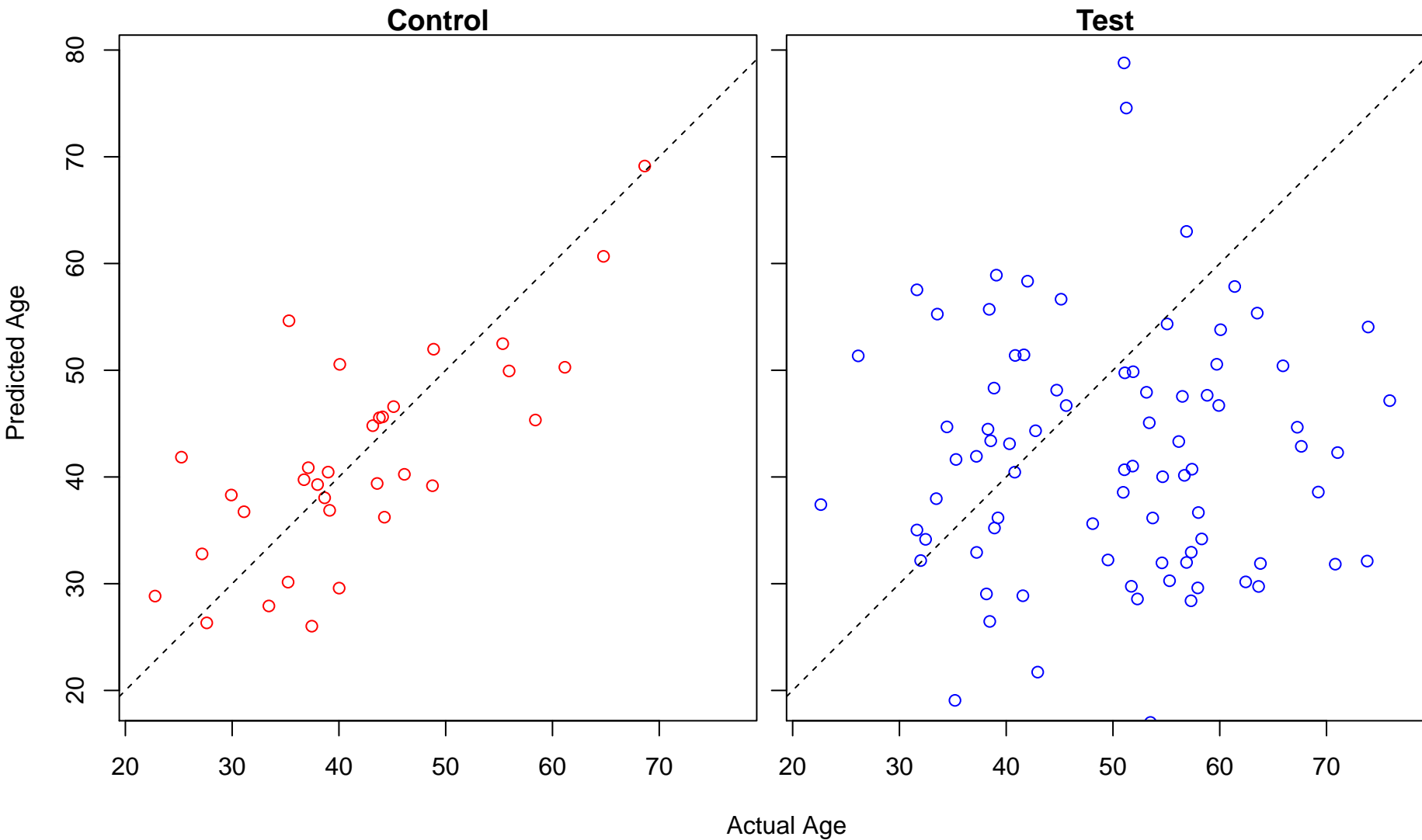
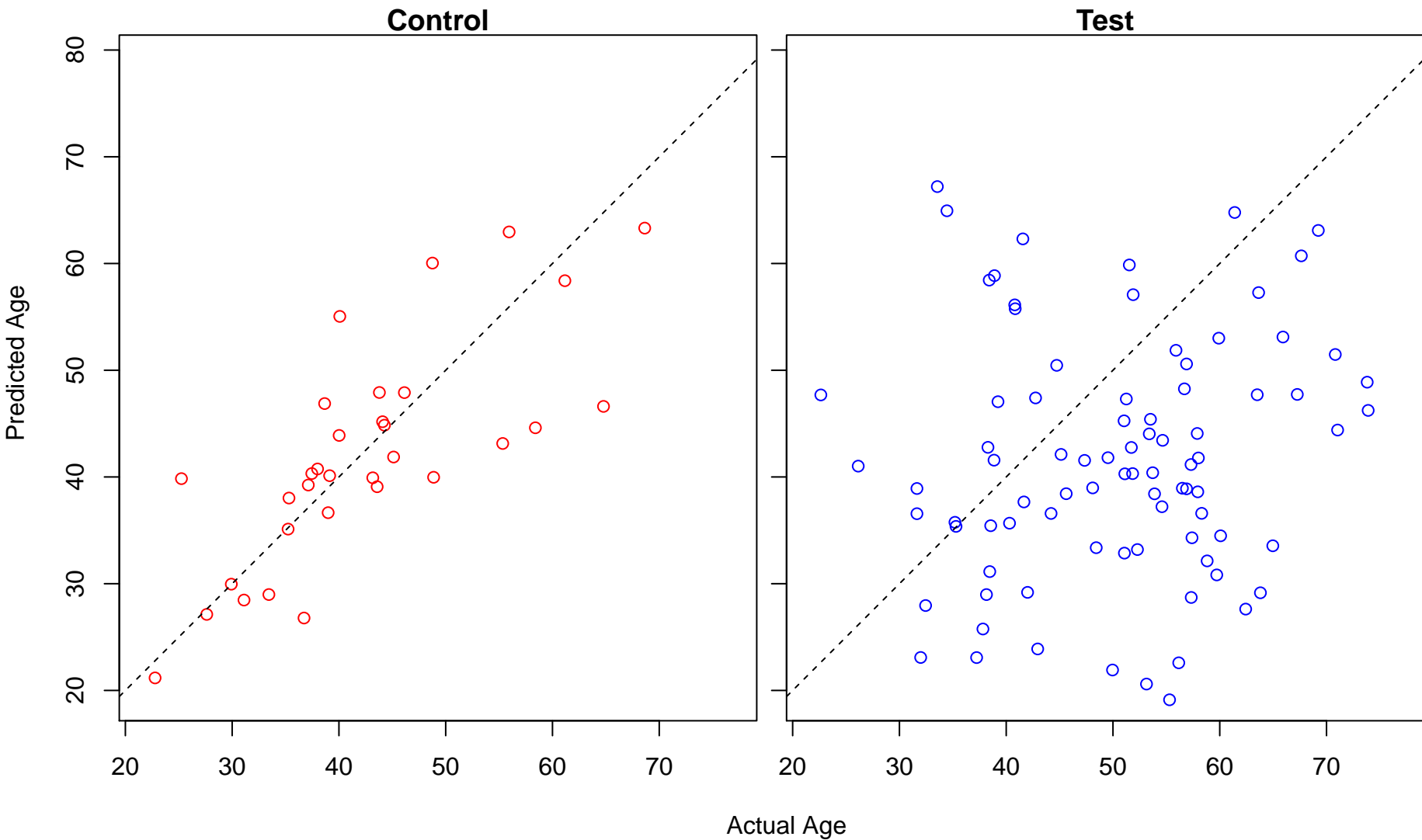


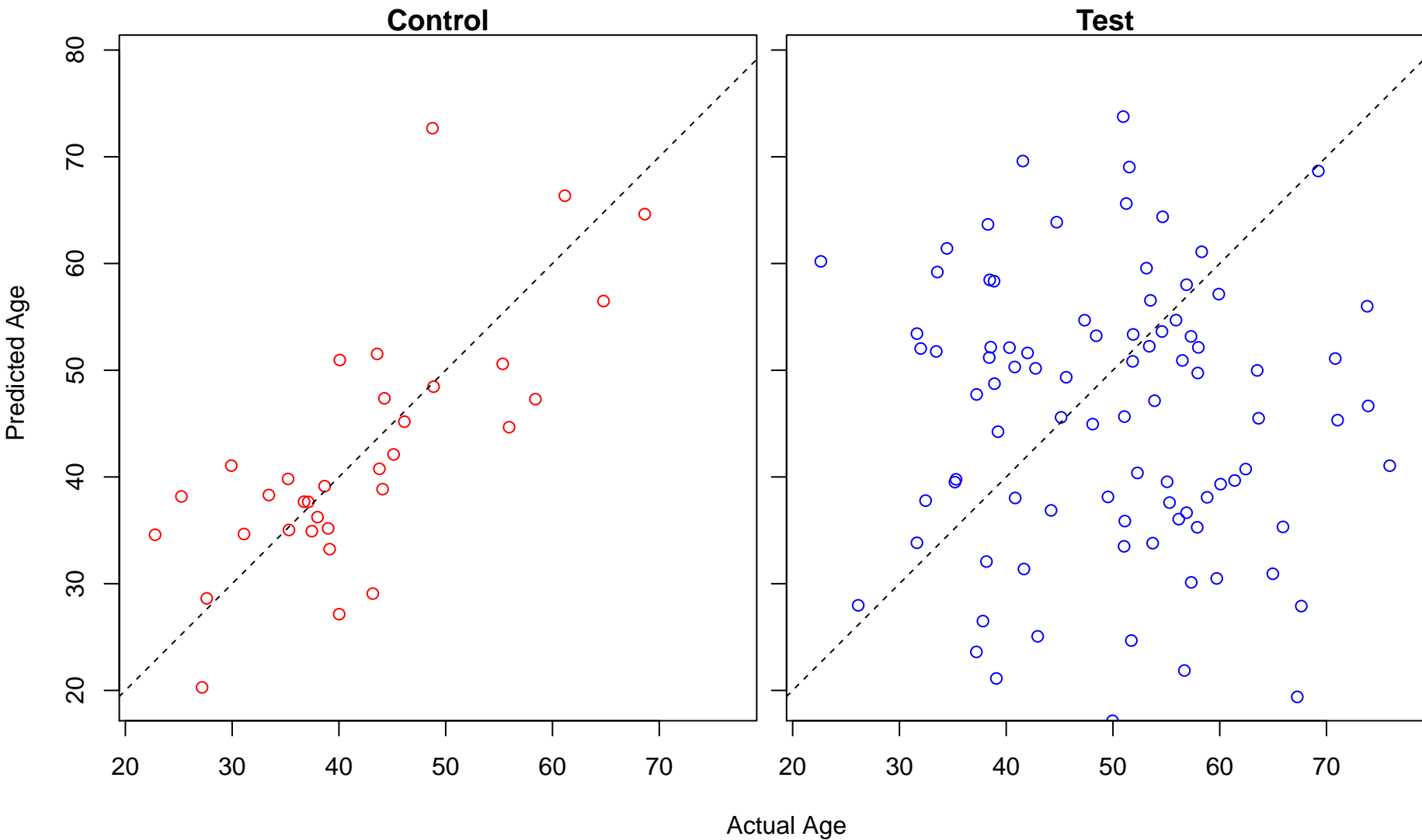
negative regulation of DNA recombination (Score: 3.523398)



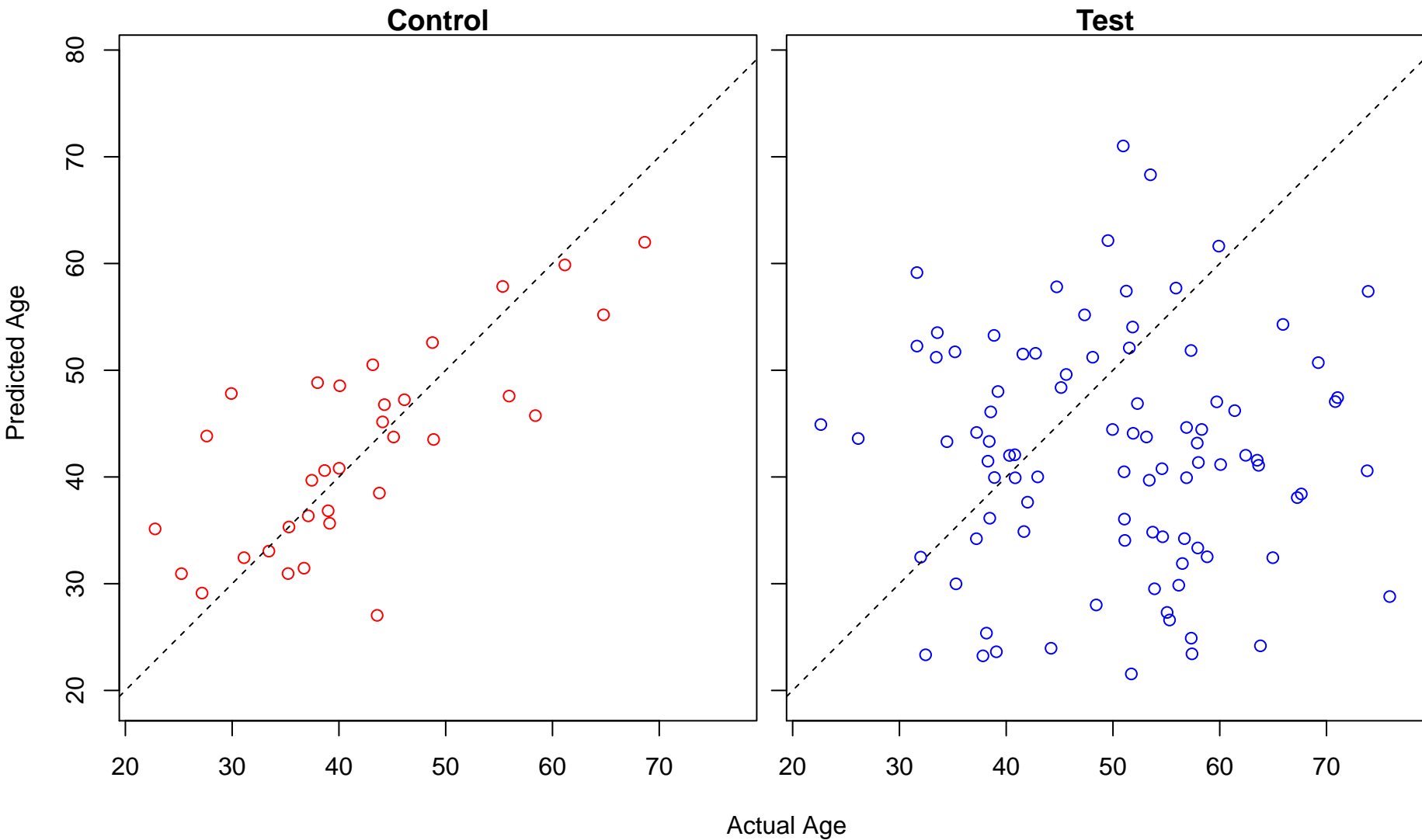
telomere maintenance via recombination (Score: 3.105962)



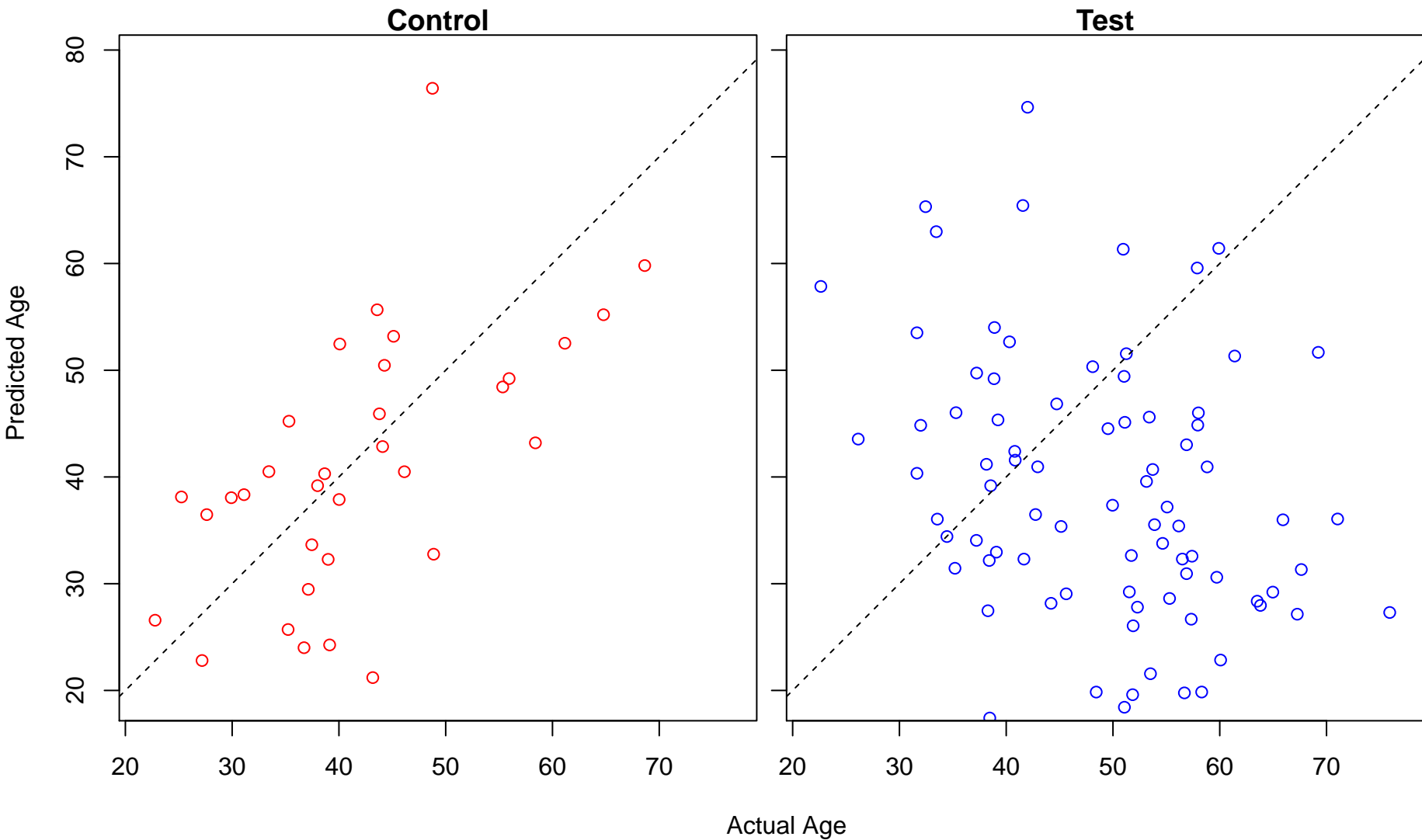
regulation of epidermal growth factor receptor signaling pathway (Score: 2.623669)



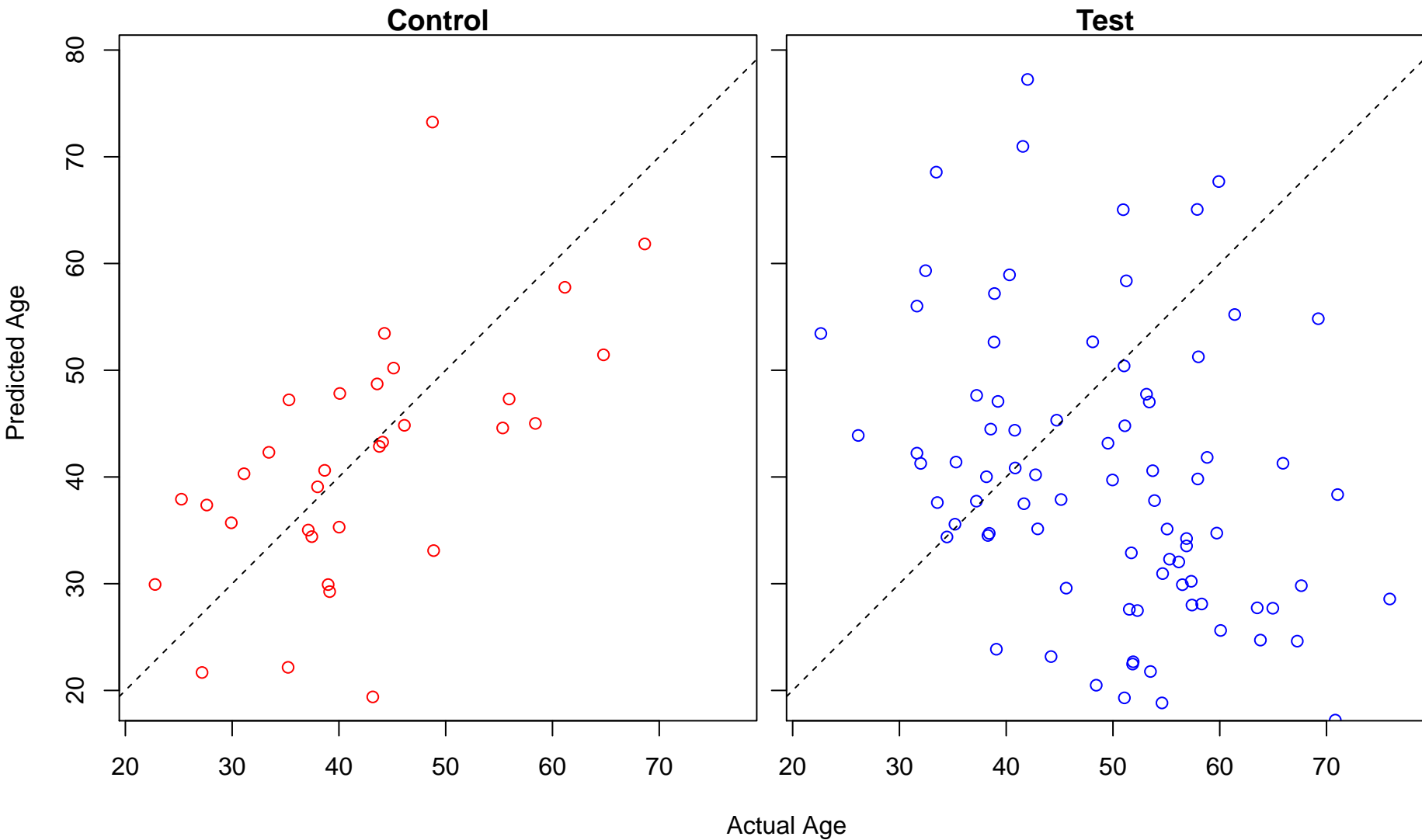
phototransduction (Score: 2.519601)



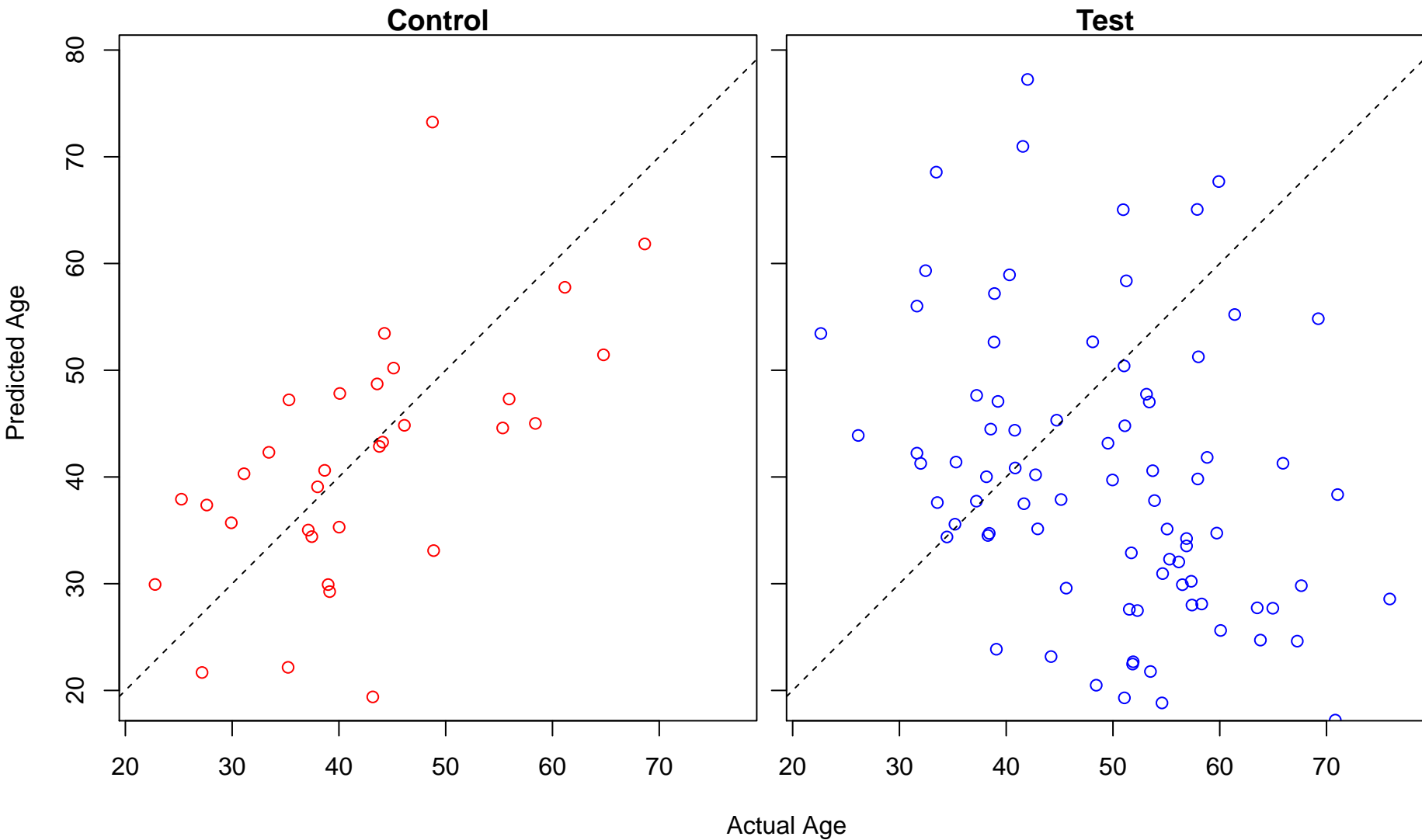
regulation of muscle organ development (Score: 2.485790)



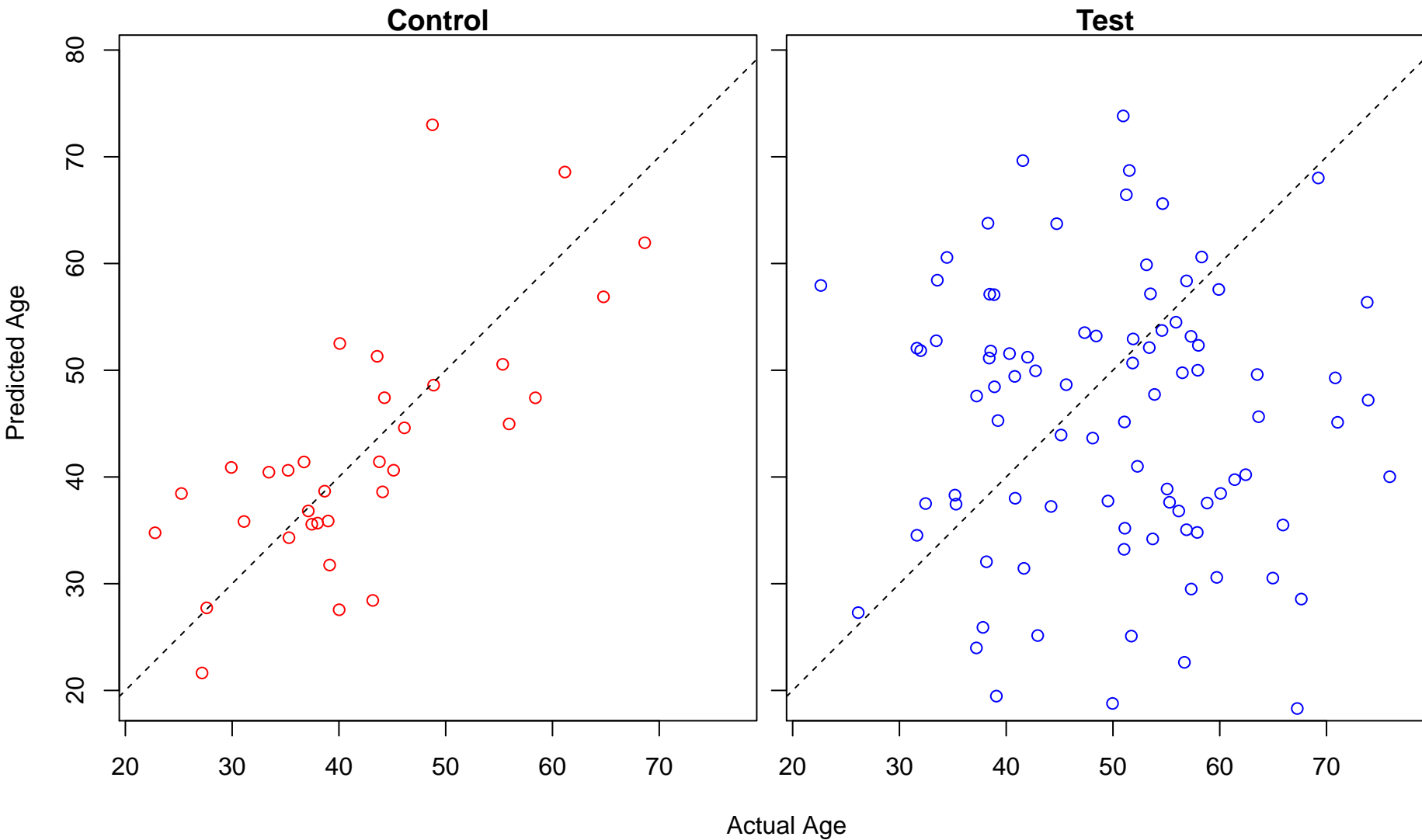
regulation of striated muscle tissue development (Score: 2.456245)



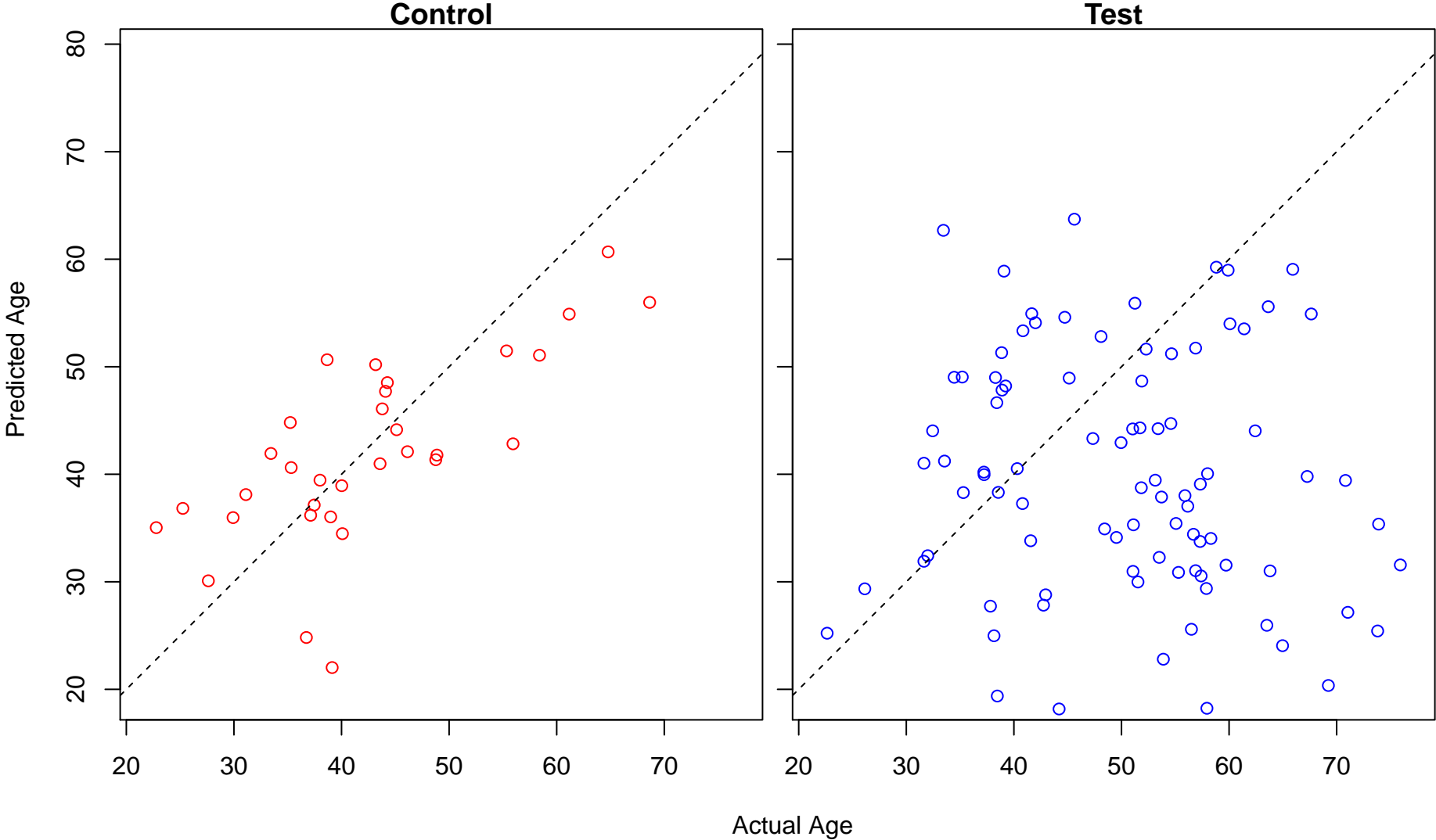
regulation of muscle tissue development (Score: 2.456245)



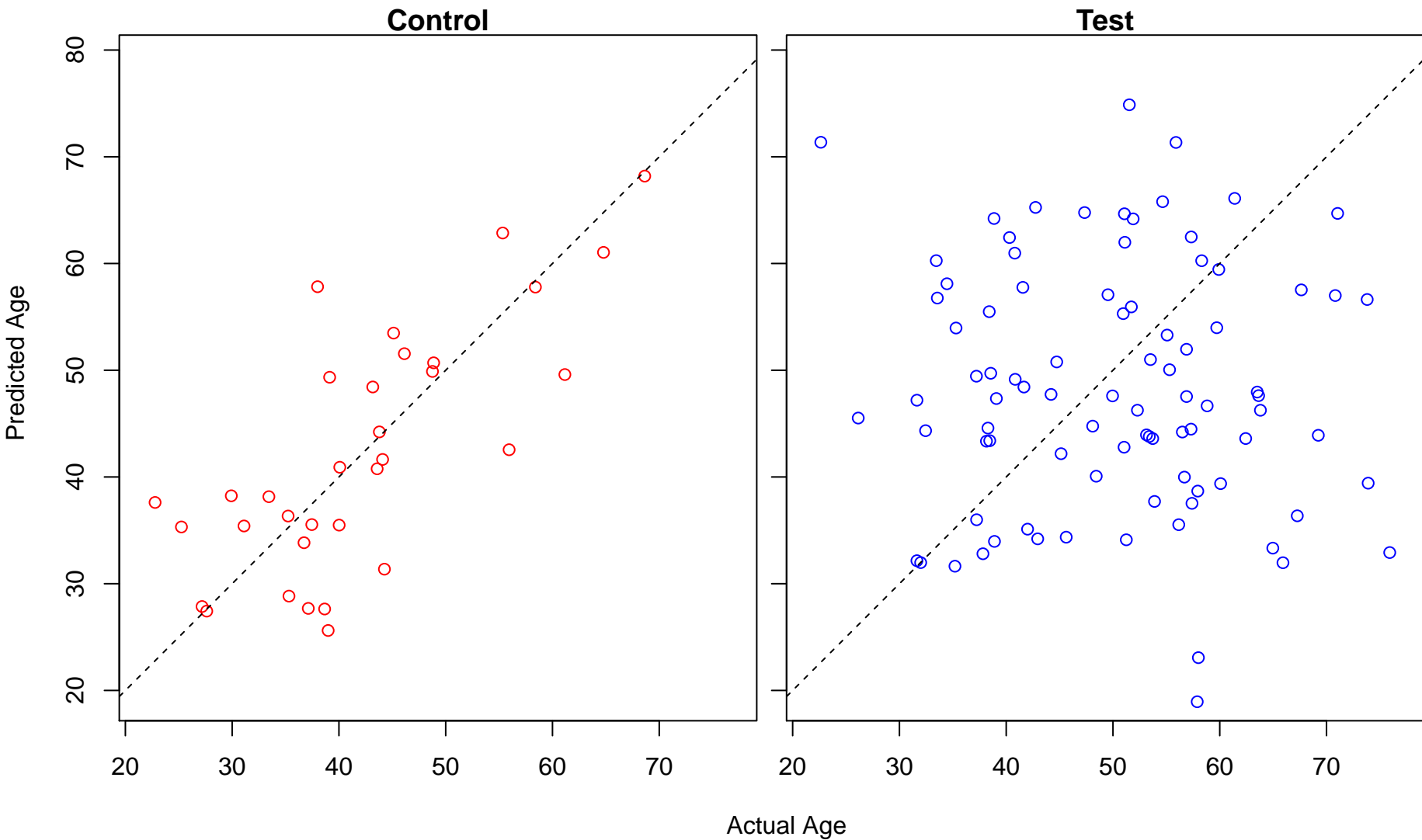
regulation of ERBB signaling pathway (Score: 2.429822)



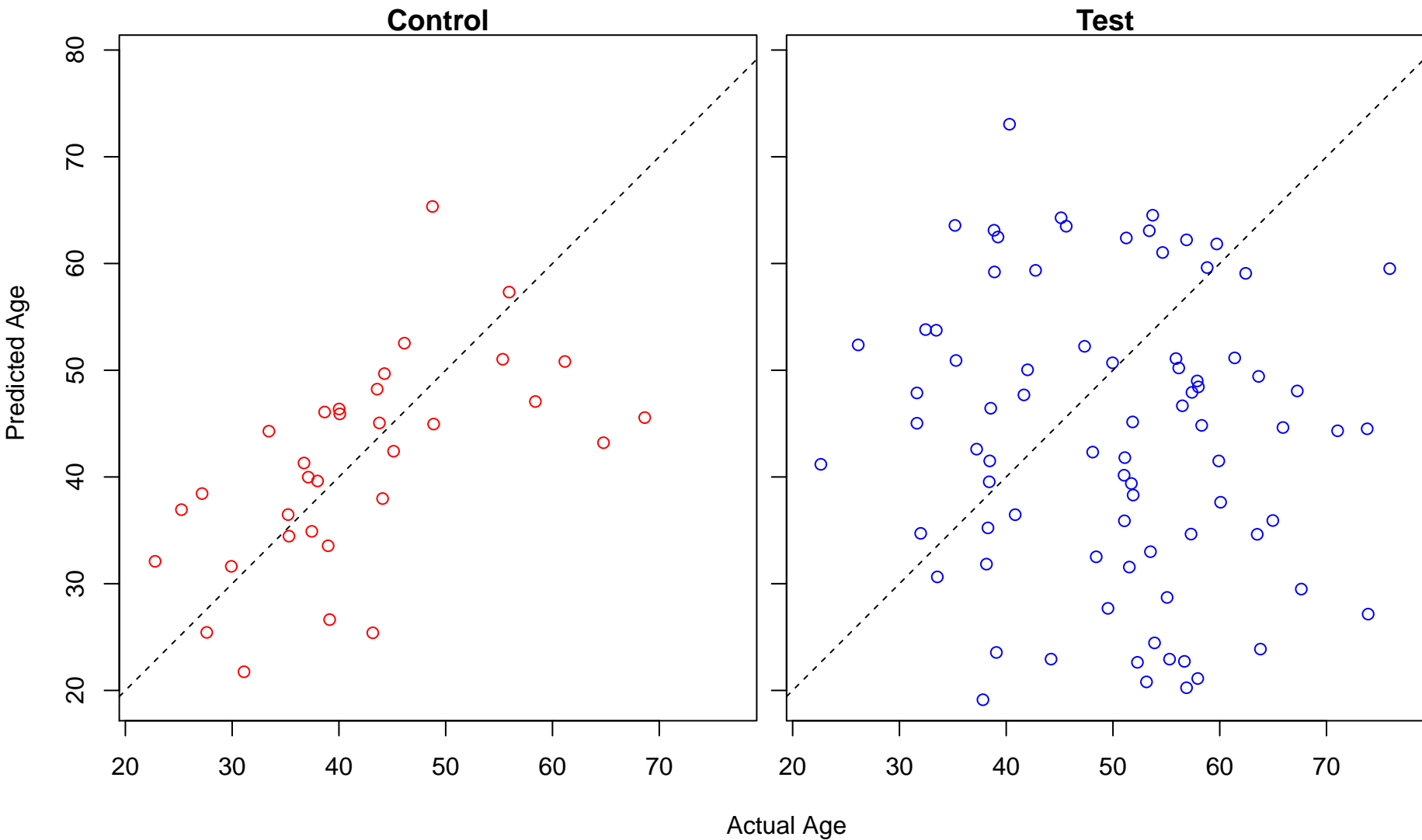
negative regulation of transcription from RNA polymerase II promoter in response to stress (Score: 2.42)



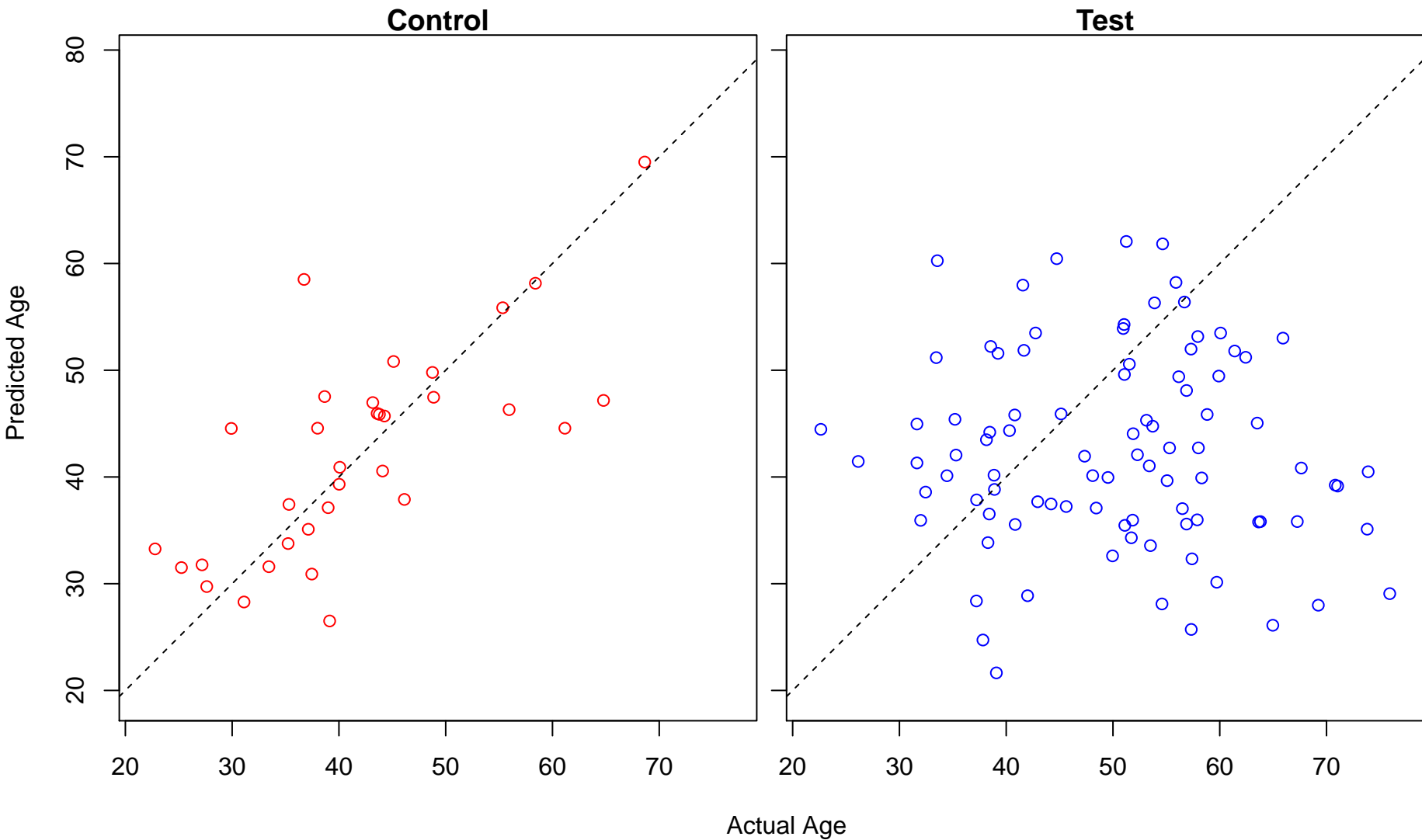
negative regulation of cation channel activity (Score: 2.335707)



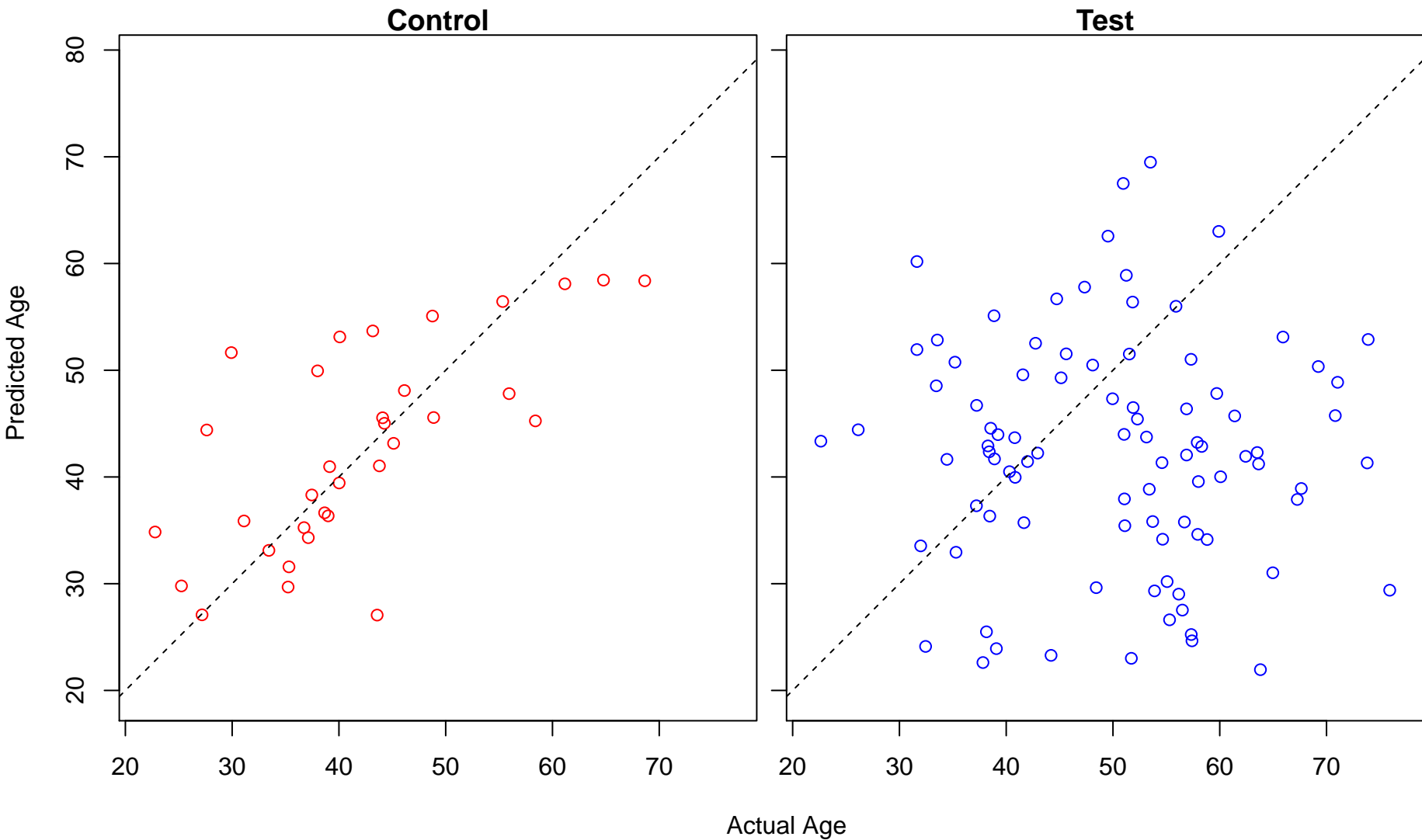
regulation of anion transport (Score: 2.256929)



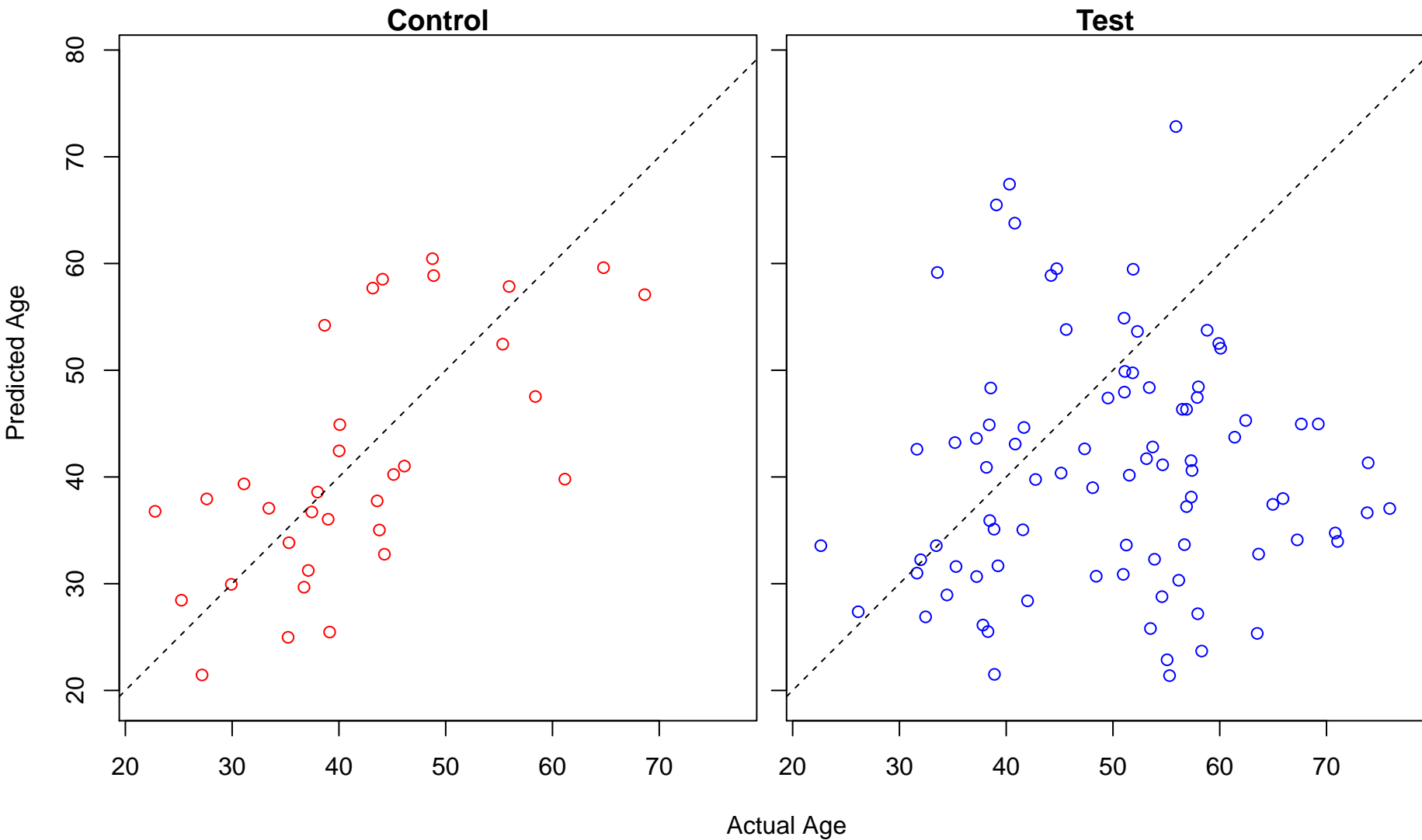
tumor necrosis factor-mediated signaling pathway (Score: 2.254703)



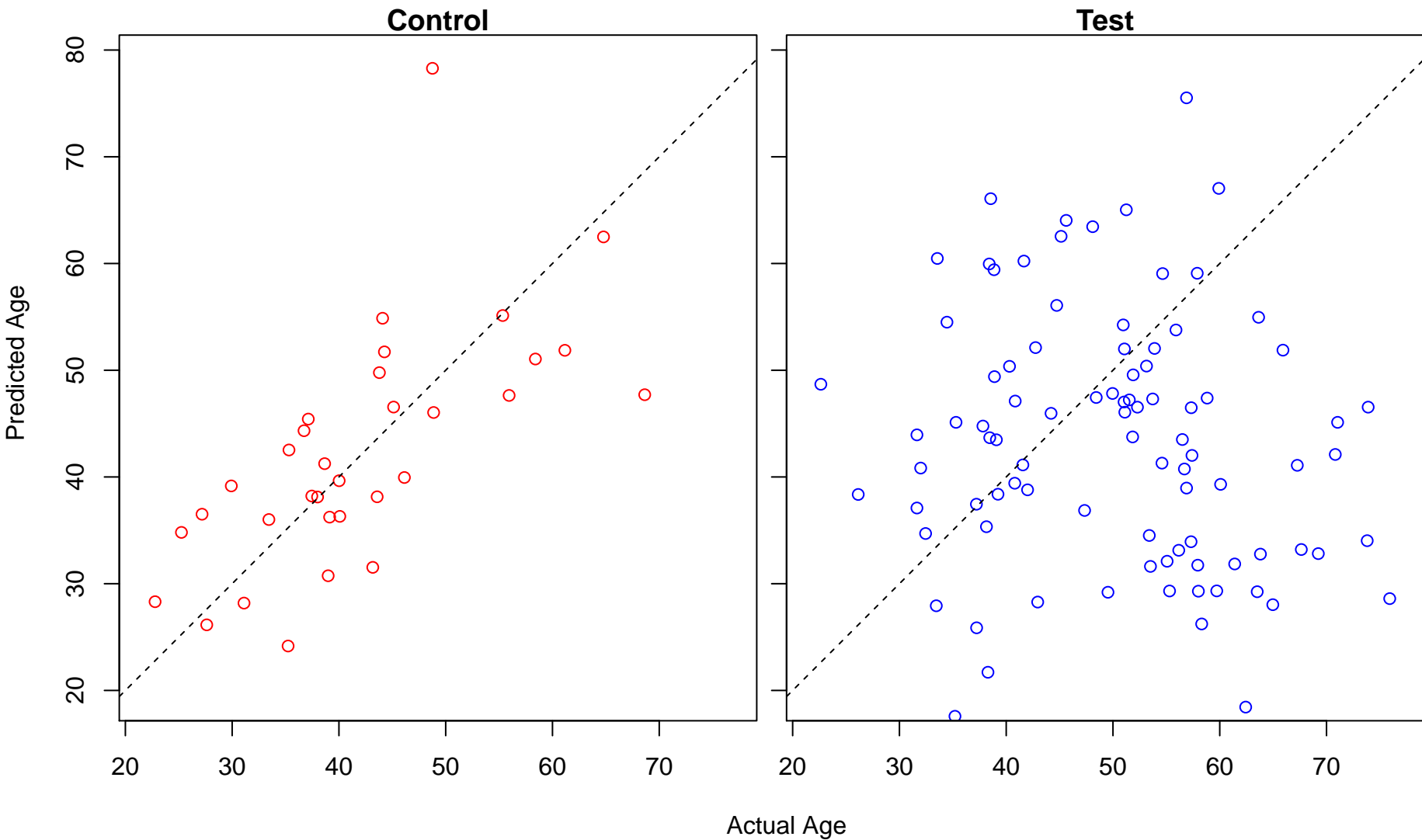
detection of visible light (Score: 2.211972)



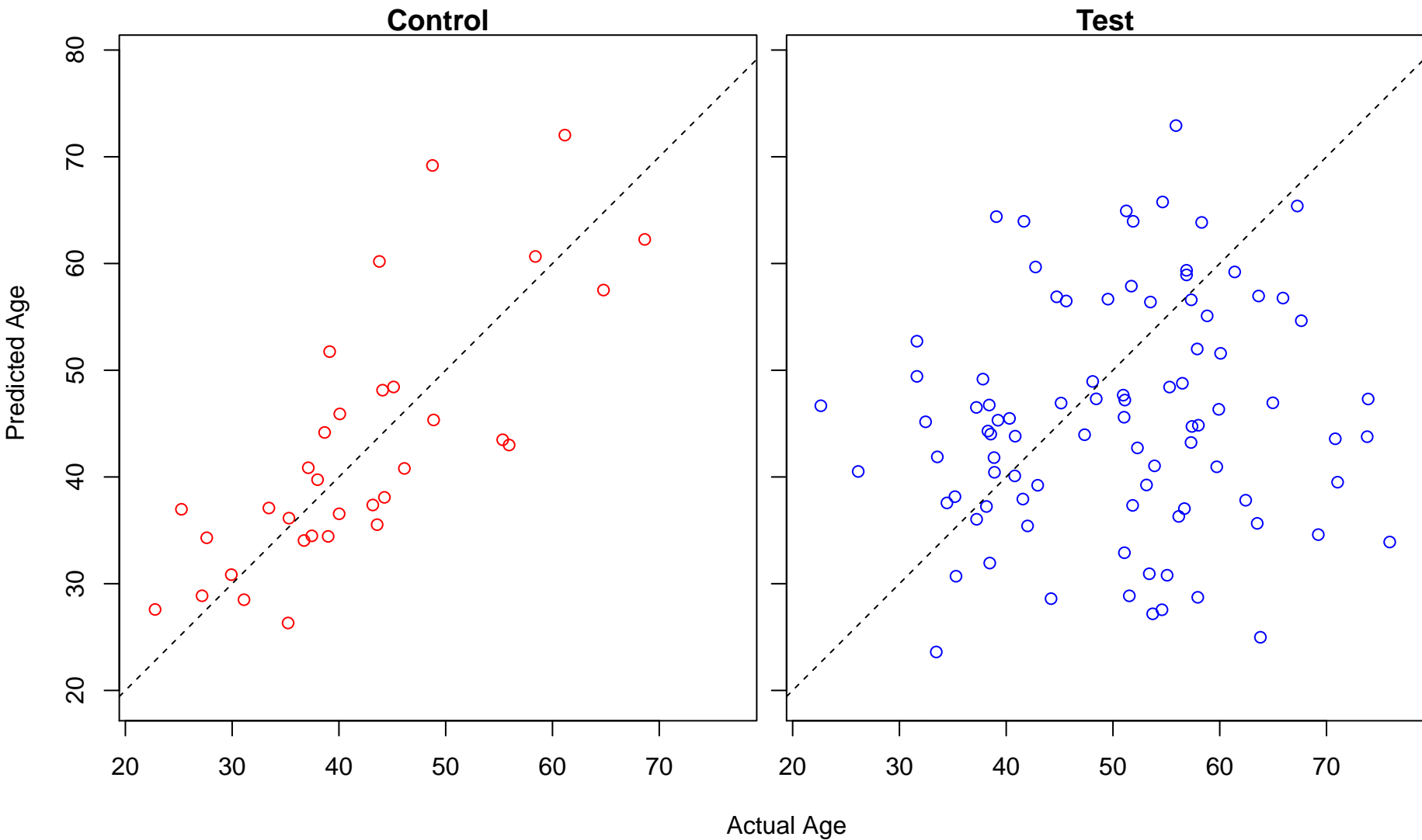
regulation of sodium ion transmembrane transporter activity (Score: 2.159195)



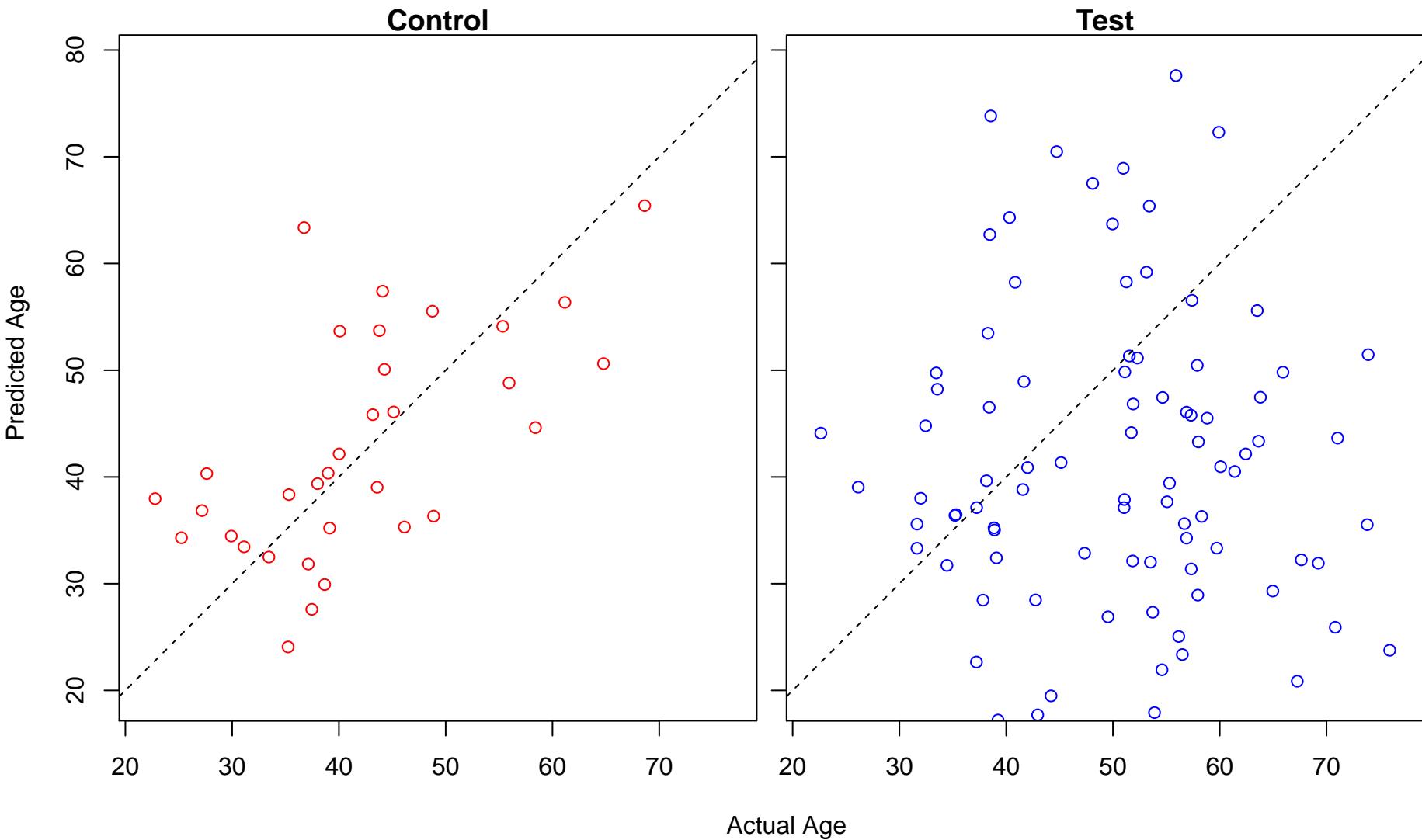
negative regulation of protein acetylation (Score: 2.145266)



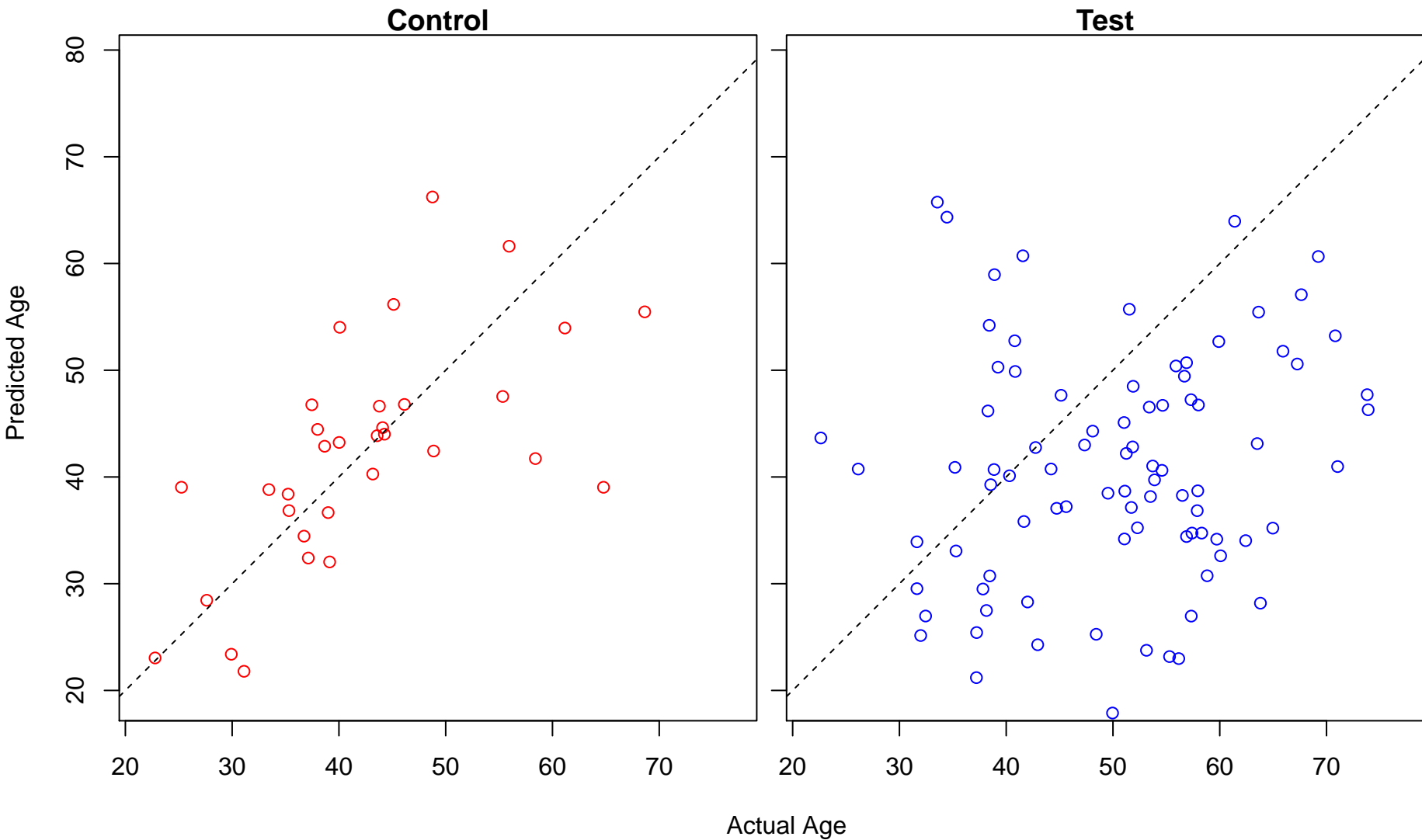
regulation of leukocyte degranulation (Score: 2.142261)



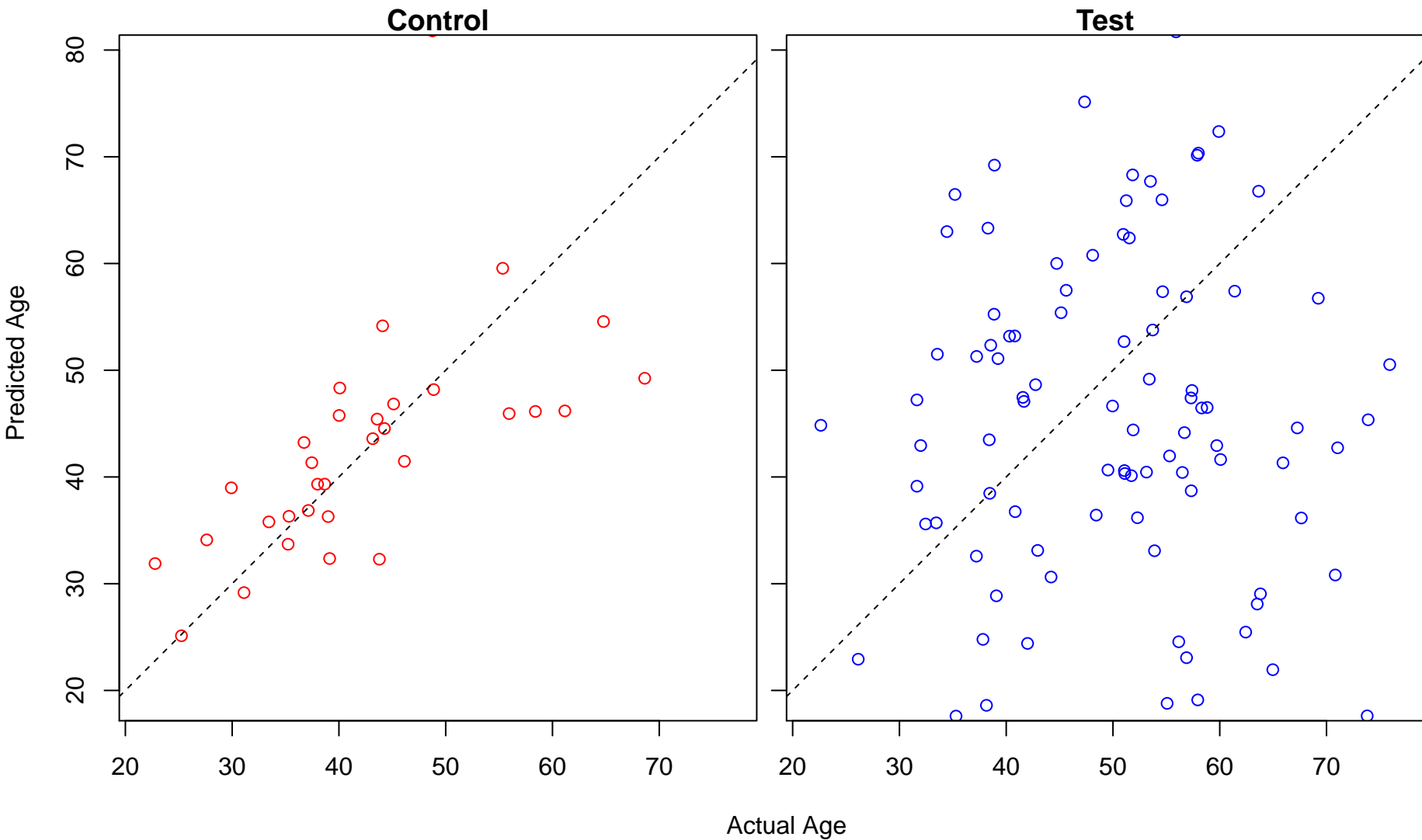
positive regulation of JUN kinase activity (Score: 2.141354)



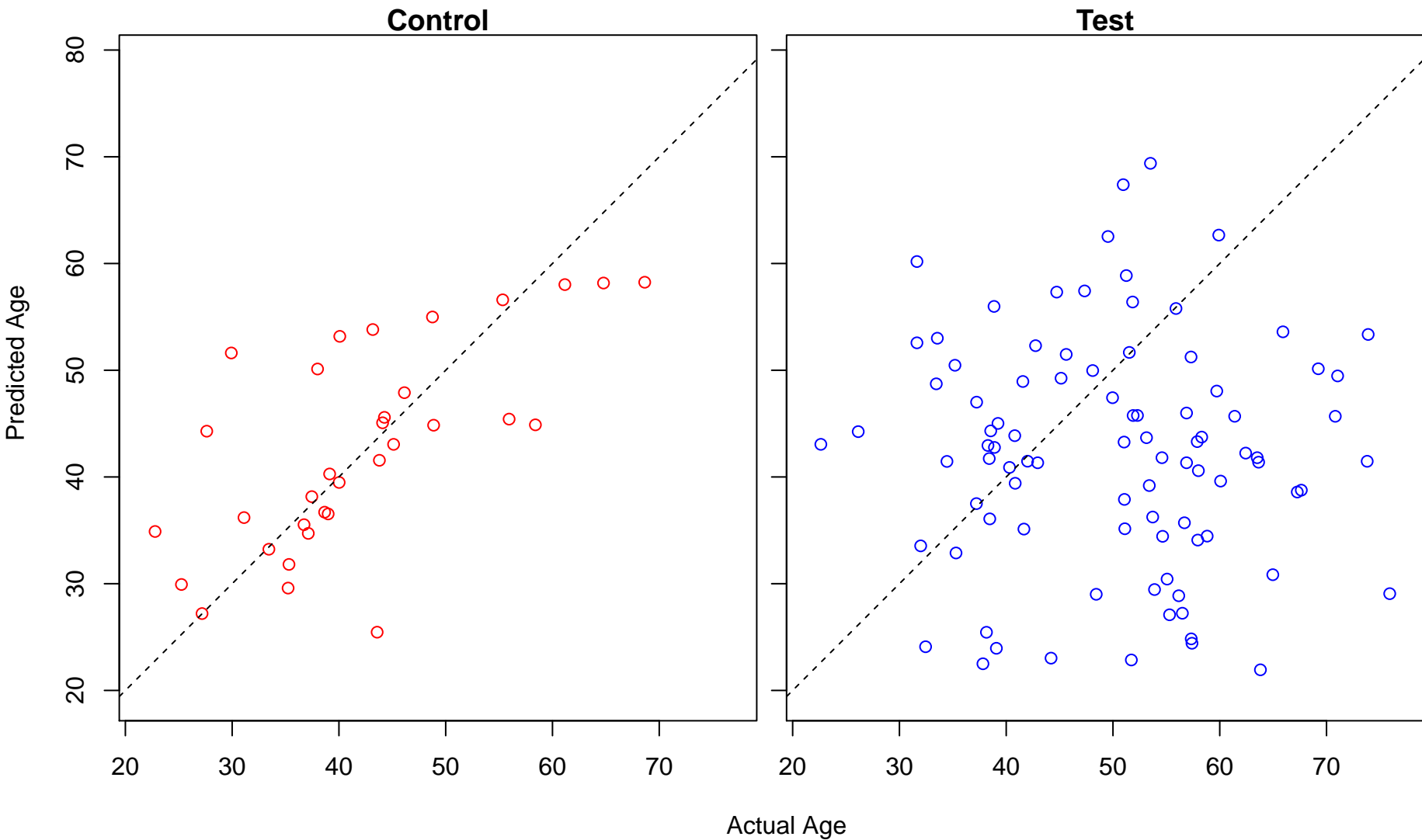
mitotic recombination (Score: 2.137083)



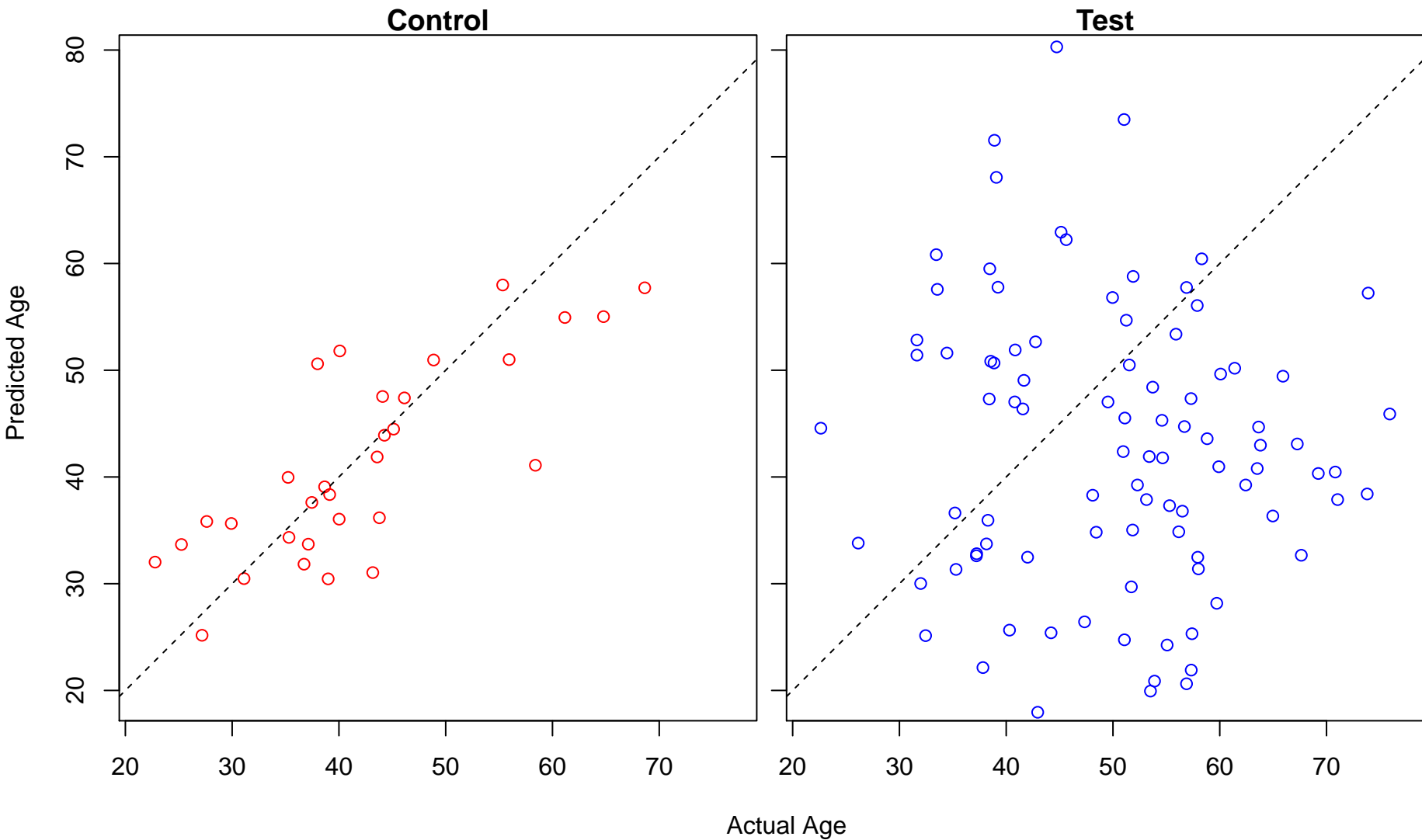
regulation of phosphoprotein phosphatase activity (Score: 2.116385)



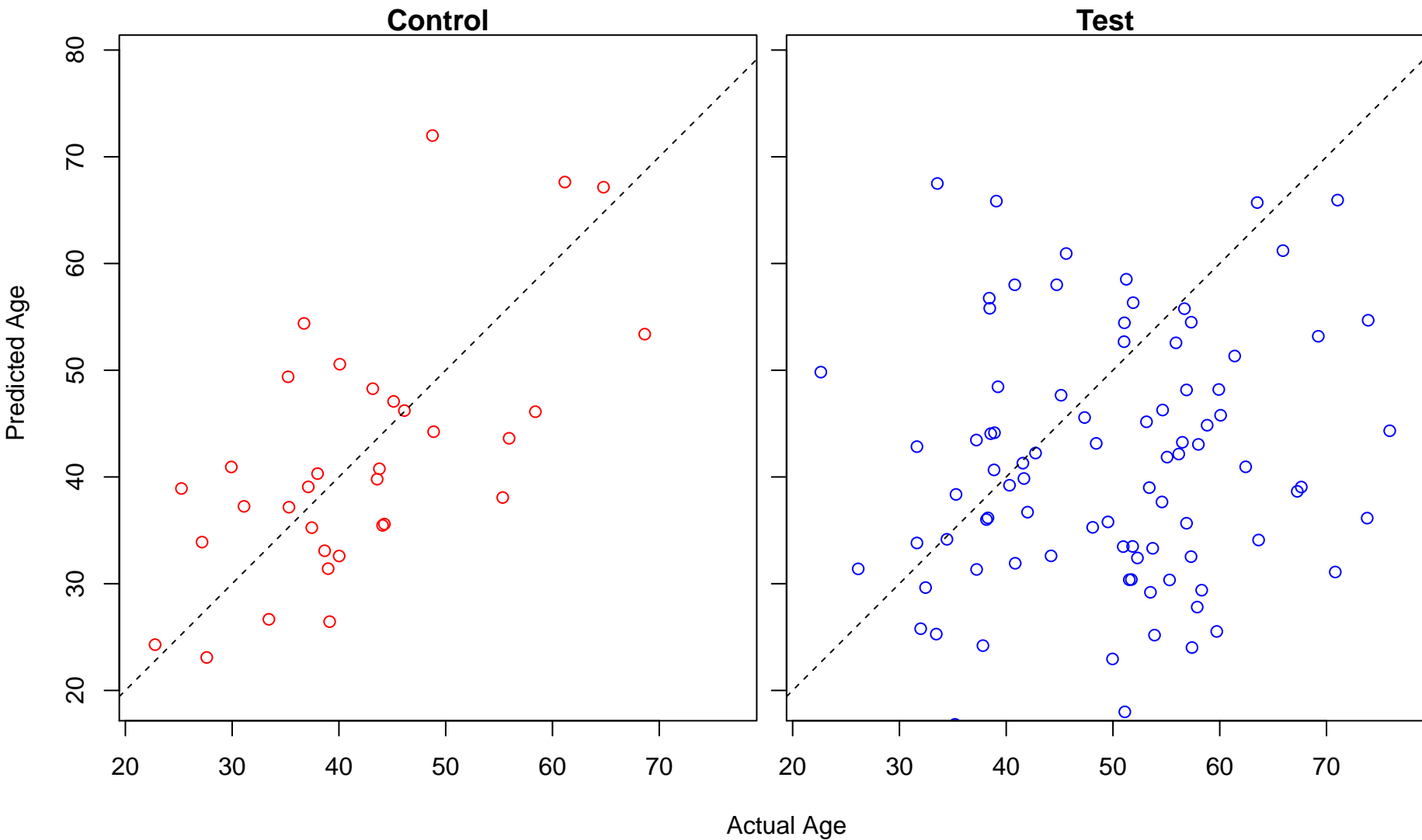
detection of light stimulus (Score: 2.101962)



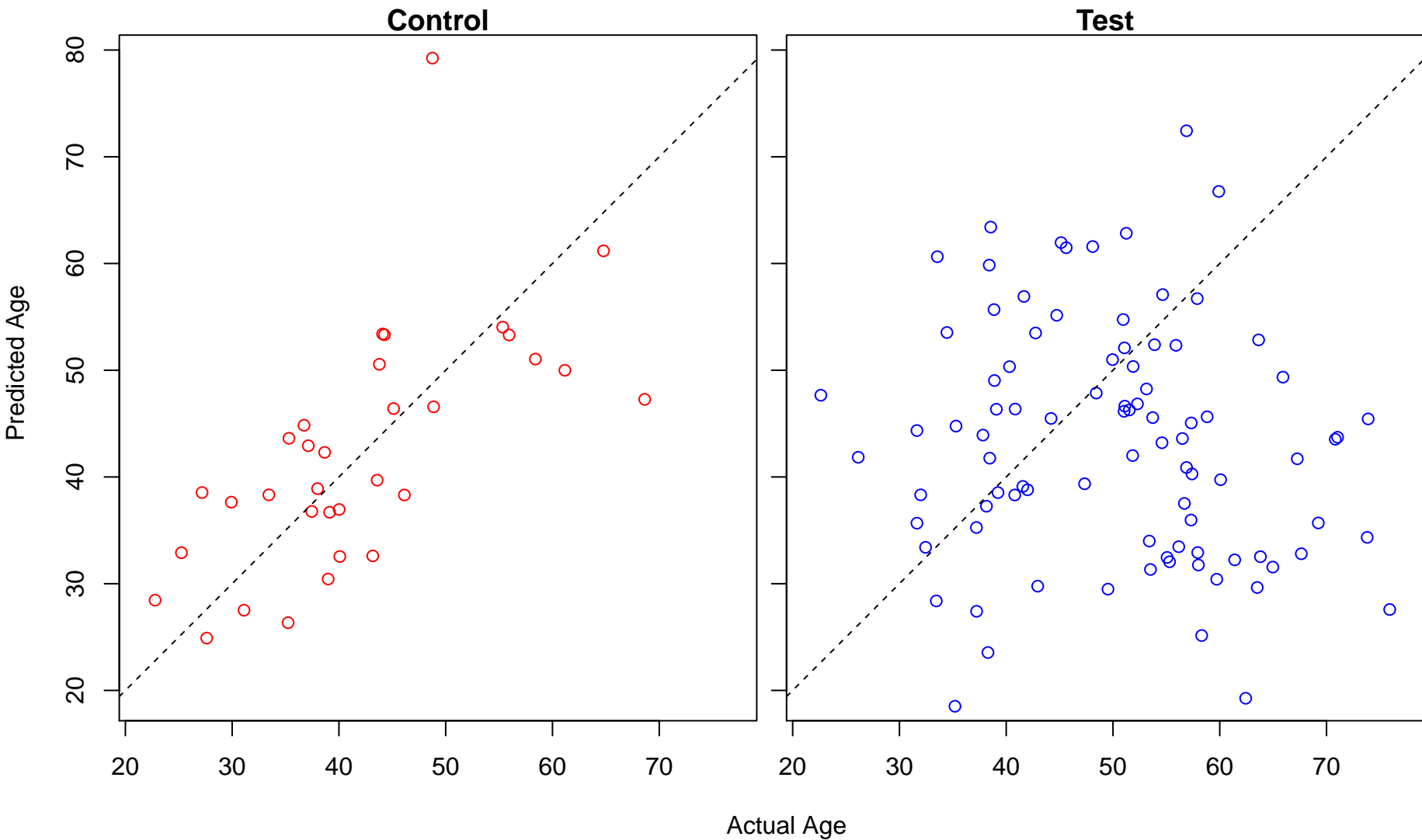
regulation of blood vessel endothelial cell migration (Score: 2.076074)



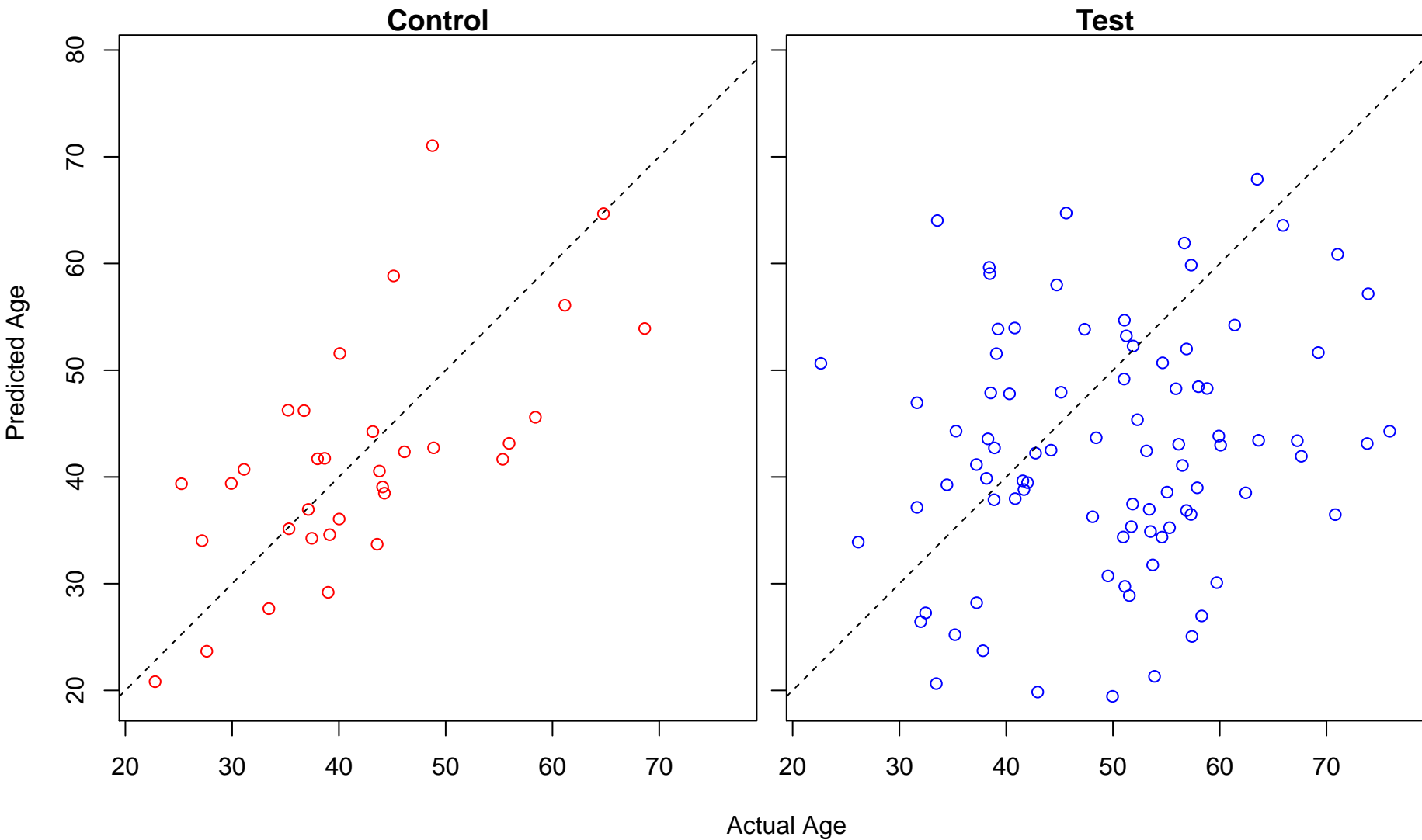
cellular response to molecule of bacterial origin (Score: 2.034874)



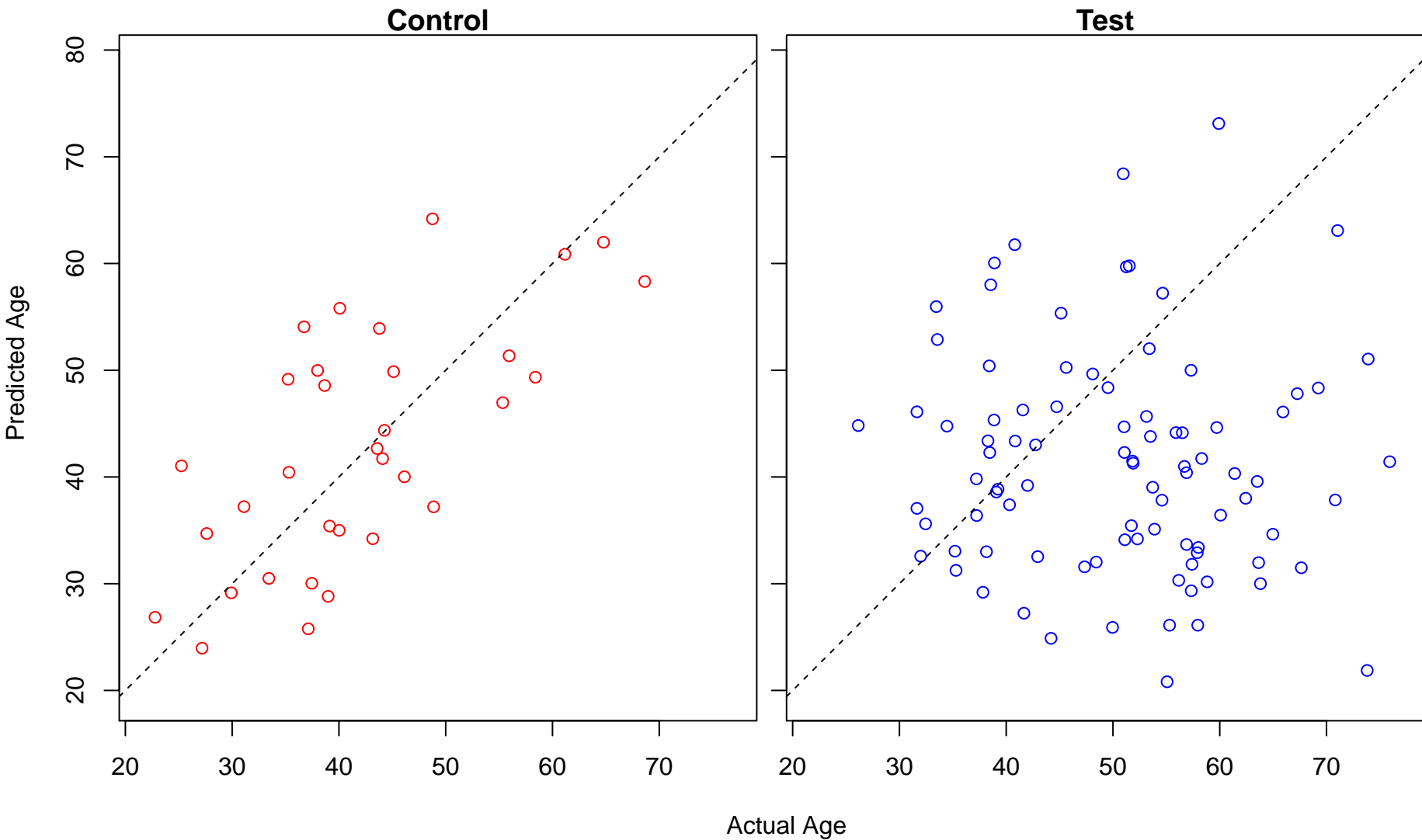
negative regulation of peptidyl-lysine acetylation (Score: 2.034557)



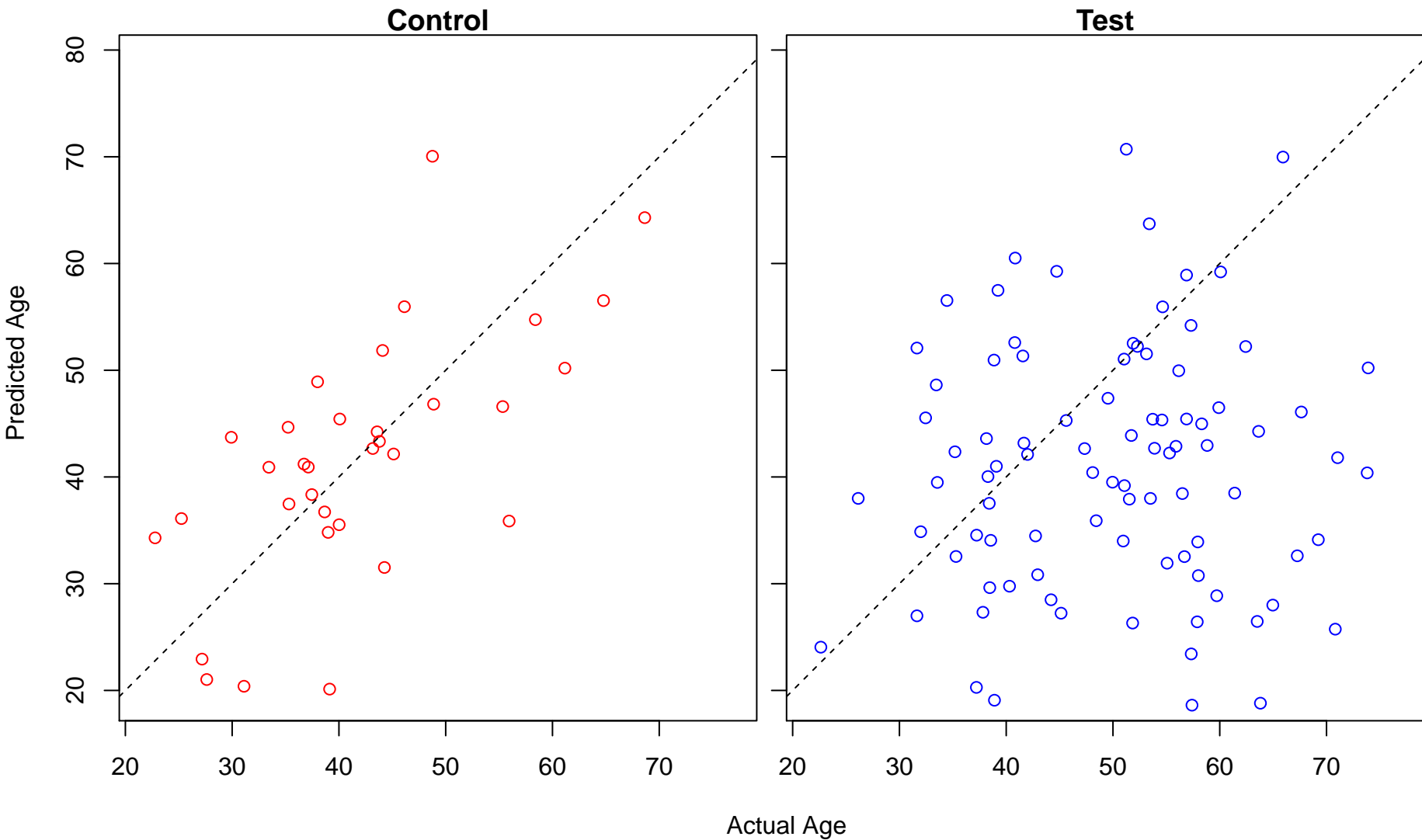
cellular response to biotic stimulus (Score: 2.027429)



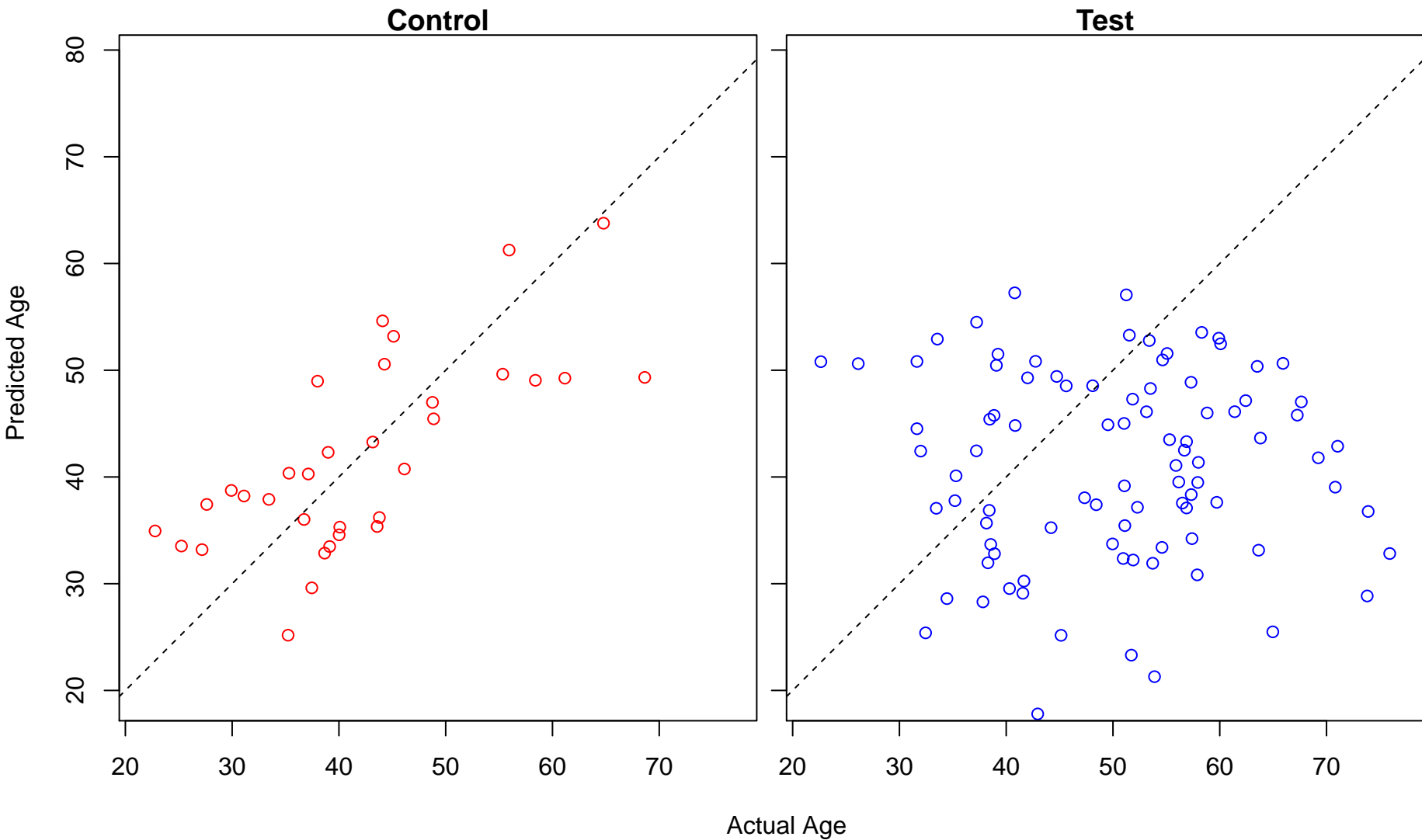
organophosphate catabolic process (Score: 2.023764)



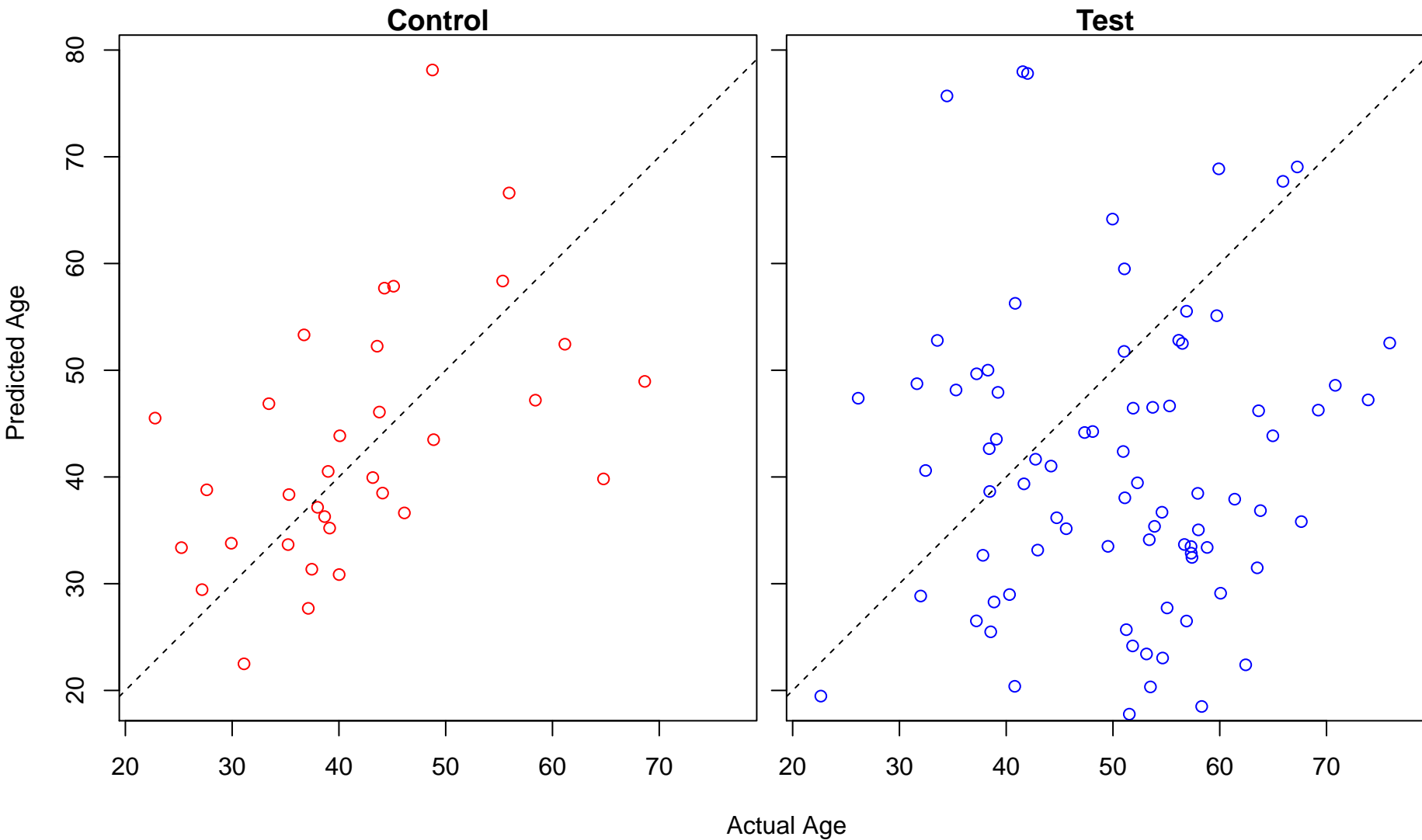
regulation of transcription from RNA polymerase II promoter in response to stress (Score: 2.01823)



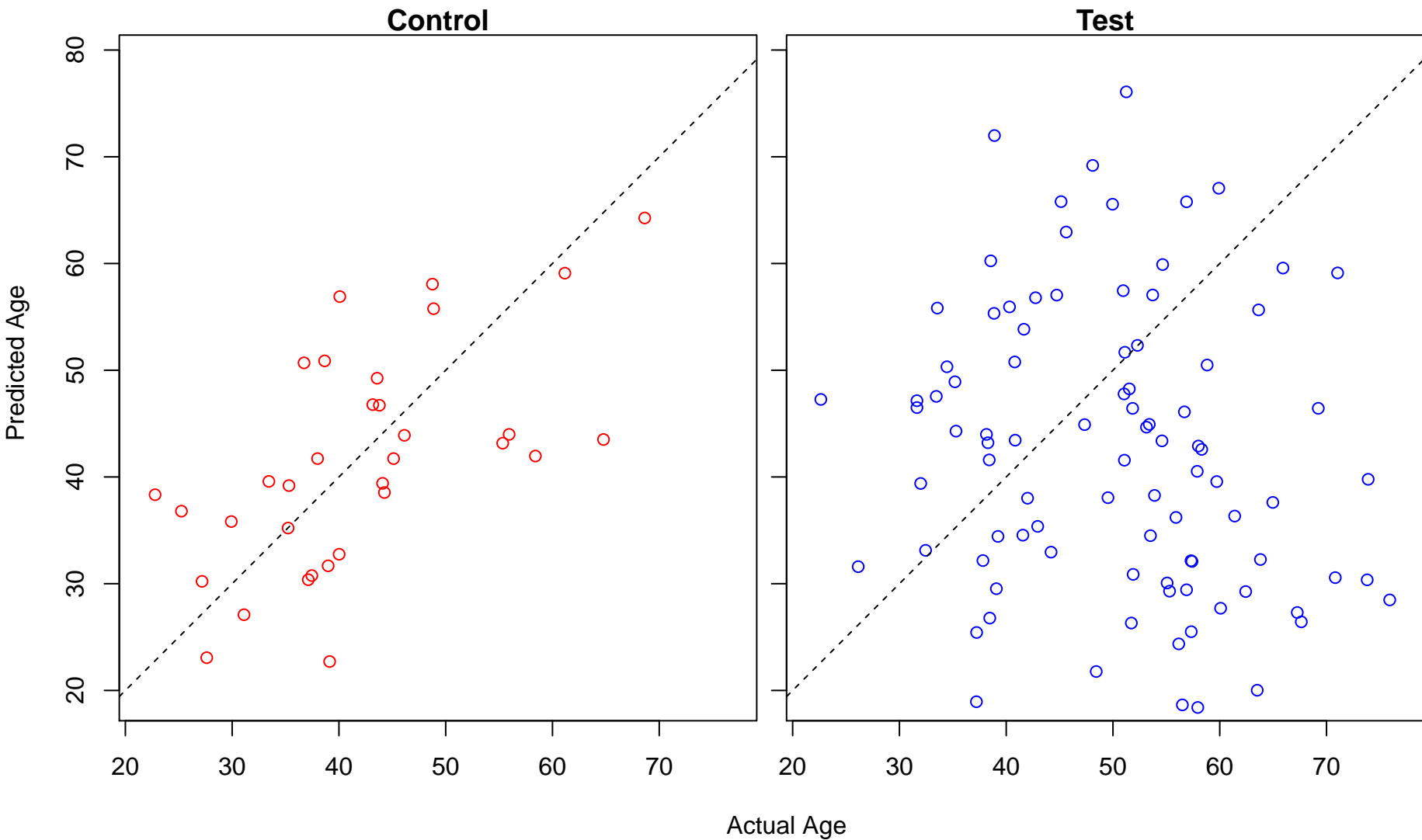
intestinal absorption (Score: 2.018197)



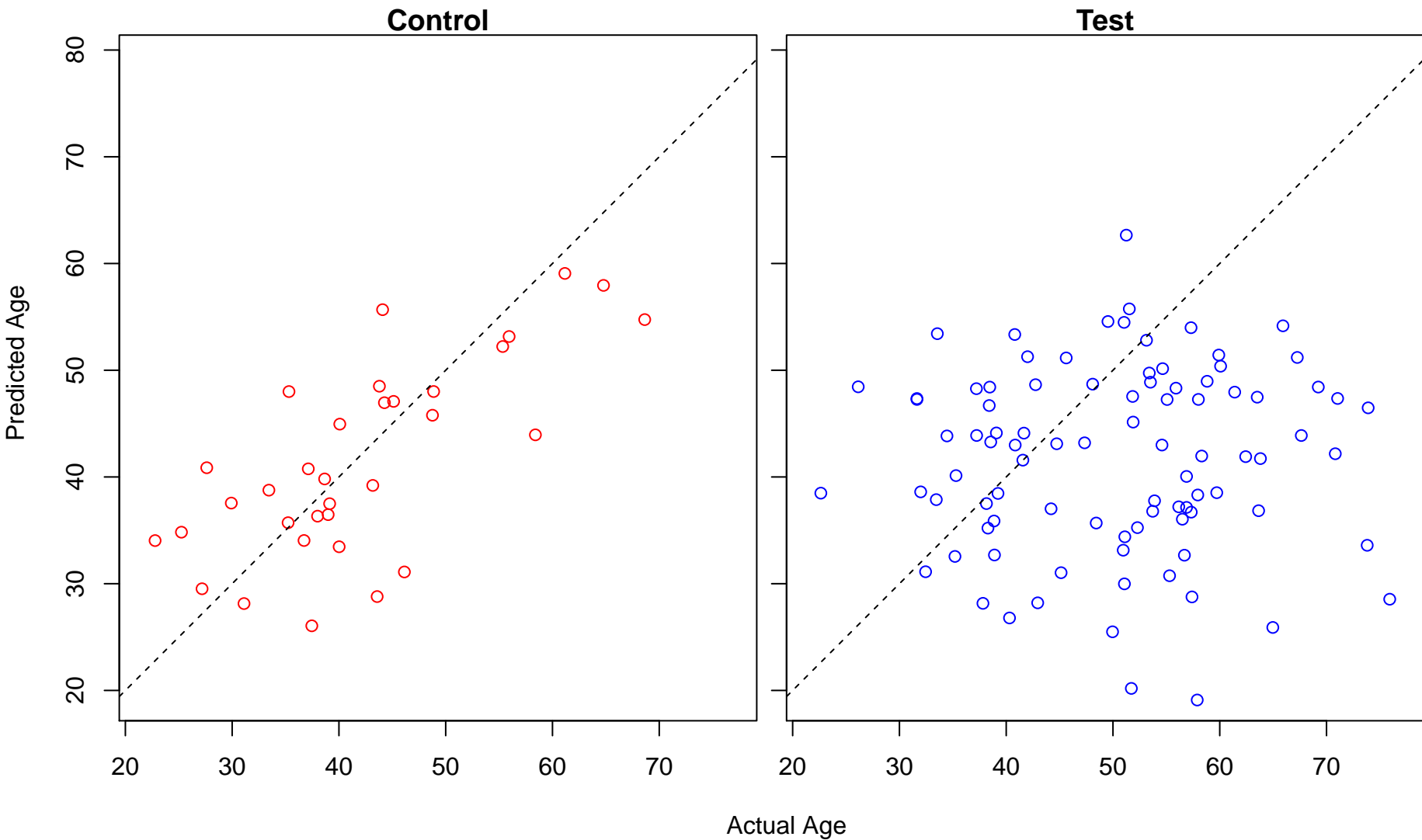
regulation of centrosome cycle (Score: 1.981333)



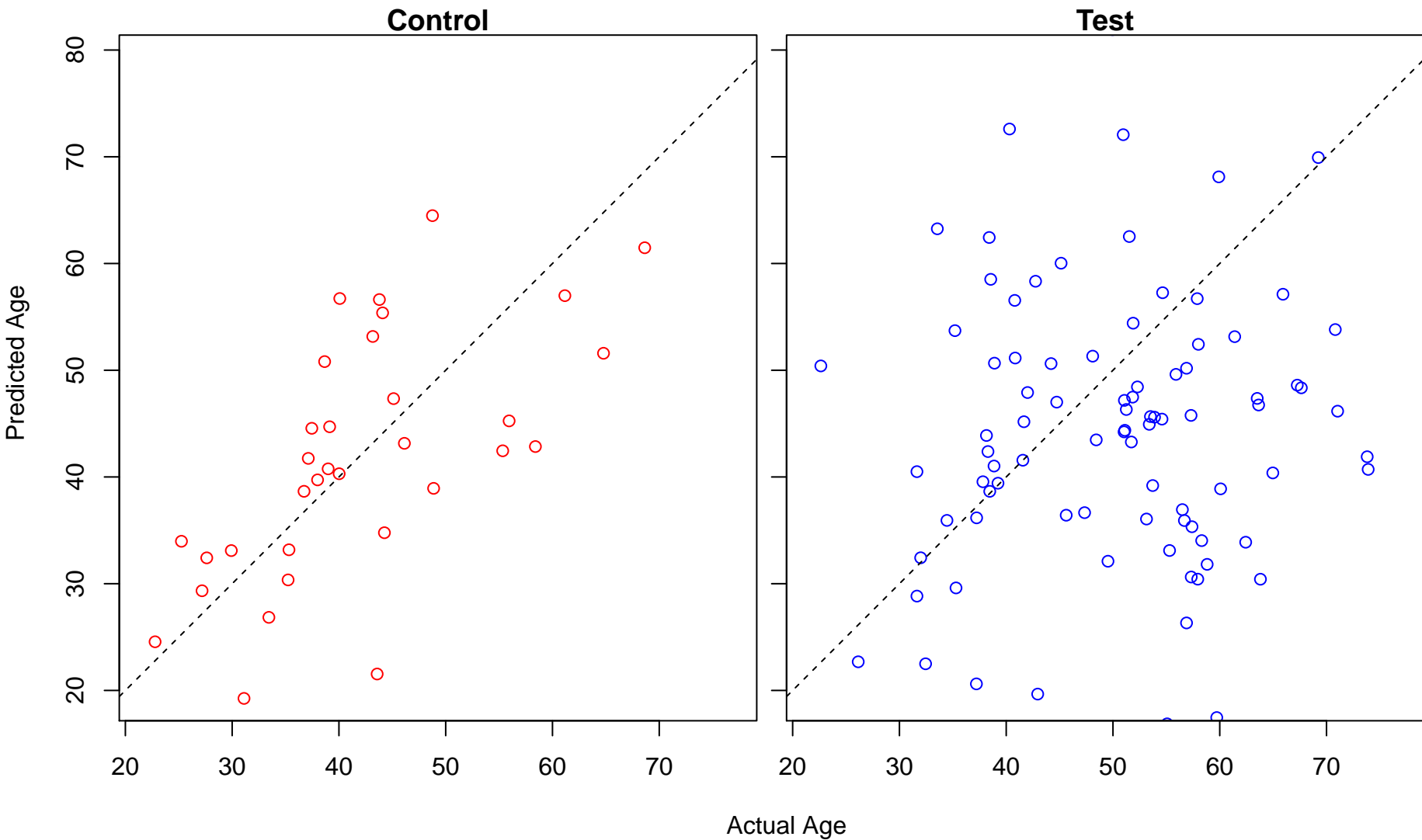
regulation of peptidyl-lysine acetylation (Score: 1.975792)



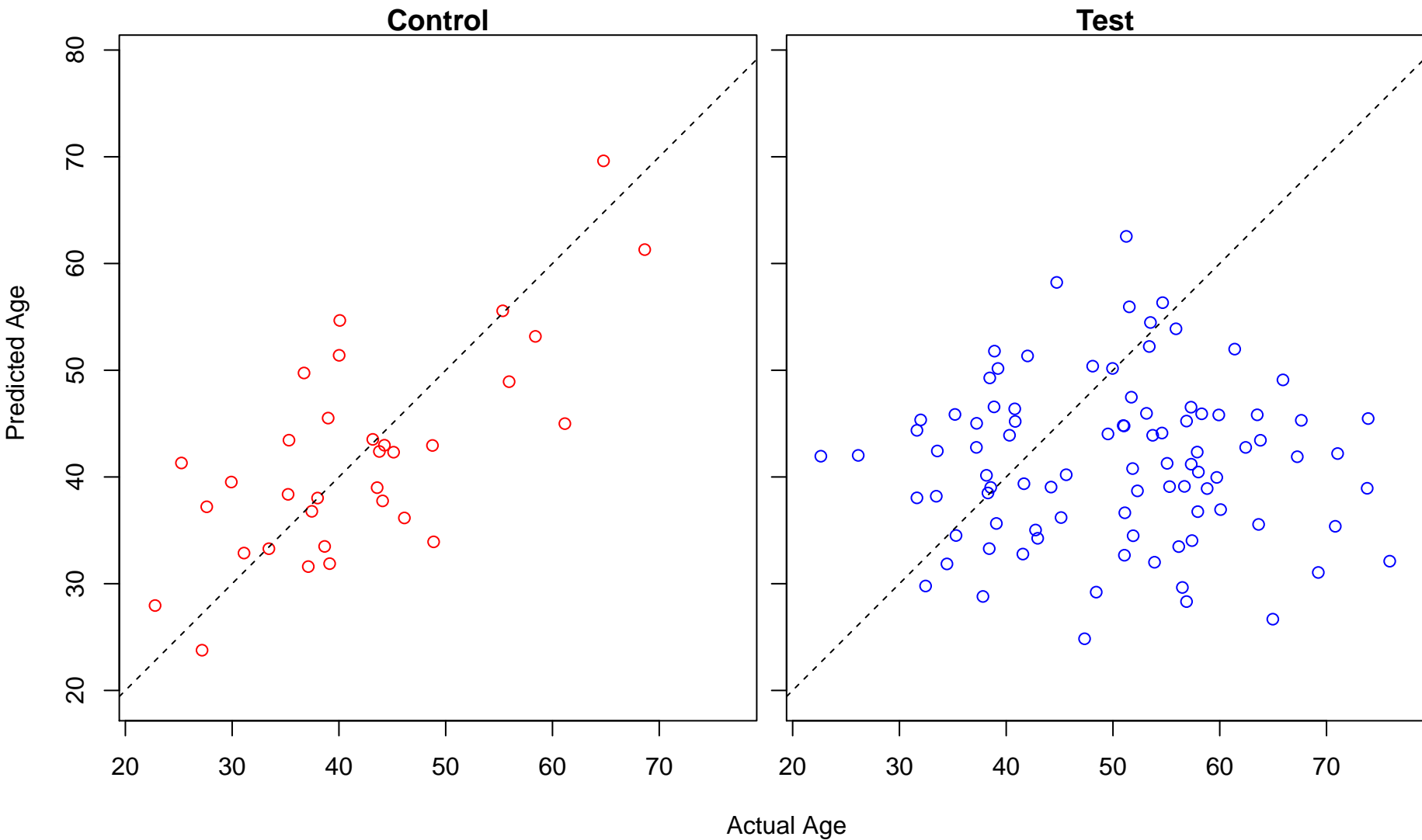
digestion (Score: 1.950334)



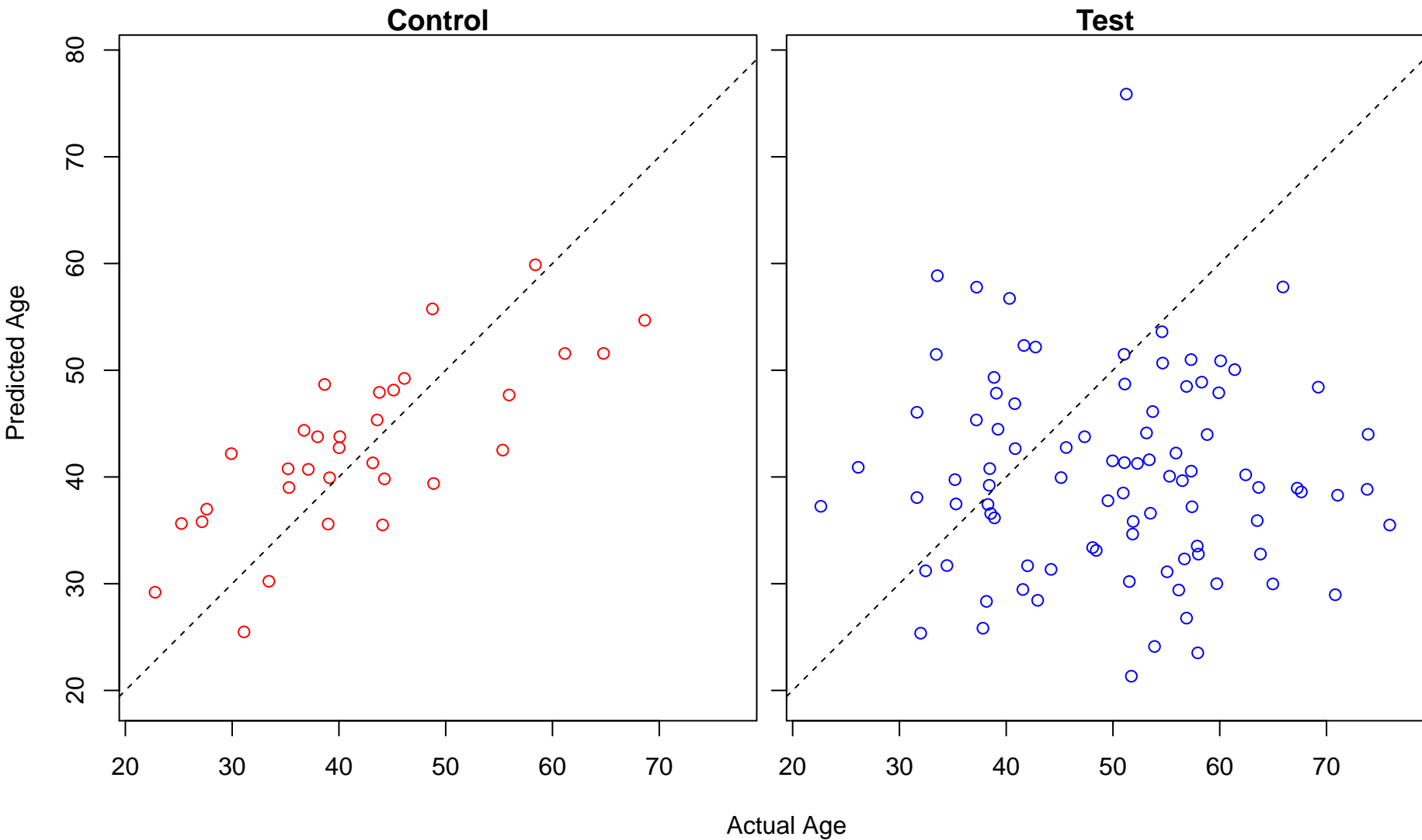
DNA strand elongation (Score: 1.948764)



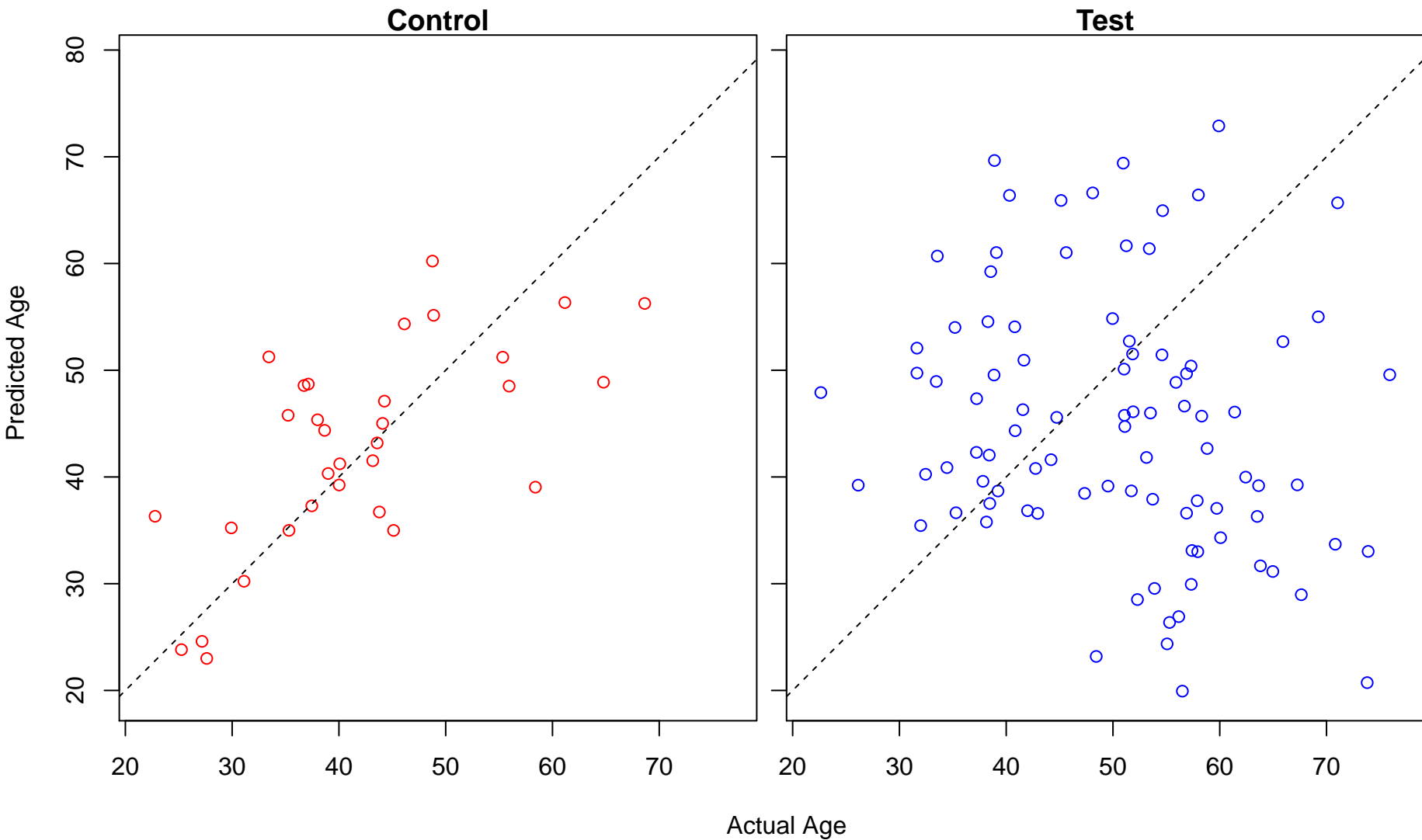
bile acid and bile salt transport (Score: 1.945938)



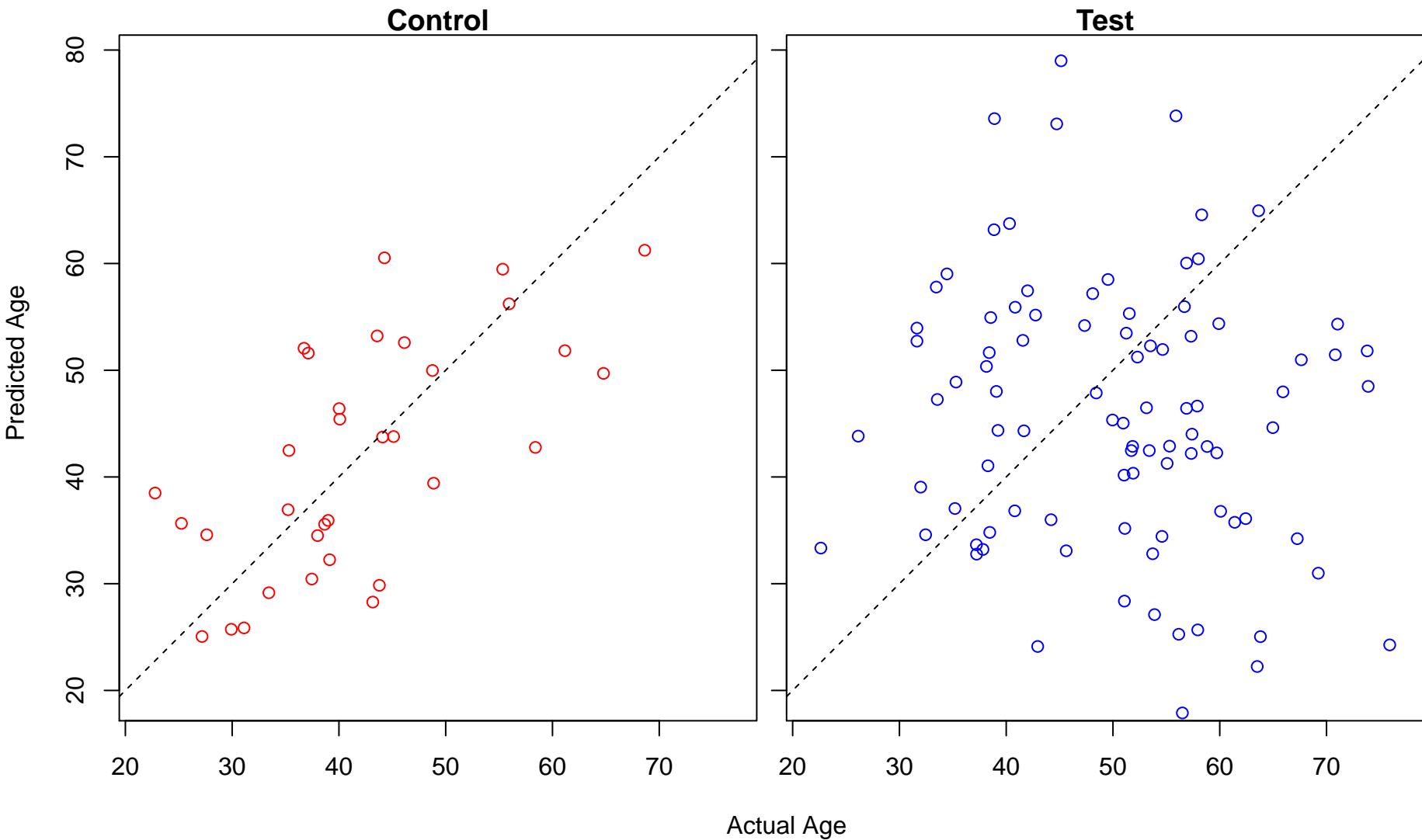
regulation of cholesterol metabolic process (Score: 1.936383)



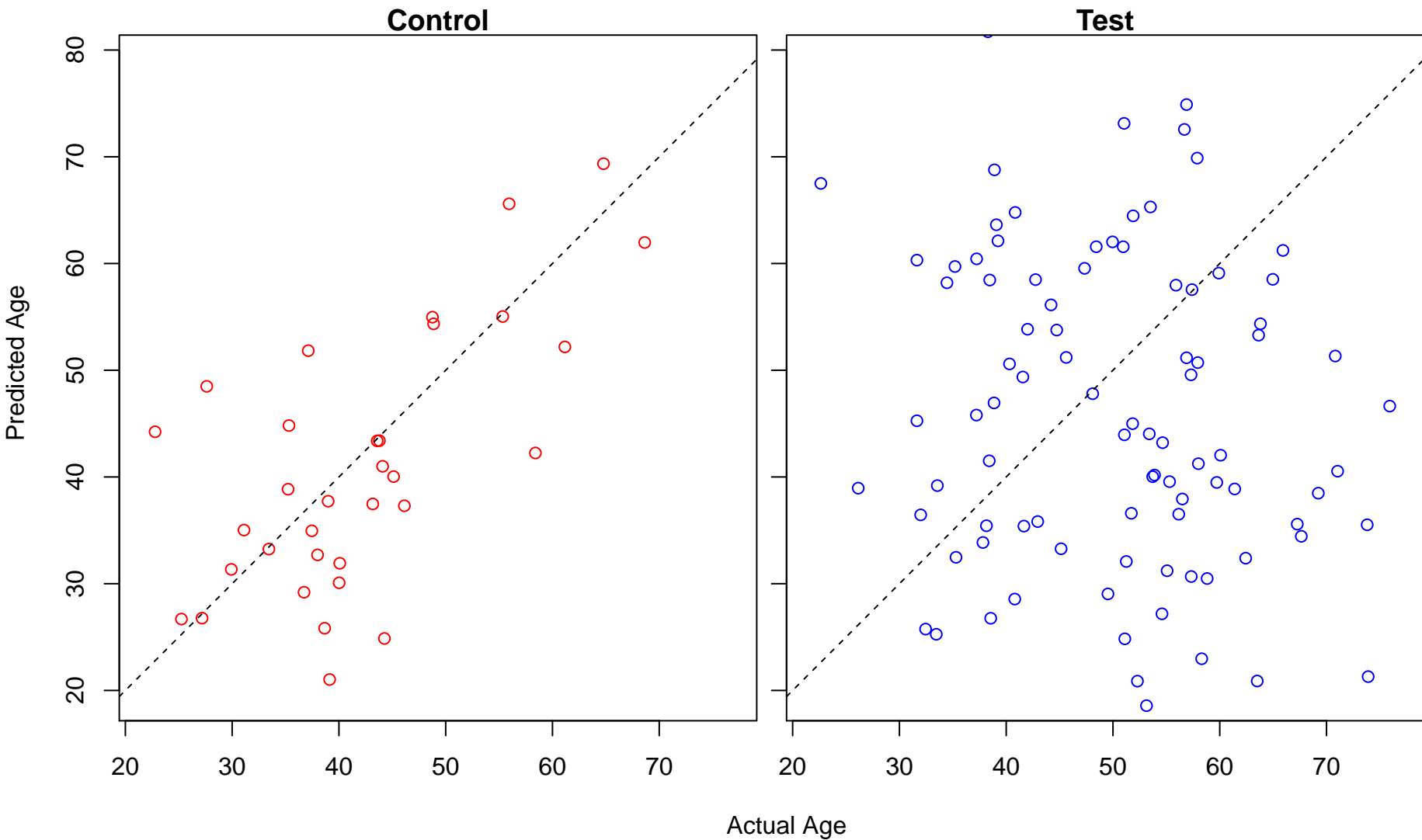
regulation of transcription from RNA polymerase I promoter (Score: 1.894826)



