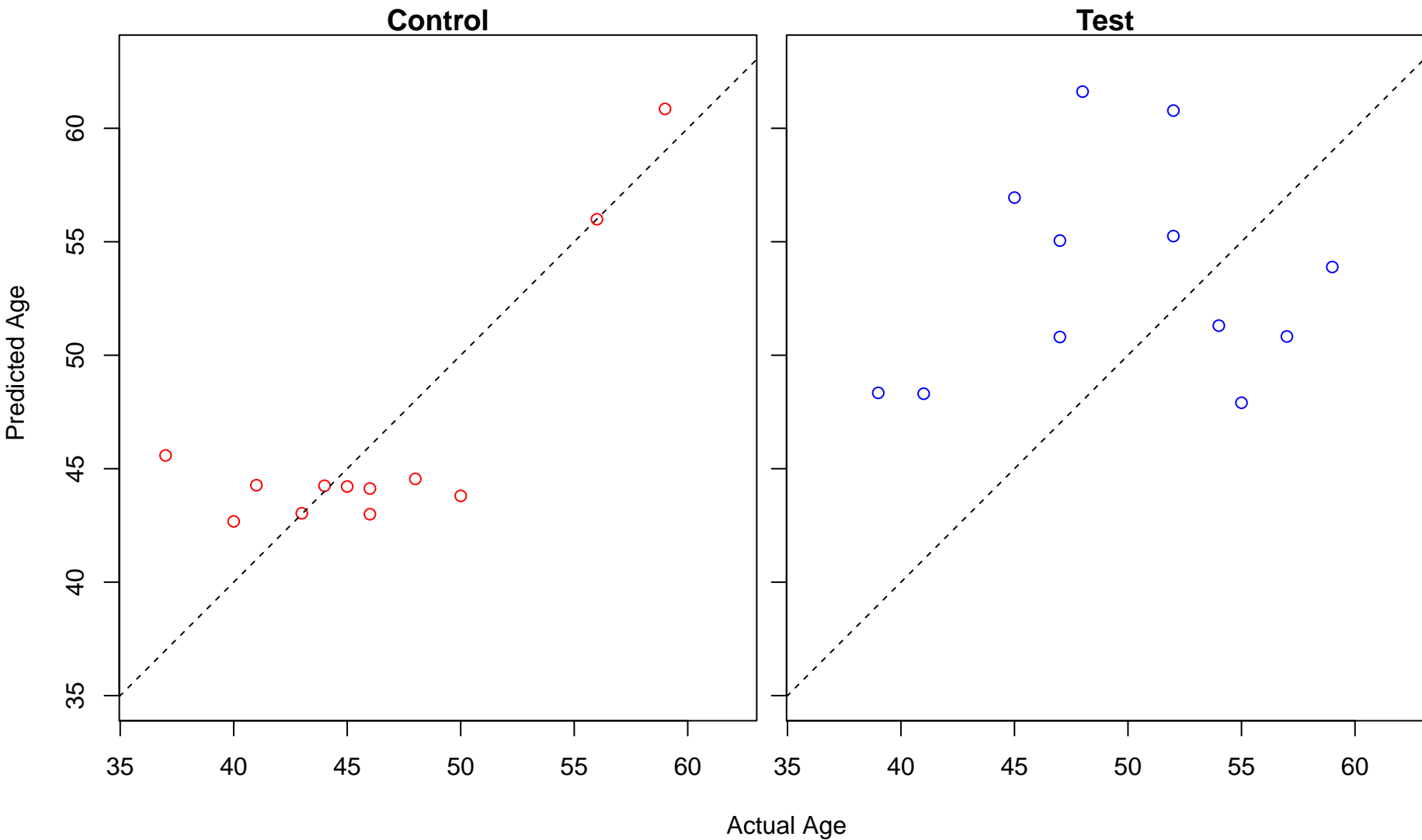
membrane raft assembly (Score: 3.007874)



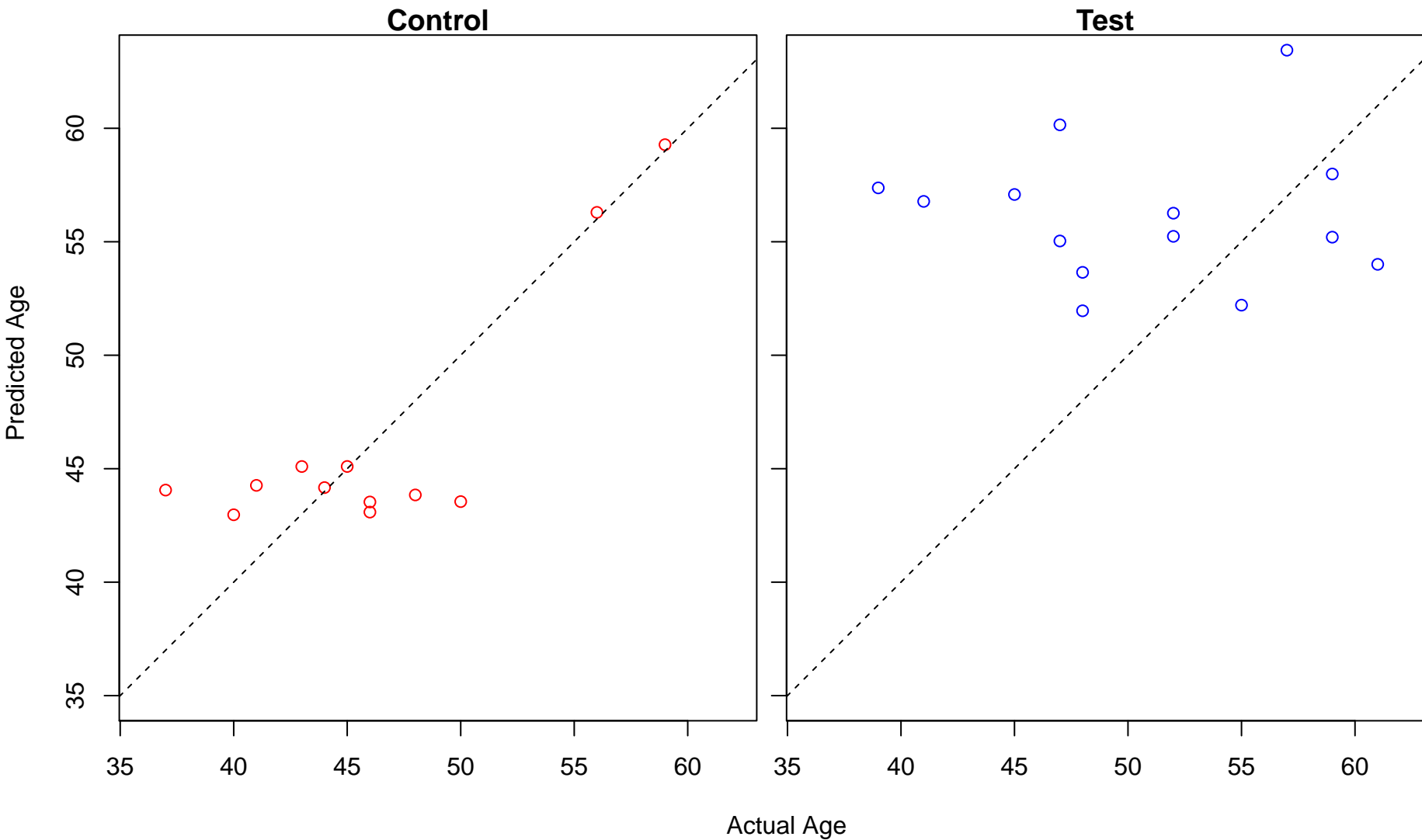
neural tube formation (Score: 3.007752)



fatty acid beta-oxidation using acyl-CoA dehydrogenase (Score: 3.006333)

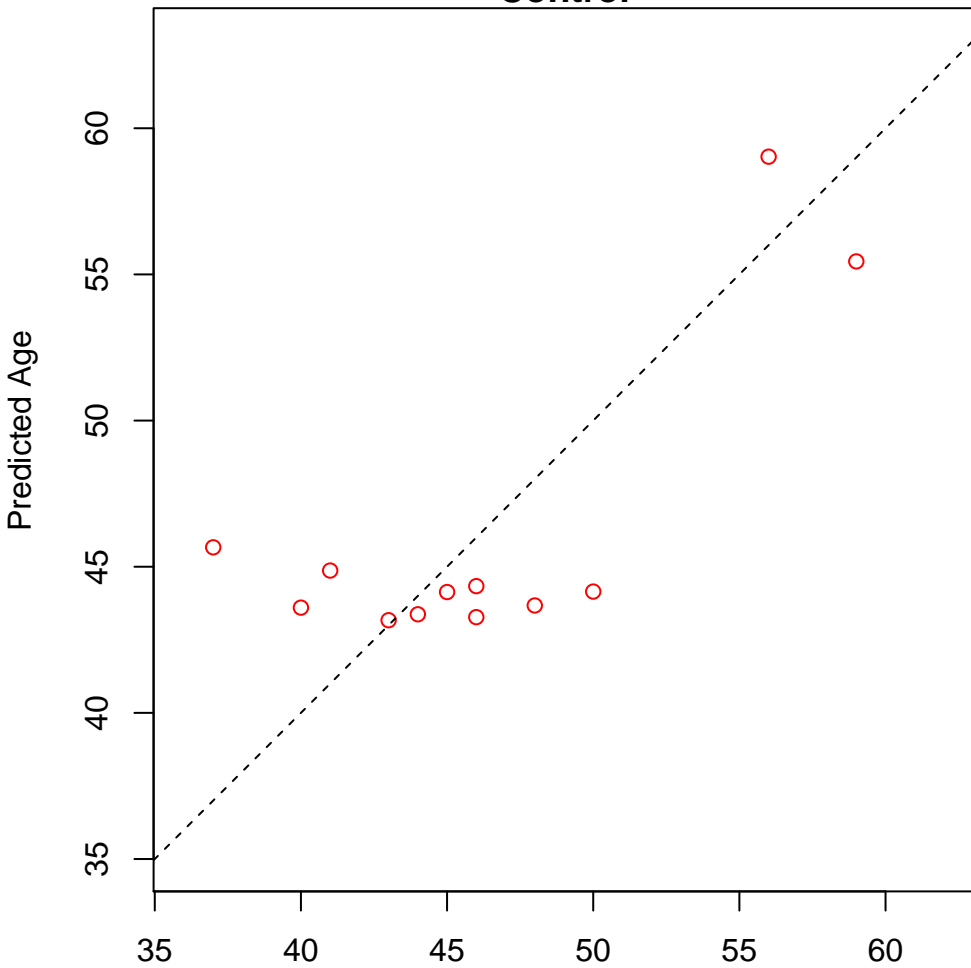


galactose metabolic process (Score: 3.005963)

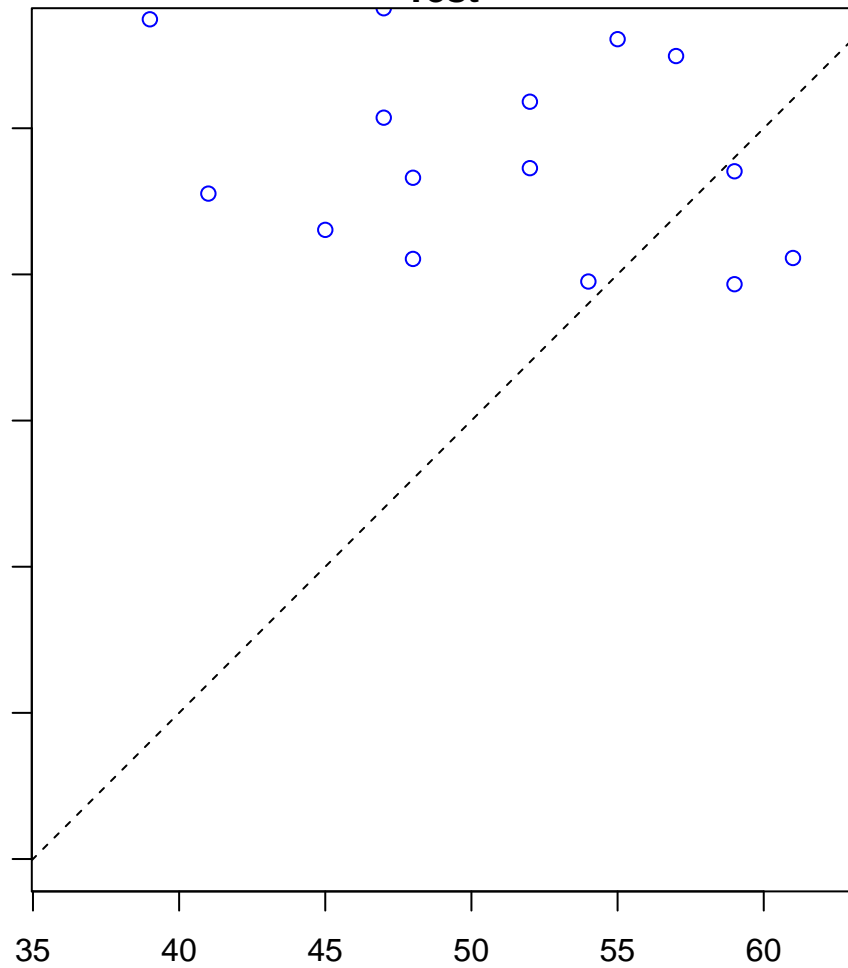


response to transition metal nanoparticle (Score: 3.005473)

Control

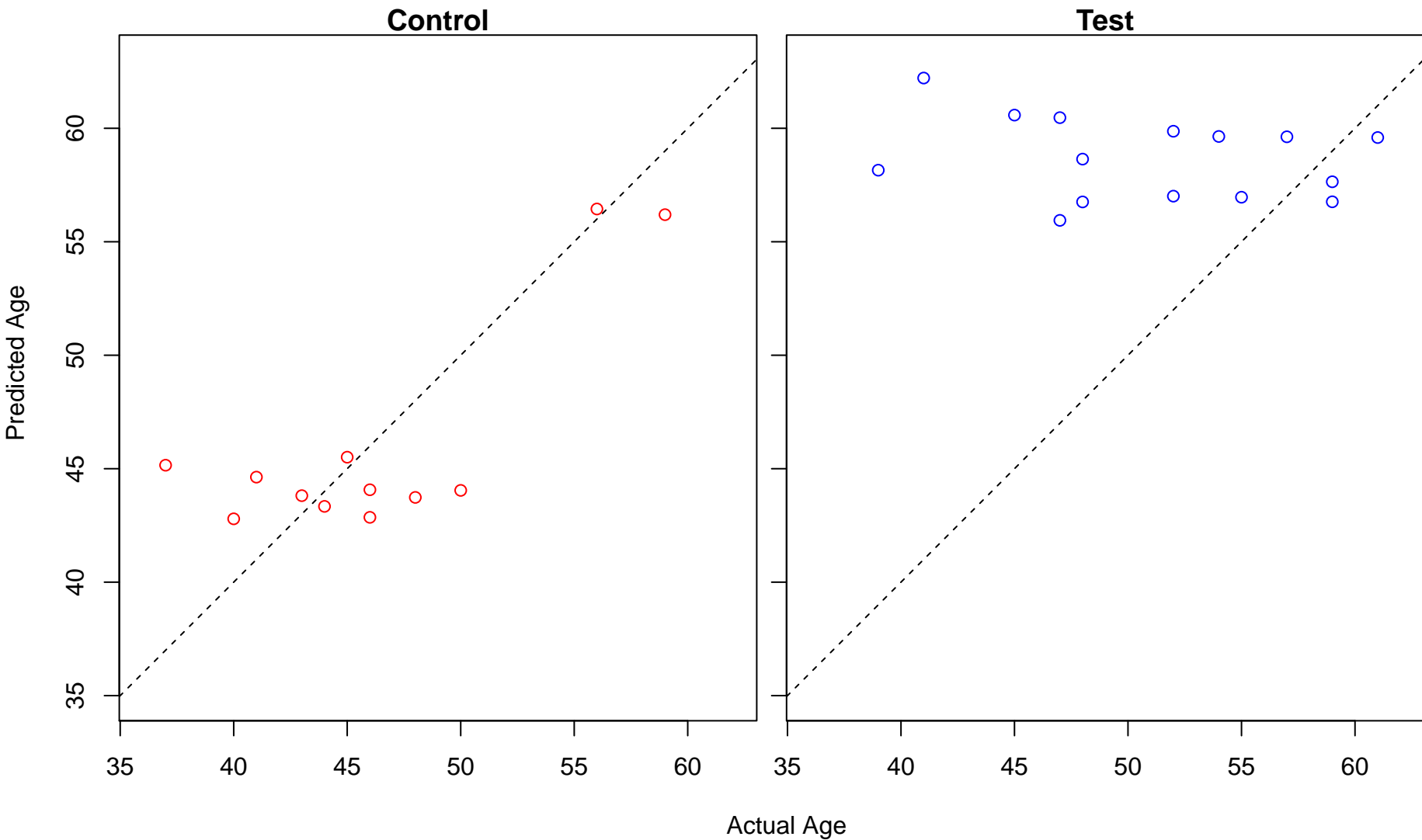


Test

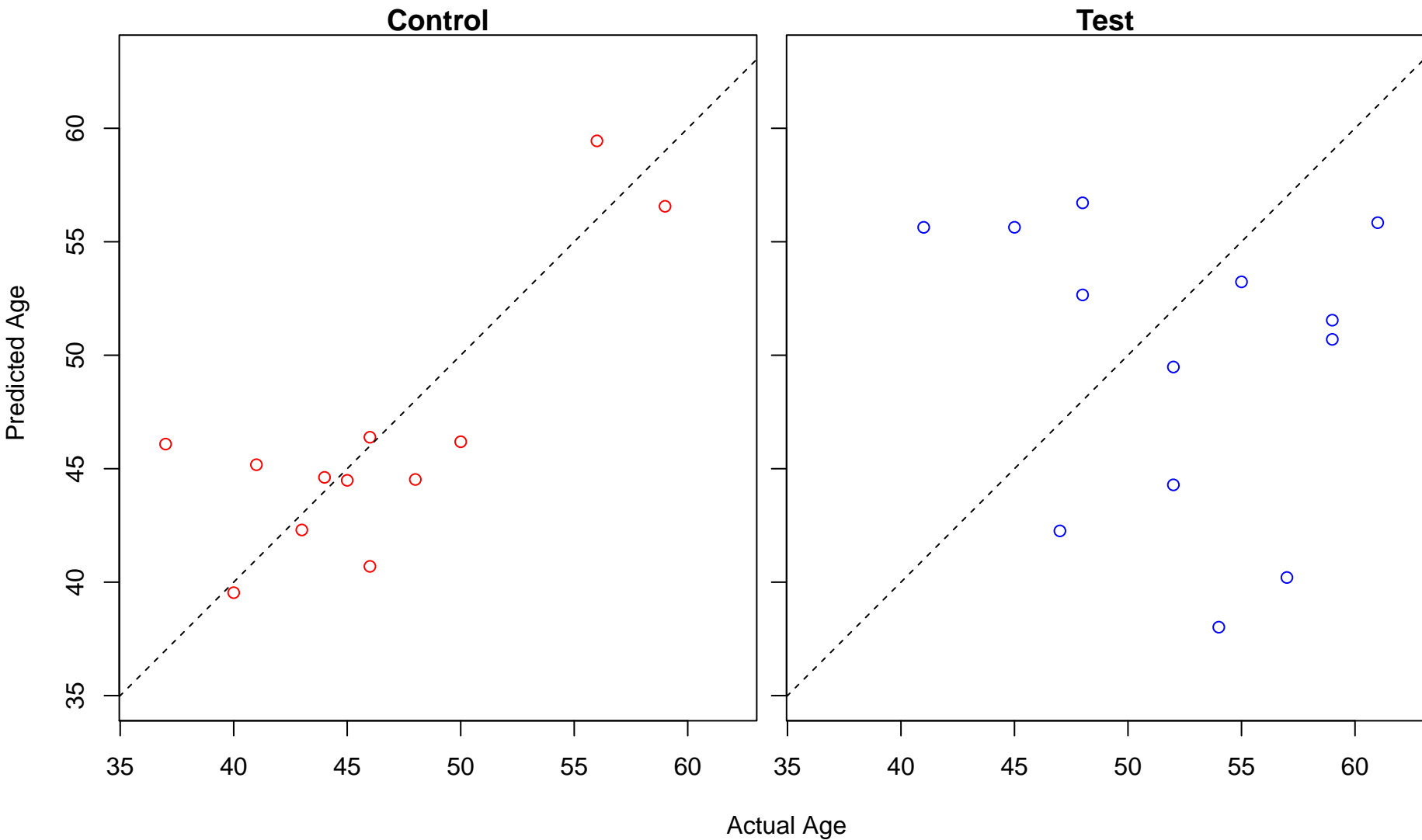


Actual Age

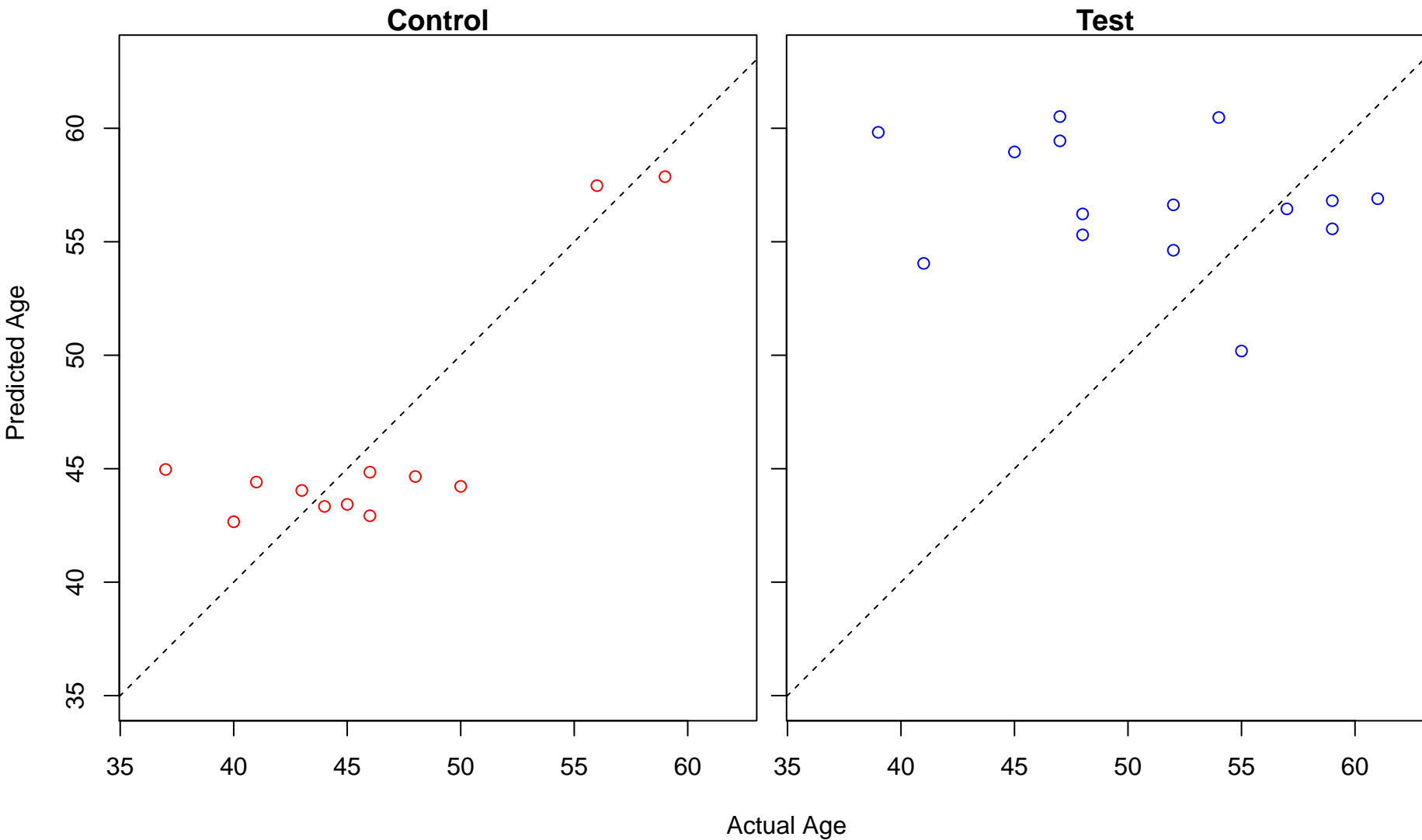
negative regulation of protein complex assembly (Score: 3.005056)



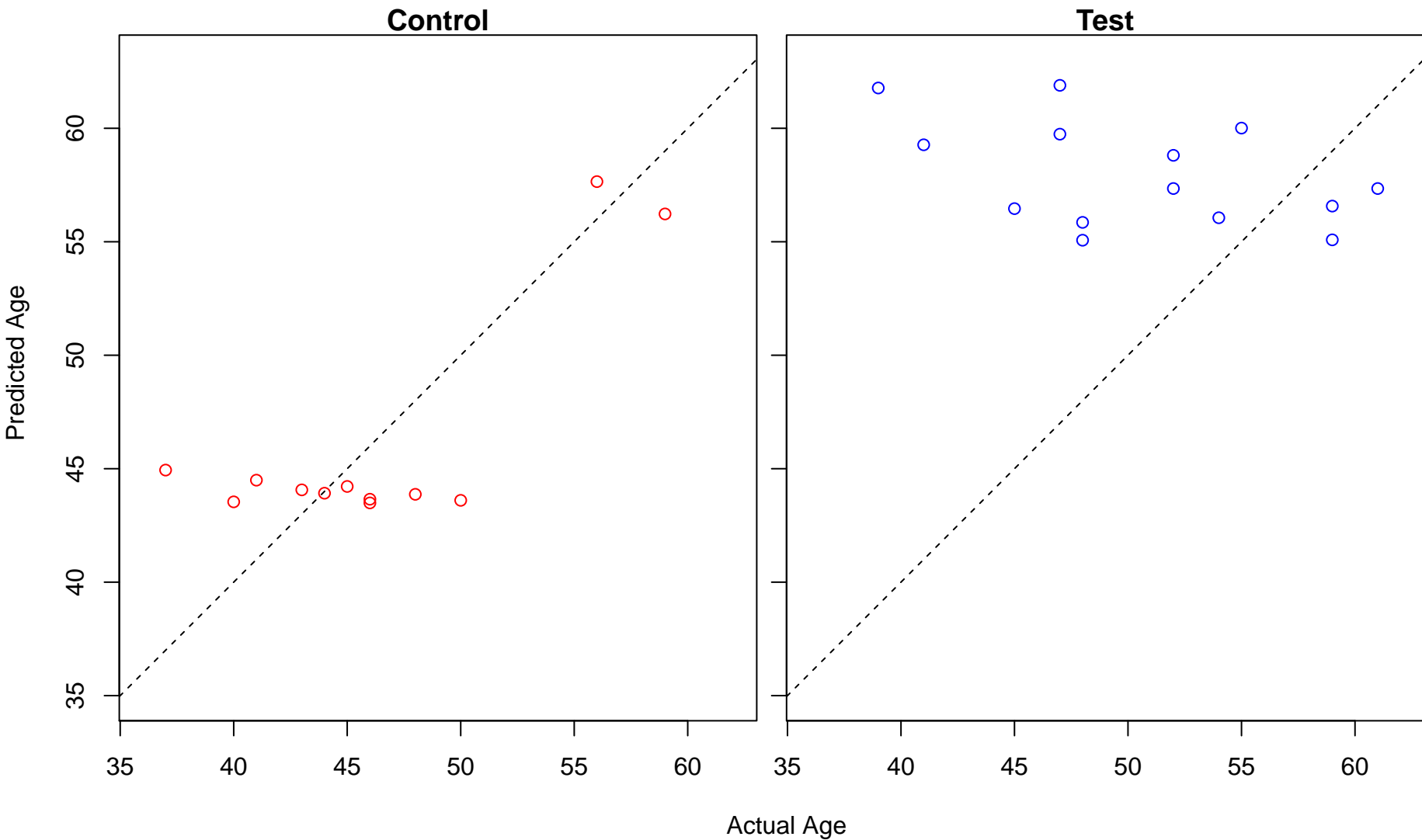
endocytosis (Score: 3.004907)



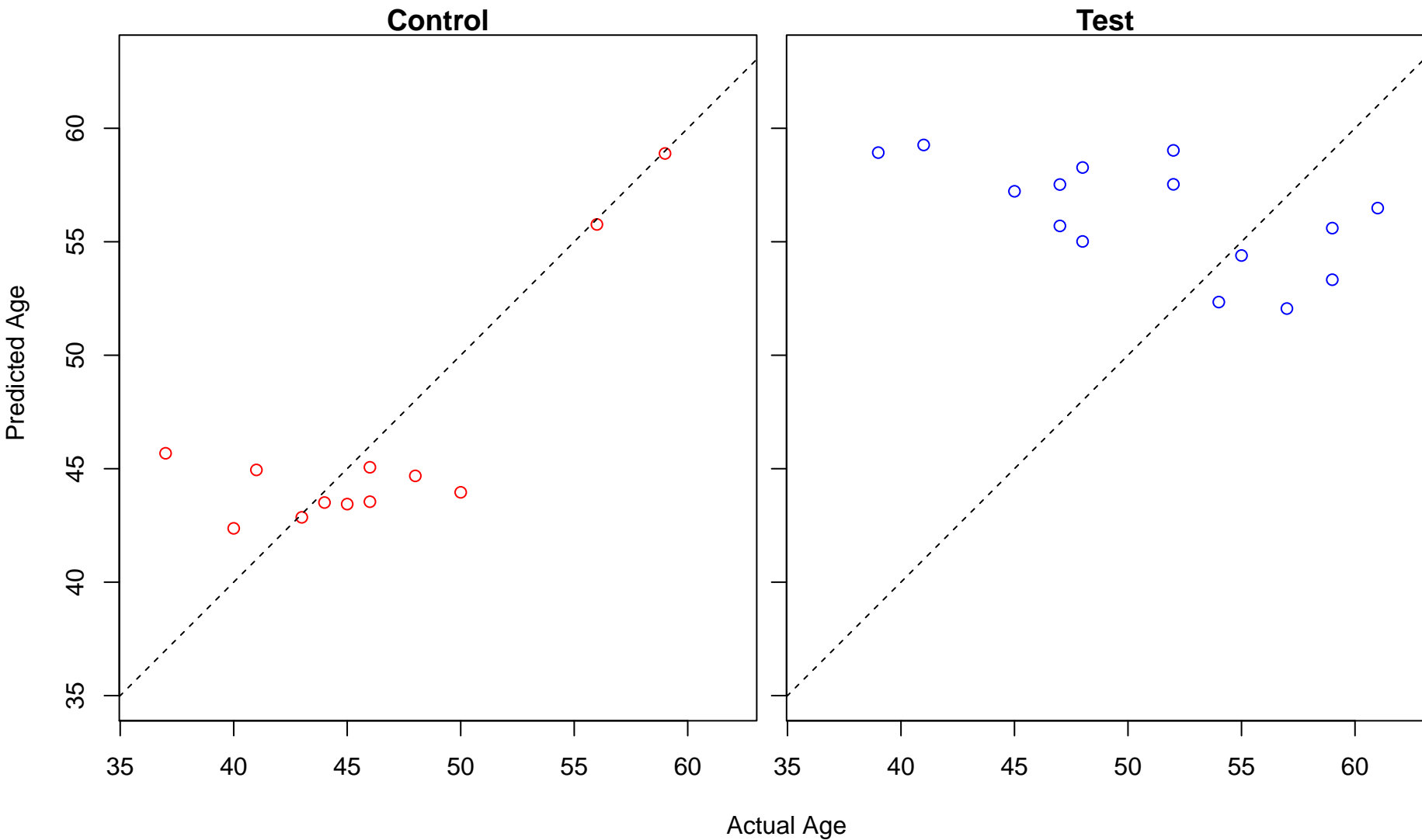
learning (Score: 3.003246)



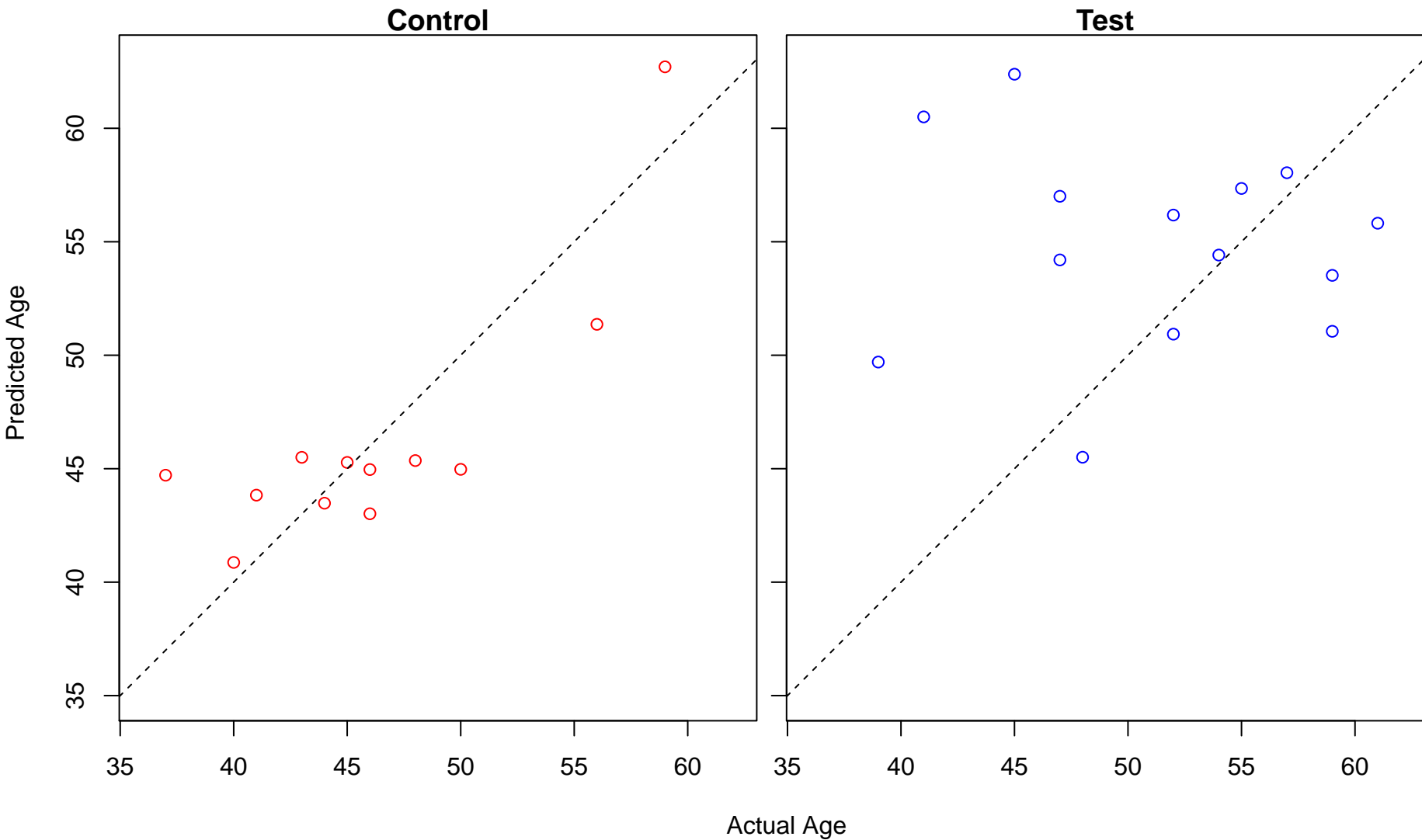
cation homeostasis (Score: 3.001999)



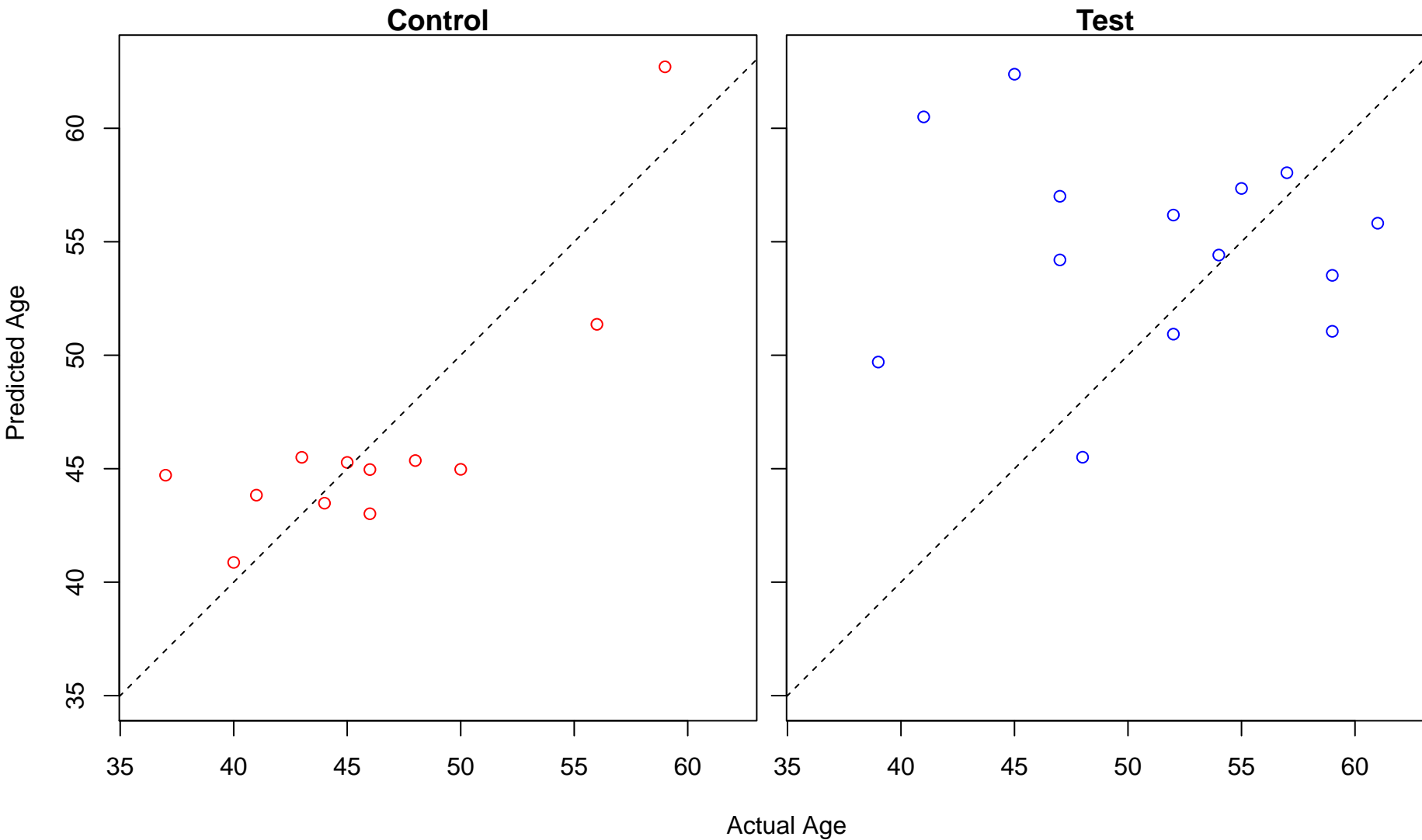
regulation of DNA-templated transcription, initiation (Score: 3.001012)



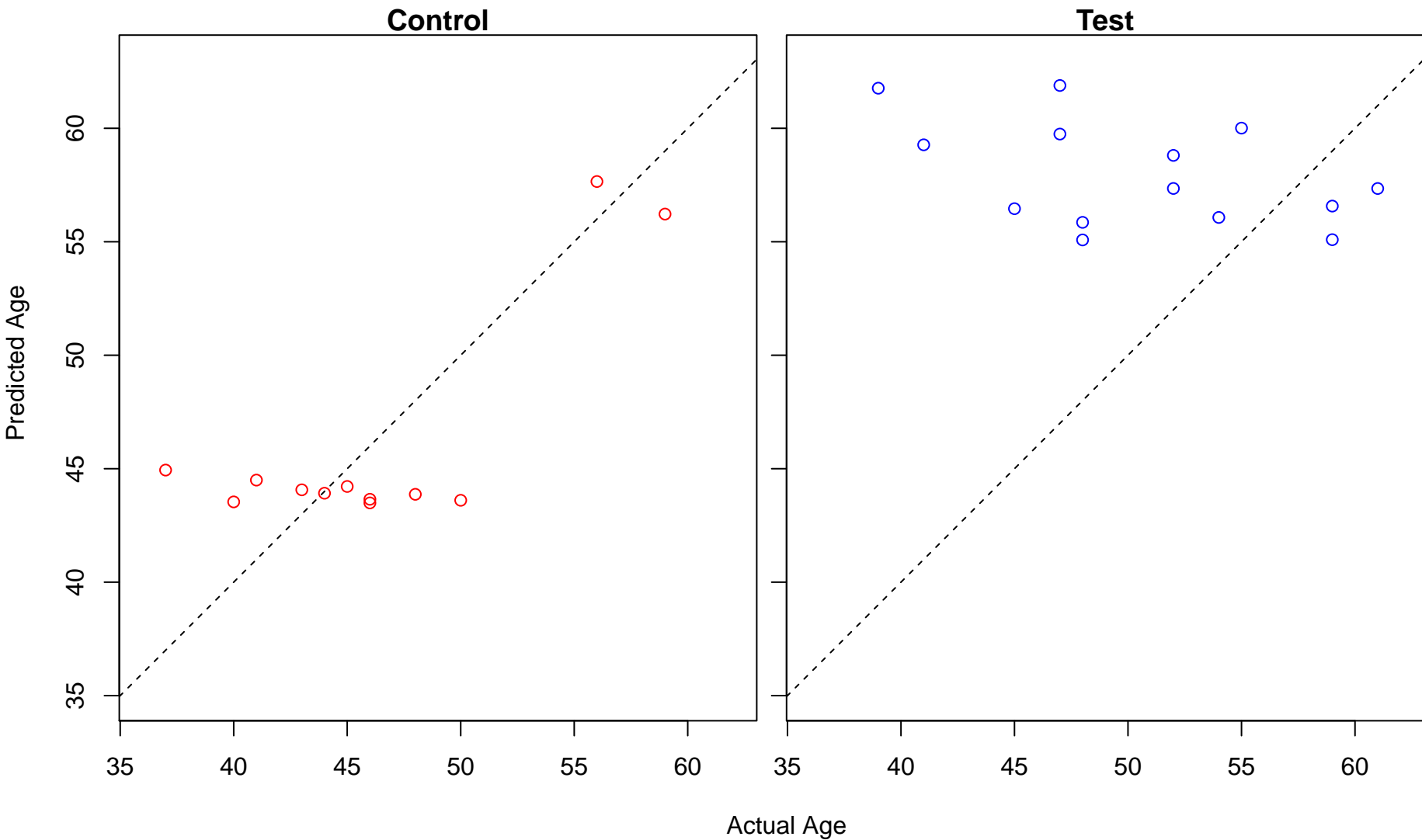
embryo development ending in birth or egg hatching (Score: 3.000571)



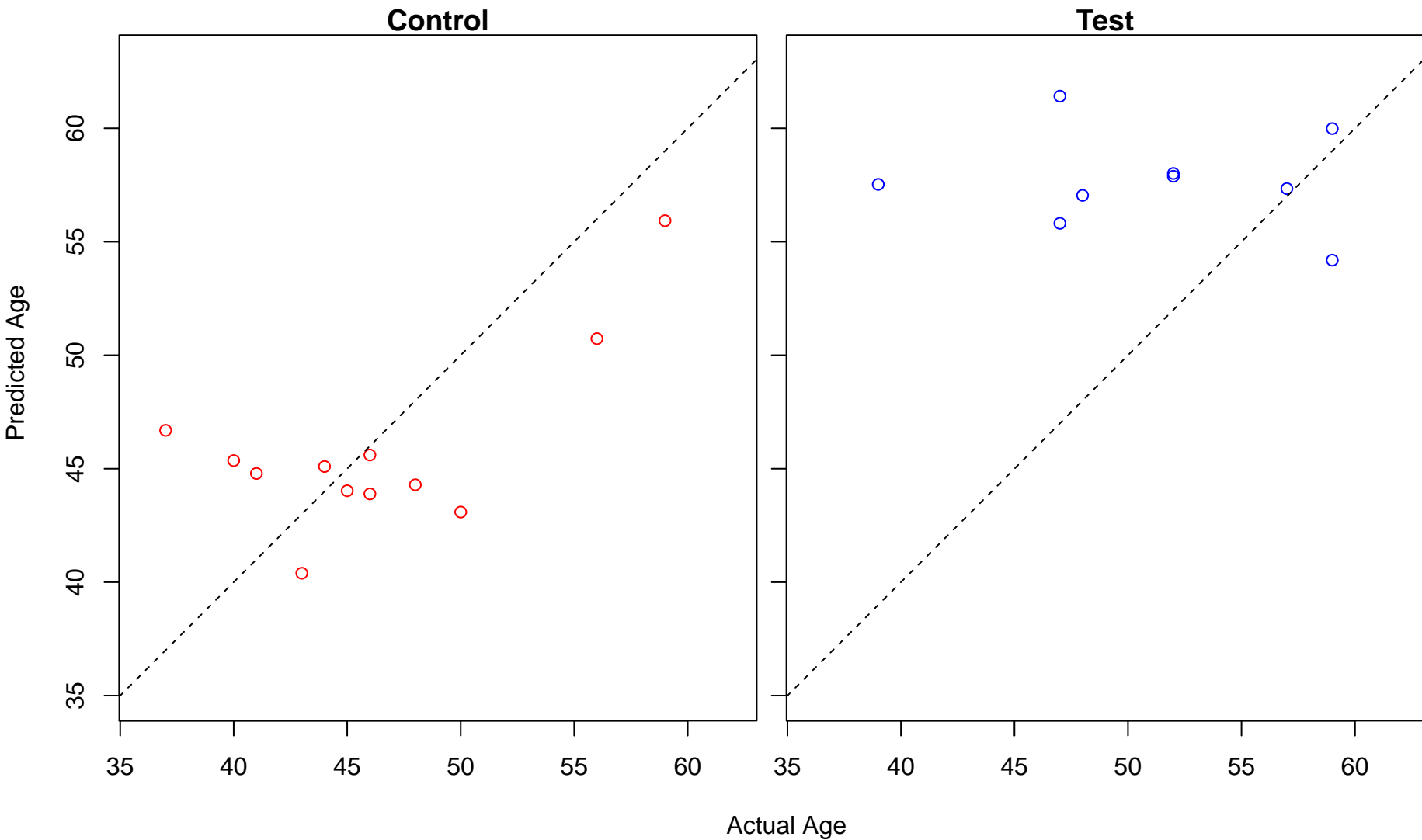
chordate embryonic development (Score: 3.000571)



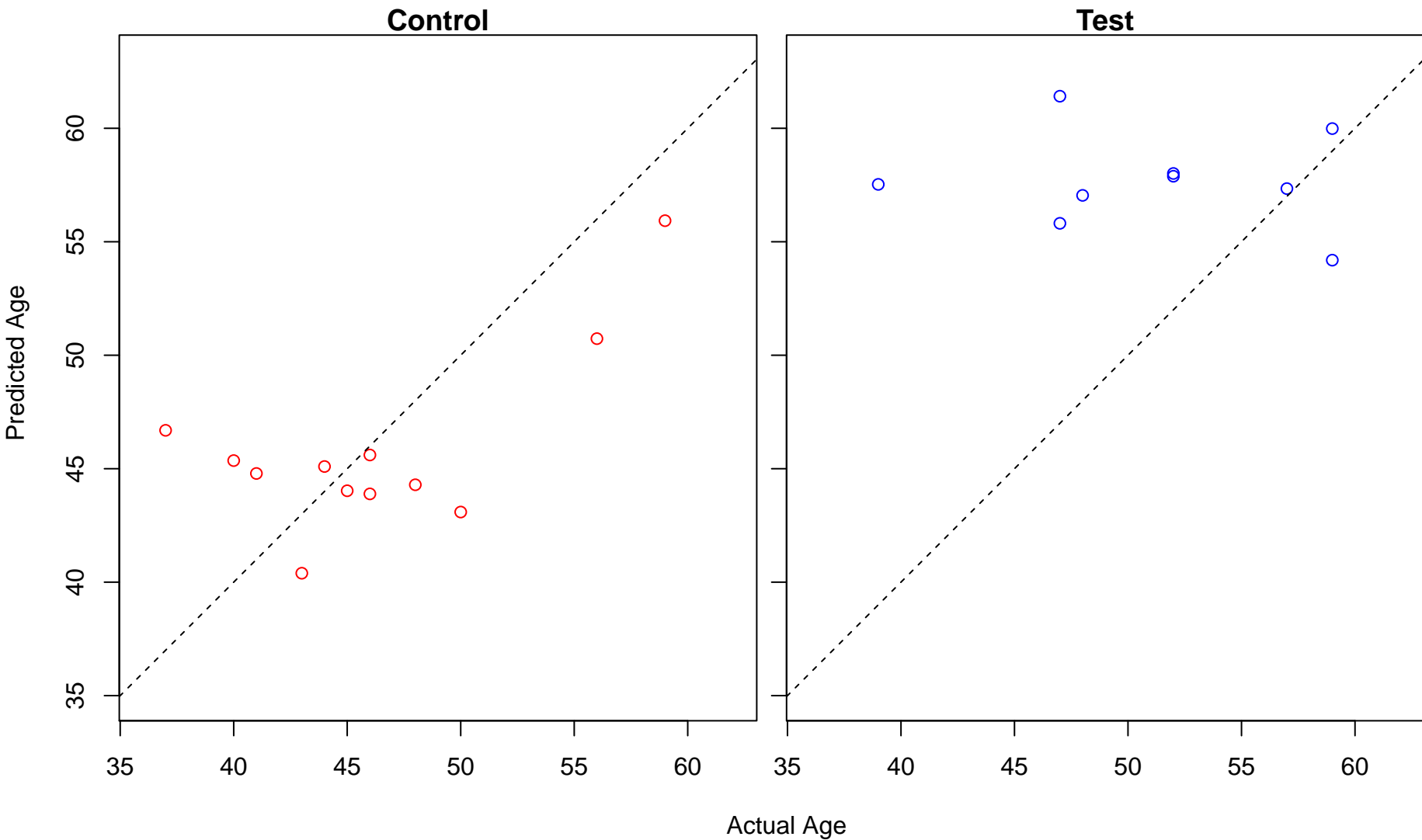
inorganic ion homeostasis (Score: 3.000533)



detection of light stimulus involved in visual perception (Score: 2.999764)

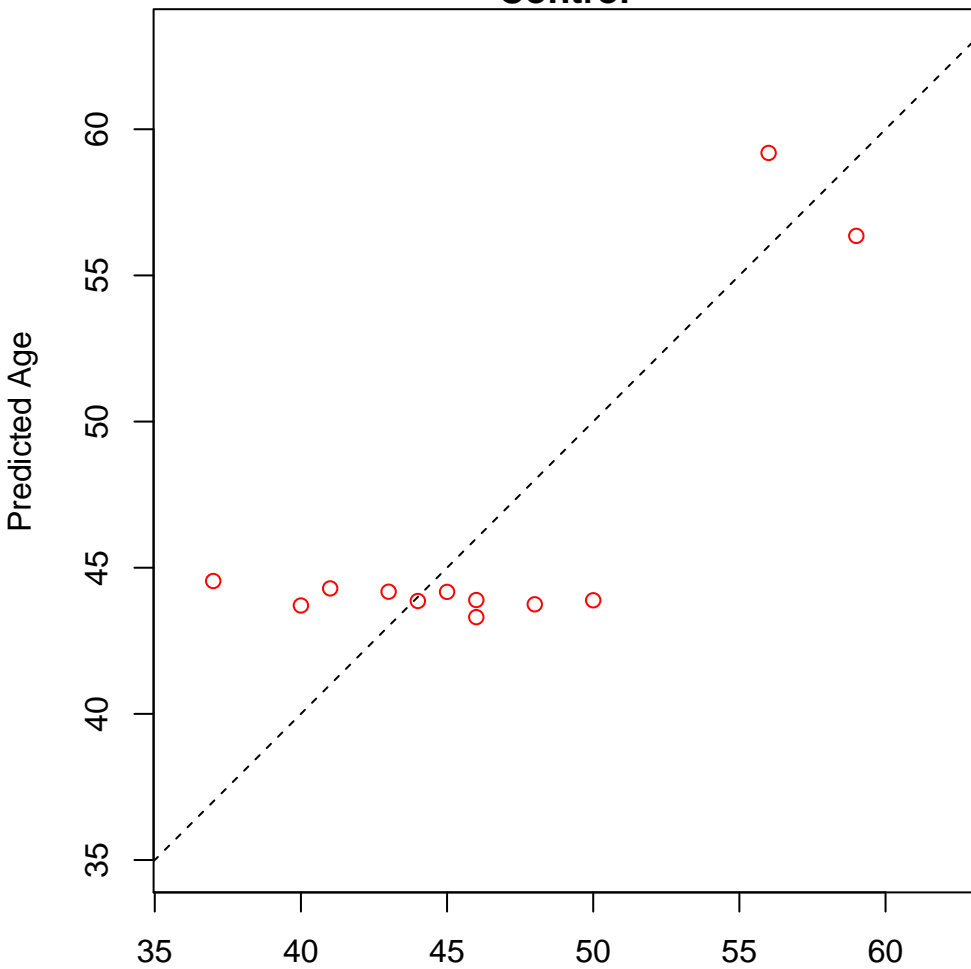


detection of light stimulus involved in sensory perception (Score: 2.999764)

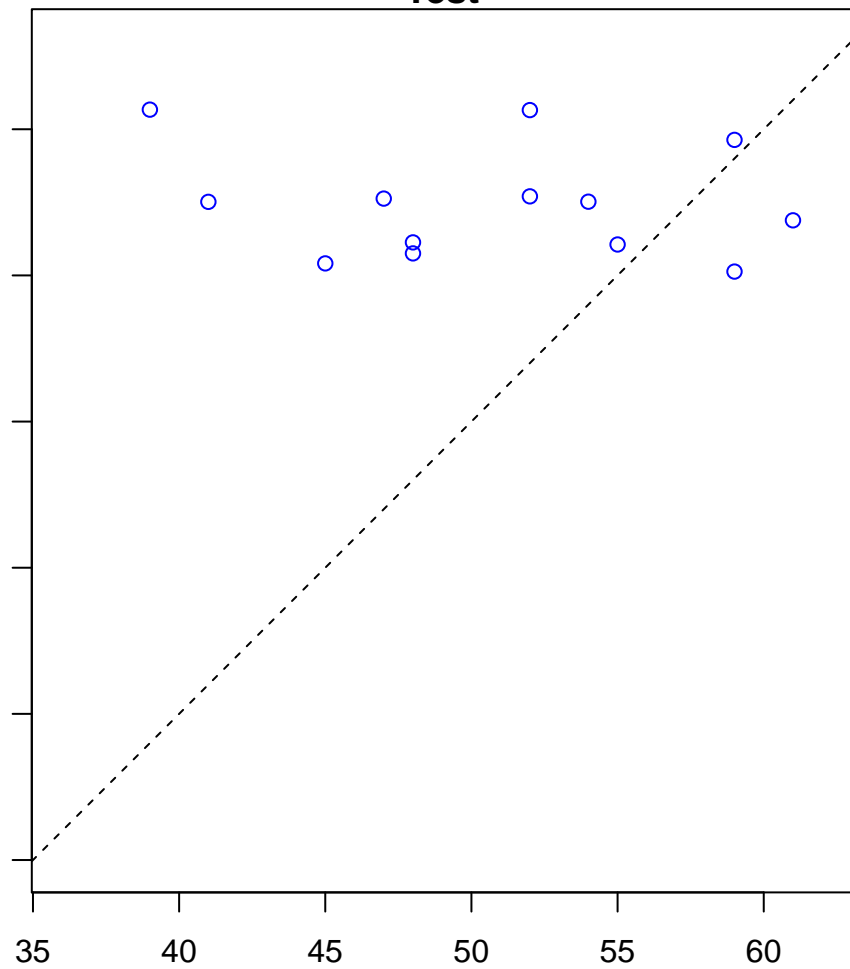


proteasomal protein catabolic process (Score: 2.998176)

Control

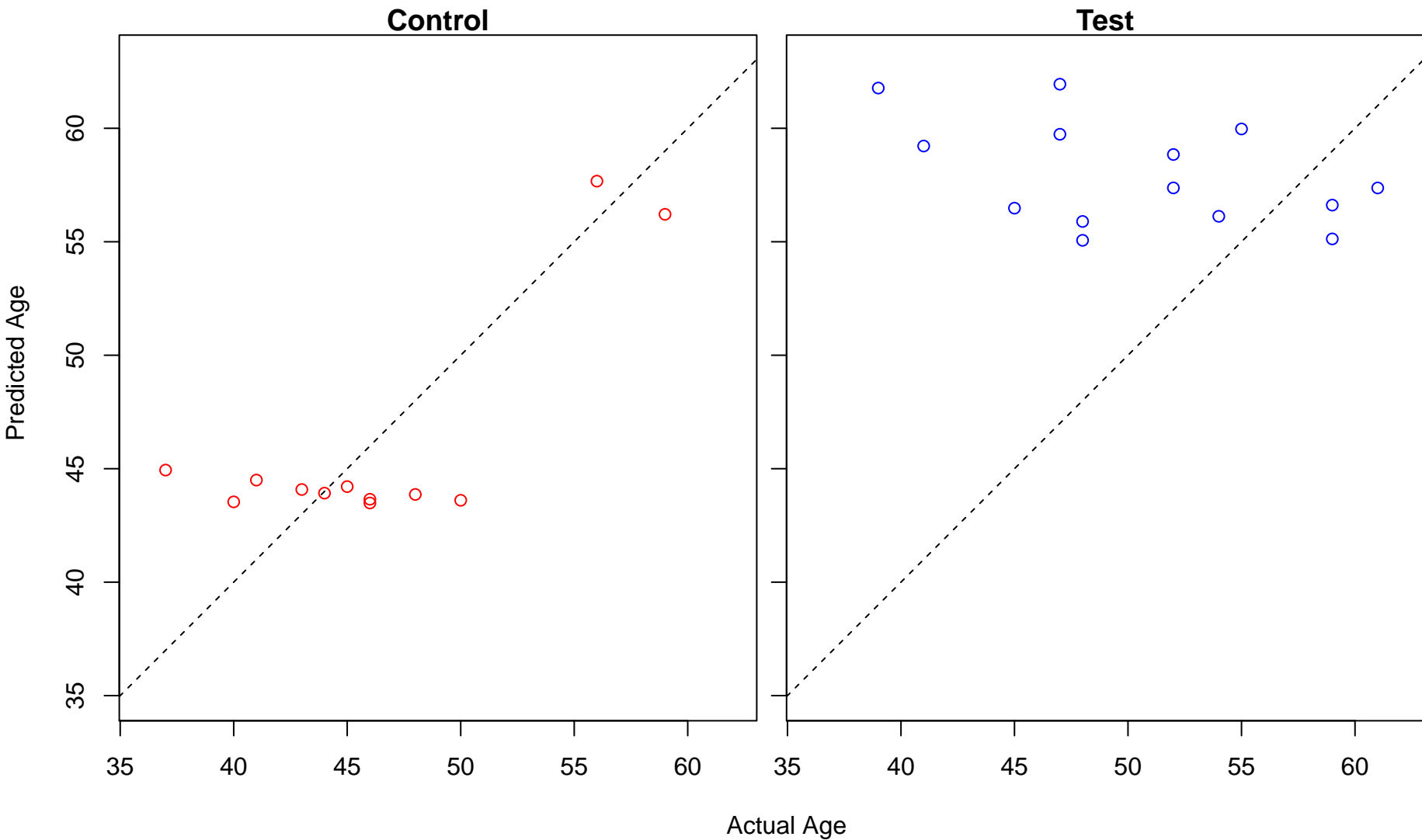


Test

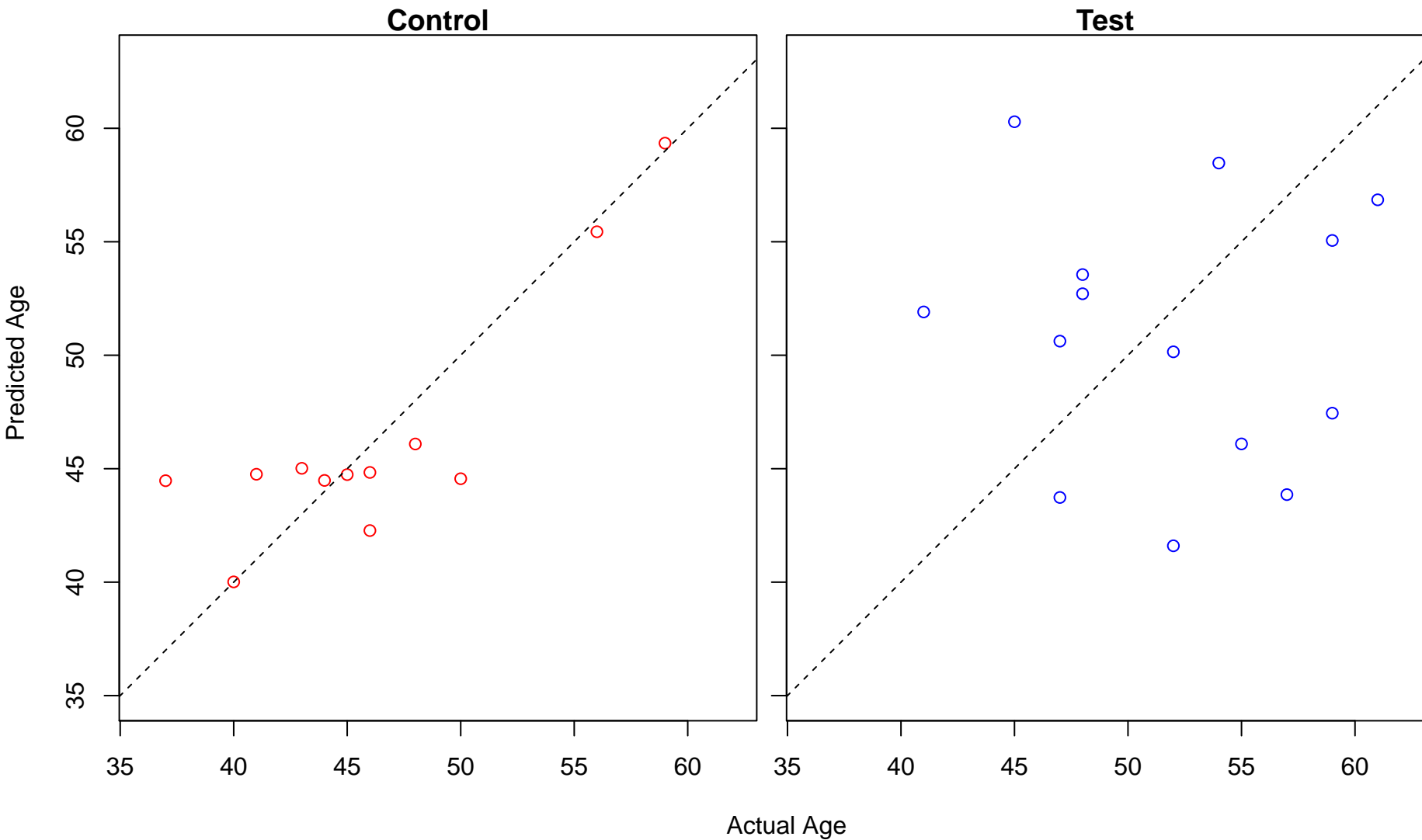


Actual Age

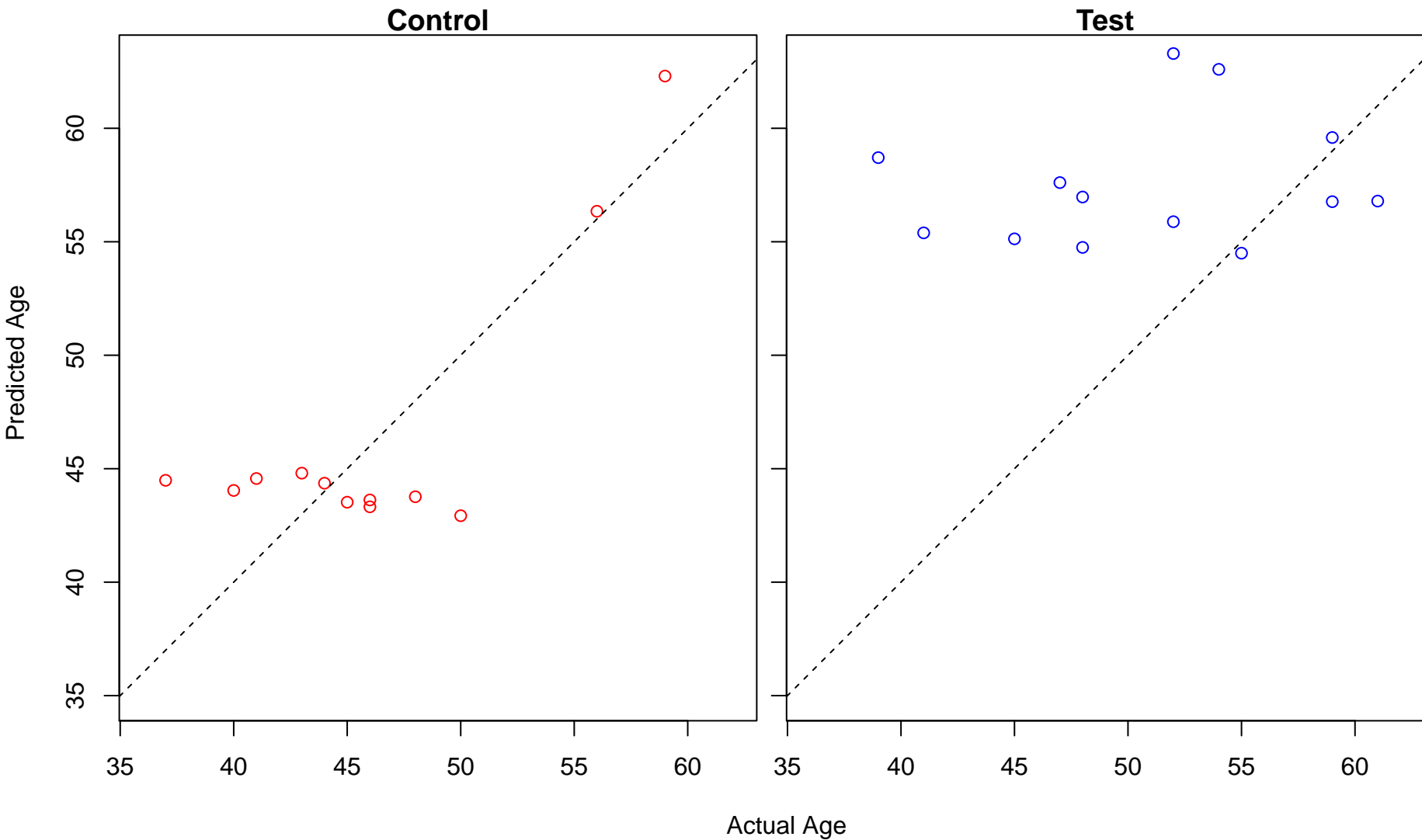
ion homeostasis (Score: 2.997523)



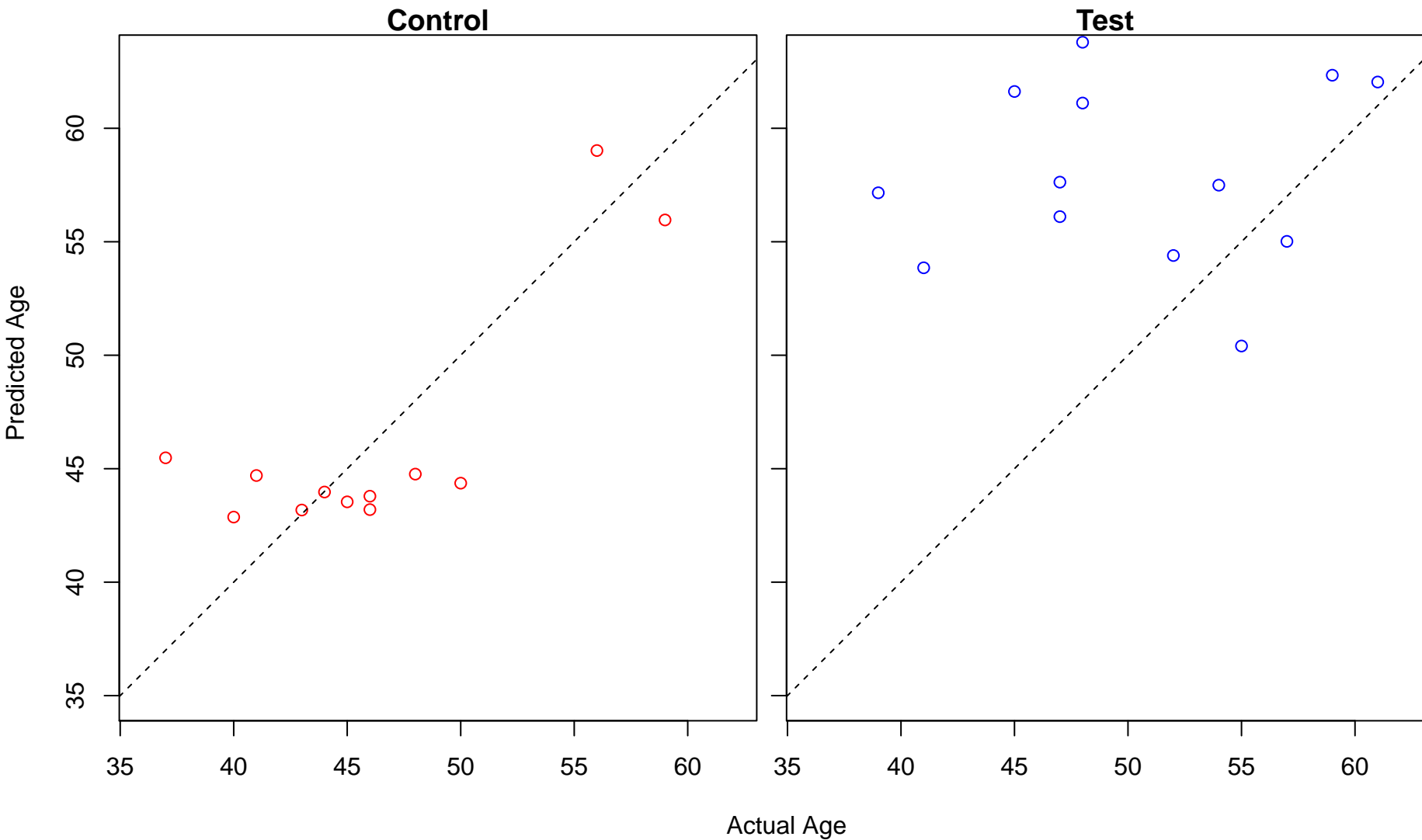
regulation of intracellular protein transport (Score: 2.996411)



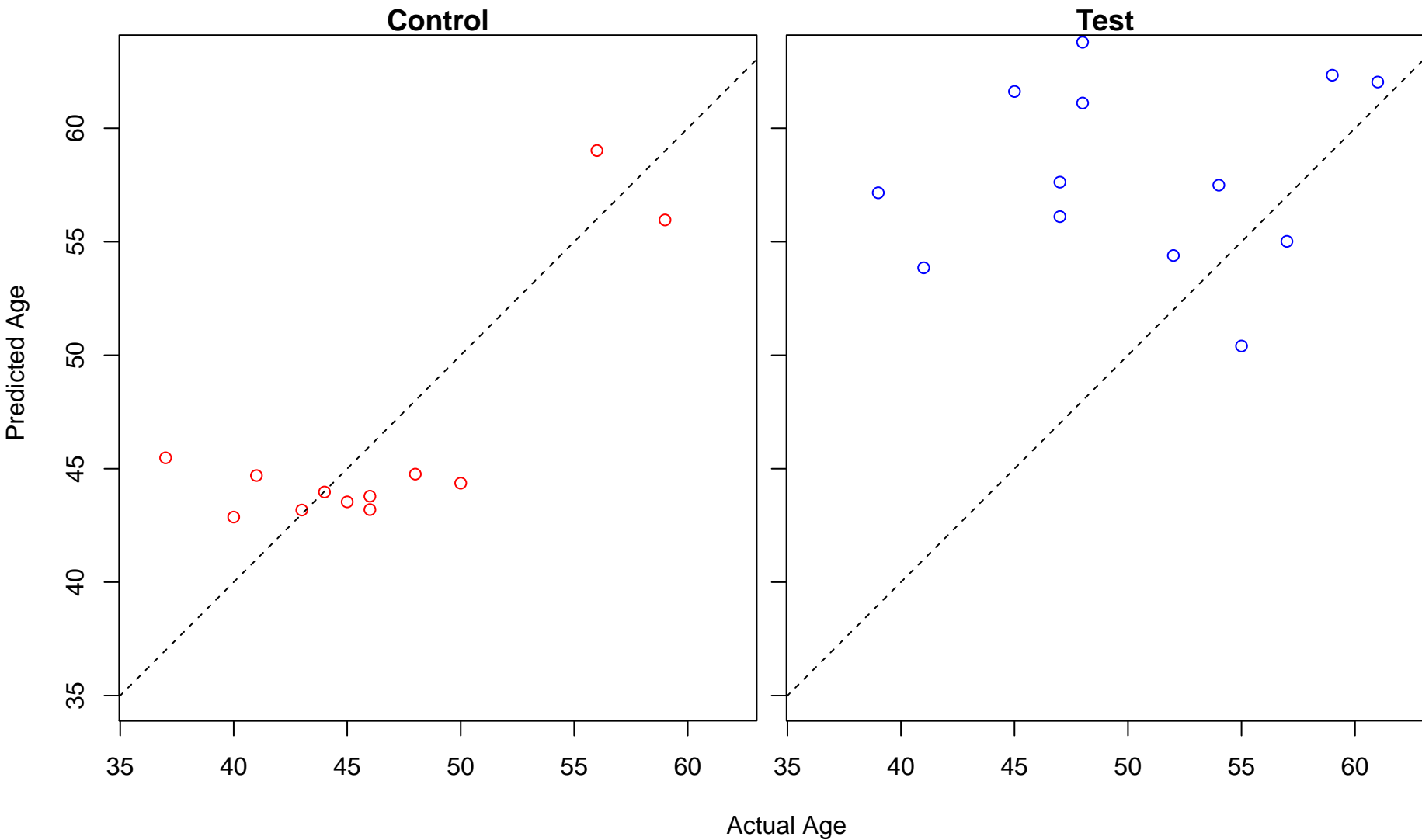
positive regulation of lyase activity (Score: 2.995490)



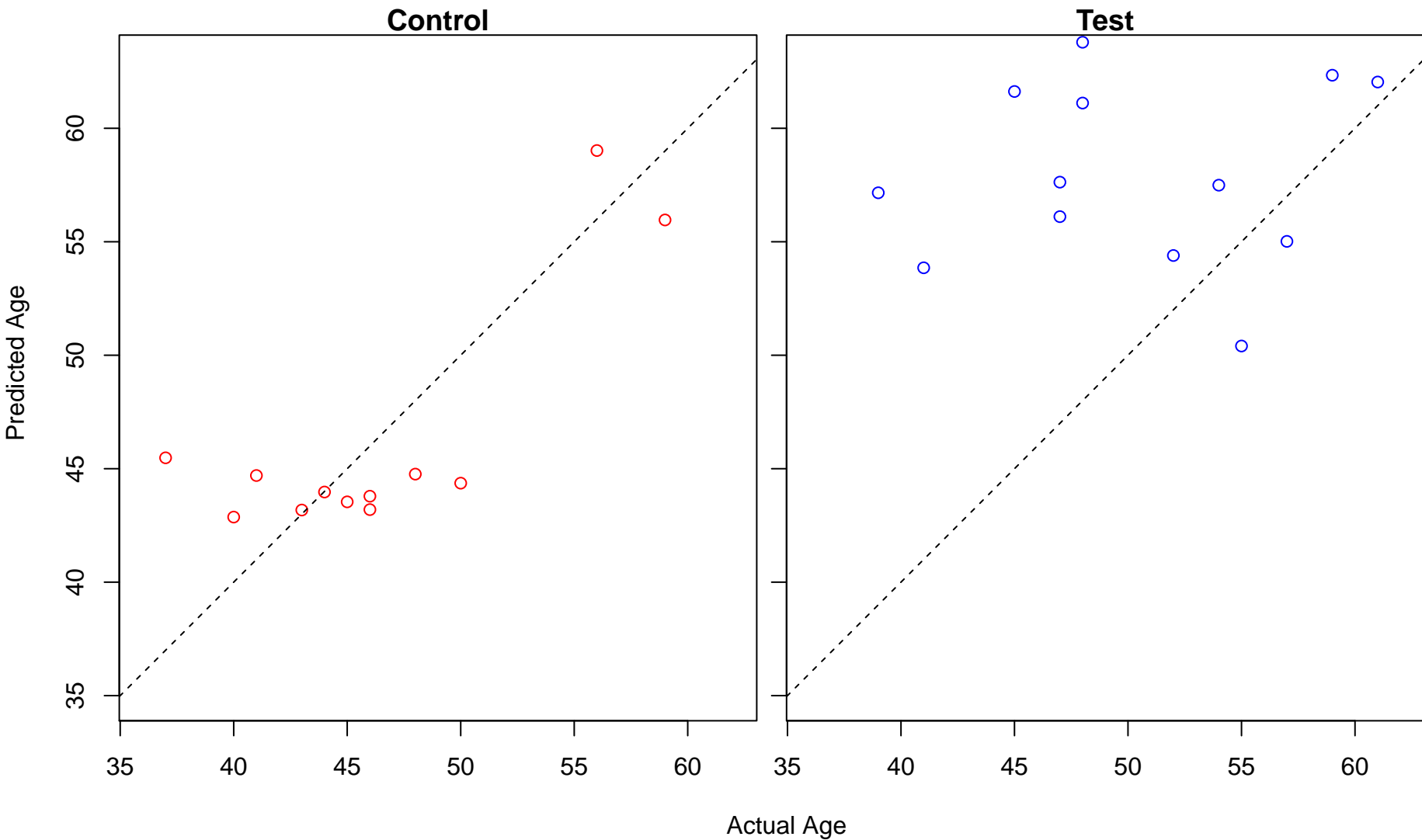
regulation of glucocorticoid biosynthetic process (Score: 2.993949)



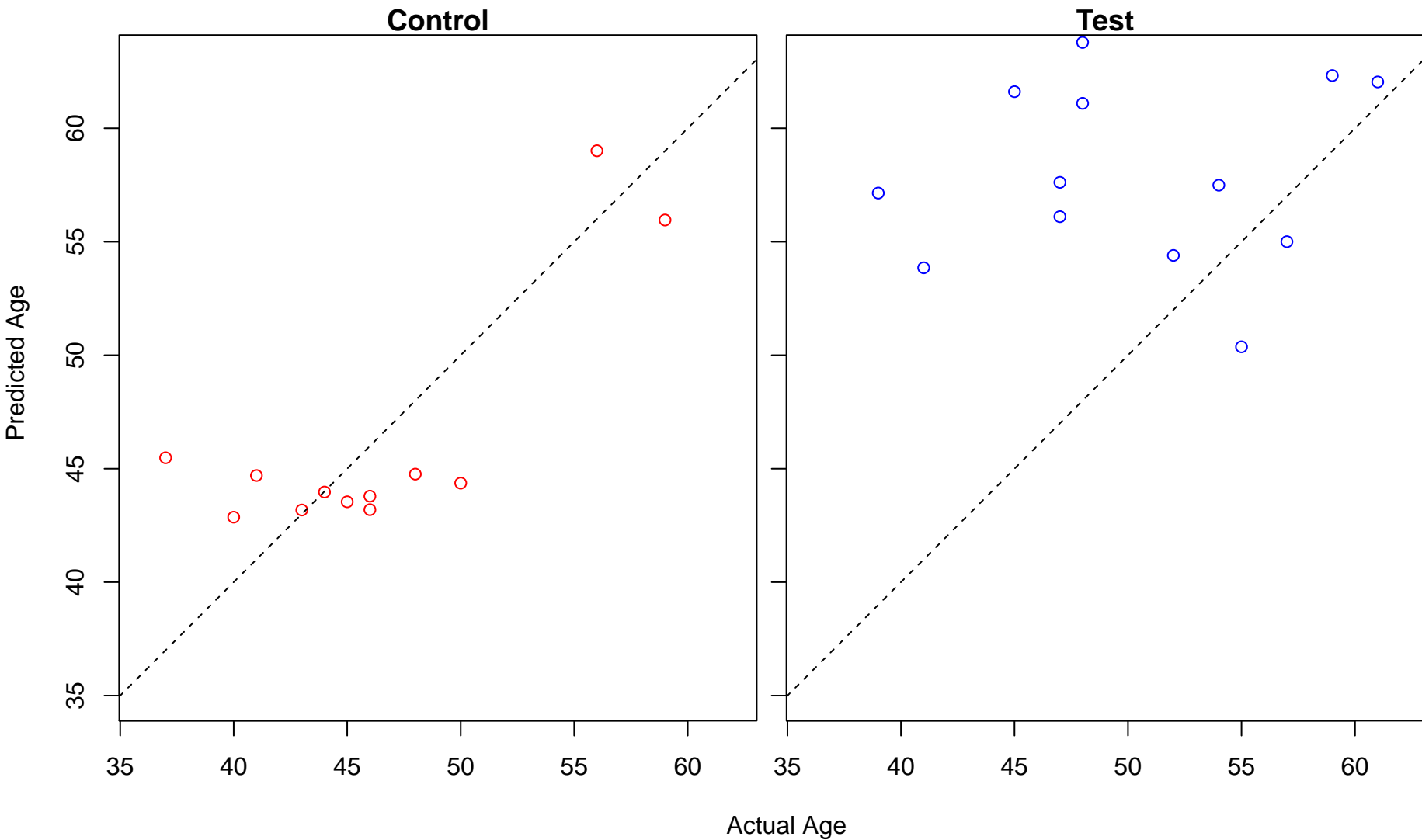
negative regulation of hormone biosynthetic process (Score: 2.993949)



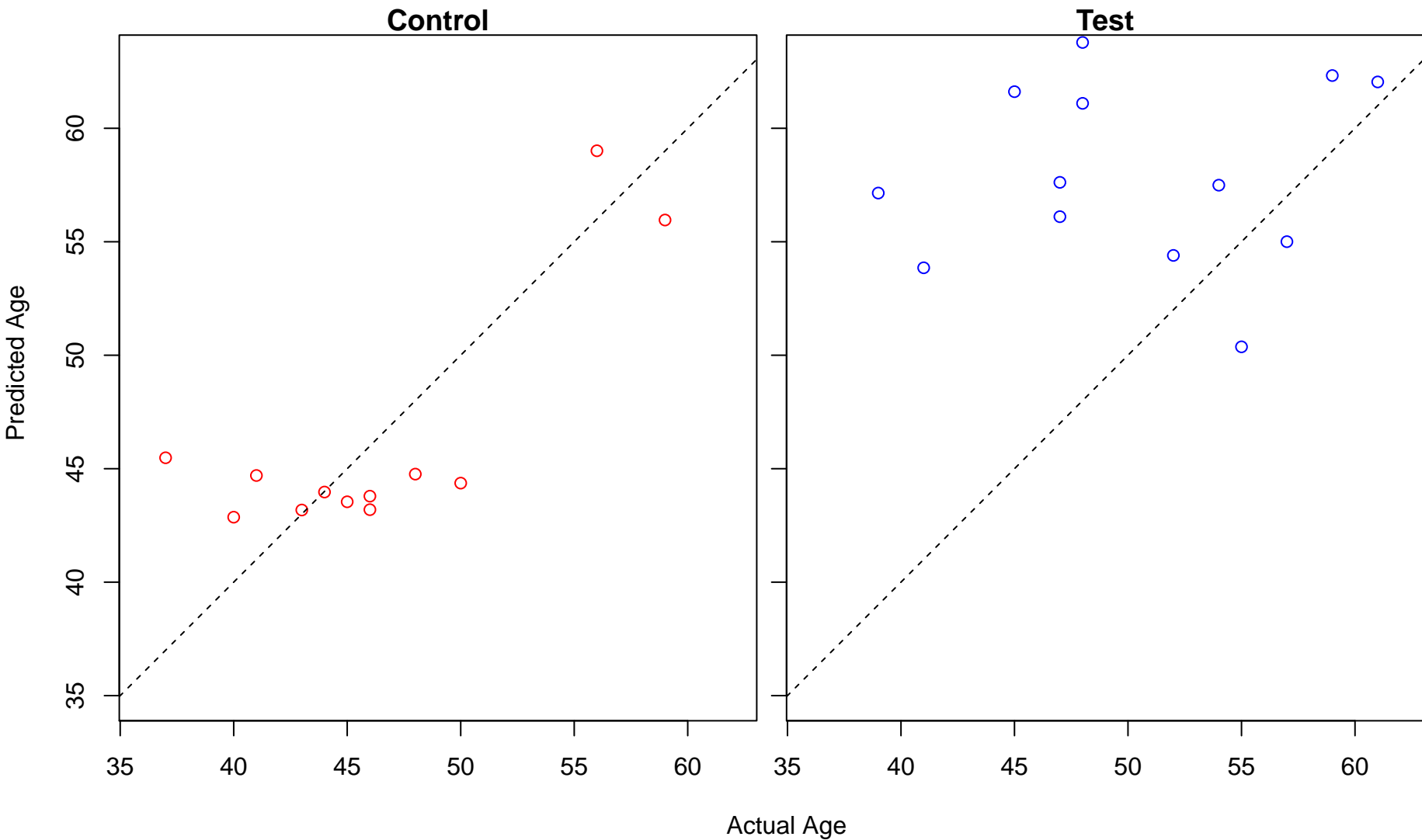
regulation of cortisol biosynthetic process (Score: 2.993949)



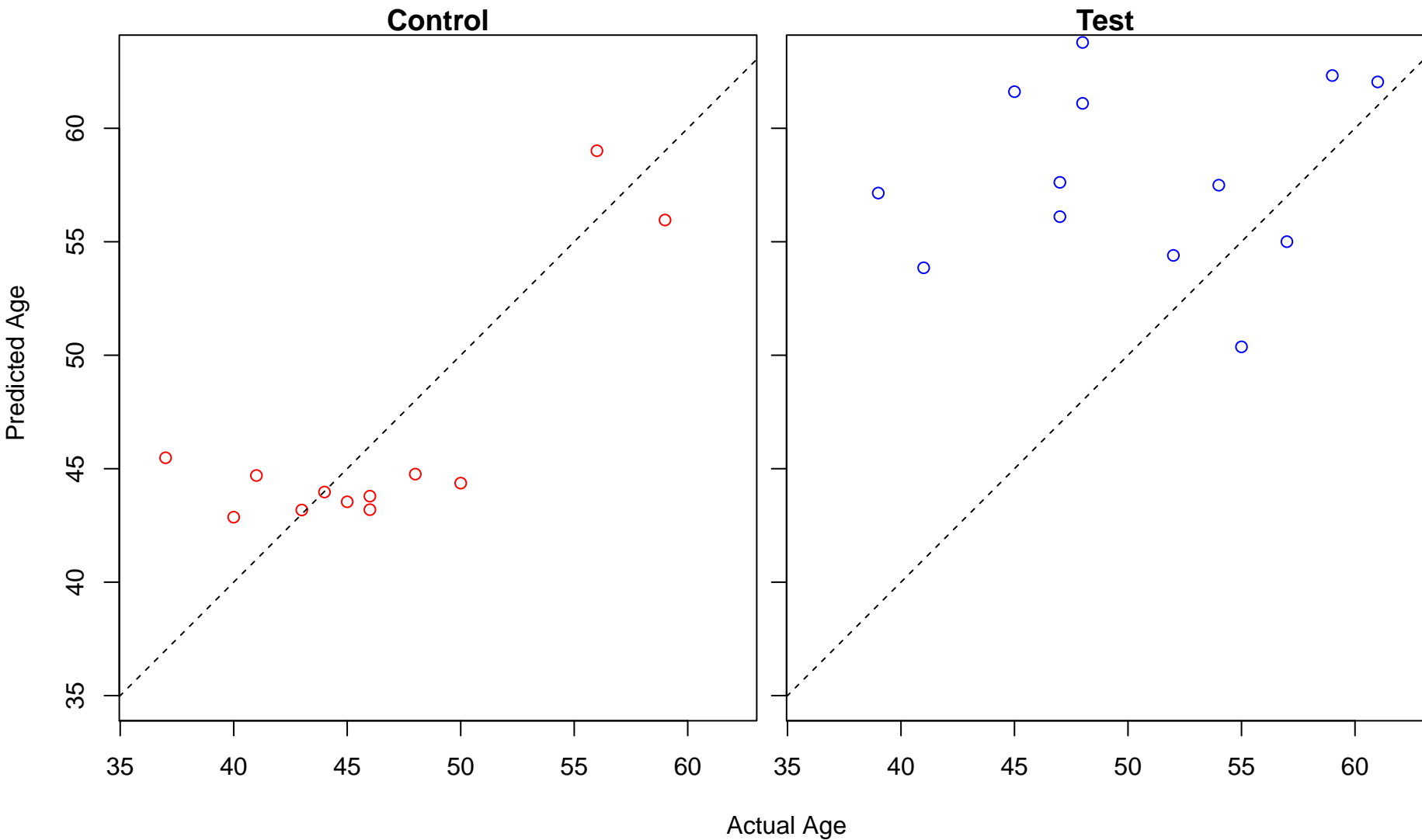
regulation of aldosterone metabolic process (Score: 2.993115)



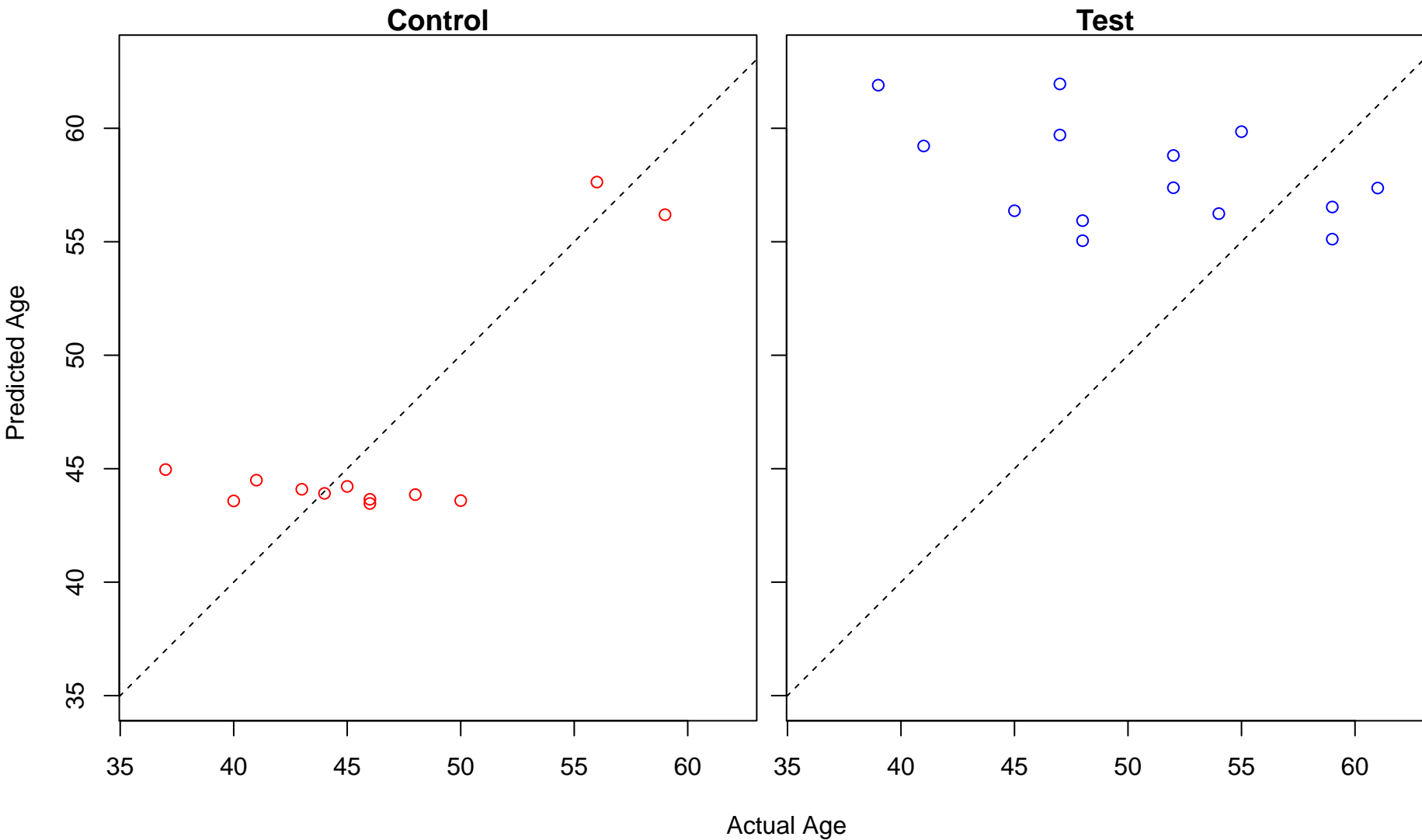
regulation of aldosterone biosynthetic process (Score: 2.993115)



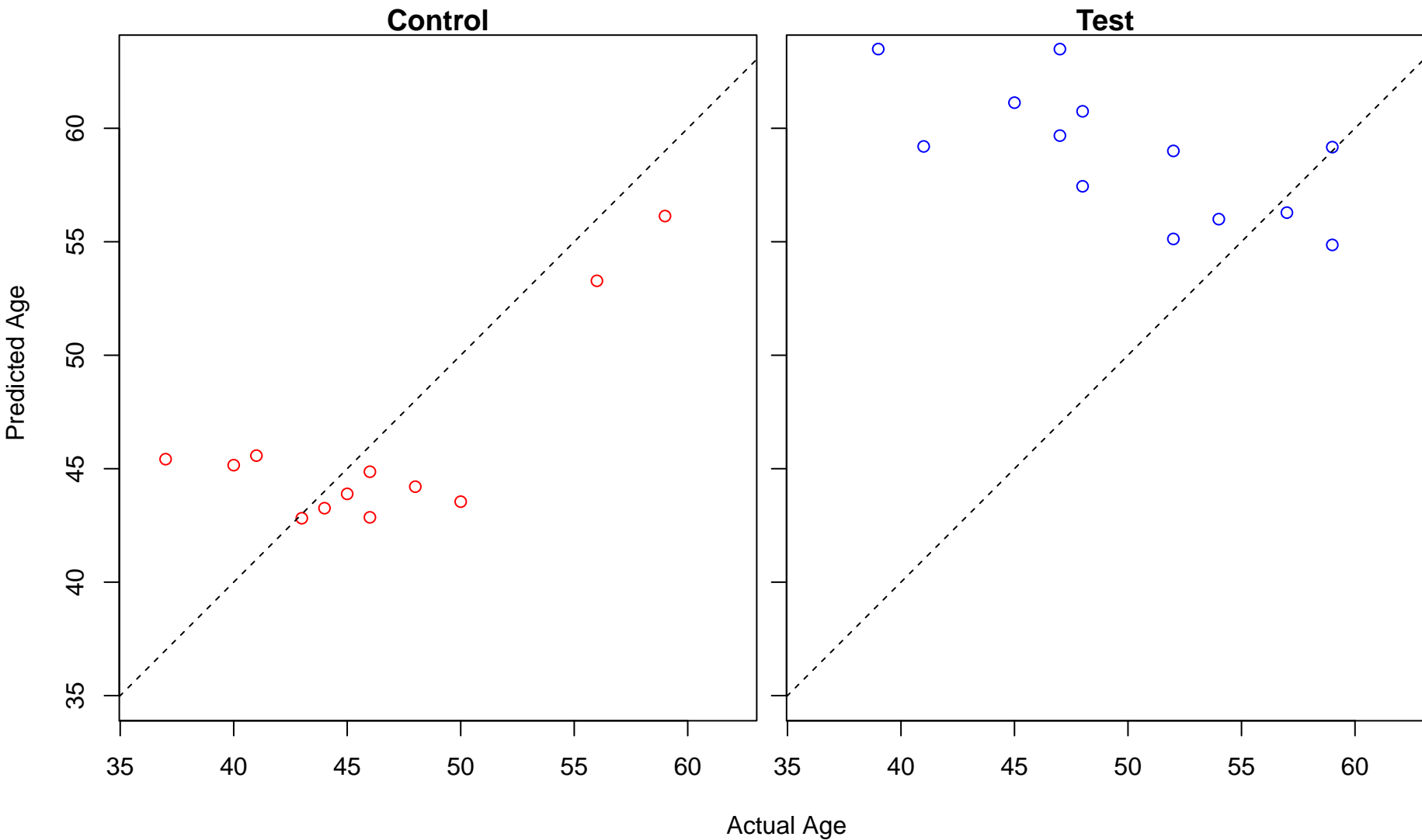
regulation of steroid hormone biosynthetic process (Score: 2.993115)



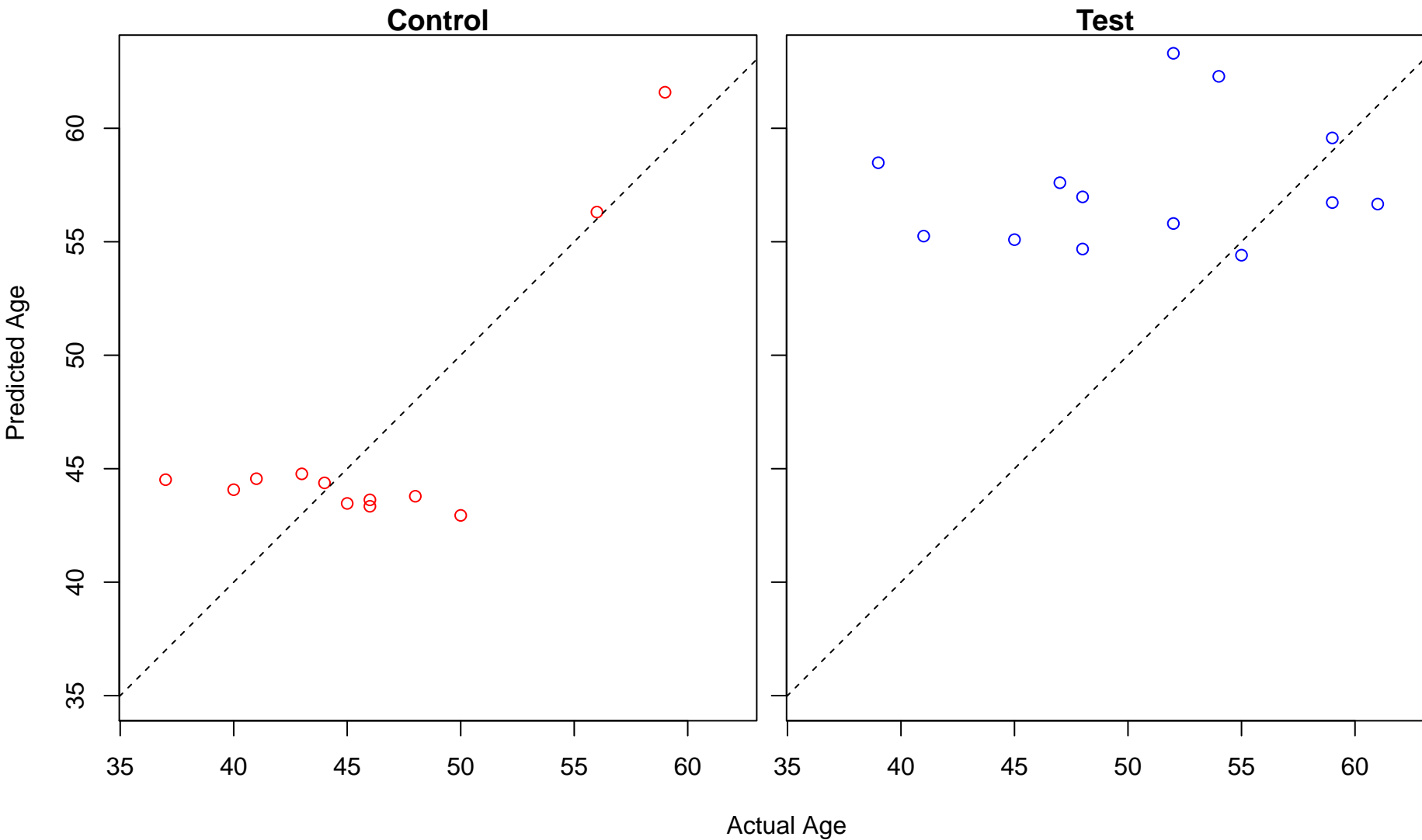
cellular chemical homeostasis (Score: 2.988603)



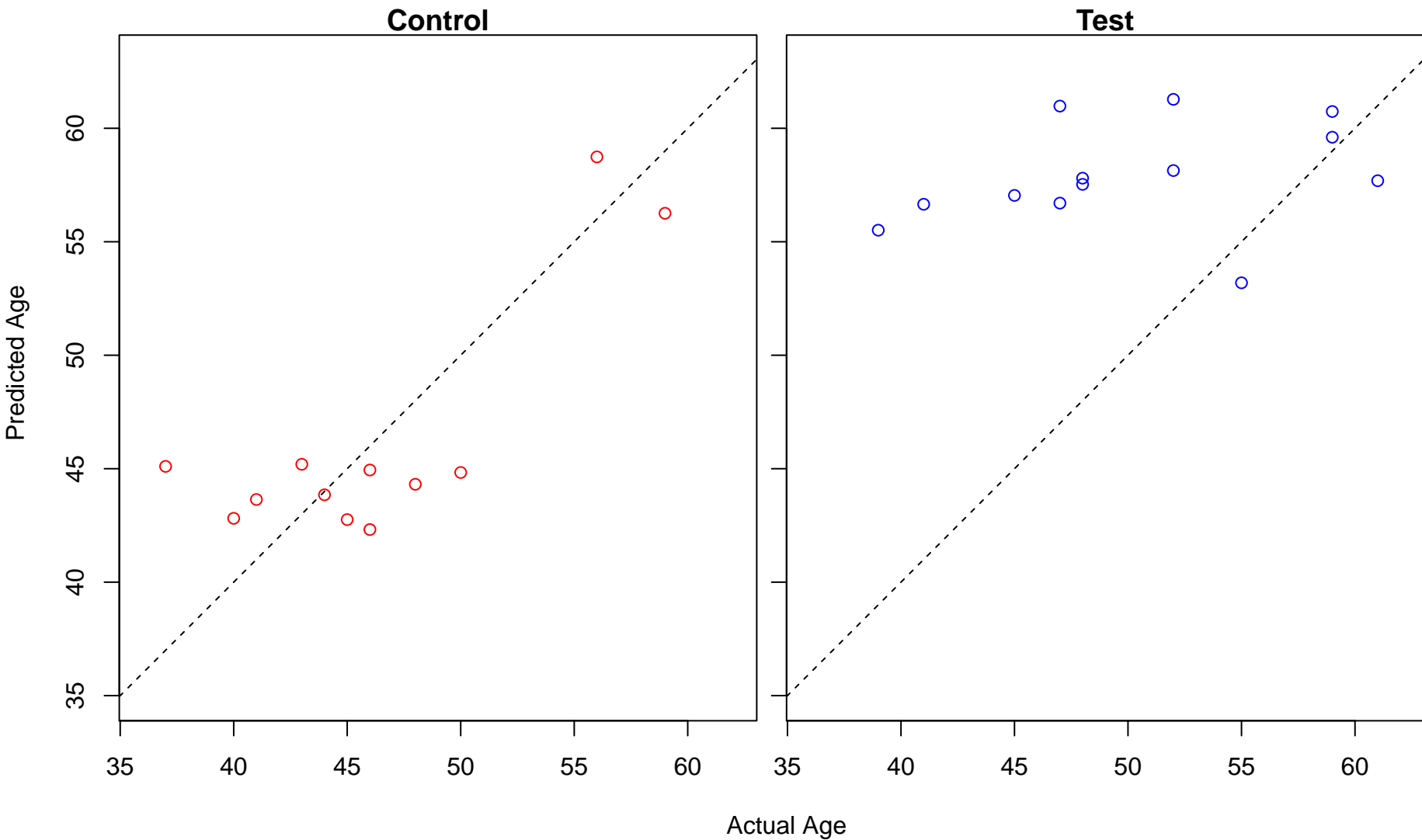
chemosensory behavior (Score: 2.988086)



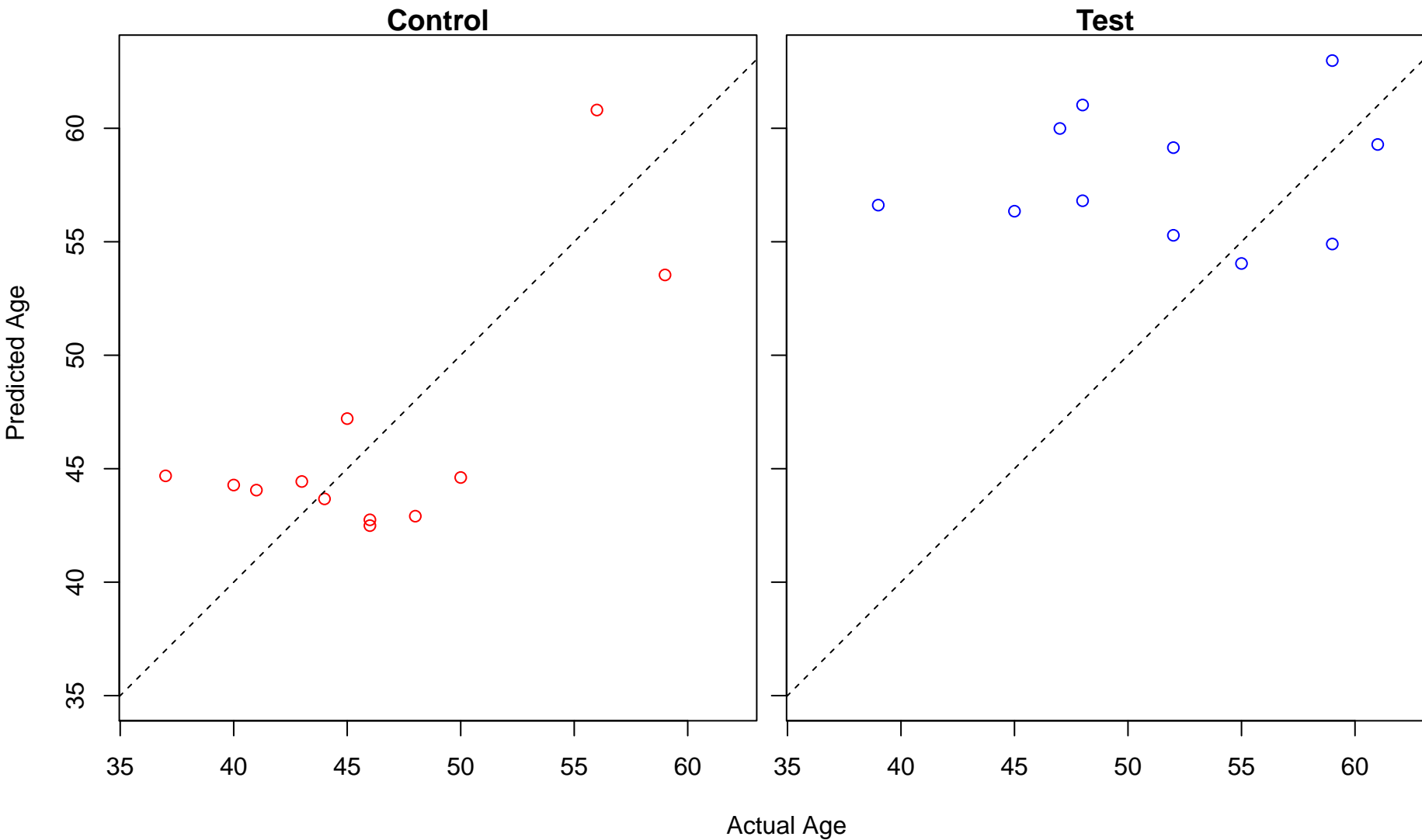
regulation of lyase activity (Score: 2.984341)



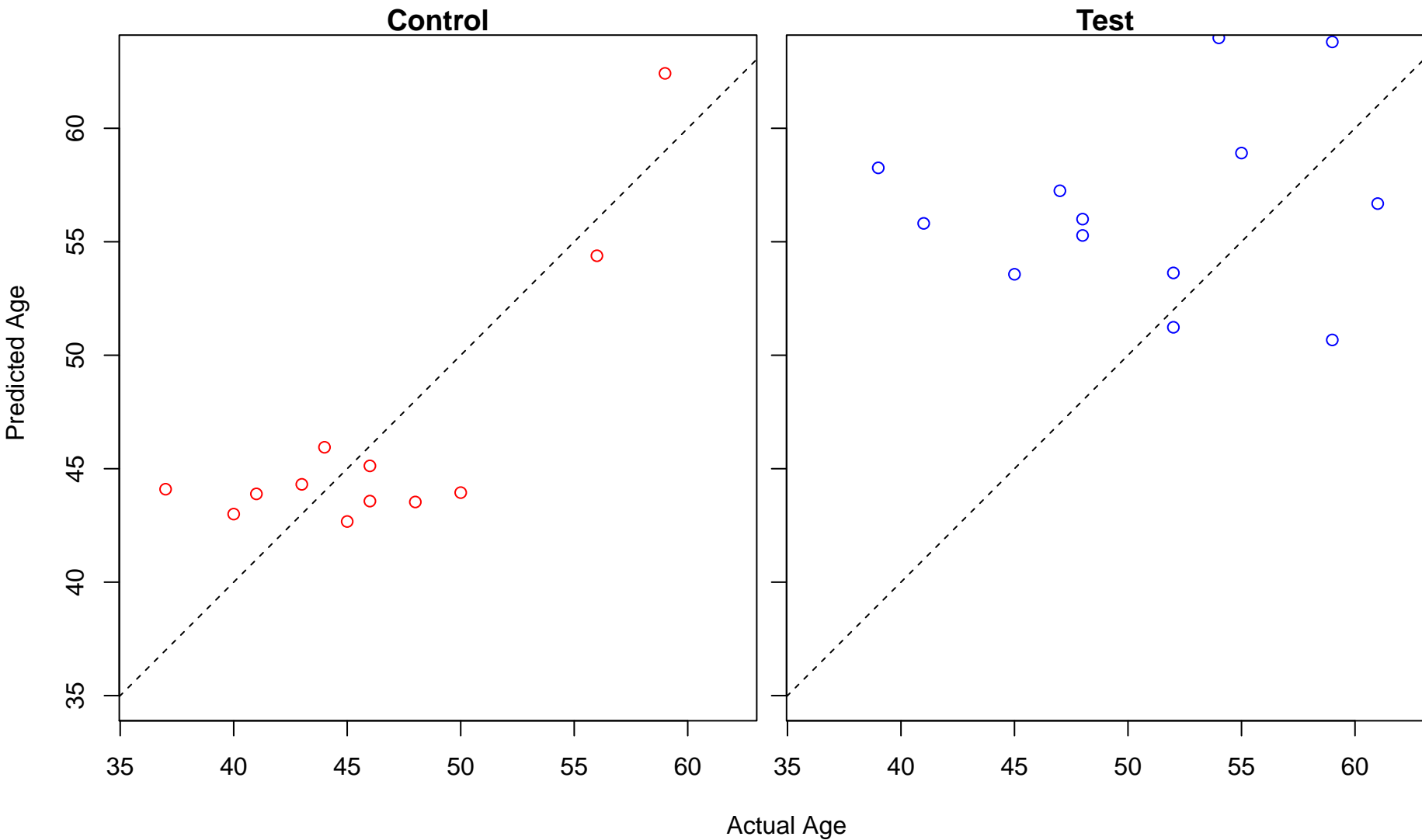
regulation of synaptic transmission, GABAergic (Score: 2.984037)



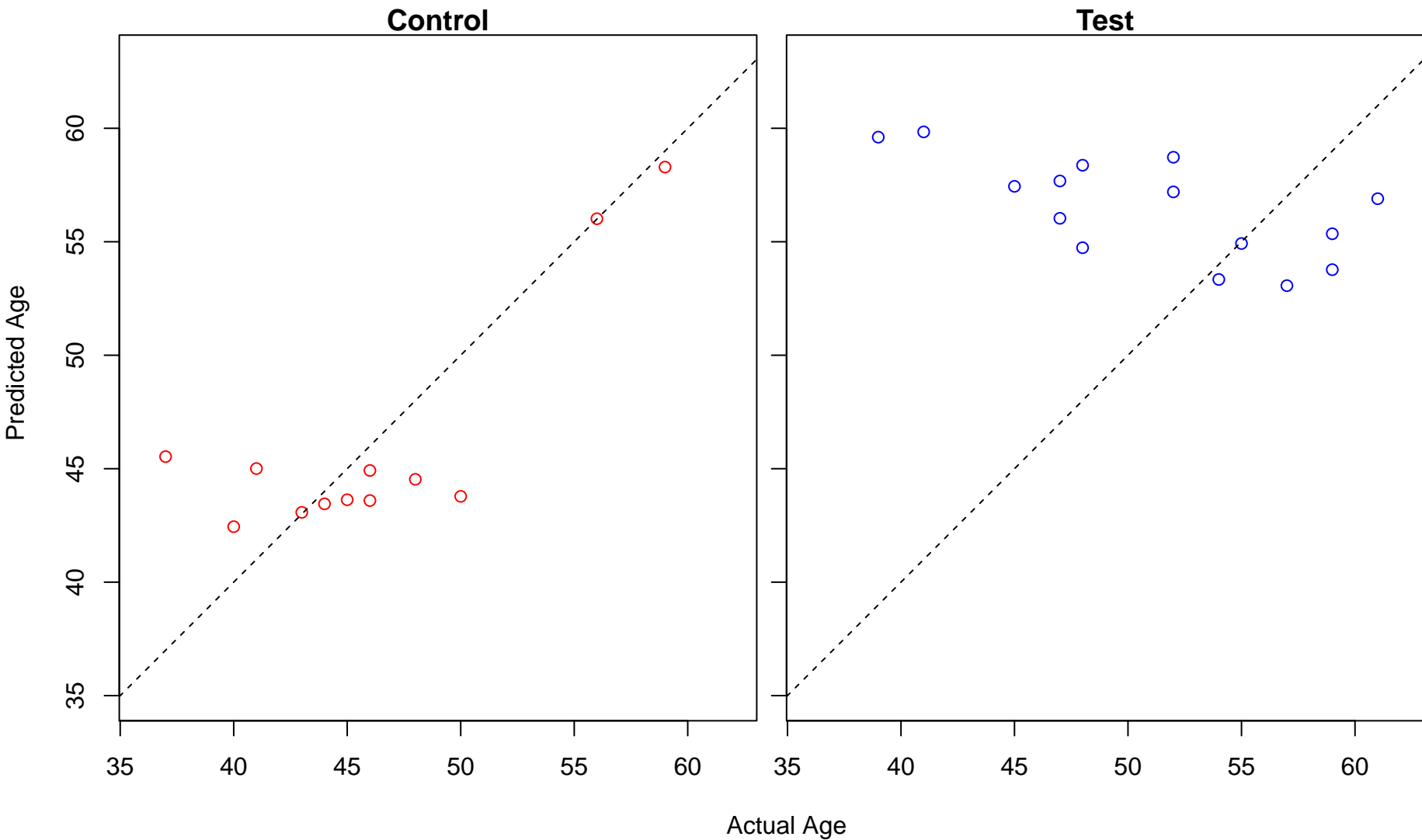
regulation of tissue remodeling (Score: 2.982441)



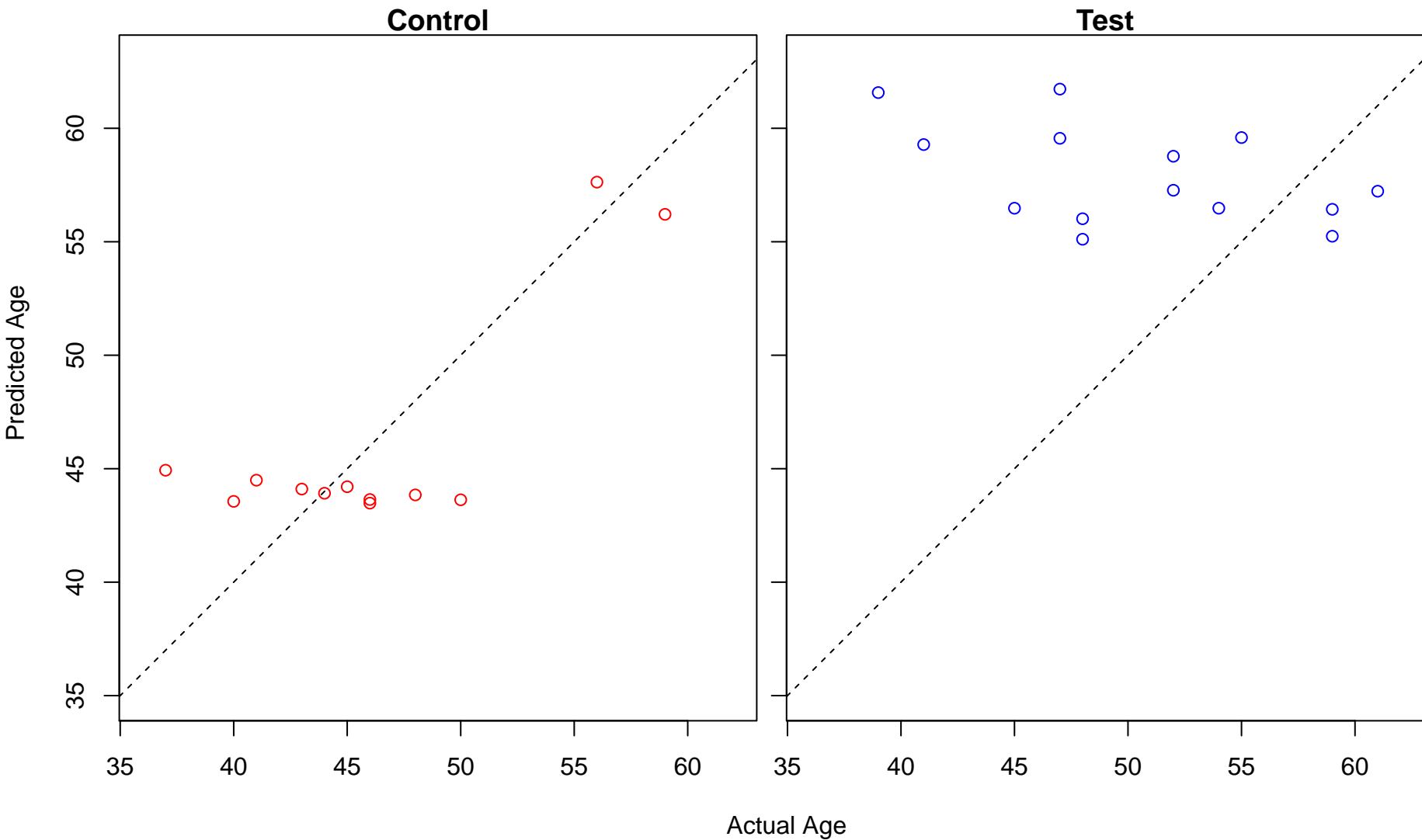
actin filament severing (Score: 2.982044)



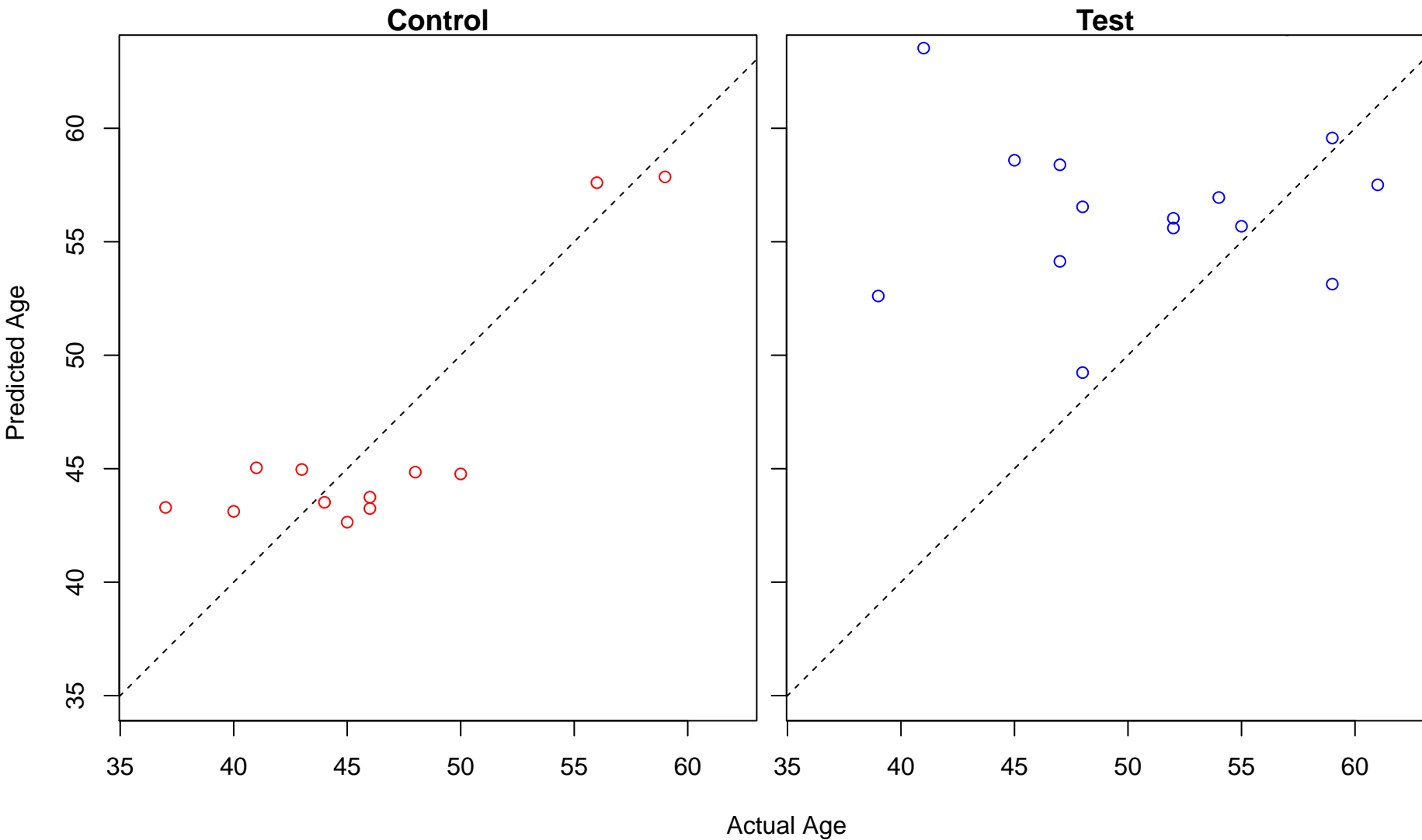
apoptotic nuclear changes (Score: 2.981096)



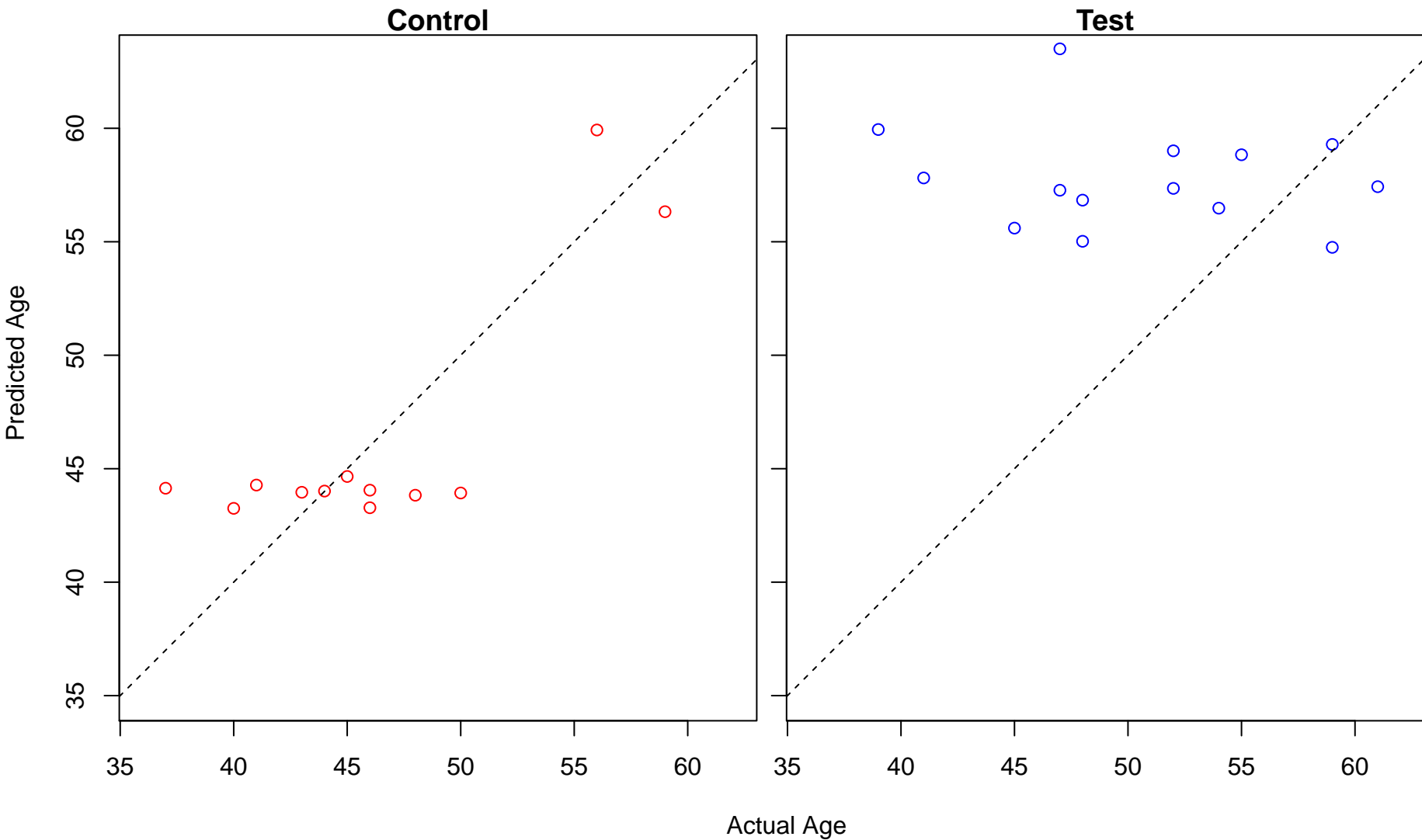
cellular homeostasis (Score: 2.978394)



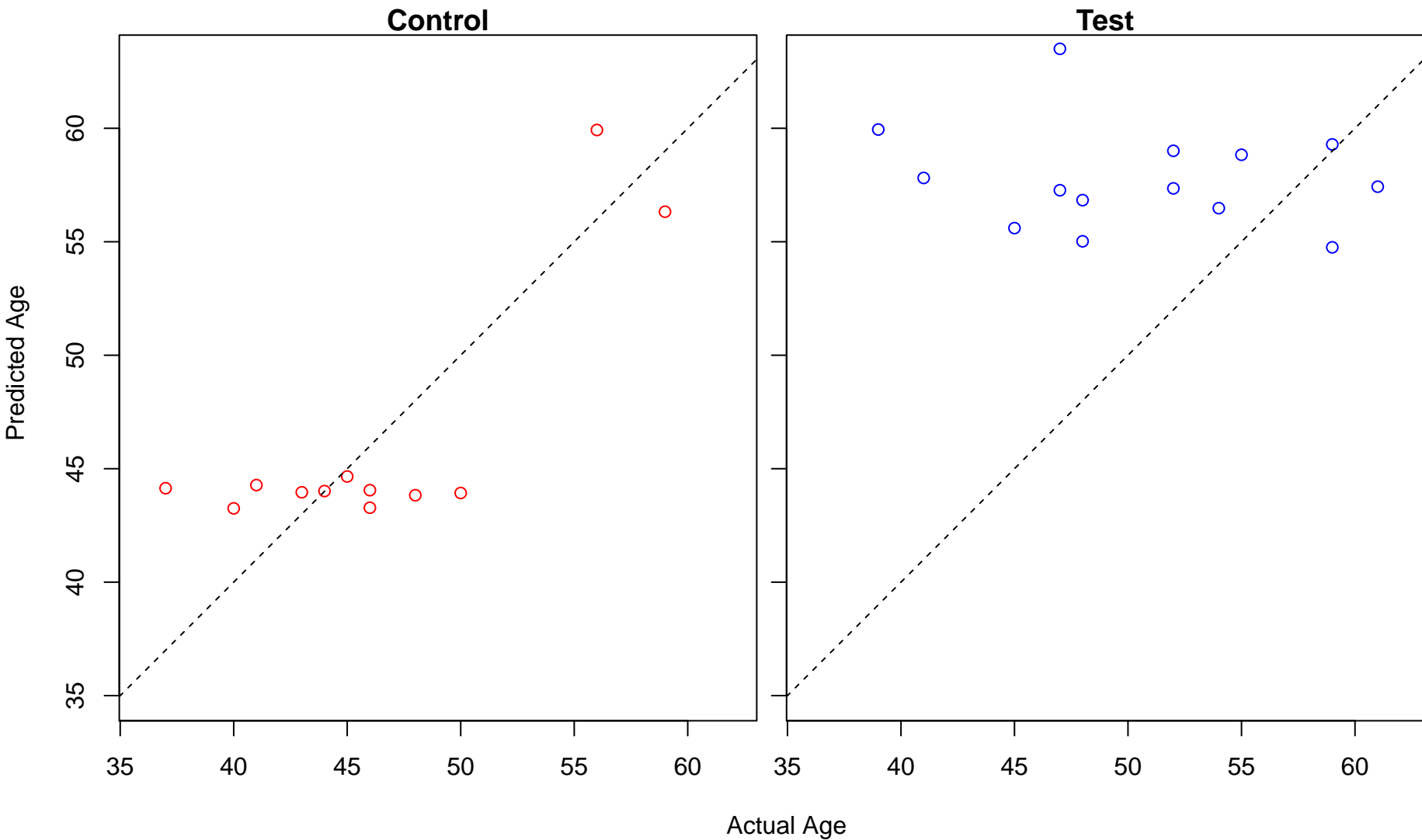
protein homooligomerization (Score: 2.978212)



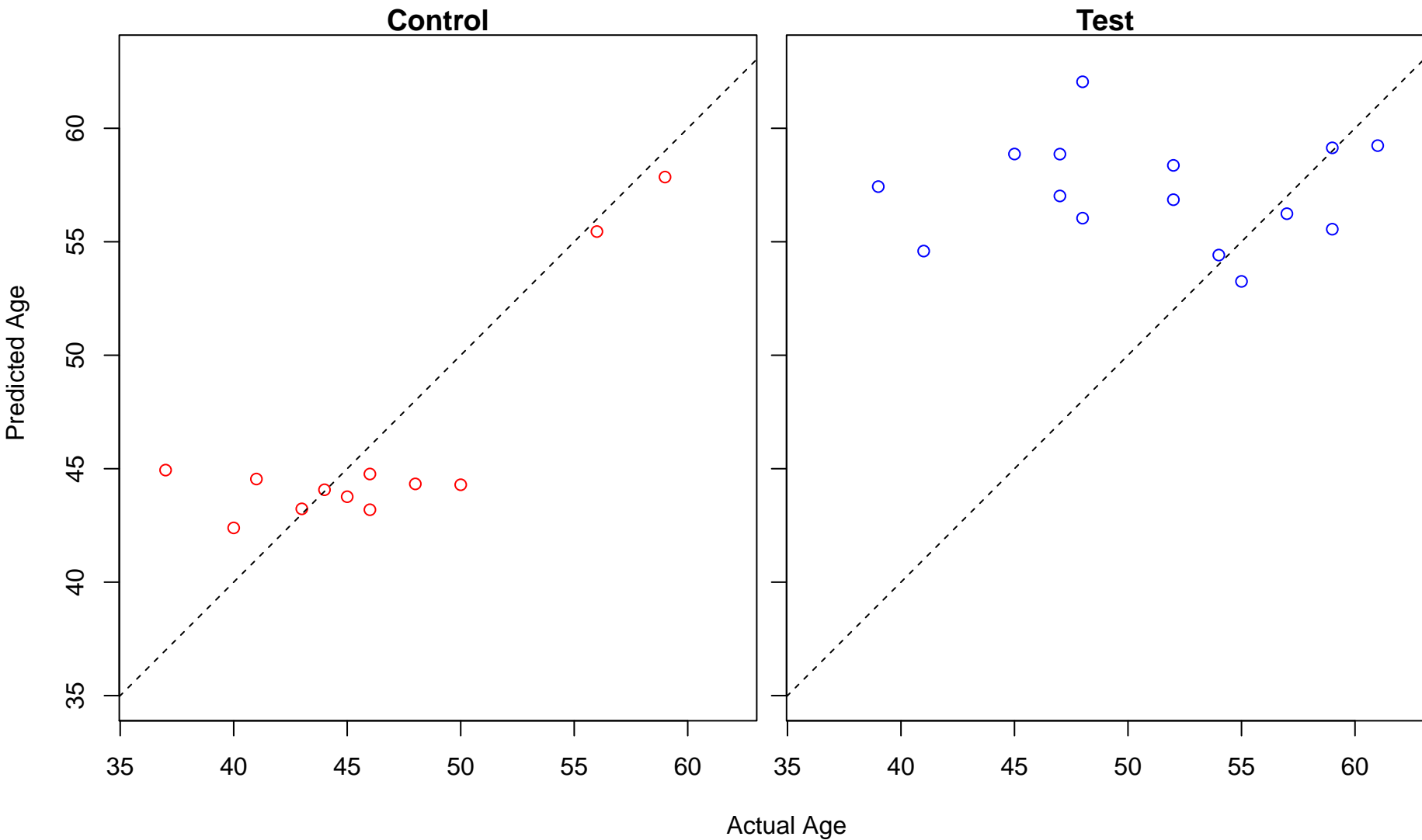
G2/M transition of mitotic cell cycle (Score: 2.974507)



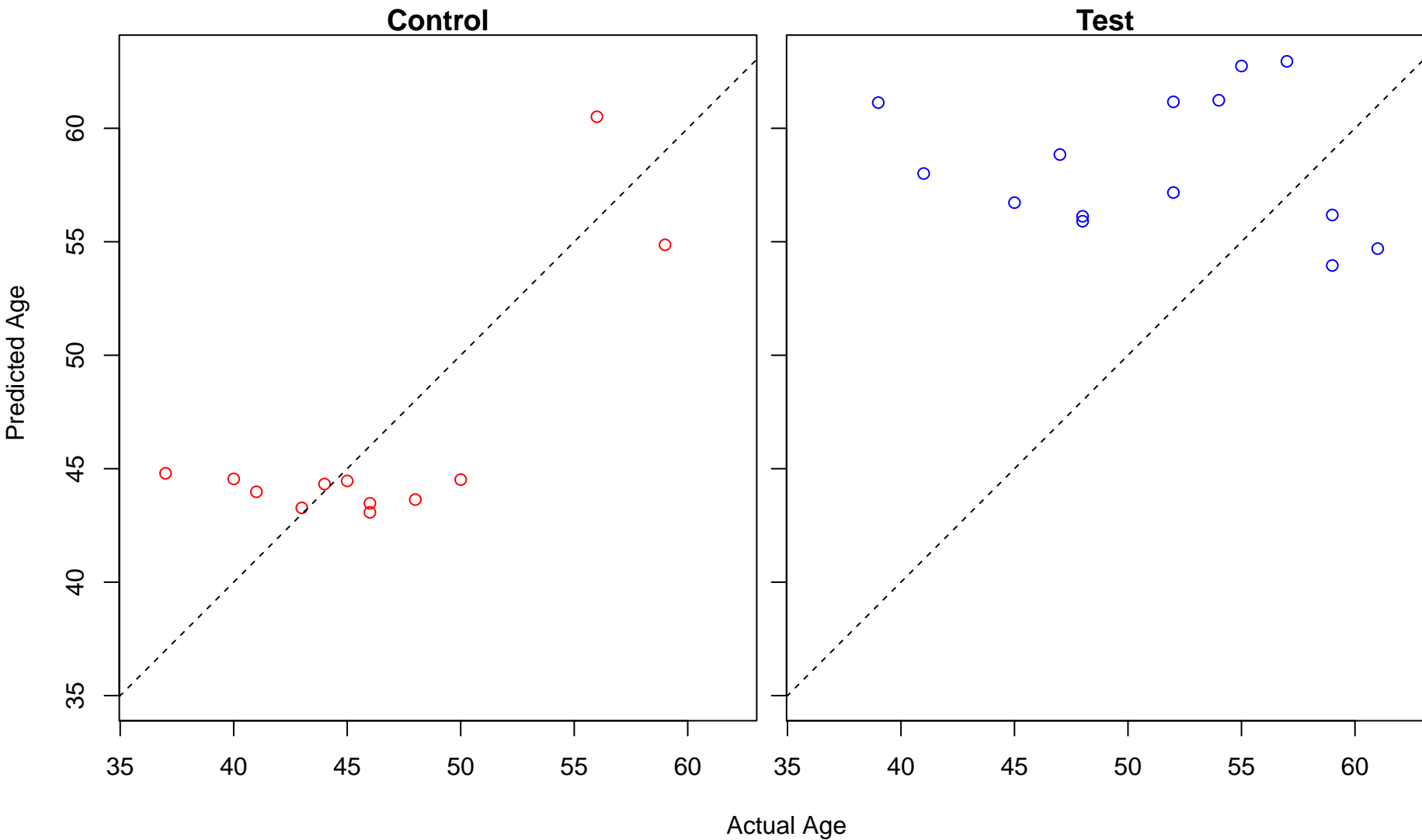
cell cycle G2/M phase transition (Score: 2.974507)



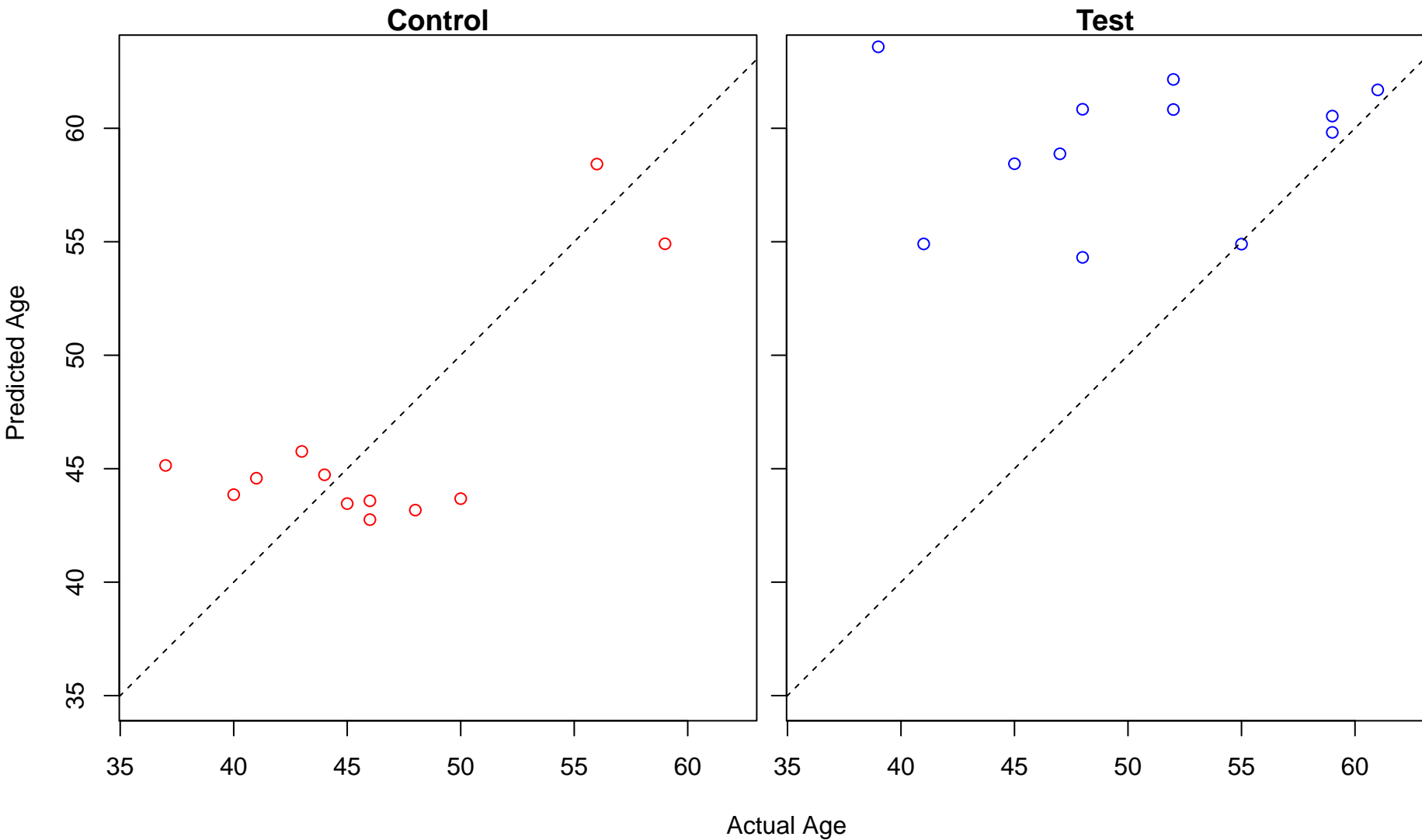
ganglion development (Score: 2.974202)



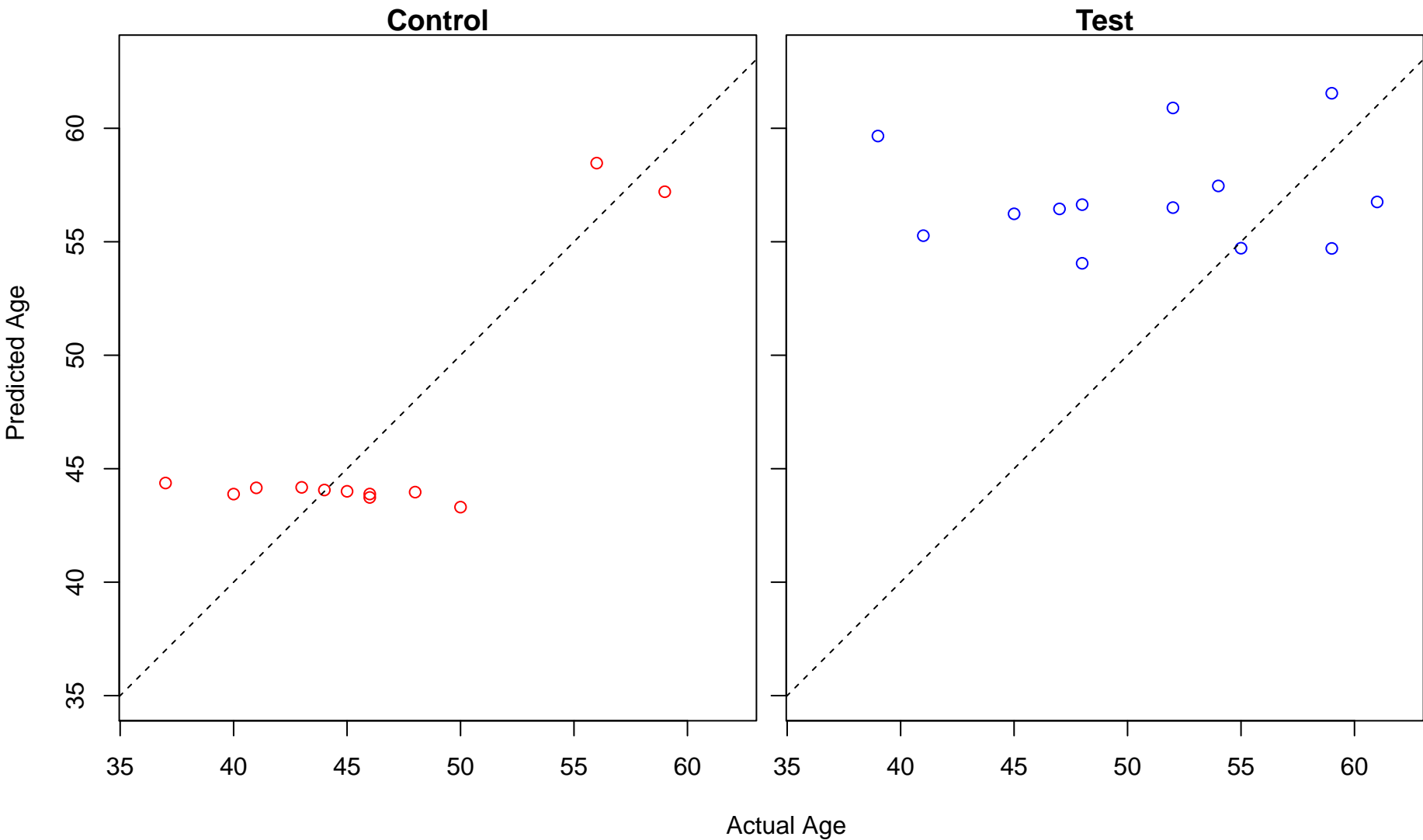
cellular senescence (Score: 2.972265)



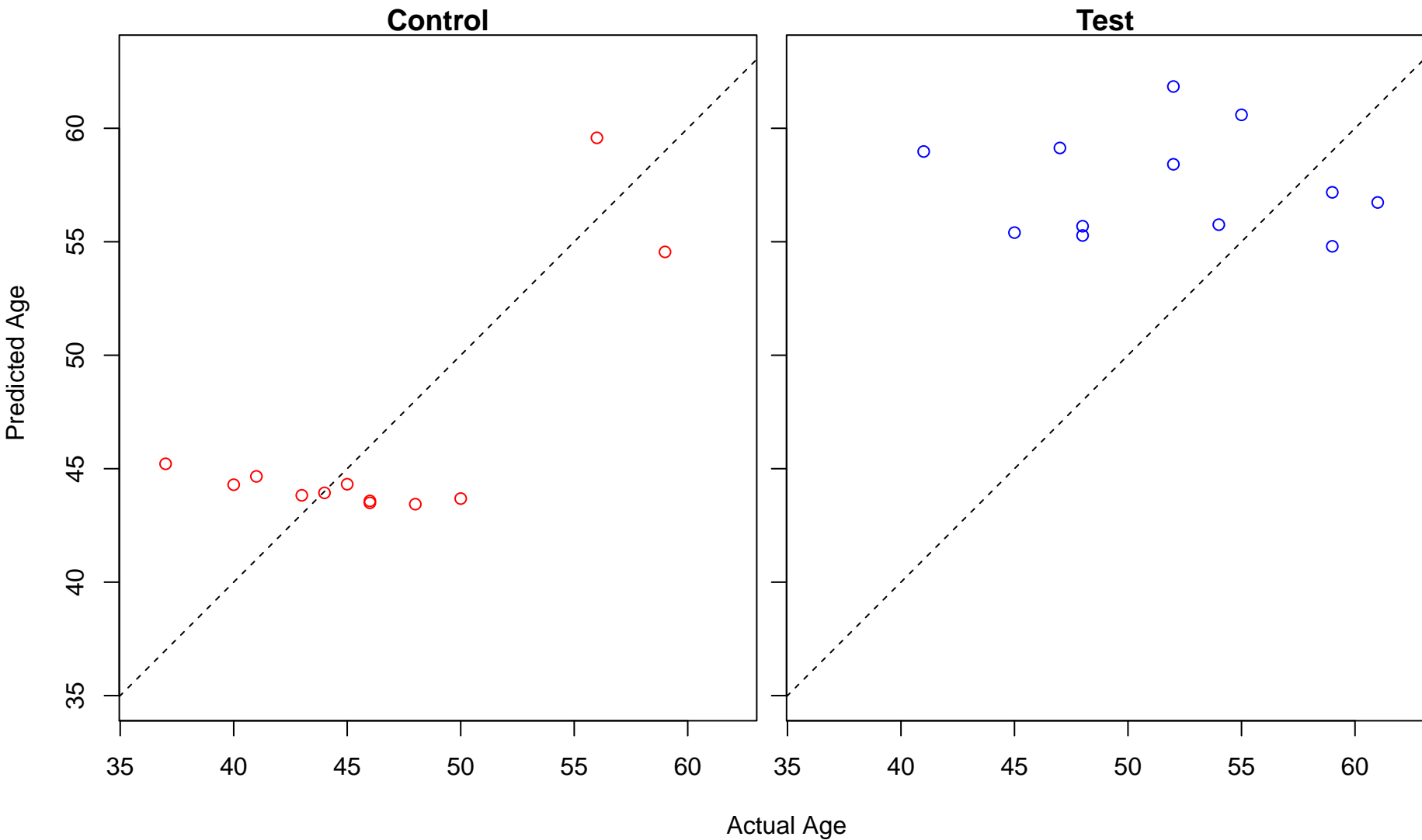
cellular response to vascular endothelial growth factor stimulus (Score: 2.969051)



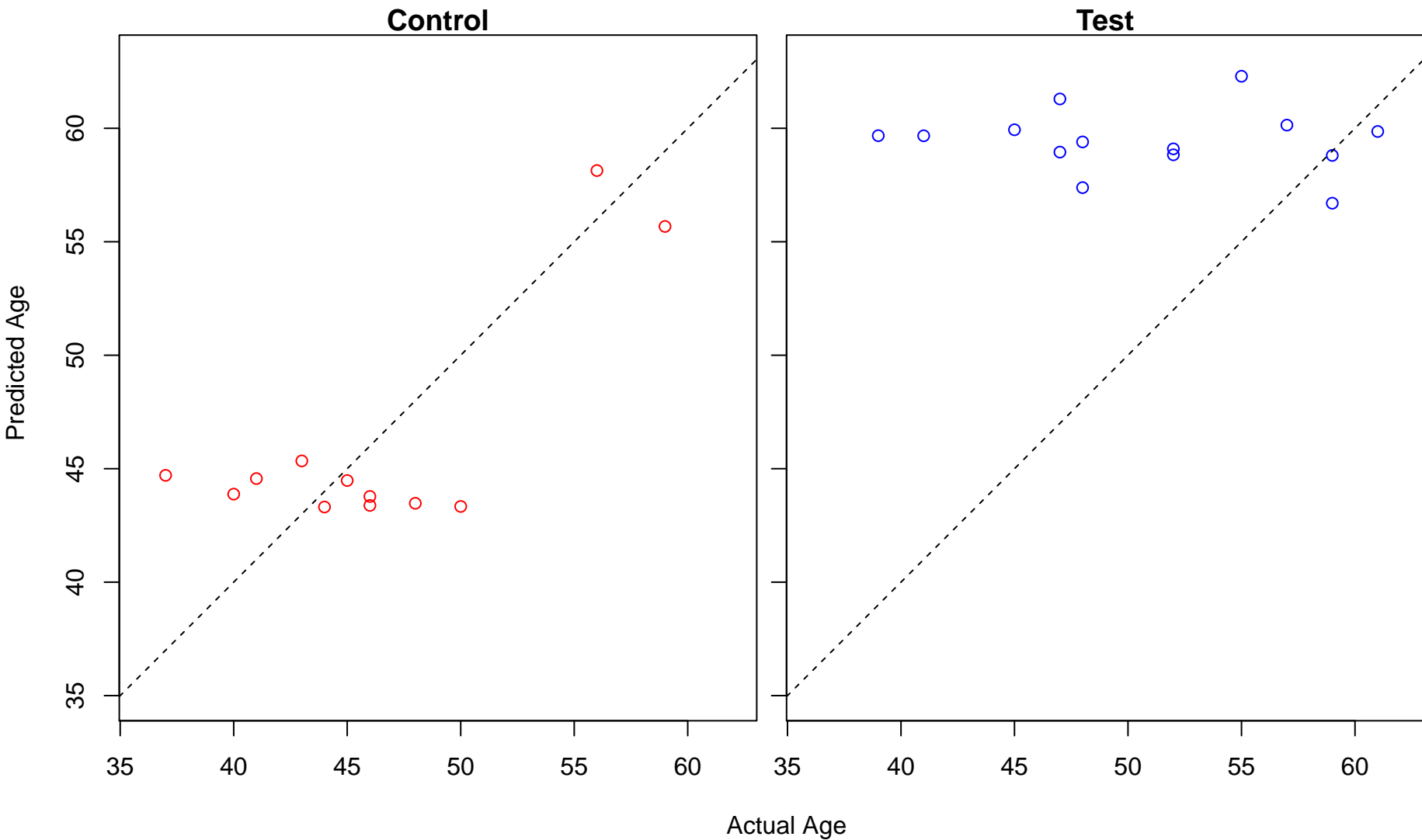
SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (Score: 2.968382)



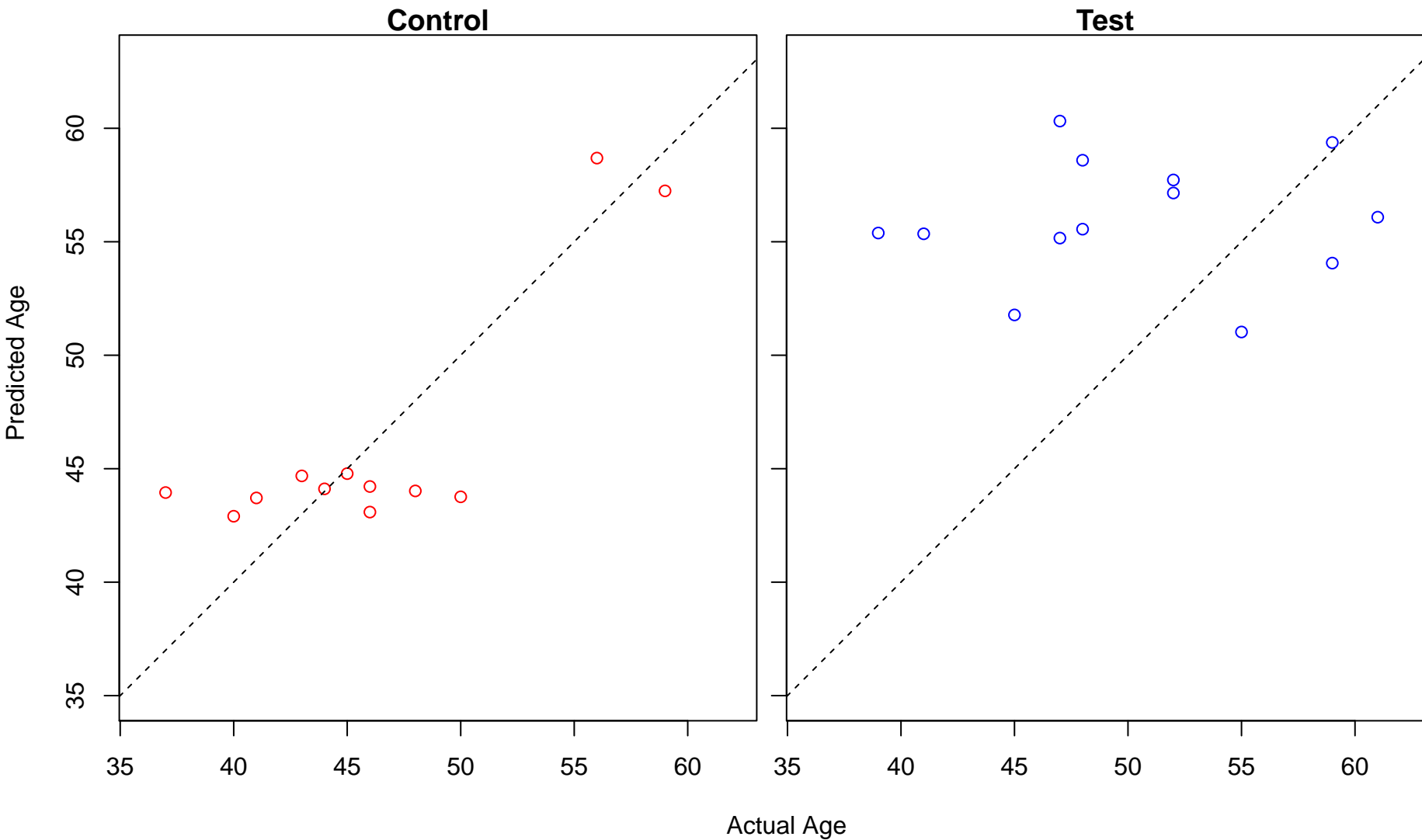
response to biotic stimulus (Score: 2.967343)



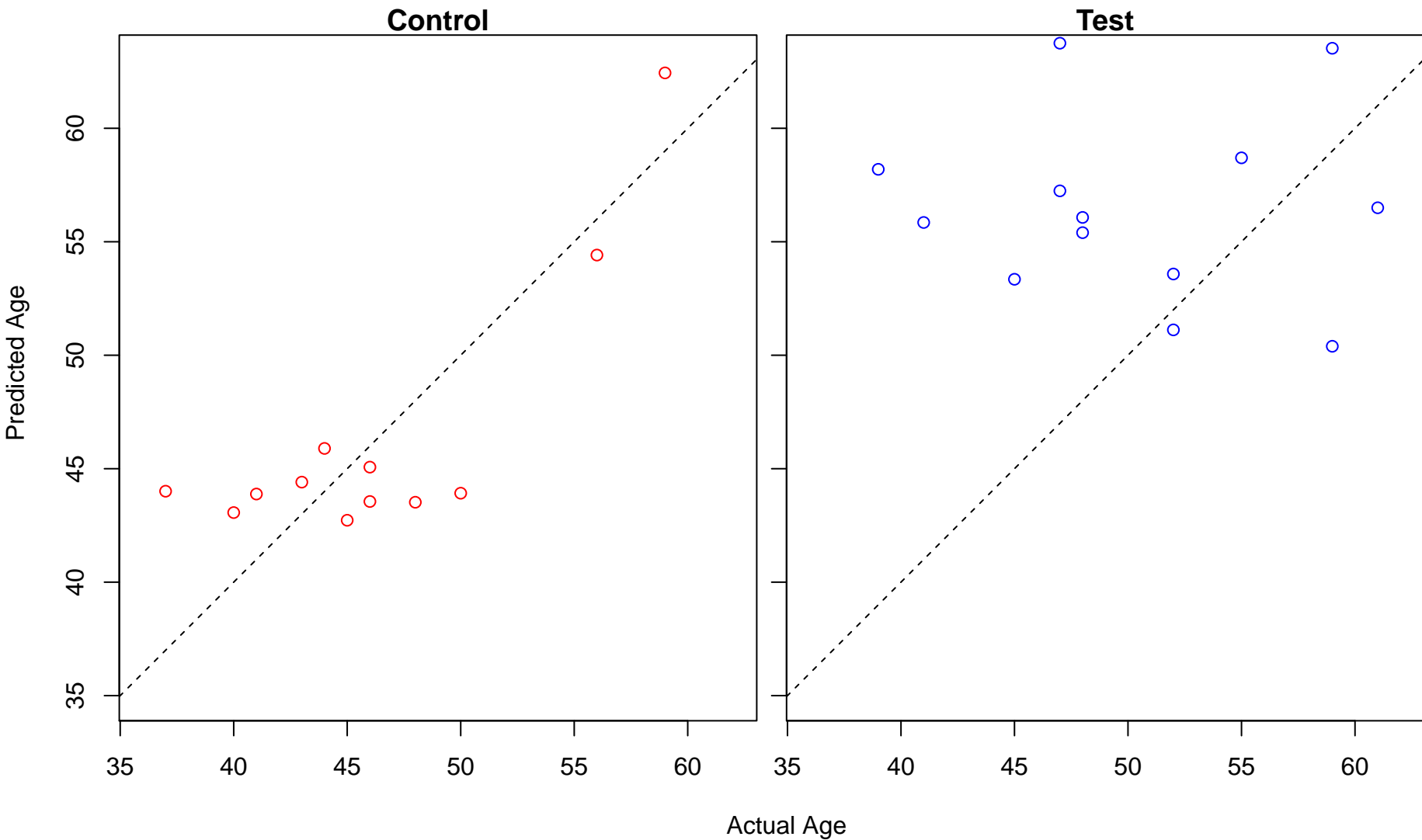
negative regulation of reactive oxygen species metabolic process (Score: 2.967214)



histone arginine methylation (Score: 2.965700)

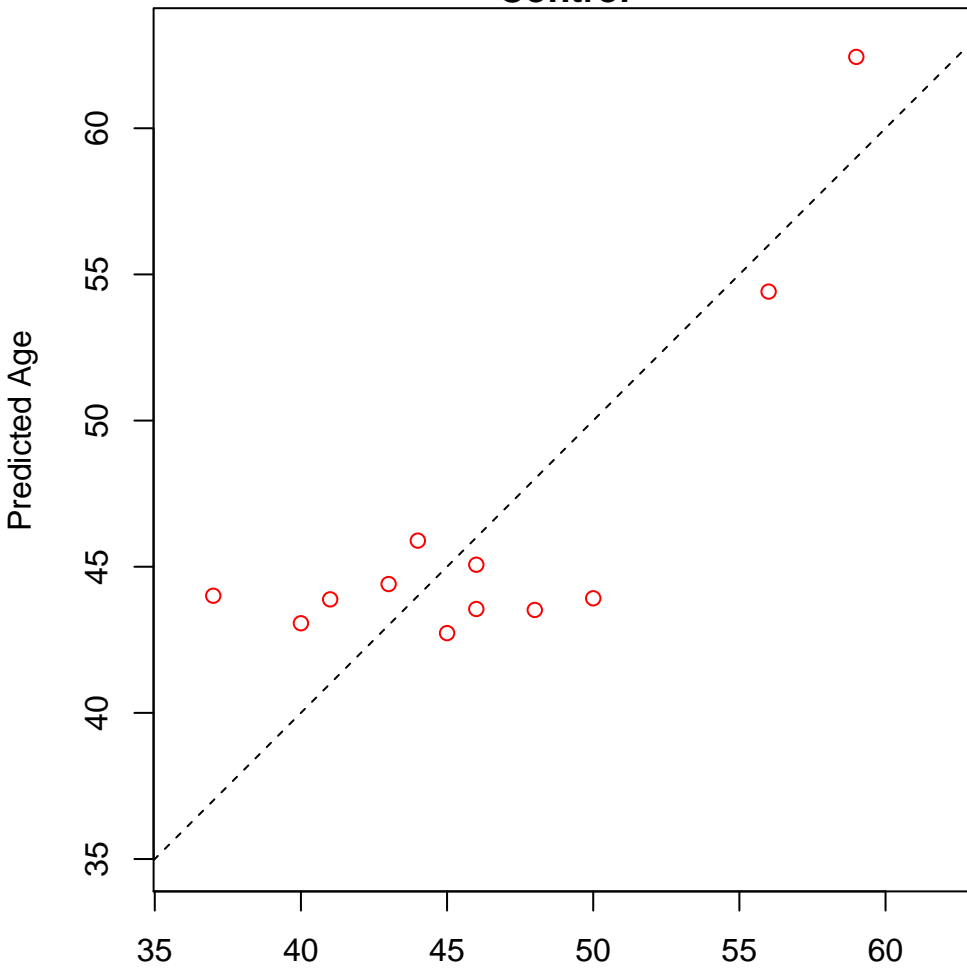


positive regulation of protein processing (Score: 2.962742)

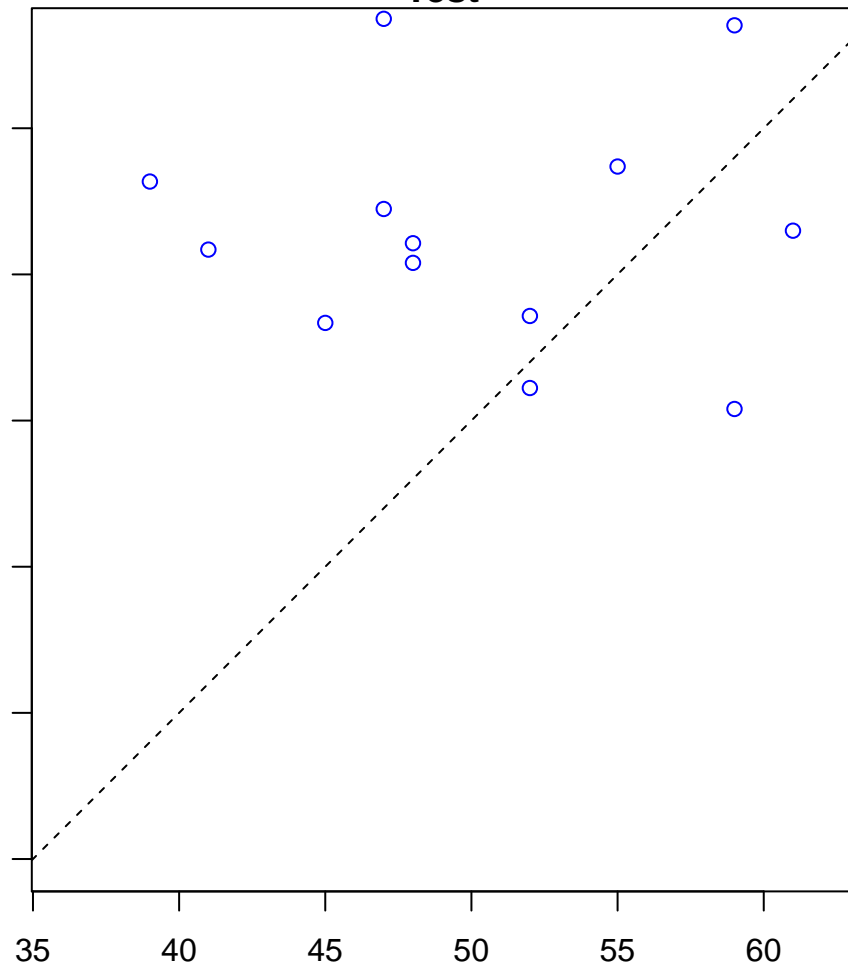


positive regulation of protein maturation (Score: 2.960666)

Control

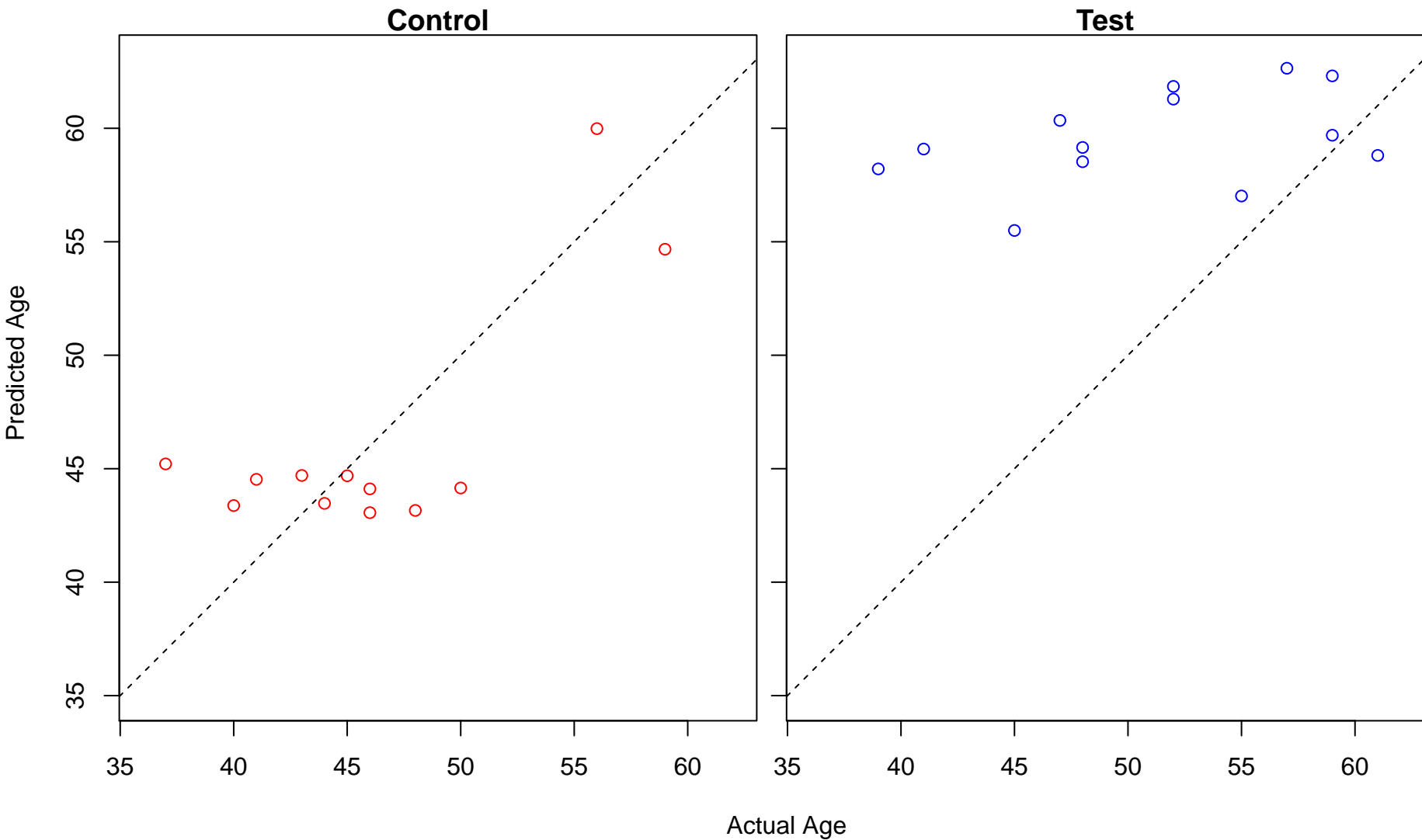


Test

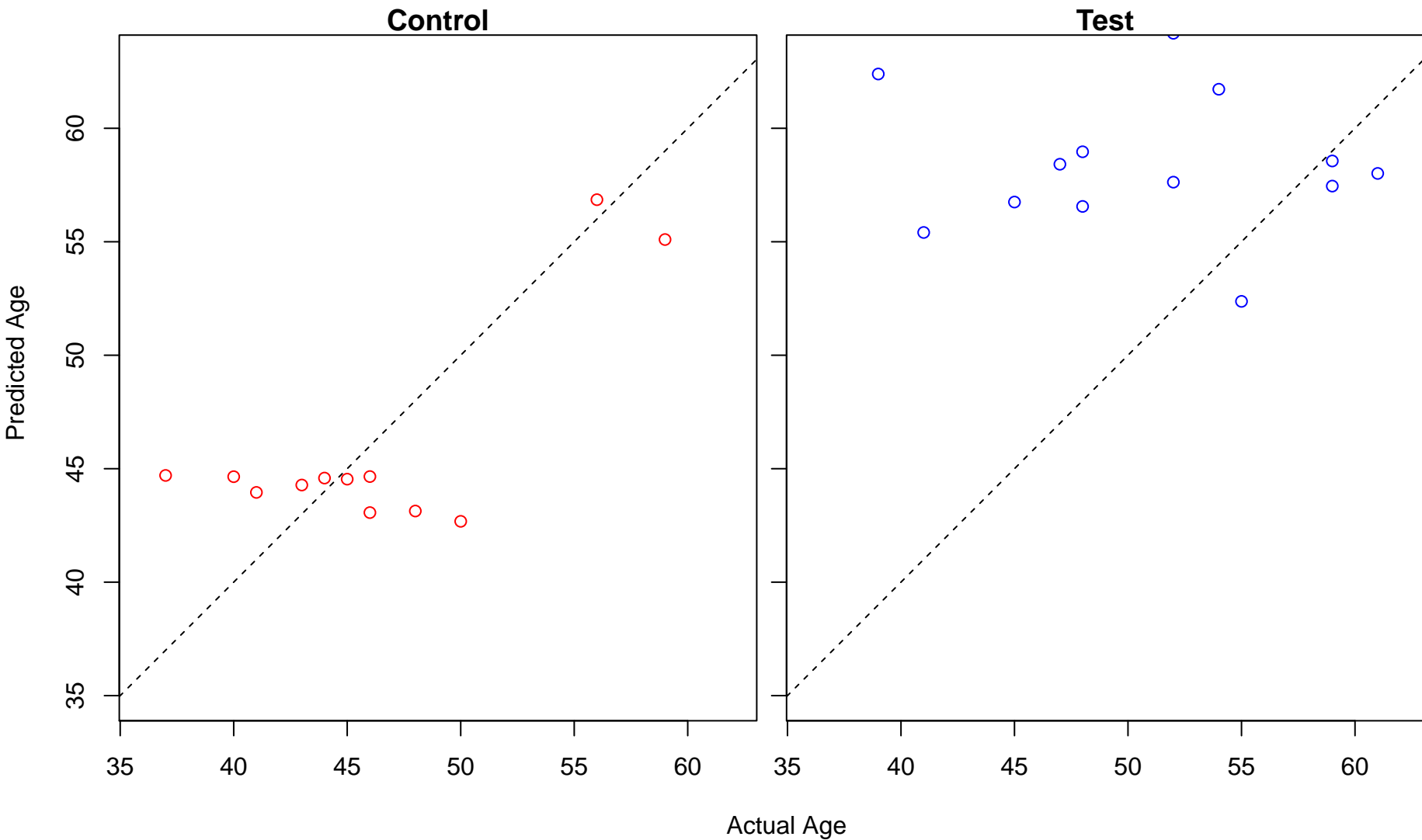


Actual Age

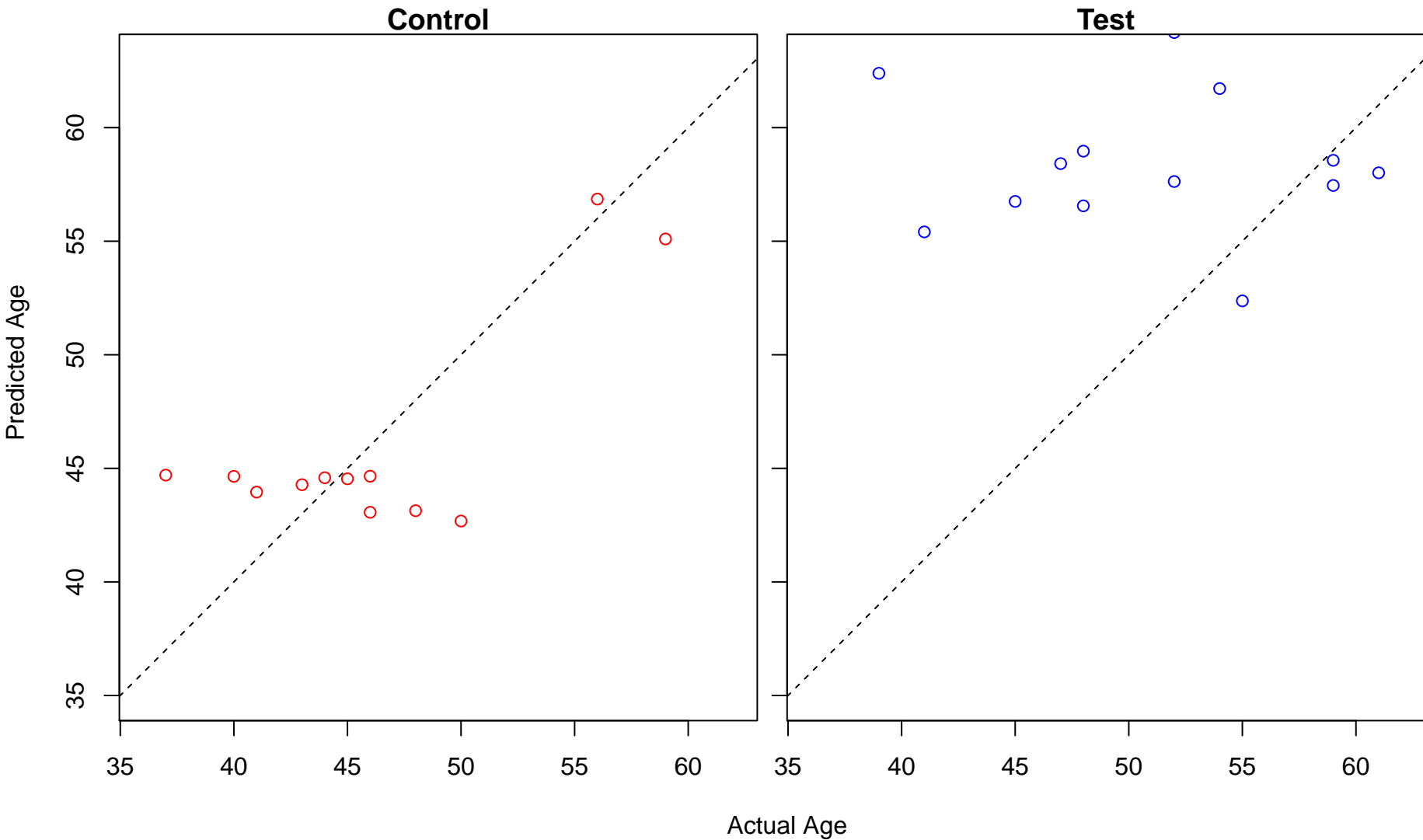
intracellular estrogen receptor signaling pathway (Score: 2.959756)



mitochondrial ATP synthesis coupled proton transport (Score: 2.959698)

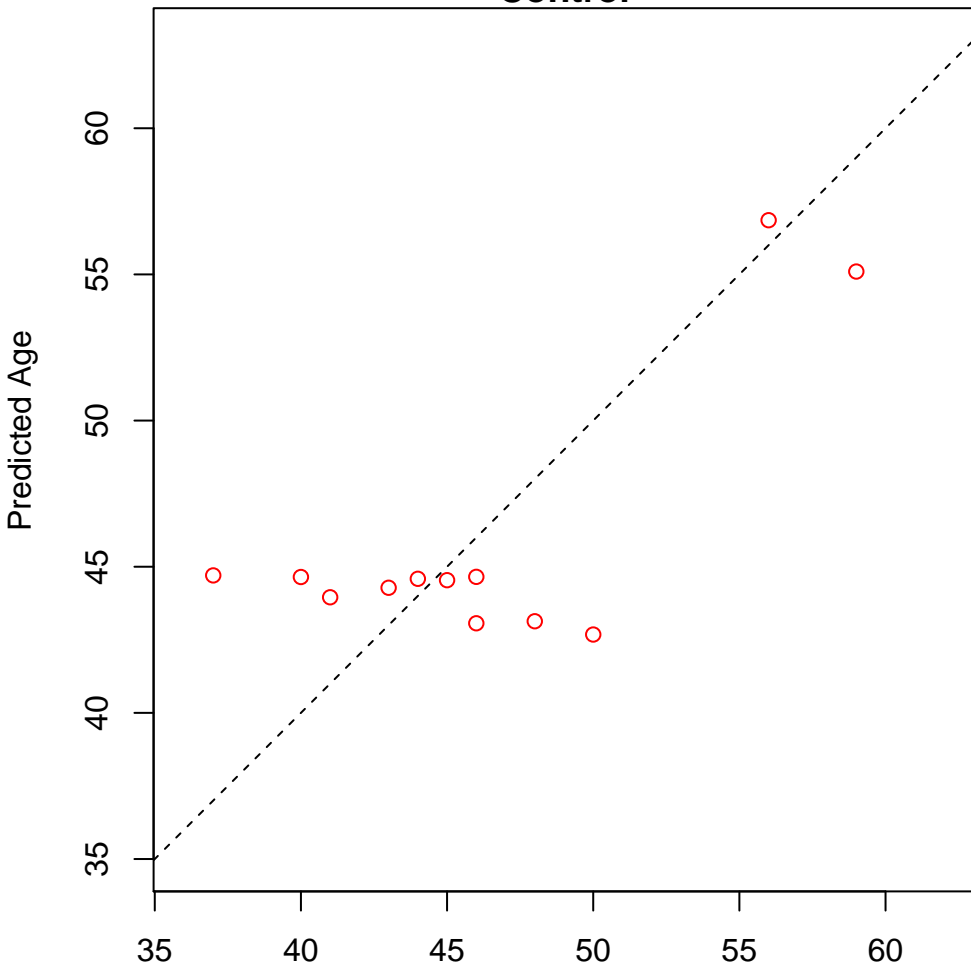


energy coupled proton transport, down electrochemical gradient (Score: 2.959696)

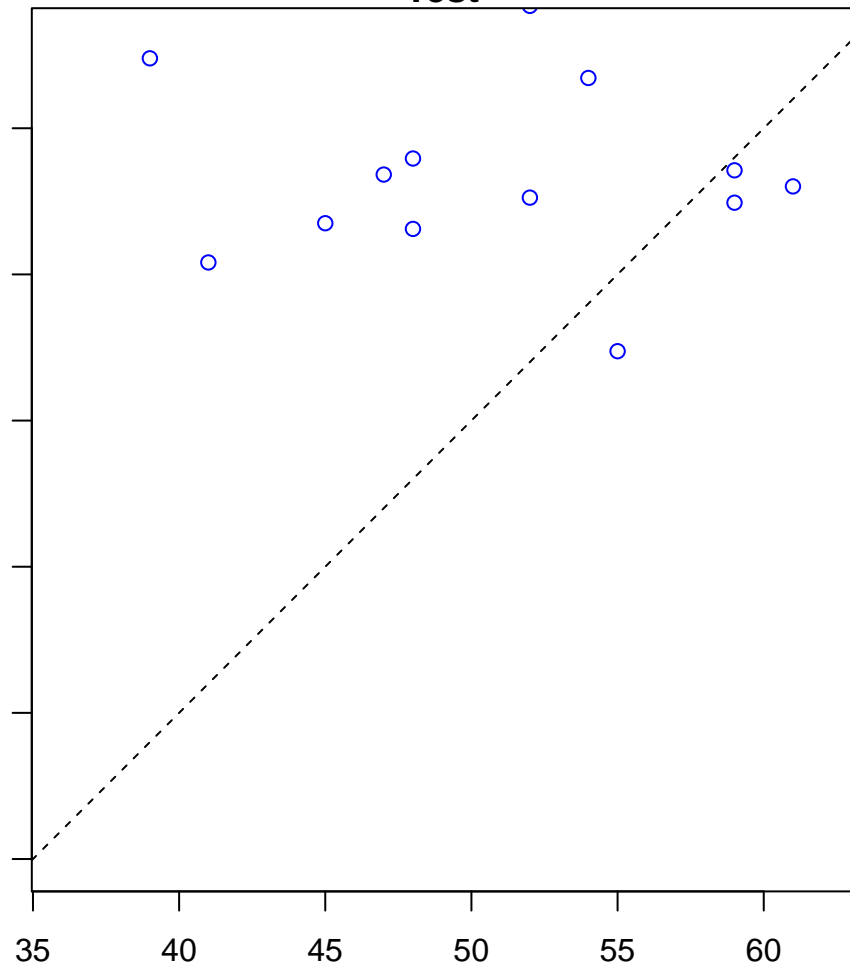


ATP synthesis coupled proton transport (Score: 2.959696)

Control

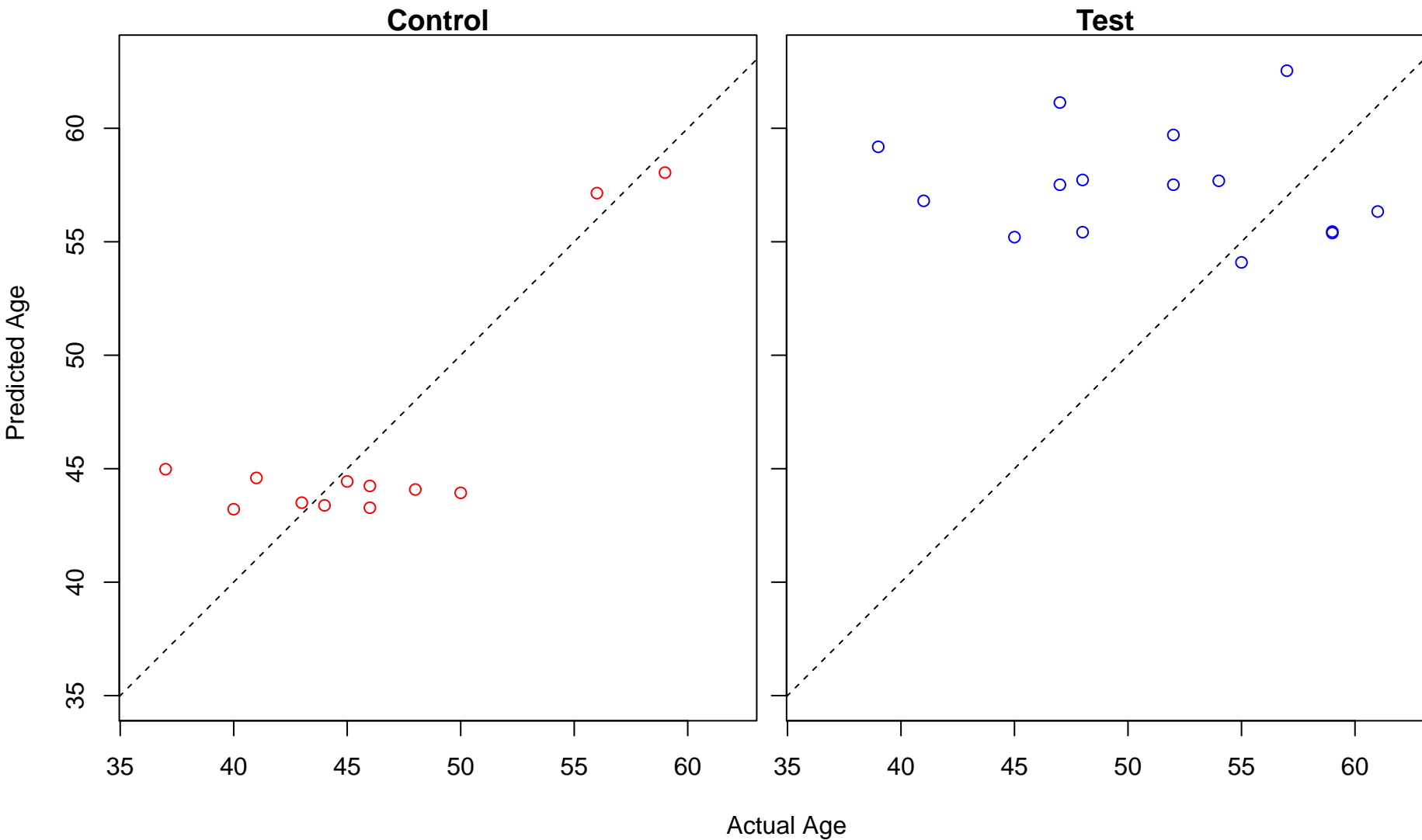


Test

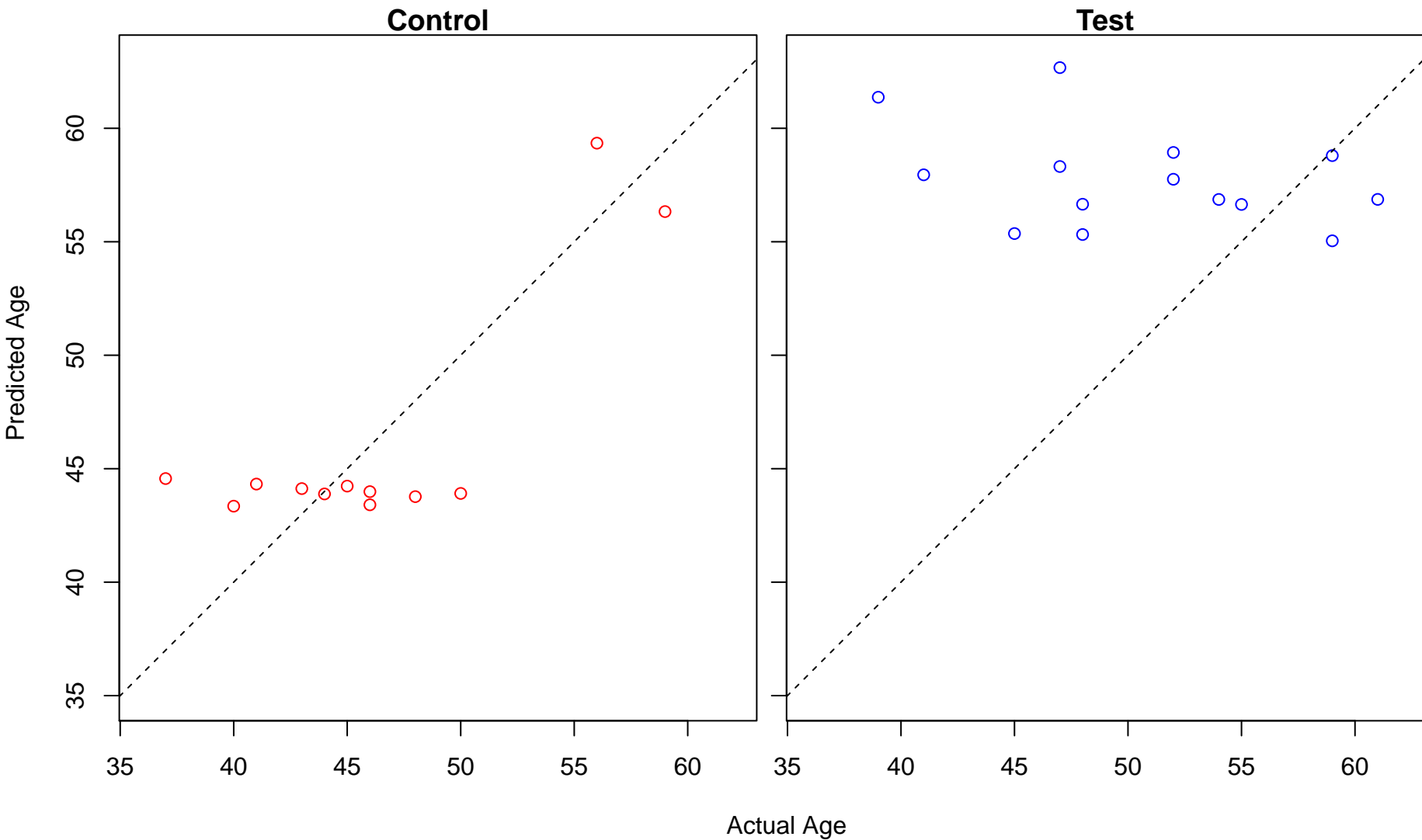


Actual Age

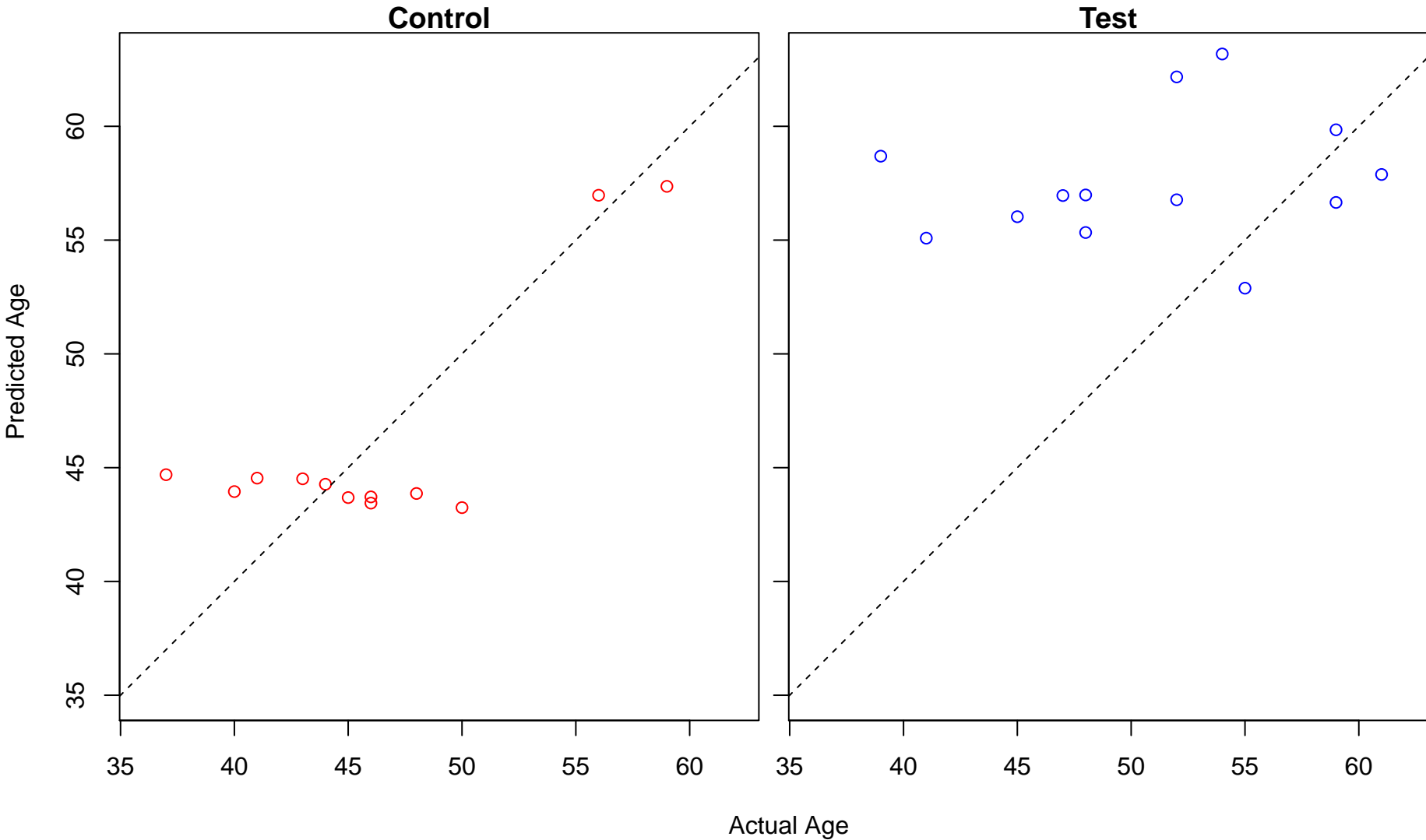
regulation of epithelial cell migration (Score: 2.959457)



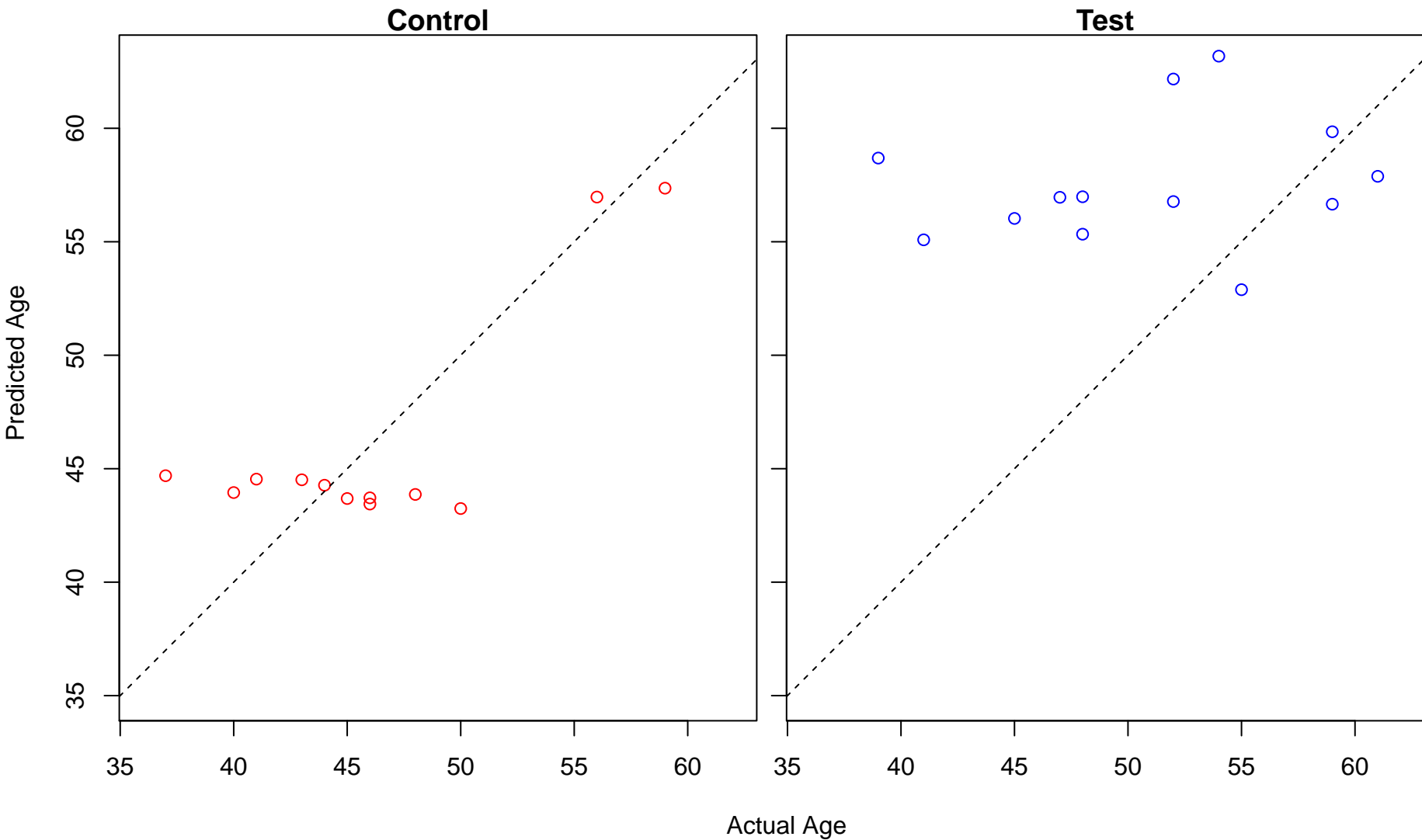
cellular response to fibroblast growth factor stimulus (Score: 2.958923)



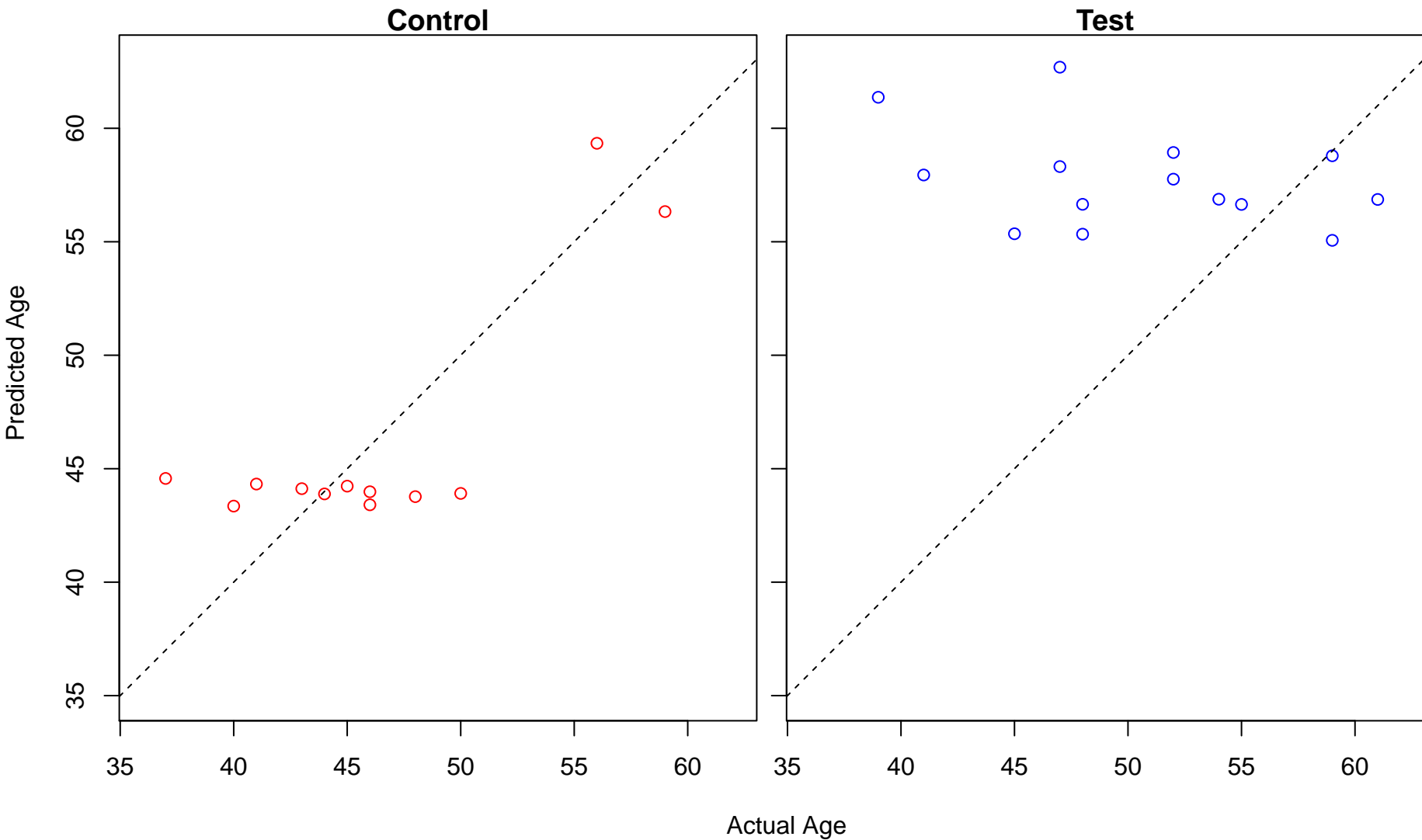
regulation of nucleoside metabolic process (Score: 2.958523)



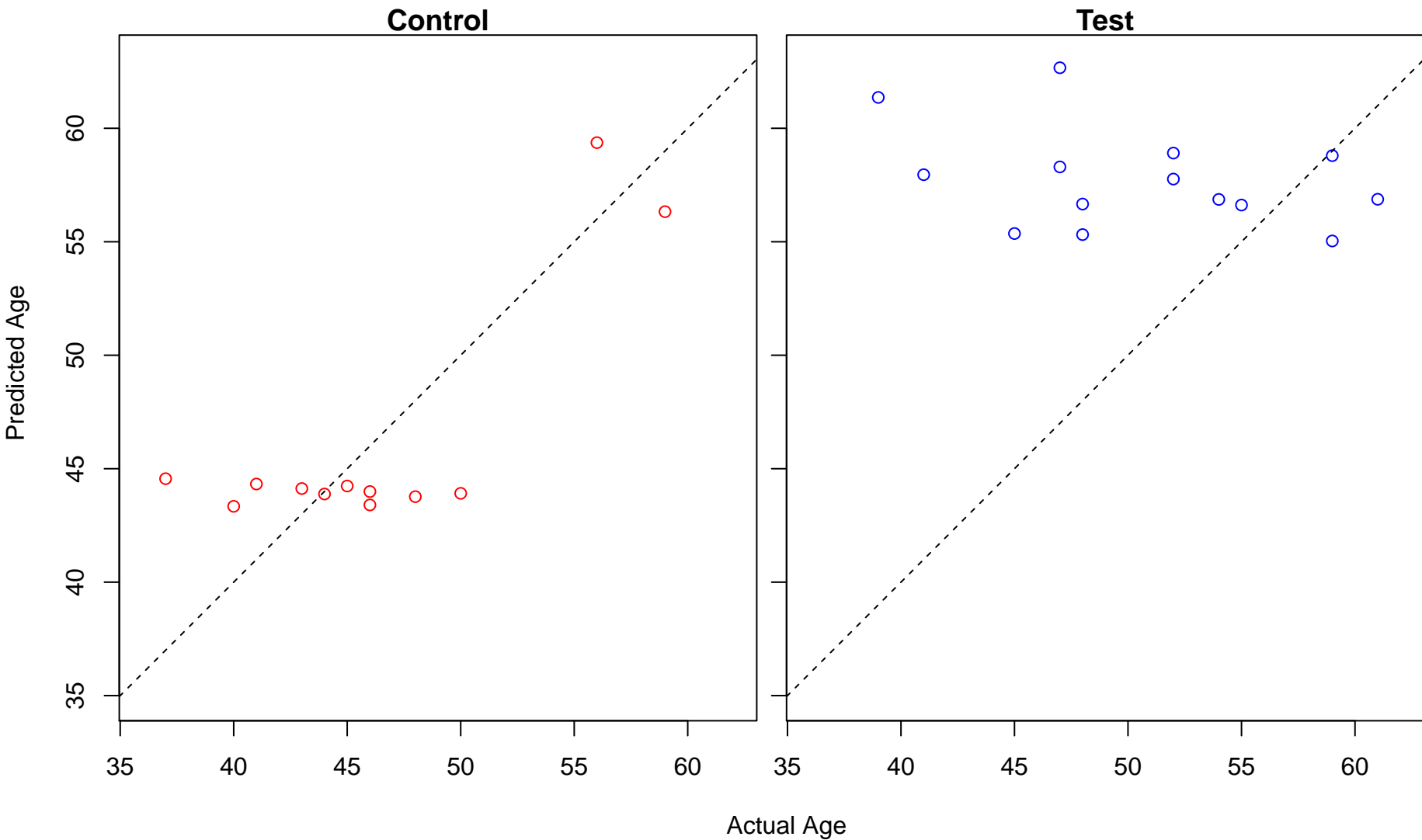
regulation of ATP metabolic process (Score: 2.958523)



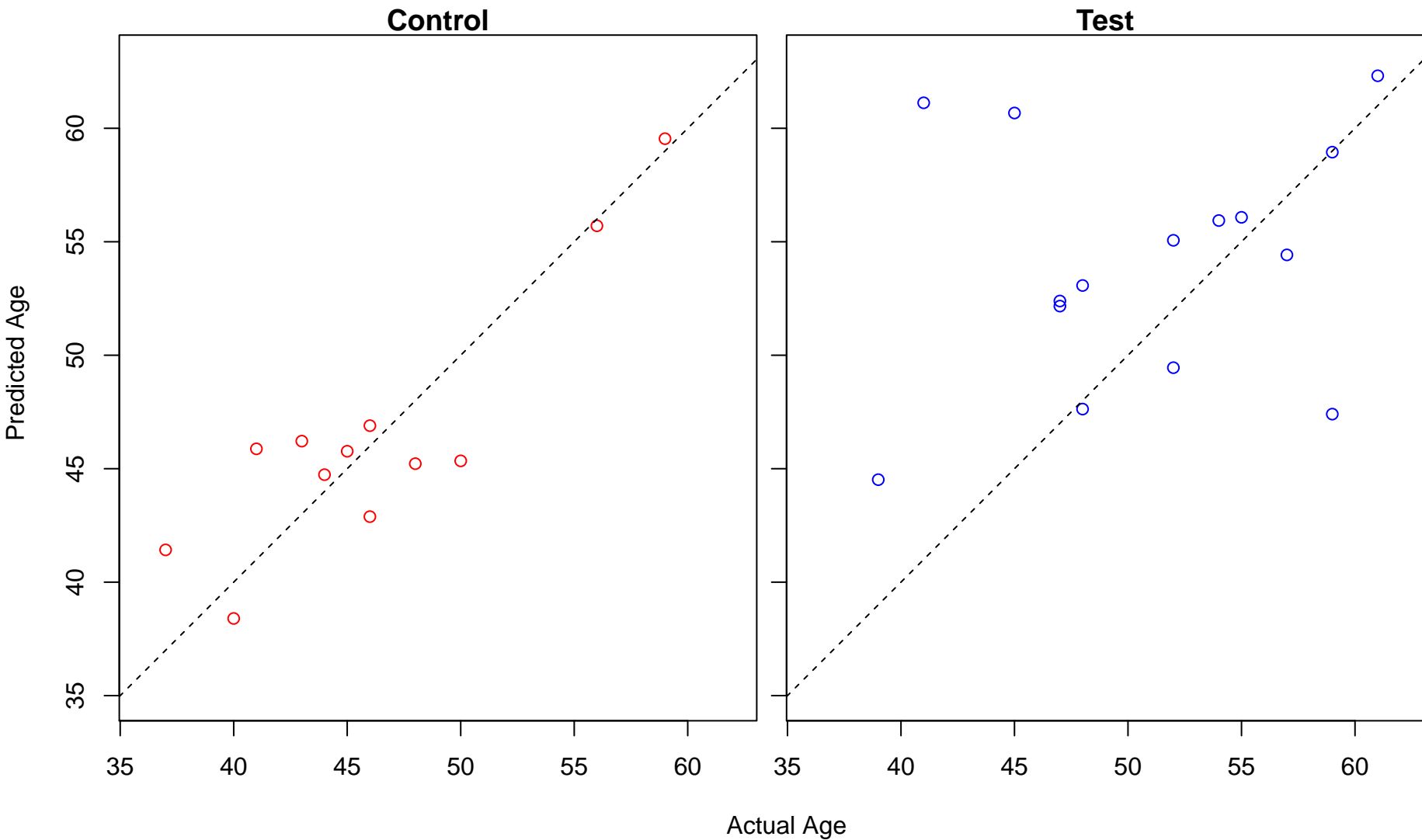
response to fibroblast growth factor (Score: 2.957865)



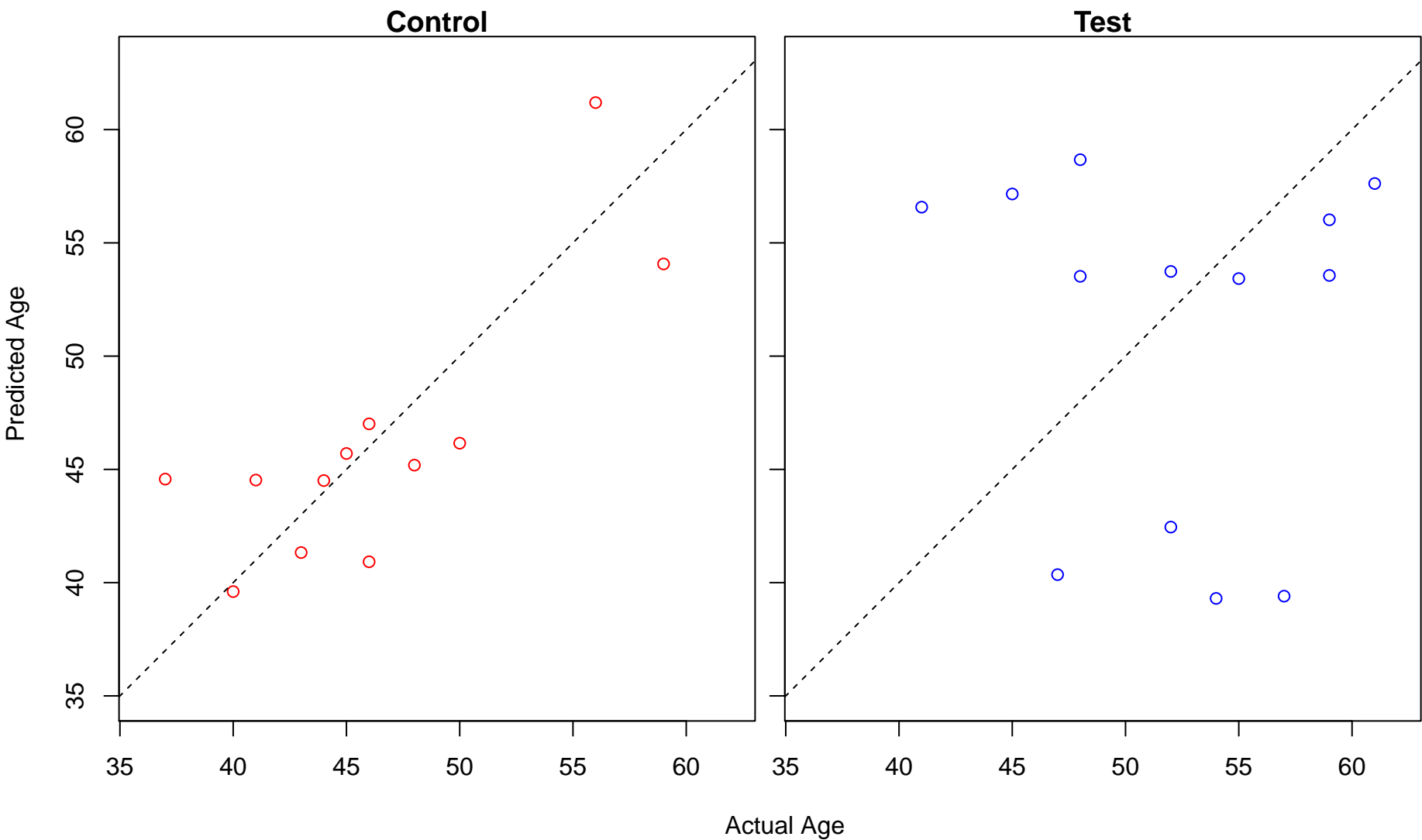
fibroblast growth factor receptor signaling pathway (Score: 2.956755)



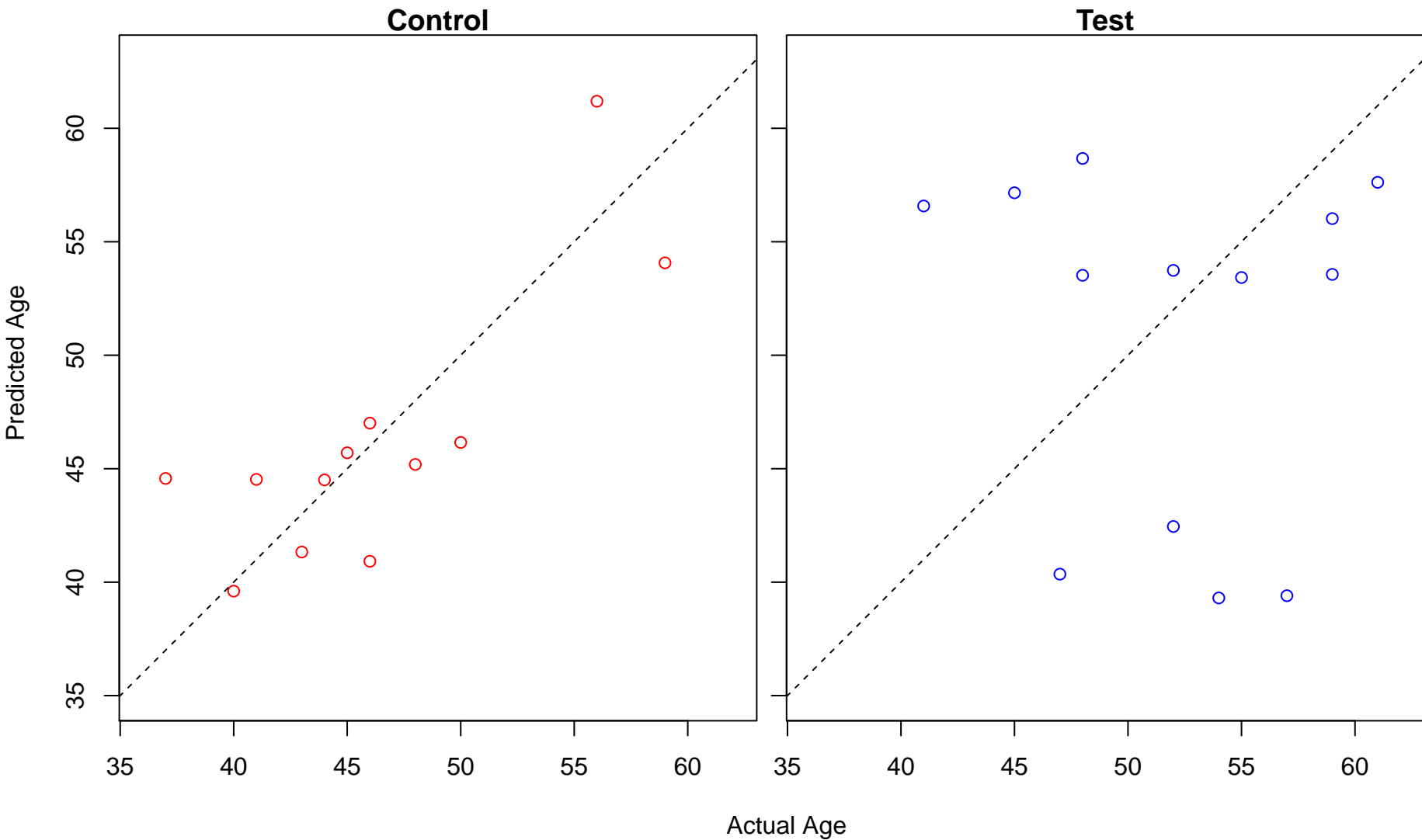
positive regulation of homeostatic process (Score: 2.955958)



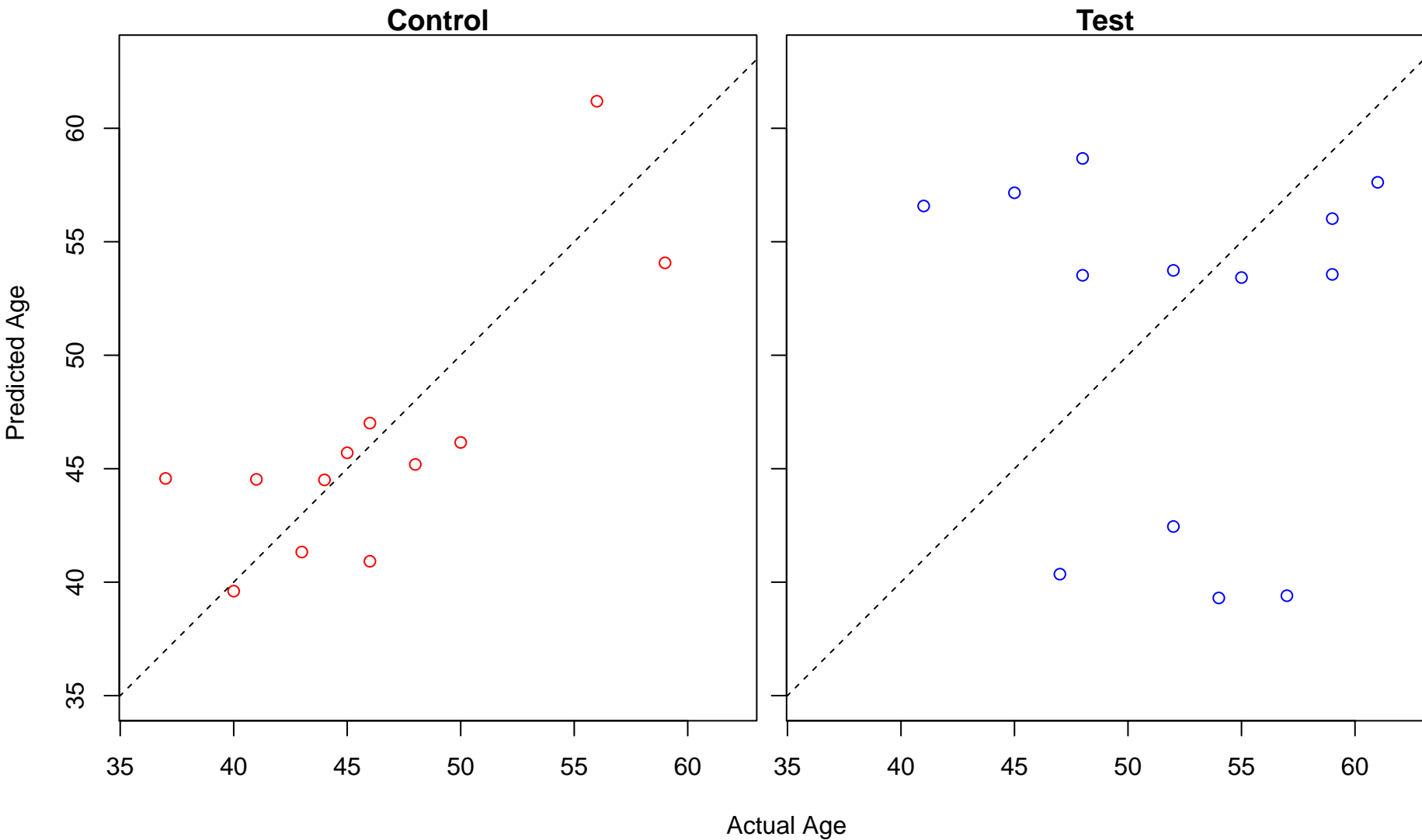
immune response–regulating cell surface receptor signaling pathway involved in phagocytosis (Score: 2)



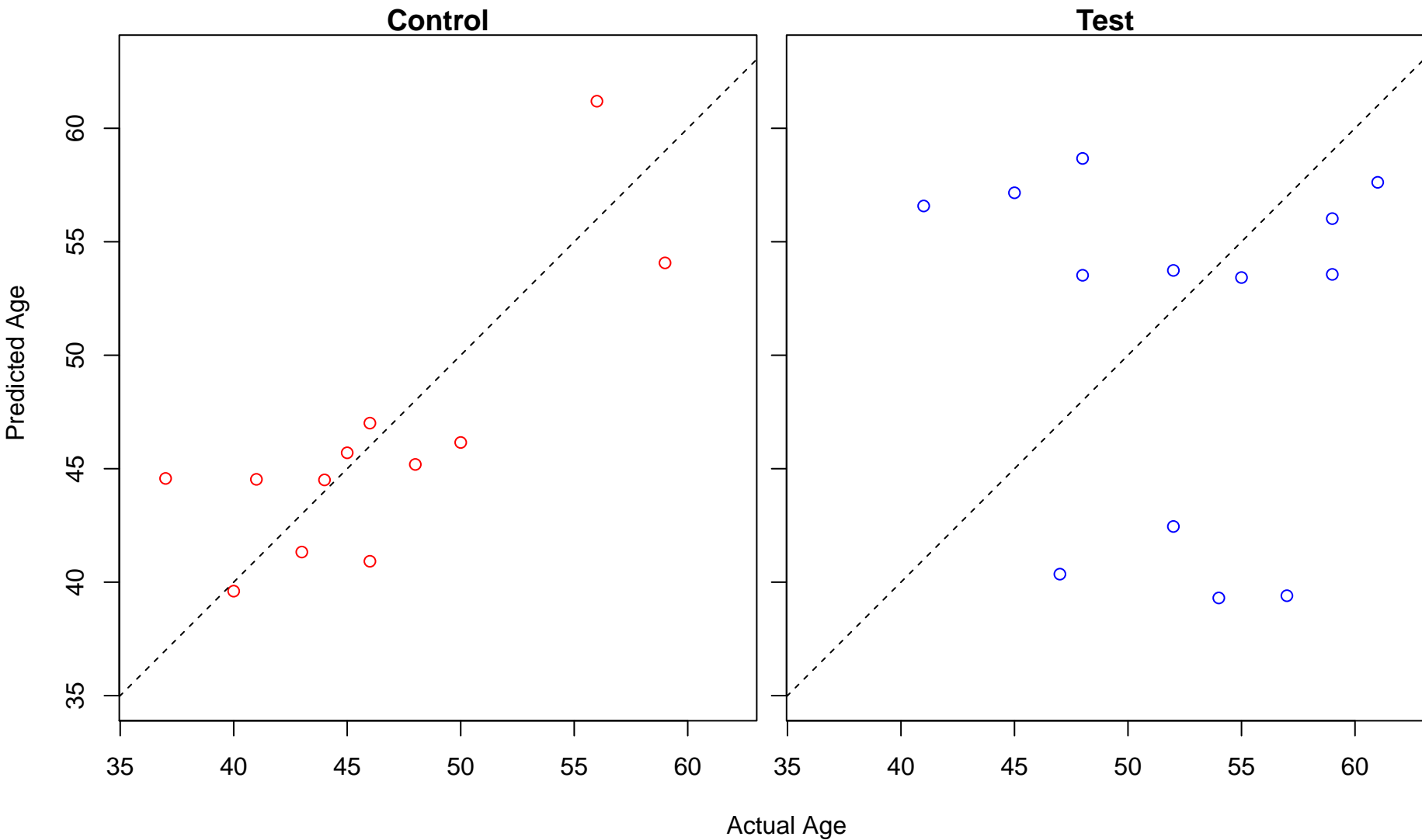
Fc-gamma receptor signaling pathway (Score: 2.954631)



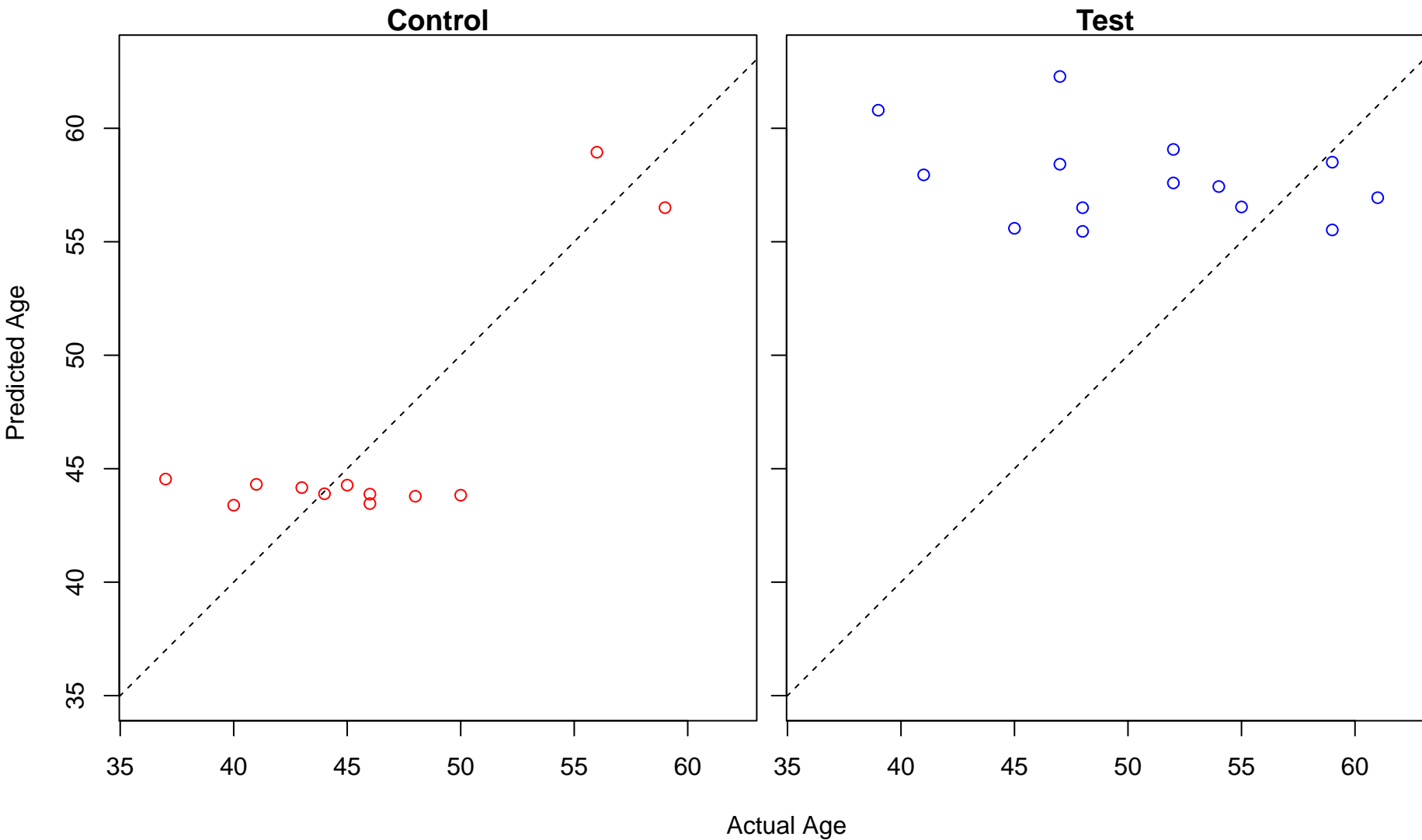
Fc-gamma receptor signaling pathway involved in phagocytosis (Score: 2.954631)



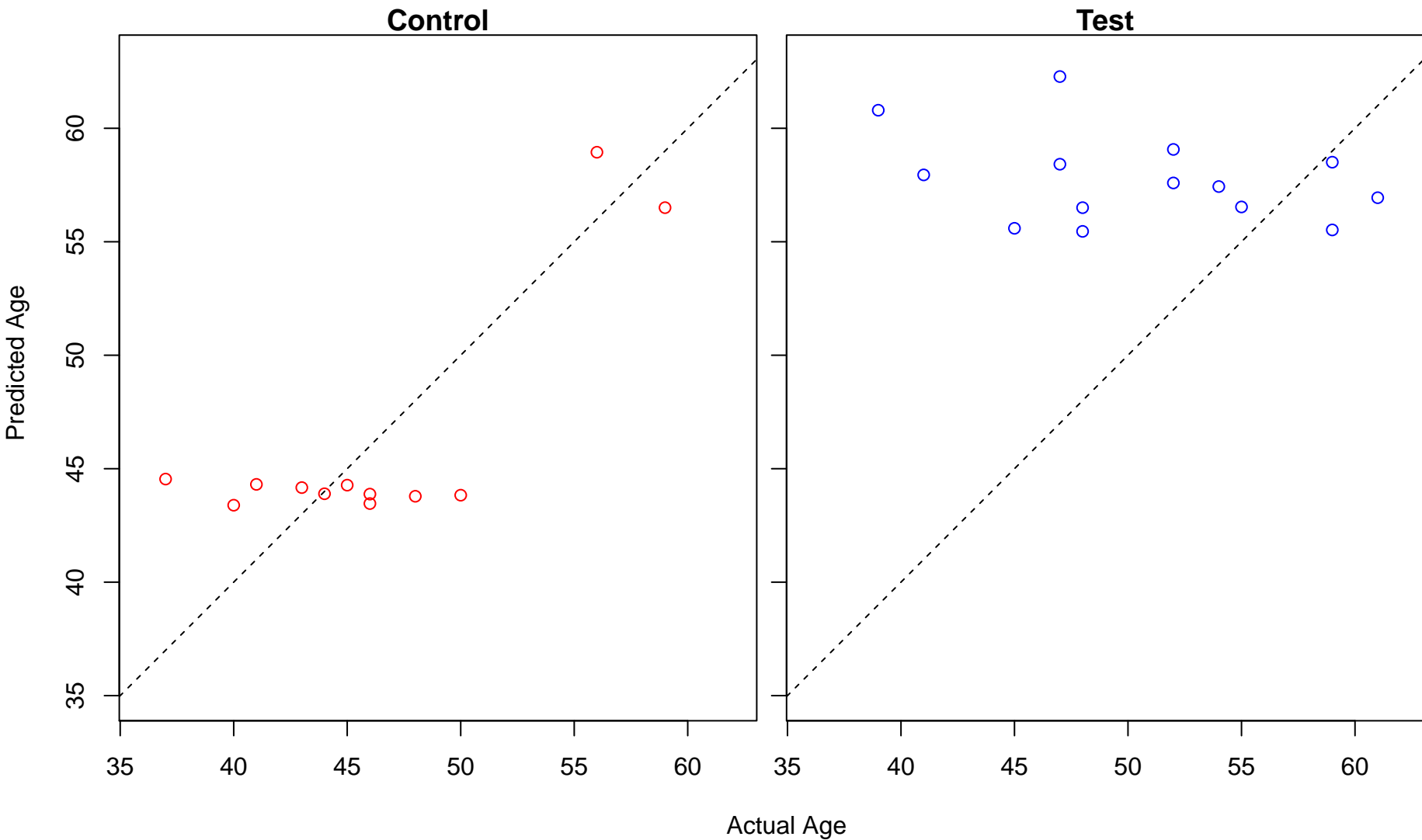
Fc receptor mediated stimulatory signaling pathway (Score: 2.954274)



neurotrophin TRK receptor signaling pathway (Score: 2.953691)

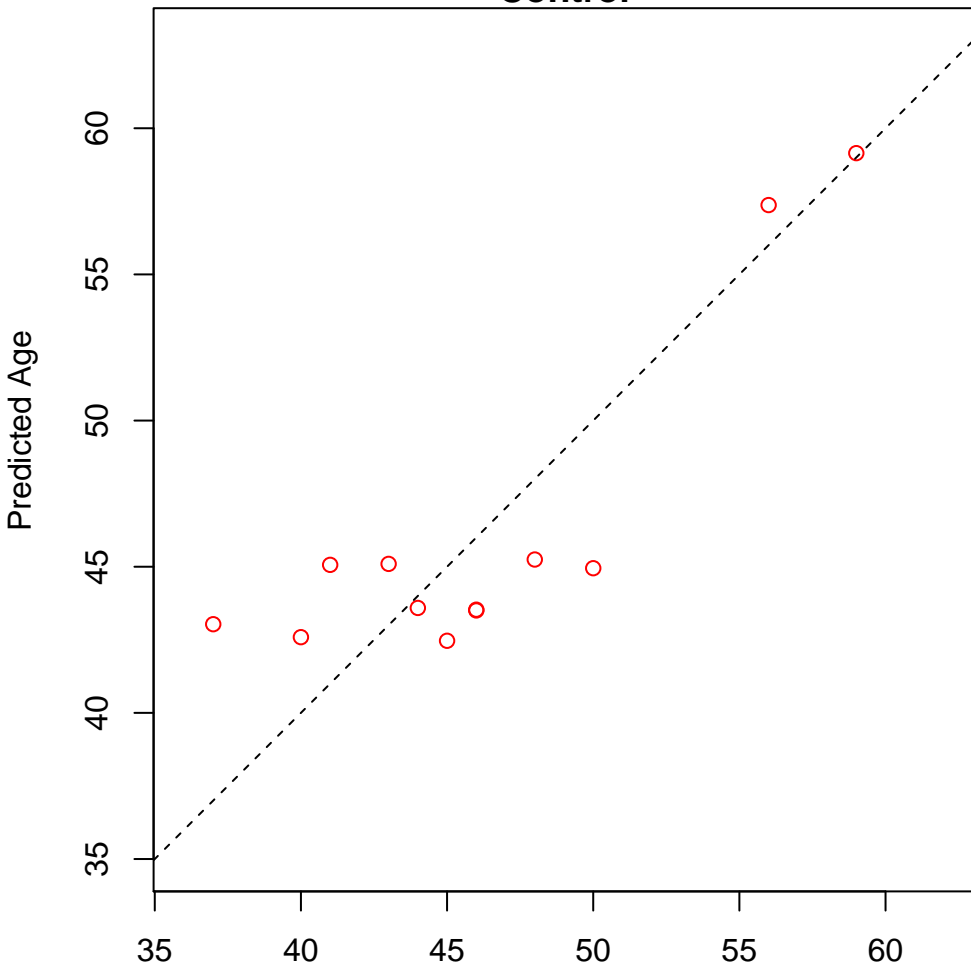


neurotrophin signaling pathway (Score: 2.953441)

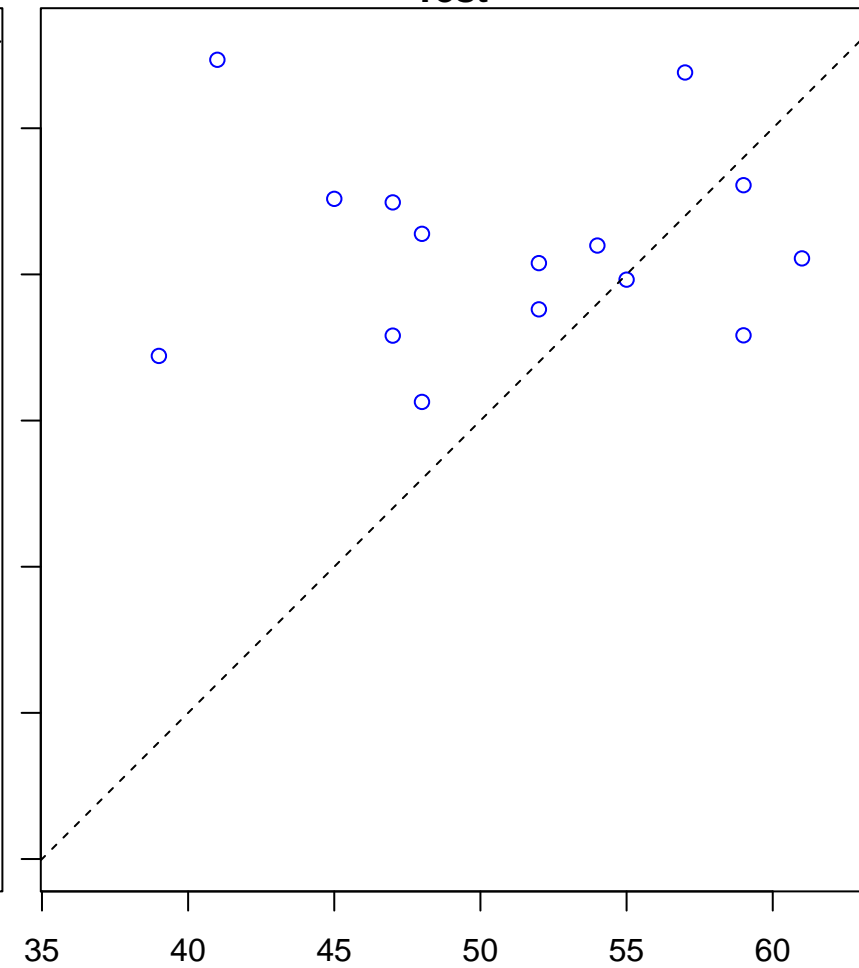


response to organophosphorus (Score: 2.952778)

Control

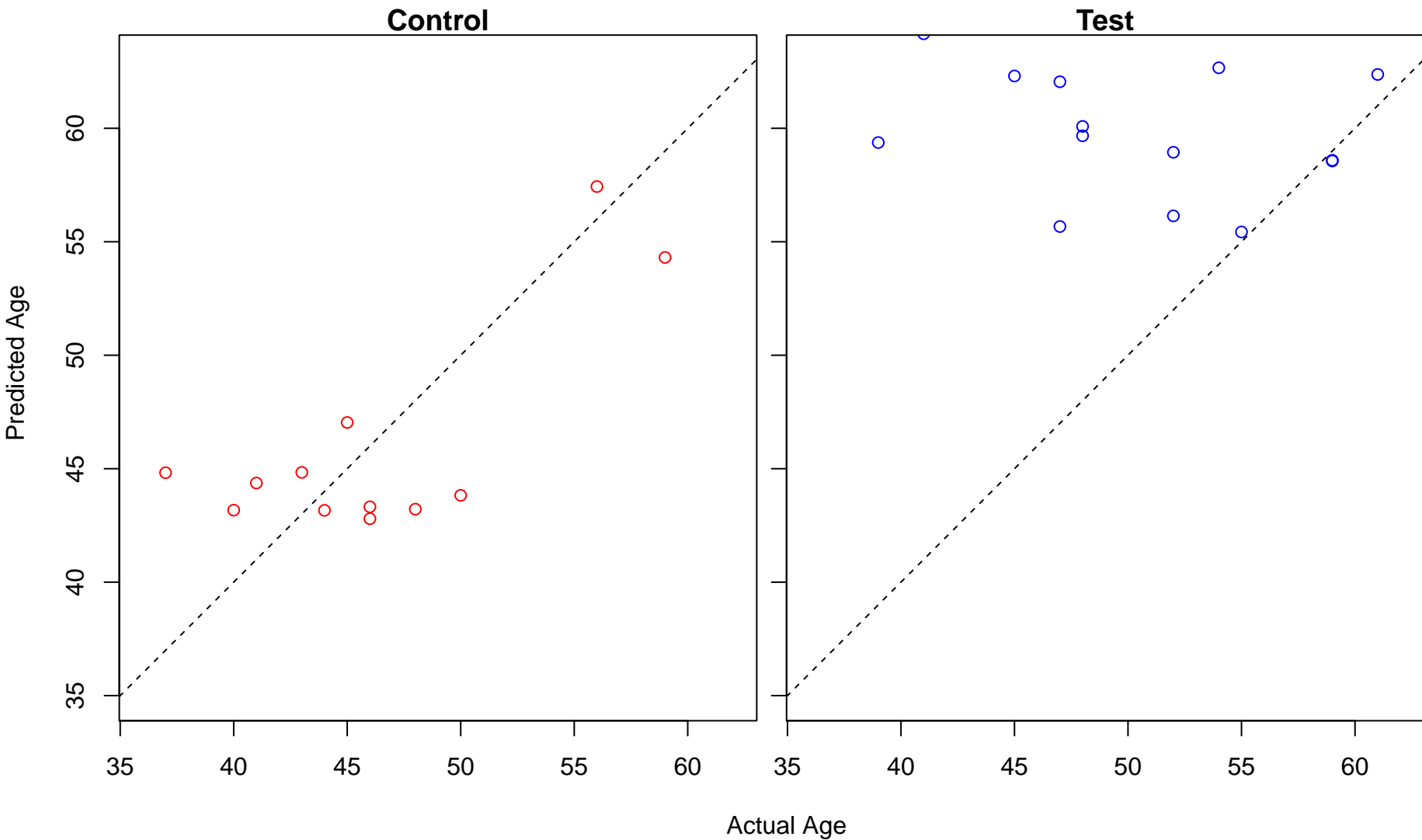


Test

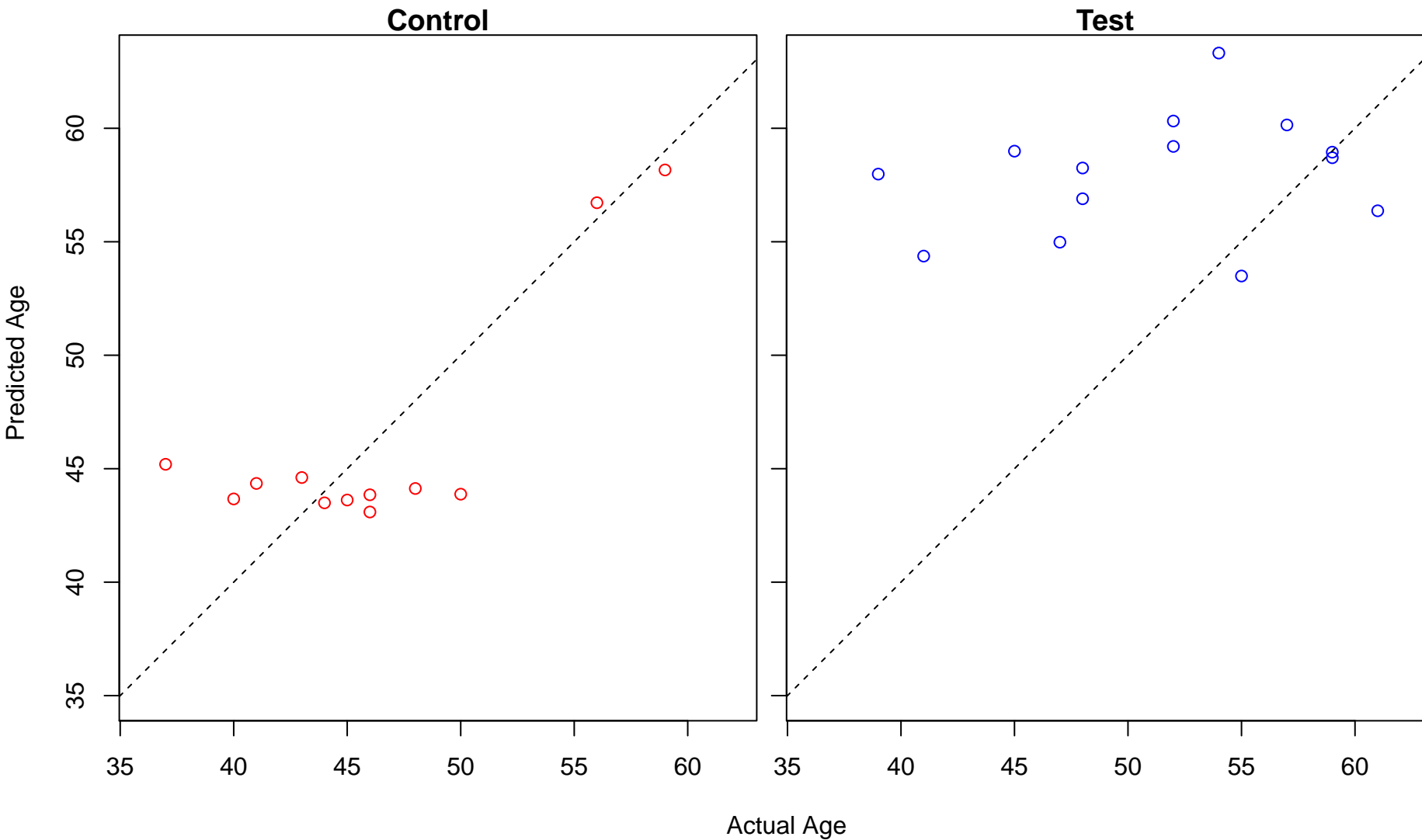


Actual Age

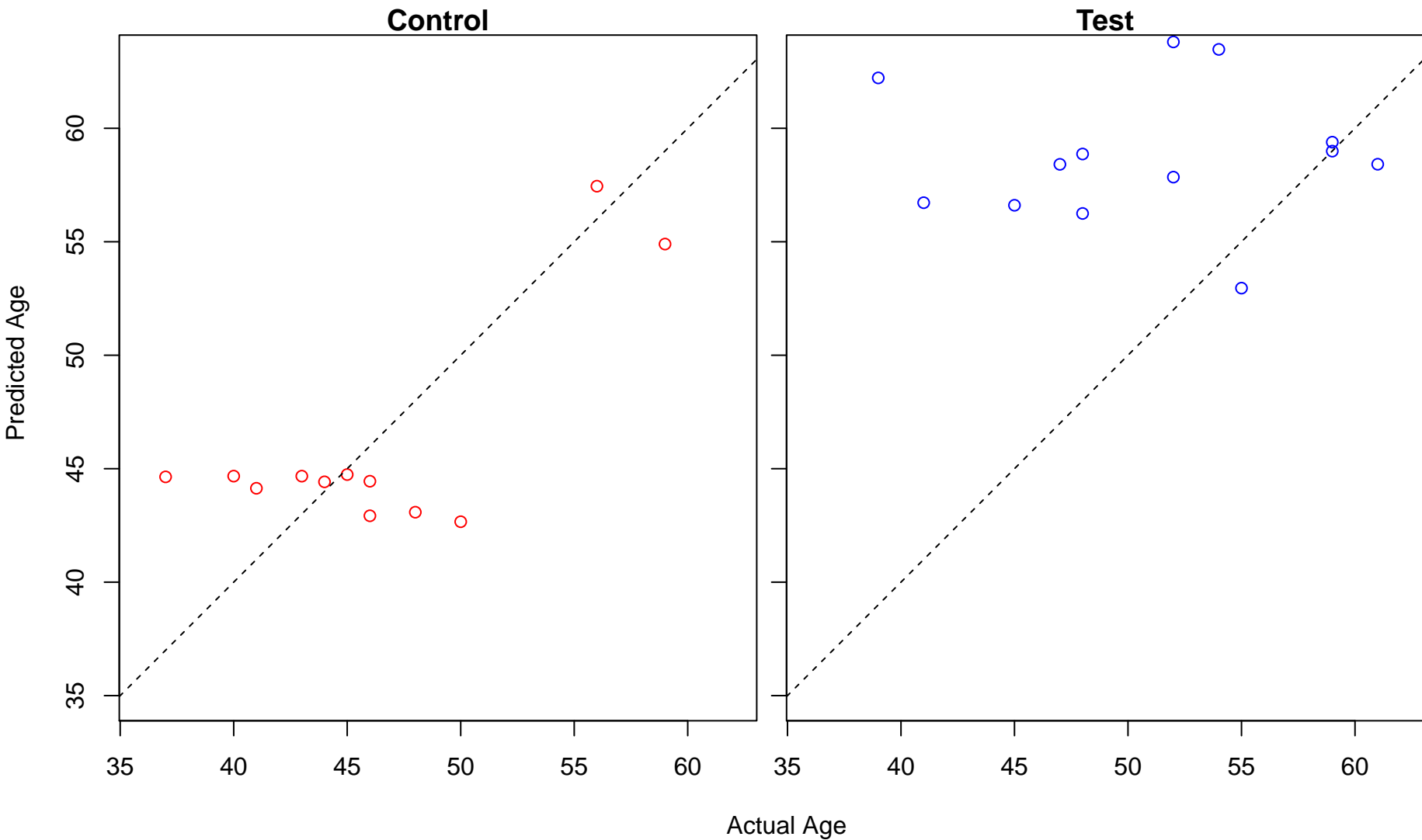
glial cell development (Score: 2.952396)



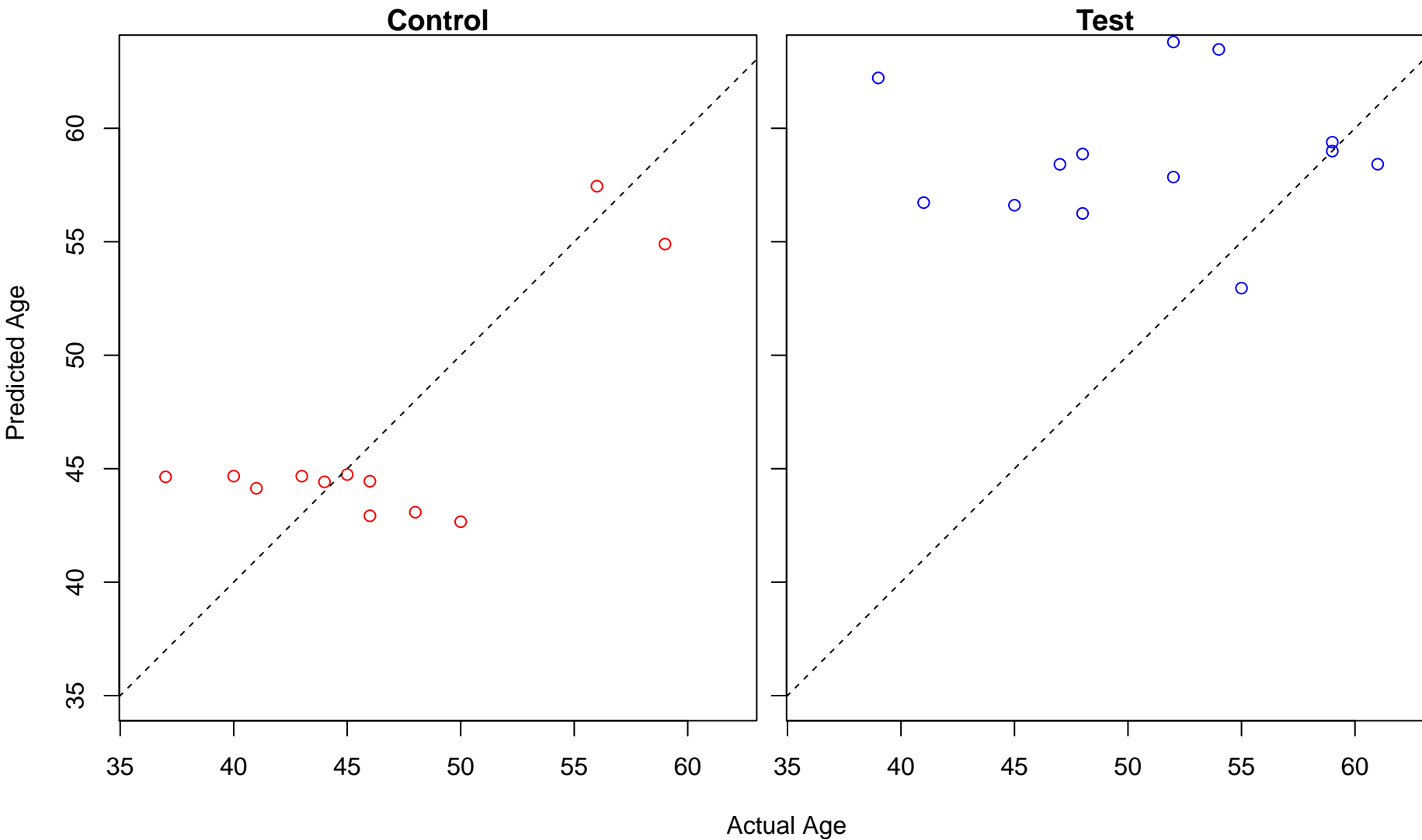
abscission (Score: 2.950367)



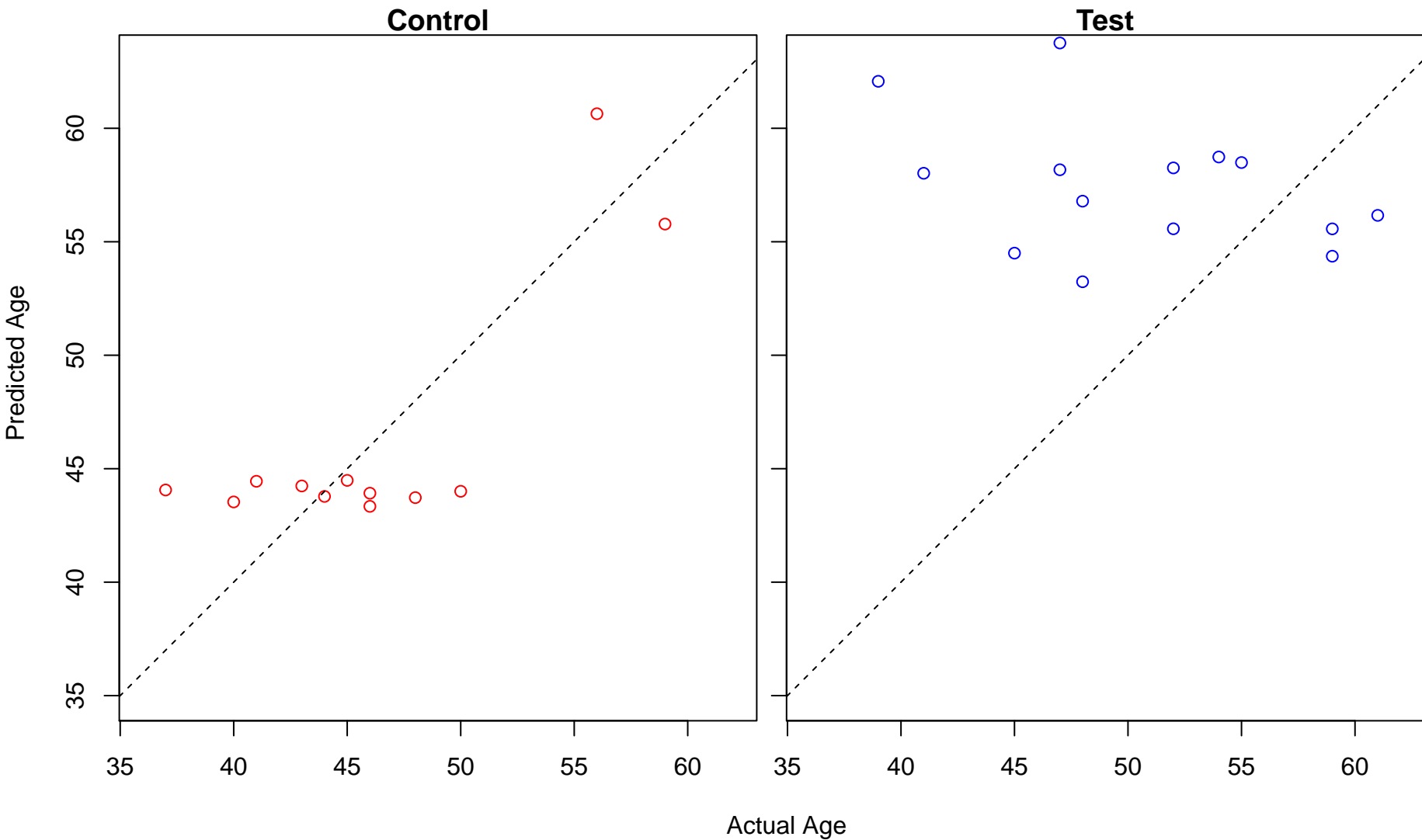
proton transport (Score: 2.949944)



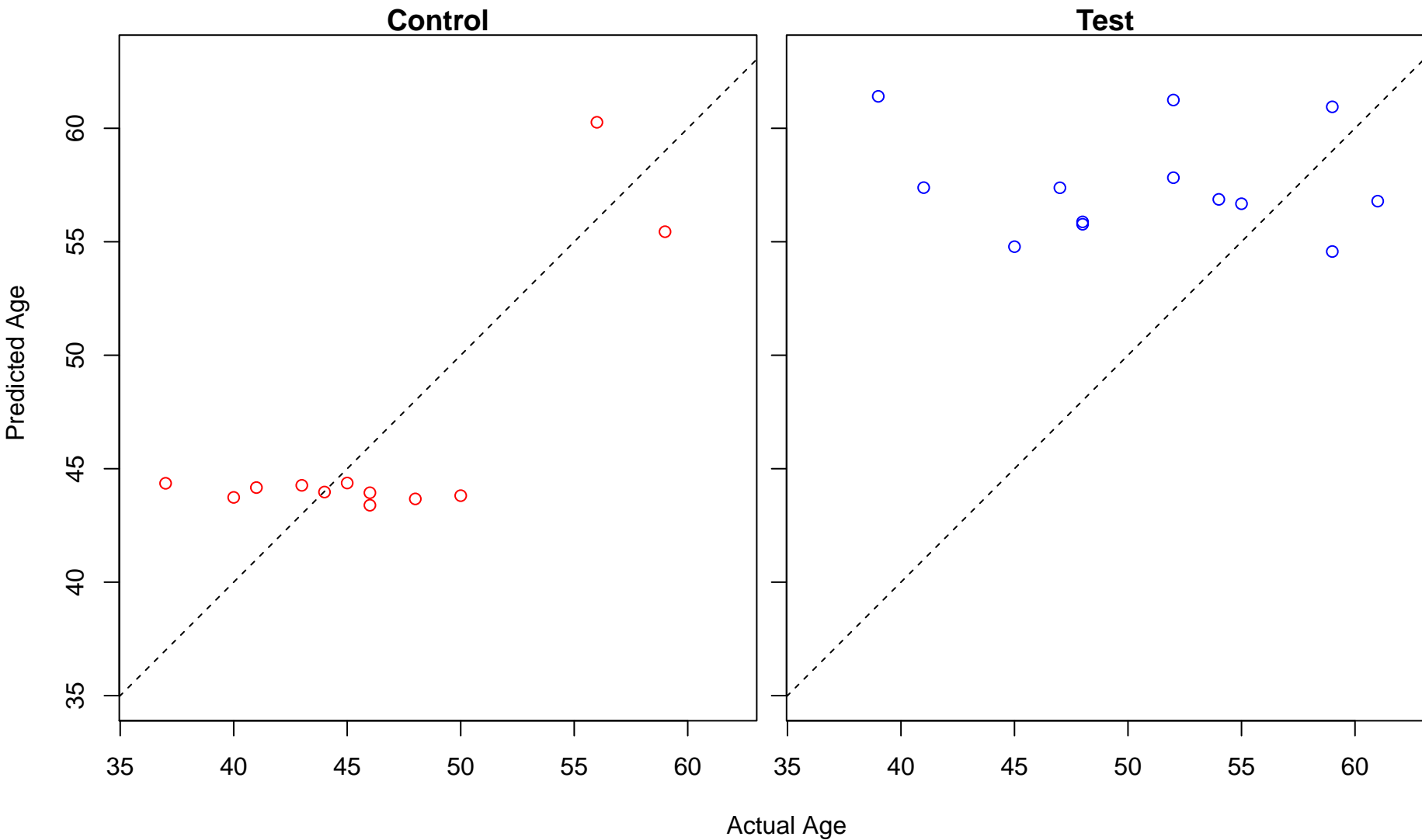
hydrogen transport (Score: 2.949653)



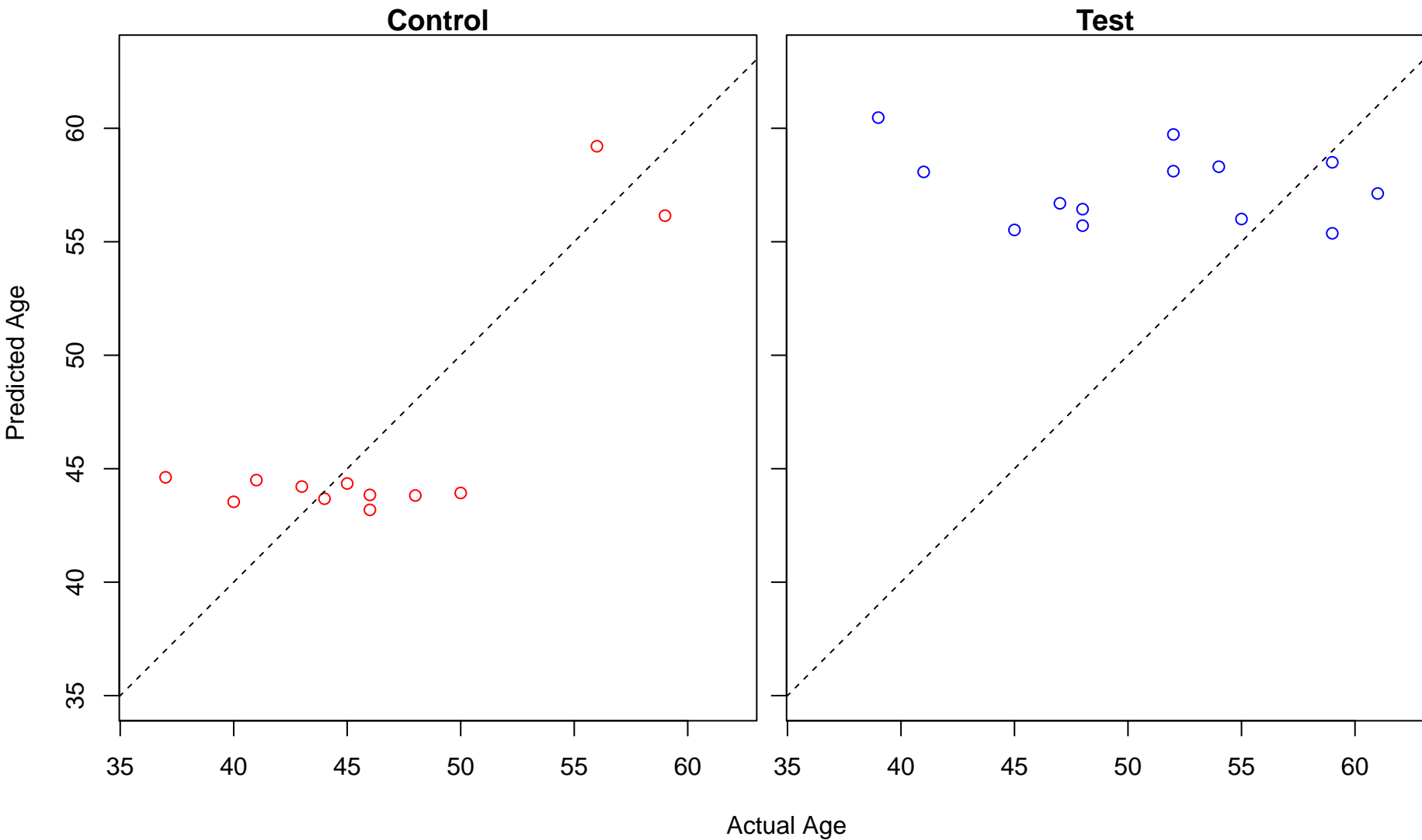
cytoskeleton-dependent intracellular transport (Score: 2.949320)



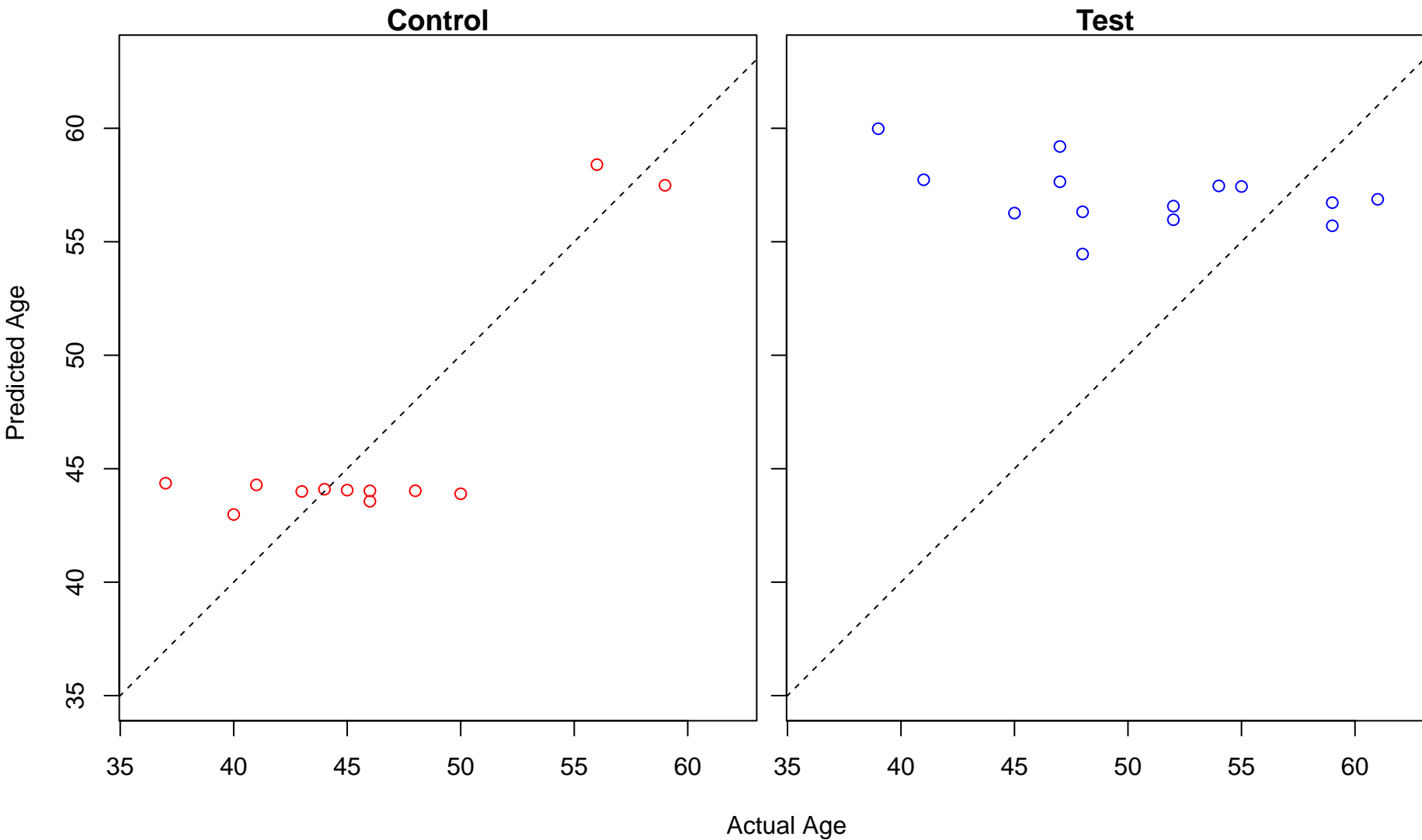
rhythmic process (Score: 2.949180)



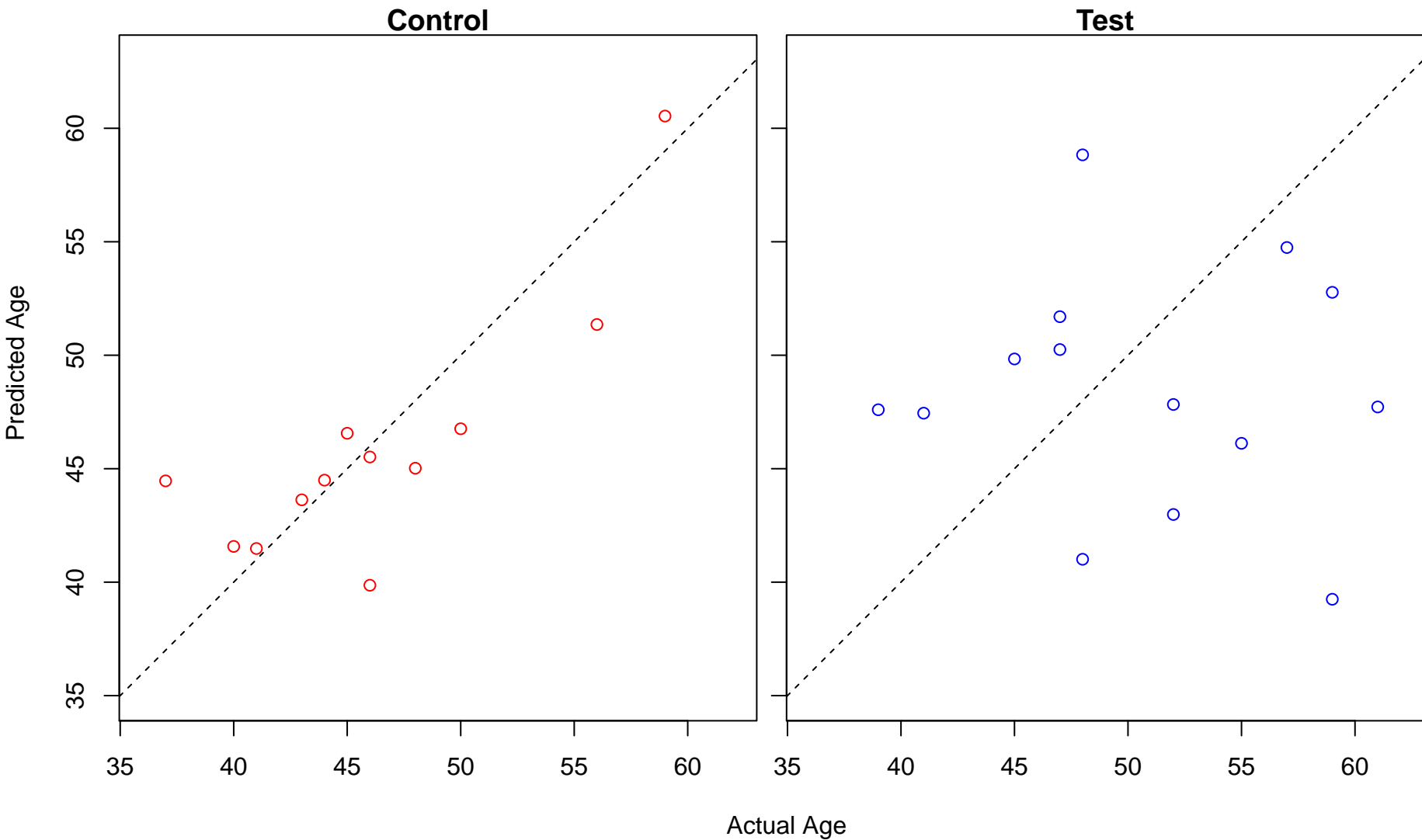
regulation of cellular protein catabolic process (Score: 2.948753)



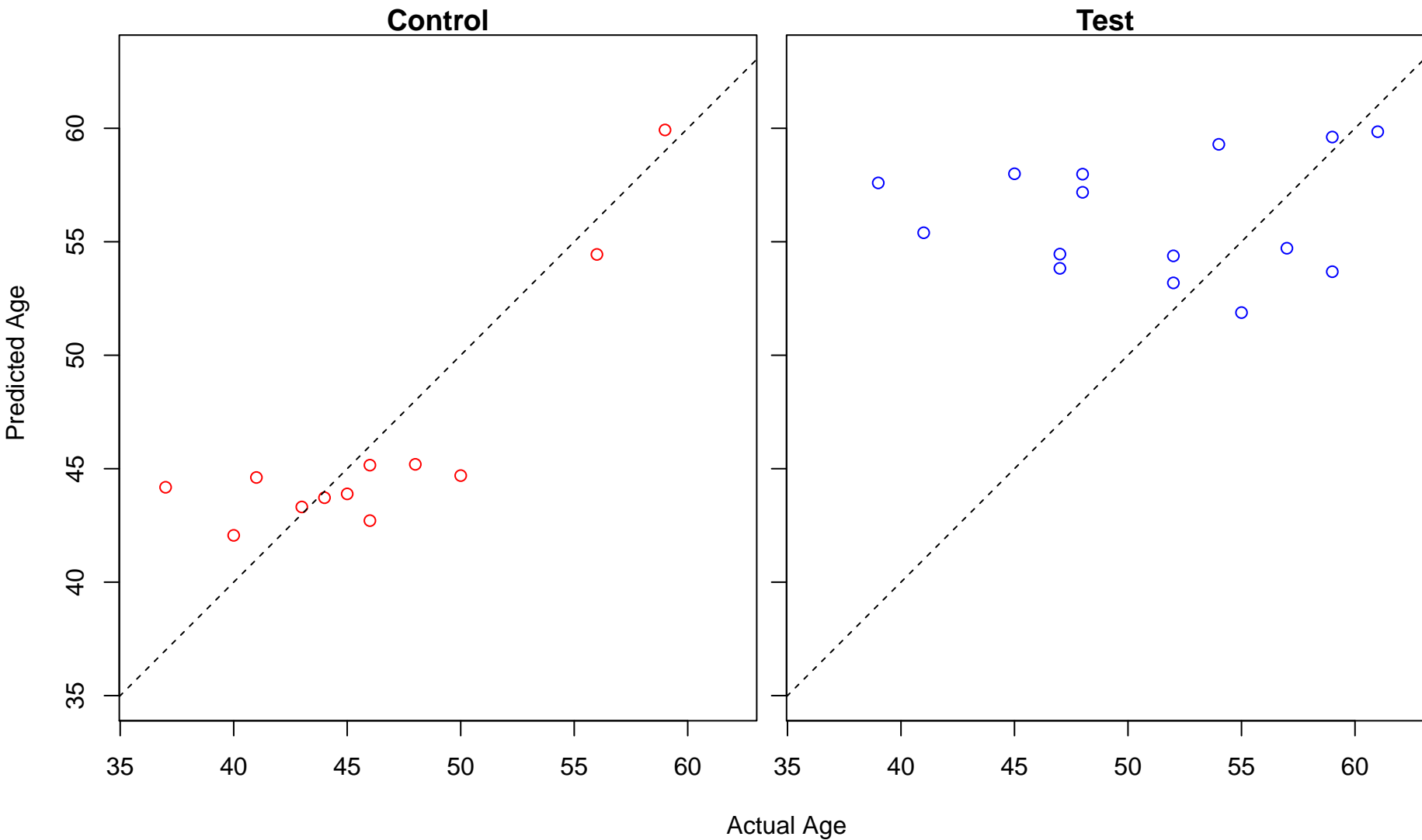
negative regulation of intracellular transport (Score: 2.947067)



monovalent inorganic cation transport (Score: 2.946960)

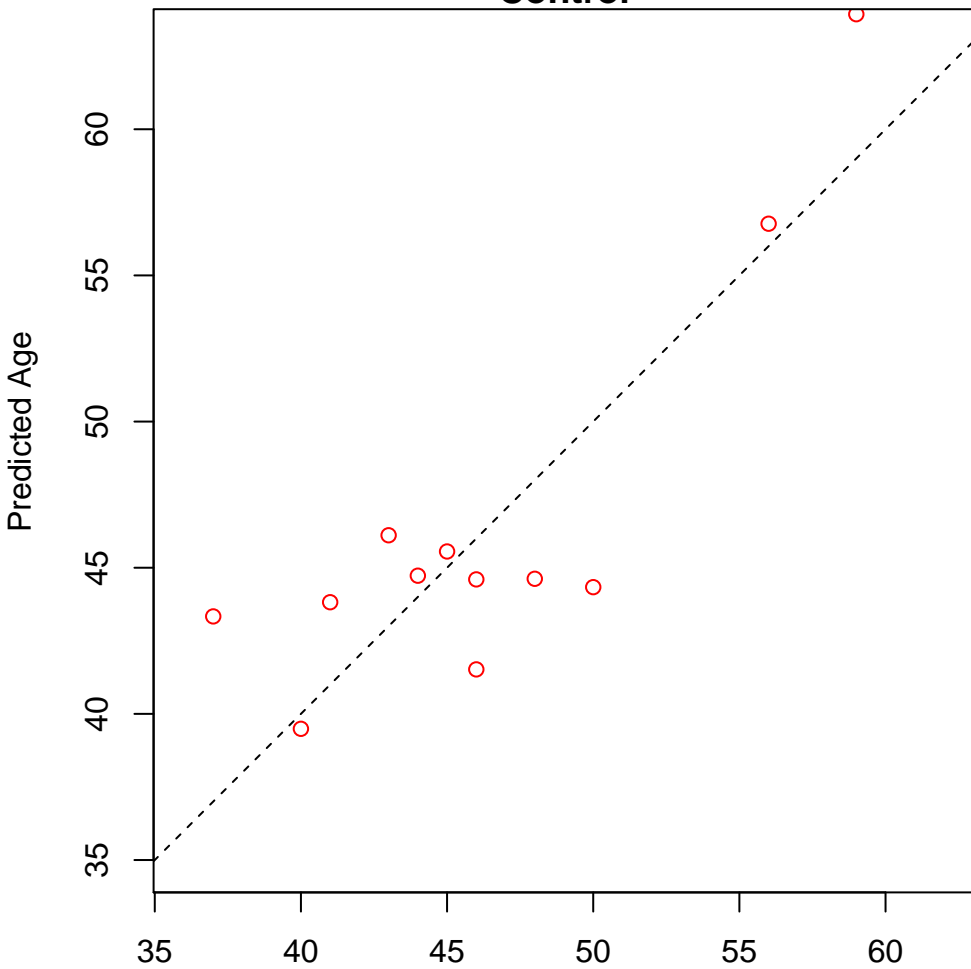


extracellular matrix assembly (Score: 2.946519)

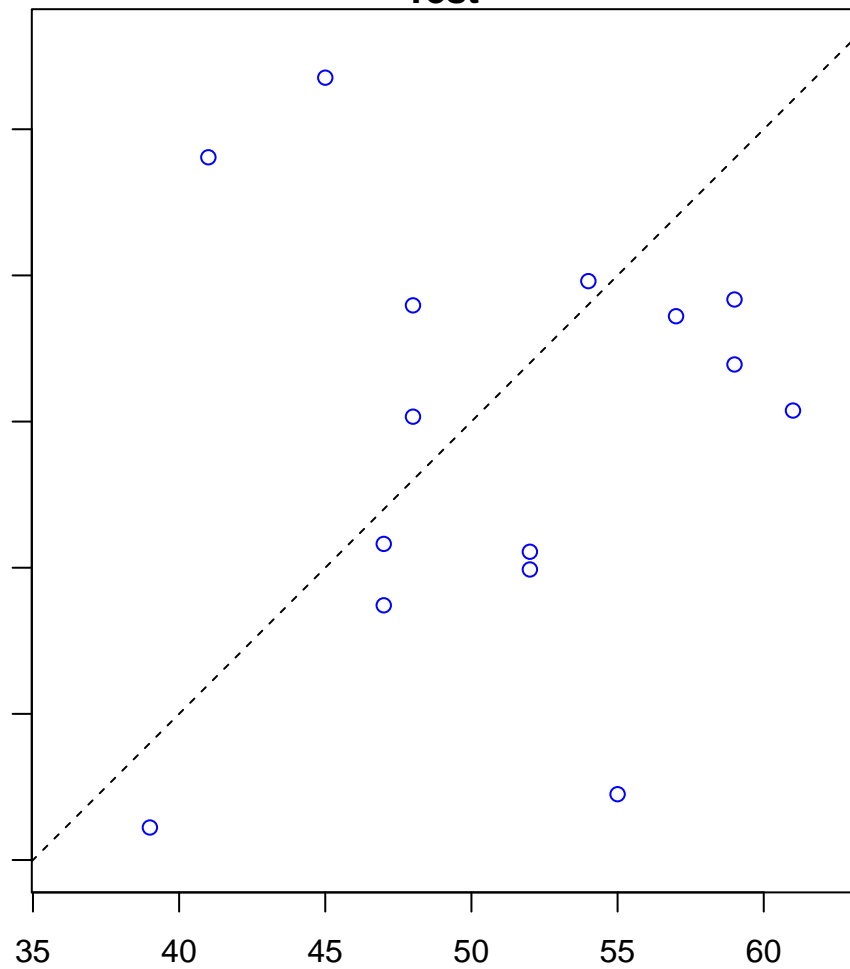


regulation of anatomical structure size (Score: 2.942421)

Control

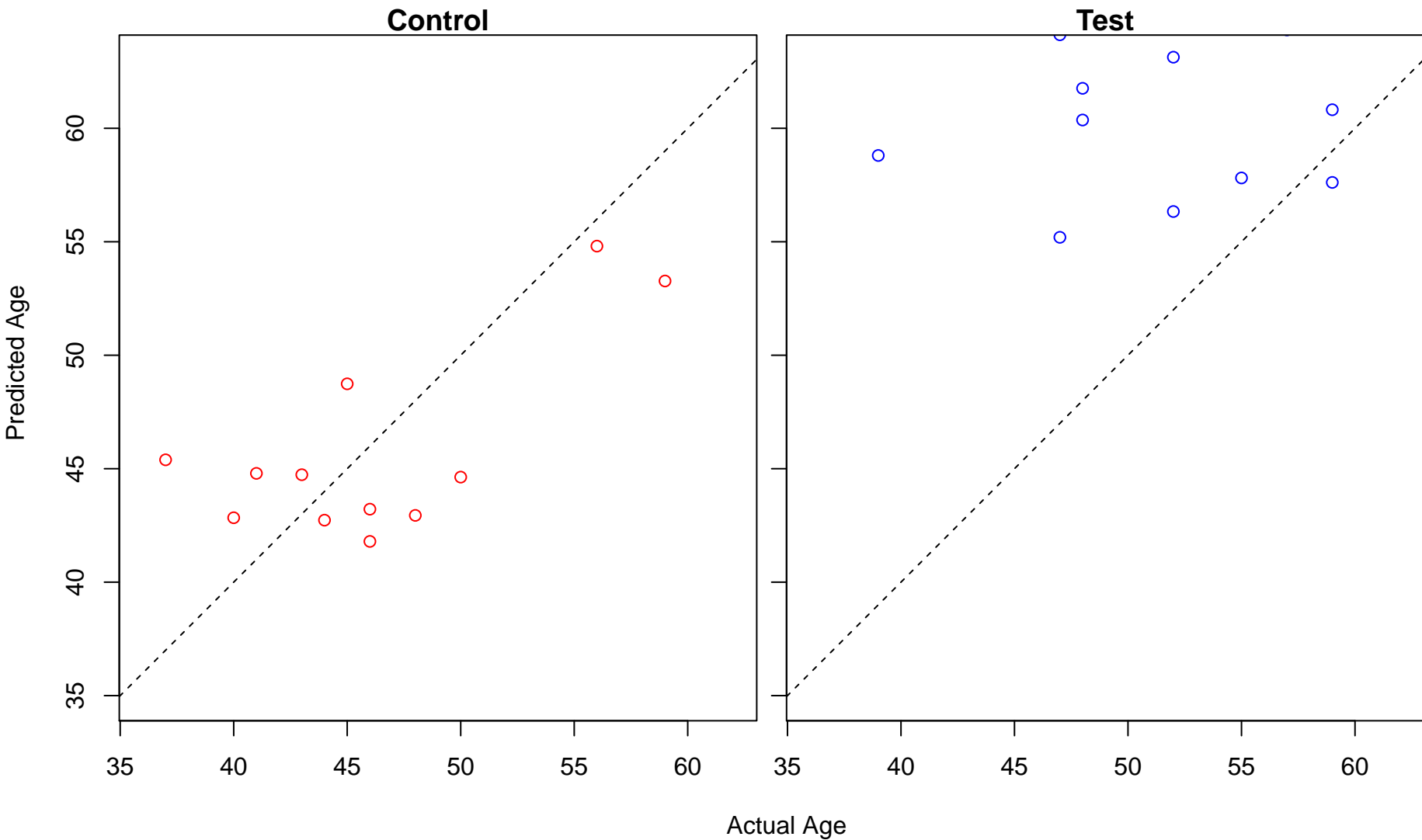


Test

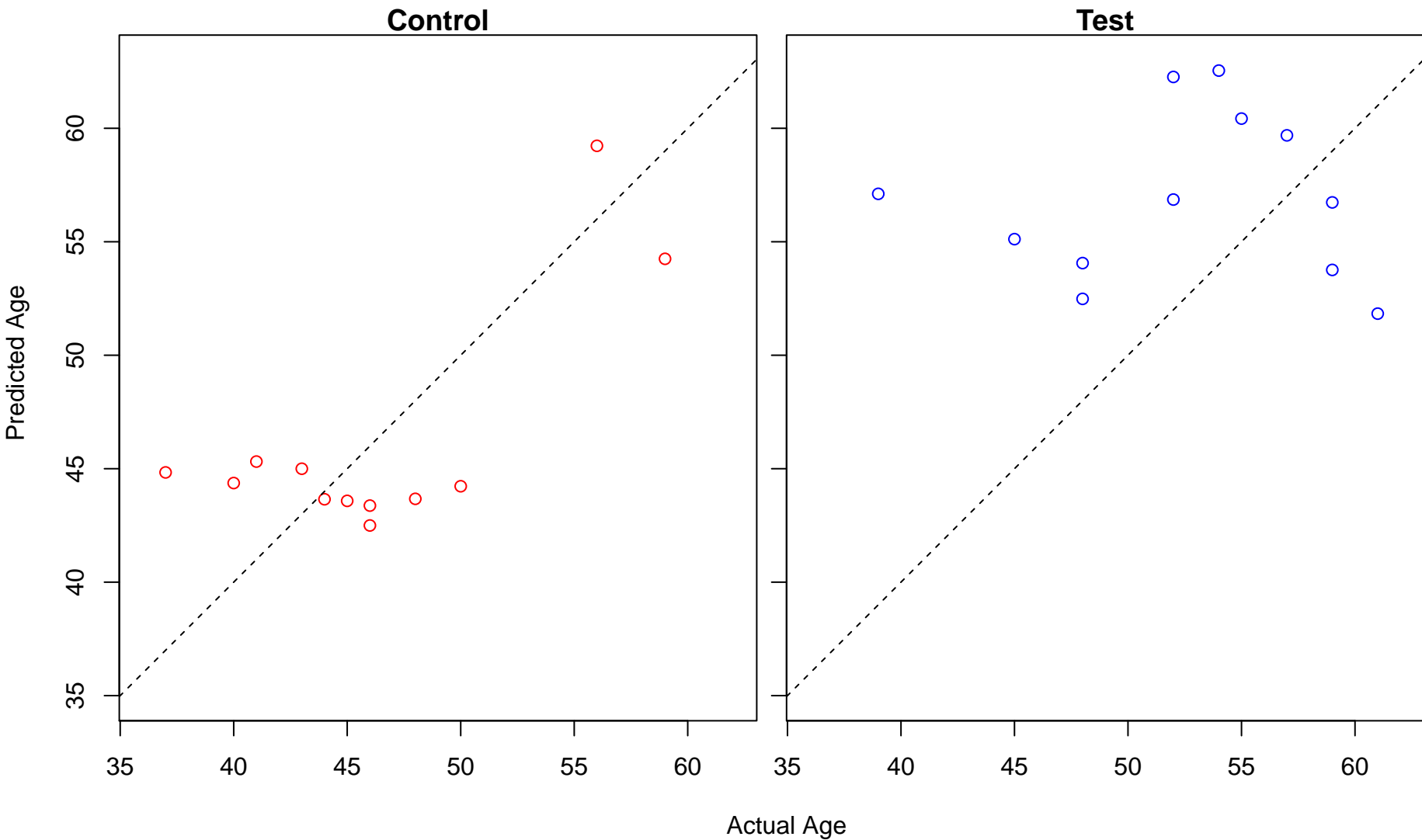


Actual Age

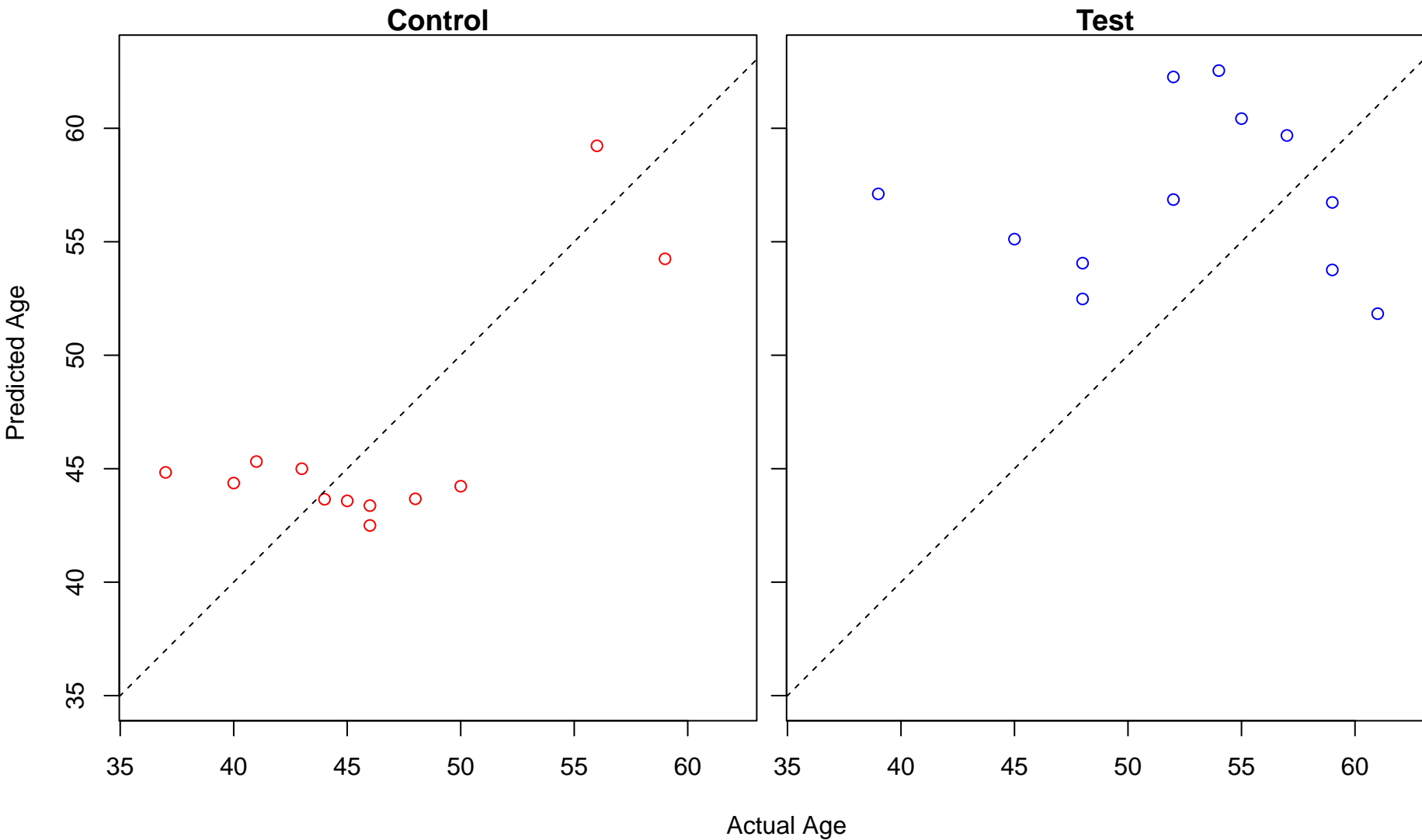
regulation of amyloid precursor protein catabolic process (Score: 2.941041)



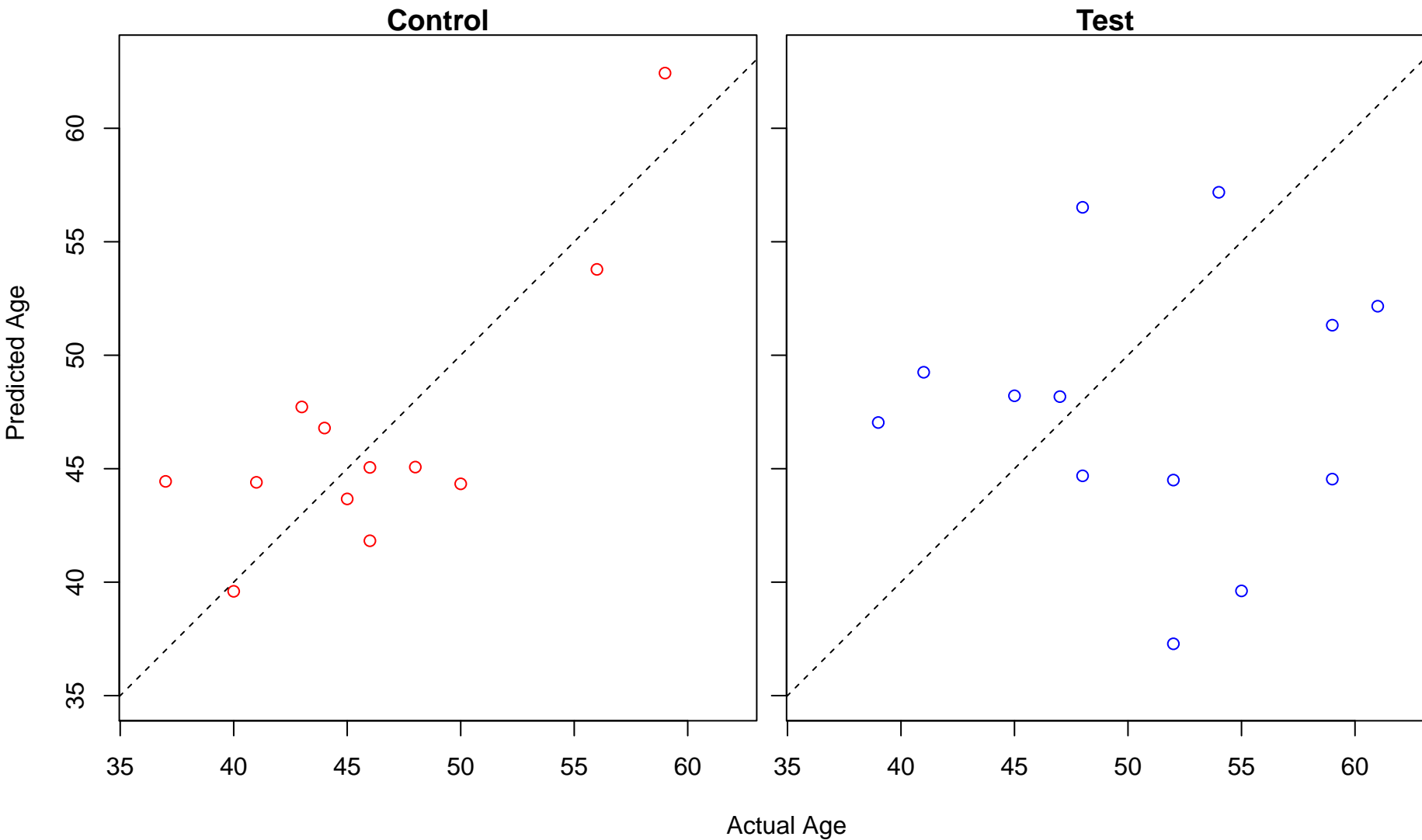
DNA damage response, signal transduction resulting in transcription (Score: 2.940948)



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

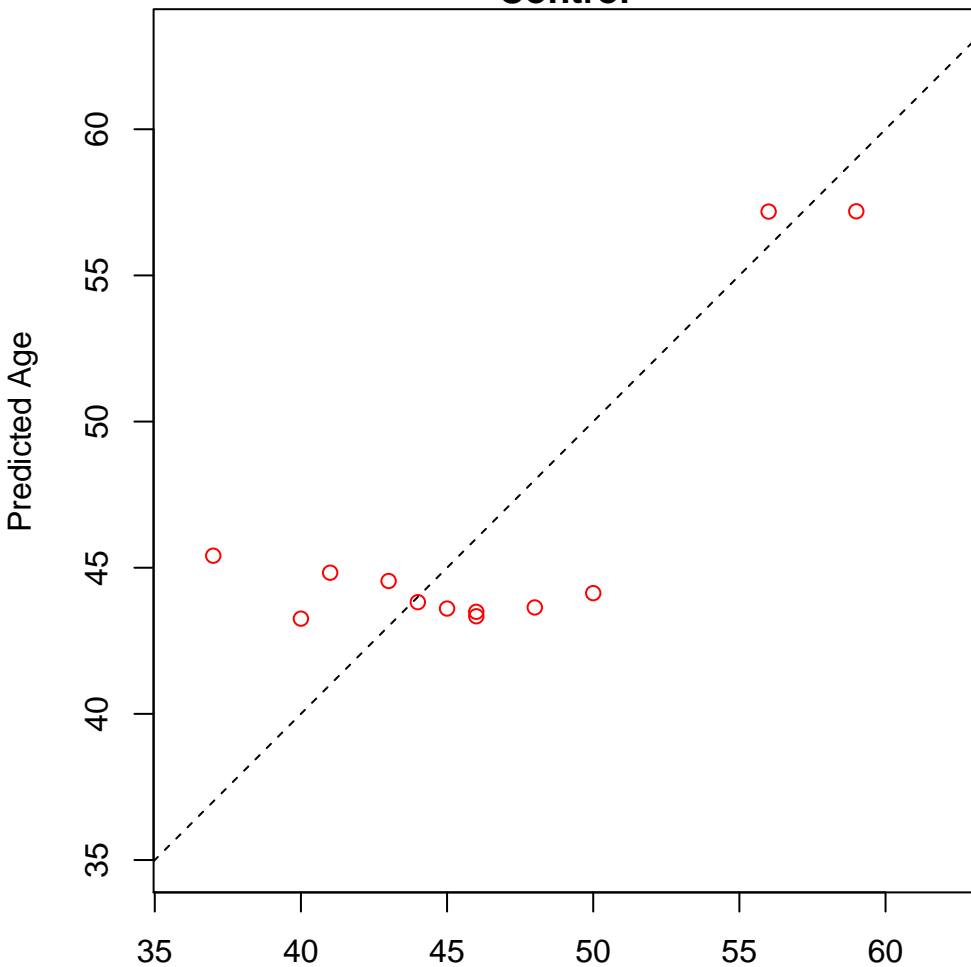


regulation of metal ion transport (Score: 2.940428)

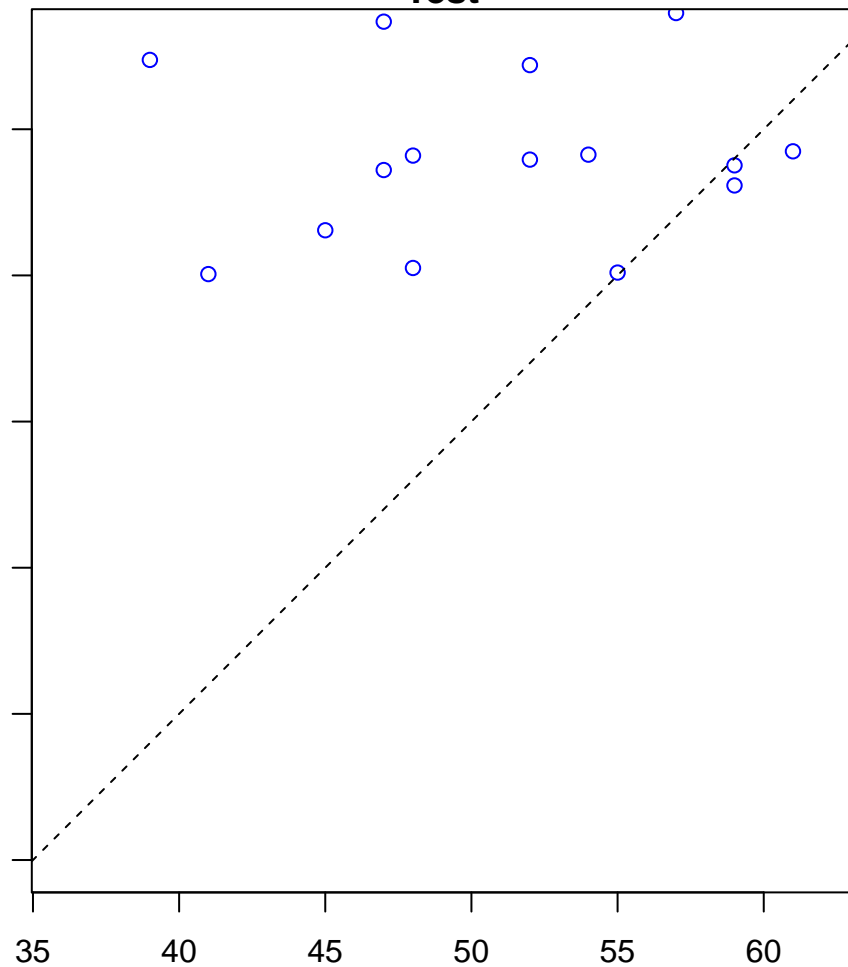


alpha-amino acid catabolic process (Score: 2.938799)