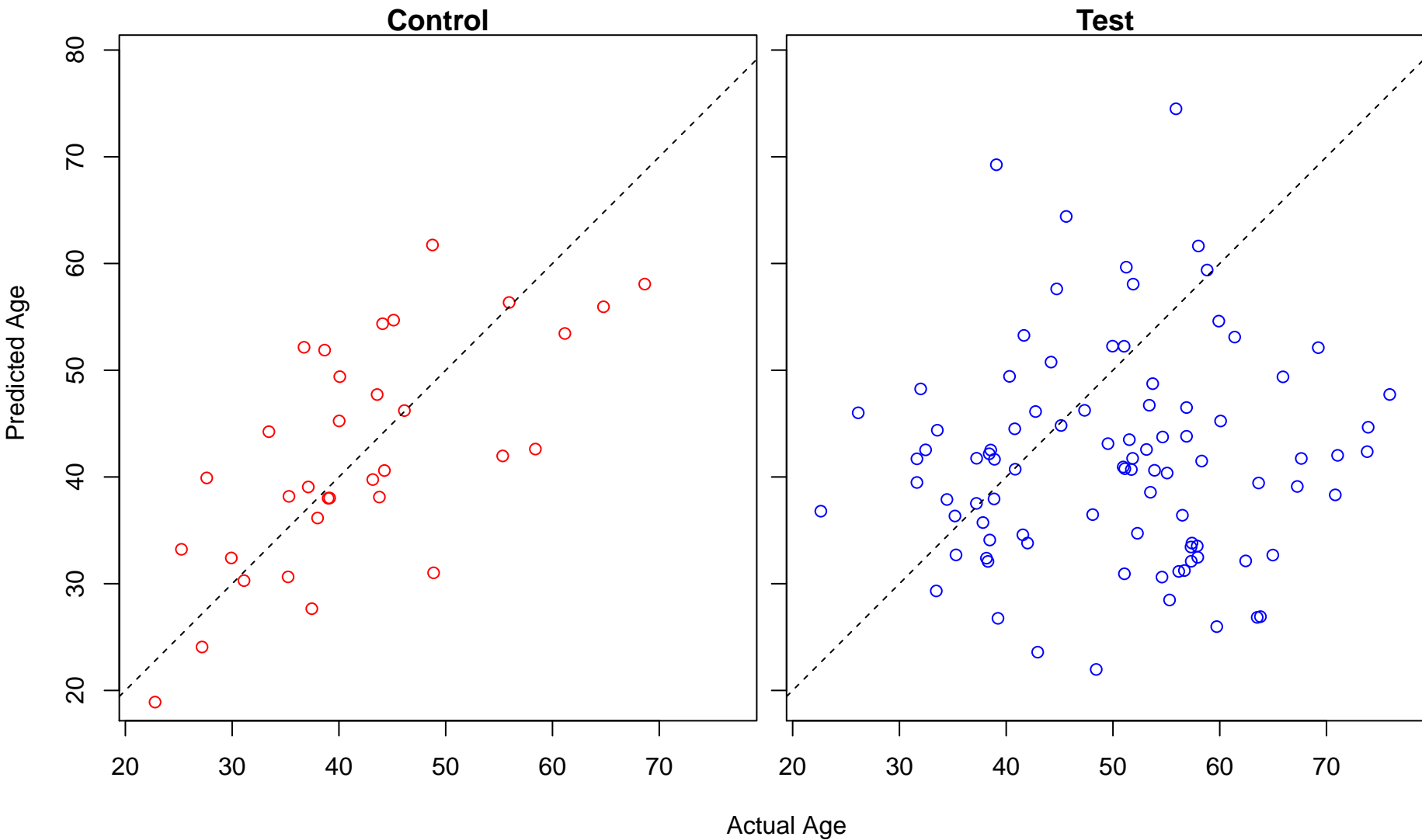
regulation of nitric oxide biosynthetic process (Score: 1.894568)



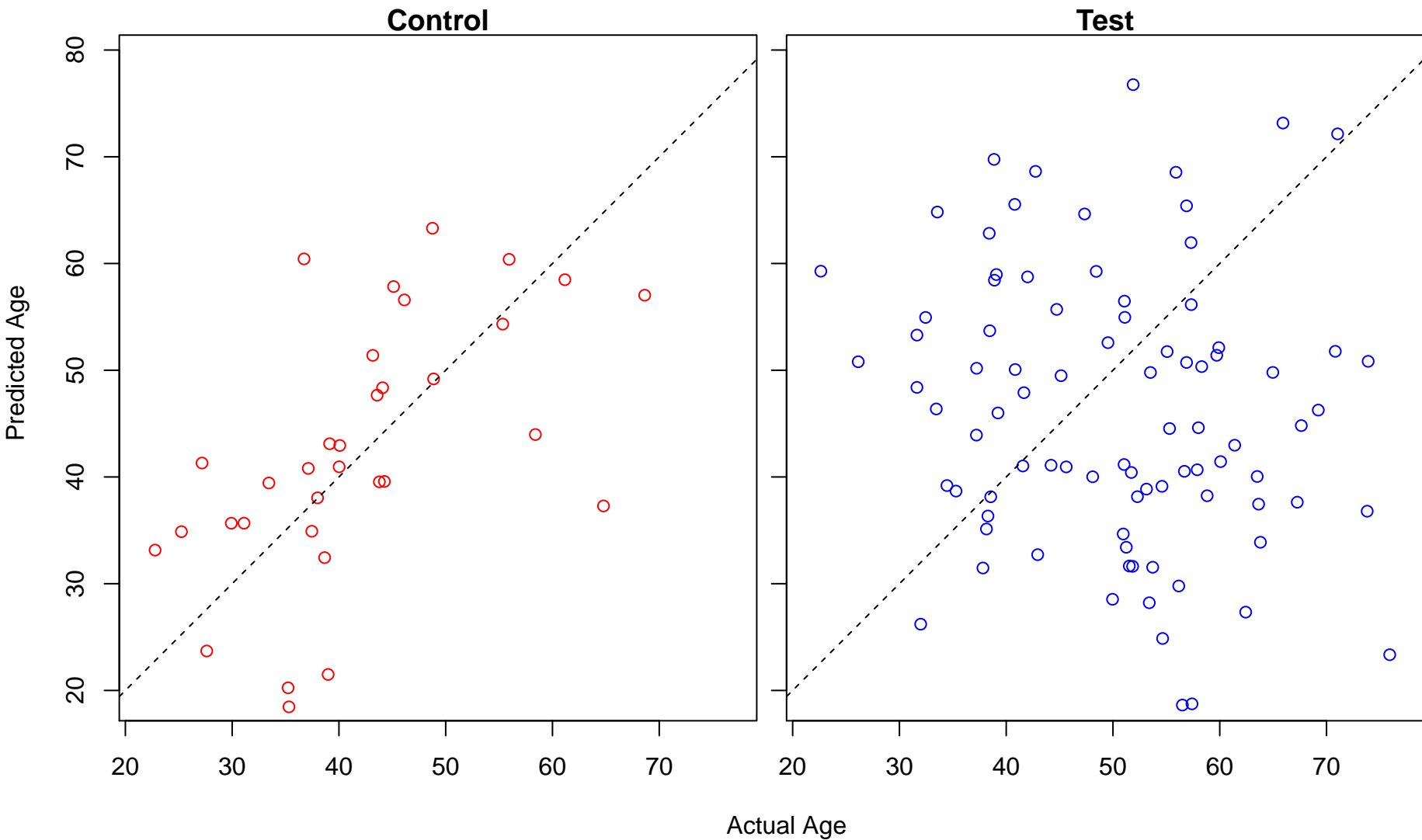
protein heterooligomerization (Score: 1.890288)



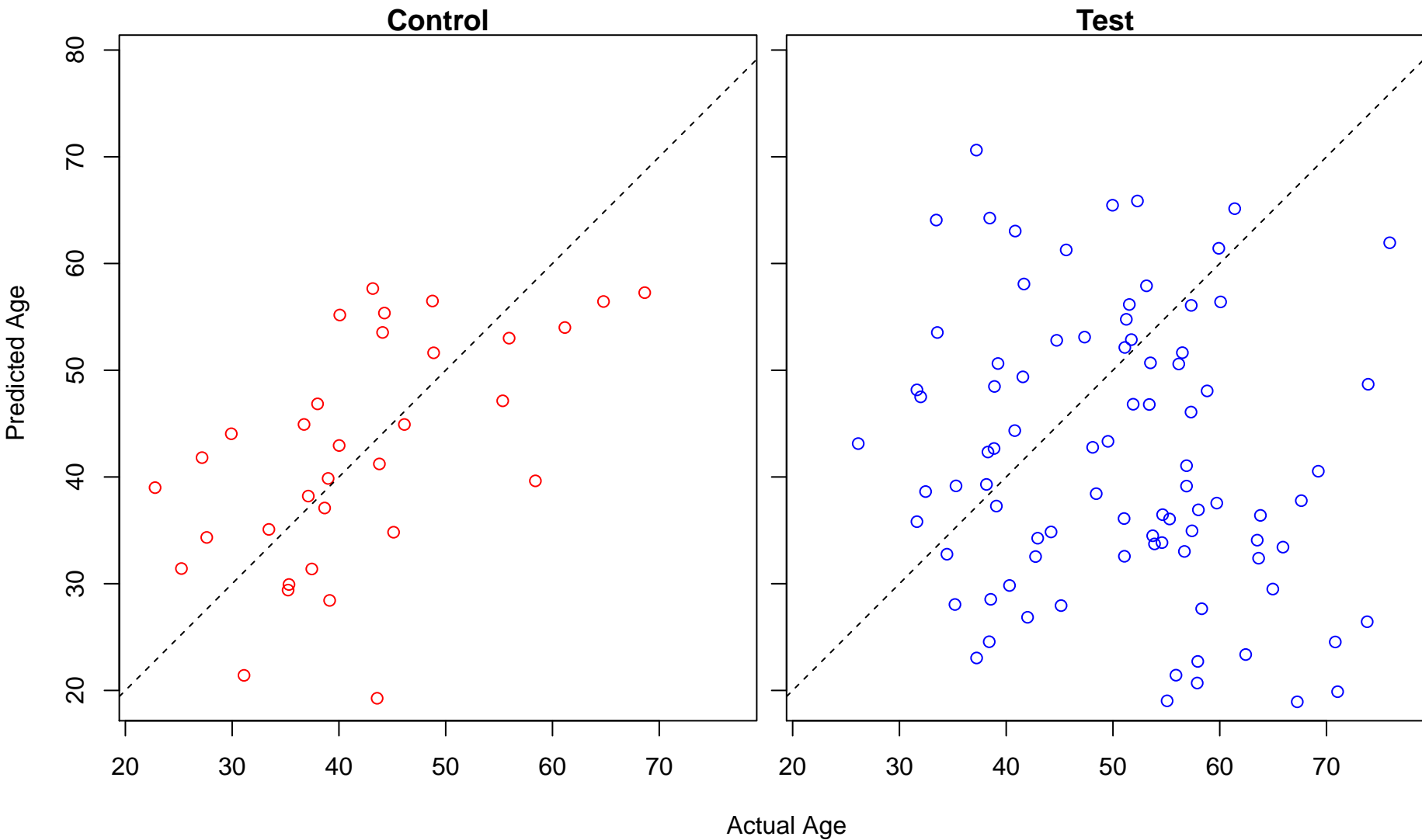
positive regulation of transporter activity (Score: 1.877813)



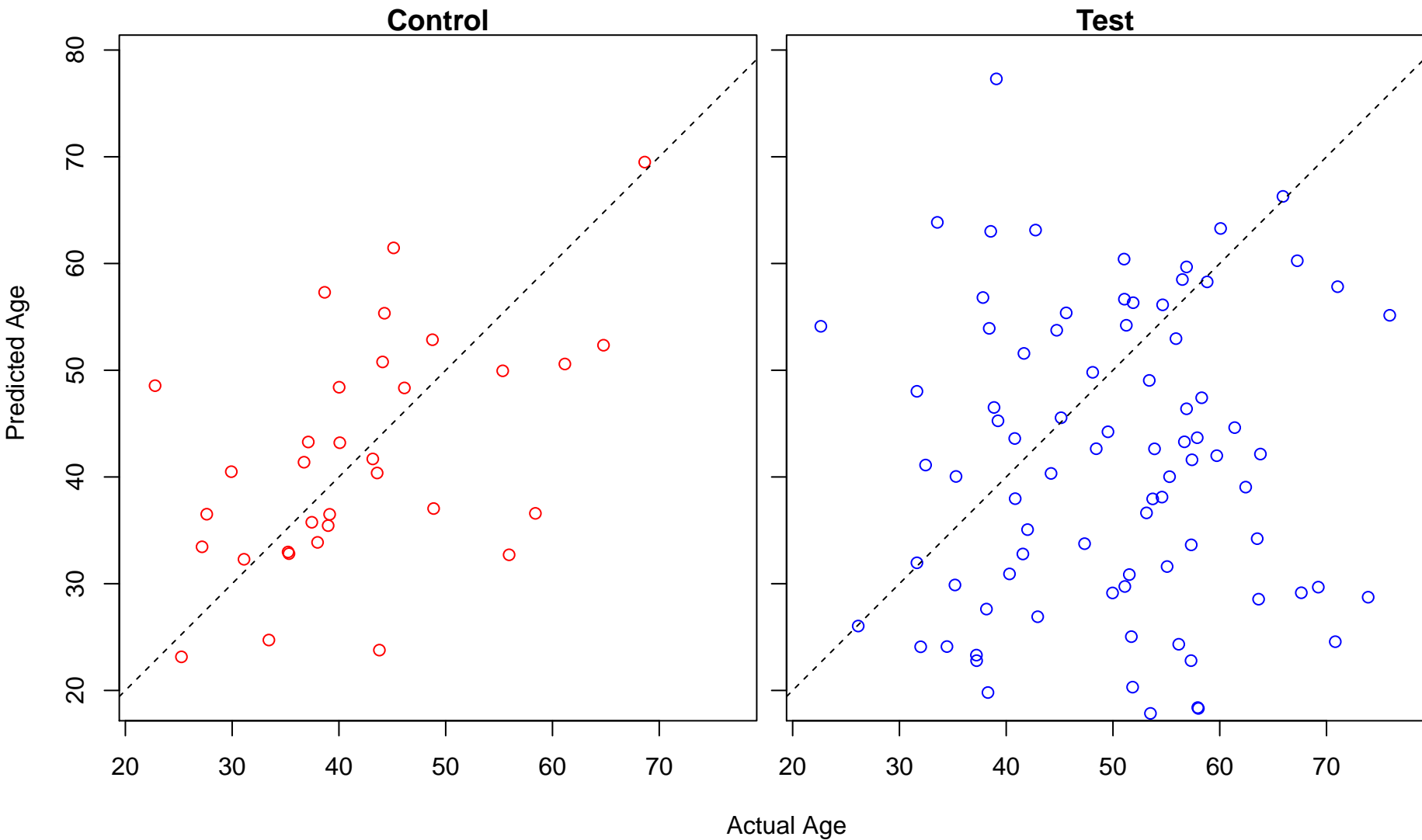
regulation of alpha-beta T cell differentiation (Score: 1.869673)



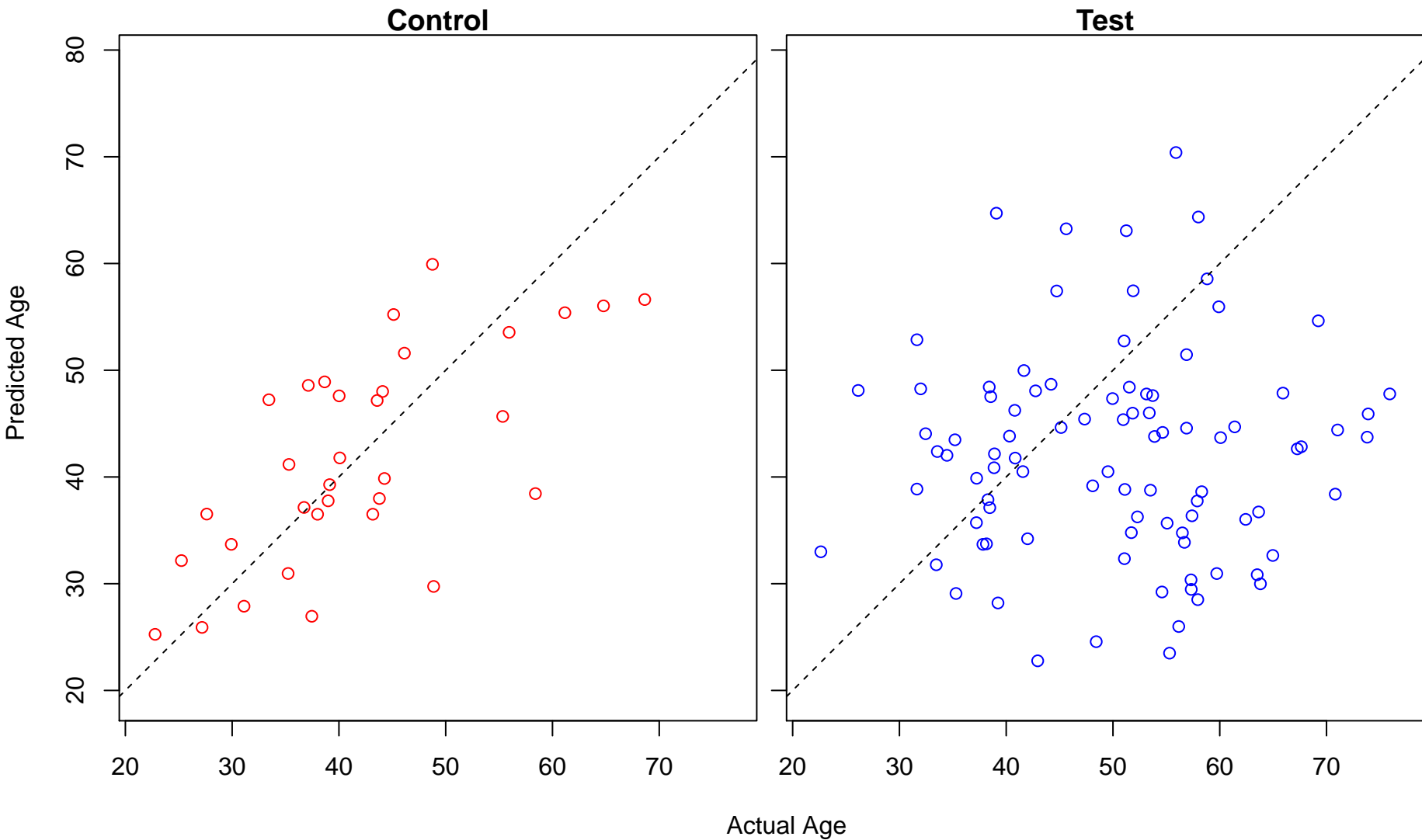
cytochrome complex assembly (Score: 1.860558)



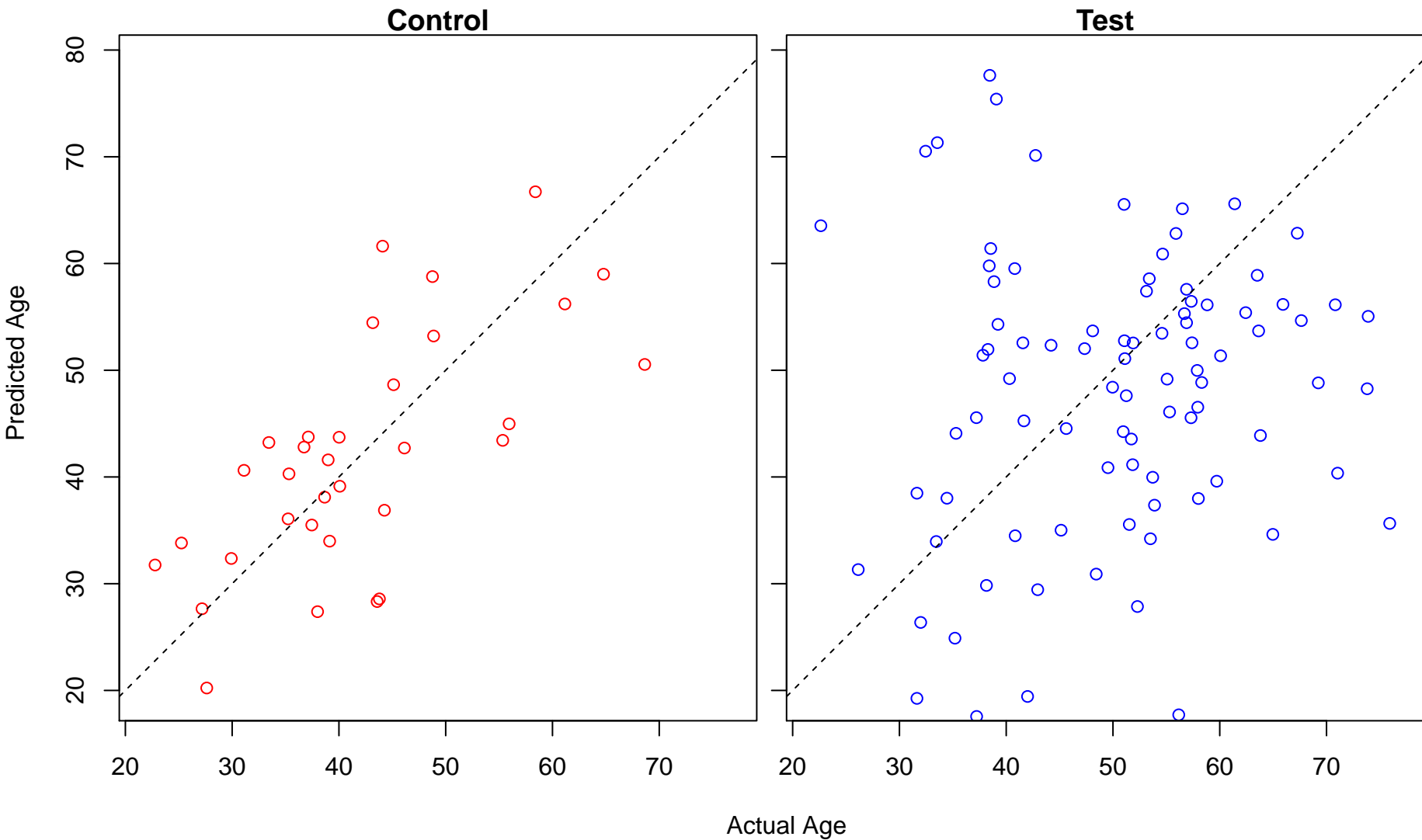
CD4-positive, alpha-beta T cell activation (Score: 1.853263)



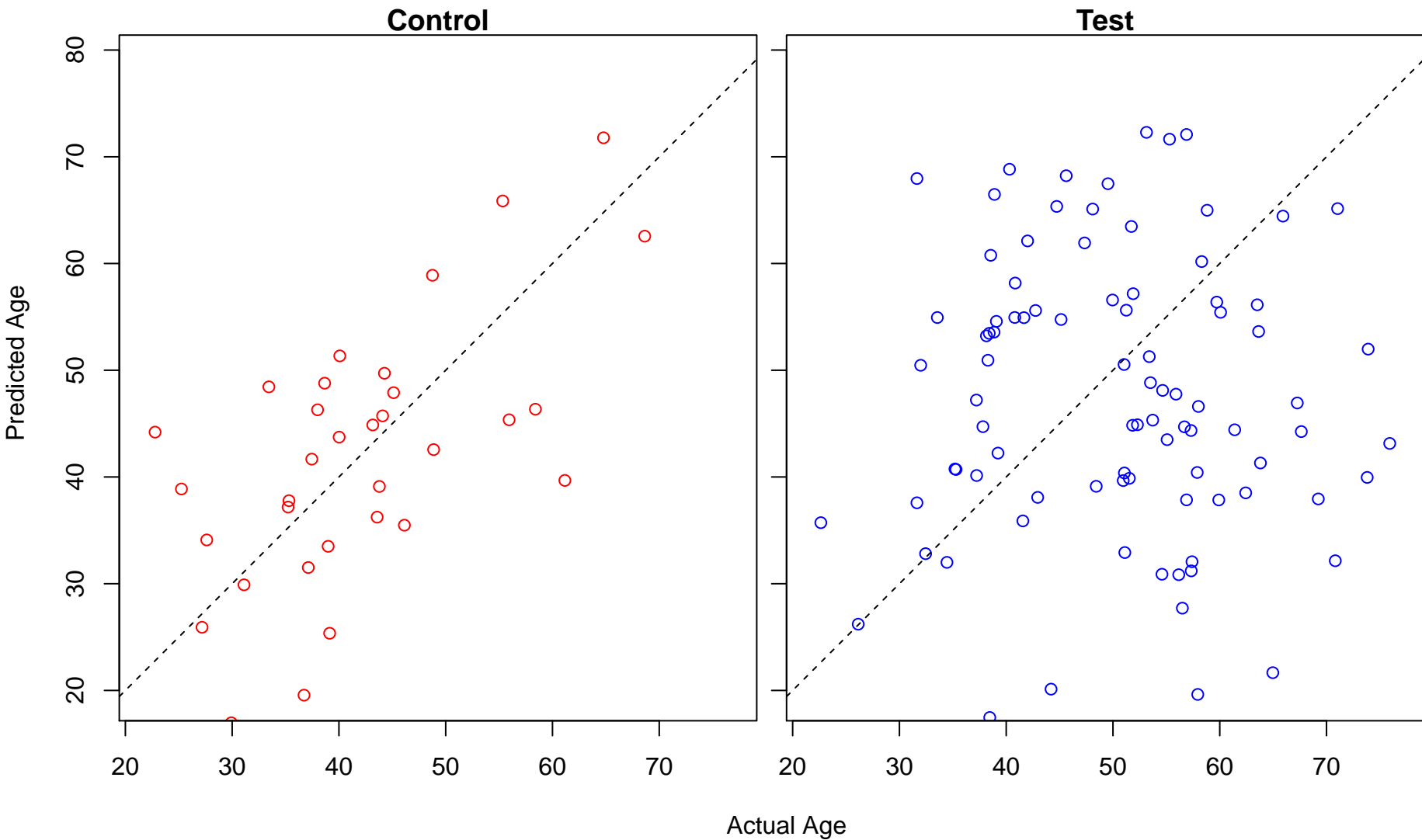
positive regulation of ion transmembrane transporter activity (Score: 1.849434)



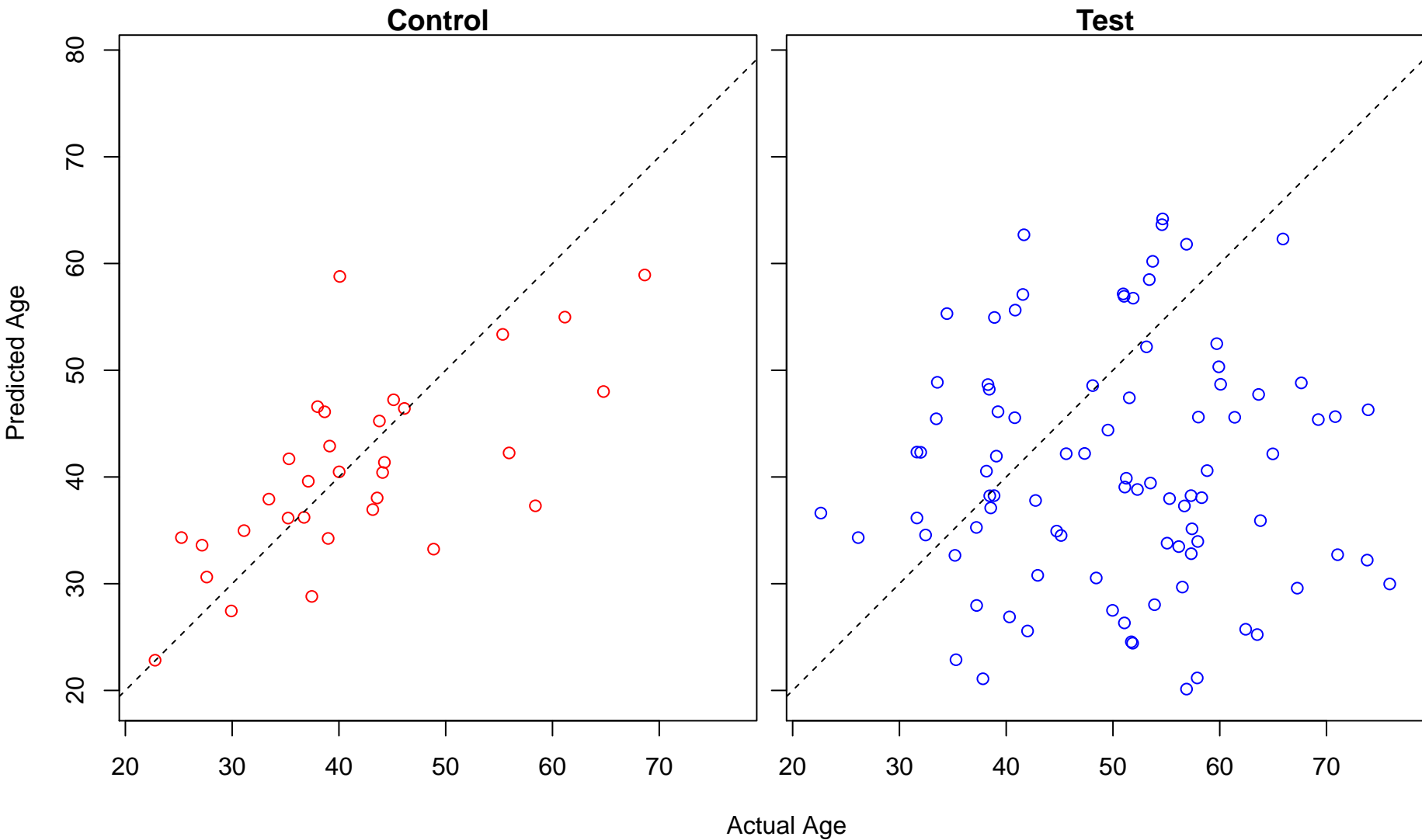
acute inflammatory response (Score: 1.843626)



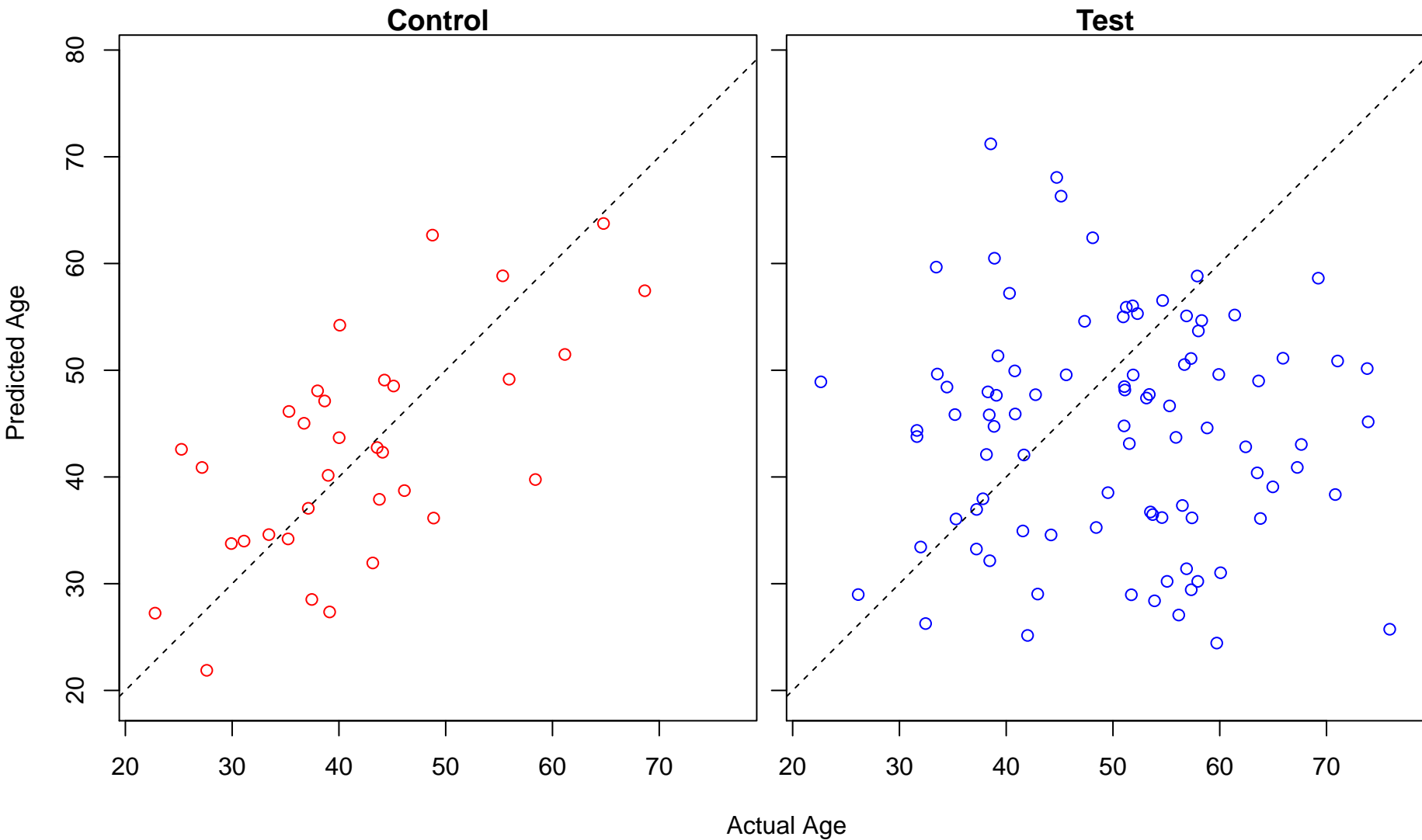
regulation of NF-kappaB import into nucleus (Score: 1.815769)



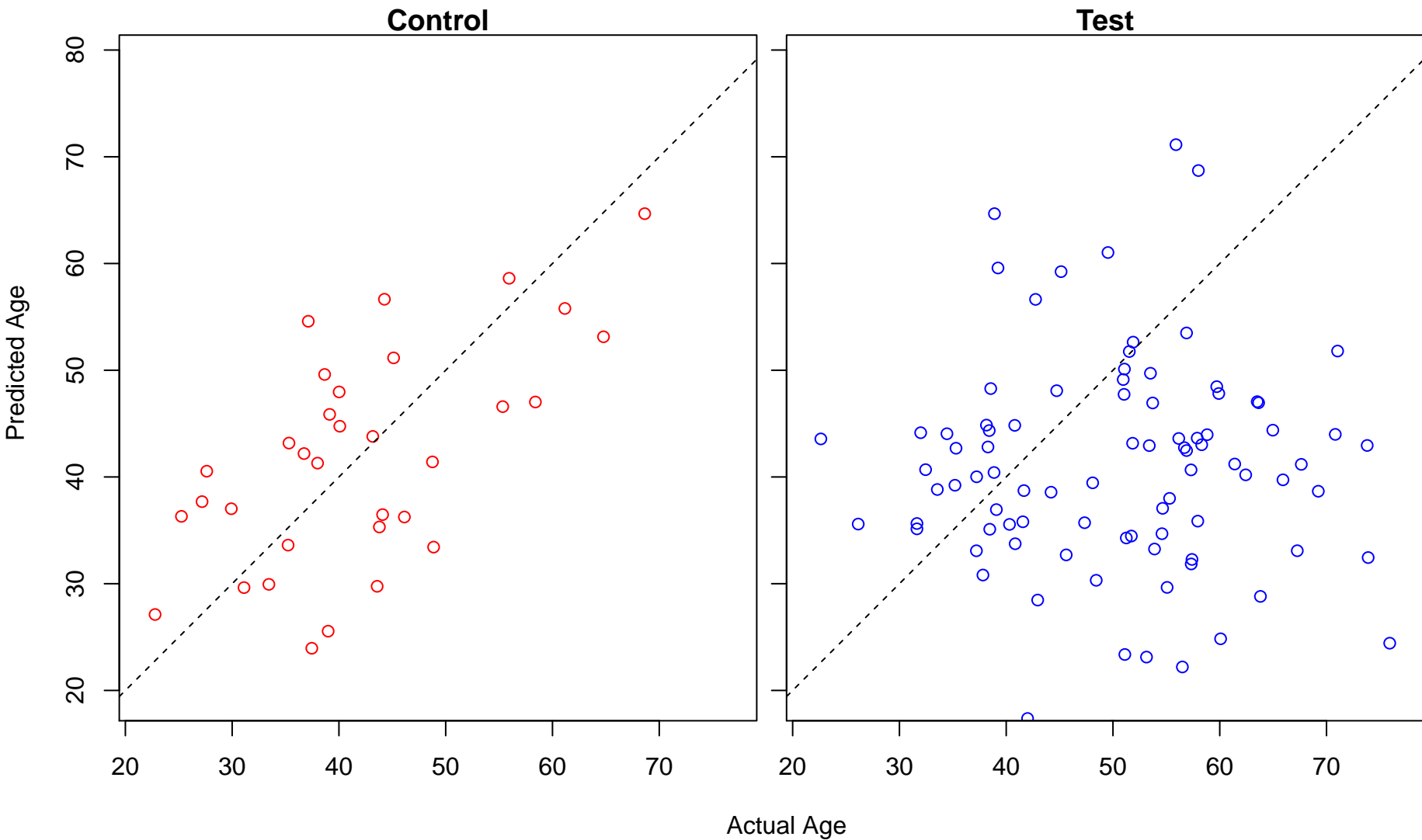
non-recombinational repair (Score: 1.772003)



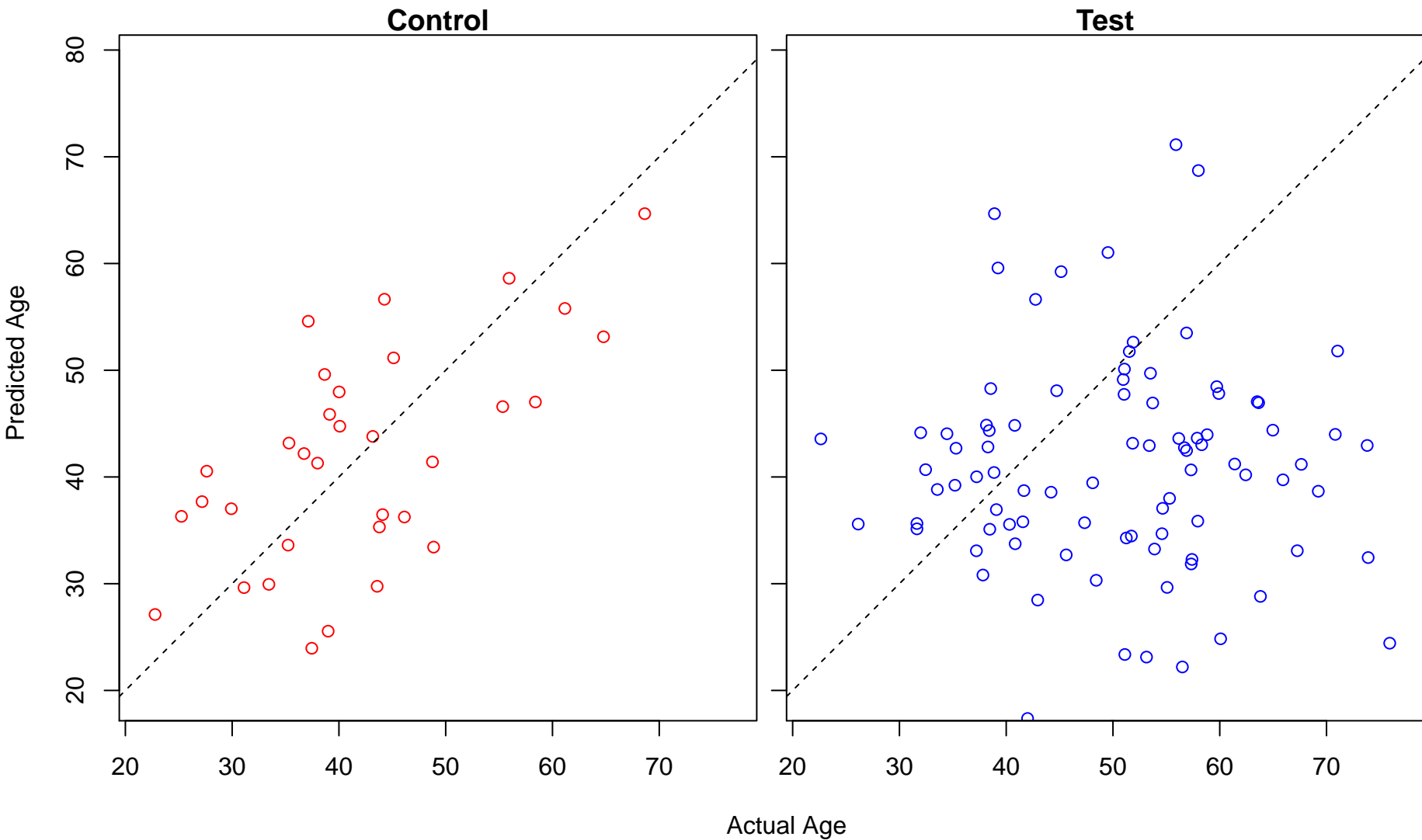
intracellular protein transmembrane transport (Score: 1.769502)



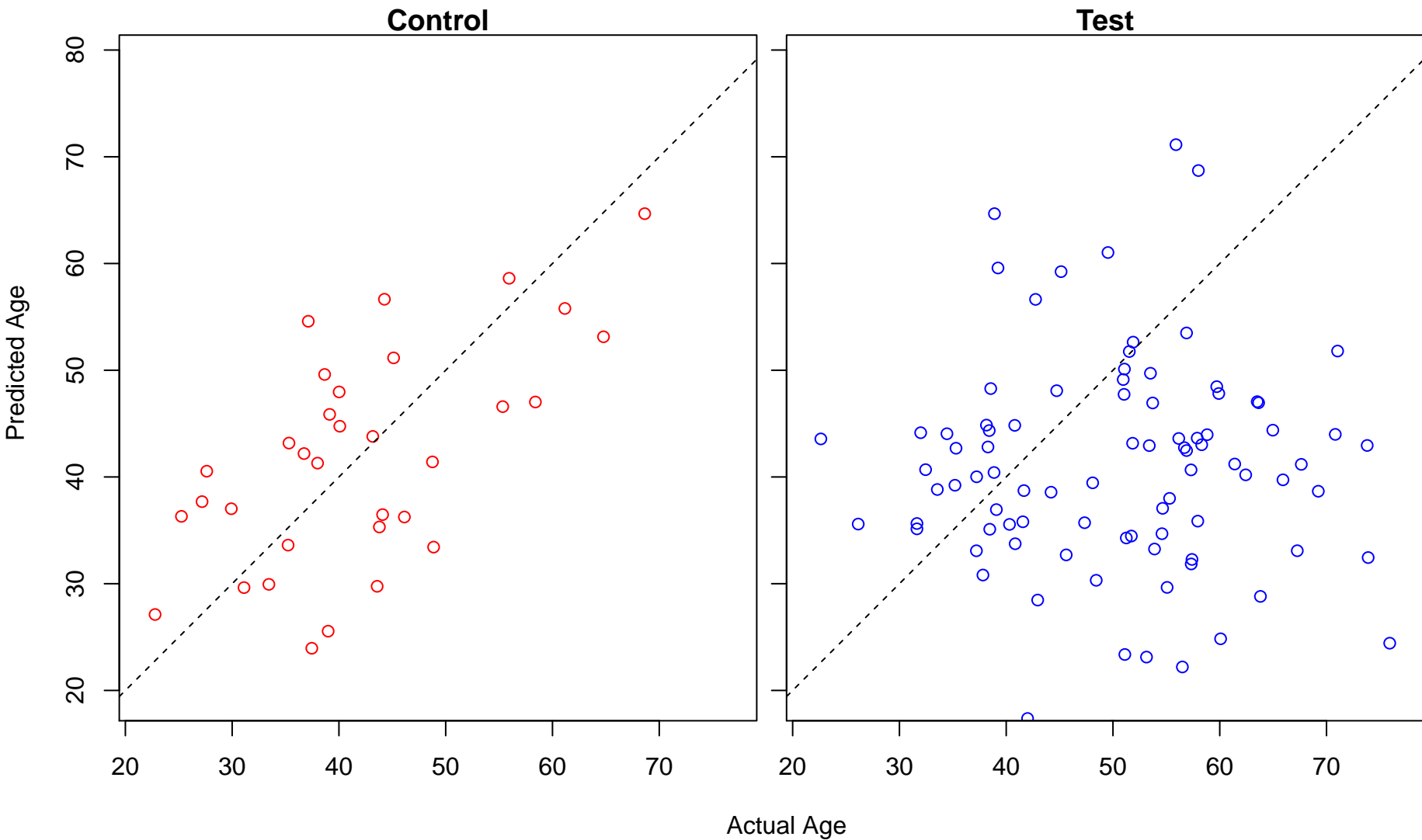
ferric iron transport (Score: 1.762852)



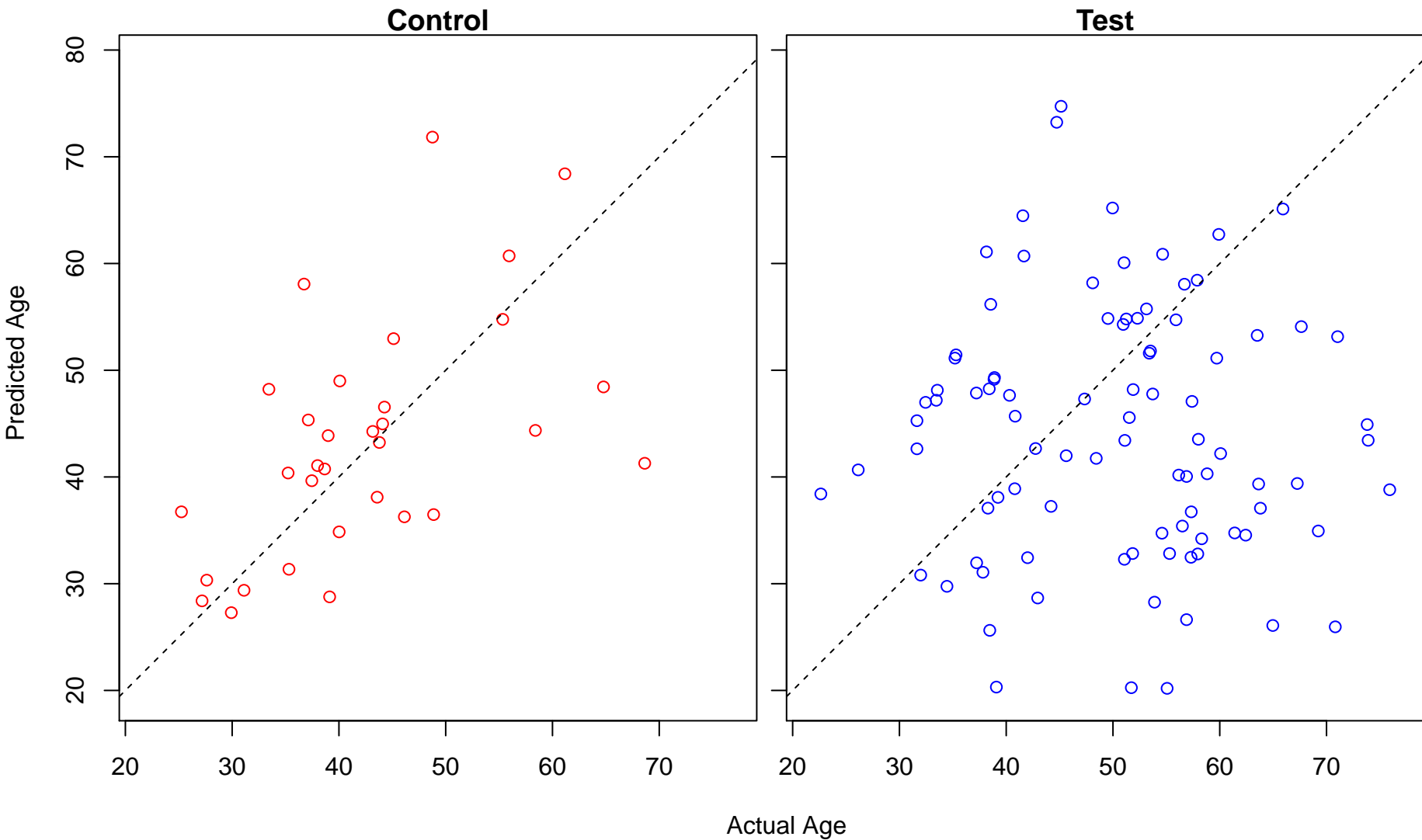
transferrin transport (Score: 1.762852)



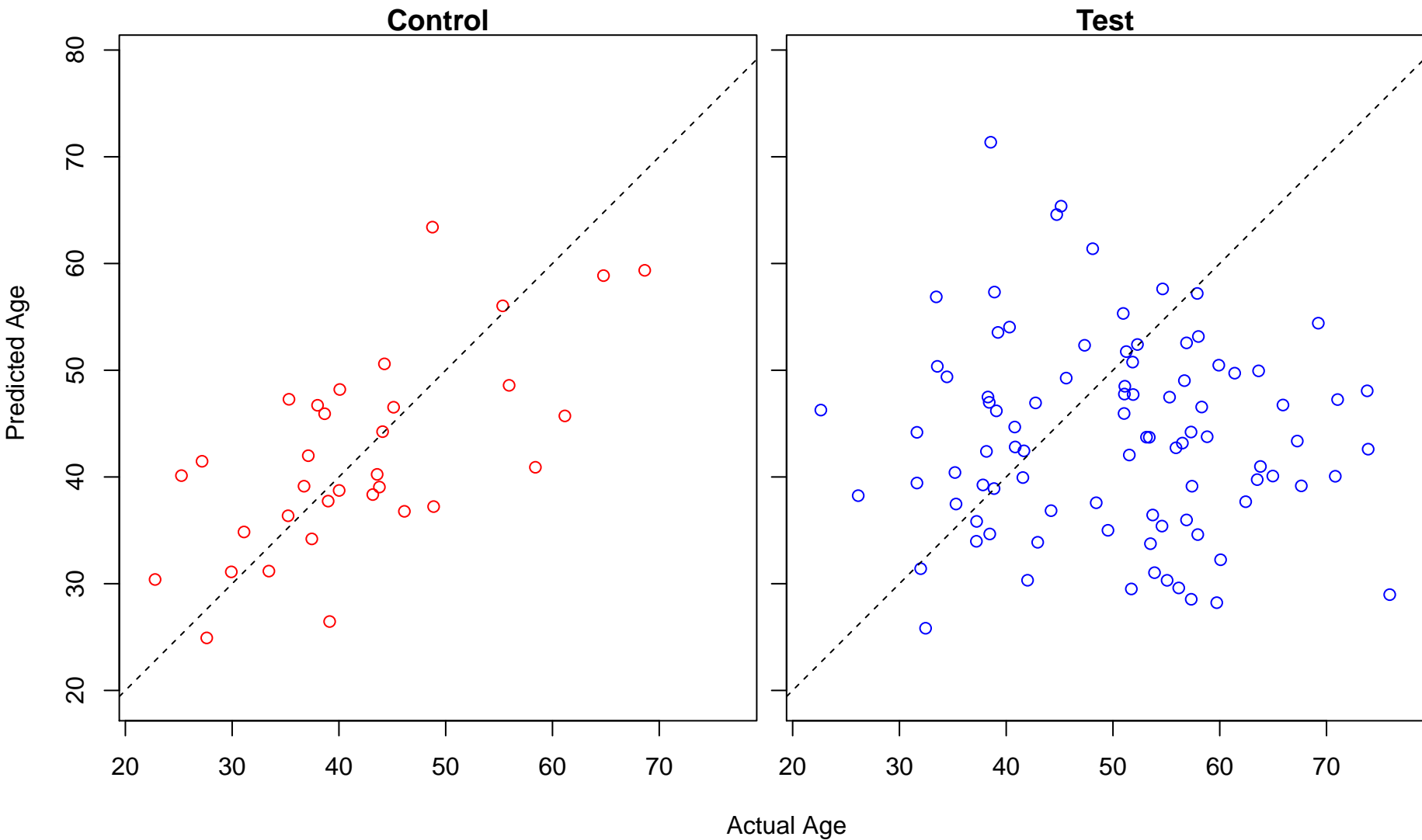
trivalent inorganic cation transport (Score: 1.762852)



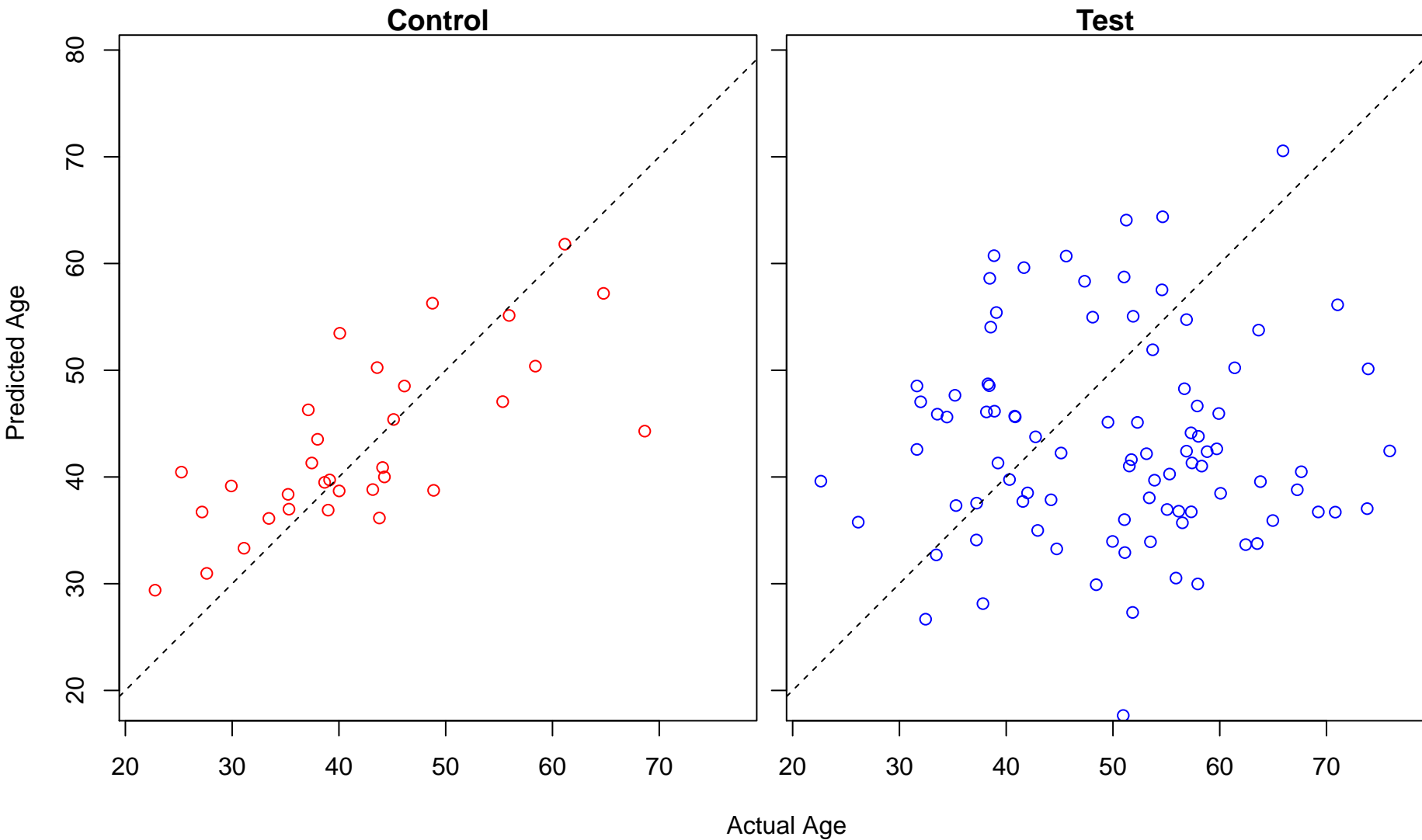
regulation of cellular amino acid metabolic process (Score: 1.745313)



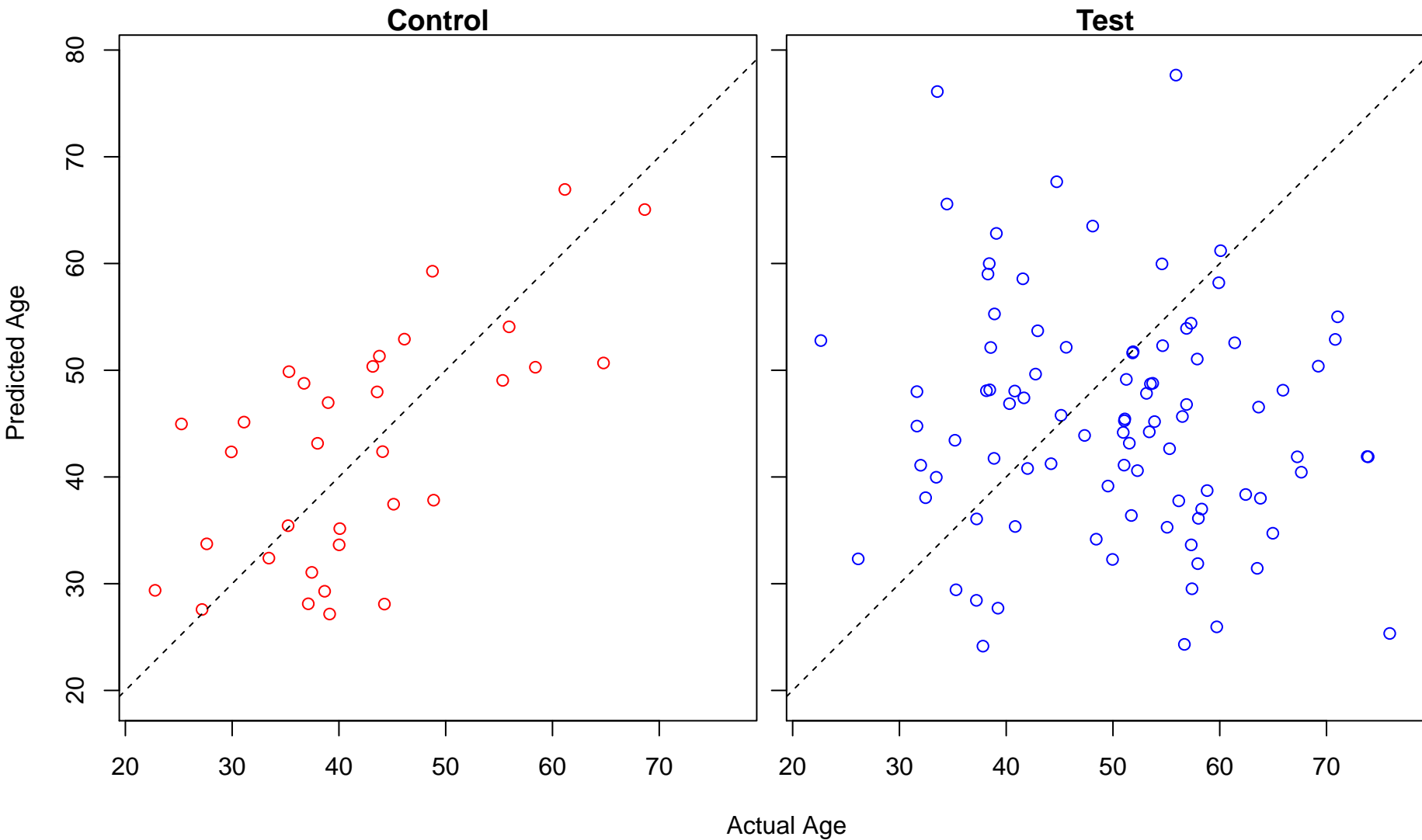
intracellular protein transmembrane import (Score: 1.742555)



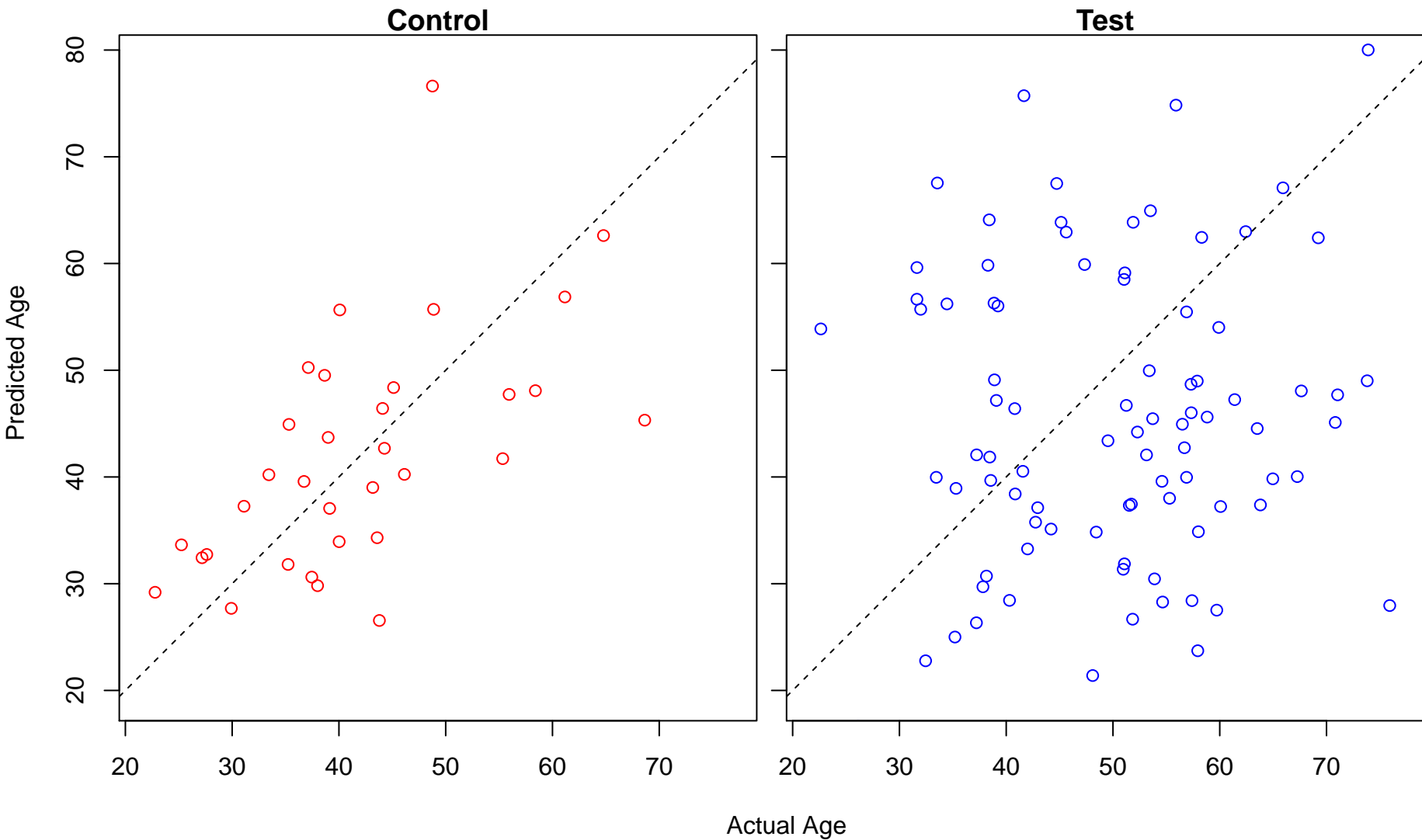
CDP-choline pathway (Score: 1.740718)



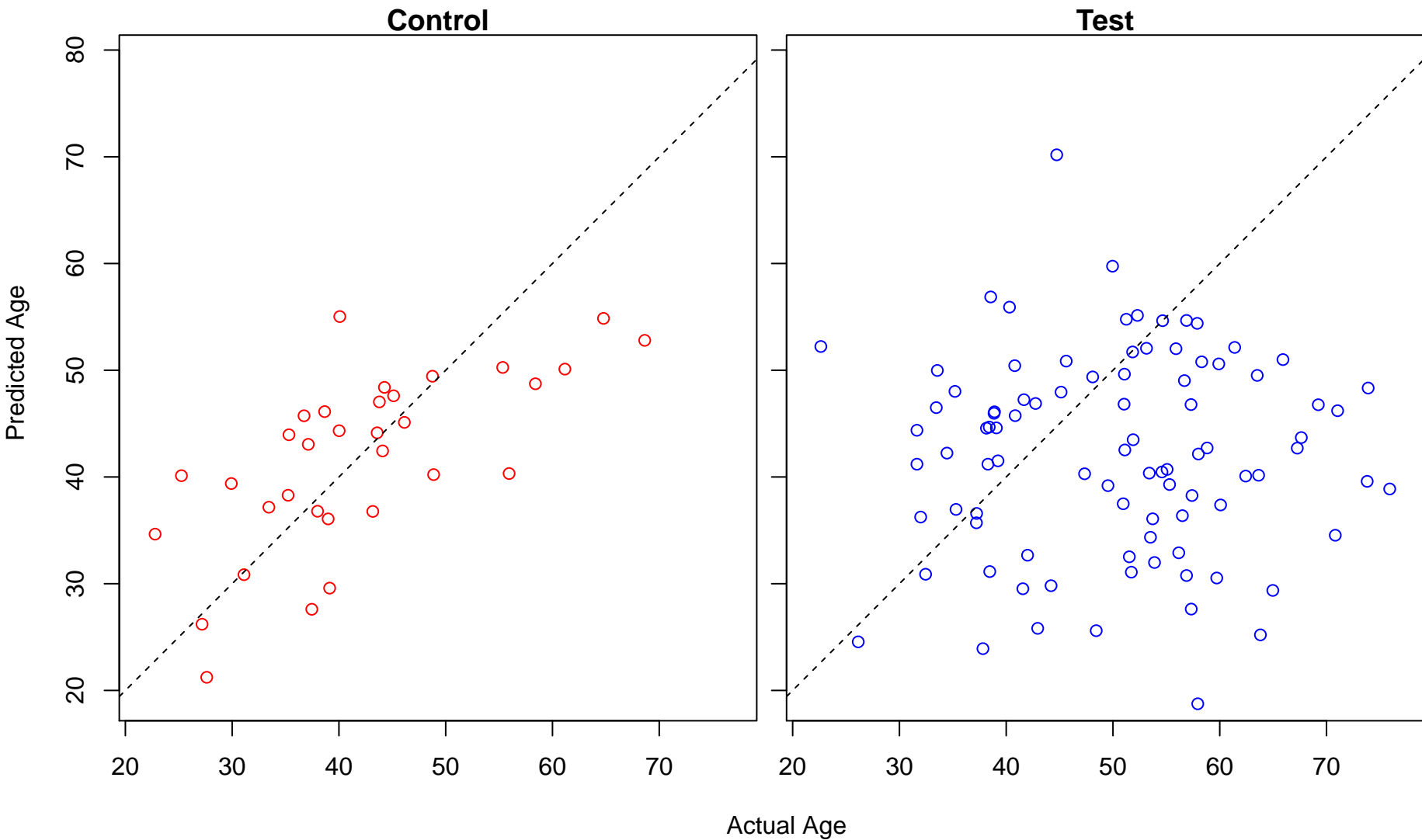
spermatid development (Score: 1.736839)



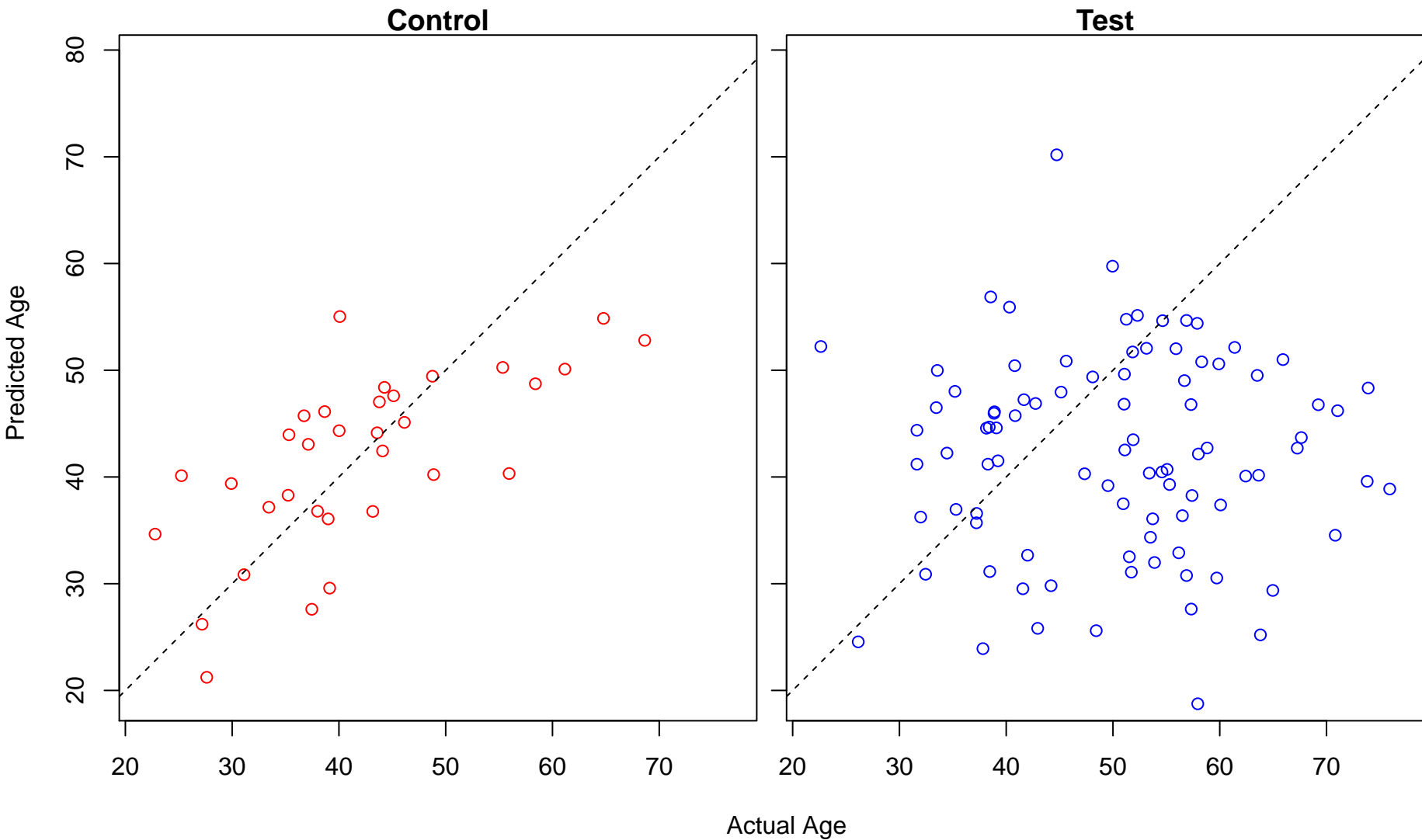
neural nucleus development (Score: 1.733624)



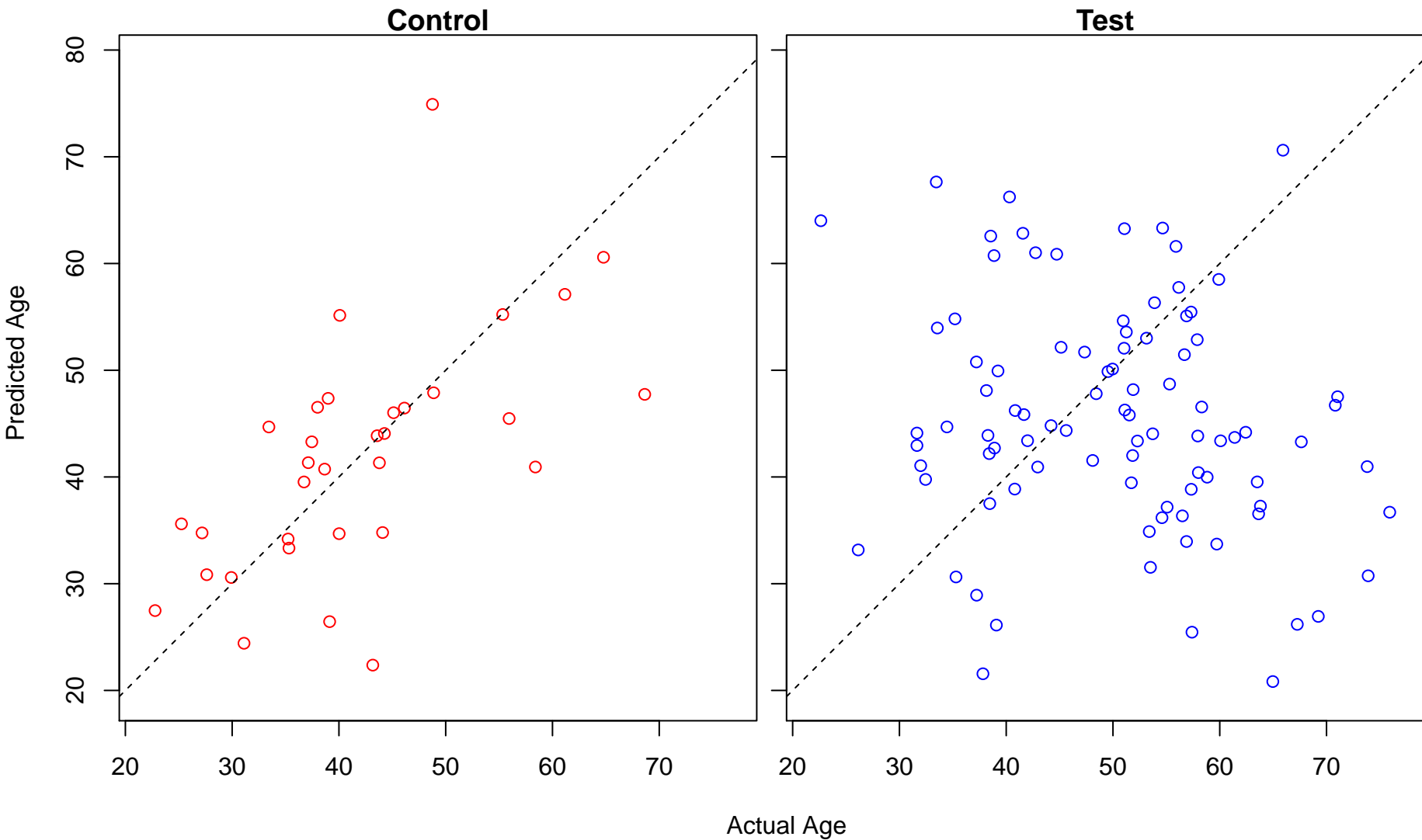
peroxisomal membrane transport (Score: 1.713007)



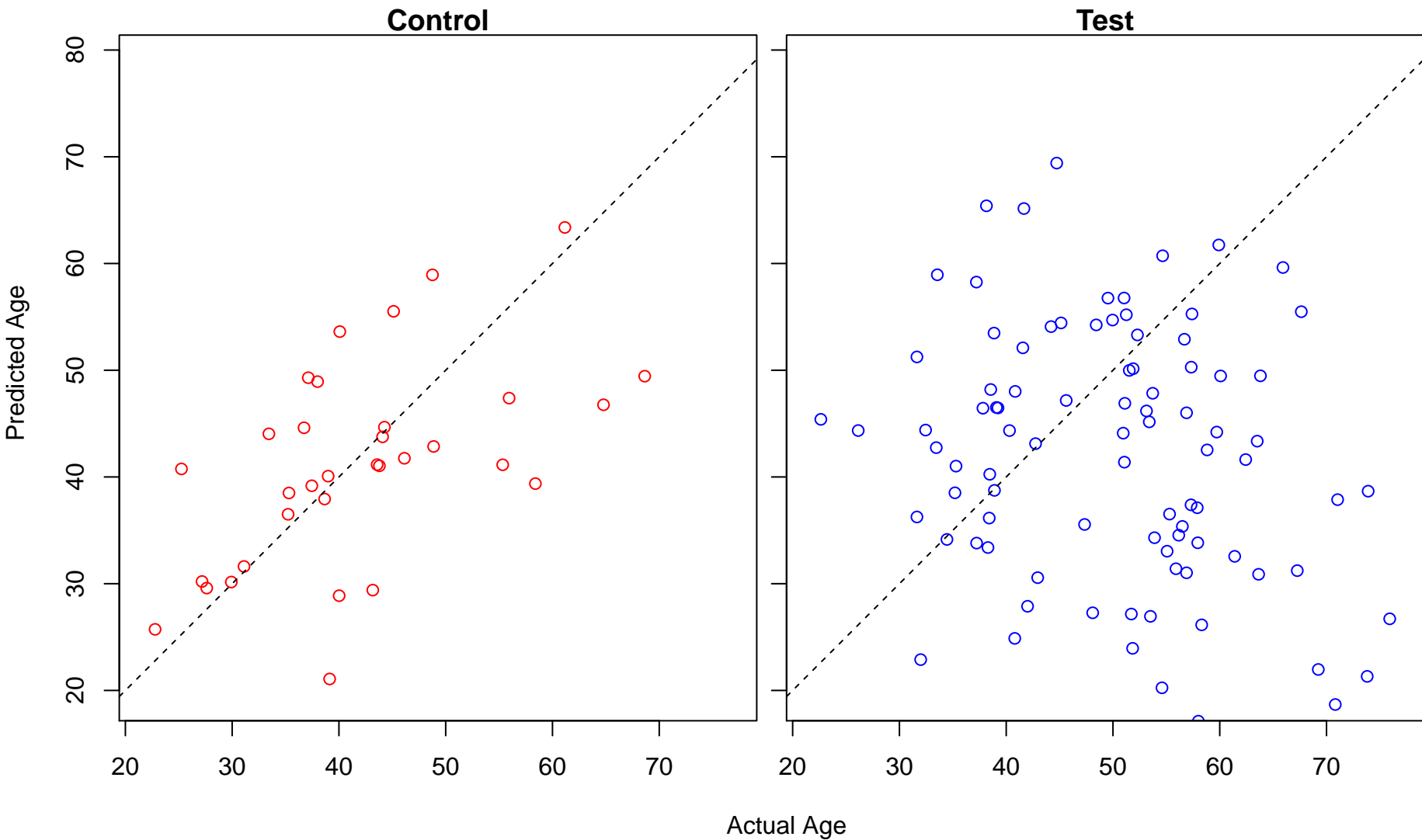
protein import into peroxisome membrane (Score: 1.713007)



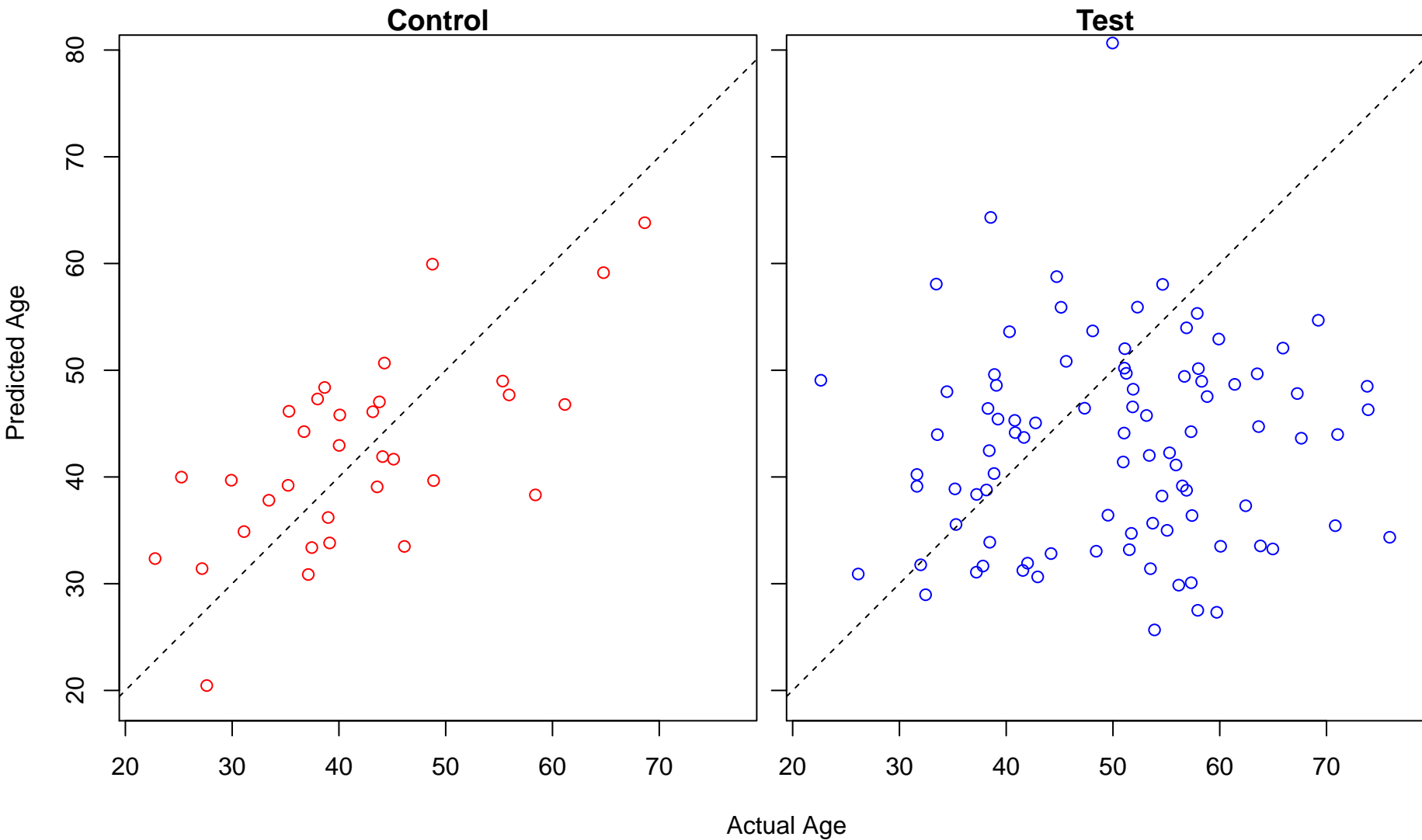
negative regulation of G1/S transition of mitotic cell cycle (Score: 1.687354)



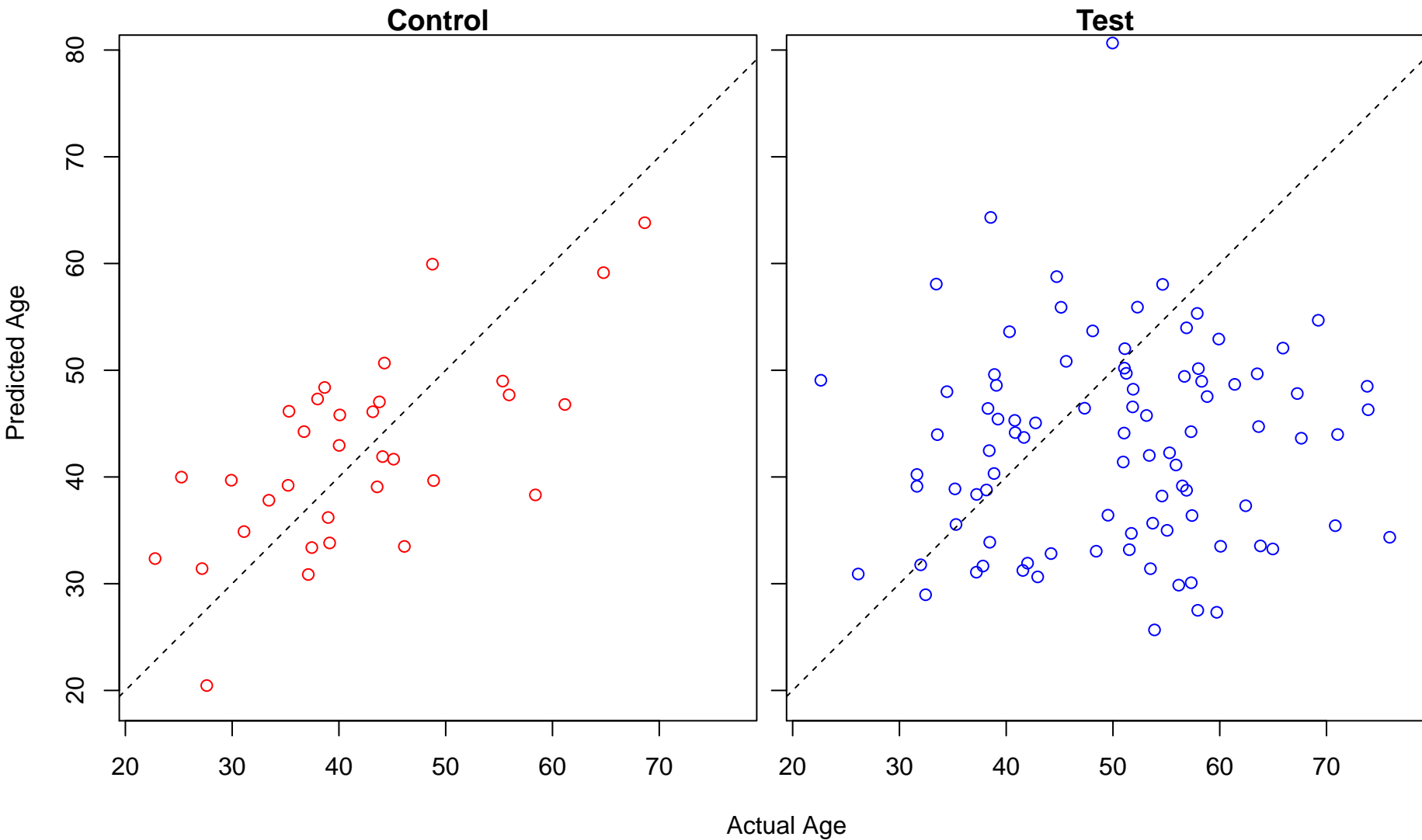
polyamine metabolic process (Score: 1.672605)



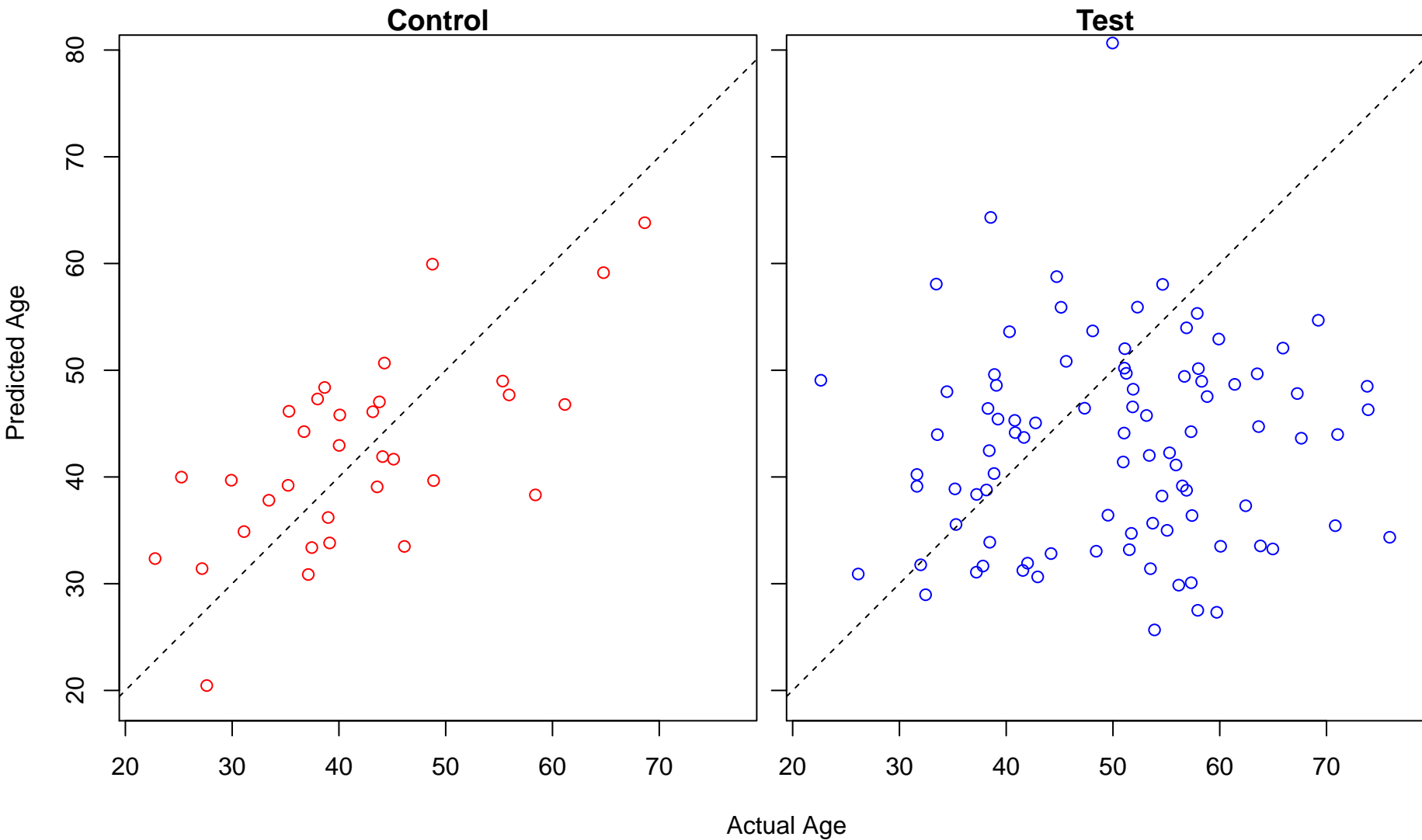
protein targeting to peroxisome (Score: 1.668135)



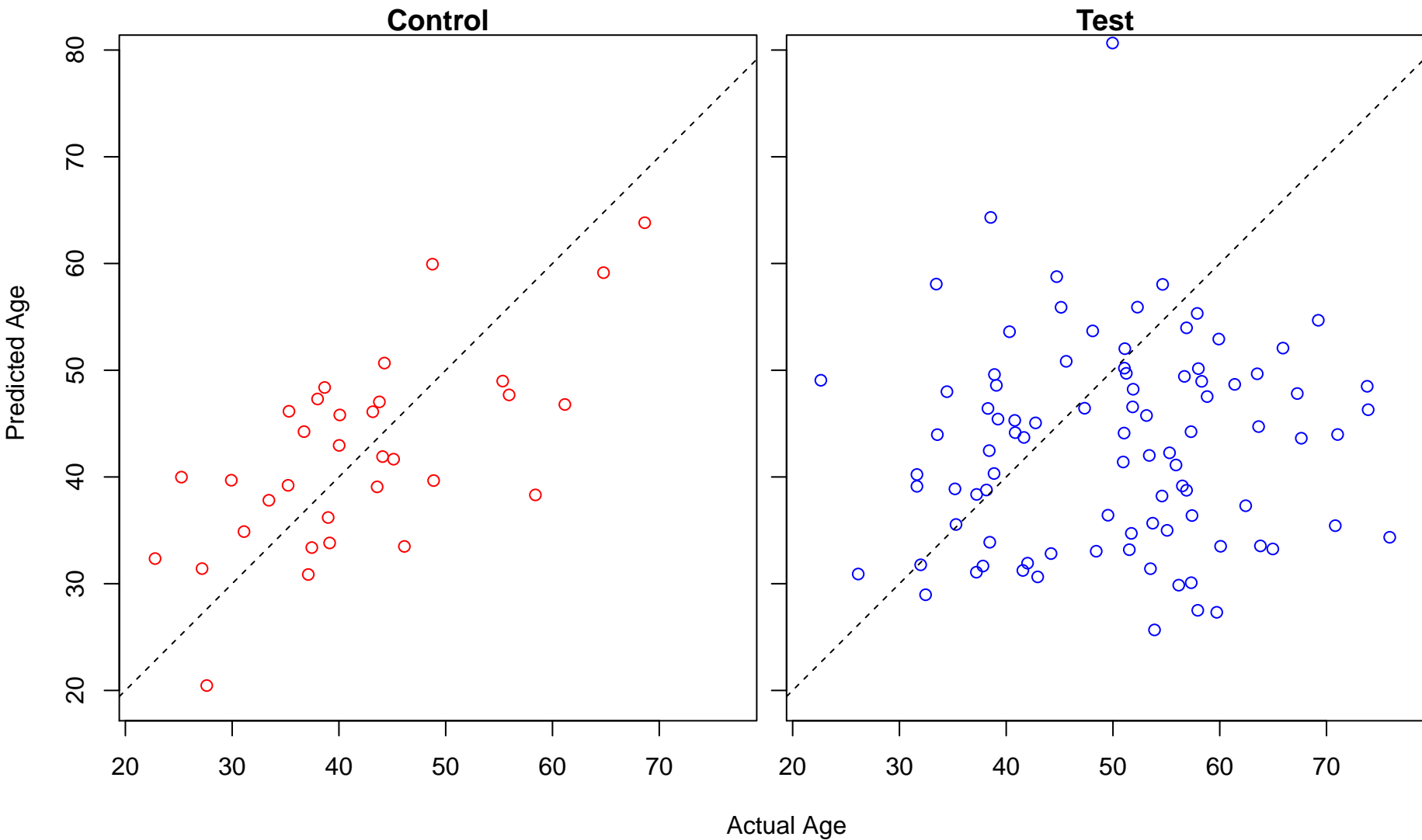
peroxisomal transport (Score: 1.668135)



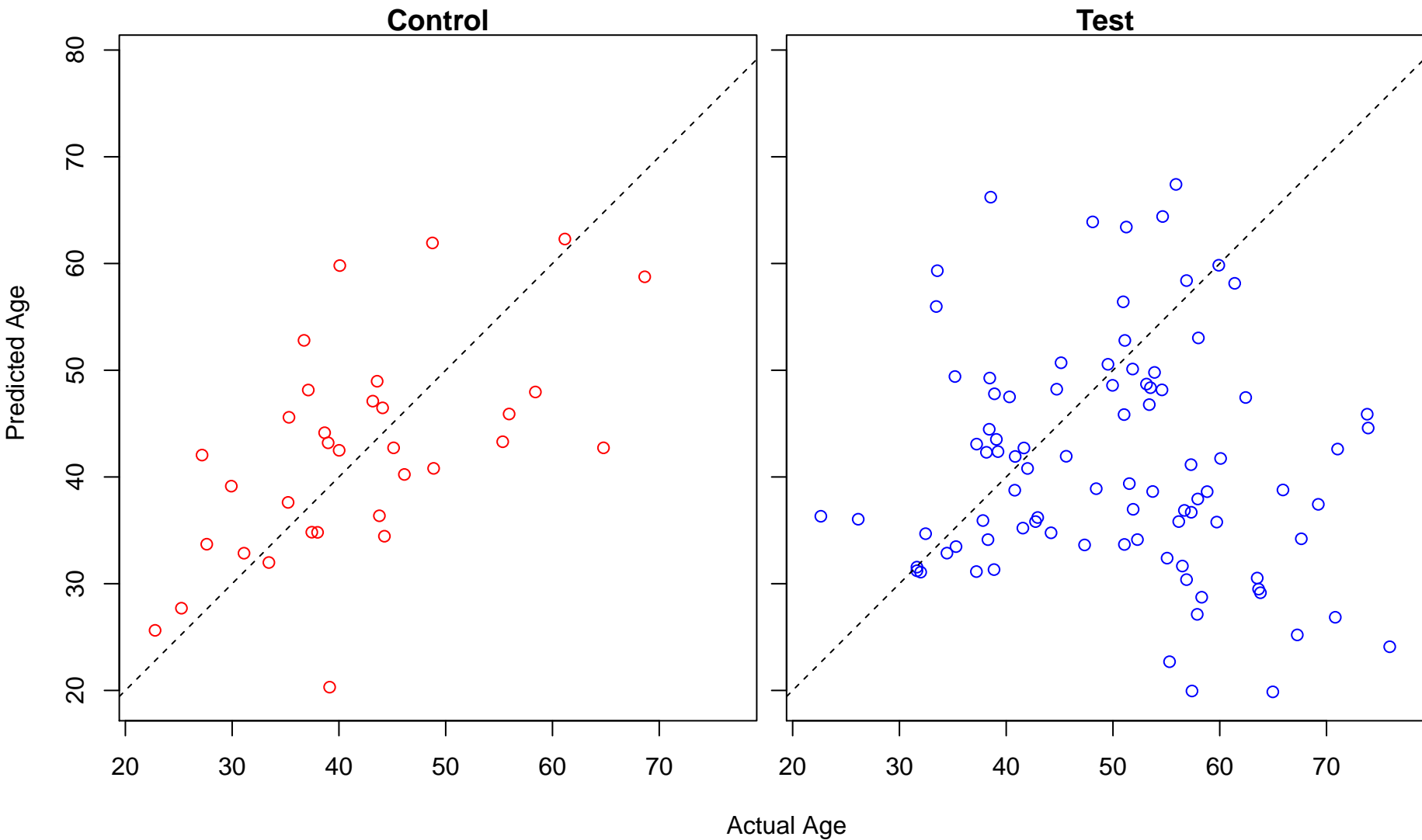
protein localization to peroxisome (Score: 1.668135)



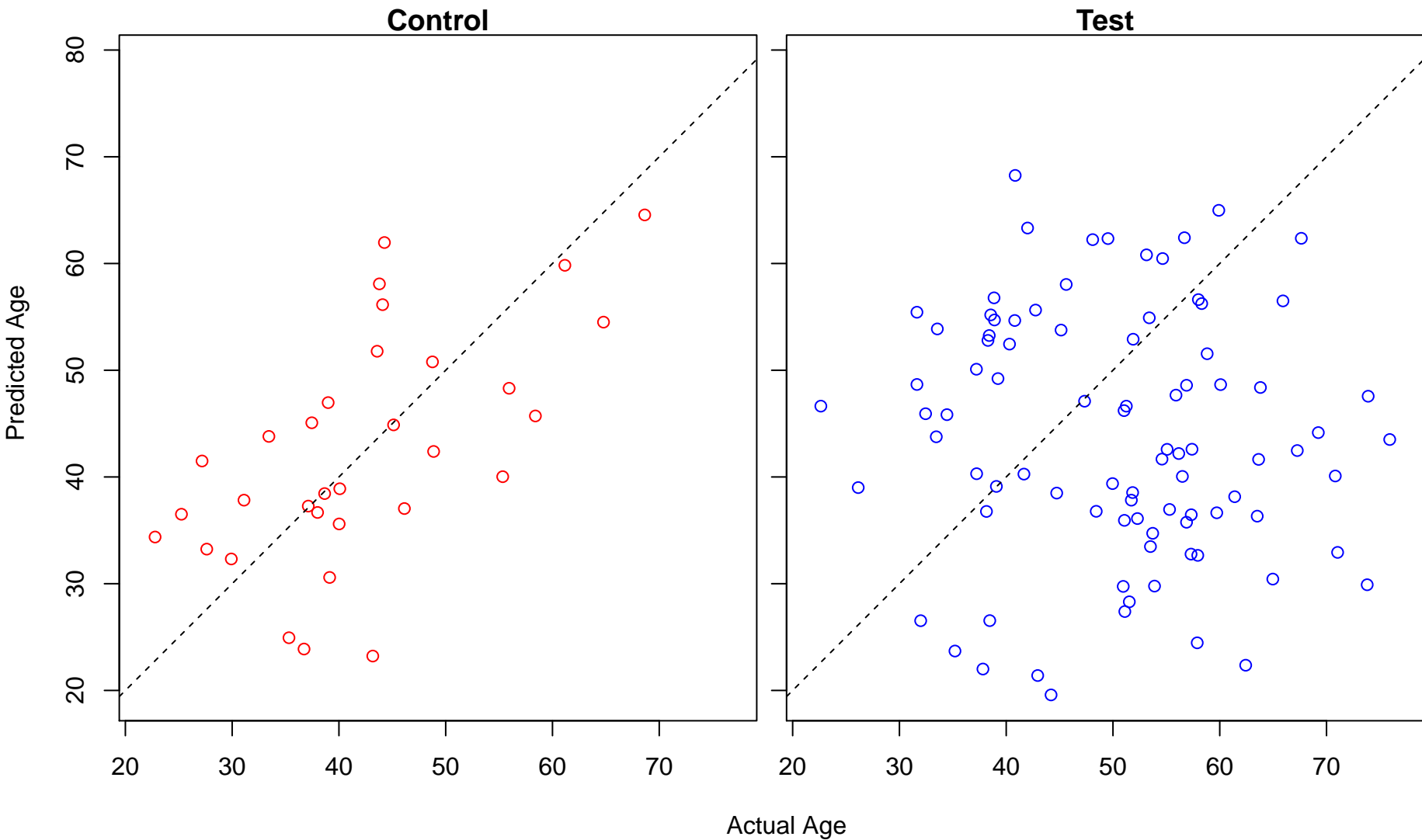
establishment of protein localization to peroxisome (Score: 1.668135)



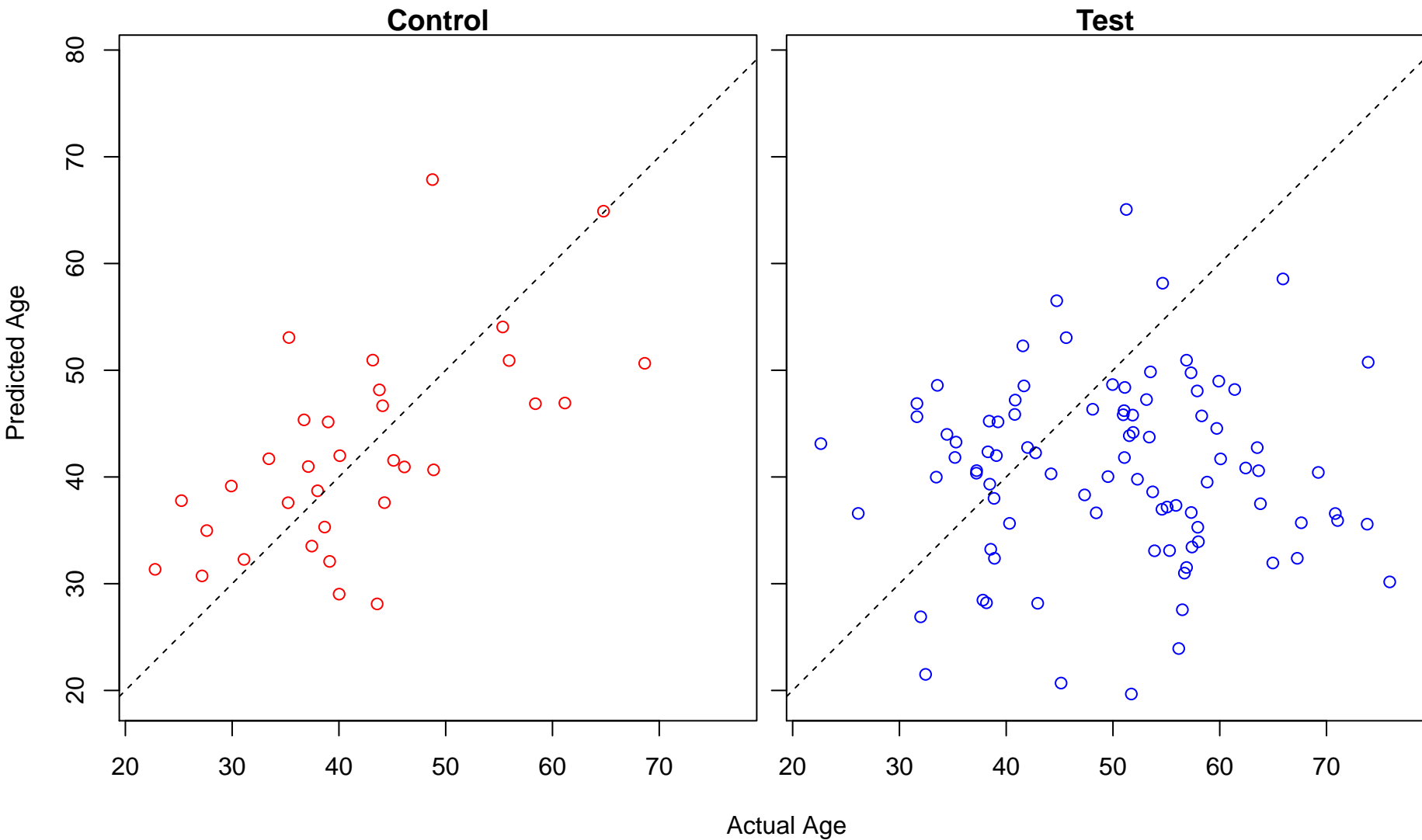
rhythmic process (Score: 1.664958)



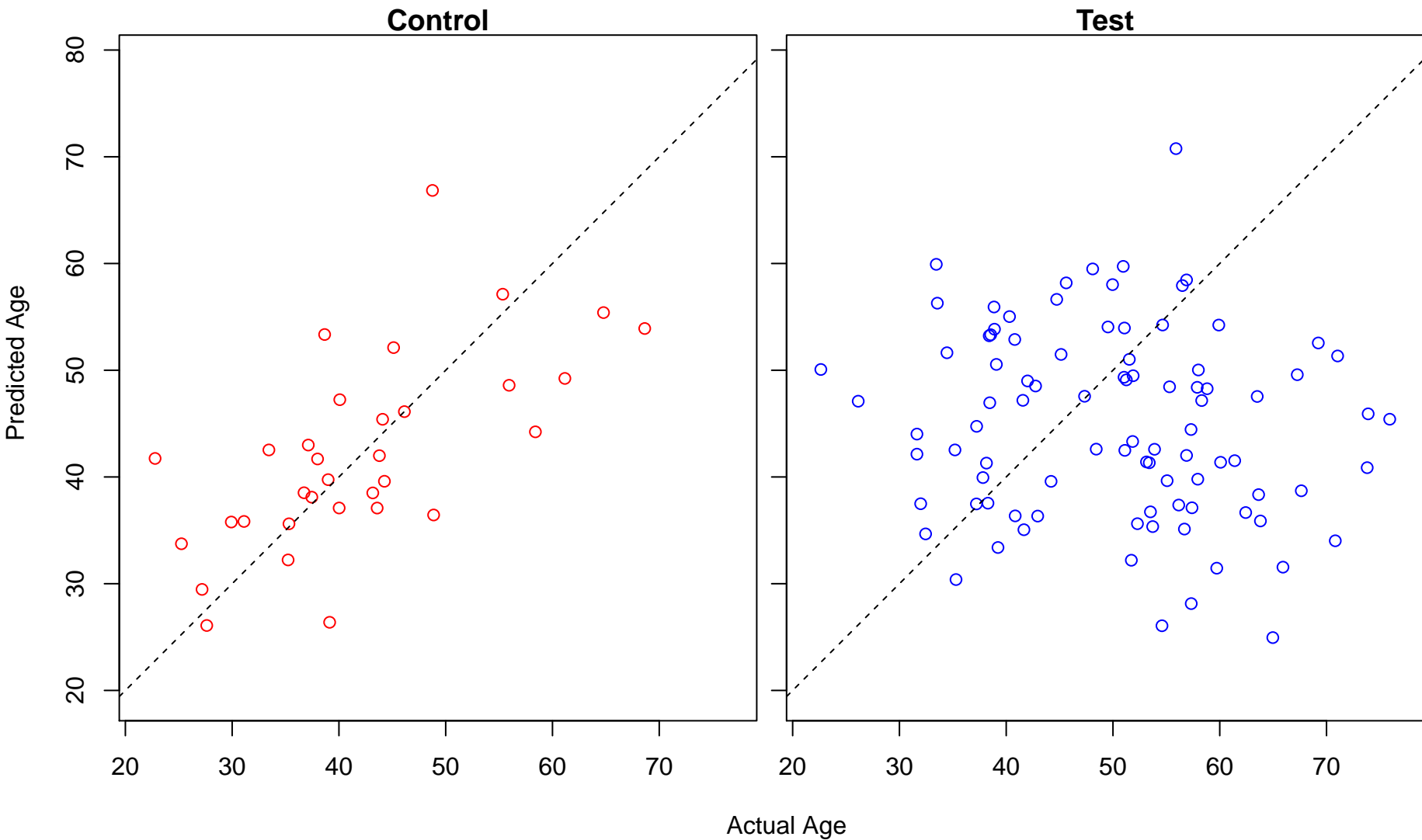
female gamete generation (Score: 1.664574)



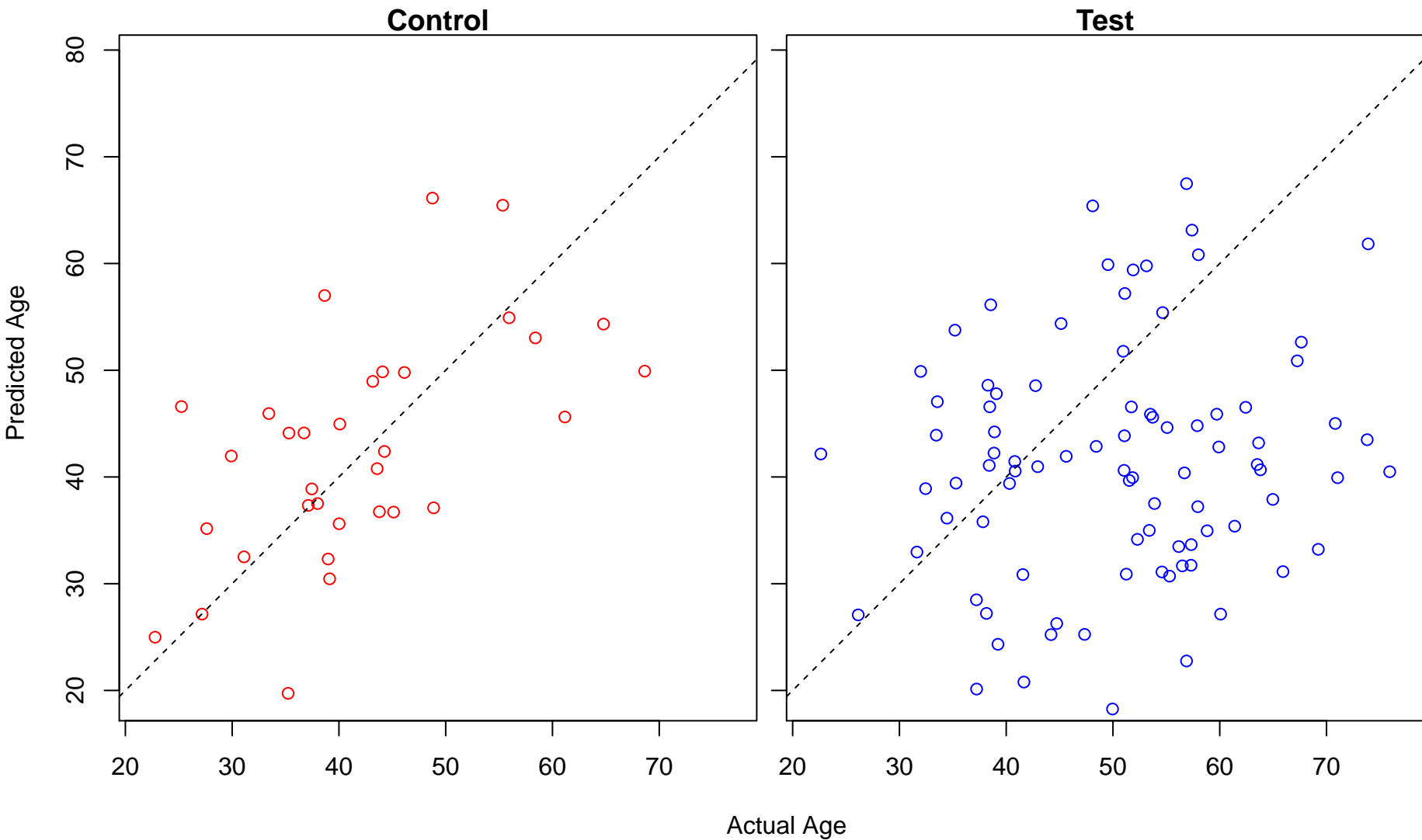
cellular aldehyde metabolic process (Score: 1.662779)



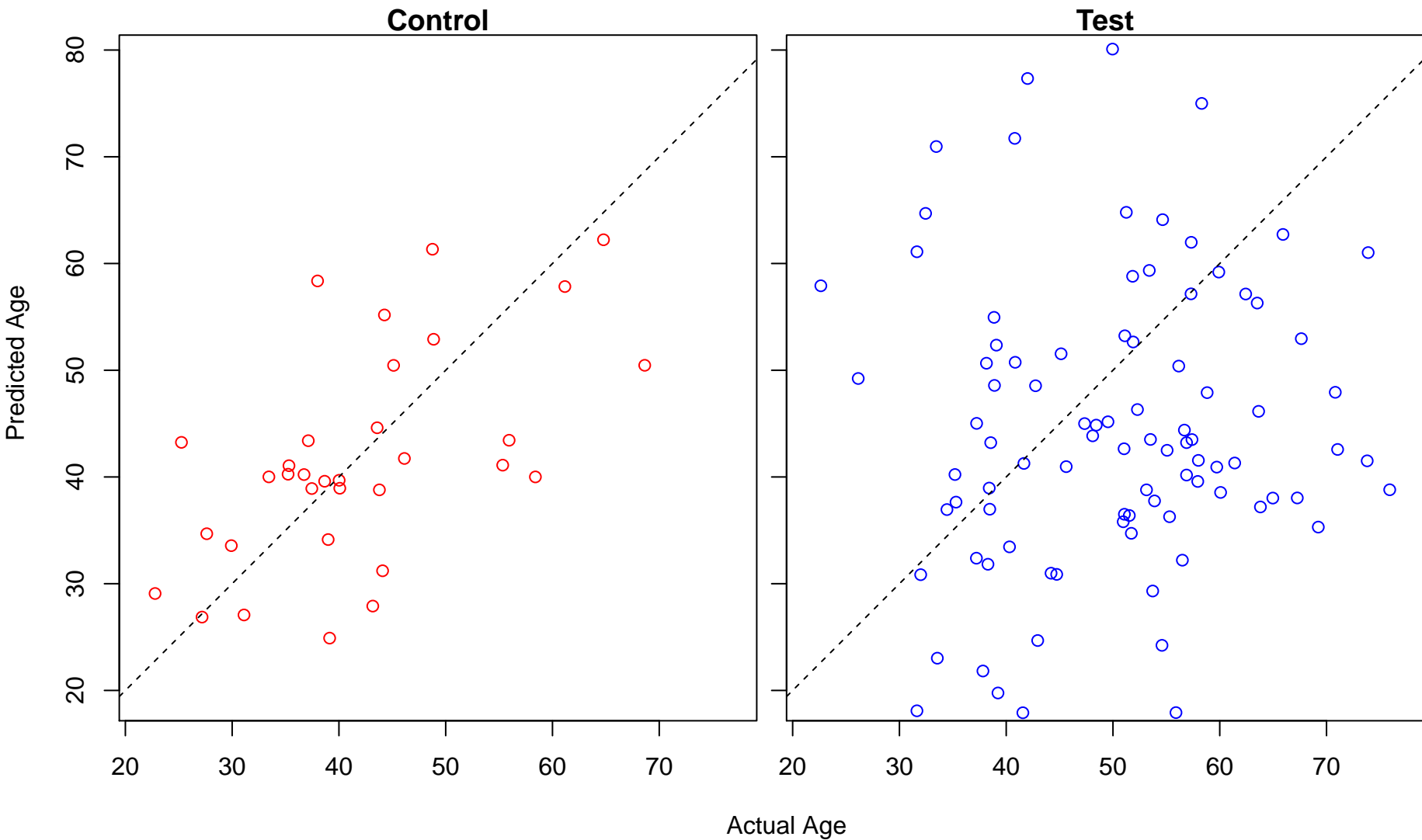
positive regulation of tumor necrosis factor production (Score: 1.660236)



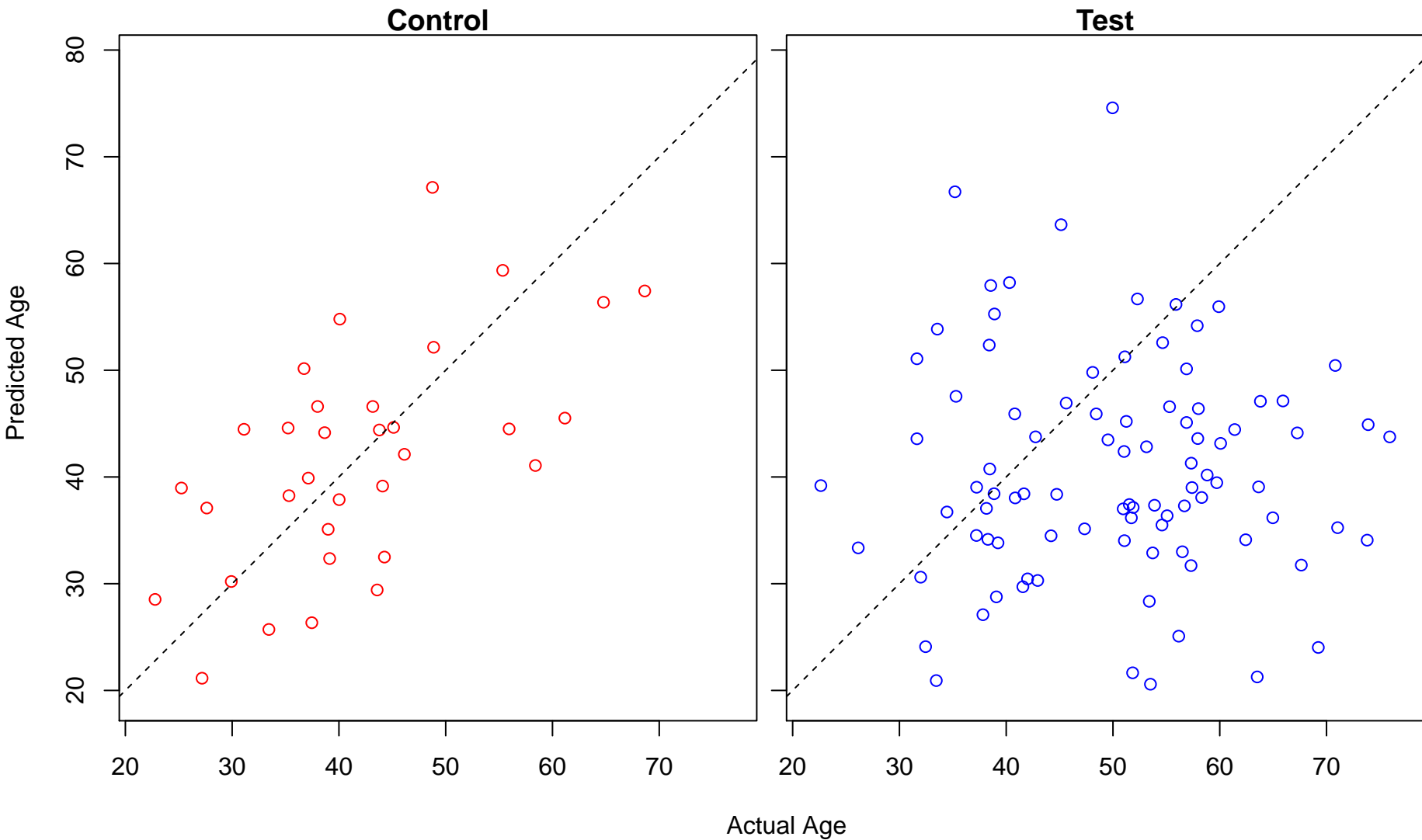
mesenchymal cell development (Score: 1.658160)



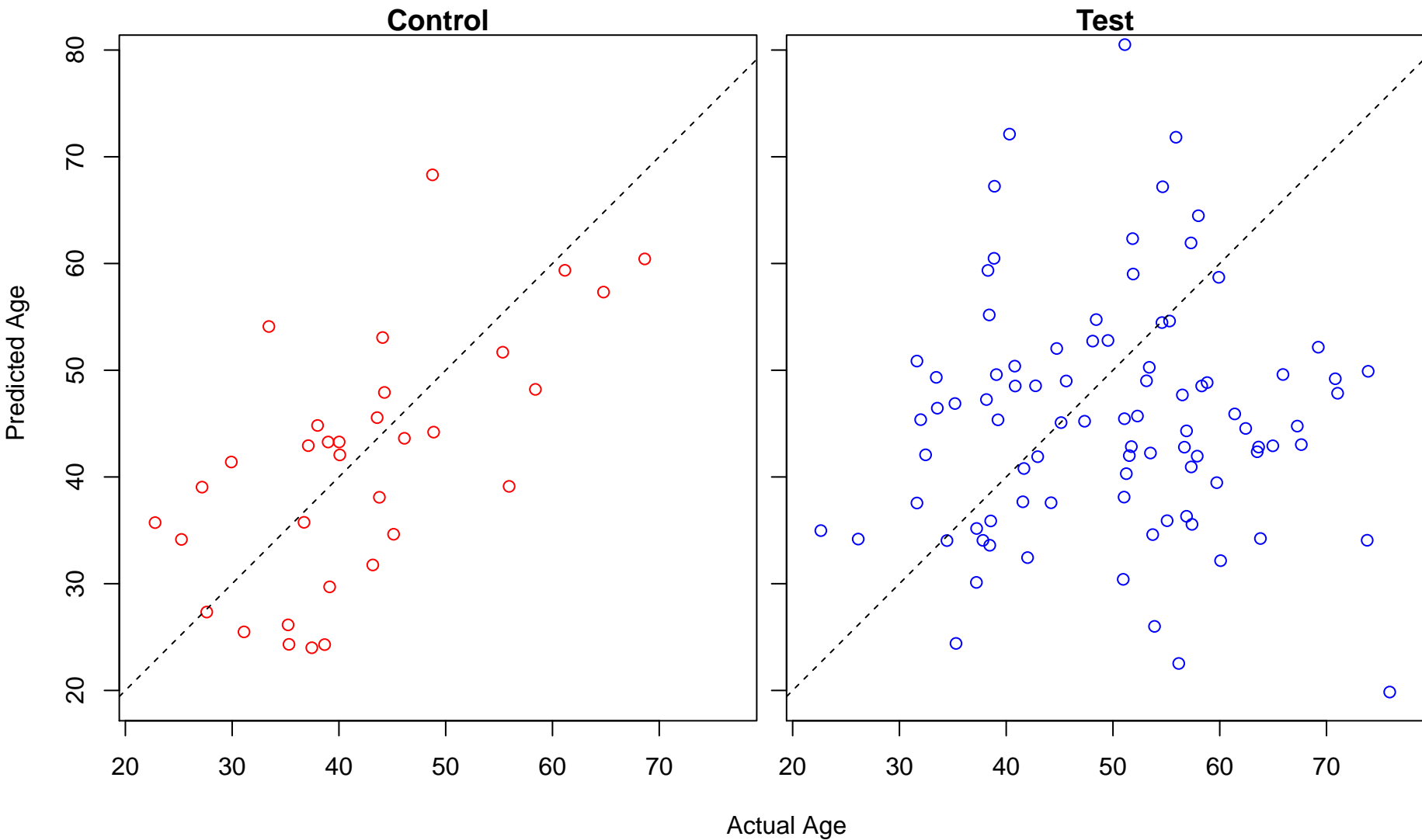
negative regulation of G2/M transition of mitotic cell cycle (Score: 1.648245)



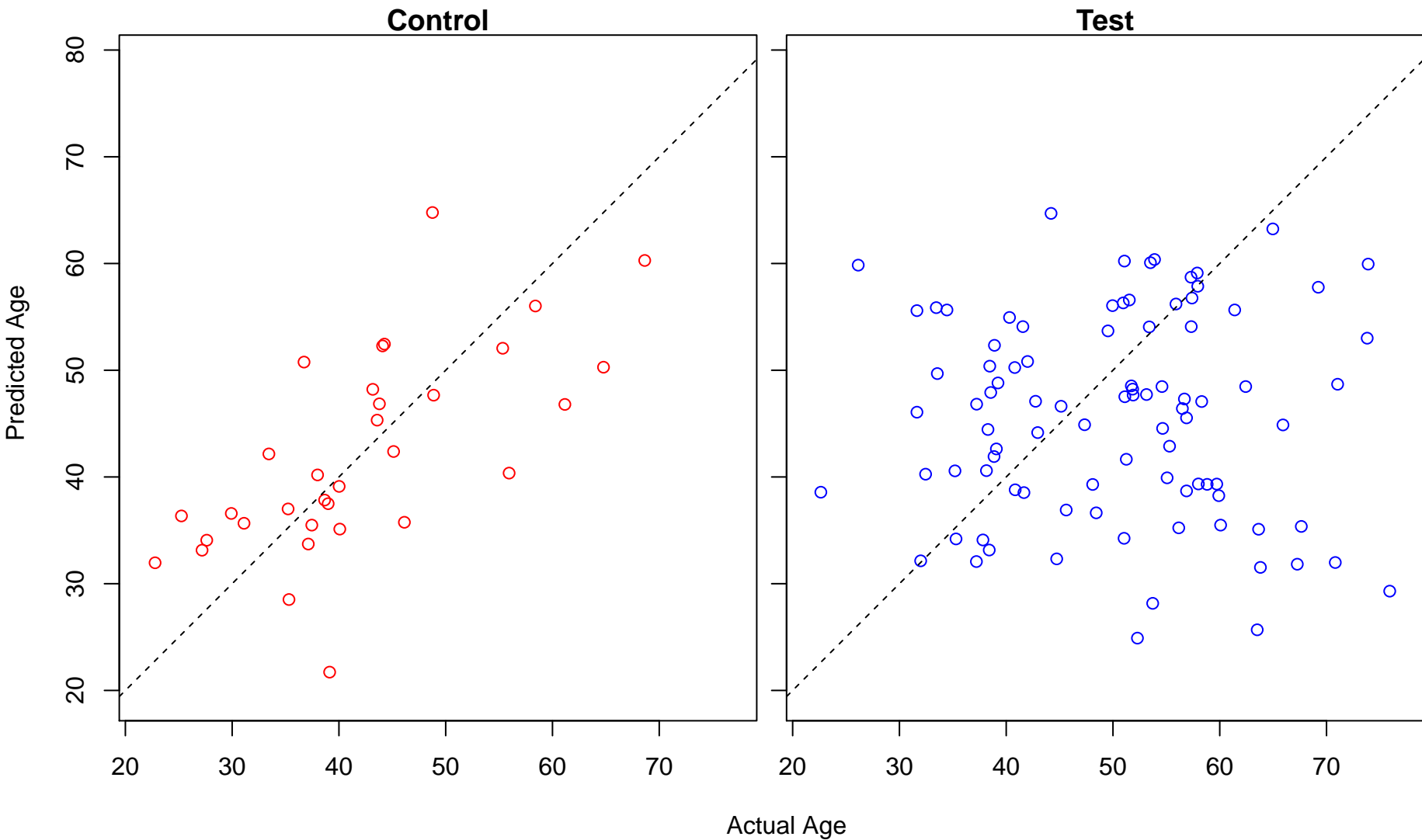
cholesterol metabolic process (Score: 1.642843)



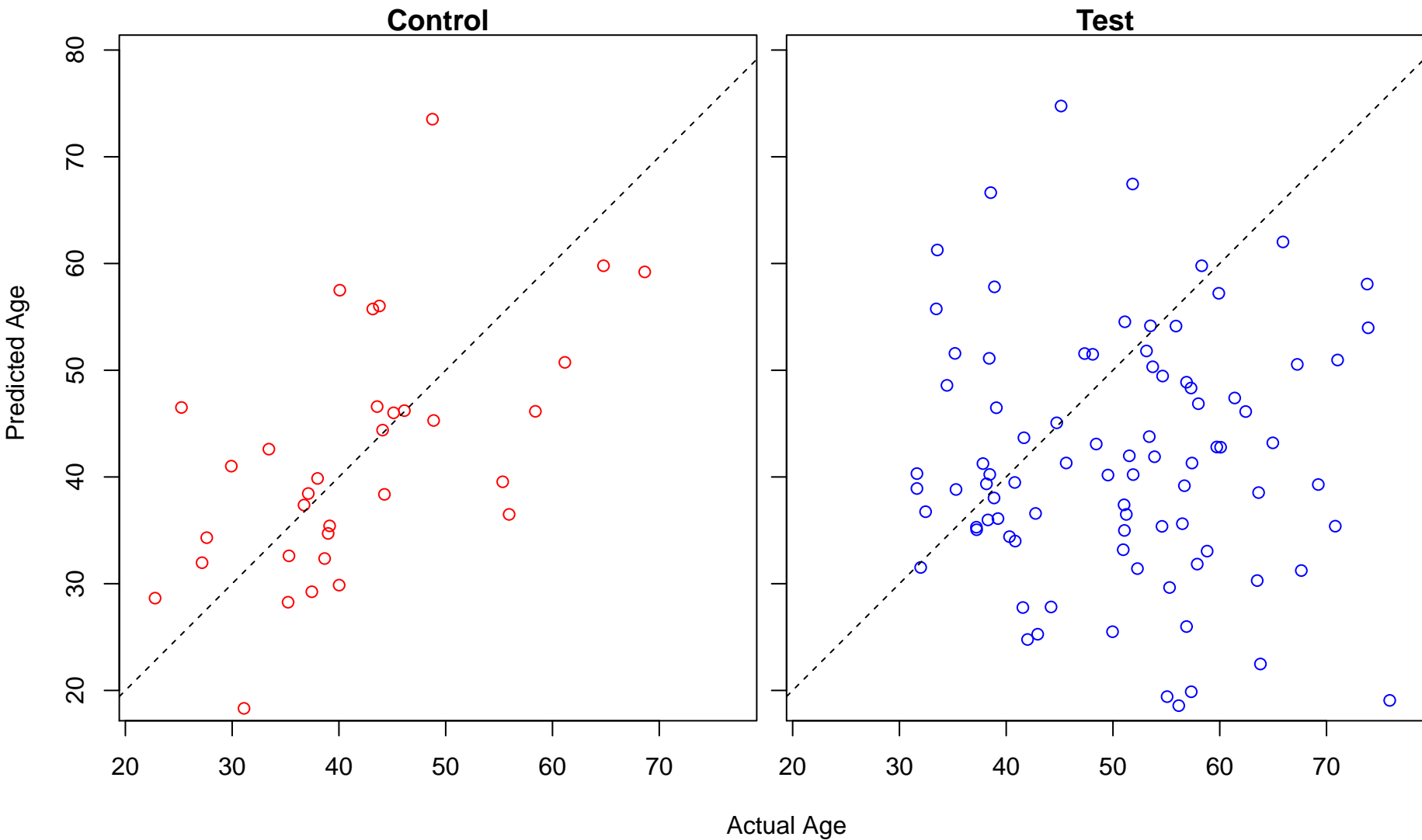
pigmentation (Score: 1.639270)



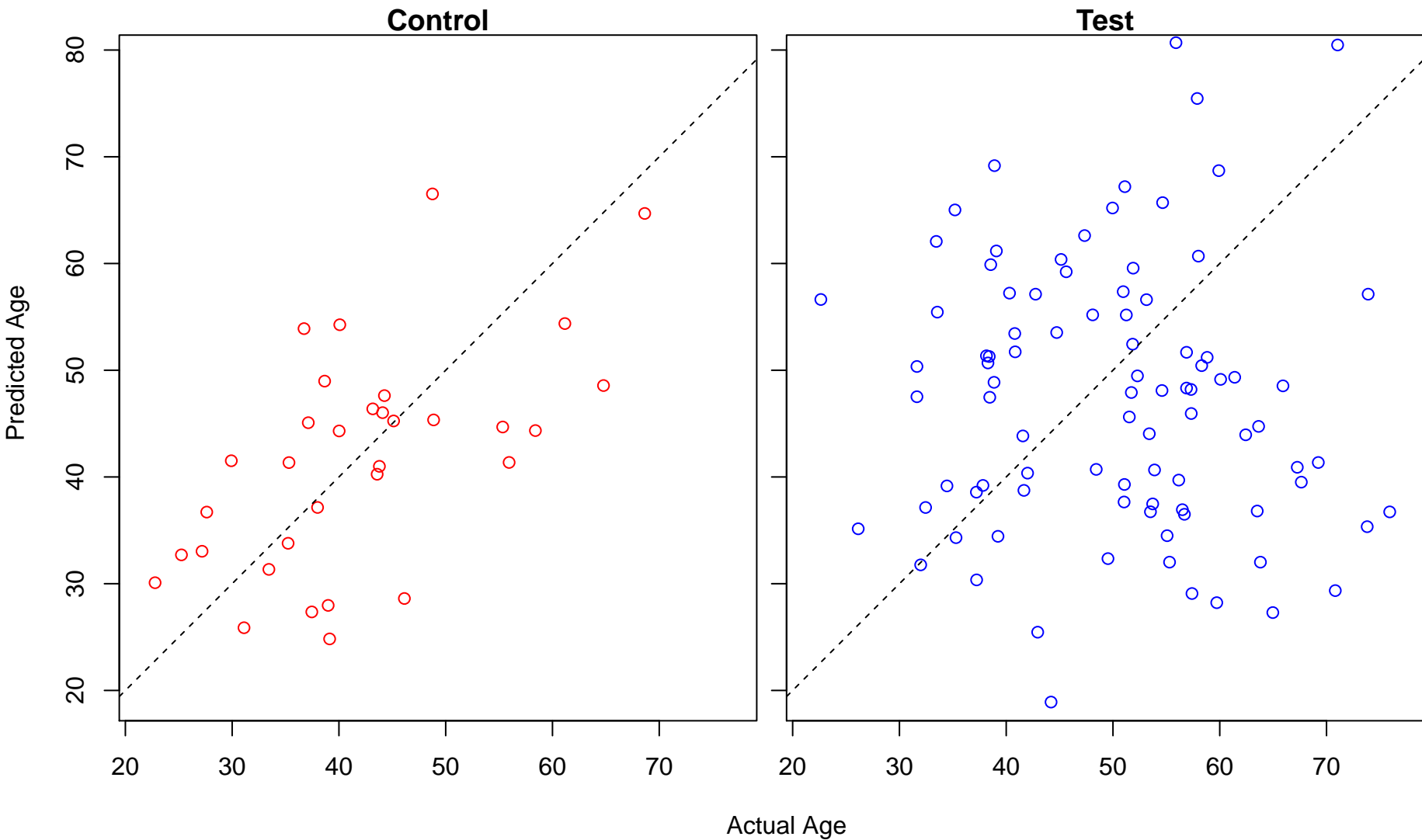
humoral immune response mediated by circulating immunoglobulin (Score: 1.637263)