Control

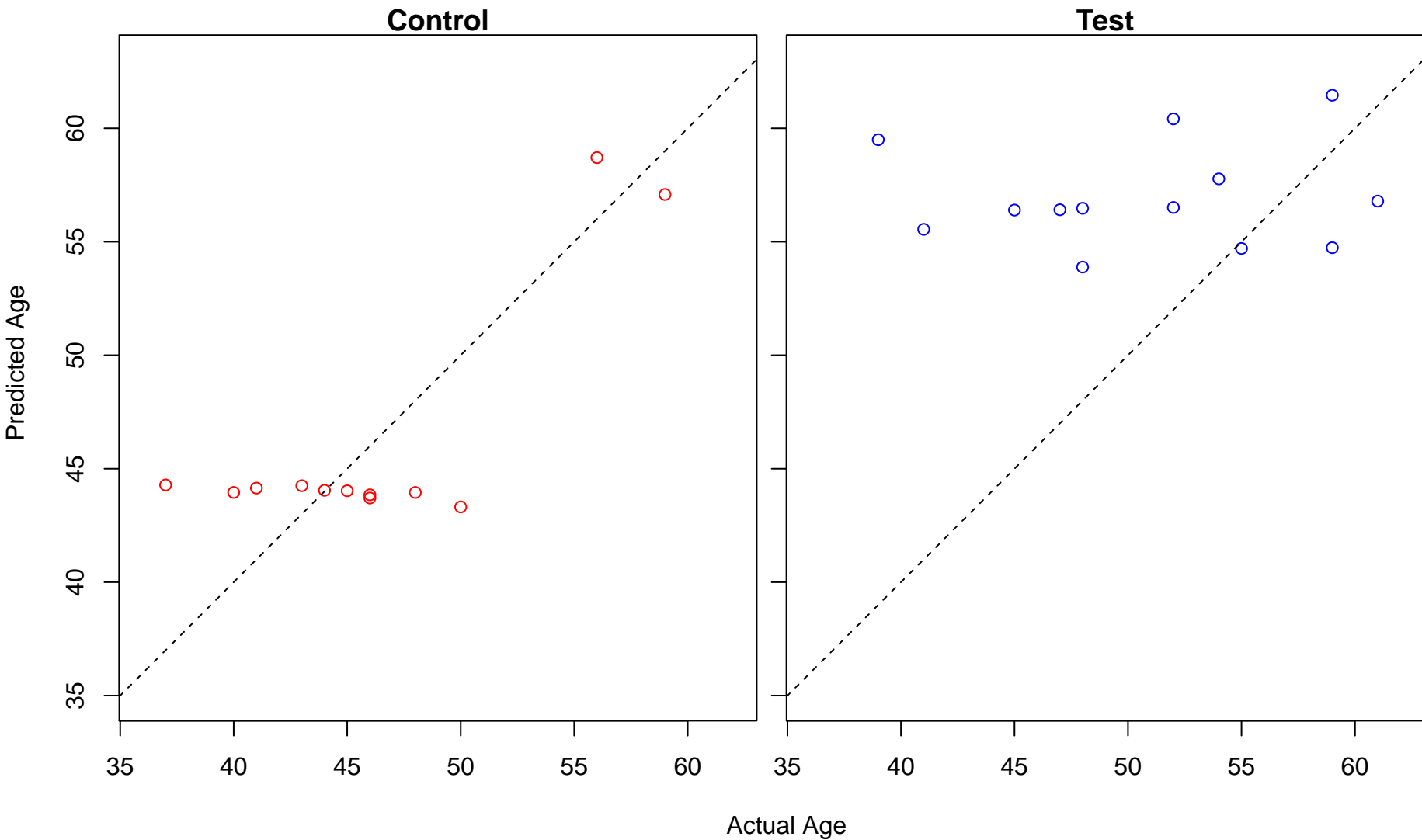


Test

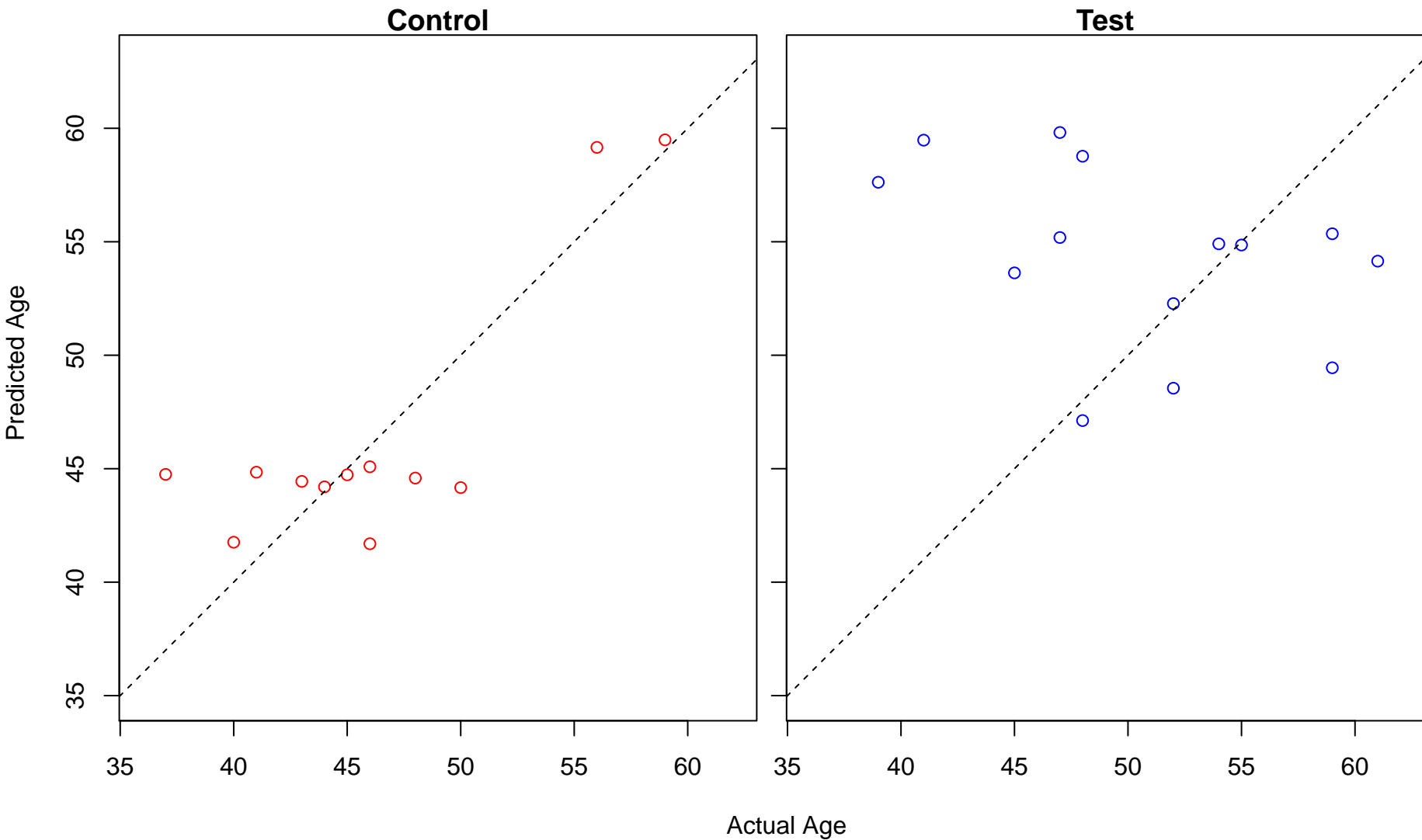


Actual Age

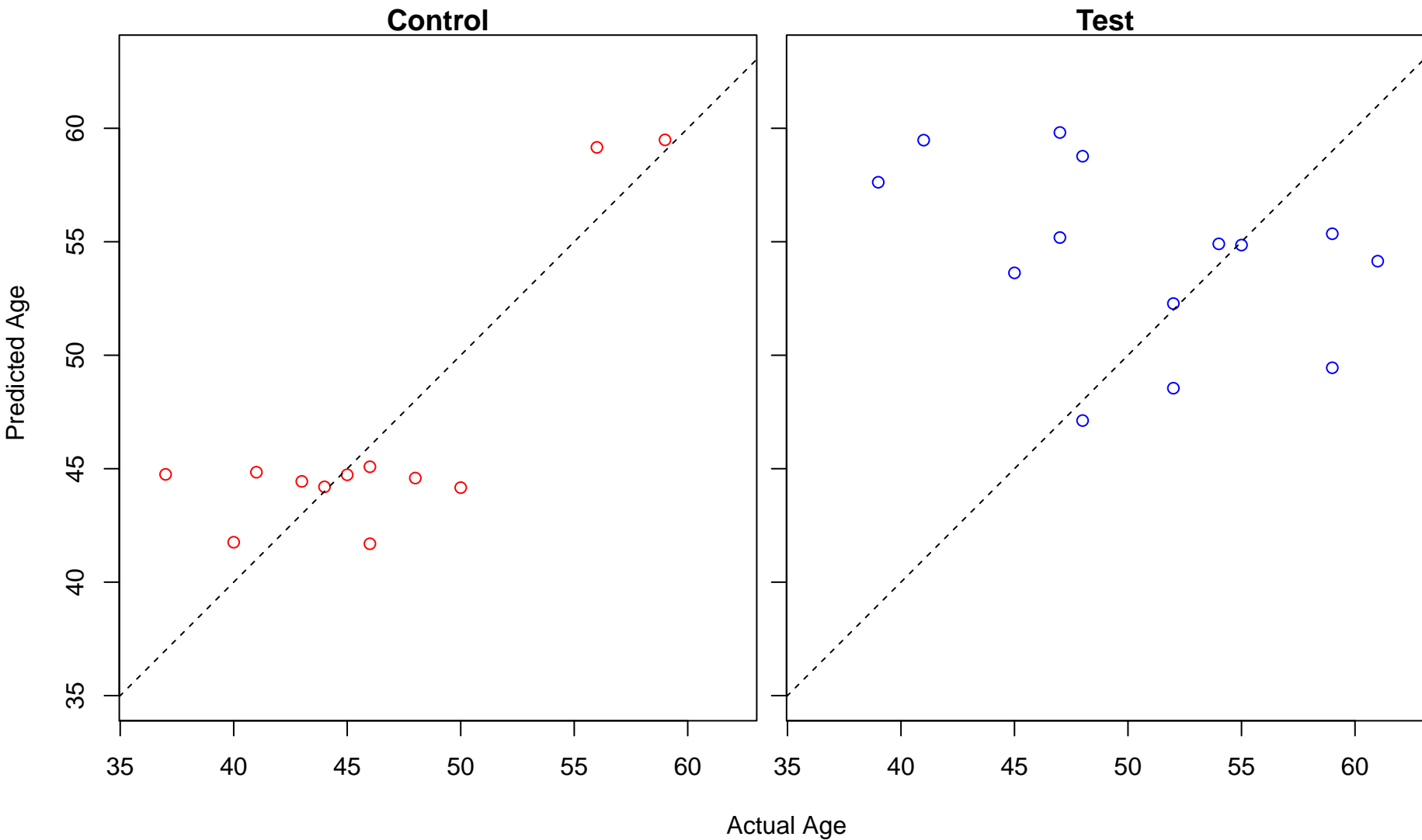
histone H2A monoubiquitination (Score: 2.936082)



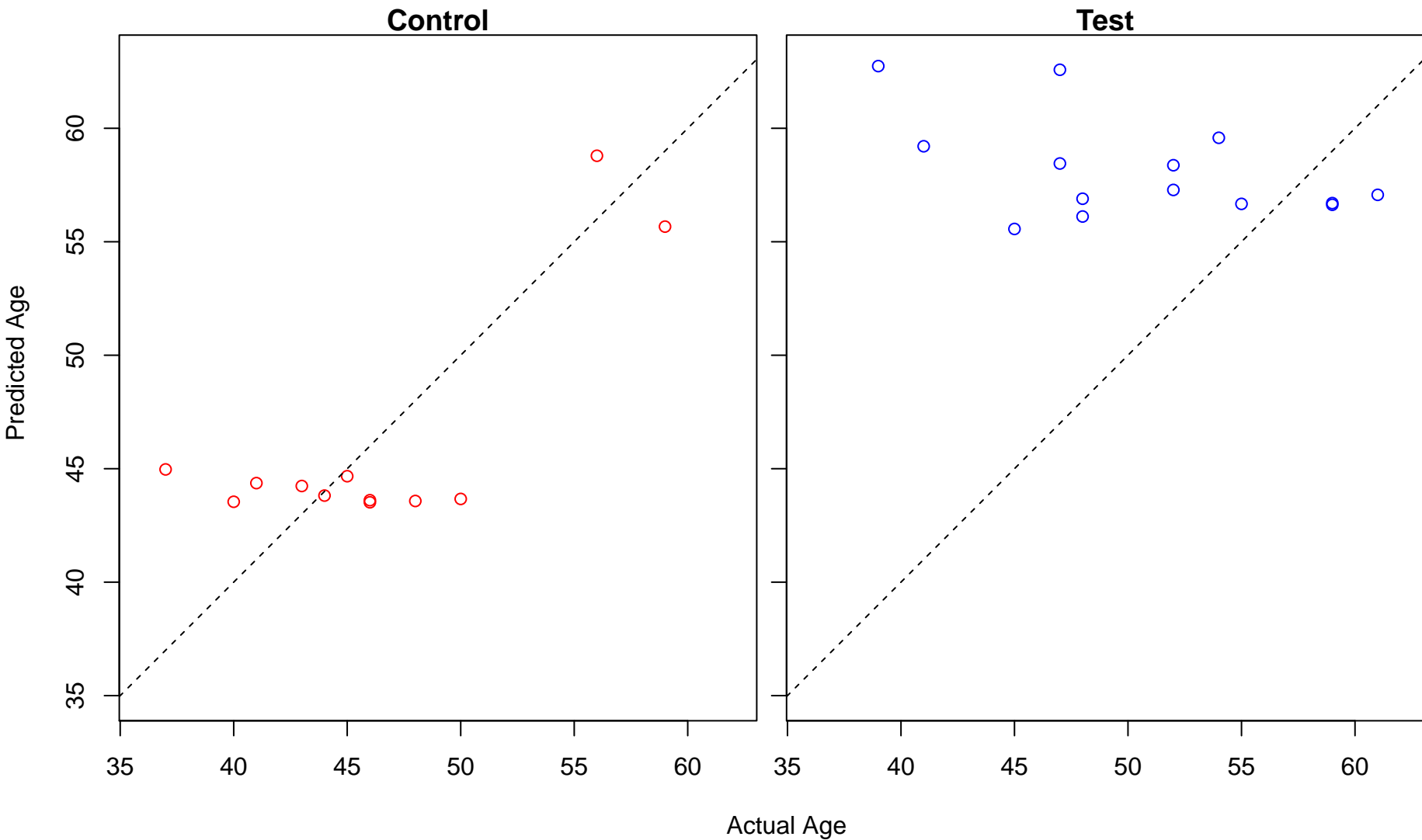
stimulatory C-type lectin receptor signaling pathway (Score: 2.934385)



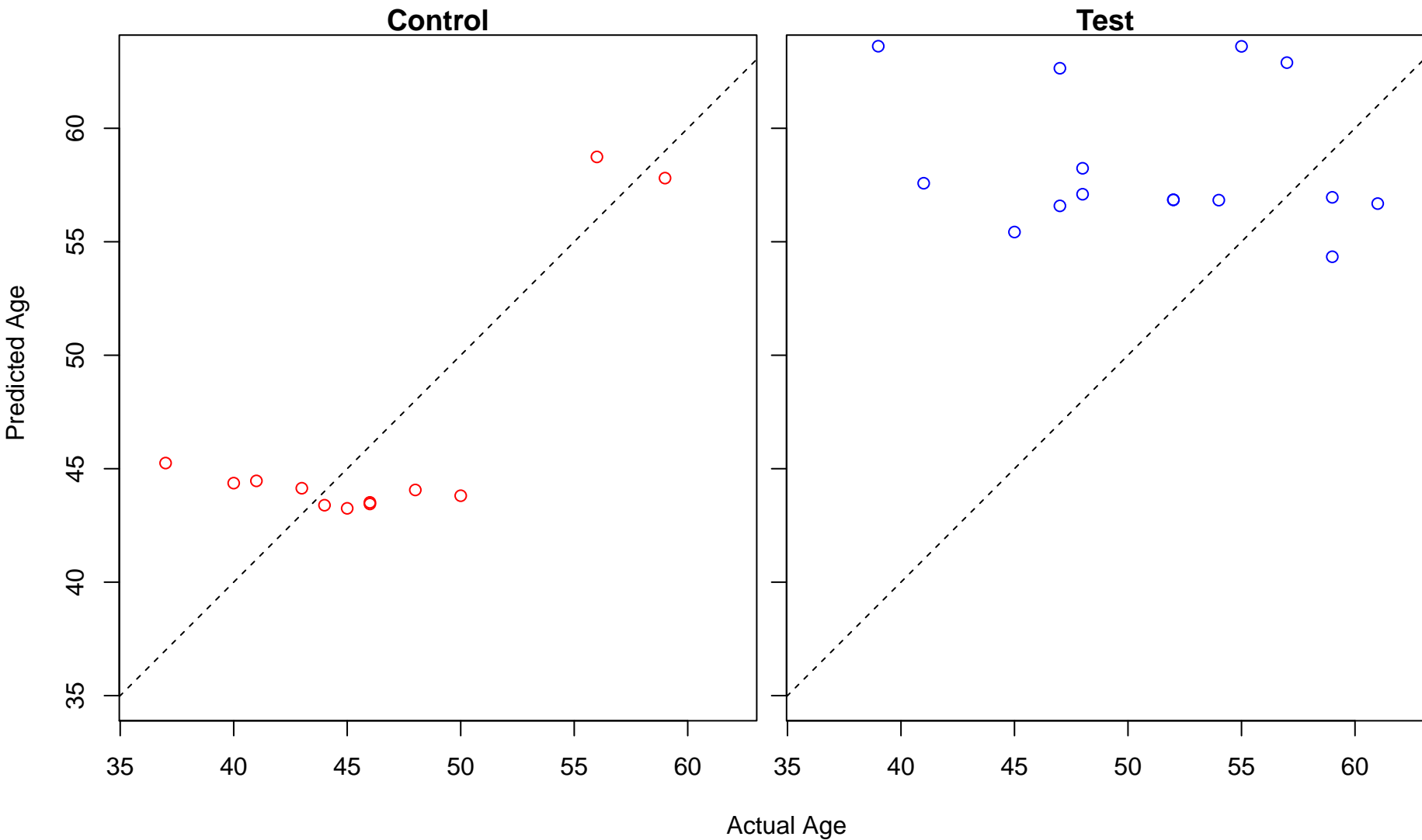
innate immune response activating cell surface receptor signaling pathway (Score: 2.934325)



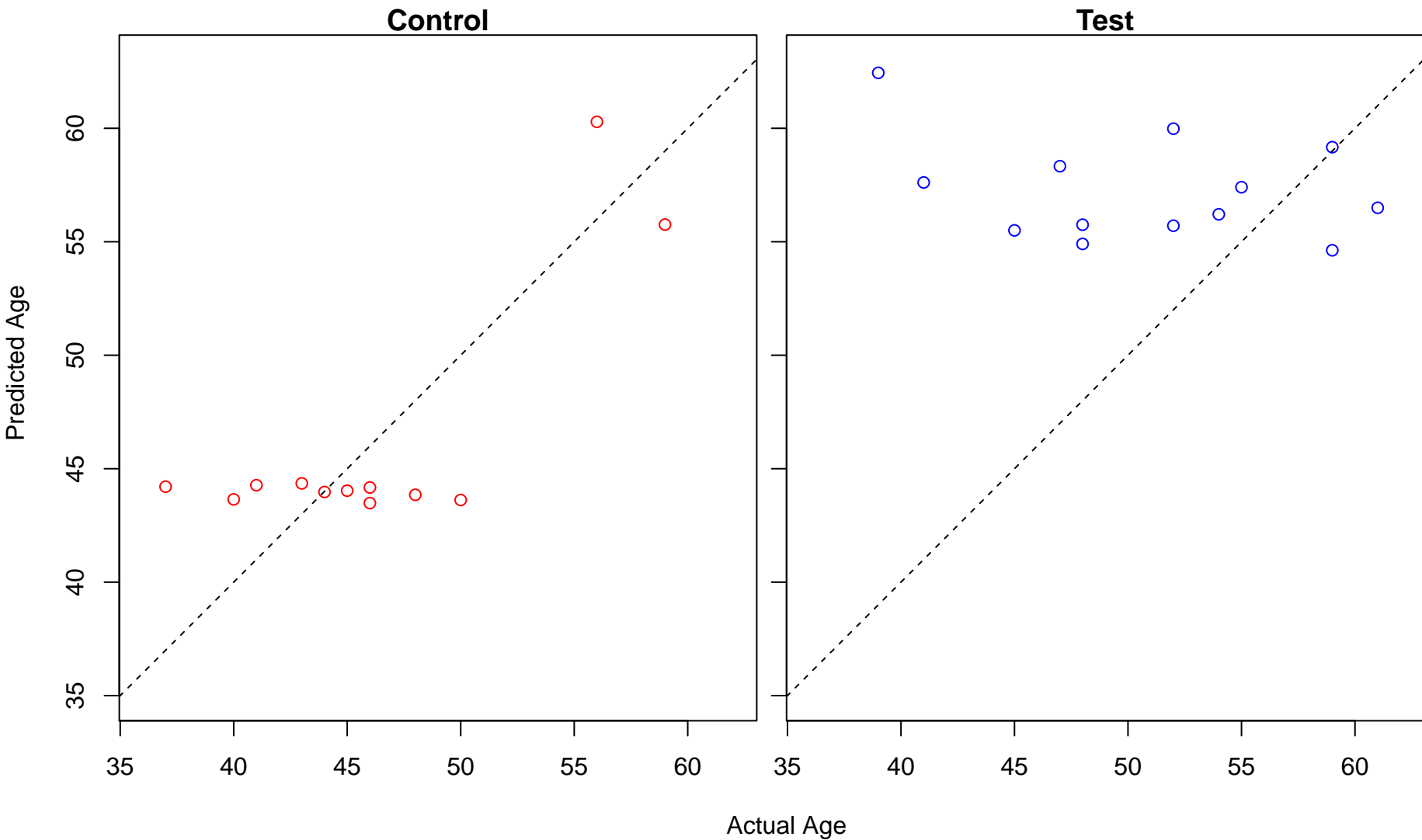
exocytosis (Score: 2.933912)



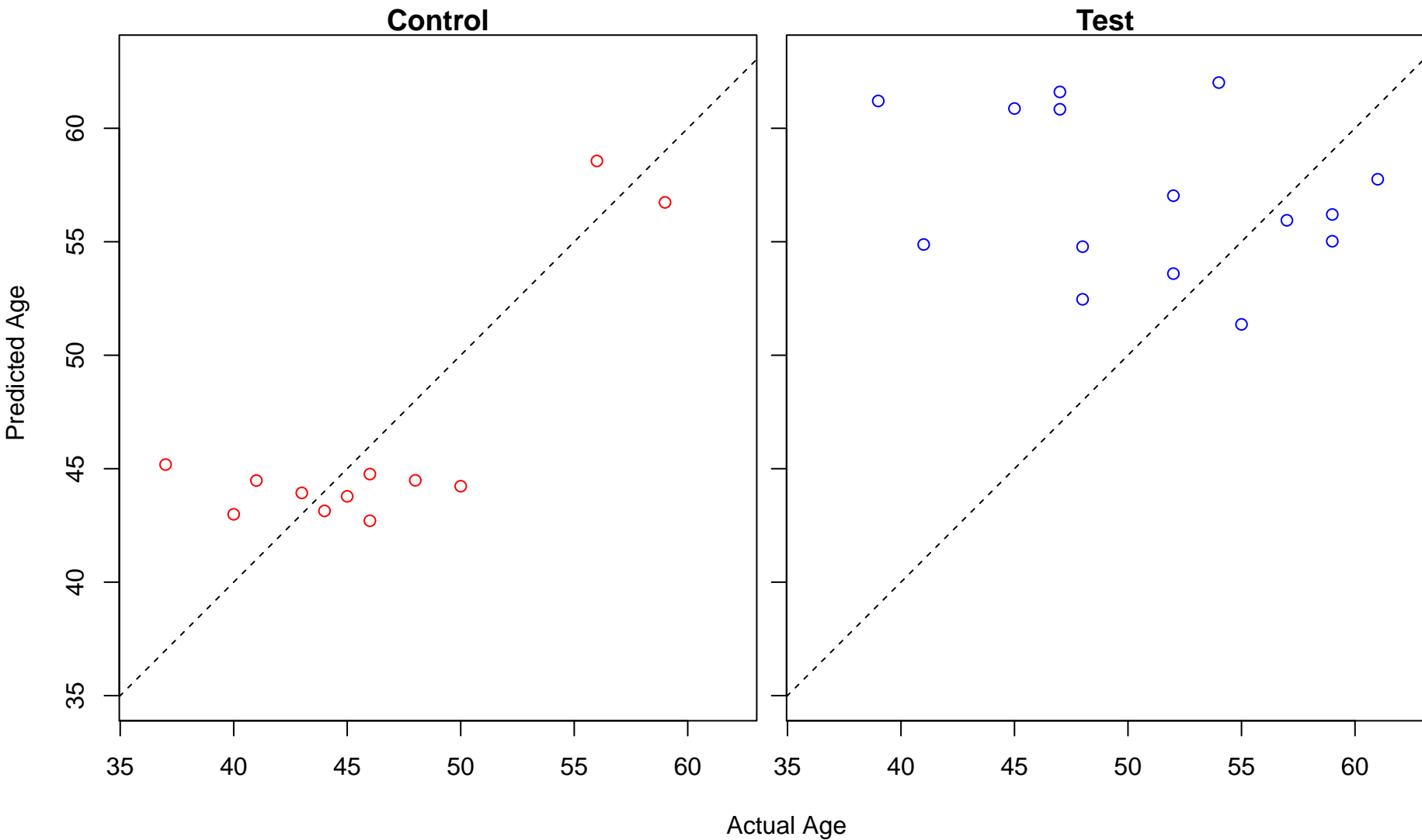
positive regulation of gene expression, epigenetic (Score: 2.932144)



establishment of localization by movement along microtubule (Score: 2.931901)

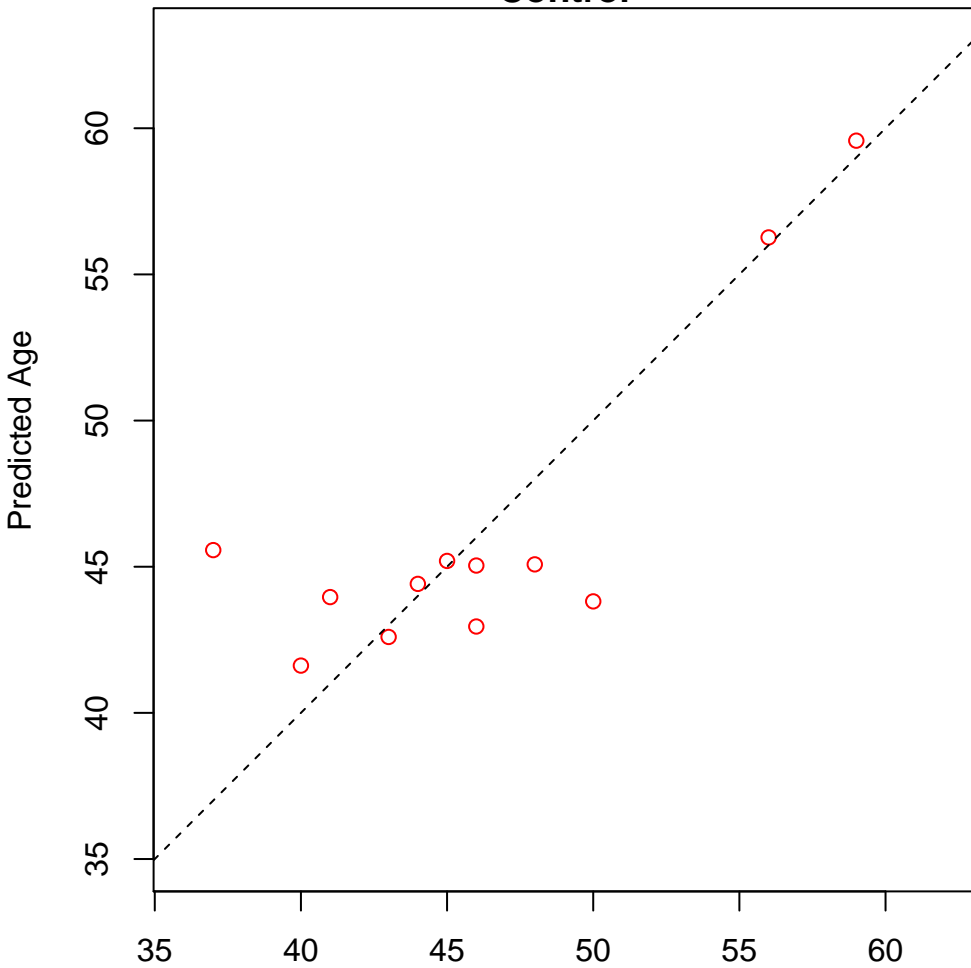


ionotropic glutamate receptor signaling pathway (Score: 2.928966)

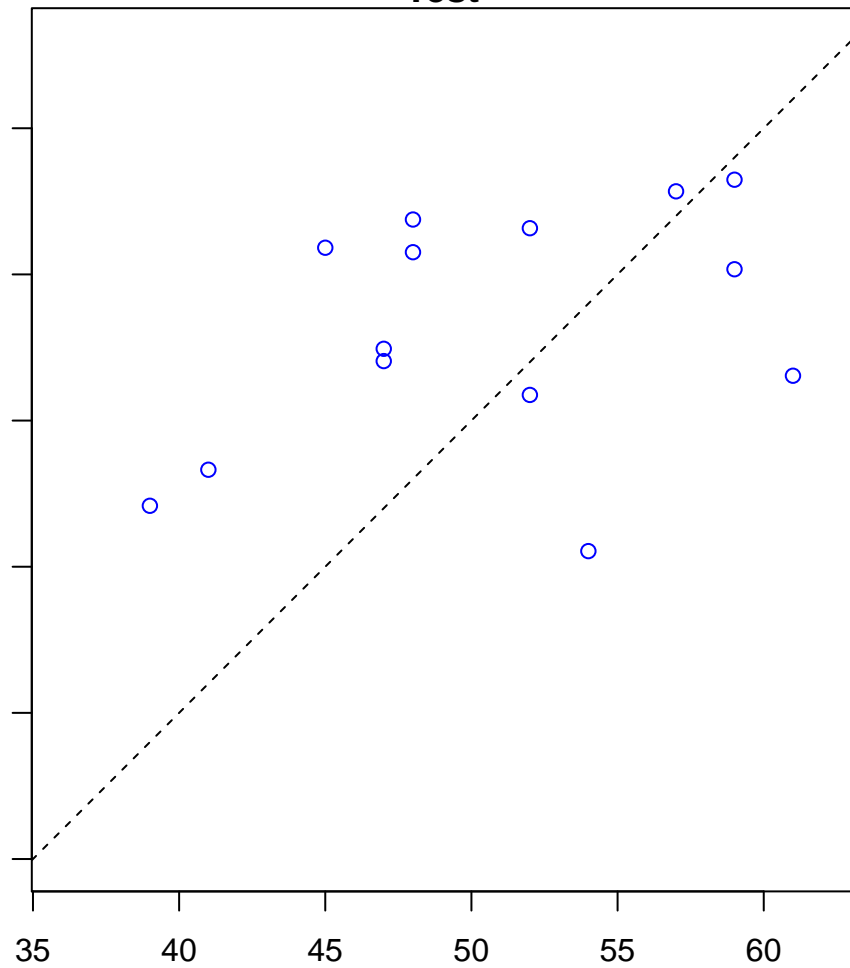


protein localization to Golgi apparatus (Score: 2.928625)

Control

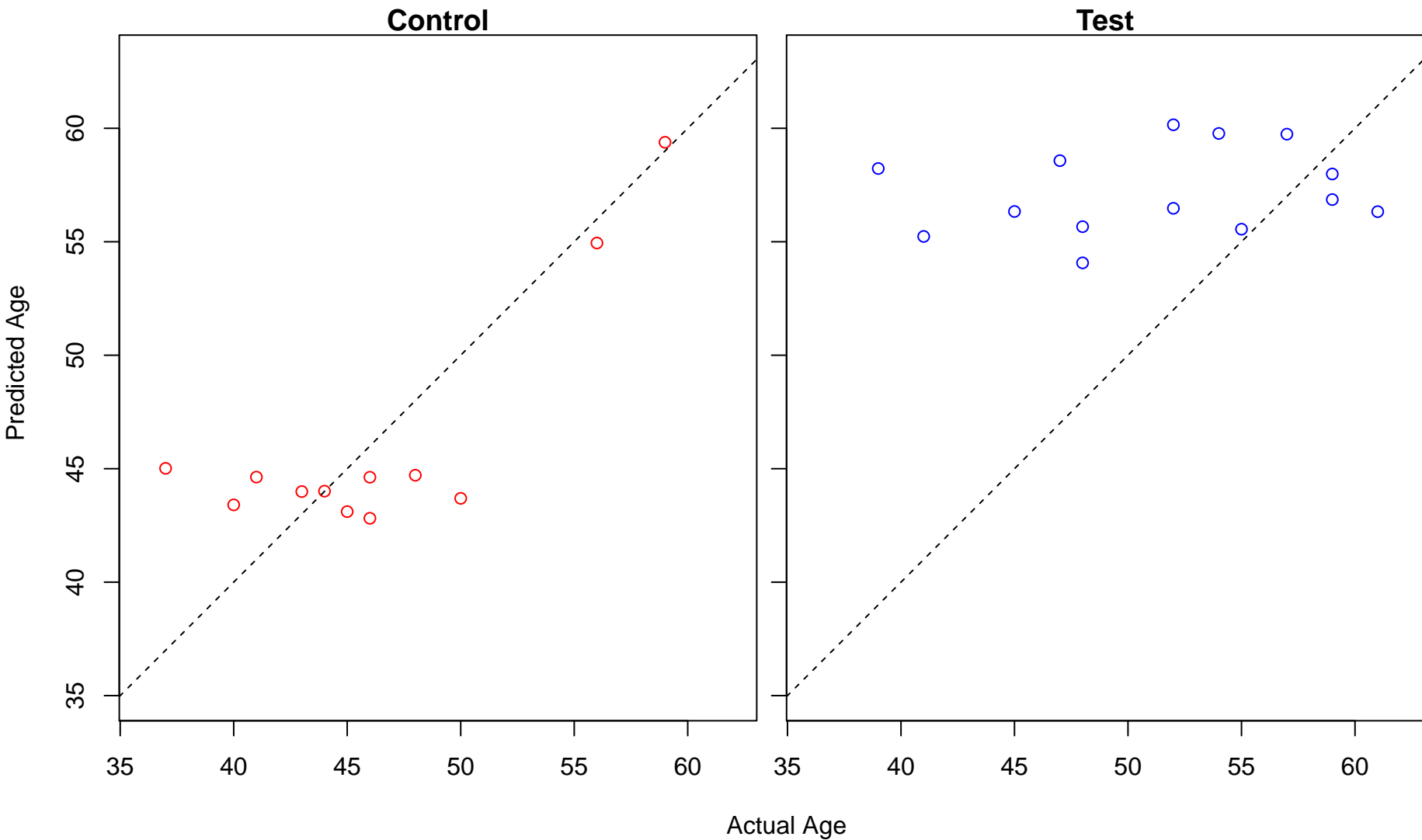


Test

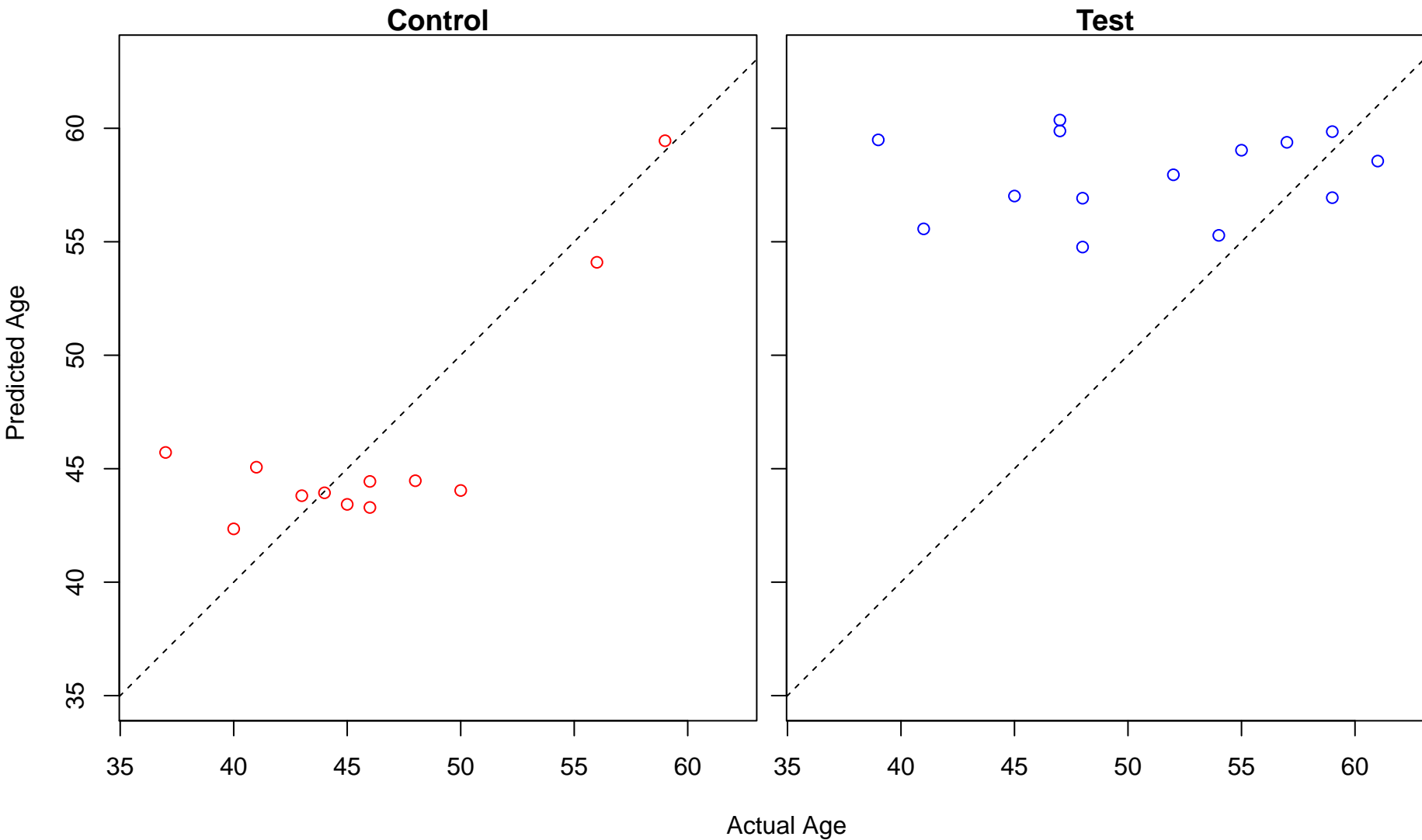


Actual Age

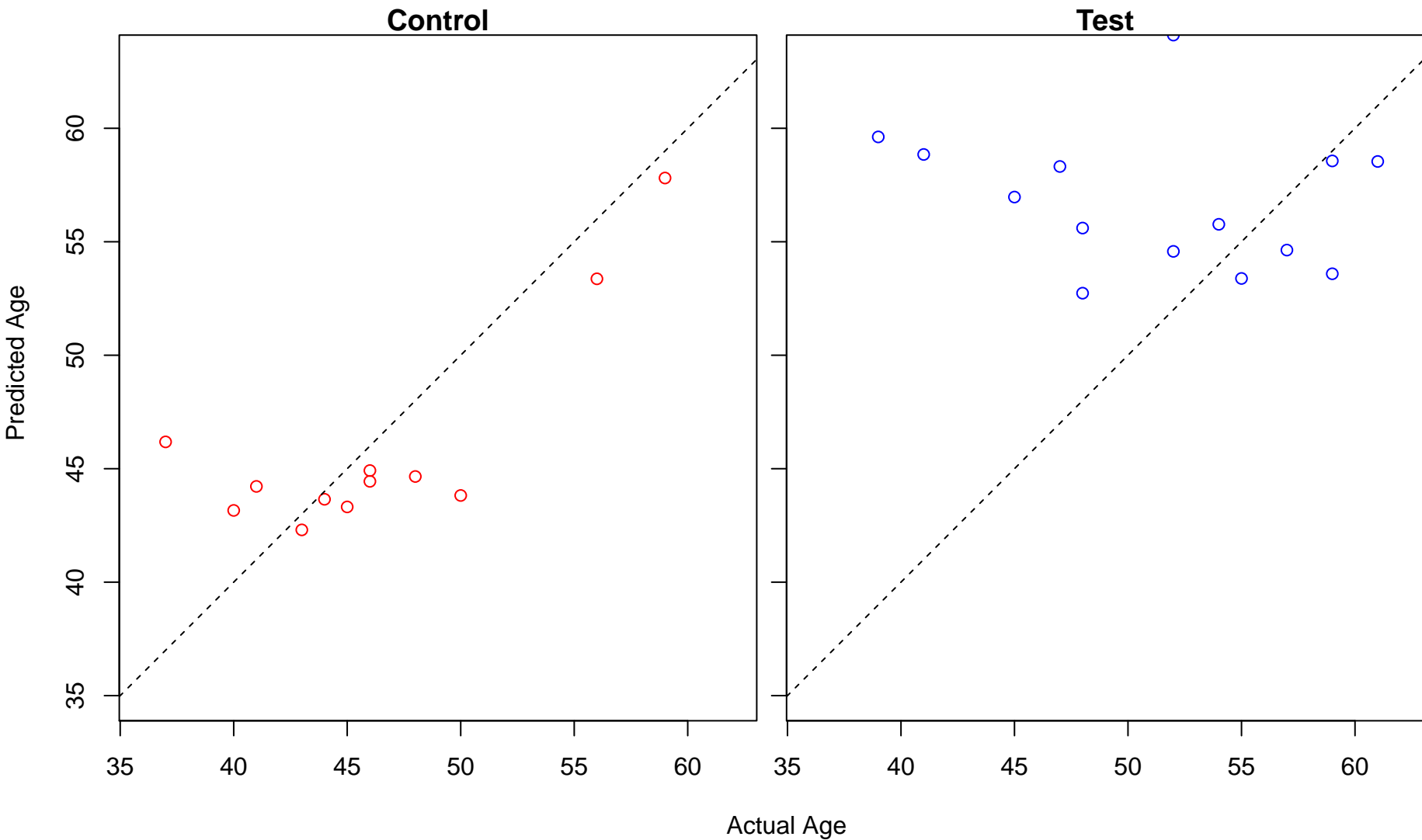
adherens junction assembly (Score: 2.927462)



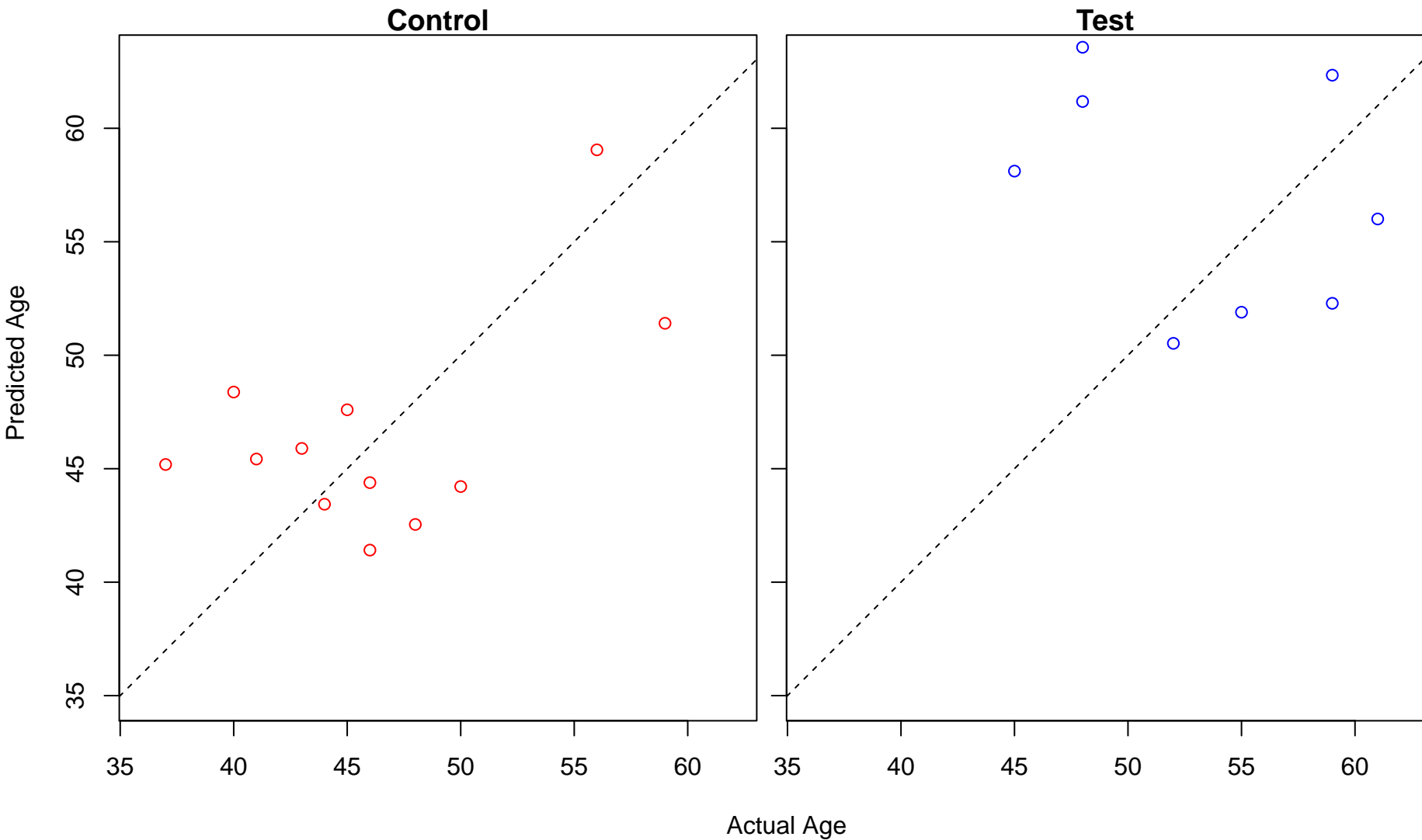
negative regulation of tumor necrosis factor–mediated signaling pathway (Score: 2.927160)



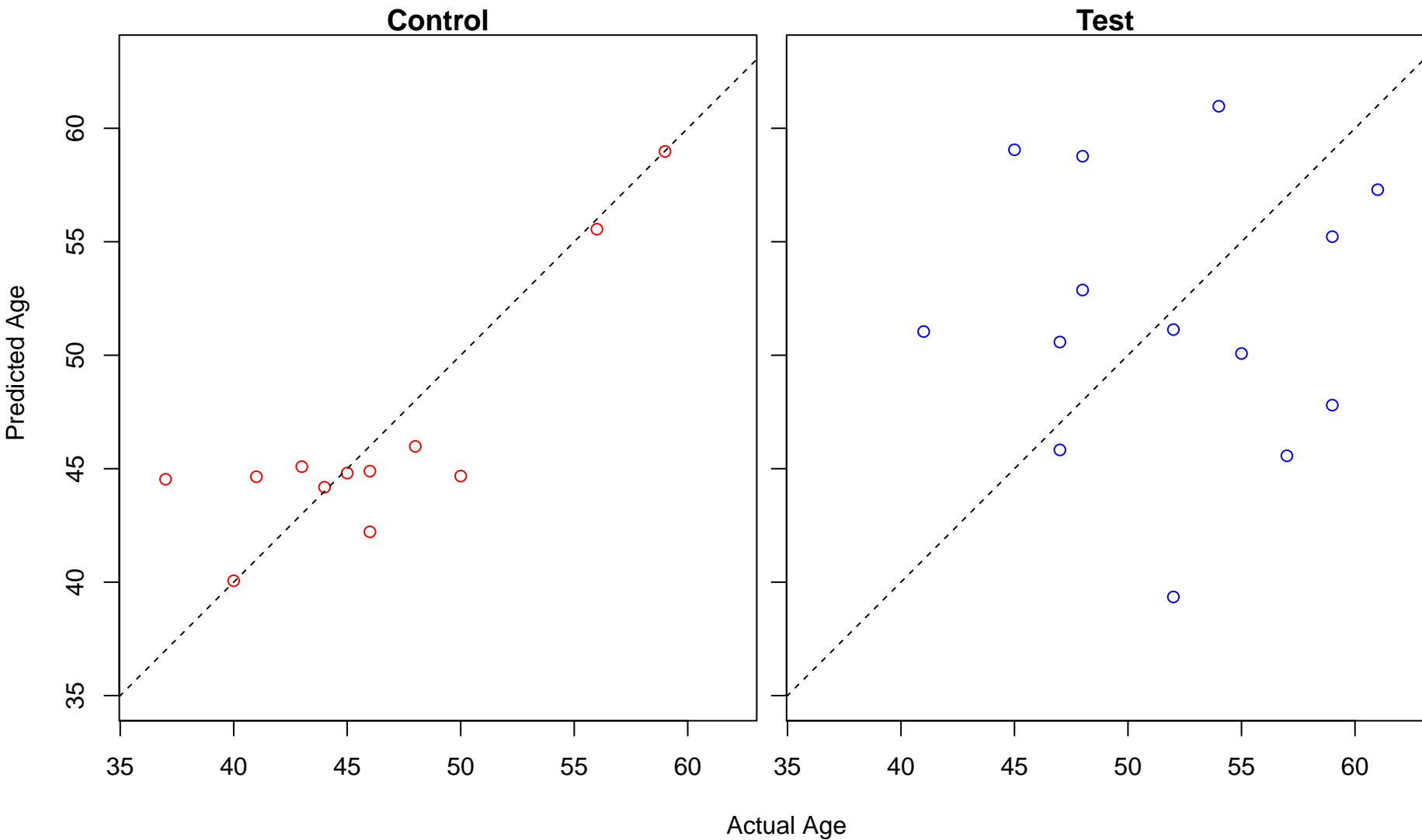
vitamin D metabolic process (Score: 2.92379)



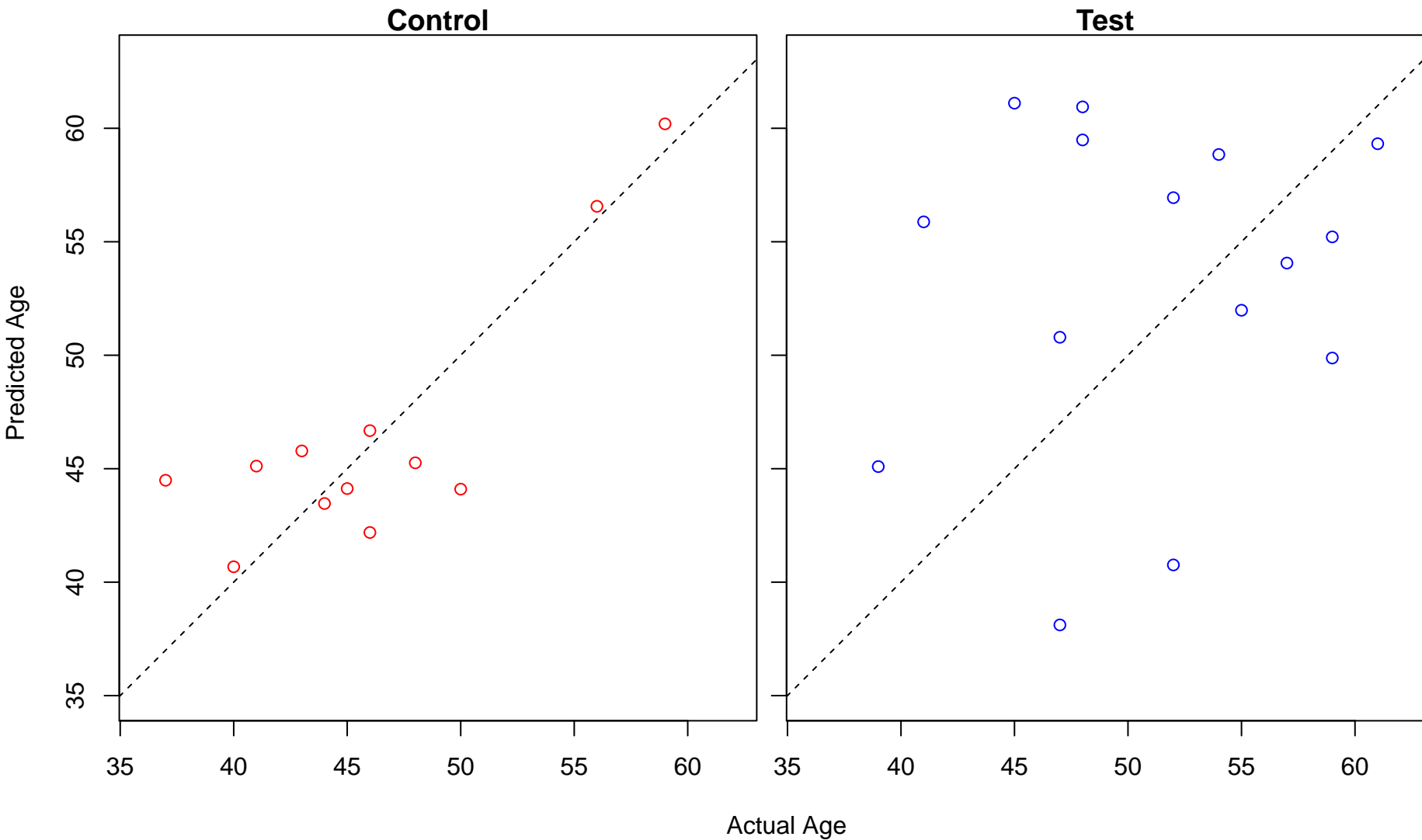
regulation of phospholipid catabolic process (Score: 2.922583)



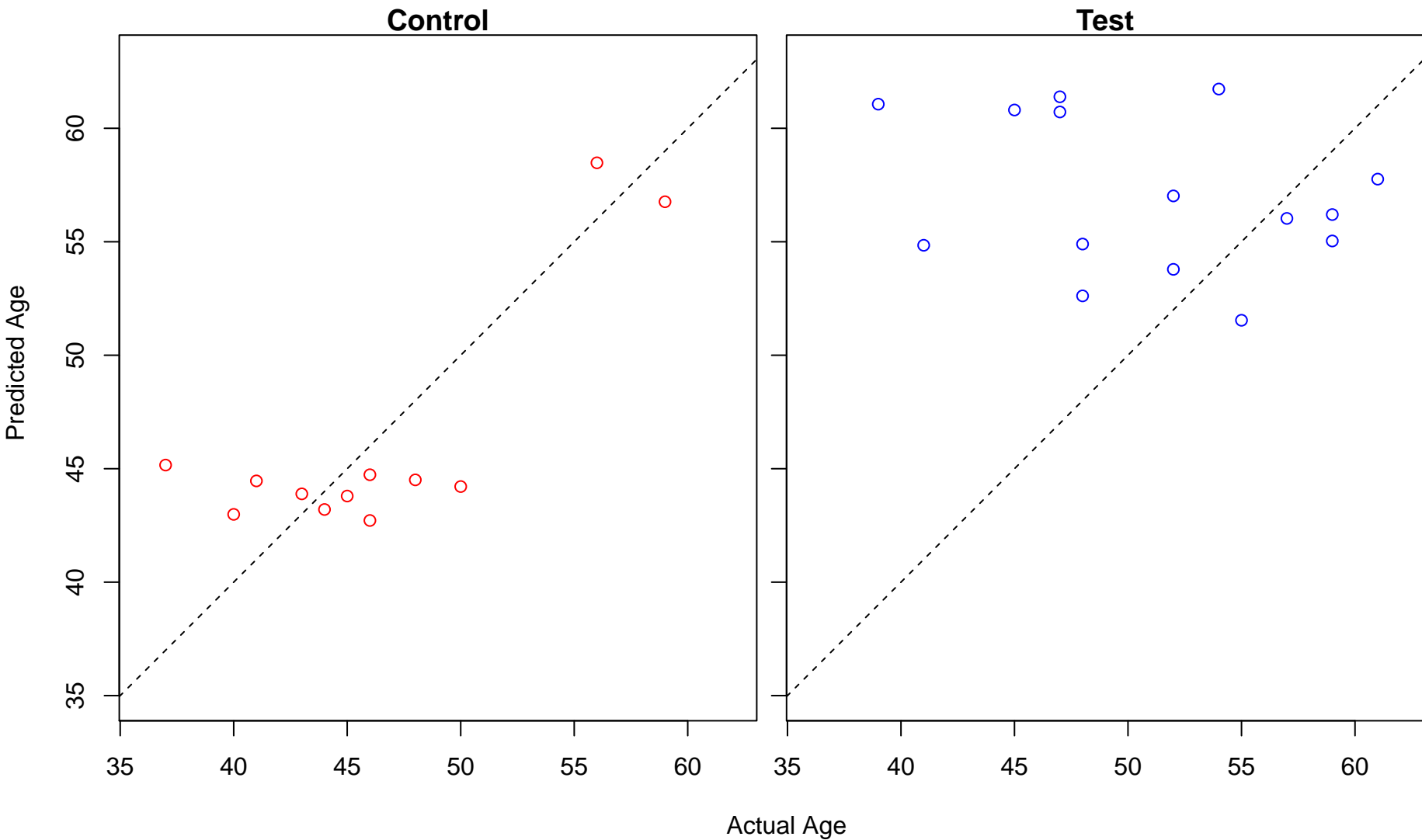
positive regulation of intracellular protein transport (Score: 2.922523)



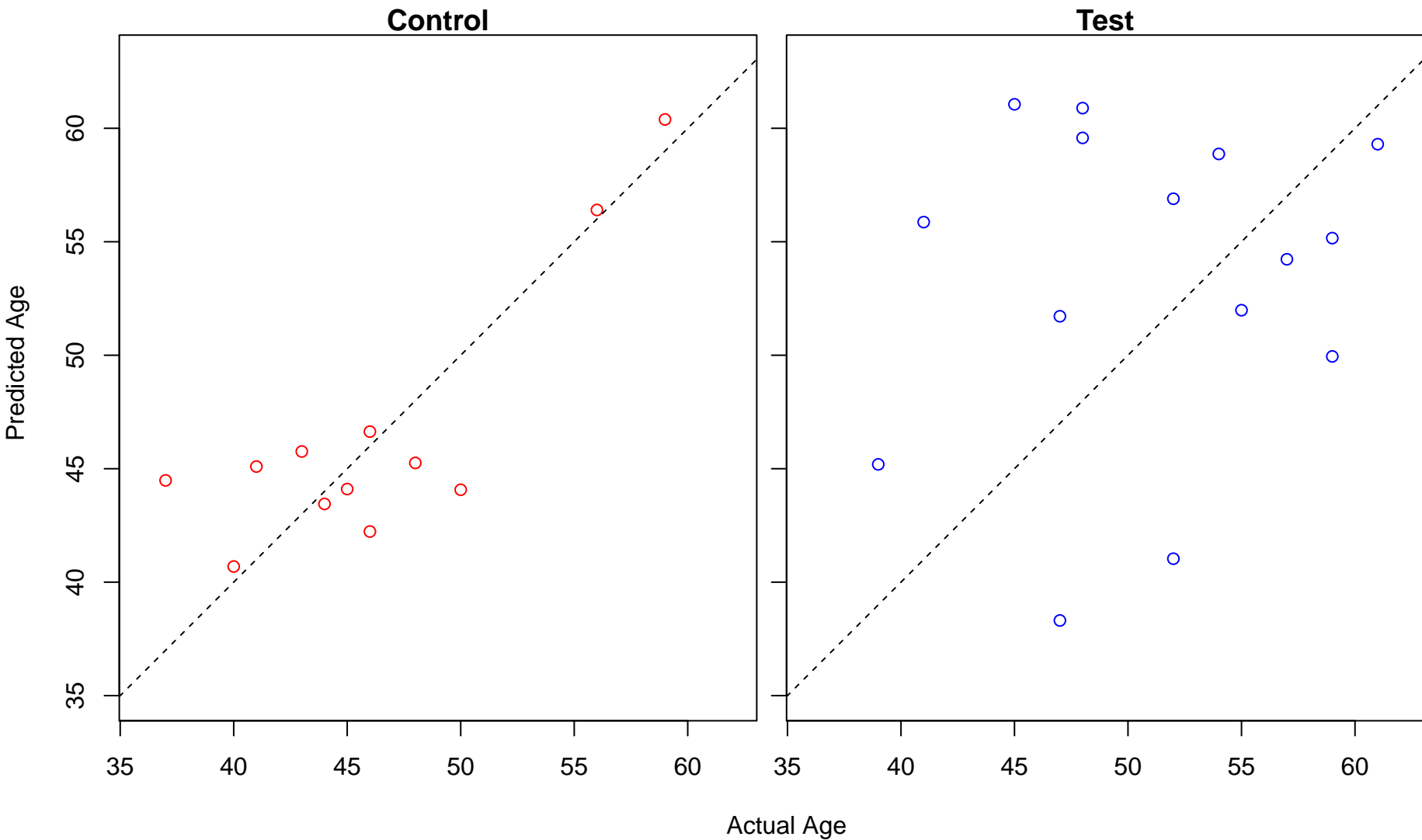
negative regulation of potassium ion transmembrane transporter activity (Score: 2.921471)



glutamate receptor signaling pathway (Score: 2.921364)

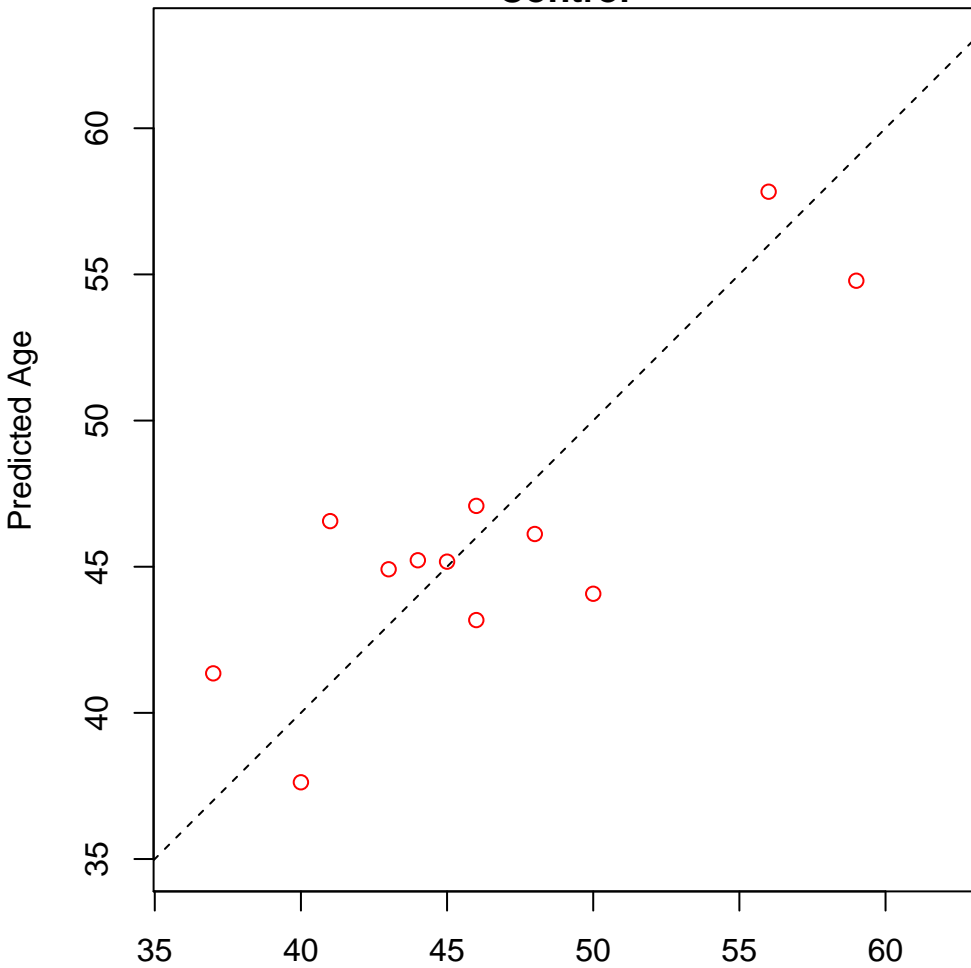


negative regulation of potassium ion transmembrane transport (Score: 2.920078)

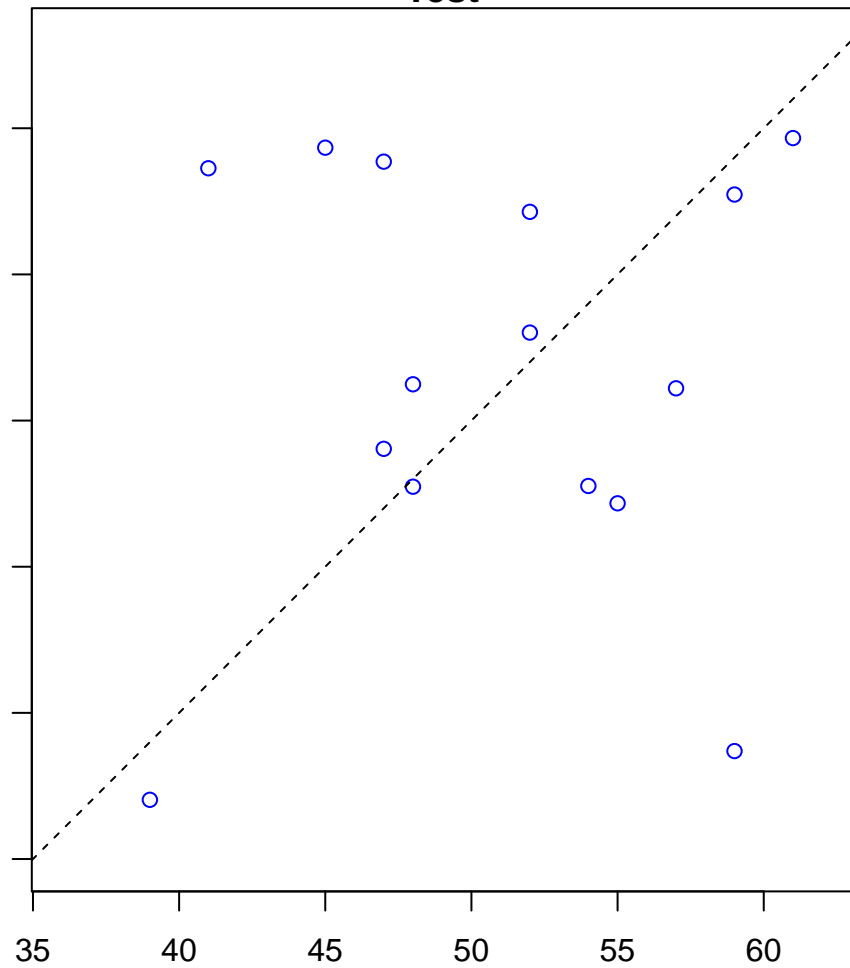


regulation of lymphocyte proliferation (Score: 2.919020)

Control

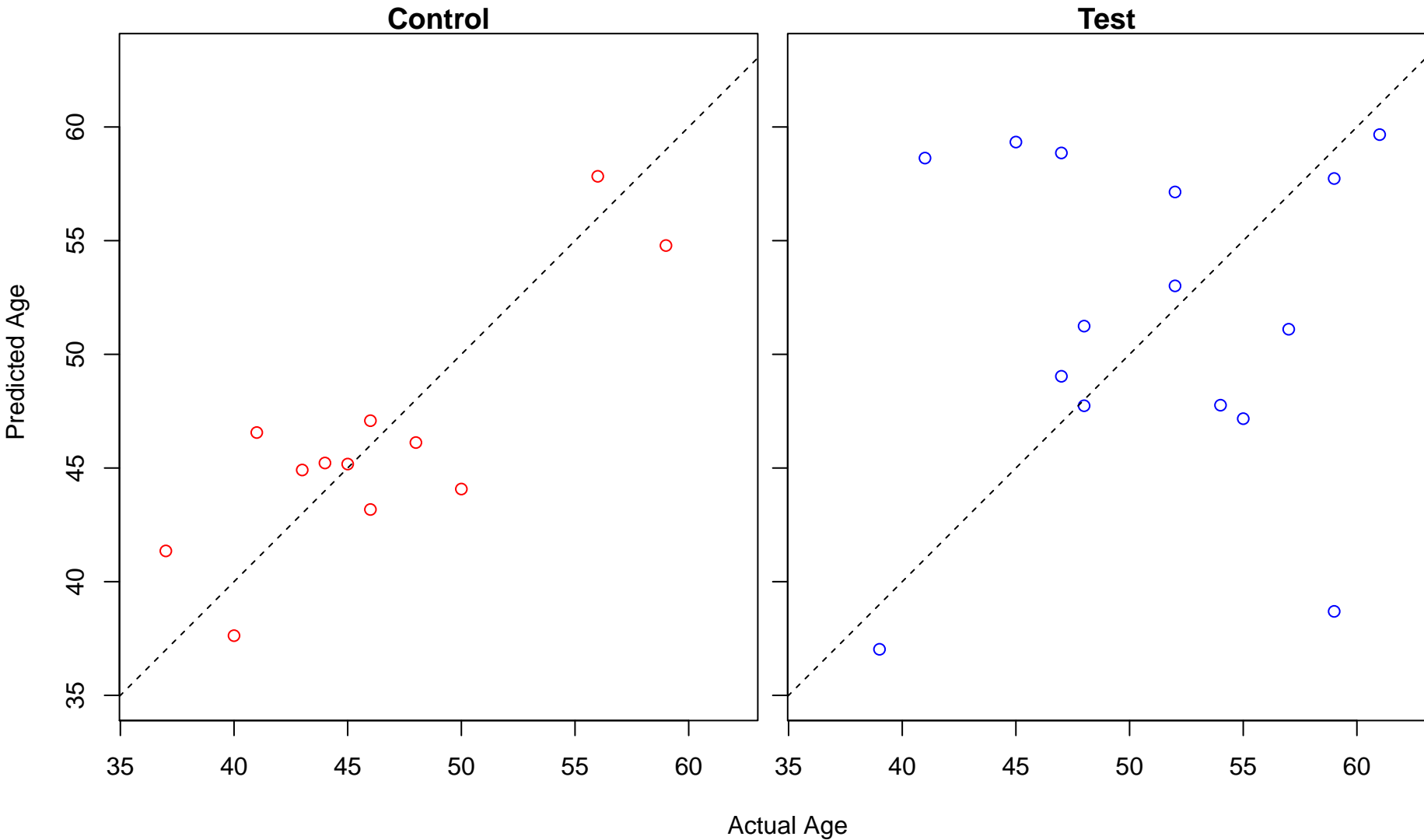


Test

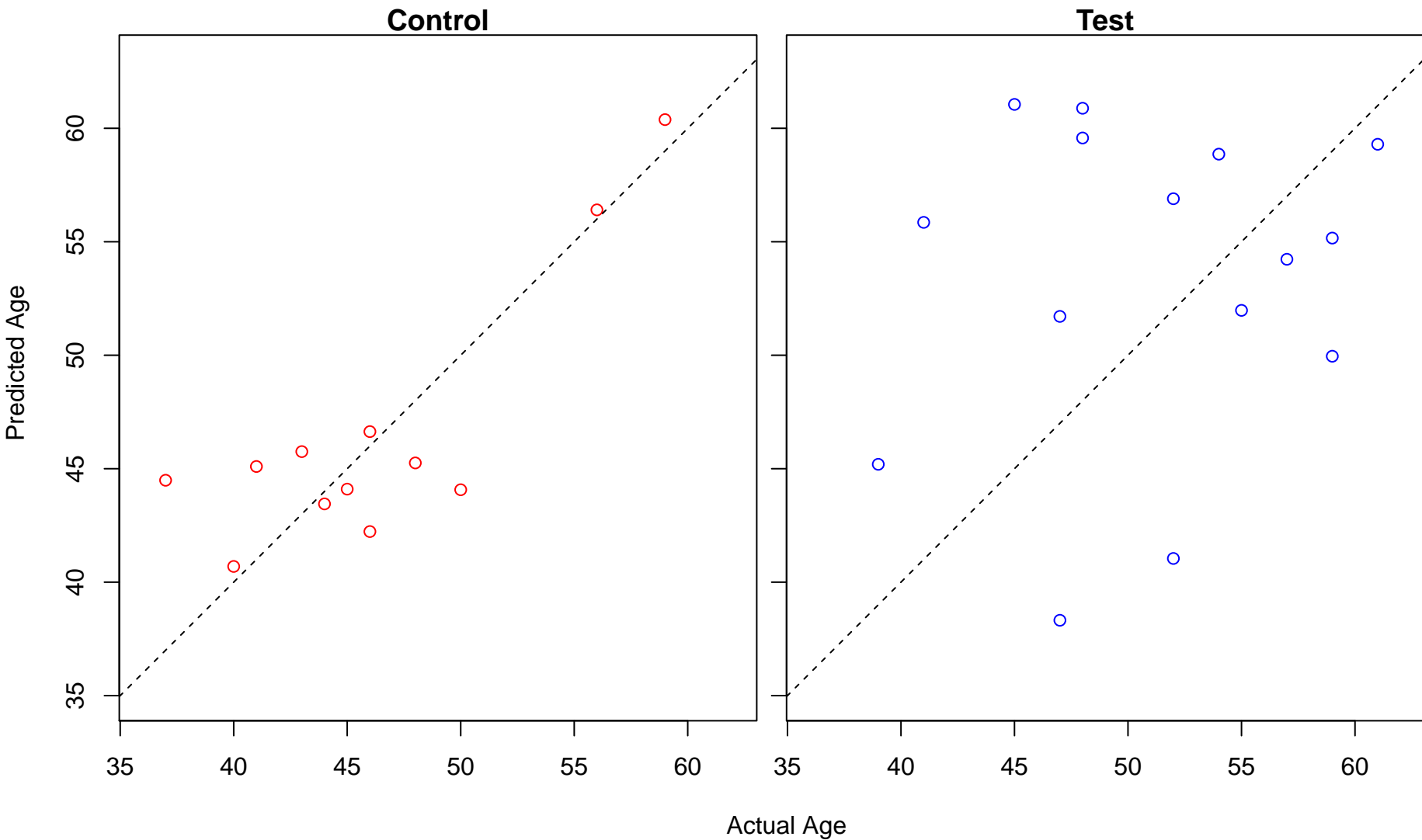


Actual Age

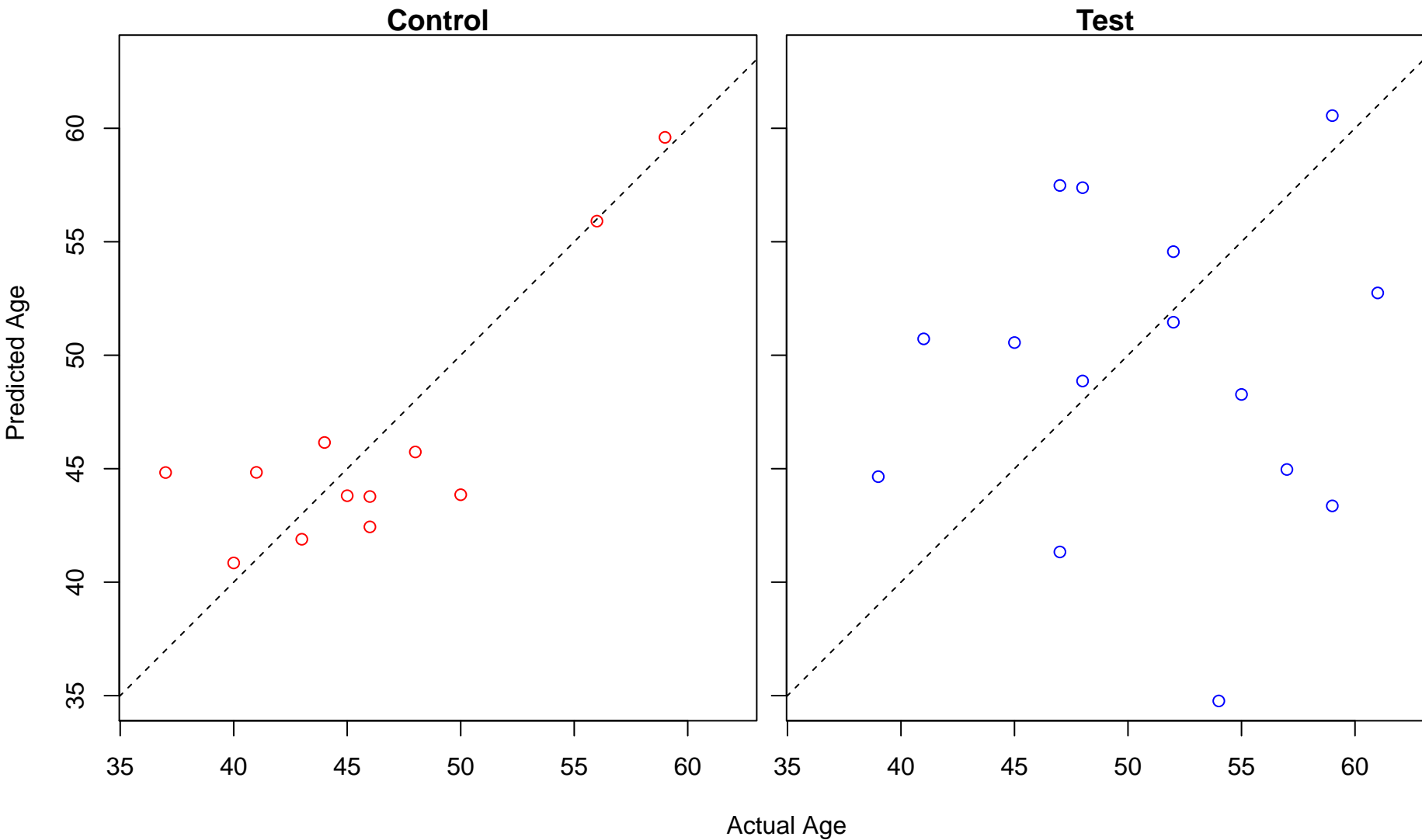
regulation of mononuclear cell proliferation (Score: 2.918998)



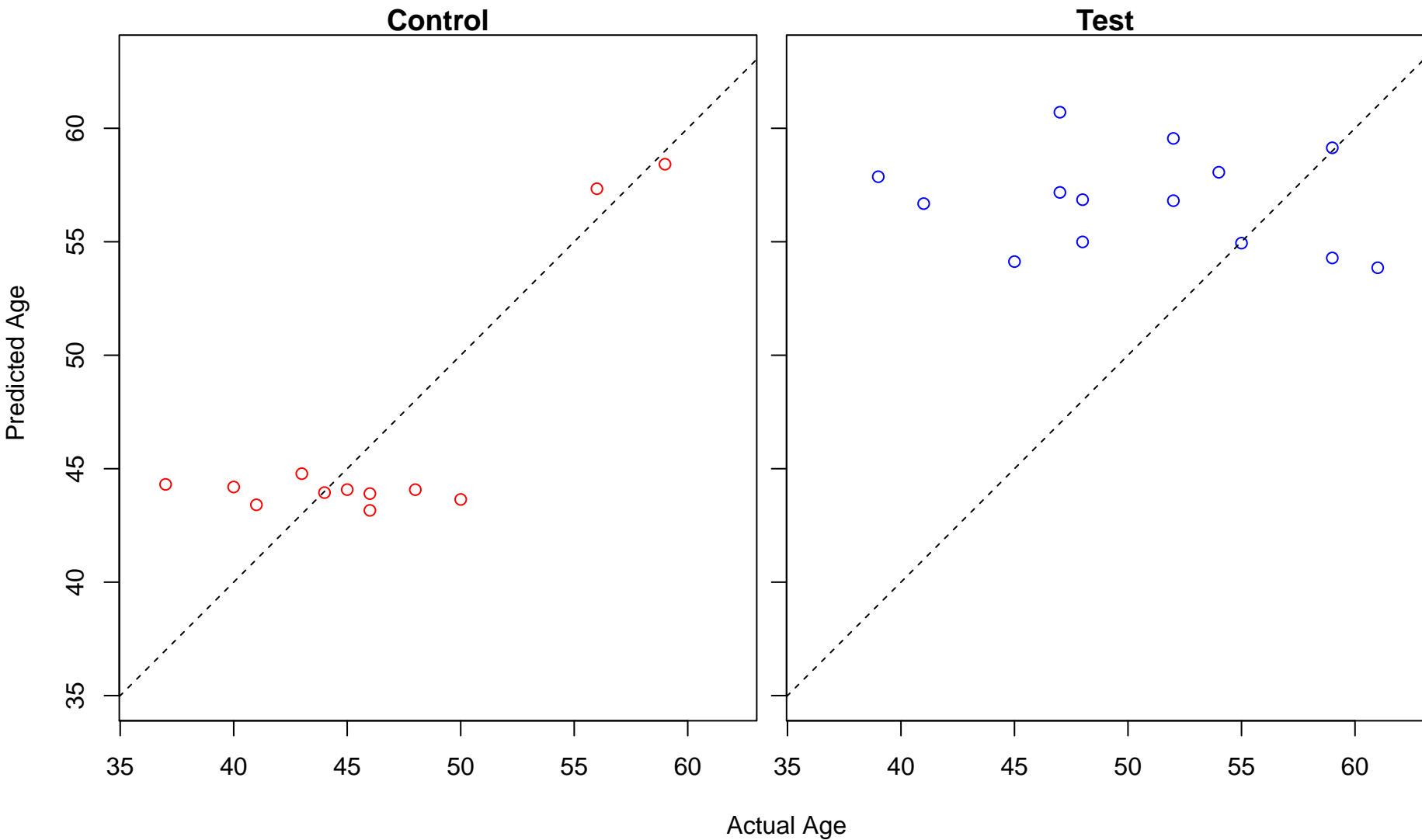
negative regulation of potassium ion transport (Score: 2.916794)



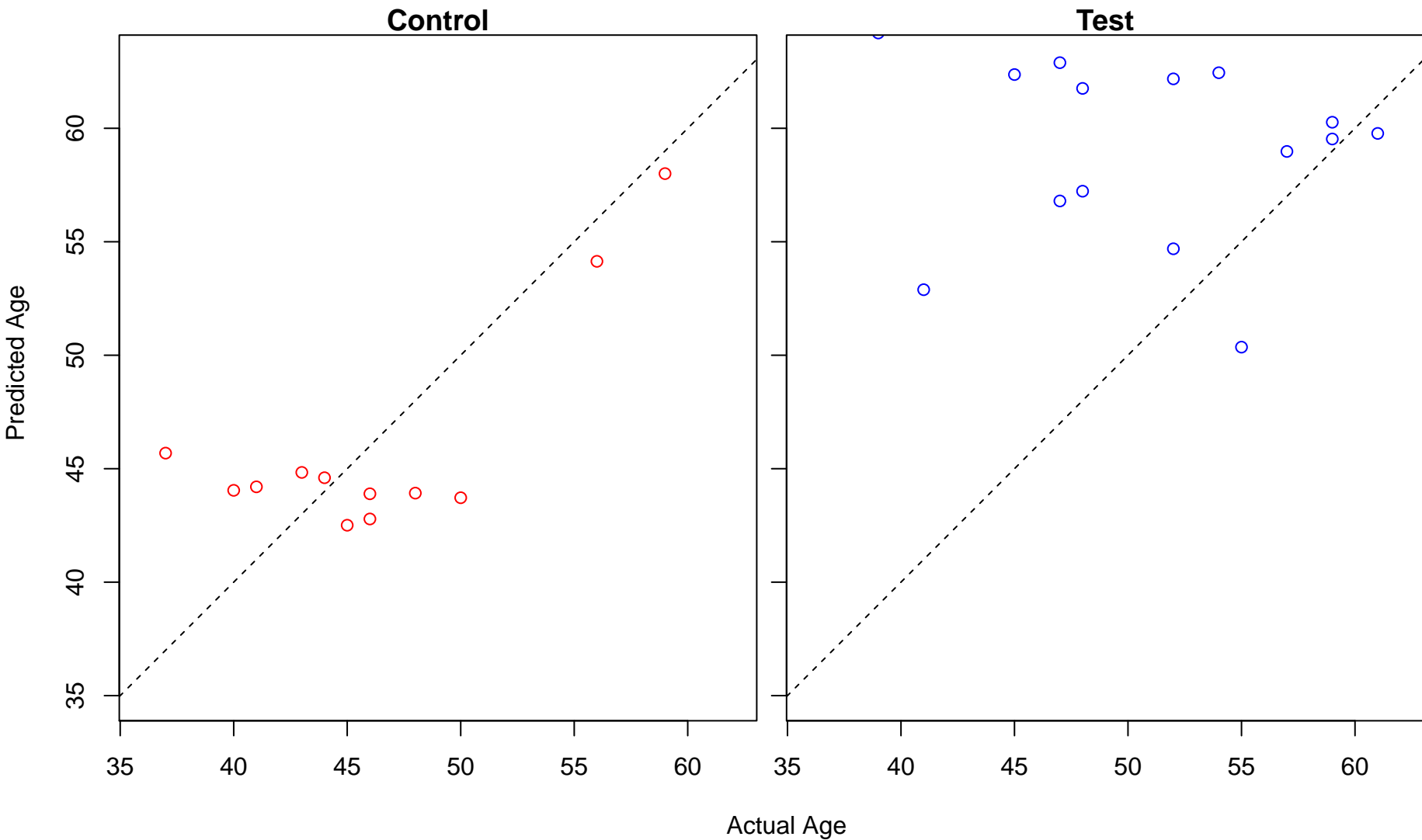
regulation of DNA endoreduplication (Score: 2.916547)



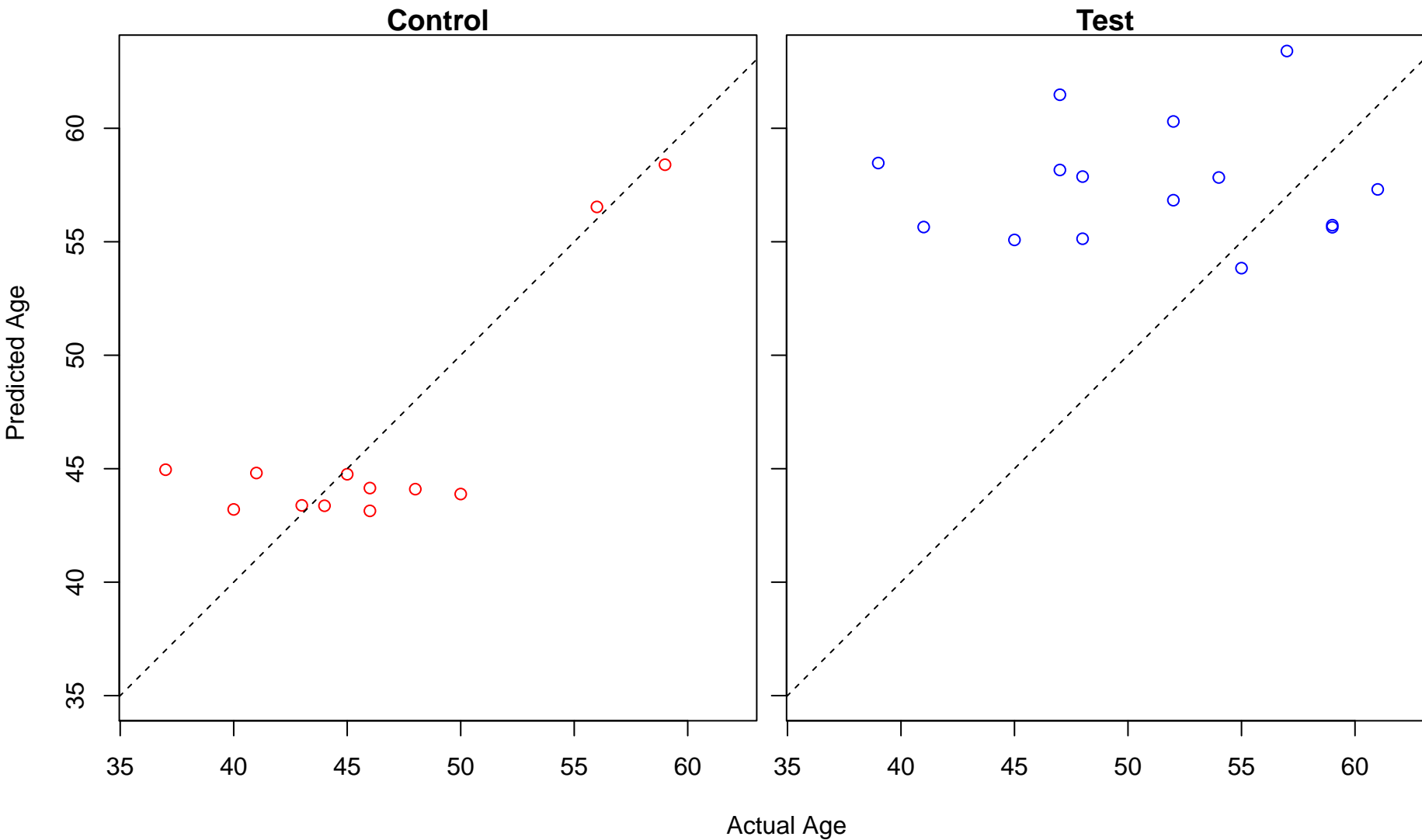
cytokinetic process (Score: 2.916275)



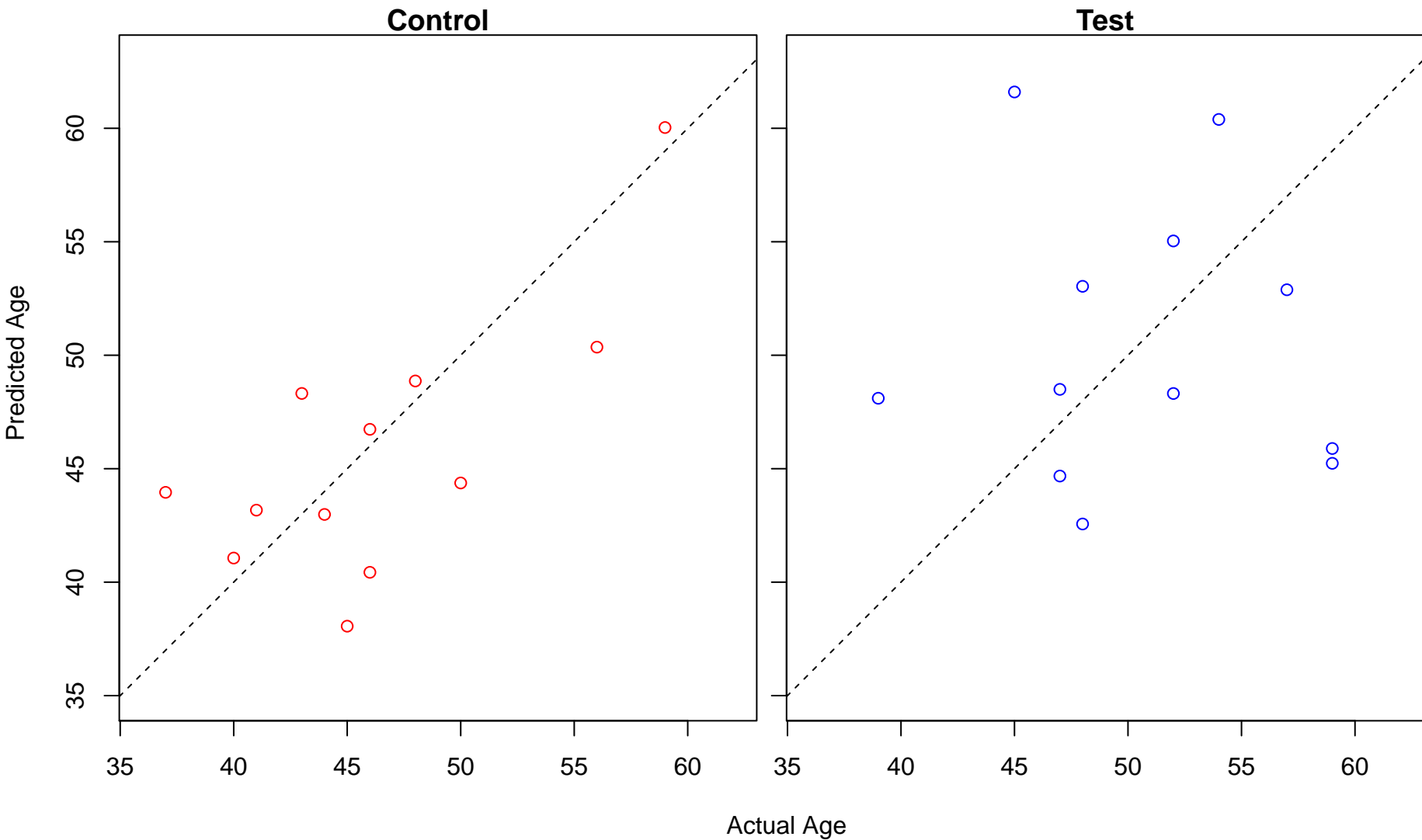
regulation of glucocorticoid metabolic process (Score: 2.915456)



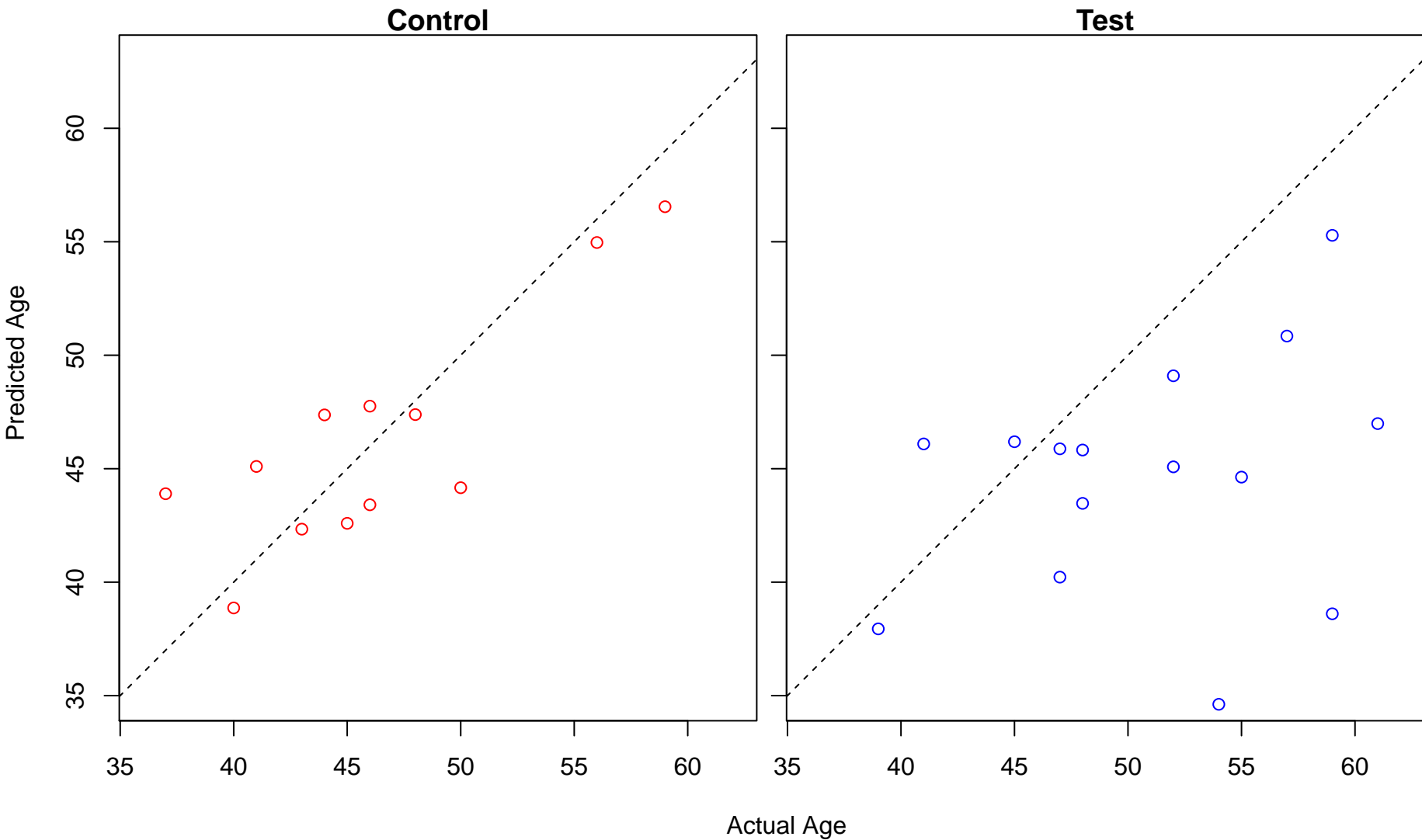
negative regulation of cytoskeleton organization (Score: 2.914134)



positive regulation of lipid storage (Score: 2.914017)

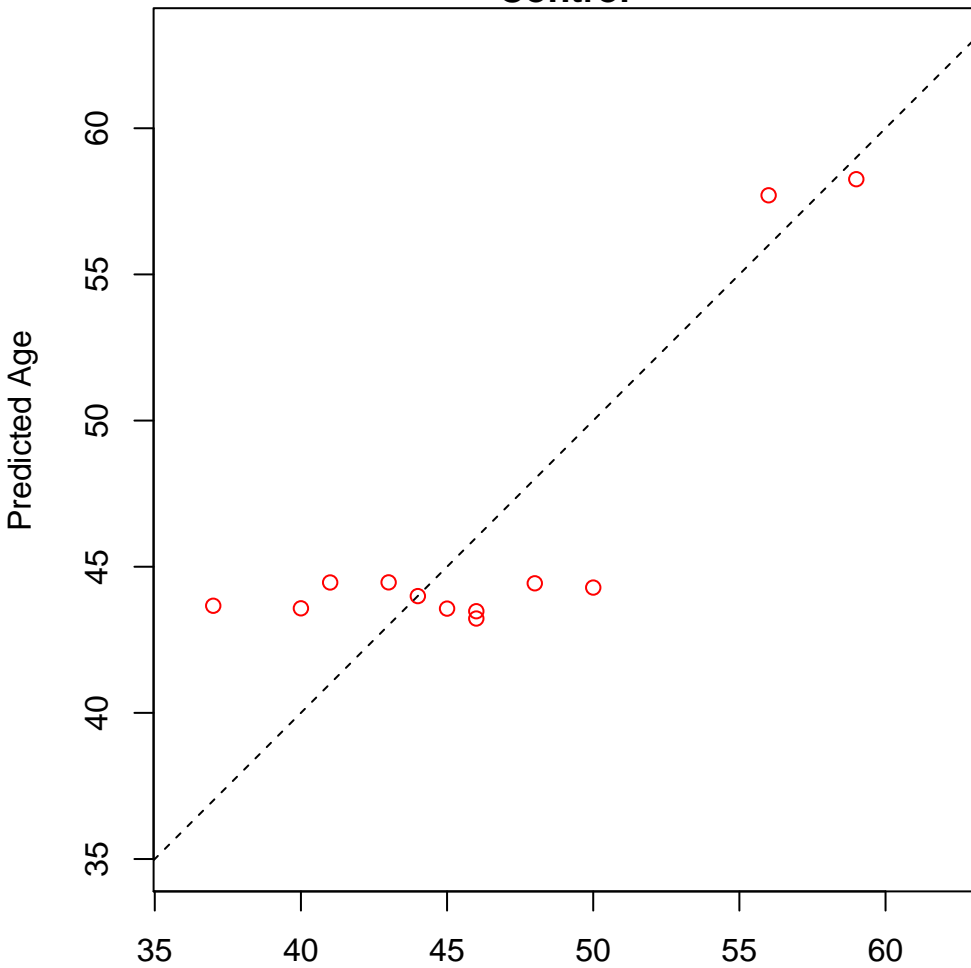


leukocyte activation (Score: 2.909721)

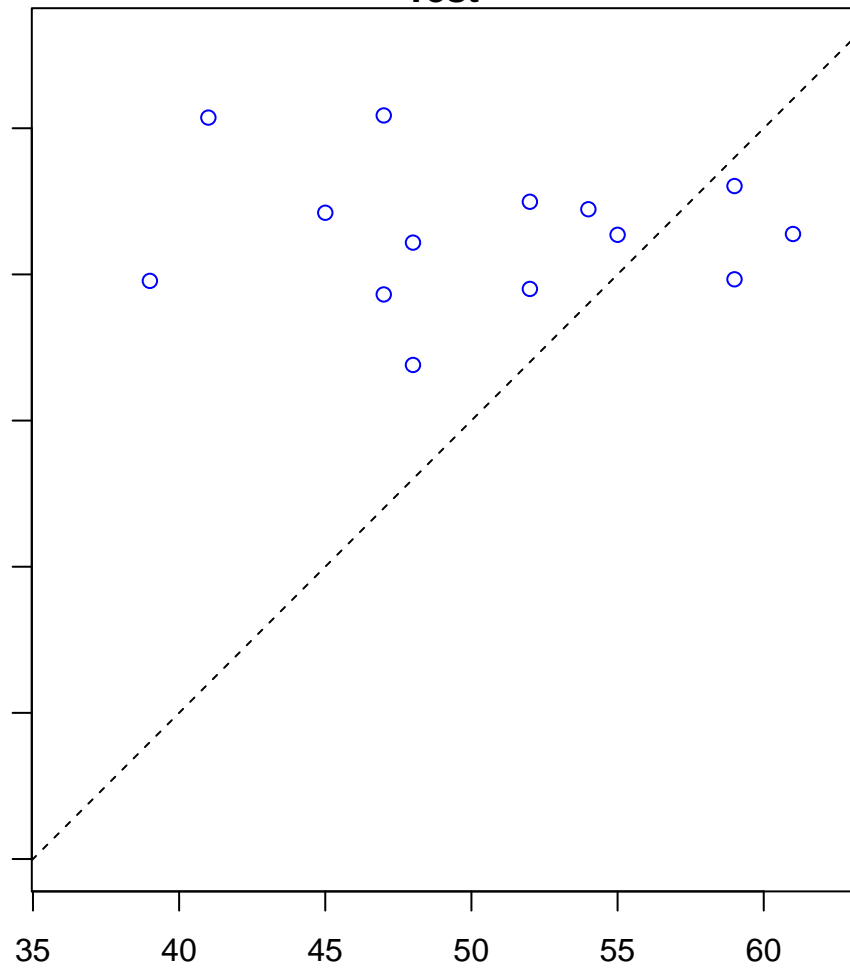


glycosyl compound metabolic process (Score: 2.907921)

Control

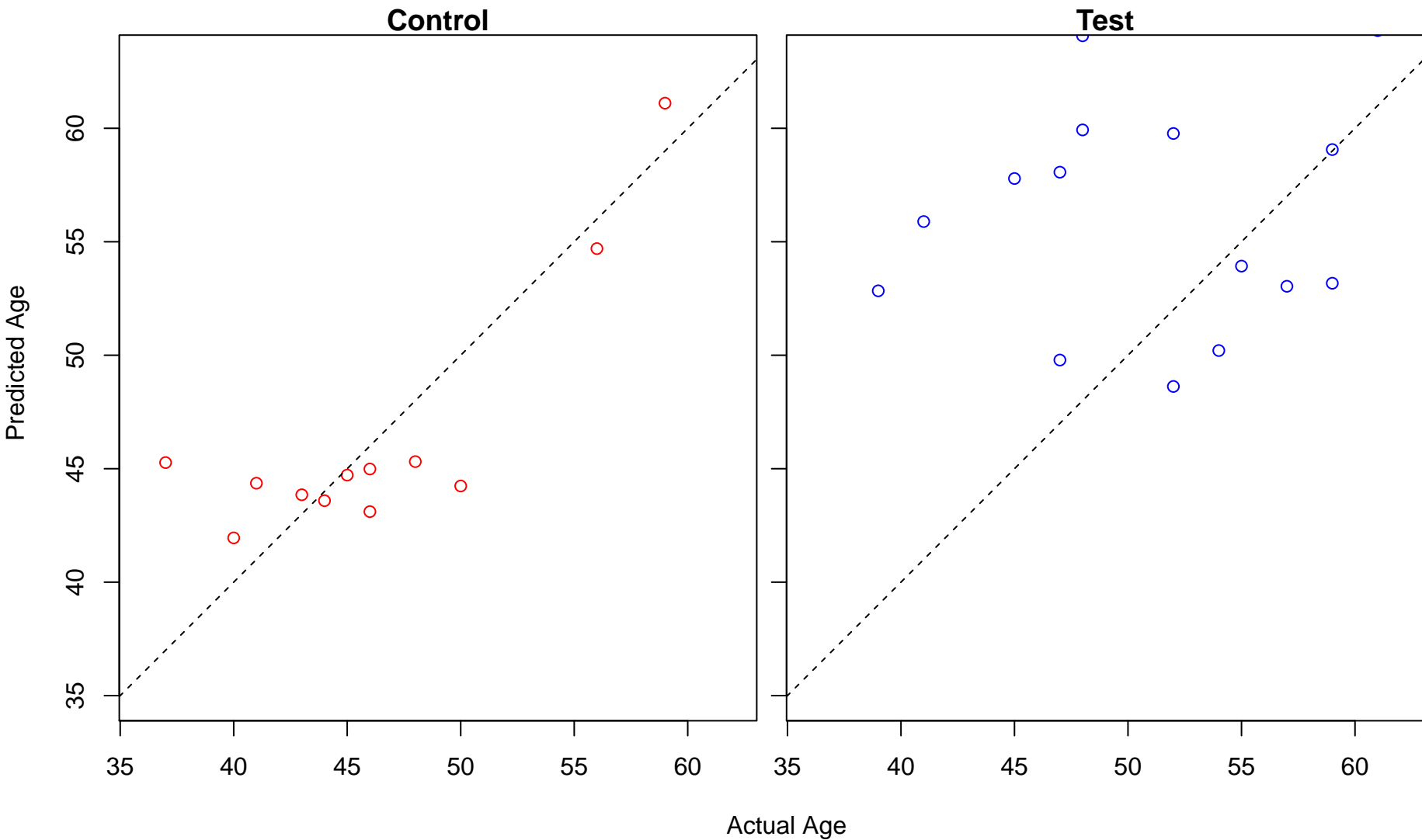


Test

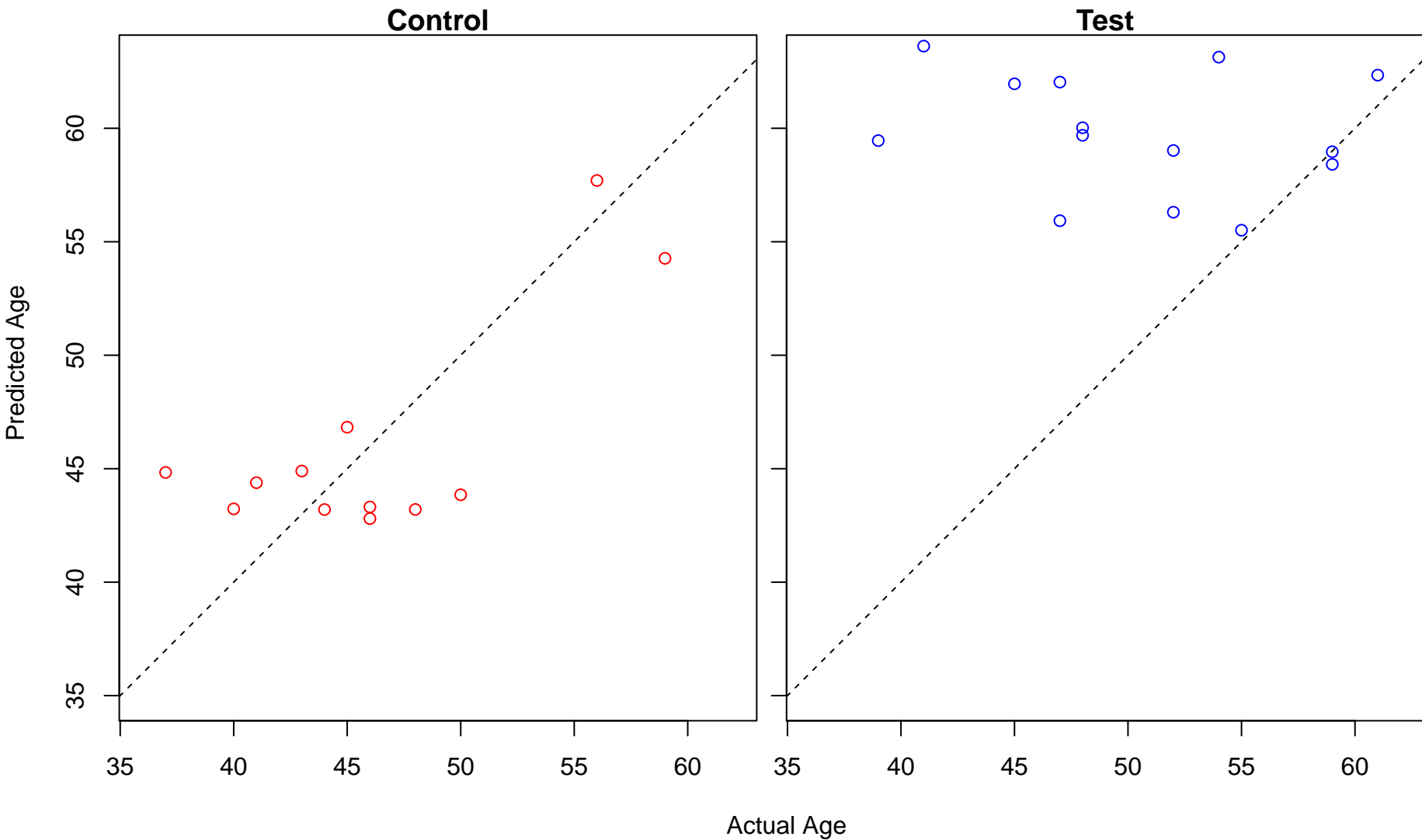


Actual Age

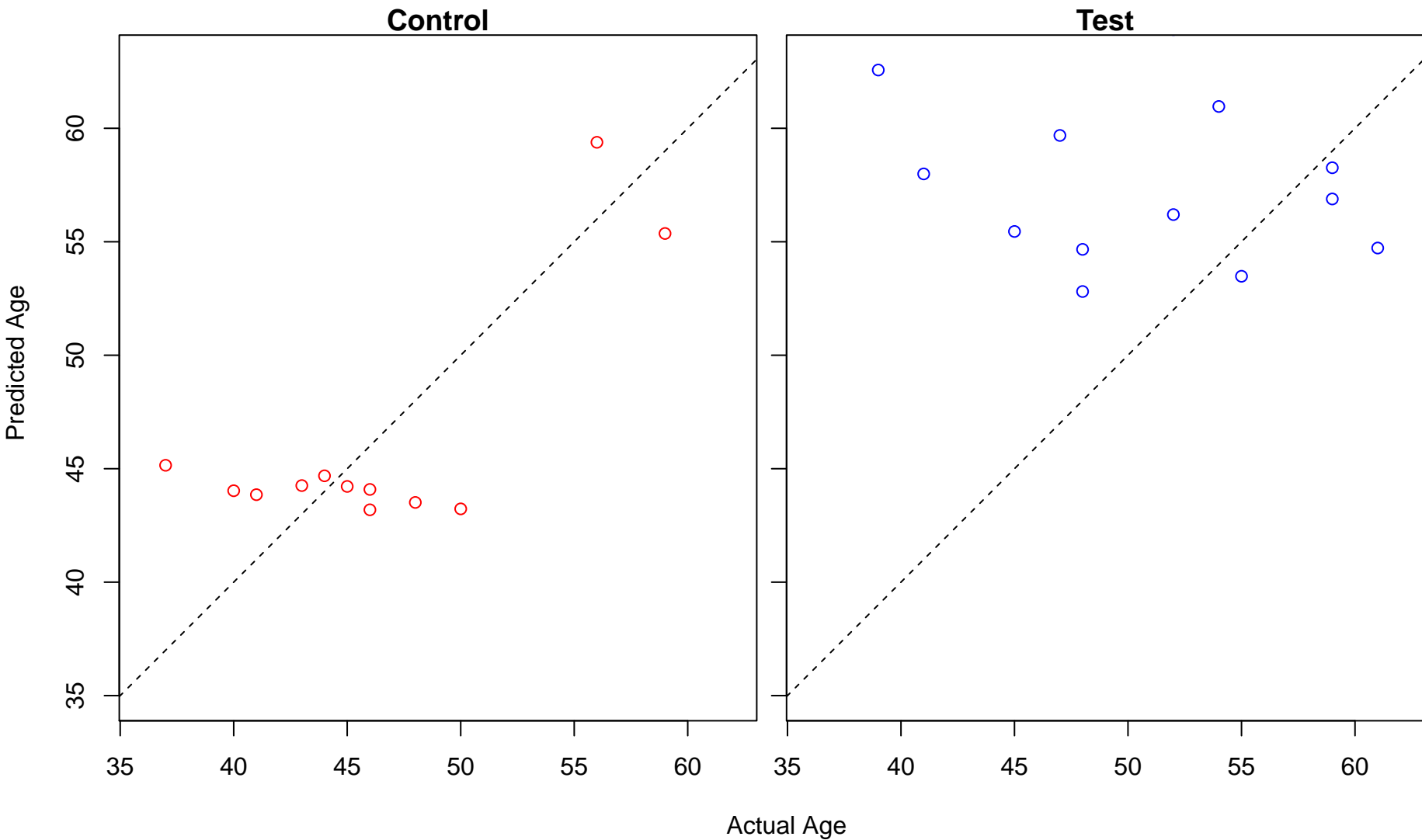
regulation of protein localization to cell surface (Score: 2.907749)



glial cell differentiation (Score: 2.907526)

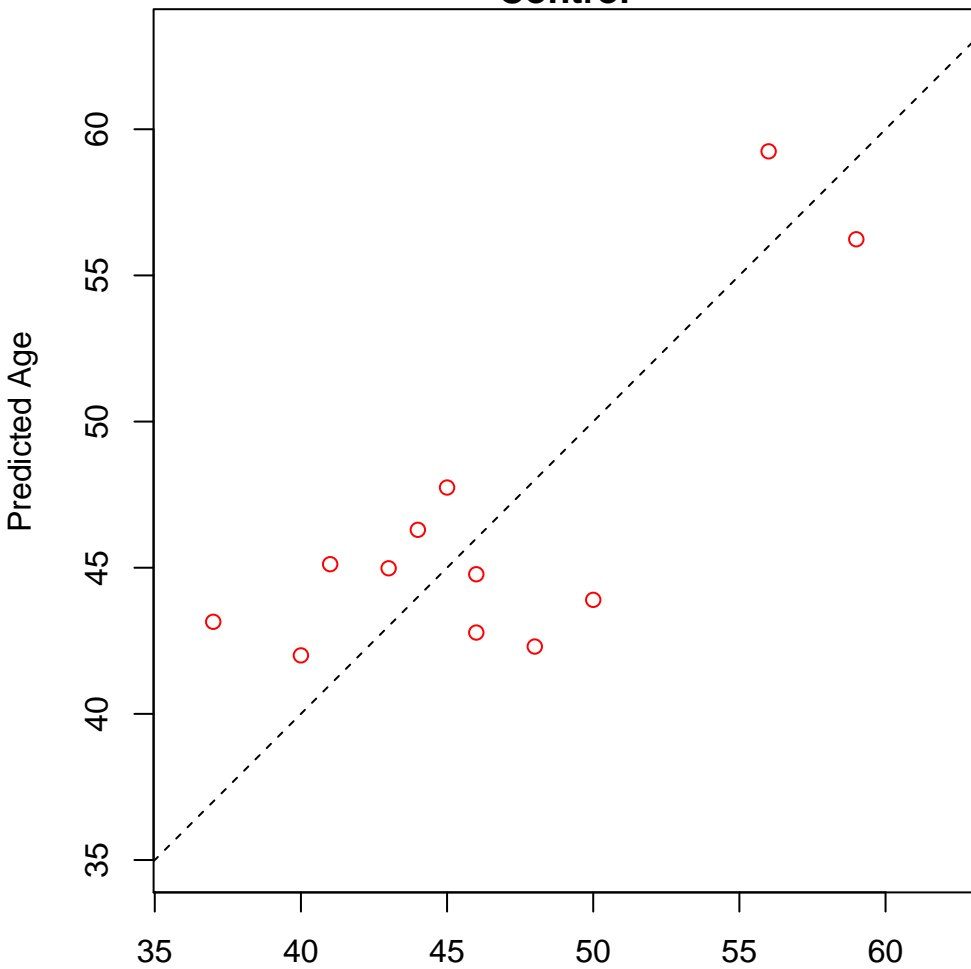


developmental pigmentation (Score: 2.905545)

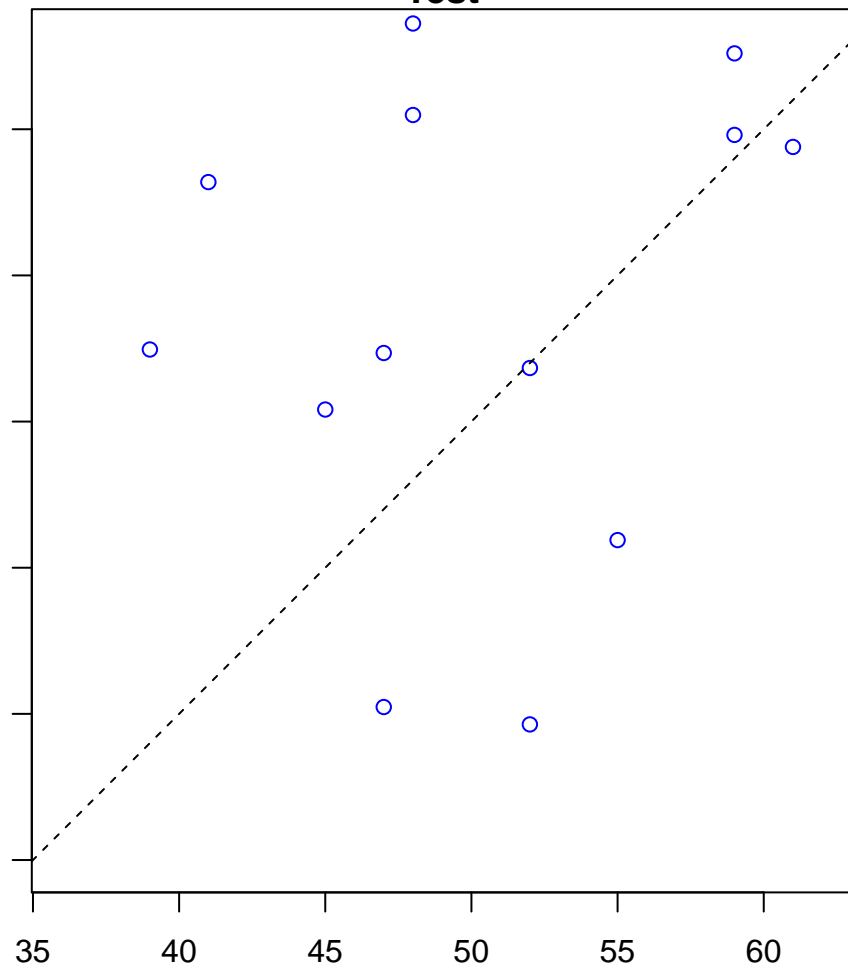


angiogenesis involved in wound healing (Score: 2.904054)

Control

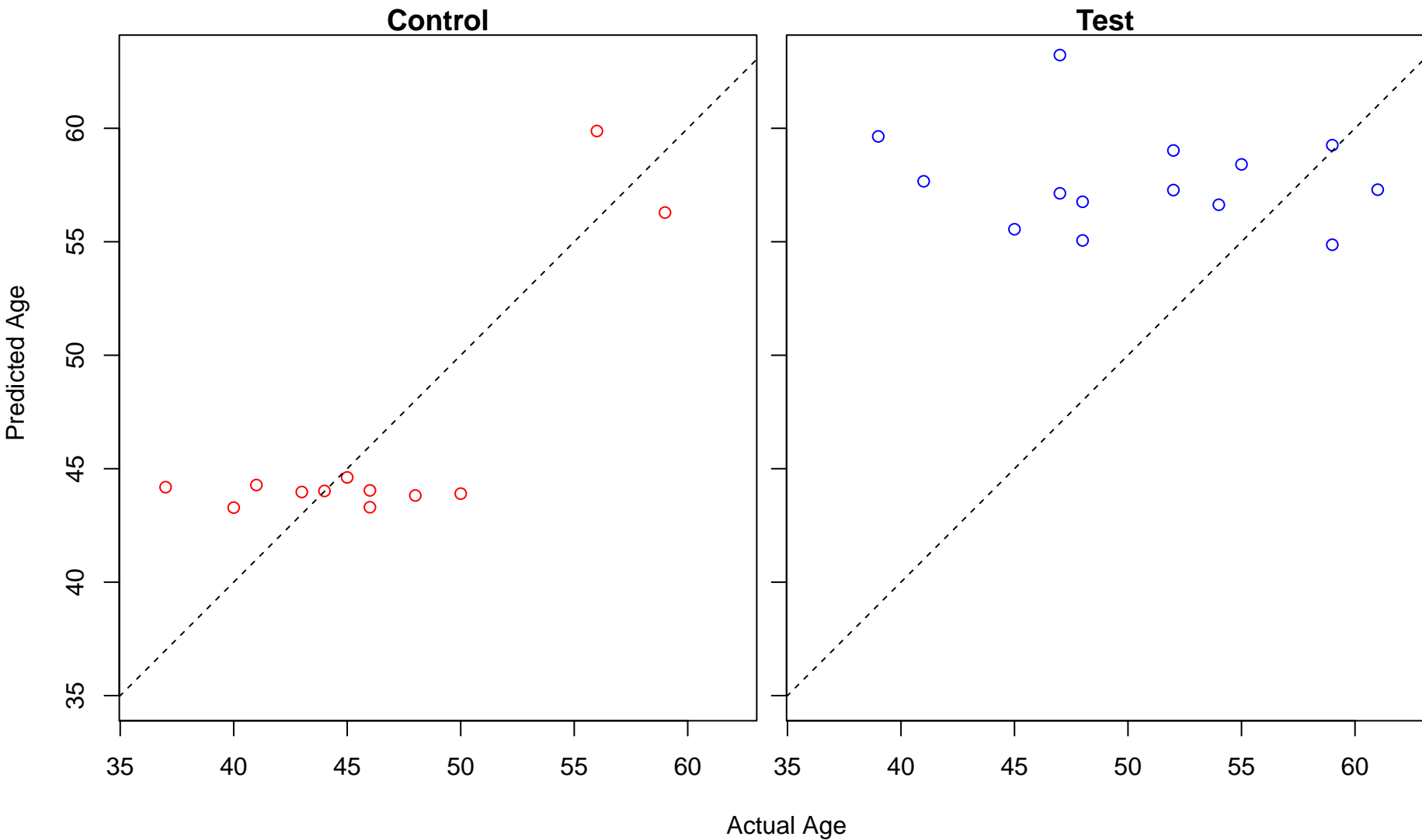


Test

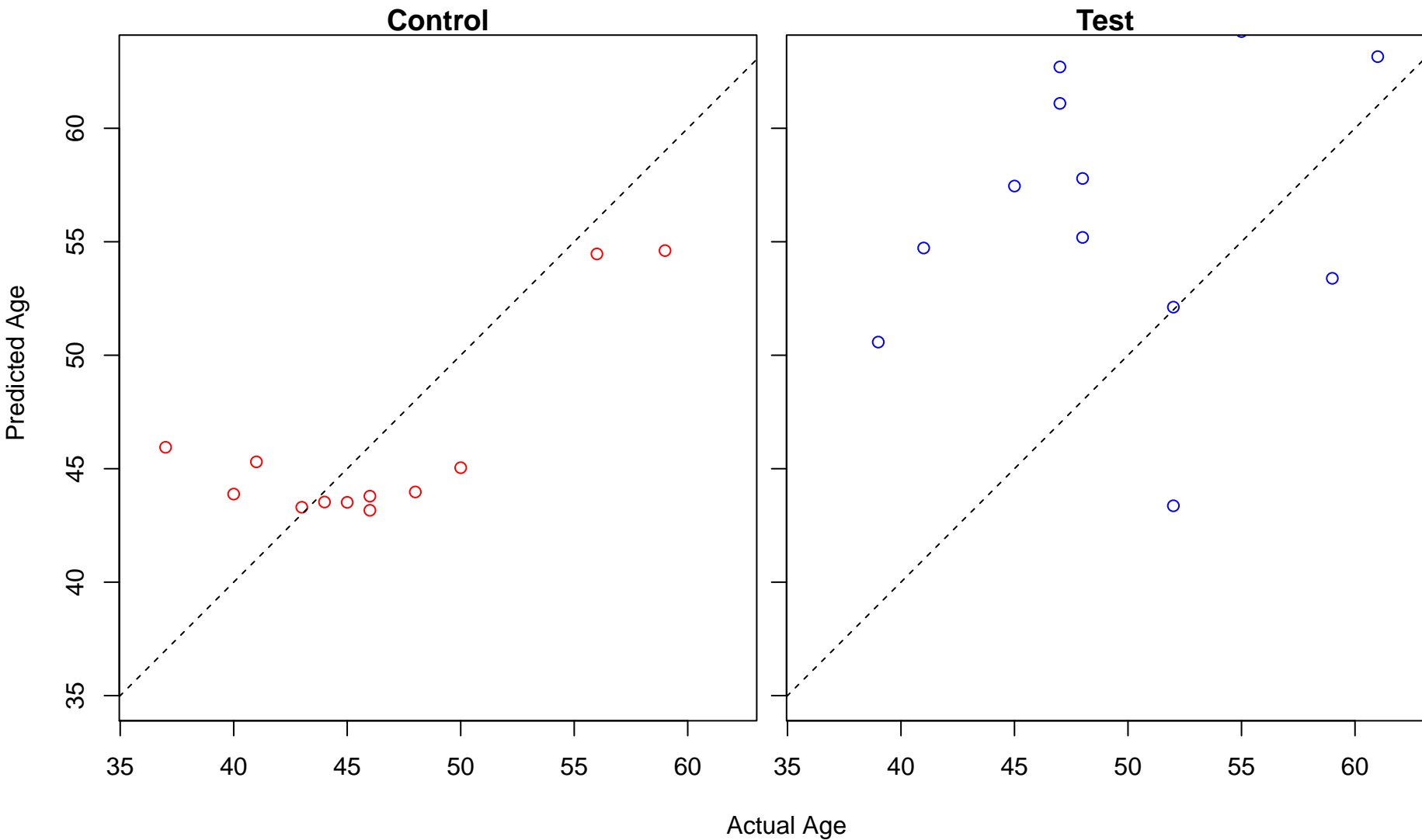


Actual Age

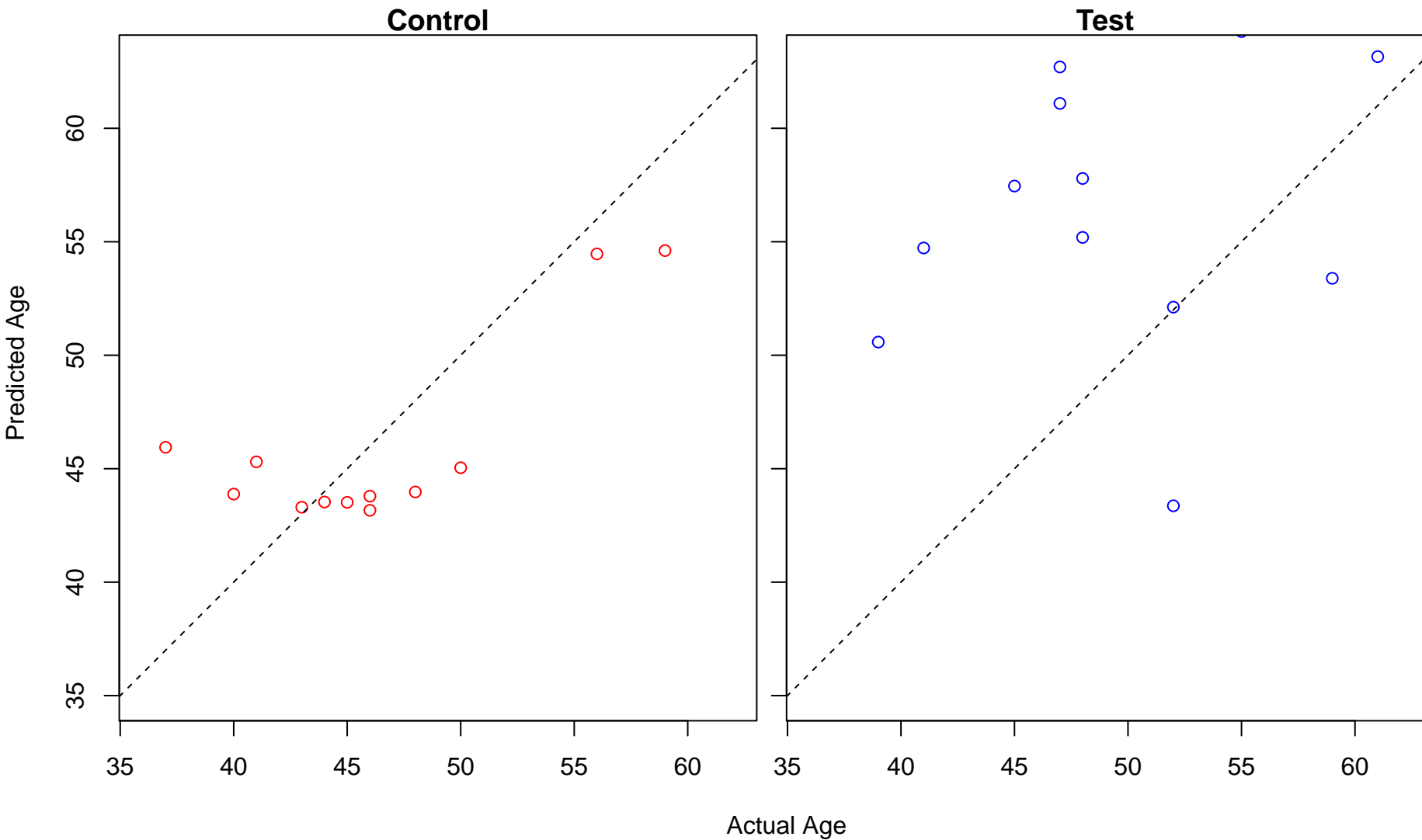
mitotic cell cycle phase transition (Score: 2.902627)



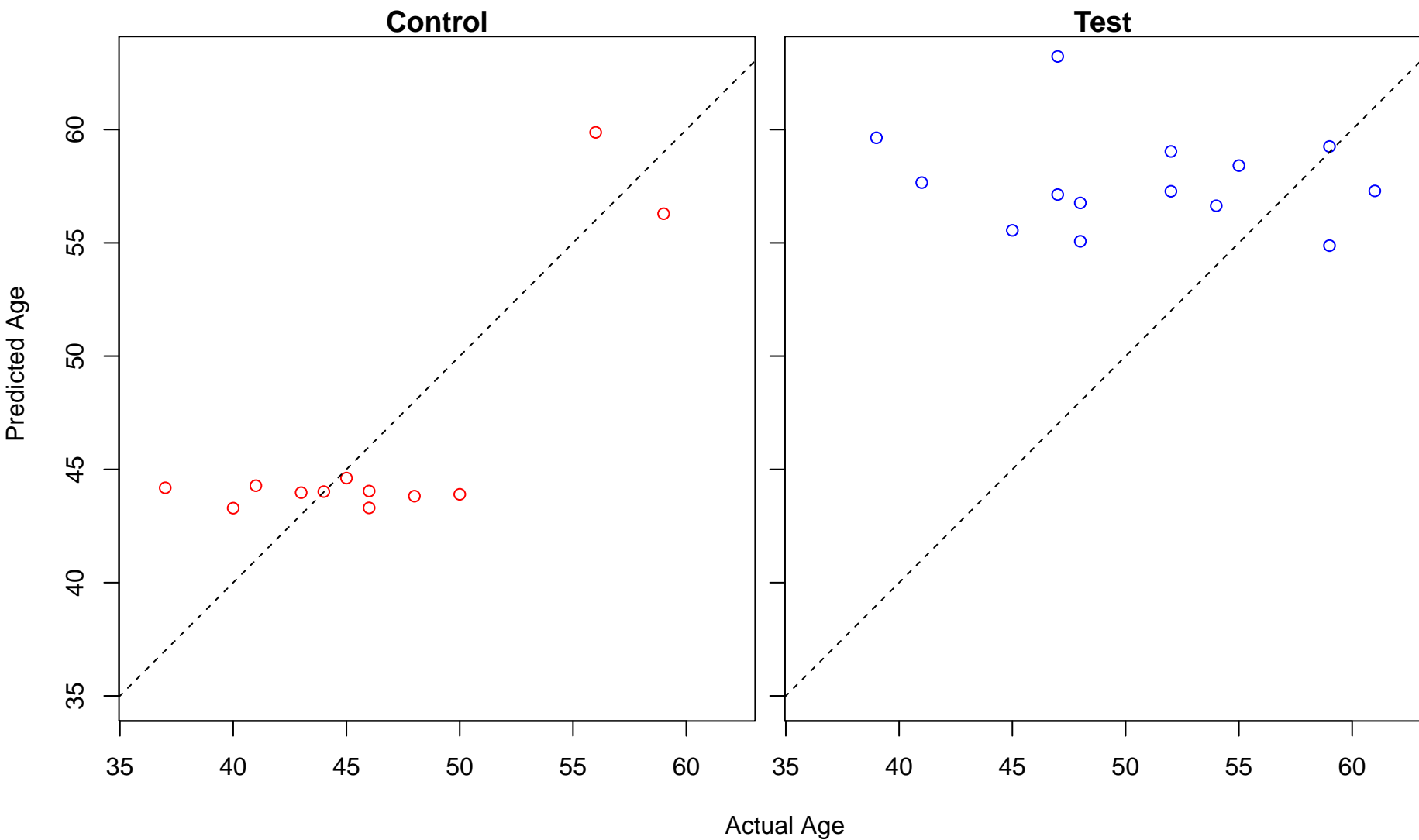
response to isoquinoline alkaloid (Score: 2.902334)



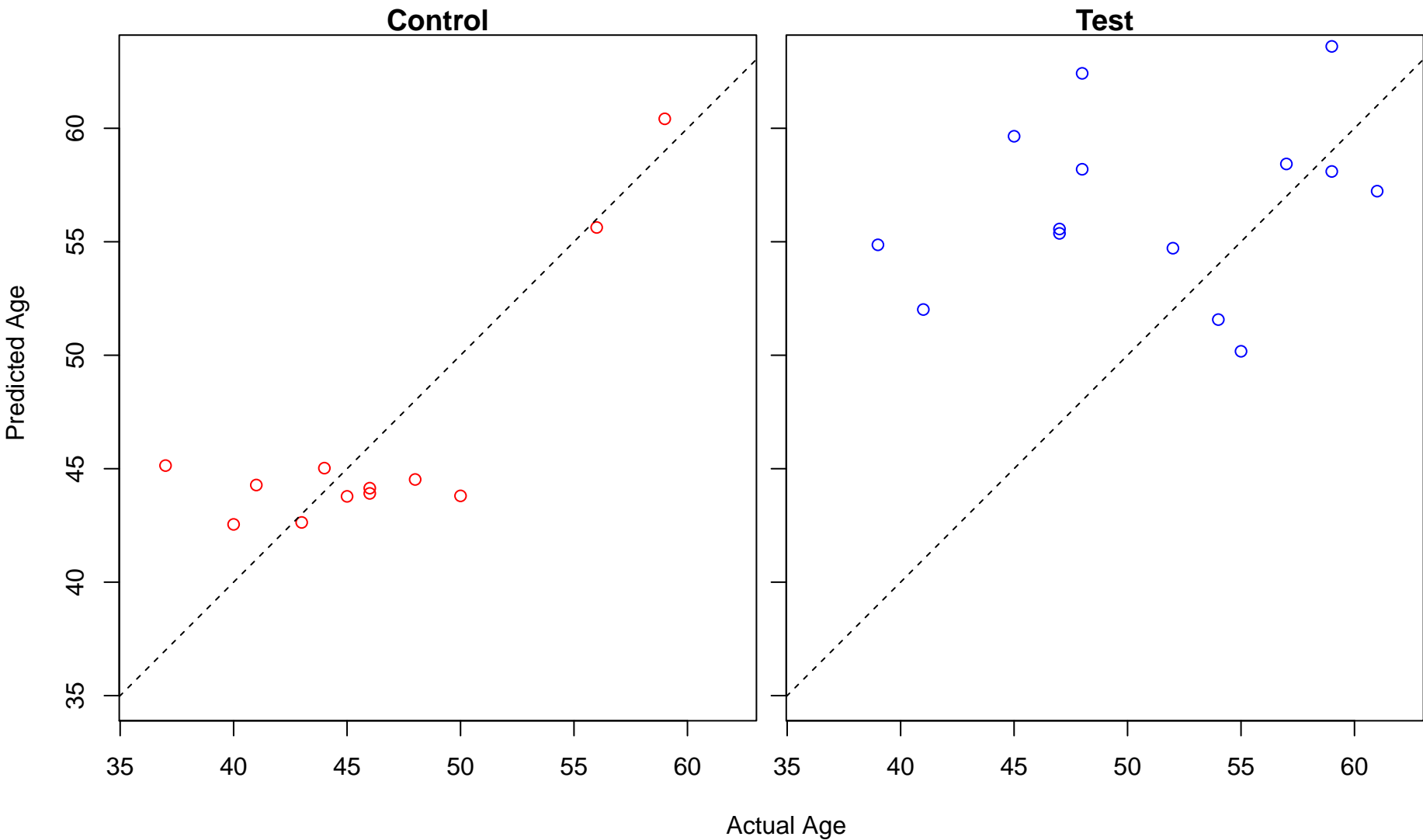
response to morphine (Score: 2.902334)



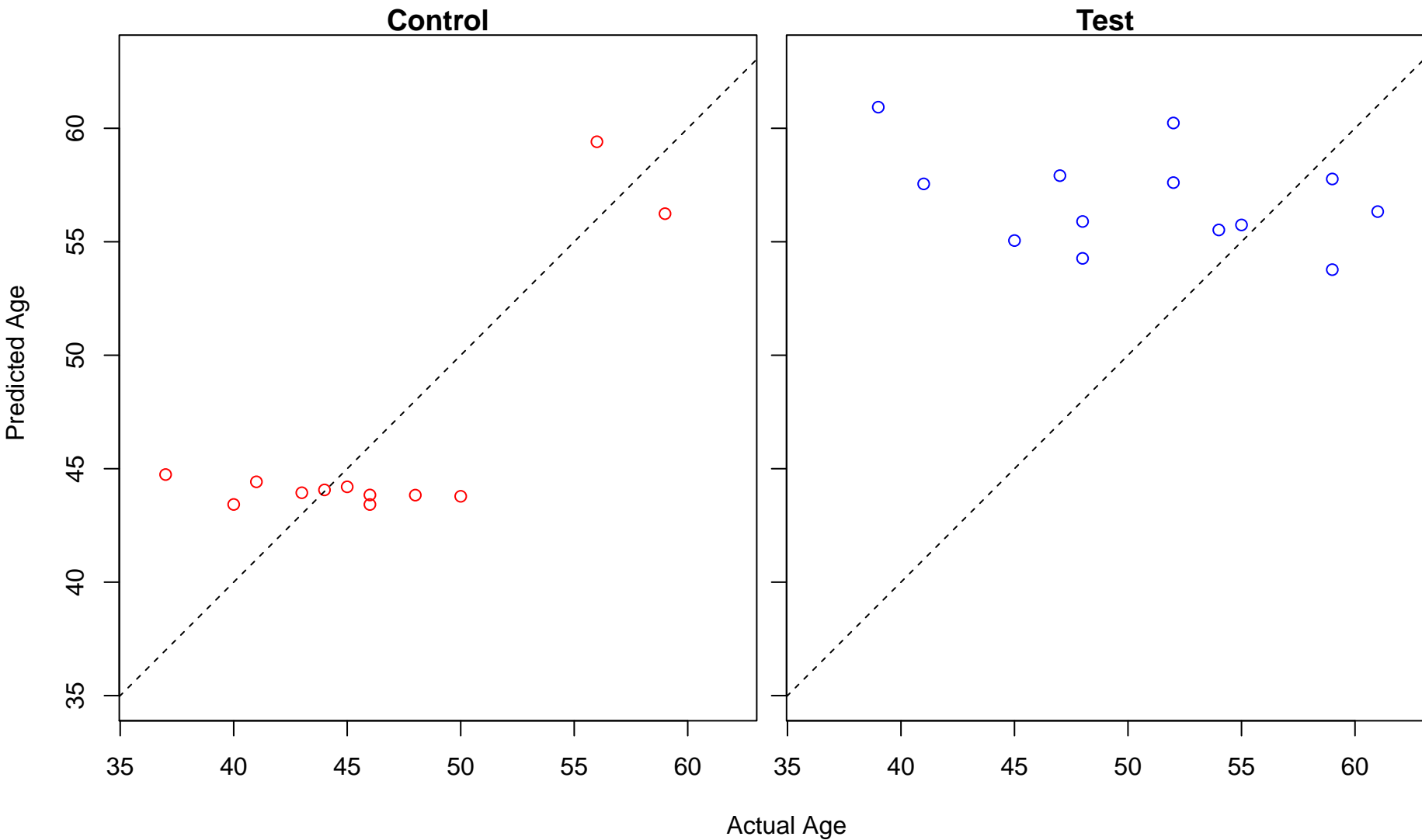
cell cycle phase transition (Score: 2.902098)



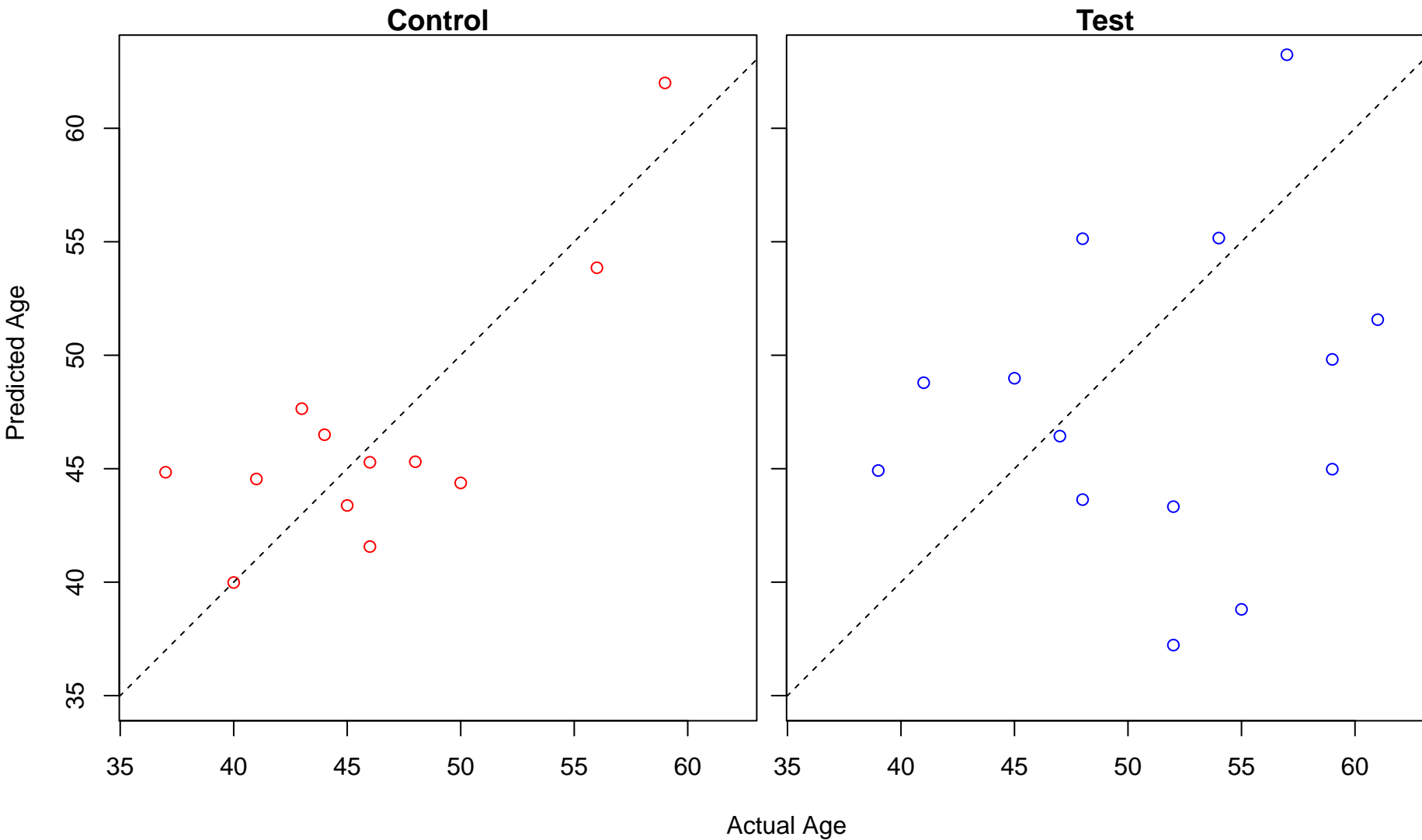
Negative regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis (Score: 1)



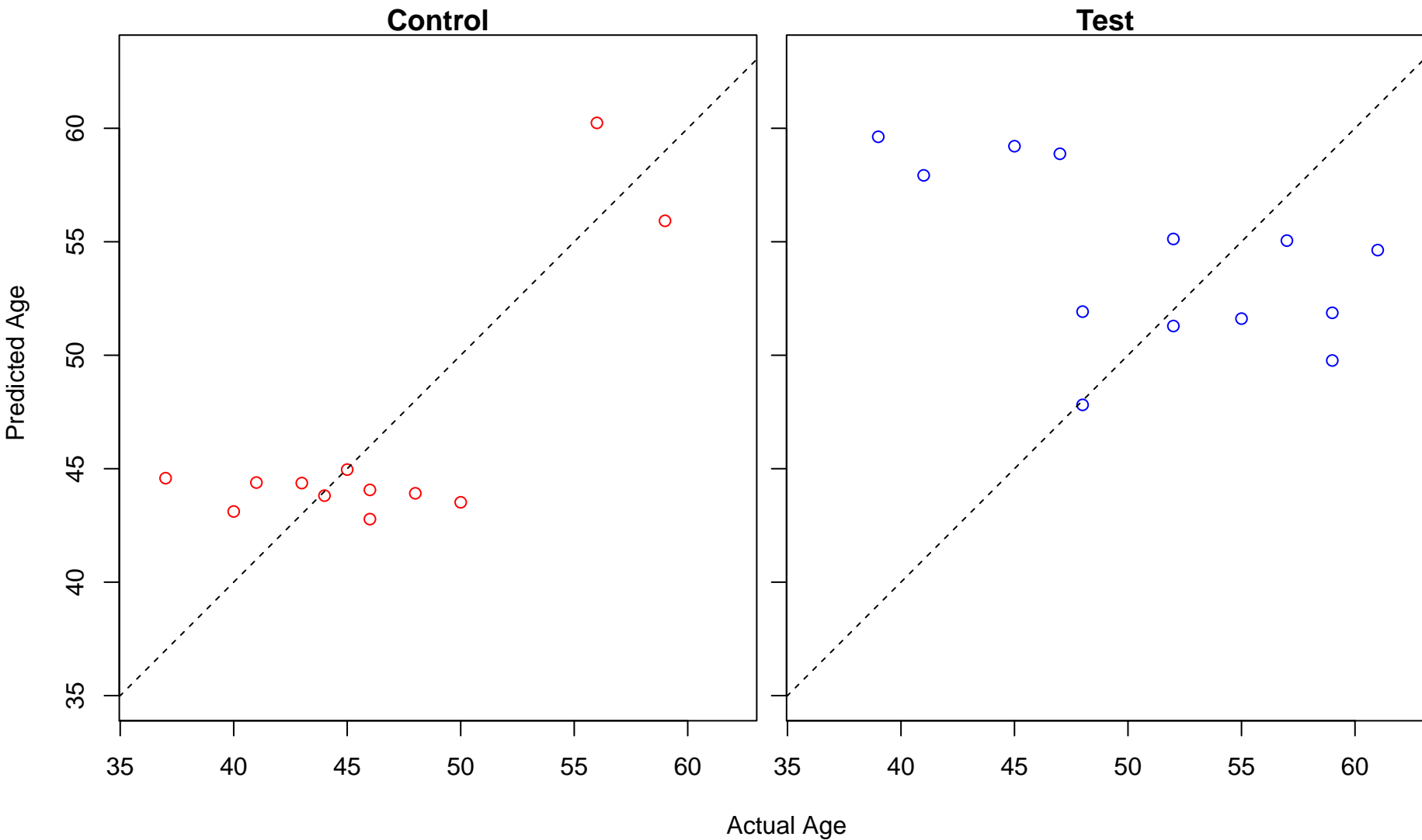
positive regulation of MAP kinase activity (Score: 2.899151)



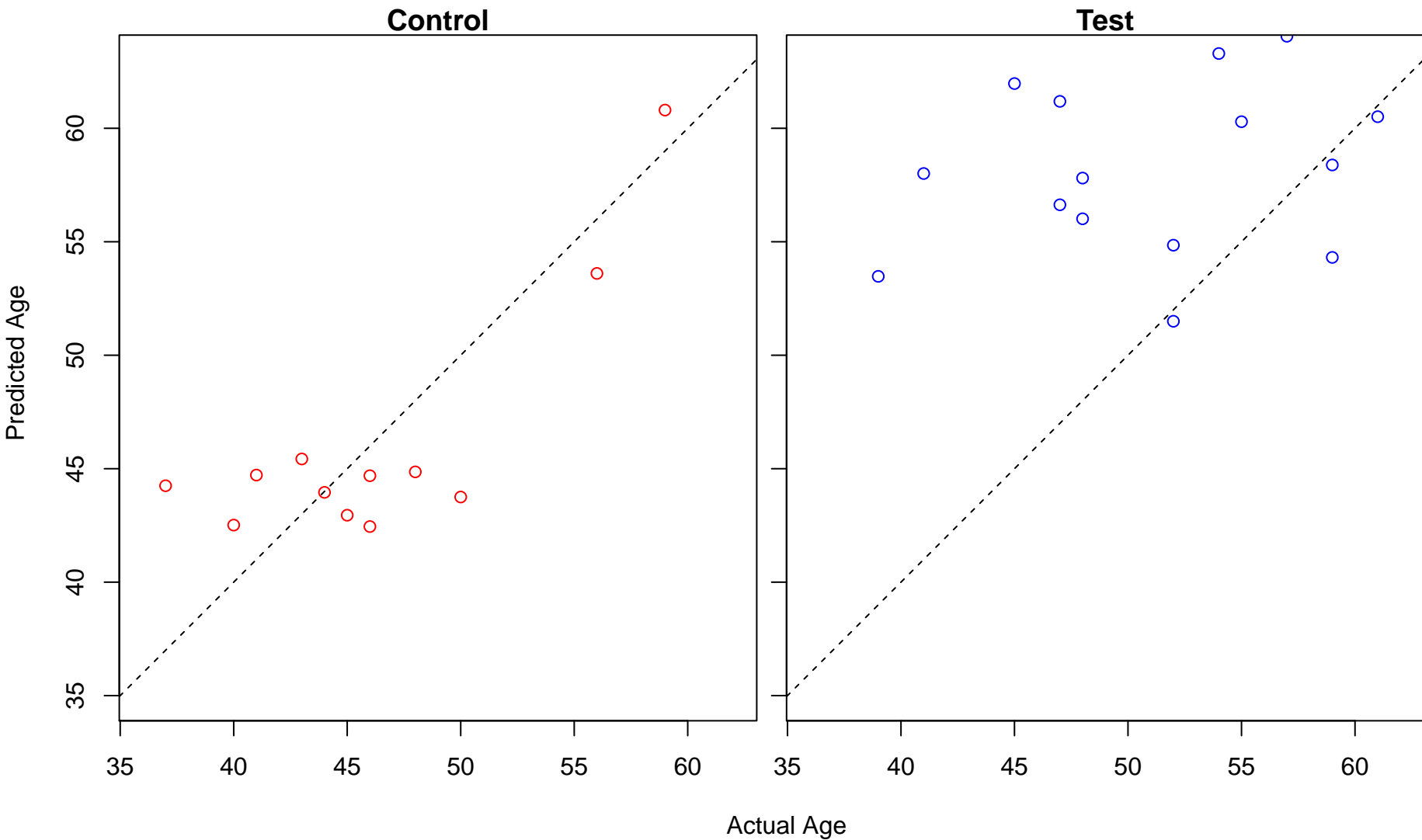
regulation of ion transport (Score: 2.898668)



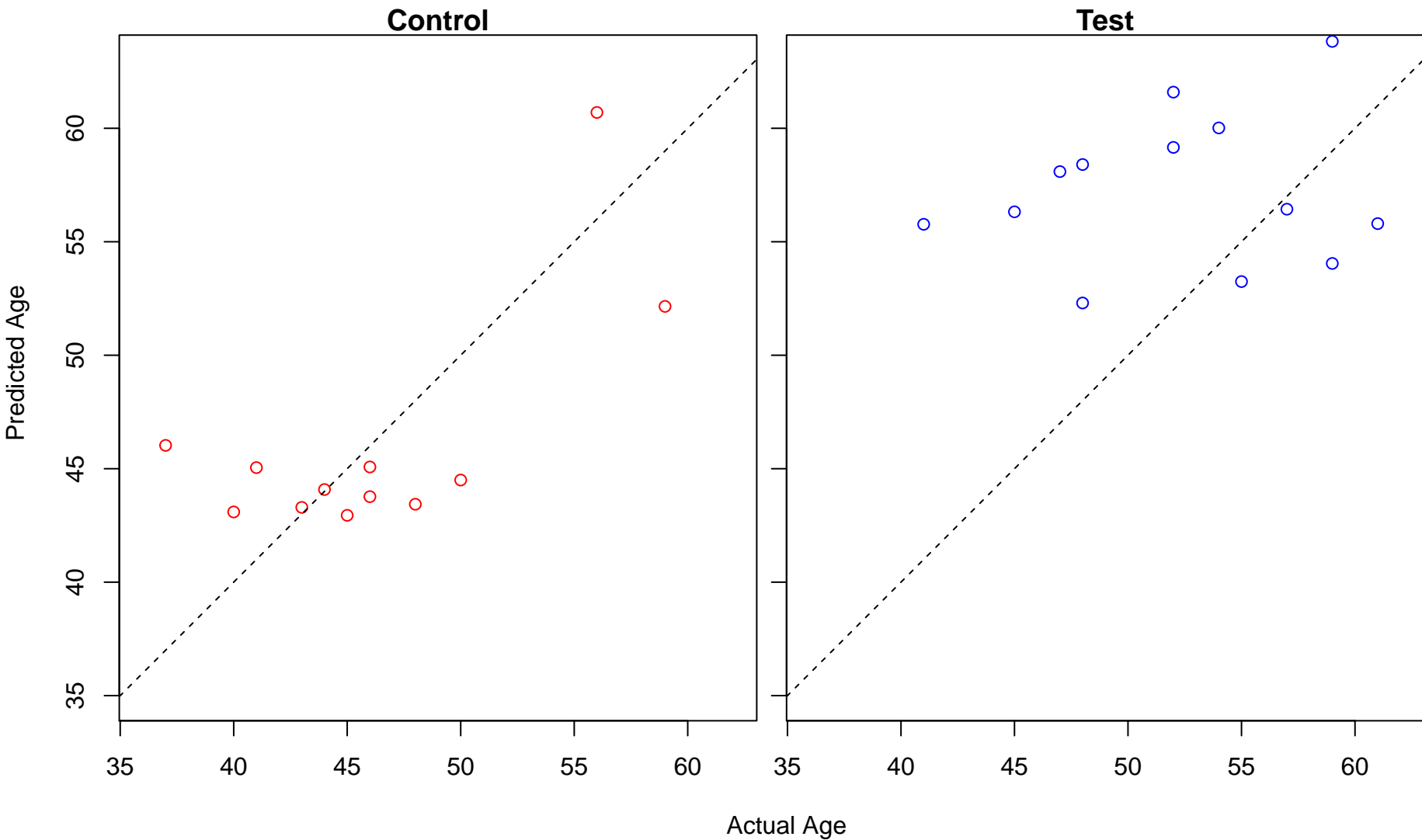
regulation of extracellular matrix disassembly (Score: 2.897083)



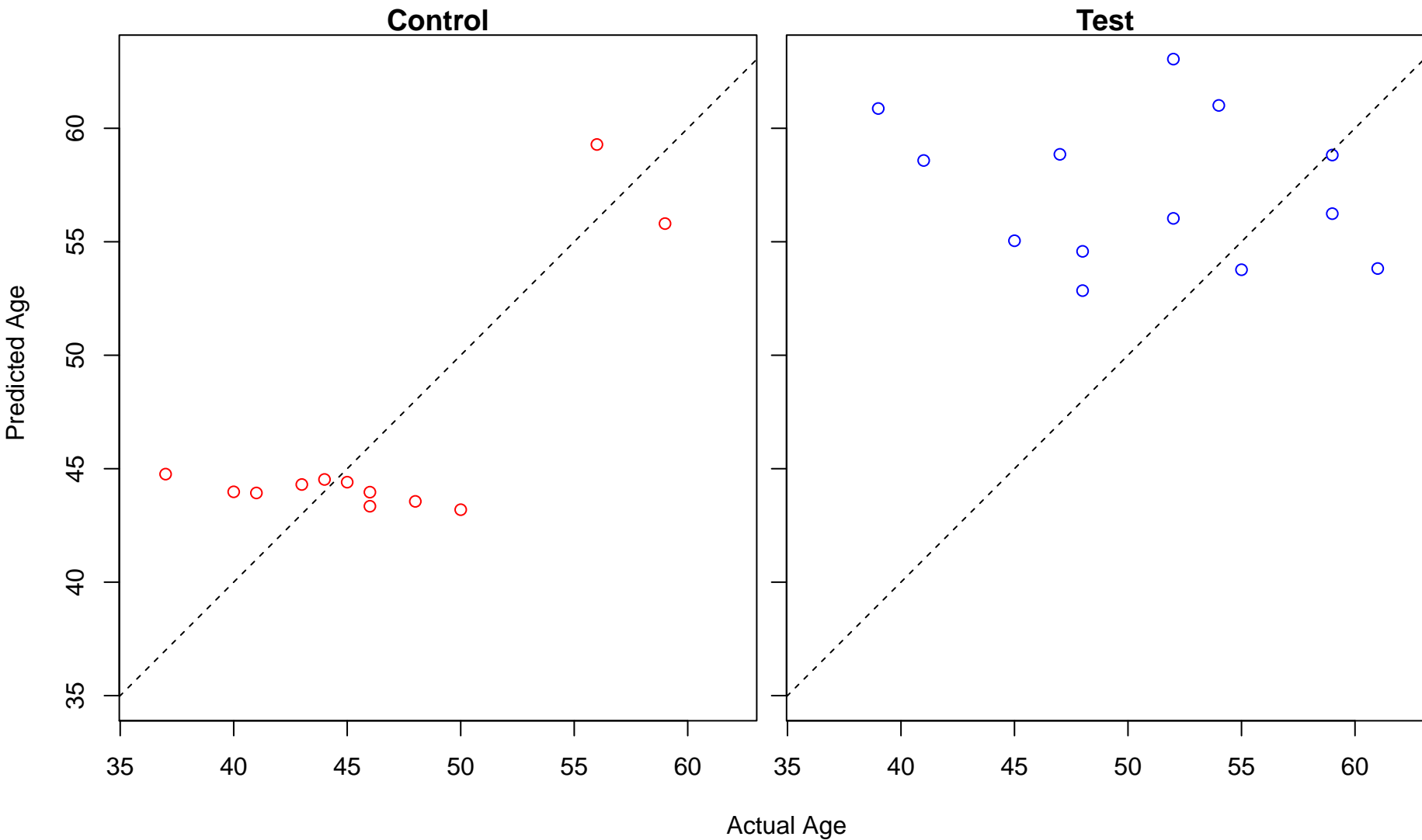
regulation of intrinsic apoptotic signaling pathway (Score: 2.895967)



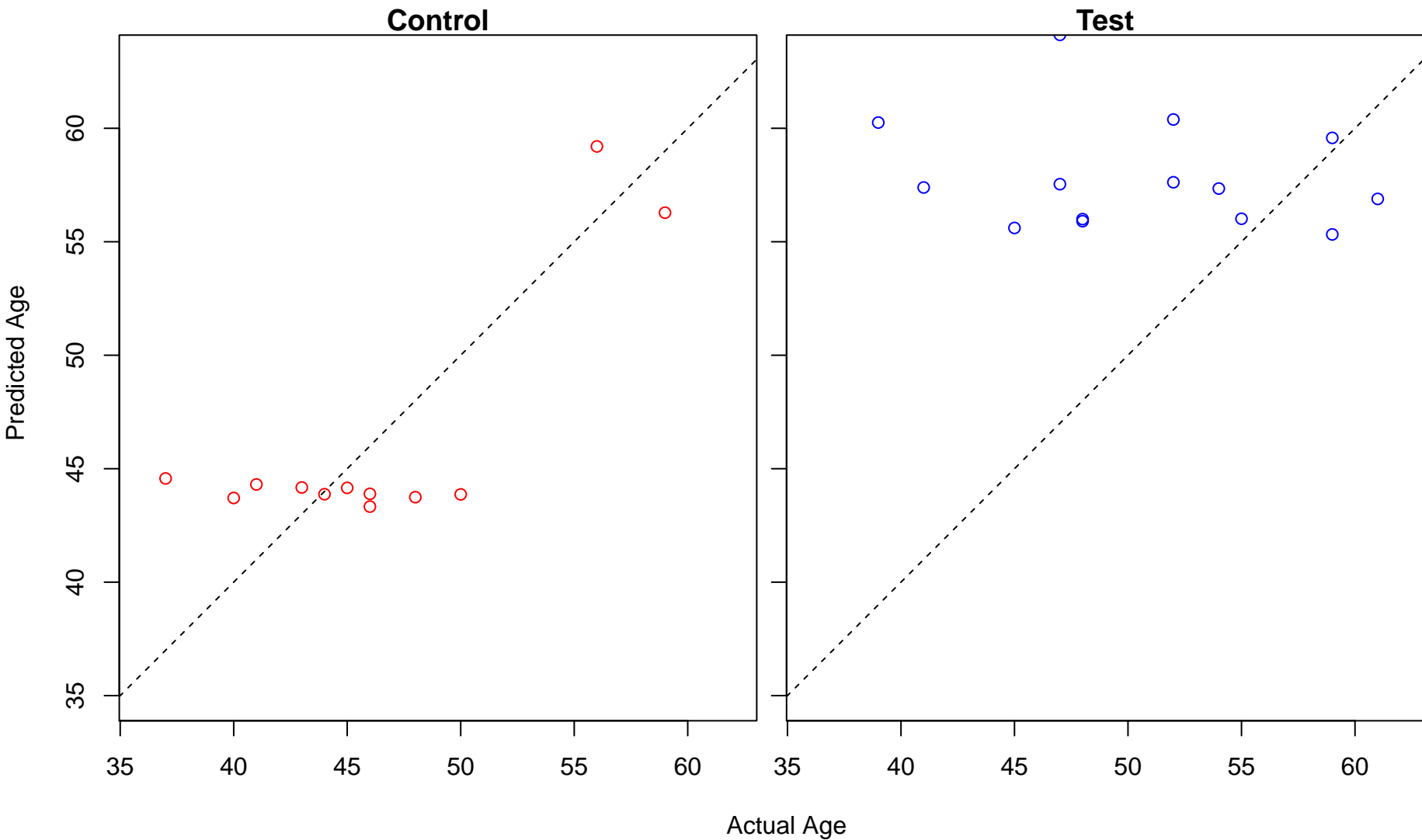
regulation of tooth mineralization (Score: 2.895571)



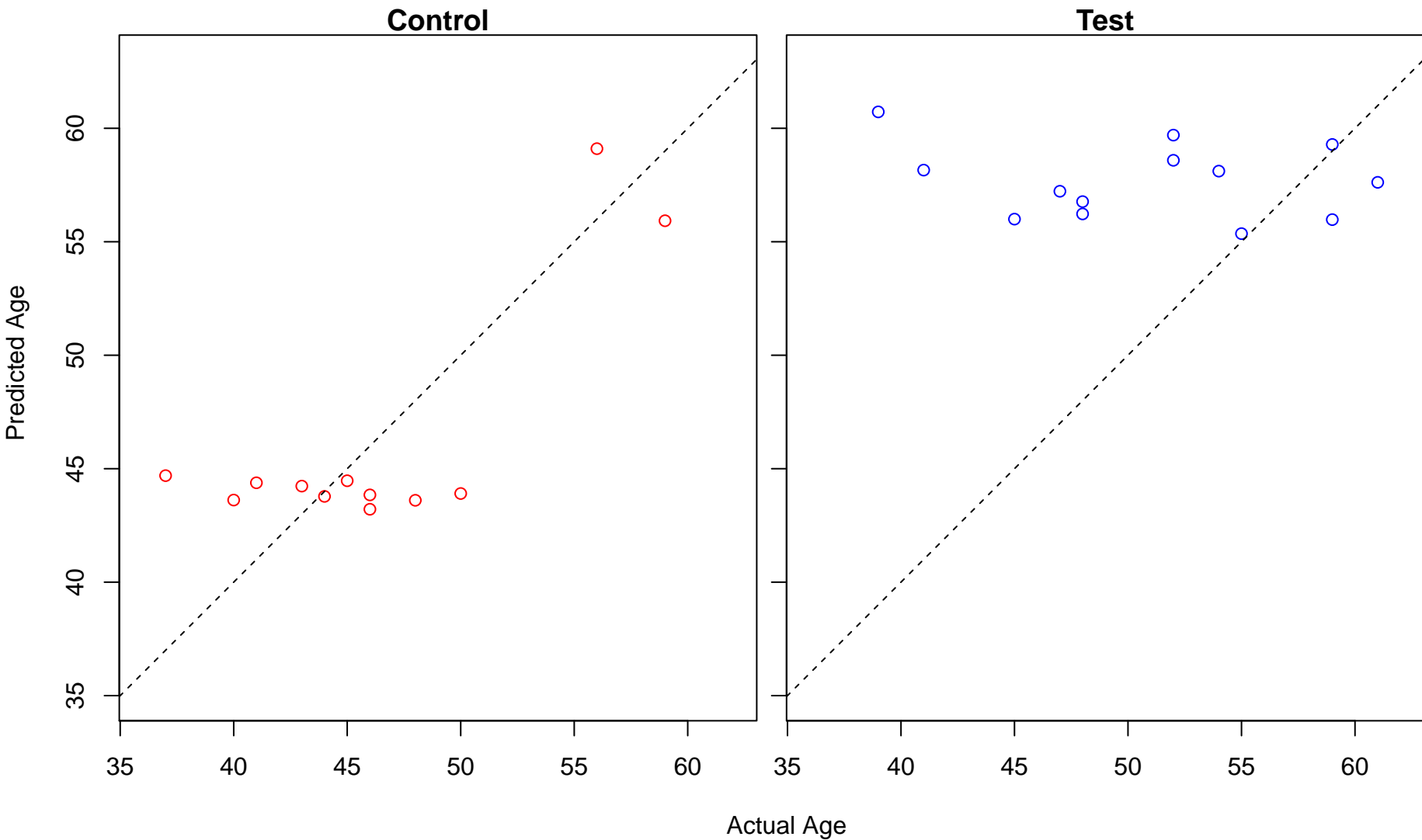
cellular pigmentation (Score: 2.894861)



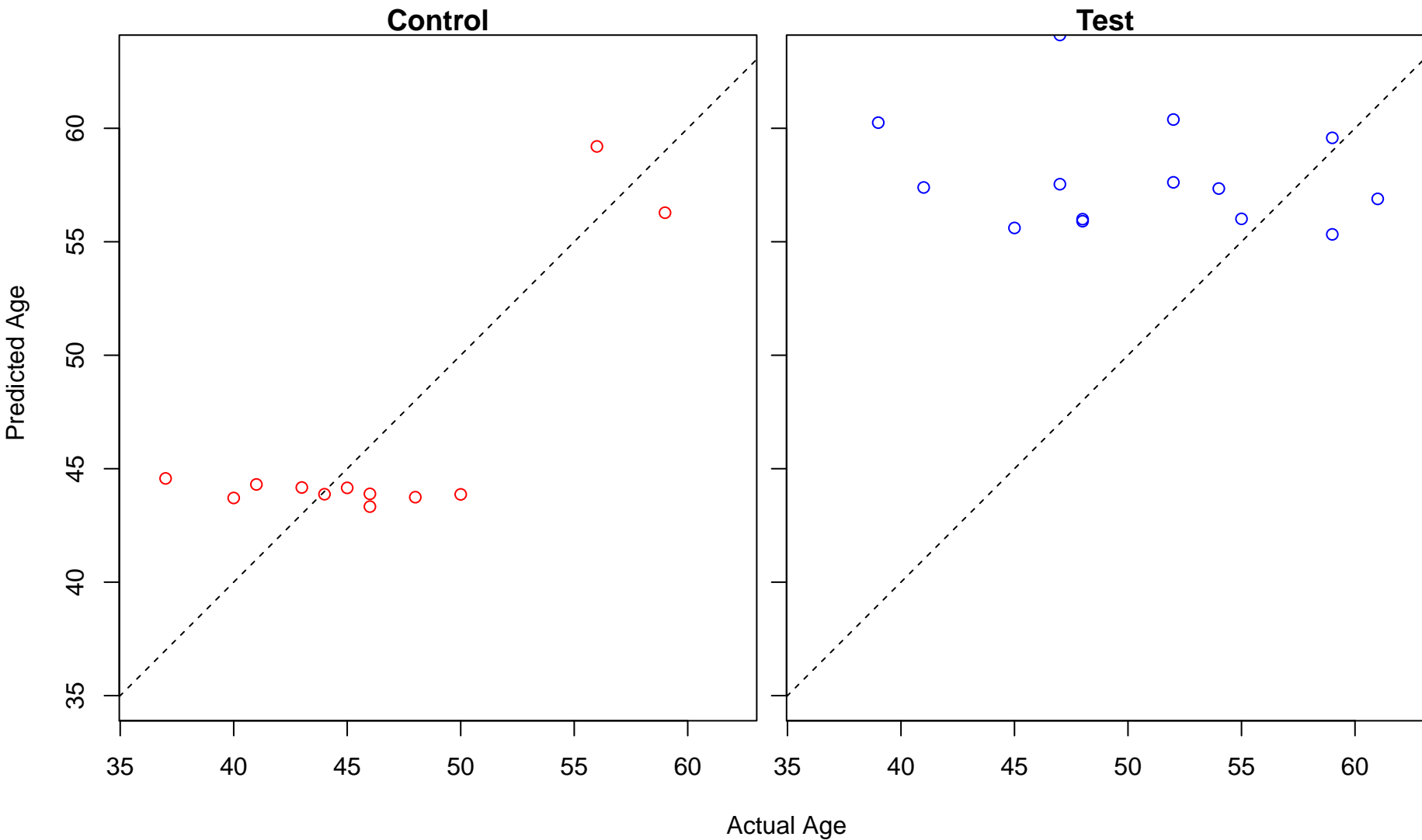
ubiquitin-dependent protein catabolic process (Score: 2.894734)



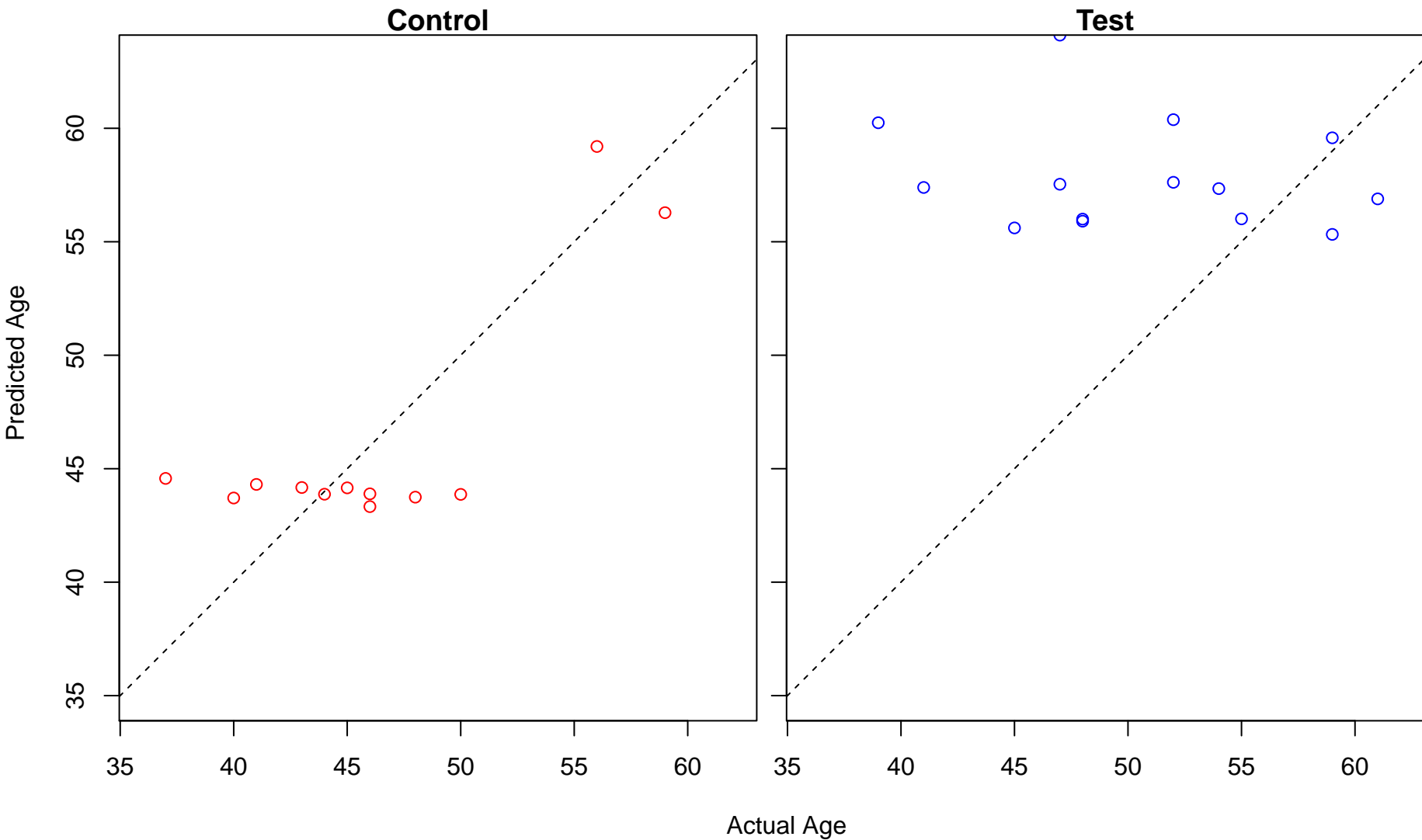
positive regulation of cellular catabolic process (Score: 2.894655)



modification-dependent protein catabolic process (Score: 2.893665)

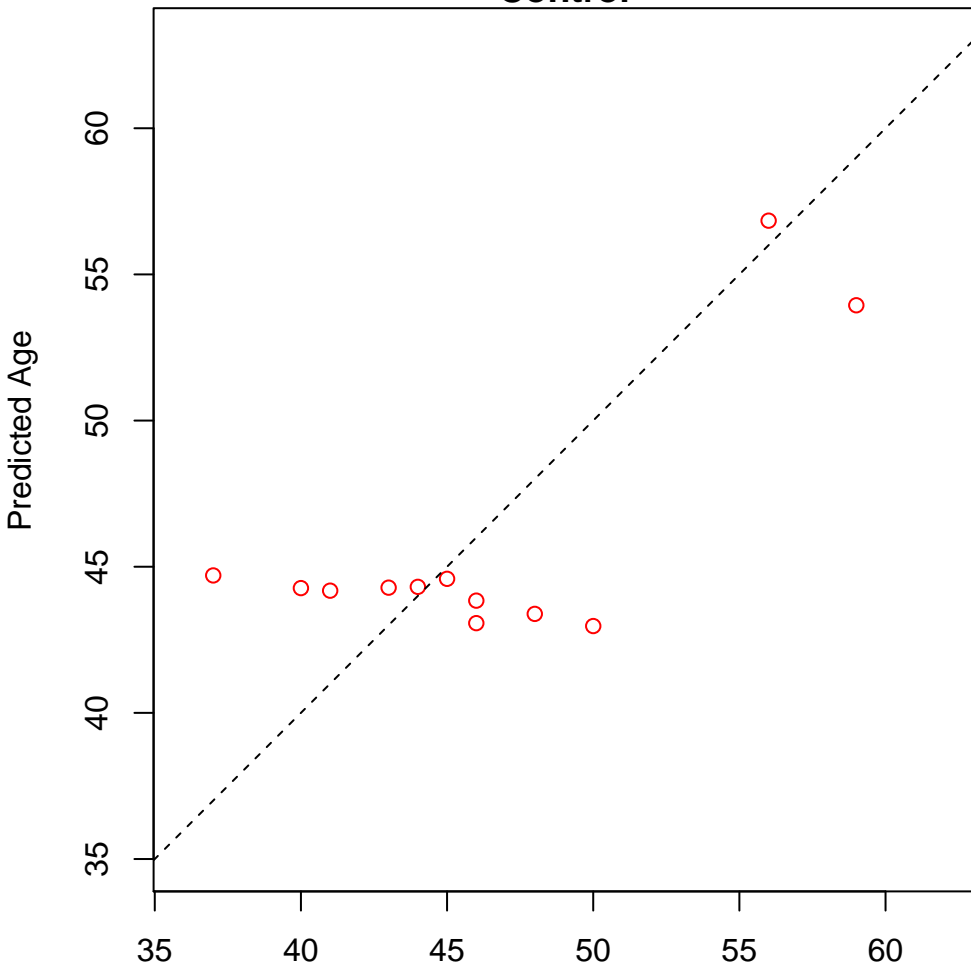


modification-dependent macromolecule catabolic process (Score: 2.893247)

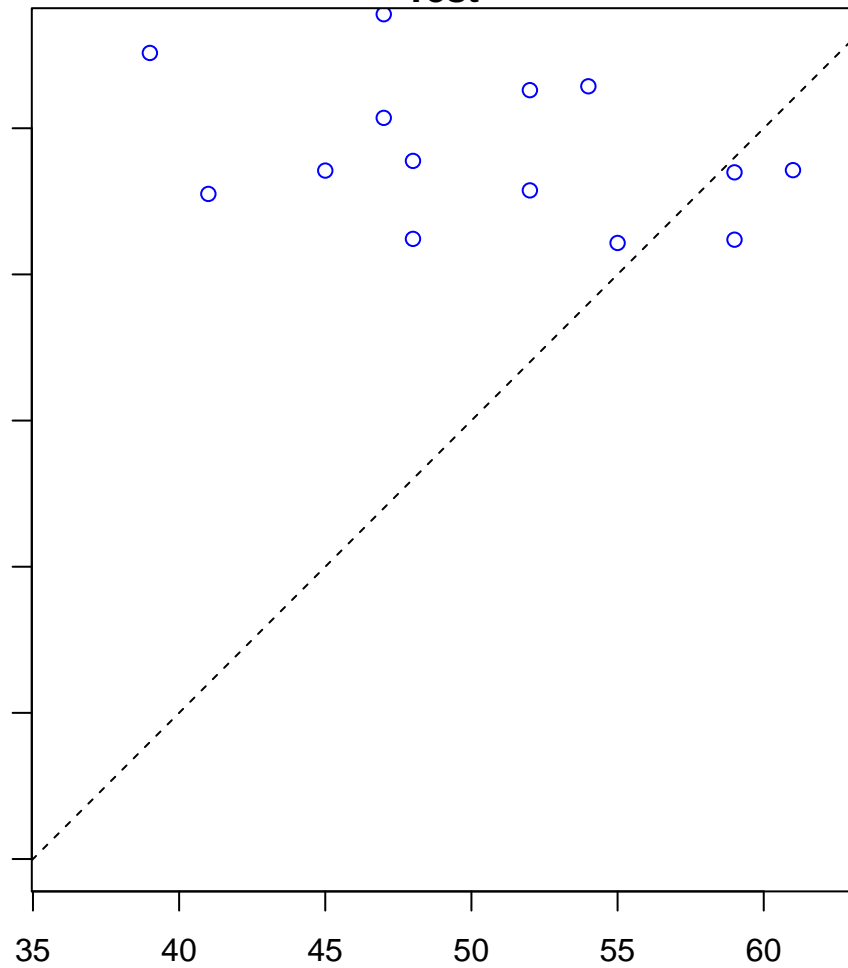


ribose phosphate biosynthetic process (Score: 2.892638)

Control

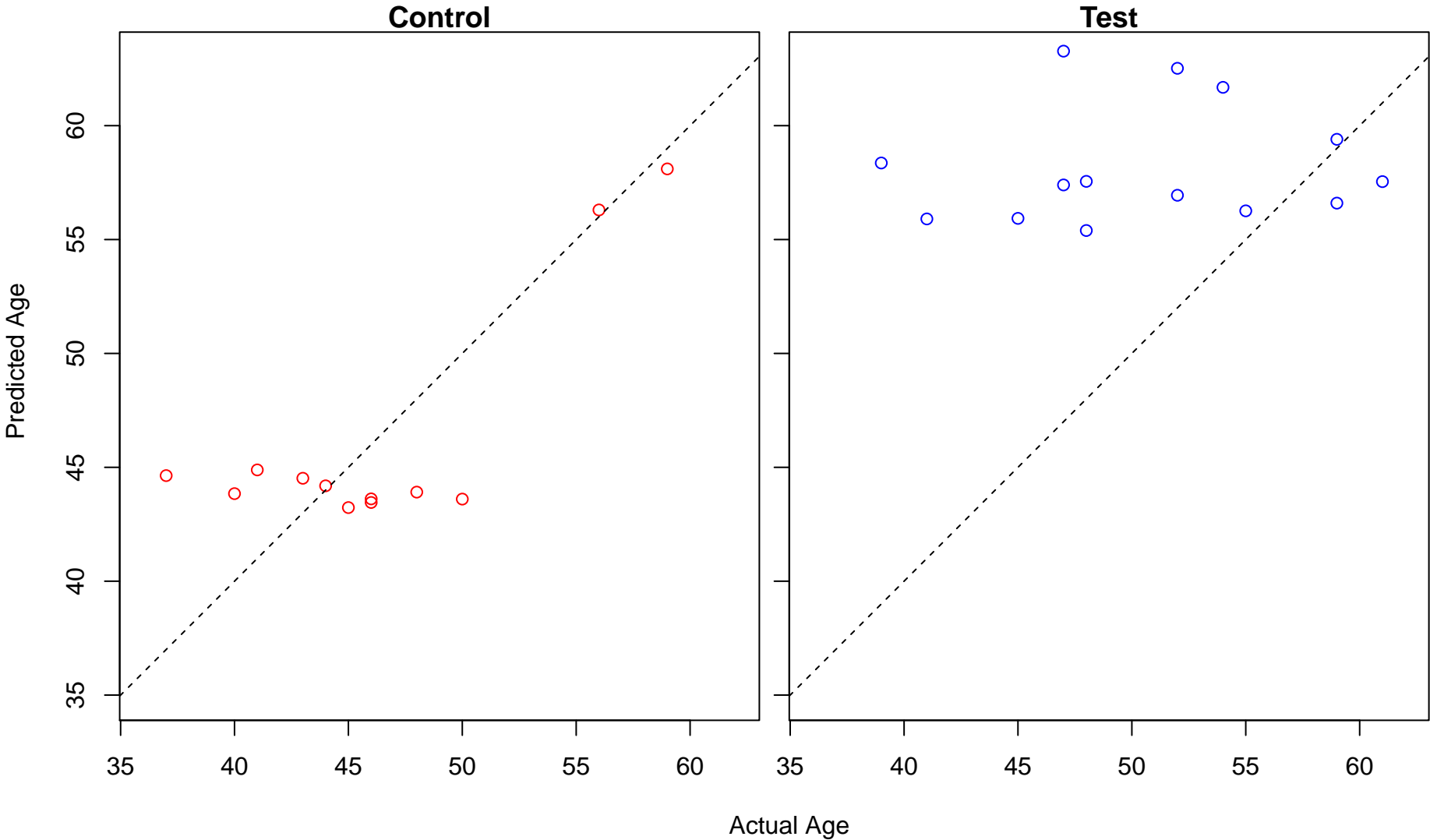


Test



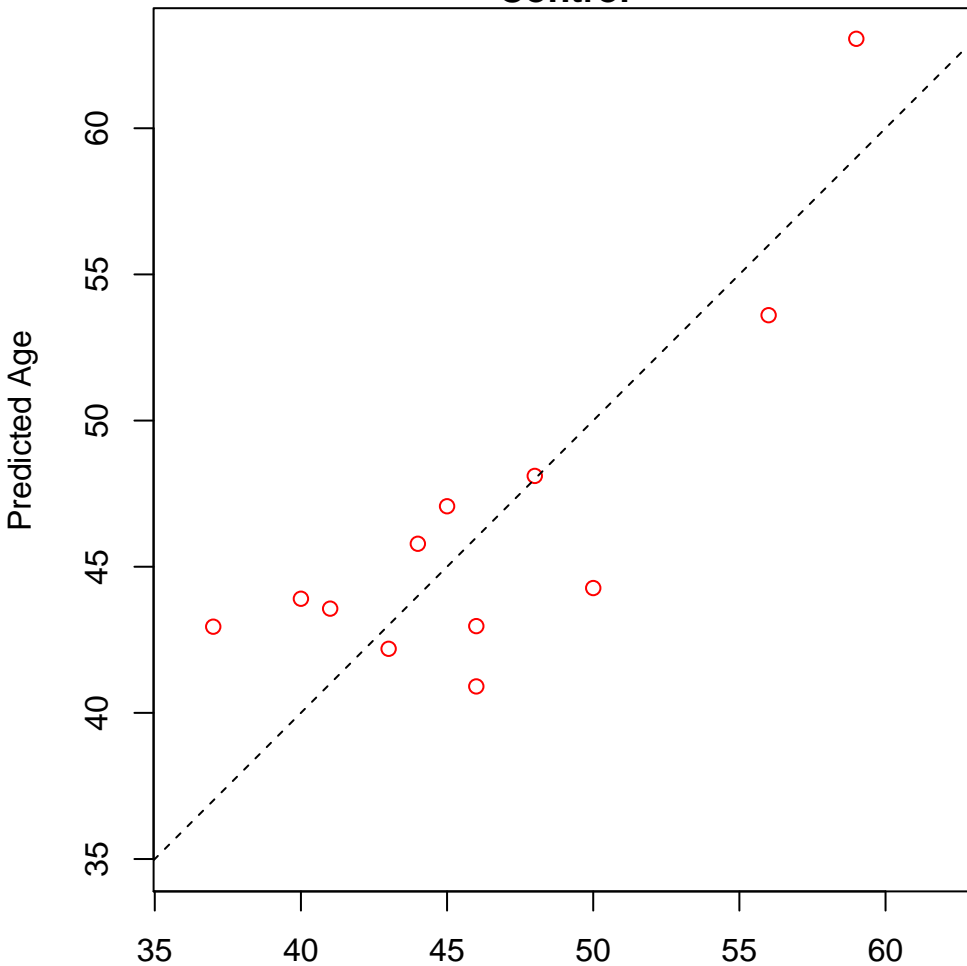
Actual Age

negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway (Score: 2.8912)

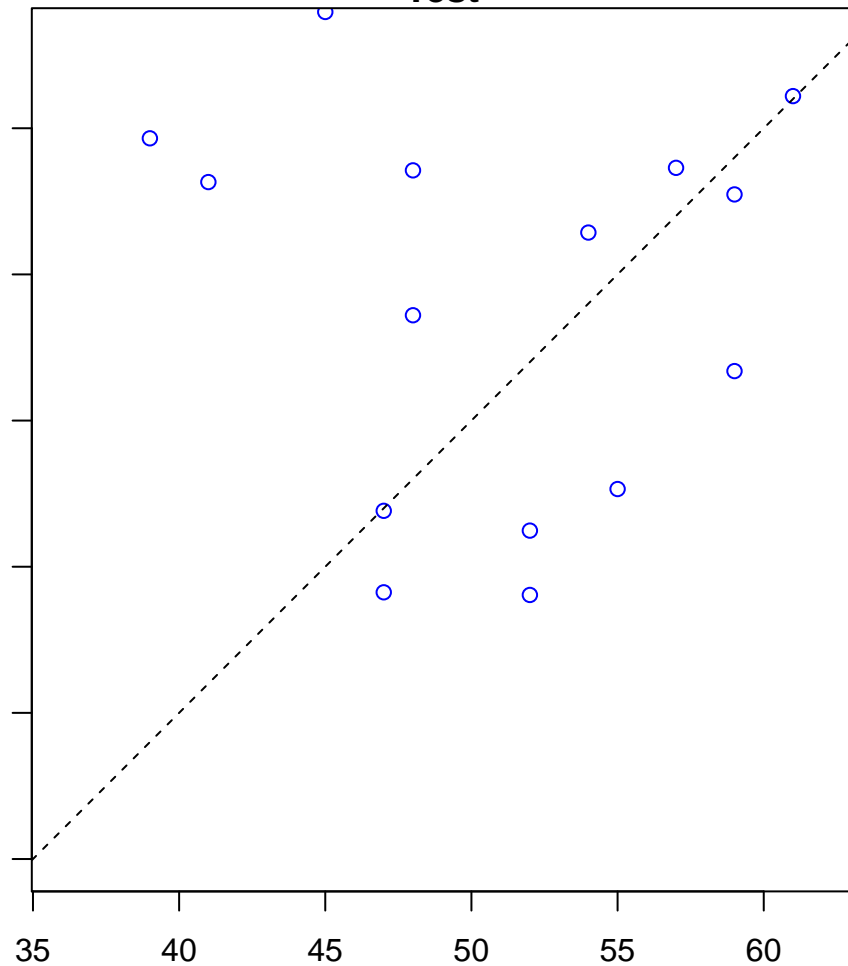


regulation of neurotransmitter uptake (Score: 2.890650)

Control

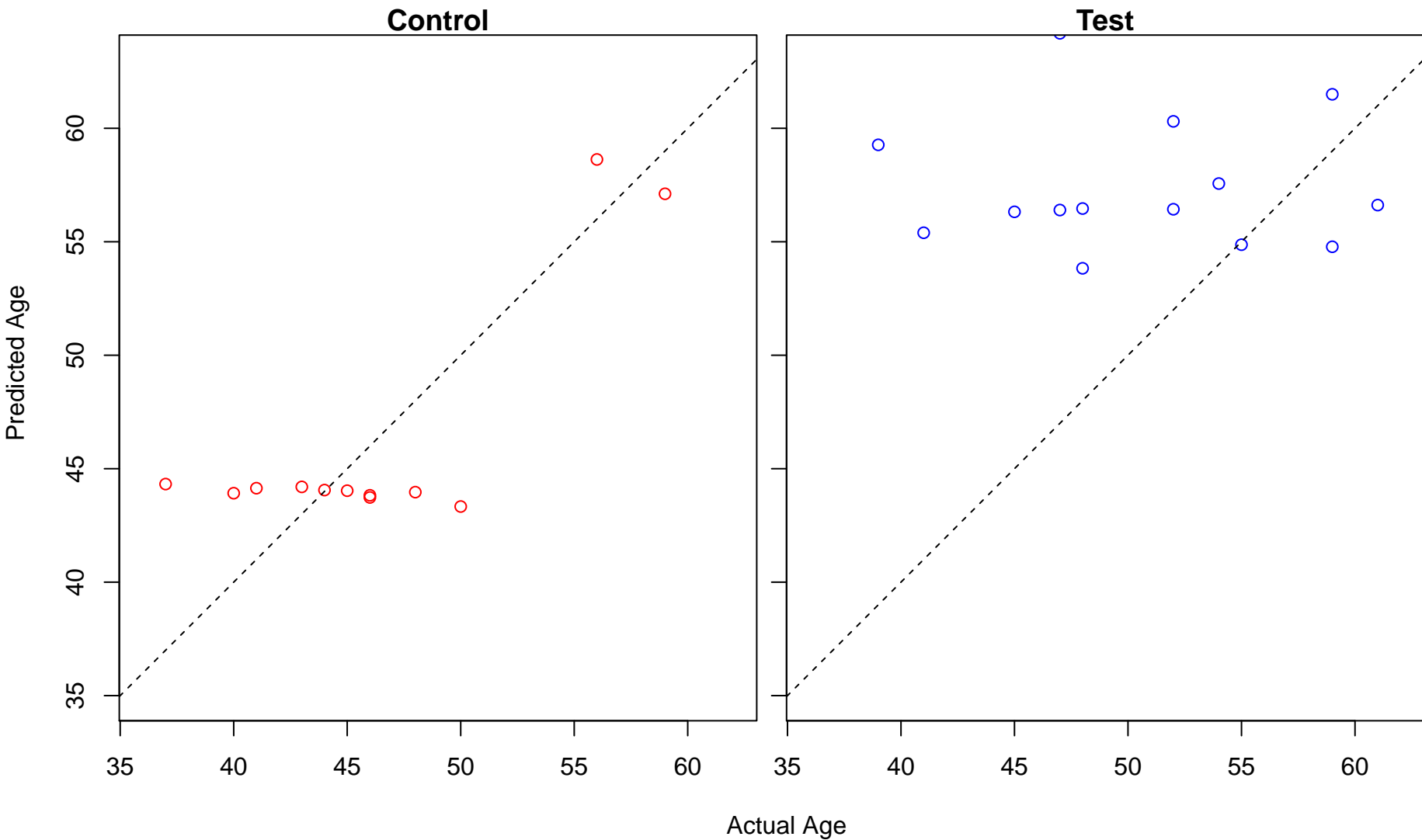


Test

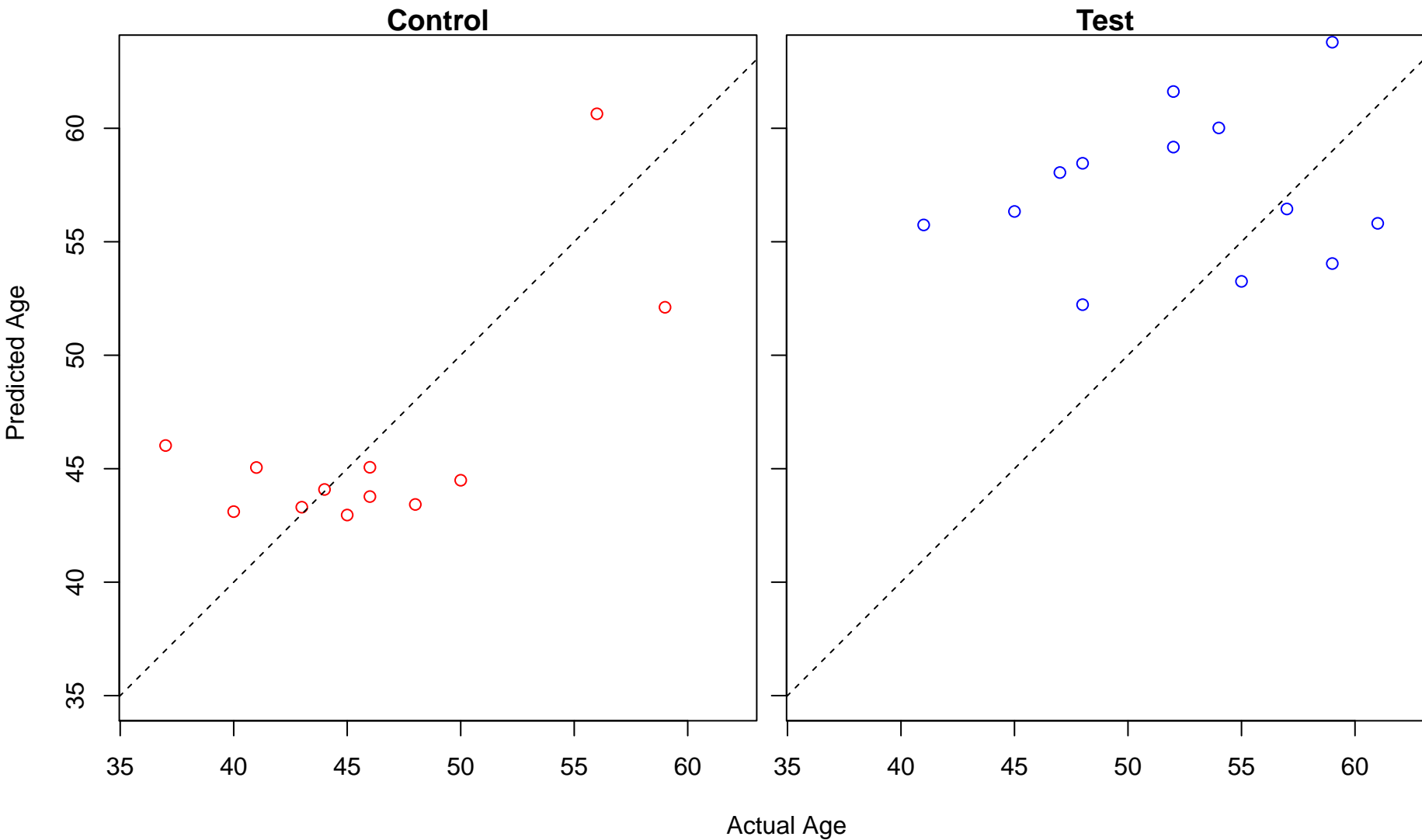


Actual Age

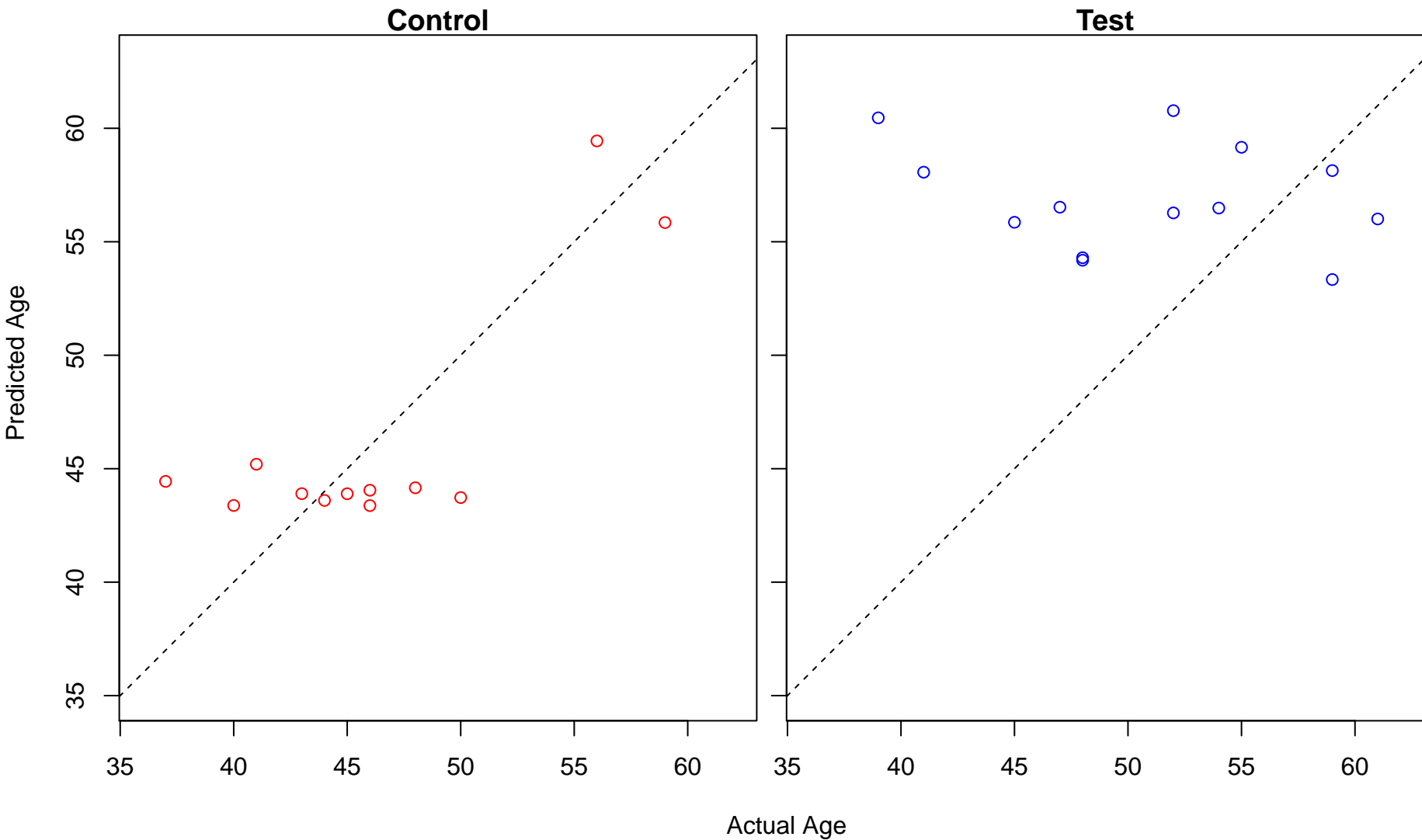
histone H2A ubiquitination (Score: 2.890488)



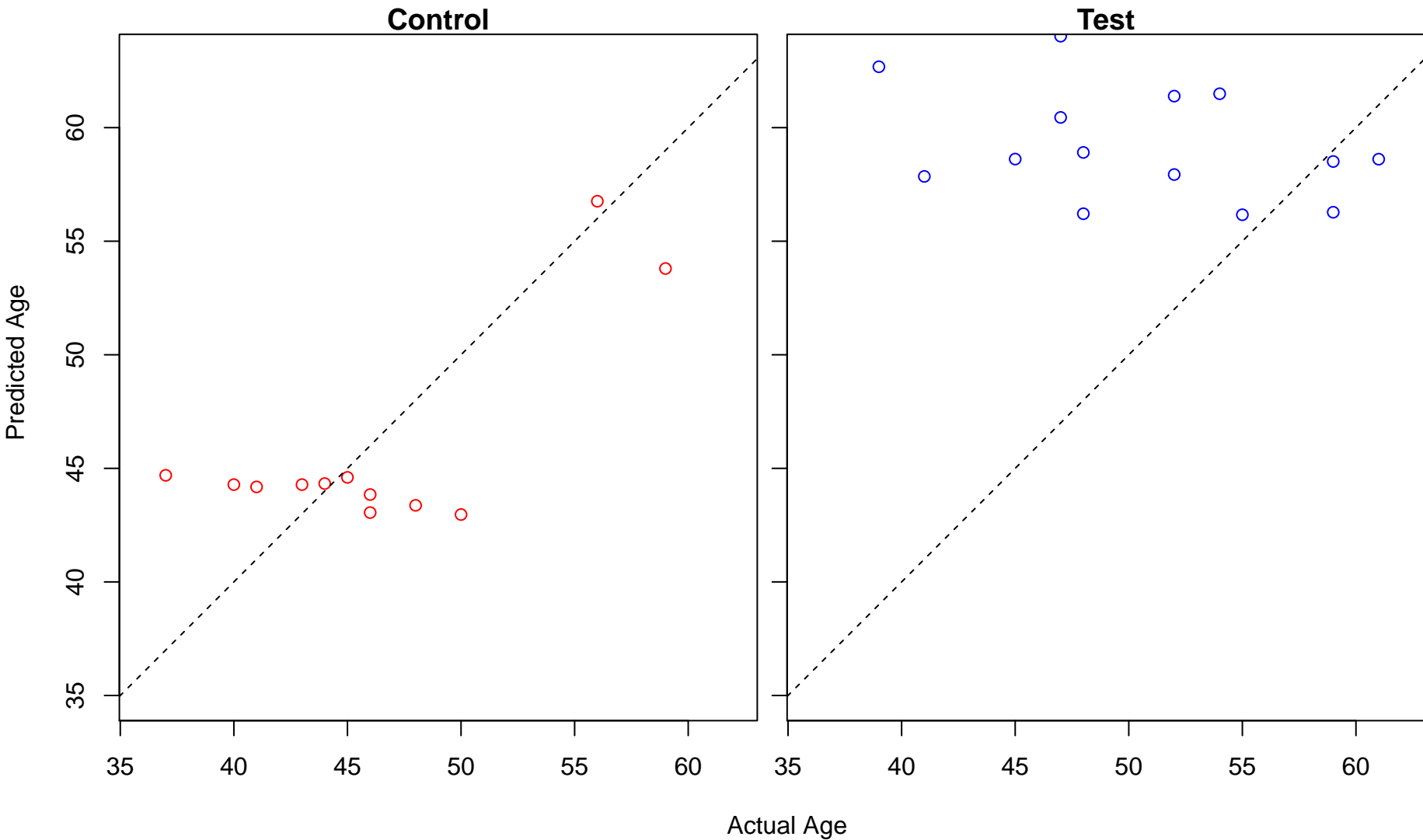
regulation of odontogenesis (Score: 2.888014)



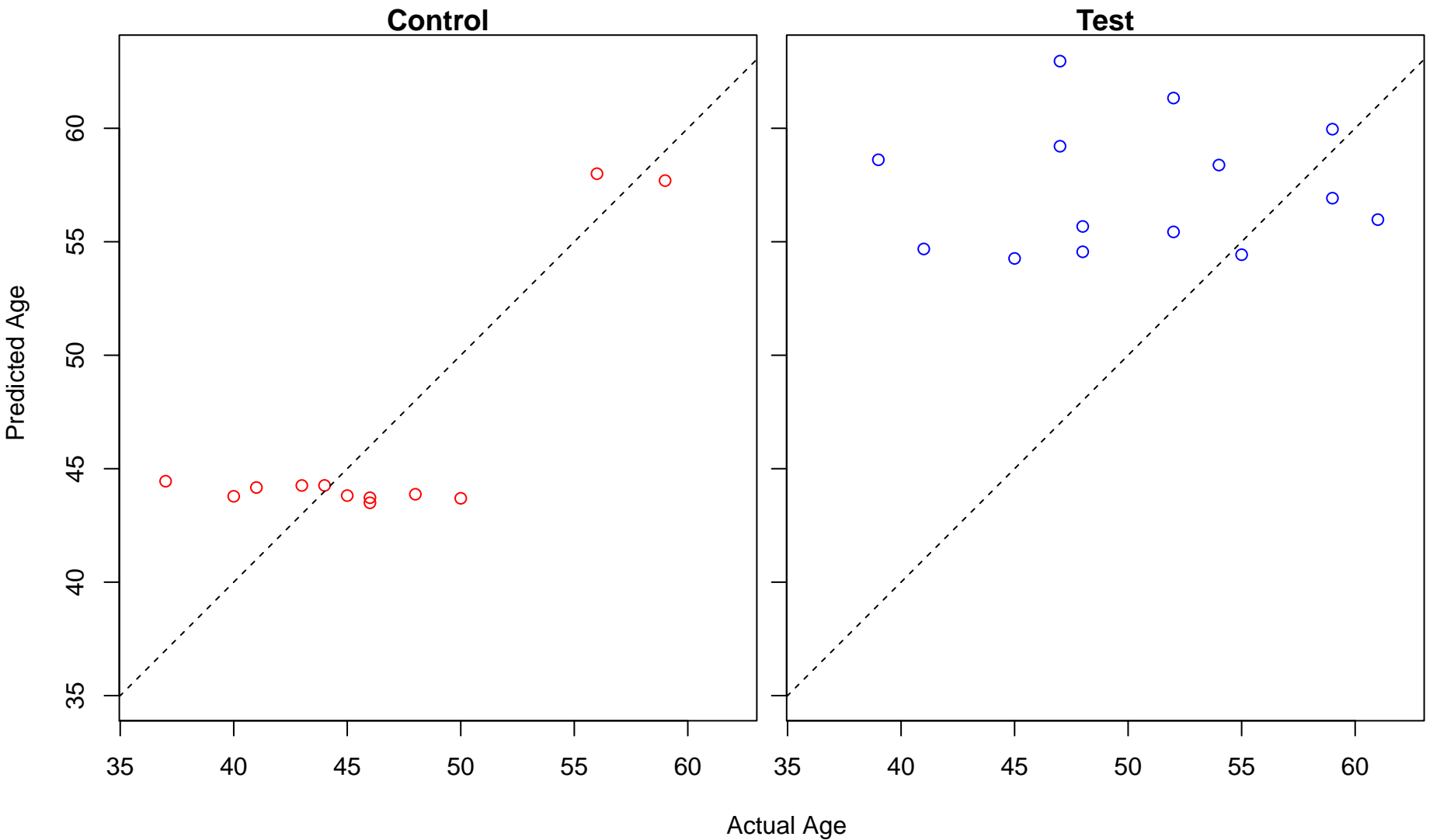
blood vessel morphogenesis (Score: 2.887859)



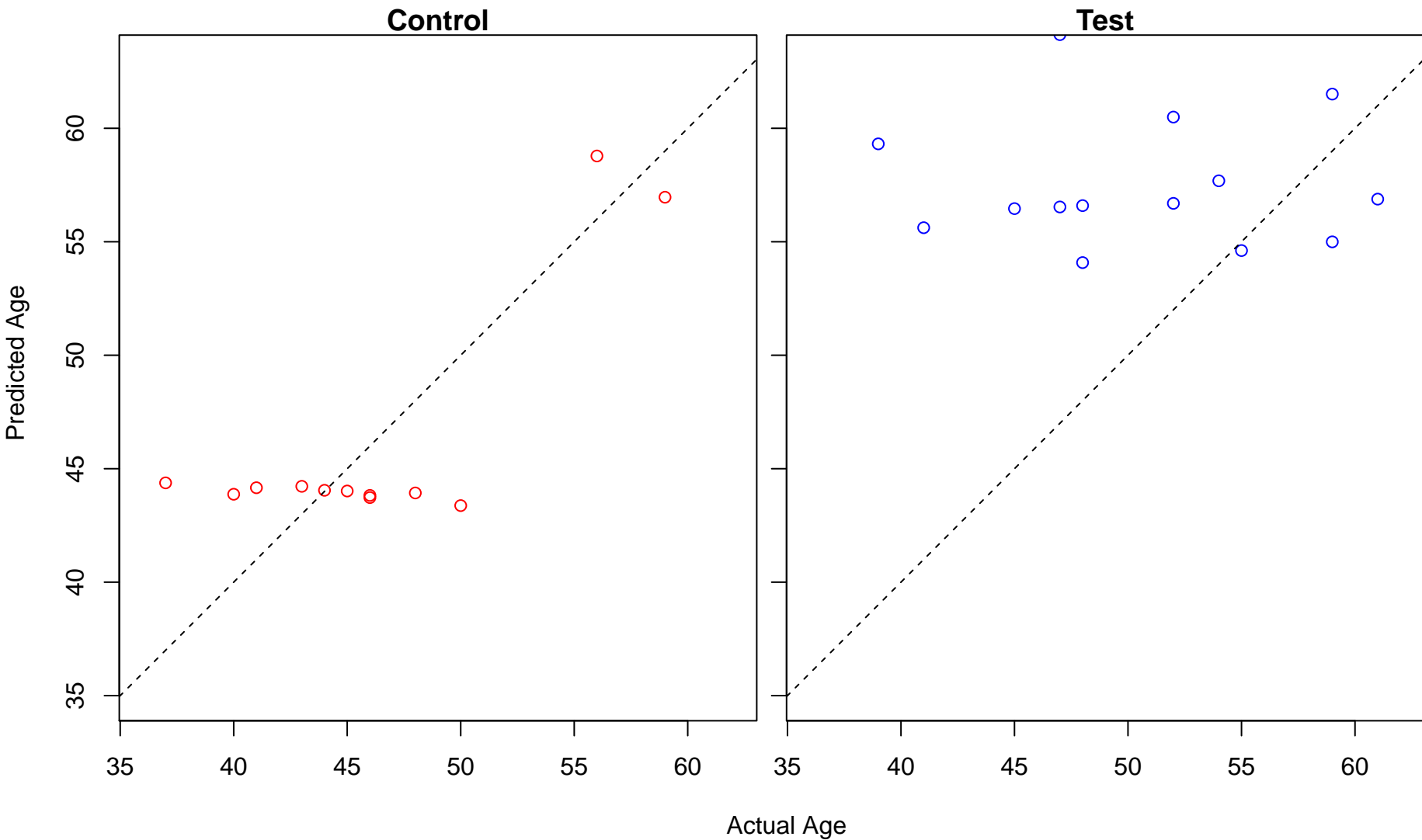
ribonucleotide biosynthetic process (Score: 2.886869)



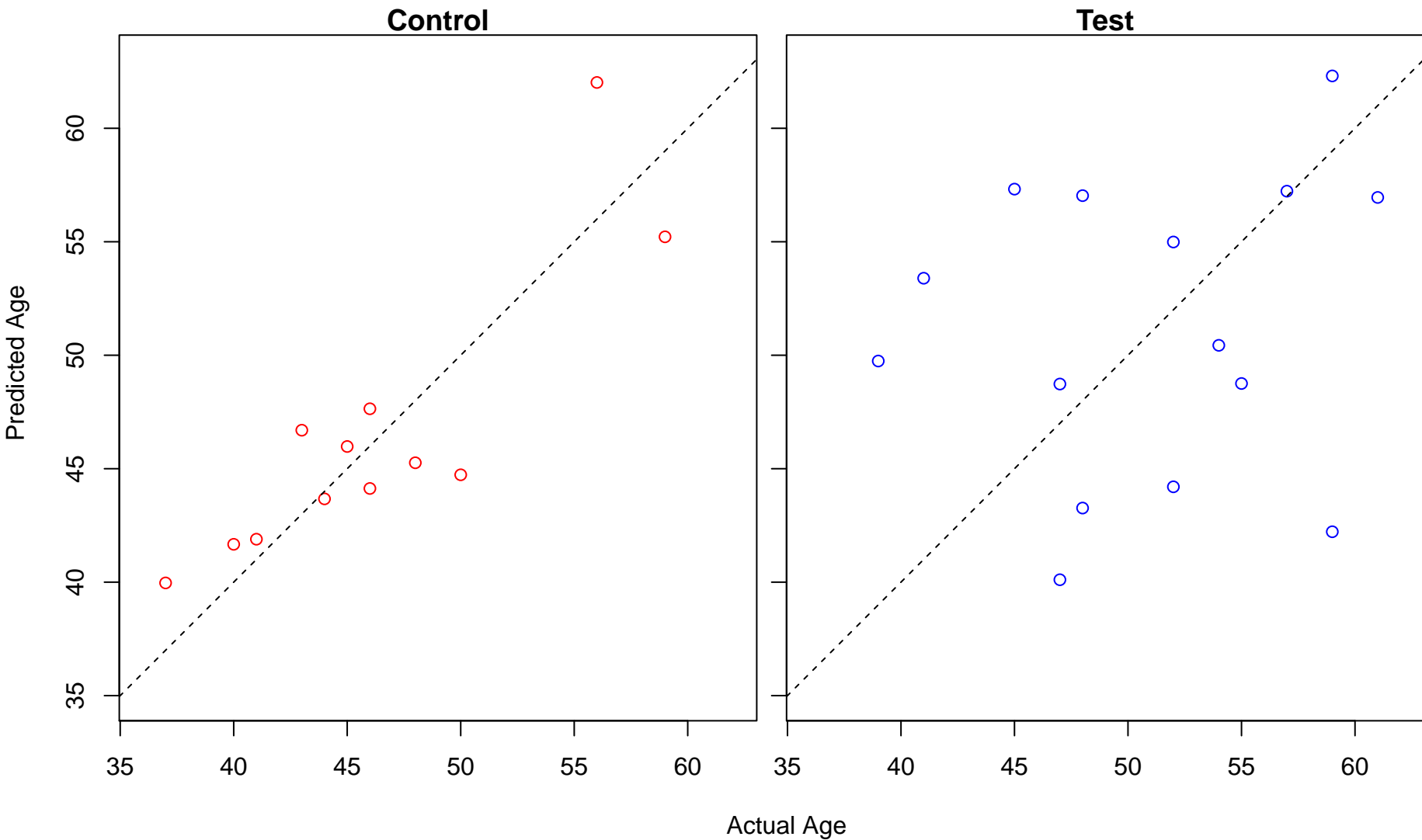
ve regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (S



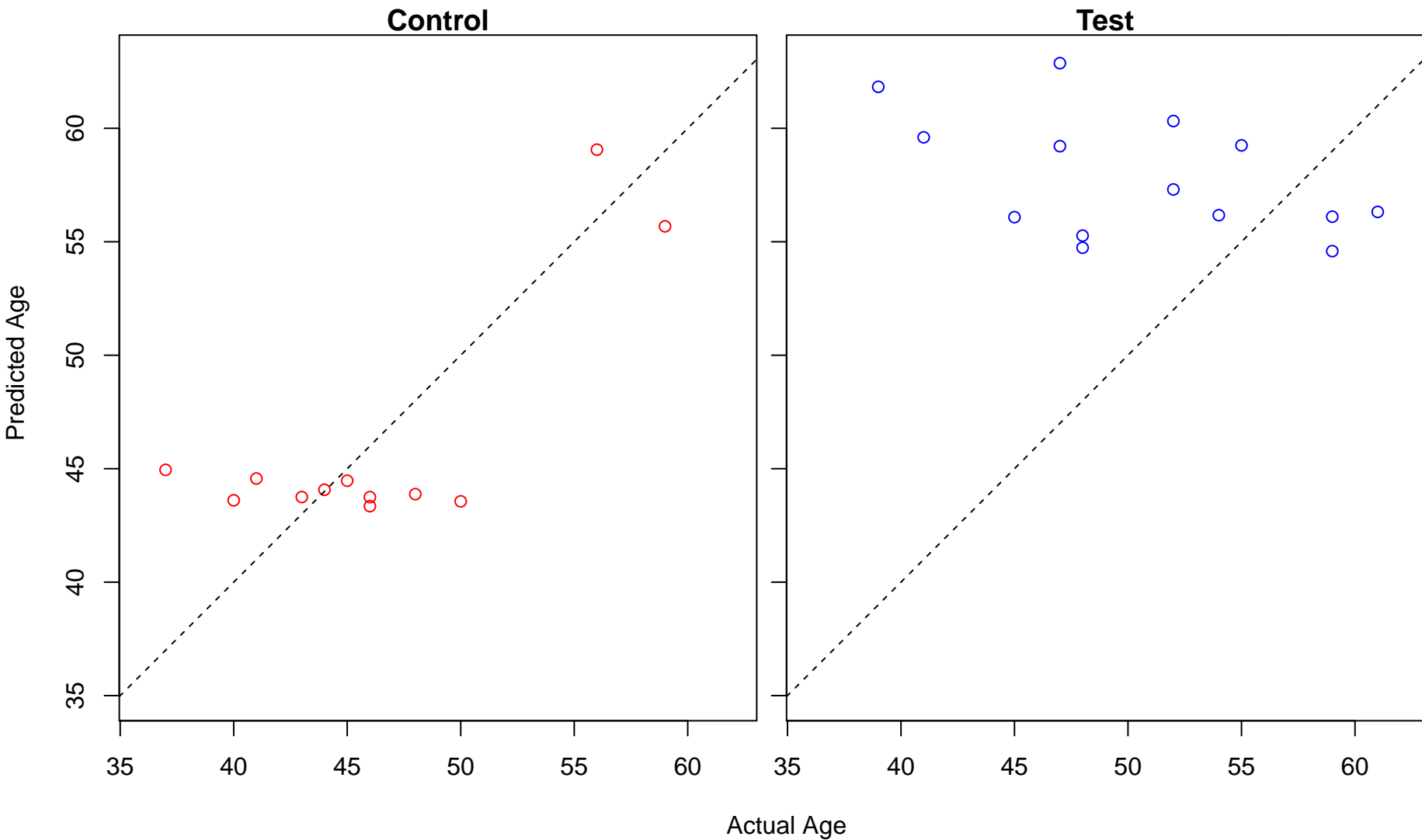
histone monoubiquitination (Score: 2.883345)



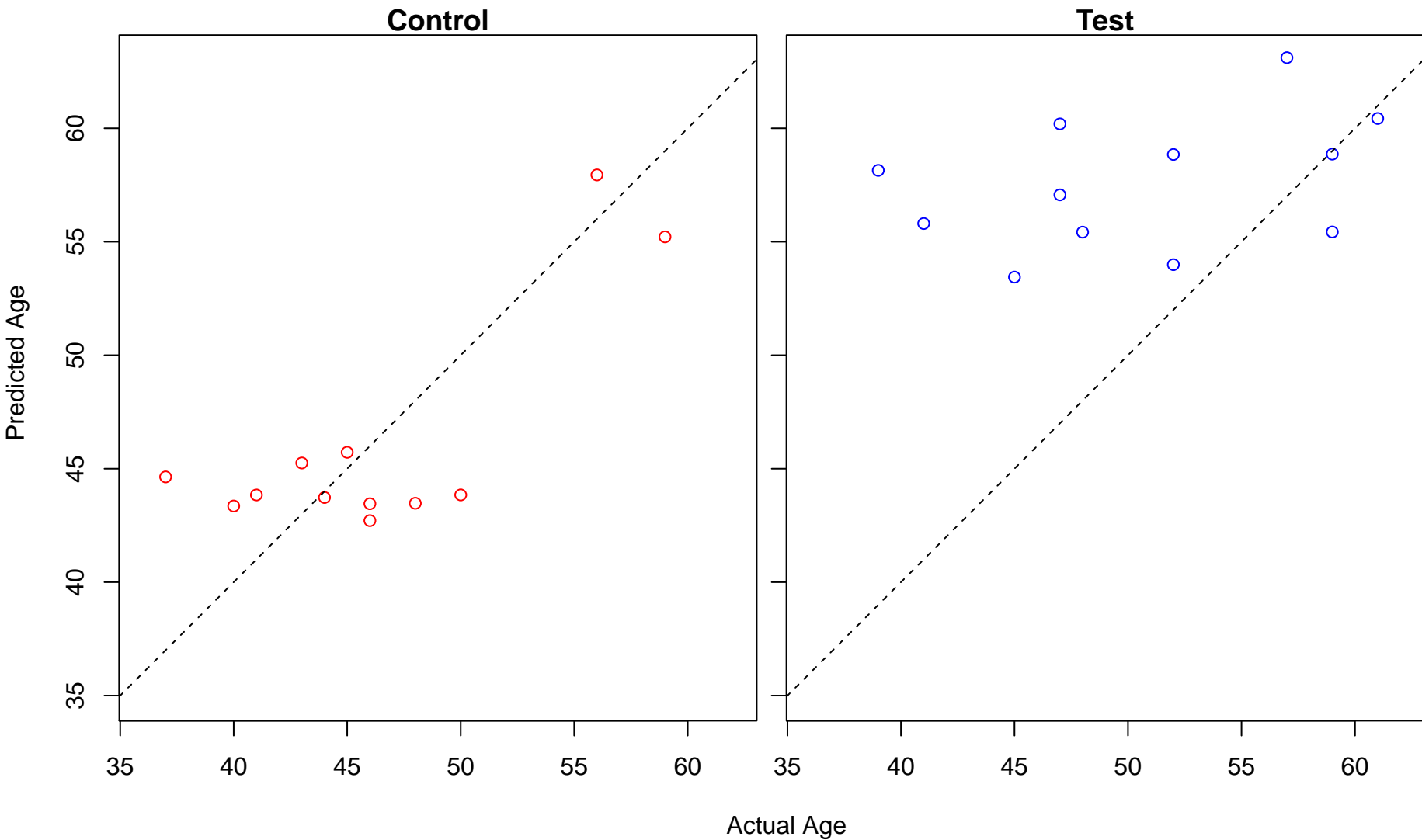
regulation of extent of cell growth (Score: 2.882725)



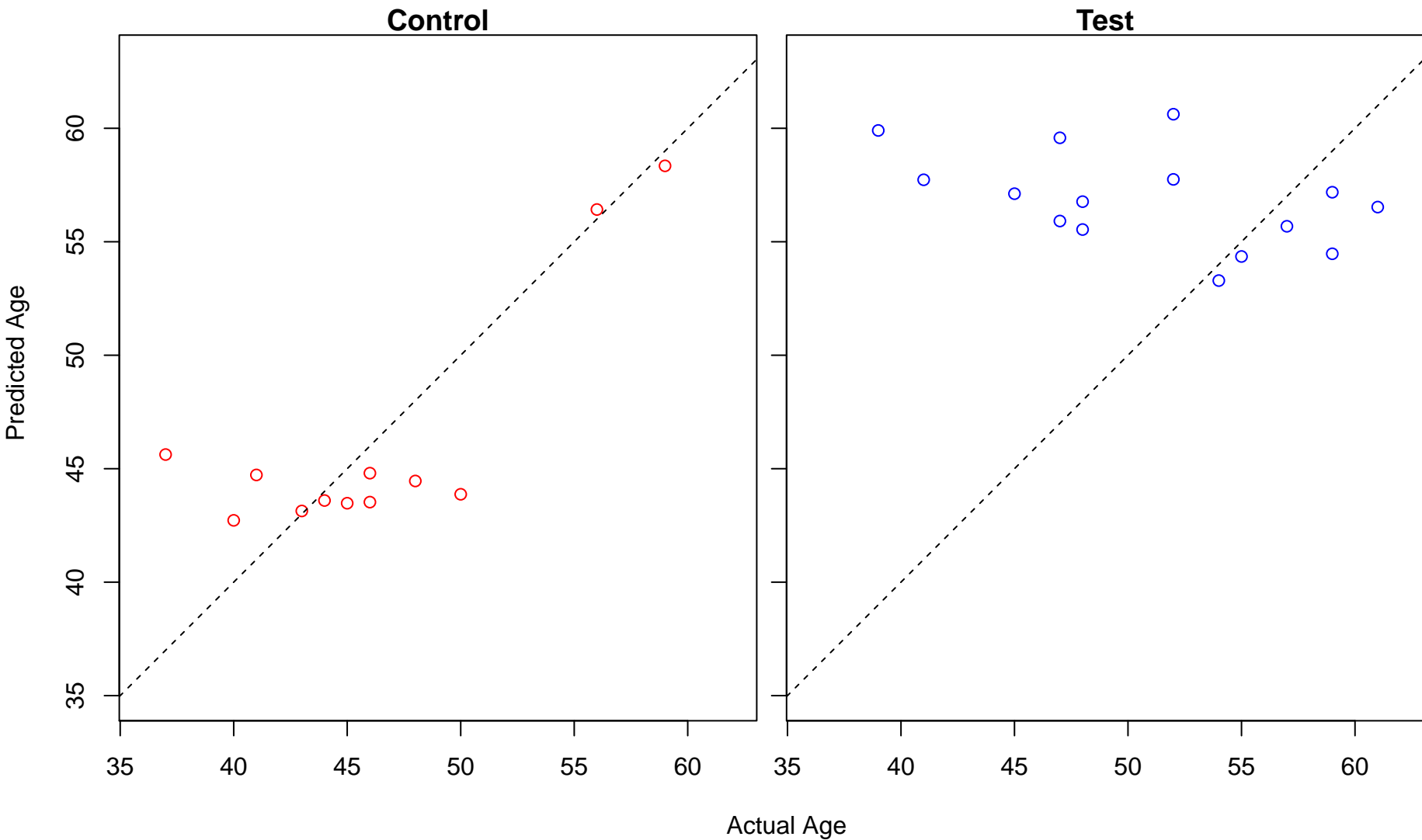
cell migration (Score: 2.881237)



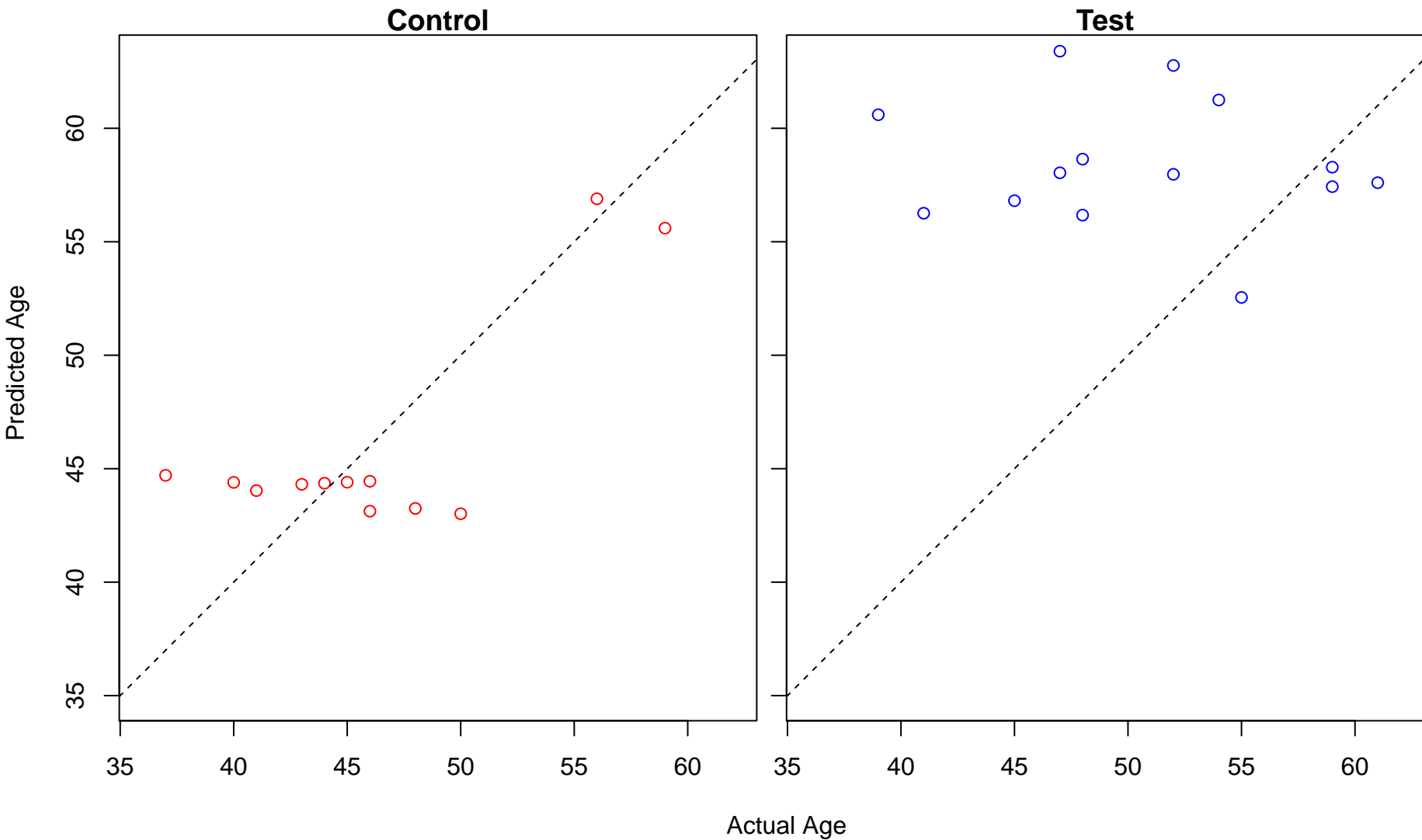
cellular response to exogenous dsRNA (Score: 2.880781)



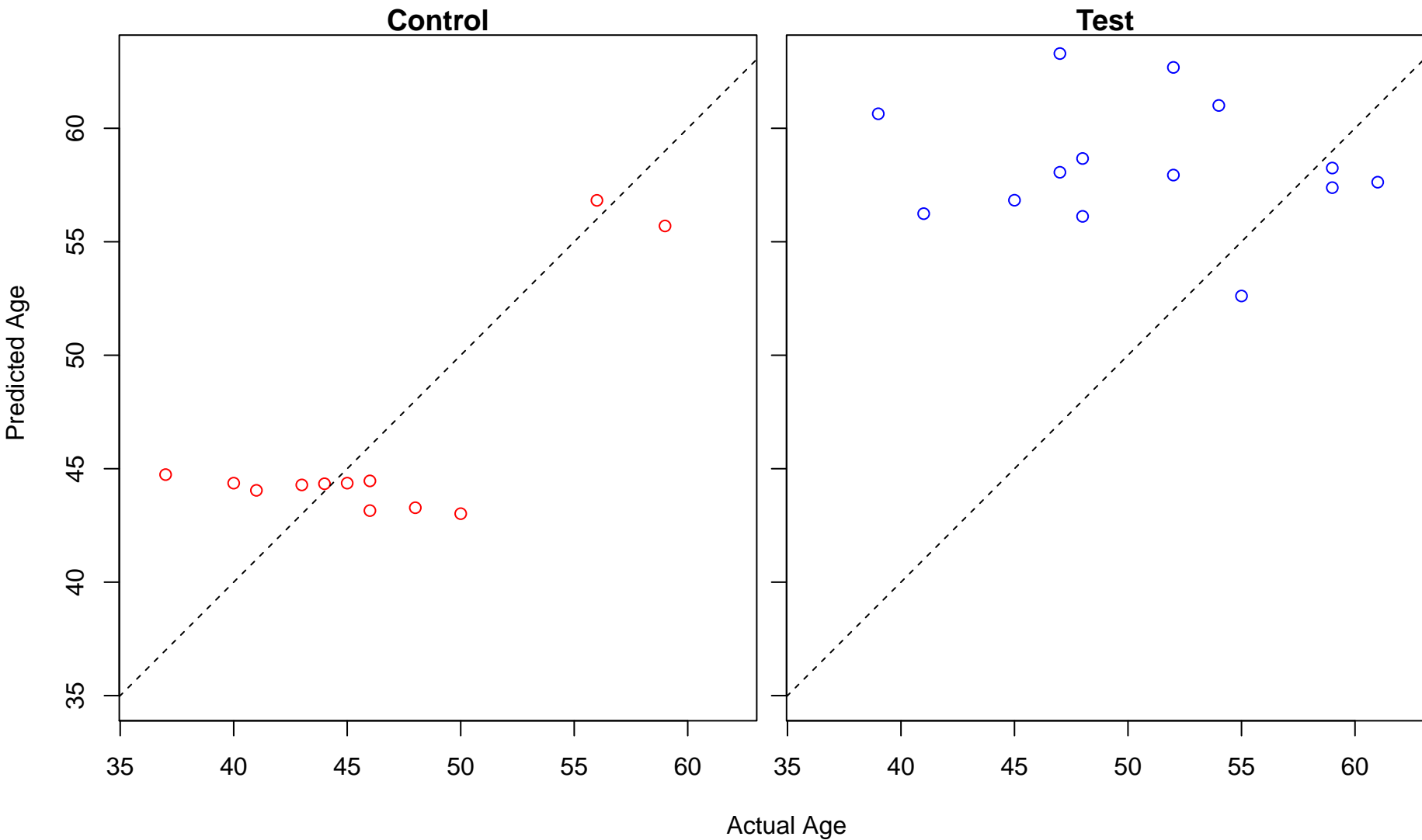
cytokine secretion (Score: 2.878855)



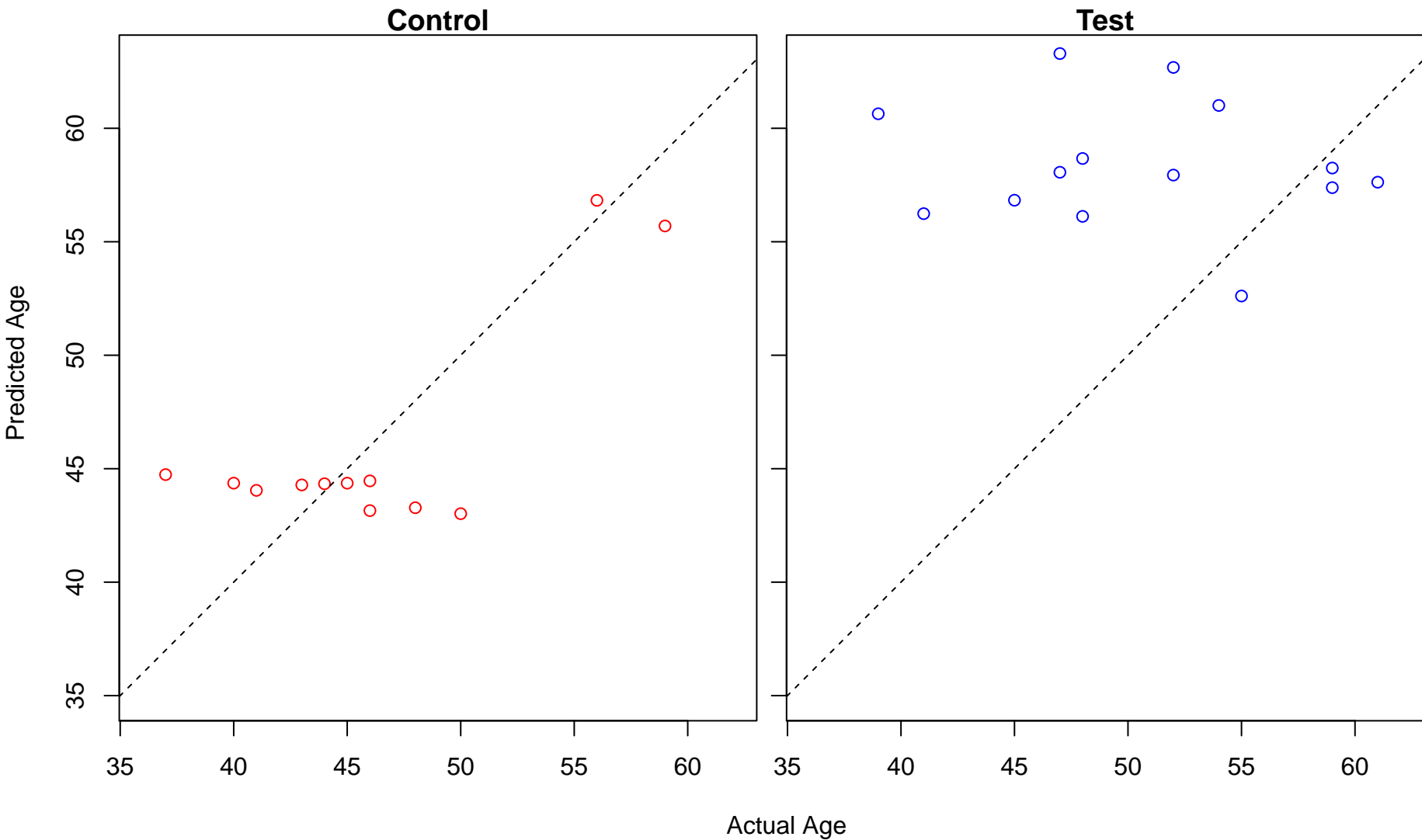
ribonucleoside biosynthetic process (Score: 2.878563)



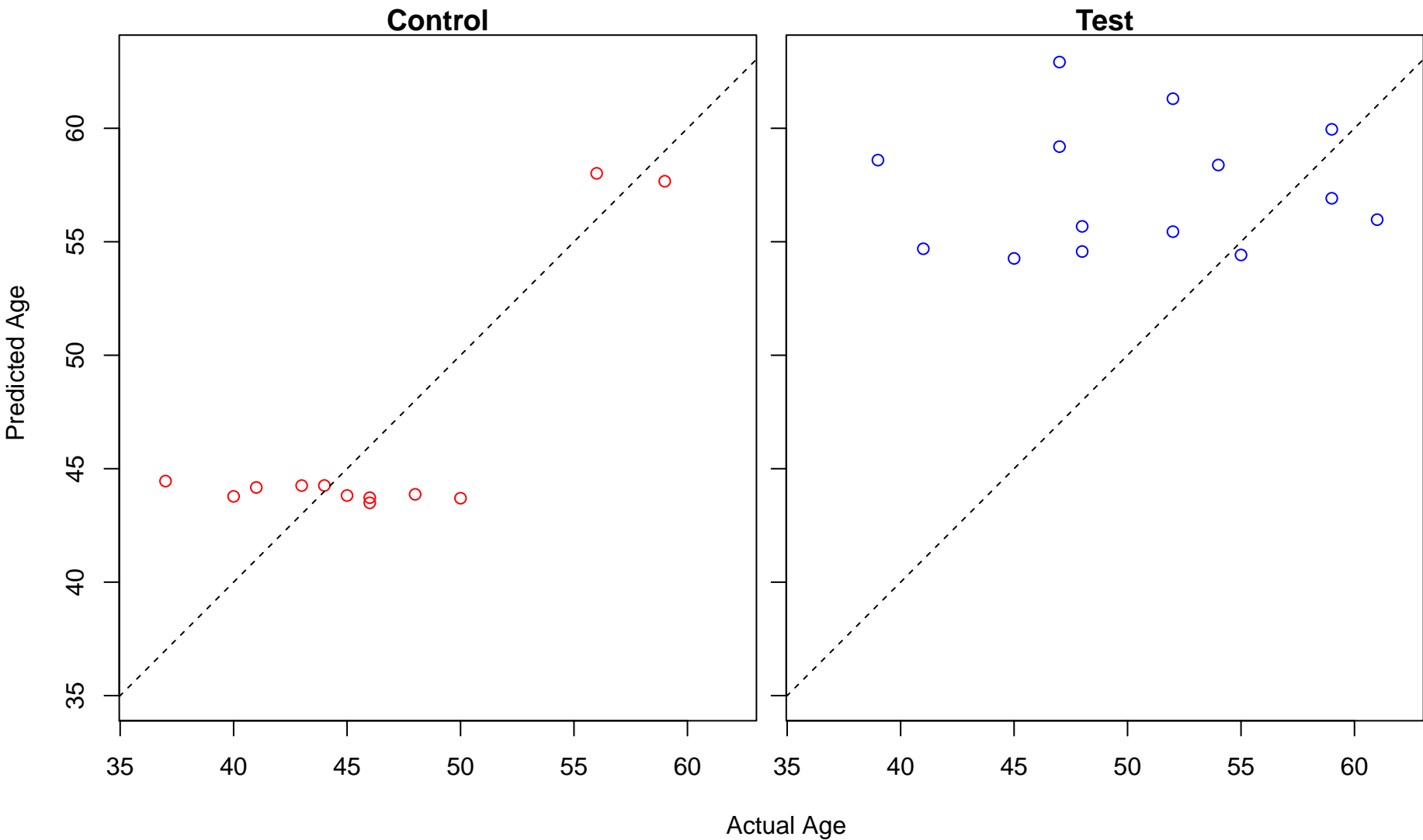
nucleoside biosynthetic process (Score: 2.877559)



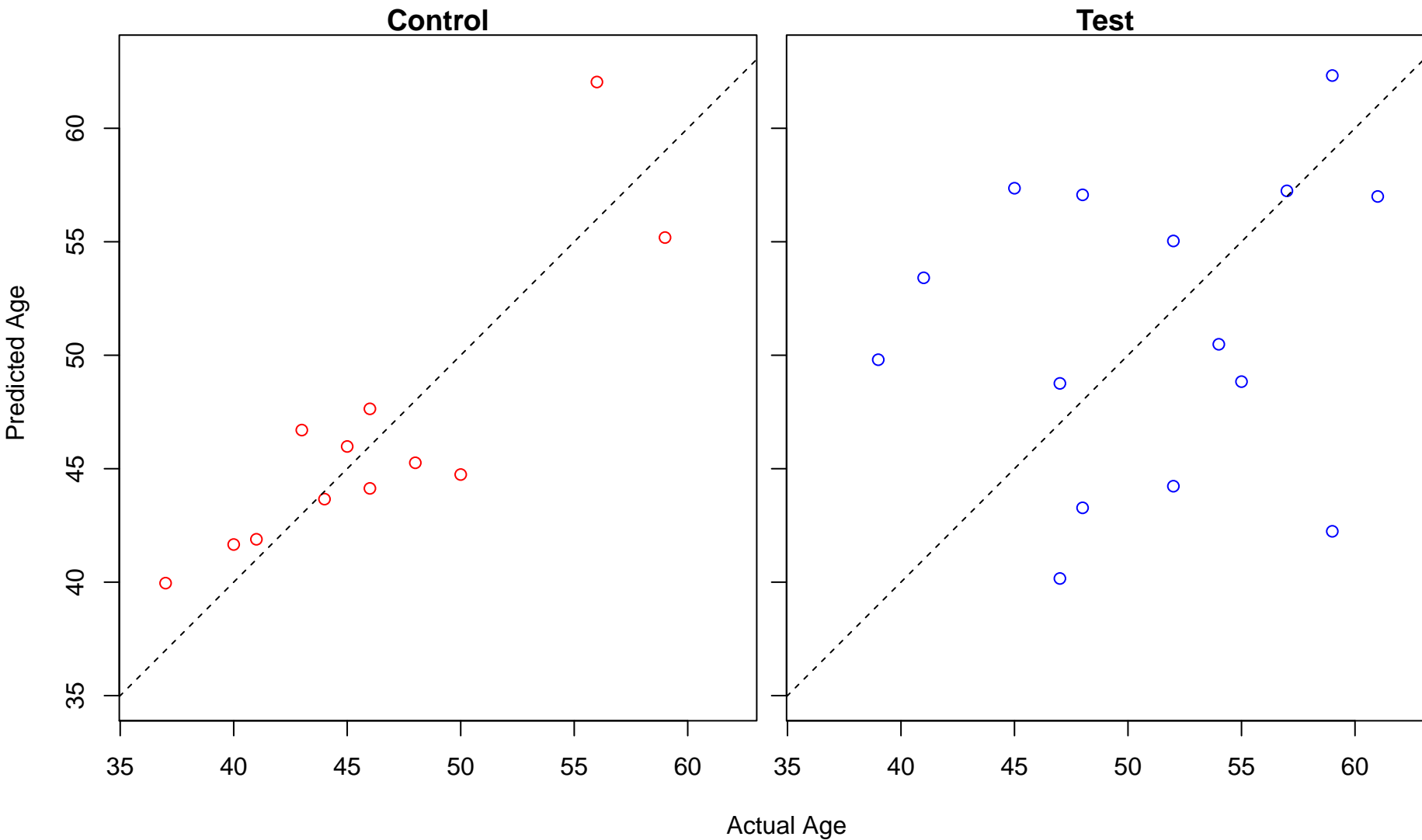
glycosyl compound biosynthetic process (Score: 2.877555)



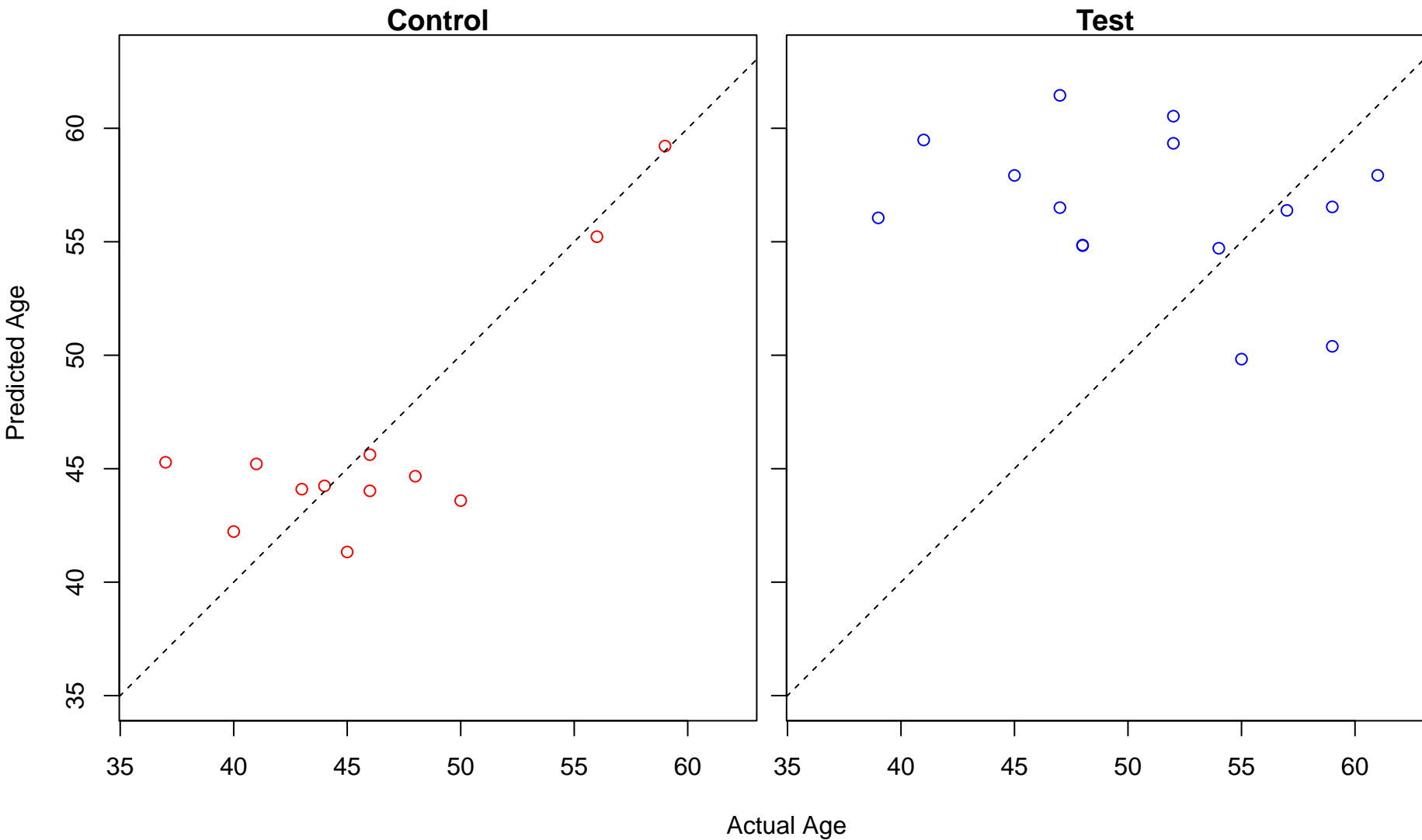
The regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (S



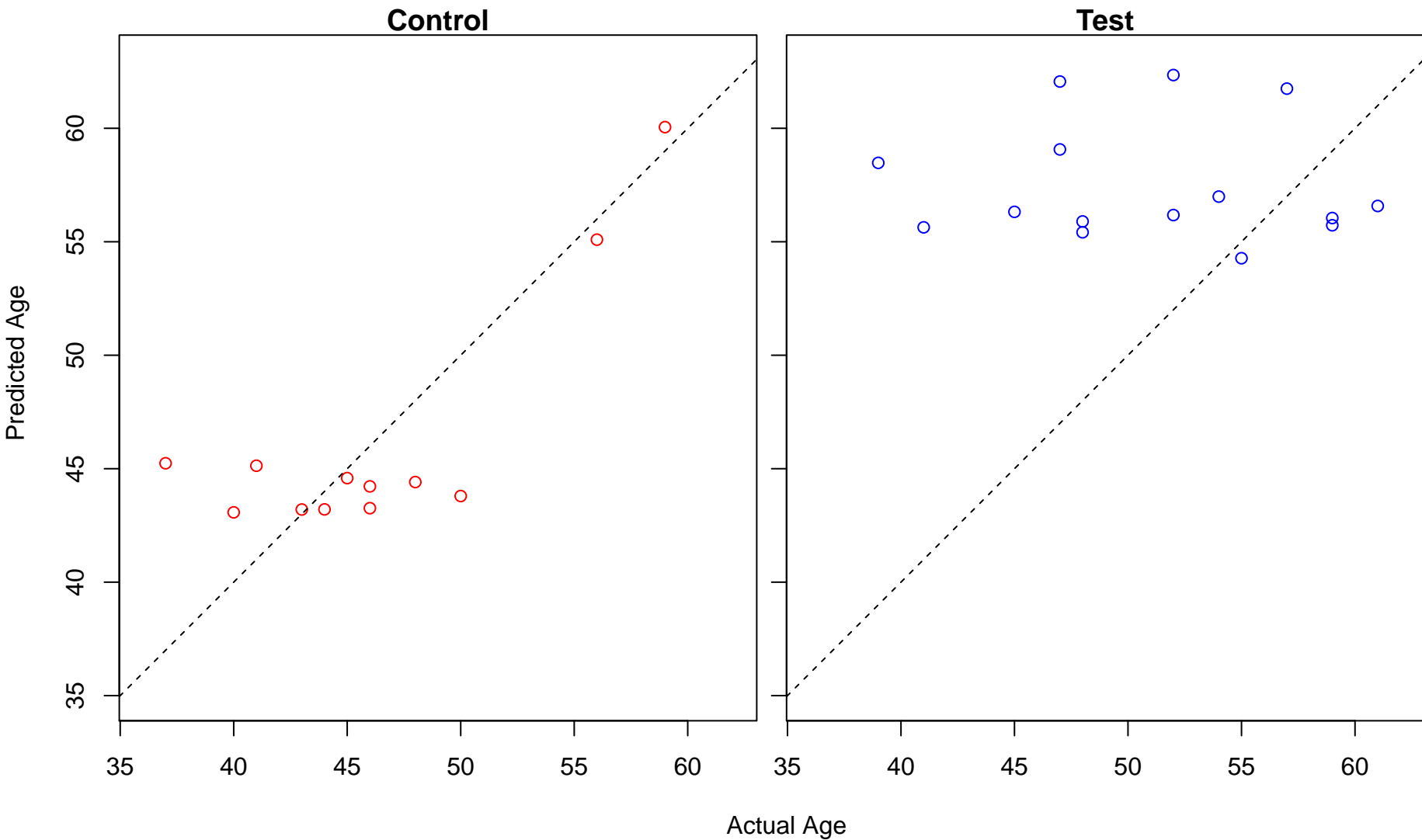
regulation of axon extension (Score: 2.876617)



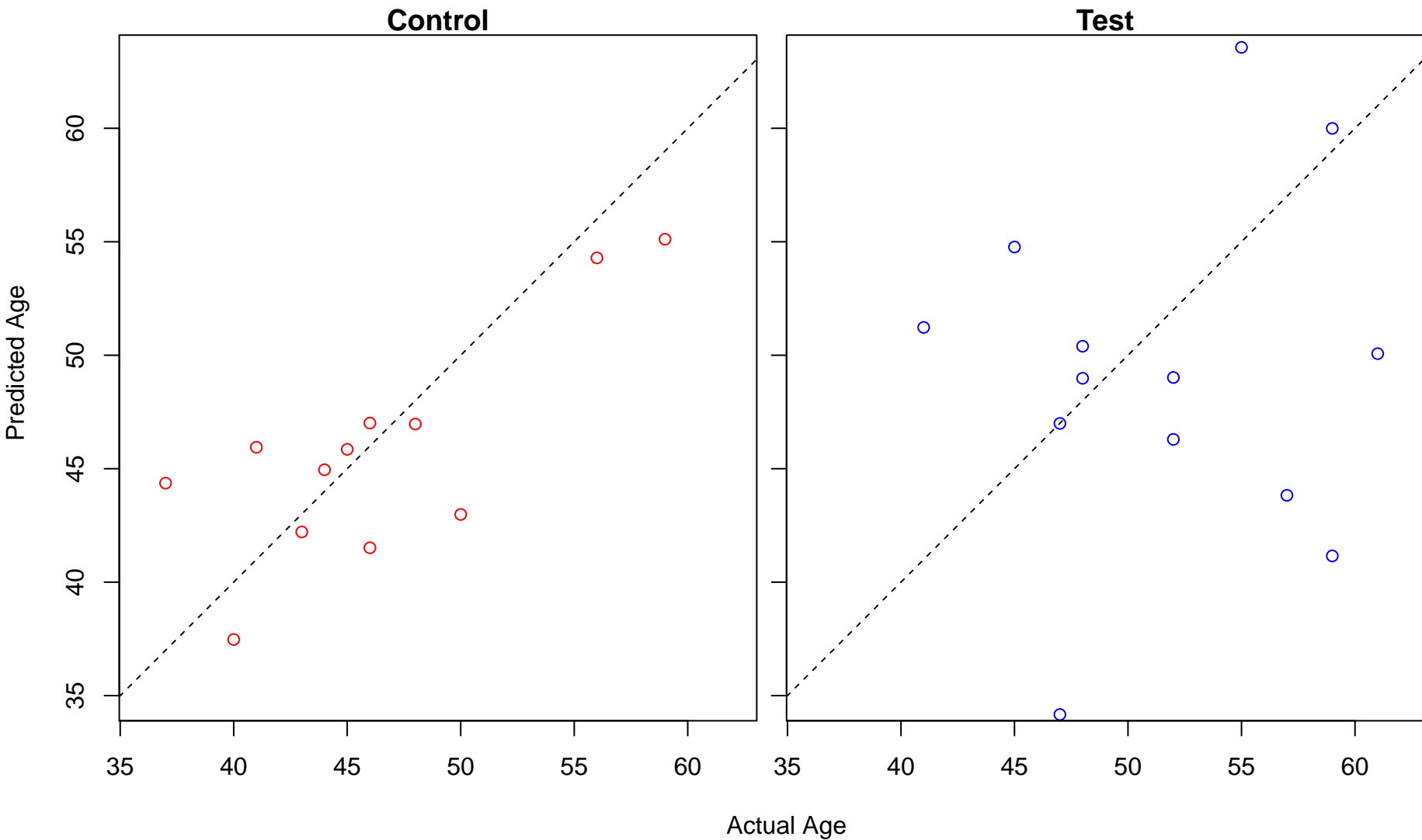
regulation of leukocyte migration (Score: 2.875830)



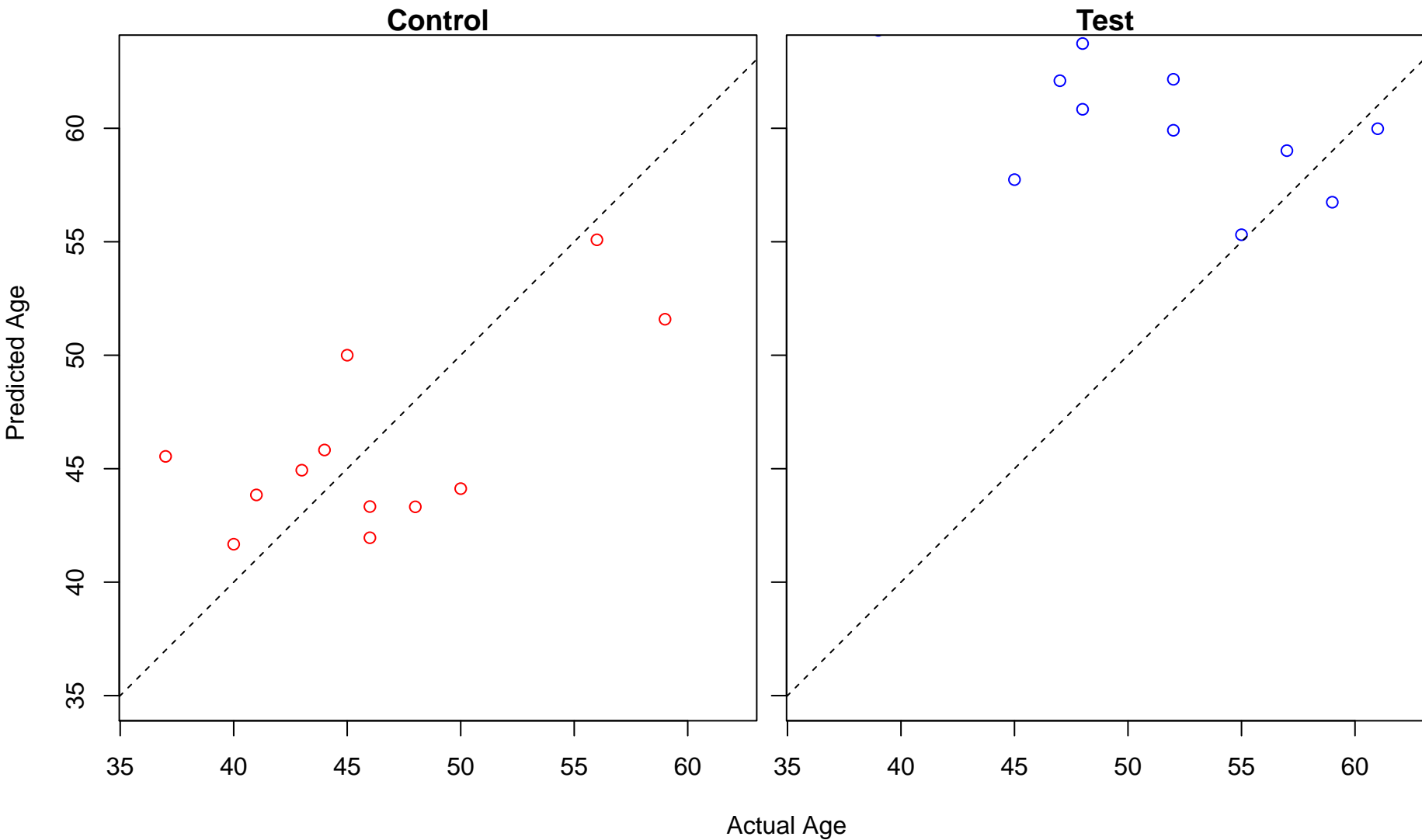
regulation of morphogenesis of a branching structure (Score: 2.875794)



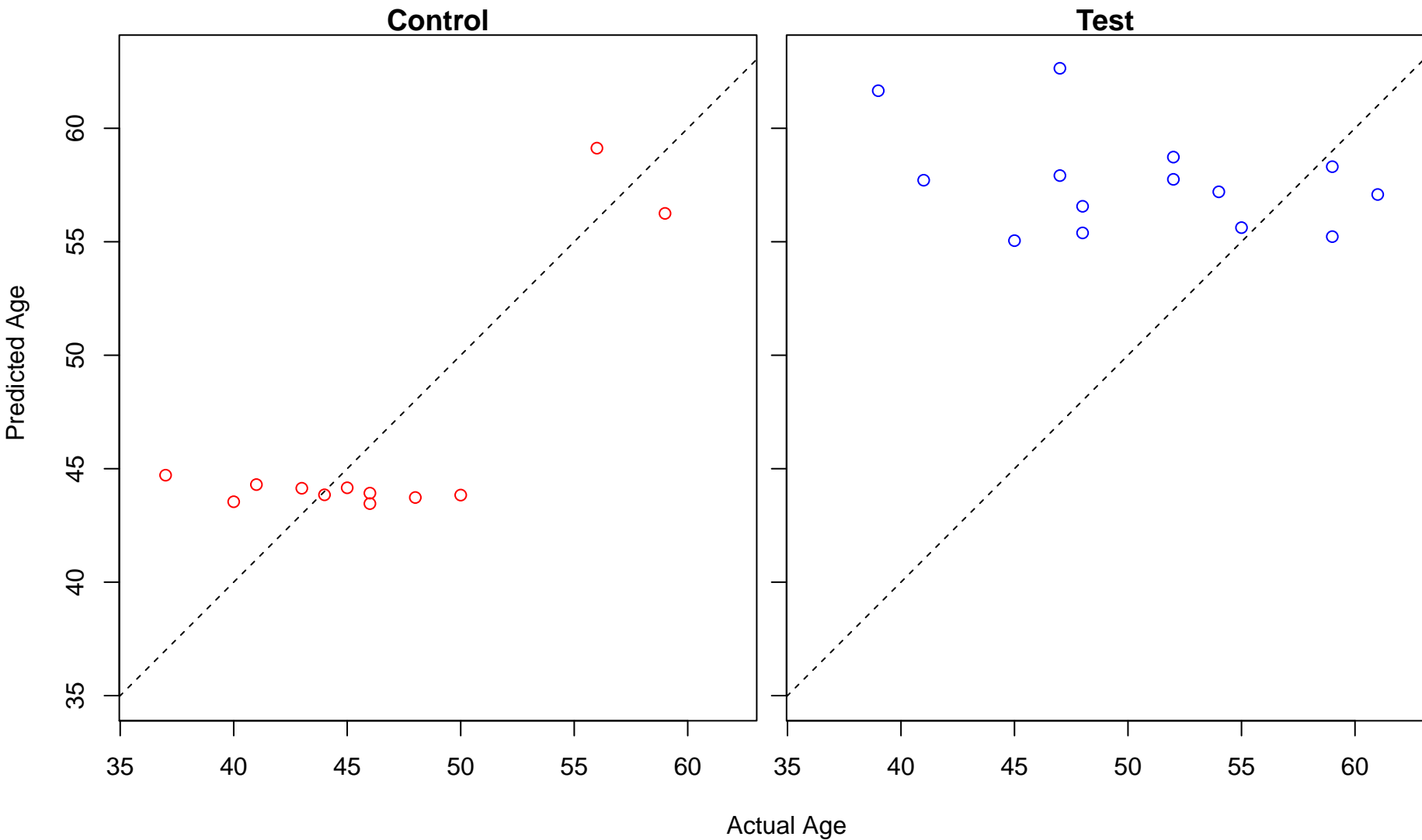
positive regulation of immune effector process (Score: 2.875291)



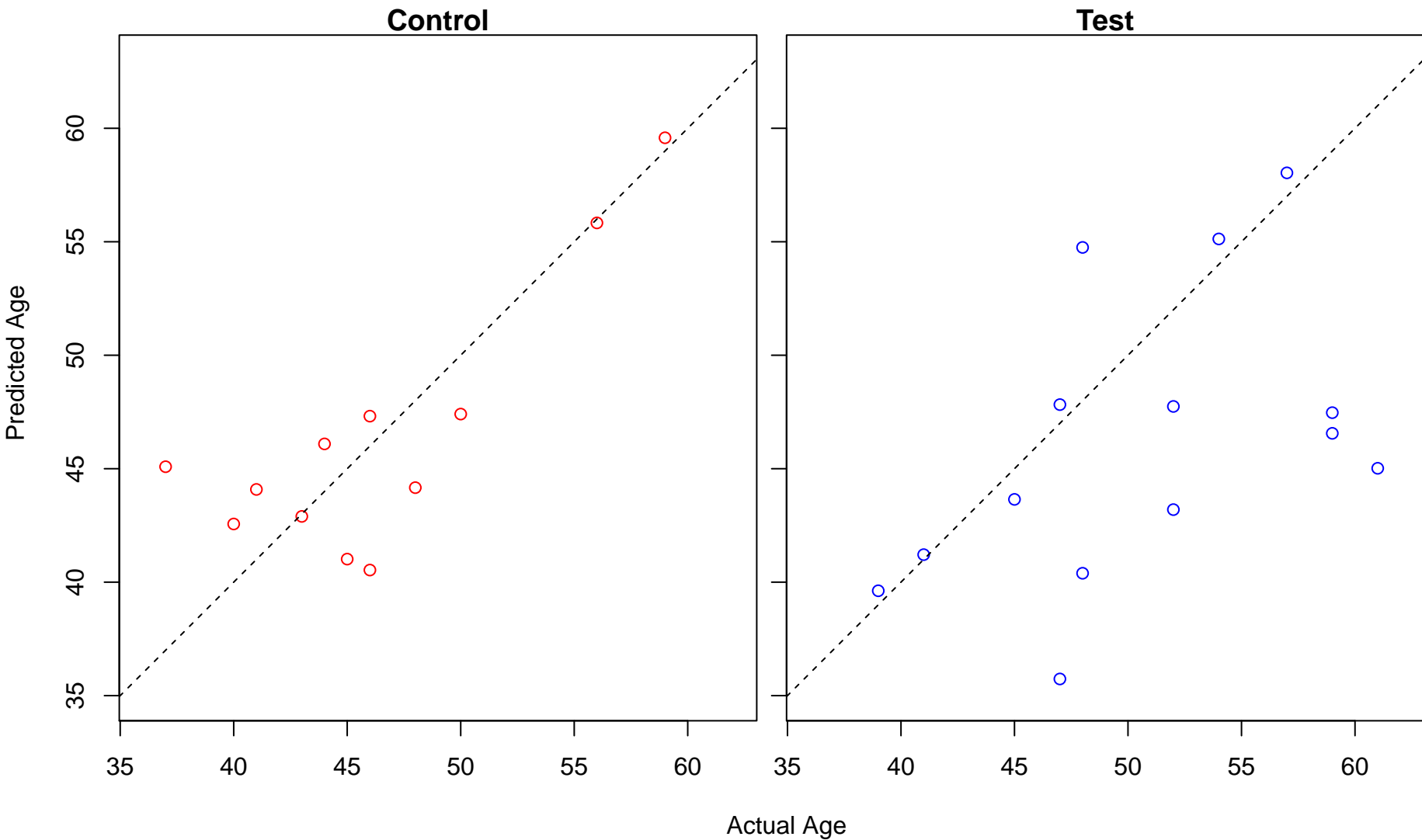
riboflavin transport (Score: 2.872673)



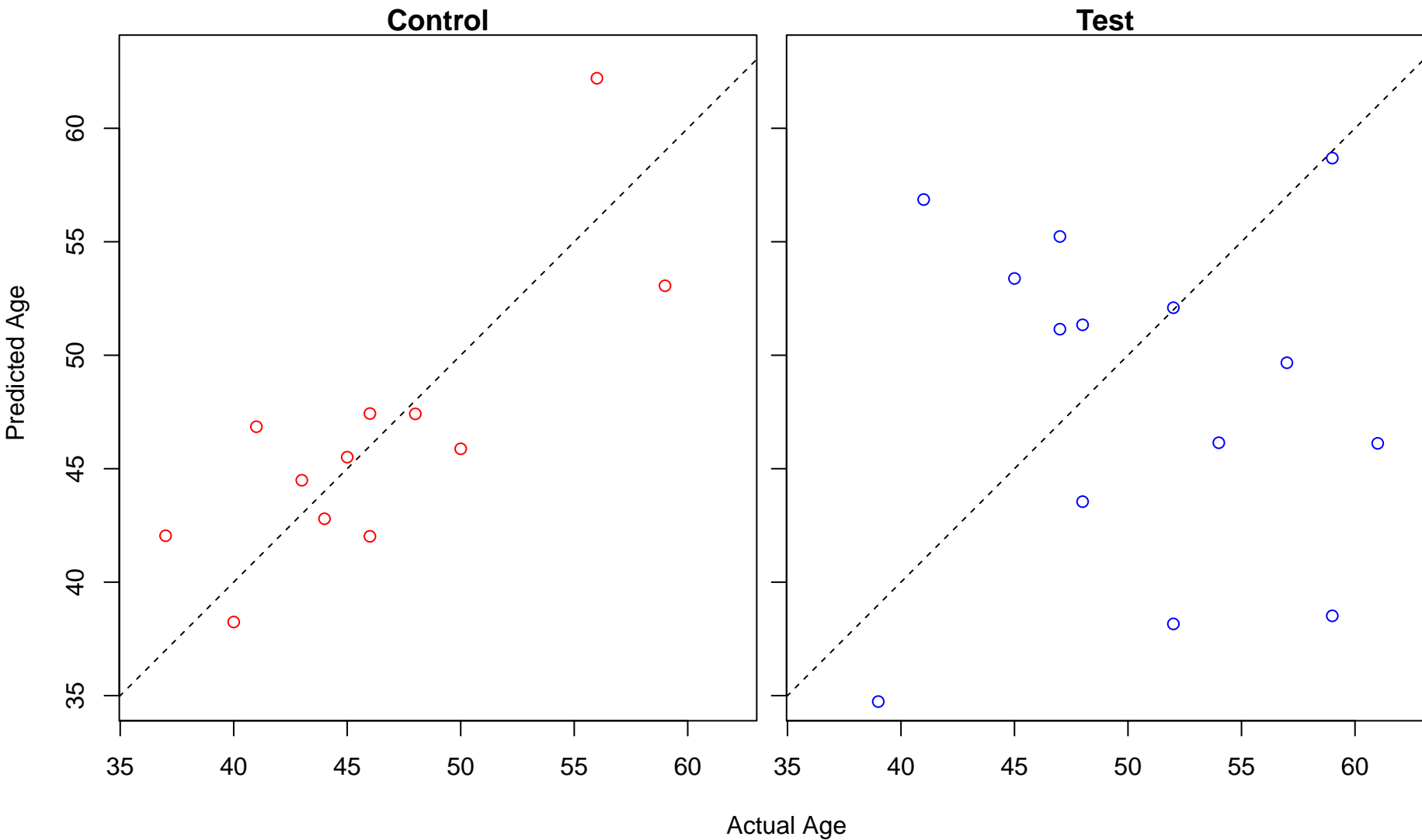
insulin receptor signaling pathway (Score: 2.872436)



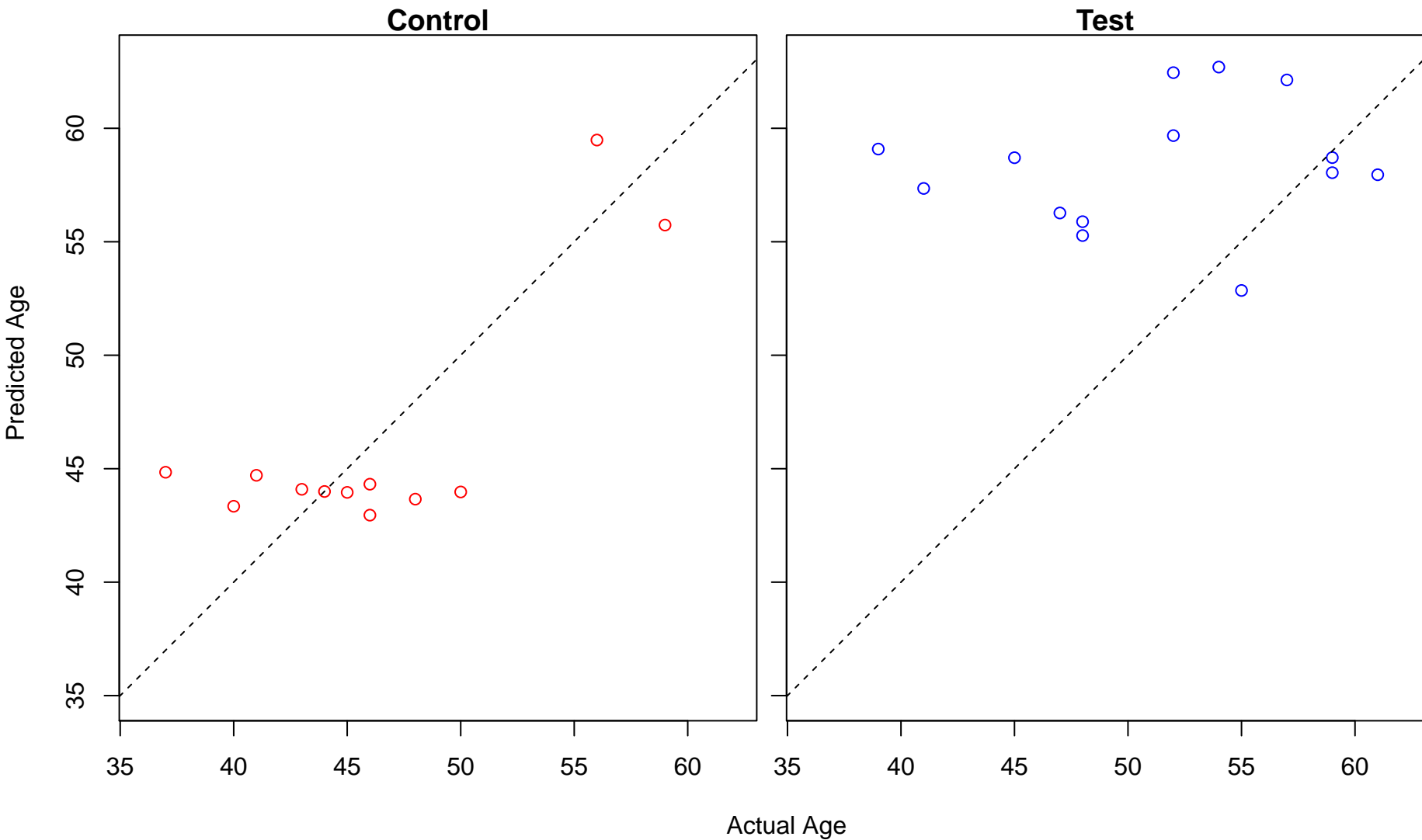
regulation of sodium ion transport (Score: 2.872120)



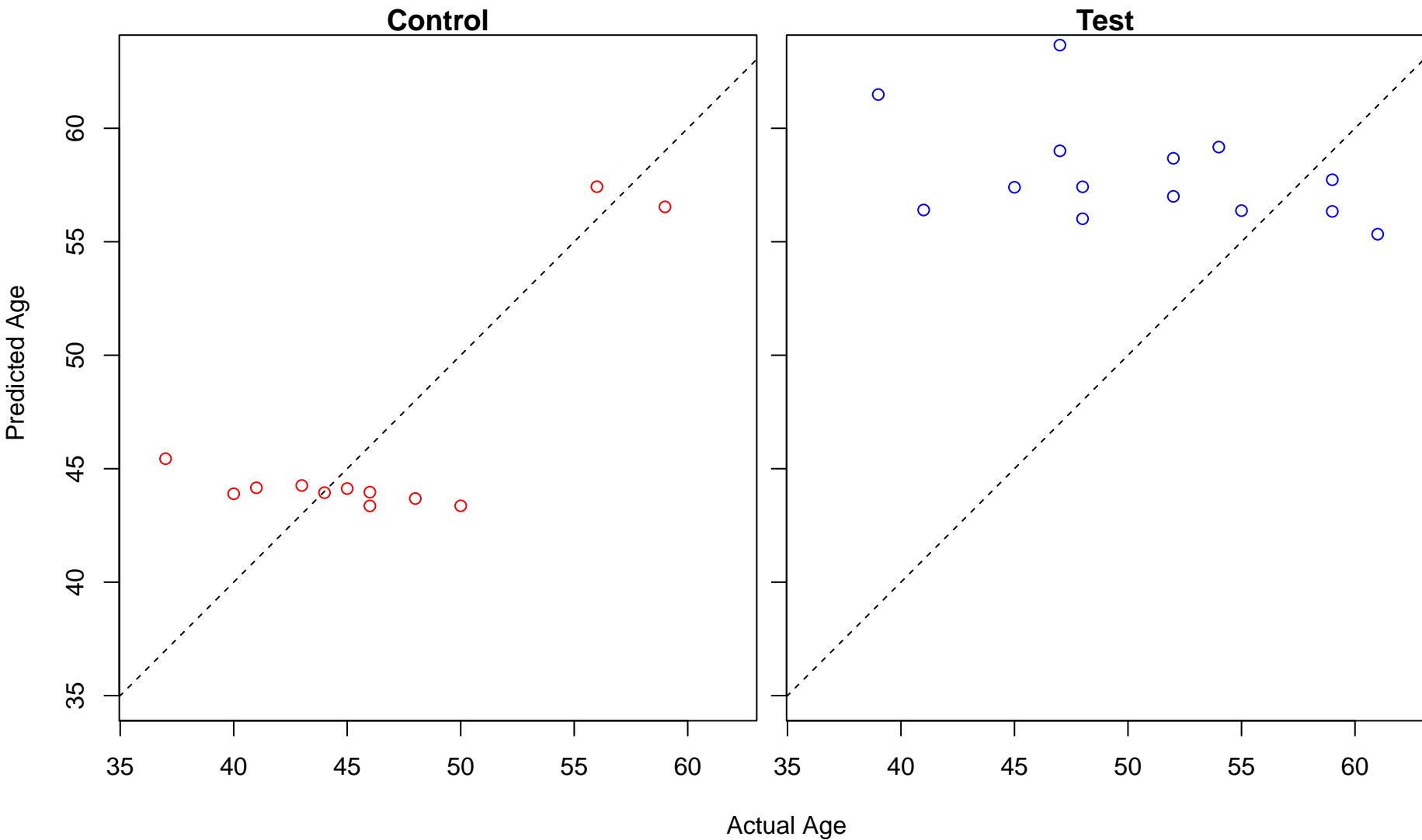
myeloid cell differentiation (Score: 2.871369)



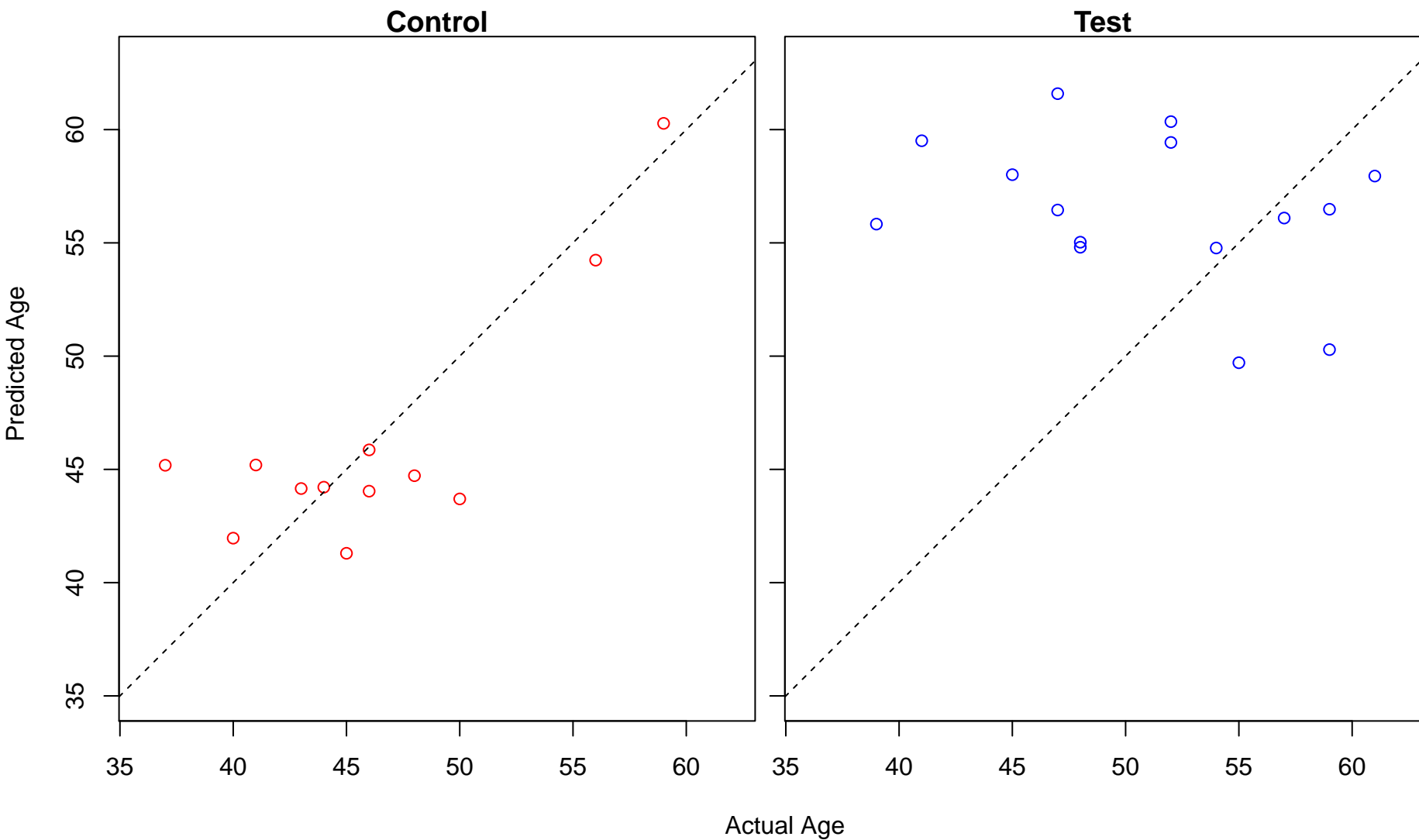
actomyosin structure organization (Score: 2.870353)



actin filament-based movement (Score: 2.870258)

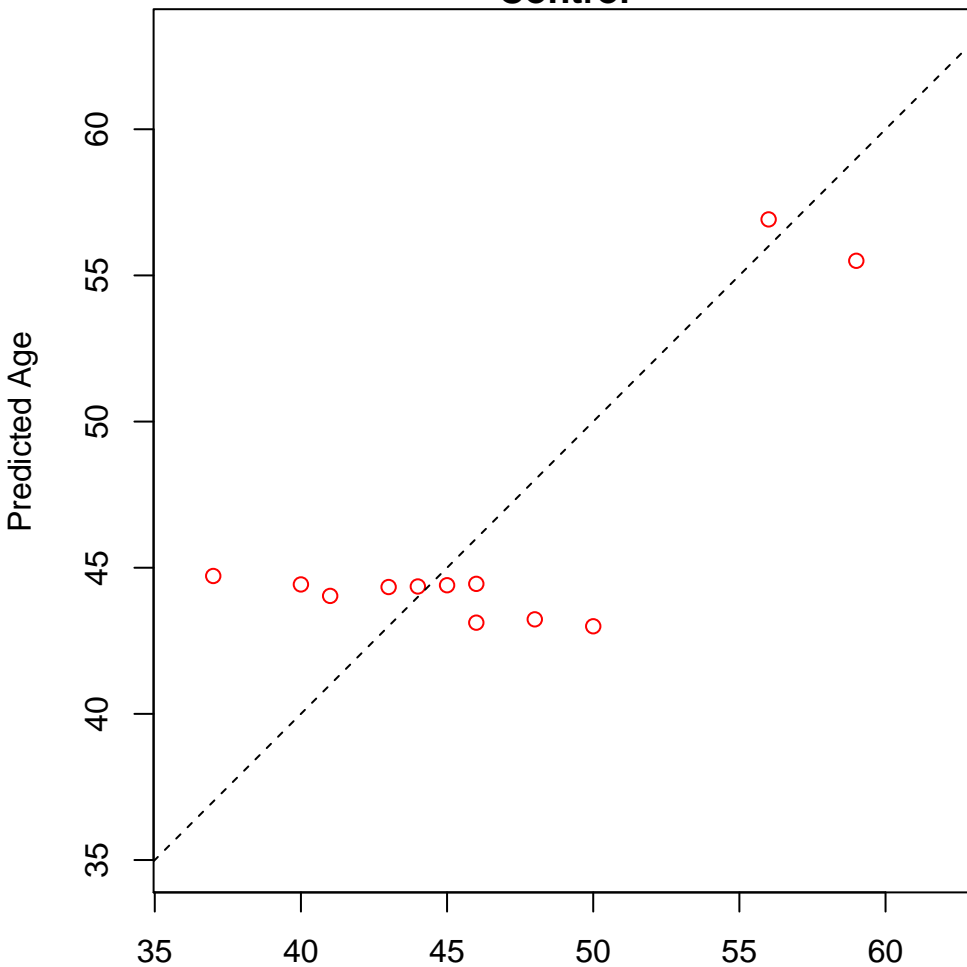


positive regulation of leukocyte migration (Score: 2.870067)

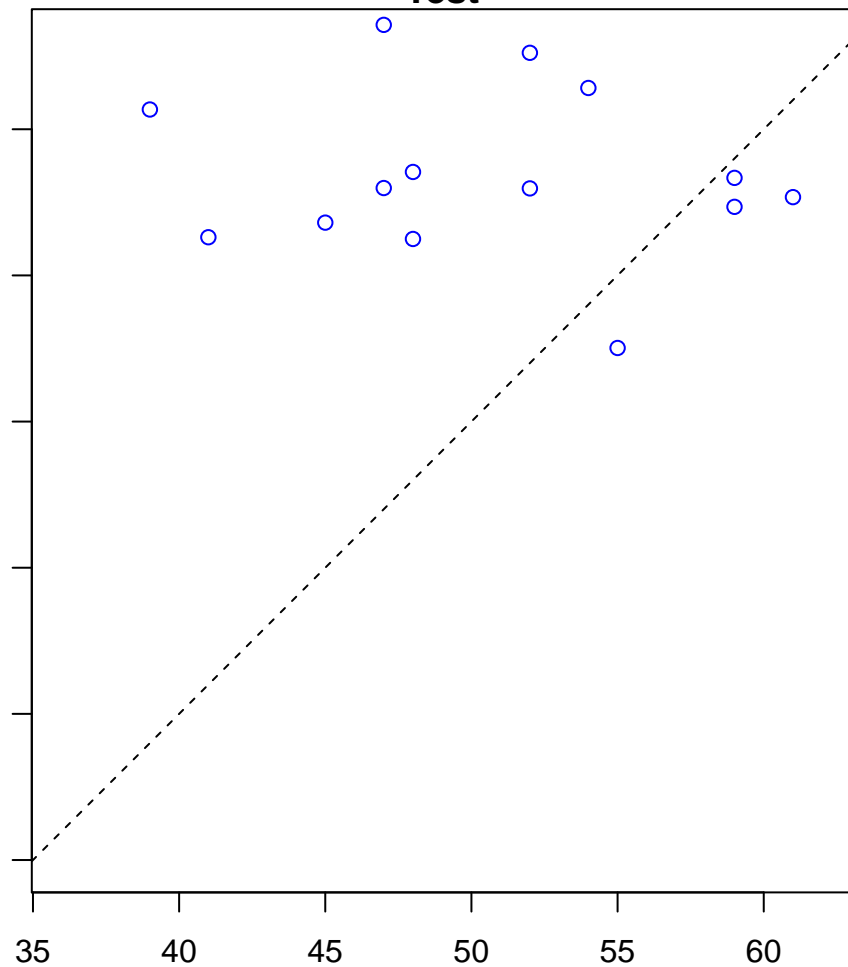


purine nucleoside biosynthetic process (Score: 2.868816)

Control

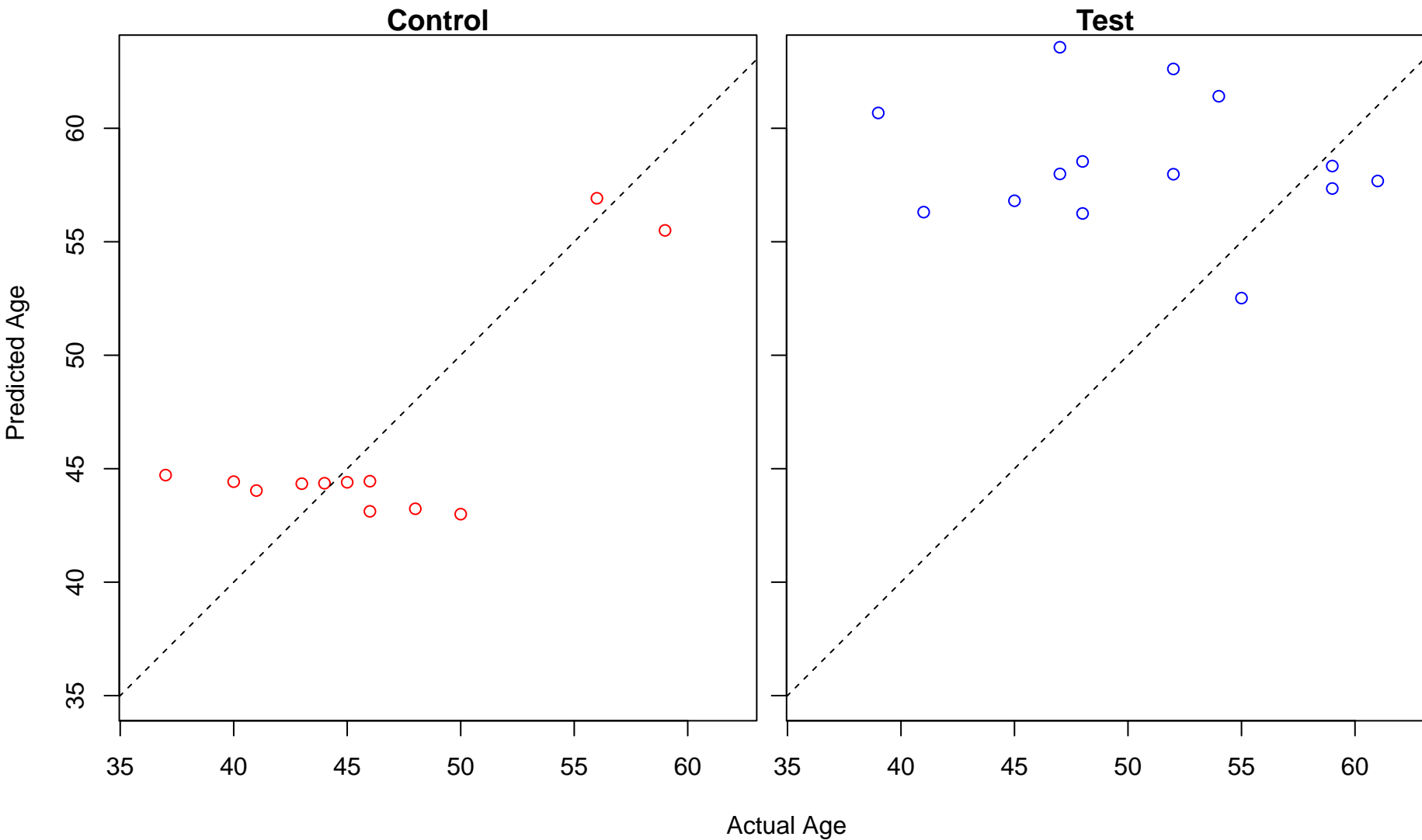


Test

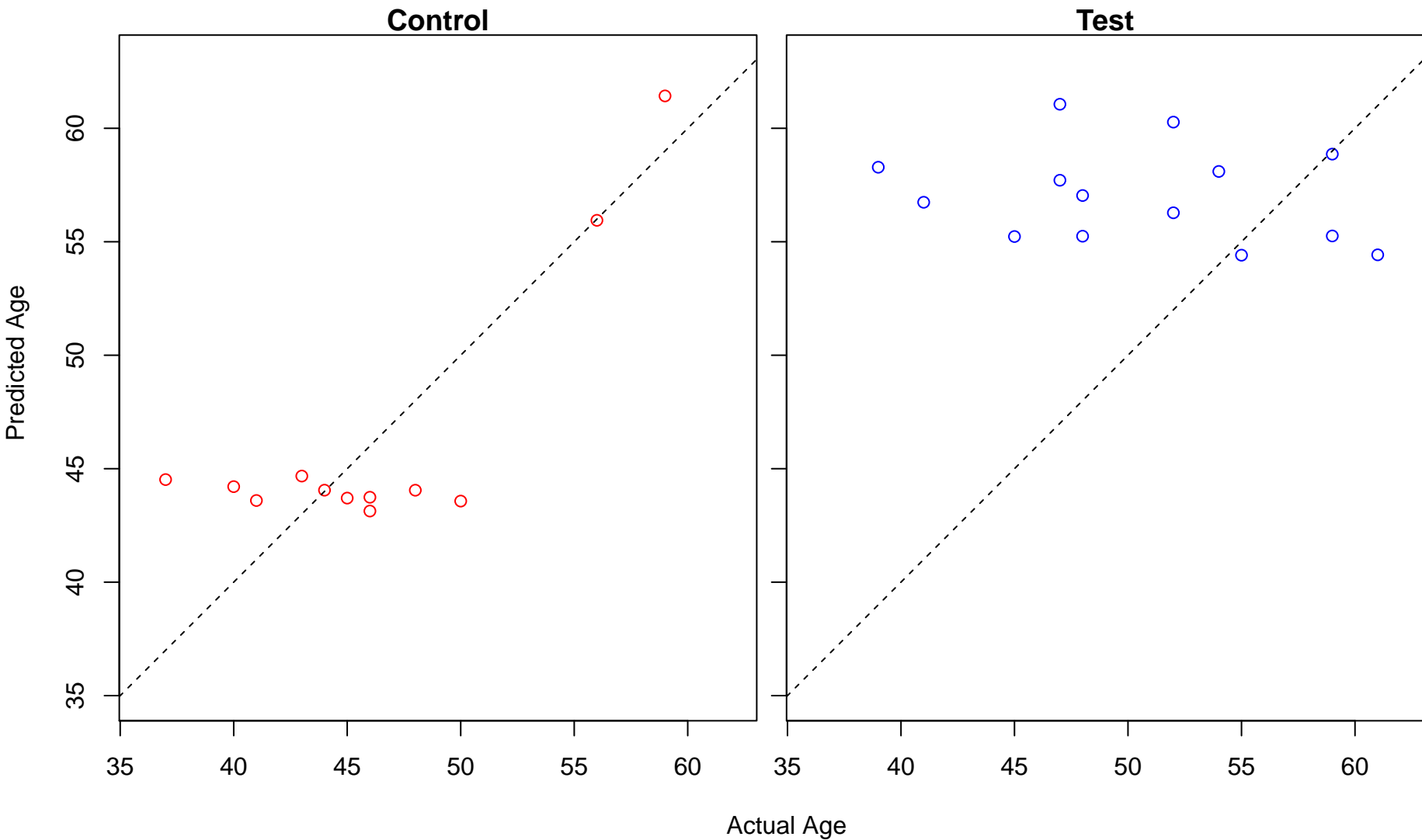


Actual Age

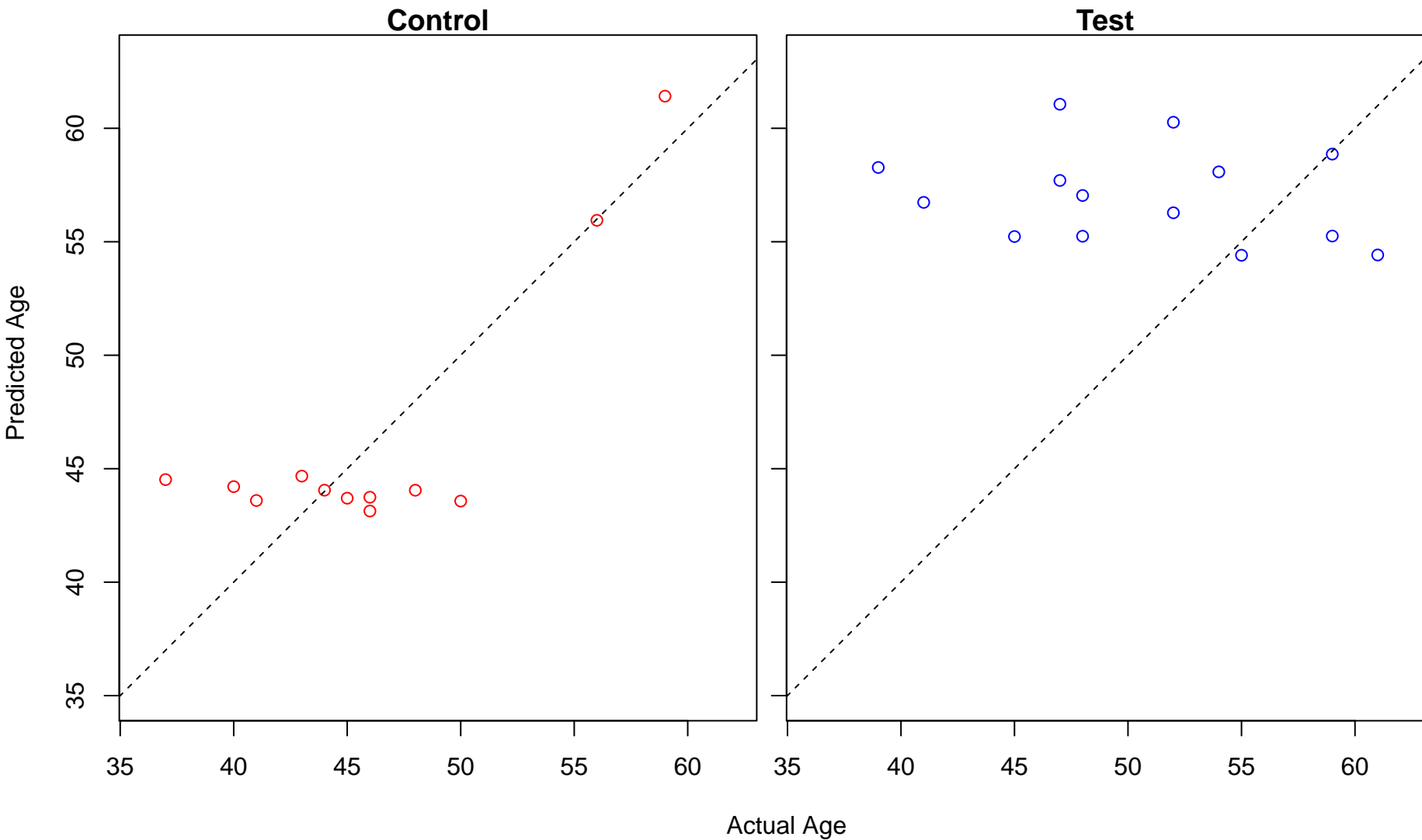
purine ribonucleoside biosynthetic process (Score: 2.868816)