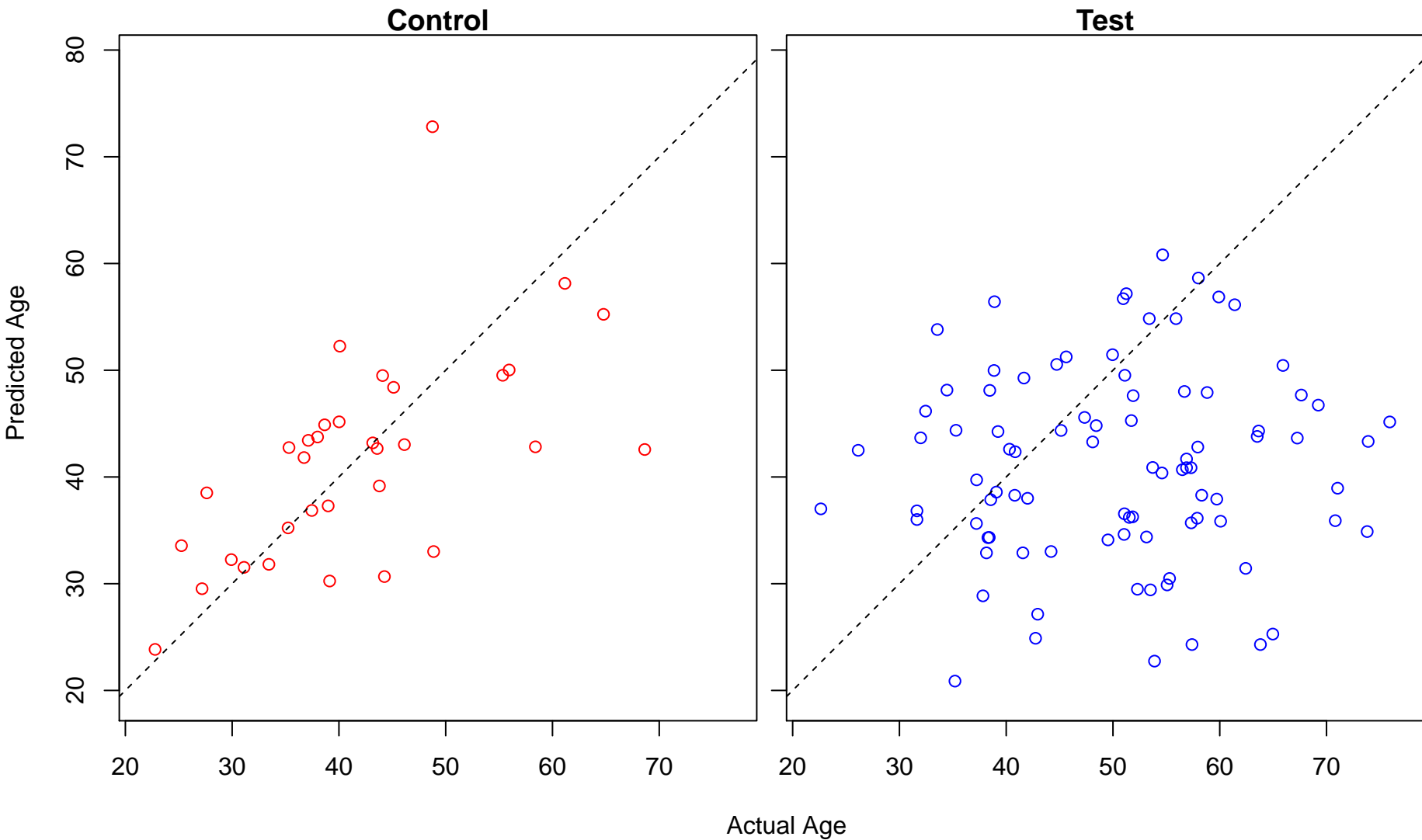
ceramide metabolic process (Score: 1.636283)



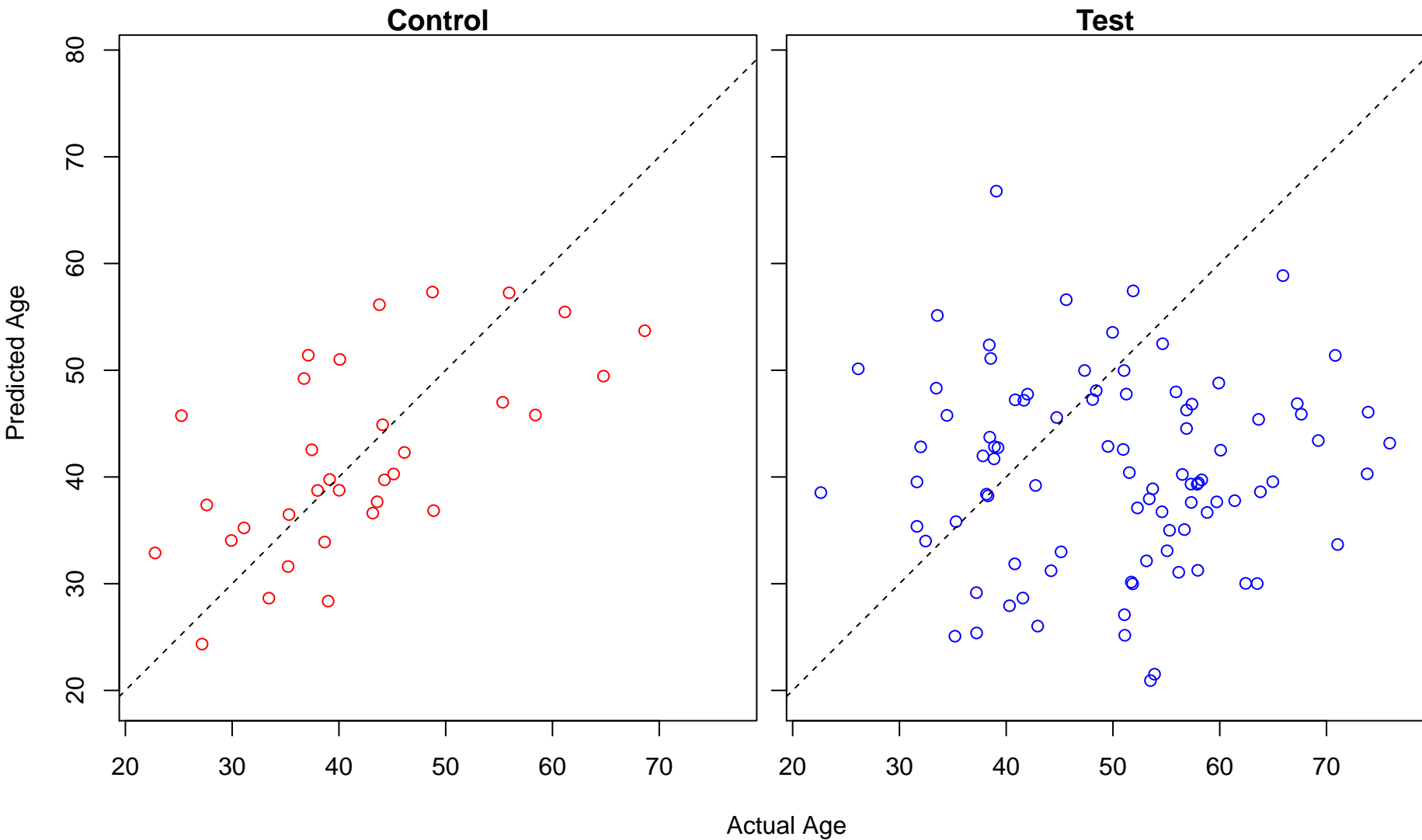
negative regulation of NF-kappaB transcription factor activity (Score: 1.633137)



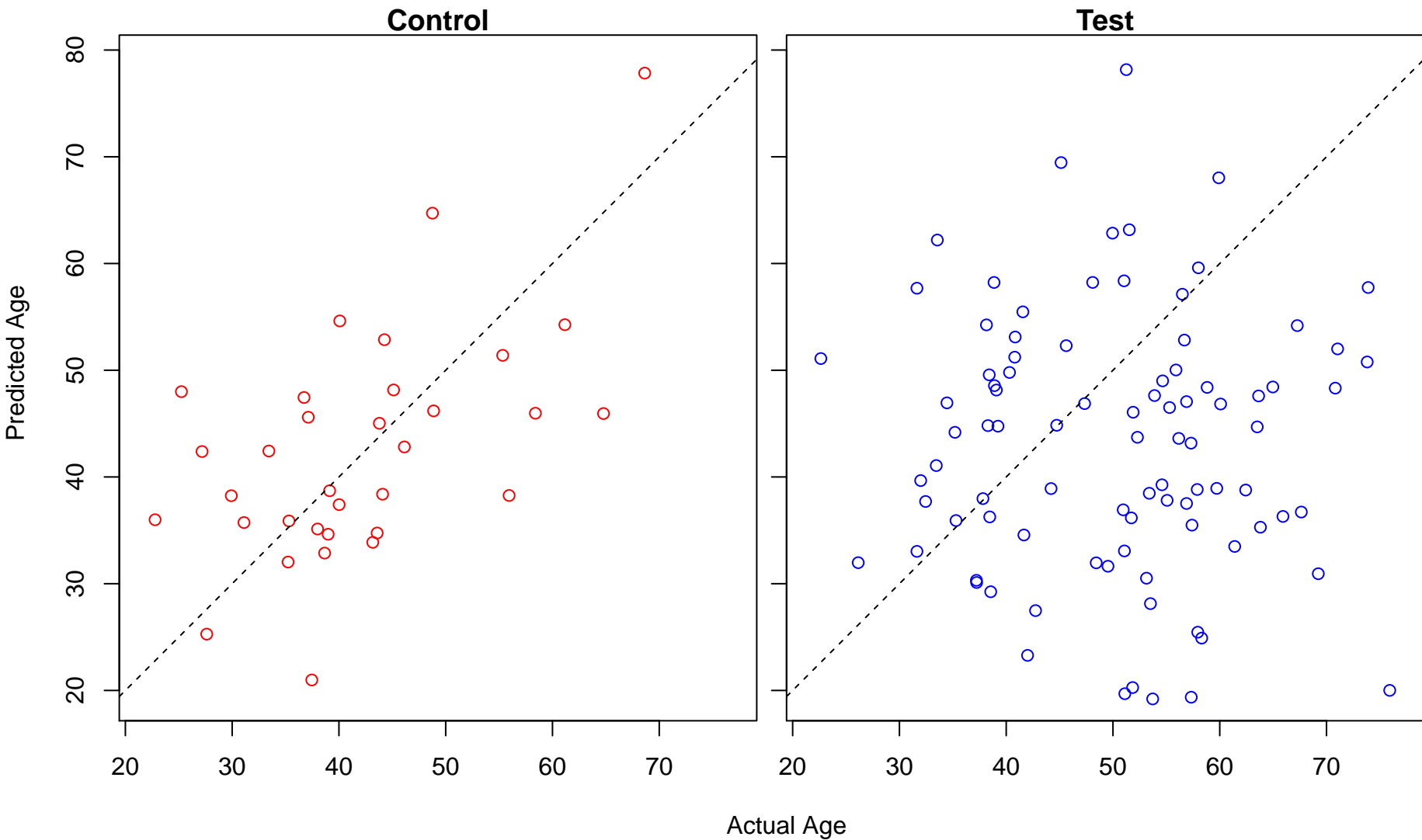
protein autophosphorylation (Score: 1.628861)



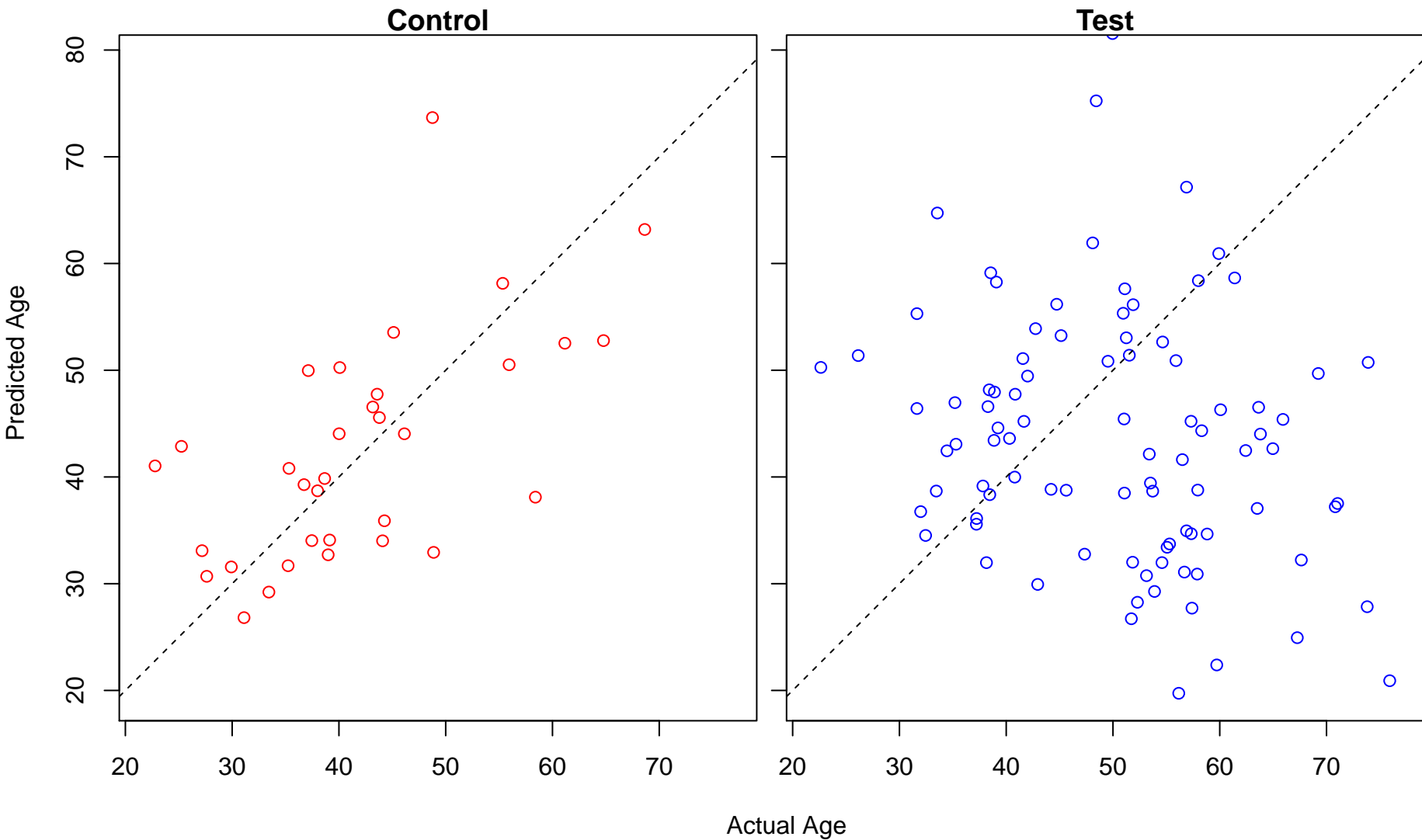
blood coagulation, intrinsic pathway (Score: 1.624854)



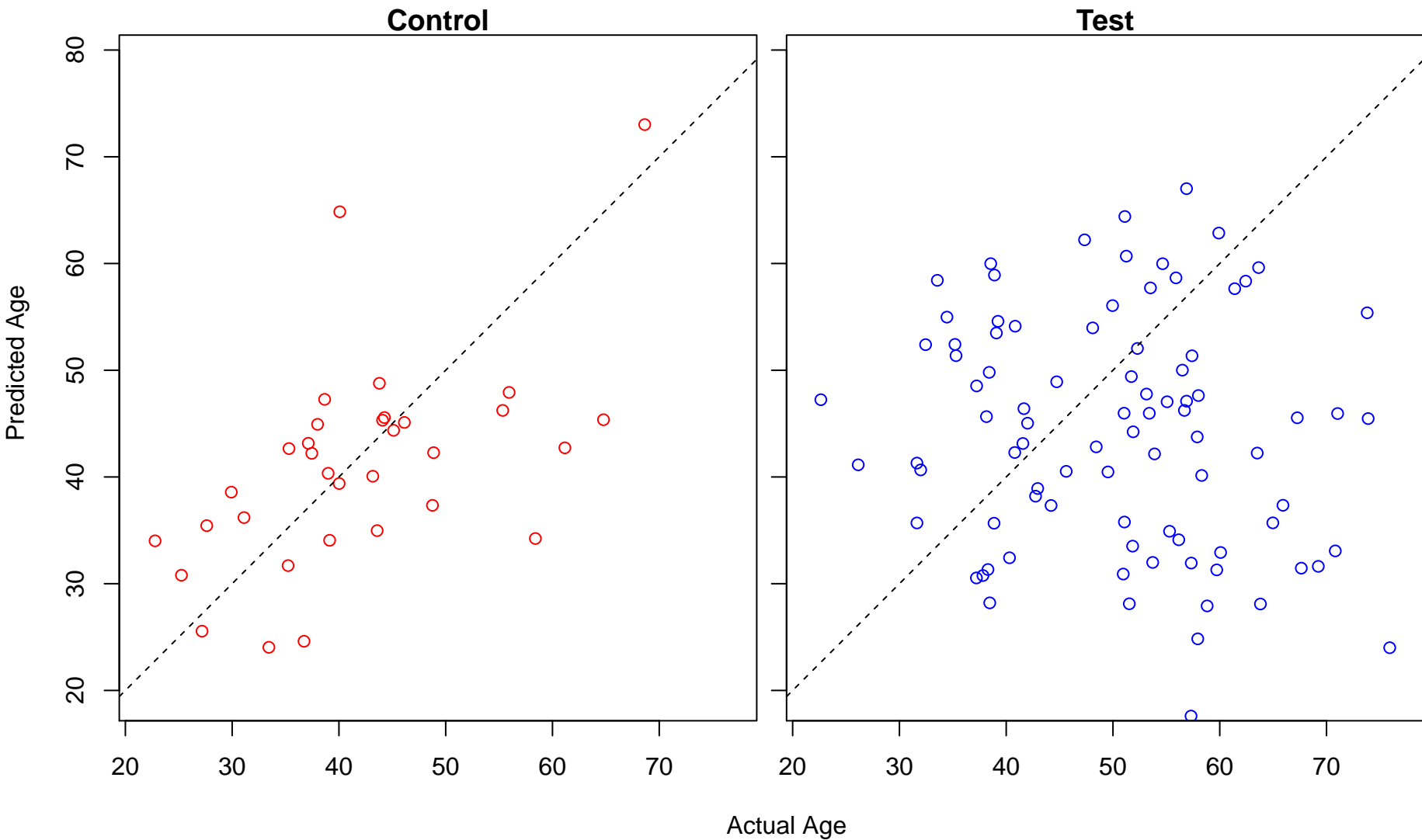
regulation of axonogenesis (Score: 1.615536)



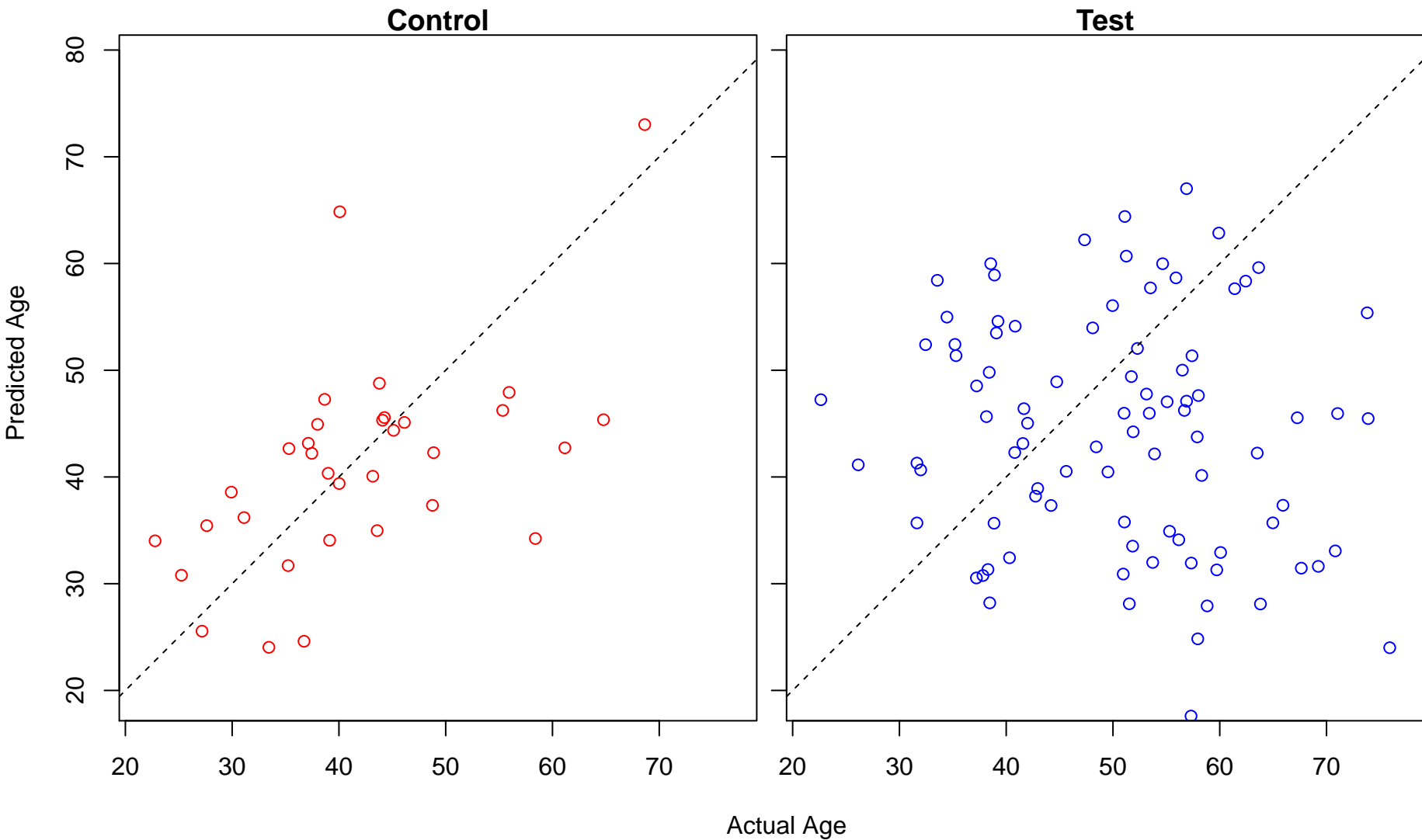
response to UV (Score: 1.612841)



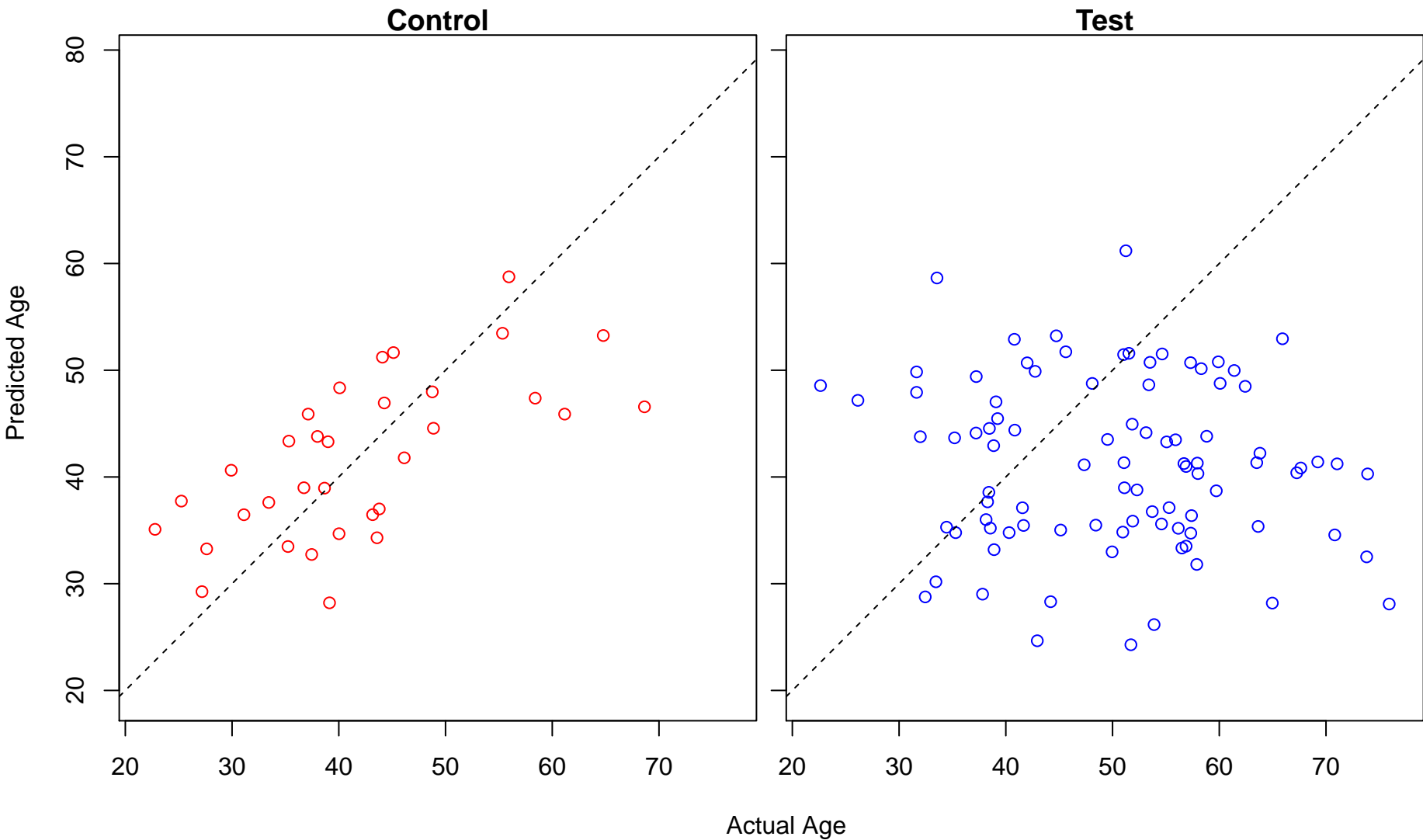
reproductive structure development (Score: 1.602611)



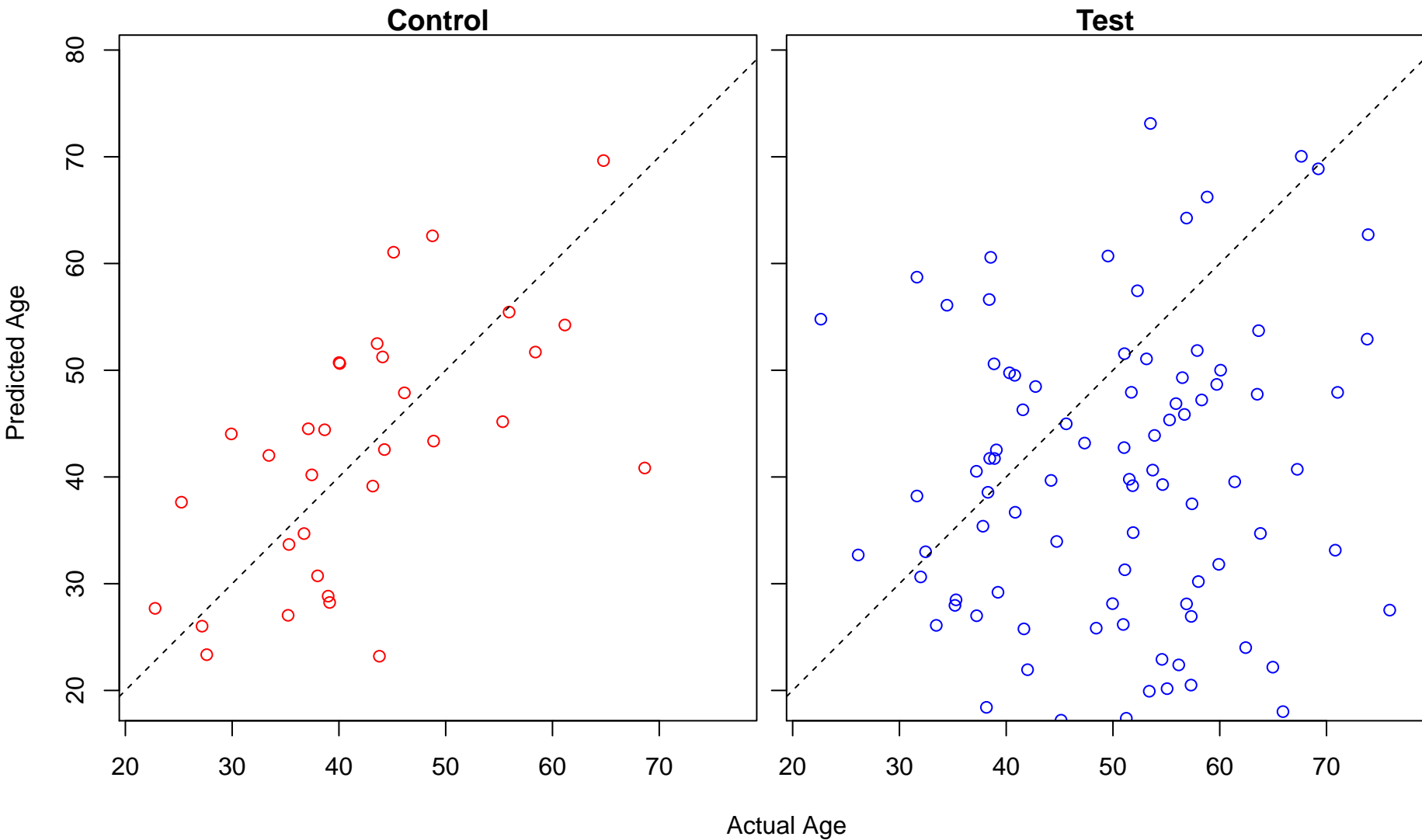
reproductive system development (Score: 1.602611)



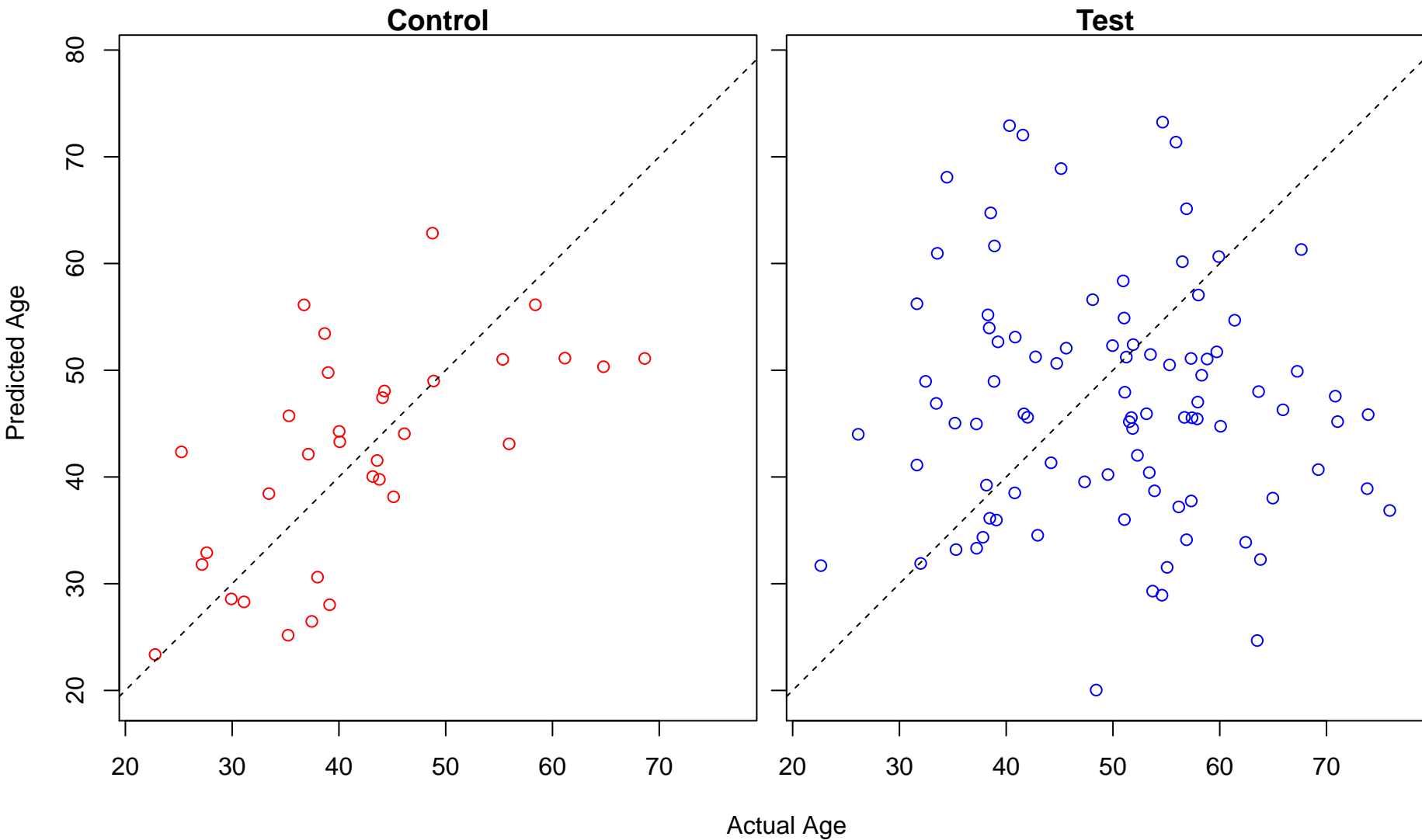
digestive system process (Score: 1.599313)



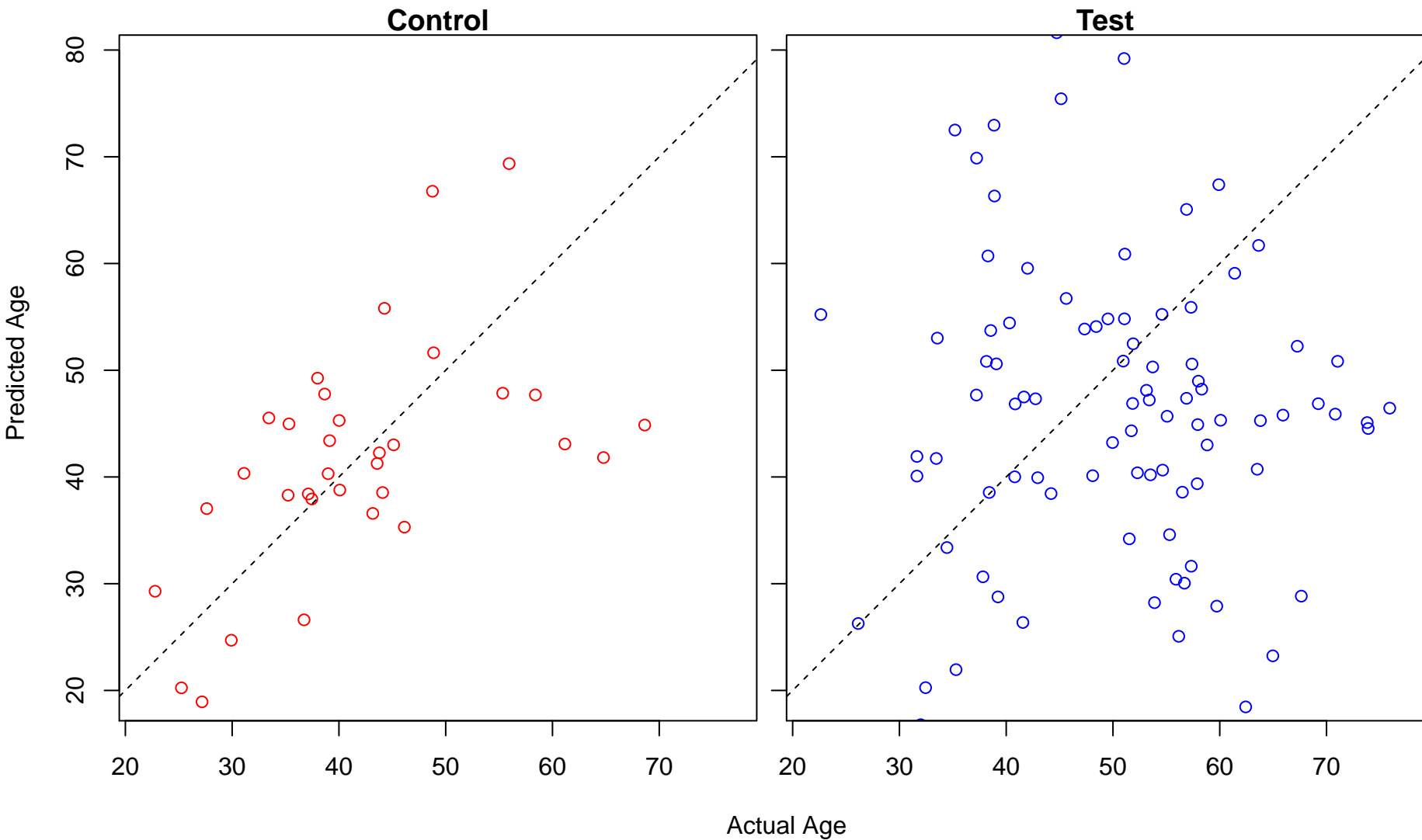
keratan sulfate metabolic process (Score: 1.596589)



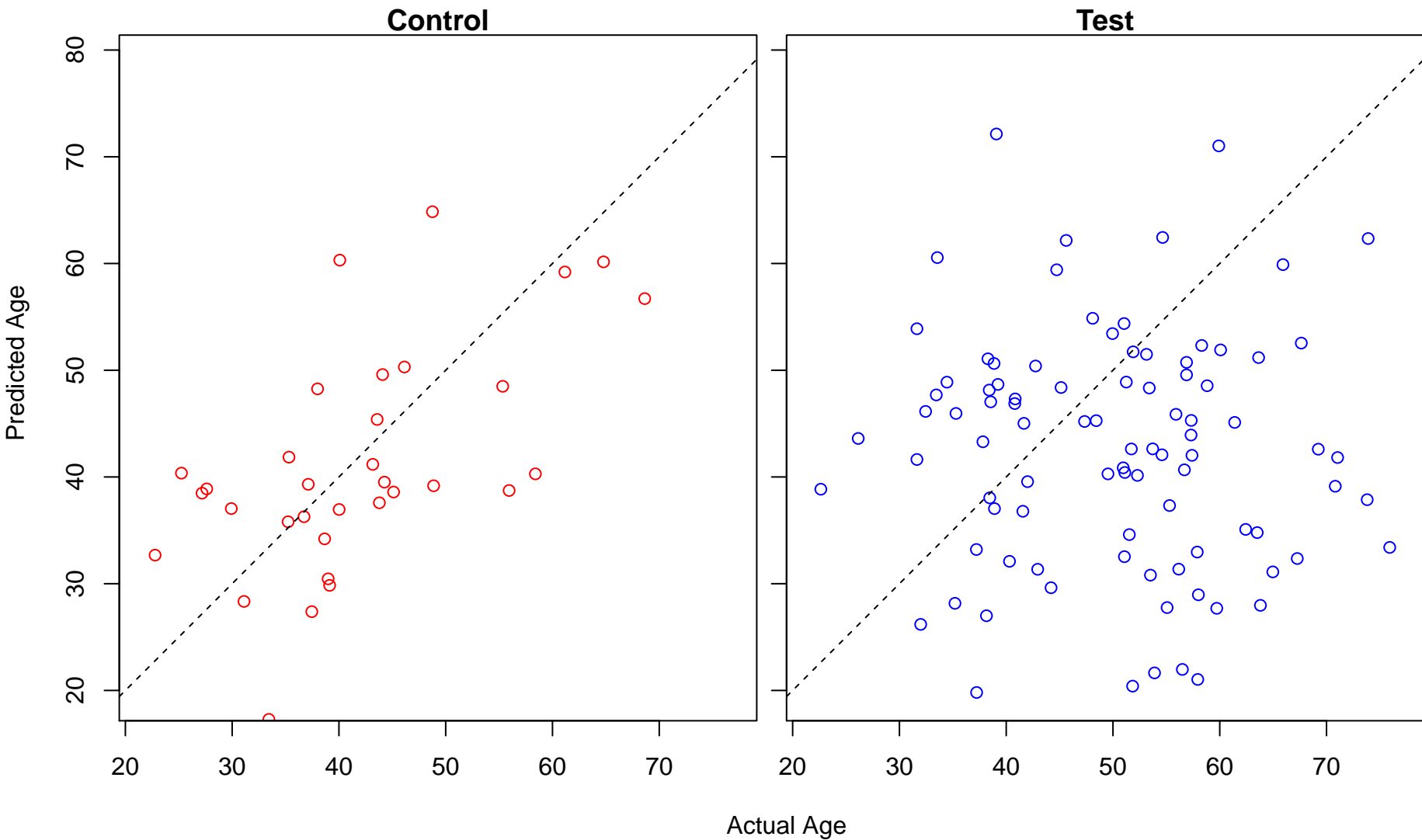
cellular glucose homeostasis (Score: 1.595559)



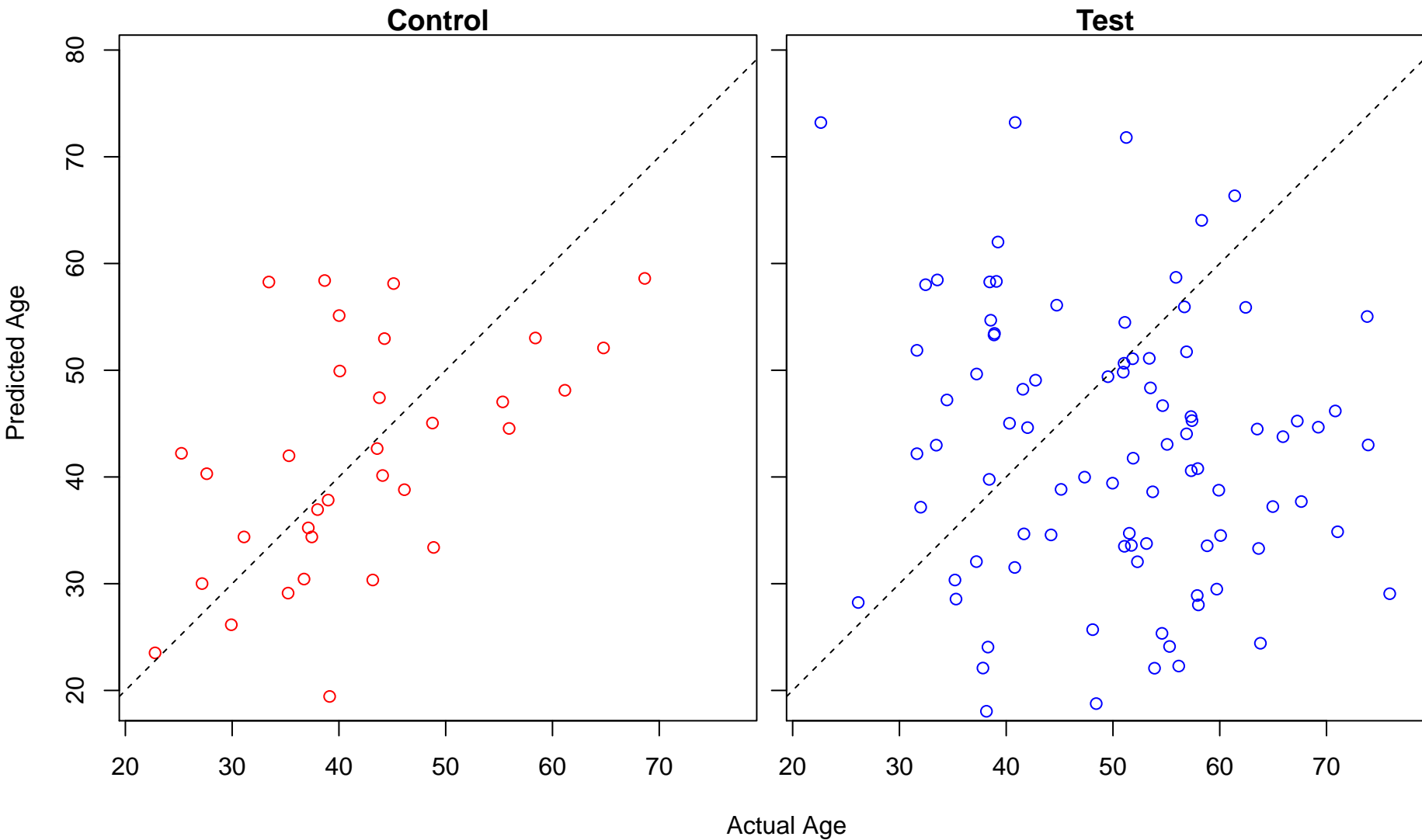
glutathione metabolic process (Score: 1.583300)



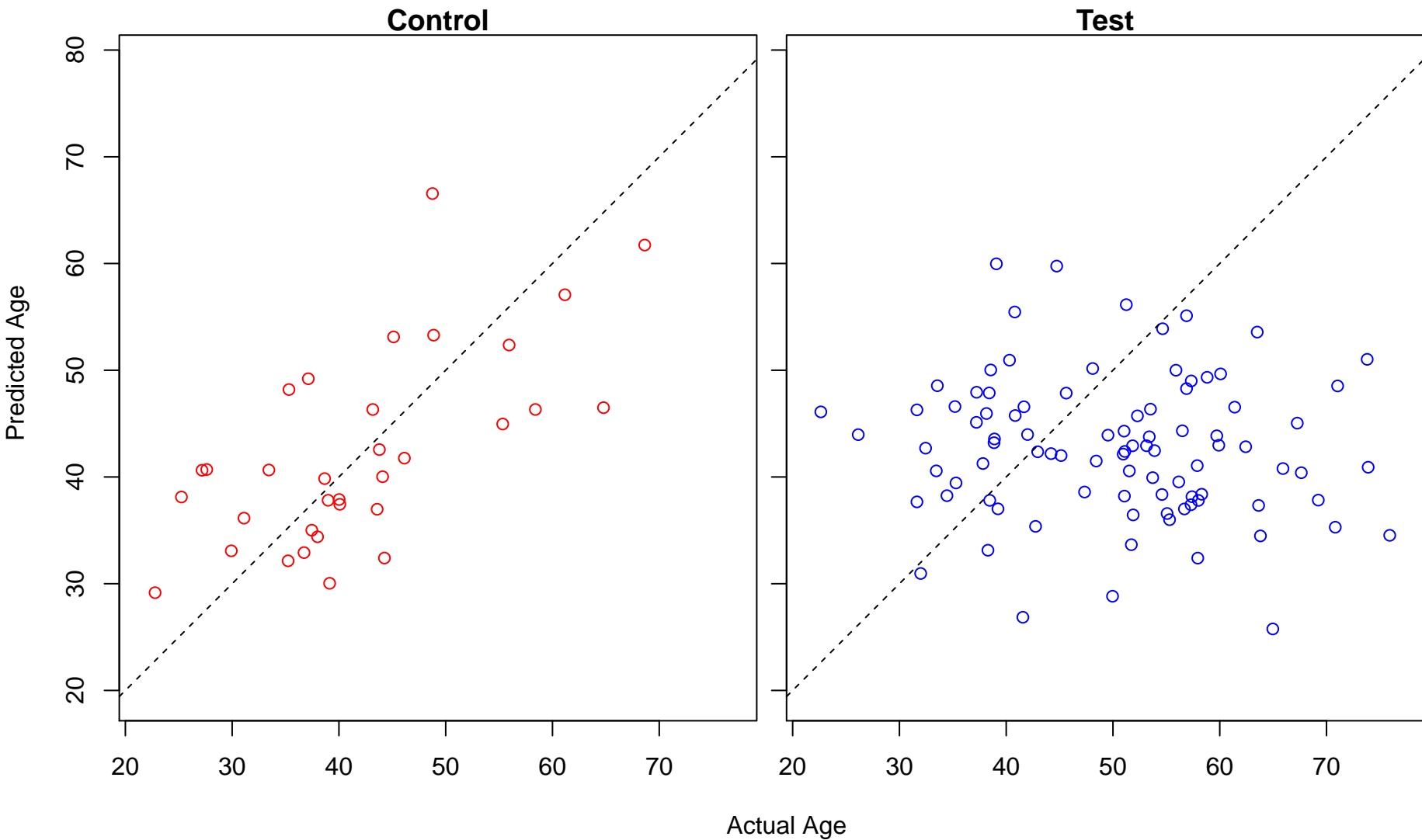
lipid modification (Score: 1.582694)



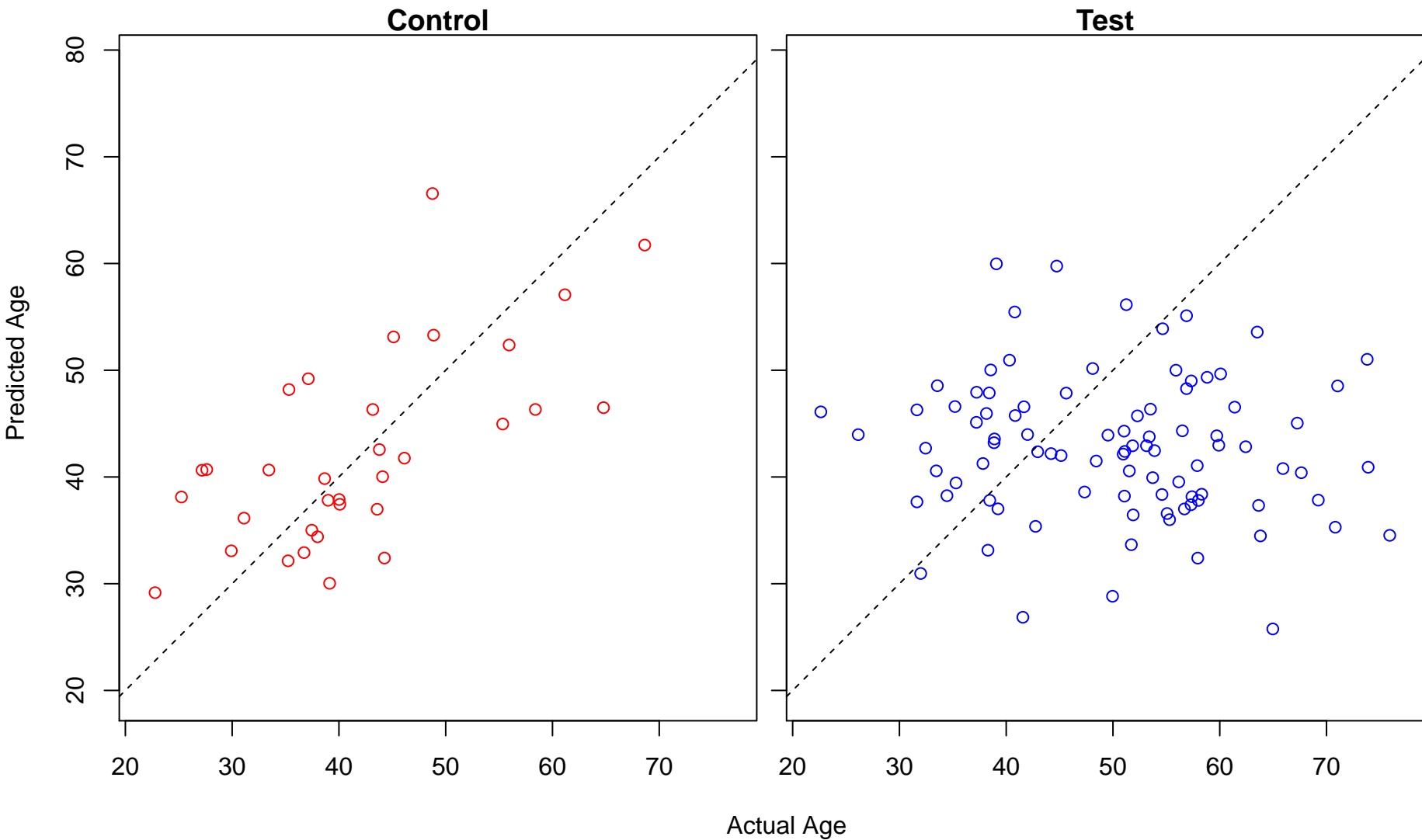
endocrine process (Score: 1.576076)



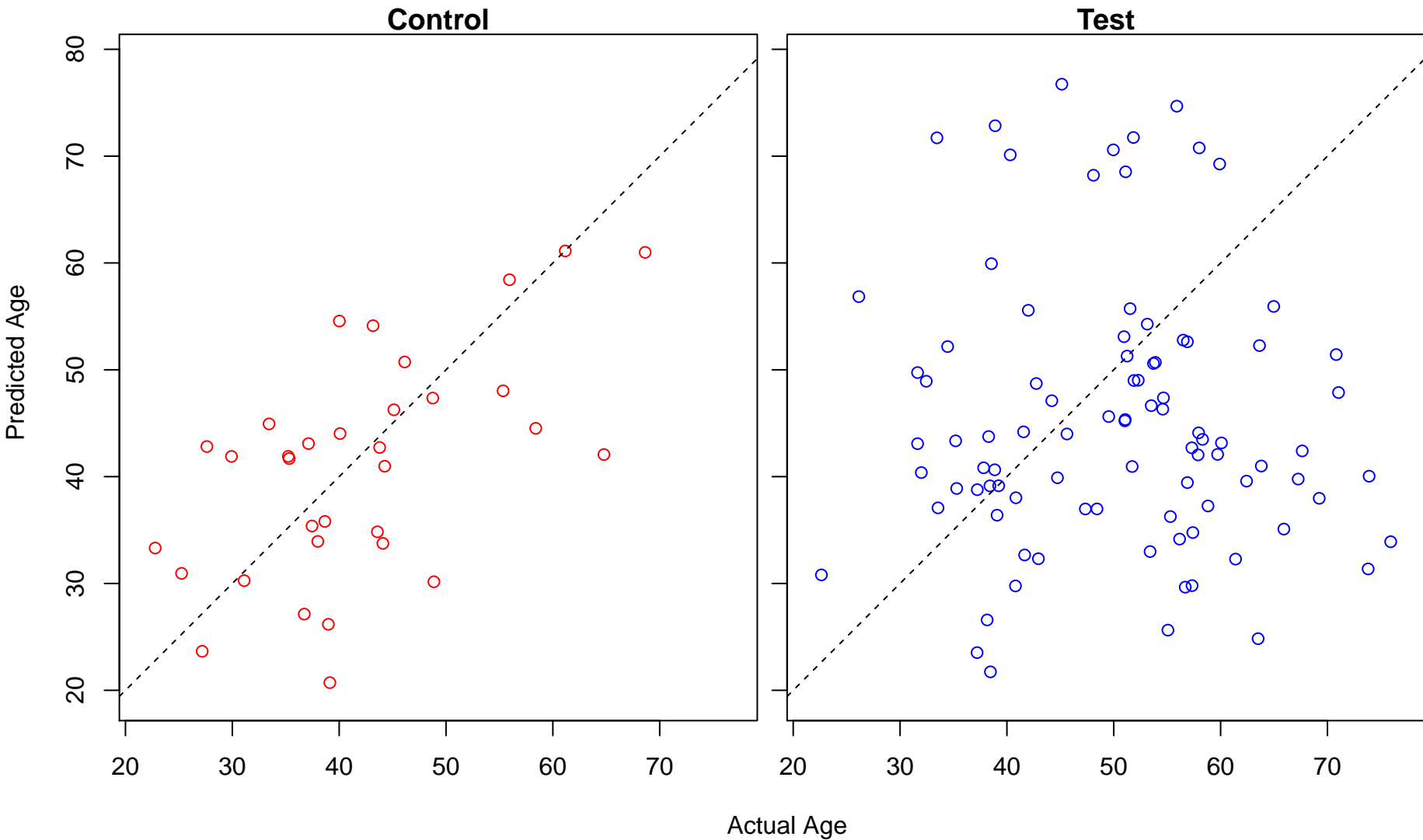
rhythmic behavior (Score: 1.575655)



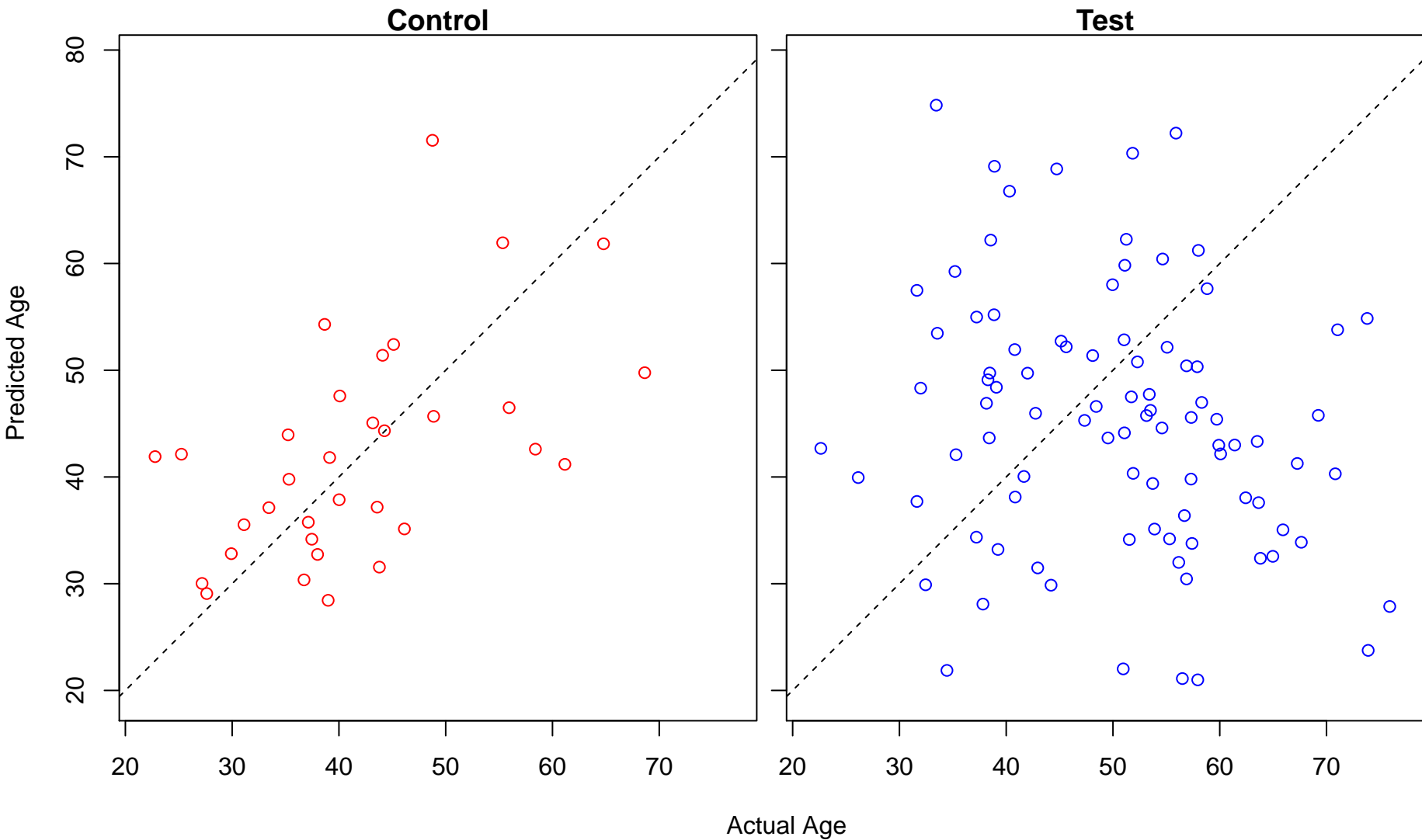
circadian behavior (Score: 1.575655)



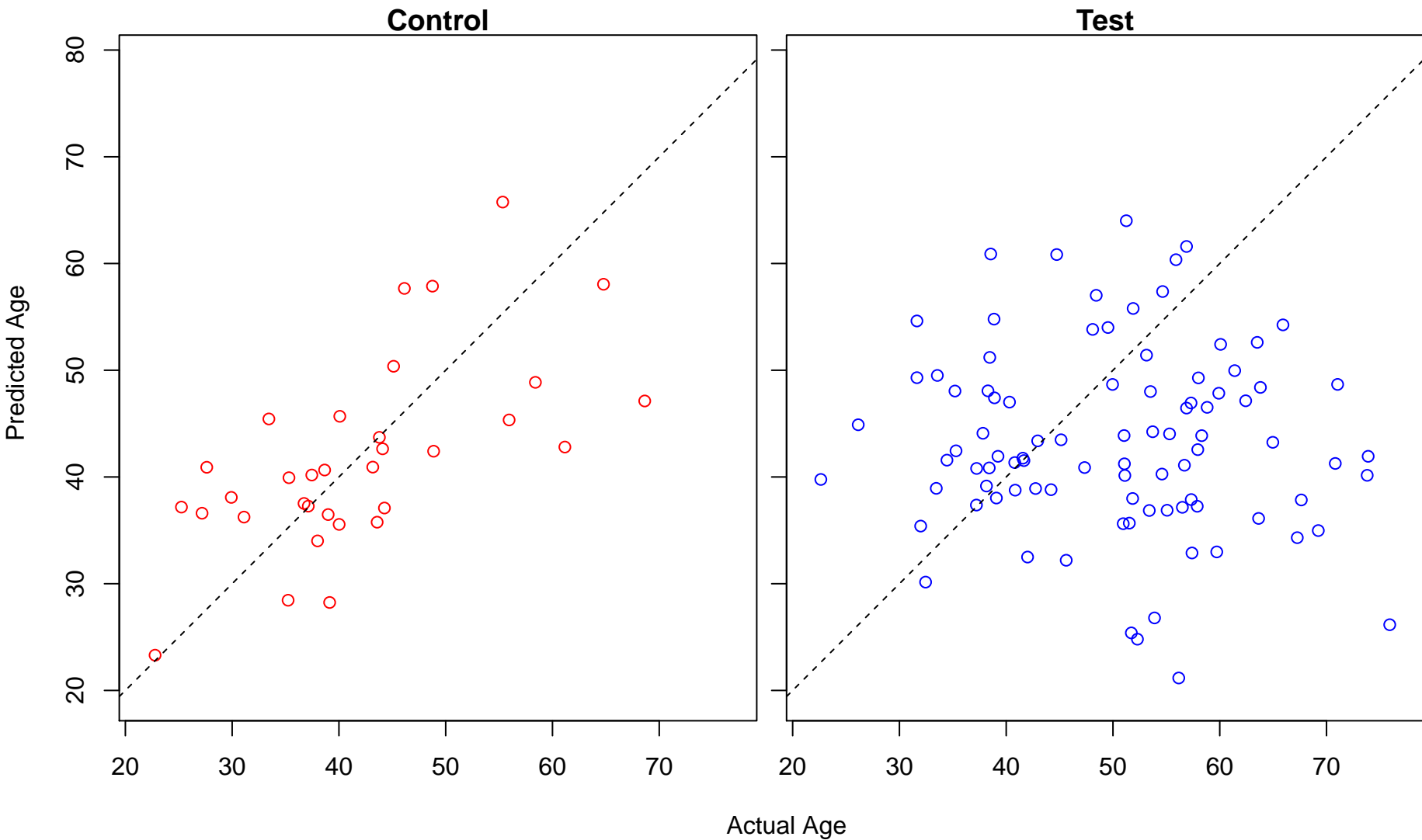
regulation of ryanodine-sensitive calcium-release channel activity (Score: 1.565901)



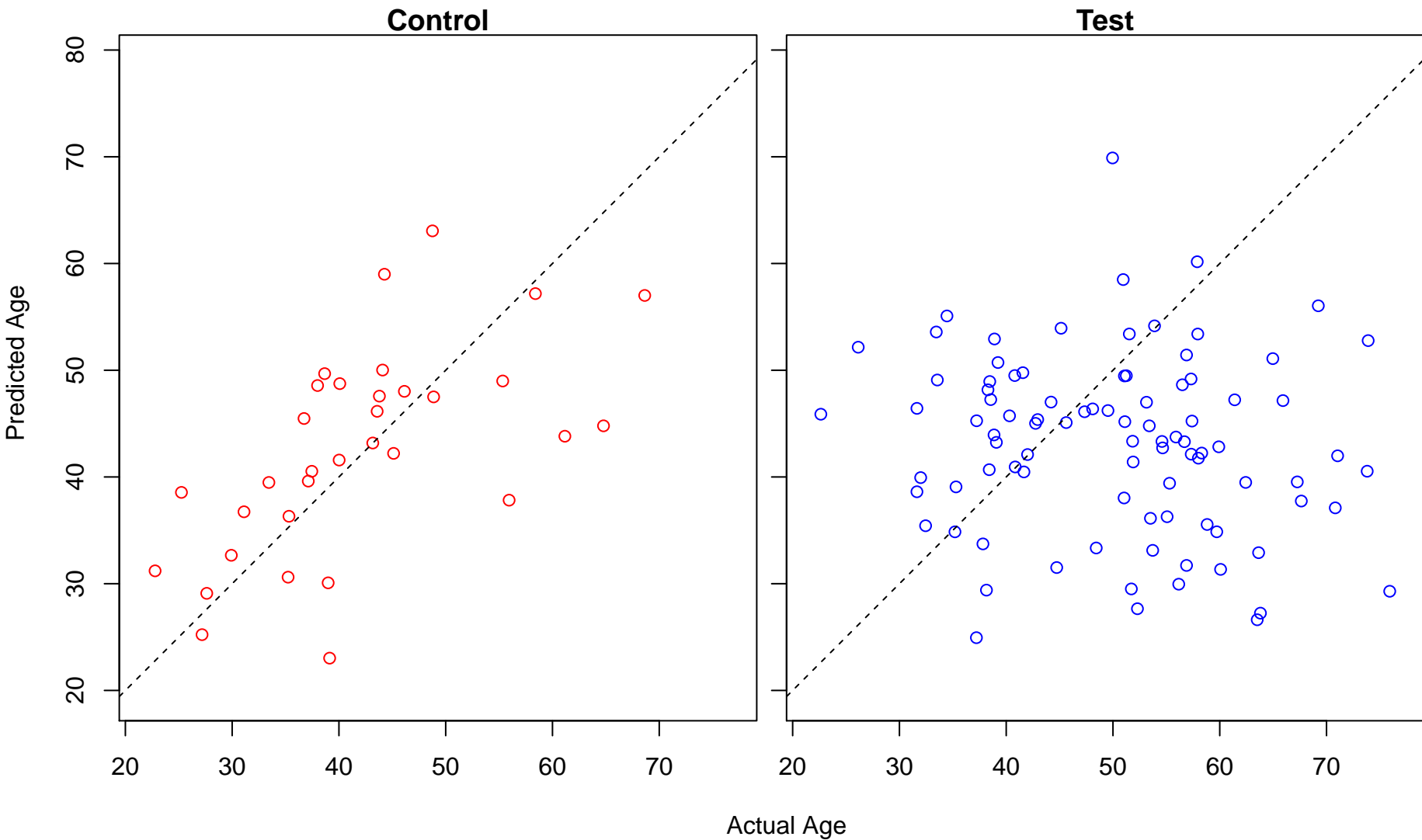
establishment of mitotic spindle localization (Score: 1.552776)



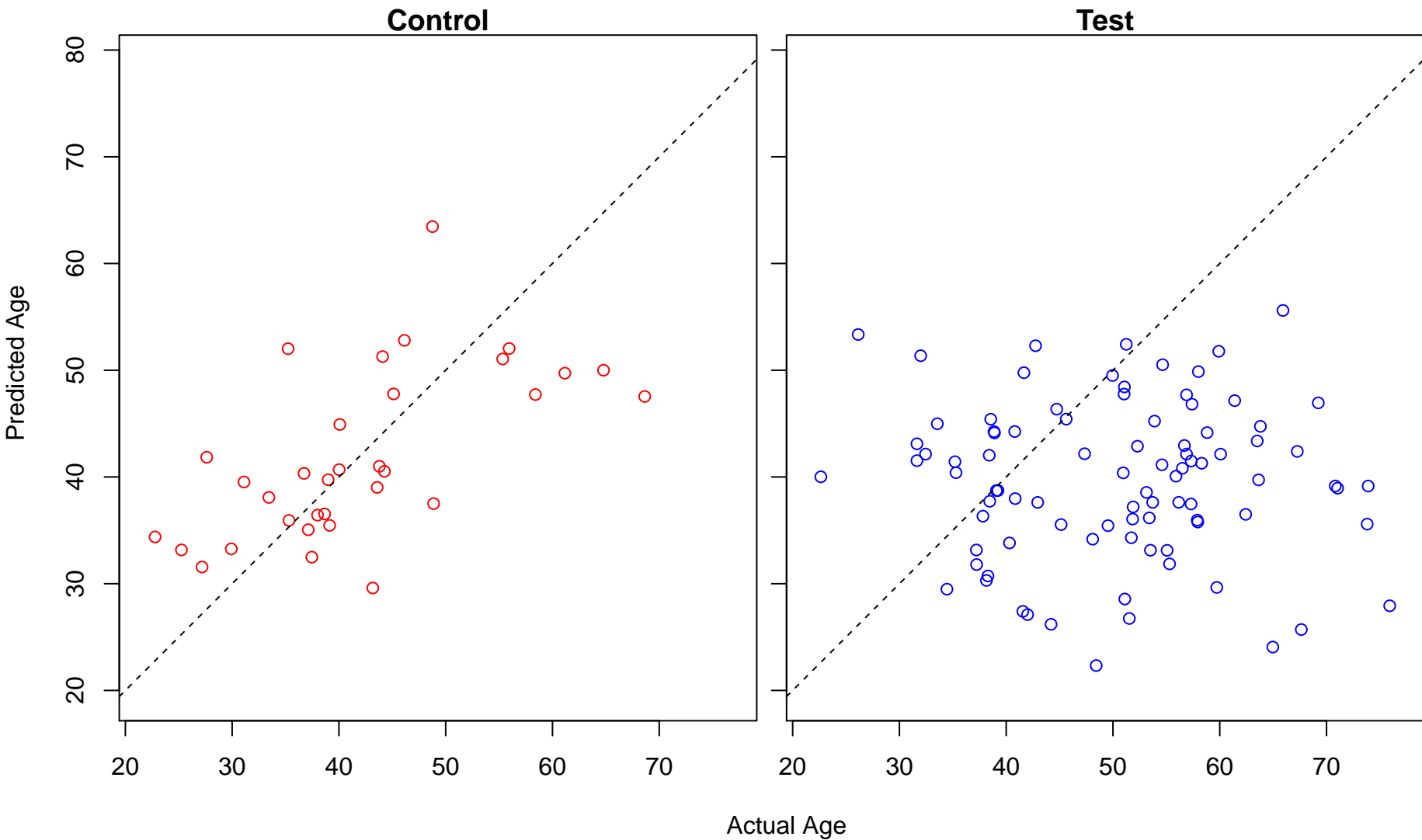
microtubule organizing center organization (Score: 1.551349)



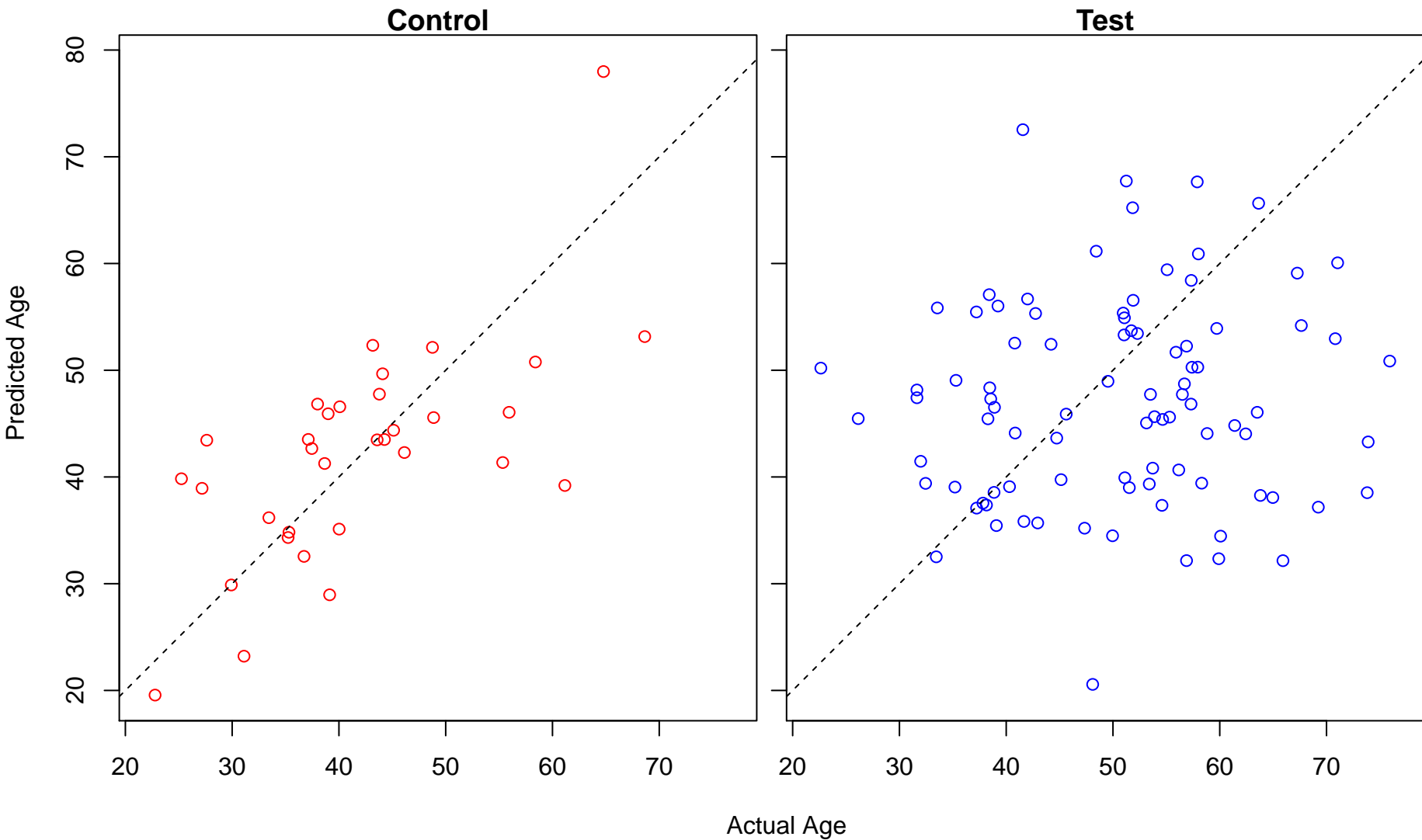
complement activation (Score: 1.550614)



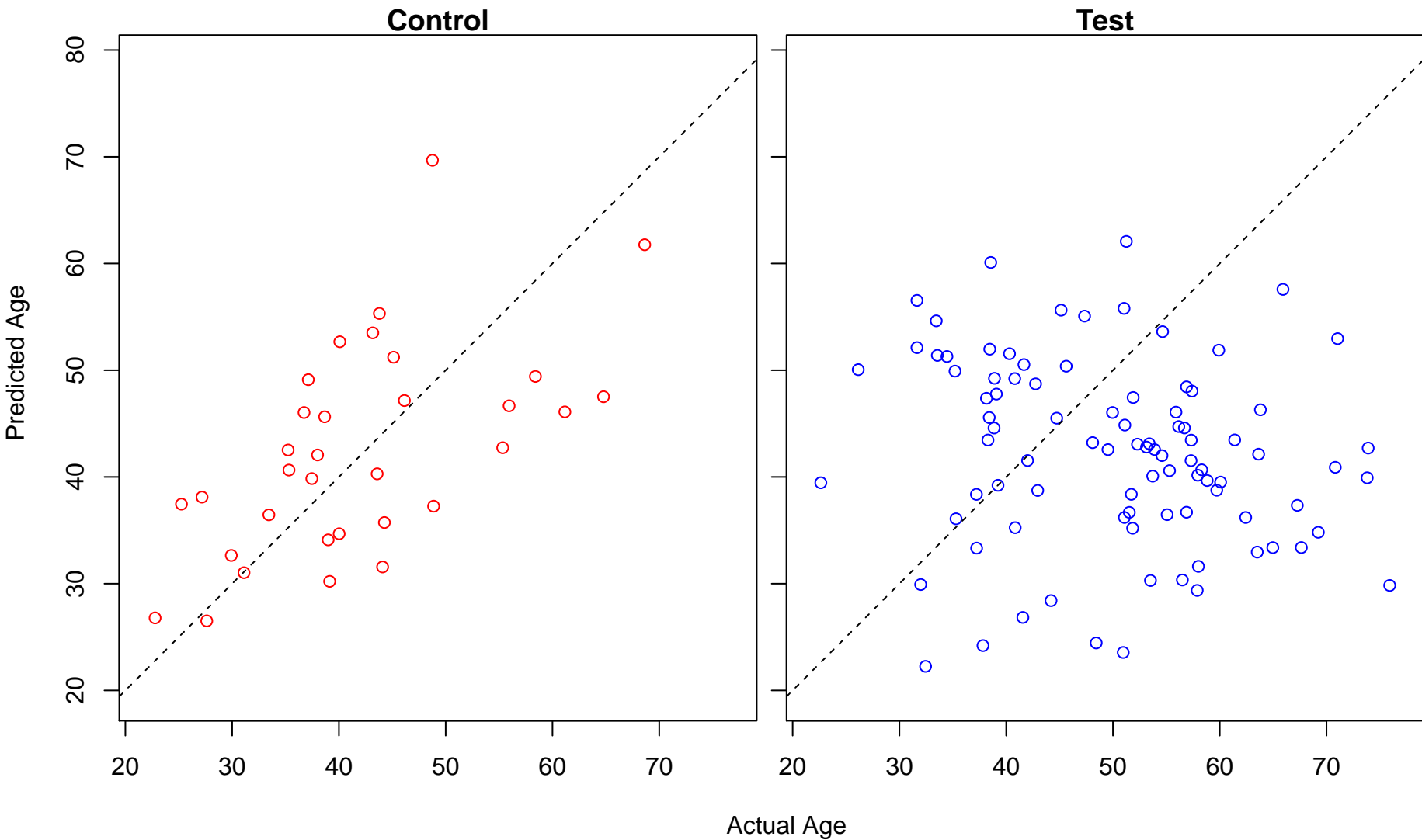
cell communication involved in cardiac conduction (Score: 1.544338)



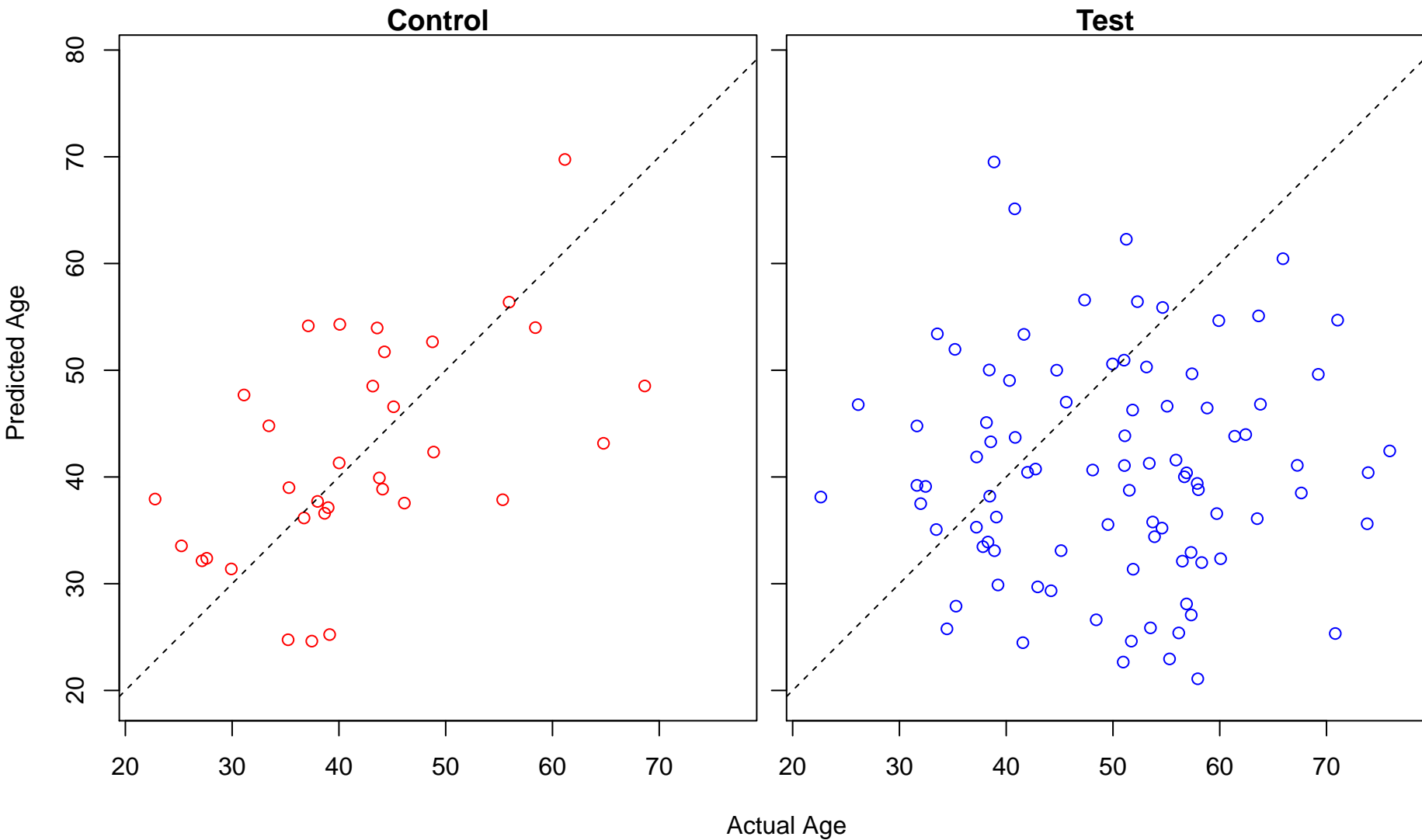
dorsal/ventral pattern formation (Score: 1.540382)



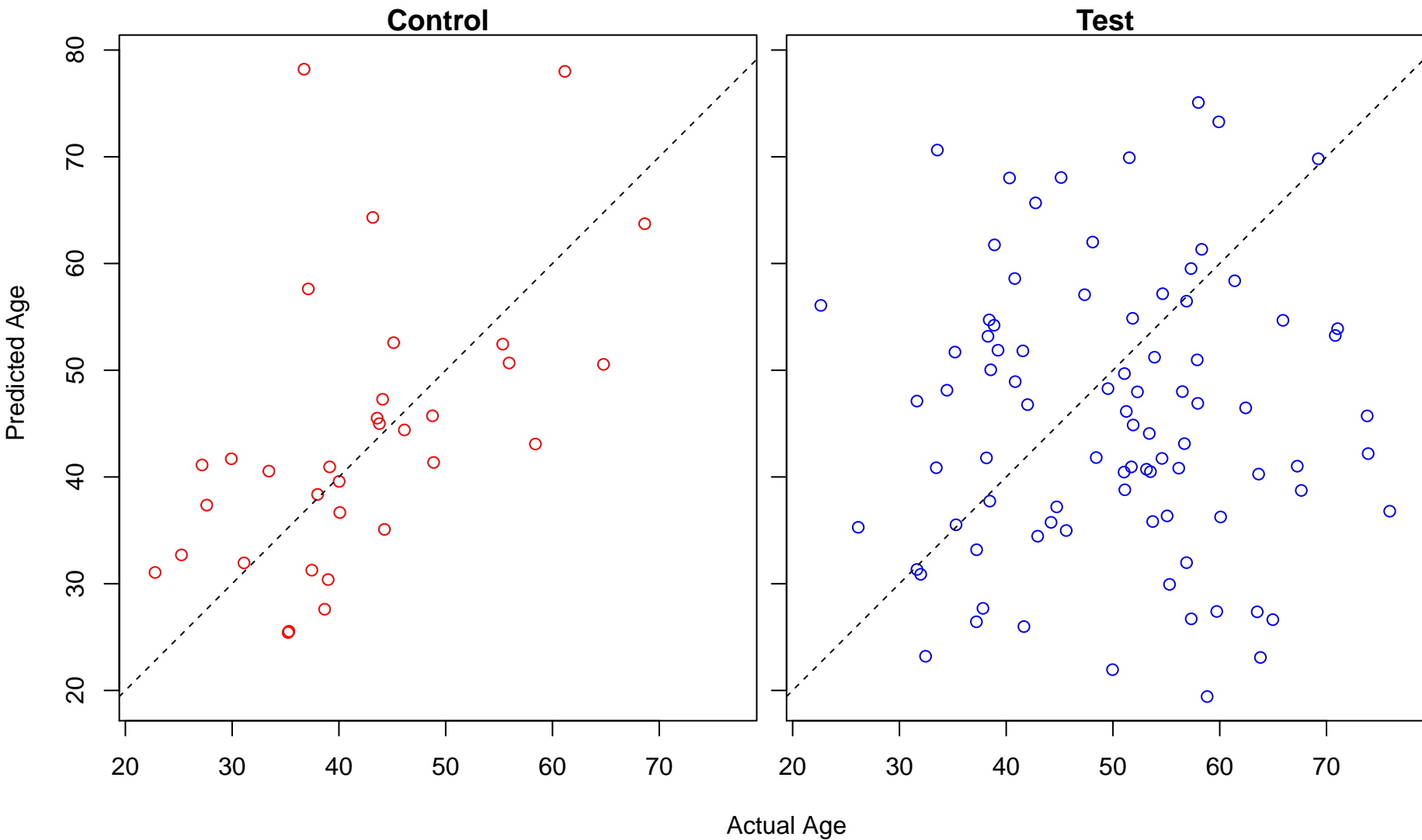
alcohol biosynthetic process (Score: 1.537787)



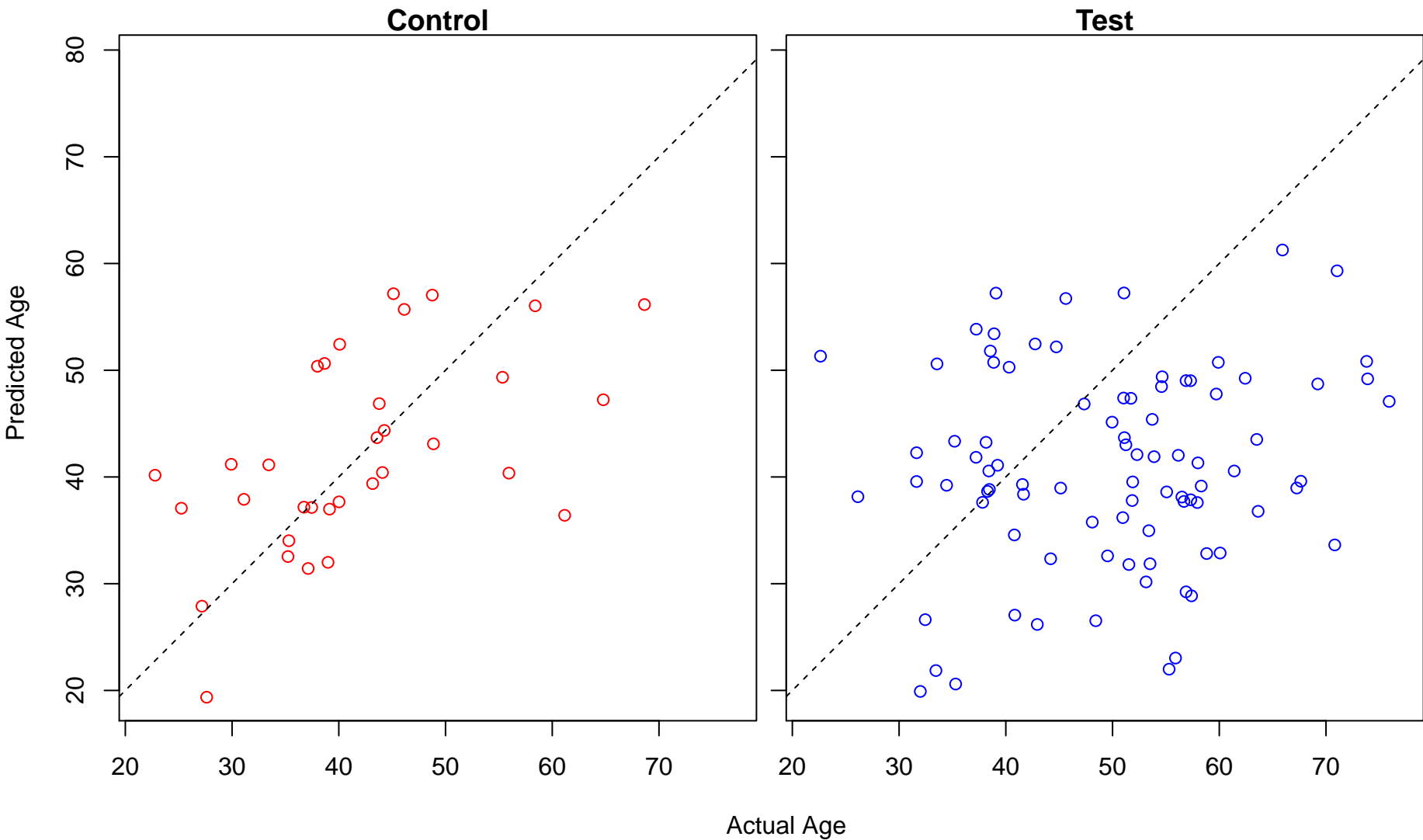
negative regulation of synaptic transmission (Score: 1.535113)



DNA damage response, detection of DNA damage (Score: 1.530234)

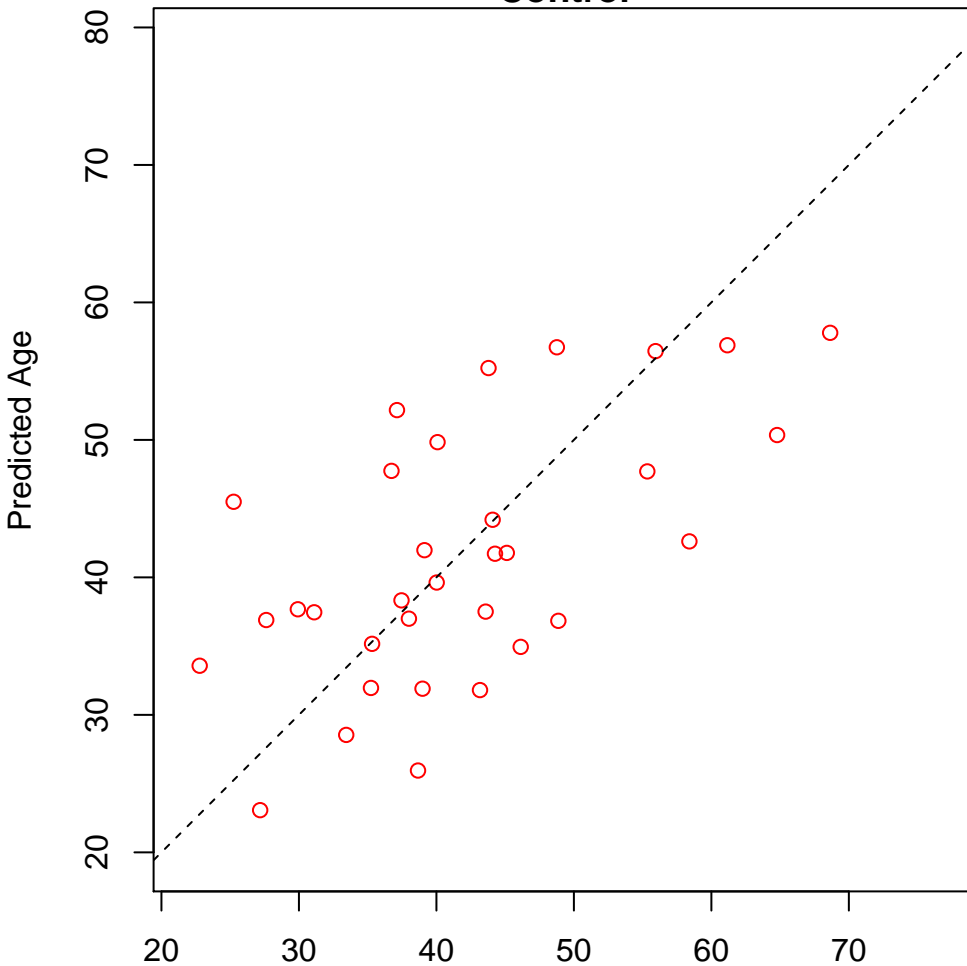


synapse organization (Score: 1.525872)

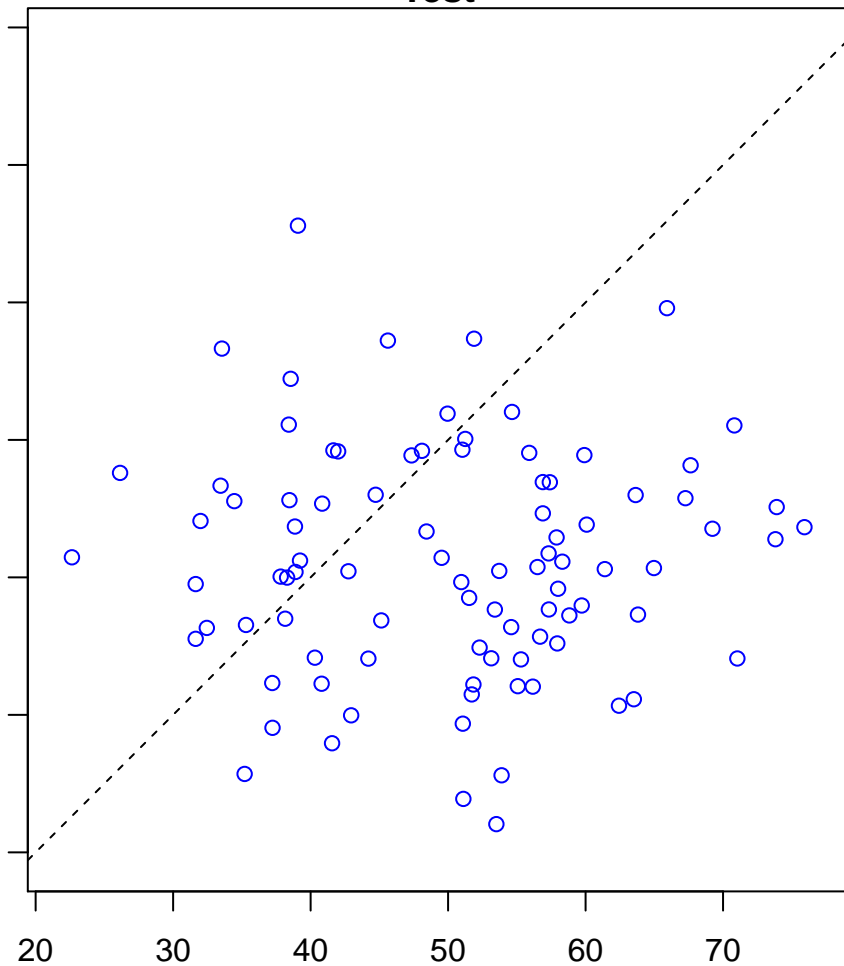


blood coagulation, fibrin clot formation (Score: 1.511570)

Control

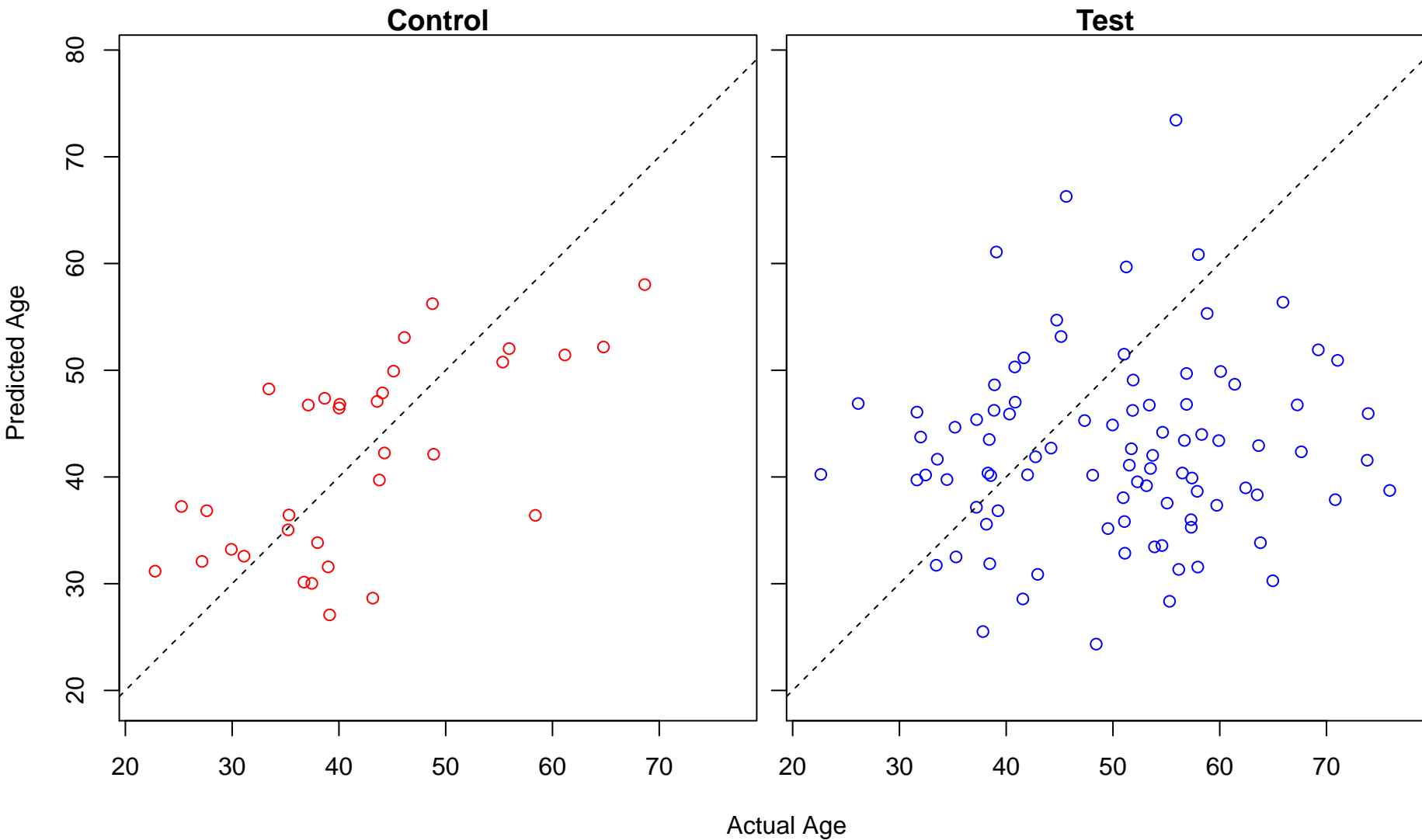


Test

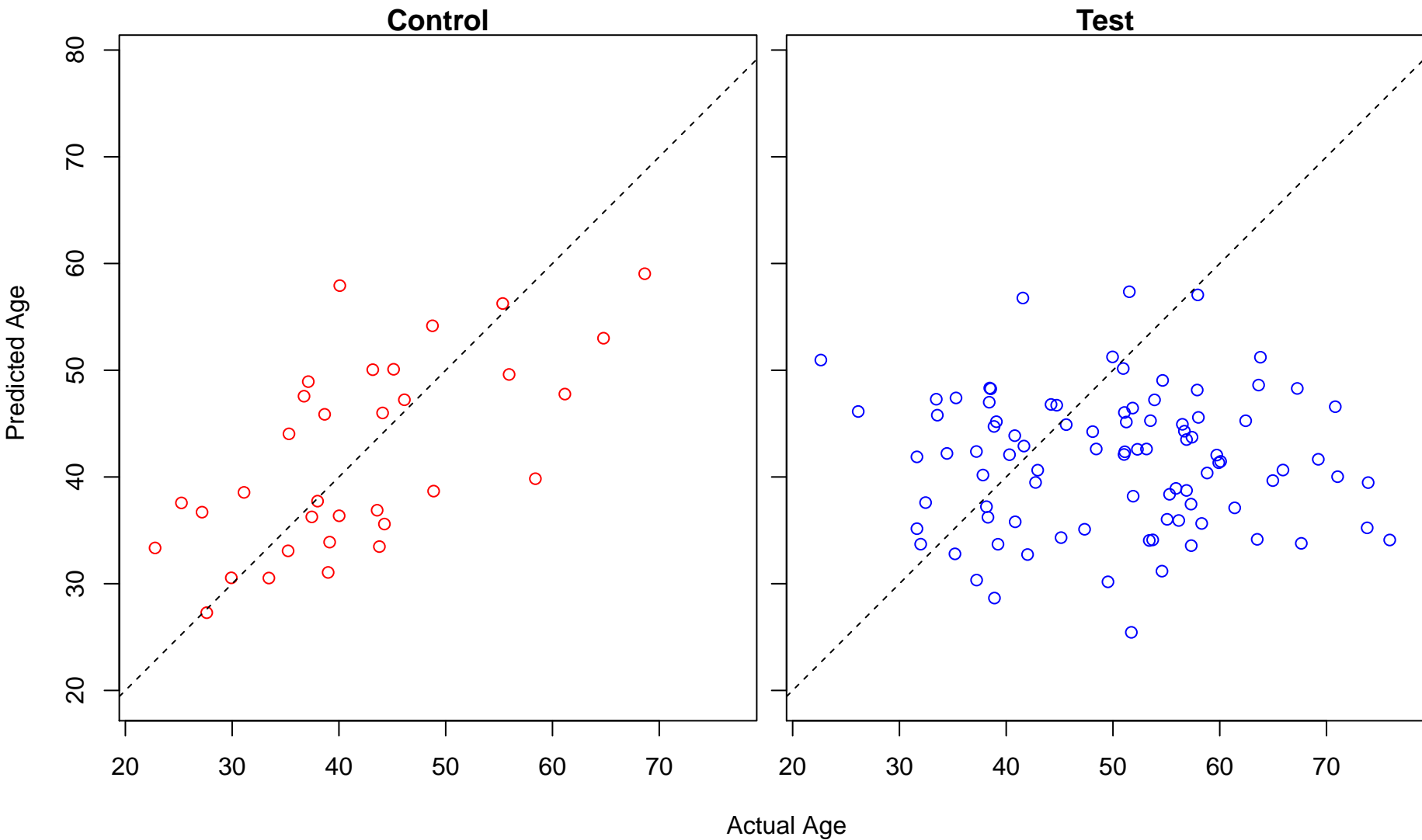


Actual Age

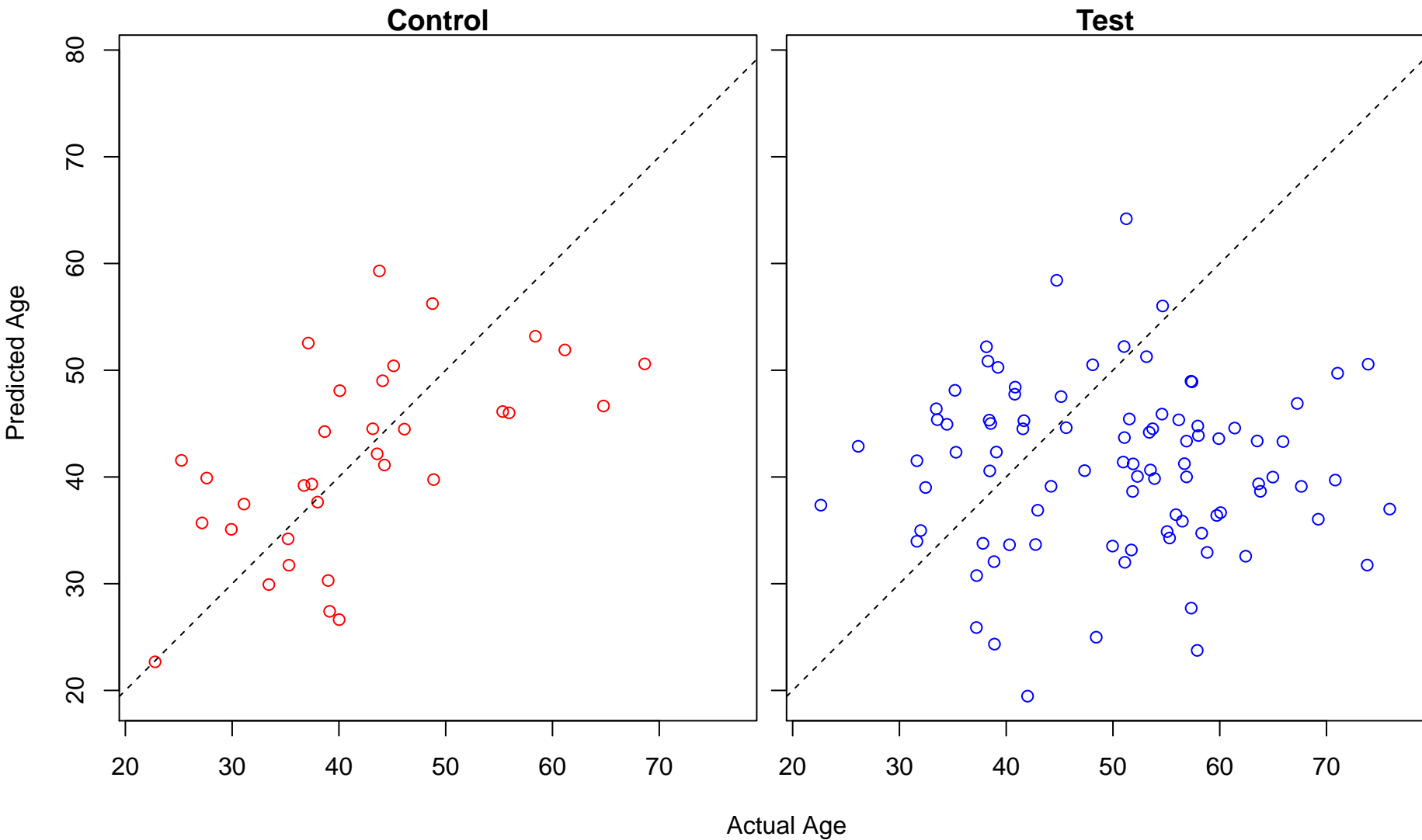
positive regulation of ion transmembrane transport (Score: 1.497628)



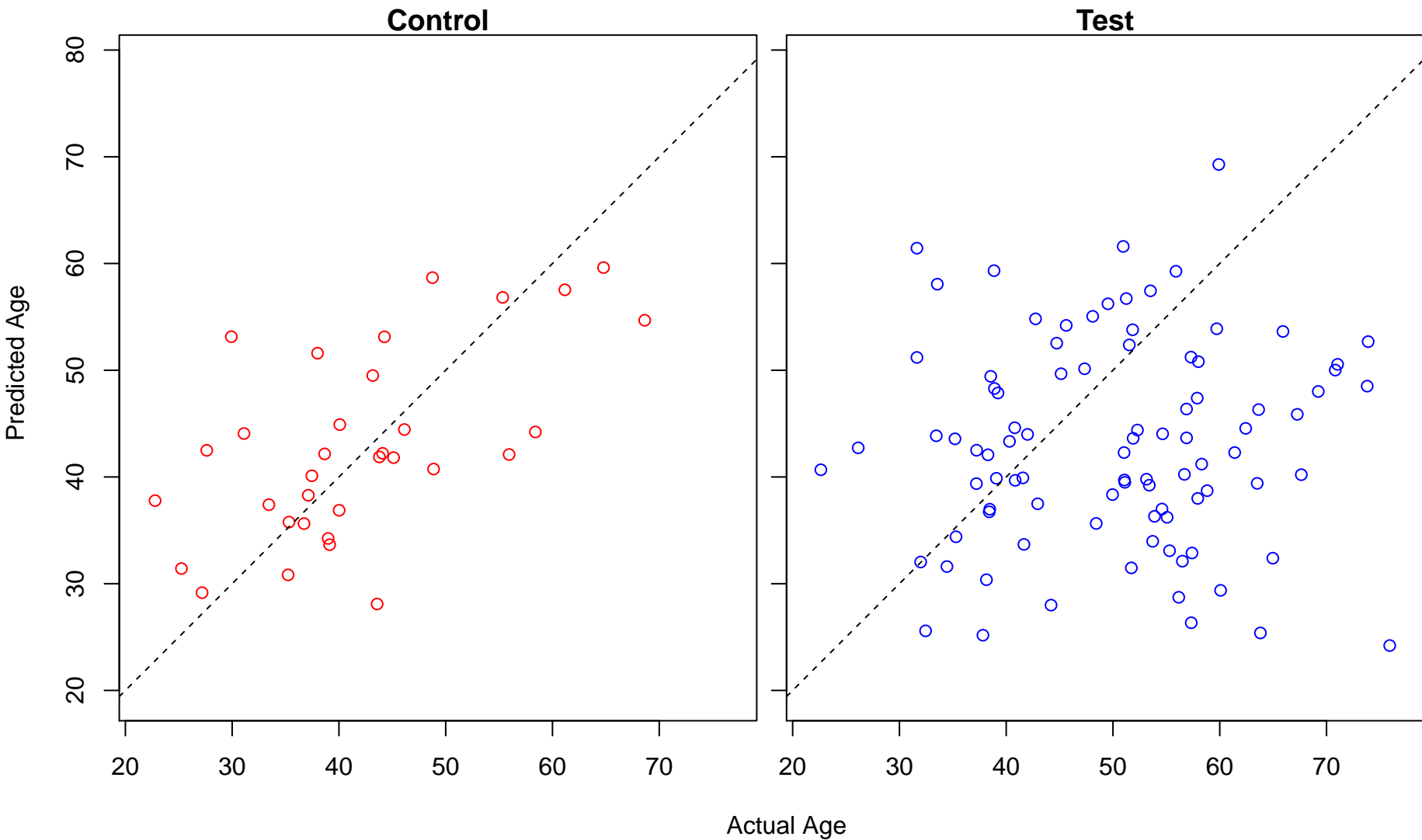
transmission of nerve impulse (Score: 1.495499)



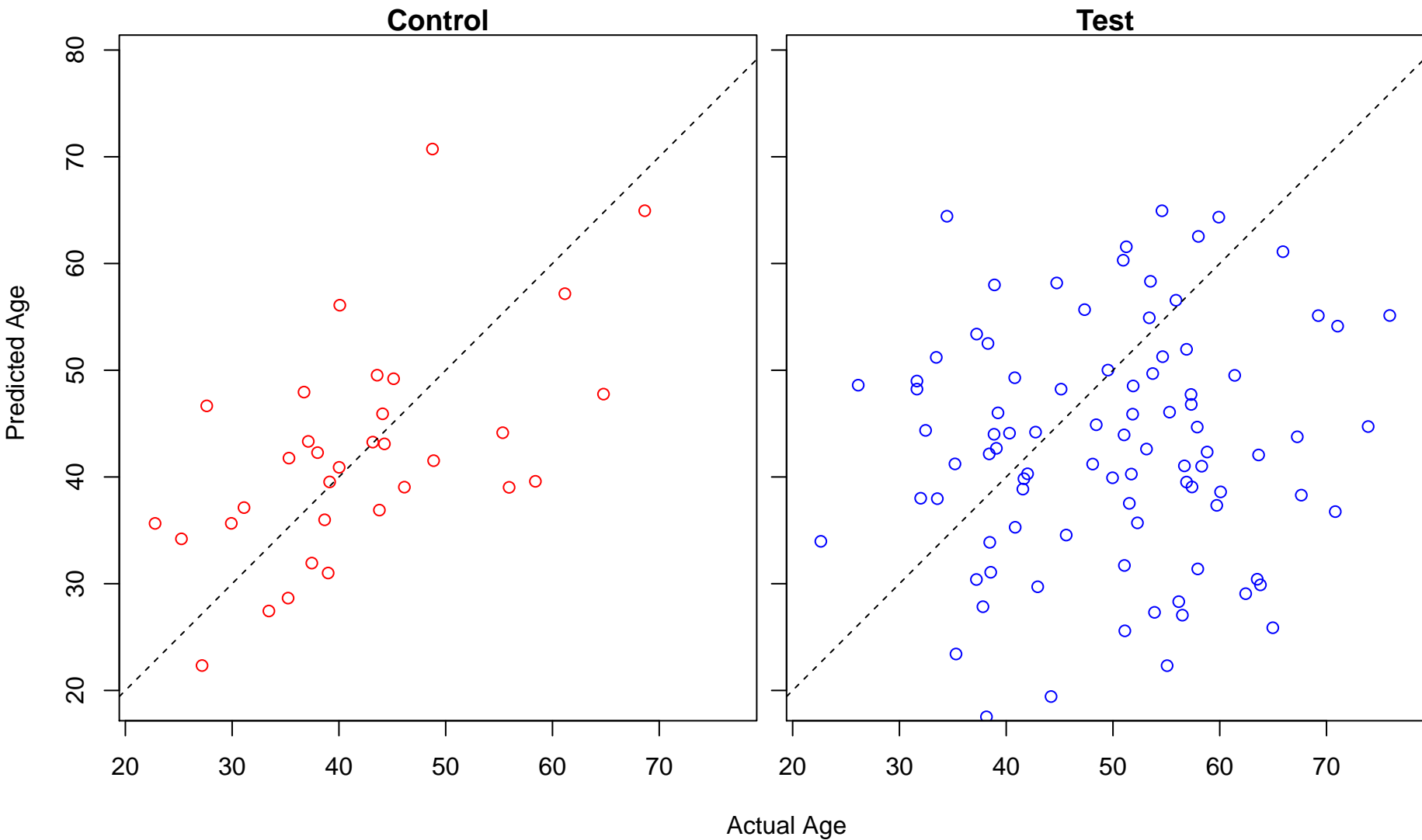
phosphatidylethanolamine metabolic process (Score: 1.493600)



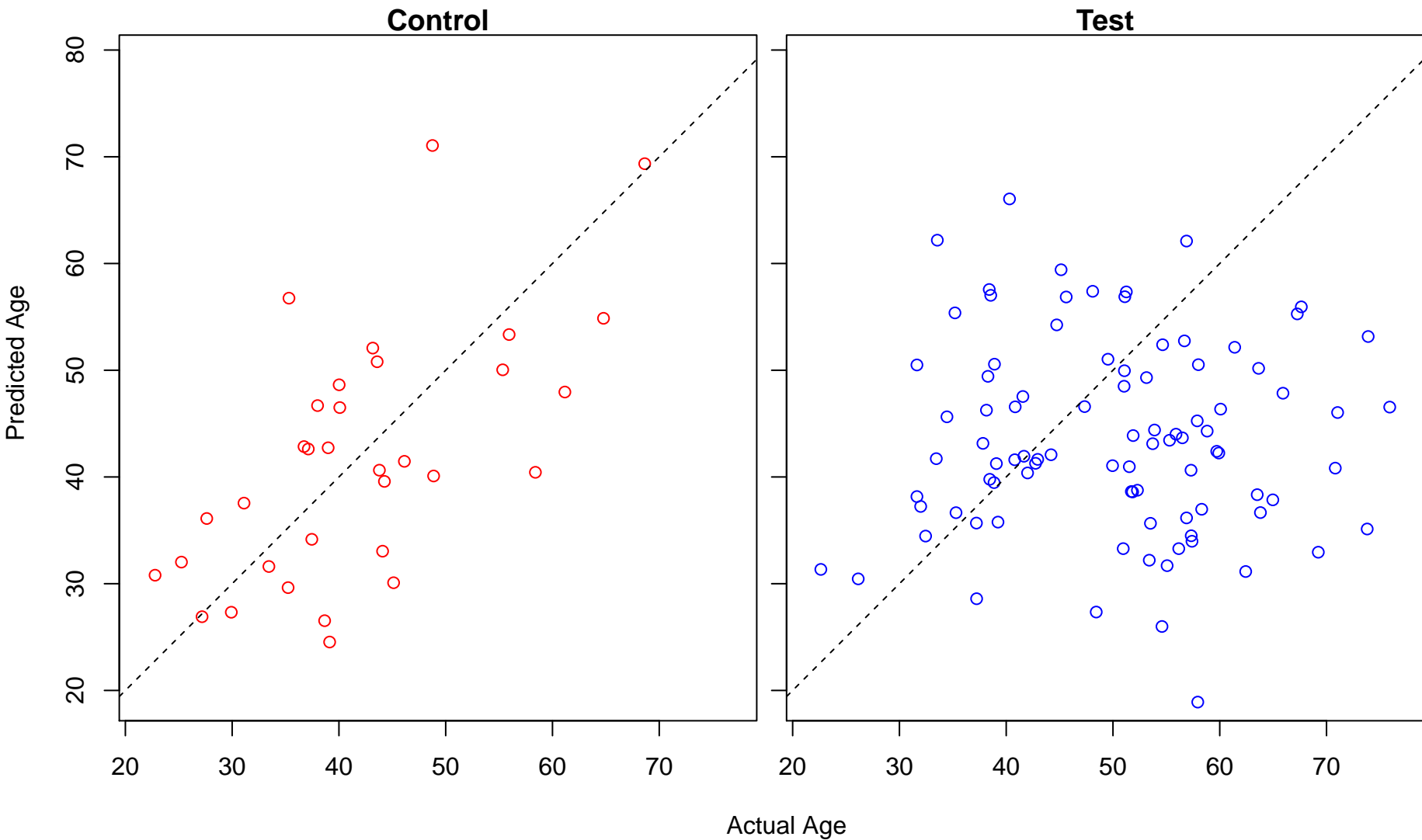
detection of abiotic stimulus (Score: 1.491576)



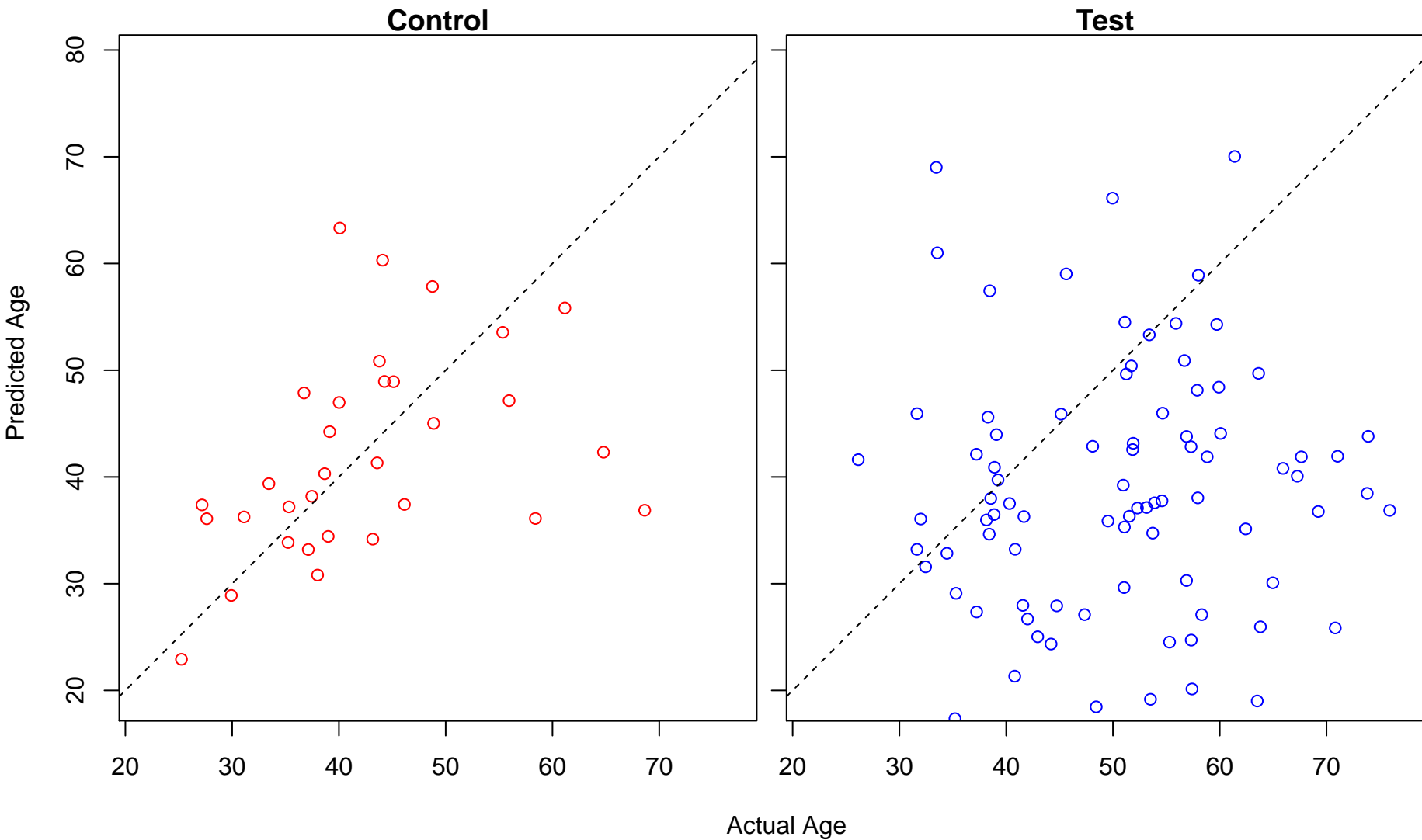
regulation of phosphatase activity (Score: 1.490411)



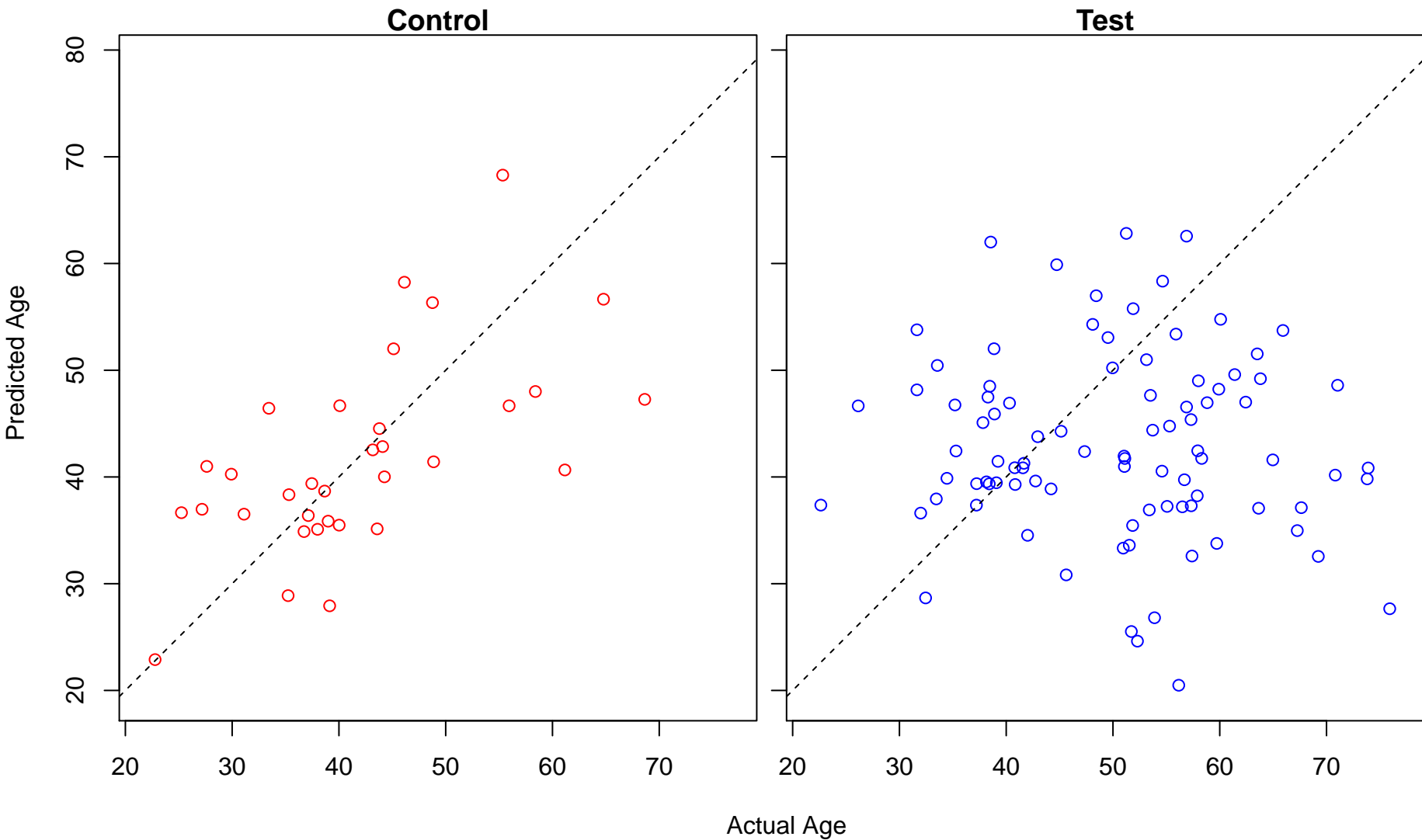
negative regulation of fat cell differentiation (Score: 1.490140)



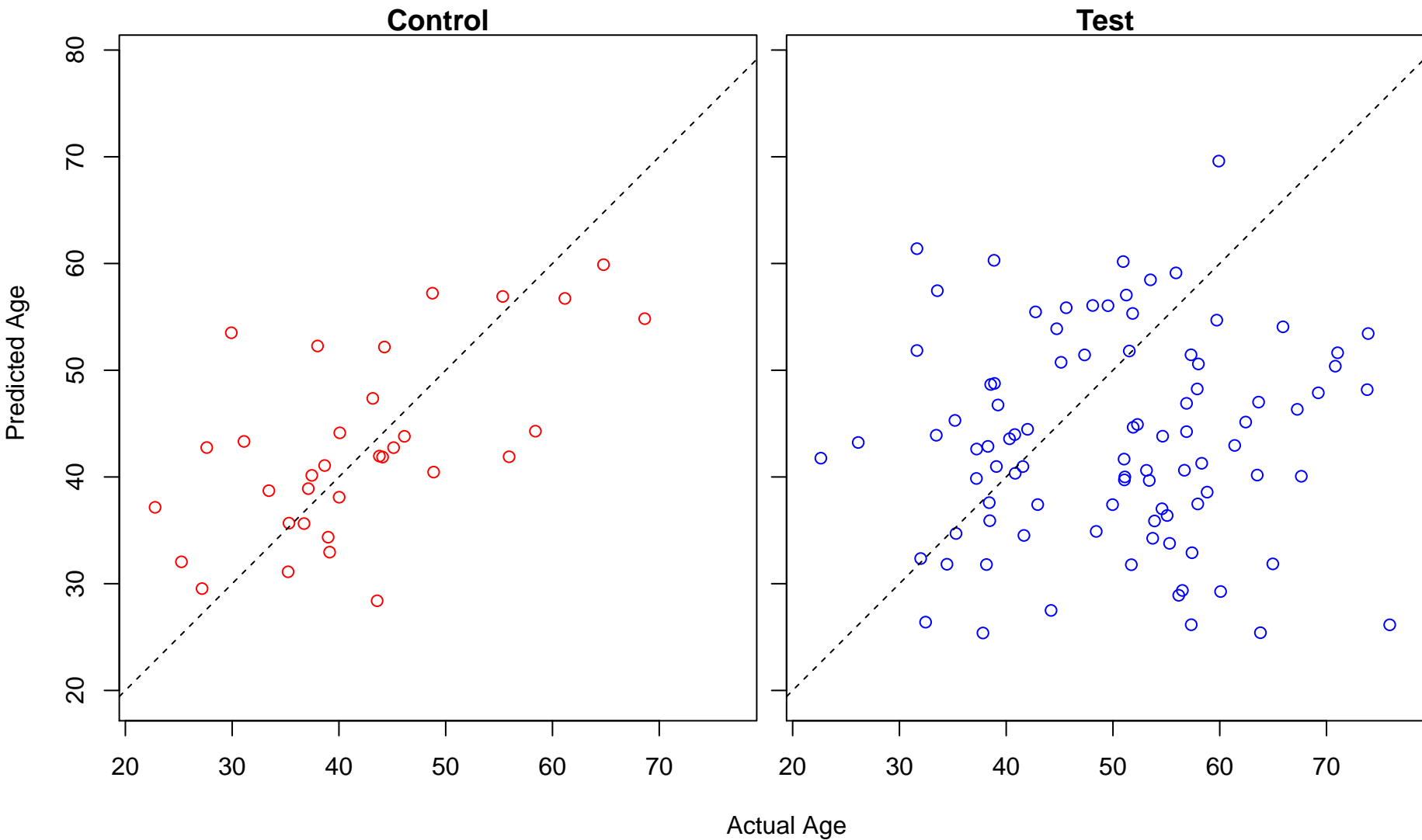
regulation of lipid kinase activity (Score: 1.488920)



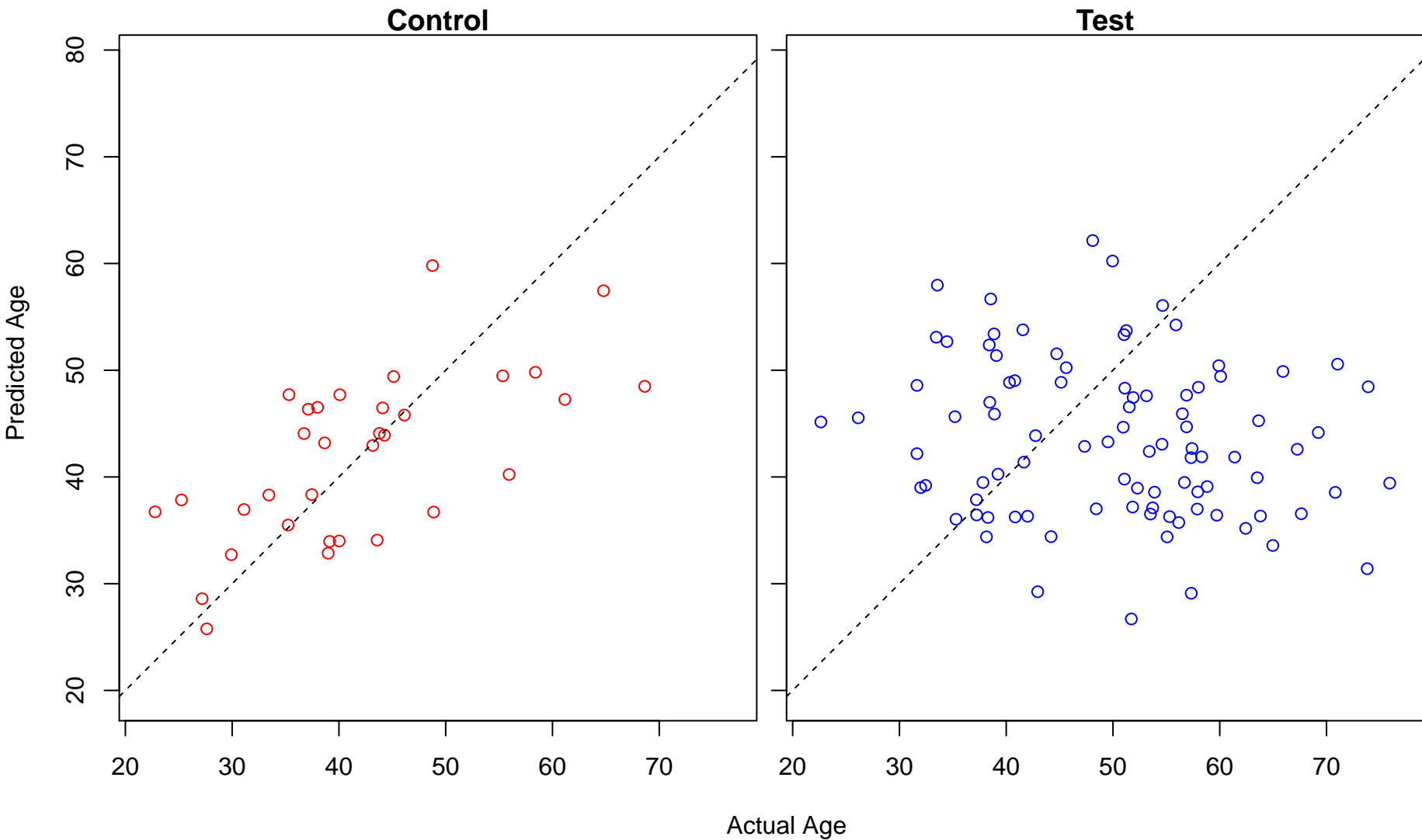
centrosome organization (Score: 1.484433)