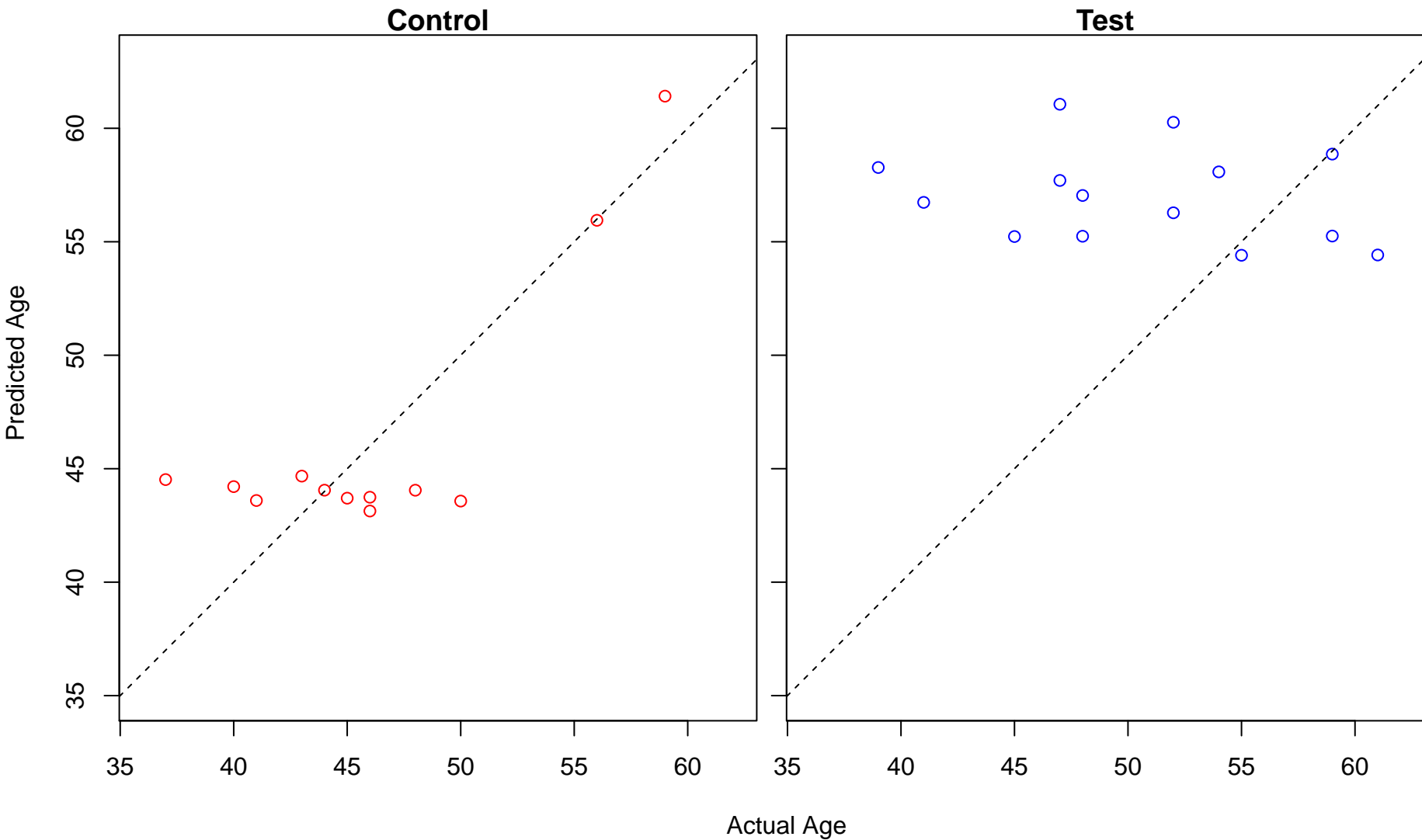
epiboly (Score: 2.868741)



wound healing, spreading of cells (Score: 2.868333)

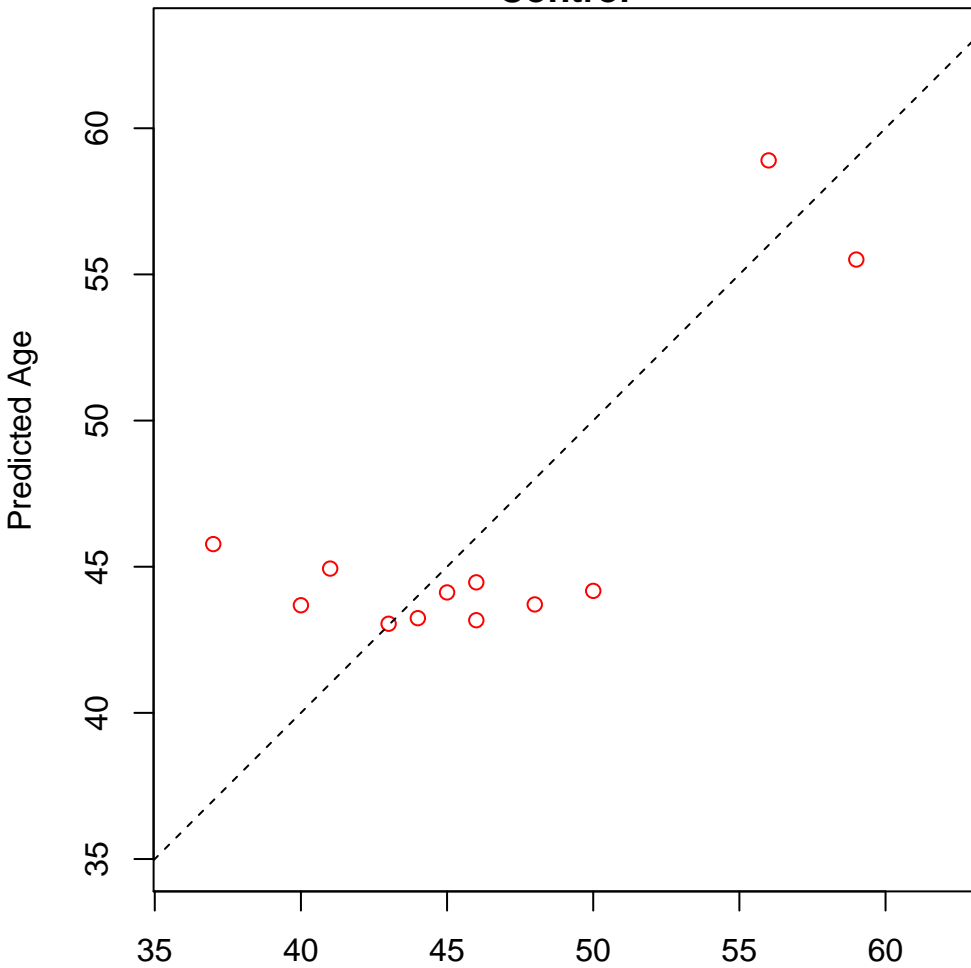


epiboly involved in wound healing (Score: 2.868333)

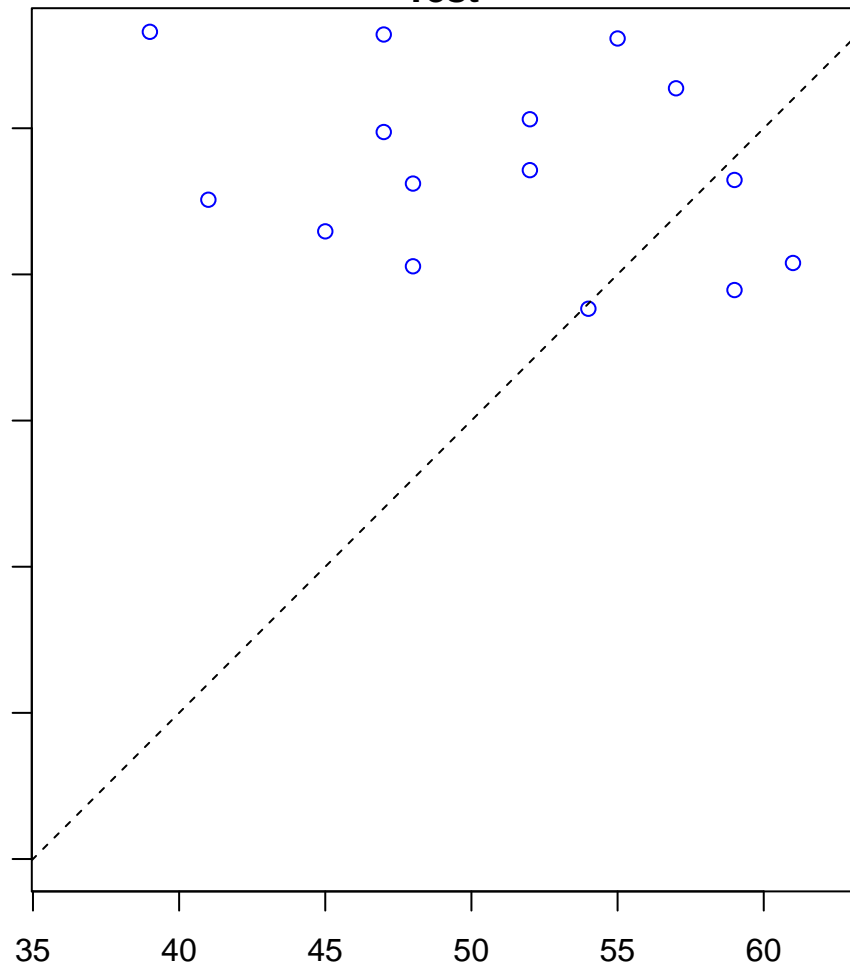


regulation of membrane depolarization (Score: 2.867848)

Control

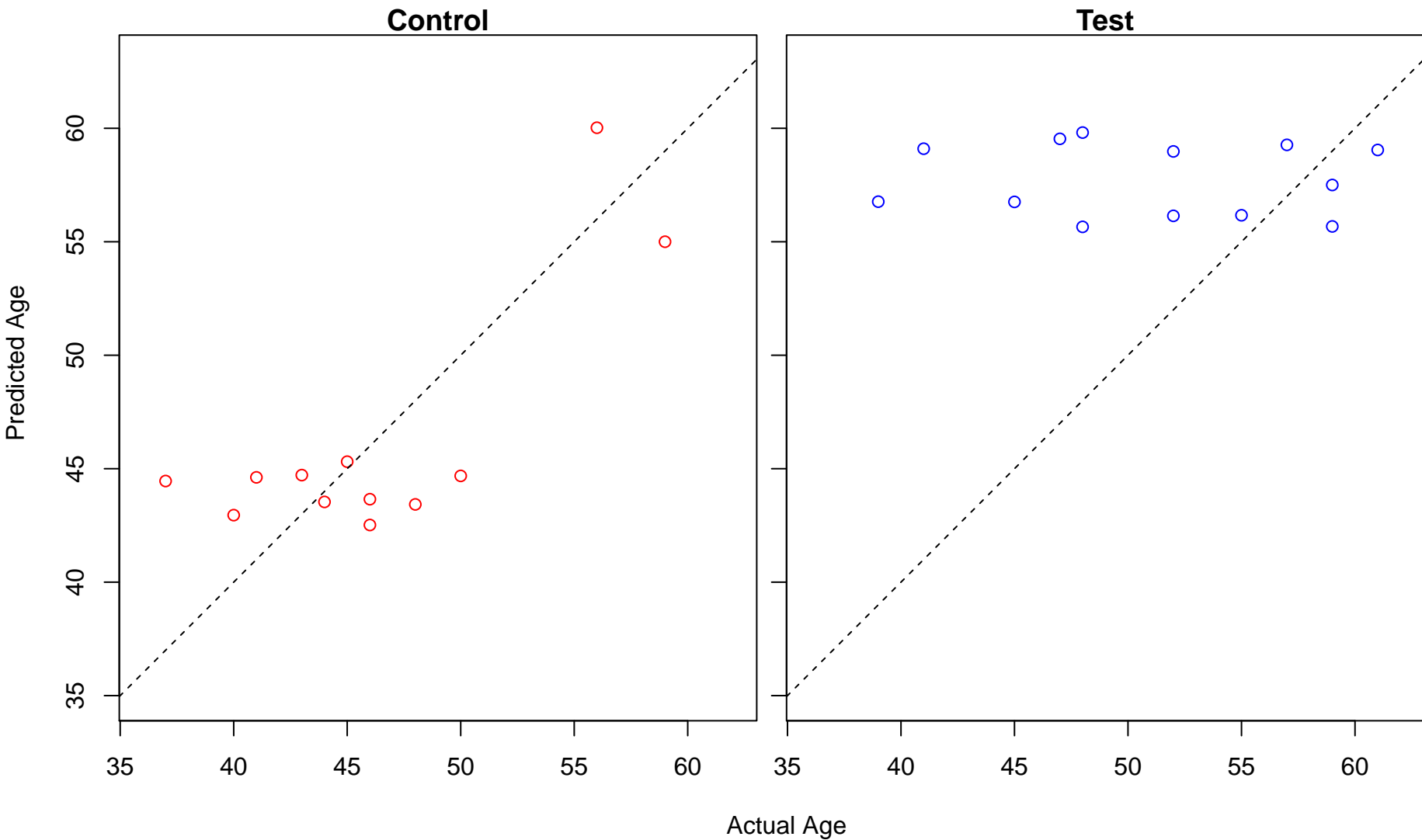


Test

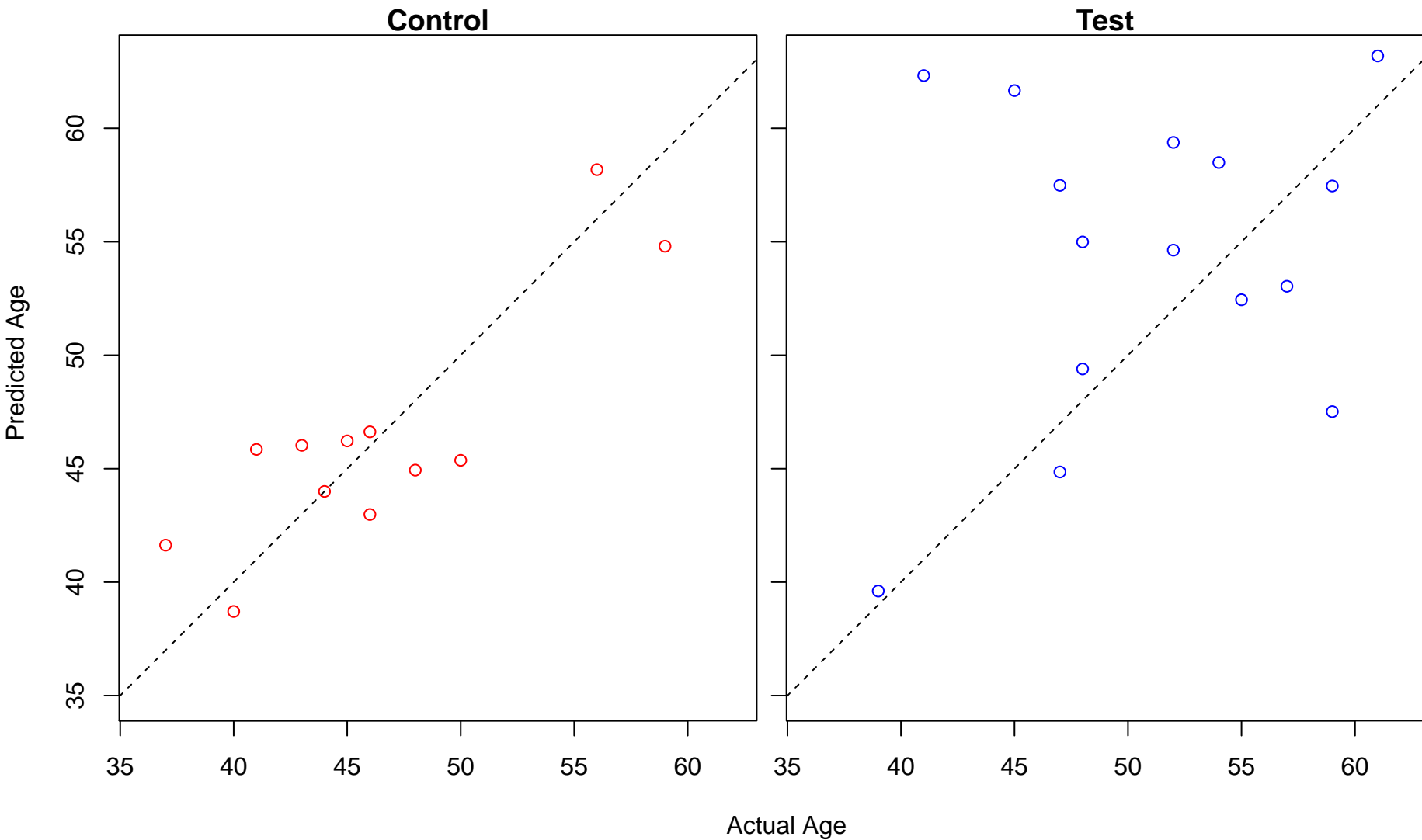


Actual Age

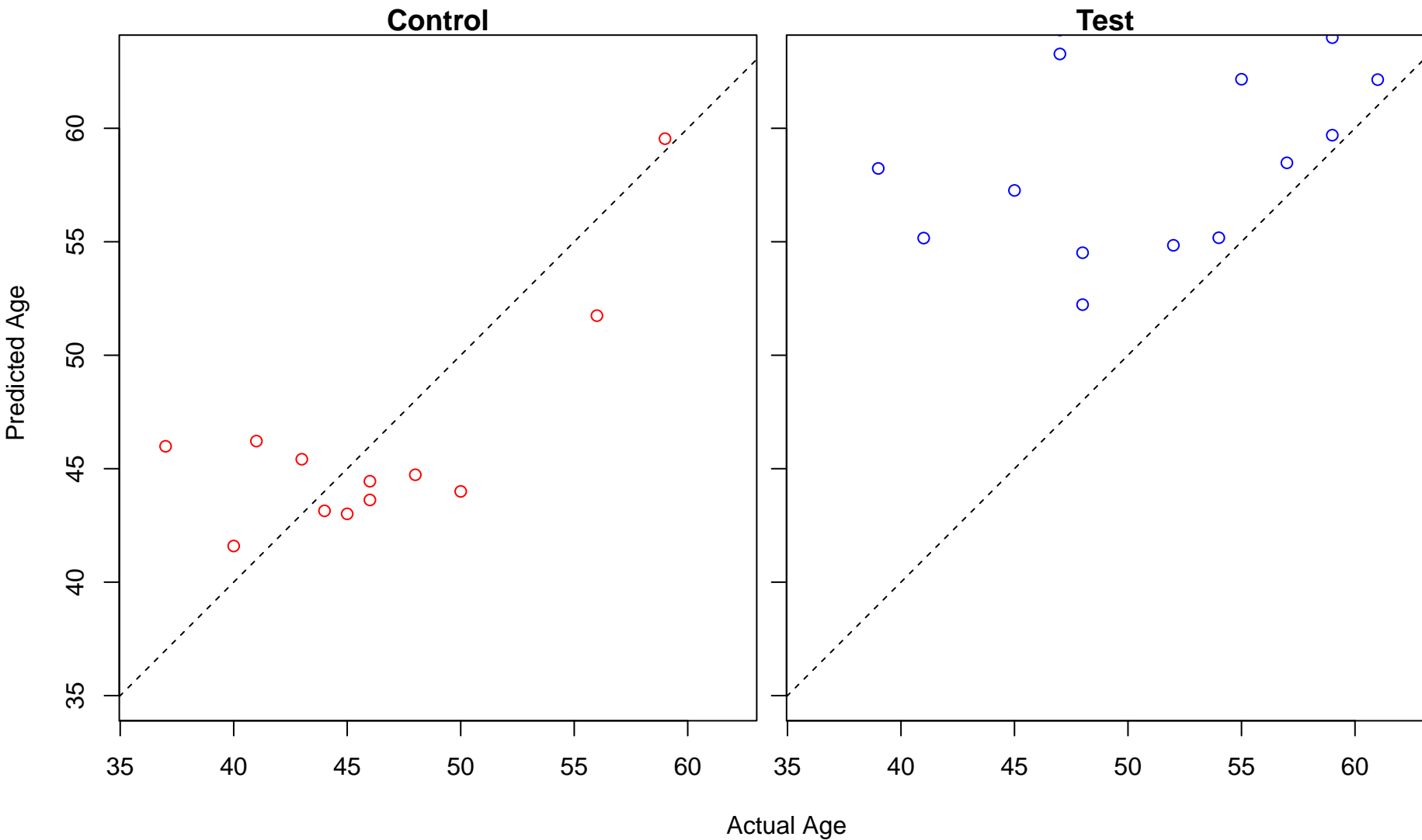
embryonic epithelial tube formation (Score: 2.864284)



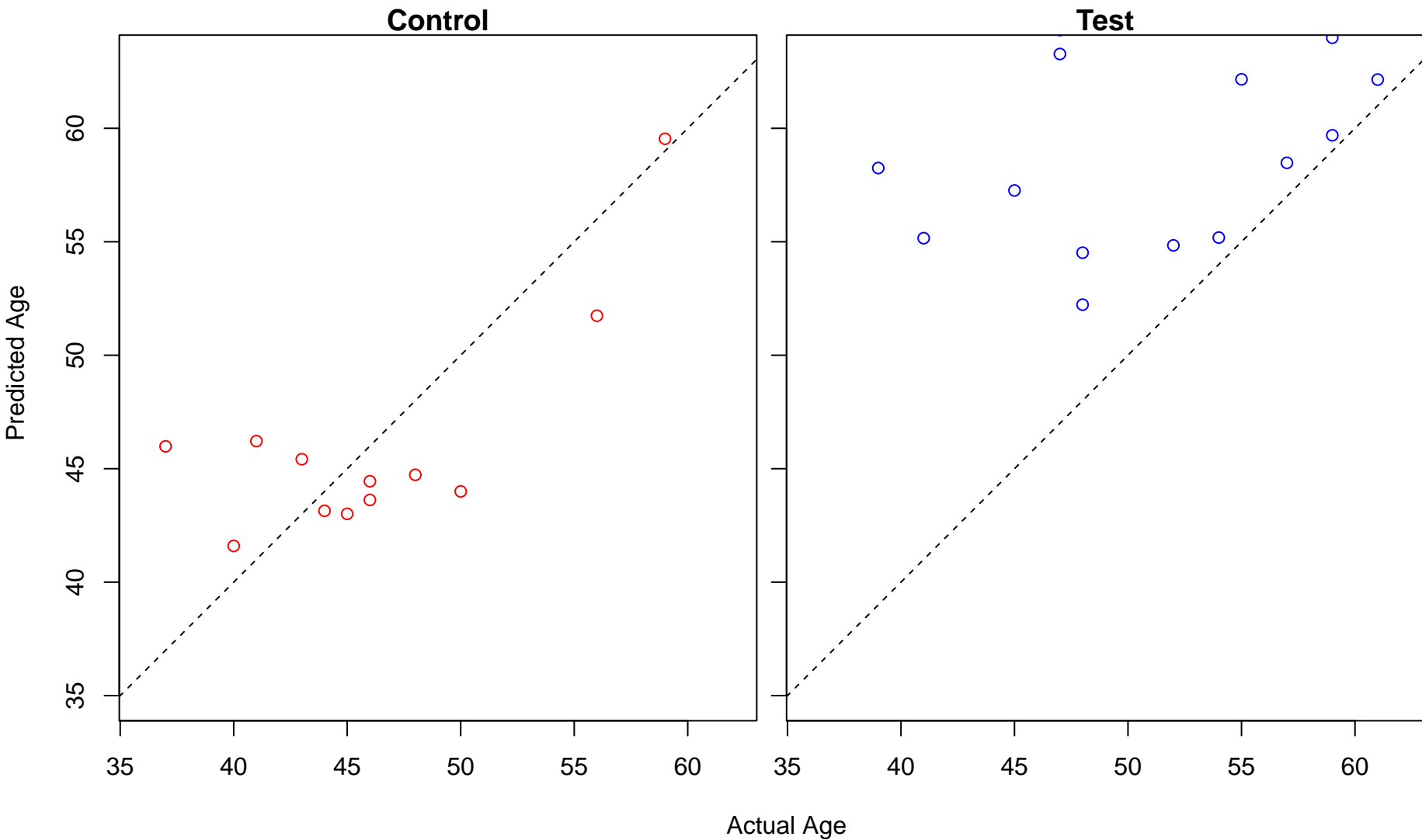
inflammatory response (Score: 2.863807)



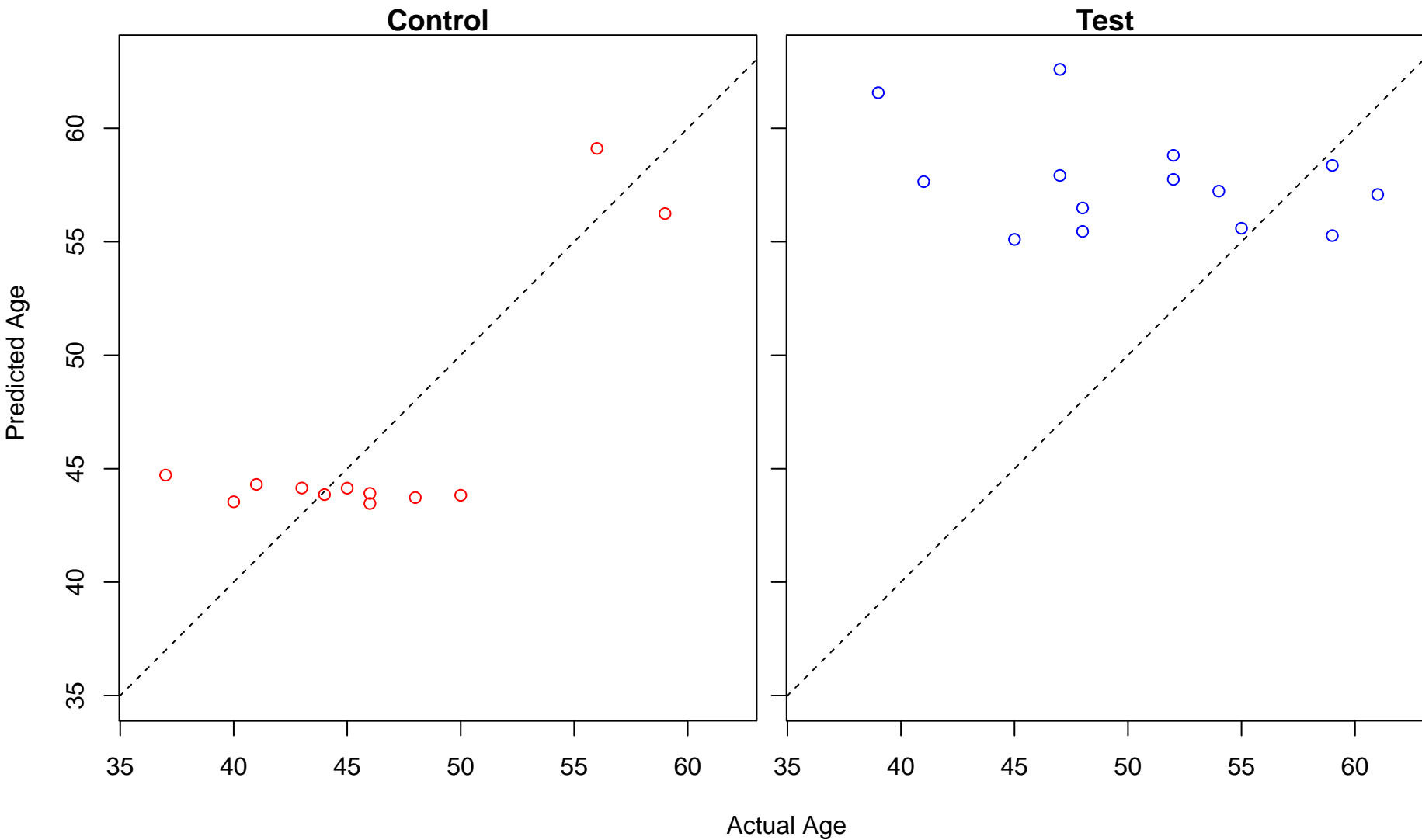
interleukin-1 beta secretion (Score: 2.862111)



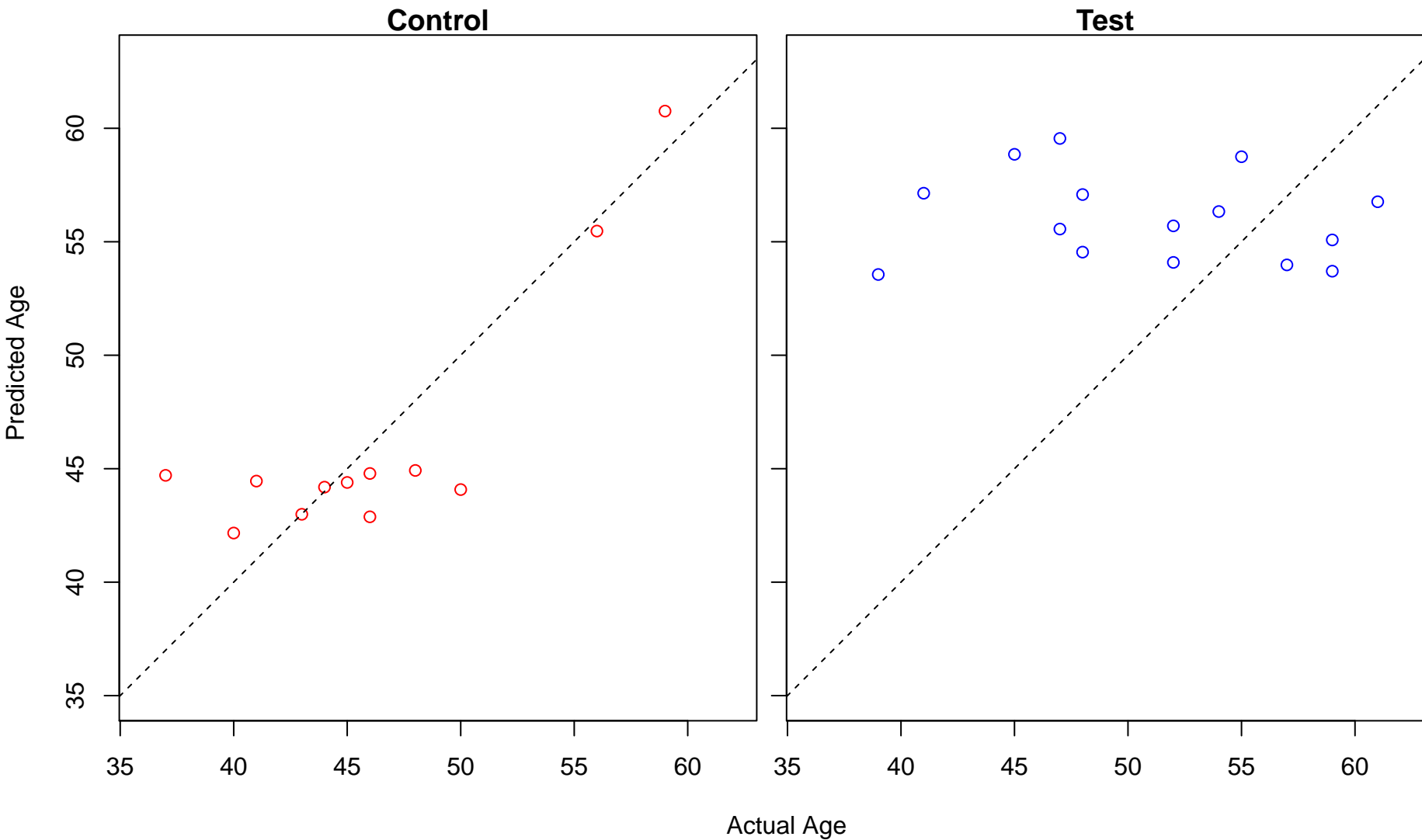
interleukin-1 beta production (Score: 2.861242)



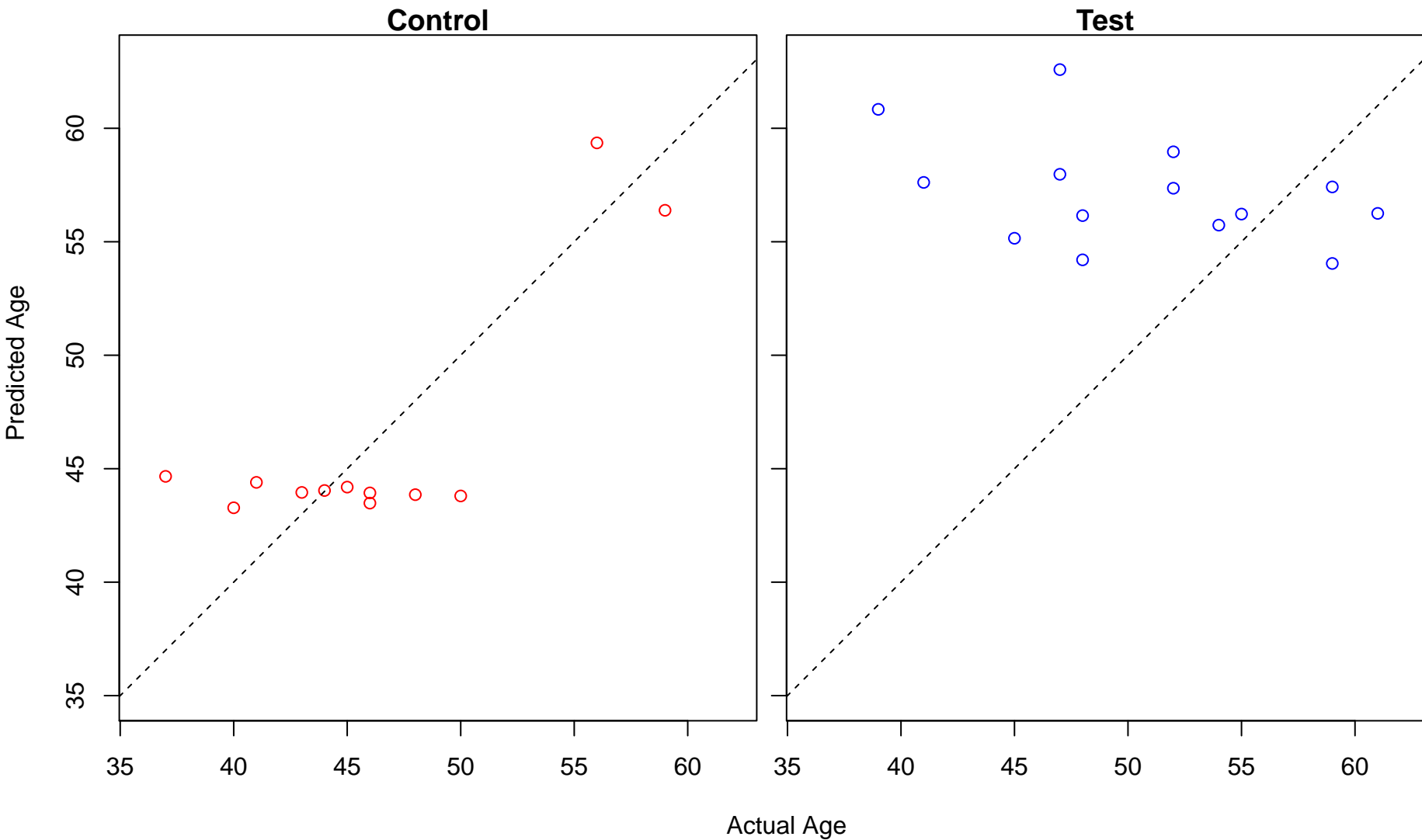
cellular response to insulin stimulus (Score: 2.858806)



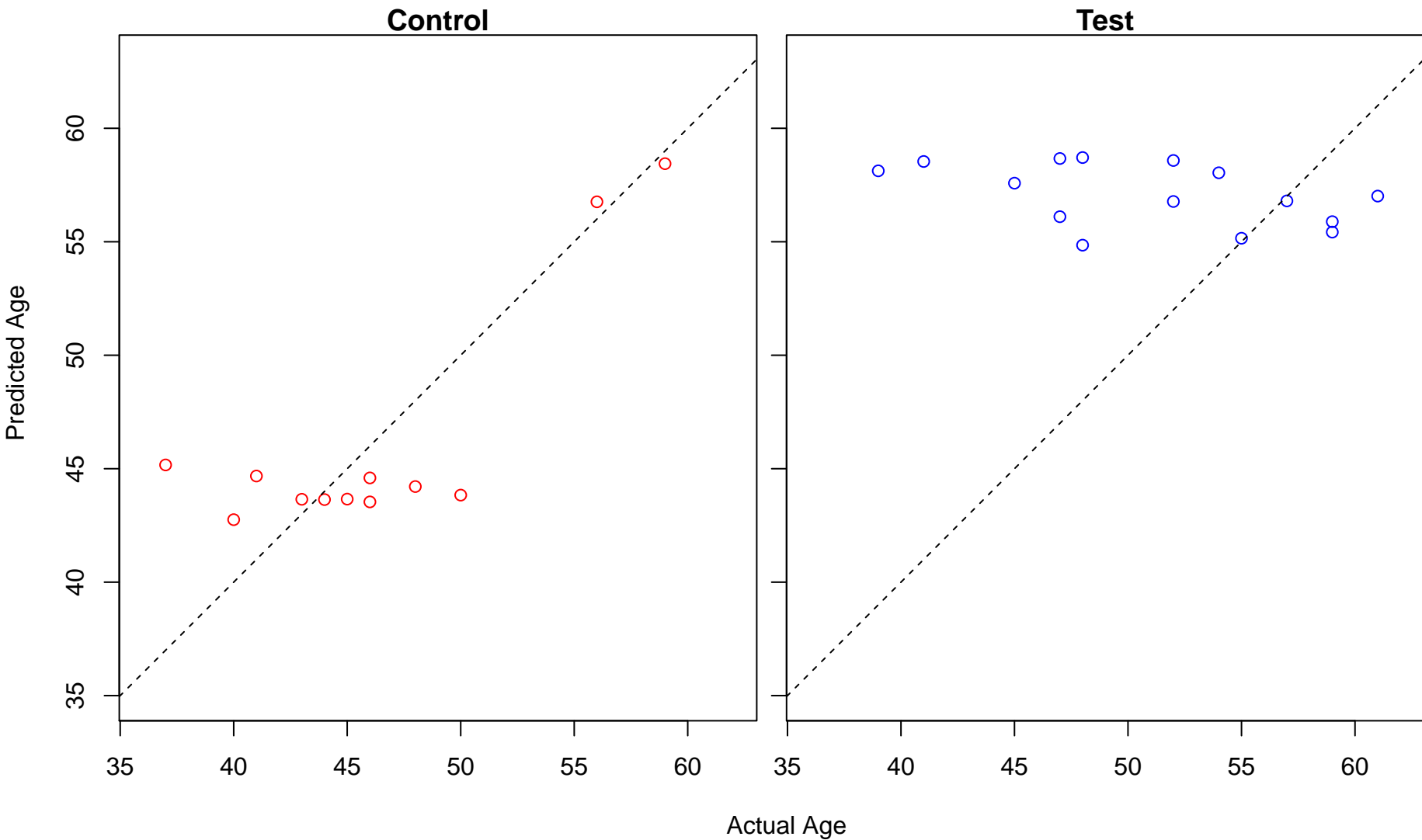
telencephalon development (Score: 2.856485)



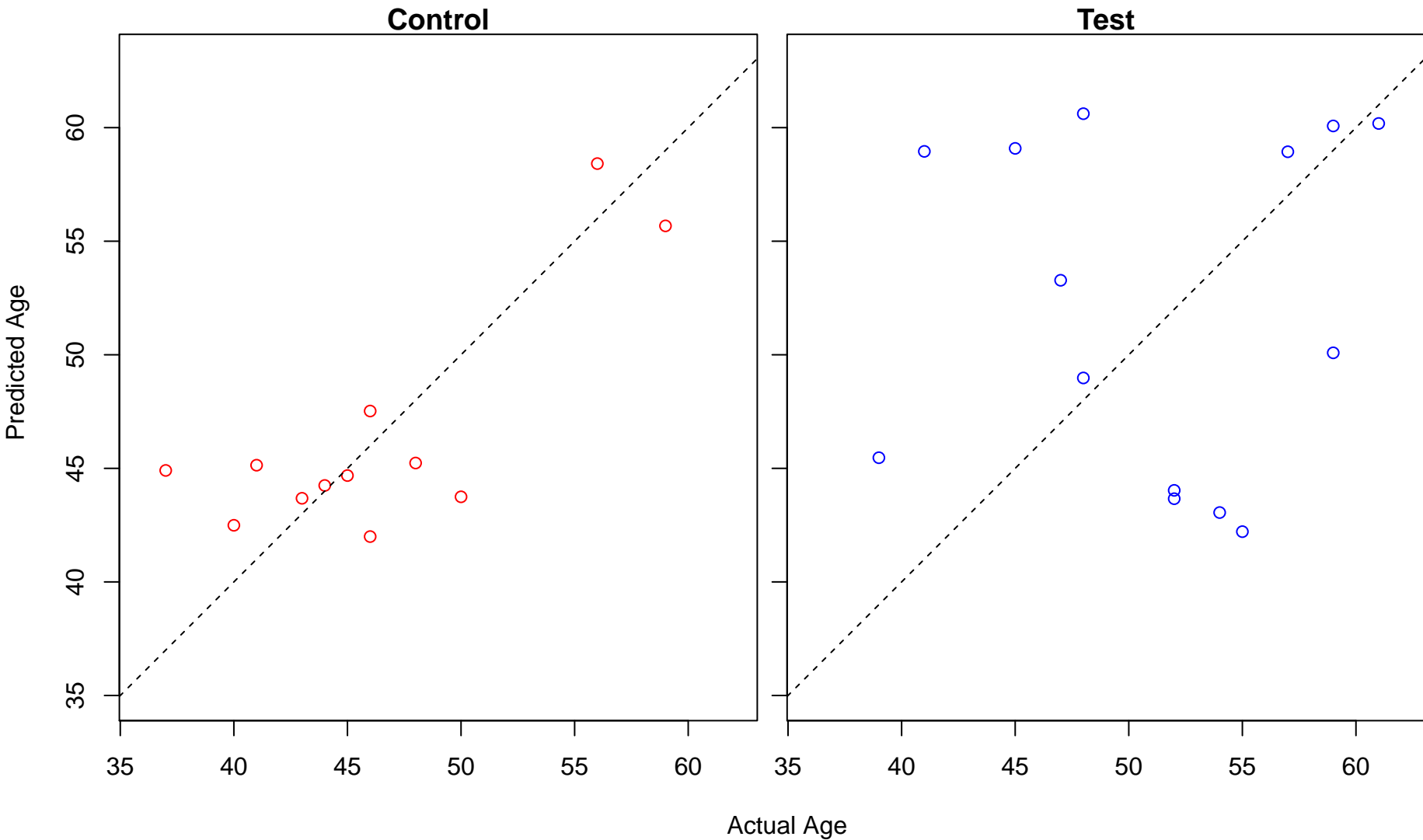
positive regulation of protein serine/threonine kinase activity (Score: 2.853698)



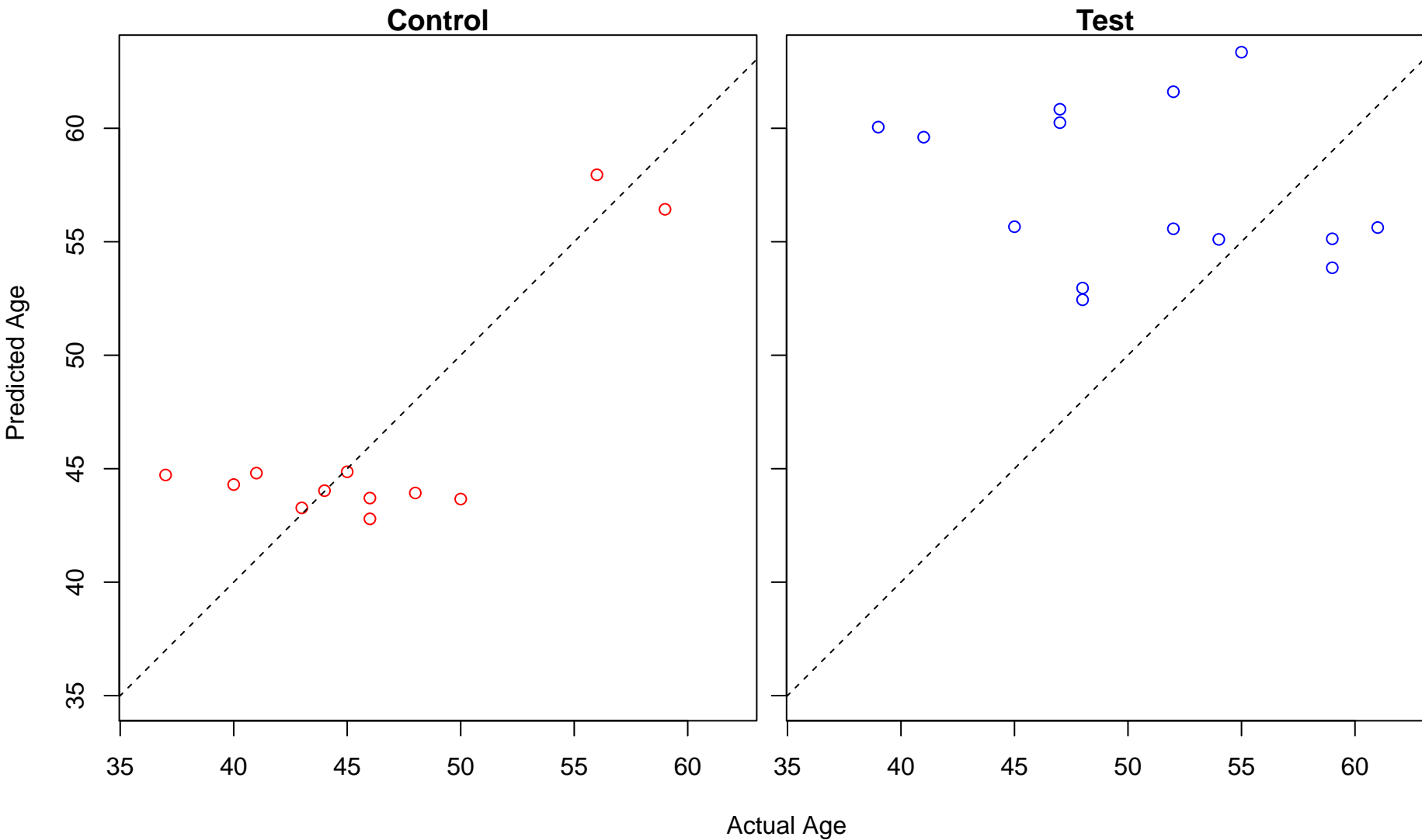
DNA geometric change (Score: 2.853255)



regulation of proteasomal ubiquitin-dependent protein catabolic process (Score: 2.852067)

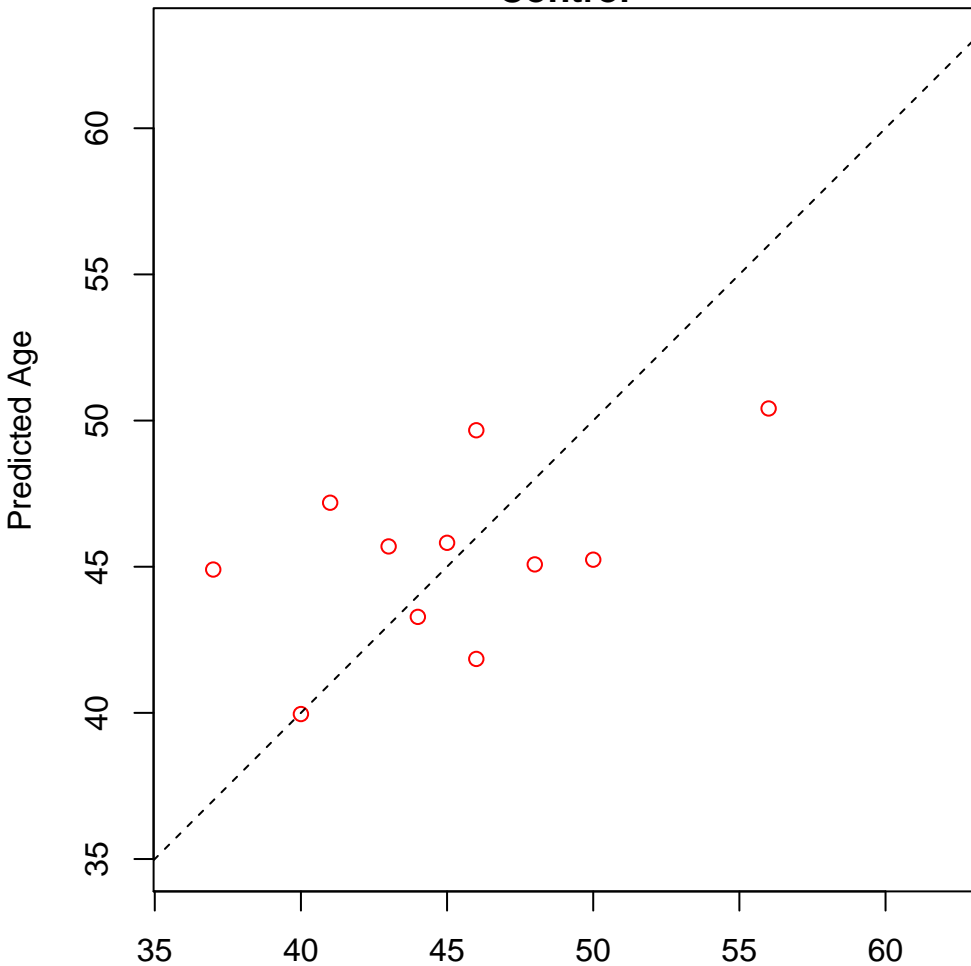


regulation of cell-substrate adhesion (Score: 2.852045)

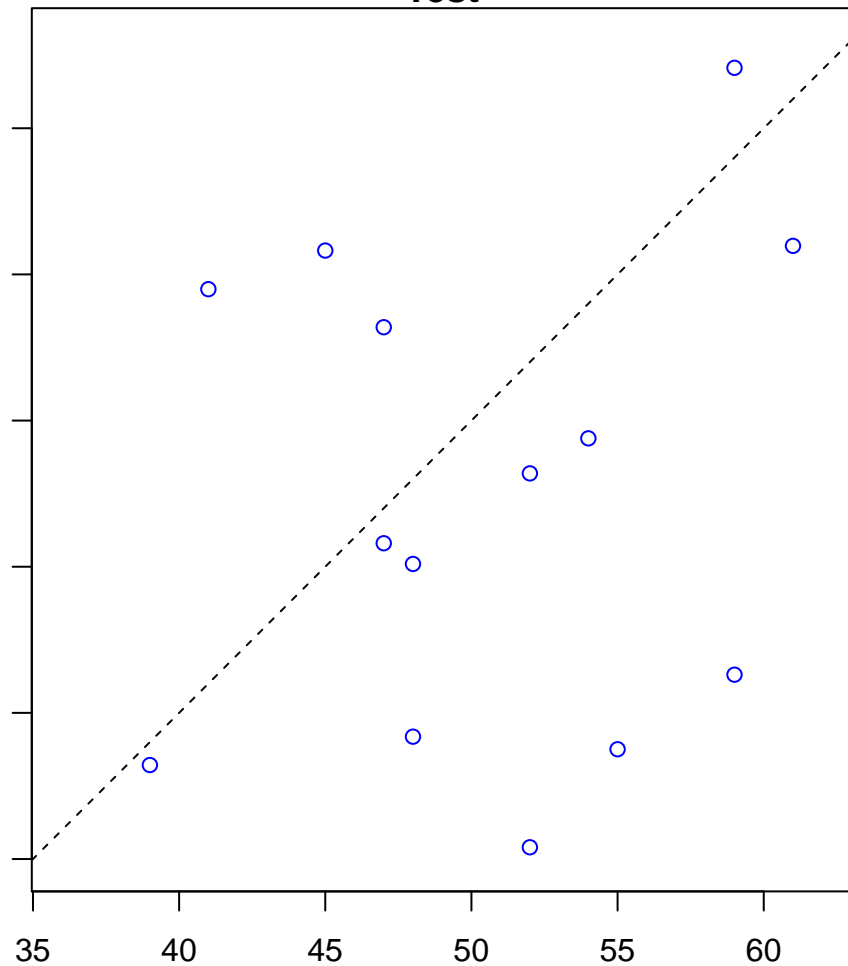


positive regulation of peptide secretion (Score: 2.850013)

Control

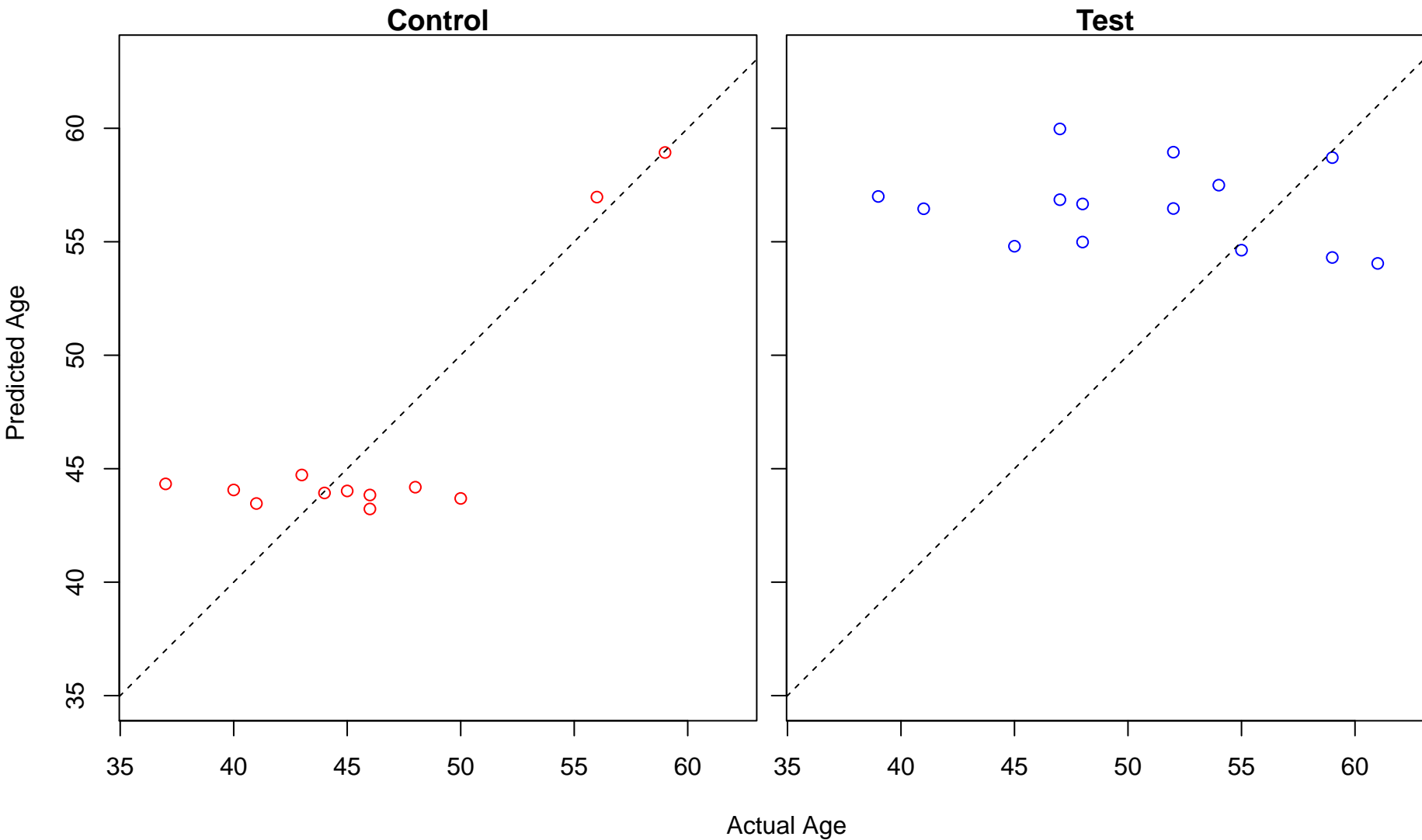


Test

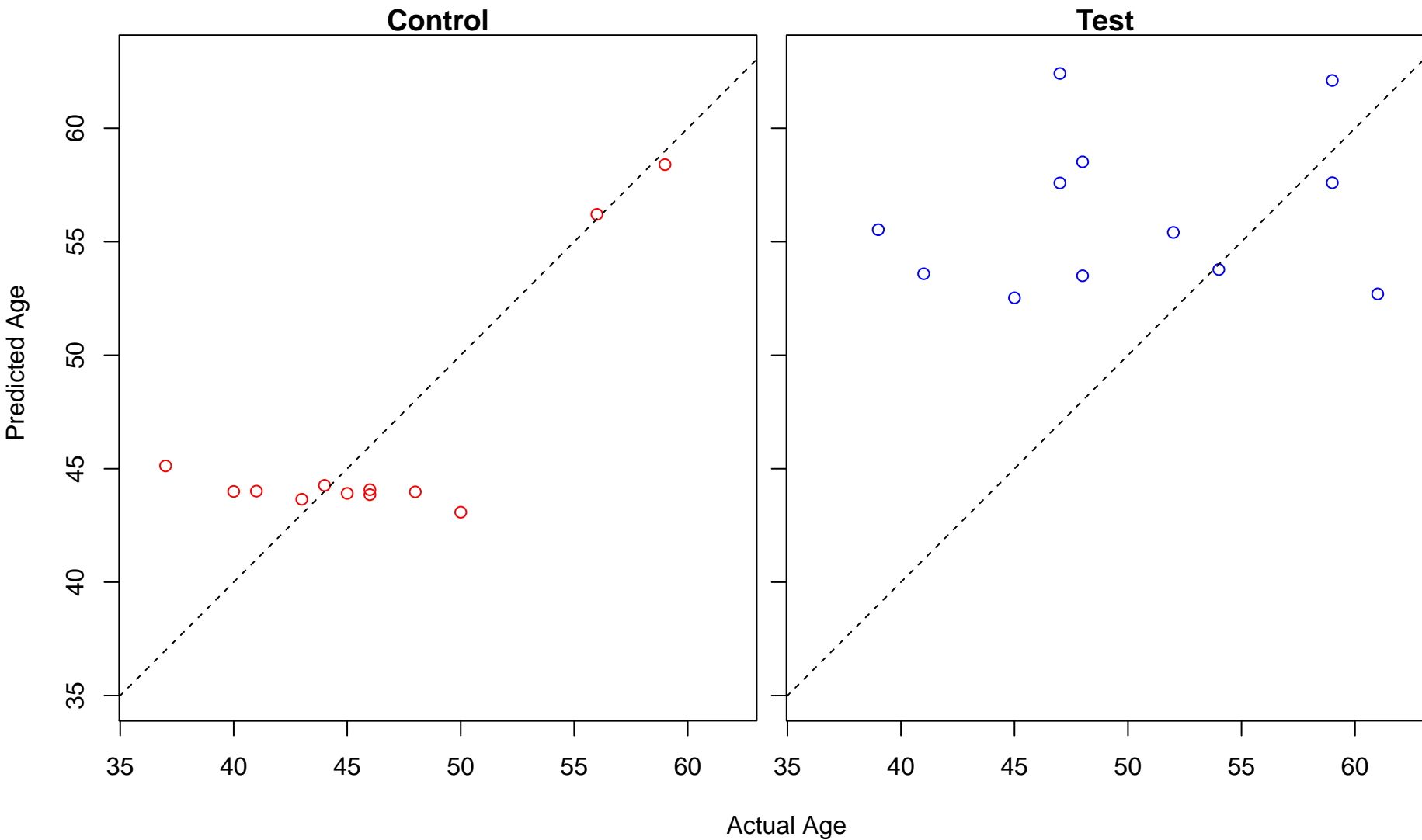


Actual Age

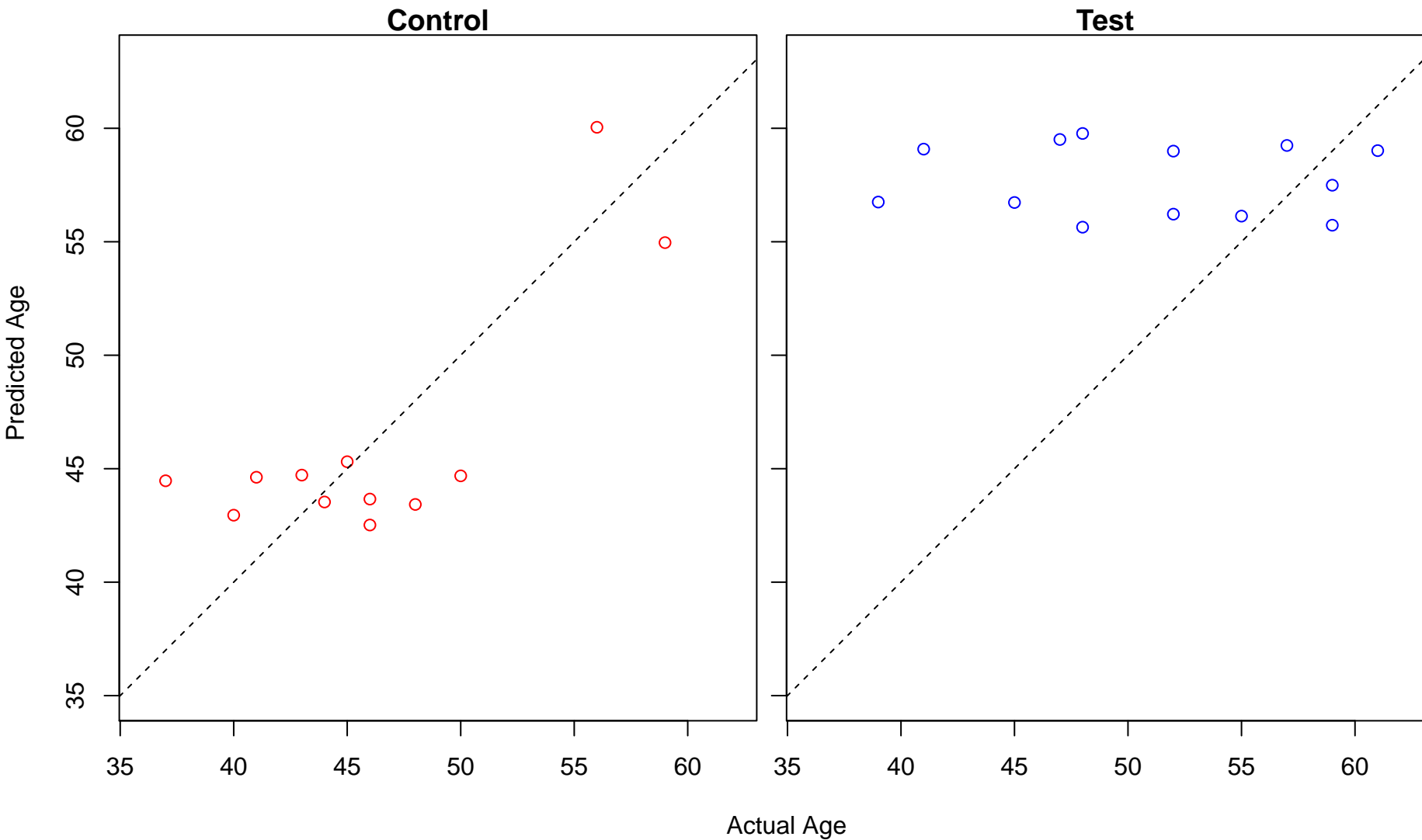
apolipoprotein A-I-mediated signaling pathway (Score: 2.849675)



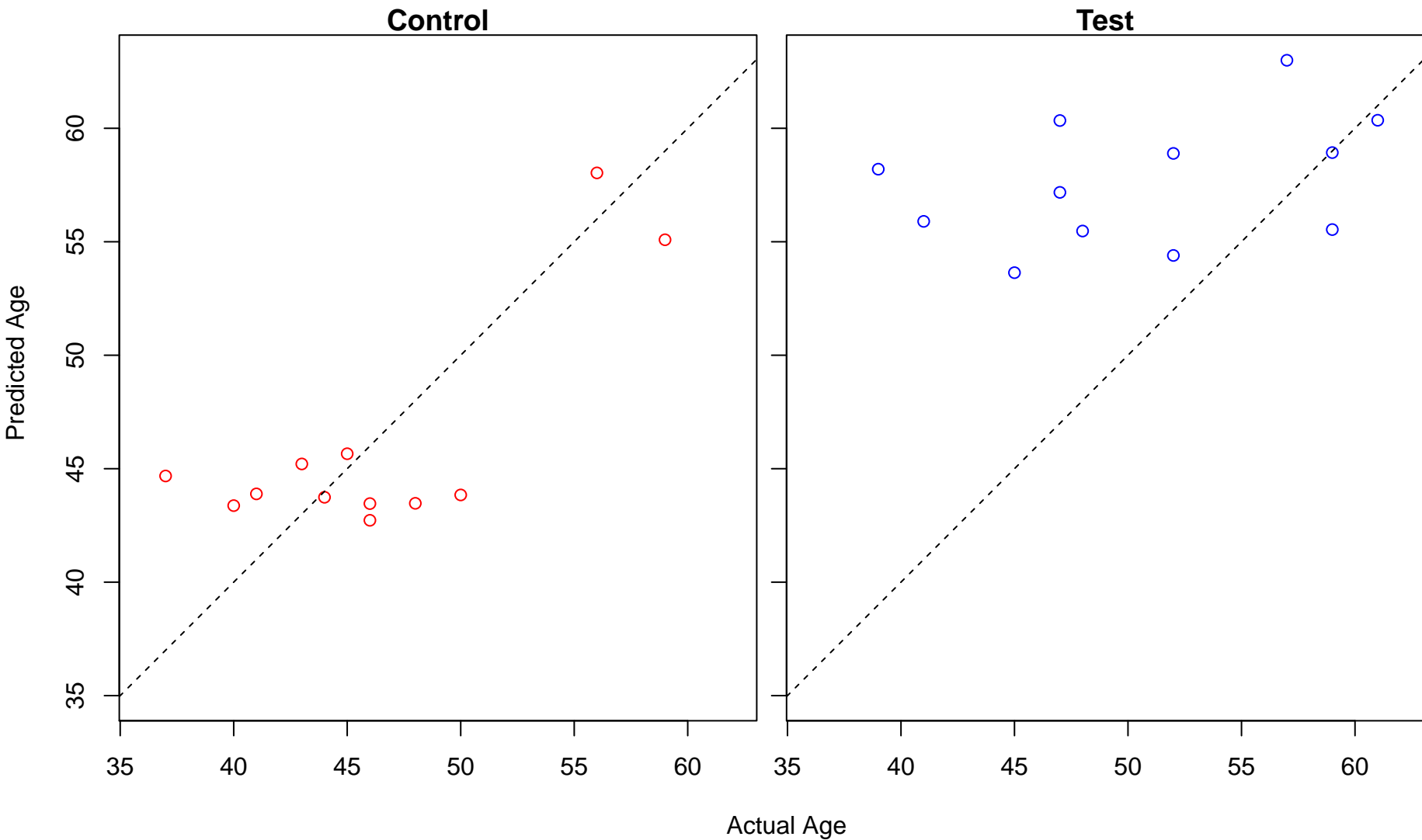
positive regulation of pathway-restricted SMAD protein phosphorylation (Score: 2.849403)



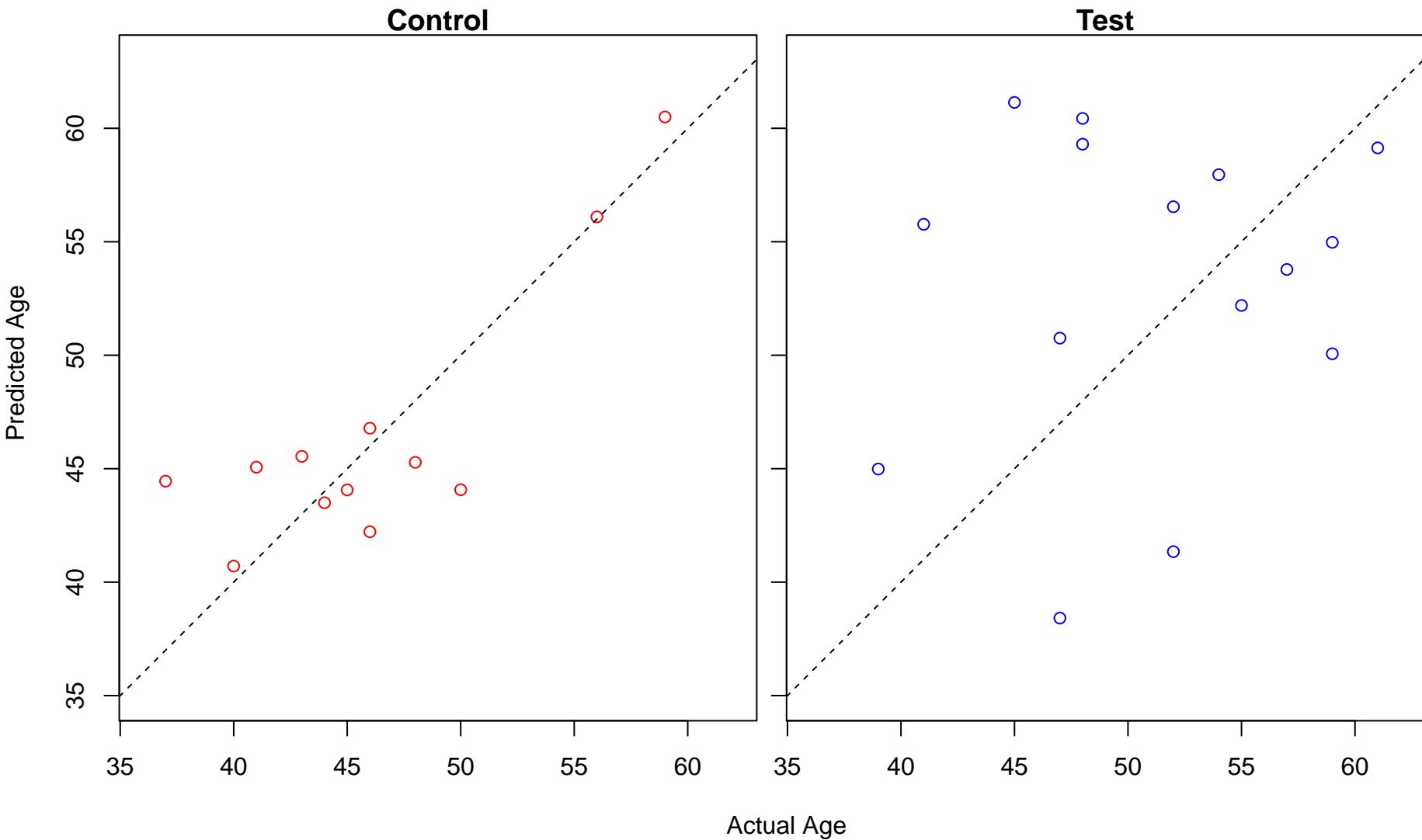
epithelial tube formation (Score: 2.849042)



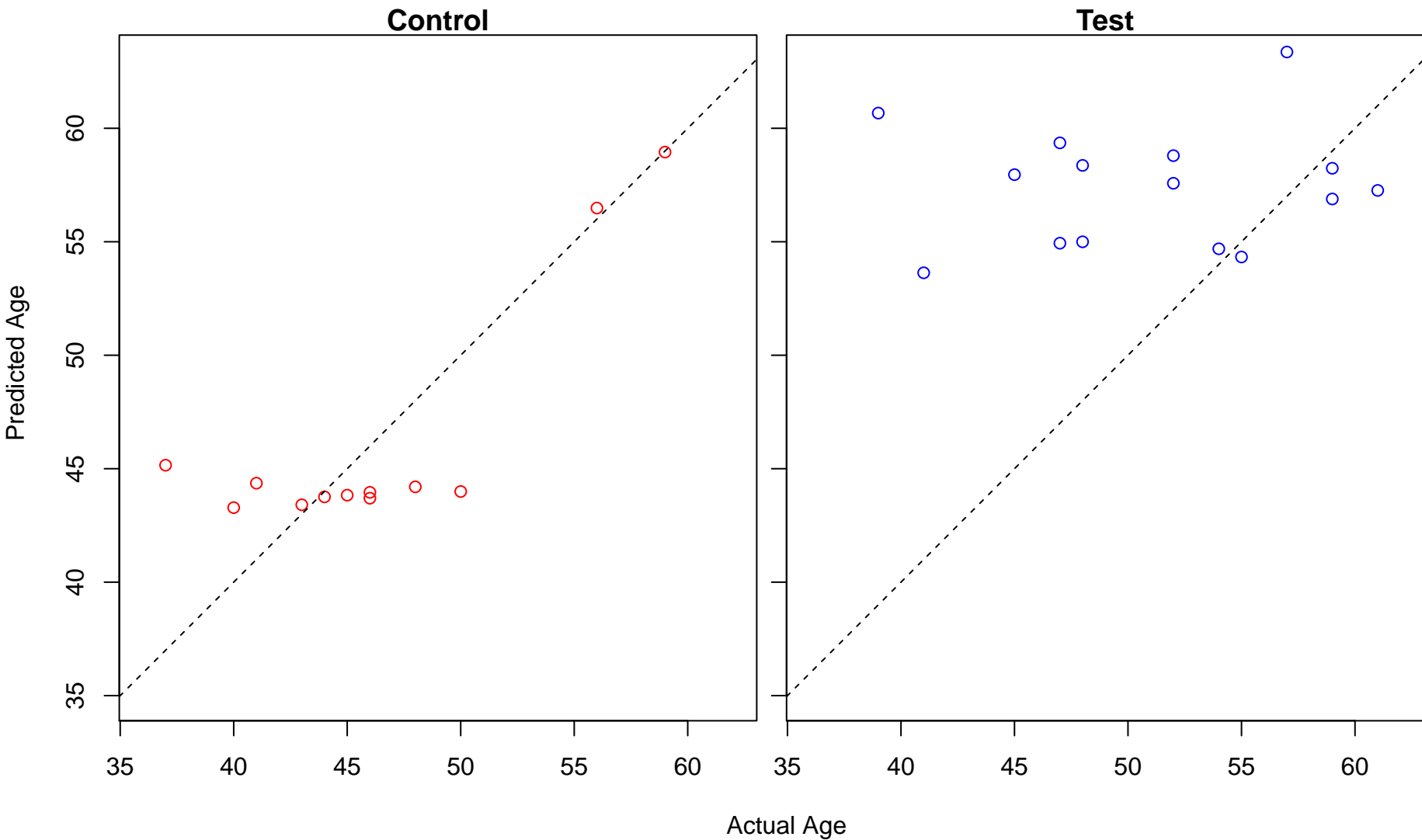
response to exogenous dsRNA (Score: 2.848676)



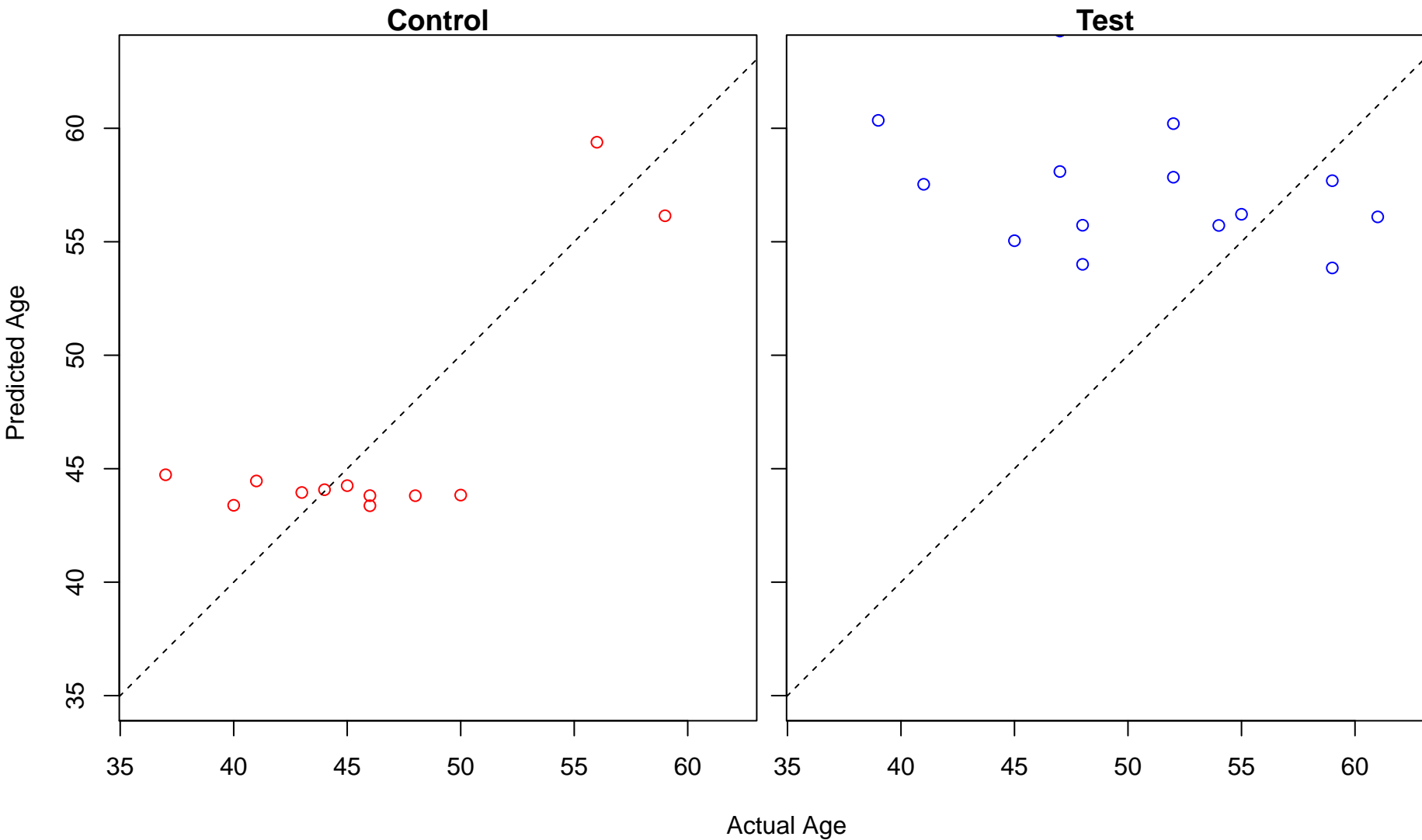
negative regulation of voltage-gated potassium channel activity (Score: 2.848225)



pyrimidine nucleoside metabolic process (Score: 2.847778)

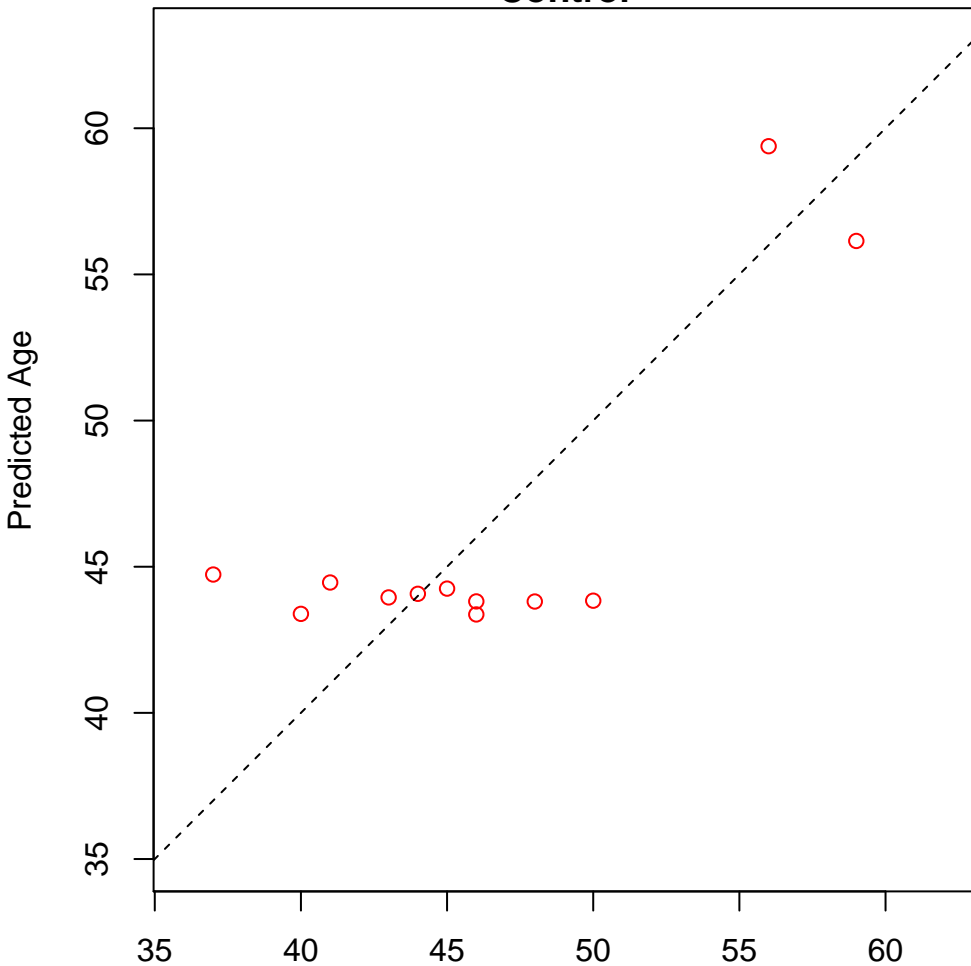


response to hypoxia (Score: 2.847552)

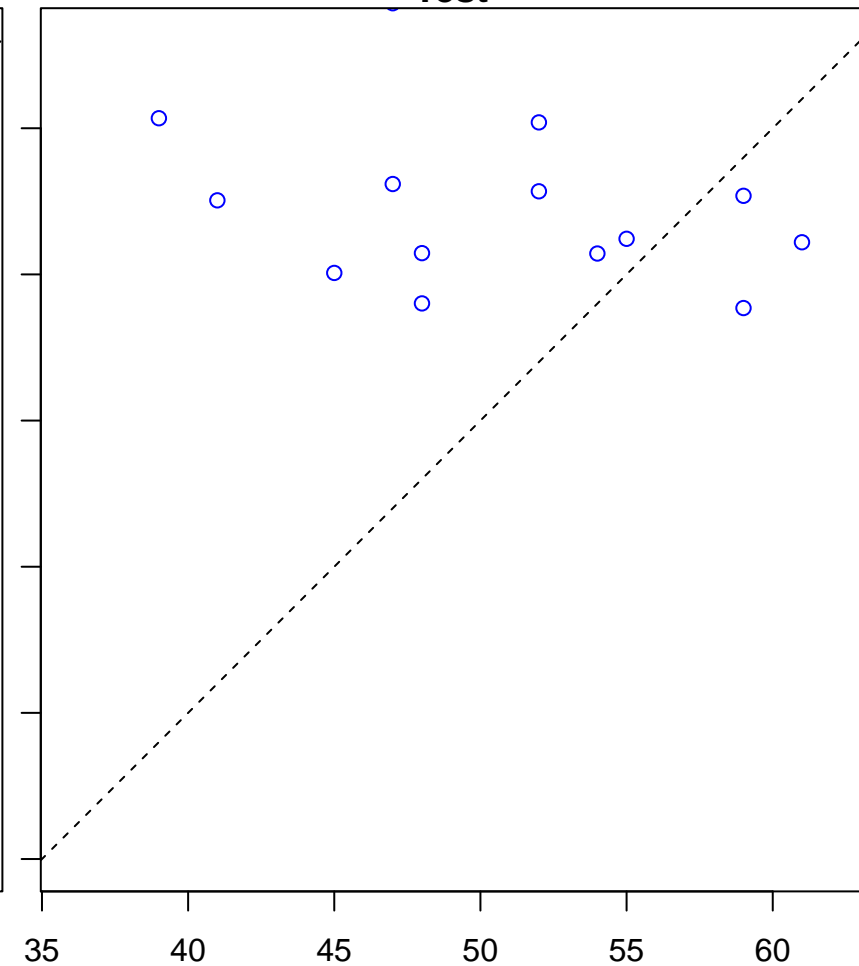


response to decreased oxygen levels (Score: 2.846659)

Control

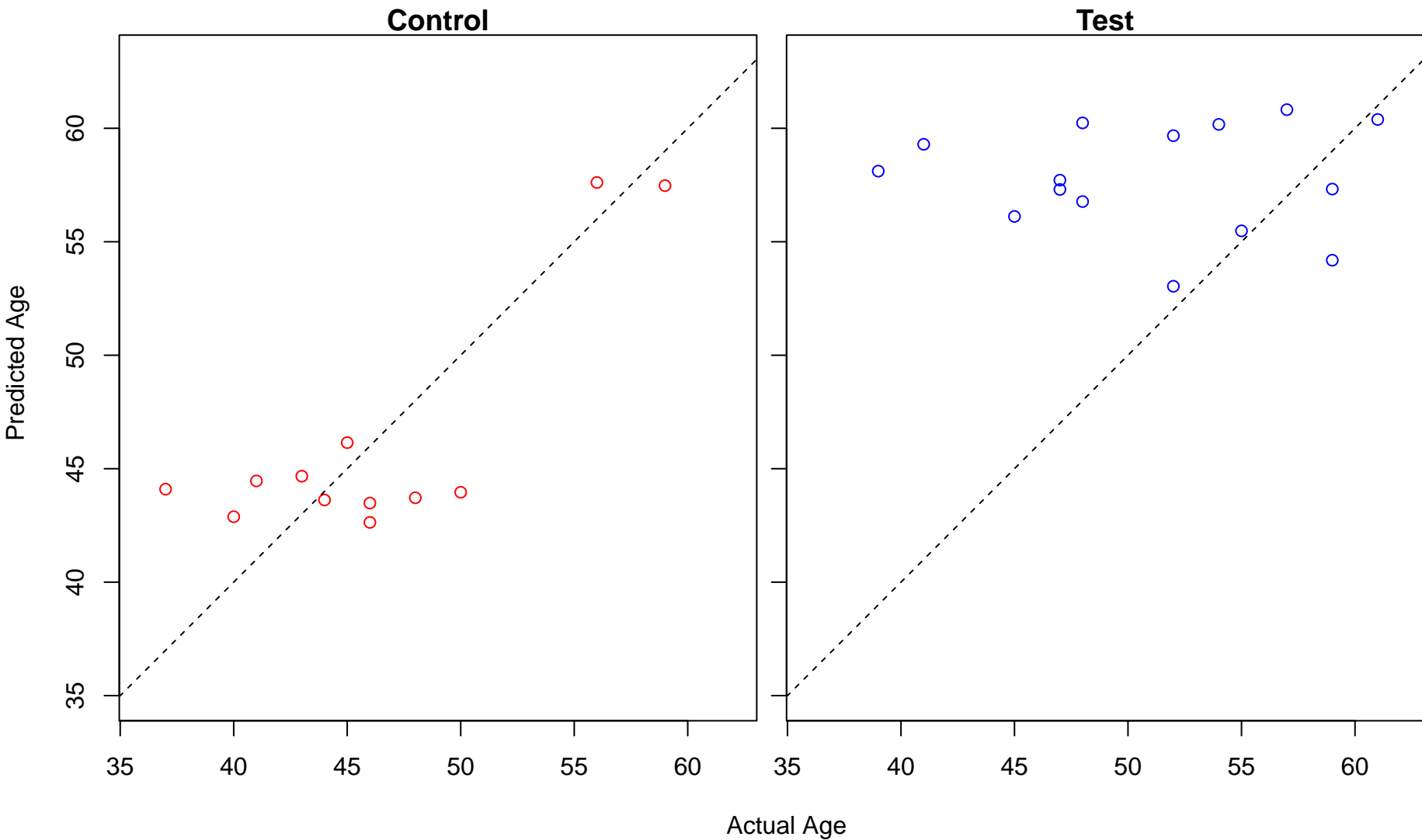


Test



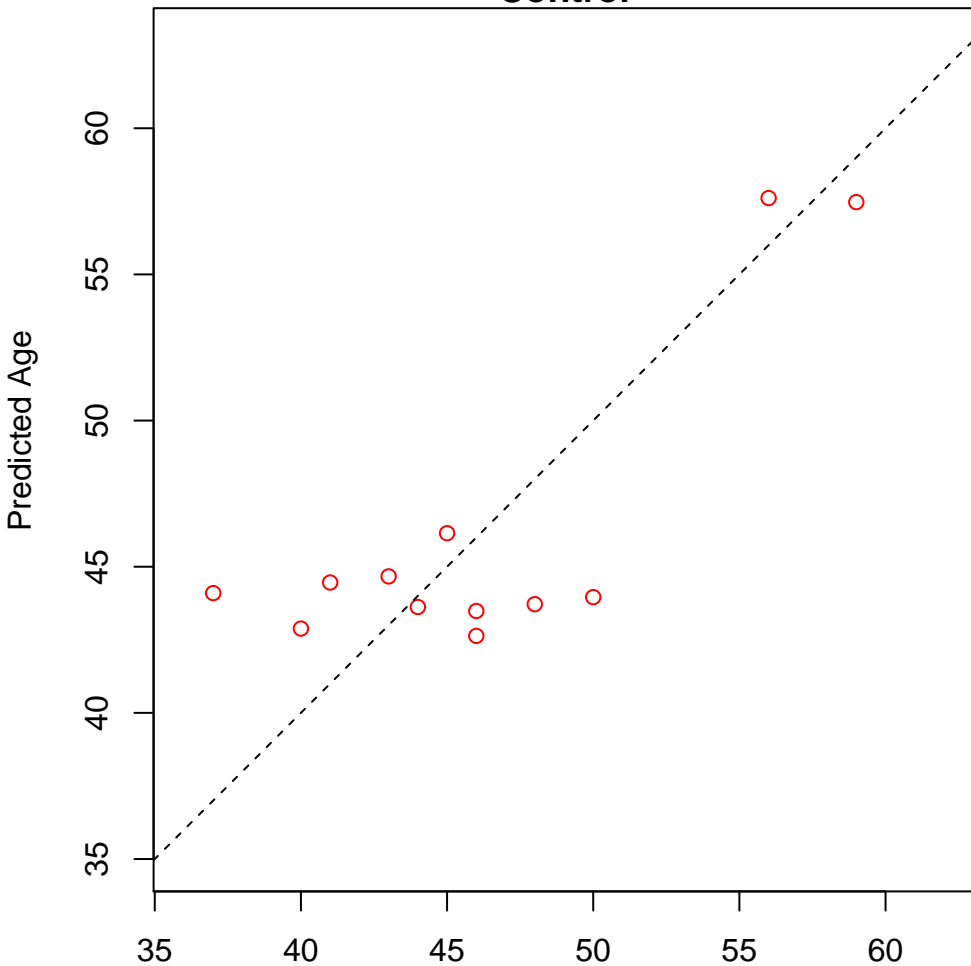
Actual Age

mitophagy in response to mitochondrial depolarization (Score: 2.846483)

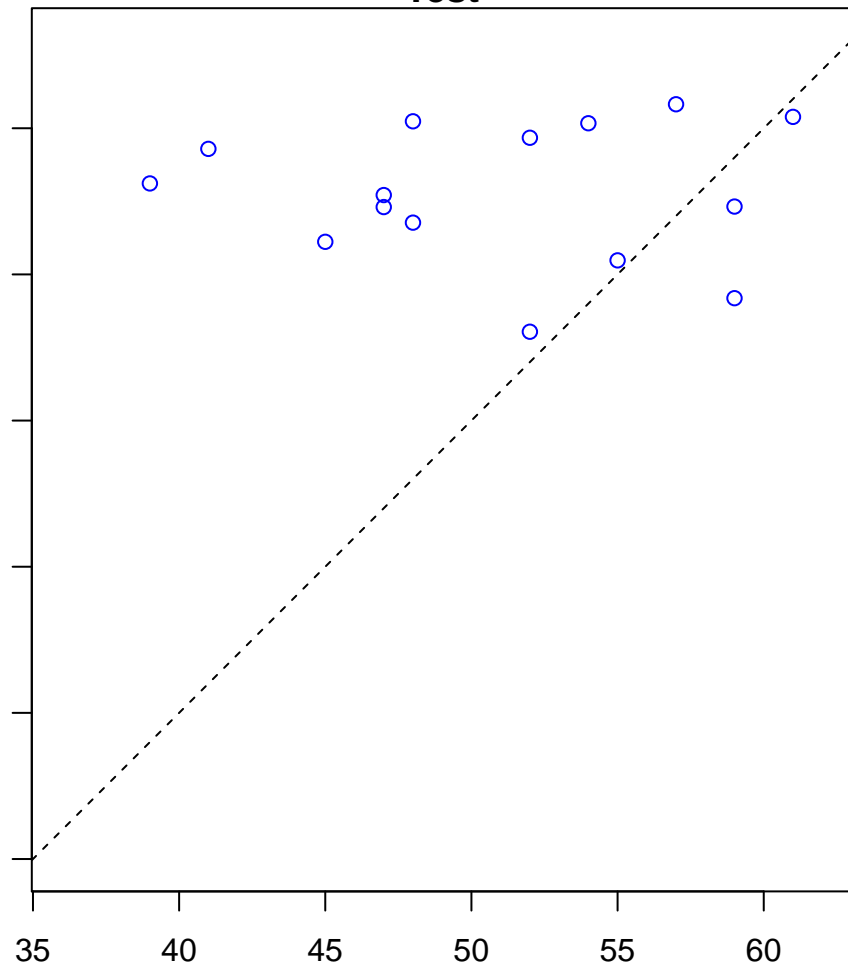


response to mitochondrial depolarisation (Score: 2.846483)

Control

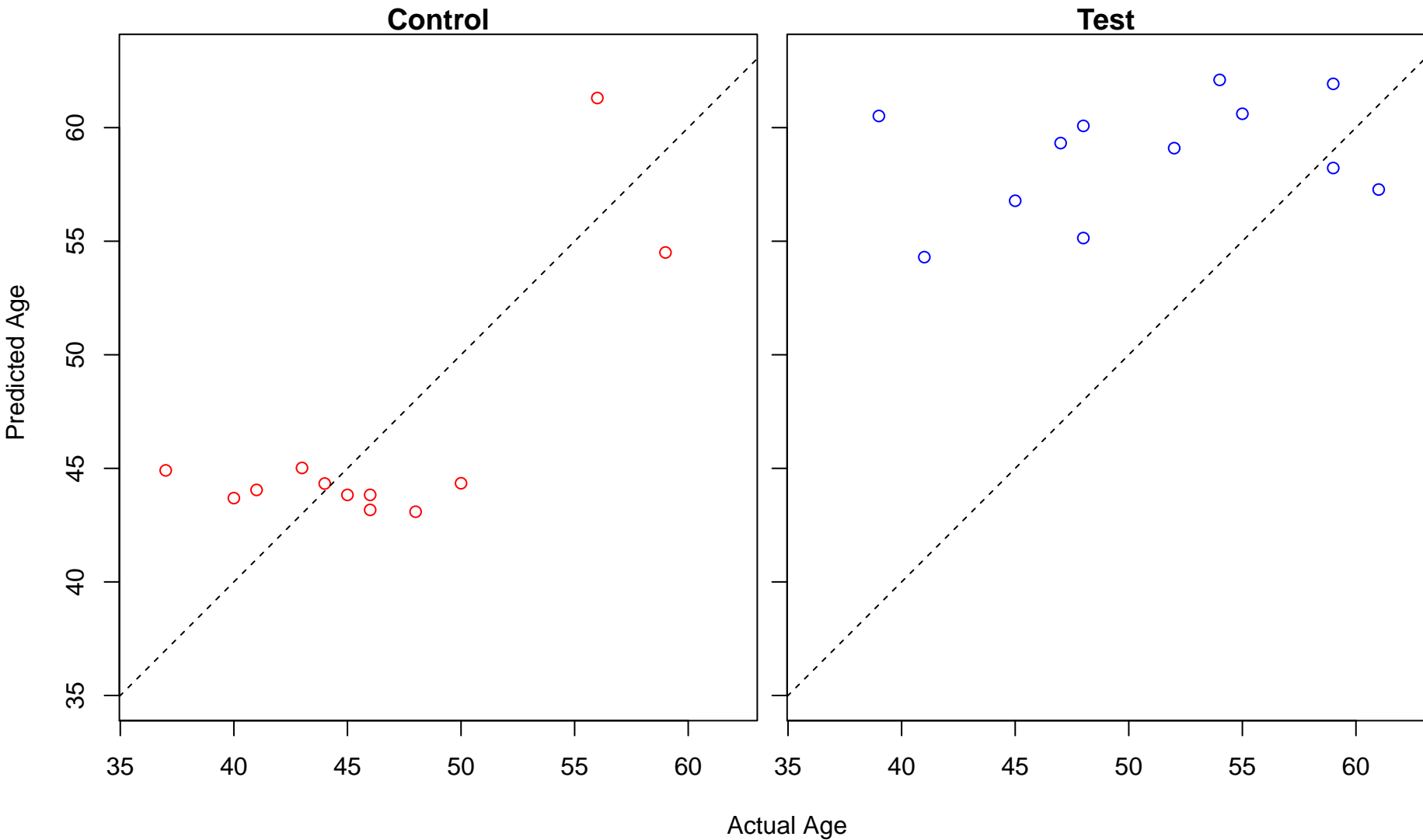


Test

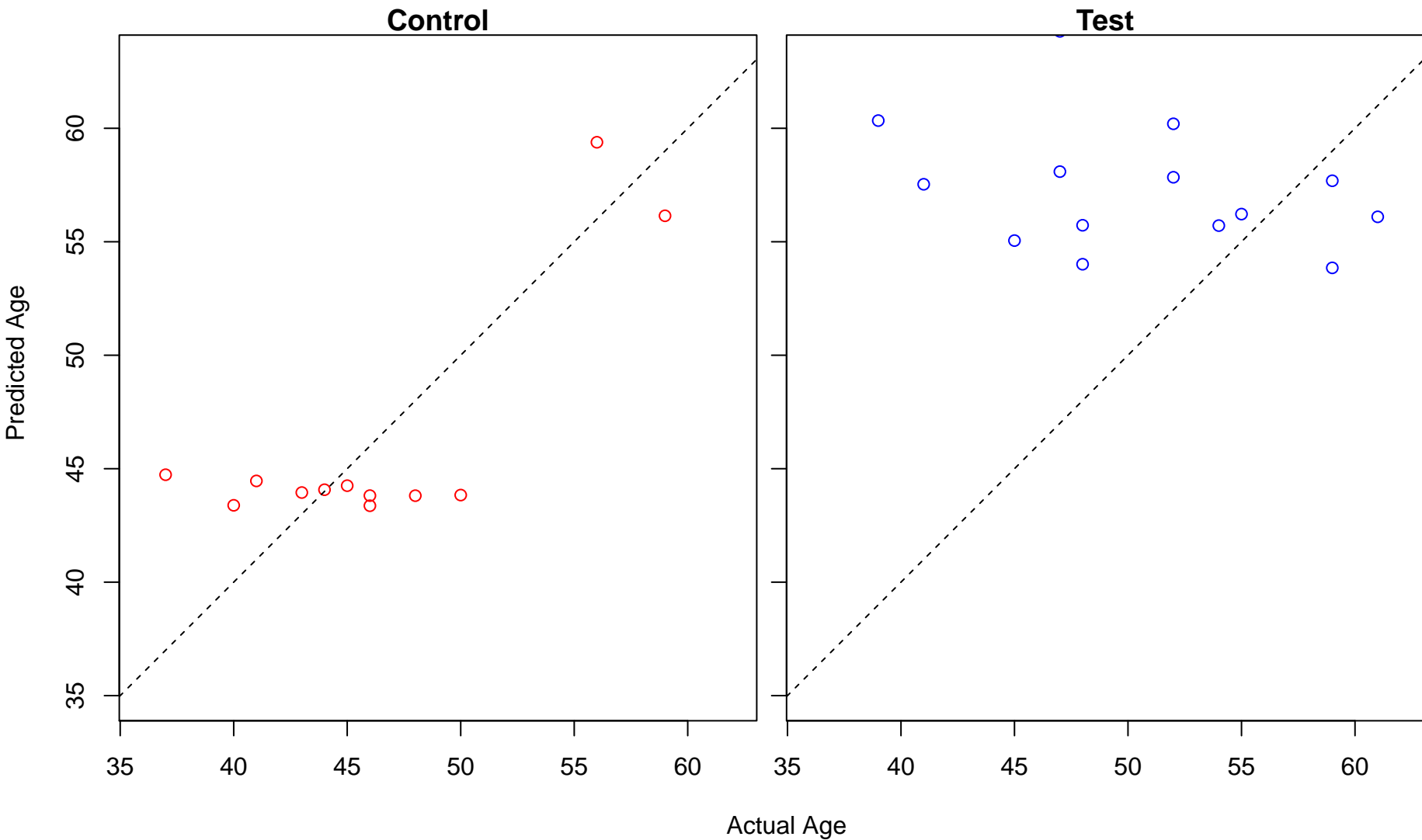


Actual Age

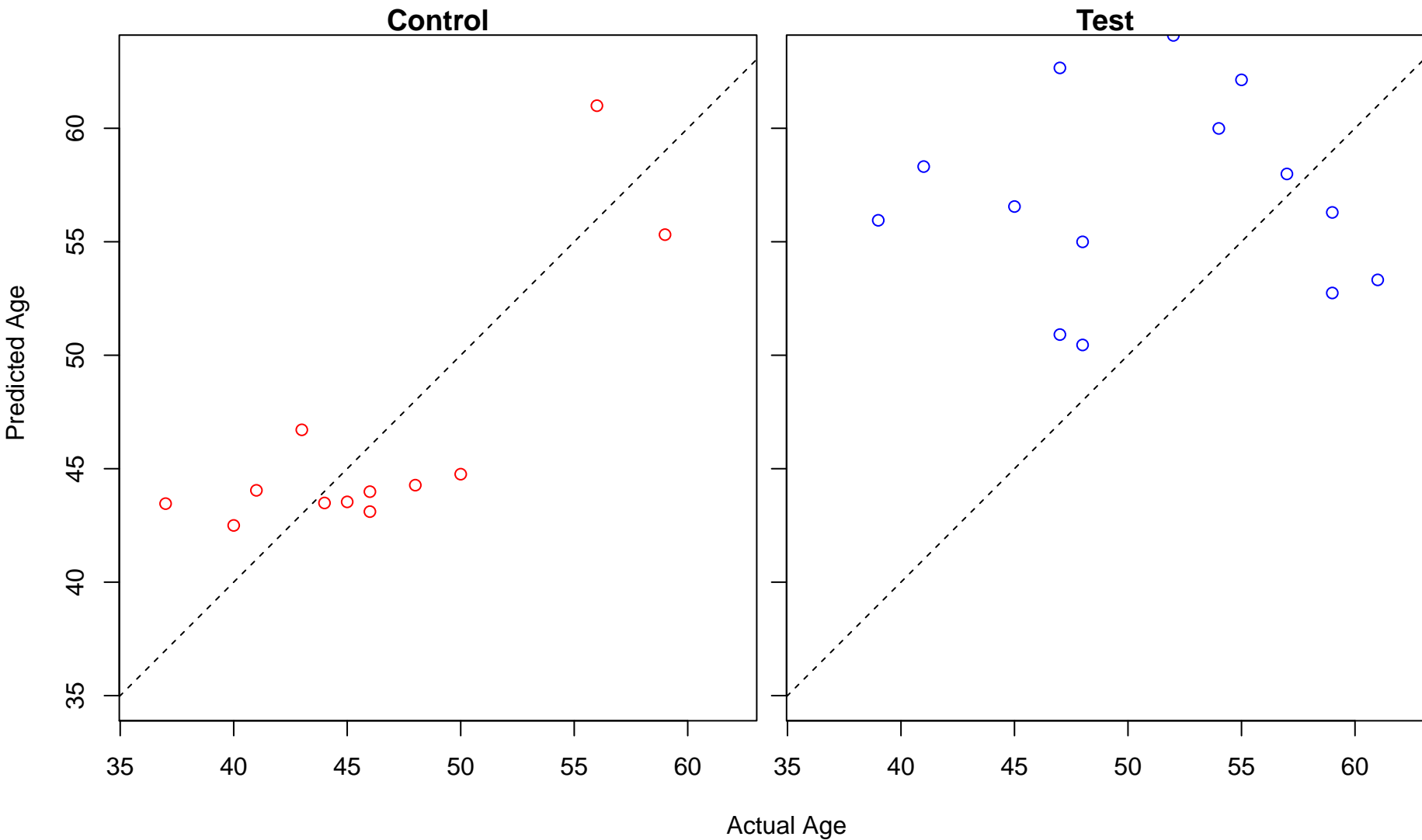
positive regulation of fat cell differentiation (Score: 2.846255)



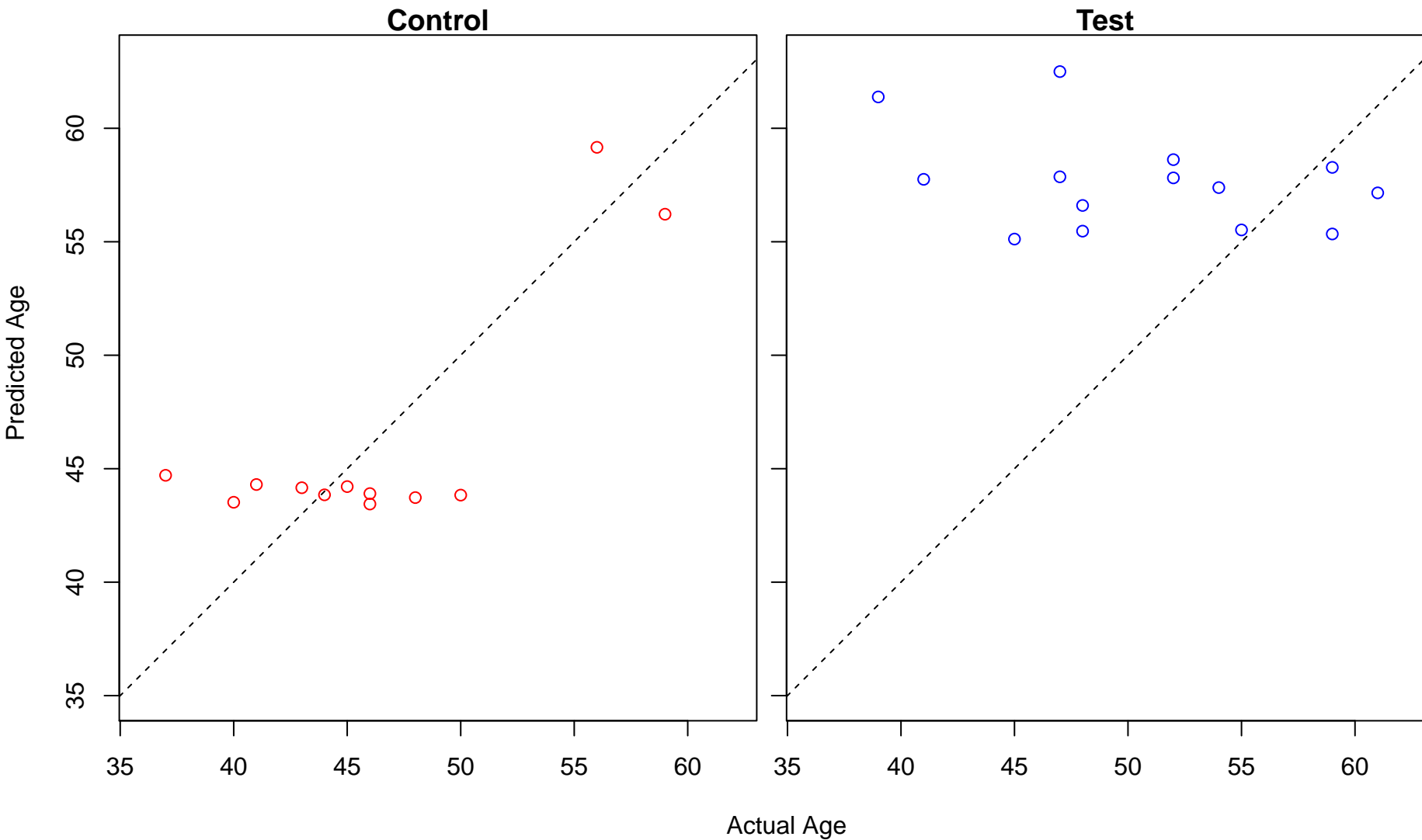
response to oxygen levels (Score: 2.845924)



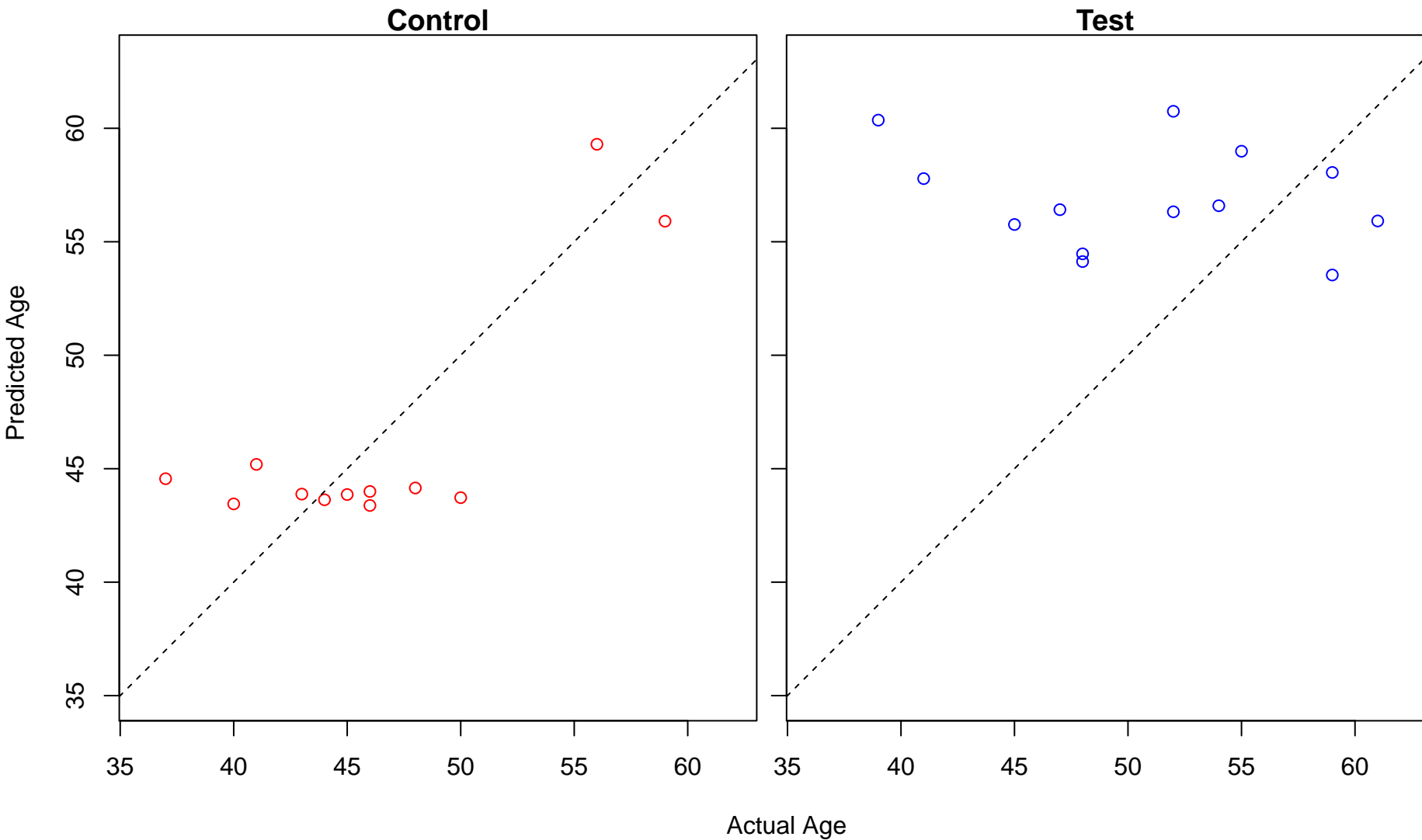
alditol metabolic process (Score: 2.845280)



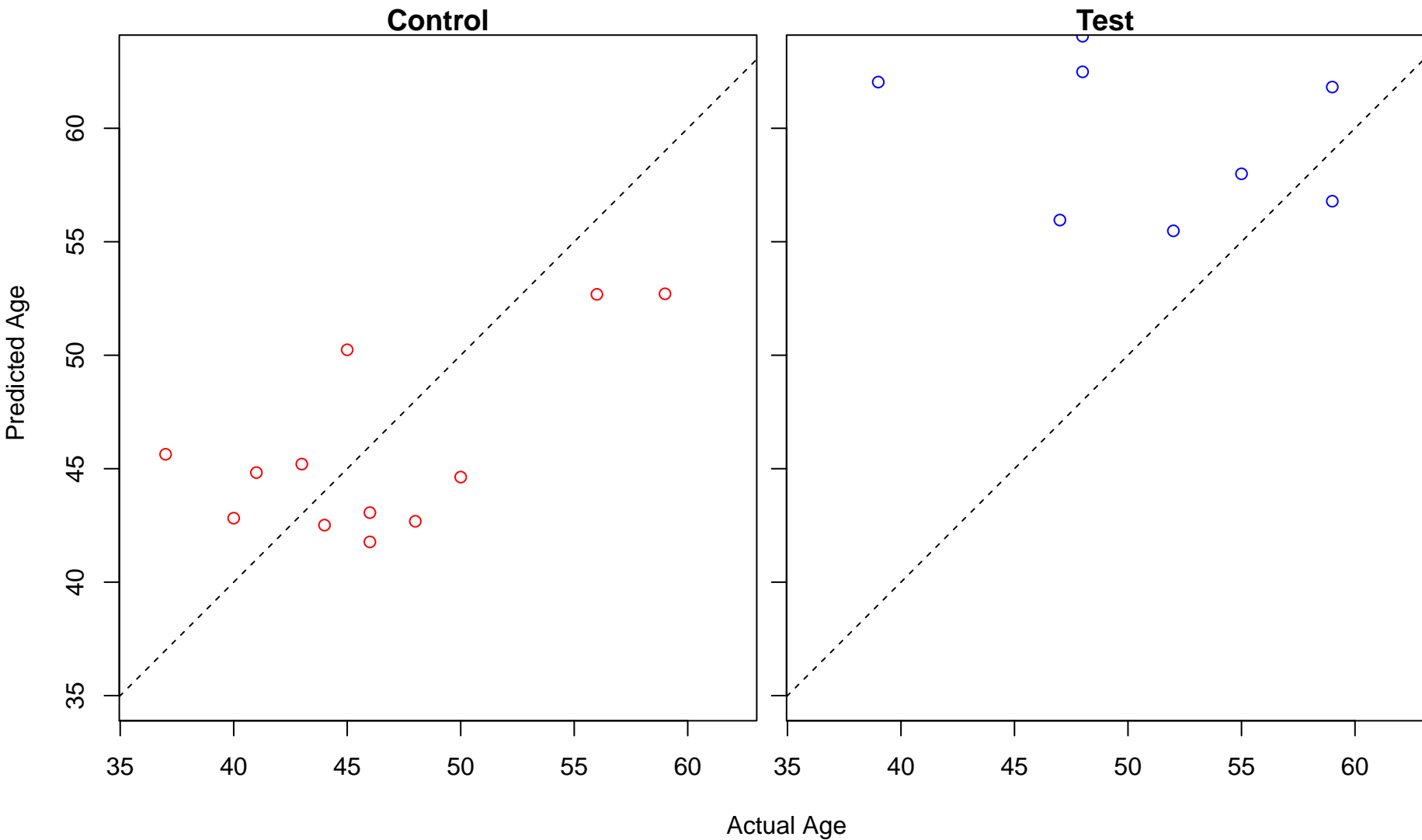
response to insulin (Score: 2.843519)



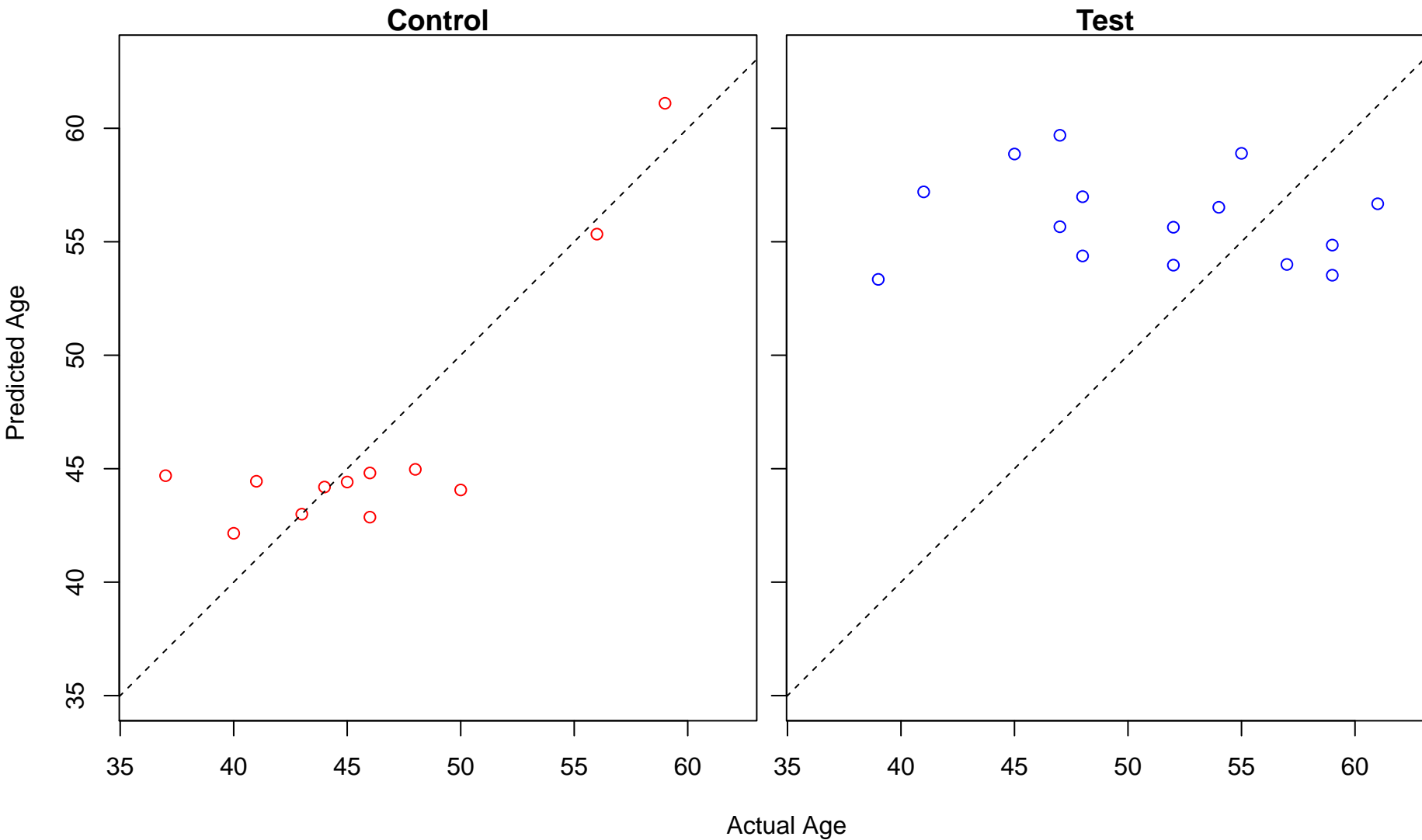
vasculature development (Score: 2.843242)



macrophage activation (Score: 2.842505)

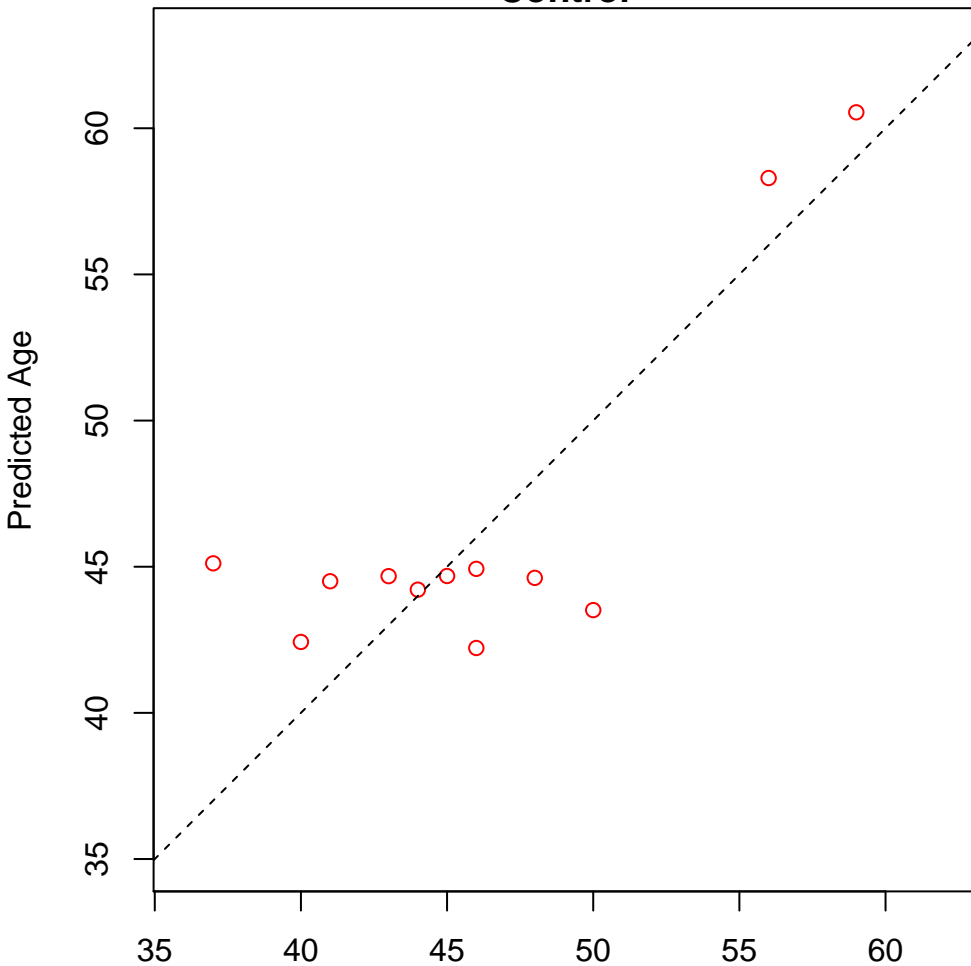


cerebral cortex cell migration (Score: 2.840958)

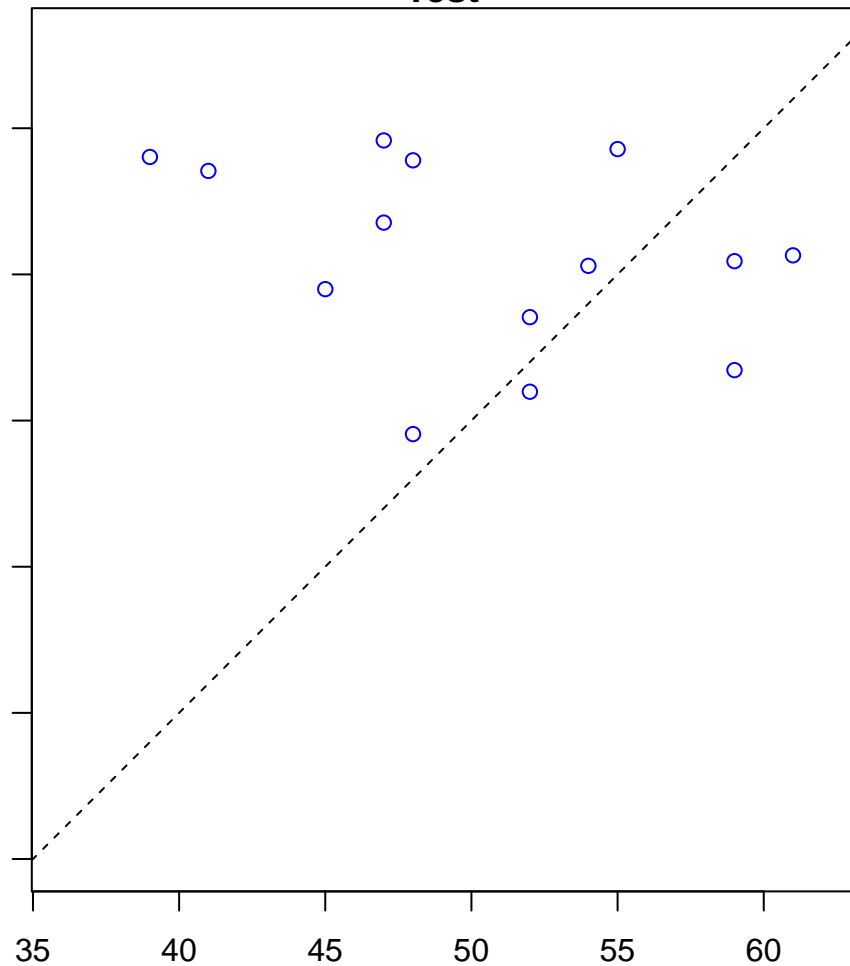


activation of protein kinase activity (Score: 2.839280)

Control

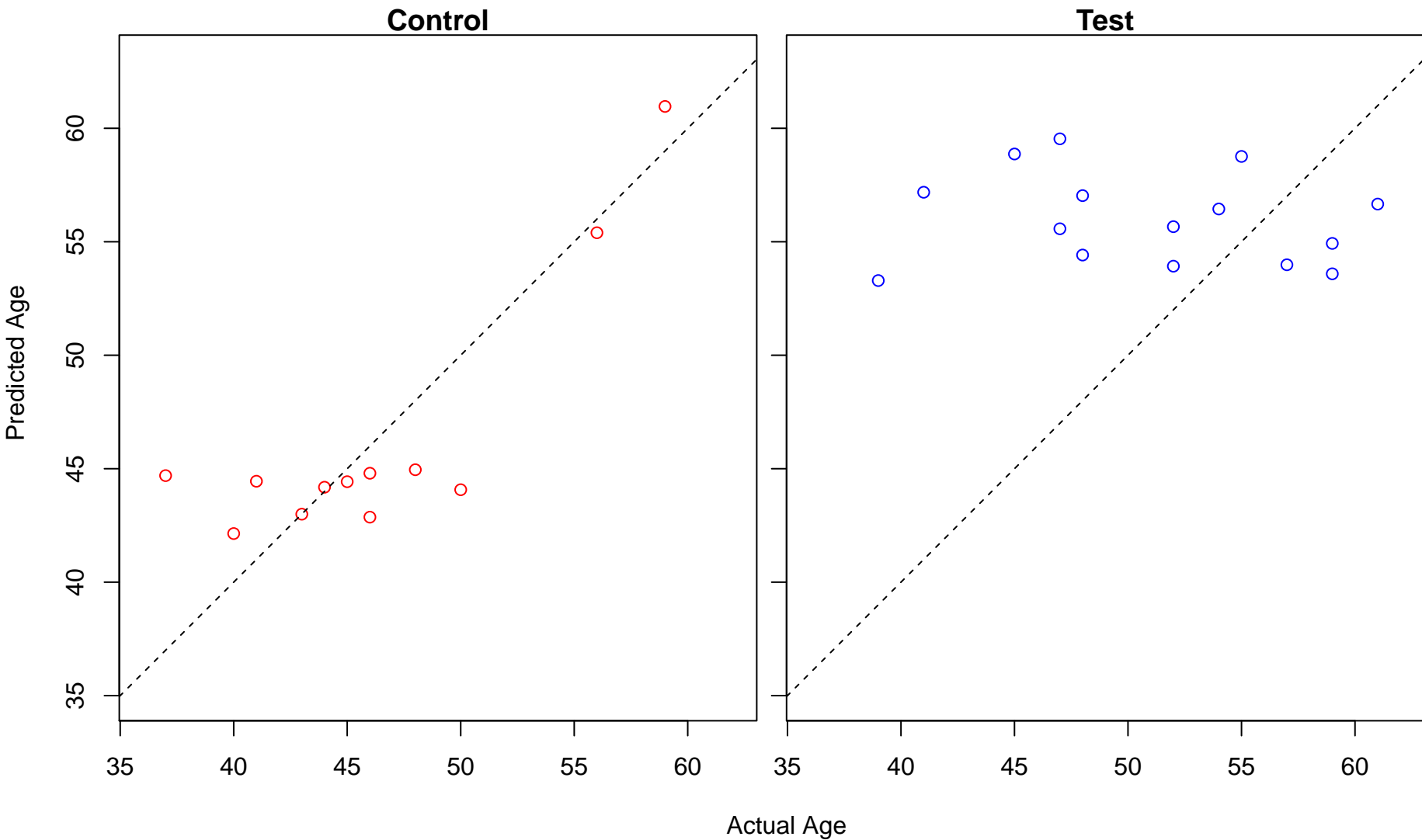


Test



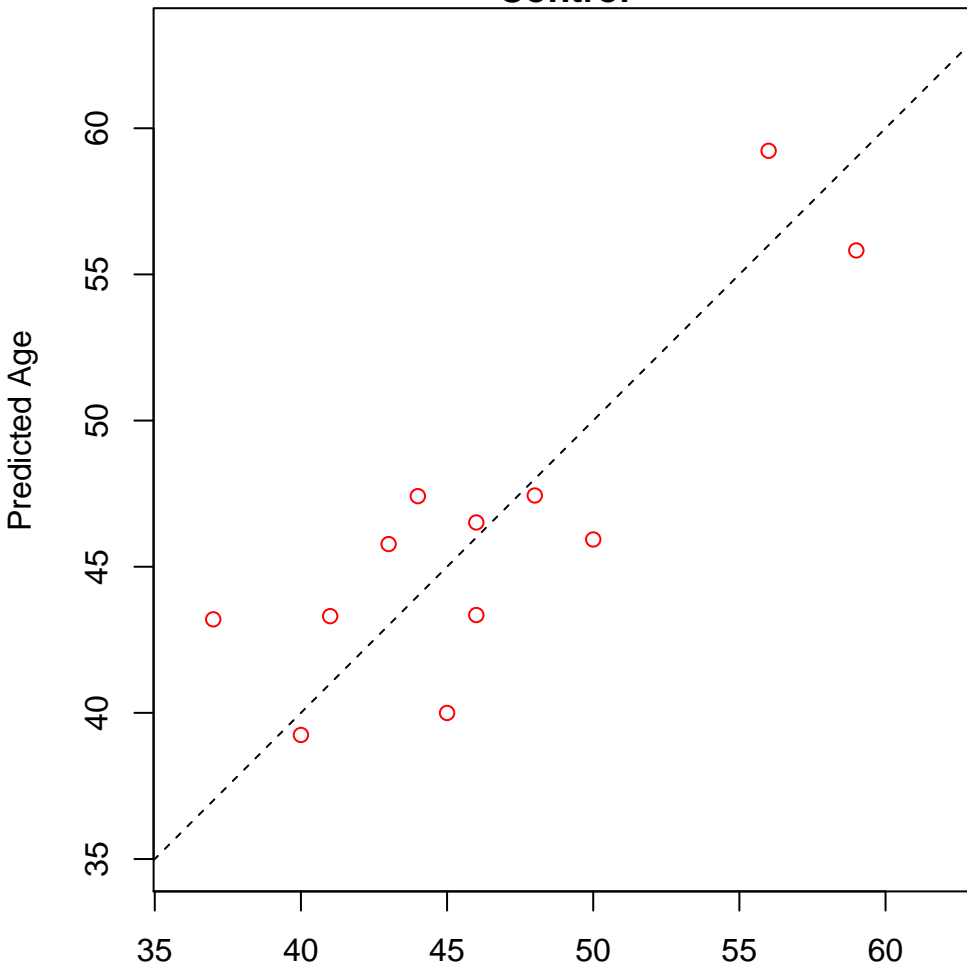
Actual Age

cerebral cortex development (Score: 2.838445)

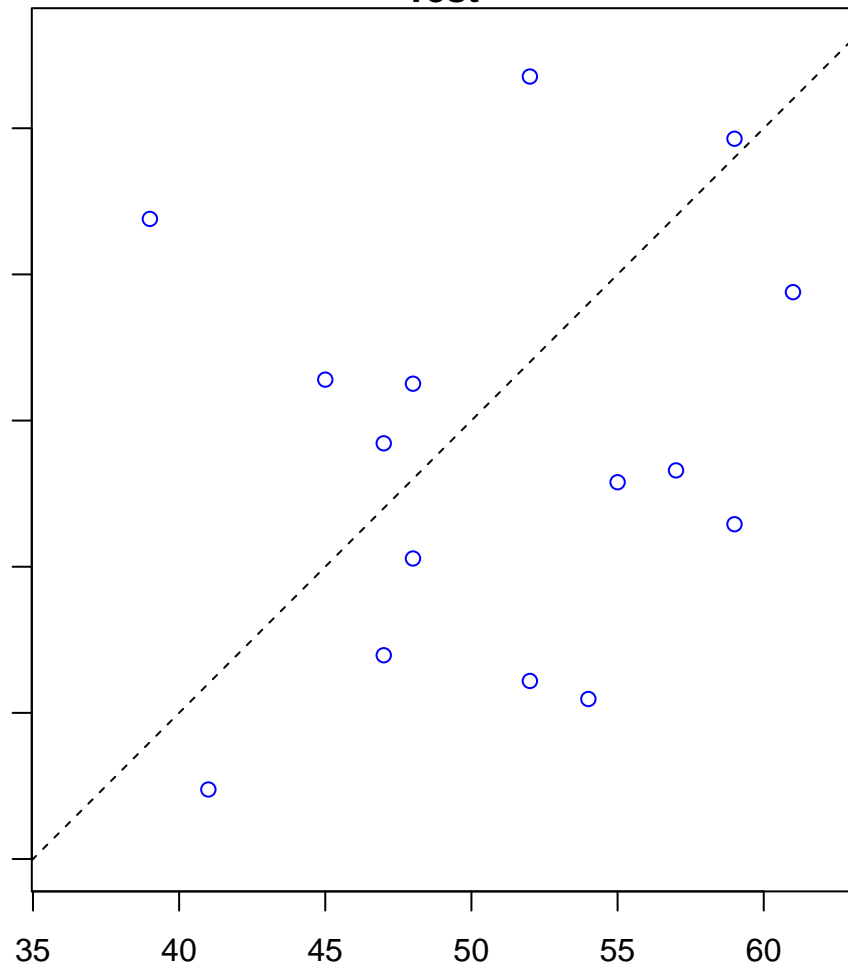


organophosphate ester transport (Score: 2.838099)

Control

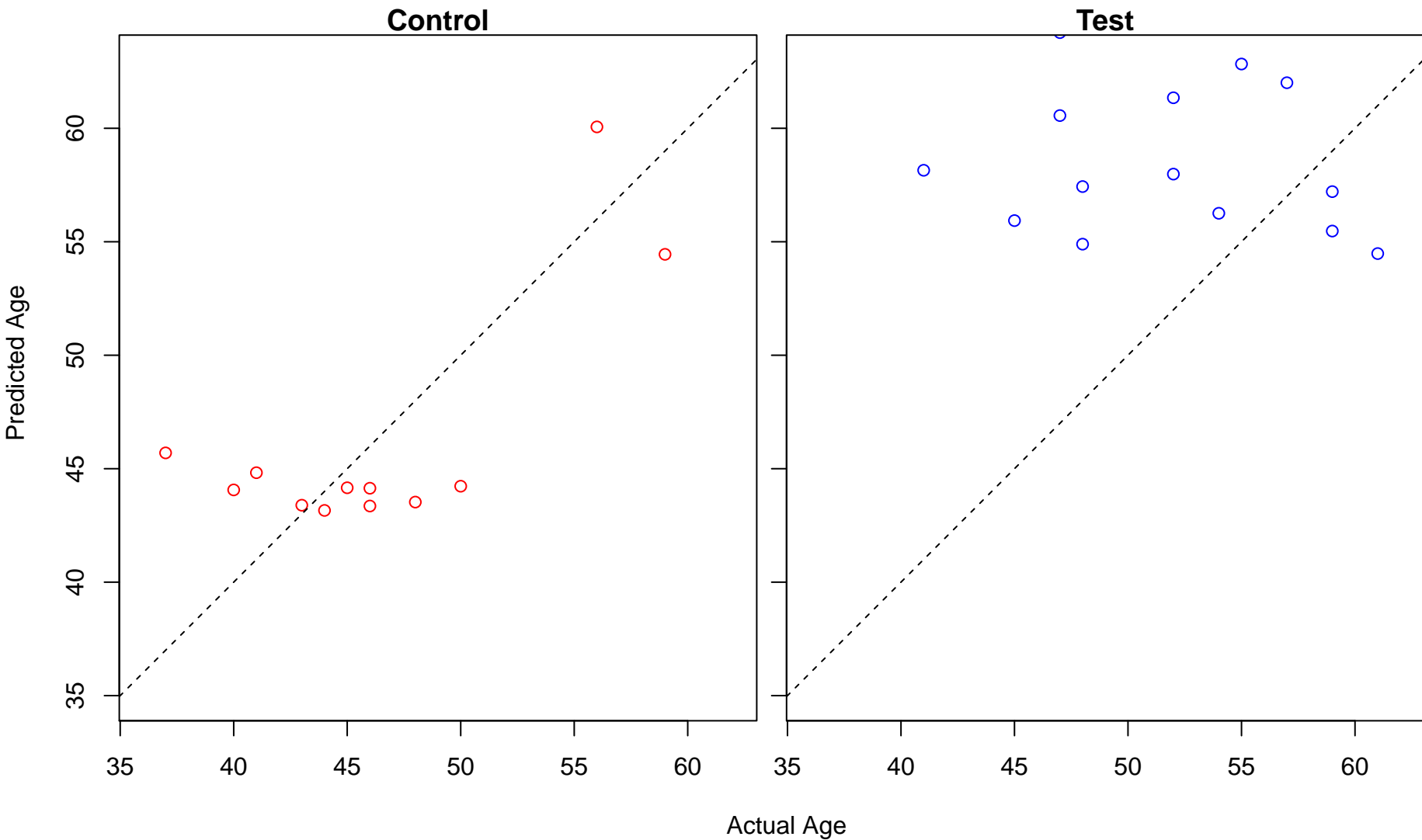


Test

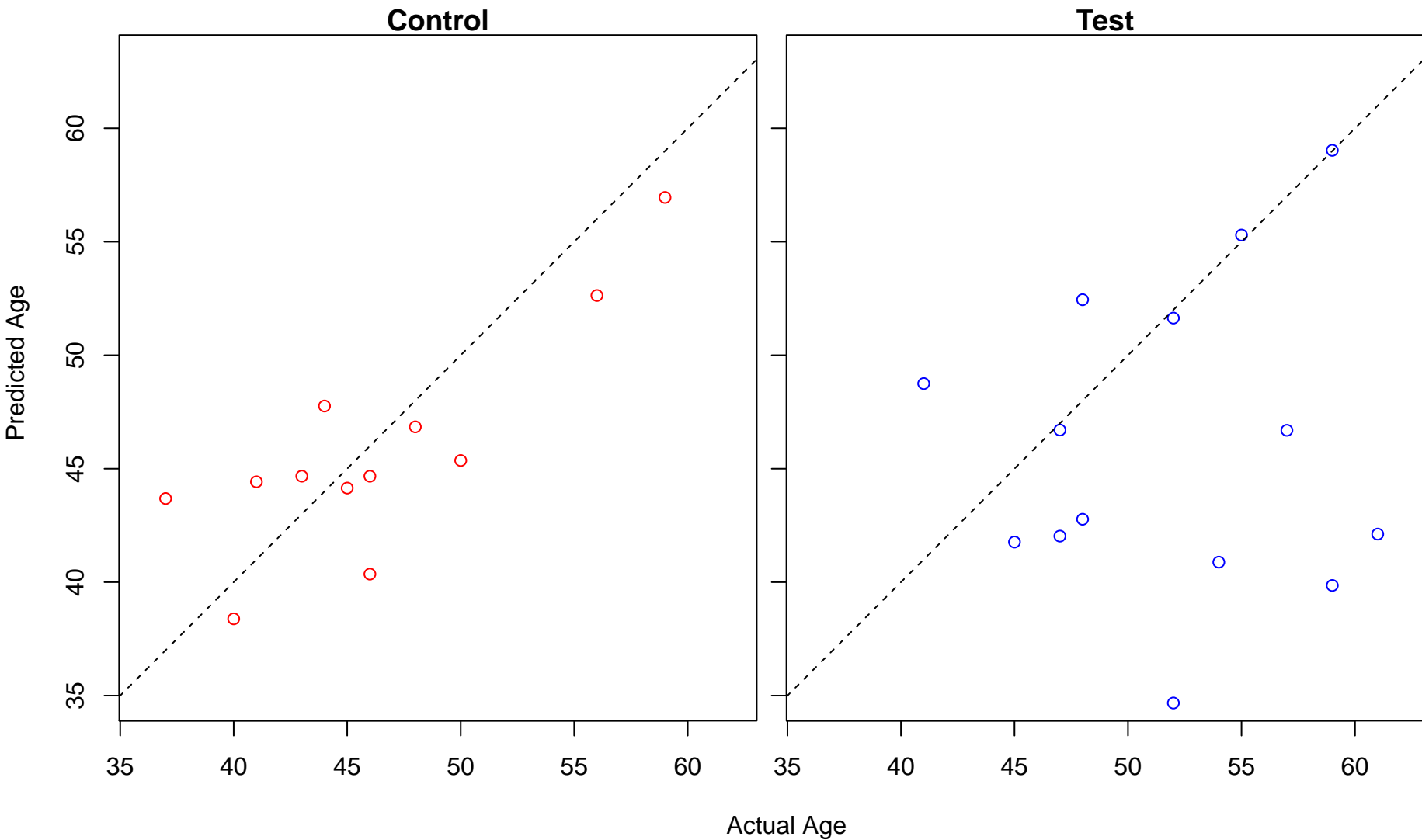


Actual Age

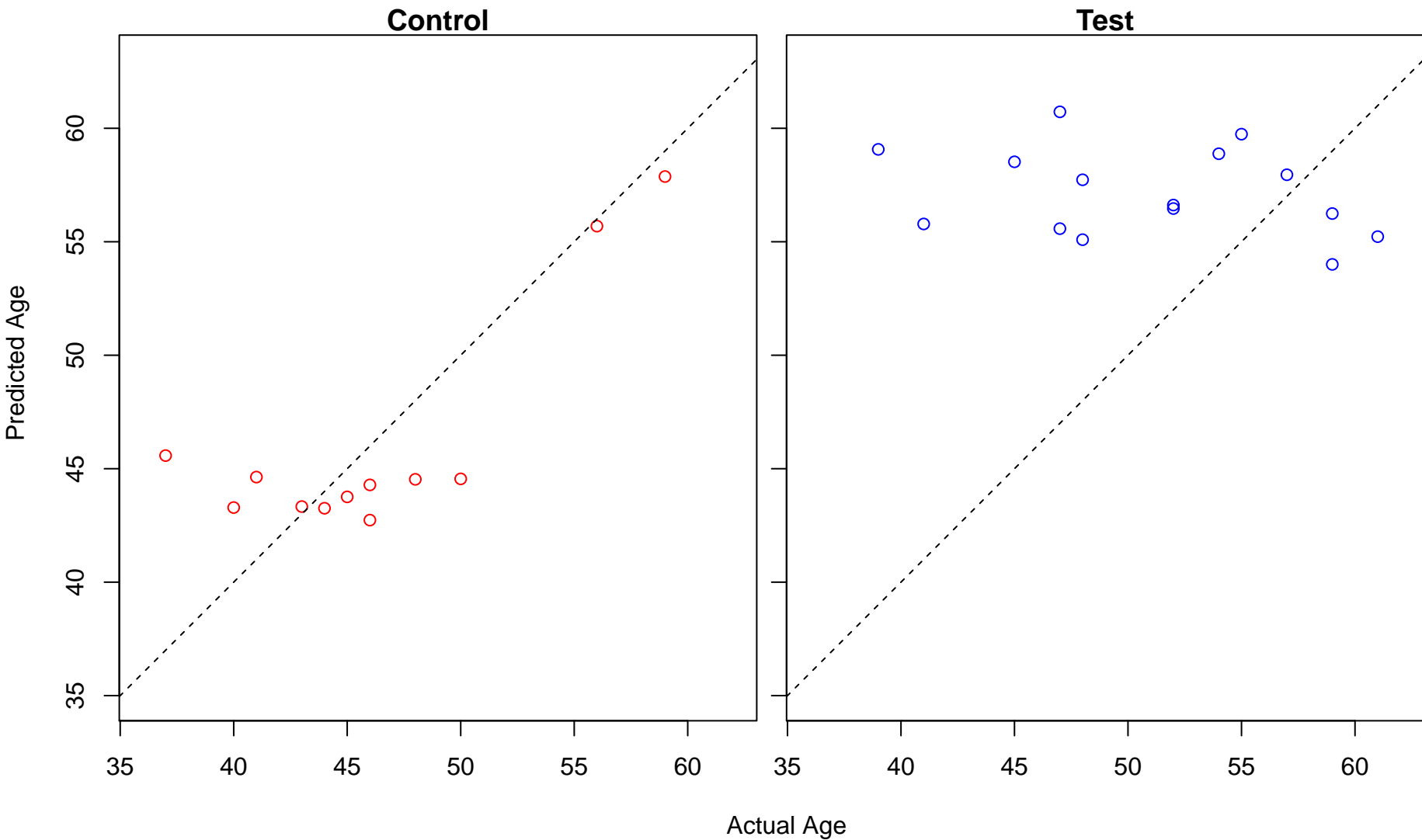
regulation of defense response to virus by virus (Score: 2.836678)



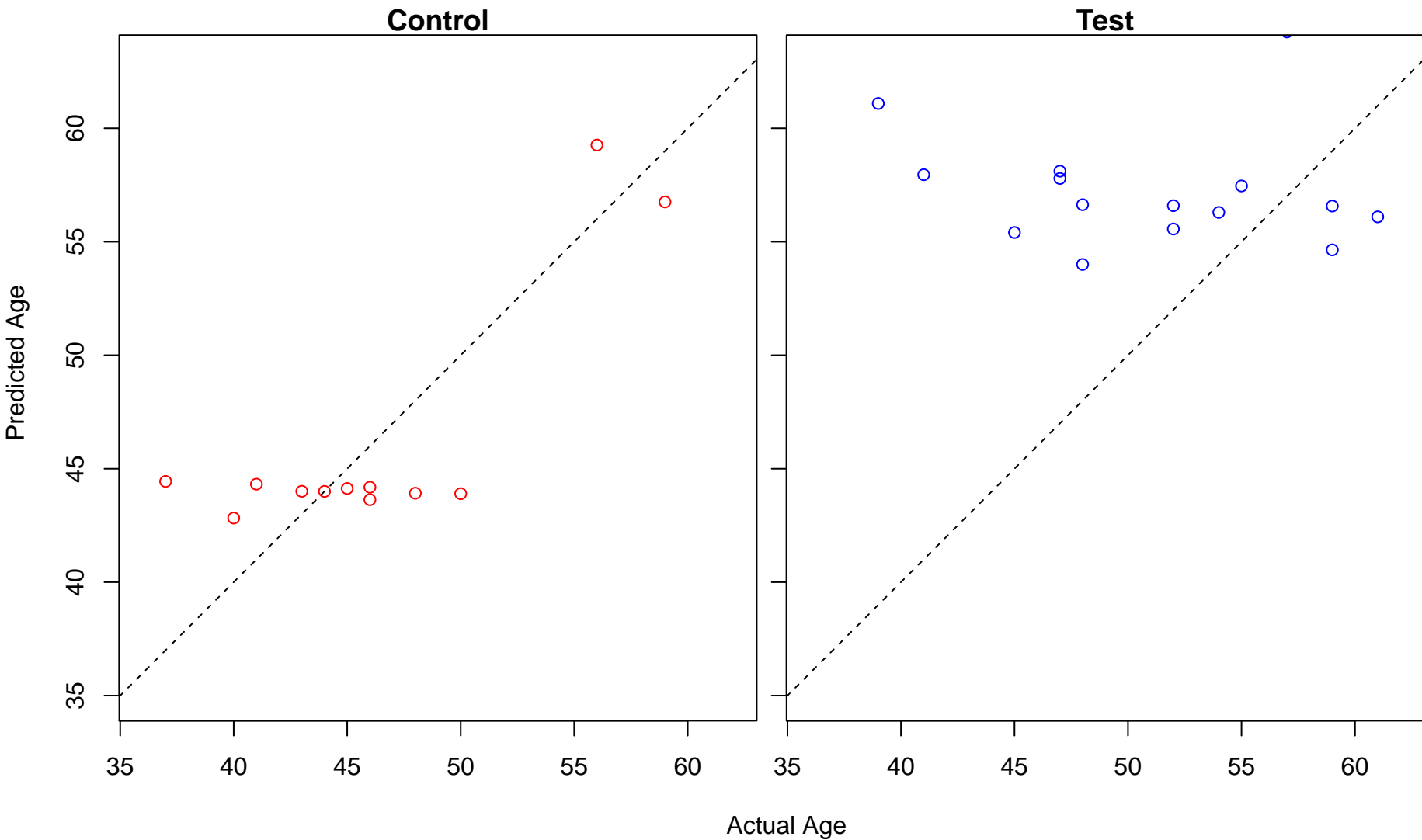
establishment of protein localization to membrane (Score: 2.834916)



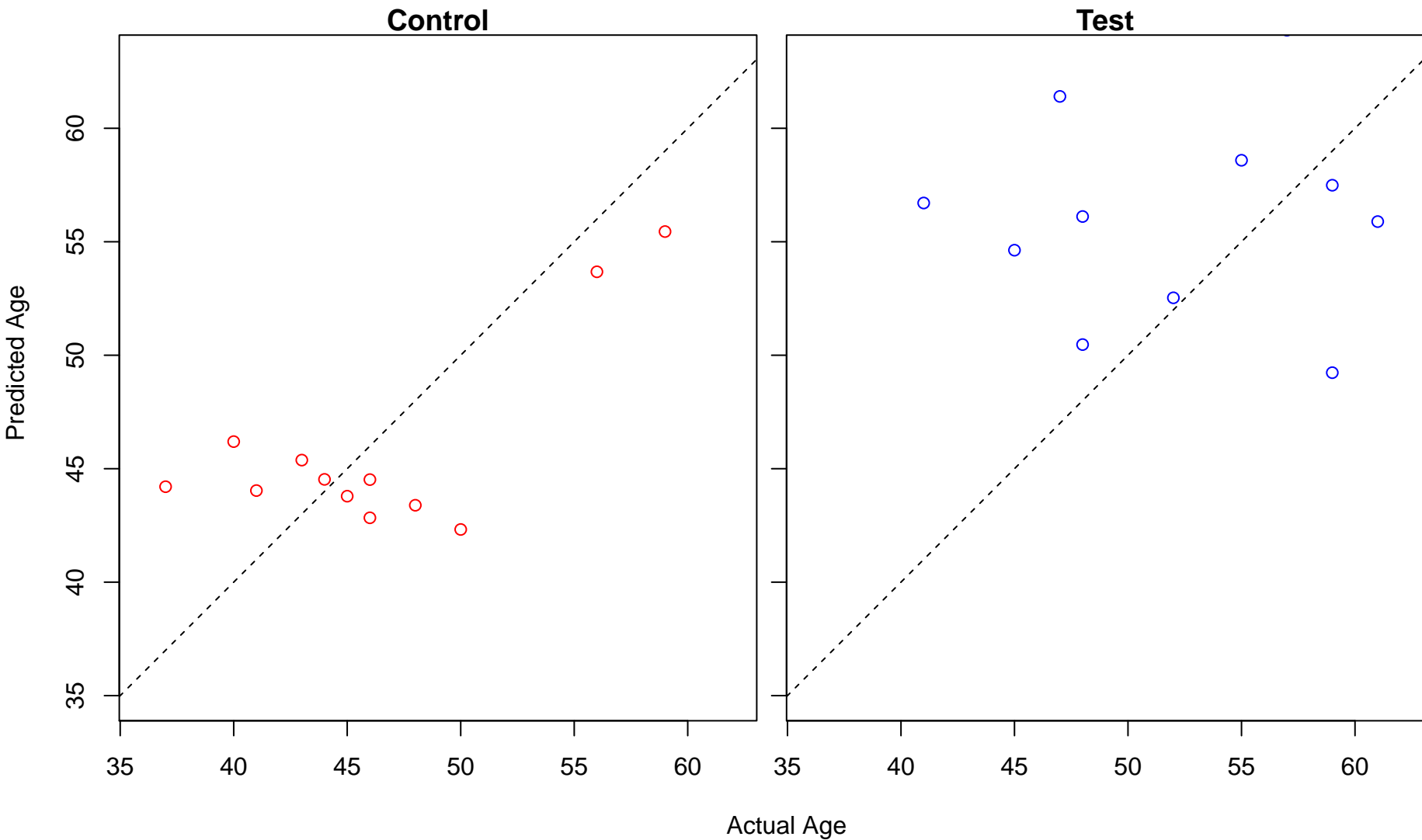
response to stimulus involved in regulation of muscle adaptation (Score: 2.833632)



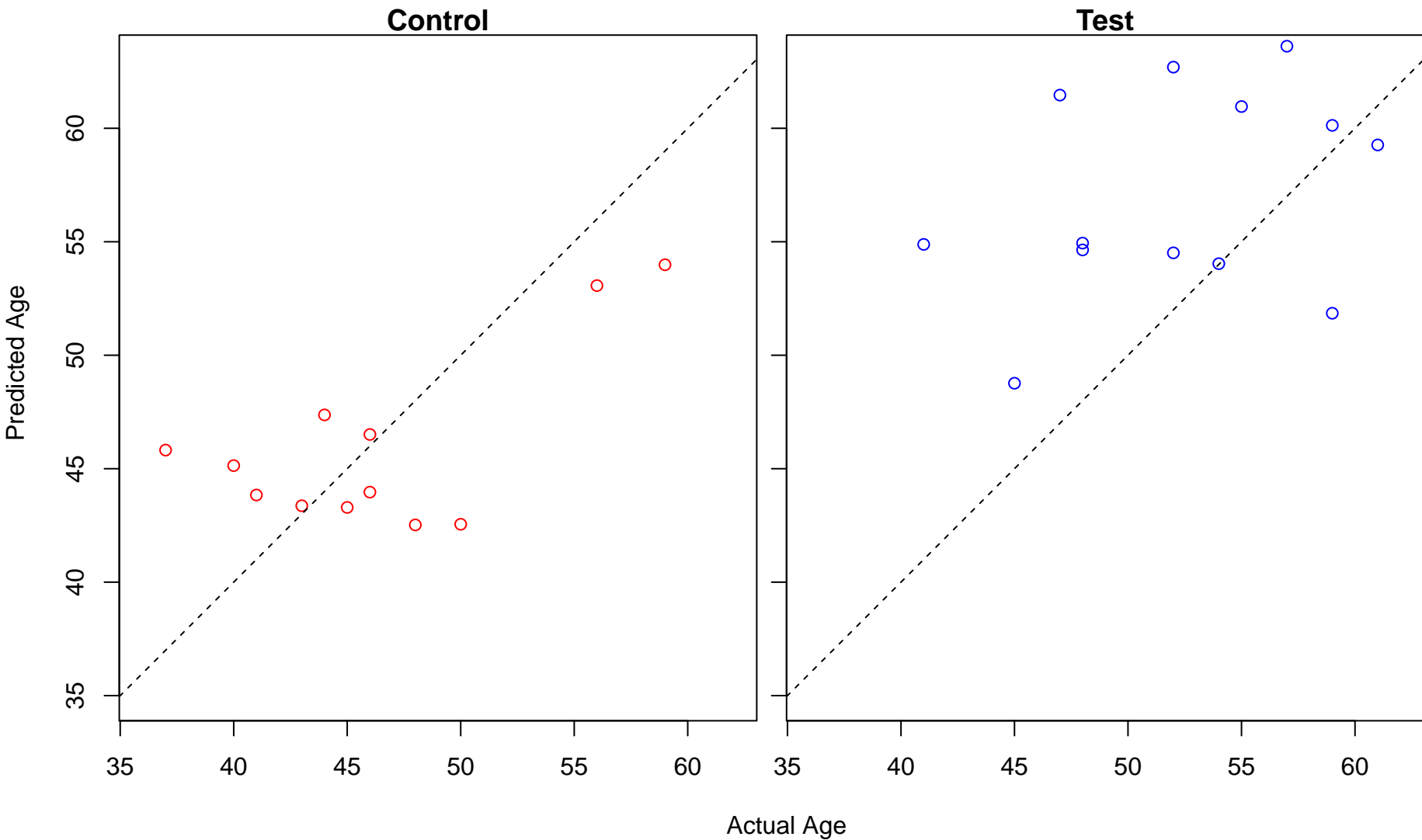
regulation of release of sequestered calcium ion into cytosol (Score: 2.833392)



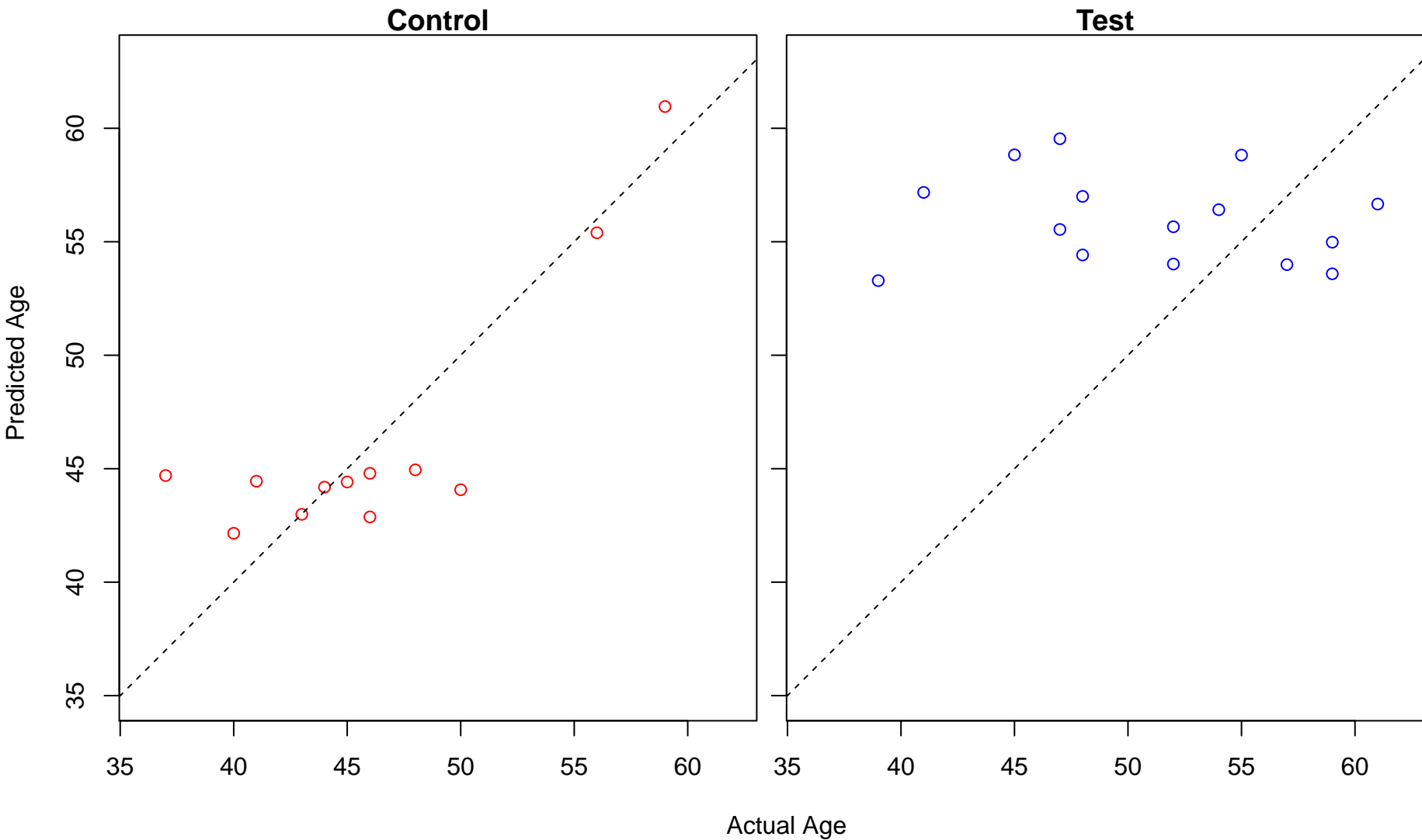
regulation of plasminogen activation (Score: 2.832988)



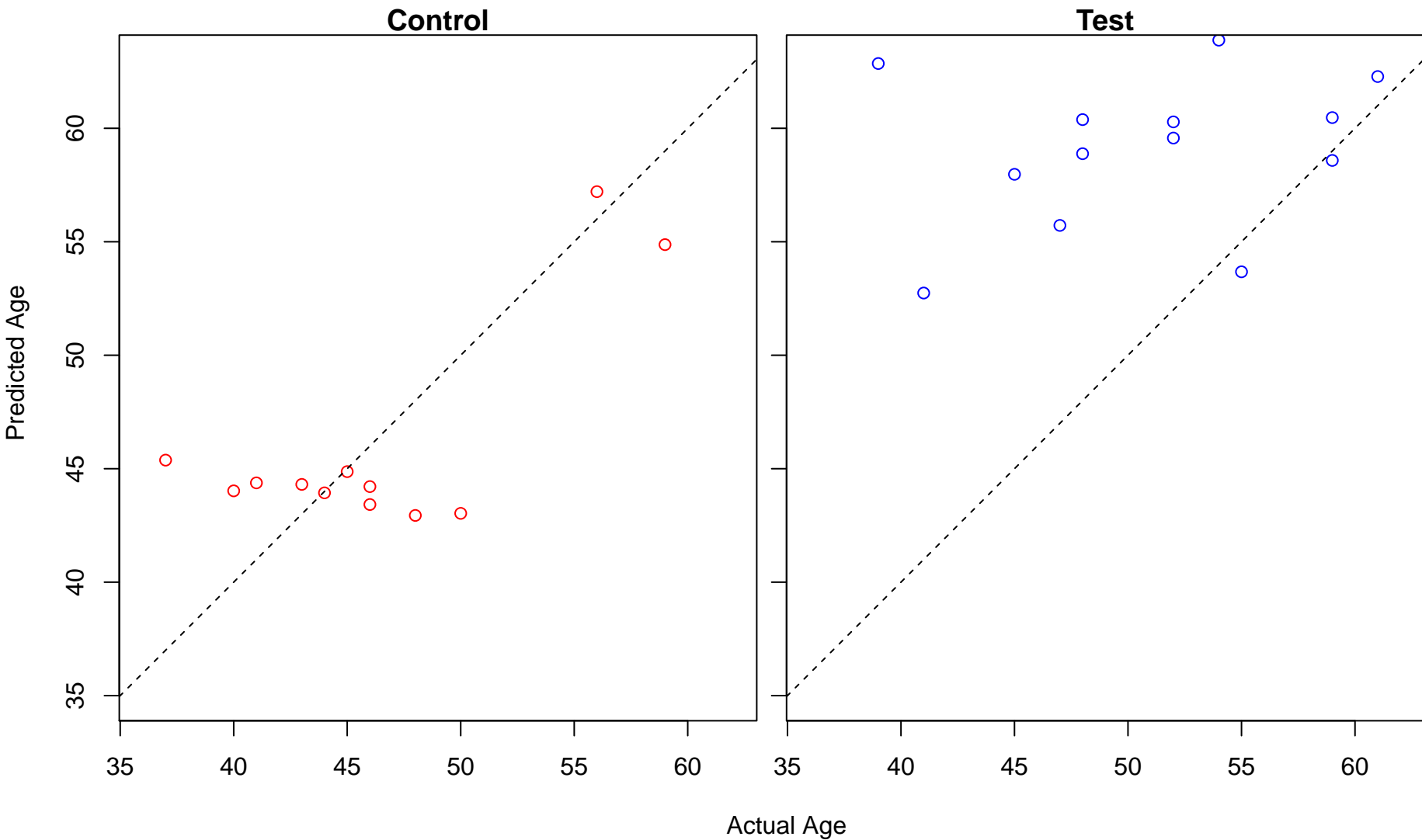
bone growth (Score: 2.832658)



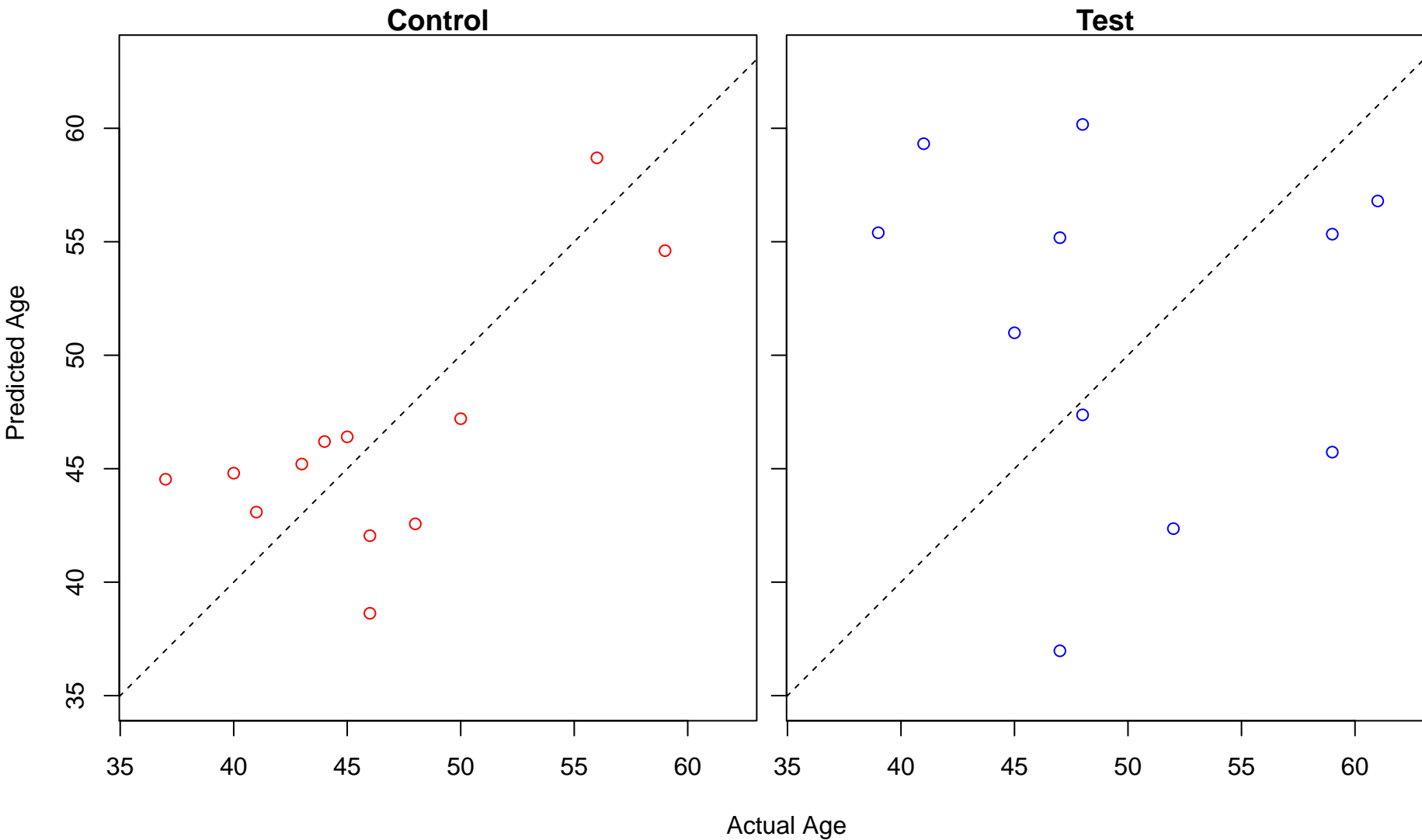
pallium development (Score: 2.832238)



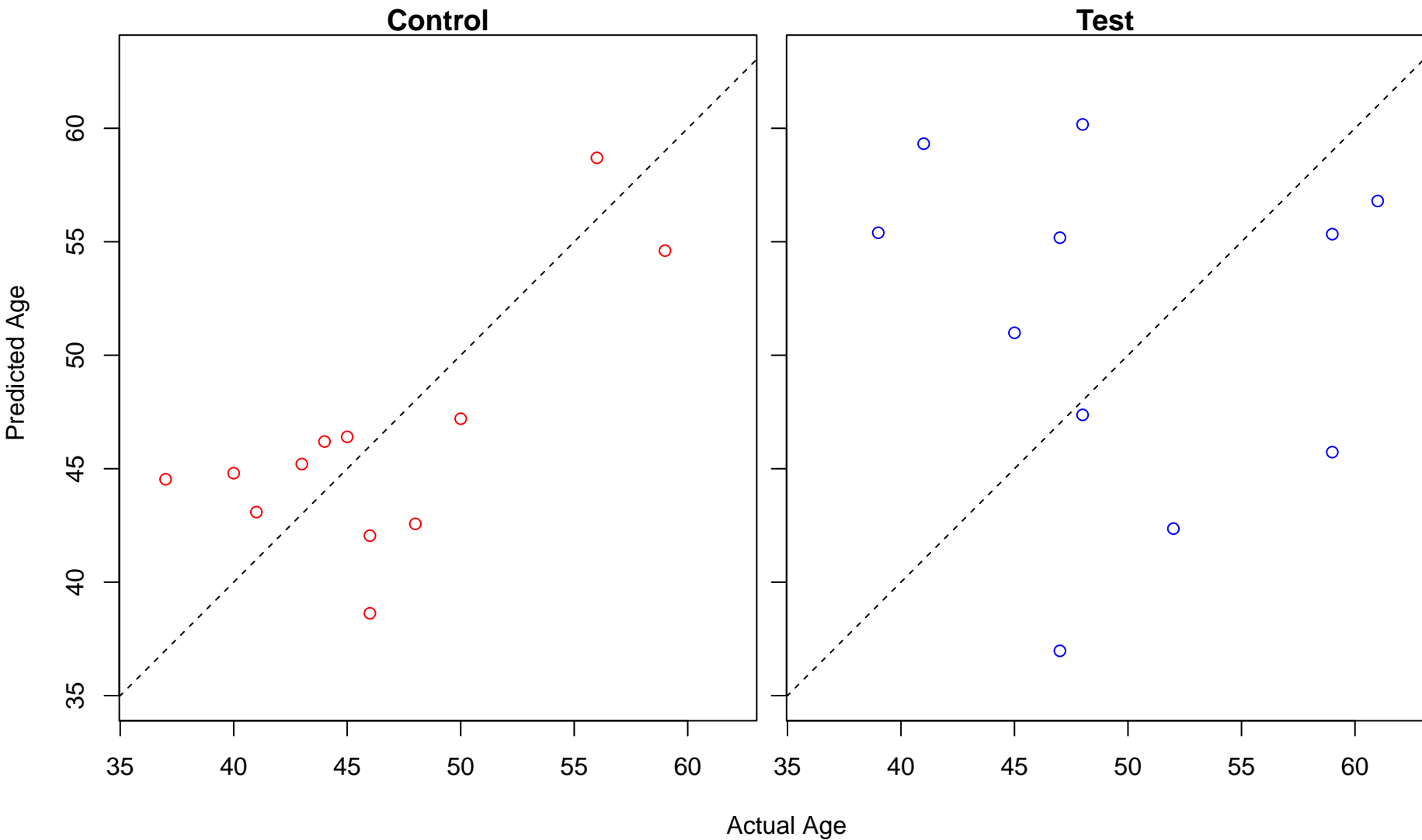
negative regulation of ATPase activity (Score: 2.831448)



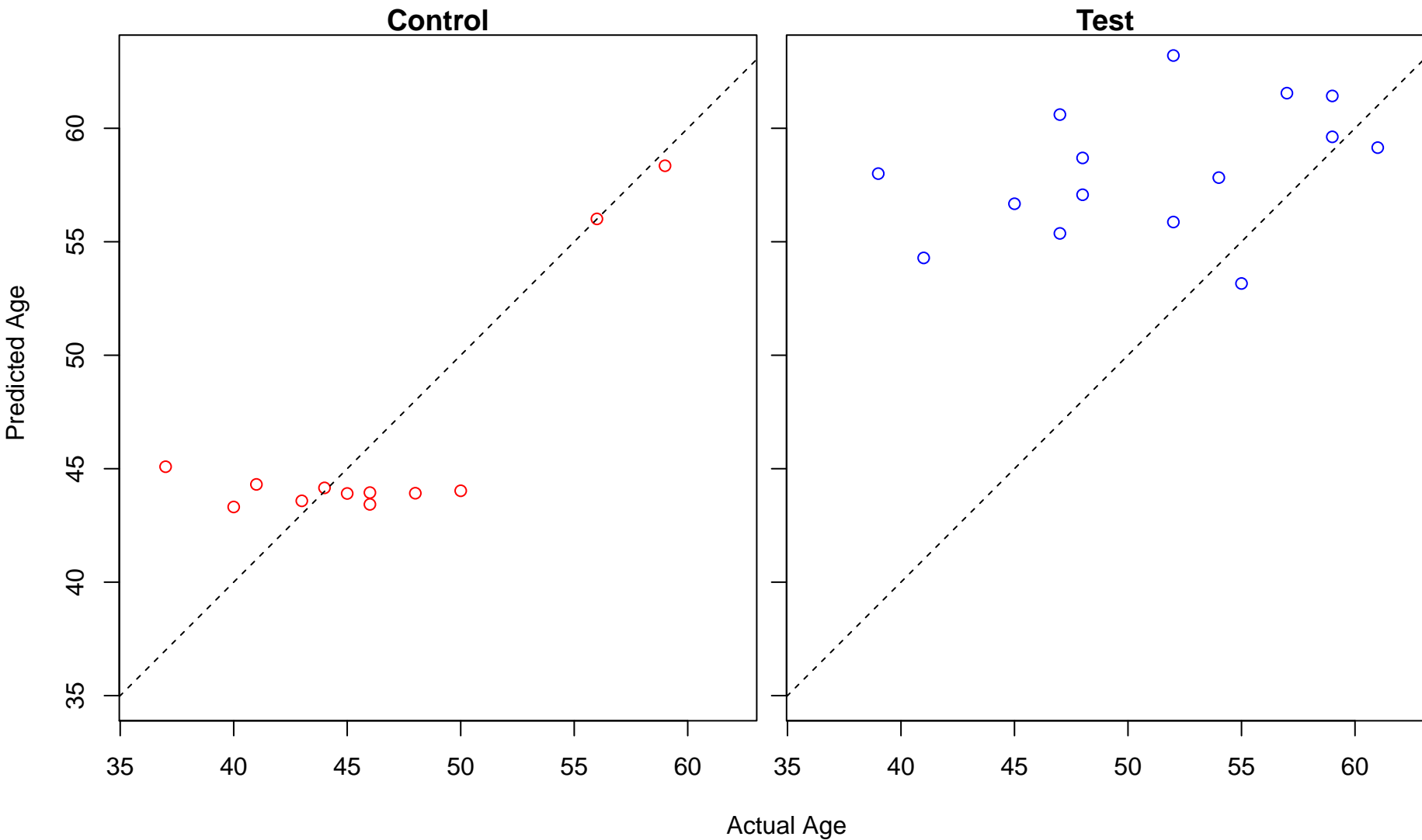
cochlea development (Score: 2.829973)



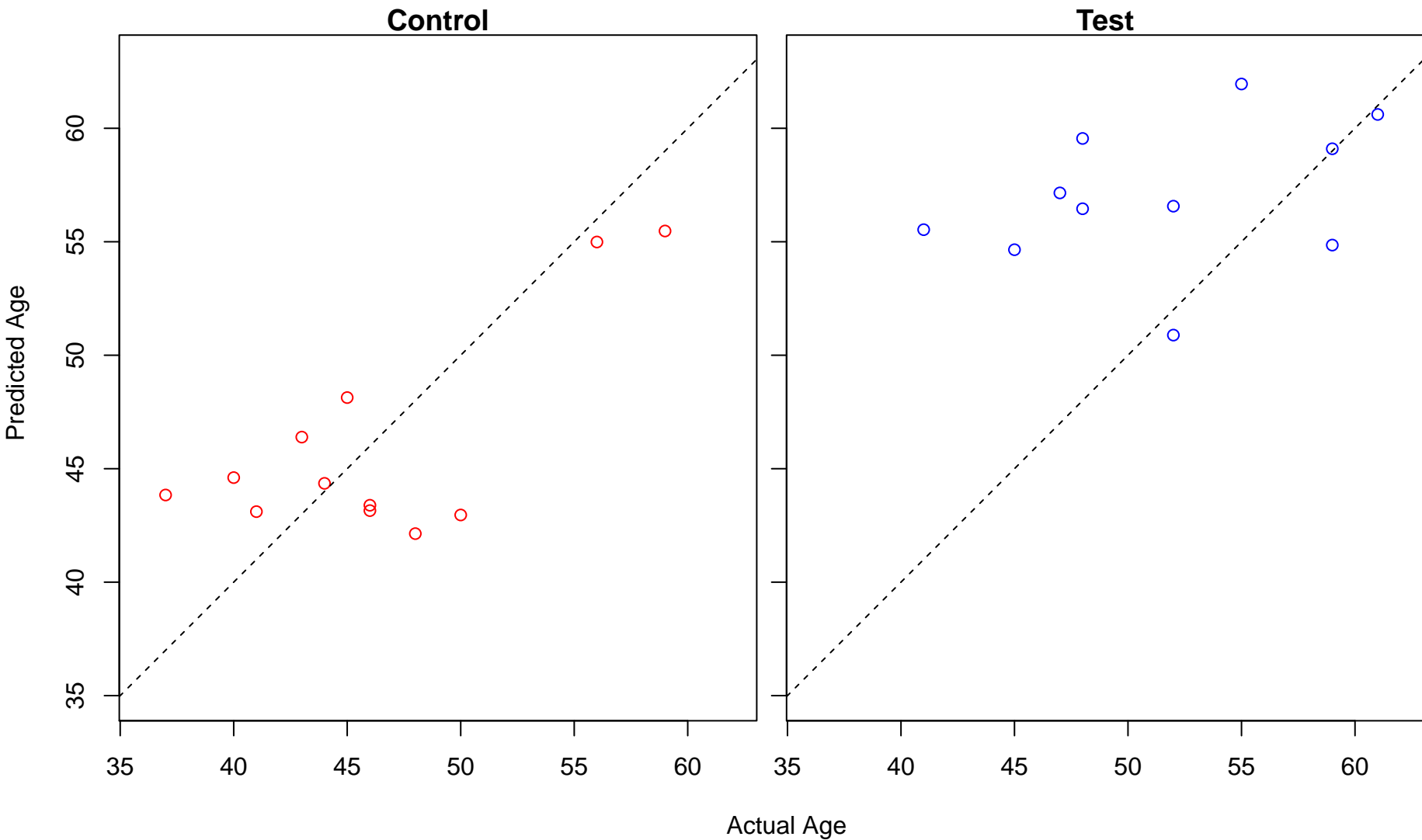
cochlea morphogenesis (Score: 2.829973)



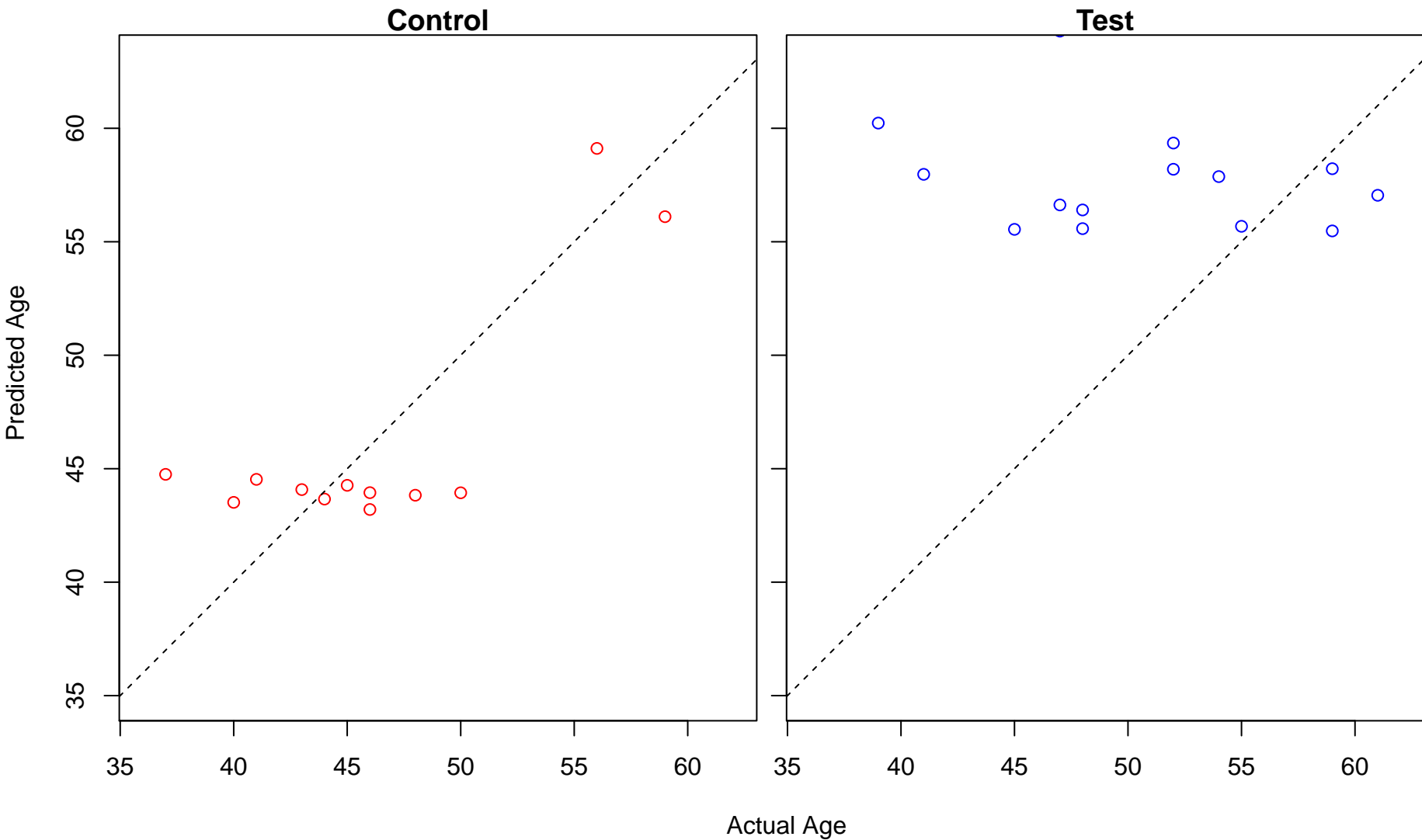
mRNA 3'-end processing by stem-loop binding and cleavage (Score: 2.826930)



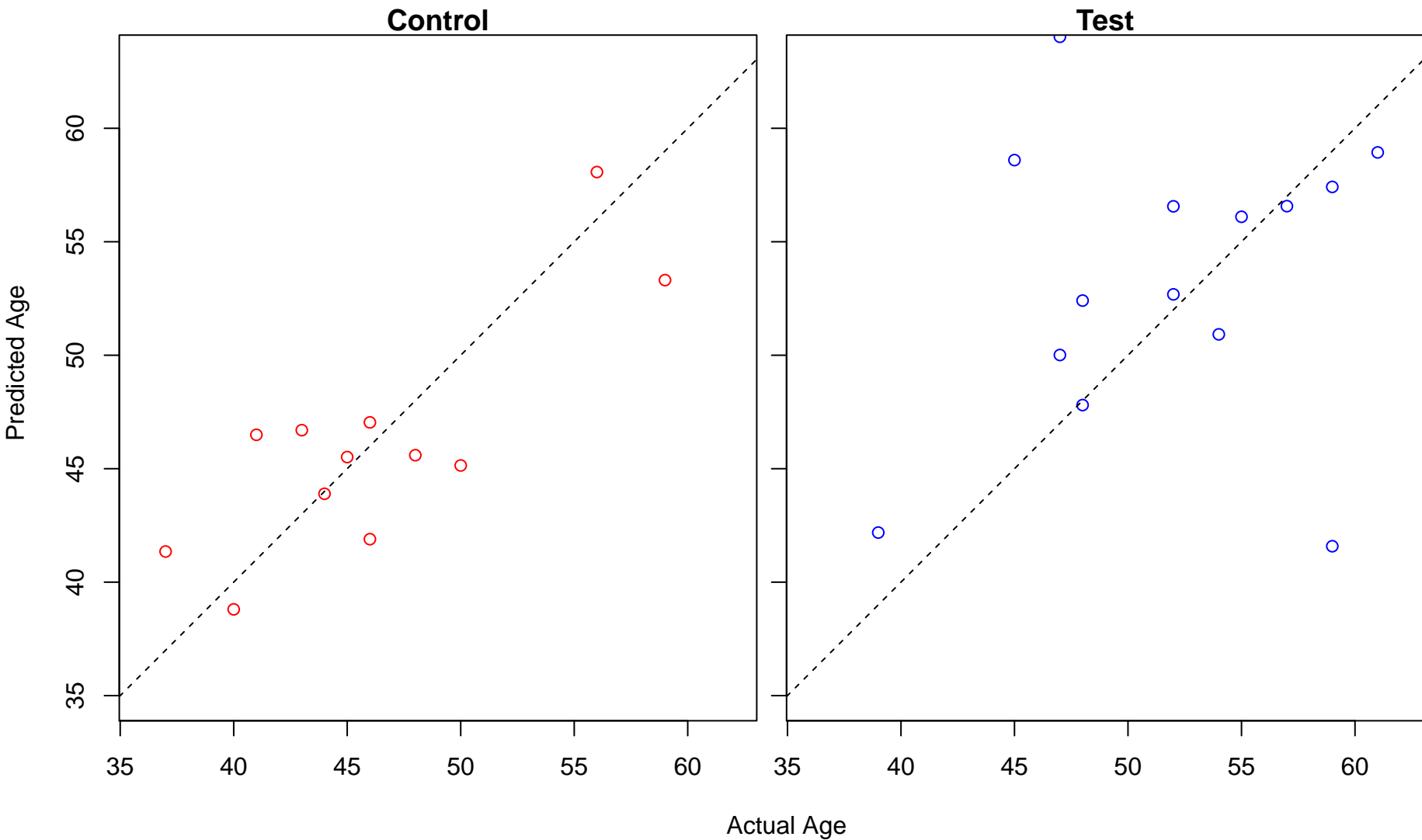
cellular response to toxic substance (Score: 2.823726)



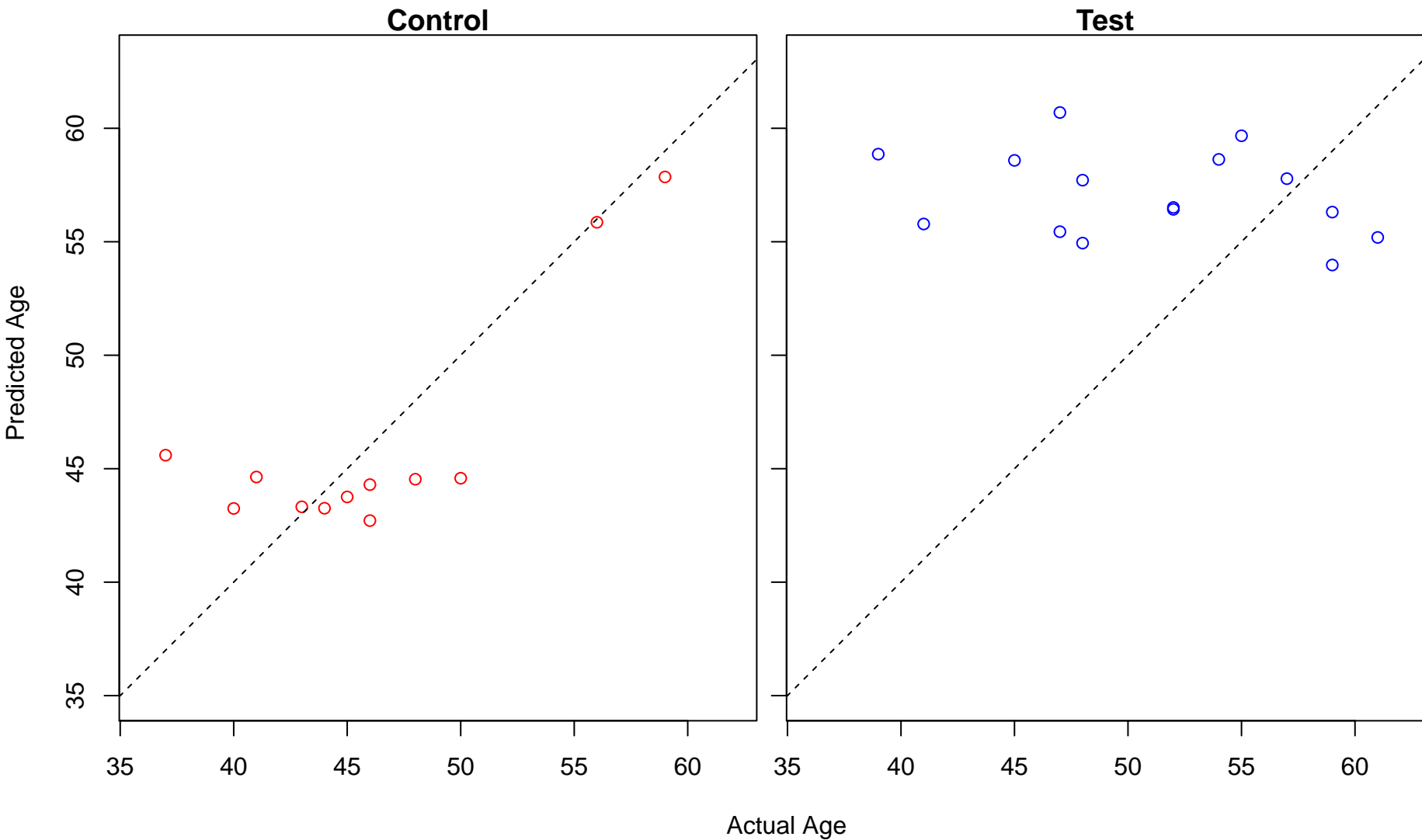
regulation of cellular catabolic process (Score: 2.823446)



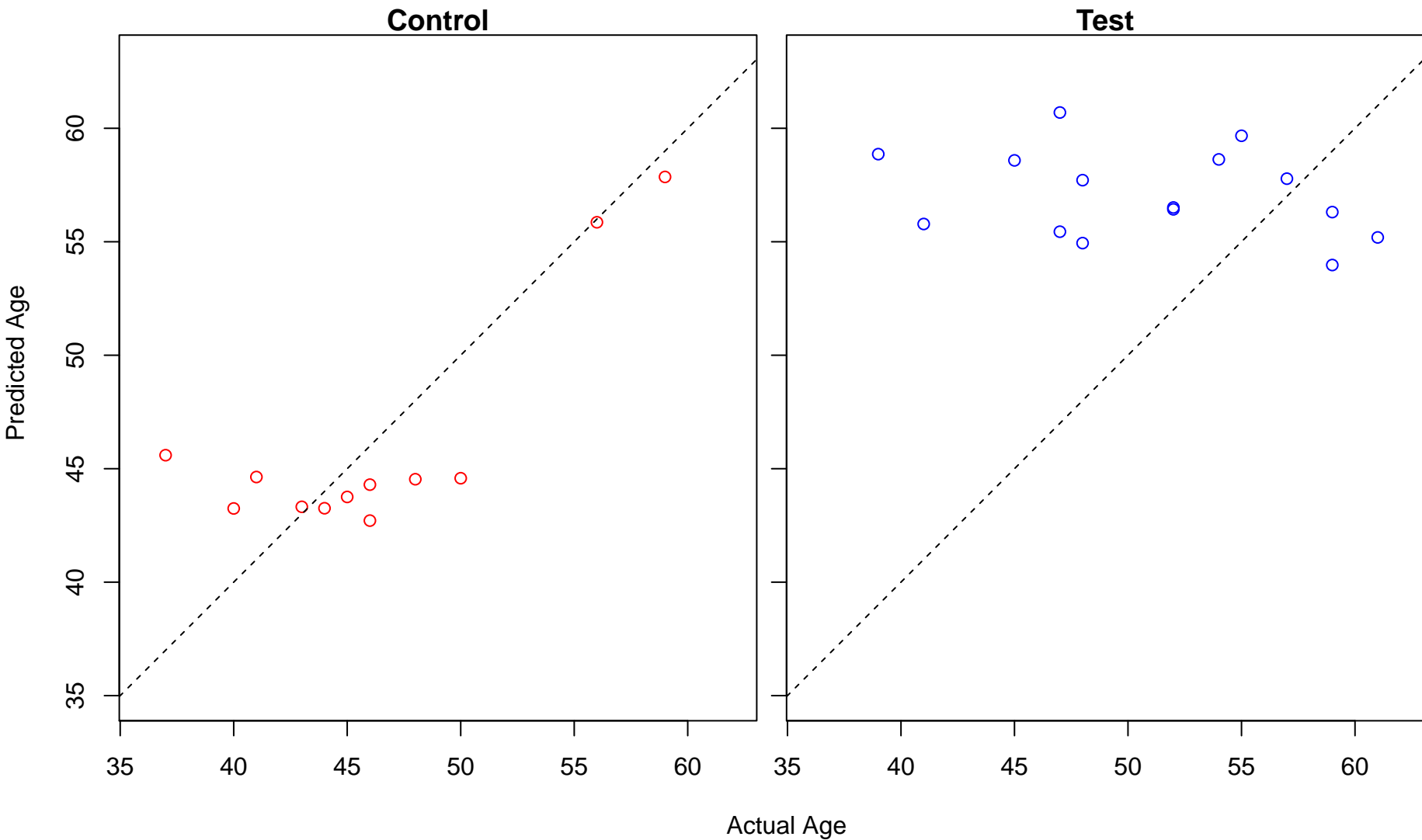
negative regulation of immune system process (Score: 2.817279)



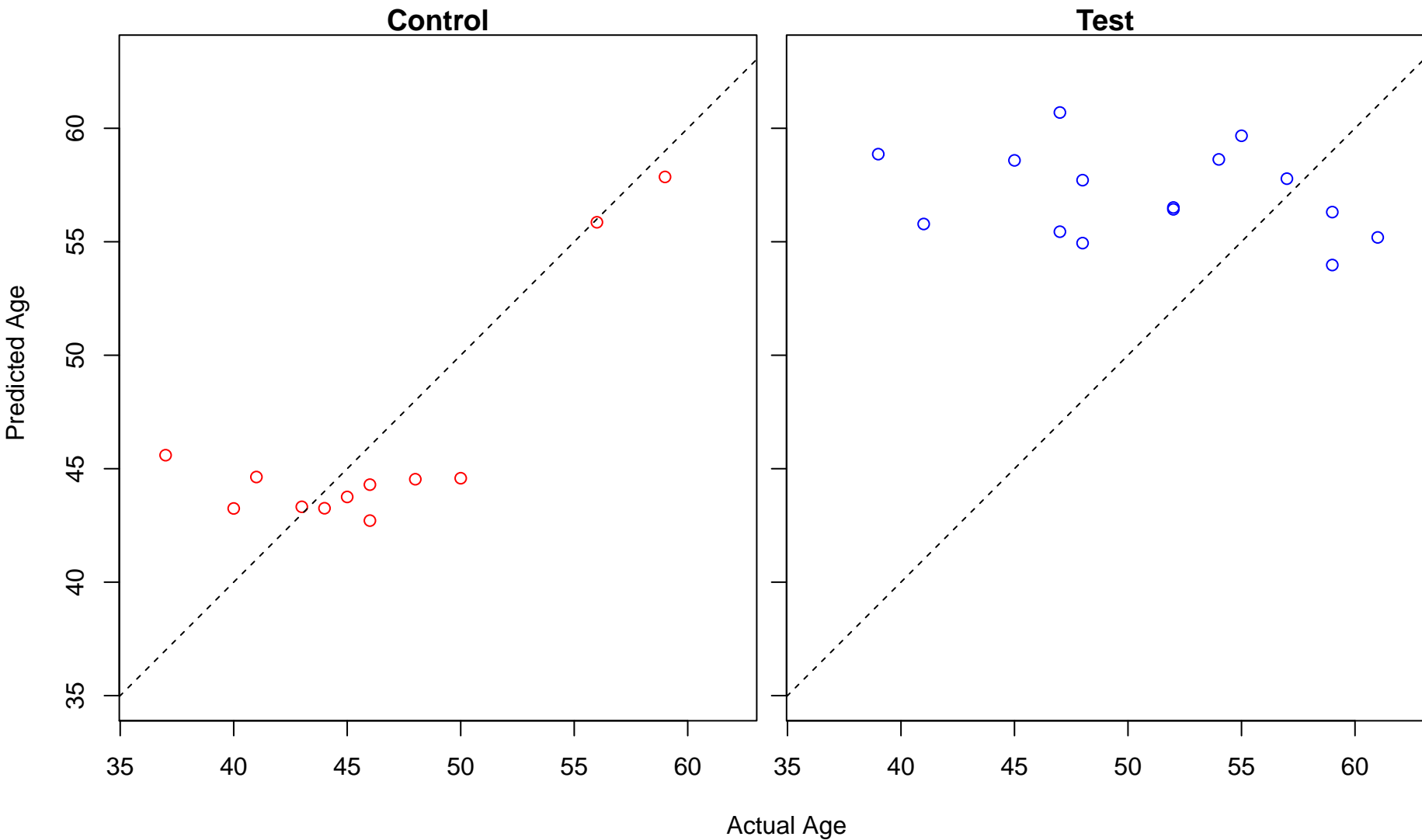
response to inactivity (Score: 2.816390)



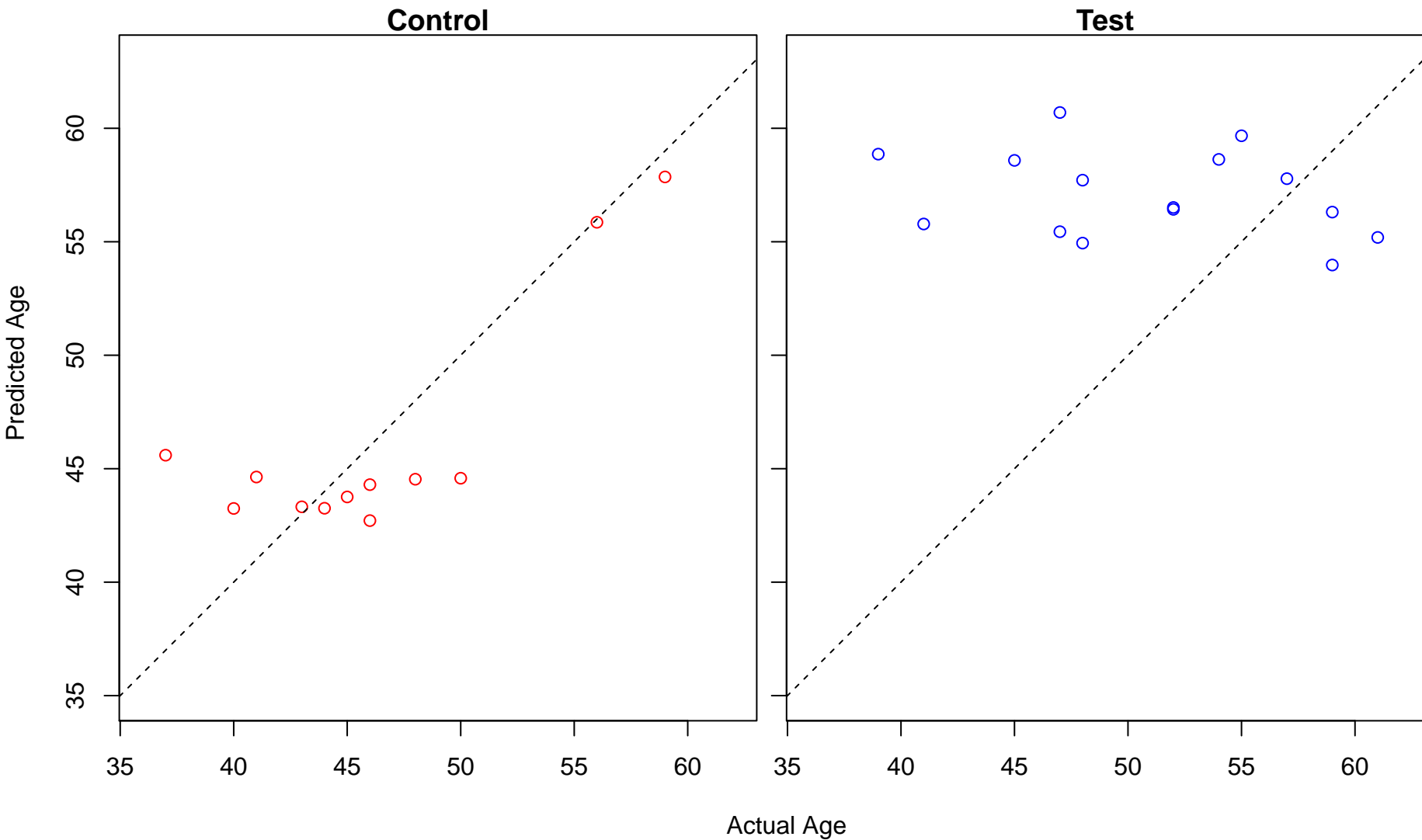
response to muscle inactivity (Score: 2.816390)



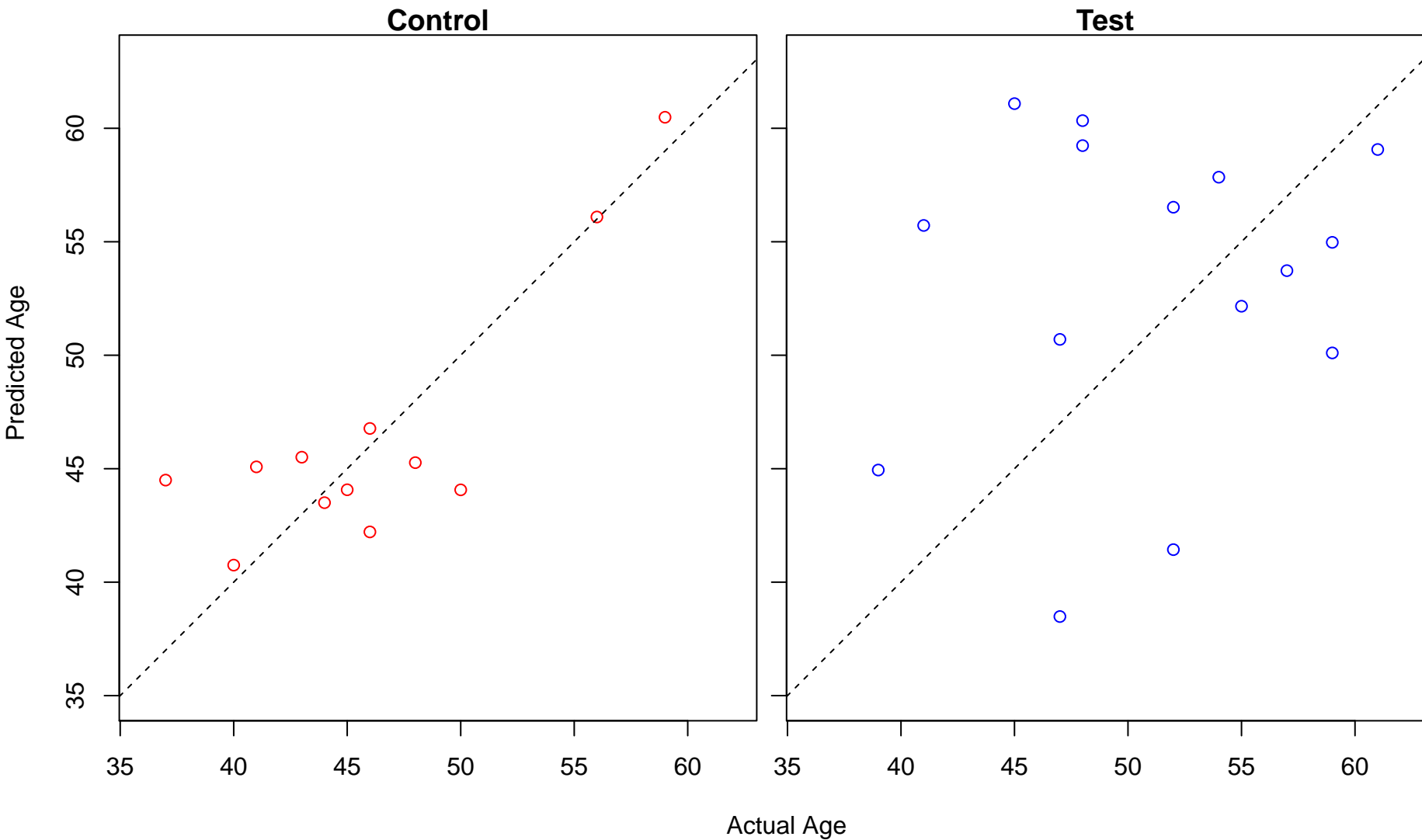
response to muscle inactivity involved in regulation of muscle adaptation (Score: 2.816390)



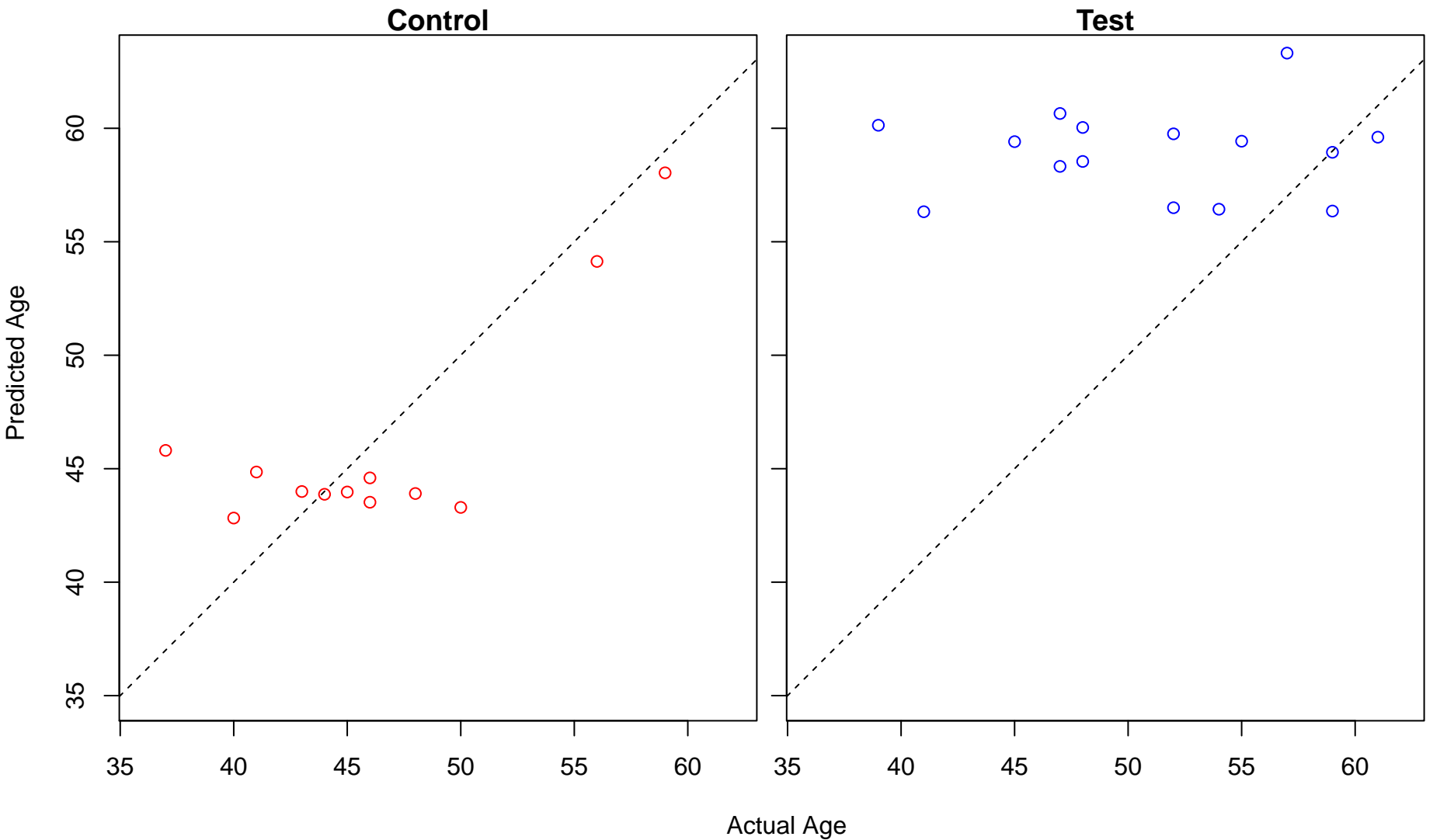
response to denervation involved in regulation of muscle adaptation (Score: 2.816390)



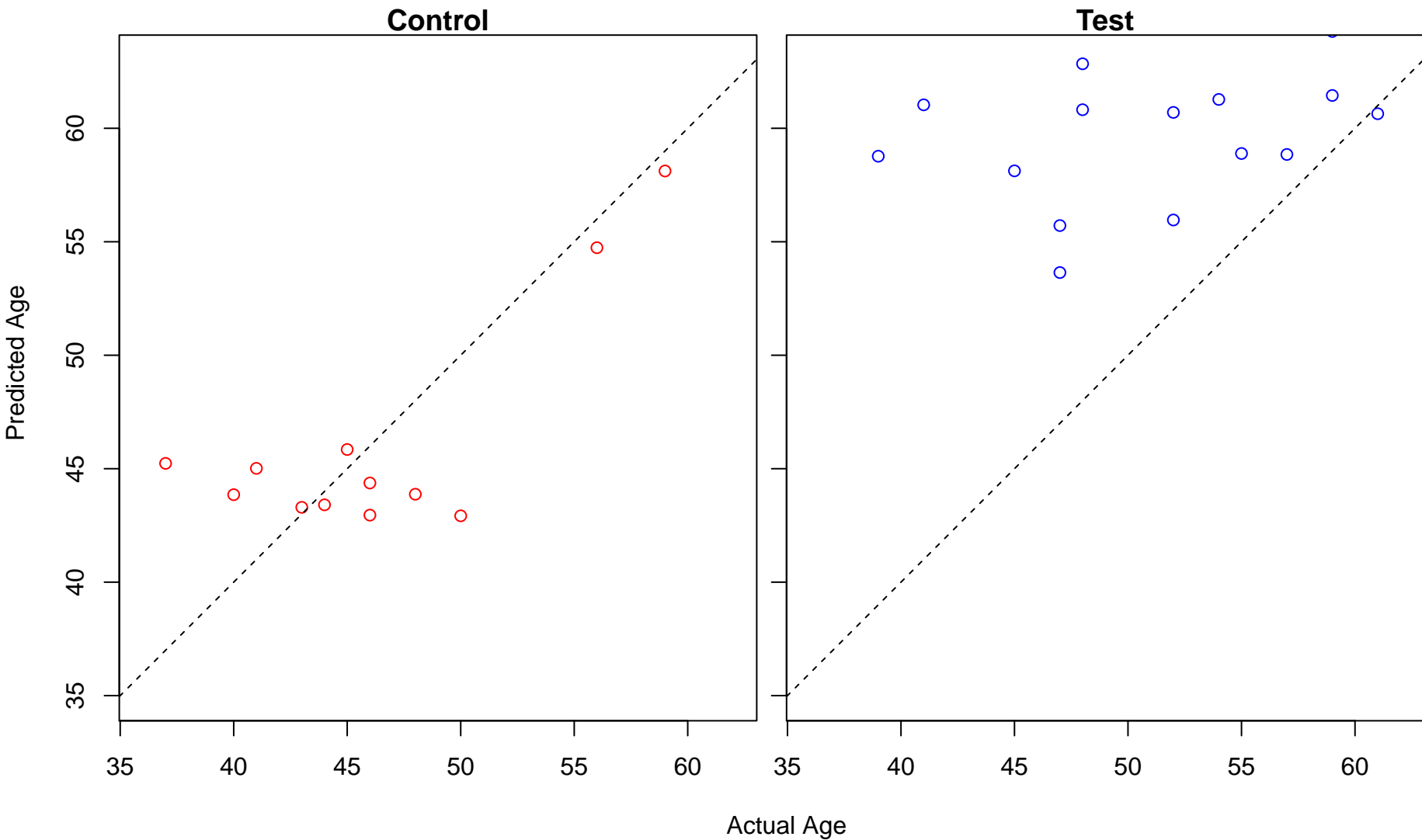
regulation of delayed rectifier potassium channel activity (Score: 2.815049)



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

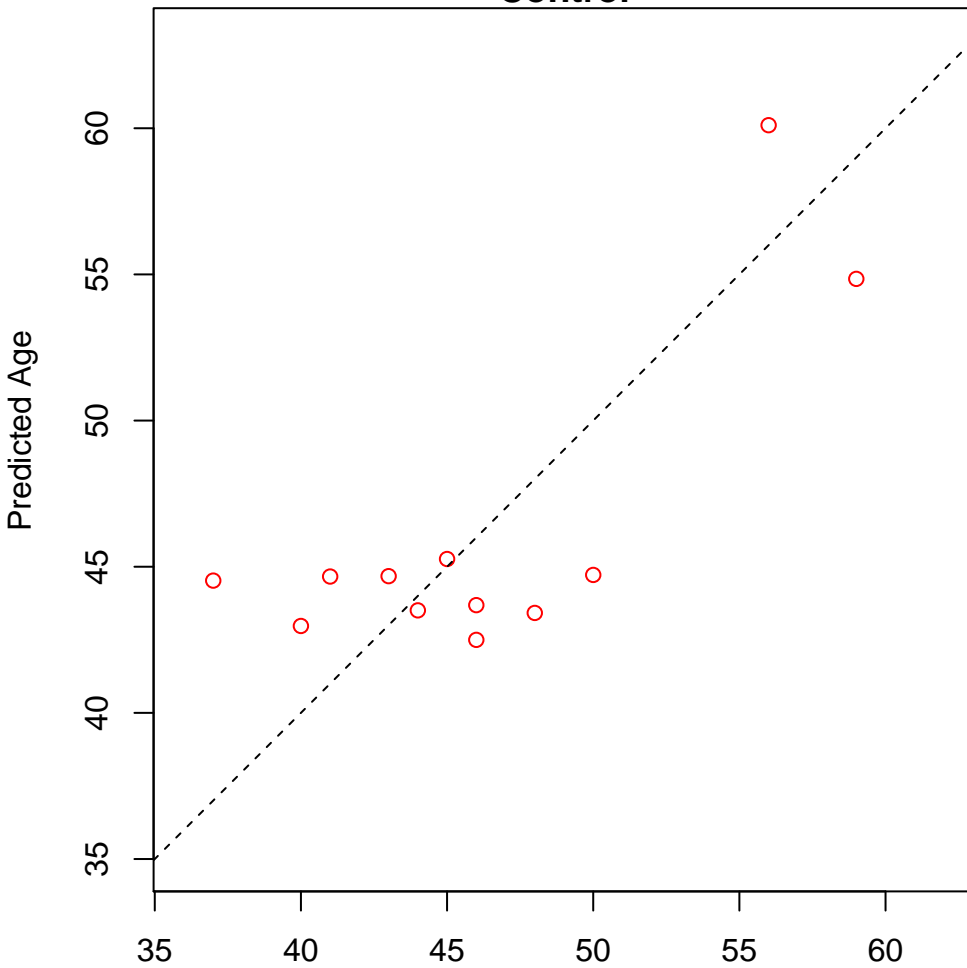


negative regulation of voltage-gated calcium channel activity (Score: 2.814312)

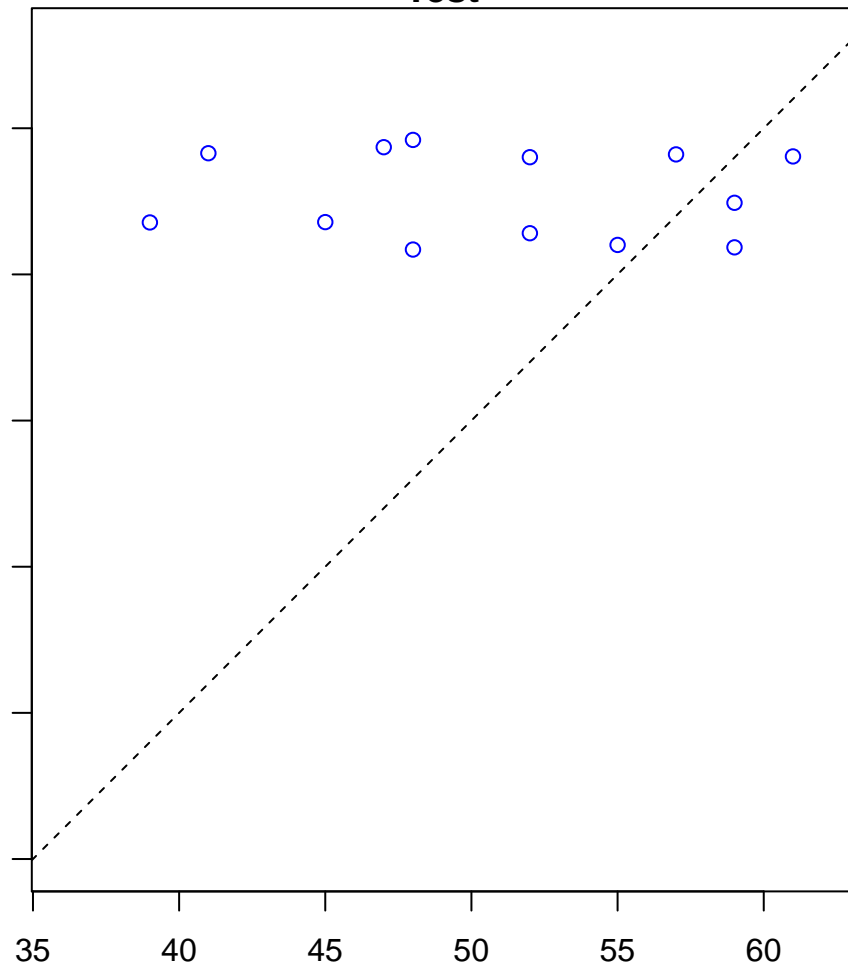


morphogenesis of embryonic epithelium (Score: 2.814250)

Control

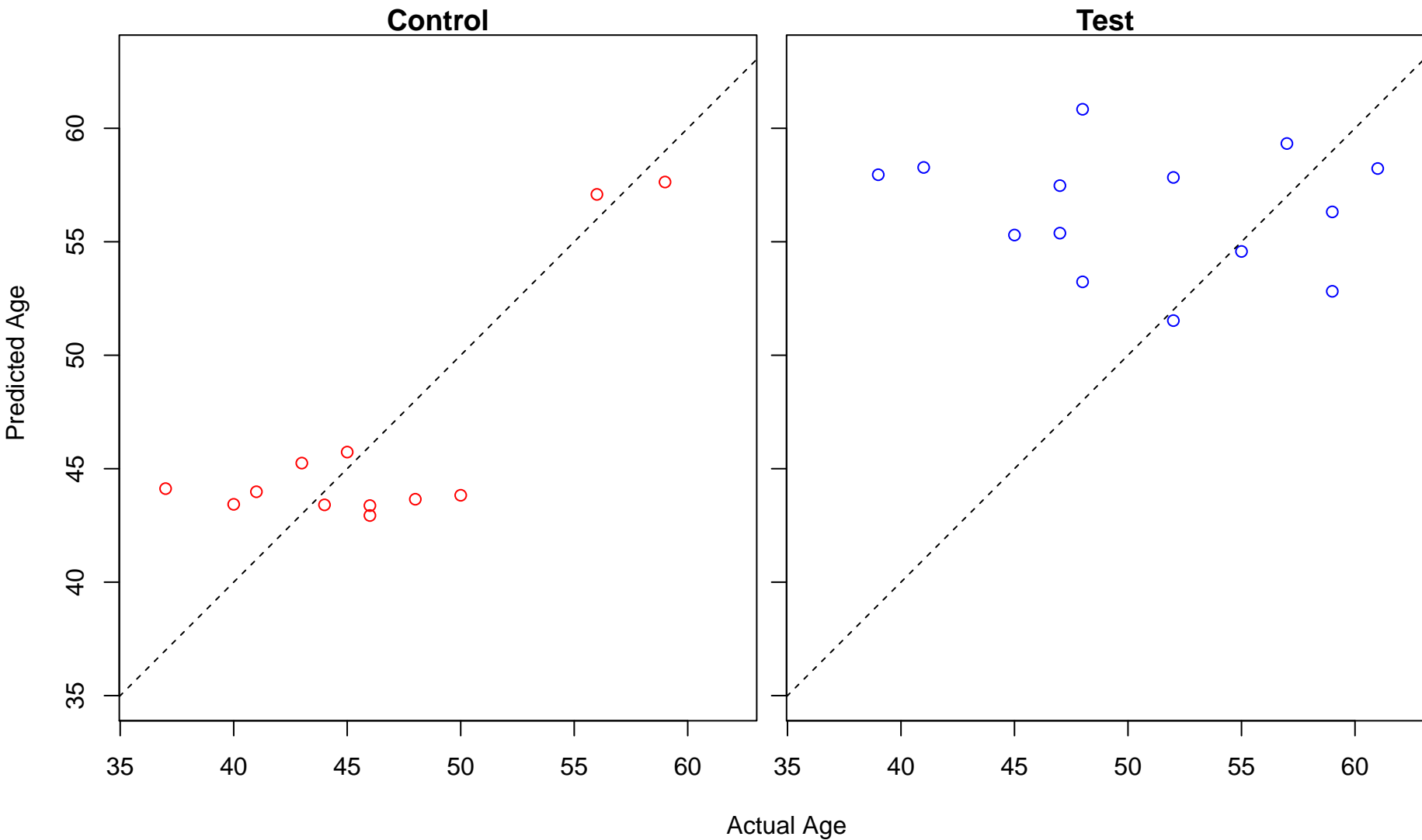


Test

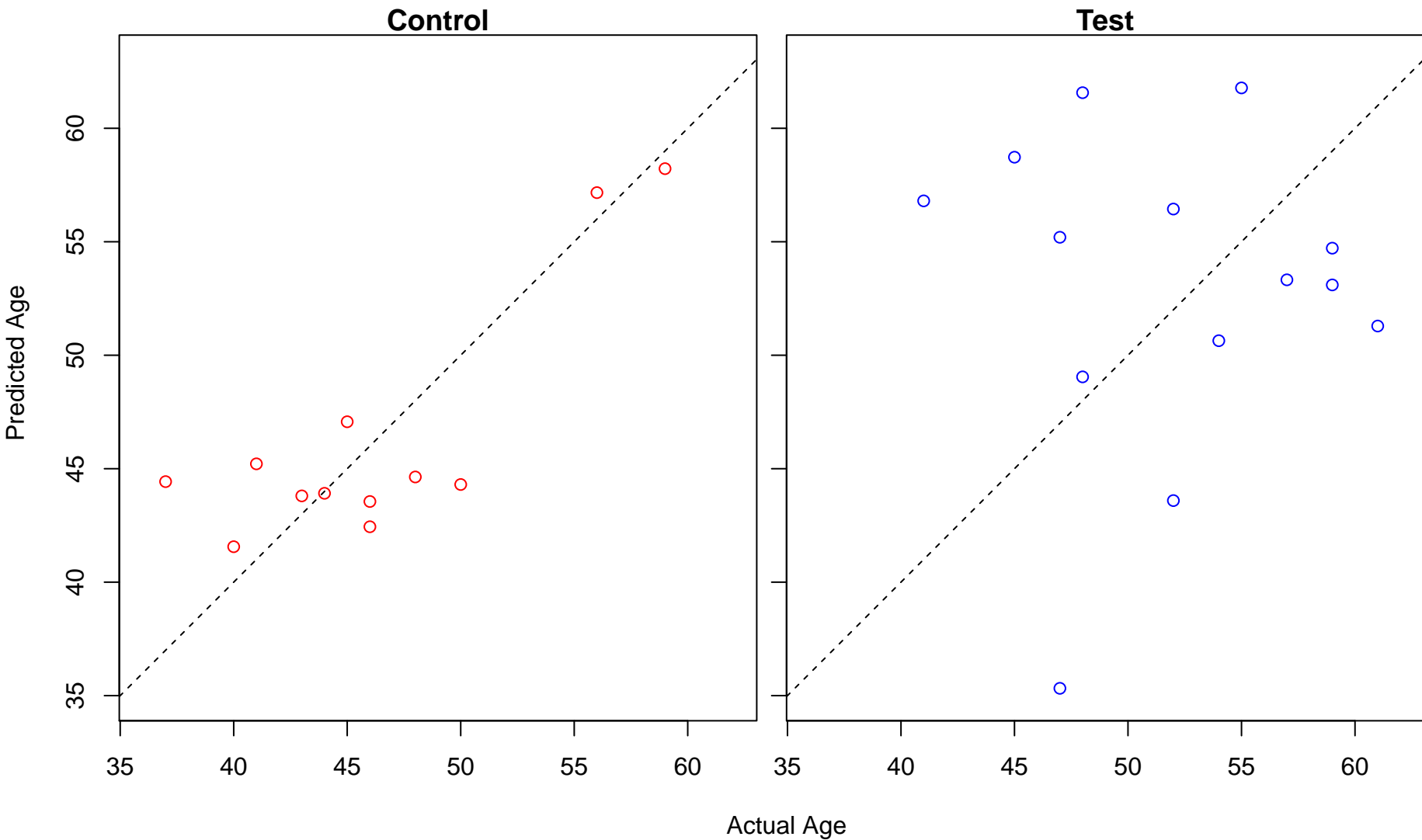


Actual Age

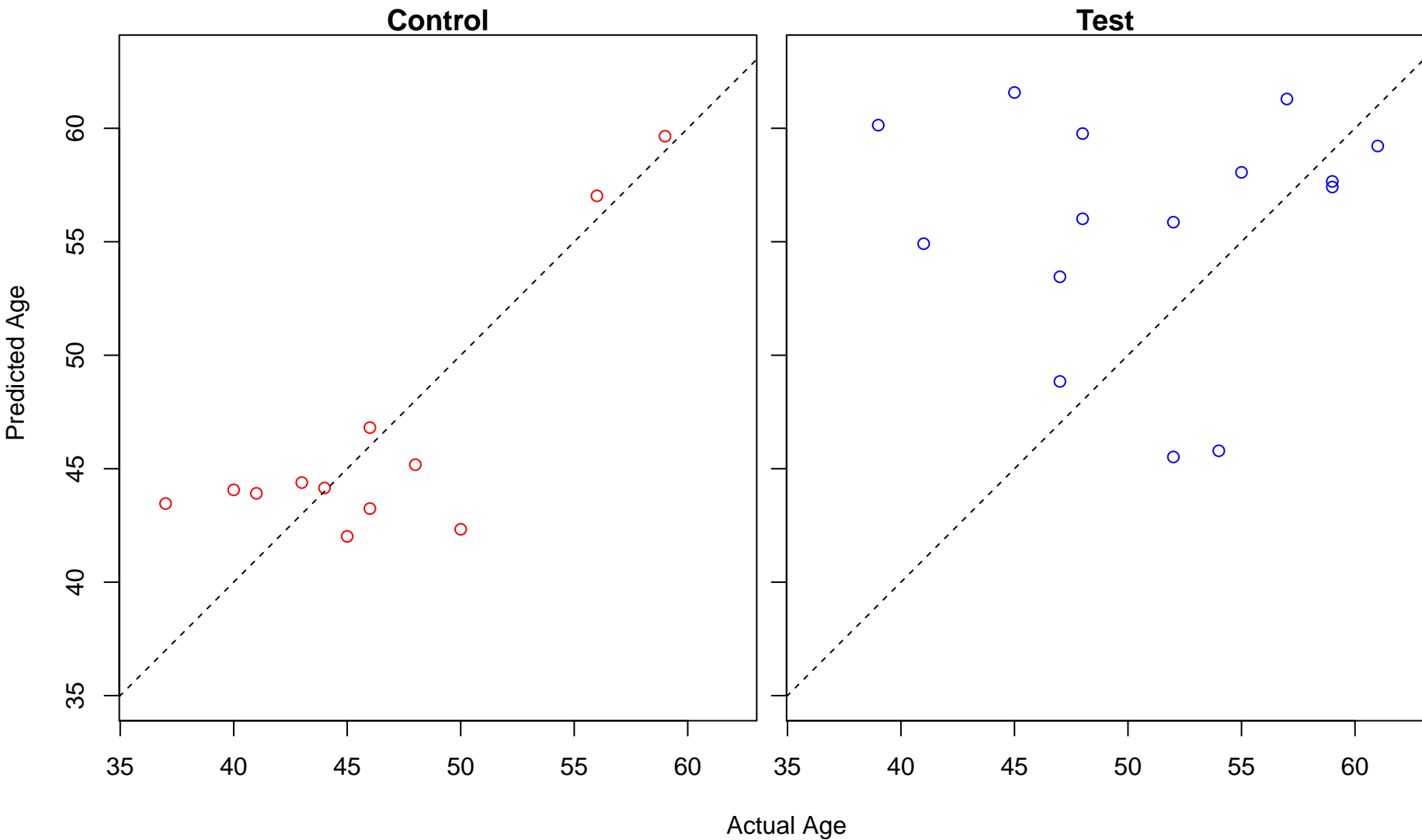
phenol-containing compound metabolic process (Score: 2.809209)



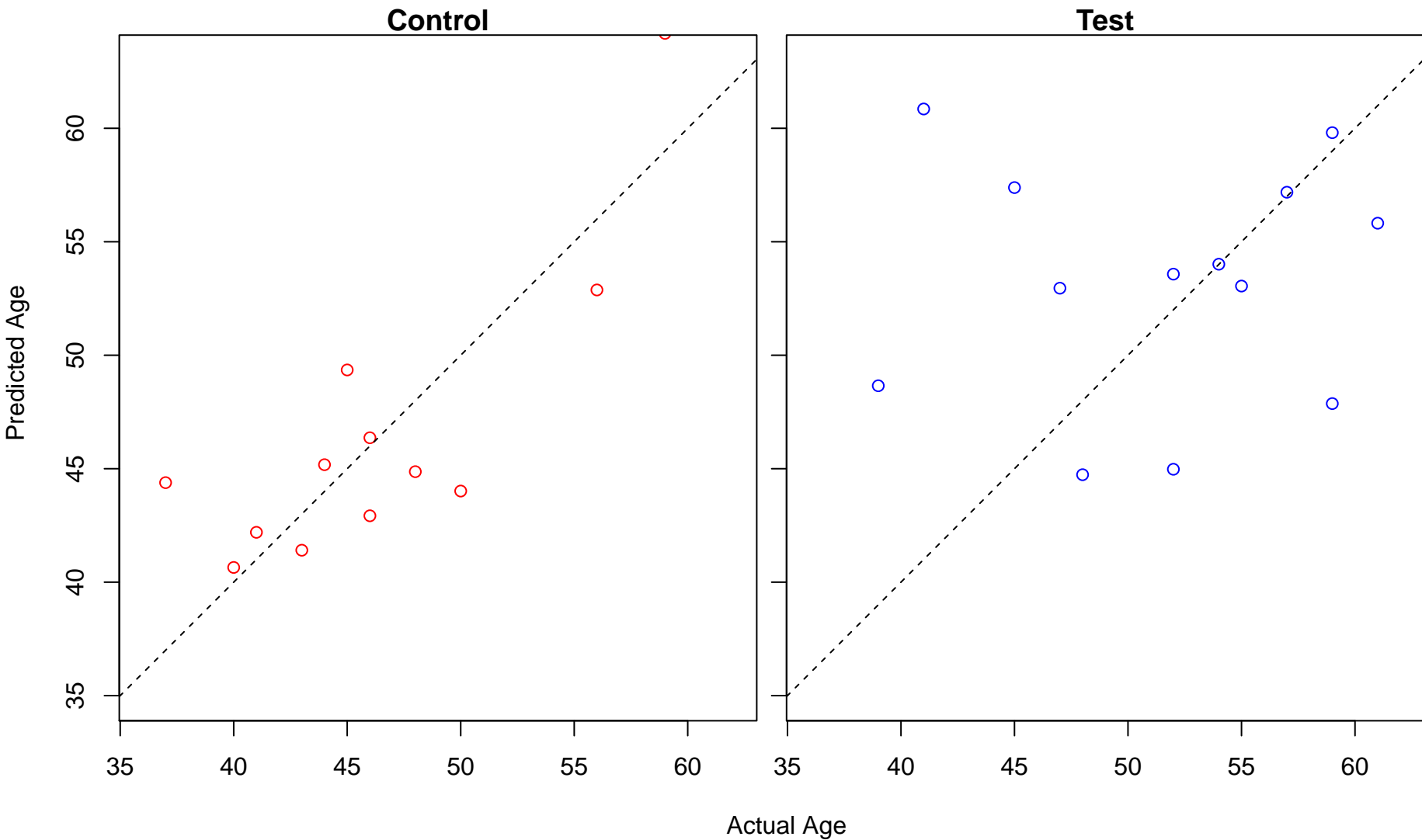
regulation of microtubule polymerization or depolymerization (Score: 2.806411)



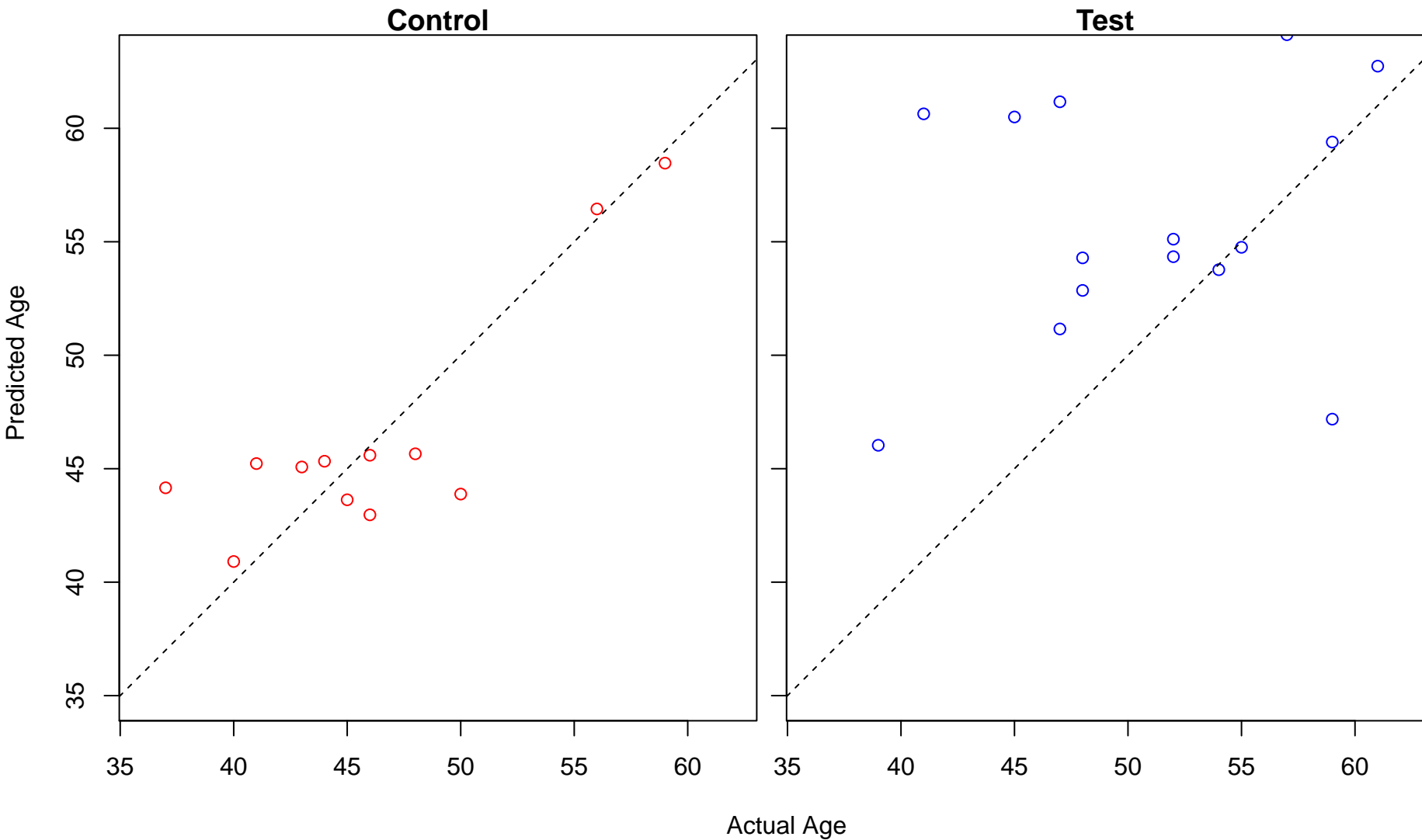
Schwann cell differentiation (Score: 2.806313)



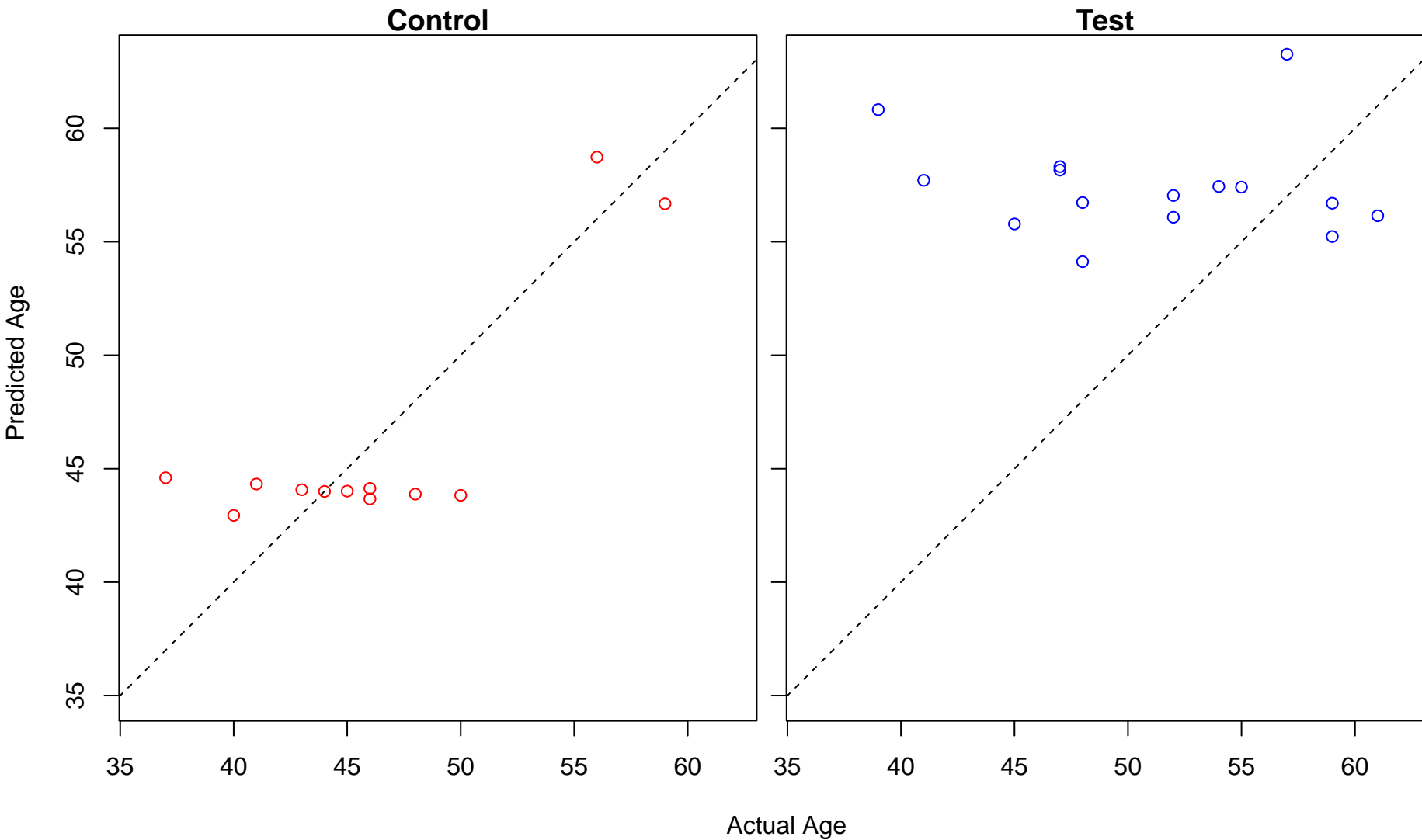
gland development (Score: 2.804199)



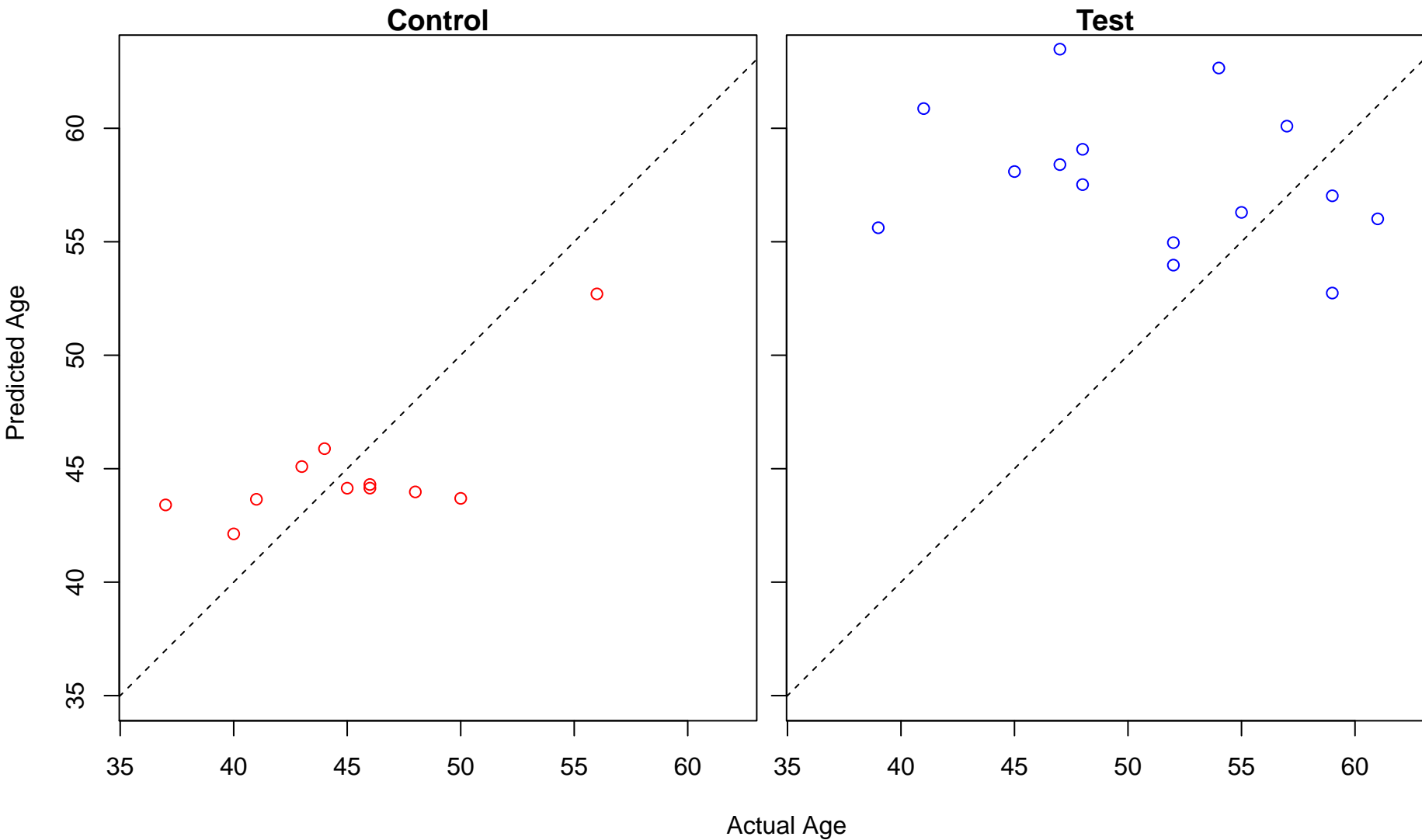
positive regulation of cytokine production (Score: 2.803186)



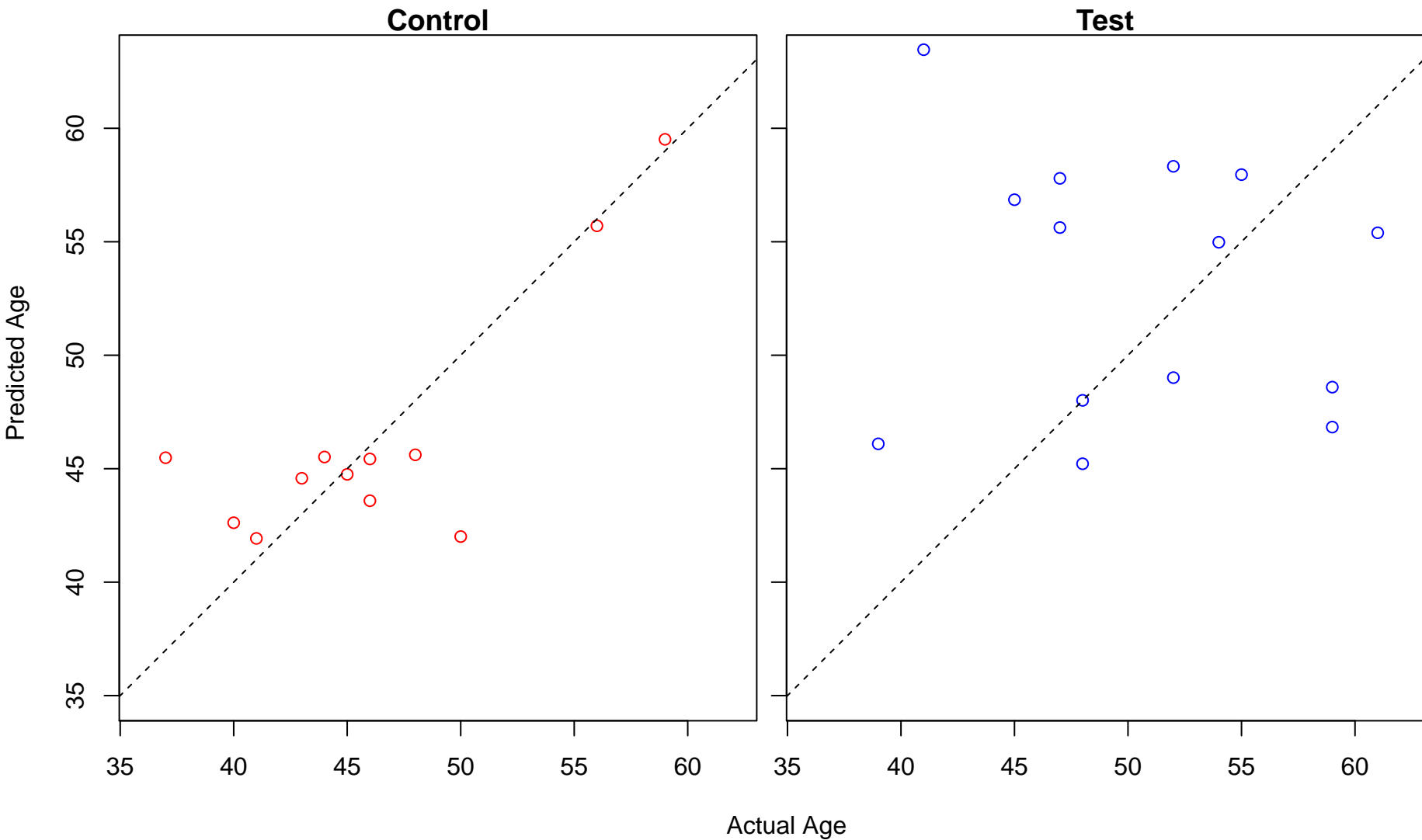
cellular response to abiotic stimulus (Score: 2.799979)



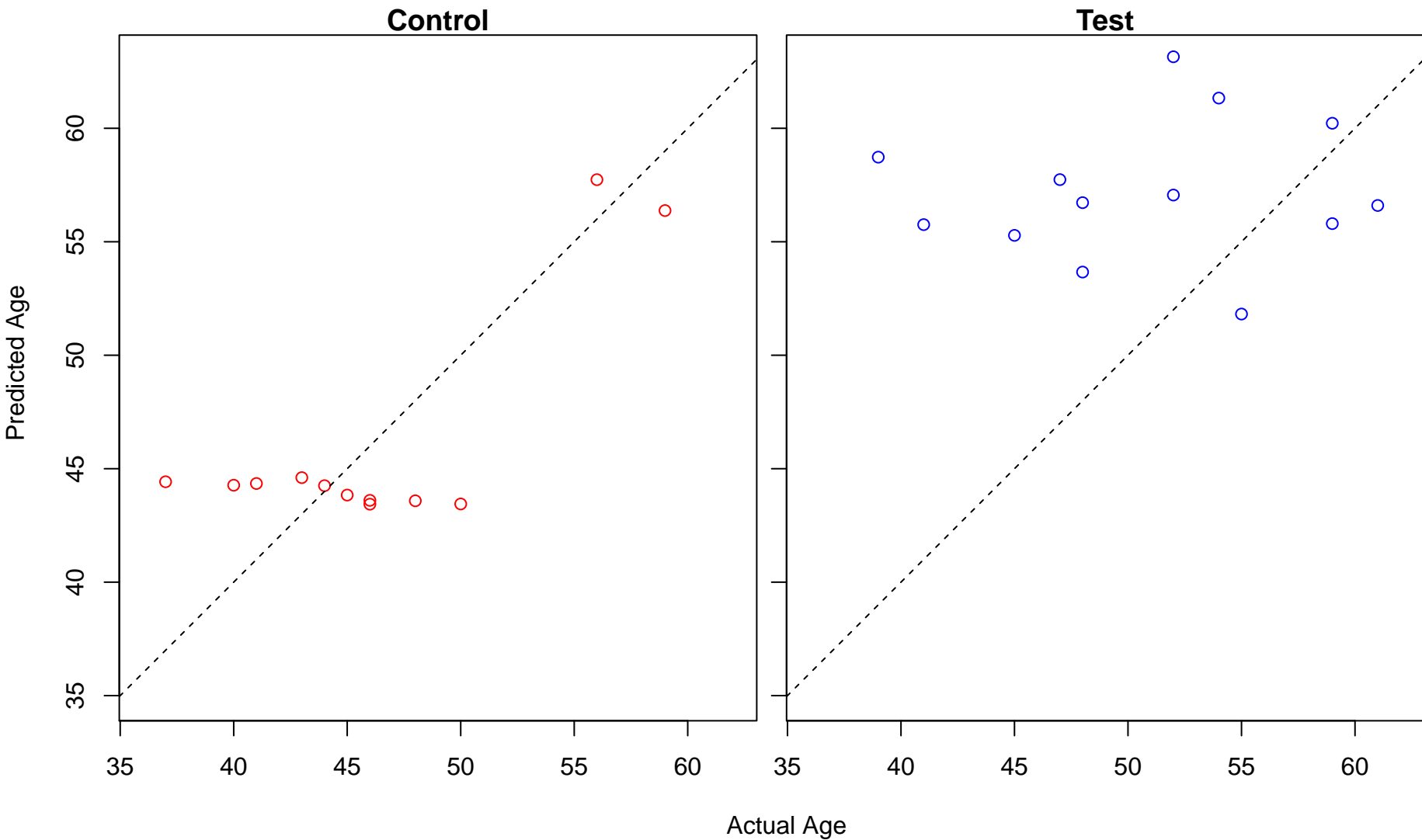
cardiac muscle tissue growth (Score: 2.799437)



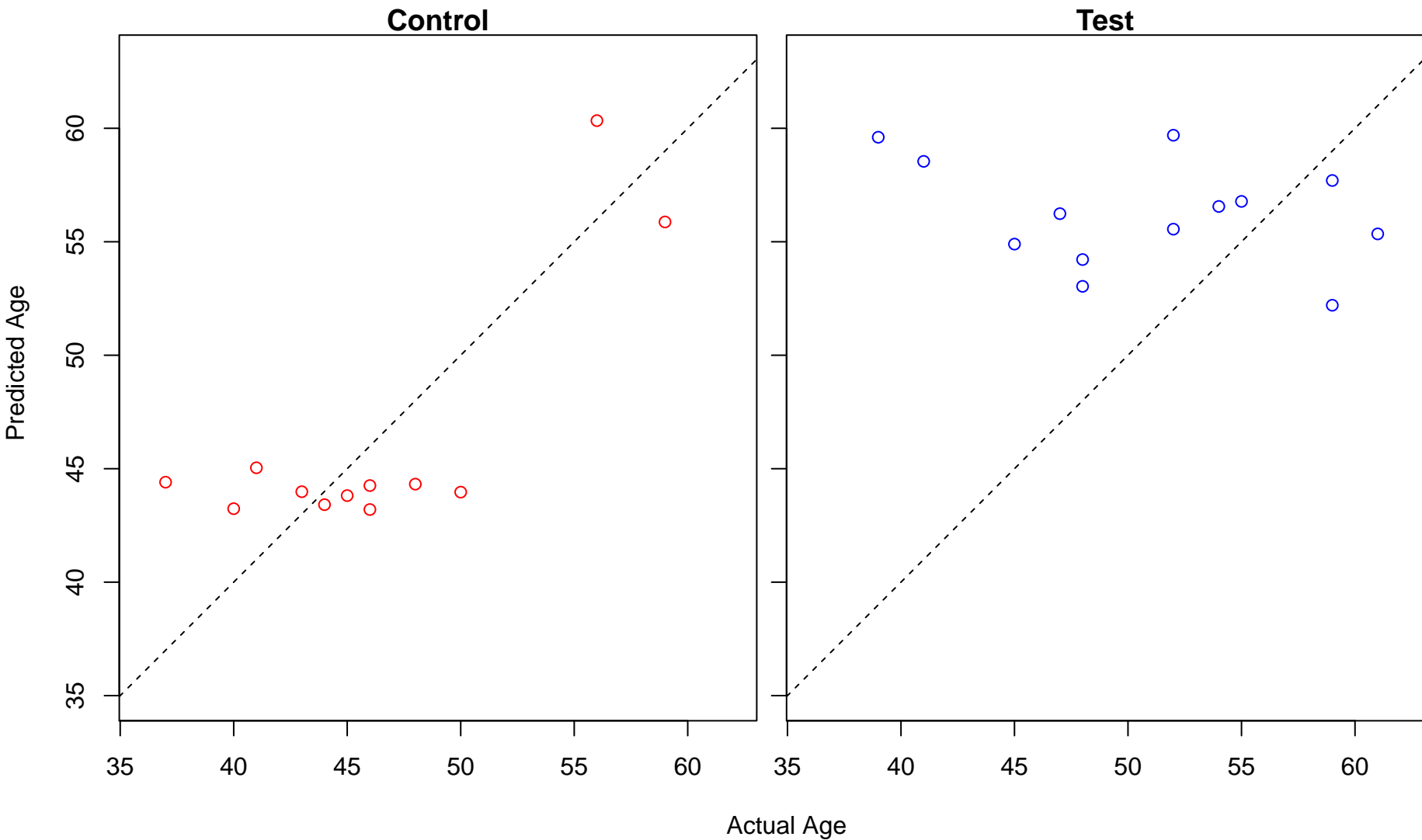
positive regulation of endocytosis (Score: 2.798962)



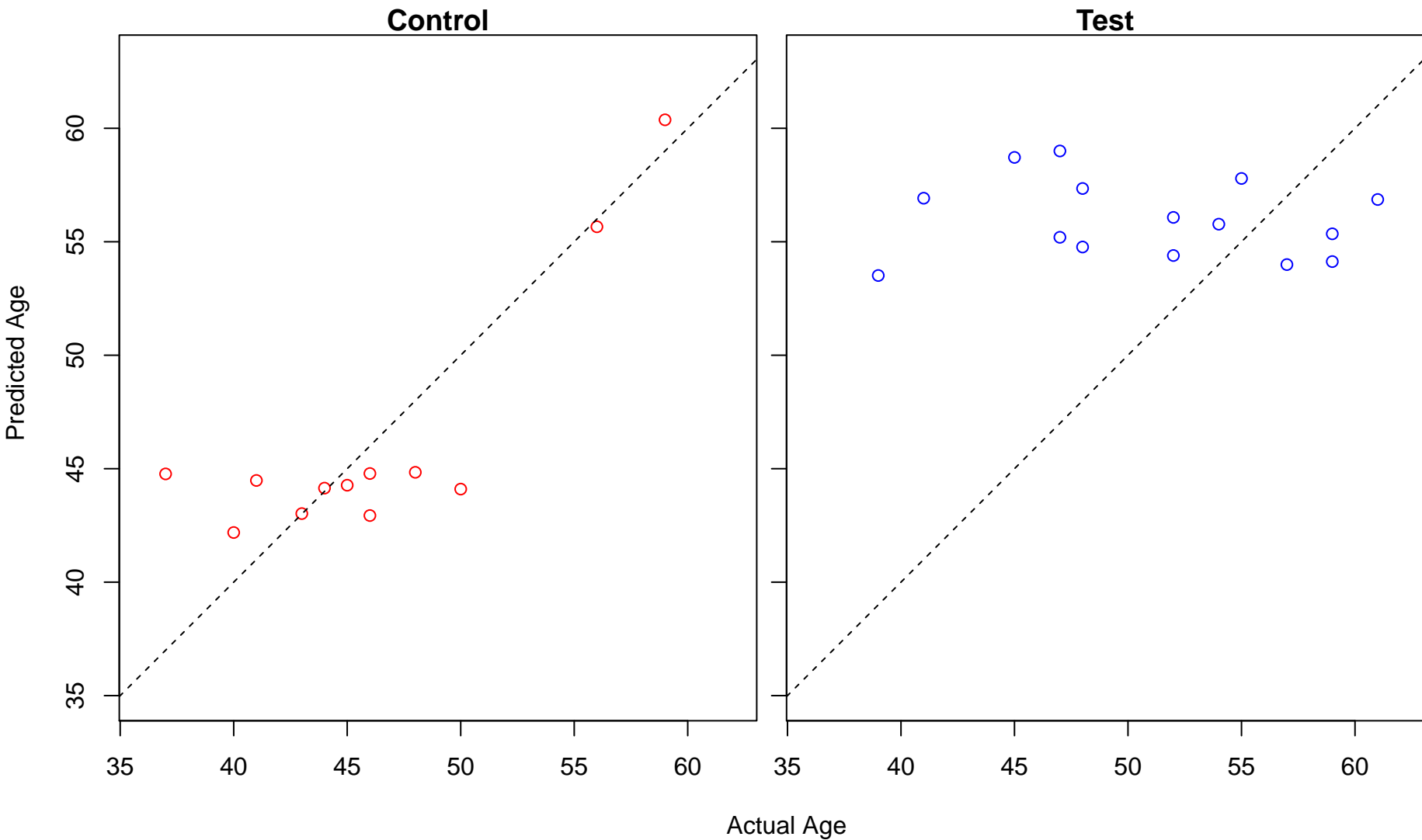
negative regulation of protein acetylation (Score: 2.796832)



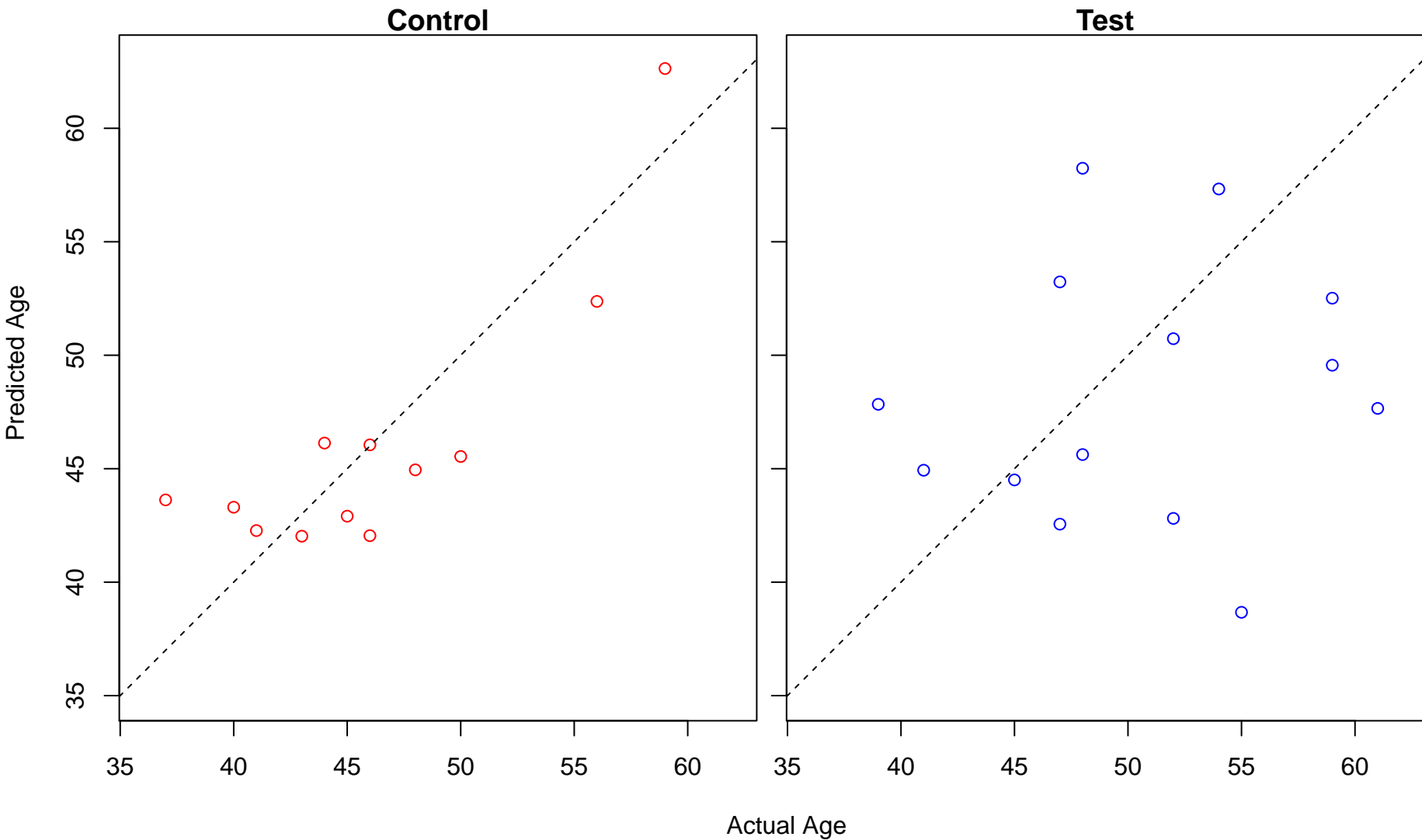
membrane assembly (Score: 2.796591)



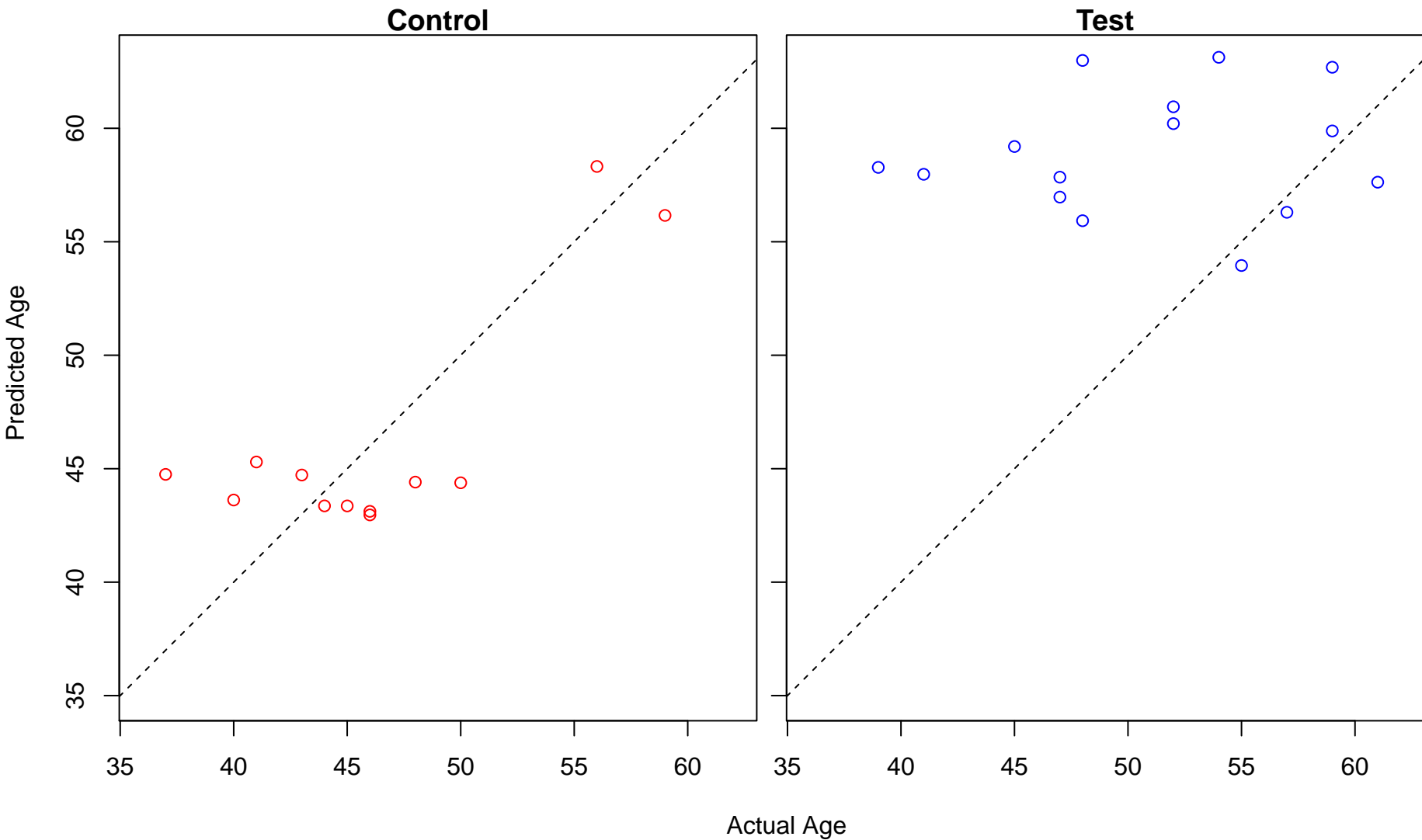
forebrain development (Score: 2.796489)



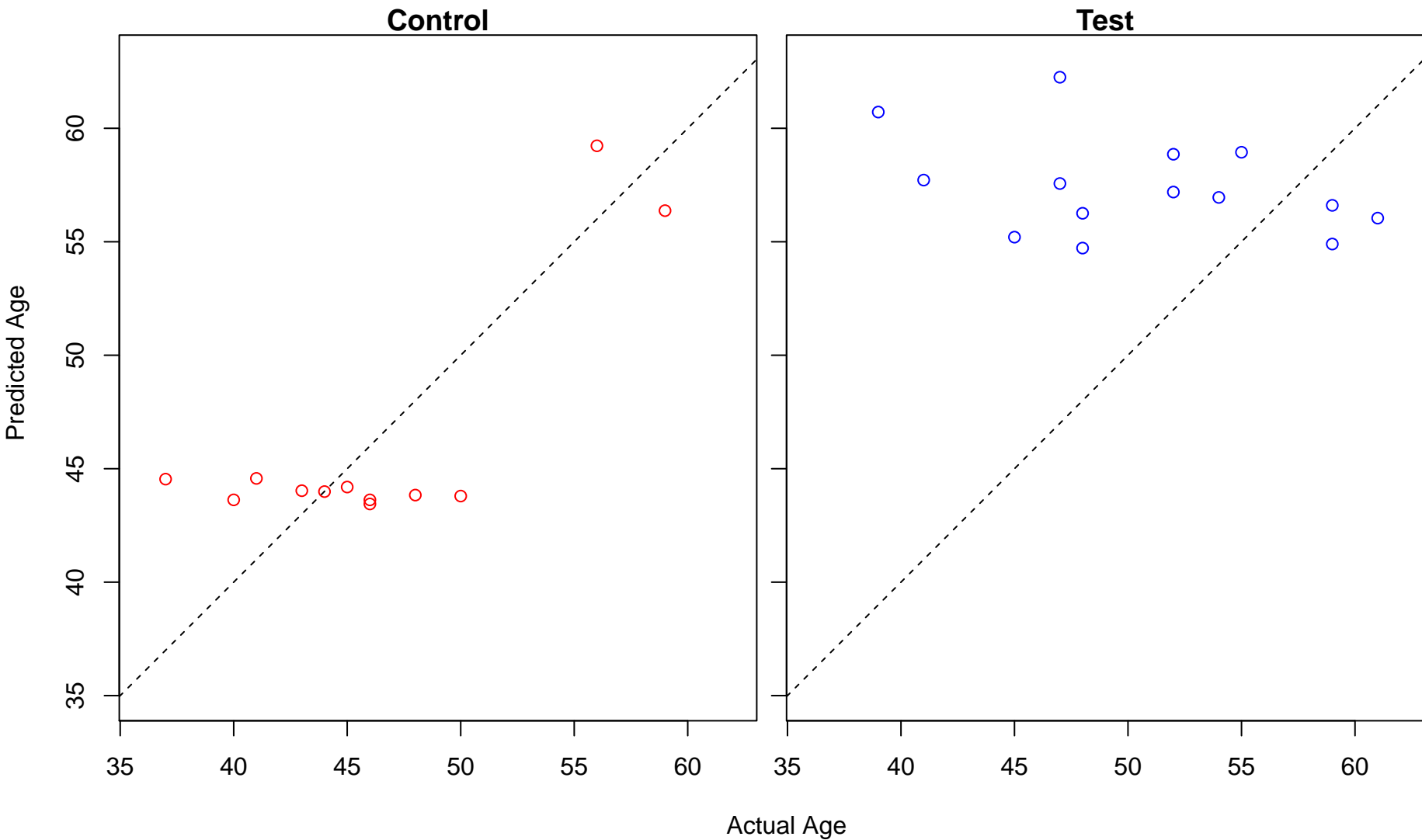
regulation of ATPase activity (Score: 2.795820)



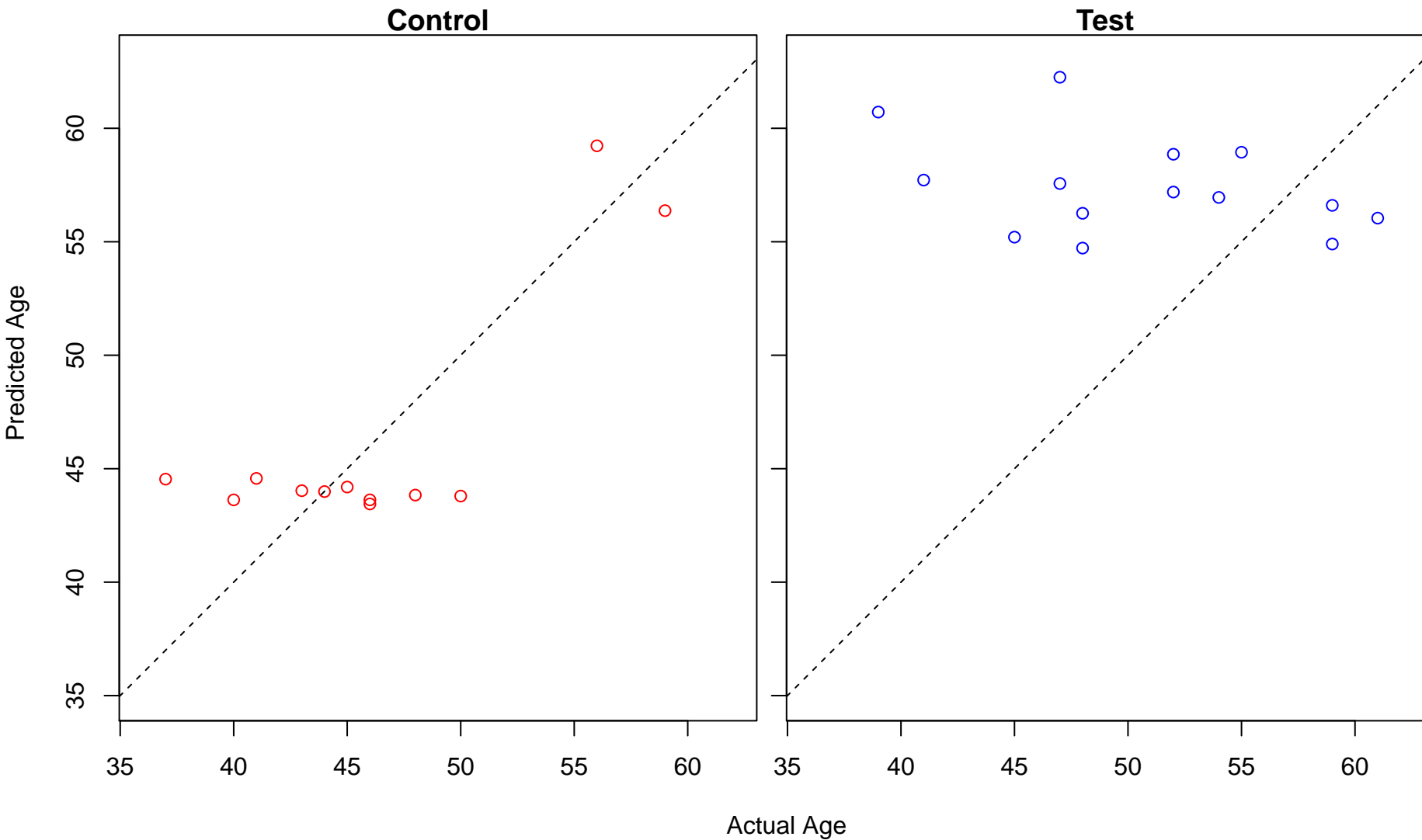
negative regulation of catenin import into nucleus (Score: 2.793880)



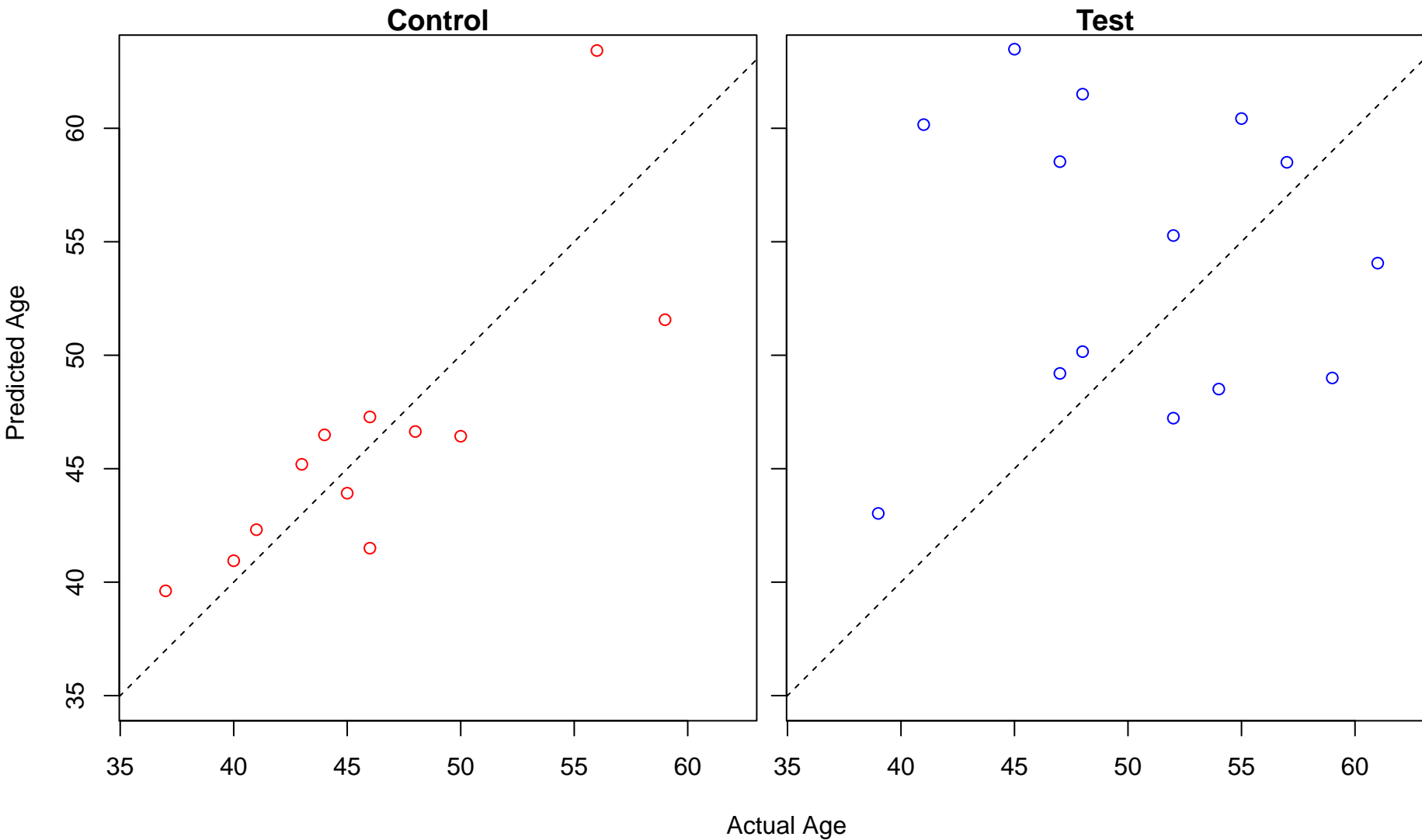
axon guidance (Score: 2.792546)



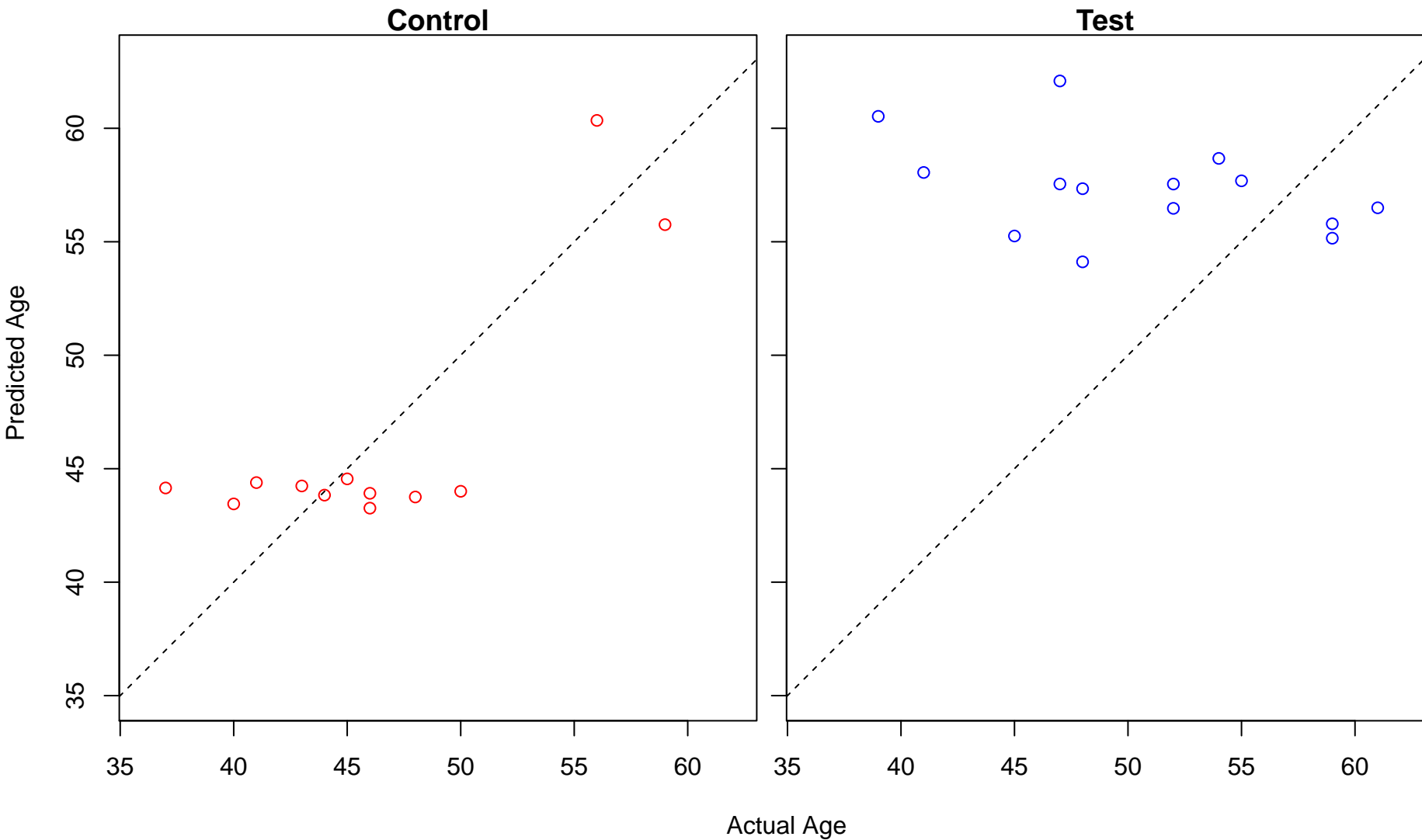
neuron projection guidance (Score: 2.792546)



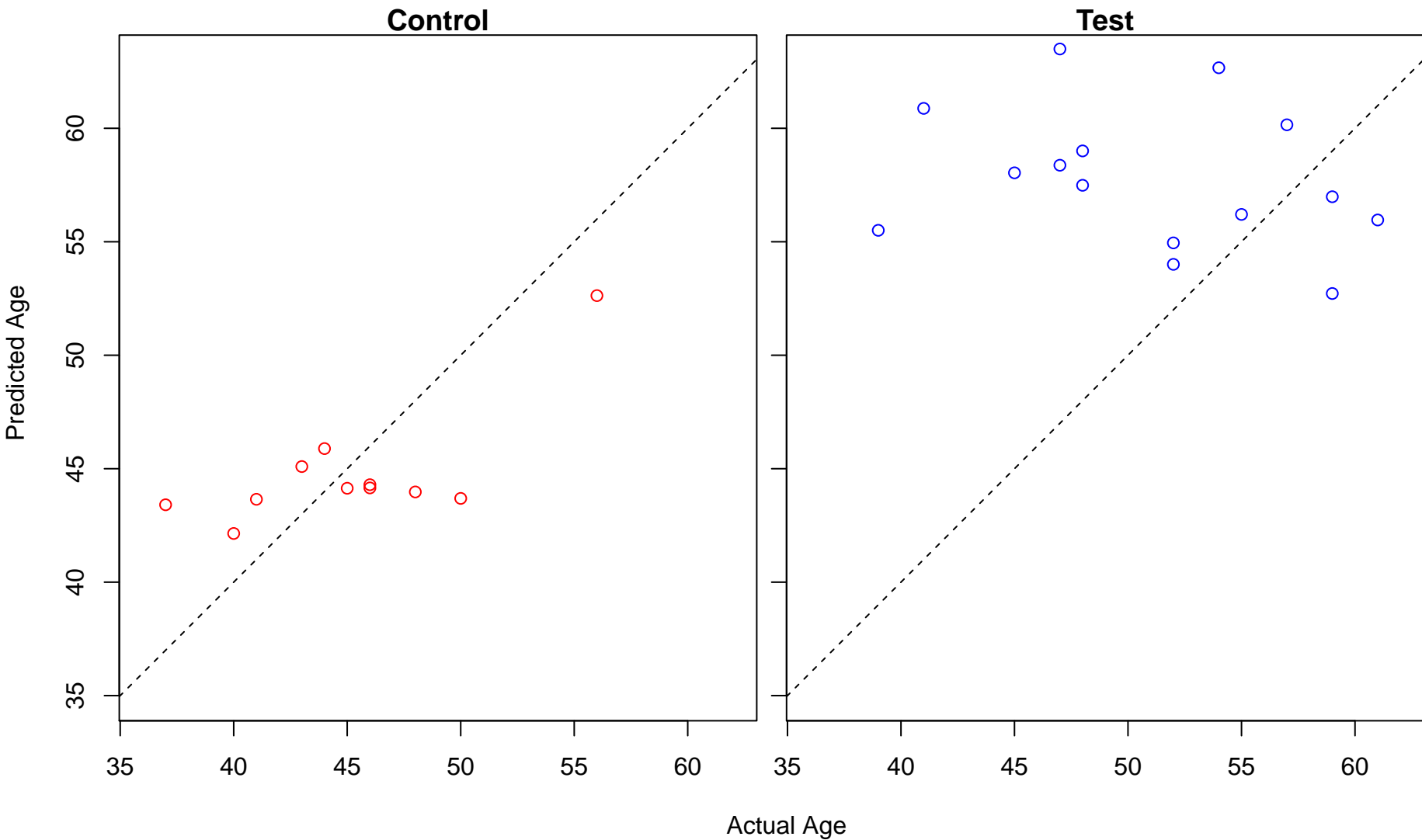
positive regulation of protein complex assembly (Score: 2.791737)



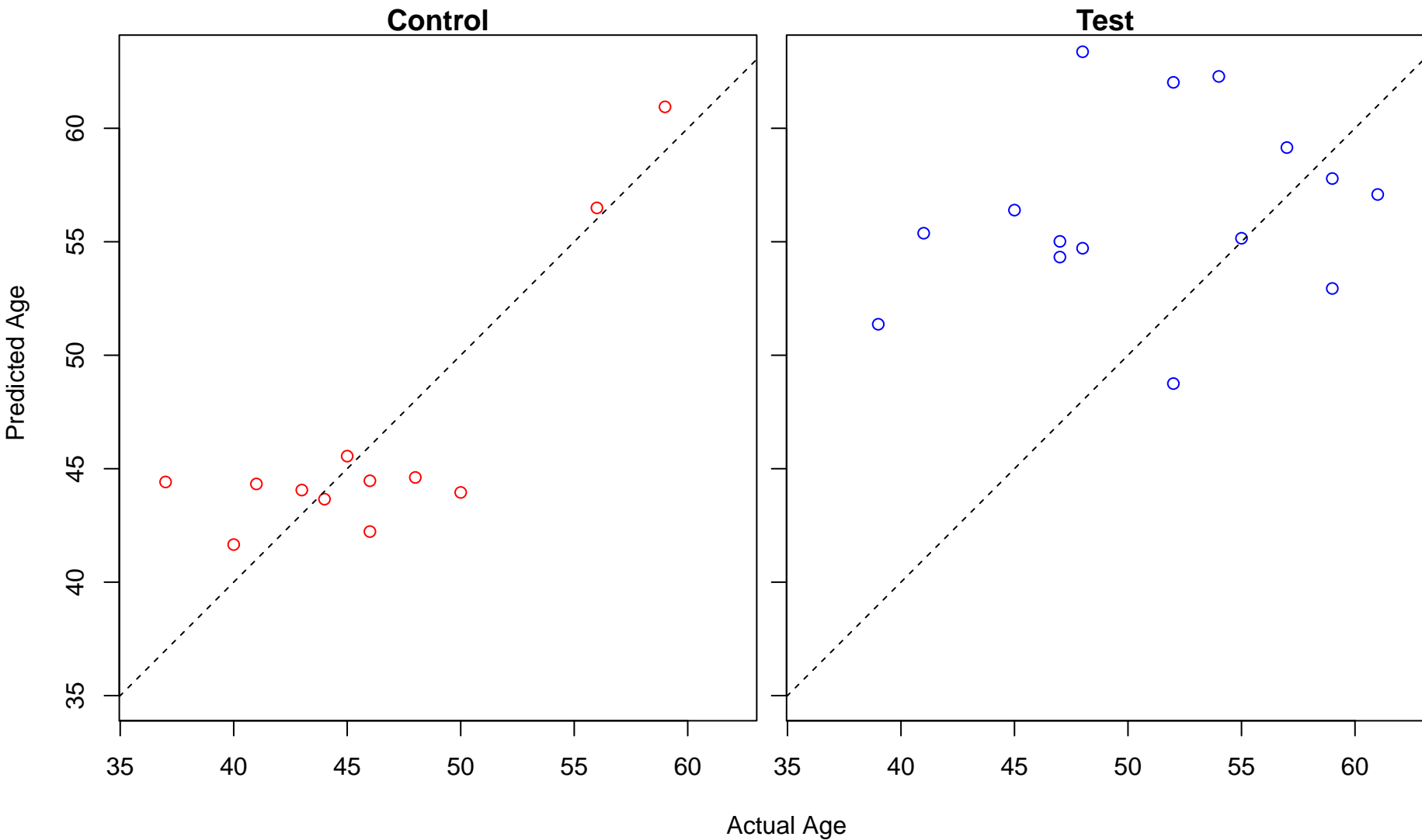
microtubule-based process (Score: 2.791420)



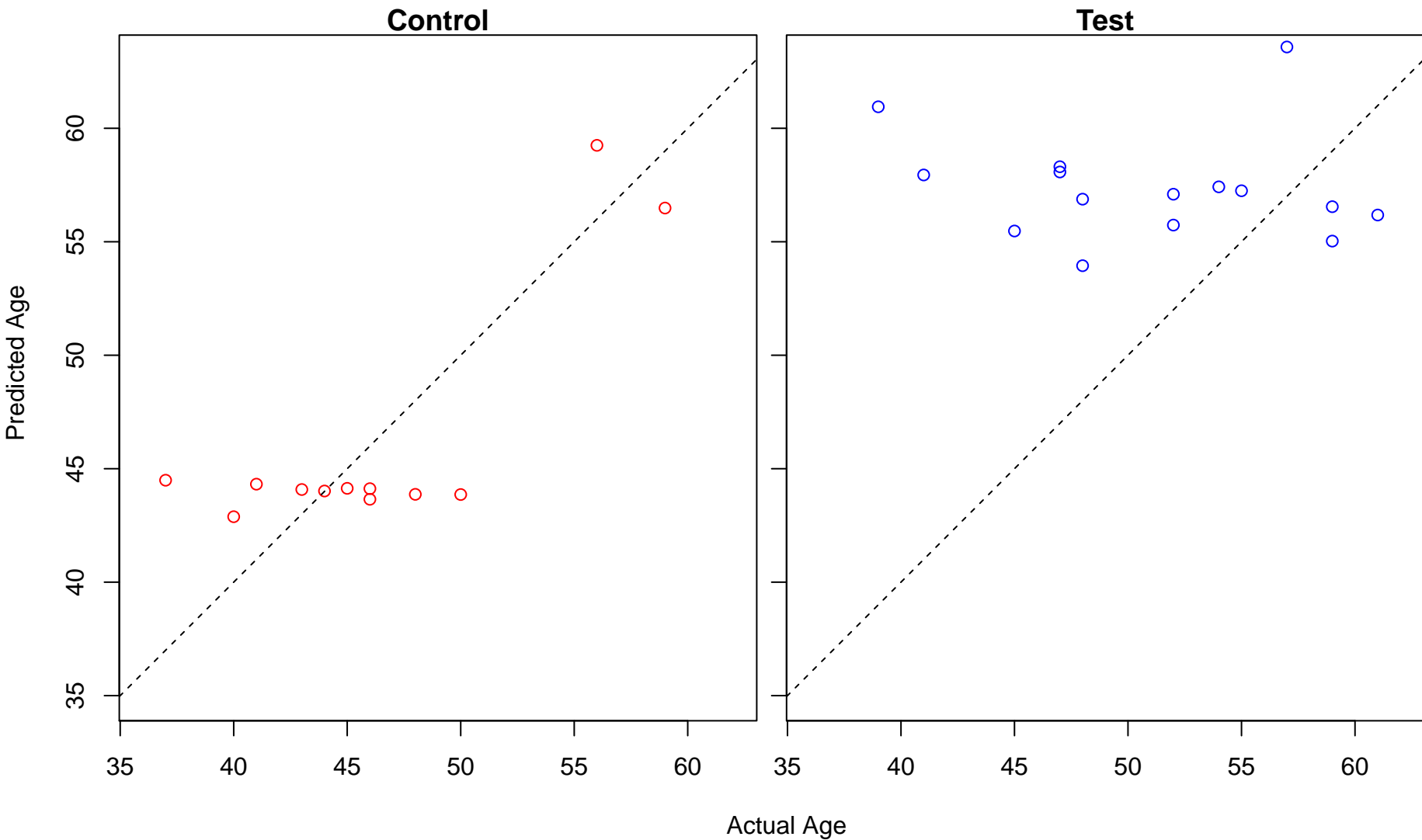
heart growth (Score: 2.789537)



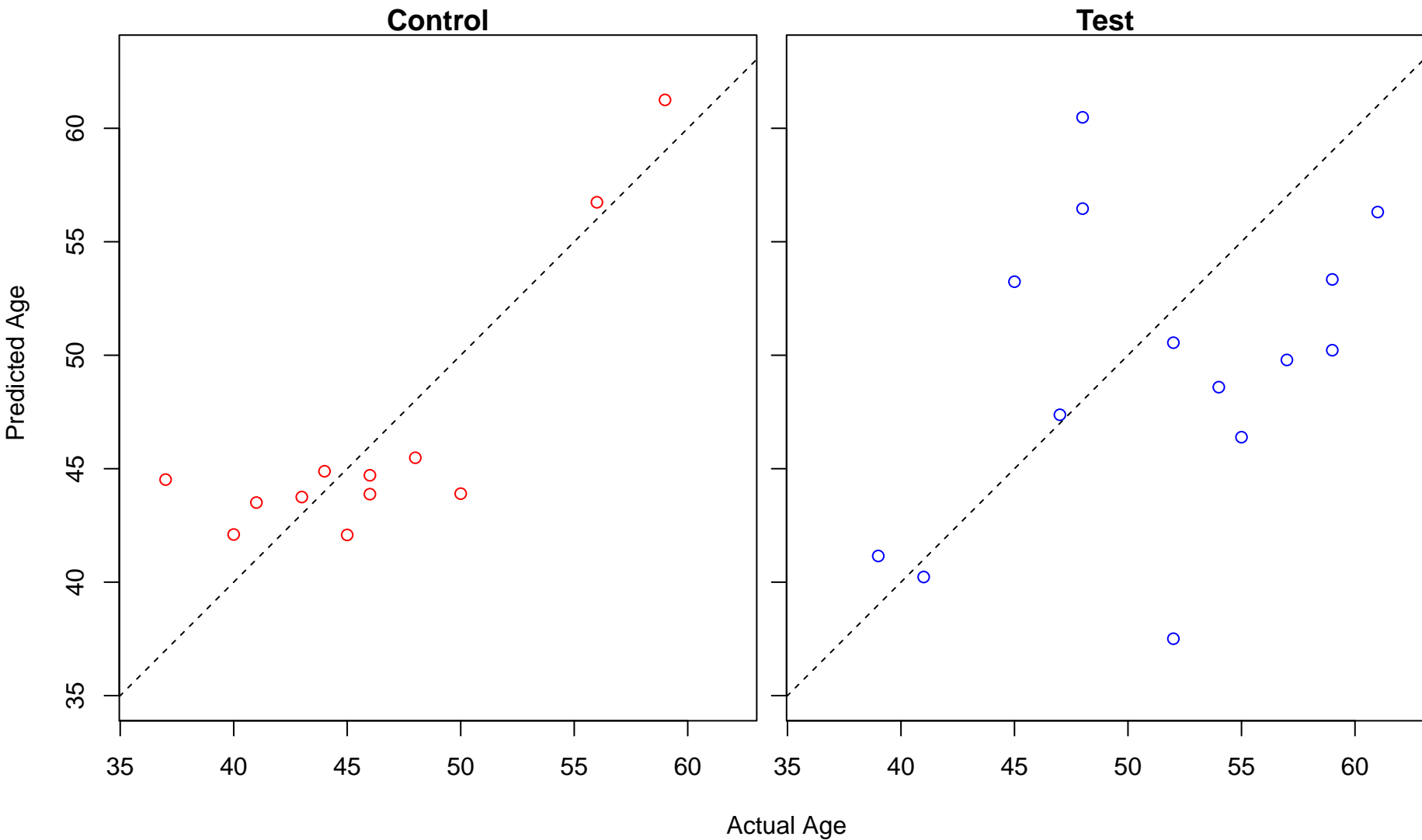
outer dynein arm assembly (Score: 2.789467)



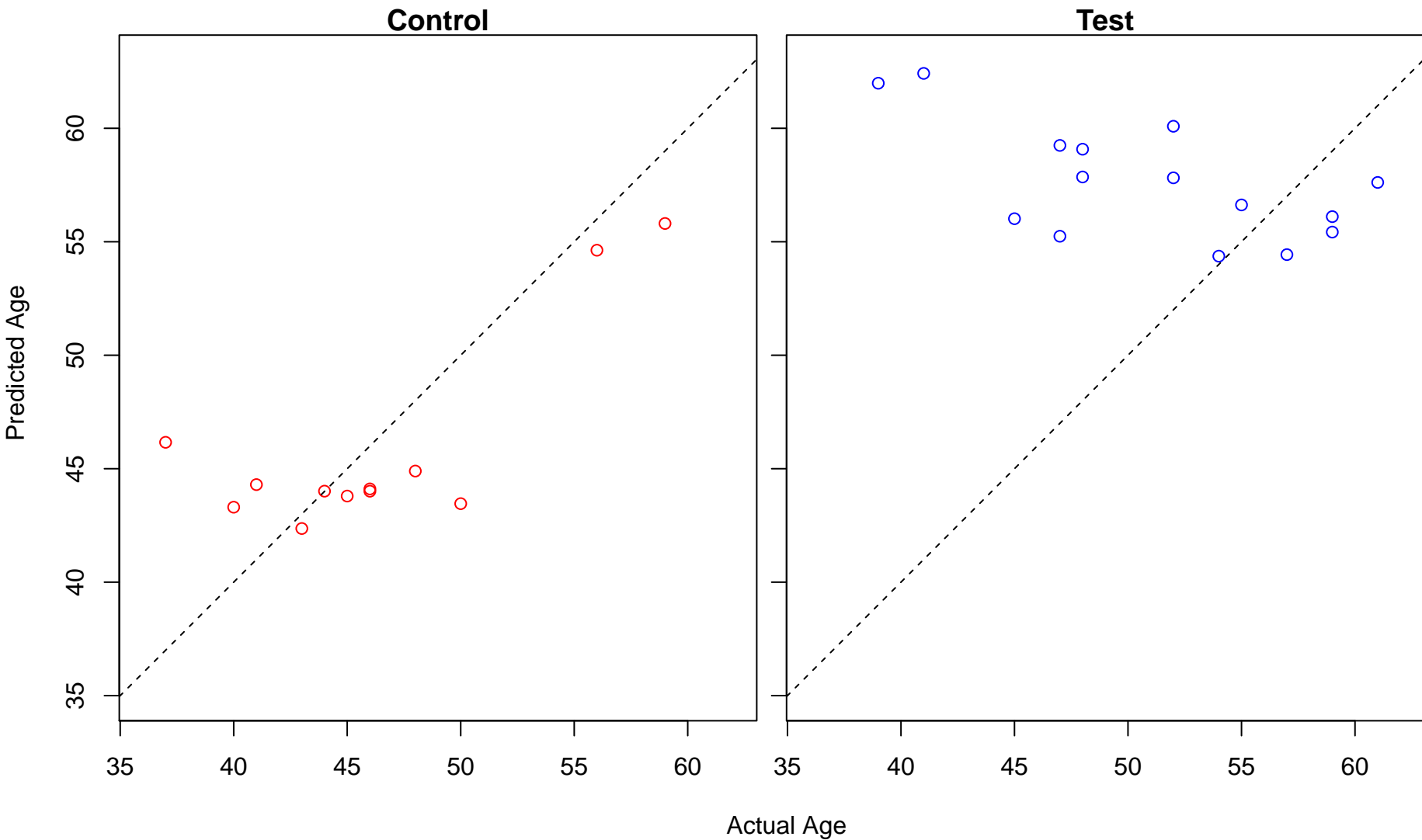
cellular response to radiation (Score: 2.789368)