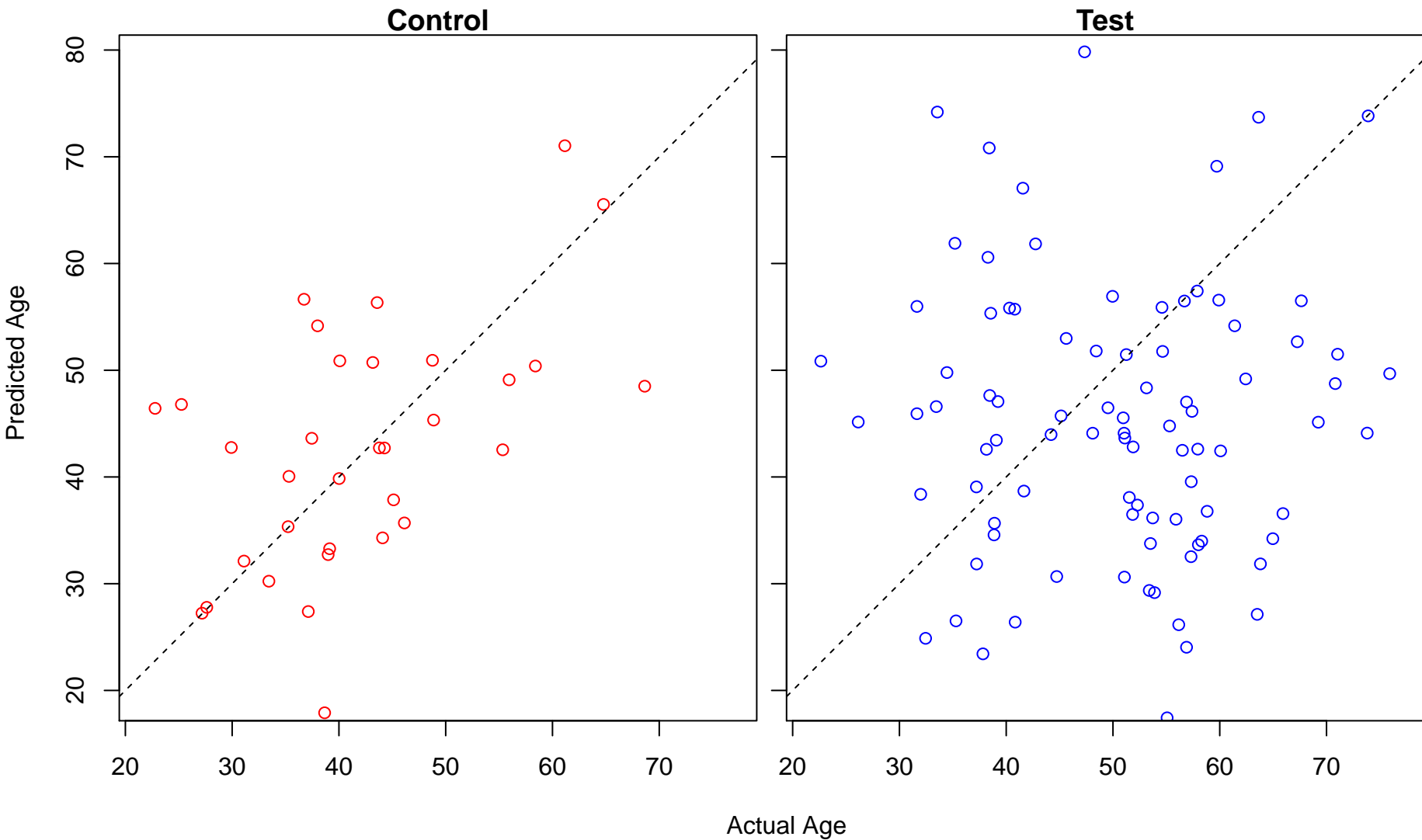
detection of external stimulus (Score: 1.482637)



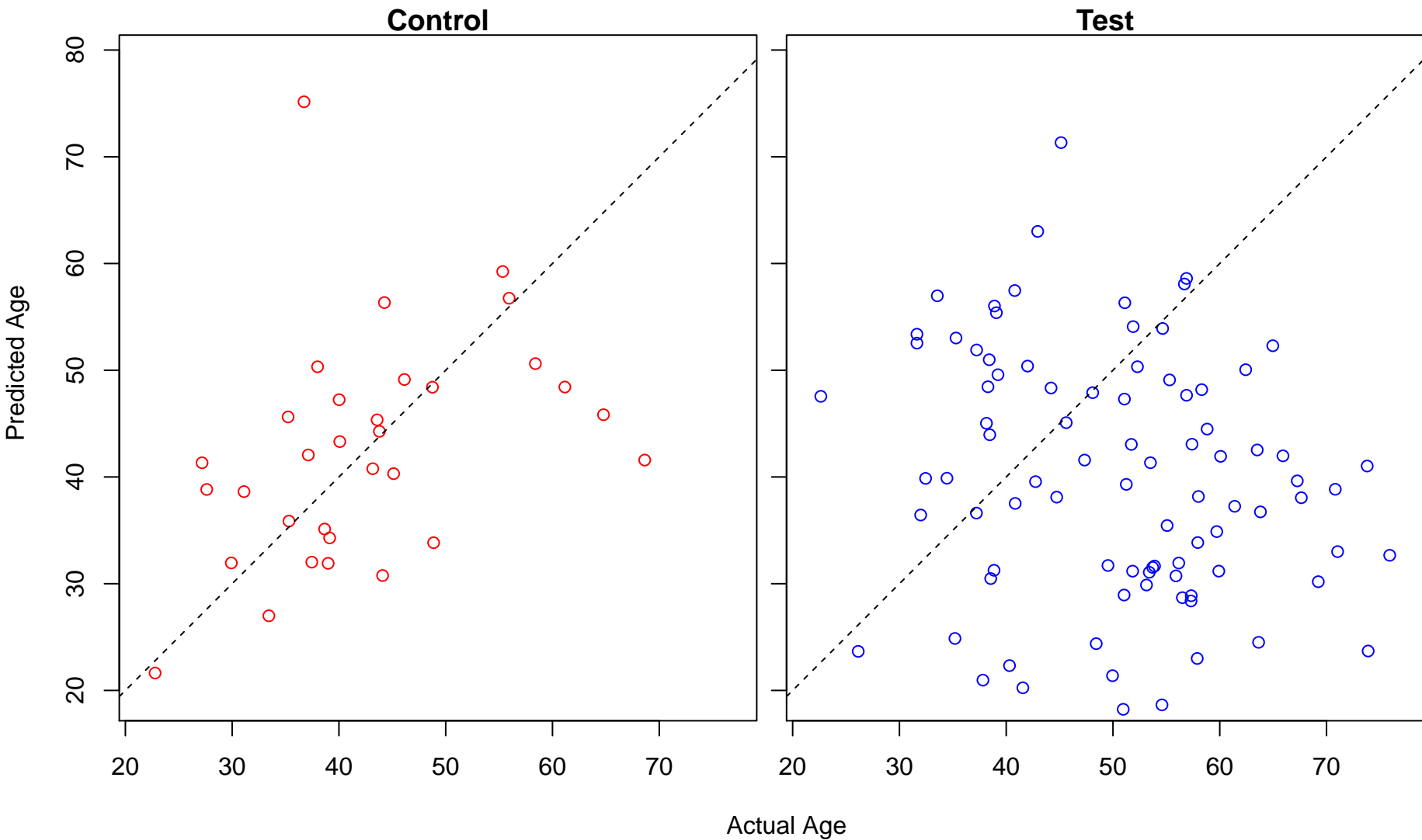
glial cell proliferation (Score: 1.480510)



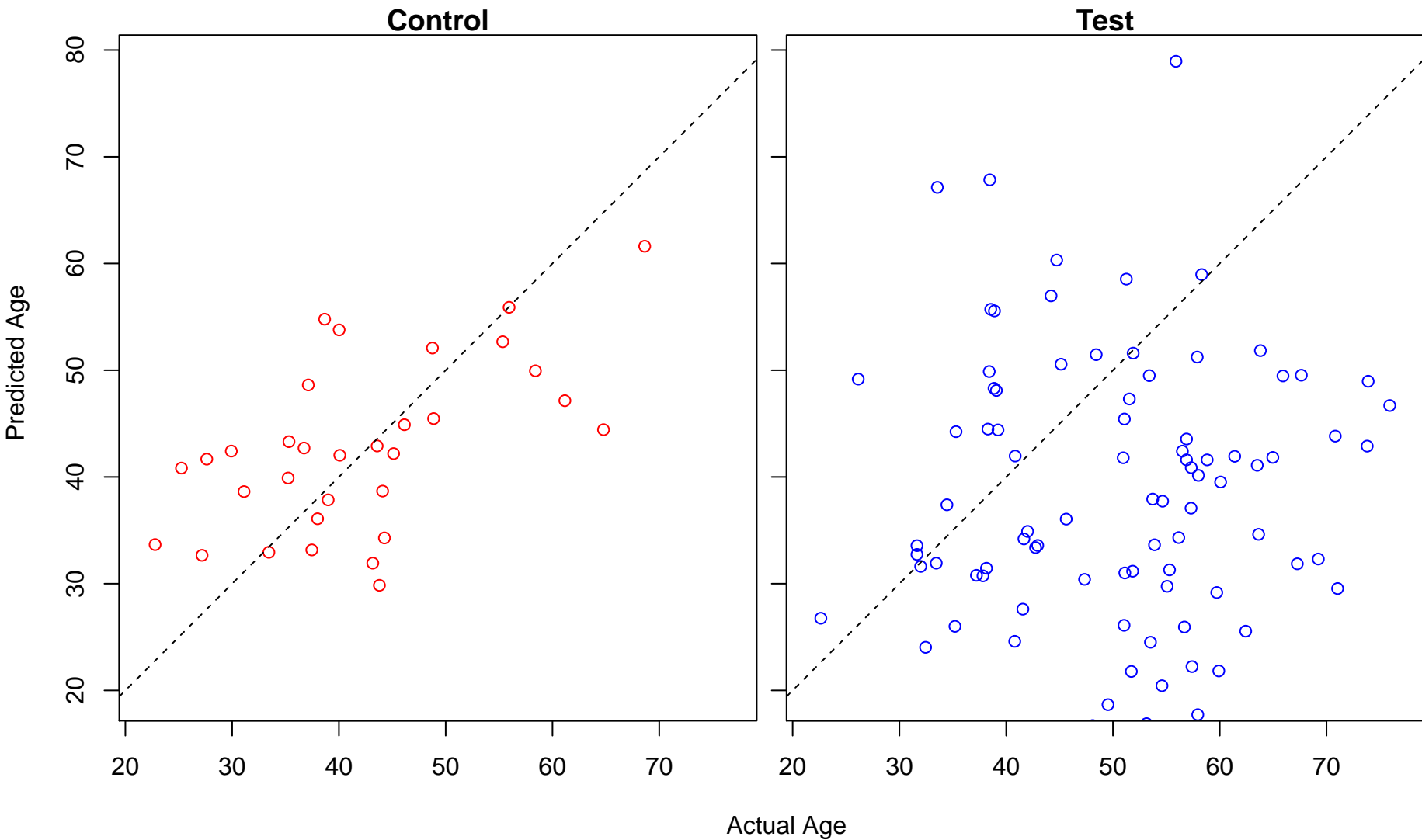
positive regulation of adaptive immune response (Score: 1.478704)



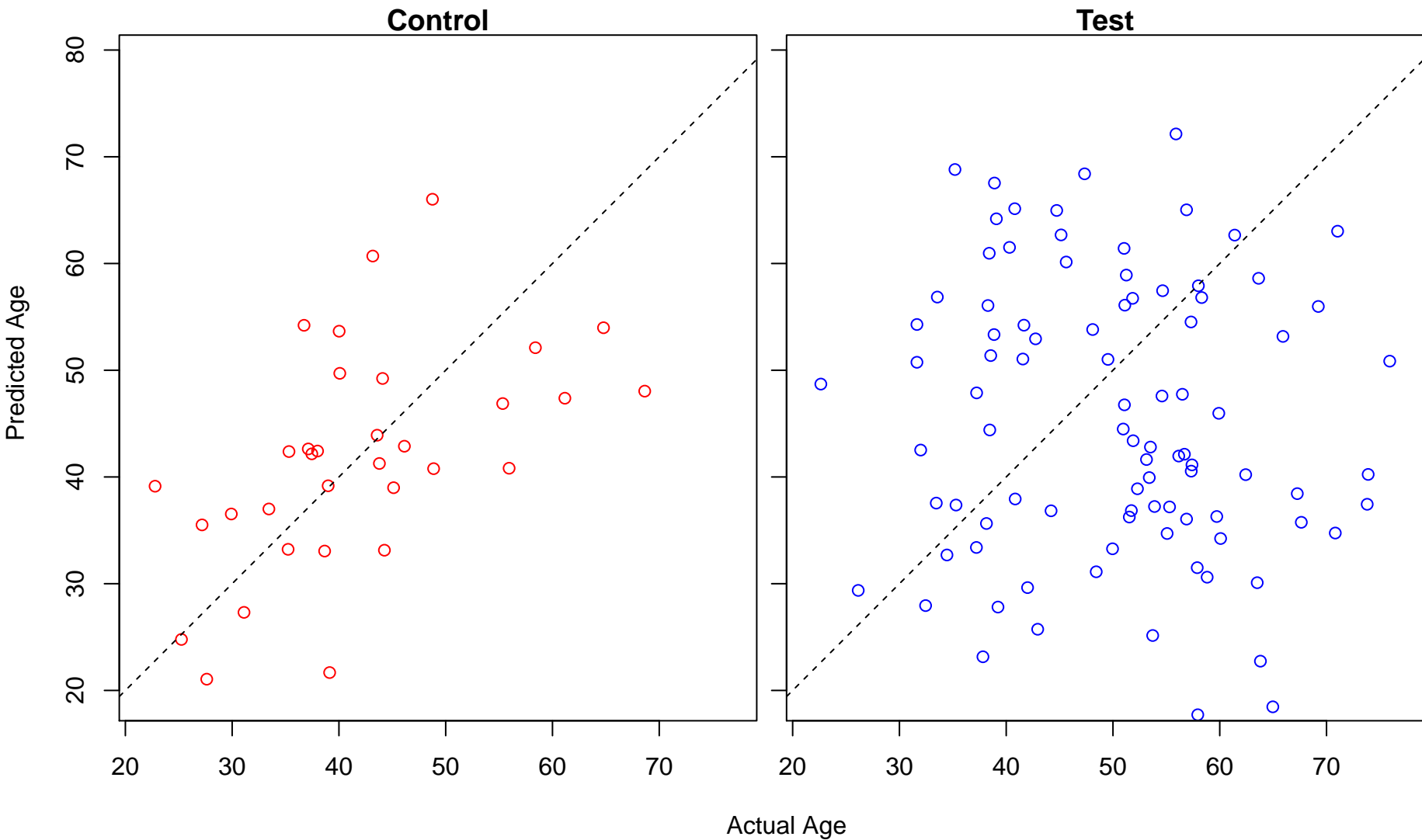
smoothened signaling pathway (Score: 1.477033)



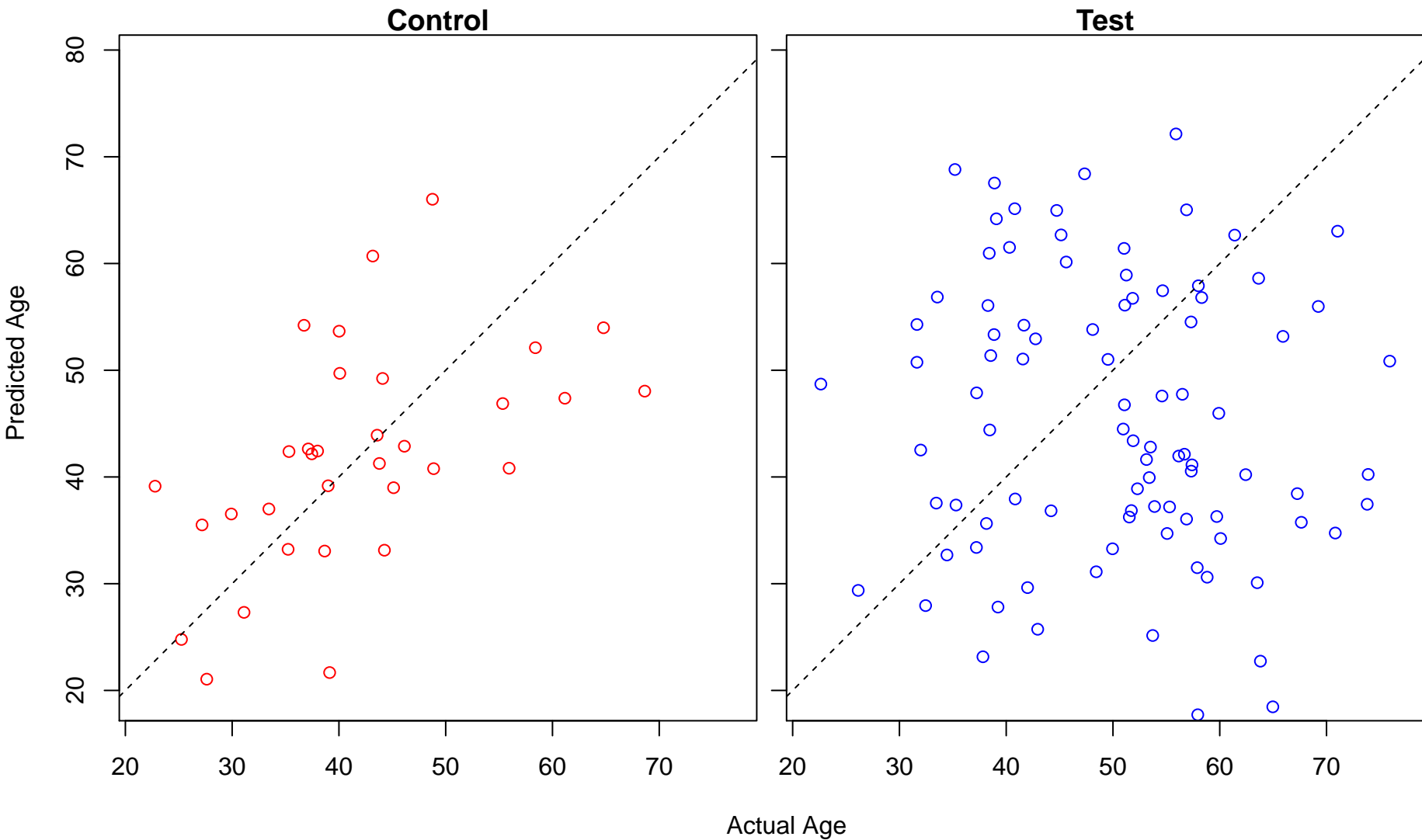
dendritic cell differentiation (Score: 1.475047)



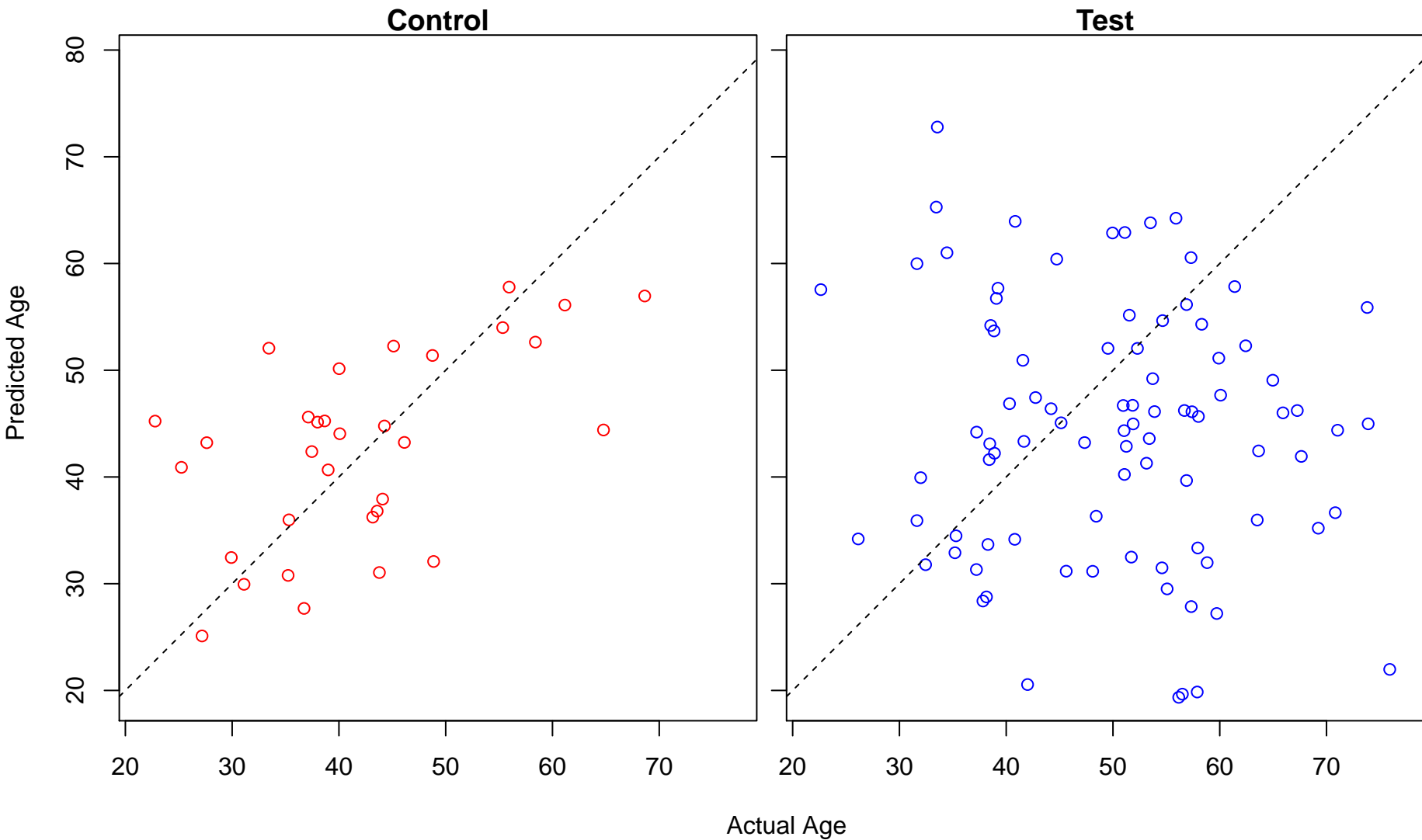
regulation of response to extracellular stimulus (Score: 1.474963)



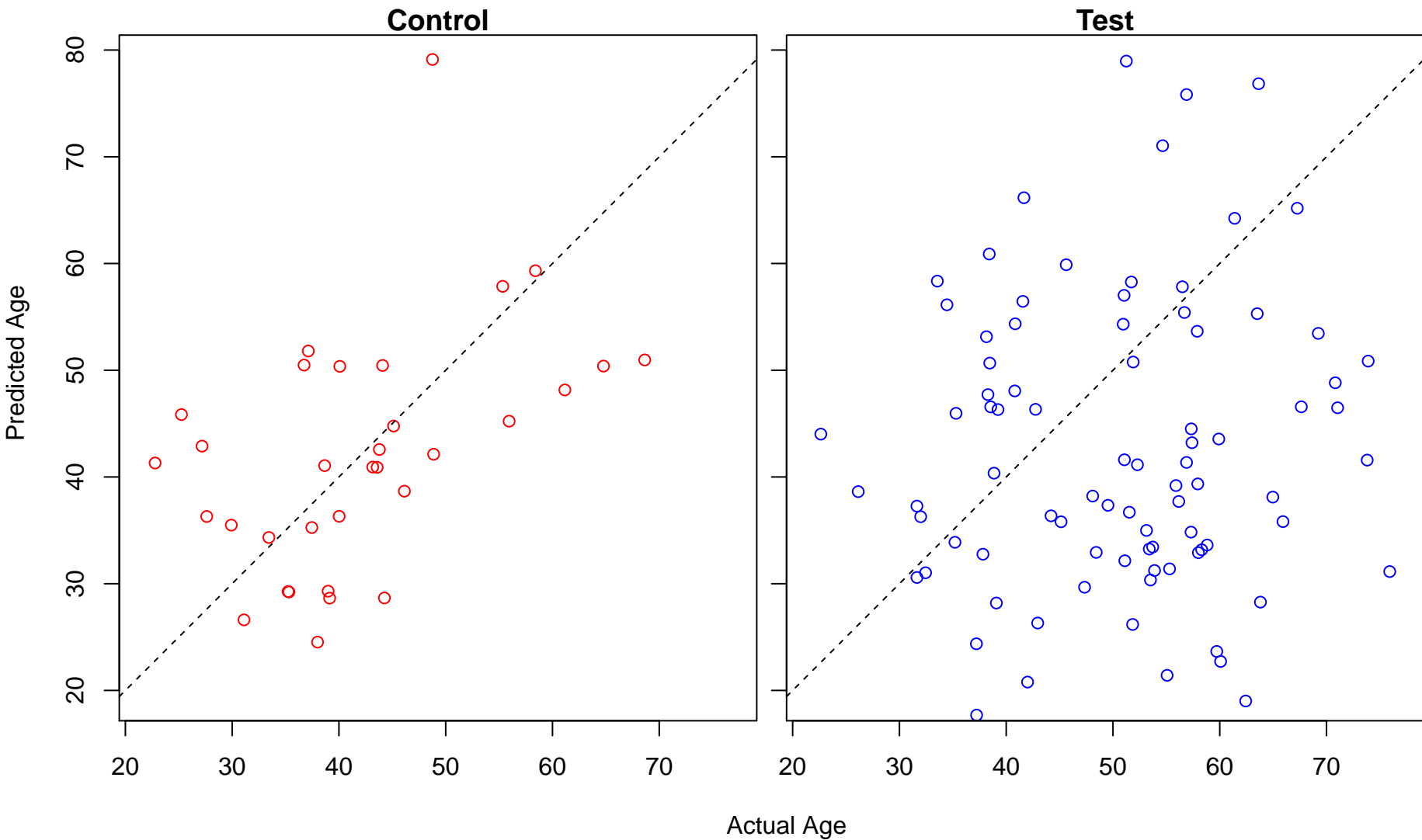
regulation of response to nutrient levels (Score: 1.474963)



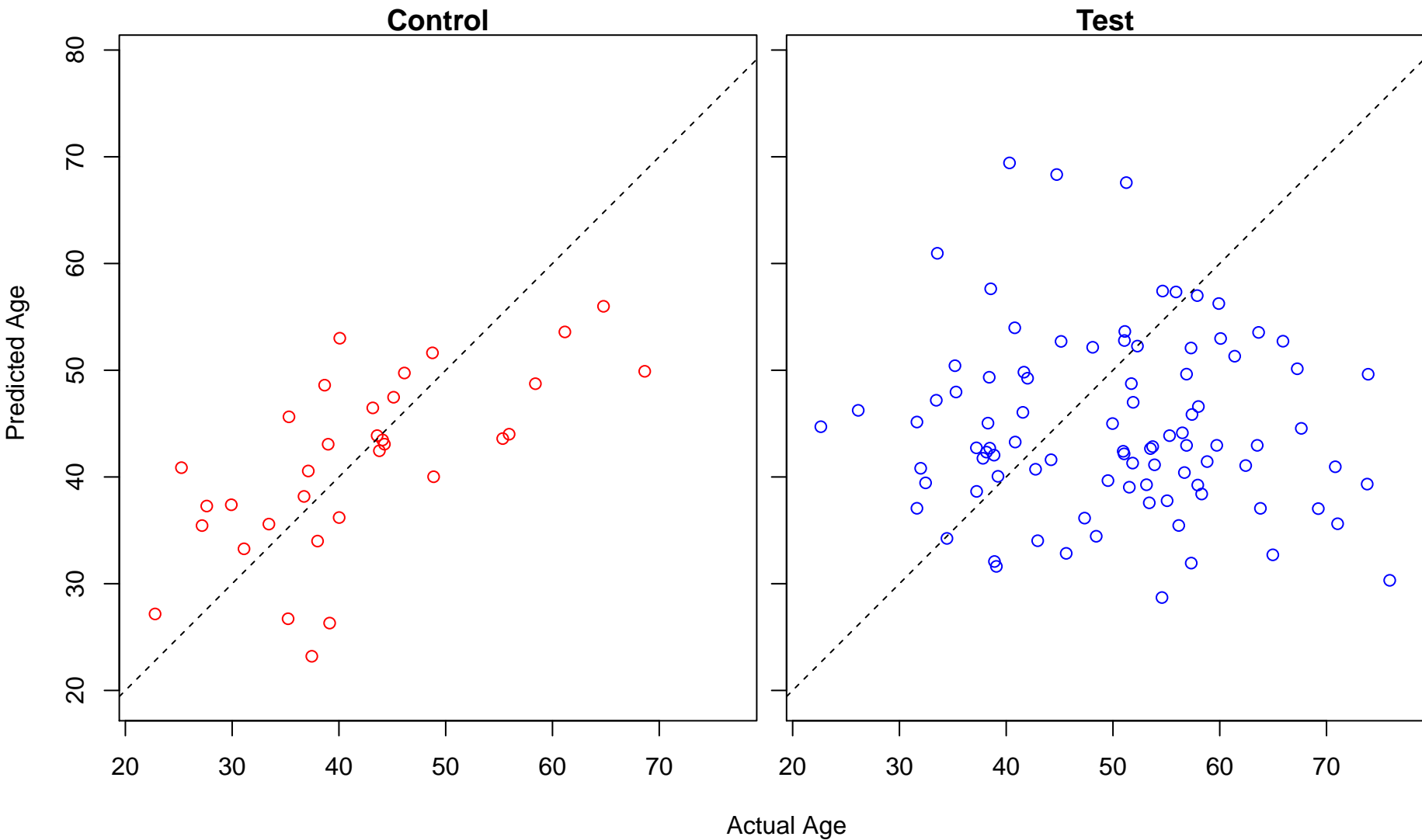
regulation of systemic arterial blood pressure by renin–angiotensin (Score: 1.469770)



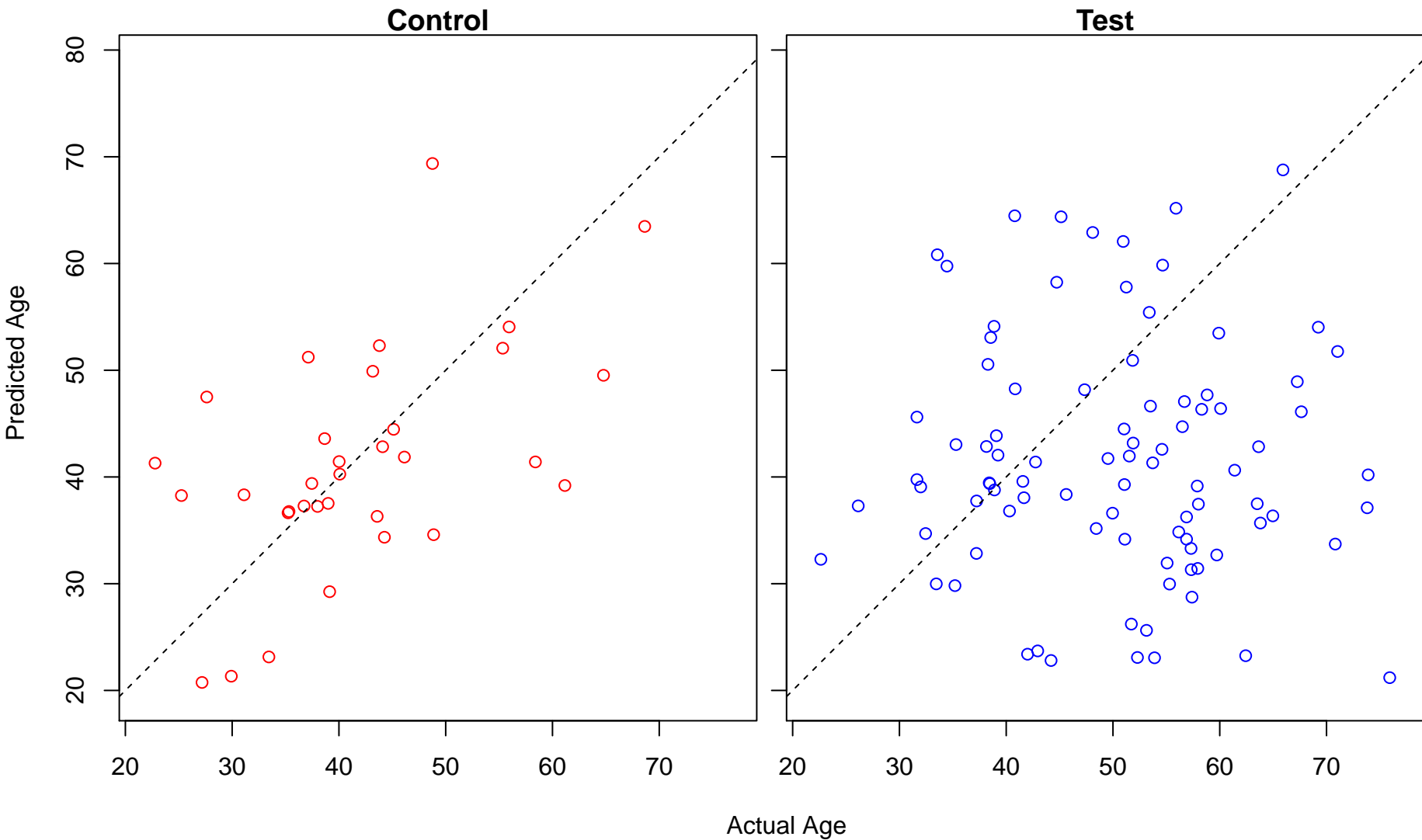
cellular carbohydrate catabolic process (Score: 1.469122)



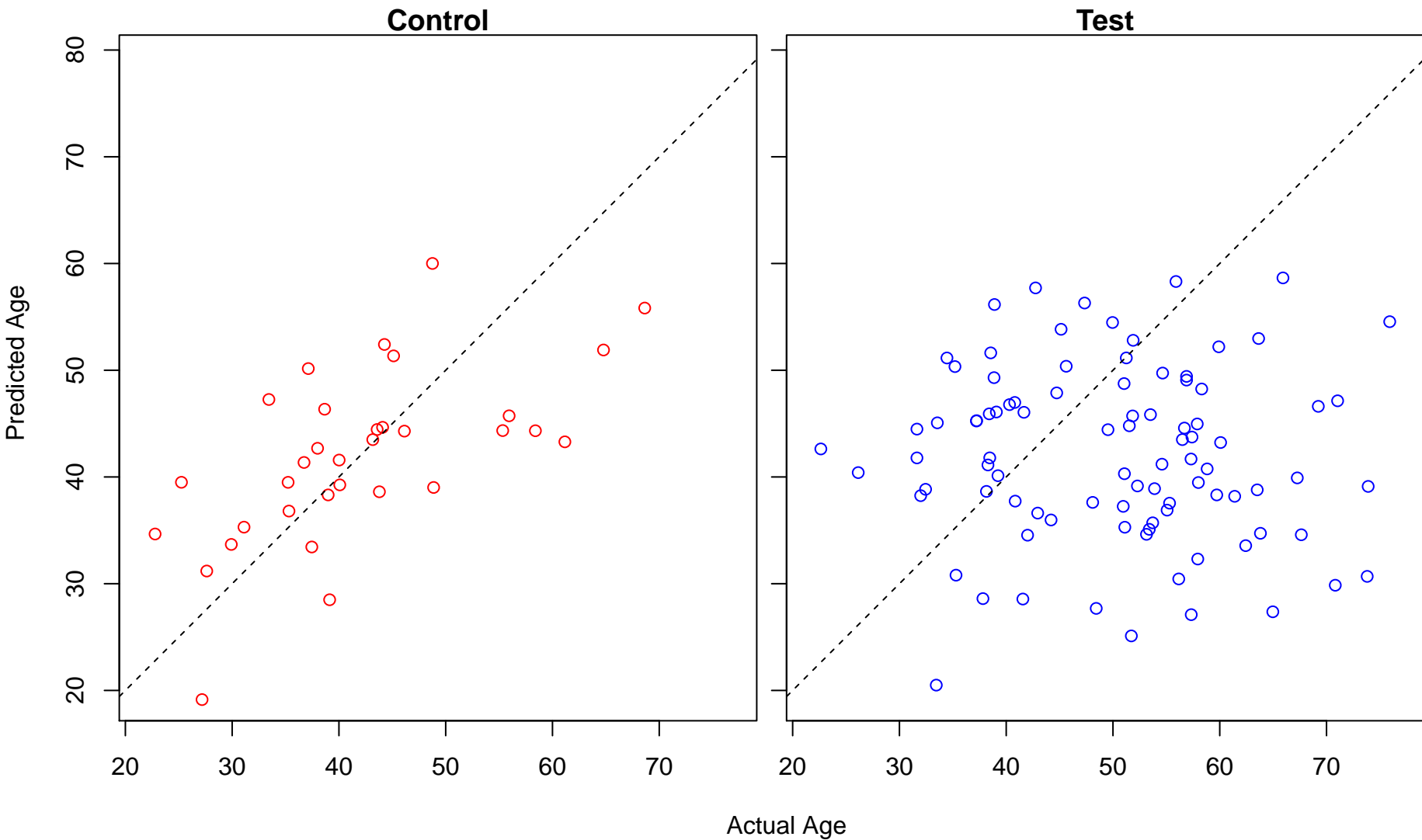
temperature homeostasis (Score: 1.466882)



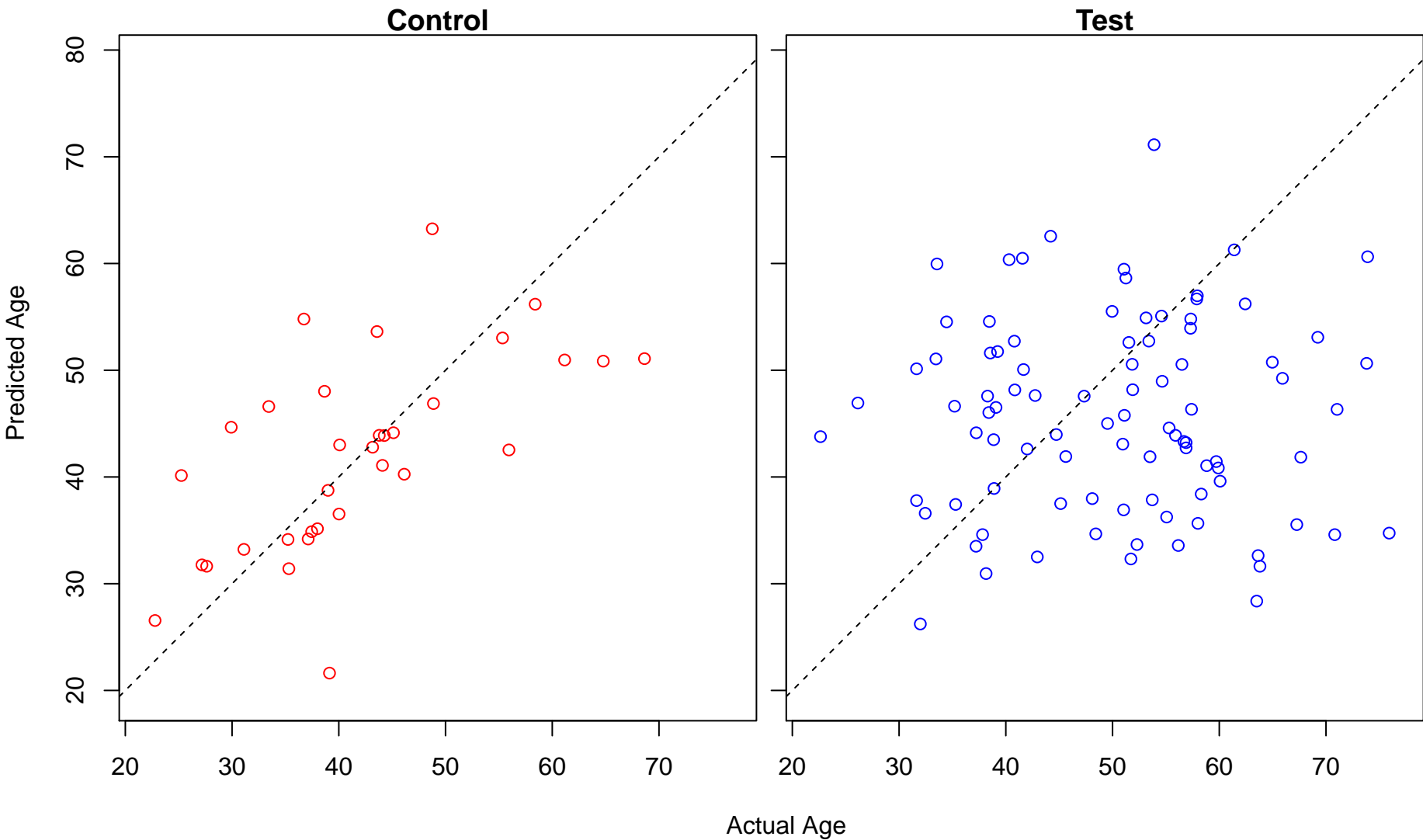
cytokinesis (Score: 1.465197)



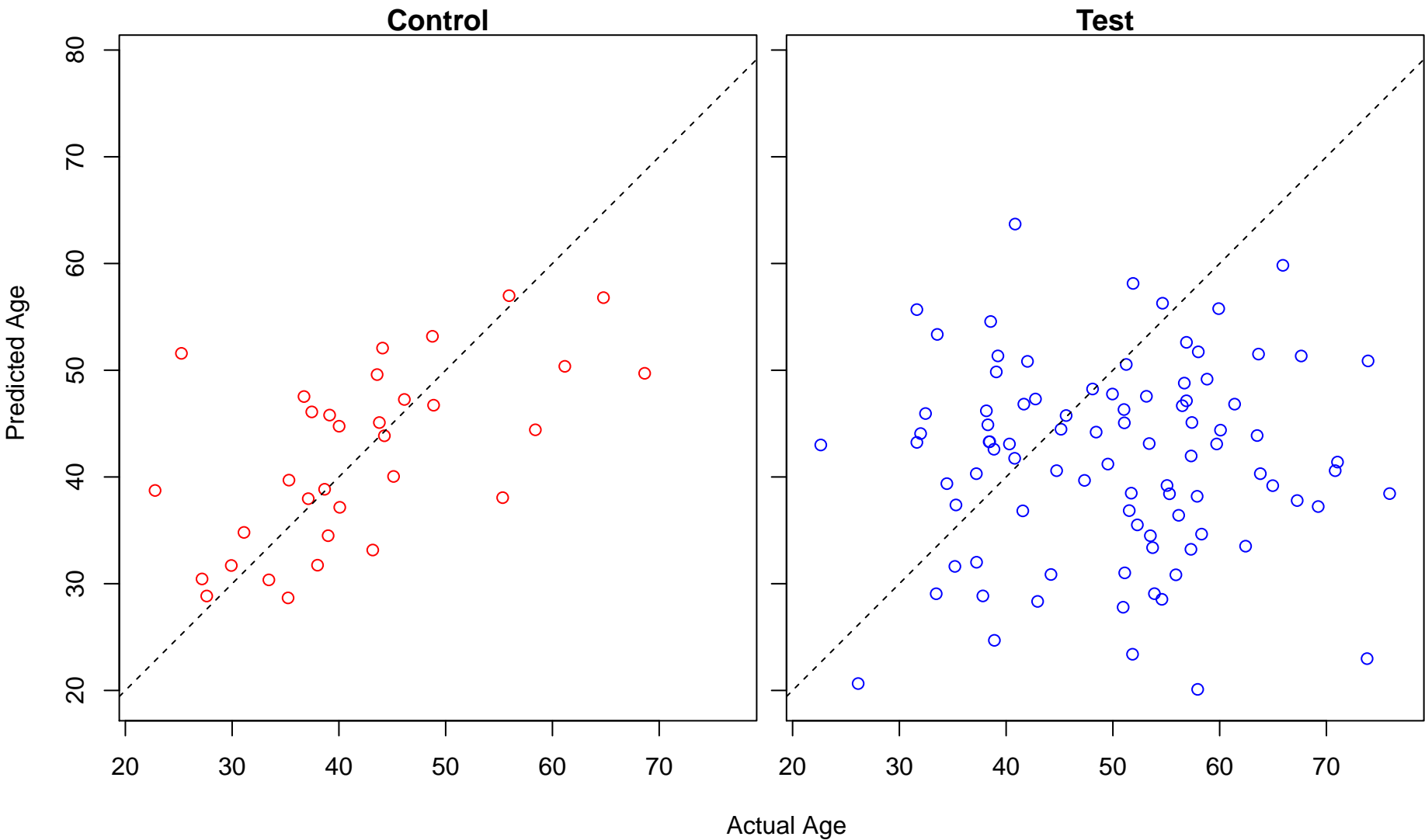
positive regulation of ATPase activity (Score: 1.460583)



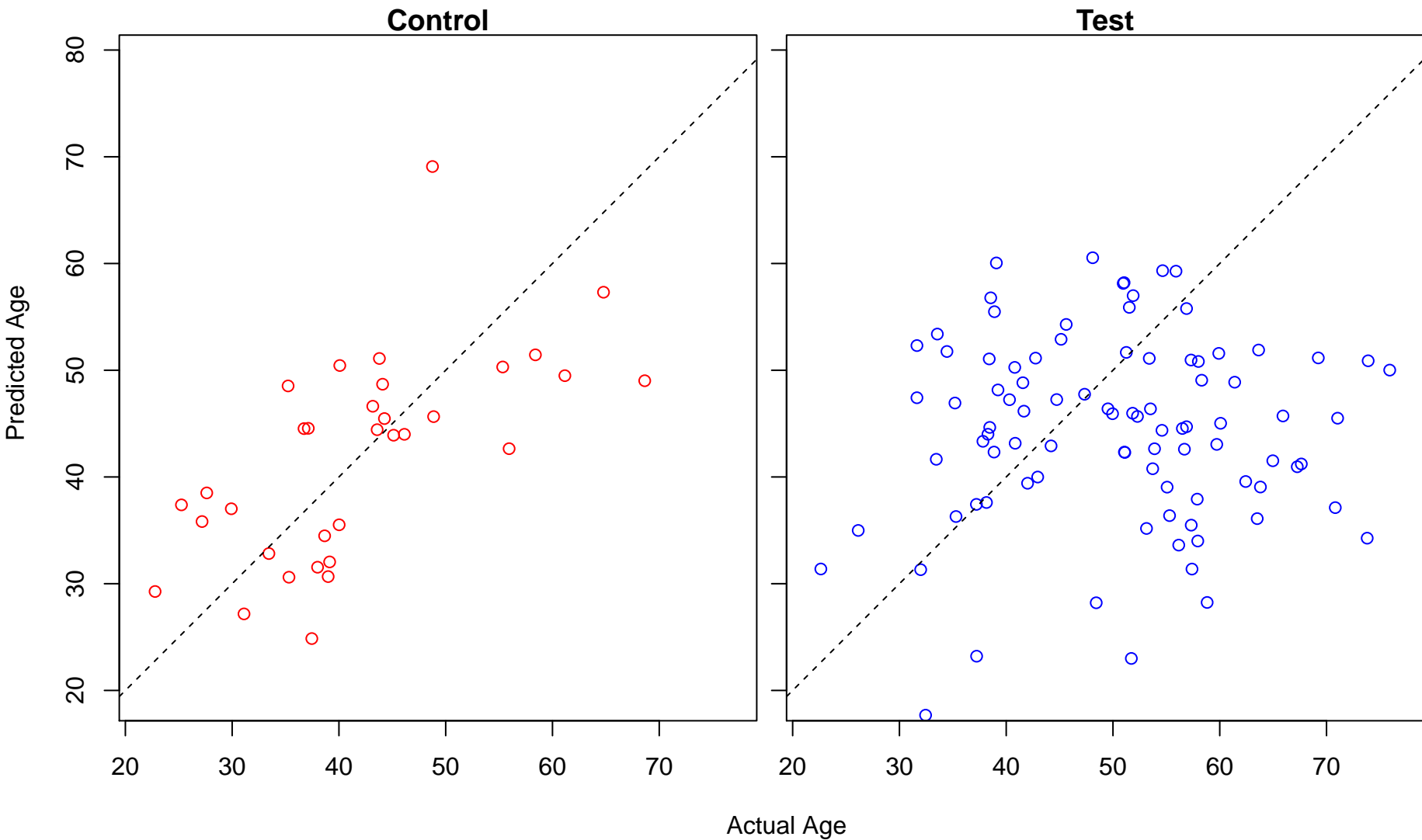
response based on somatic recombination of immune receptors built from immunoglobulin superfamily c



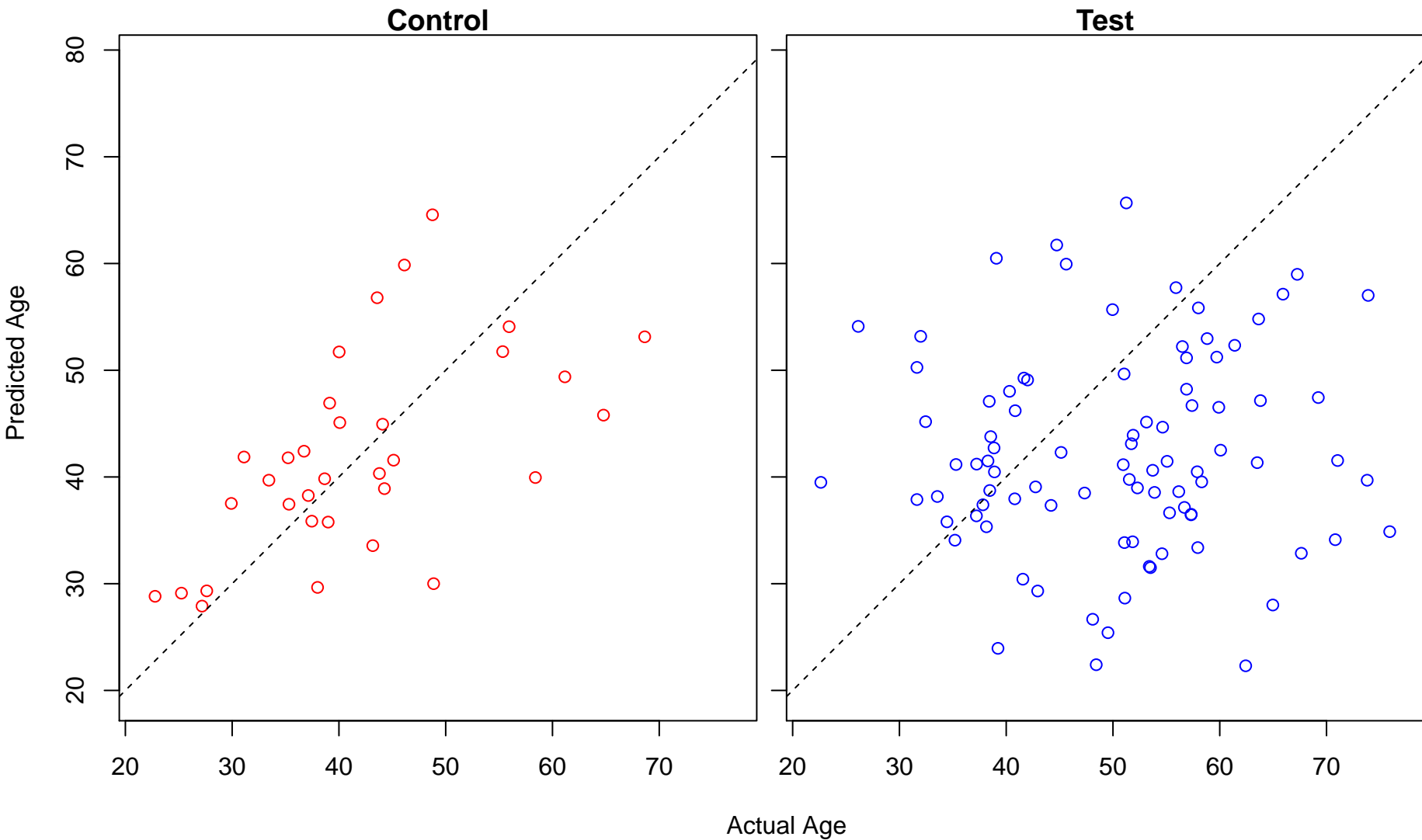
activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c (Score: 1)



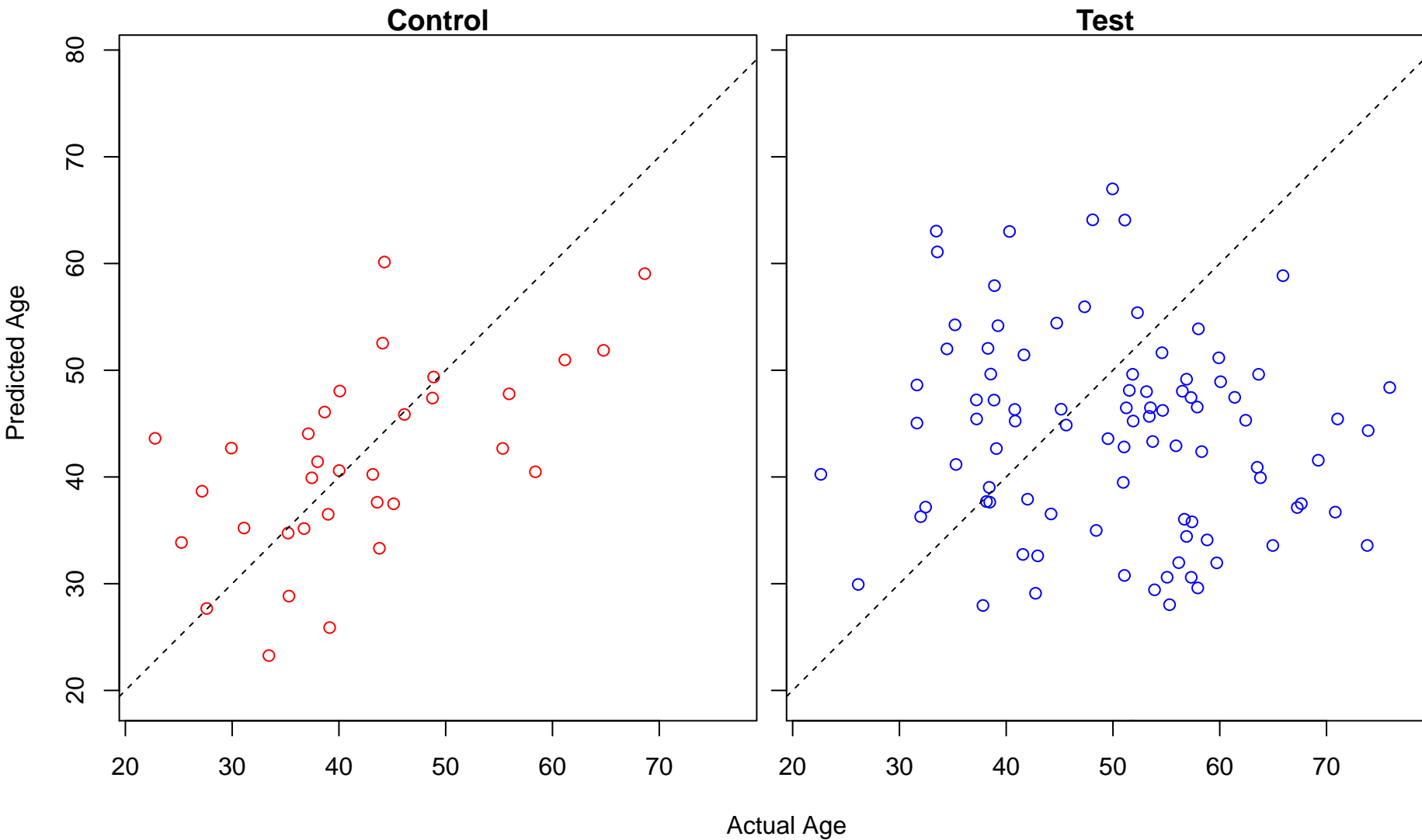
'de novo' posttranslational protein folding (Score: 1.449210)



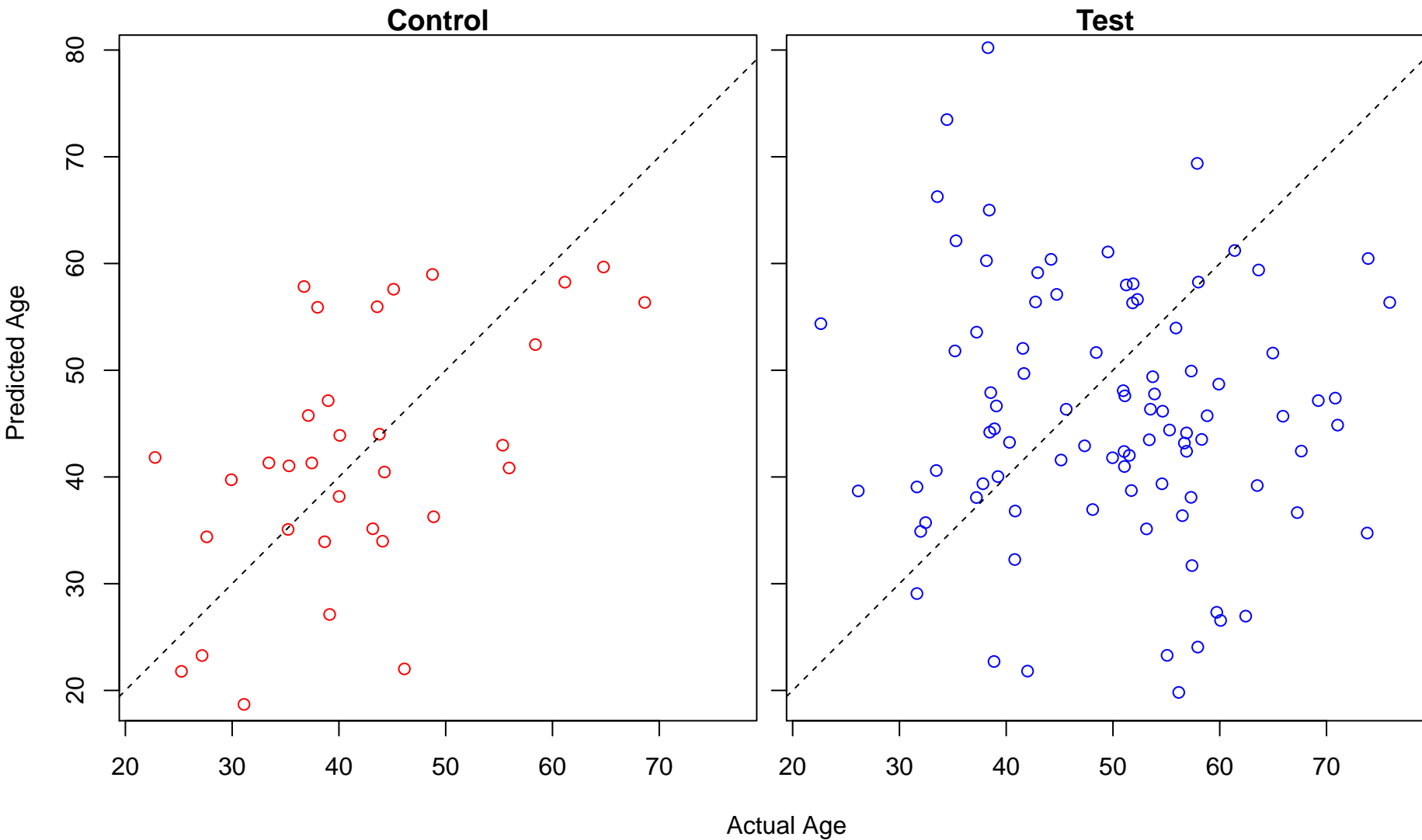
positive regulation of potassium ion transport (Score: 1.447921)



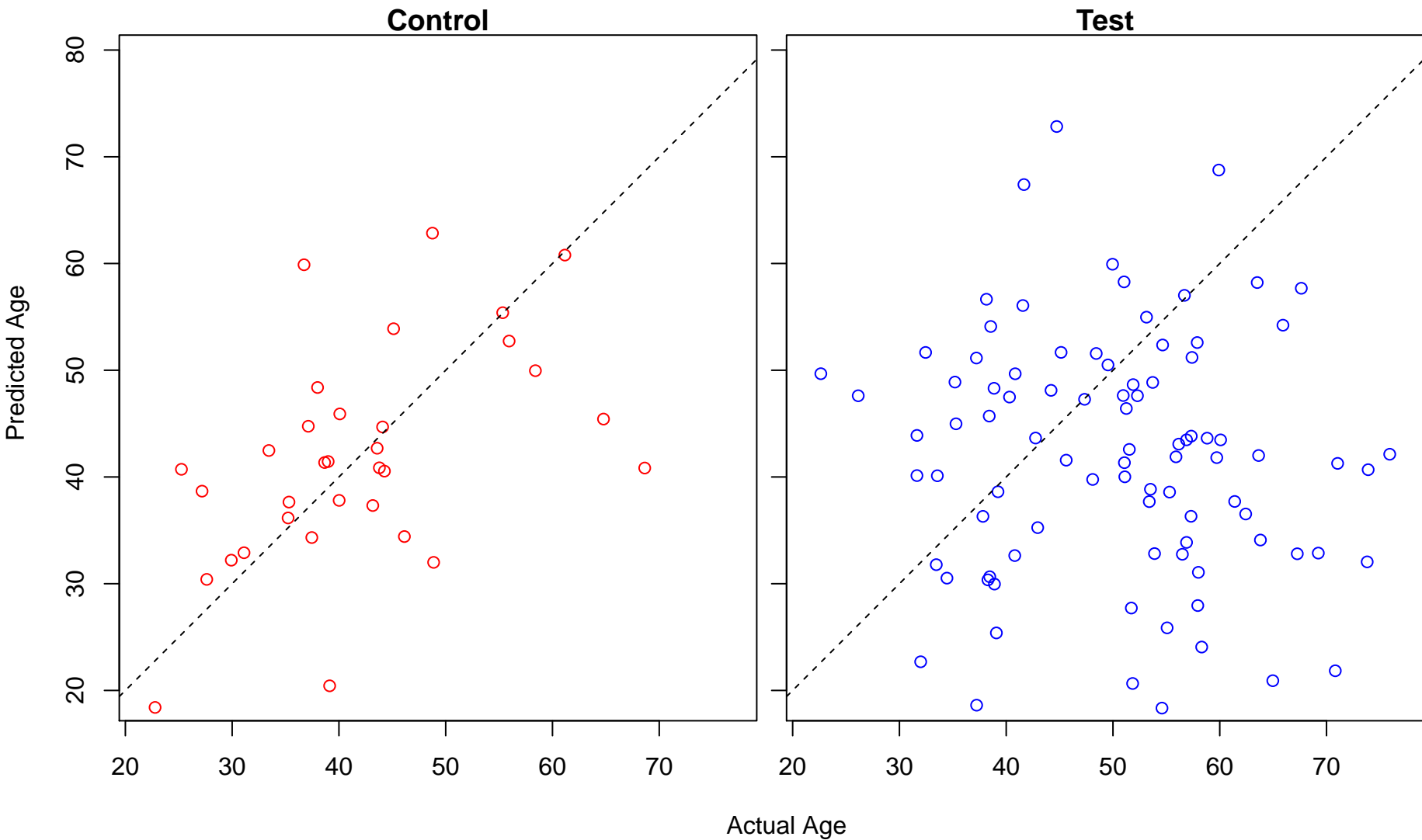
peptidyl-arginine N-methylation (Score: 1.444514)



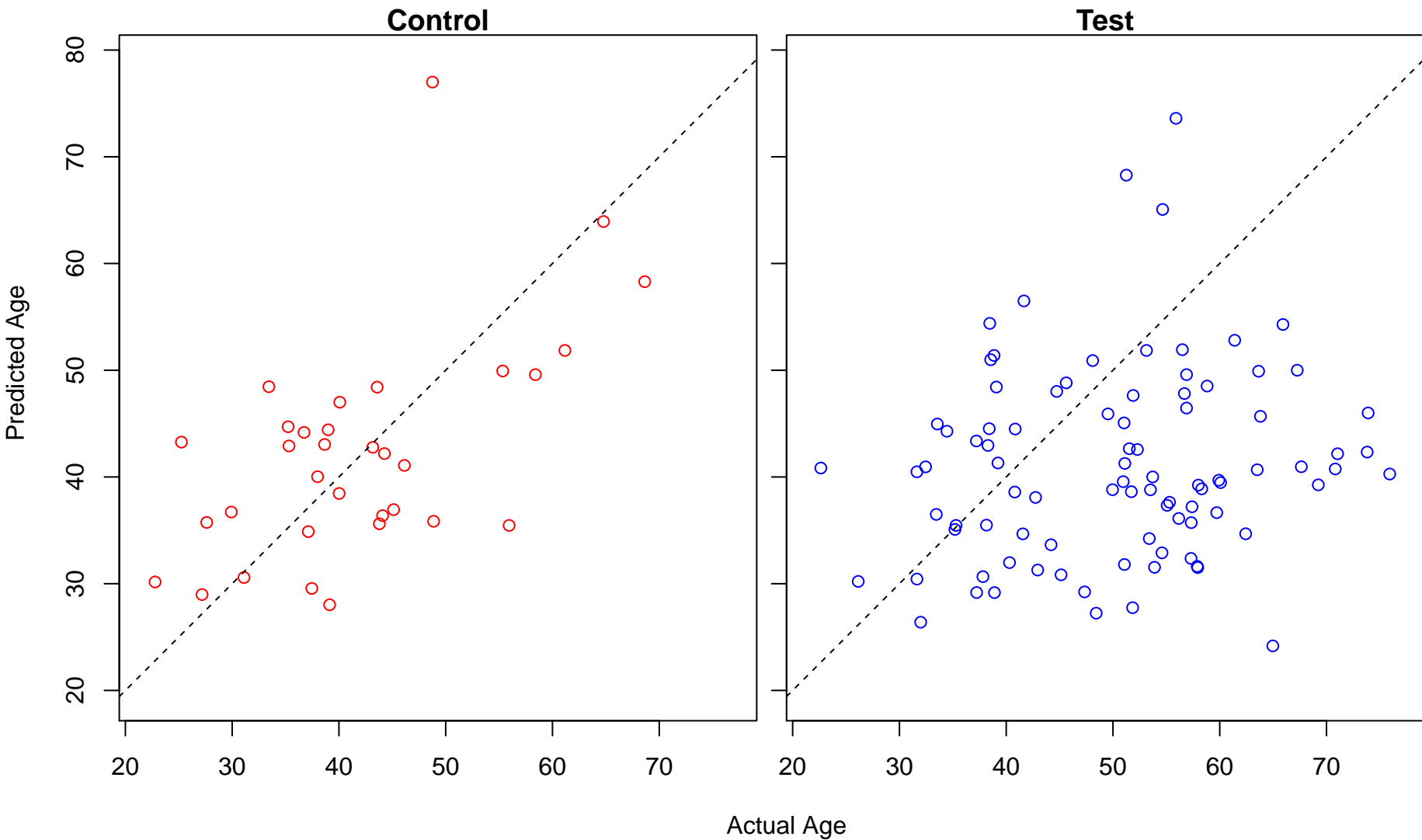
developmental growth involved in morphogenesis (Score: 1.444456)



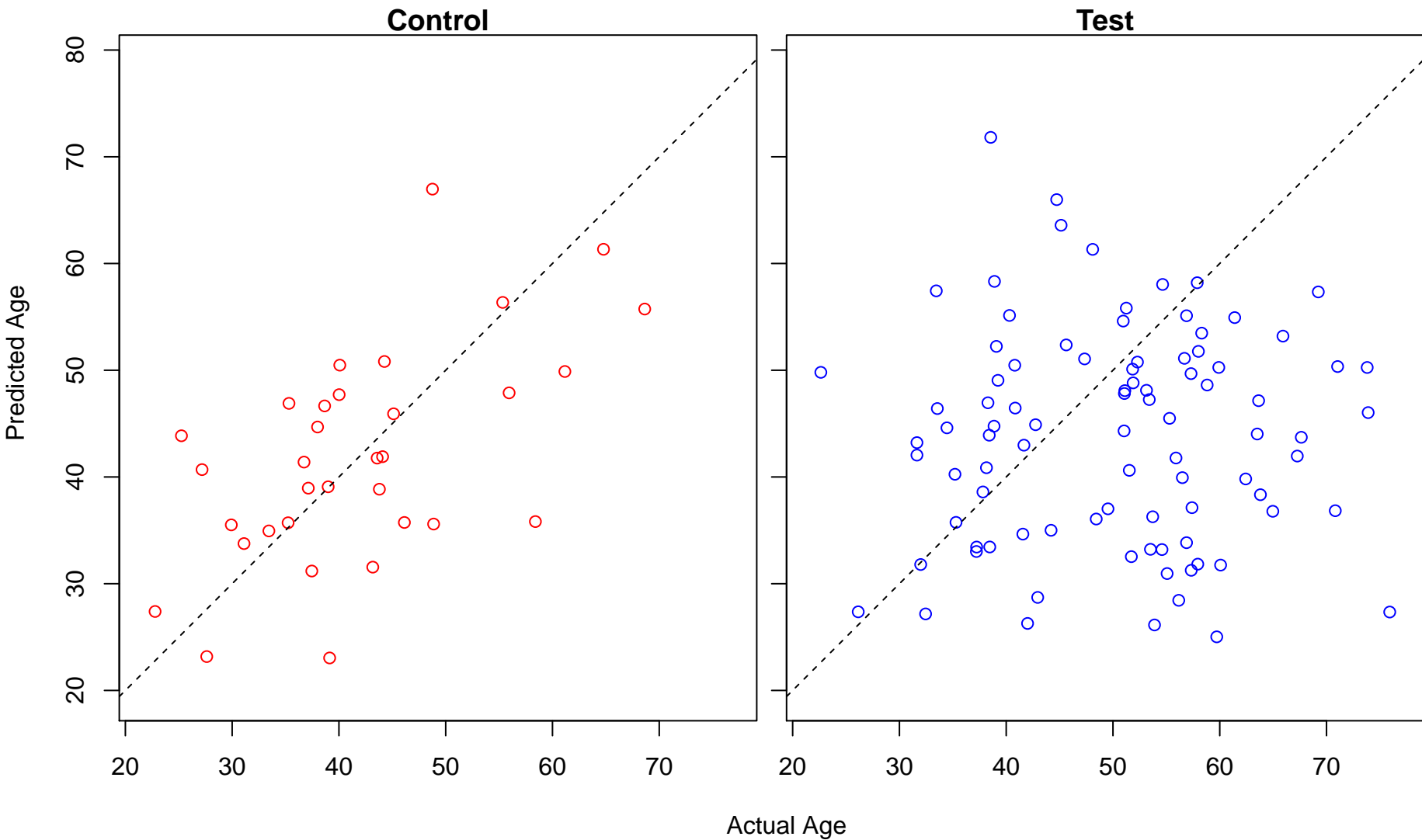
regulation of cellular amine metabolic process (Score: 1.444337)



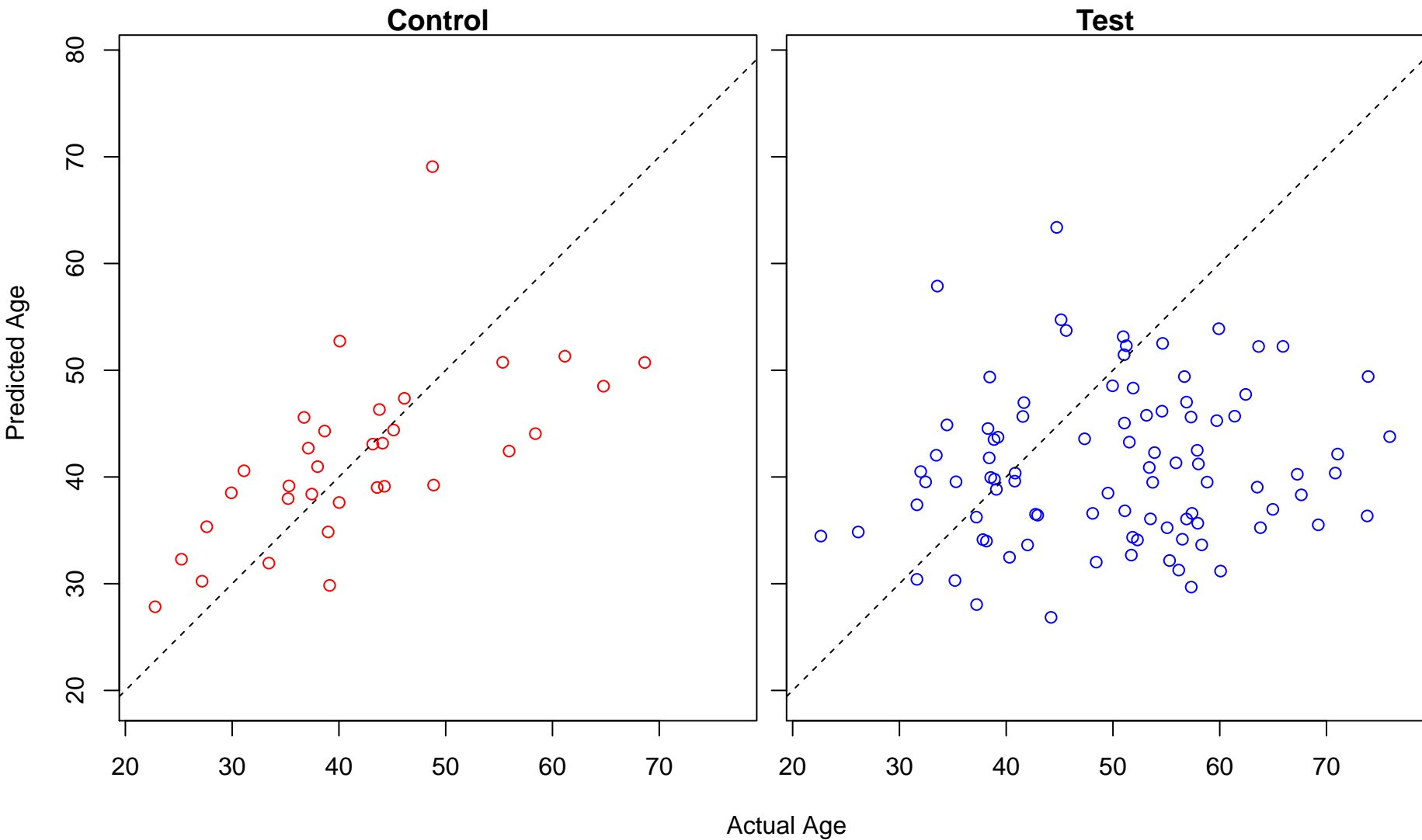
protein localization to Golgi apparatus (Score: 1.443080)



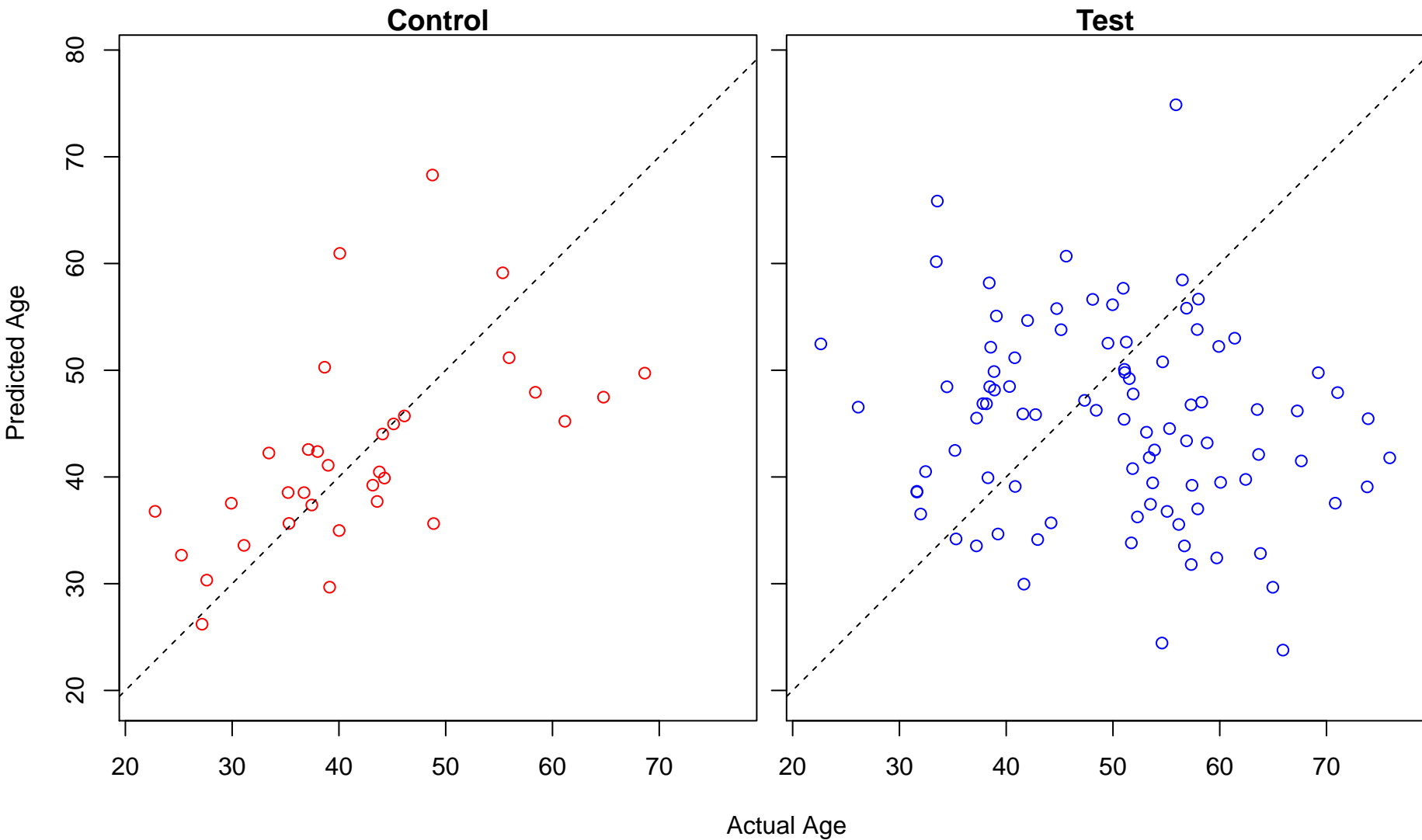
protein transmembrane transport (Score: 1.436769)



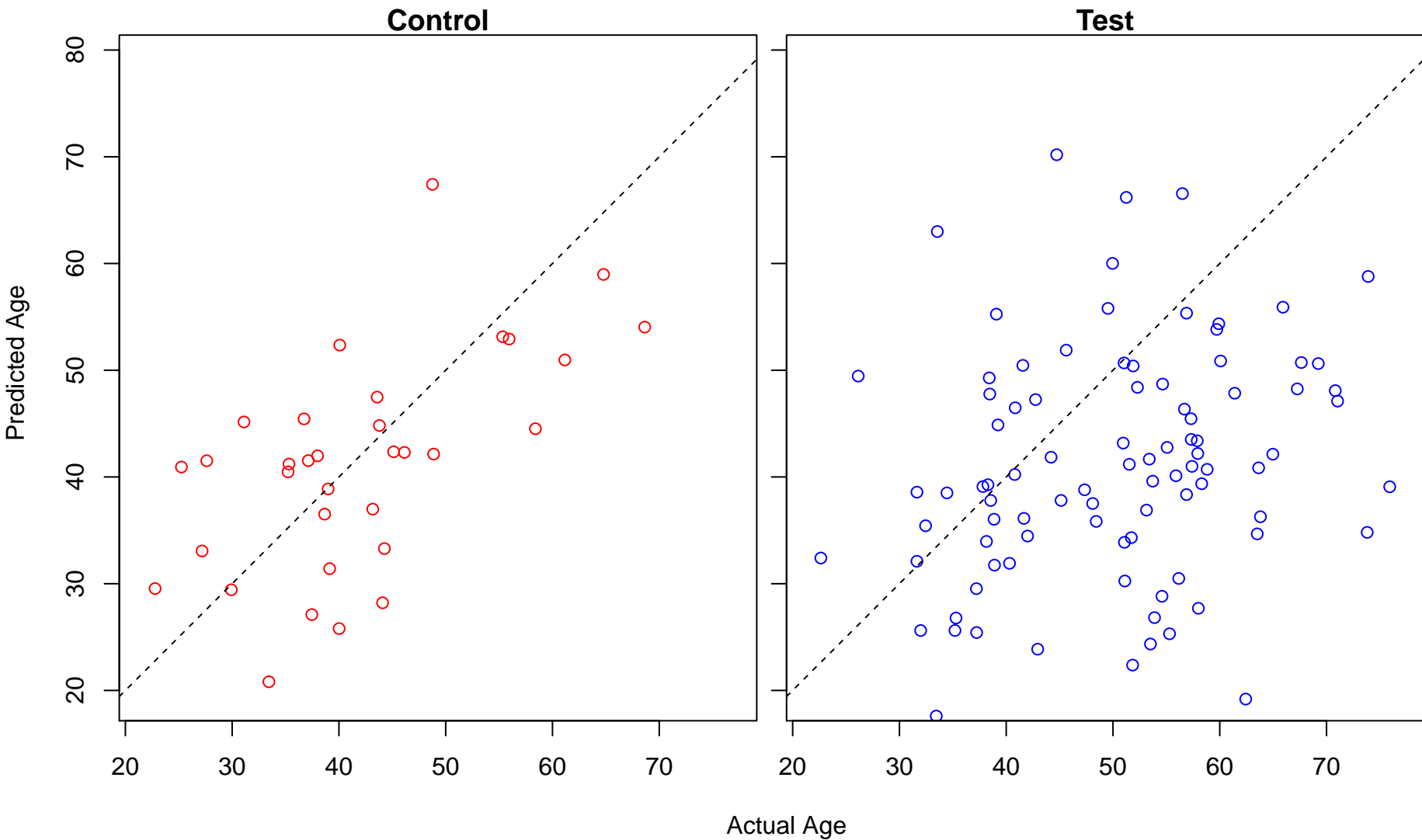
epidermal growth factor receptor signaling pathway (Score: 1.436582)



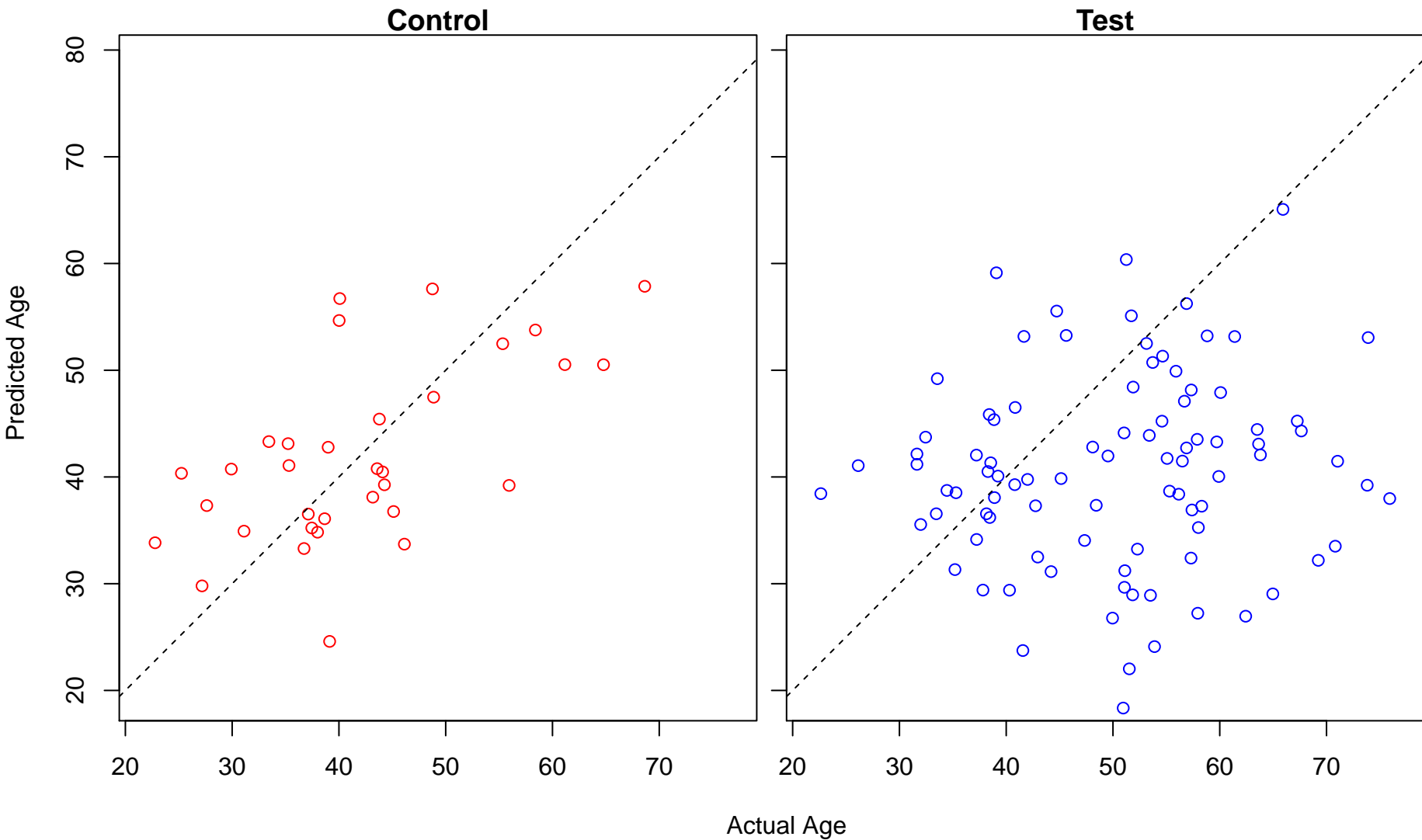
regulation of tumor necrosis factor production (Score: 1.431886)



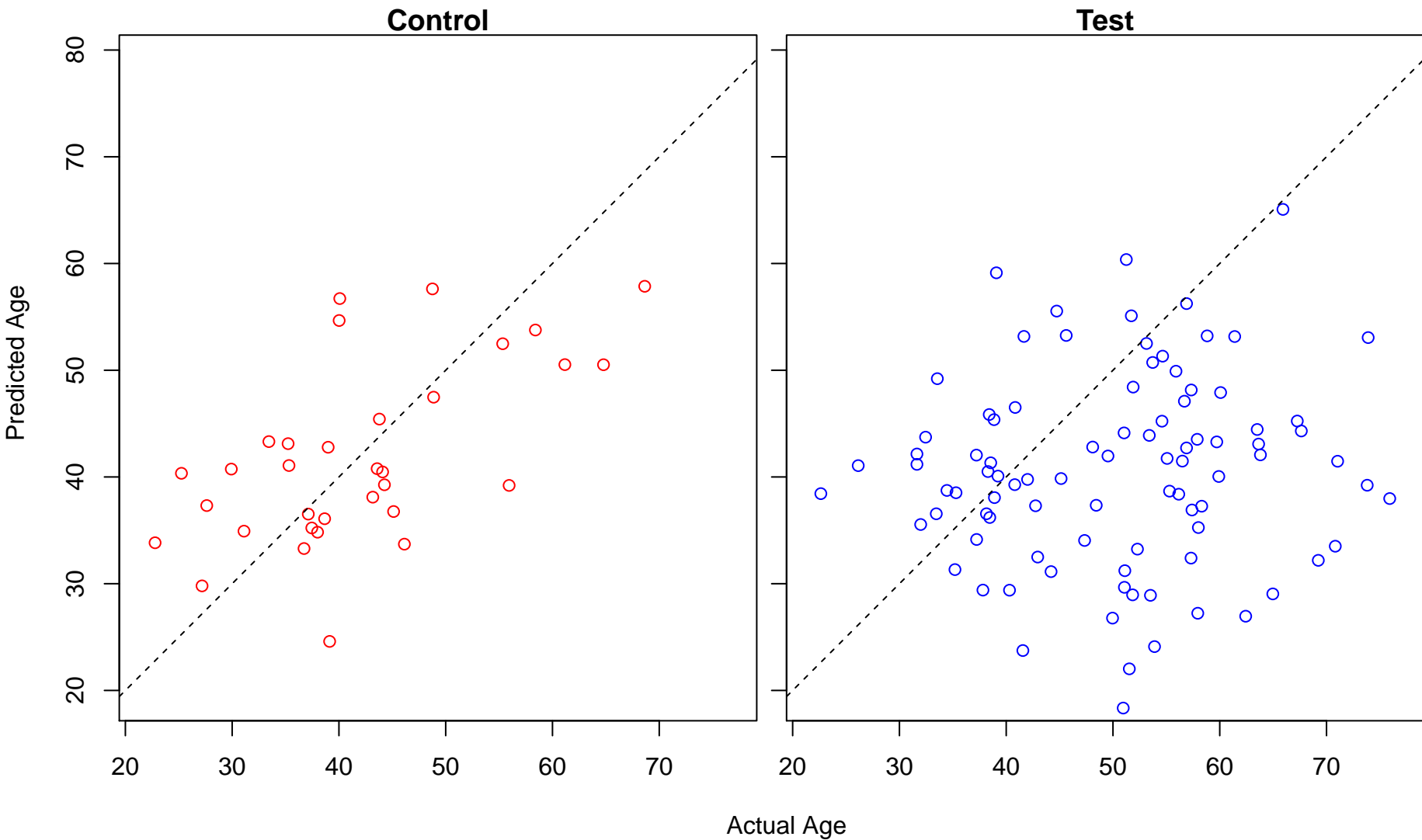
nucleobase metabolic process (Score: 1.431749)



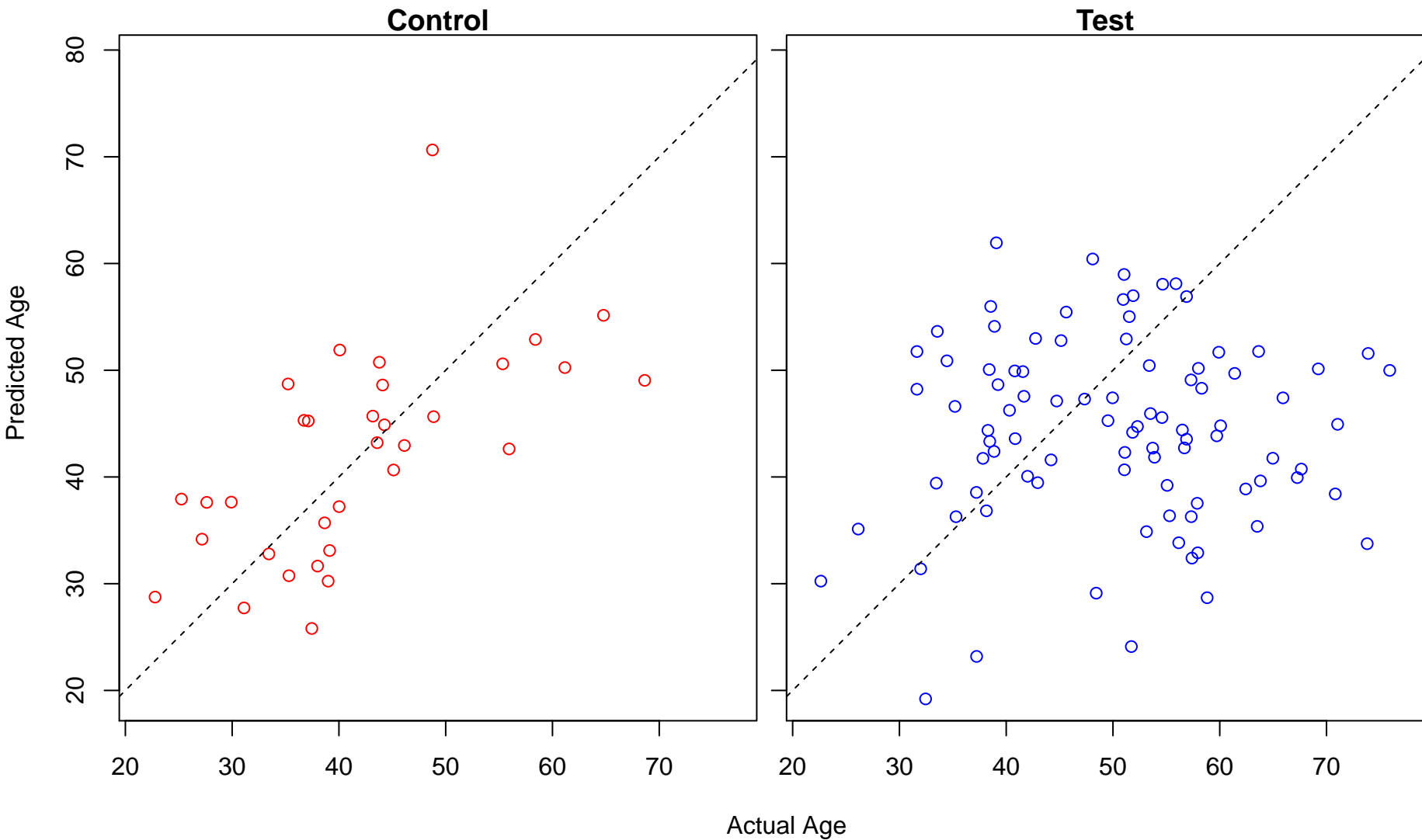
protein targeting to Golgi (Score: 1.431706)



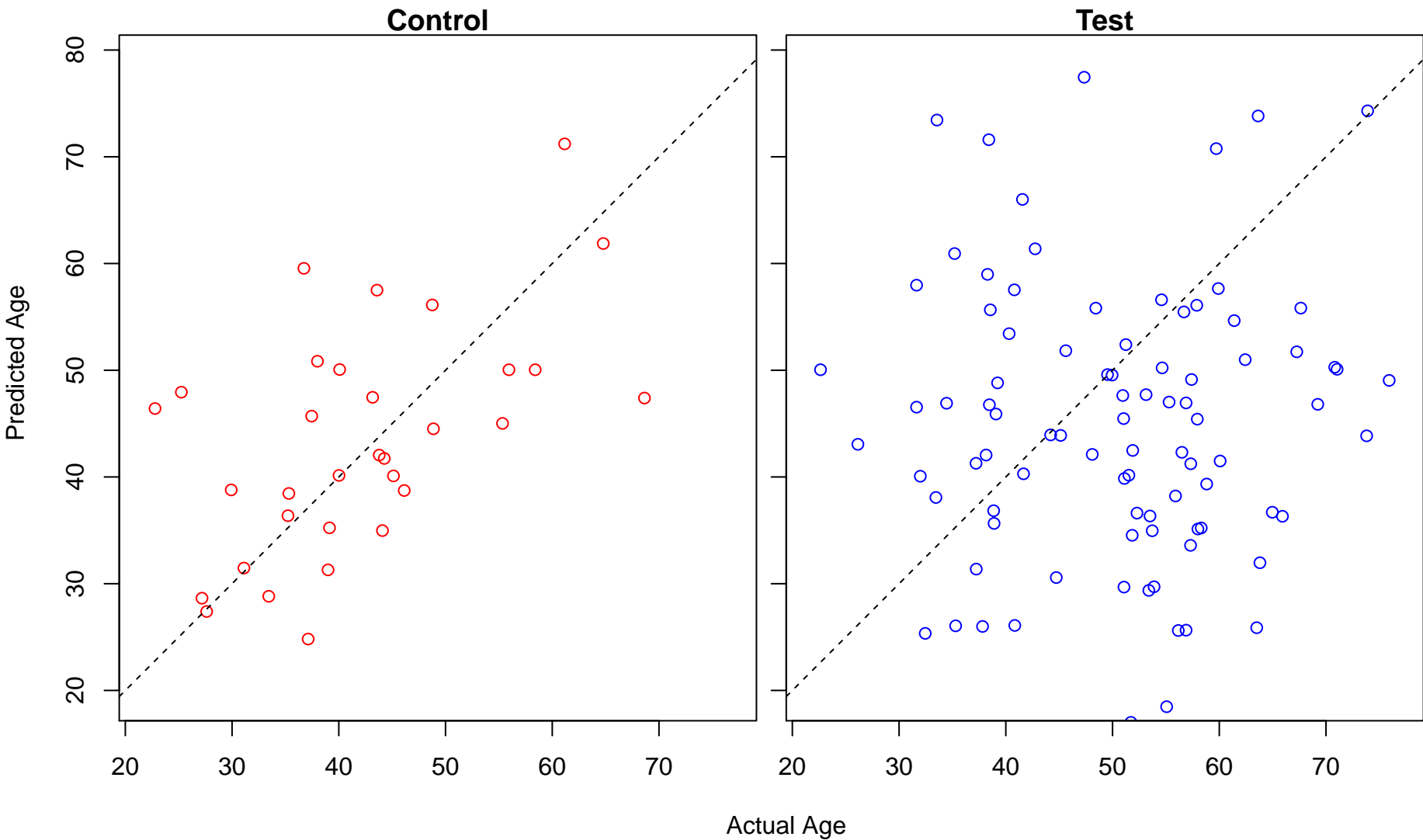
retrograde transport, vesicle recycling within Golgi (Score: 1.431706)



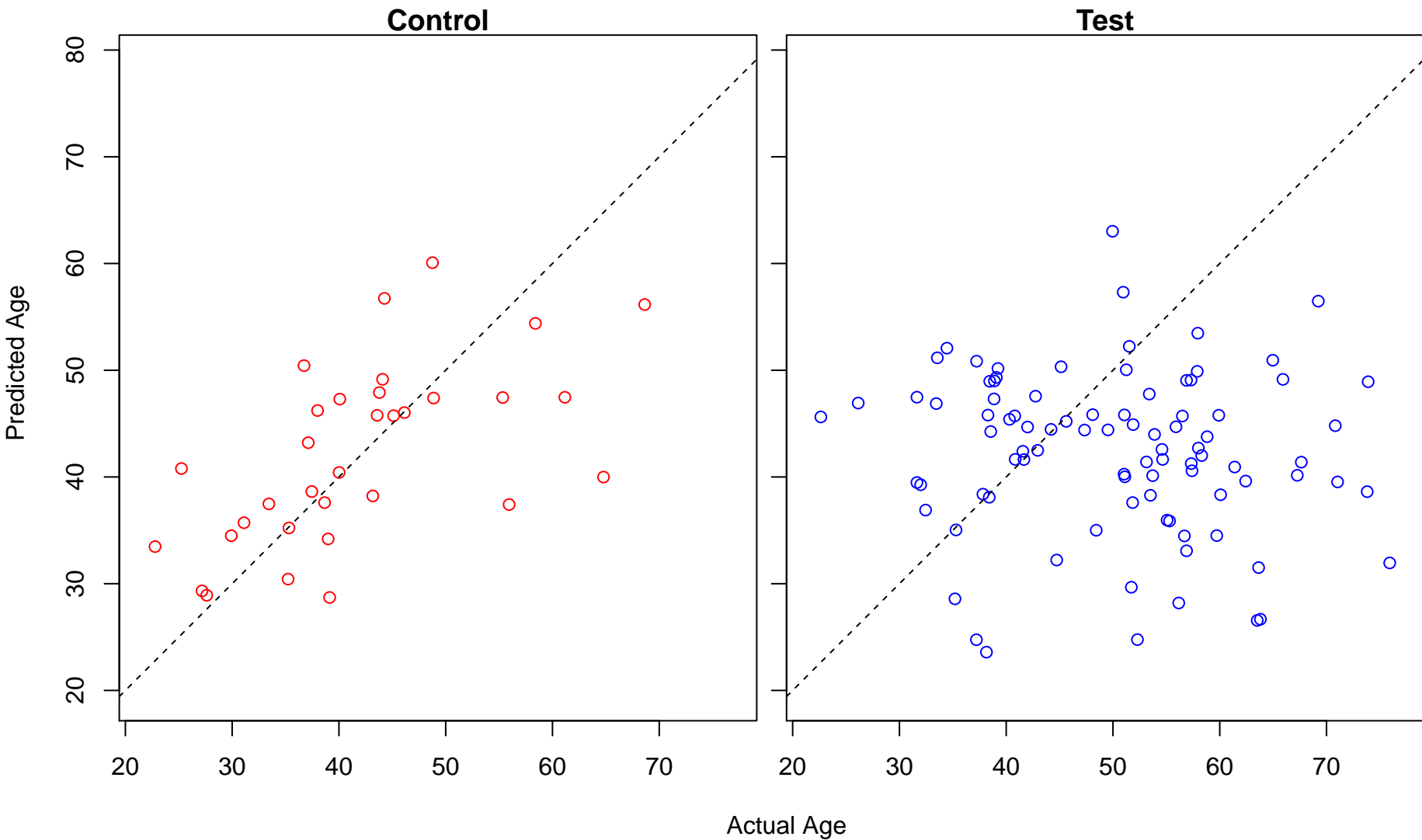
'de novo' protein folding (Score: 1.429691)



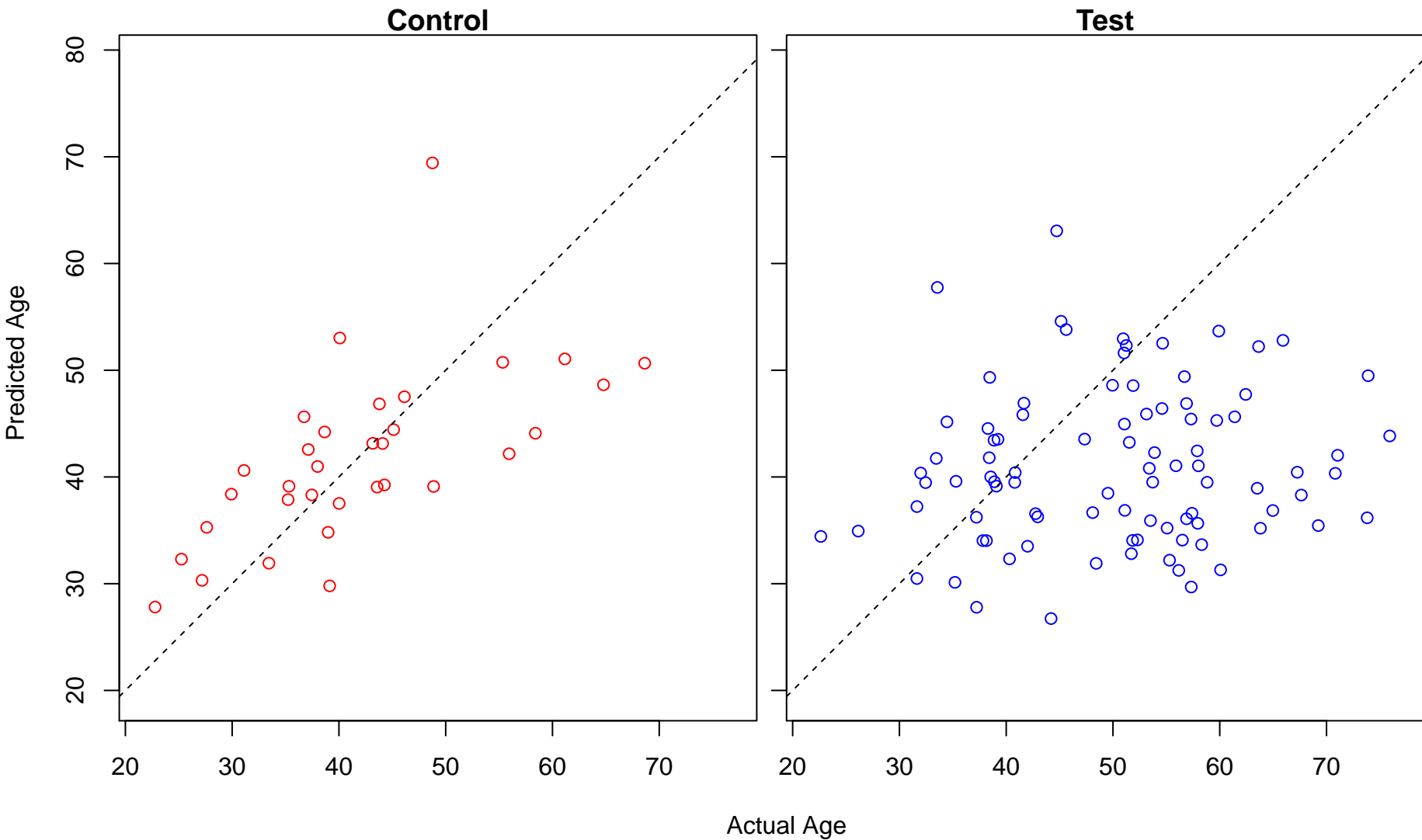
ve immune response based on somatic recombination of immune receptors built from immunoglobulin su



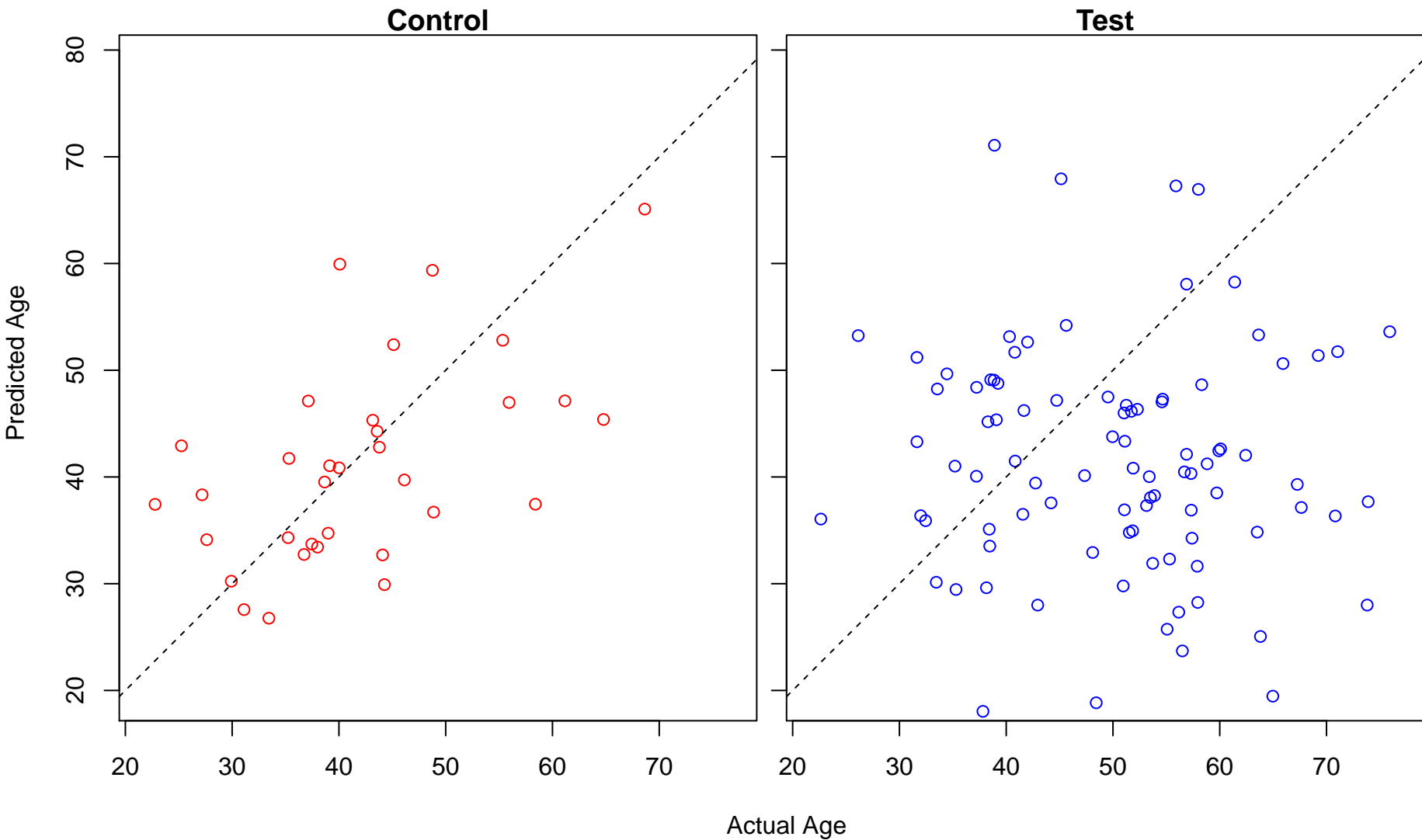
protein activation cascade (Score: 1.427161)



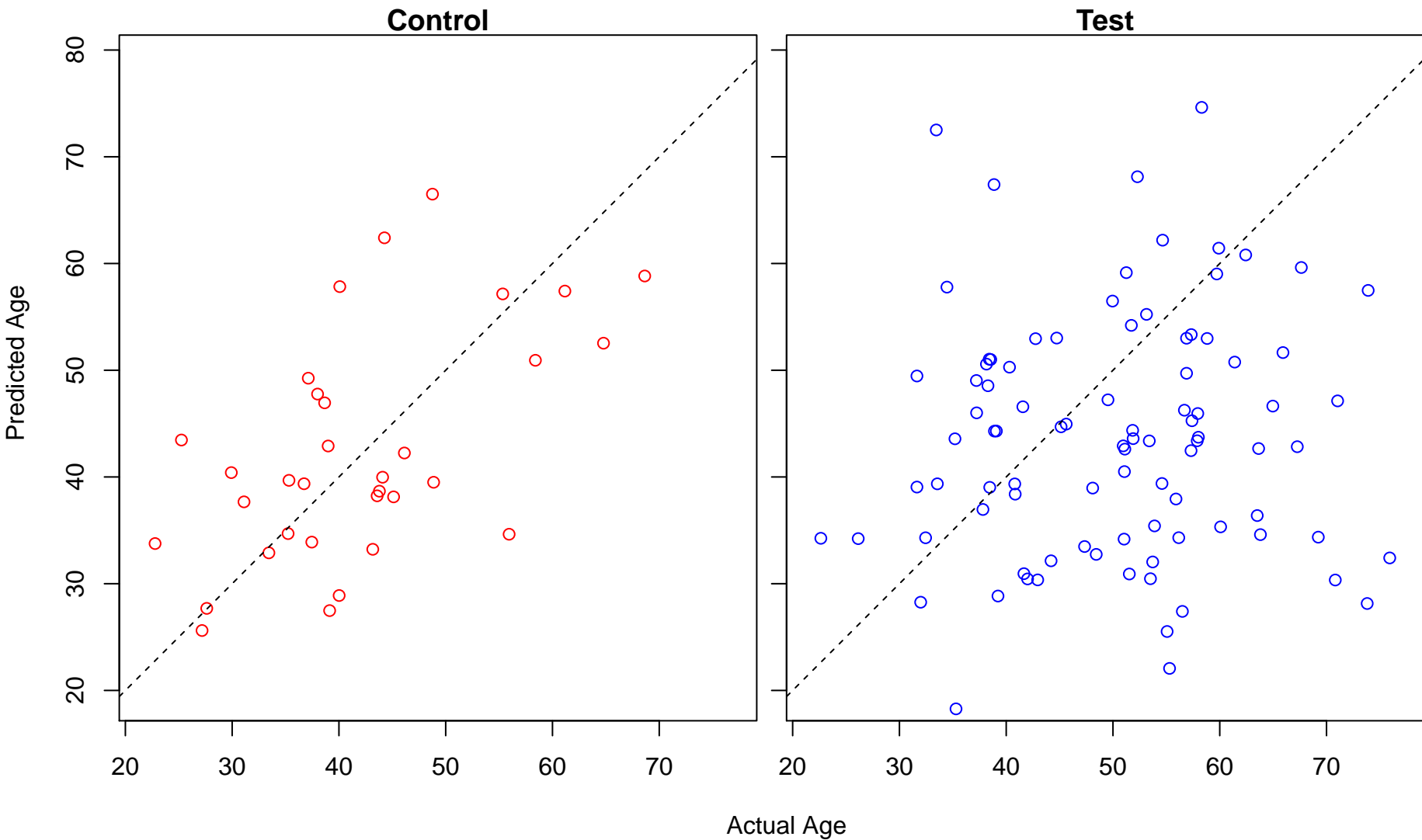
ERBB signaling pathway (Score: 1.426746)



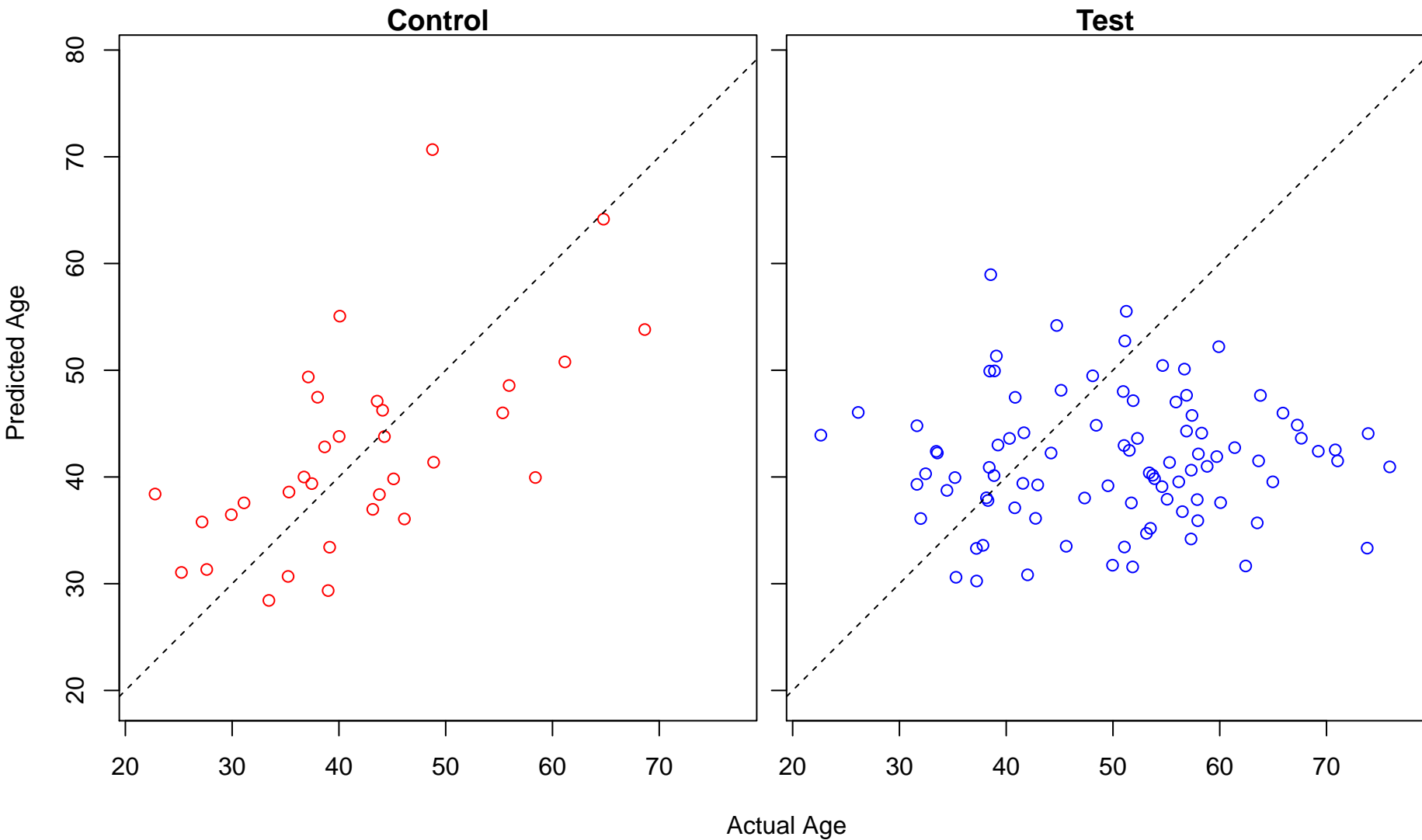
positive regulation of DNA biosynthetic process (Score: 1.424736)



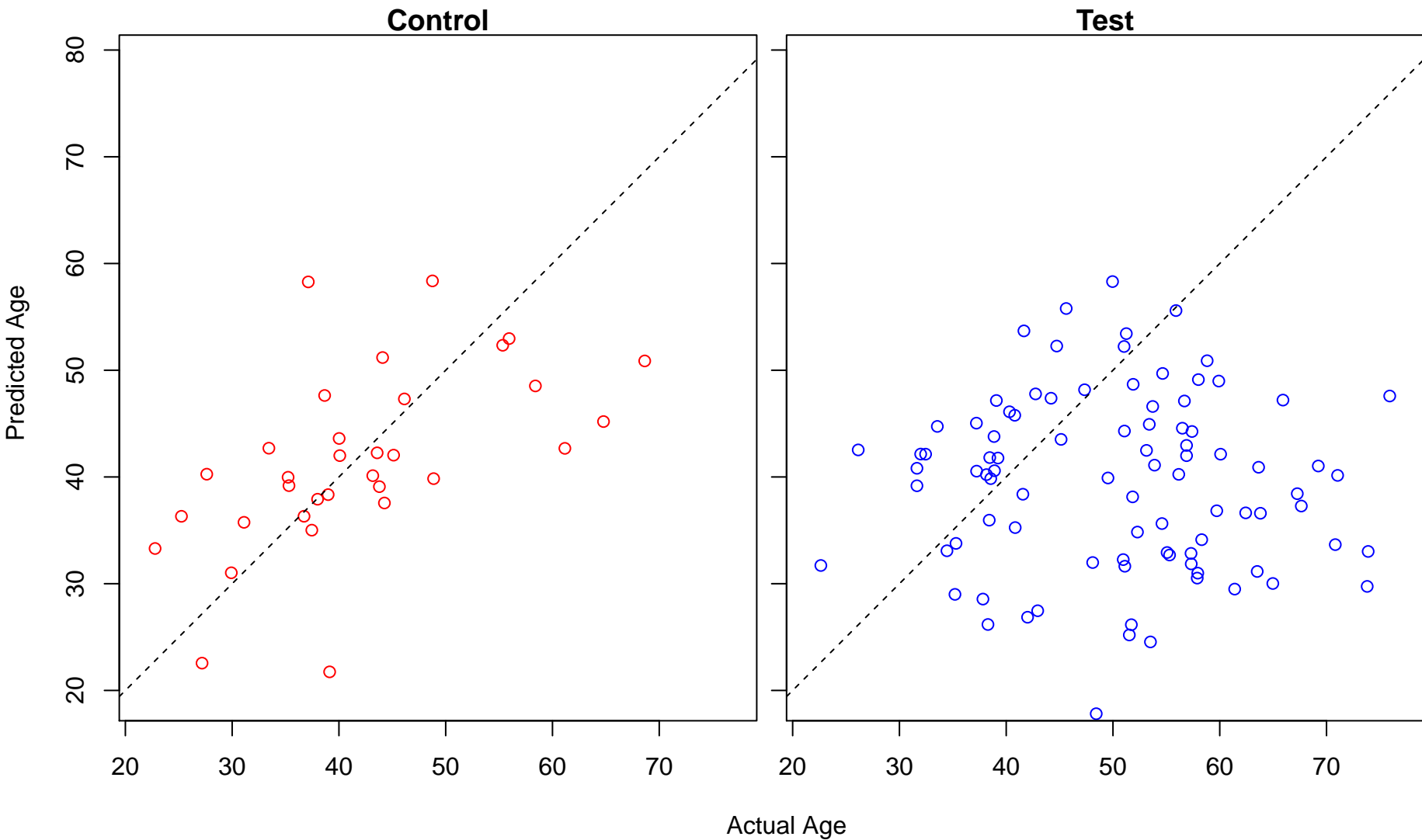
developmental maturation (Score: 1.423757)



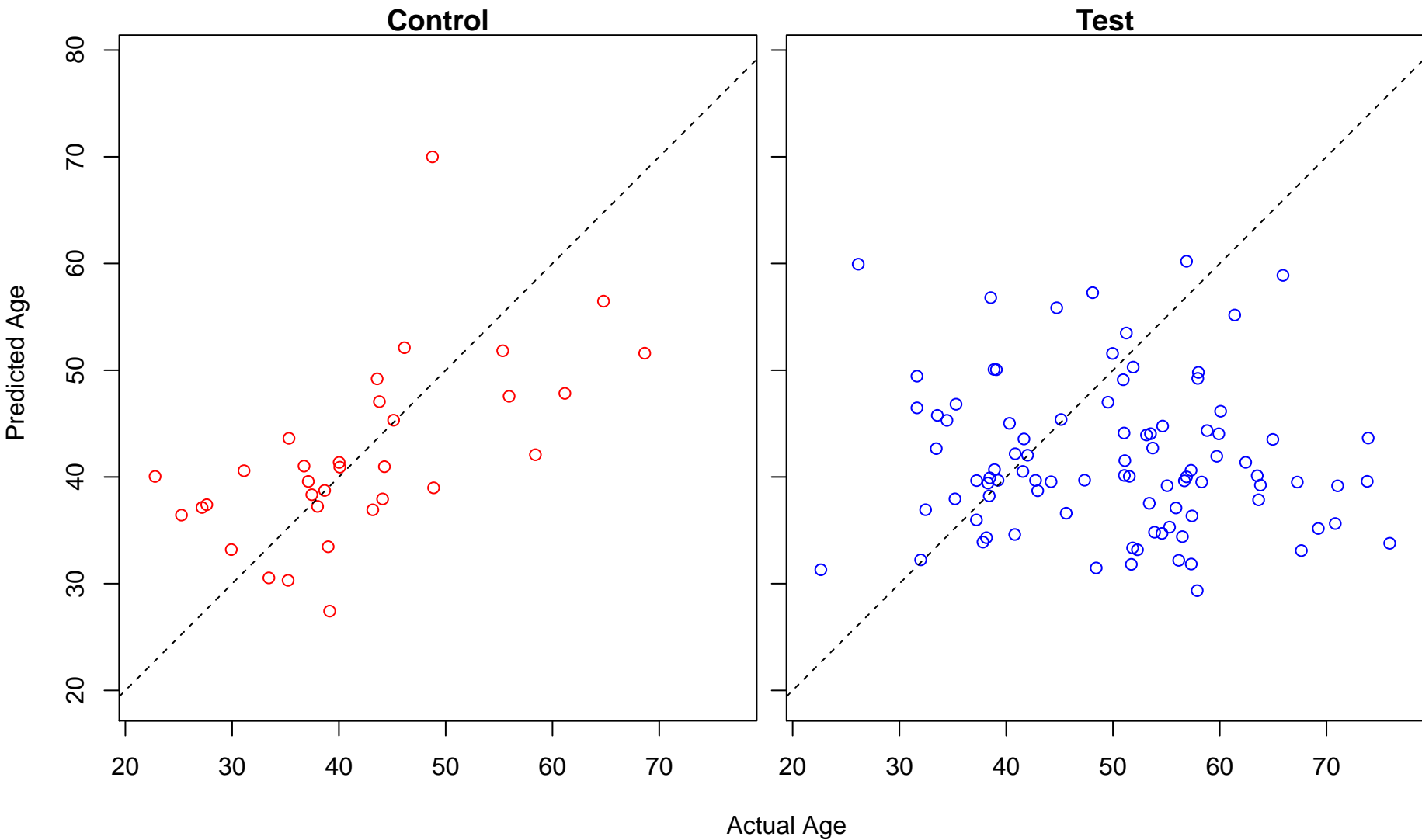
positive regulation of mitochondrial fission (Score: 1.418930)



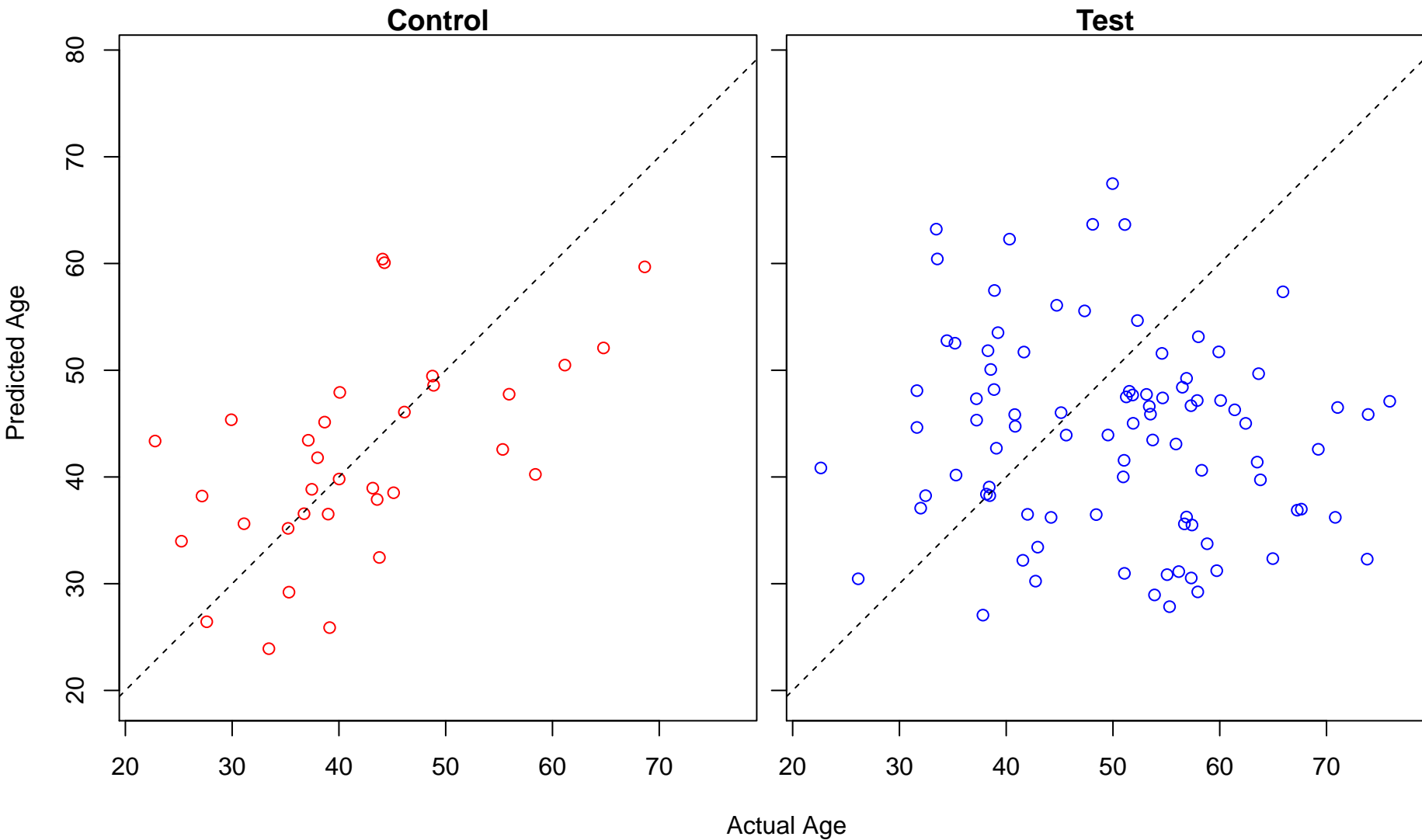
positive regulation of sodium ion transport (Score: 1.418253)



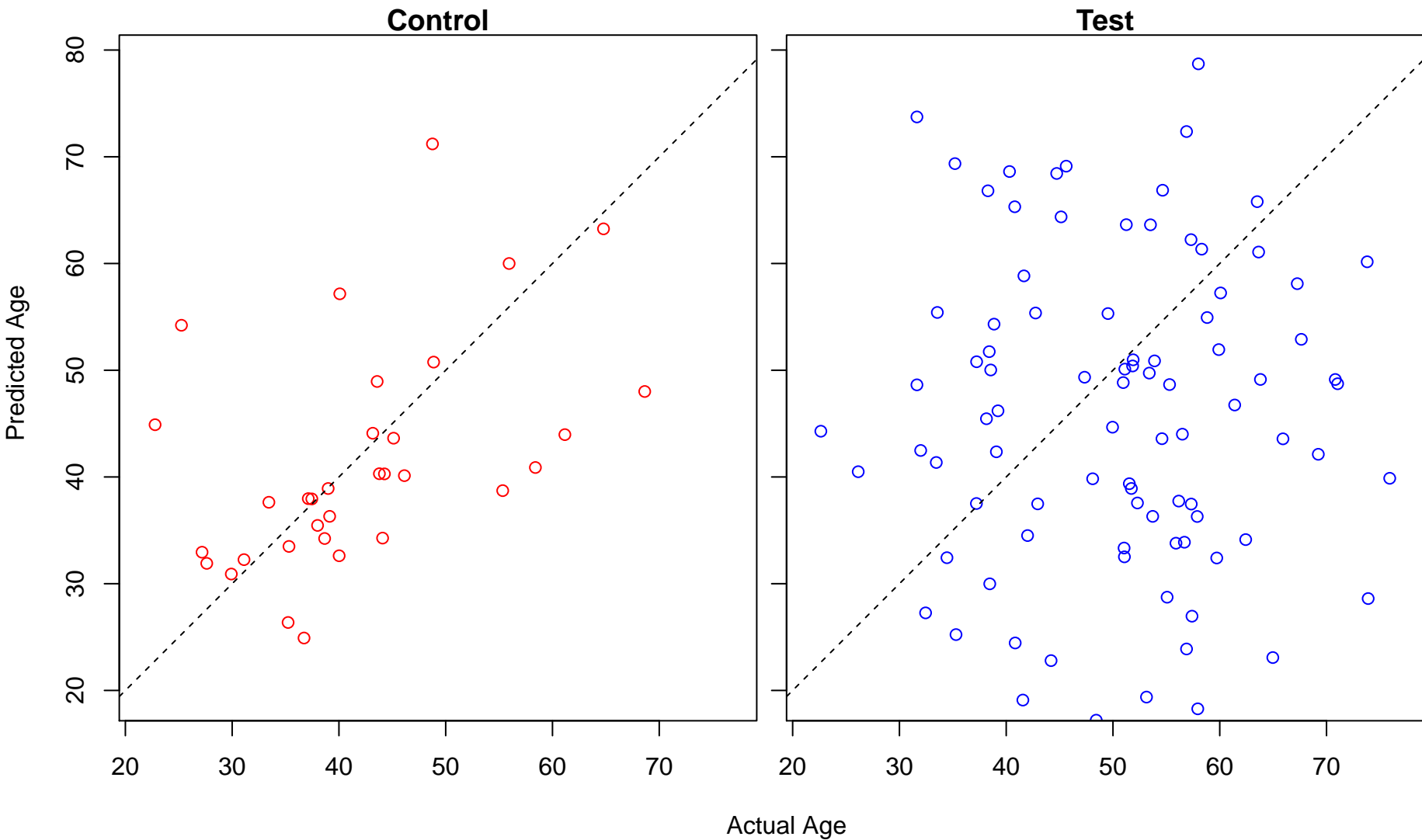
G2 DNA damage checkpoint (Score: 1.414084)



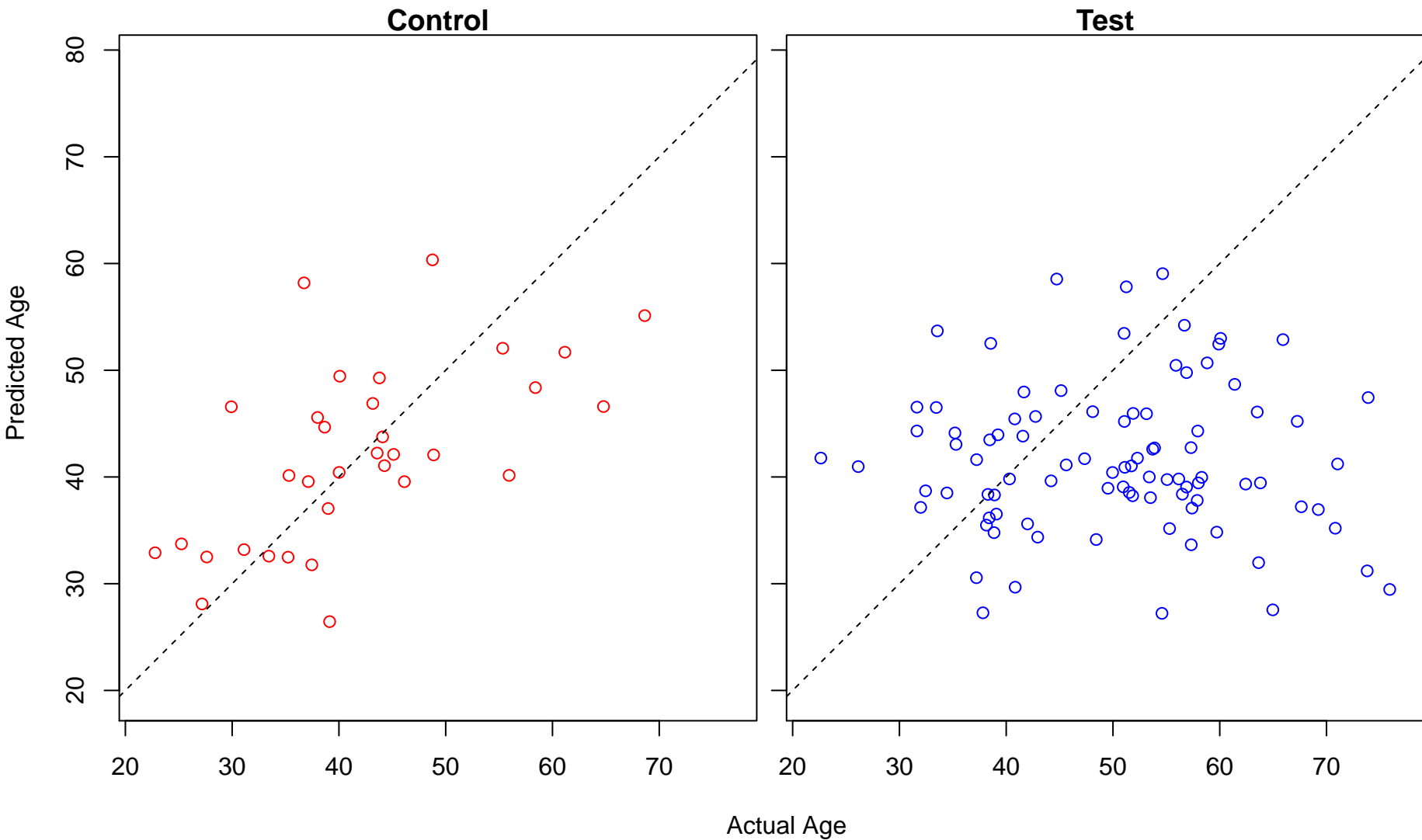
peptidyl-arginine methylation (Score: 1.413088)