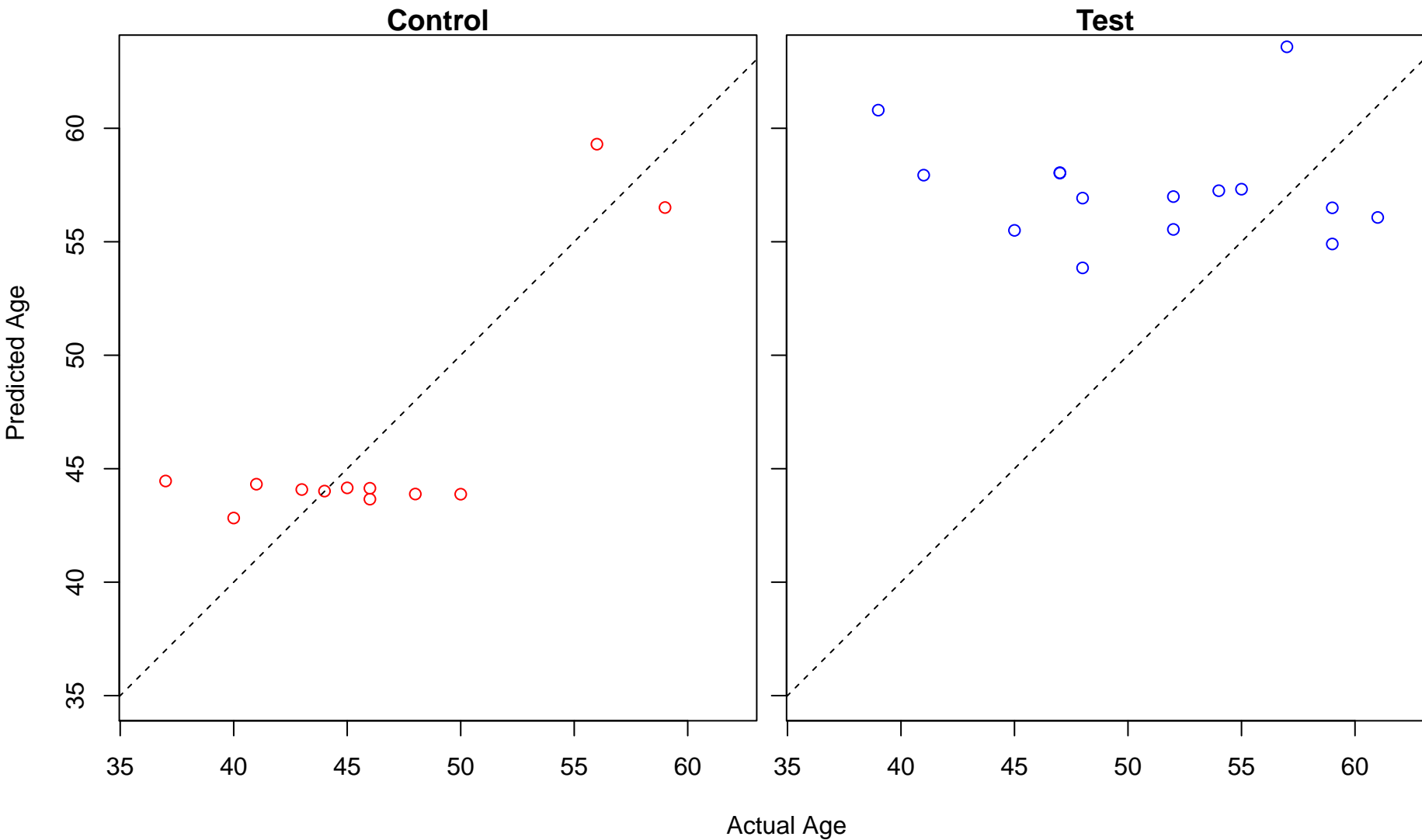
gamete generation (Score: 2.786773)



microtubule depolymerization (Score: 2.786421)

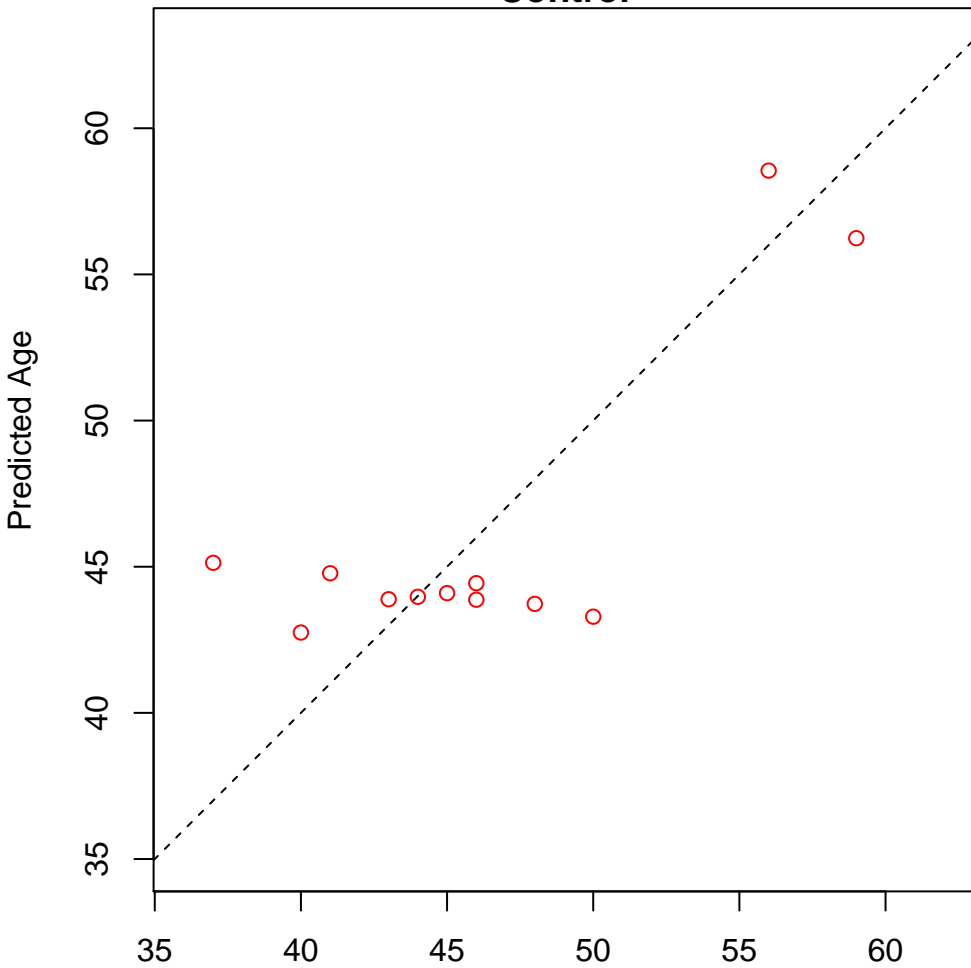


cellular response to light stimulus (Score: 2.786381)

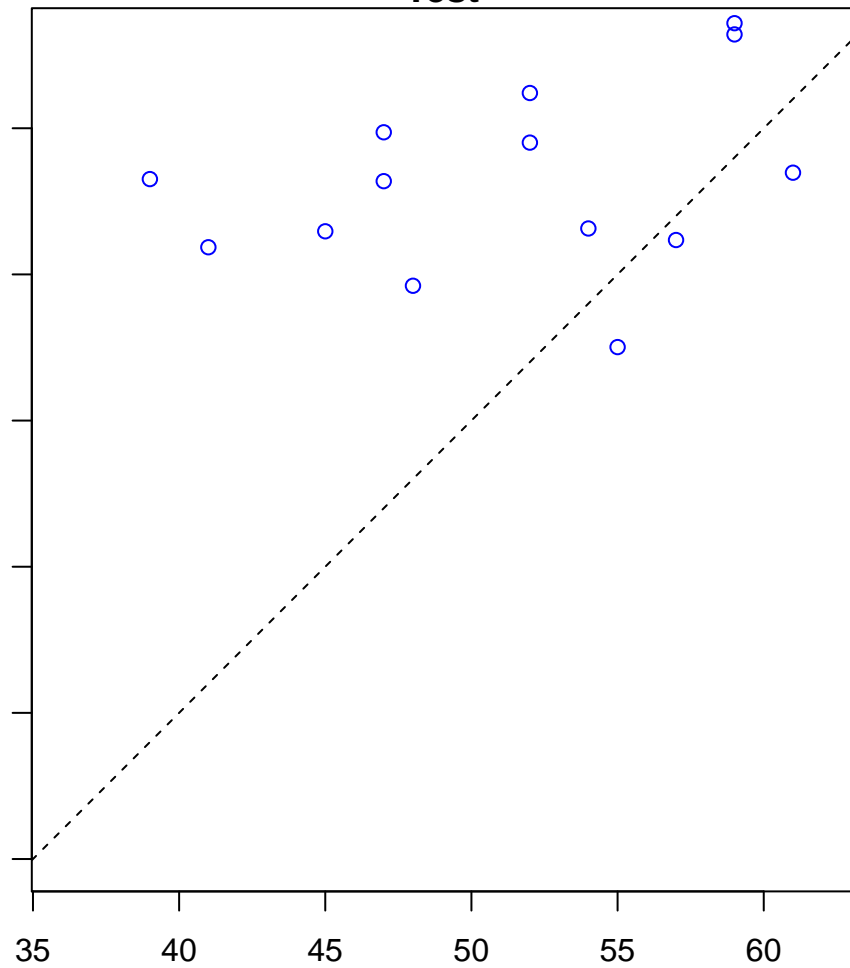


short-chain fatty acid catabolic process (Score: 2.785954)

Control

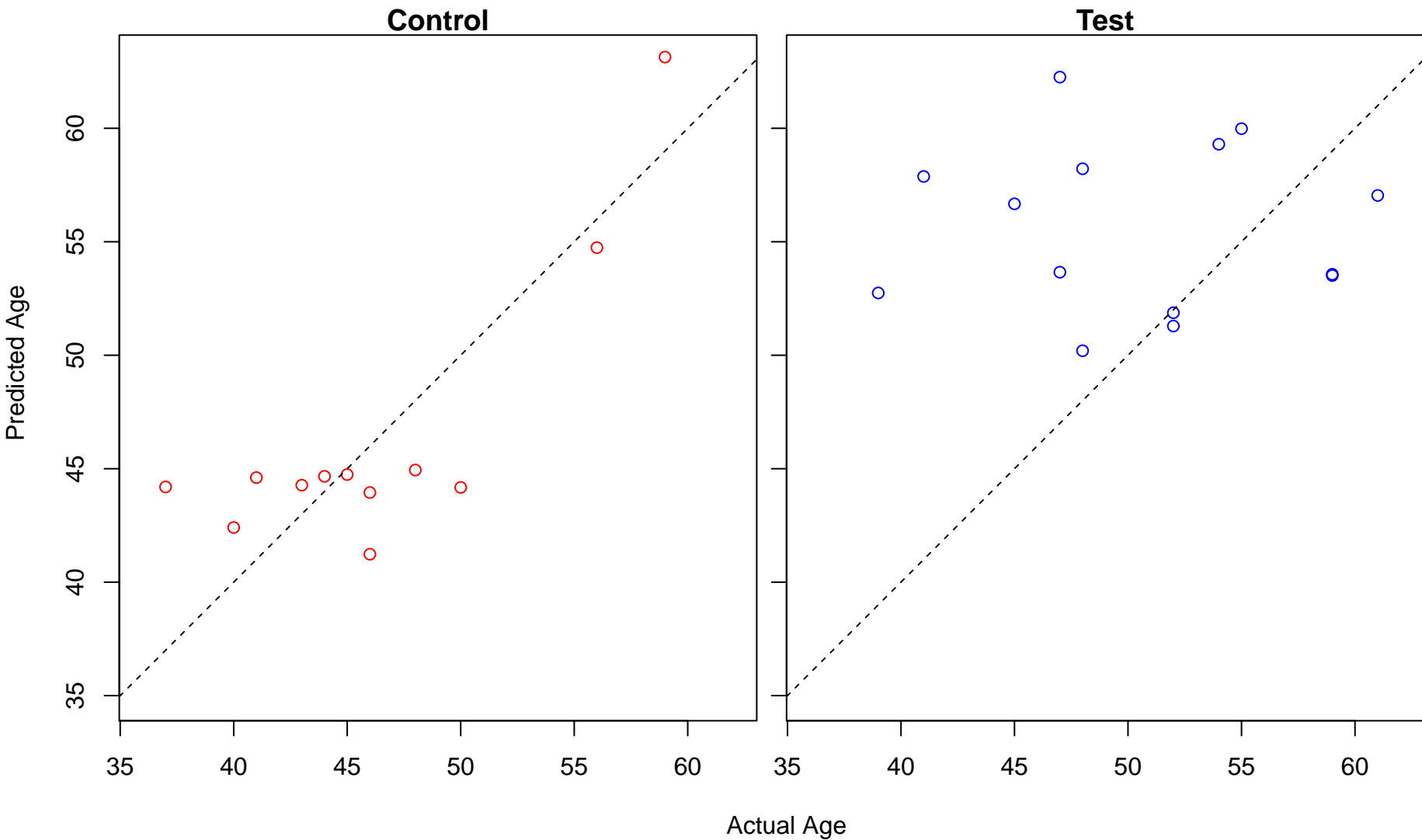


Test

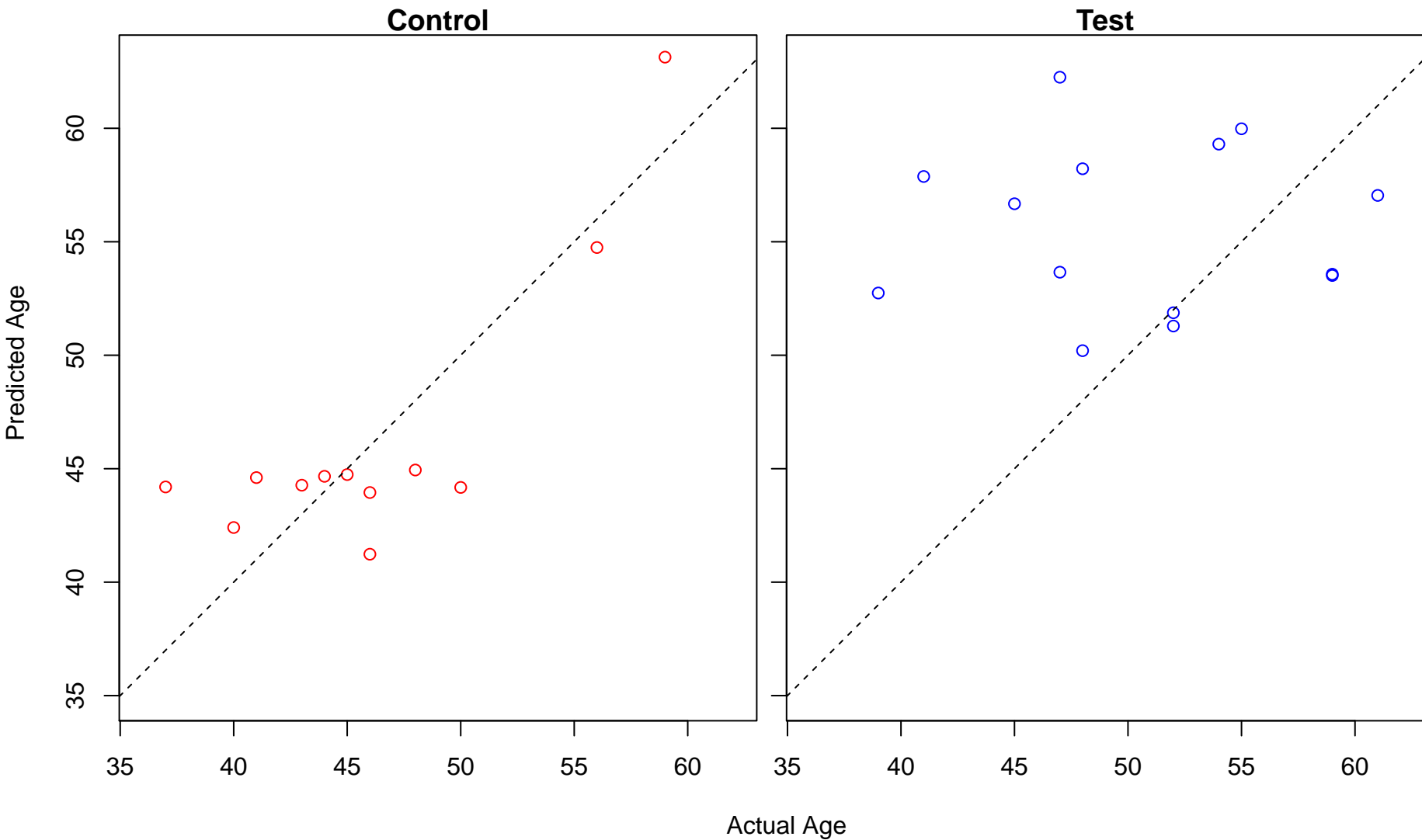


Actual Age

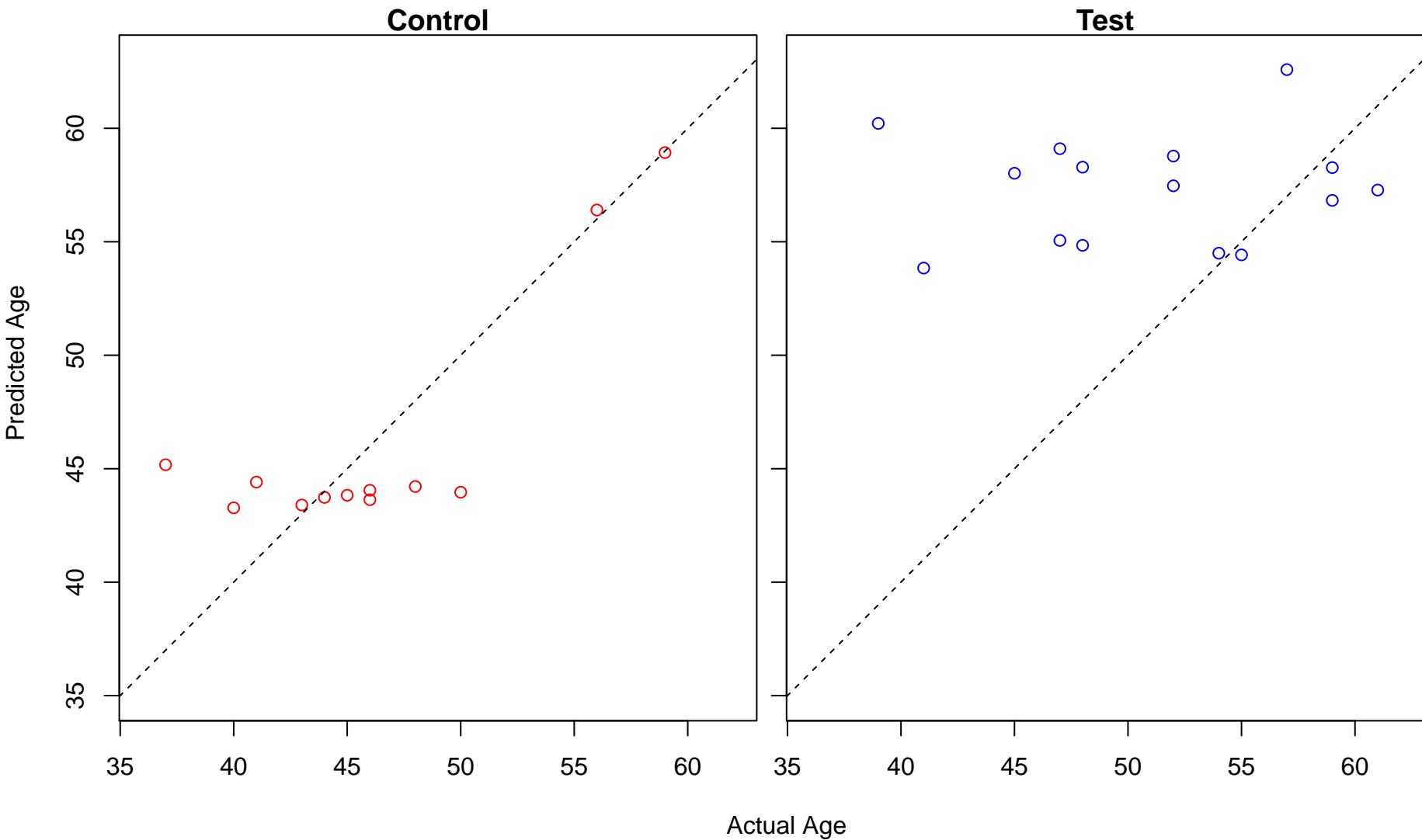
regulation of mRNA stability (Score: 2.785633)



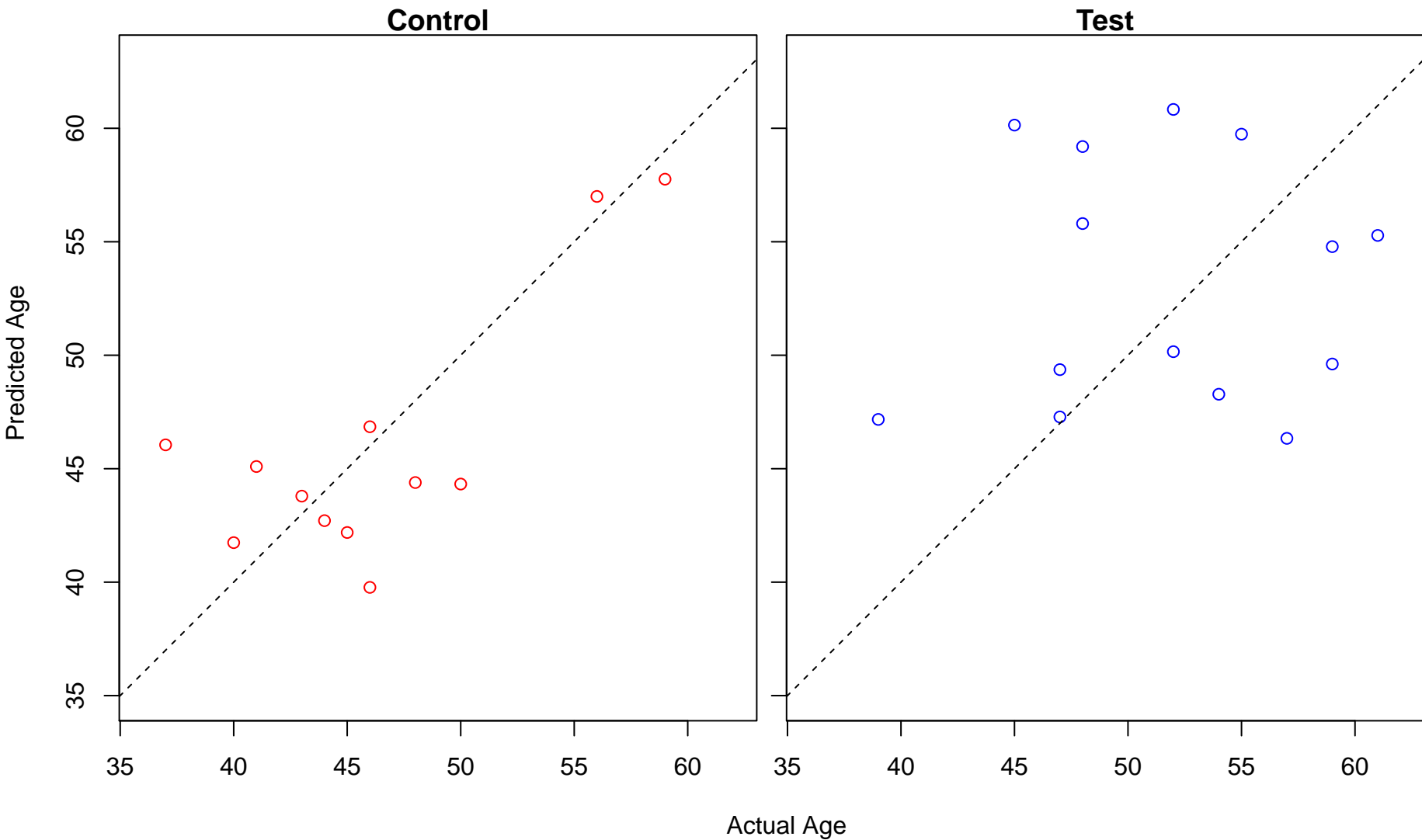
regulation of RNA stability (Score: 2.785605)



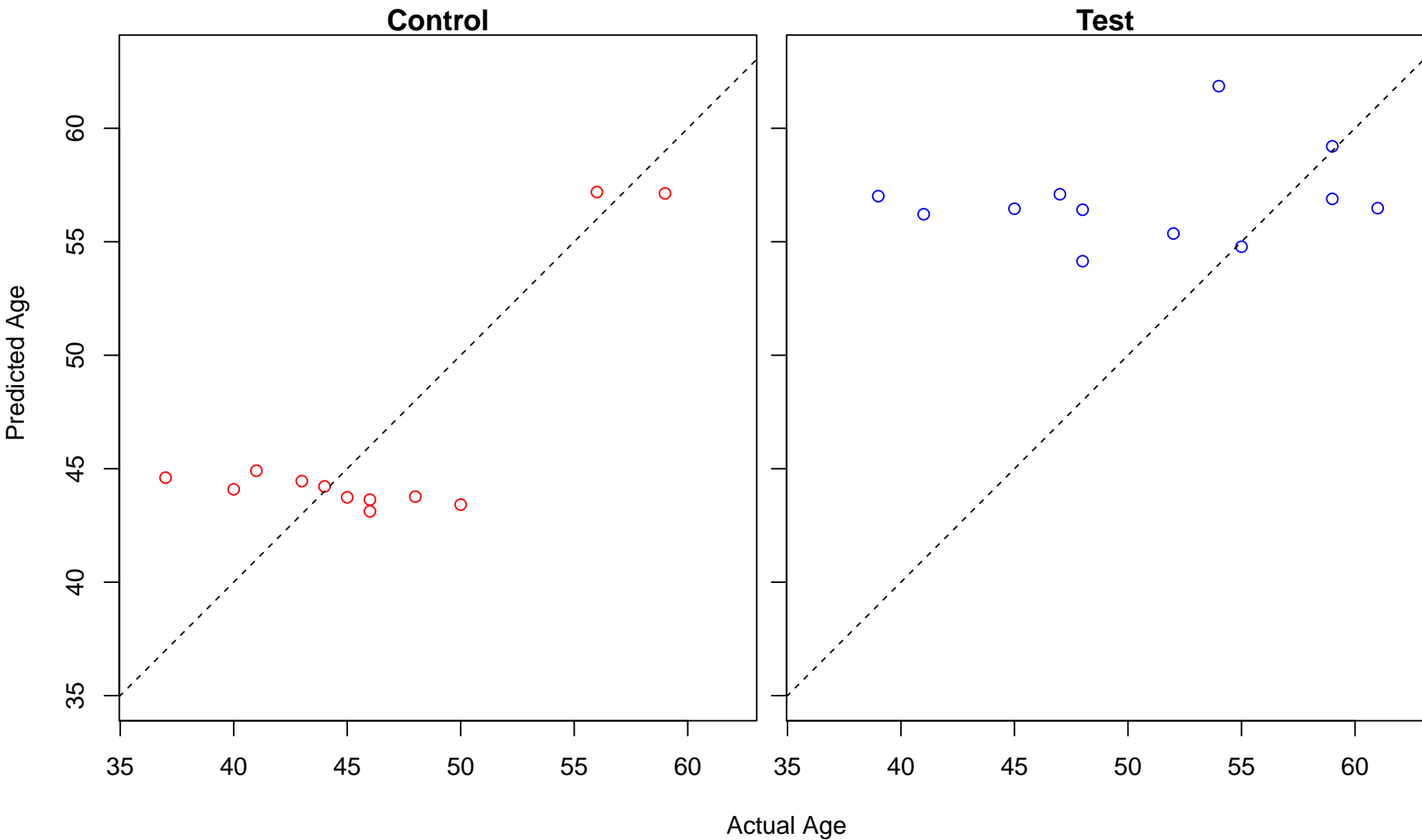
pyrimidine-containing compound metabolic process (Score: 2.784499)



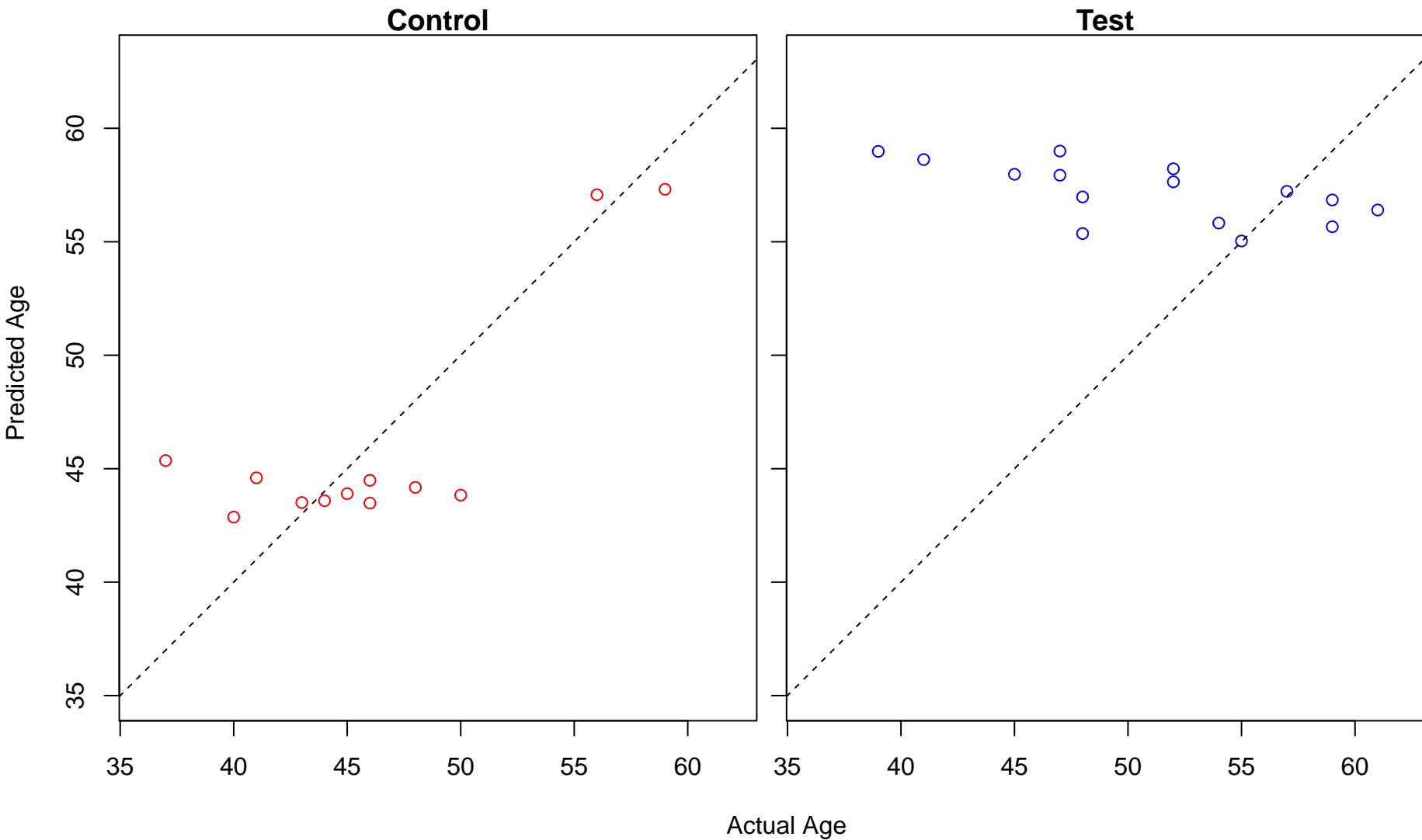
regulation of synapse assembly (Score: 2.782365)



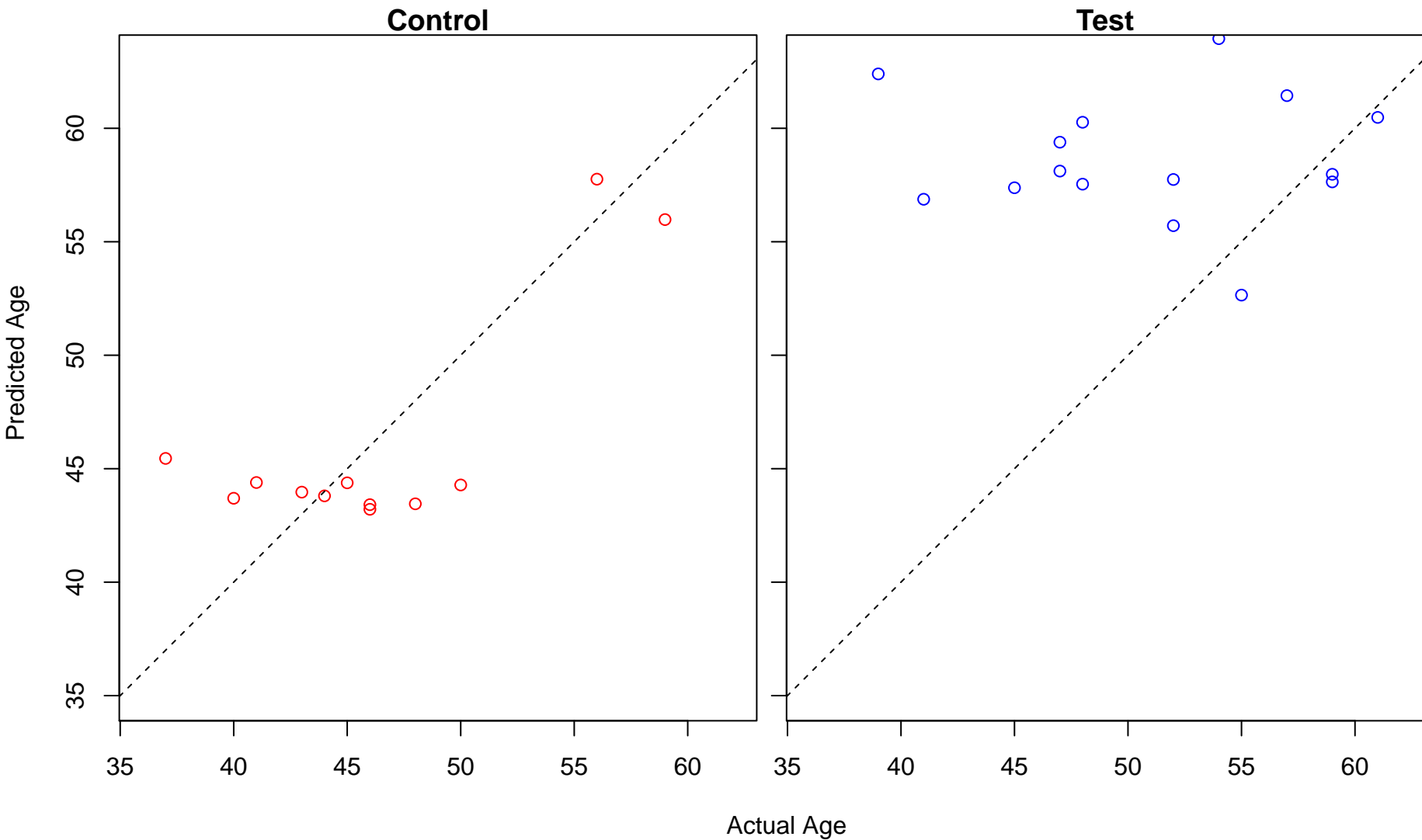
regulation of protein homodimerization activity (Score: 2.780375)



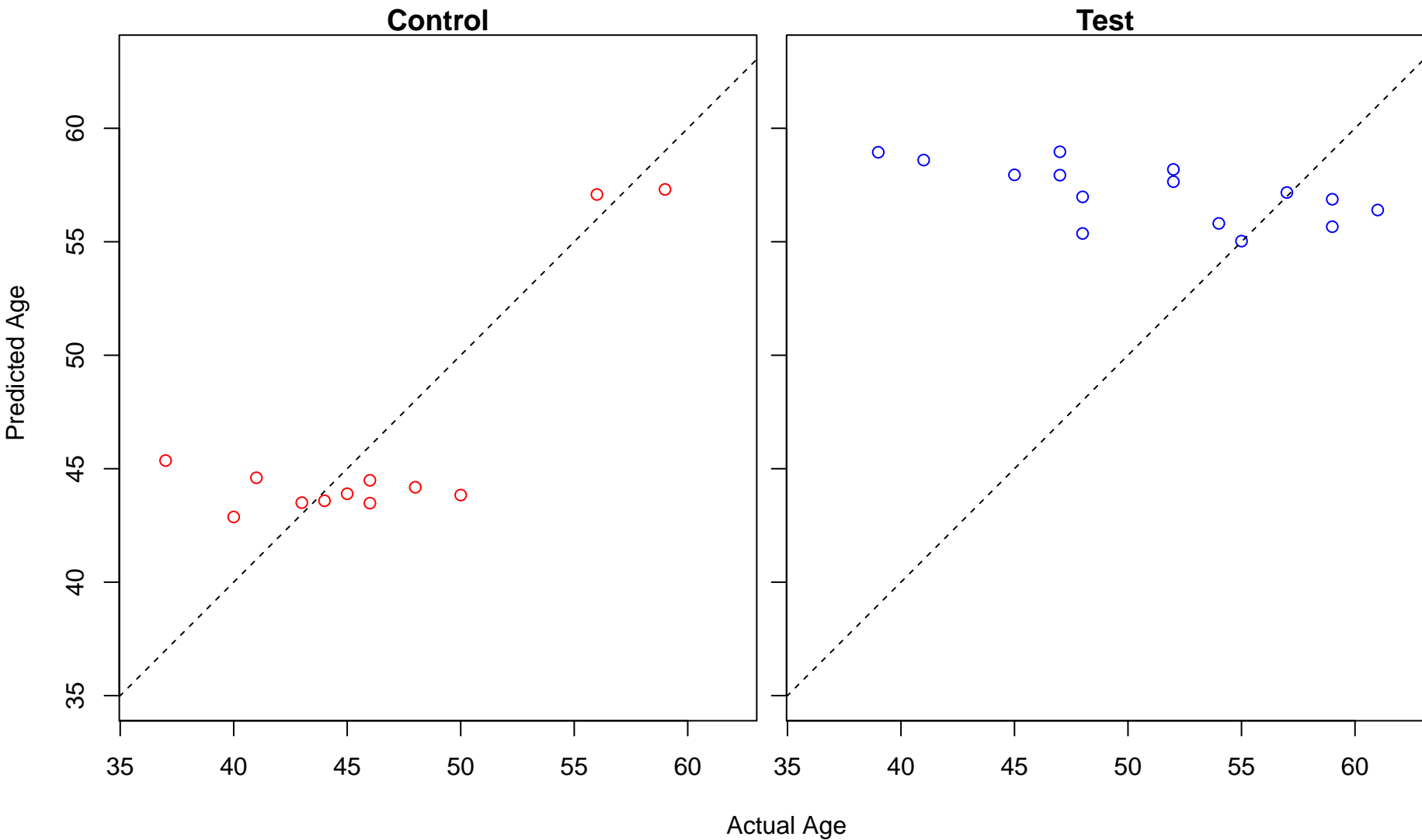
cellular component disassembly involved in execution phase of apoptosis (Score: 2.779662)



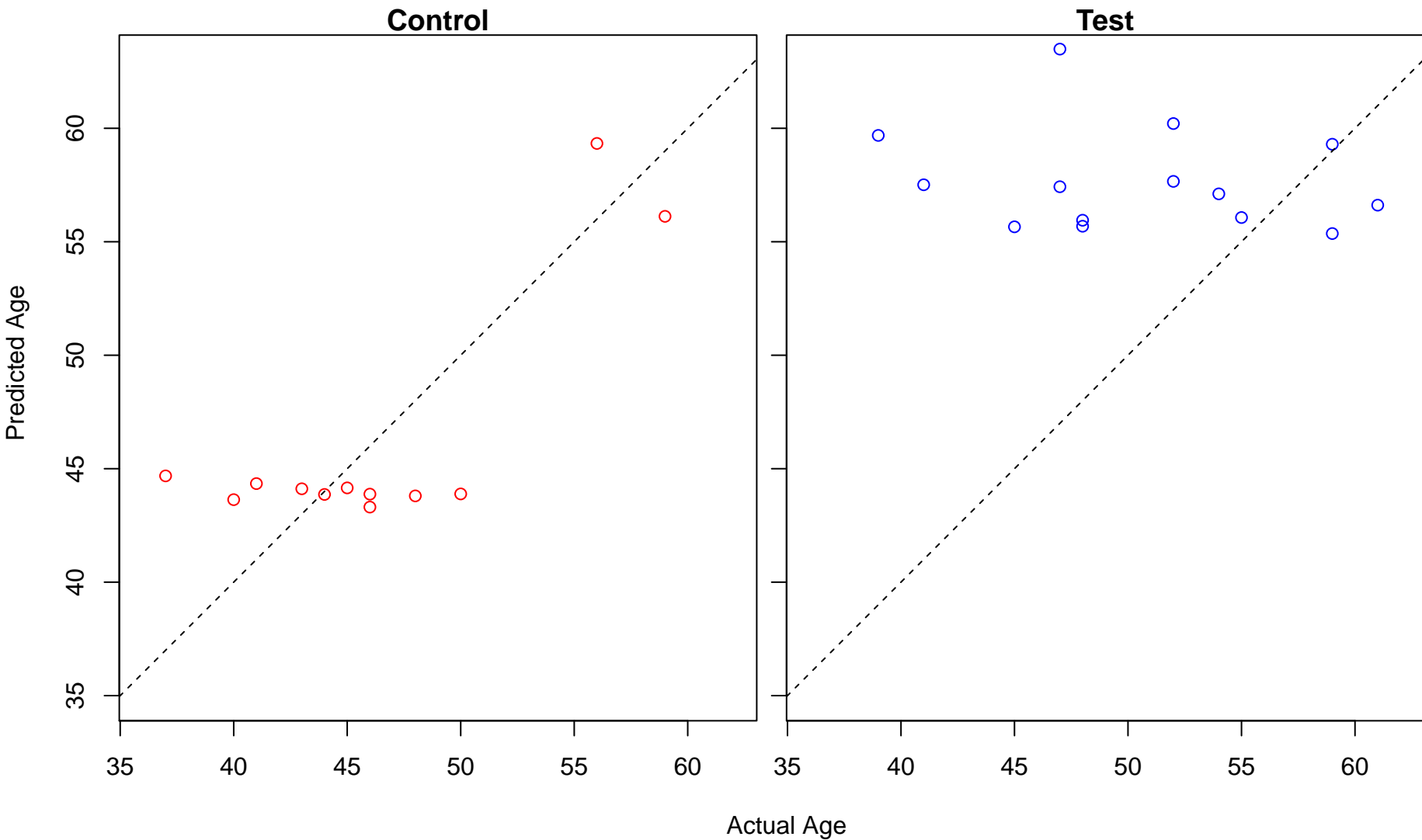
regulation of lipid kinase activity (Score: 2.776746)



execution phase of apoptosis (Score: 2.772433)

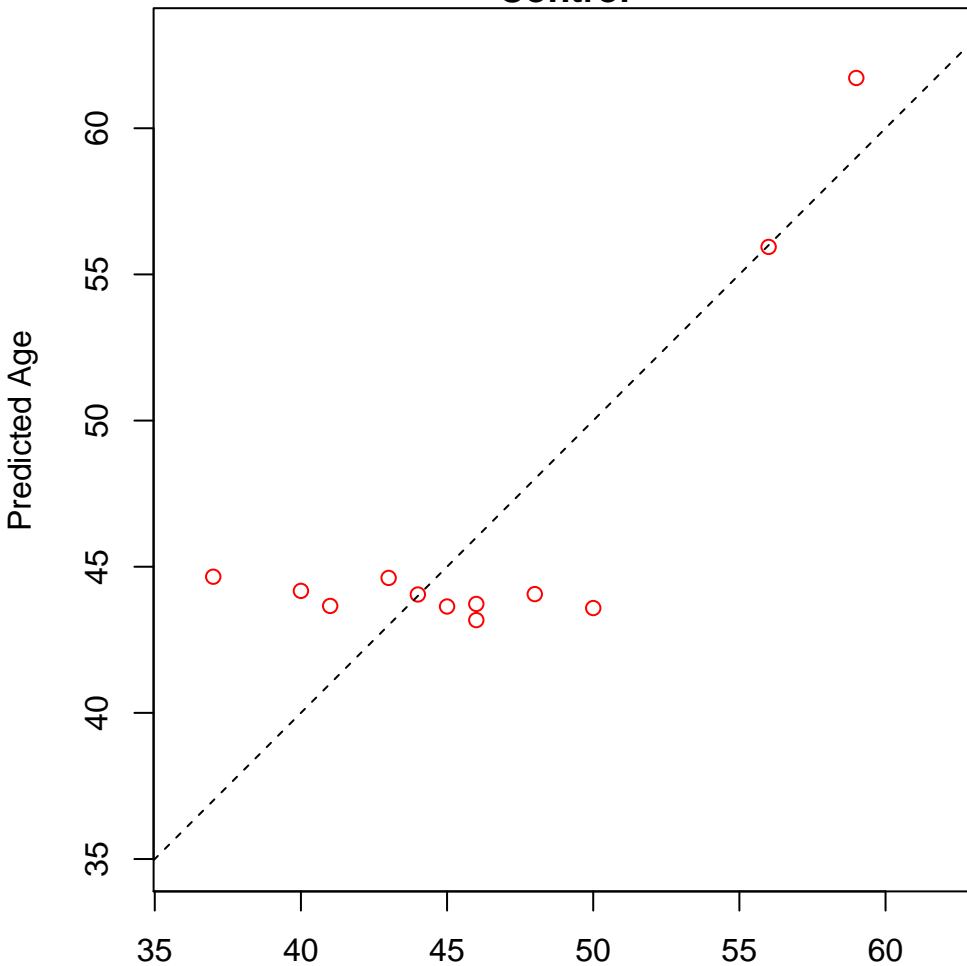


proteolysis involved in cellular protein catabolic process (Score: 2.770871)

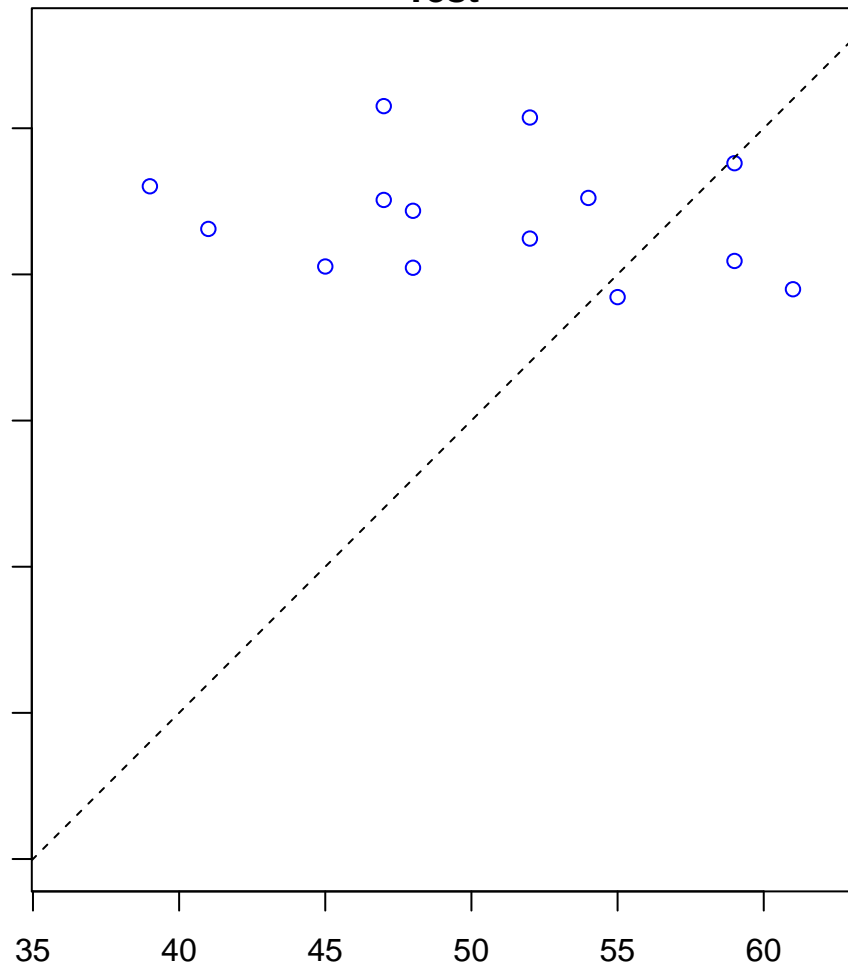


morphogenesis of an epithelial sheet (Score: 2.769149)

Control

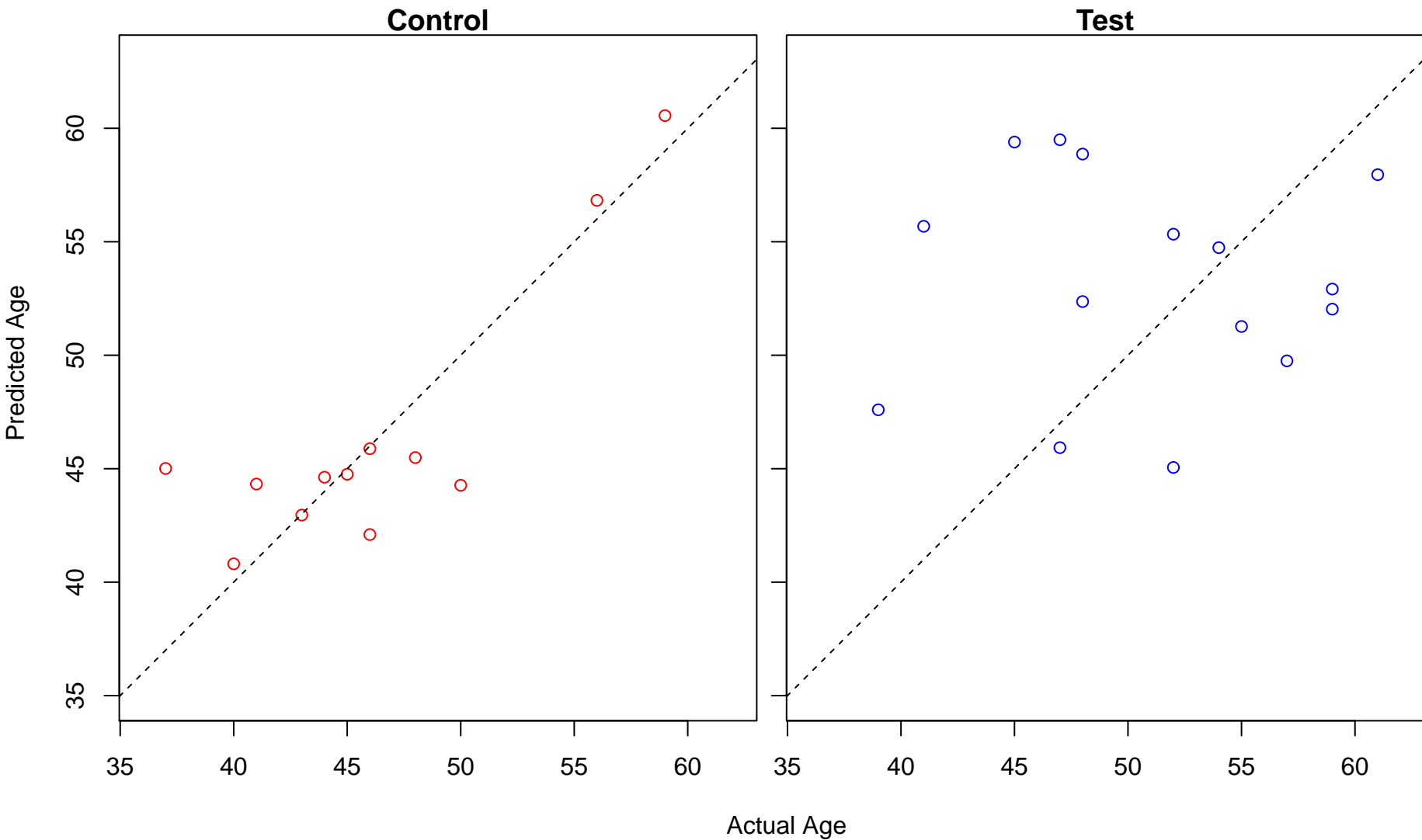


Test

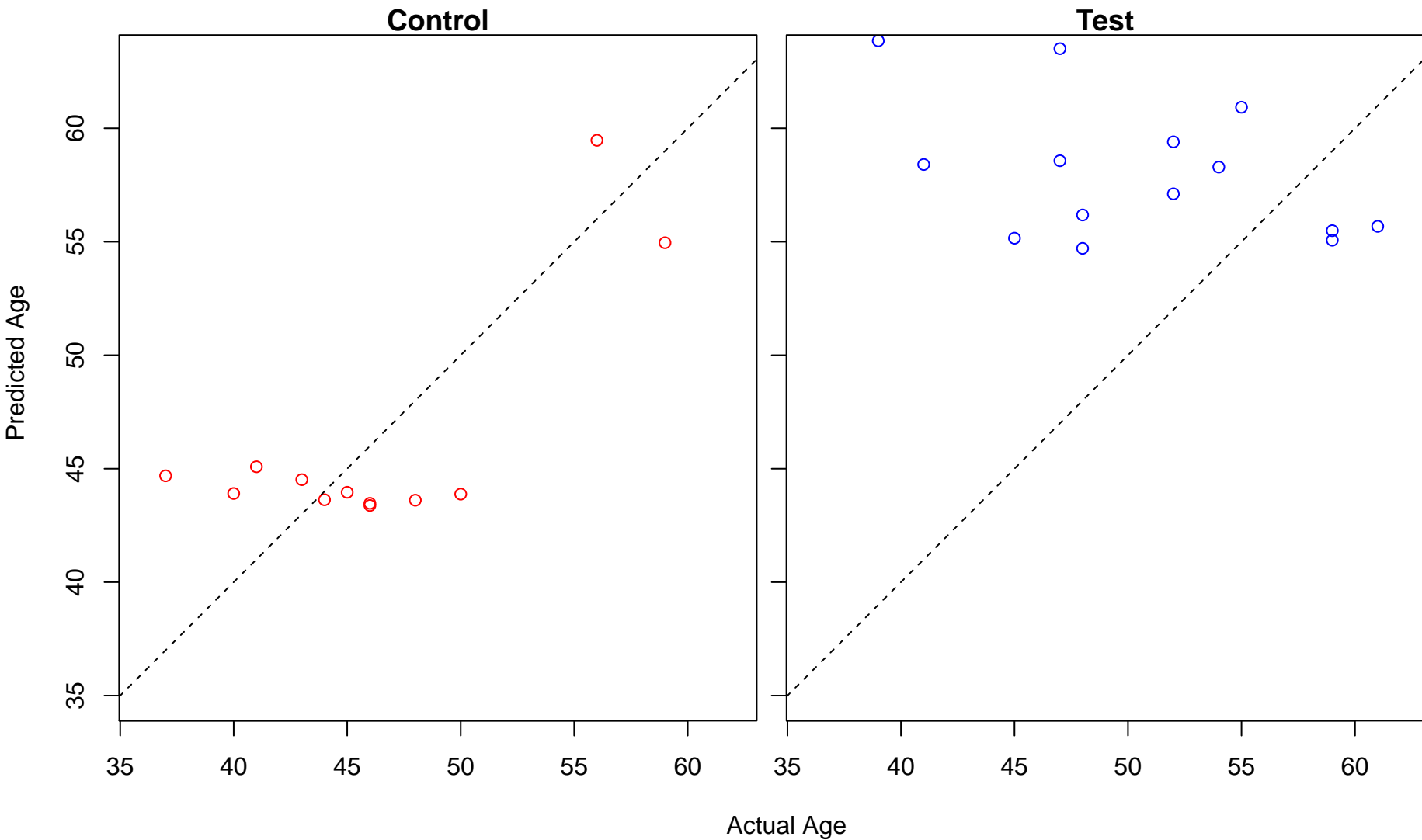


Actual Age

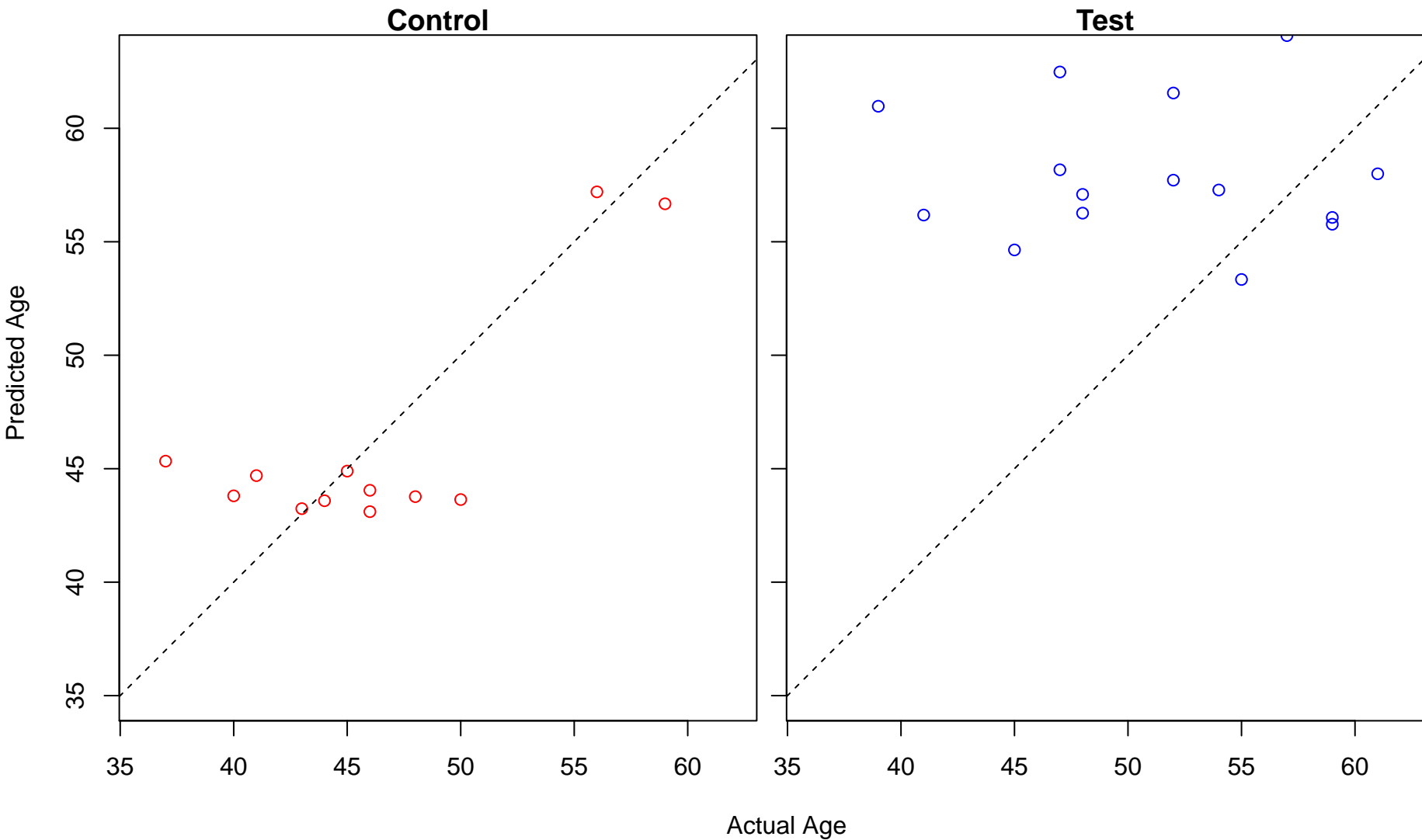
brain development (Score: 2.769119)



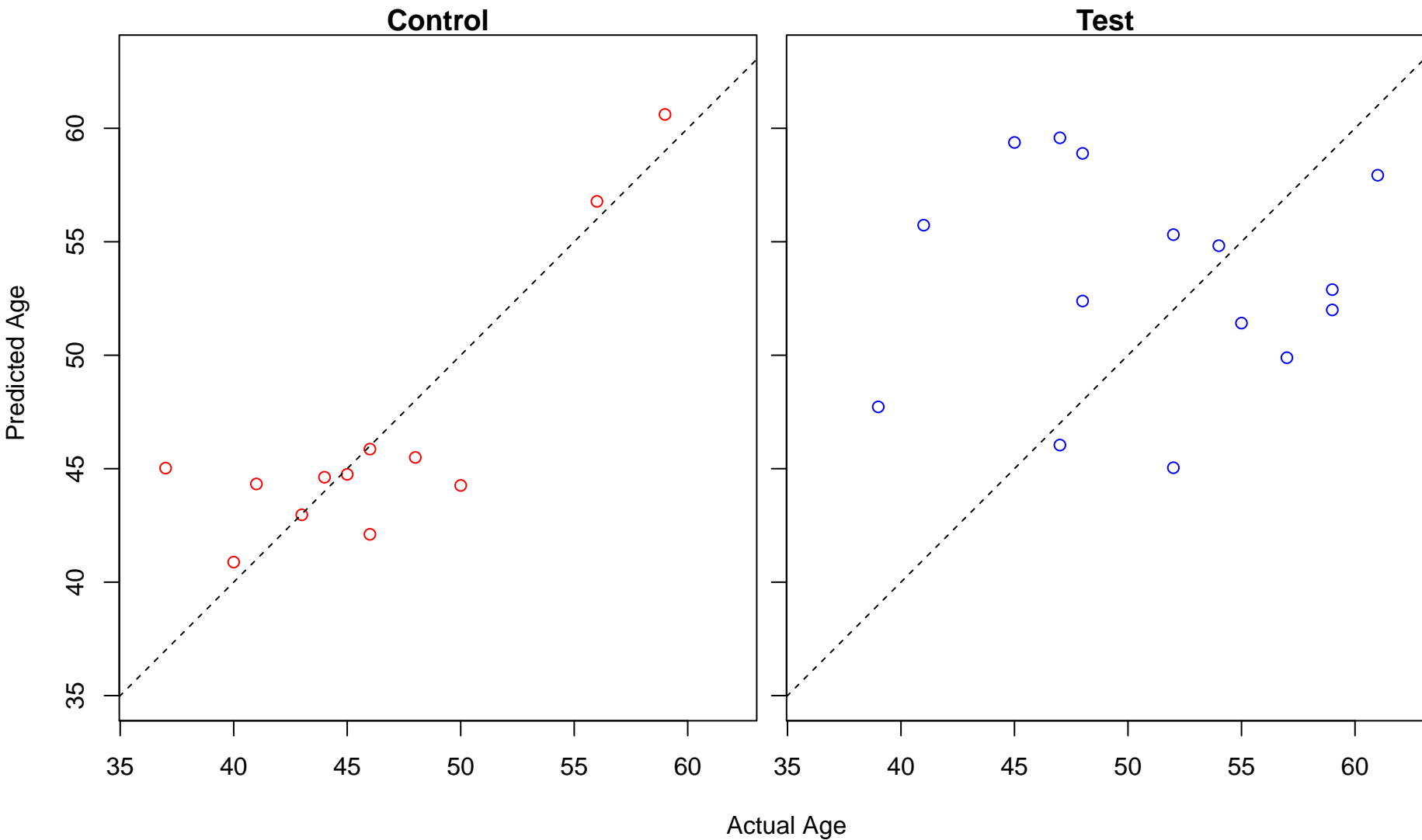
multicellular organismal homeostasis (Score: 2.768611)



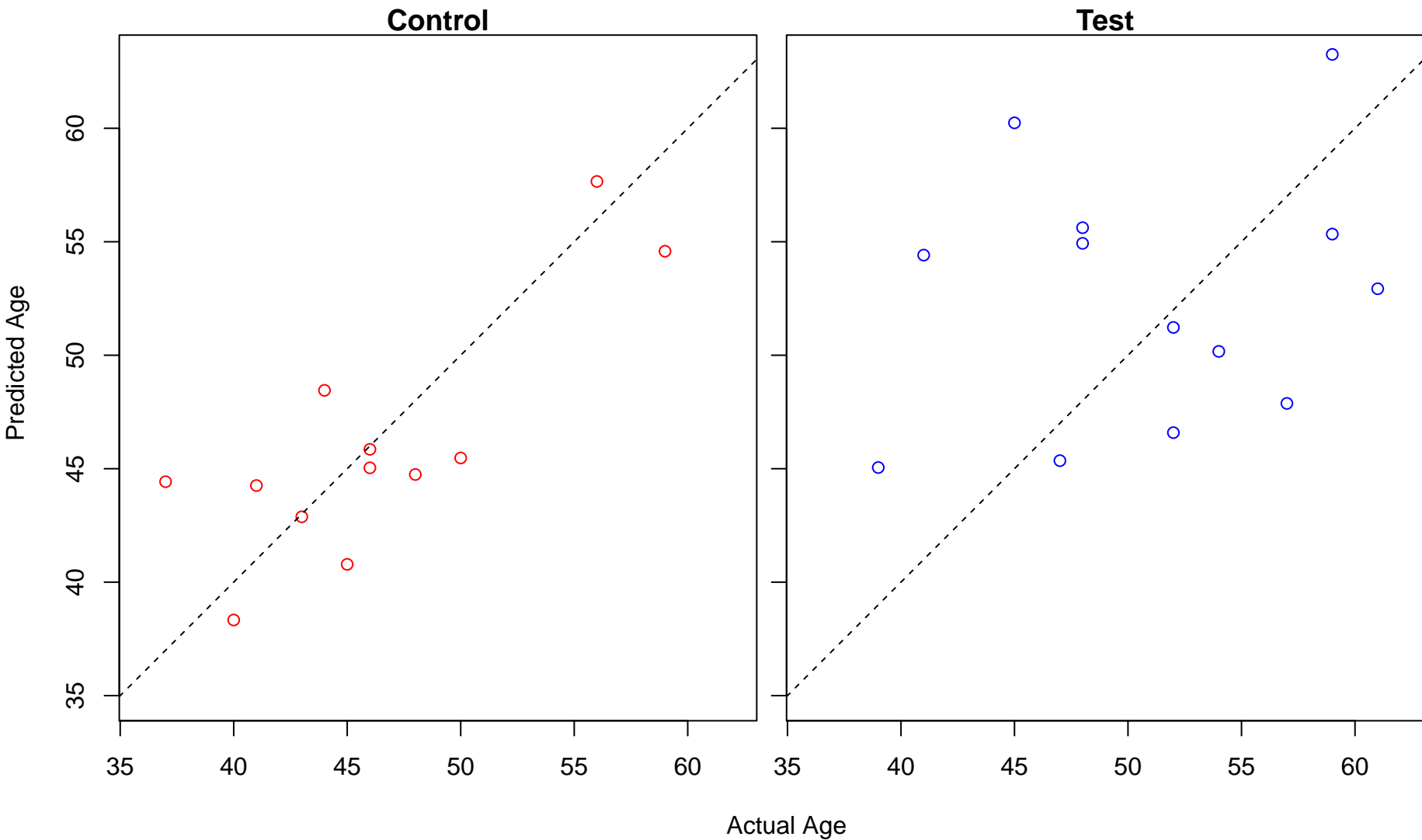
regulation of organ morphogenesis (Score: 2.765228)



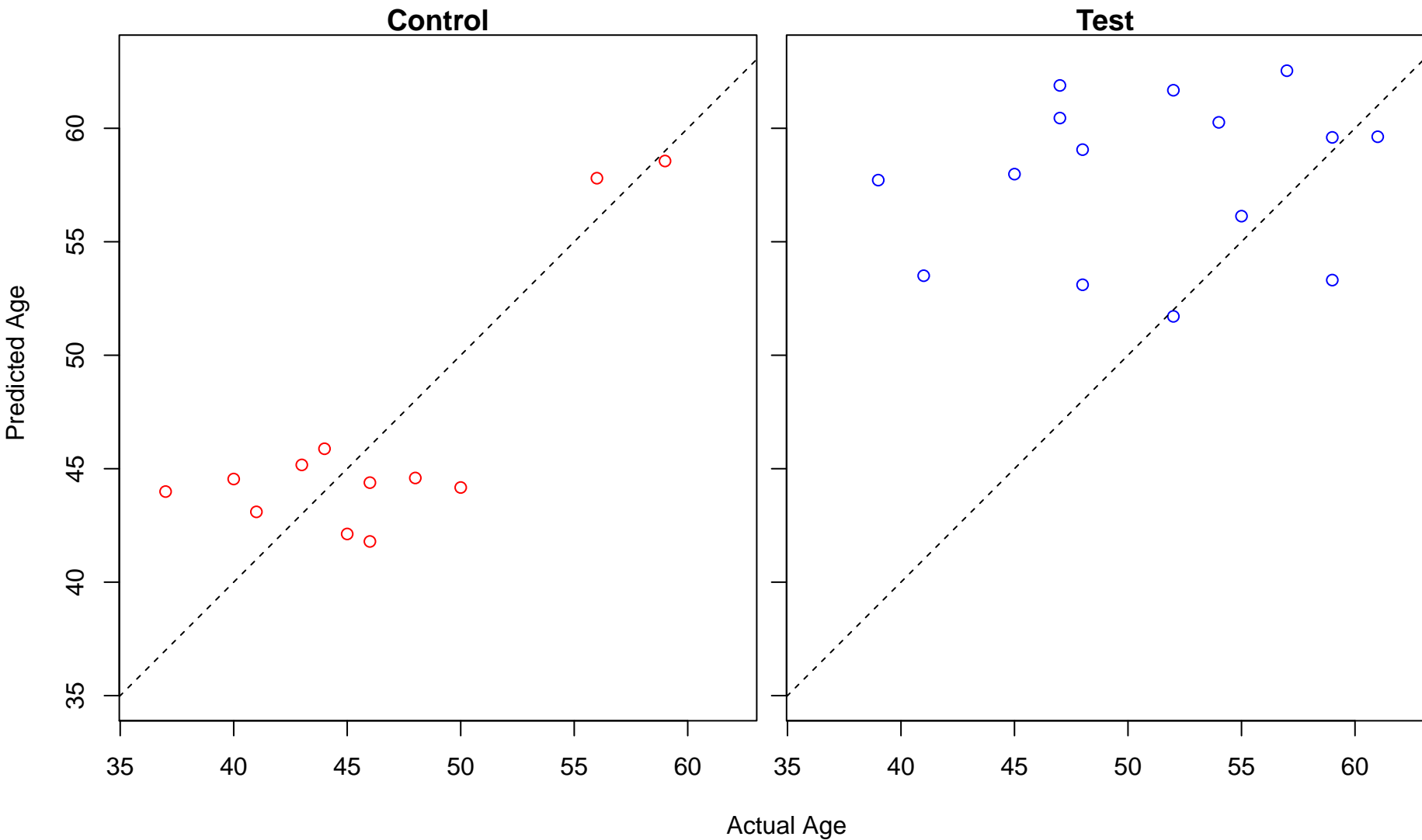
head development (Score: 2.764929)



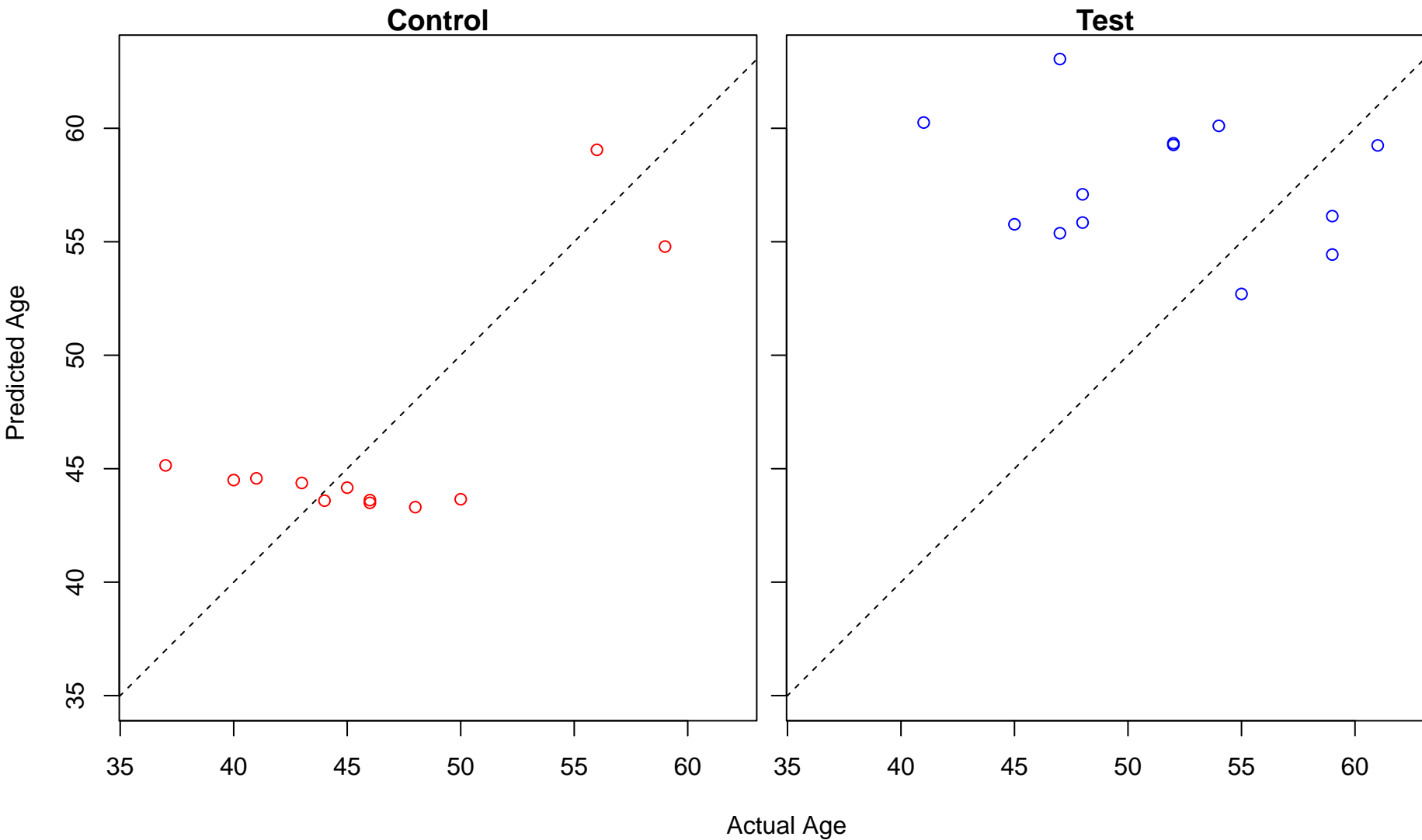
regulation of establishment or maintenance of cell polarity (Score: 2.762269)



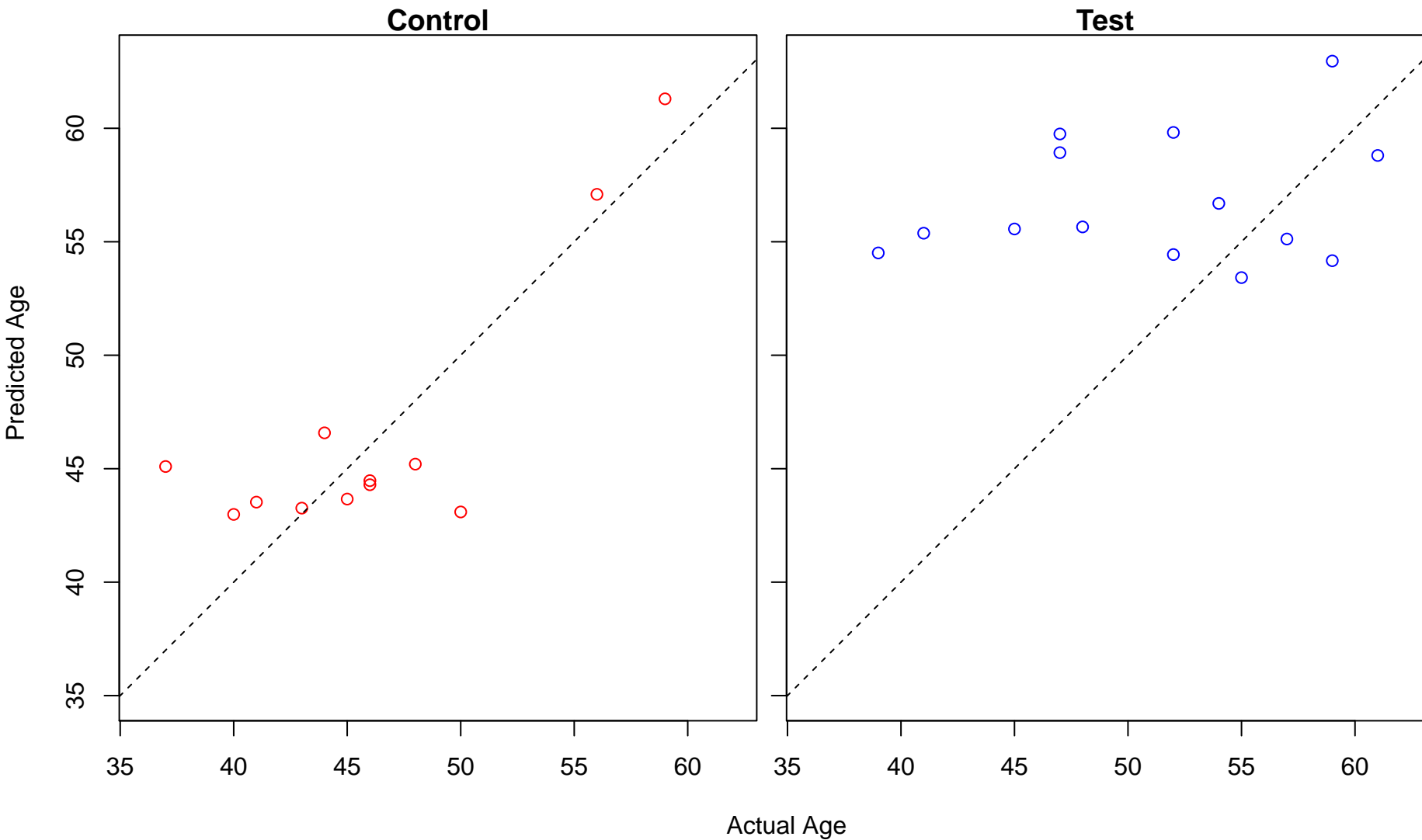
regulation of intracellular steroid hormone receptor signaling pathway (Score: 2.760956)



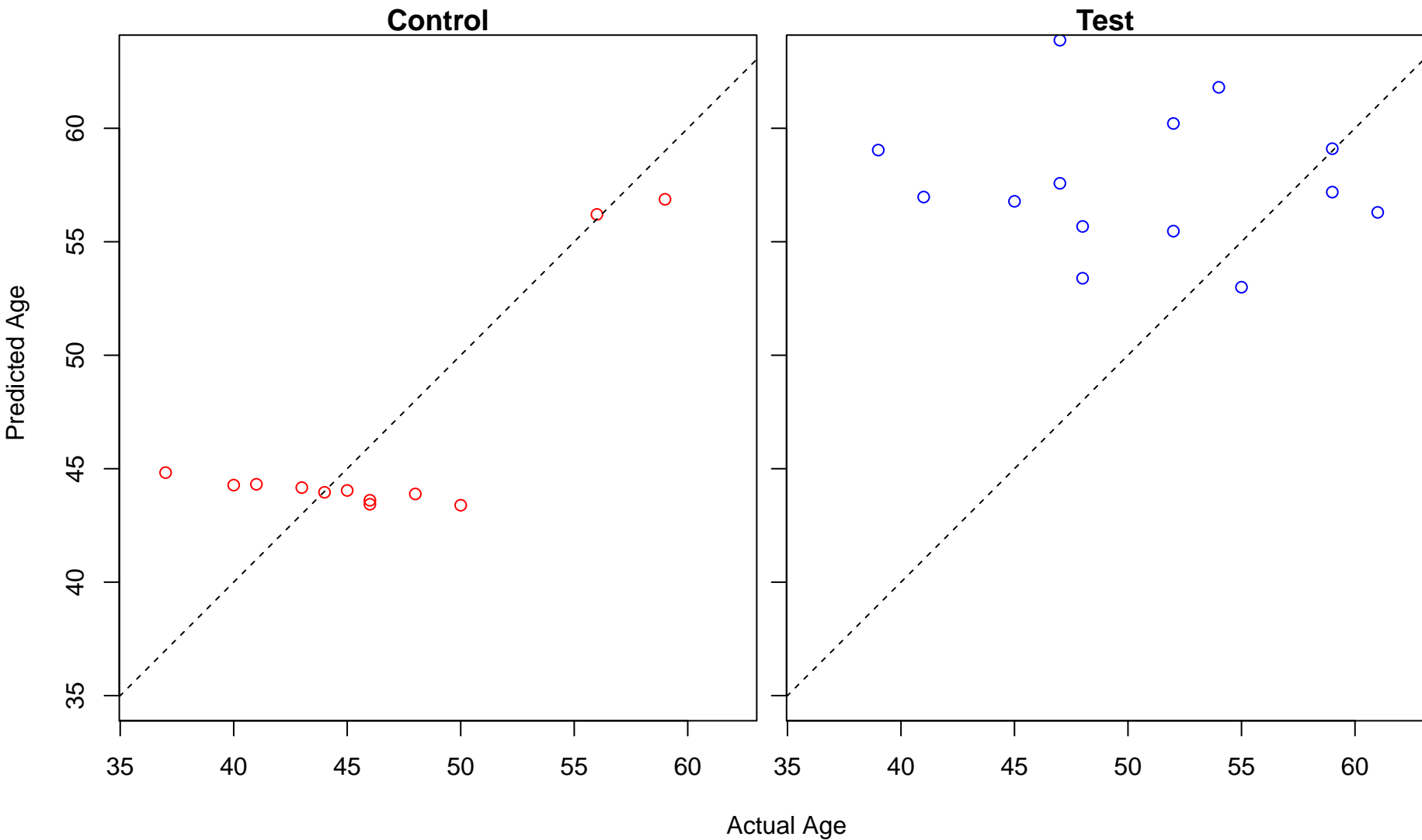
negative regulation of cellular amide metabolic process (Score: 2.760400)



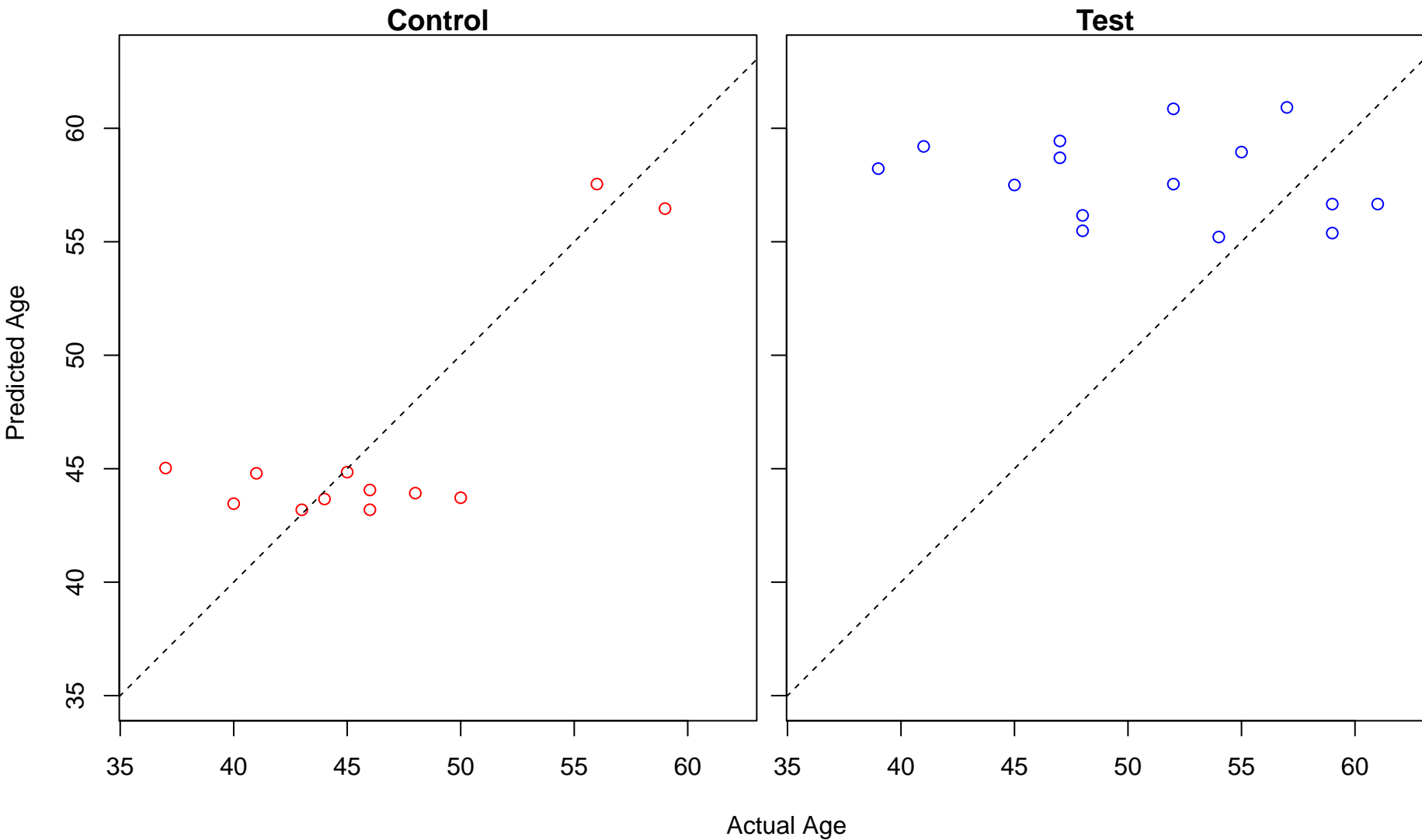
peptidyl-serine phosphorylation (Score: 2.759491)



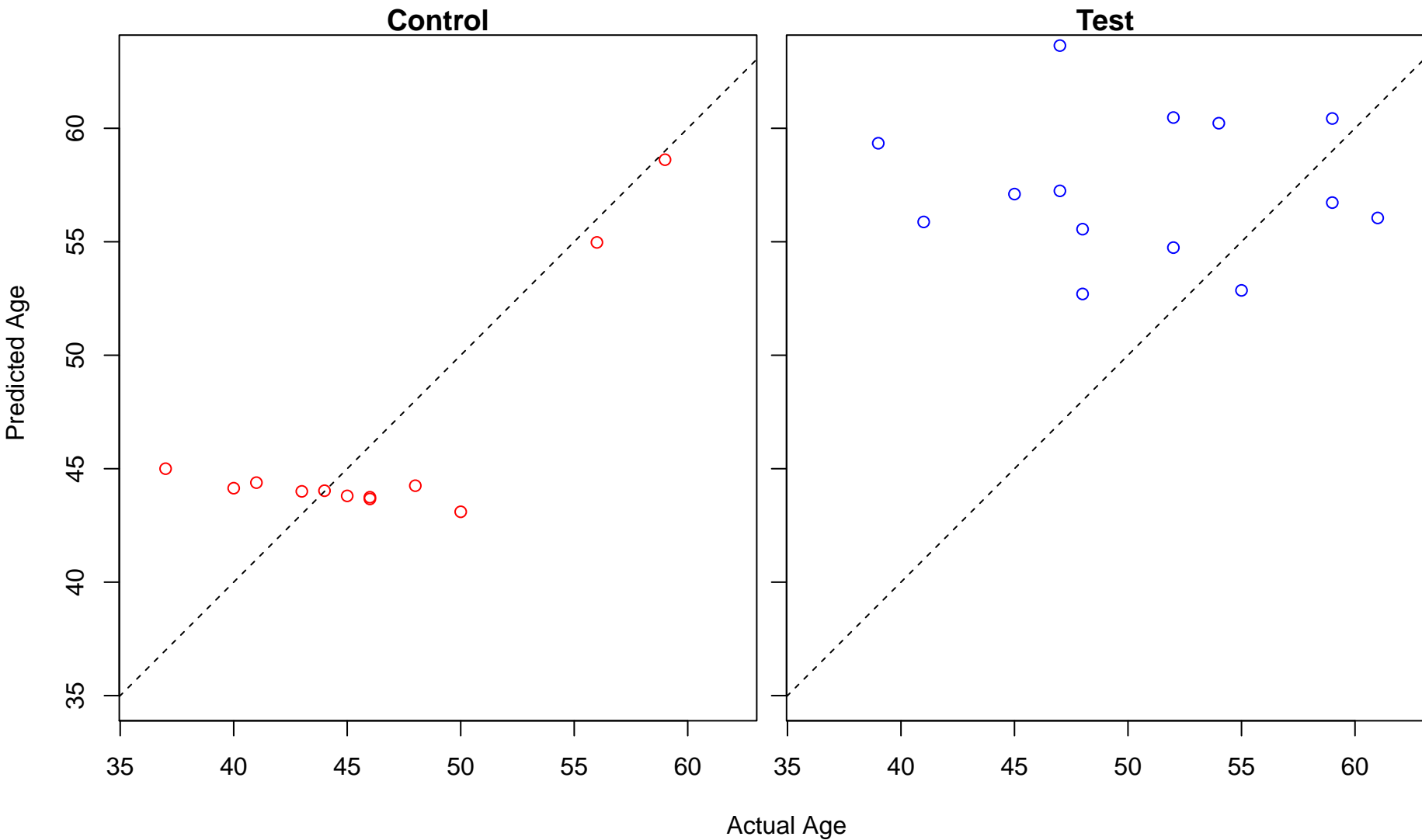
regulation of pH (Score: 2.757783)



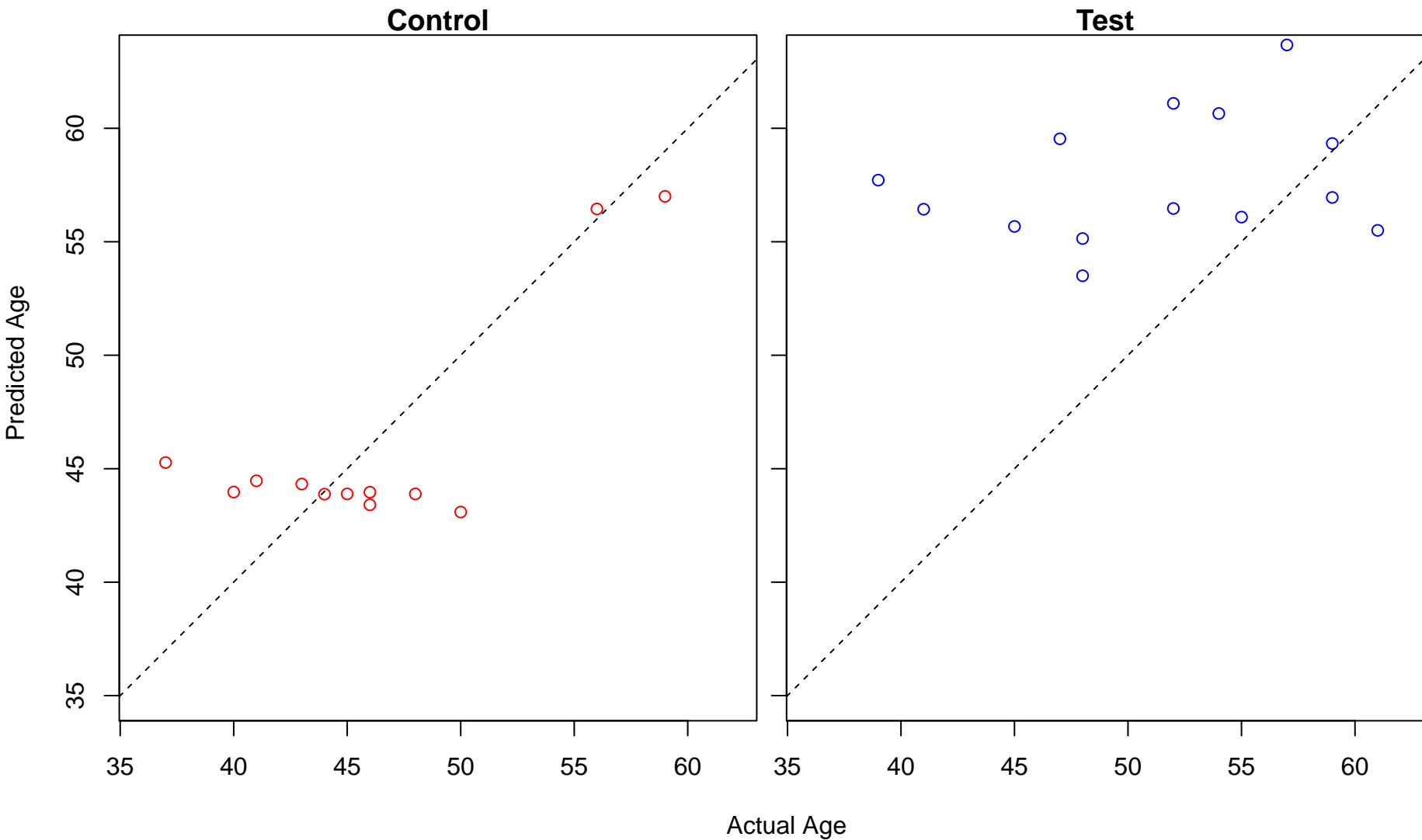
negative regulation of cell differentiation (Score: 2.757461)



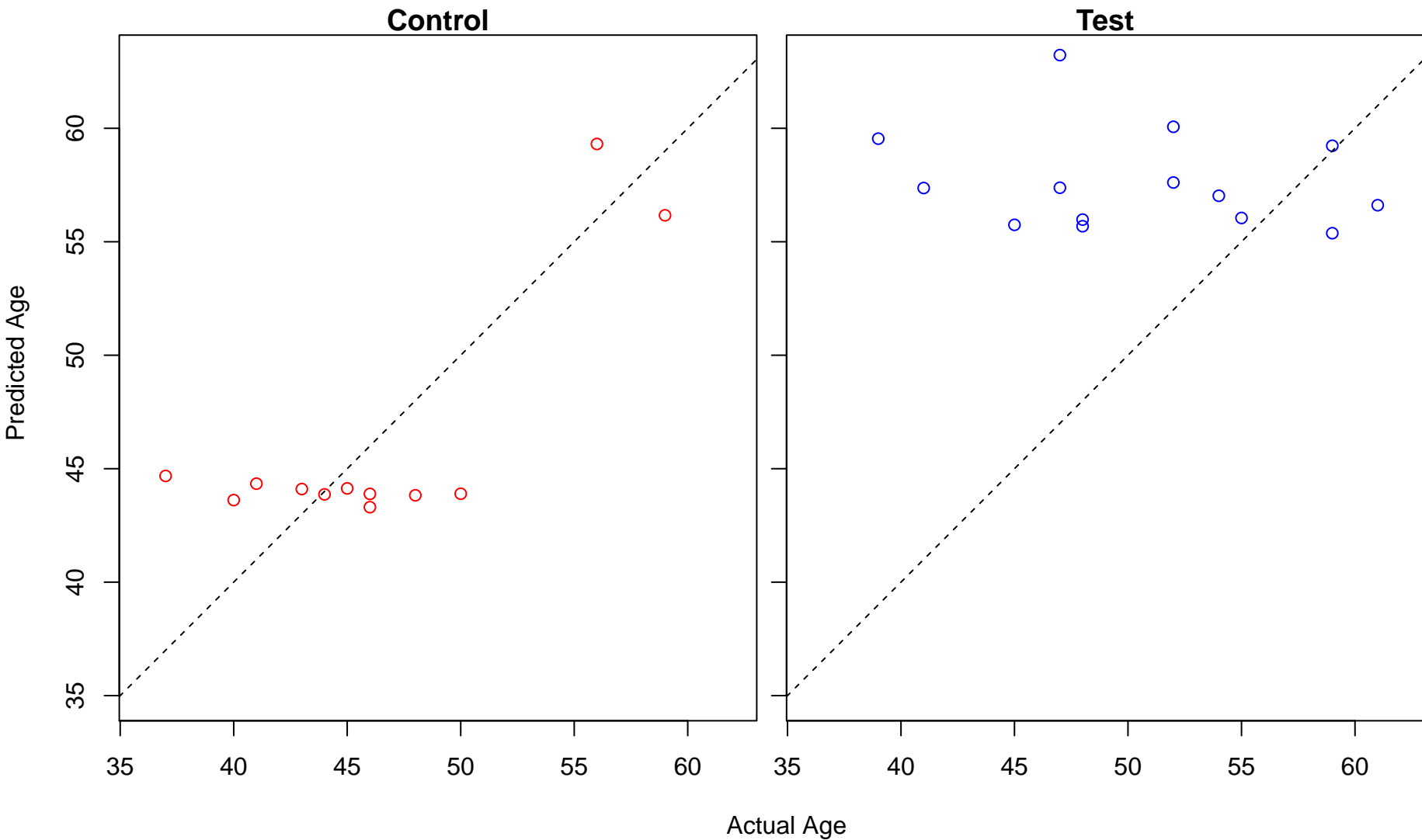
intracellular pH reduction (Score: 2.754589)



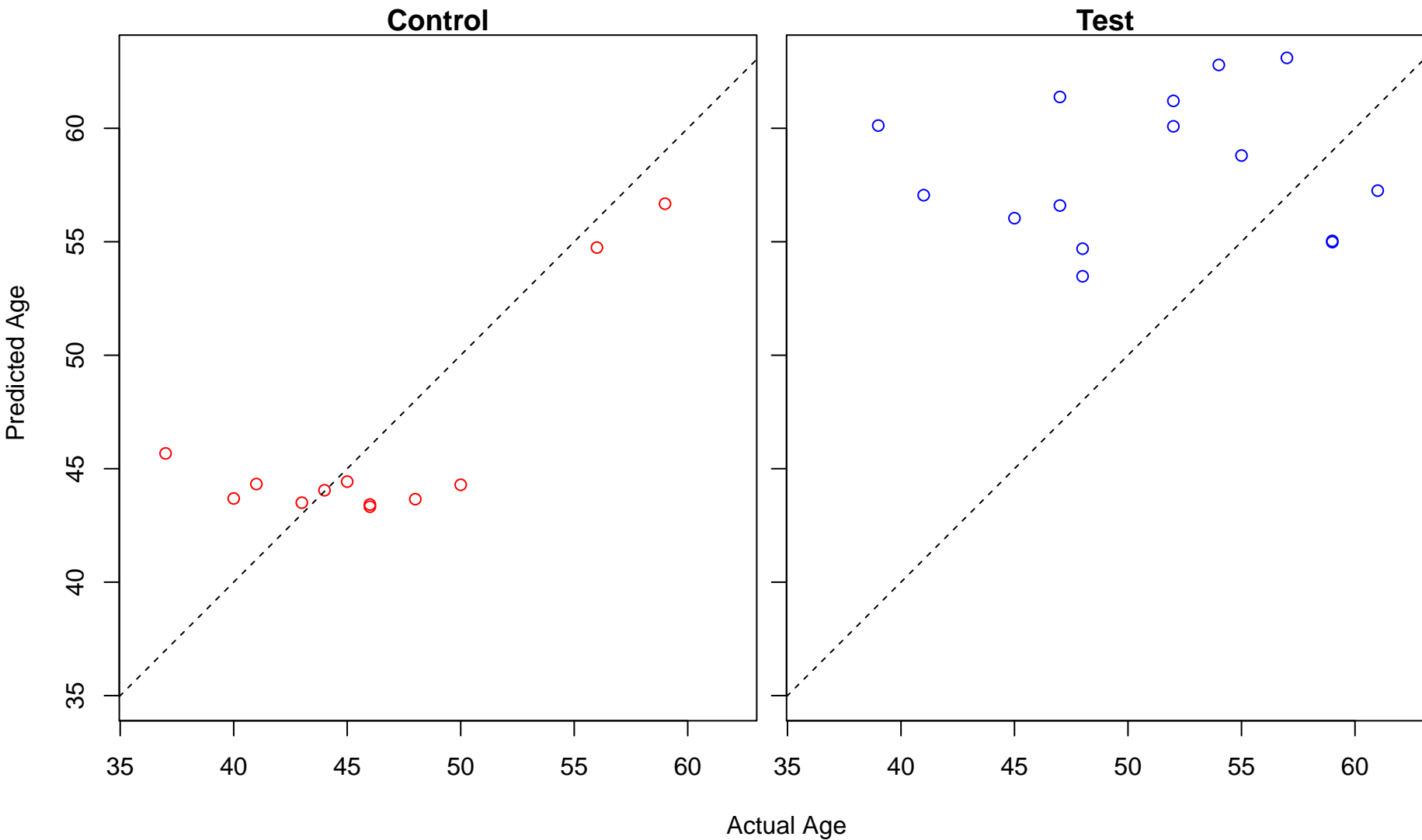
positive regulation of exocytosis (Score: 2.752533)



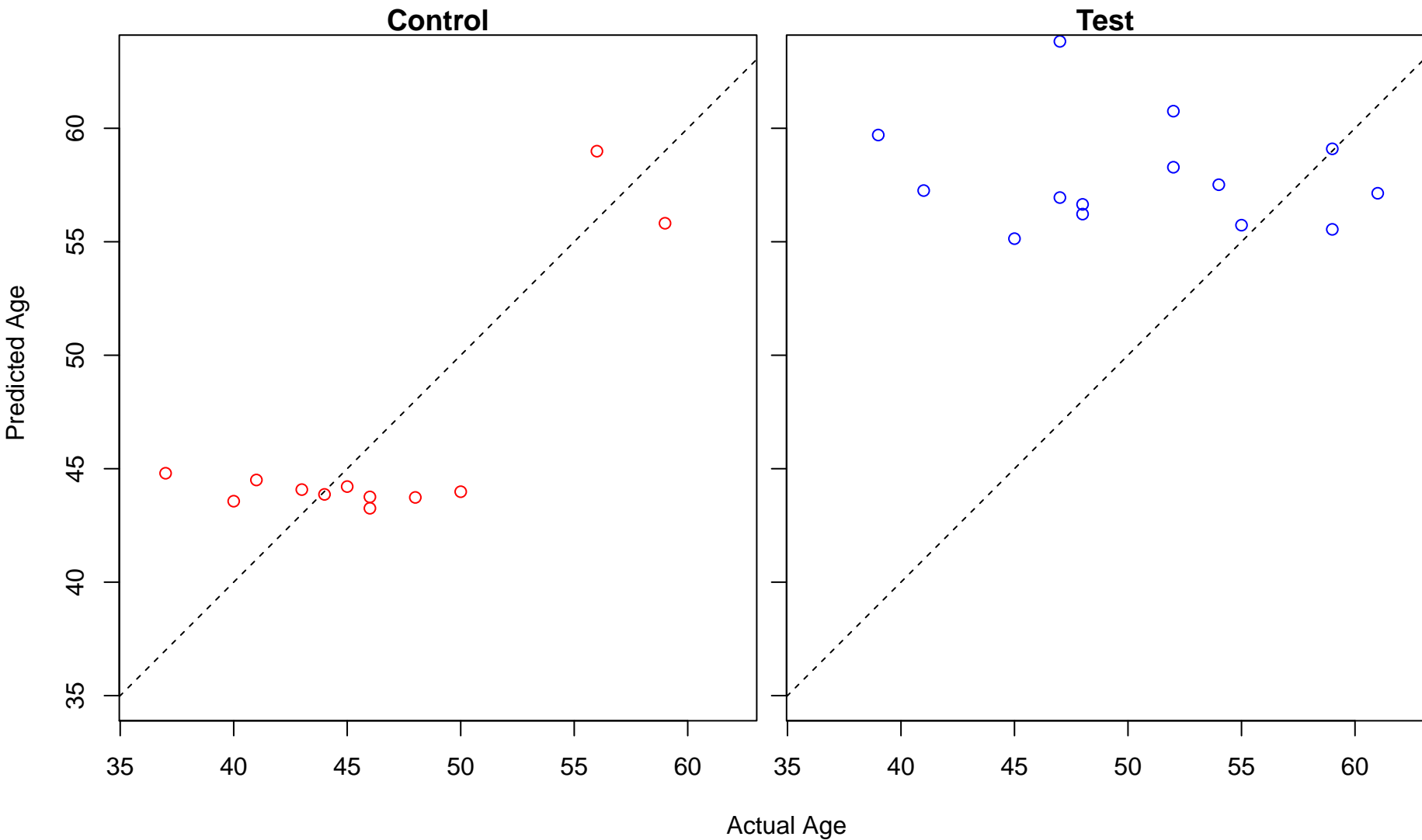
cellular protein catabolic process (Score: 2.751868)



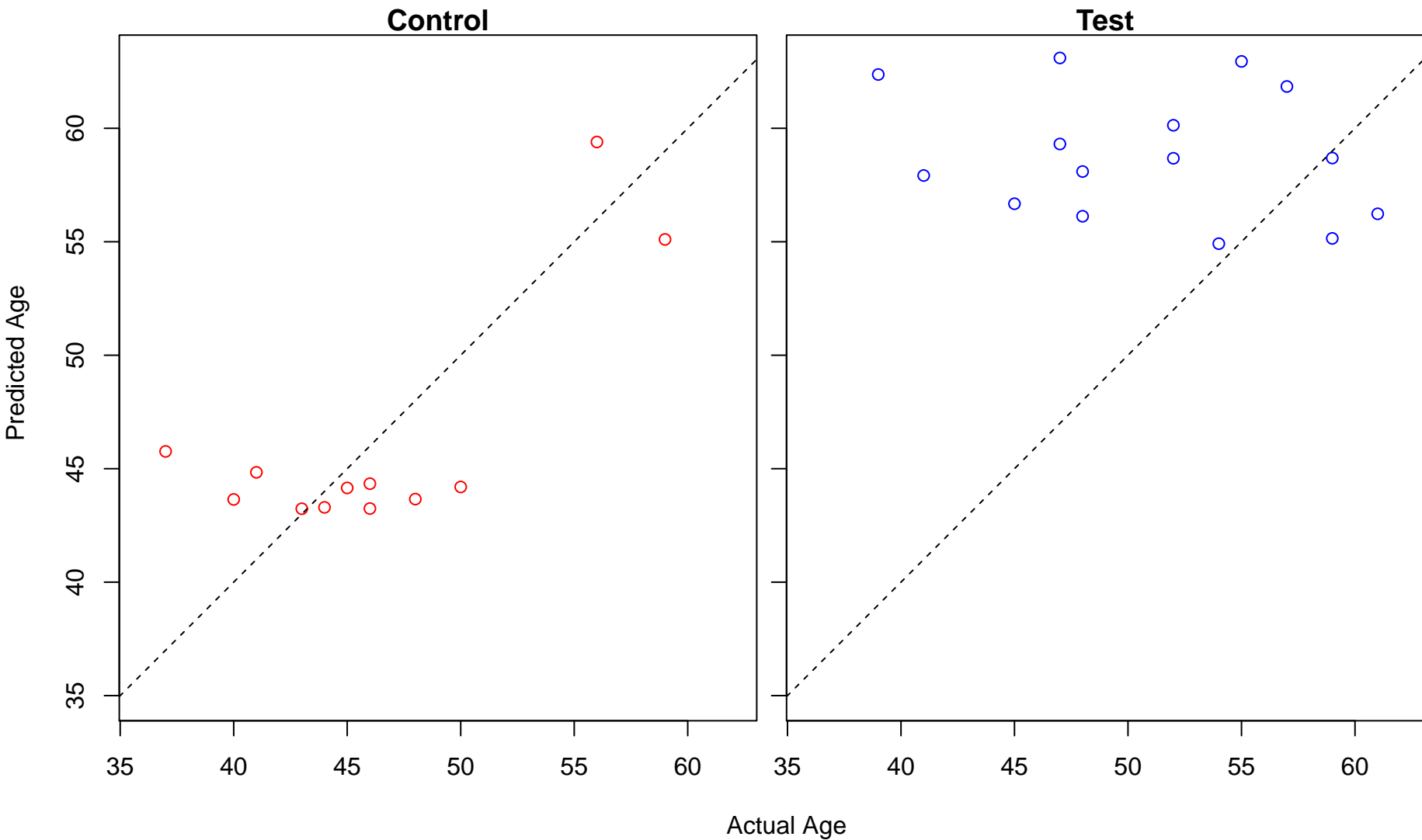
DNA deamination (Score: 2.750316)



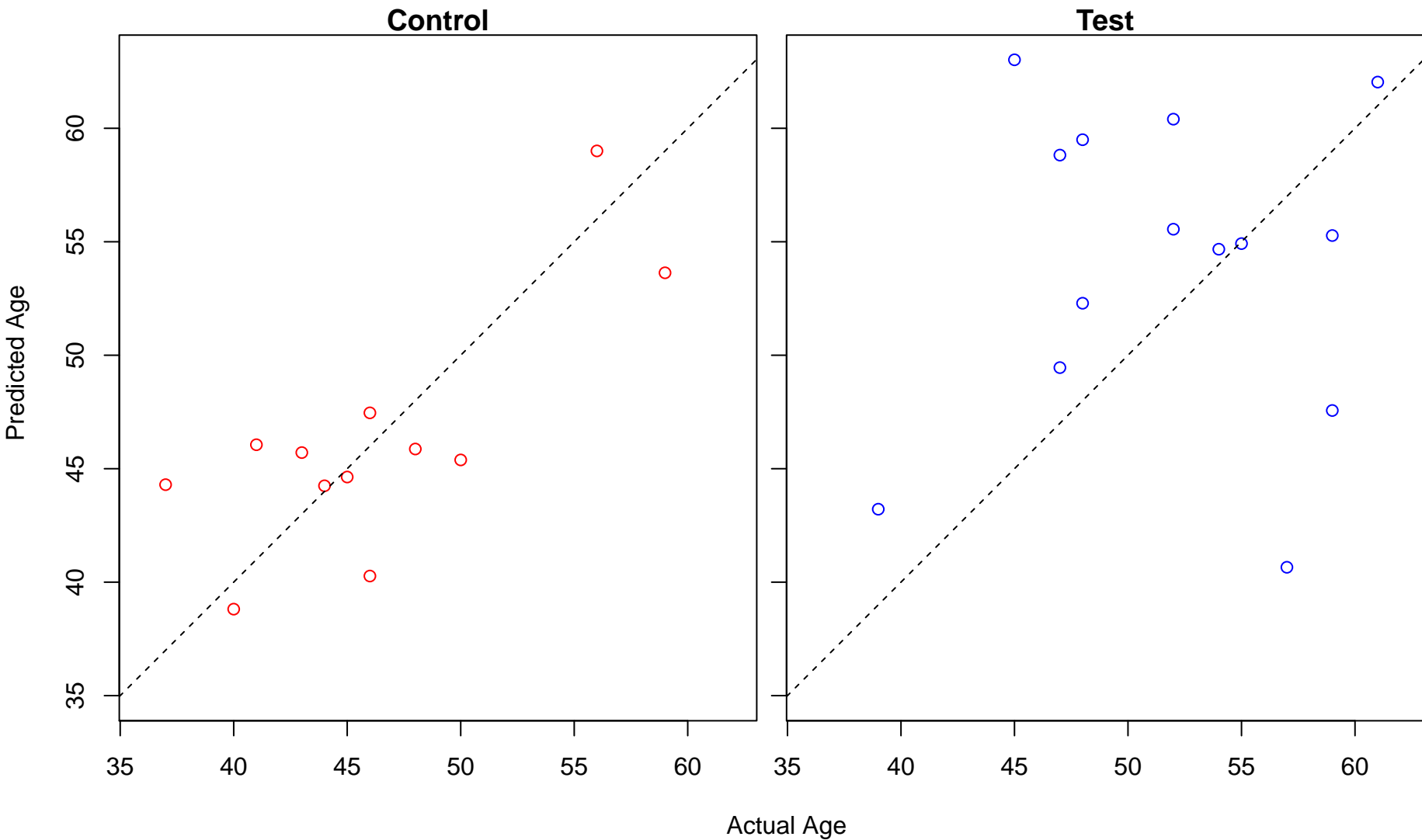
negative regulation of transferase activity (Score: 2.750296)



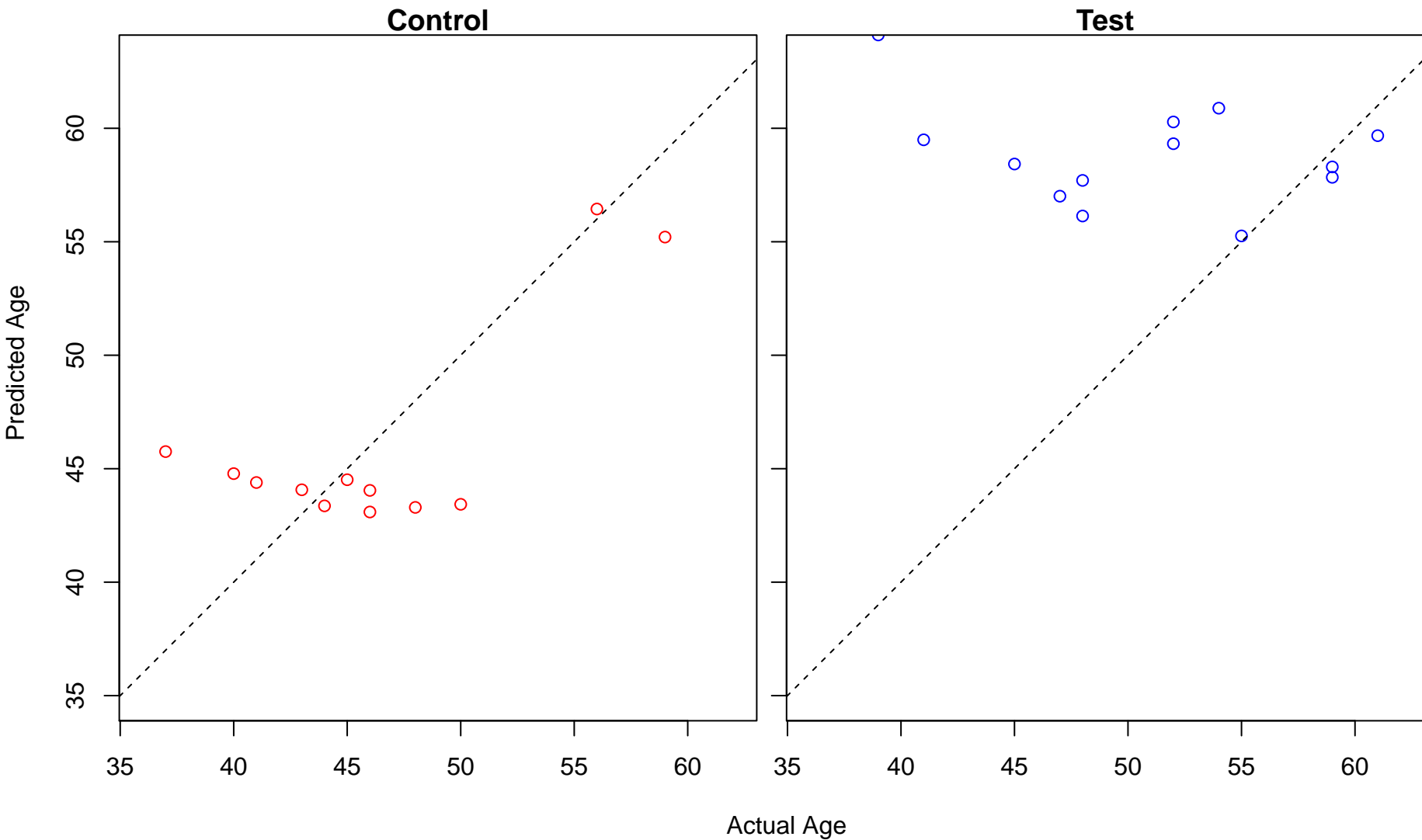
cellular response to biotic stimulus (Score: 2.749971)



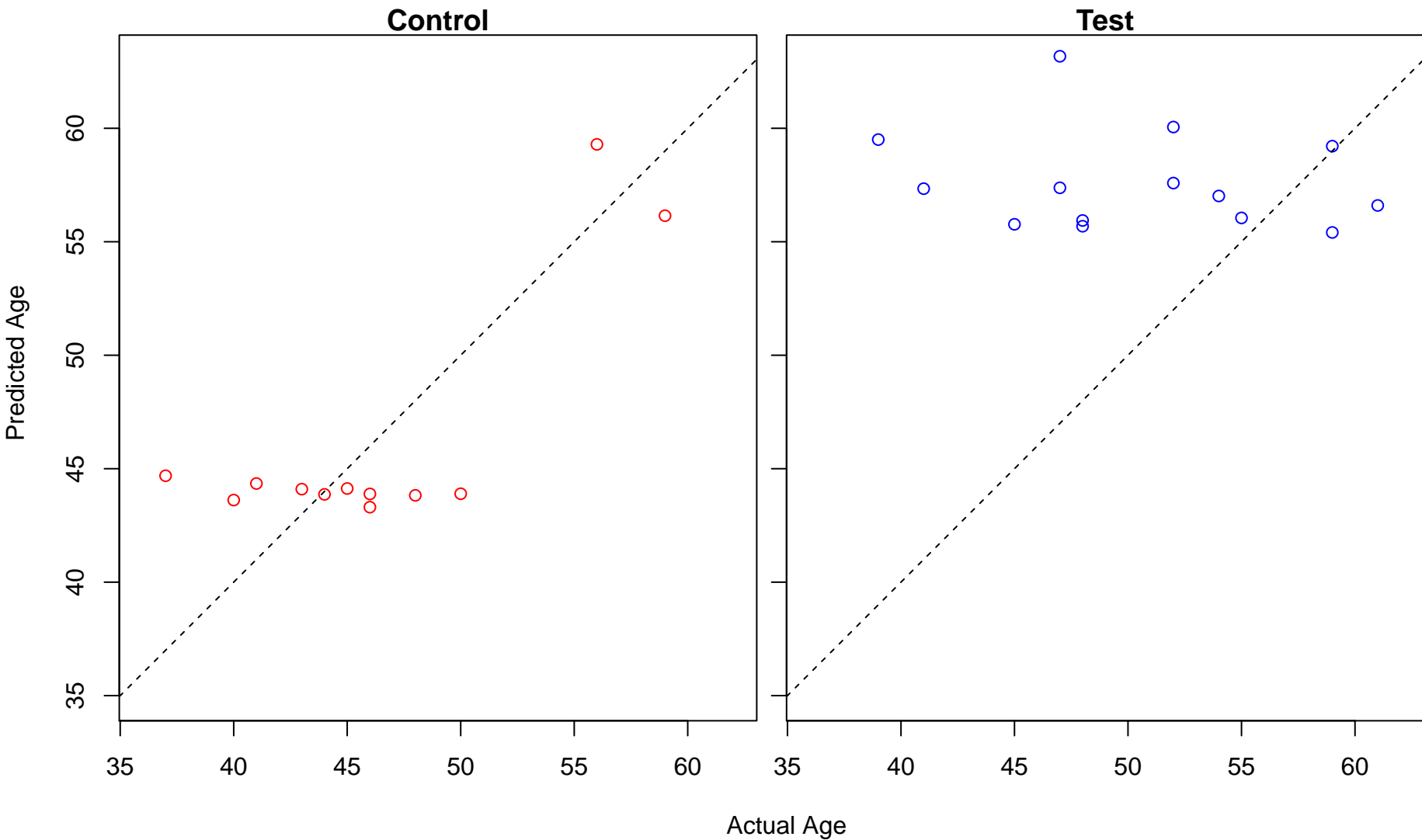
regulation of cytokine secretion (Score: 2.742666)



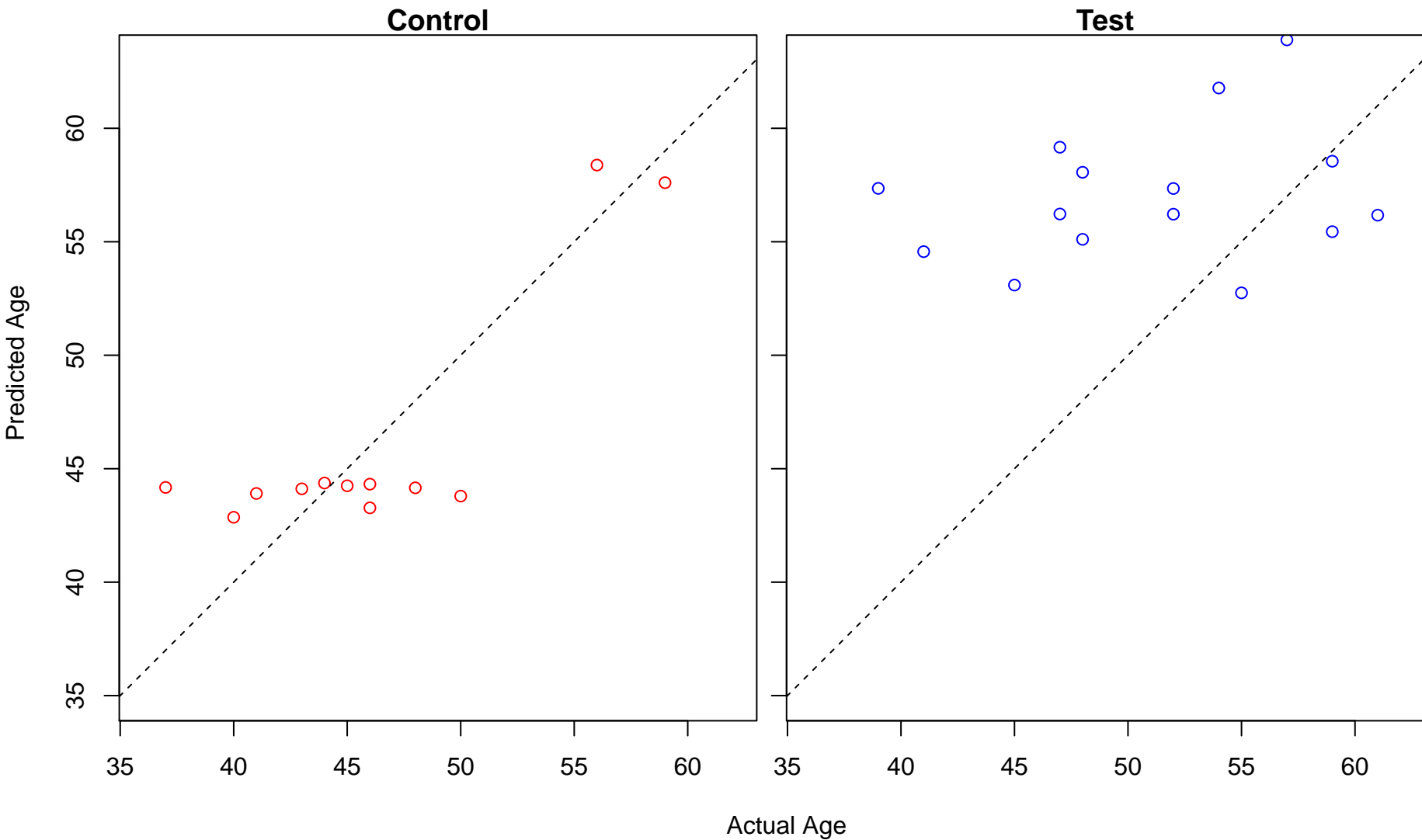
positive regulation of cellular amide metabolic process (Score: 2.741264)



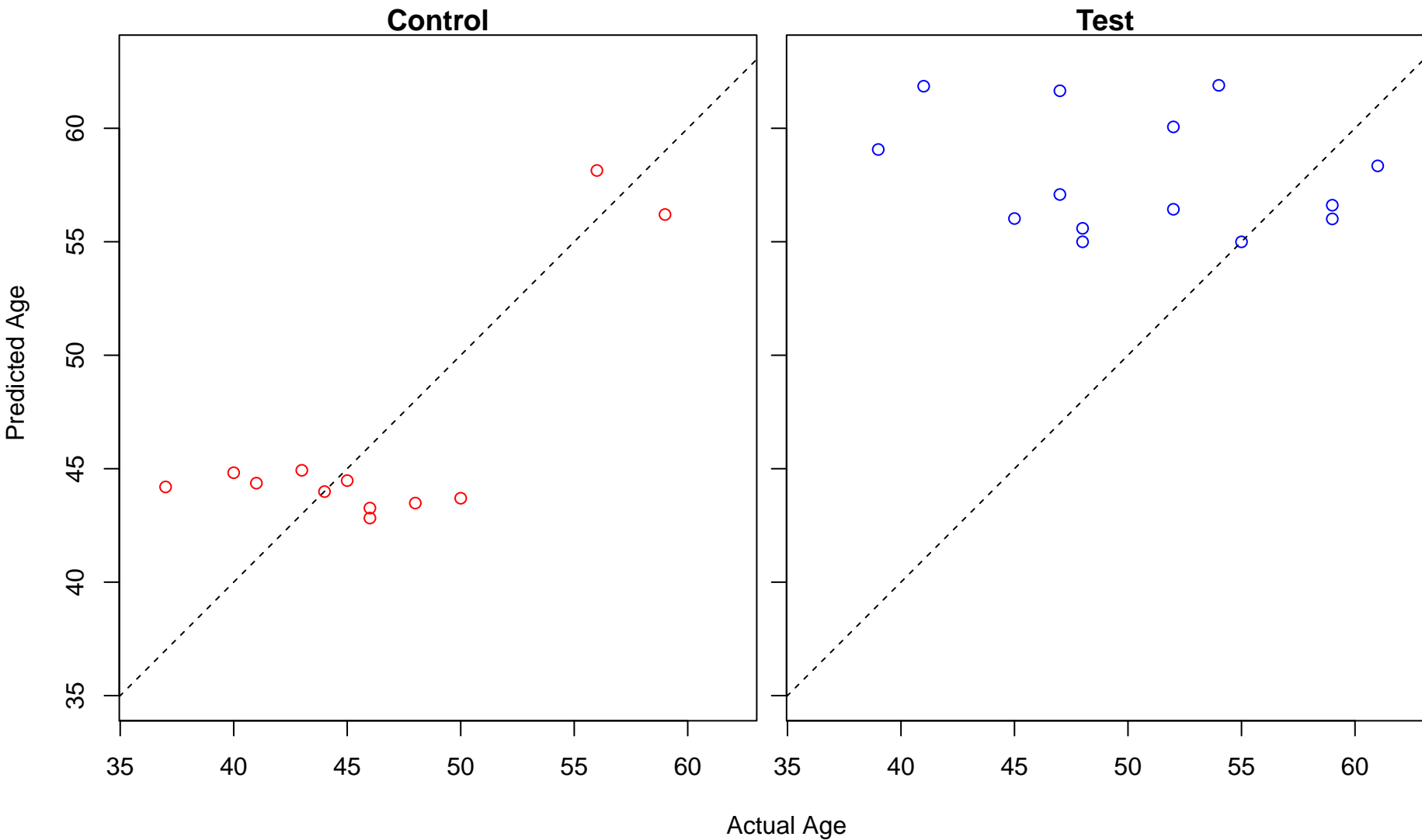
protein catabolic process (Score: 2.740432)



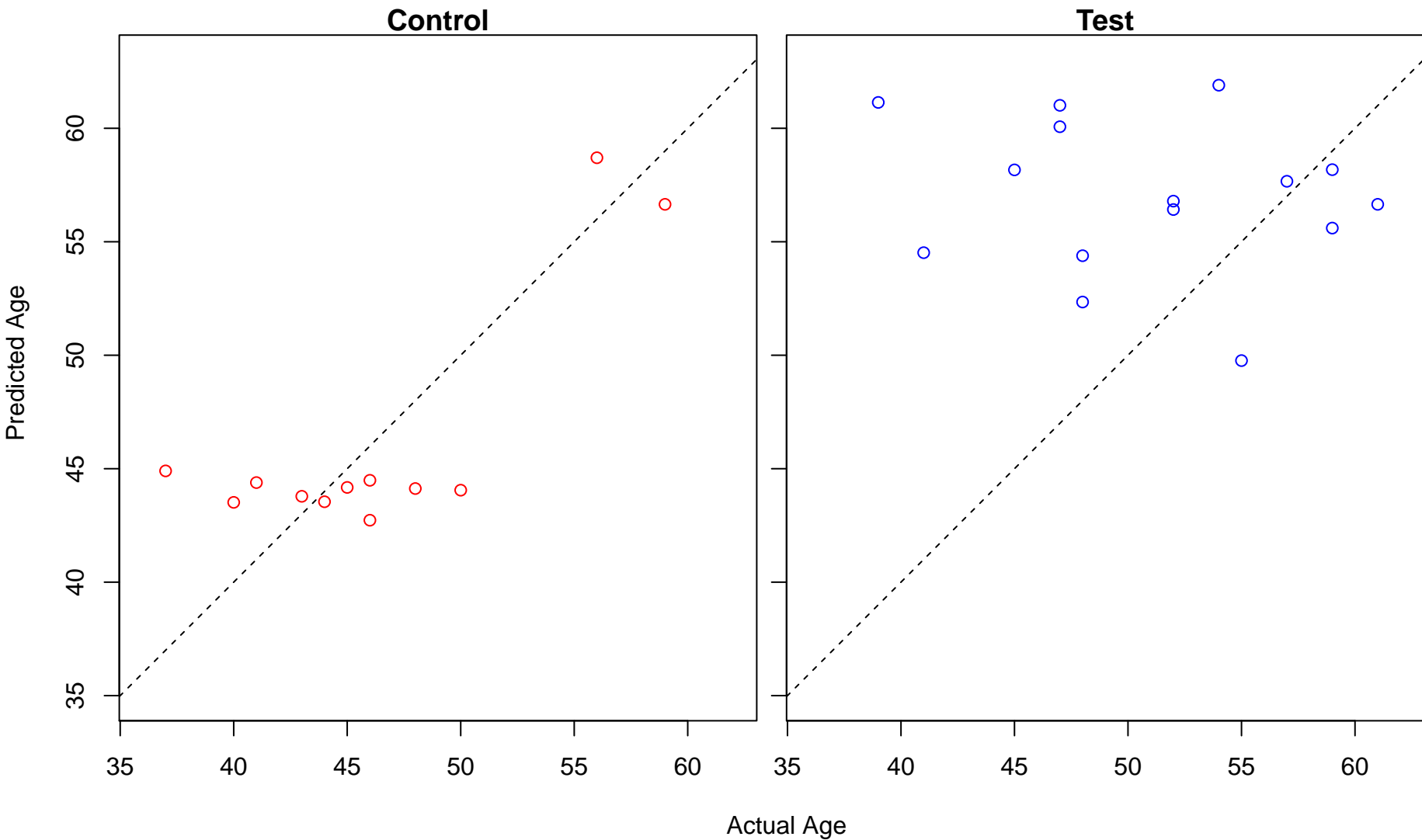
peptidyl-arginine modification (Score: 2.740358)



pyruvate metabolic process (Score: 2.740154)

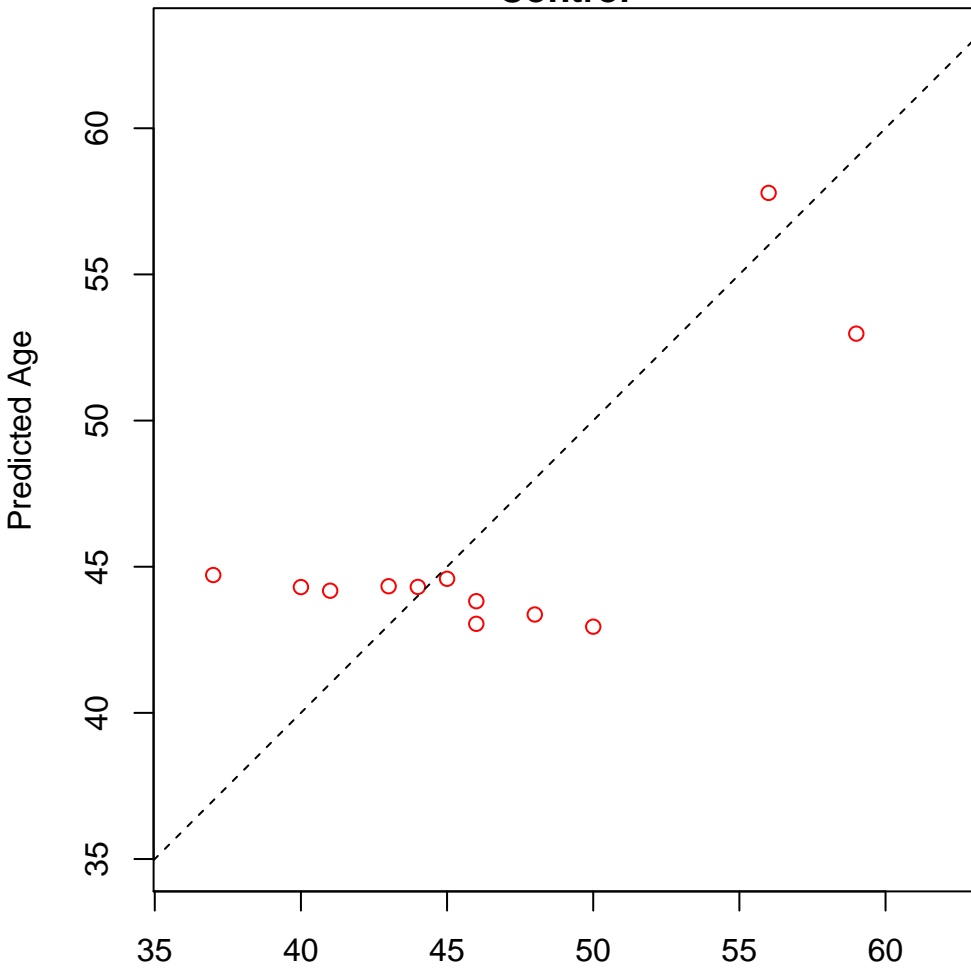


regulation of epidermal growth factor-activated receptor activity (Score: 2.739555)

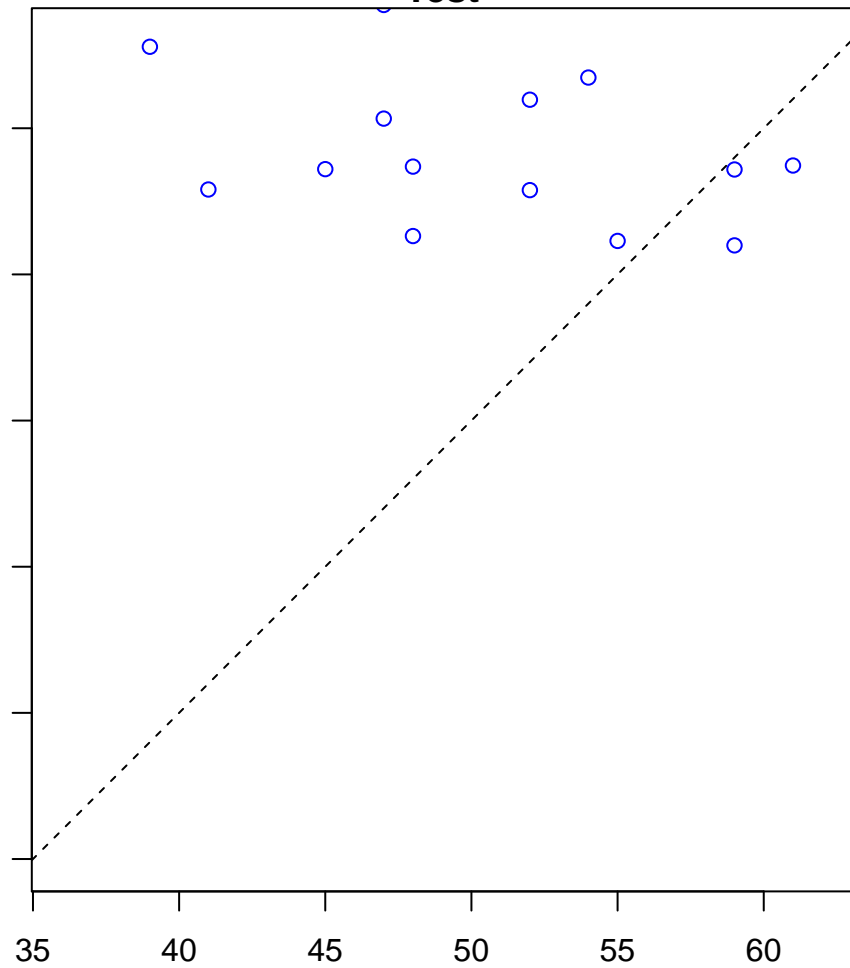


purine nucleotide biosynthetic process (Score: 2.737030)

Control

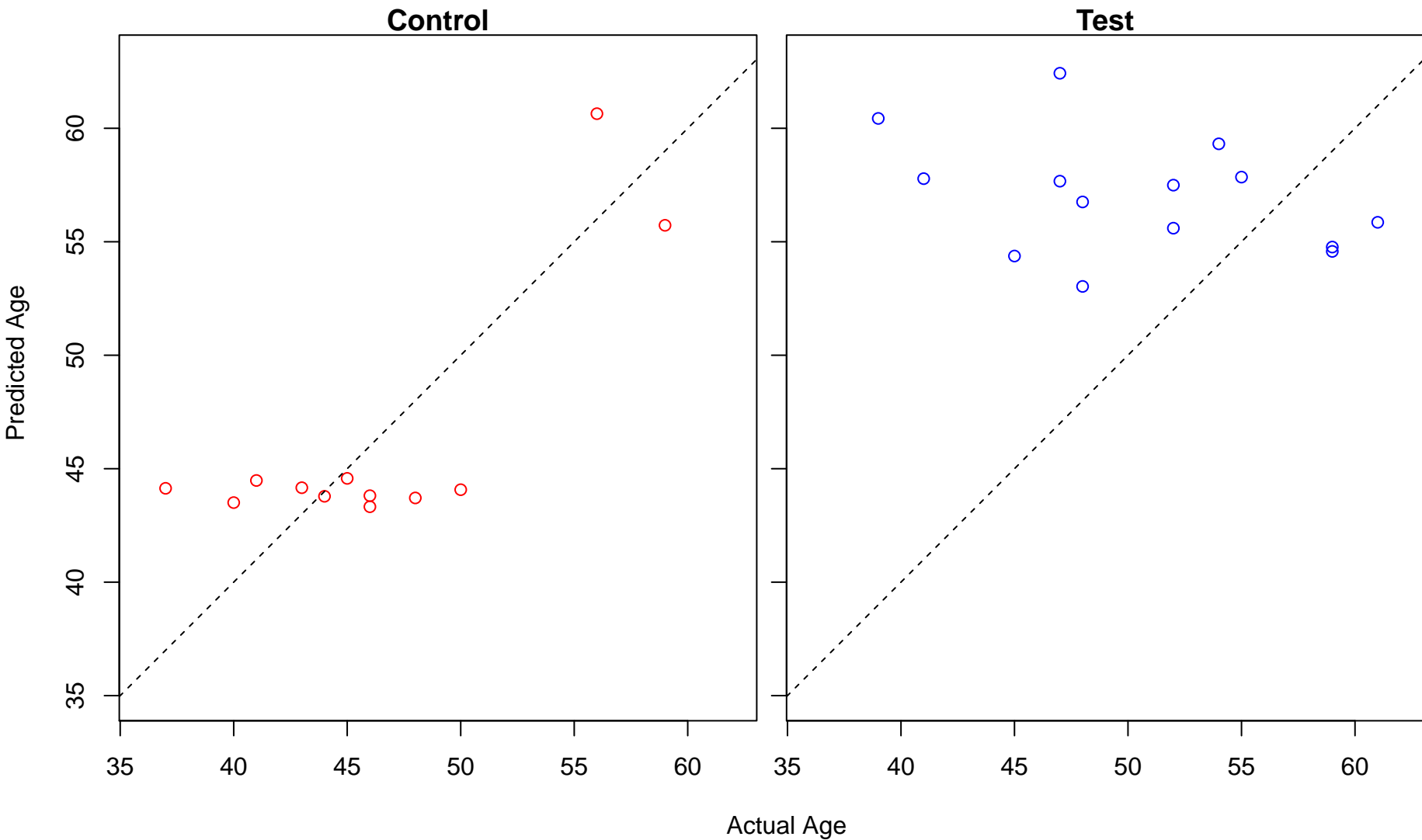


Test

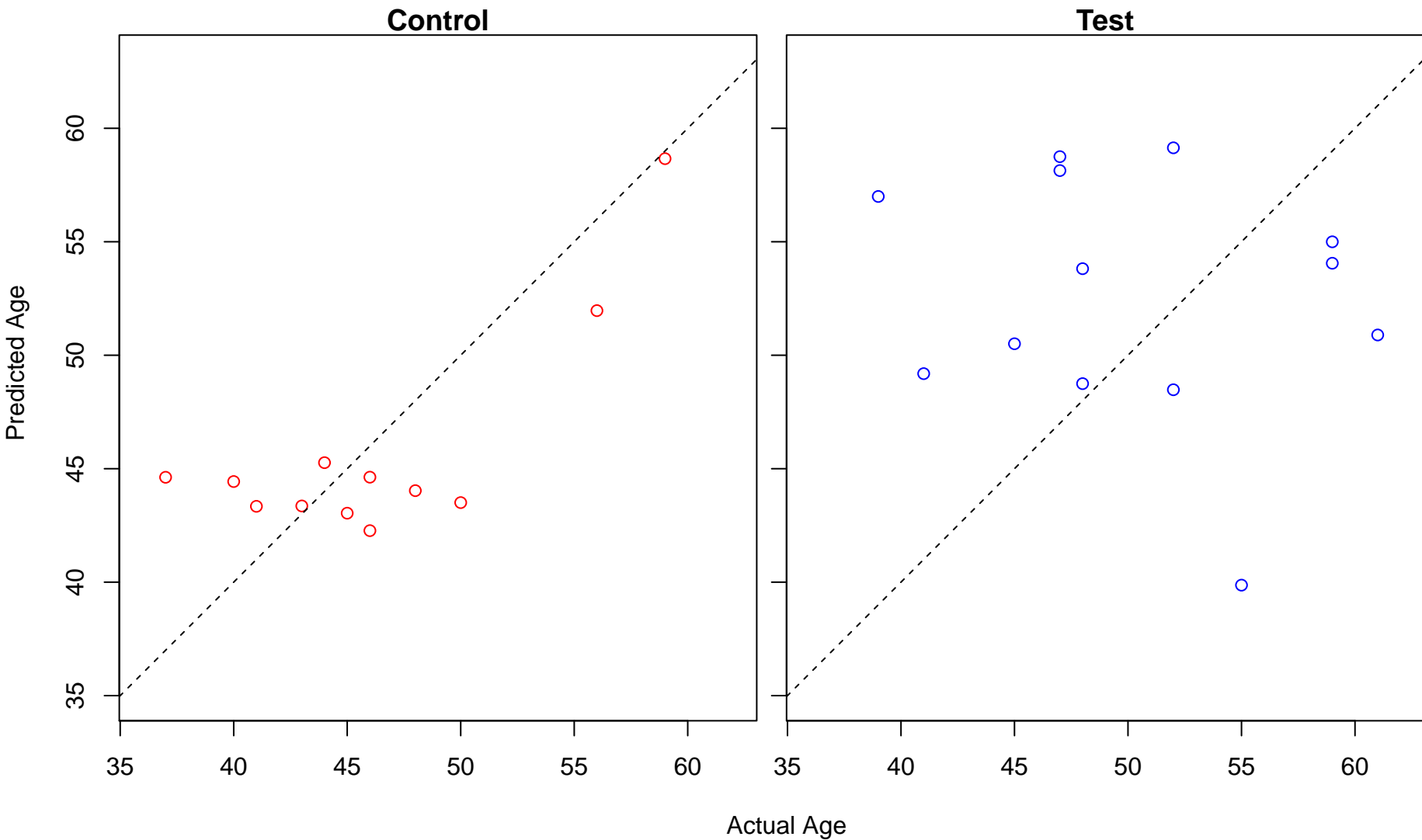


Actual Age

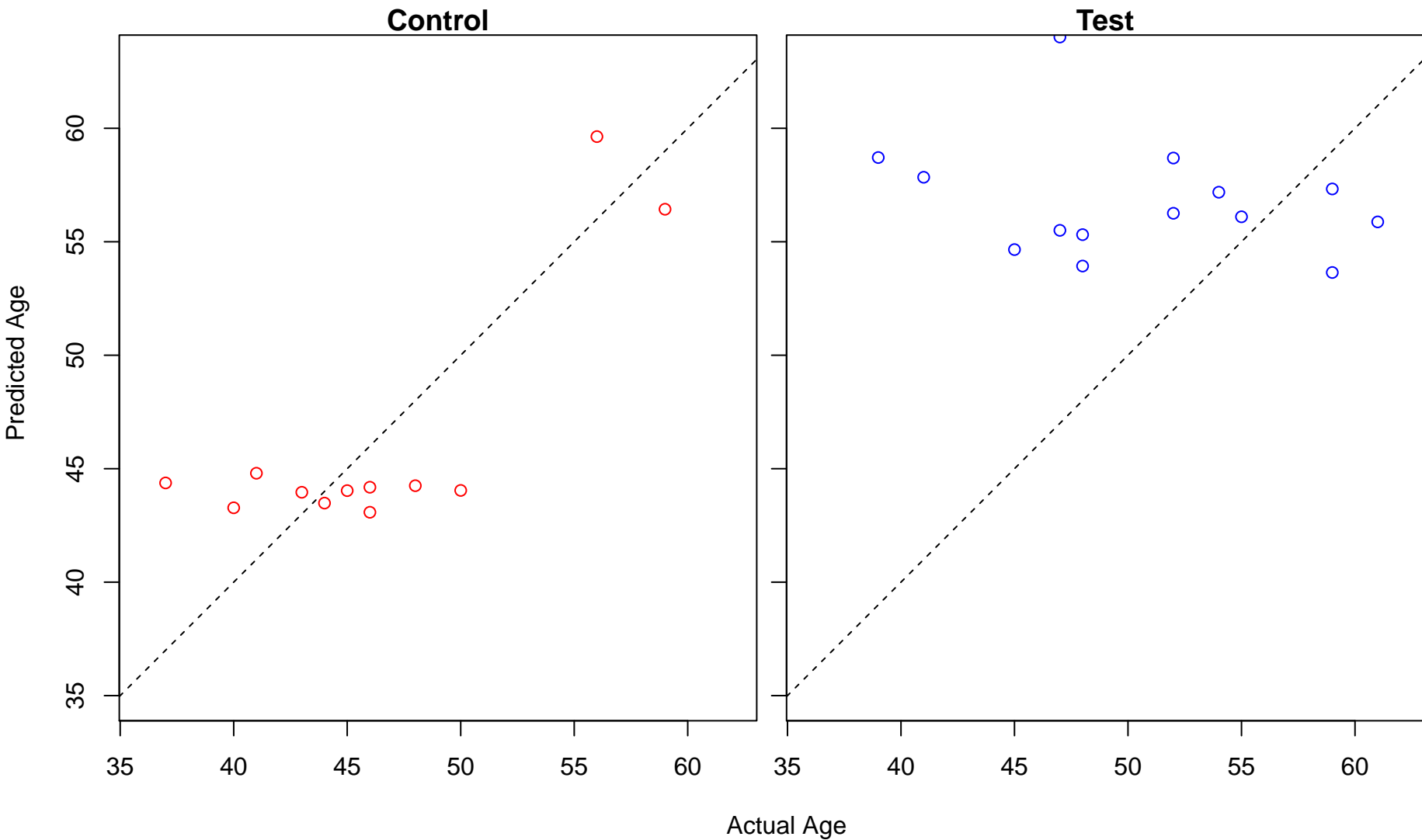
cell division (Score: 2.735728)



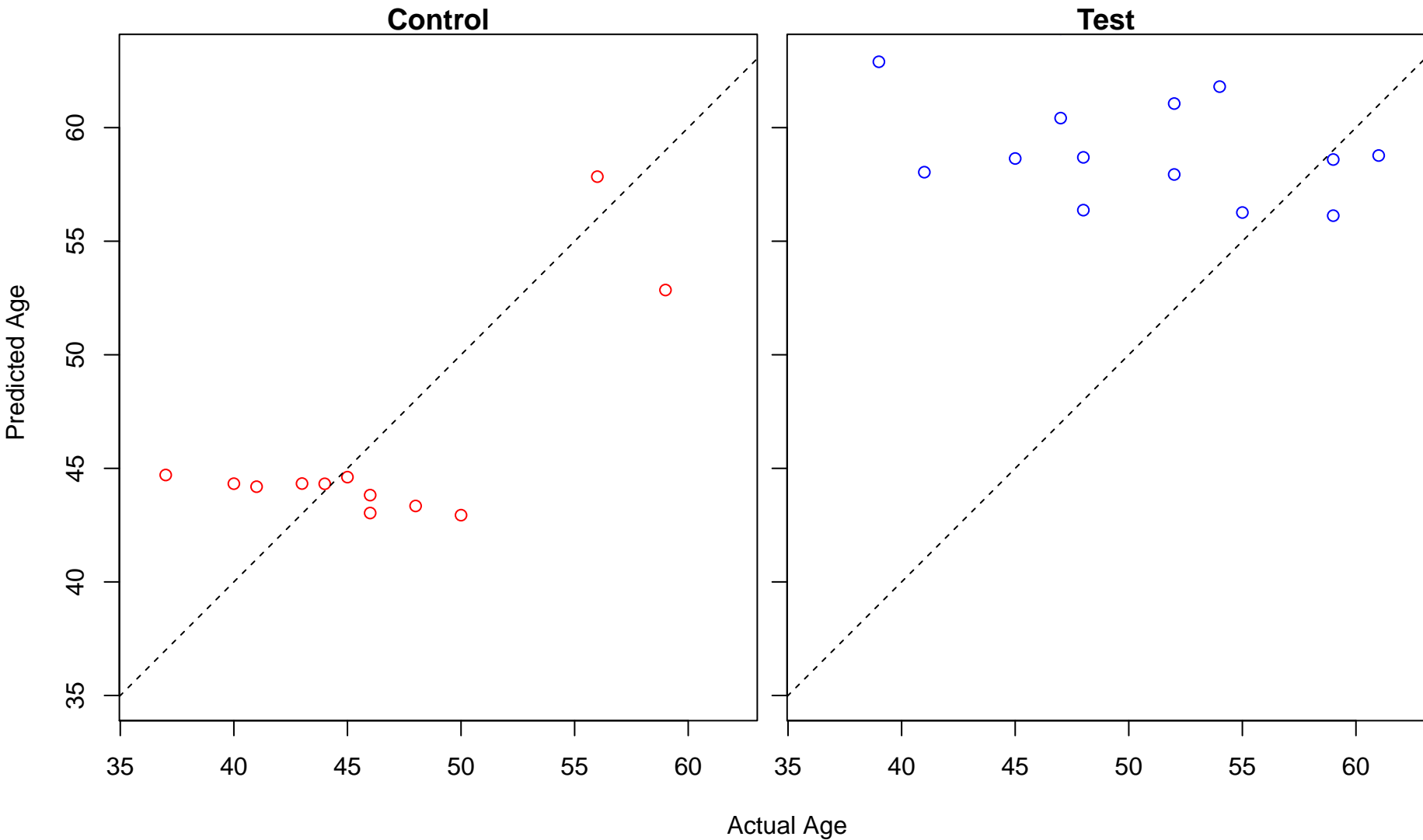
monovalent inorganic cation homeostasis (Score: 2.733212)



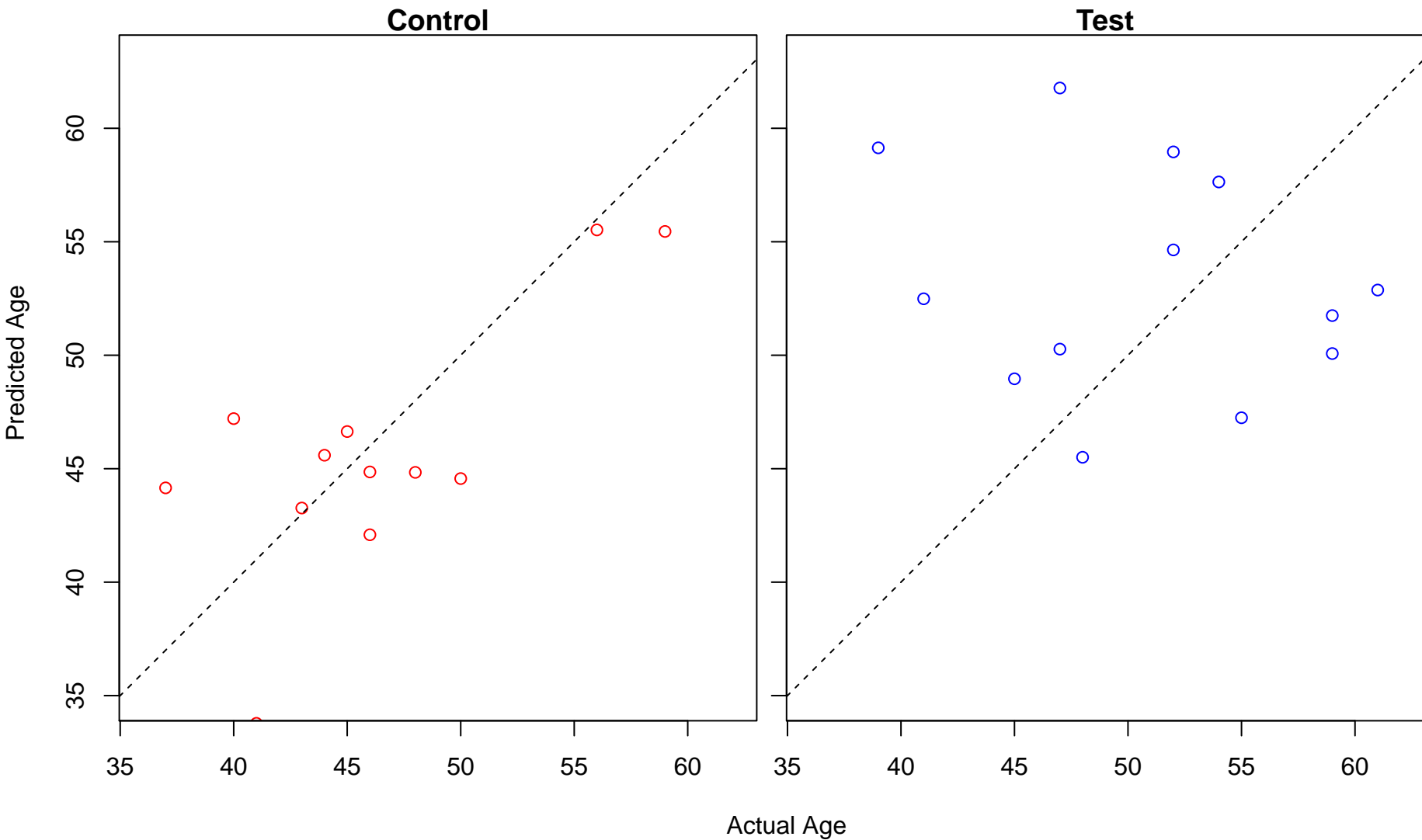
negative regulation of cellular protein catabolic process (Score: 2.732197)



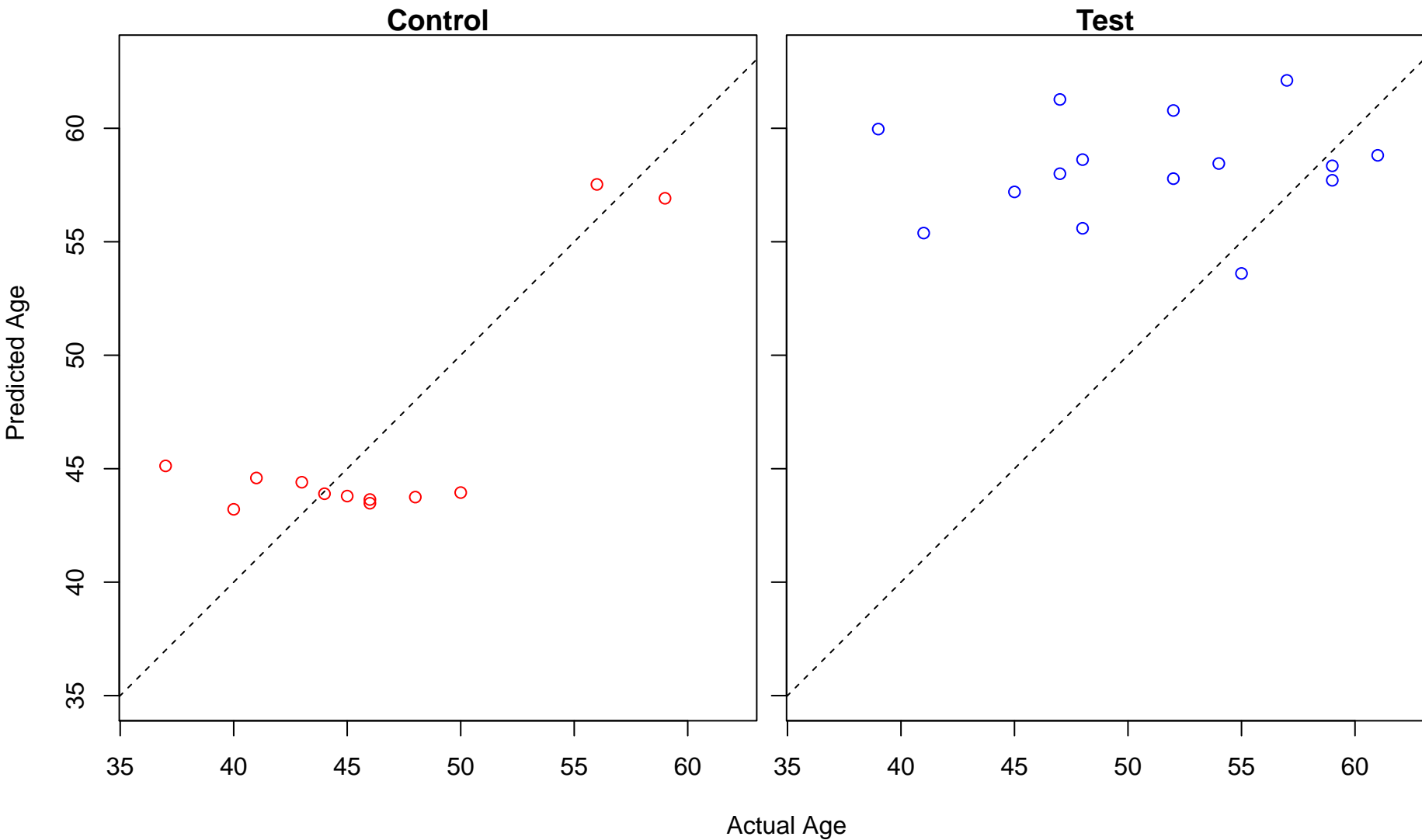
purine ribonucleotide biosynthetic process (Score: 2.731045)



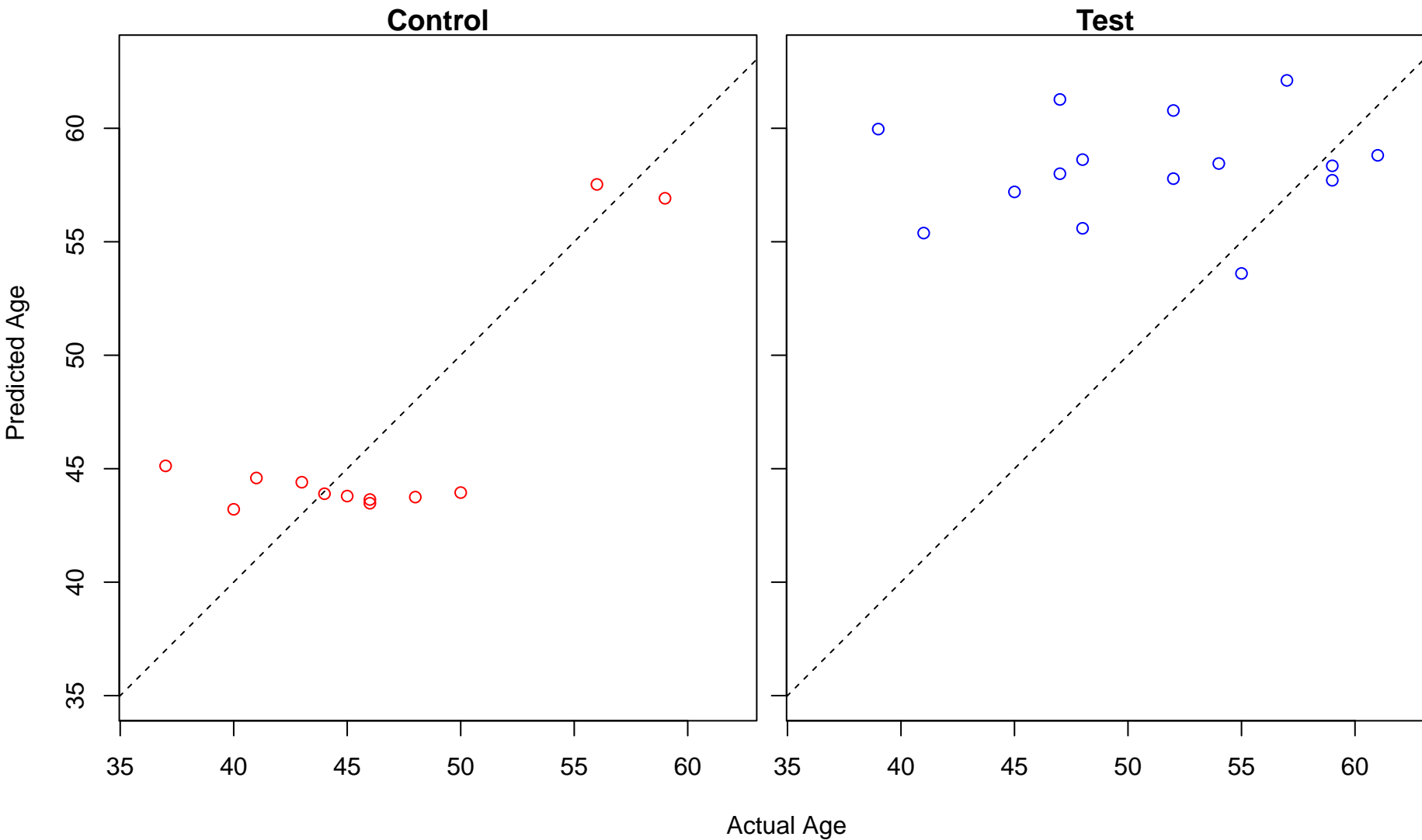
regulation of mitochondrial depolarization (Score: 2.729077)



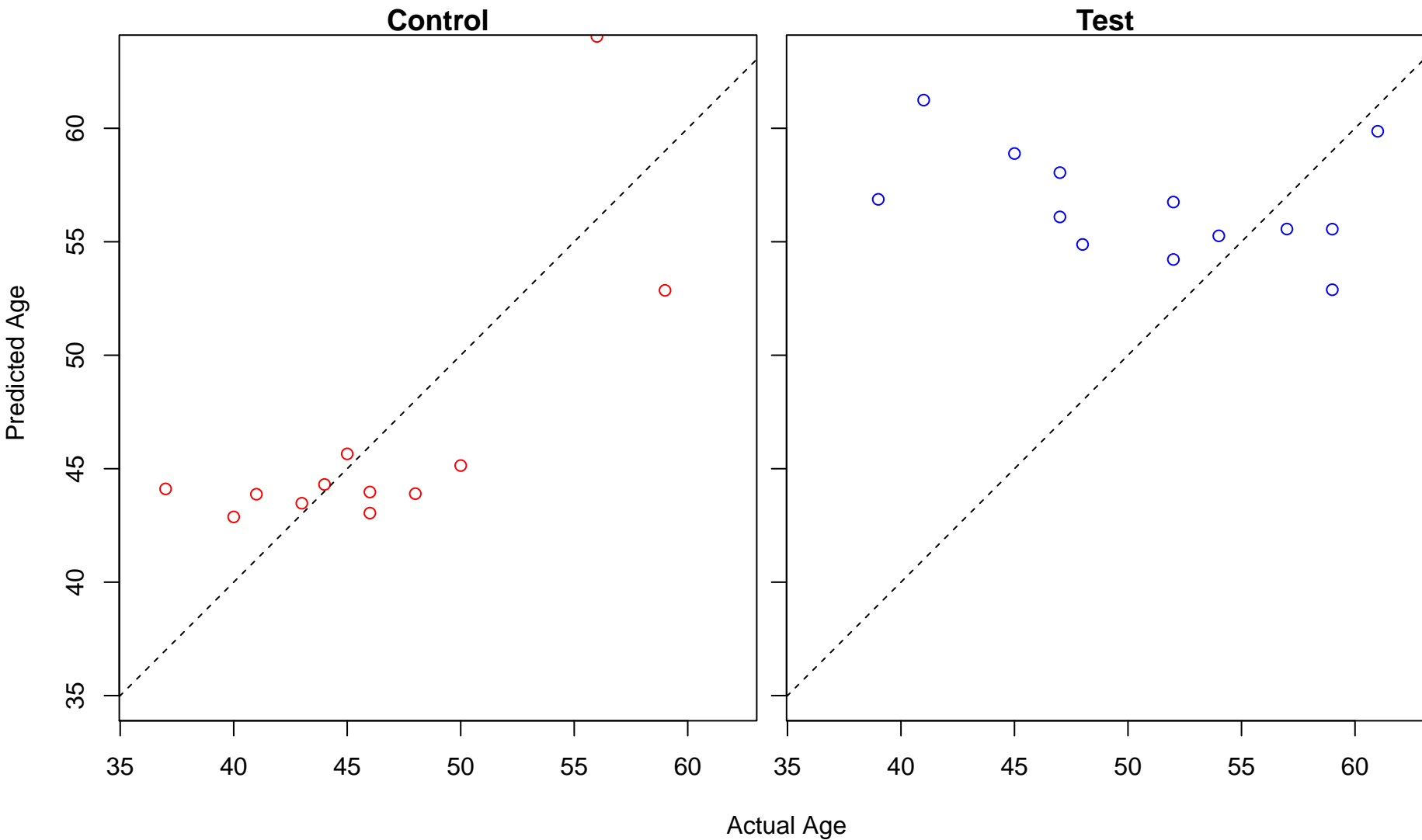
organic acid catabolic process (Score: 2.728994)



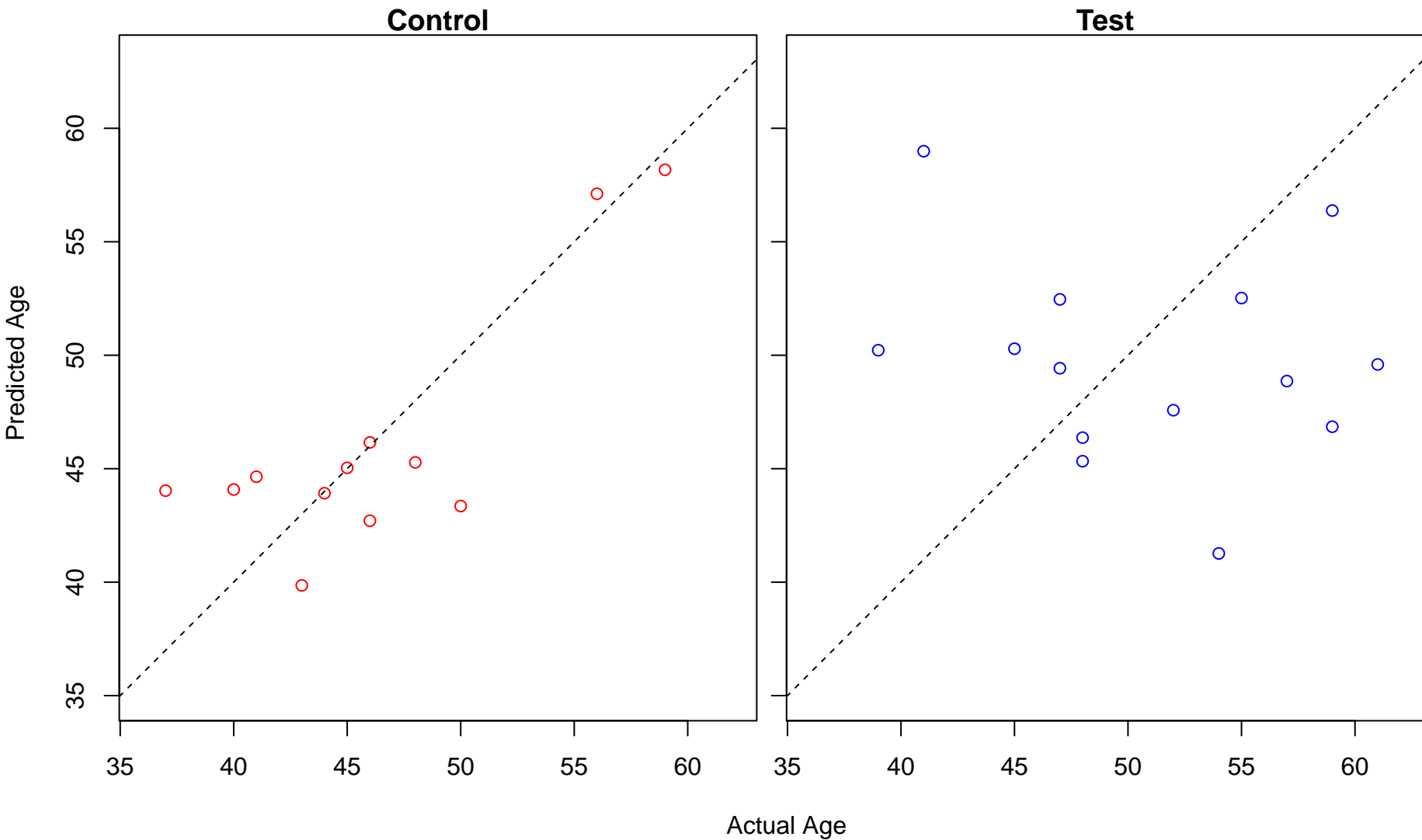
carboxylic acid catabolic process (Score: 2.728994)



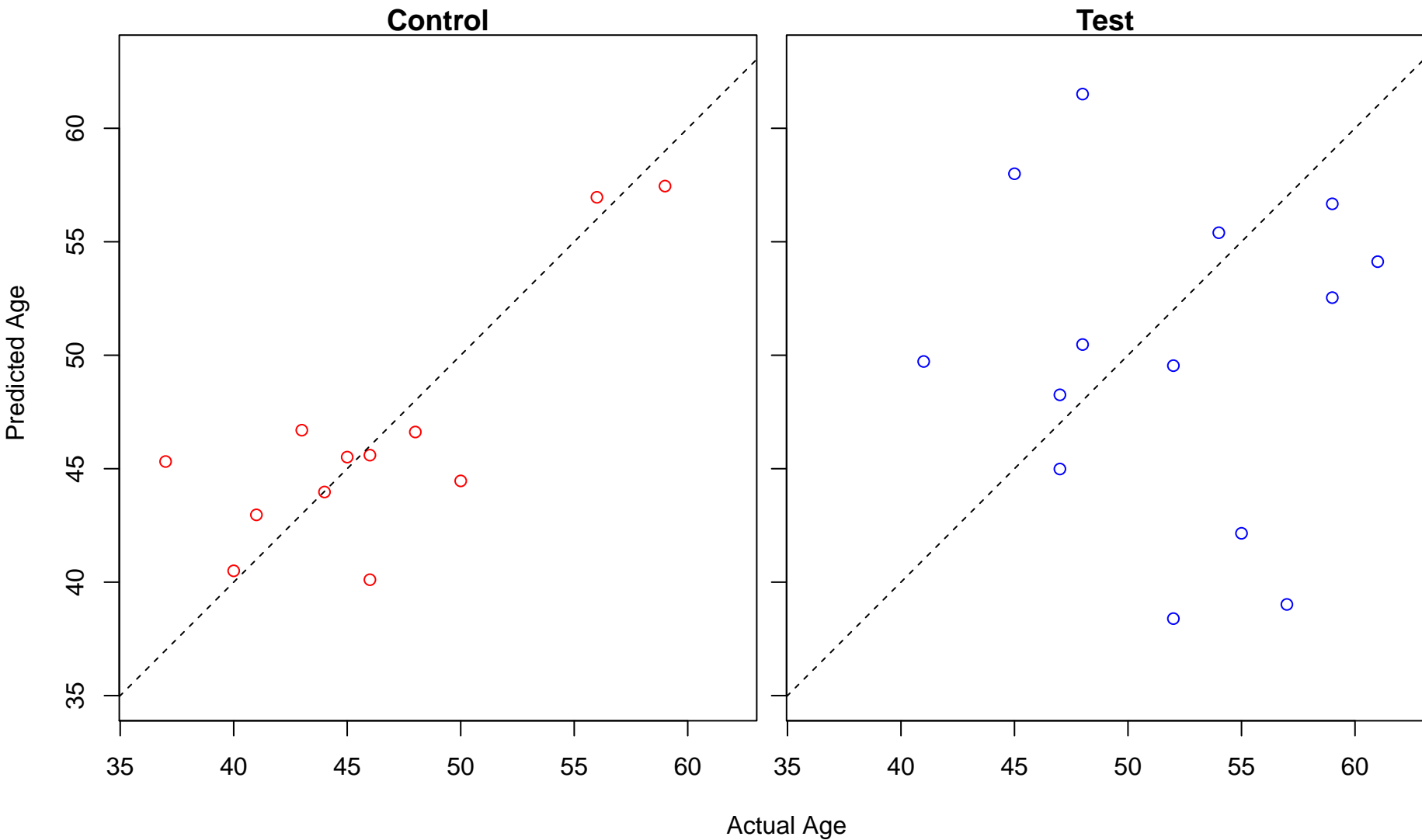
protein O-linked fucosylation (Score: 2.721148)



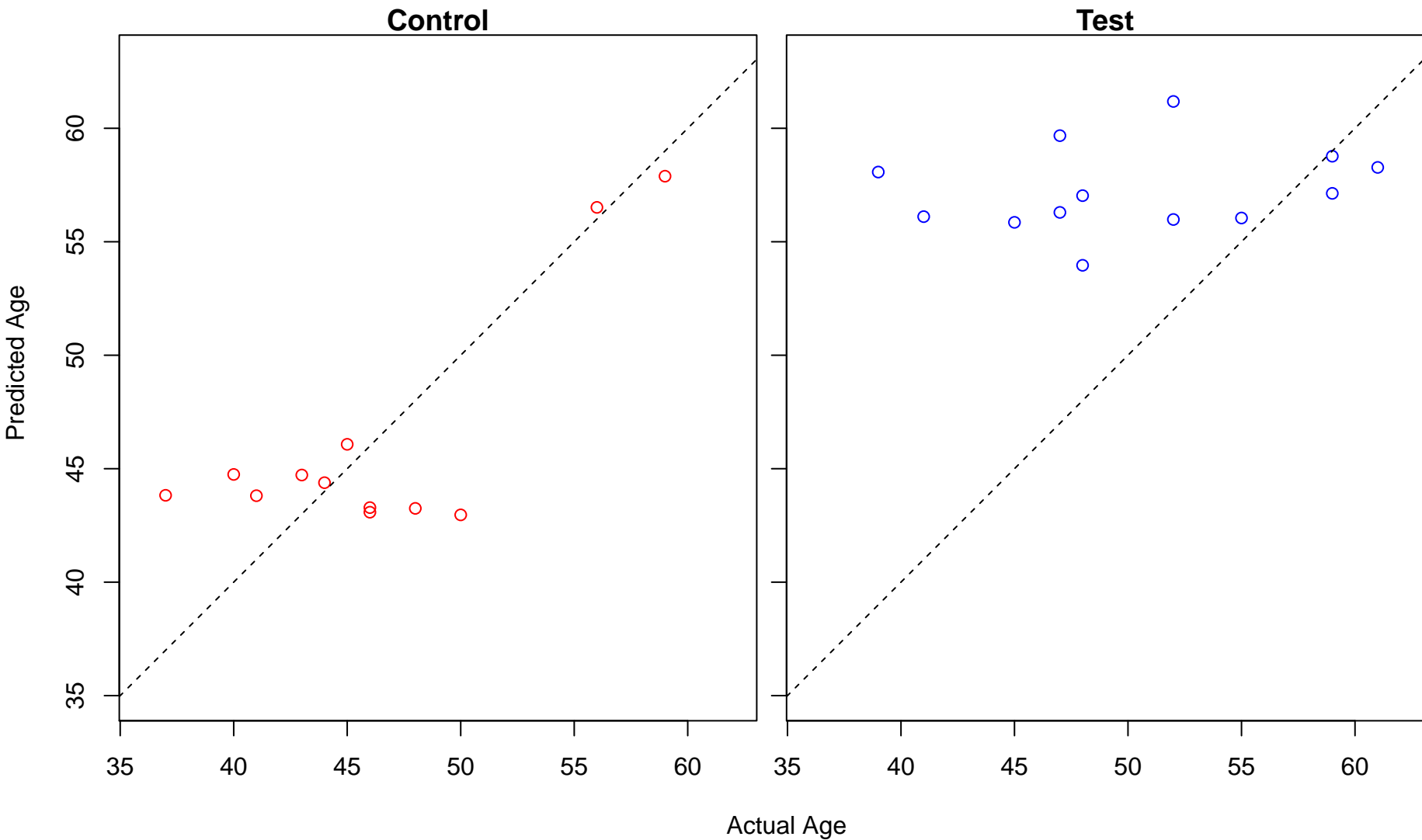
monovalent inorganic anion homeostasis (Score: 2.719308)



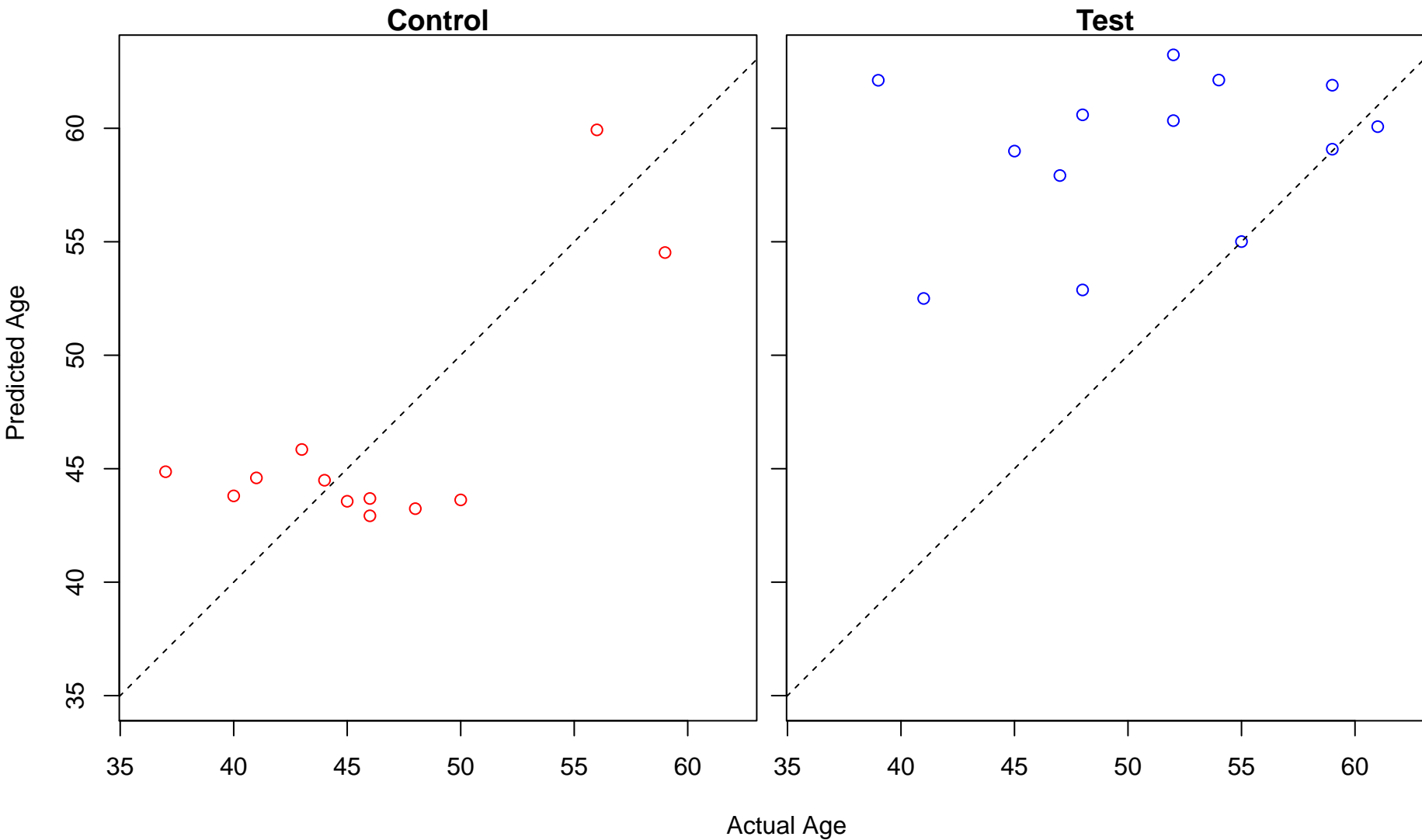
regulation of growth (Score: 2.719209)



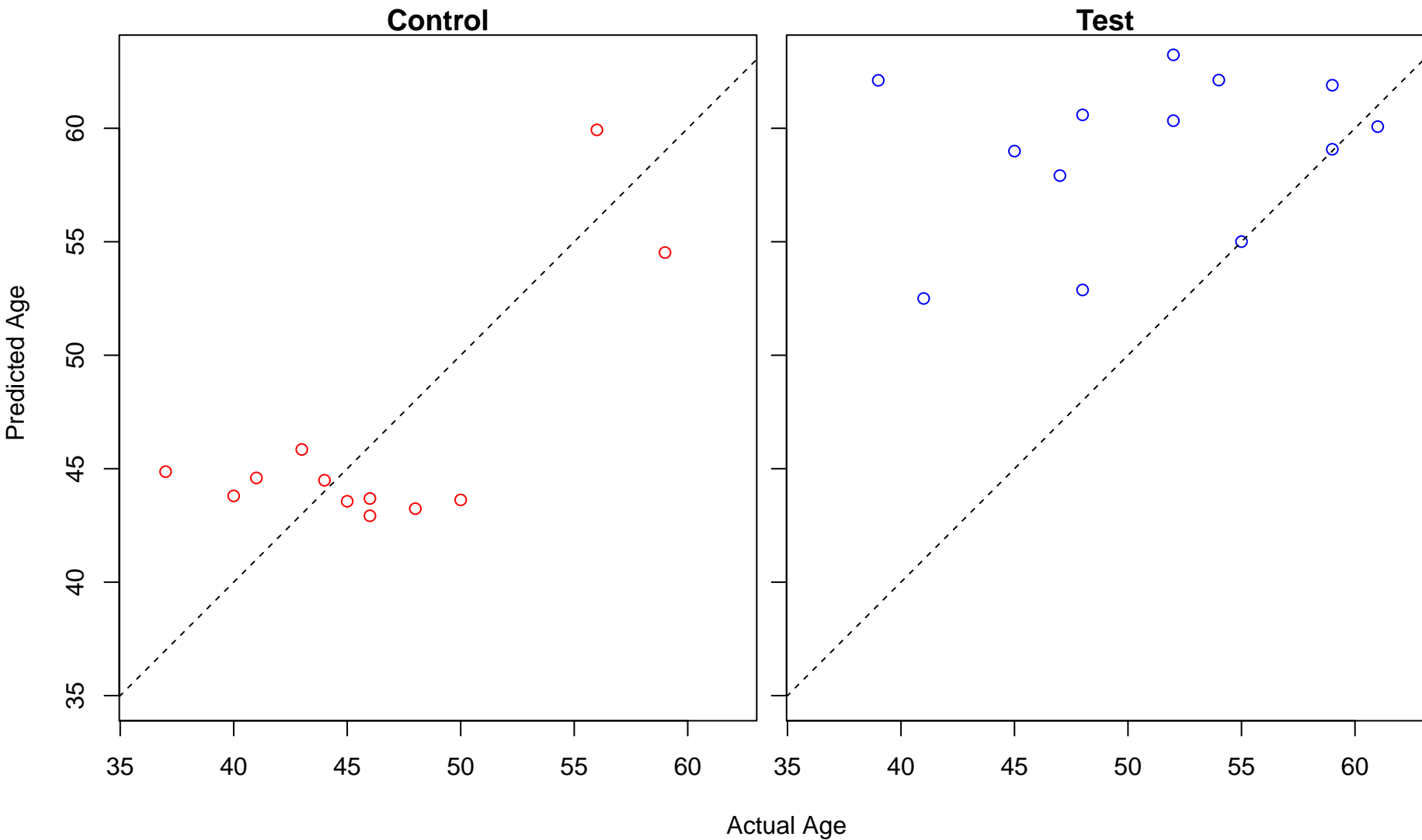
ATP synthesis coupled electron transport (Score: 2.718424)



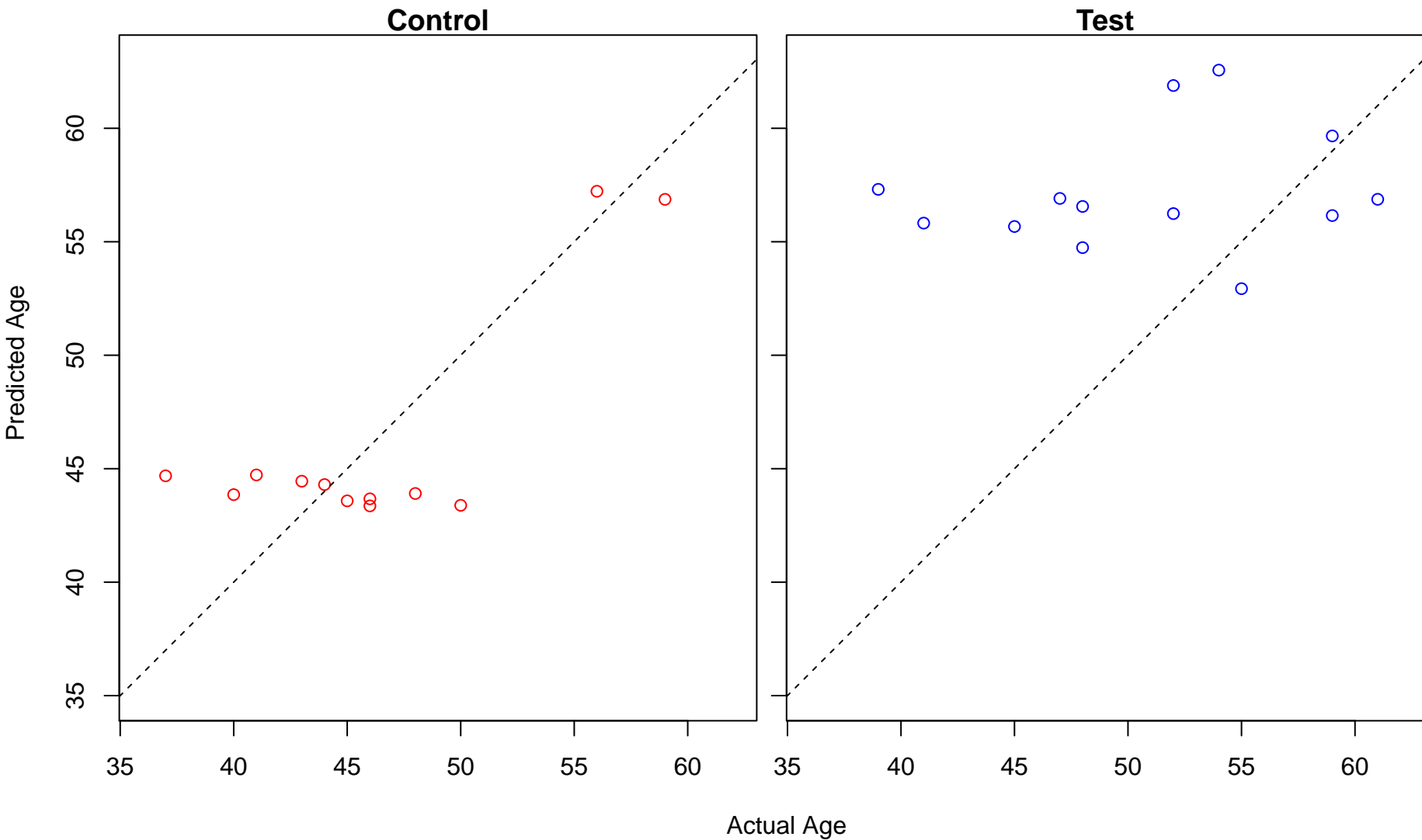
positive regulation of B cell differentiation (Score: 2.718217)



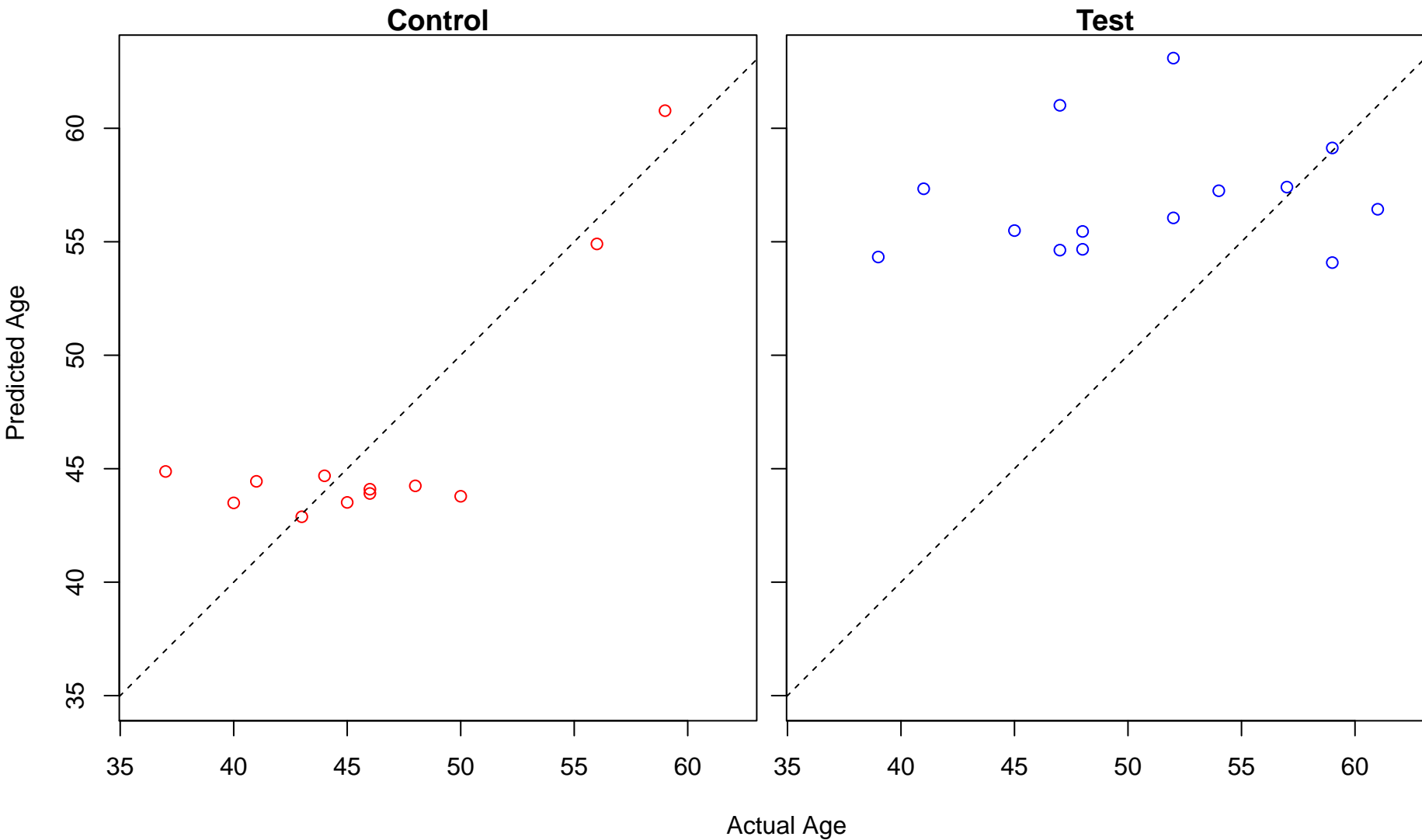
regulation of B cell differentiation (Score: 2.717365)



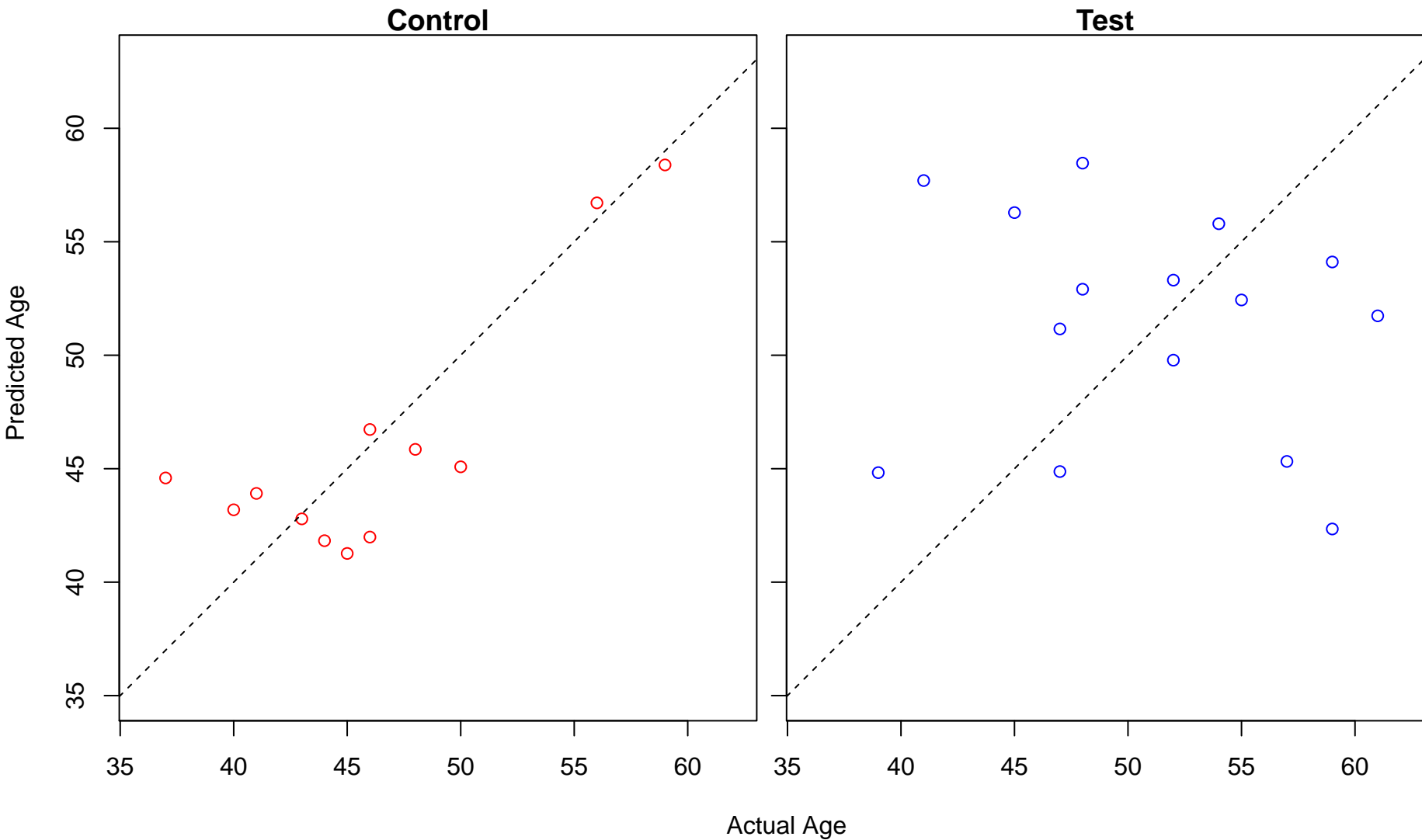
regulation of generation of precursor metabolites and energy (Score: 2.714514)



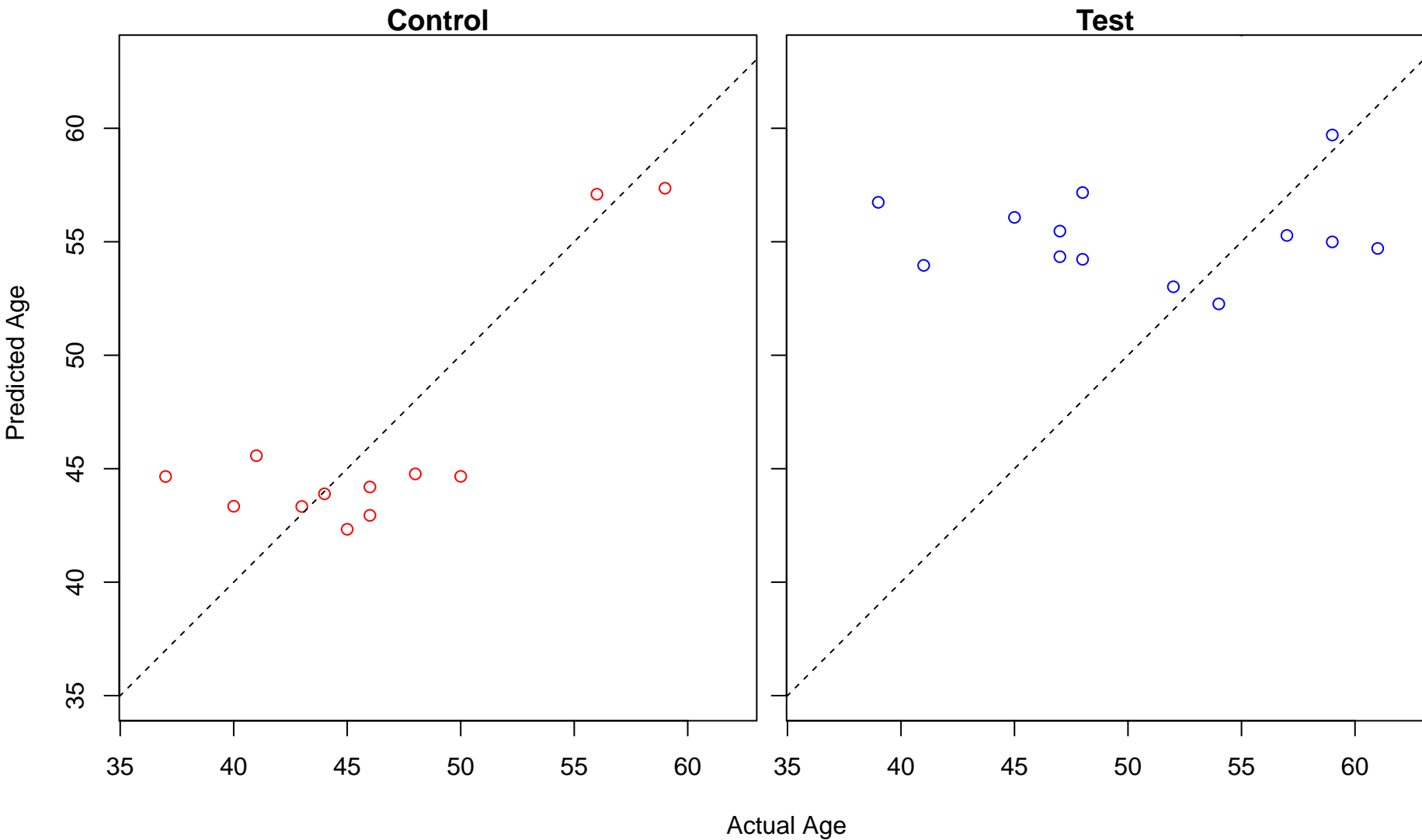
positive regulation of excitatory postsynaptic potential (Score: 2.714174)



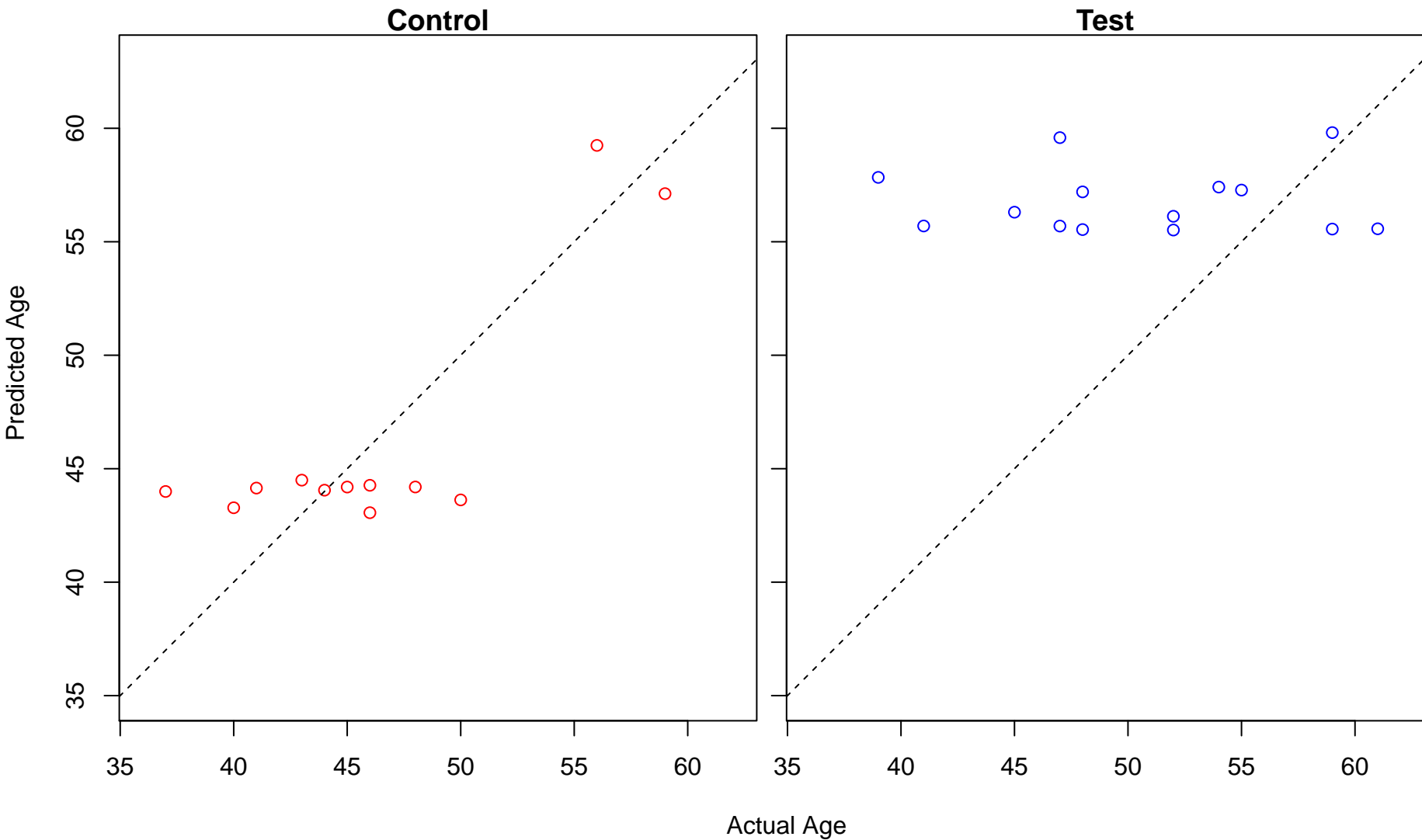
positive regulation of synaptic transmission, glutamatergic (Score: 2.712389)



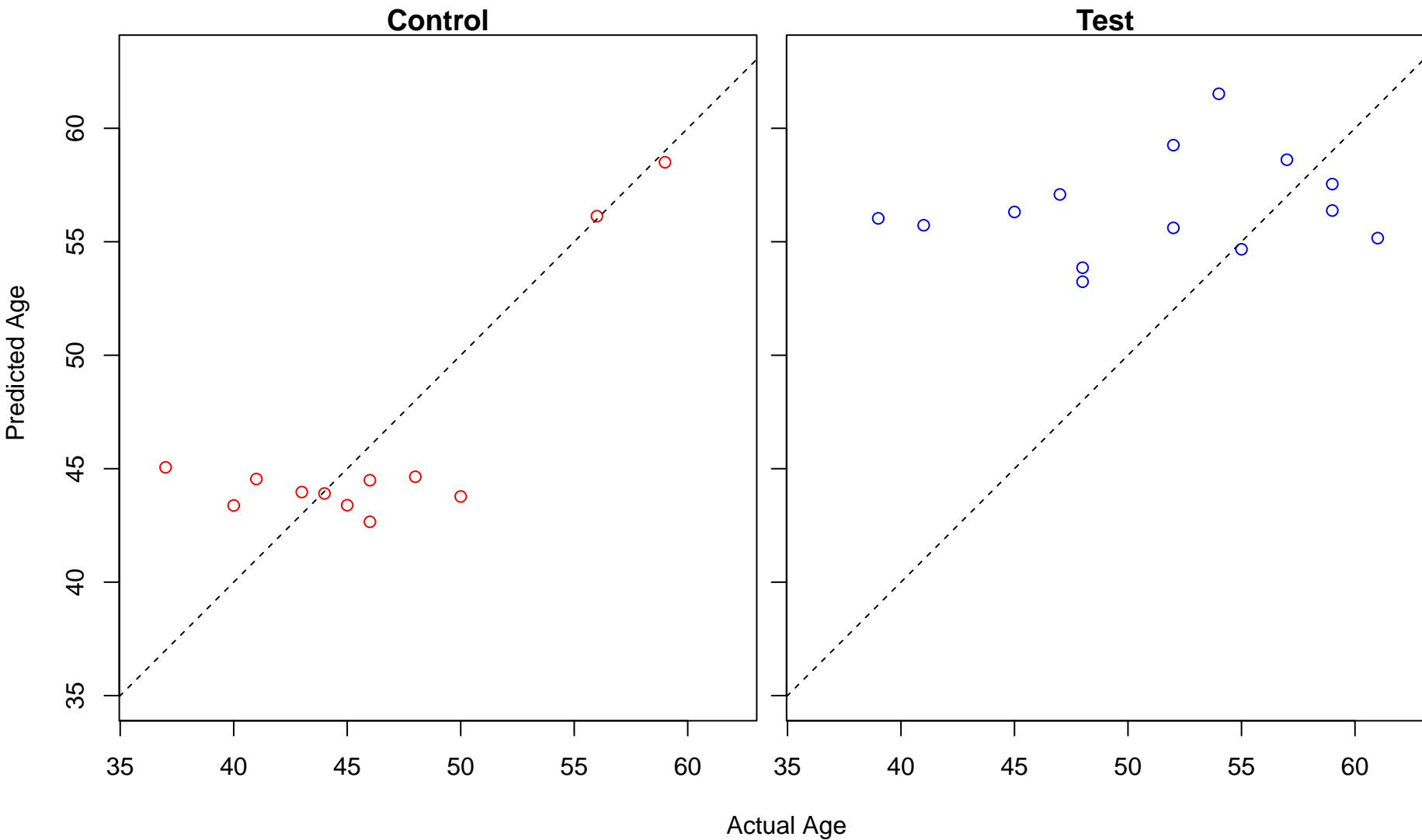
regulation of transforming growth factor beta2 production (Score: 2.712033)



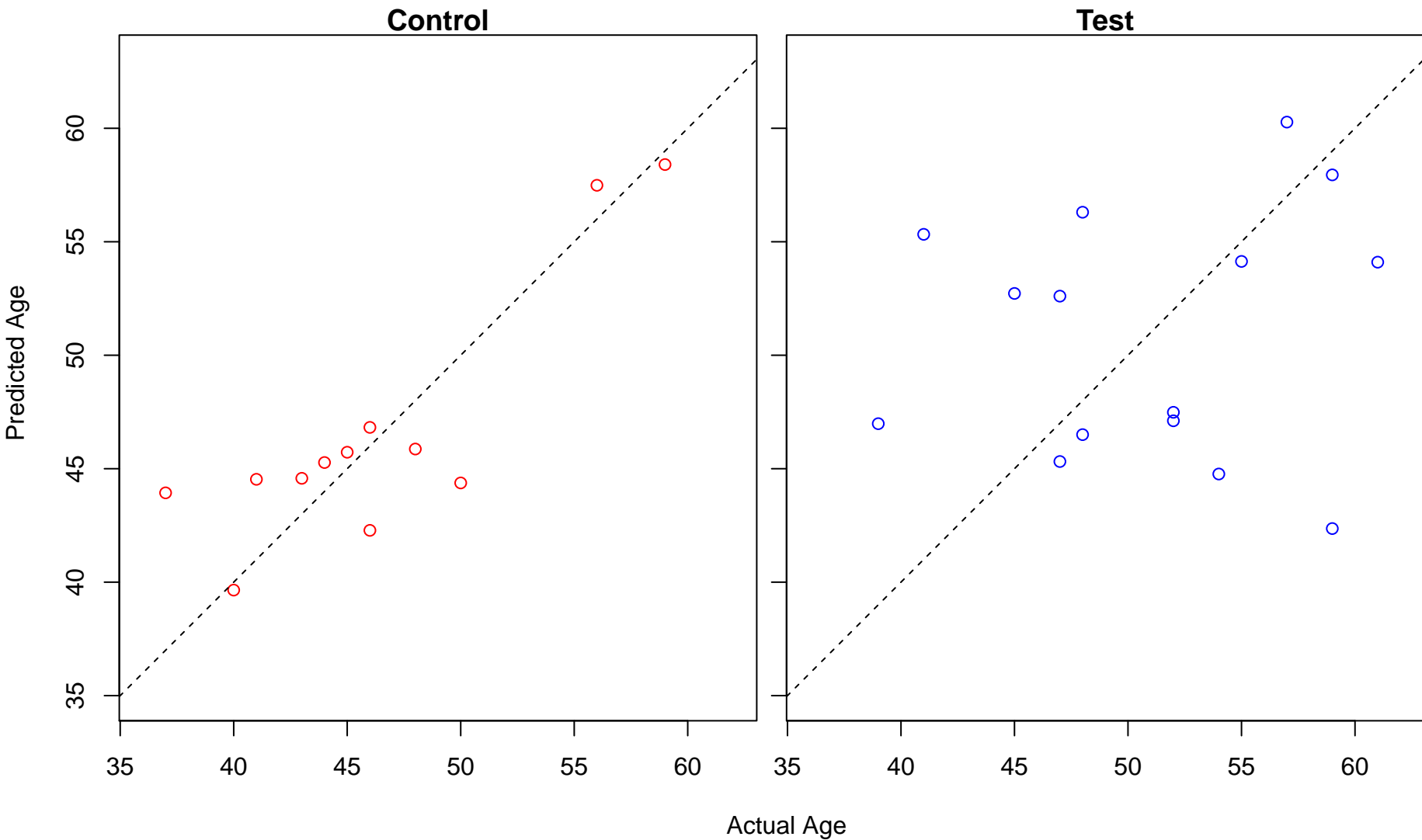
centriole replication (Score: 2.711514)



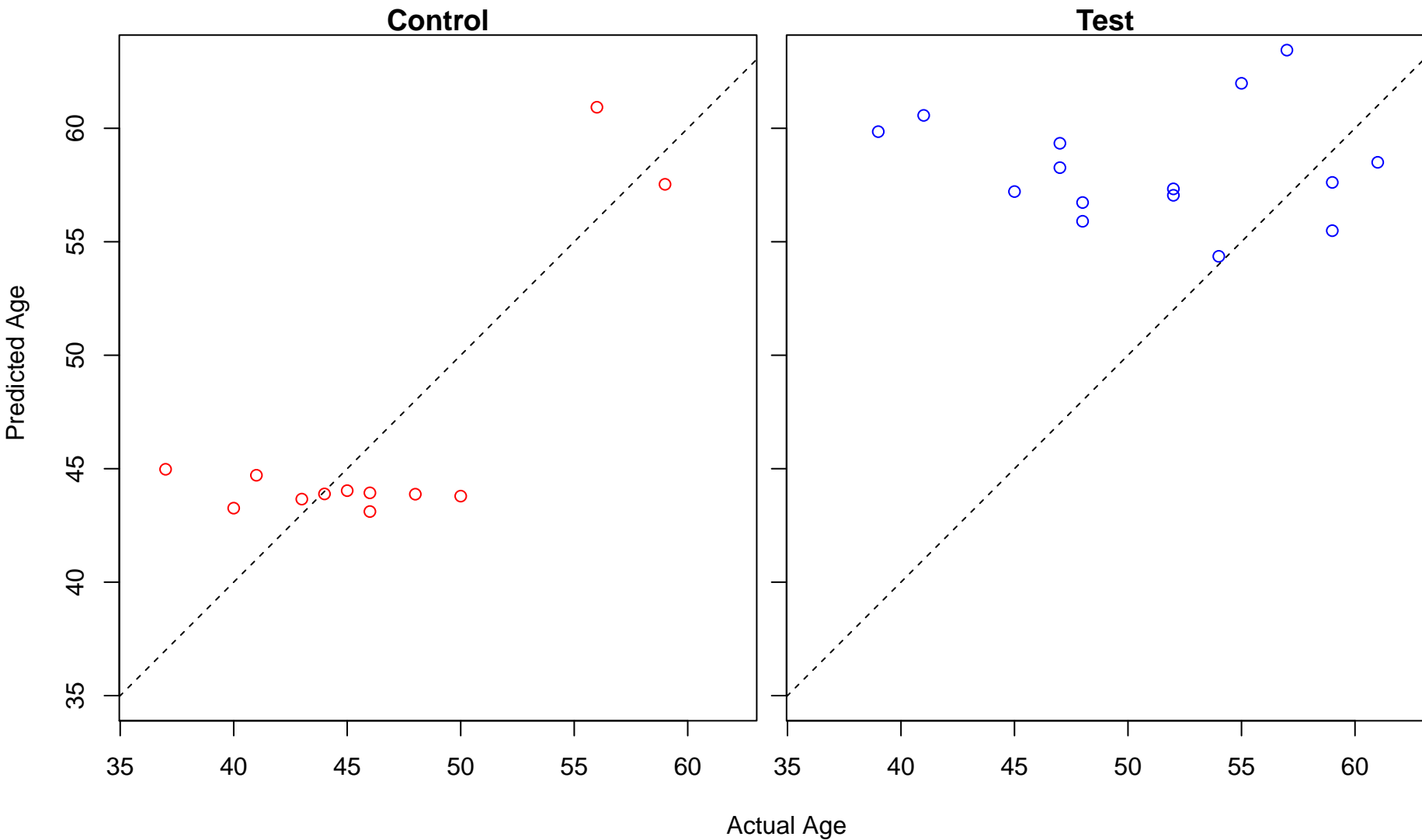
cell-substrate junction assembly (Score: 2.709325)



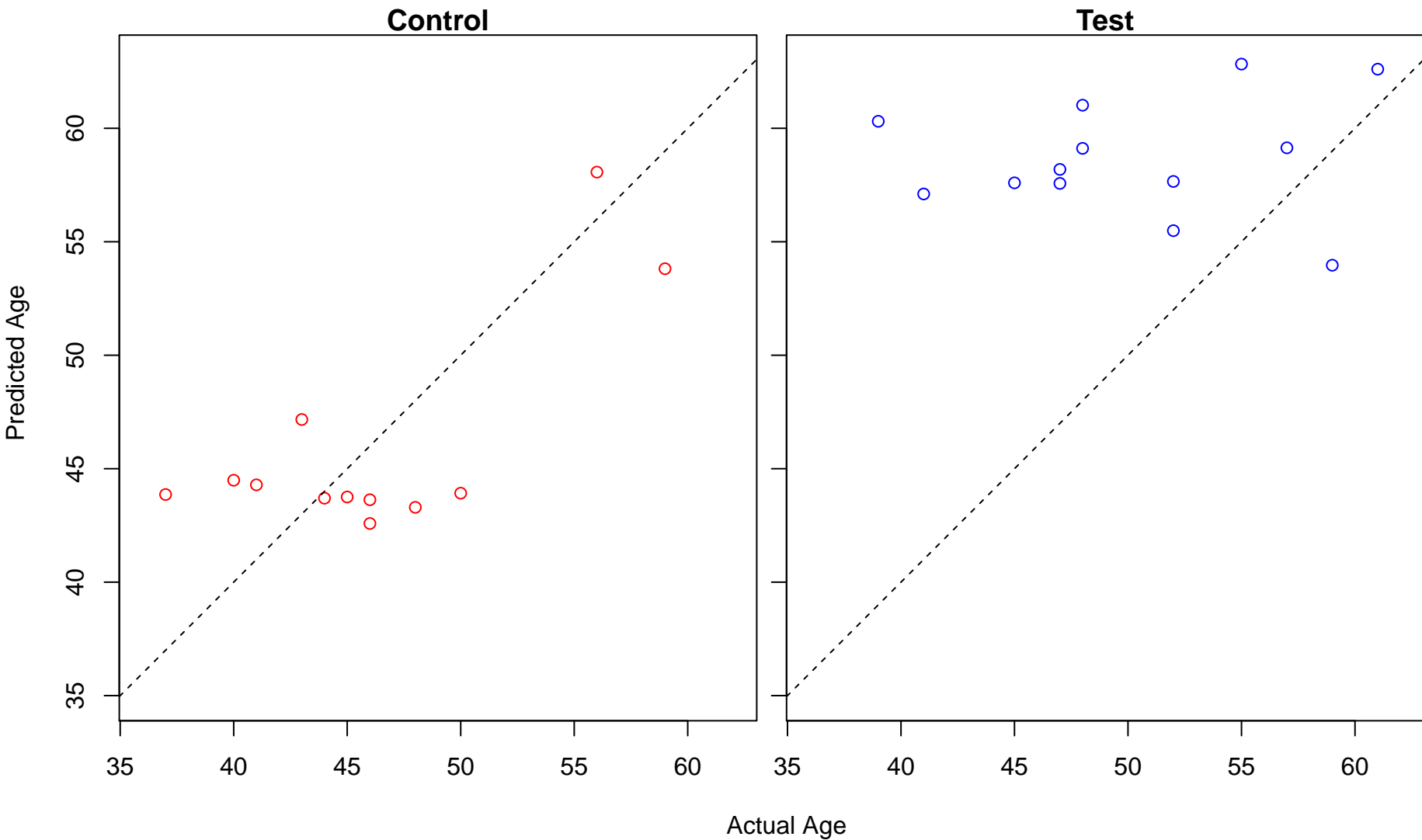
positive regulation of innate immune response (Score: 2.700350)



receptor-mediated endocytosis (Score: 2.699536)

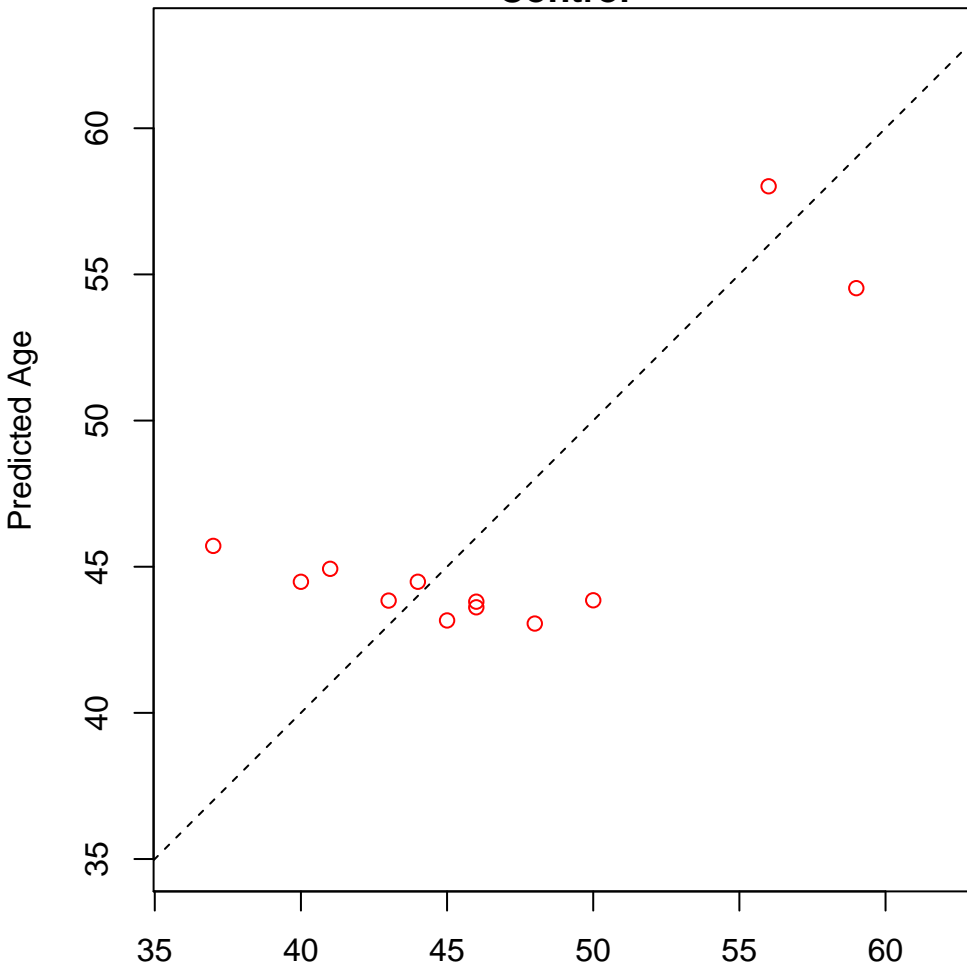


temperature homeostasis (Score: 2.695715)

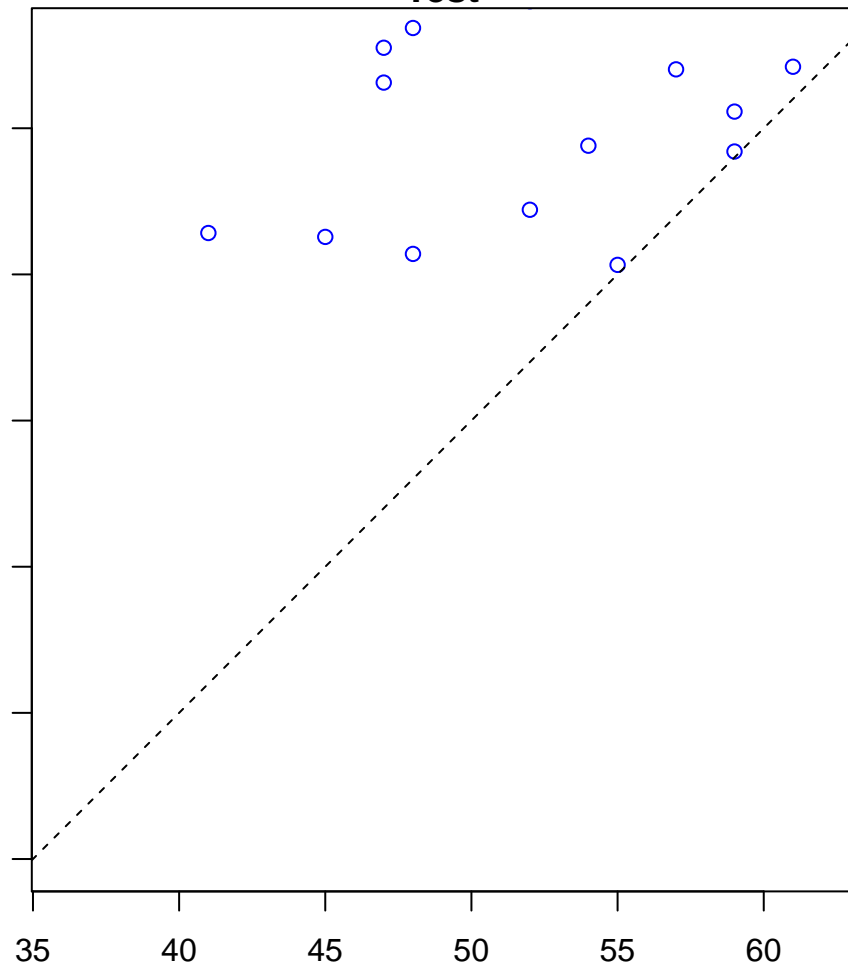


epithelial to mesenchymal transition (Score: 2.694728)

Control

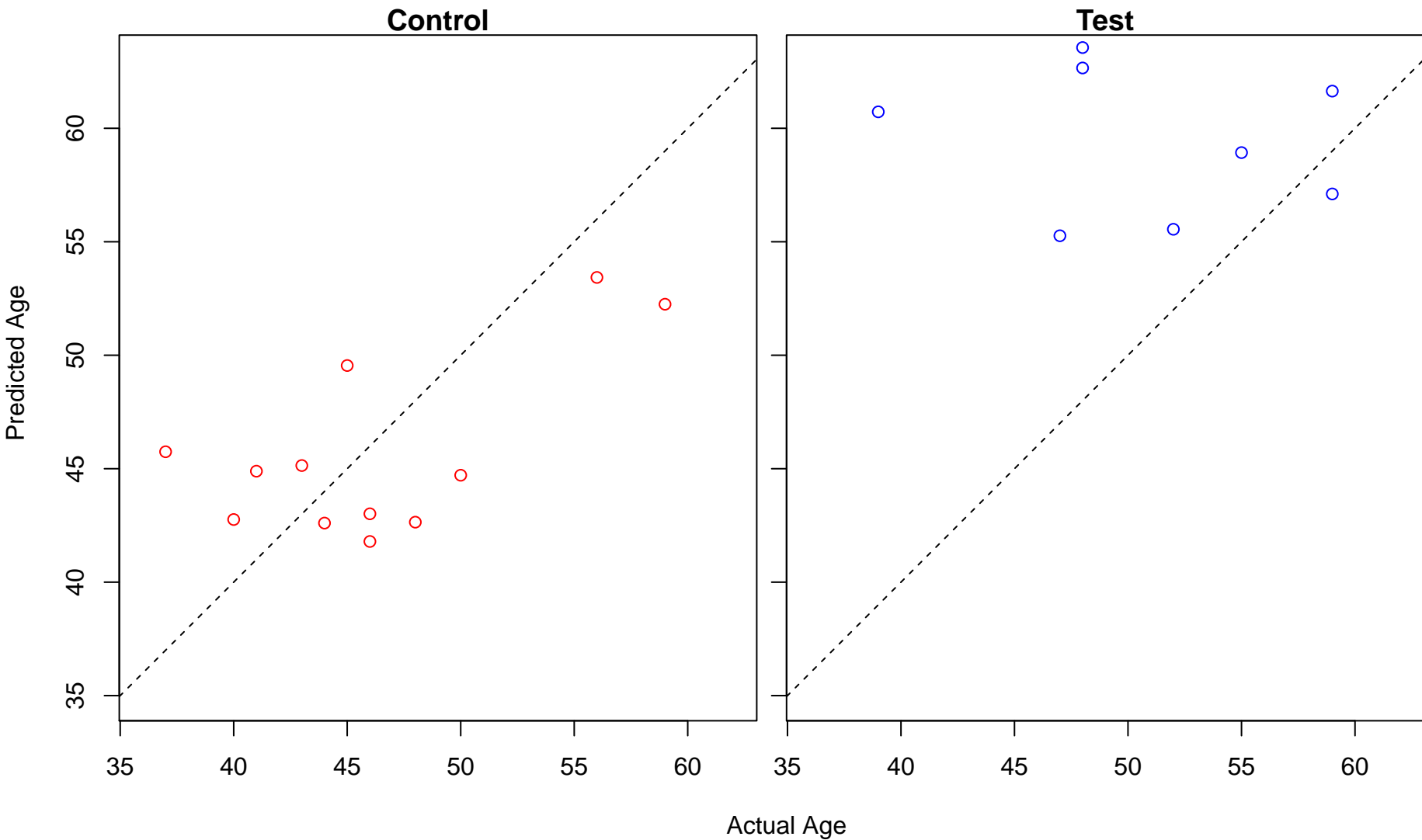


Test

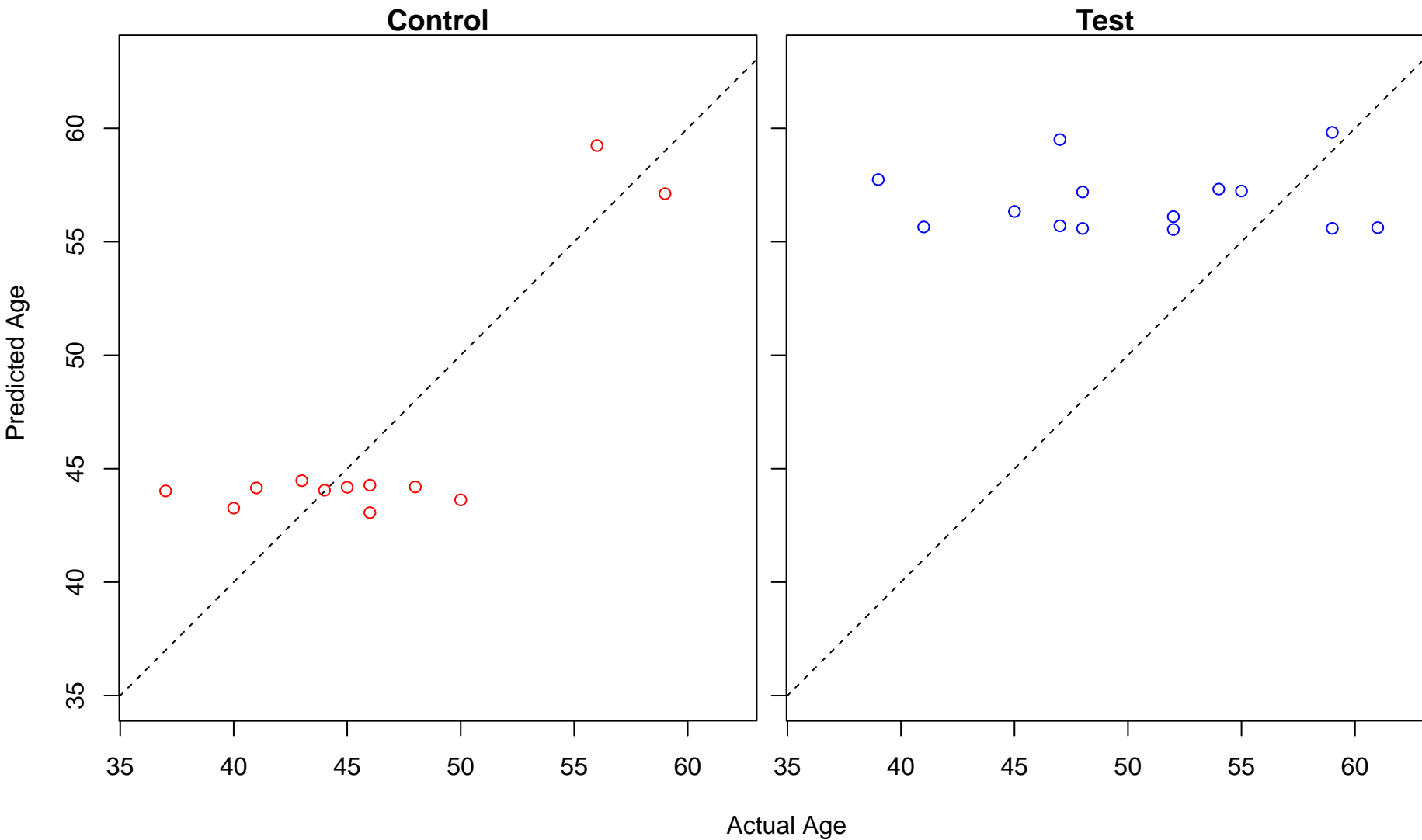


Actual Age

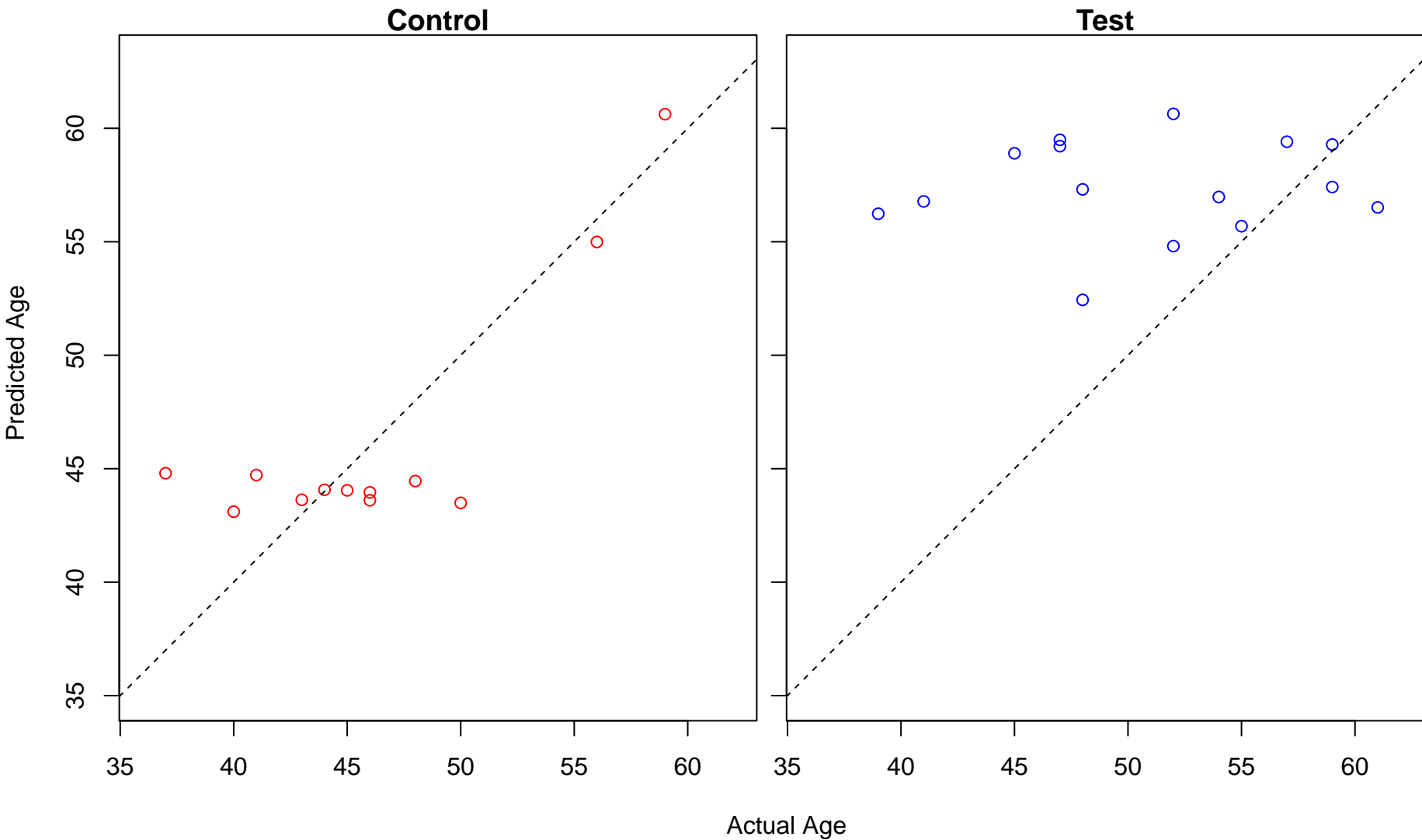
positive regulation of neuron death (Score: 2.694115)



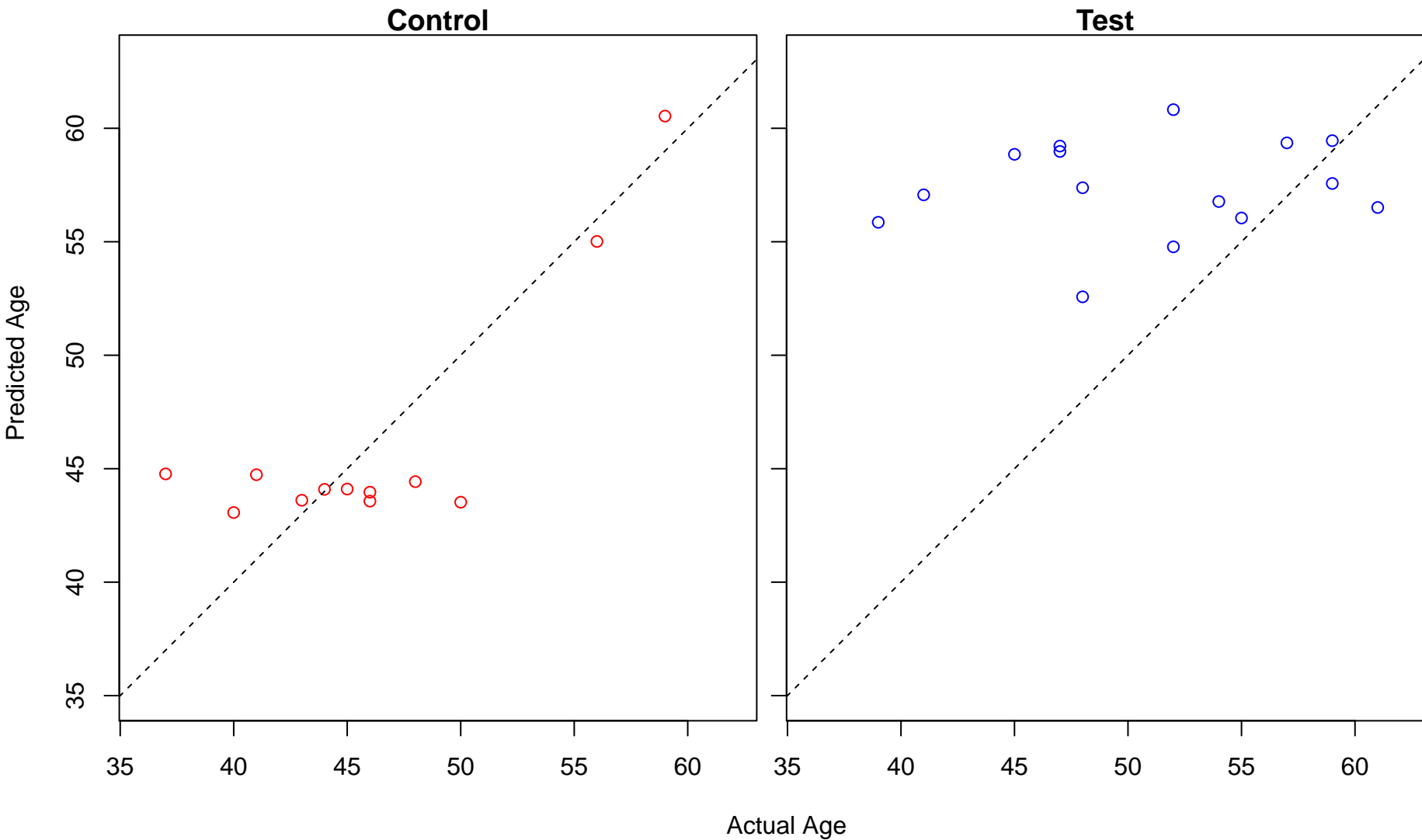
centrosome duplication (Score: 2.693094)



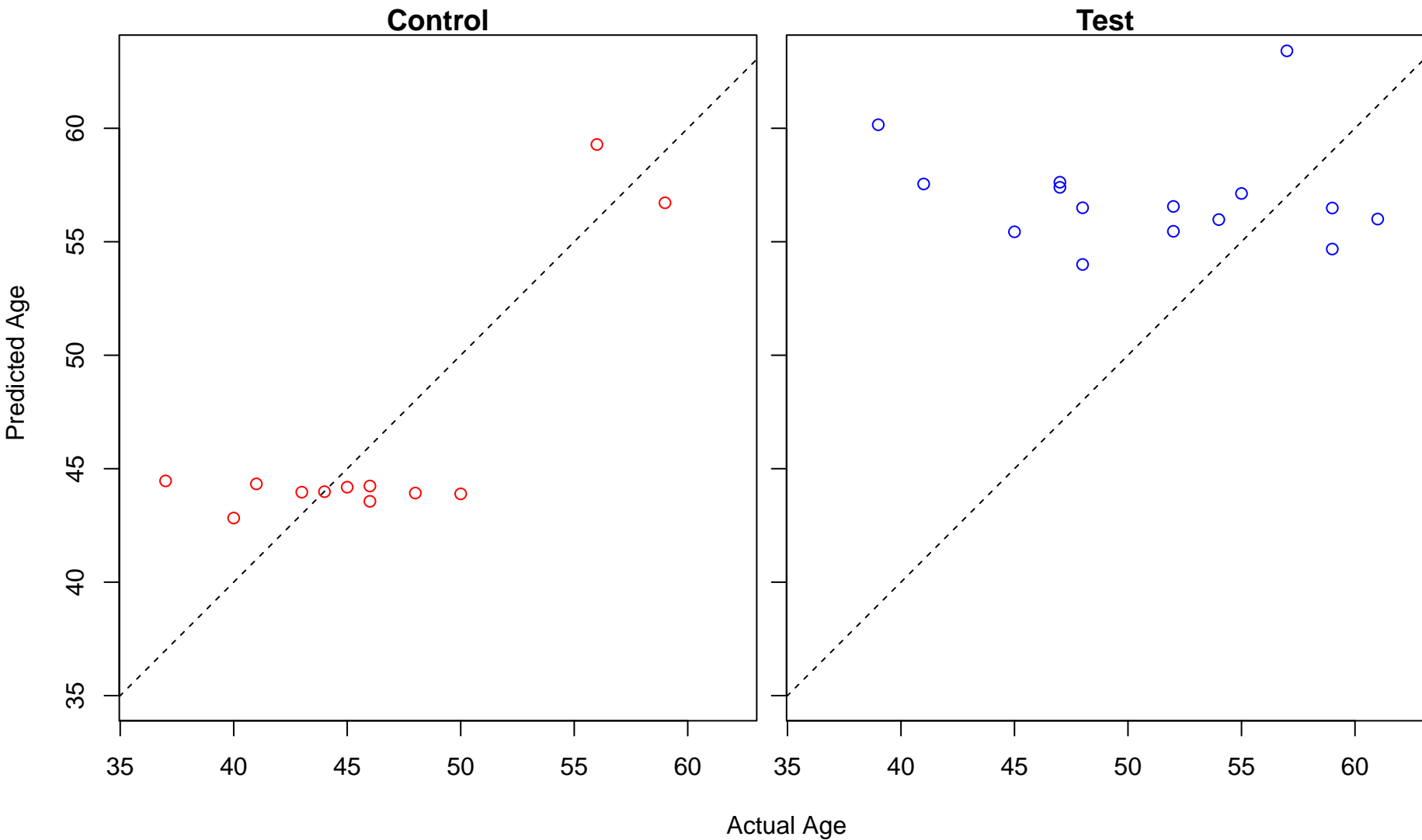
neuron recognition (Score: 2.692084)



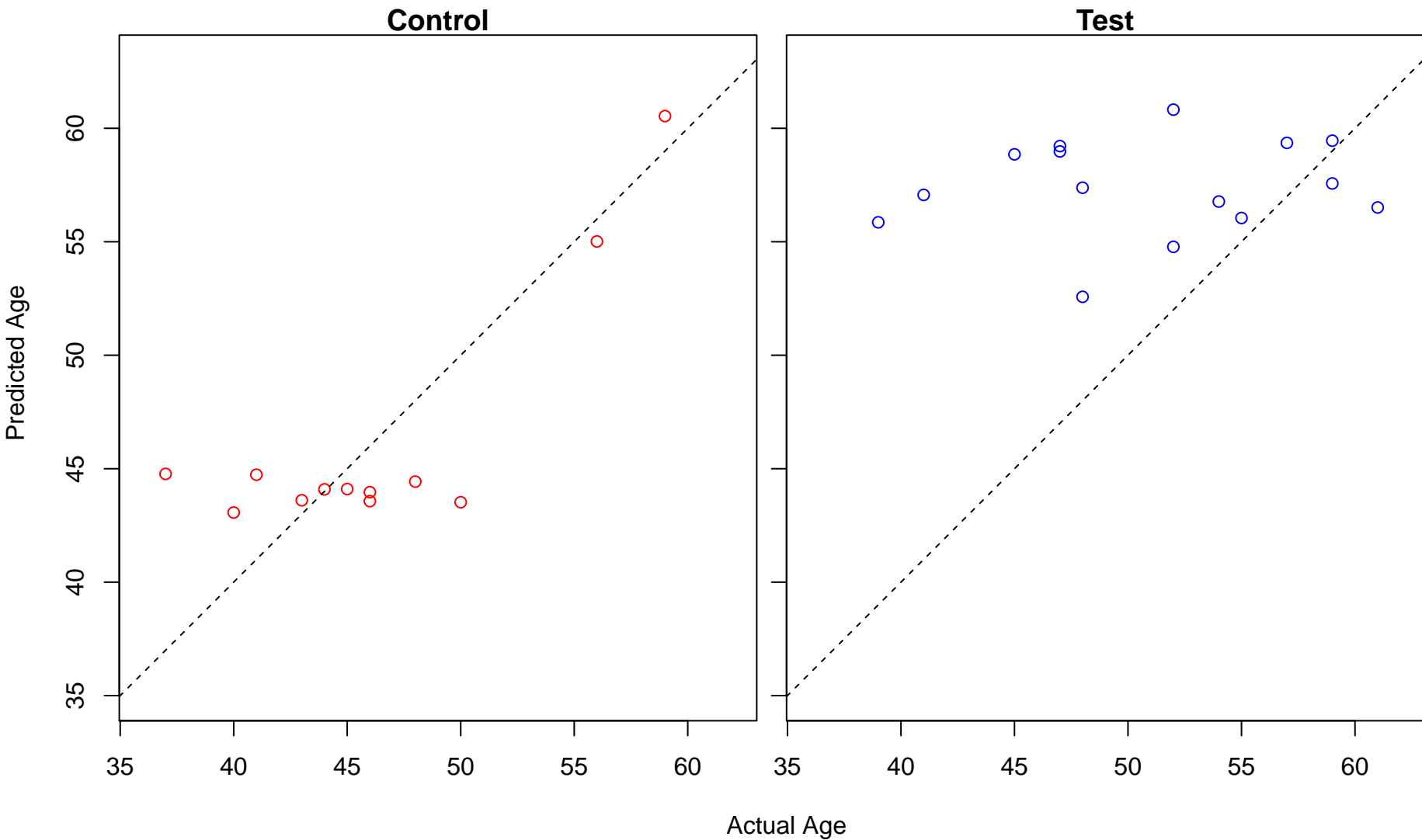
cerebral cortex radially oriented cell migration (Score: 2.692029)



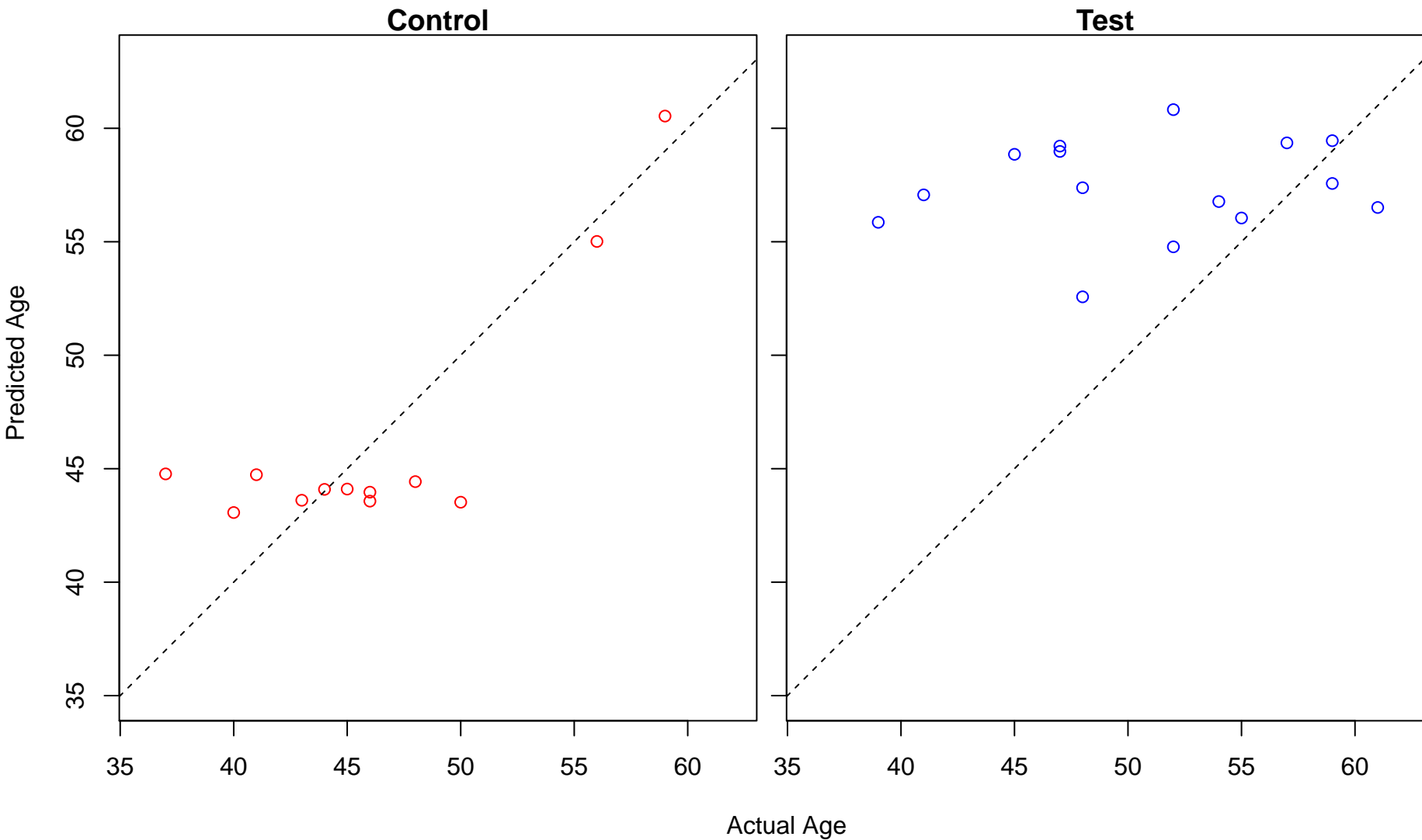
negative regulation of ion transmembrane transporter activity (Score: 2.691923)



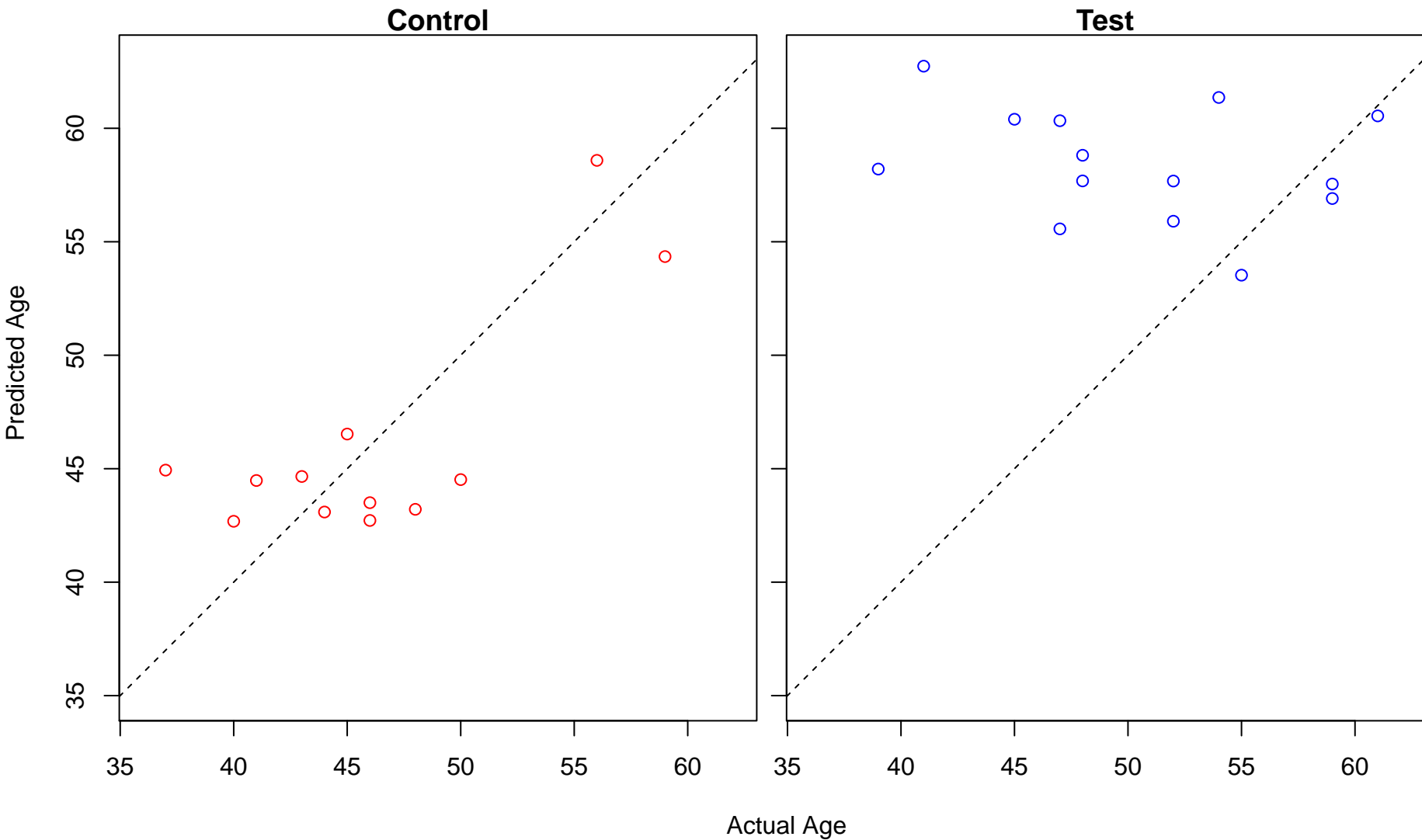
cerebral cortex radial glia guided migration (Score: 2.691905)



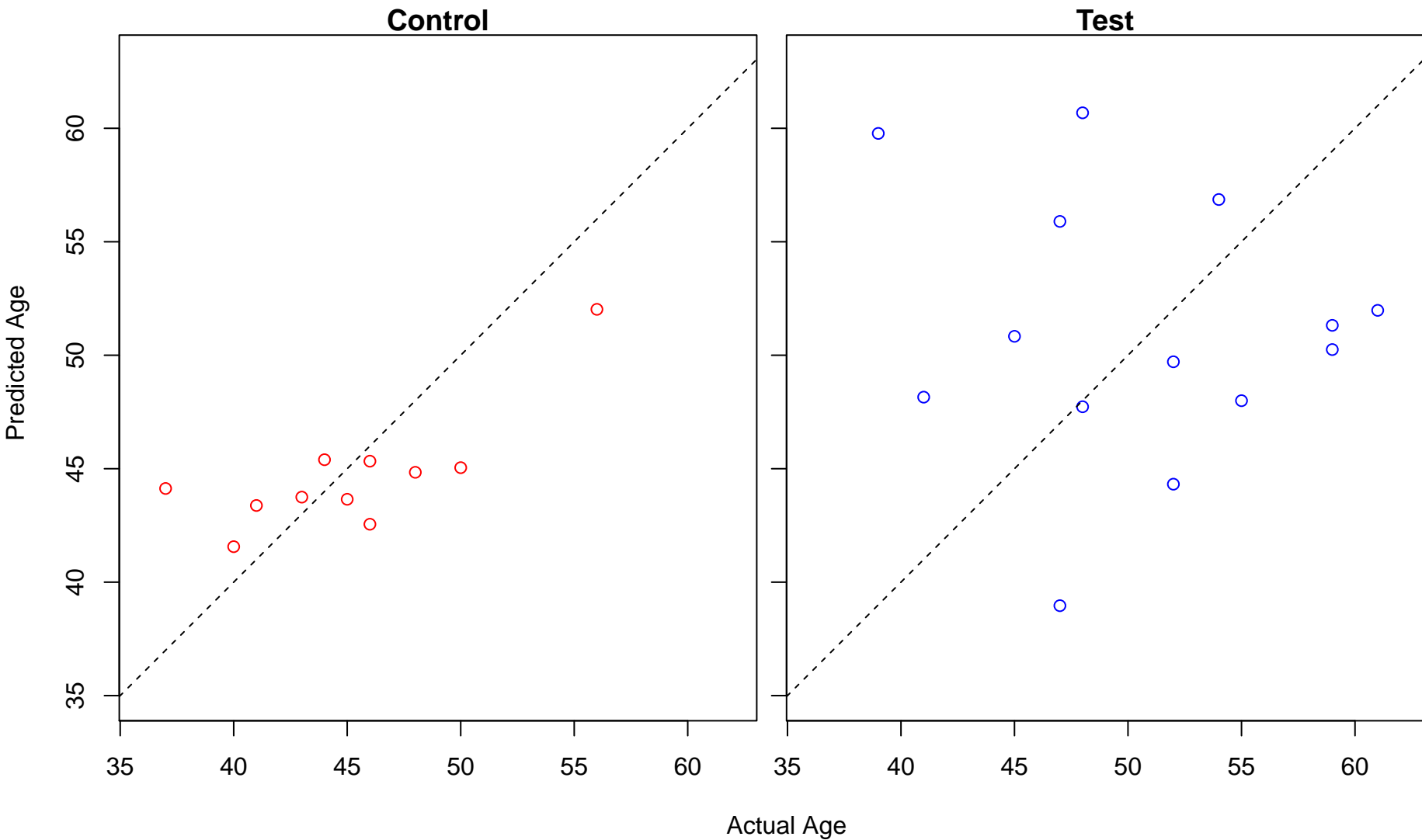
telencephalon glial cell migration (Score: 2.691905)



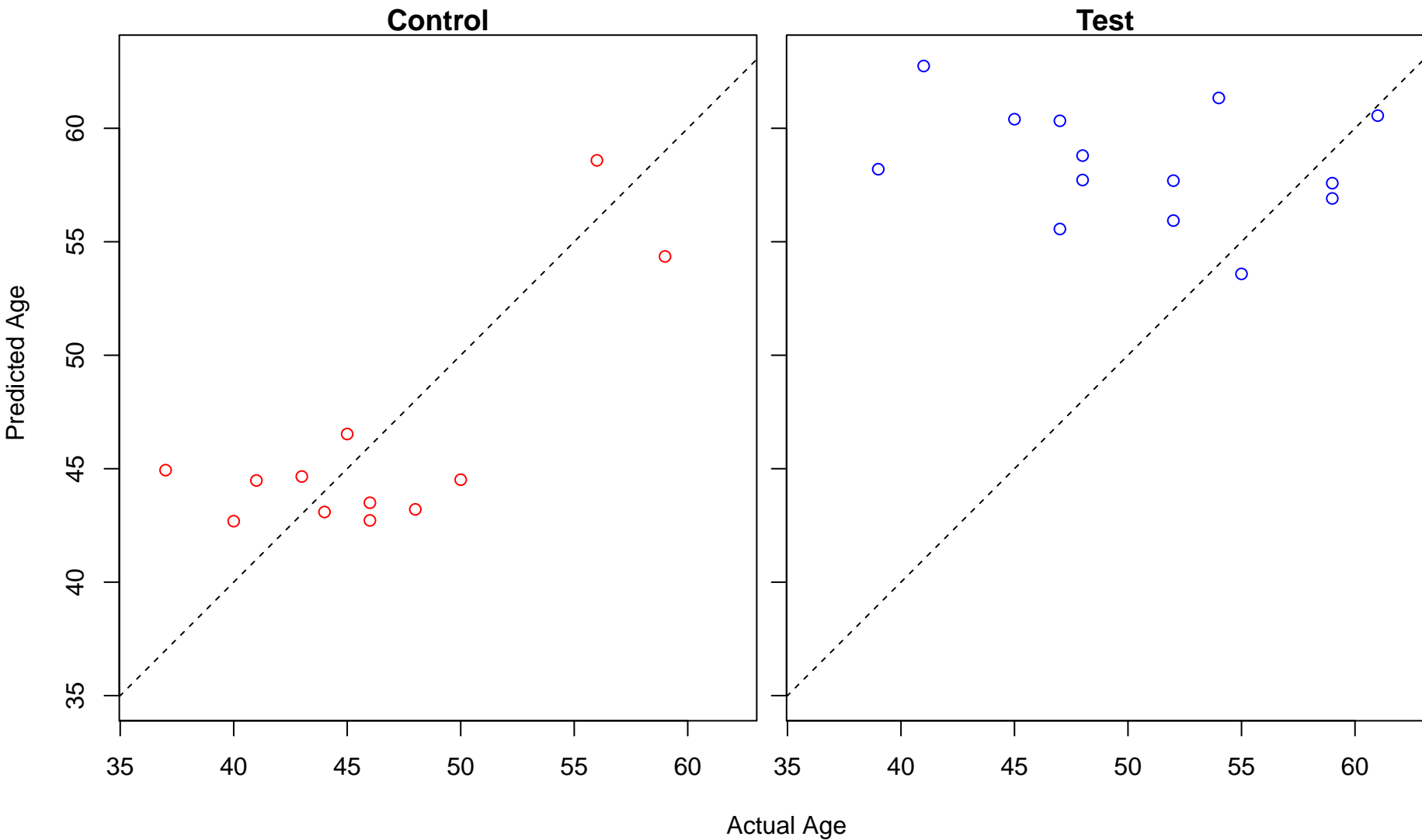
myelination (Score: 2.691795)



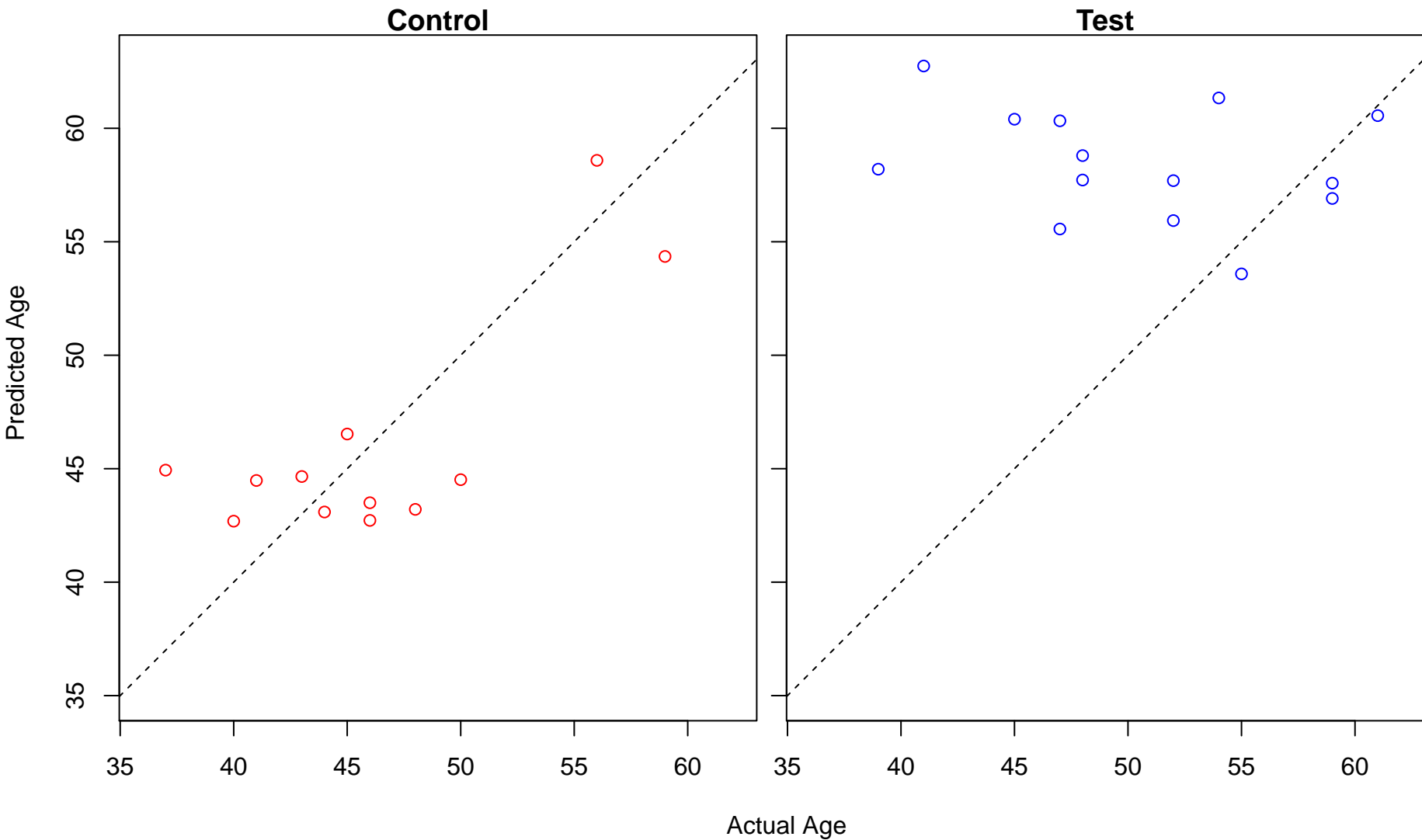
positive regulation of ion transmembrane transport (Score: 2.691718)



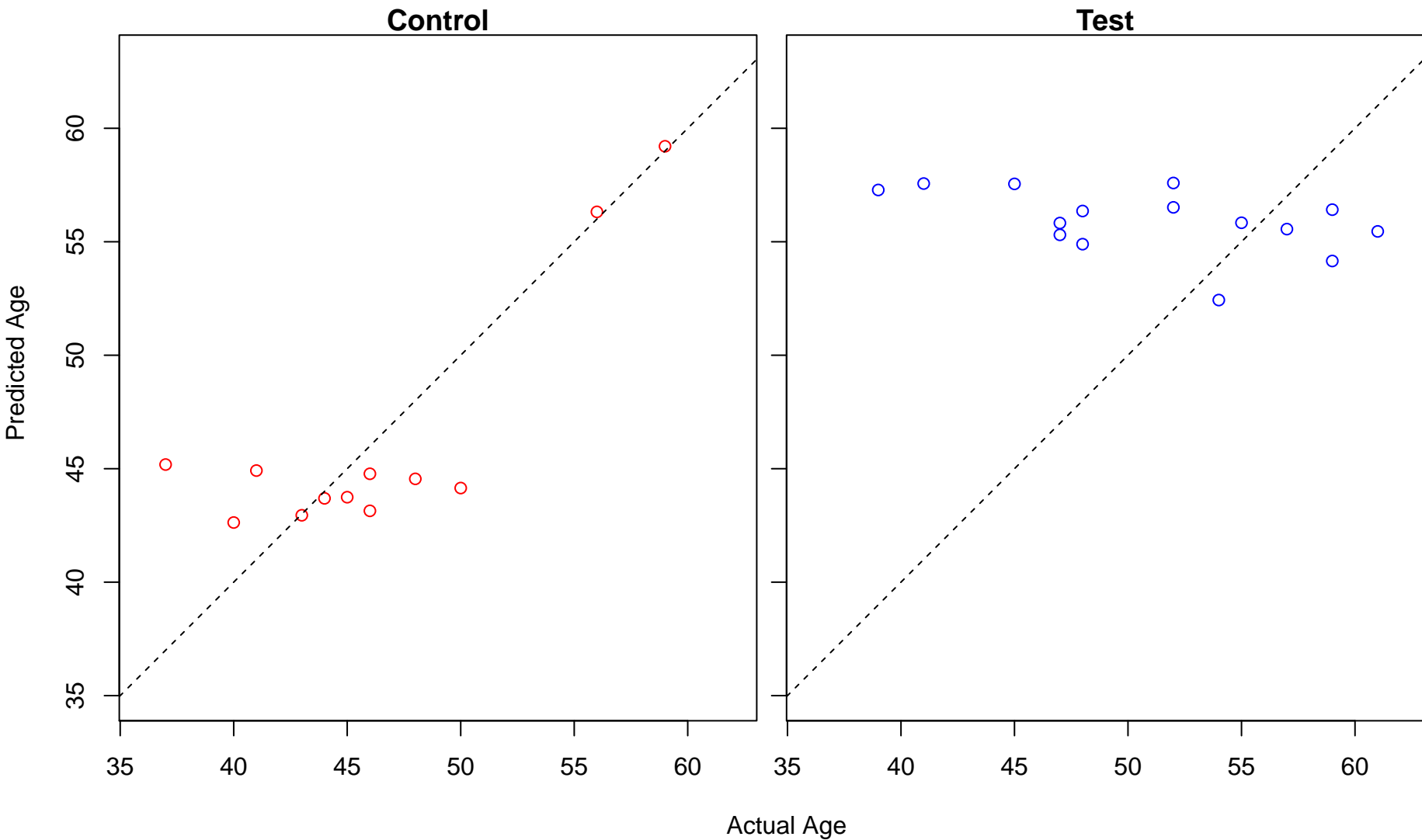
ensheathment of neurons (Score: 2.690856)



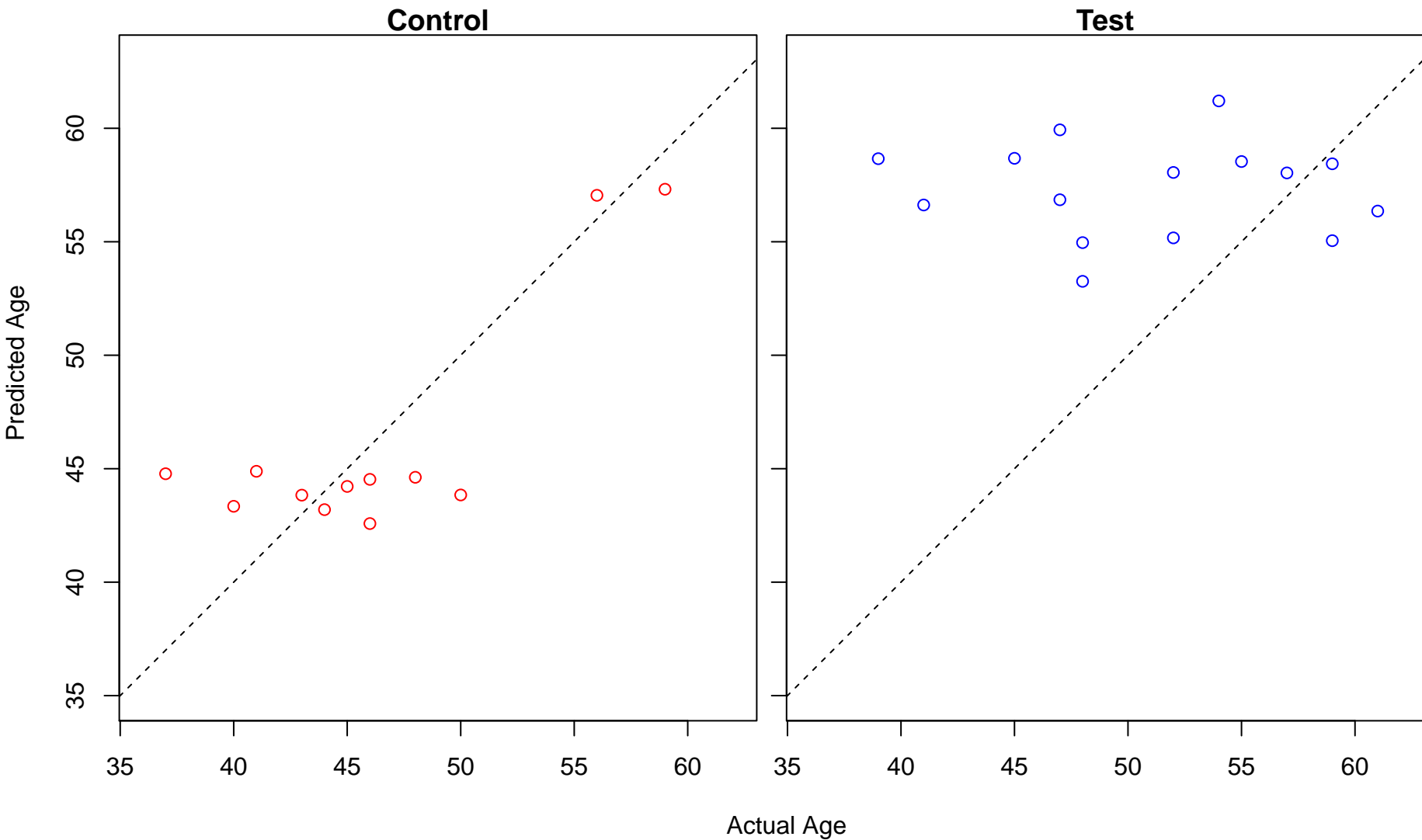
axon ensheathment (Score: 2.690856)



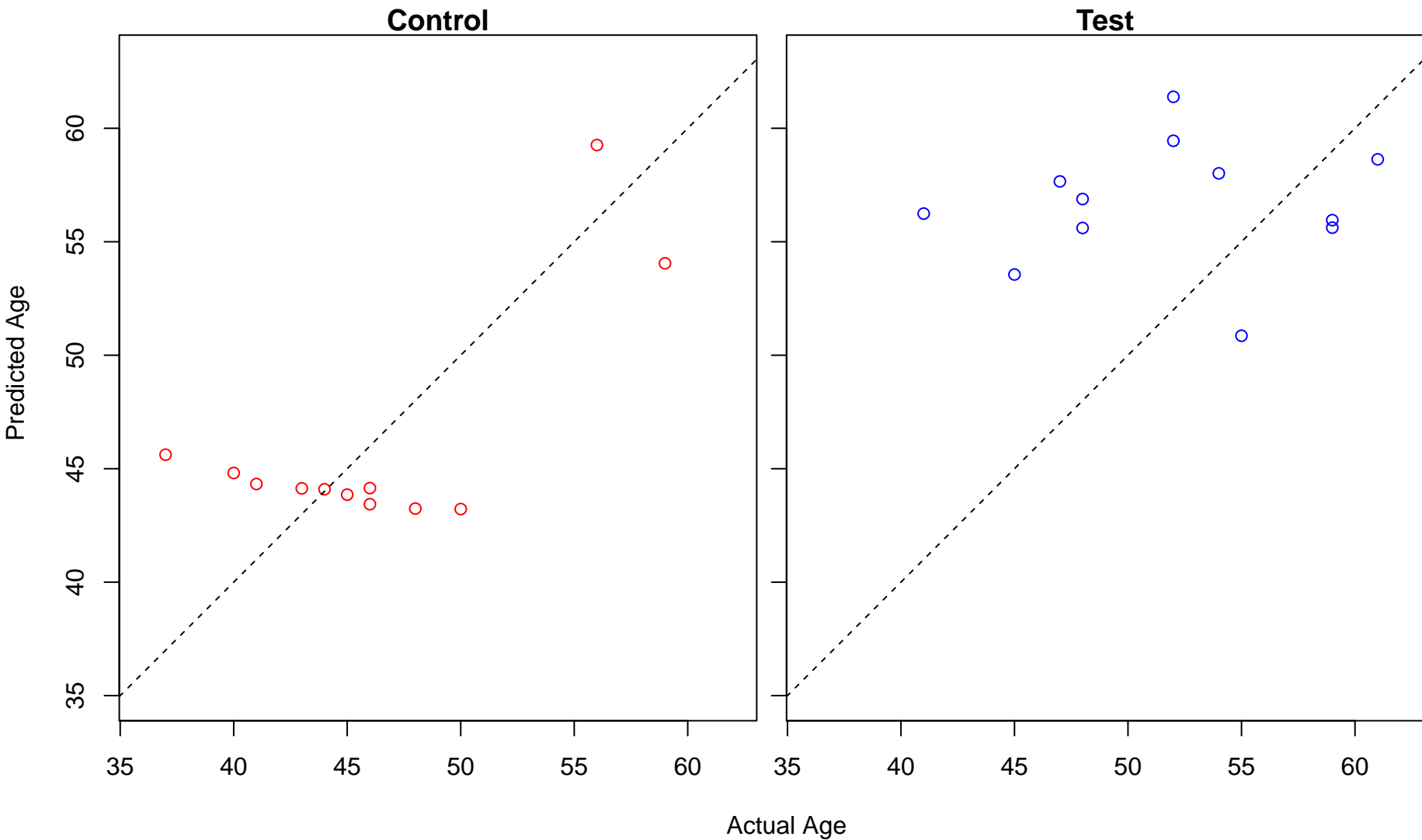
lymphocyte activation involved in immune response (Score: 2.690008)



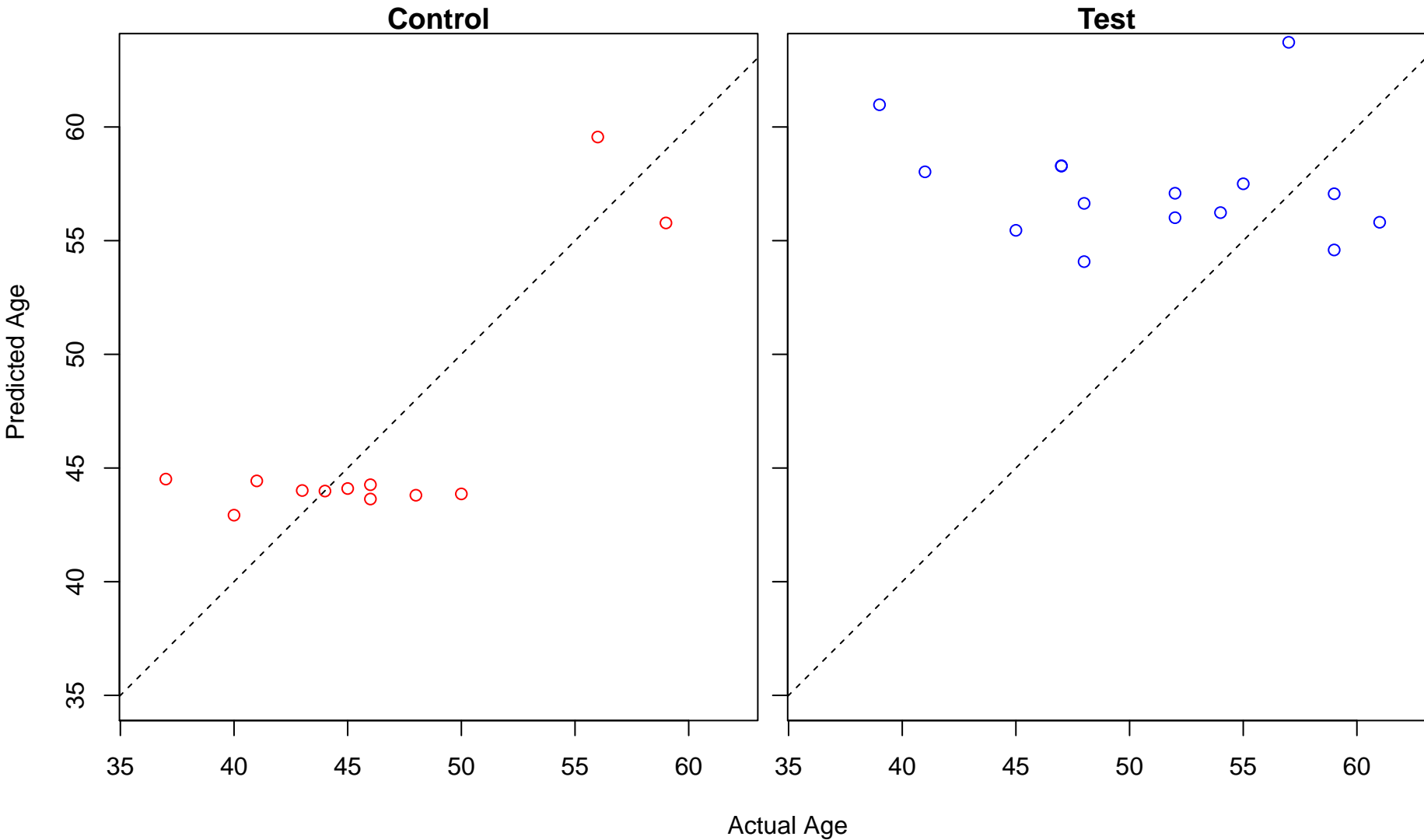
heparan sulfate proteoglycan metabolic process (Score: 2.689838)



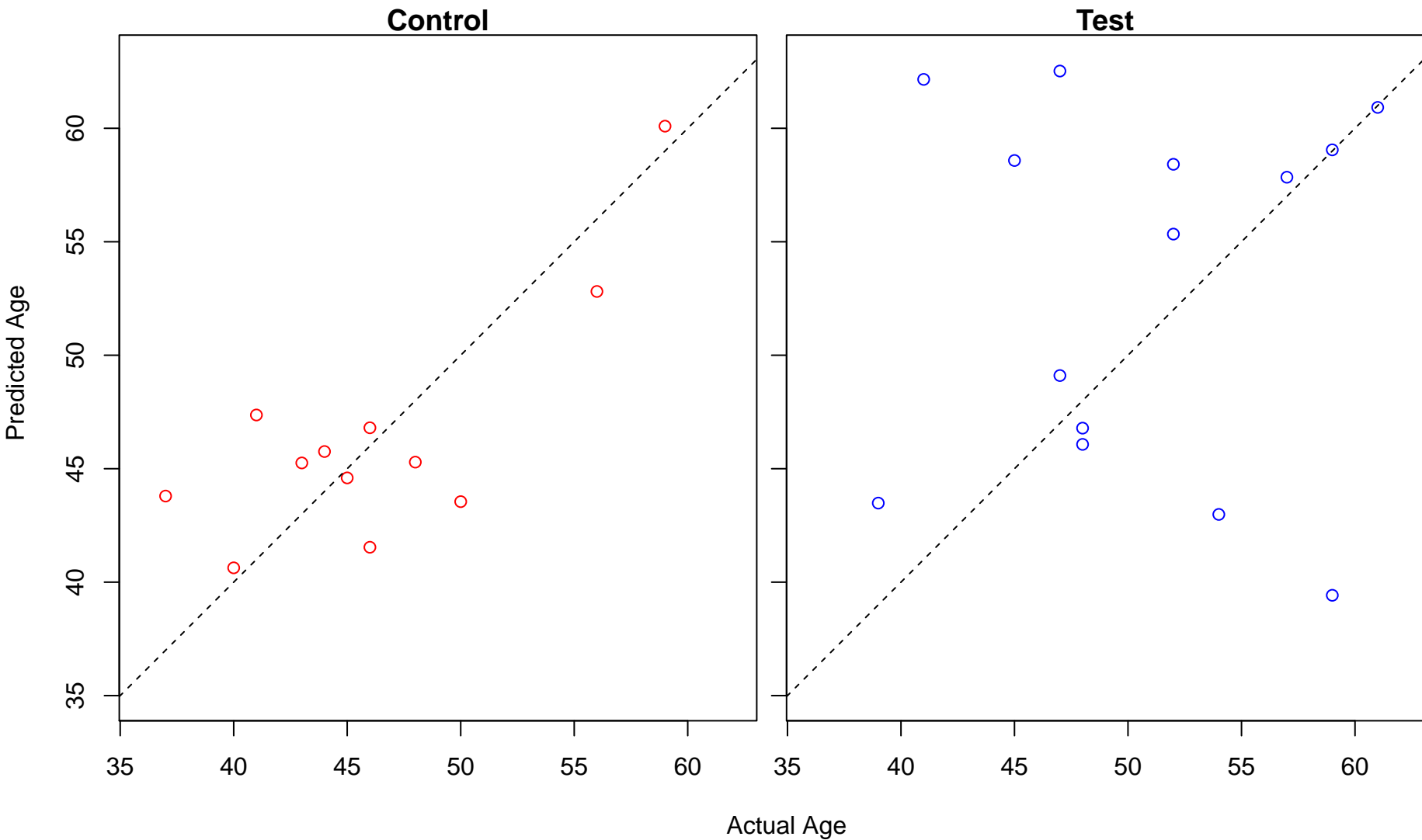
ribosomal small subunit biogenesis (Score: 2.688939)



regulation of G-protein coupled receptor protein signaling pathway (Score: 2.685559)

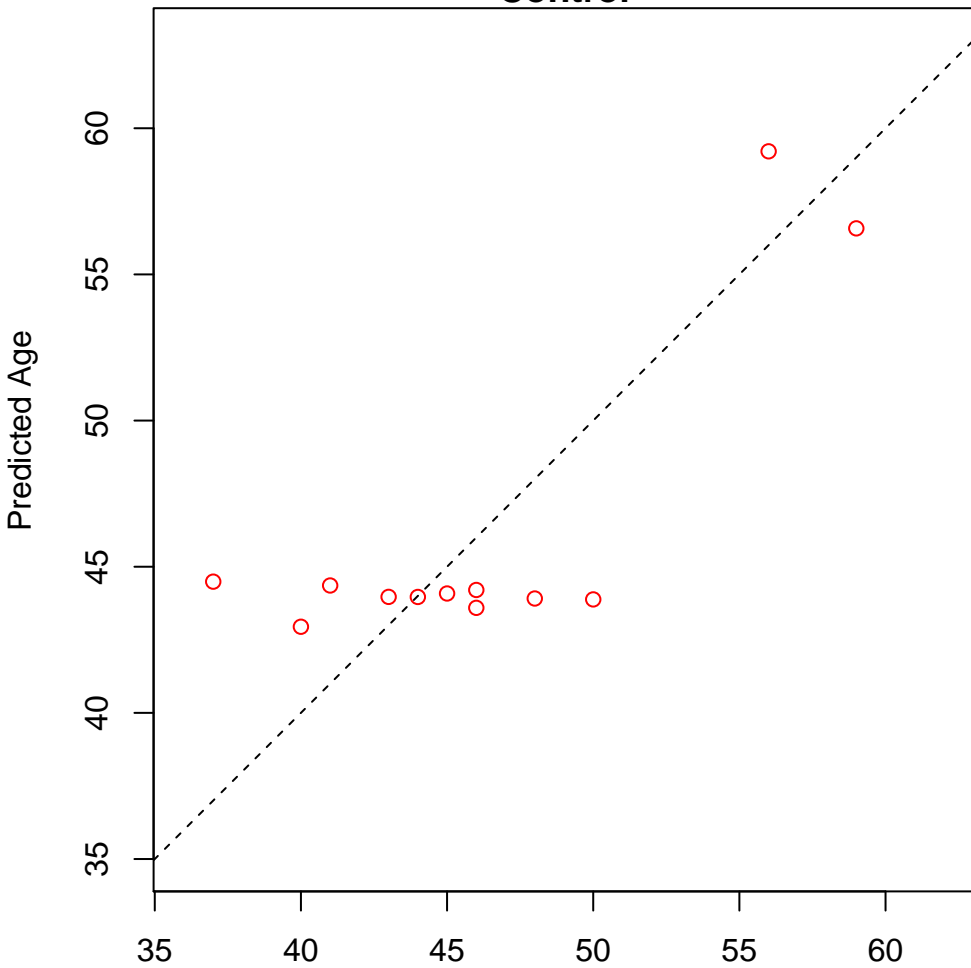


response to bacterium (Score: 2.684979)

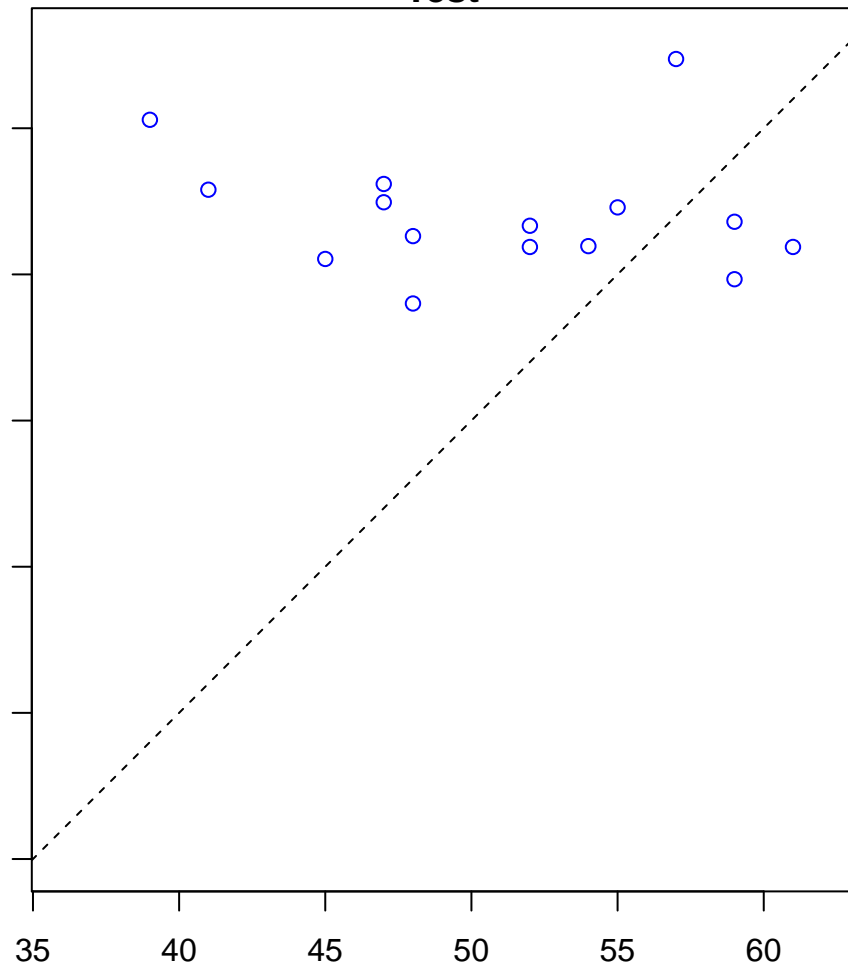


regulation of protein dephosphorylation (Score: 2.68292)

Control

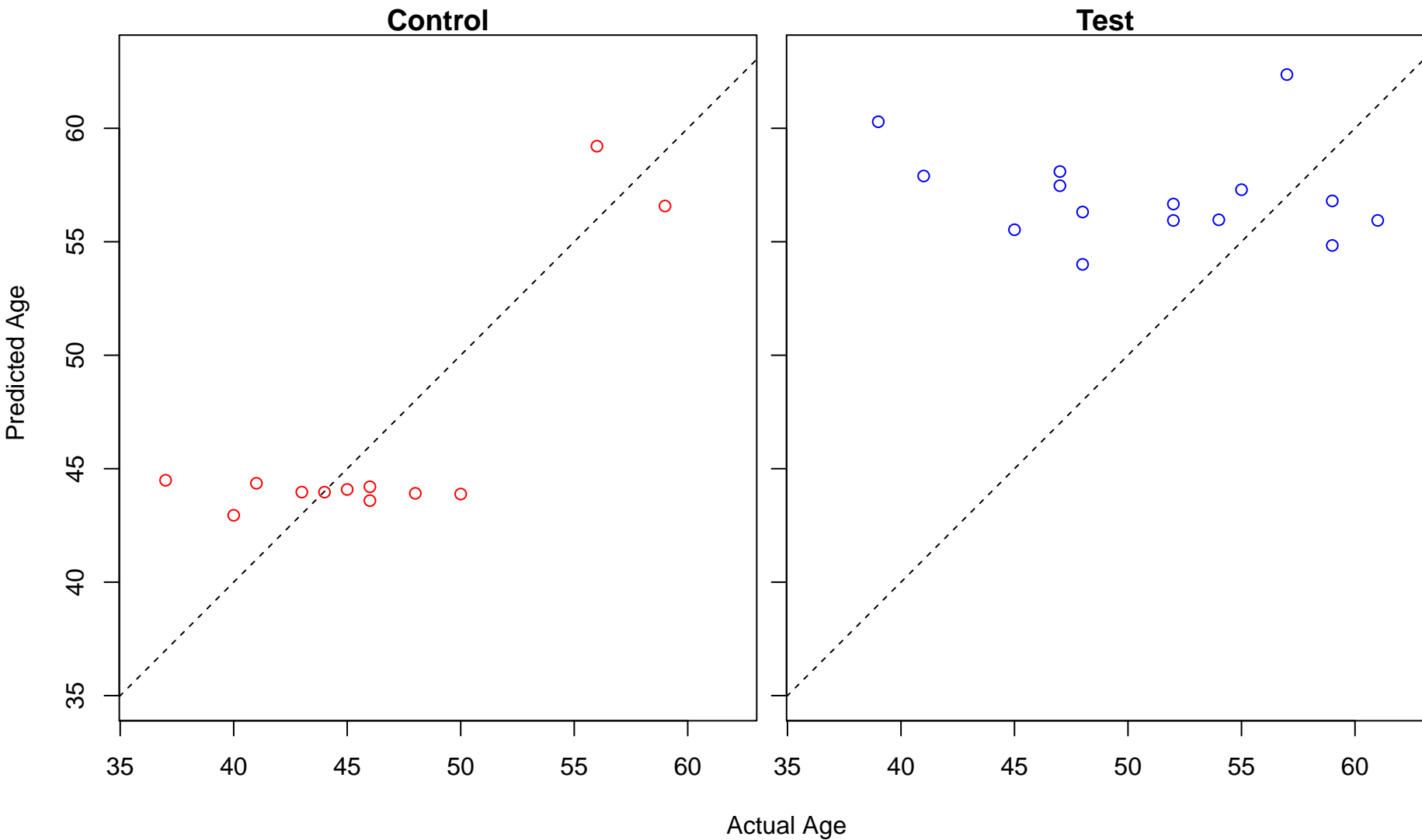


Test

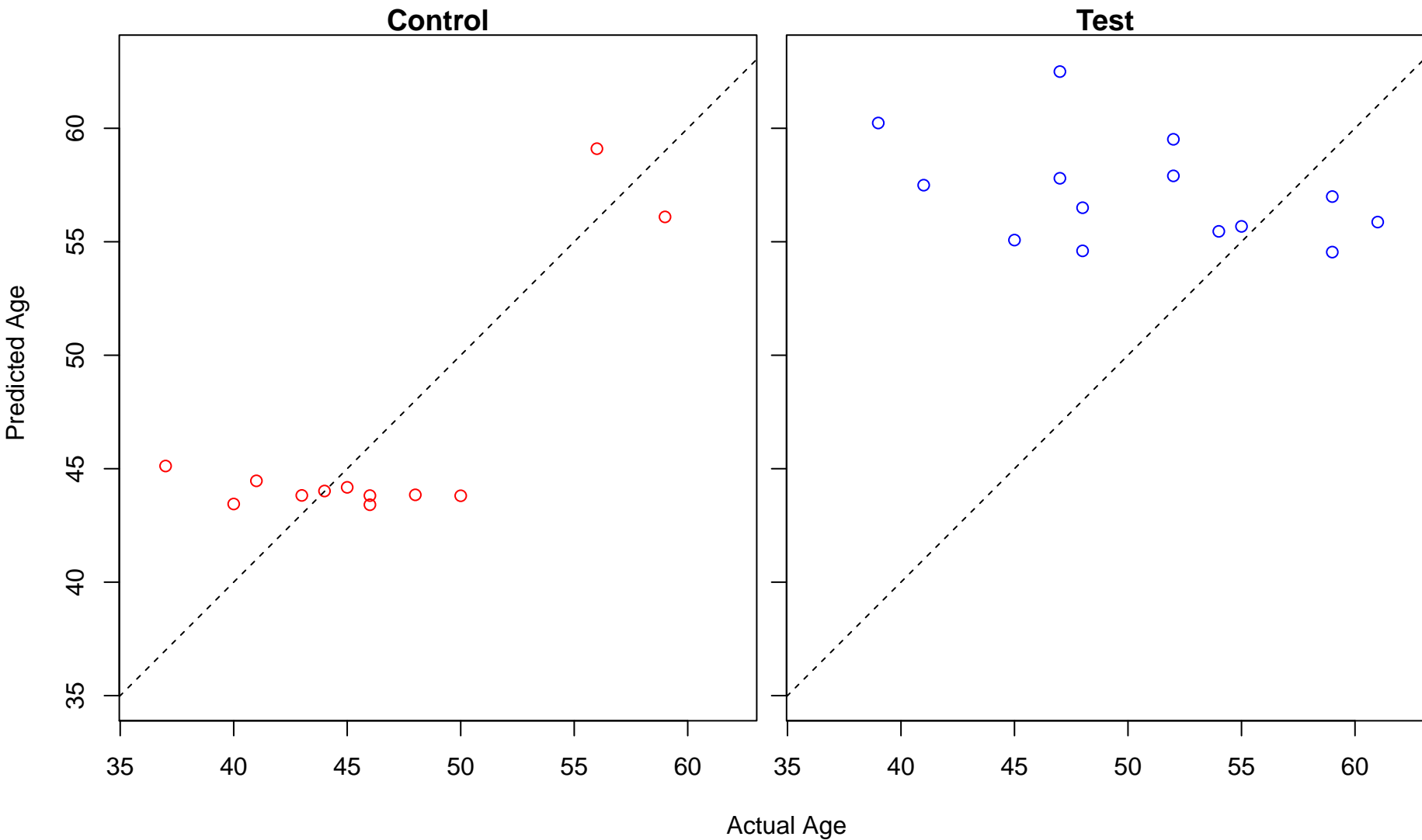


Actual Age

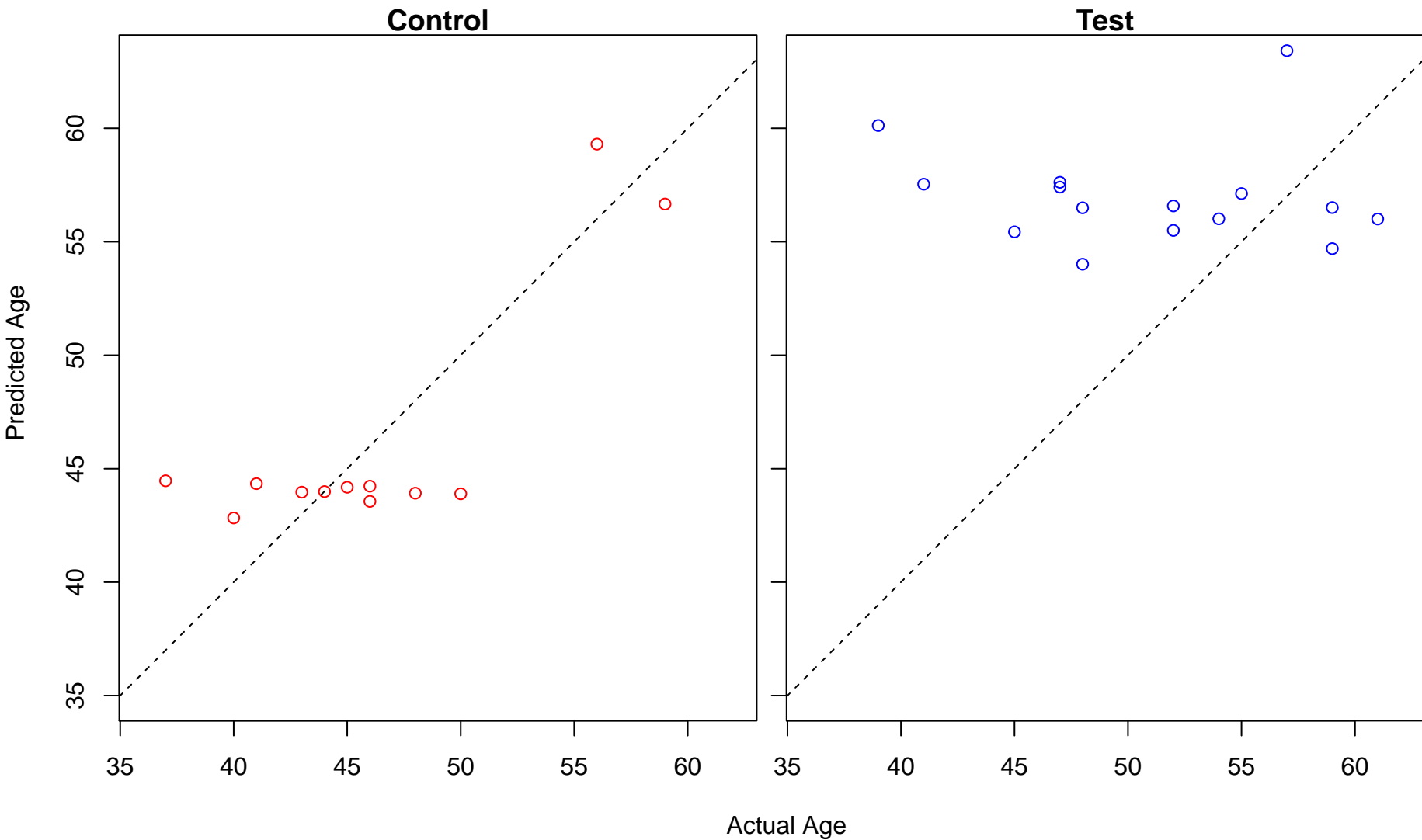
regulation of dephosphorylation (Score: 2.682192)



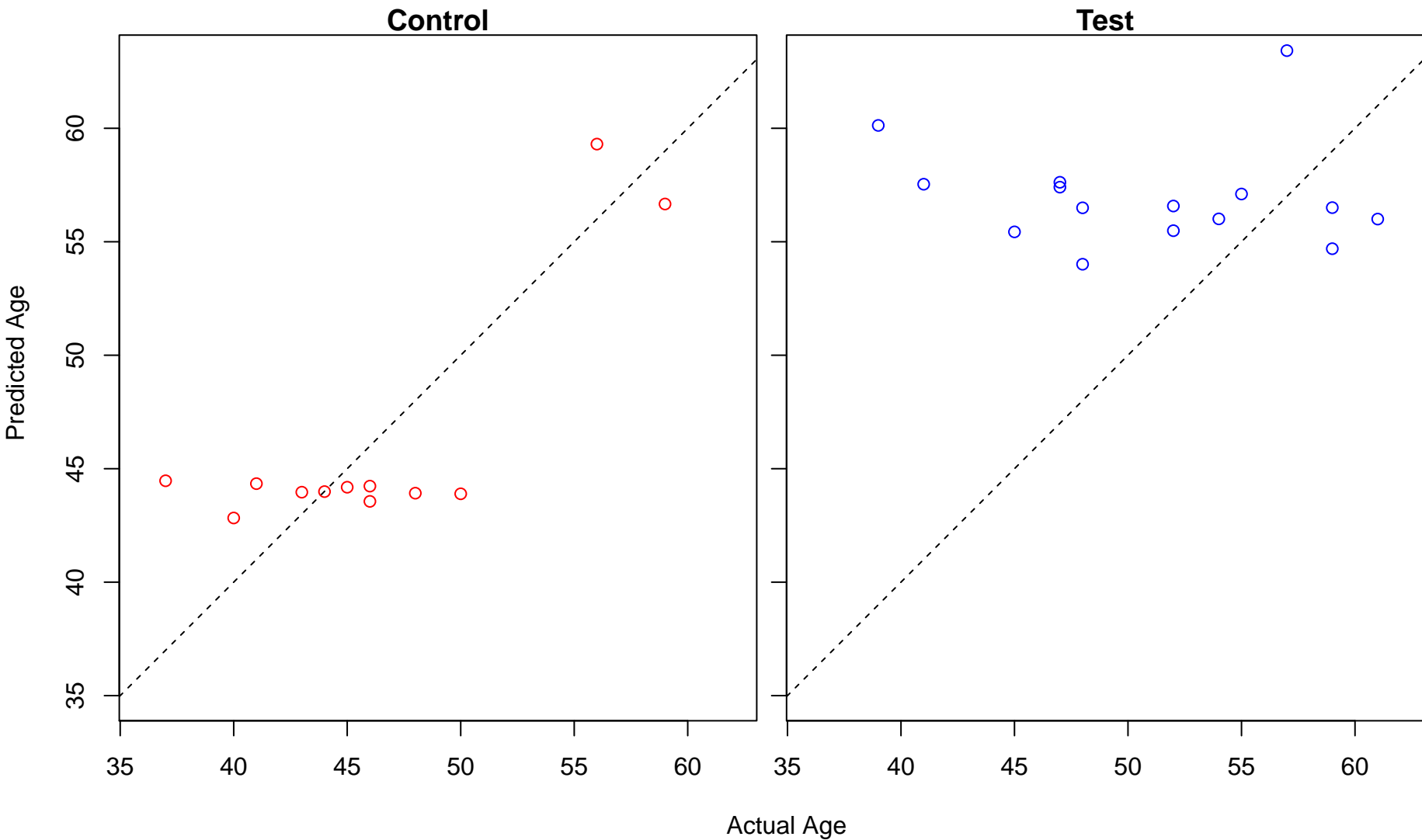
negative regulation of cytokine production (Score: 2.681585)



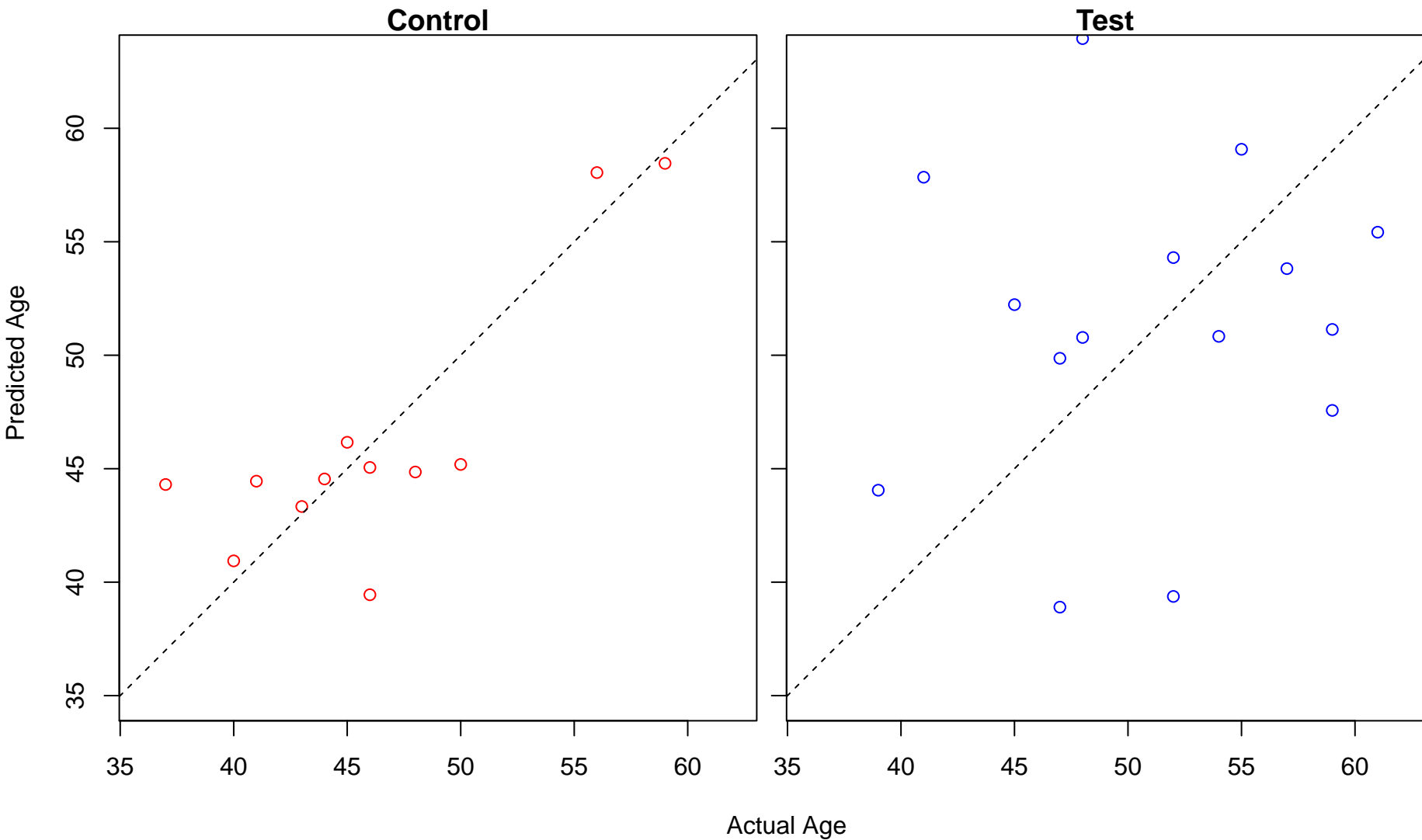
negative regulation of transmembrane transport (Score: 2.681134)



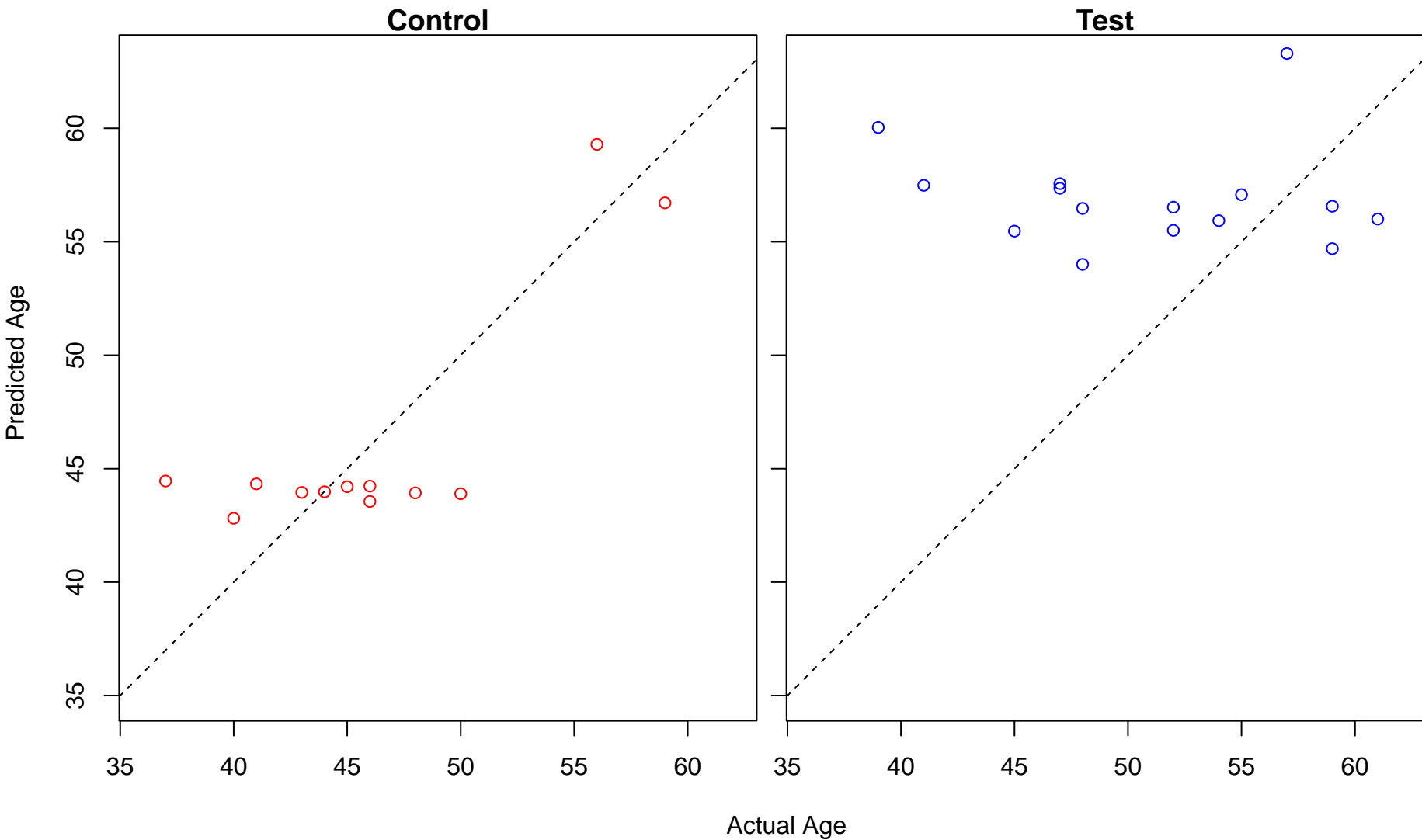
negative regulation of ion transmembrane transport (Score: 2.681102)



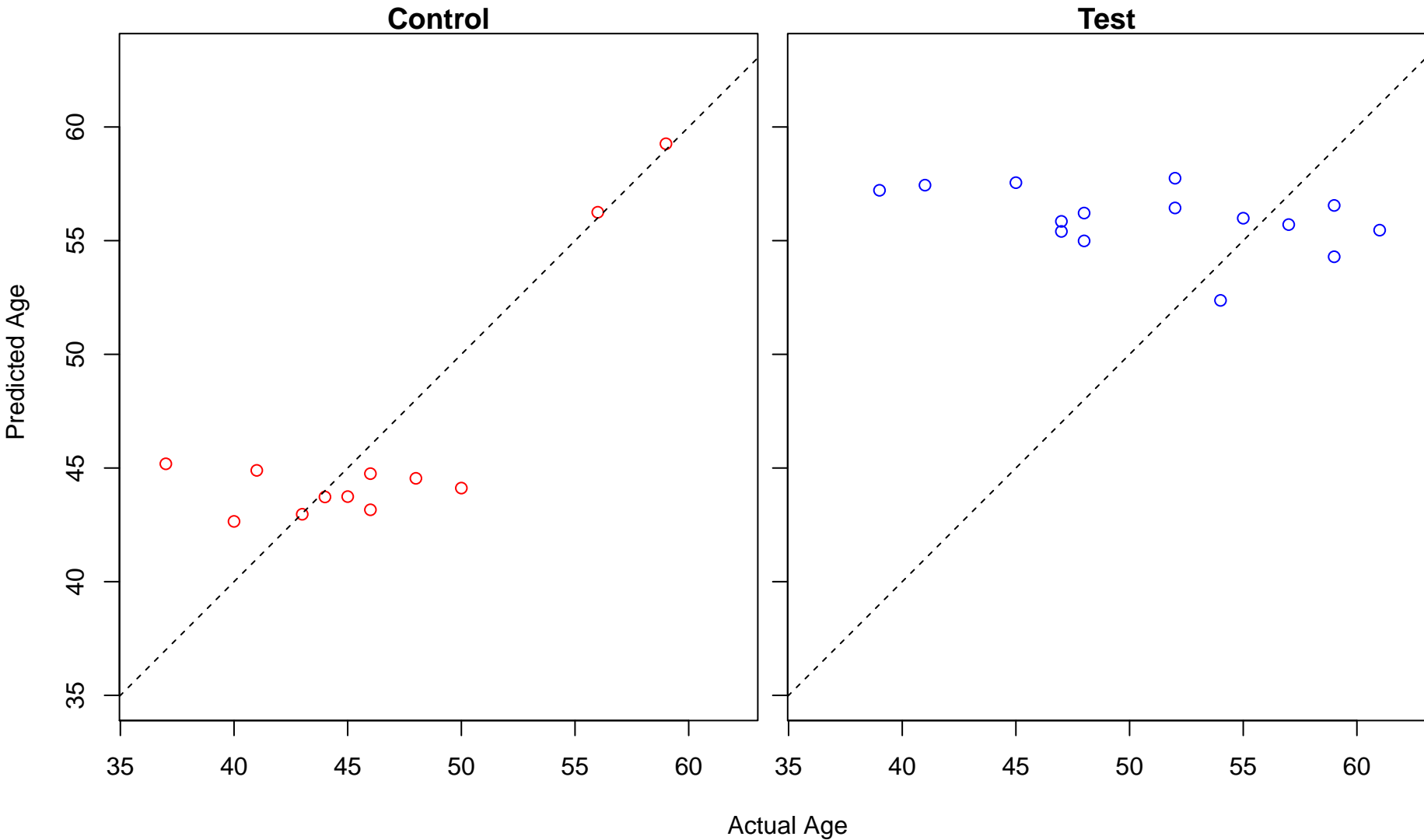
autophagy (Score: 2.679260)



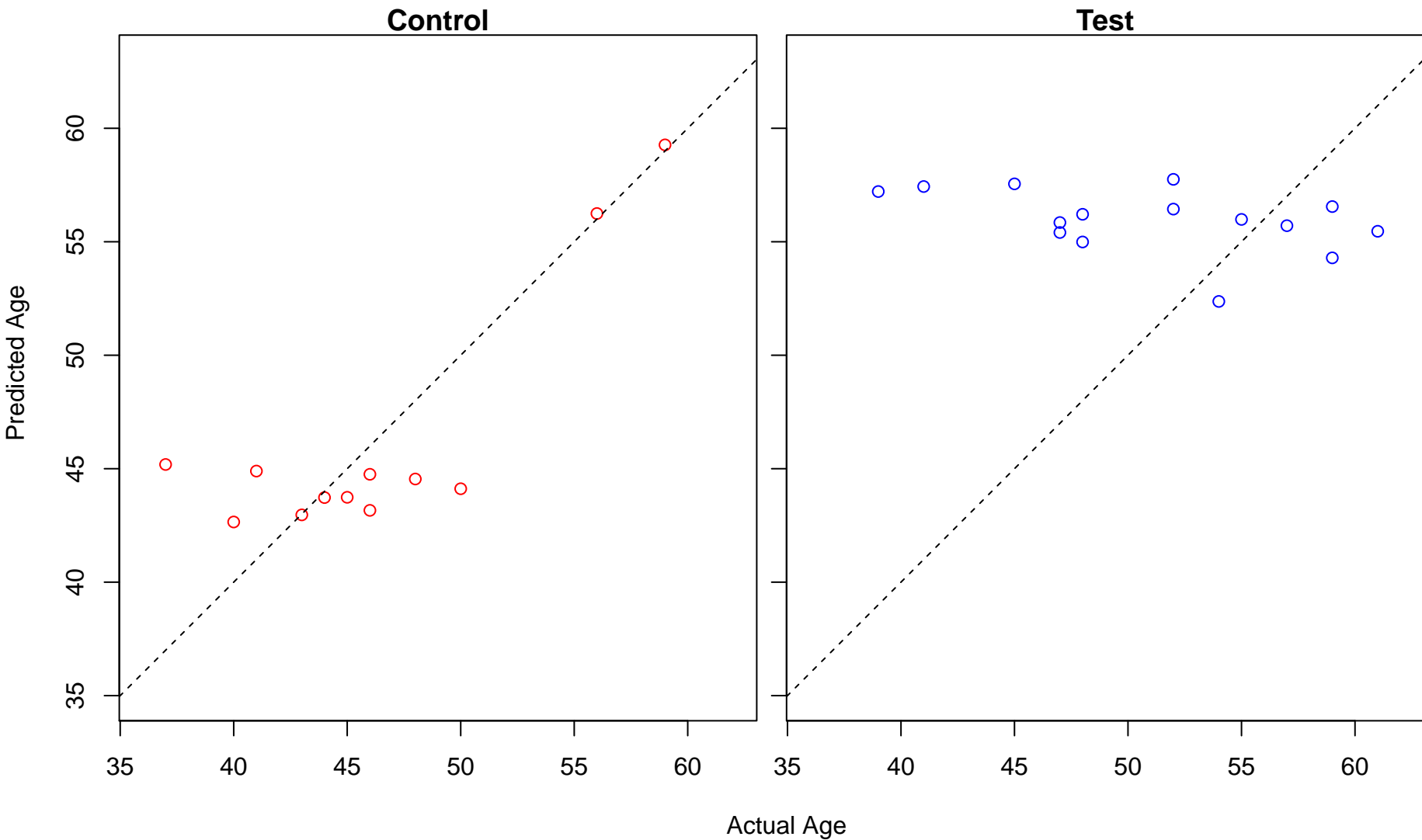
negative regulation of transporter activity (Score: 2.678060)



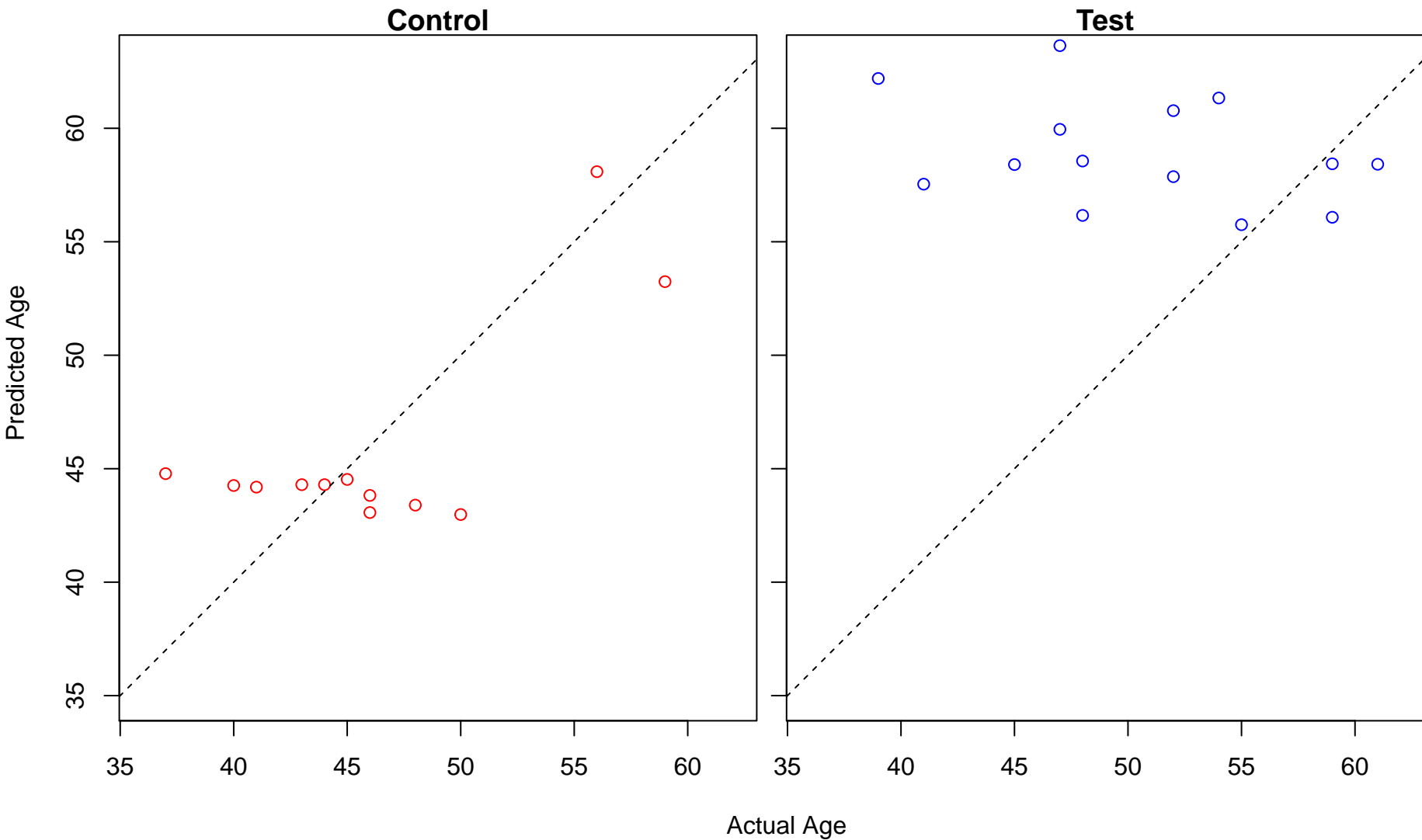
cell activation involved in immune response (Score: 2.676703)



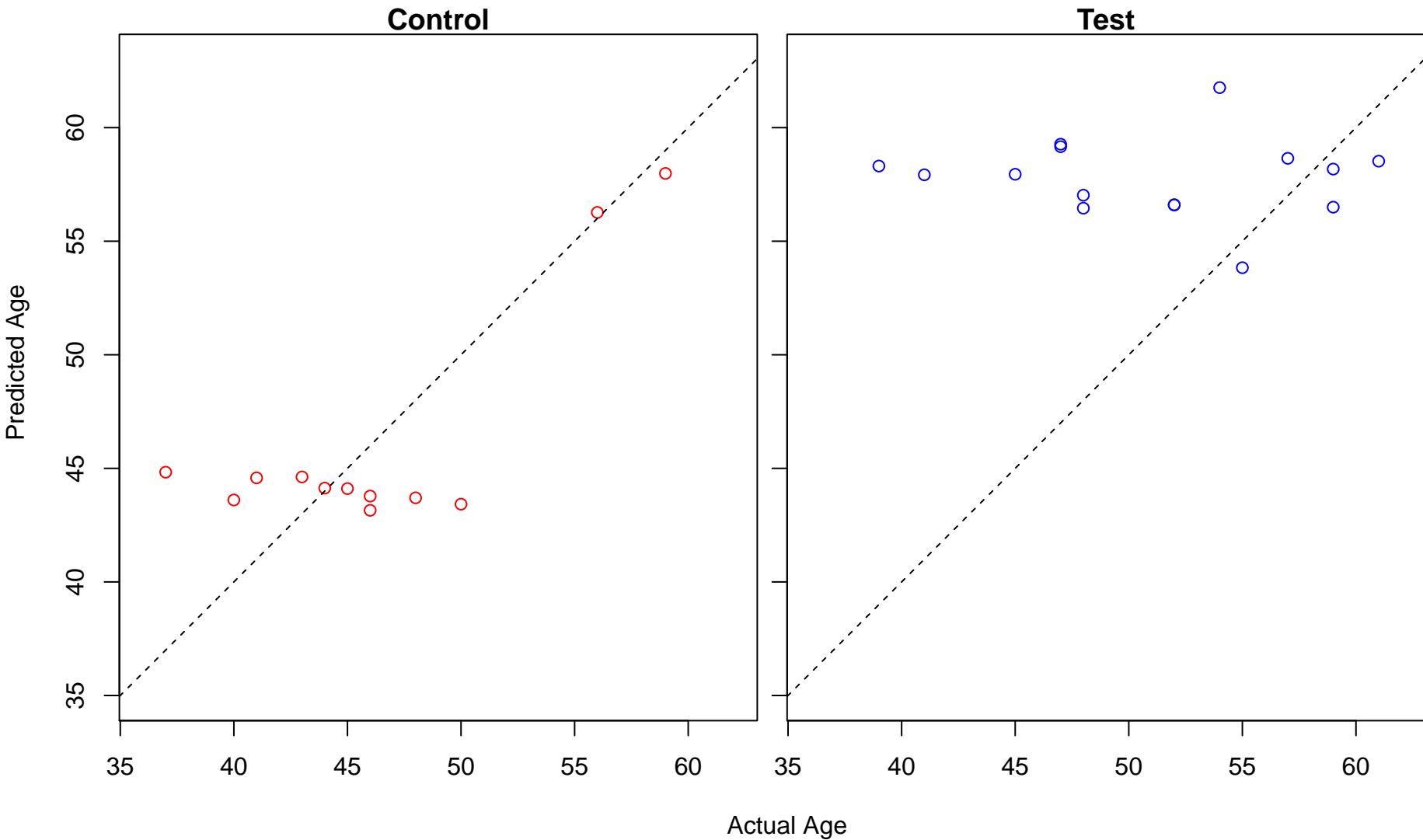
leukocyte activation involved in immune response (Score: 2.675957)



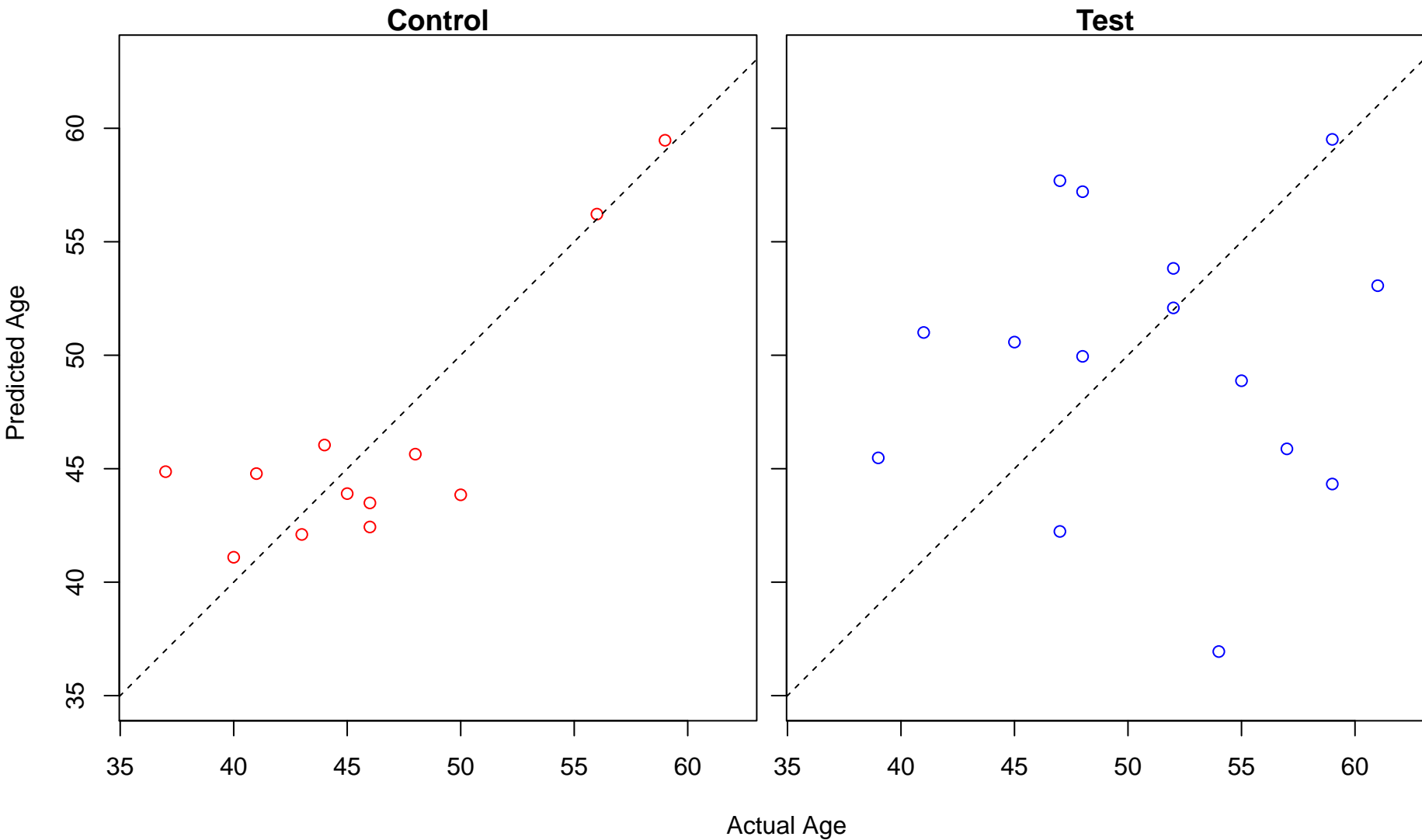
purine-containing compound biosynthetic process (Score: 2.674688)



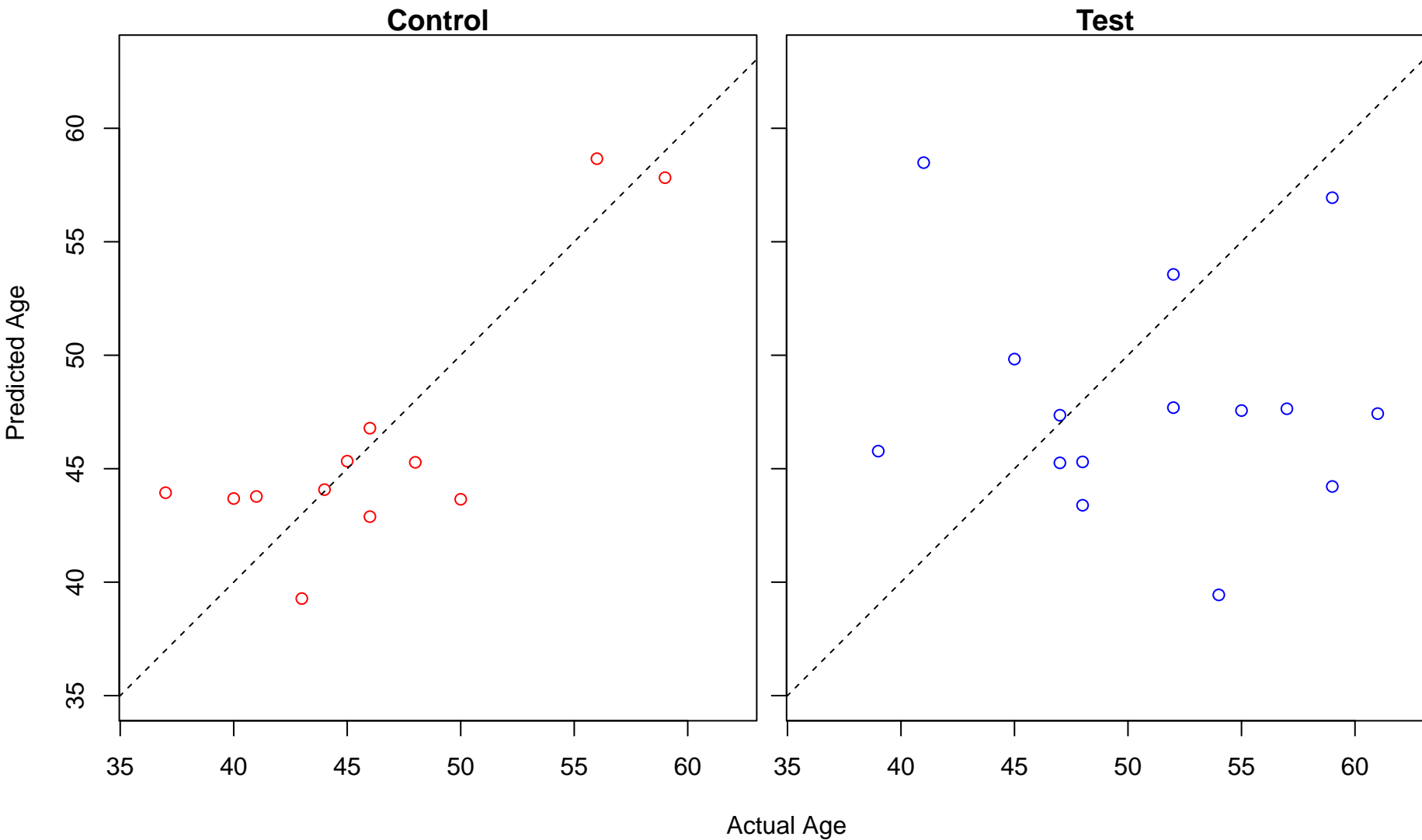
positive regulation of transcription from RNA polymerase I promoter (Score: 2.669863)



negative regulation of DNA-dependent DNA replication (Score: 2.665728)

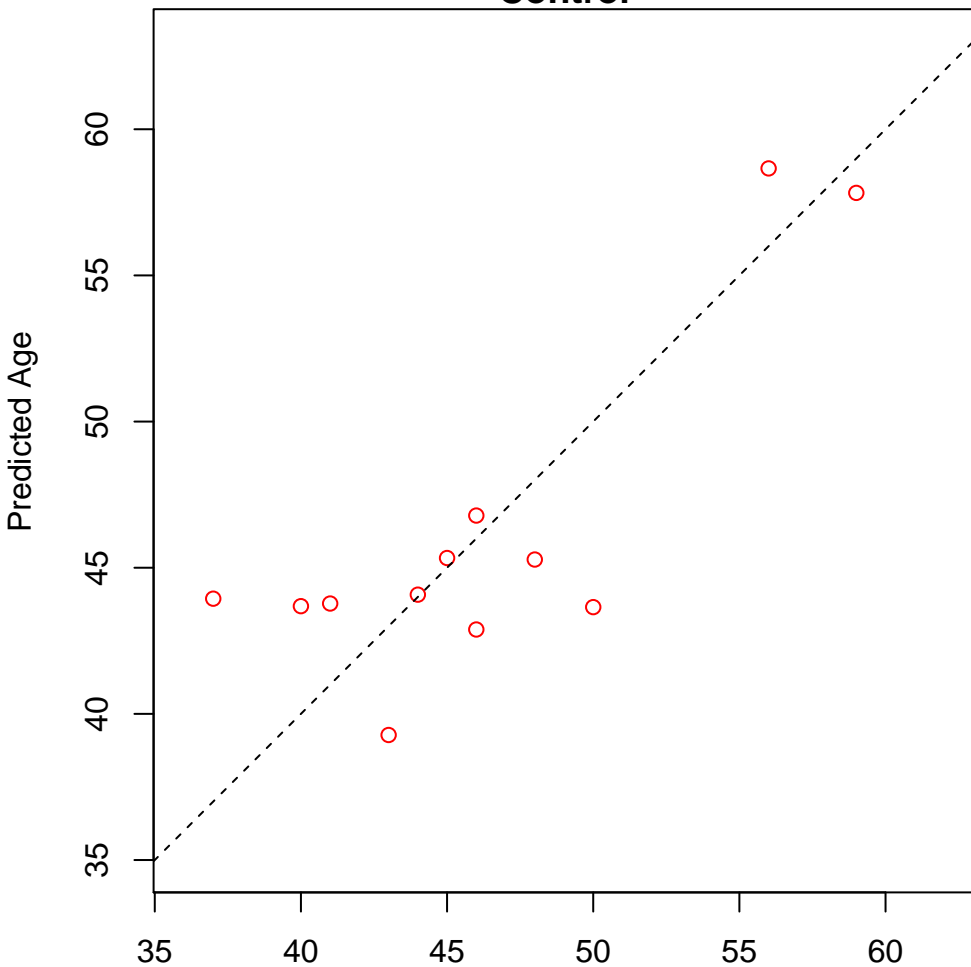


phosphate ion homeostasis (Score: 2.663383)

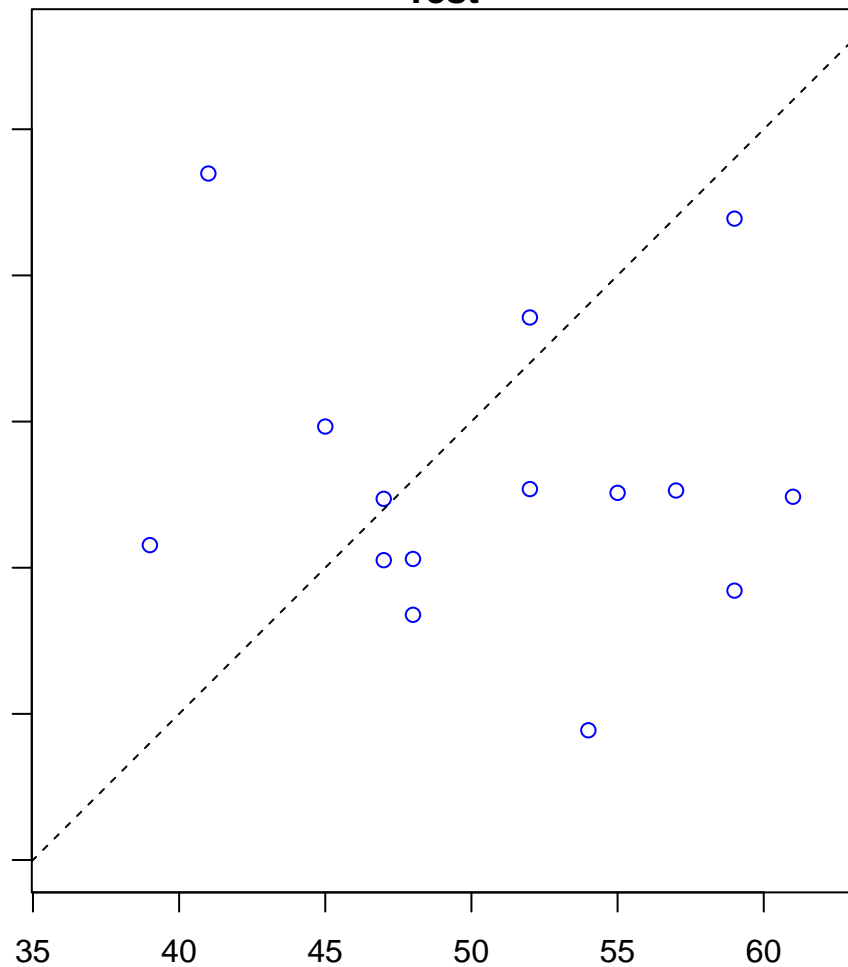


trivalent inorganic anion homeostasis (Score: 2.663383)

Control

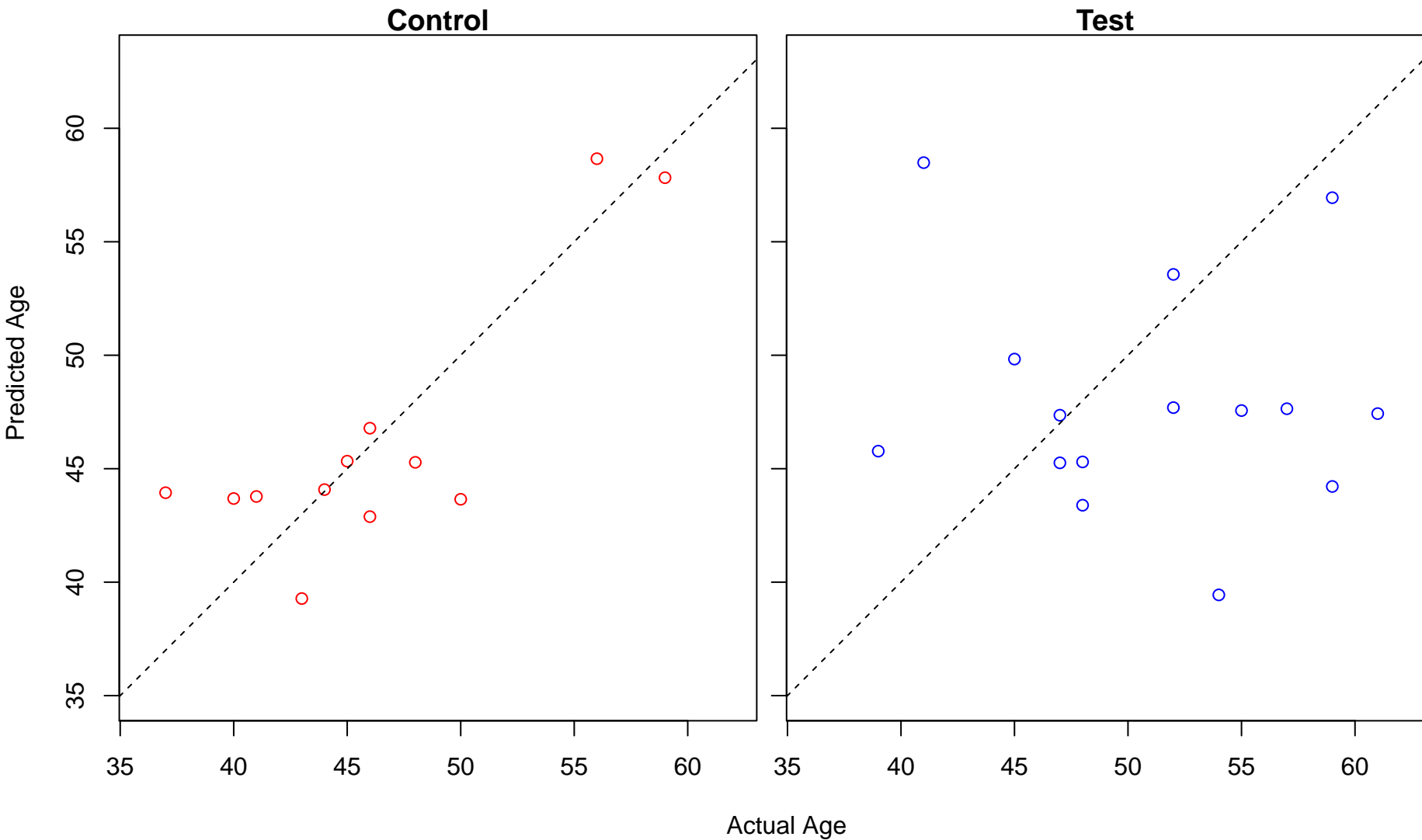


Test

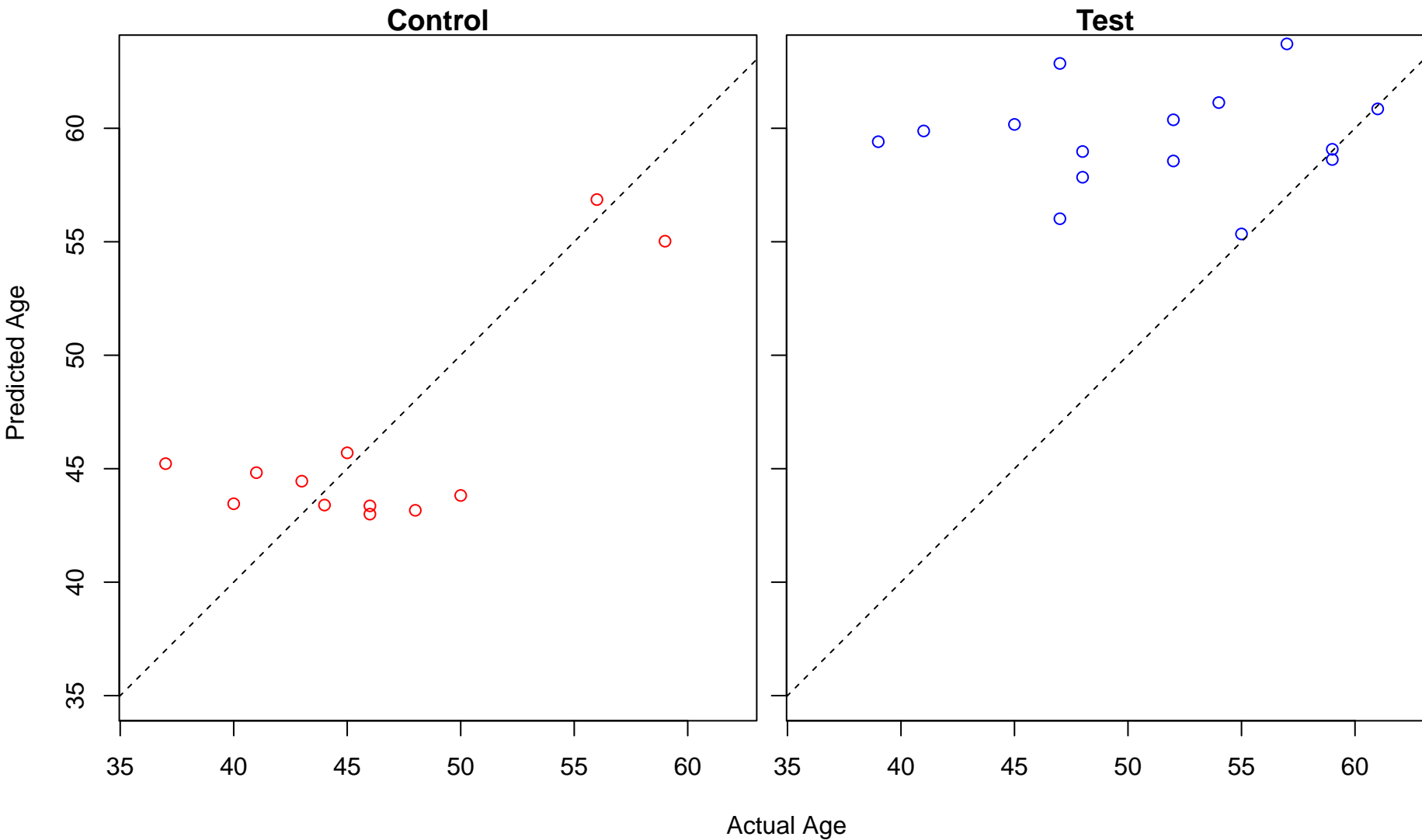


Actual Age

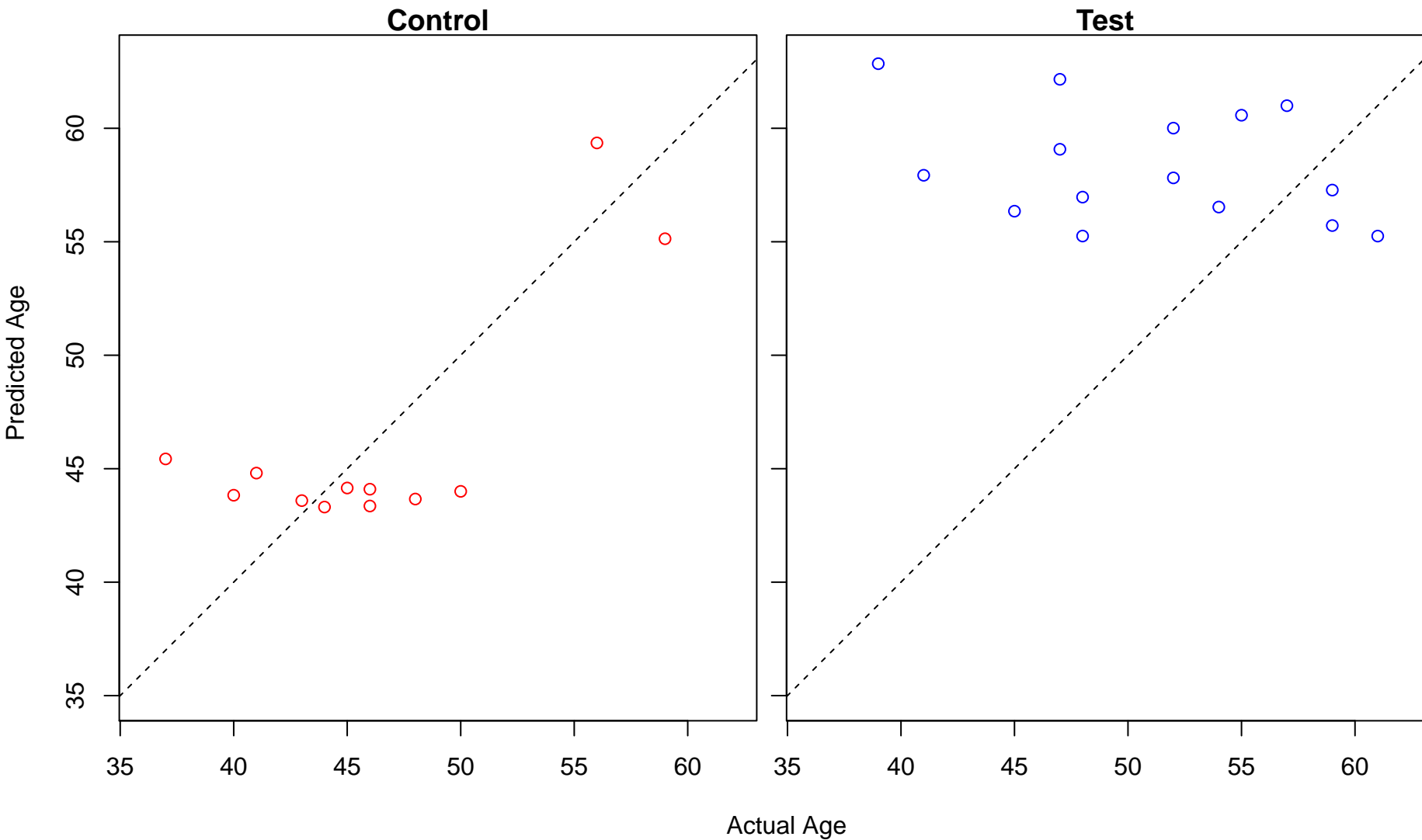
divalent inorganic anion homeostasis (Score: 2.663345)



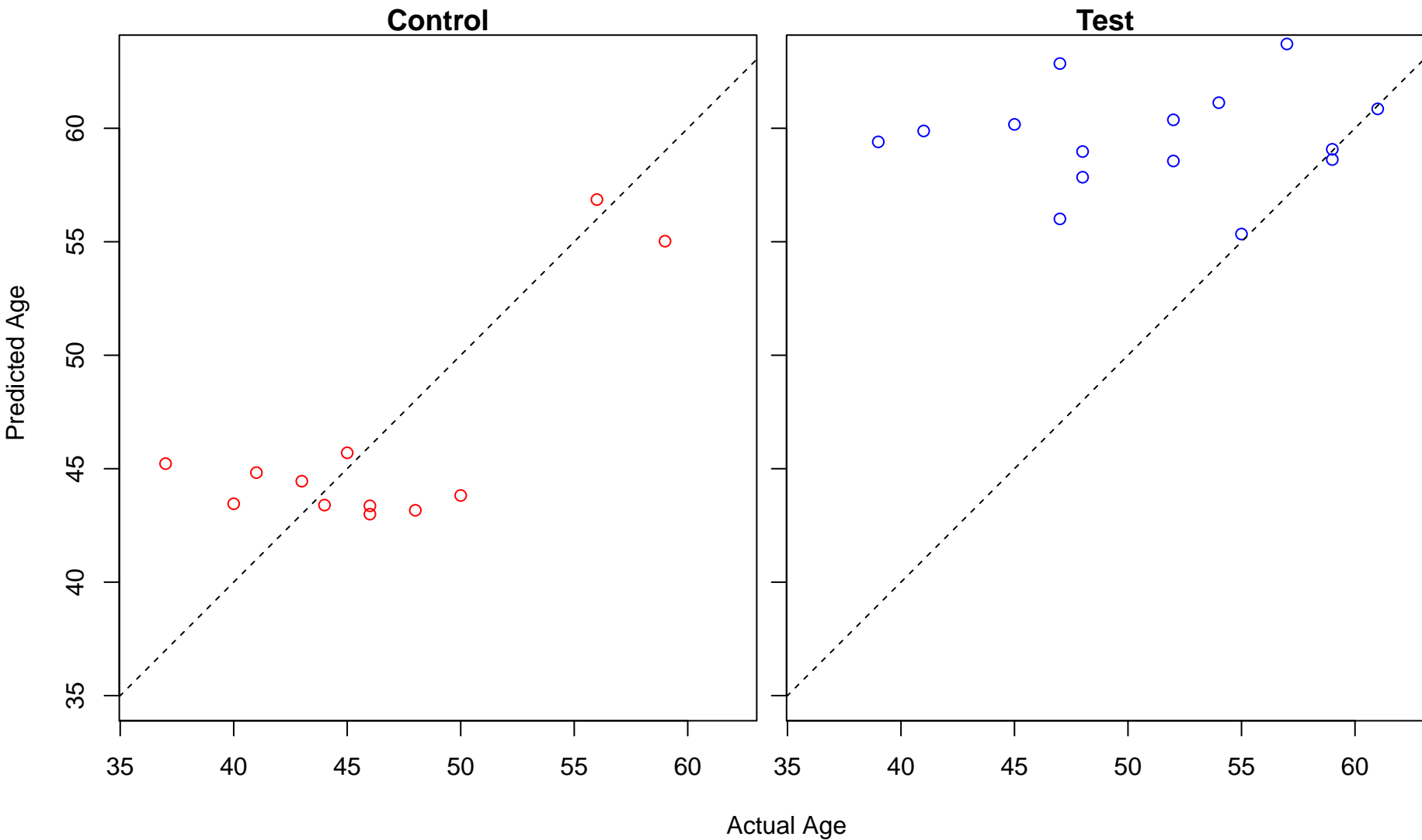
positive regulation of proteasomal protein catabolic process (Score: 2.662096)



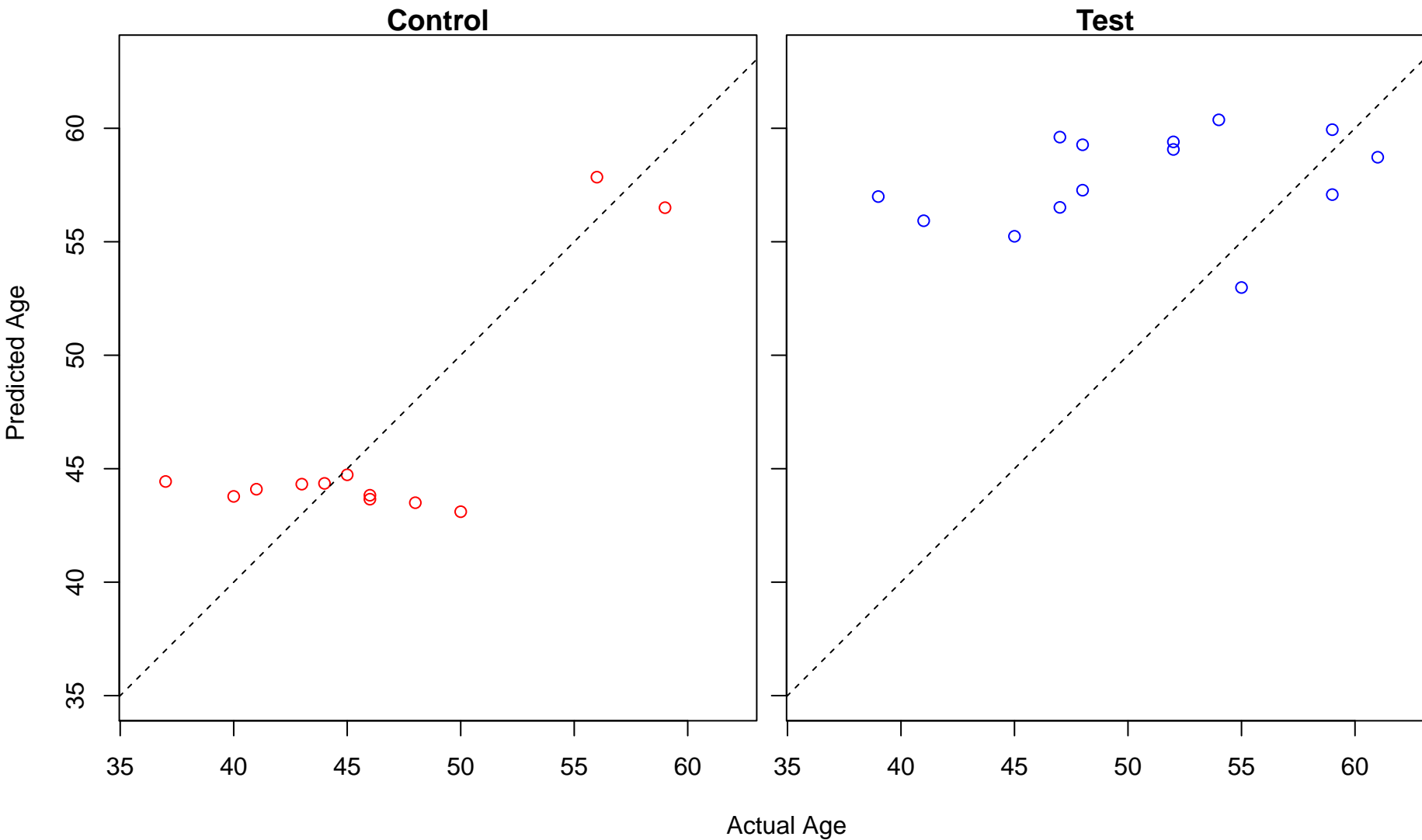
regulation of response to biotic stimulus (Score: 2.661644)



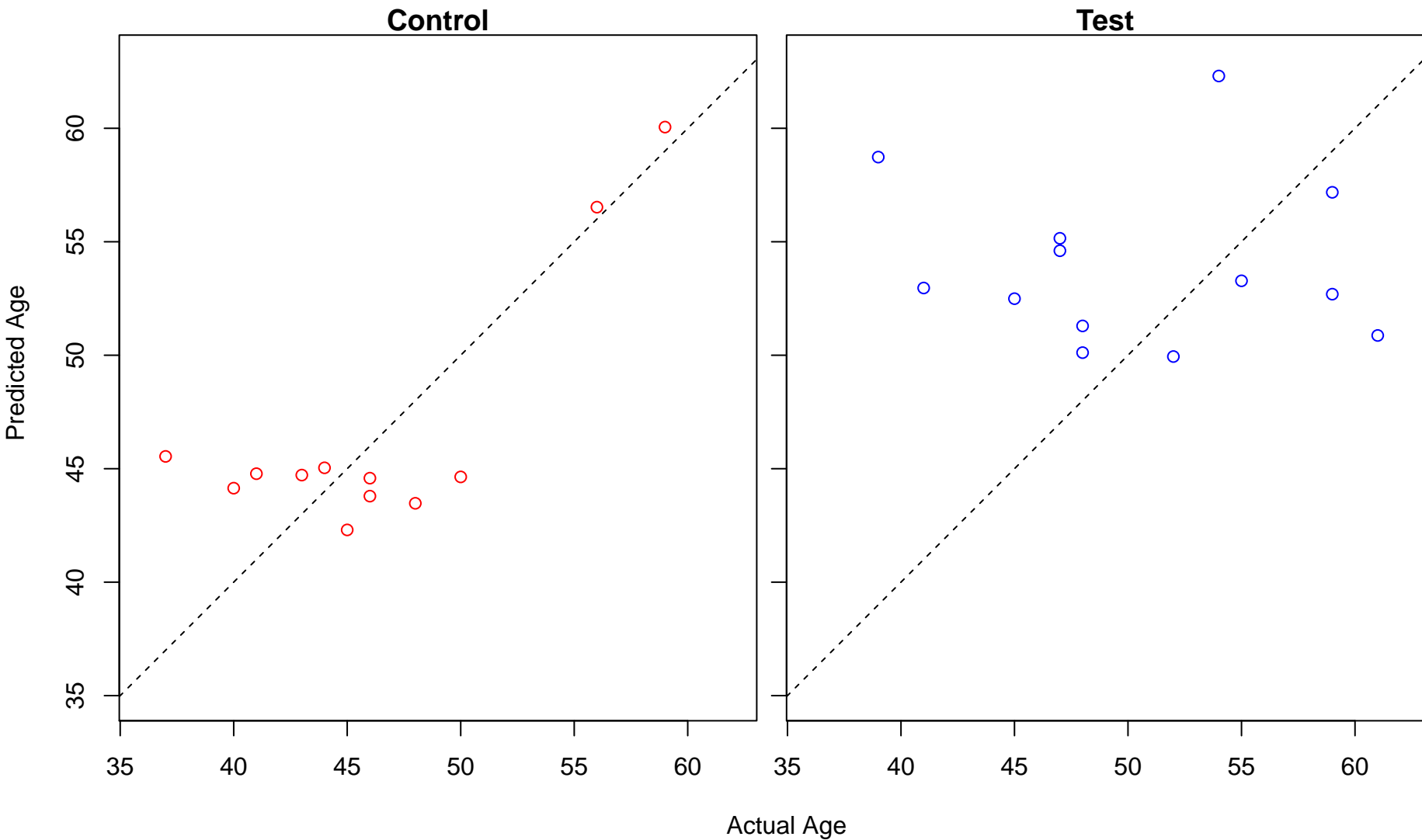
positive regulation of proteasomal ubiquitin-dependent protein catabolic process (Score: 2.661257)



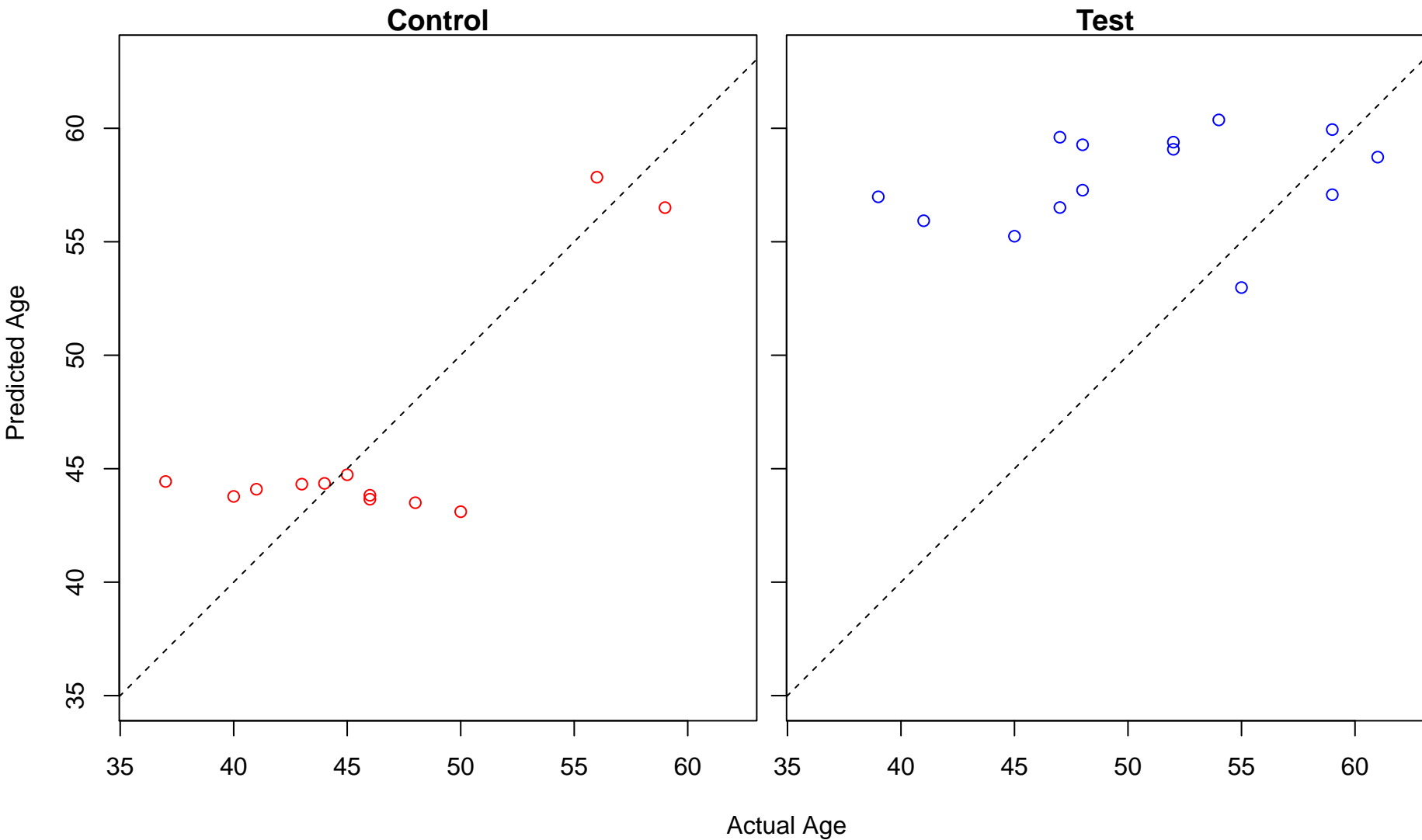
7-methylguanosine RNA capping (Score: 2.661151)



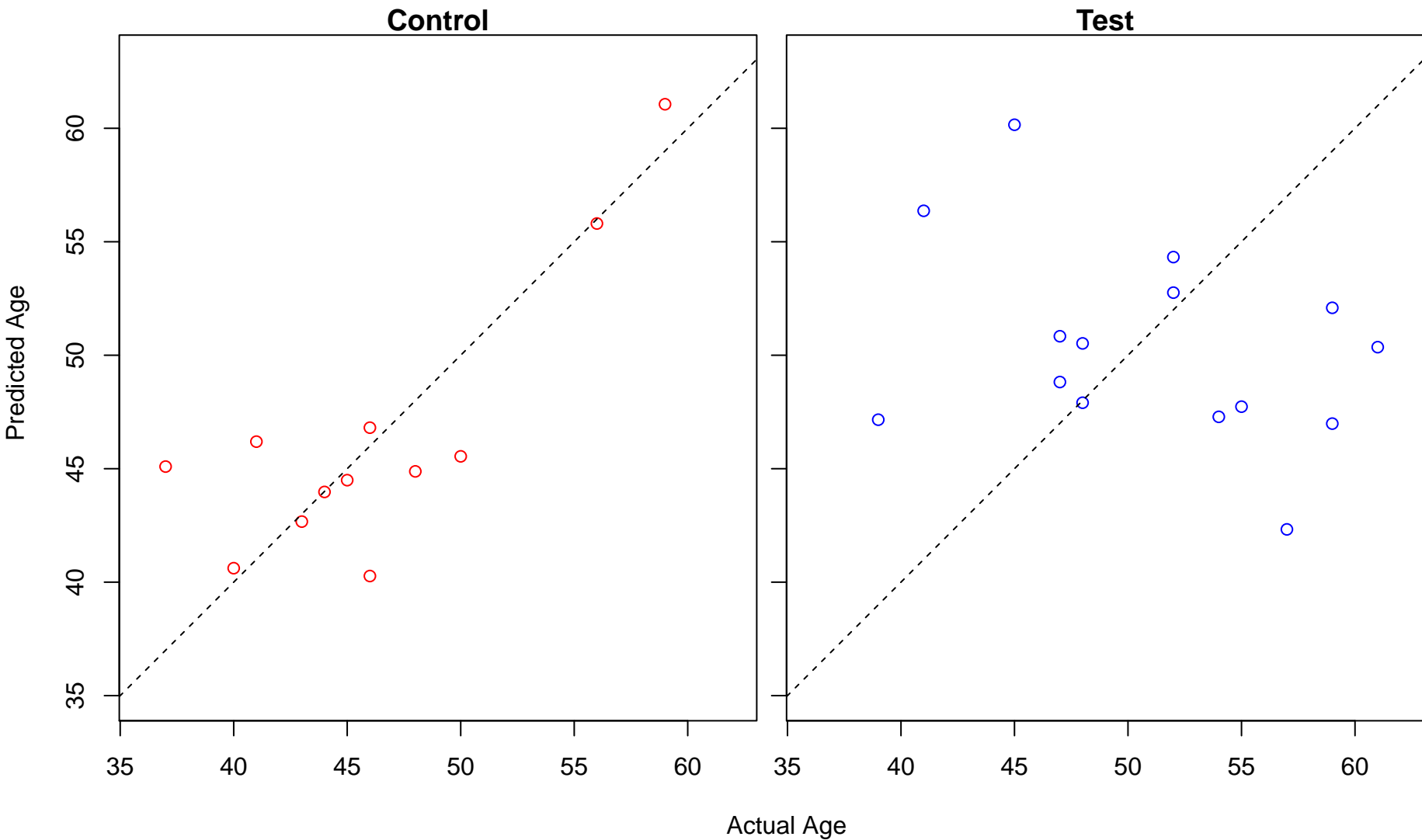
positive regulation of protein kinase A signaling (Score: 2.661039)



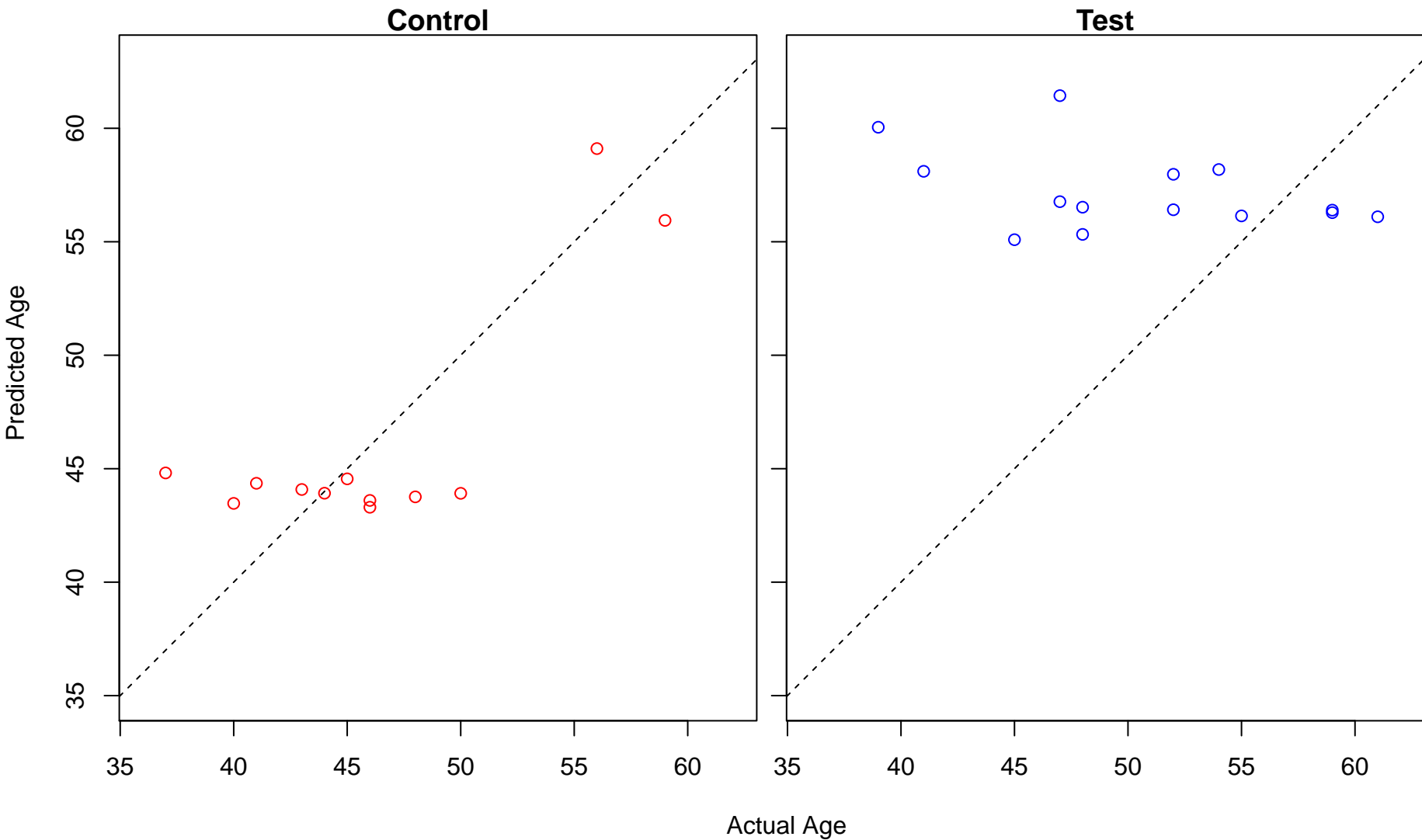
7-methylguanosine mRNA capping (Score: 2.660841)



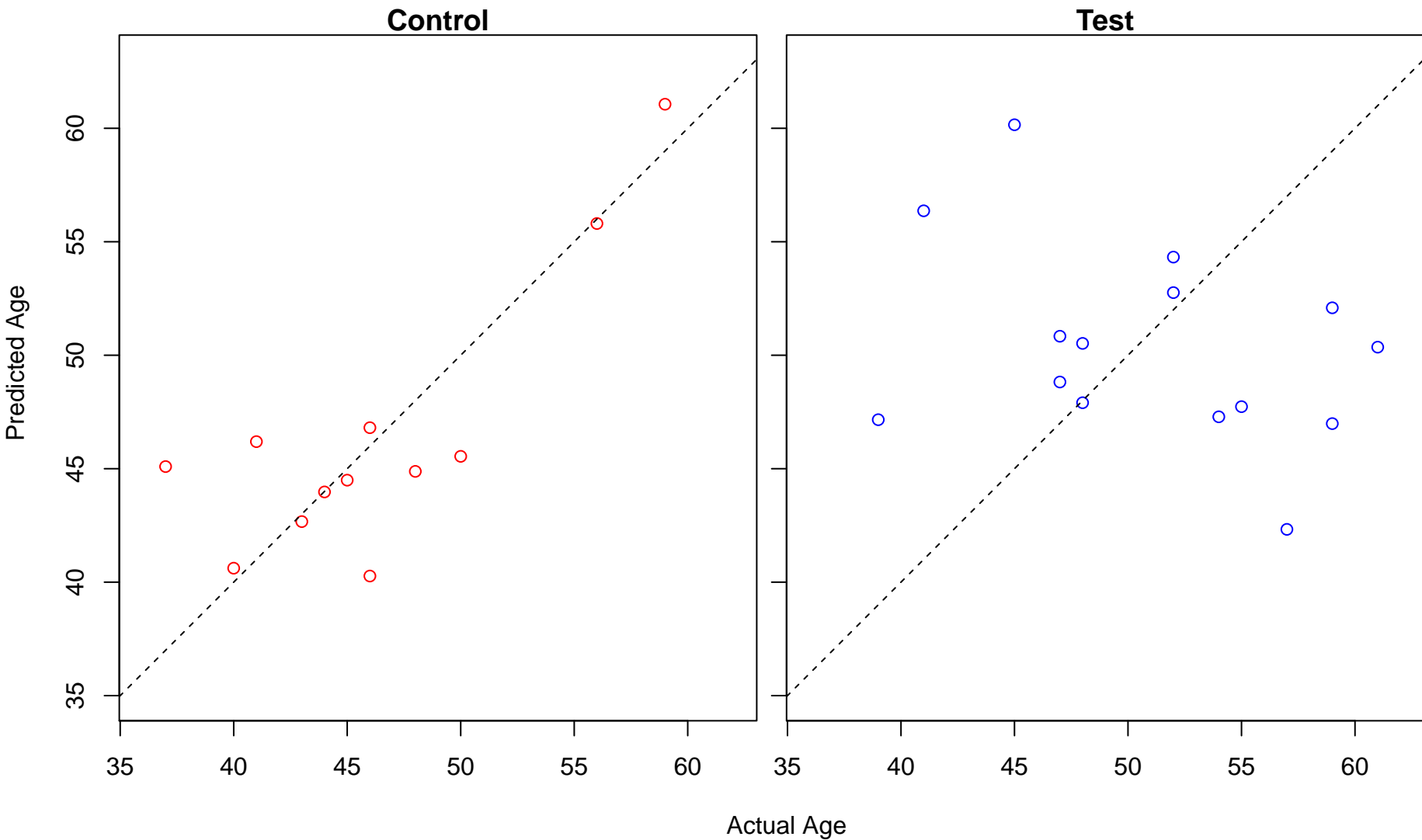
regulation of intracellular pH (Score: 2.660680)



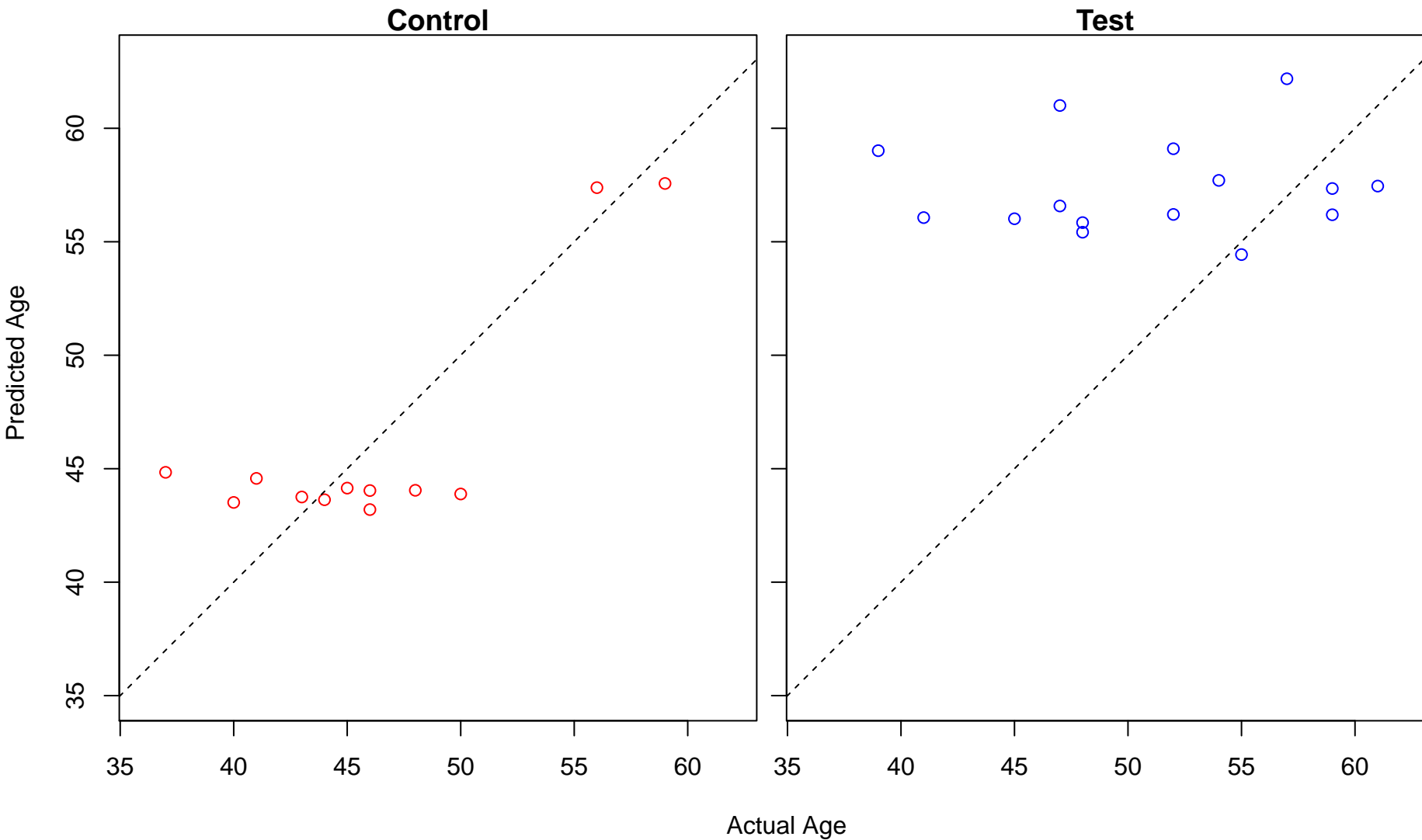
secretion by cell (Score: 2.660669)



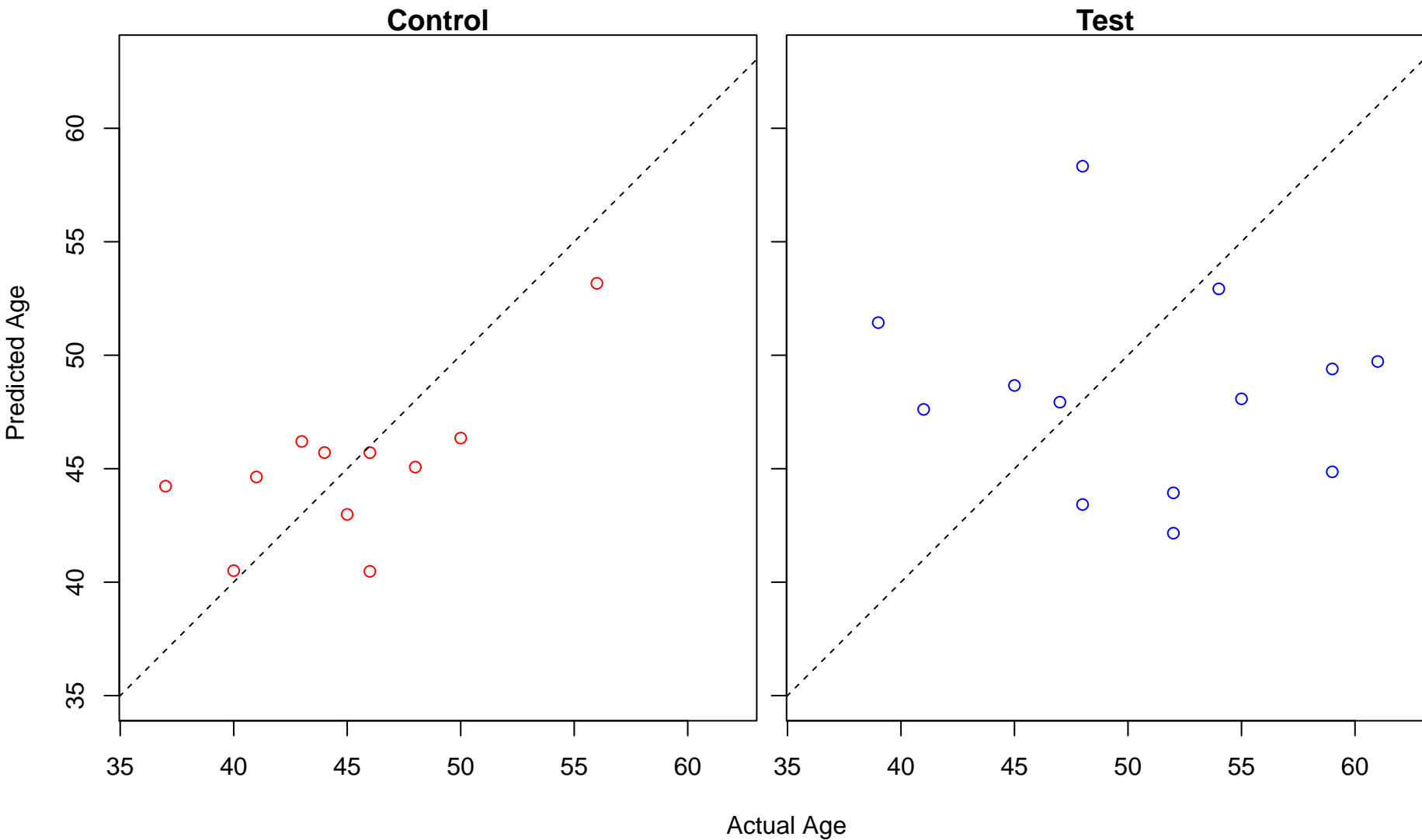
regulation of cellular pH (Score: 2.660635)



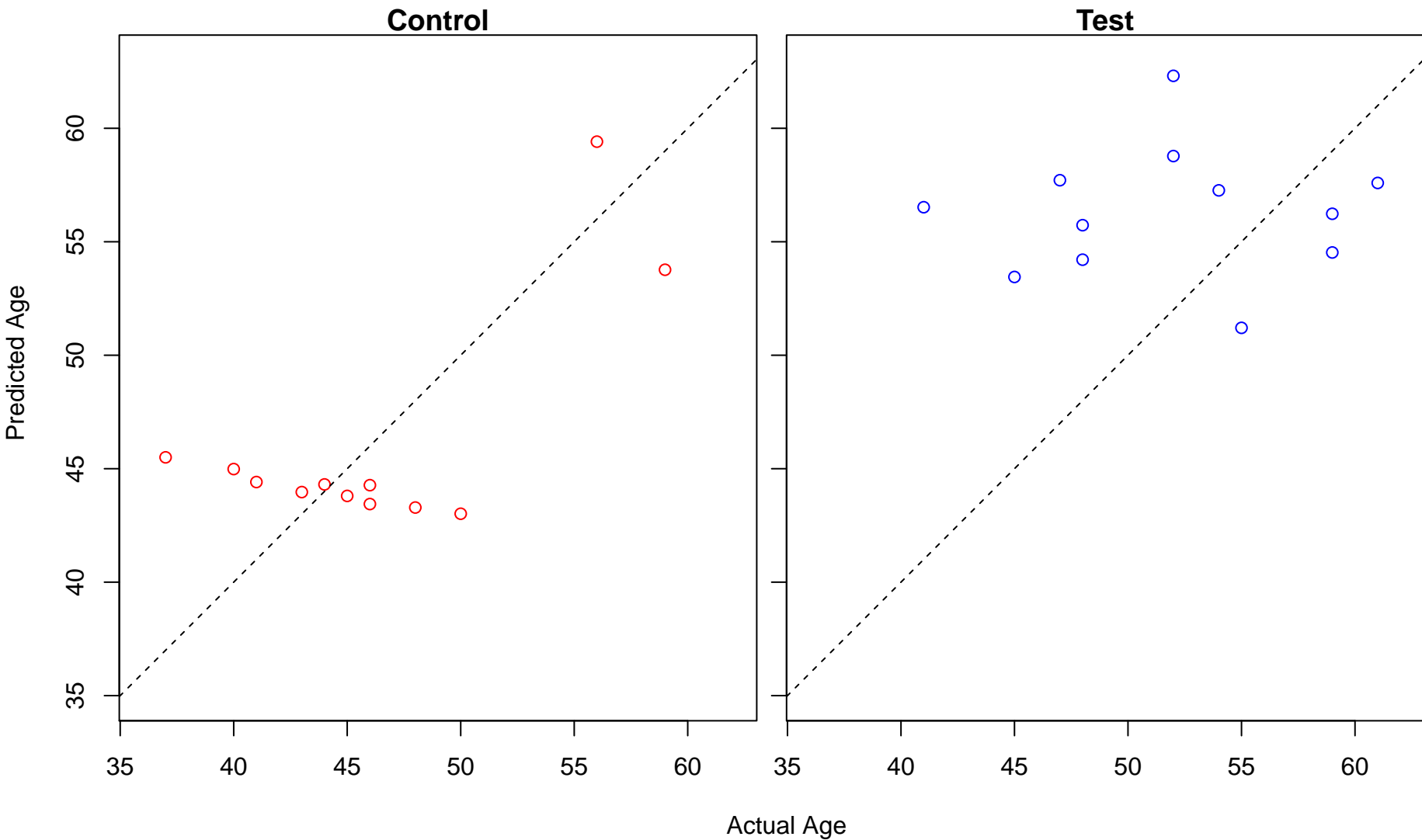
negative regulation of organelle organization (Score: 2.660612)



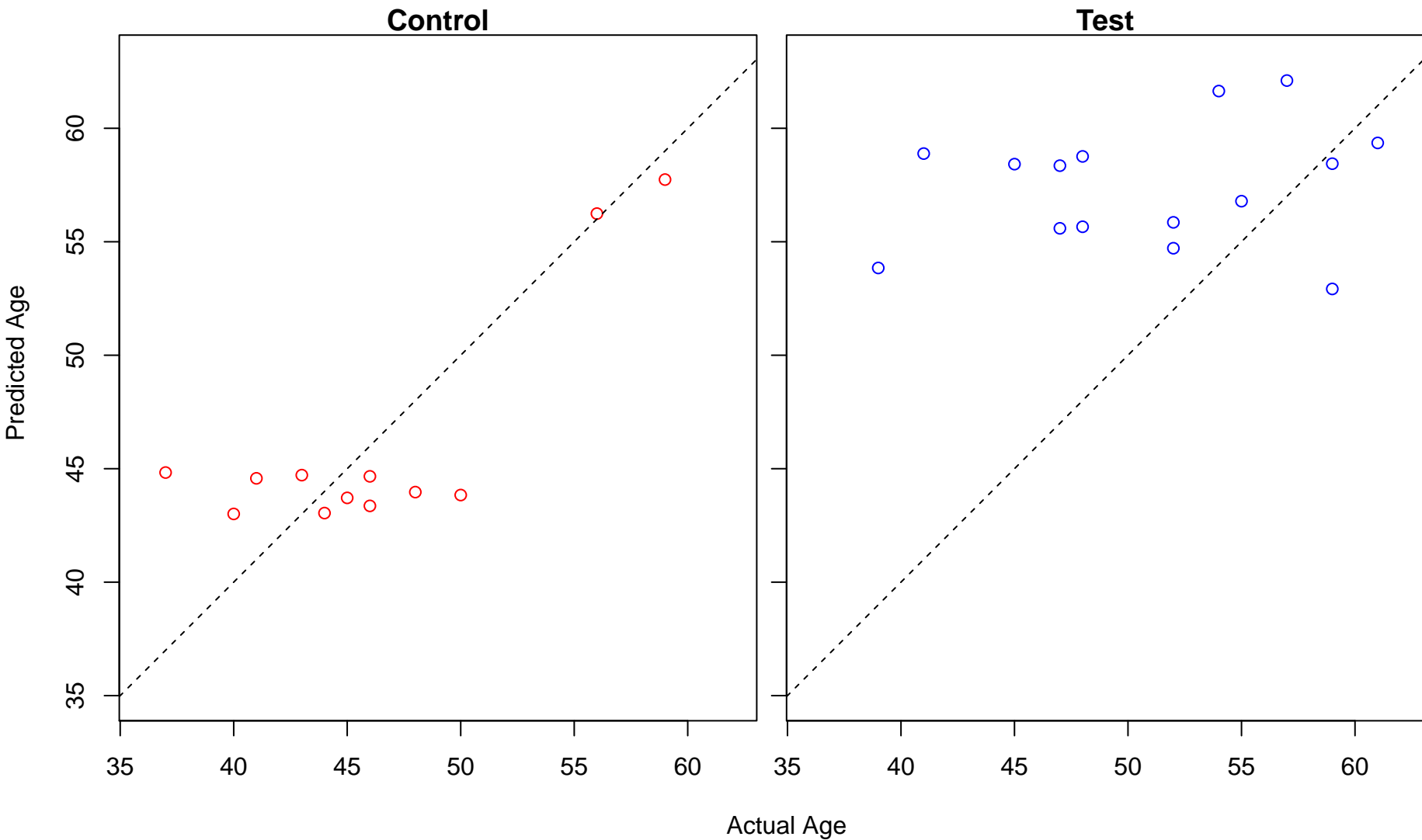
regulation of ion transmembrane transport (Score: 2.659880)



erythrocyte homeostasis (Score: 2.657856)

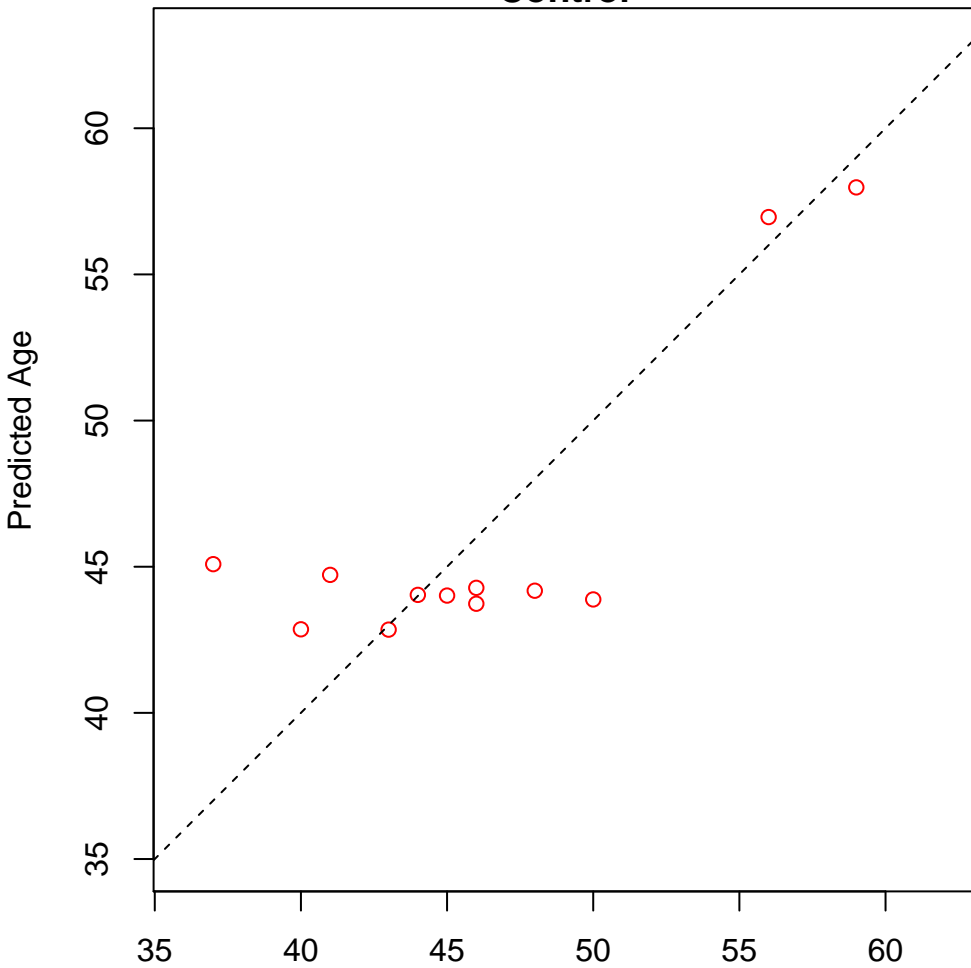


membrane protein ectodomain proteolysis (Score: 2.657288)

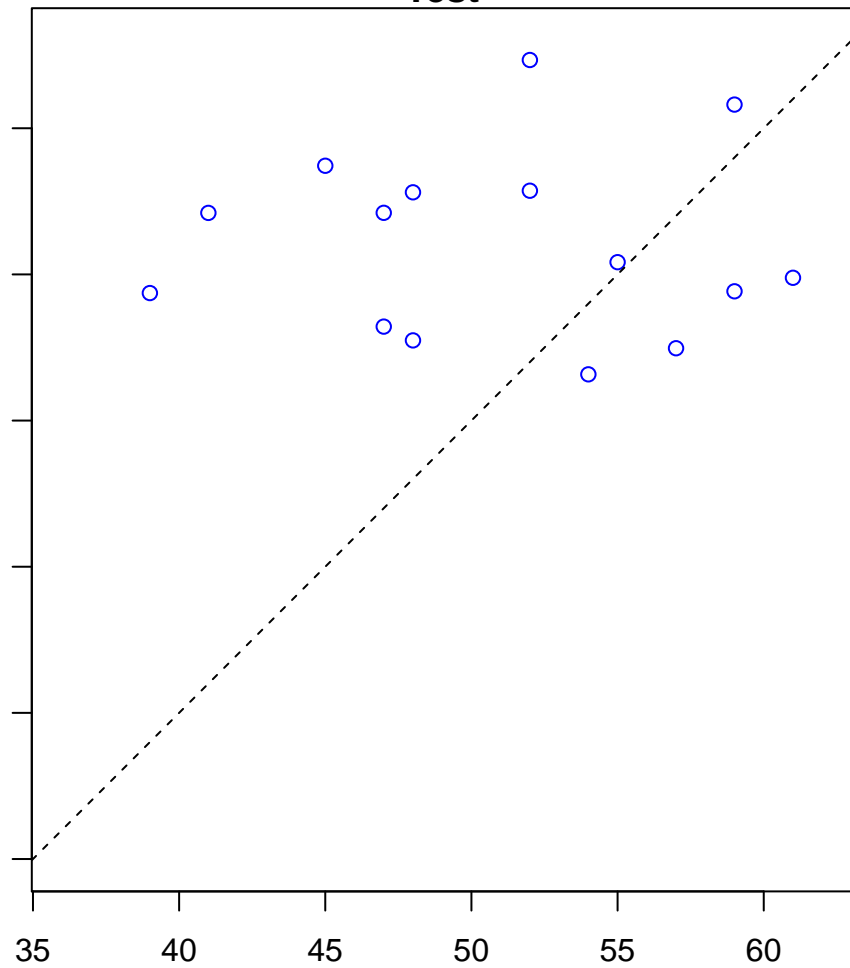


pyrimidine nucleotide metabolic process (Score: 2.655494)

Control

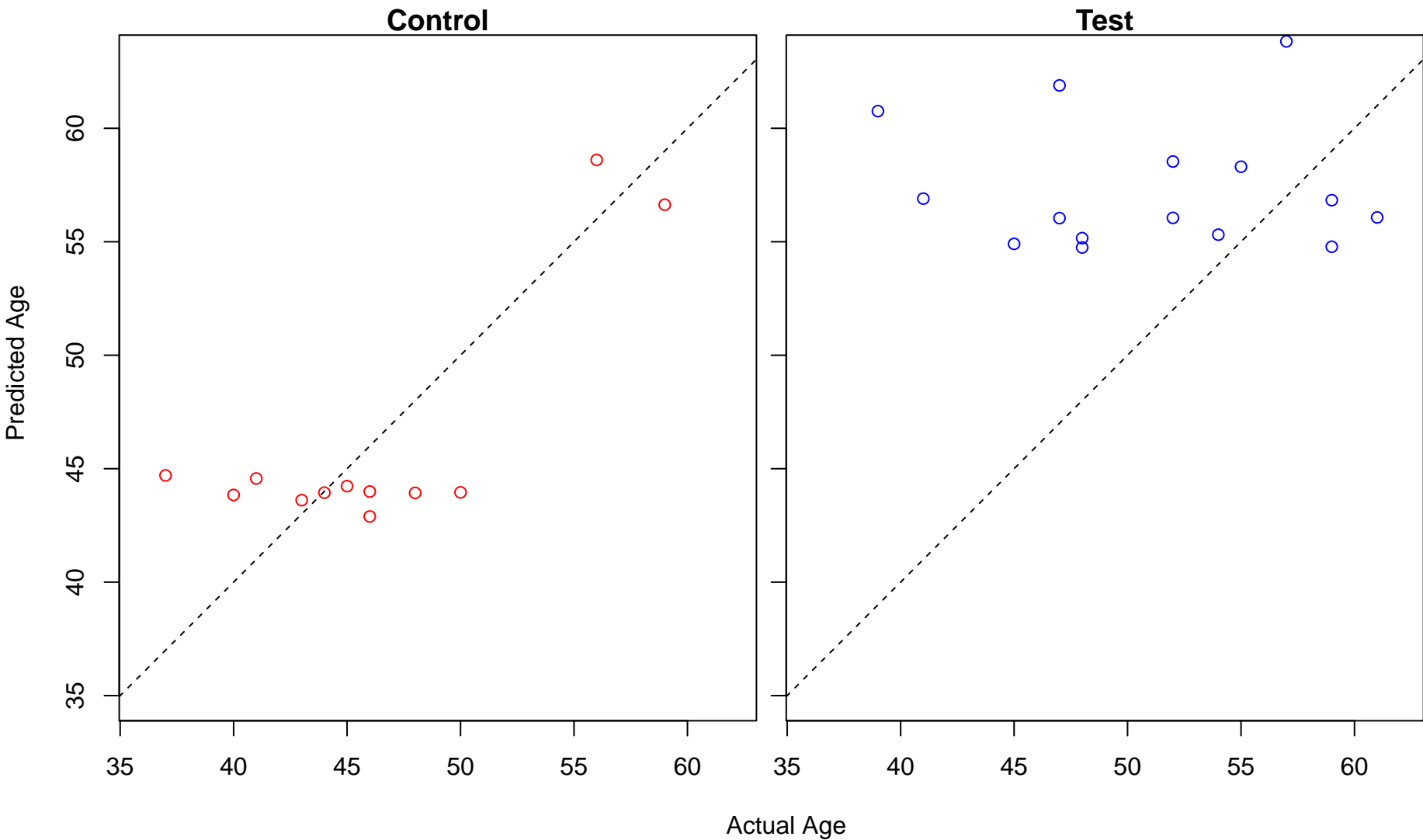


Test

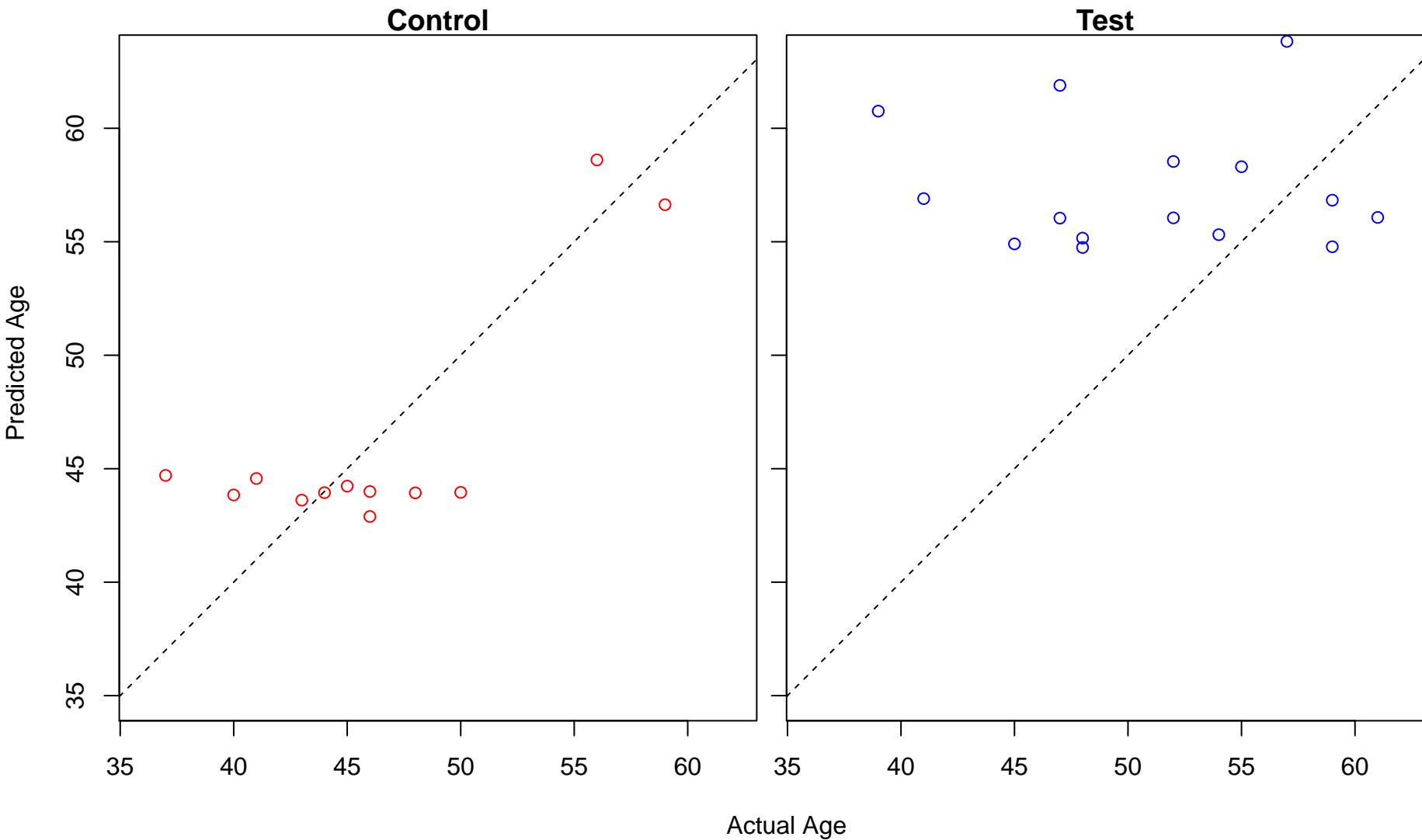


Actual Age

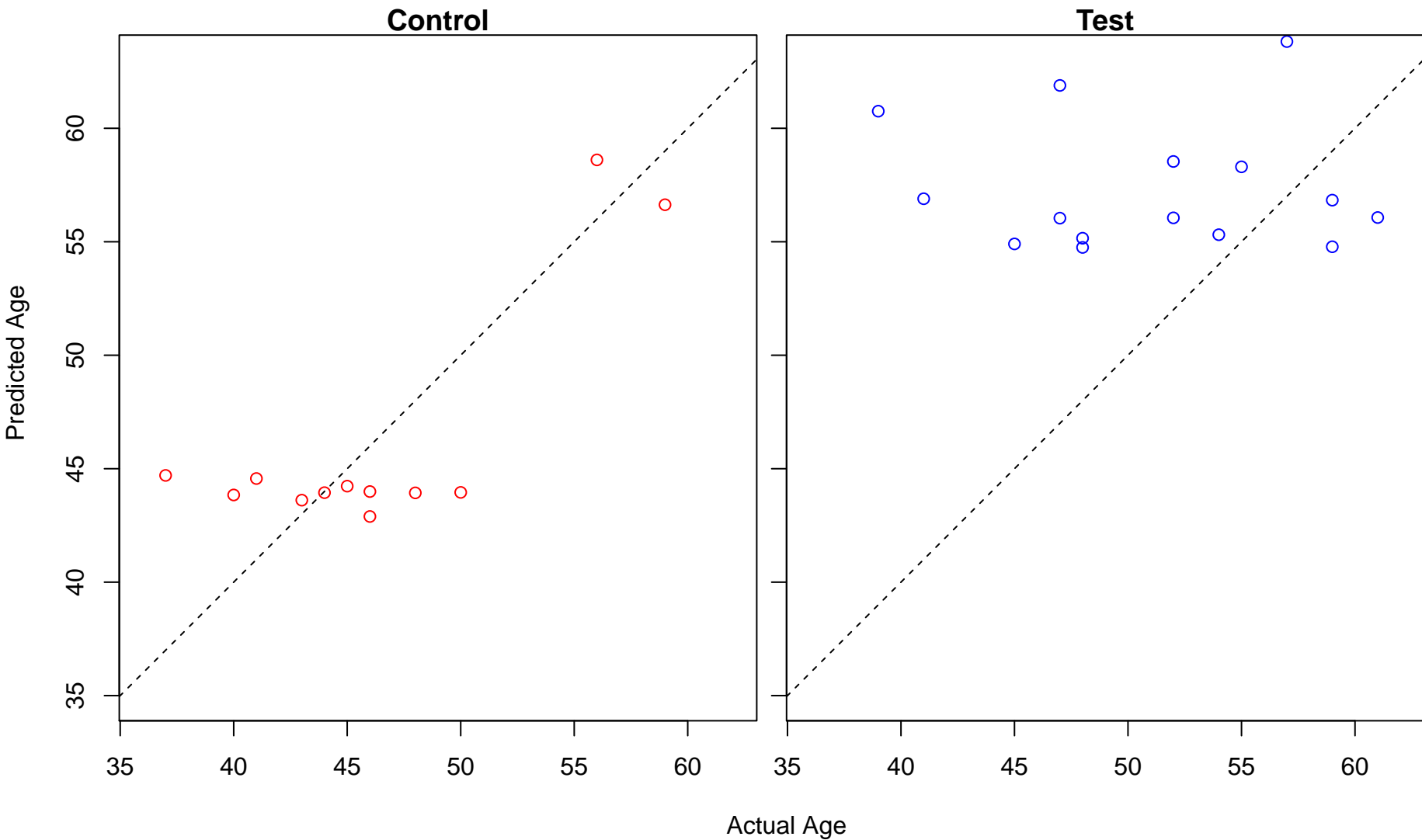
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (Score: 2.6547)



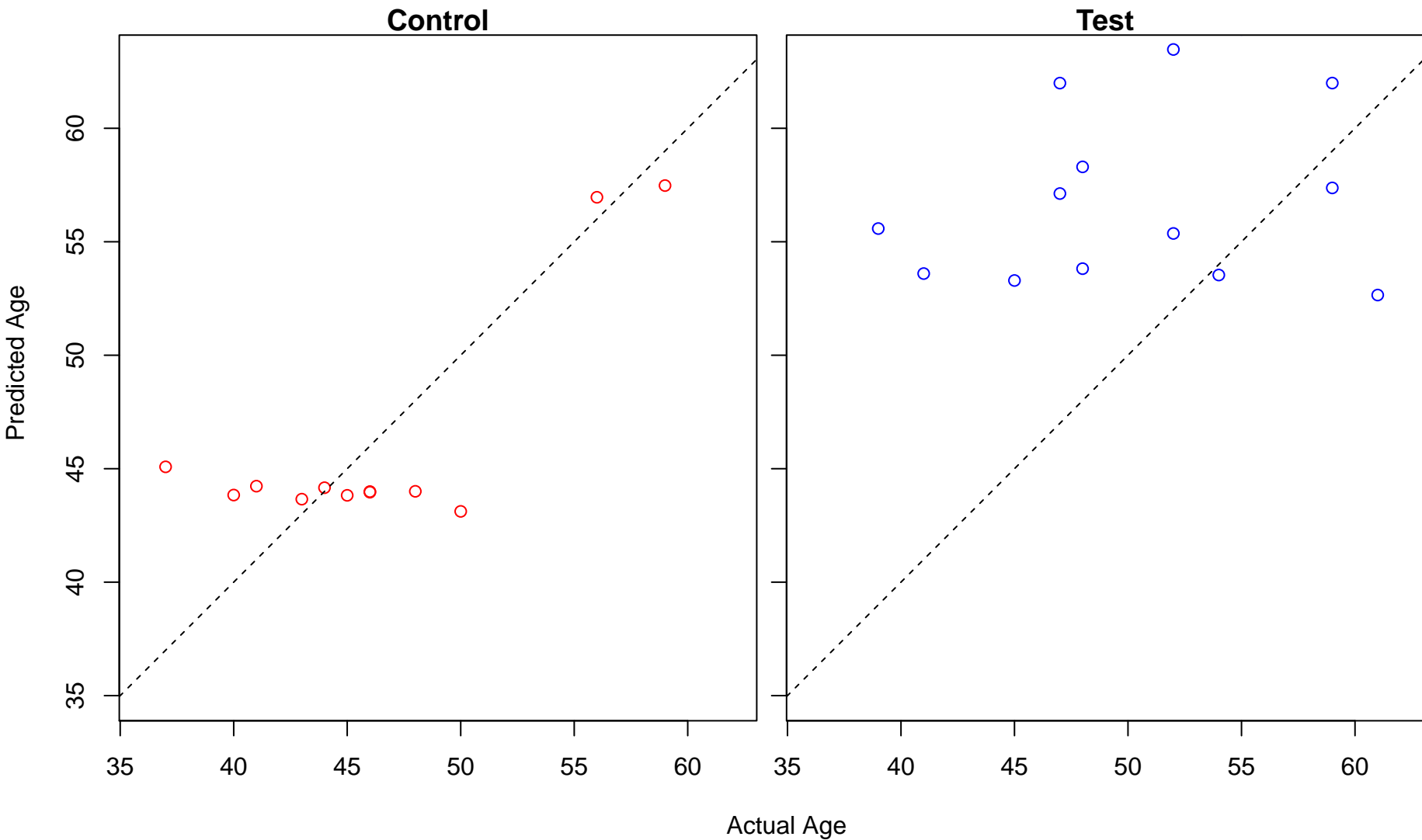
mRNA splicing, via spliceosome (Score: 2.654709)



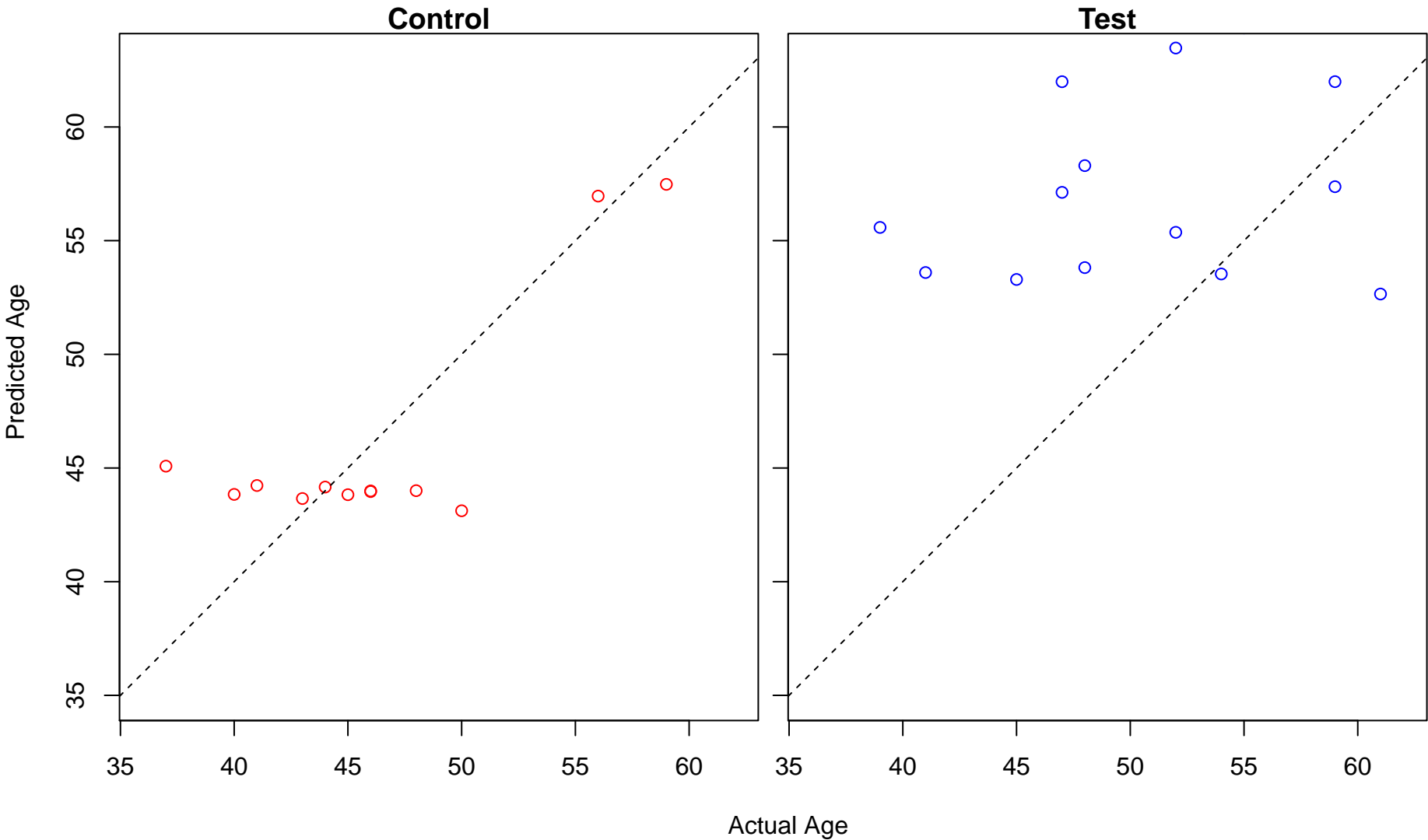
RNA splicing, via transesterification reactions (Score: 2.653873)



positive regulation of transforming growth factor beta receptor signaling pathway (Score: 2.652994)

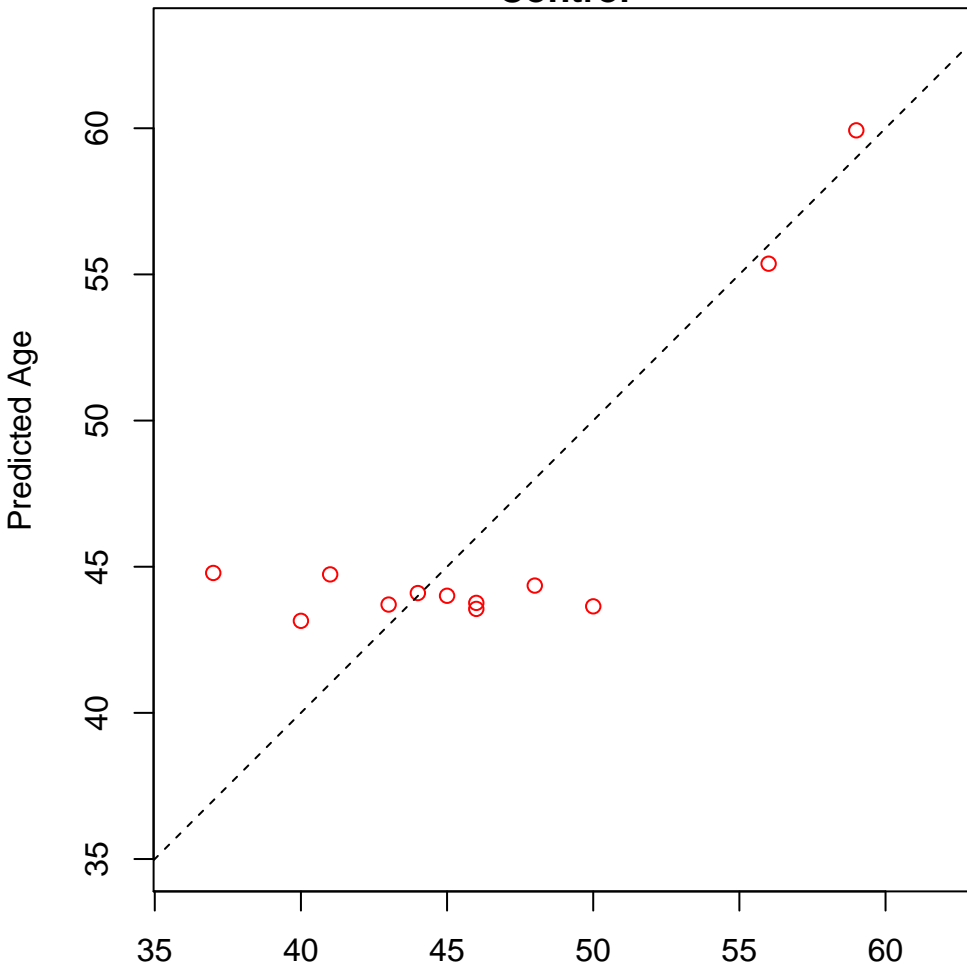


positive regulation of cellular response to transforming growth factor beta stimulus (Score: 2.65299)

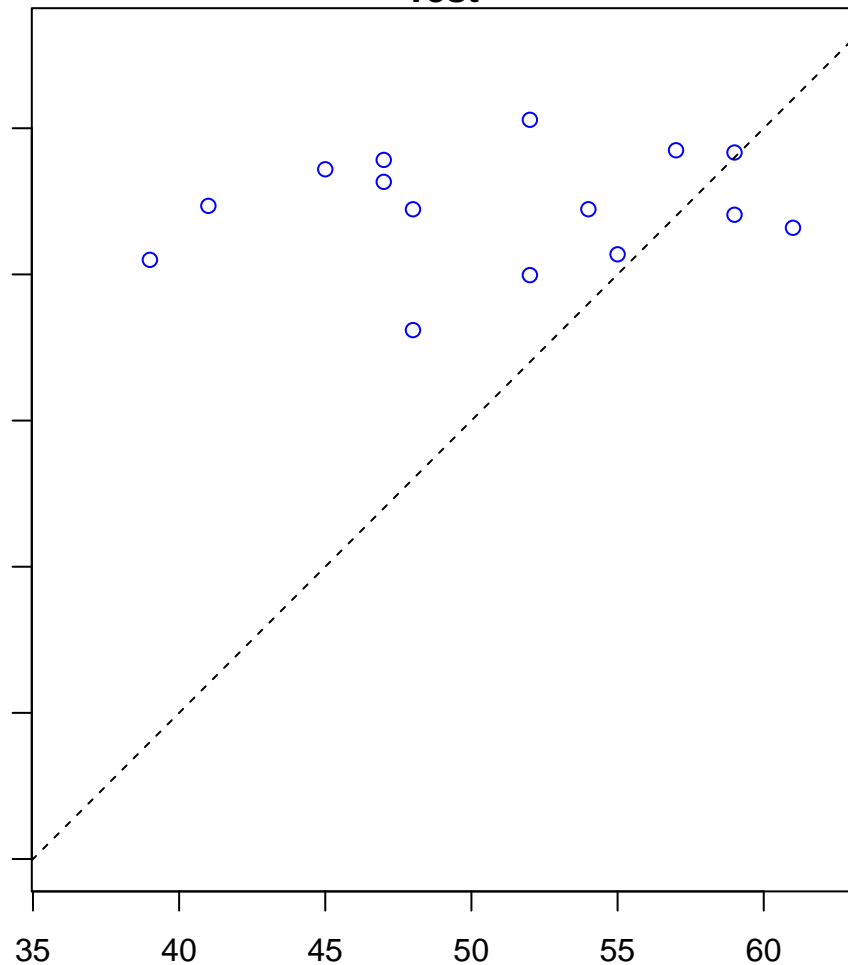


endoplasmic reticulum organization (Score: 2.652709)

Control

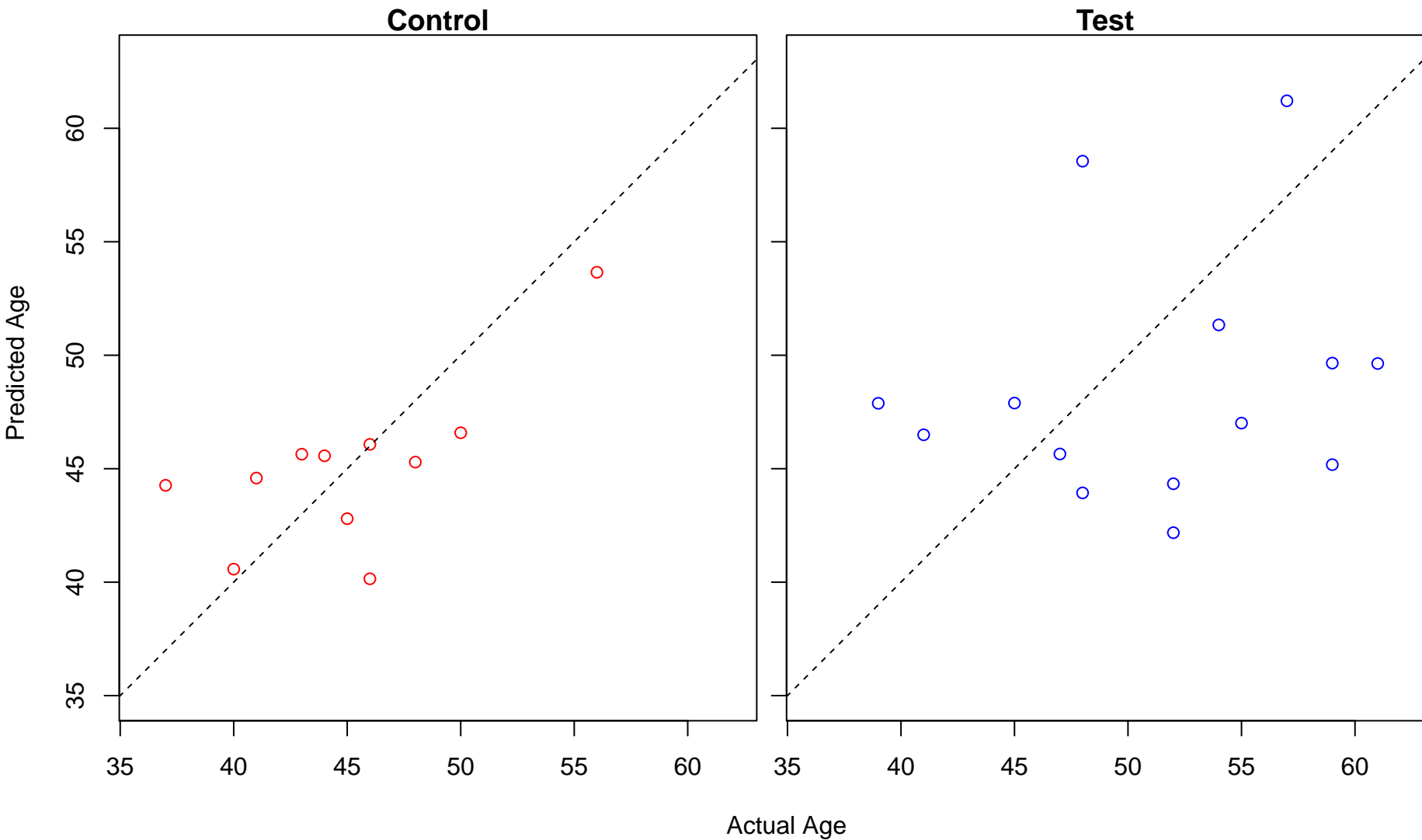


Test

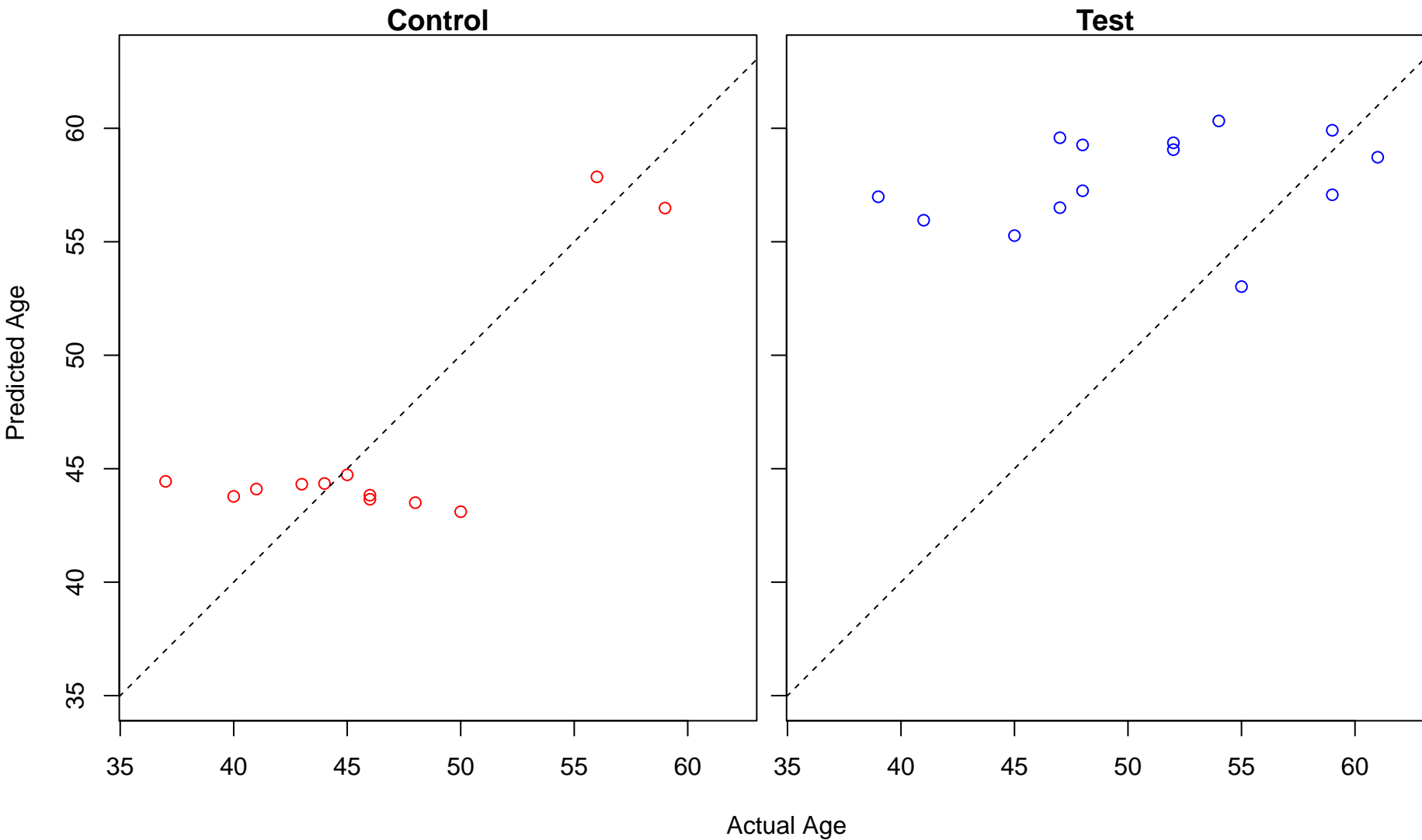


Actual Age

regulation of transmembrane transport (Score: 2.652040)

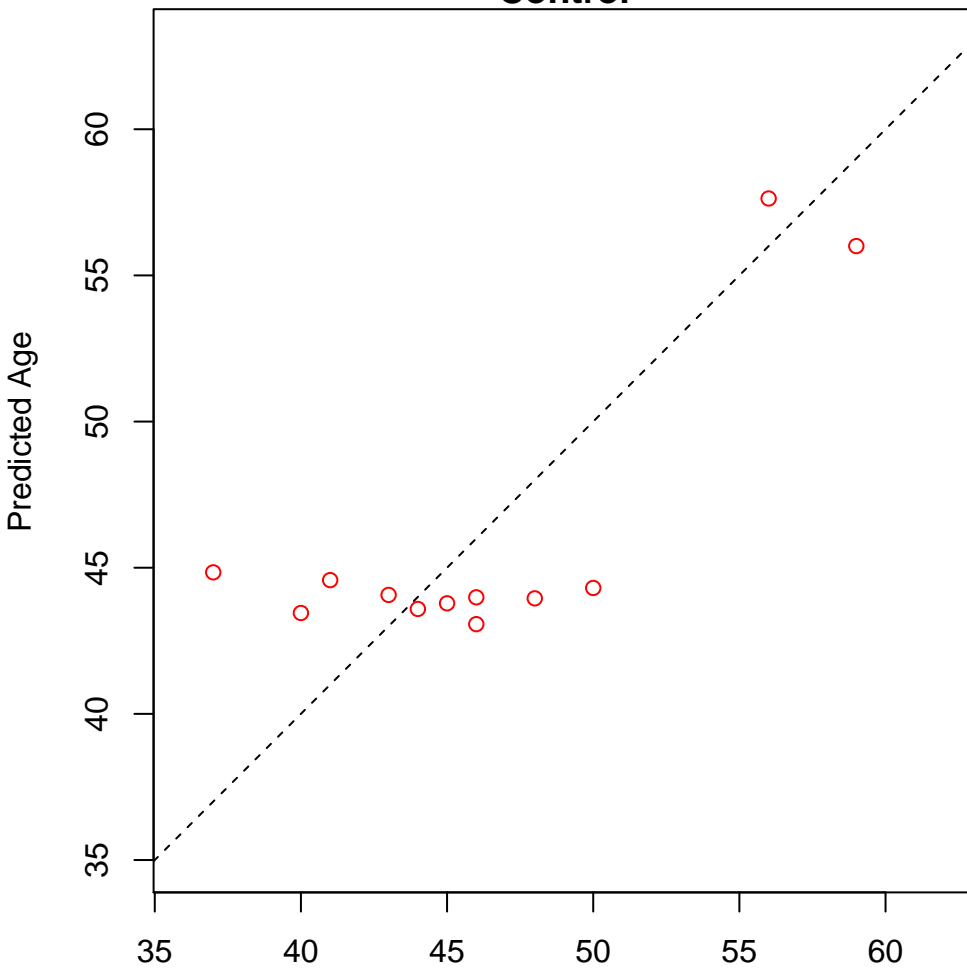


RNA capping (Score: 2.652031)

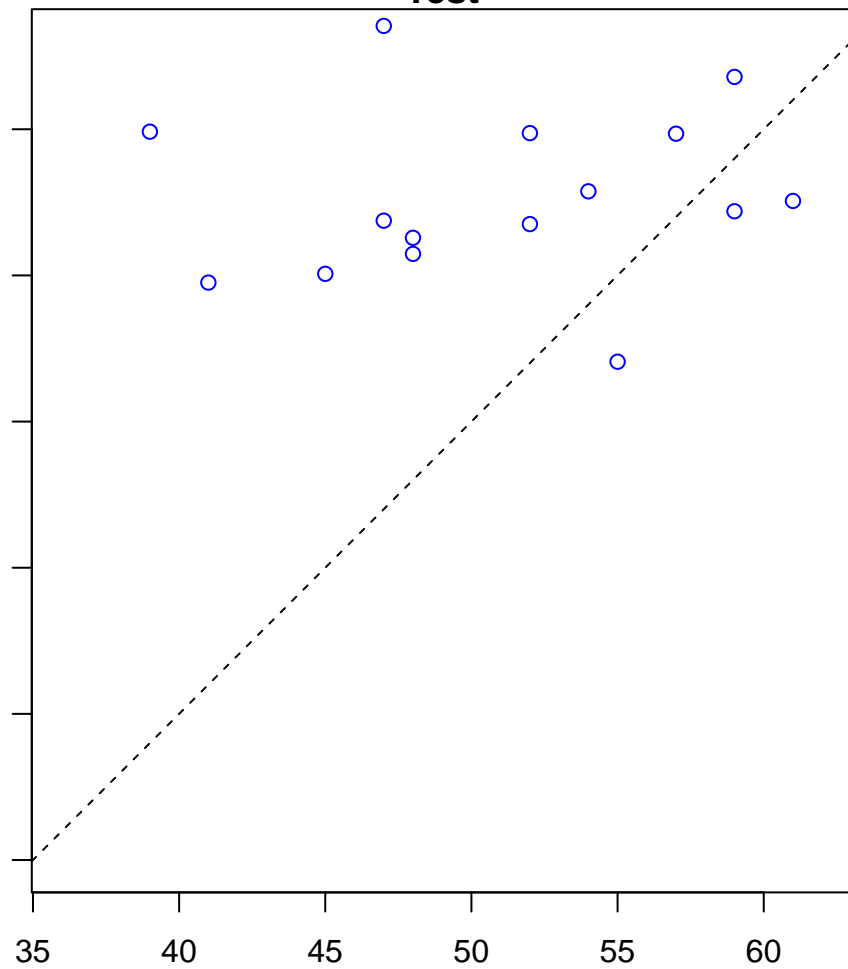


embryonic skeletal system development (Score: 2.648591)

Control

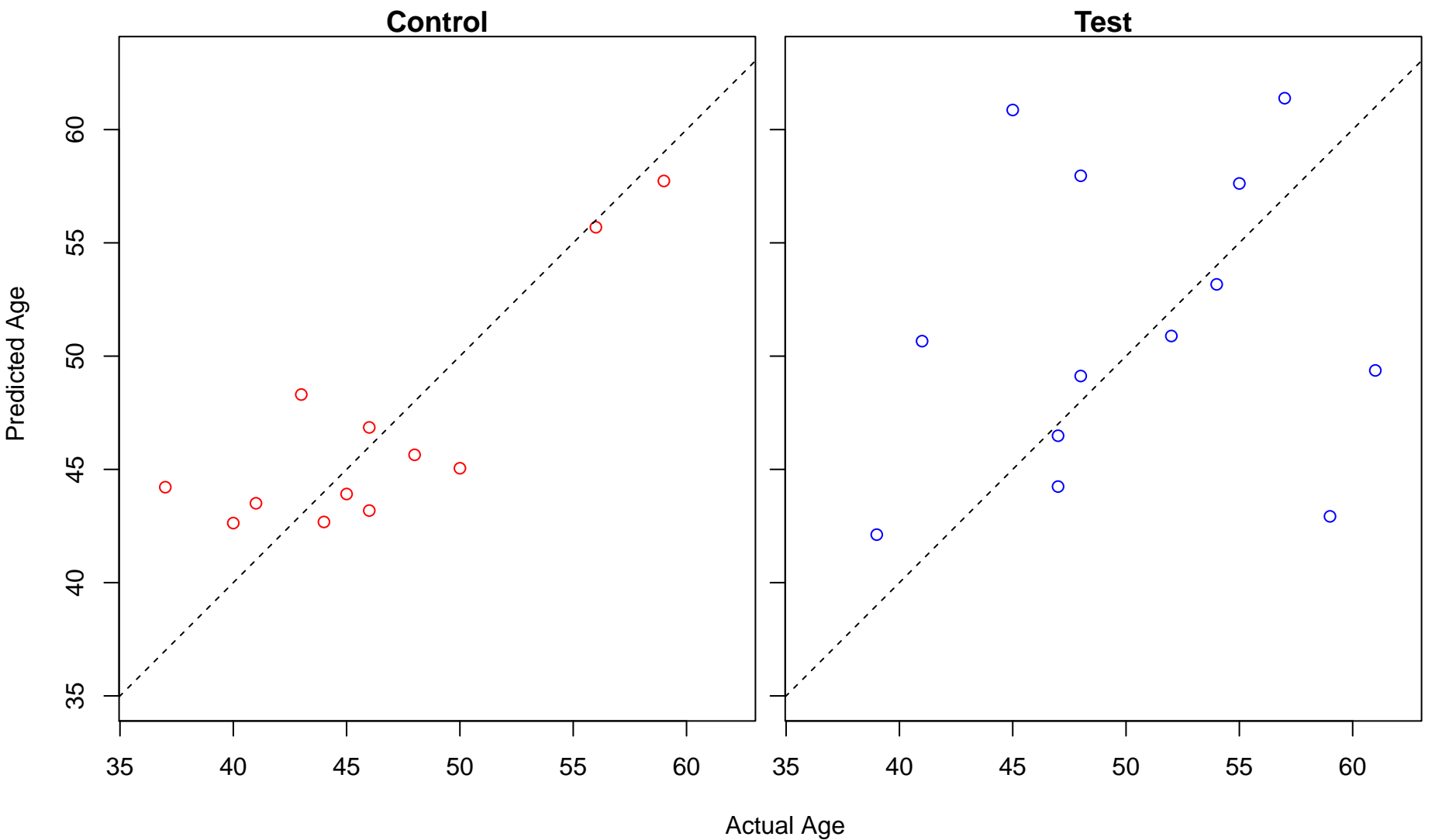


Test

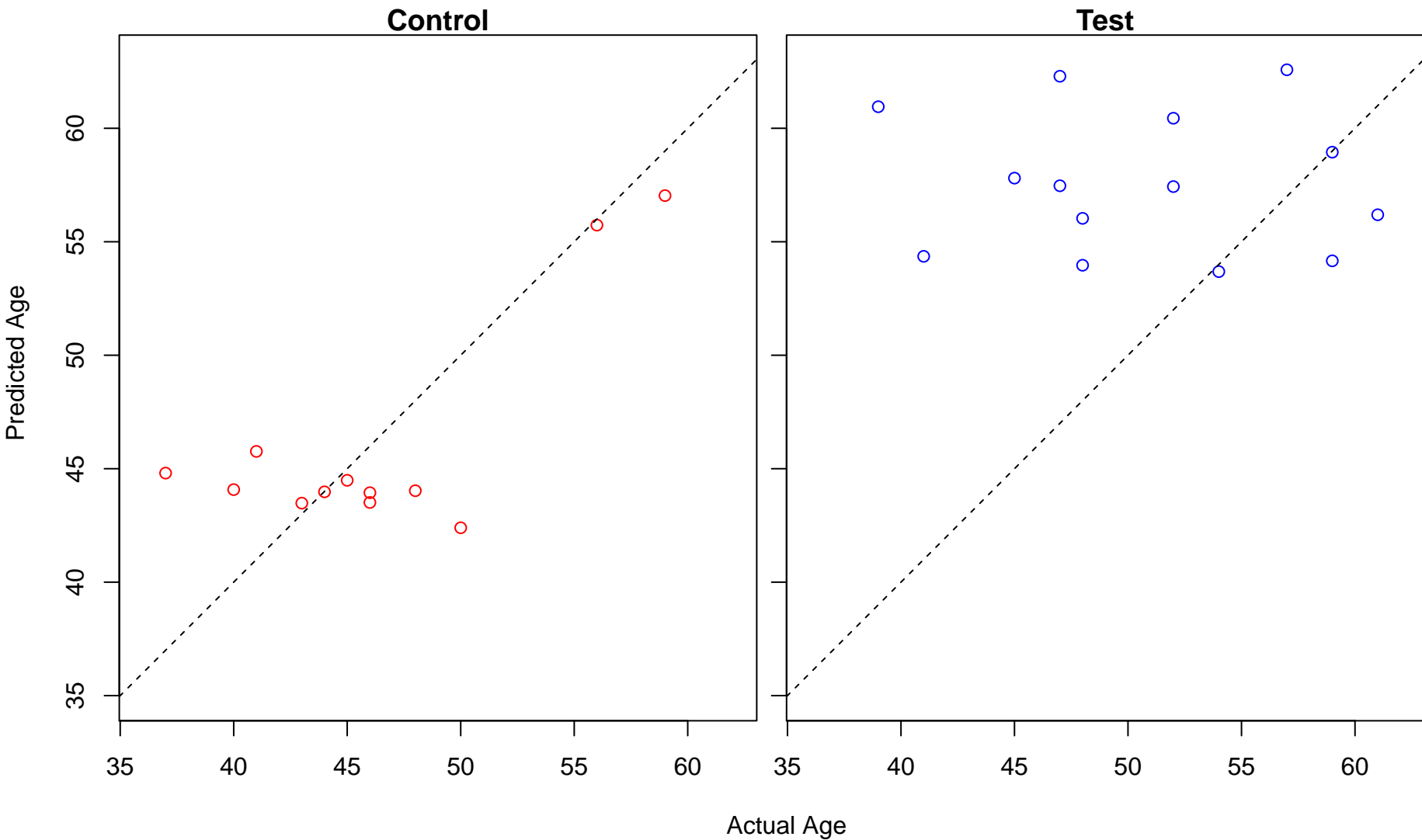


Actual Age

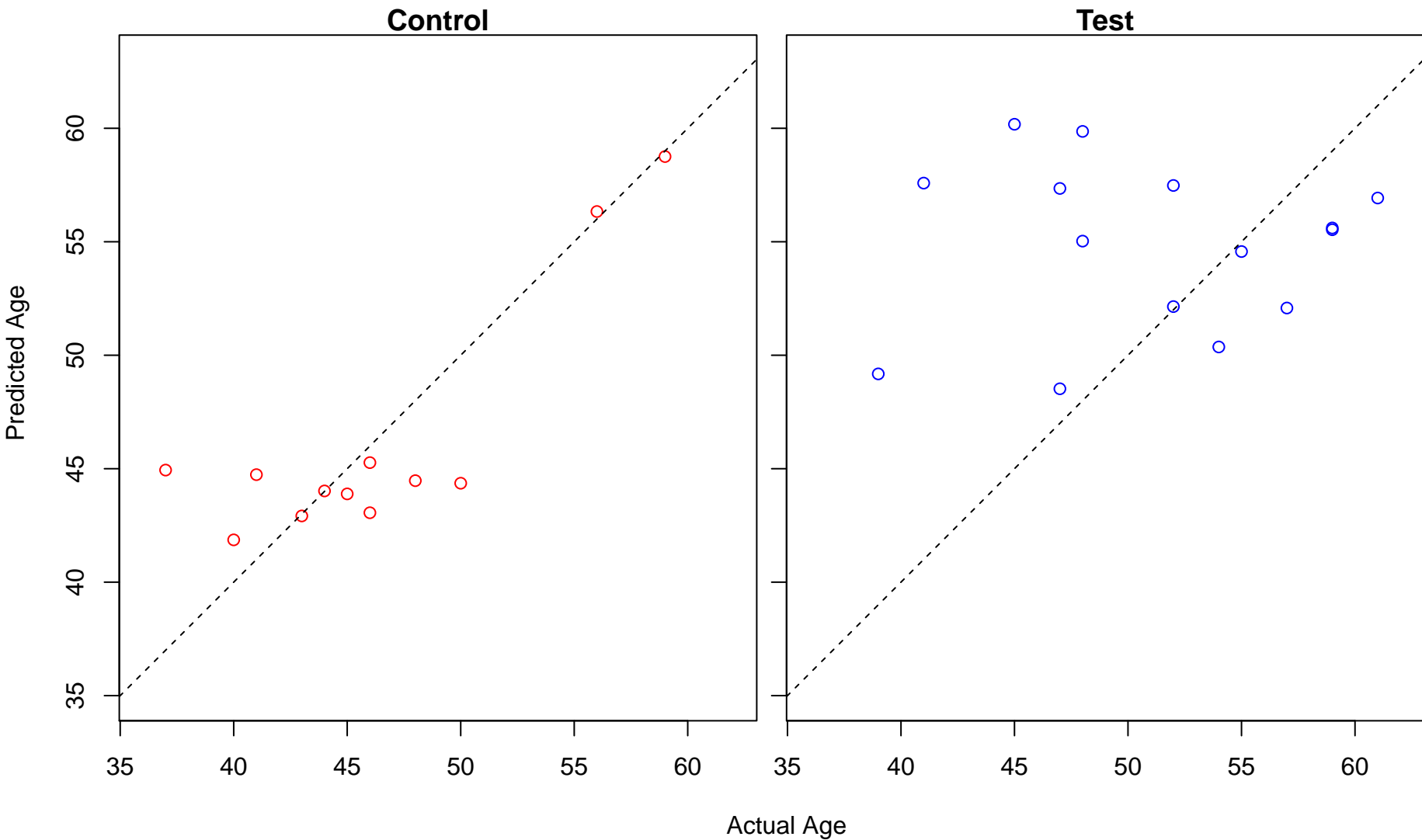
ulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimul



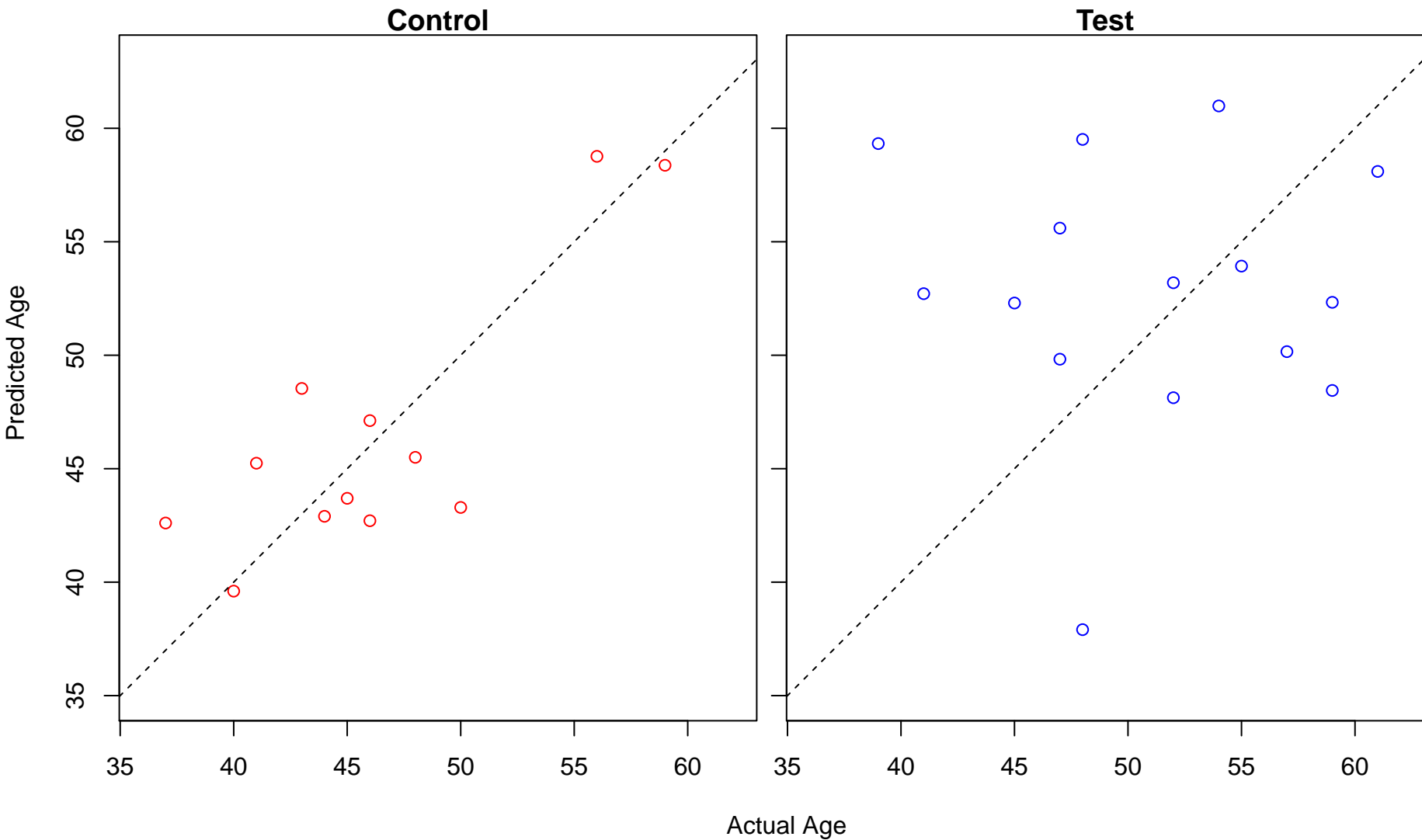
cellular biogenic amine biosynthetic process (Score: 2.644311)



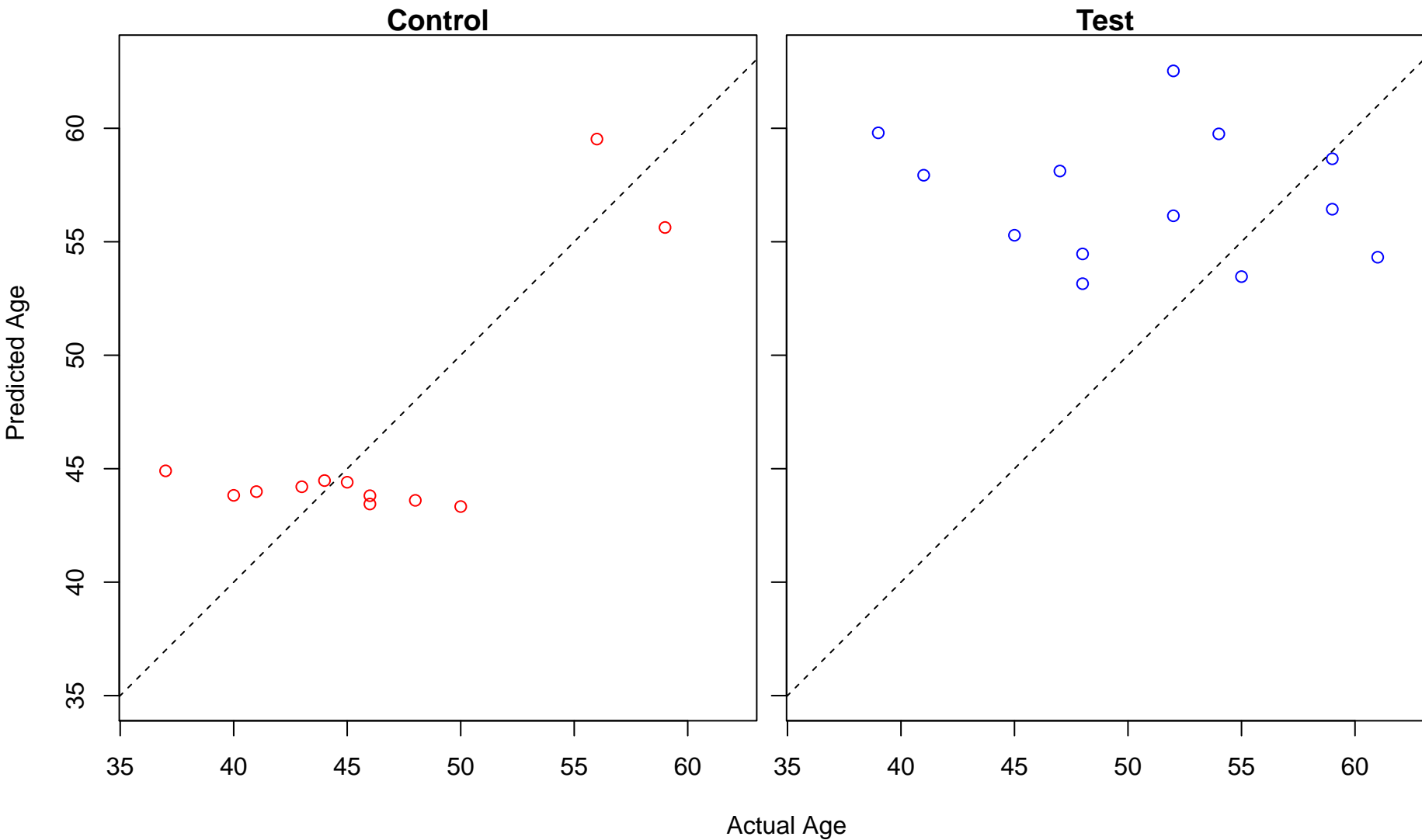
nonmotile primary cilium assembly (Score: 2.643944)



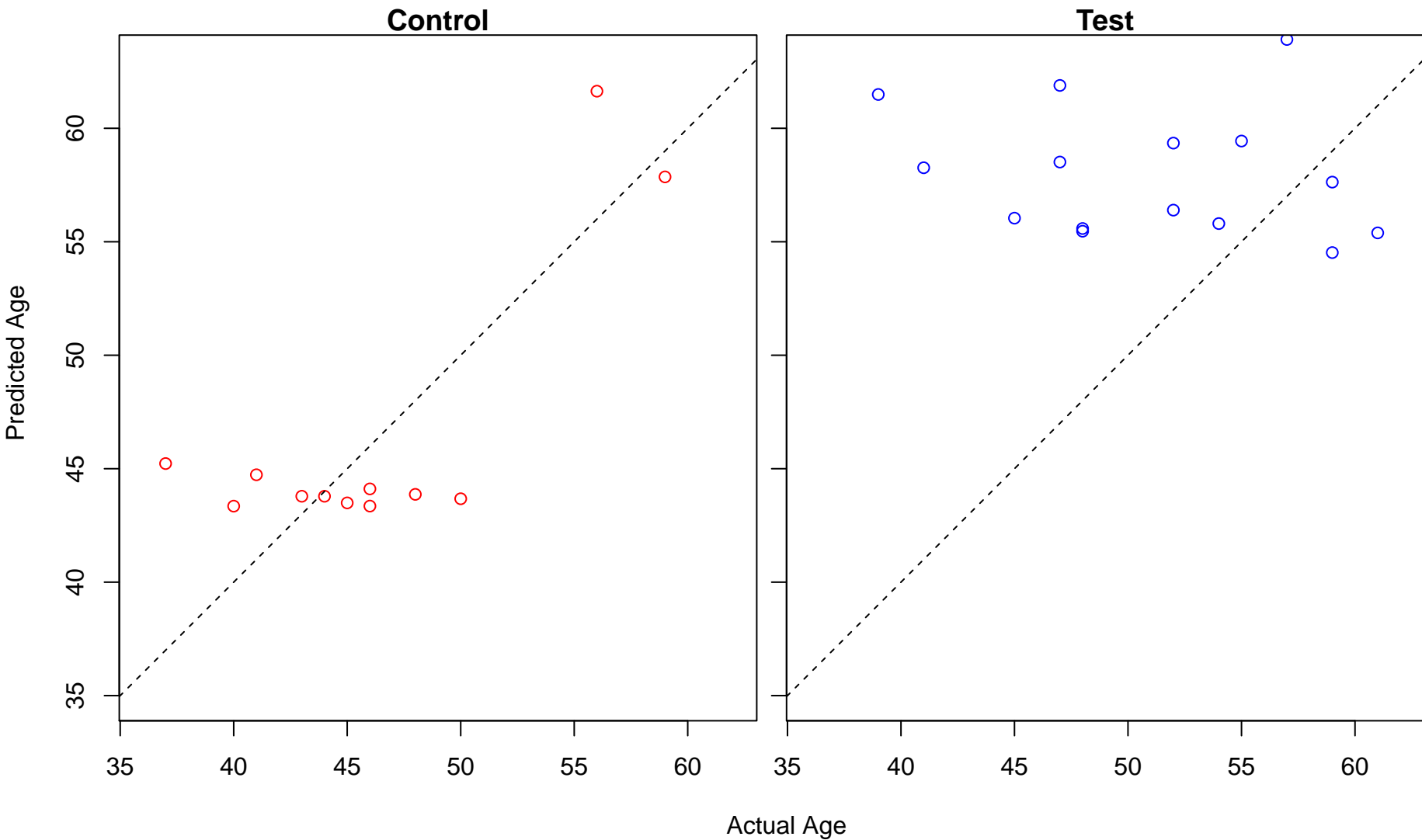
regulation of synaptic plasticity (Score: 2.643794)



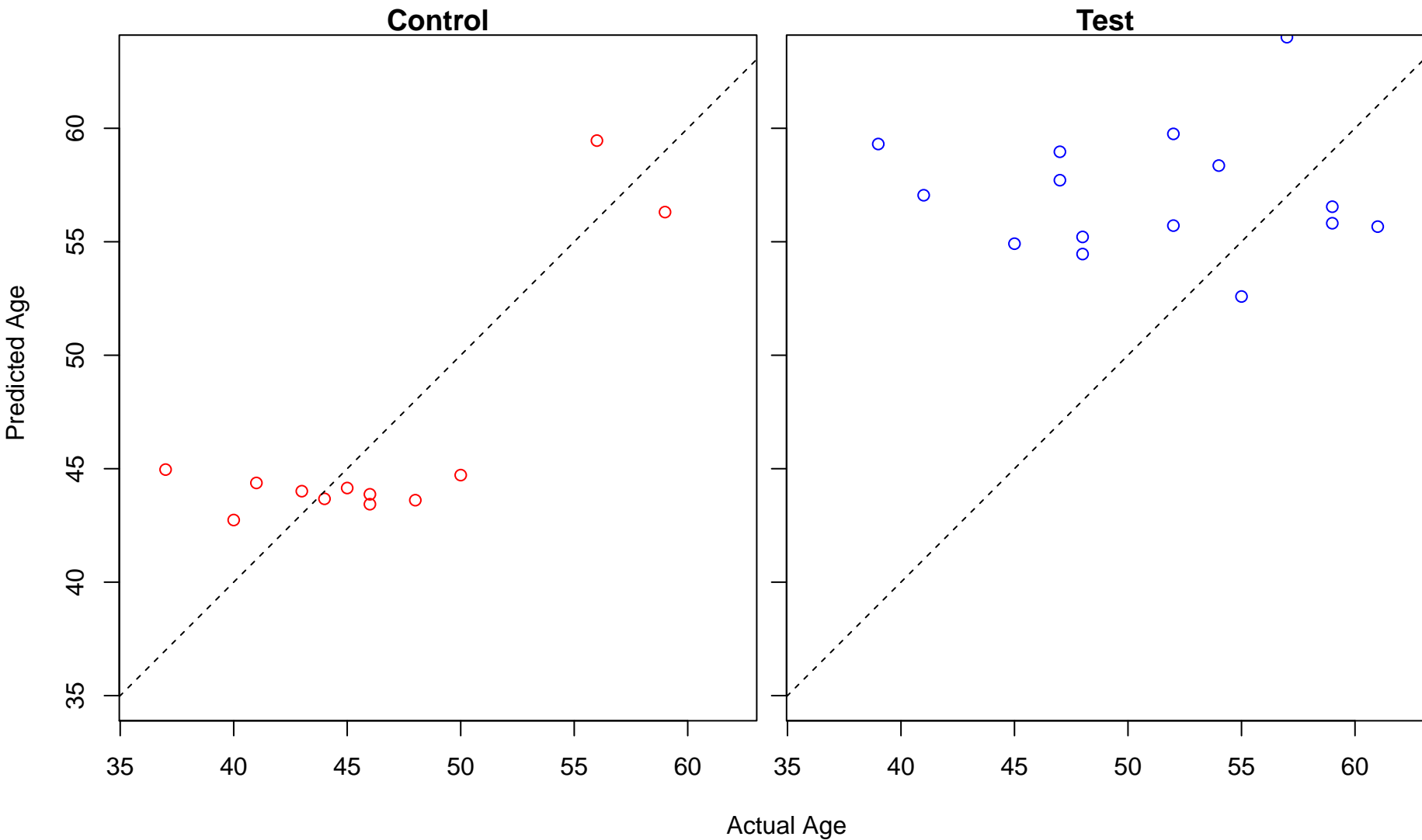
pigmentation (Score: 2.643457)



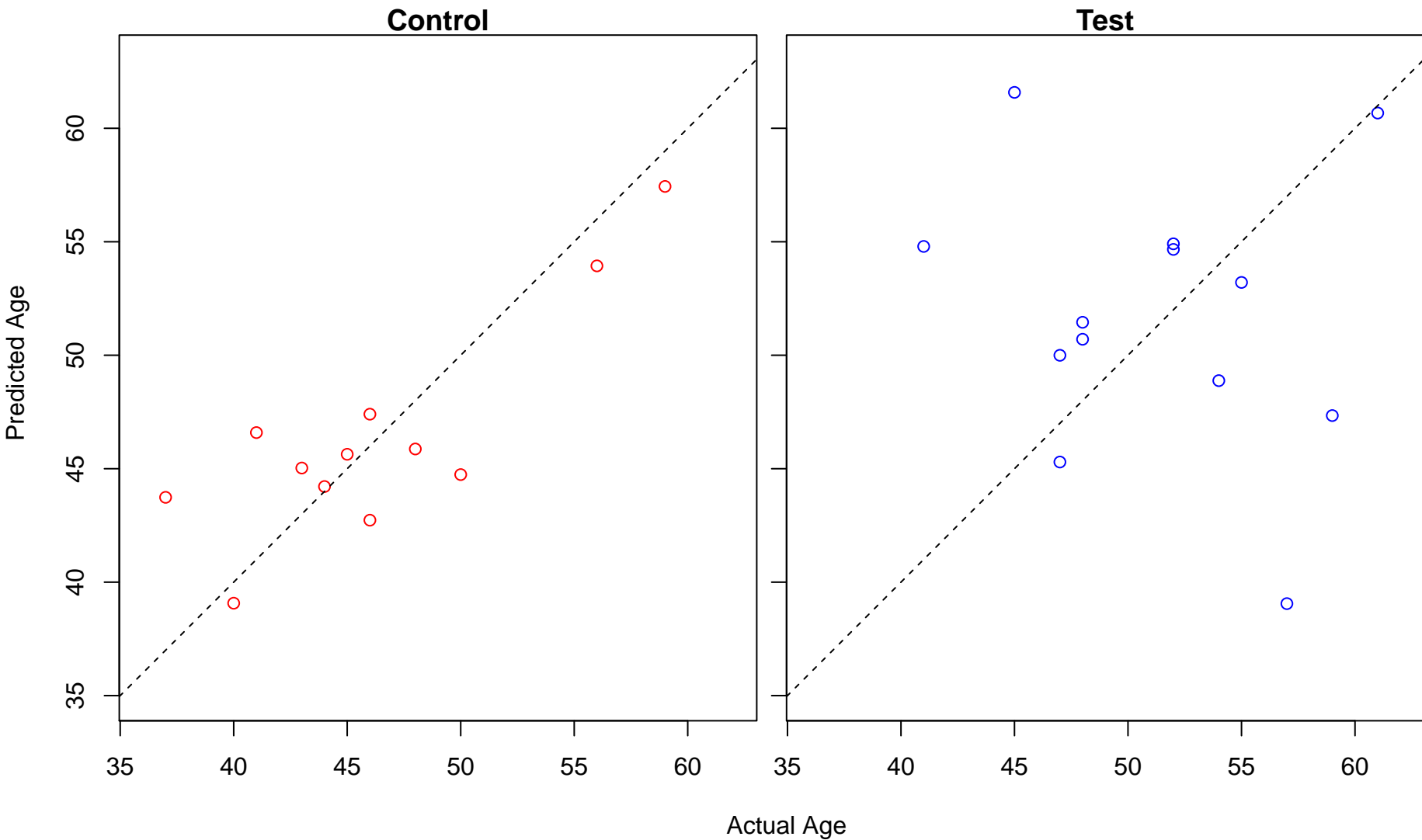
response to inorganic substance (Score: 2.638517)



membrane fusion (Score: 2.638389)

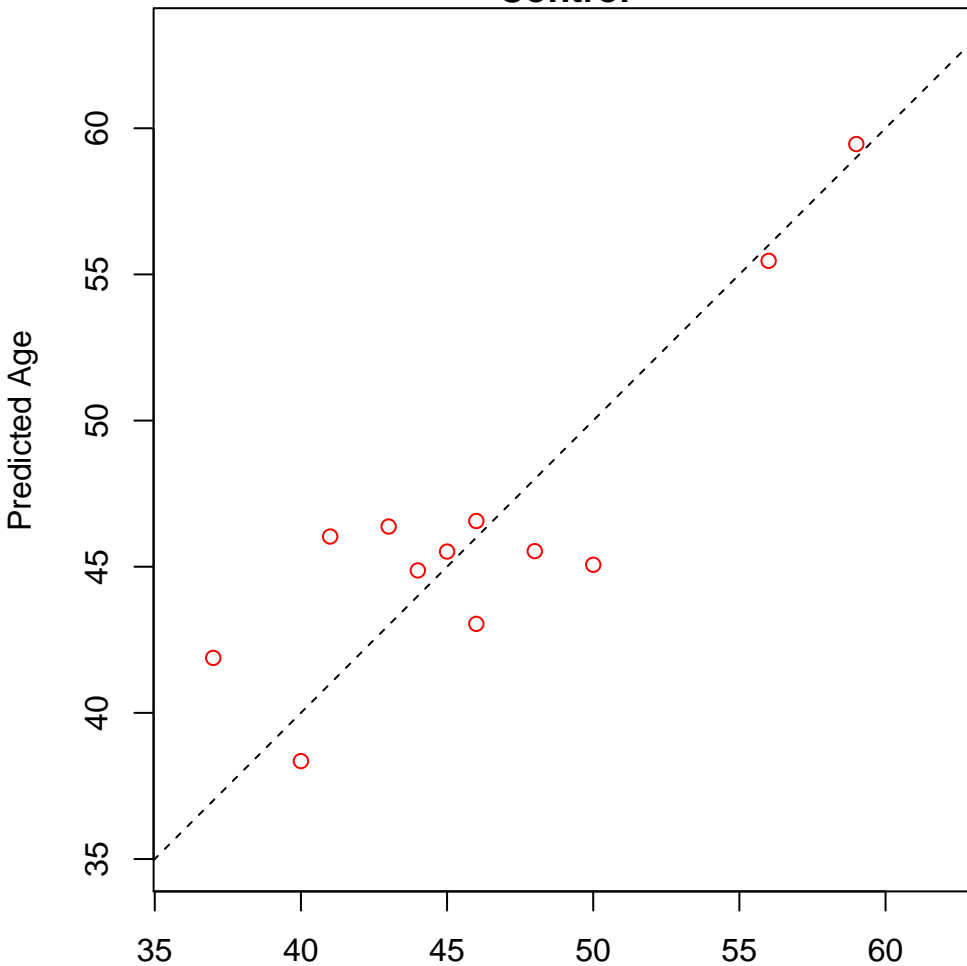


regulation of insulin secretion (Score: 2.638212)

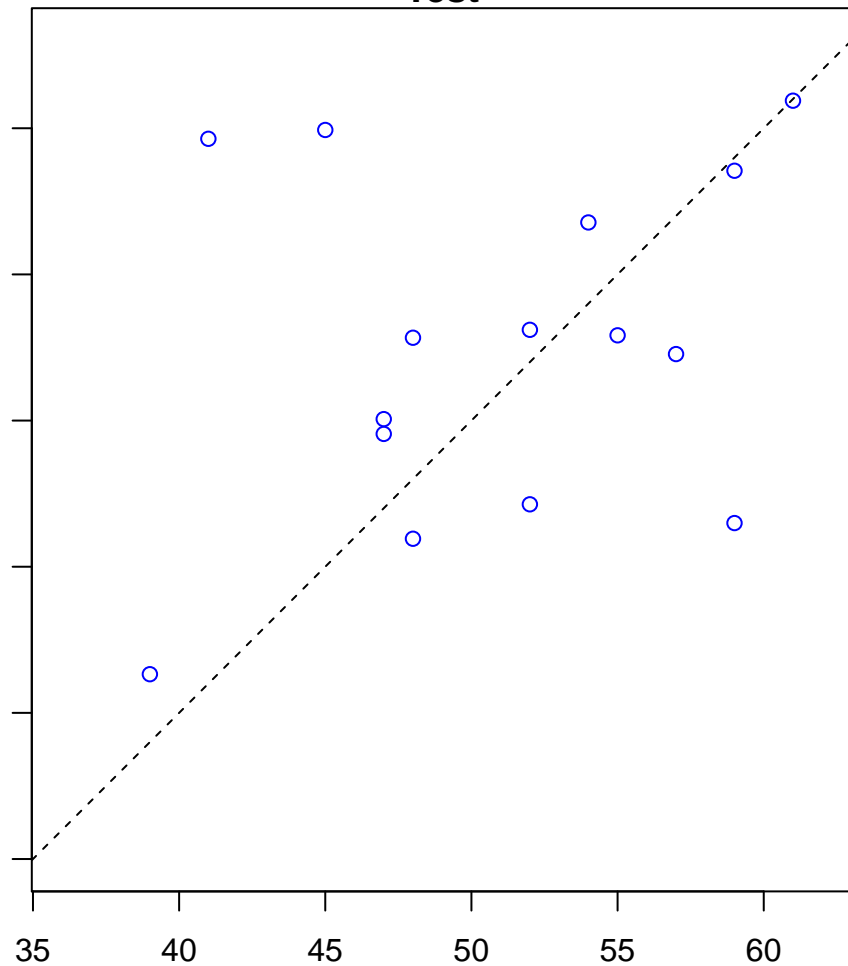


regulation of homeostatic process (Score: 2.637842)

Control



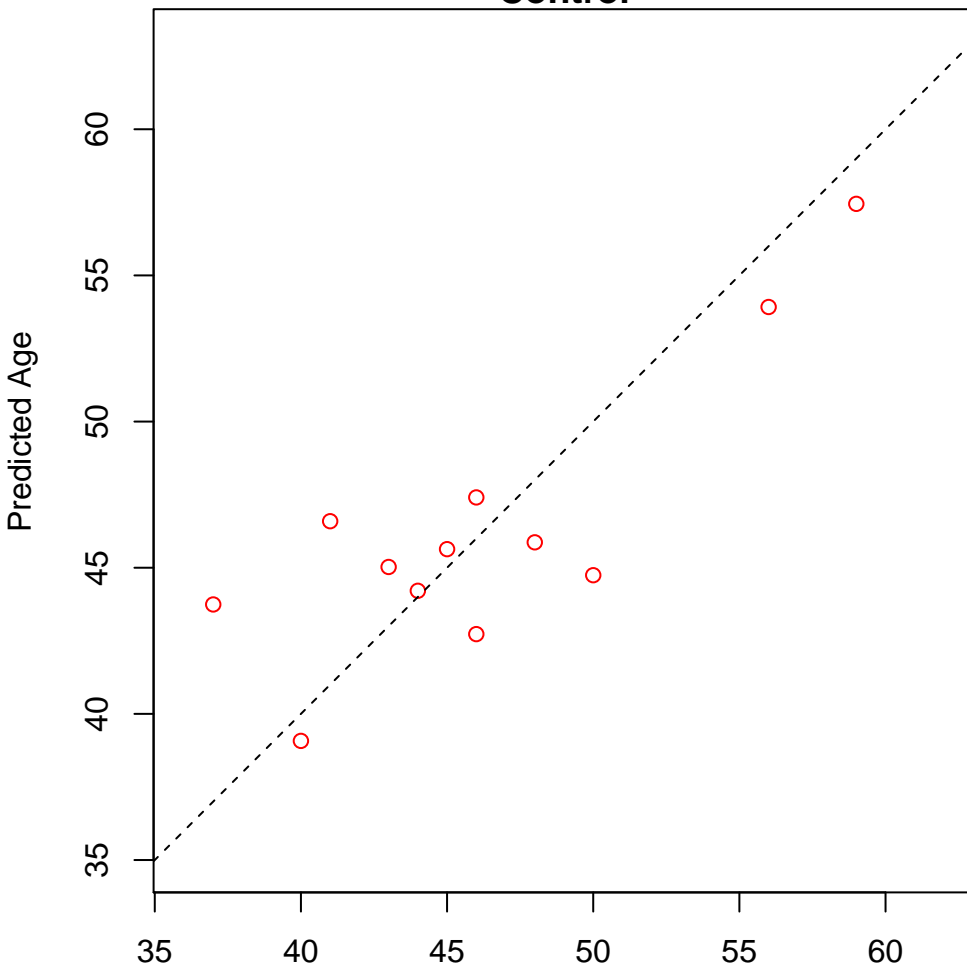
Test



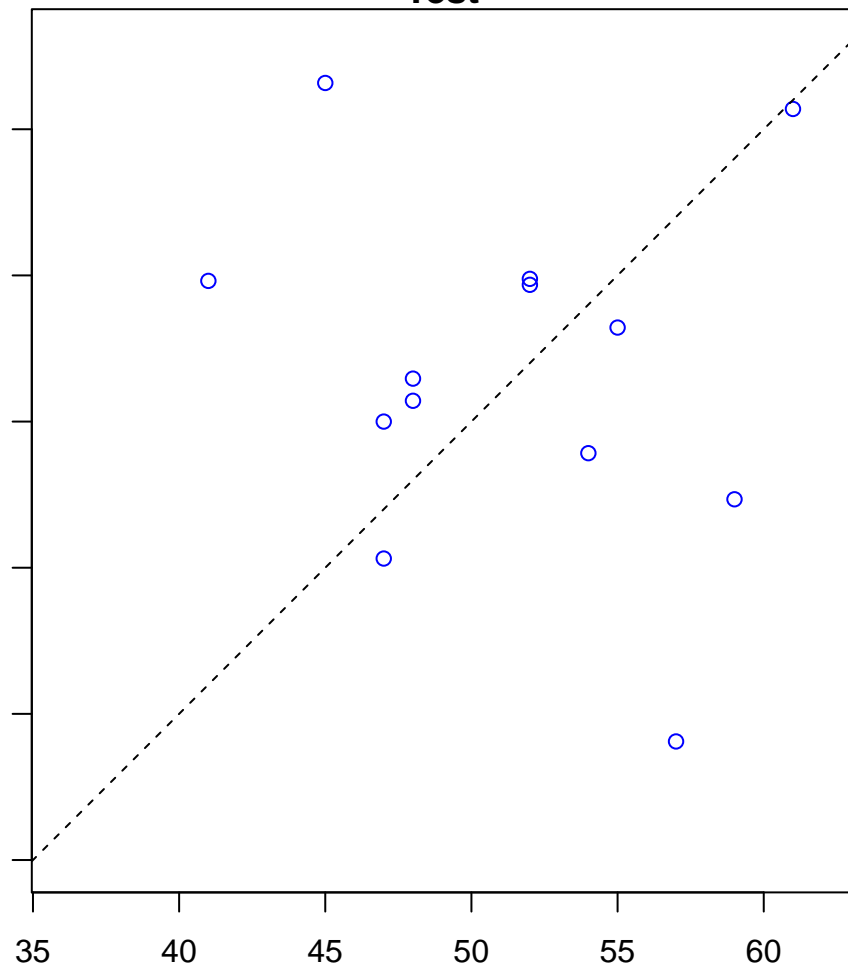
Actual Age

regulation of peptide hormone secretion (Score: 2.635987)

Control



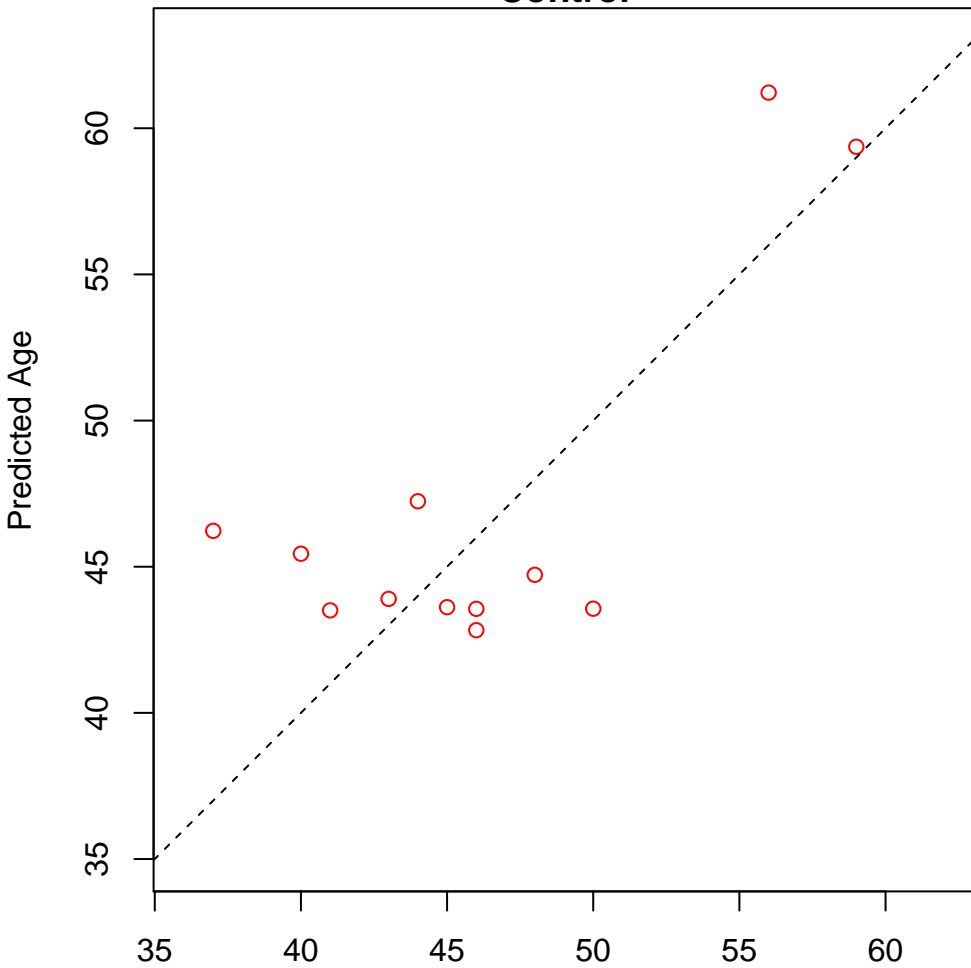
Test



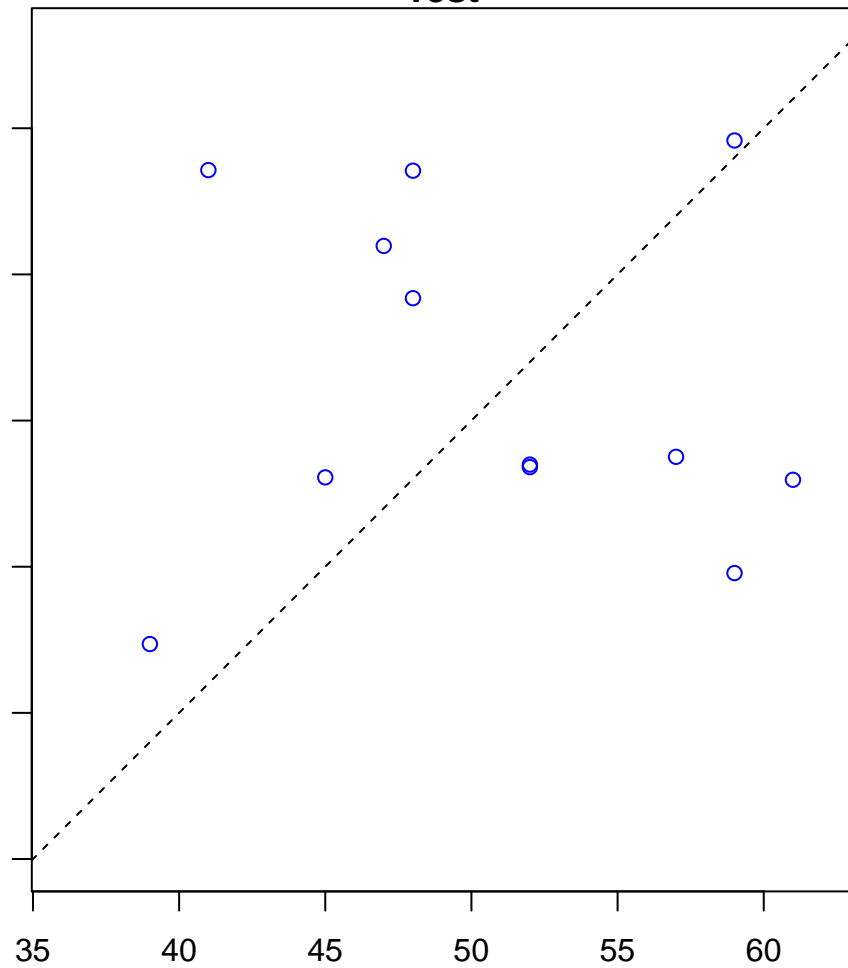
Actual Age

regulation of circadian sleep/wake cycle (Score: 2.635163)

Control

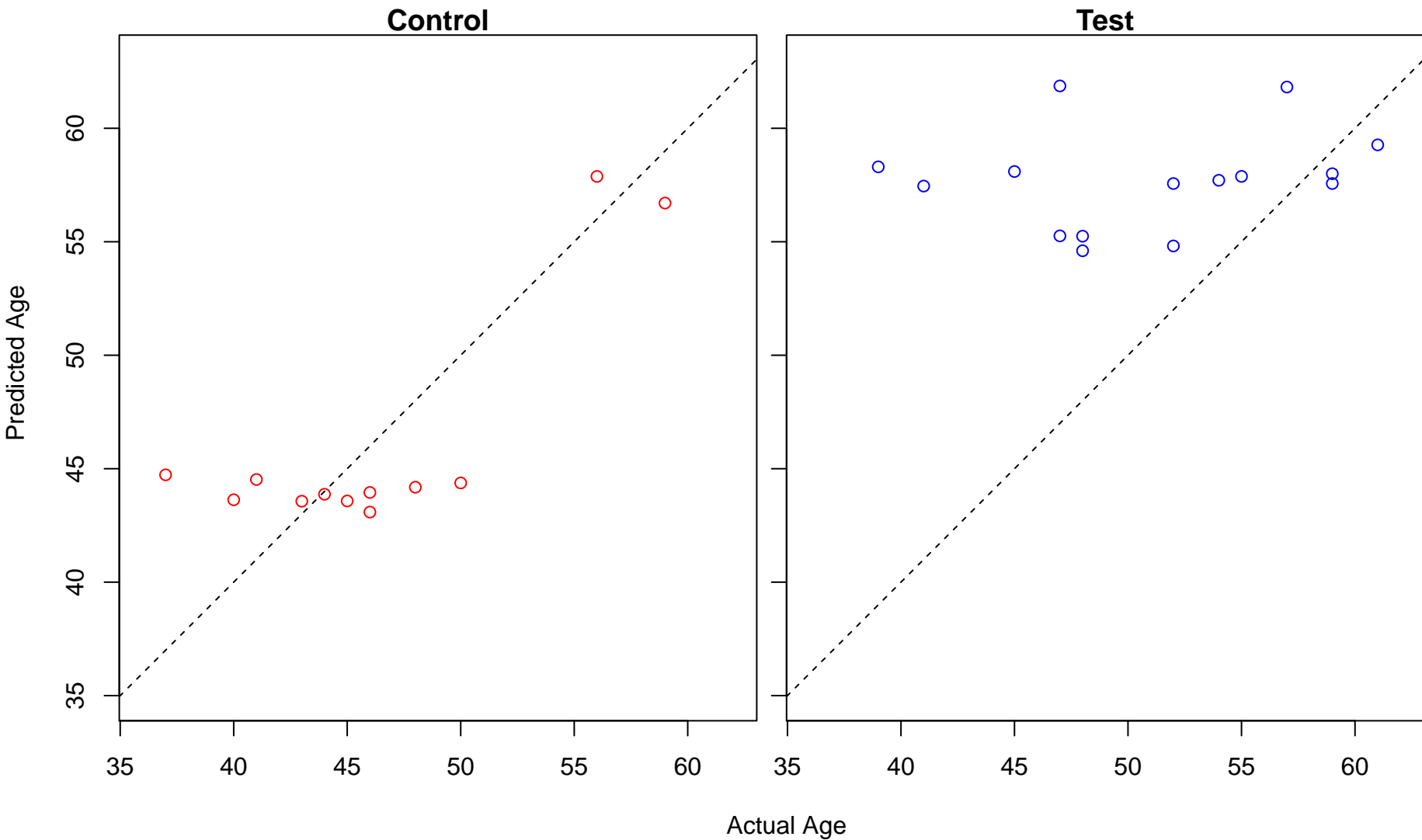


Test

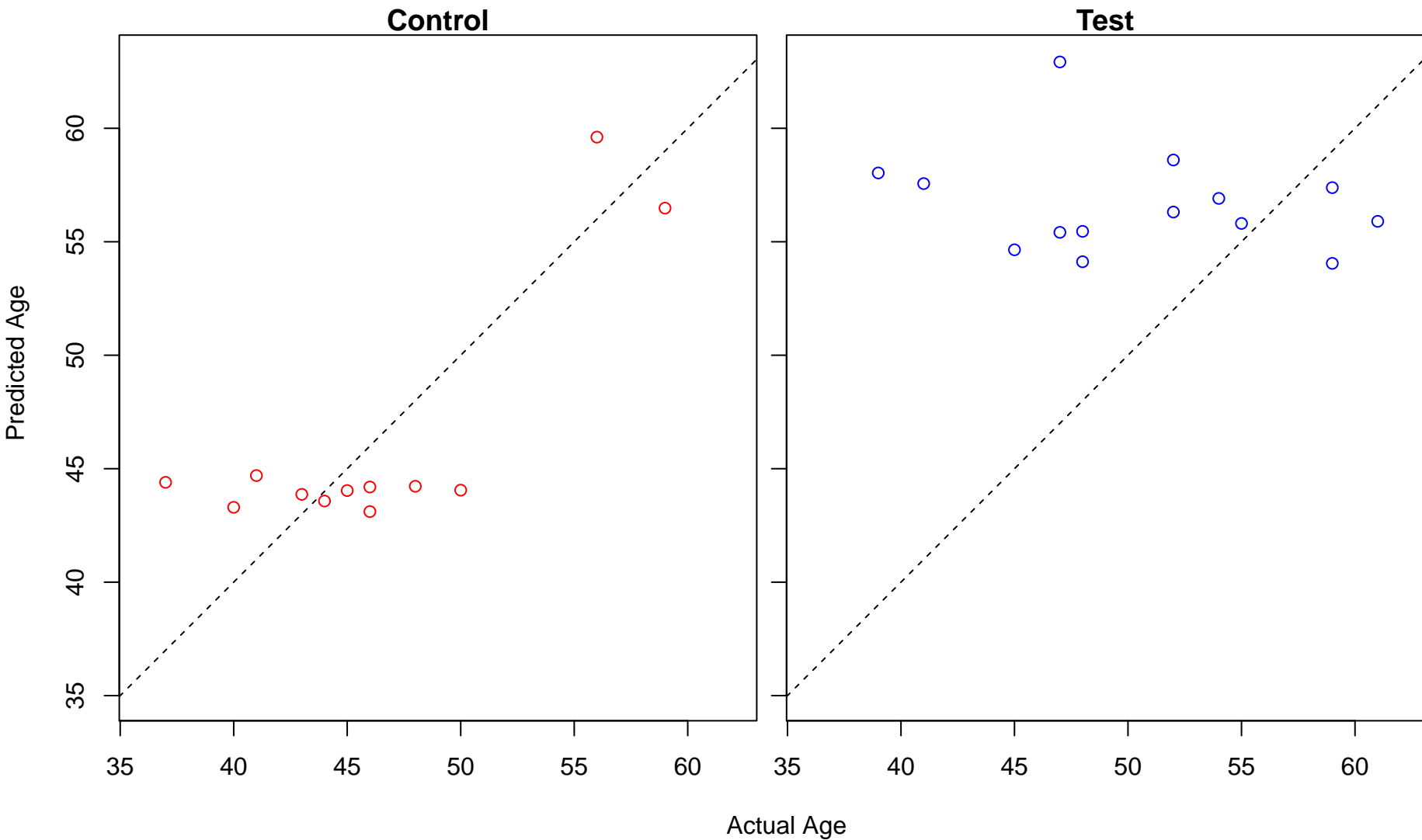


Actual Age

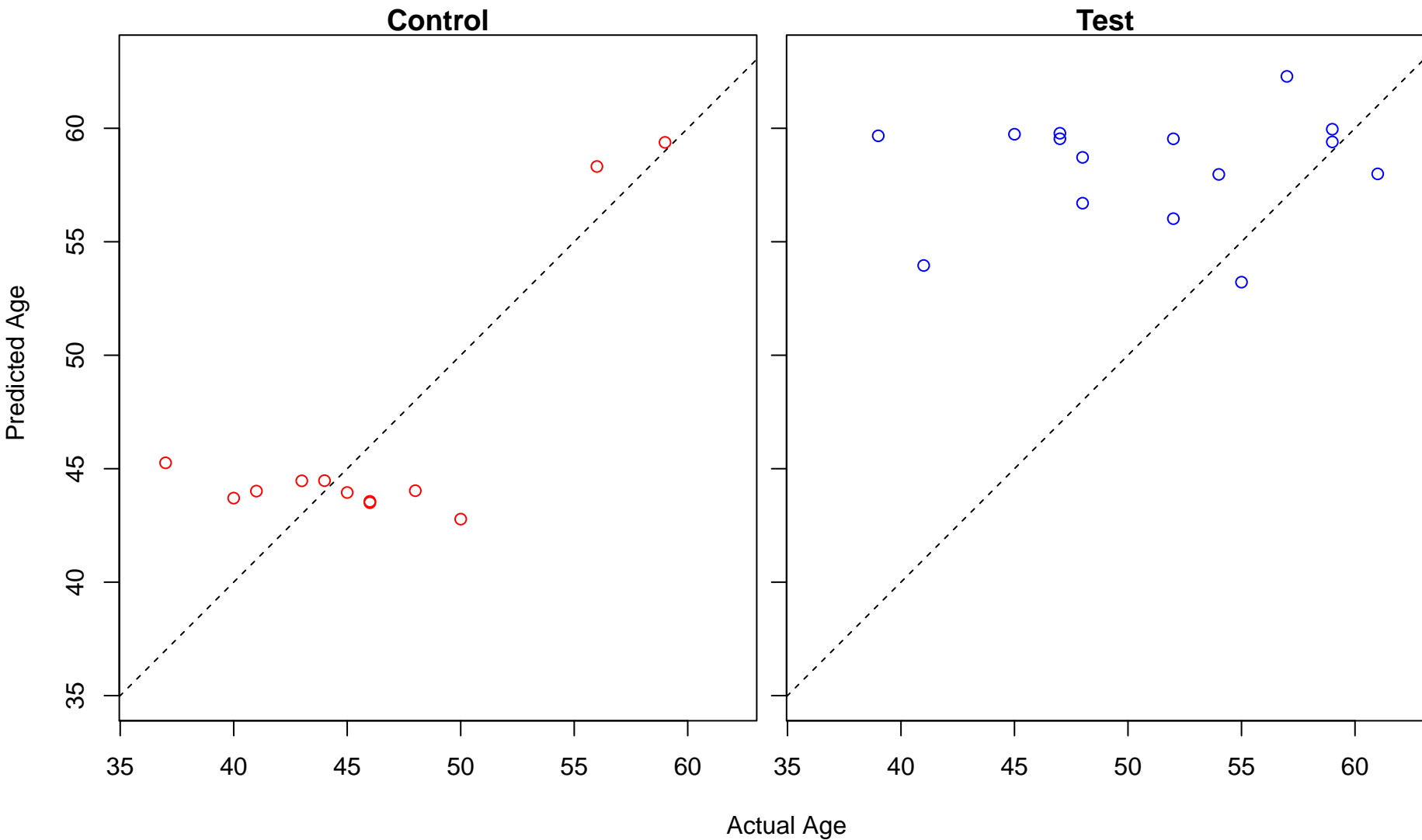
positive regulation of mRNA metabolic process (Score: 2.633826)



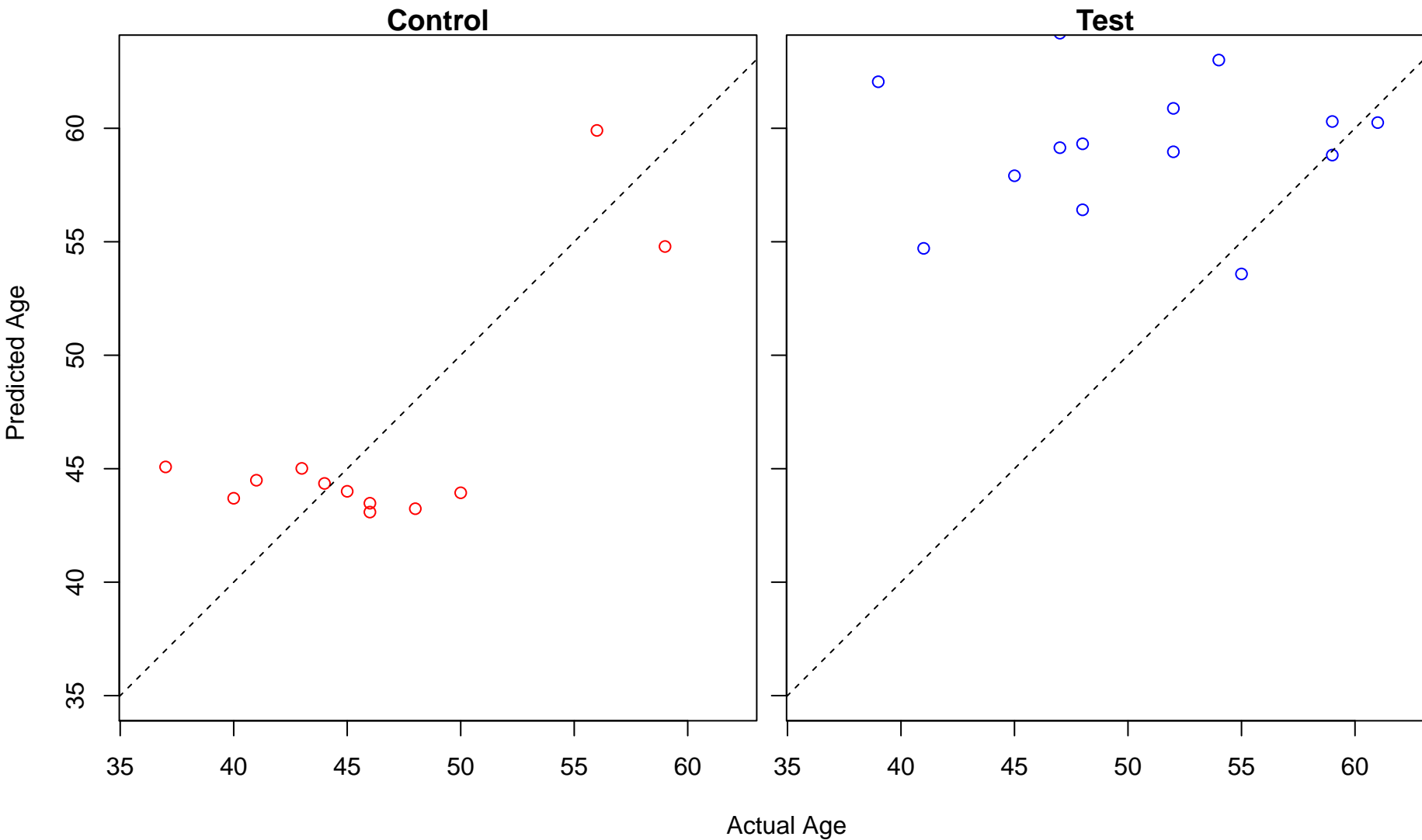
negative regulation of protein catabolic process (Score: 2.633551)



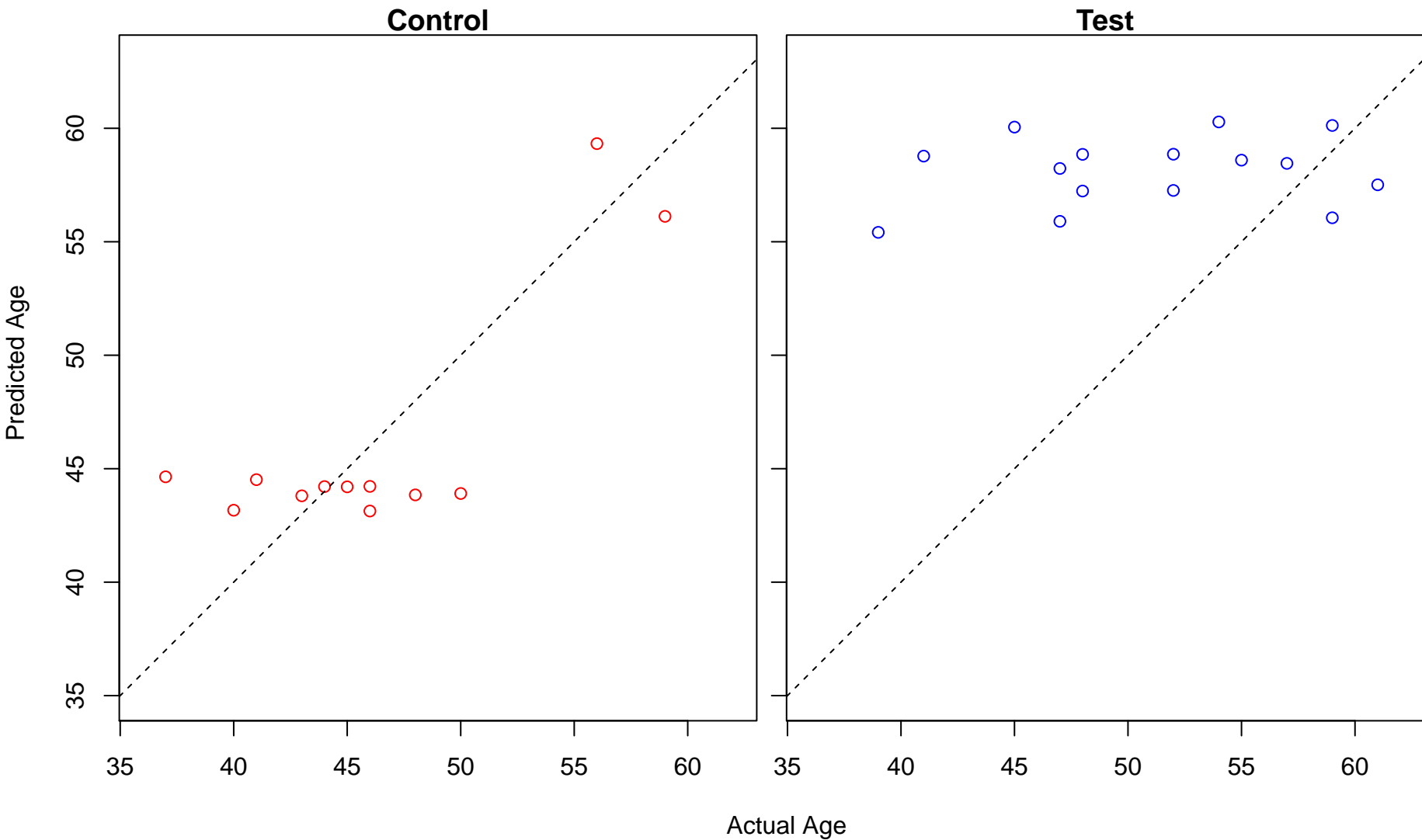
histone H3-K4 trimethylation (Score: 2.632553)



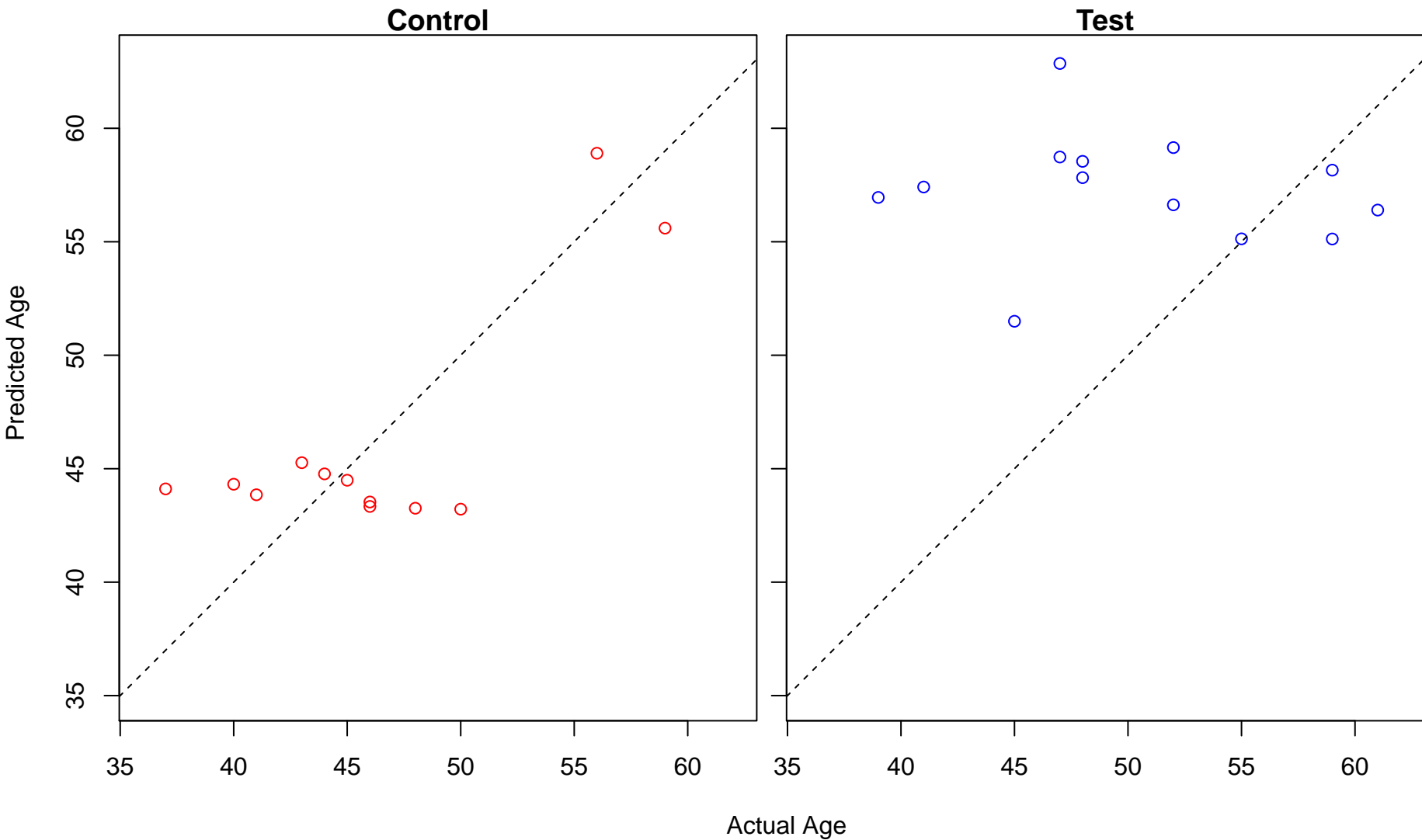
positive regulation of phospholipid metabolic process (Score: 2.632229)



regulation of translational initiation in response to stress (Score: 2.630714)

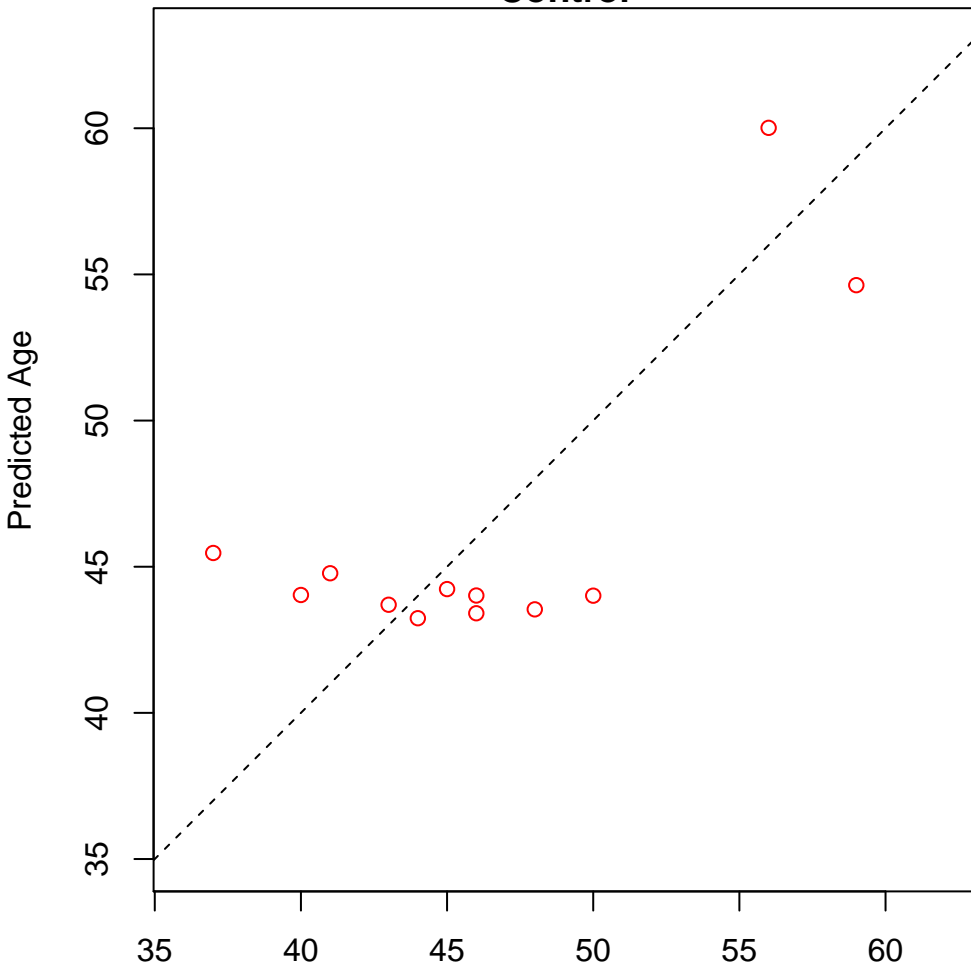


synaptic vesicle exocytosis (Score: 2.630227)

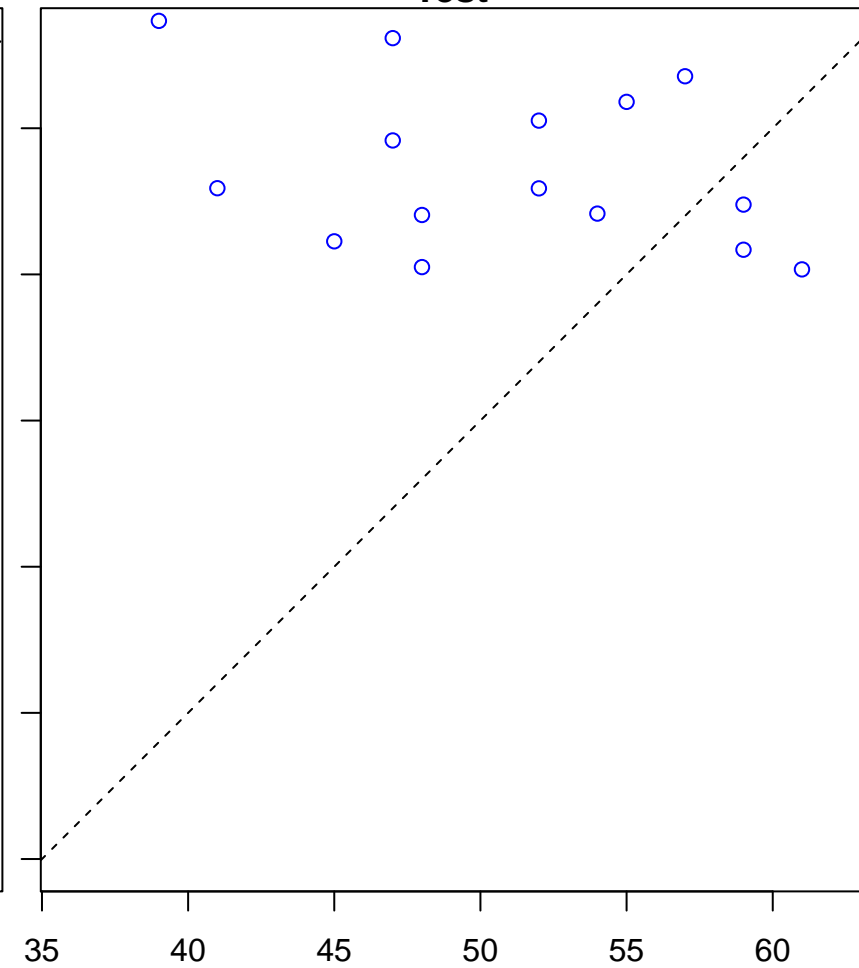


regulation of defense response to virus (Score: 2.626448)

Control

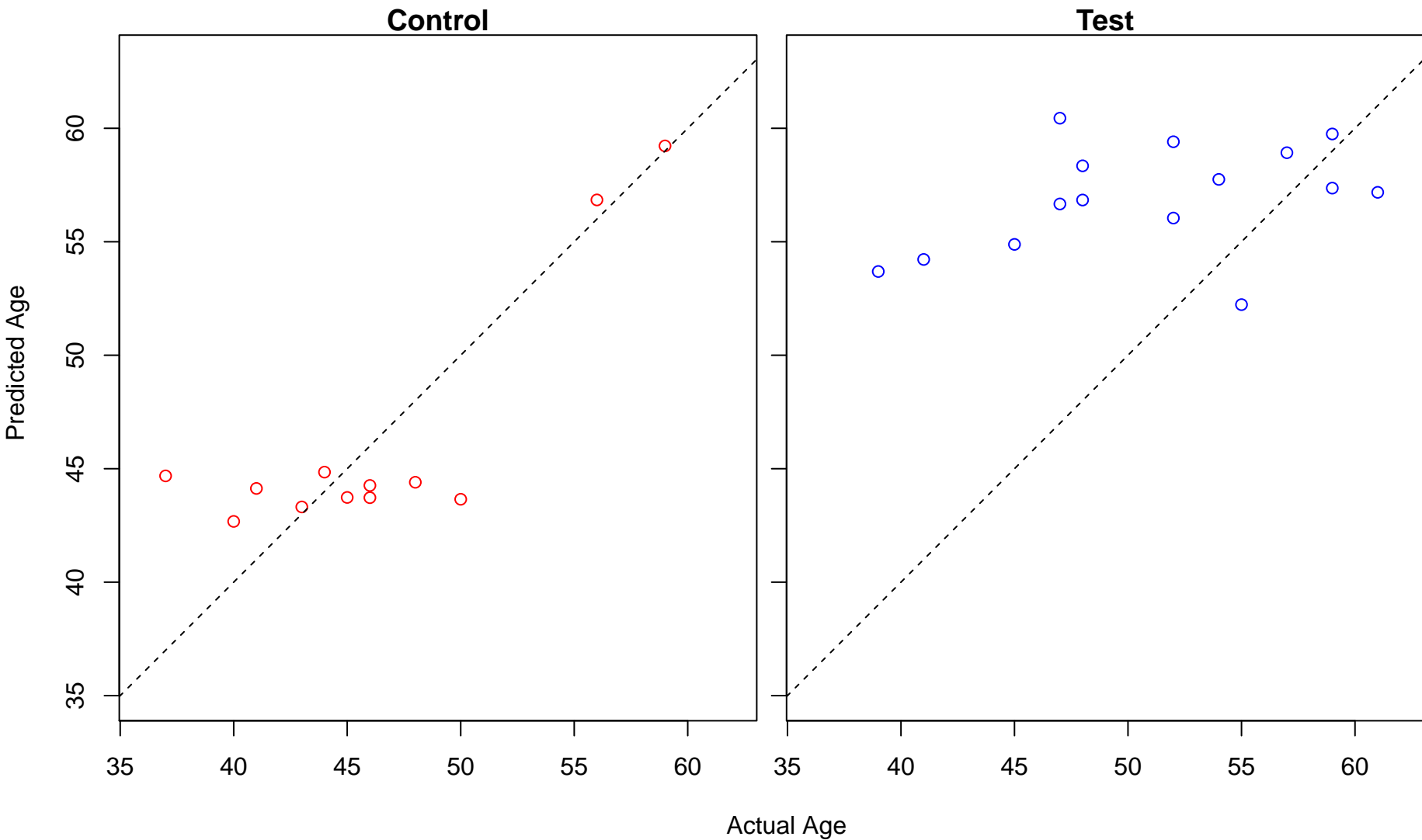


Test

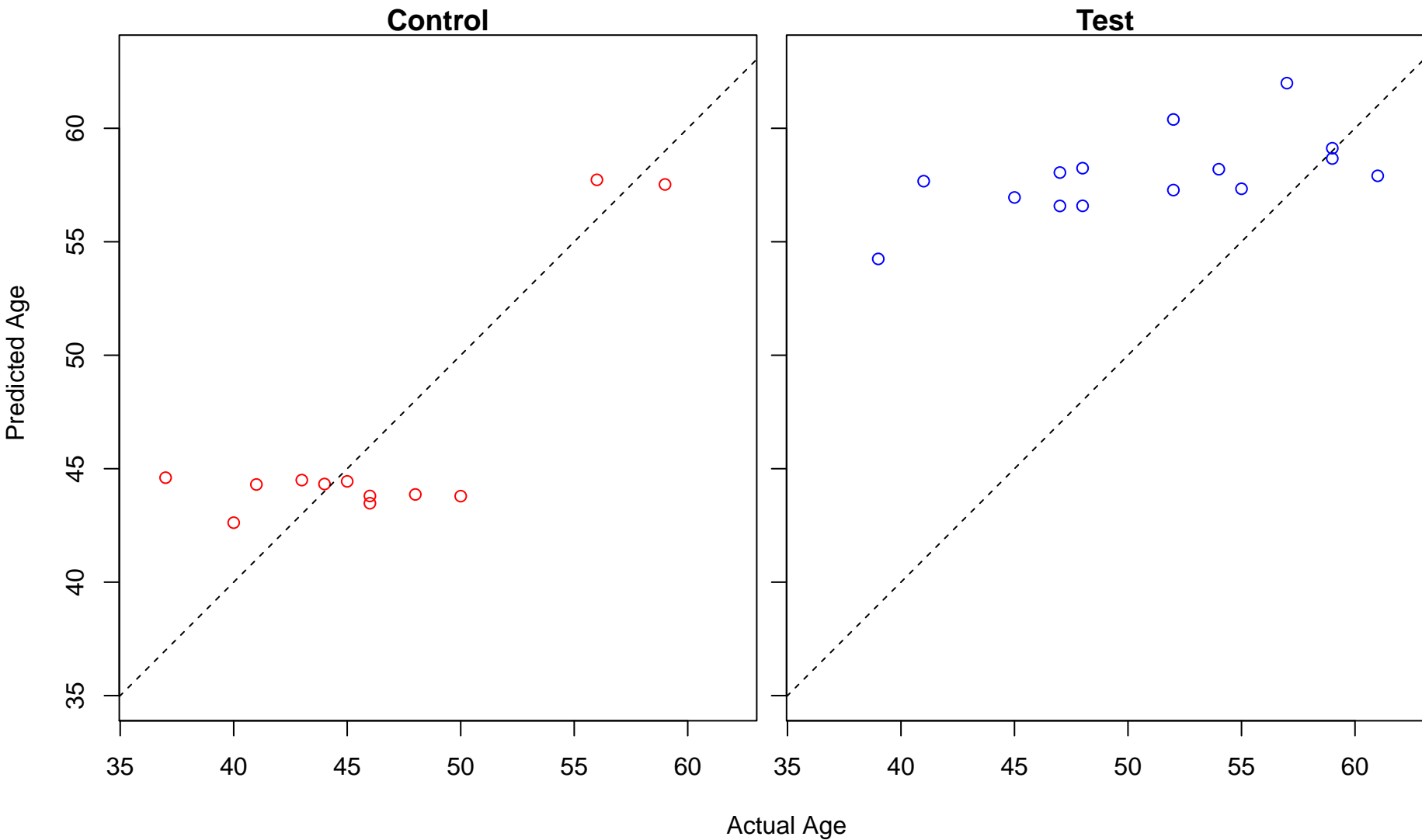


Actual Age

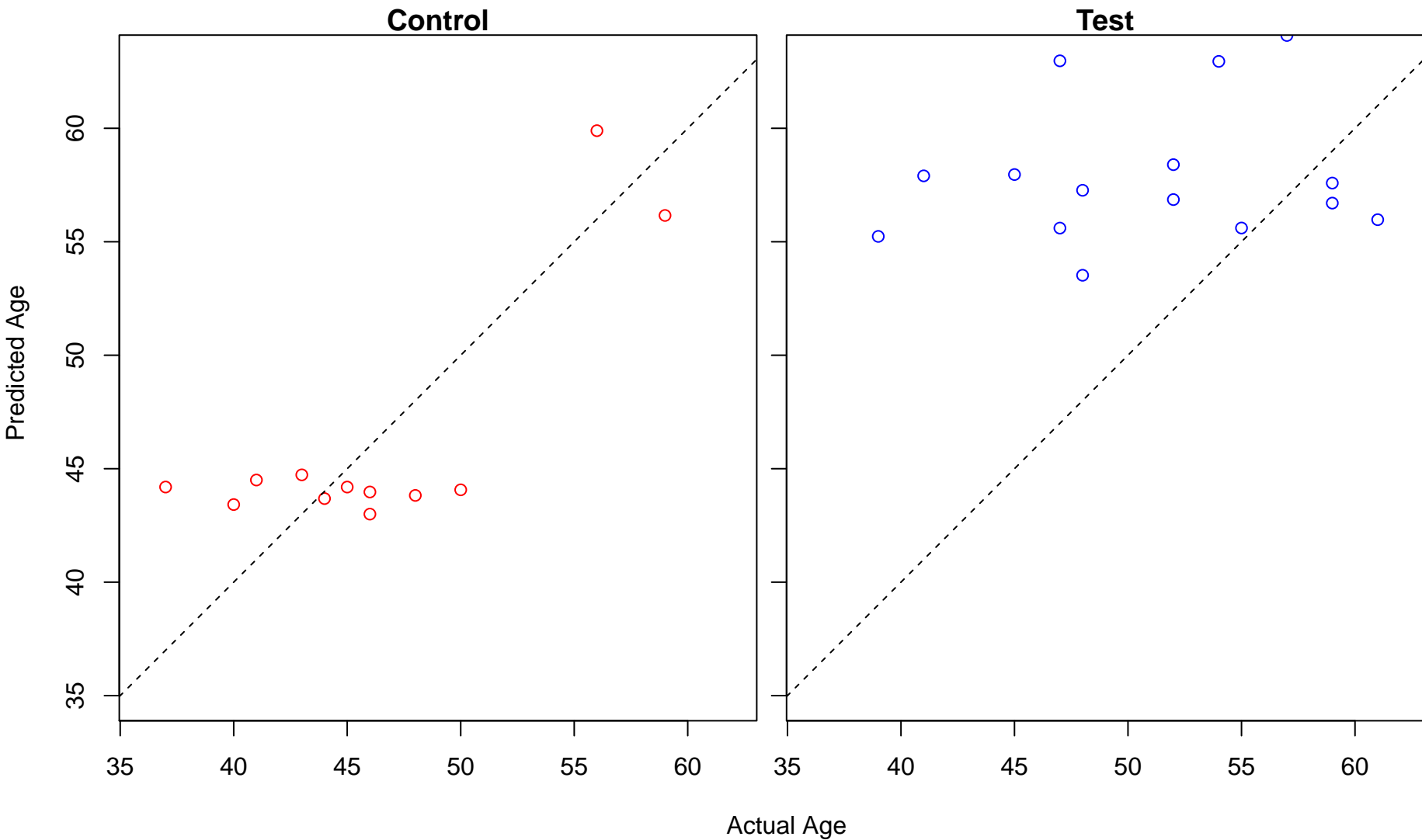
DNA replication initiation (Score: 2.622048)



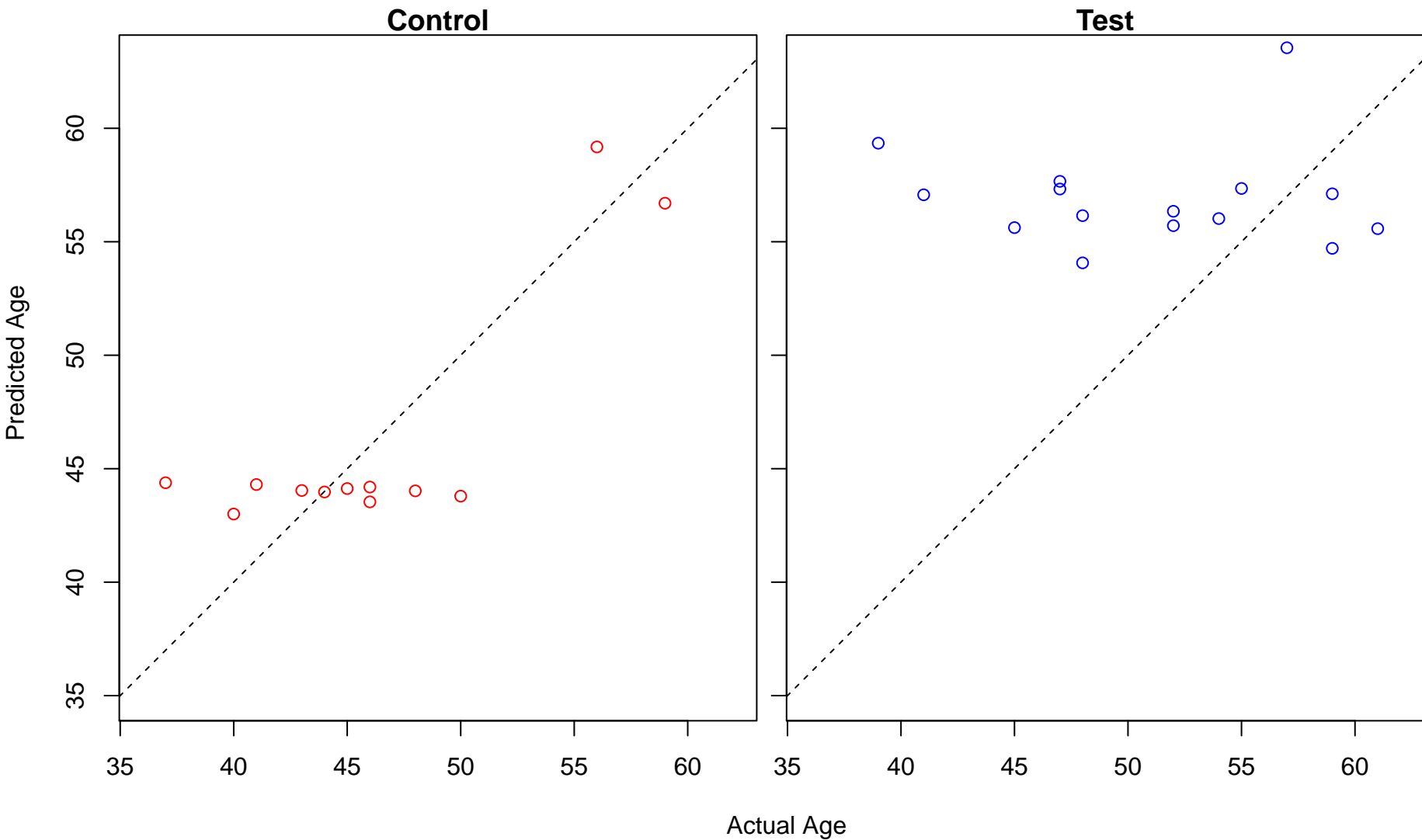
lysosome localization (Score: 2.621325)



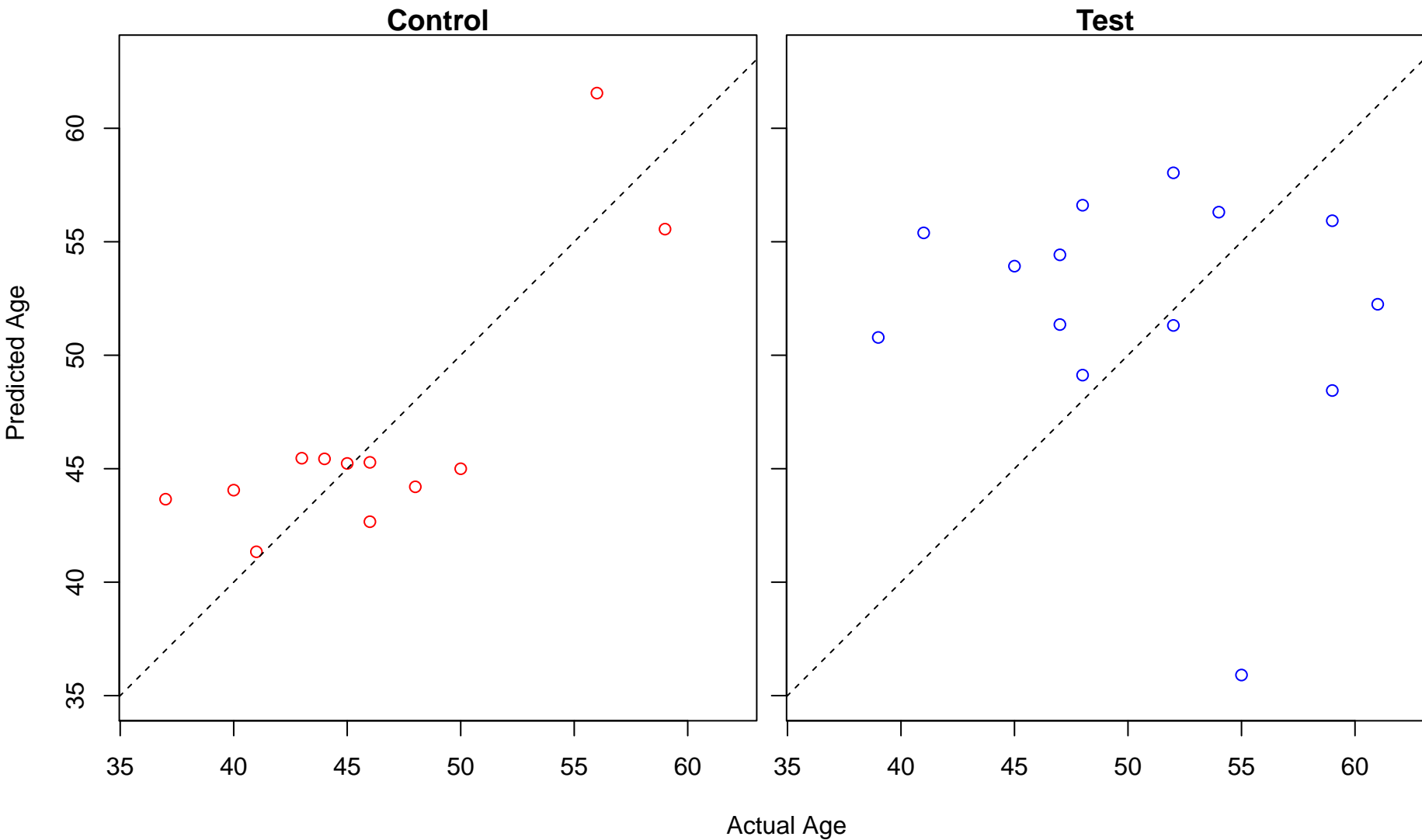
cellular response to alcohol (Score: 2.620615)



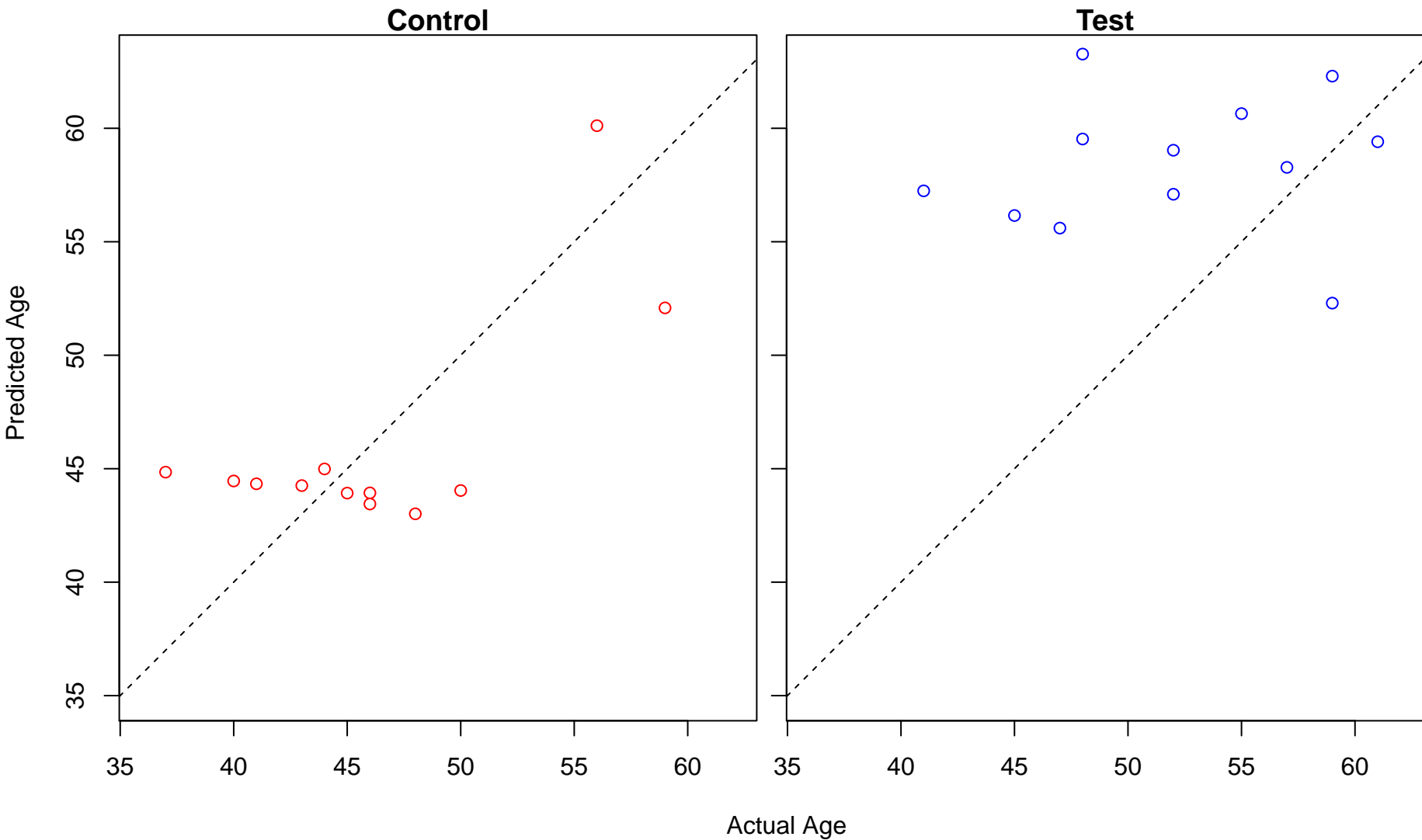
regulation of cytokinesis (Score: 2.619137)



striated muscle cell development (Score: 2.617829)

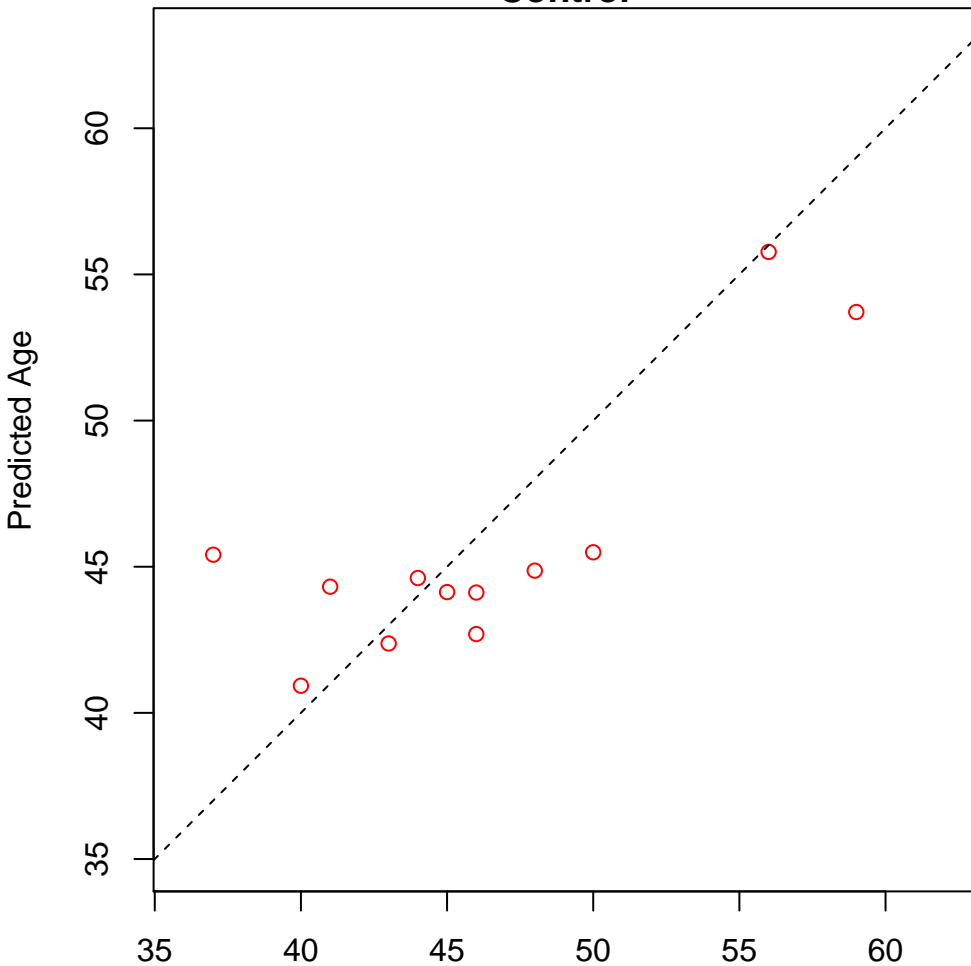


carbon catabolite regulation of transcription (Score: 2.617753)

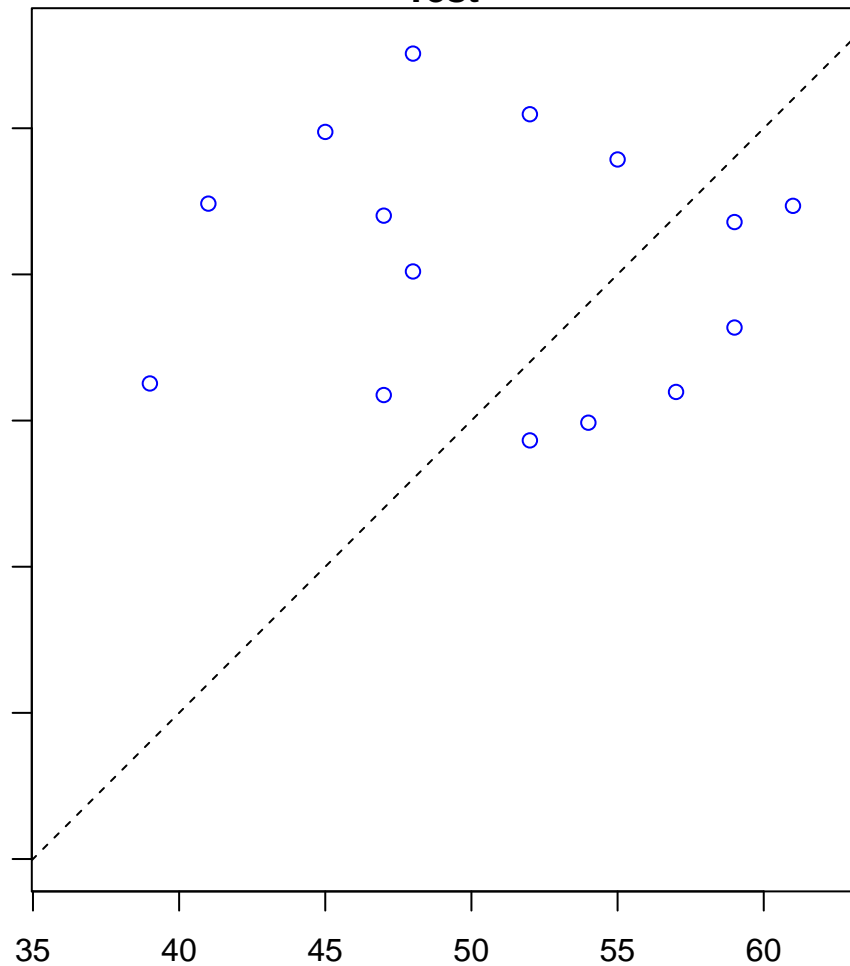


embryonic heart tube development (Score: 2.615049)

Control

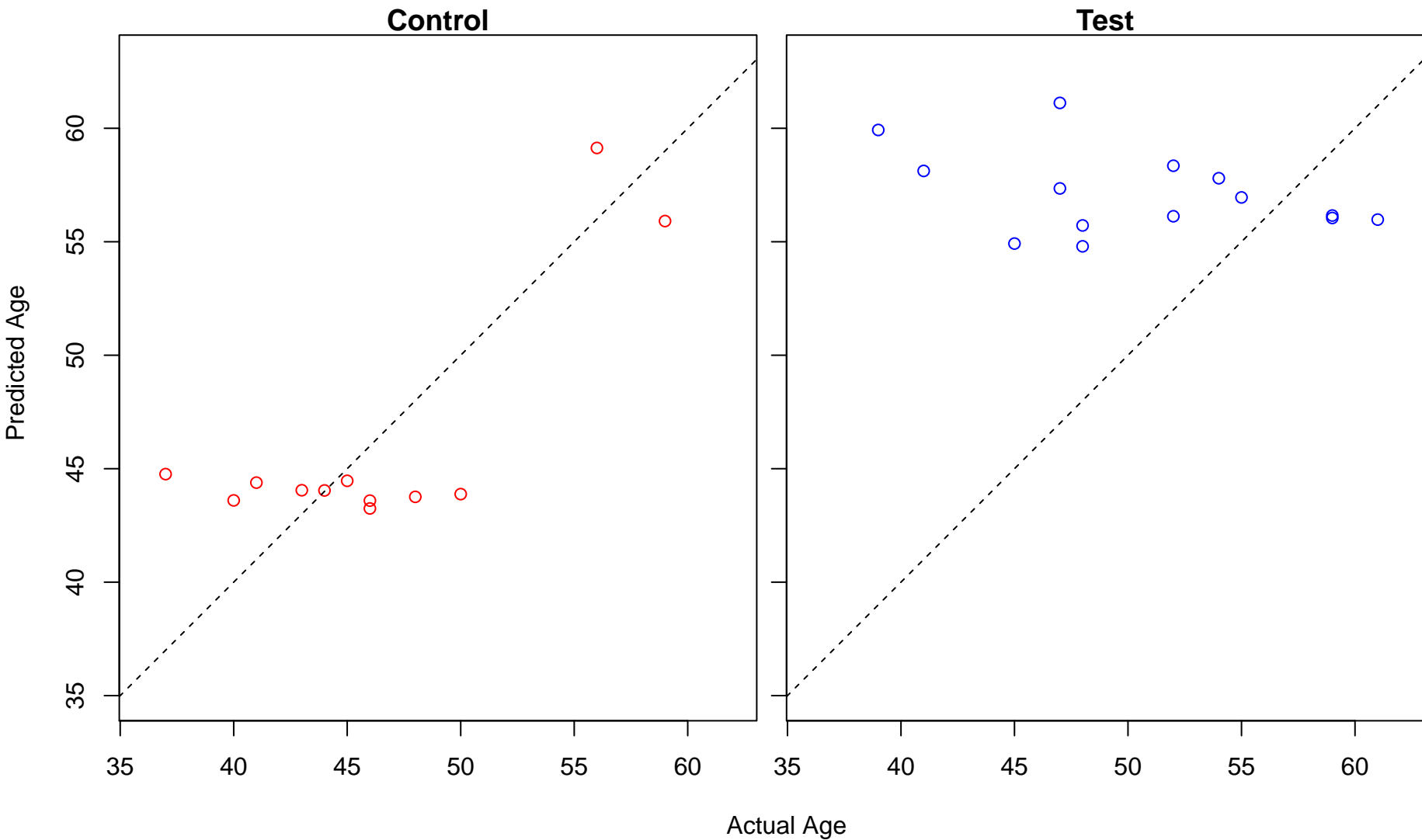


Test

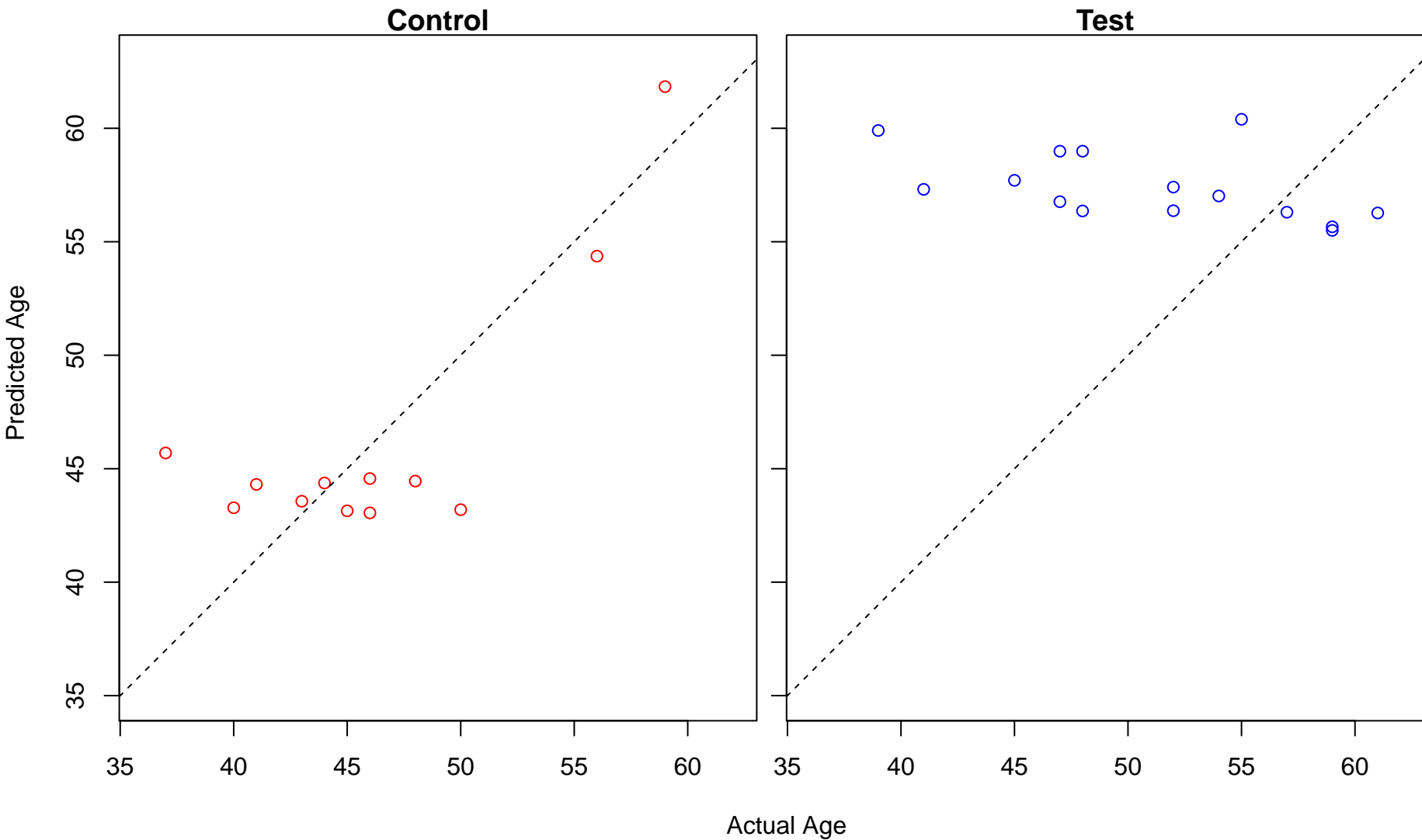


Actual Age

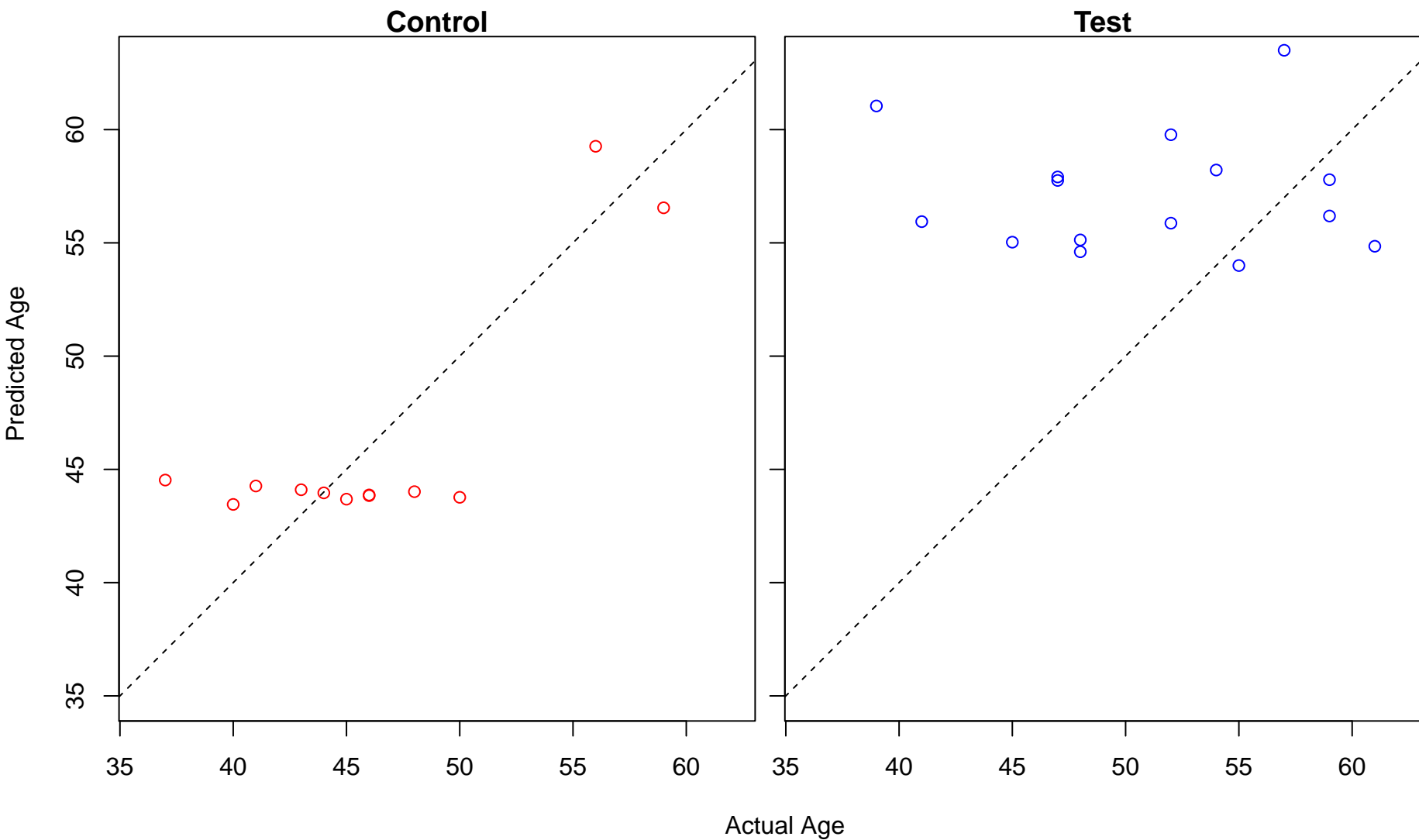
secretion (Score: 2.614437)



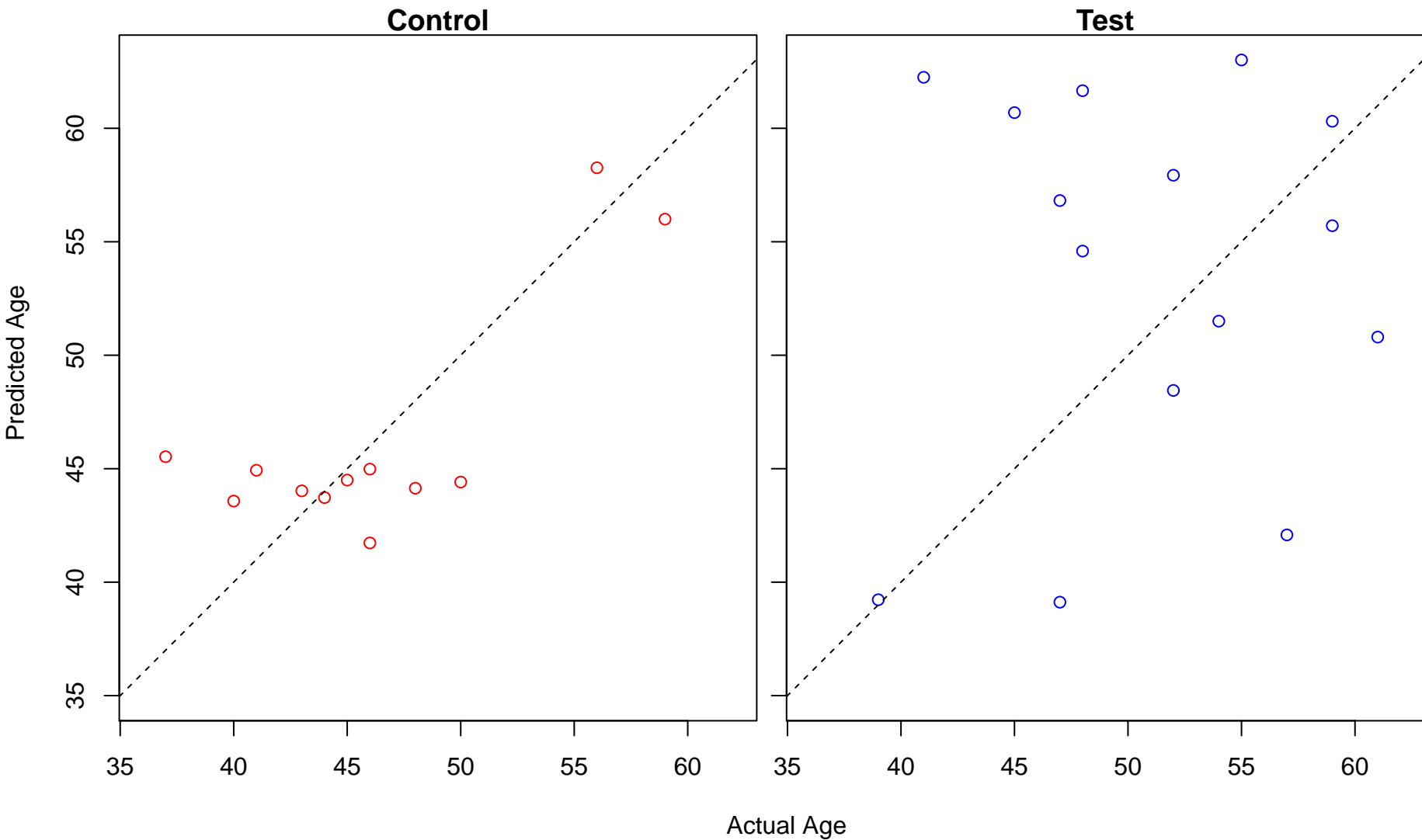
histone H4-K16 acetylation (Score: 2.613002)



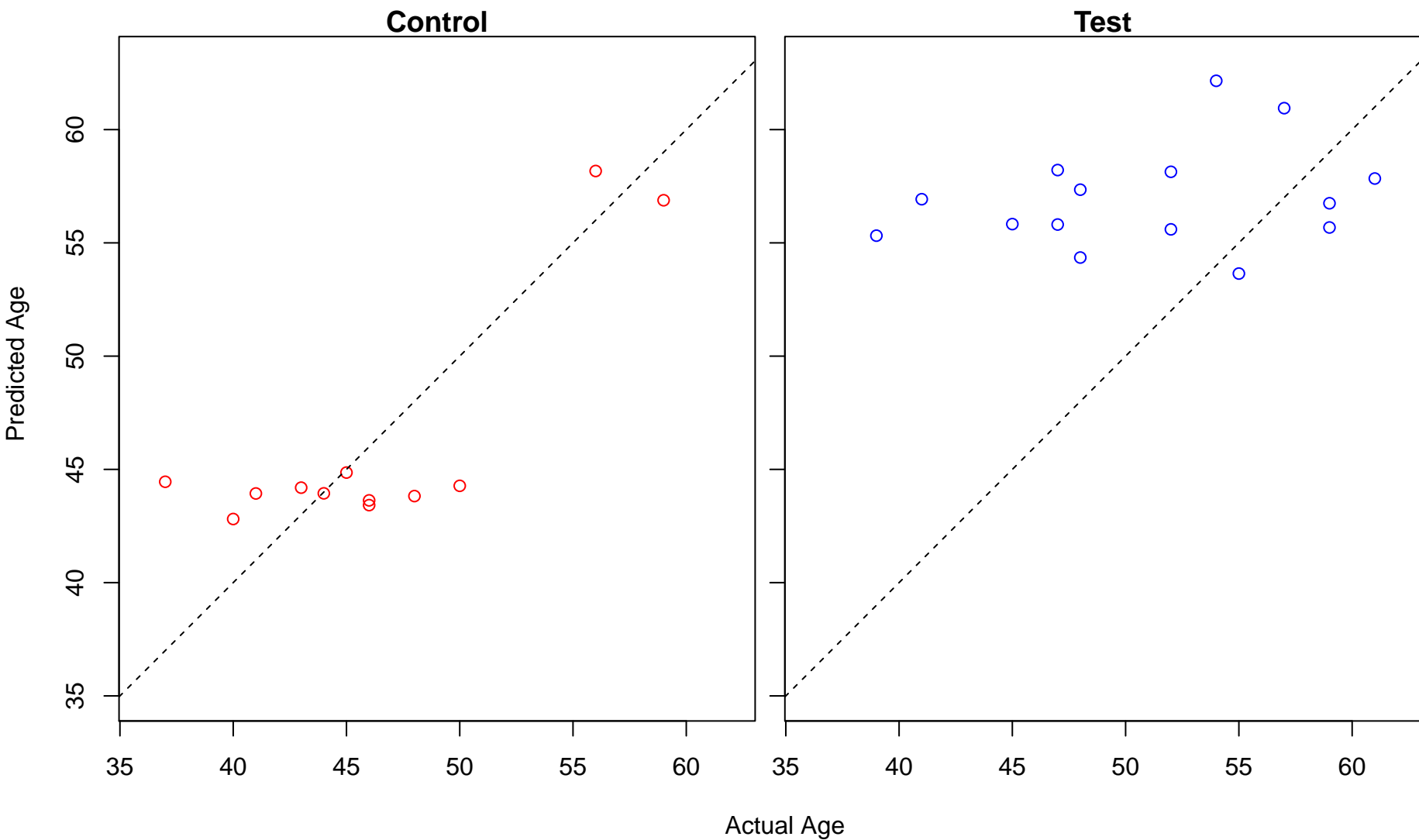
positive regulation of viral release from host cell (Score: 2.611777)



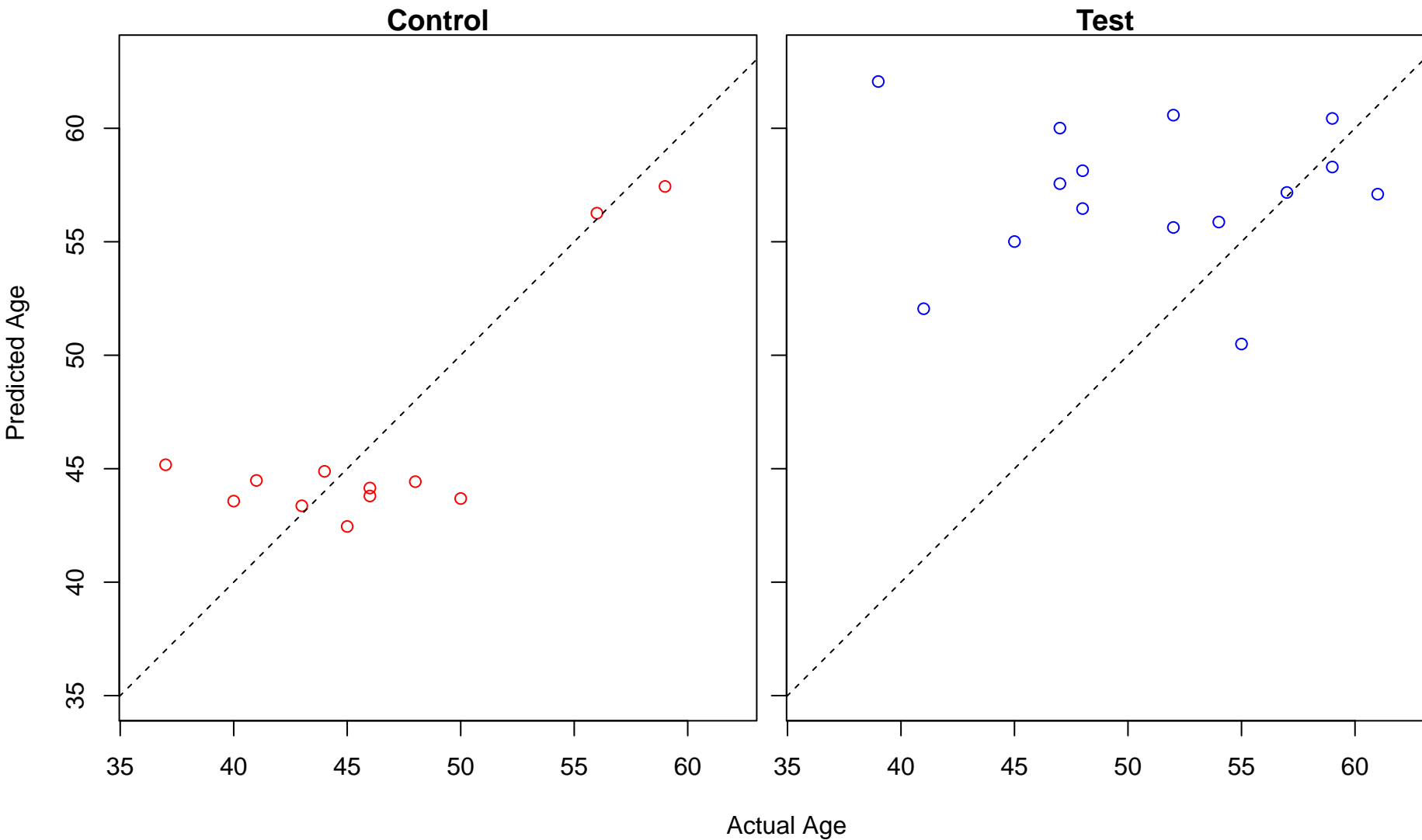
regulation of execution phase of apoptosis (Score: 2.609508)



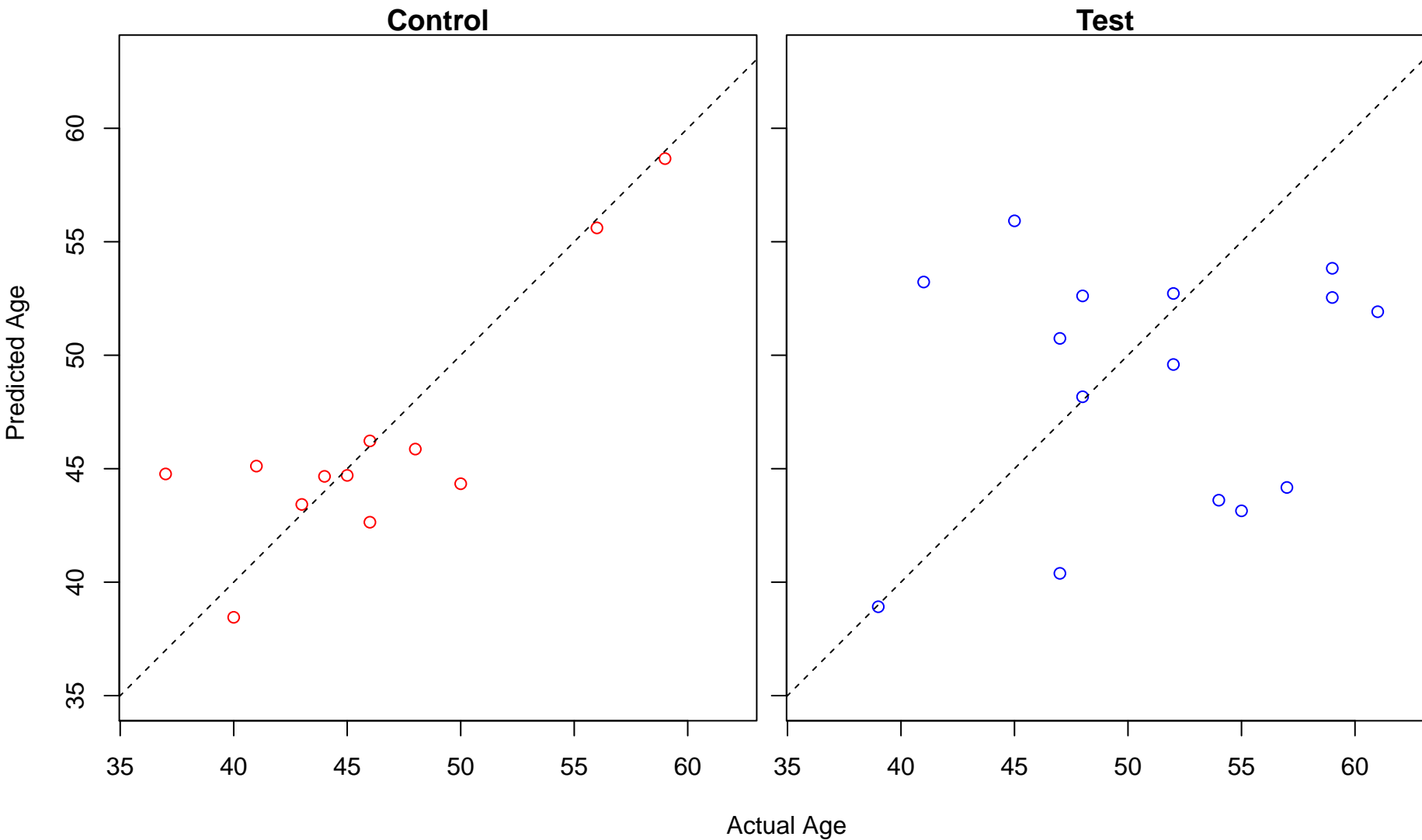
response to UV (Score: 2.608649)



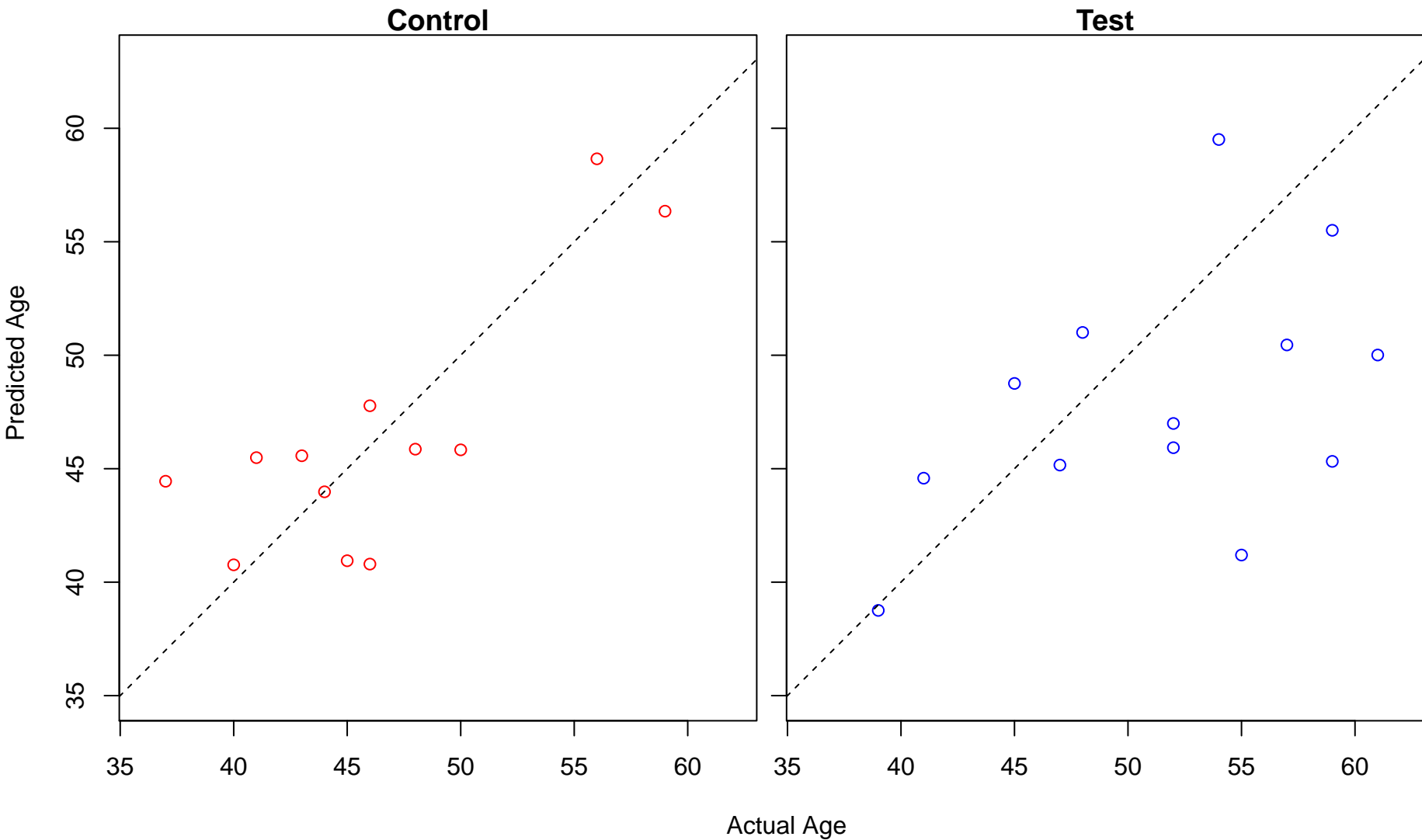
steroid hormone mediated signaling pathway (Score: 2.607612)



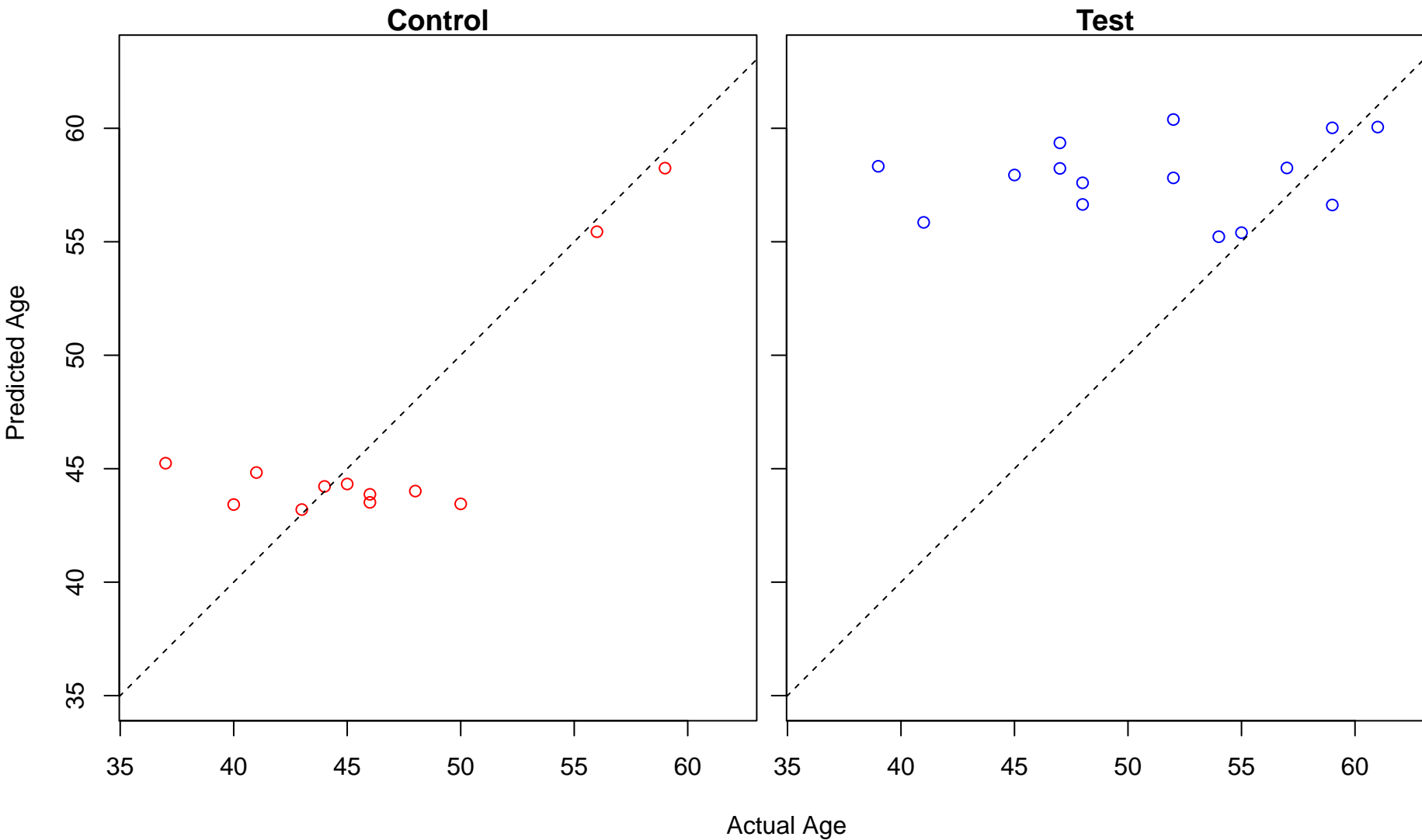
regulation of viral transcription (Score: 2.607486)



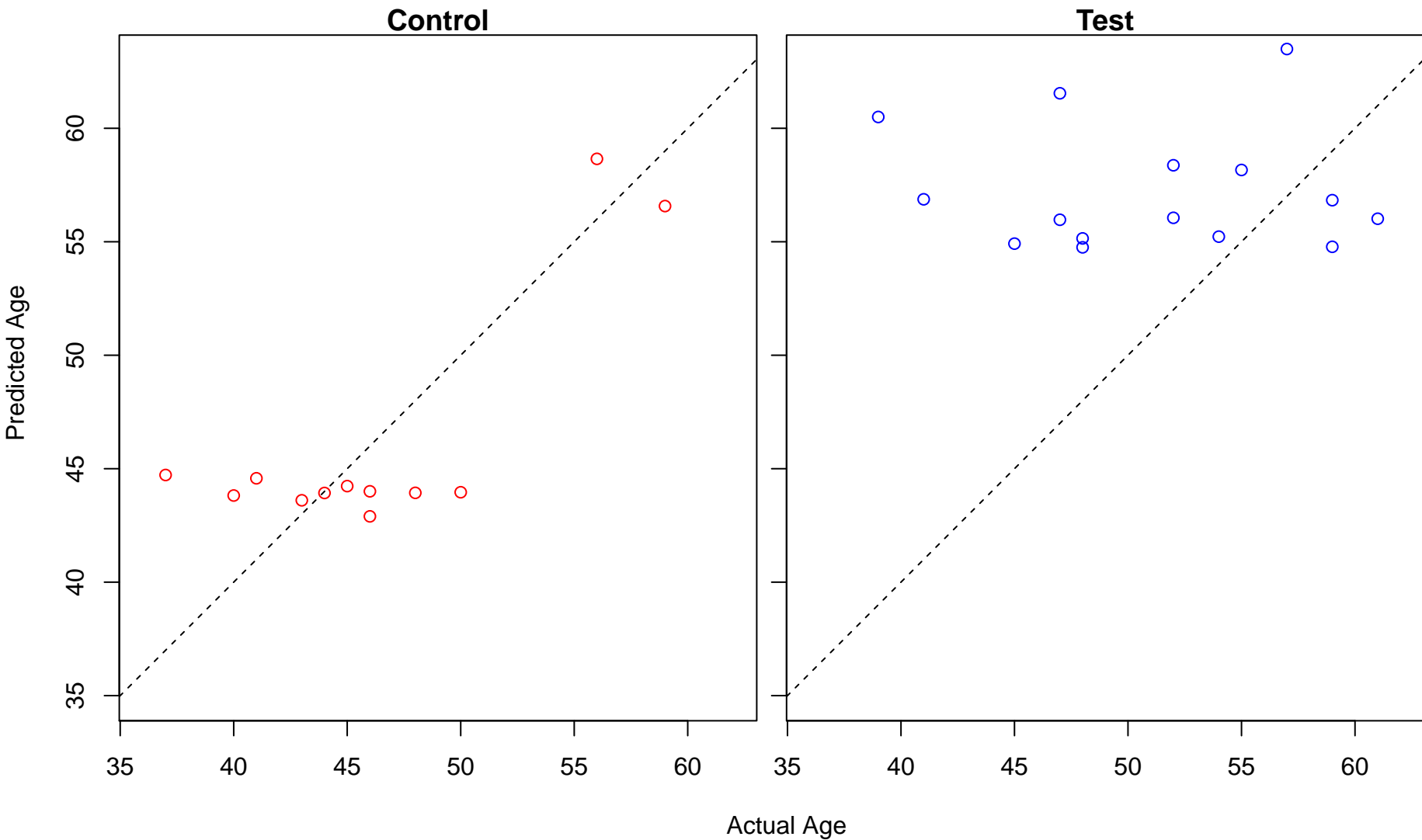
regulation of dendrite development (Score: 2.607029)



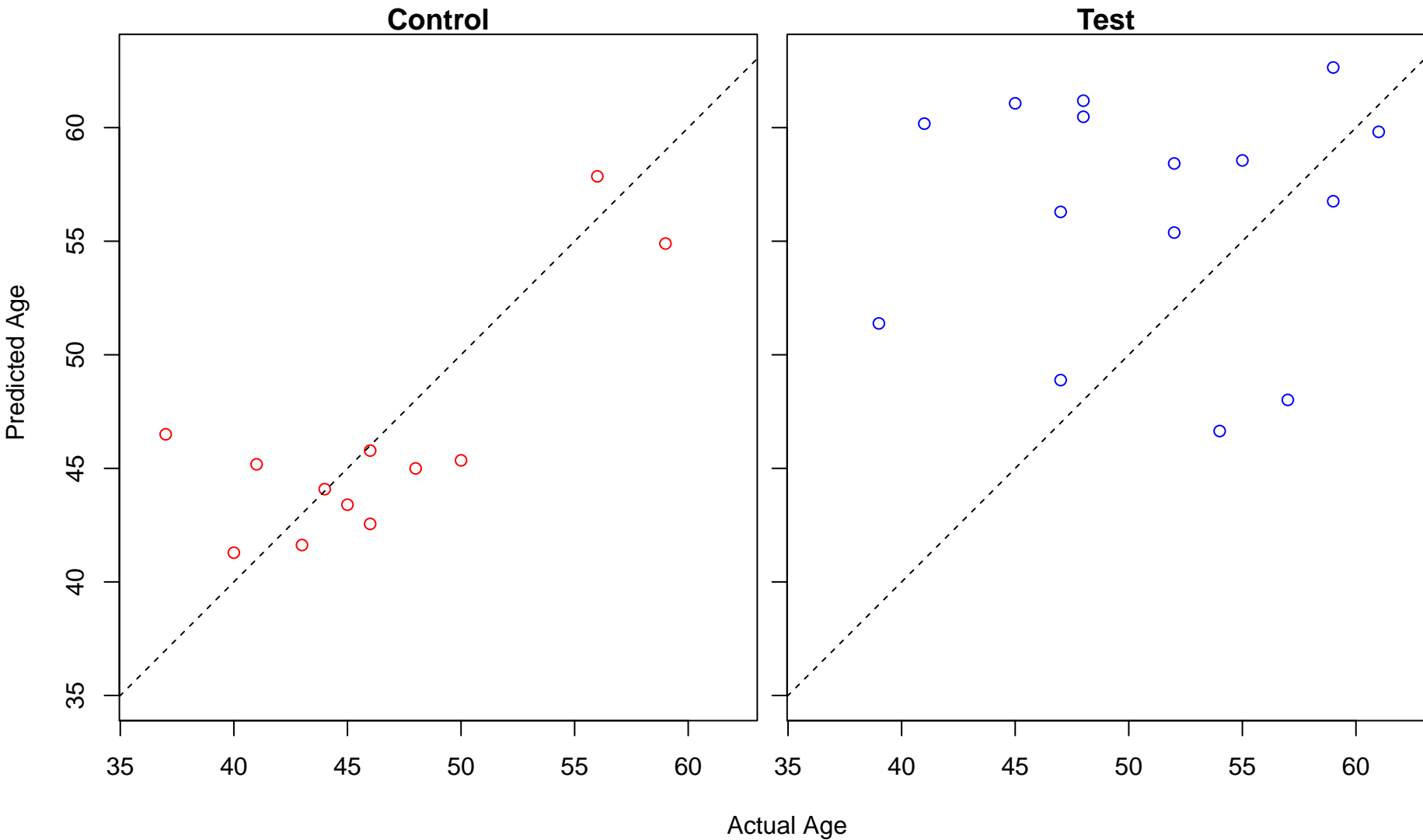
response to dsRNA (Score: 2.605183)



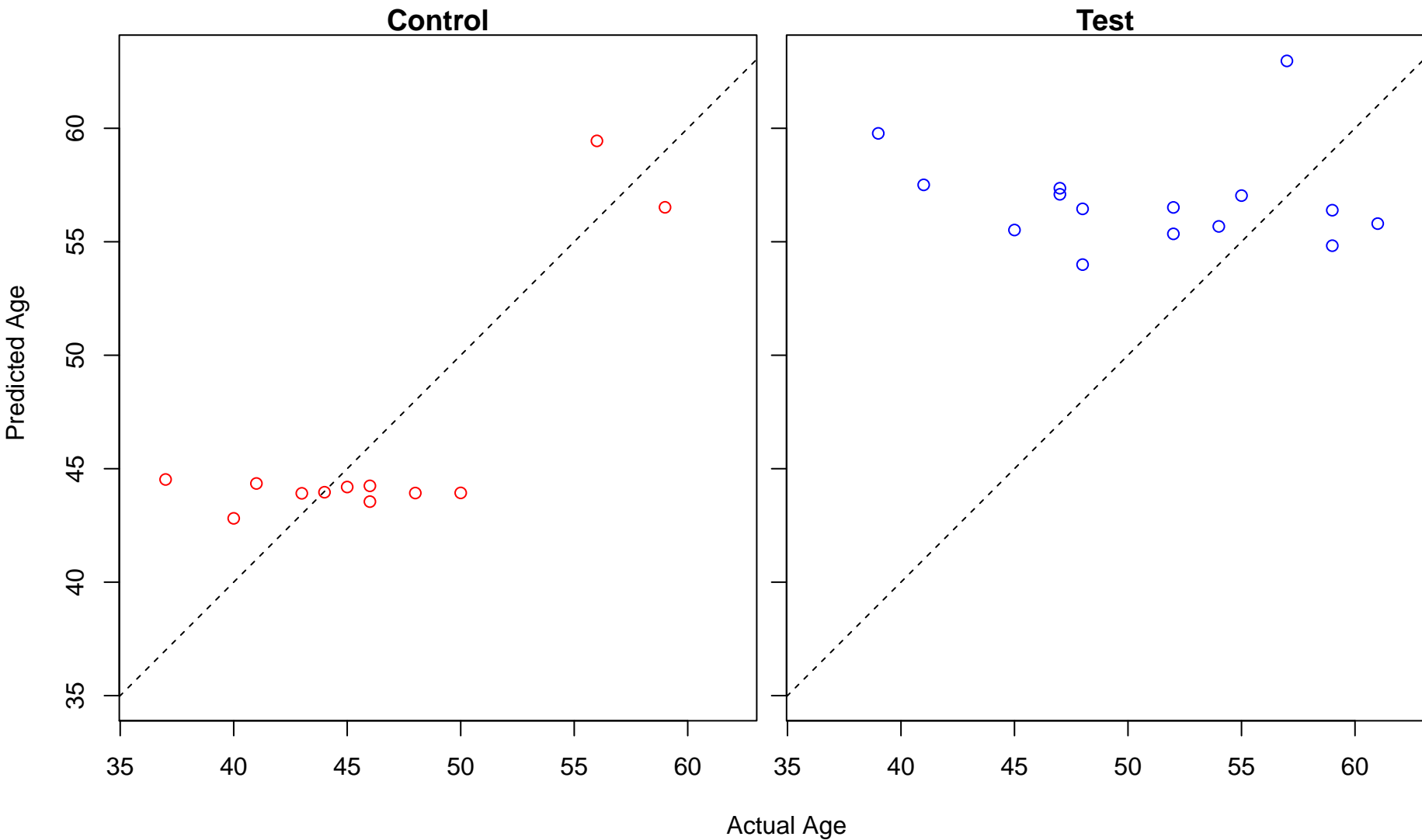
RNA splicing (Score: 2.604610)



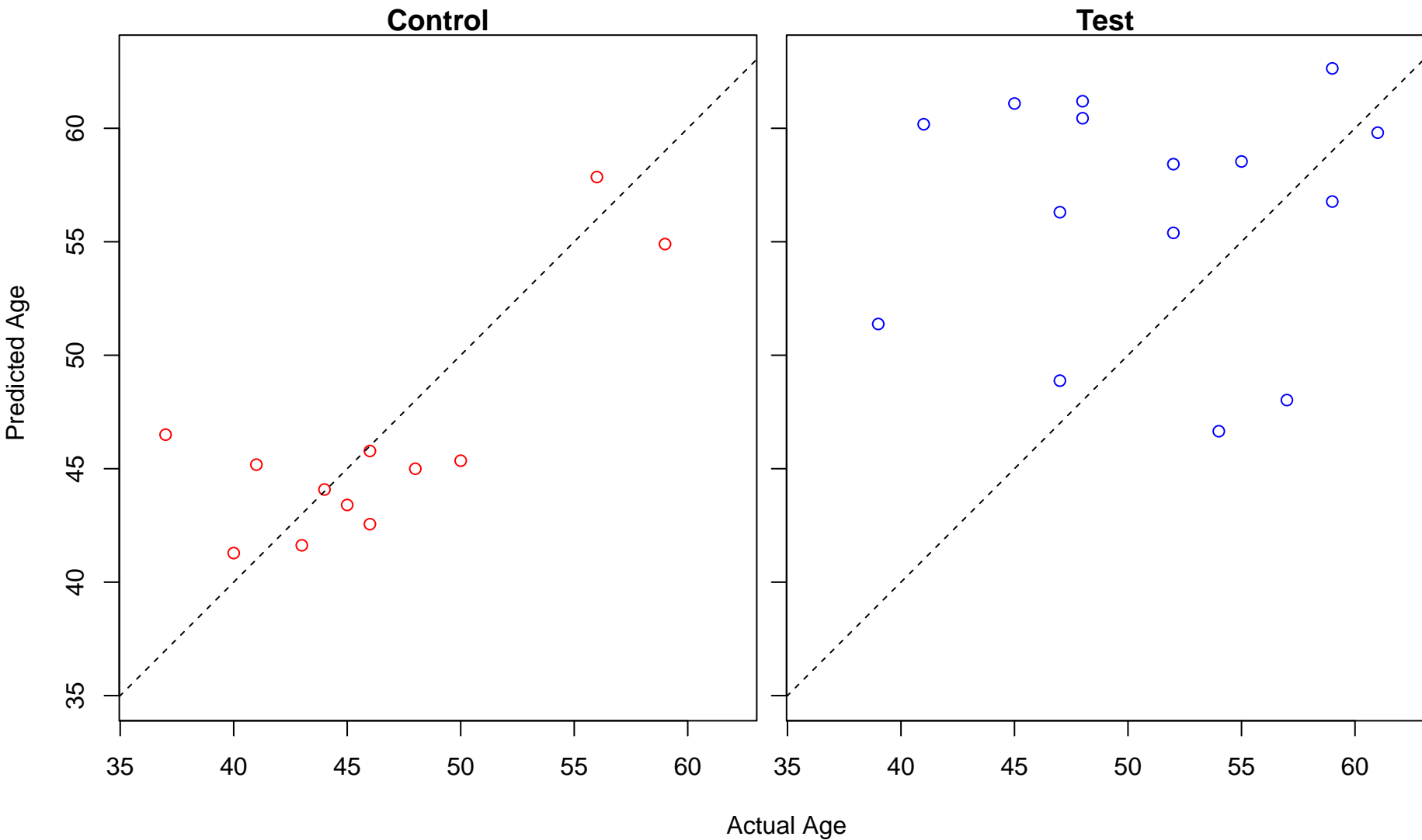
vascular smooth muscle contraction (Score: 2.603603)



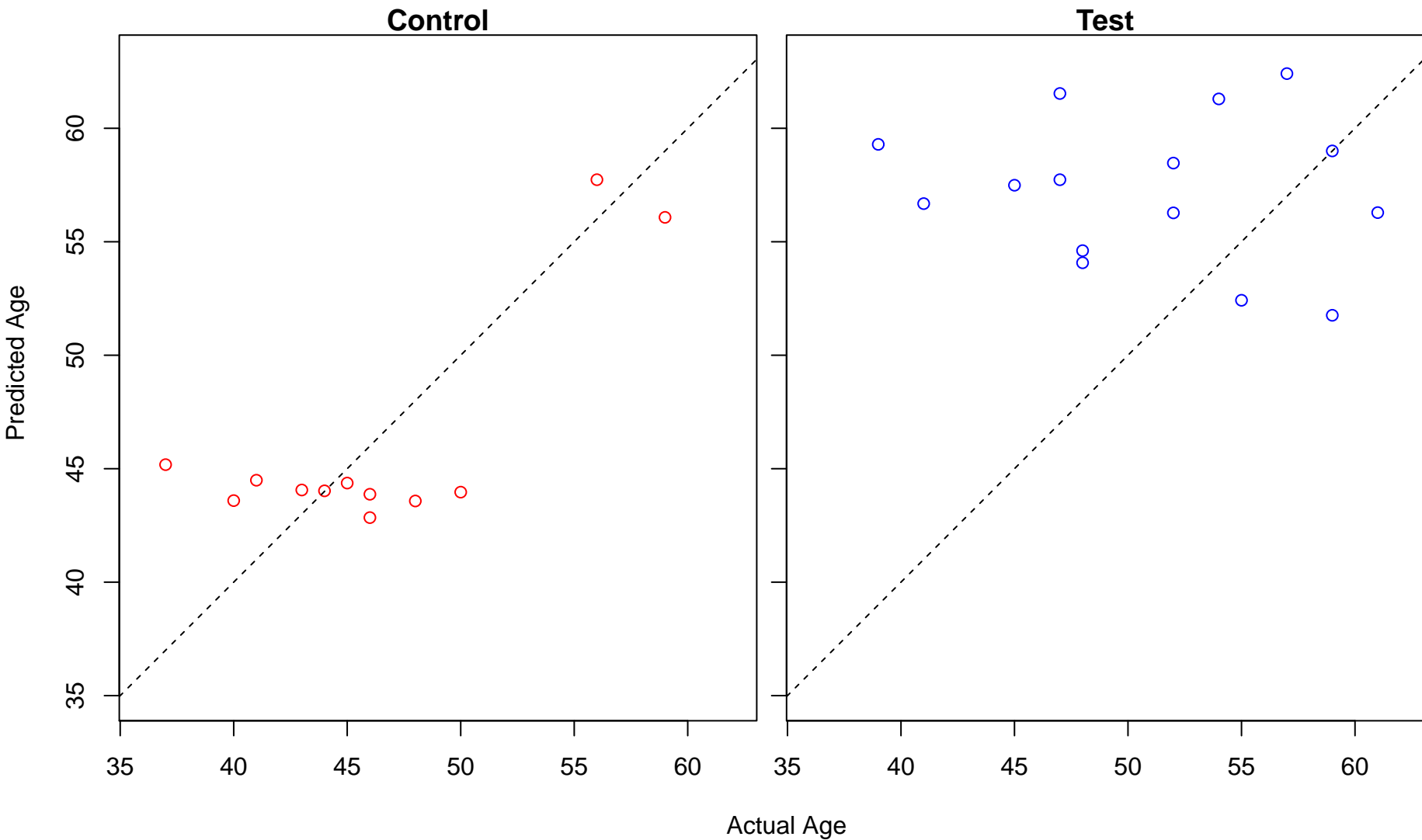
regulation of cation channel activity (Score: 2.603529)



vasoconstriction (Score: 2.603474)

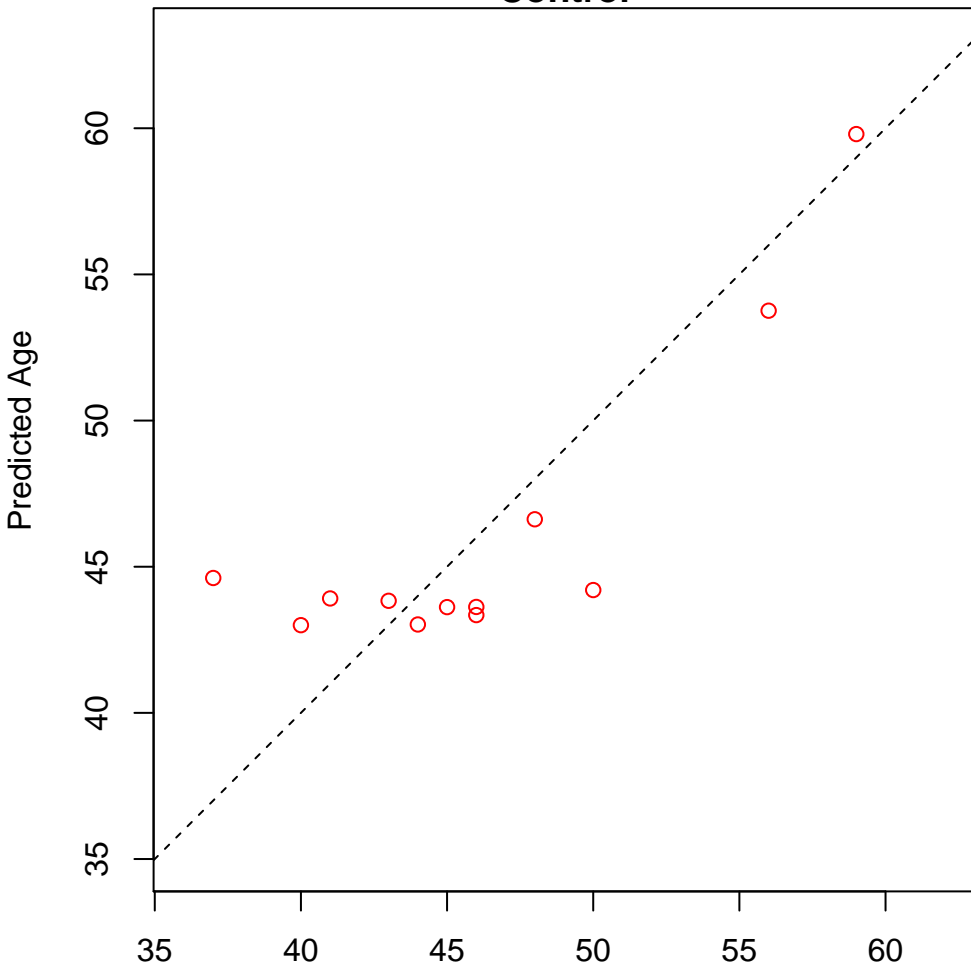


inorganic anion transmembrane transport (Score: 2.598357)

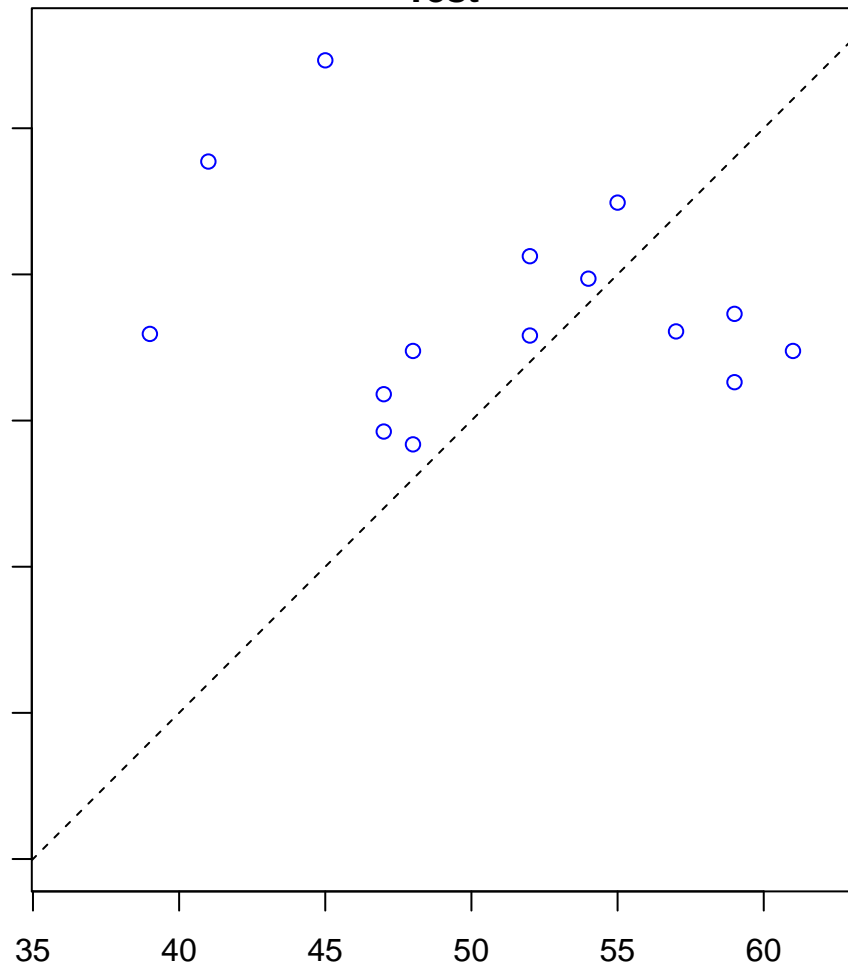


neuromuscular synaptic transmission (Score: 2.594865)