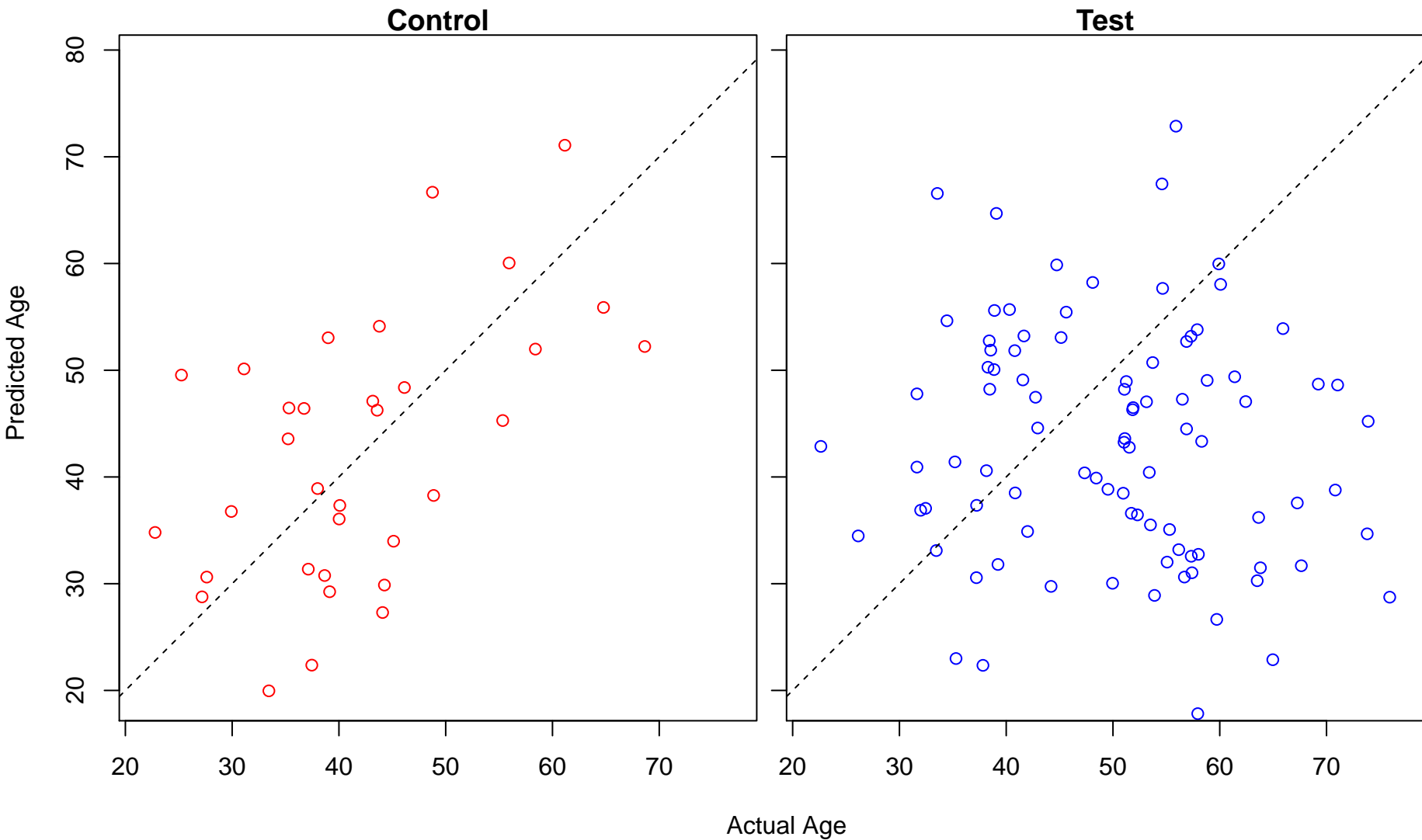
visual perception (Score: 1.410511)



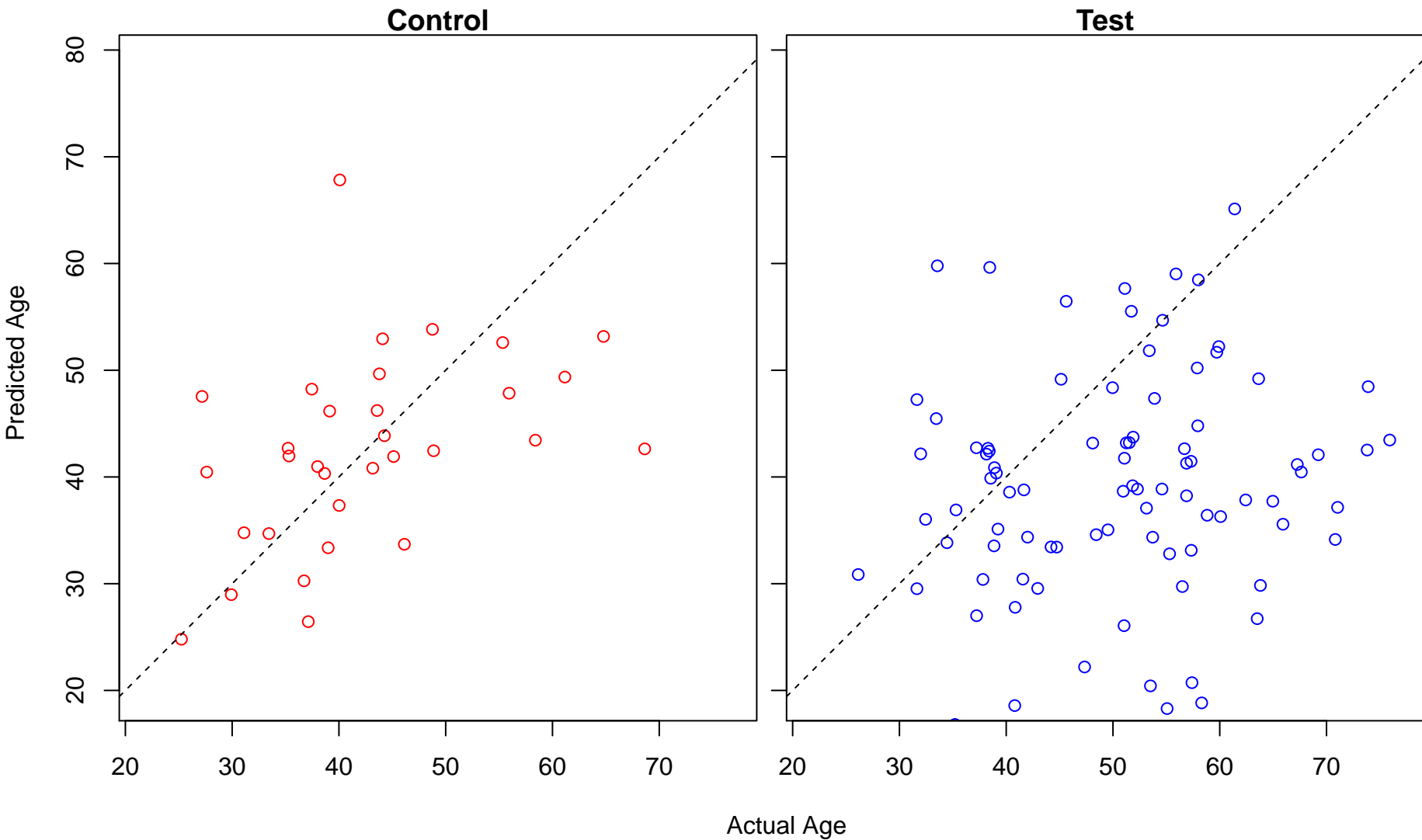
cellular response to tumor necrosis factor (Score: 1.409771)



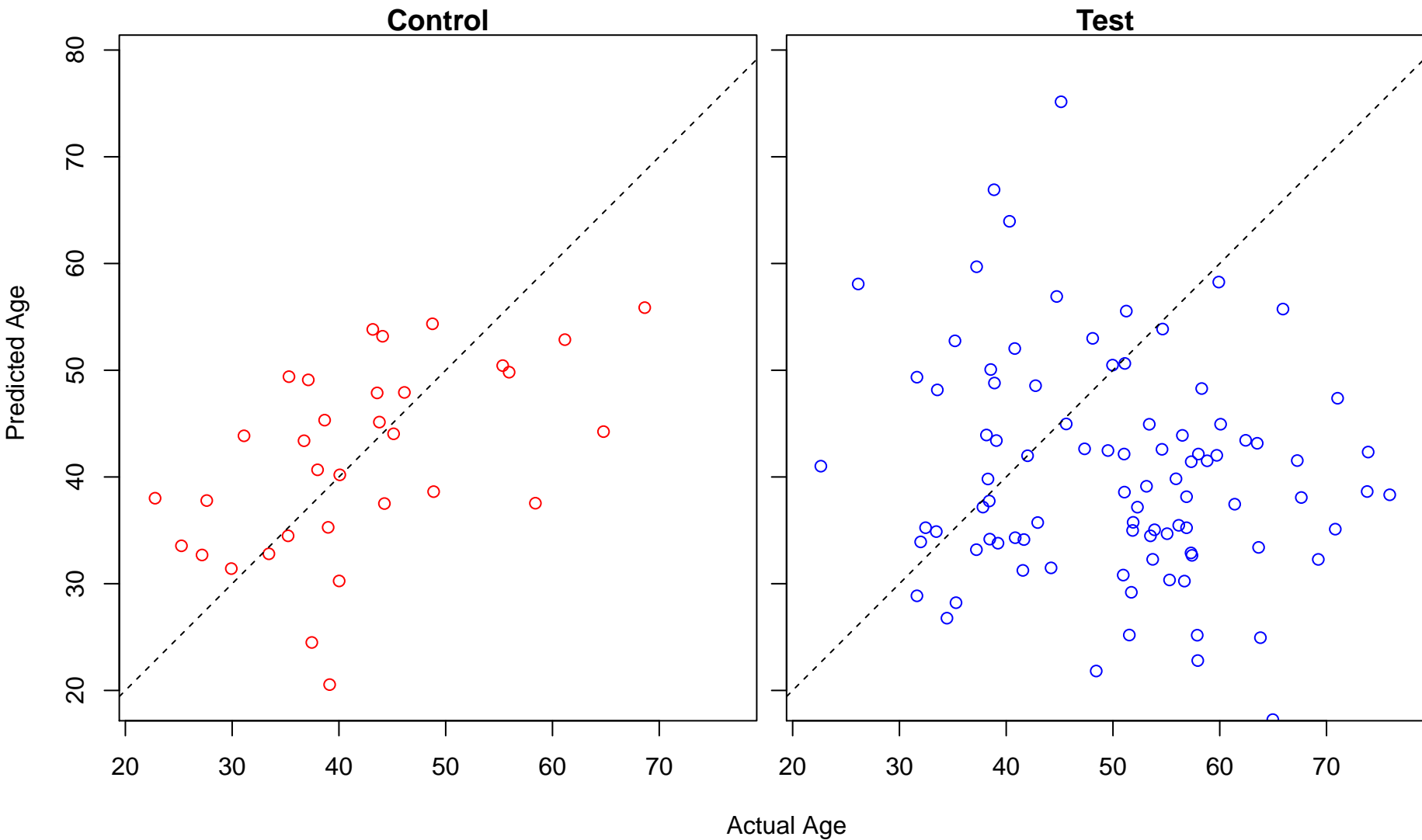
spermatid differentiation (Score: 1.409531)



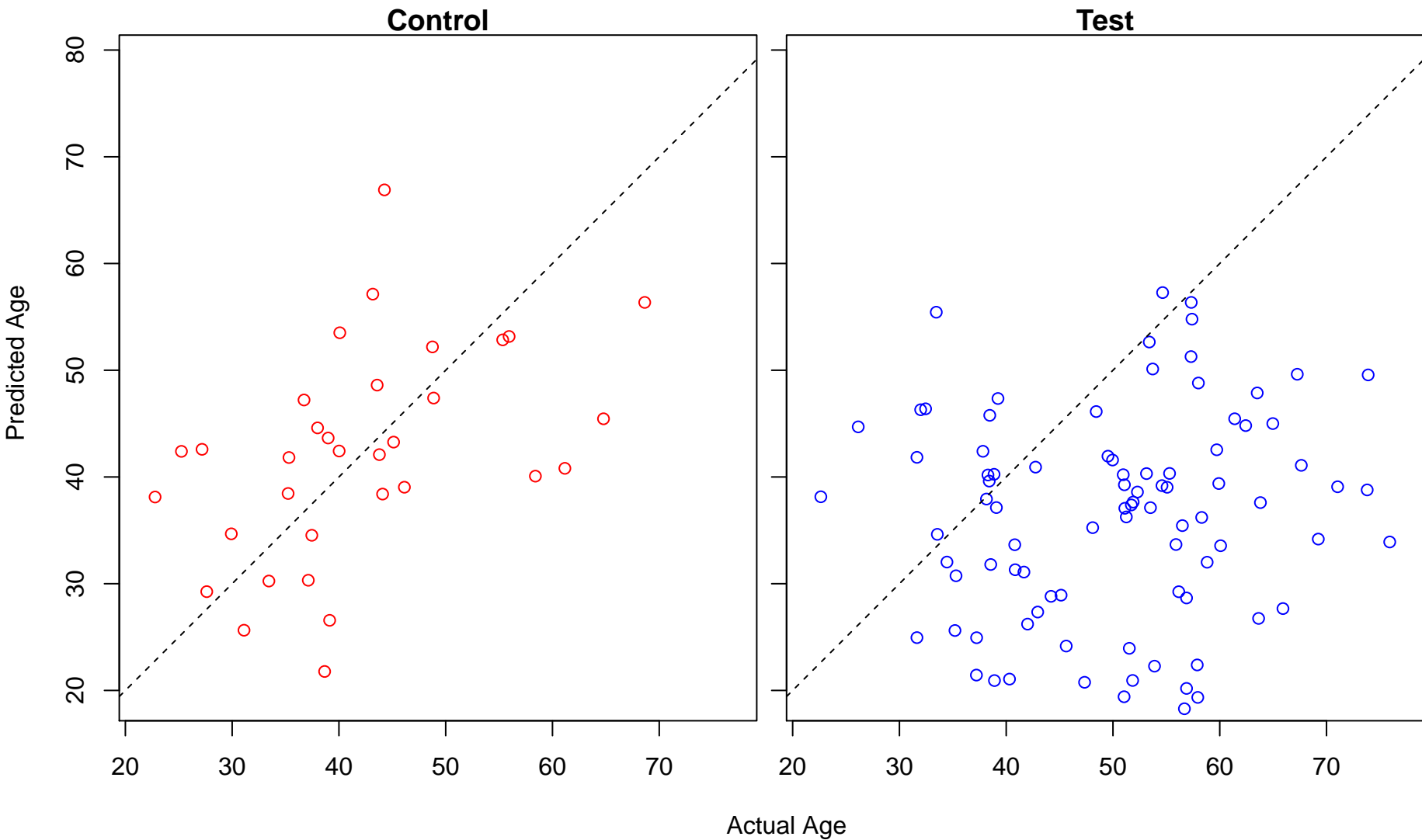
regulation of phosphatidylinositol 3-kinase activity (Score: 1.408553)



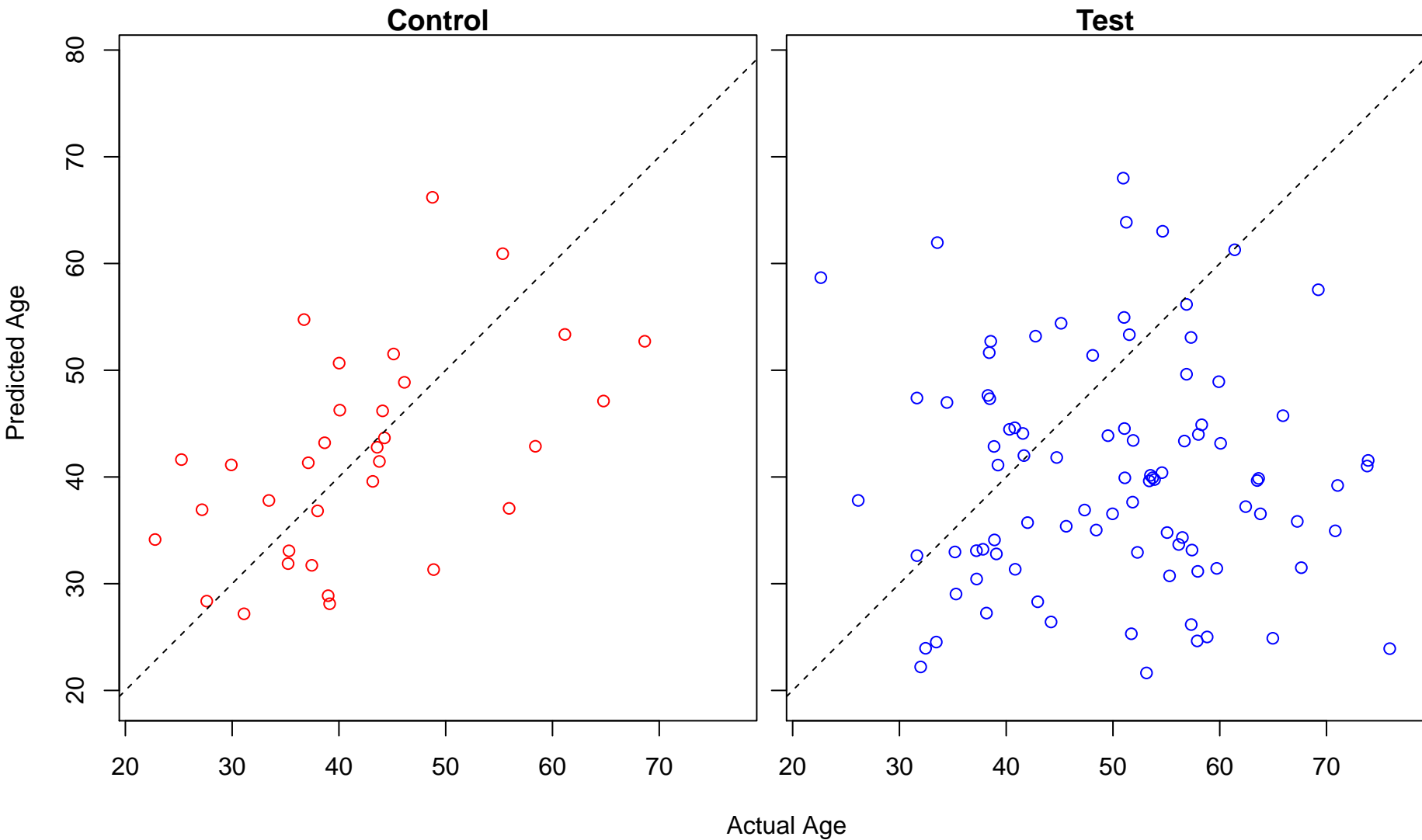
microtubule bundle formation (Score: 1.407627)



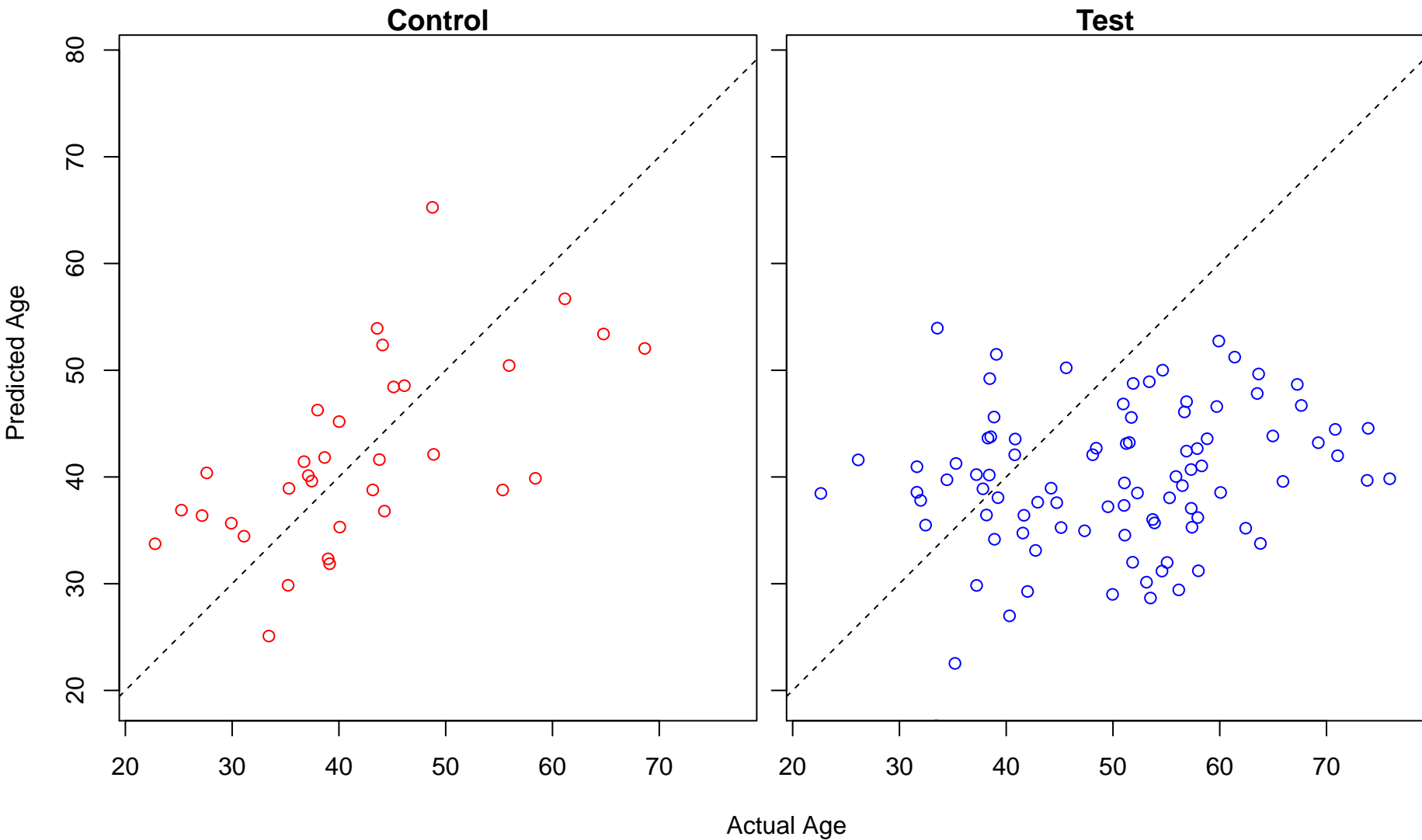
negative regulation of interleukin-8 production (Score: 1.406358)



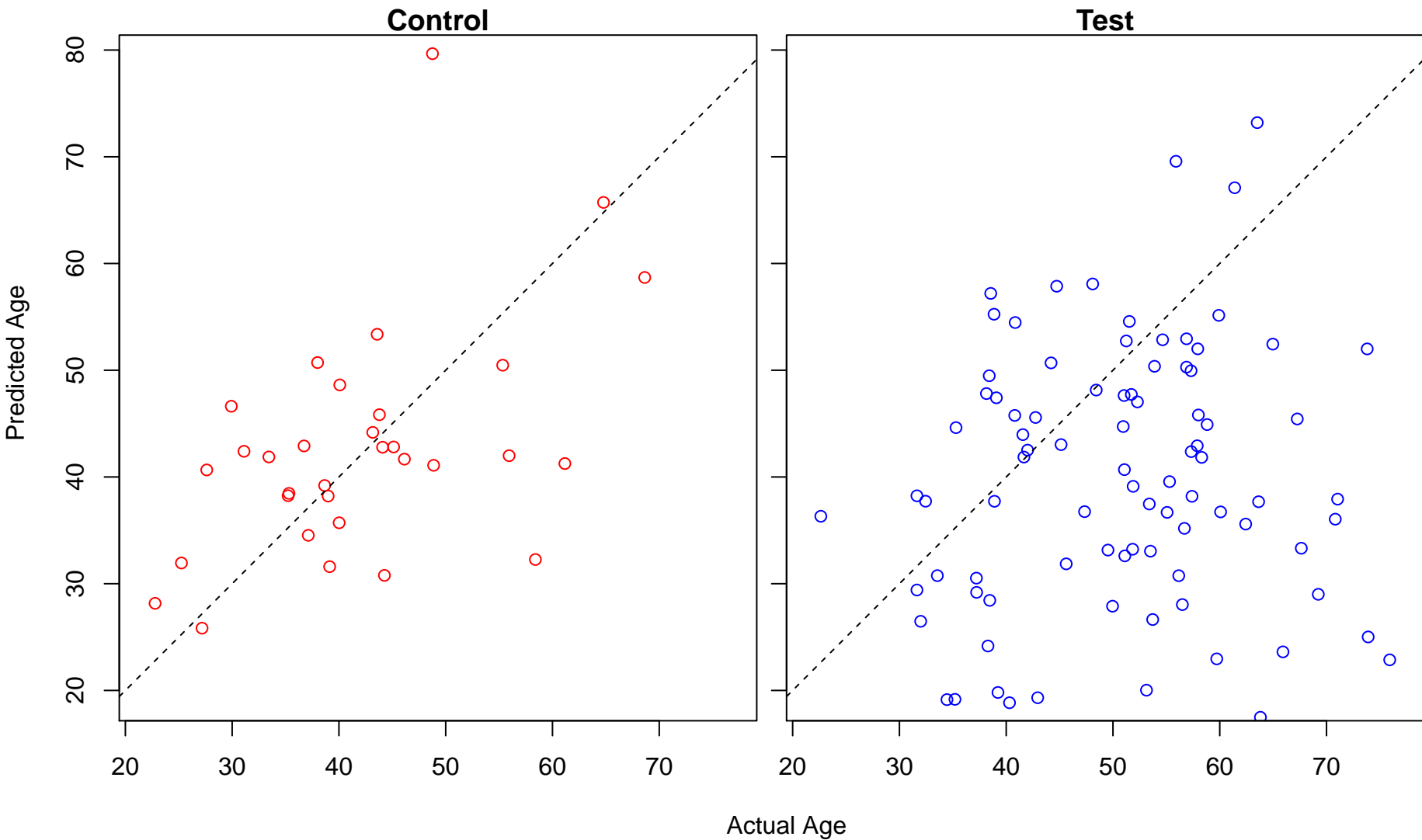
DNA biosynthetic process (Score: 1.405621)



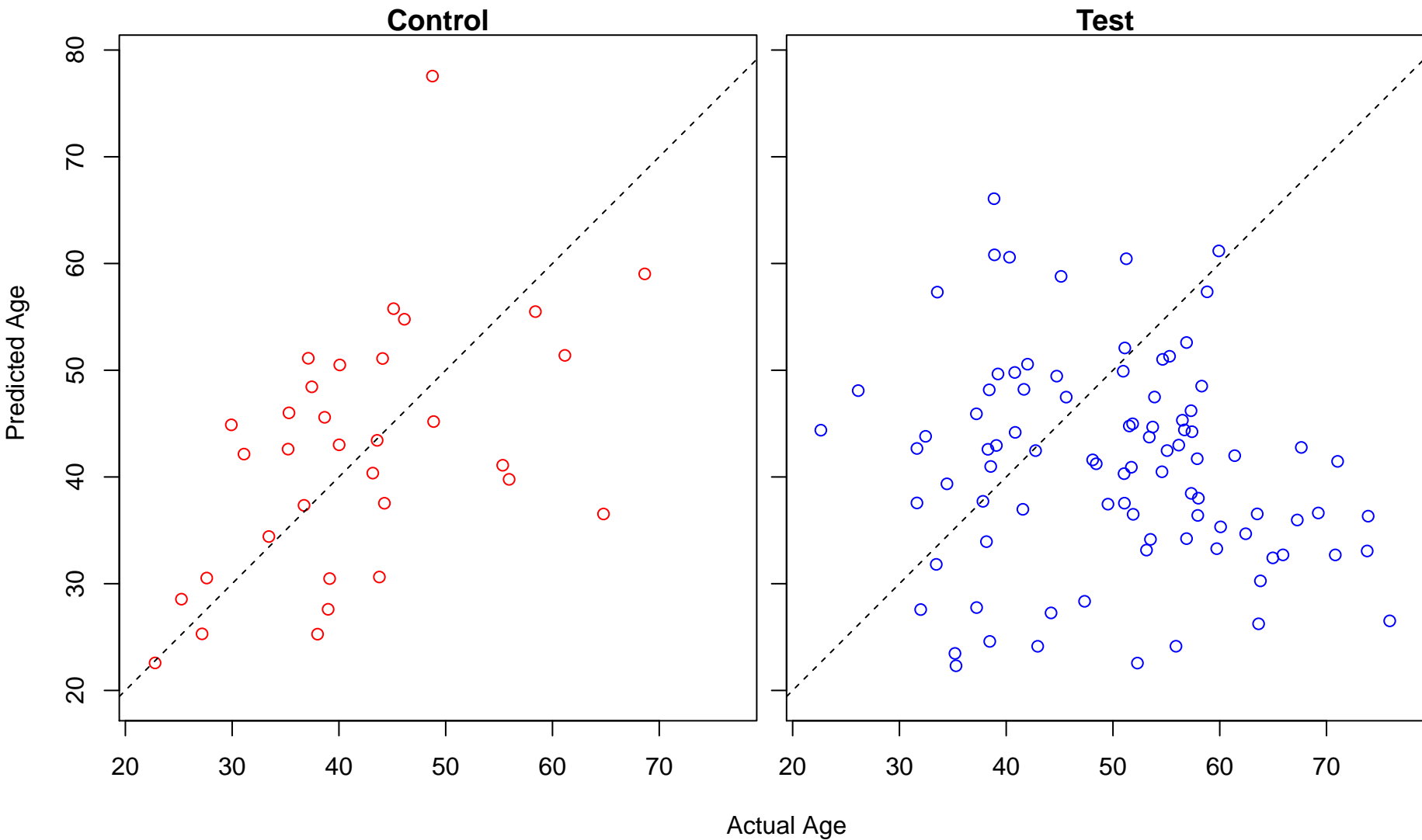
positive regulation of focal adhesion assembly (Score: 1.404724)



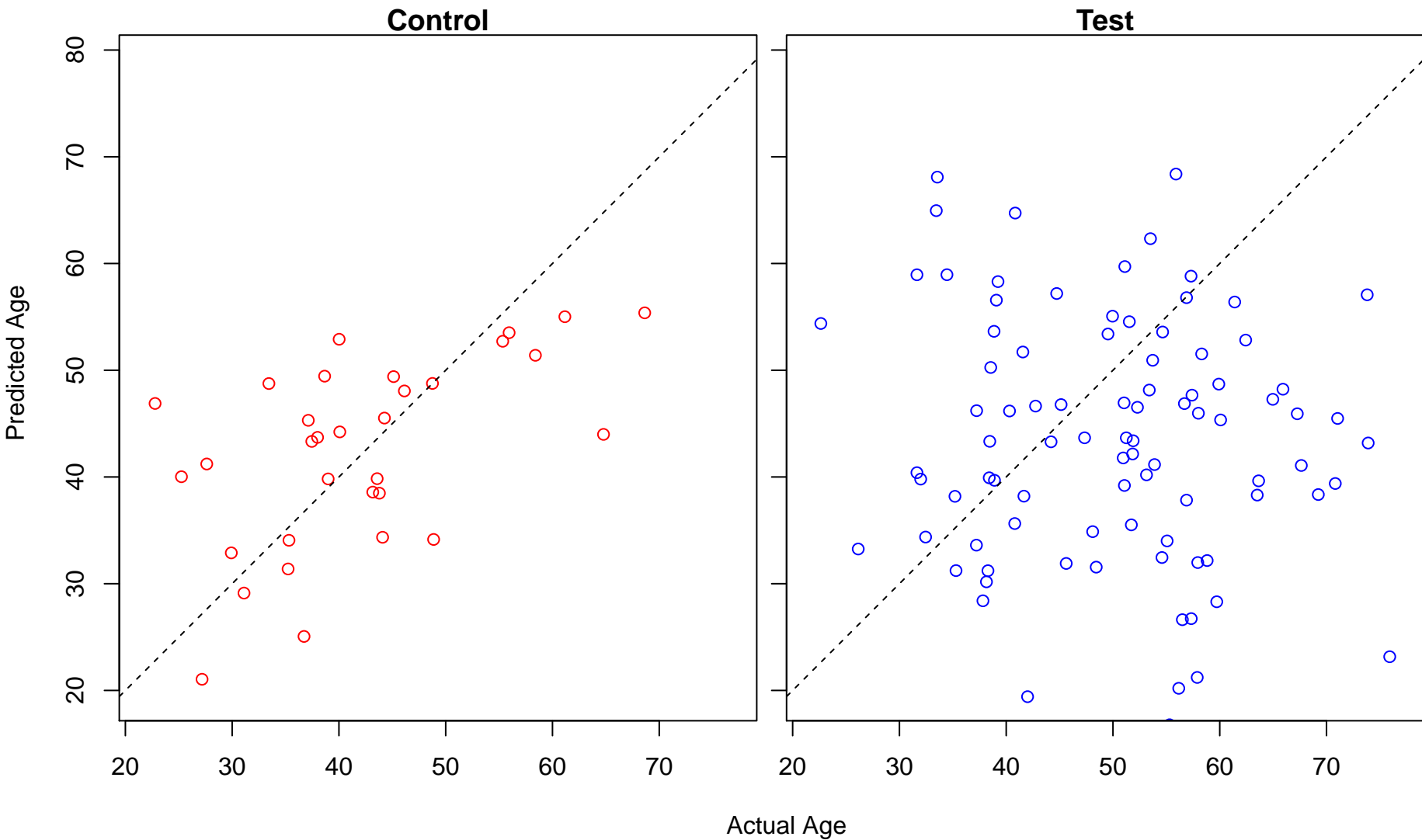
neuron recognition (Score: 1.404628)



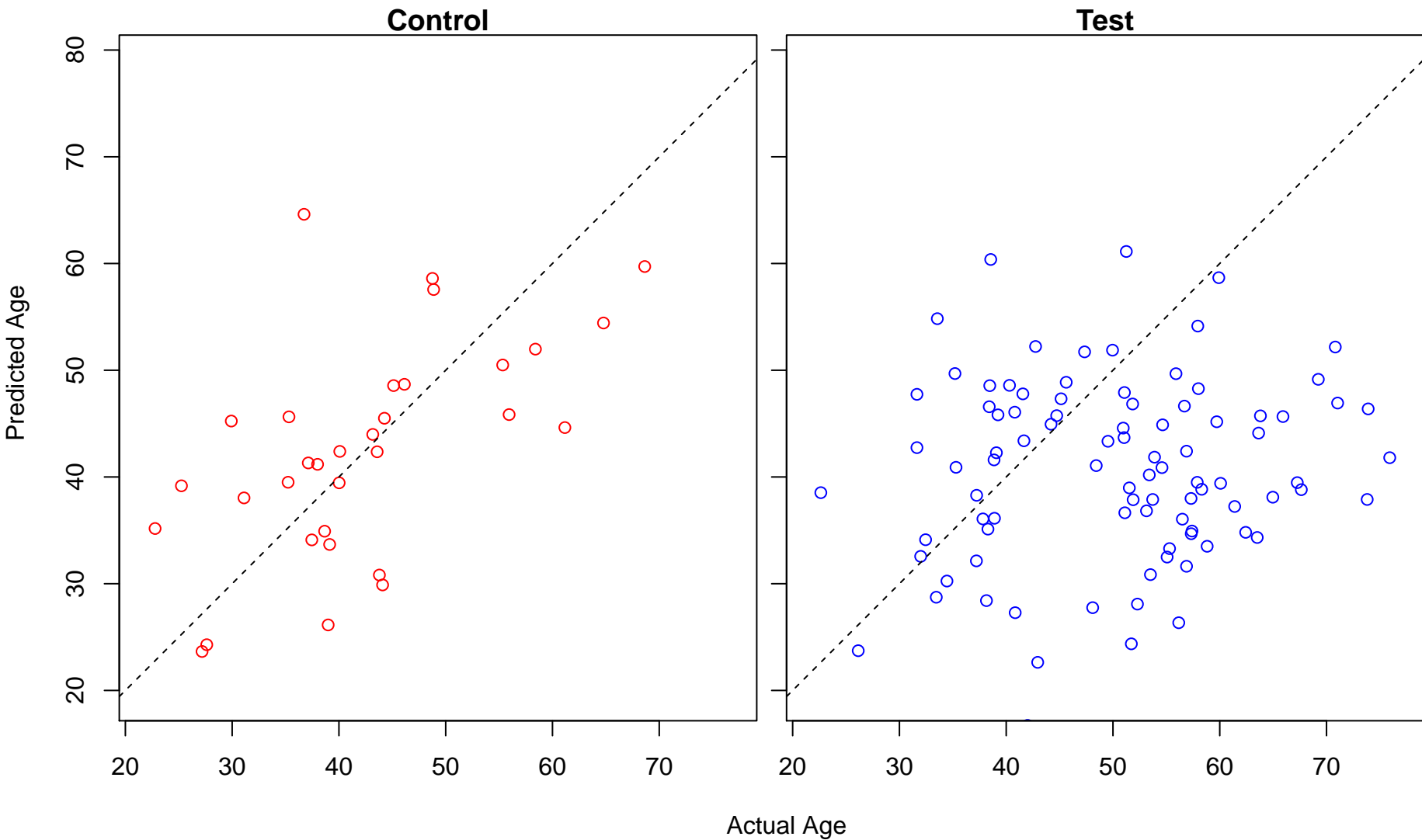
camera-type eye morphogenesis (Score: 1.404227)



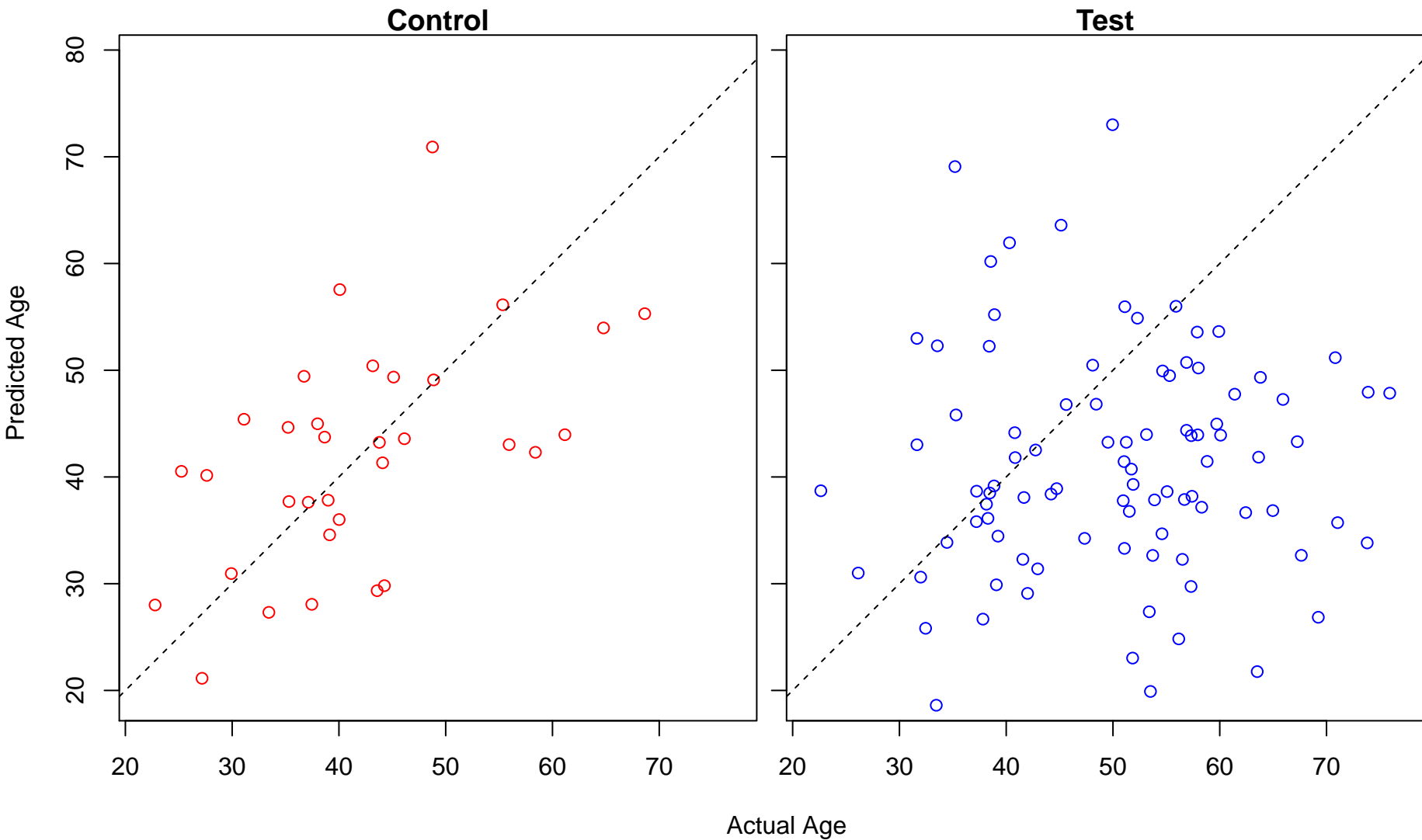
regulation of systemic arterial blood pressure by circulatory renin–angiotensin (Score: 1.404097)



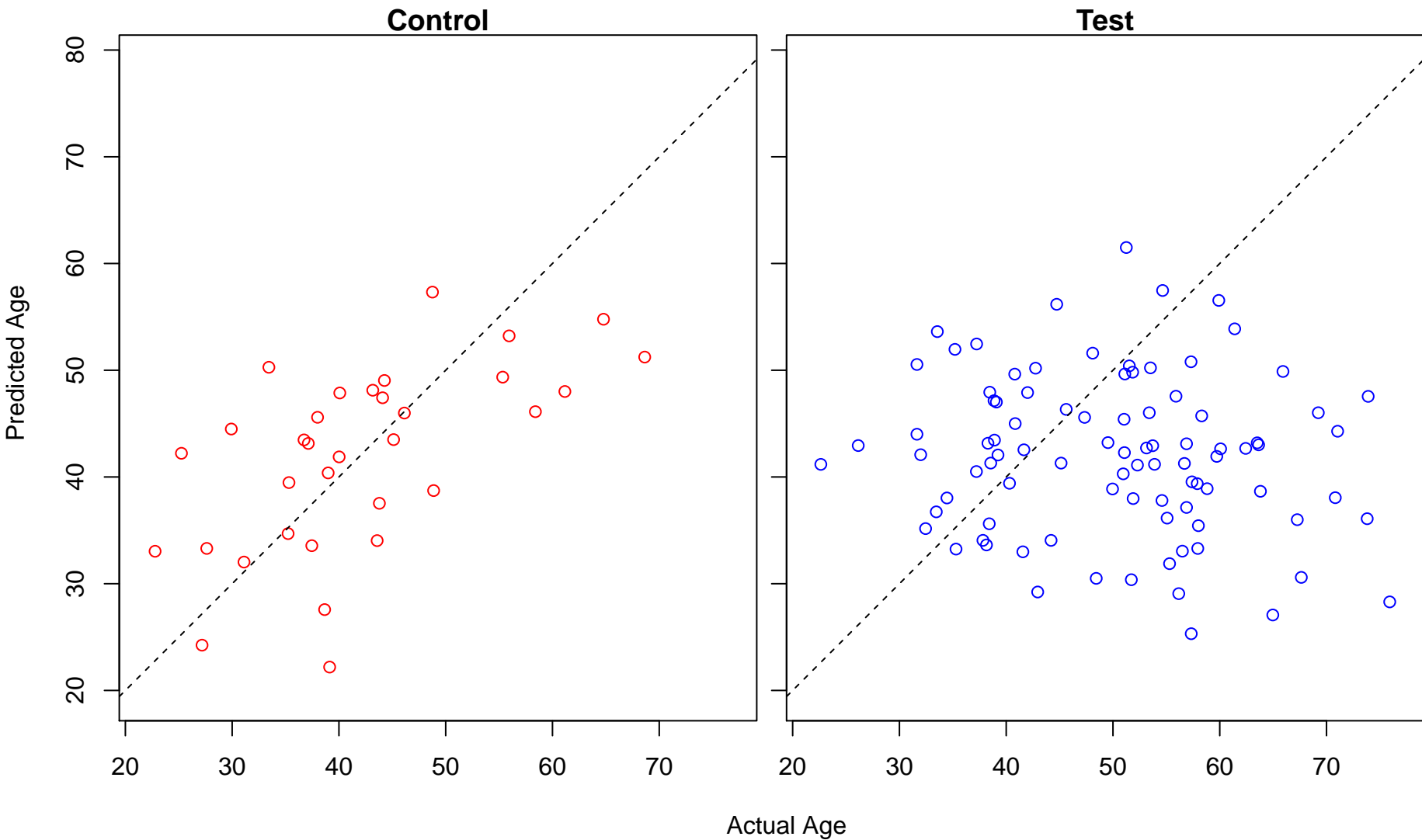
regulation of production of molecular mediator of immune response (Score: 1.402223)



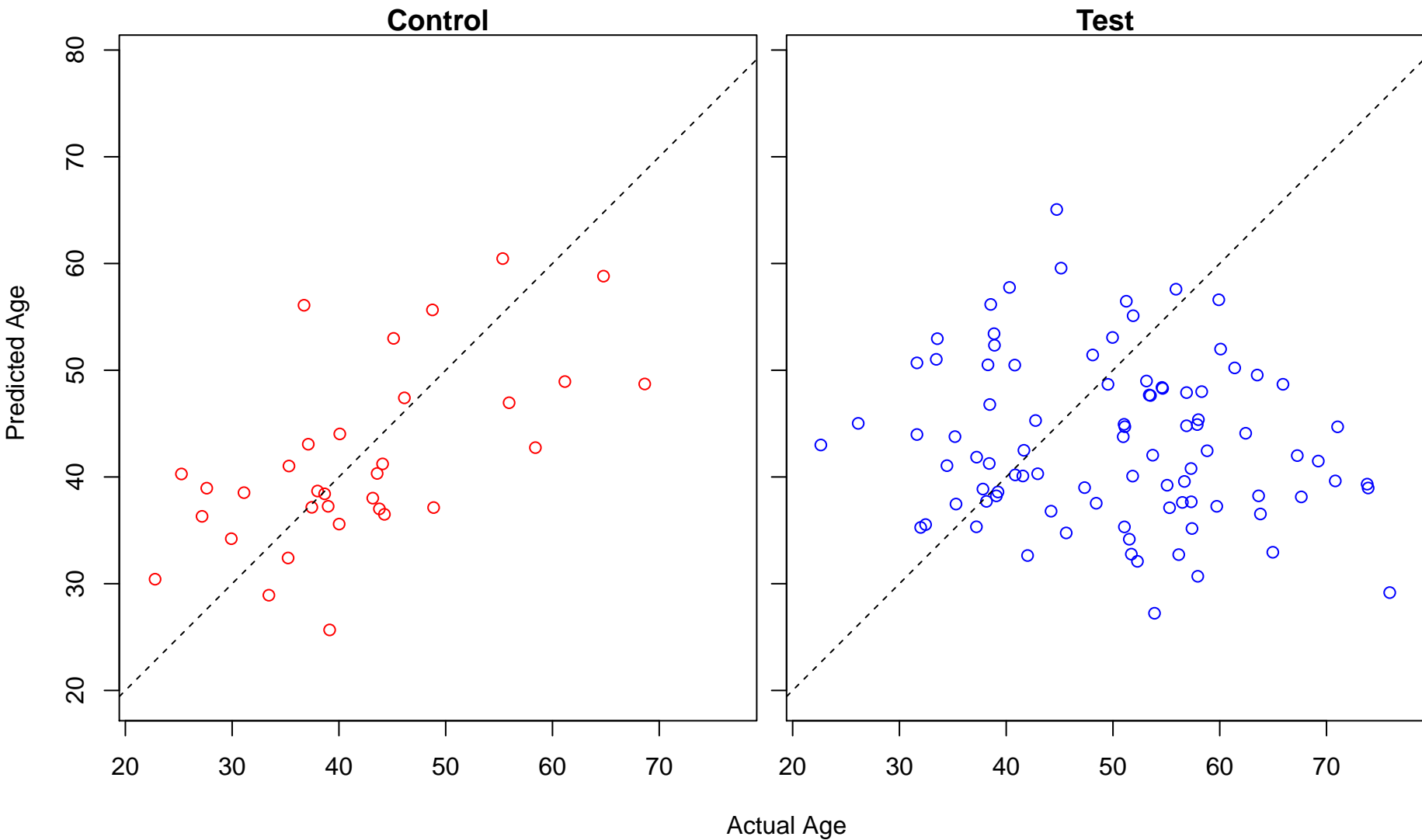
sterol metabolic process (Score: 1.398154)



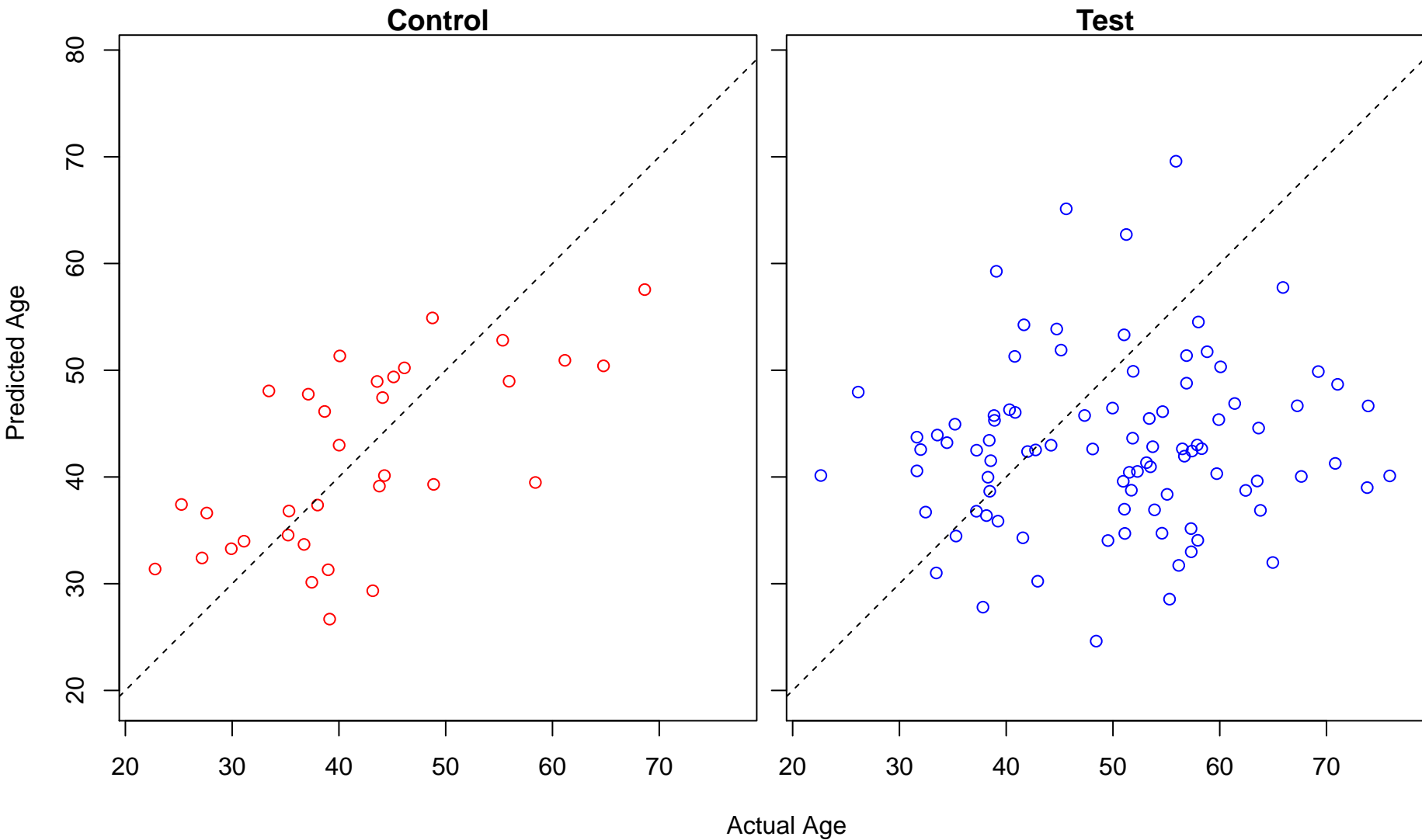
response to organophosphorus (Score: 1.391429)



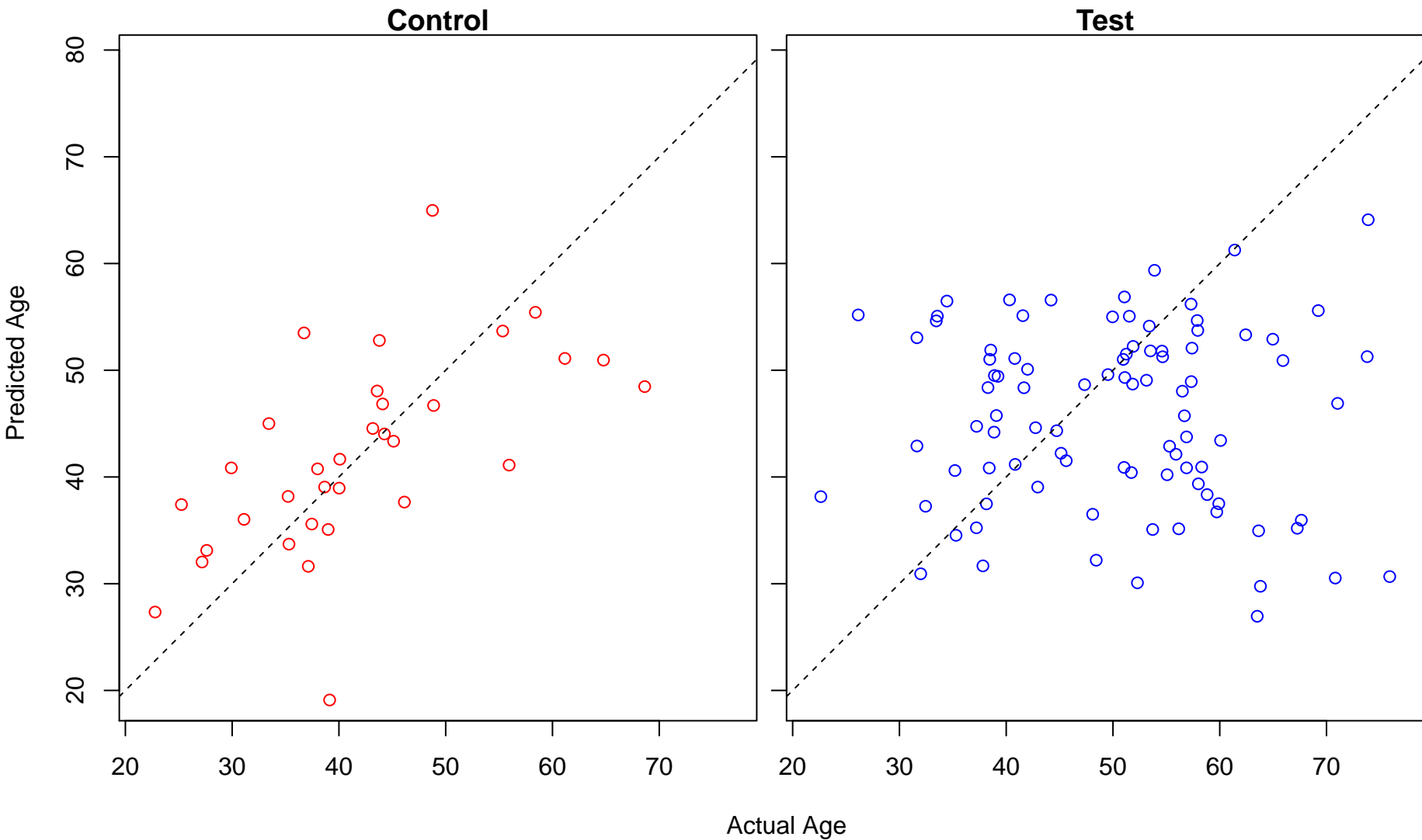
microtubule cytoskeleton organization (Score: 1.391175)



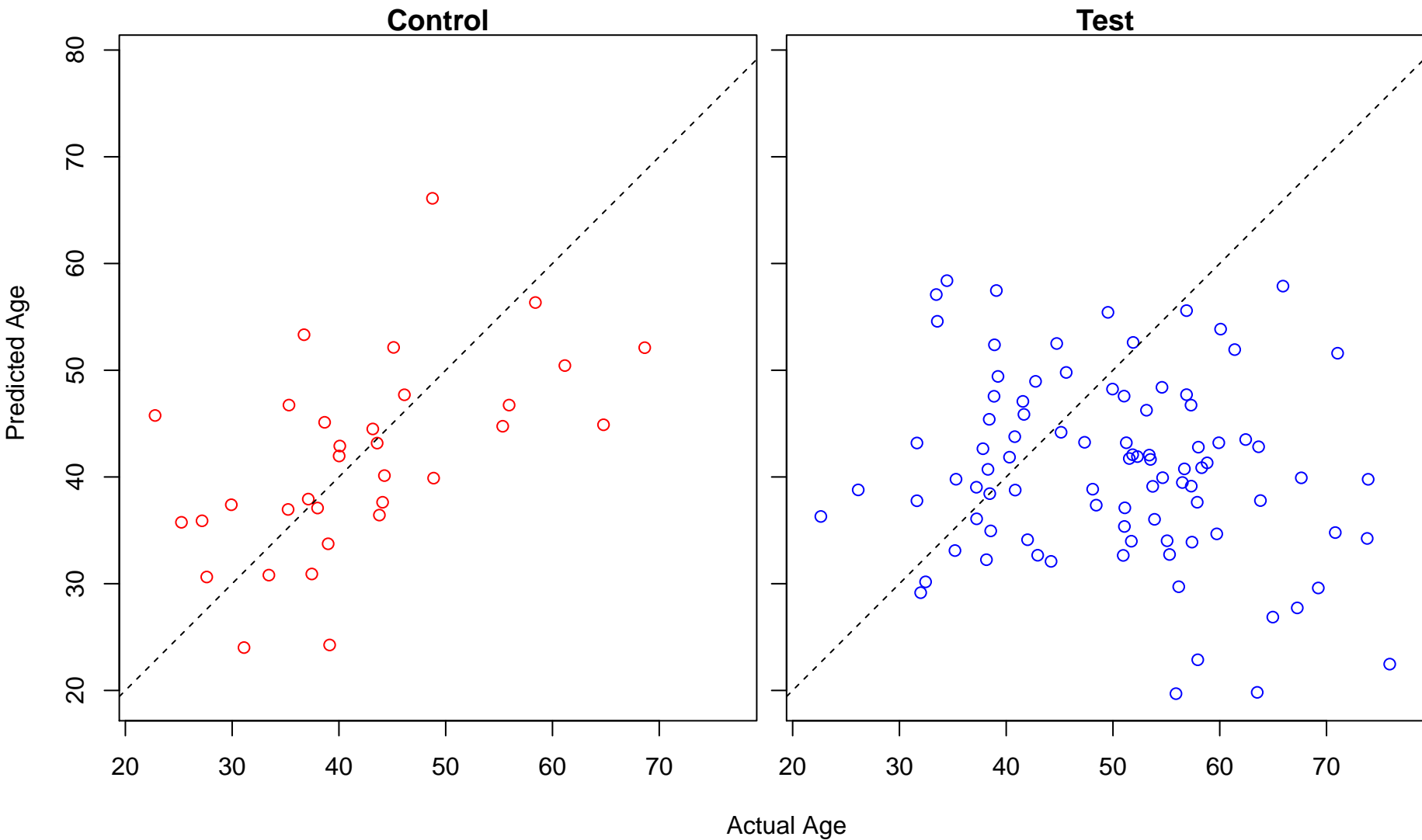
positive regulation of transmembrane transport (Score: 1.389979)



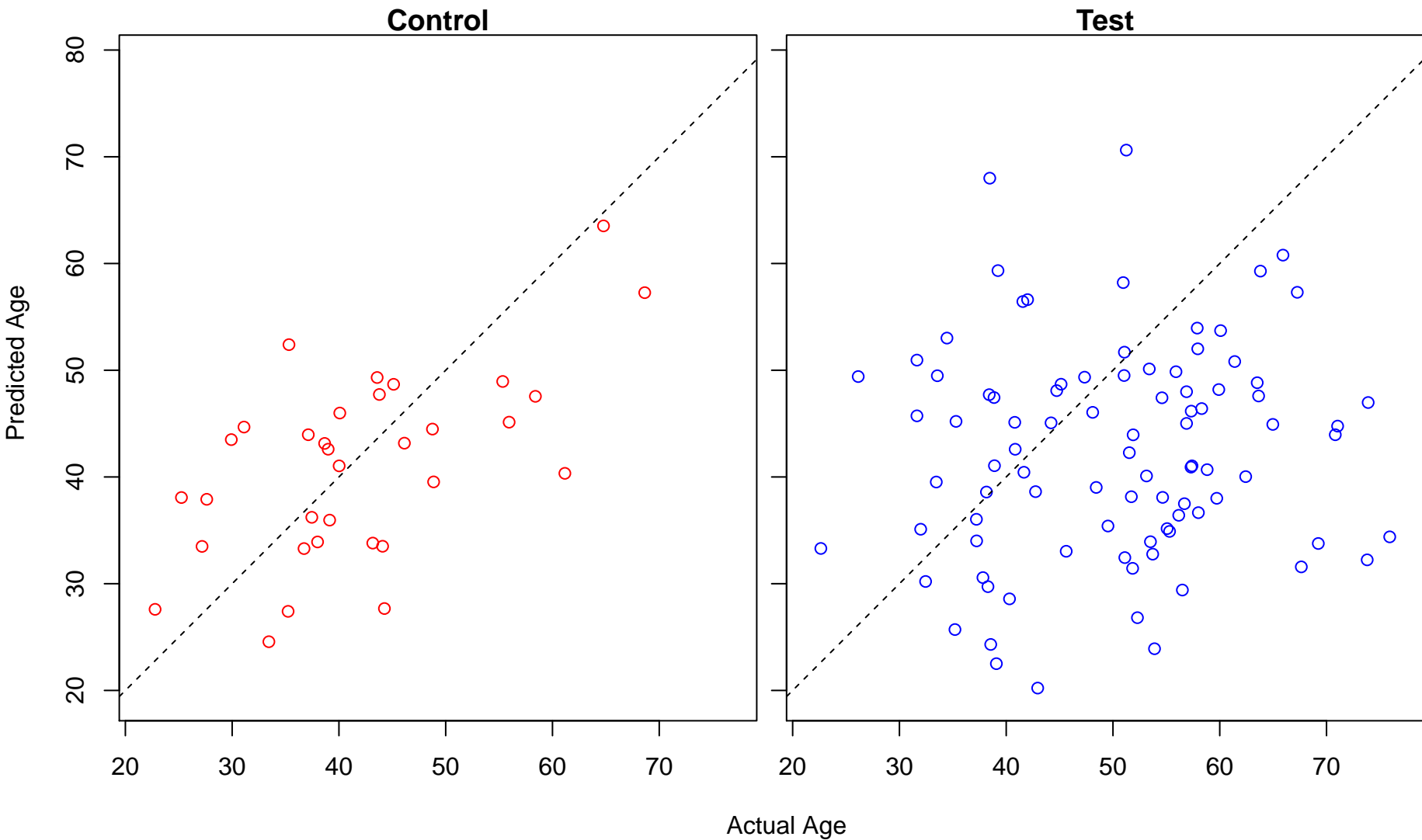
immunoglobulin mediated immune response (Score: 1.388763)



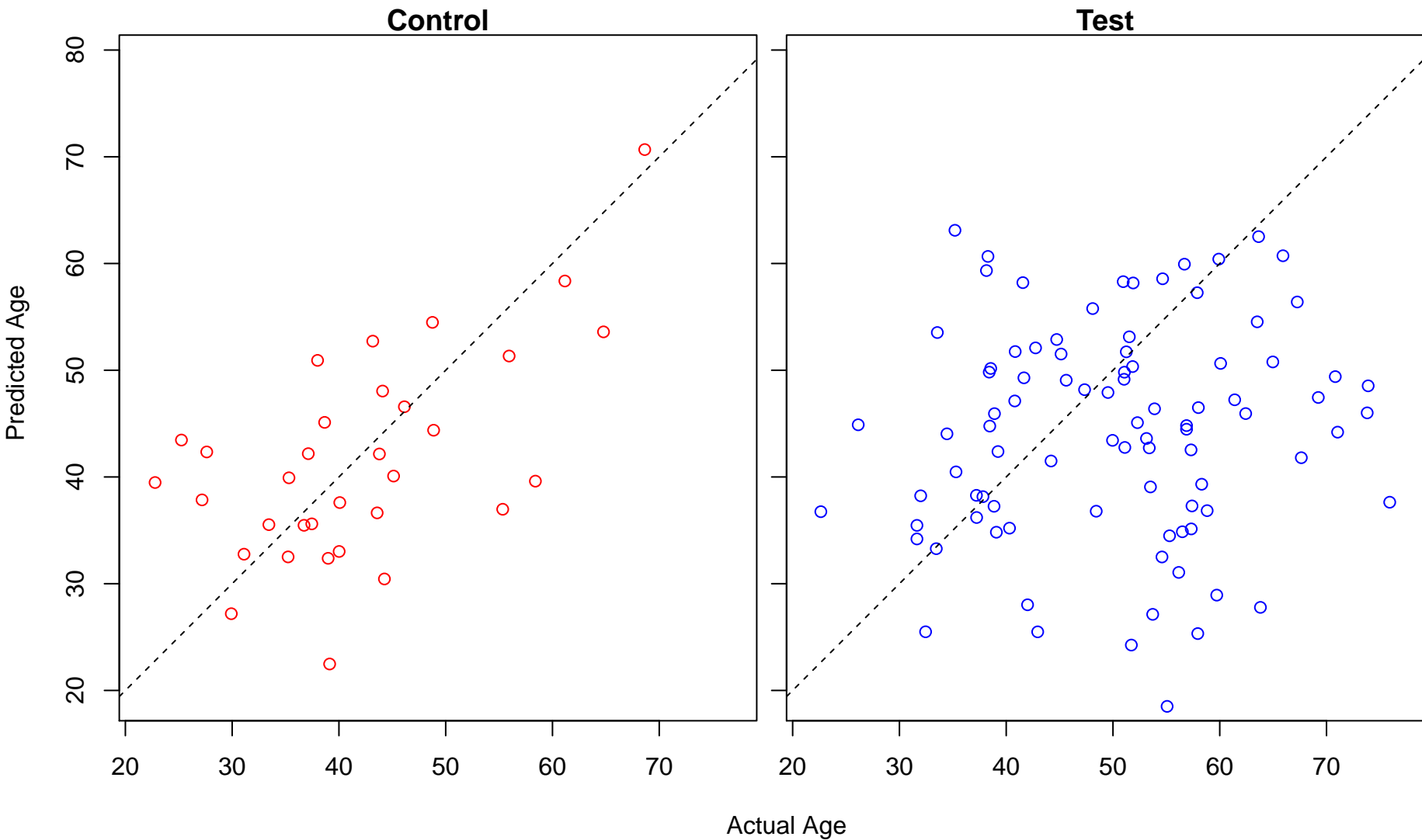
mitochondrial RNA metabolic process (Score: 1.381076)



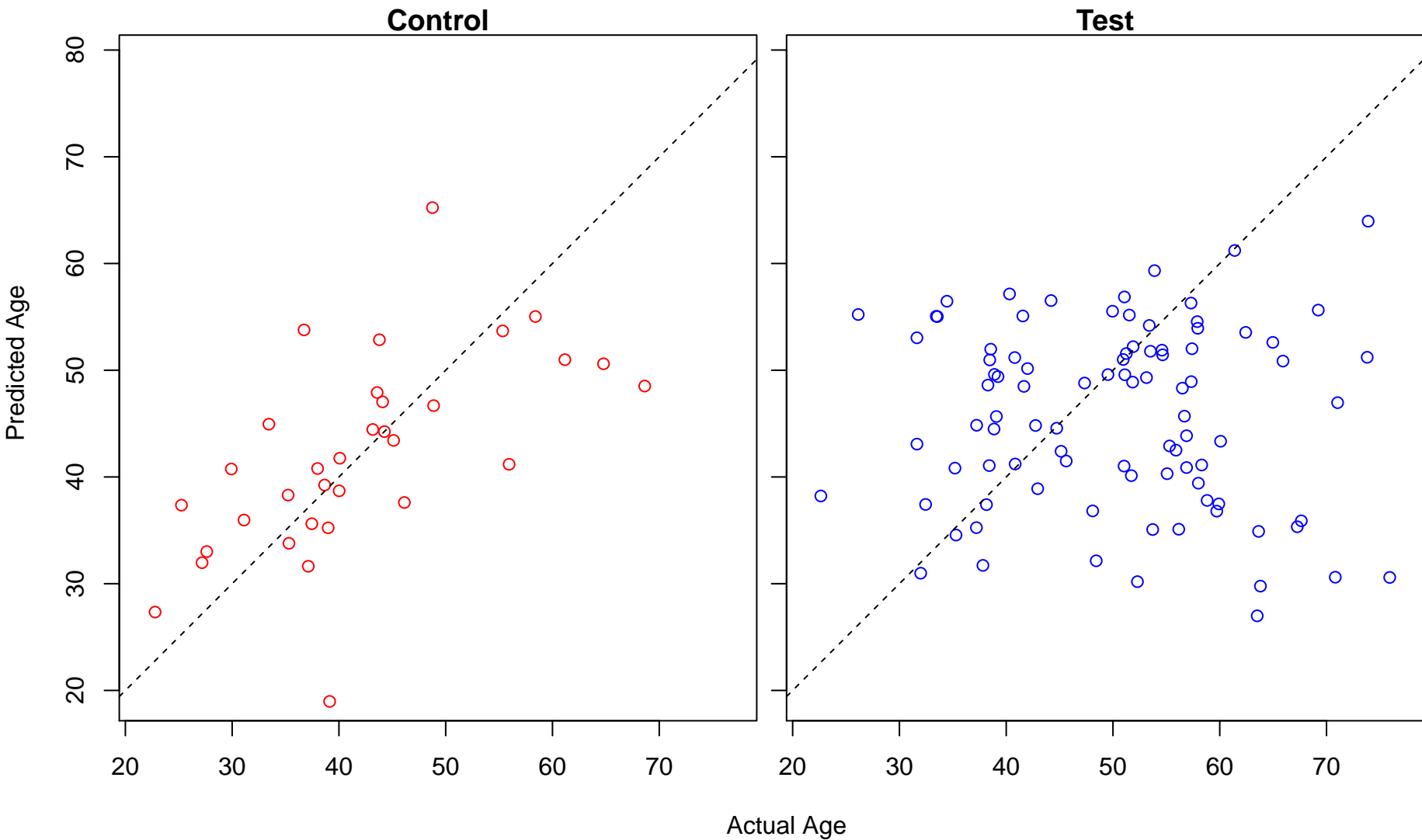
phosphatidylethanolamine acyl-chain remodeling (Score: 1.380653)



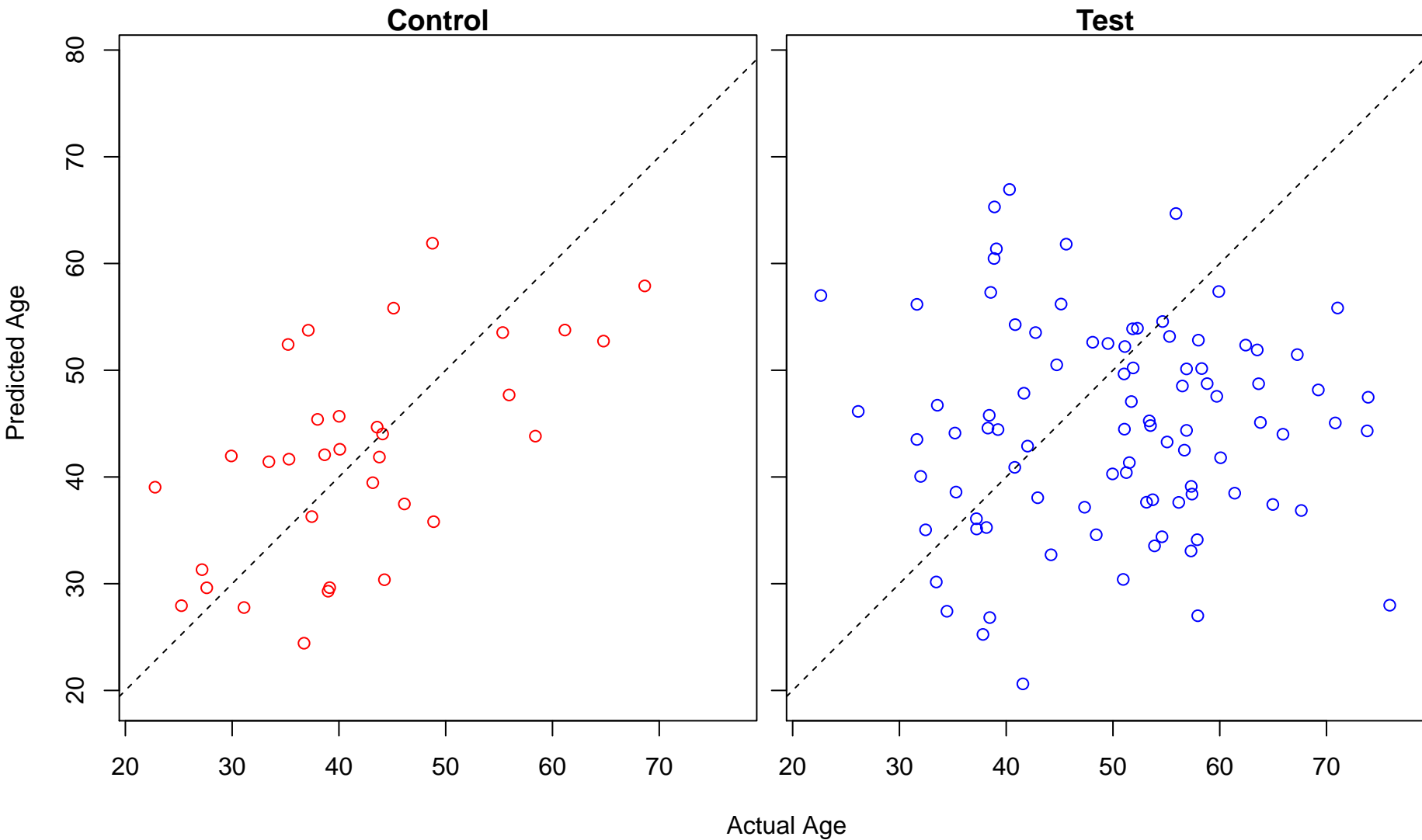
response to antibiotic (Score: 1.379602)



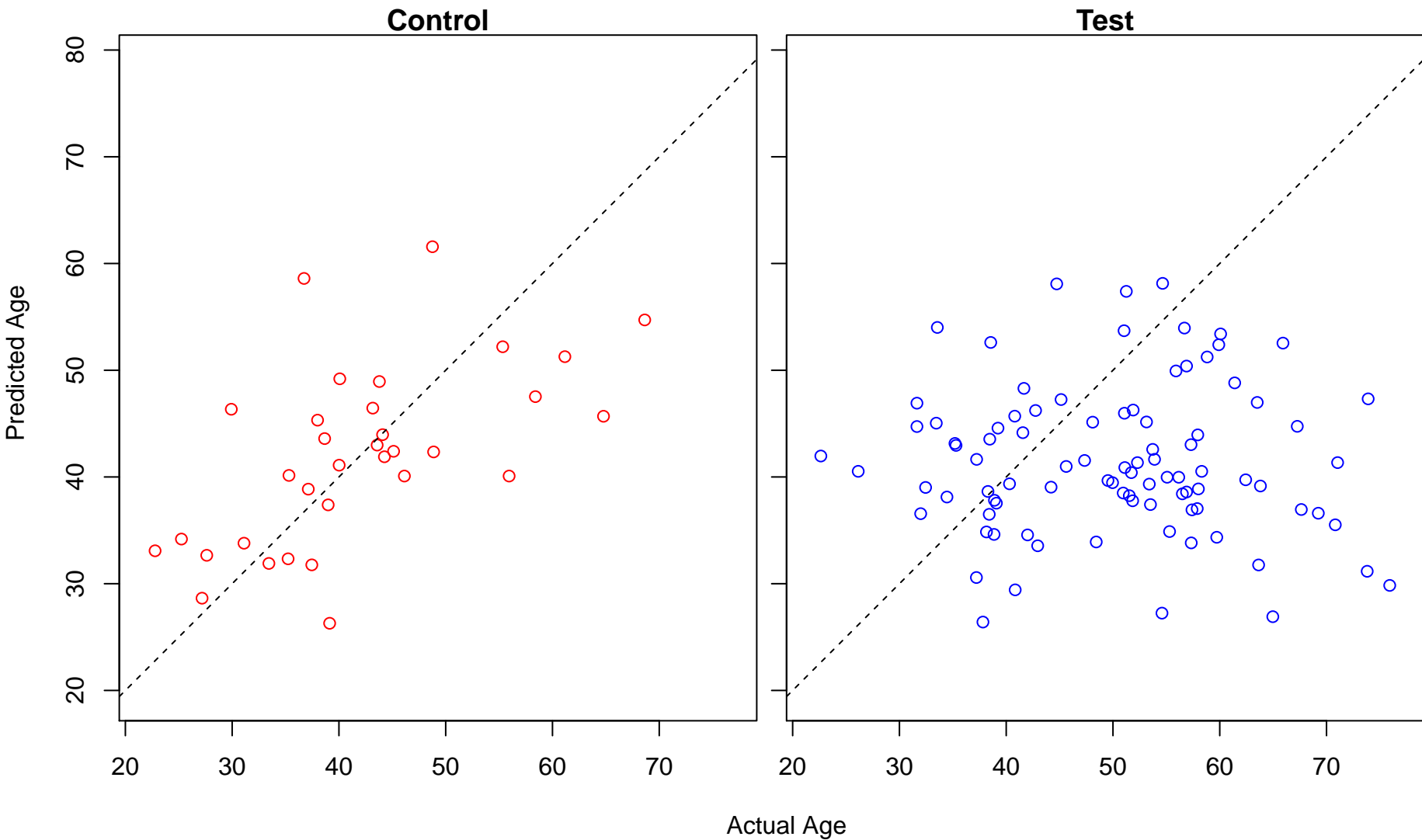
B cell mediated immunity (Score: 1.378421)



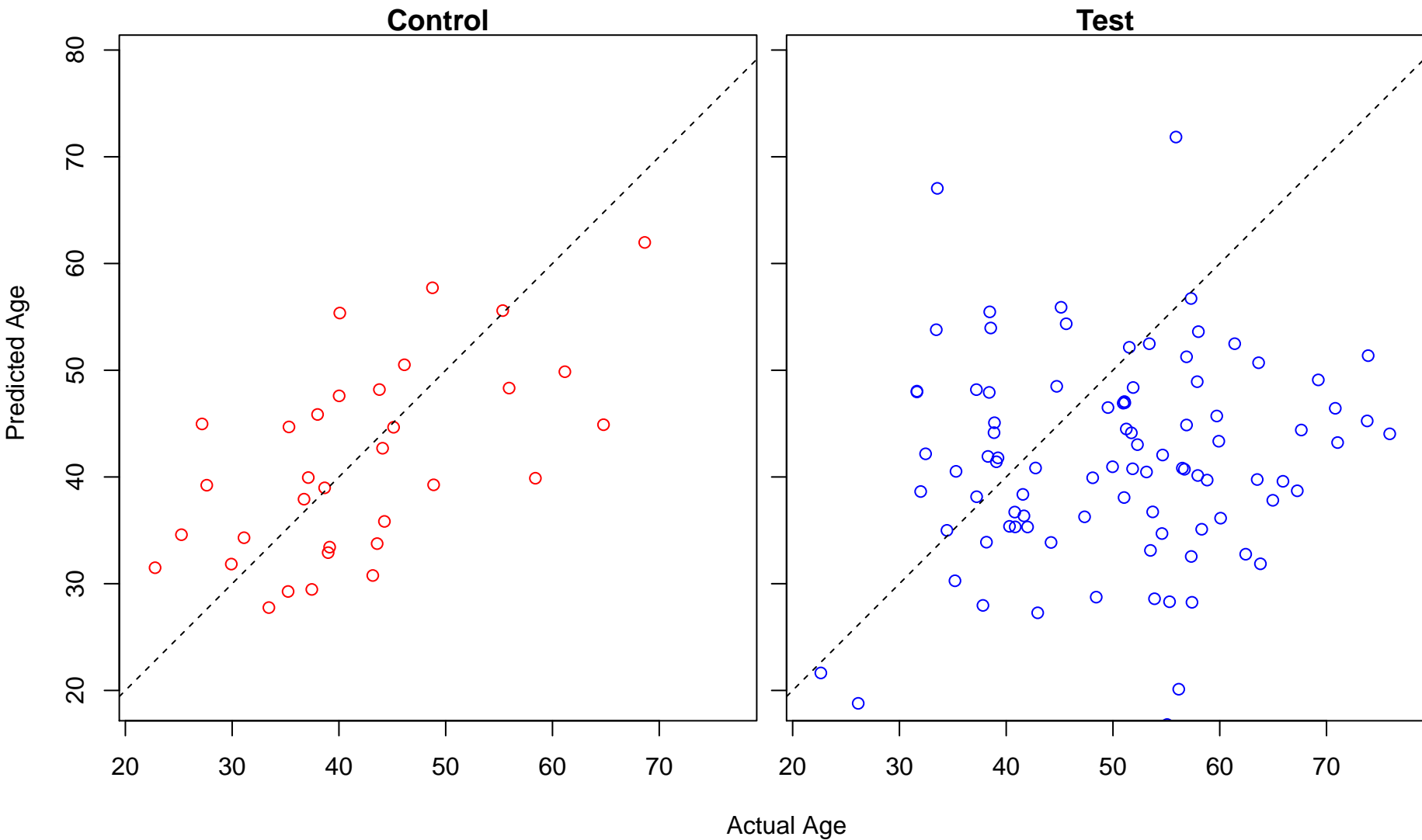
detection of mechanical stimulus (Score: 1.373742)



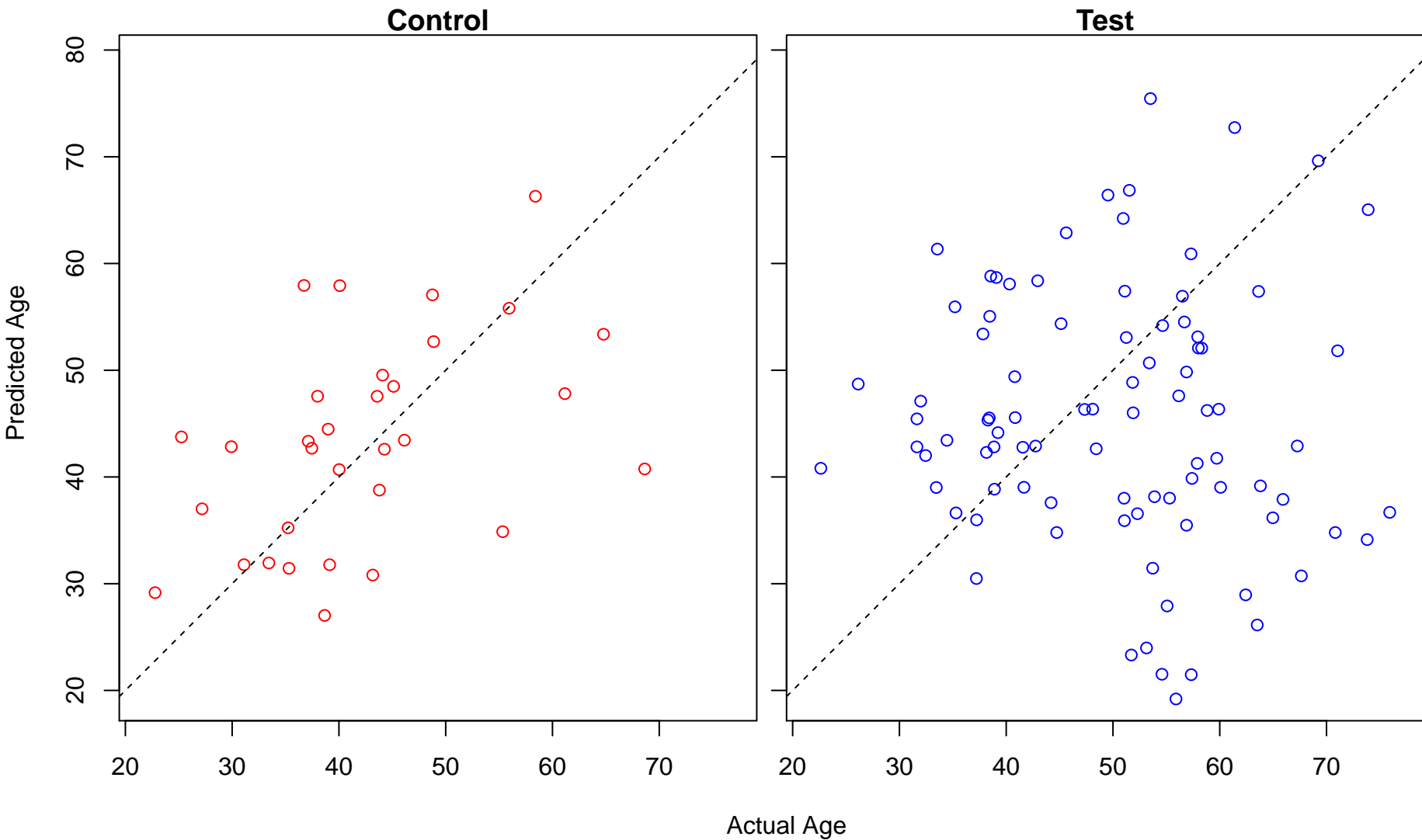
response to tumor necrosis factor (Score: 1.372548)



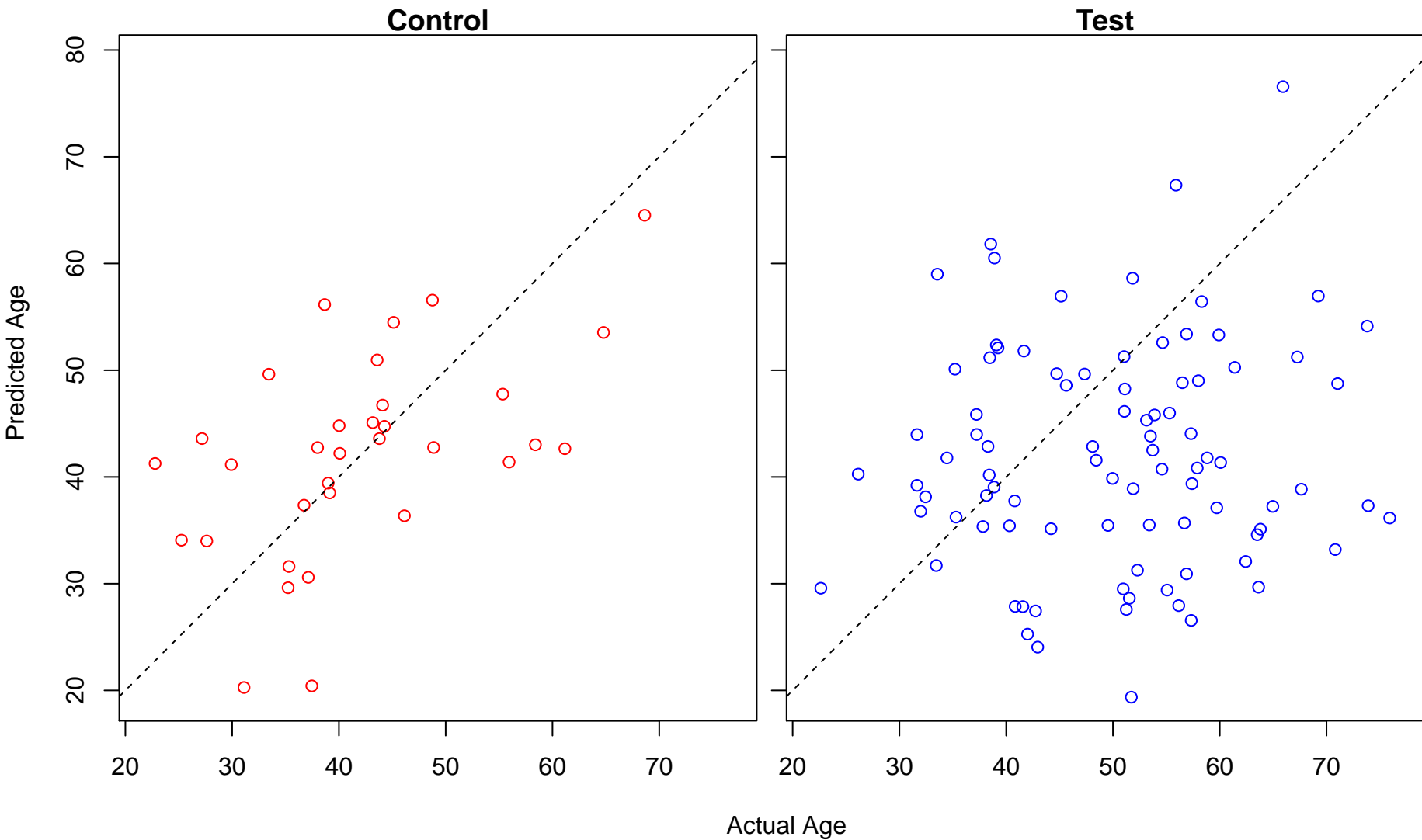
positive regulation of lipid metabolic process (Score: 1.366153)



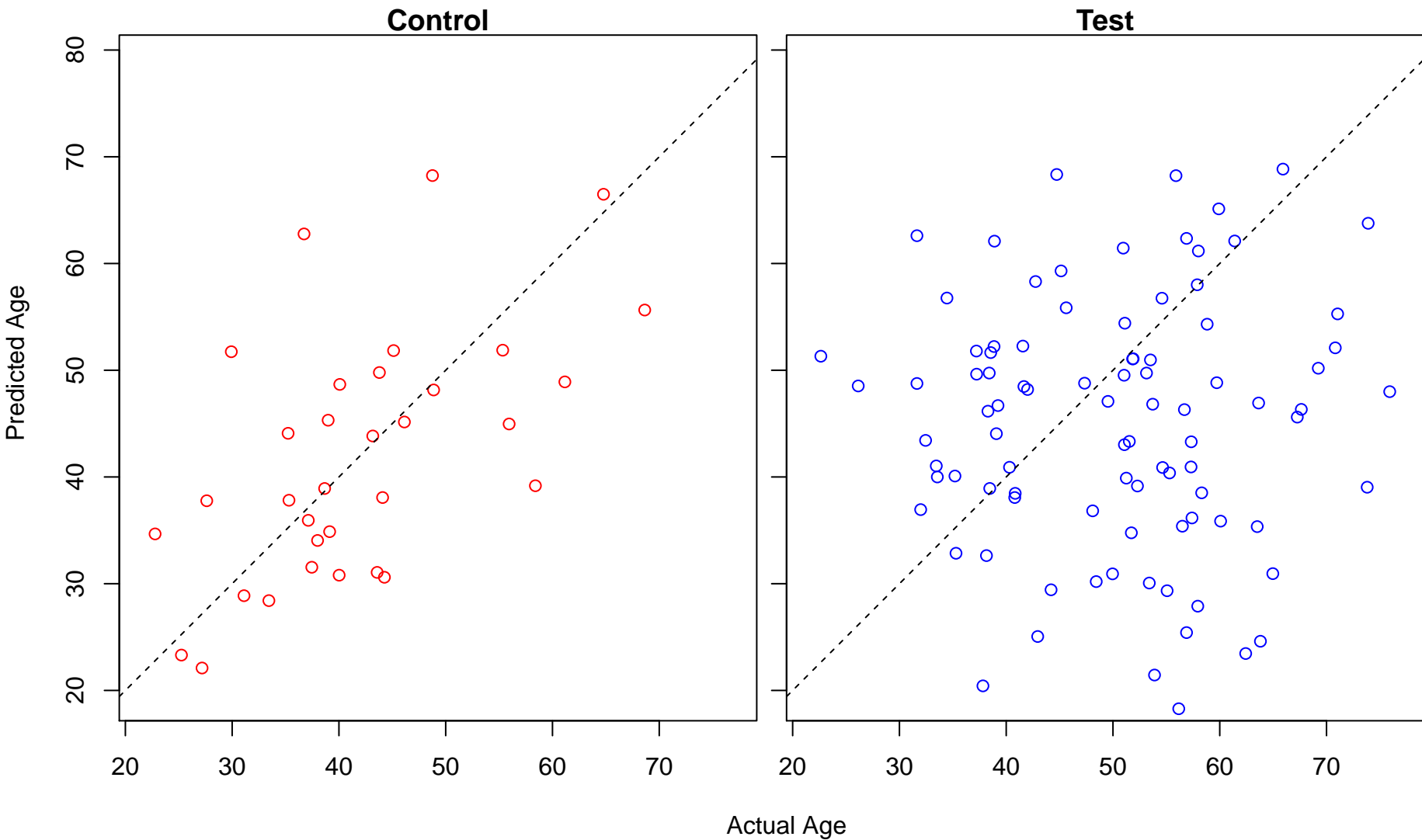
positive regulation of epidermal cell differentiation (Score: 1.362013)



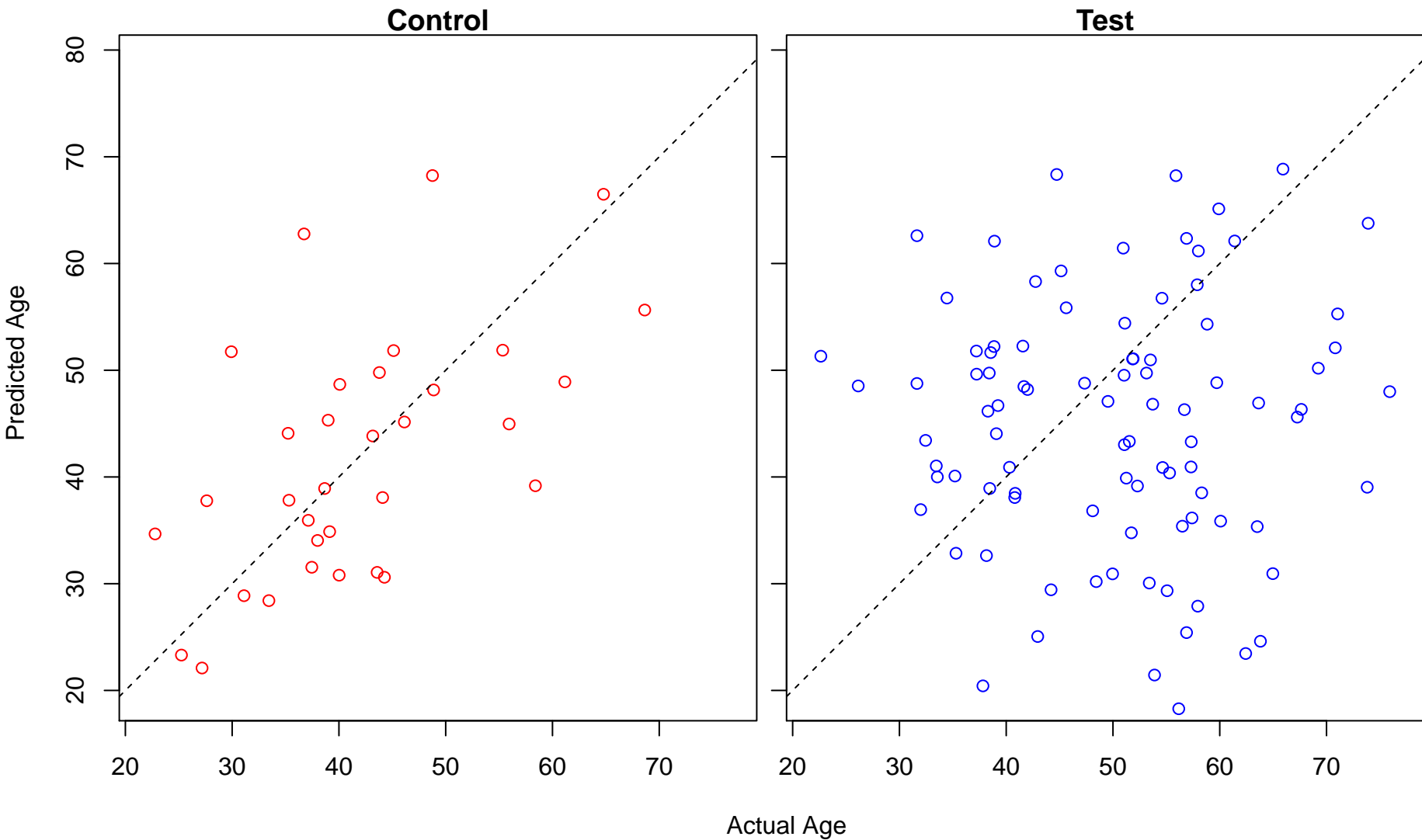
ceramide biosynthetic process (Score: 1.361657)



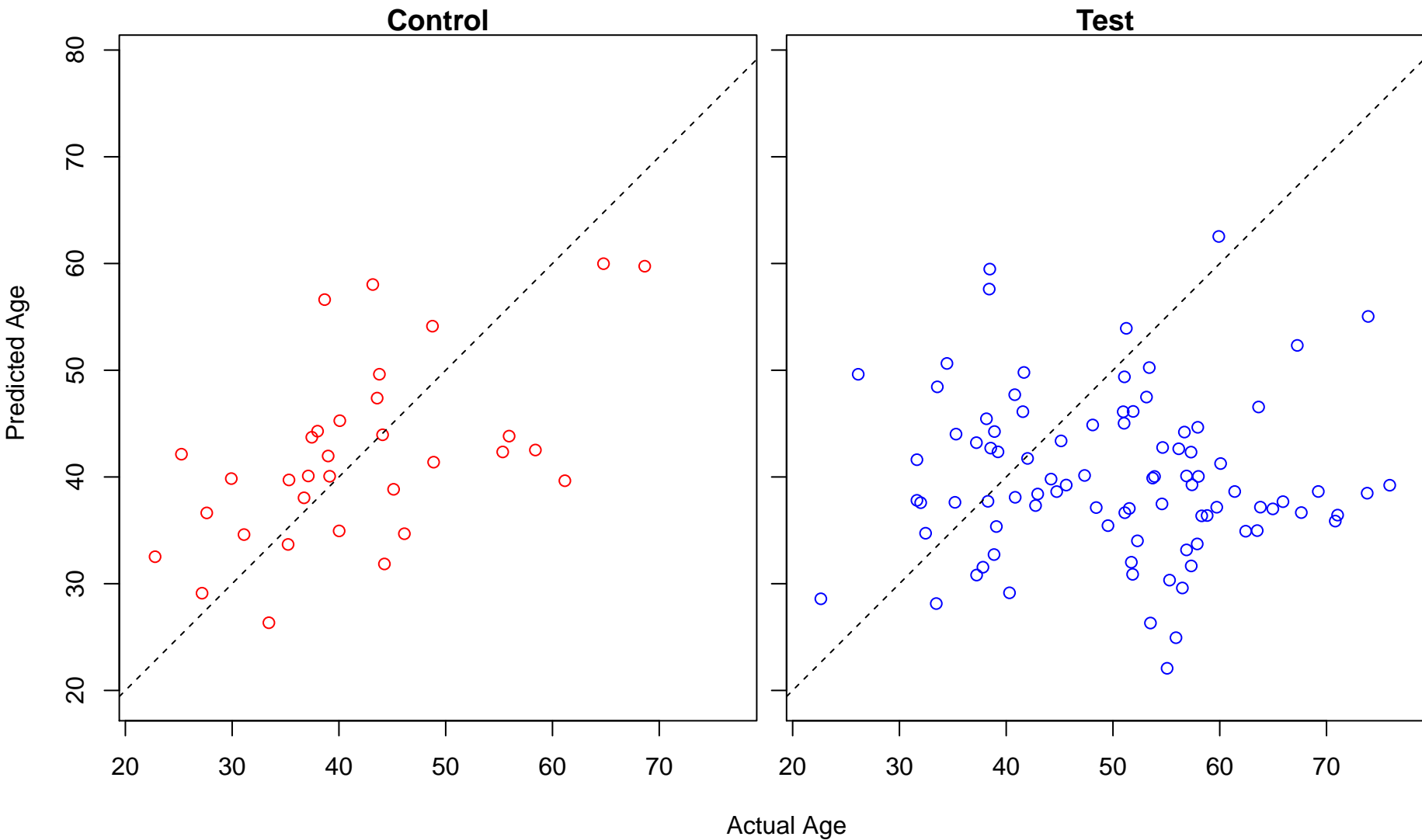
positive regulation of dephosphorylation (Score: 1.359154)



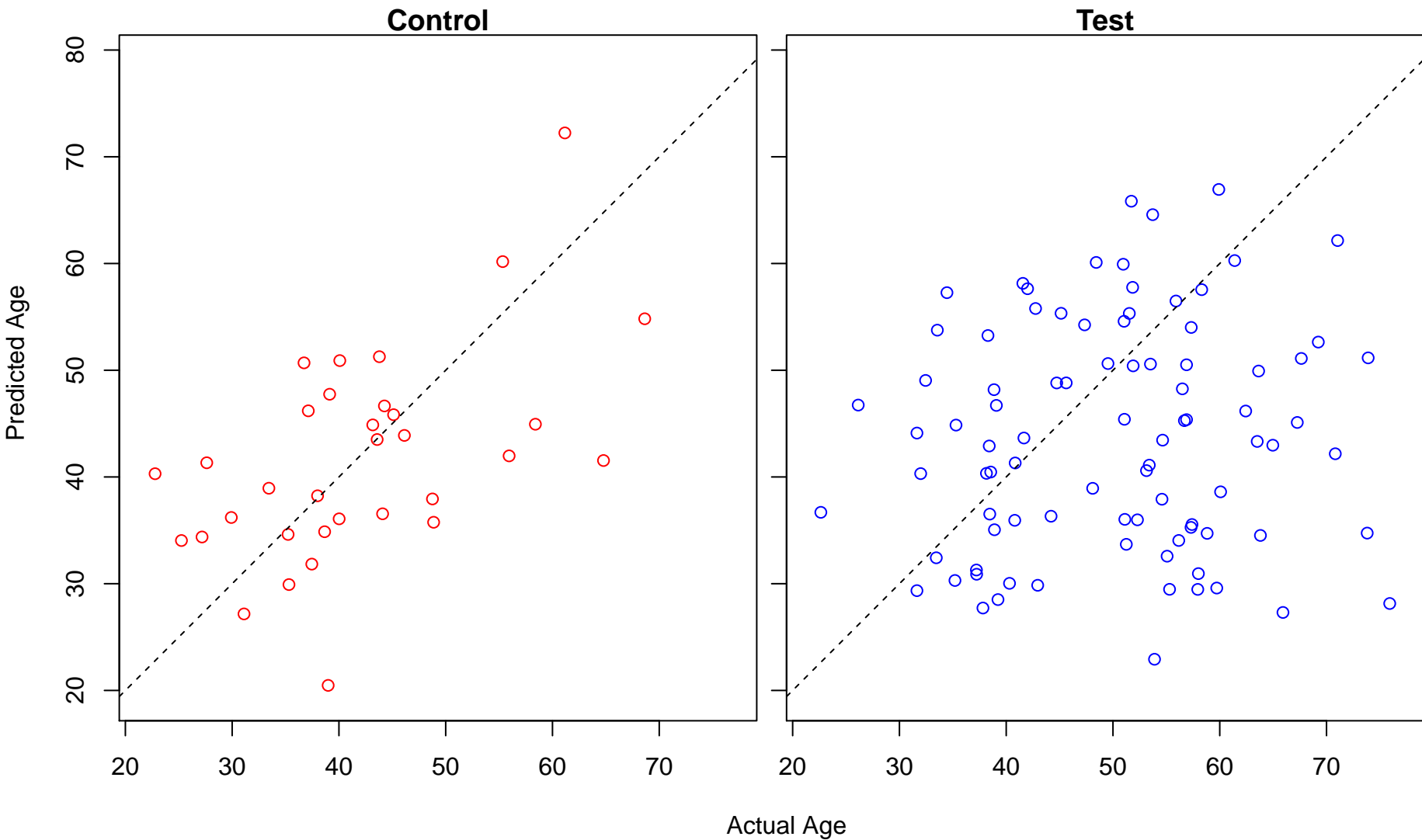
positive regulation of protein dephosphorylation (Score: 1.359154)



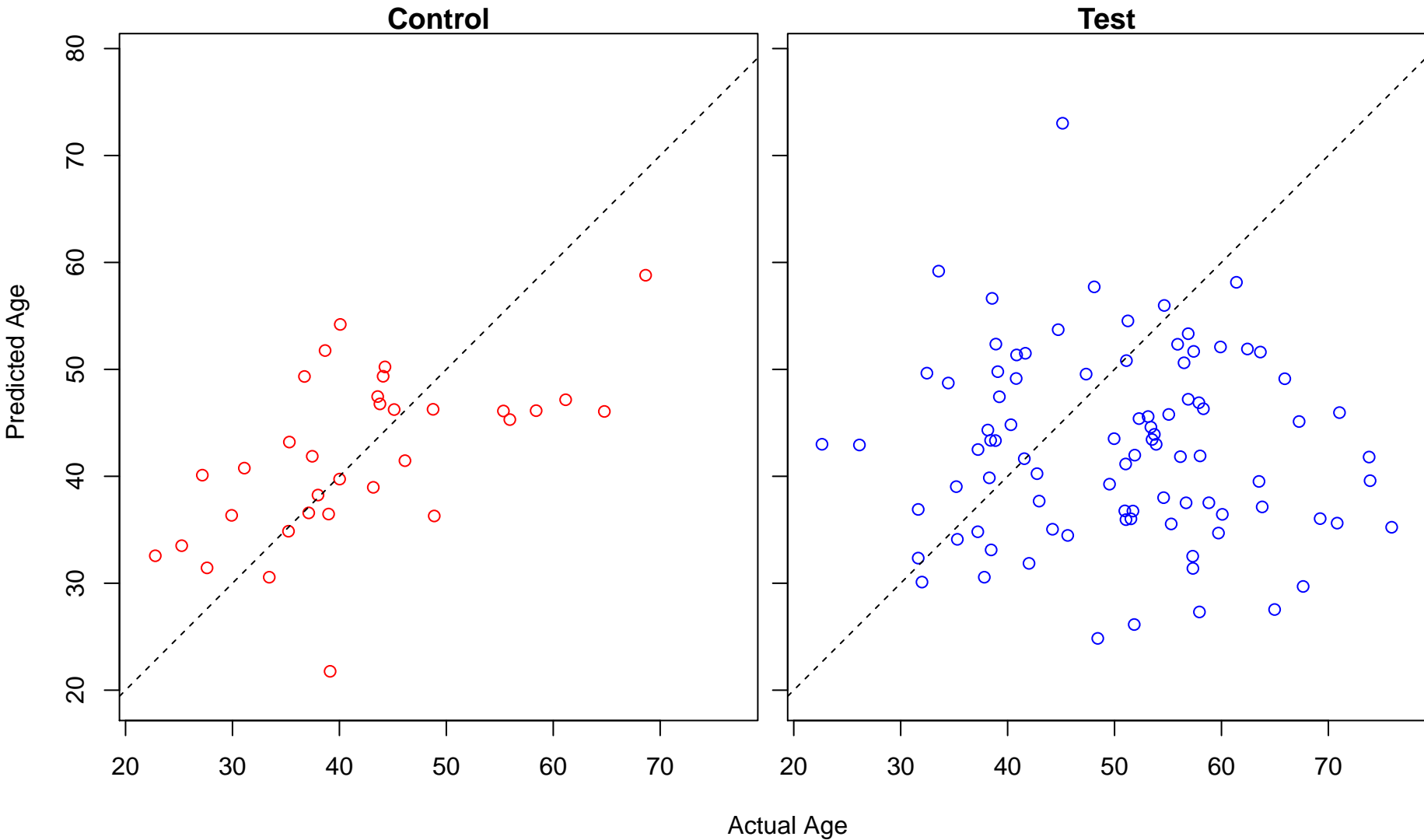
phospholipid catabolic process (Score: 1.358688)



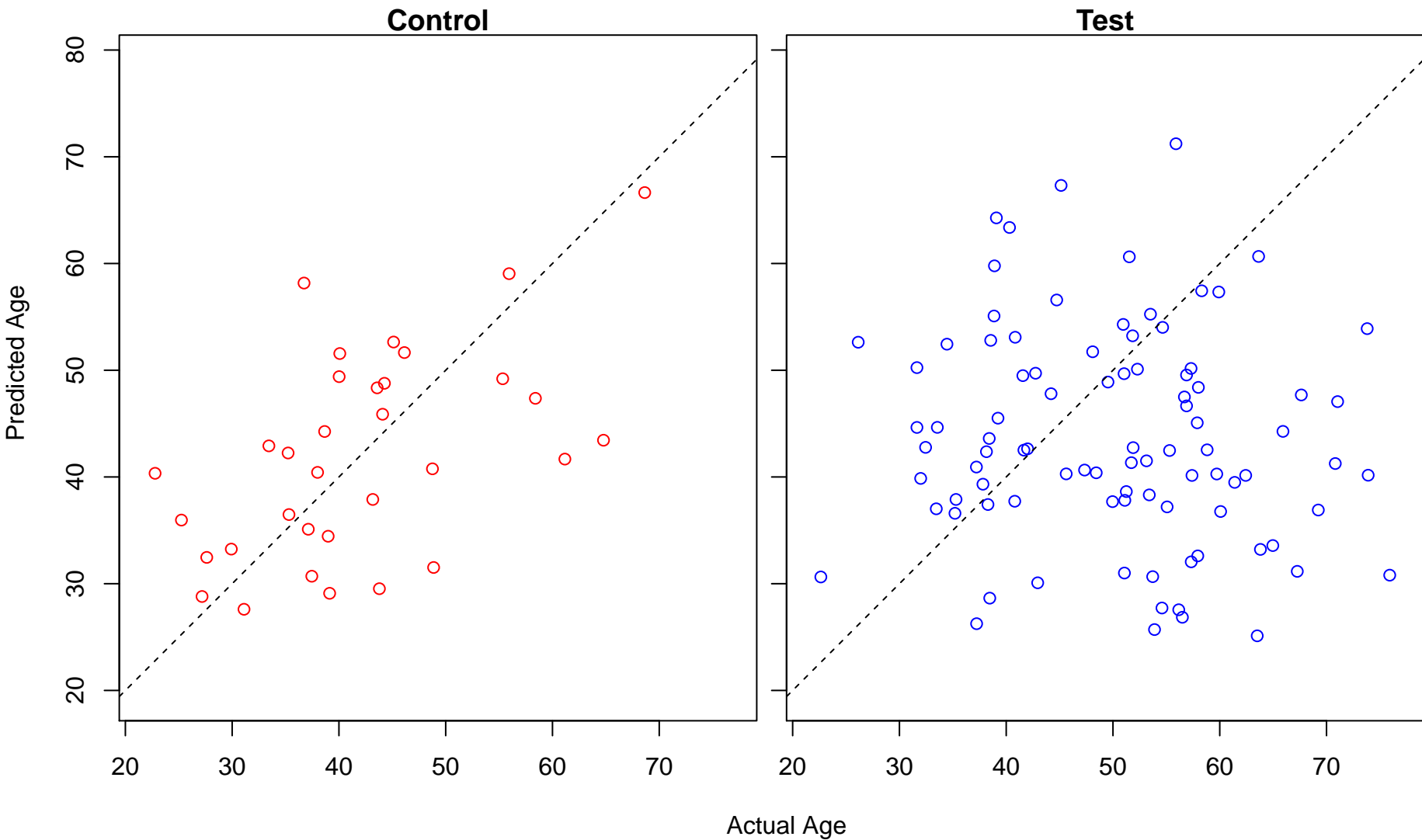
negative regulation of calcium ion transmembrane transporter activity (Score: 1.354762)



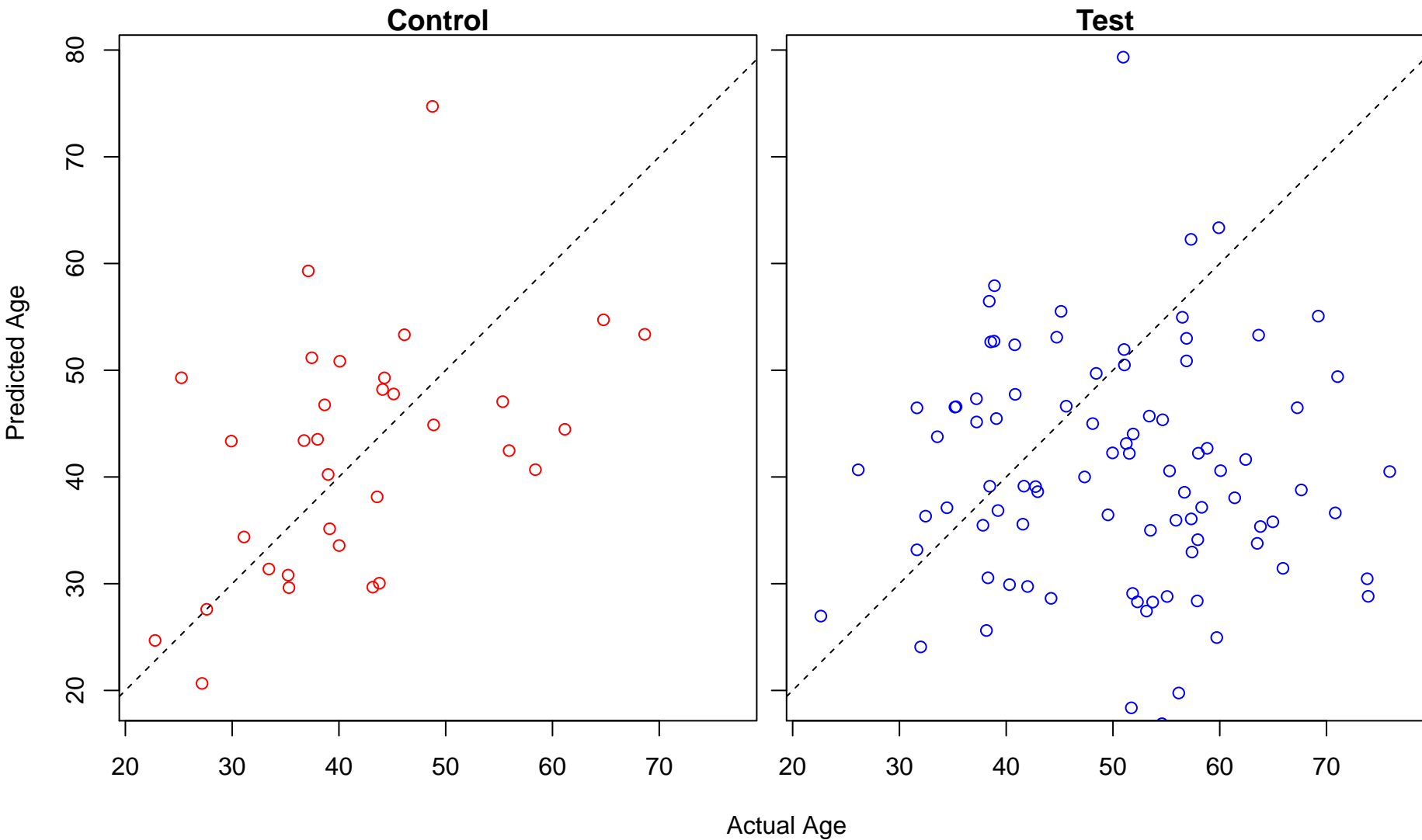
developmental process involved in reproduction (Score: 1.354084)



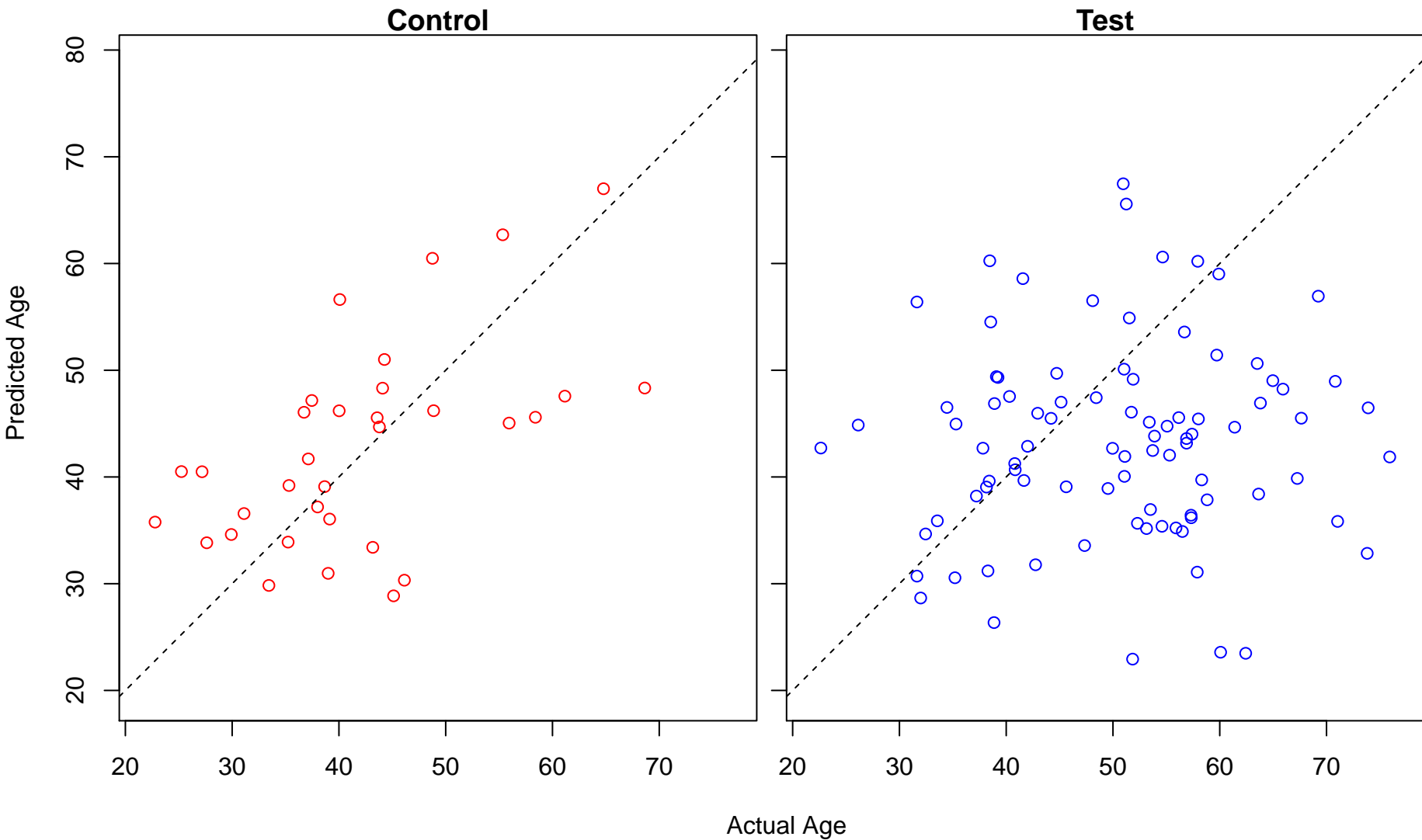
positive regulation of nitric oxide biosynthetic process (Score: 1.350859)



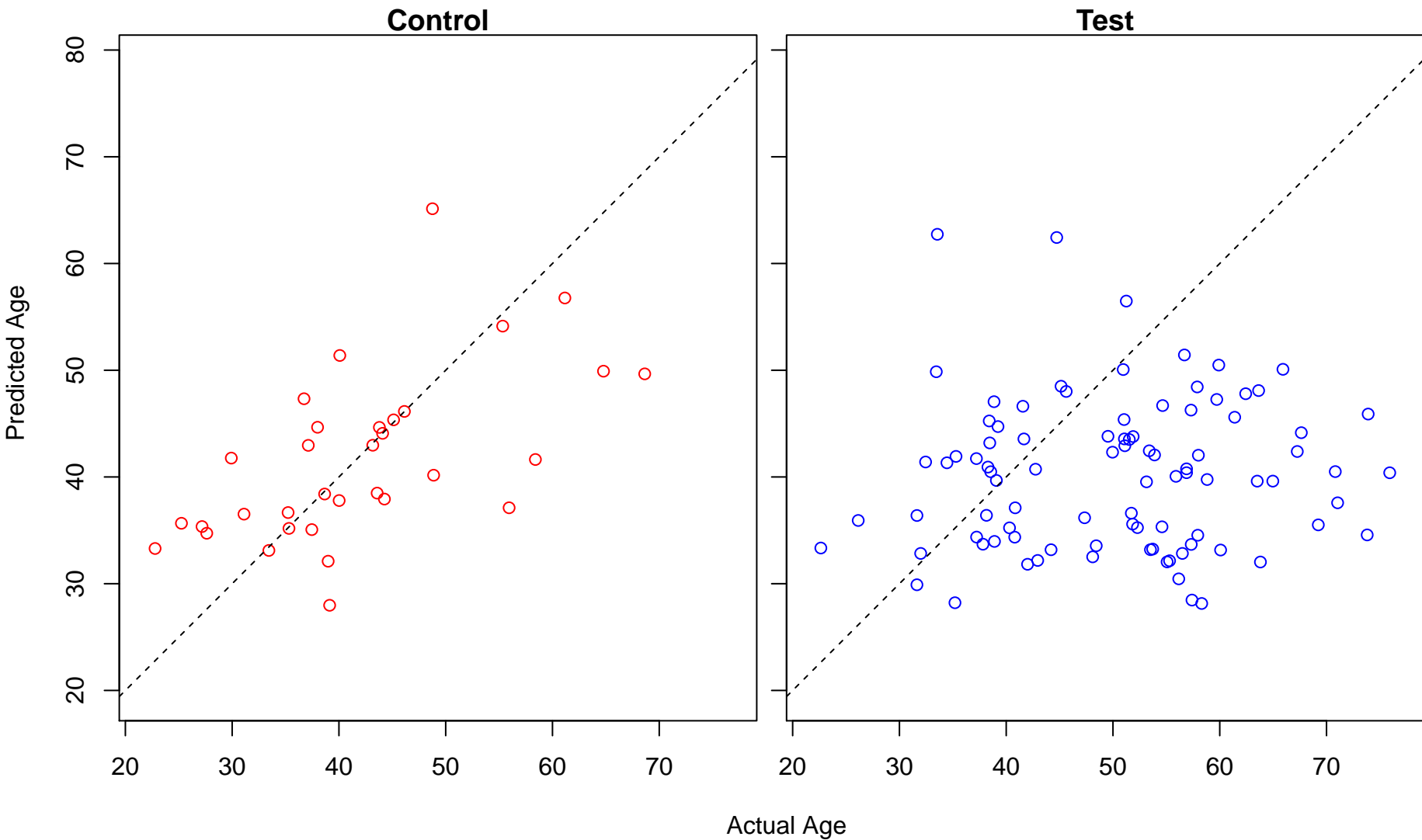
protein-lipid complex subunit organization (Score: 1.346865)



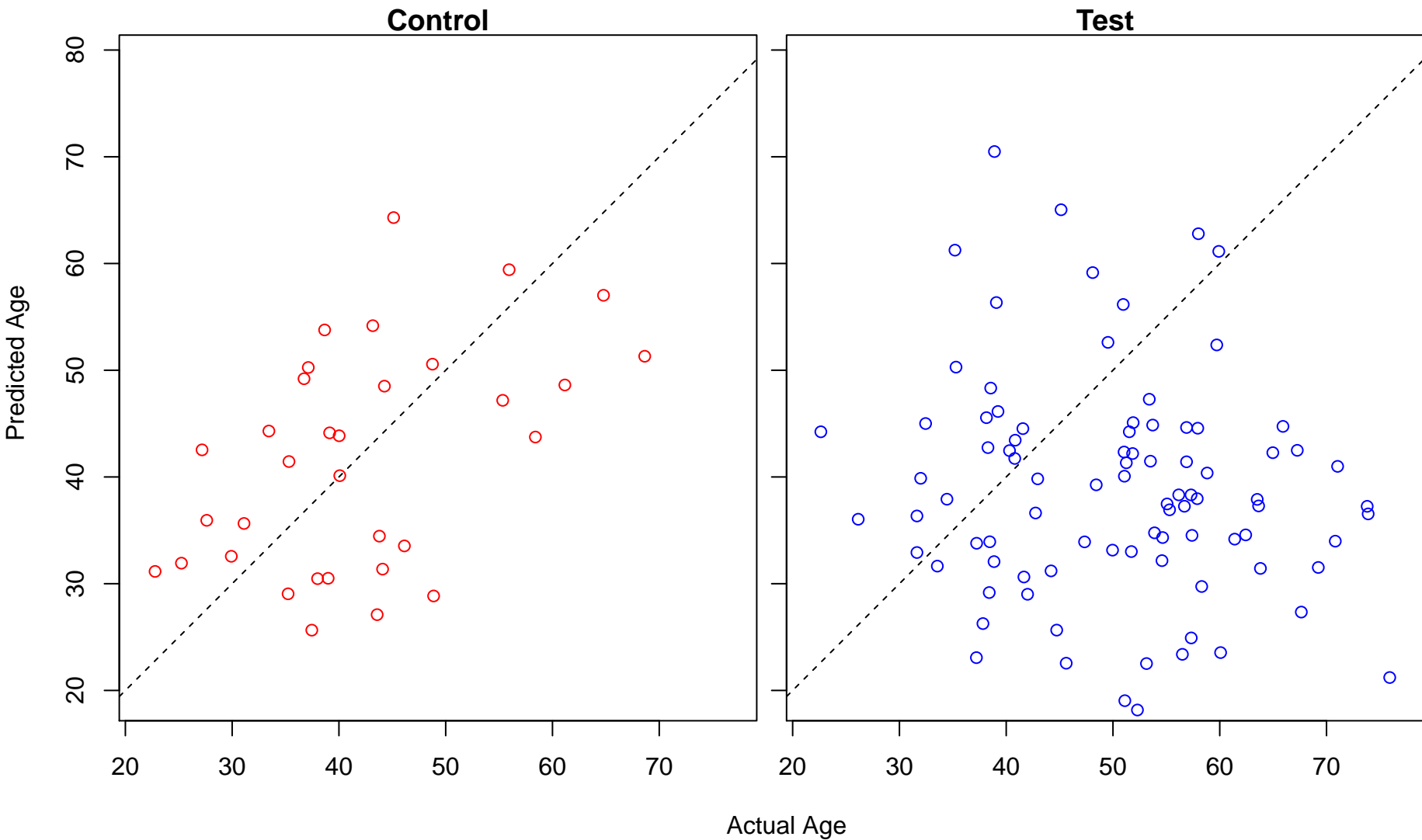
mitochondrion morphogenesis (Score: 1.346125)



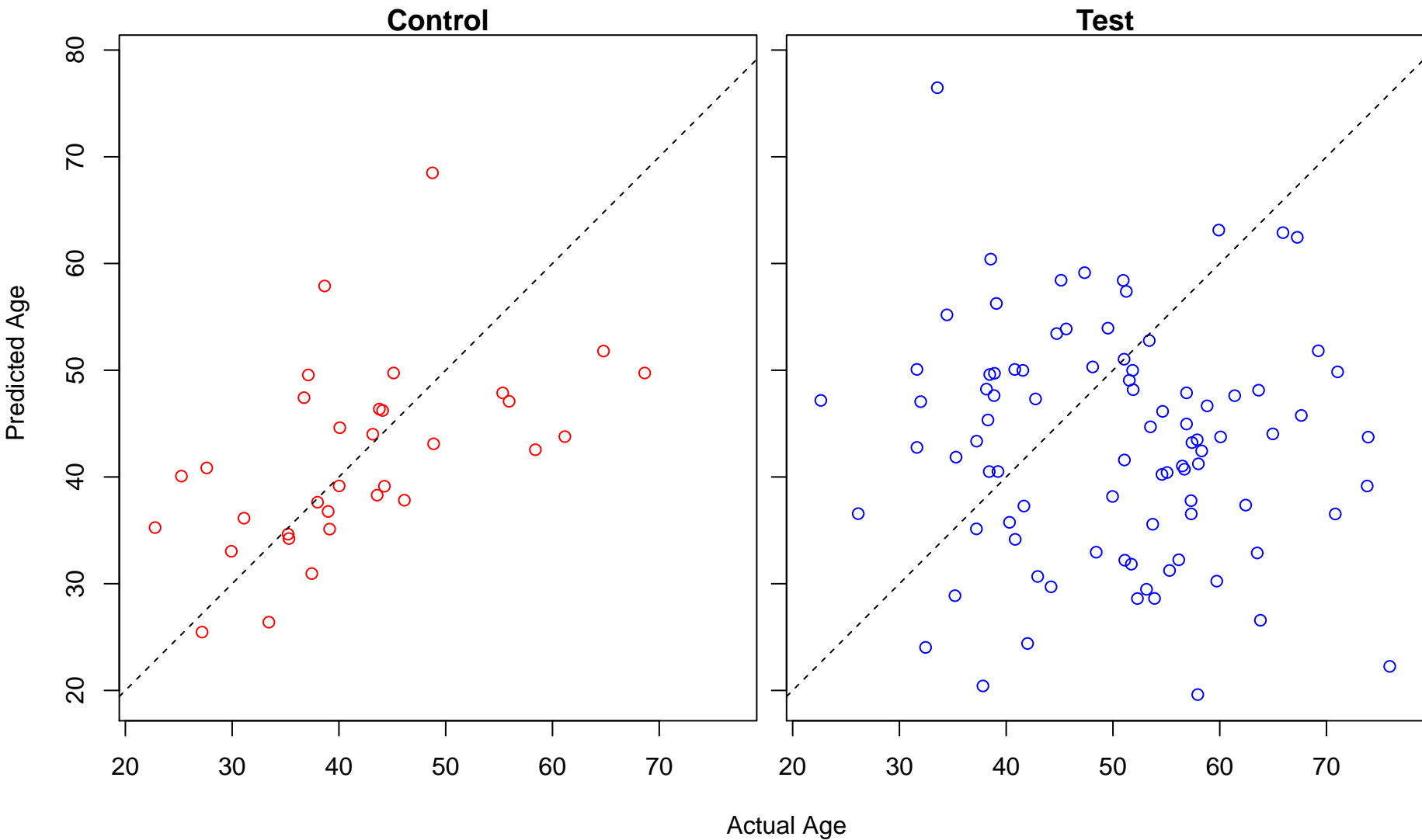
fibroblast growth factor receptor signaling pathway (Score: 1.345785)



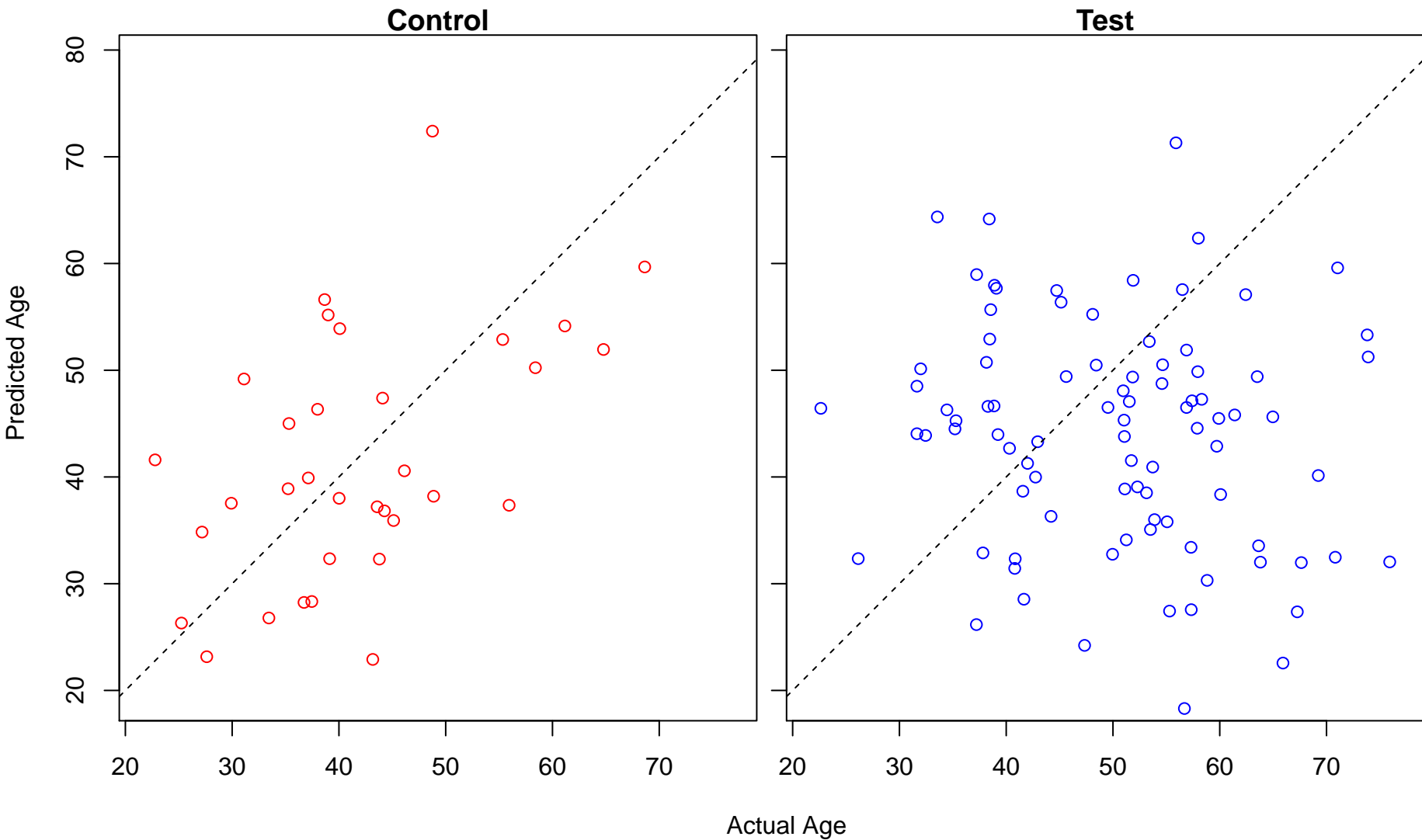
iron ion transport (Score: 1.343848)