Control

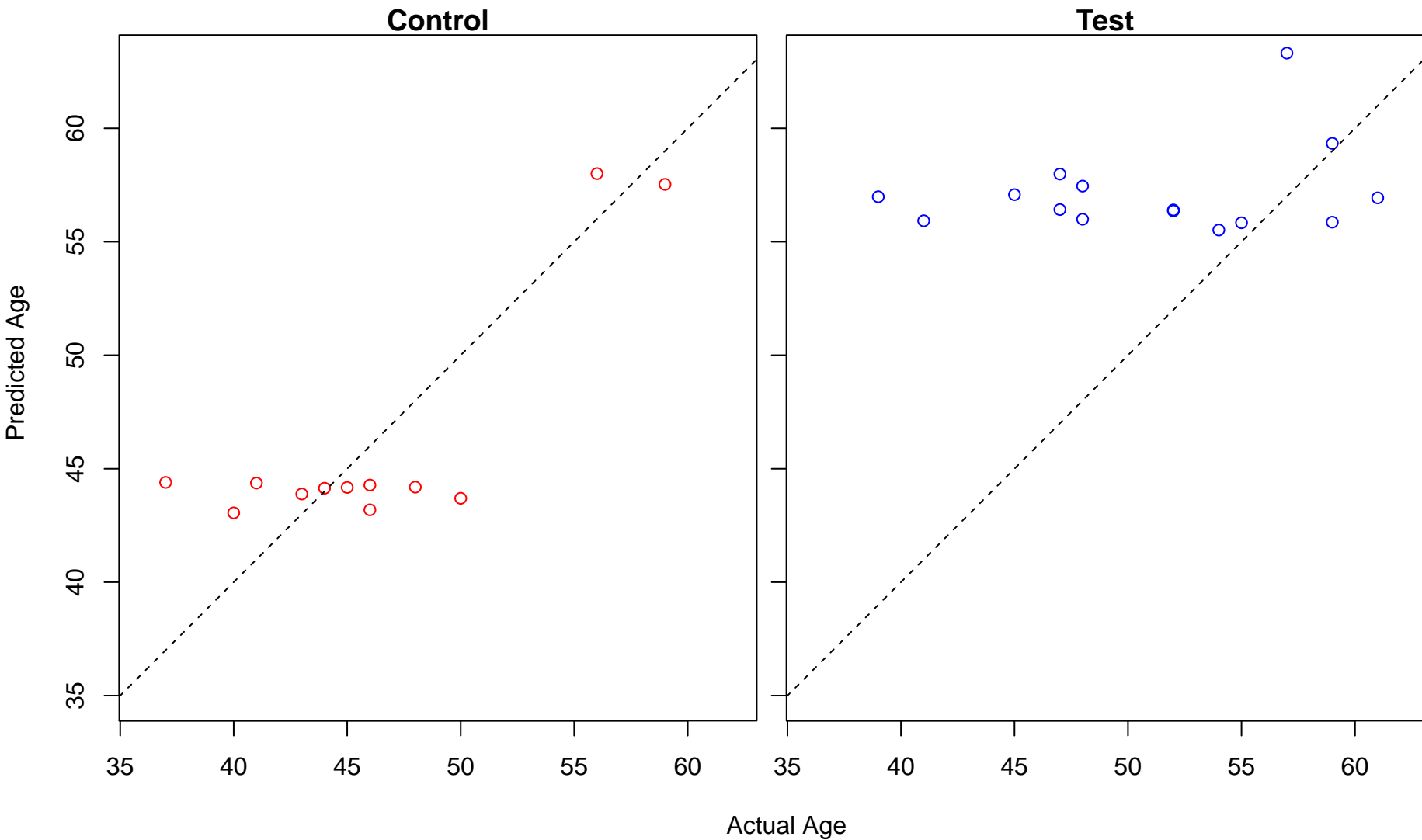


Test

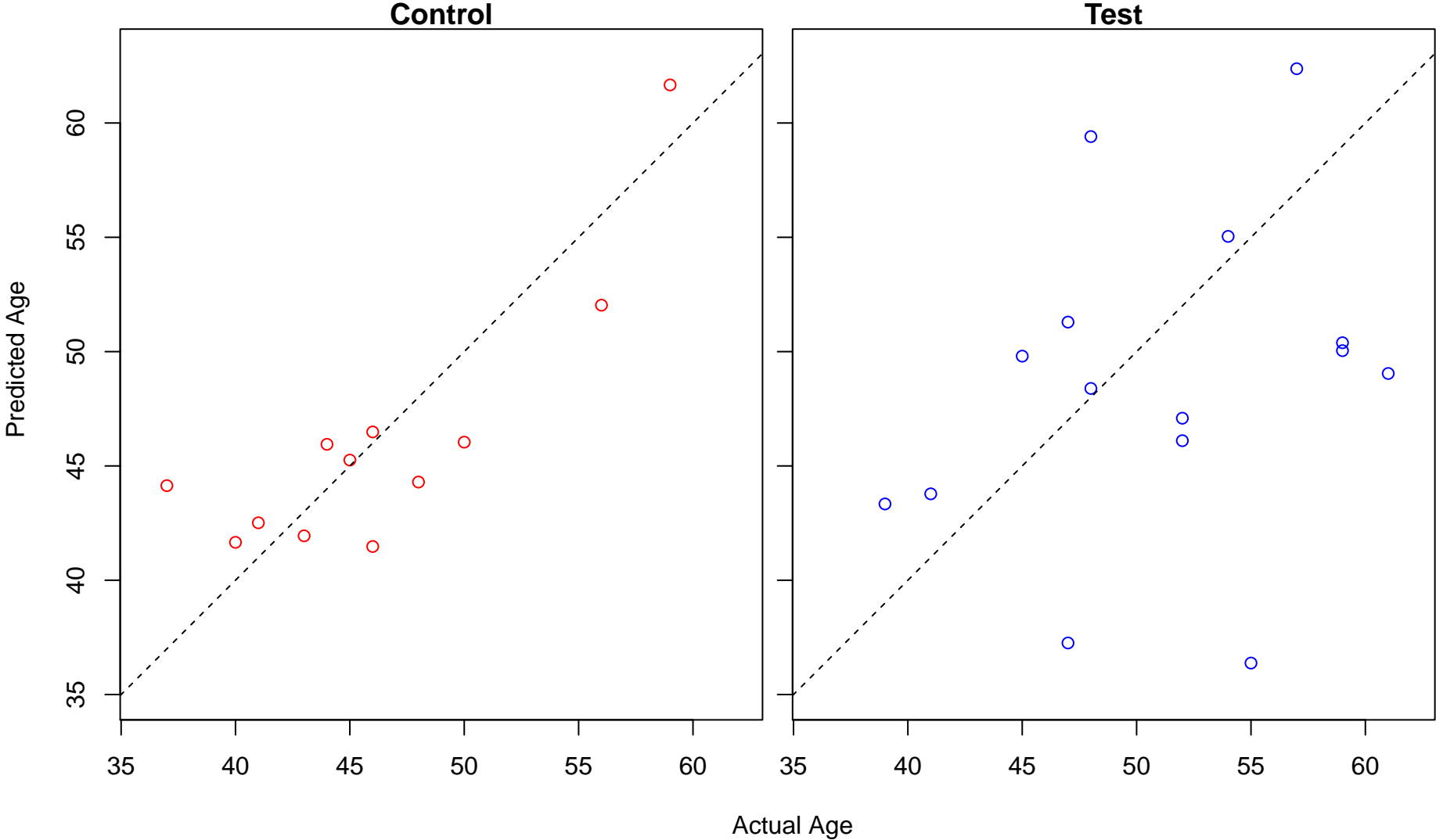


Actual Age

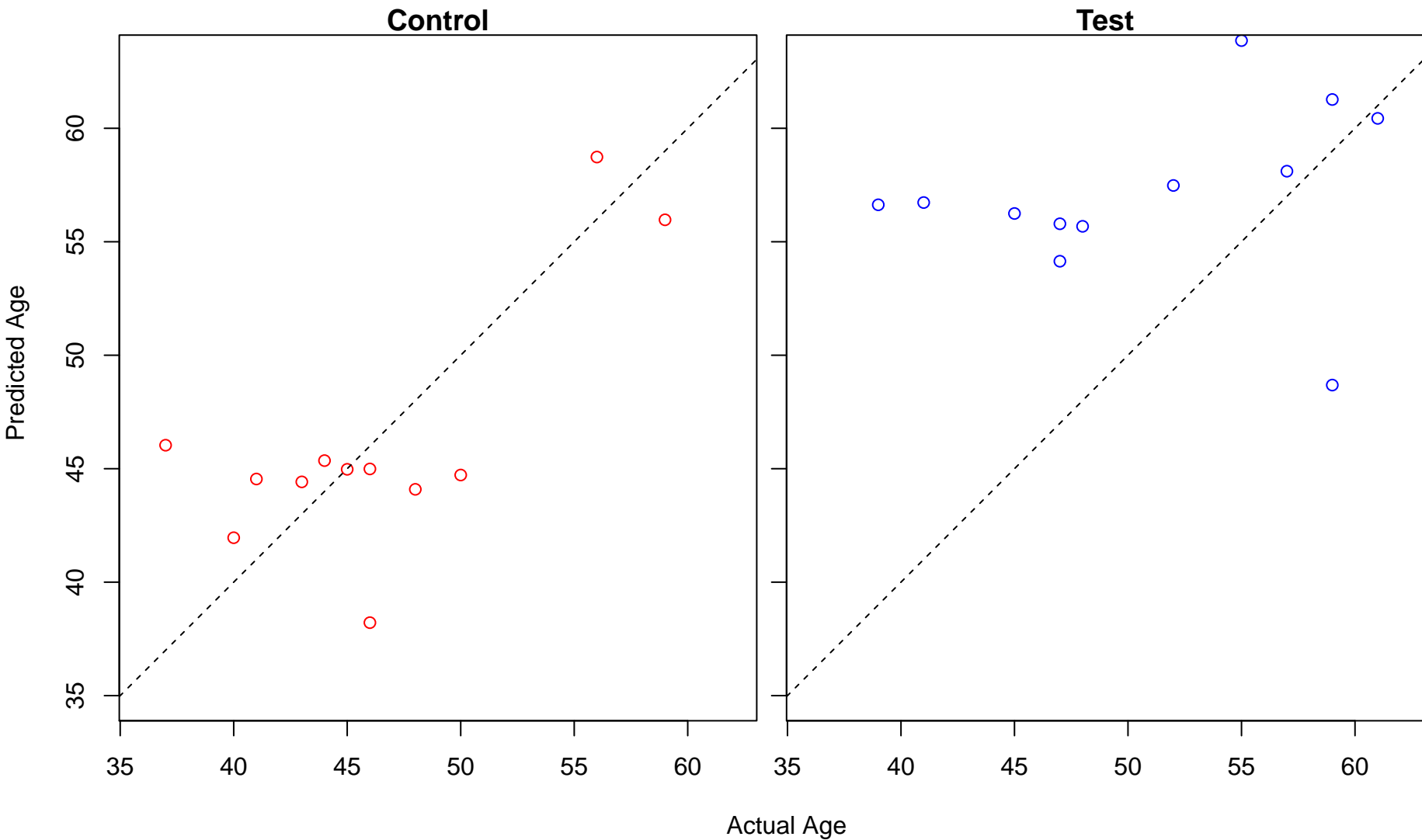
centrosome organization (Score: 2.594410)



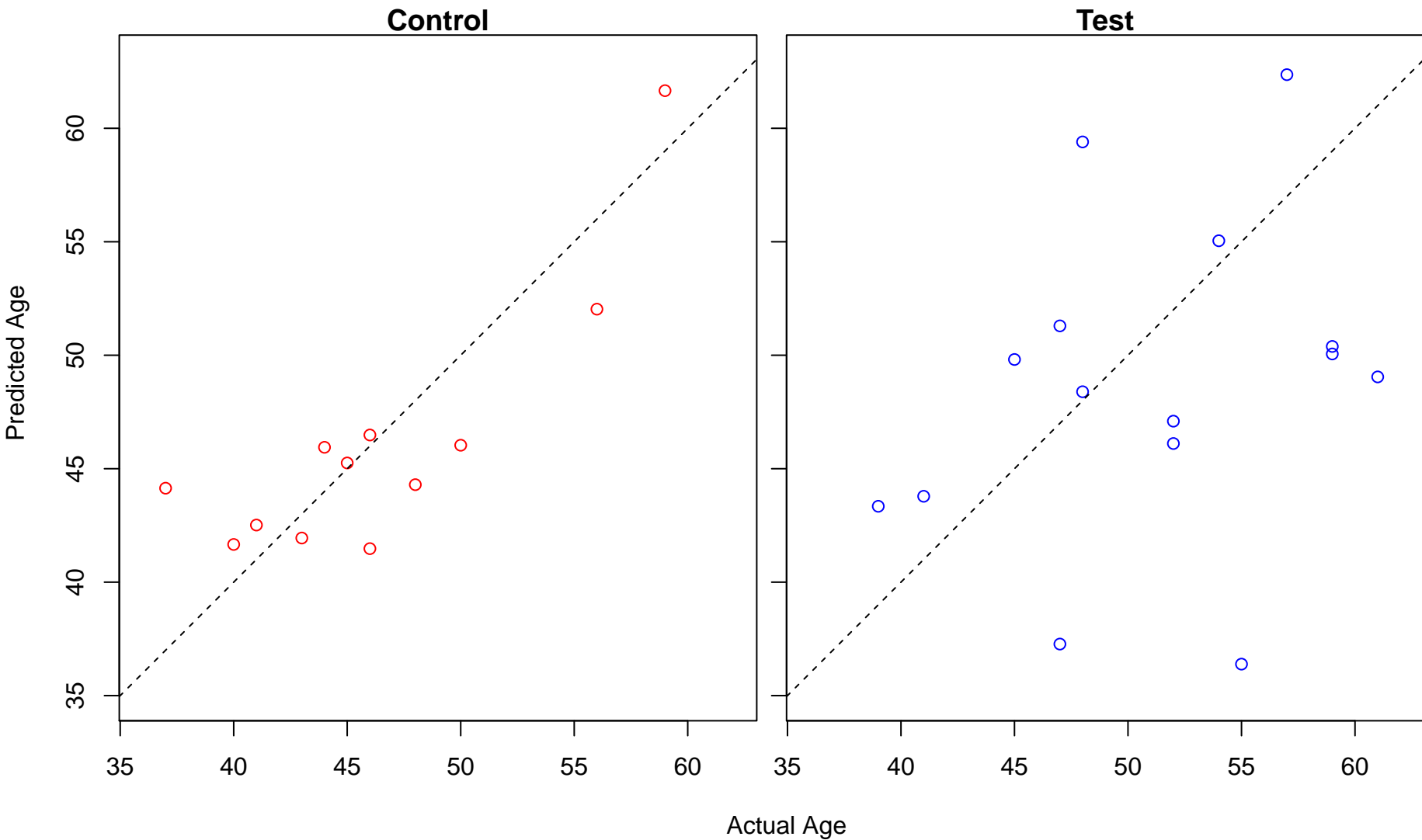
regulation of potassium ion transmembrane transporter activity (Score: 2.594306)



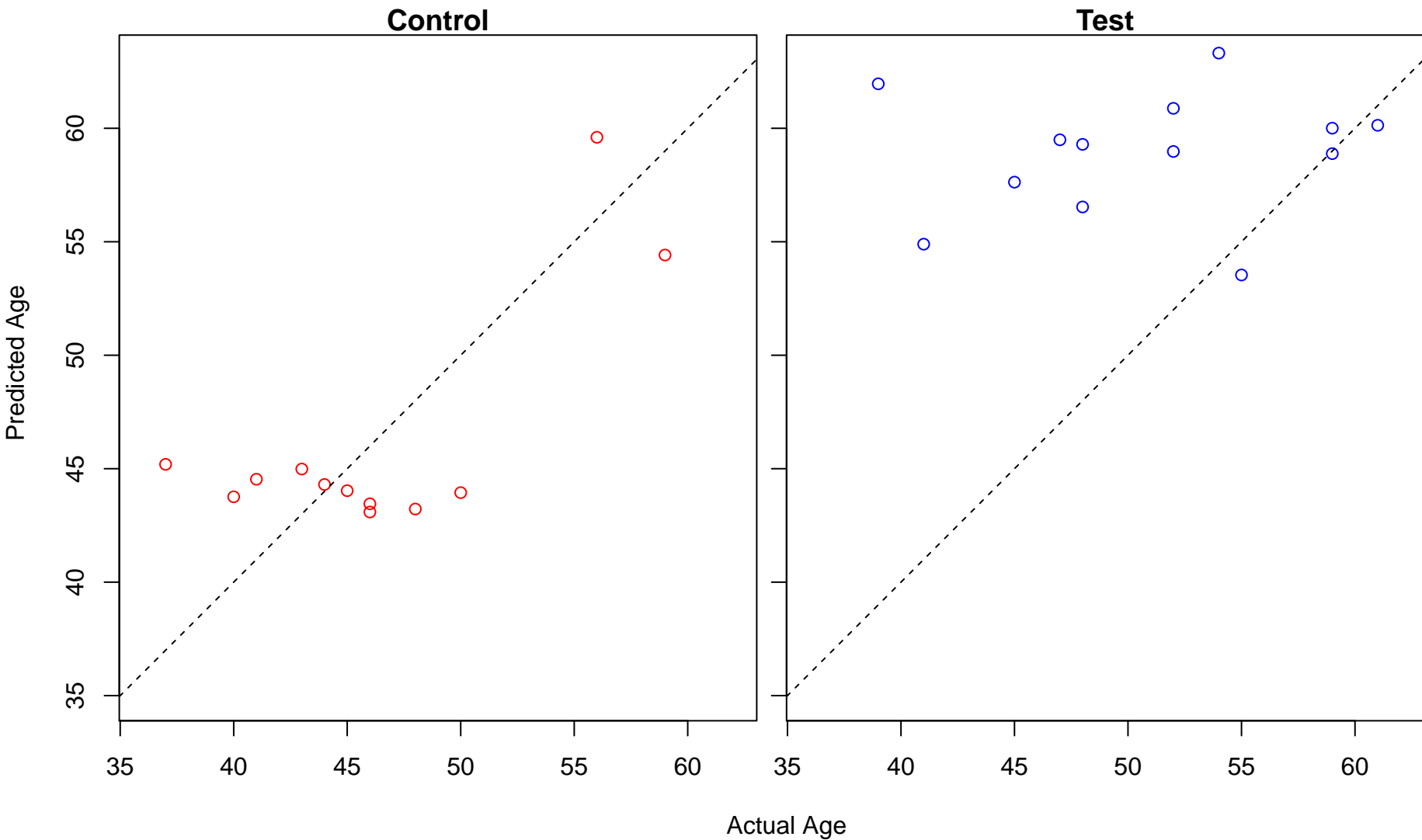
response to nicotine (Score: 2.593588)



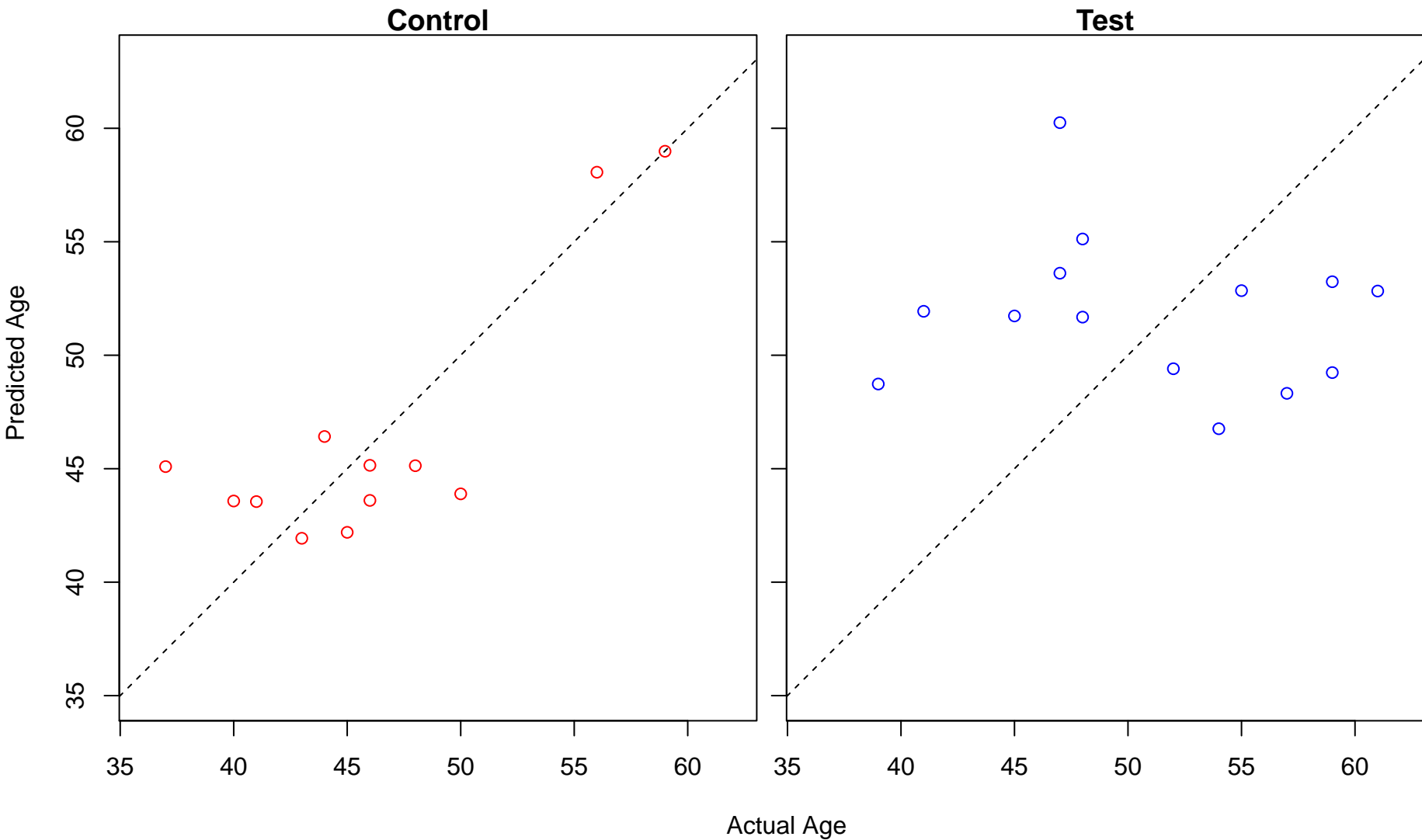
regulation of potassium ion transmembrane transport (Score: 2.591299)



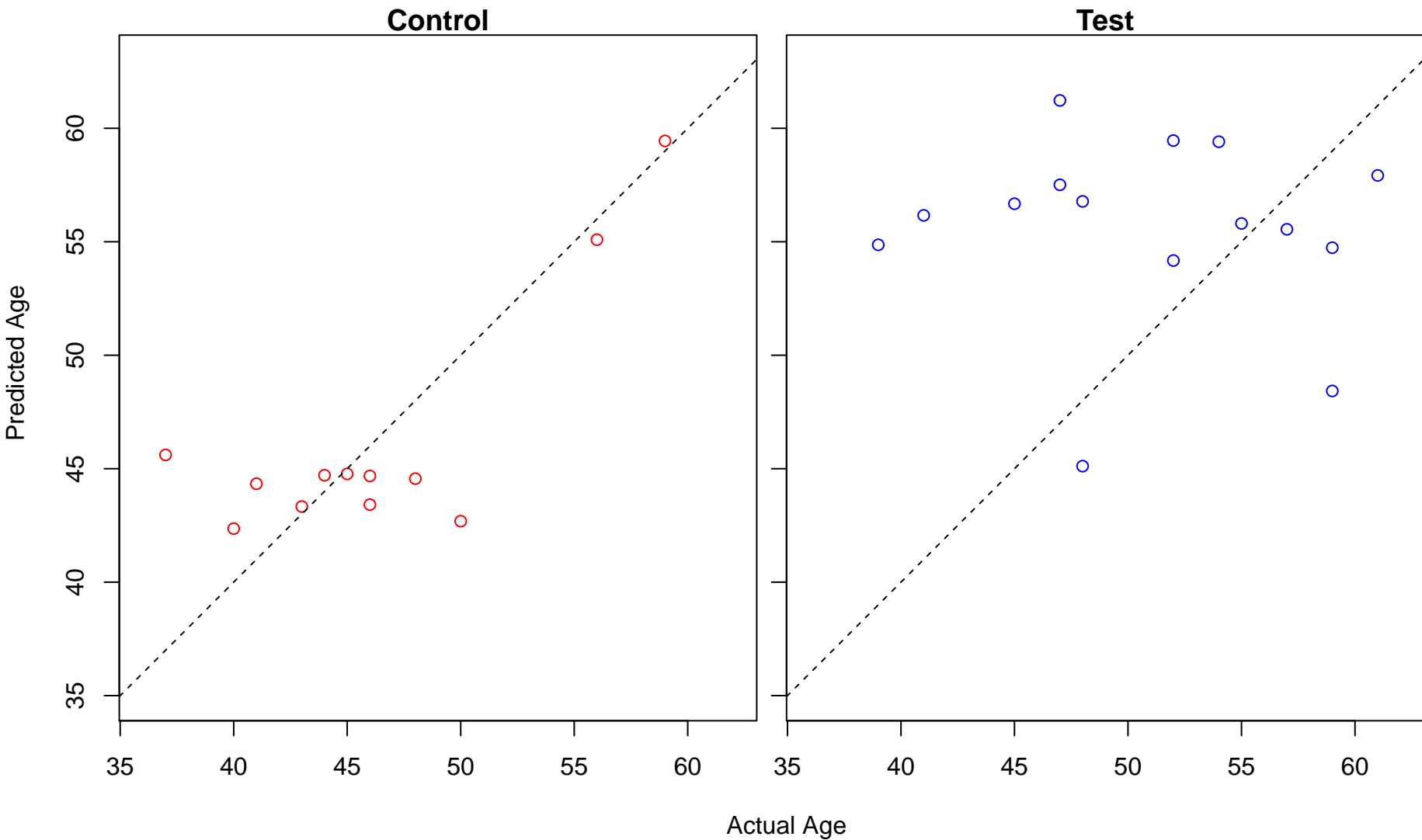
regulation of phospholipid metabolic process (Score: 2.589524)



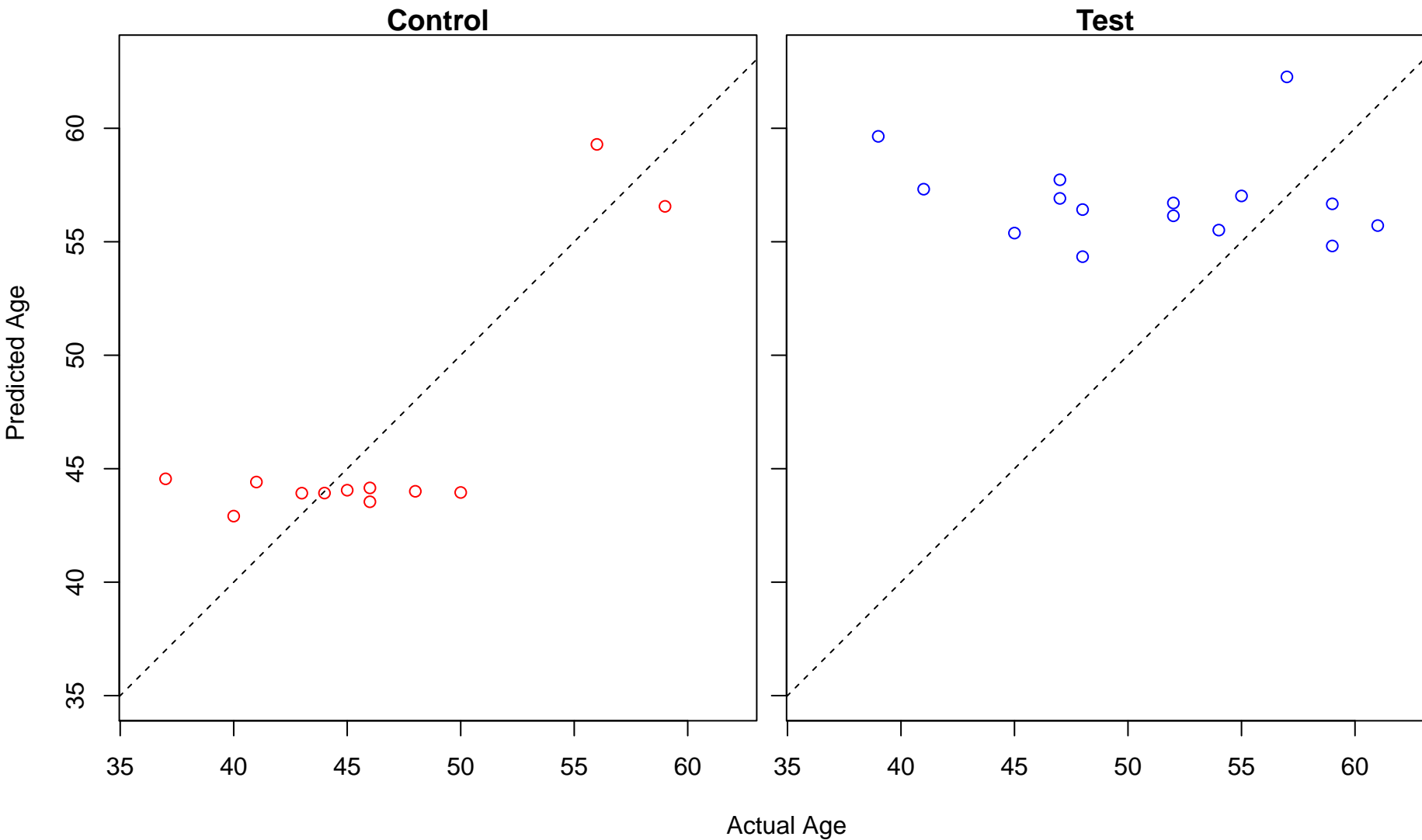
G-protein coupled acetylcholine receptor signaling pathway (Score: 2.588437)



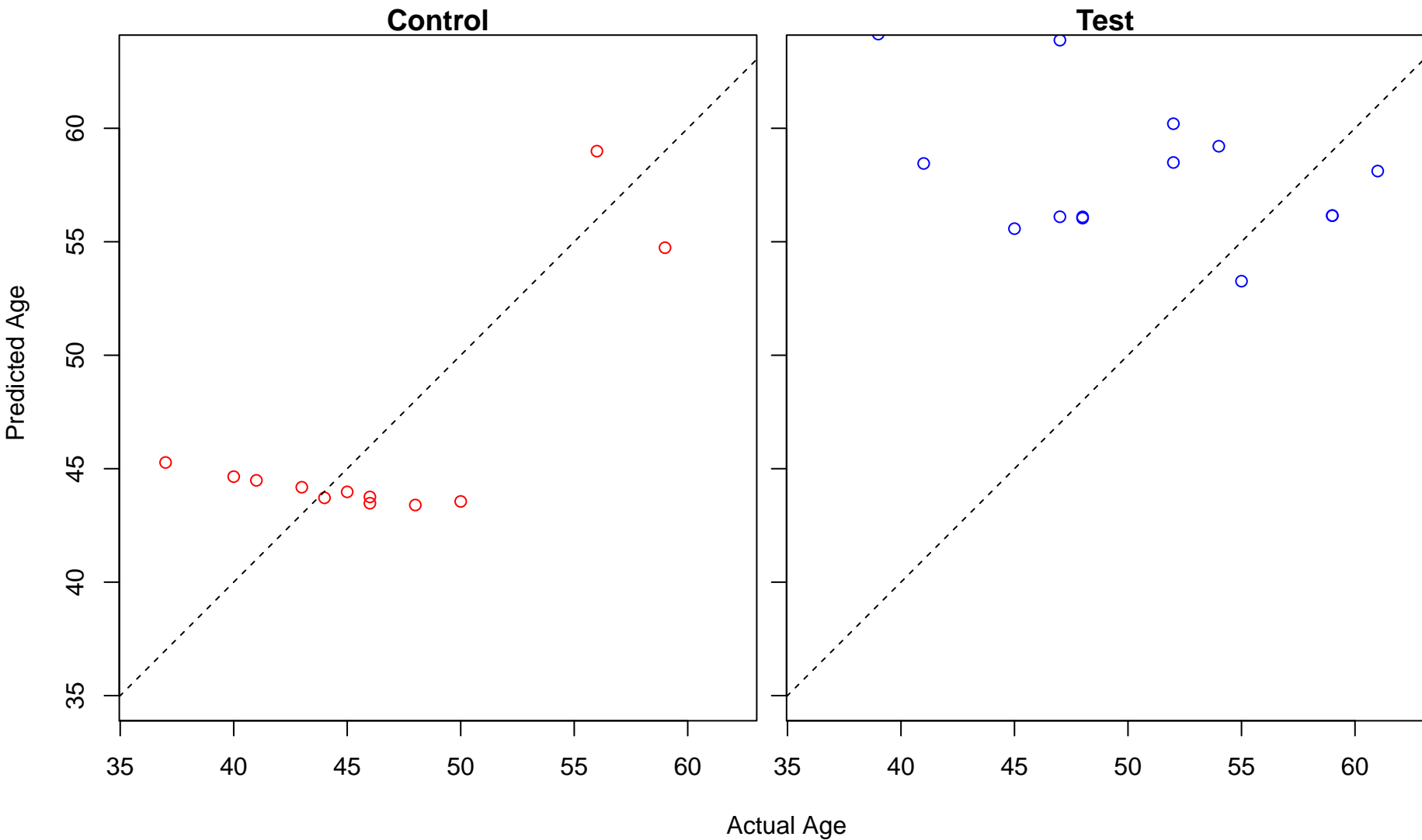
regulation of myeloid leukocyte differentiation (Score: 2.587551)



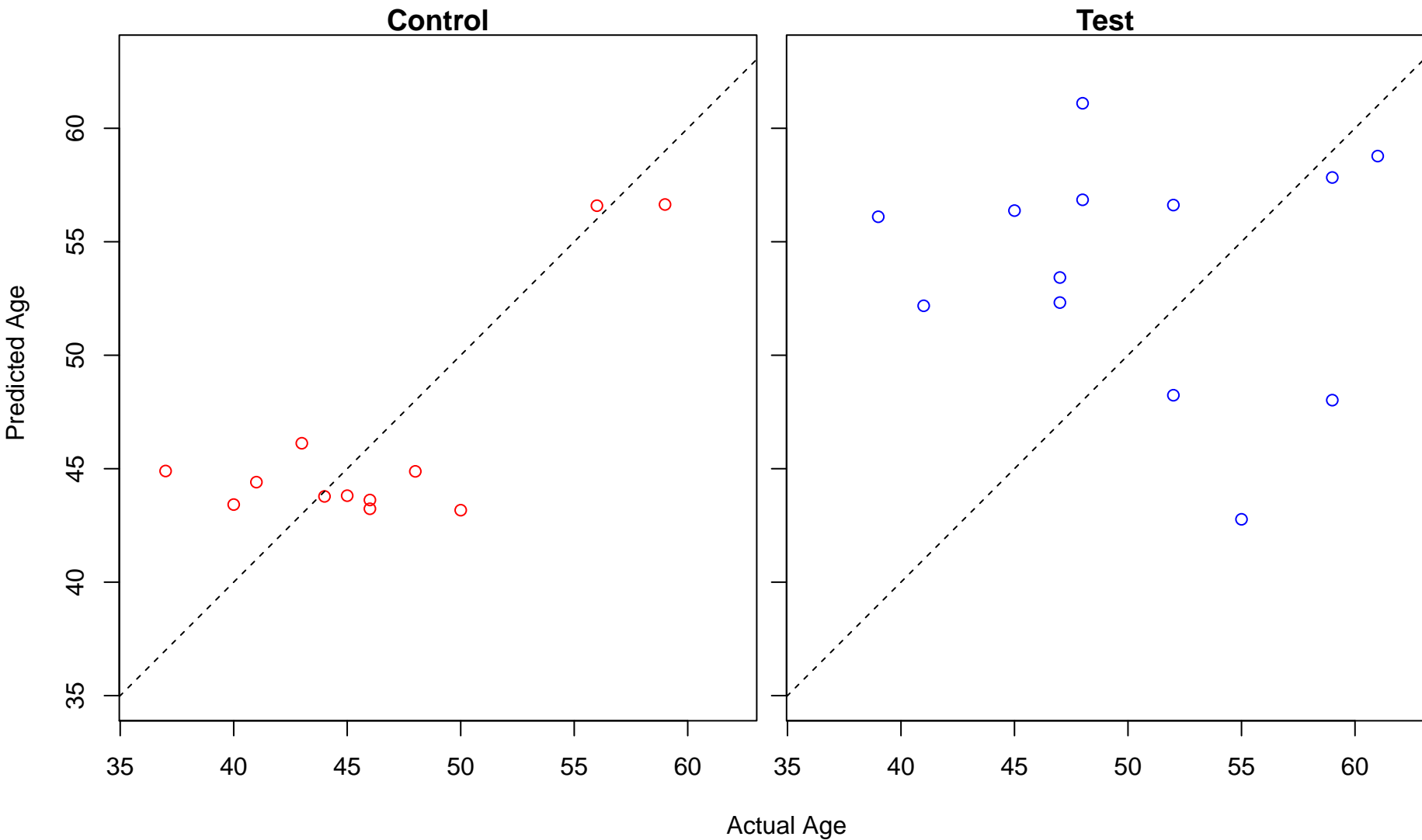
regulation of lipase activity (Score: 2.587222)



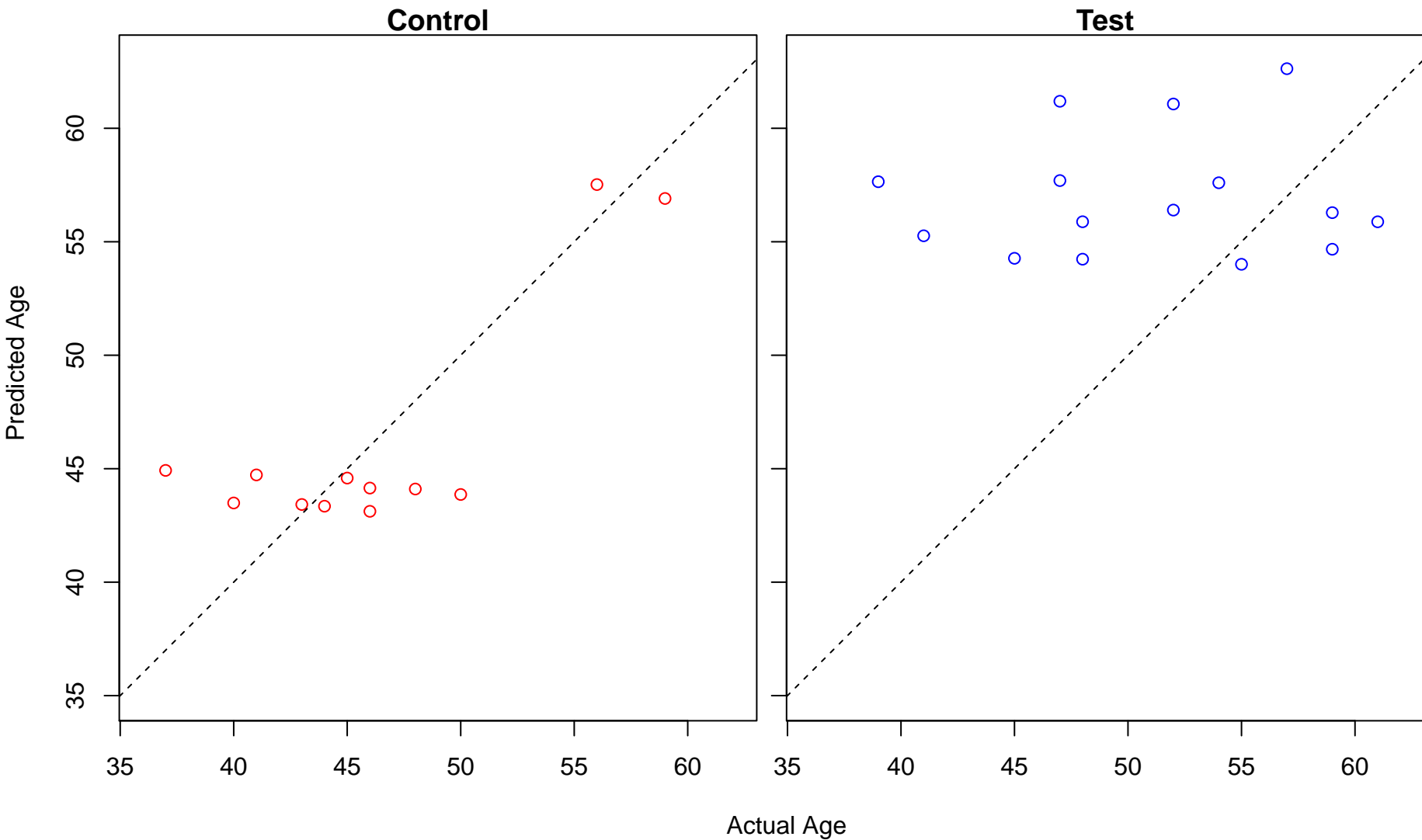
regulation of cellular amide metabolic process (Score: 2.586295)



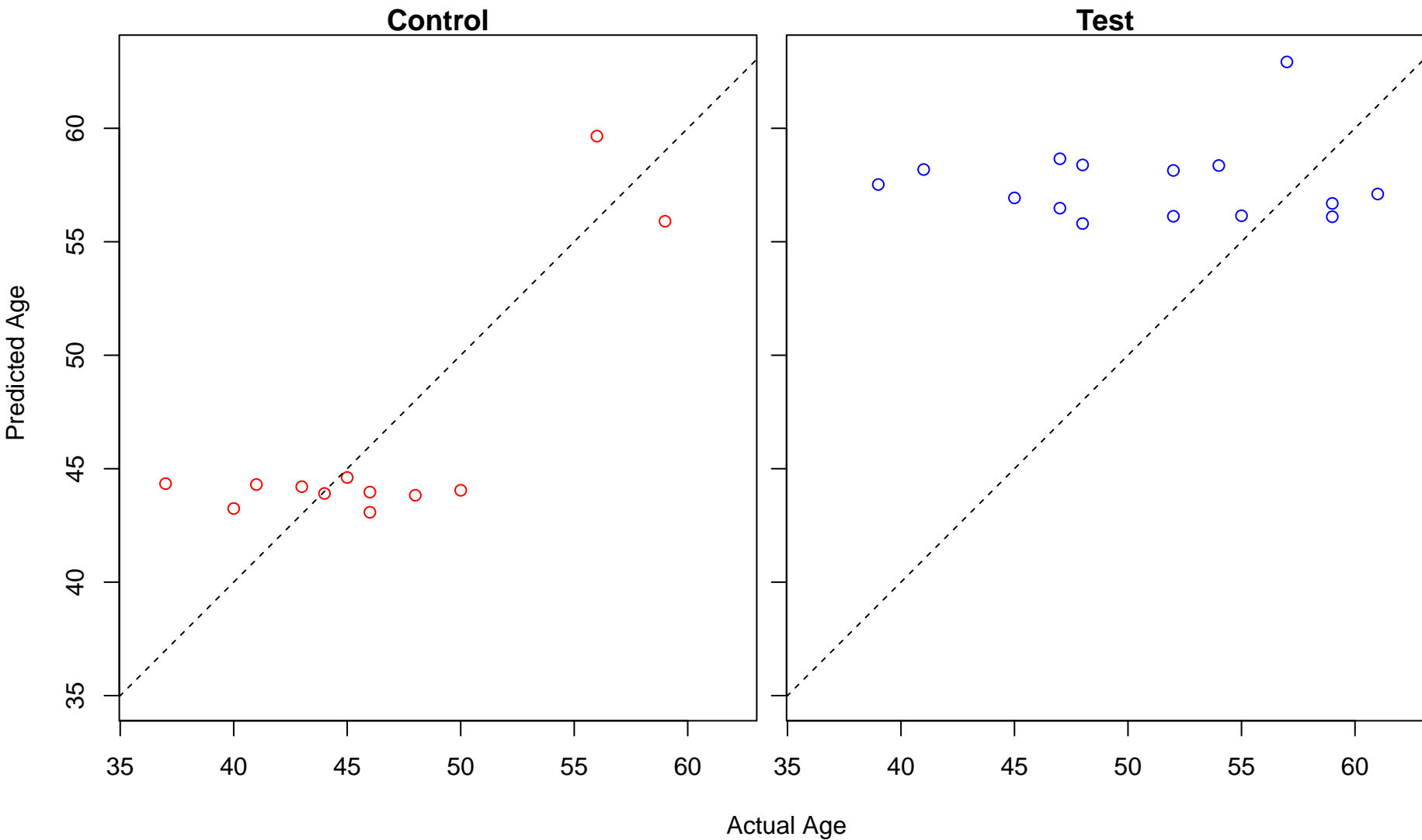
negative regulation of endopeptidase activity (Score: 2.580495)



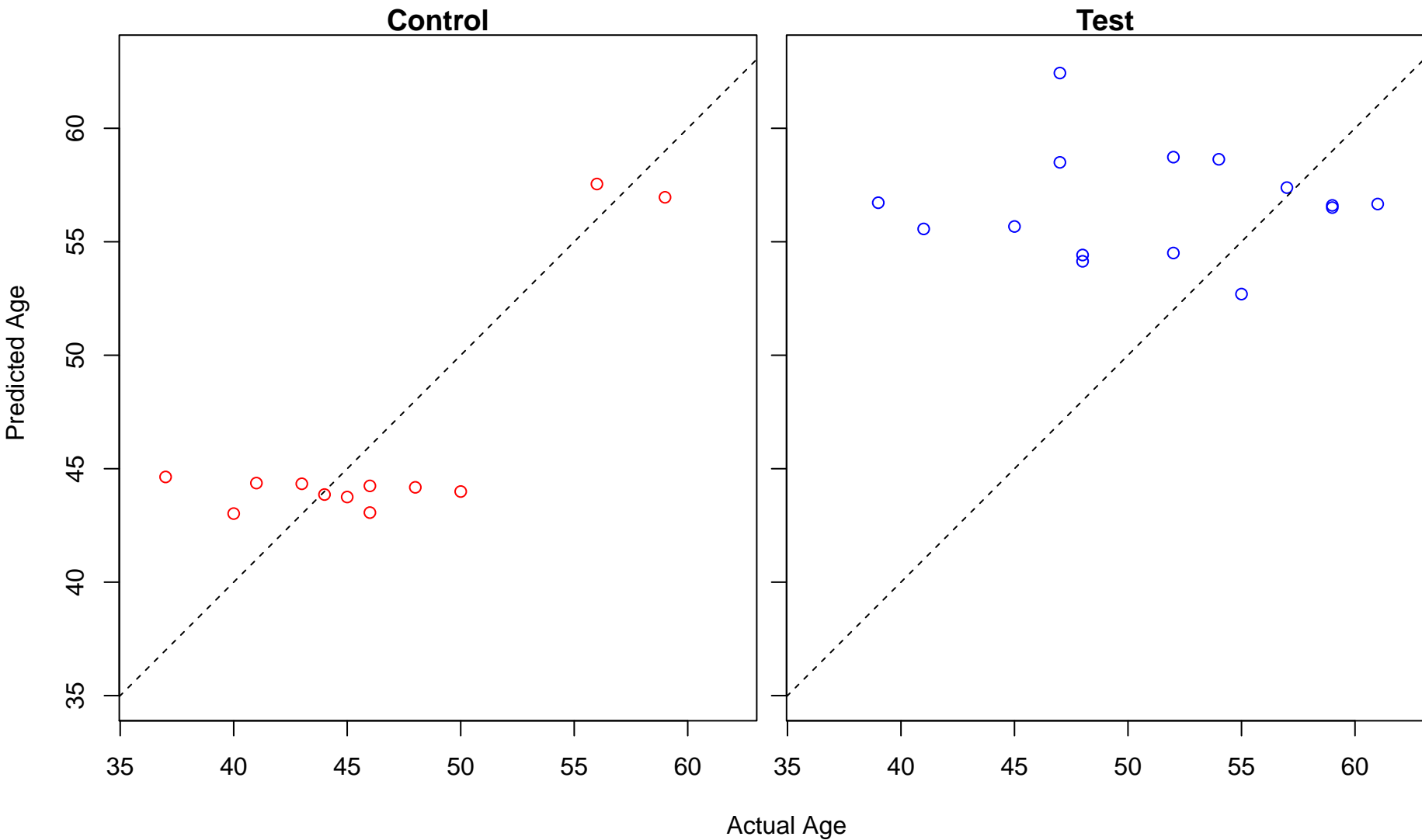
regulation of cell projection assembly (Score: 2.578928)



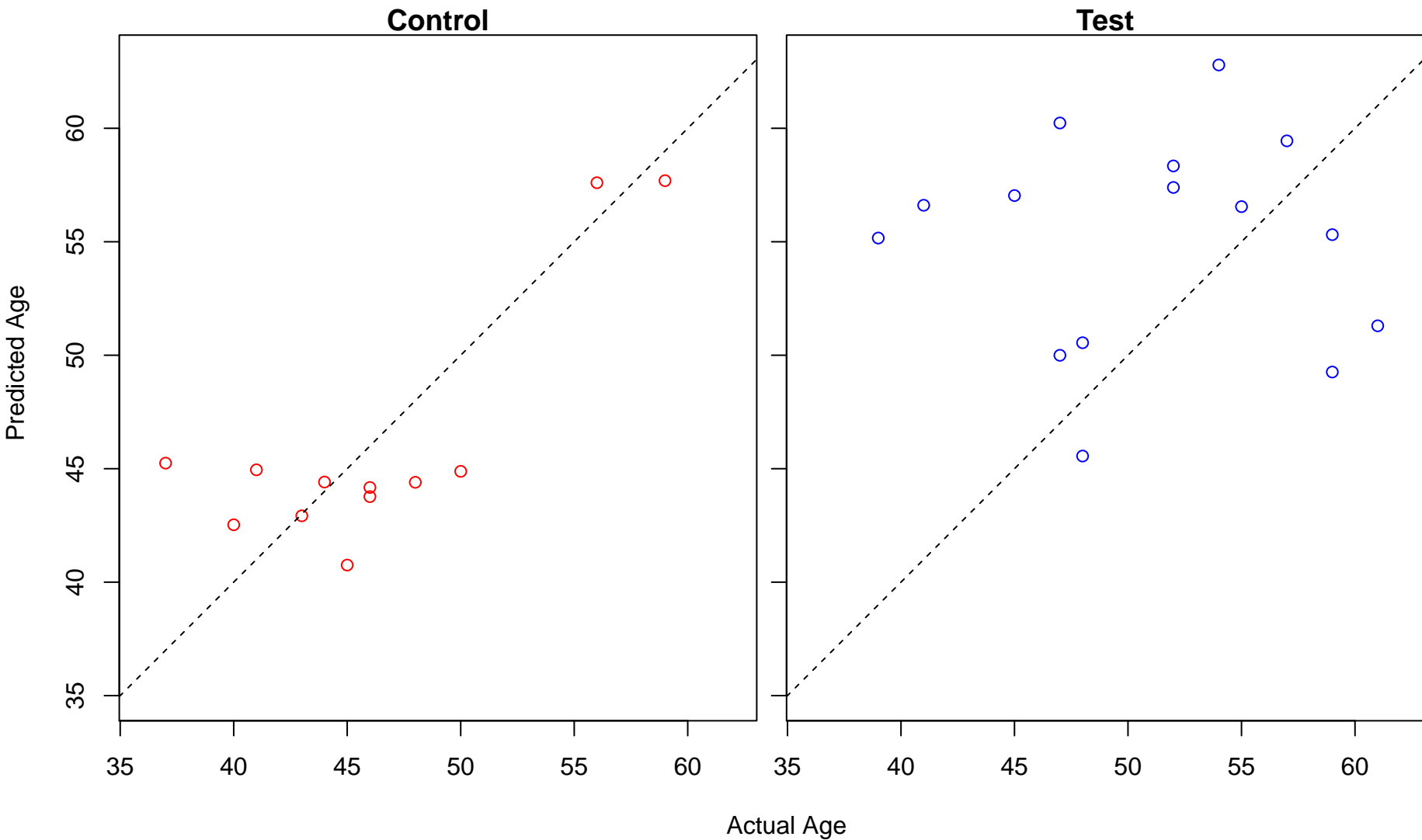
microtubule cytoskeleton organization (Score: 2.577037)



protein localization to cell surface (Score: 2.574232)

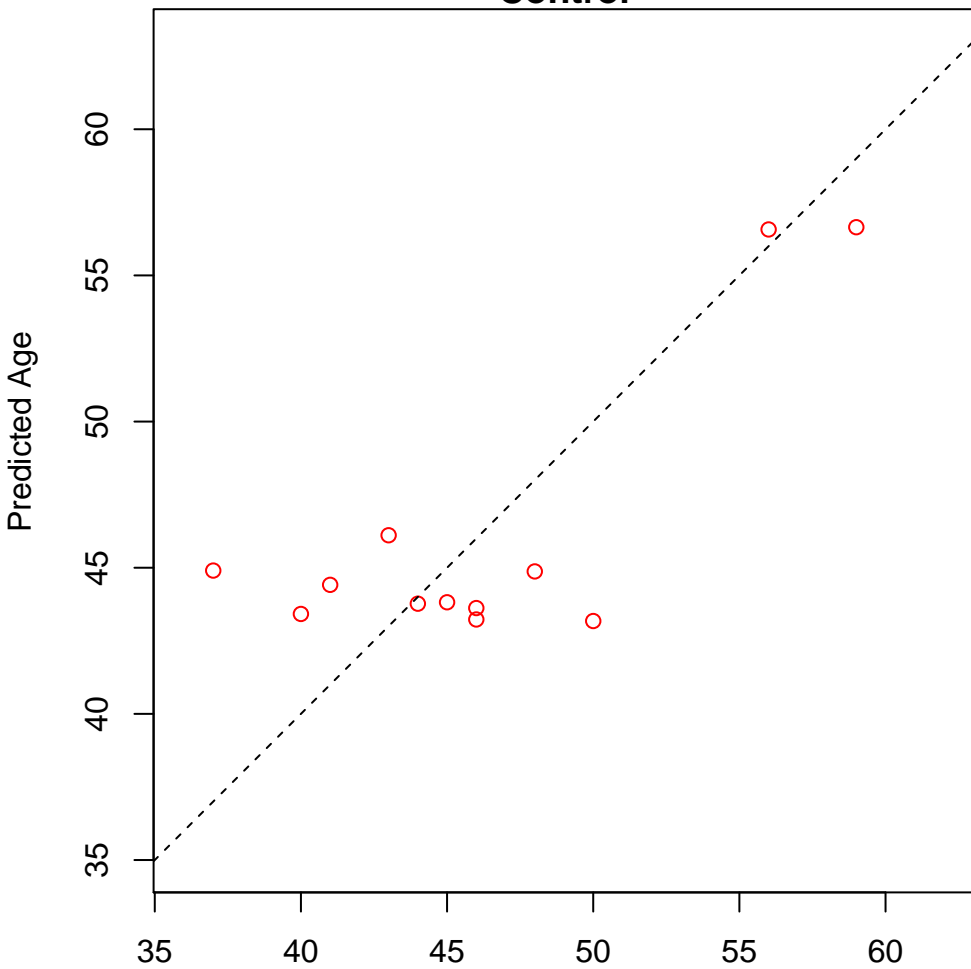


oxidative demethylation (Score: 2.573686)

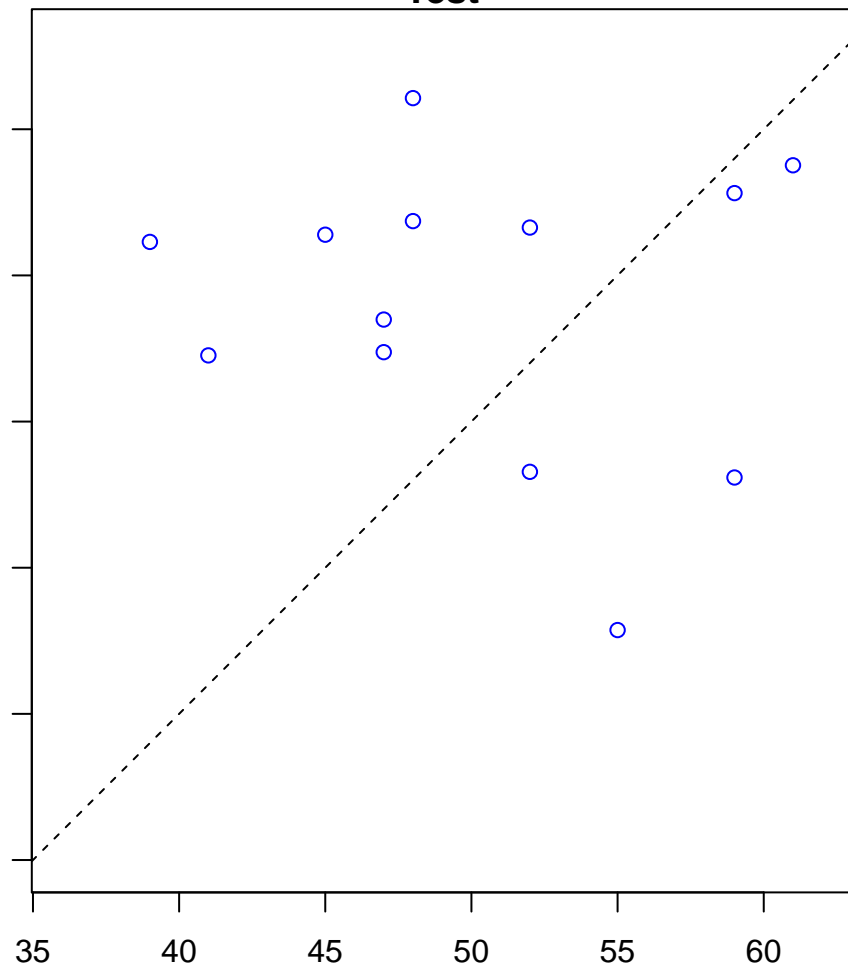


negative regulation of peptidase activity (Score: 2.572973)

Control

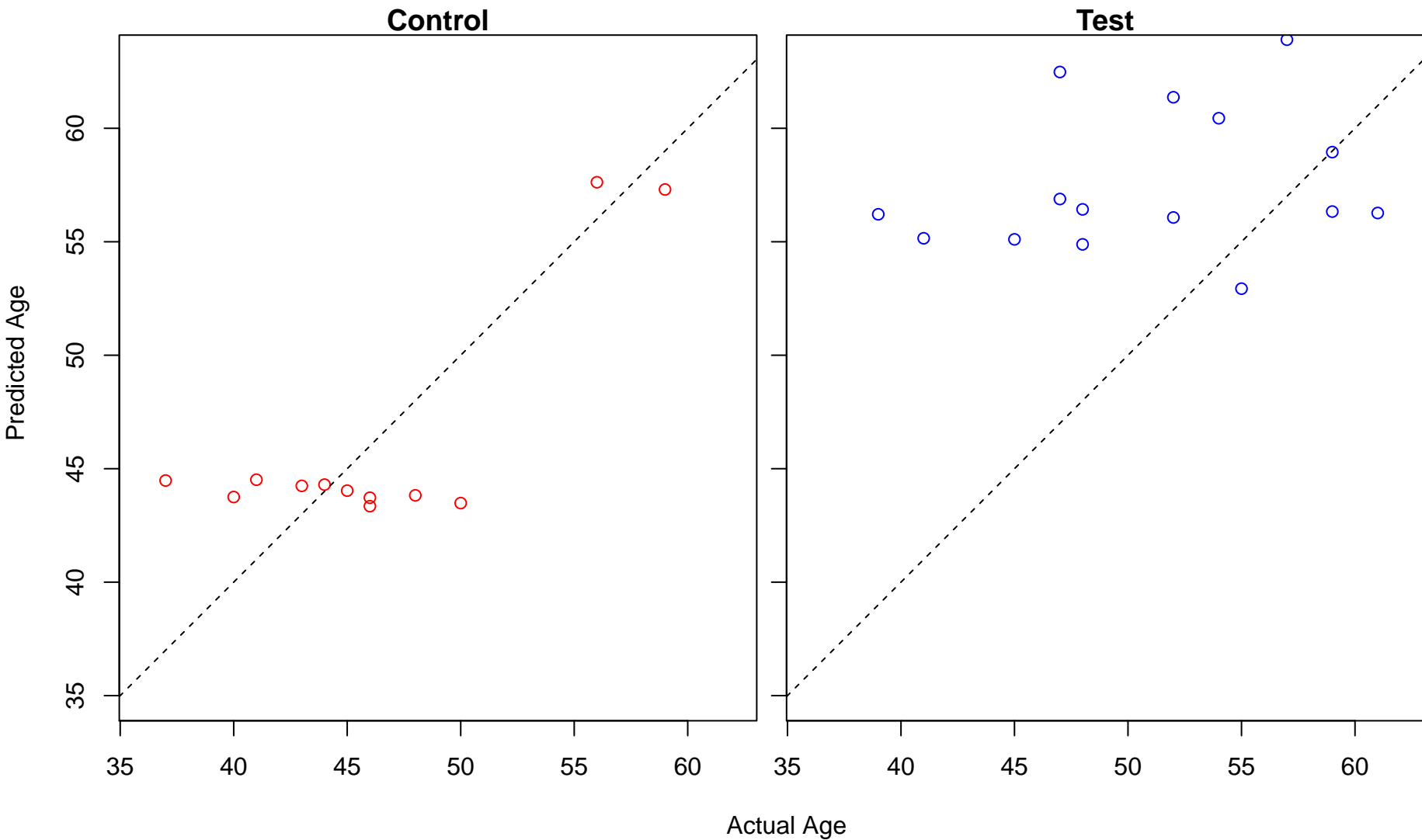


Test



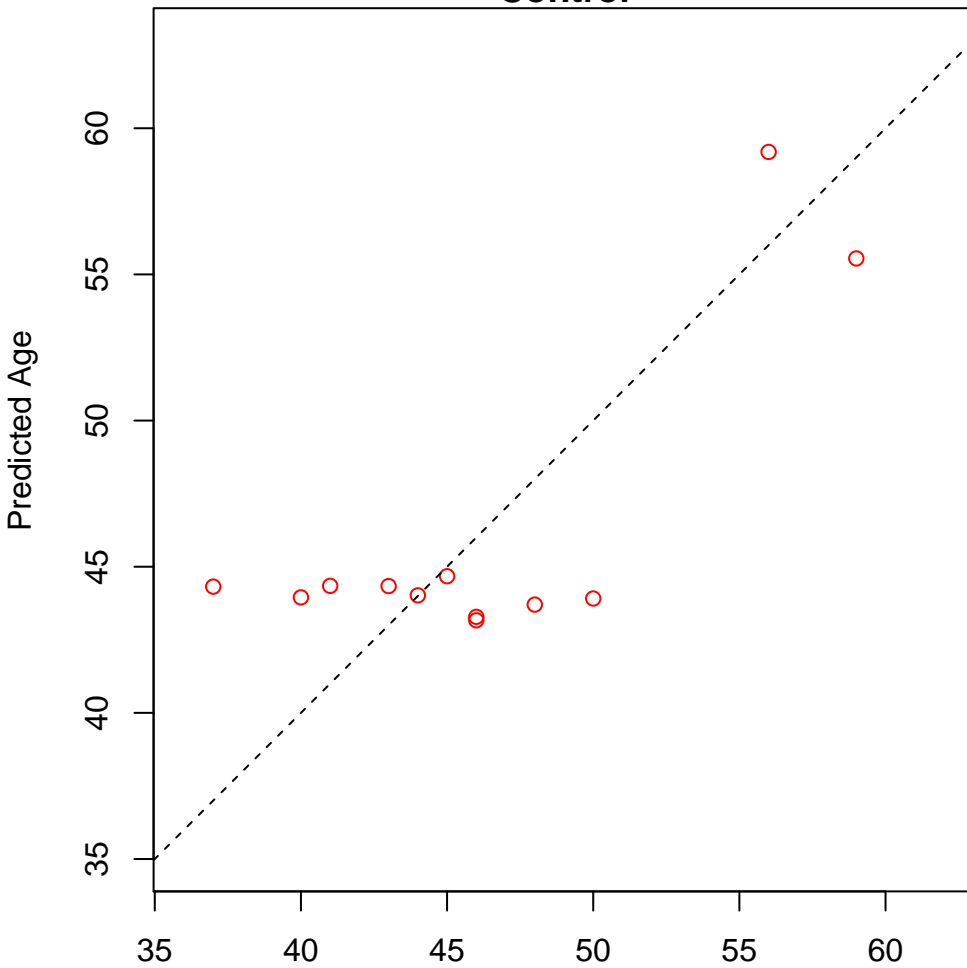
Actual Age

negative regulation of intracellular protein transport (Score: 2.571111)

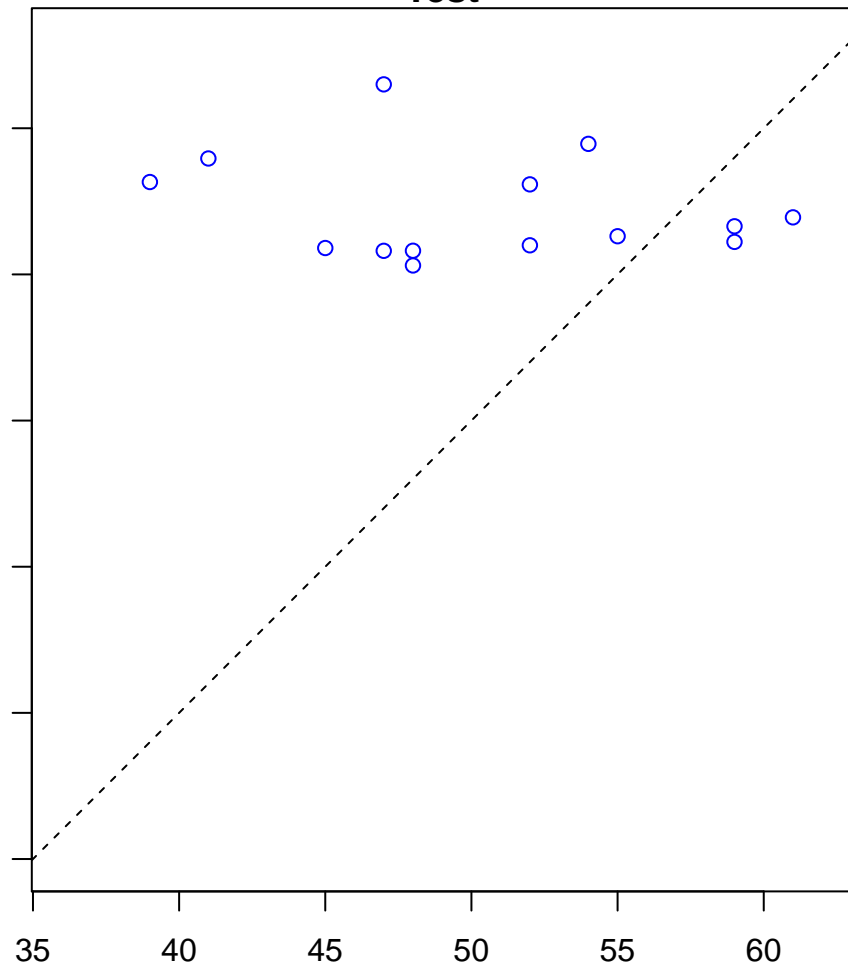


nucleoside phosphate metabolic process (Score: 2.570427)

Control

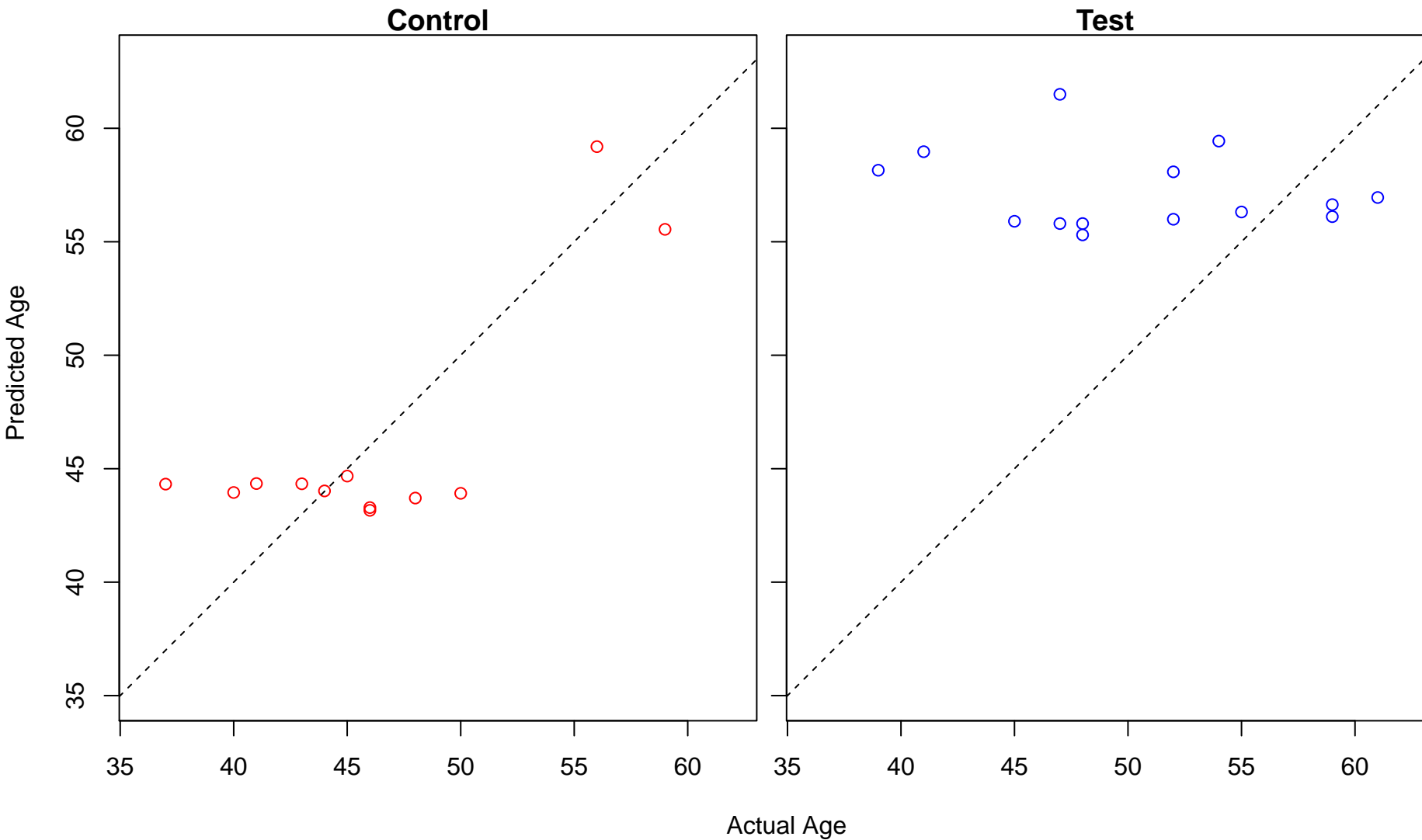


Test

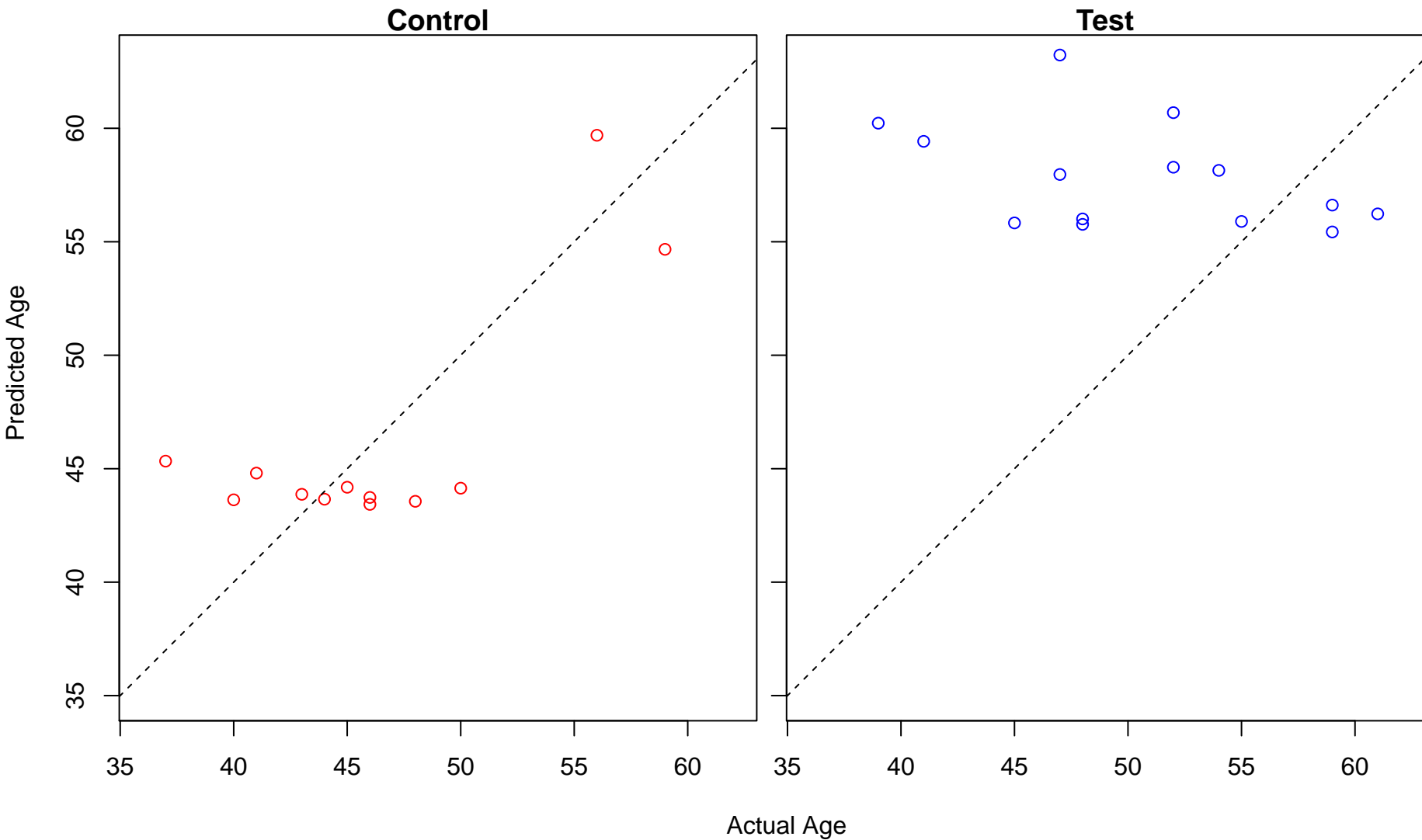


Actual Age

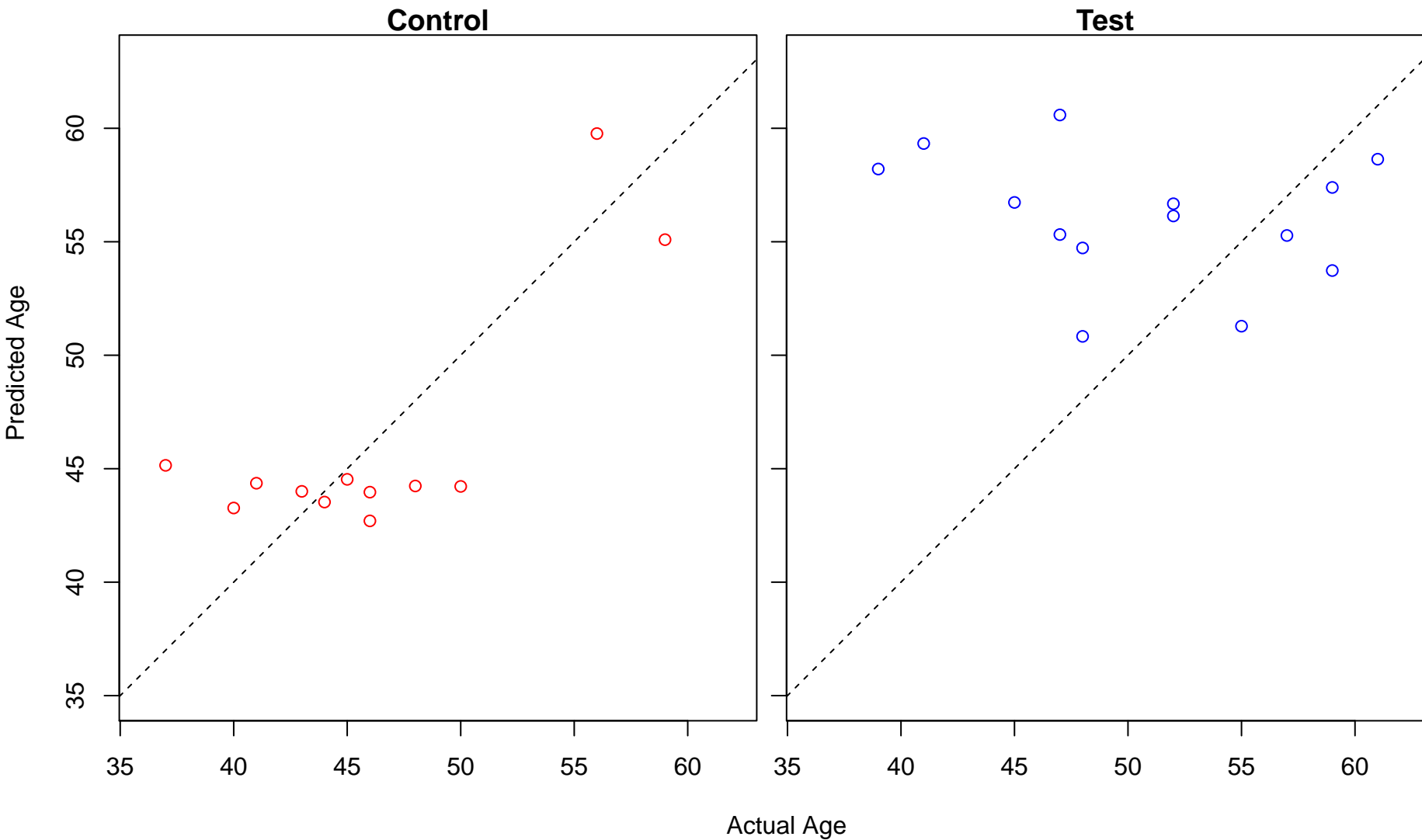
nucleotide metabolic process (Score: 2.569652)



positive regulation of cellular component movement (Score: 2.569357)

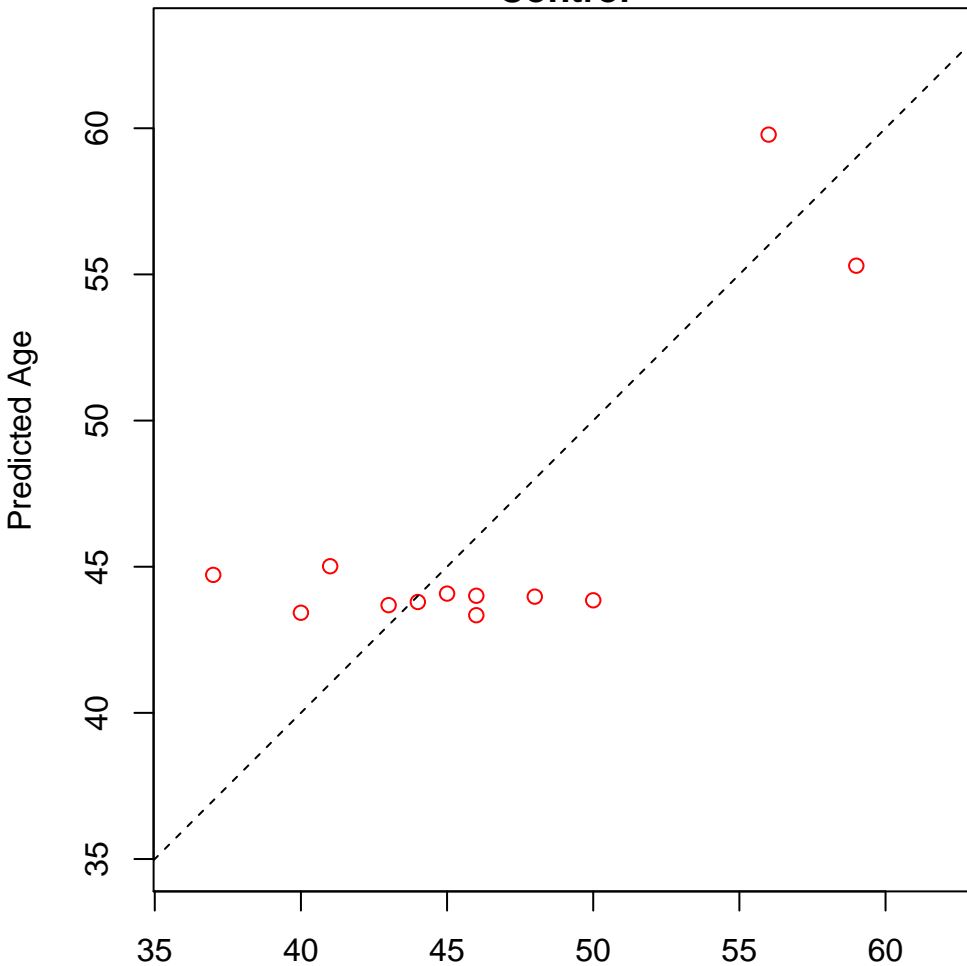


hemidesmosome assembly (Score: 2.568261)

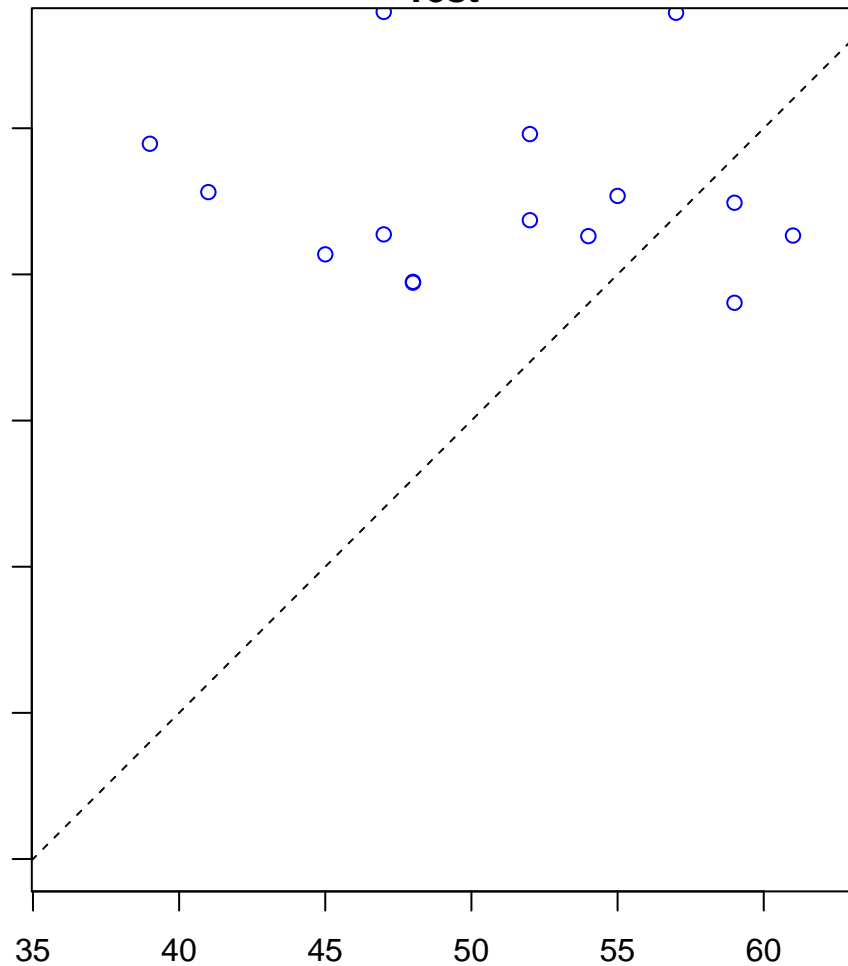


cardiovascular system development (Score: 2.567036)

Control

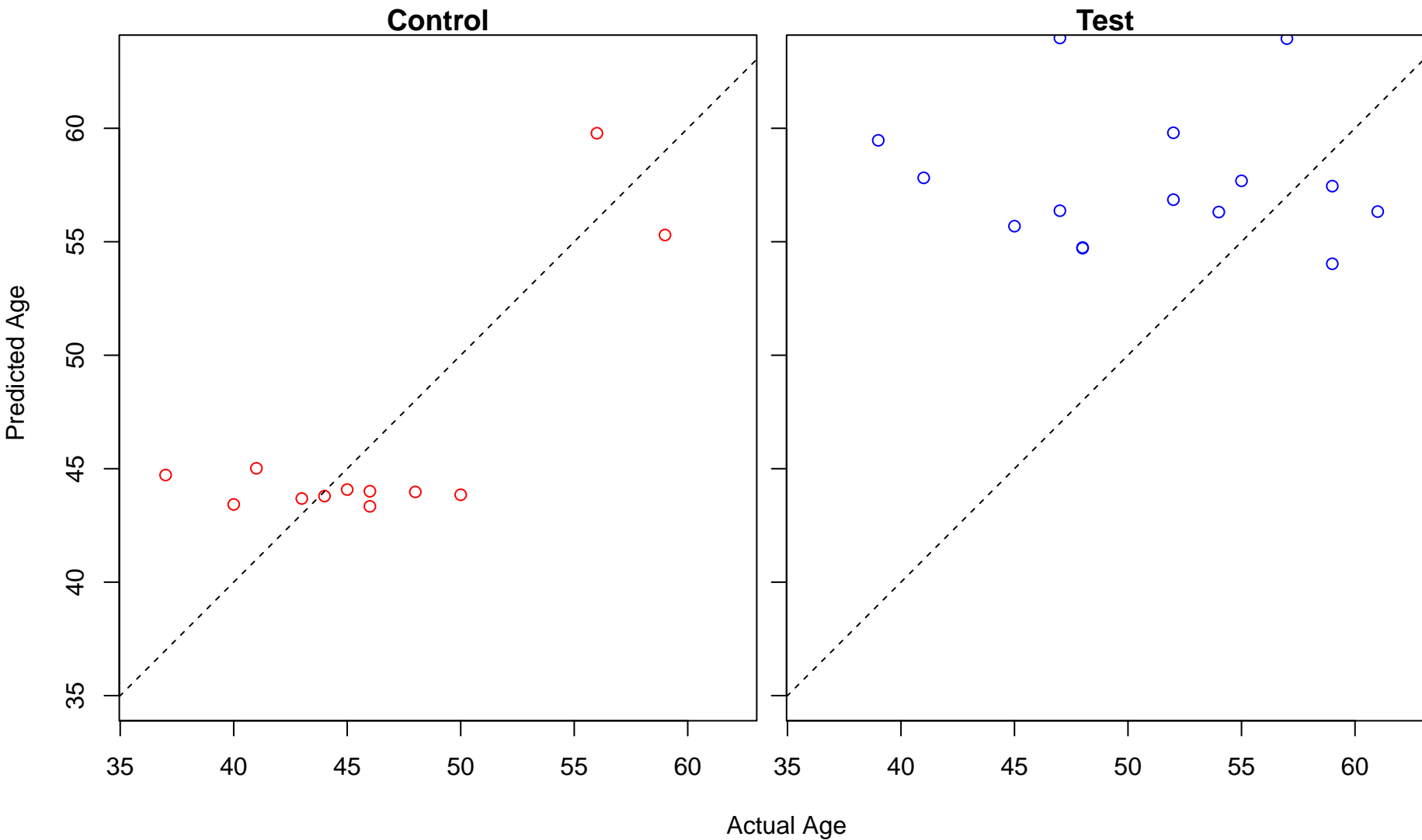


Test

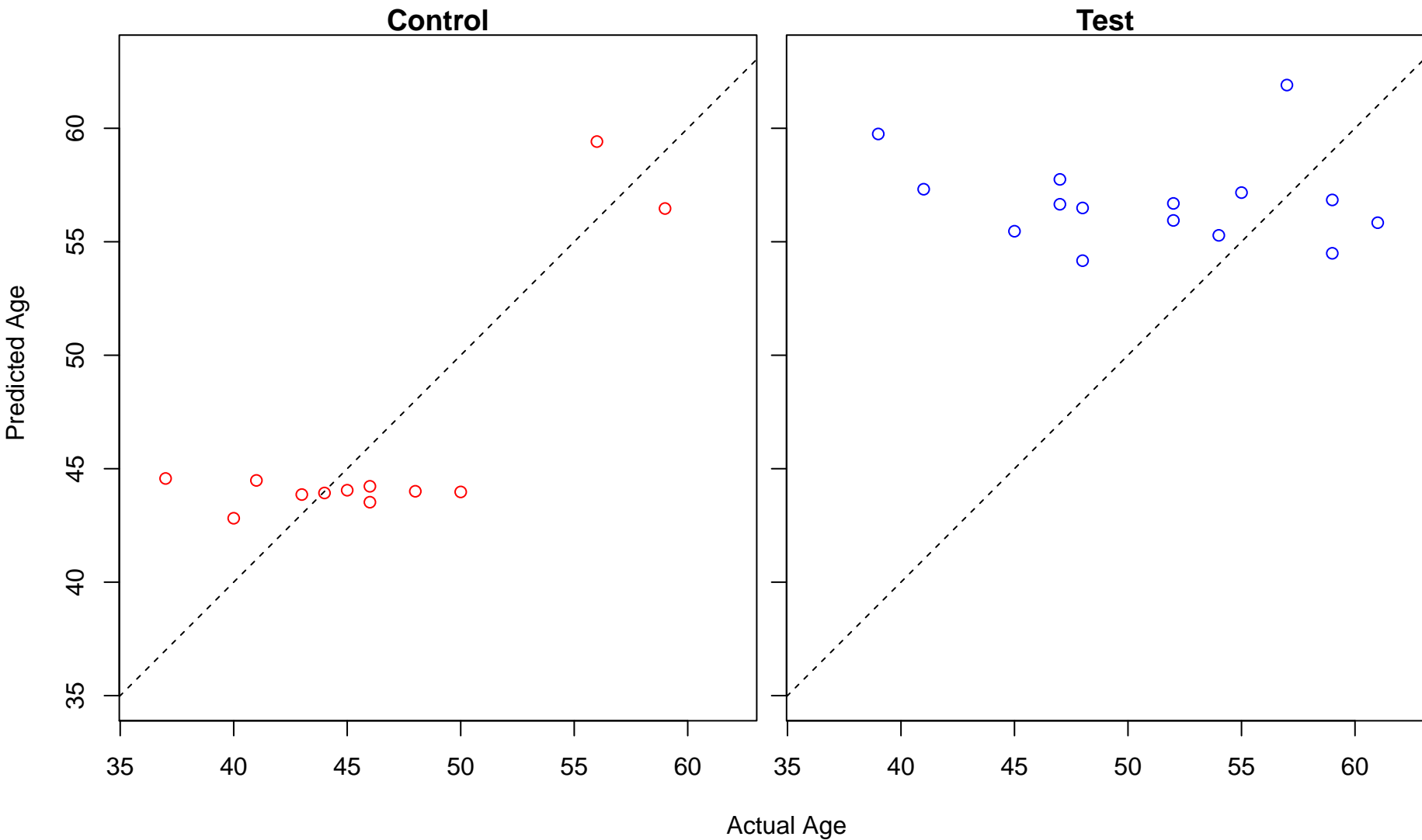


Actual Age

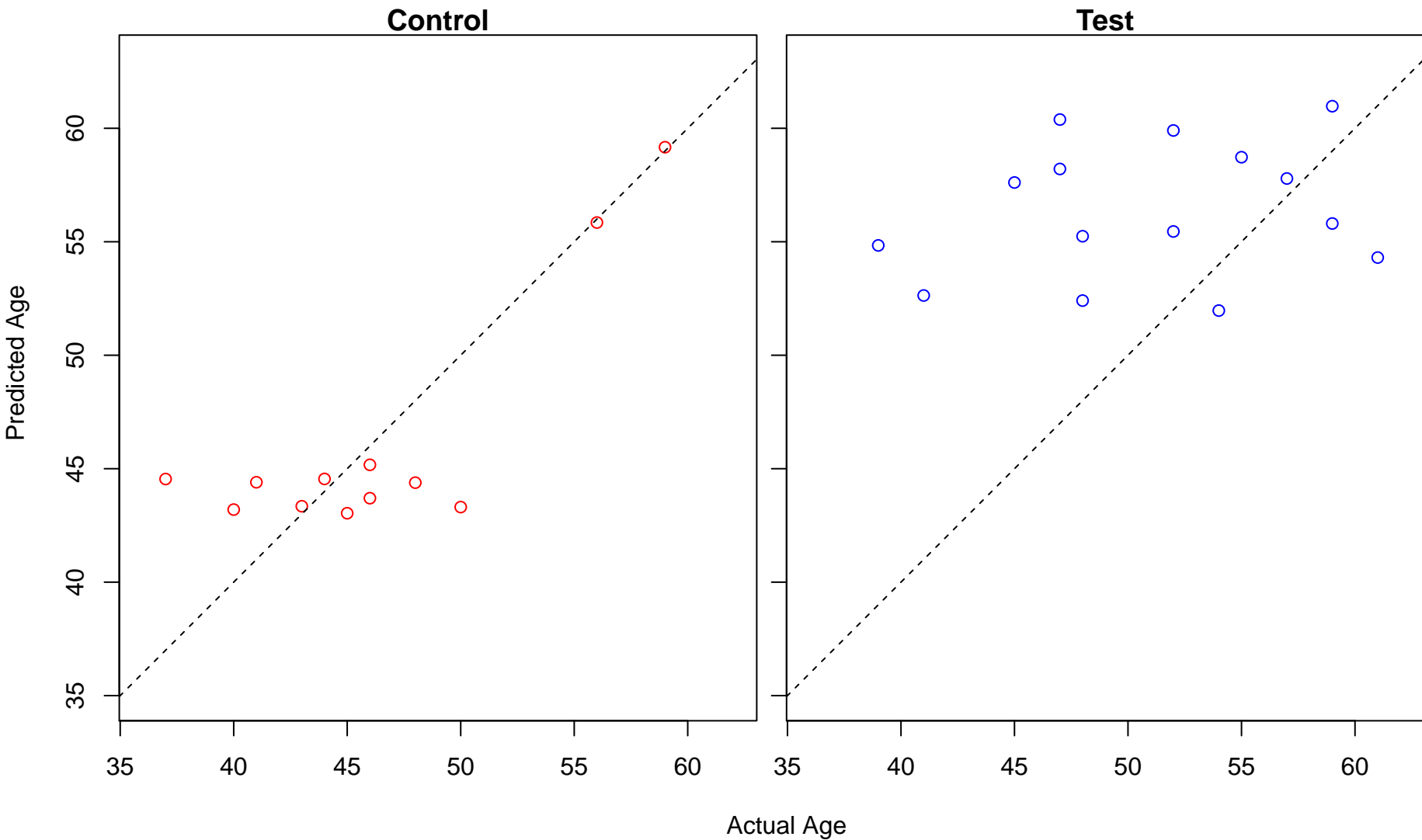
circulatory system development (Score: 2.567036)



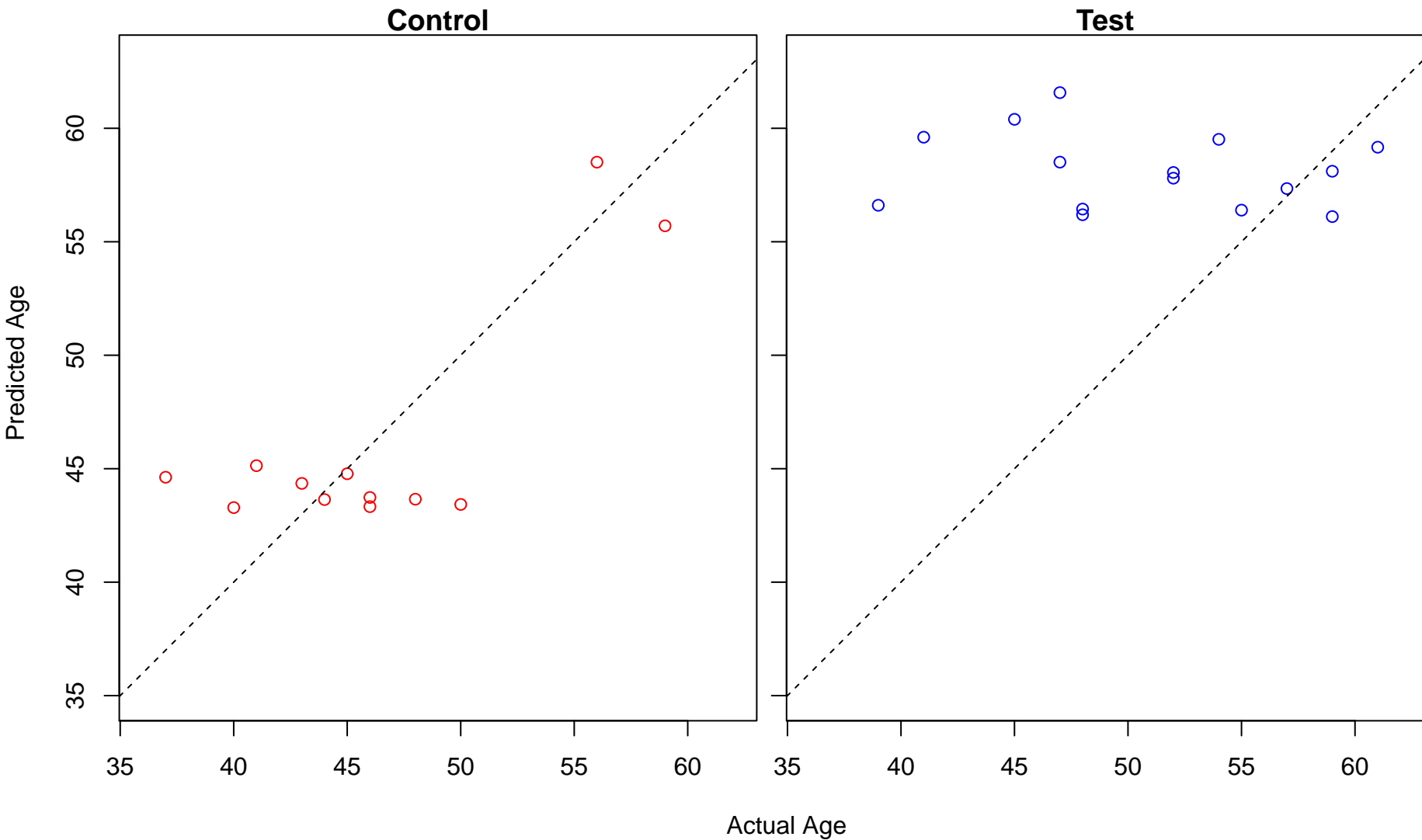
regulation of phospholipase activity (Score: 2.566919)



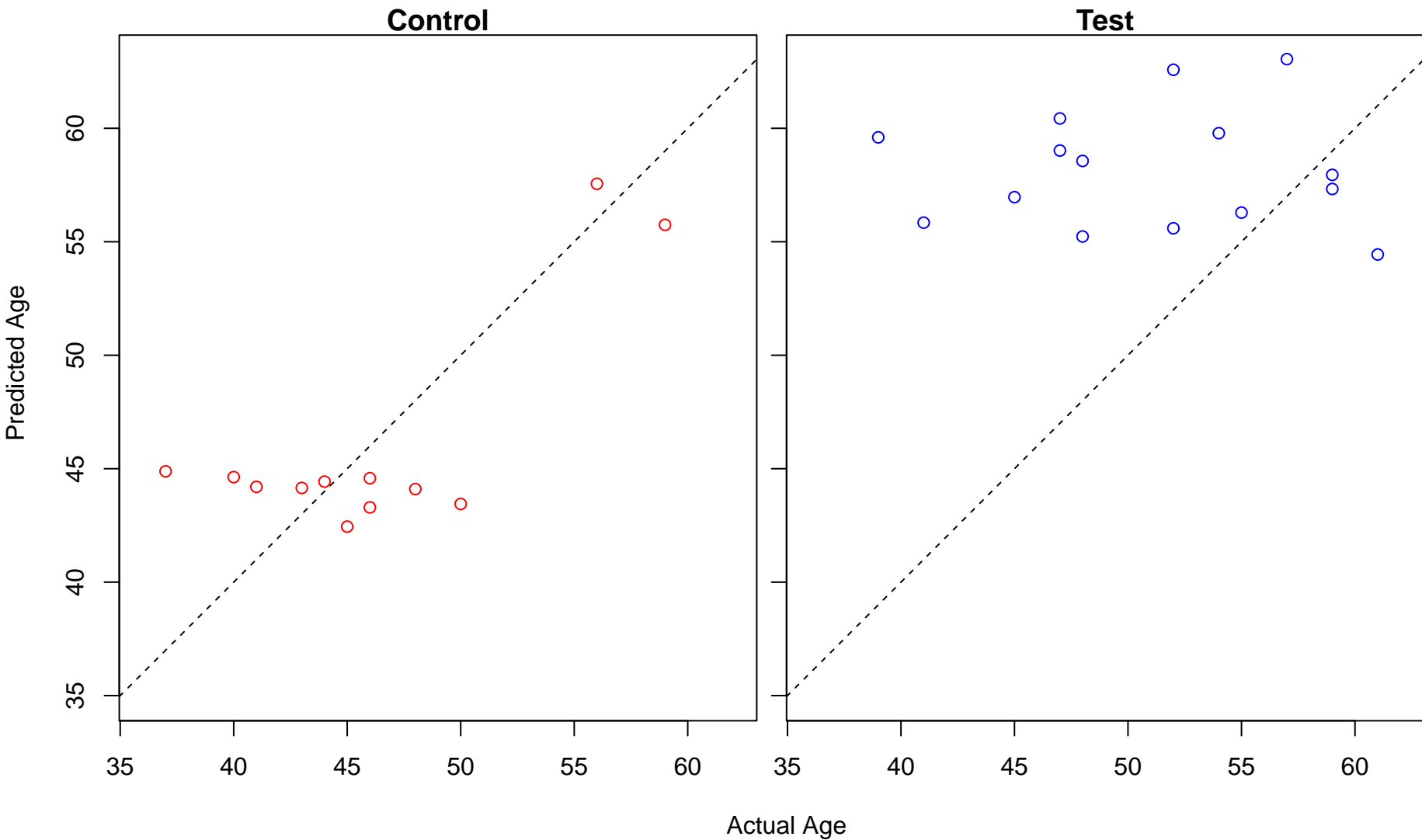
snRNA transcription from RNA polymerase II promoter (Score: 2.565794)



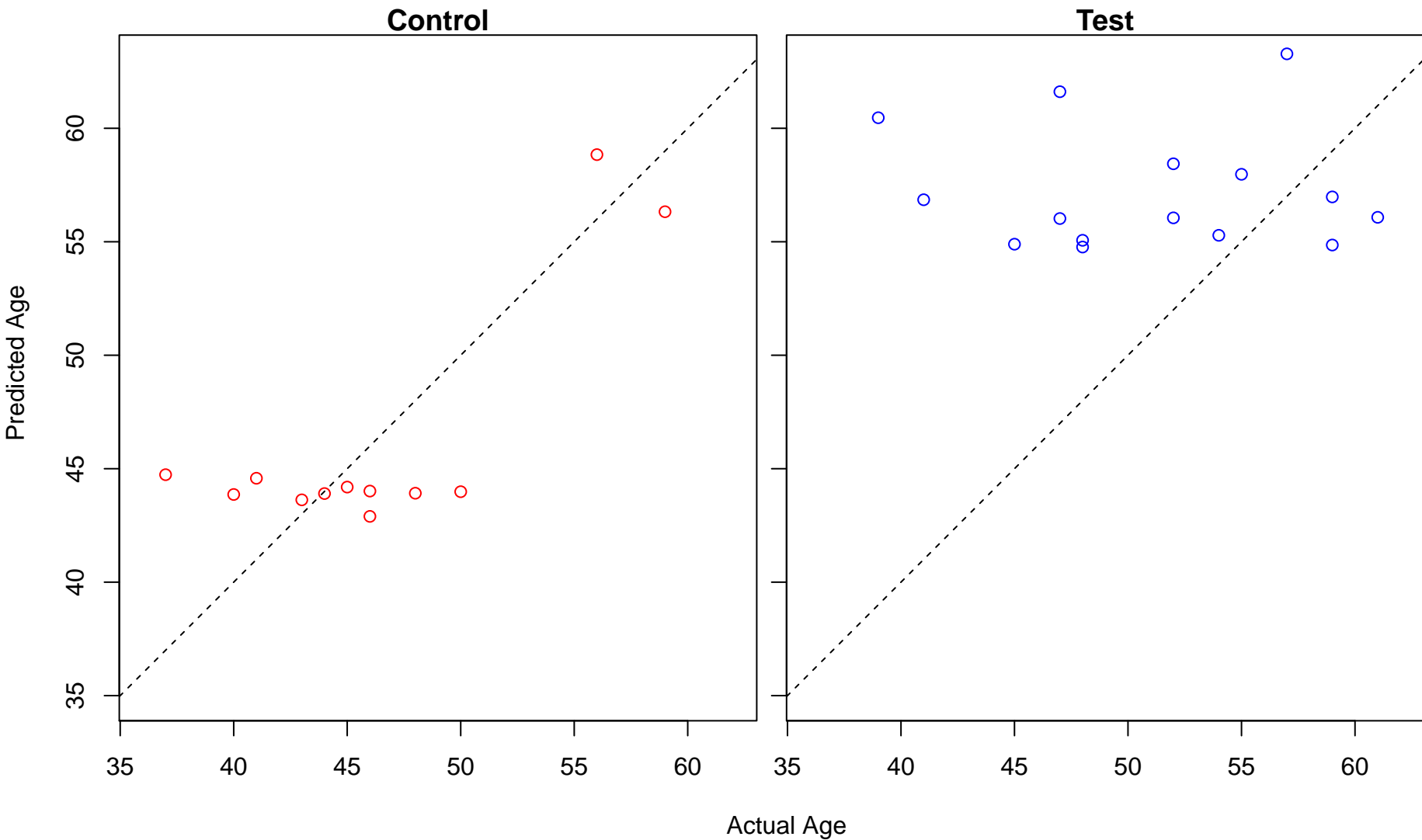
cardiac conduction (Score: 2.562422)



folic acid-containing compound metabolic process (Score: 2.559872)

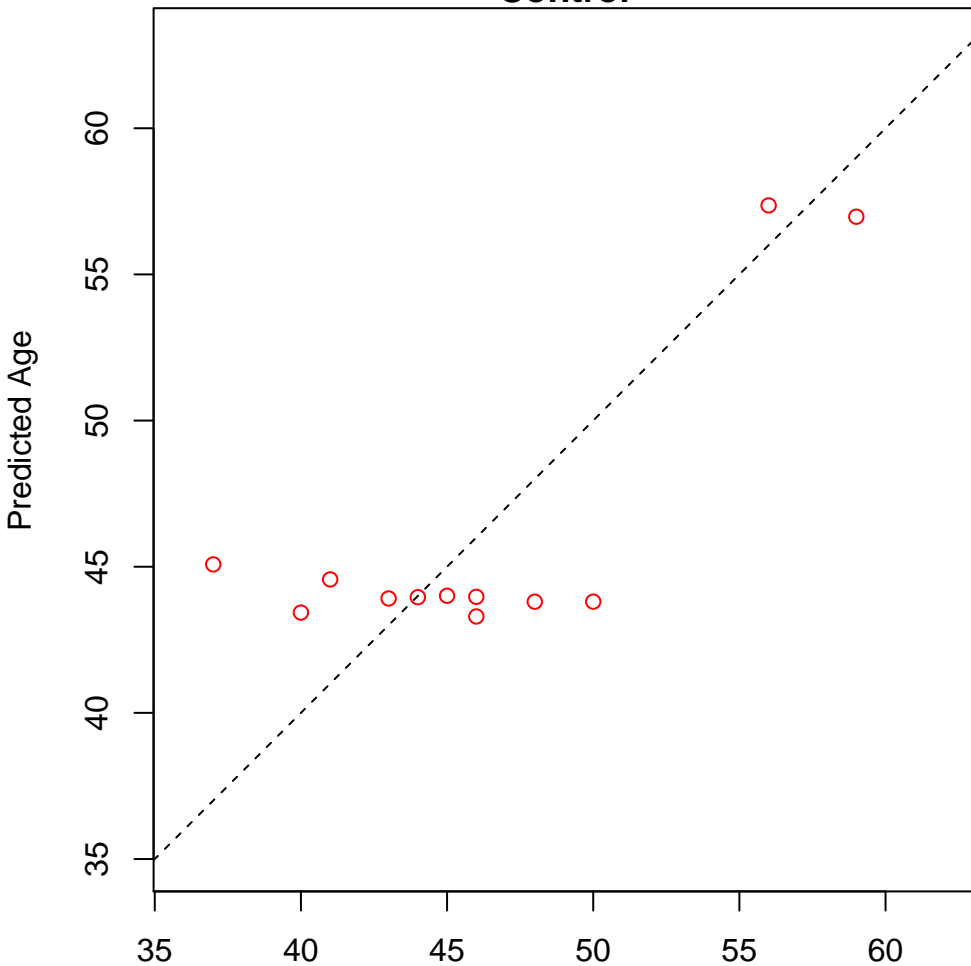


mRNA processing (Score: 2.553568)

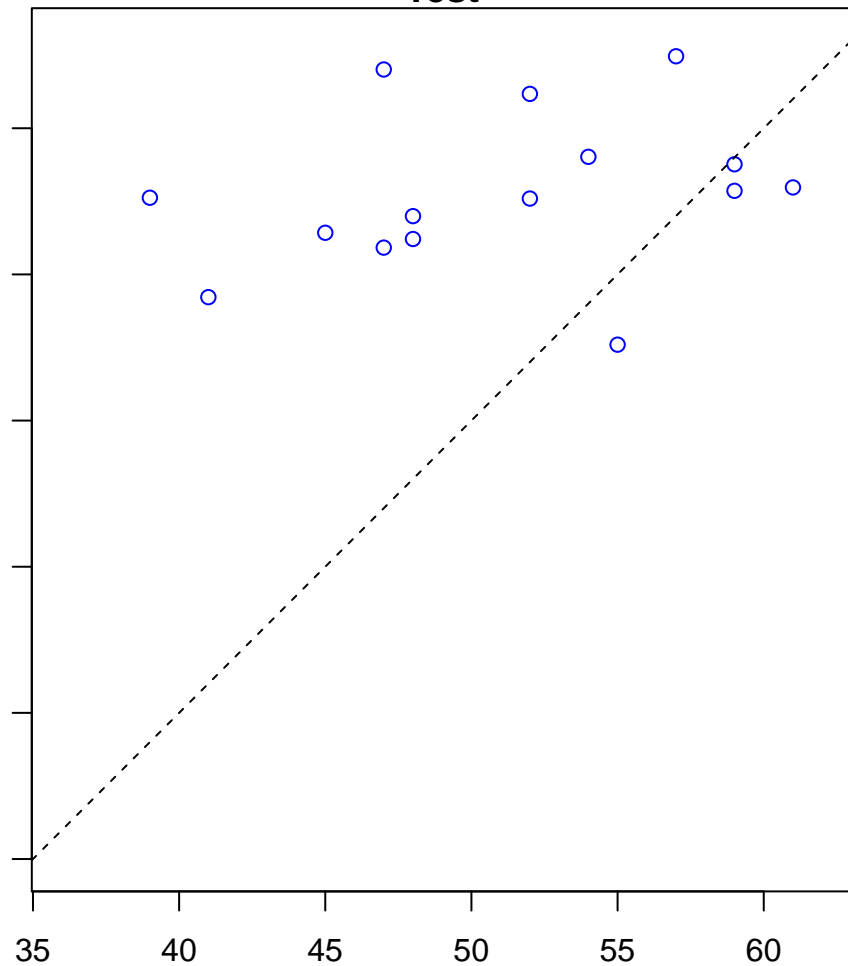


regulation of epithelial cell proliferation (Score: 2.552916)

Control

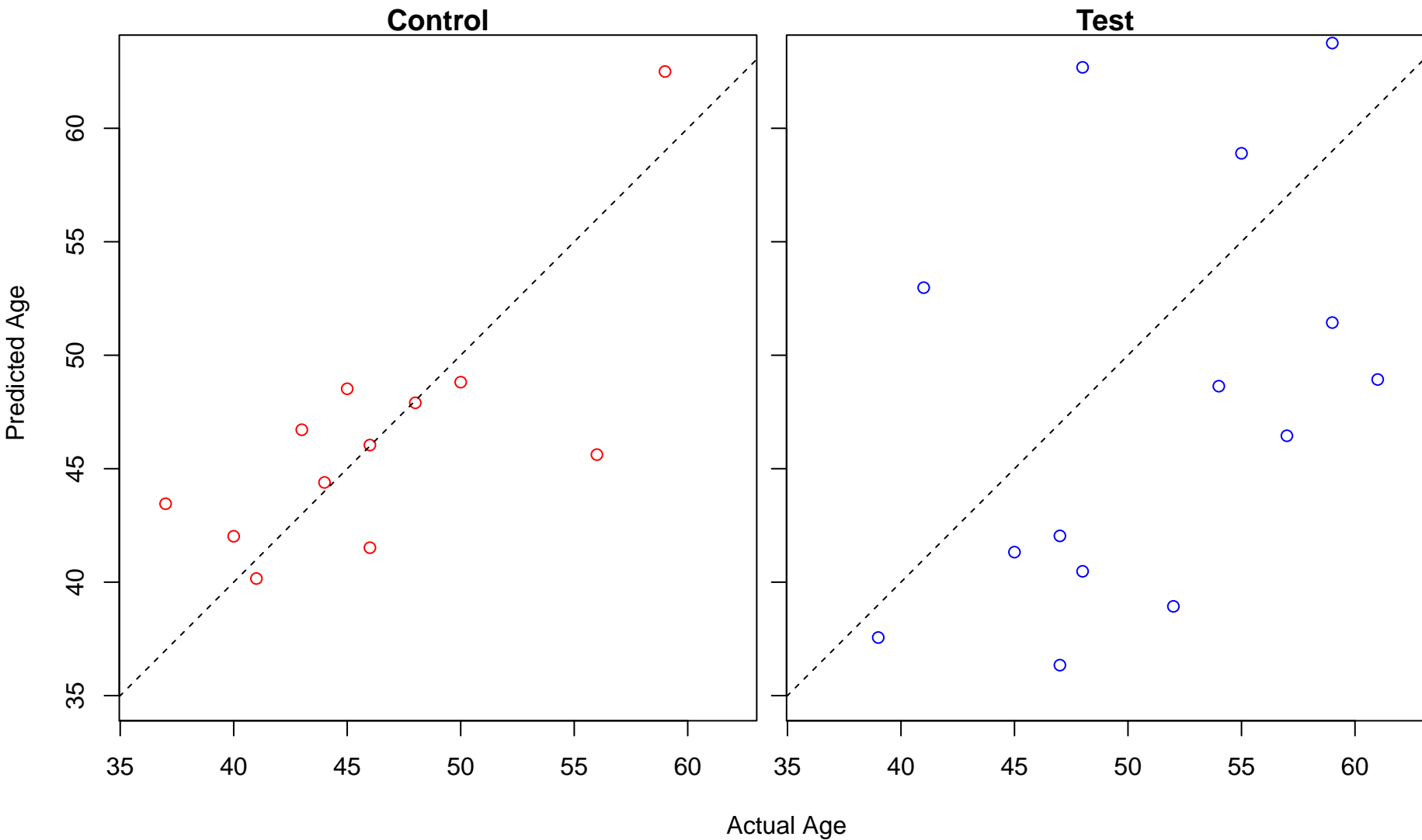


Test

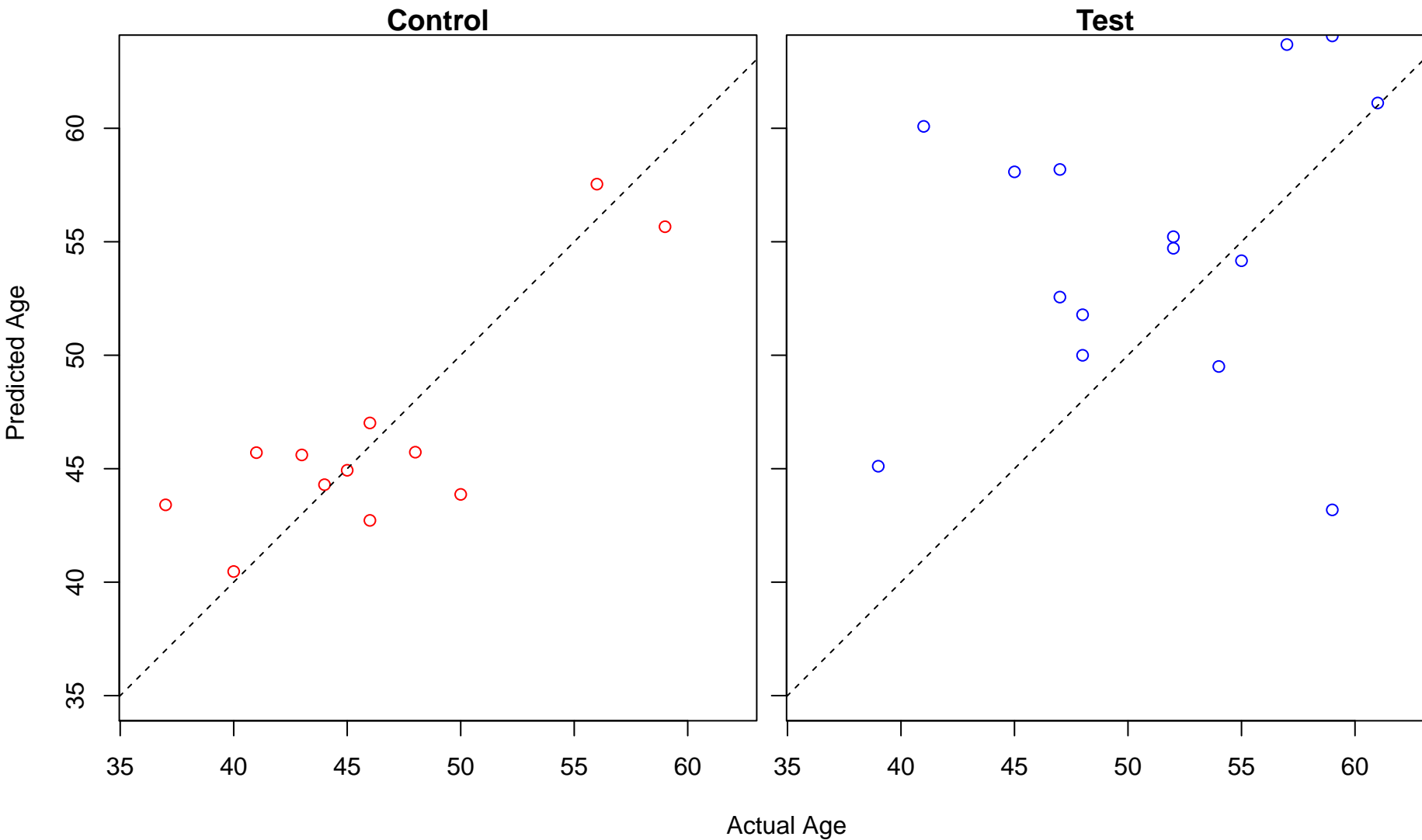


Actual Age

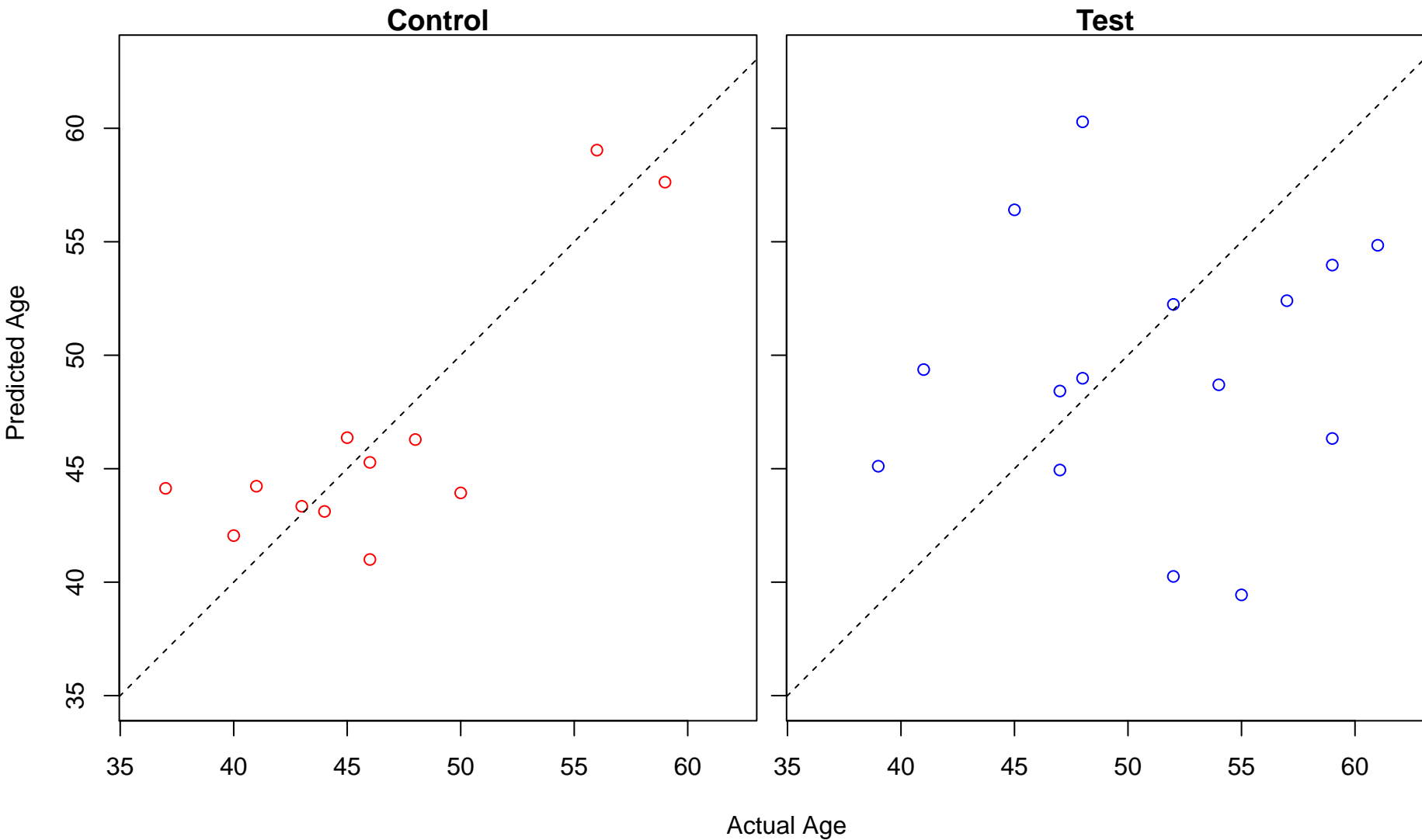
positive regulation of striated muscle cell differentiation (Score: 2.549983)



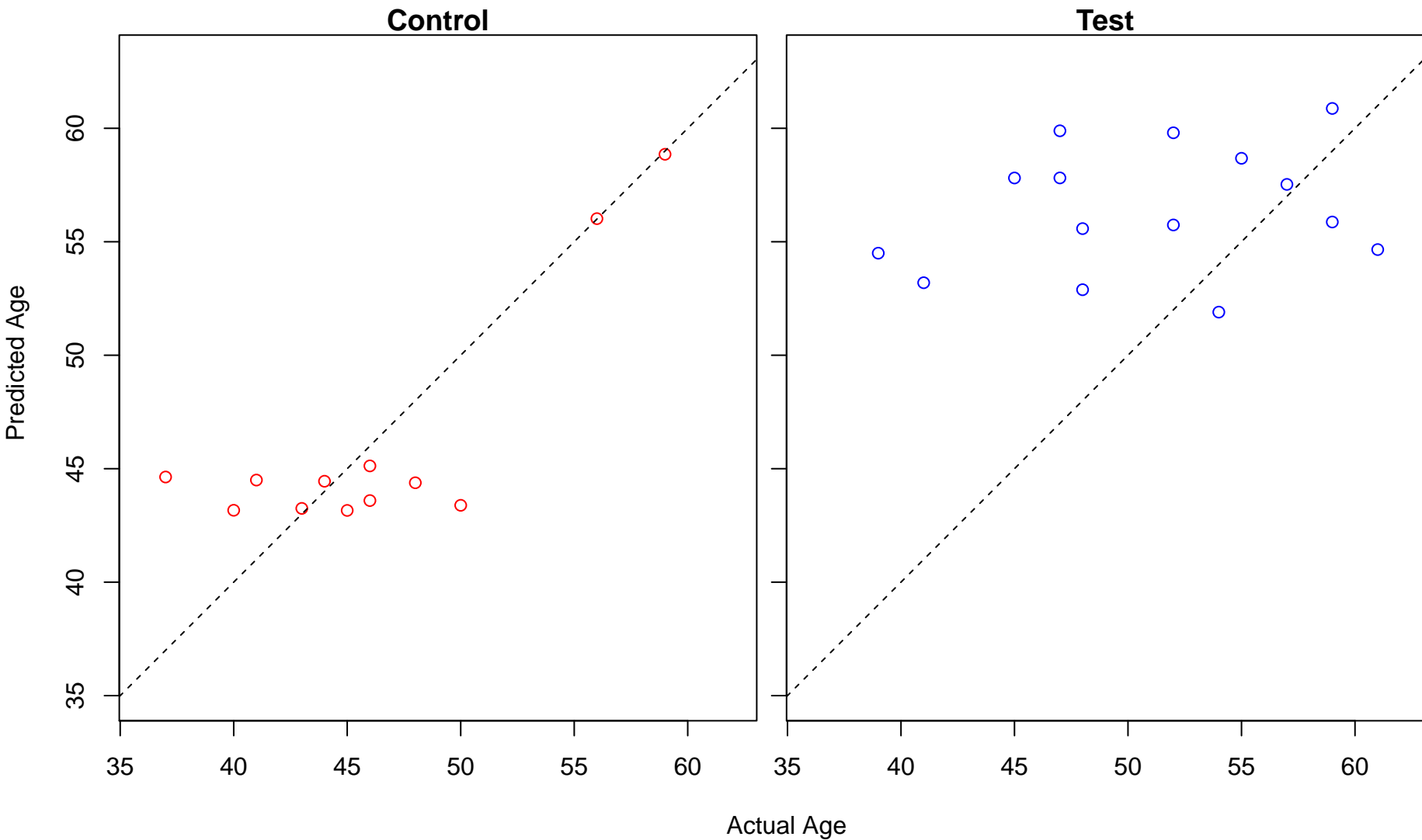
cytokine-mediated signaling pathway (Score: 2.548464)



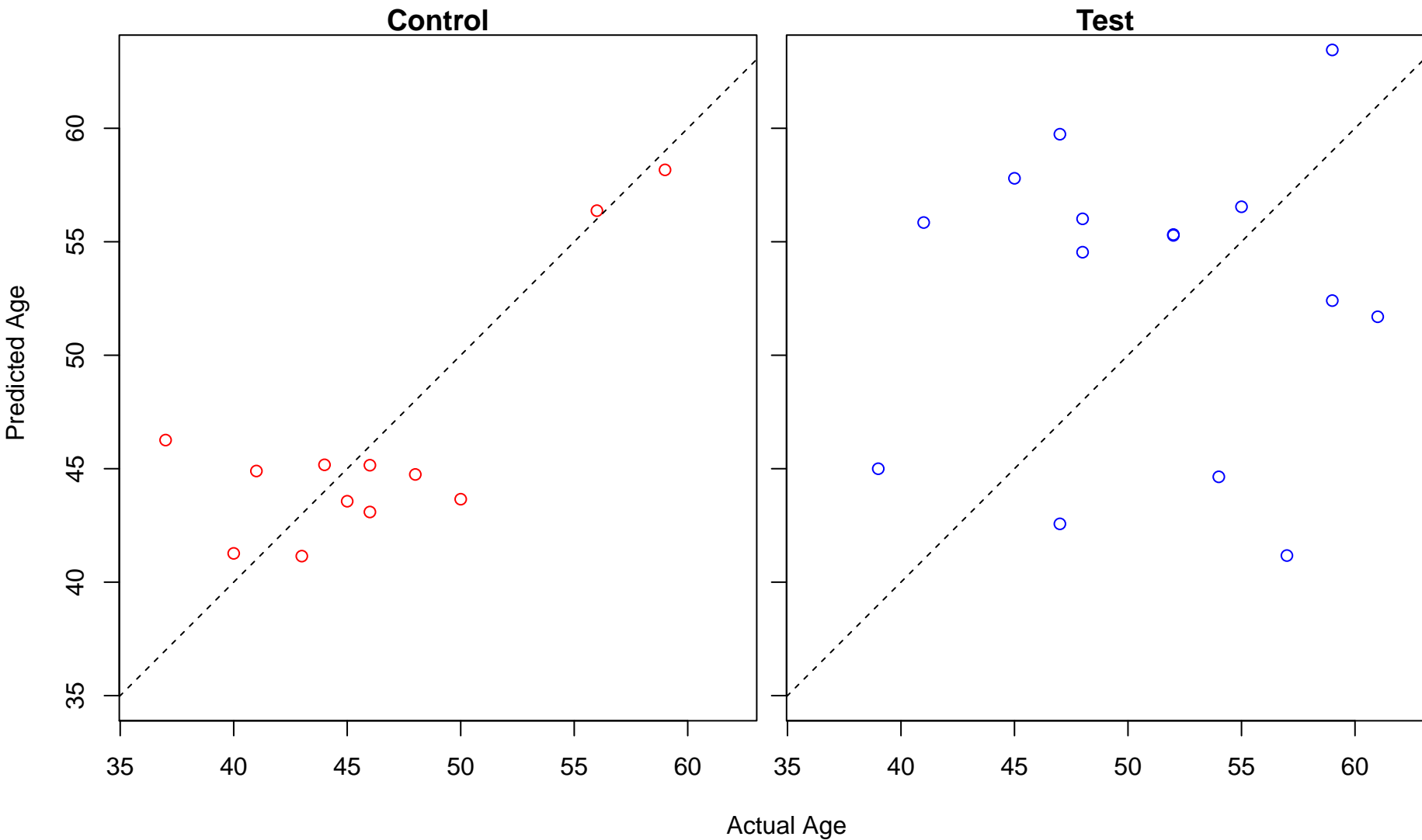
protein N-linked glycosylation (Score: 2.548354)



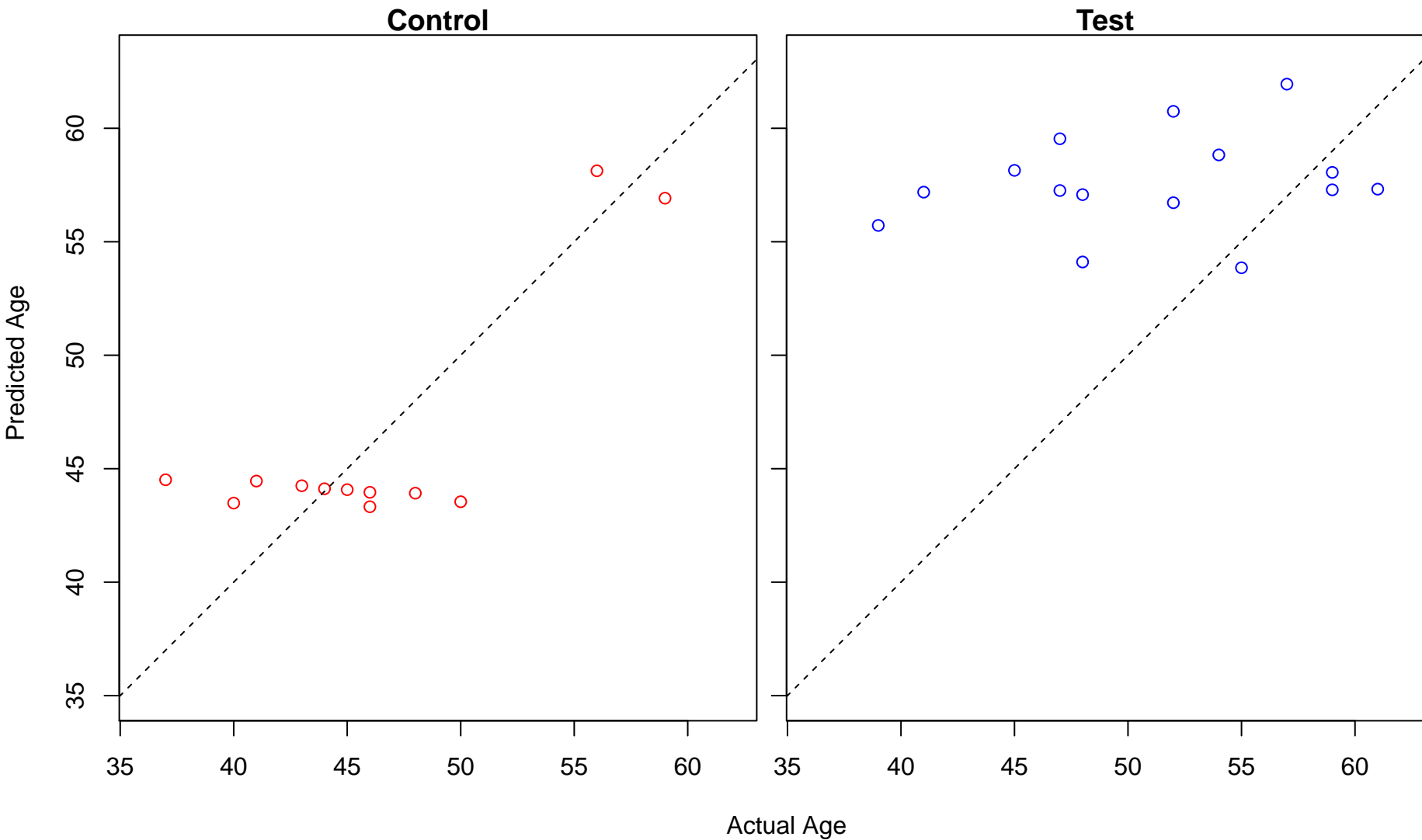
snRNA transcription (Score: 2.546054)



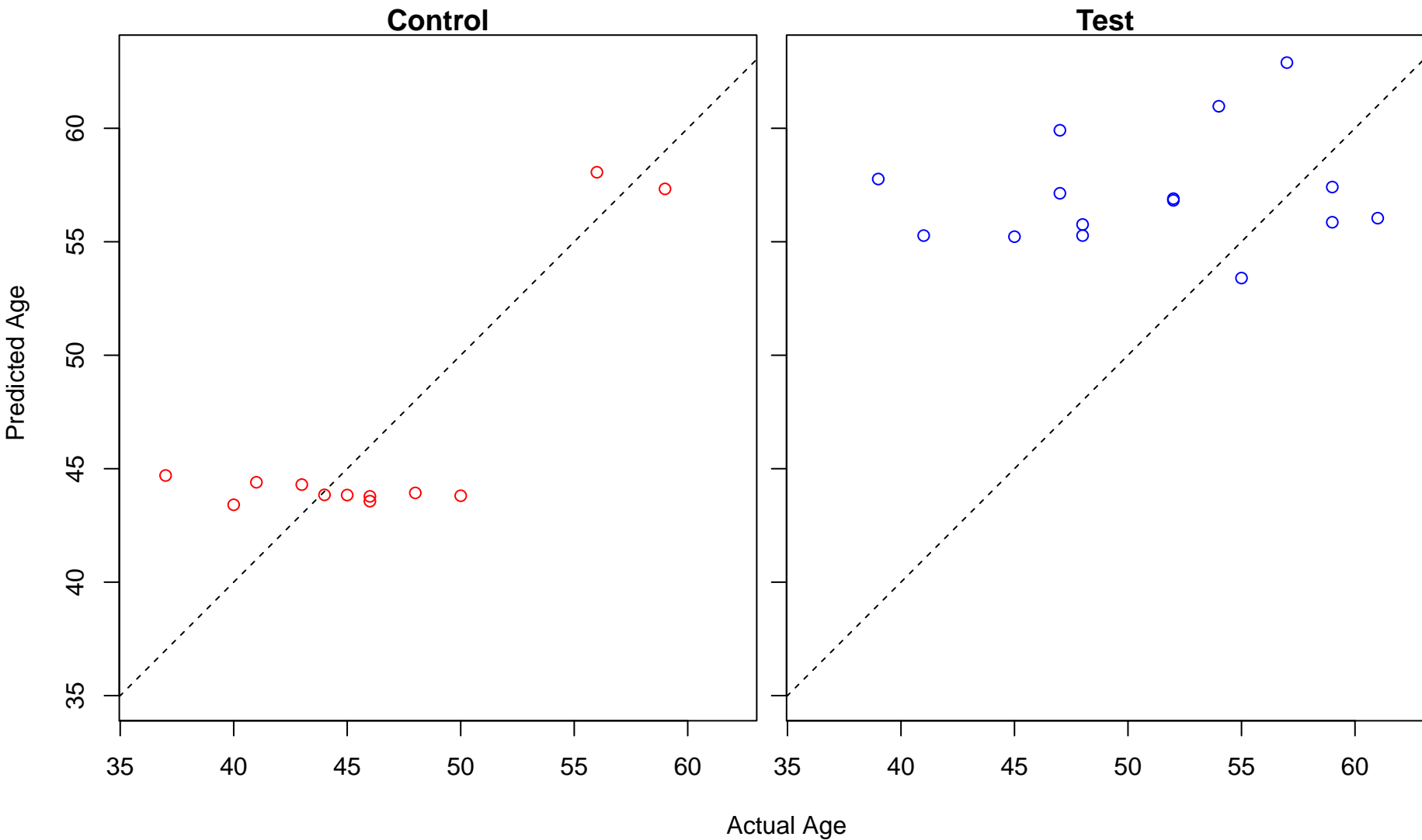
positive regulation of JUN kinase activity (Score: 2.544972)



regulation of protein localization to nucleus (Score: 2.542752)

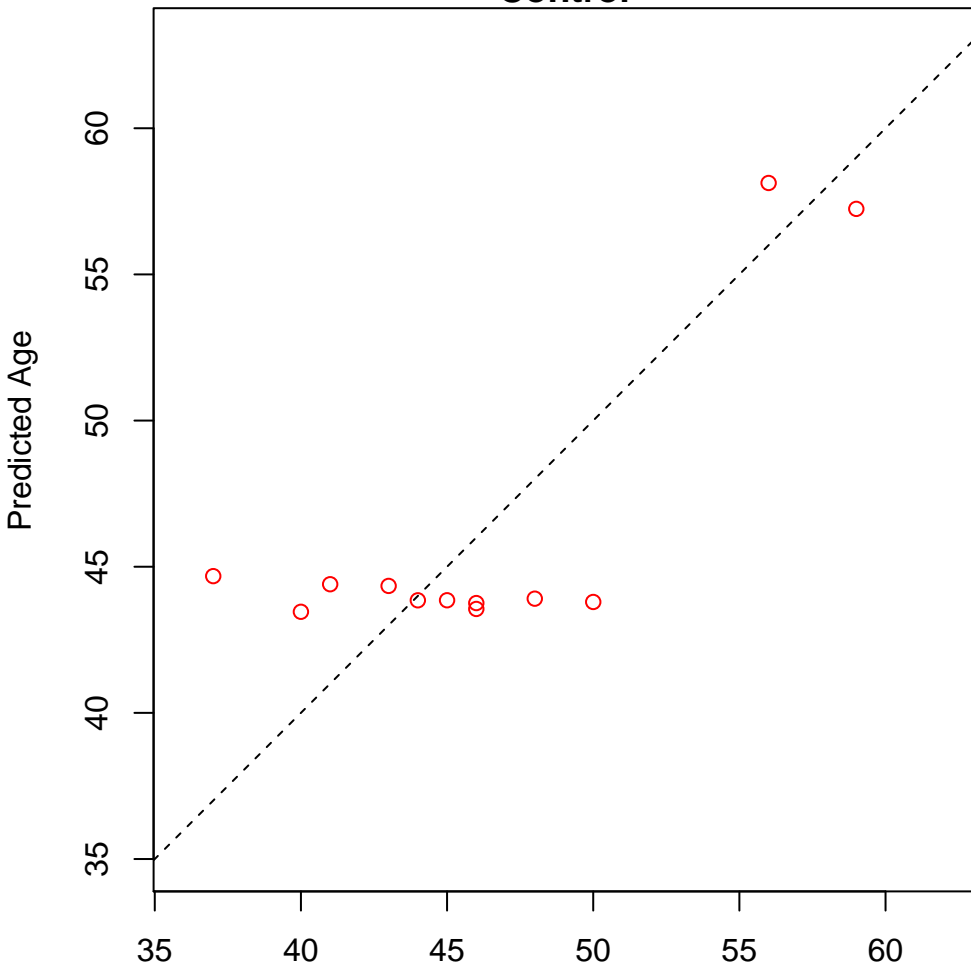


peptidyl-lysine acetylation (Score: 2.540793)

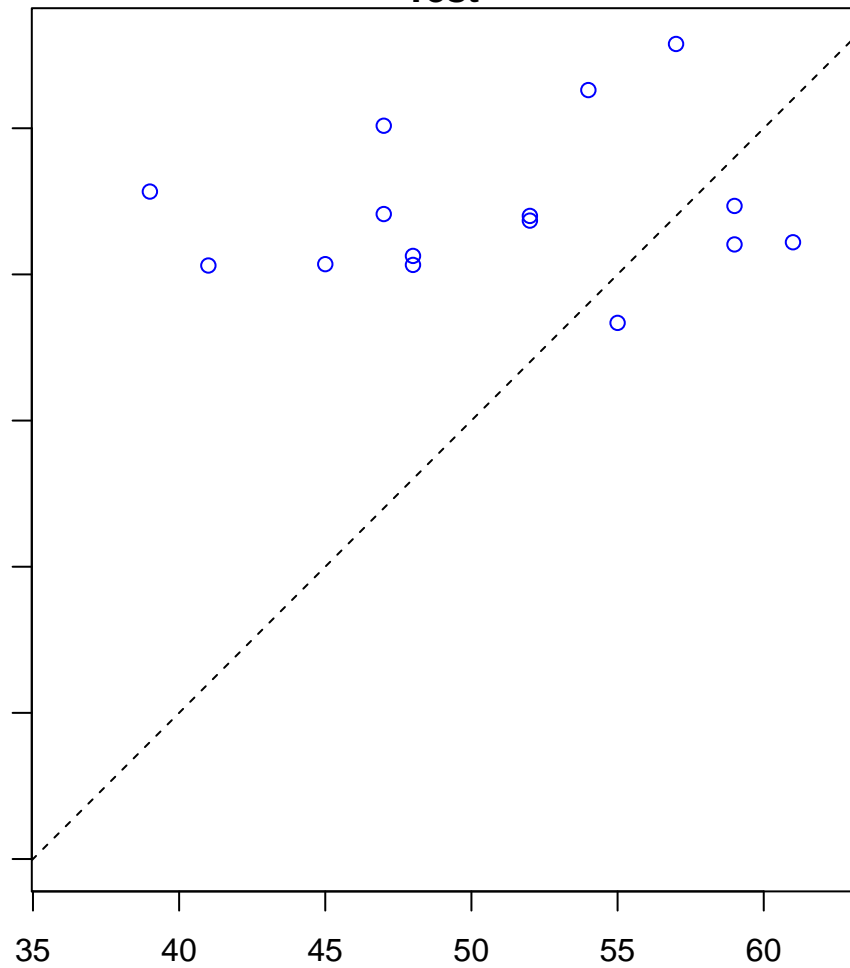


internal protein amino acid acetylation (Score: 2.539499)

Control

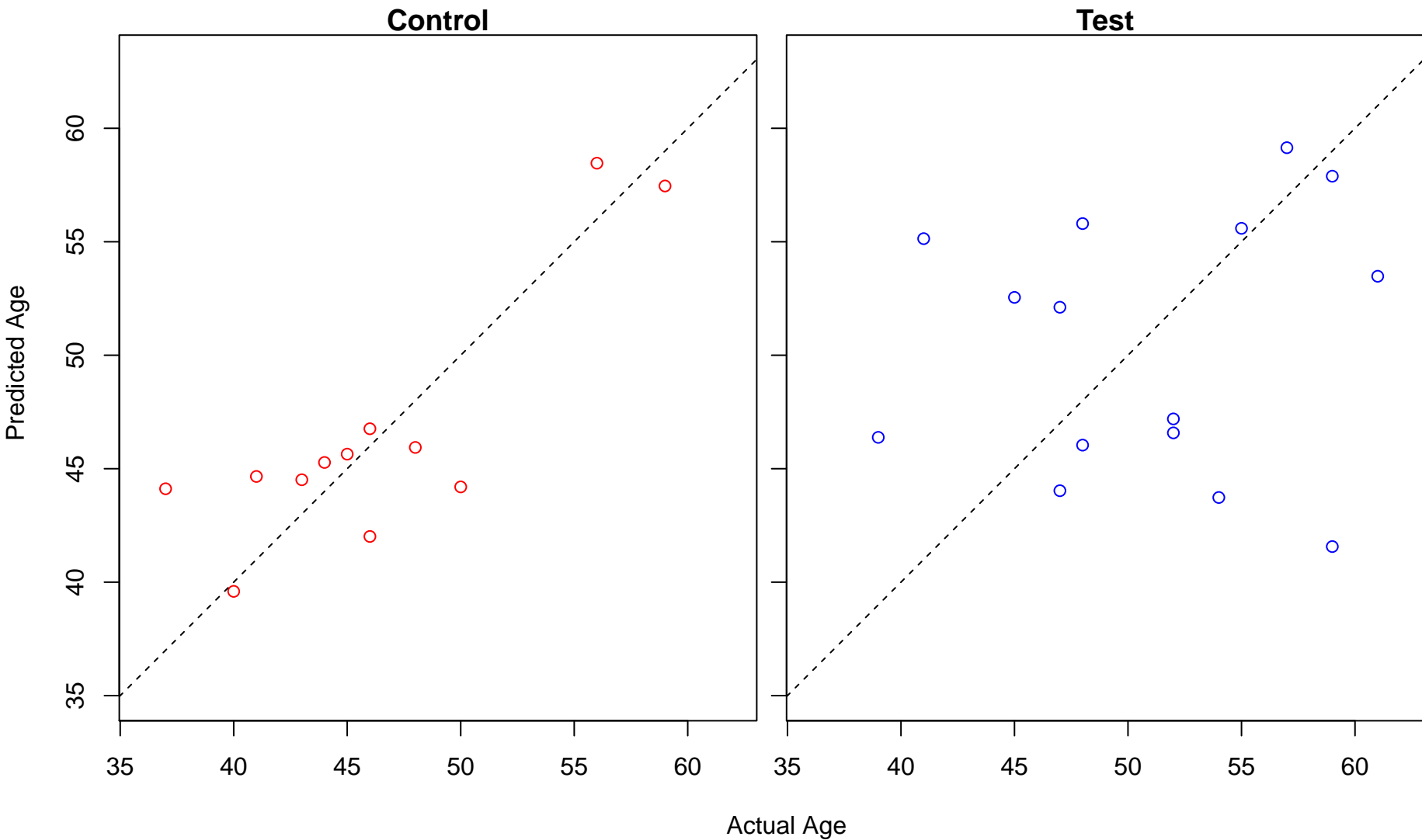


Test



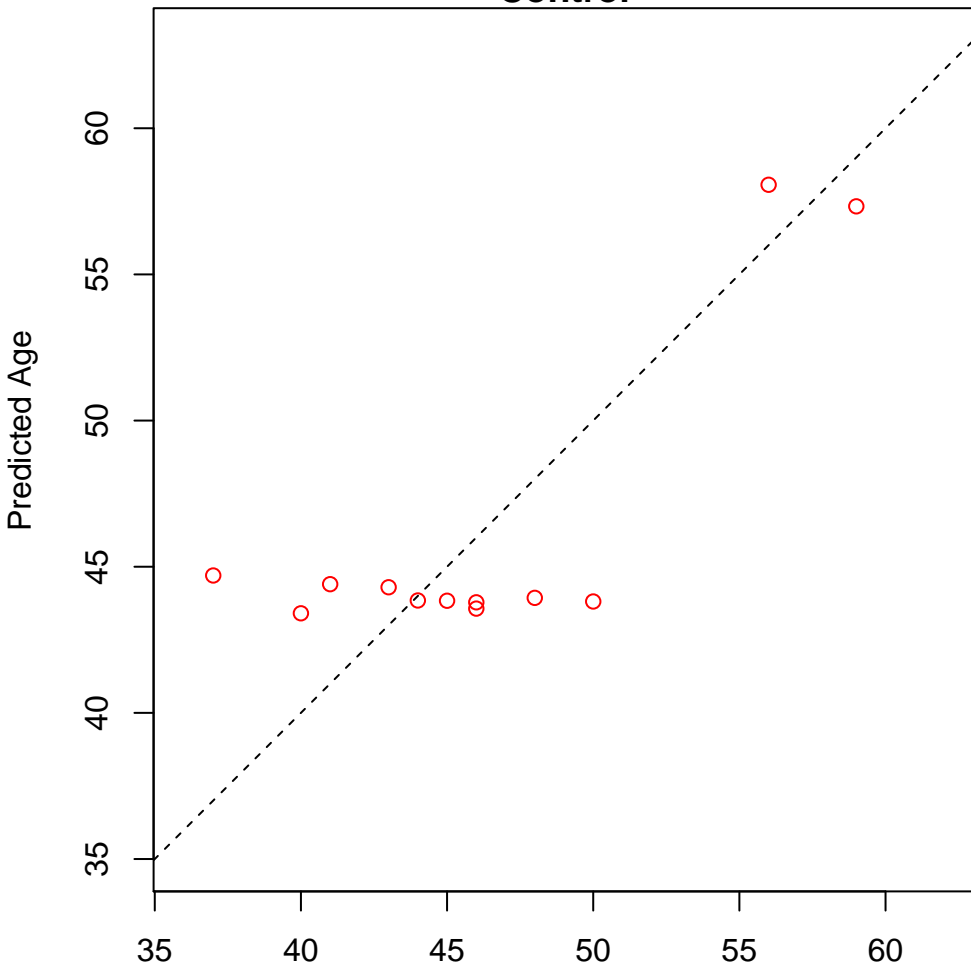
Actual Age

positive regulation of defense response (Score: 2.539294)

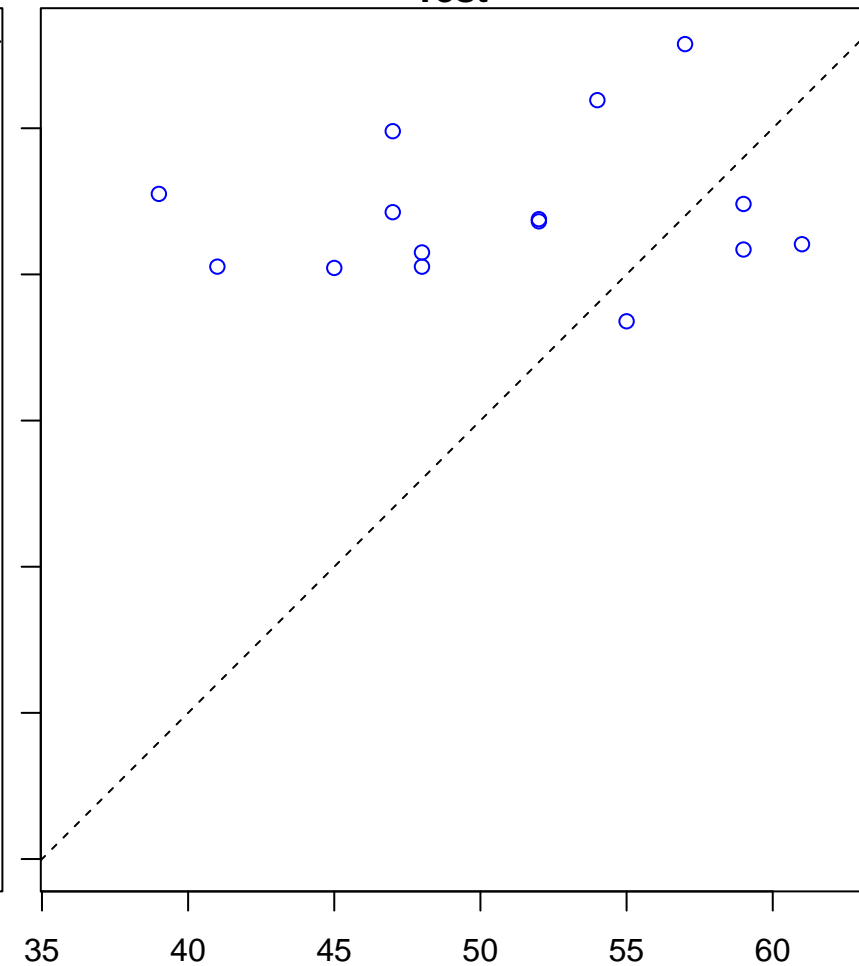


internal peptidyl-lysine acetylation (Score: 2.538591)

Control

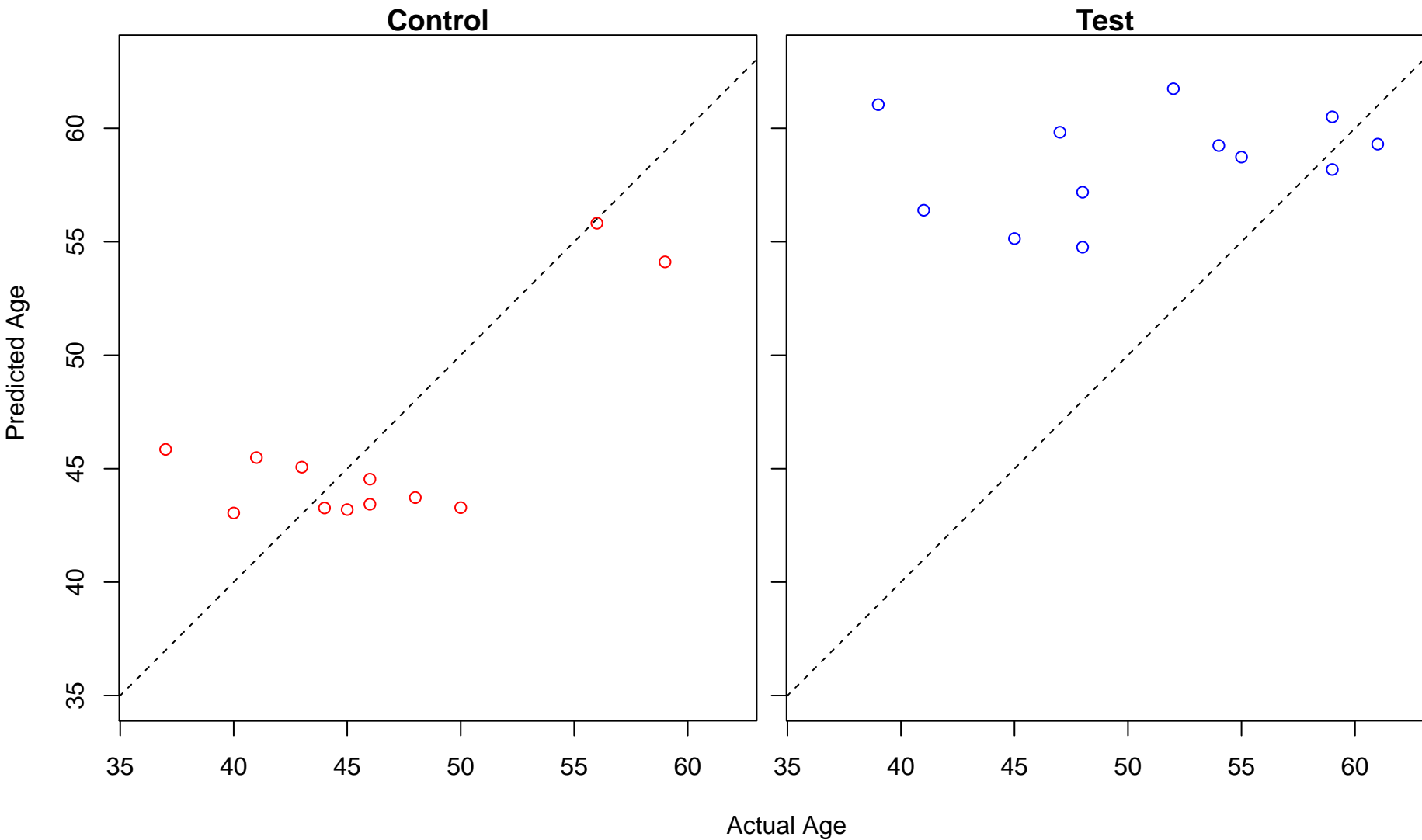


Test

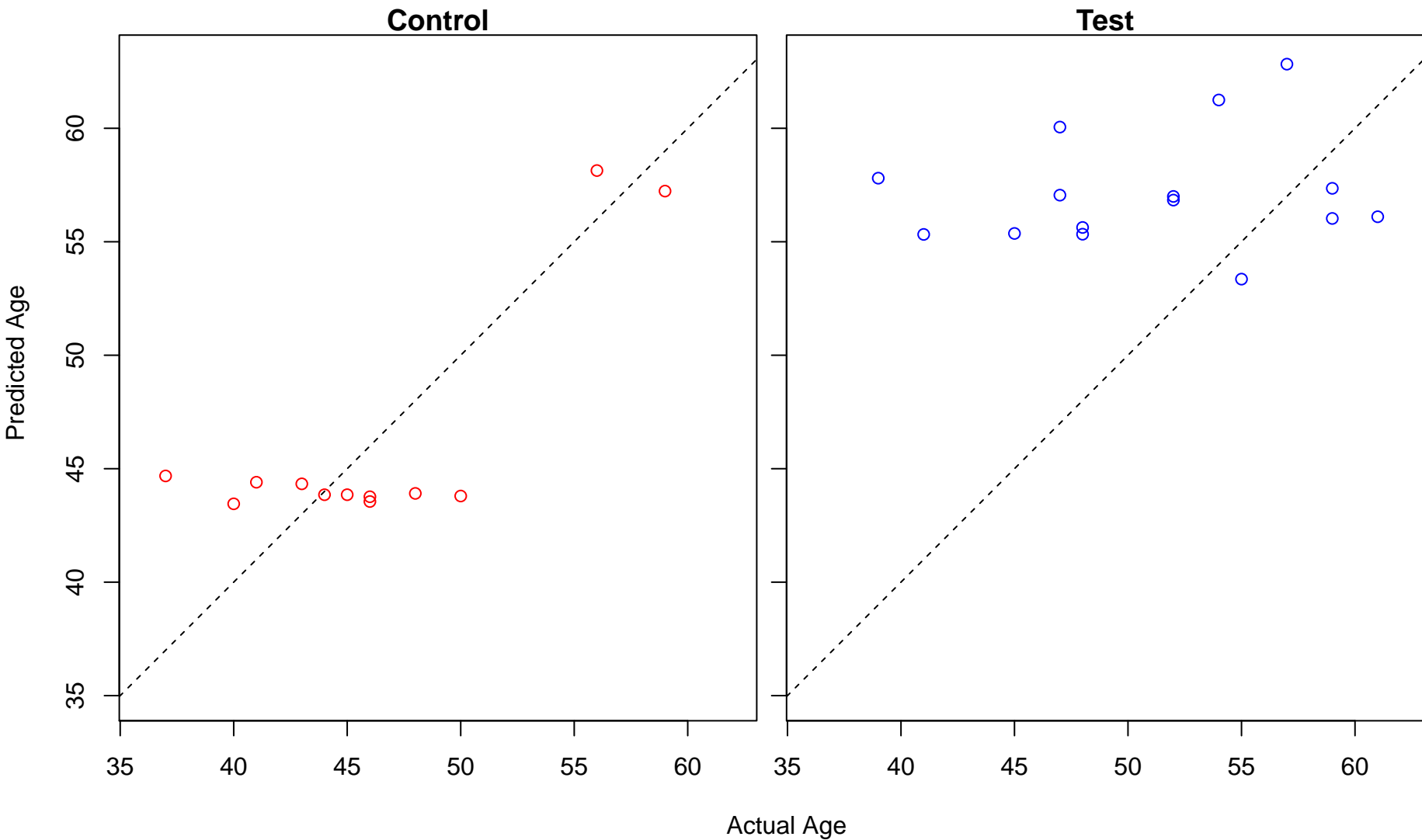


Actual Age

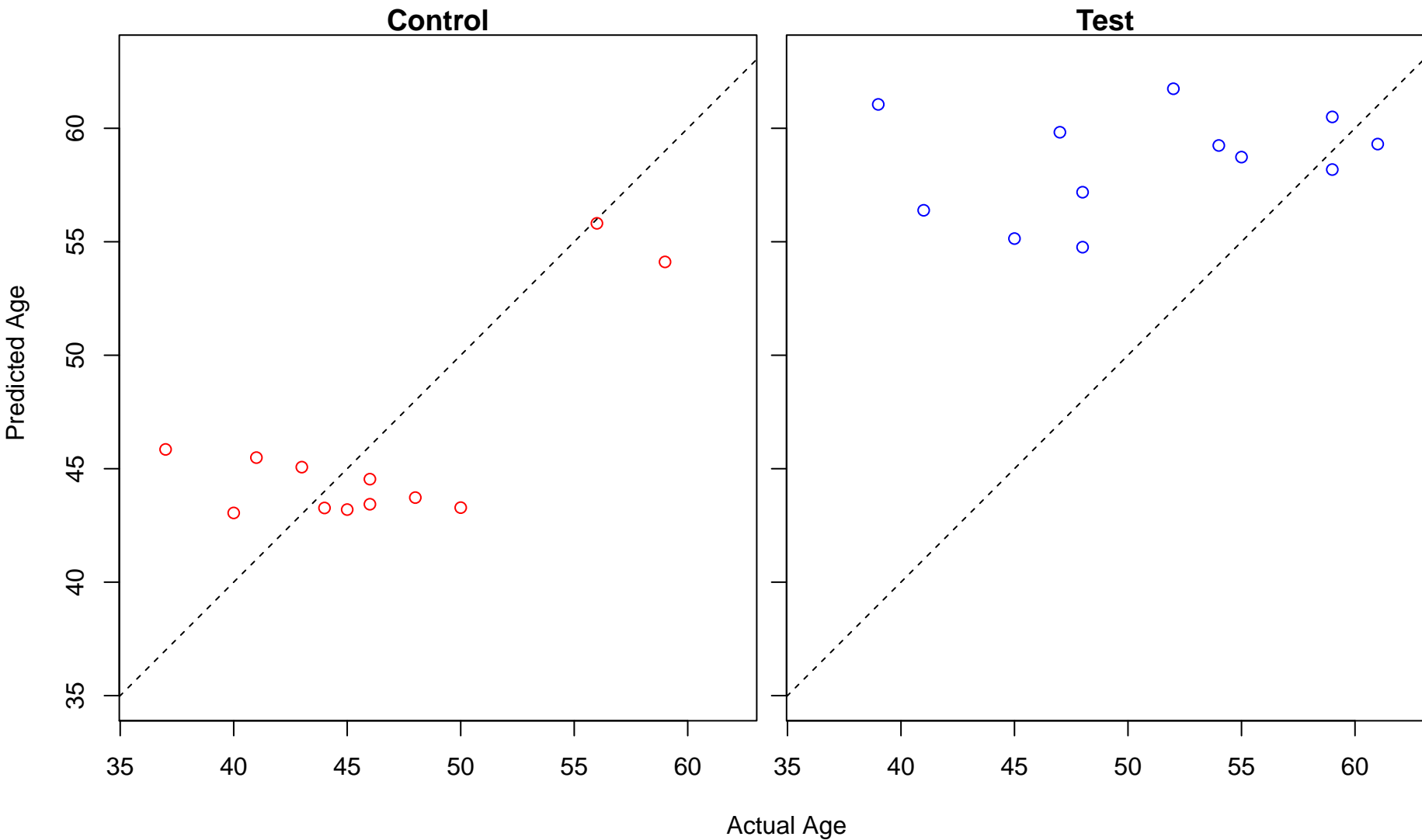
interleukin-1 secretion (Score: 2.535077)



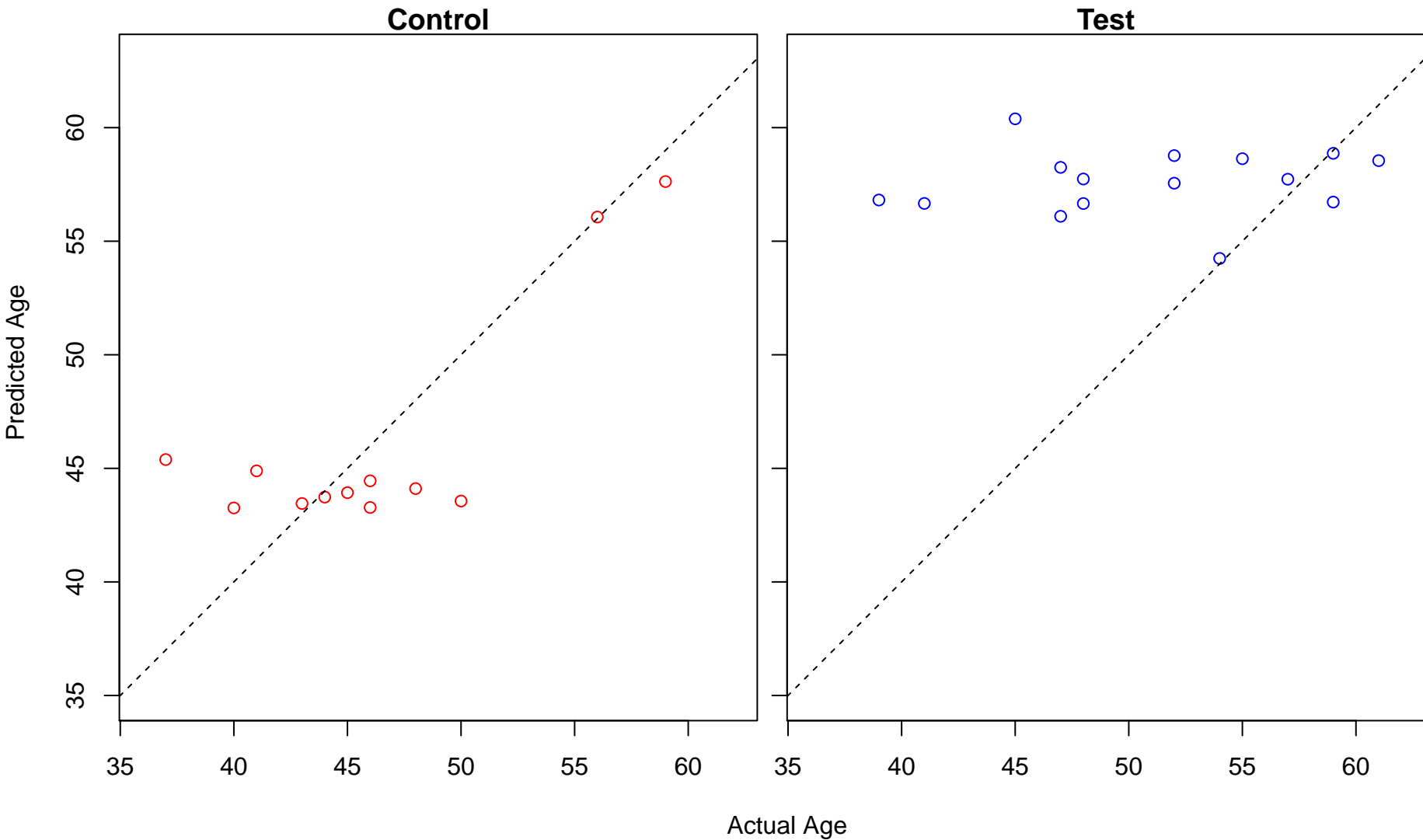
protein acetylation (Score: 2.534938)



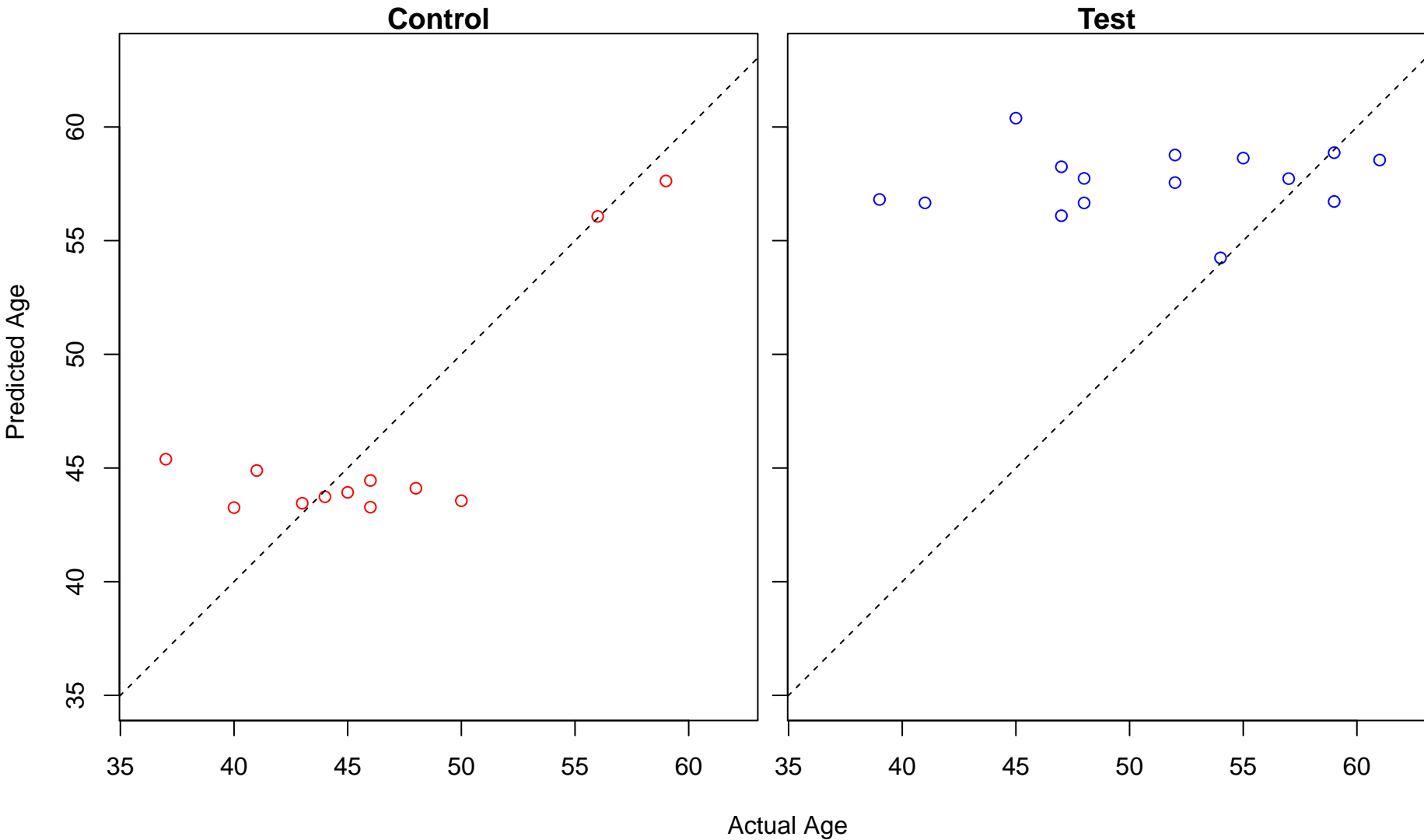
interleukin-1 production (Score: 2.534793)



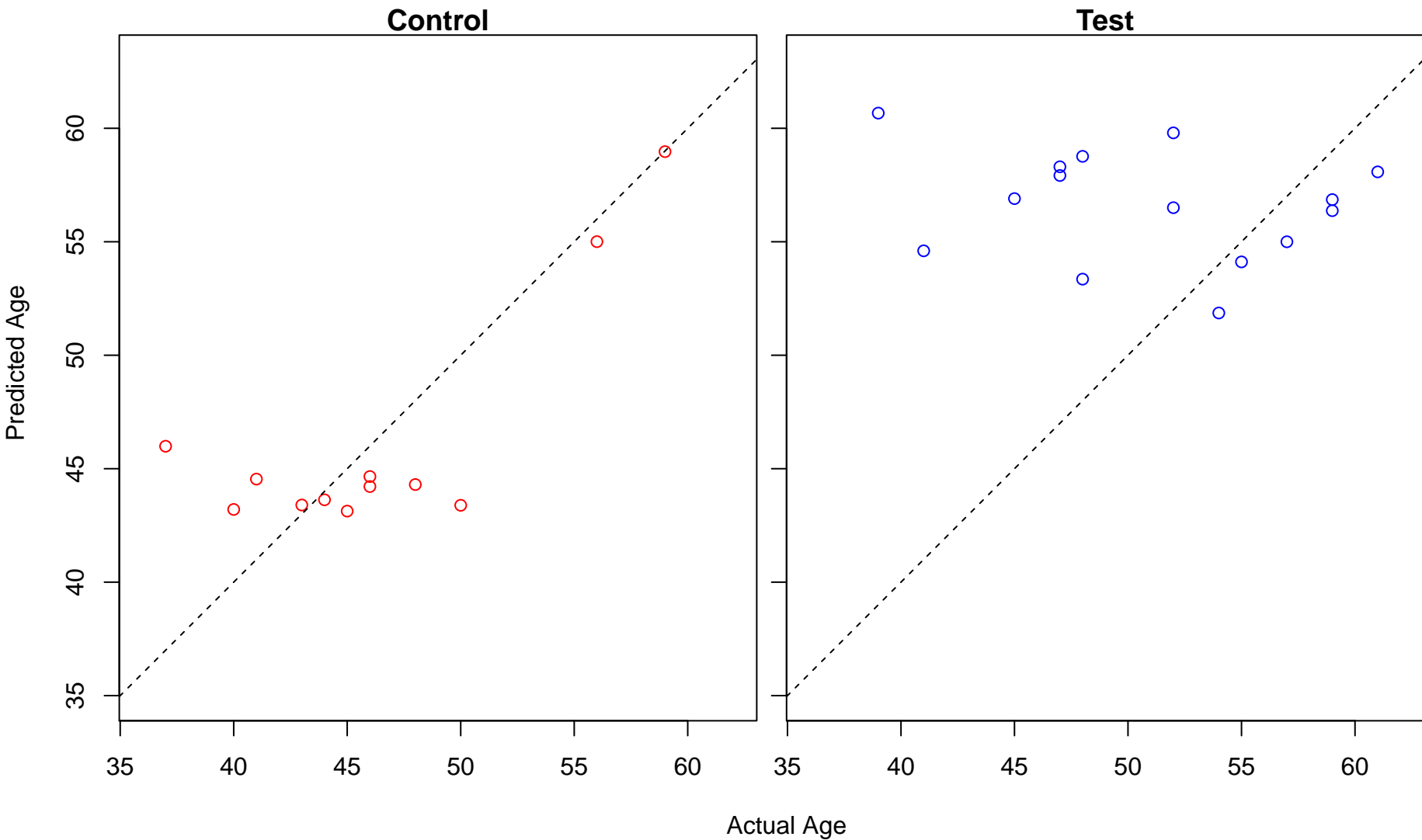
production of miRNAs involved in gene silencing by miRNA (Score: 2.53181)



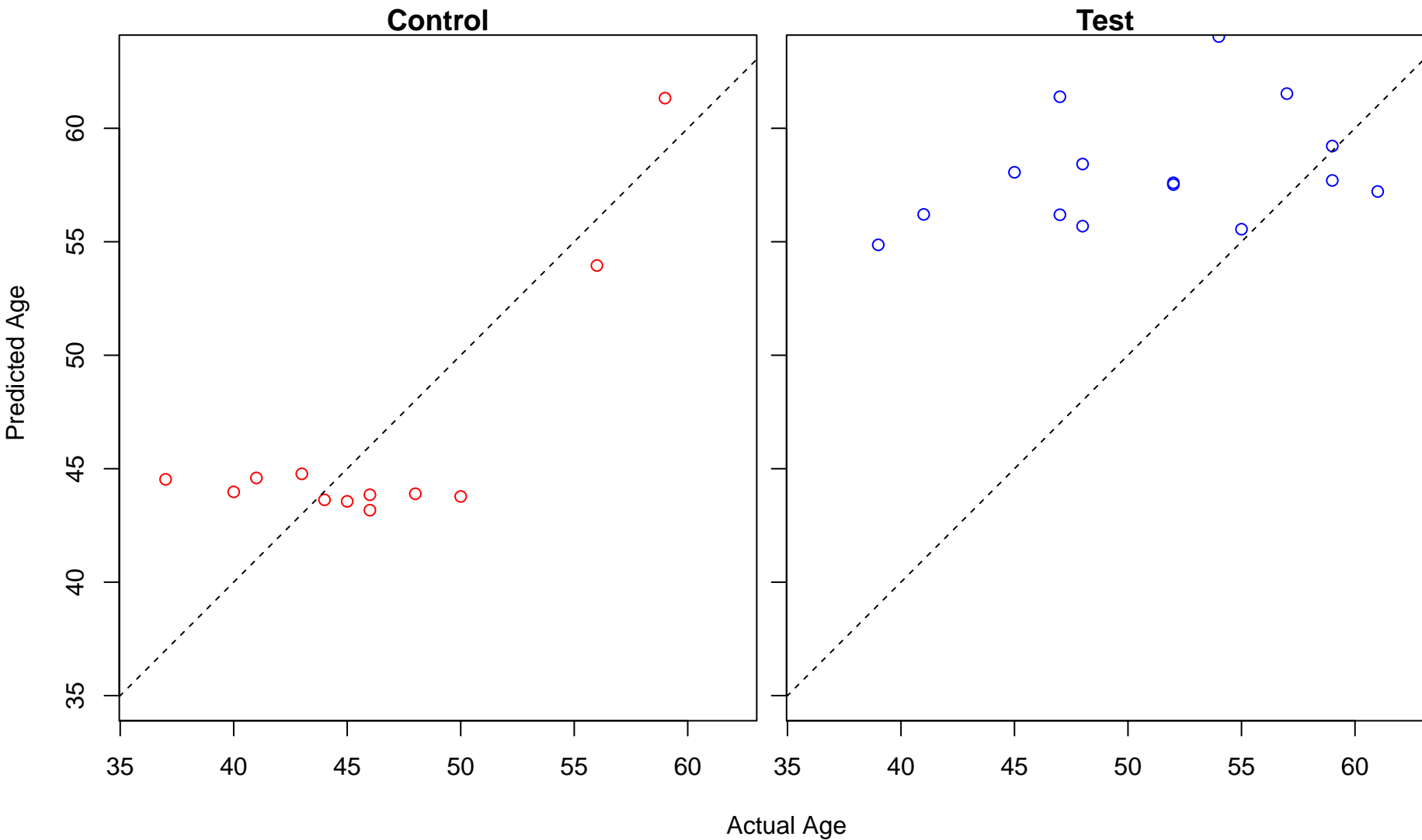
production of small RNA involved in gene silencing by RNA (Score: 2.532916)



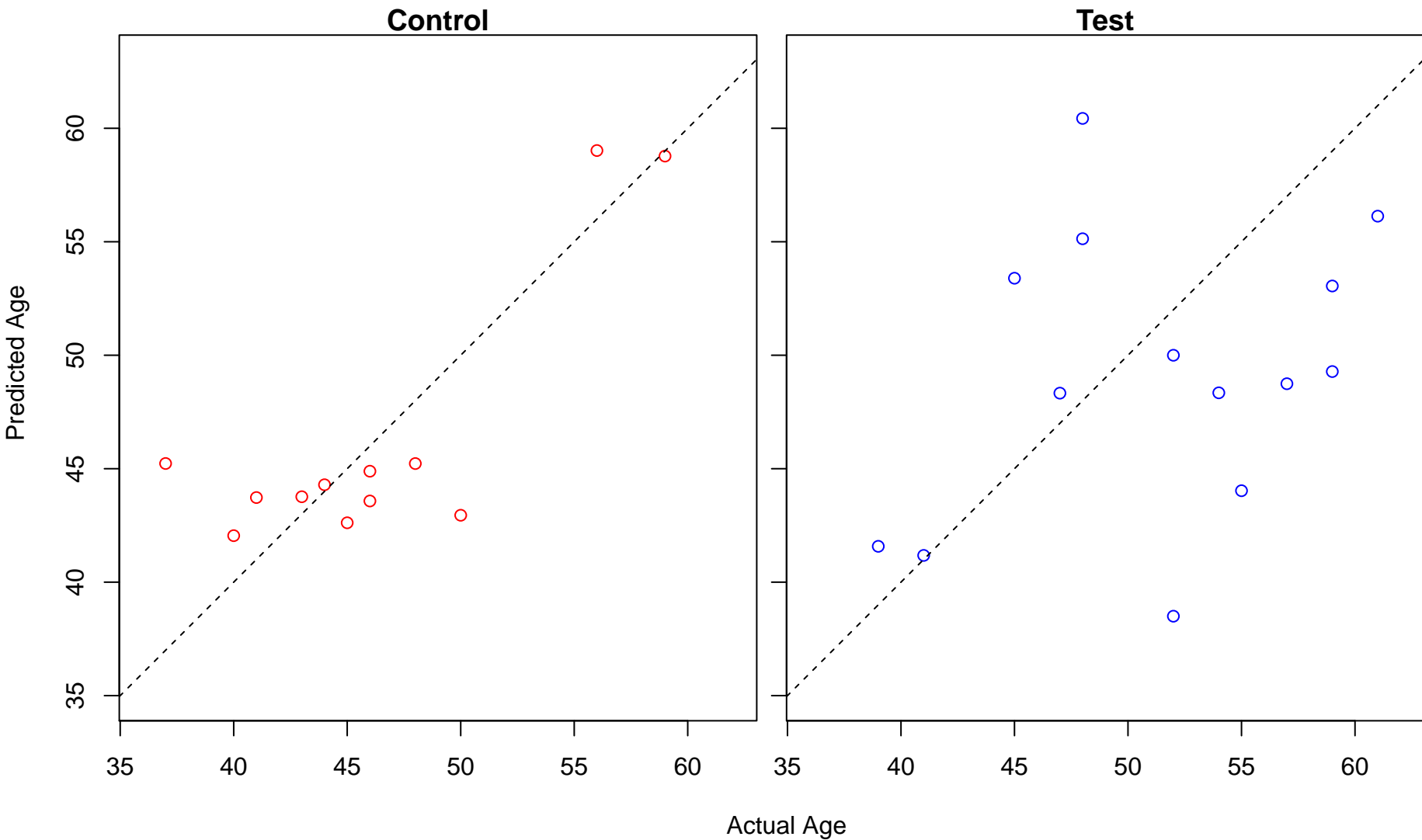
pyrimidine nucleobase metabolic process (Score: 2.532191)



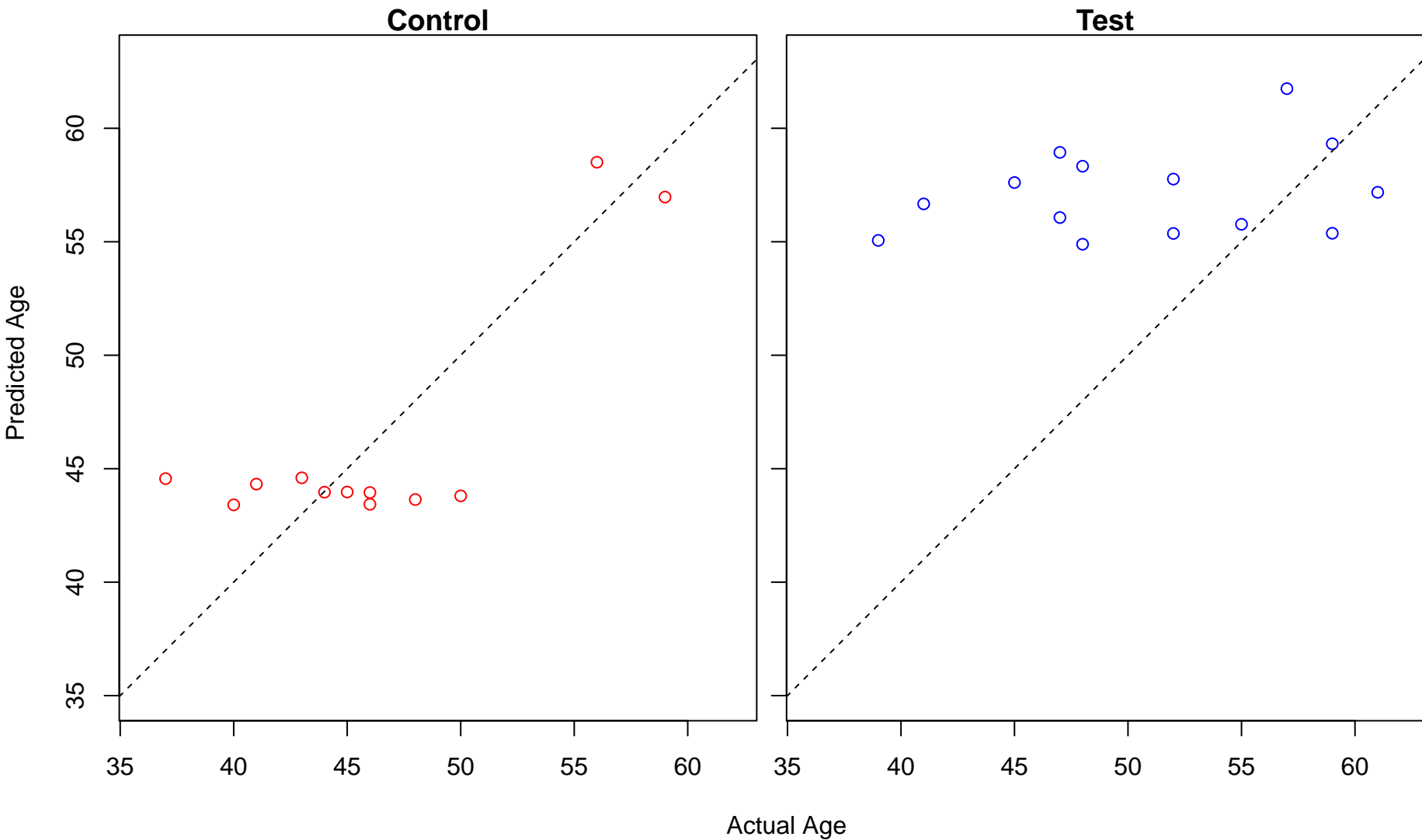
cellular response to UV (Score: 2.529382)



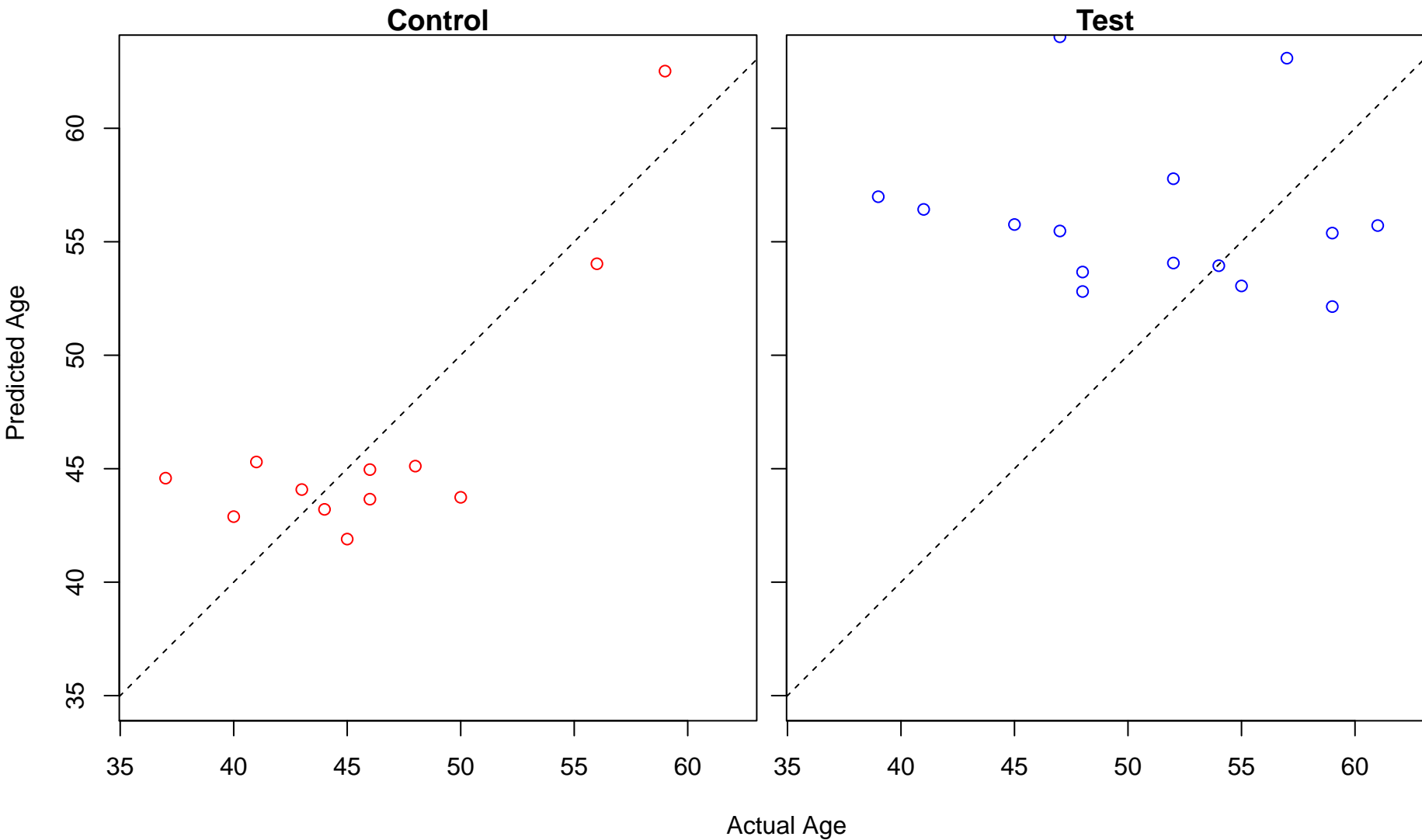
sexual reproduction (Score: 2.528185)



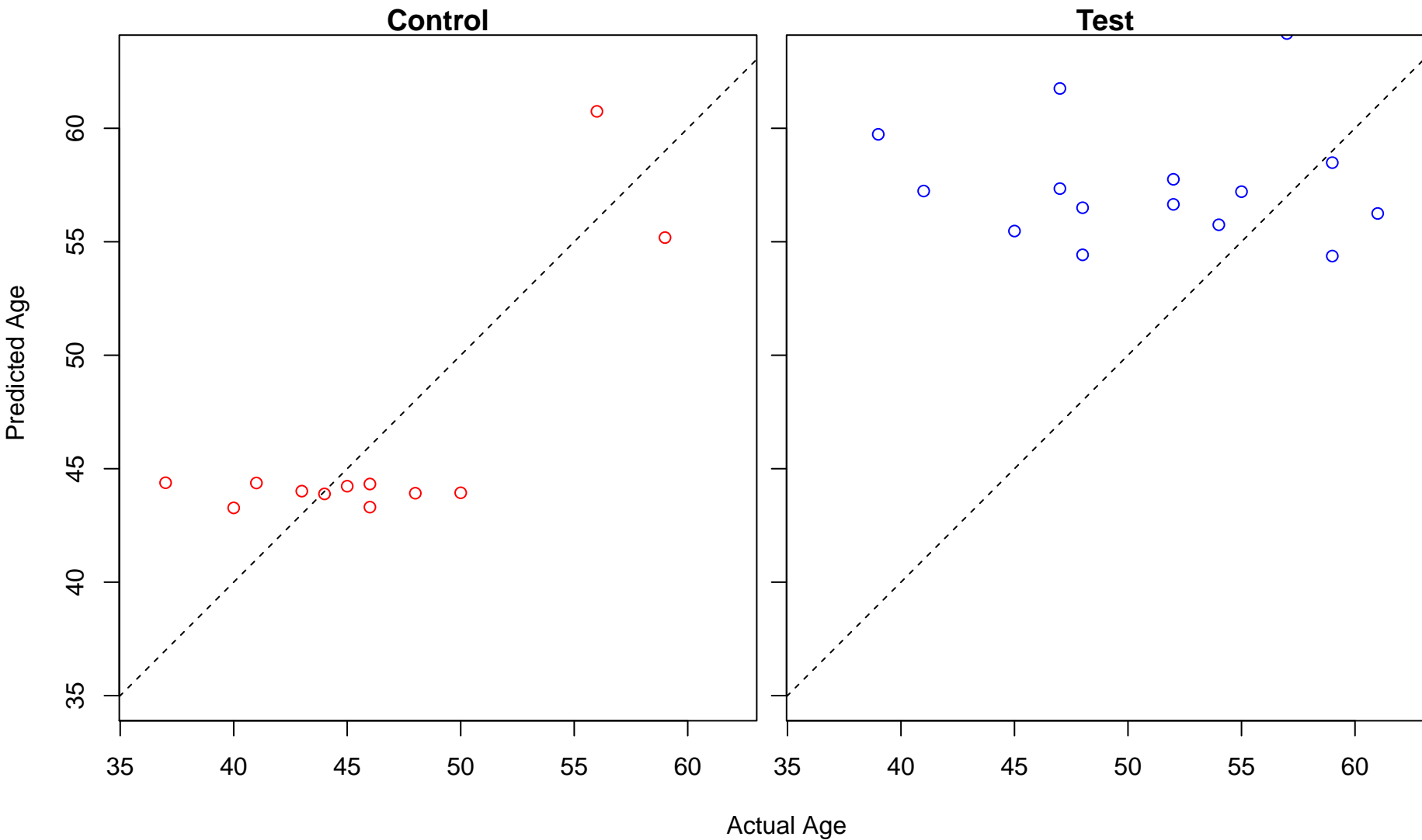
DNA duplex unwinding (Score: 2.526894)



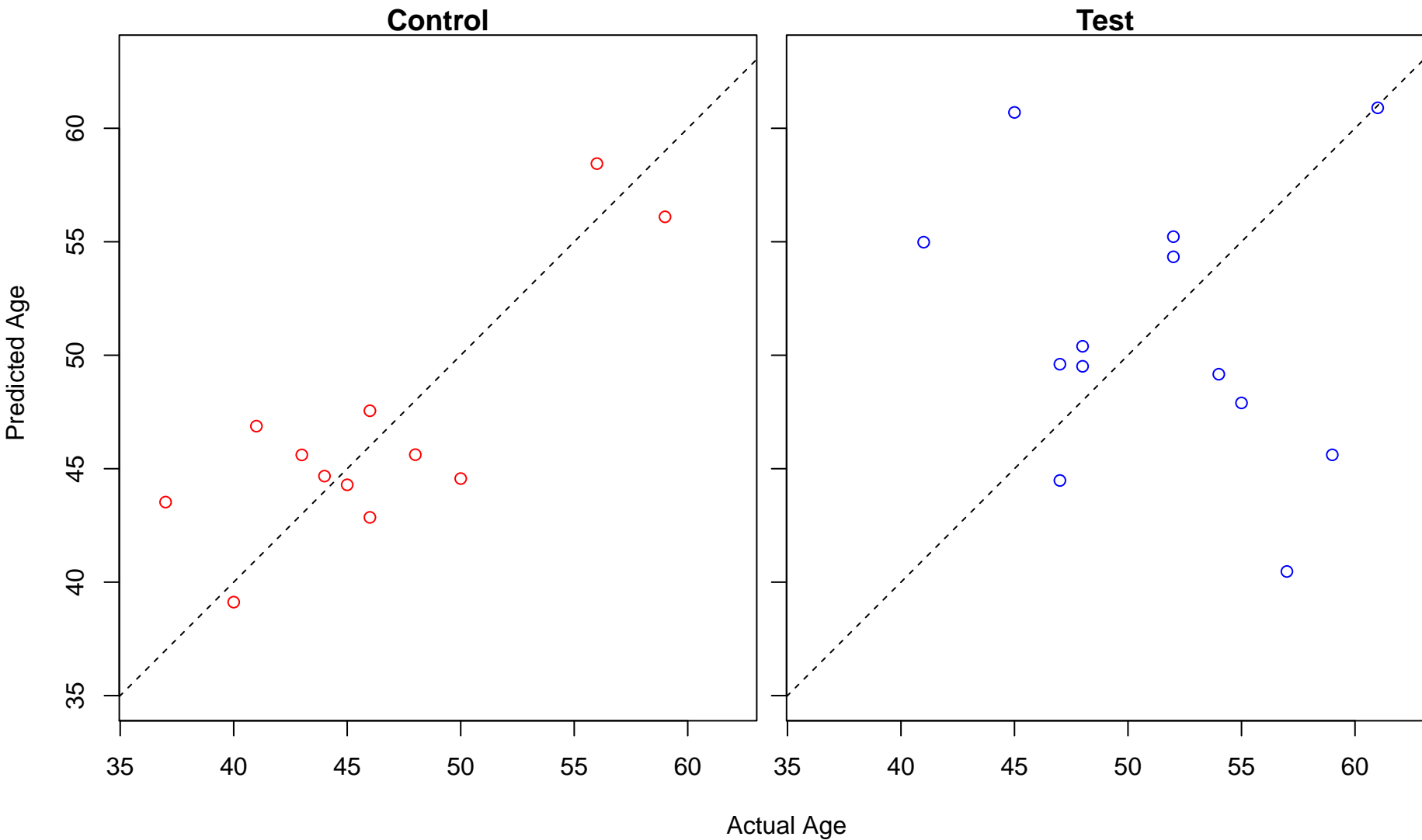
skeletal system development (Score: 2.526889)



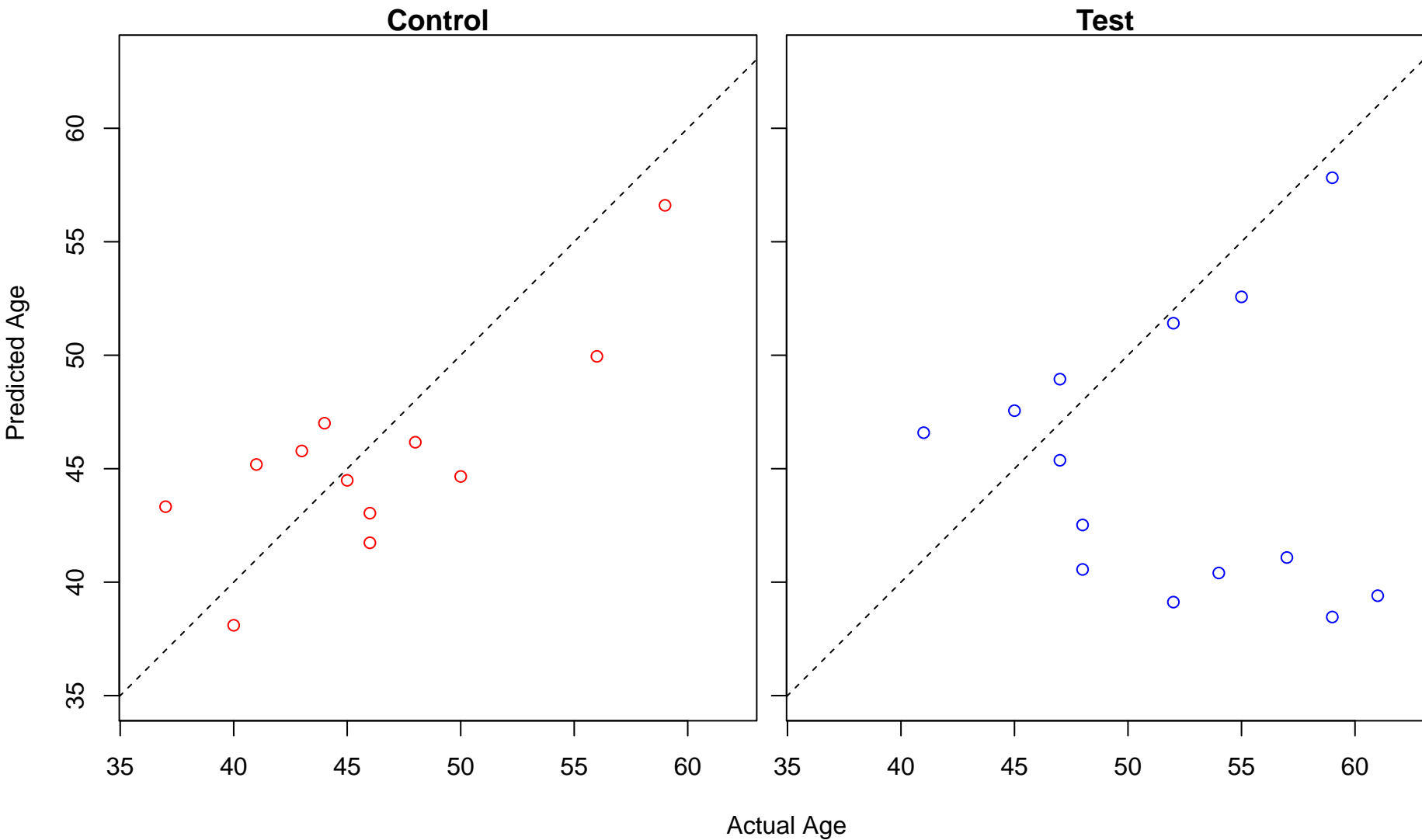
microtubule-based movement (Score: 2.523943)



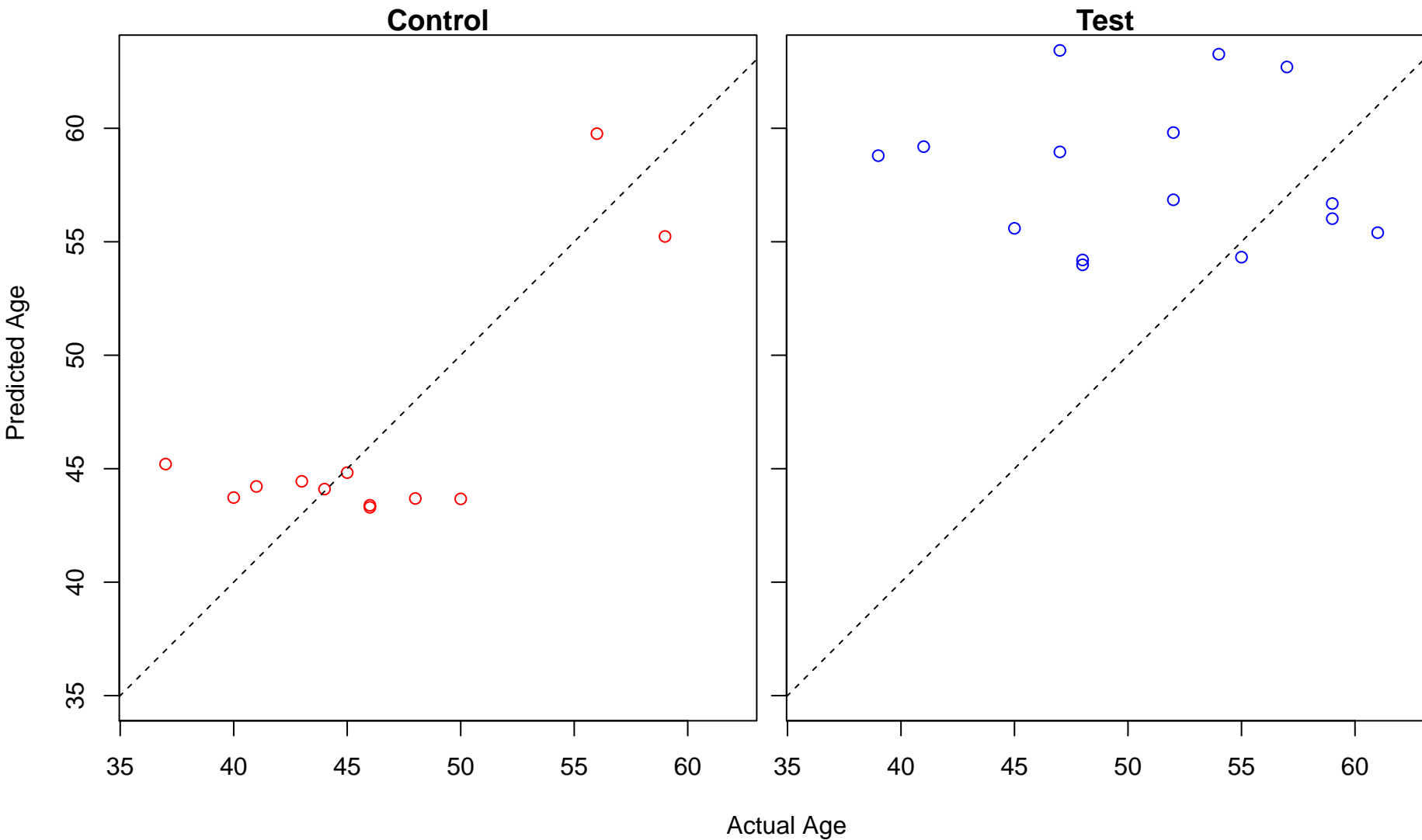
regulation of peptide transport (Score: 2.522071)



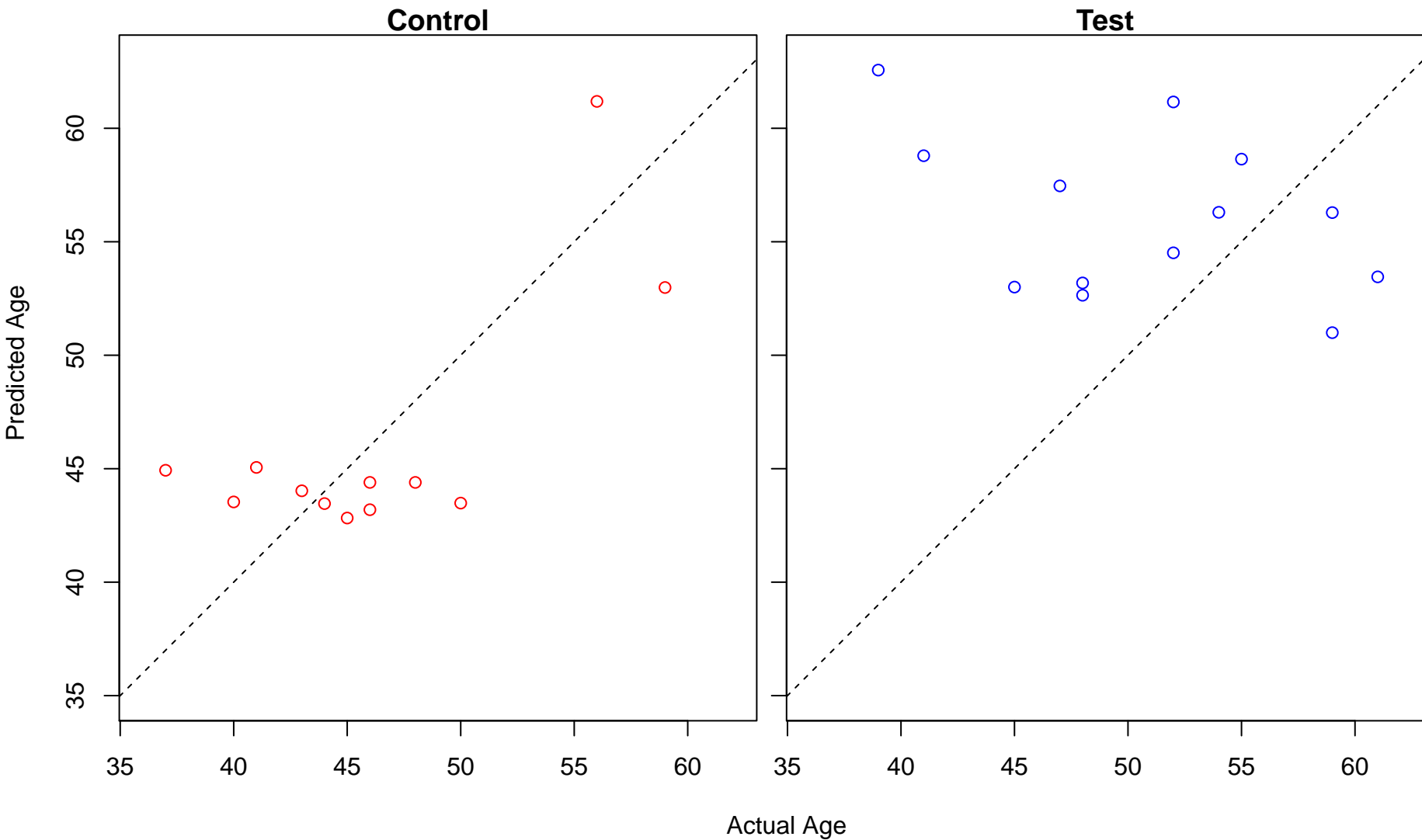
peptide biosynthetic process (Score: 2.521439)



cell-substrate adhesion (Score: 2.519107)

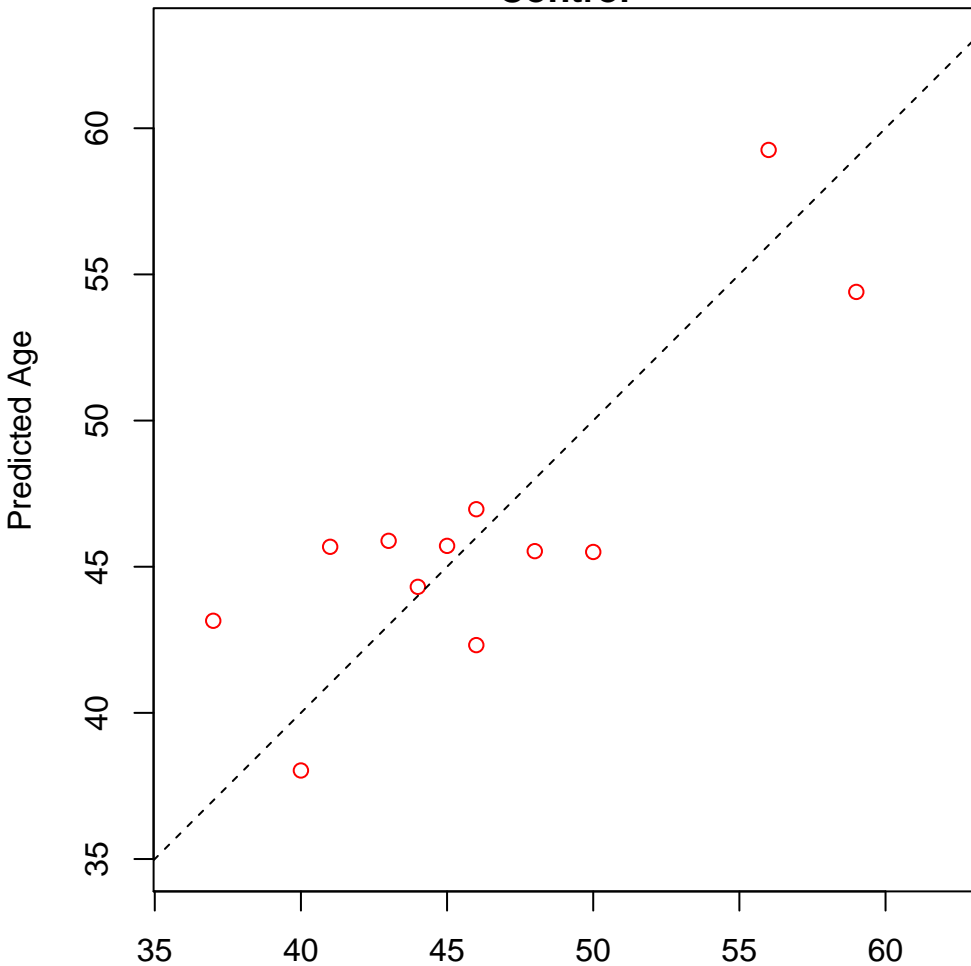


protein heterooligomerization (Score: 2.518275)

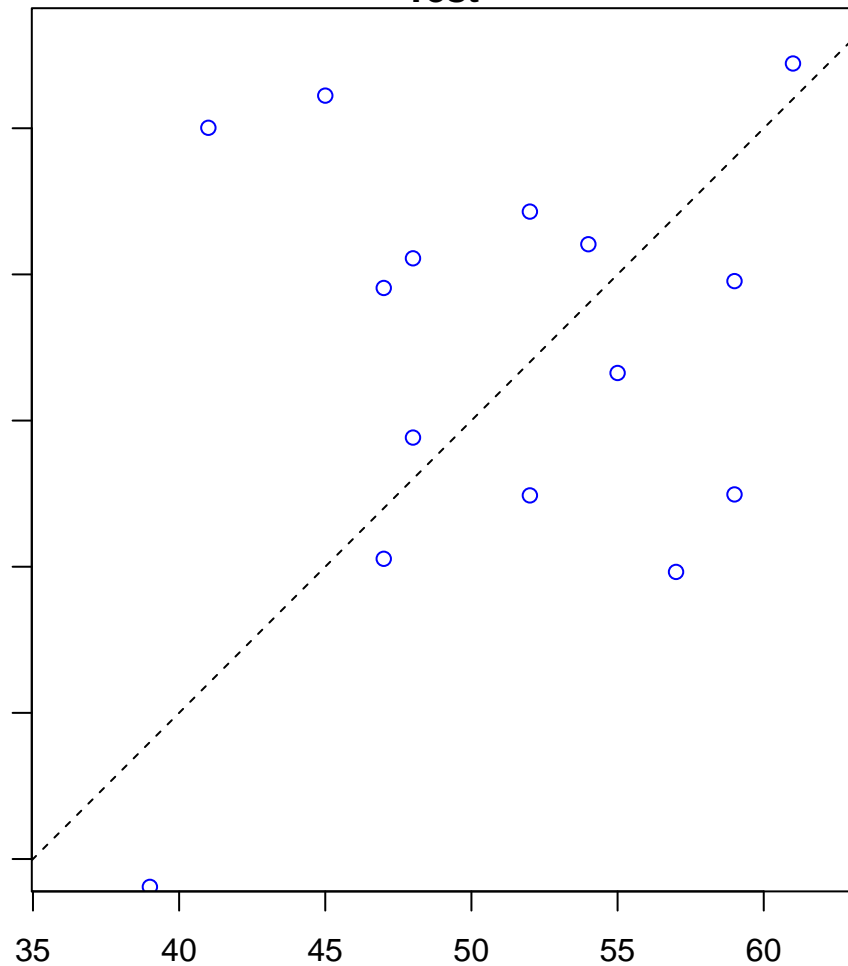


positive regulation of protein transport (Score: 2.515048)

Control

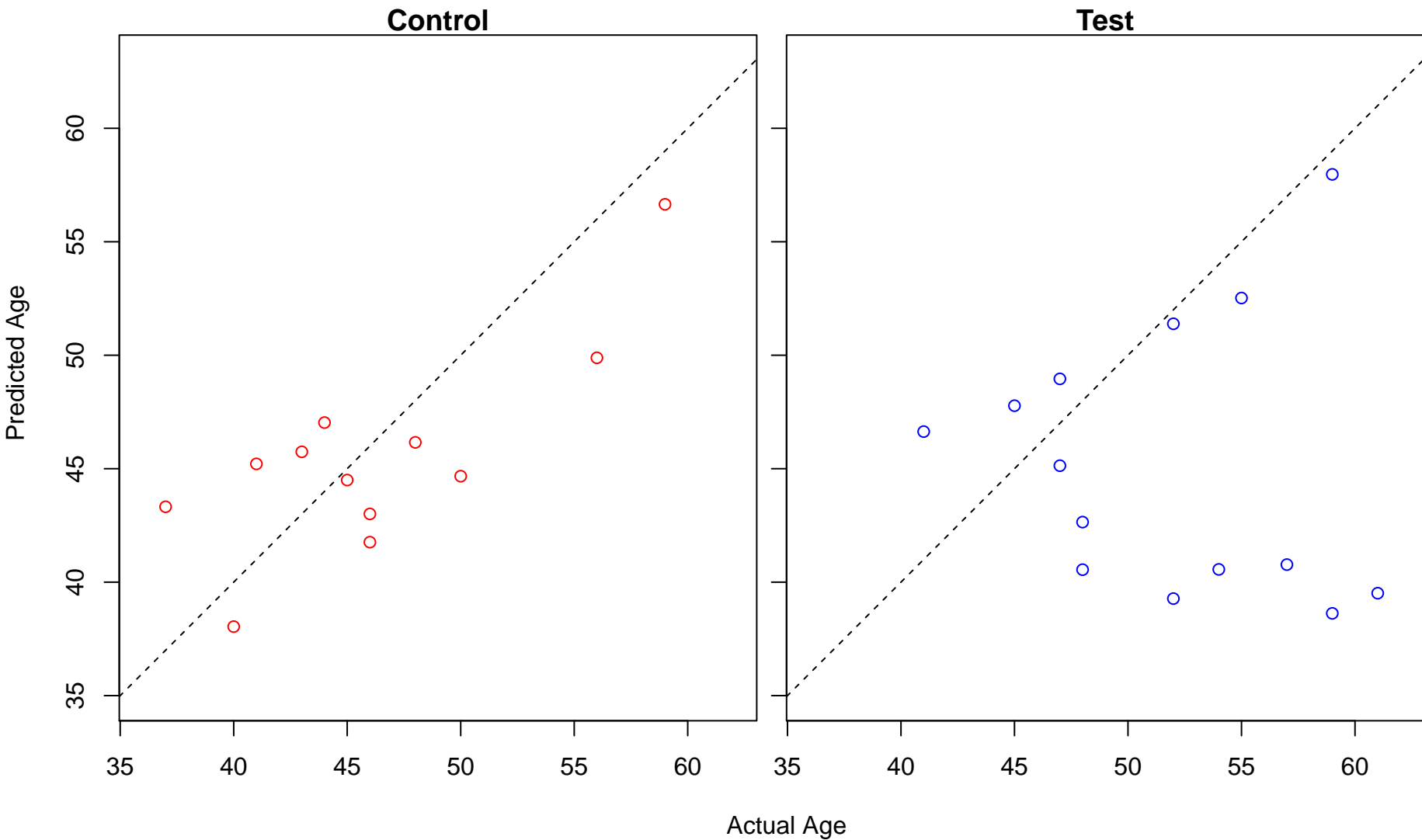


Test

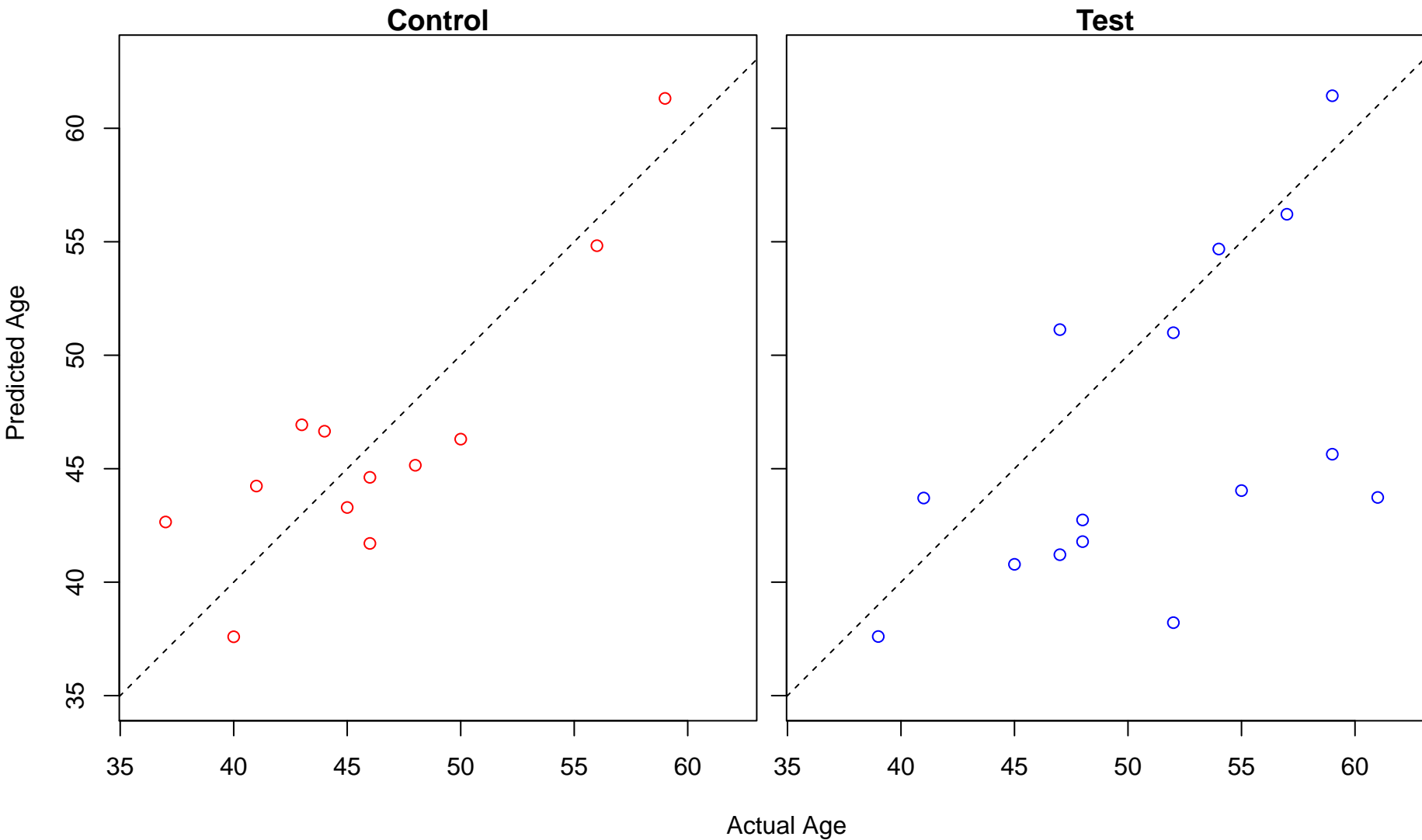


Actual Age

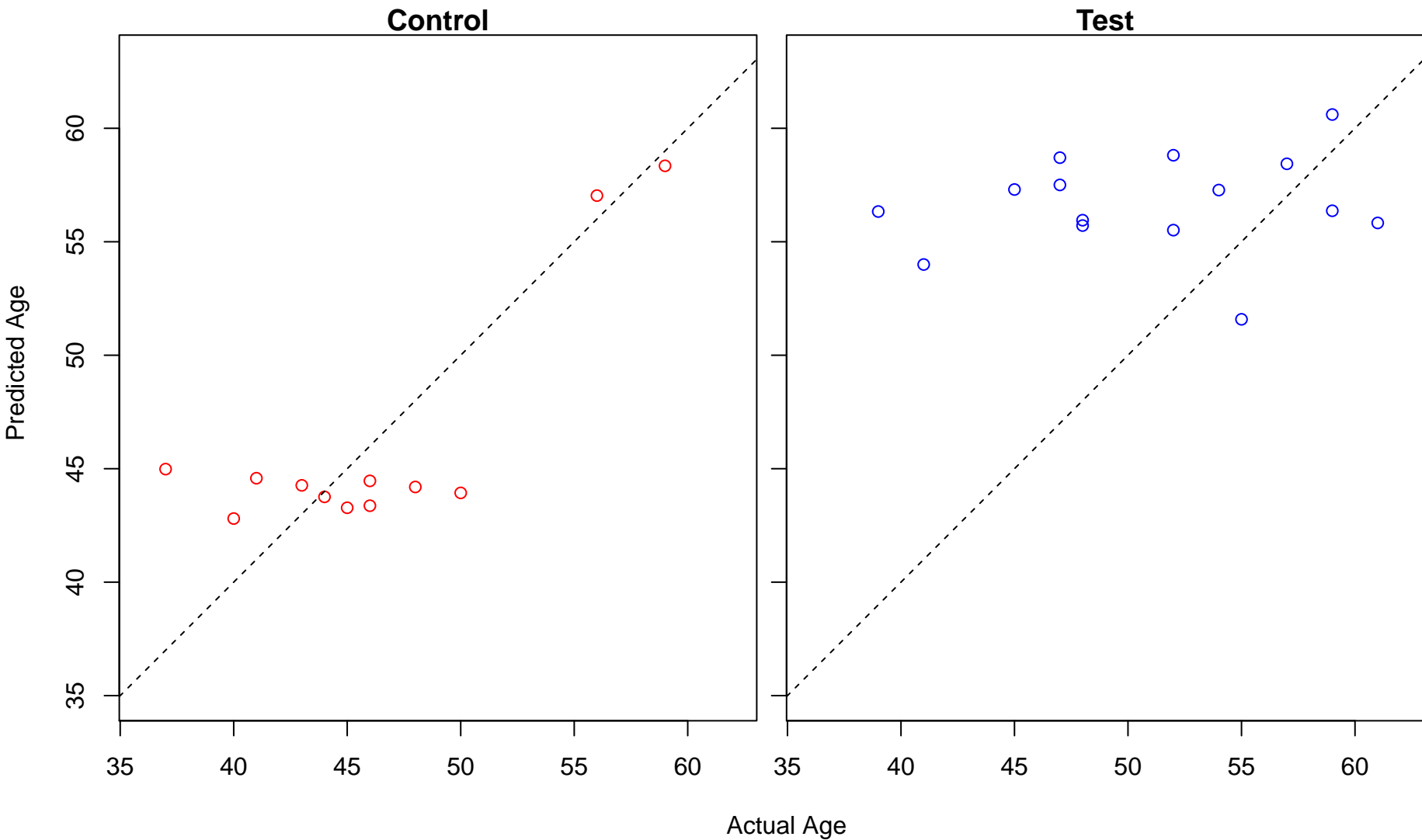
amide biosynthetic process (Score: 2.513228)



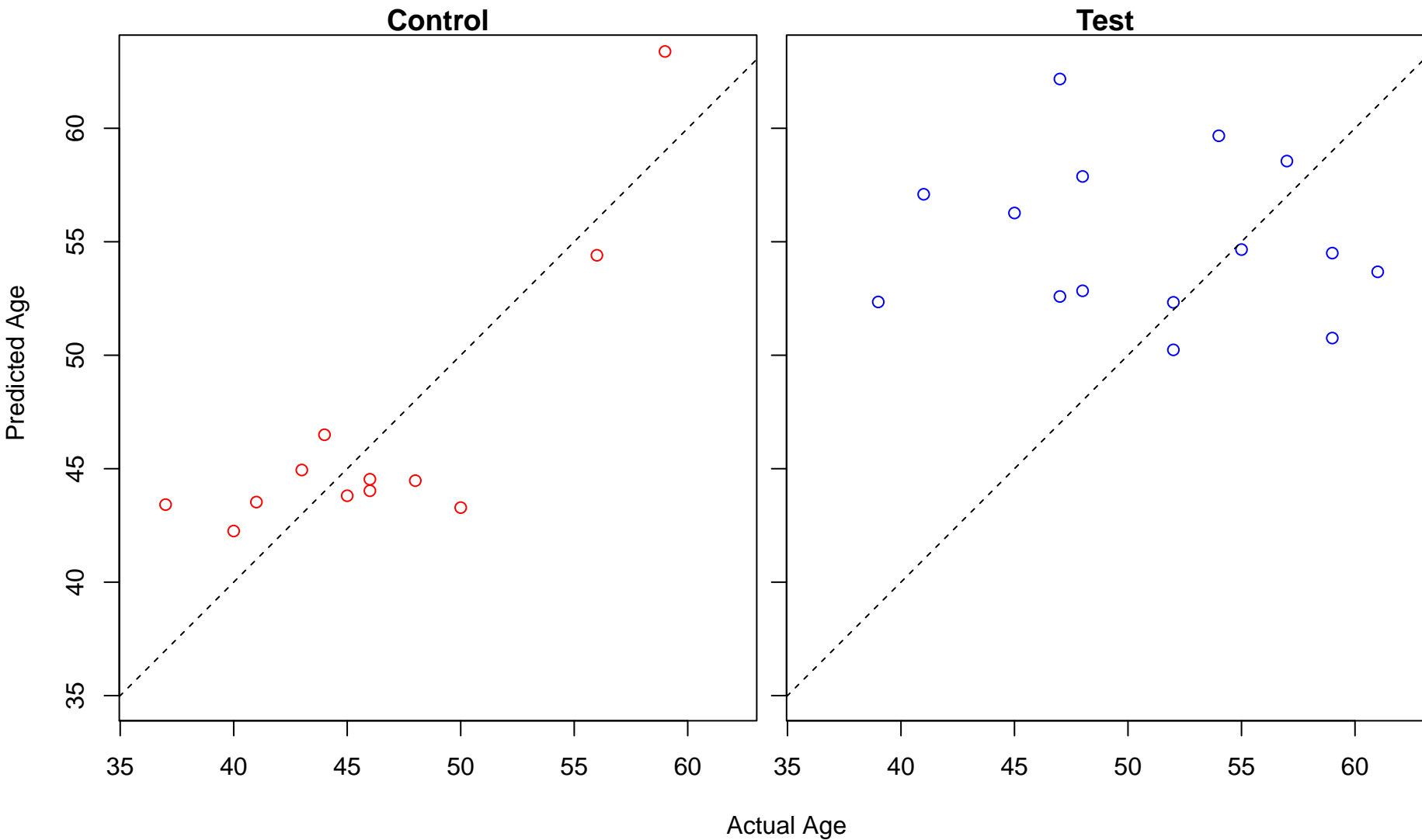
protein polymerization (Score: 2.511885)



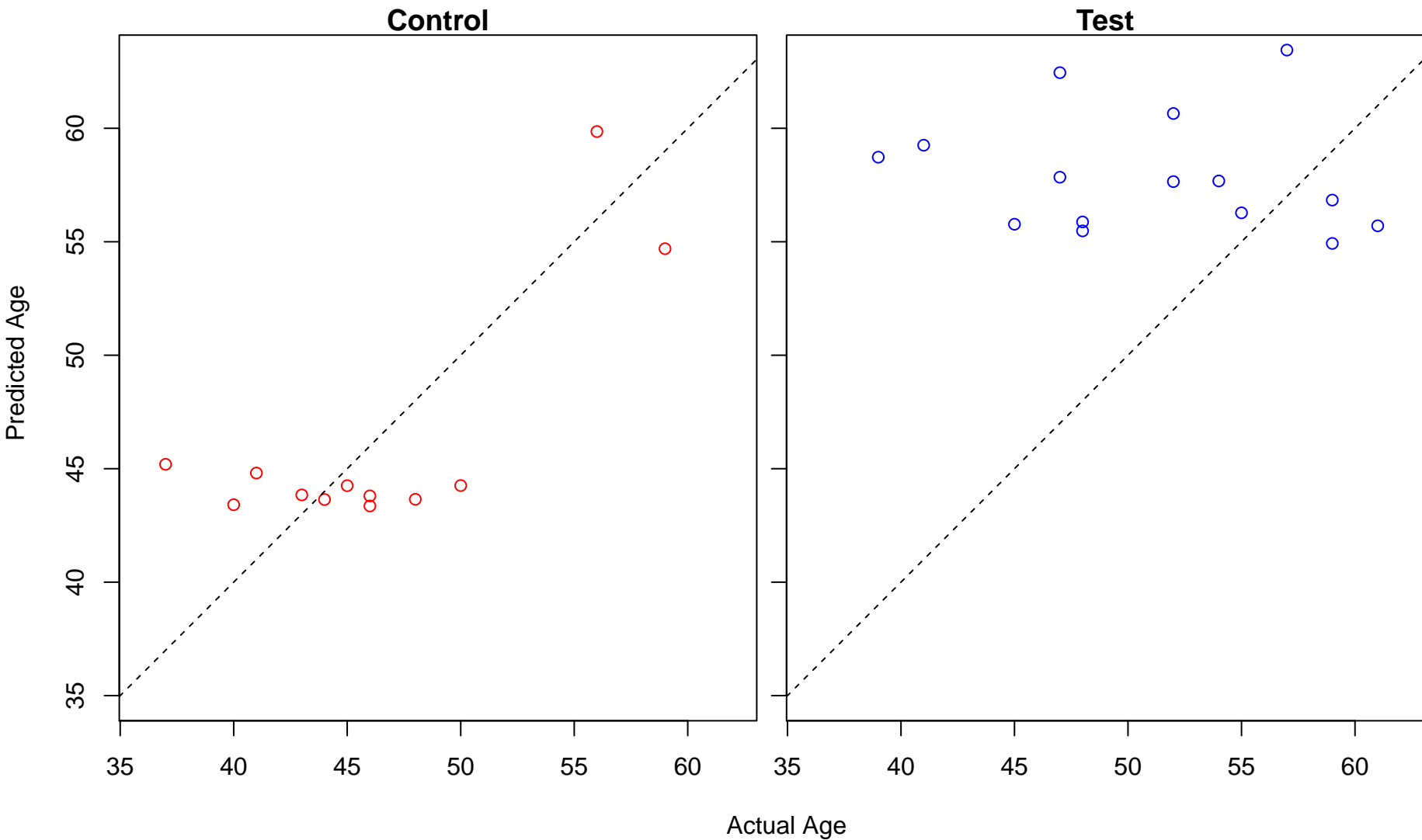
multi-organism behavior (Score: 2.510130)



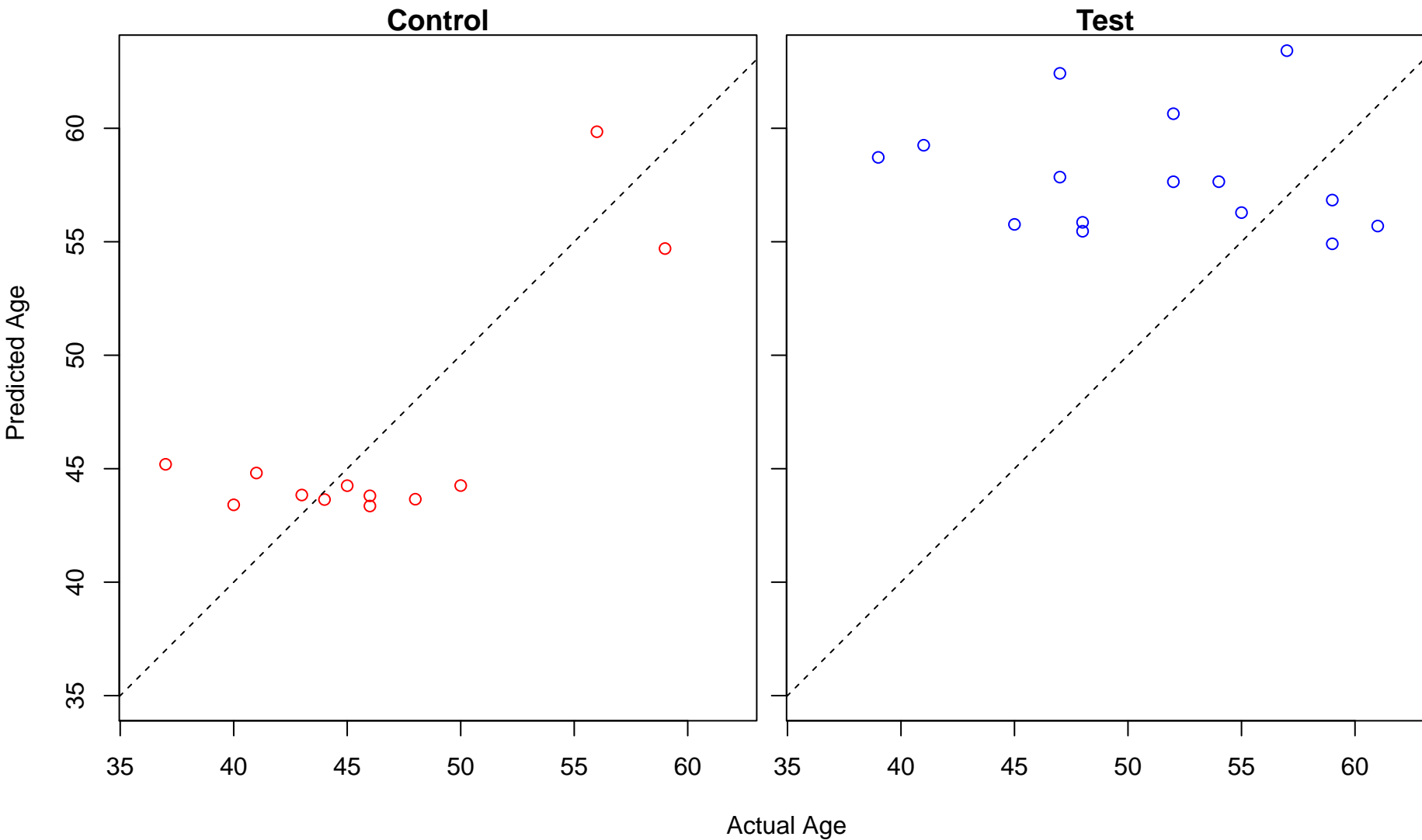
organ growth (Score: 2.509762)



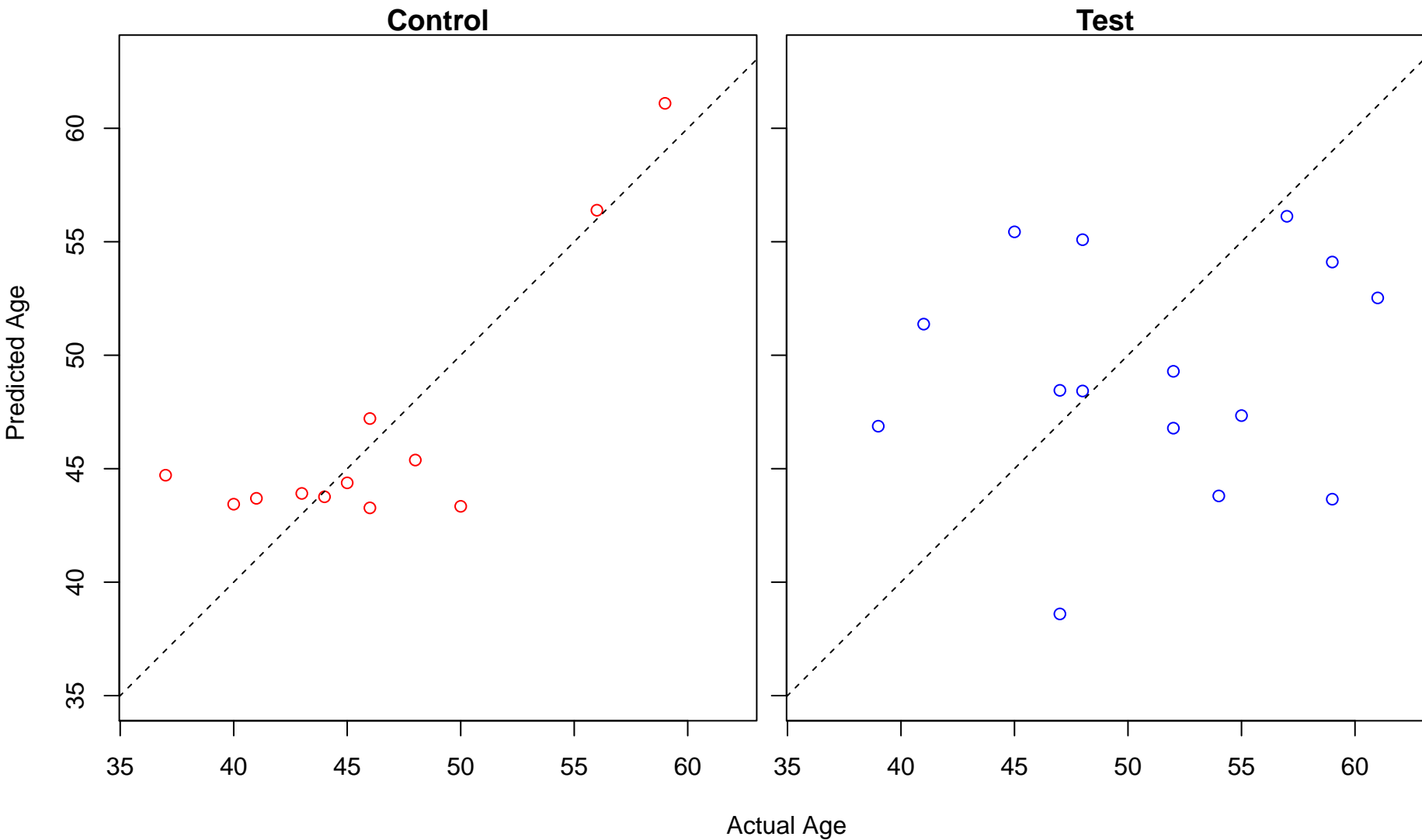
positive regulation of cell motility (Score: 2.503861)



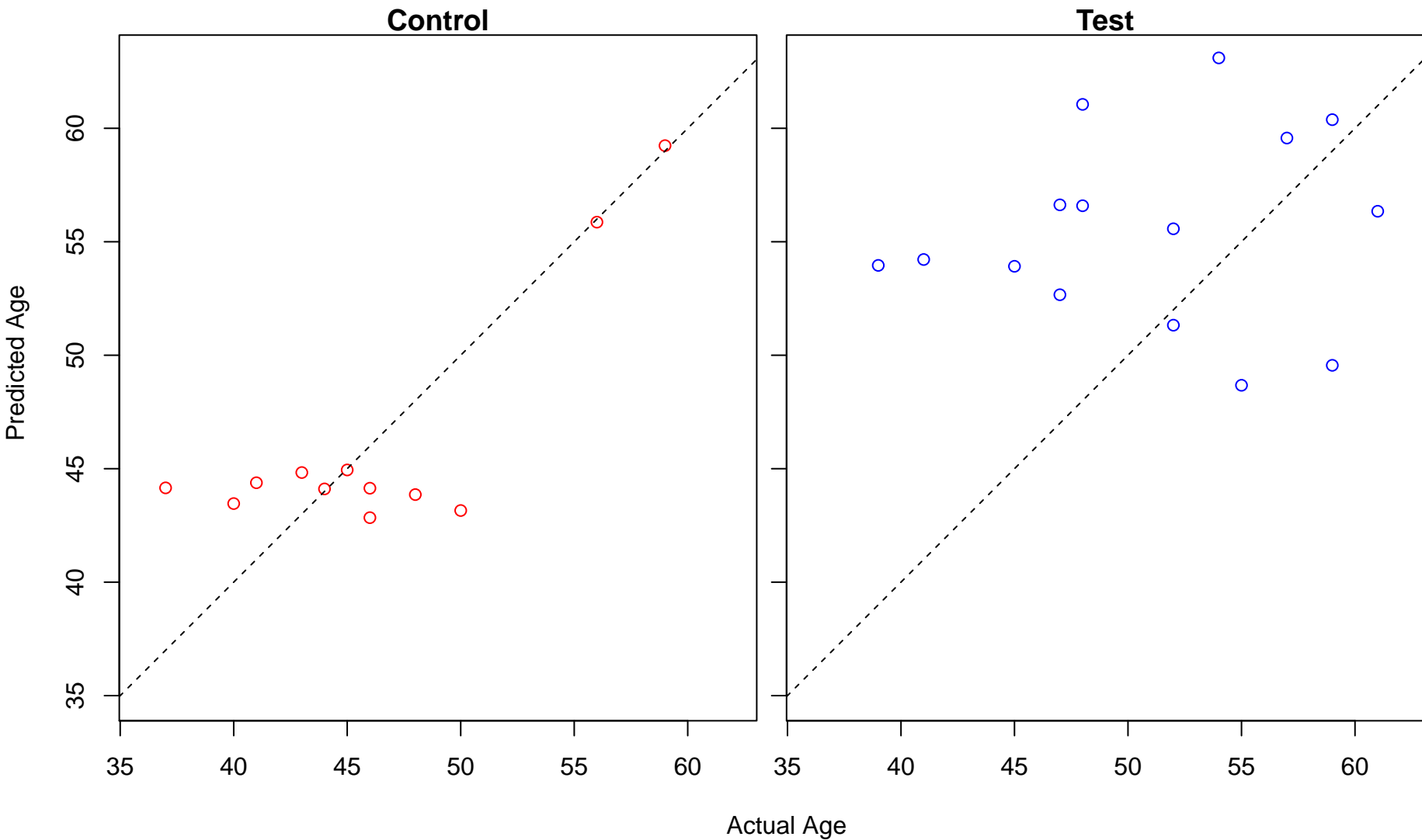
positive regulation of cell migration (Score: 2.502683)



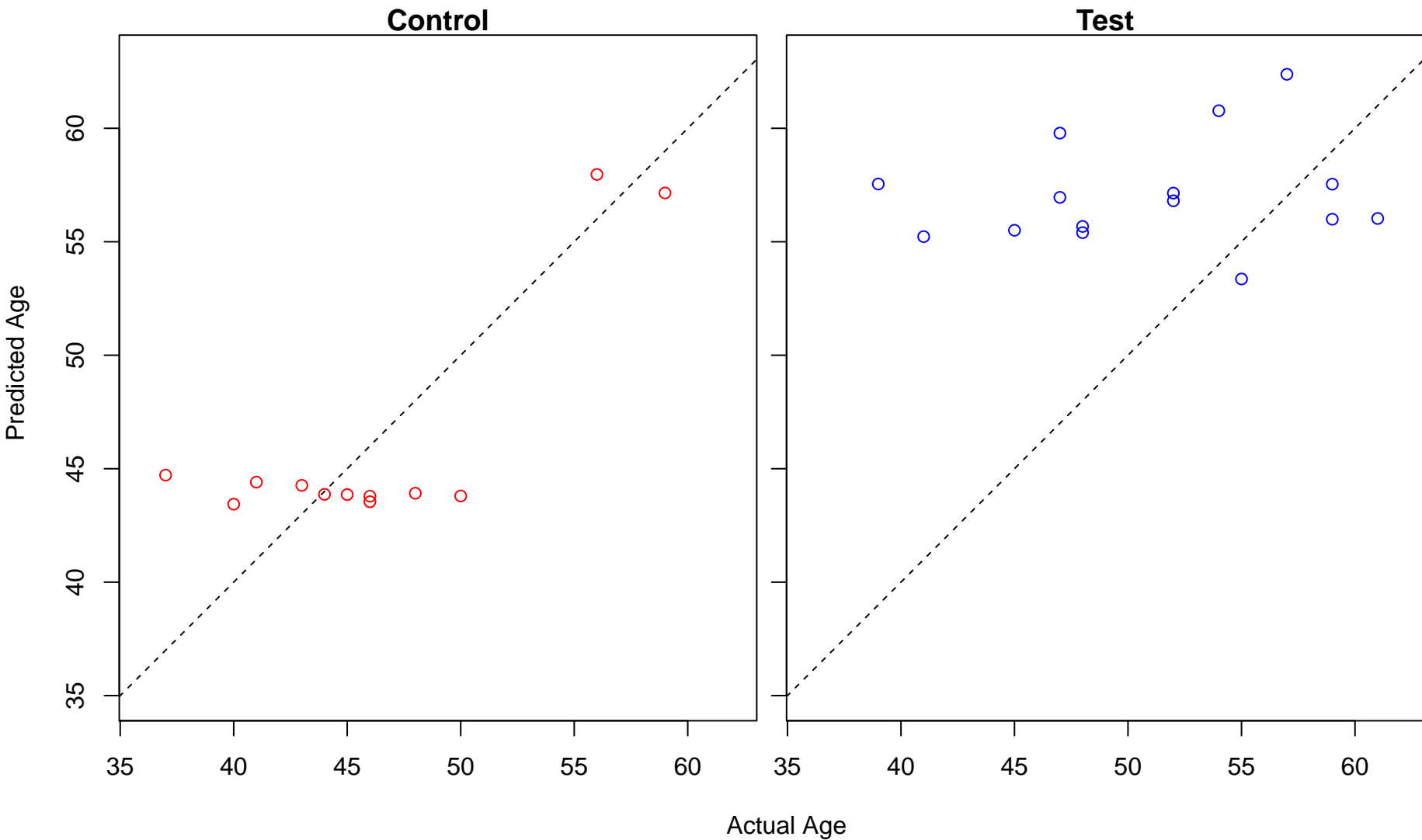
positive regulation of epithelial cell migration (Score: 2.501361)



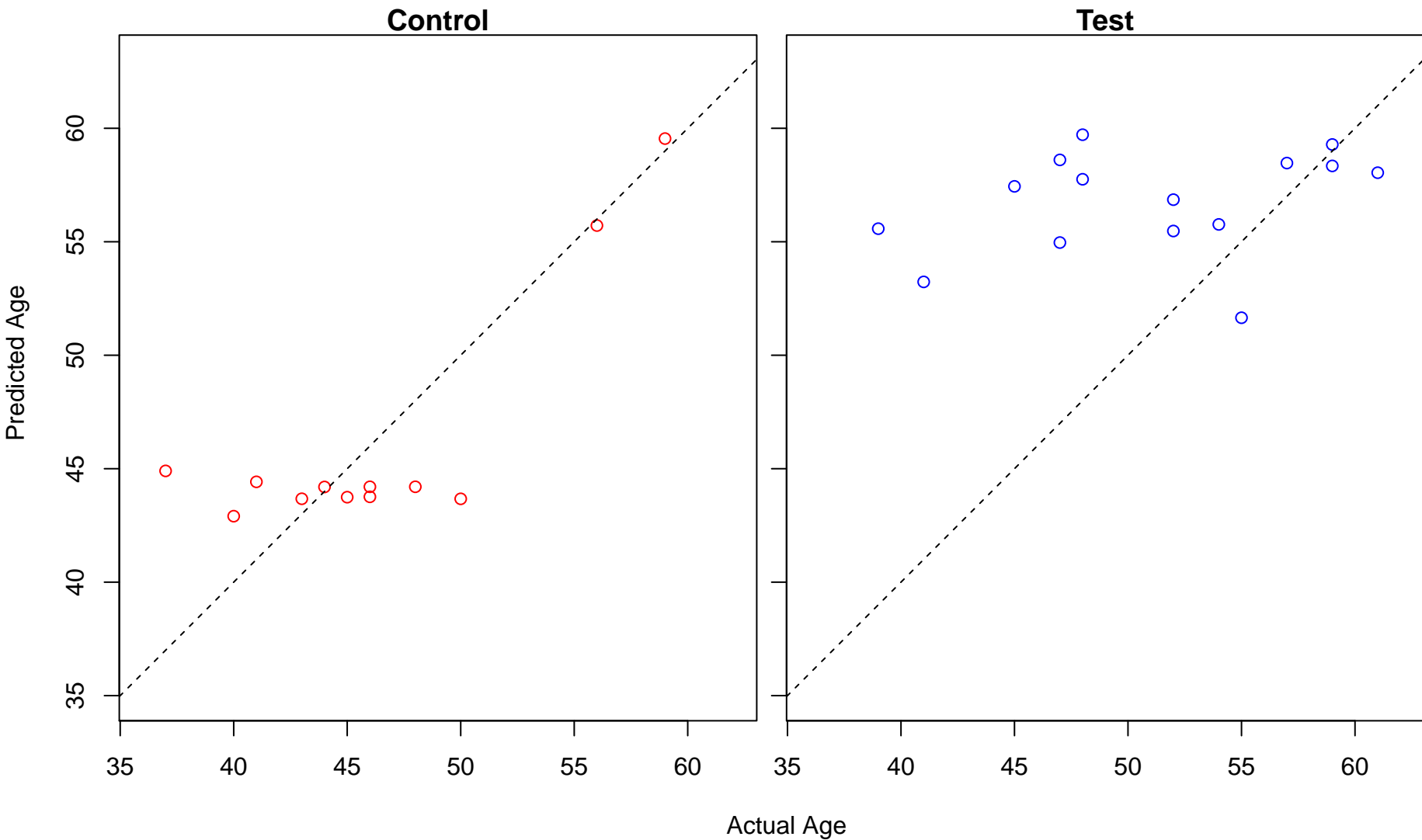
positive regulation of humoral immune response (Score: 2.500388)



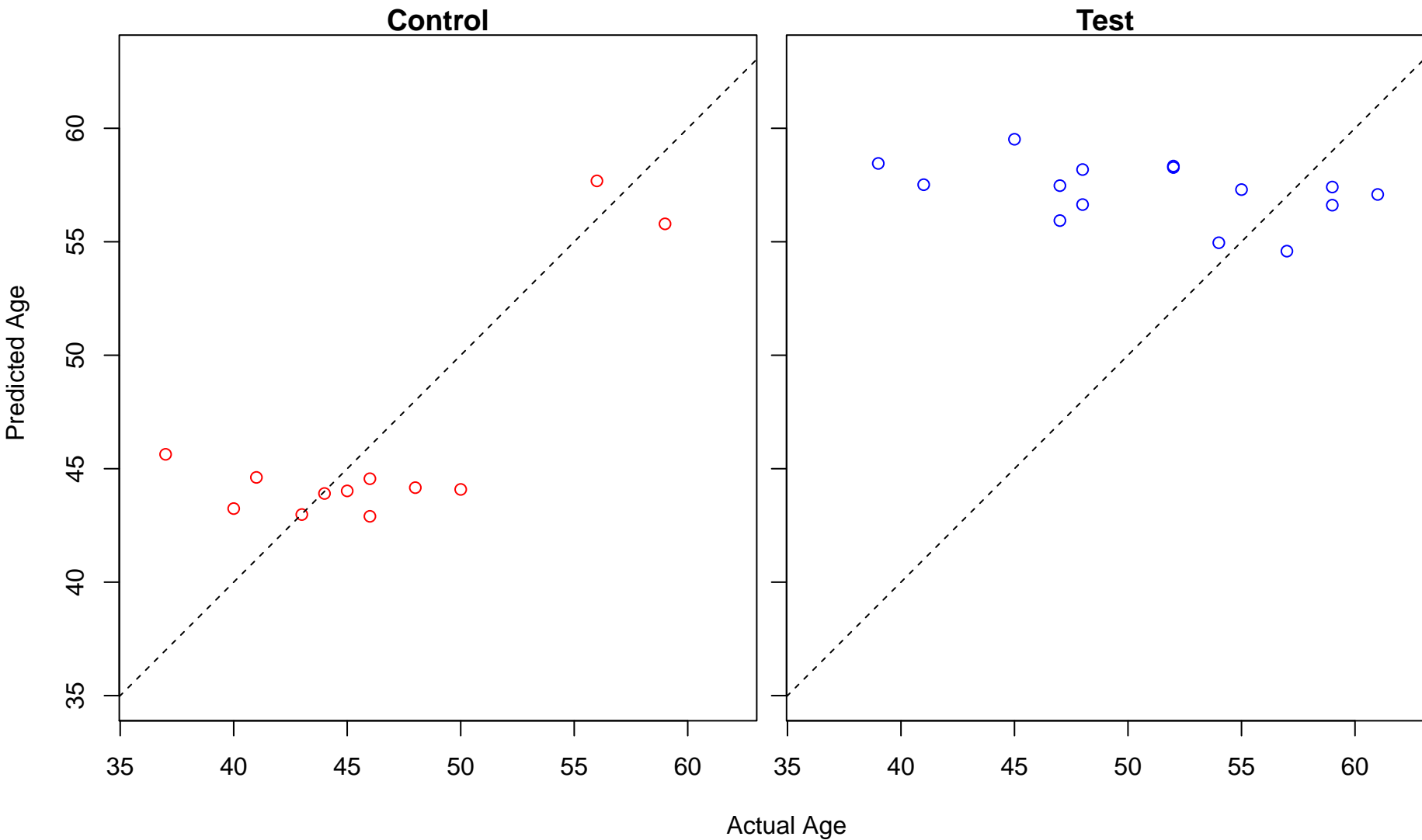
protein acylation (Score: 2.499881)



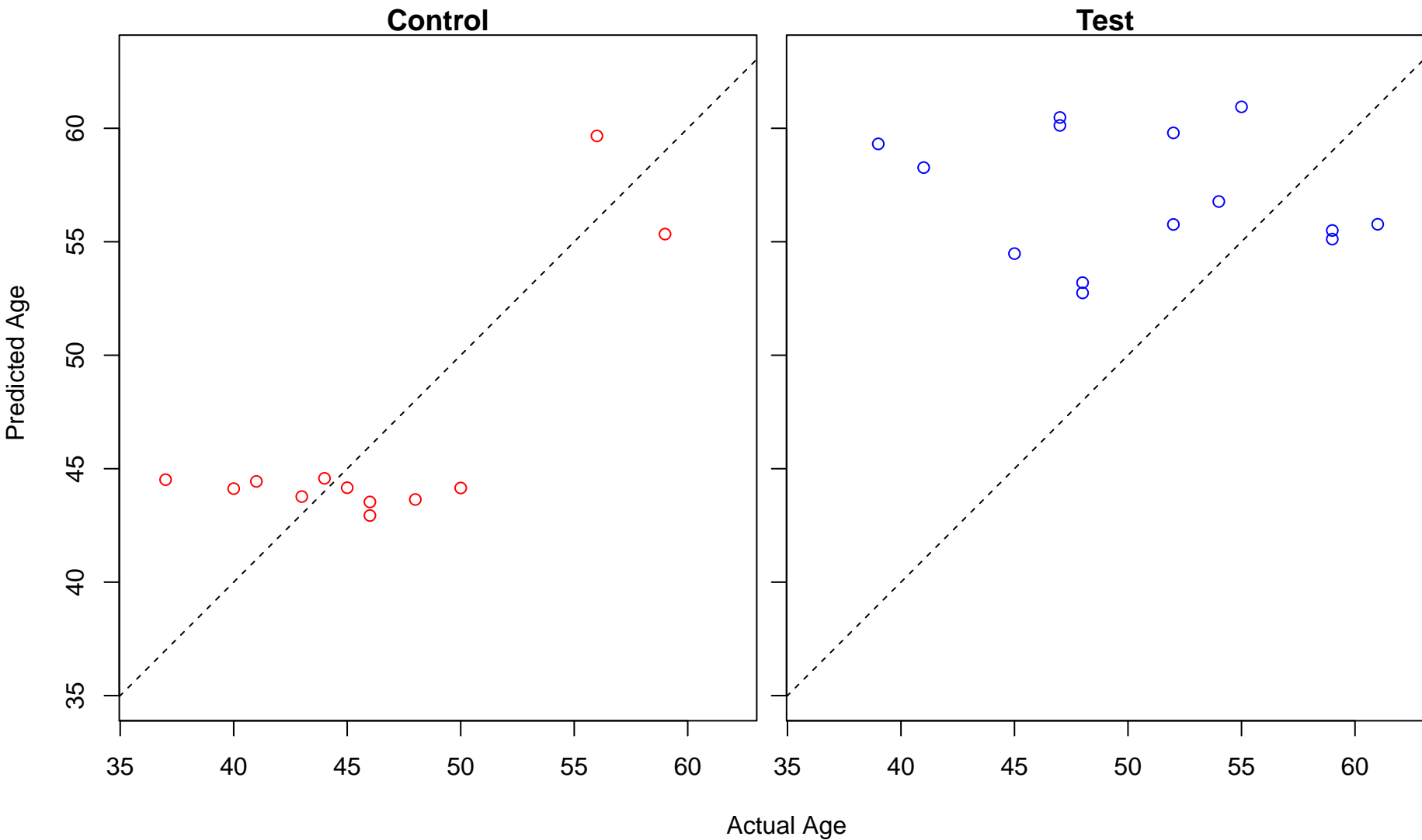
peroxisome organization (Score: 2.499296)



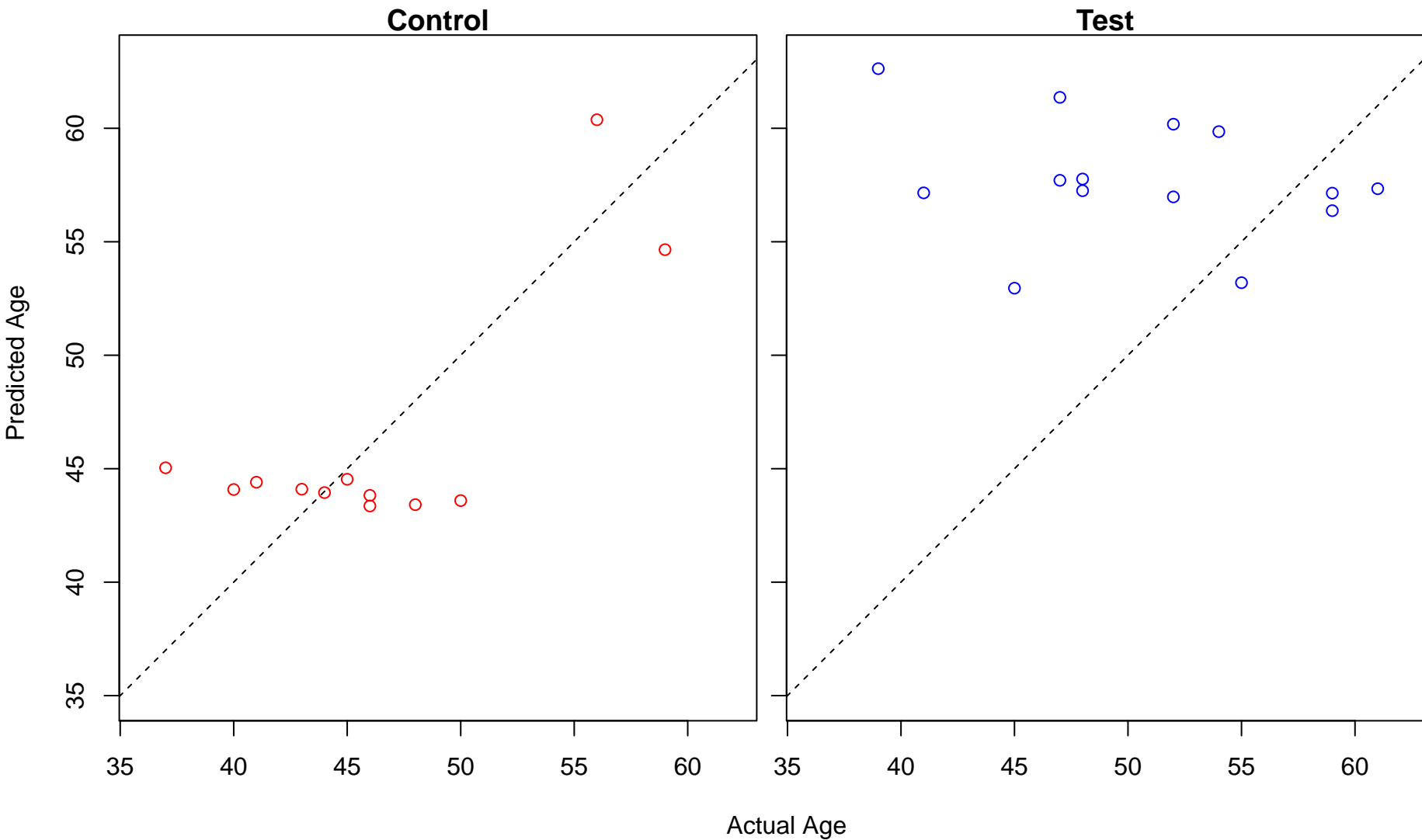
histone H3-K9 modification (Score: 2.497453)



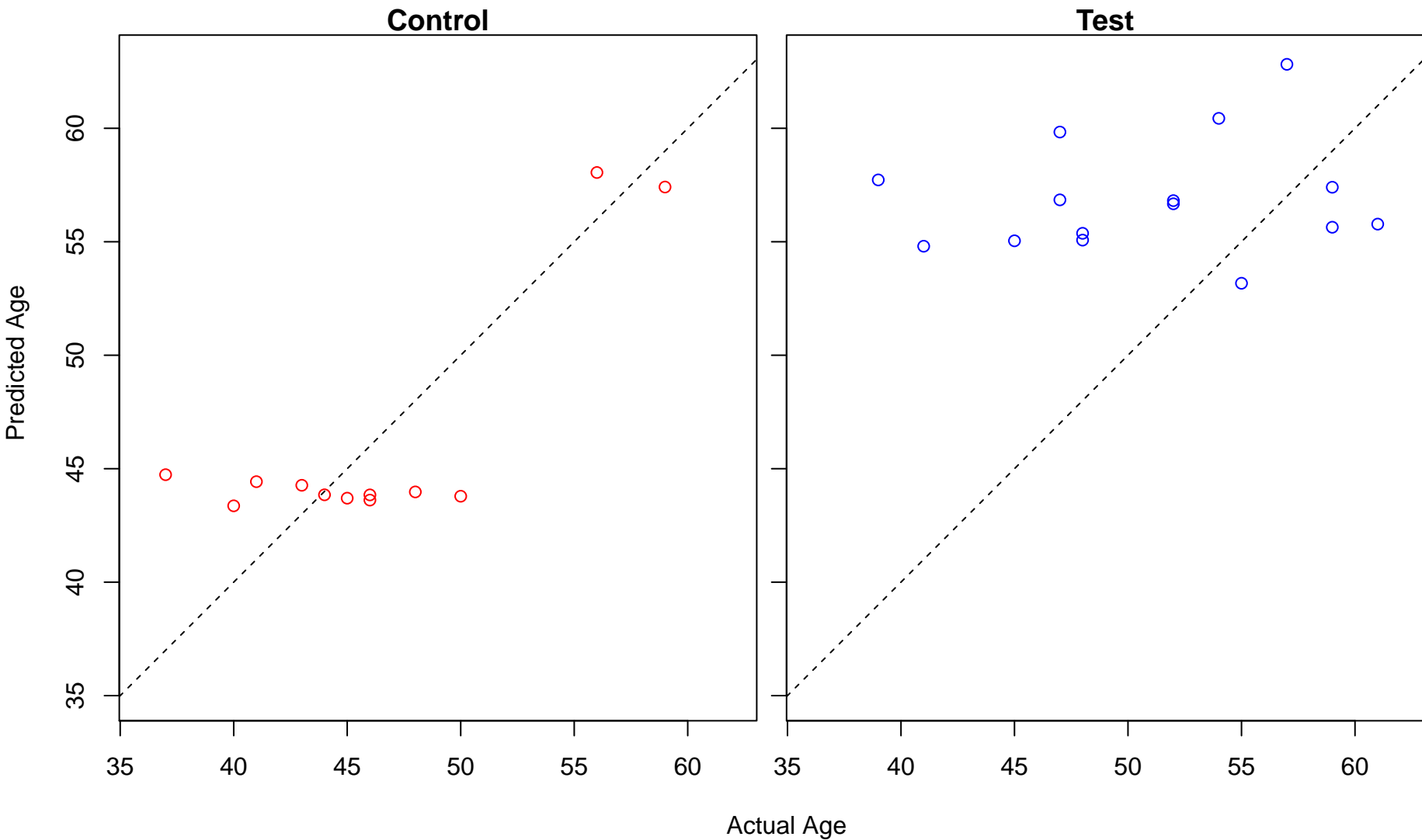
tube development (Score: 2.496005)



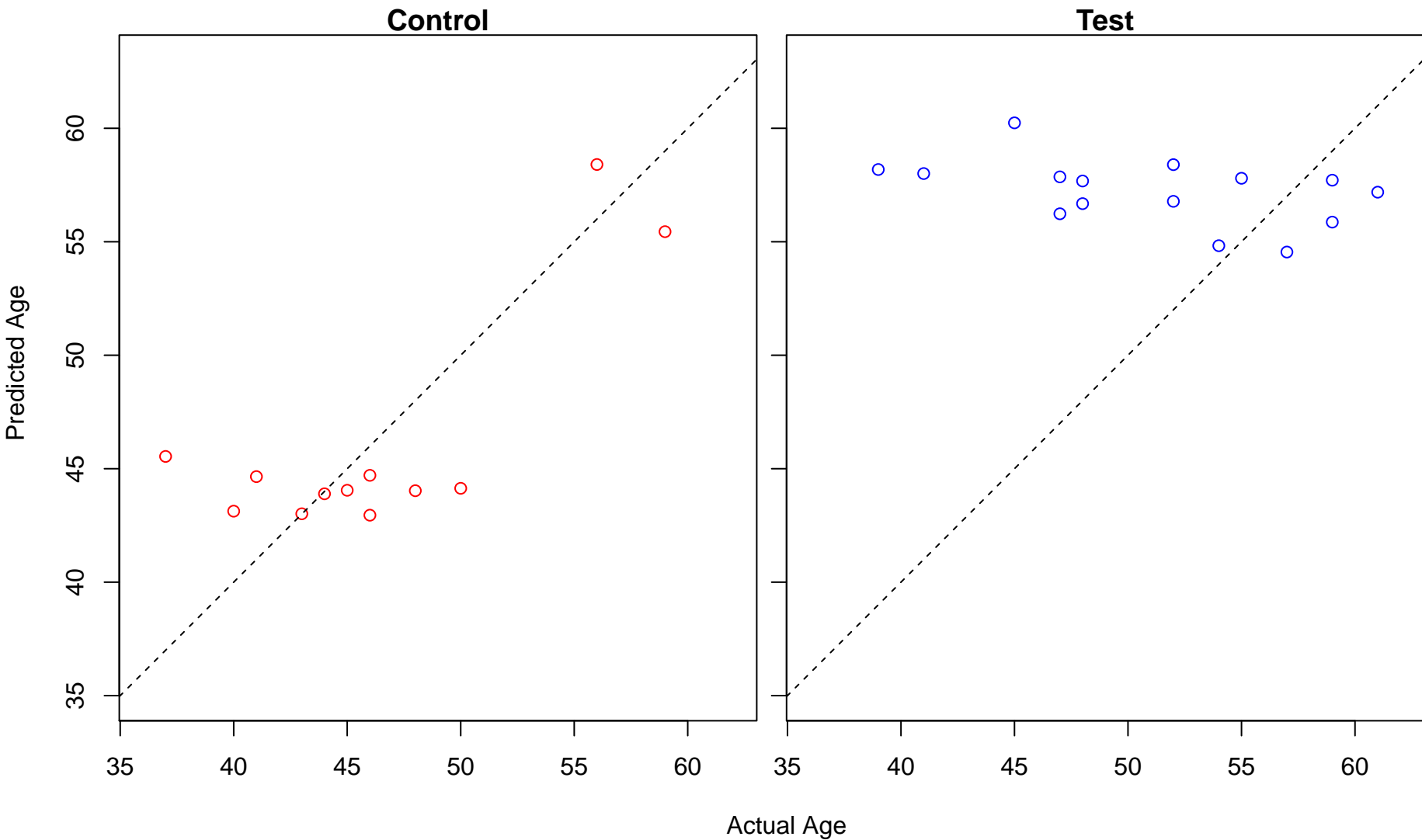
DNA replication (Score: 2.494934)



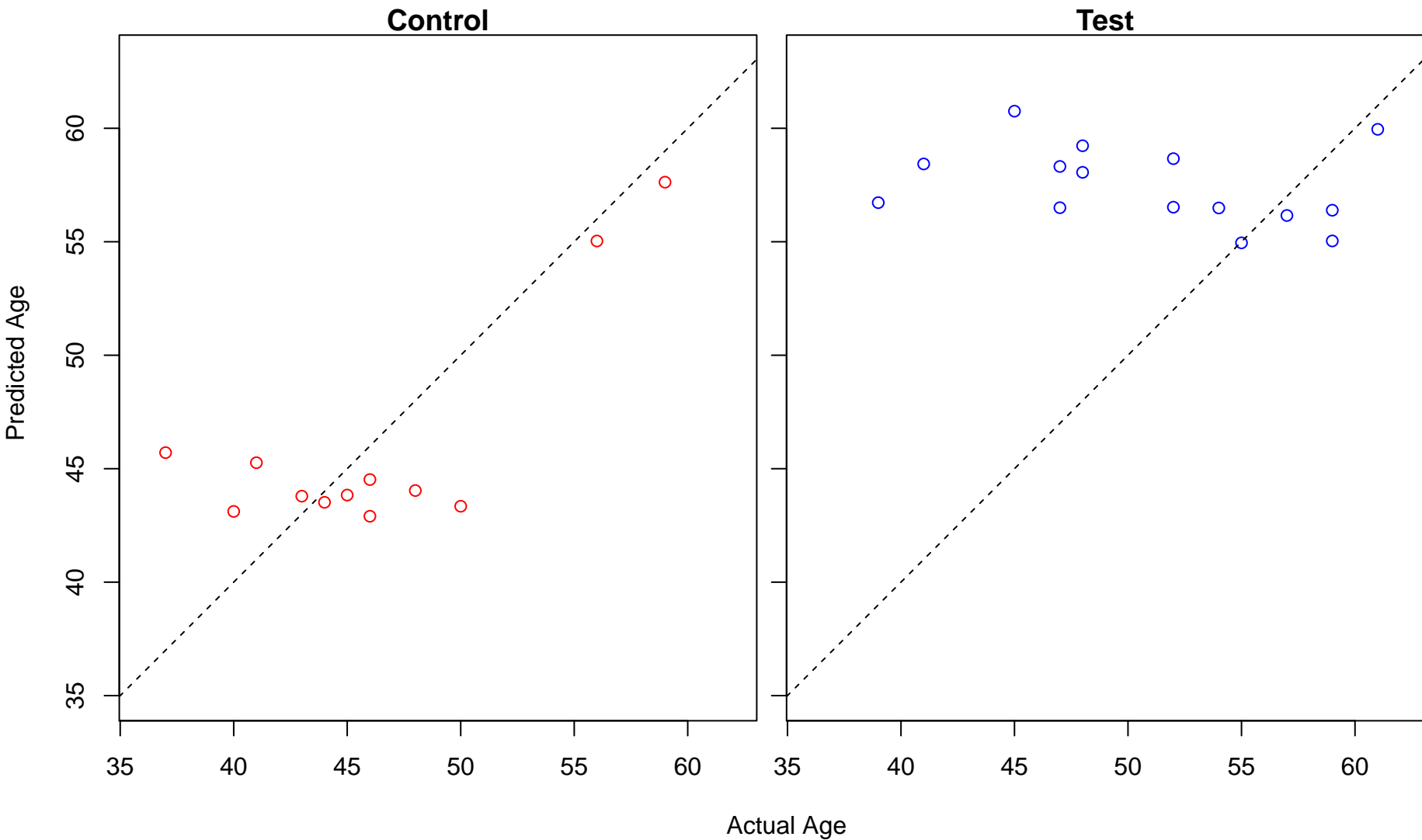
histone H4 acetylation (Score: 2.489561)



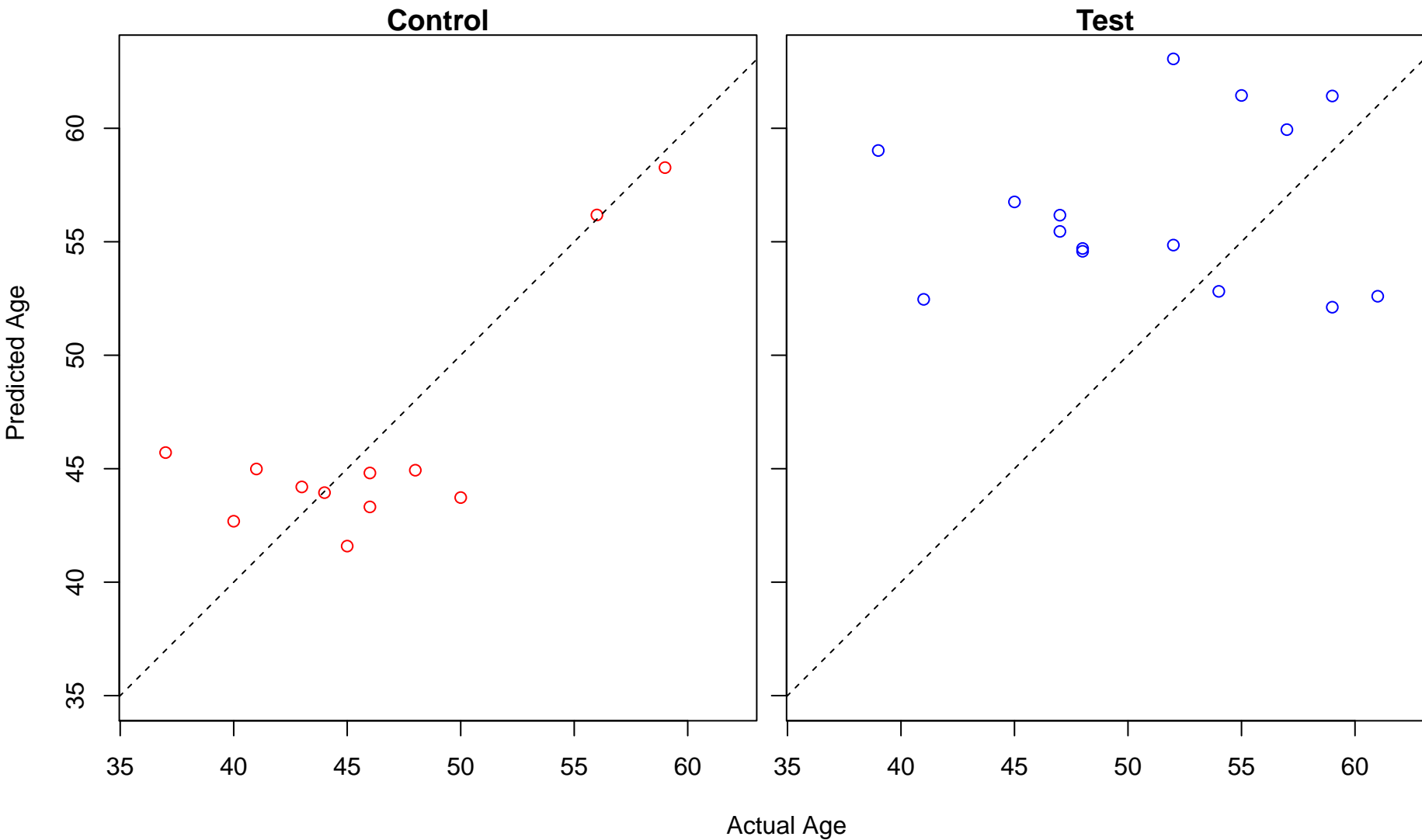
histone H3-K9 methylation (Score: 2.488866)



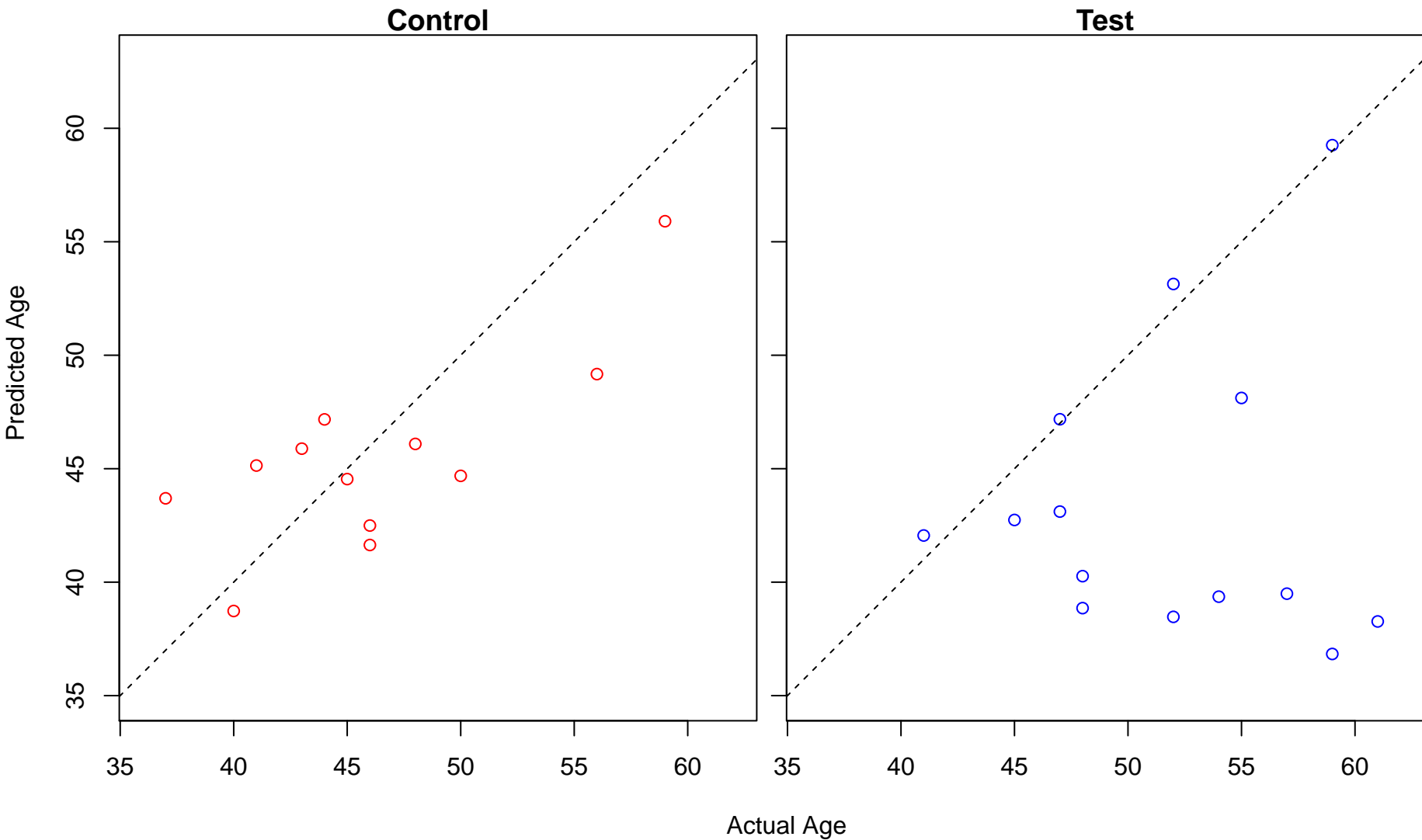
regulation of response to DNA damage stimulus (Score: 2.486199)



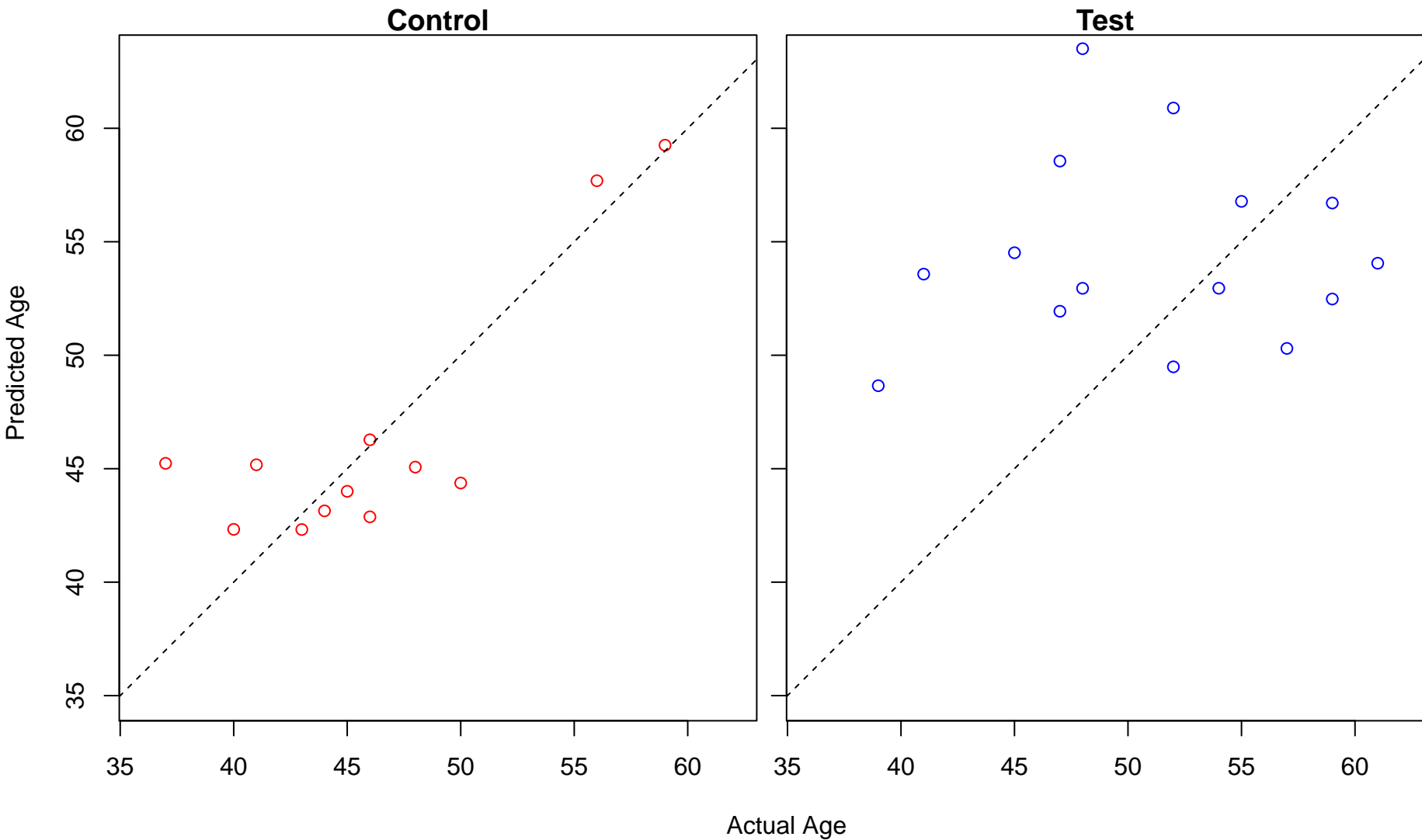
positive regulation of autophagosome assembly (Score: 2.483712)



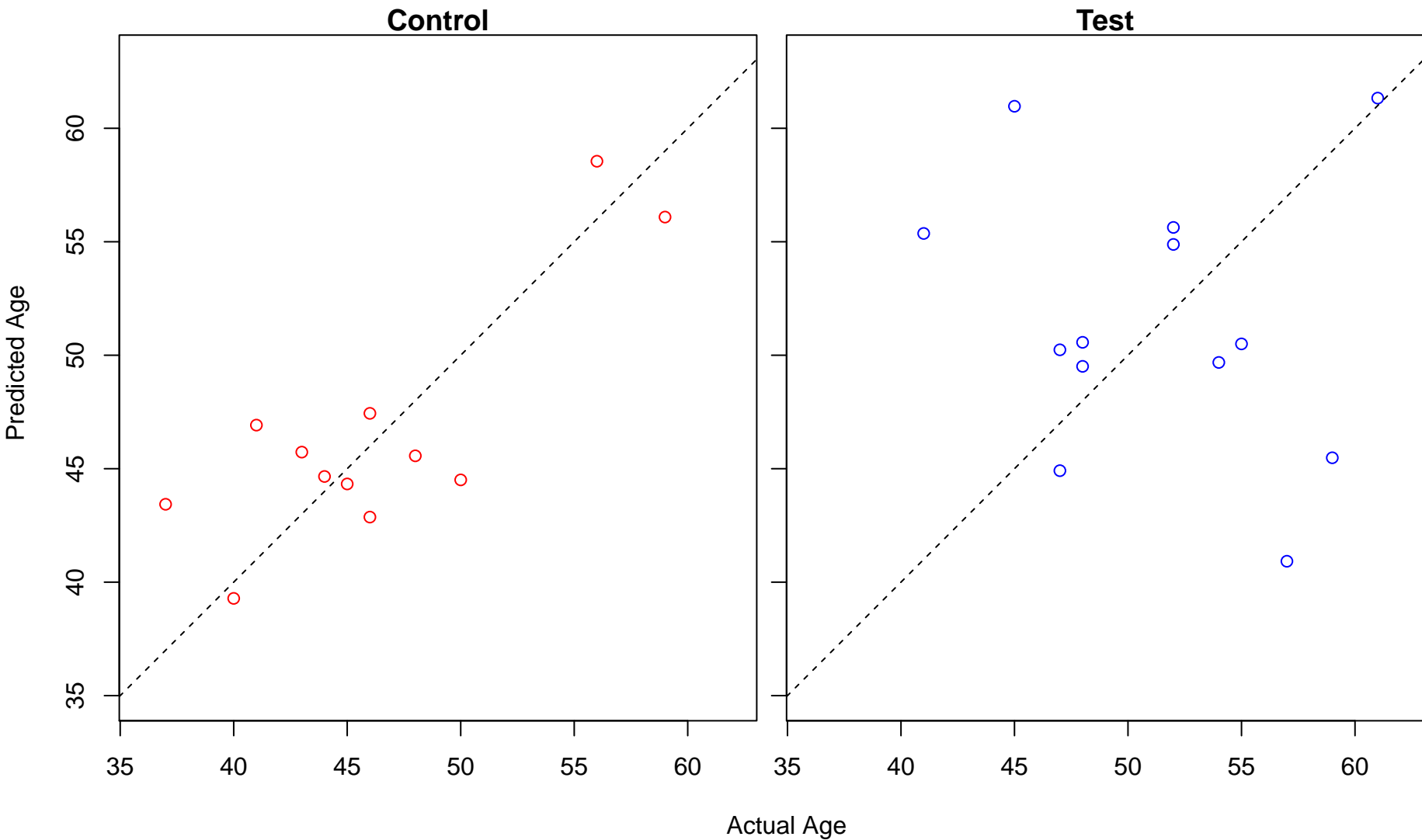
translational initiation (Score: 2.482116)



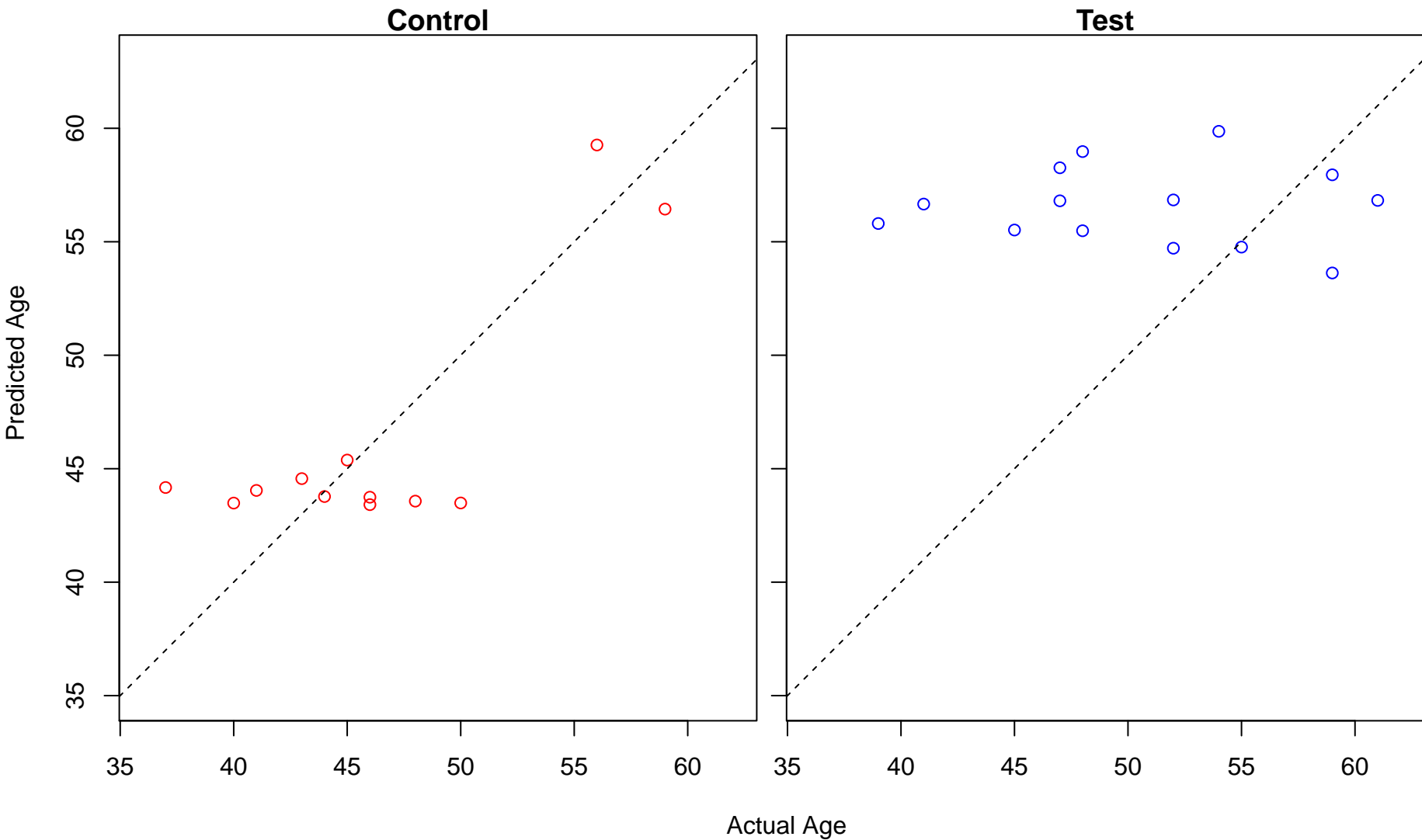
protein K11-linked ubiquitination (Score: 2.476913)



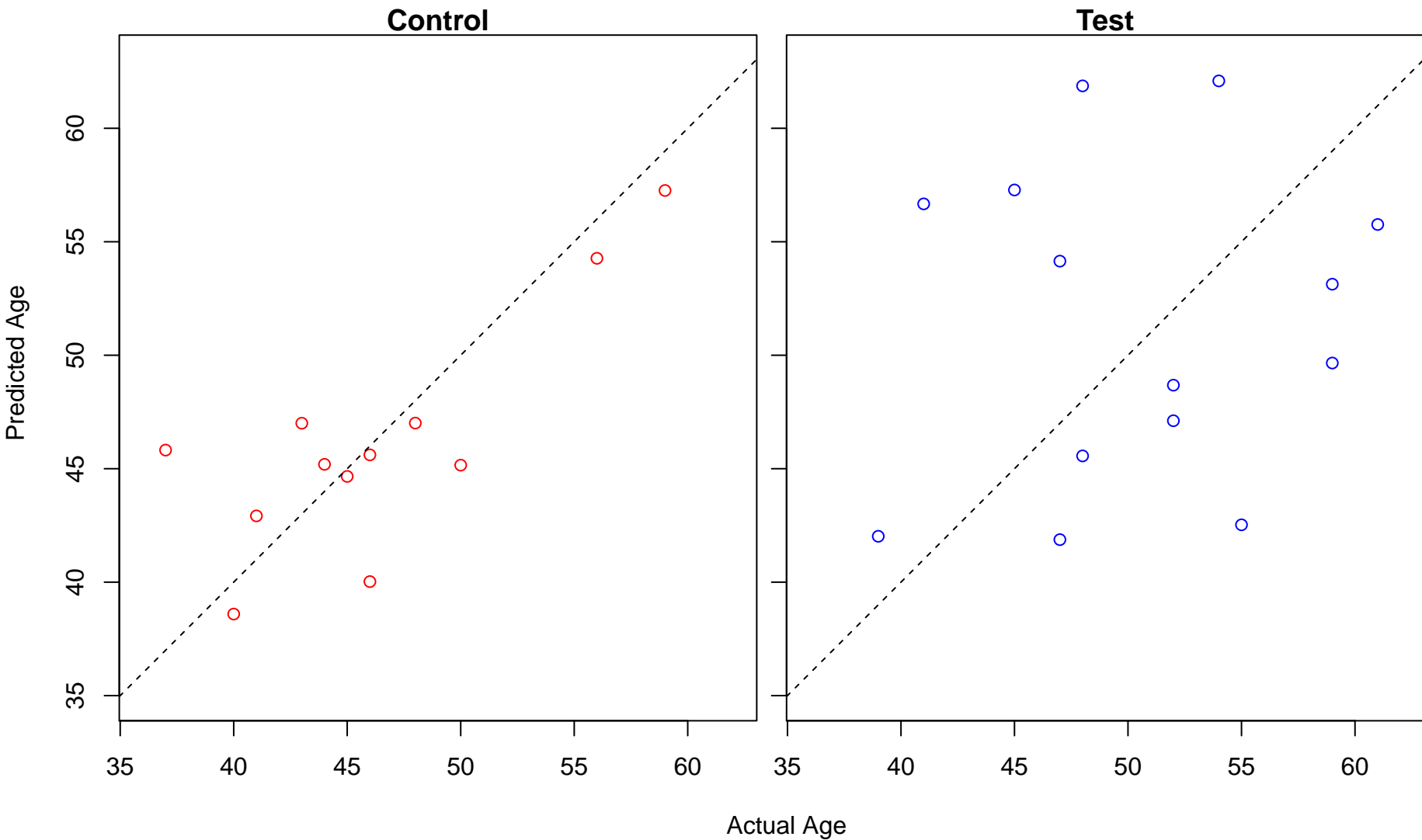
regulation of peptide secretion (Score: 2.466755)



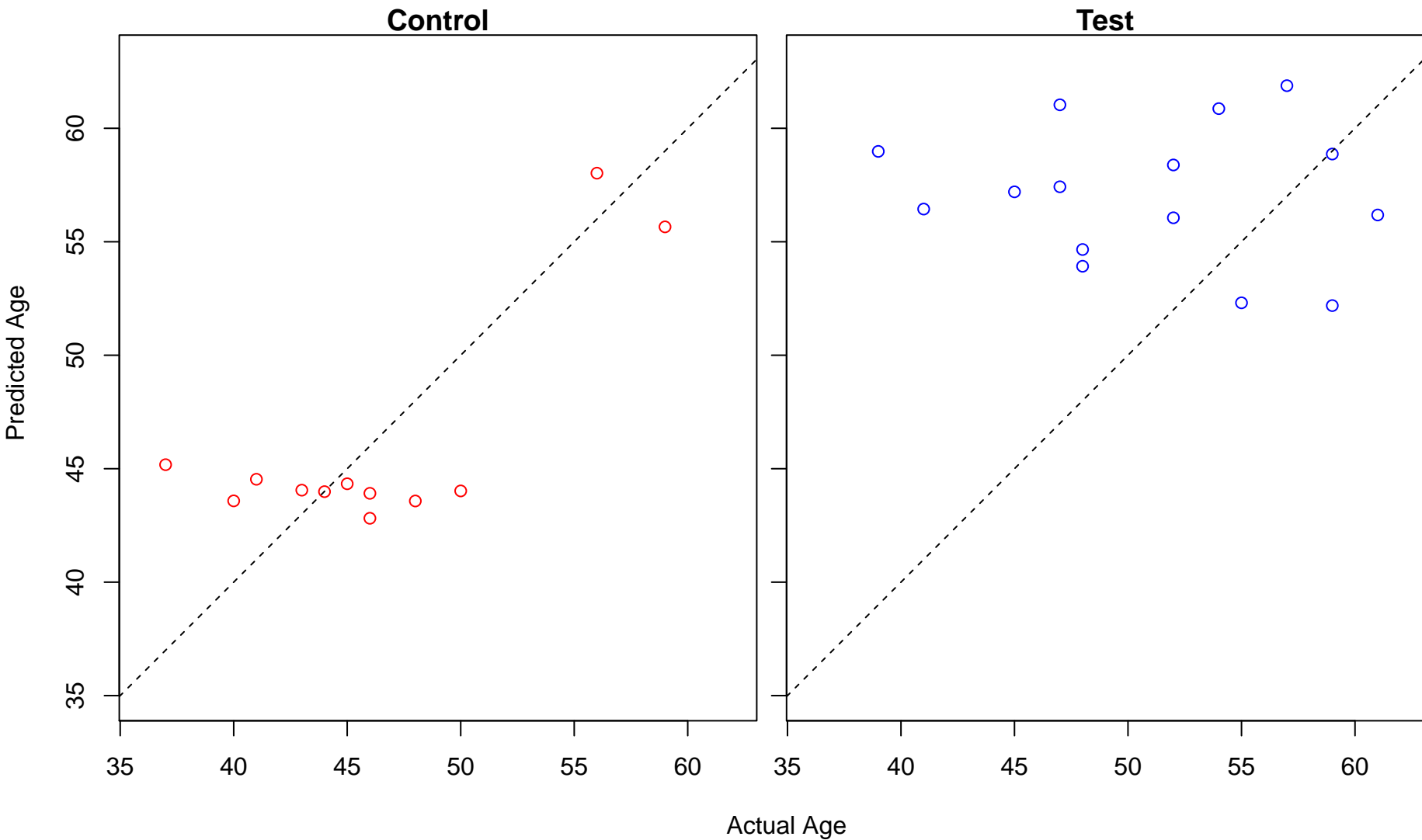
regulation of protein targeting to membrane (Score: 2.464253)



anatomical structure formation involved in morphogenesis (Score: 2.463304)

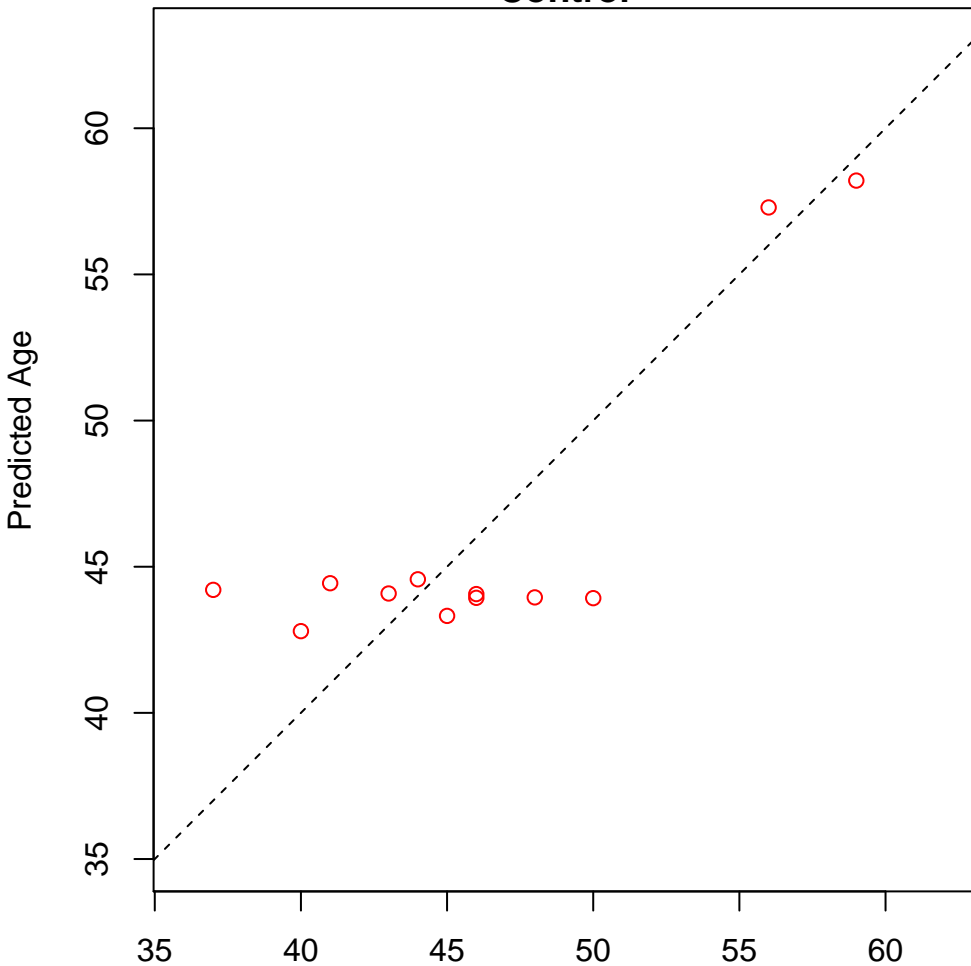


inorganic anion transport (Score: 2.463059)