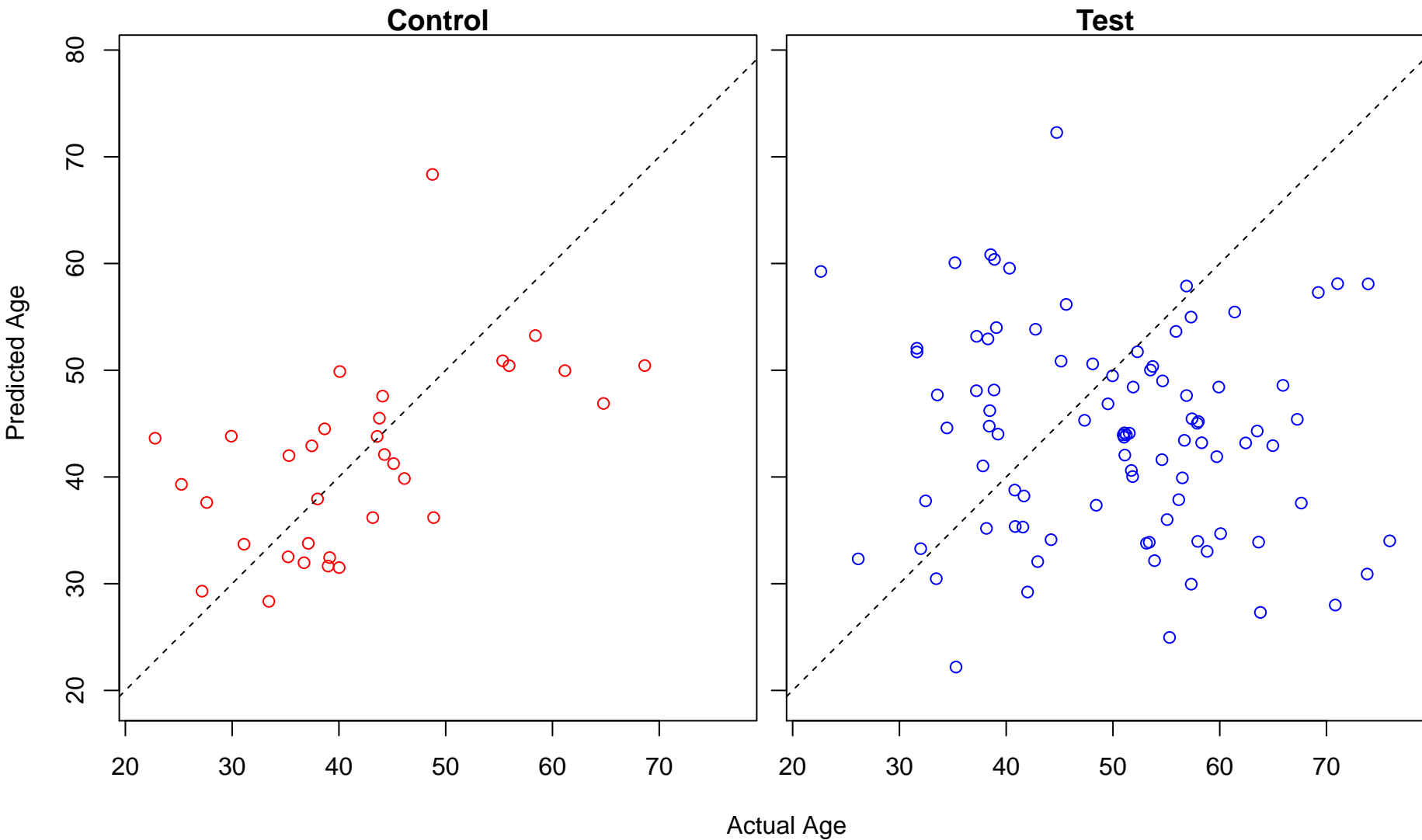
cell division (Score: 1.331700)



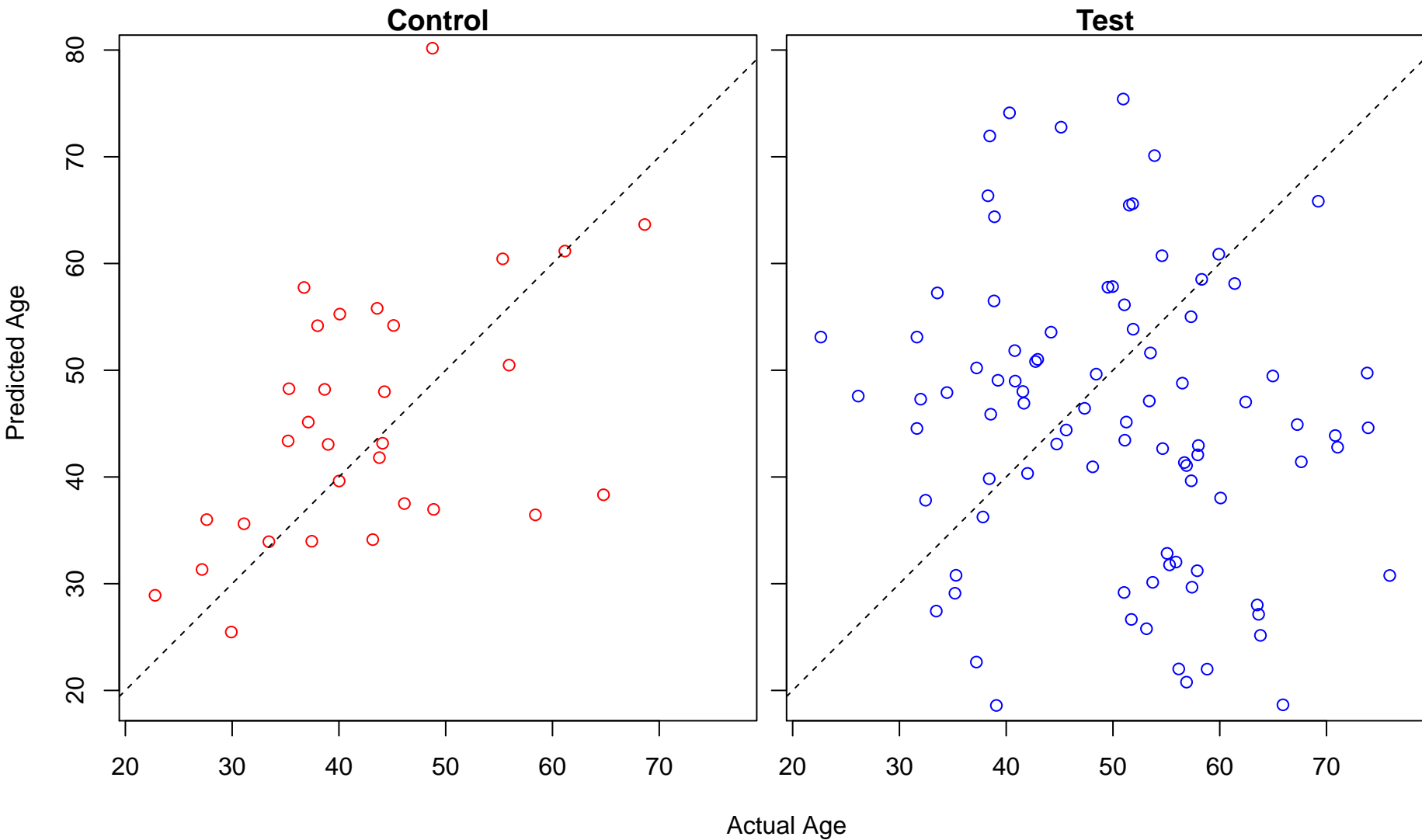
bone development (Score: 1.324946)



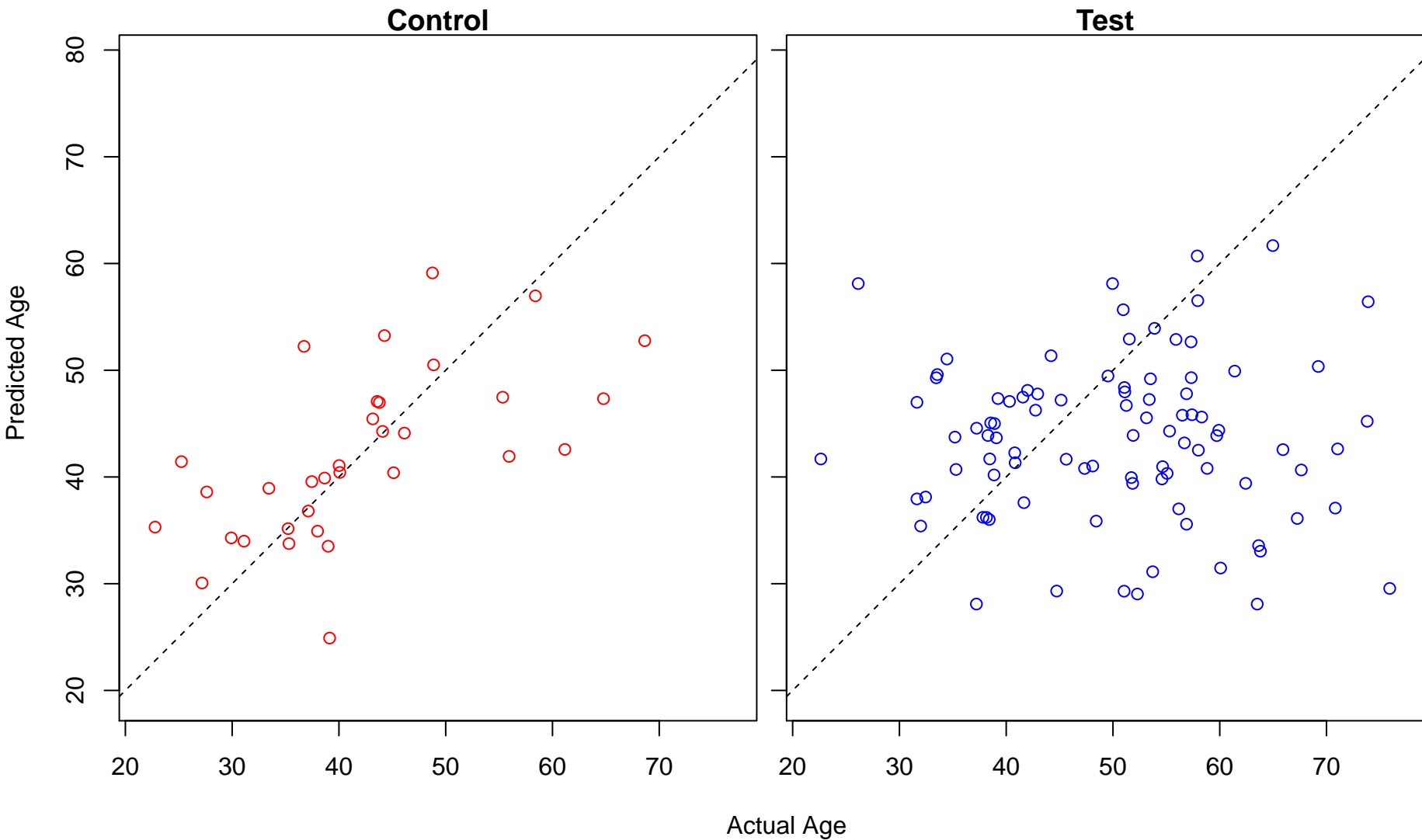
receptor clustering (Score: 1.324454)



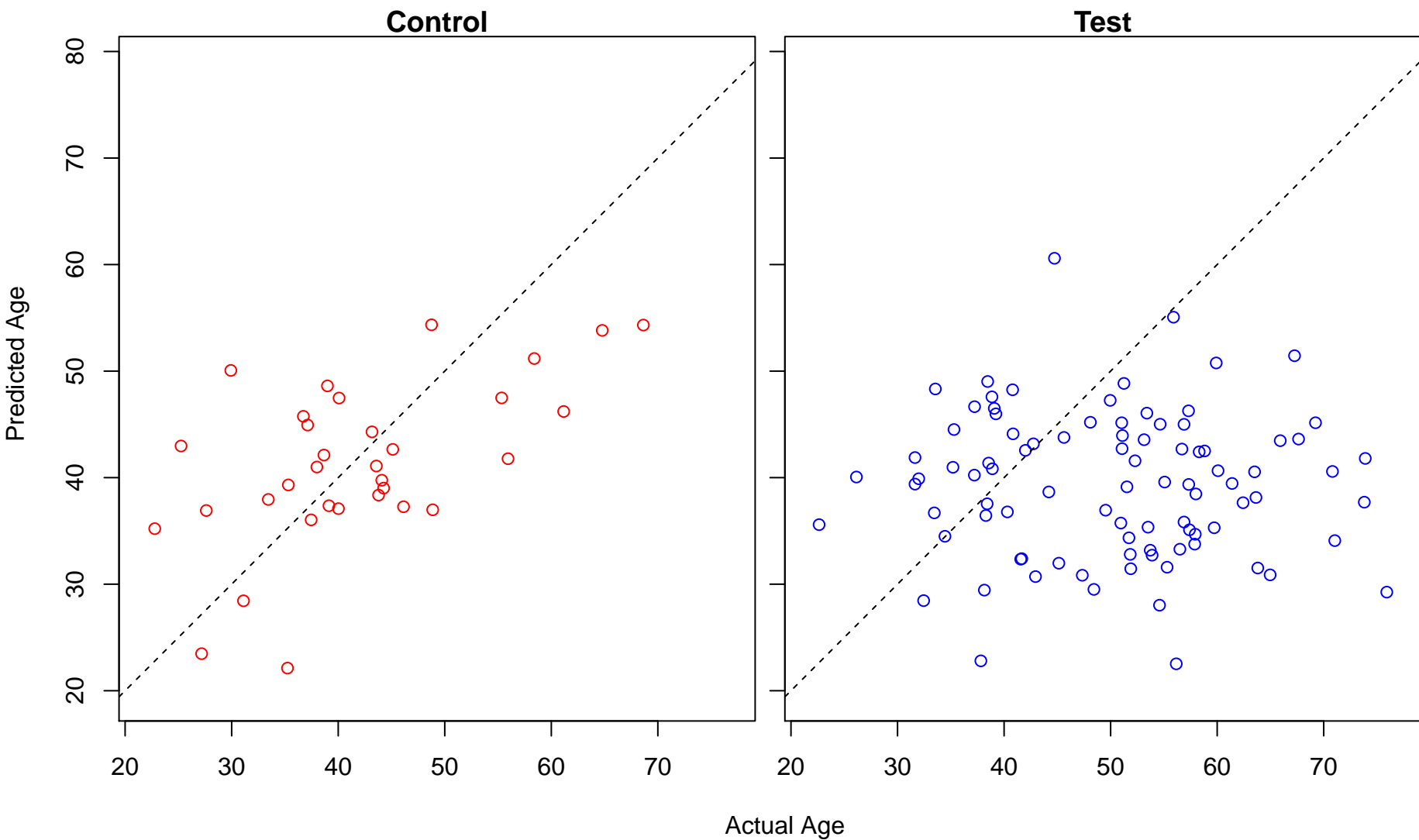
retina homeostasis (Score: 1.322754)



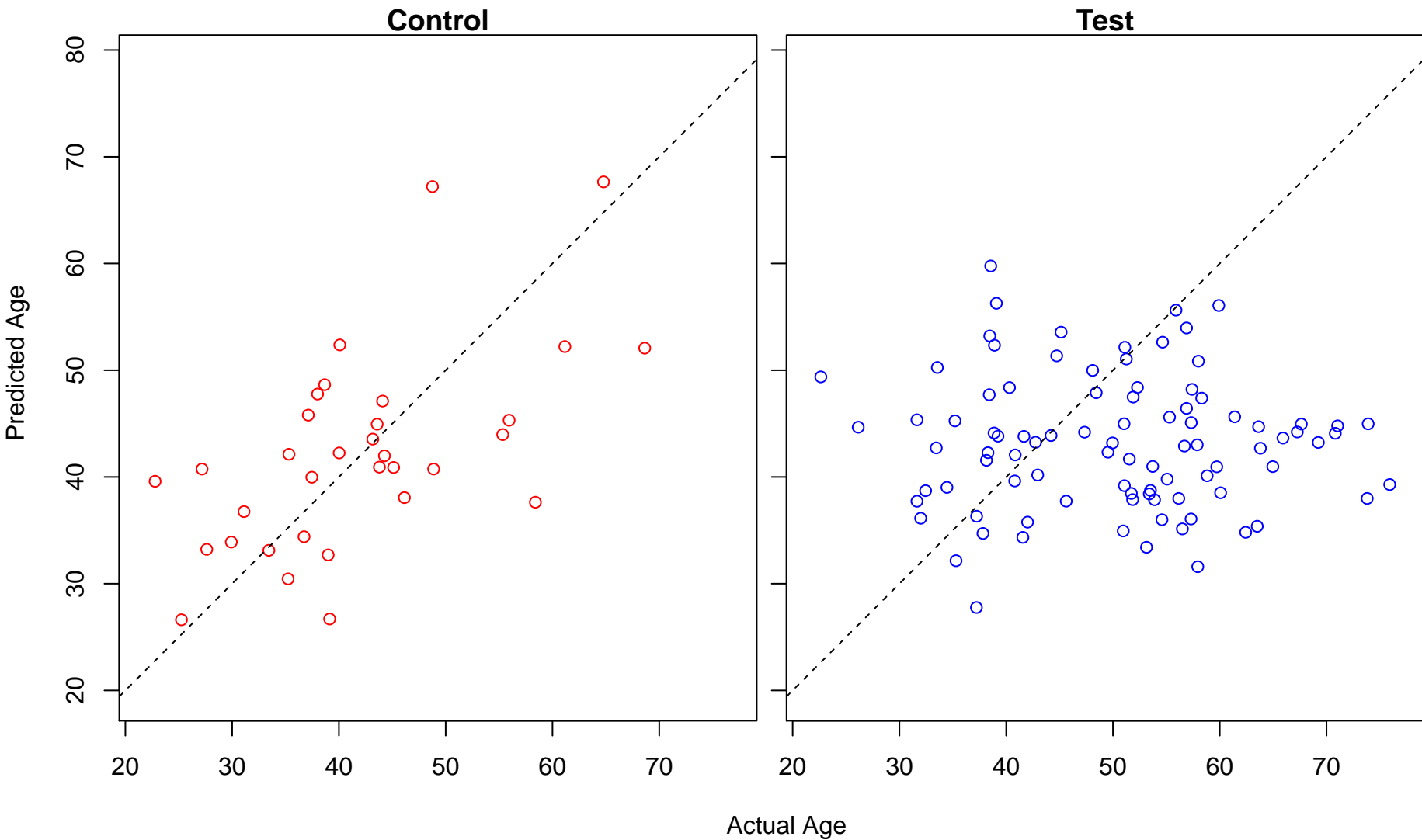
complement activation, classical pathway (Score: 1.319585)



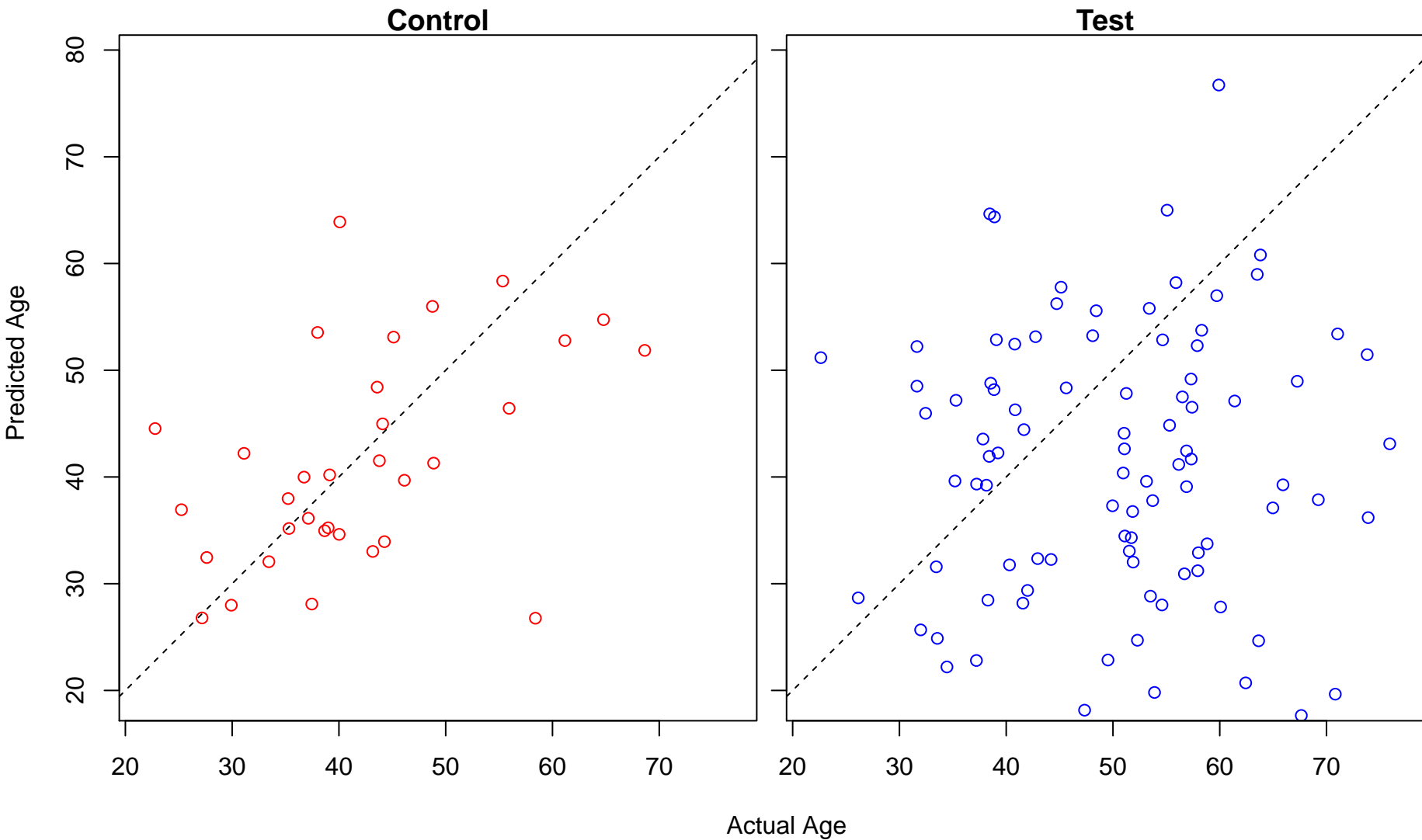
lipid homeostasis (Score: 1.319373)



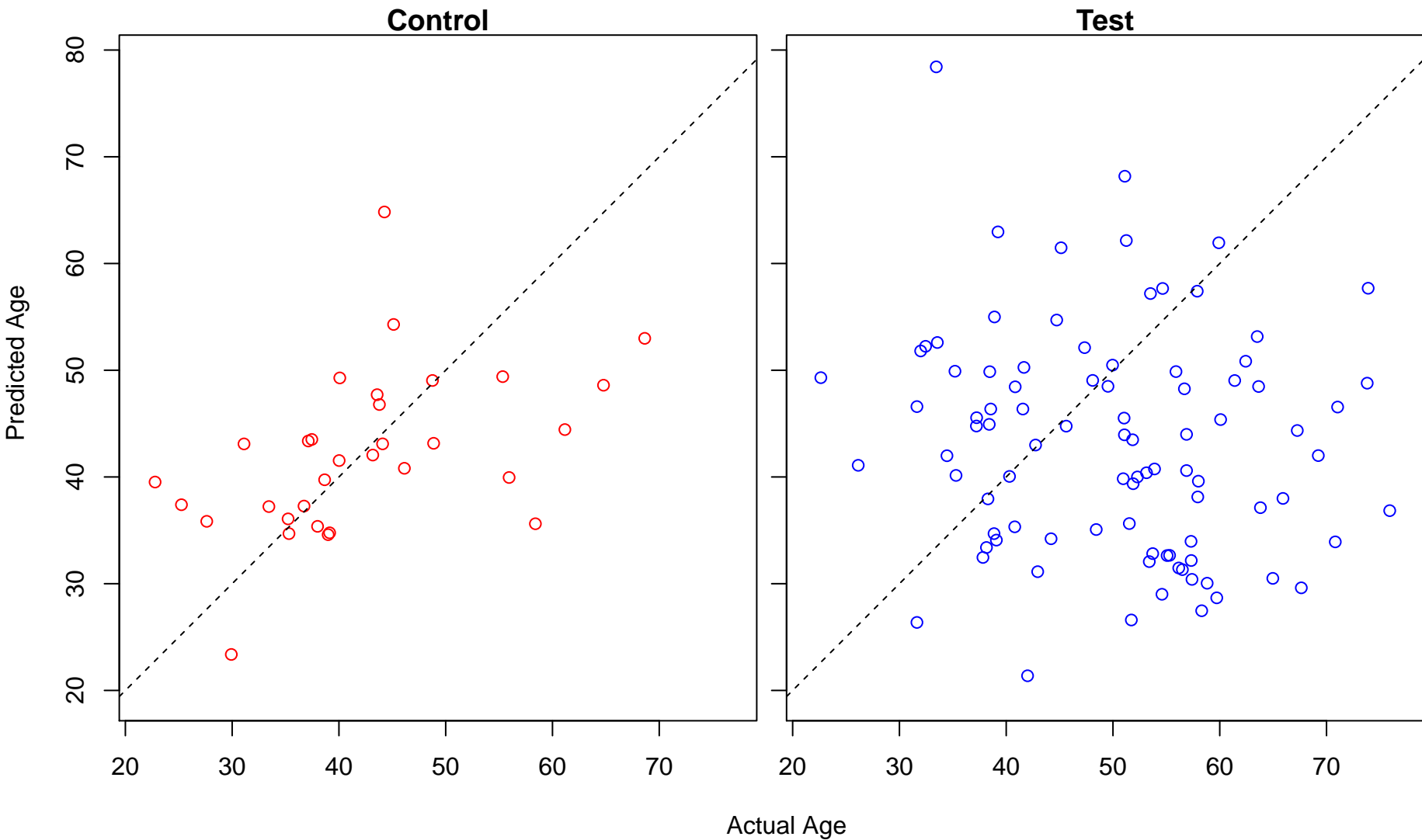
regulation of mitochondrial fission (Score: 1.312998)



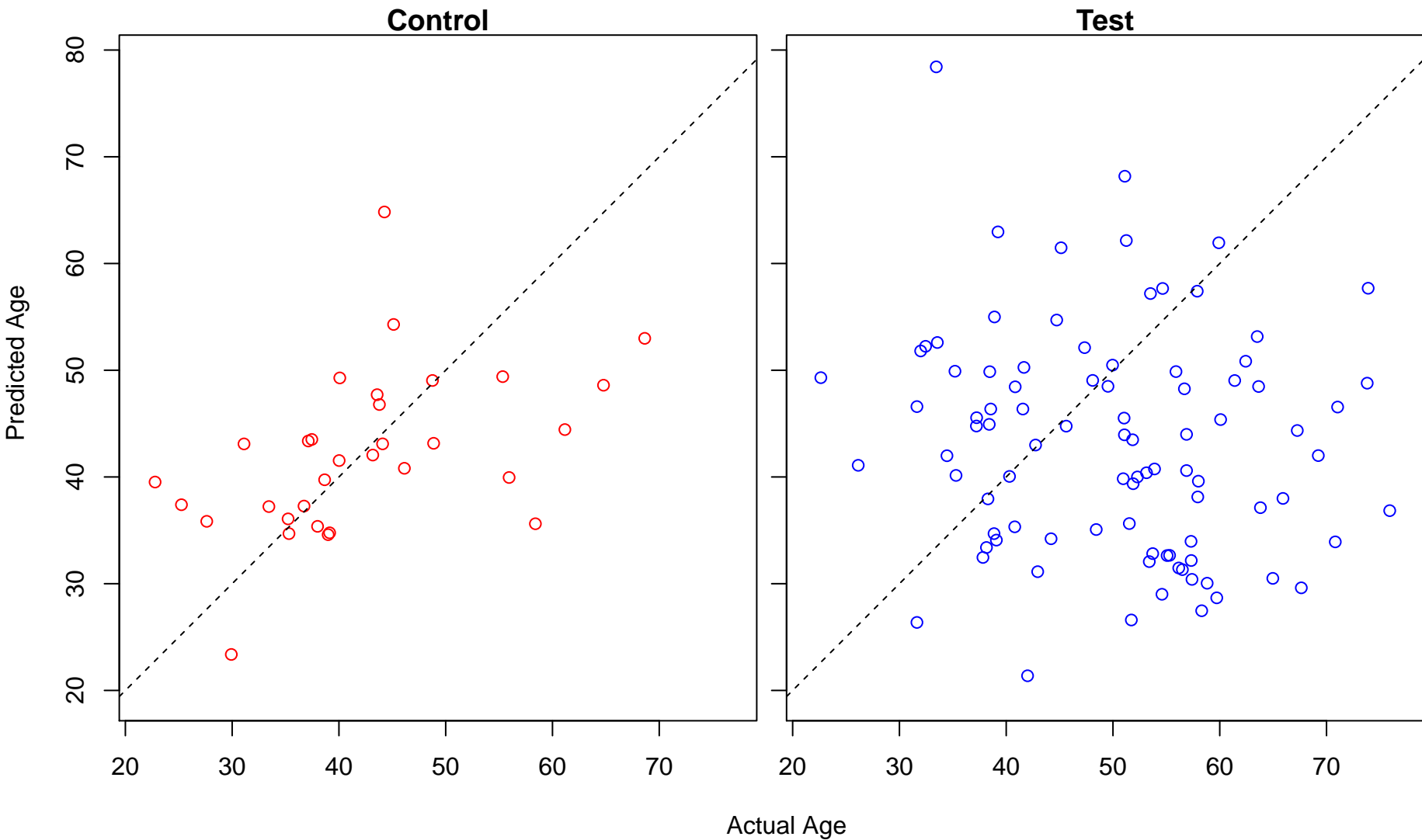
negative regulation of blood vessel endothelial cell migration (Score: 1.312713)



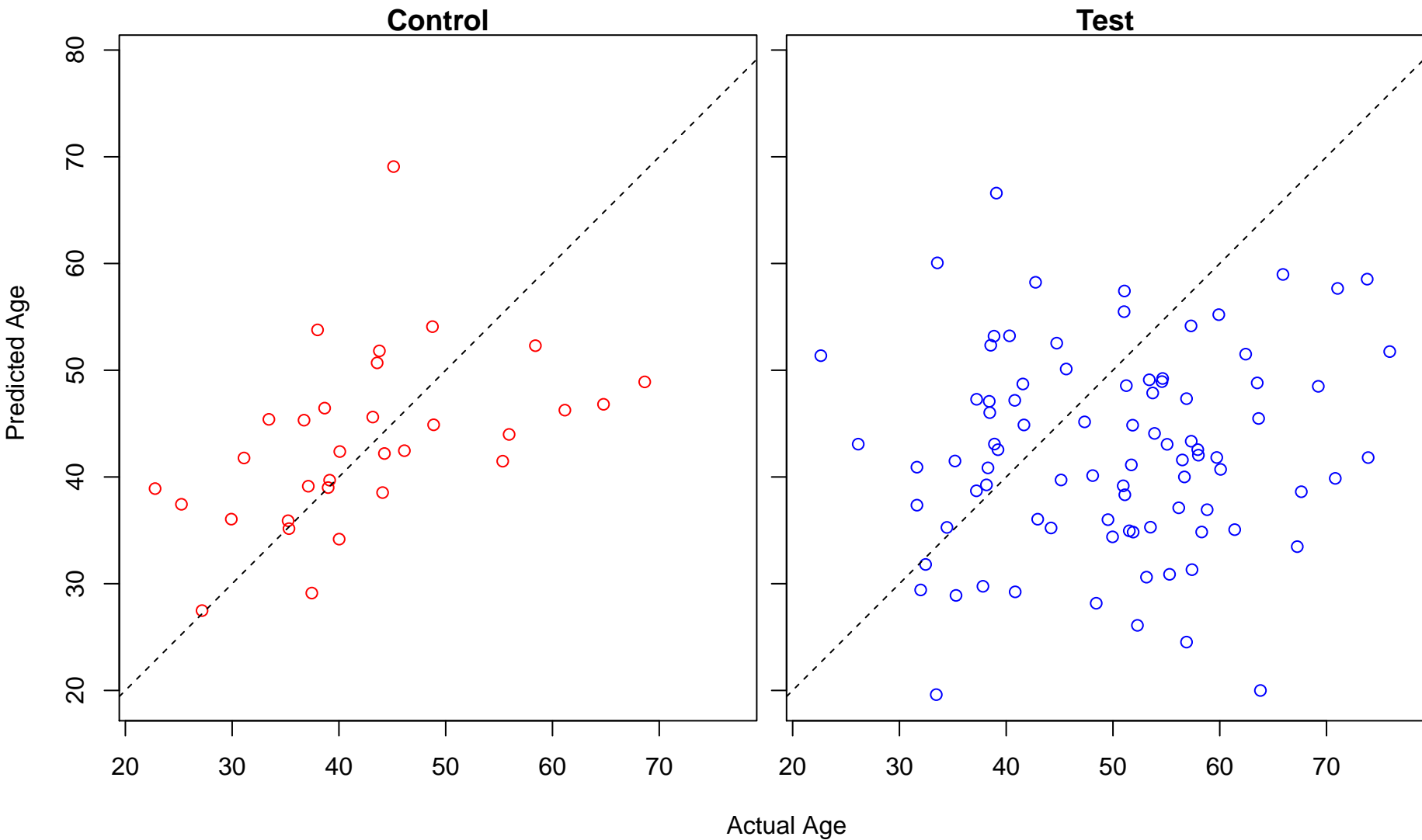
male gonad development (Score: 1.310521)



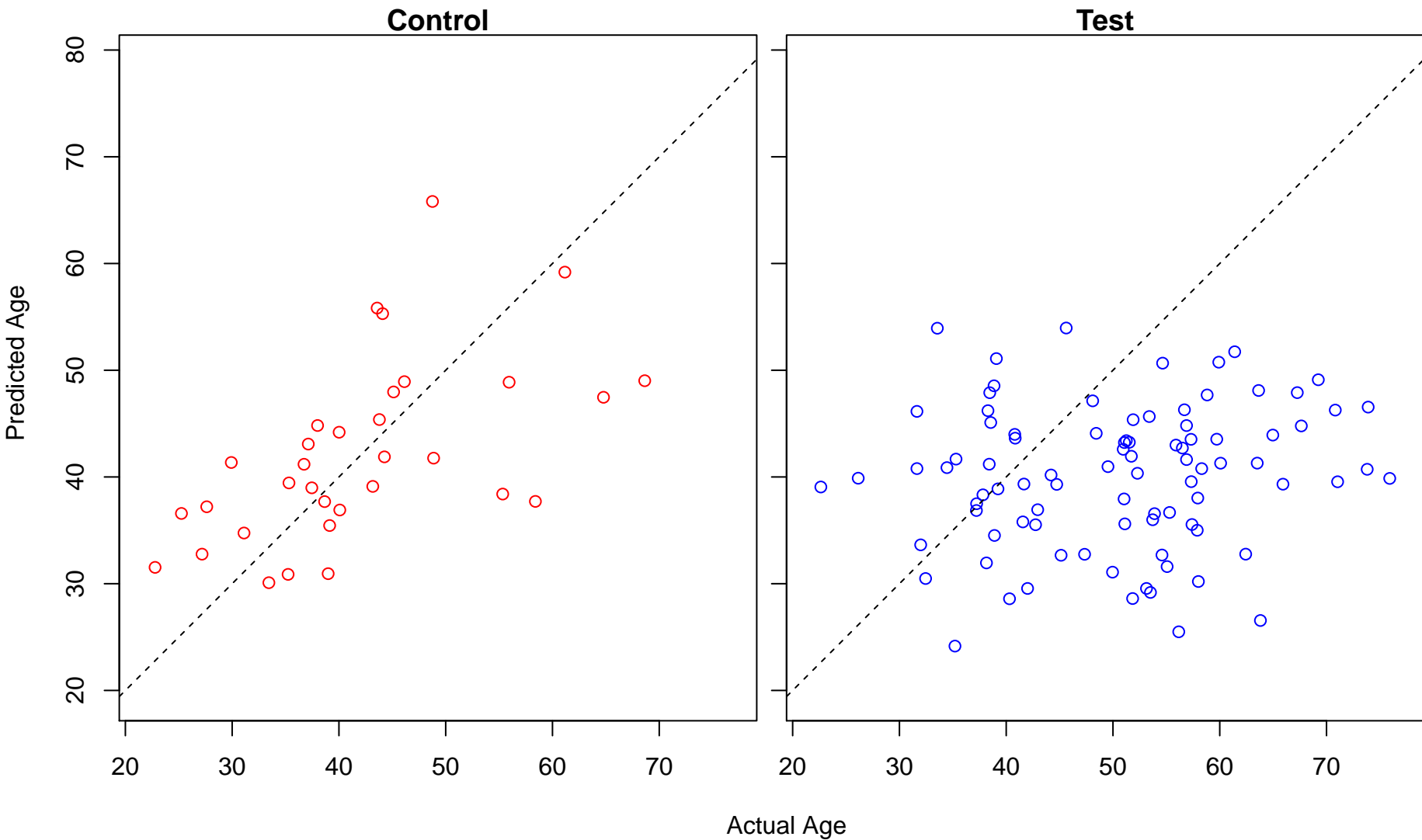
development of primary male sexual characteristics (Score: 1.310521)



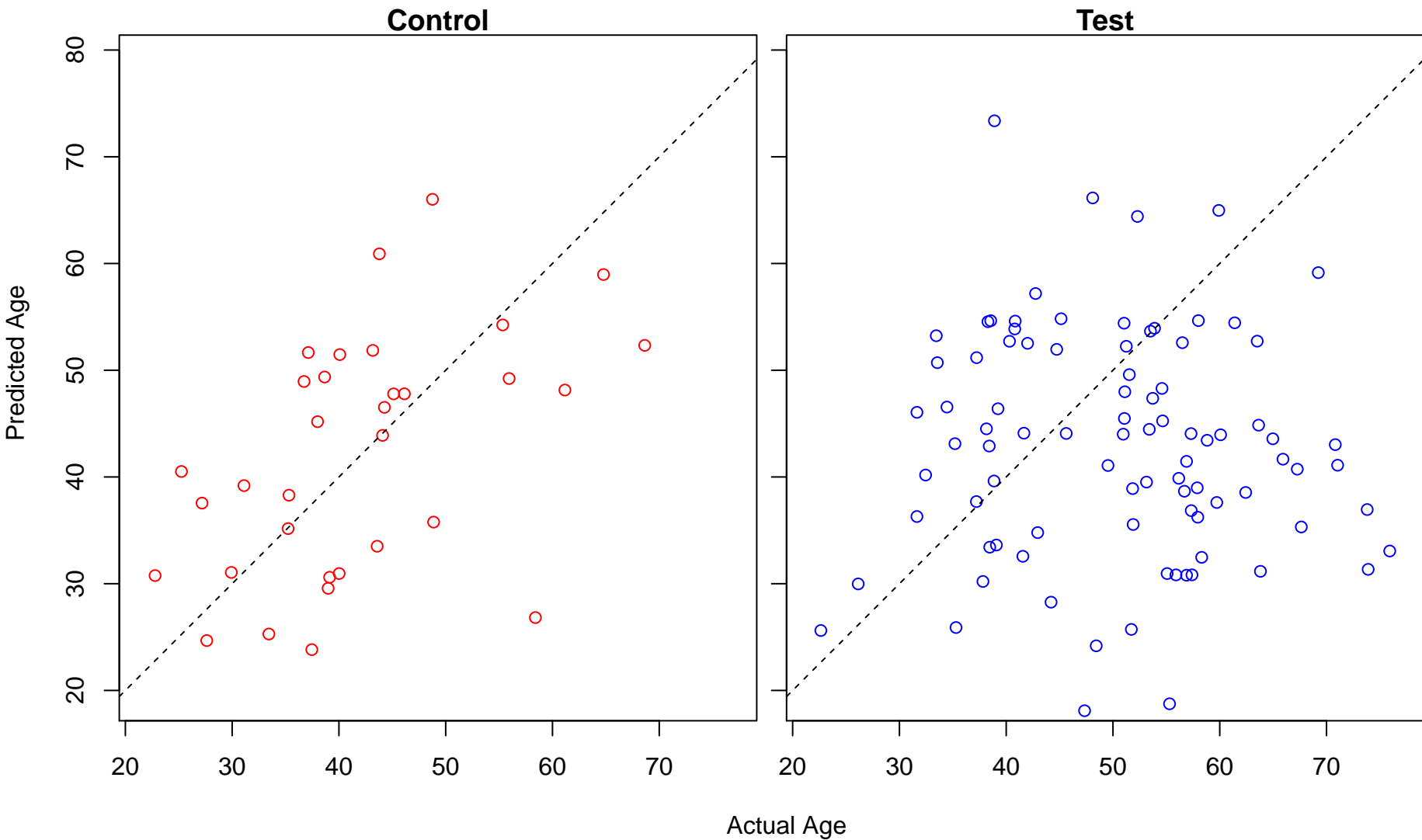
synapse assembly (Score: 1.309900)



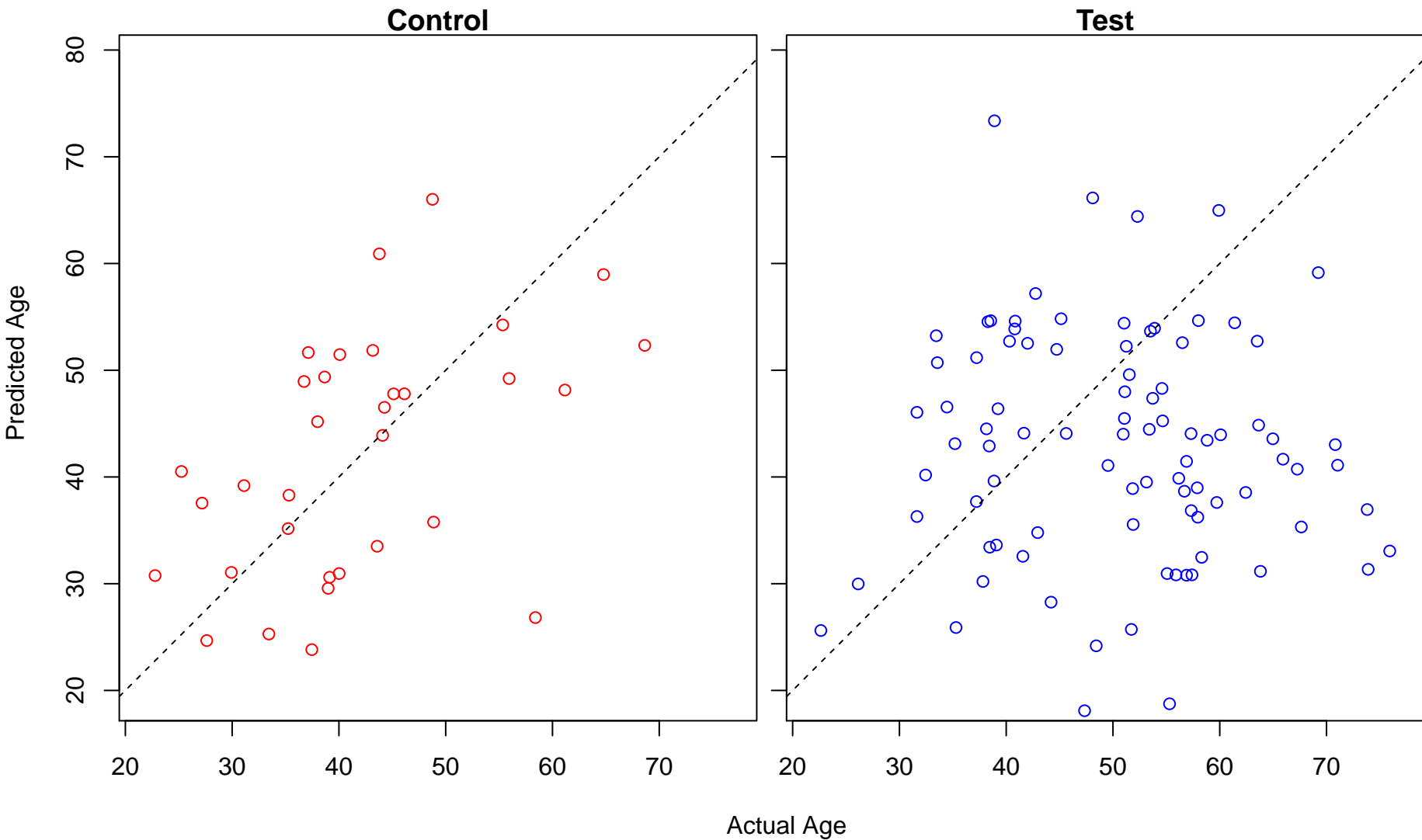
positive regulation of cell junction assembly (Score: 1.309168)



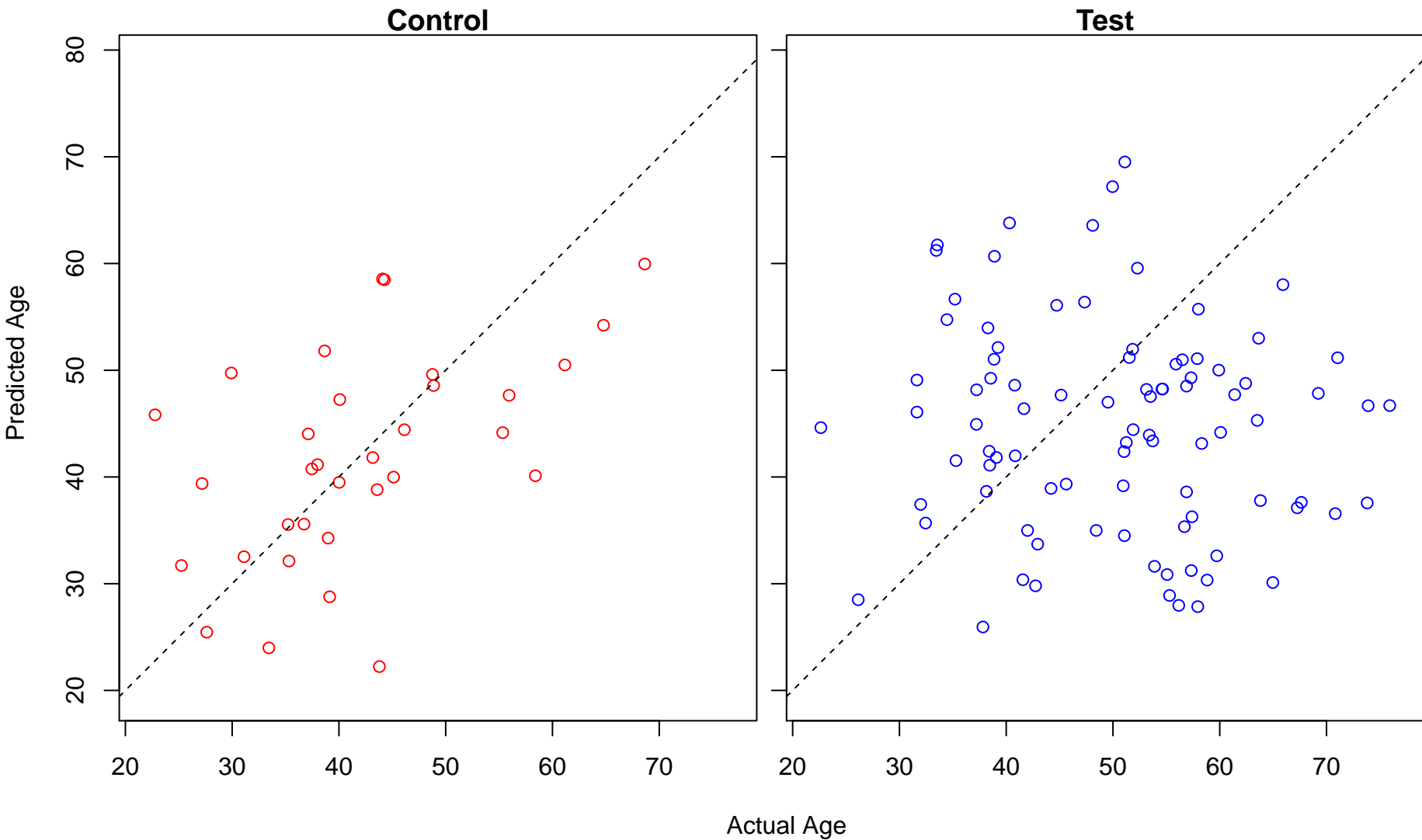
reciprocal meiotic recombination (Score: 1.306792)



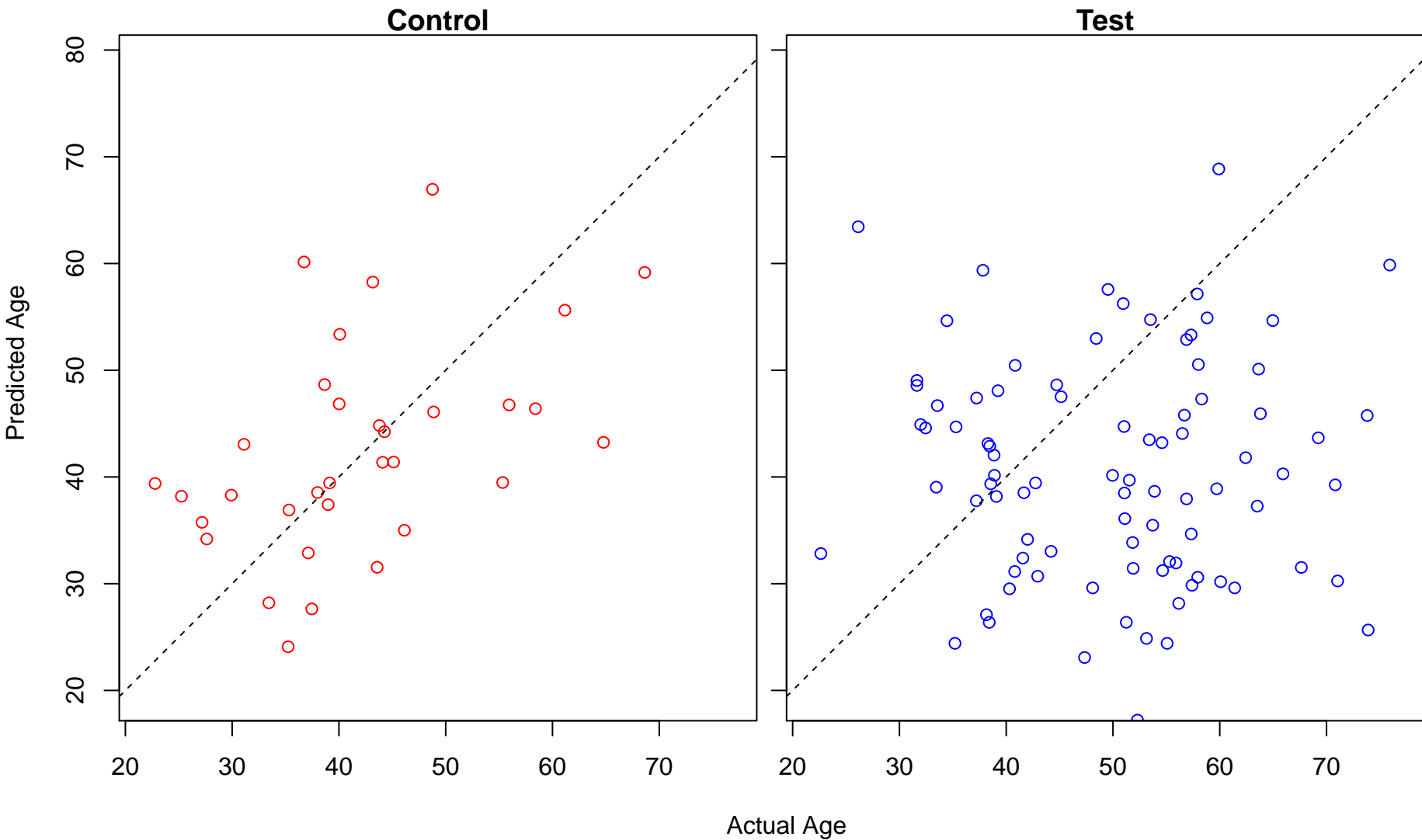
reciprocal DNA recombination (Score: 1.306792)



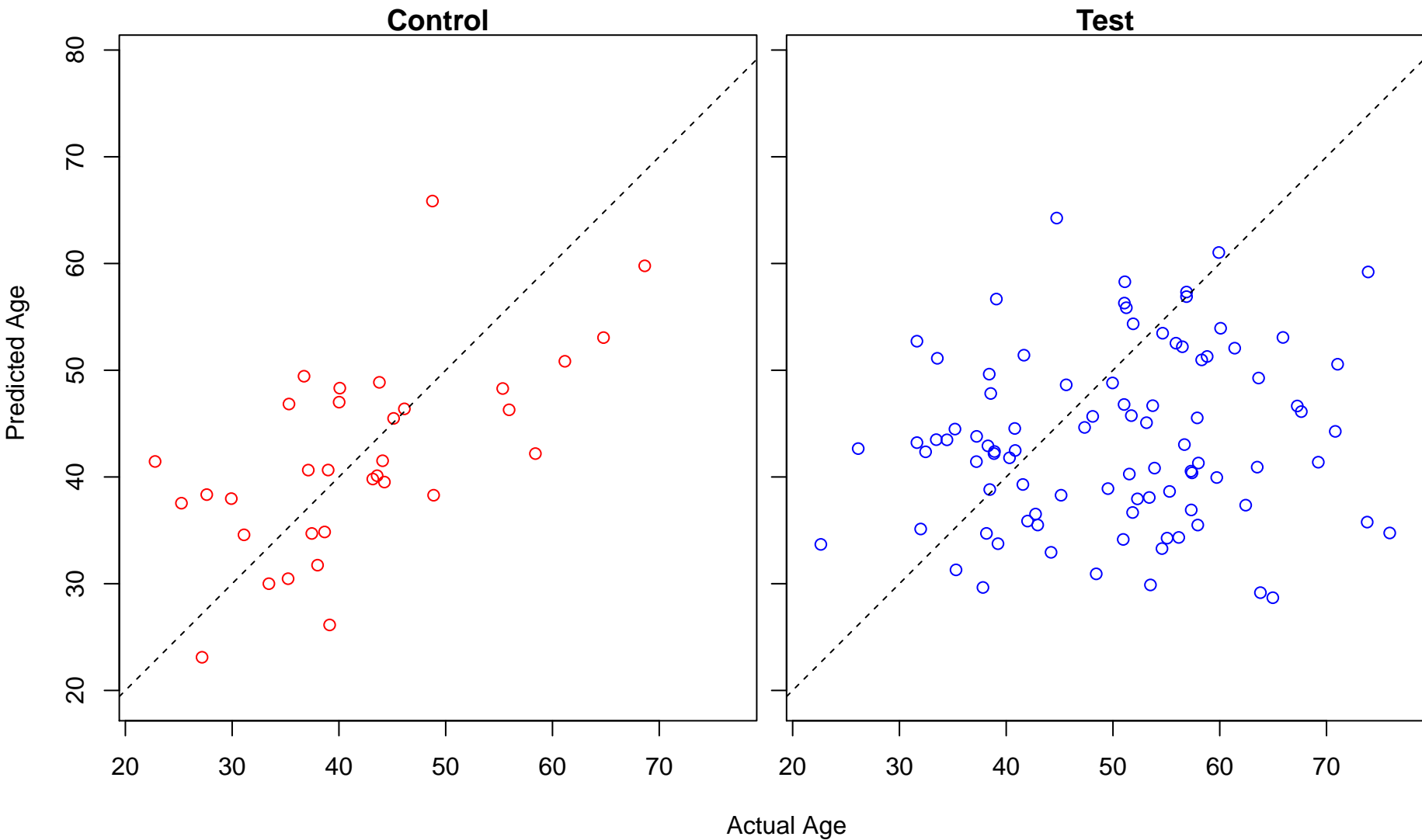
peptidyl-arginine modification (Score: 1.306223)



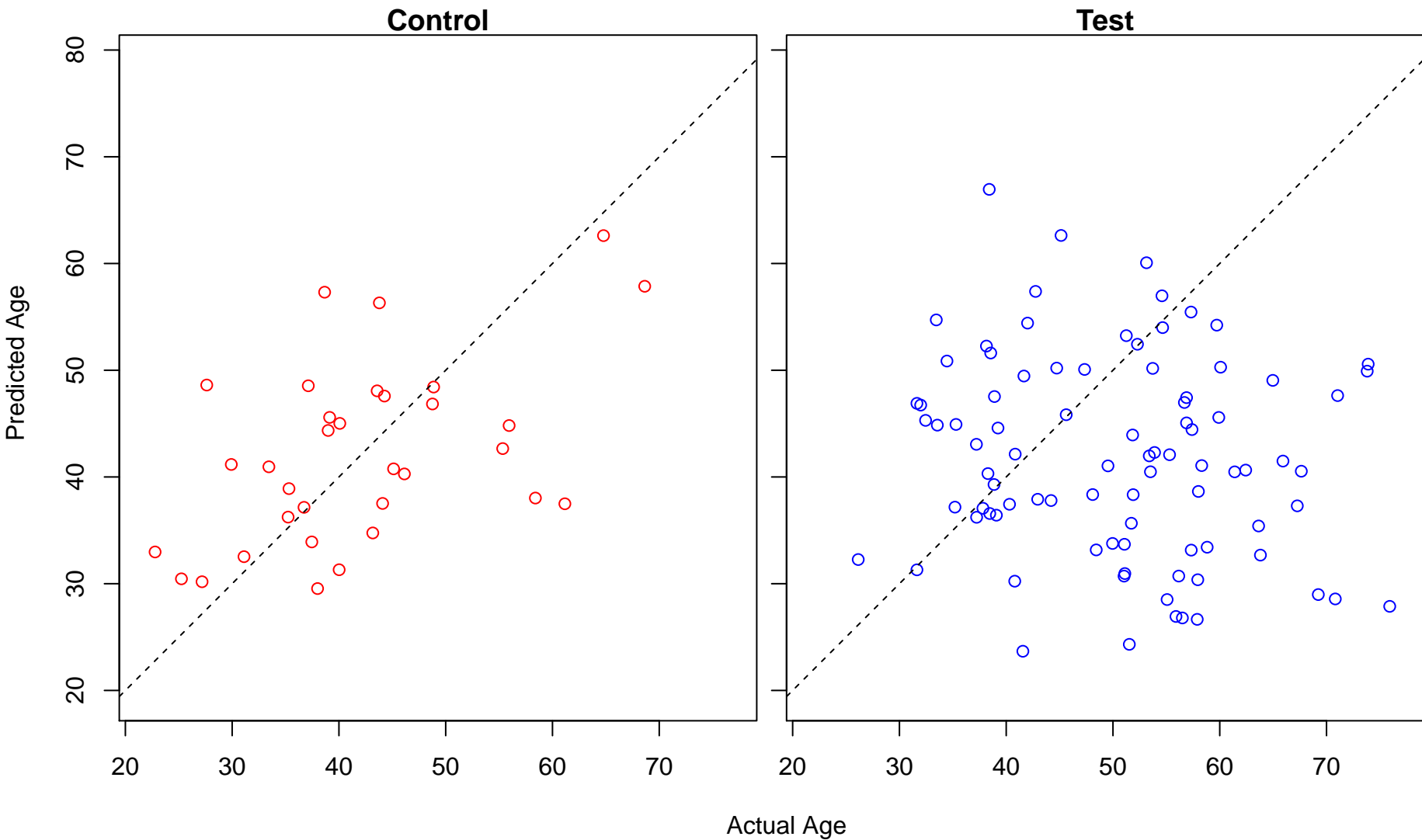
folic acid metabolic process (Score: 1.305998)



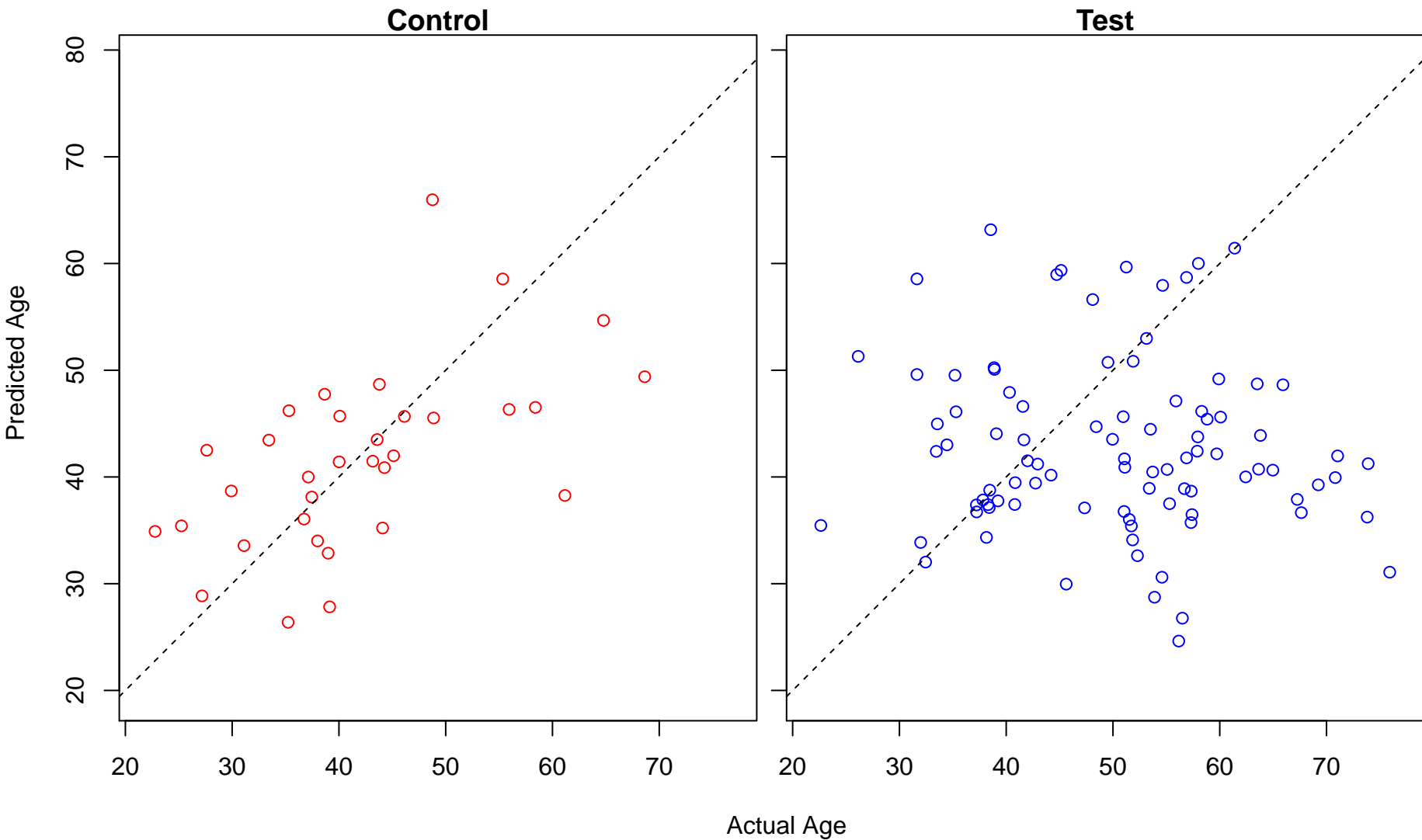
dermatan sulfate proteoglycan metabolic process (Score: 1.303763)



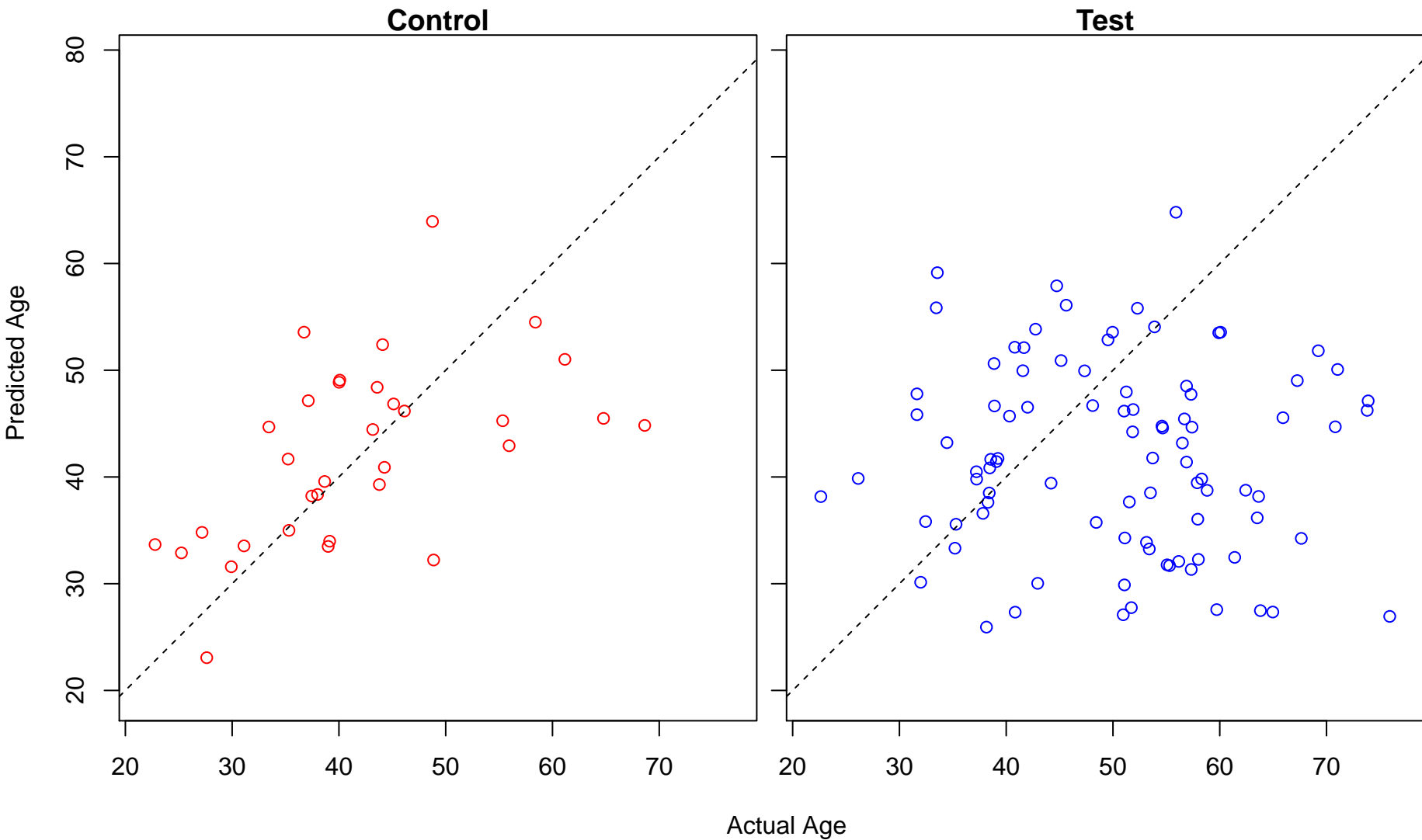
sphingolipid catabolic process (Score: 1.302734)



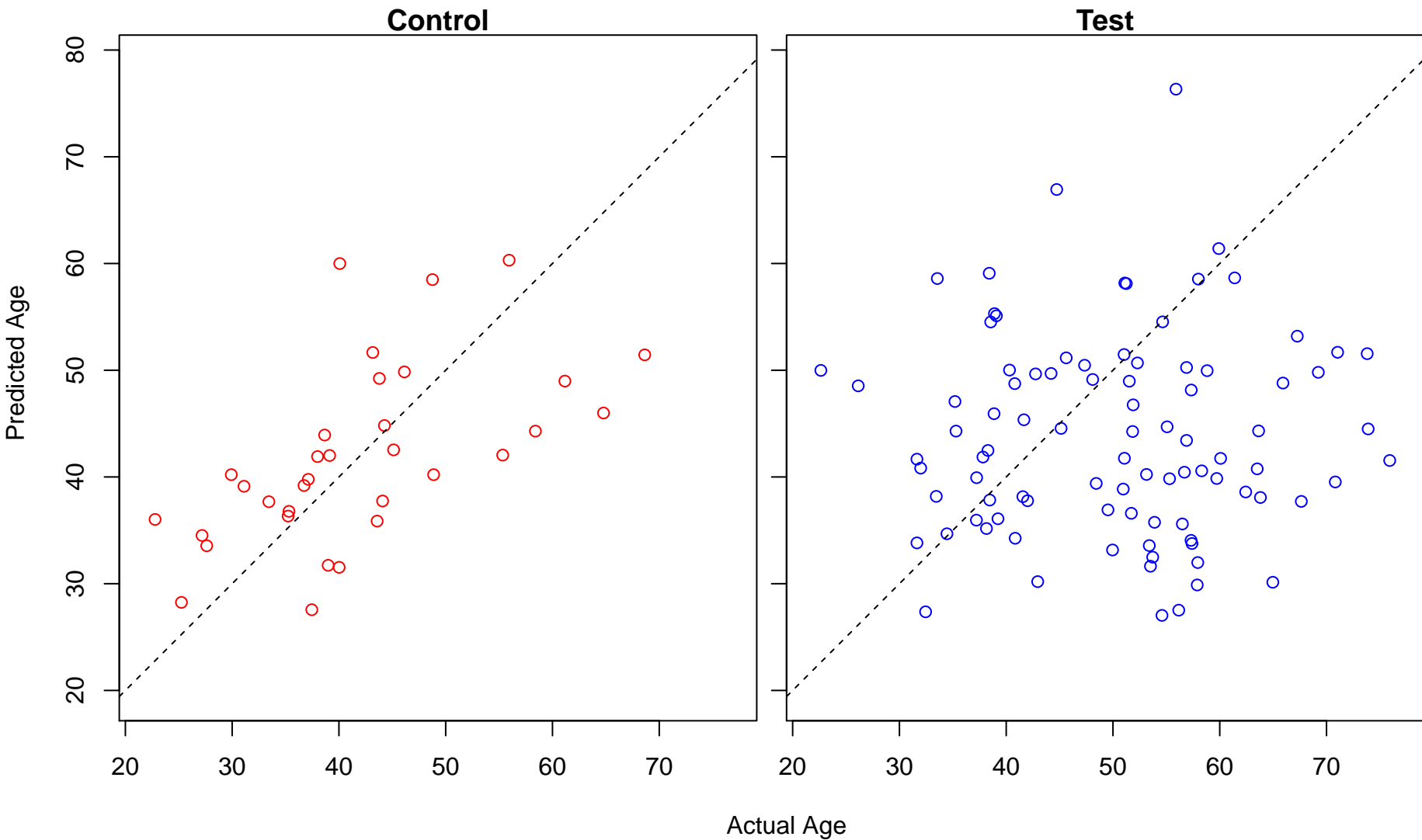
centrosome duplication (Score: 1.299040)



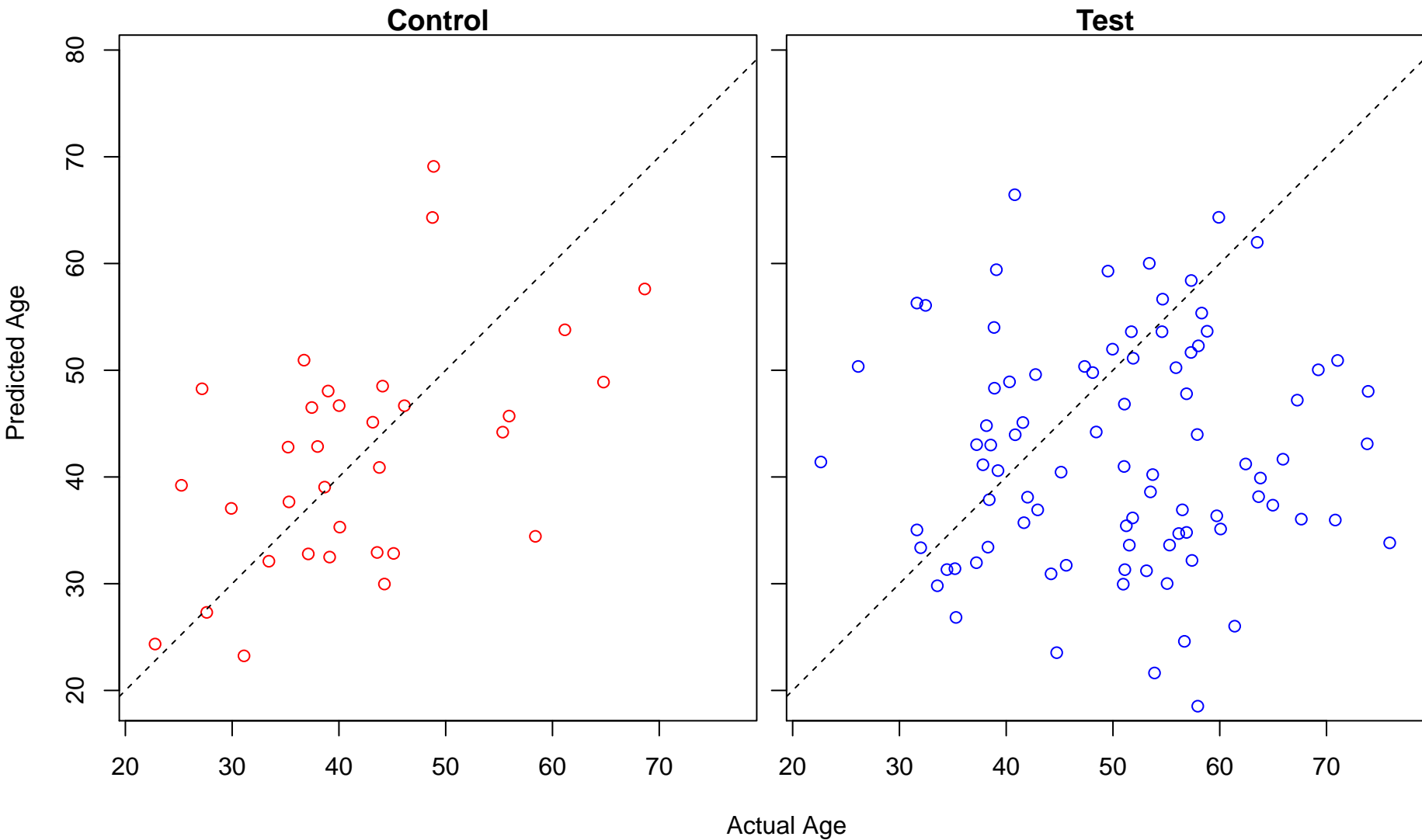
membrane depolarization (Score: 1.295317)



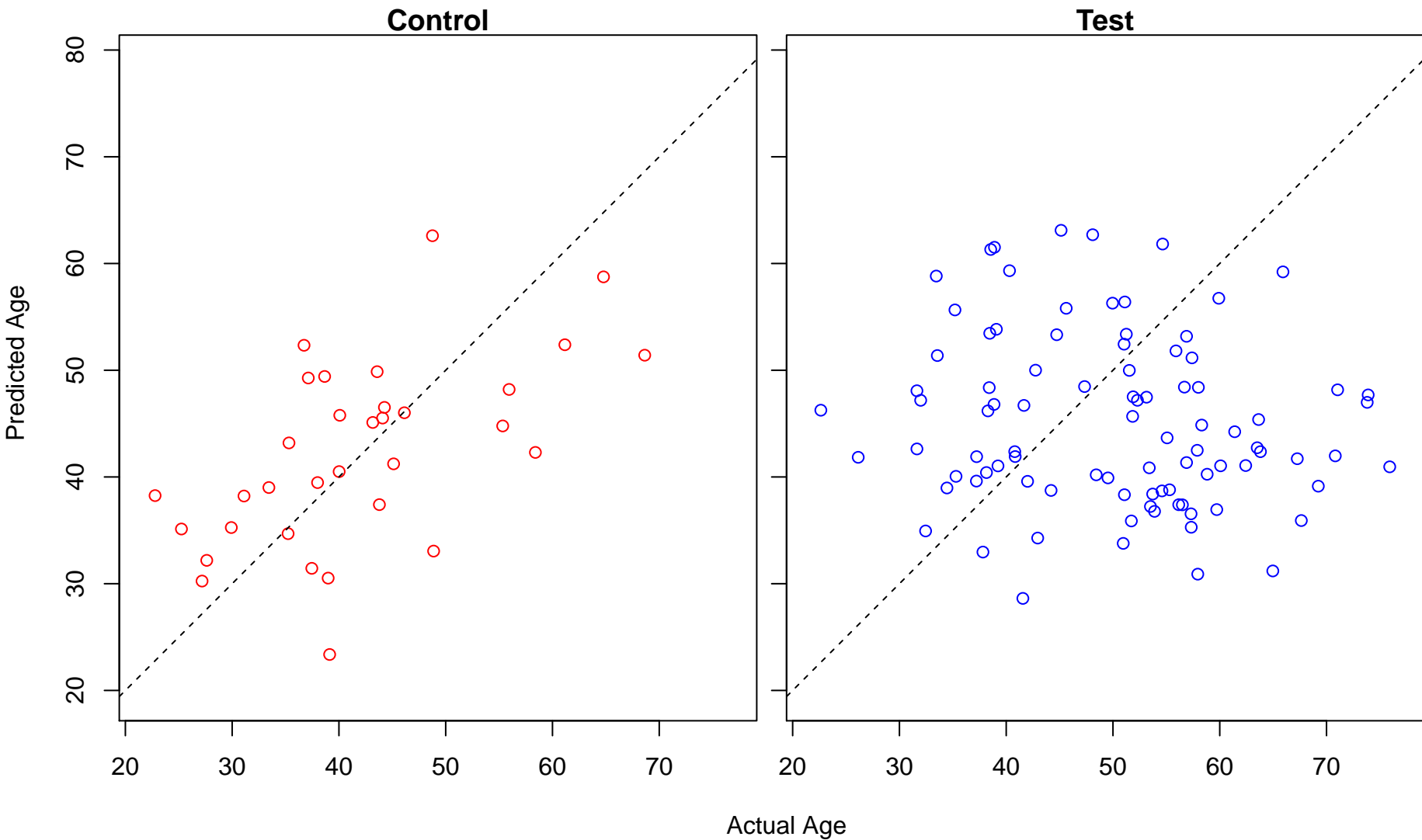
negative regulation of ion transmembrane transporter activity (Score: 1.294007)



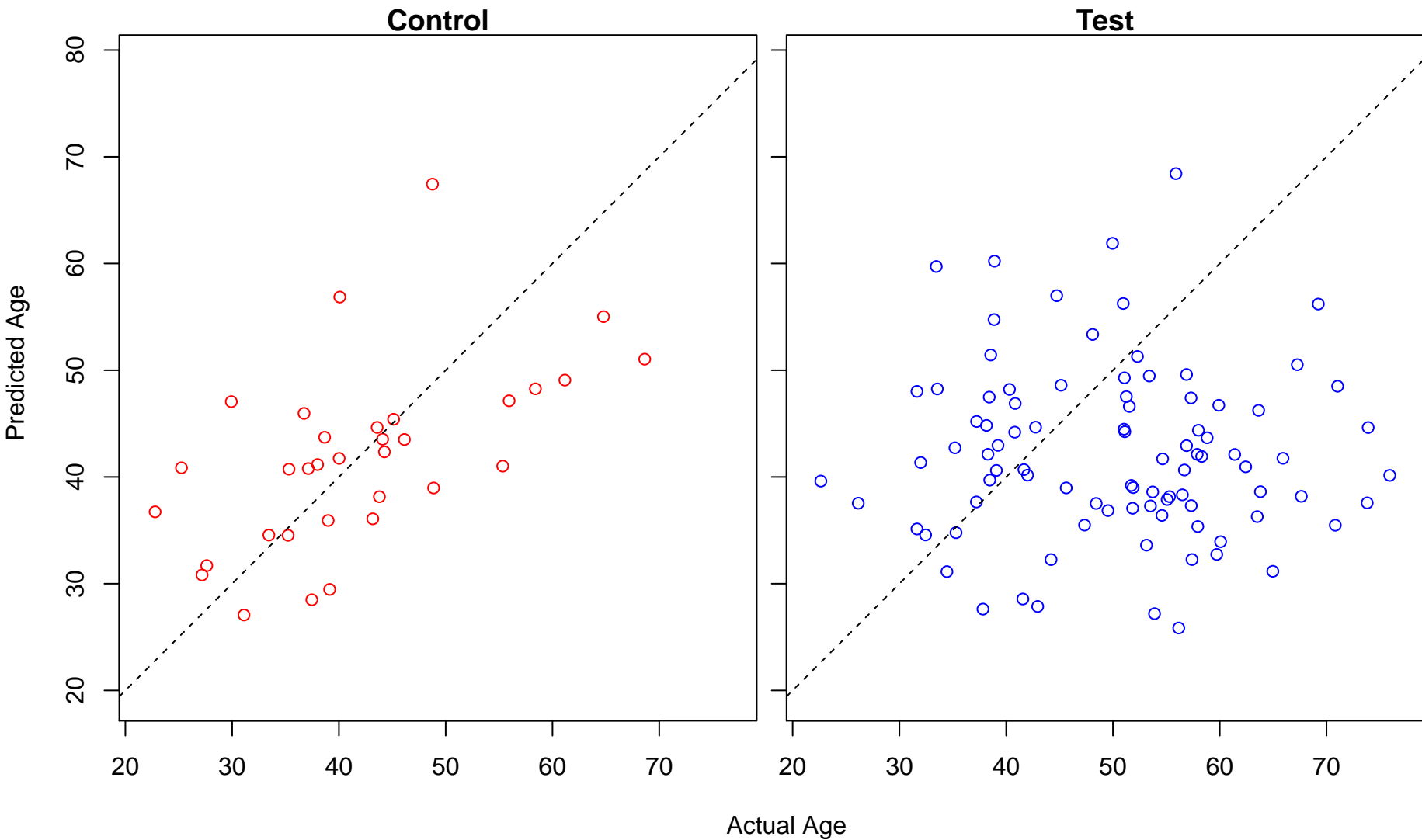
regulation of microtubule-based movement (Score: 1.293795)



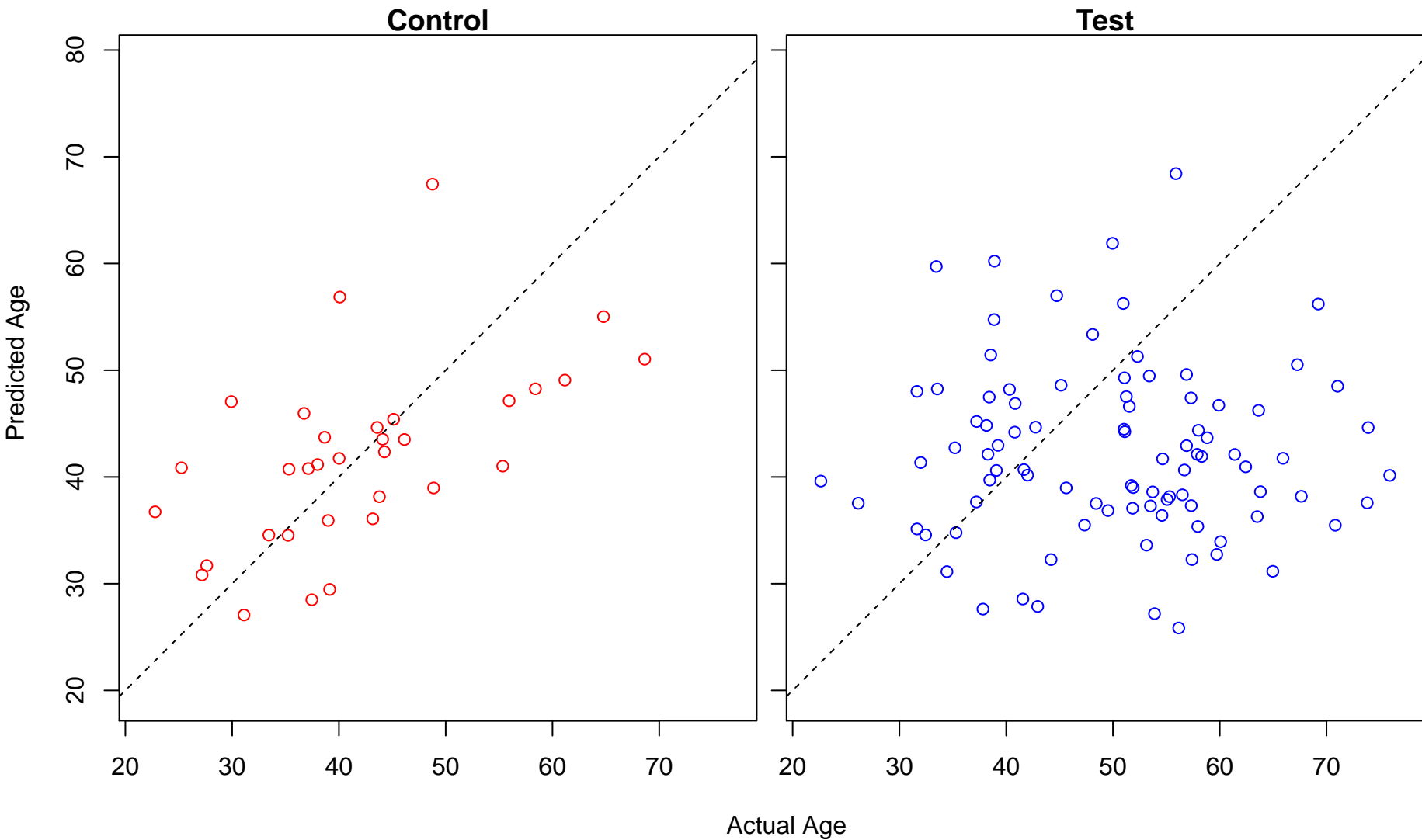
negative regulation of transcription factor import into nucleus (Score: 1.291459)



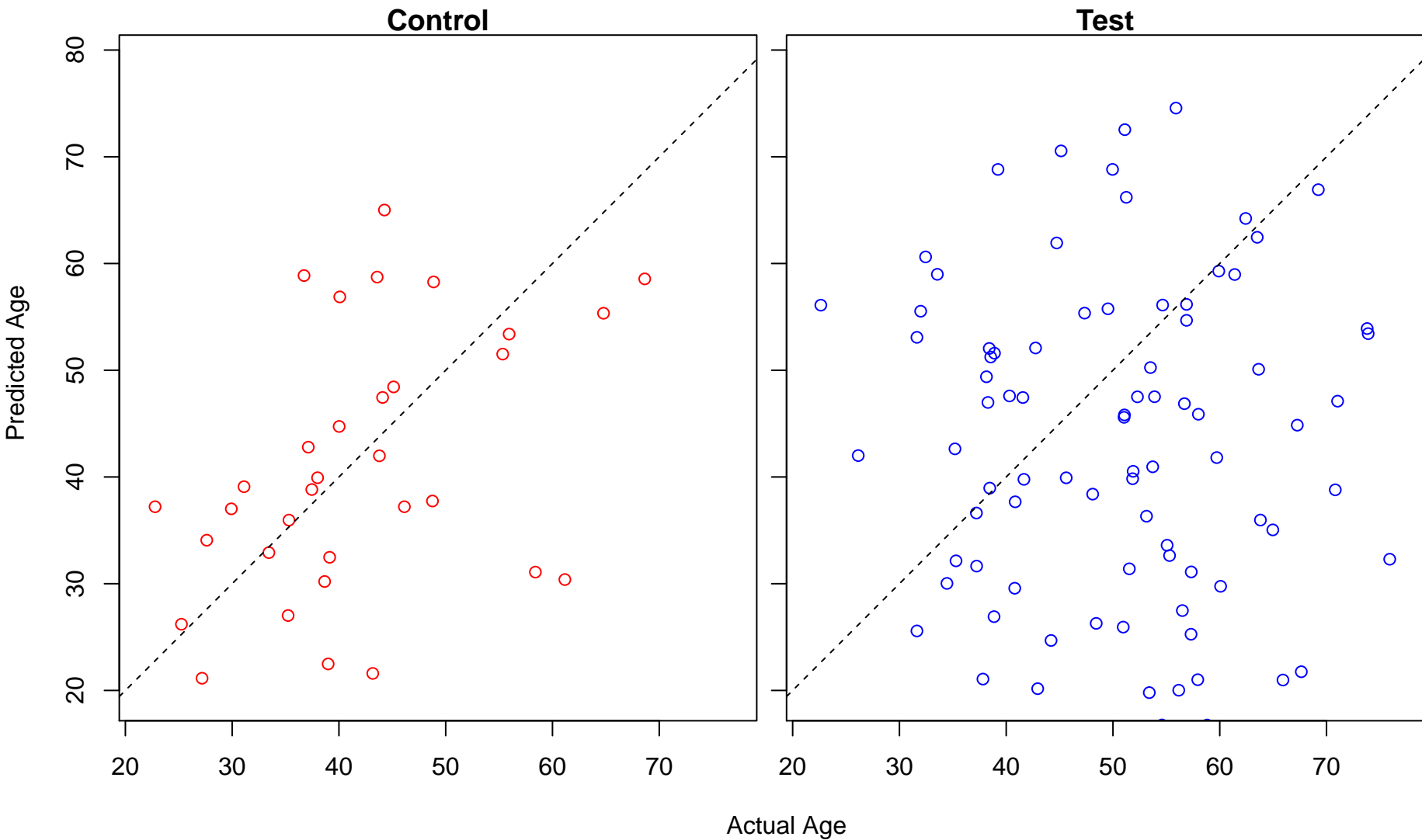
regulation of sterol transport (Score: 1.290859)



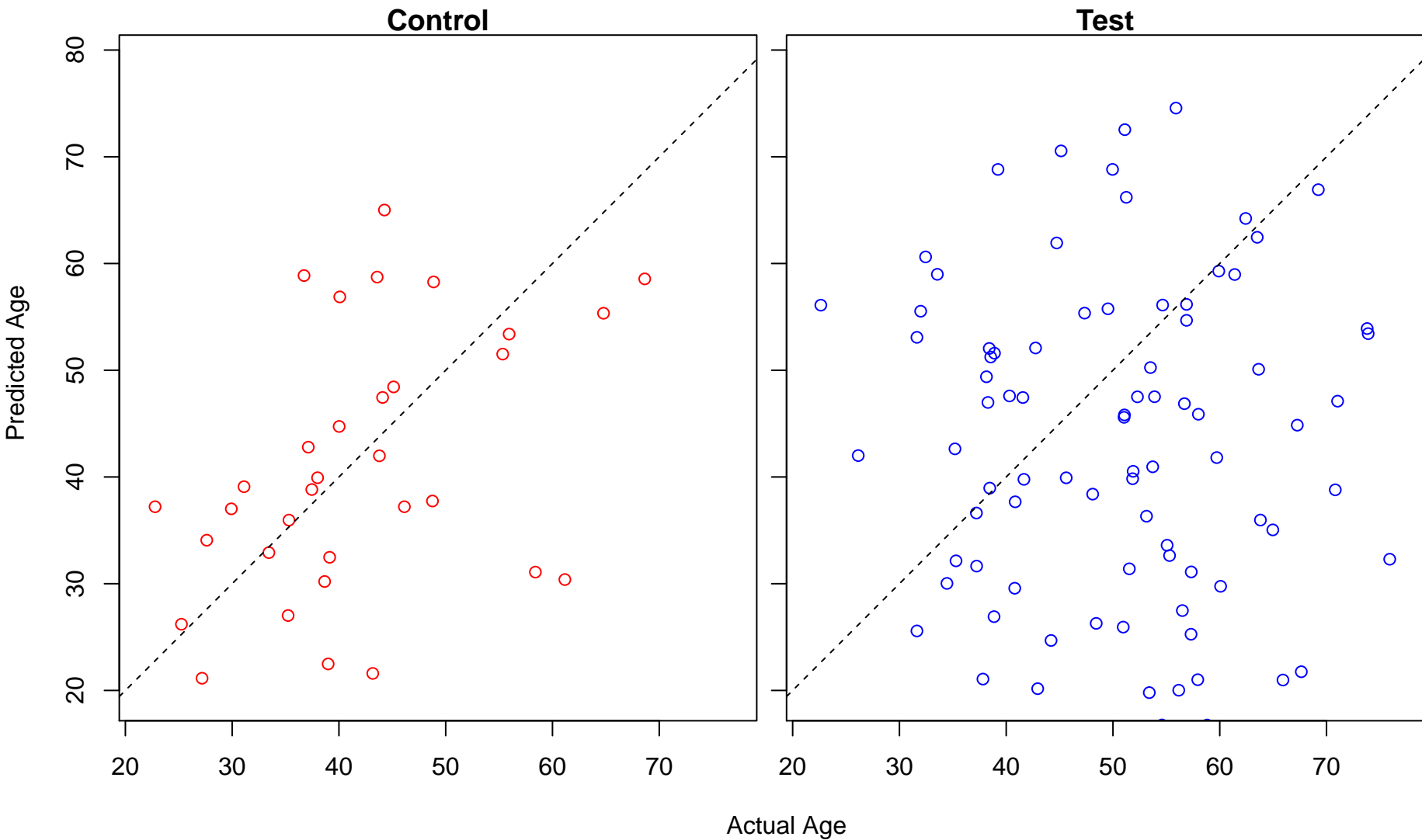
regulation of cholesterol transport (Score: 1.290859)



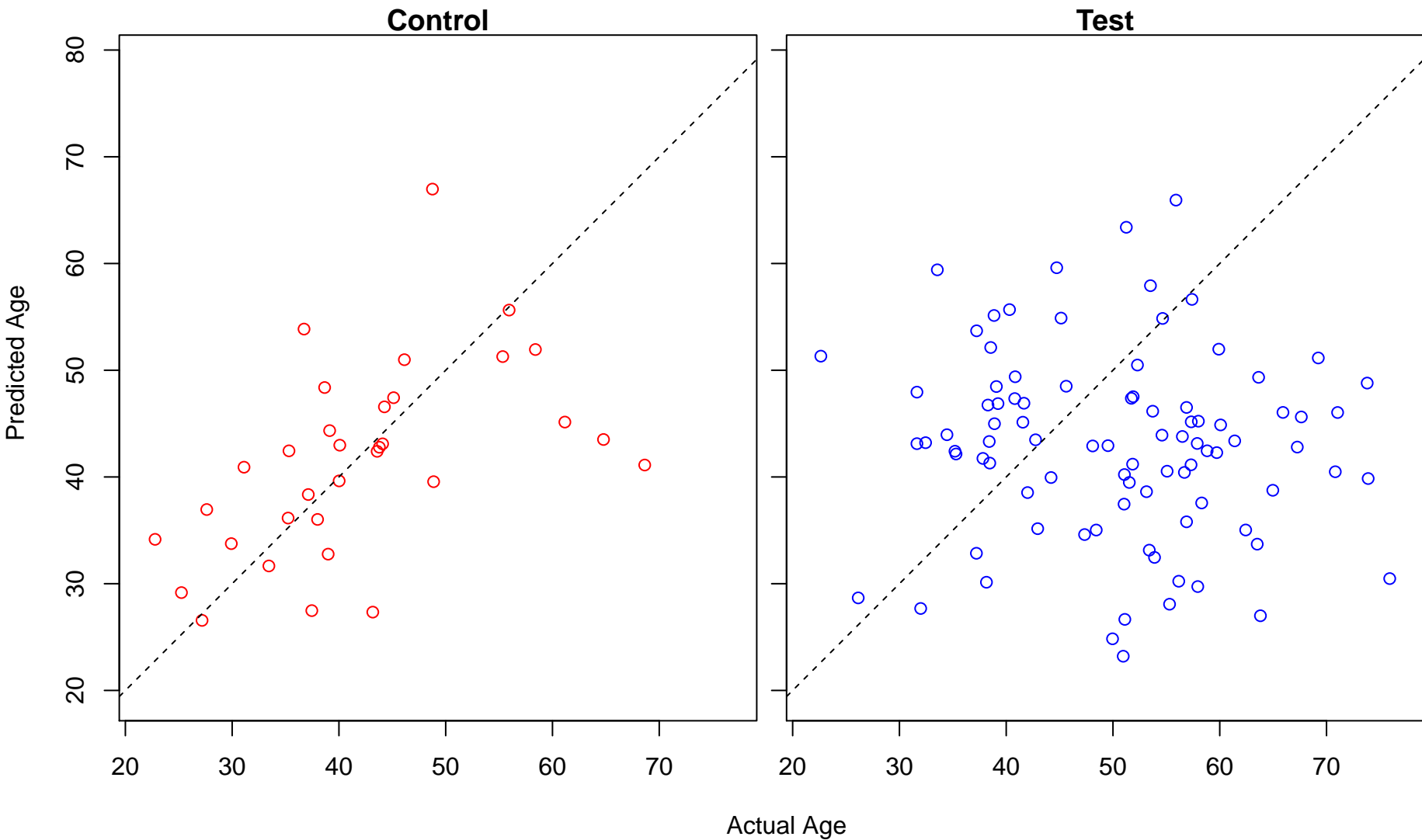
gonad development (Score: 1.285031)



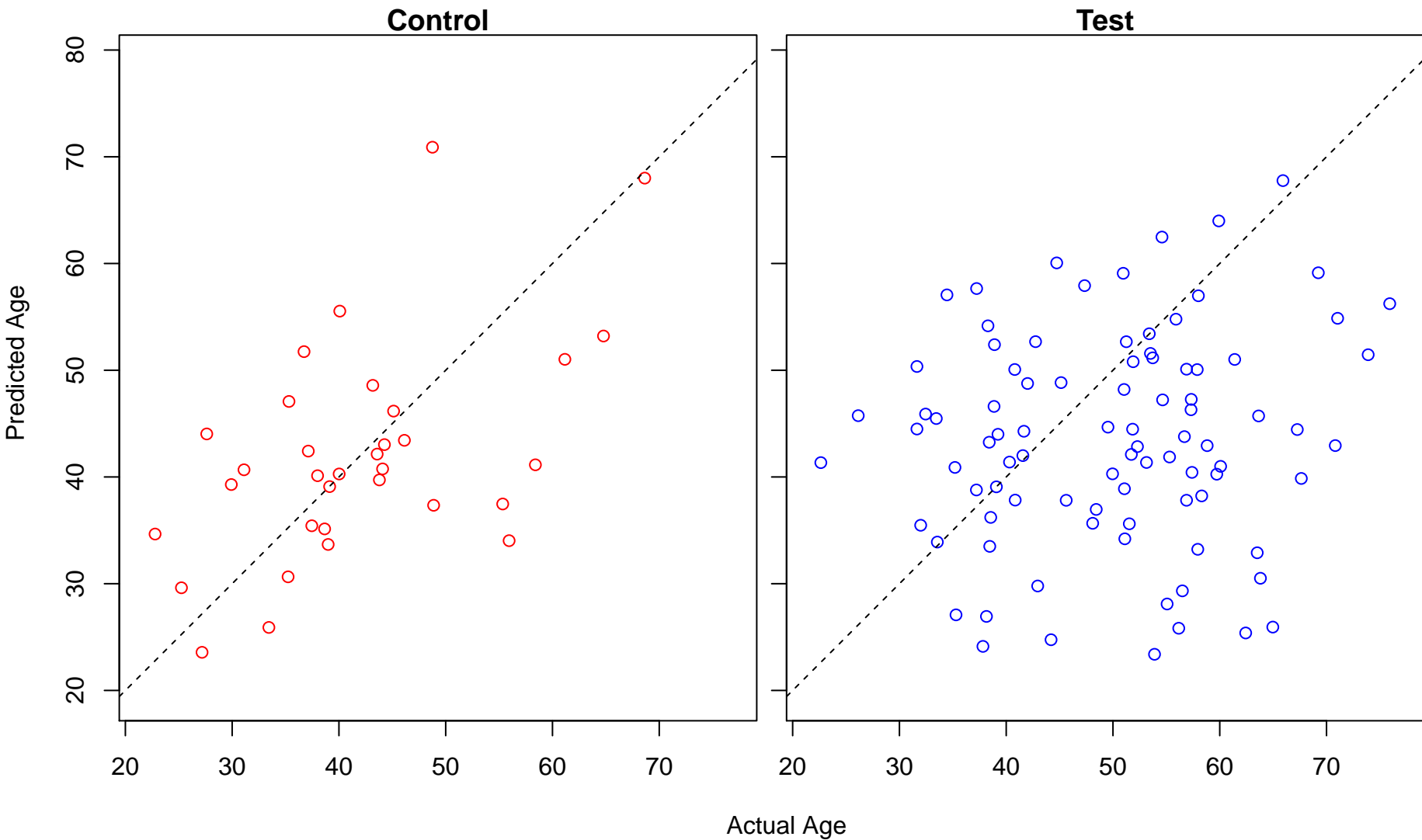
development of primary sexual characteristics (Score: 1.285031)



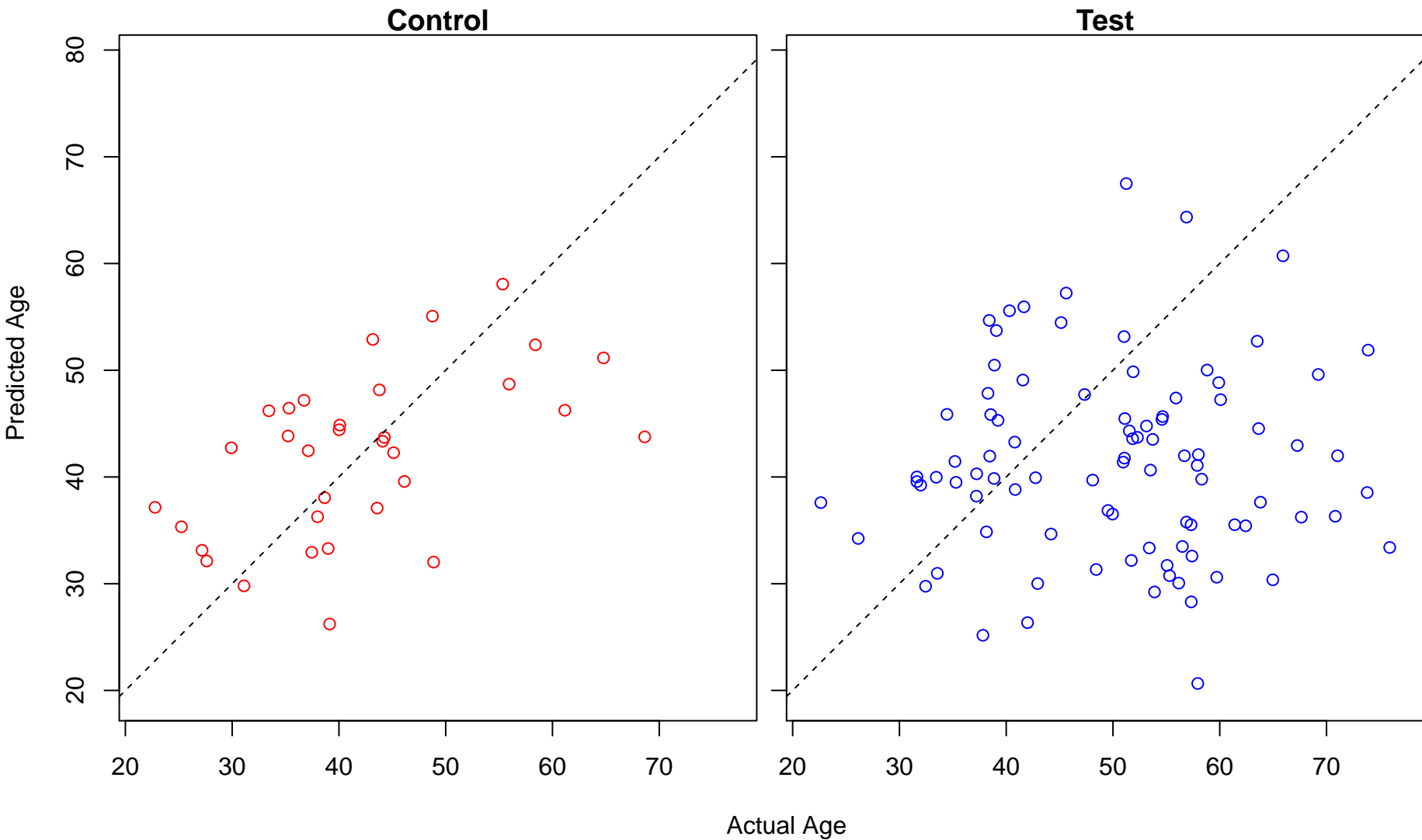
negative regulation of peptidase activity (Score: 1.284255)



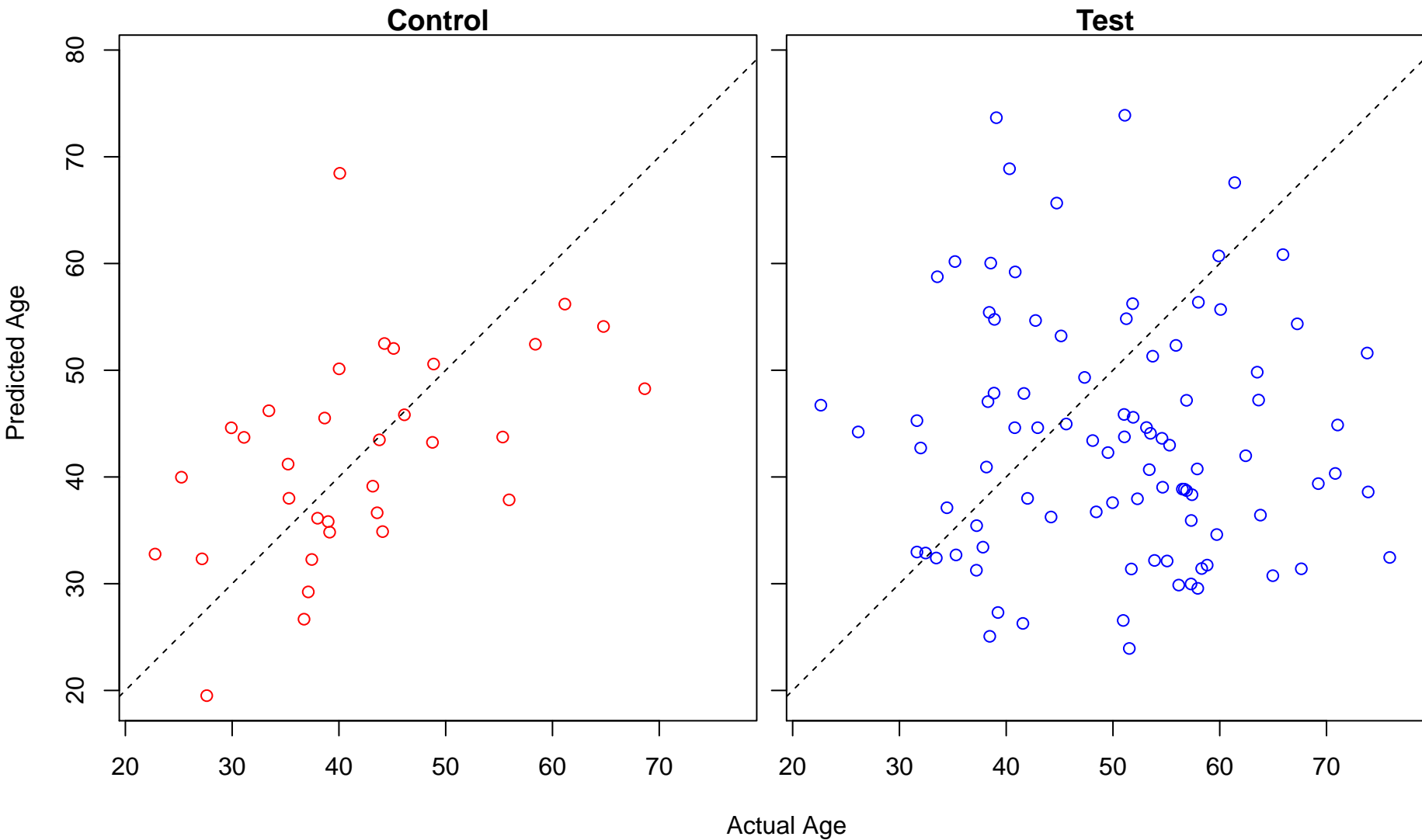
regulation of protein dephosphorylation (Score: 1.283965)



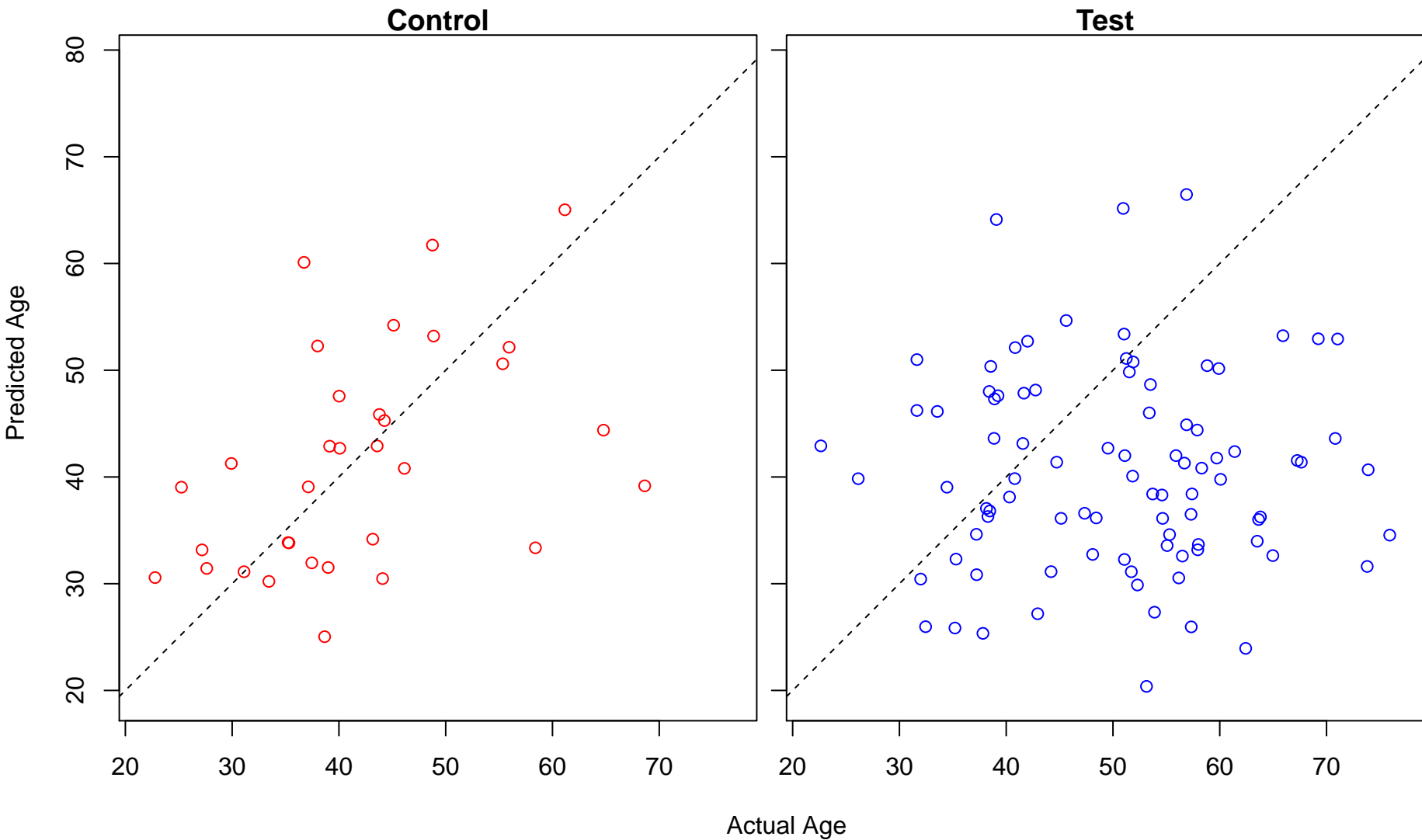
regulation of Rab protein signal transduction (Score: 1.278981)



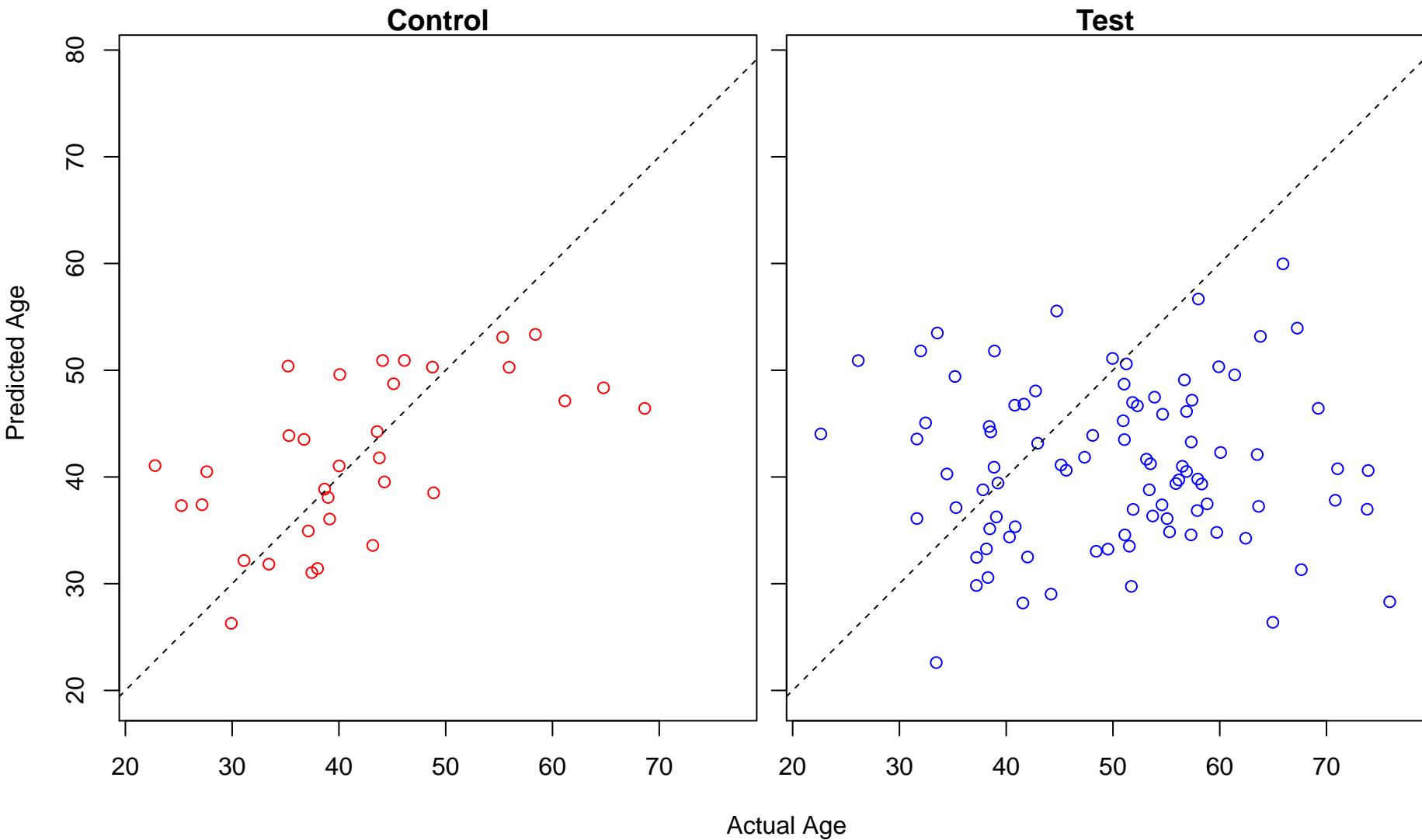
social behavior (Score: 1.277105)



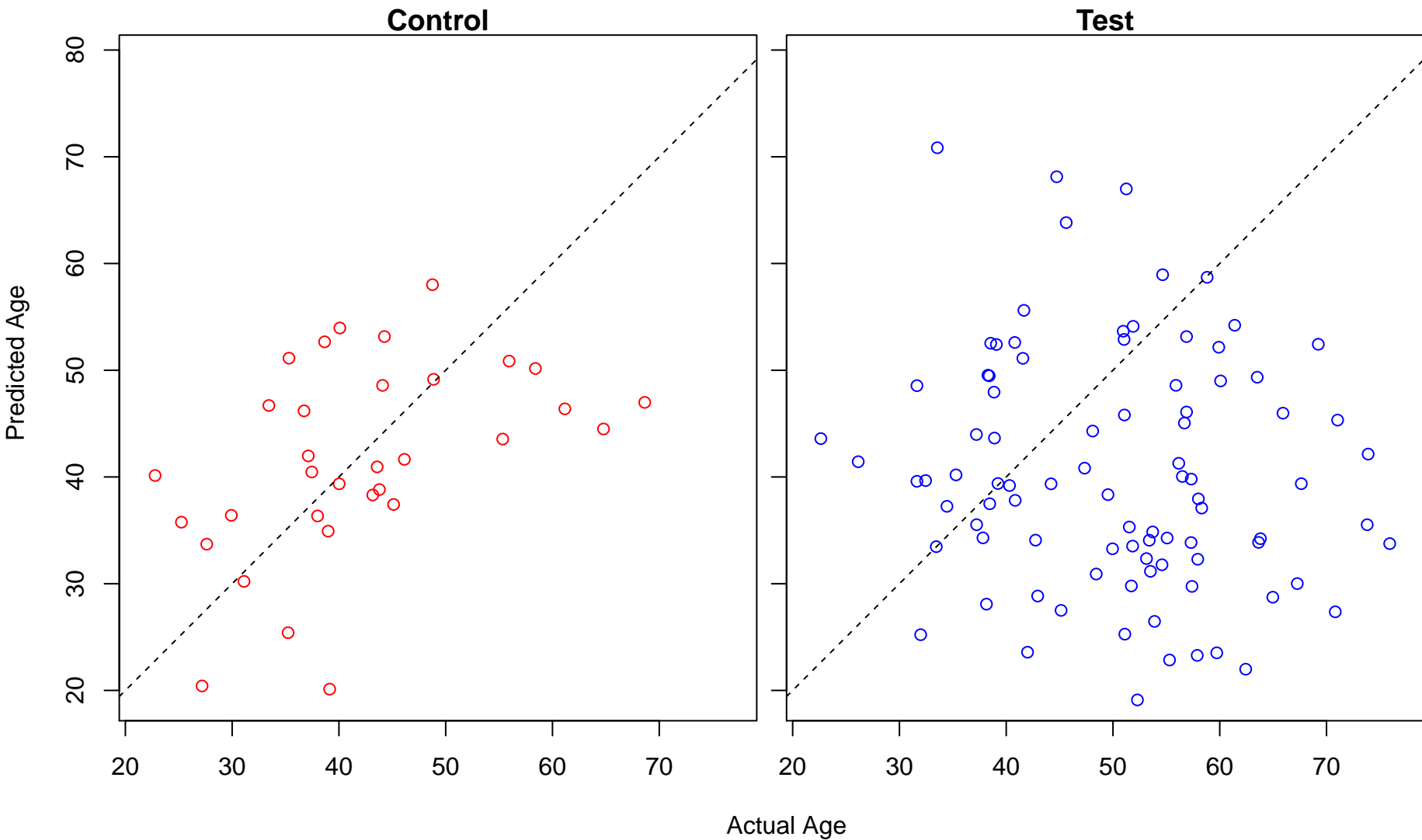
negative regulation of mRNA splicing, via spliceosome (Score: 1.276441)



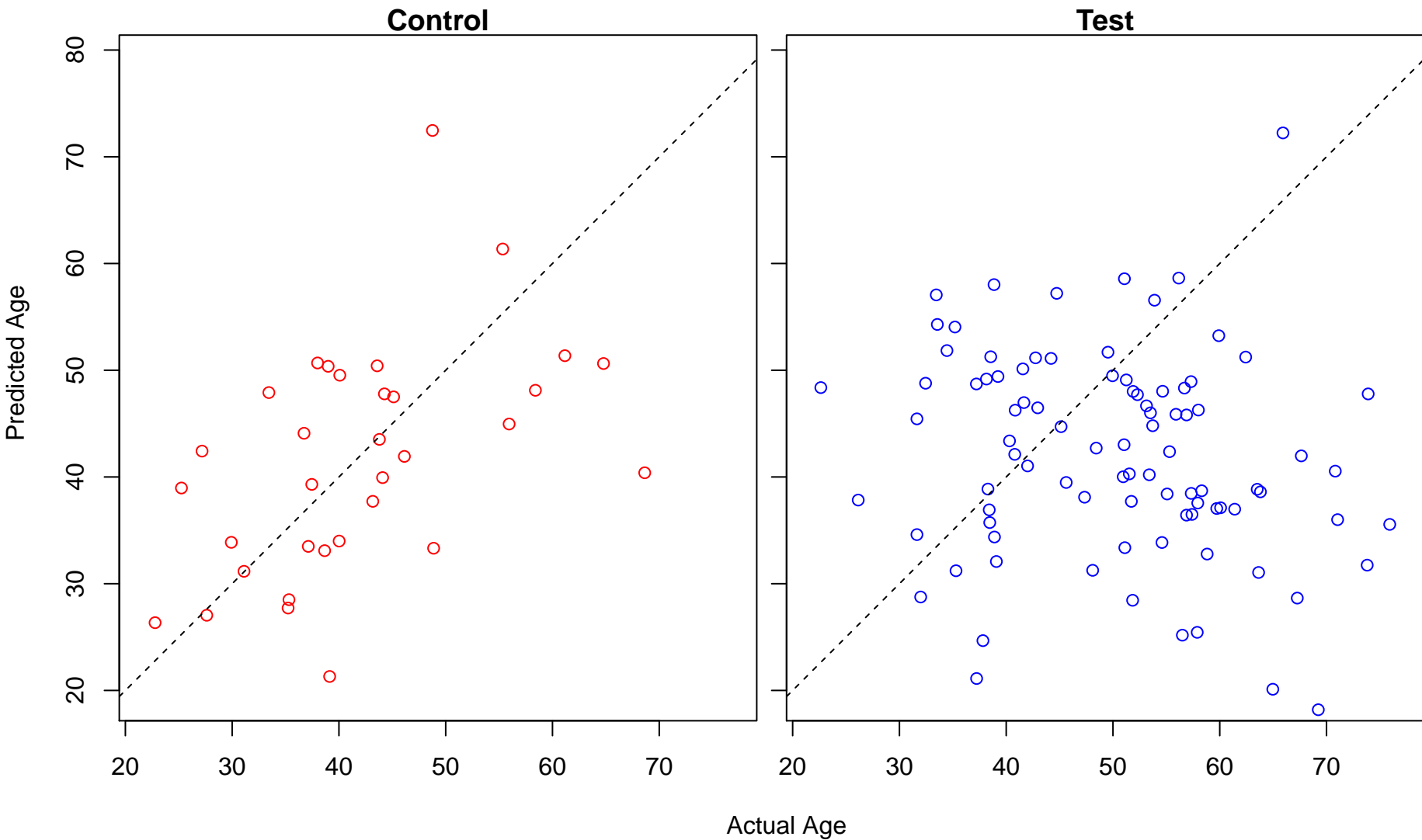
cell-cell signaling involved in cardiac conduction (Score: 1.276321)



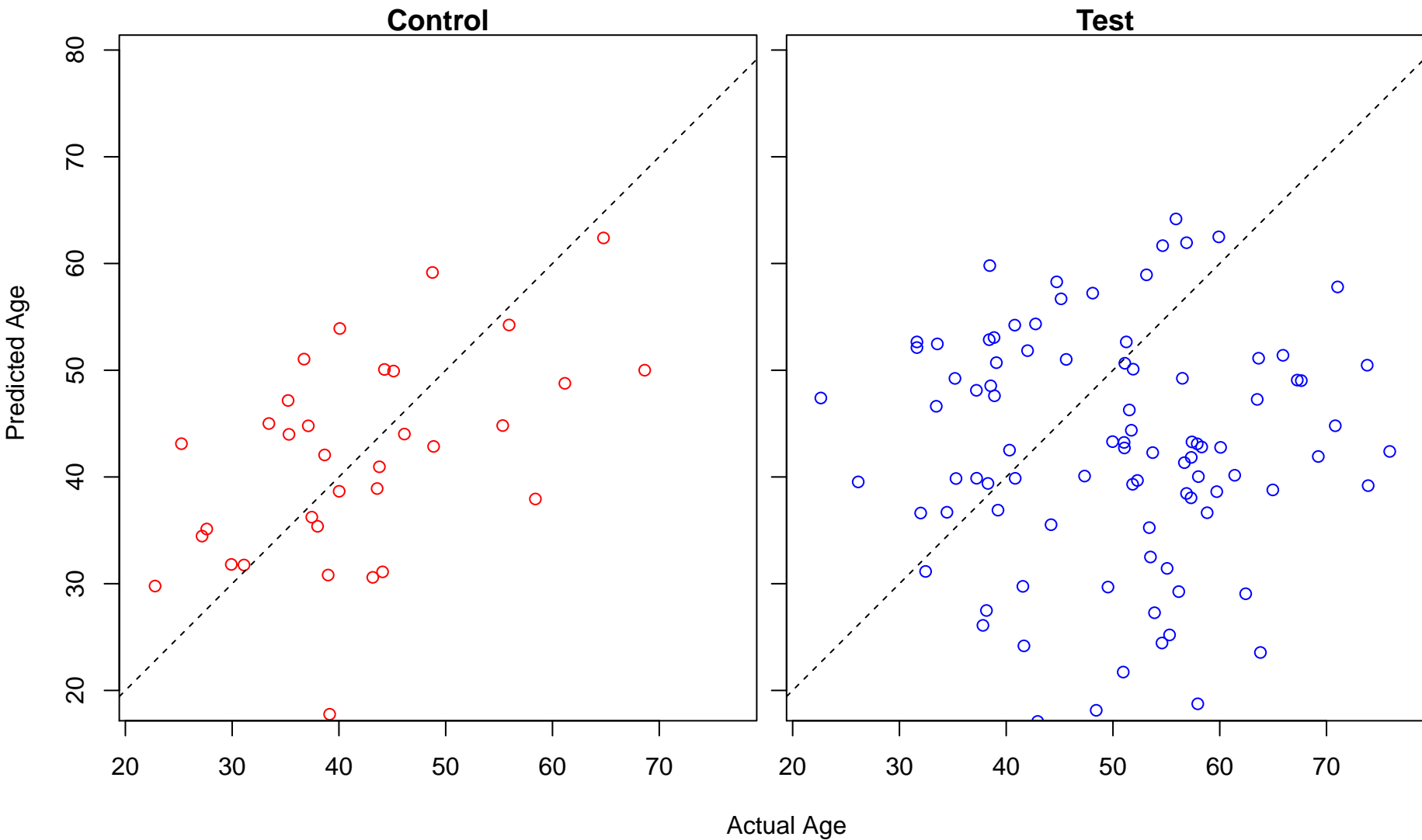
3'-UTR-mediated mRNA stabilization (Score: 1.275331)



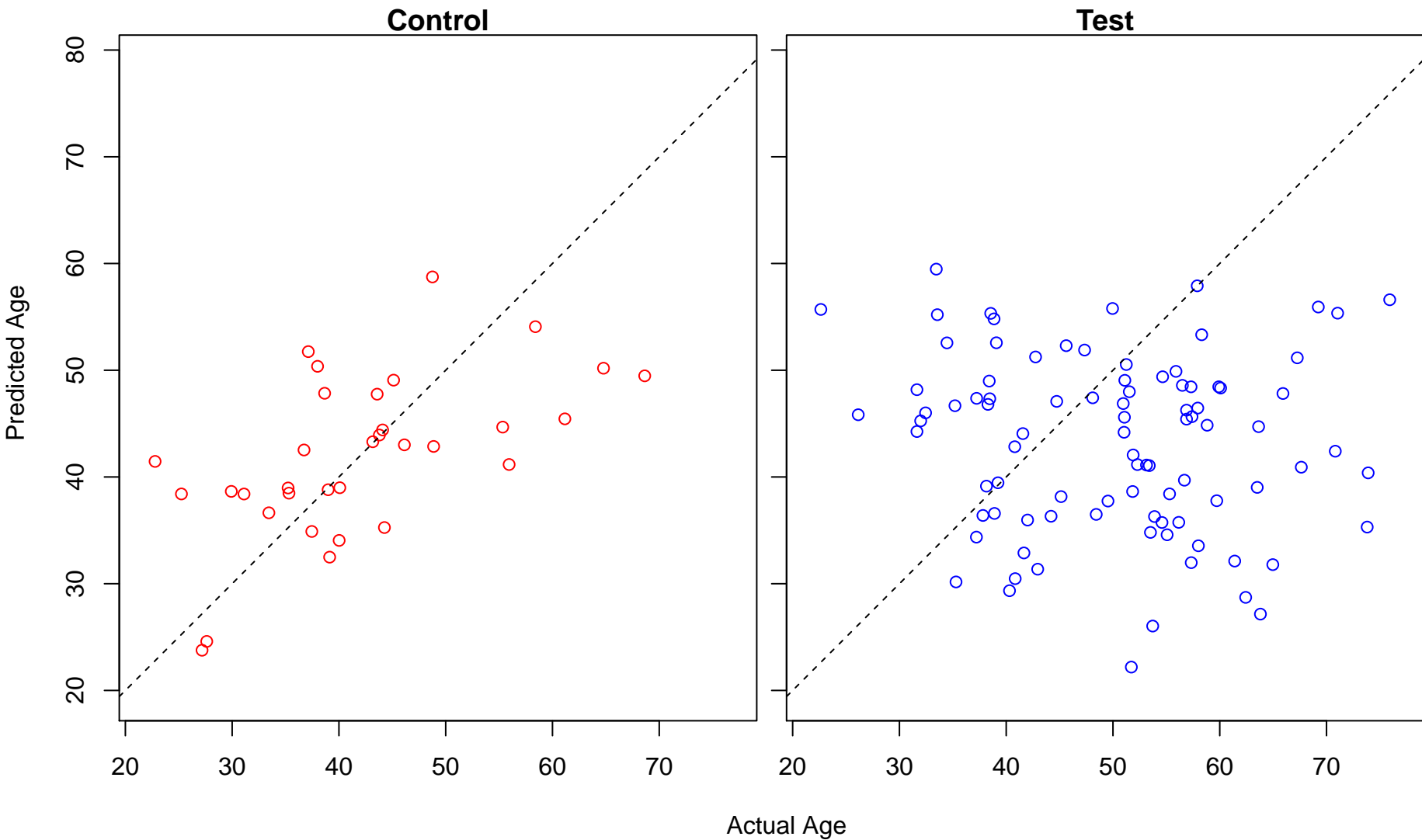
mitotic DNA damage checkpoint (Score: 1.273247)



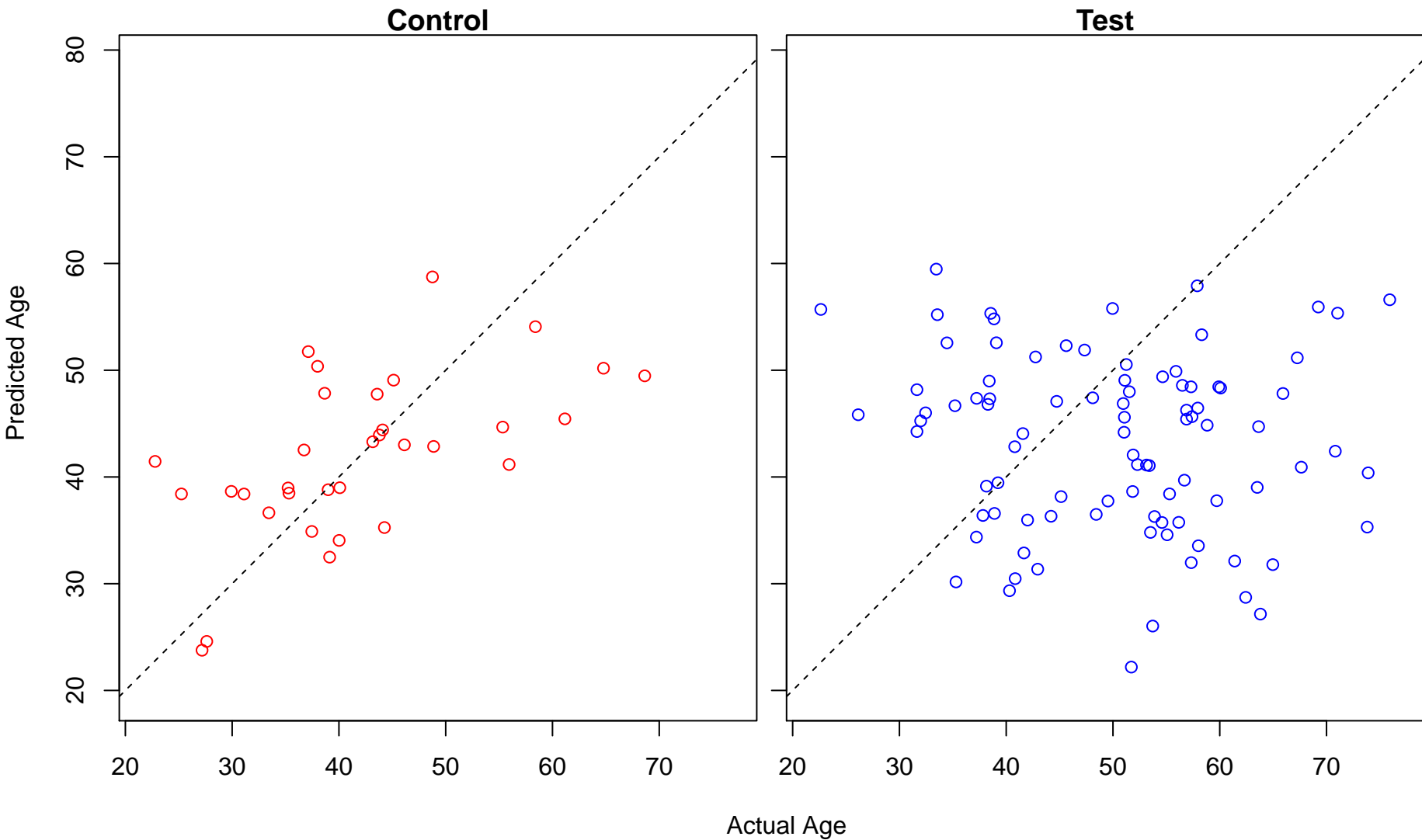
negative regulation of protein secretion (Score: 1.270509)



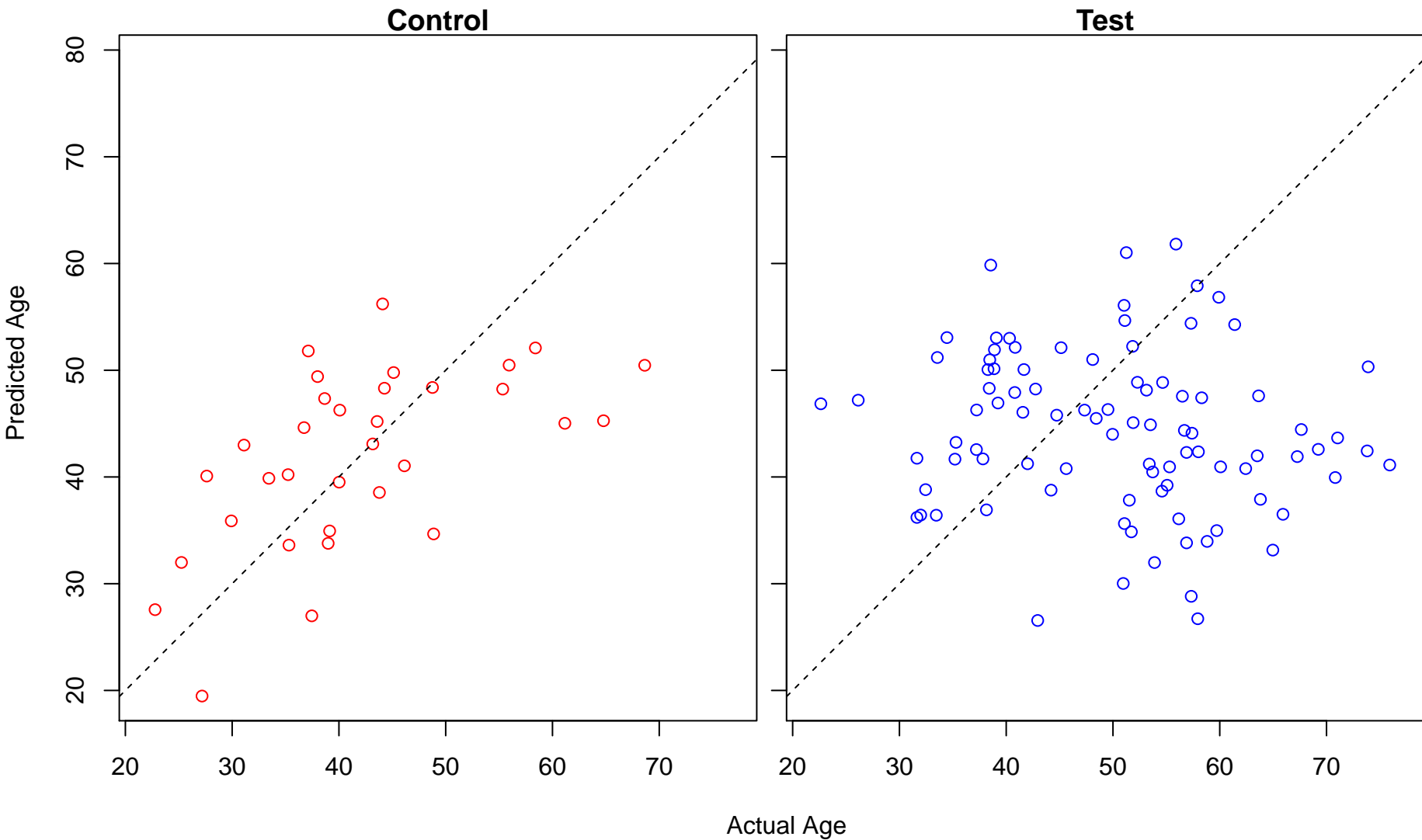
central nervous system myelination (Score: 1.262174)



axon ensheathment in central nervous system (Score: 1.262174)

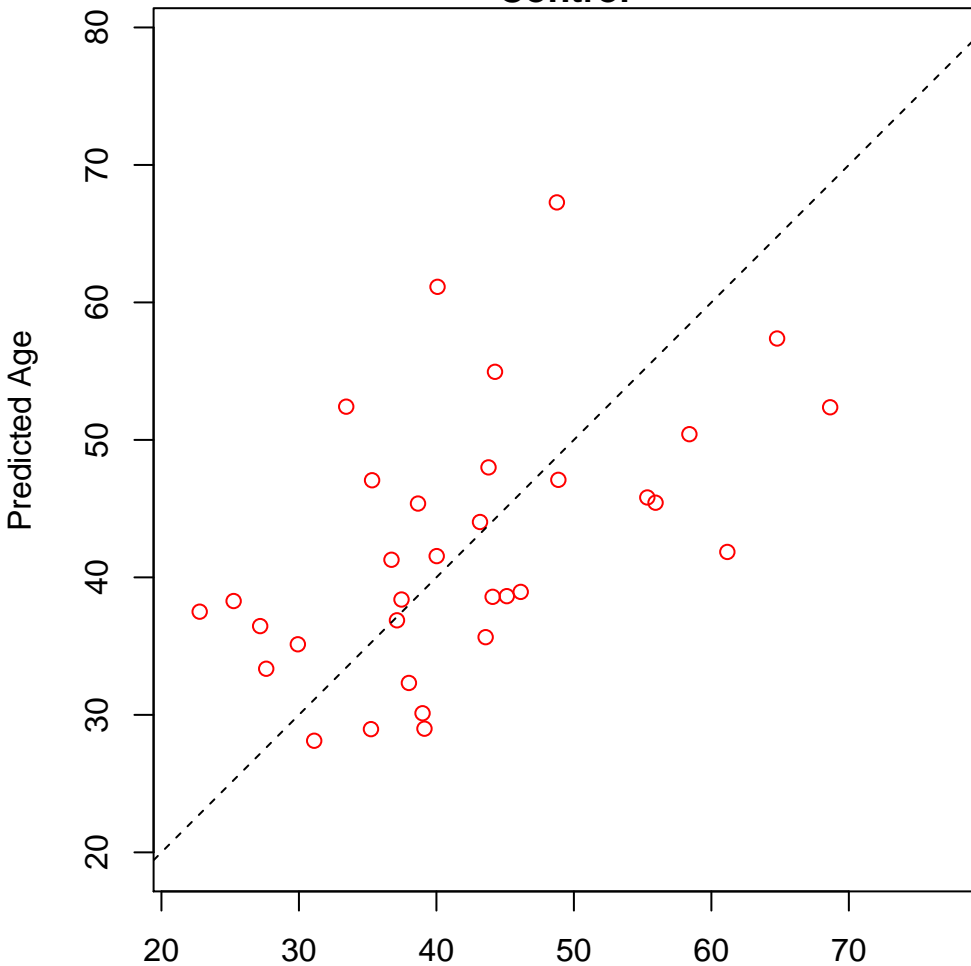


vasoconstriction (Score: 1.261207)

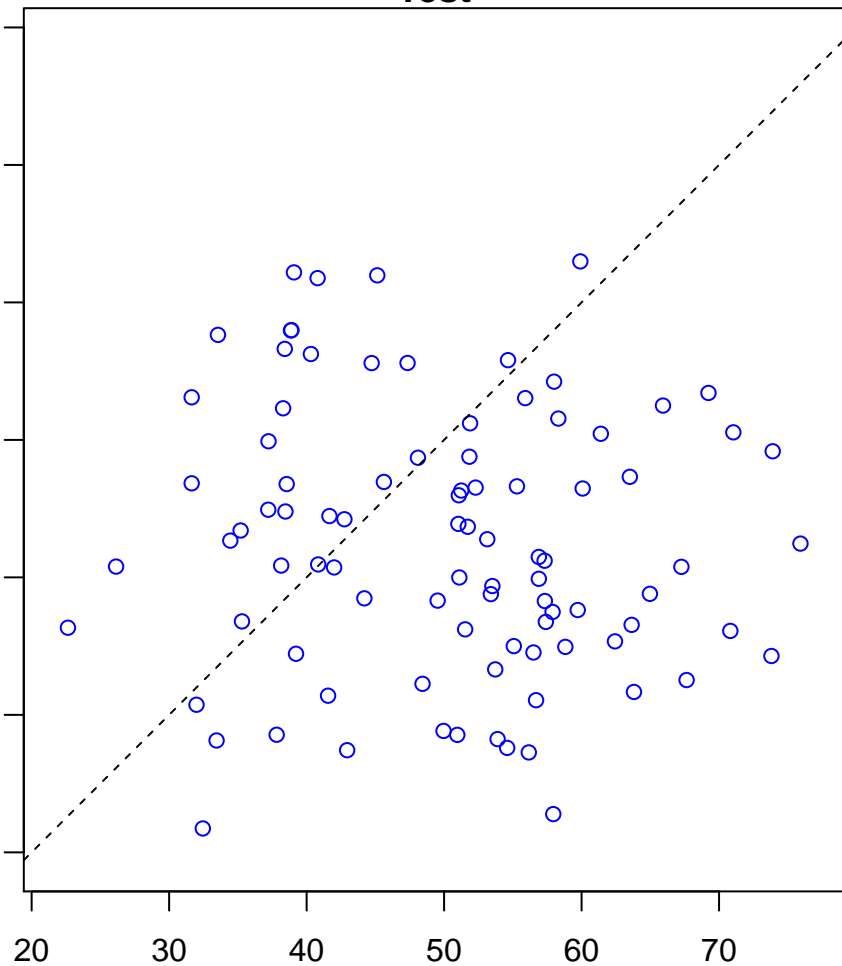


detection of molecule of bacterial origin (Score: 1.258819)

Control

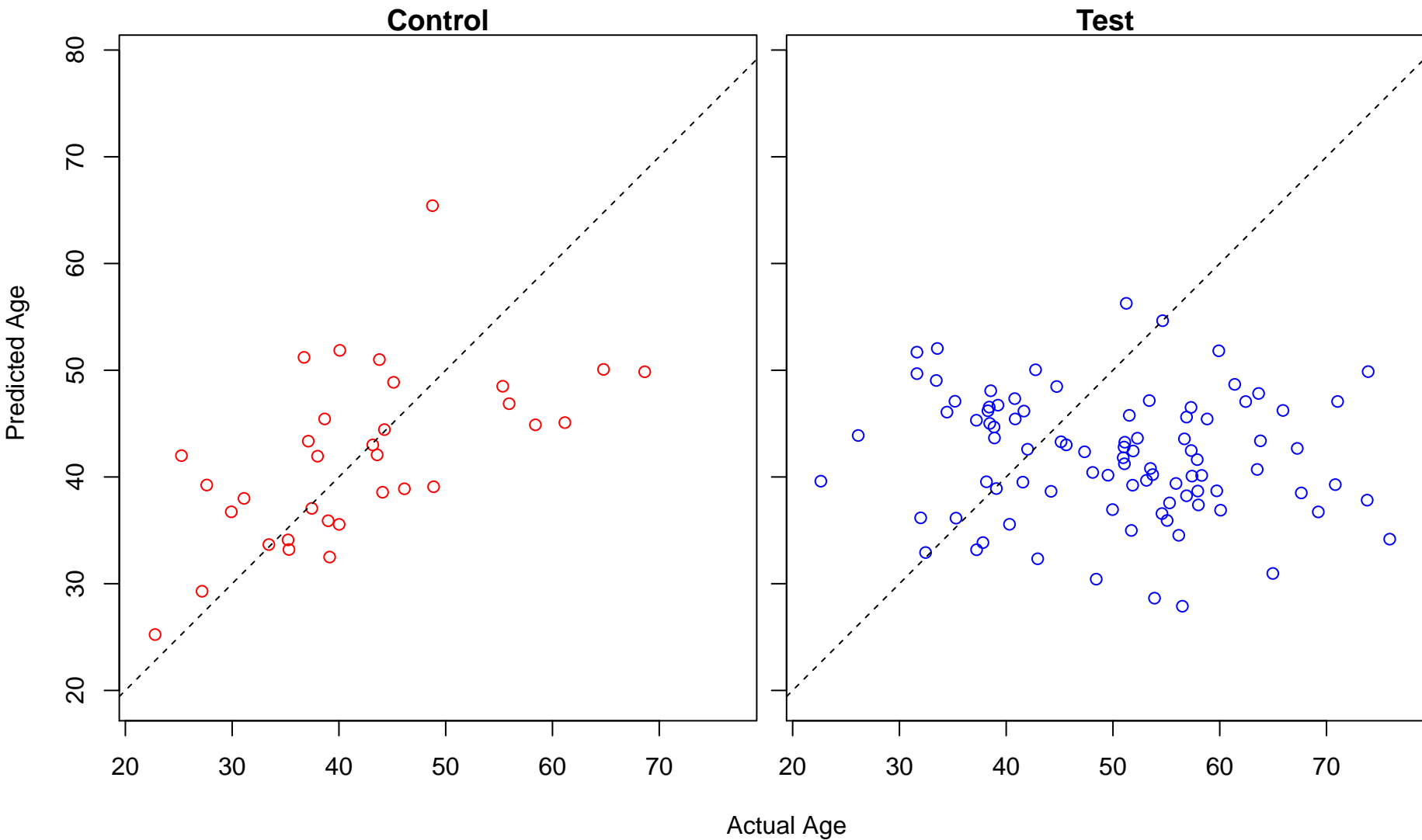


Test

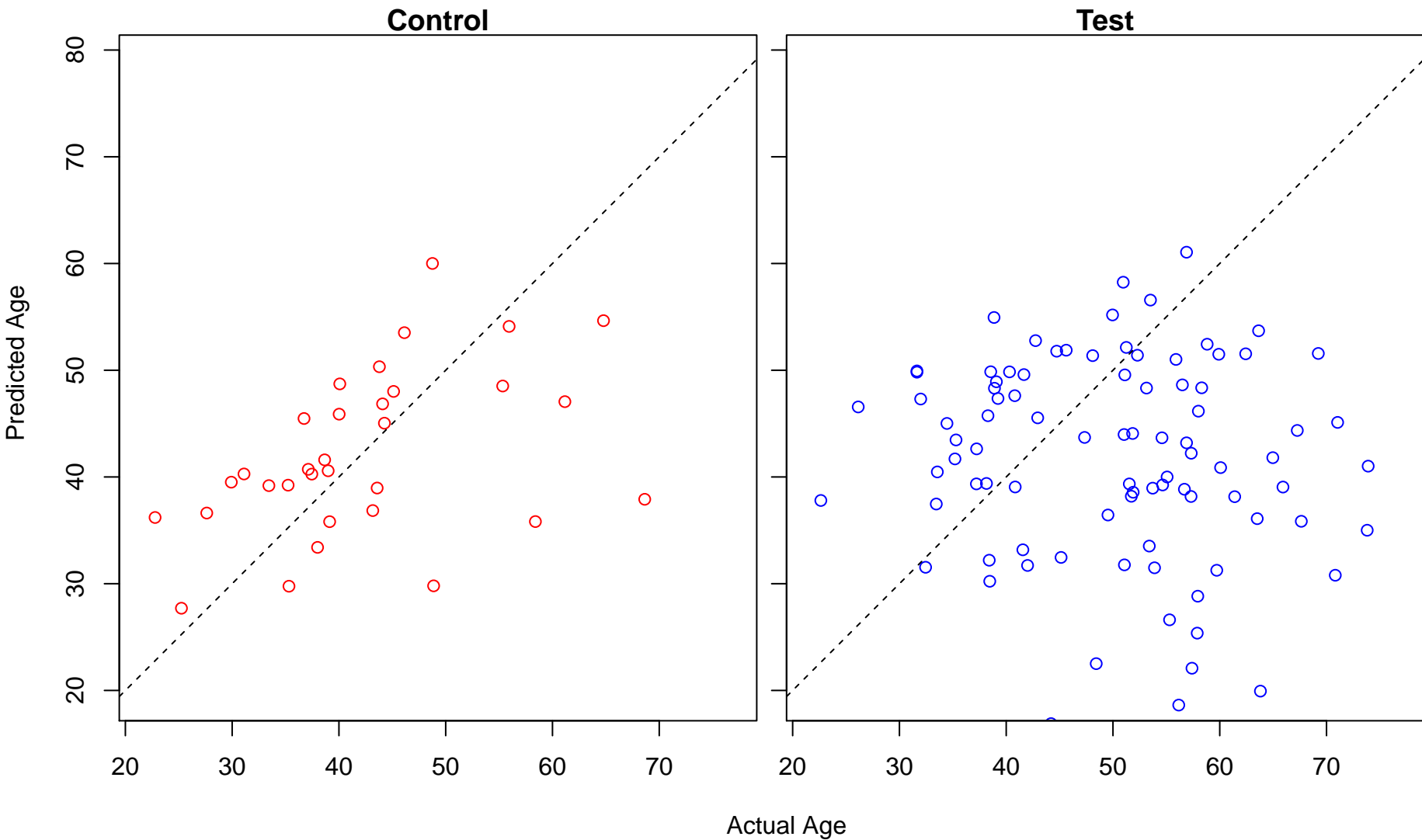


Actual Age

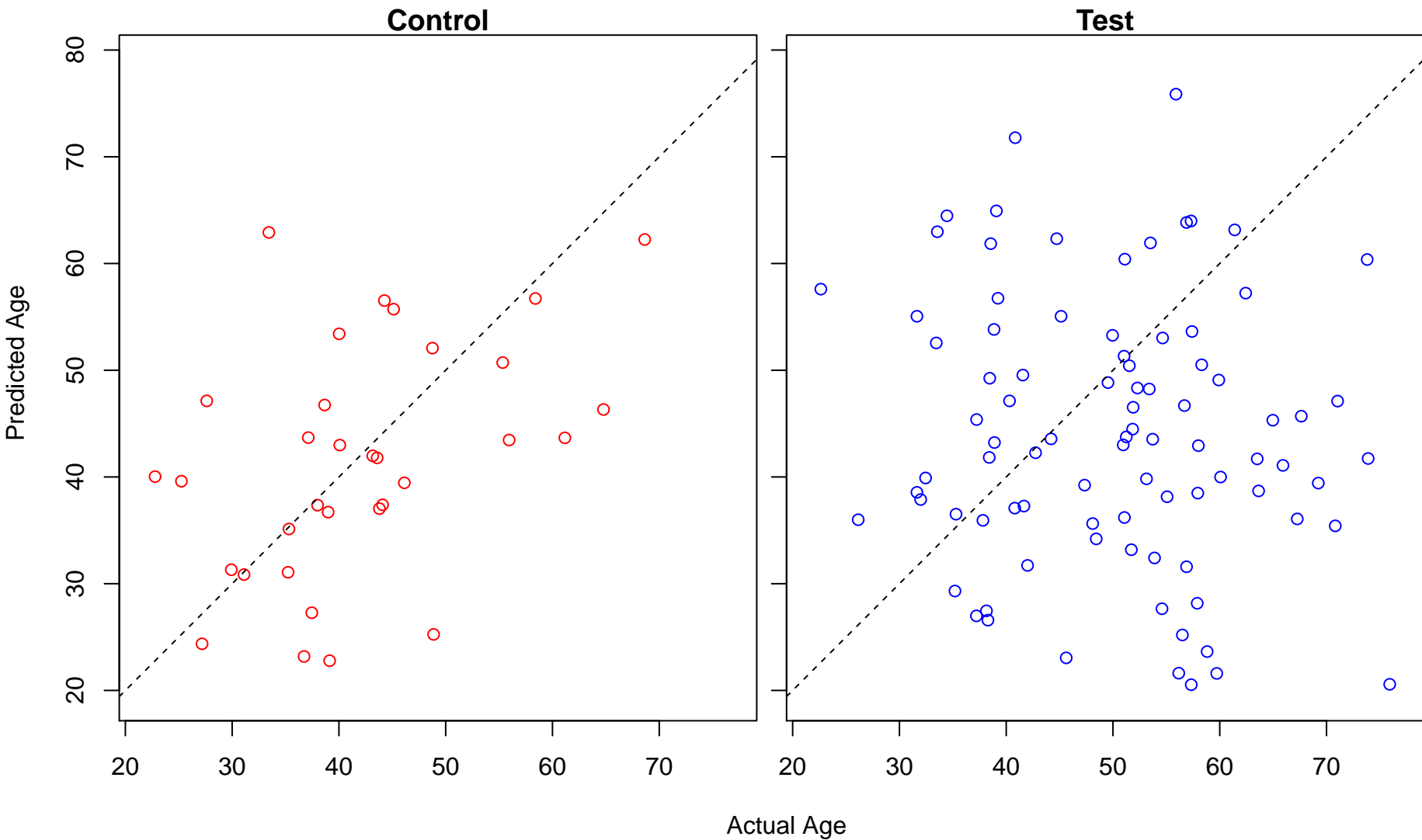
organic hydroxy compound metabolic process (Score: 1.257832)



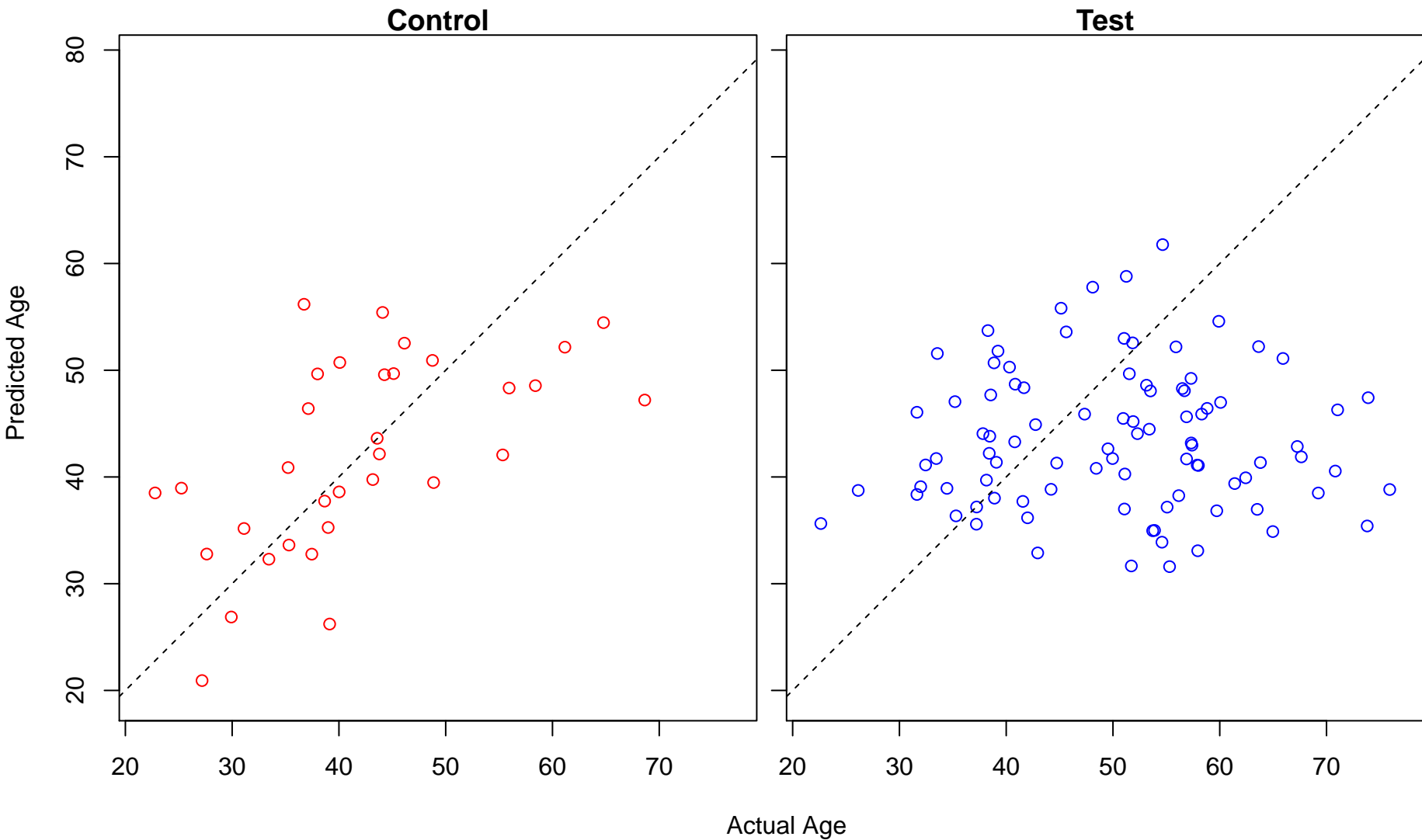
regulation of muscle system process (Score: 1.257702)



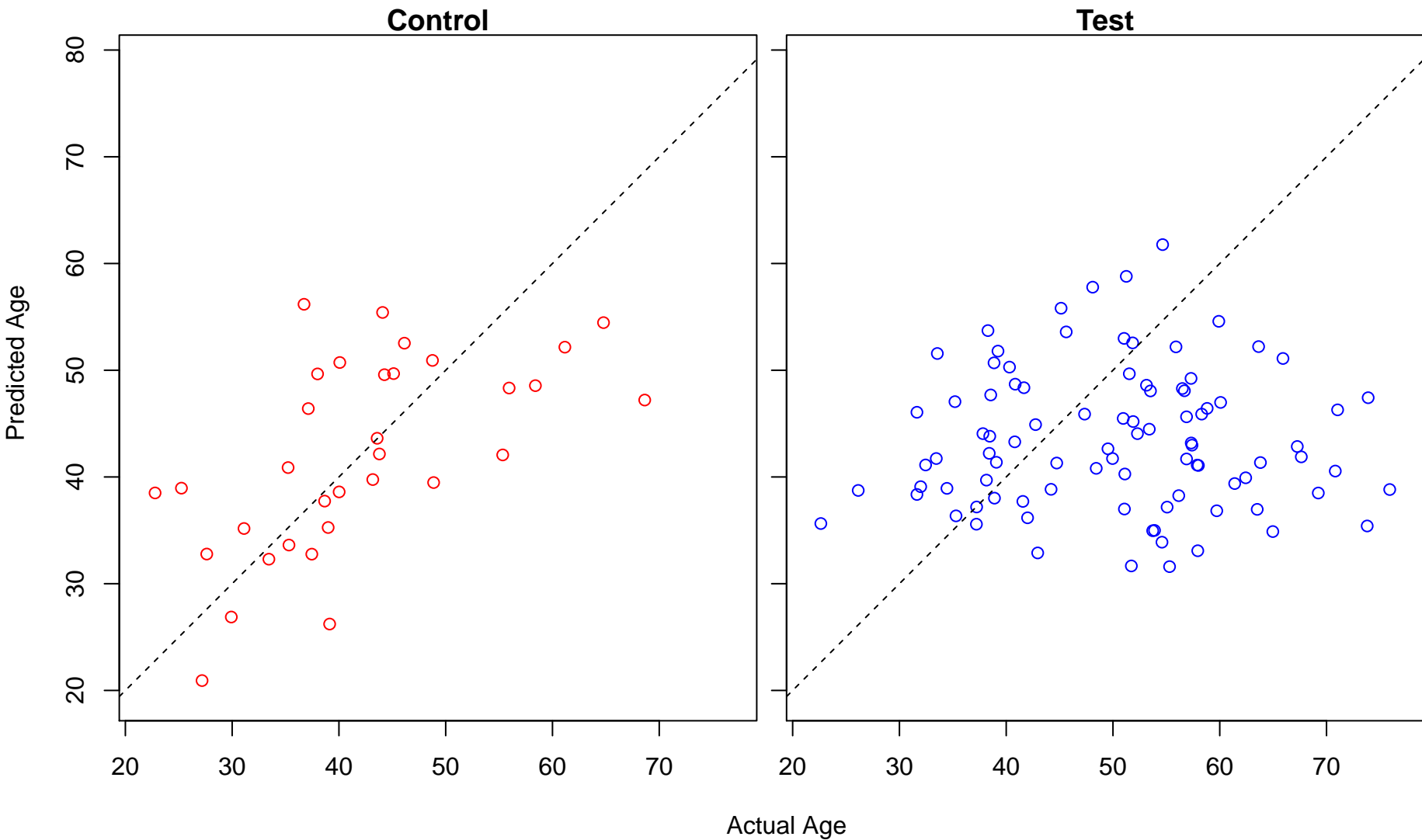
regulation of systemic arterial blood pressure by hormone (Score: 1.256266)



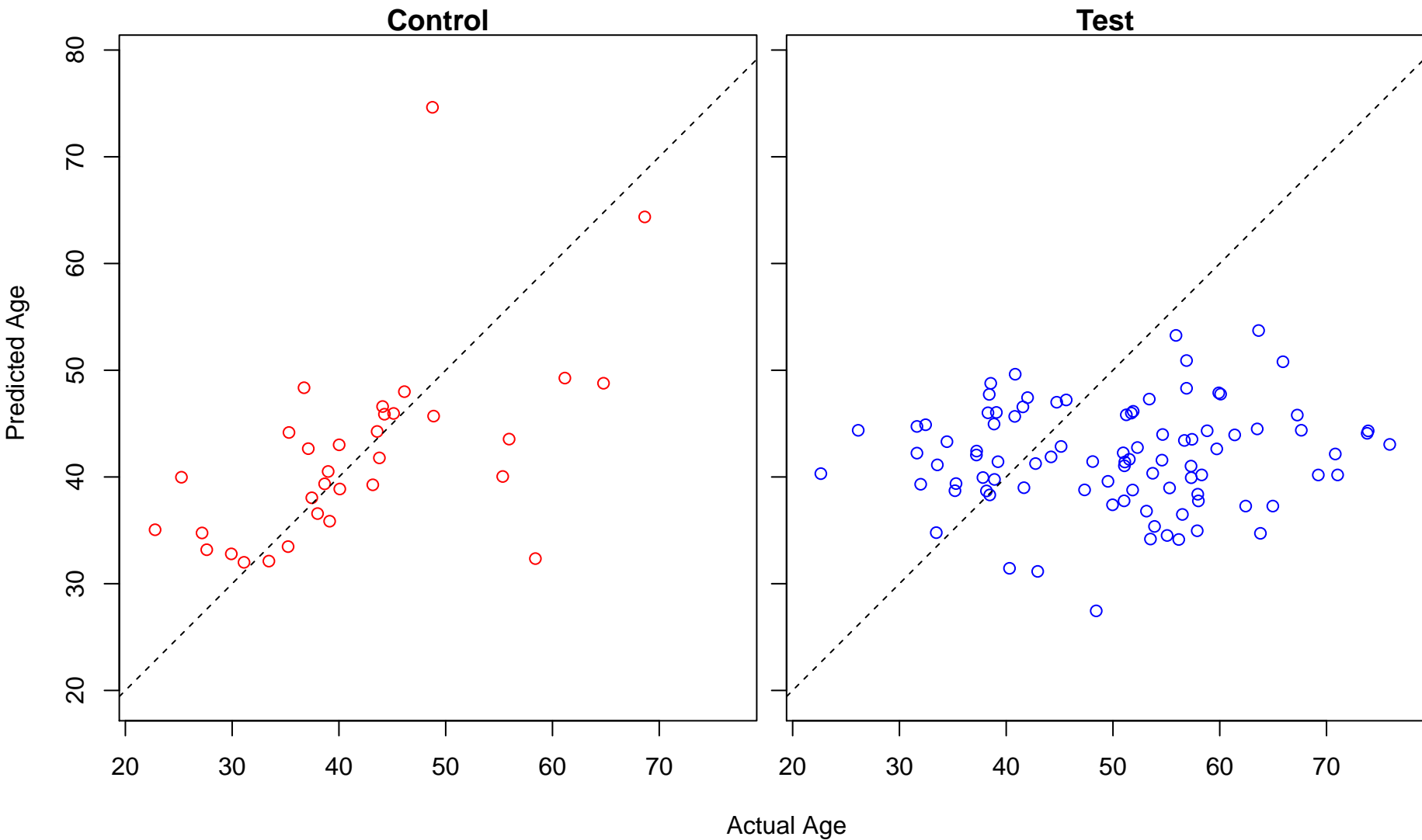
amine catabolic process (Score: 1.255488)



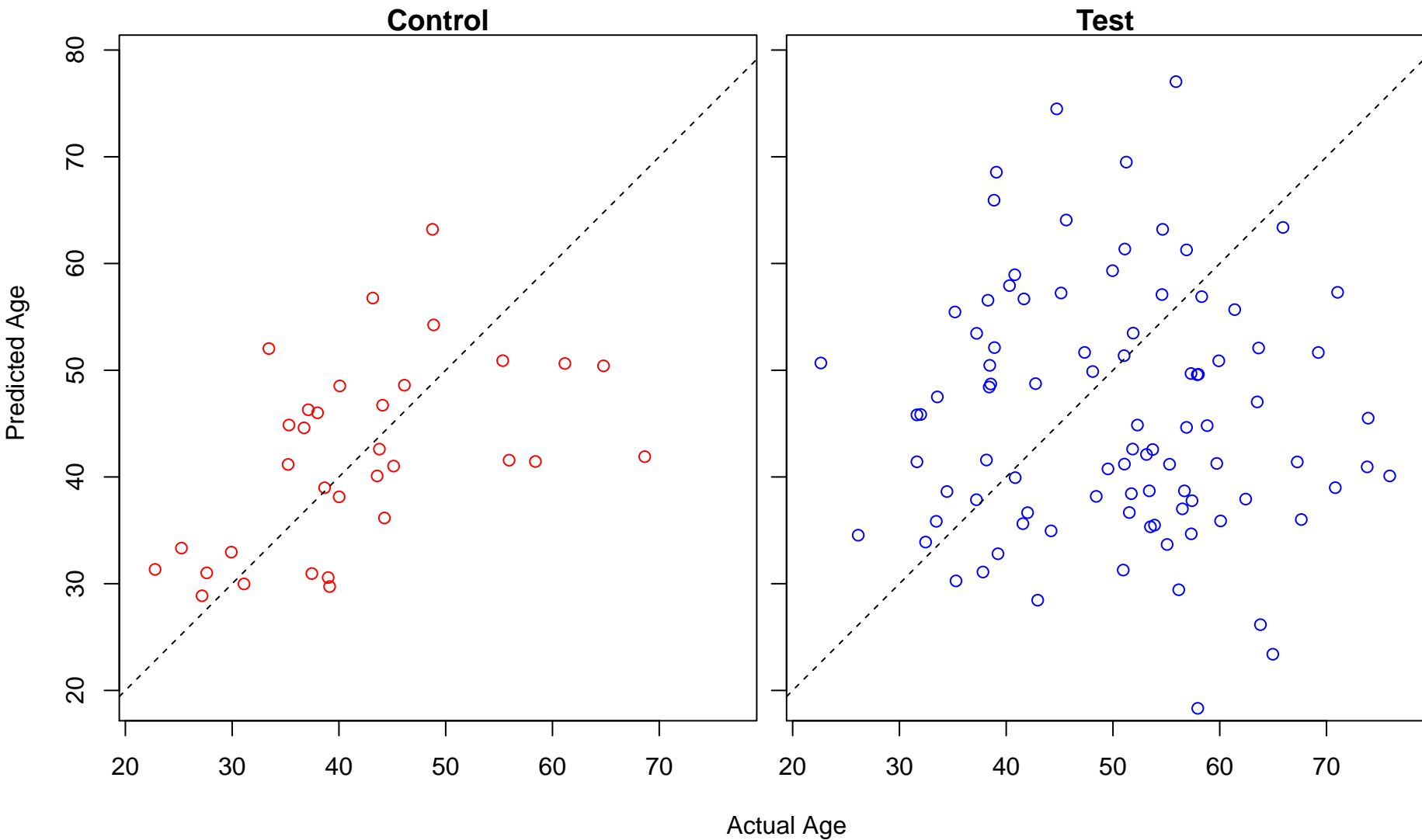
cellular biogenic amine catabolic process (Score: 1.255488)



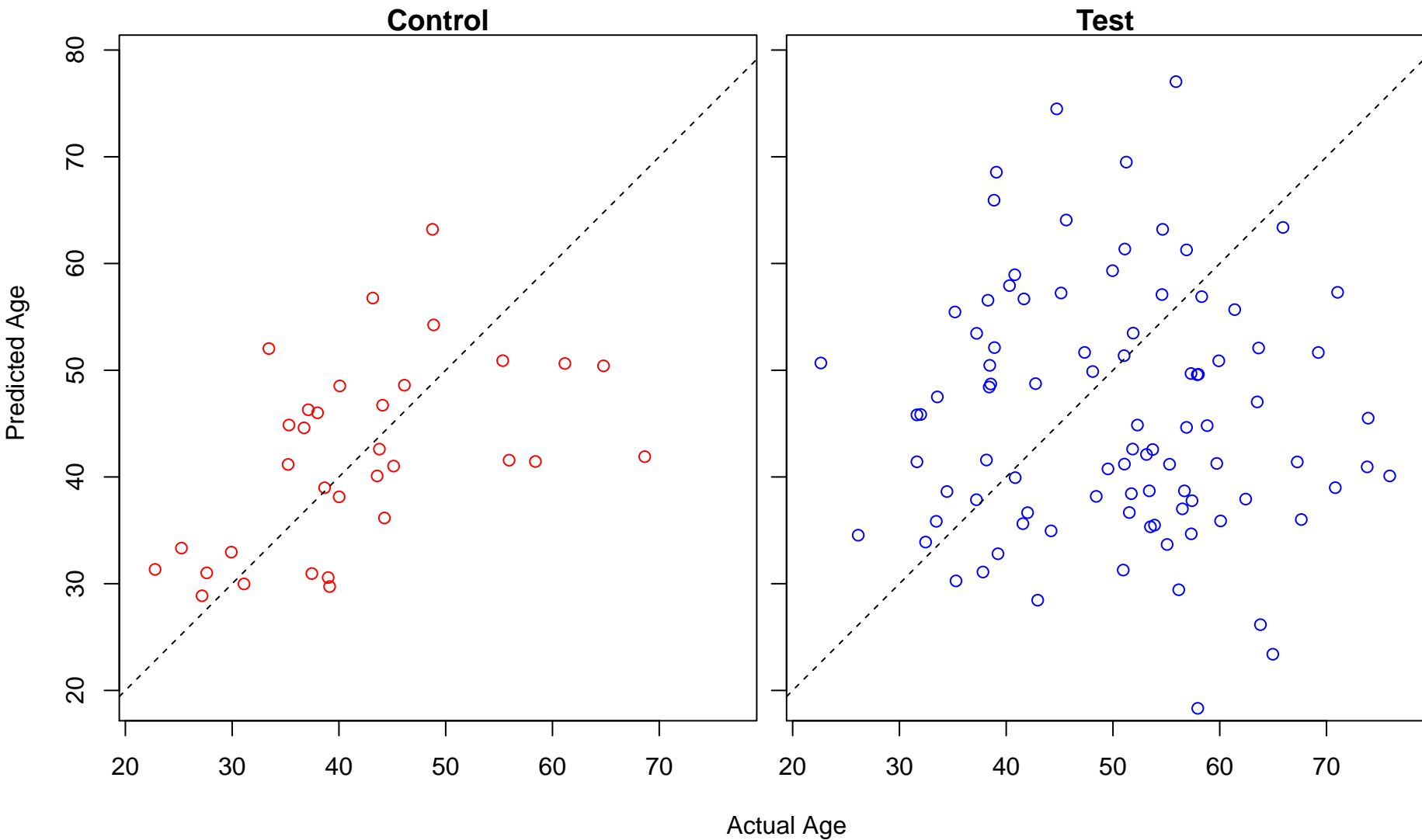
DNA replication initiation (Score: 1.253627)



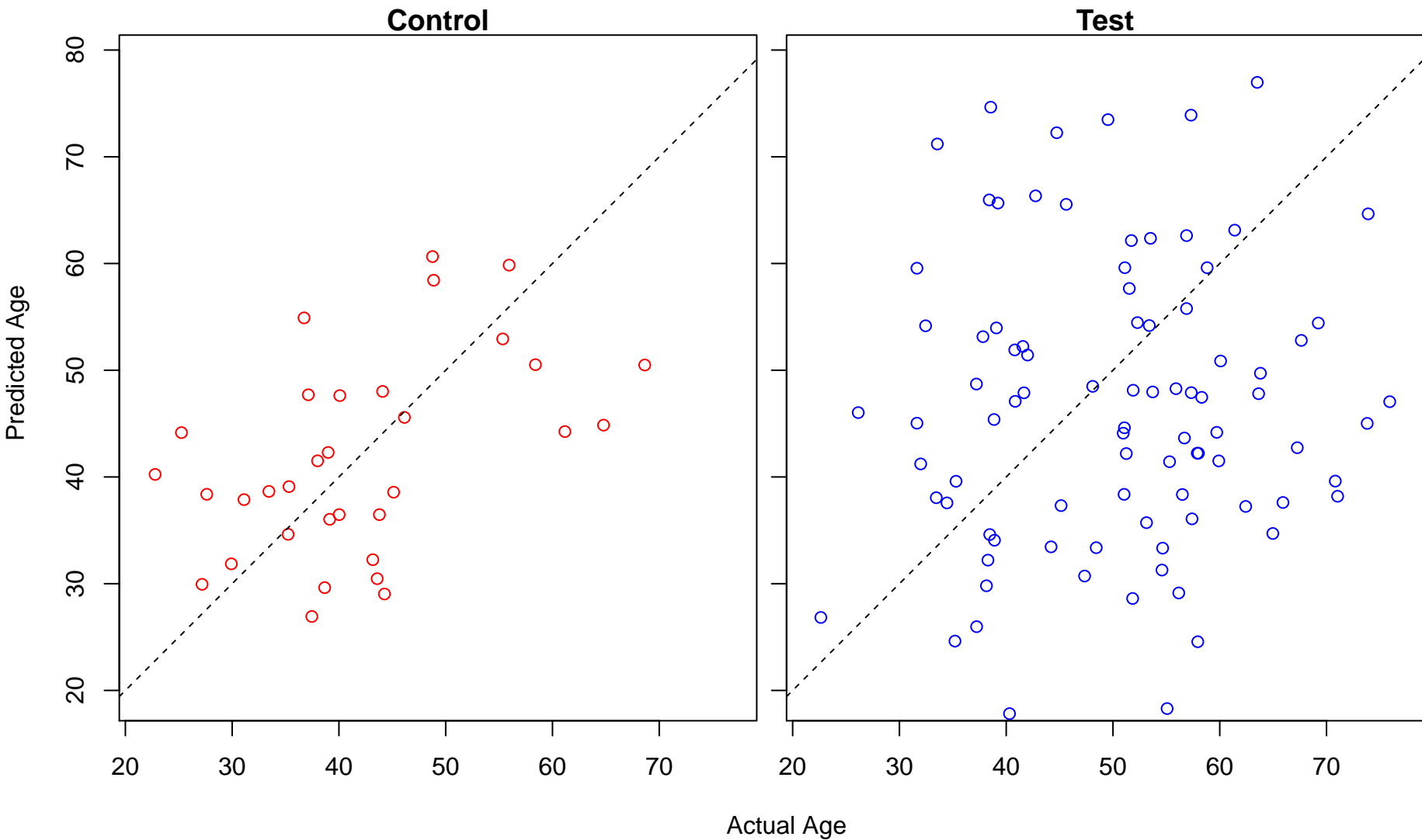
negative regulation of response to extracellular stimulus (Score: 1.252092)



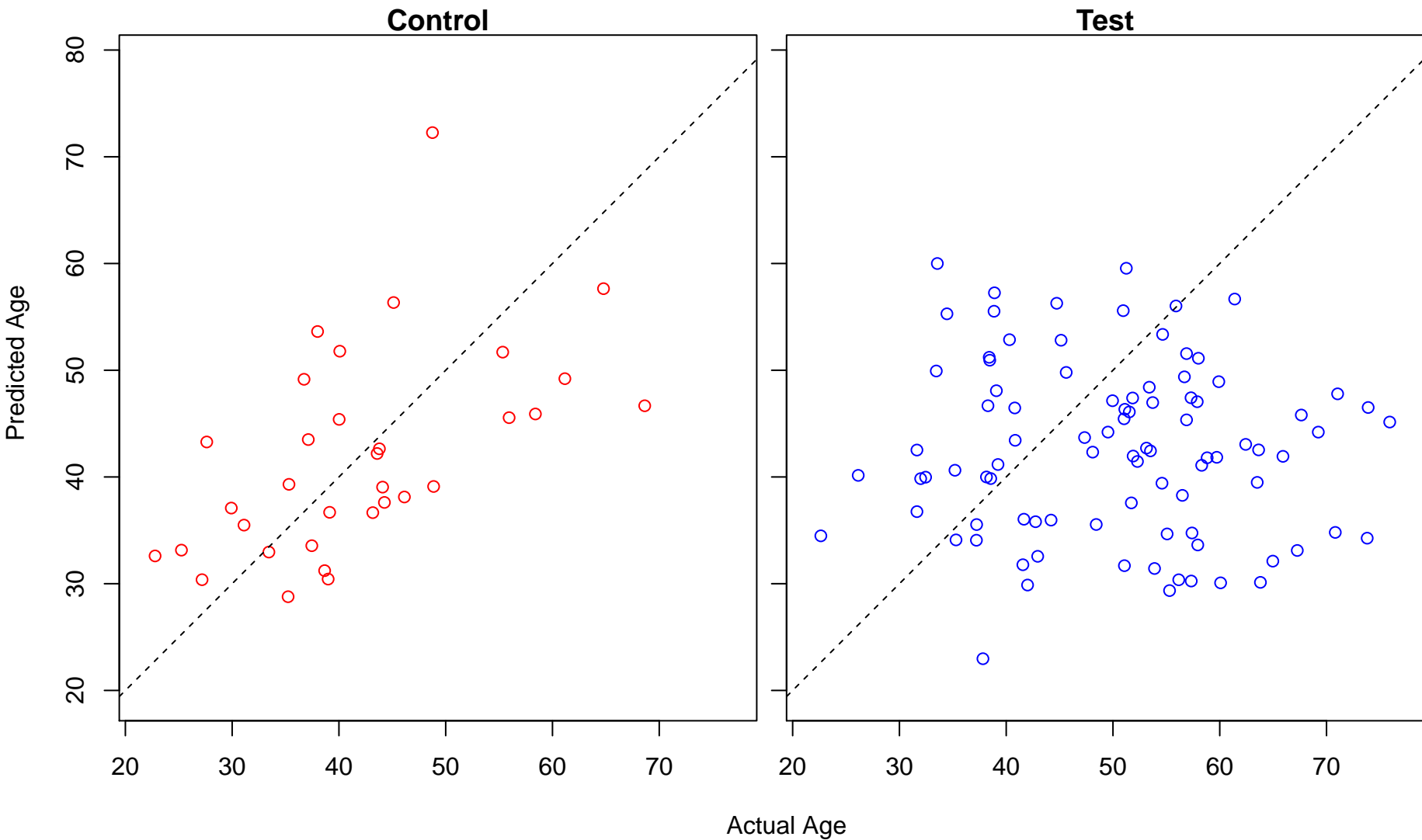
negative regulation of response to nutrient levels (Score: 1.252092)



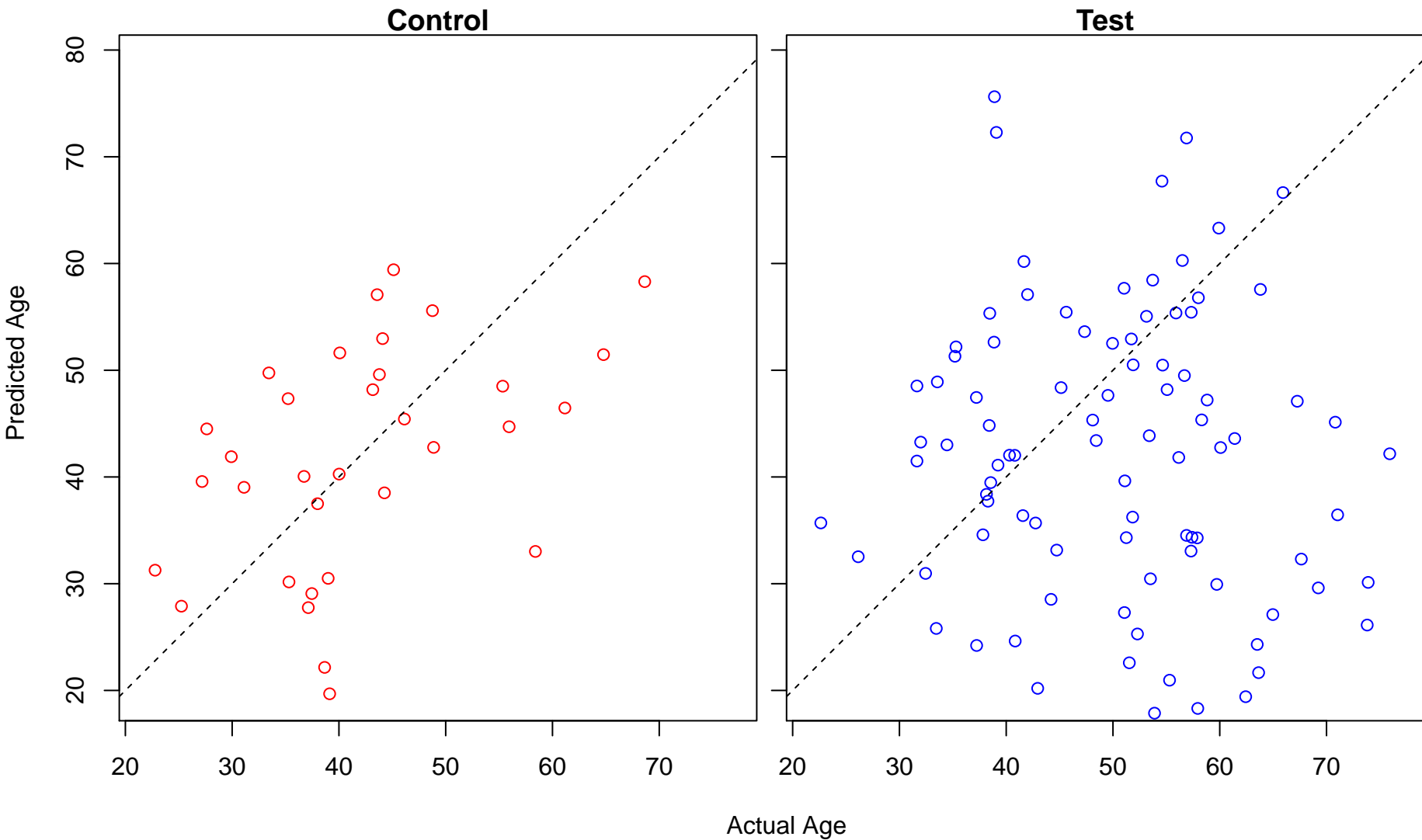
positive regulation of membrane protein ectodomain proteolysis (Score: 1.251460)



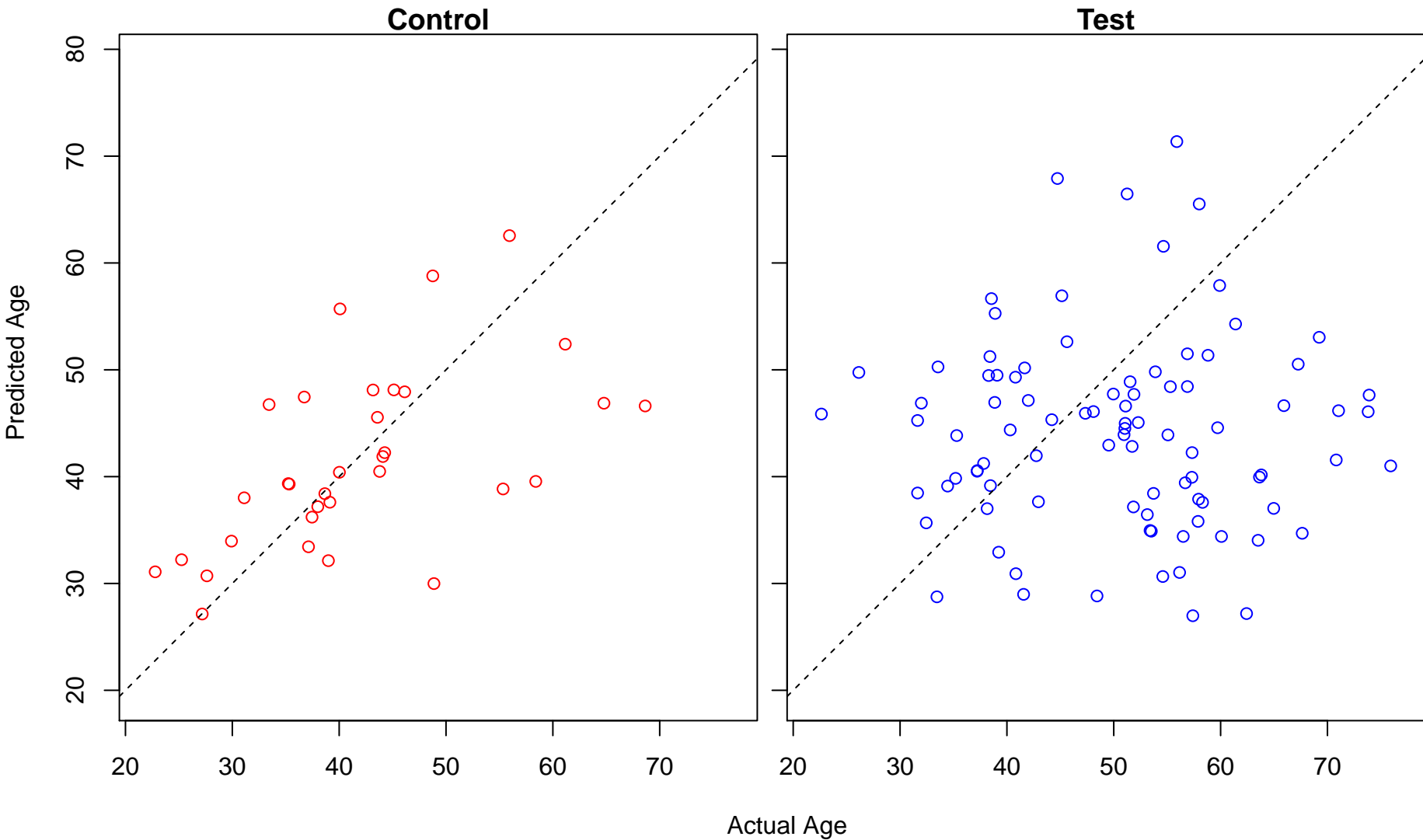
regulation of actin cytoskeleton organization (Score: 1.251224)



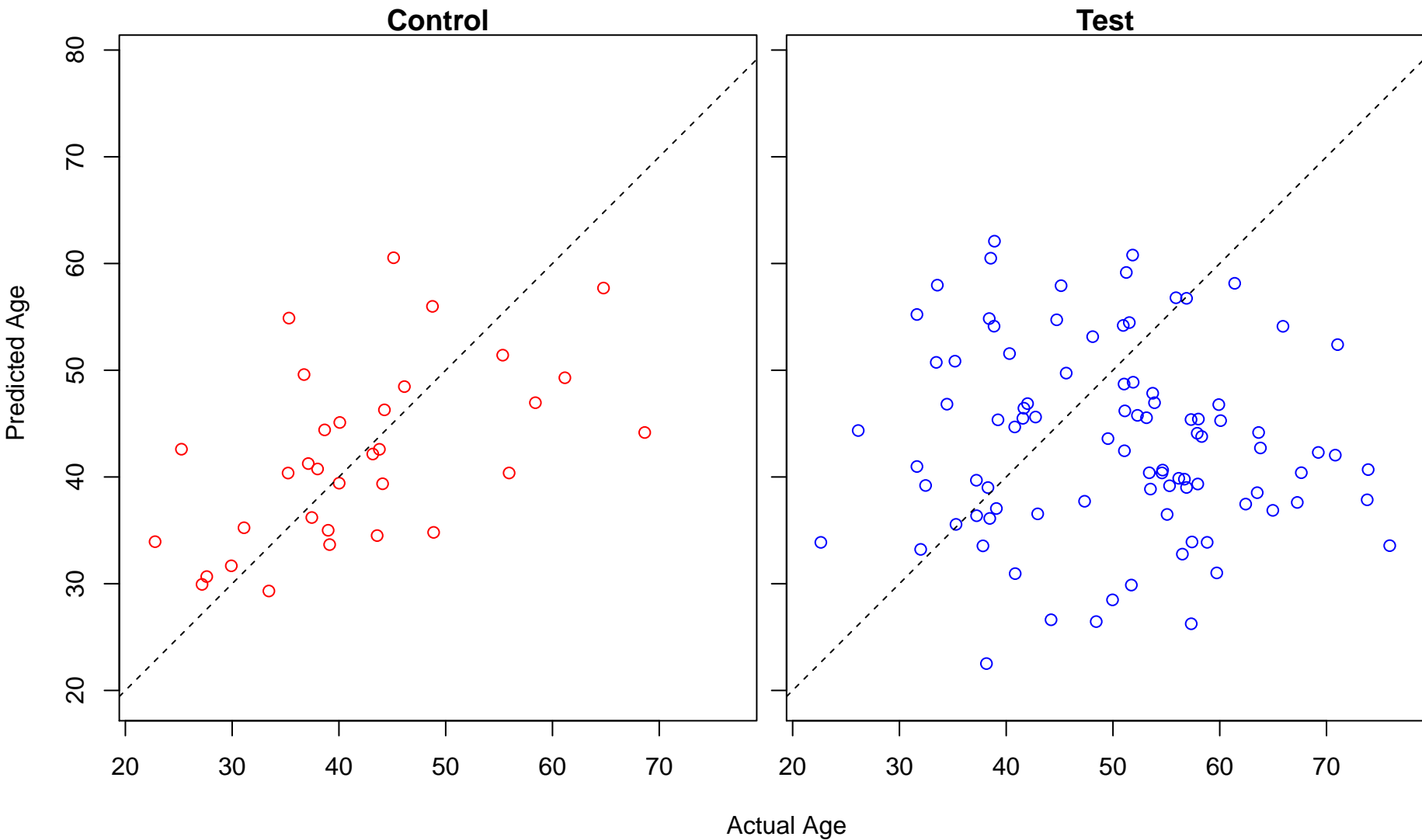
negative regulation of translational initiation (Score: 1.249807)



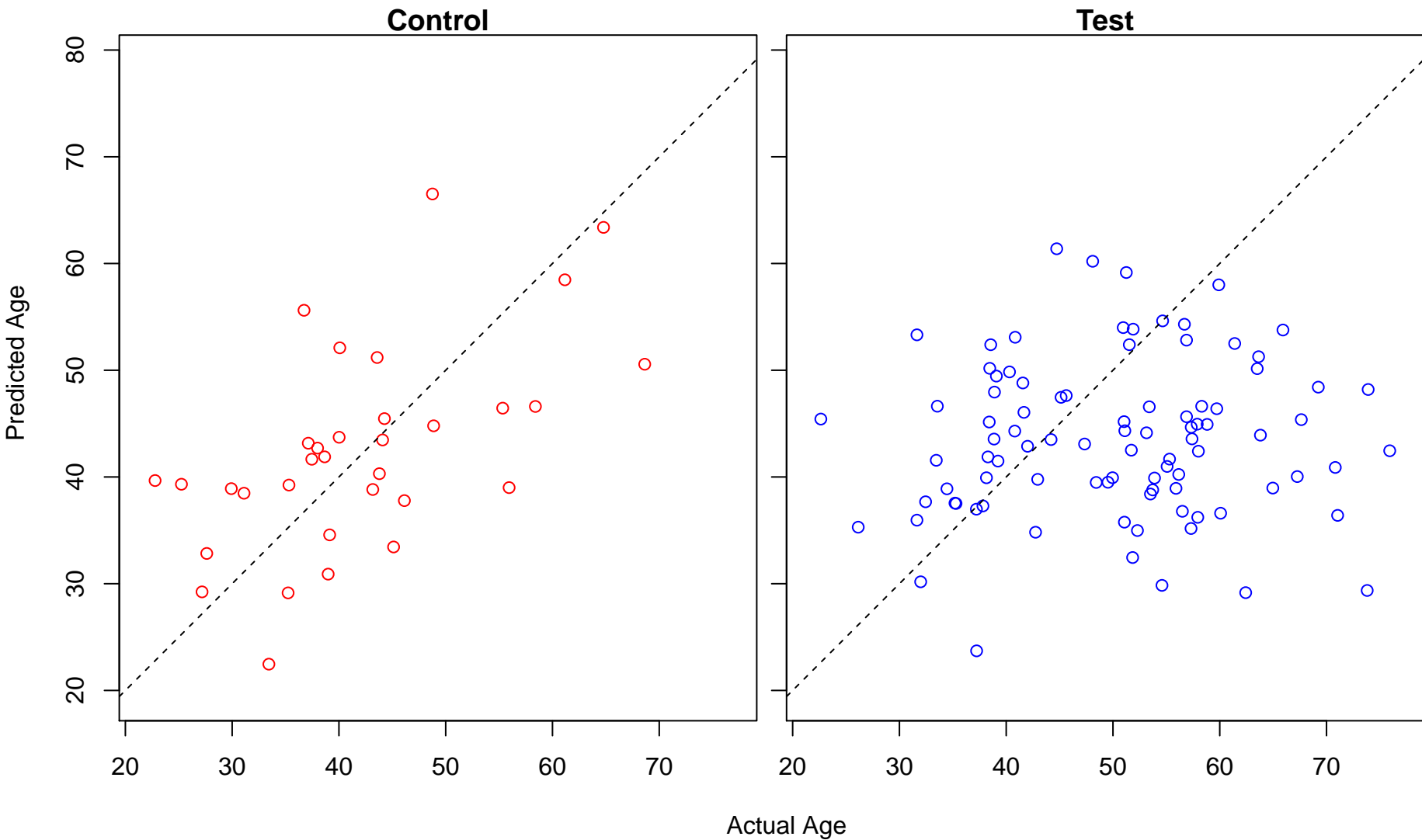
regulation of potassium ion transmembrane transporter activity (Score: 1.246077)



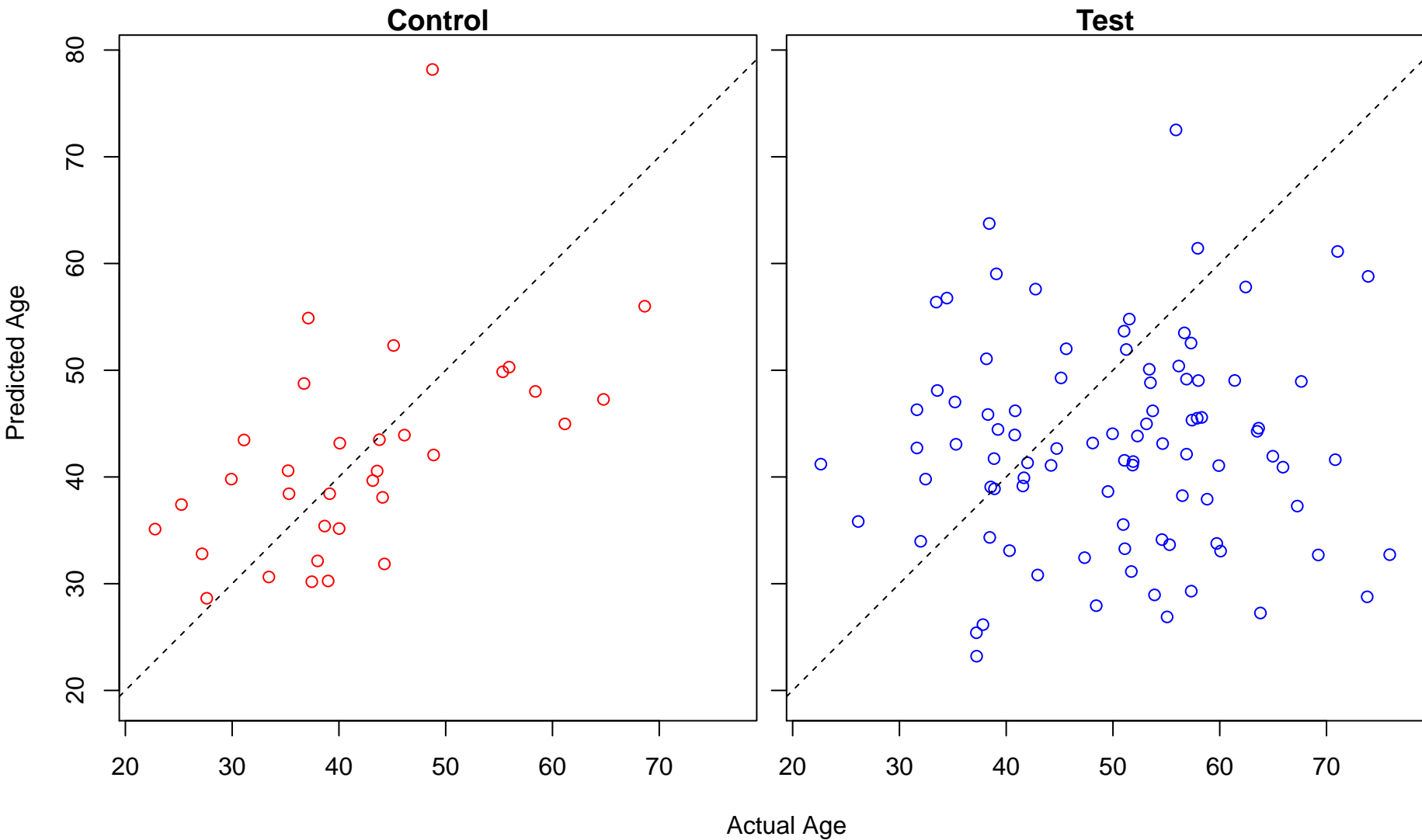
spinal cord development (Score: 1.245125)



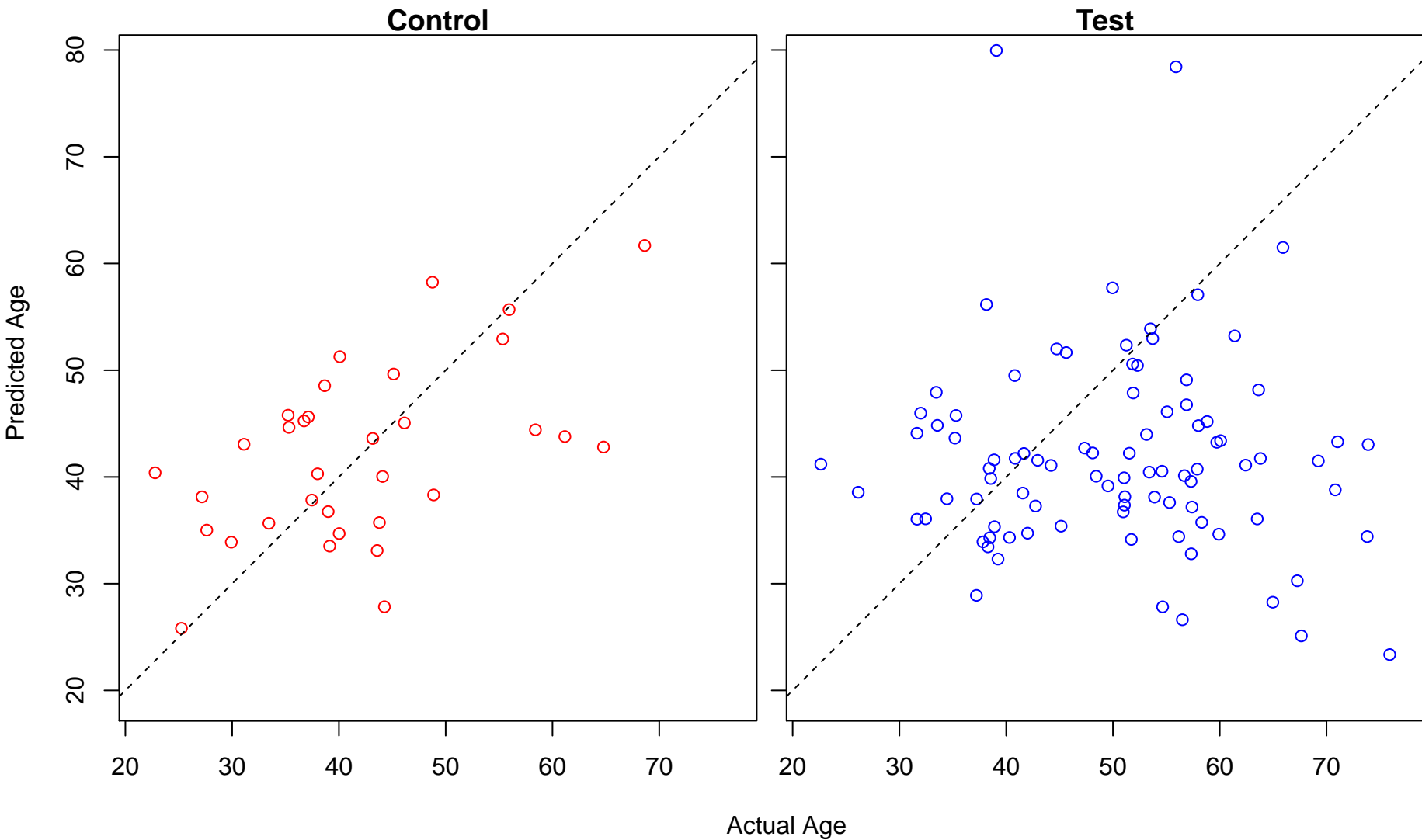
mitochondrial fragmentation involved in apoptotic process (Score: 1.243219)



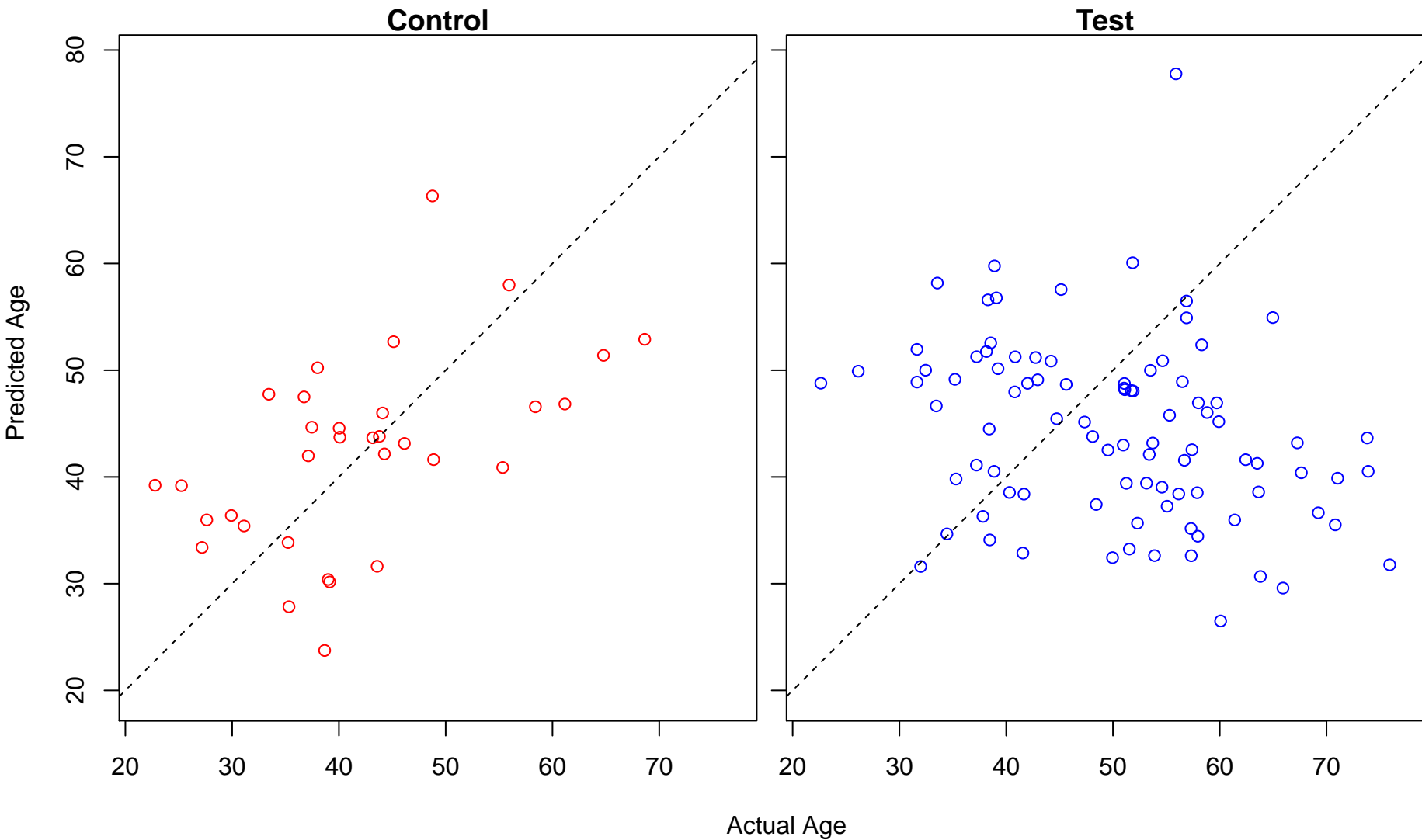
response to metal ion (Score: 1.243154)



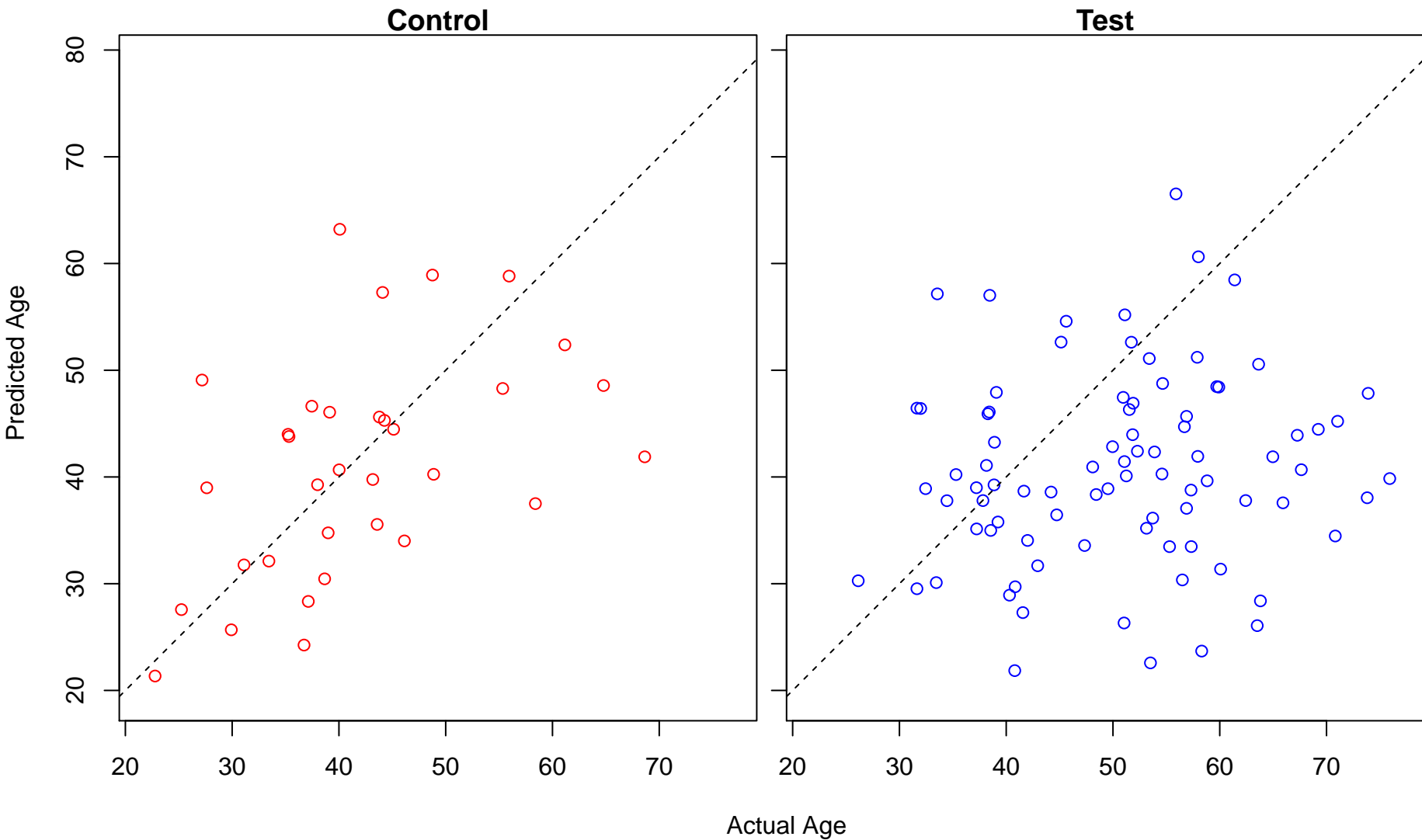
response to iron ion (Score: 1.241632)



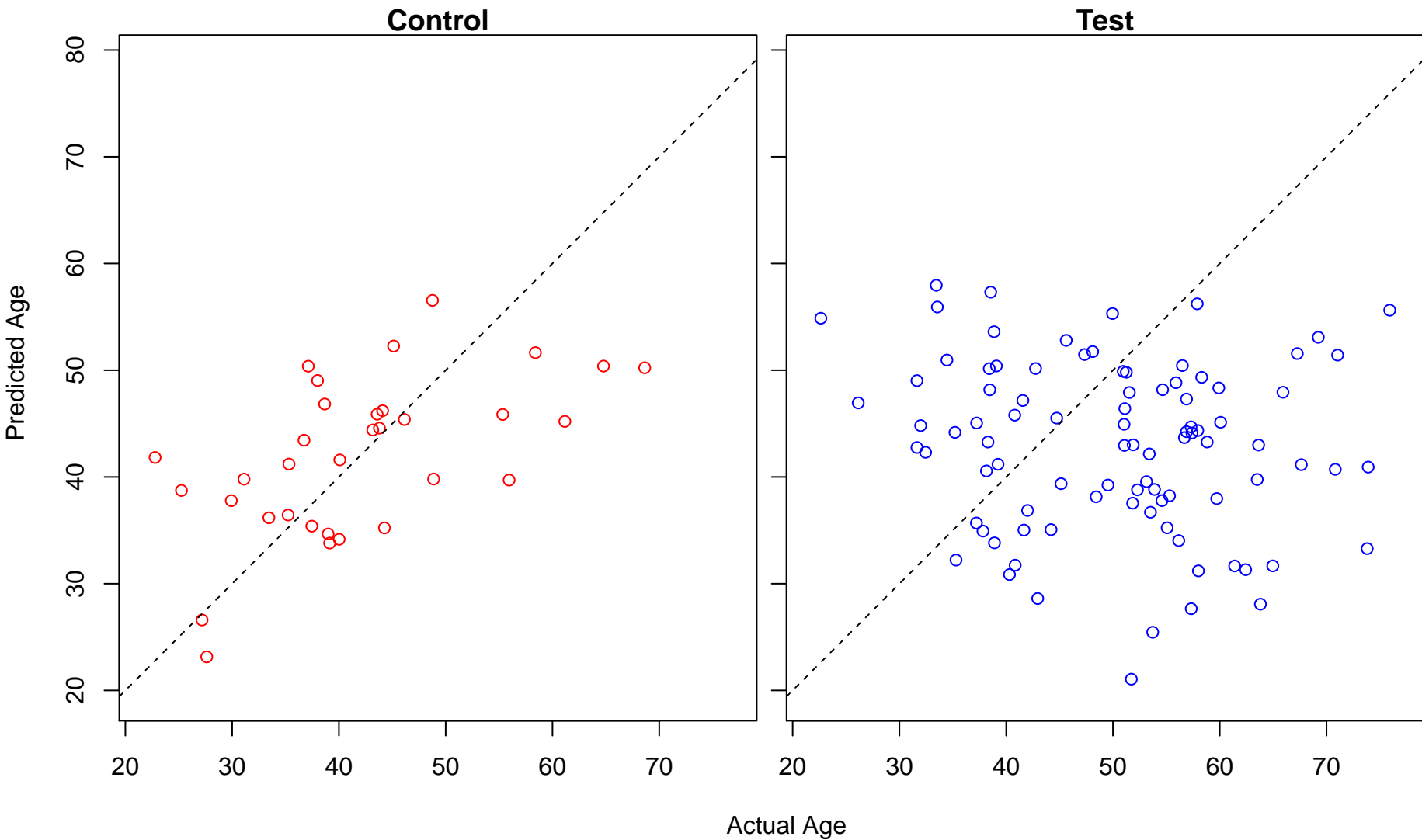
negative regulation of T cell differentiation in thymus (Score: 1.237748)



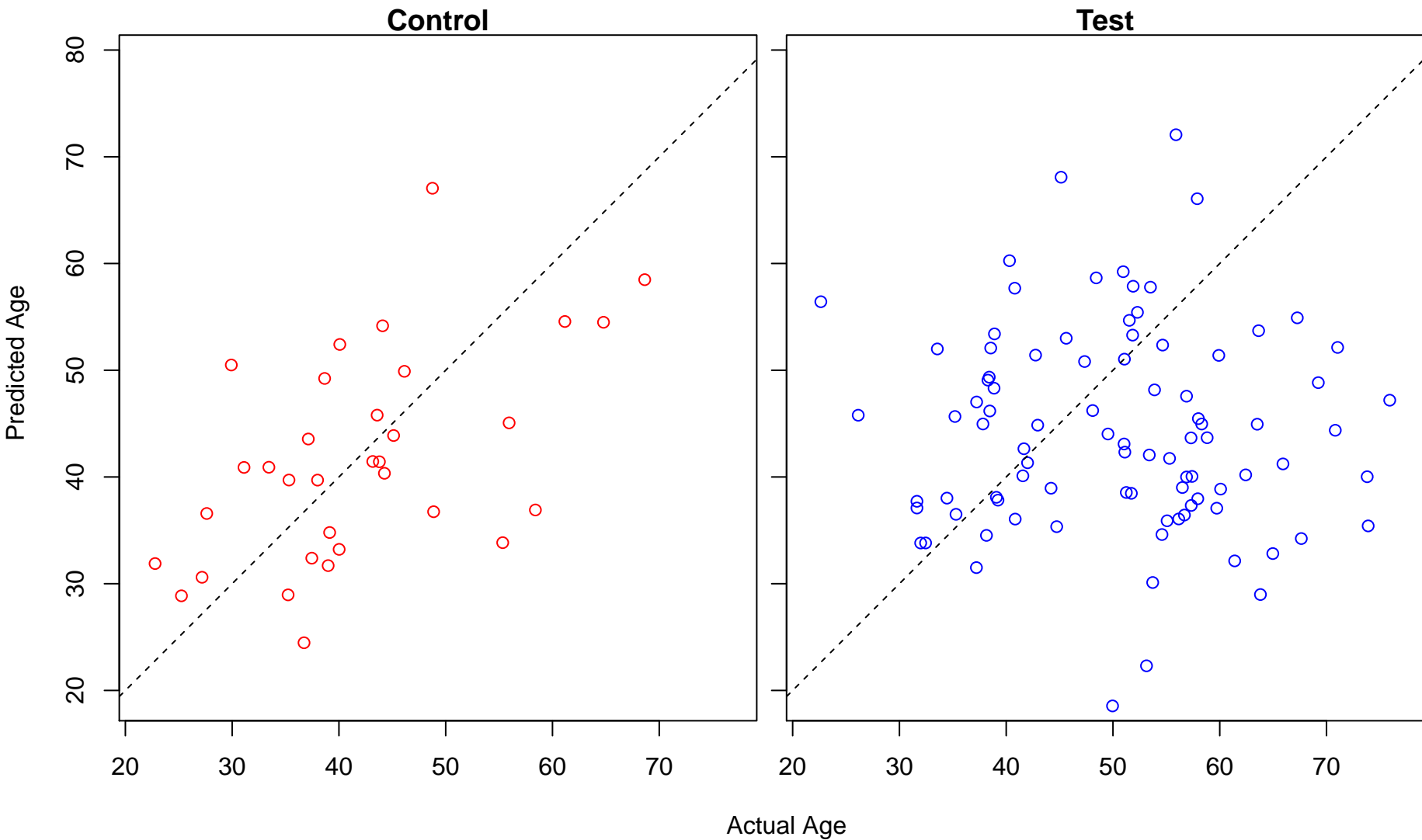
positive regulation of lipid kinase activity (Score: 1.235744)



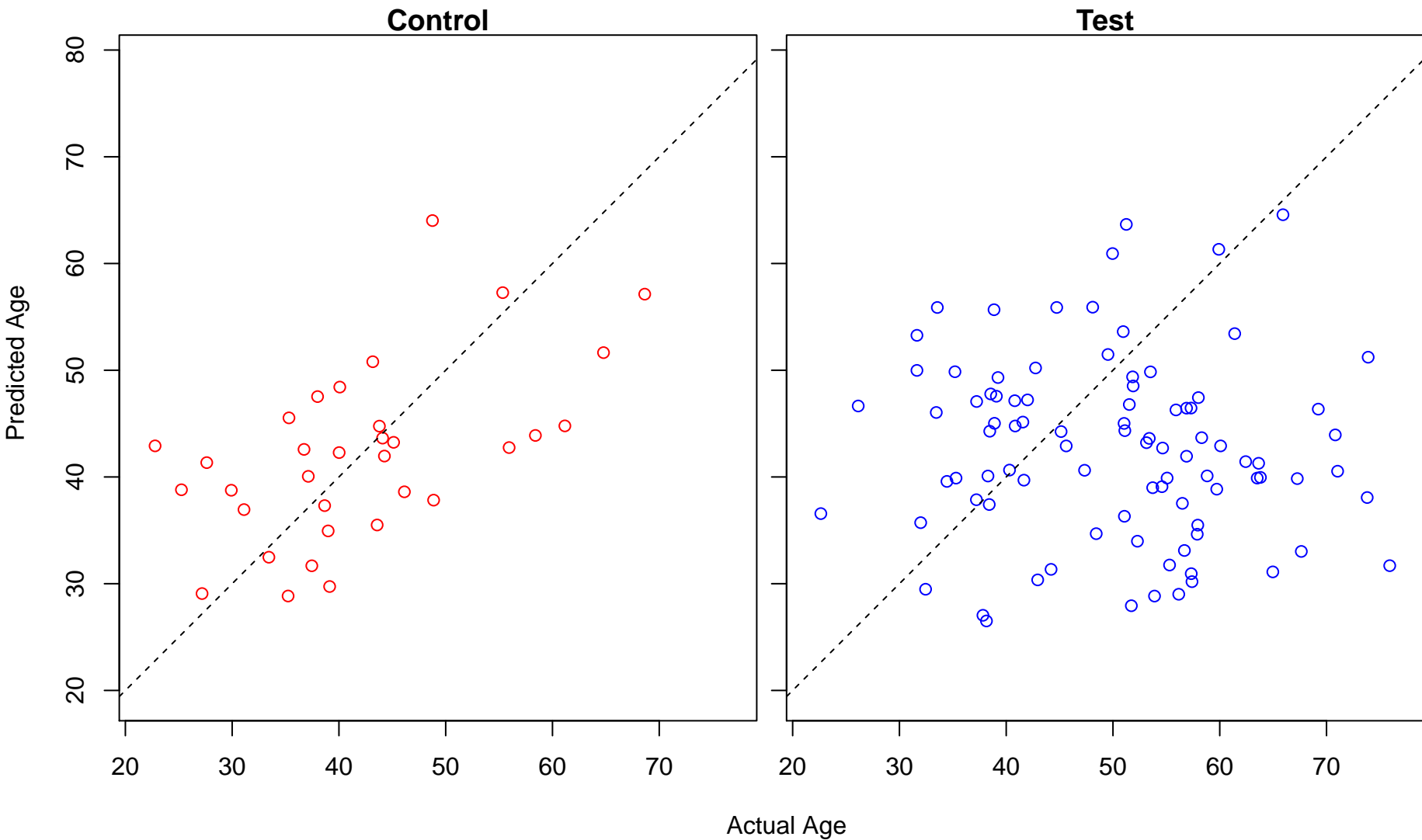
central nervous system myelin maintenance (Score: 1.232768)



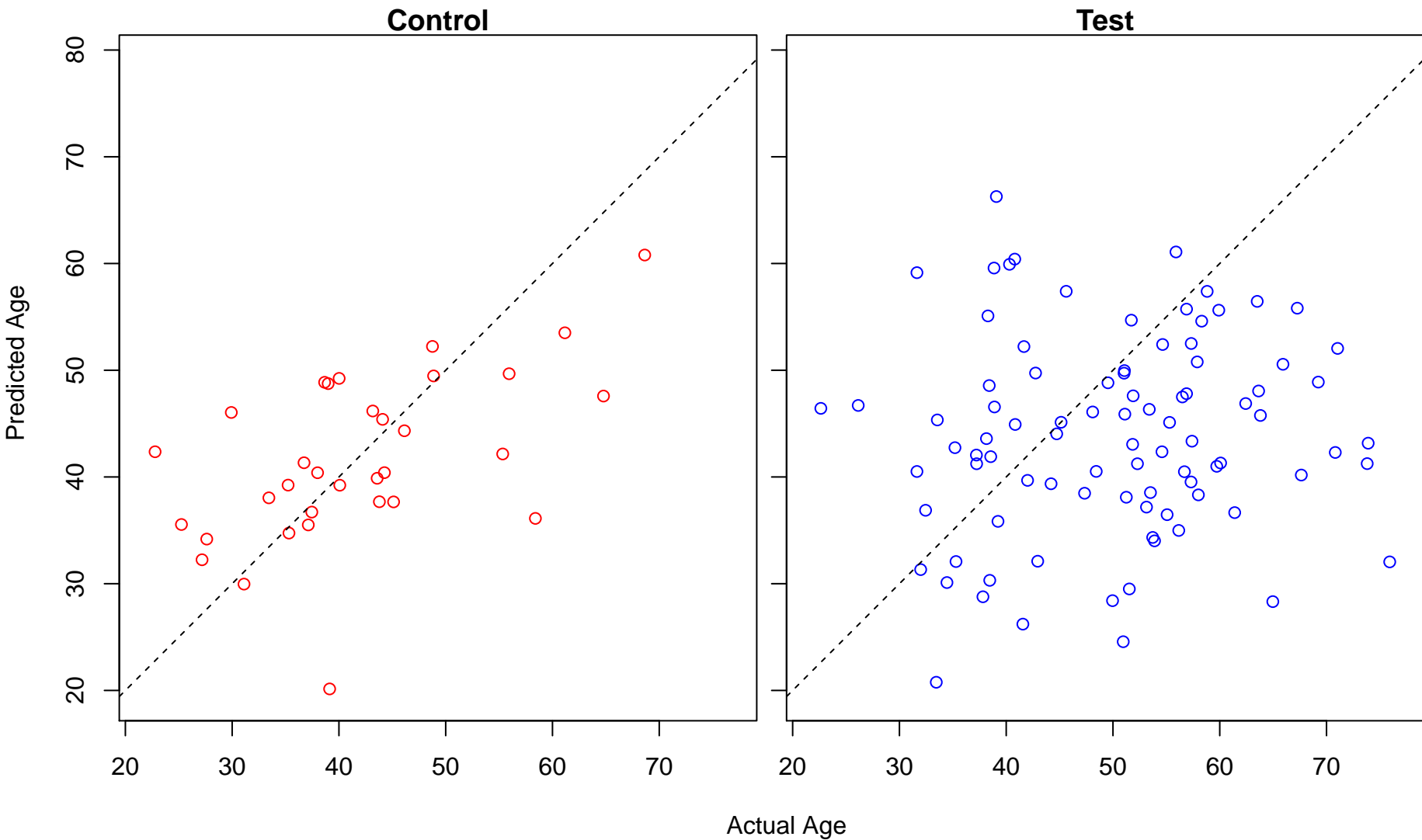
pathway-restricted SMAD protein phosphorylation (Score: 1.232521)



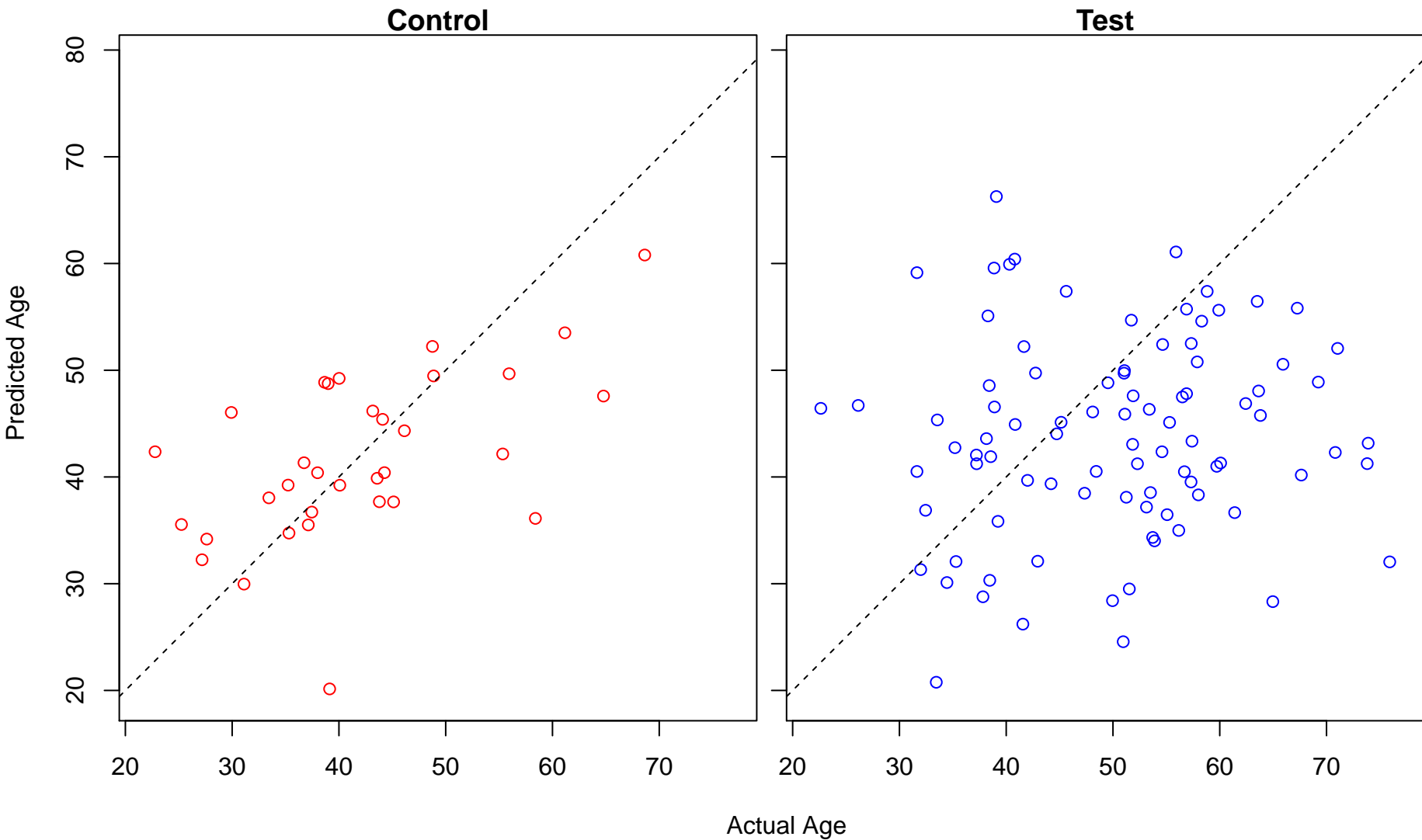
response to light stimulus (Score: 1.230425)



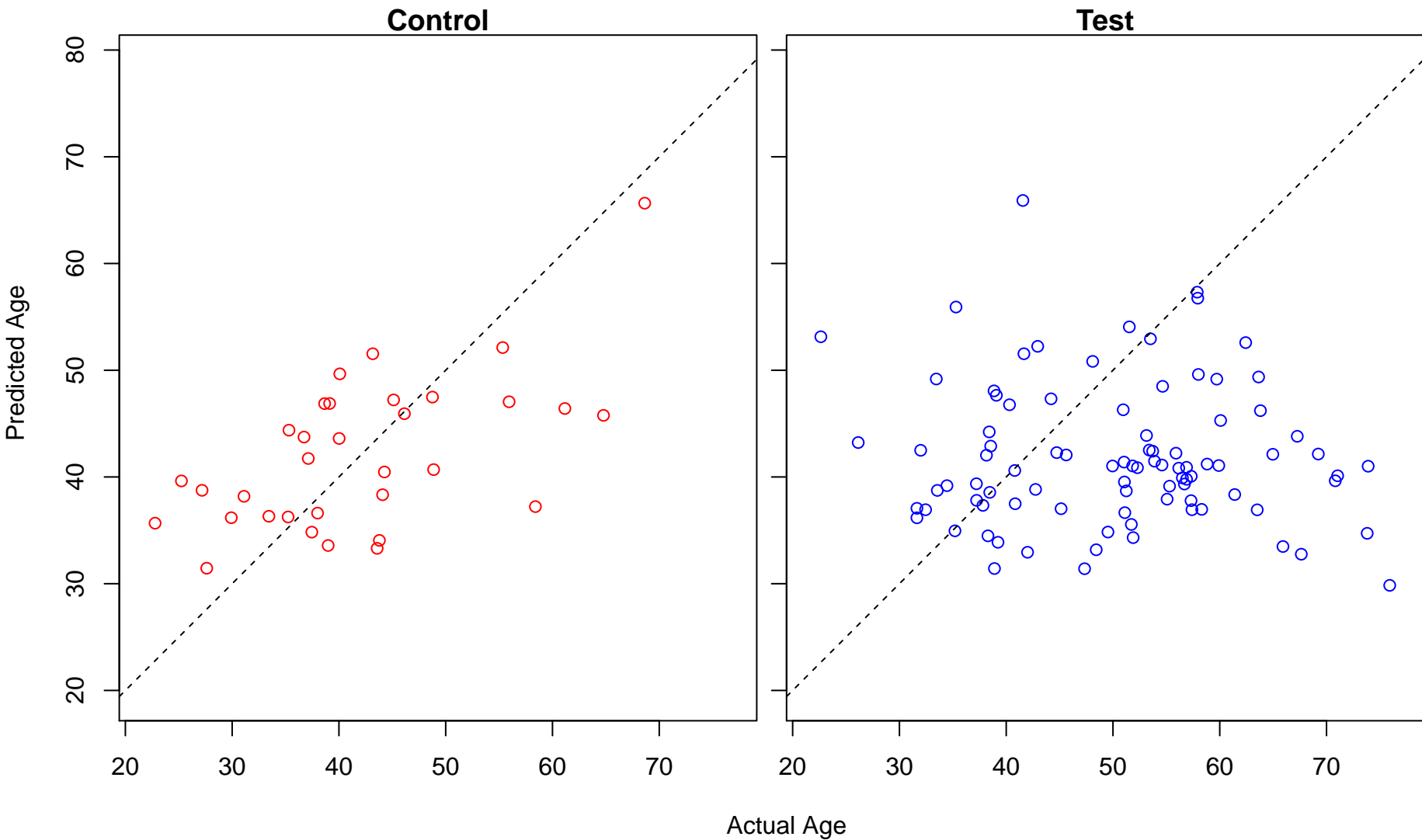
subpallium development (Score: 1.230395)



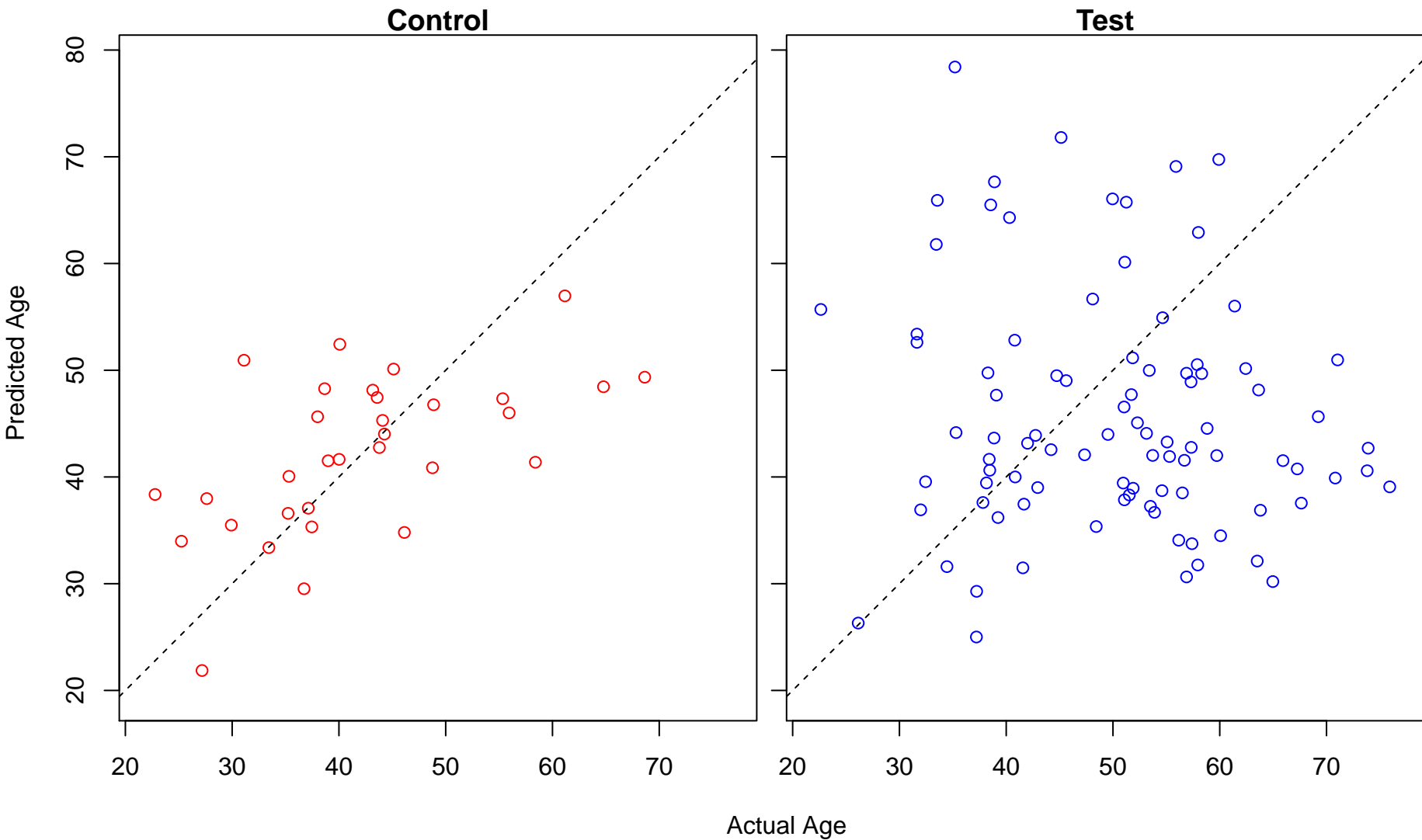
striatum development (Score: 1.230395)



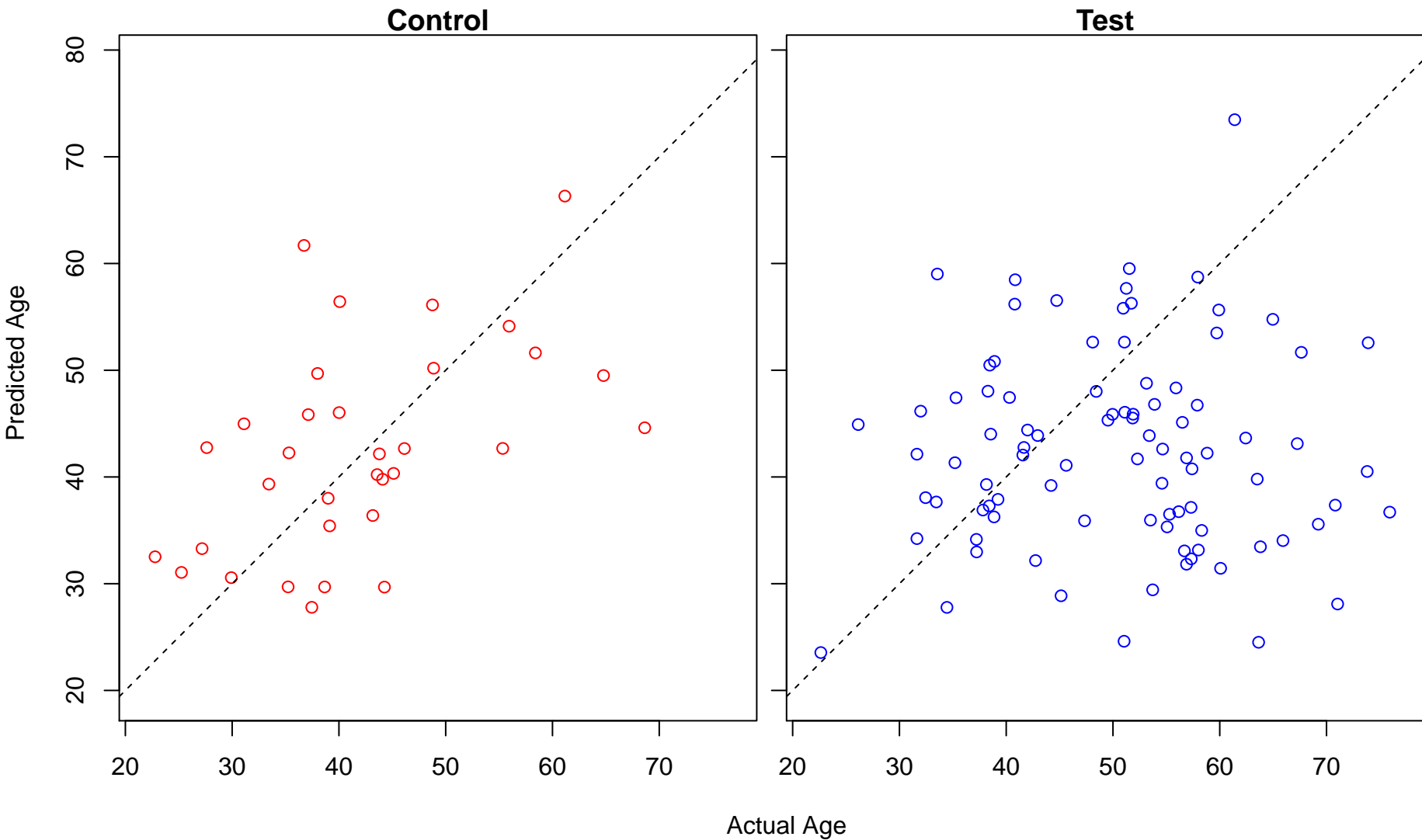
detection of calcium ion (Score: 1.227875)



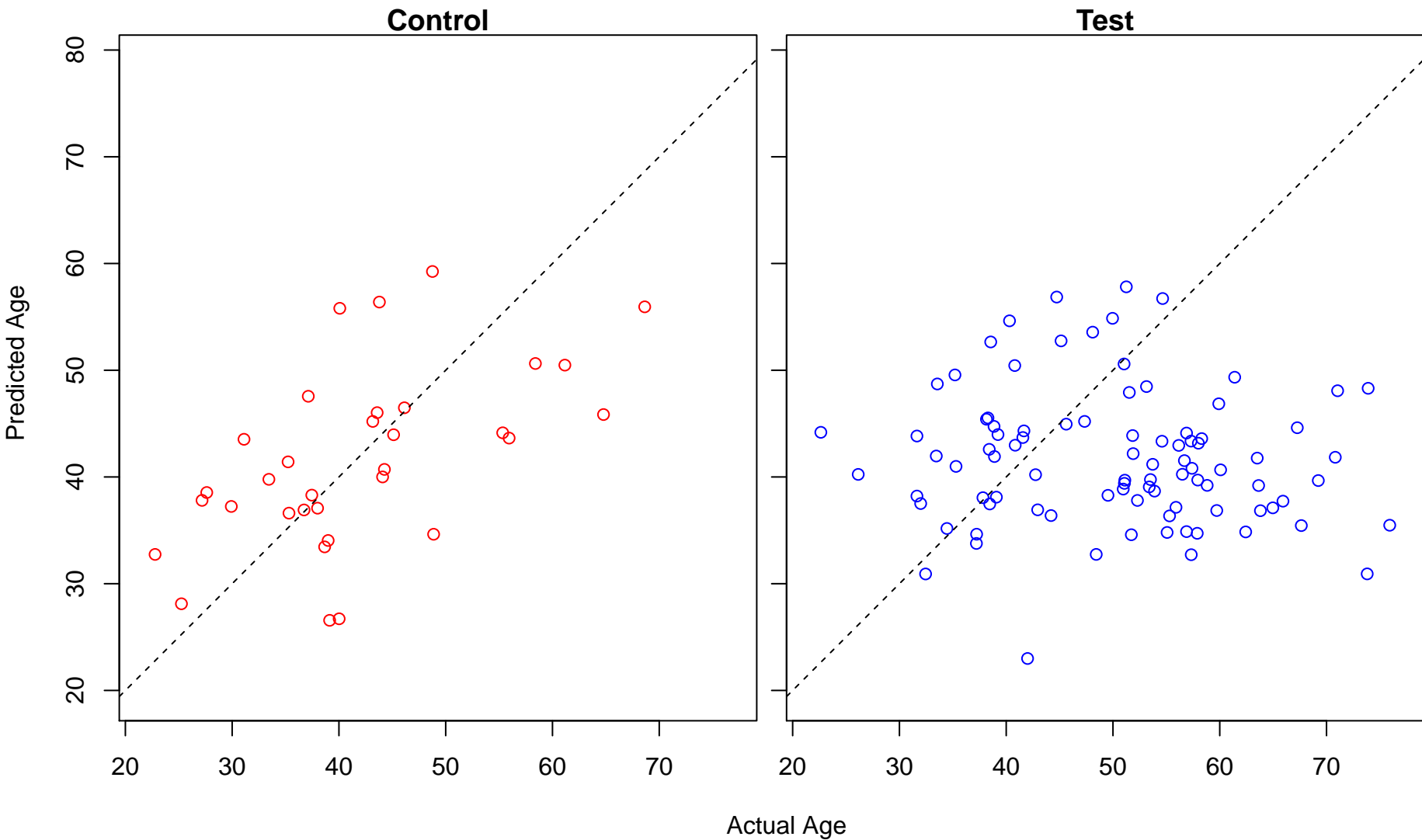
regulation of histone H3-K9 methylation (Score: 1.227607)



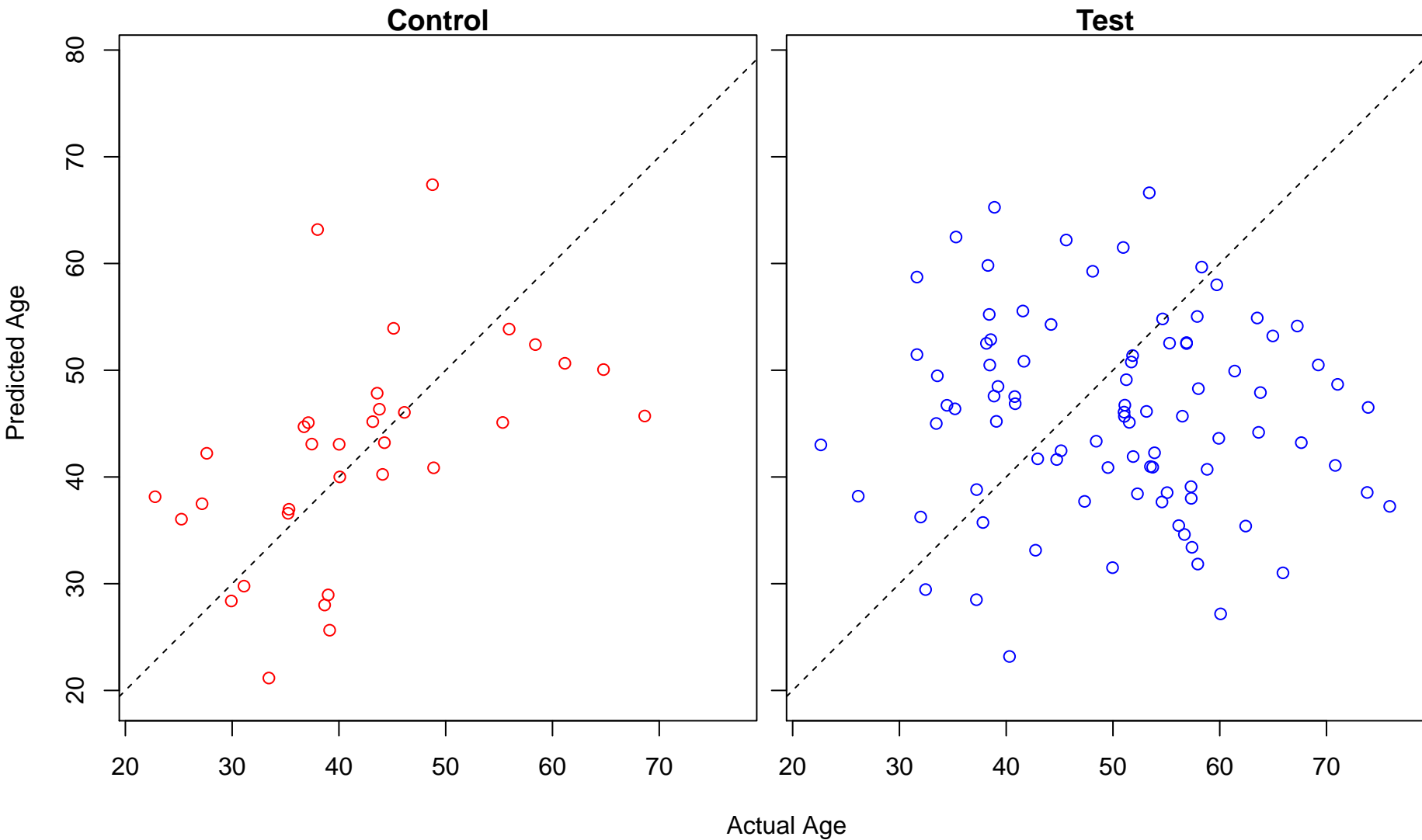
endothelial cell proliferation (Score: 1.226310)



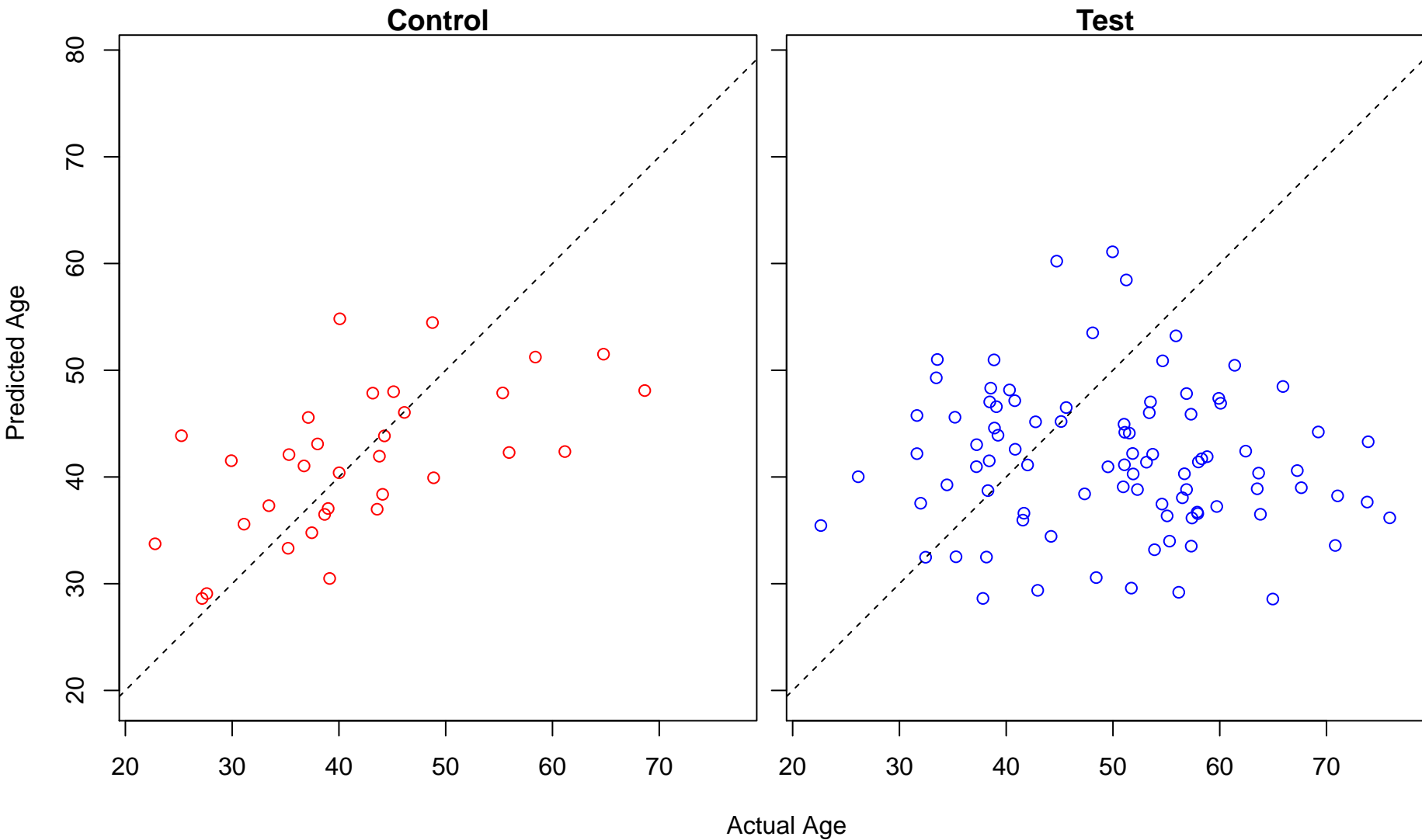
phosphatidylethanolamine biosynthetic process (Score: 1.223702)



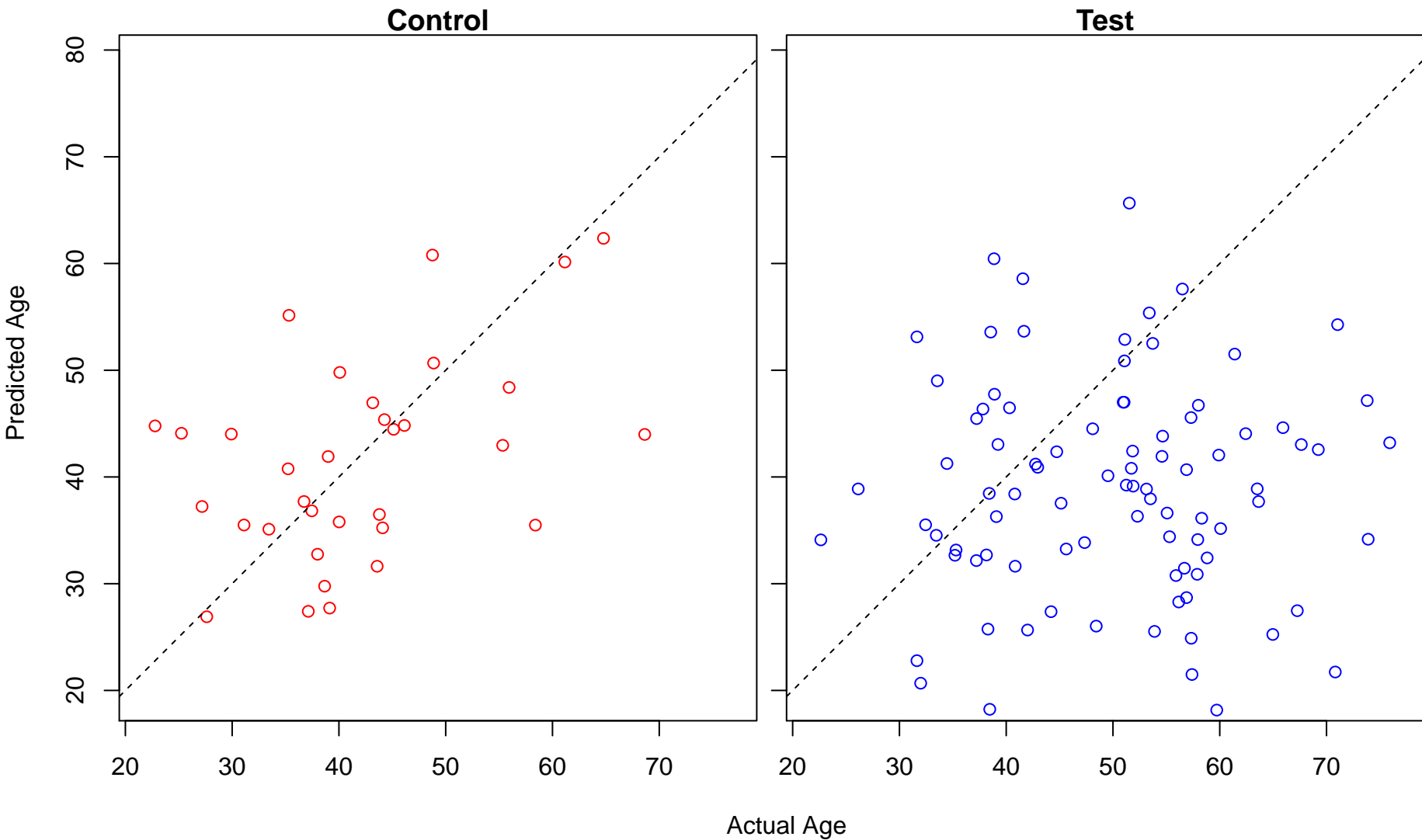
morphogenesis of an endothelium (Score: 1.223496)



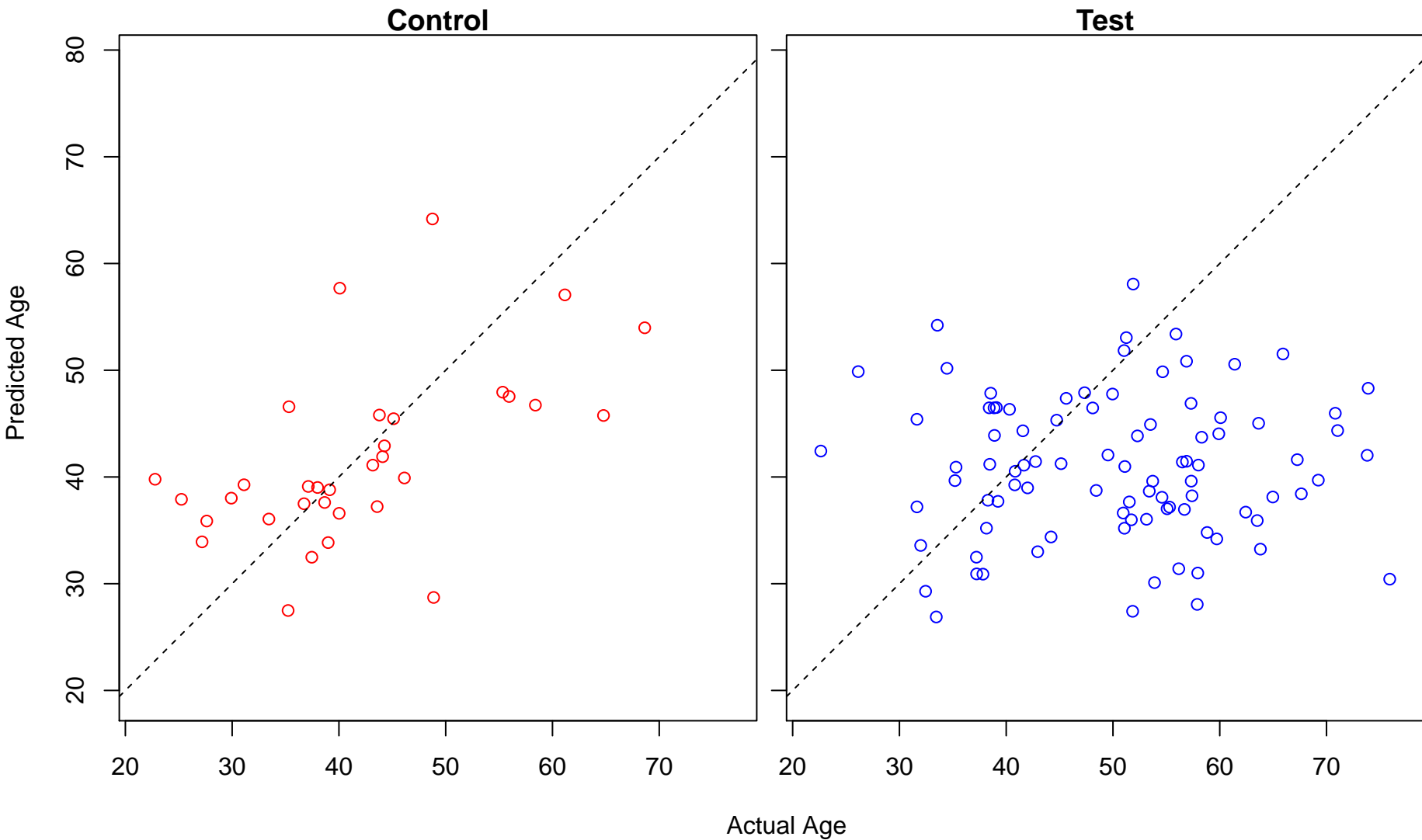
organic hydroxy compound transport (Score: 1.220334)



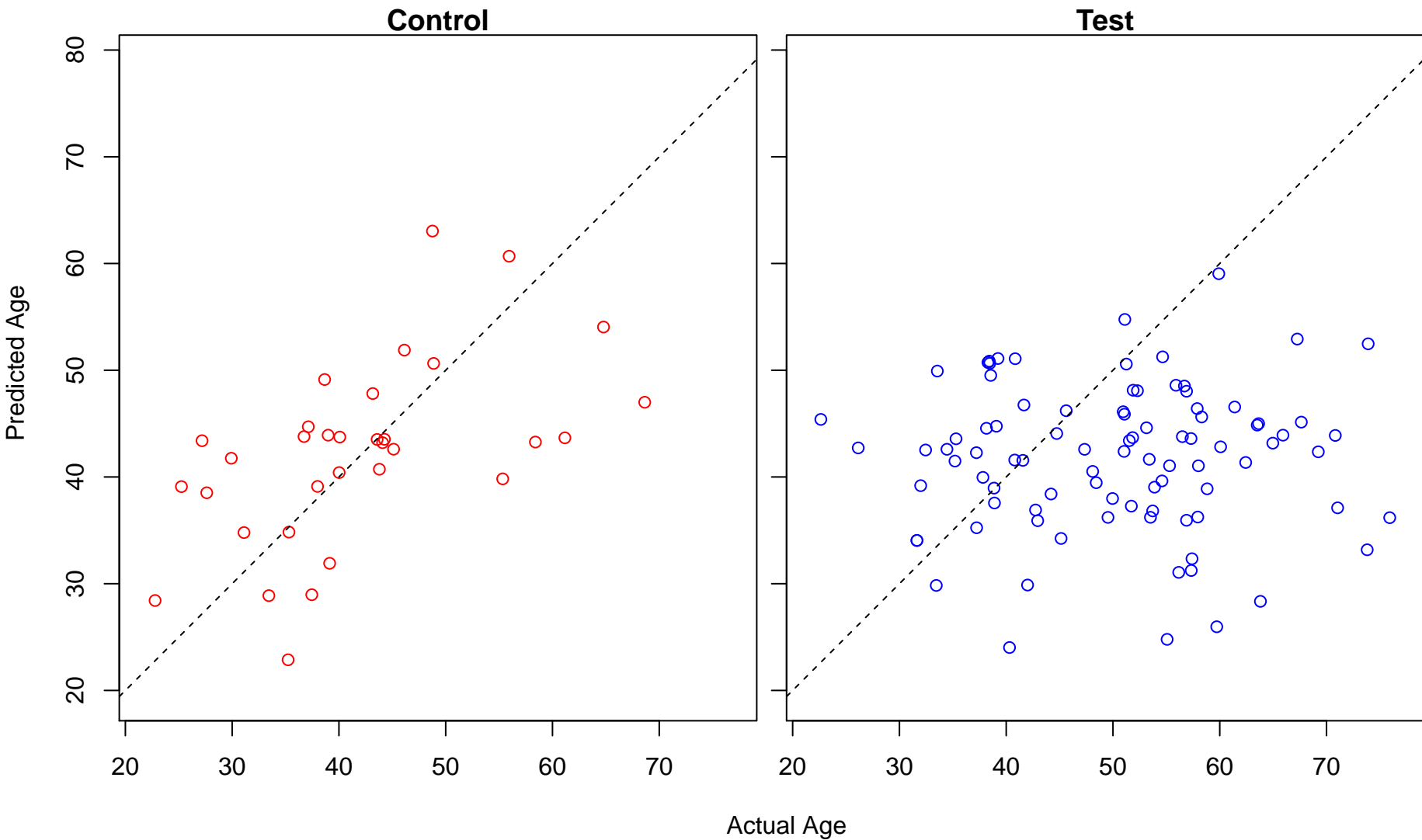
neuron migration (Score: 1.217565)



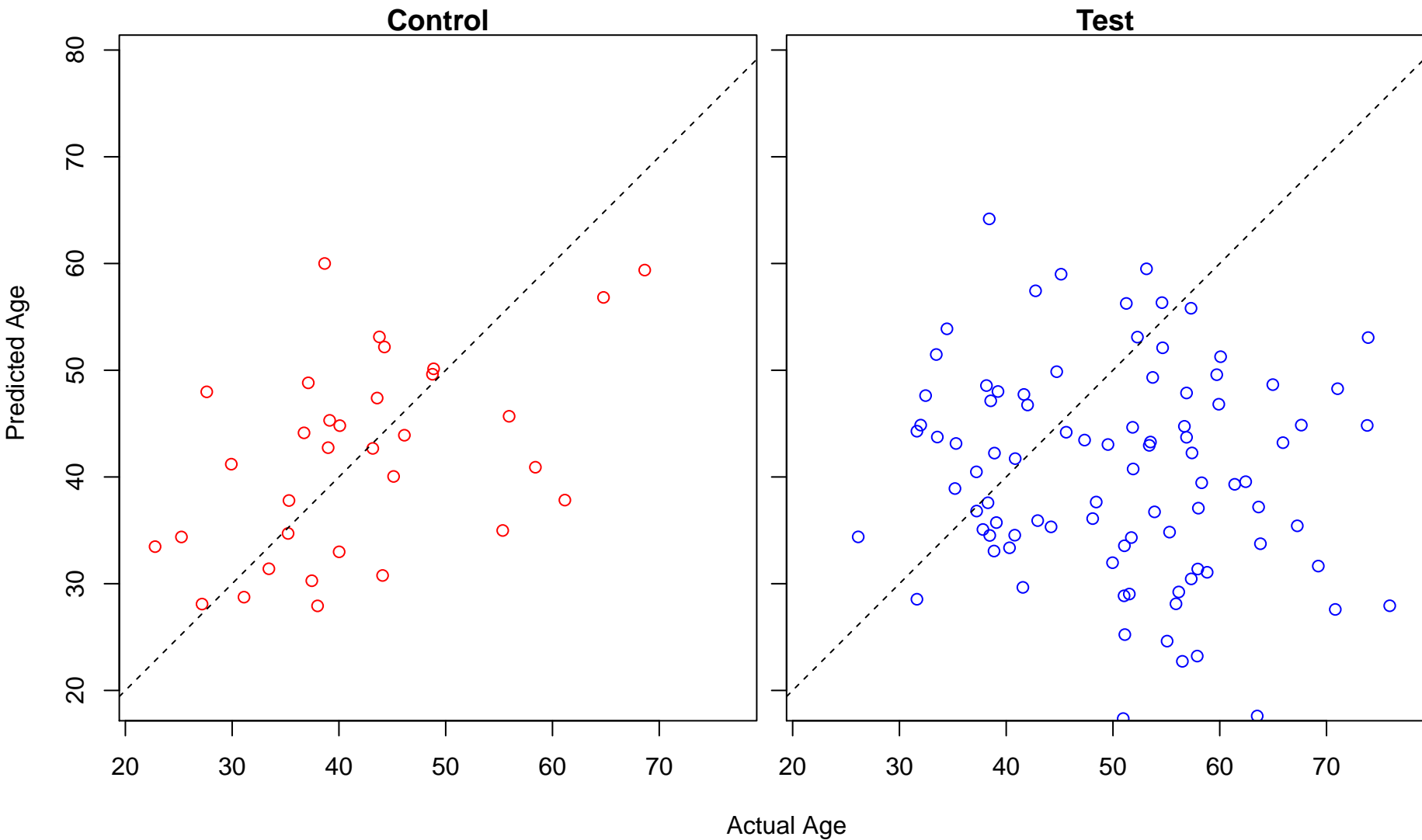
histone deubiquitination (Score: 1.212954)