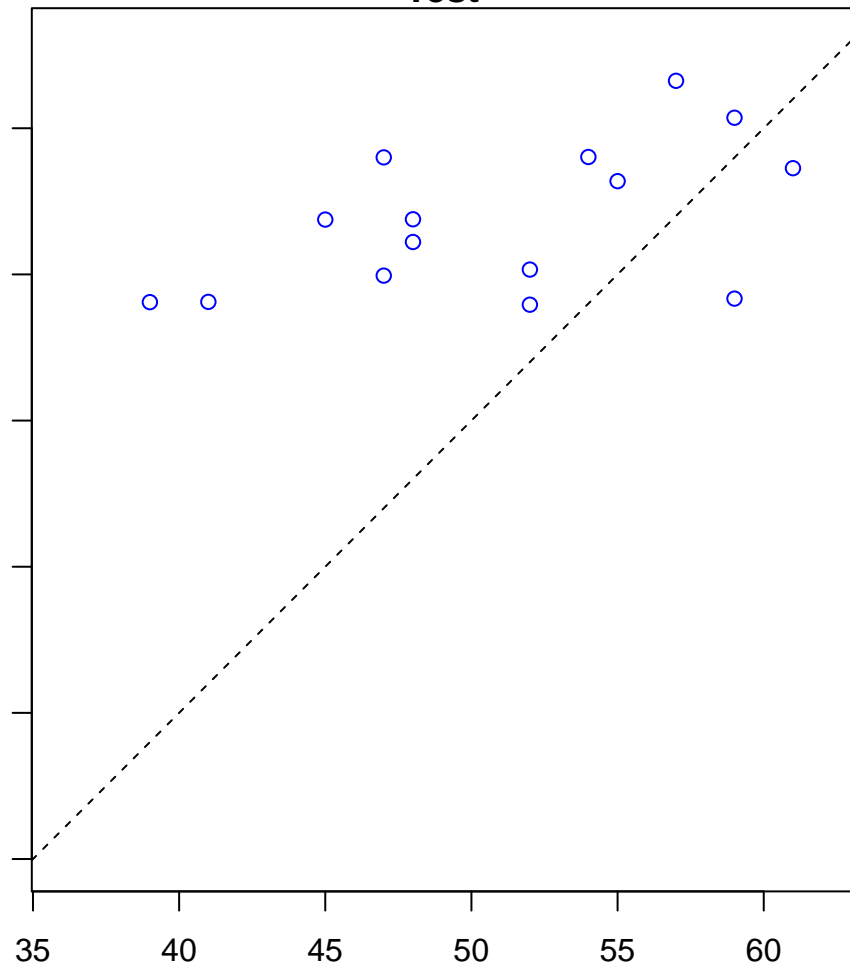


epithelial cell apoptotic process (Score: 2.460744)

Control

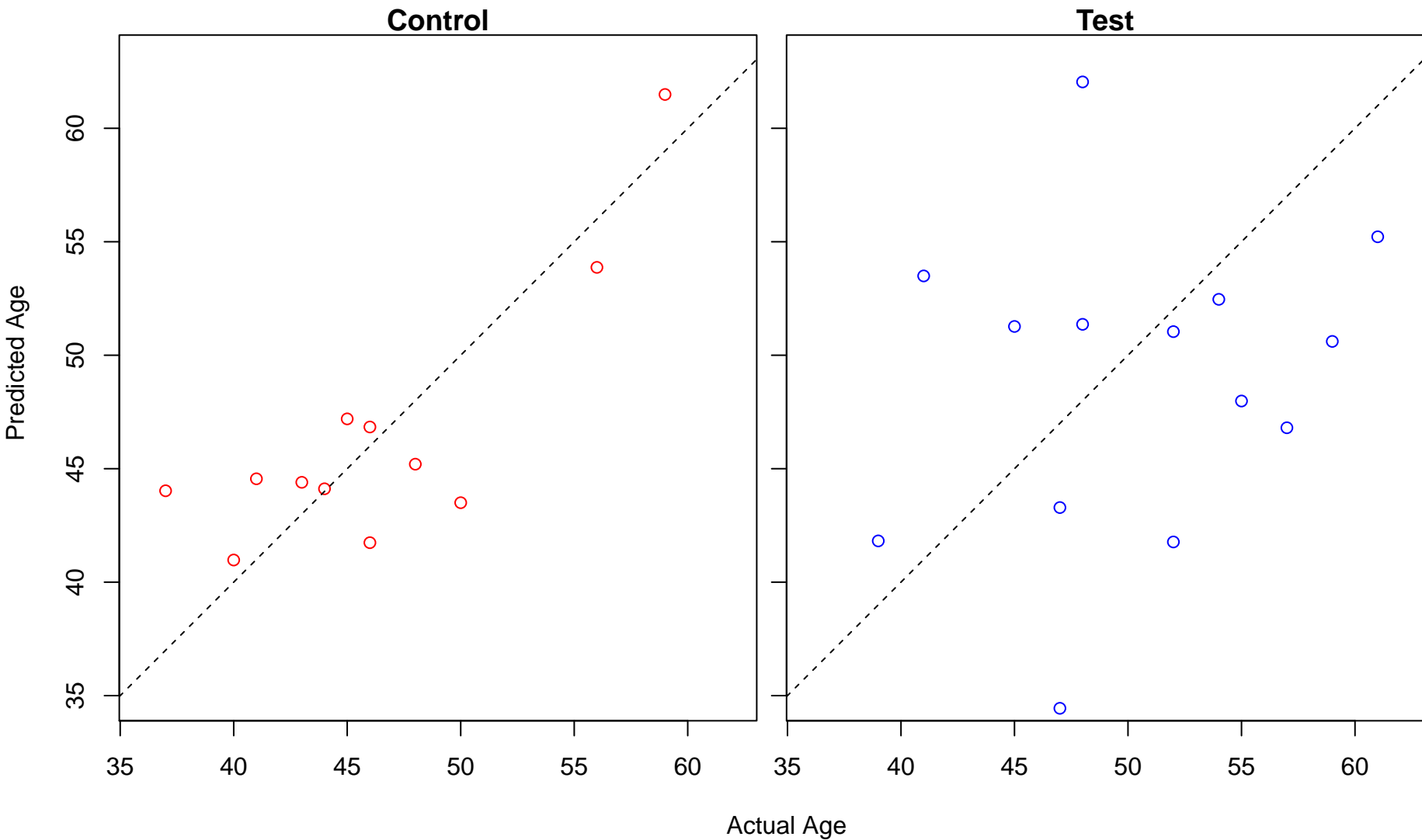


Test

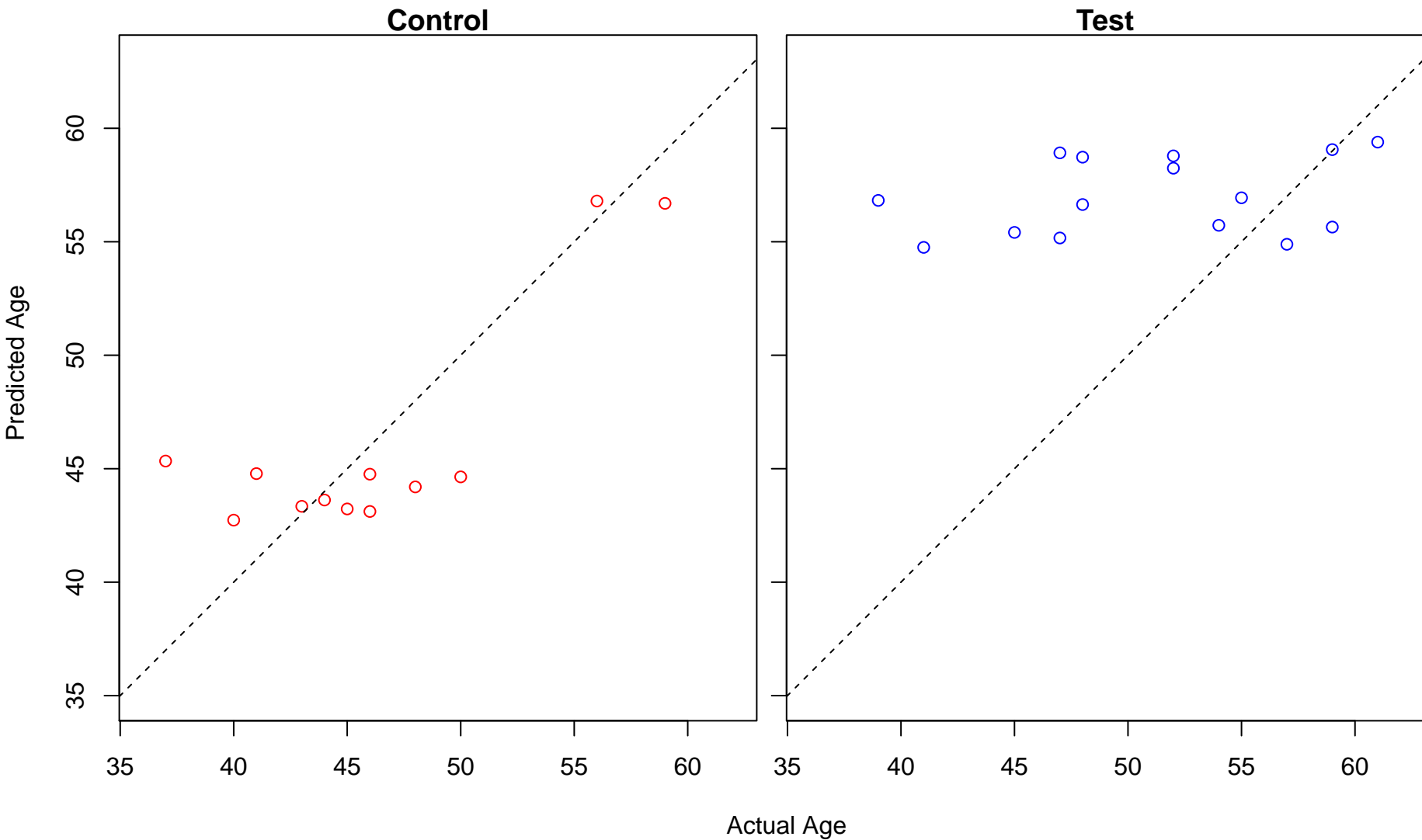


Actual Age

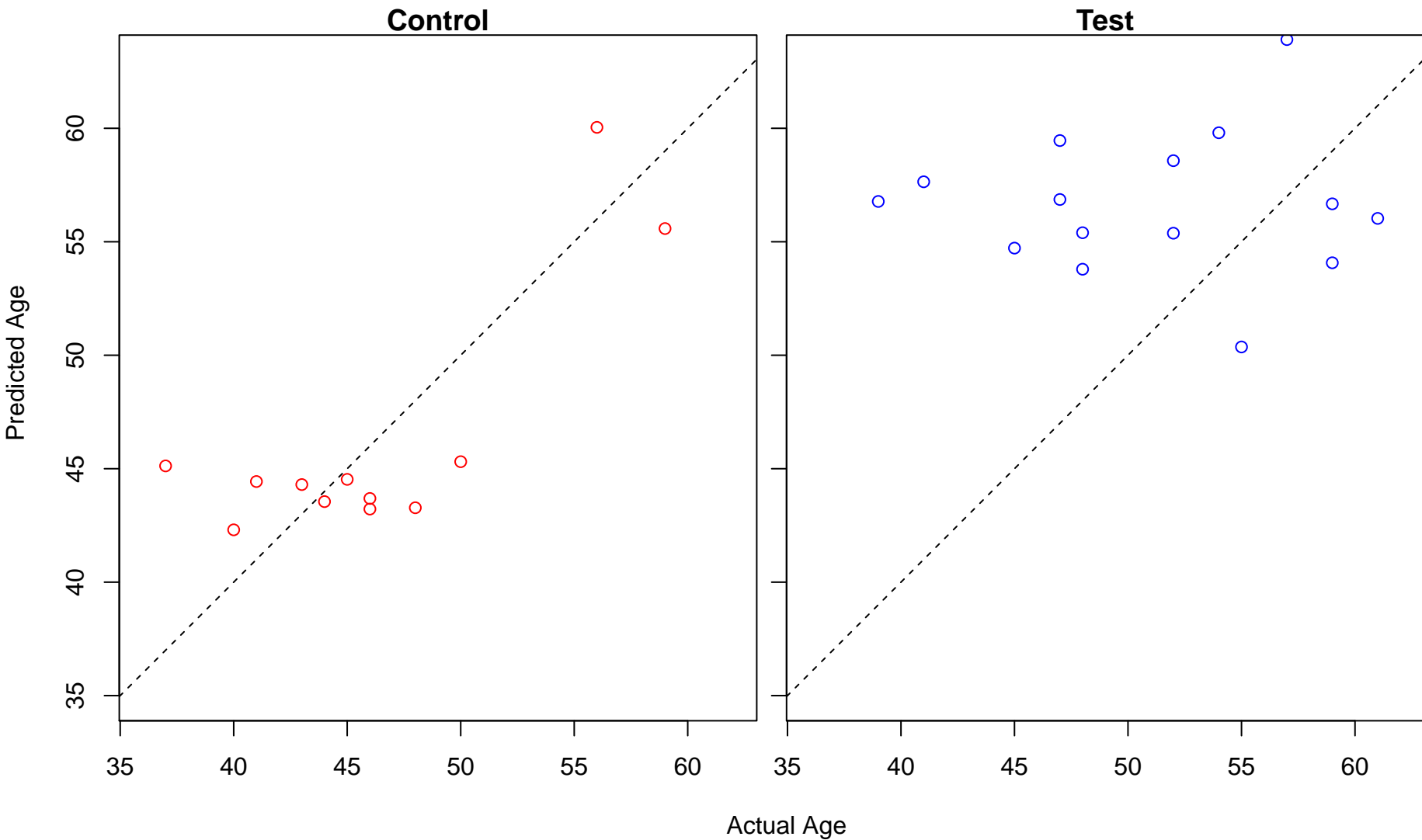
positive regulation of DNA biosynthetic process (Score: 2.454496)



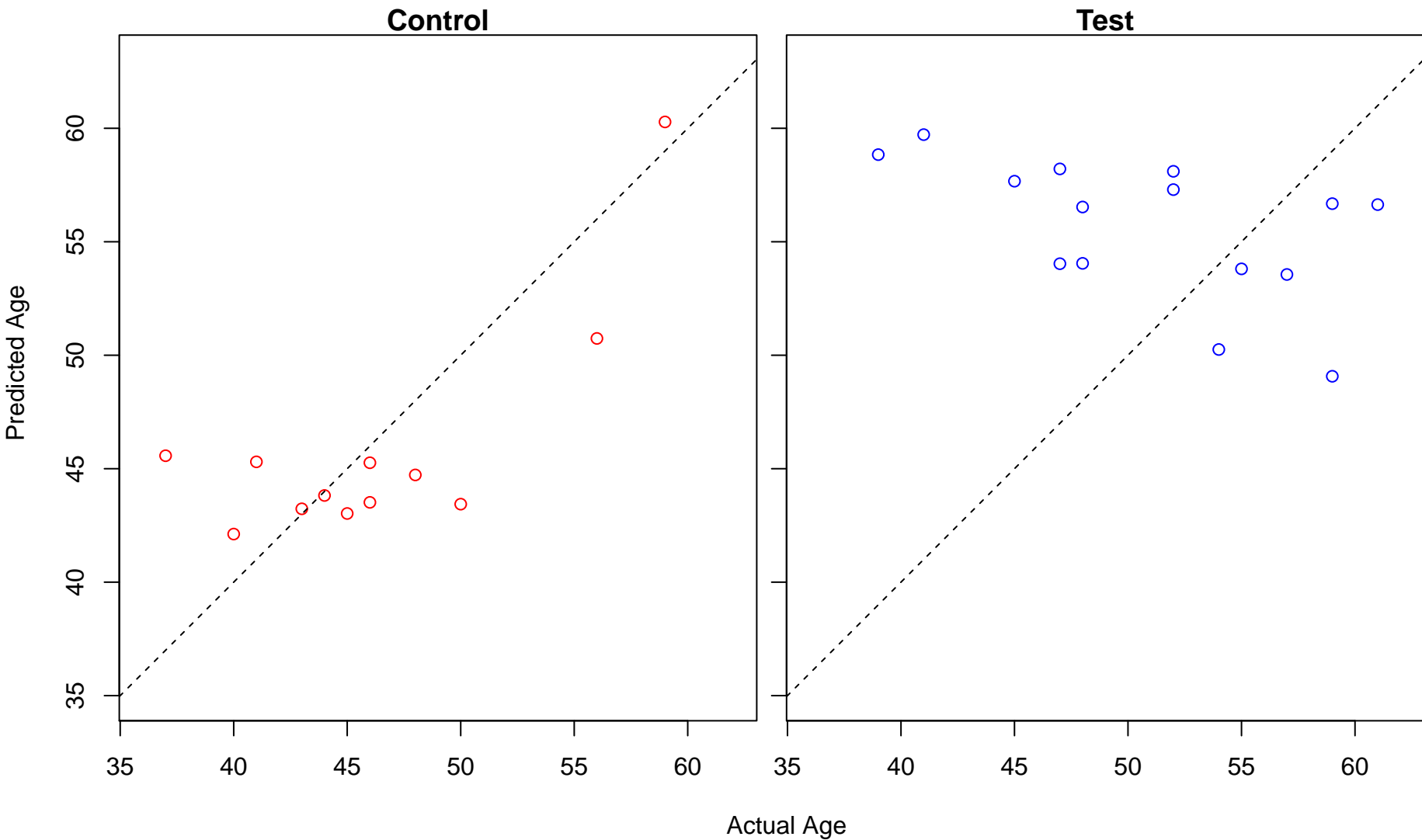
synapse assembly (Score: 2.451740)



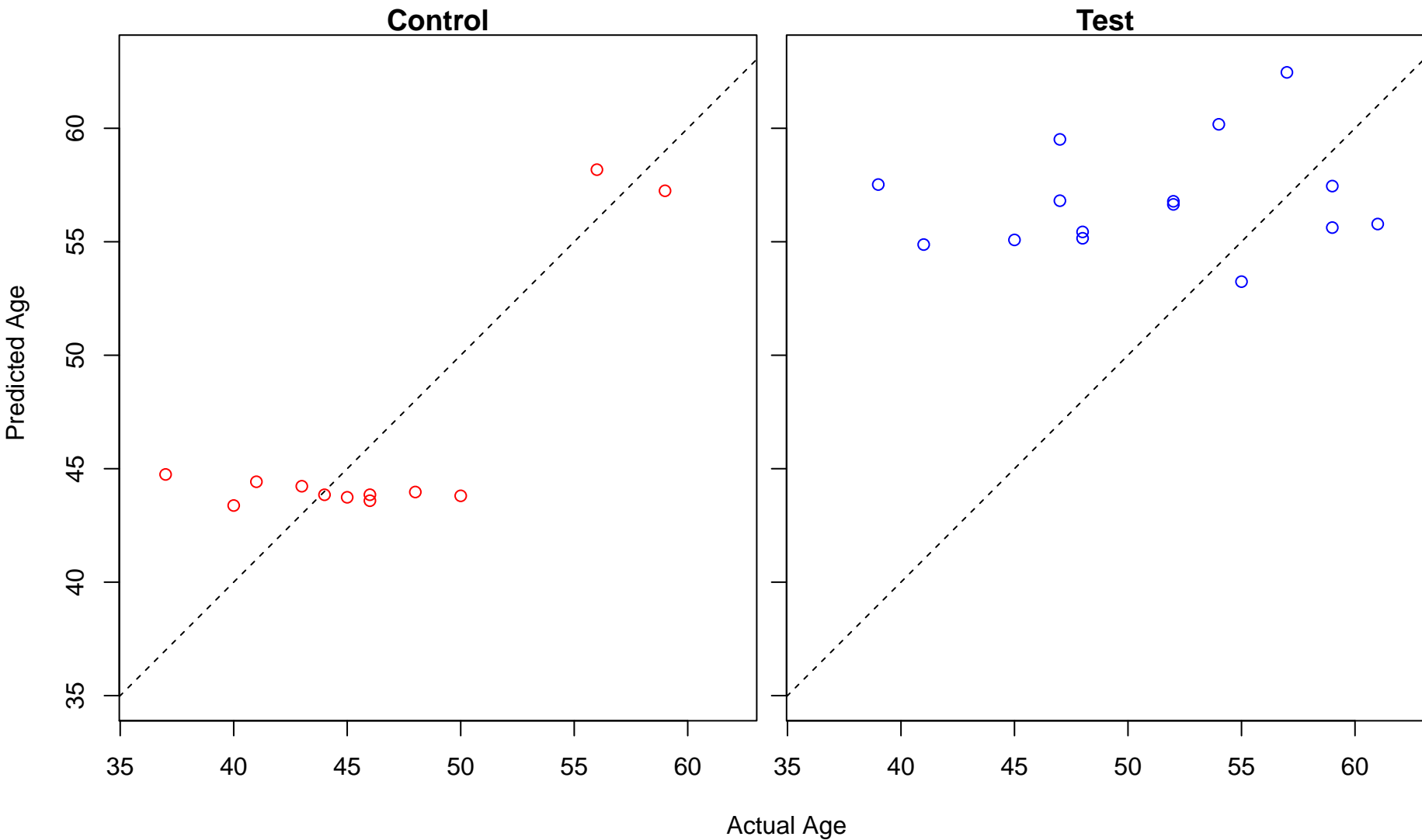
single-organism membrane fusion (Score: 2.449371)



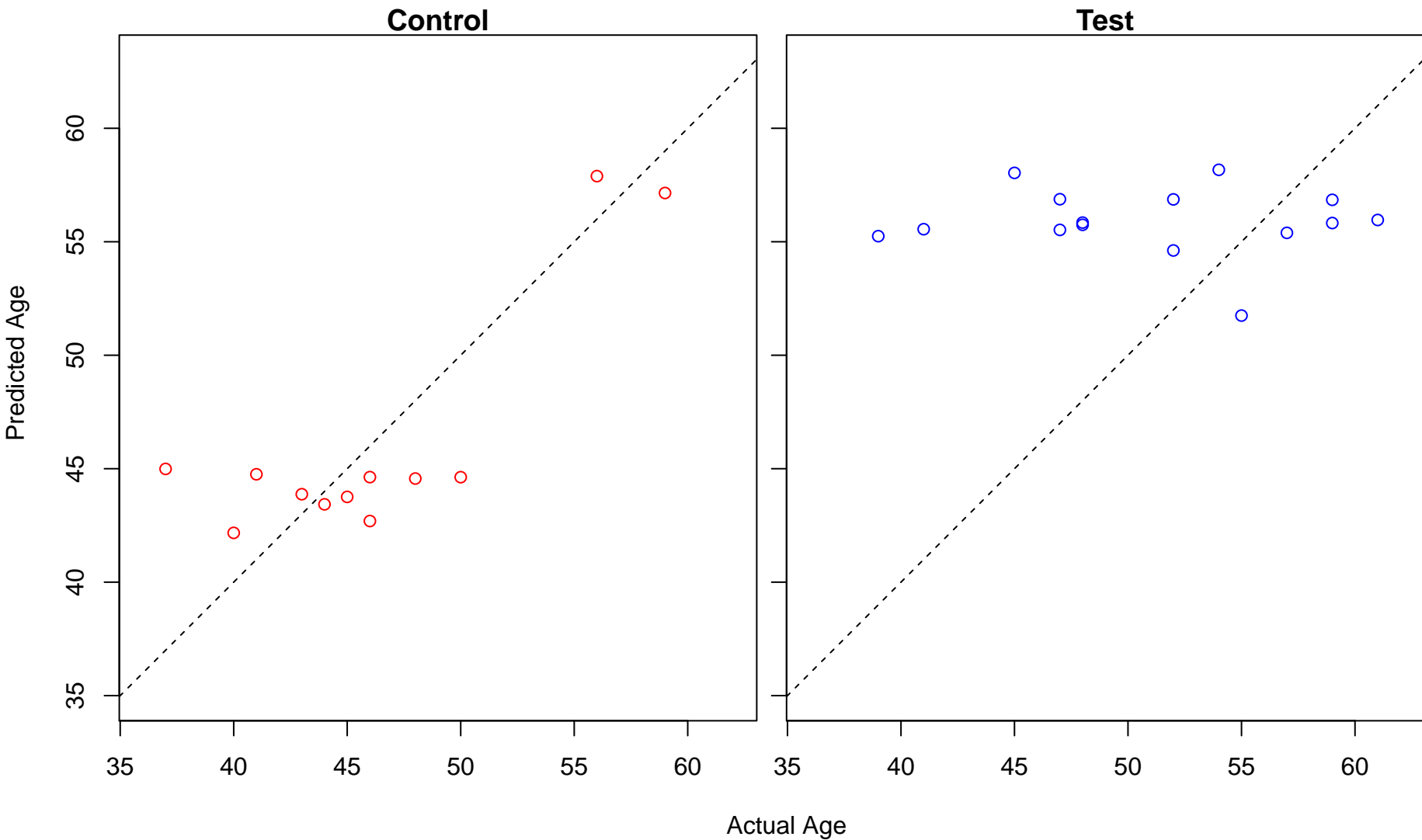
positive regulation of leukocyte differentiation (Score: 2.445078)



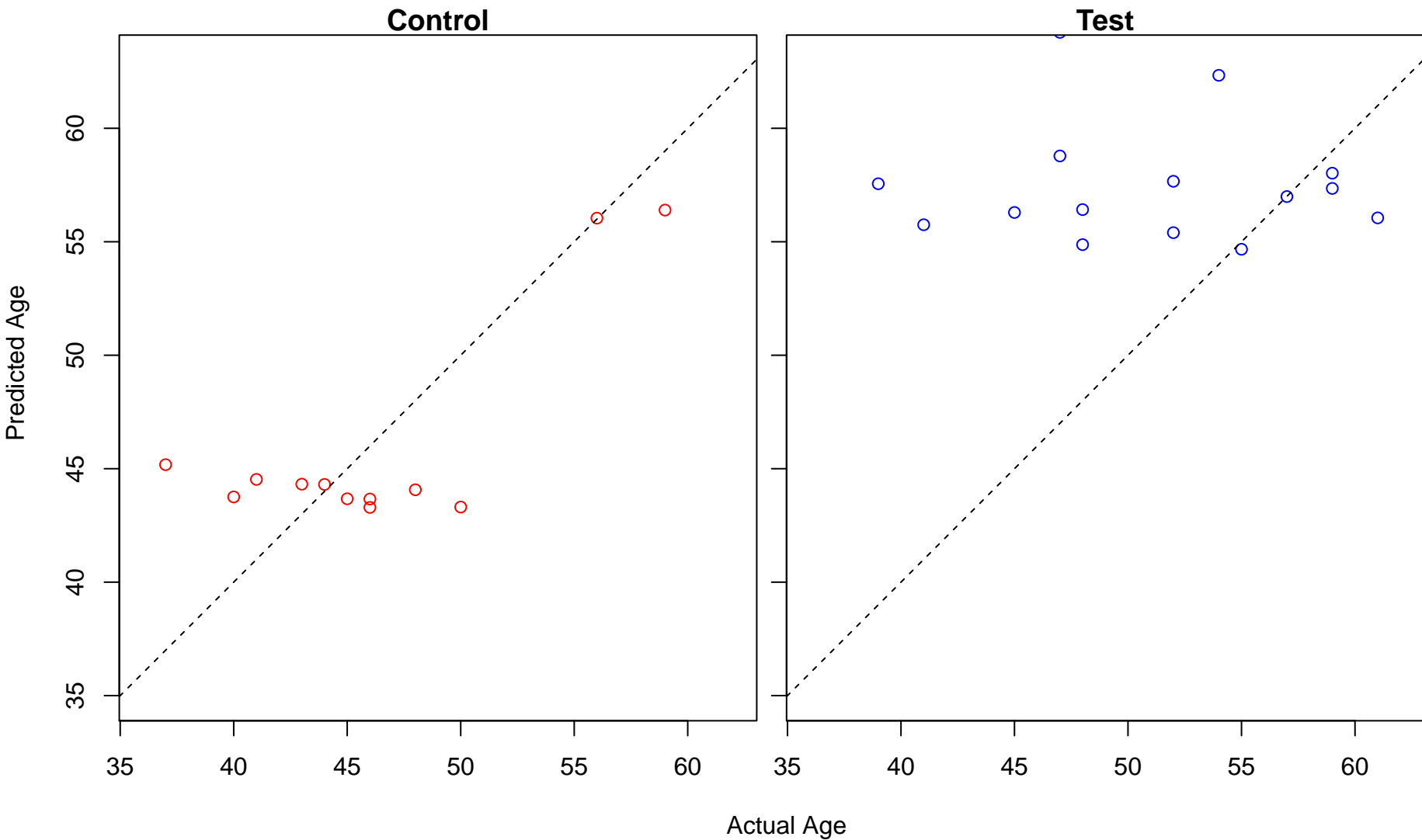
histone acetylation (Score: 2.443420)



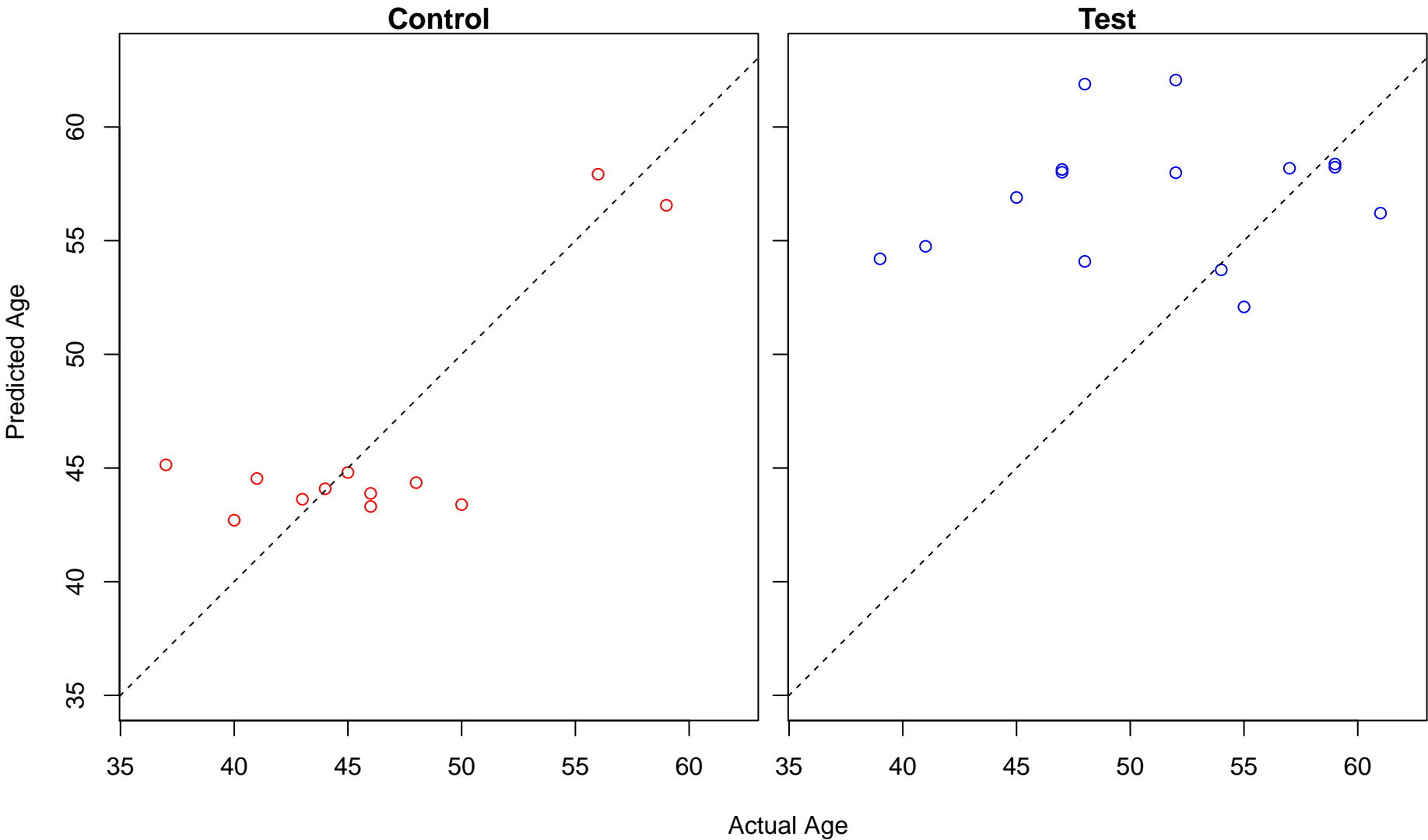
adult behavior (Score: 2.442921)



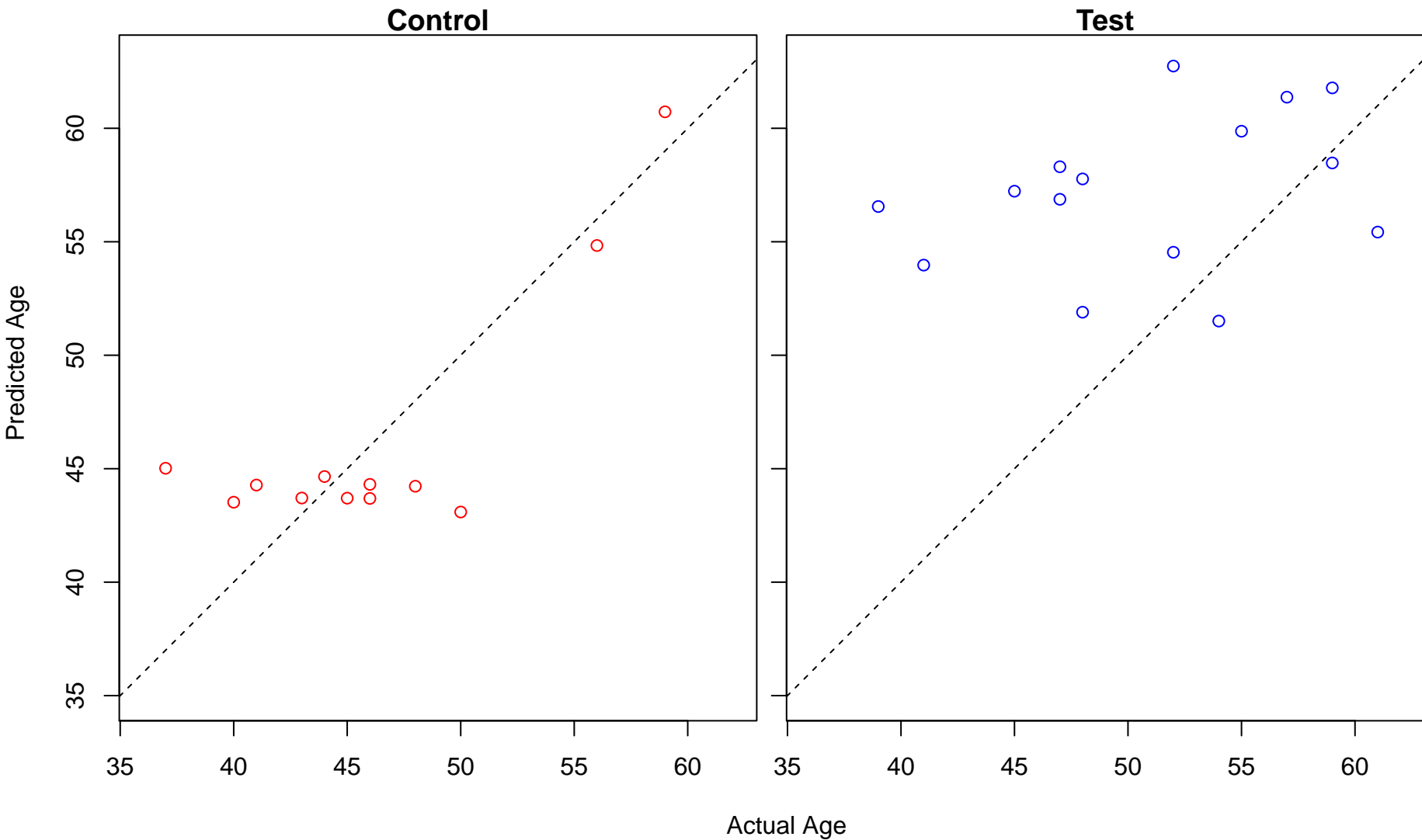
positive regulation by host of viral transcription (Score: 2.438122)



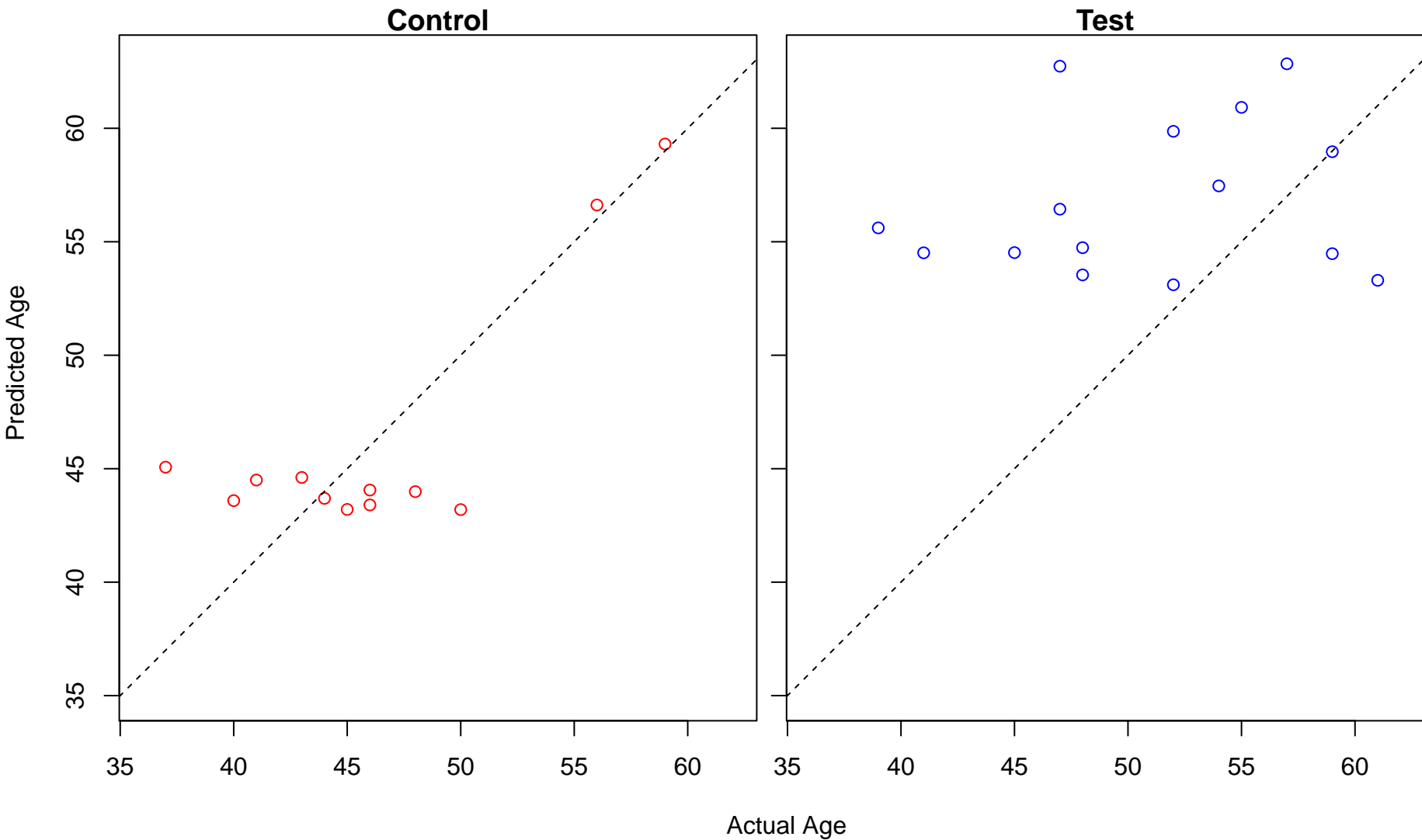
serine family amino acid catabolic process (Score: 2.435862)



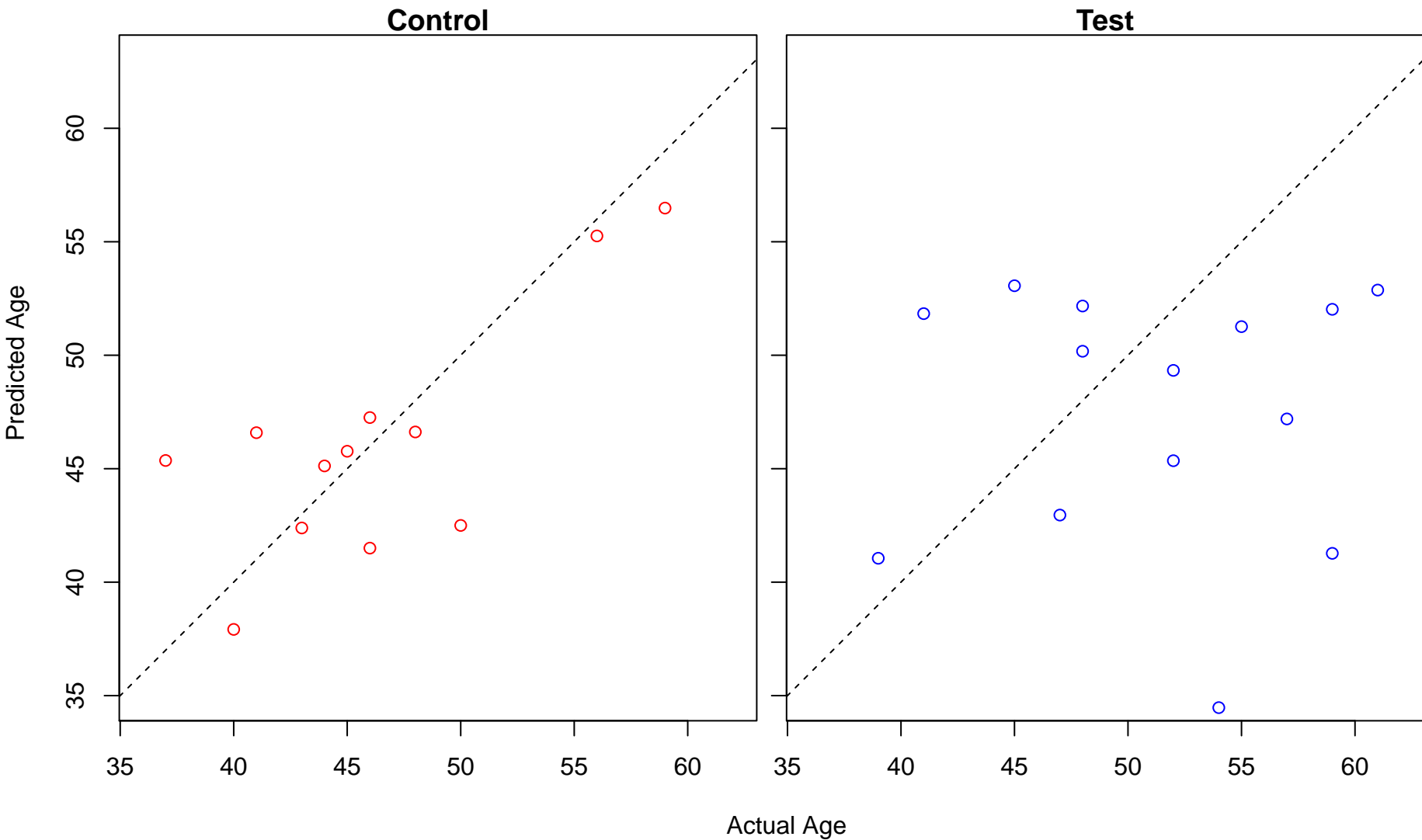
mast cell mediated immunity (Score: 2.435222)



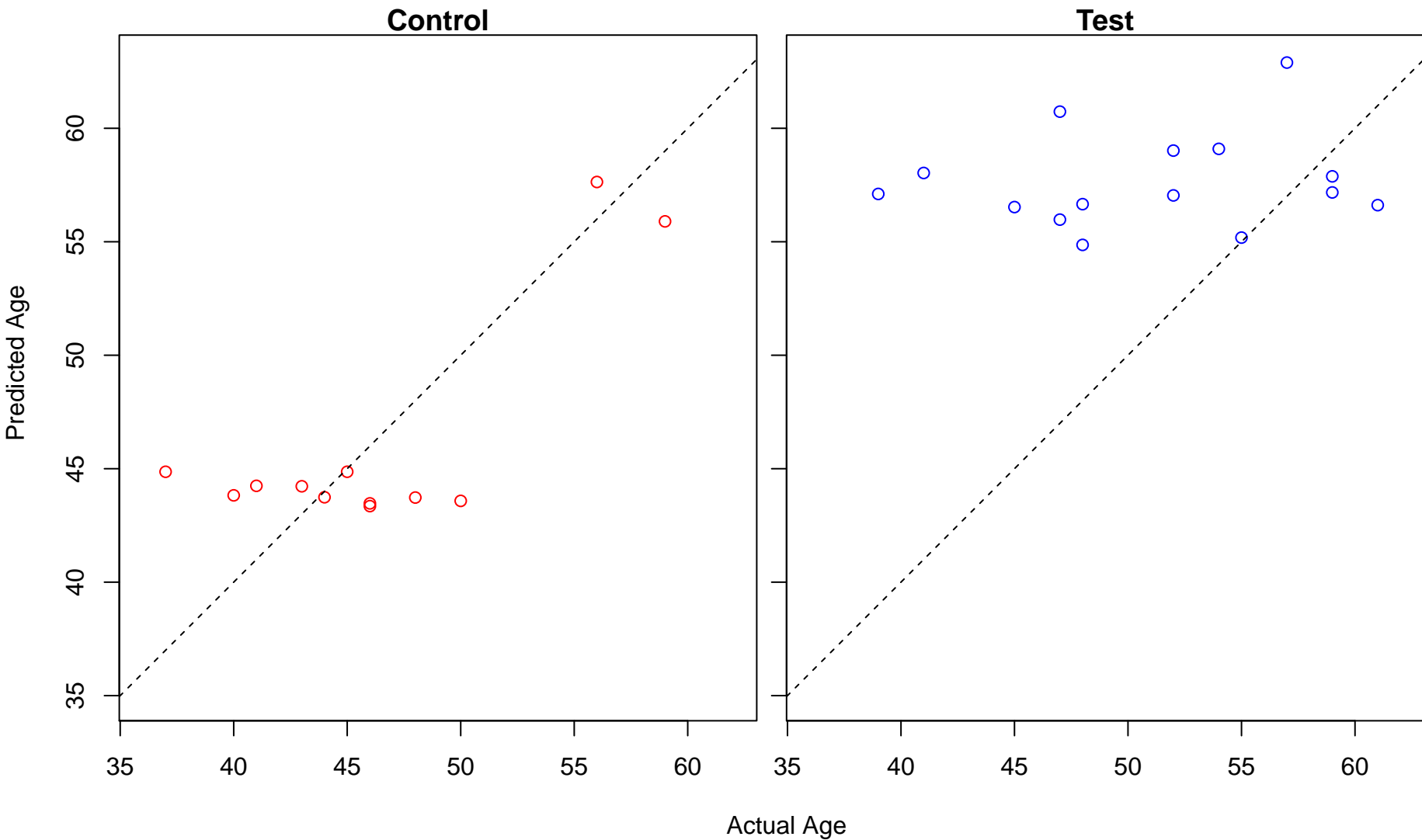
positive regulation of cAMP biosynthetic process (Score: 2.429361)



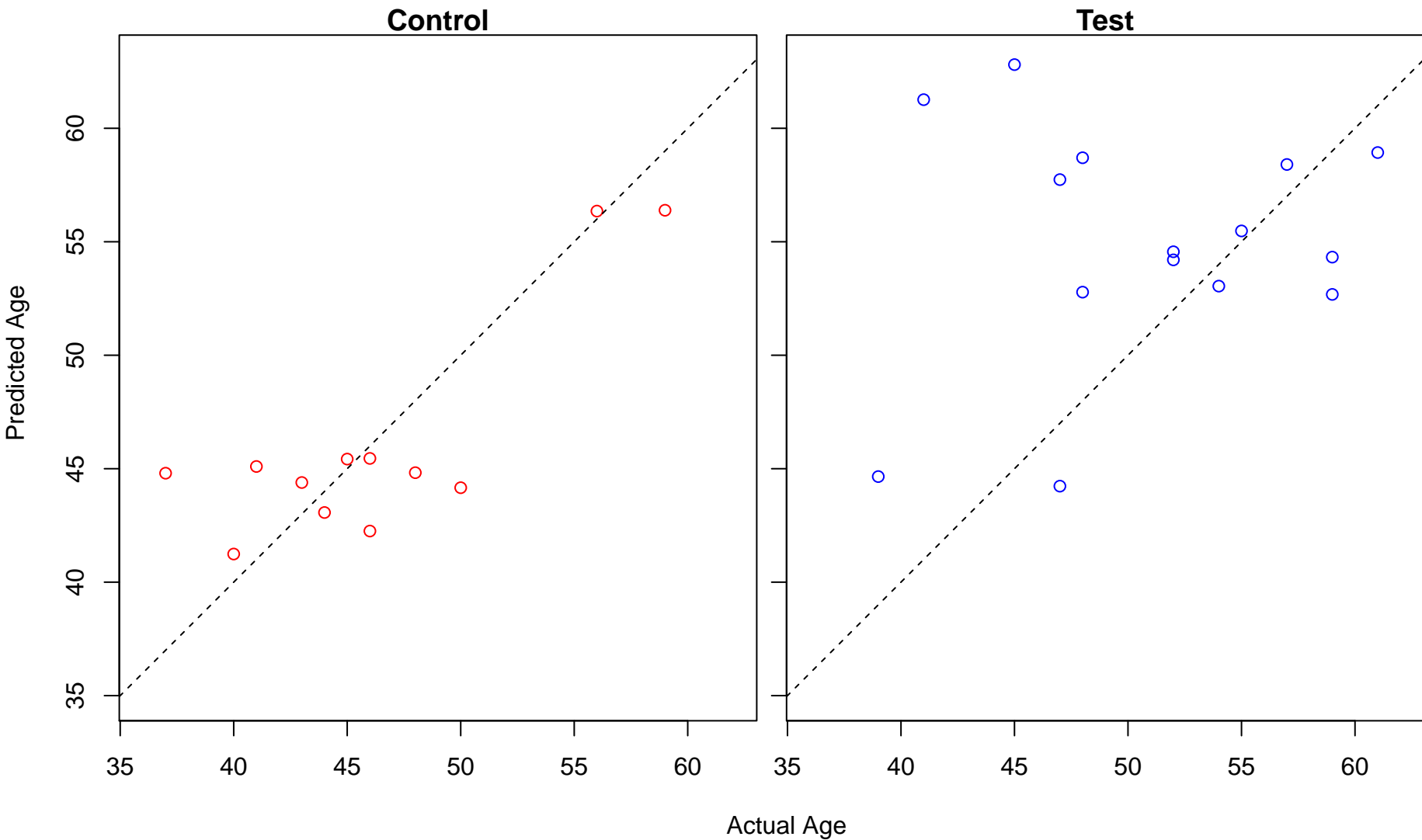
regulation of leukocyte mediated immunity (Score: 2.427155)



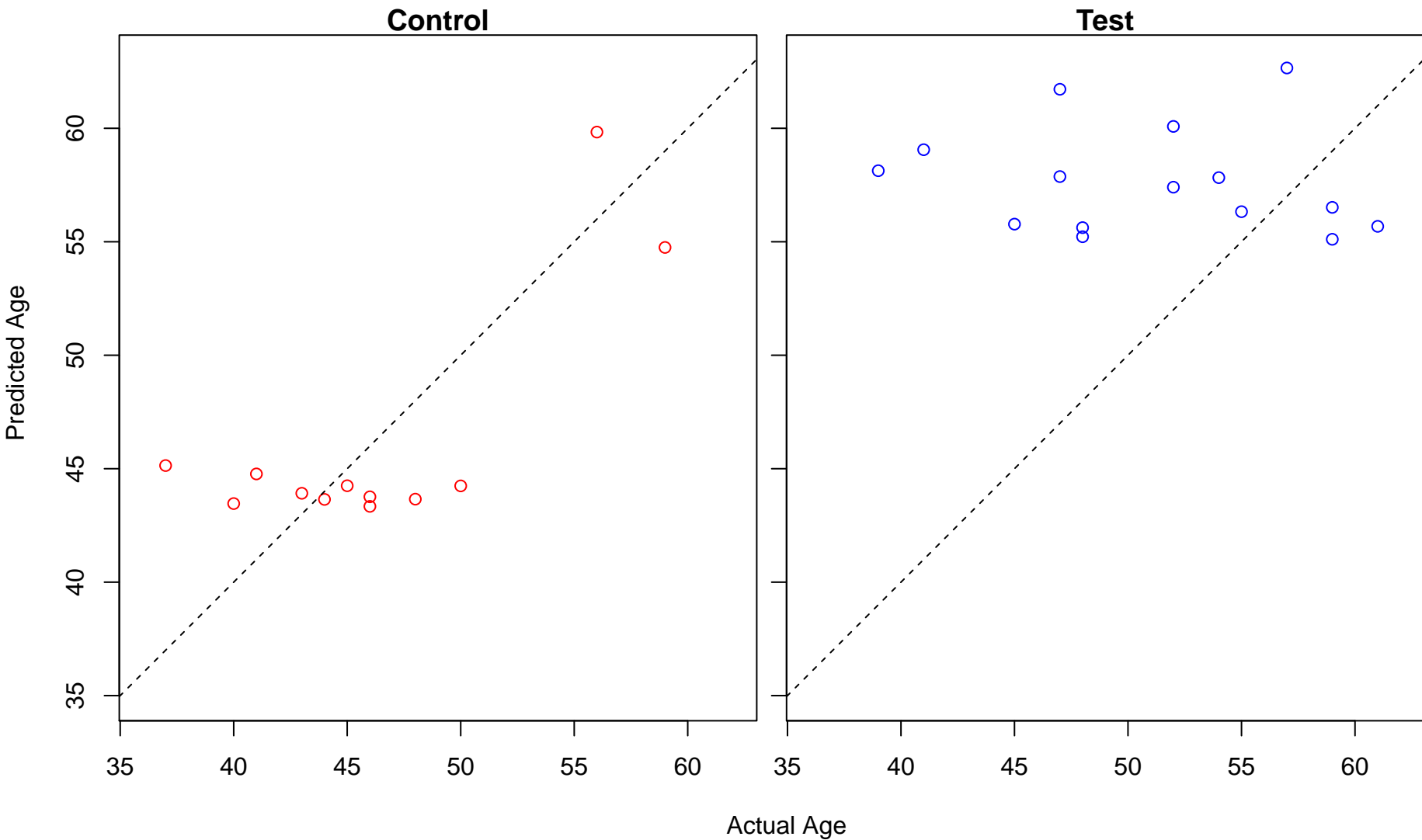
positive regulation of cellular component biogenesis (Score: 2.426210)



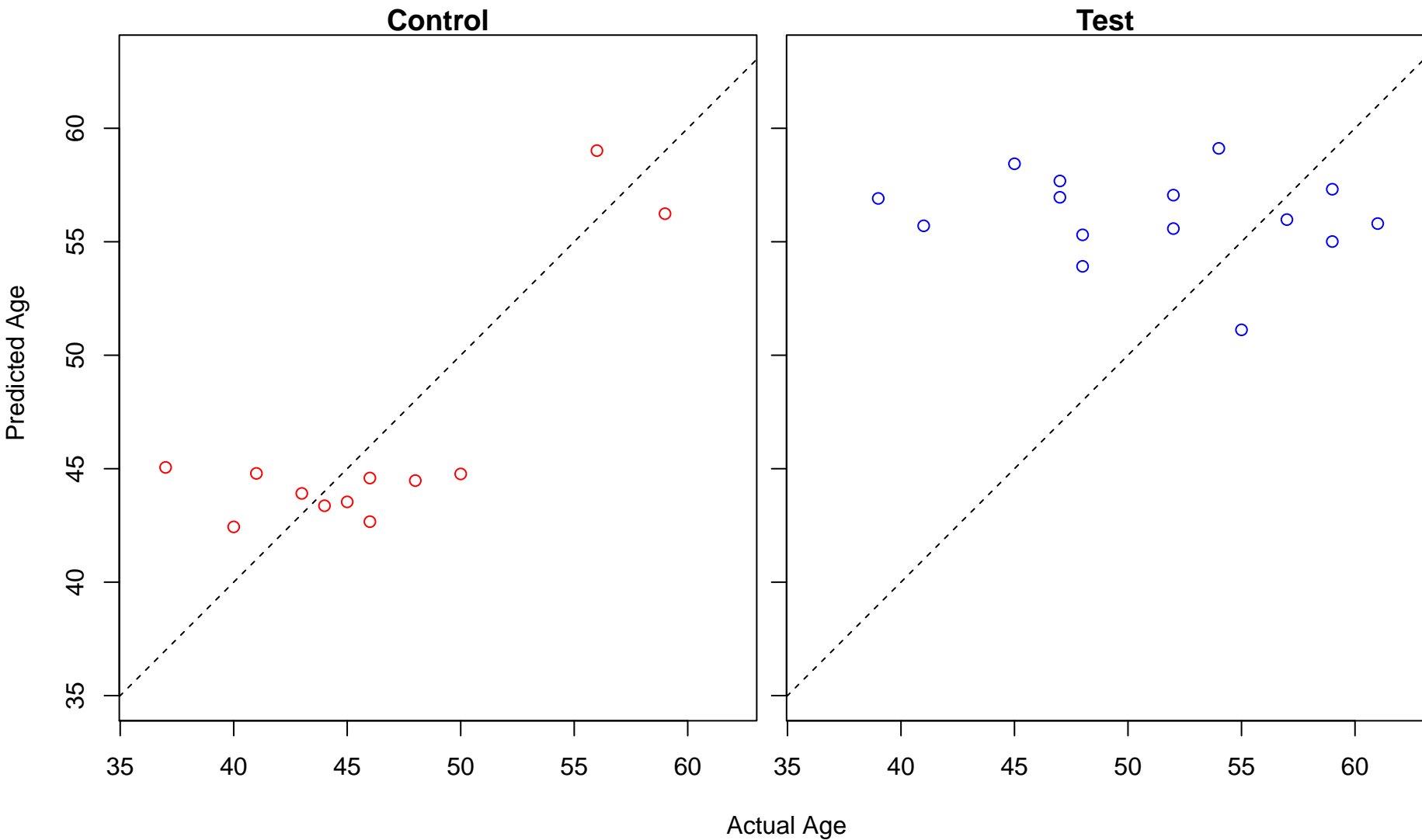
cell proliferation (Score: 2.421940)



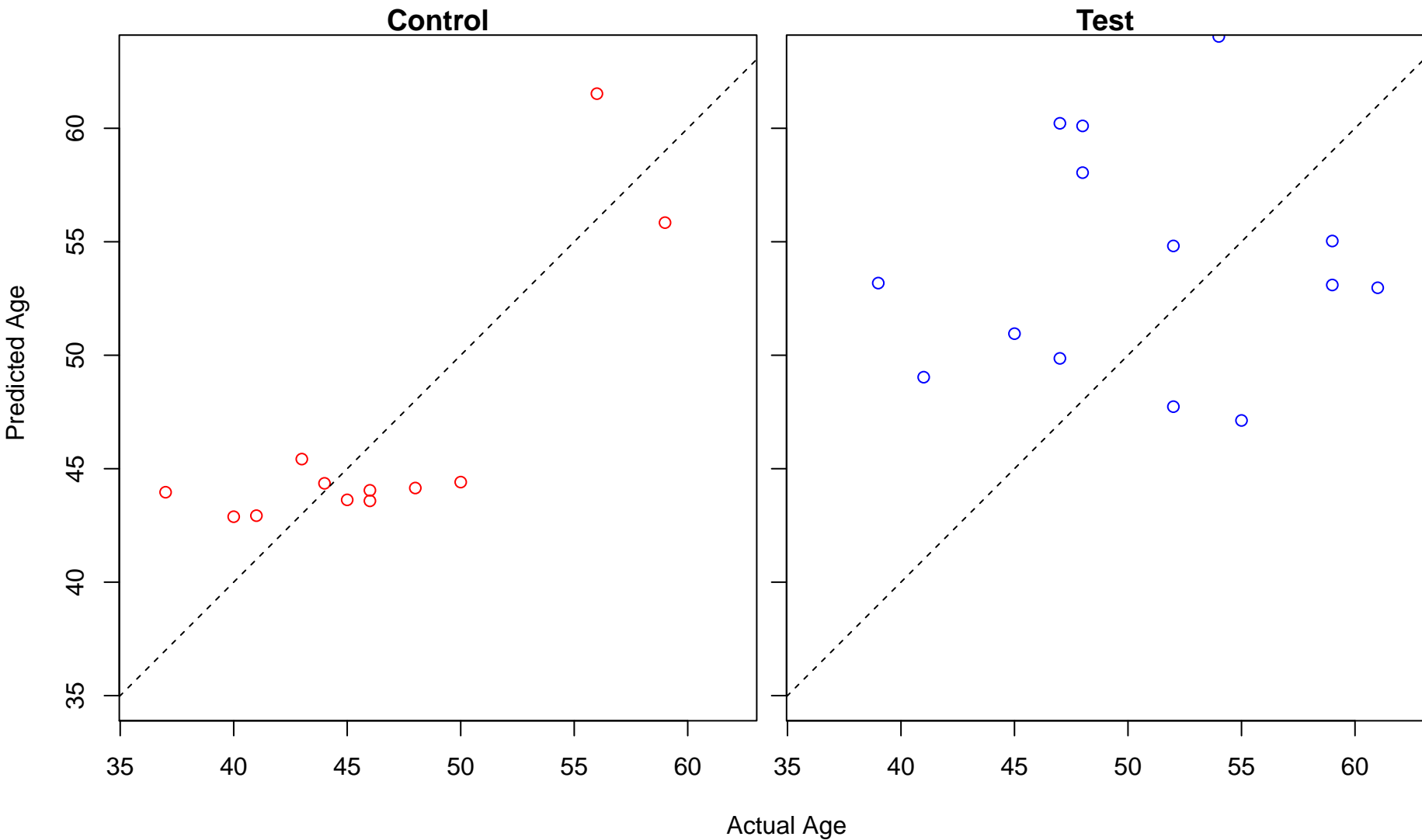
positive regulation of locomotion (Score: 2.421455)



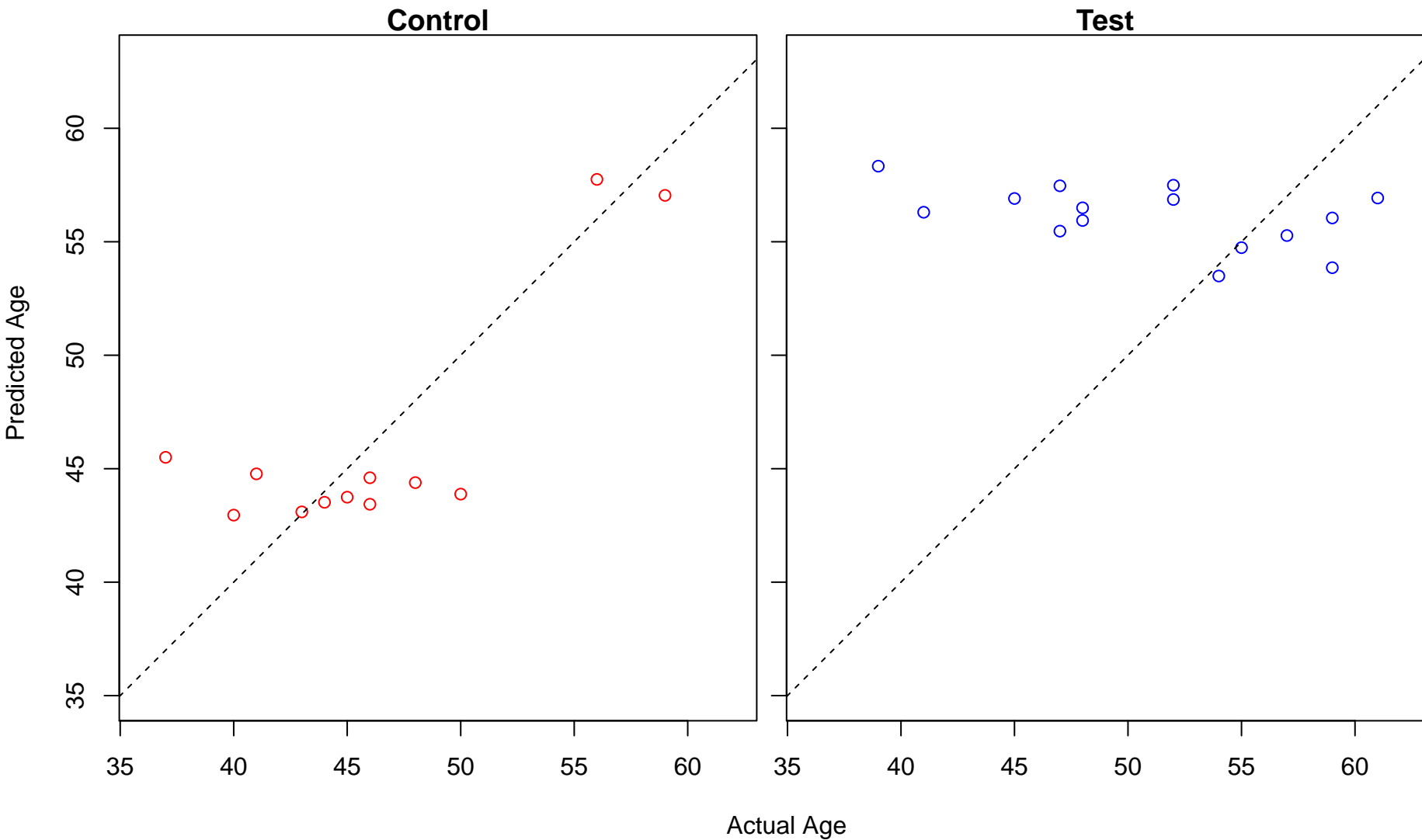
adult locomotory behavior (Score: 2.420208)



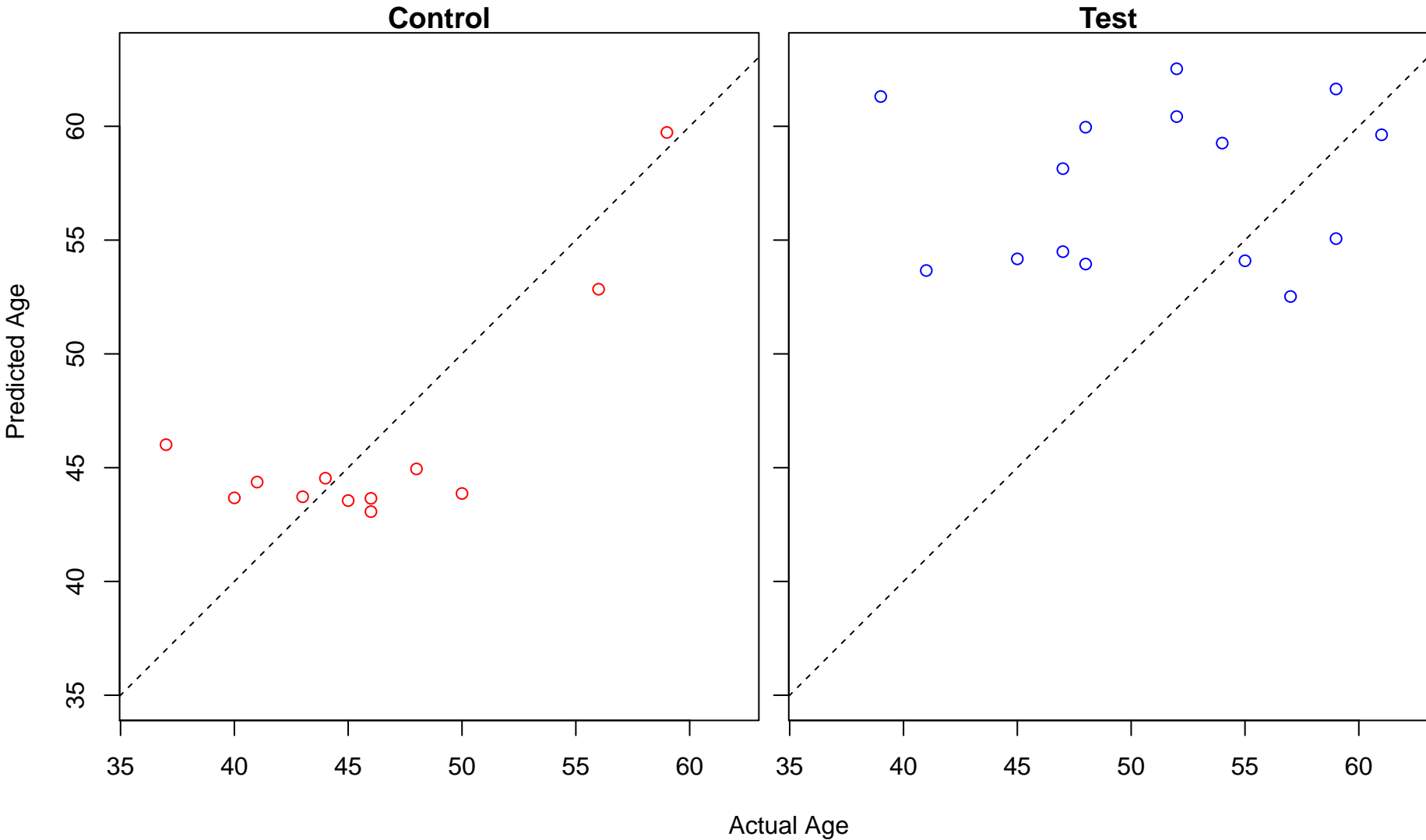
sperm-egg recognition (Score: 2.419138)



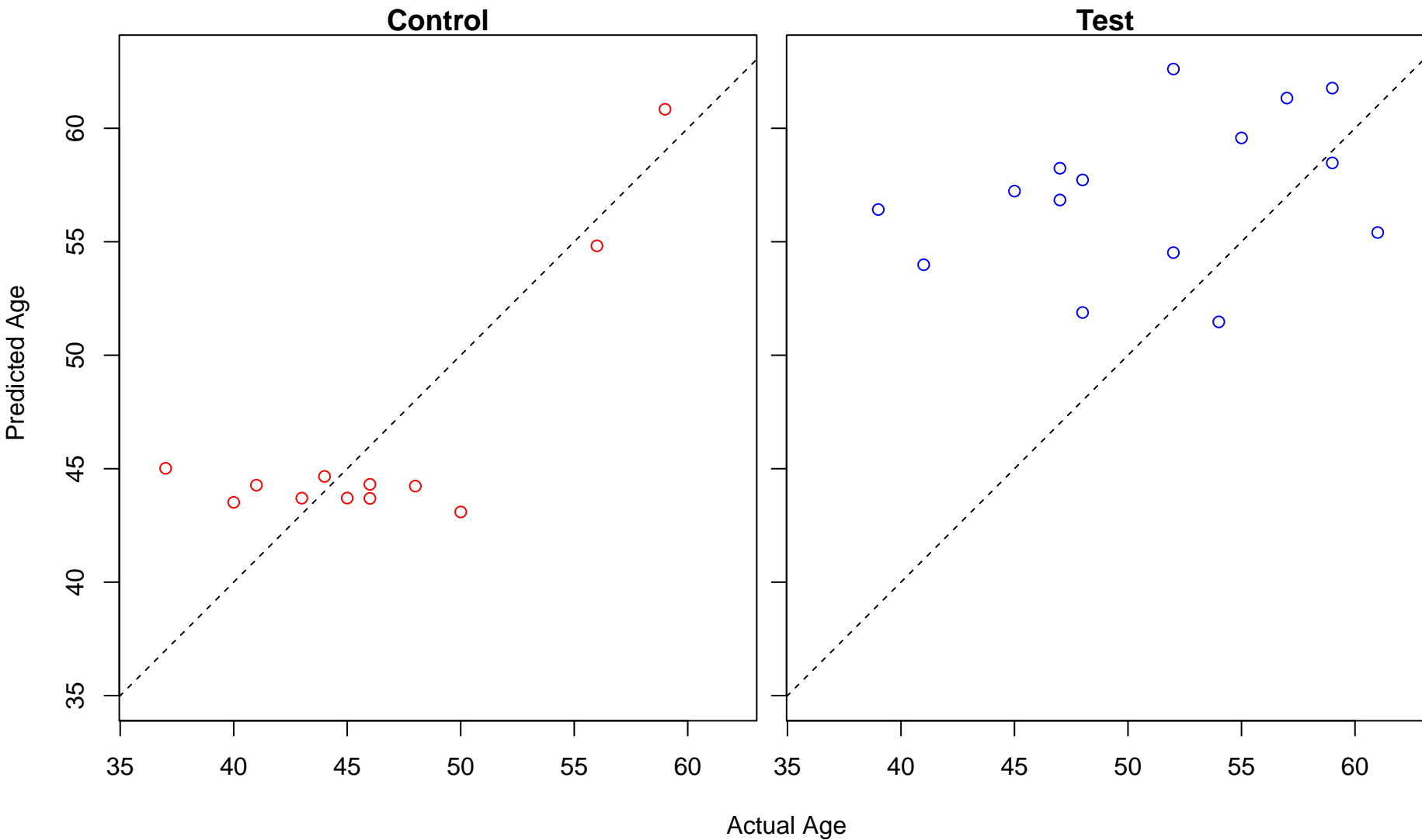
positive regulation of response to DNA damage stimulus (Score: 2.418683)



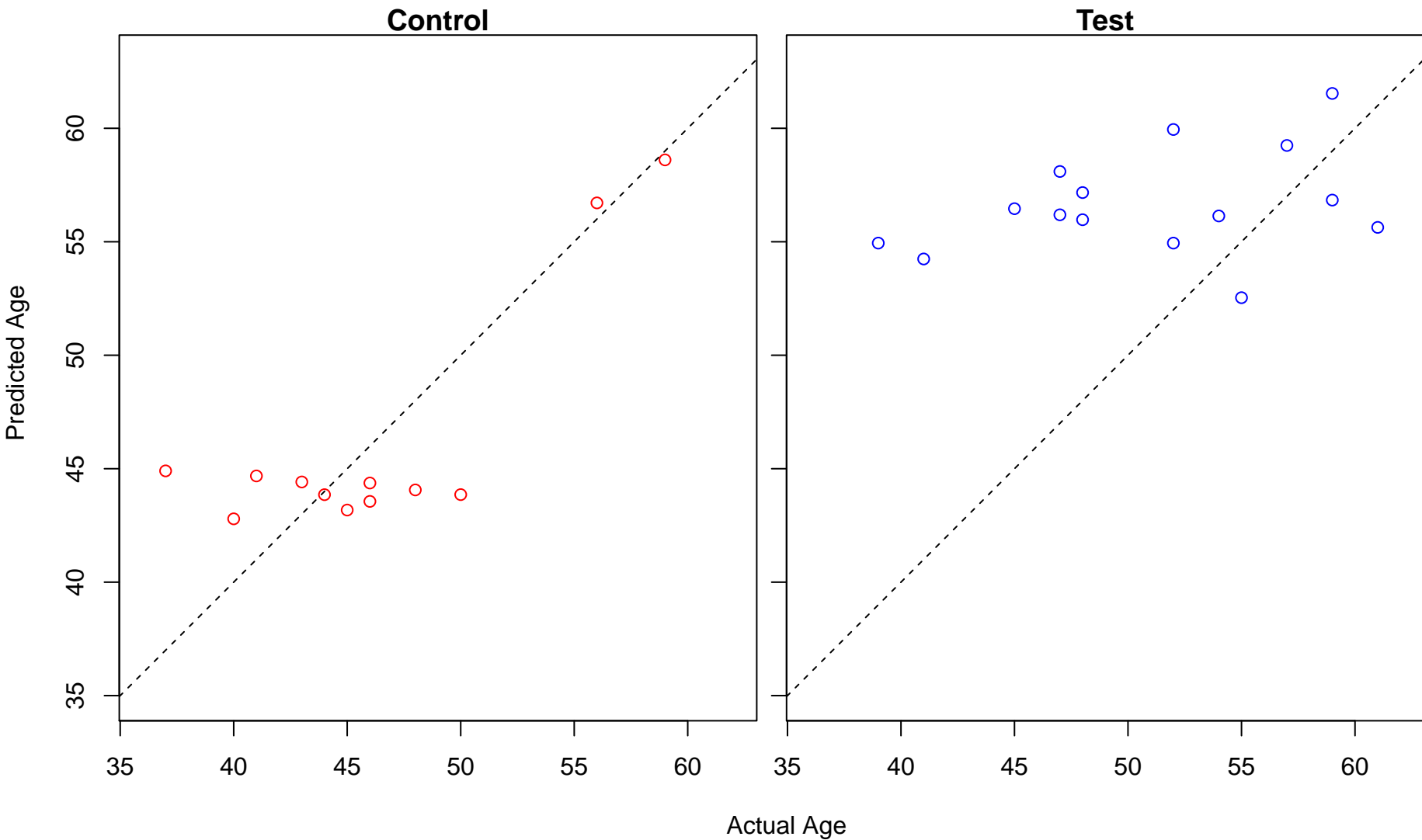
regulation of bile acid biosynthetic process (Score: 2.414318)



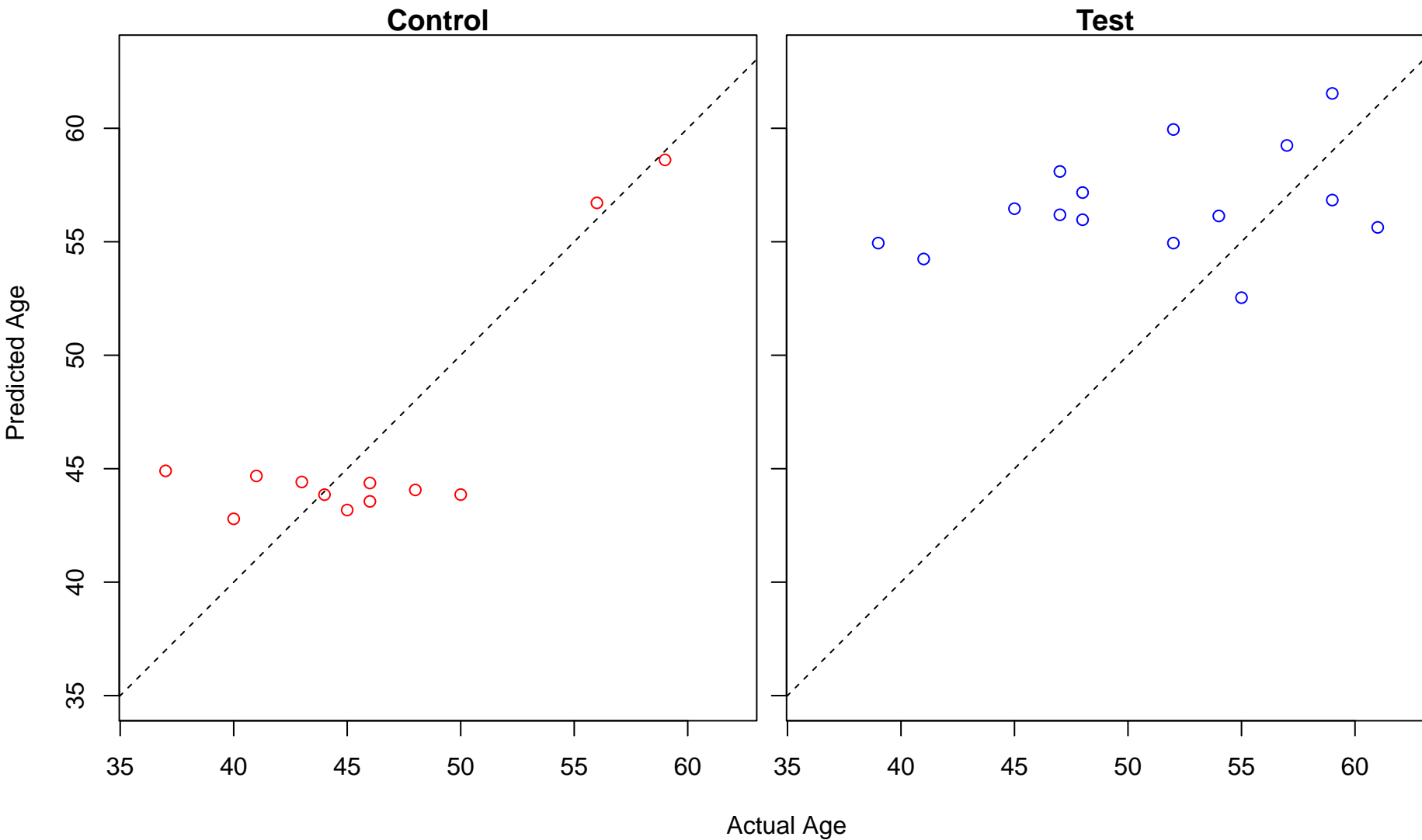
mast cell degranulation (Score: 2.414012)



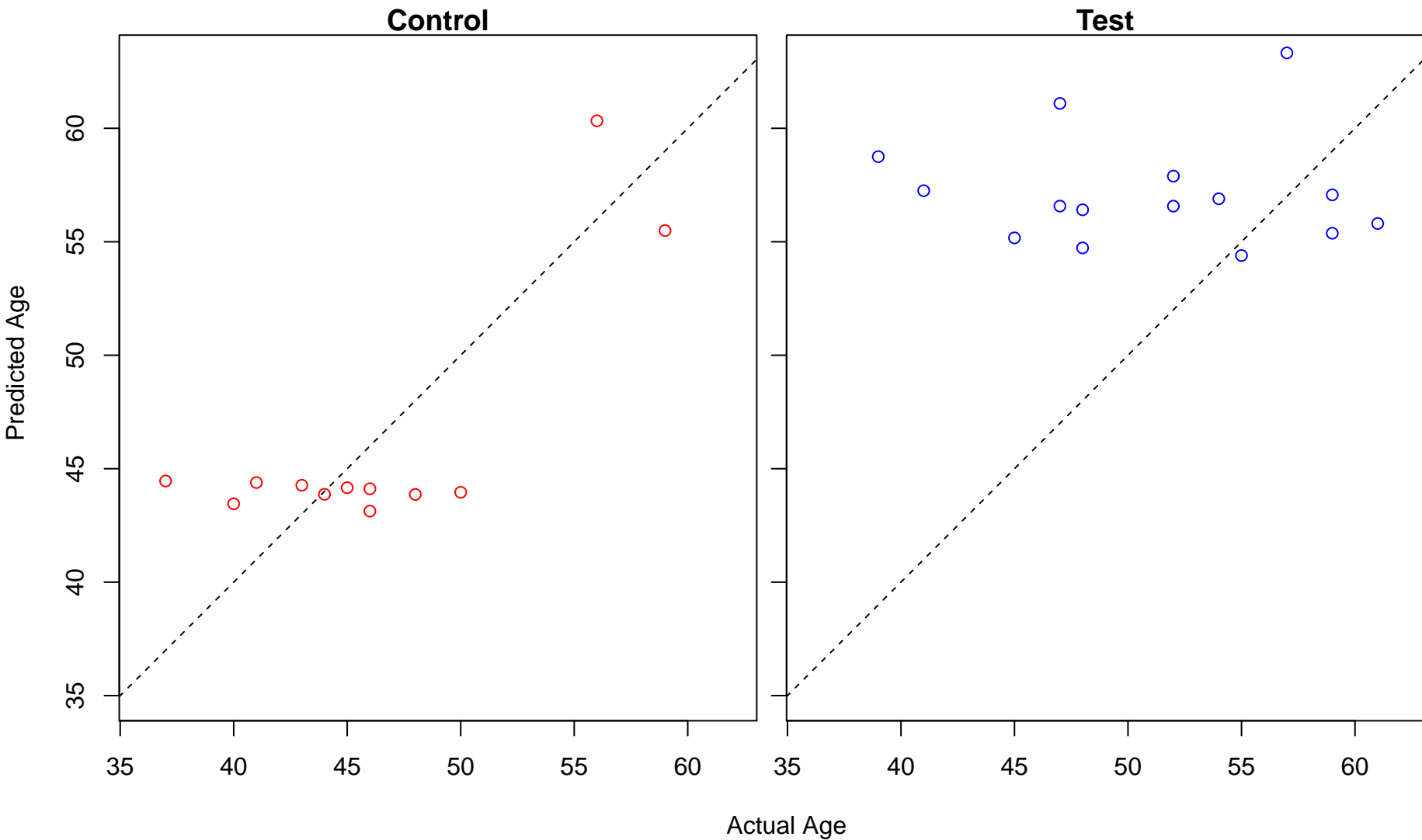
social behavior (Score: 2.411917)



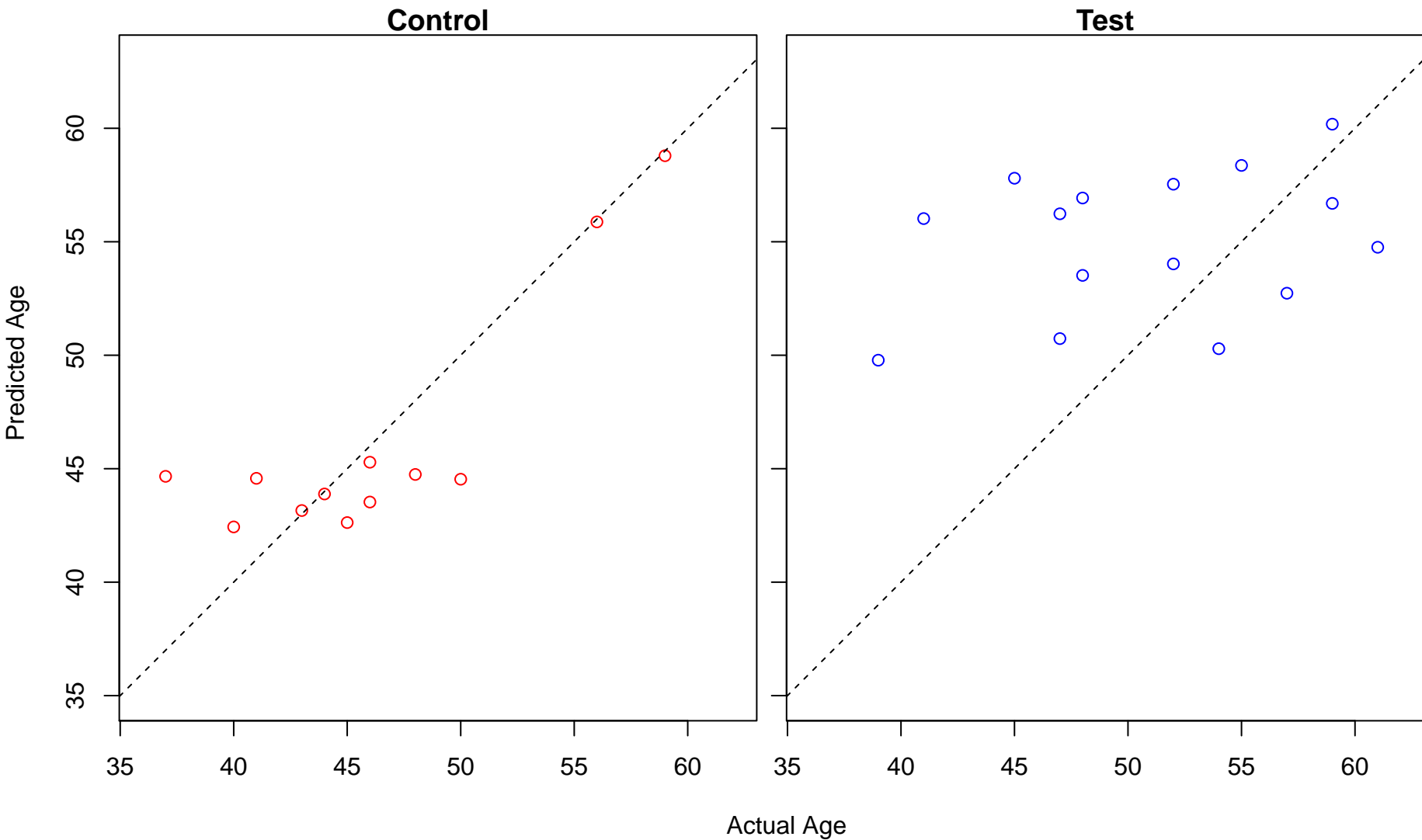
intraspecies interaction between organisms (Score: 2.411917)



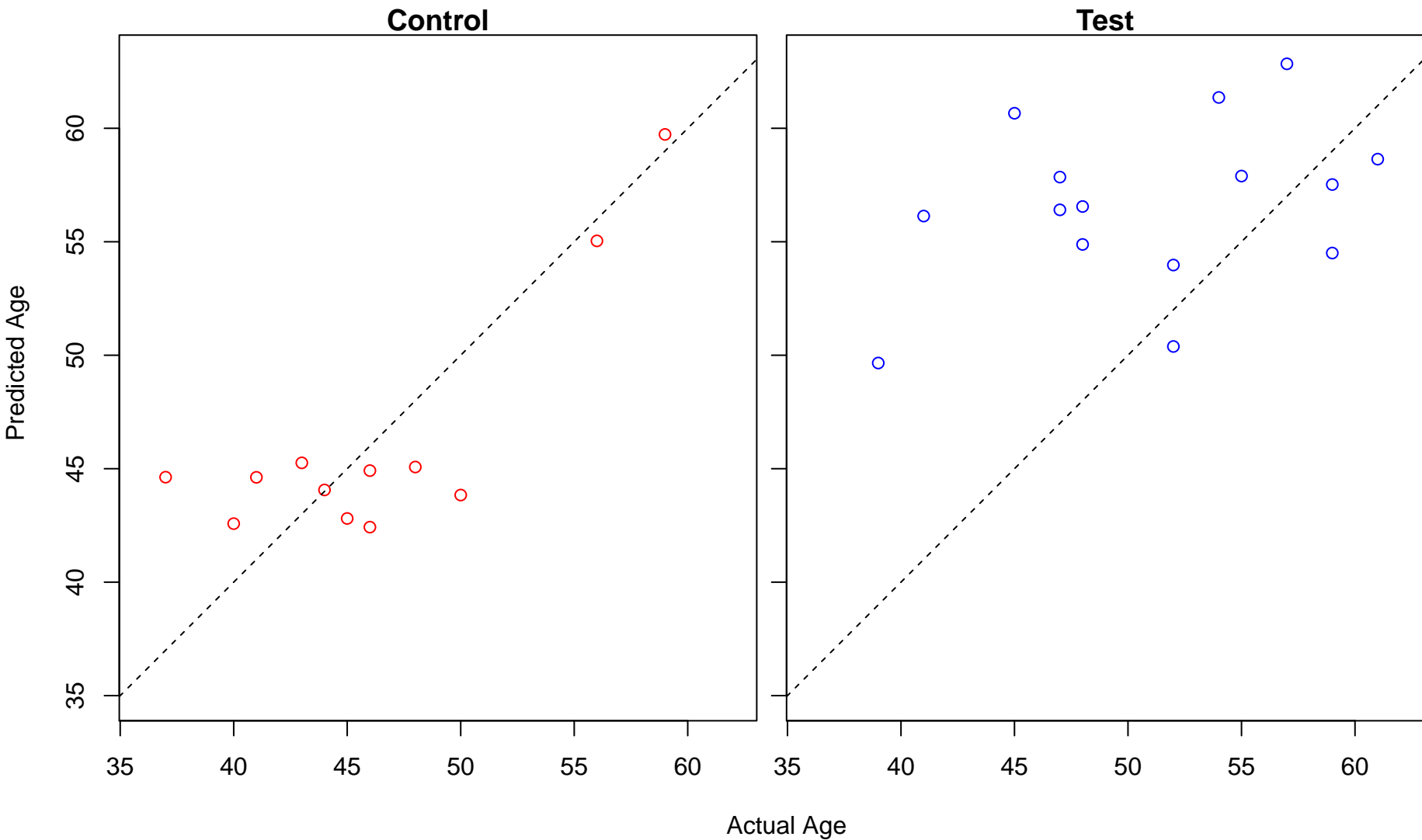
establishment of organelle localization (Score: 2.411825)



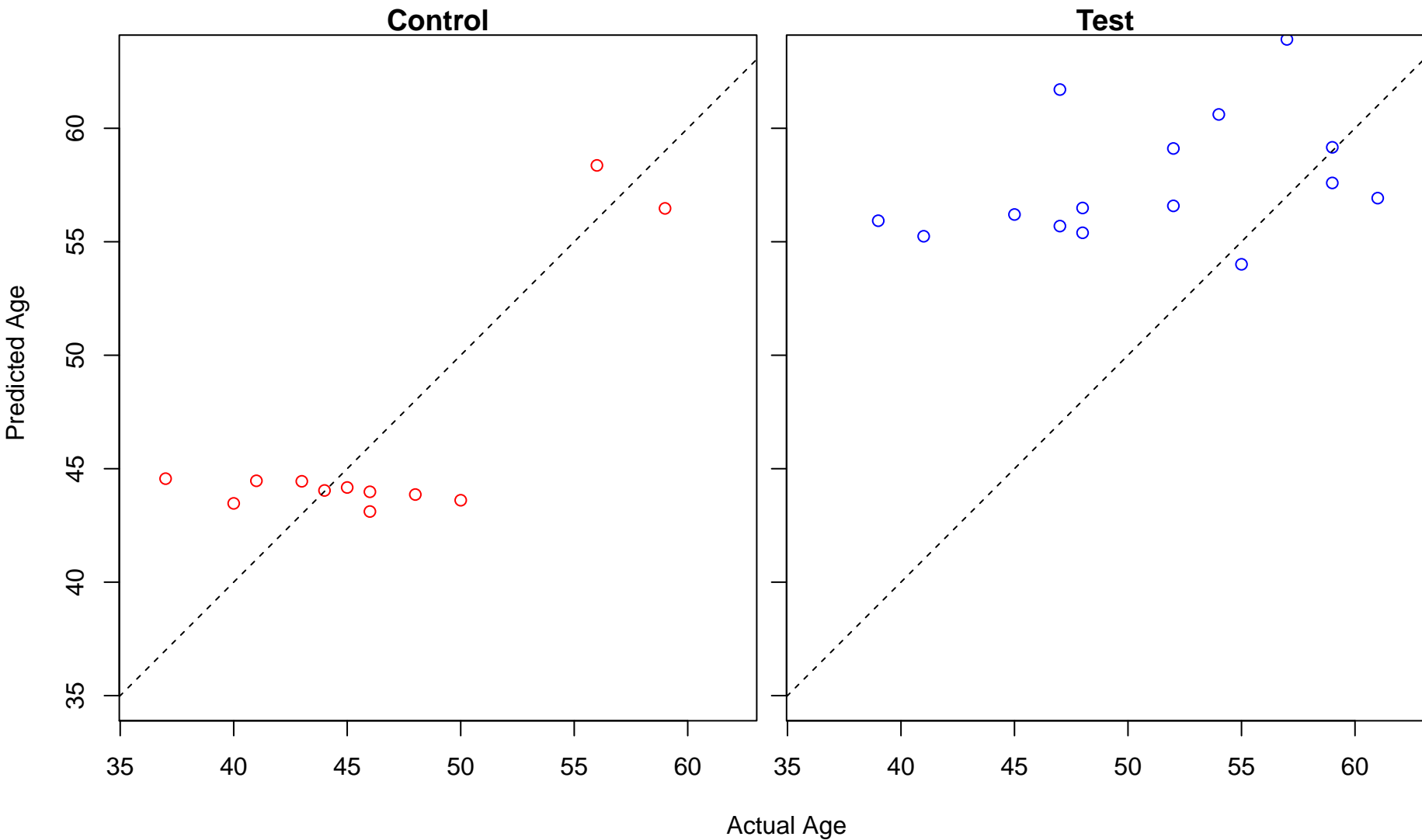
cell differentiation in hindbrain (Score: 2.411693)



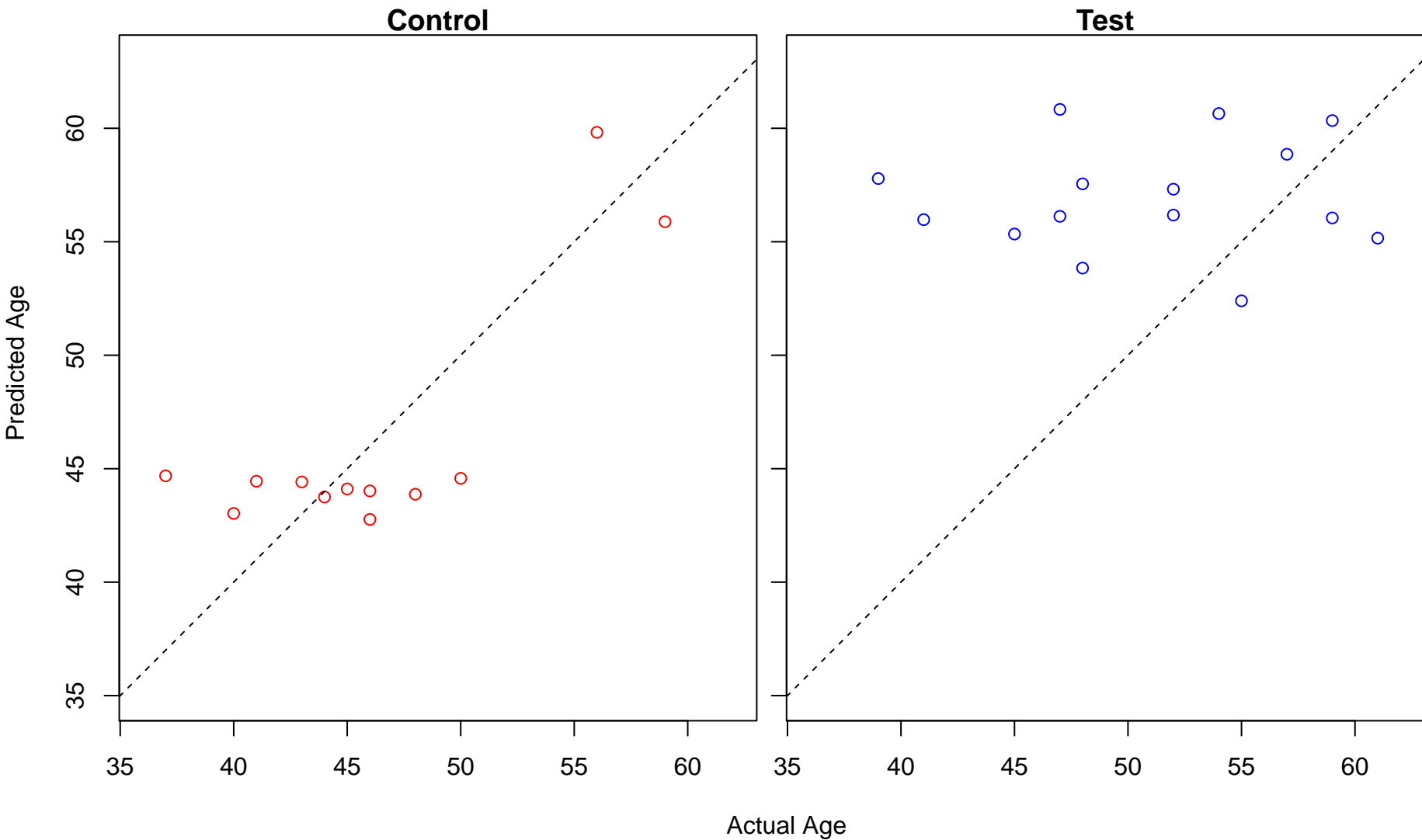
regulation of apoptotic signaling pathway (Score: 2.411315)



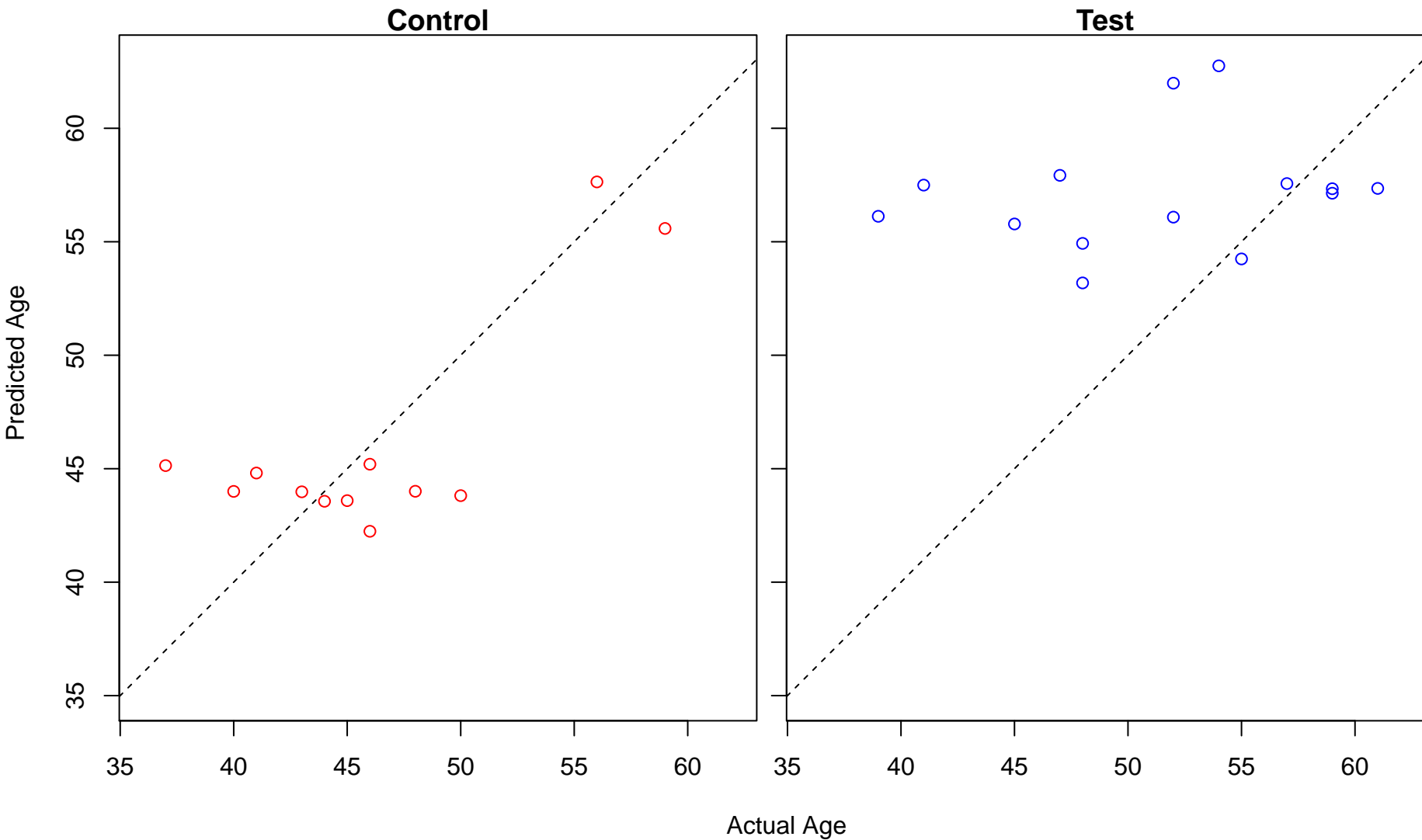
positive regulation of protein localization to nucleus (Score: 2.411059)



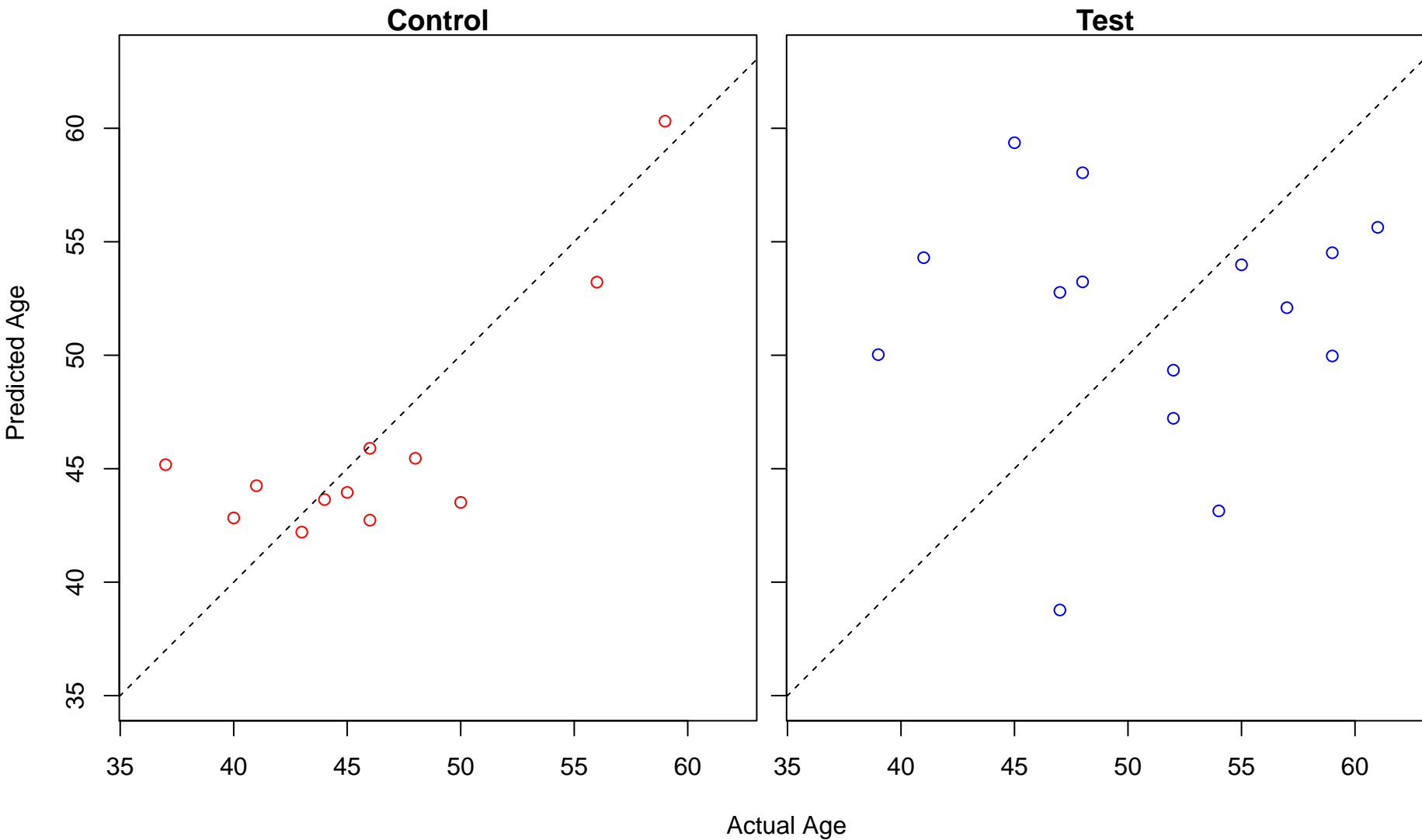
kidney morphogenesis (Score: 2.405829)



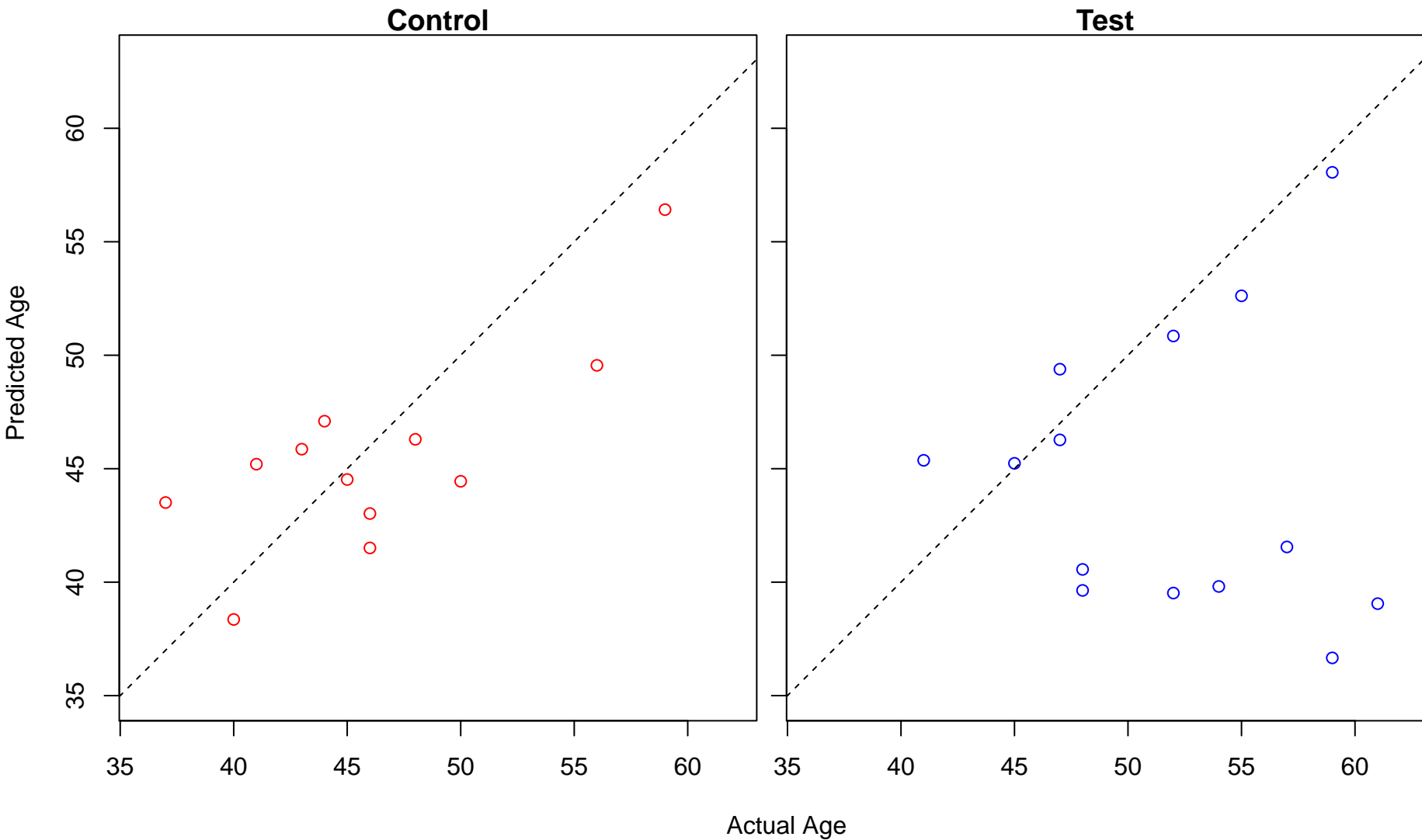
epithelial cell-cell adhesion (Score: 2.405617)



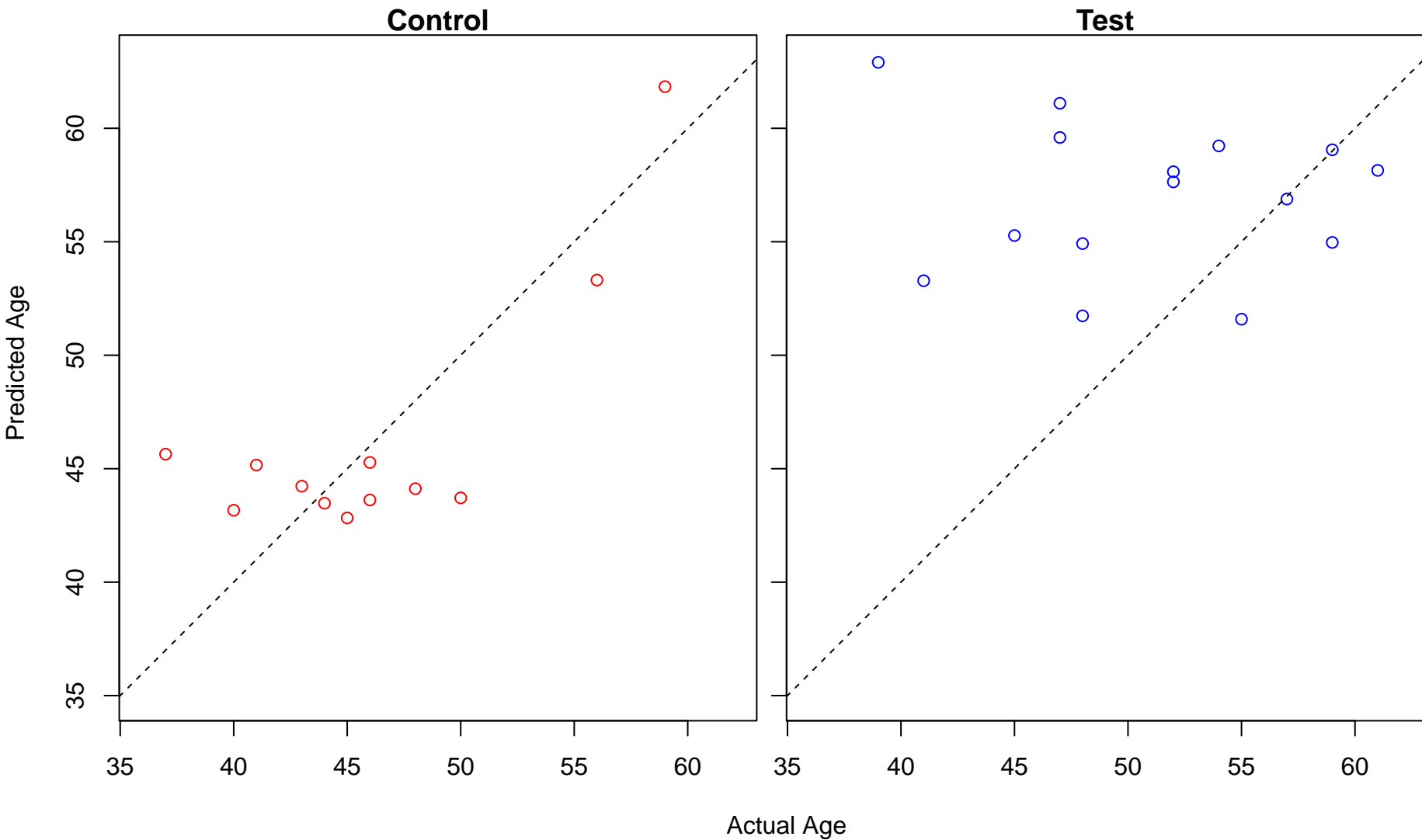
endosome to lysosome transport (Score: 2.405349)



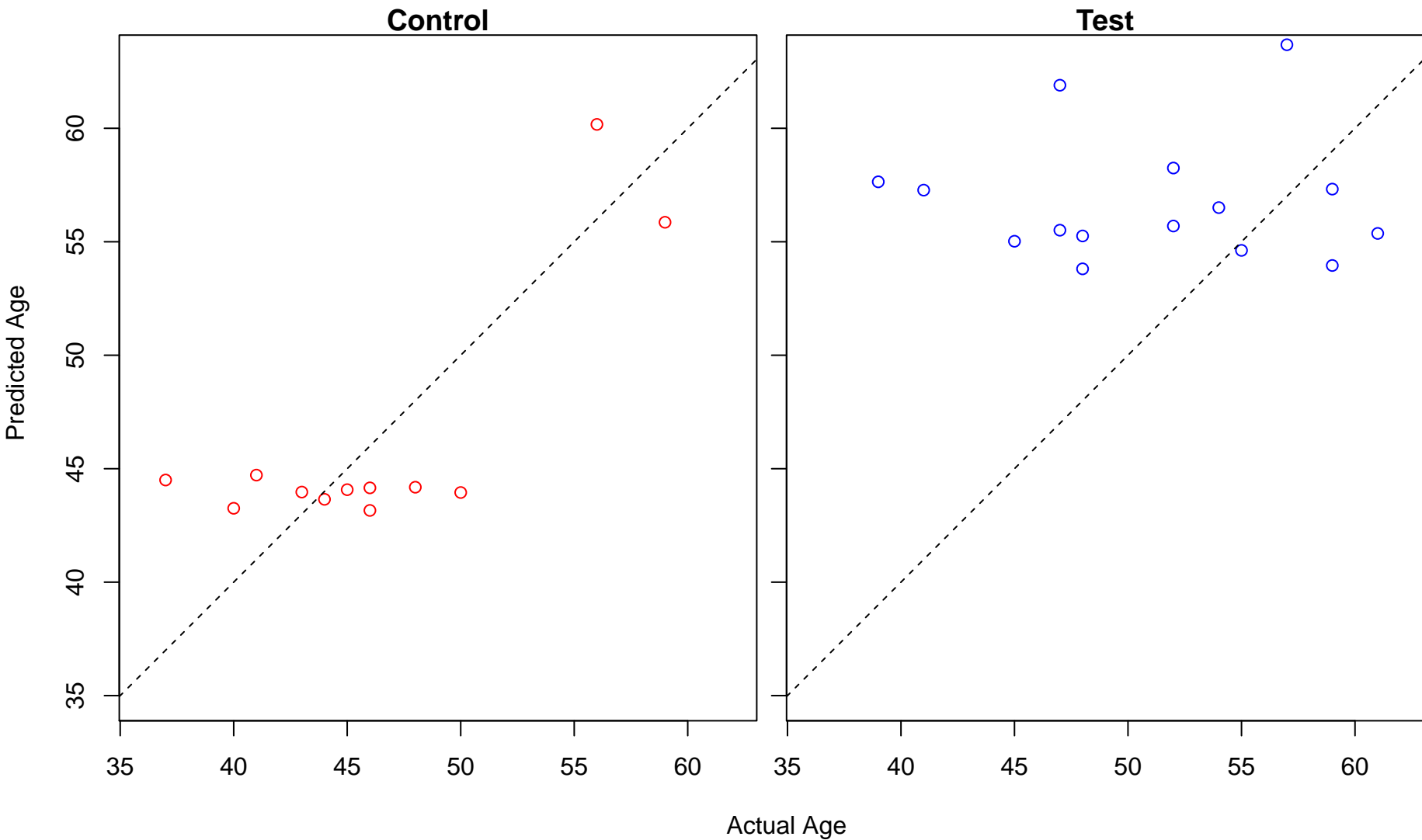
translation (Score: 2.405220)



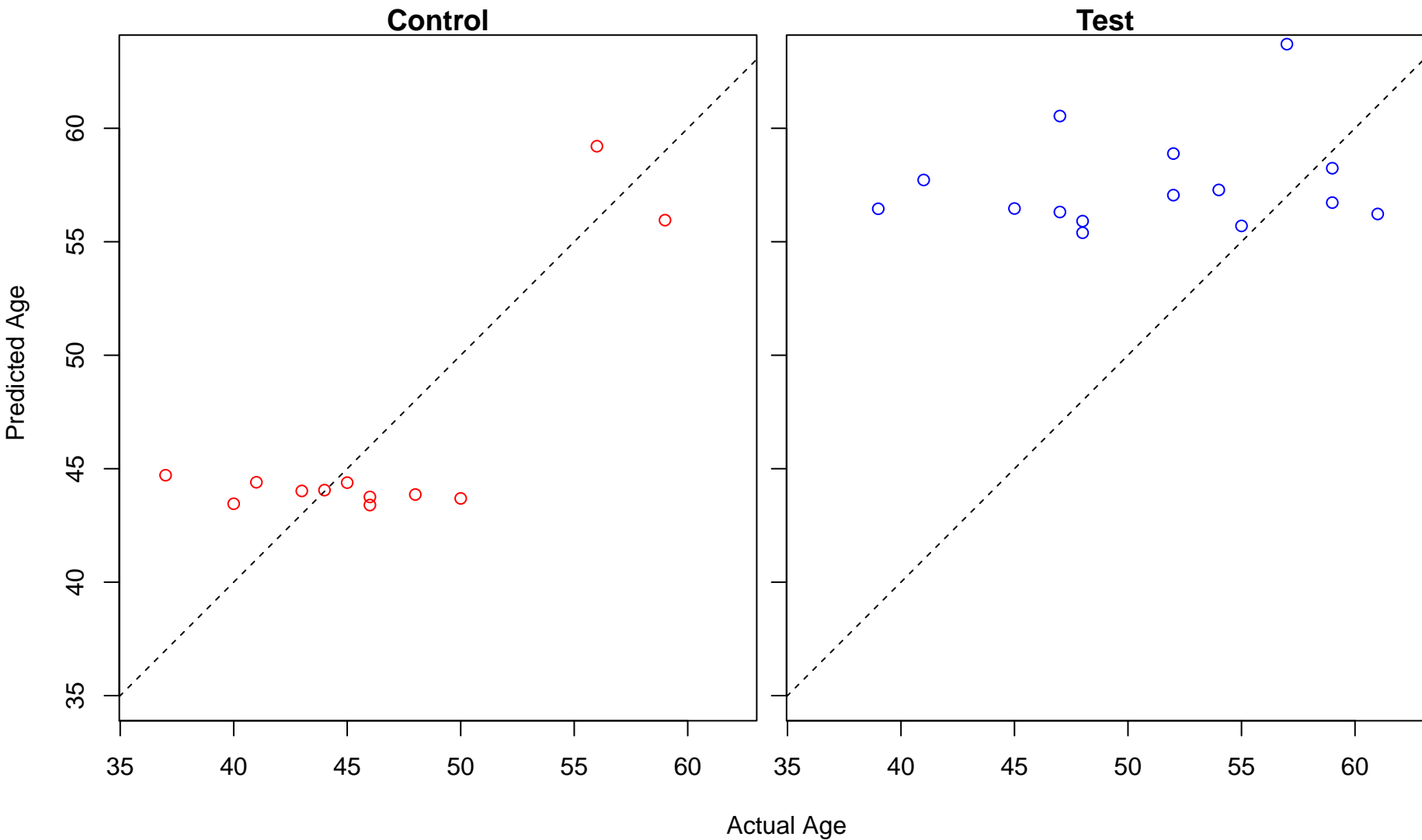
regulation of amine transport (Score: 2.404089)



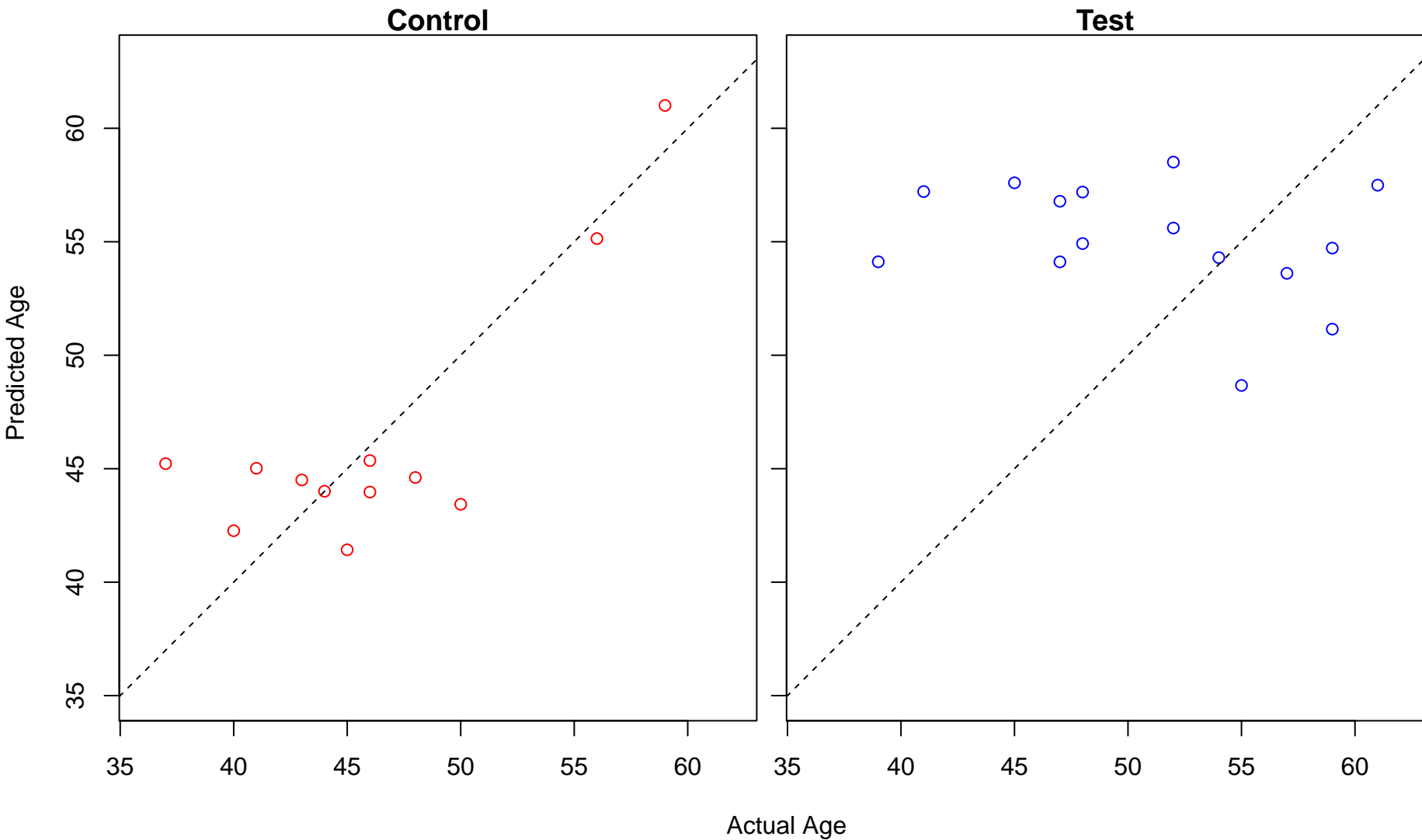
membrane budding (Score: 2.401912)



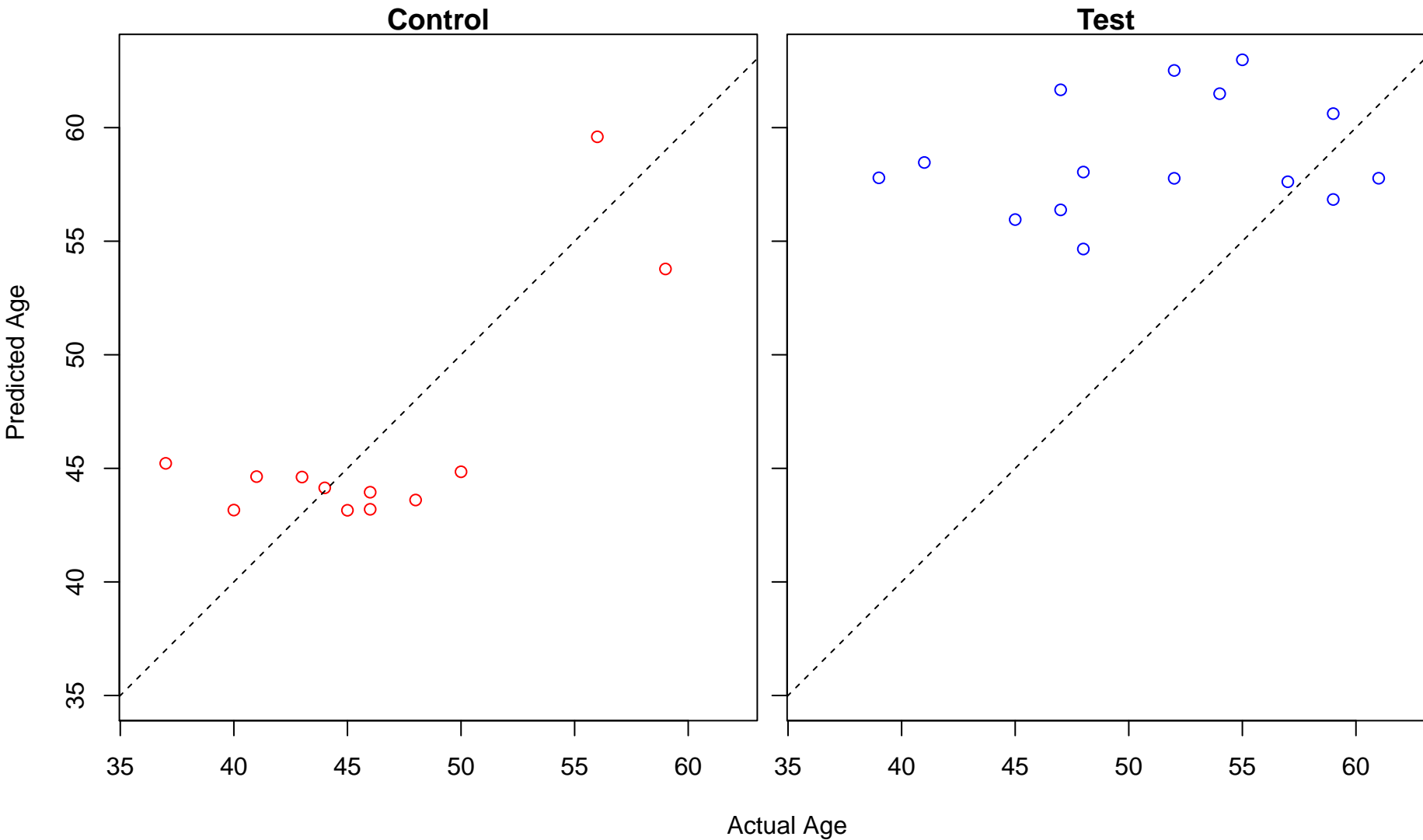
actin filament-based process (Score: 2.401754)



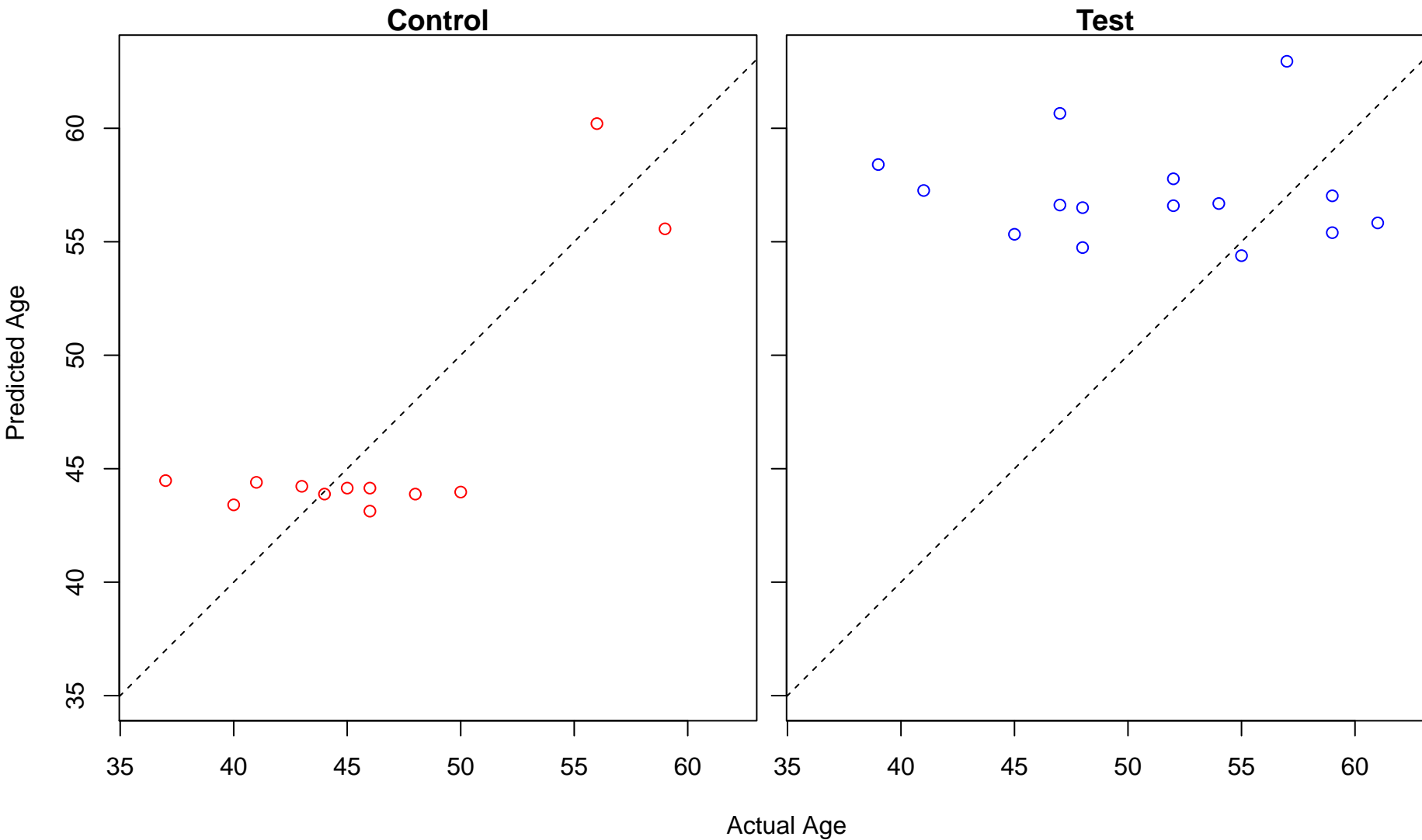
positive regulation of ERK1 and ERK2 cascade (Score: 2.401657)



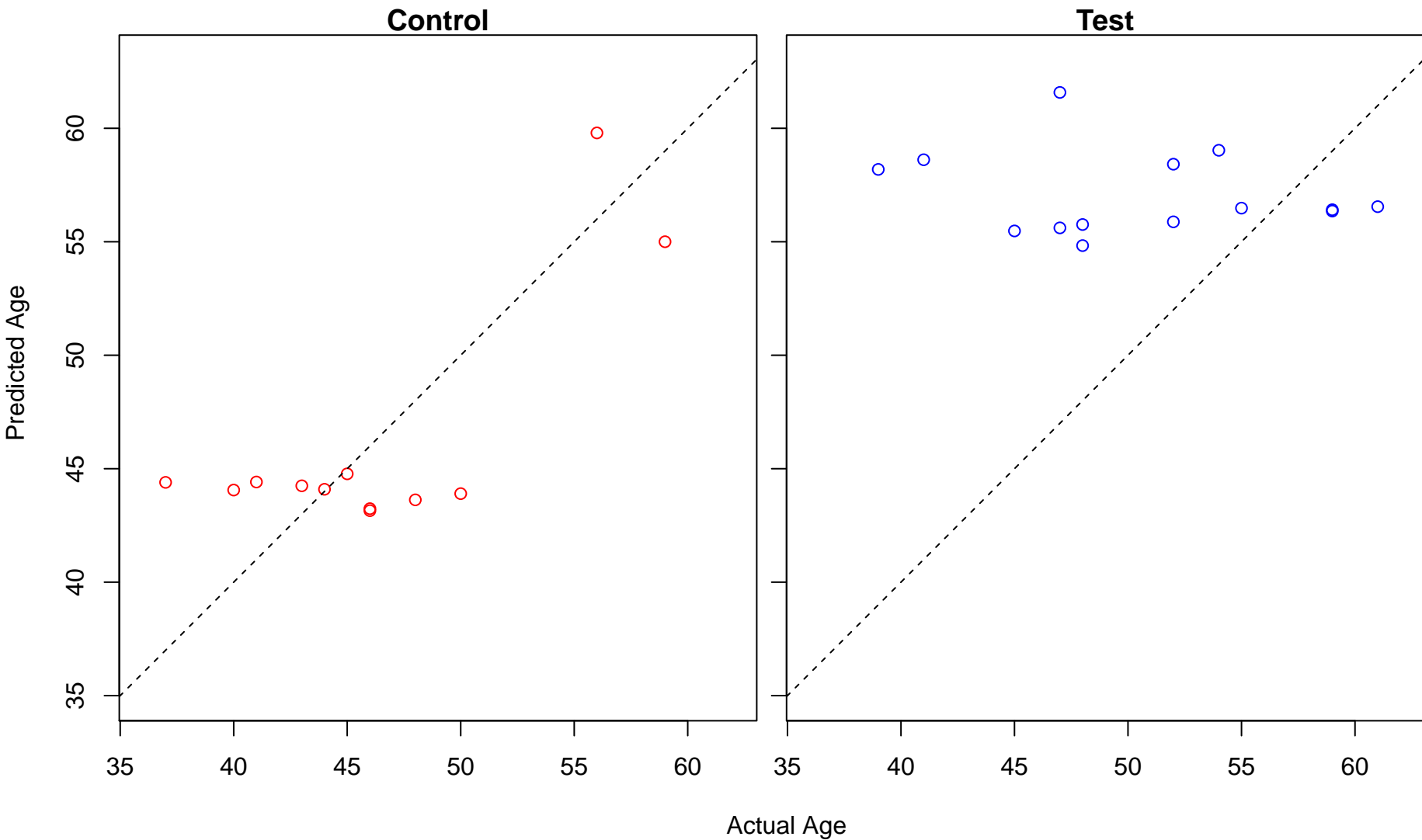
regulation of smooth muscle cell migration (Score: 2.400895)



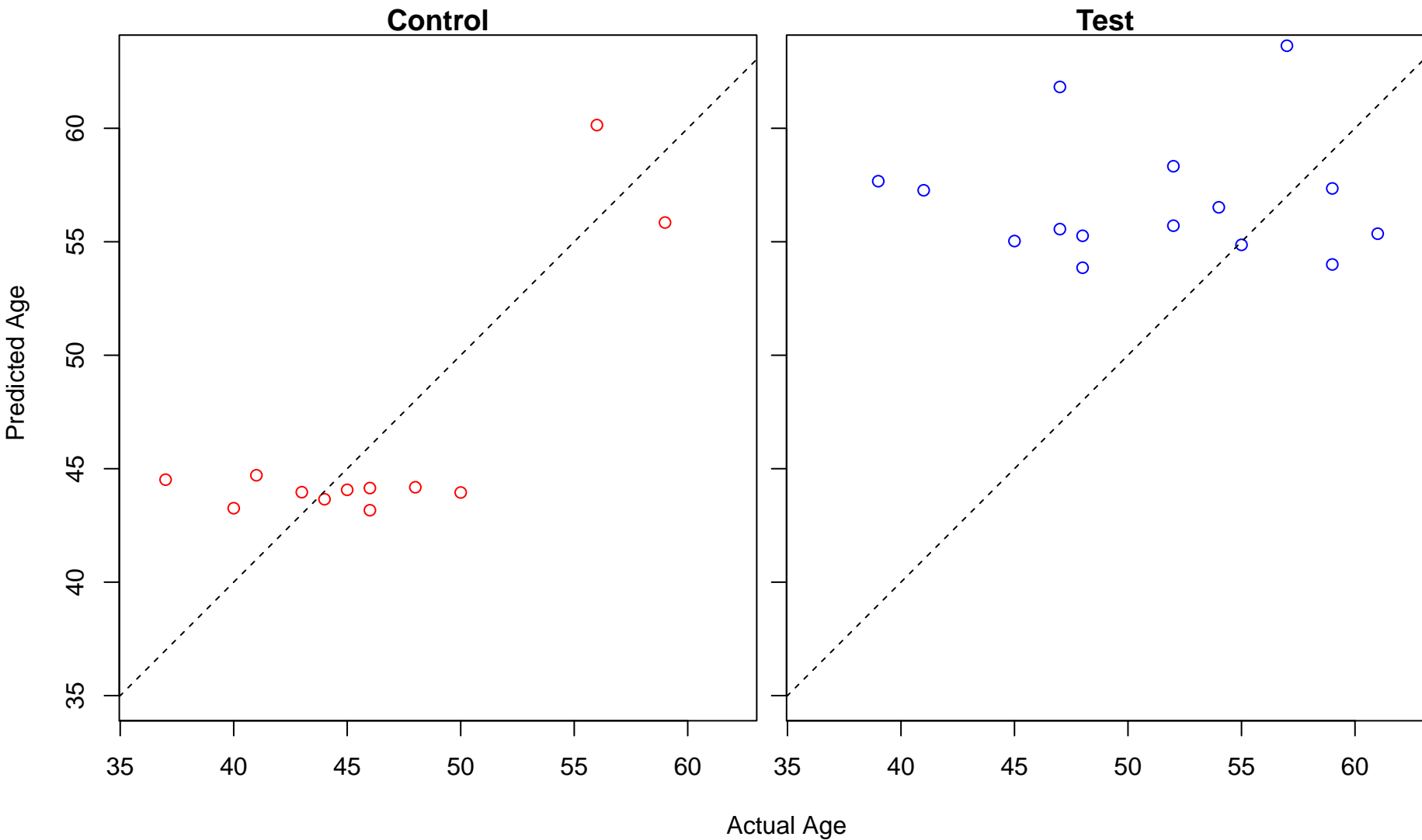
organelle localization (Score: 2.400888)



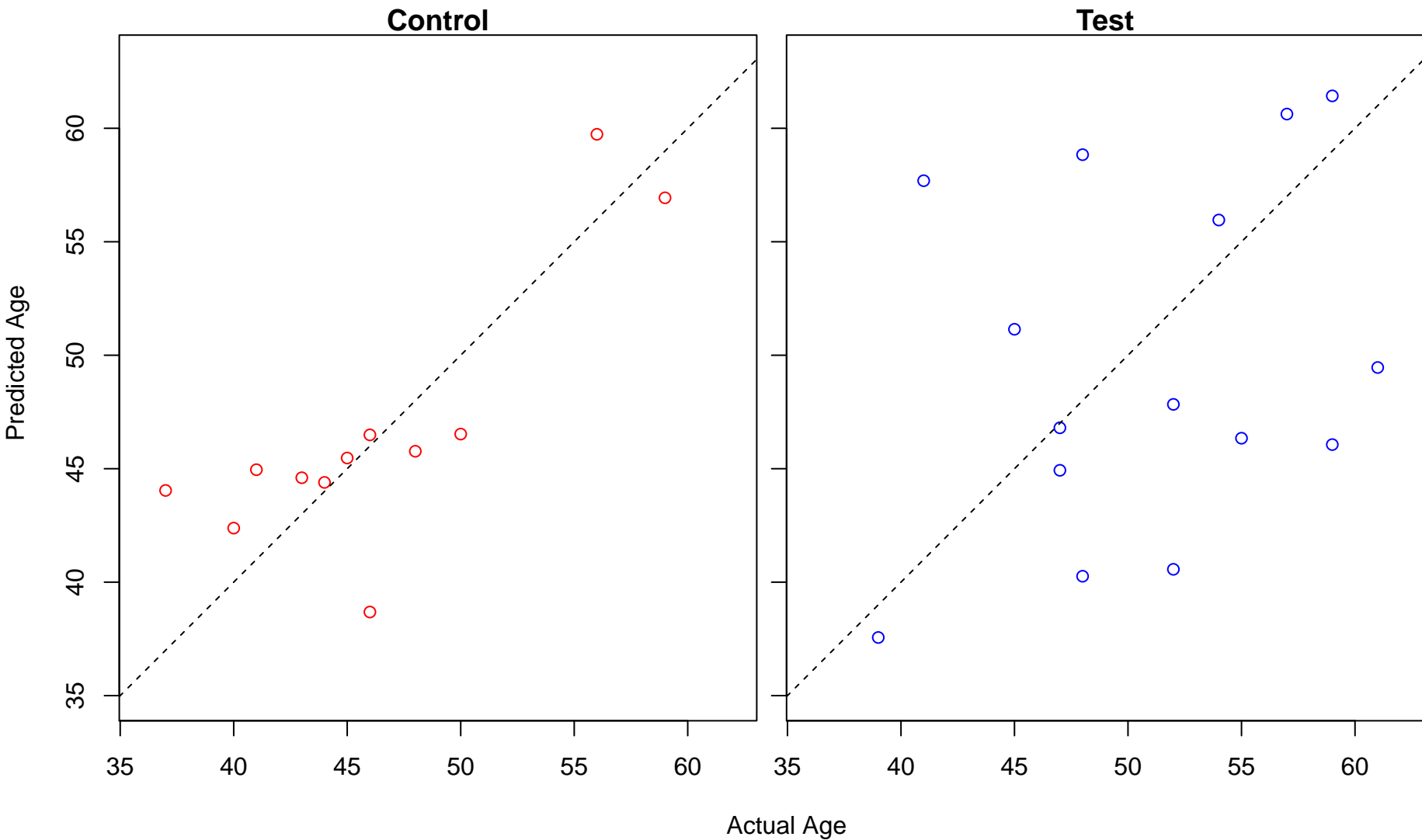
purine nucleotide metabolic process (Score: 2.399798)



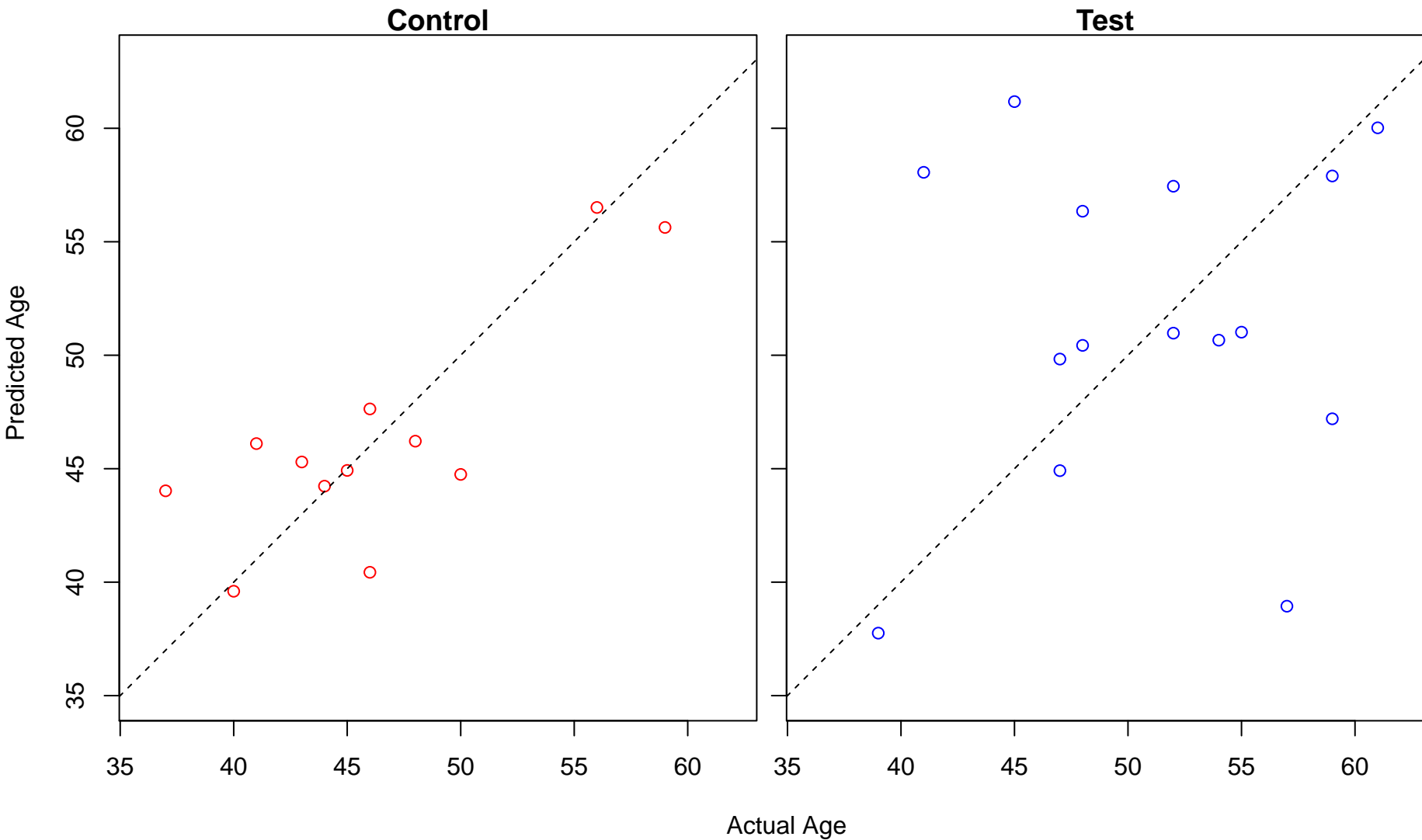
vesicle organization (Score: 2.399791)



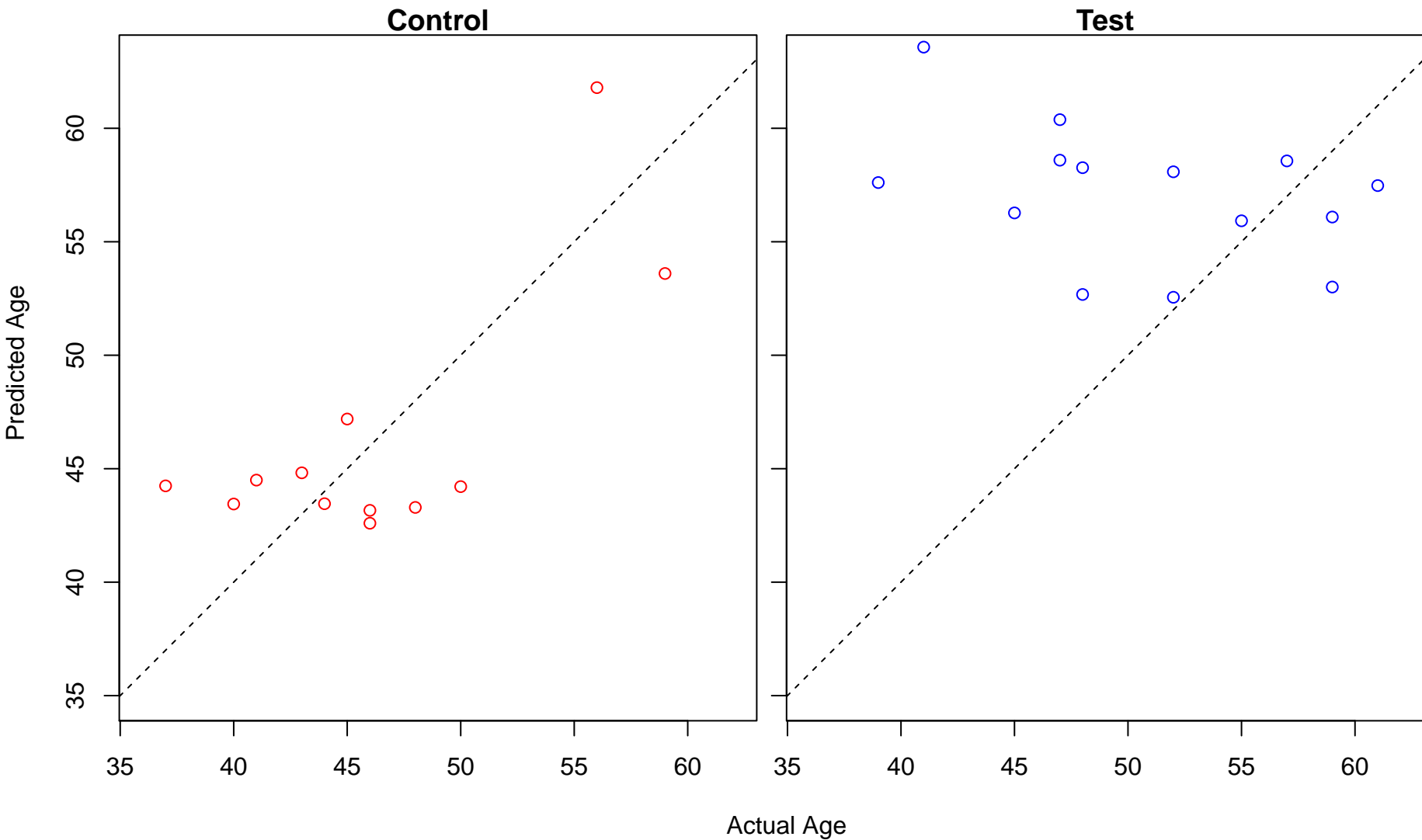
positive regulation of protein polymerization (Score: 2.399060)



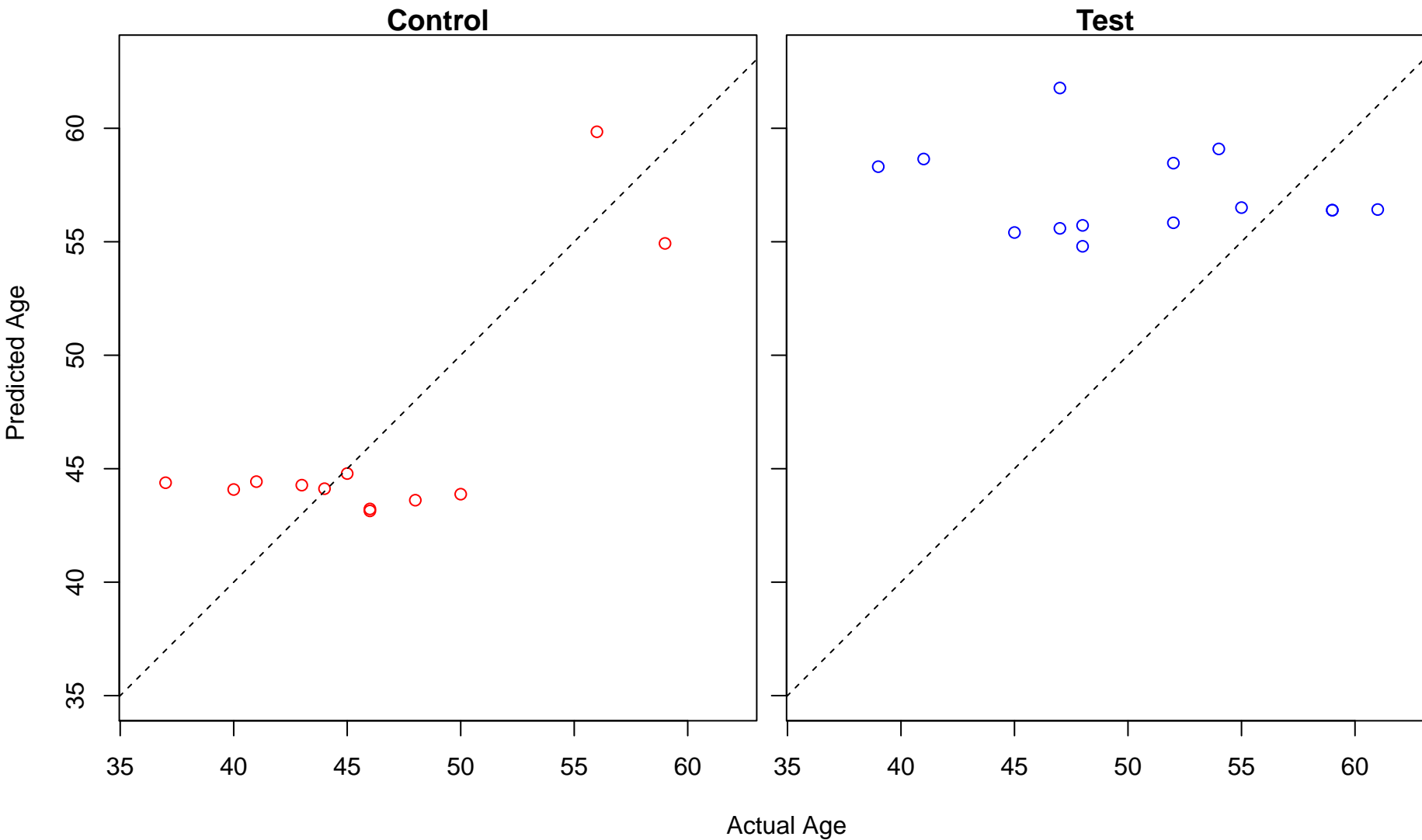
regulation of protein secretion (Score: 2.398866)



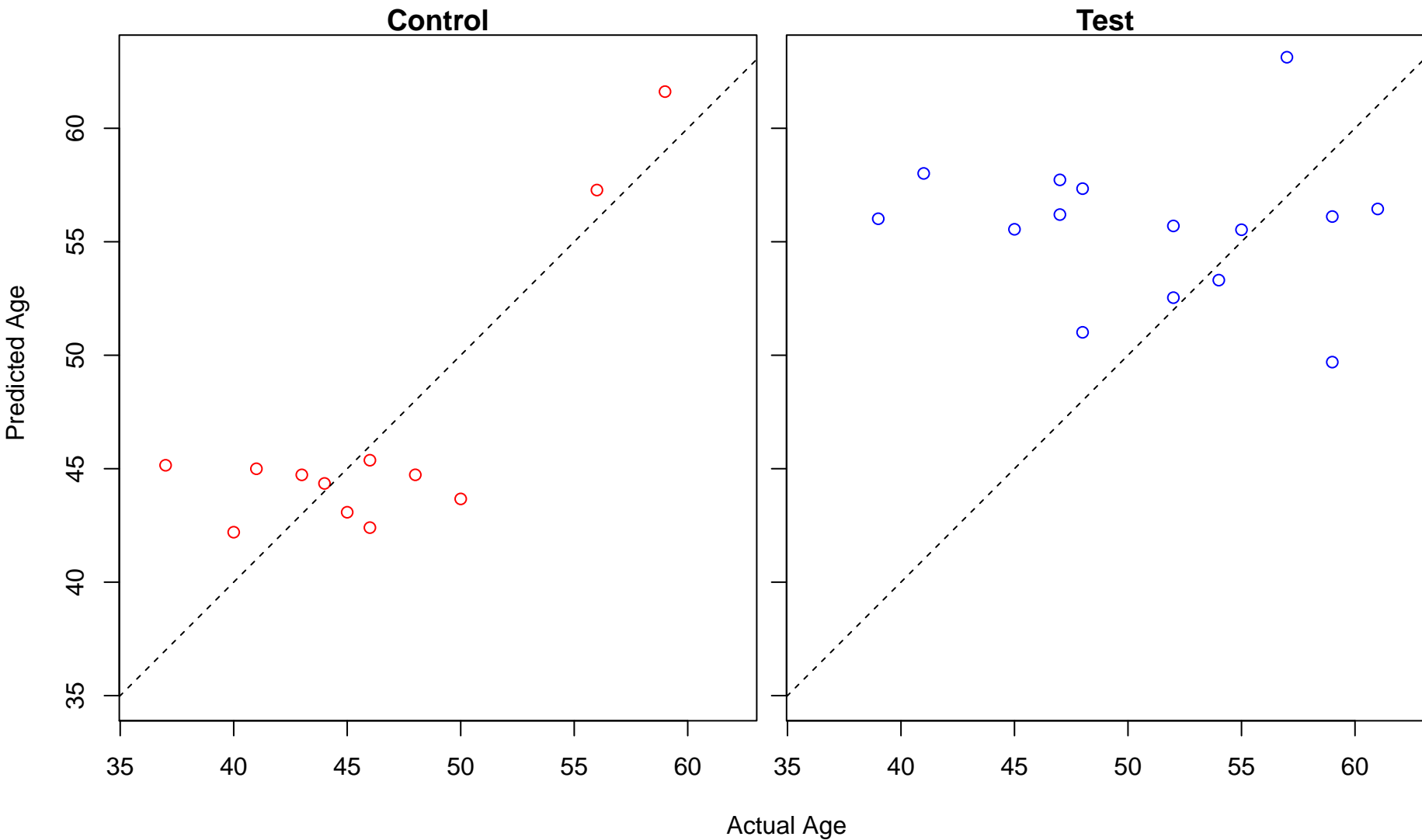
smooth muscle cell migration (Score: 2.396841)



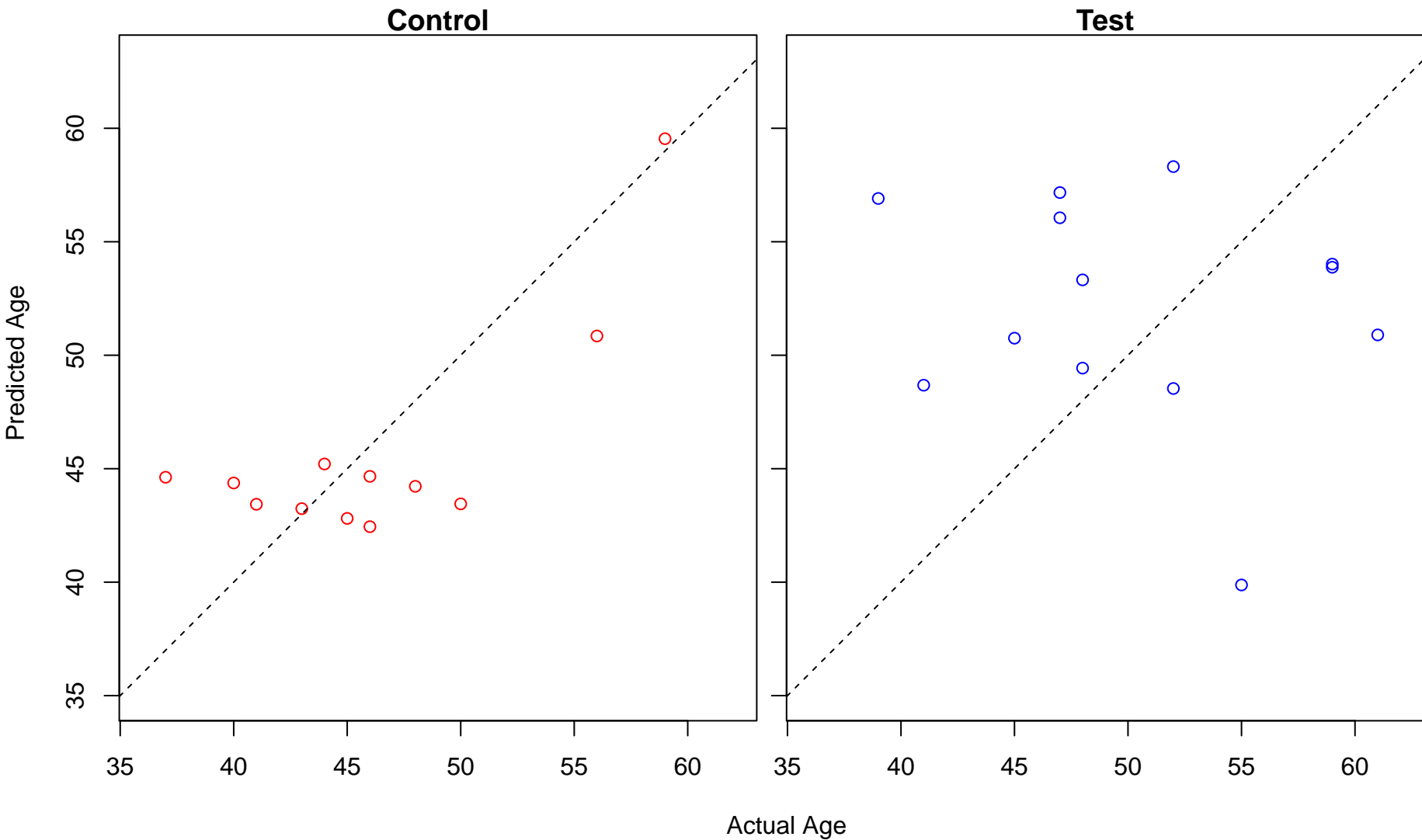
ribonucleotide metabolic process (Score: 2.396738)



positive regulation of MAPK cascade (Score: 2.393176)

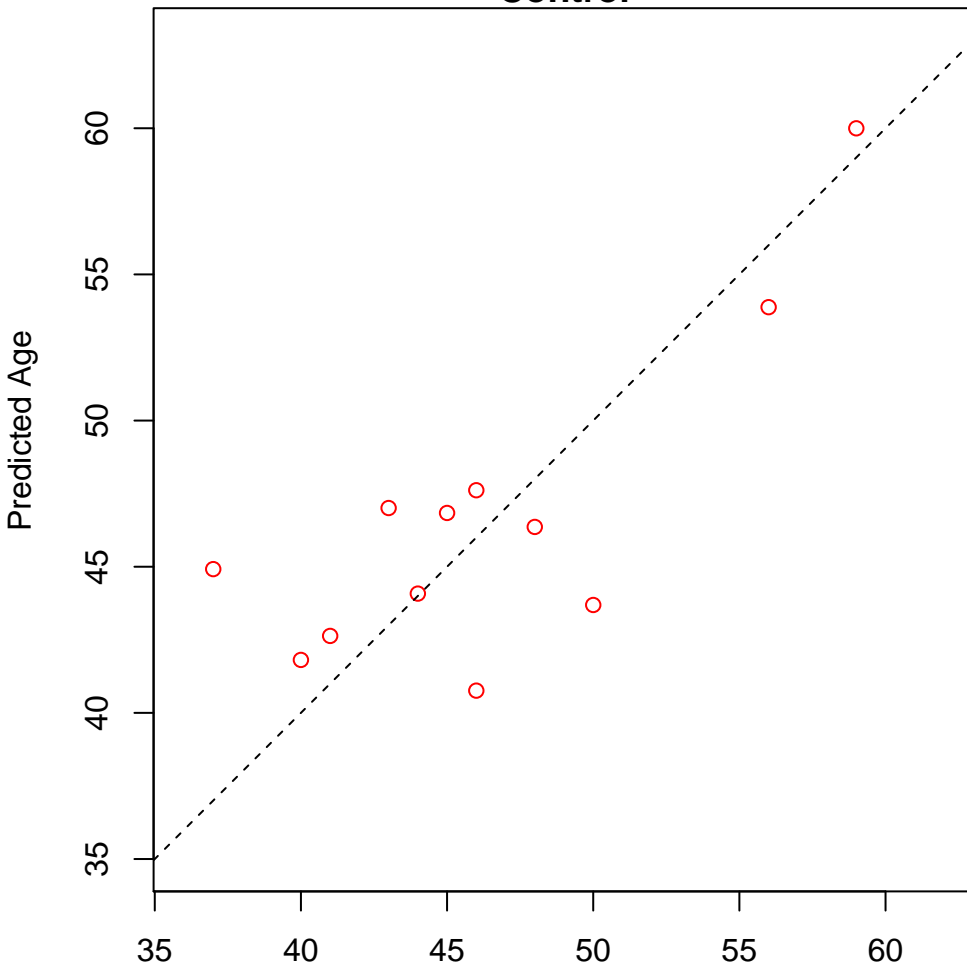


cellular monovalent inorganic cation homeostasis (Score: 2.391873)

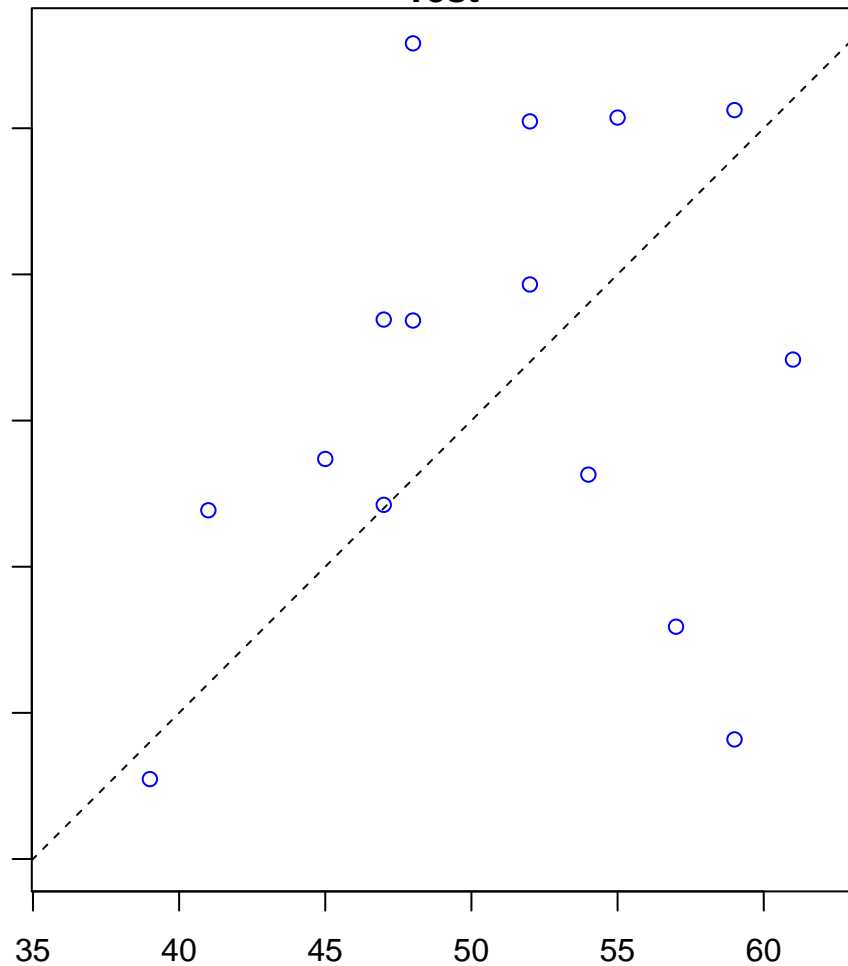


response to endoplasmic reticulum stress (Score: 2.390861)

Control

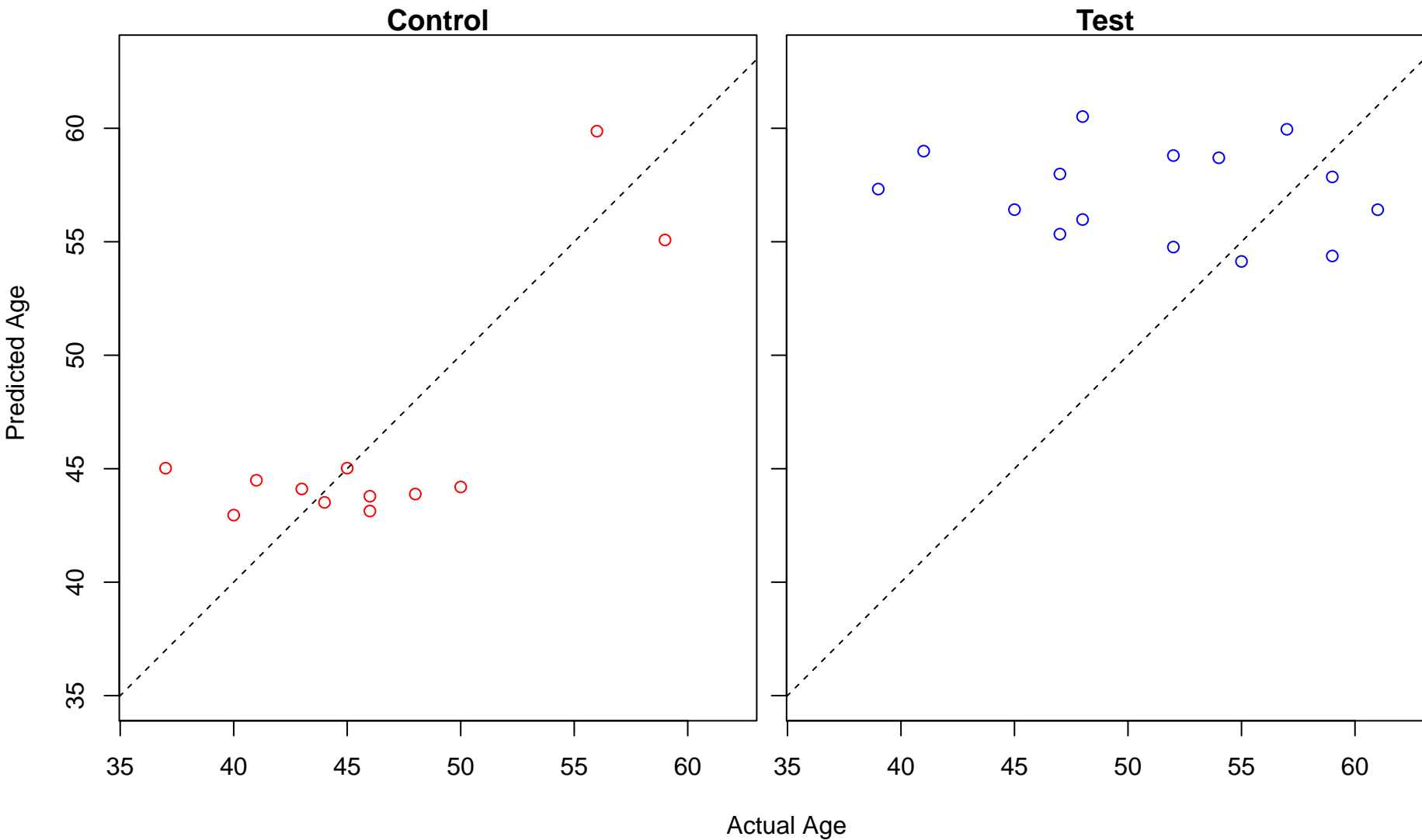


Test



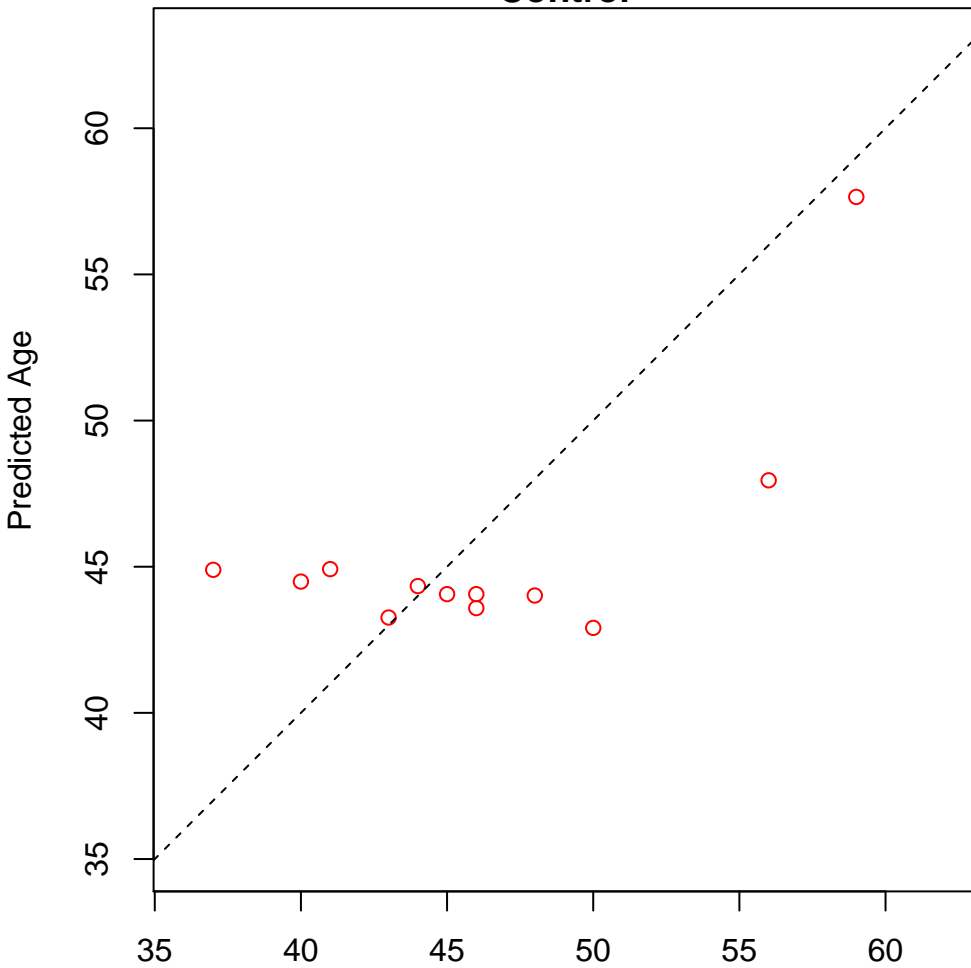
Actual Age

regulation of ERK1 and ERK2 cascade (Score: 2.389810)

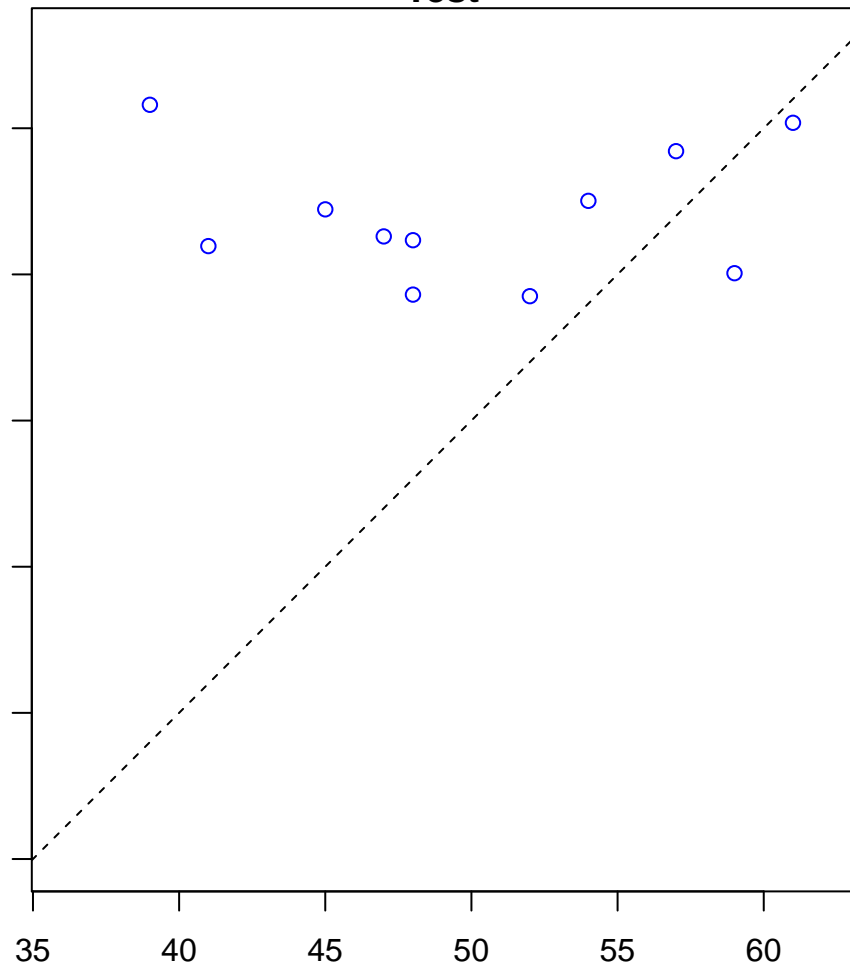


regulation of hair follicle development (Score: 2.386269)

Control

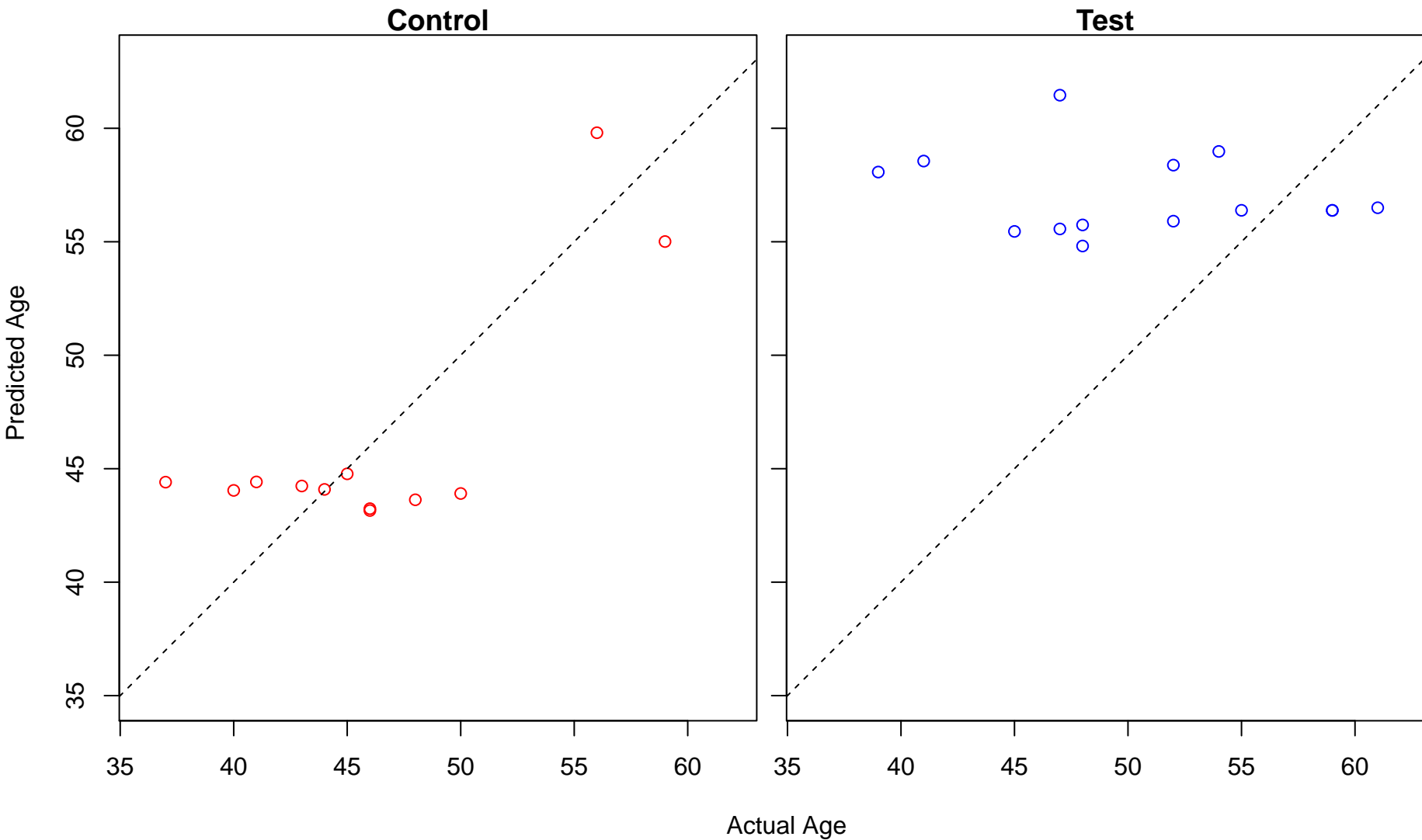


Test

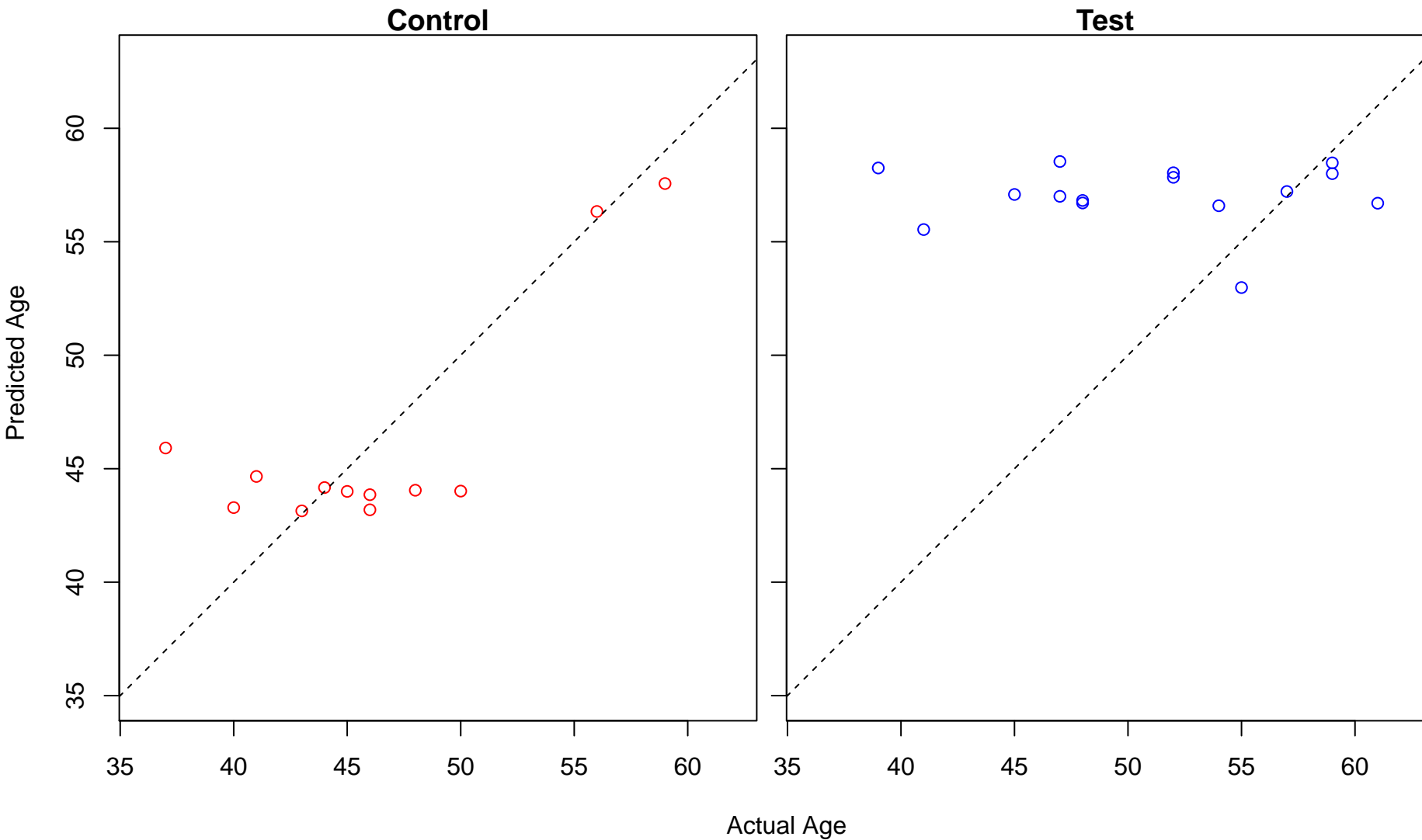


Actual Age

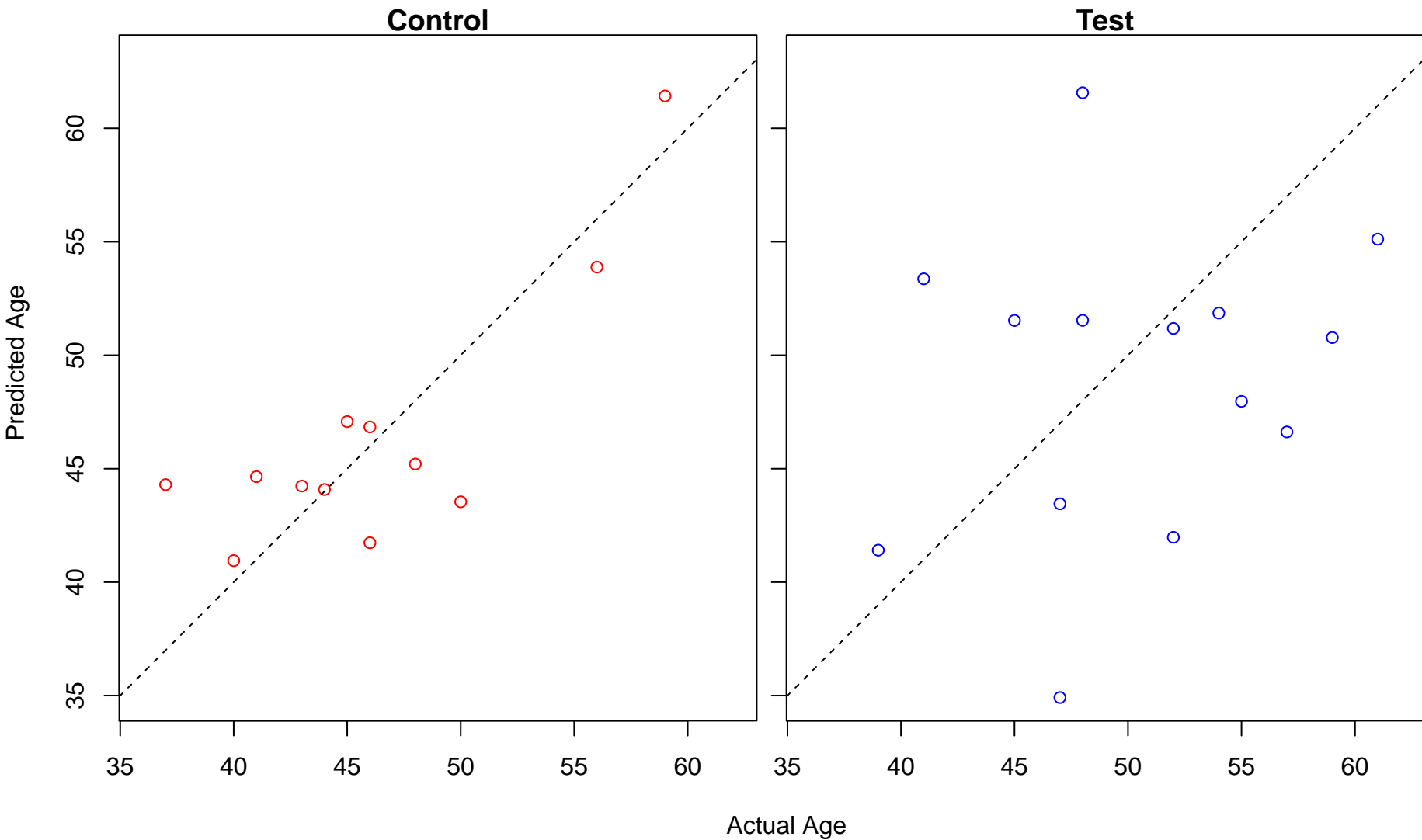
purine-containing compound metabolic process (Score: 2.382299)



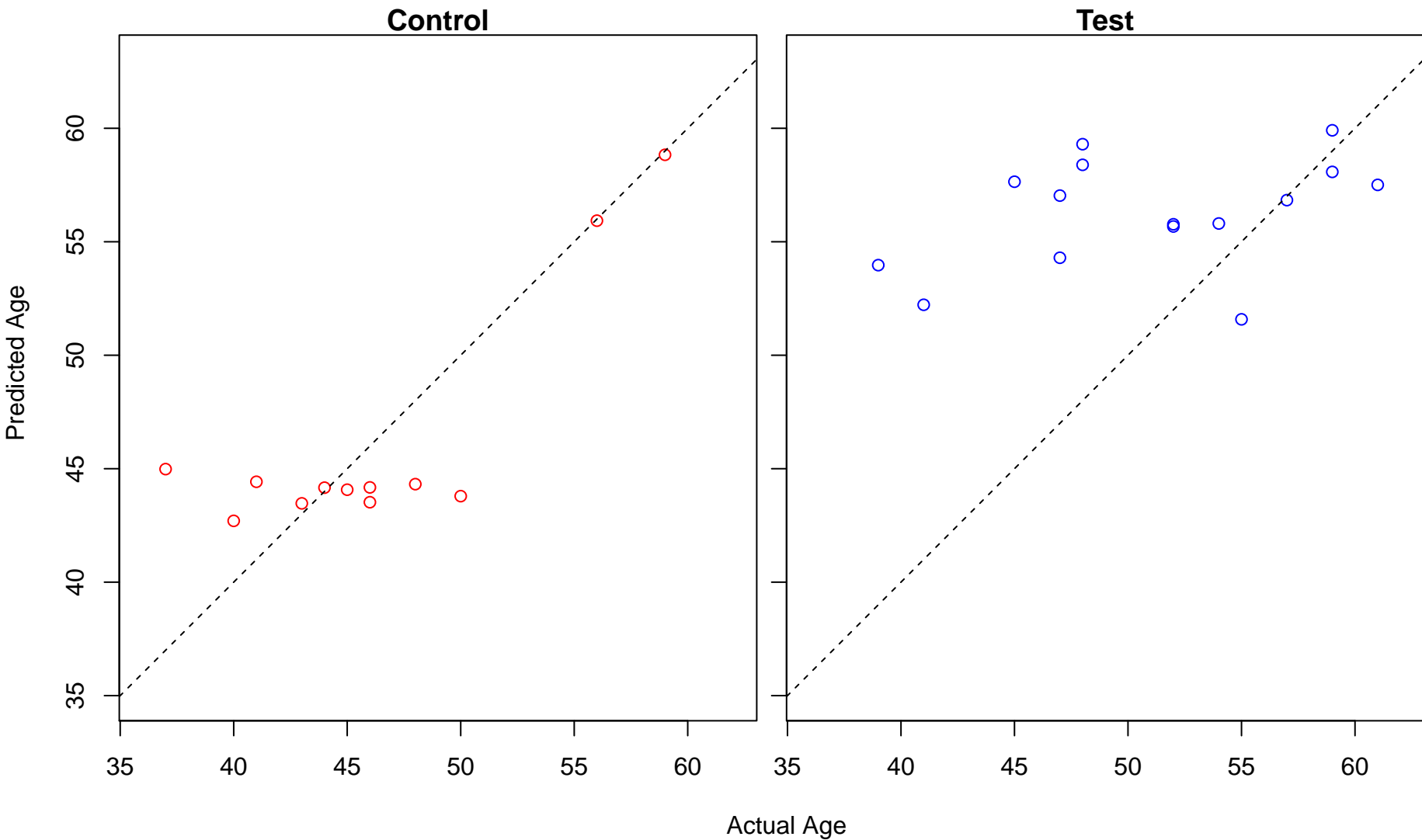
negative regulation of stem cell differentiation (Score: 2.382179)



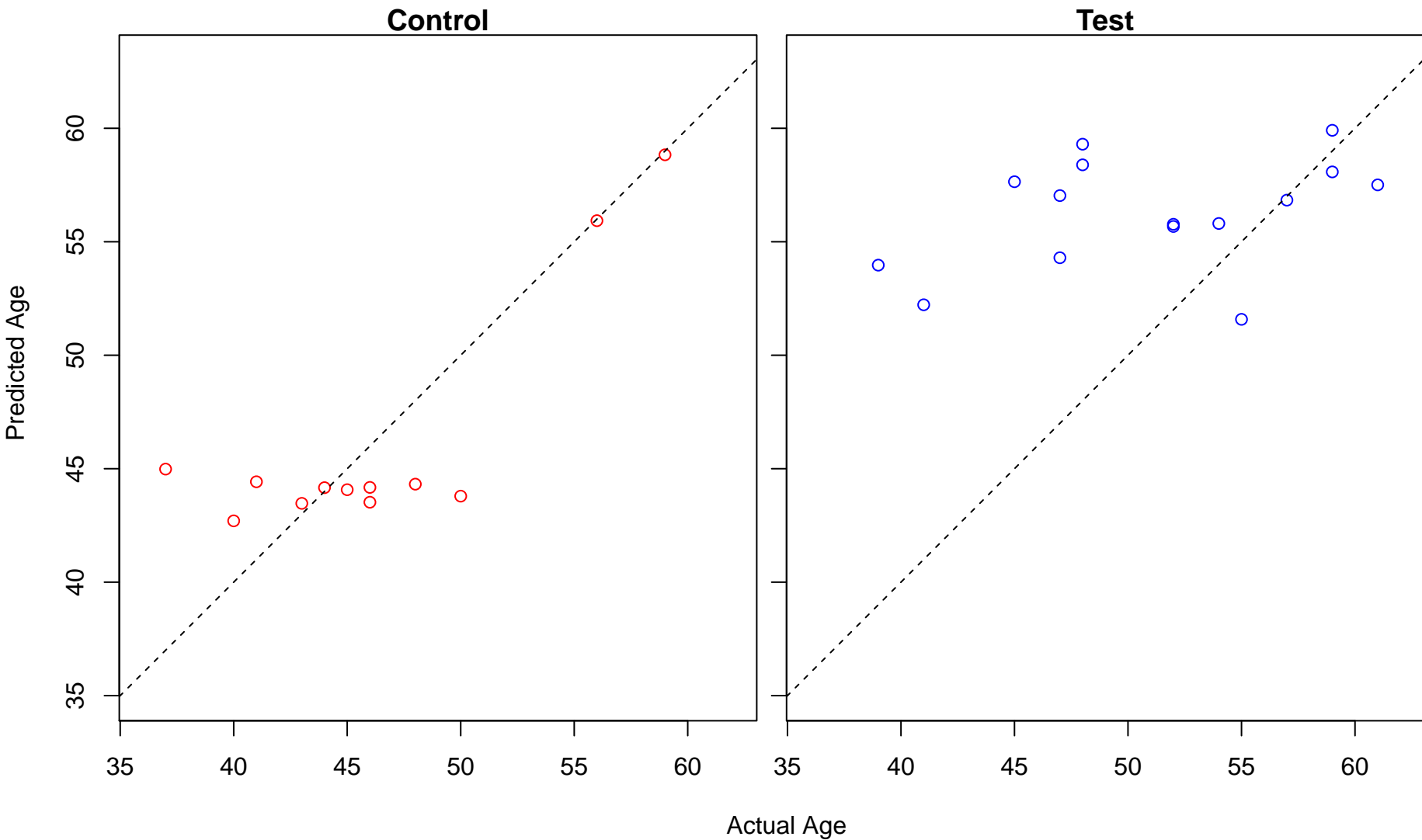
regulation of DNA biosynthetic process (Score: 2.378390)



protein targeting to peroxisome (Score: 2.366652)

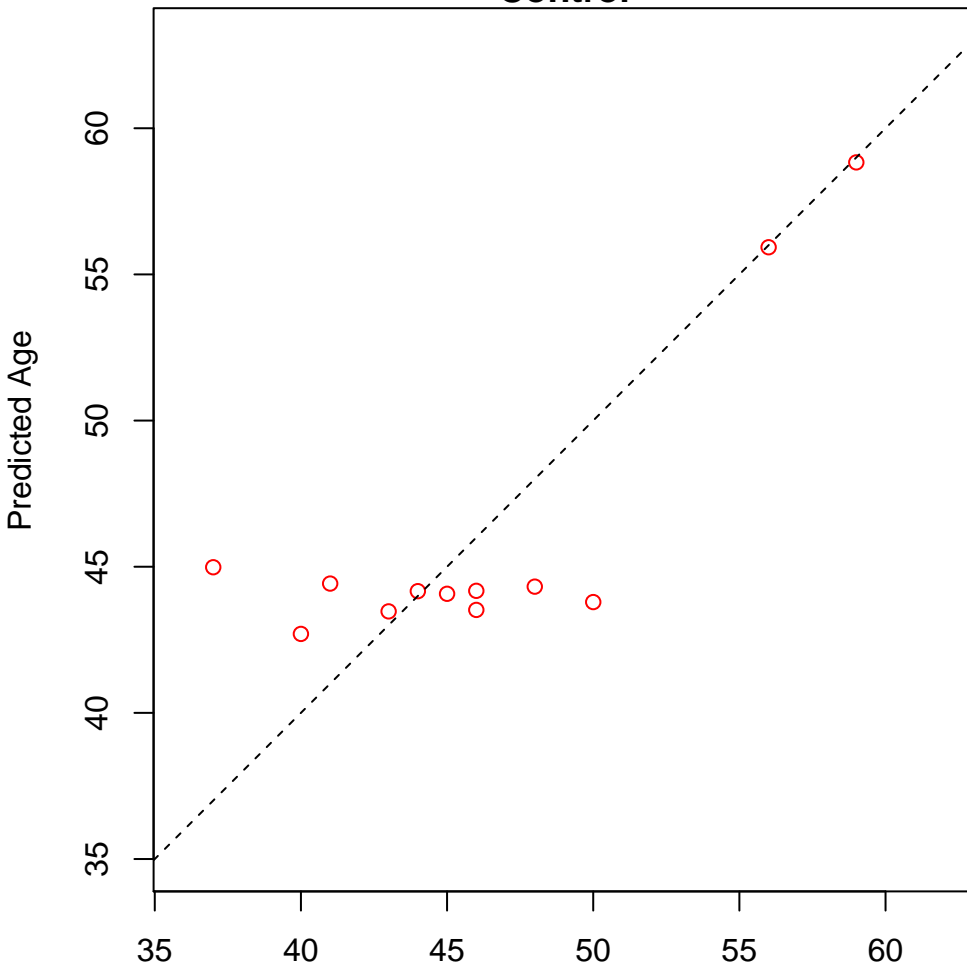


peroxisomal transport (Score: 2.366652)

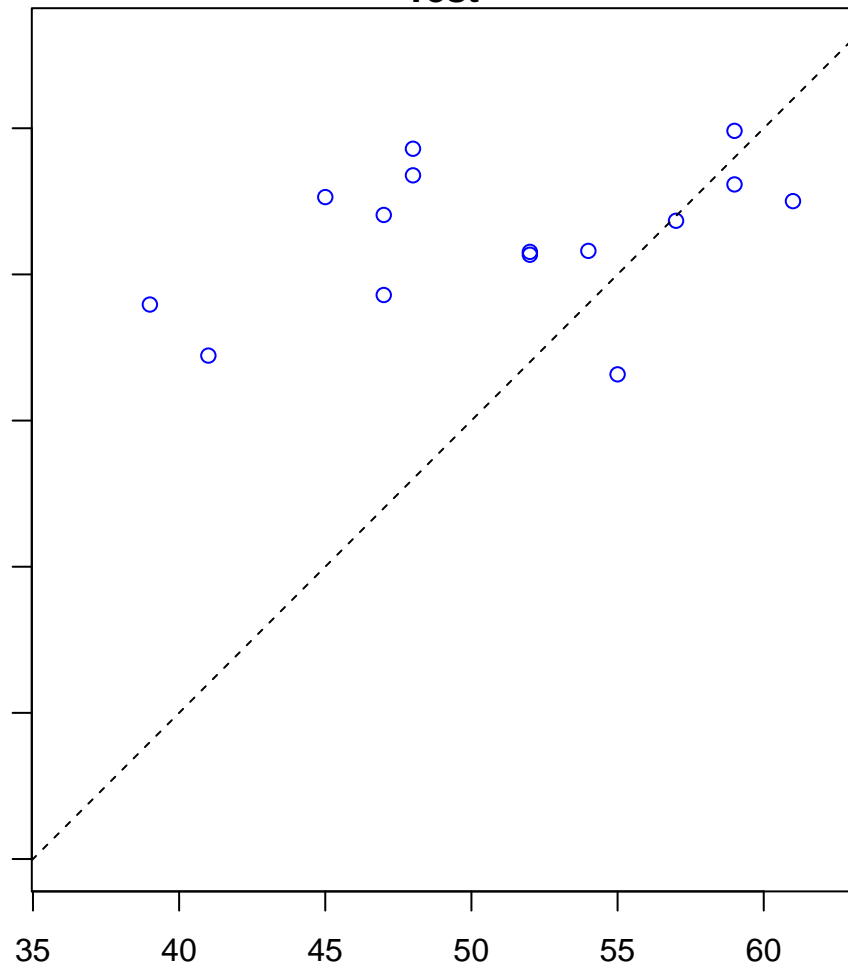


protein localization to peroxisome (Score: 2.366652)

Control

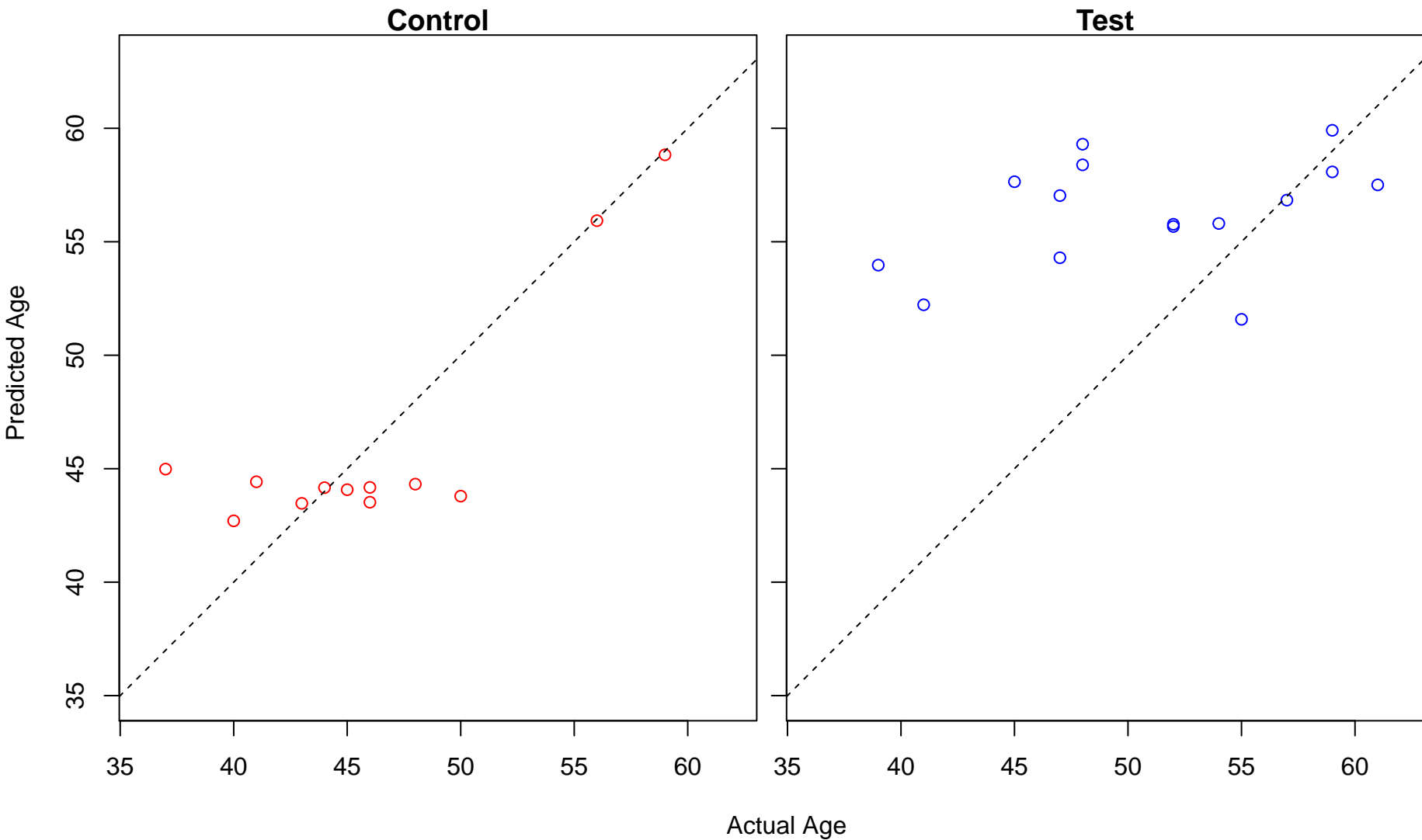


Test

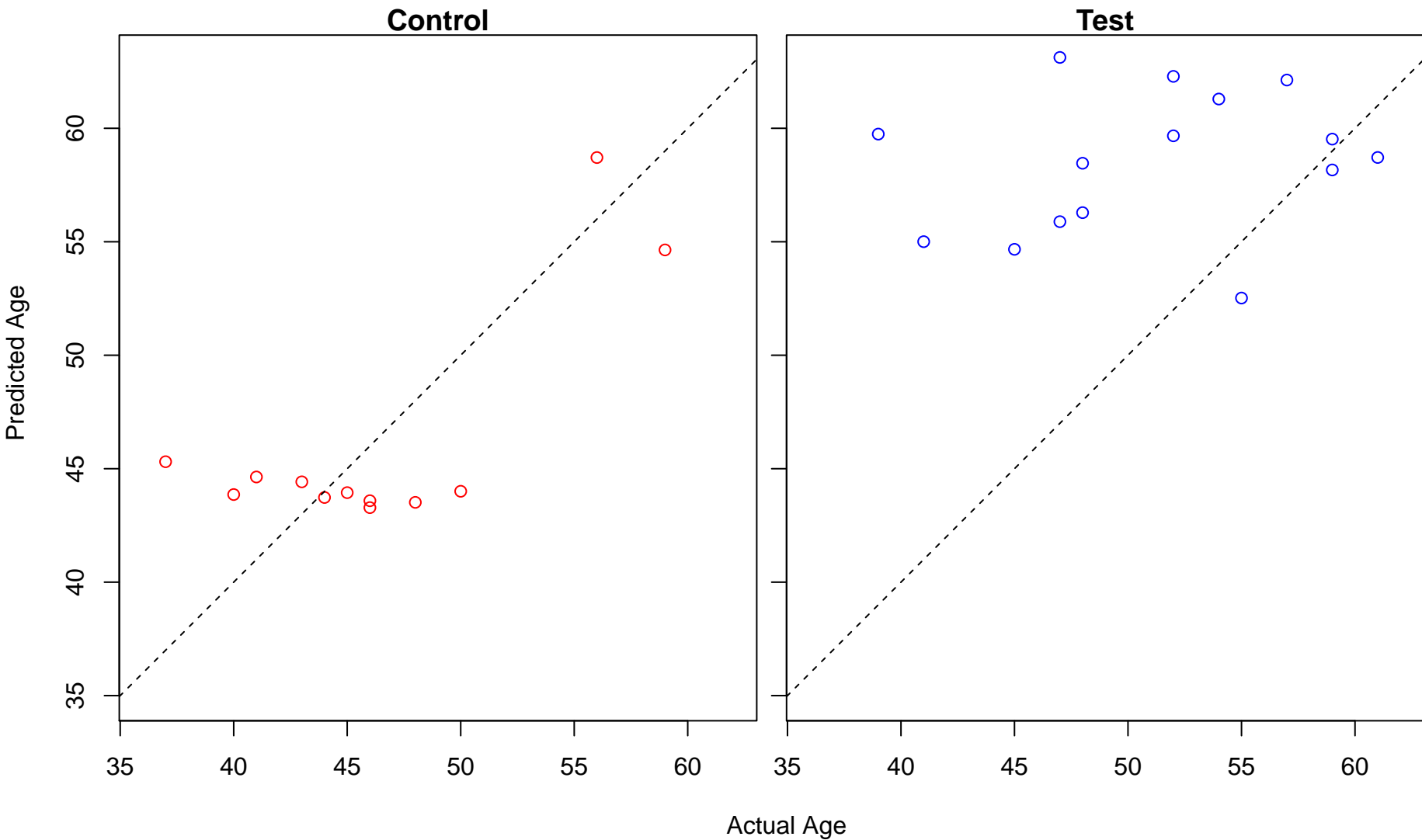


Actual Age

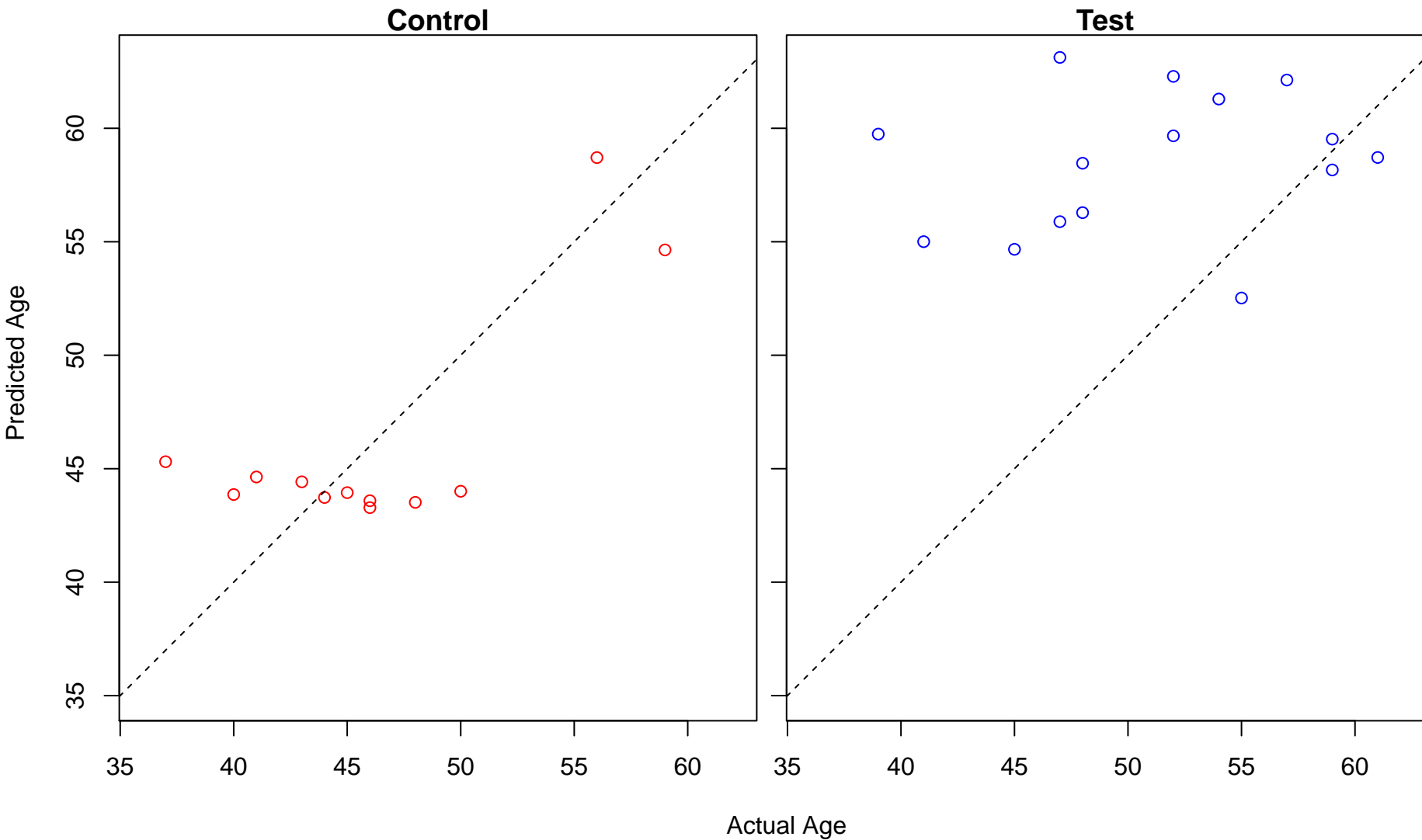
establishment of protein localization to peroxisome (Score: 2.366652)



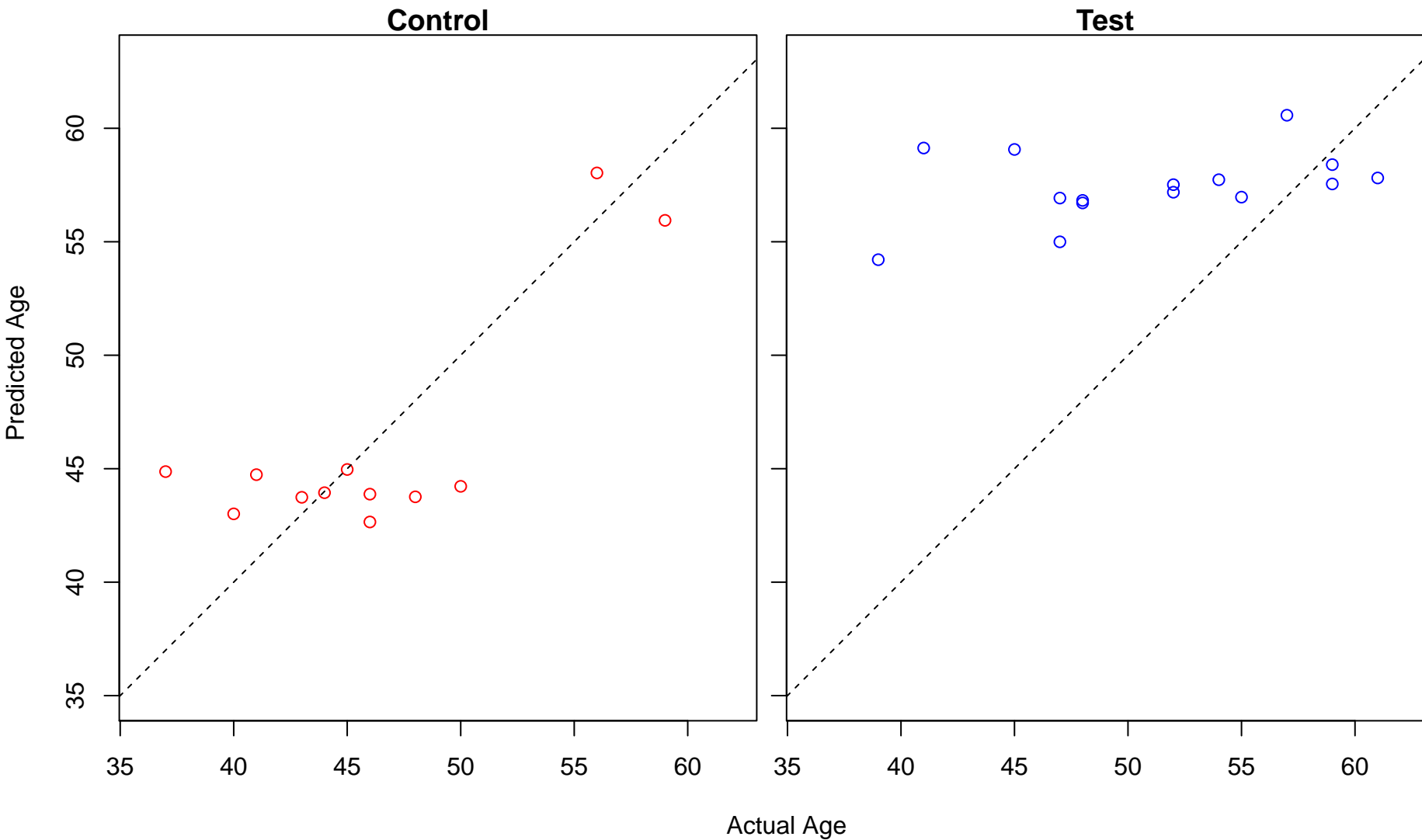
stem cell population maintenance (Score: 2.366065)



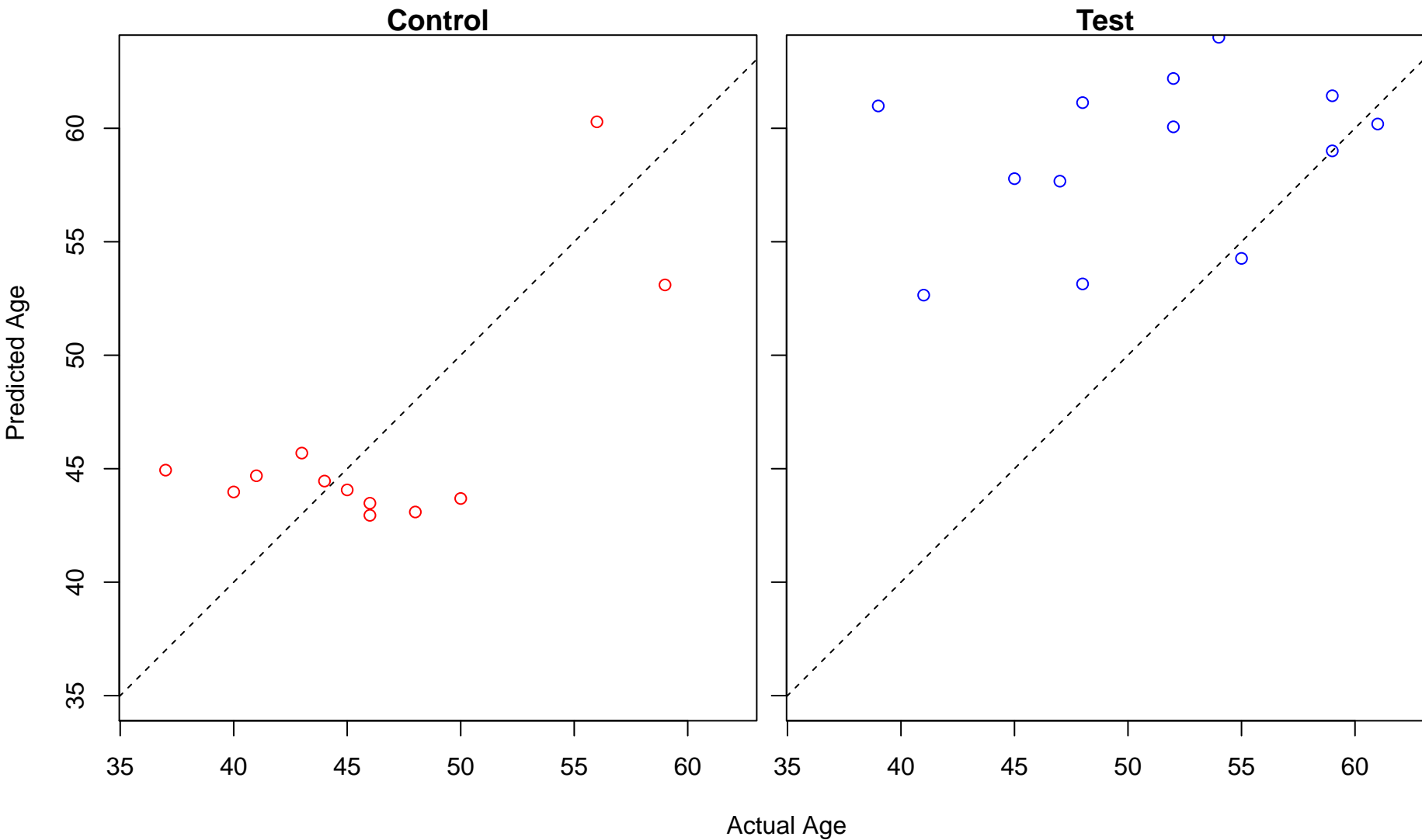
maintenance of cell number (Score: 2.366021)



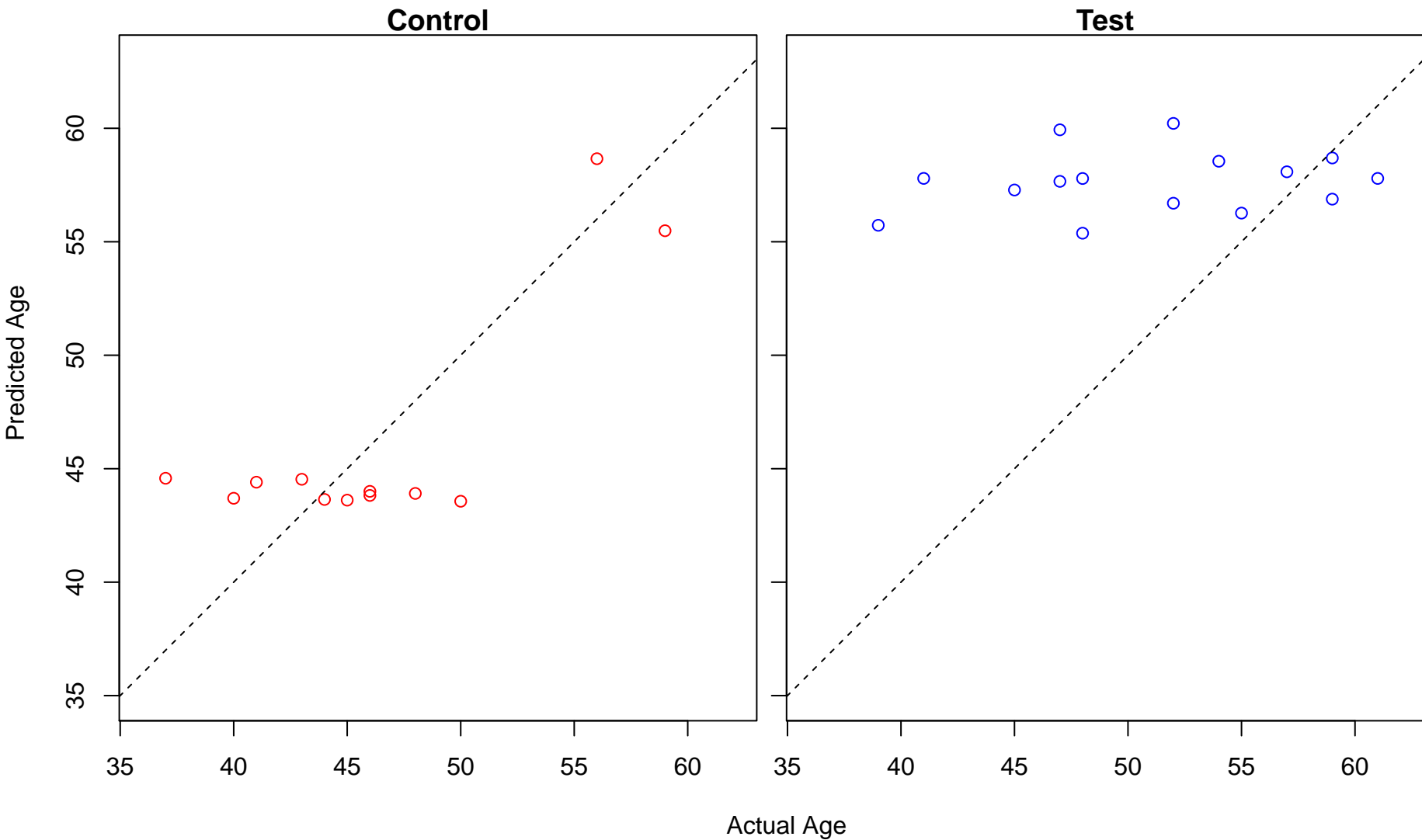
response to topologically incorrect protein (Score: 2.358177)



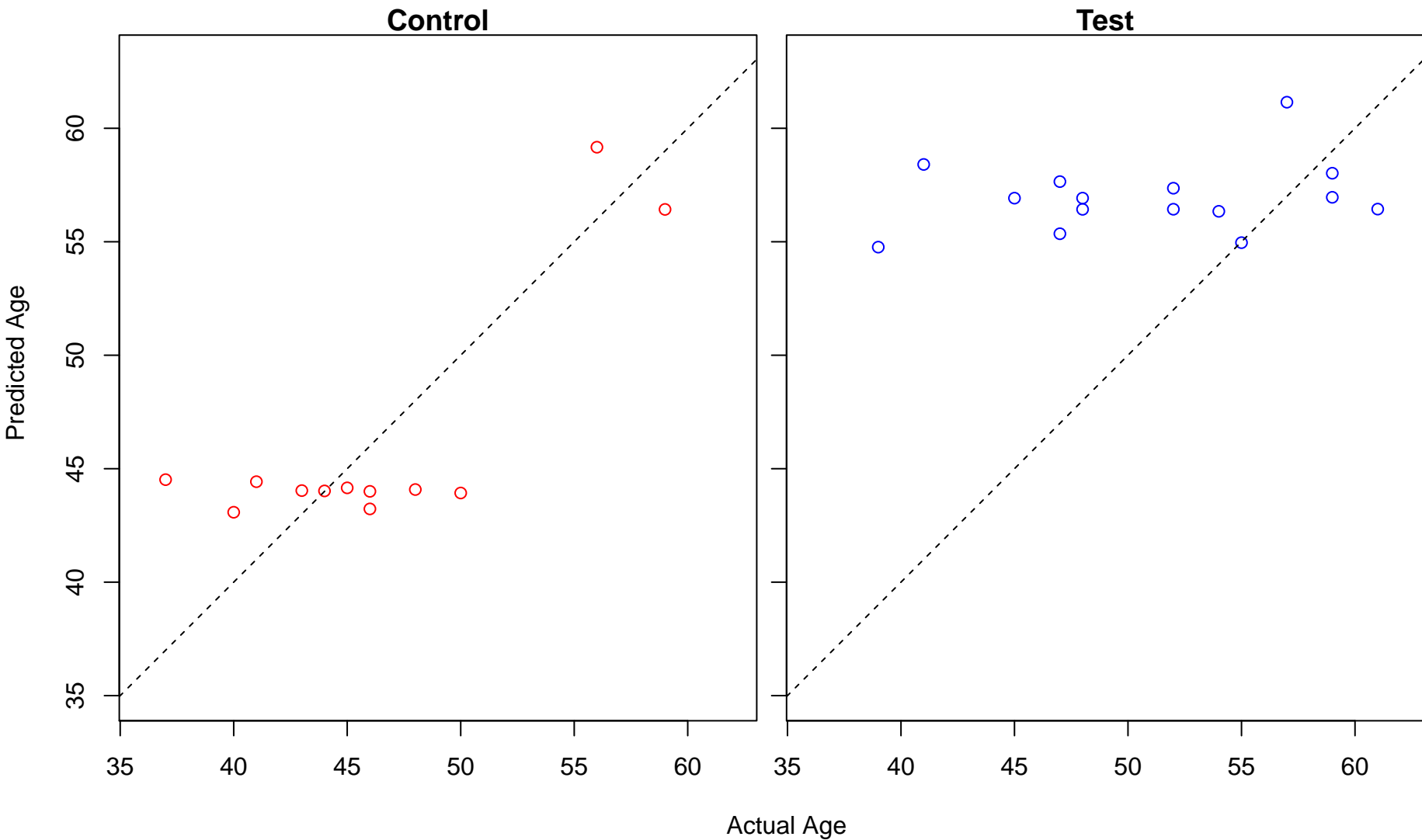
cellular response to nutrient (Score: 2.354470)



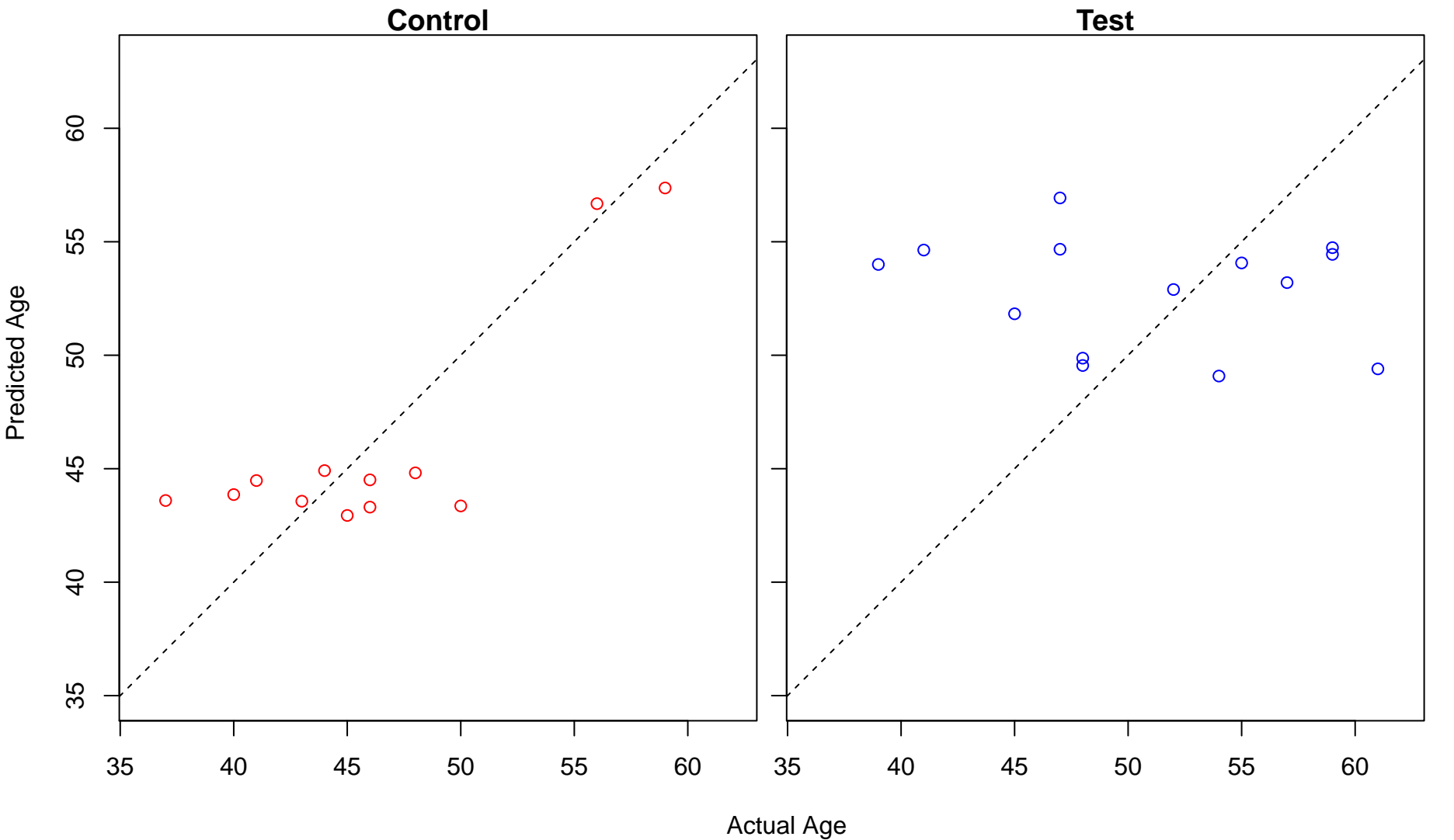
endocytic recycling (Score: 2.354441)



actin filament organization (Score: 2.354054)

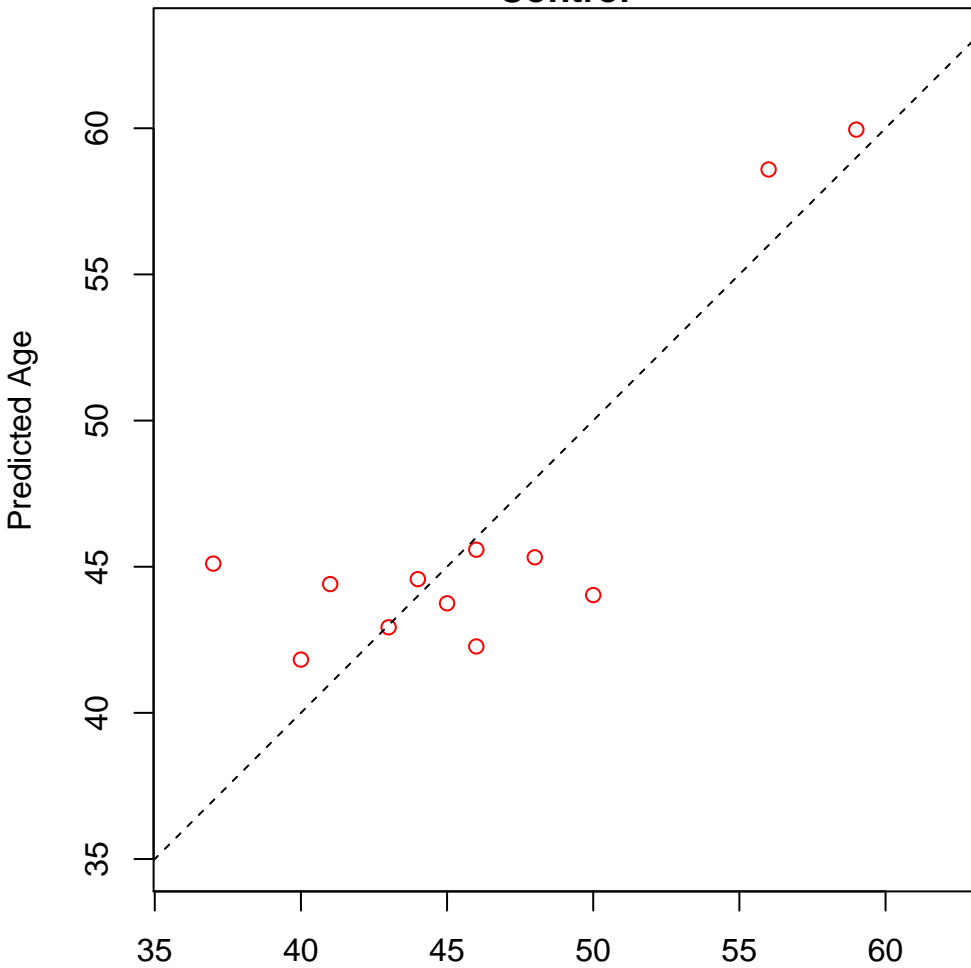


of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling

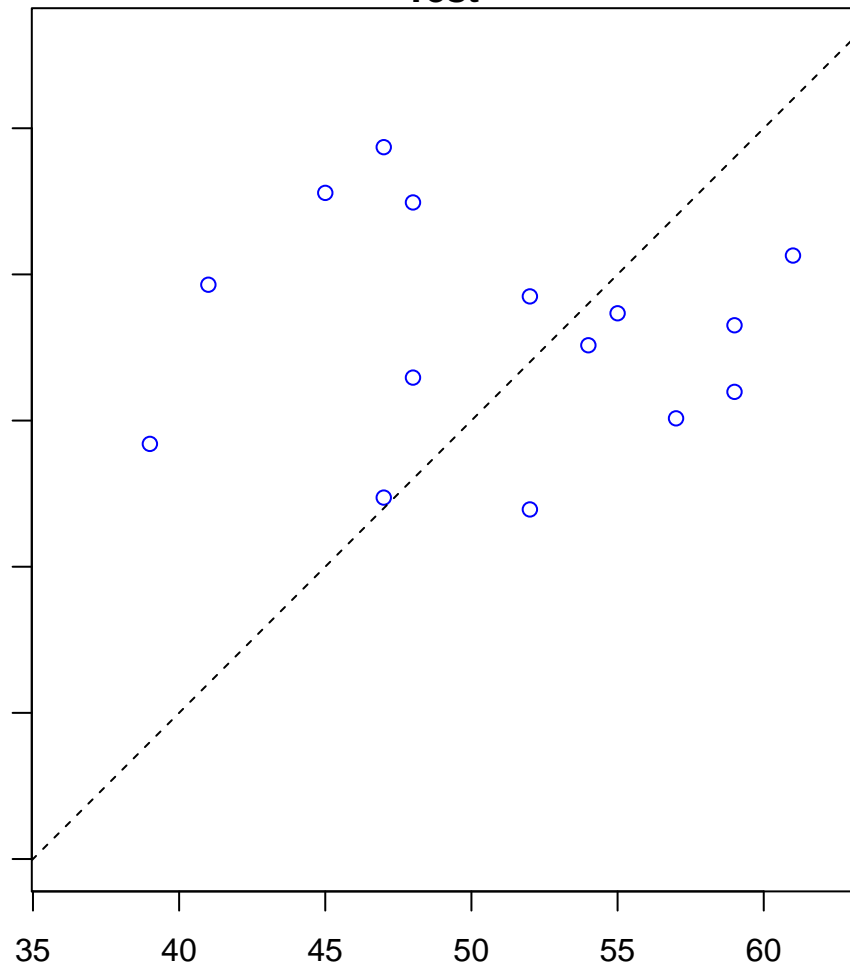


central nervous system development (Score: 2.352002)

Control

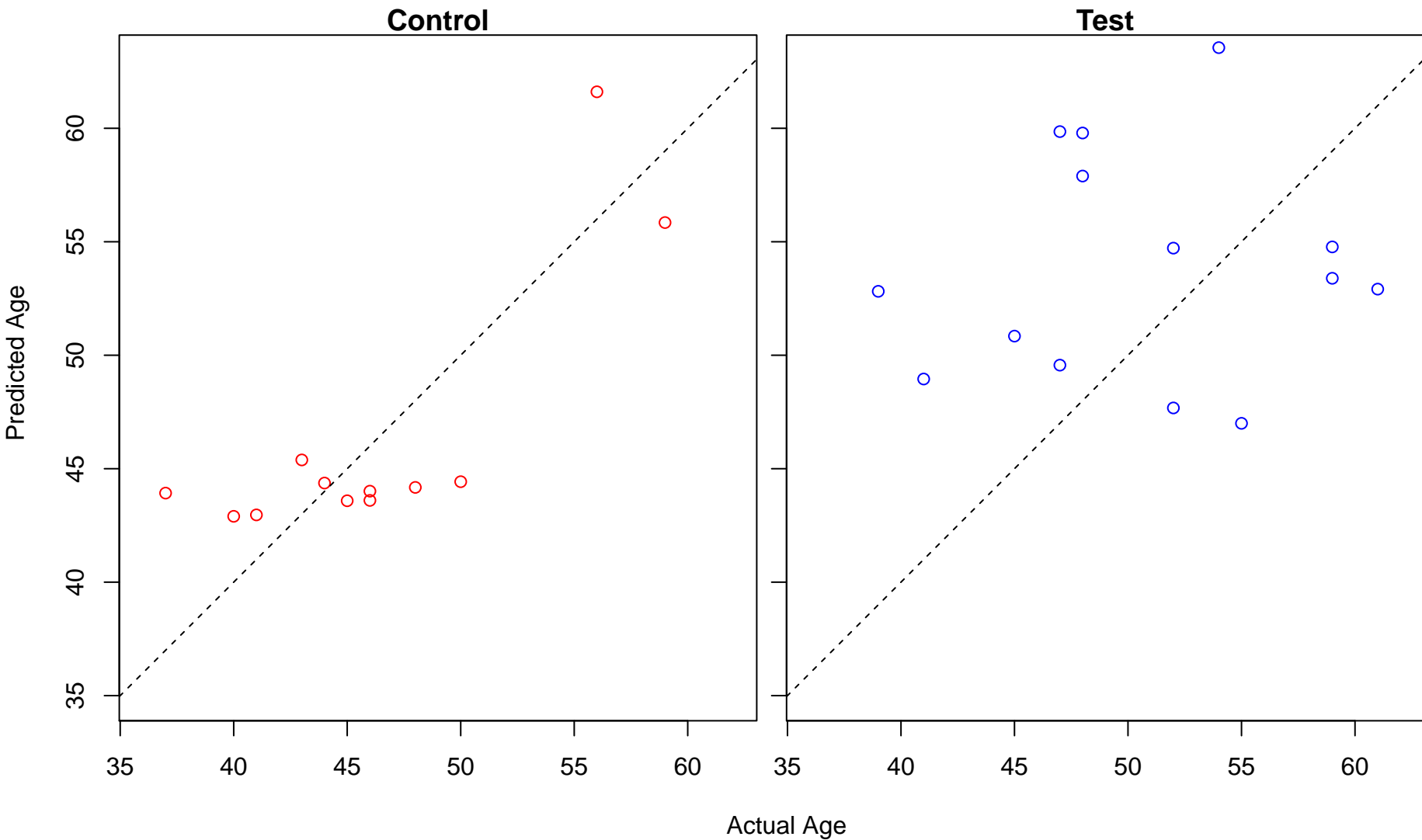


Test

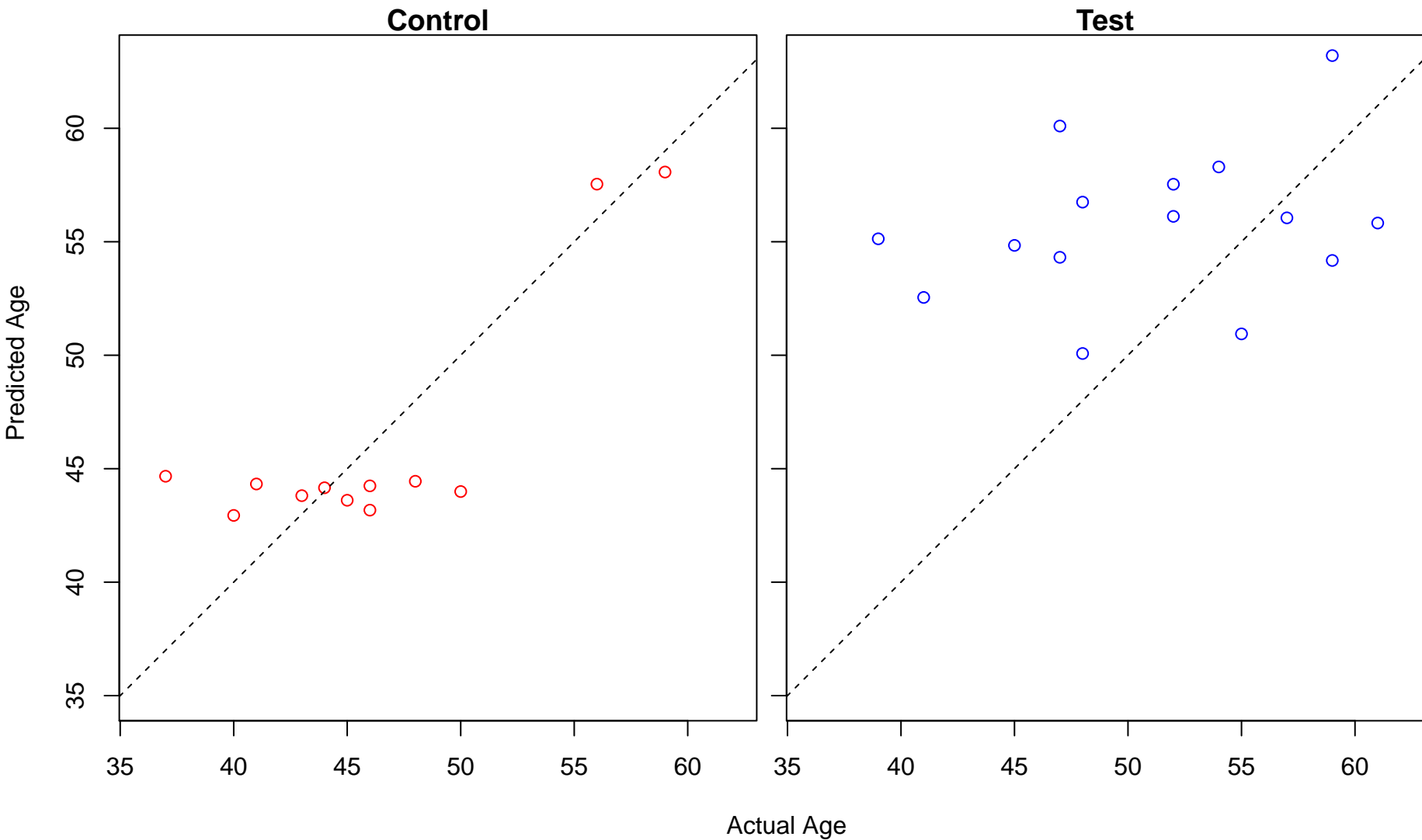


Actual Age

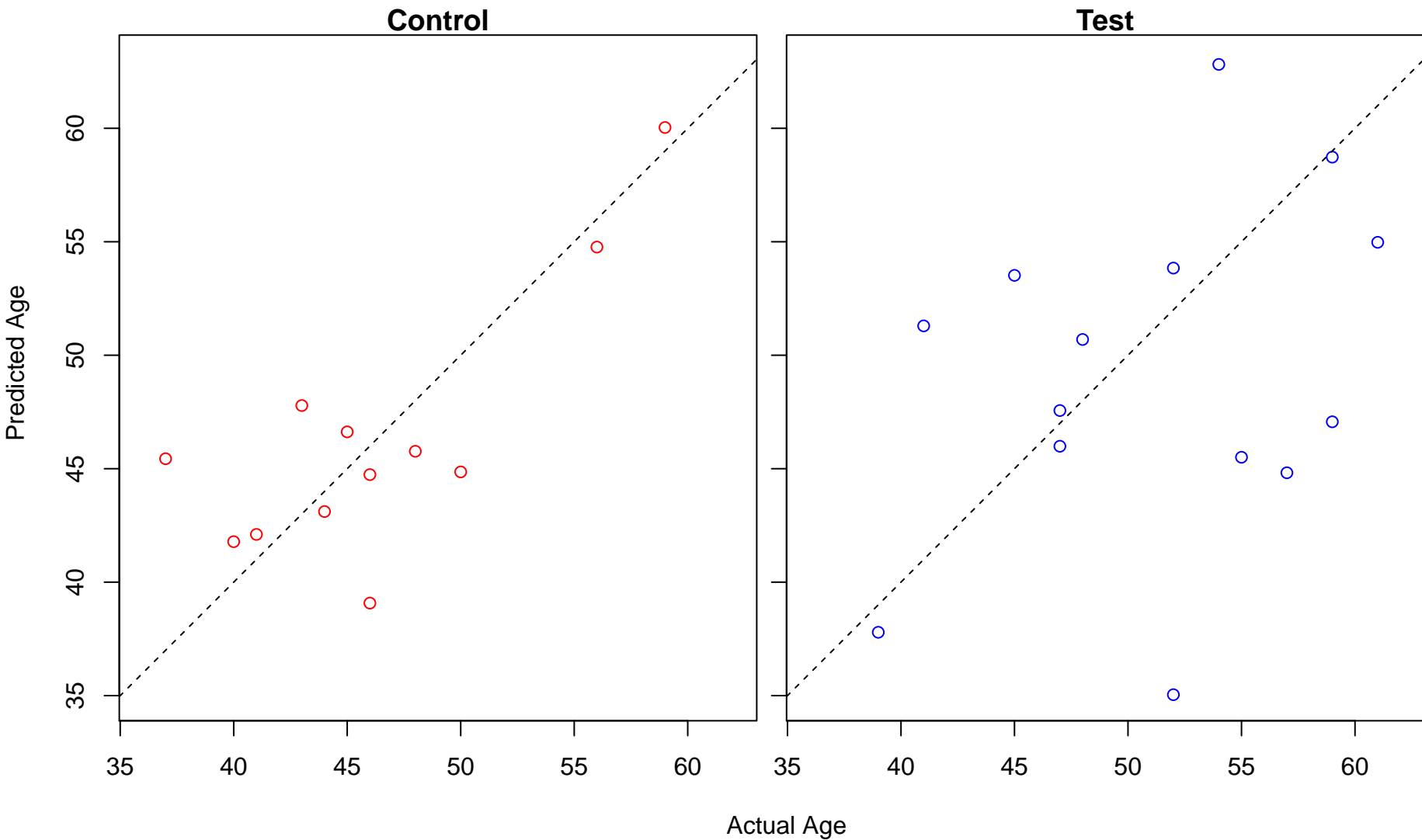
sperm capacitation (Score: 2.349804)



nephron tubule development (Score: 2.347848)

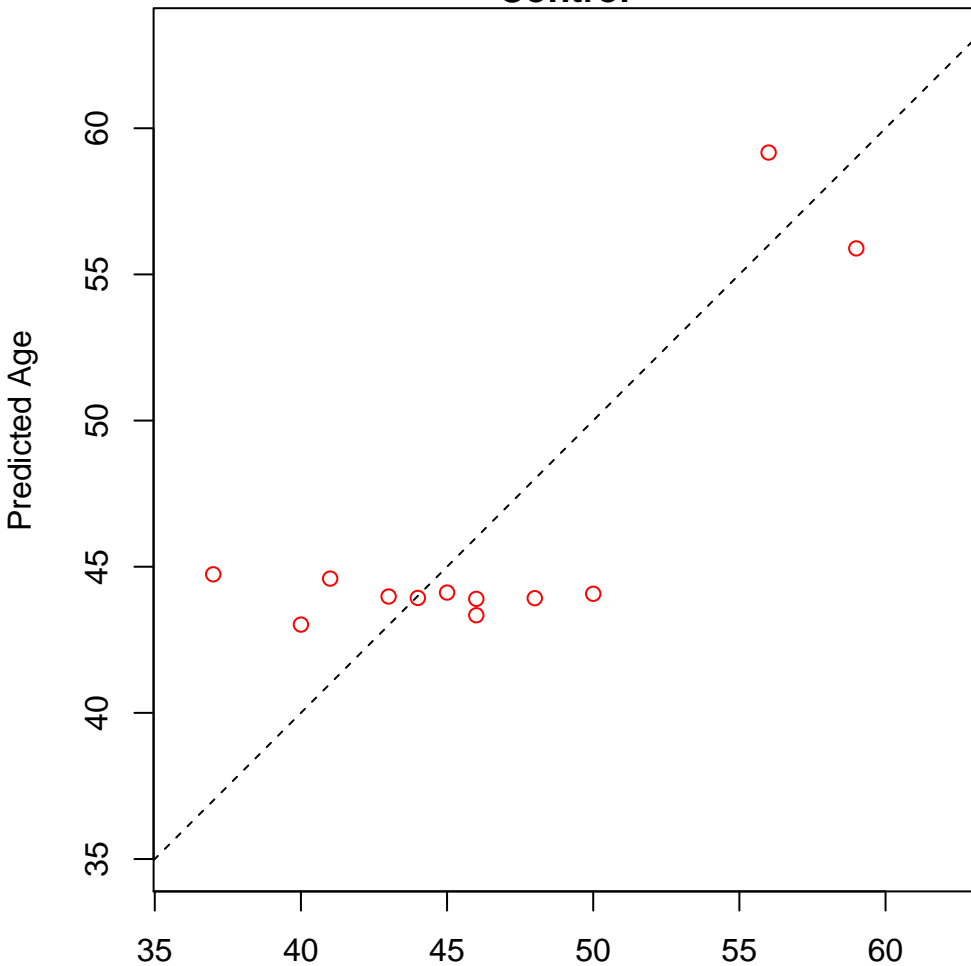


positive regulation of growth (Score: 2.347579)

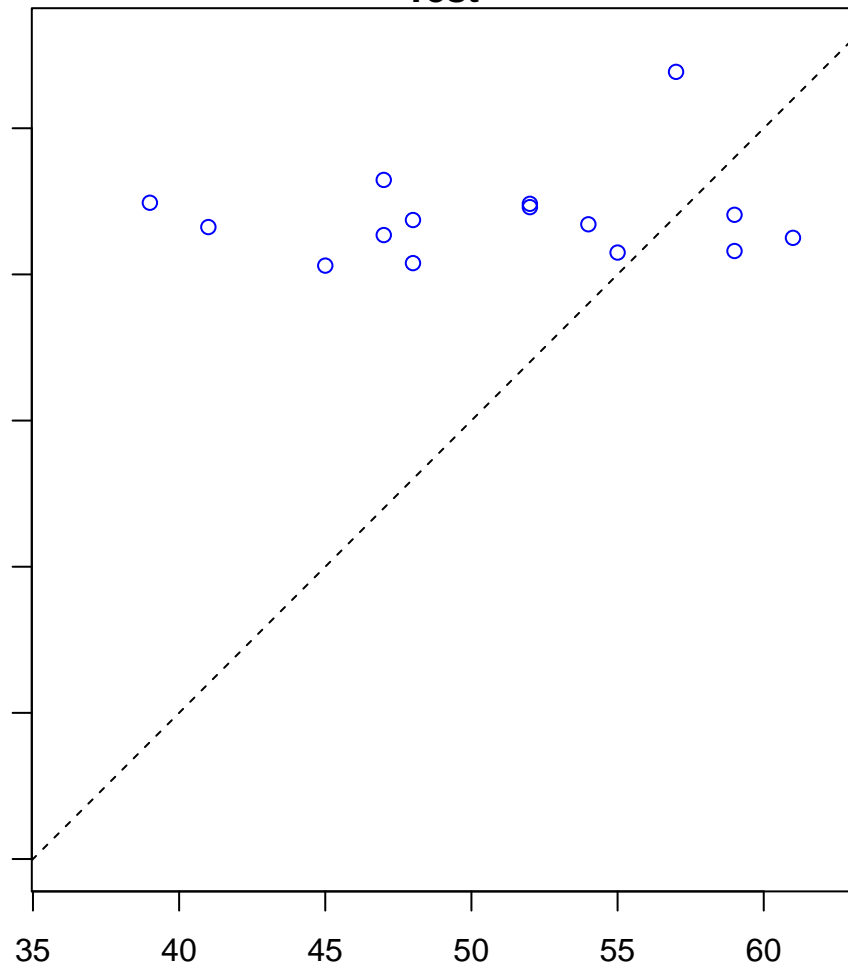


negative regulation of phosphorylation (Score: 2.345243)

Control

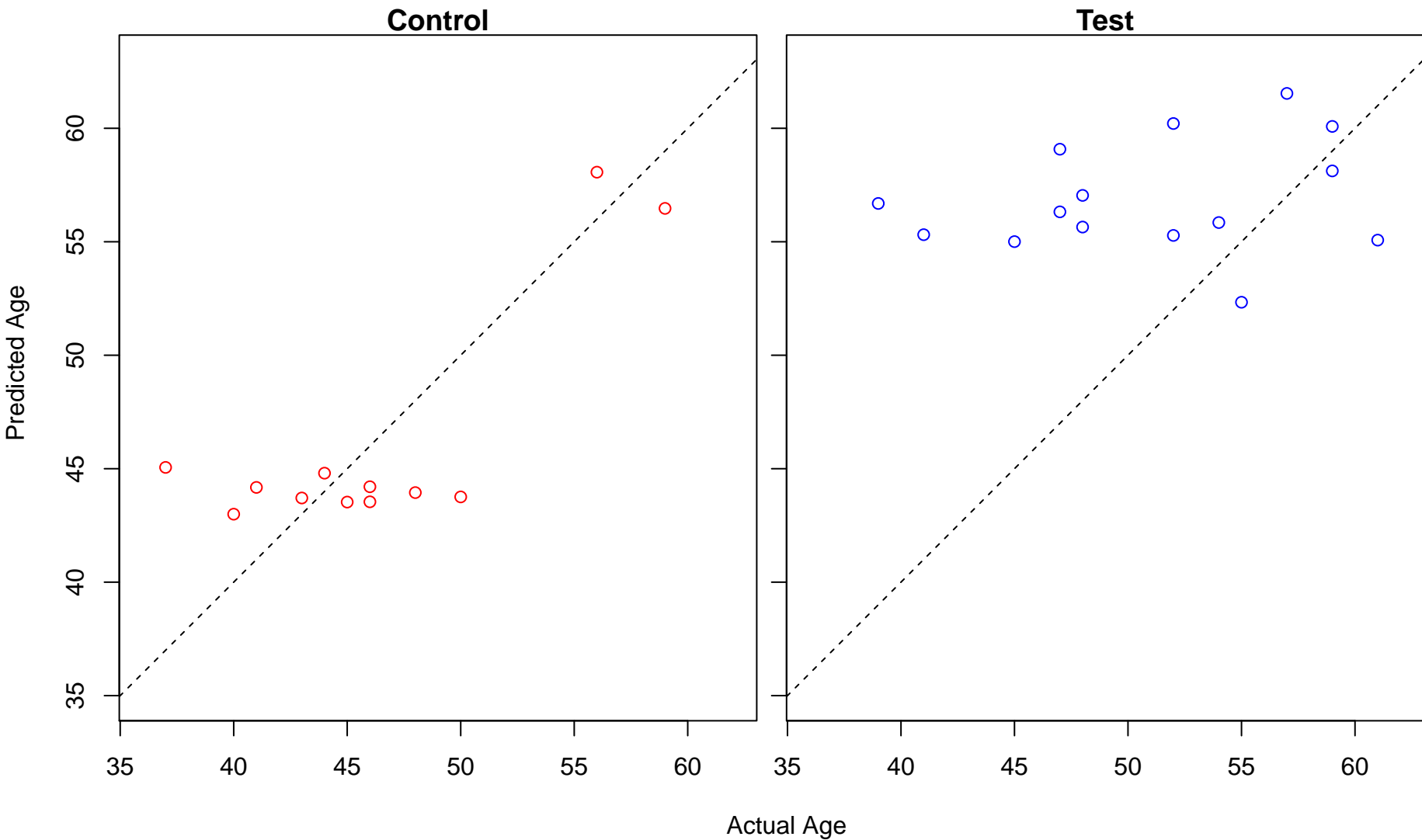


Test

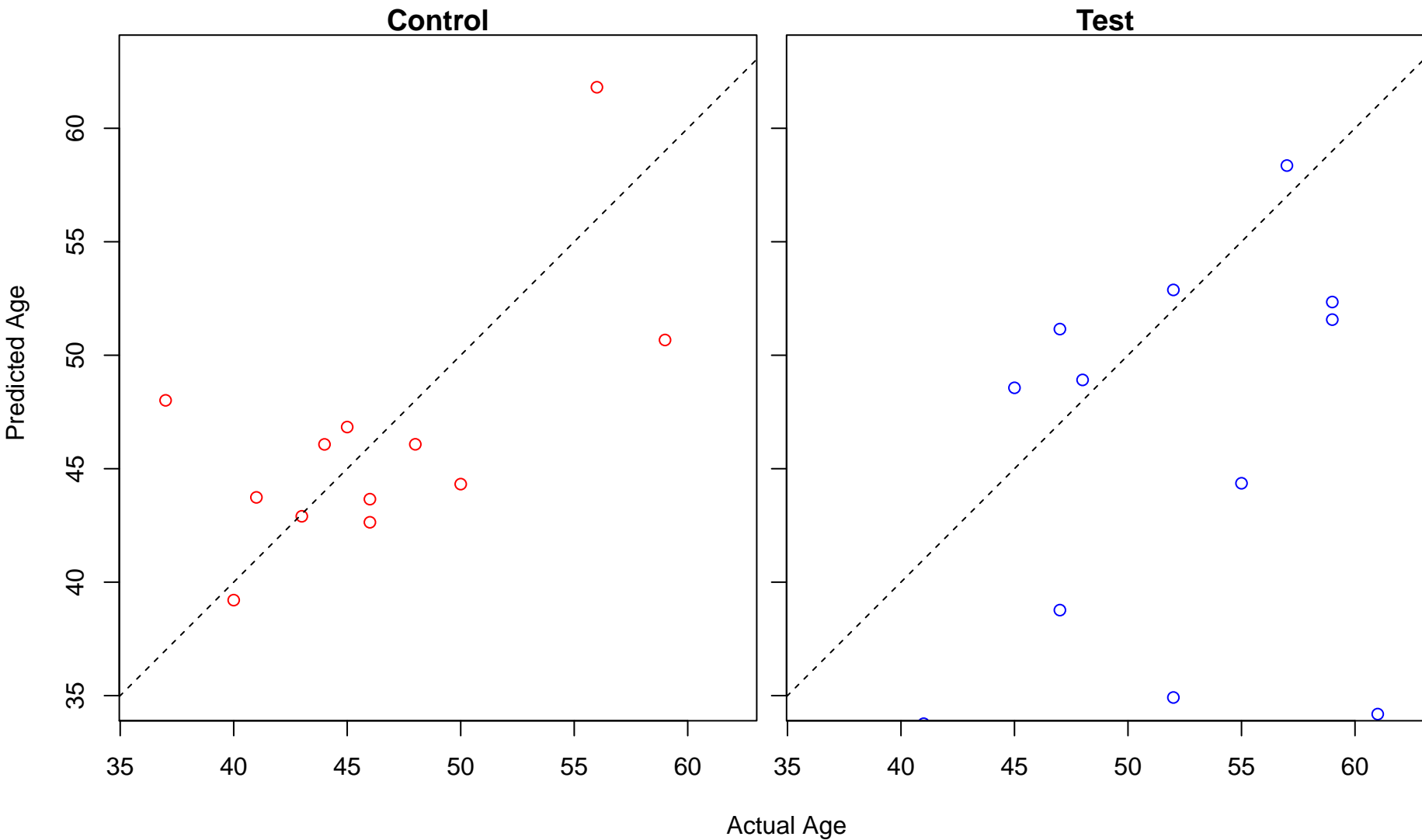


Actual Age

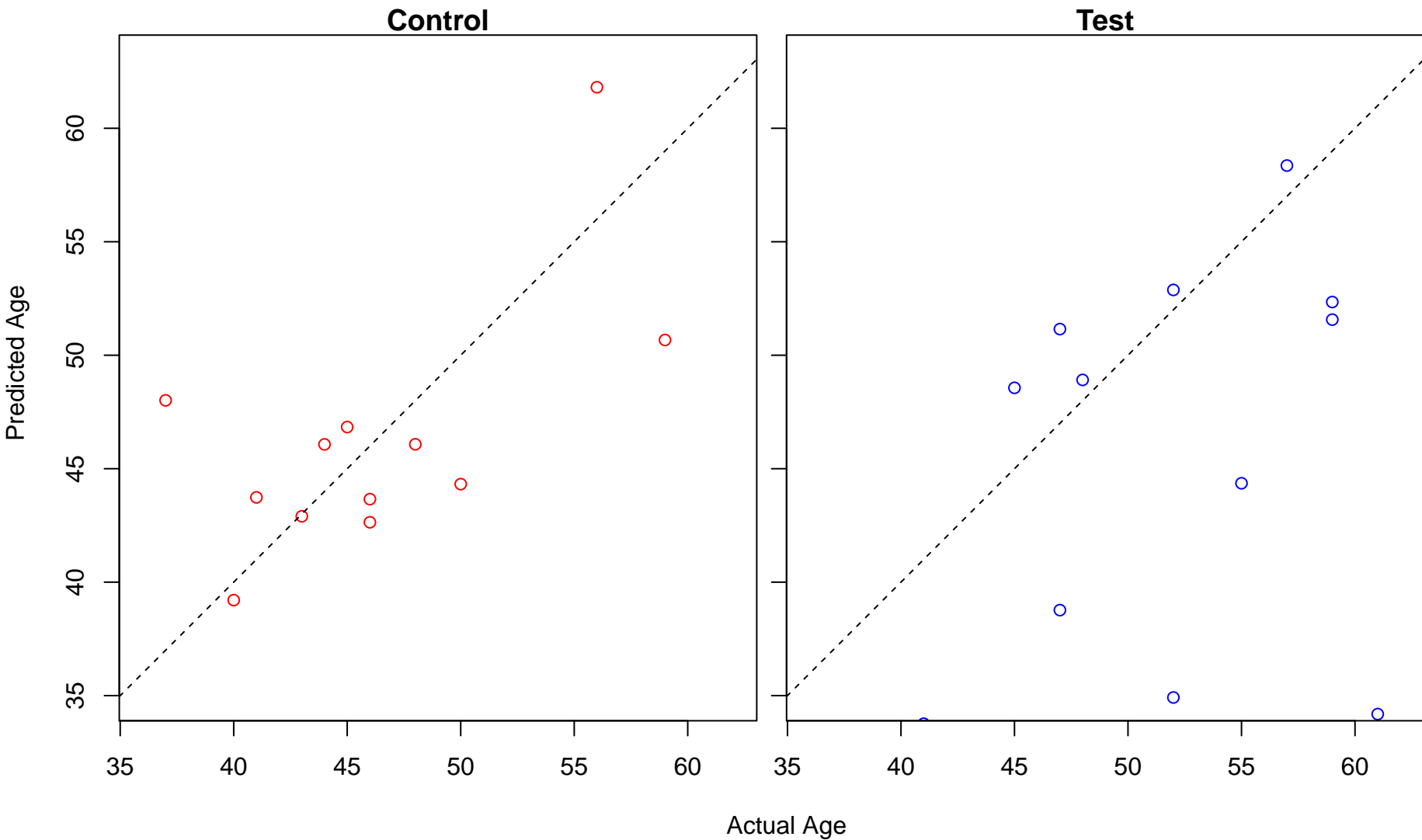
dorsal/ventral pattern formation (Score: 2.342457)



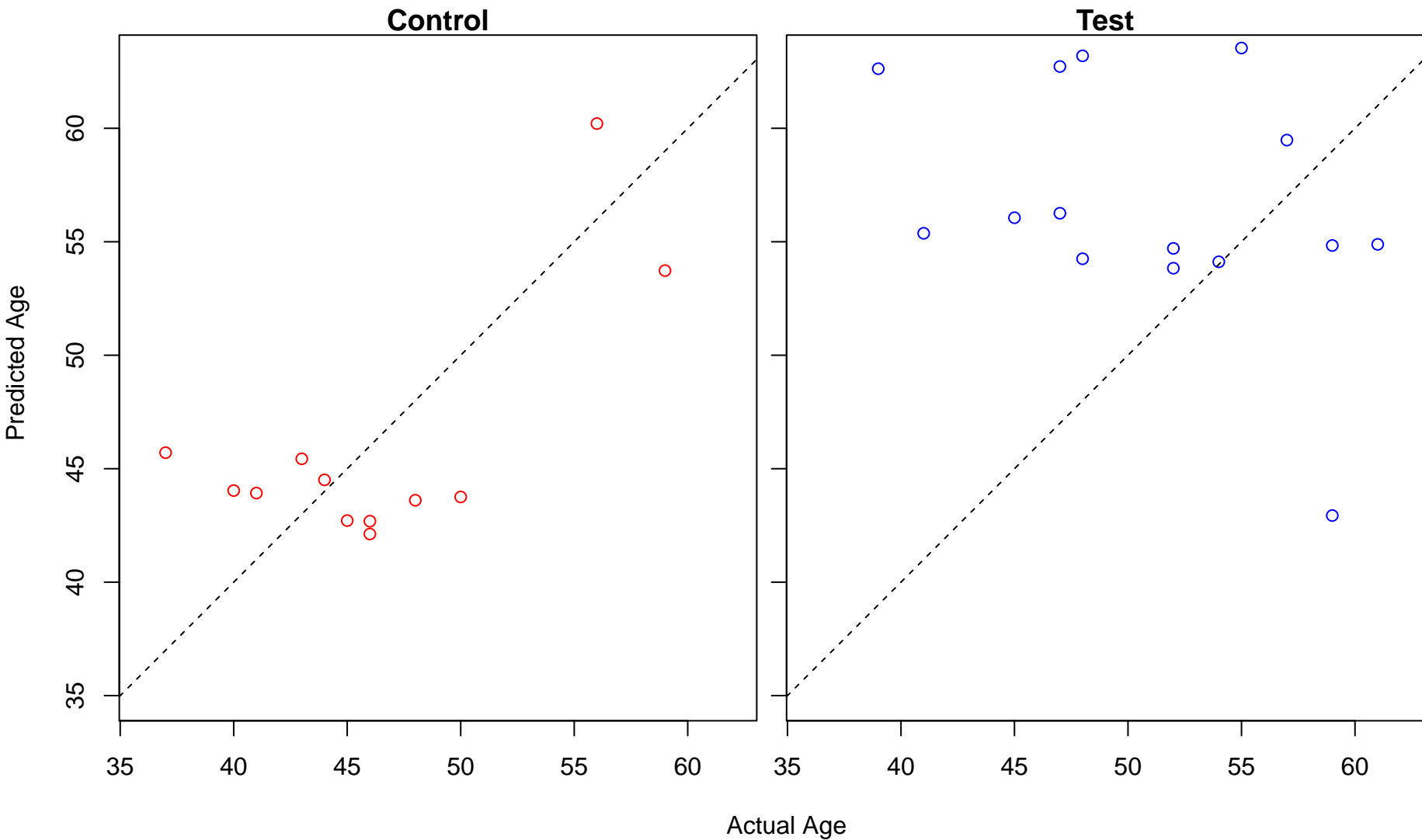
Purkinje myocyte to ventricular cardiac muscle cell signaling (Score: 2.332814)



Purkinje myocyte to ventricular cardiac muscle cell communication (Score: 2.332814)

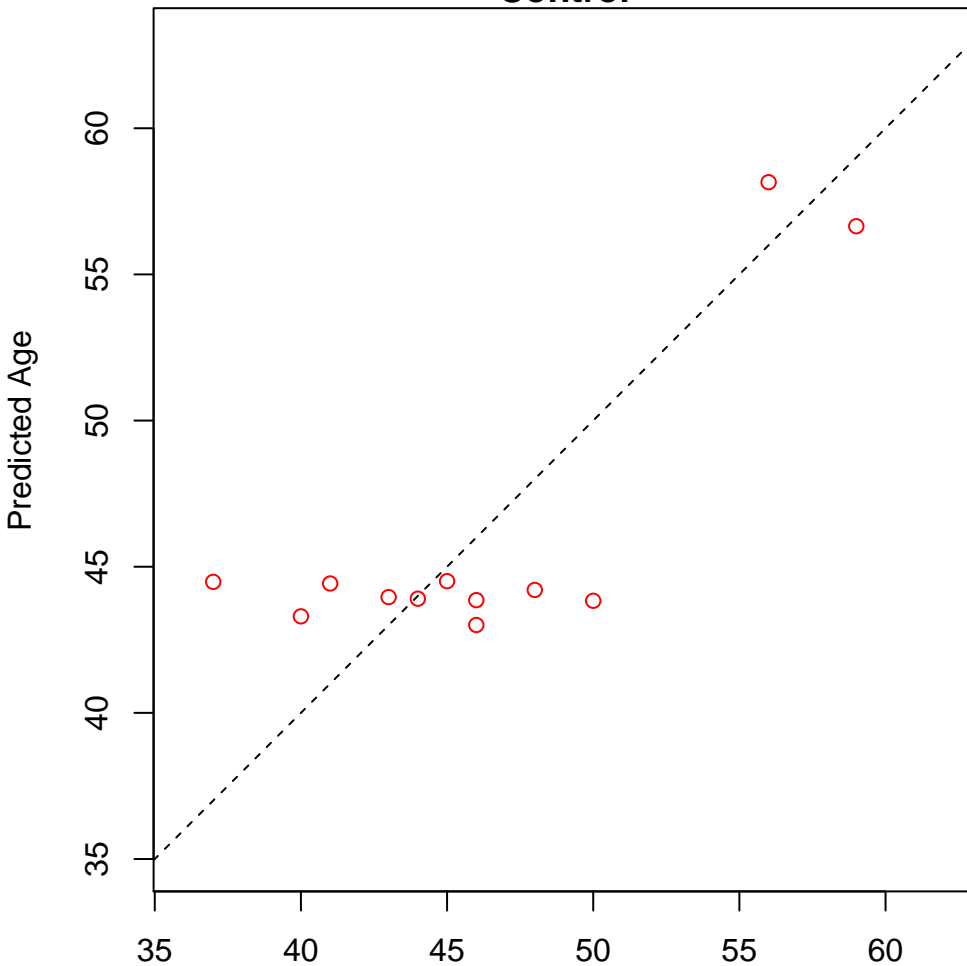


fatty acid elongation, unsaturated fatty acid (Score: 2.331047)

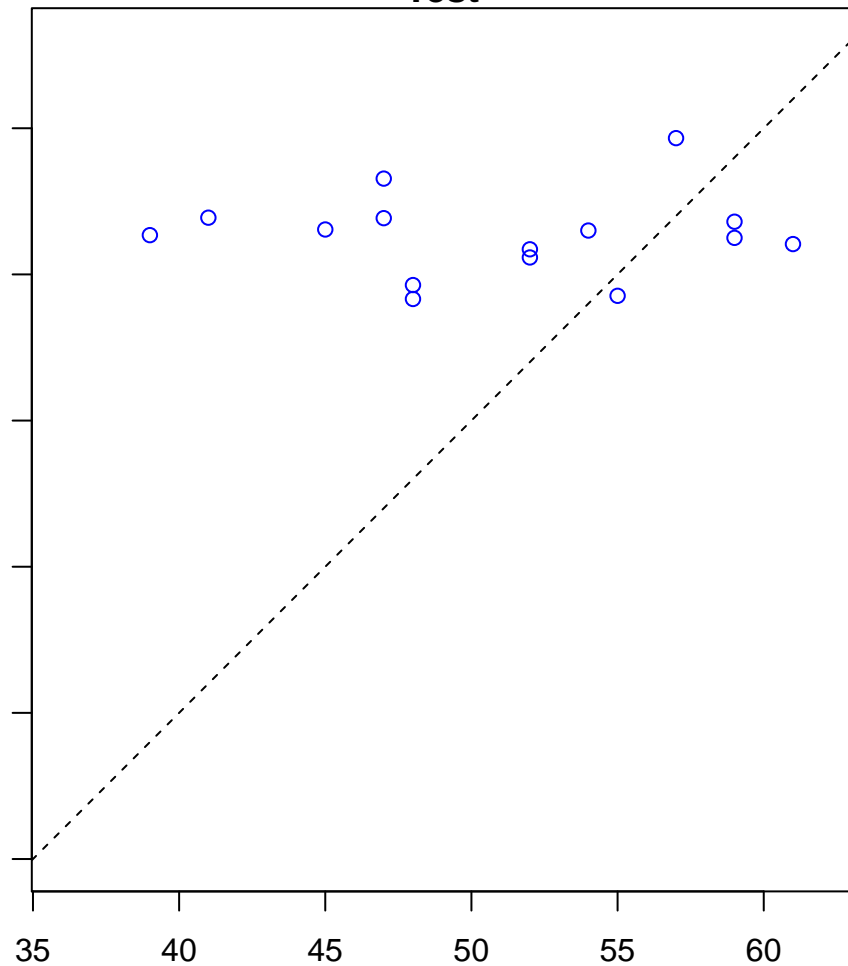


post-translational protein modification (Score: 2.329652)

Control

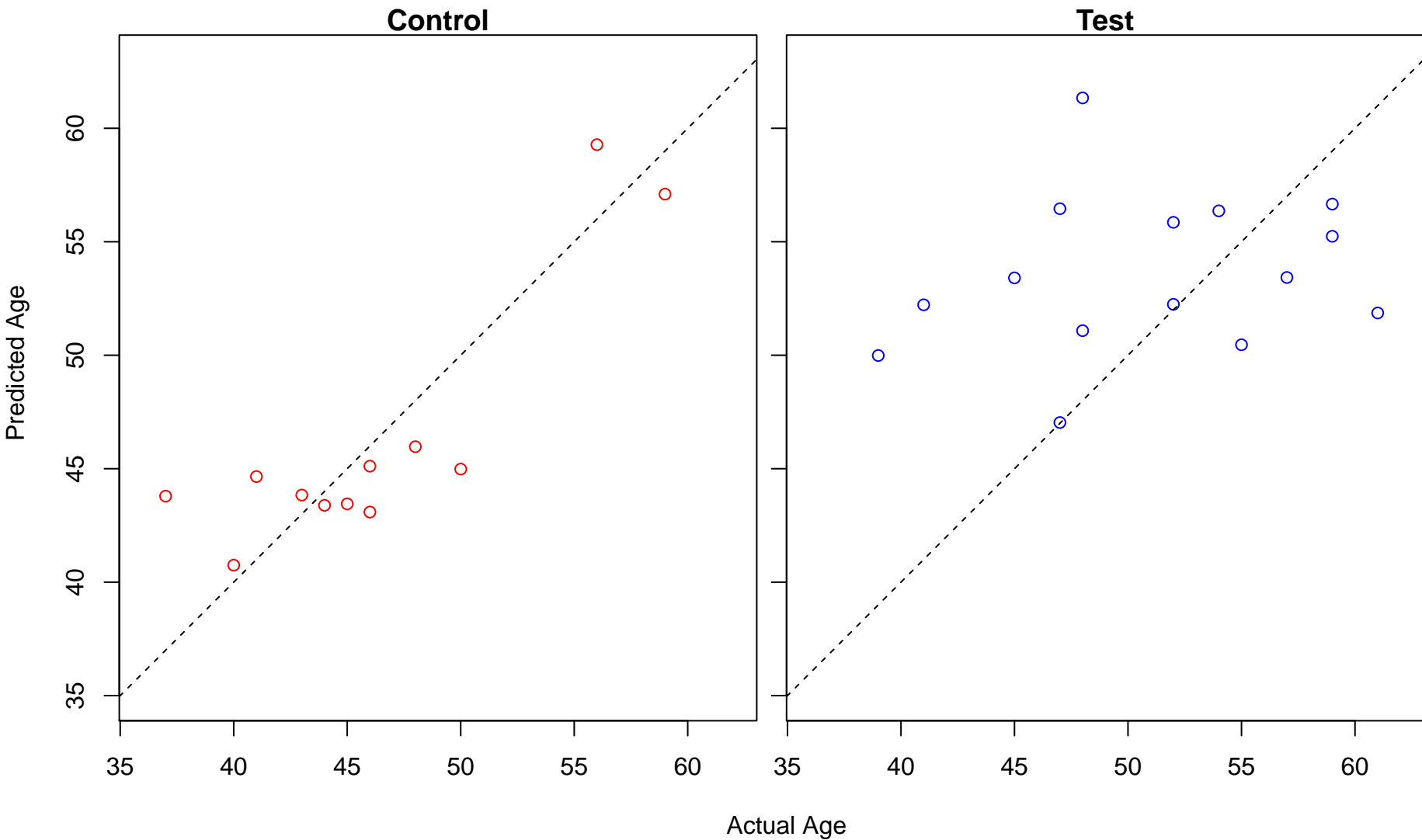


Test

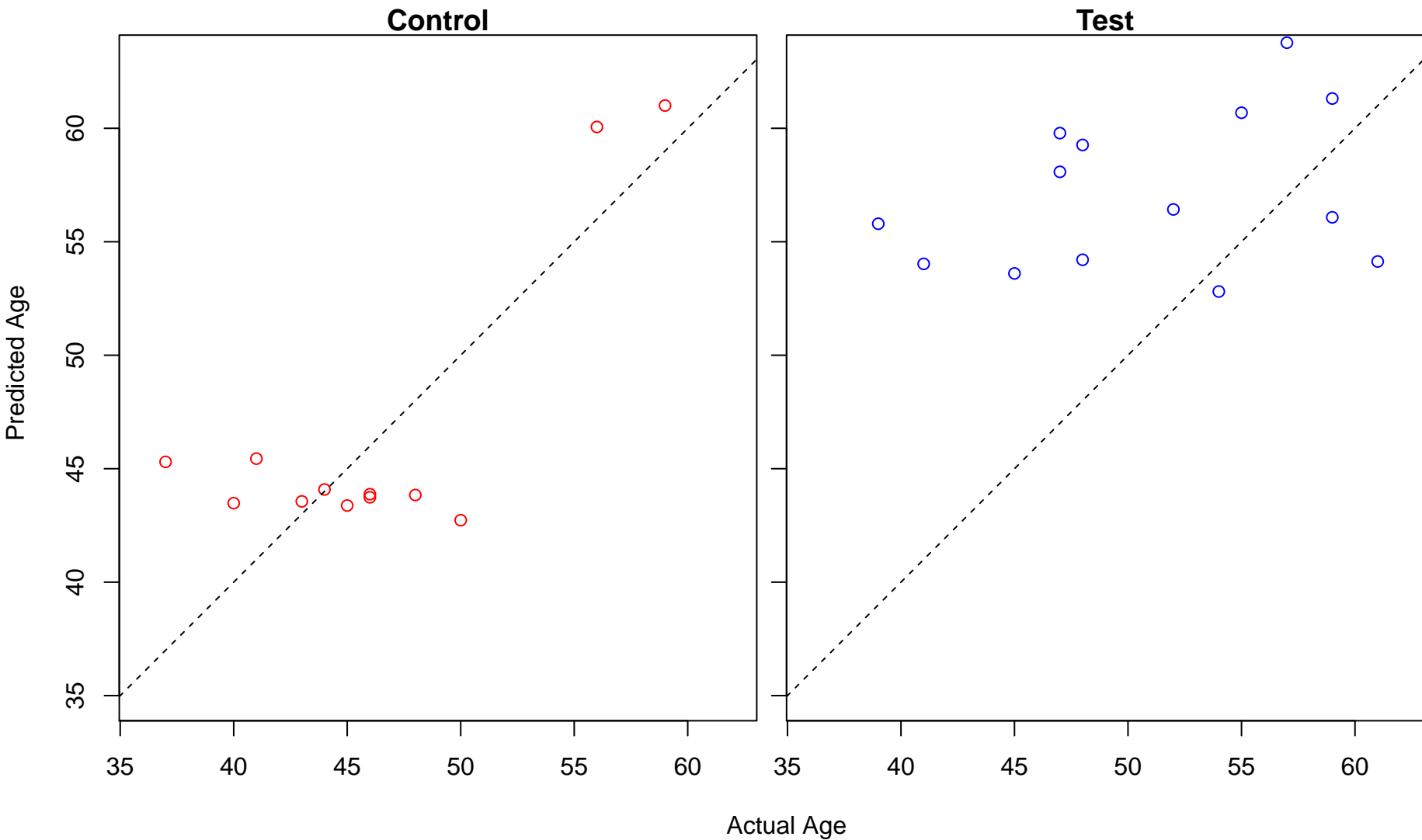


Actual Age

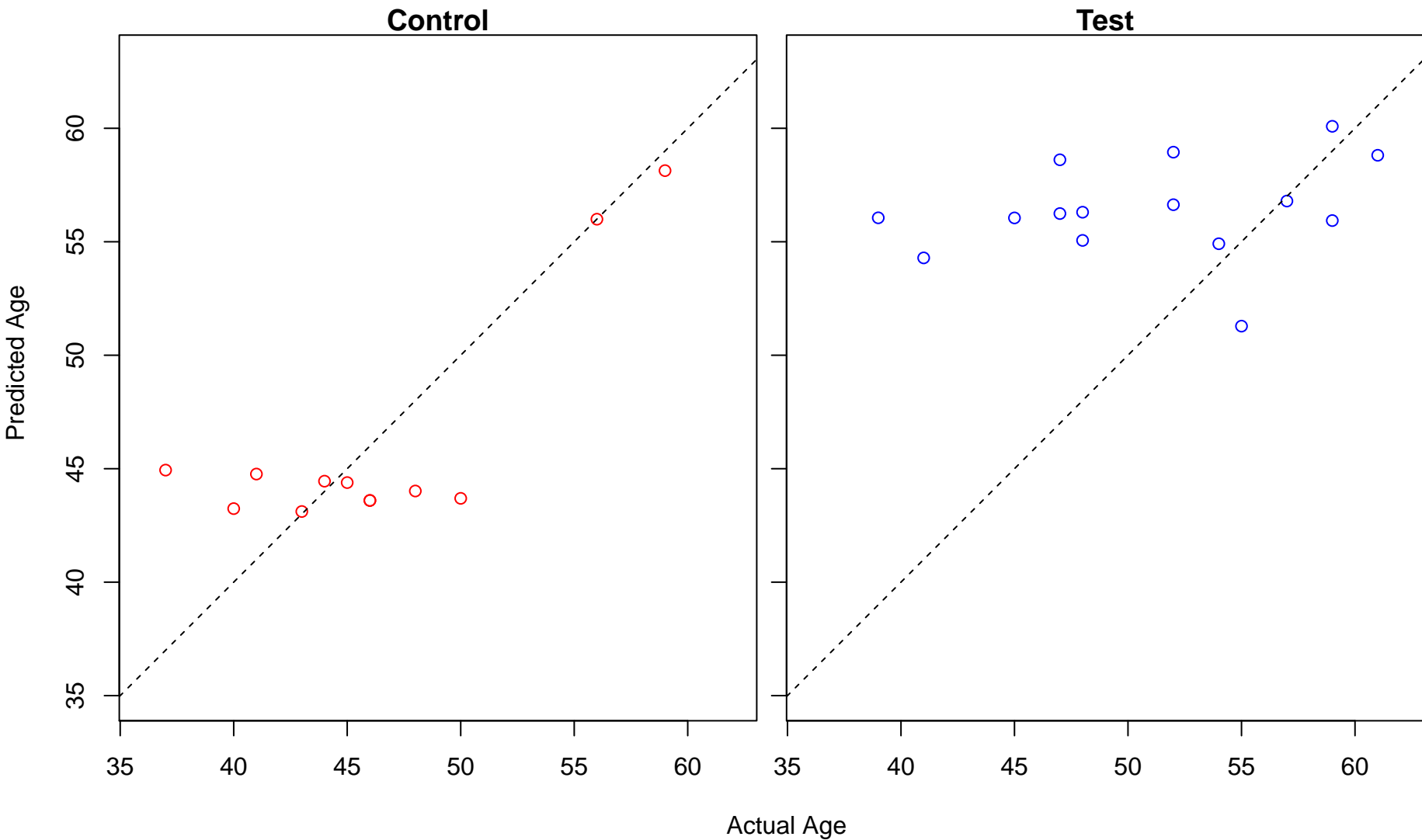
neuron cell-cell adhesion (Score: 2.325100)



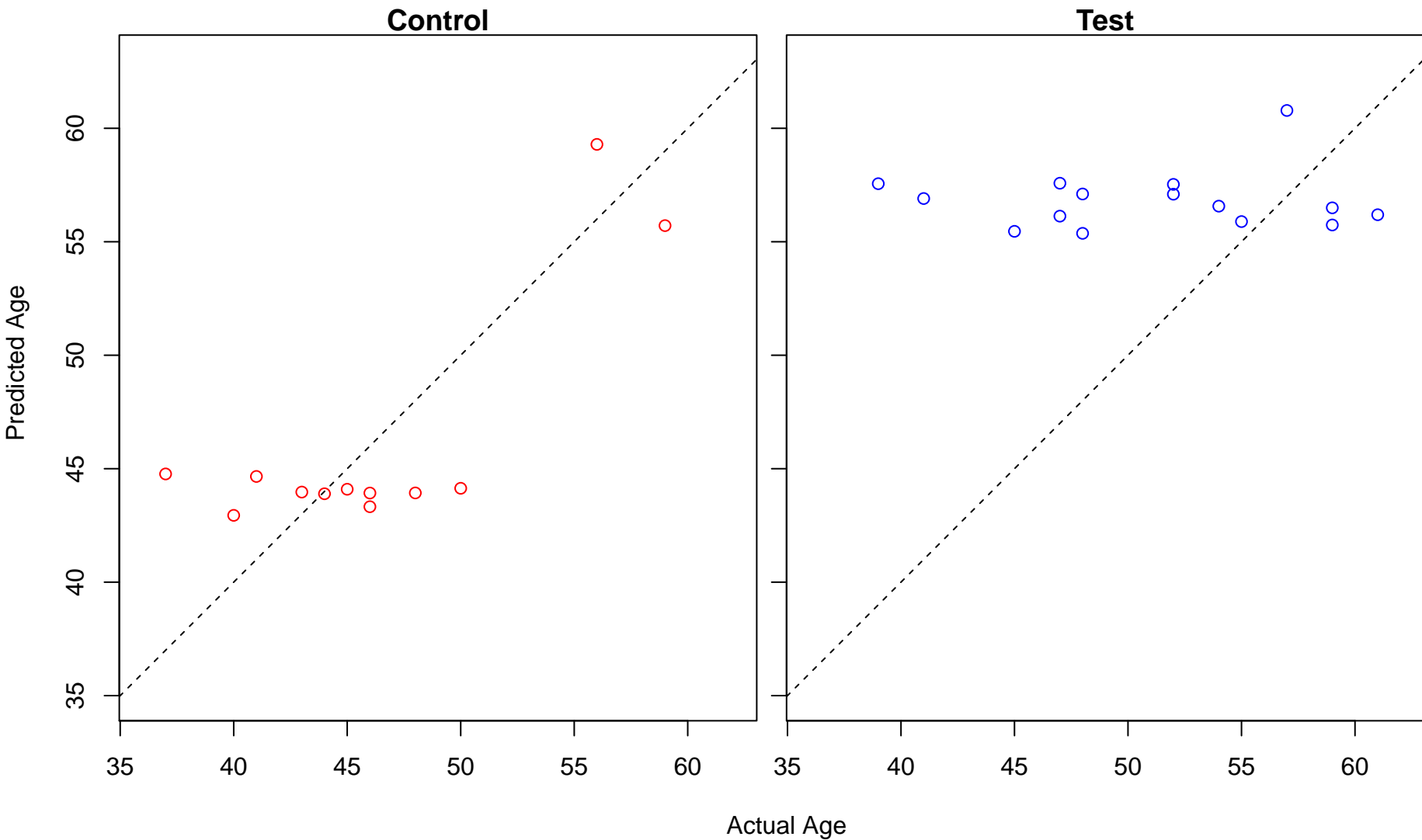
positive regulation of stem cell differentiation (Score: 2.321976)



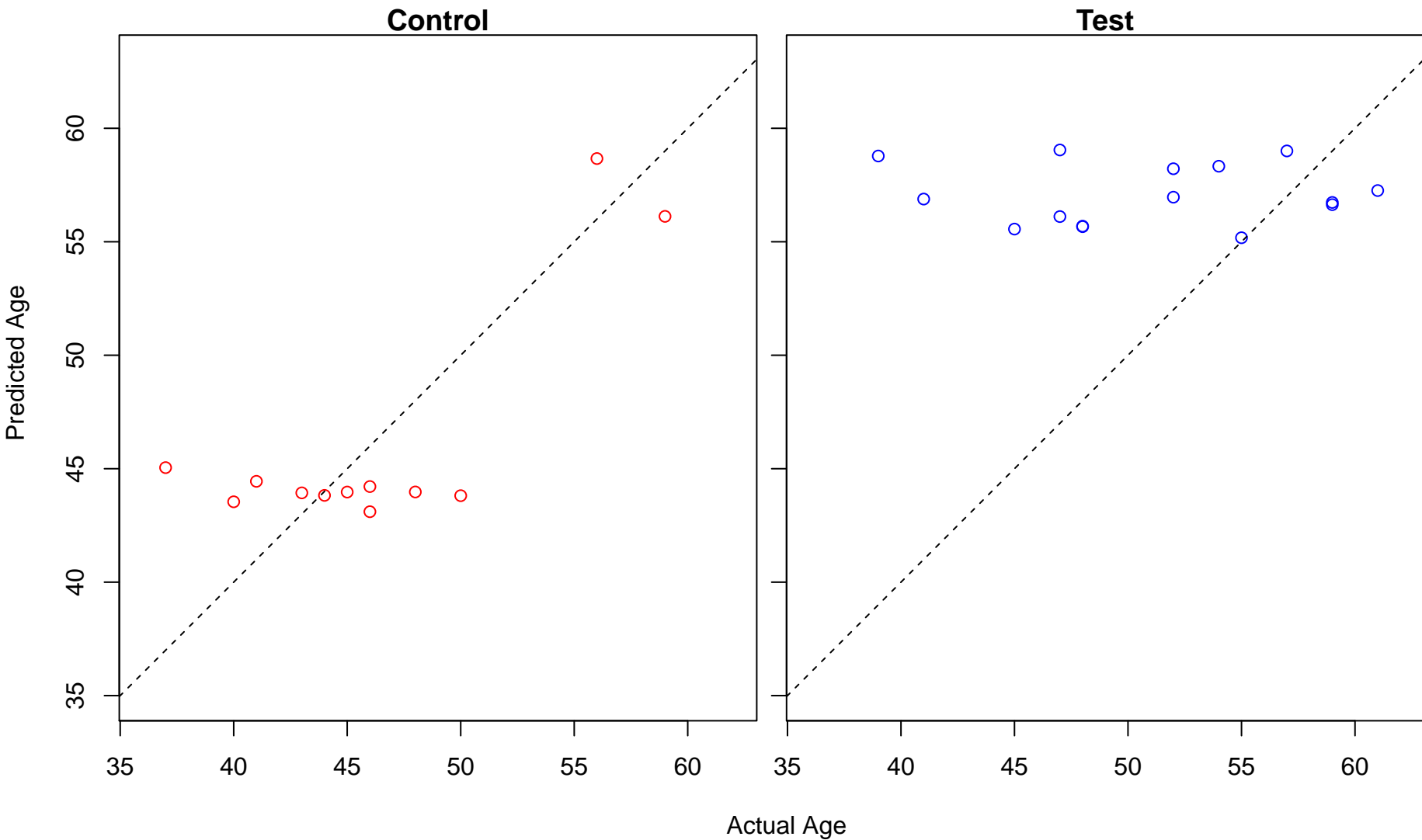
histone exchange (Score: 2.319563)



negative regulation of protein phosphorylation (Score: 2.316314)

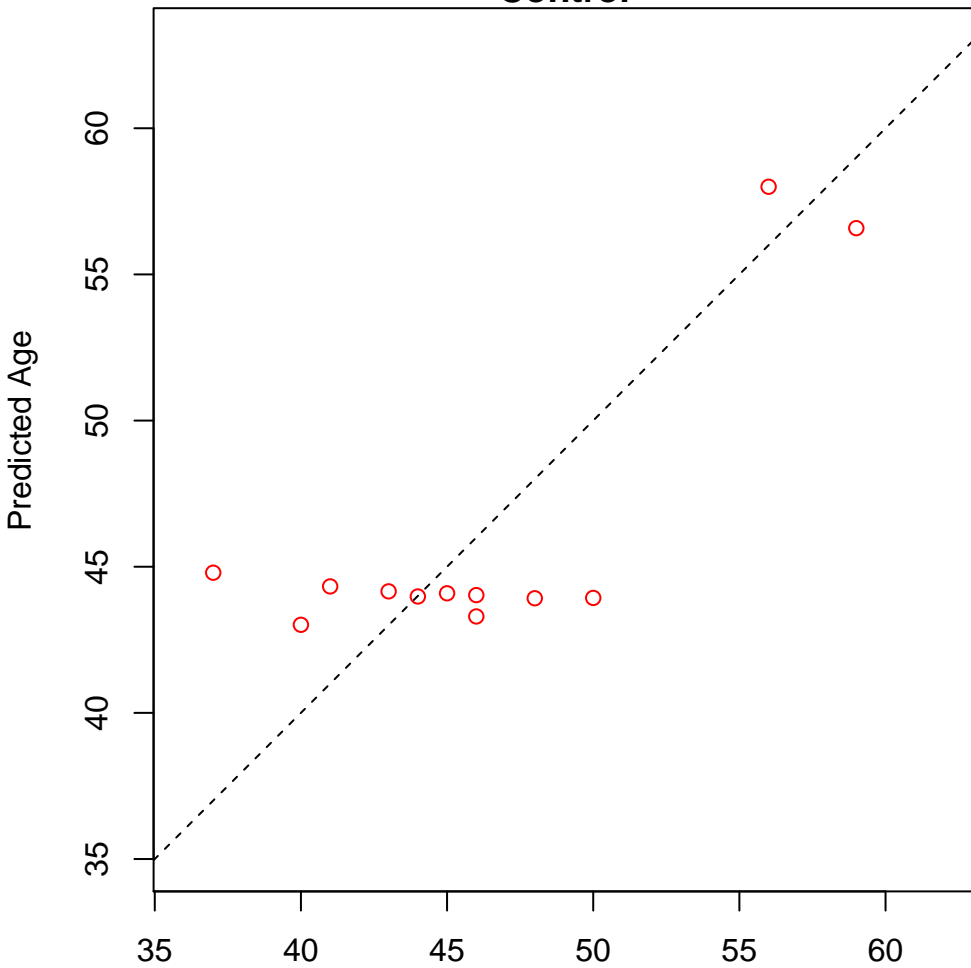


response to ionizing radiation (Score: 2.315416)

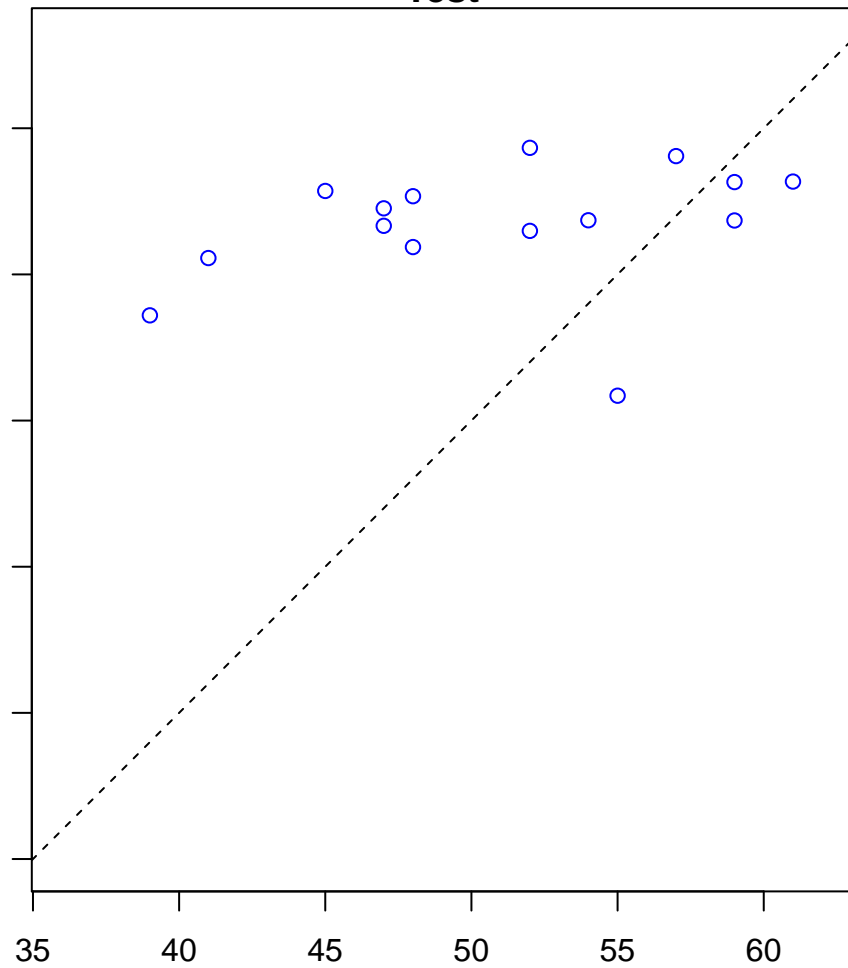


monocarboxylic acid catabolic process (Score: 2.314055)

Control

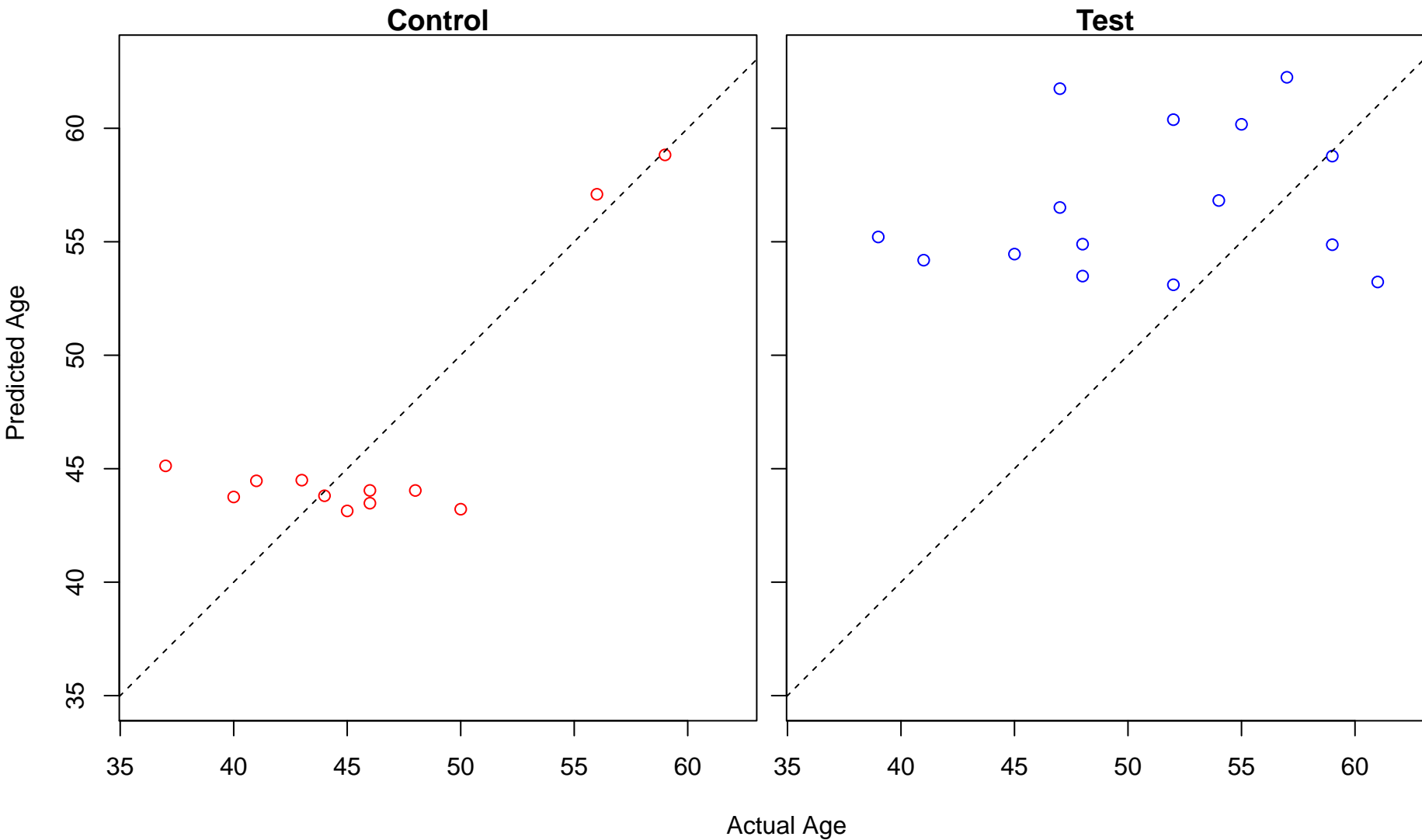


Test

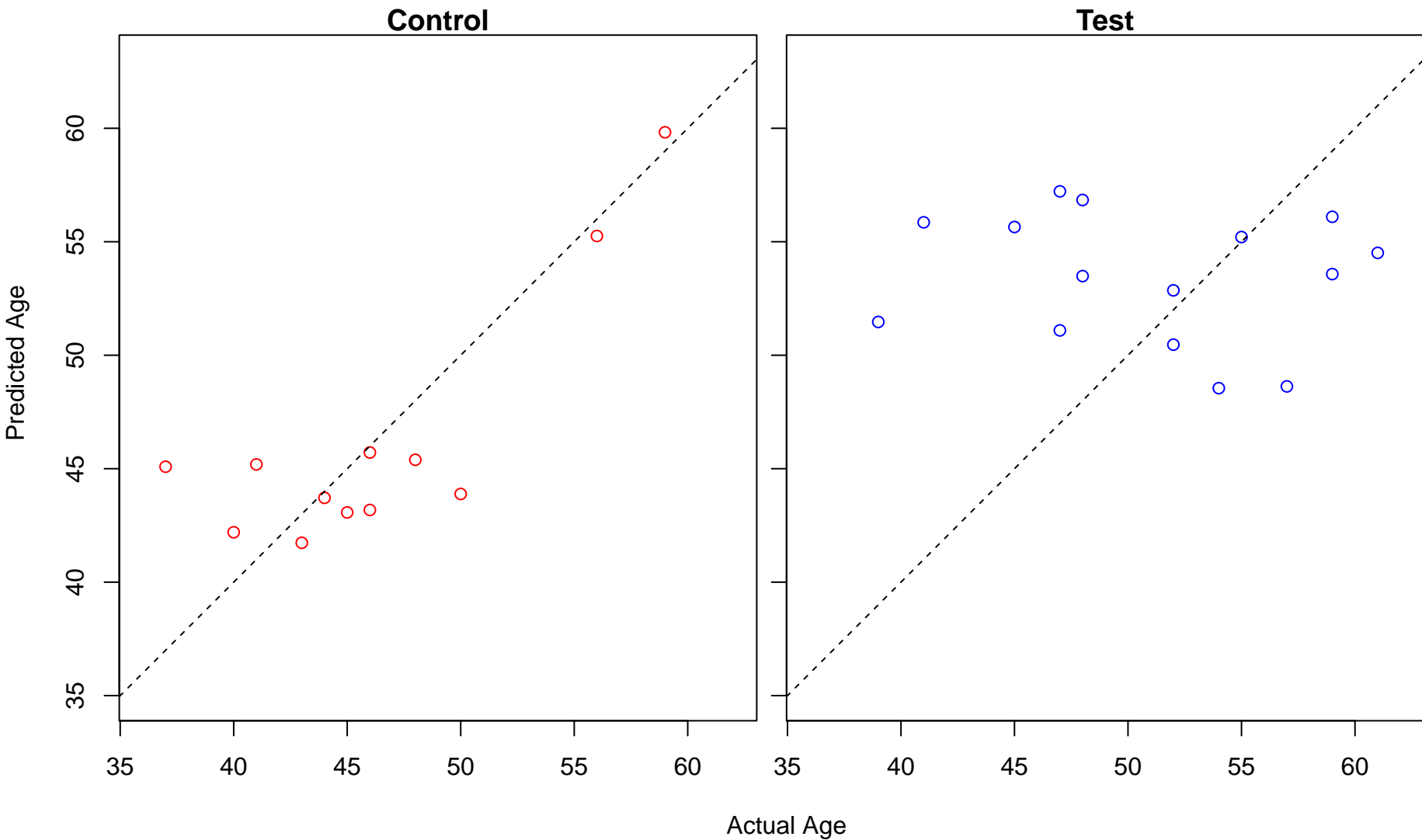


Actual Age

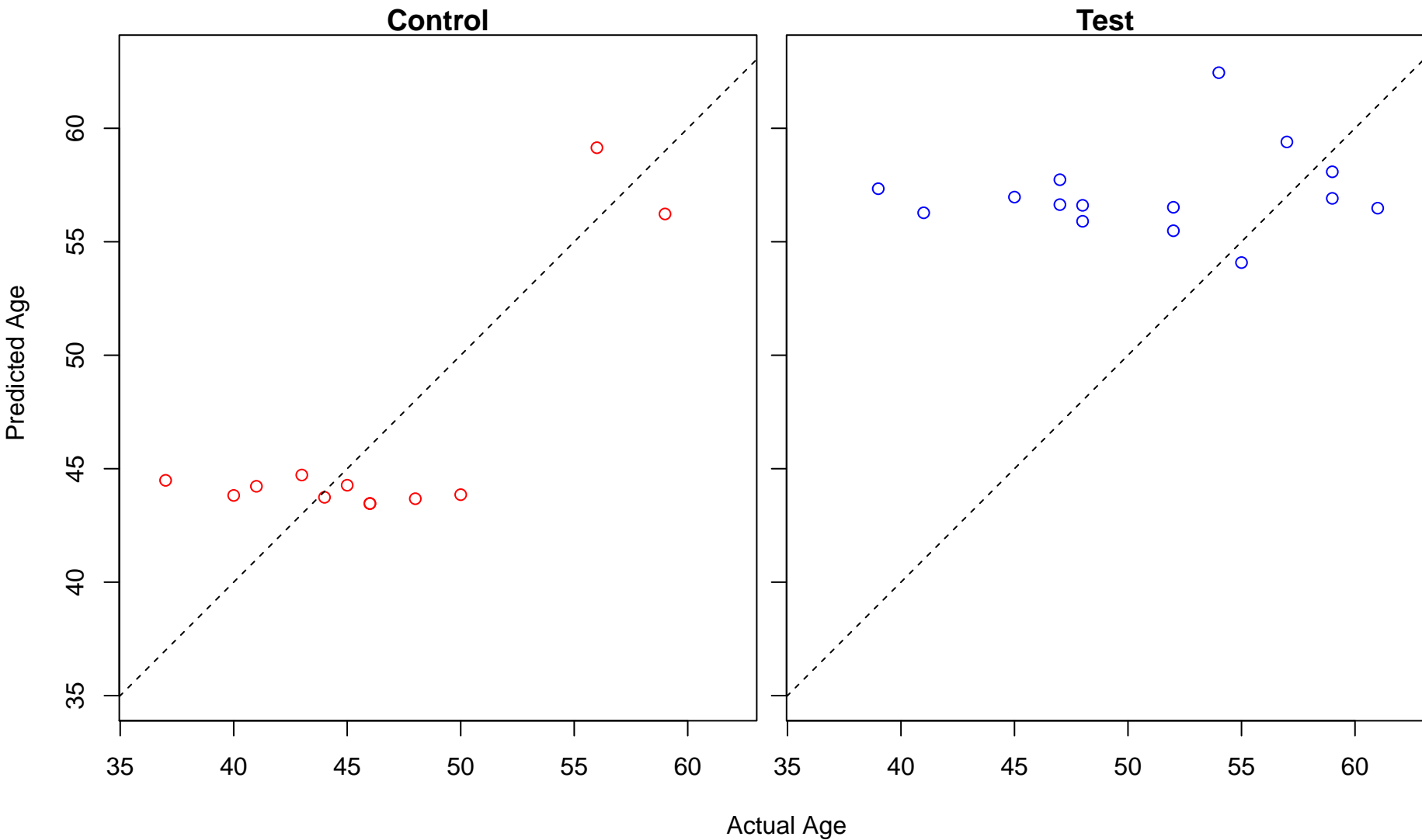
regulation of cAMP biosynthetic process (Score: 2.310793)



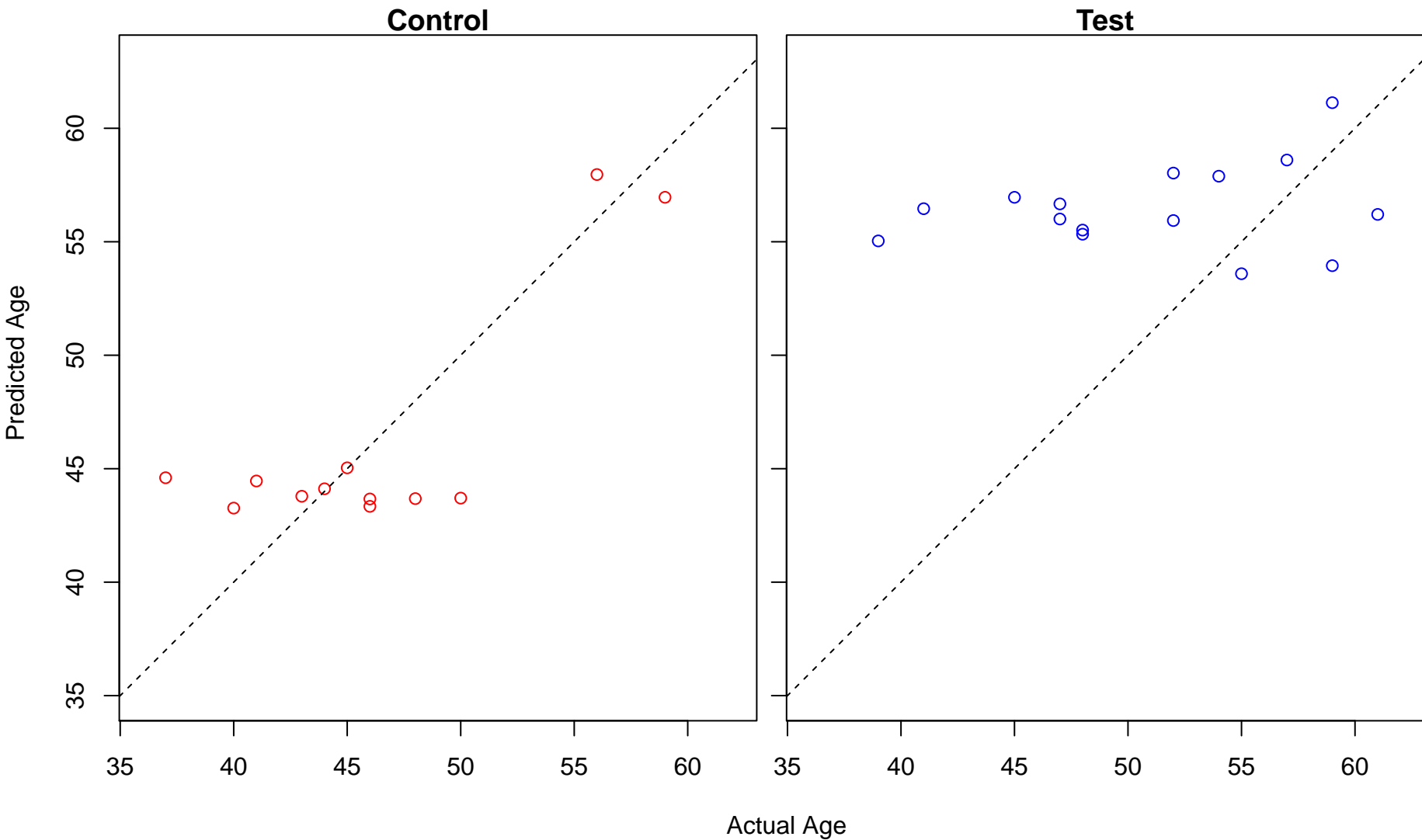
endothelial cell proliferation (Score: 2.302234)



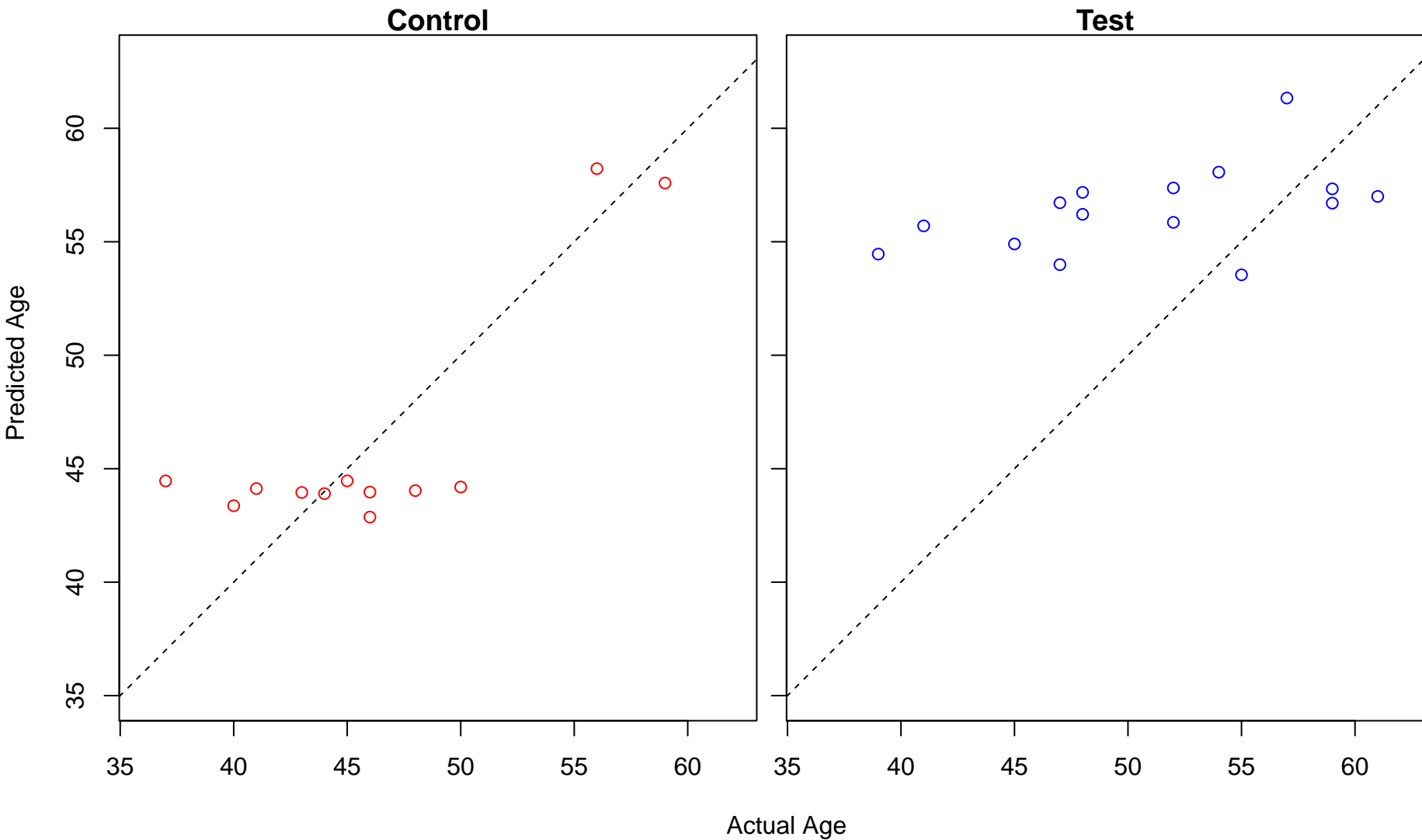
protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score: 2.297507)



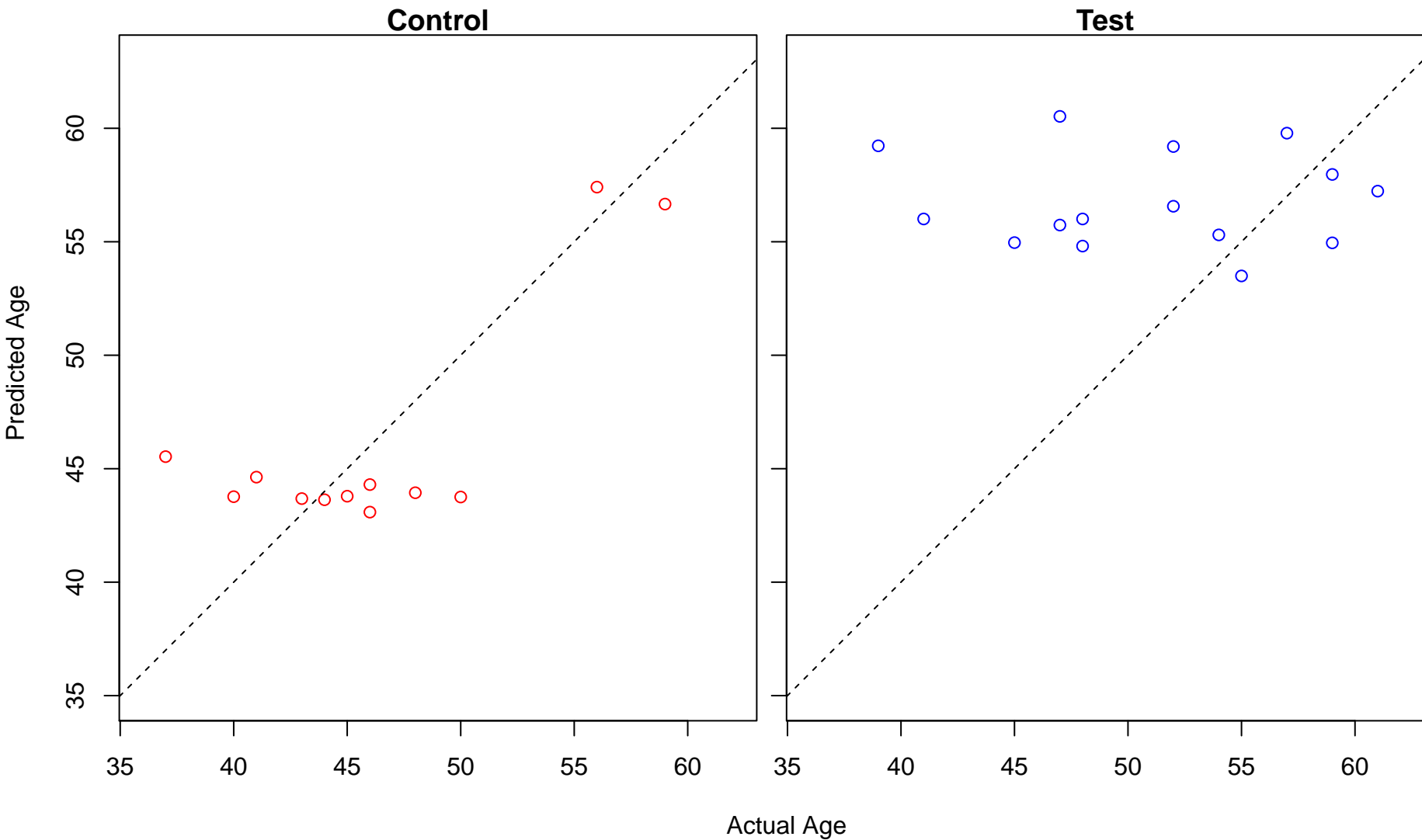
C-terminal protein amino acid modification (Score: 2.292265)



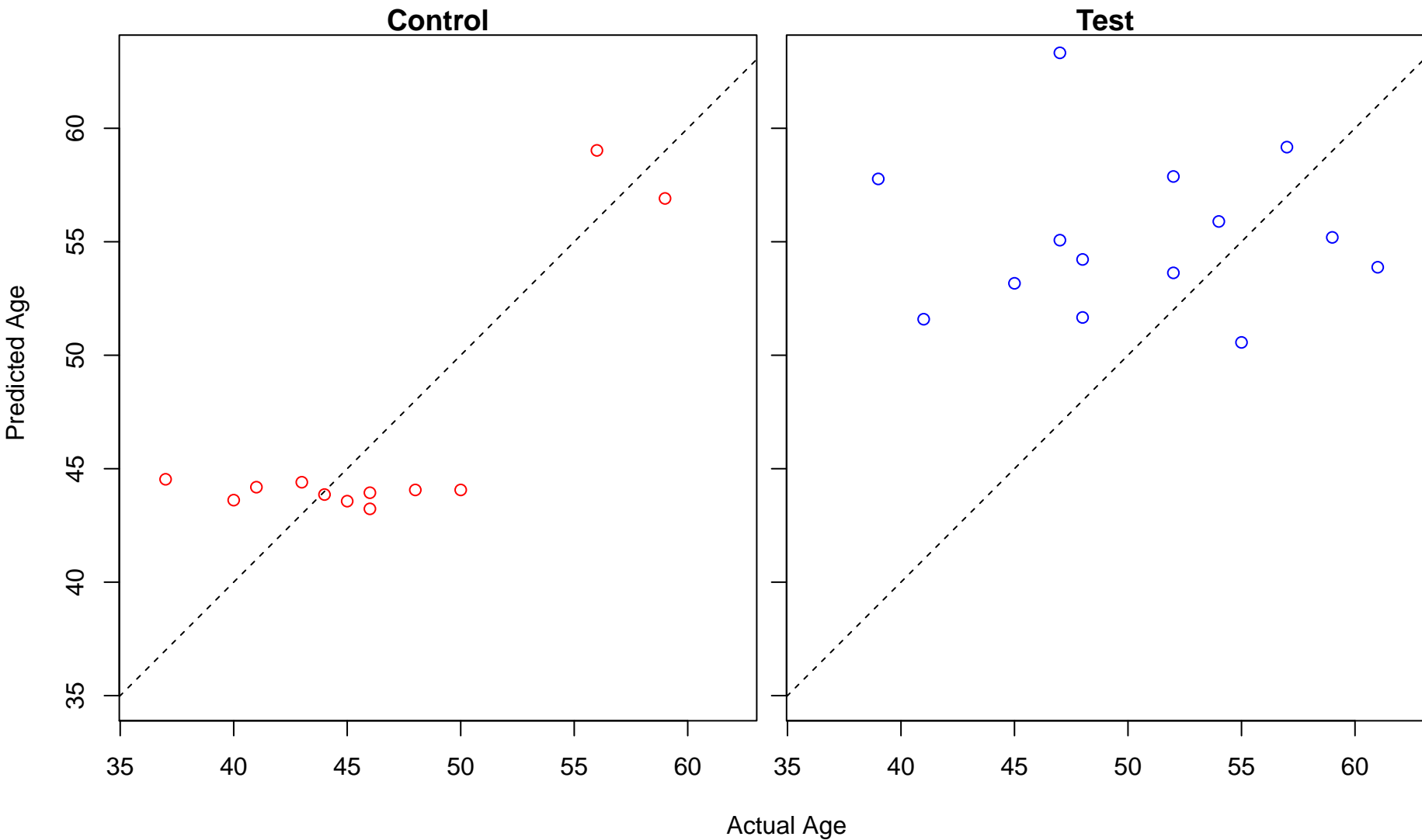
negative regulation of proteasomal ubiquitin-dependent protein catabolic process (Score: 2.28545)



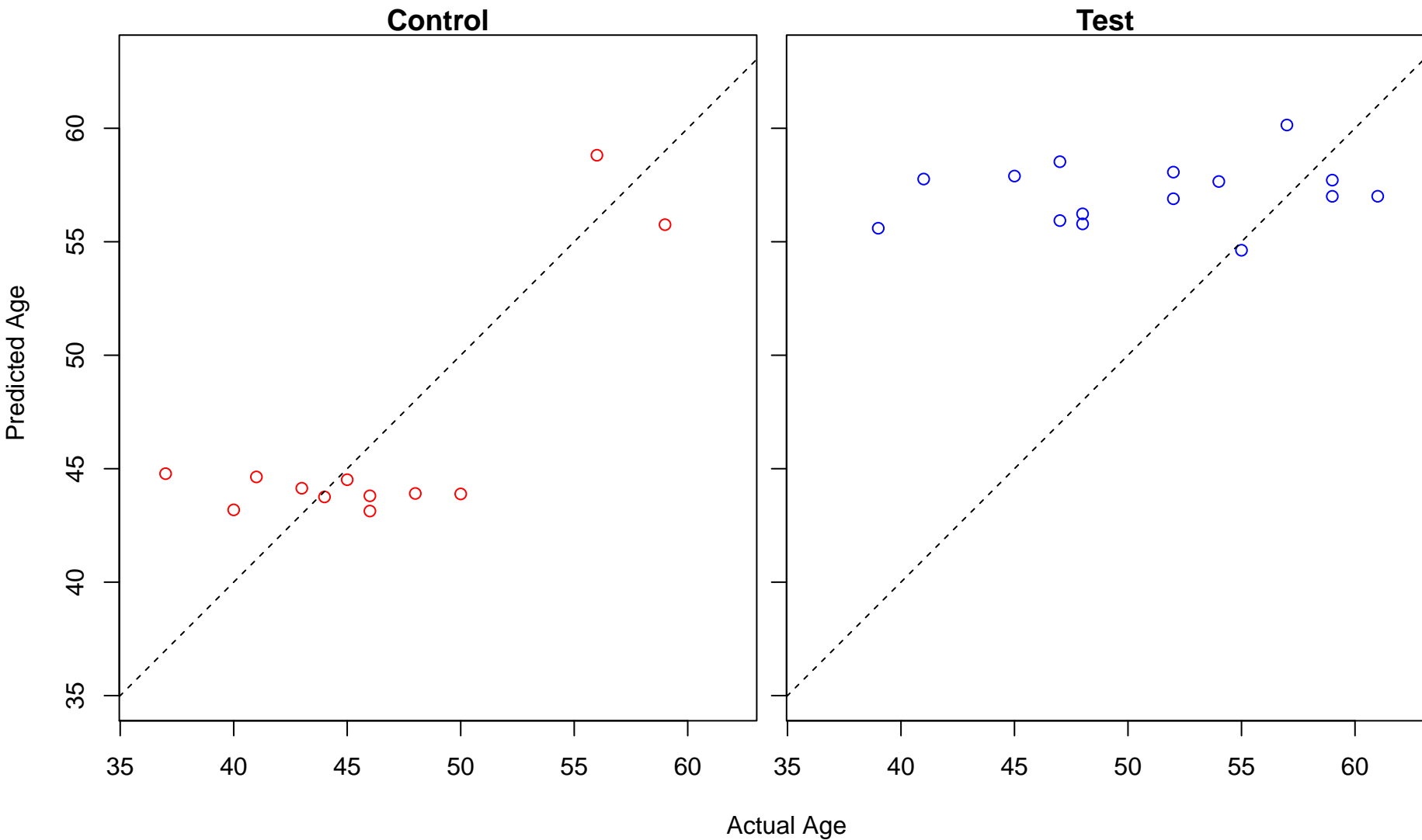
nuclear export (Score: 2.282443)



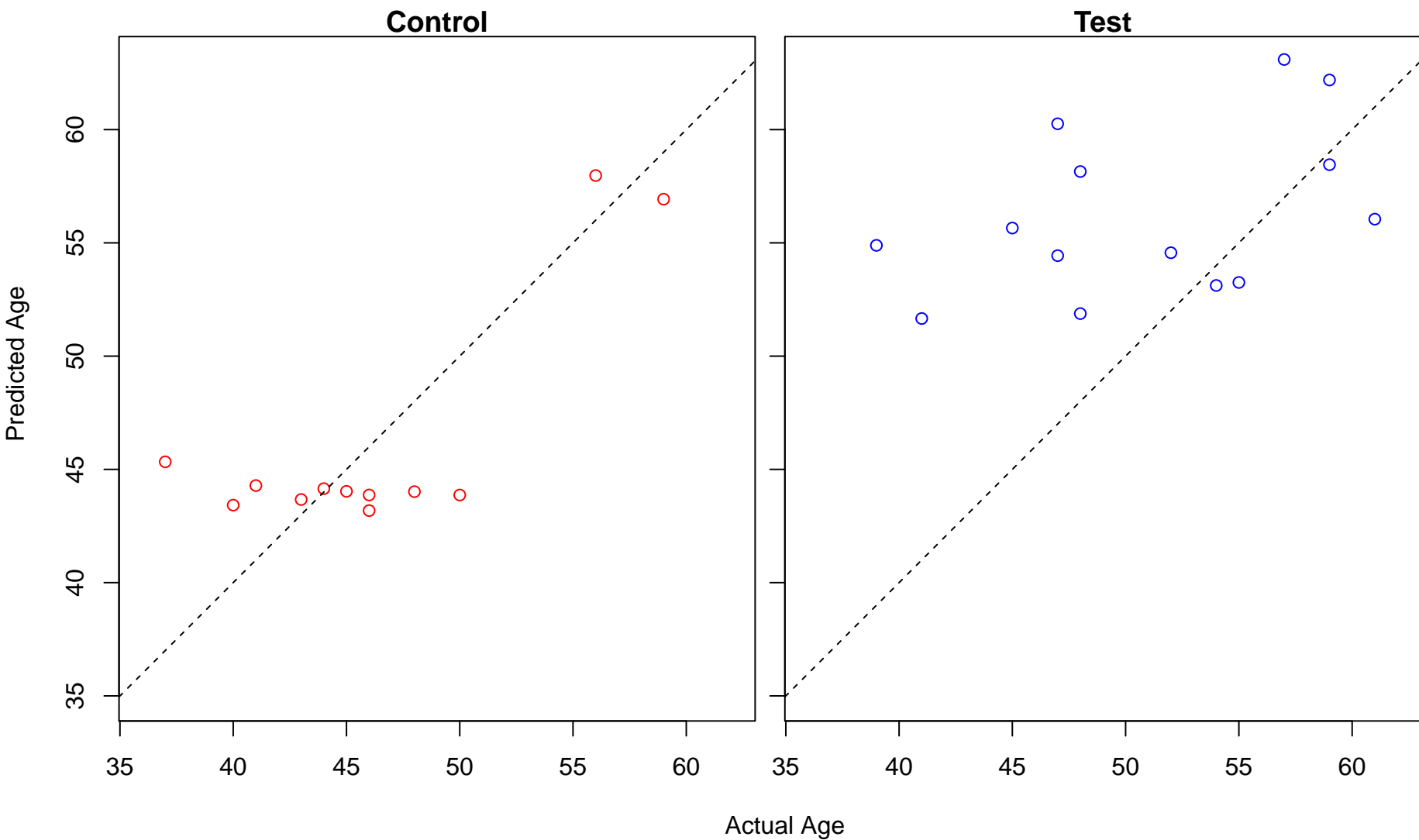
thyroid gland development (Score: 2.282293)



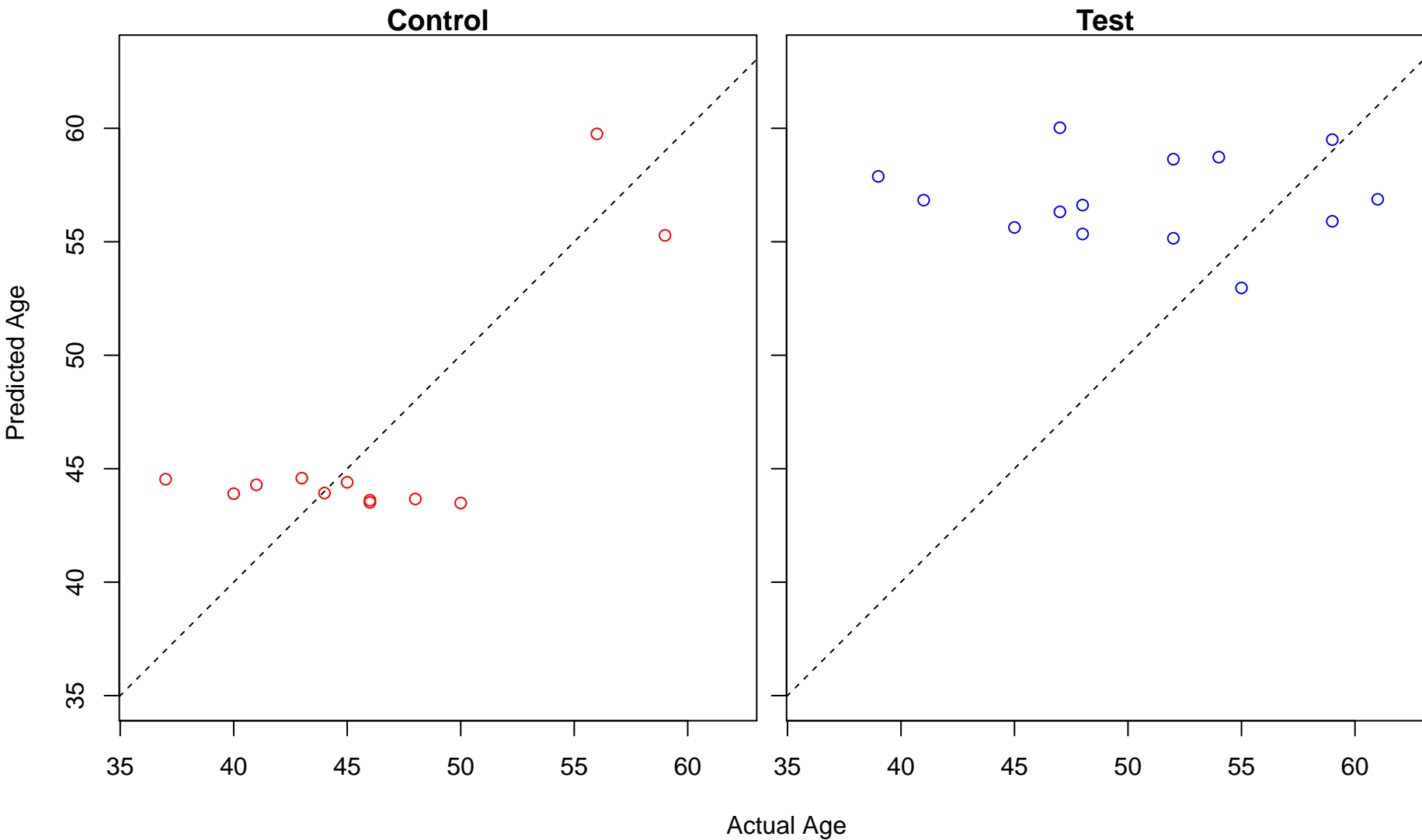
endomembrane system organization (Score: 2.278352)



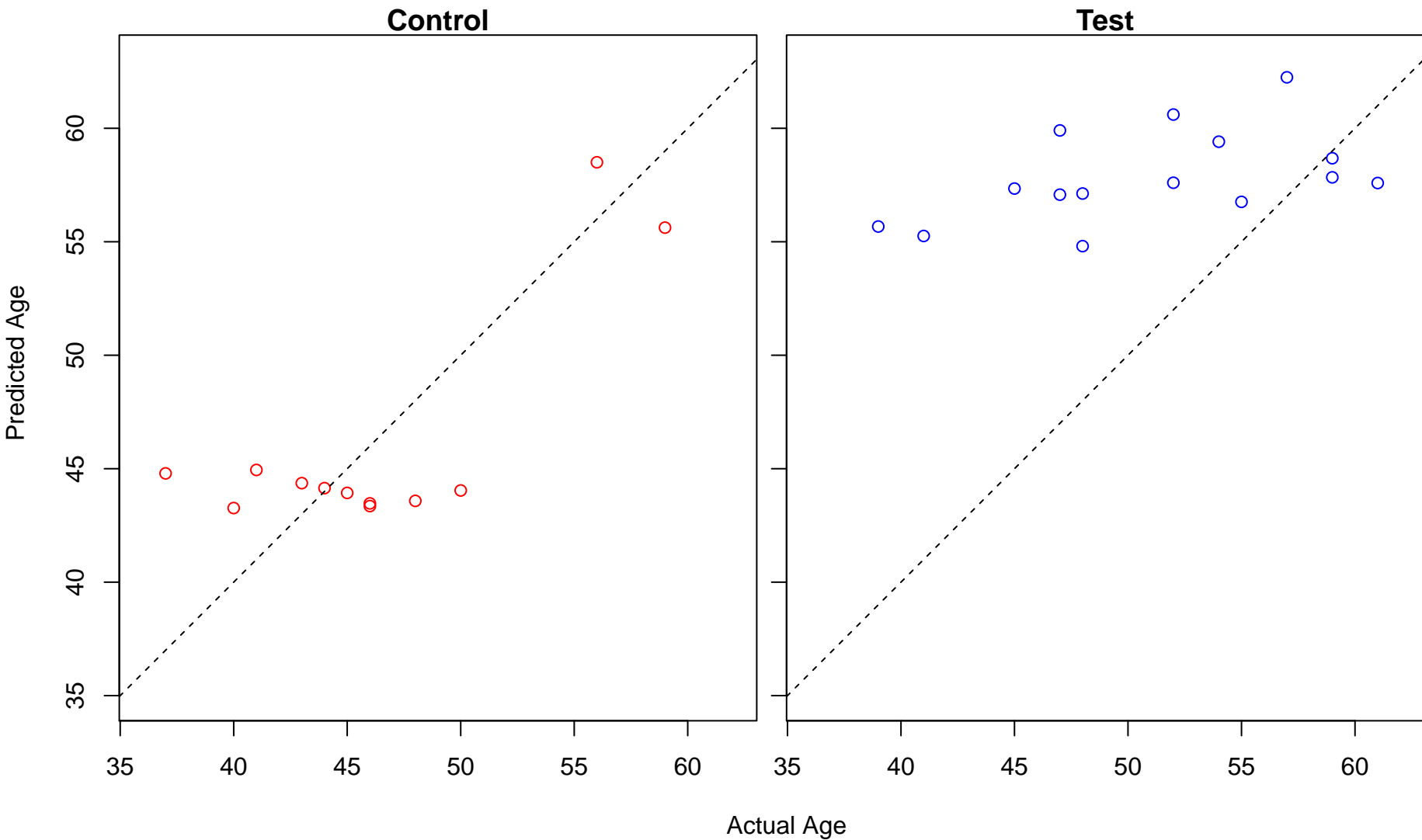
hormone secretion (Score: 2.270212)



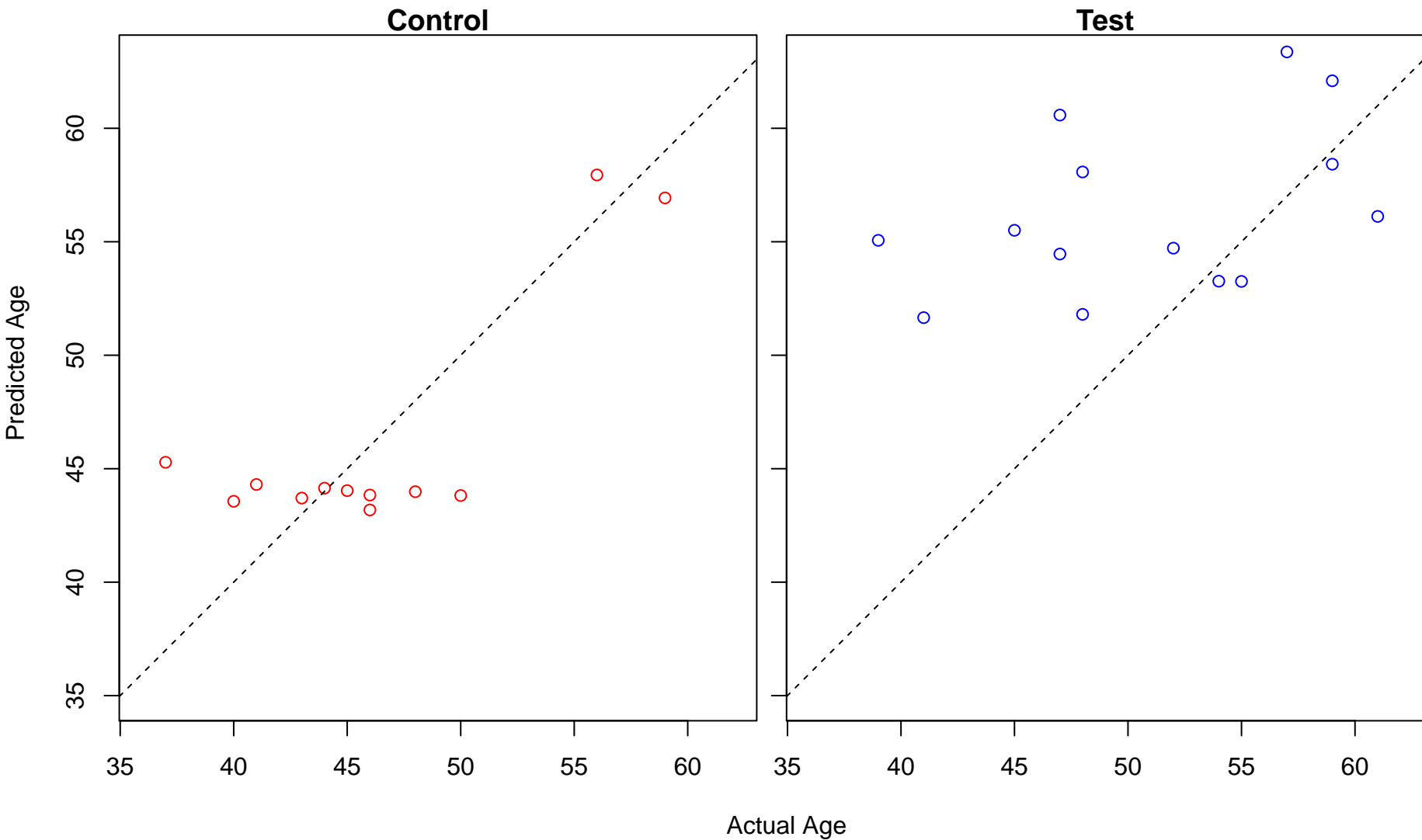
negative regulation of neuron apoptotic process (Score: 2.269678)



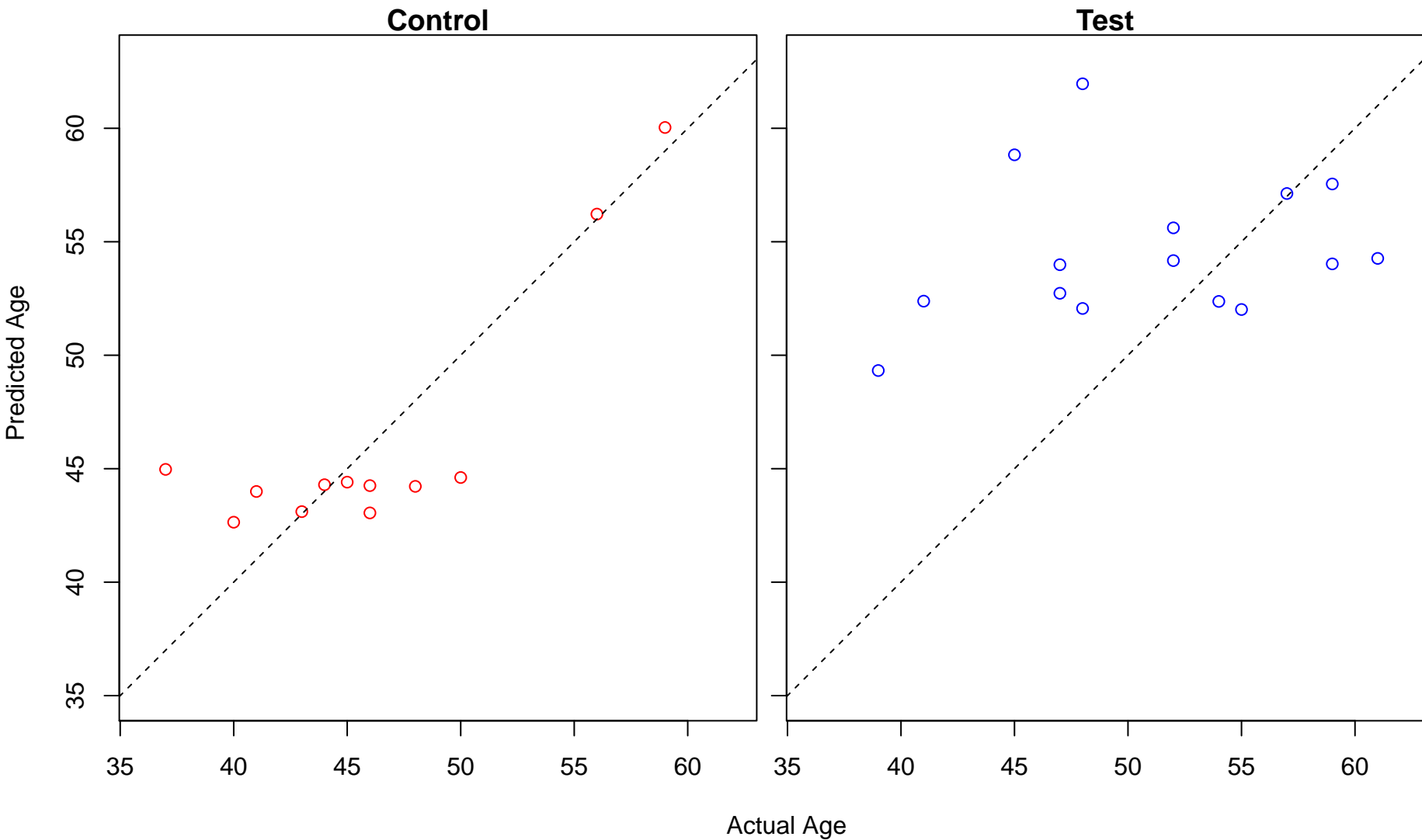
regulation of ERAD pathway (Score: 2.269084)



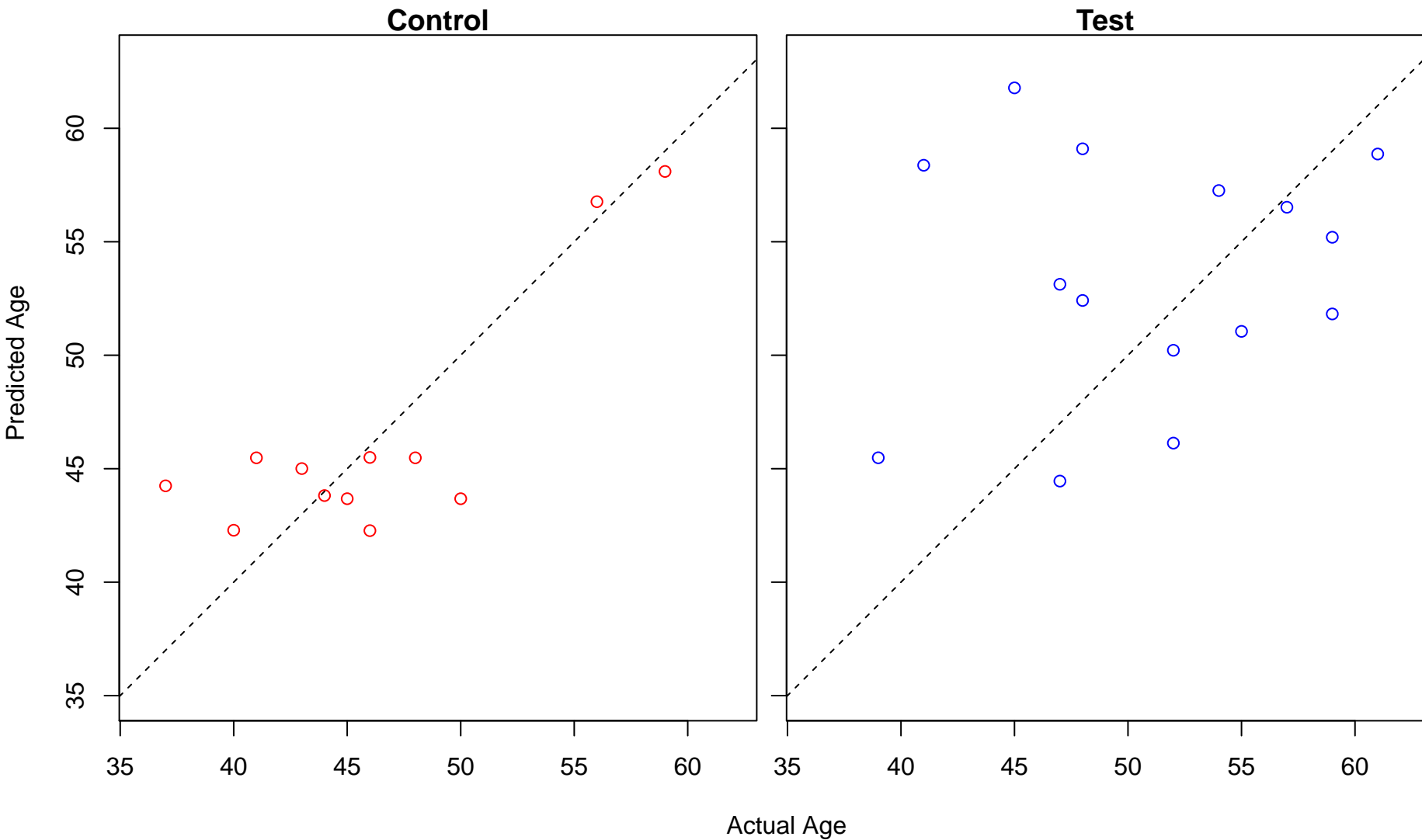
hormone transport (Score: 2.265893)



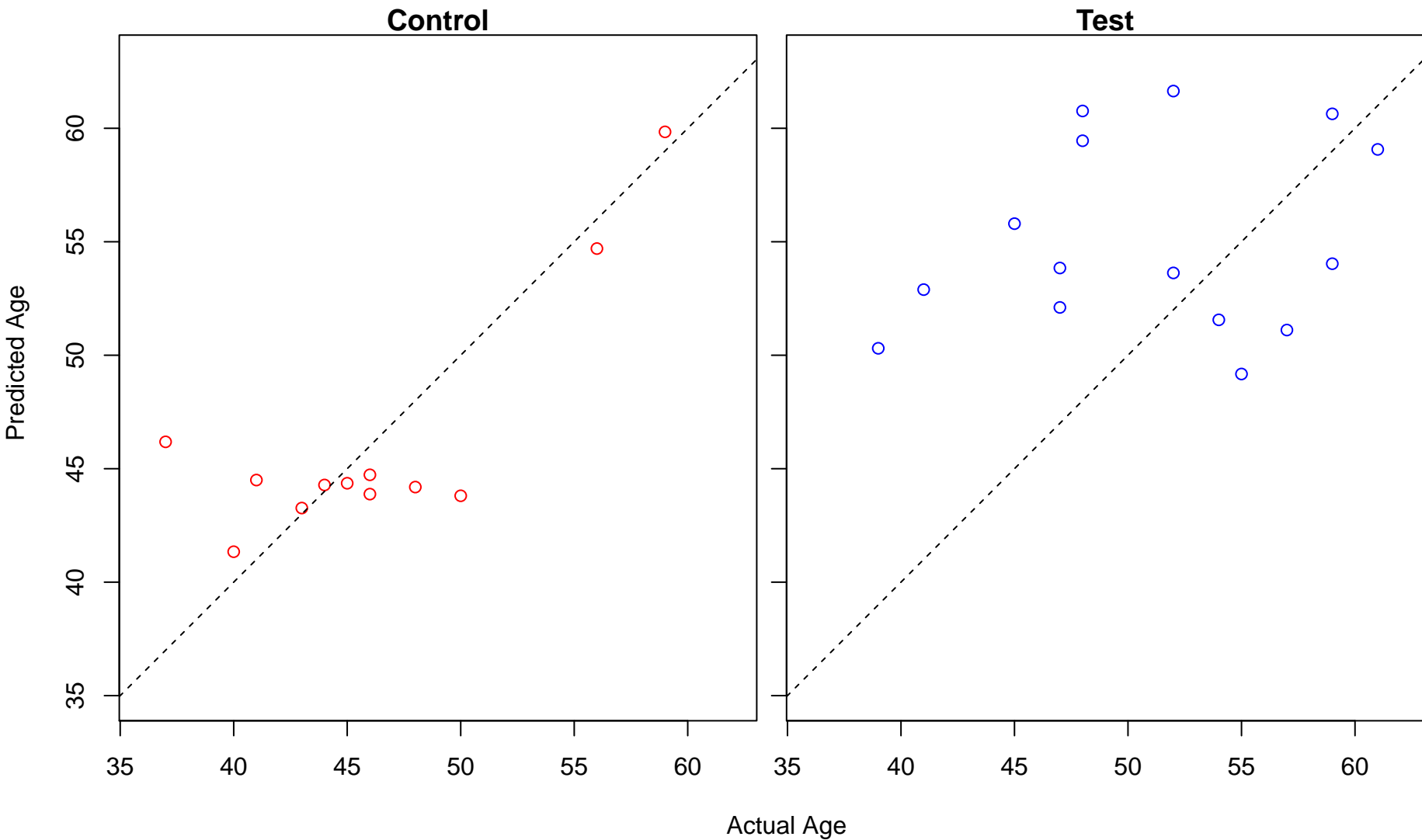
negative regulation of muscle organ development (Score: 2.265700)



negative regulation of intracellular signal transduction (Score: 2.263705)

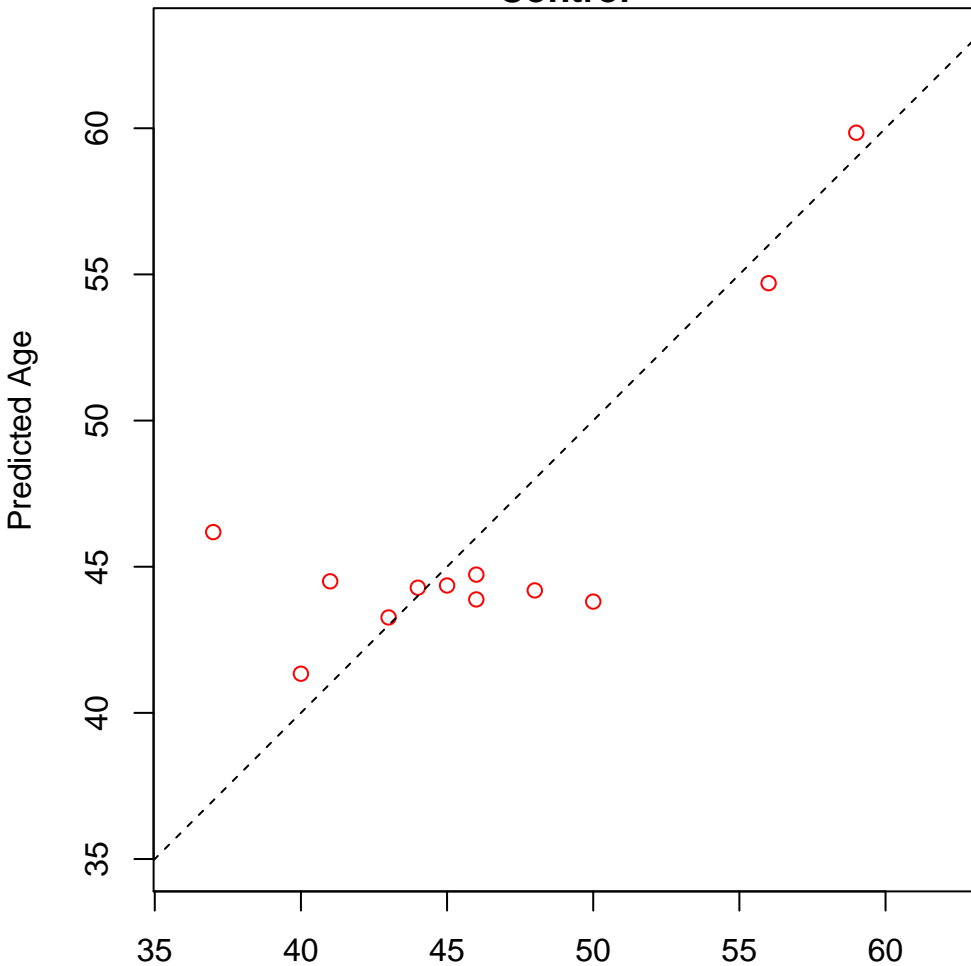


chondroitin sulfate proteoglycan biosynthetic process (Score: 2.262310)

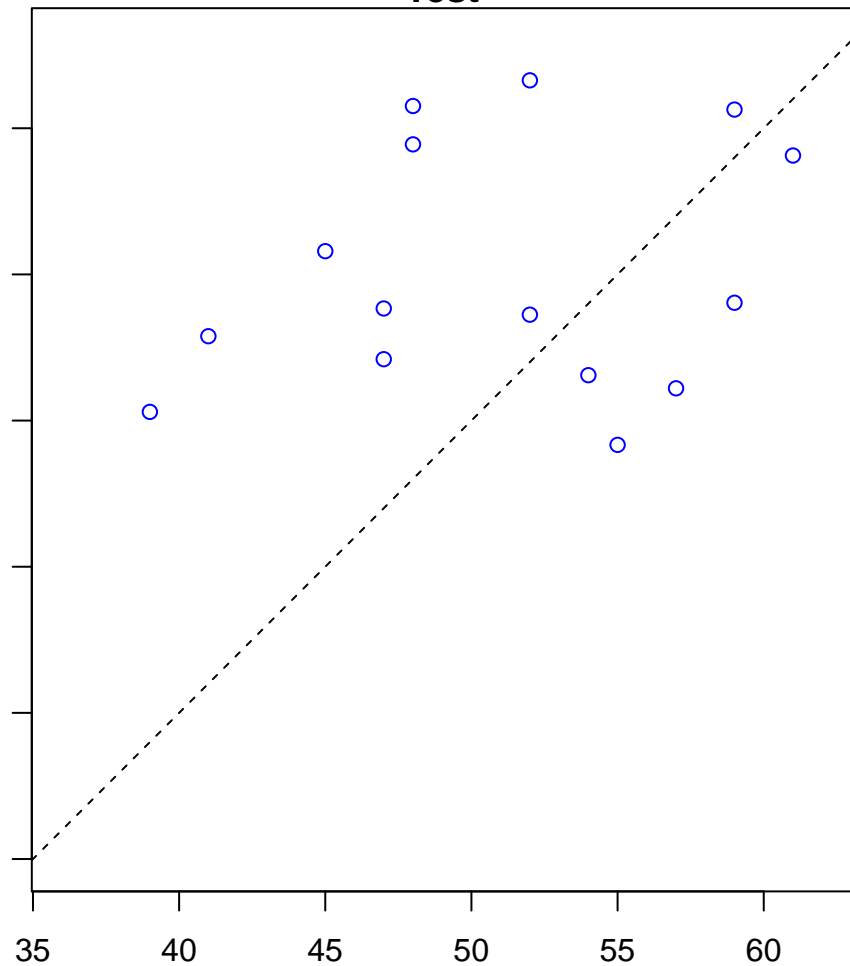


chondroitin sulfate biosynthetic process (Score: 2.261483)

Control

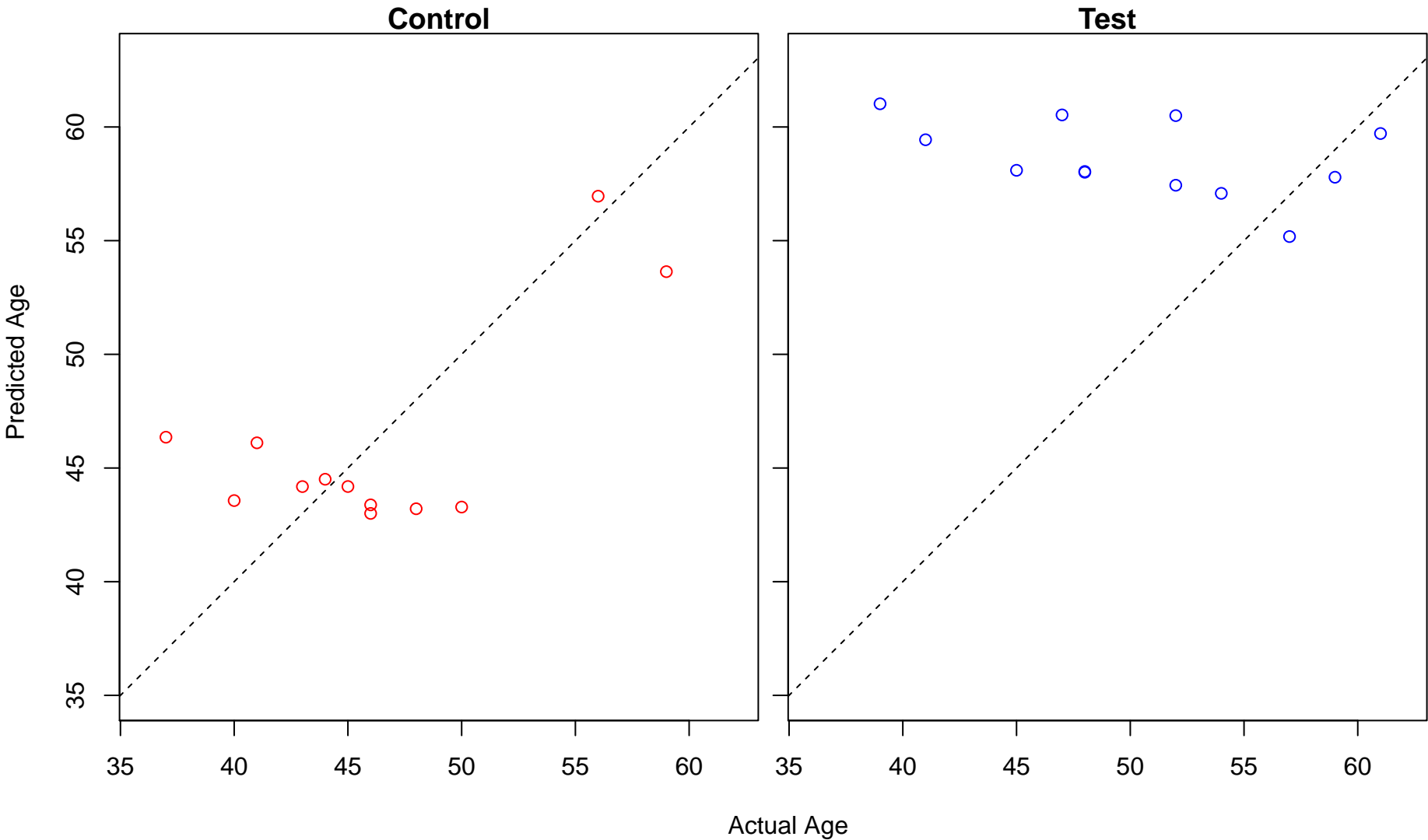


Test

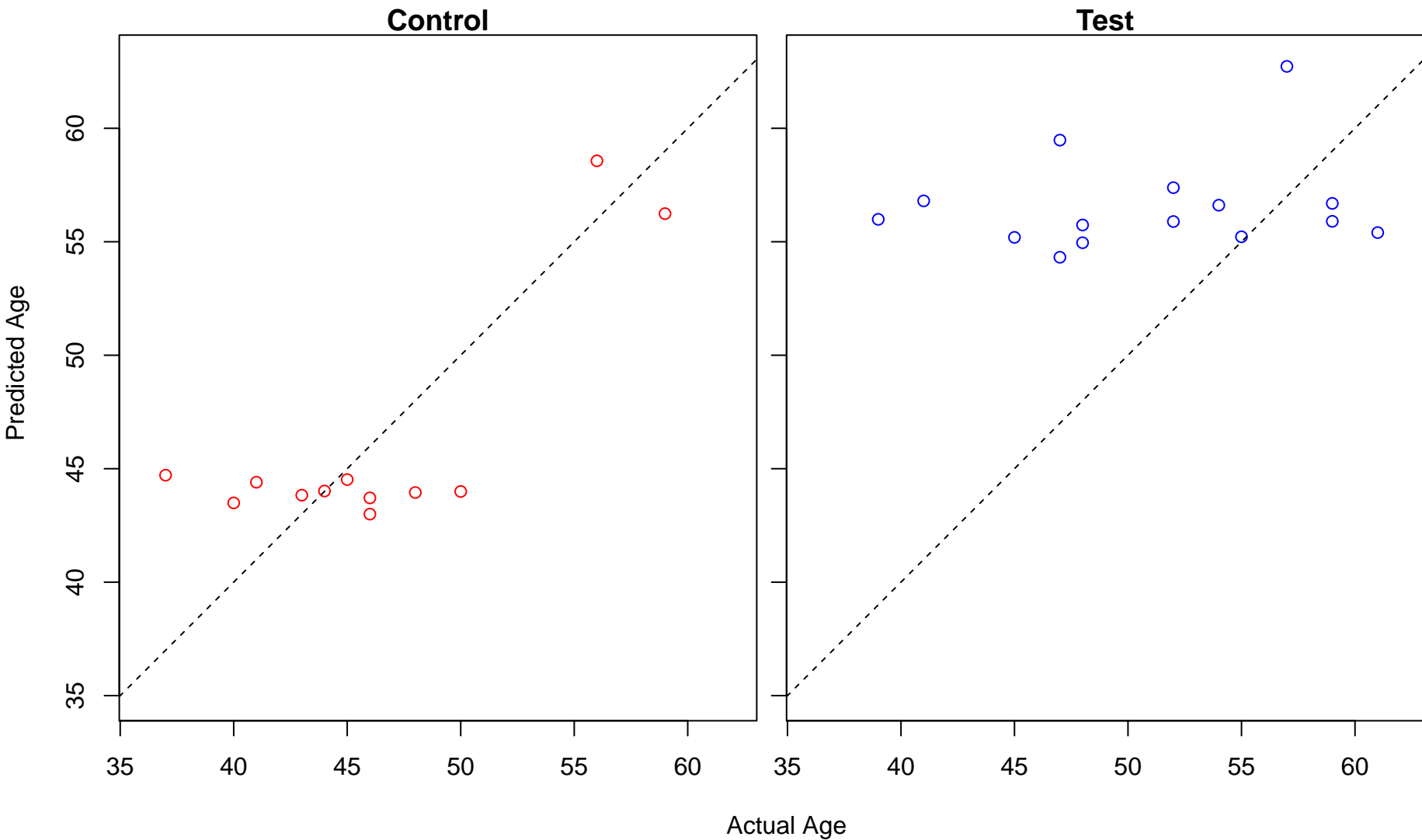


Actual Age

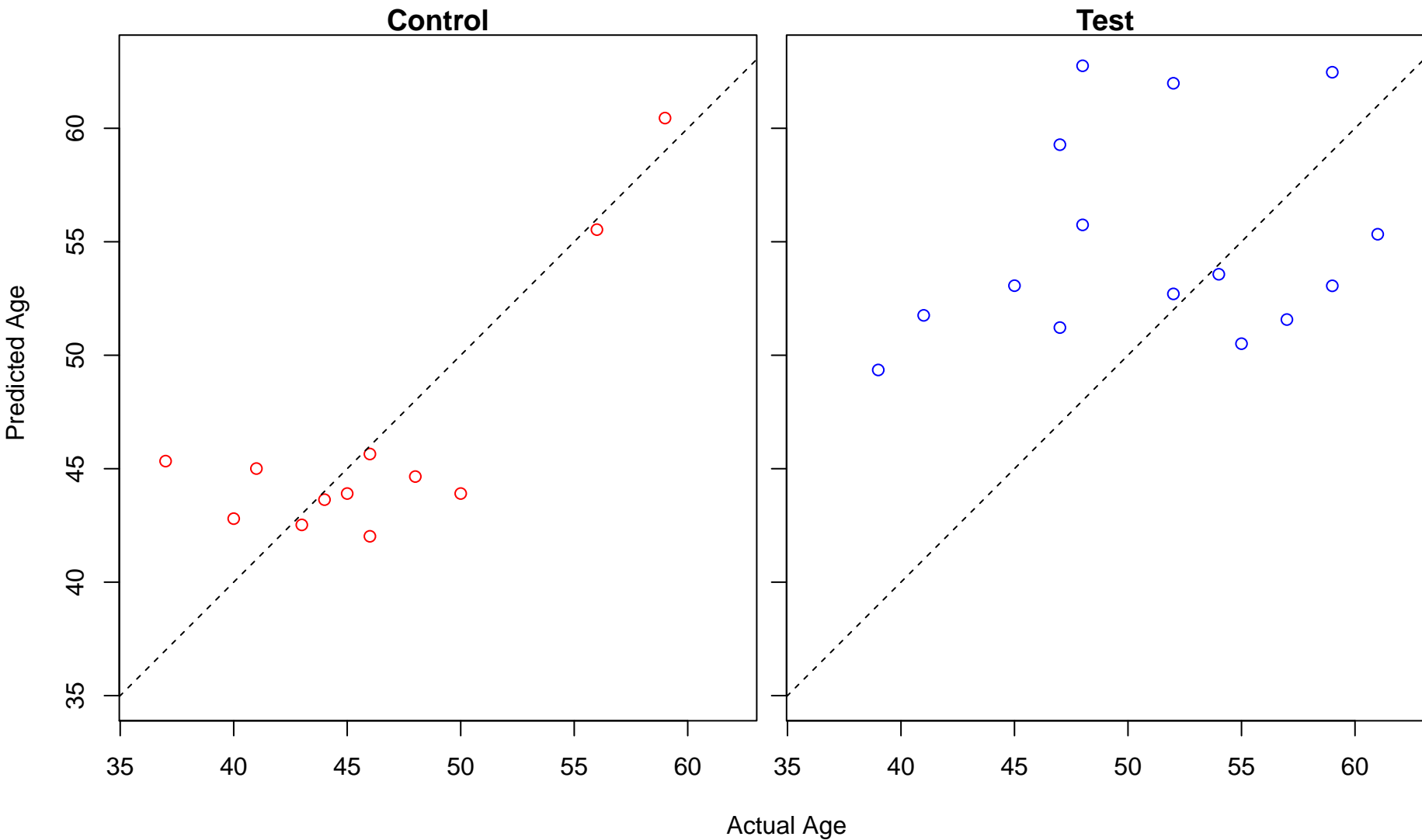
activation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 2.26)



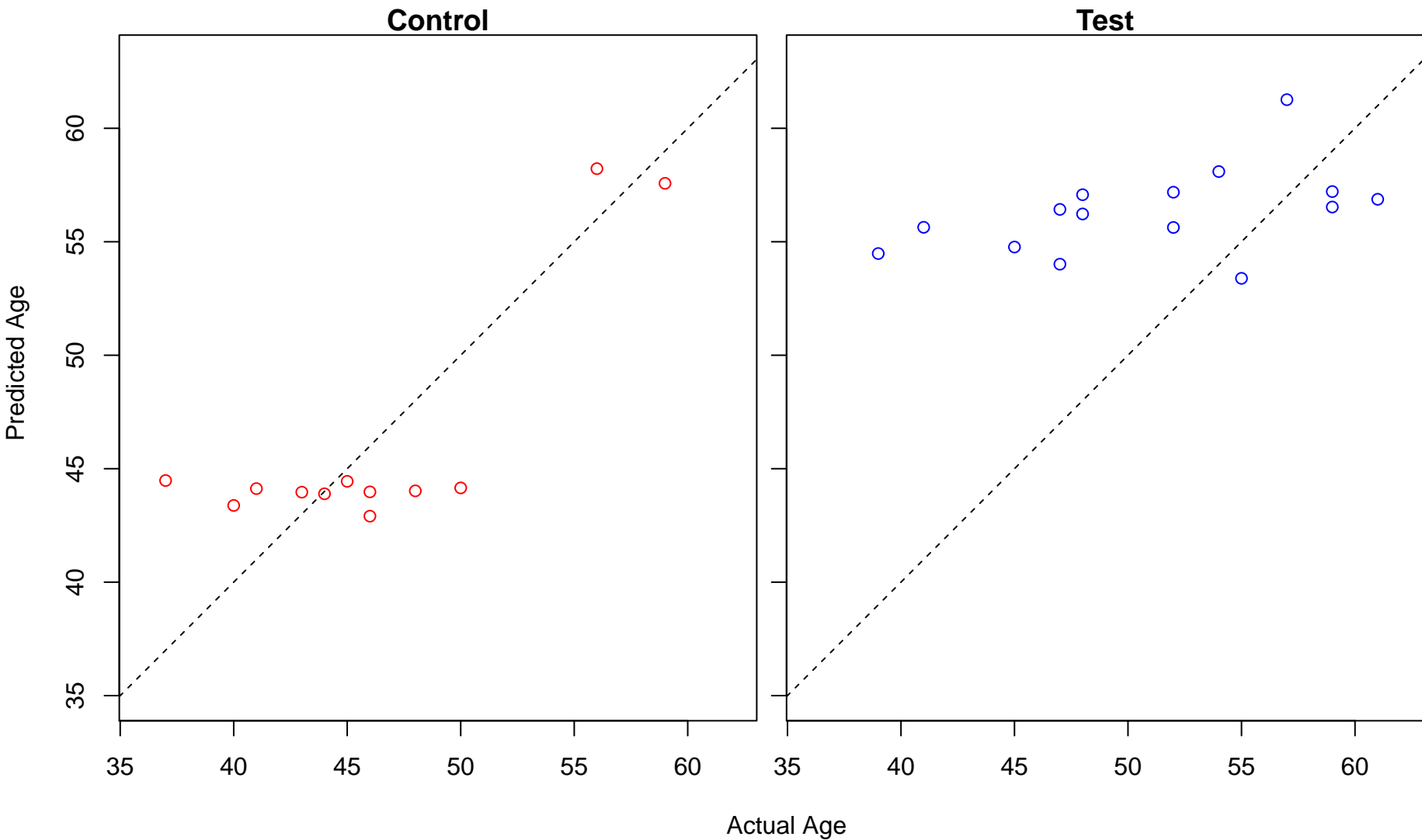
regulation of protein complex assembly (Score: 2.260721)



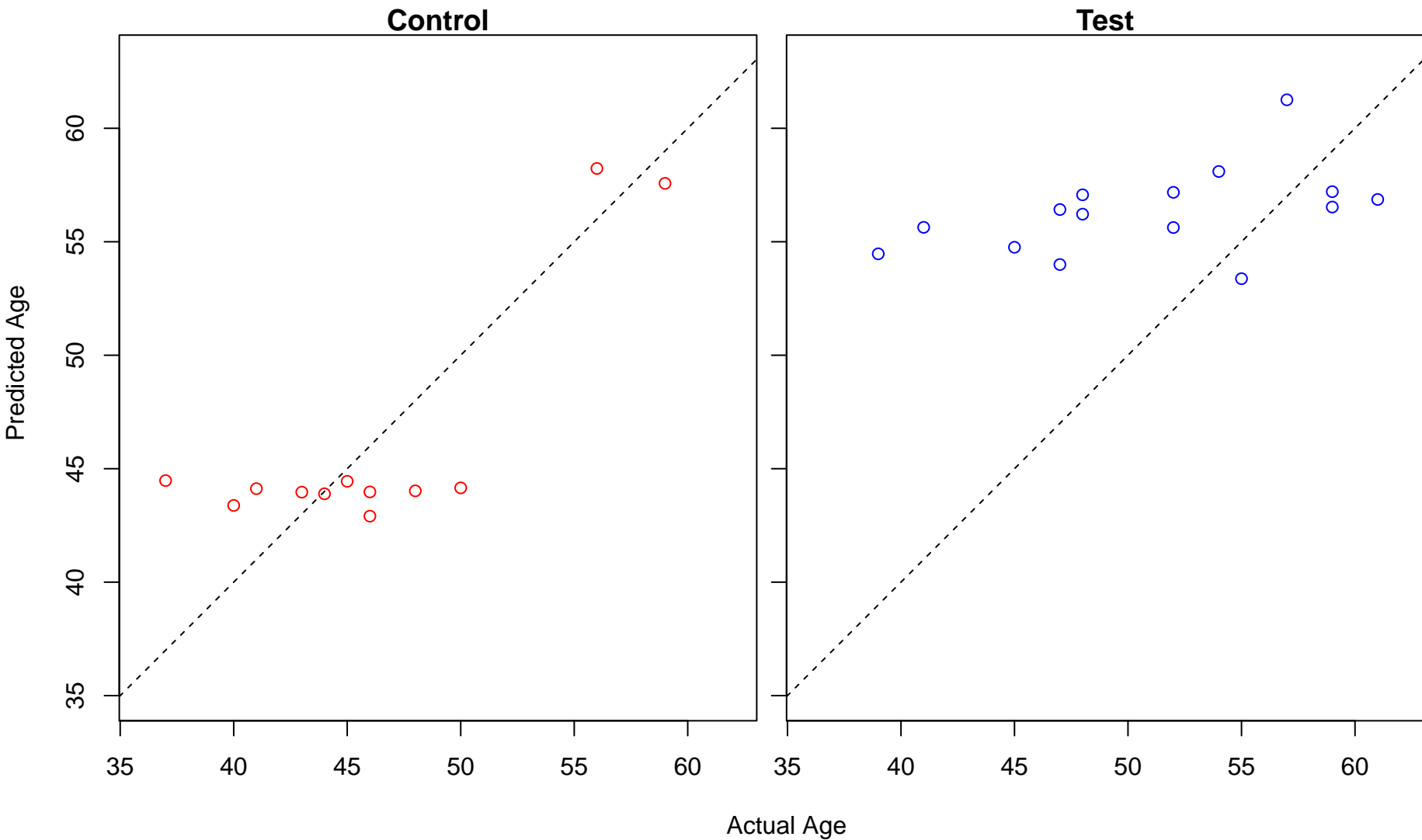
negative regulation of mitotic sister chromatid separation (Score: 2.259870)



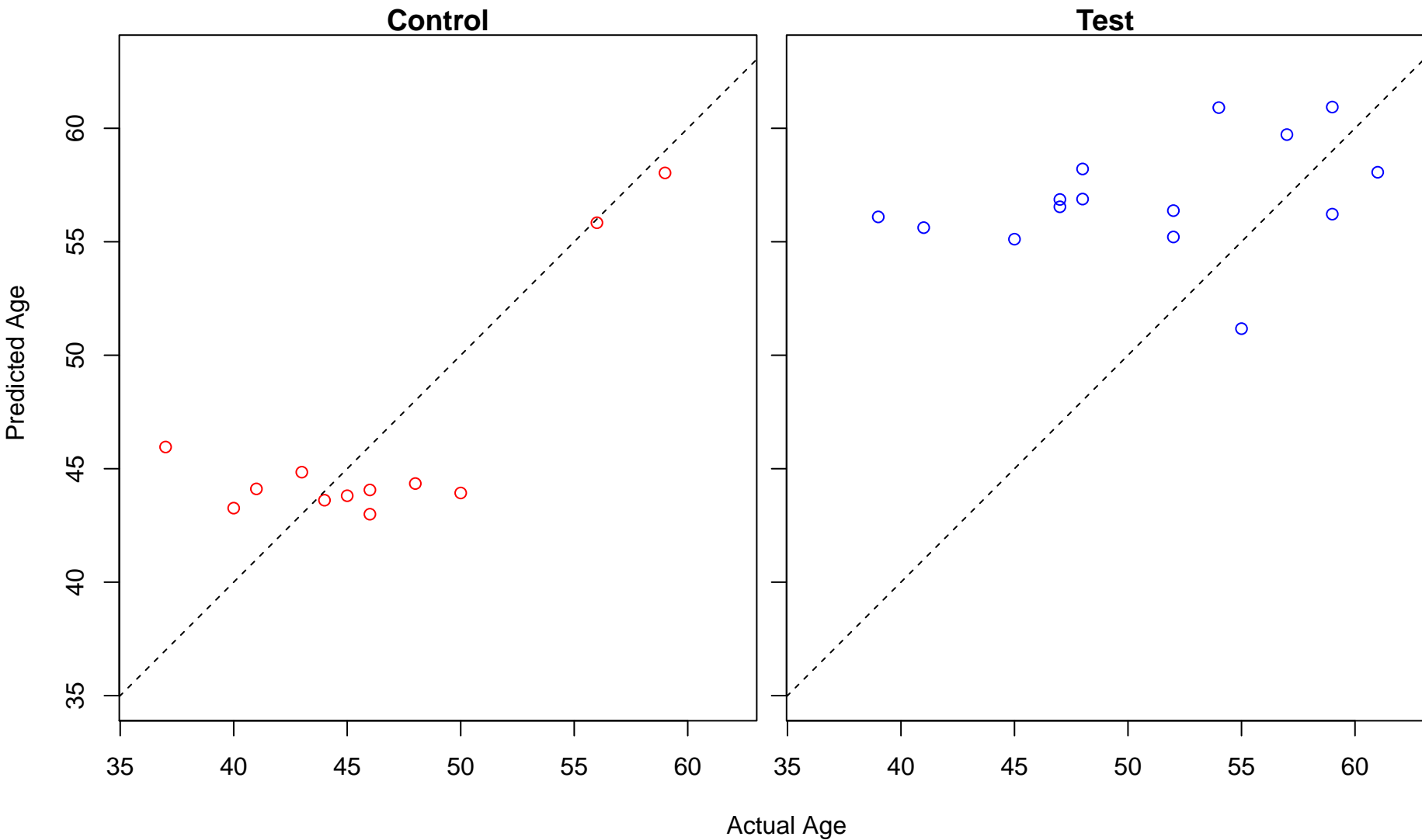
negative regulation of proteolysis involved in cellular protein catabolic process (Score: 2.259442)



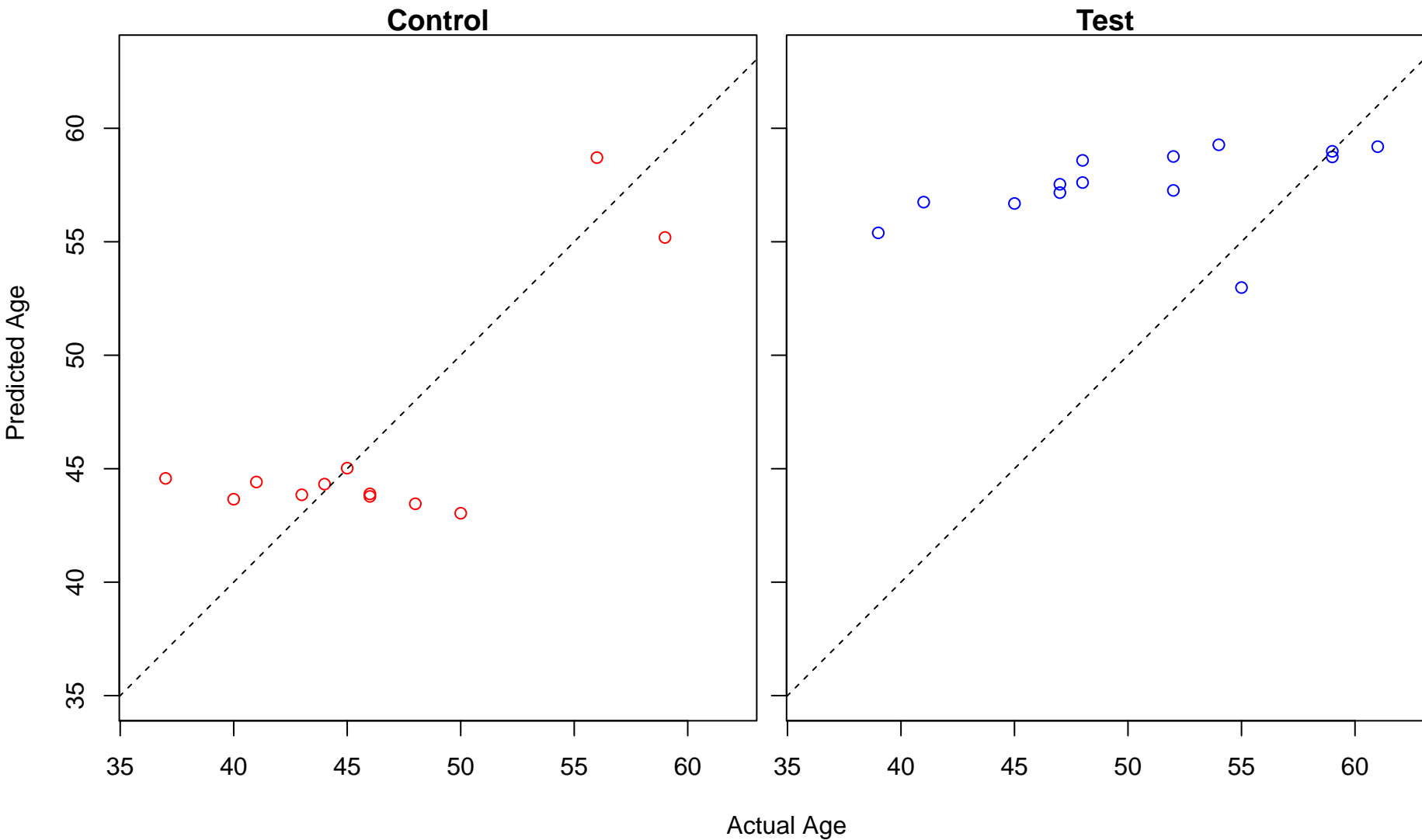
negative regulation of proteasomal protein catabolic process (Score: 2.257678)



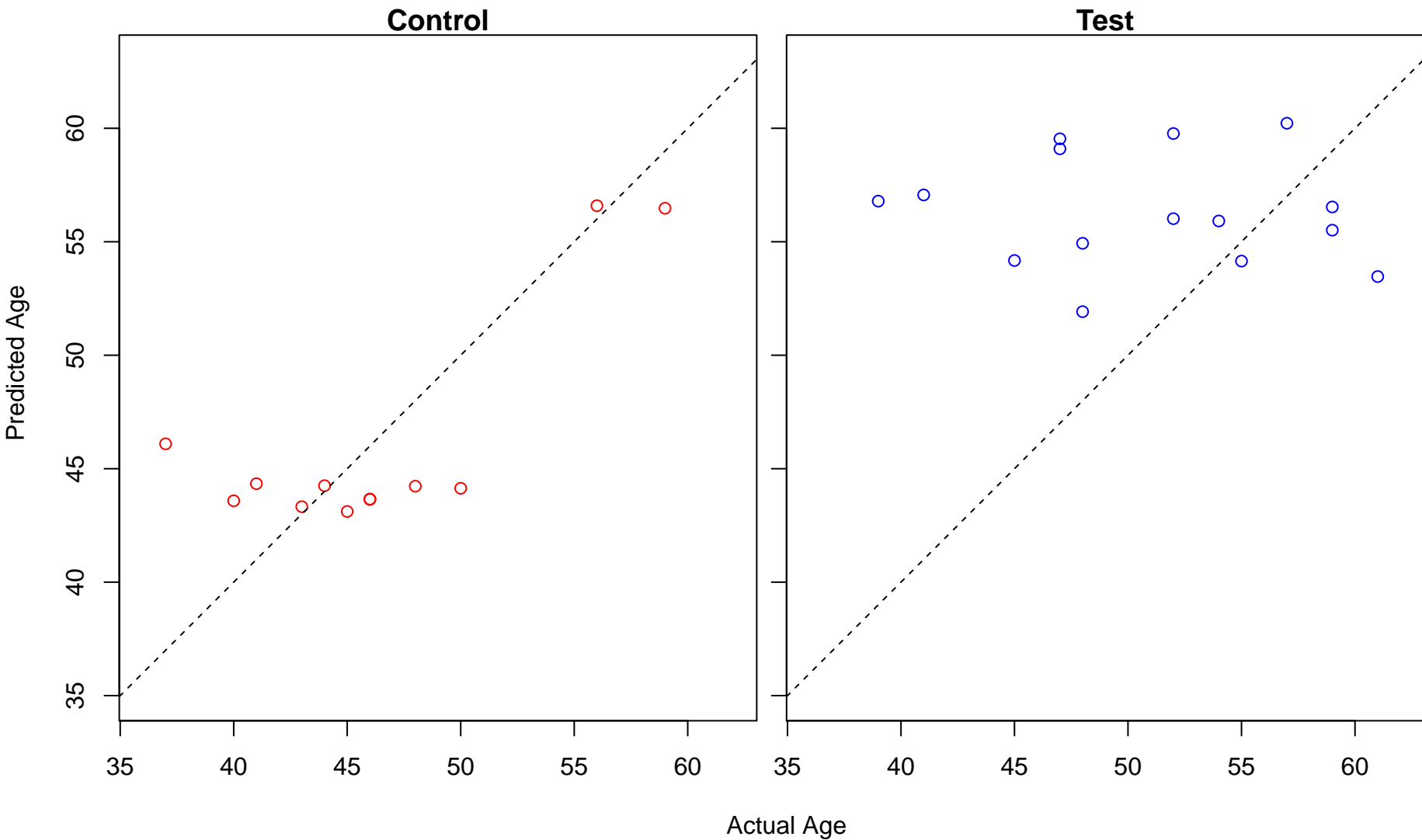
DNA strand elongation involved in DNA replication (Score: 2.250529)



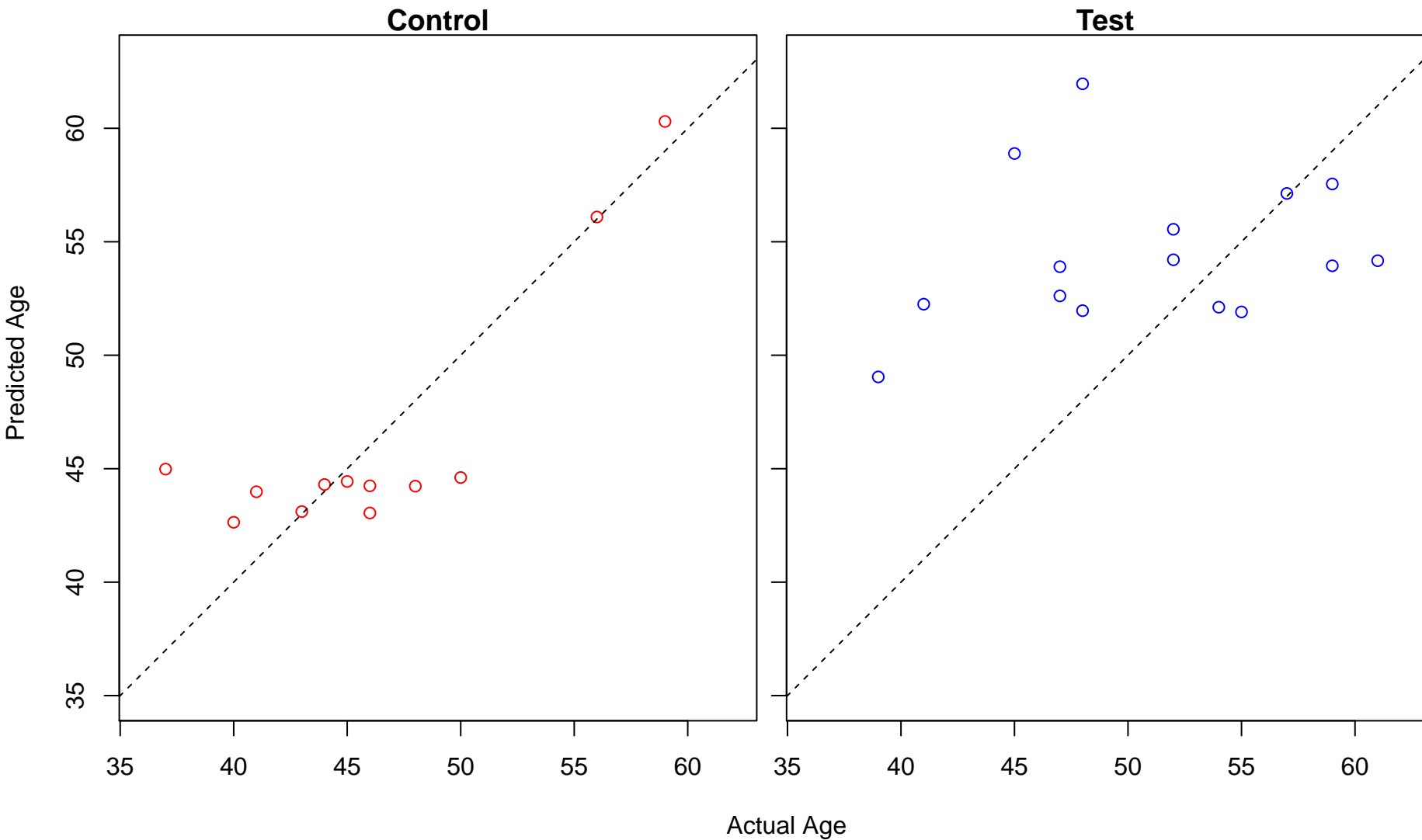
termination of RNA polymerase I transcription (Score: 2.249665)



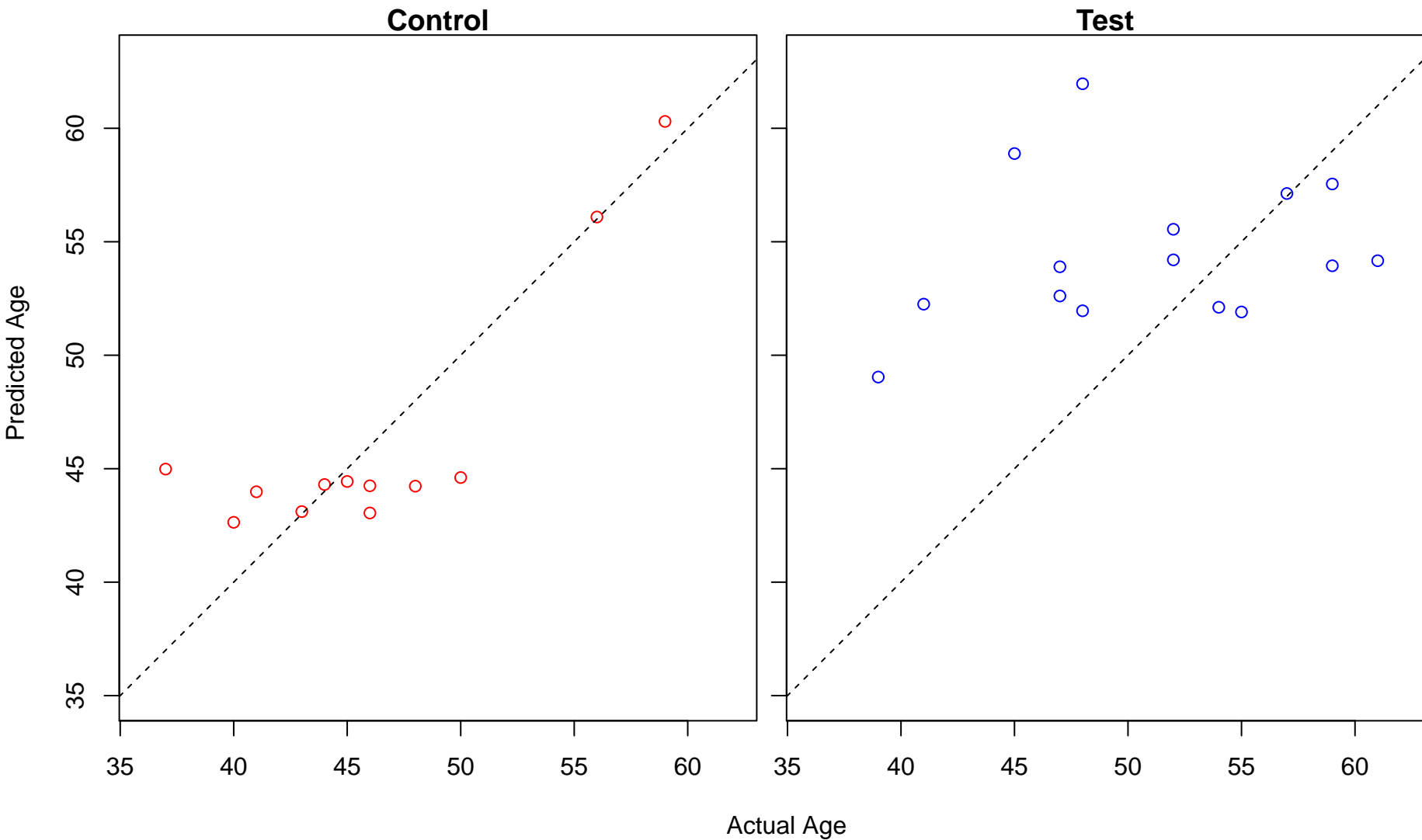
regulation of fibroblast migration (Score: 2.249032)



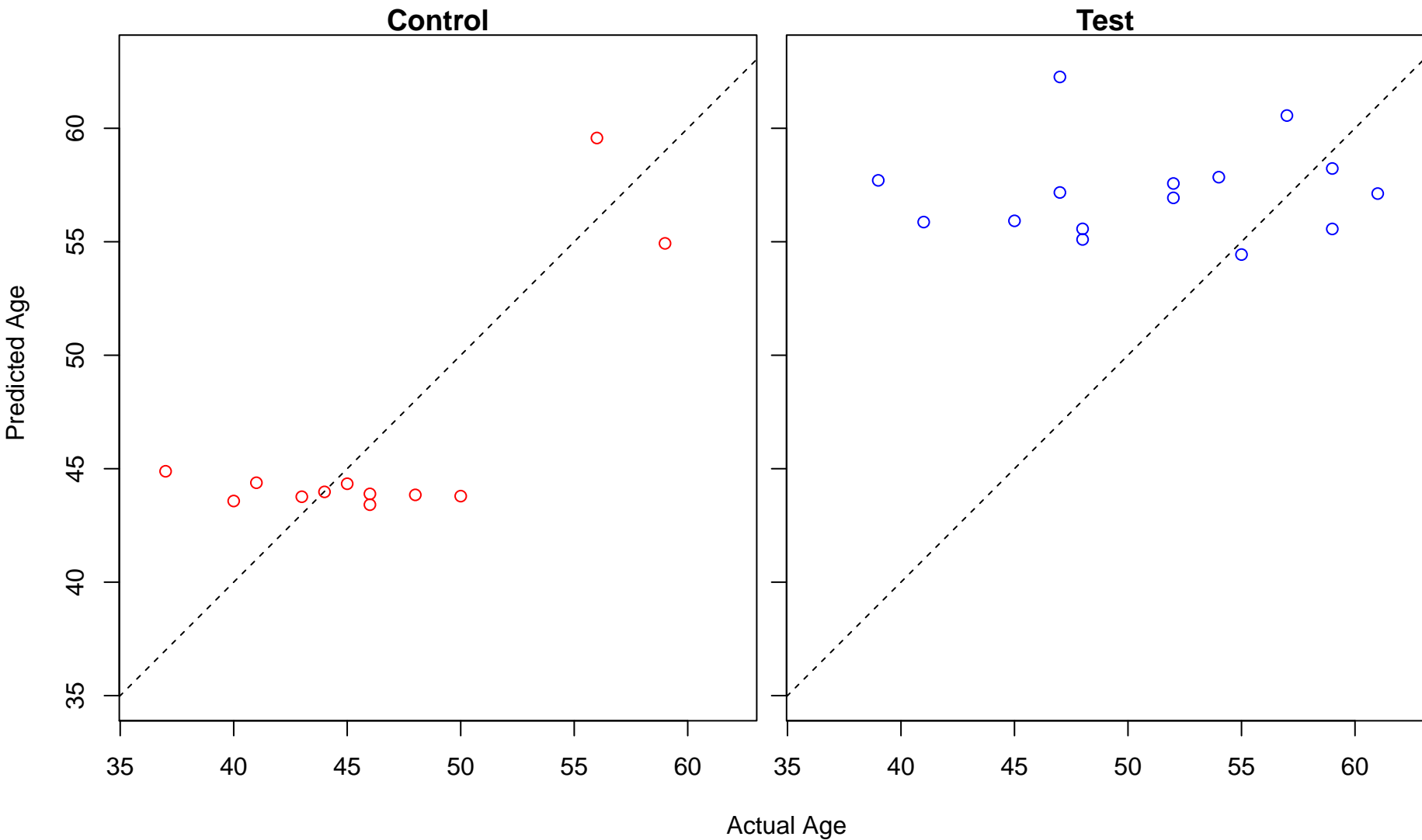
negative regulation of muscle tissue development (Score: 2.248964)



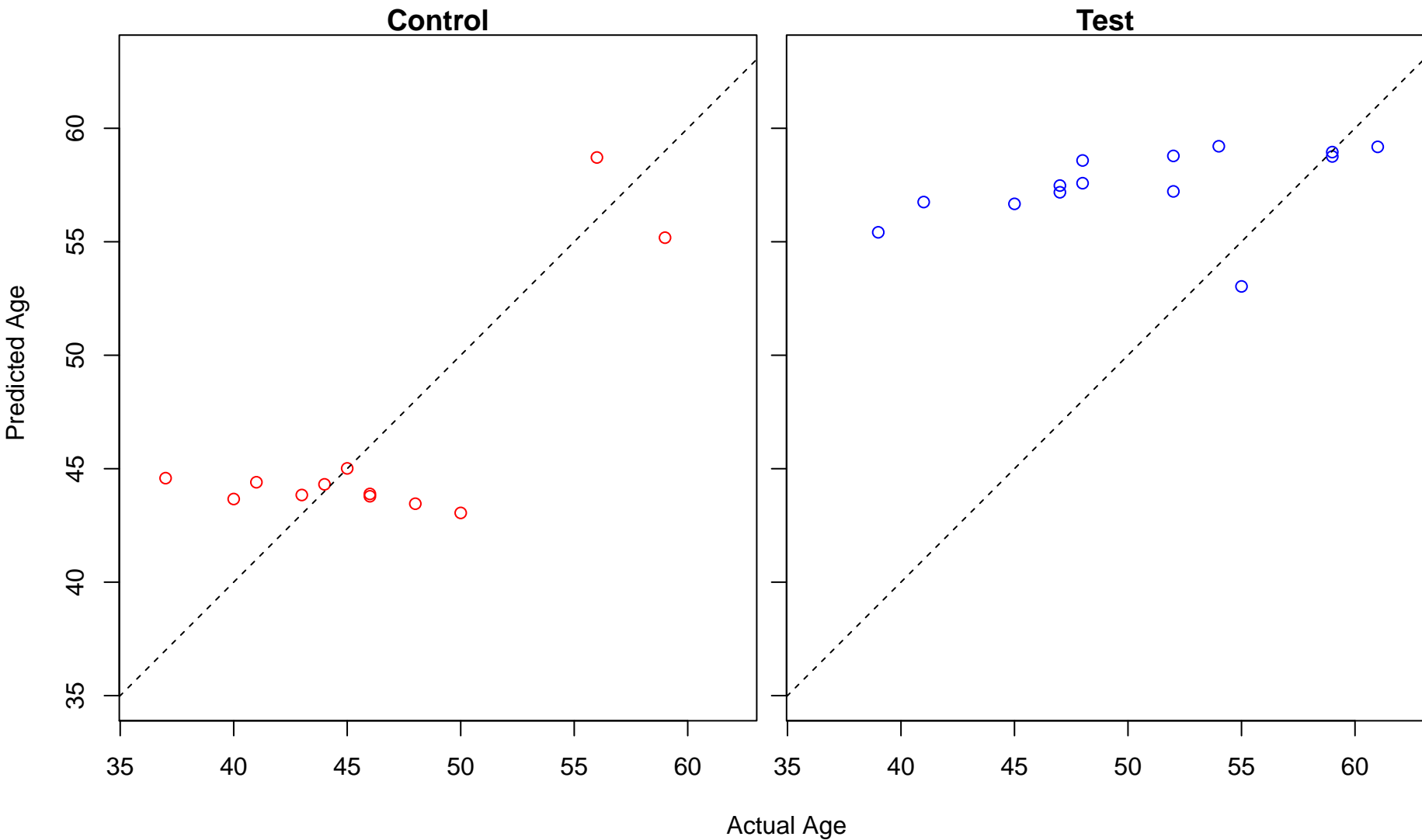
negative regulation of striated muscle tissue development (Score: 2.248837)



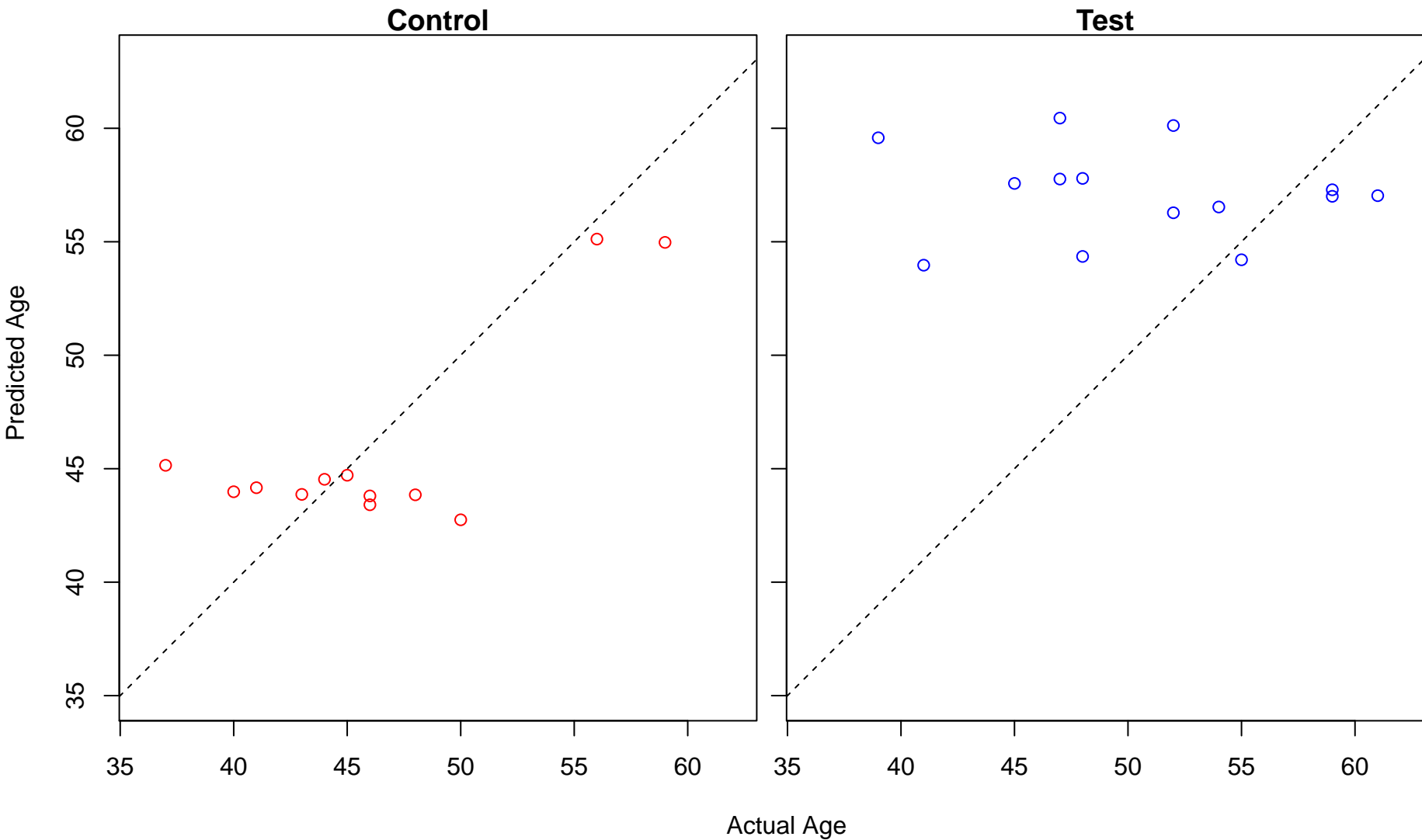
regulation of microtubule-based process (Score: 2.246776)



transcription from RNA polymerase I promoter (Score: 2.245505)

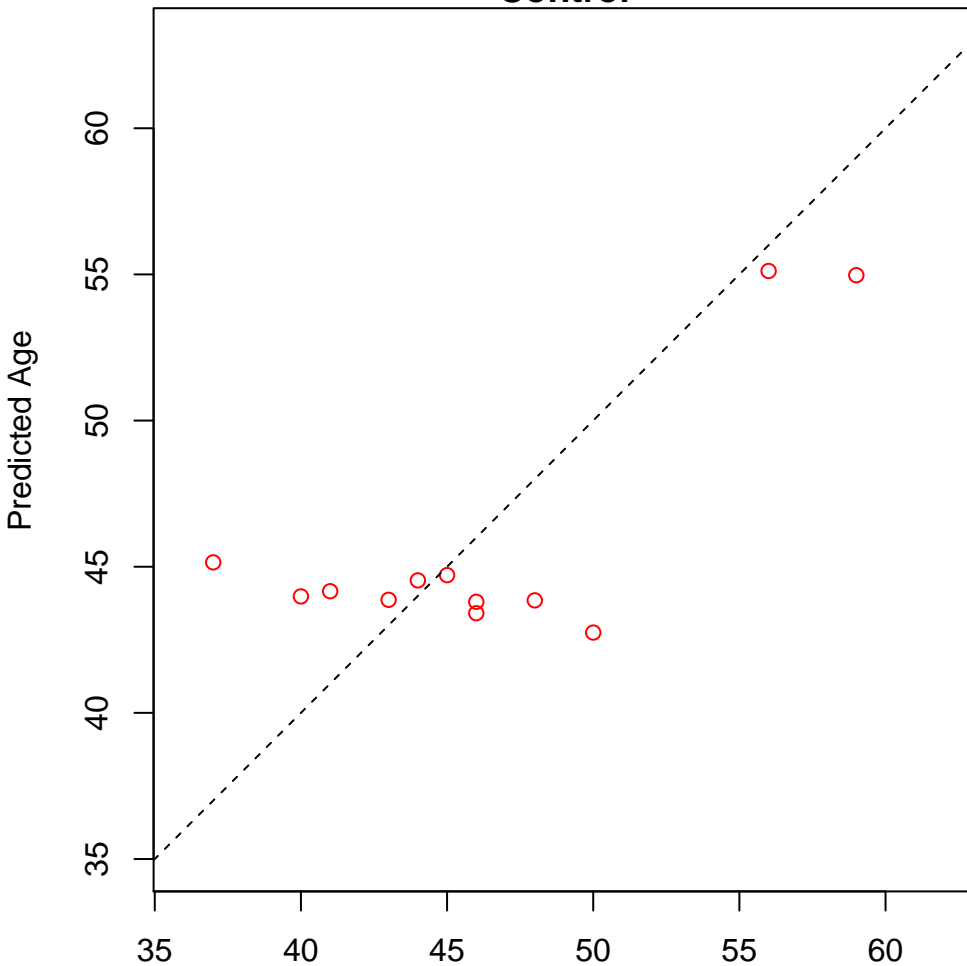


electron transport chain (Score: 2.244938)

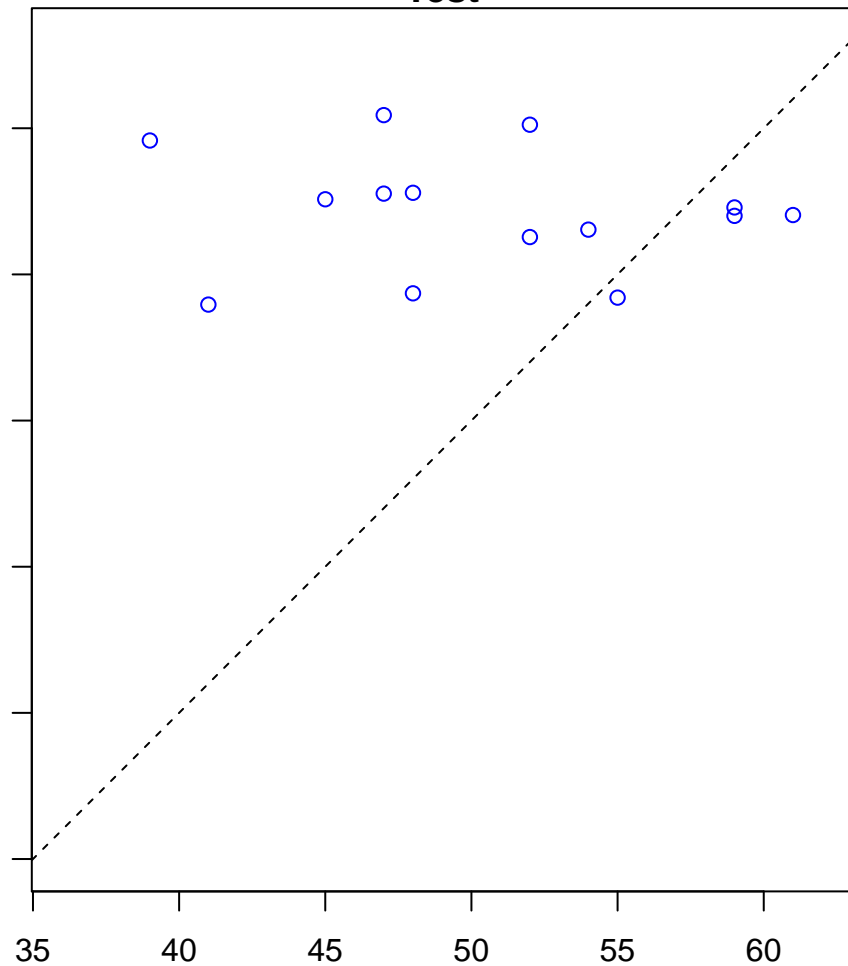


respiratory electron transport chain (Score: 2.244938)

Control

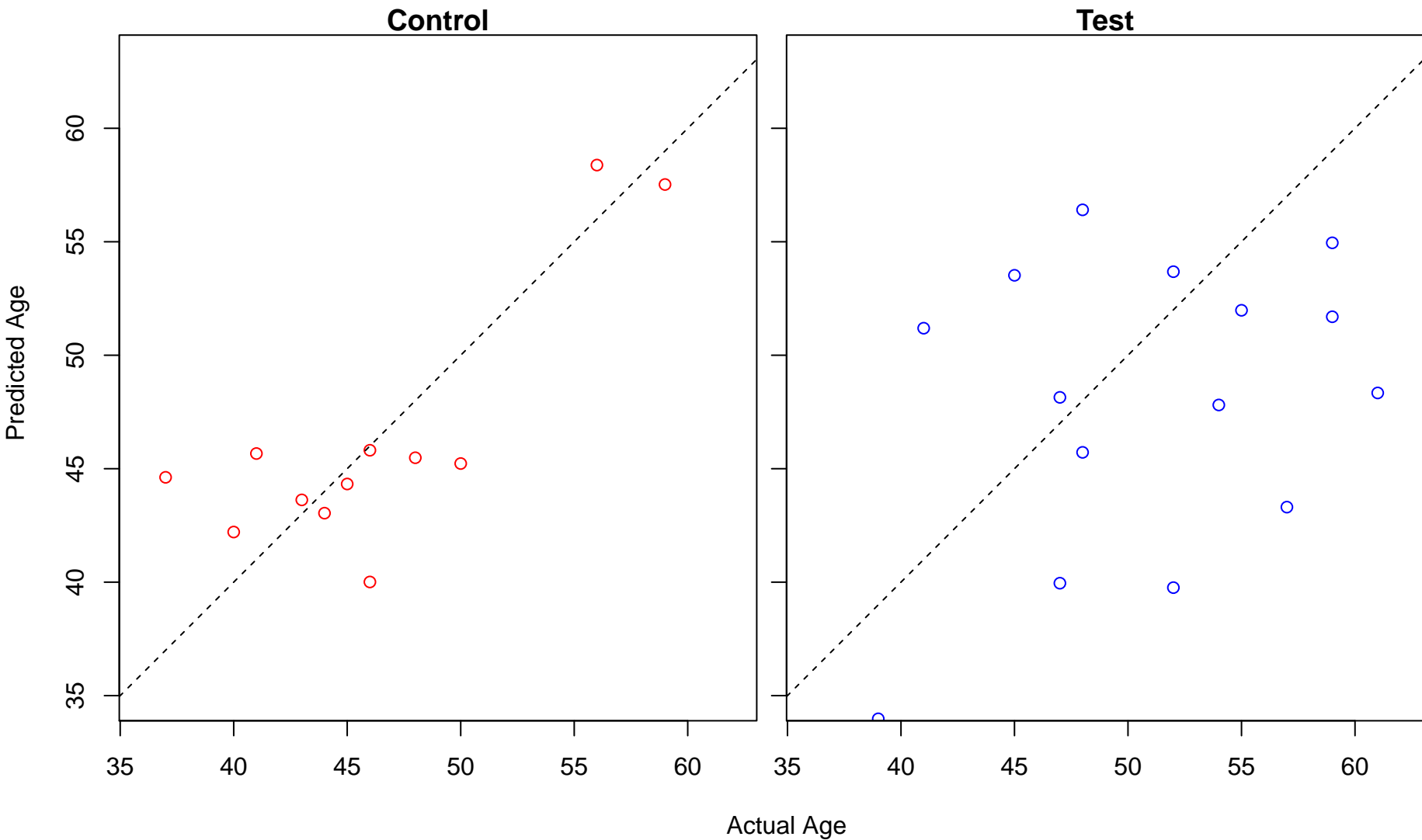


Test

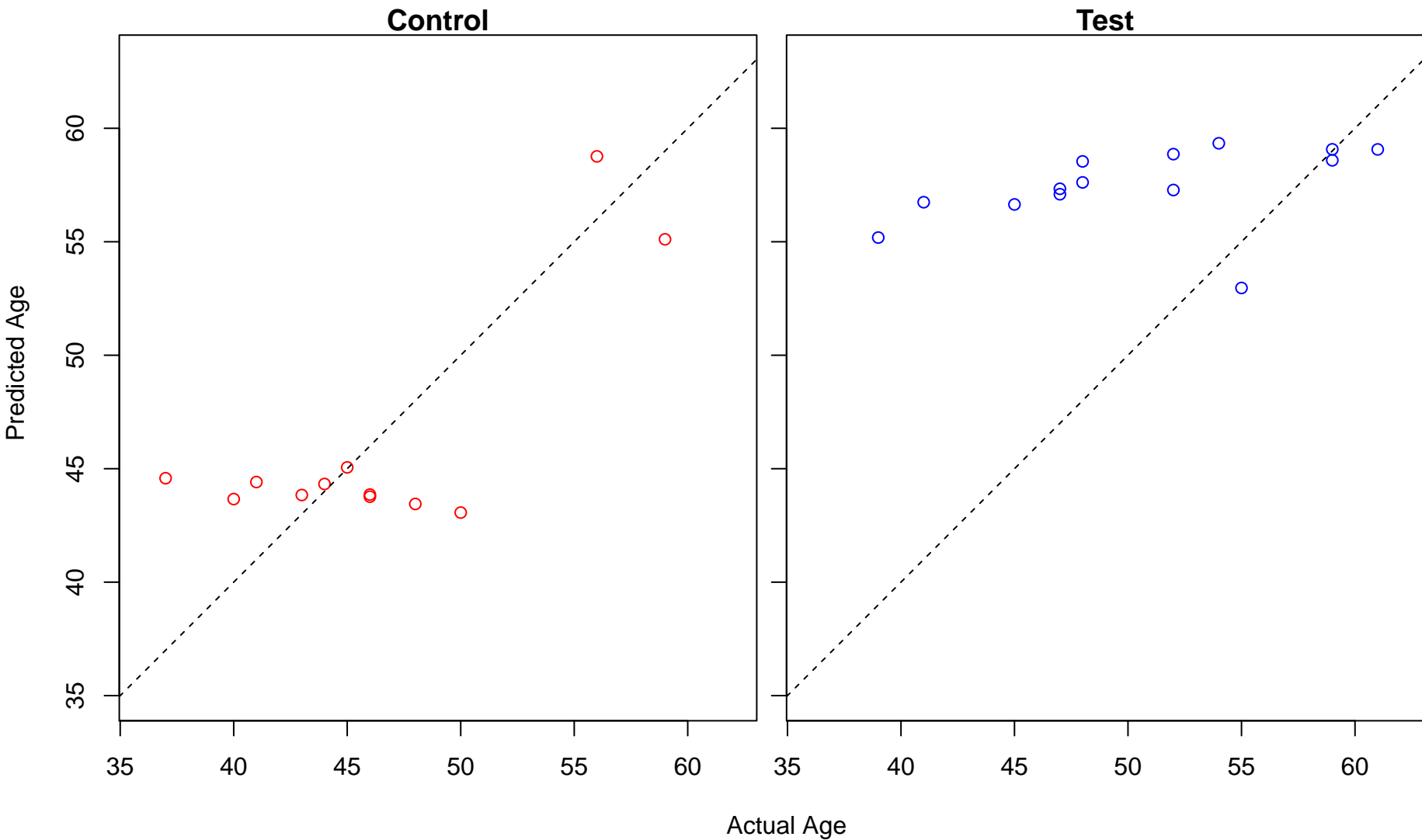


Actual Age

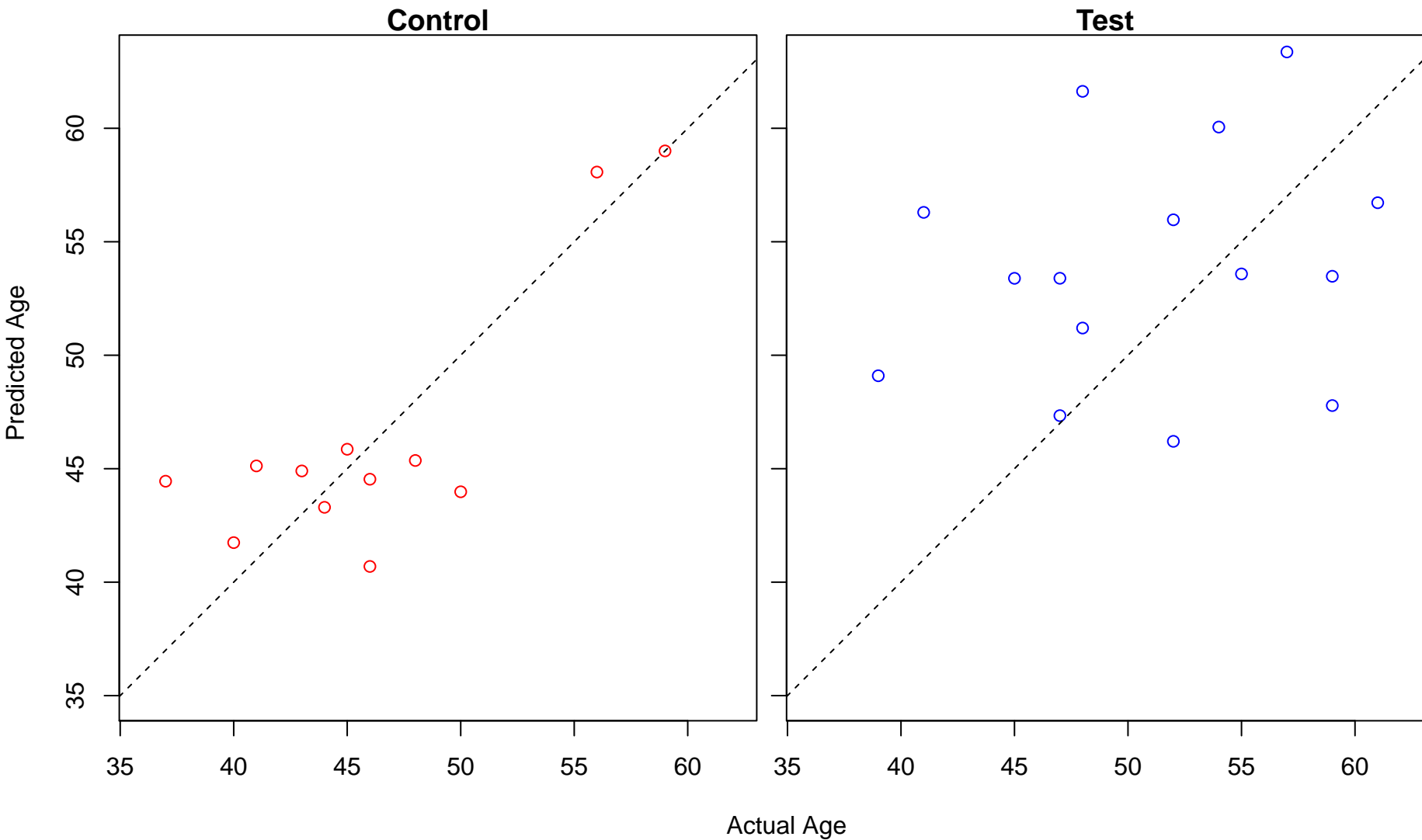
positive regulation of cytoskeleton organization (Score: 2.239358)



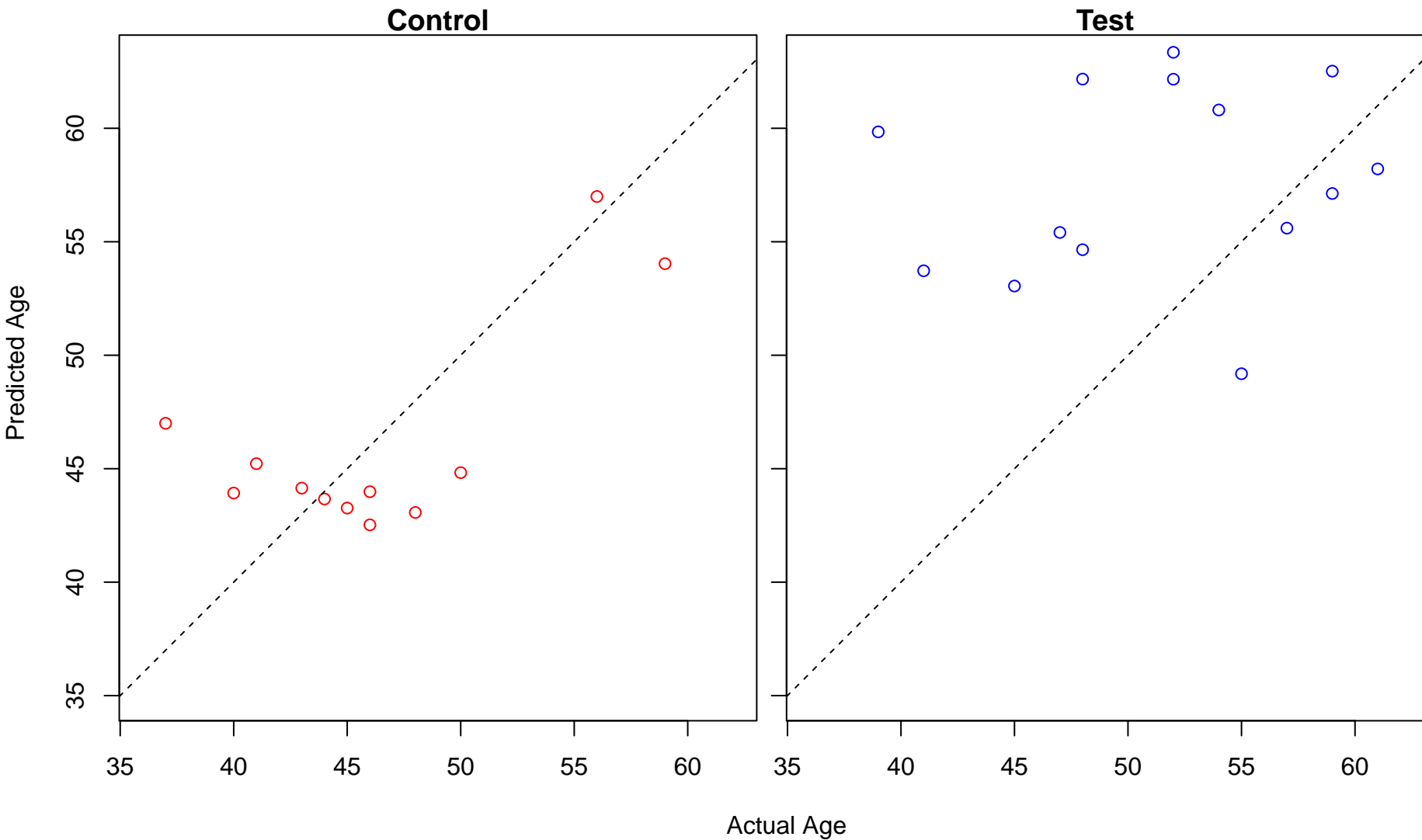
transcription initiation from RNA polymerase I promoter (Score: 2.231994)



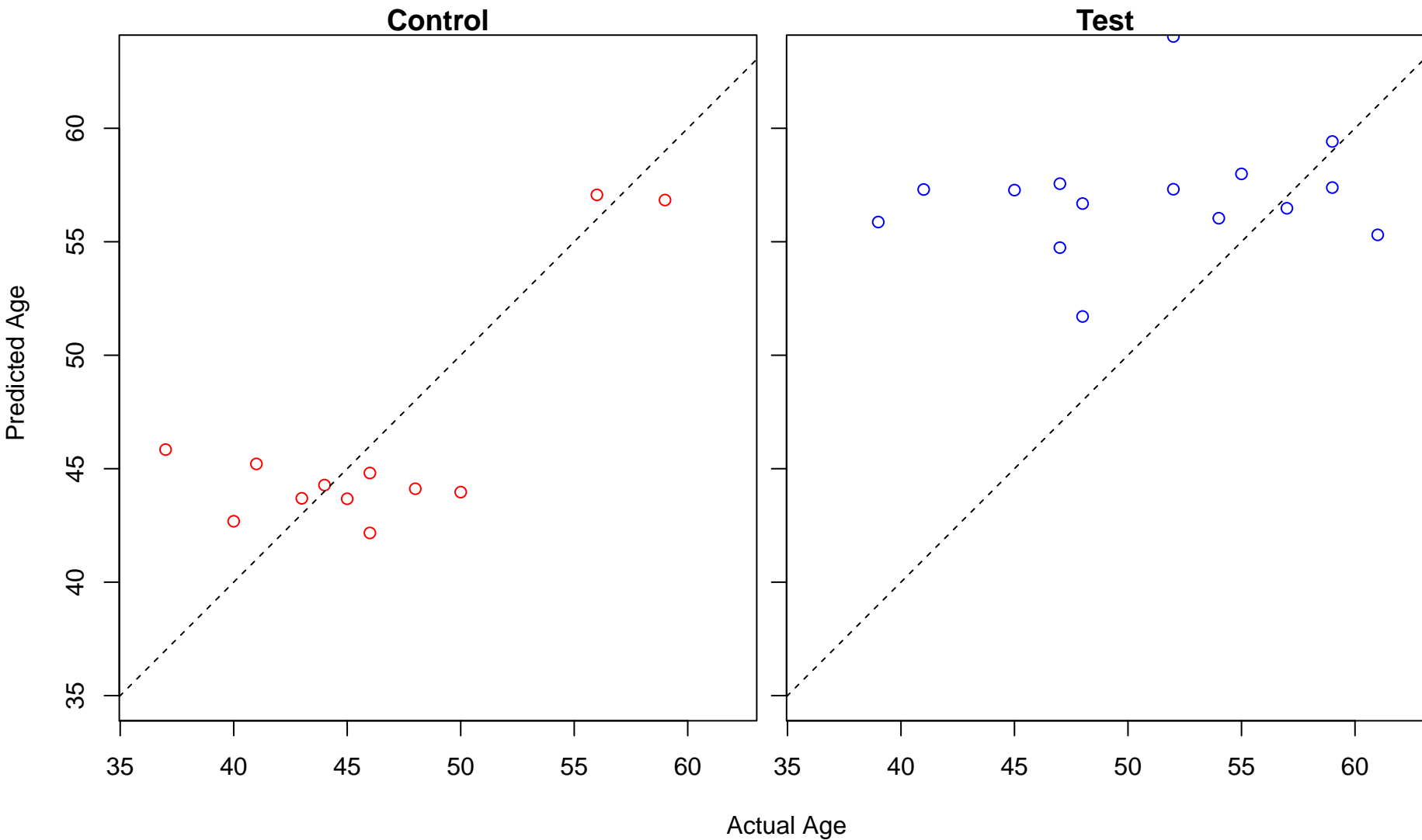
negative regulation of cellular catabolic process (Score: 2.231205)



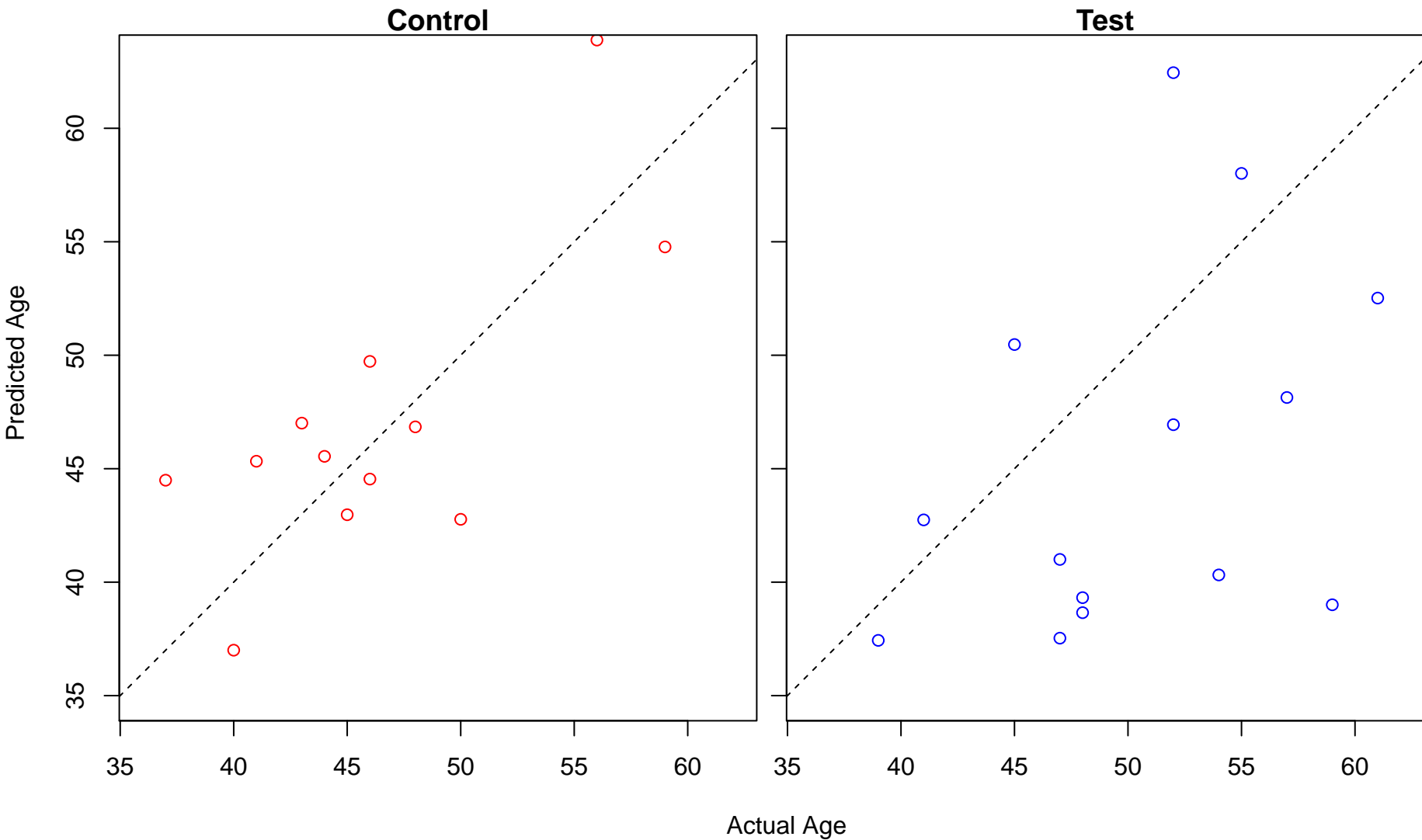
ventricular septum development (Score: 2.227734)



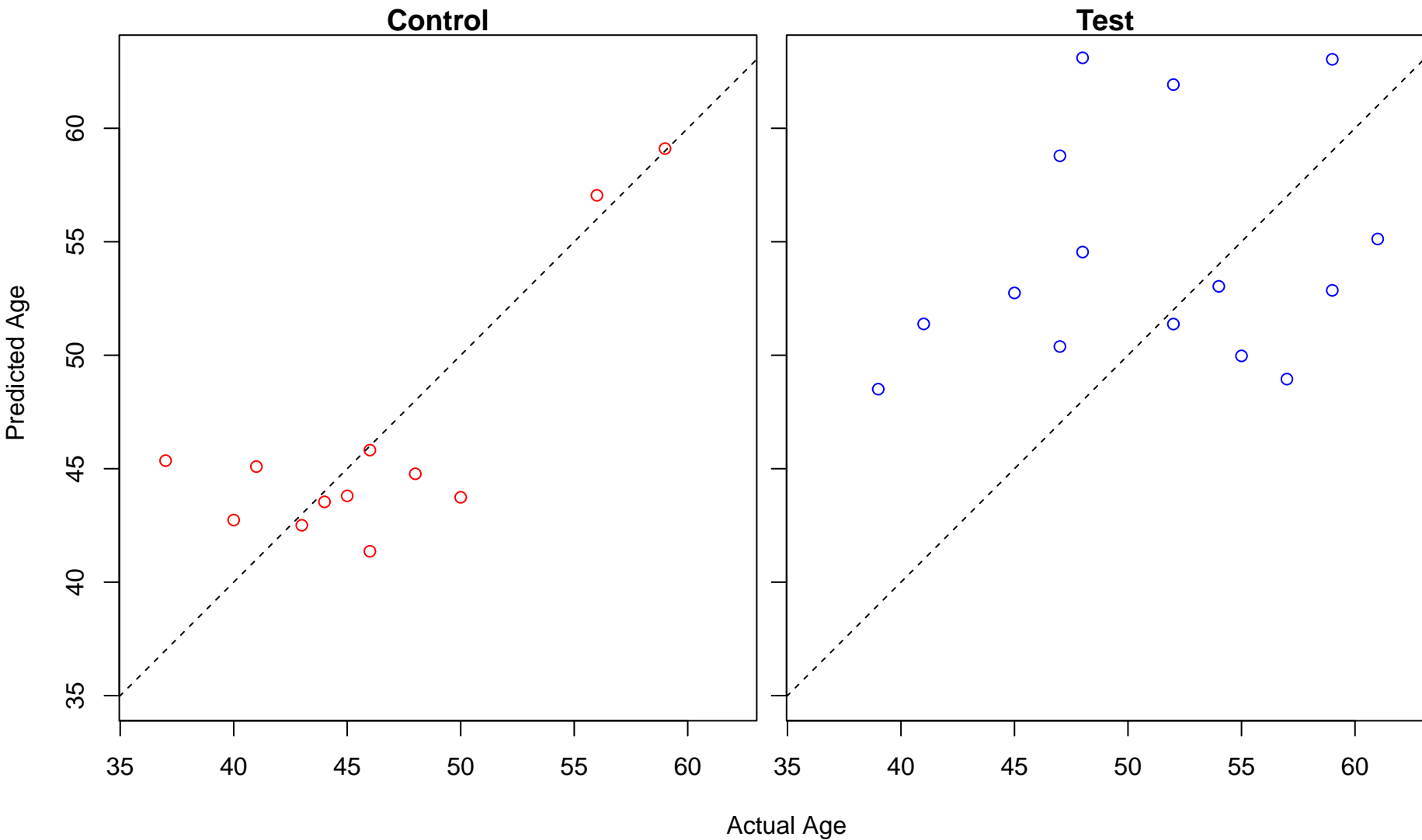
mitochondrial DNA replication (Score: 2.223505)



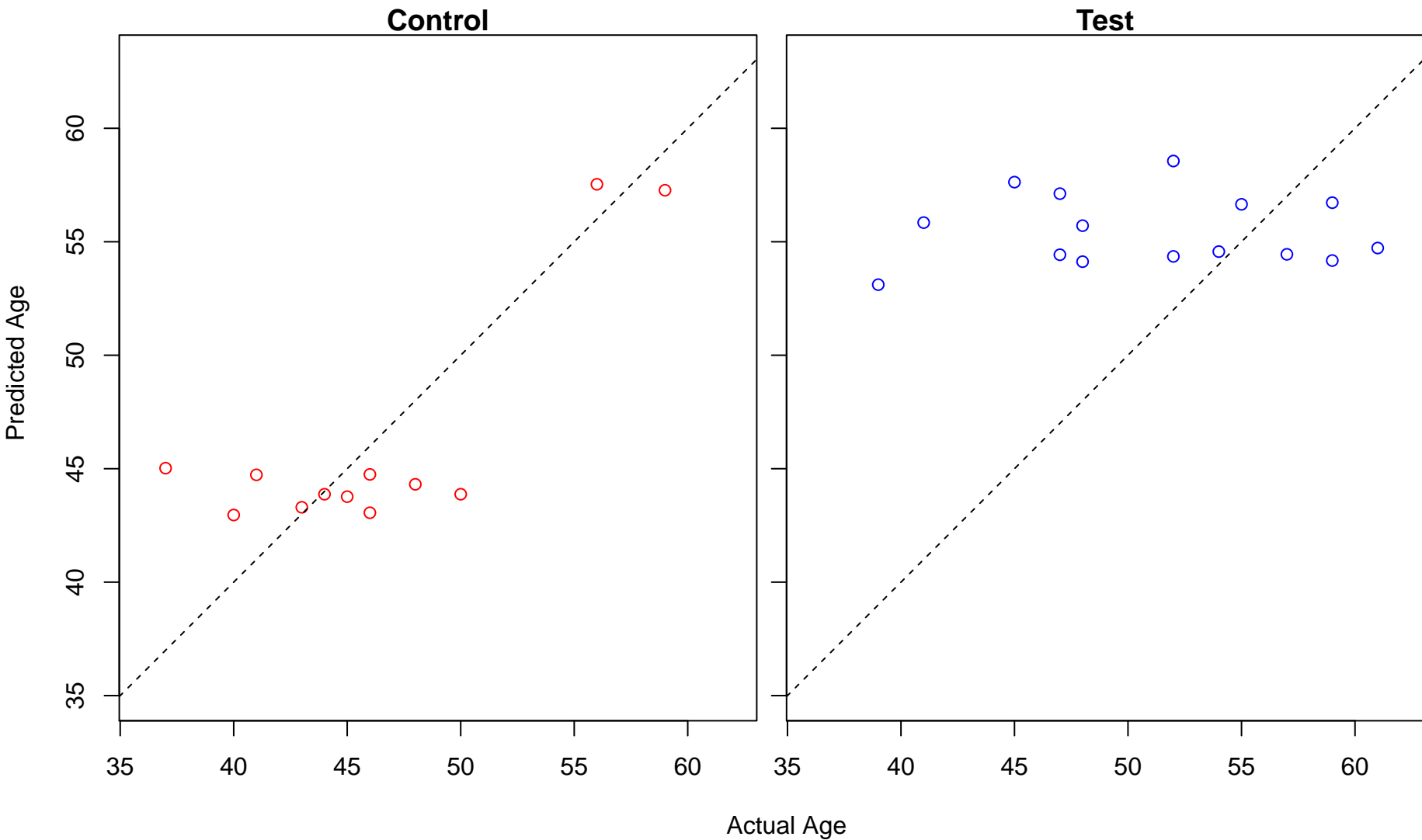
acylglycerol metabolic process (Score: 2.219877)



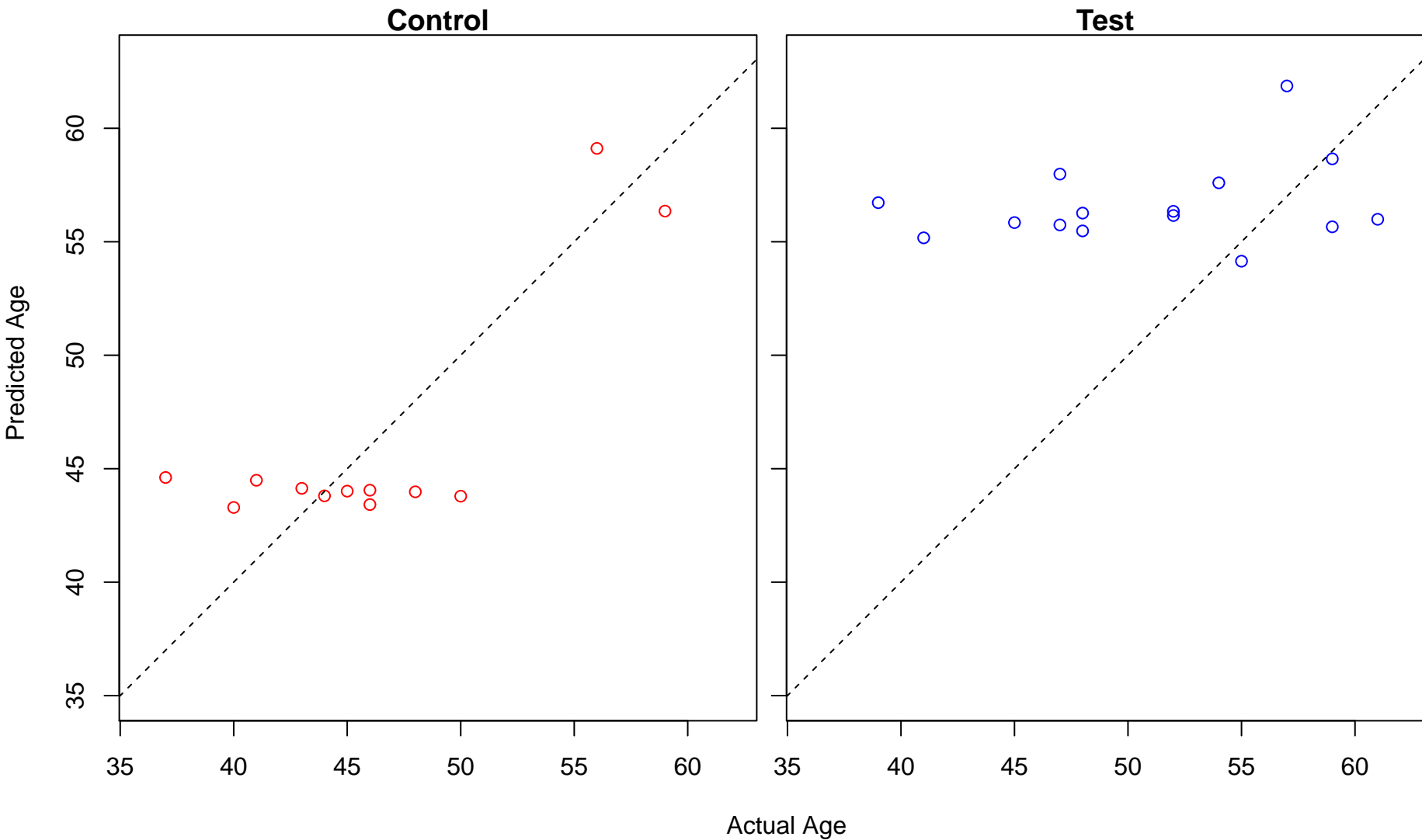
negative regulation of mitotic nuclear division (Score: 2.219597)



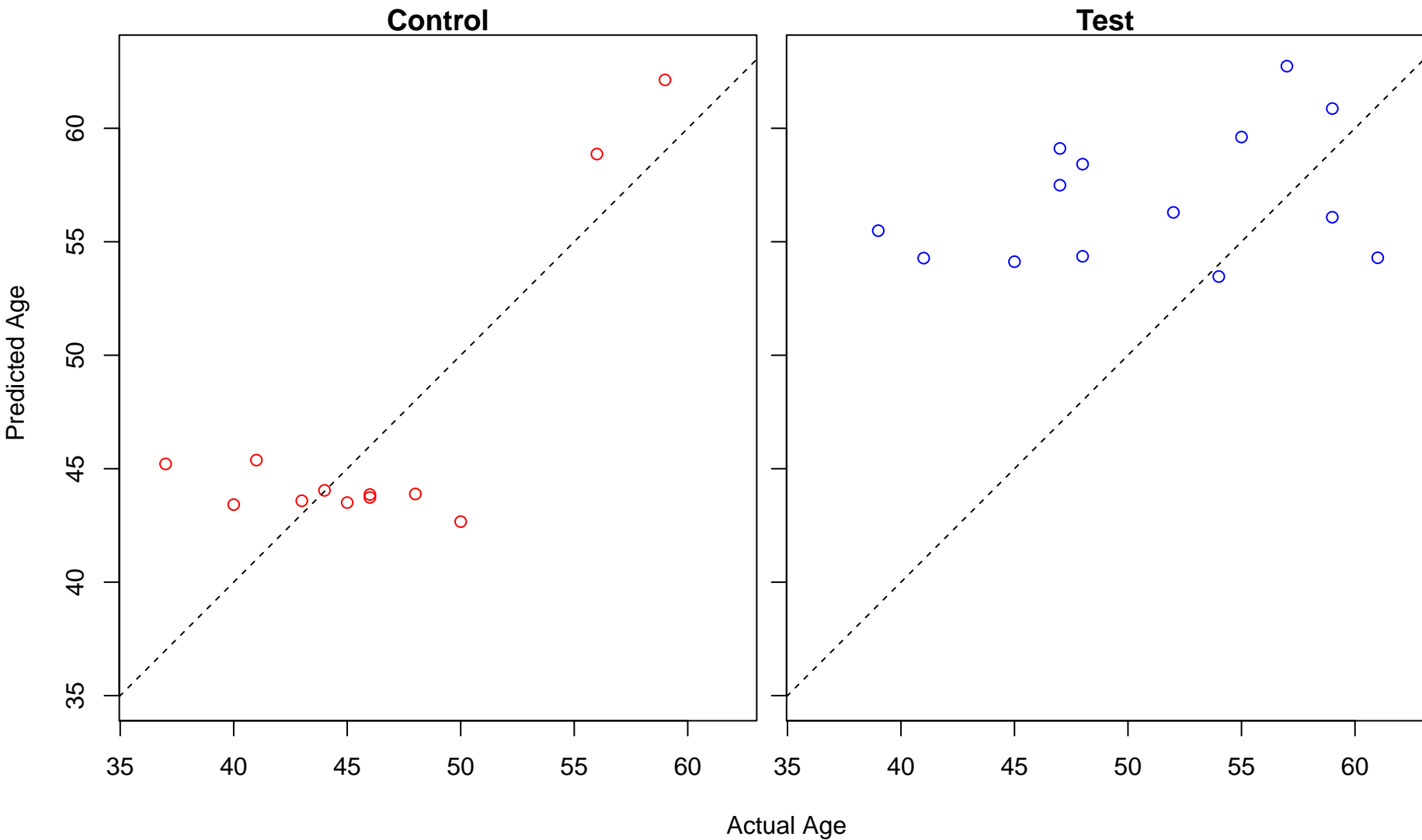
snRNA metabolic process (Score: 2.217796)



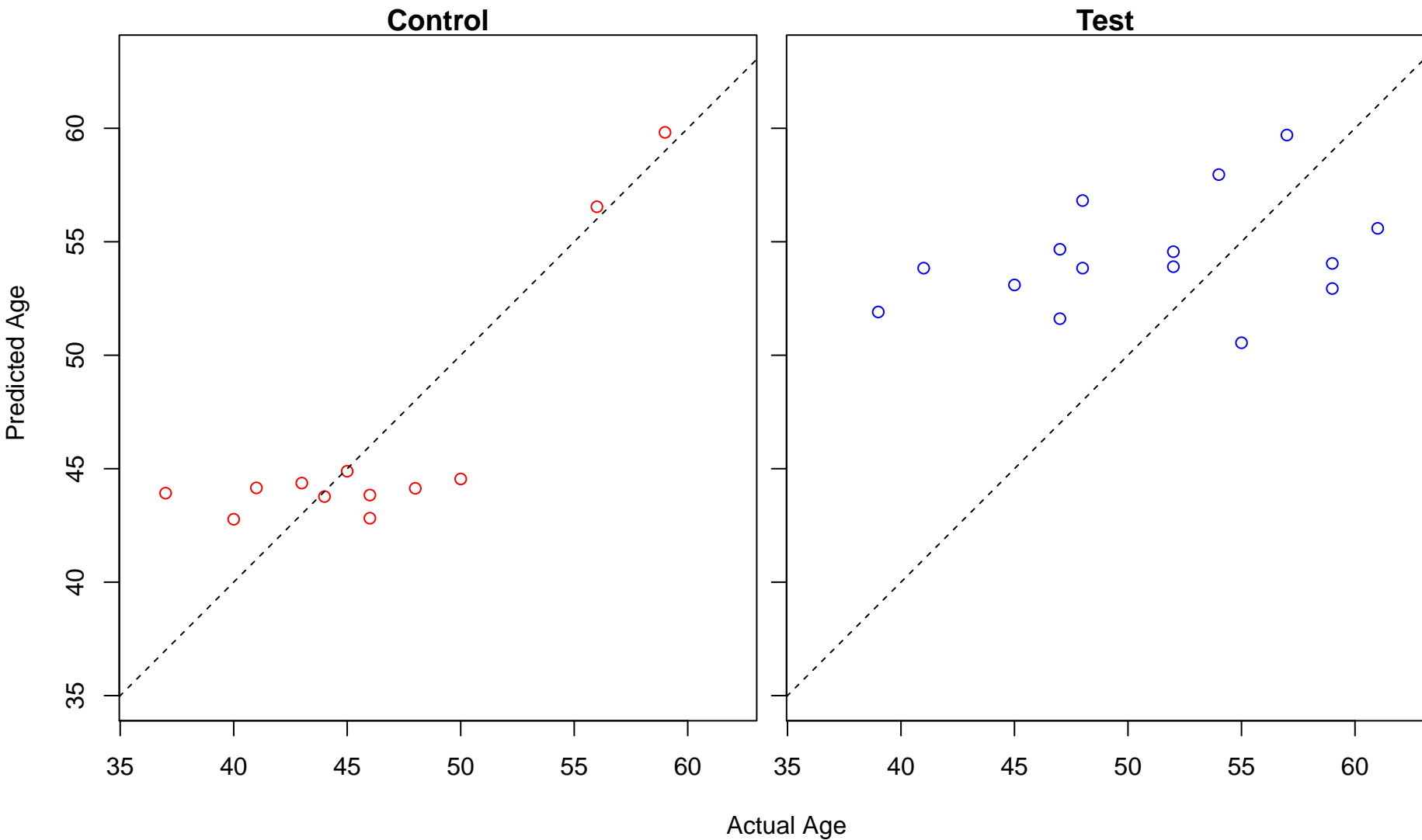
peptidyl-lysine modification (Score: 2.216618)



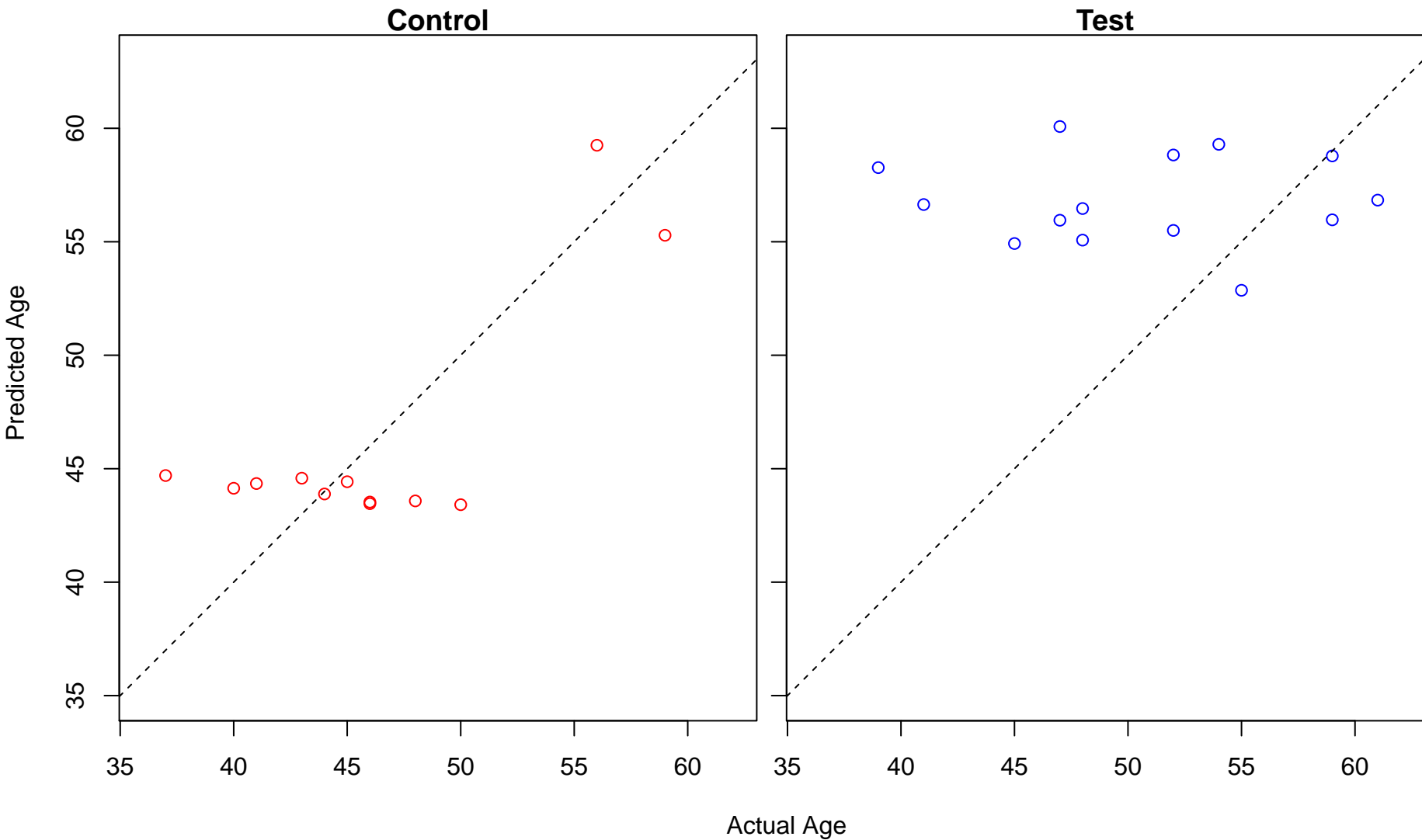
regulation of epithelial to mesenchymal transition (Score: 2.215668)



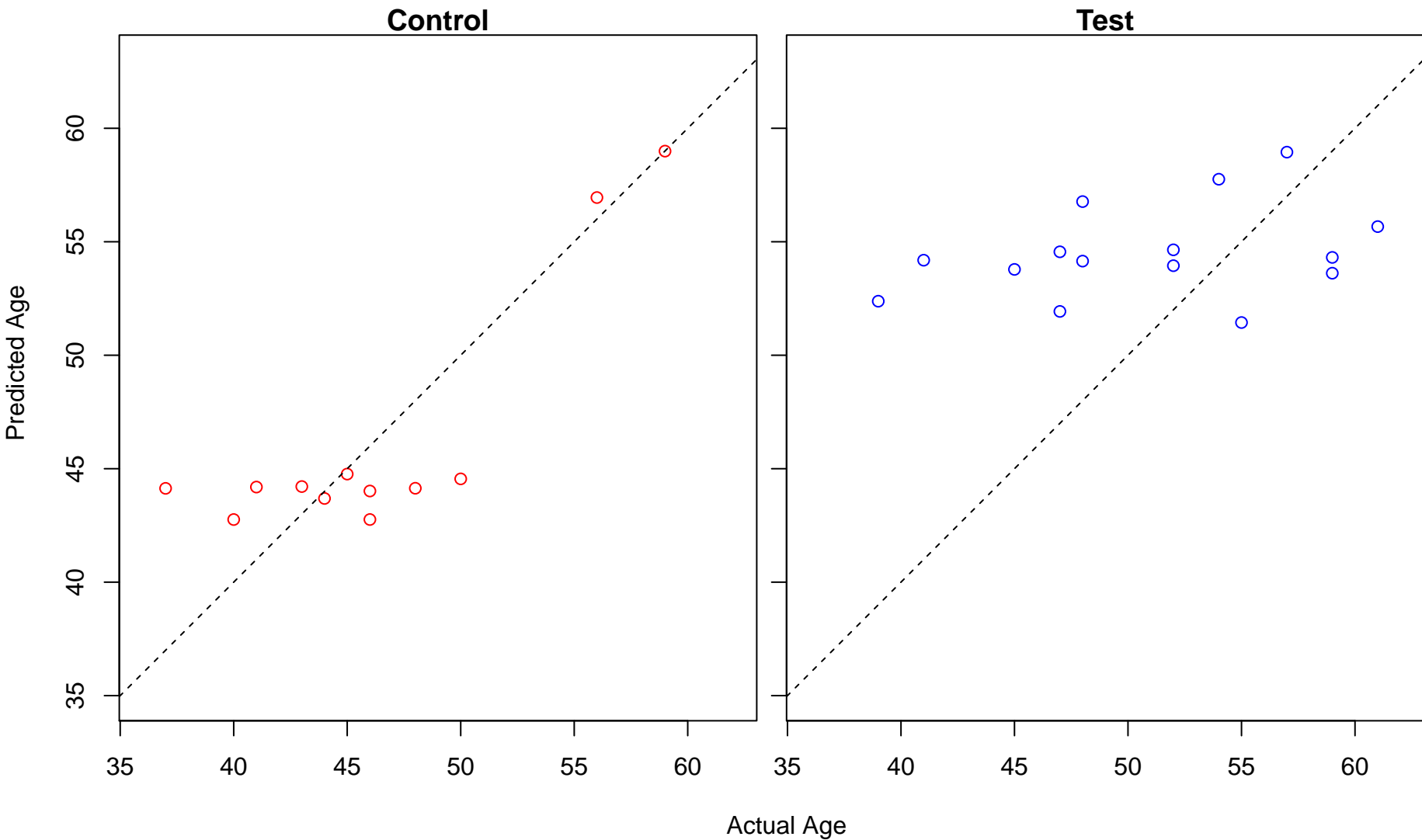
meiosis I (Score: 2.213435)



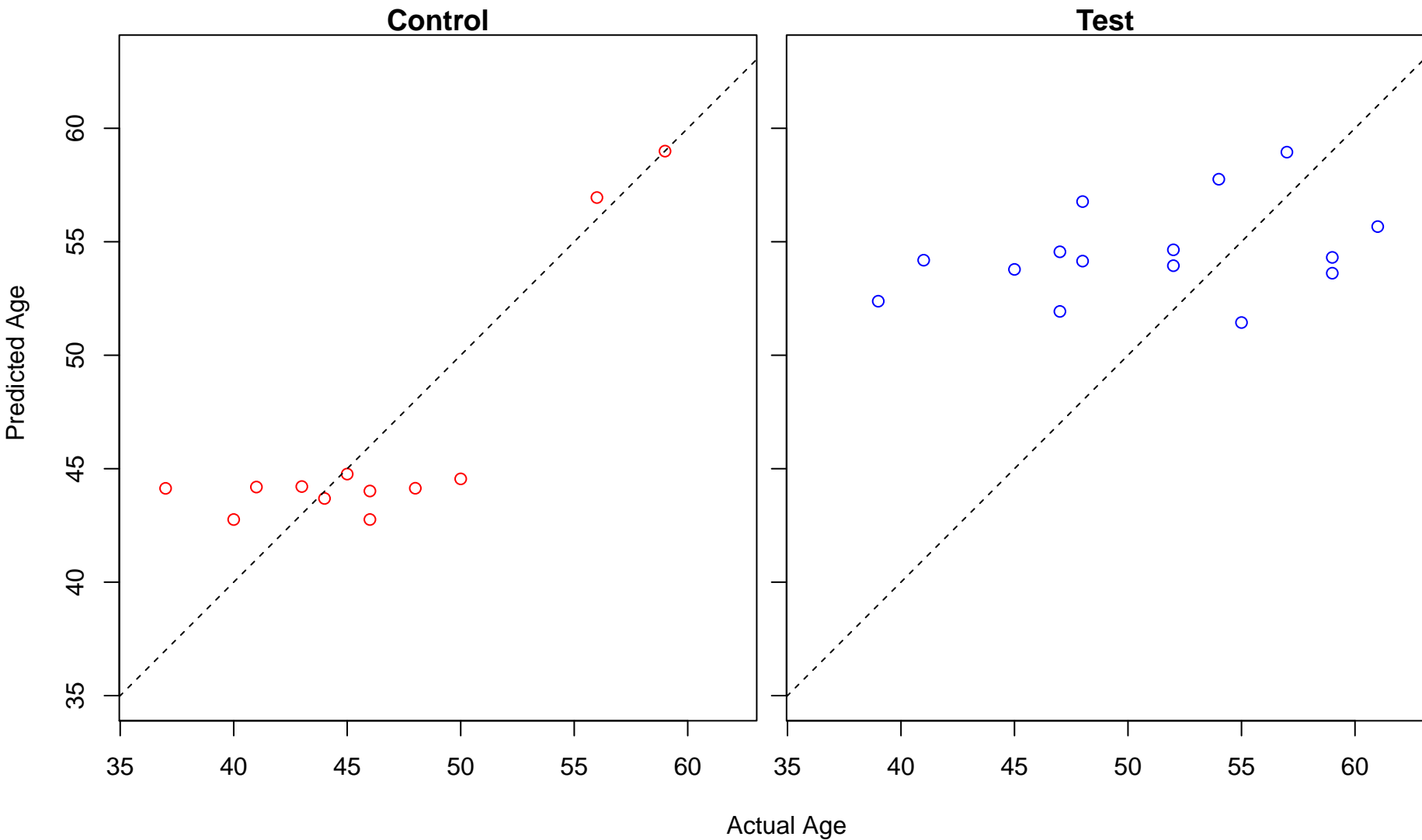
negative regulation of neuron death (Score: 2.213136)



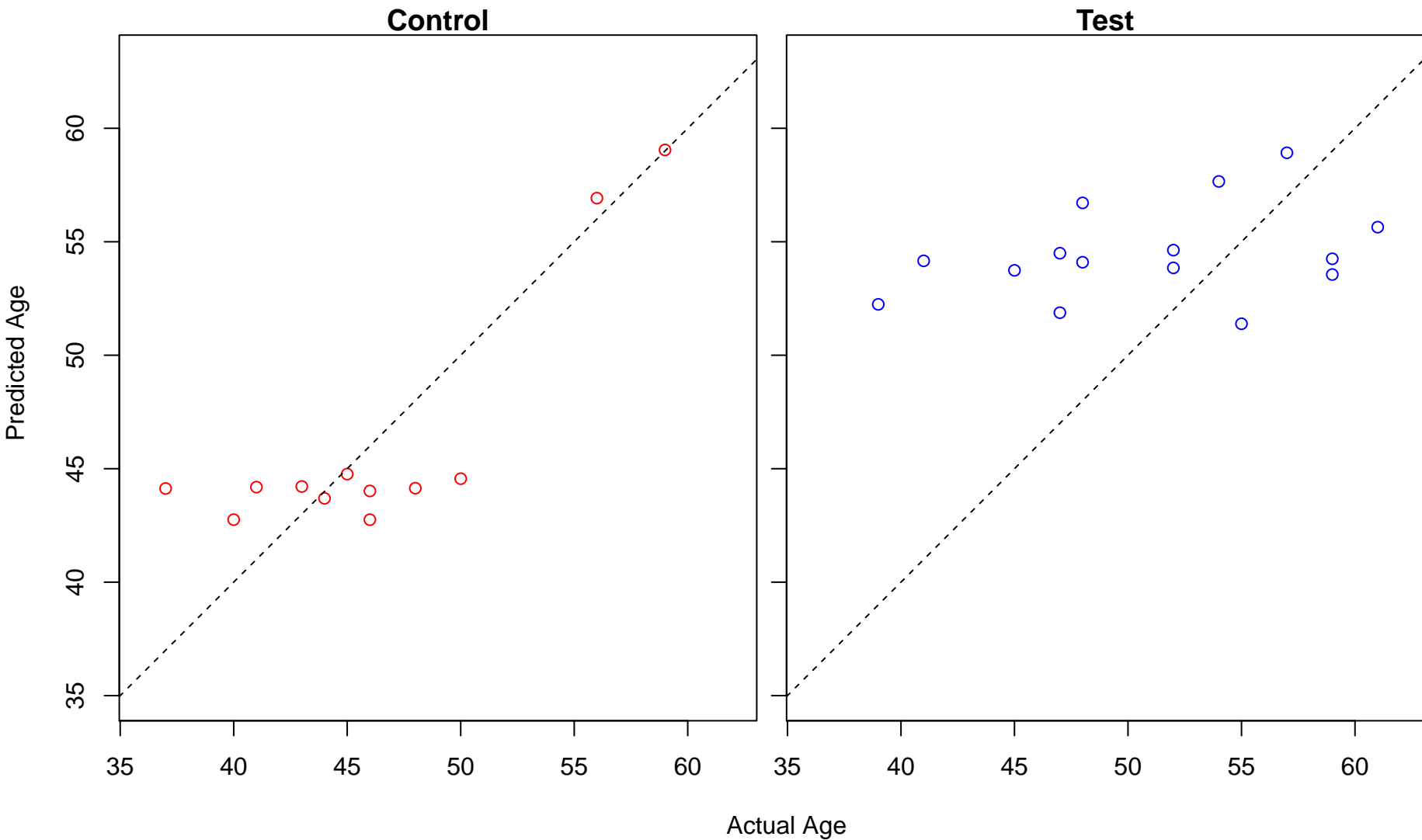
meiotic cell cycle (Score: 2.207937)



meiotic cell cycle process (Score: 2.207937)

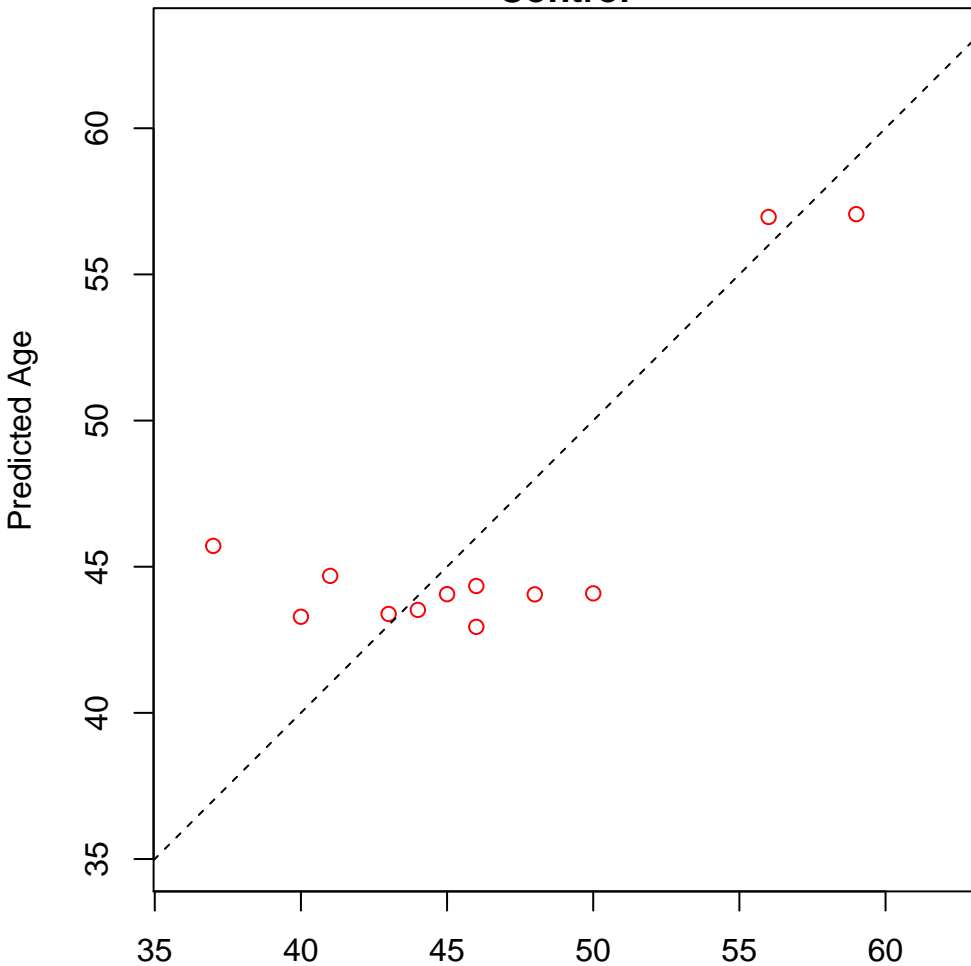


meiotic nuclear division (Score: 2.196461)

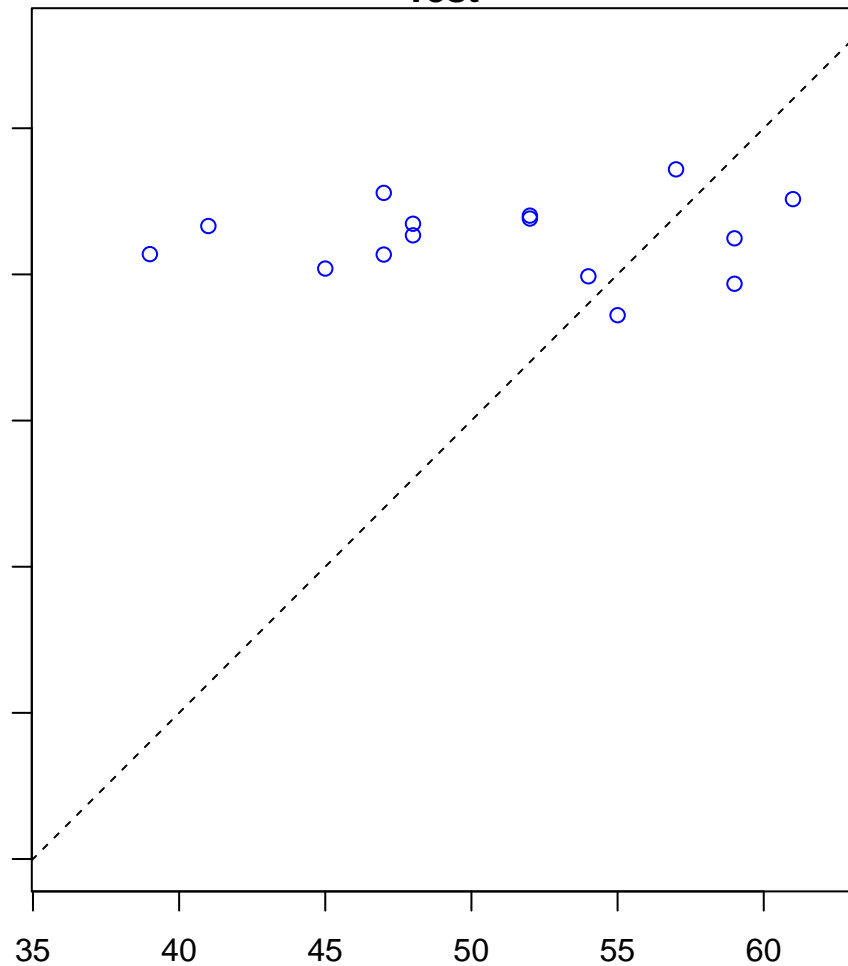


ribonucleoprotein complex localization (Score: 2.189036)

Control

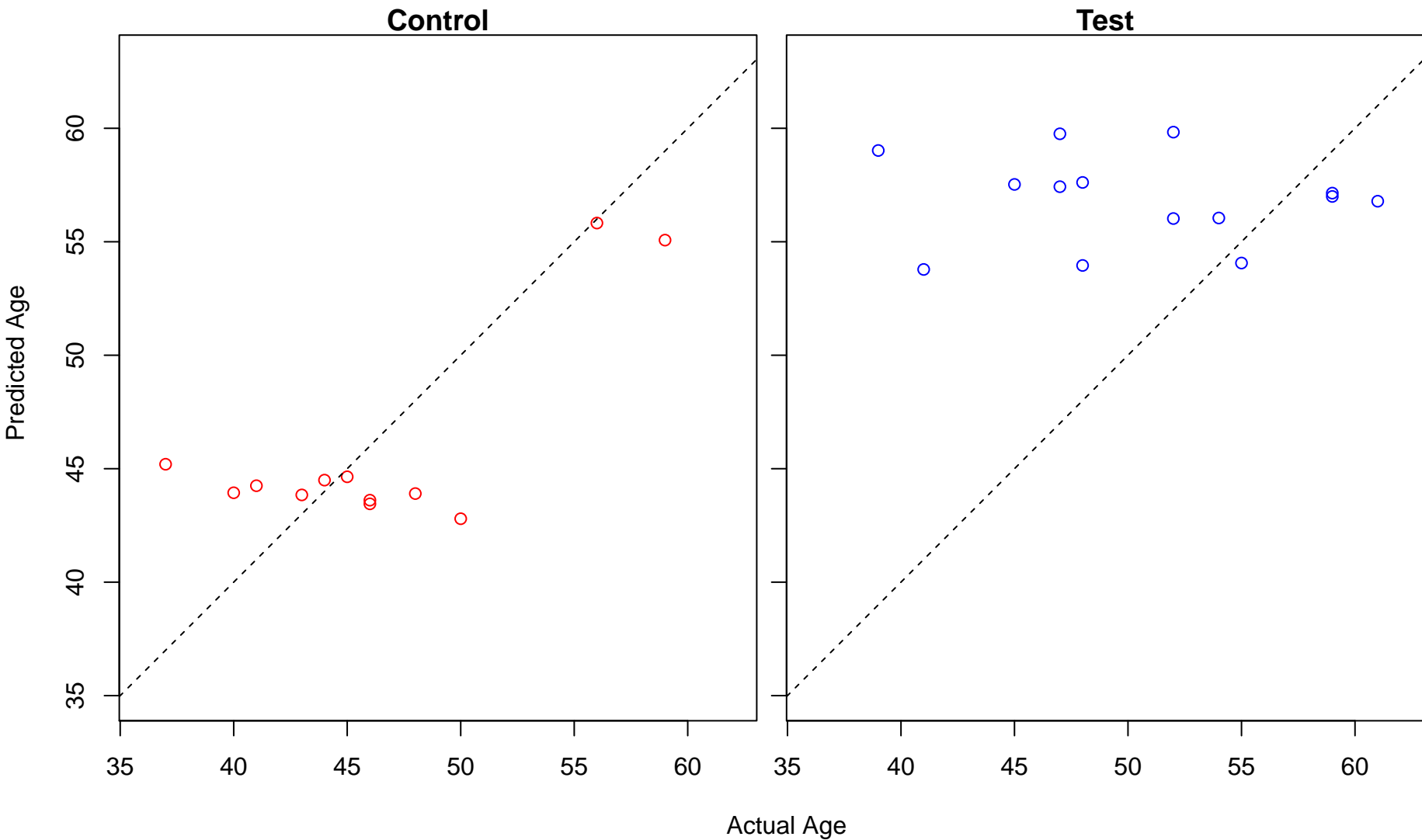


Test

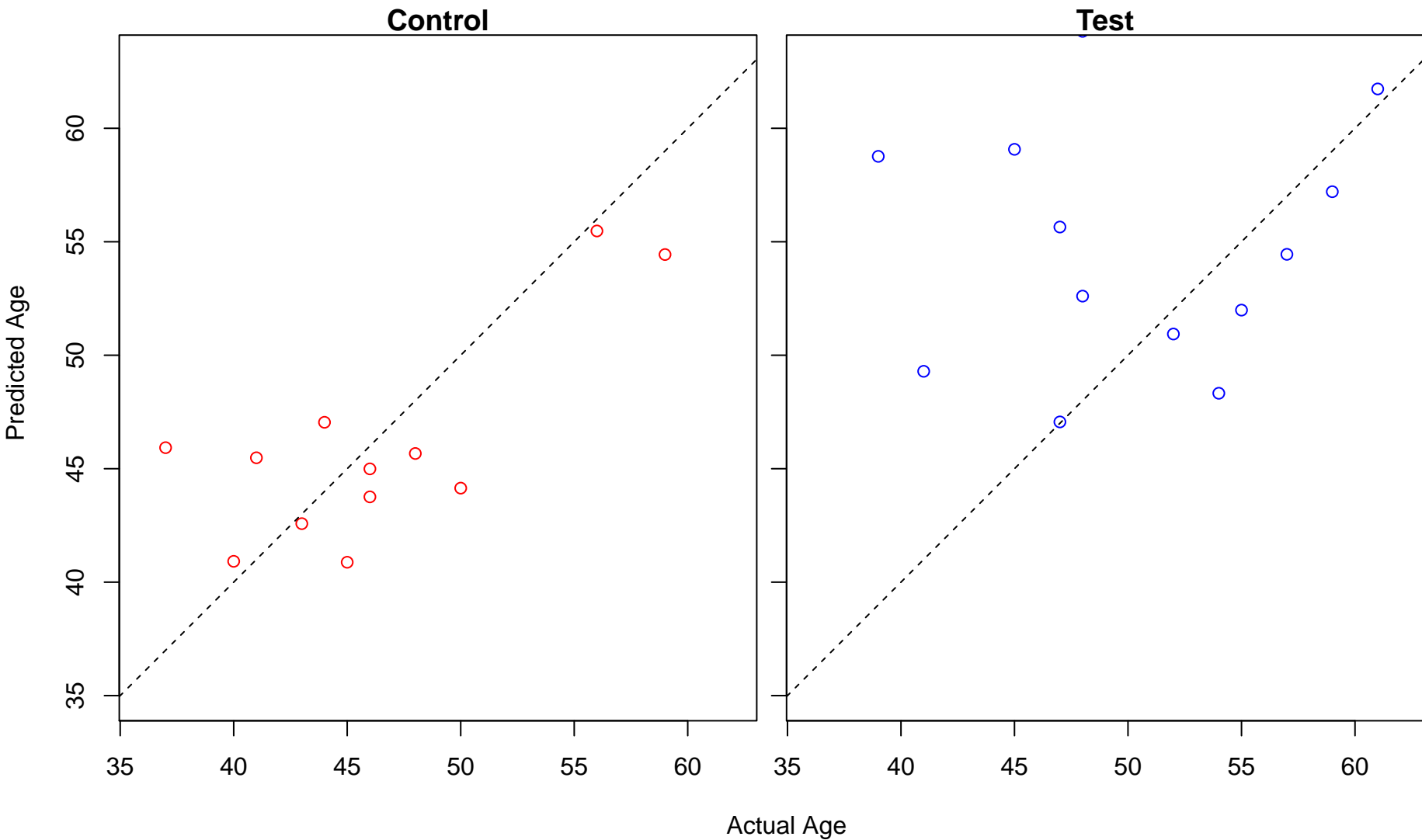


Actual Age

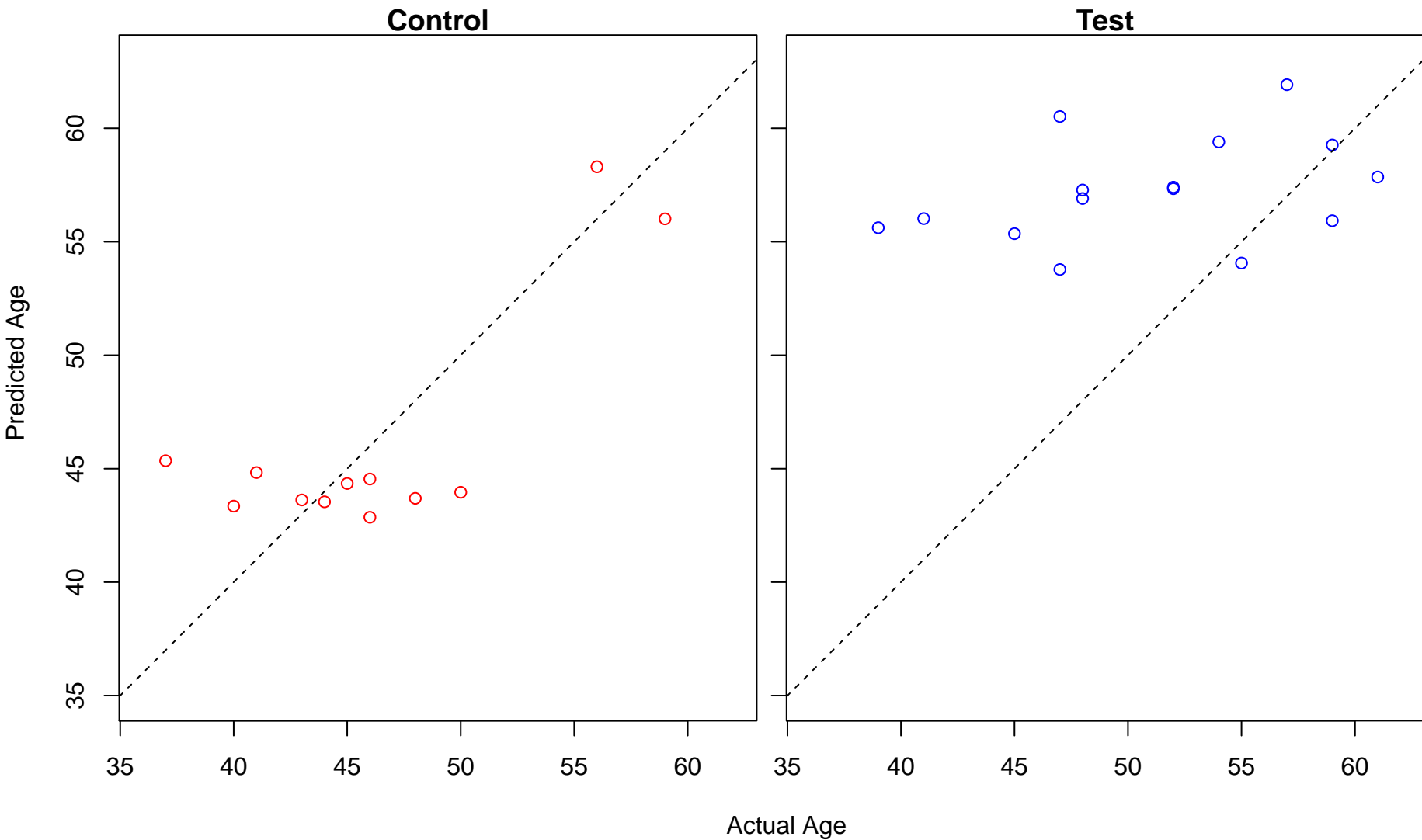
cellular respiration (Score: 2.186152)



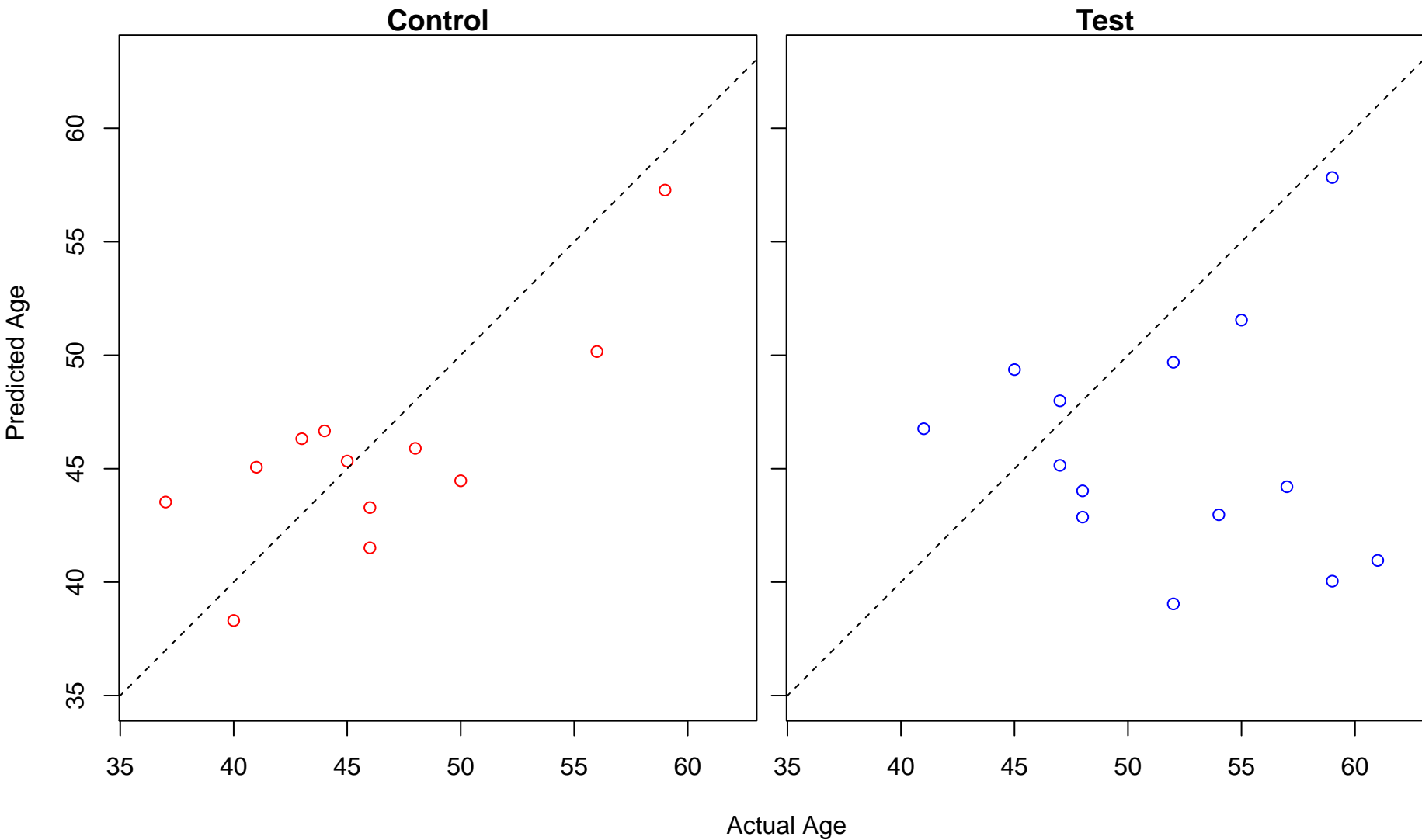
protein localization to chromosome, centromeric region (Score: 2.185697)



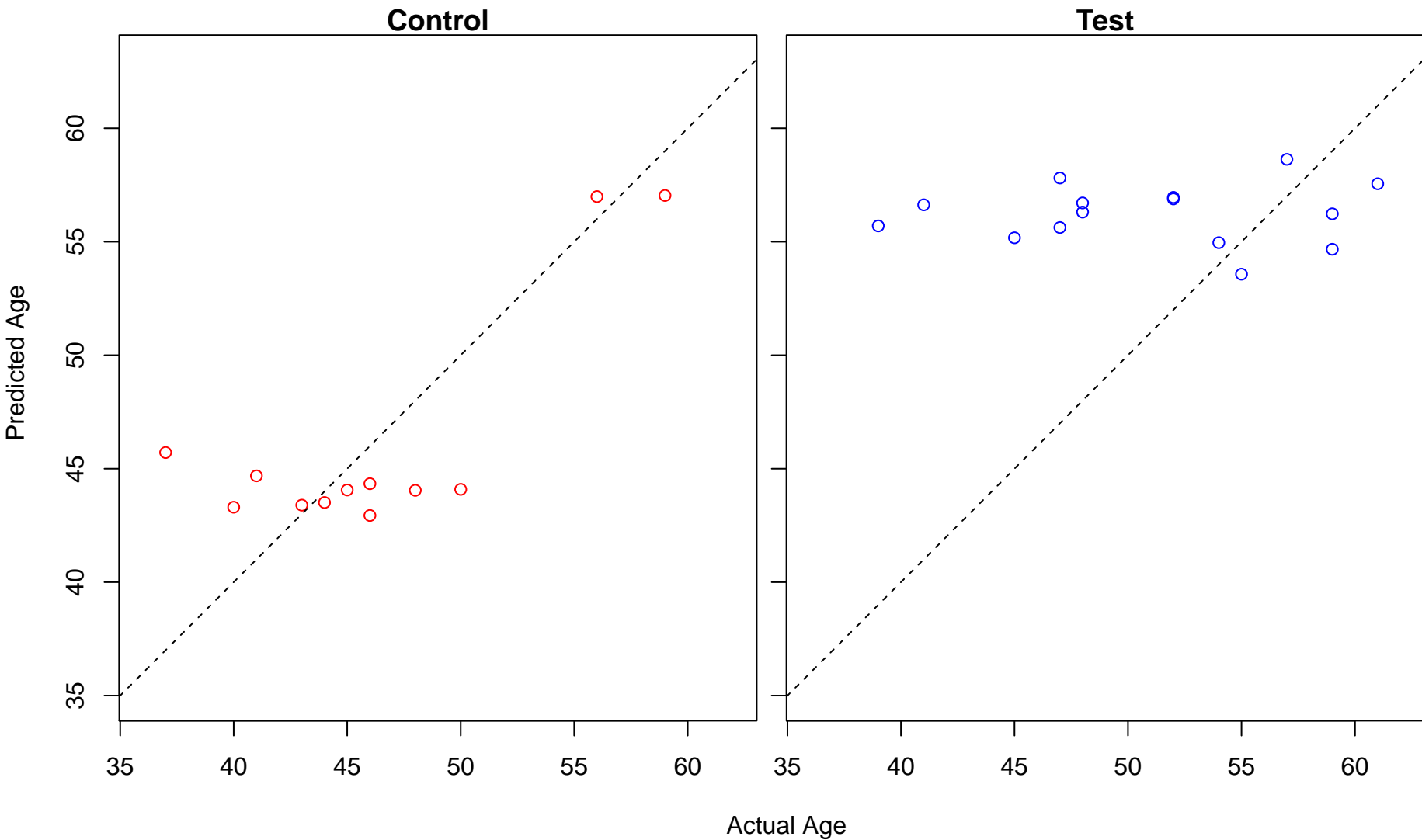
negative regulation of mRNA splicing, via spliceosome (Score: 2.184250)



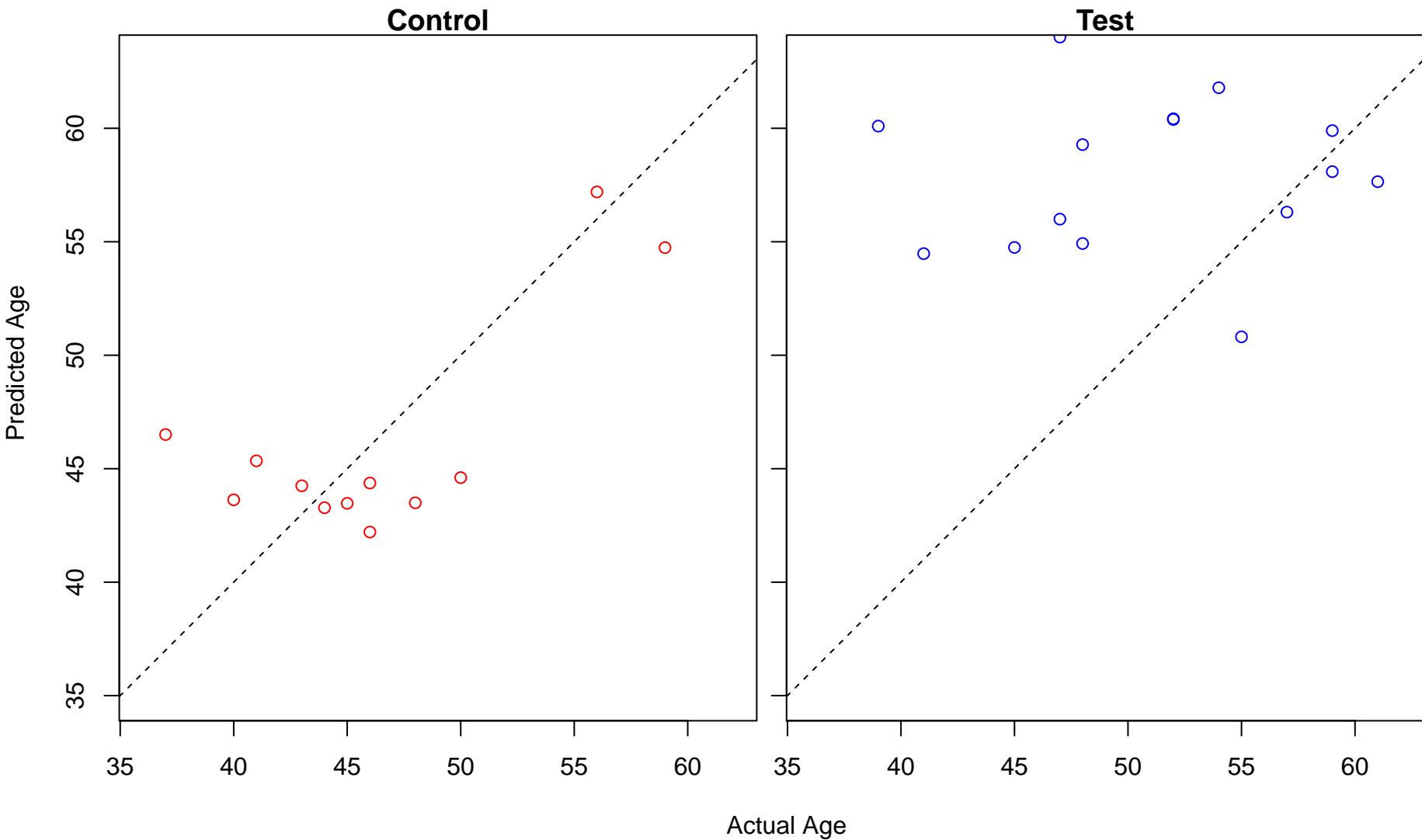
peptide metabolic process (Score: 2.181884)



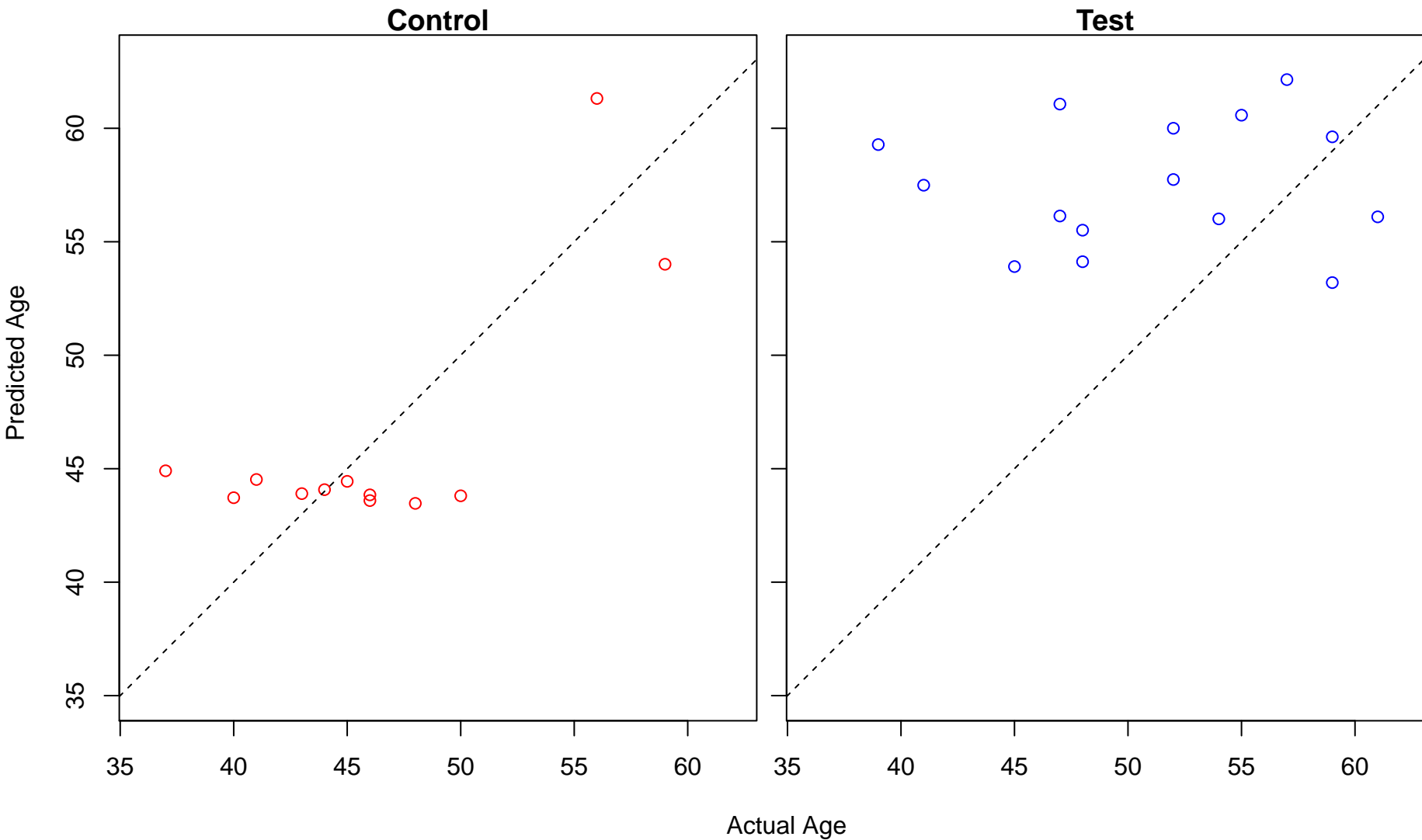
ribonucleoprotein complex export from nucleus (Score: 2.180835)



cardiac septum development (Score: 2.156205)

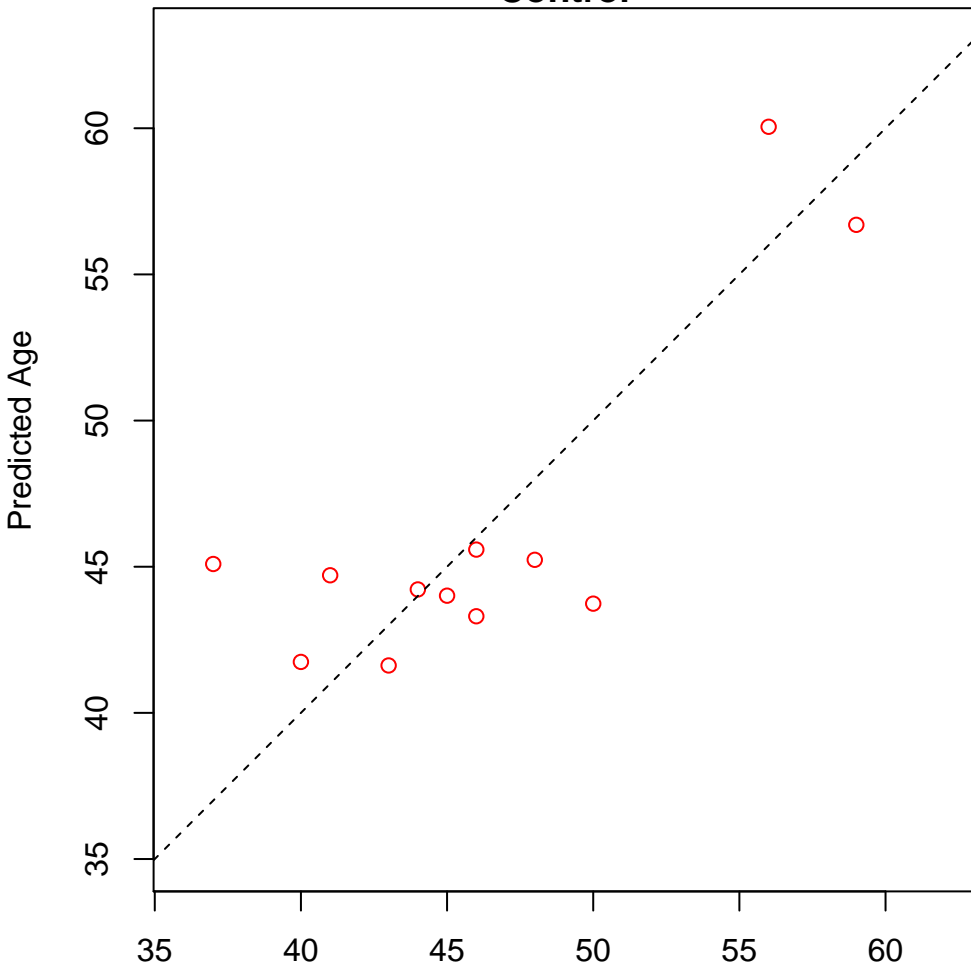


DNA conformation change (Score: 2.153258)

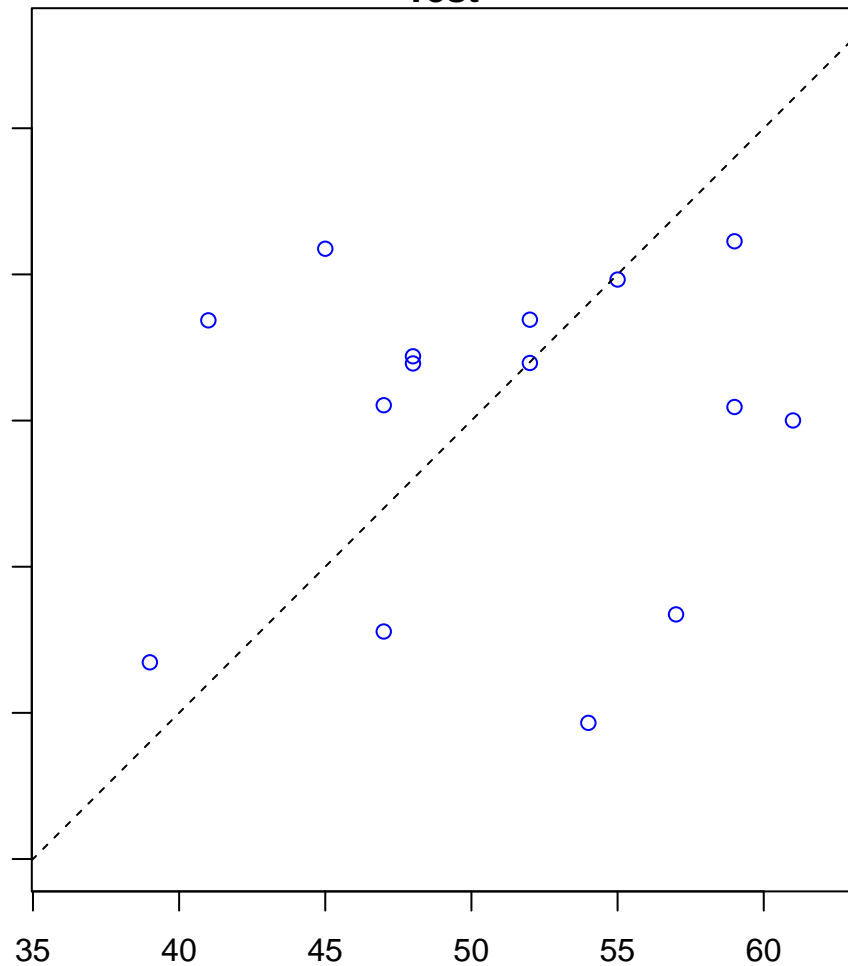


mitochondrial translational termination (Score: 2.149294)

Control

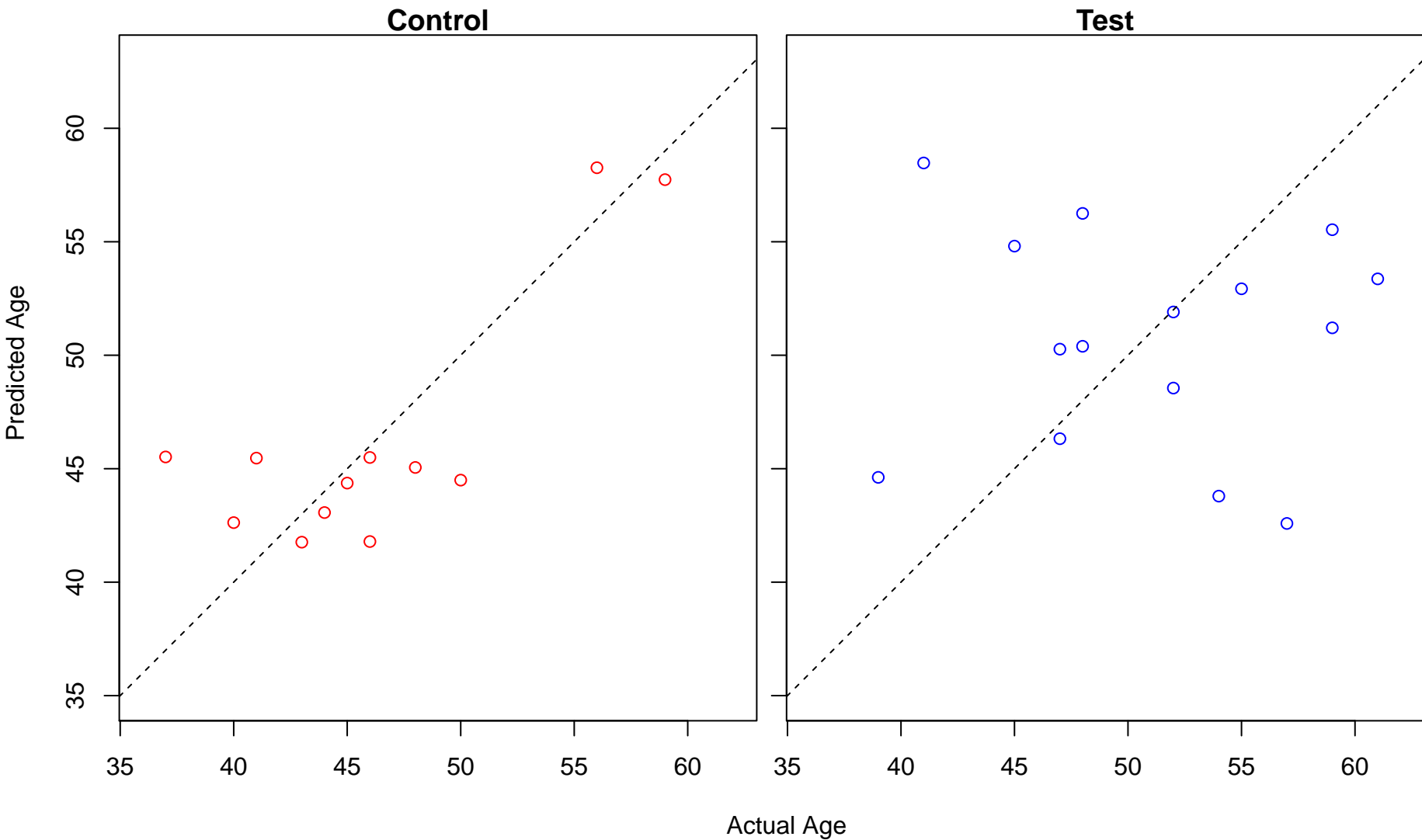


Test

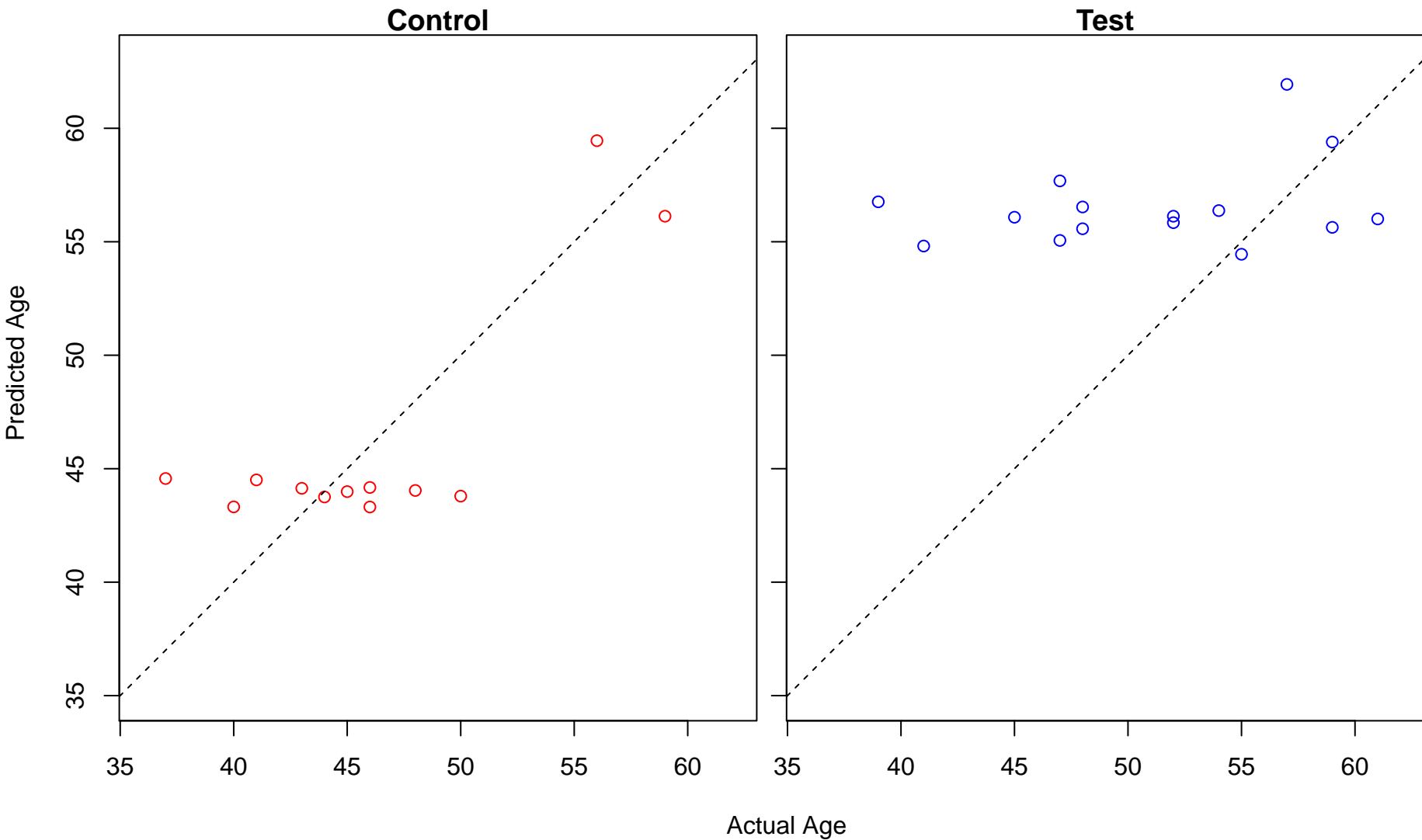


Actual Age

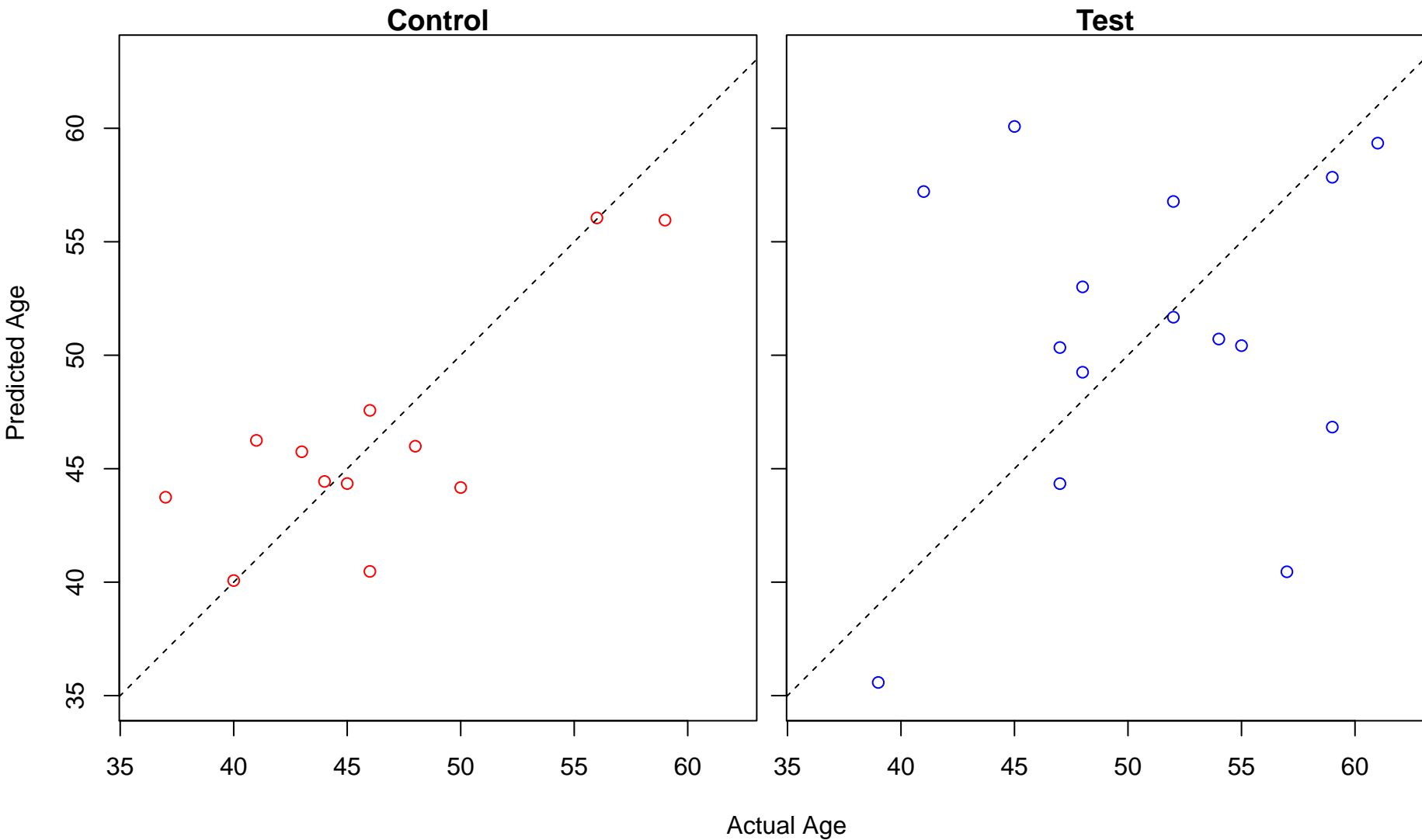
posttranslational protein targeting to membrane (Score: 2.141452)



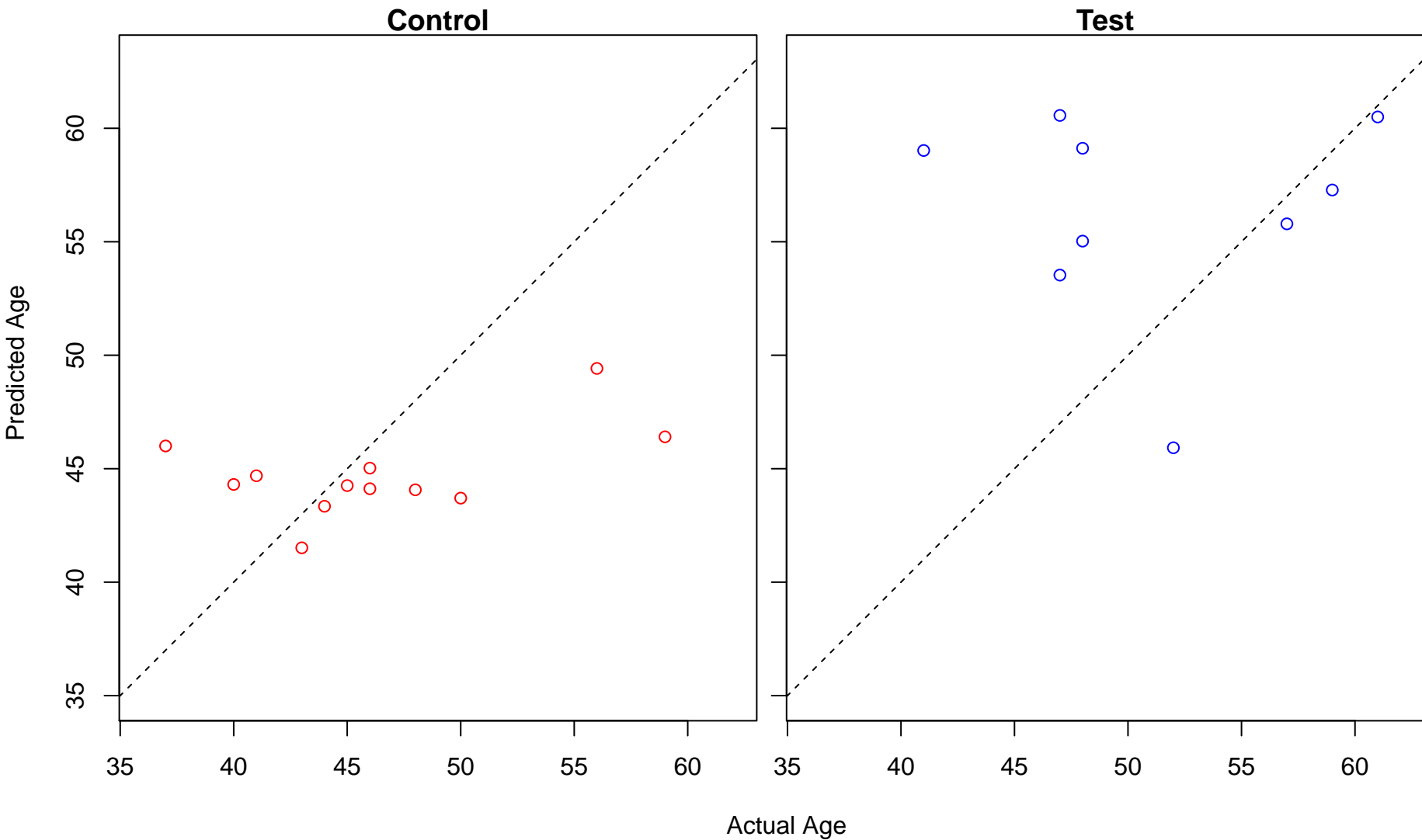
protein sumoylation (Score: 2.141110)



regulation of secretion (Score: 2.140551)

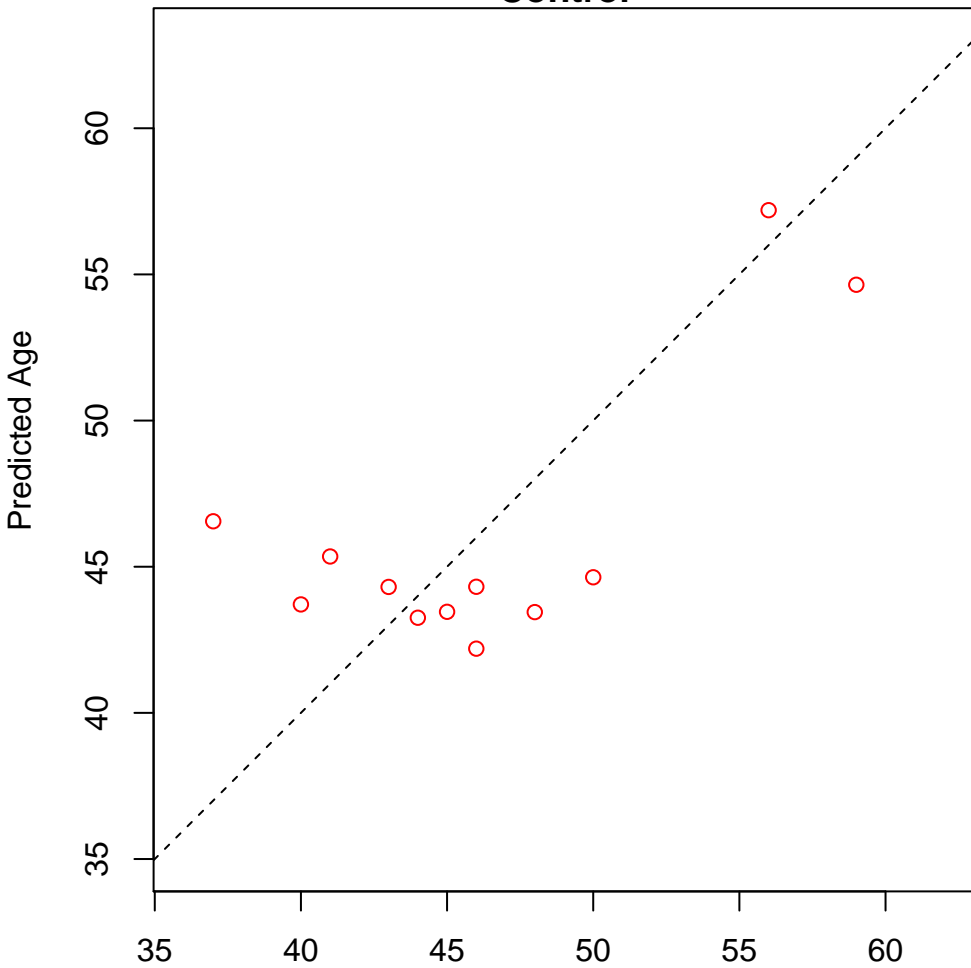


G-protein coupled purinergic receptor signaling pathway (Score: 2.133771)

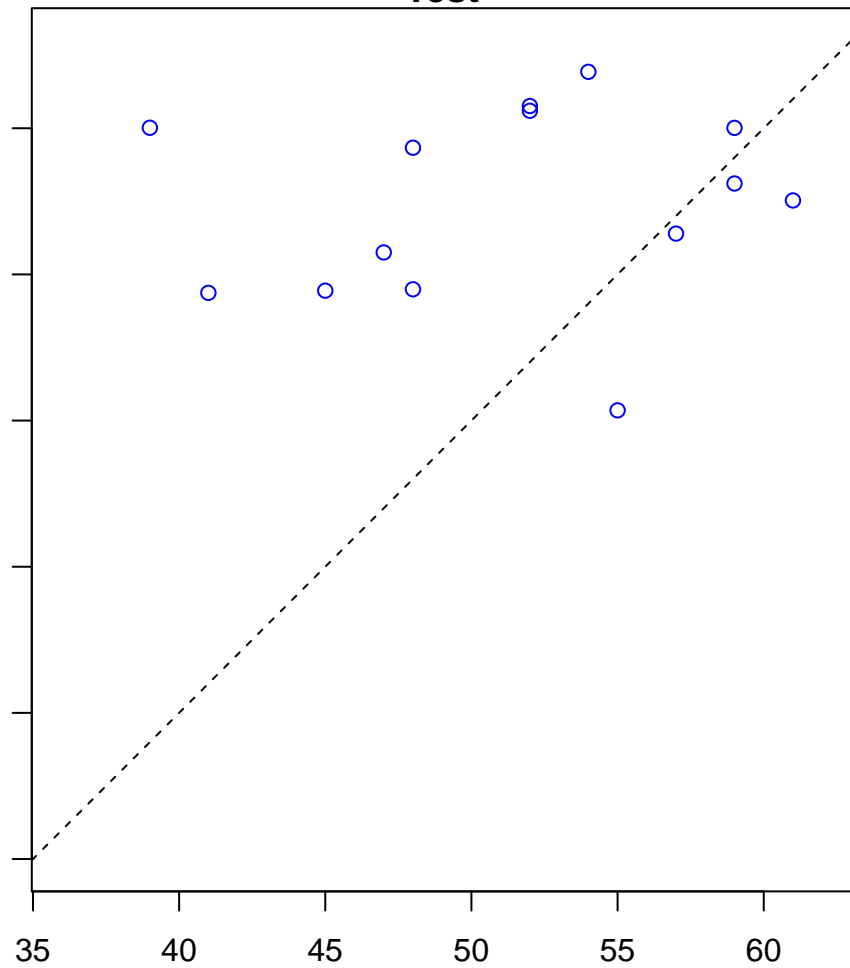


cardiac septum morphogenesis (Score: 2.131633)

Control

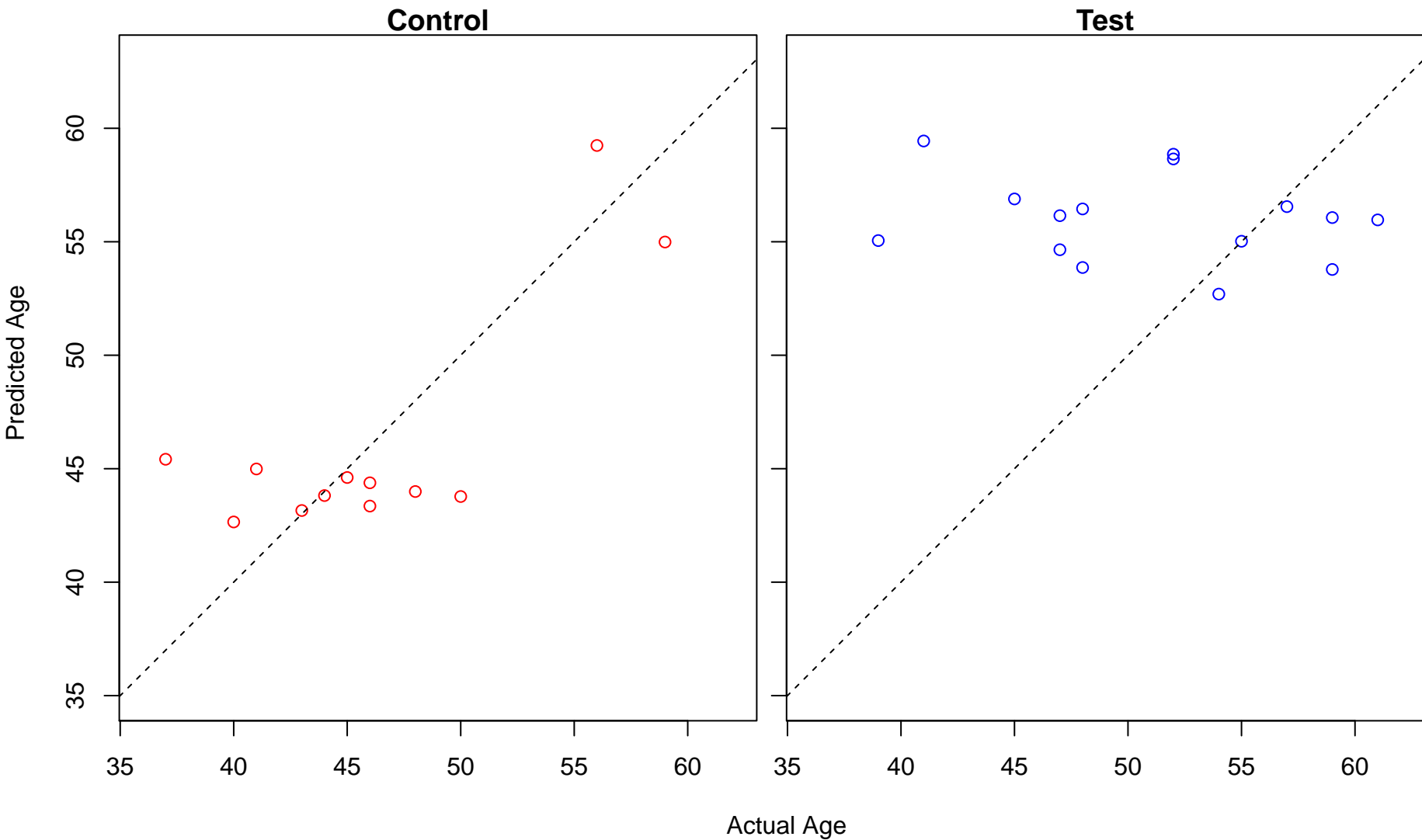


Test



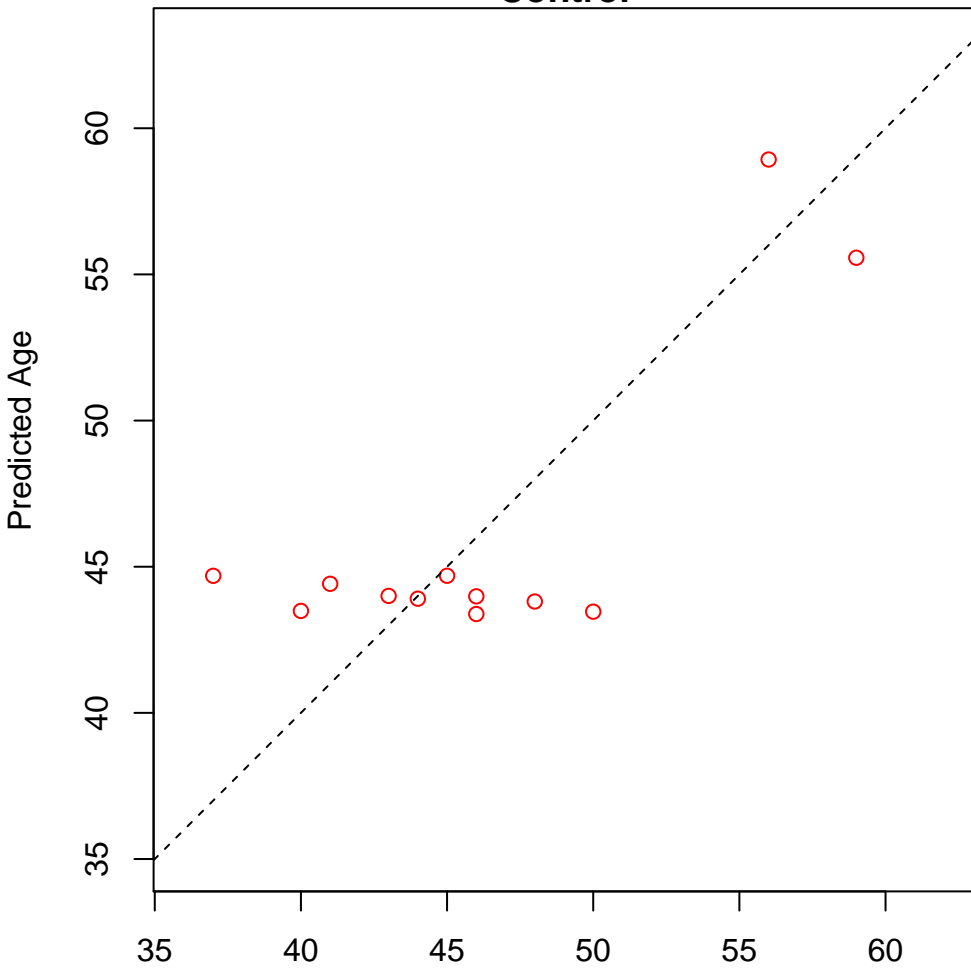
Actual Age

tissue remodeling (Score: 2.126521)

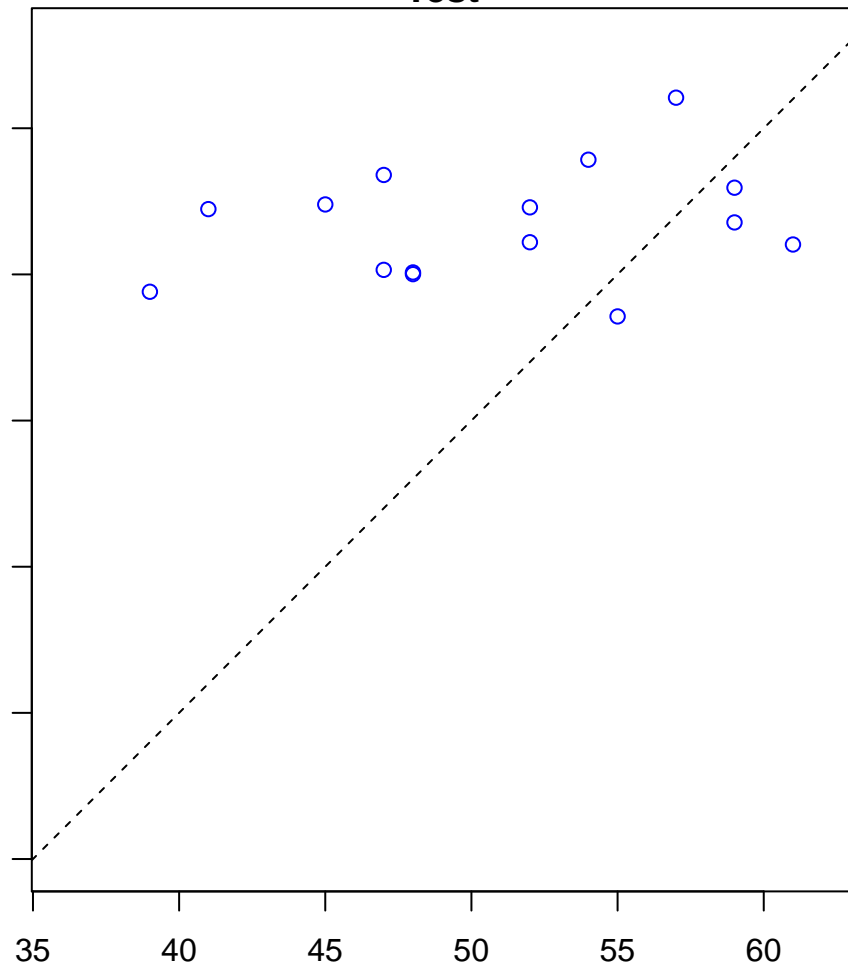


phosphatidylglycerol metabolic process (Score: 2.12350)

Control

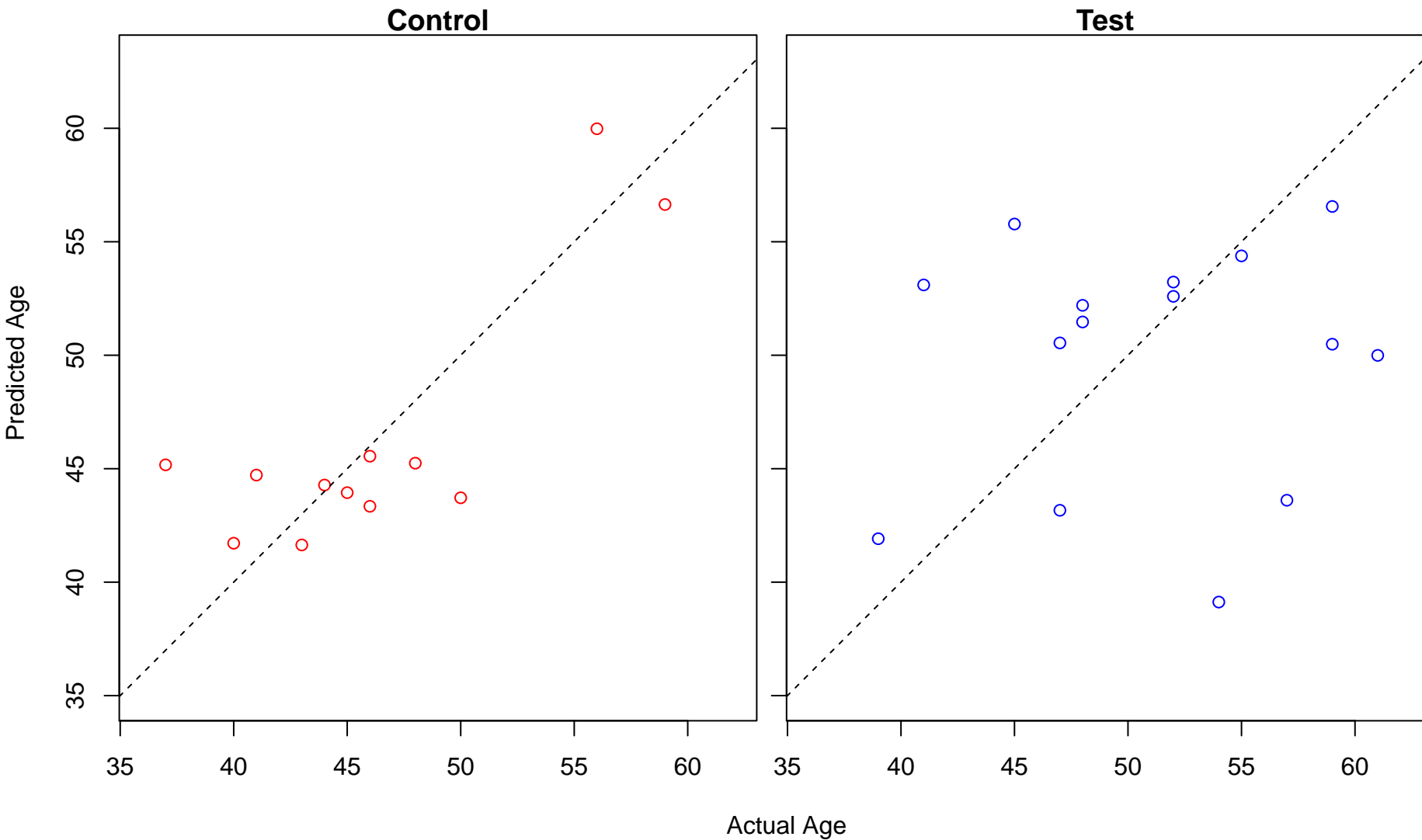


Test



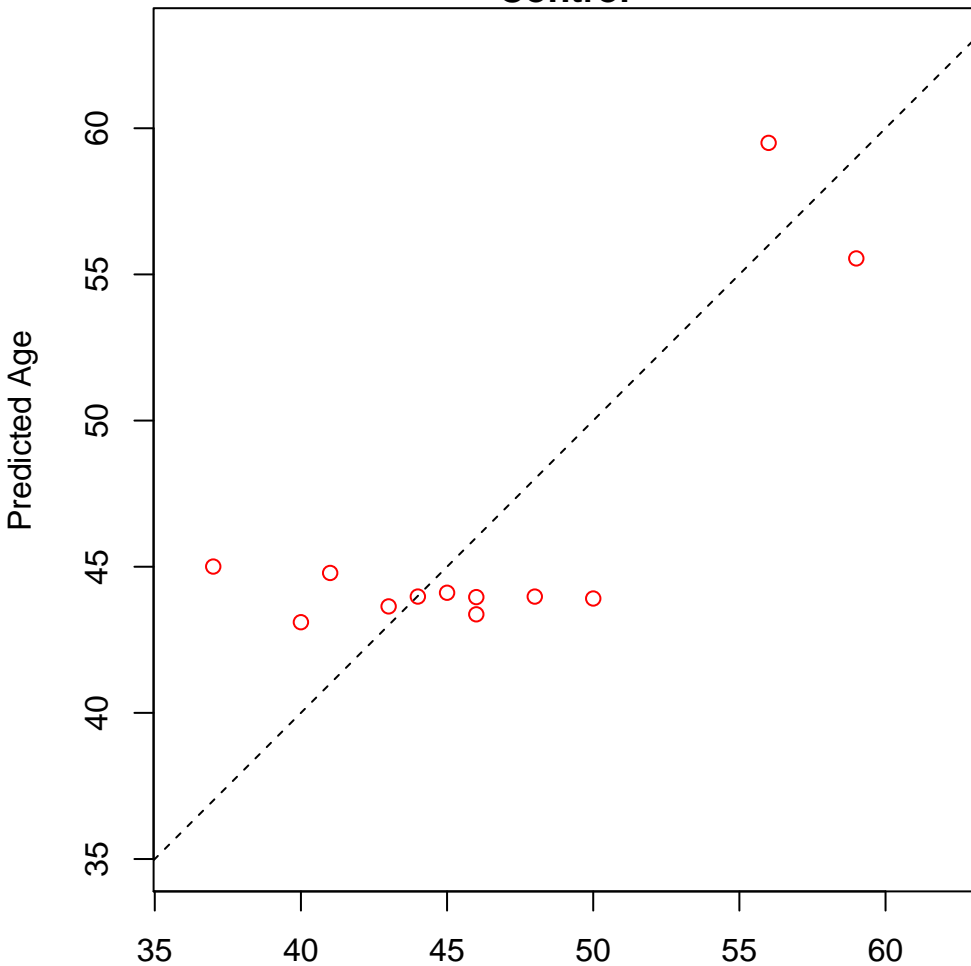
Actual Age

mitochondrial translation (Score: 2.121160)

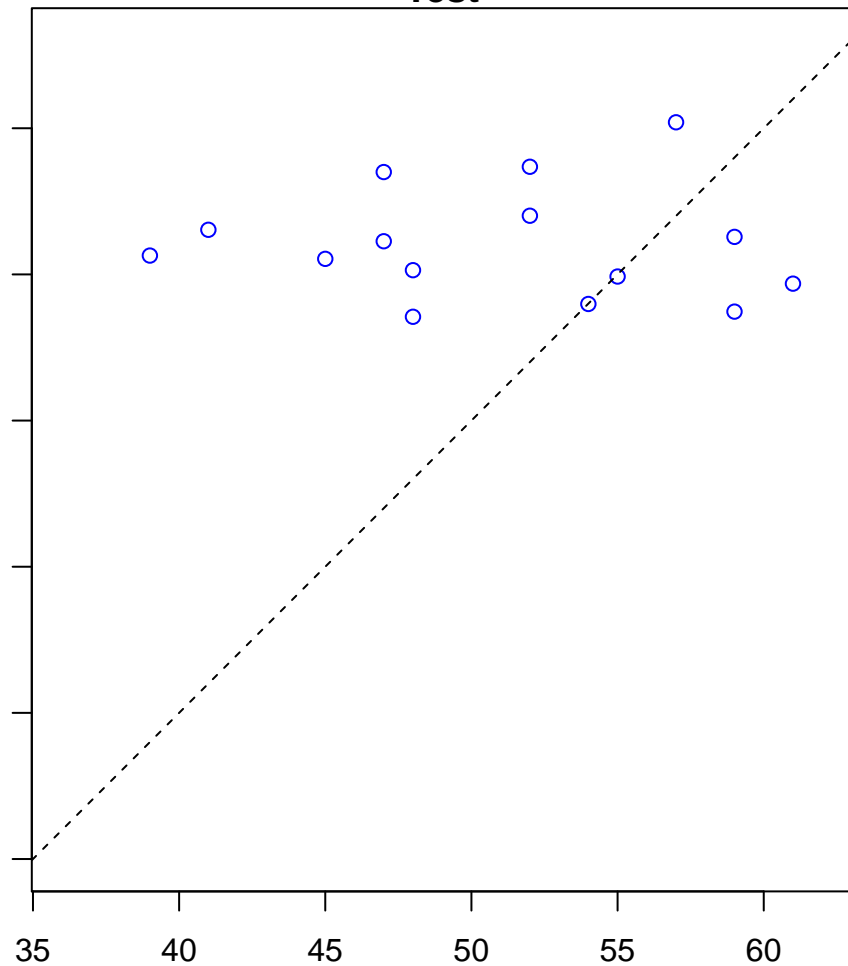


positive regulation of cell differentiation (Score: 2.117162)

Control

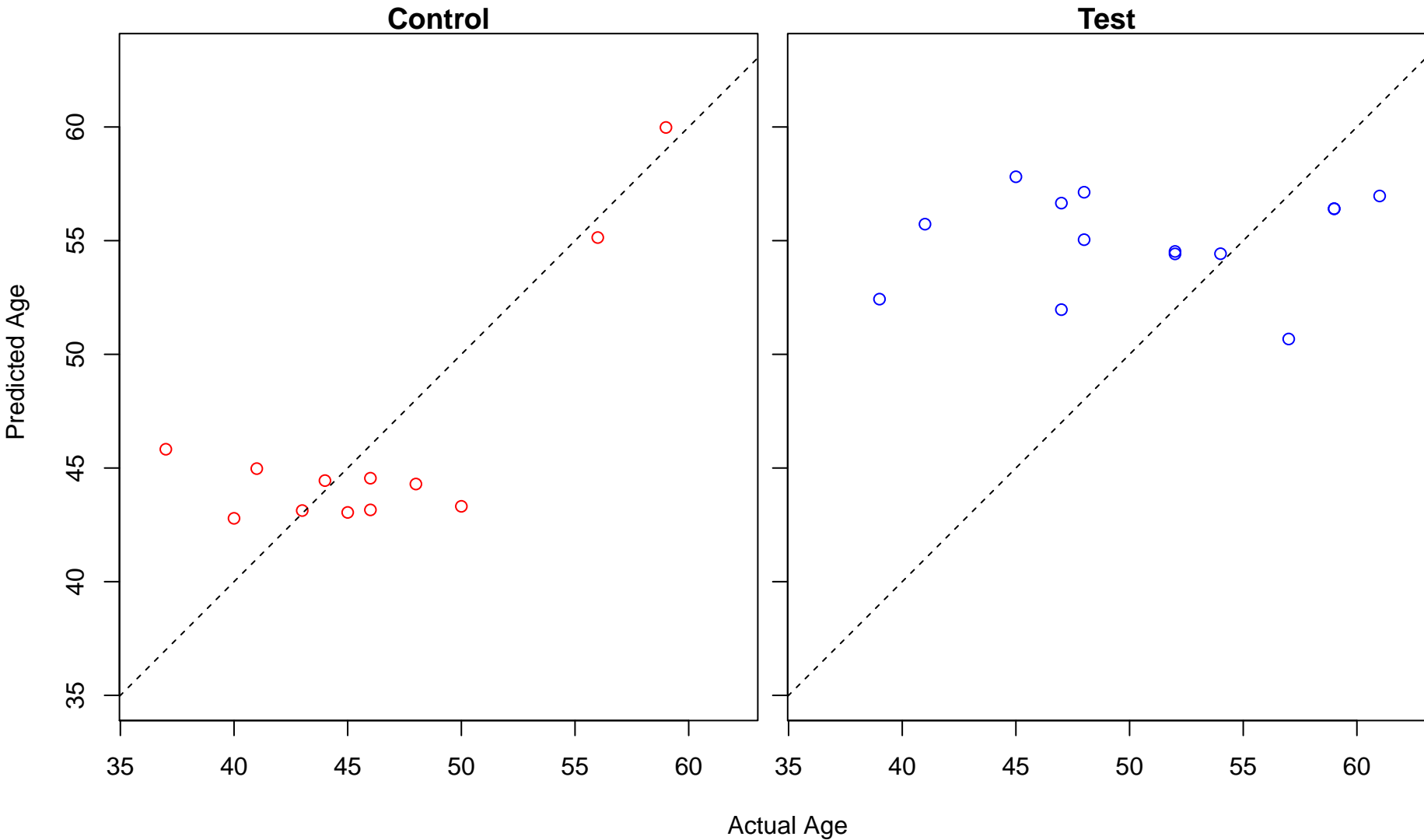


Test

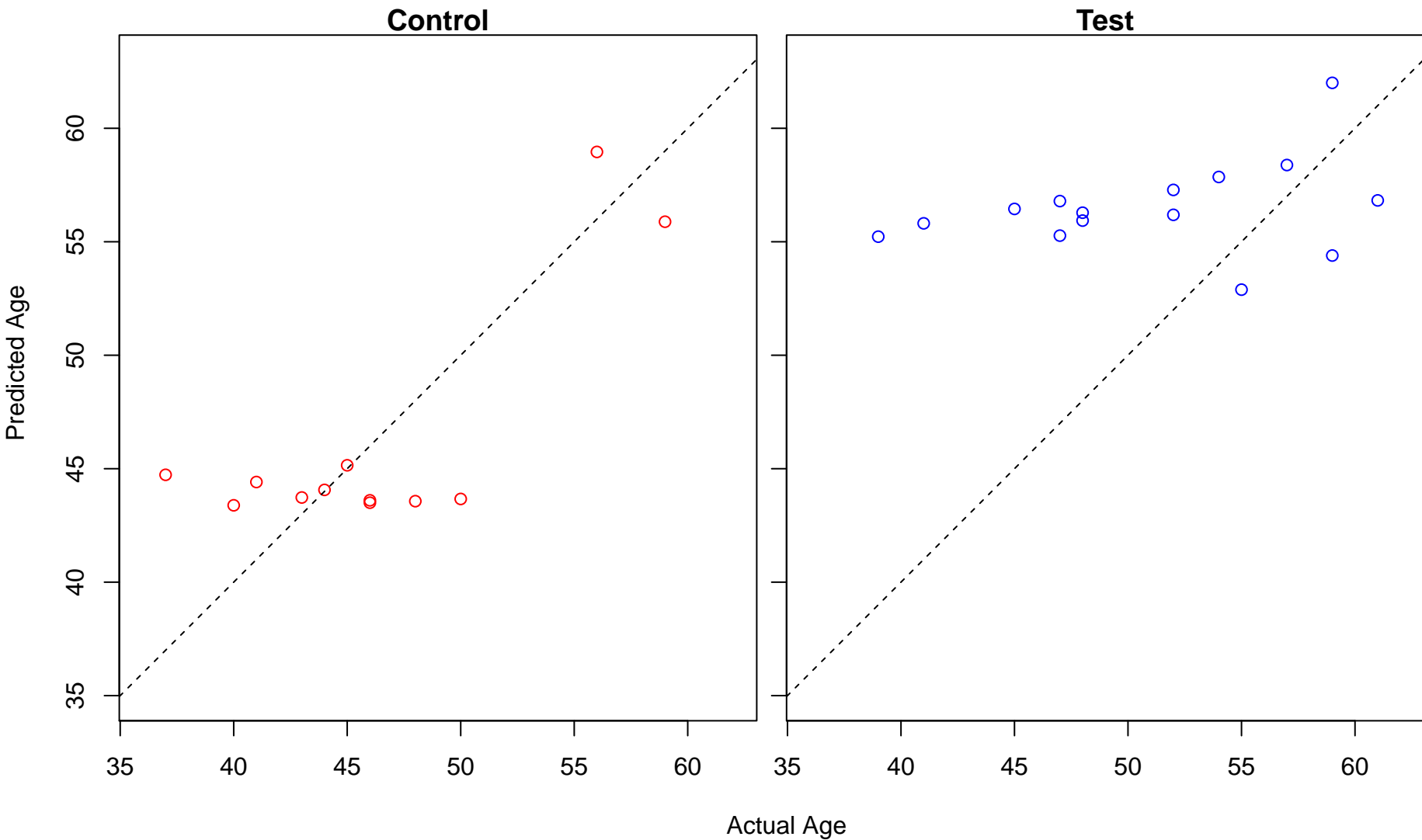


Actual Age

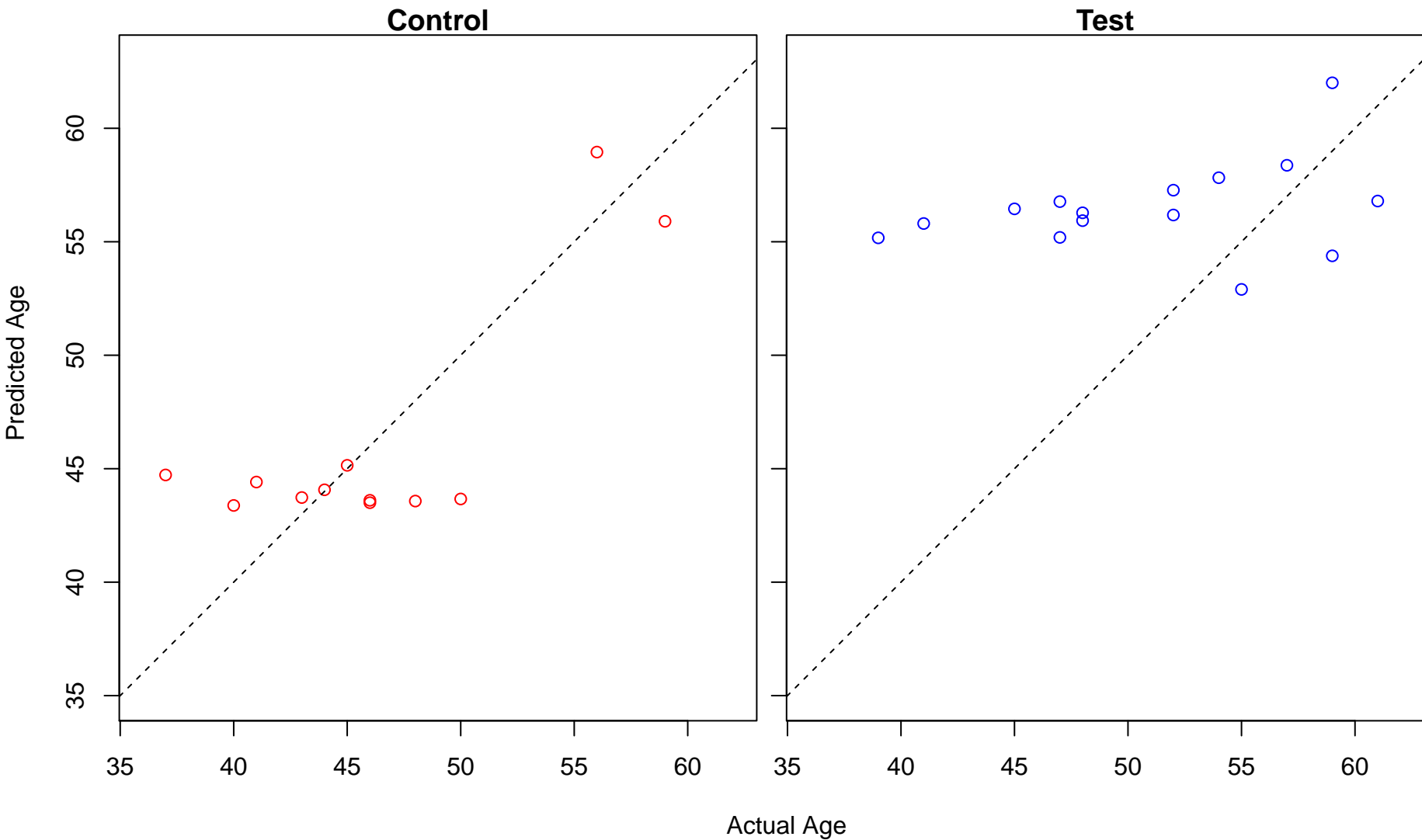
transcription from RNA polymerase III promoter (Score: 2.112856)



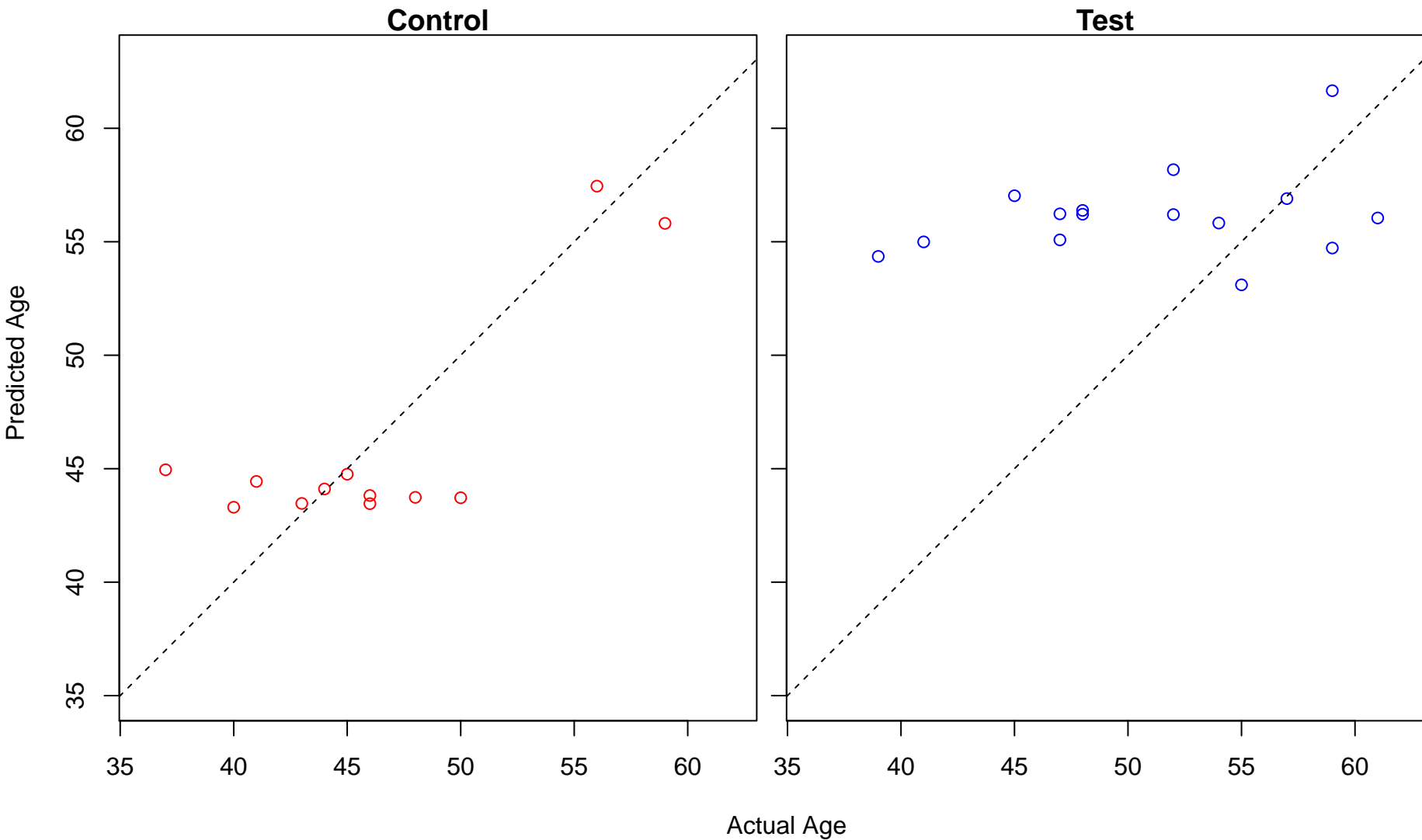
GPI anchor metabolic process (Score: 2.104130)



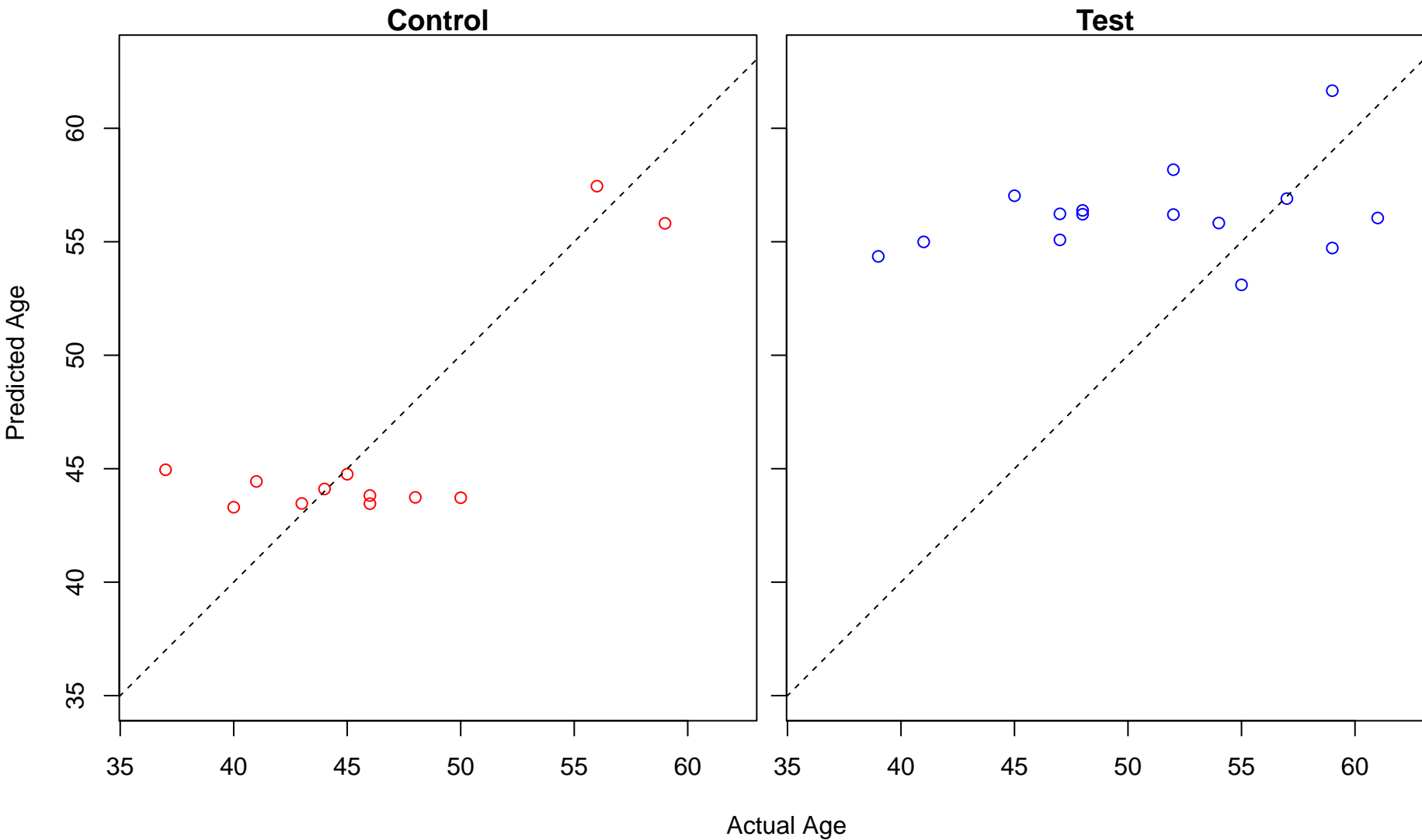
GPI anchor biosynthetic process (Score: 2.102714)



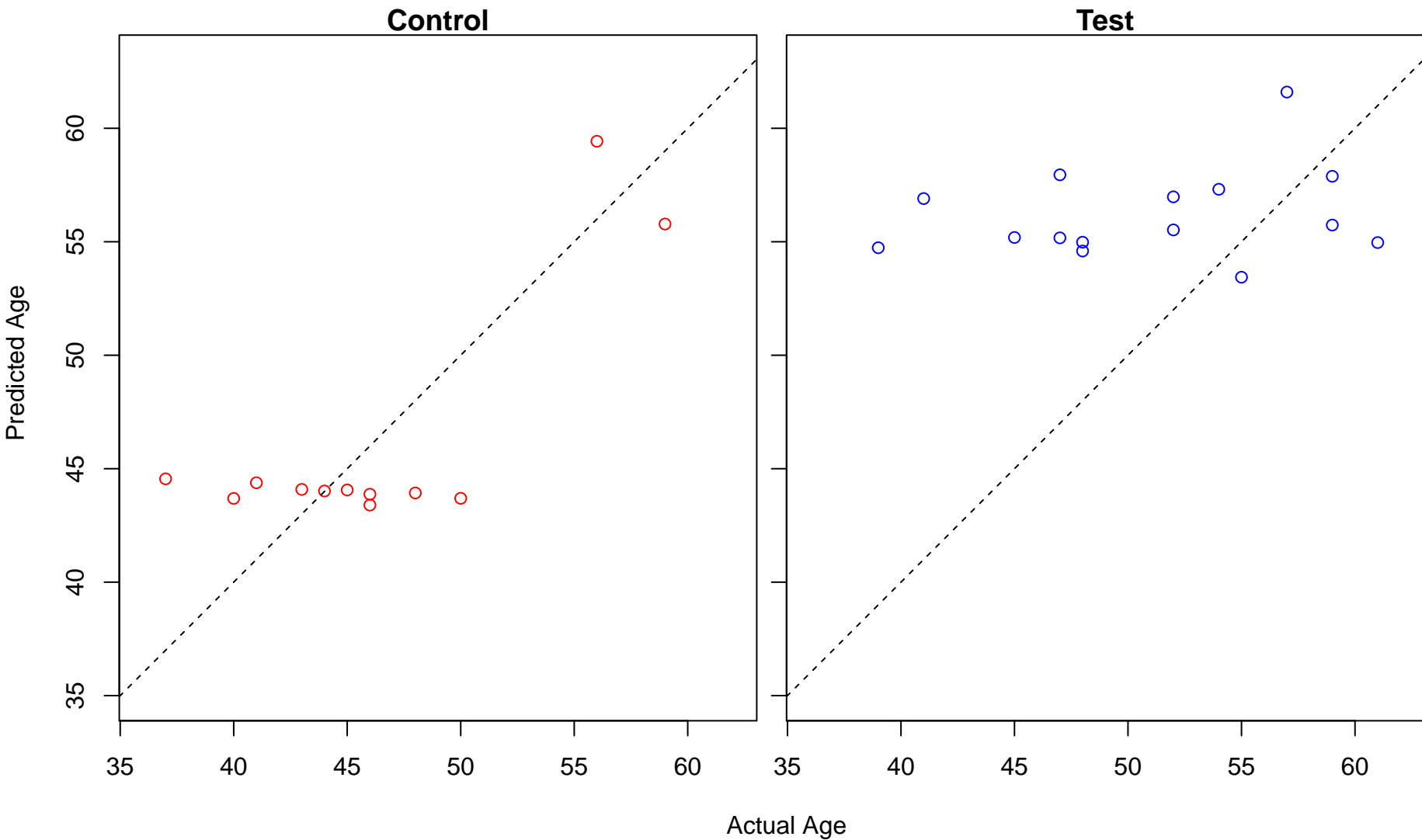
protein lipidation (Score: 2.084169)



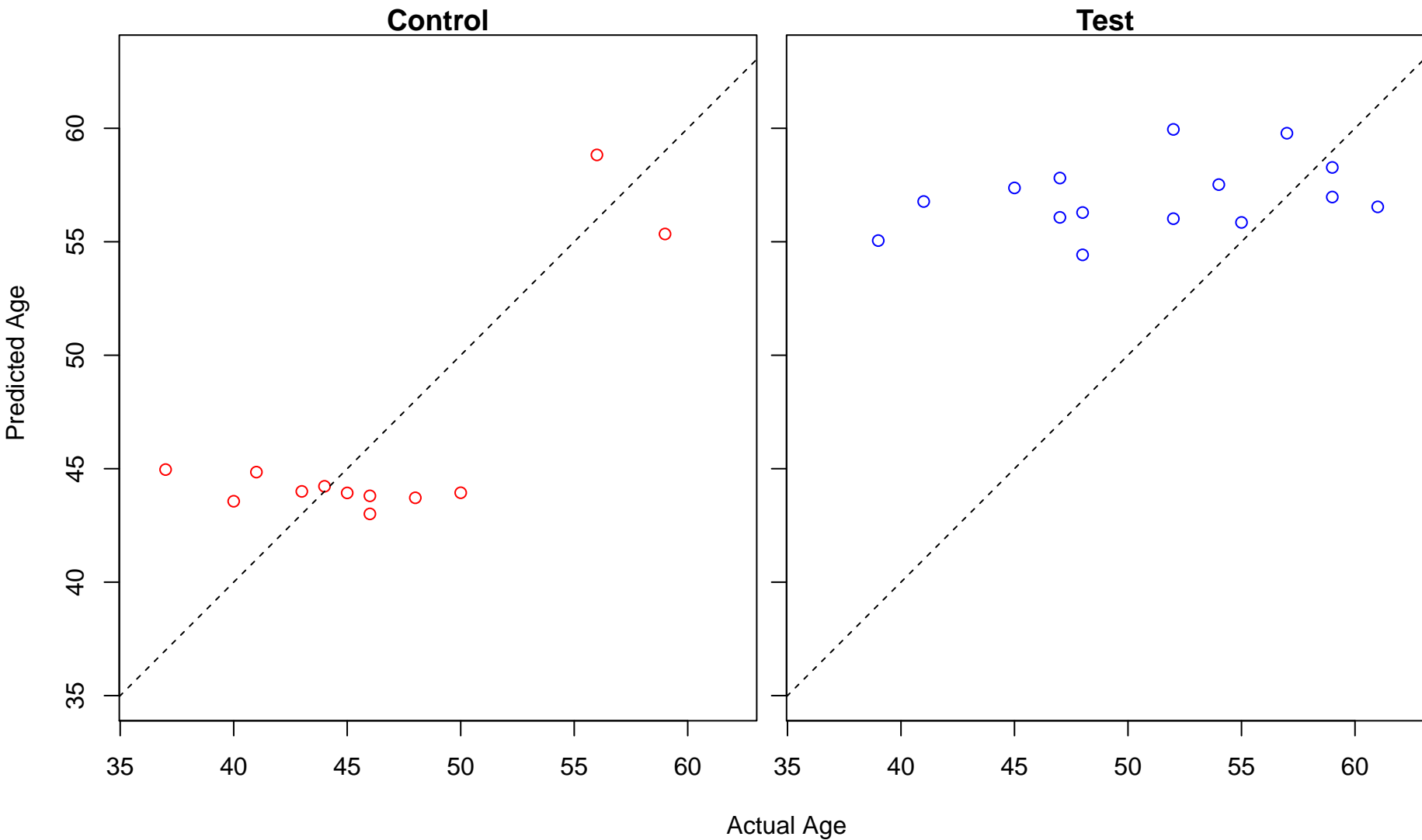
lipoprotein biosynthetic process (Score: 2.084169)



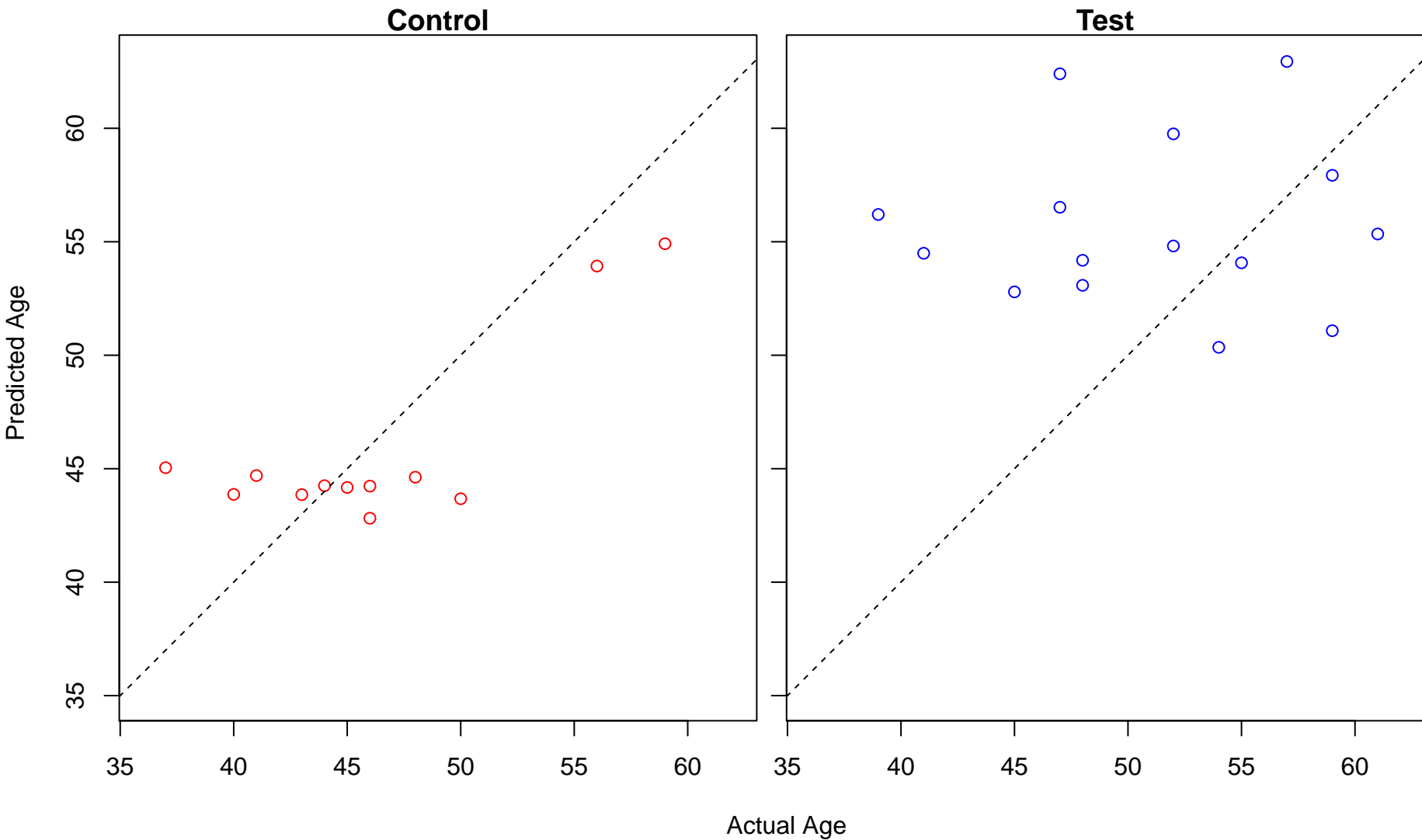
organelle fission (Score: 2.051653)



endoplasmic reticulum unfolded protein response (Score: 2.038898)

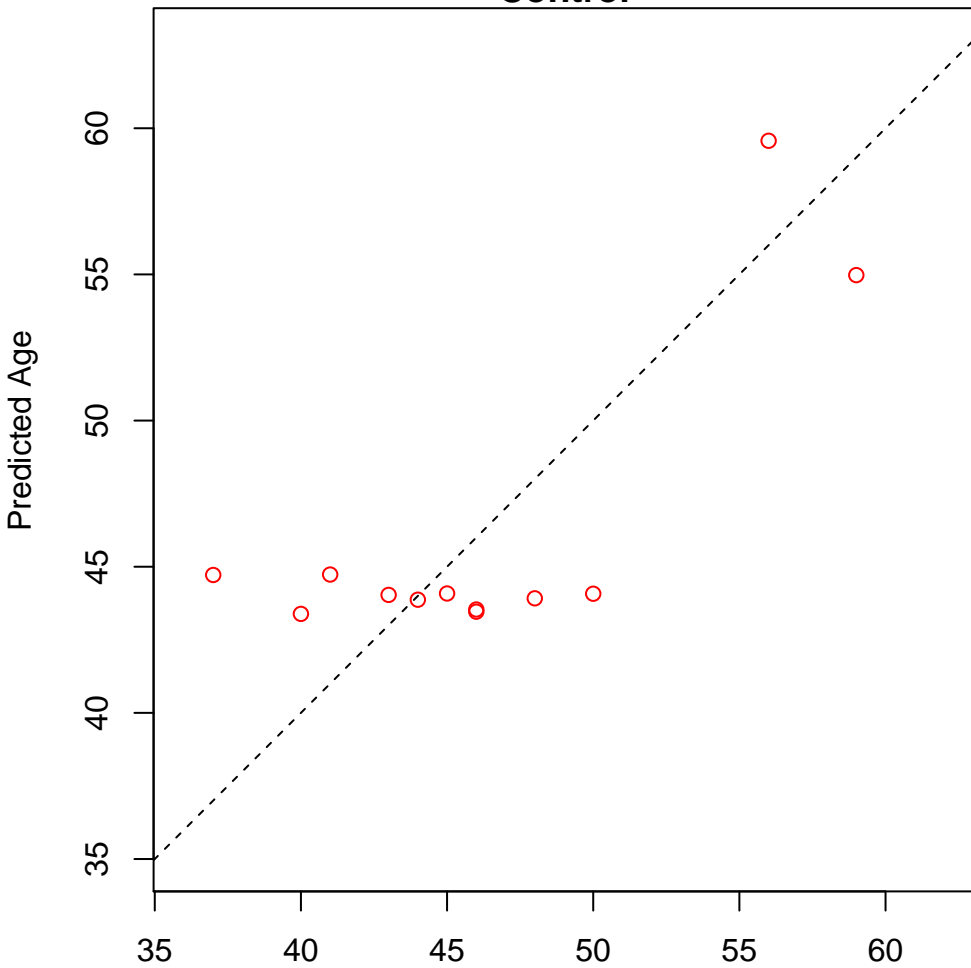


viral gene expression (Score: 2.006166)

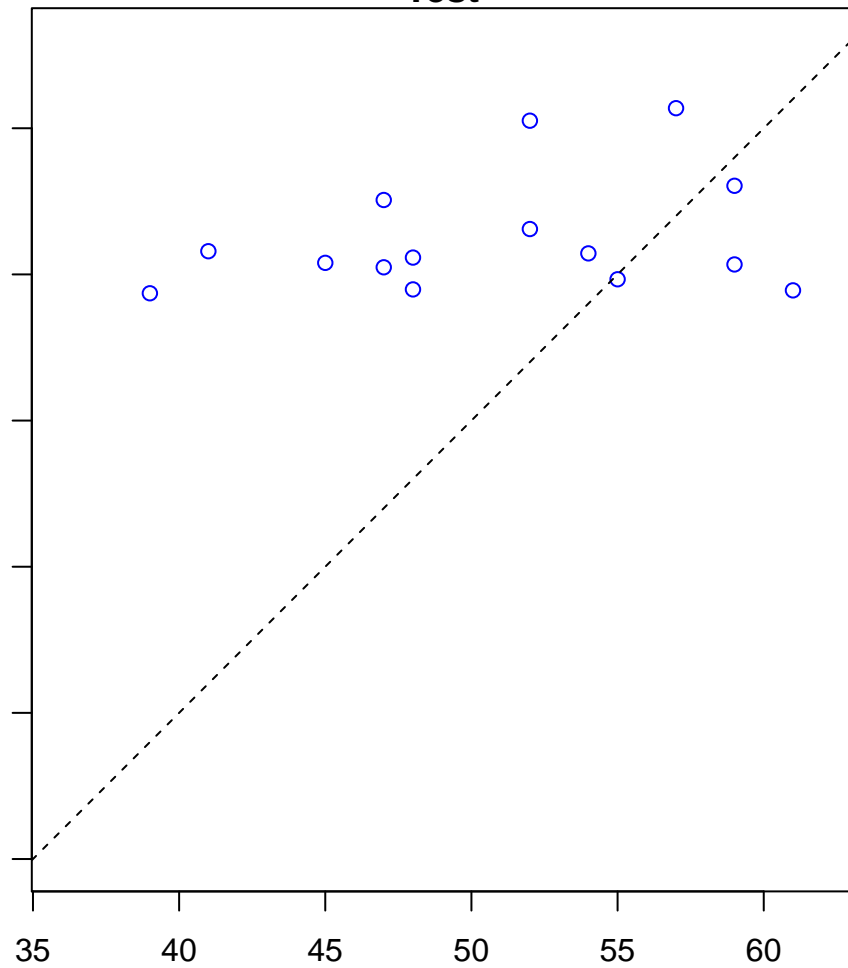


positive regulation of cell development (Score: 1.981059)

Control

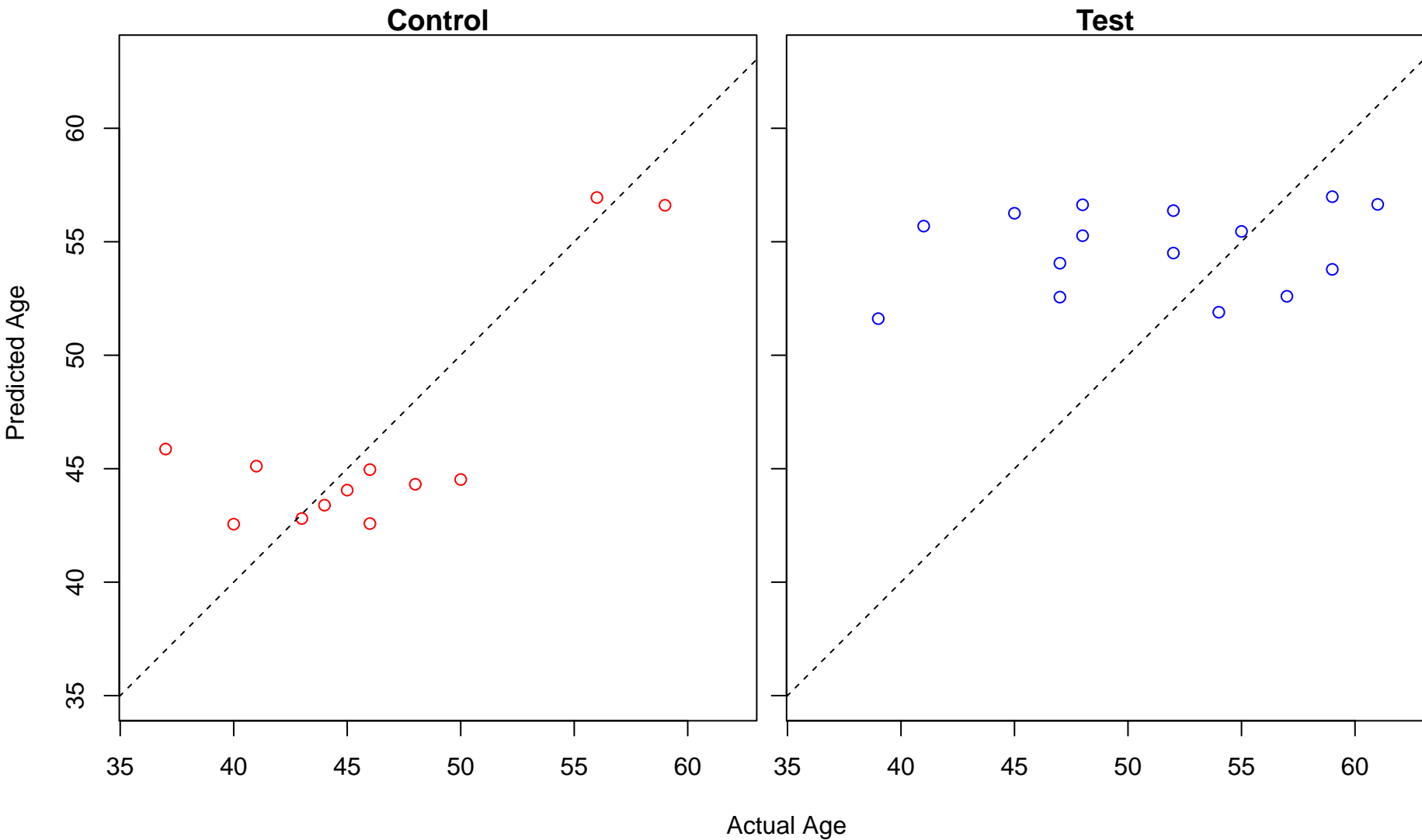


Test

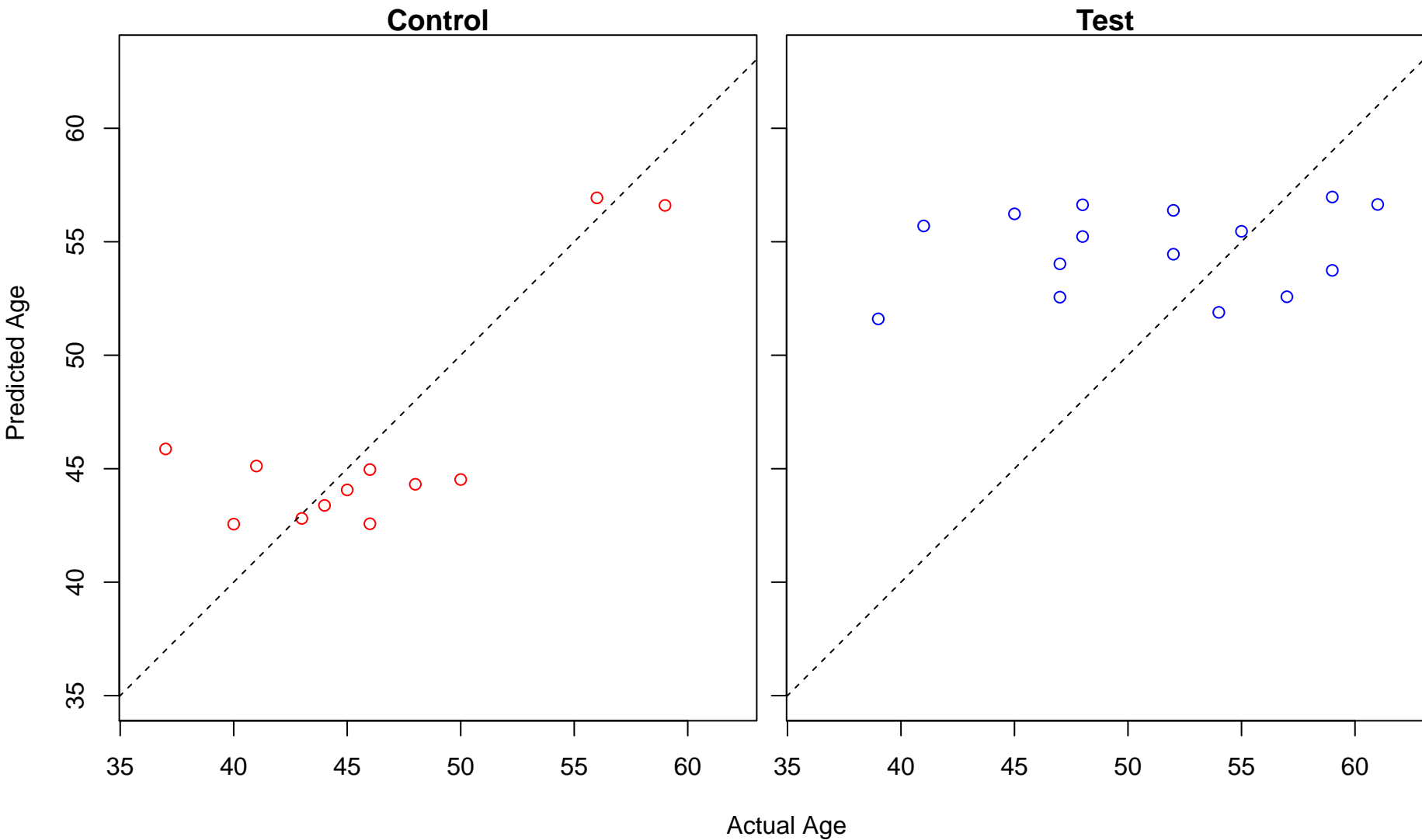


Actual Age

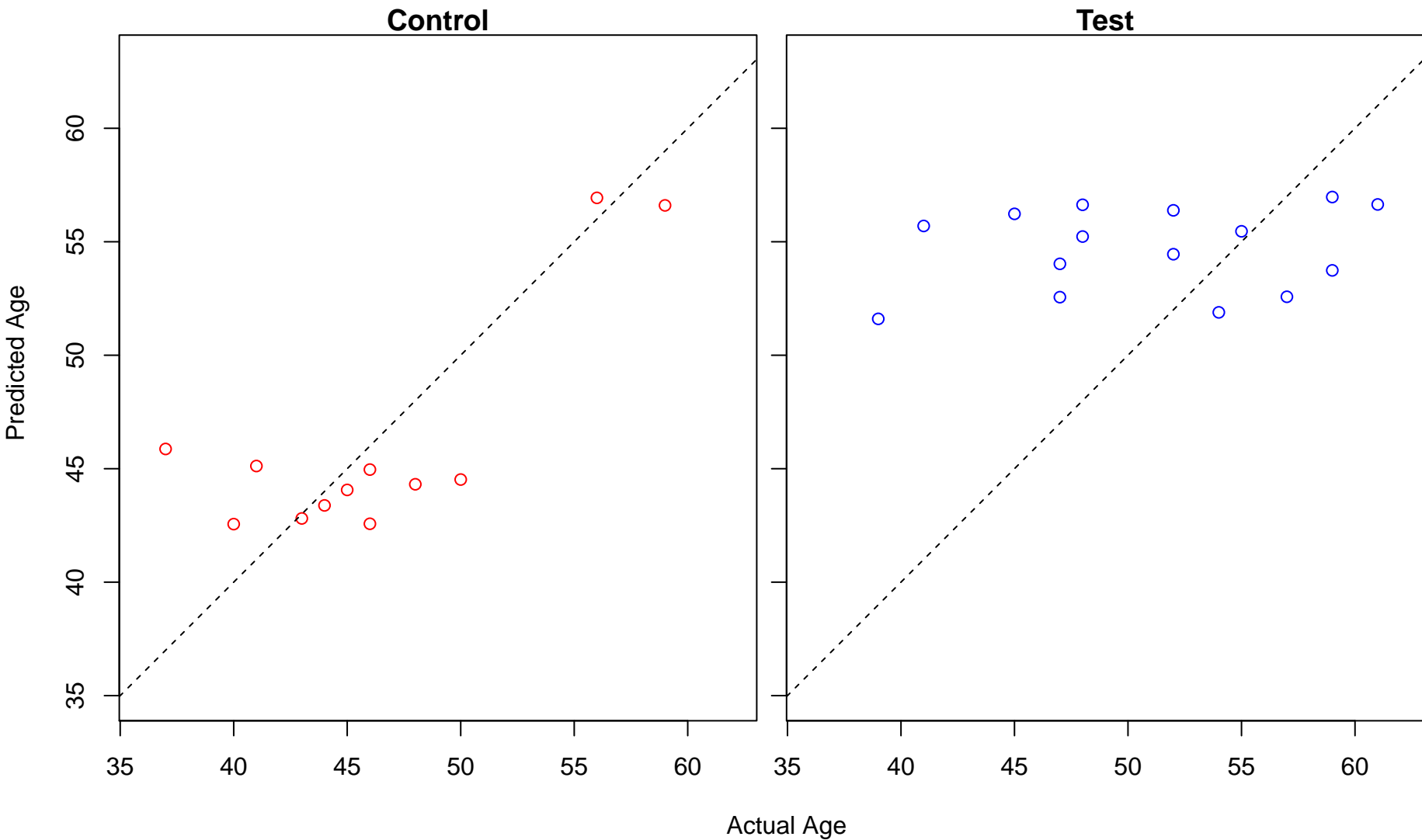
RNA export from nucleus (Score: 1.887195)



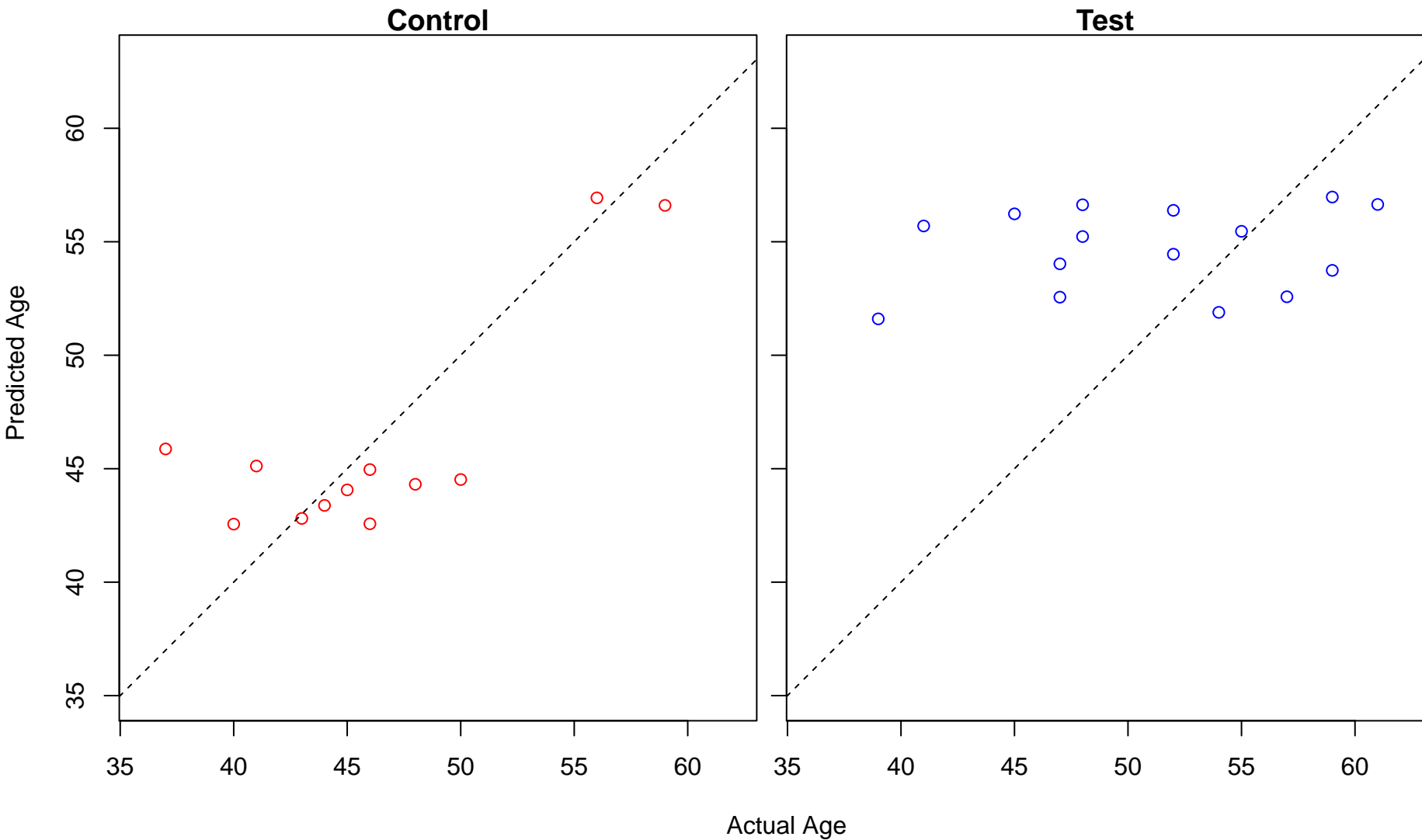
mRNA export from nucleus (Score: 1.883799)



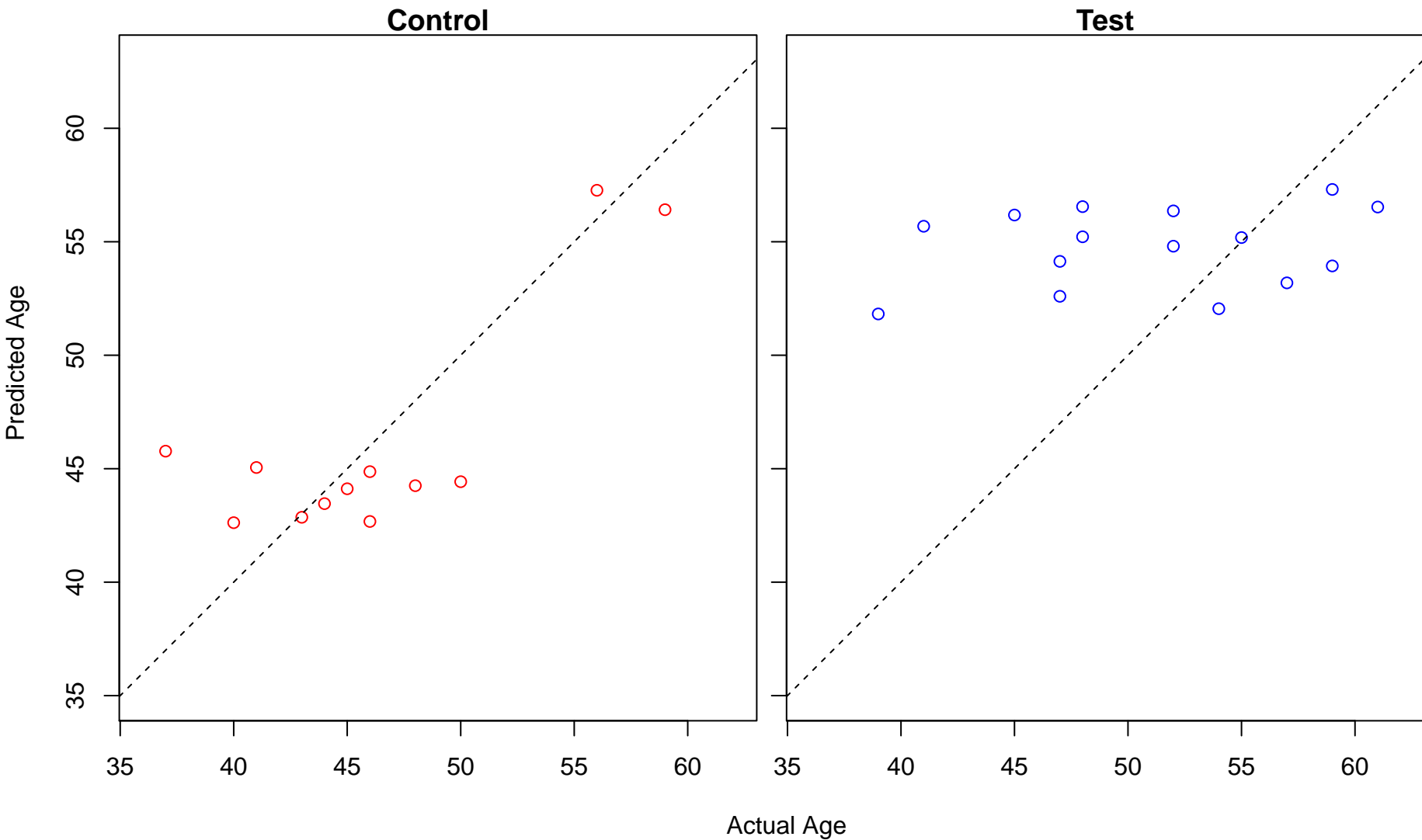
mRNA-containing ribonucleoprotein complex export from nucleus (Score: 1.883799)



mRNA transport (Score: 1.883789)



establishment of RNA localization (Score: 1.866148)



RNA transport (Score: 1.865235)