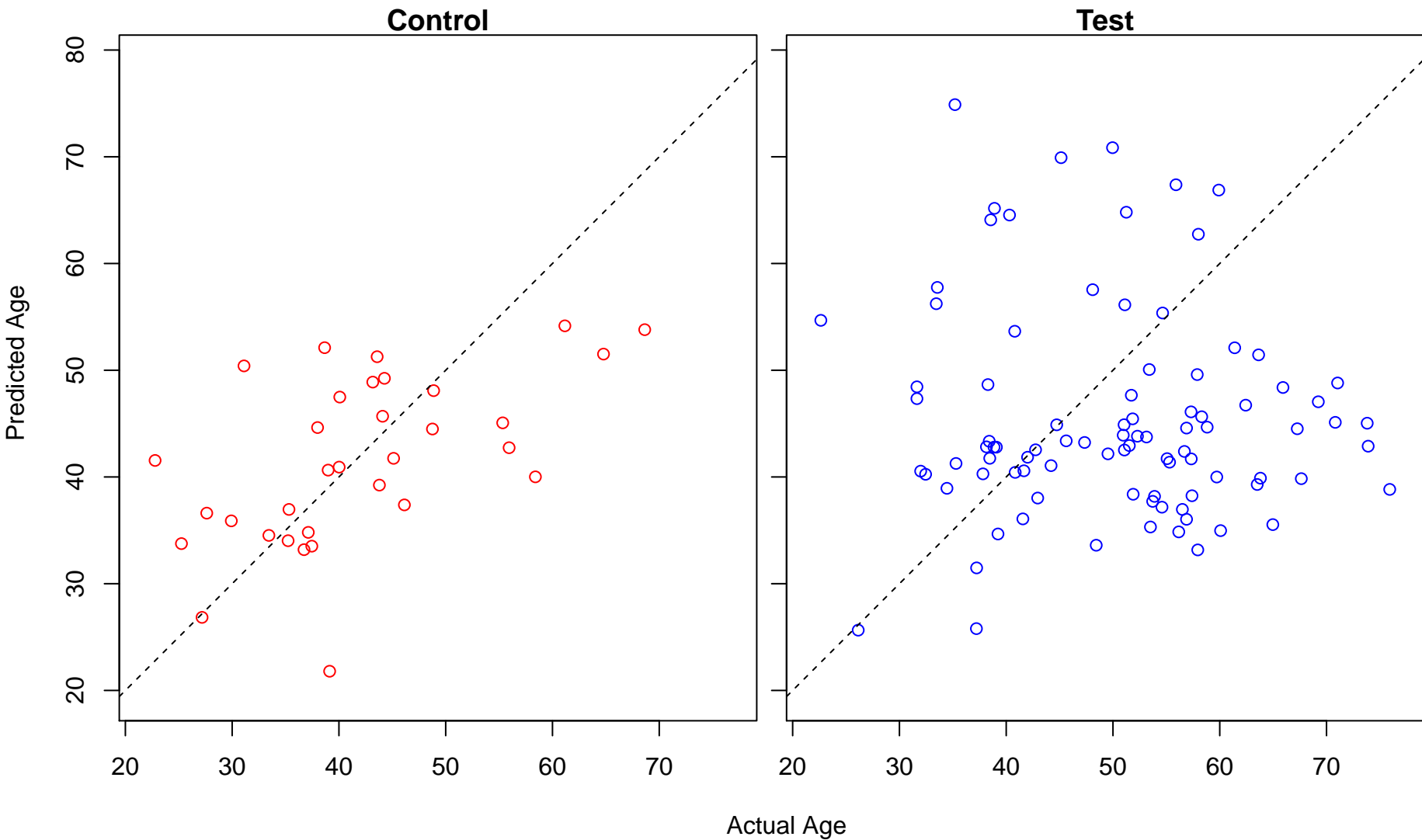
regulation of macrophage cytokine production (Score: 1.212907)



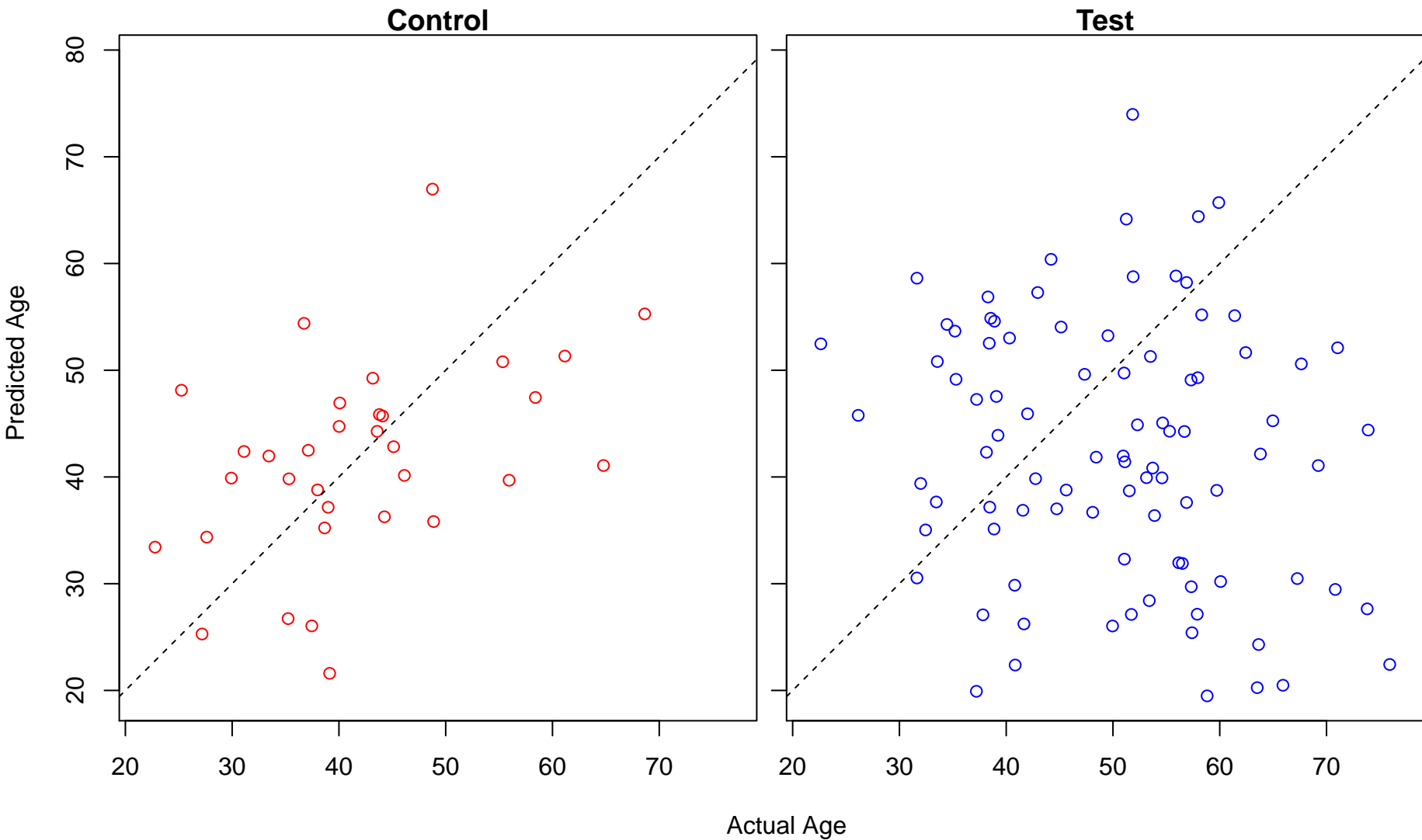
membrane lipid catabolic process (Score: 1.211713)



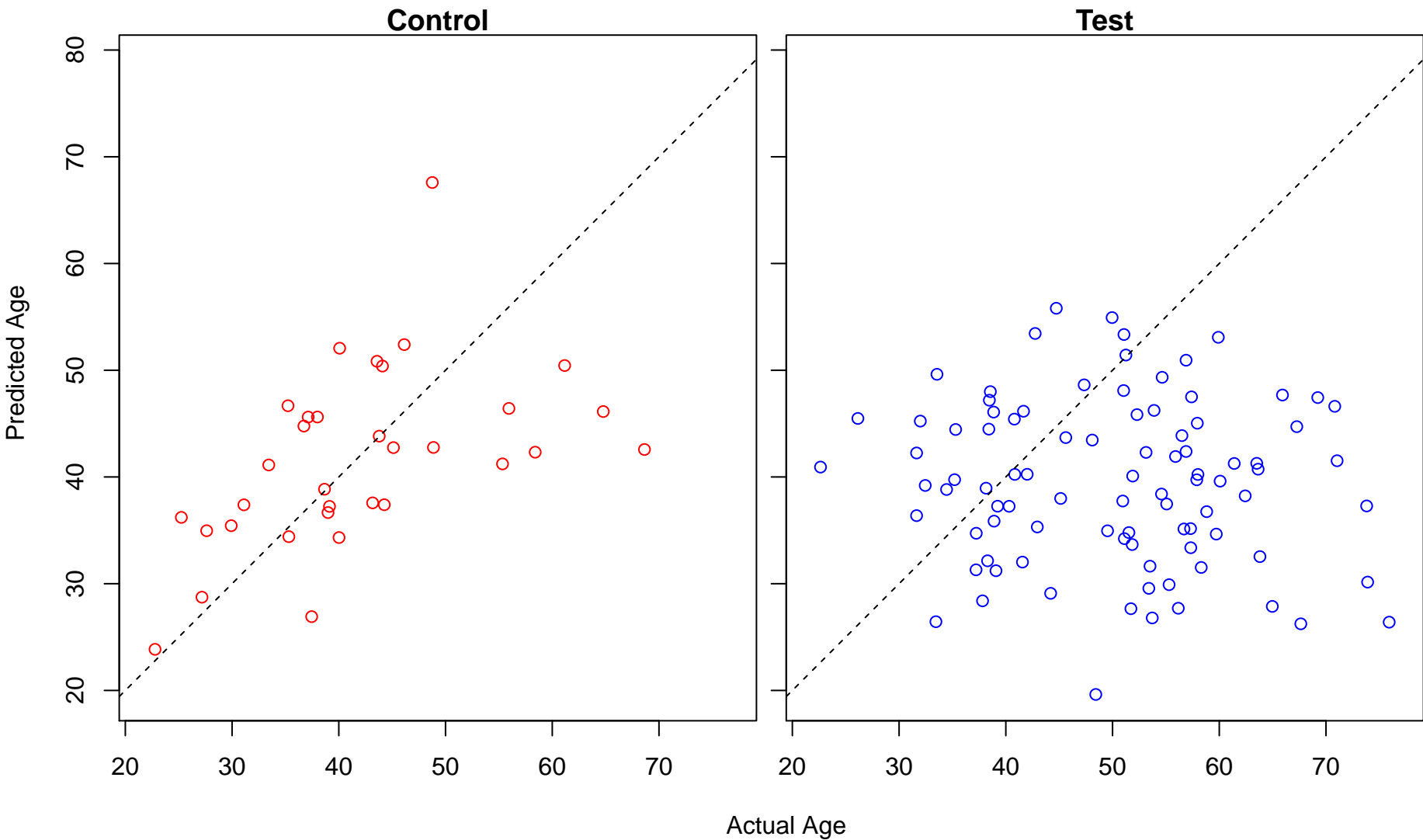
negative regulation of histone H3-K9 methylation (Score: 1.209656)



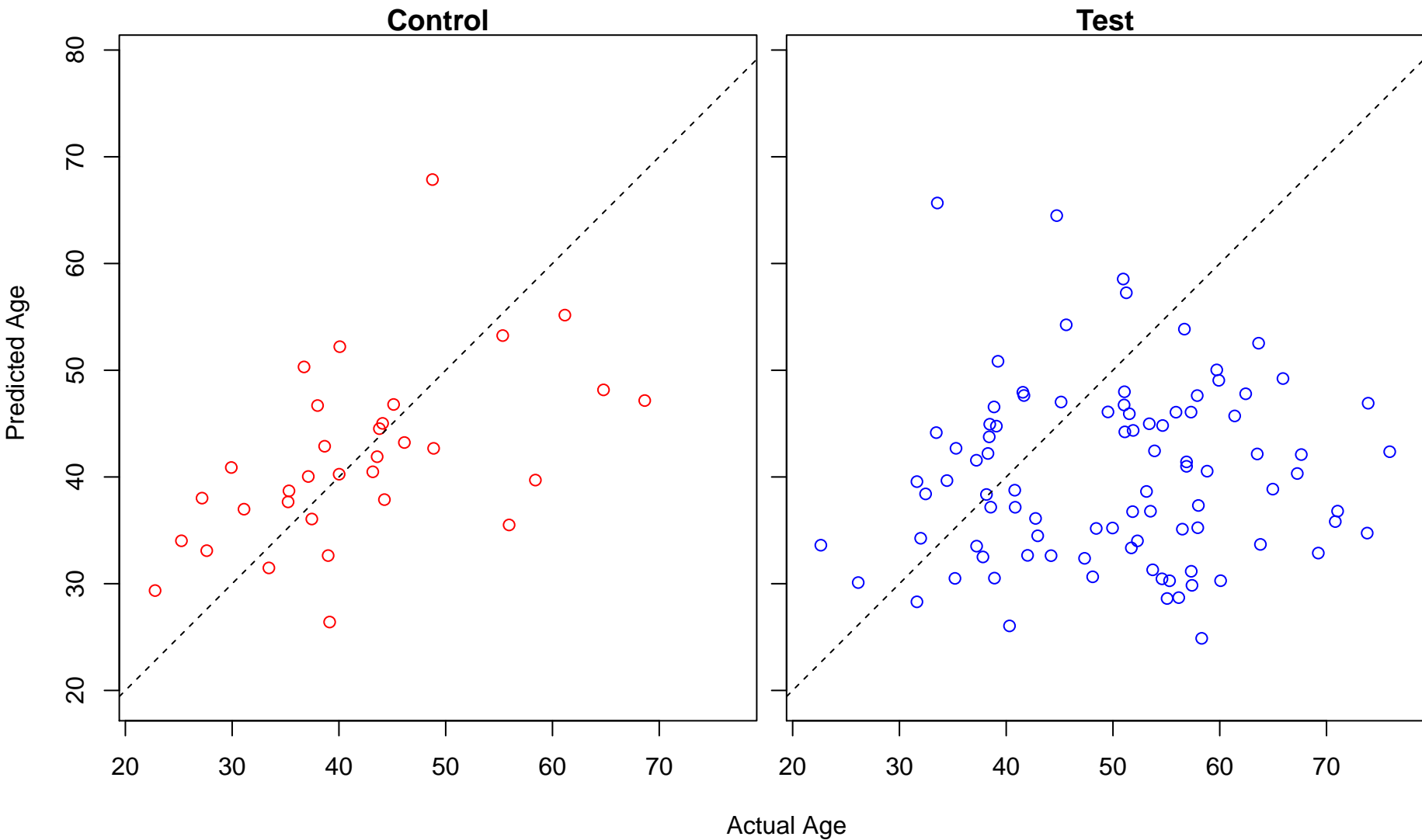
forebrain development (Score: 1.209434)



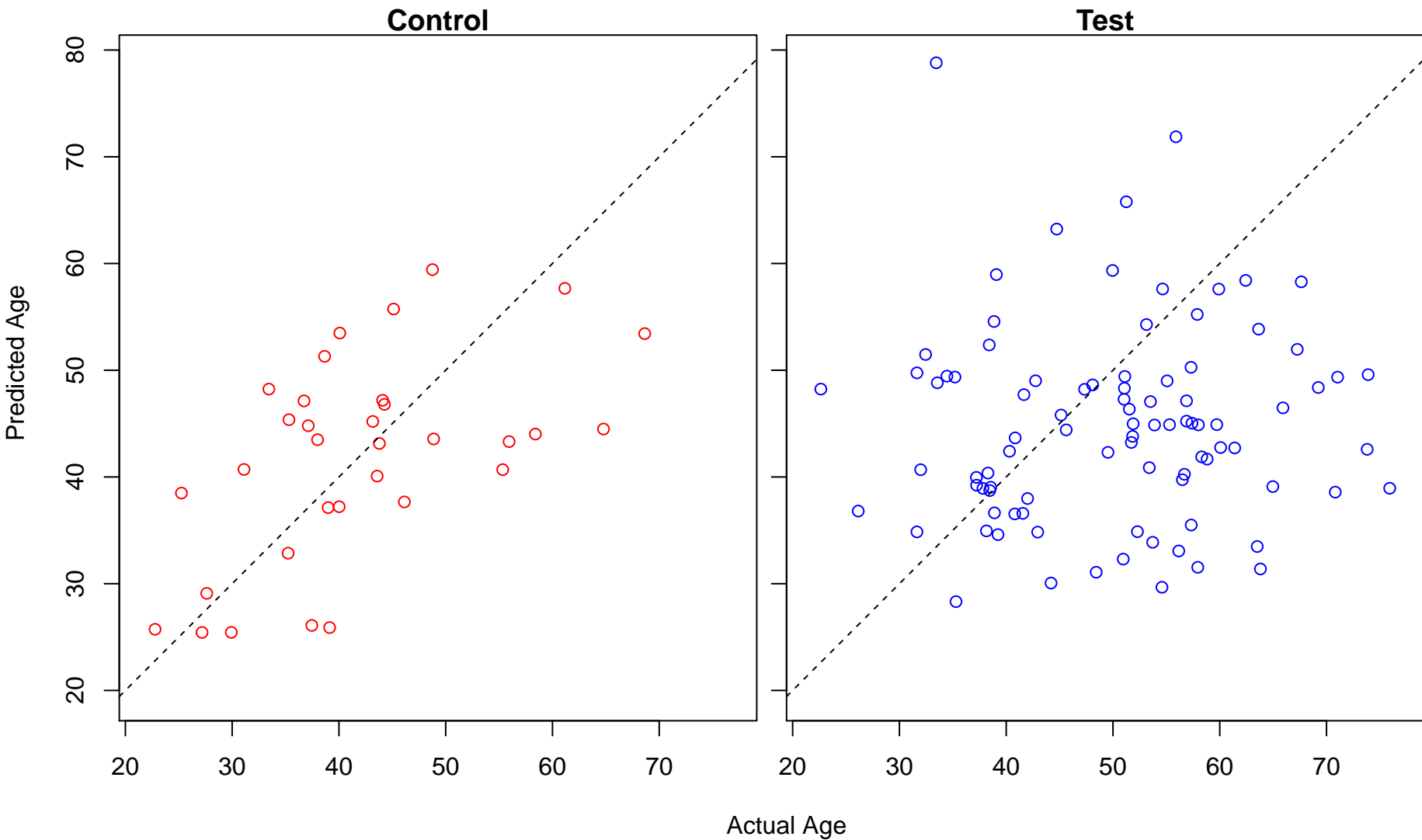
cardiac conduction (Score: 1.207277)



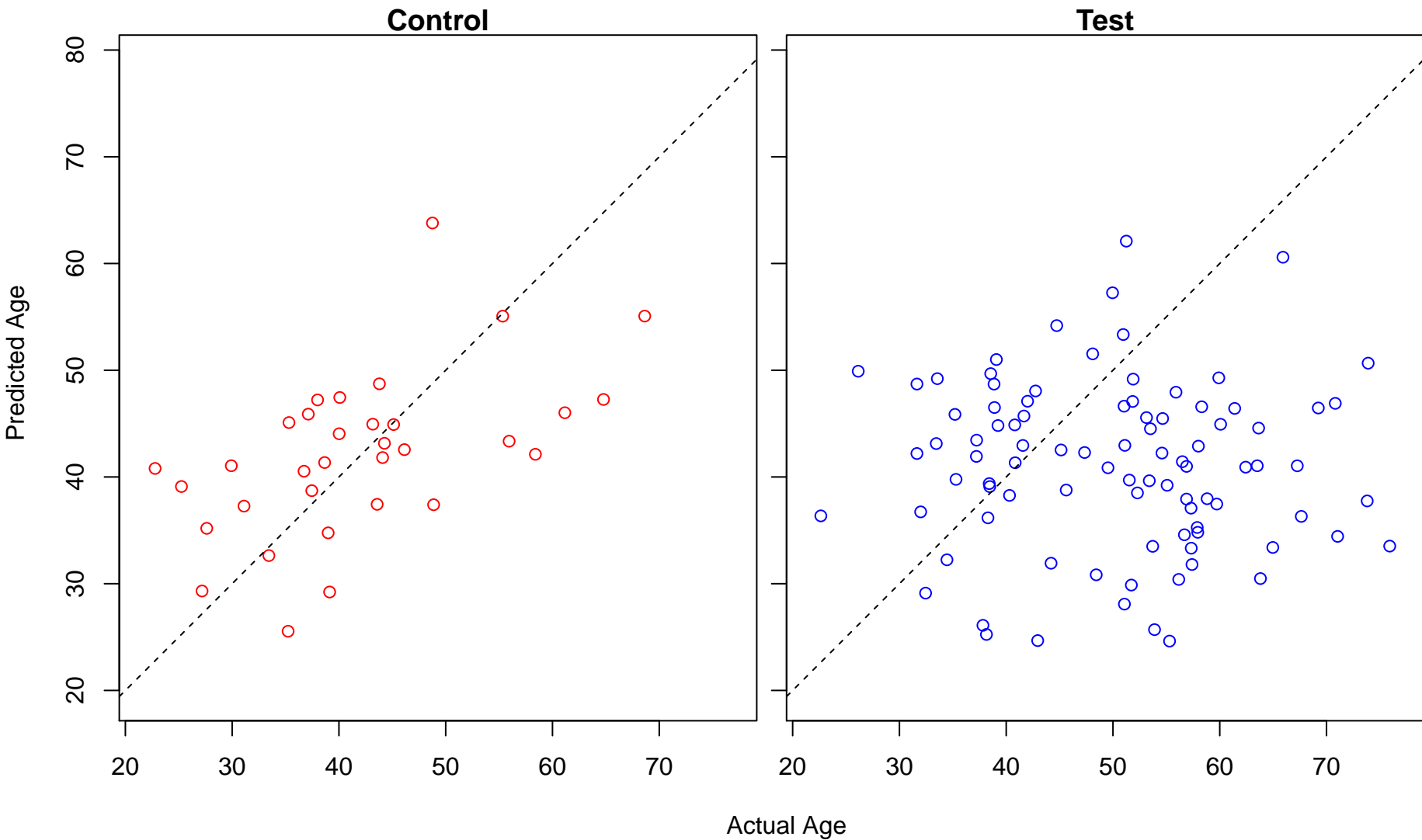
activation of MAPKK activity (Score: 1.207121)



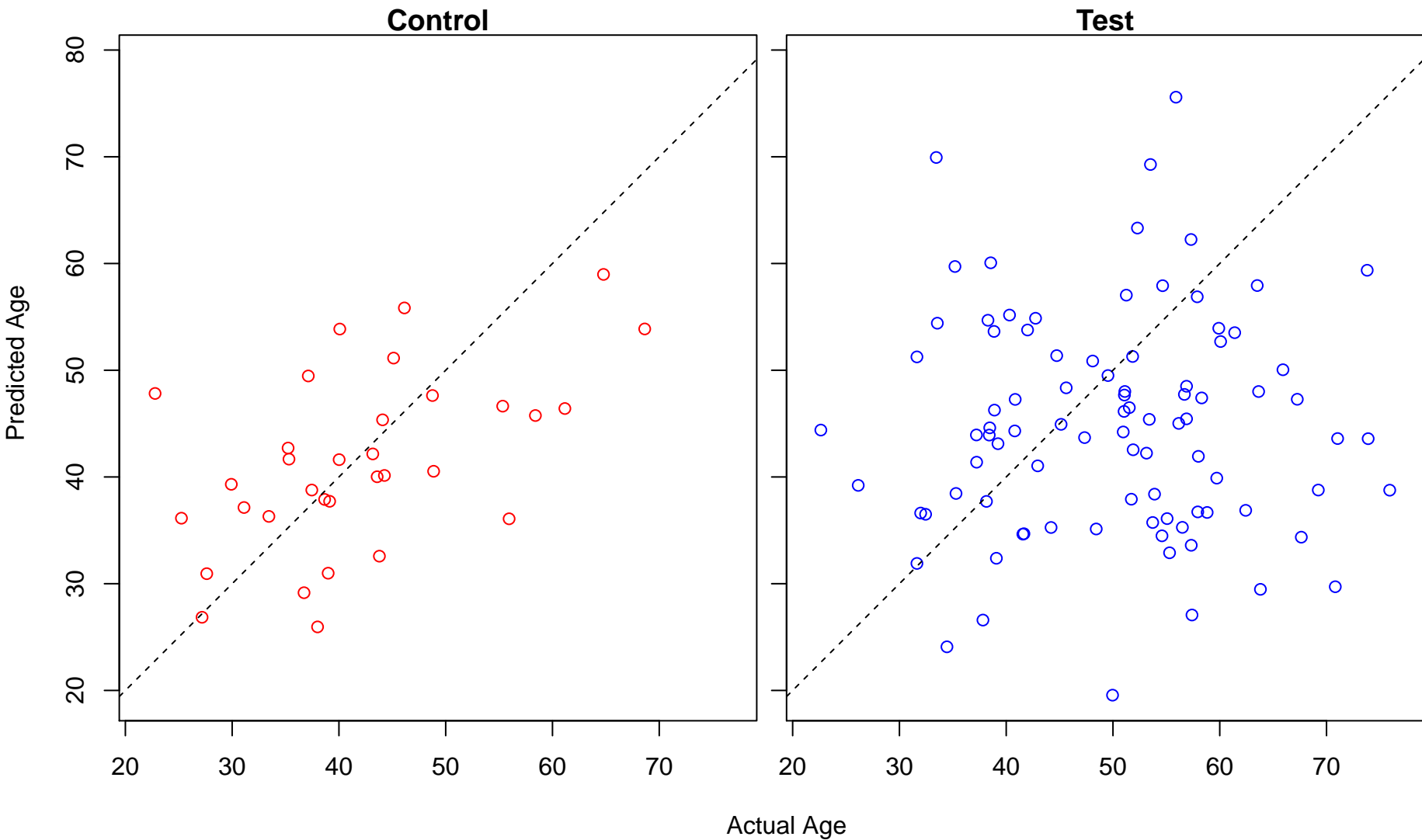
positive regulation of synaptic transmission (Score: 1.206260)



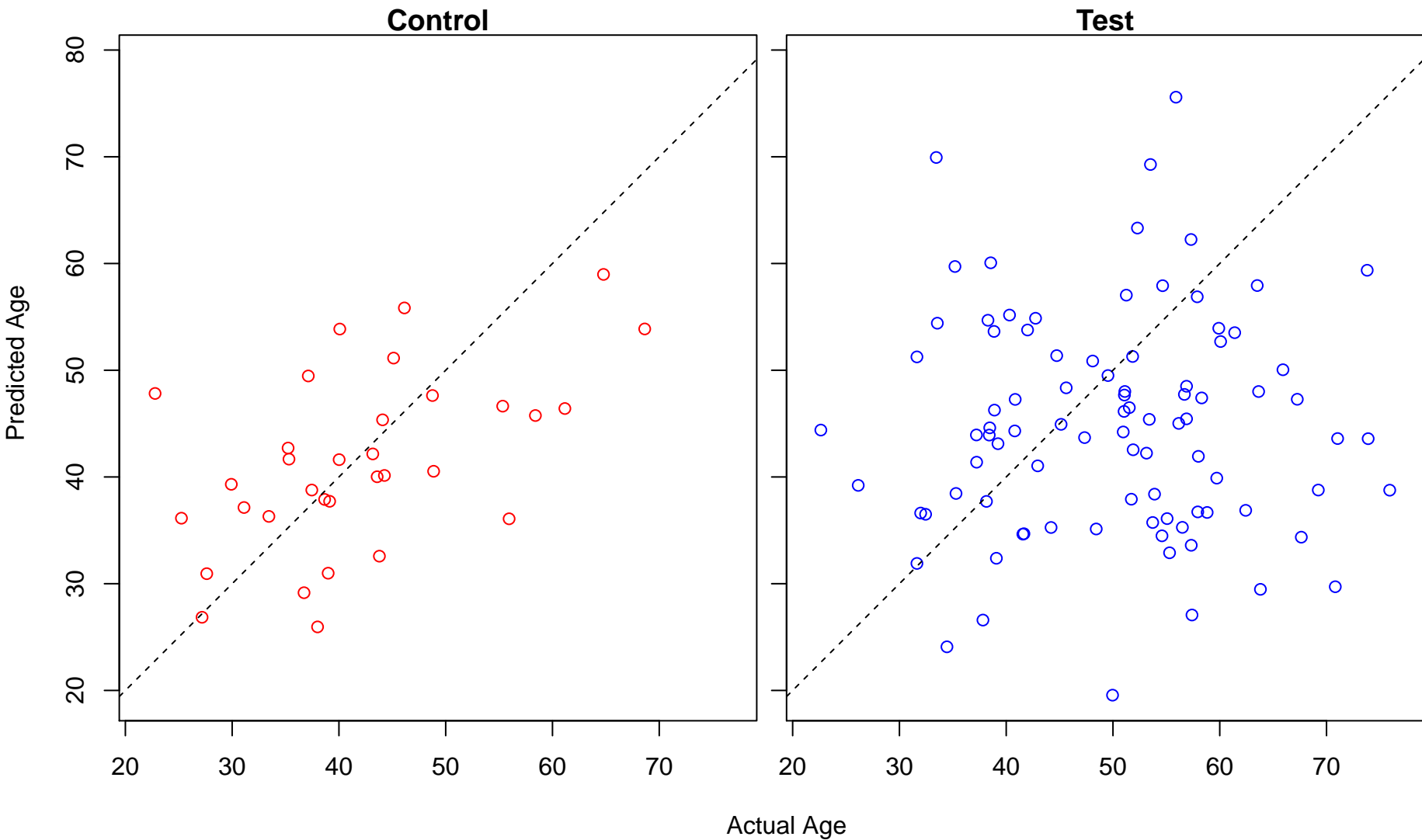
response to radiation (Score: 1.204443)



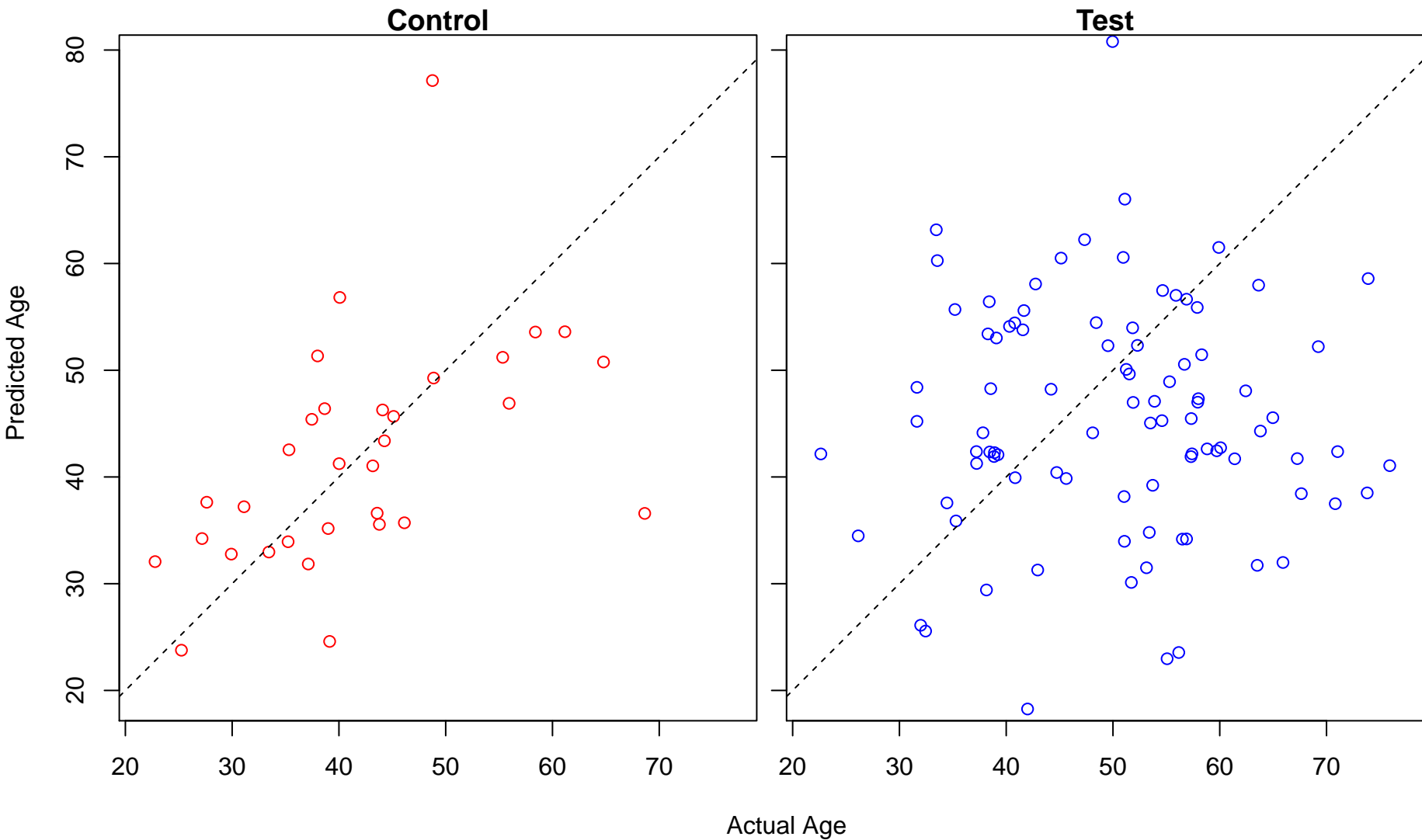
glycogen biosynthetic process (Score: 1.202429)



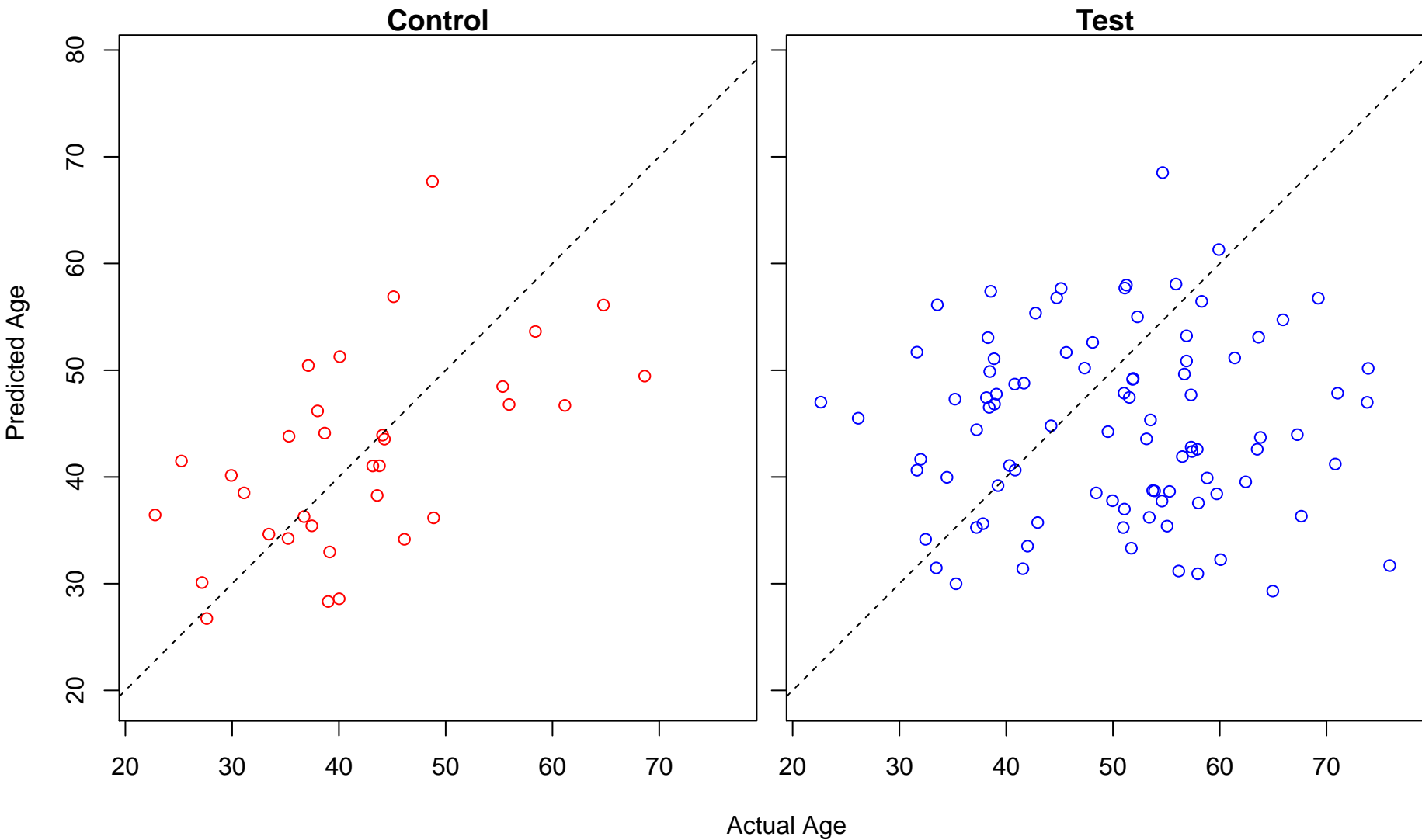
glucan biosynthetic process (Score: 1.202429)



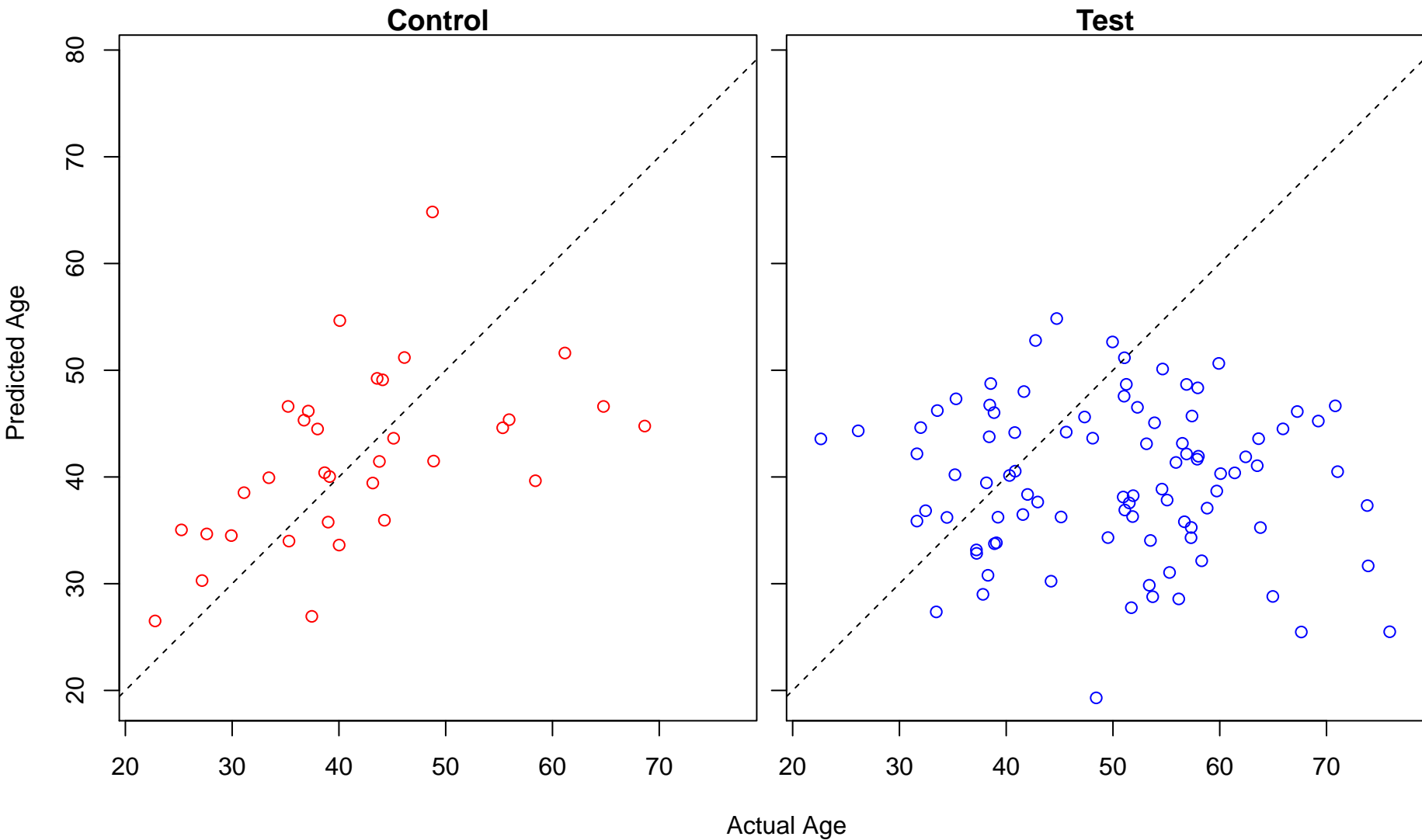
B cell differentiation (Score: 1.201932)



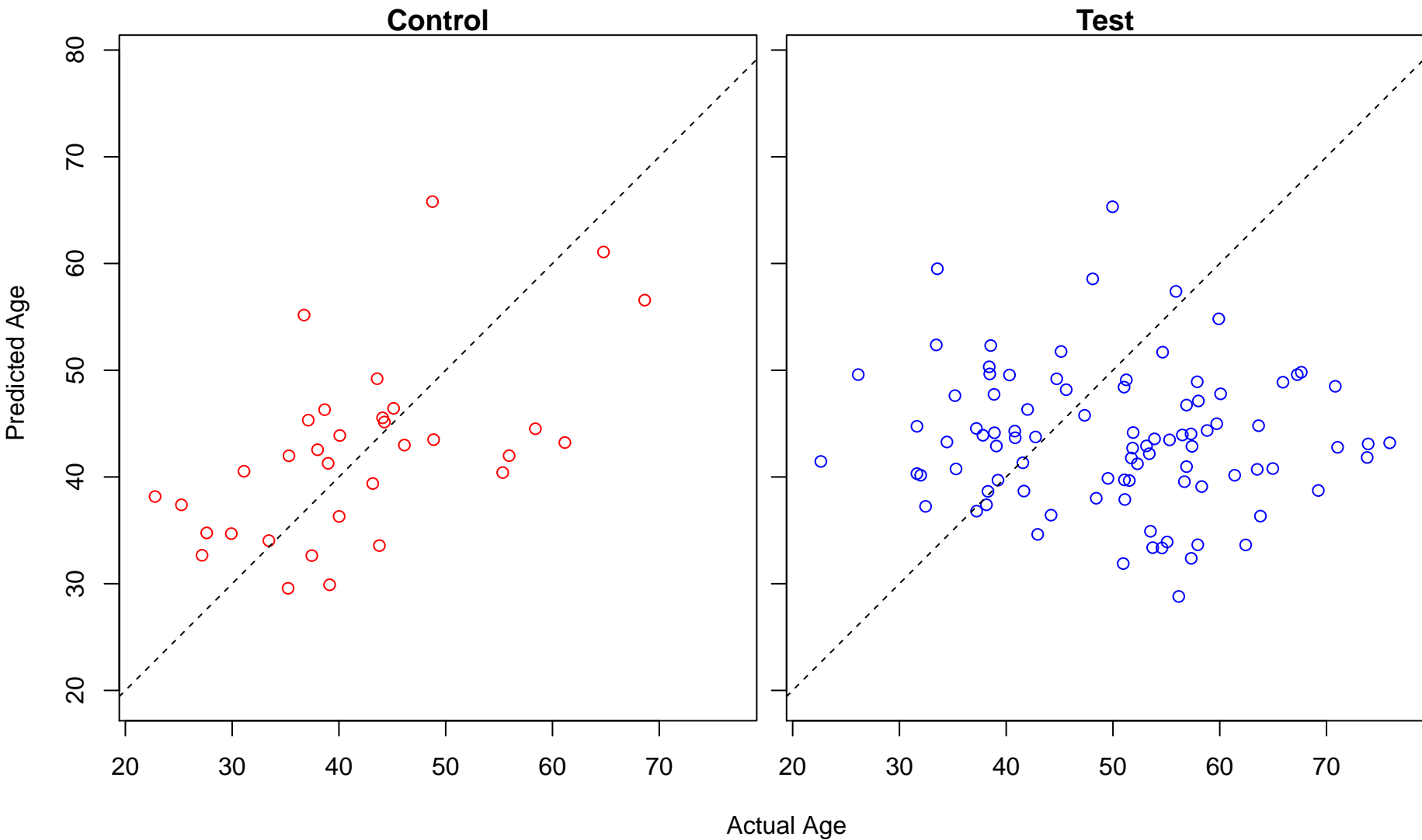
guanosine-containing compound metabolic process (Score: 1.196419)



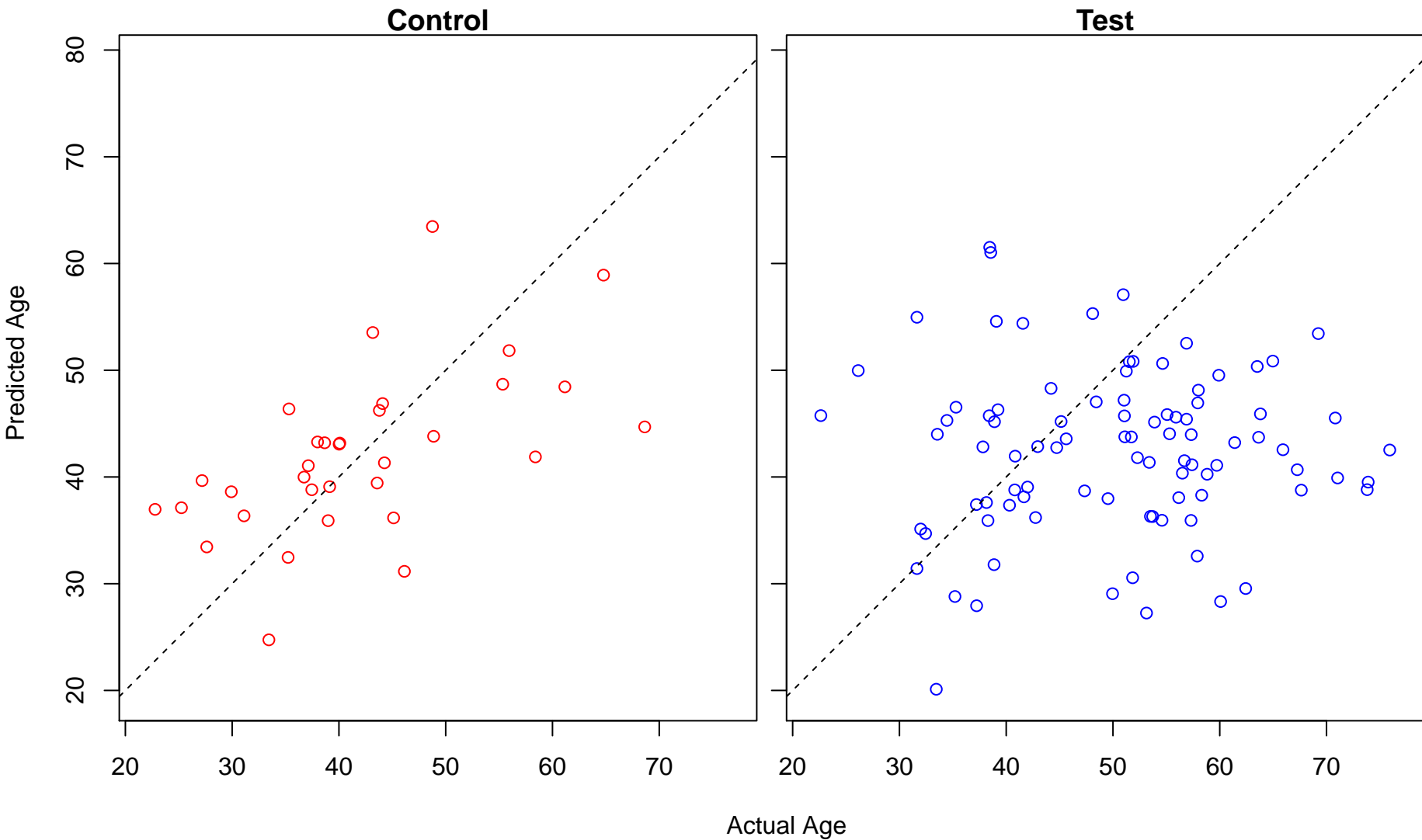
multicellular organismal signaling (Score: 1.194322)



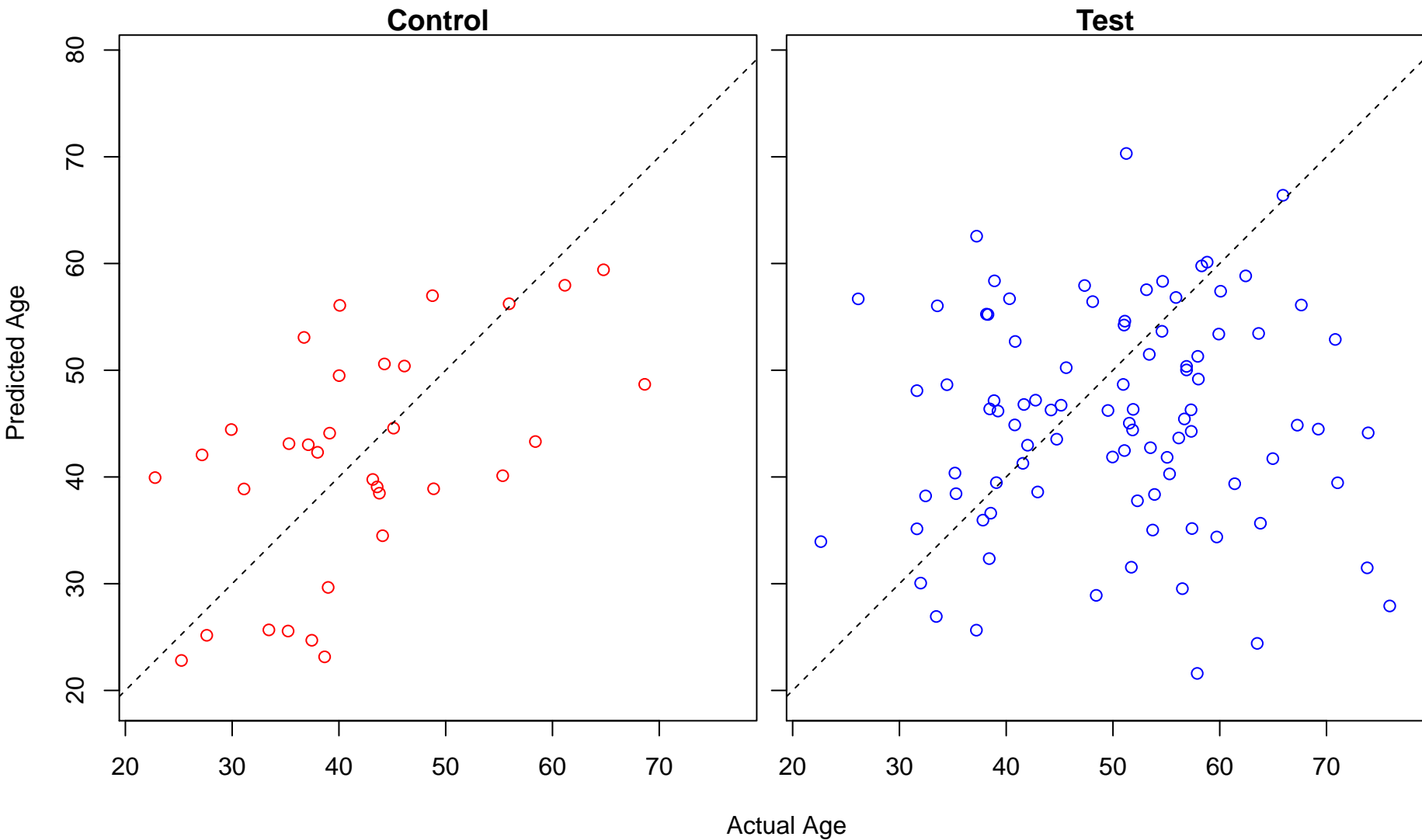
response to nitric oxide (Score: 1.189743)



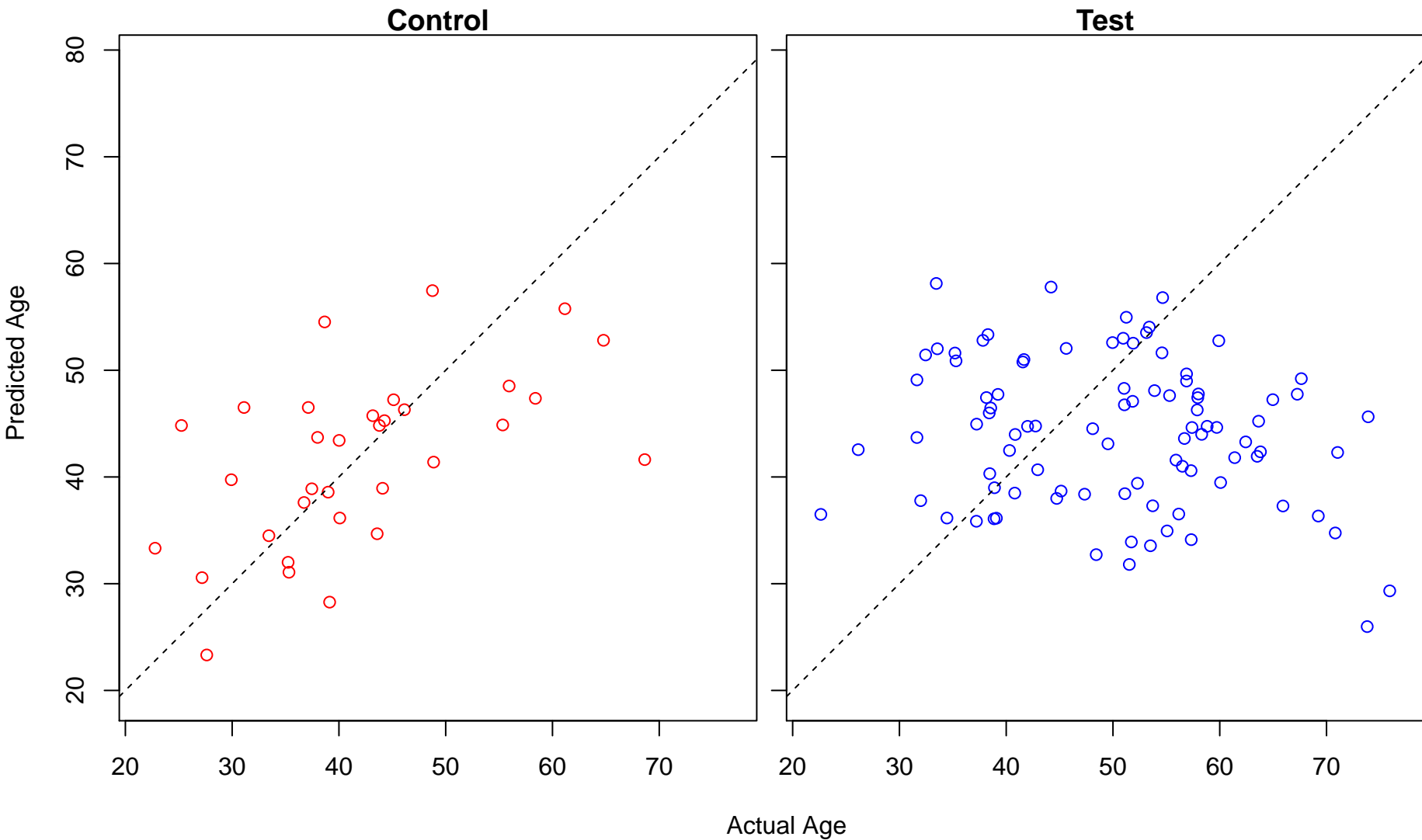
regulation of peroxisome organization (Score: 1.185802)



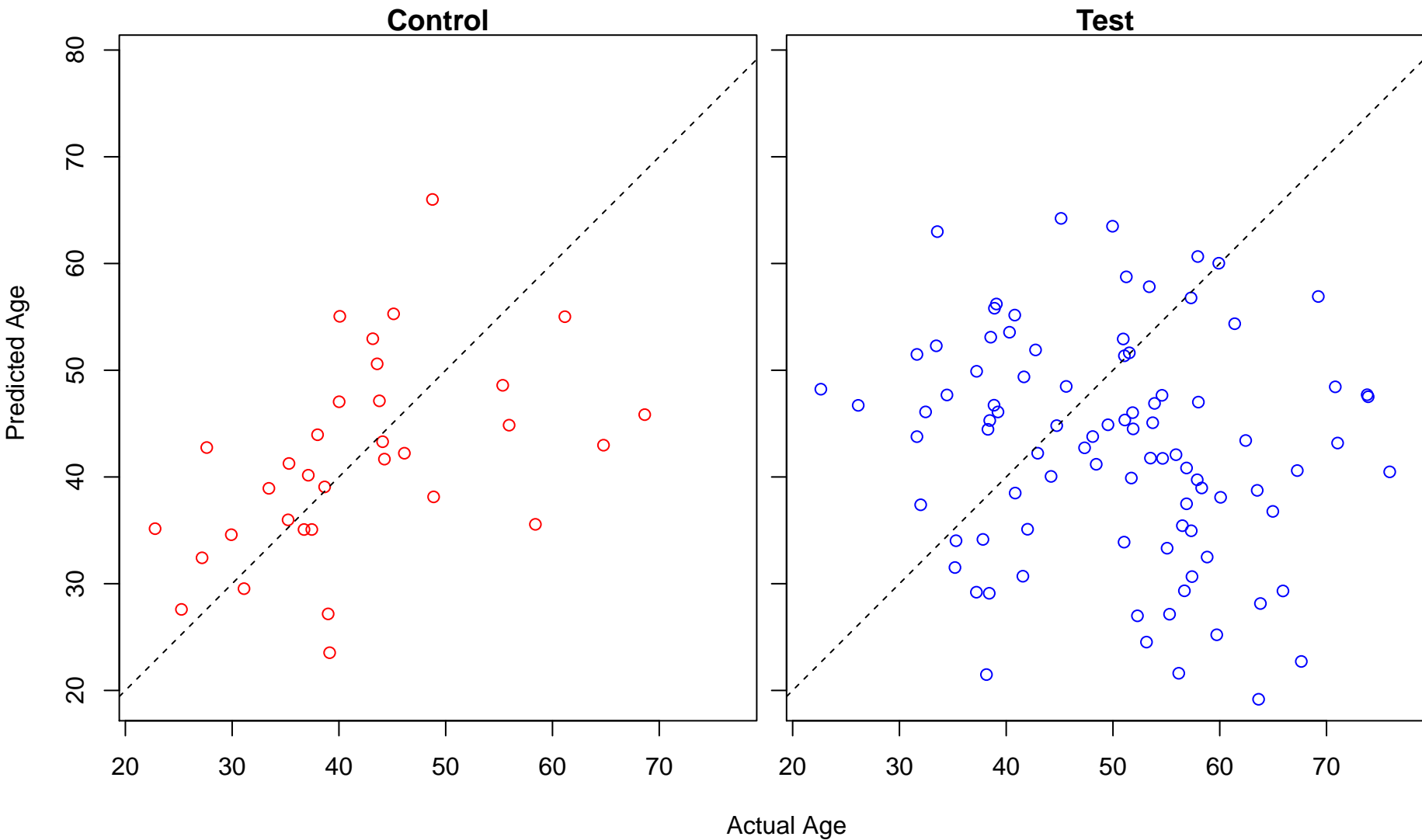
B cell receptor signaling pathway (Score: 1.185260)



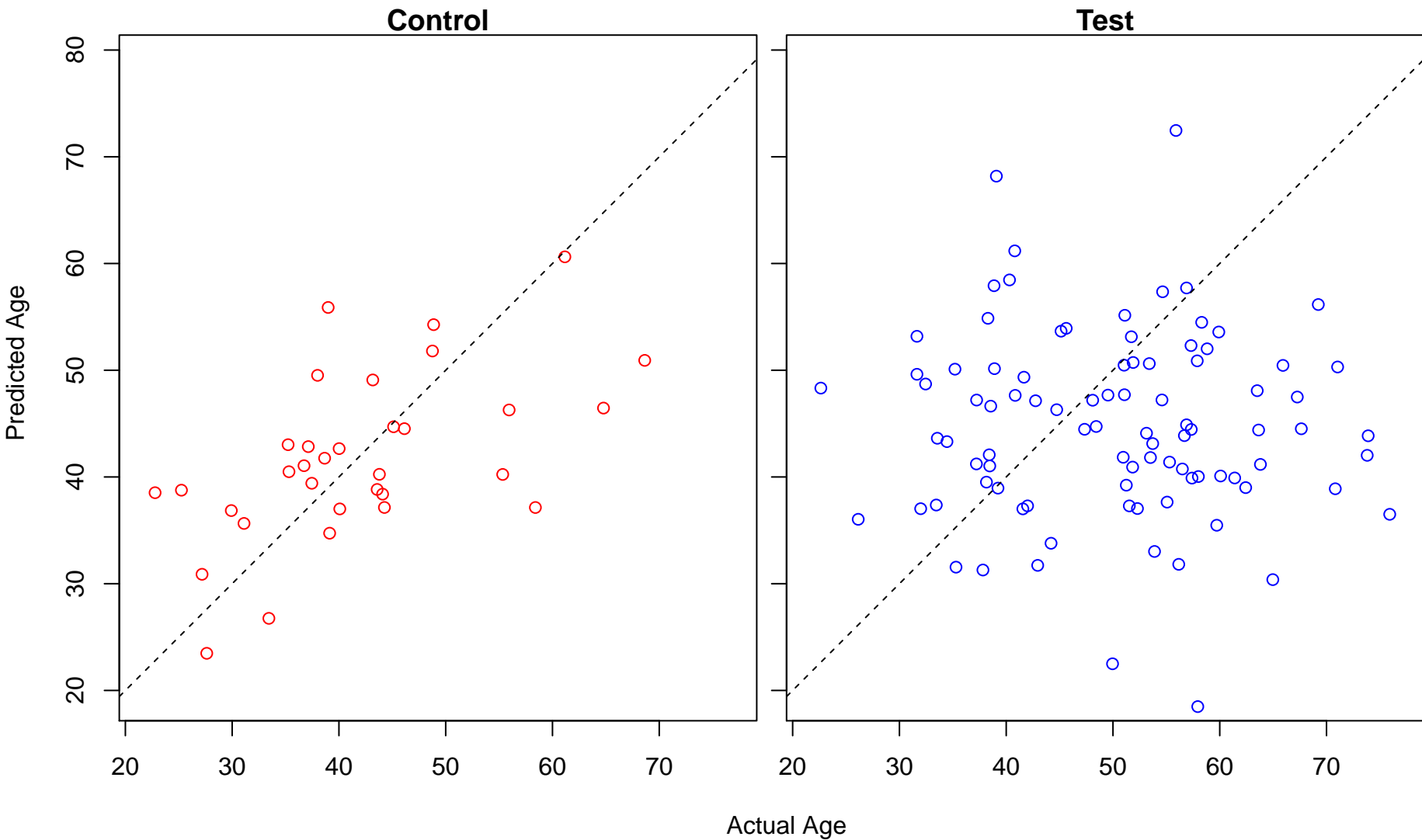
endocrine pancreas development (Score: 1.180961)



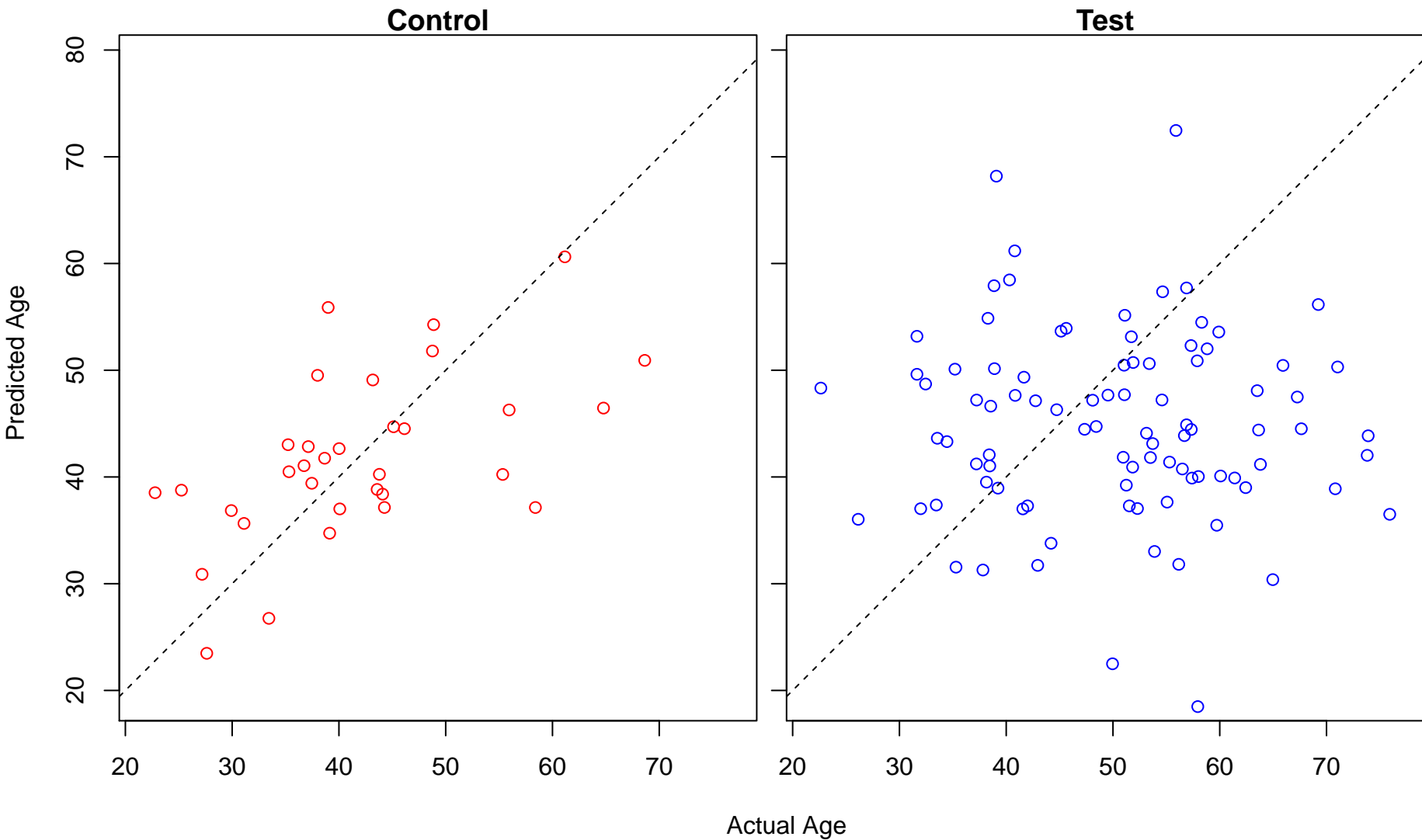
multicellular organismal homeostasis (Score: 1.180316)



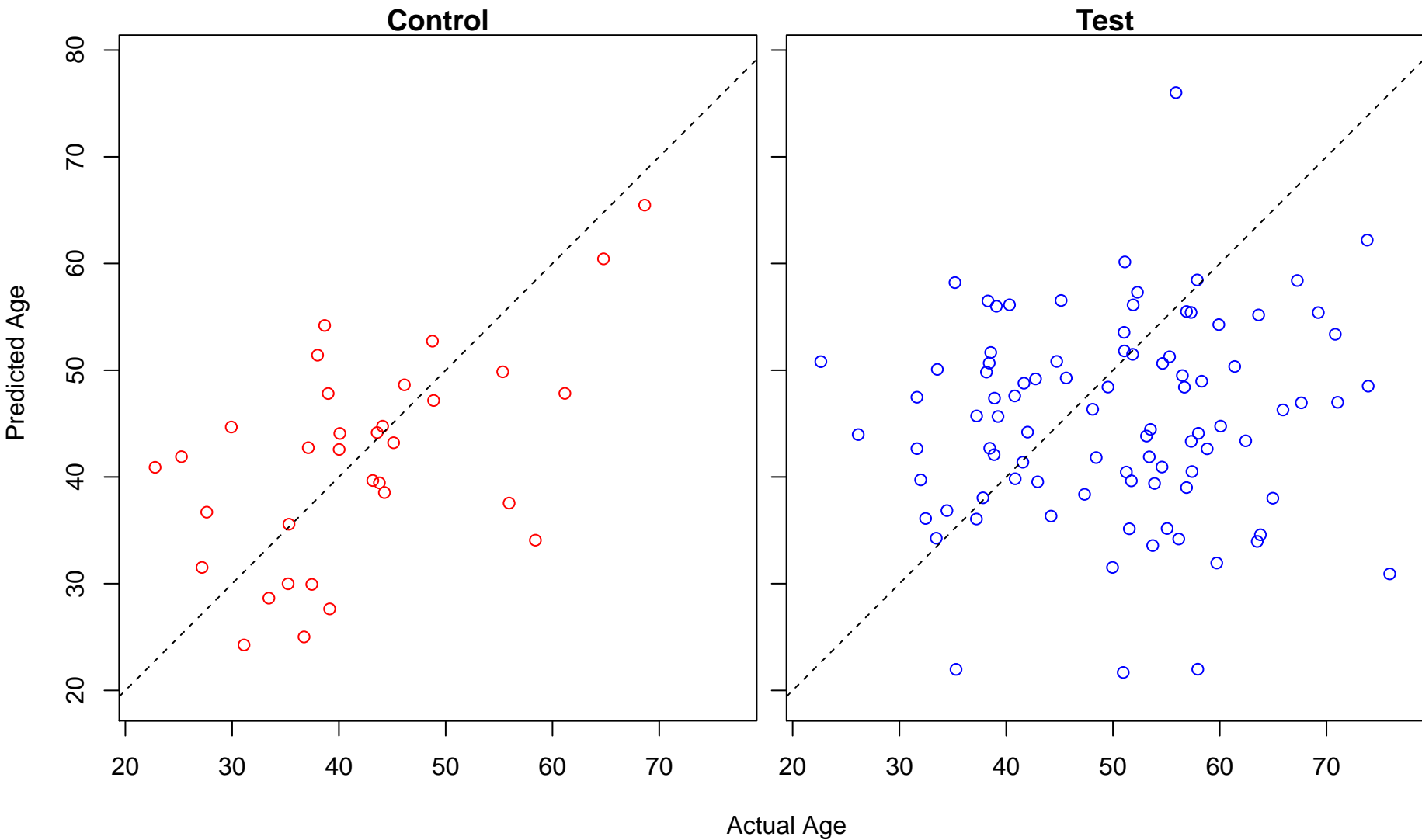
negative regulation of response to food (Score: 1.179753)



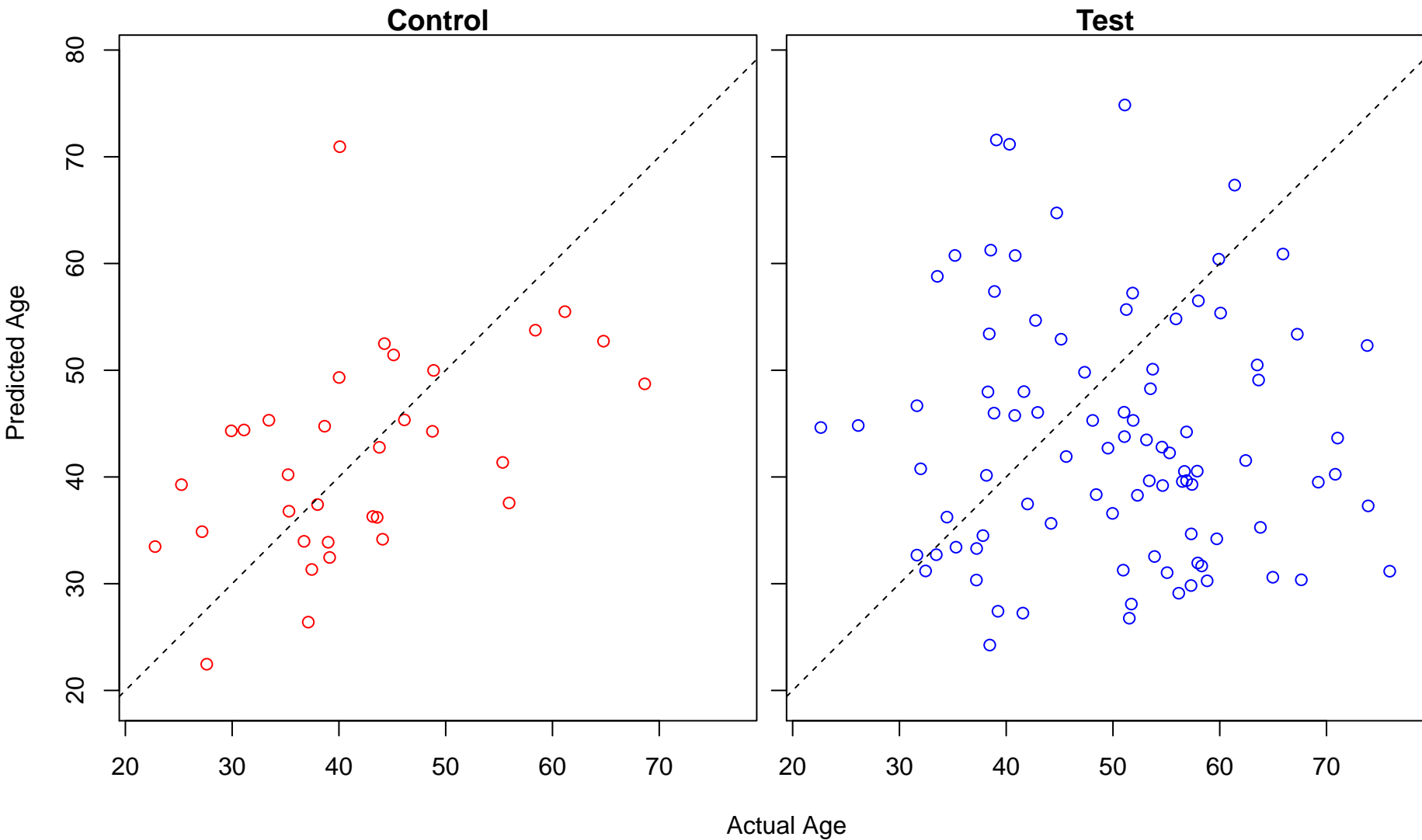
negative regulation of appetite (Score: 1.179753)



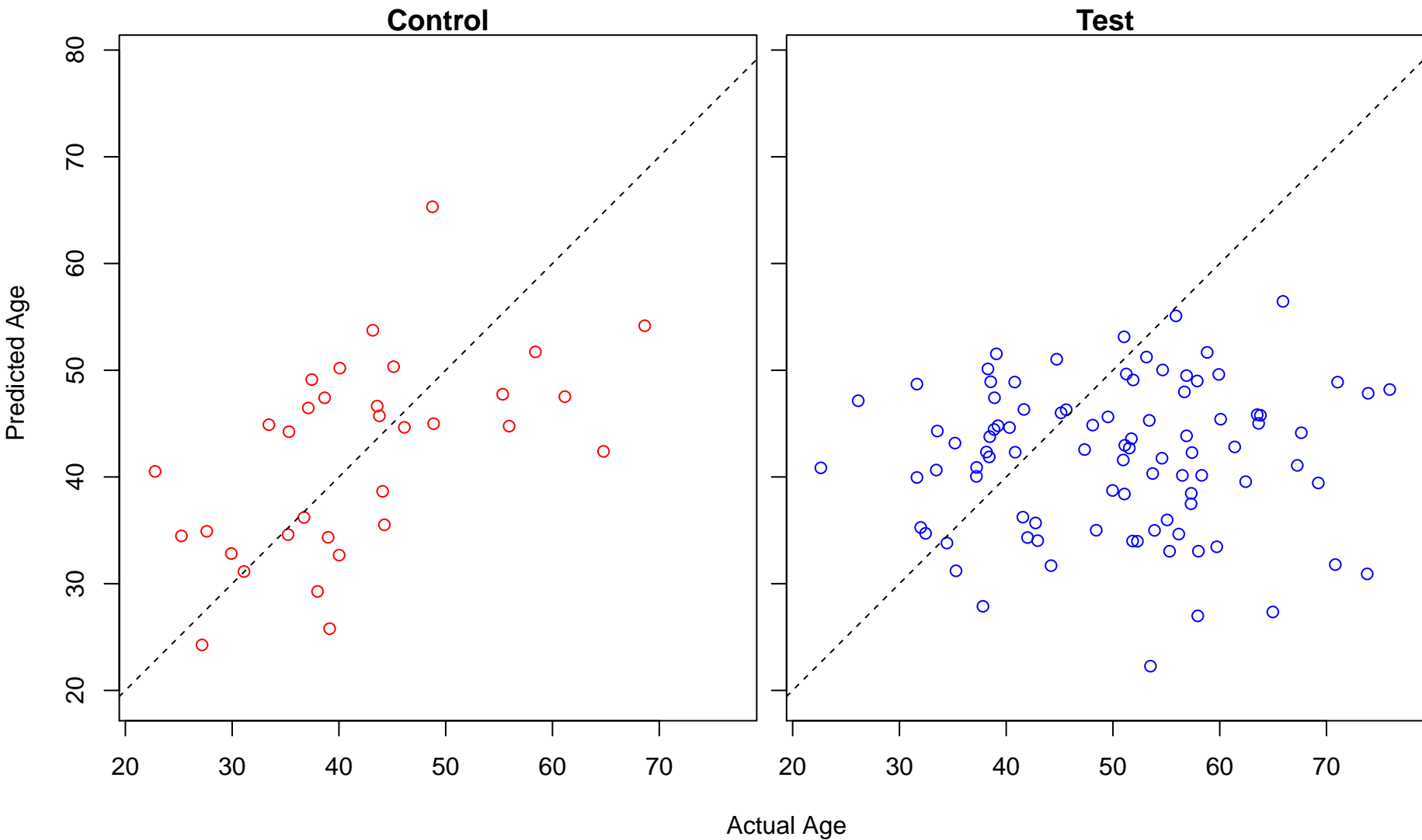
brain morphogenesis (Score: 1.178090)



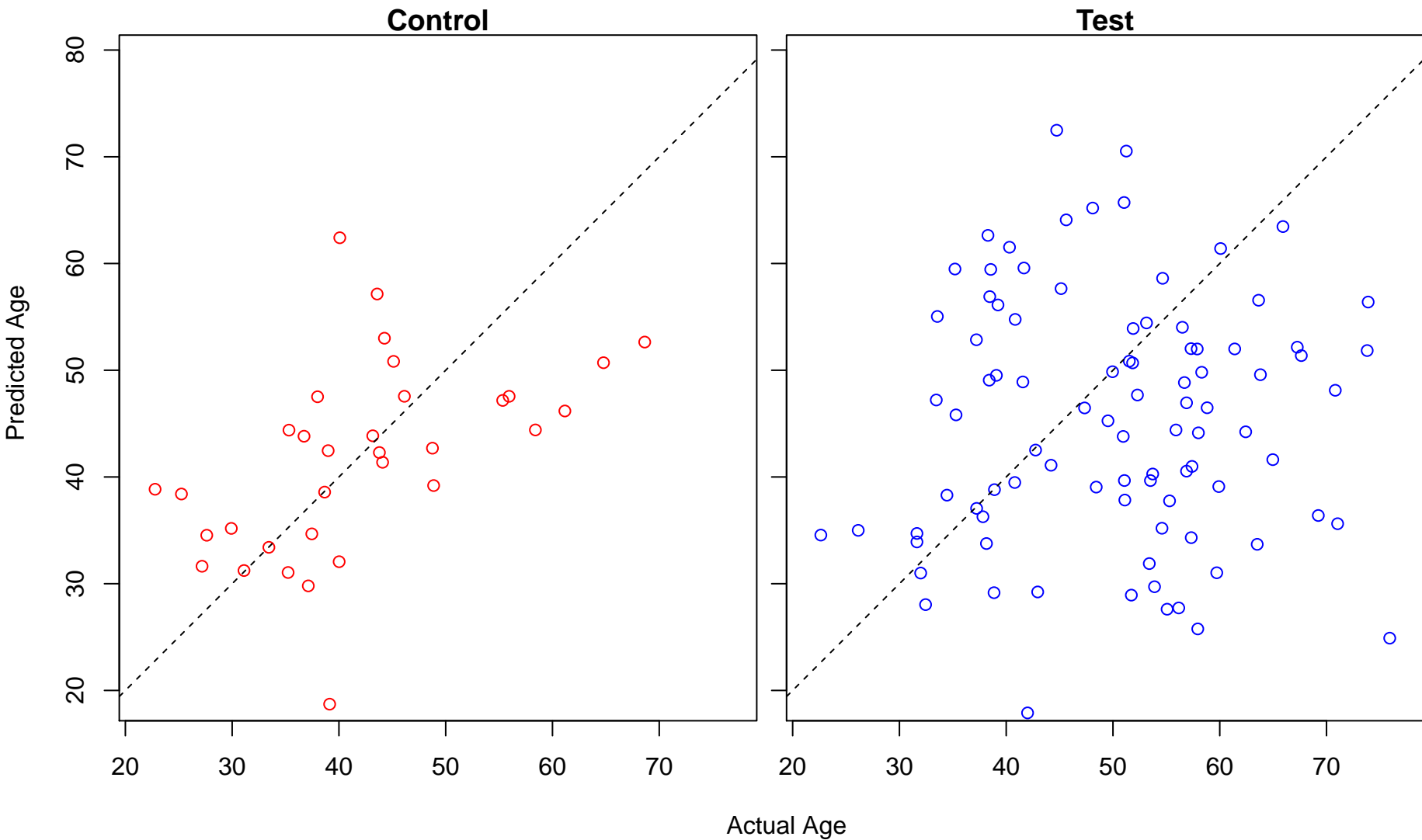
multi-organism behavior (Score: 1.177811)



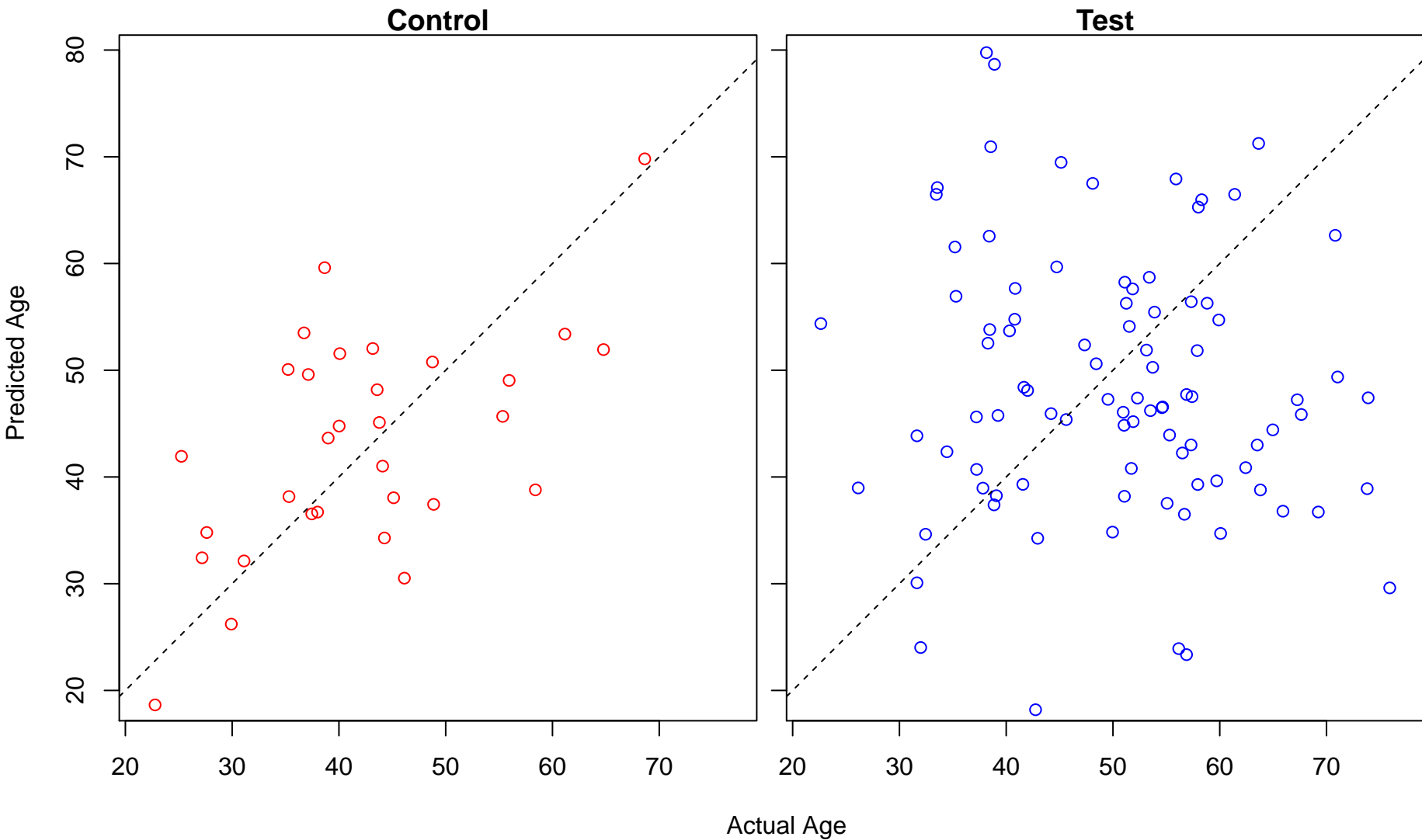
positive regulation of glucose import (Score: 1.177792)



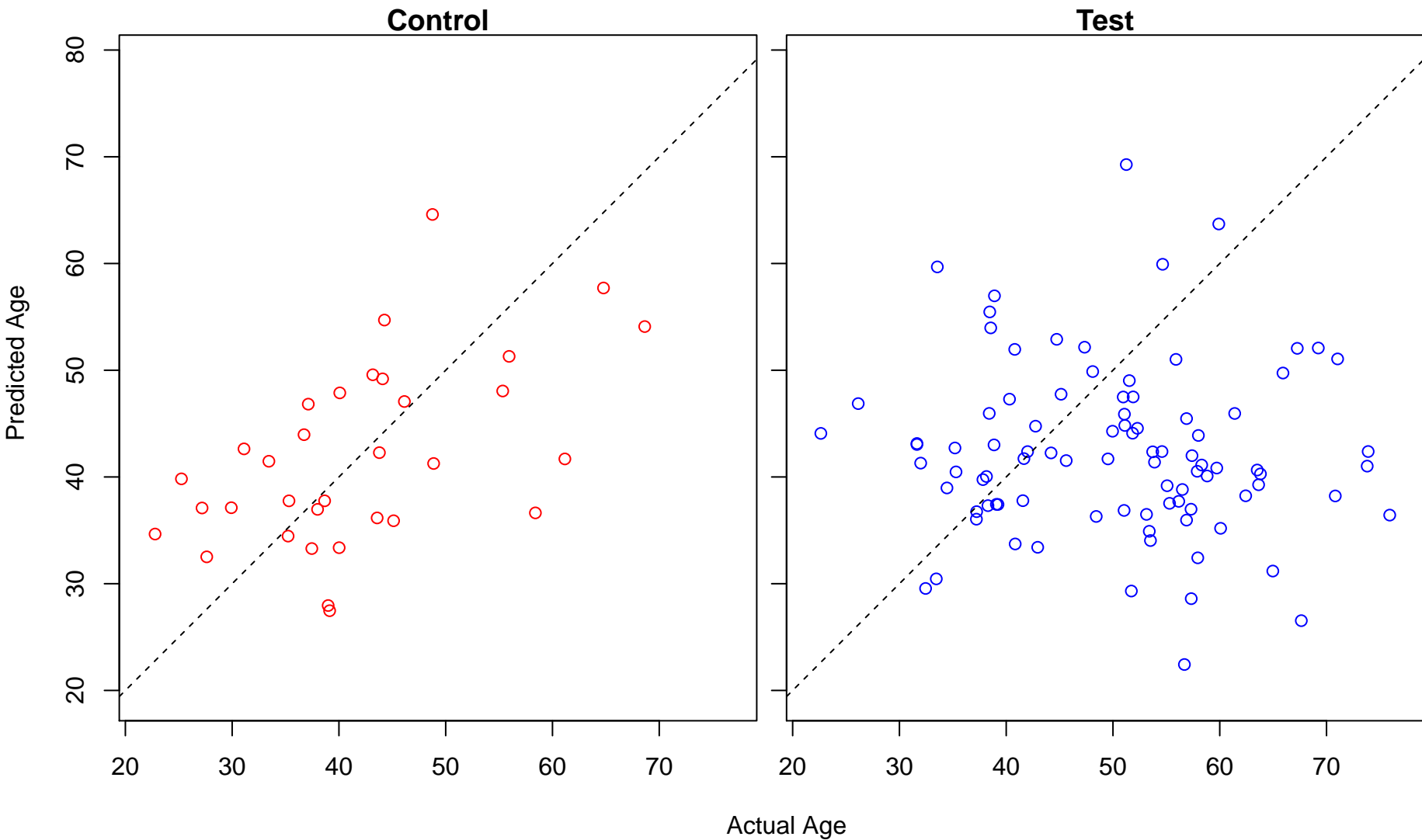
filopodium assembly (Score: 1.174716)



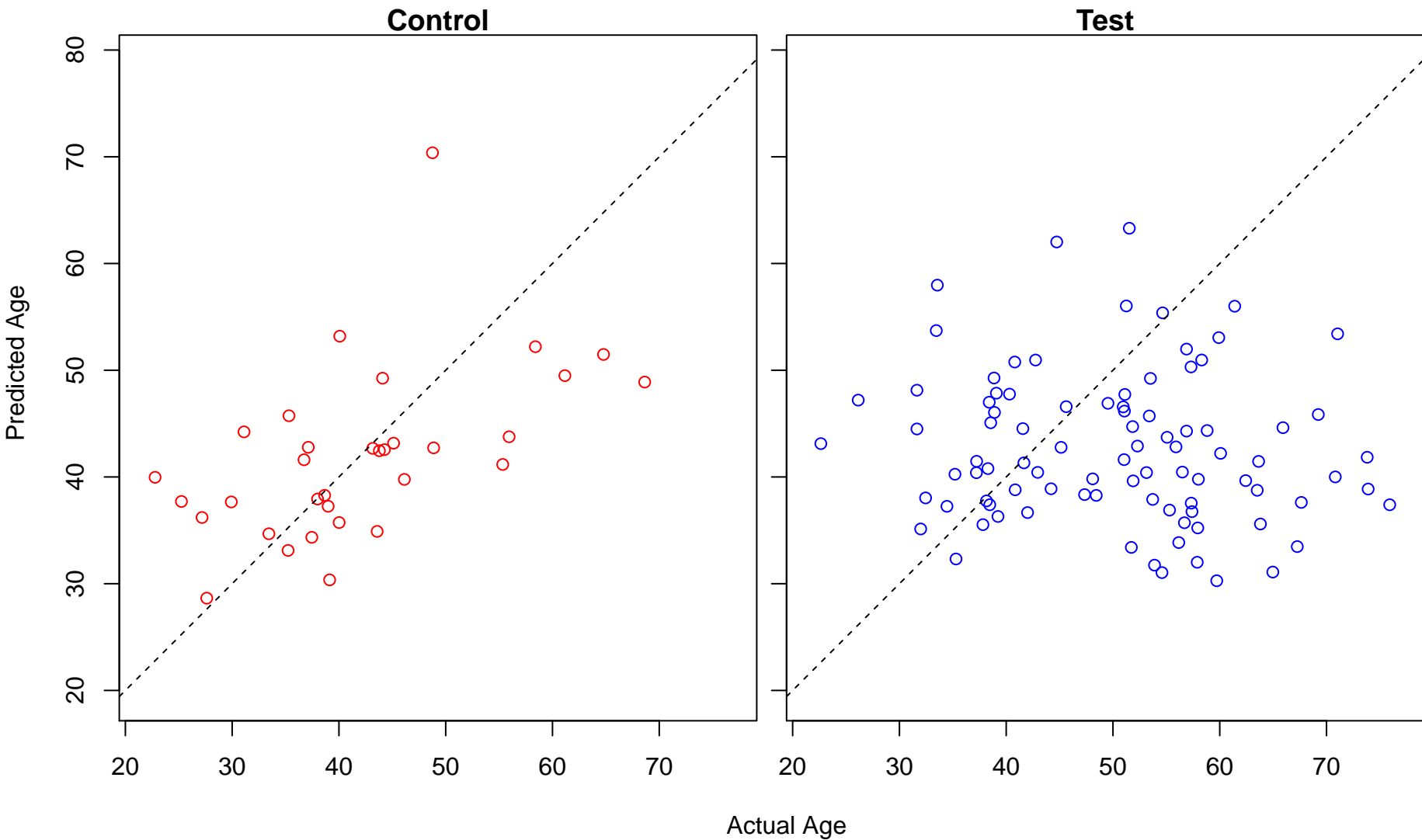
negative regulation of tumor necrosis factor production (Score: 1.173376)



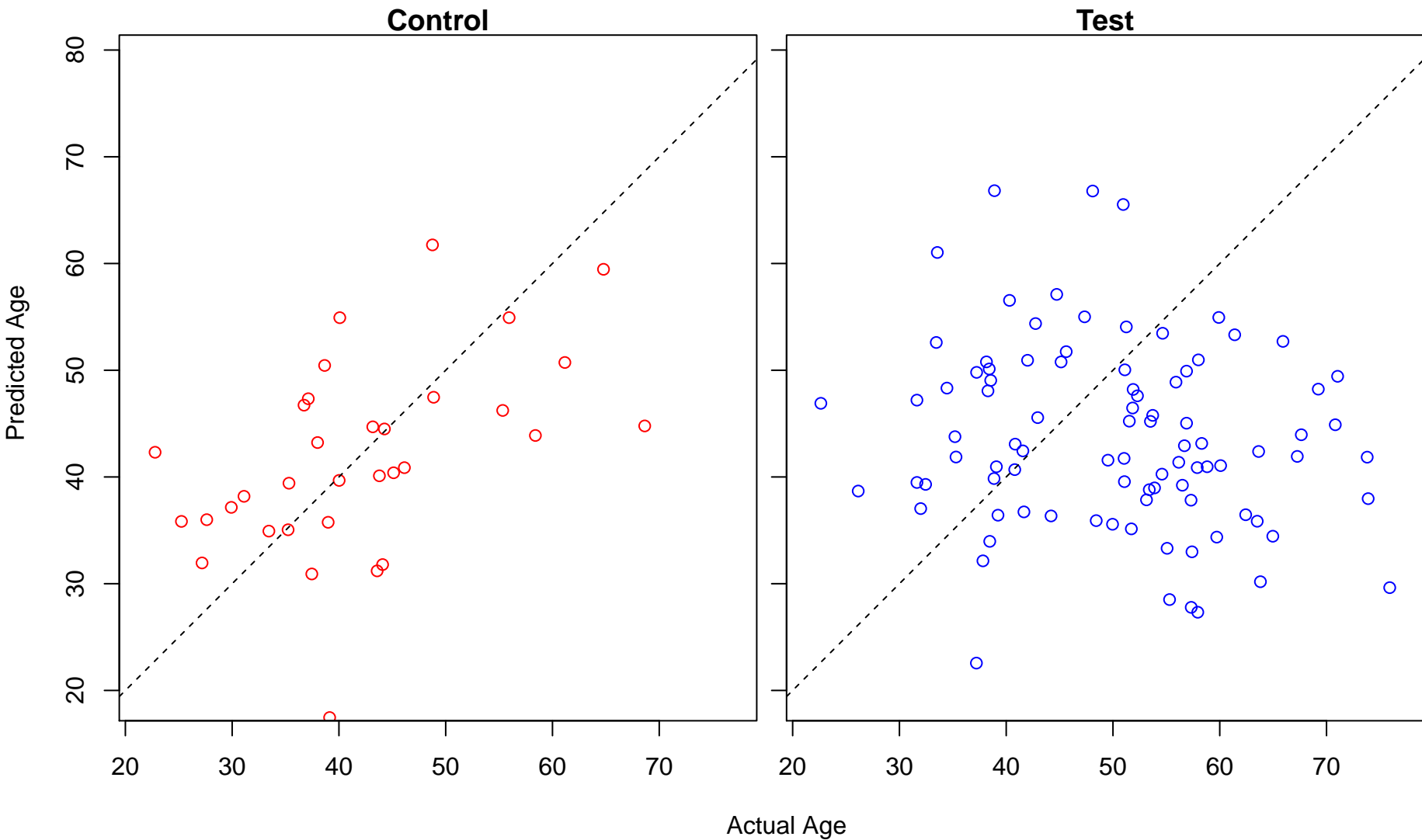
chloride transport (Score: 1.170690)



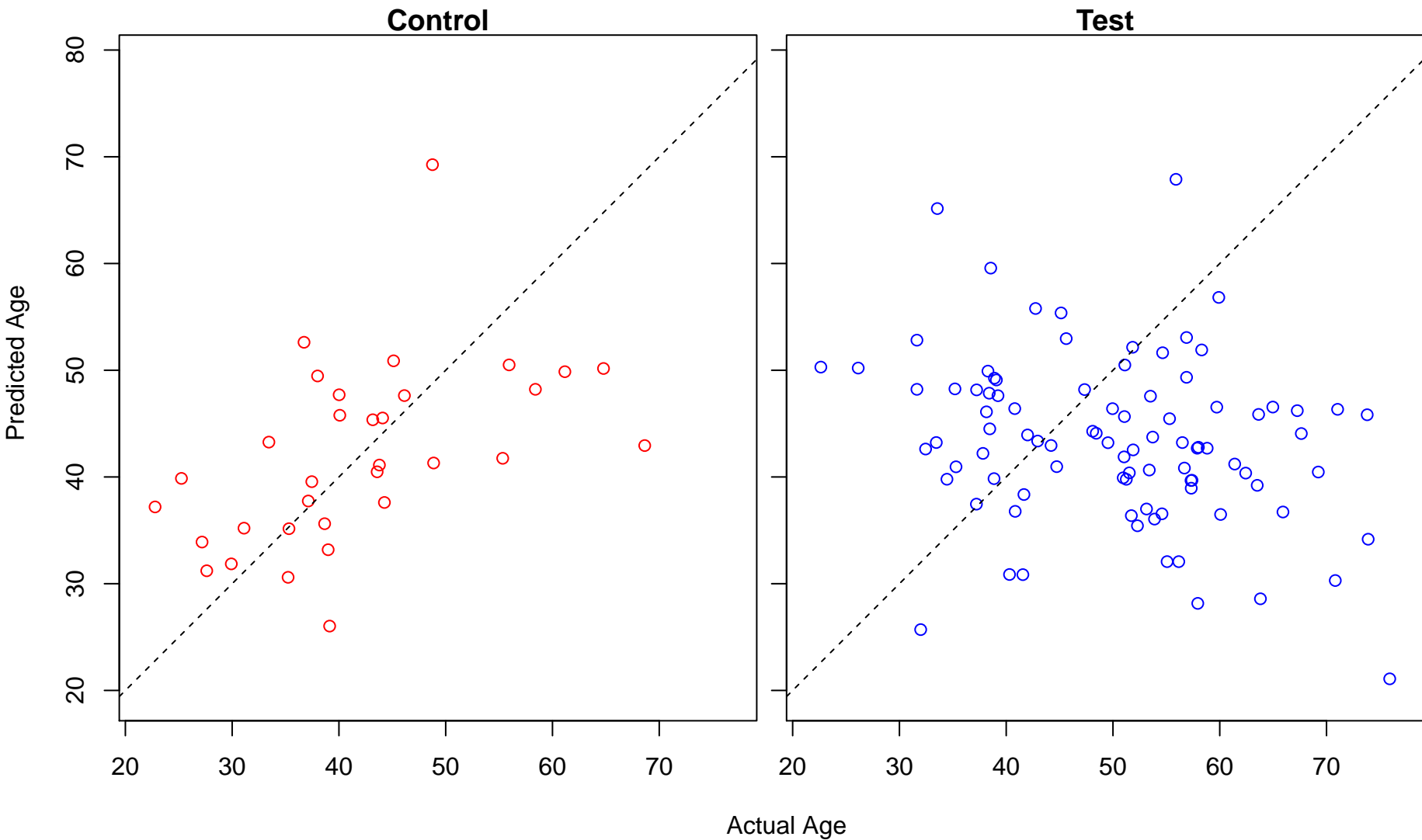
nucleotide-excision repair, DNA incision, 5'-to lesion (Score: 1.169894)



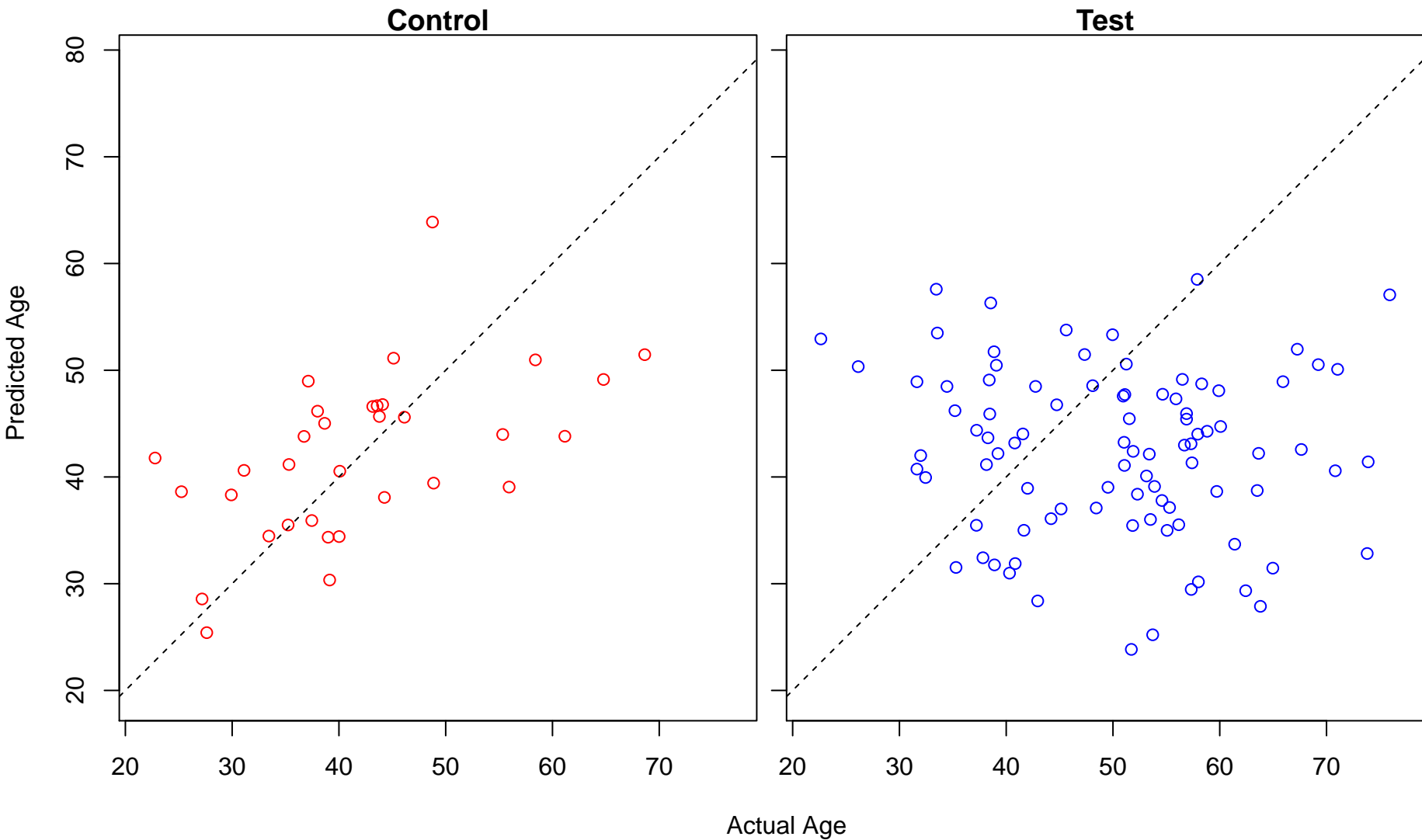
pinocytosis (Score: 1.169175)



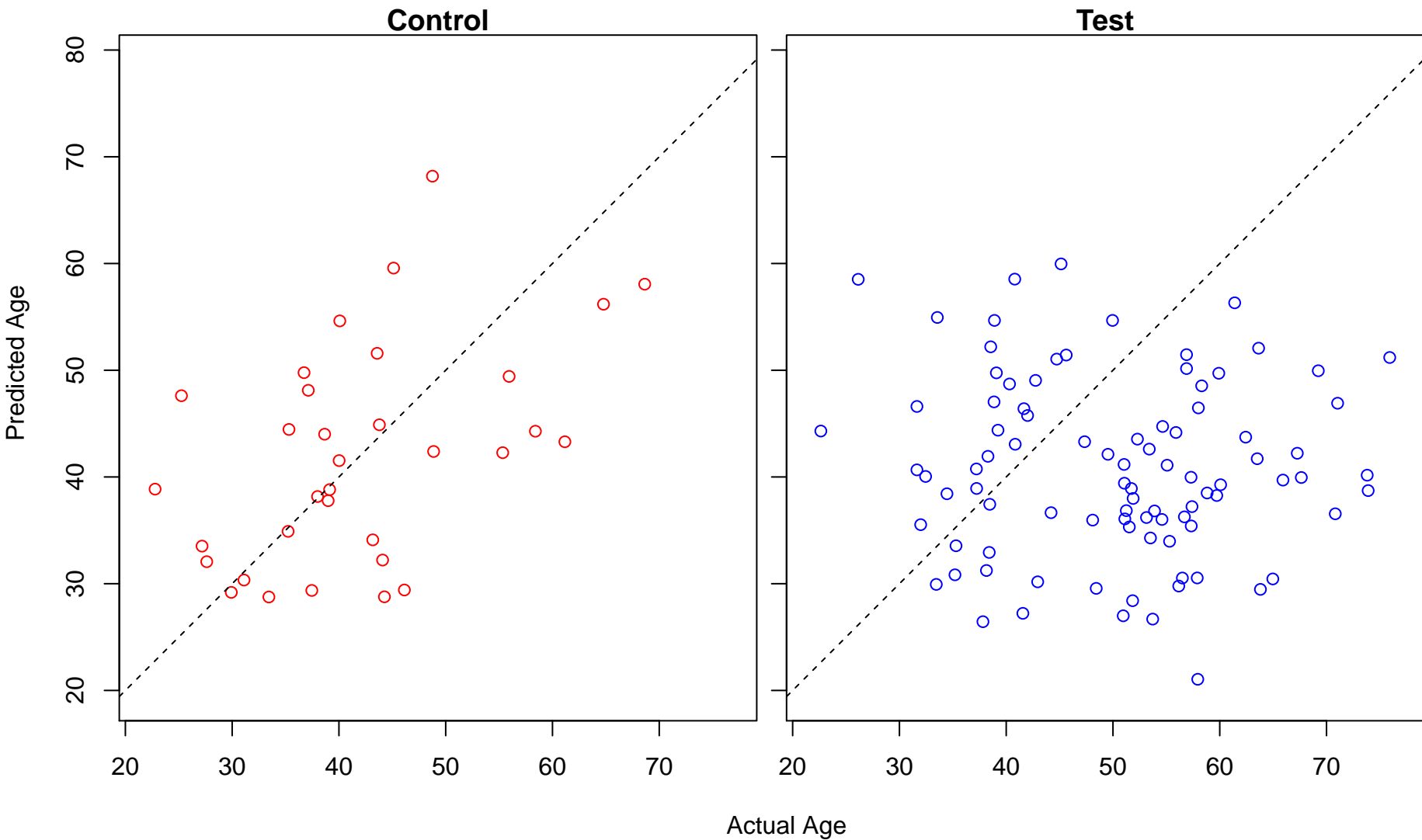
negative regulation of T cell differentiation (Score: 1.168402)



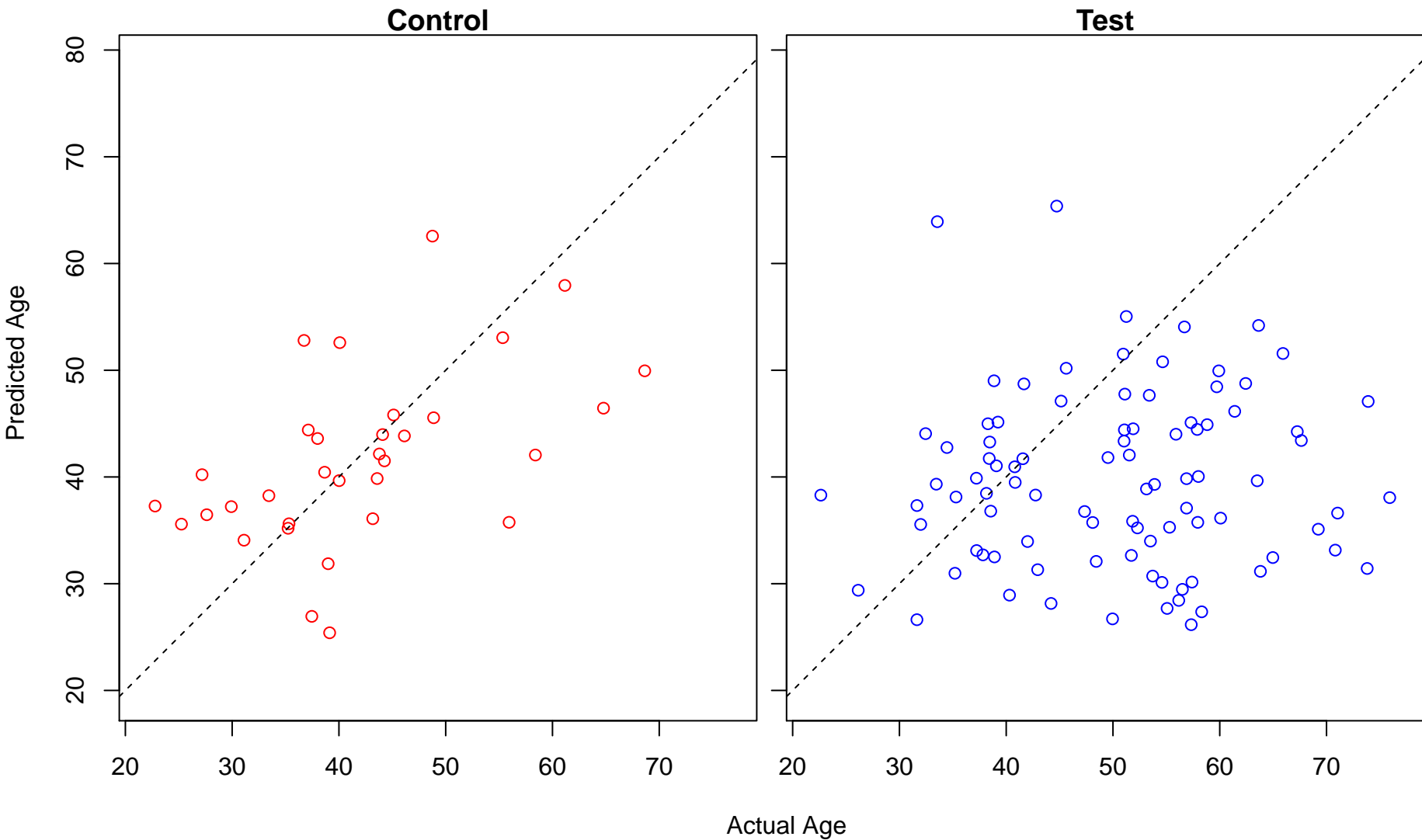
myelin maintenance (Score: 1.168200)



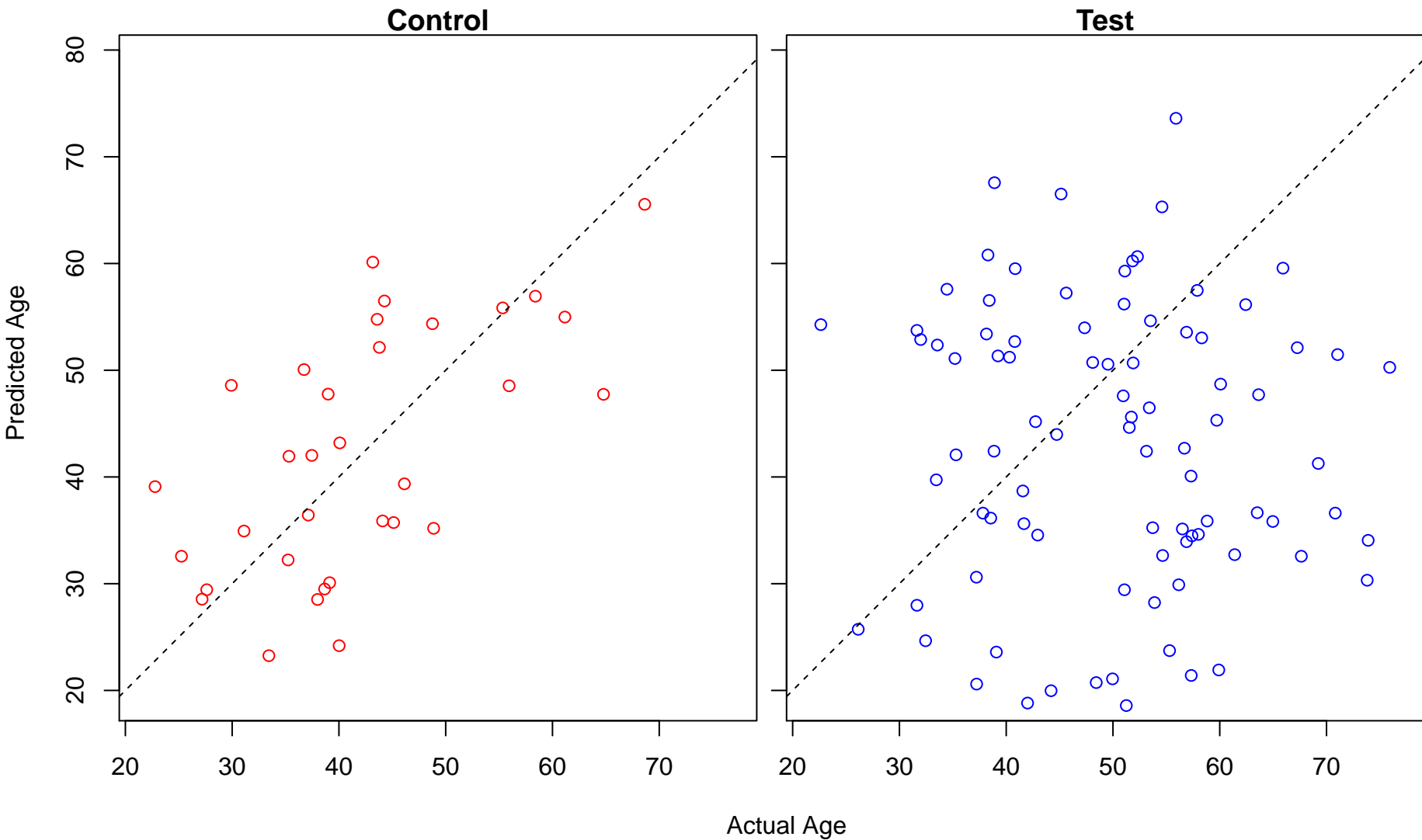
positive regulation of telomerase activity (Score: 1.167609)



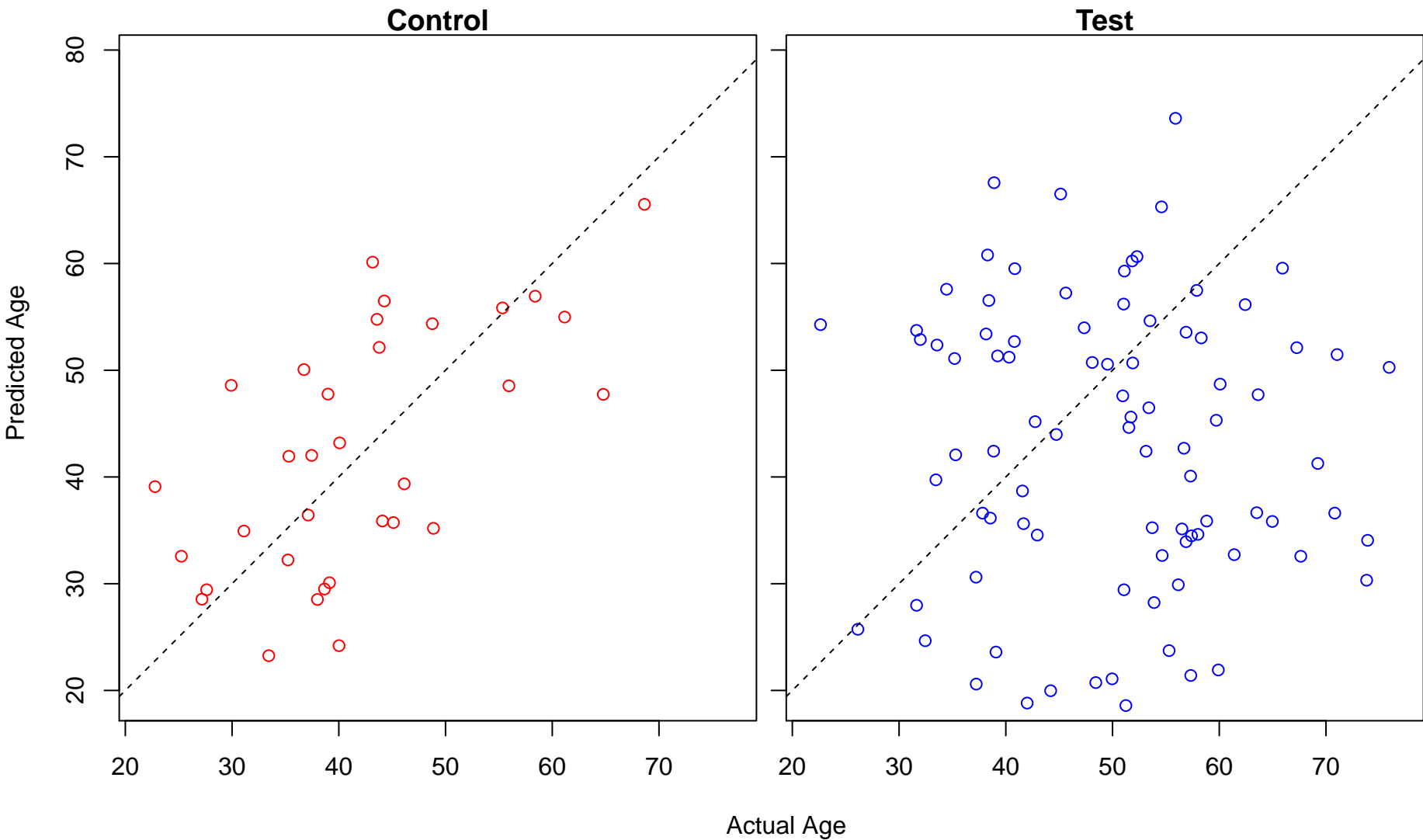
Ras protein signal transduction (Score: 1.164525)



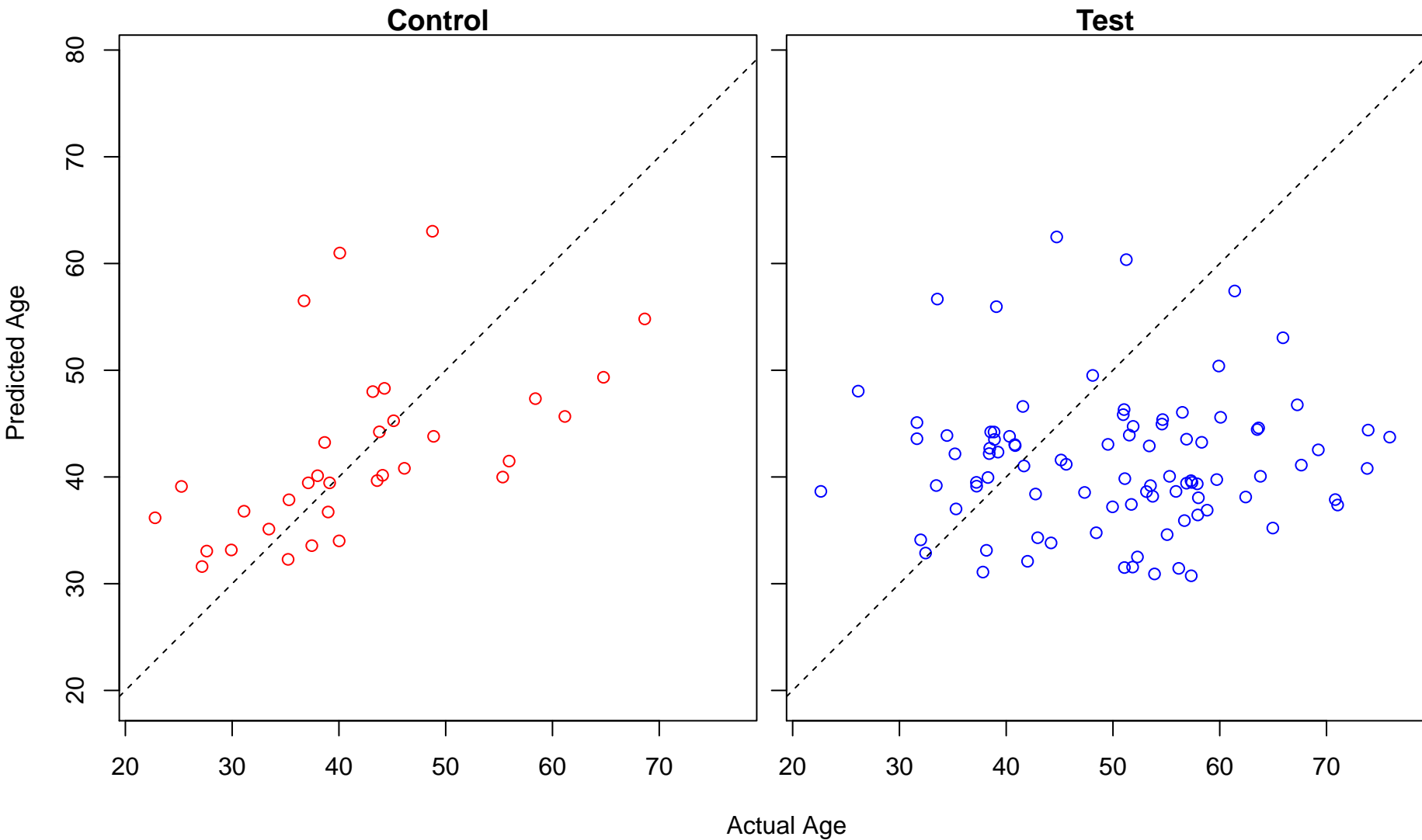
phosphatidic acid biosynthetic process (Score: 1.164123)



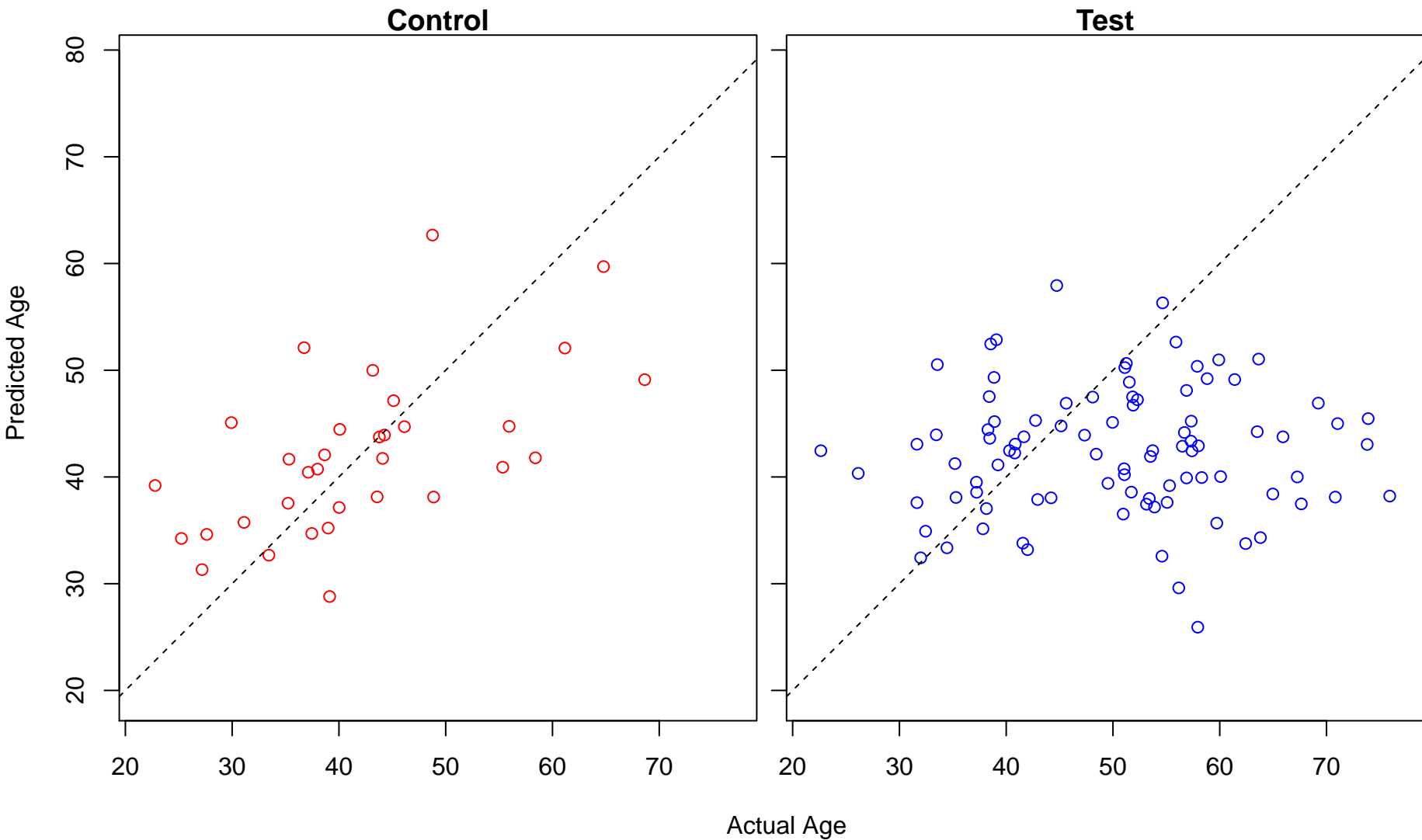
phosphatidic acid metabolic process (Score: 1.164123)



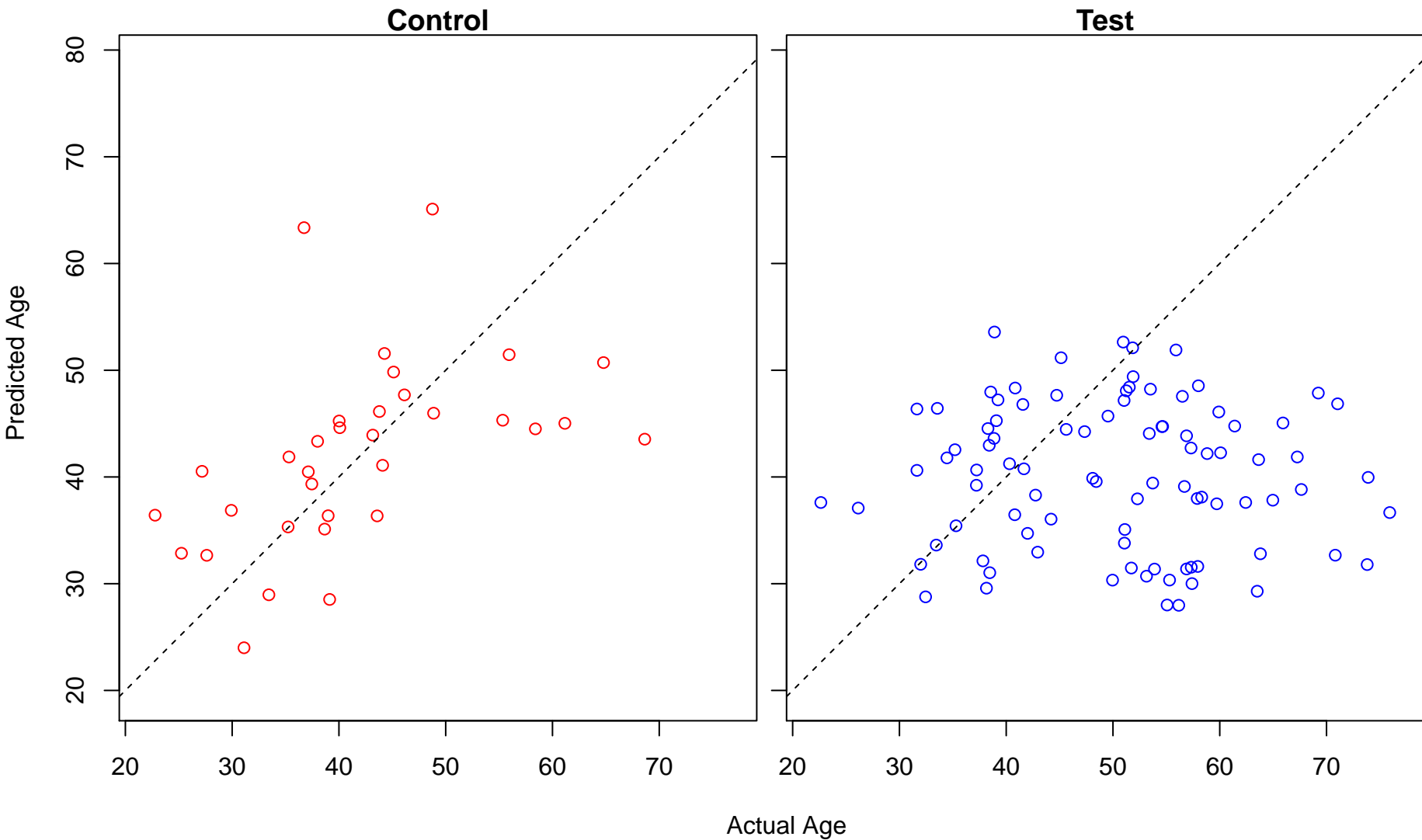
negative regulation of skeletal muscle tissue development (Score: 1.162905)



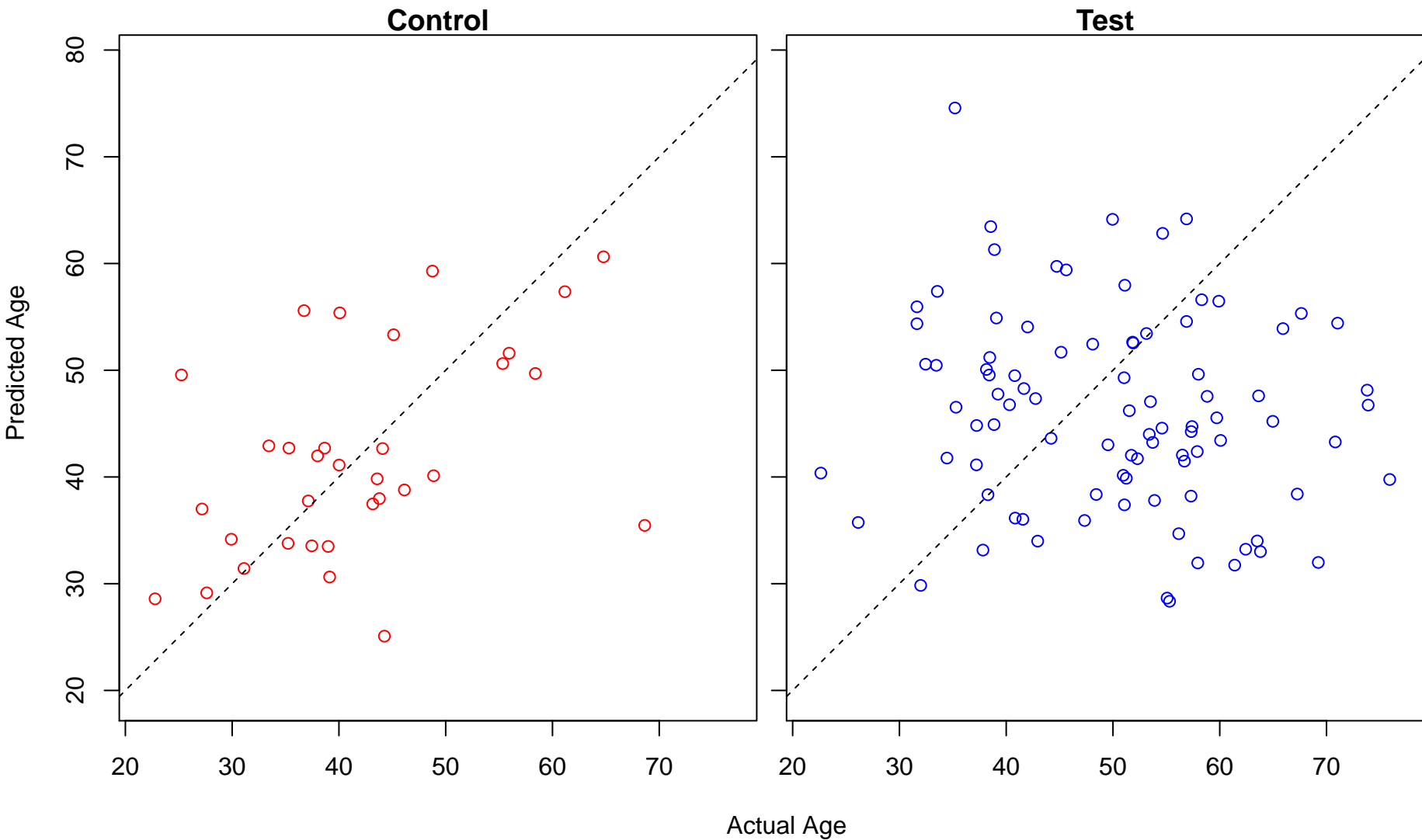
neuron death (Score: 1.158619)



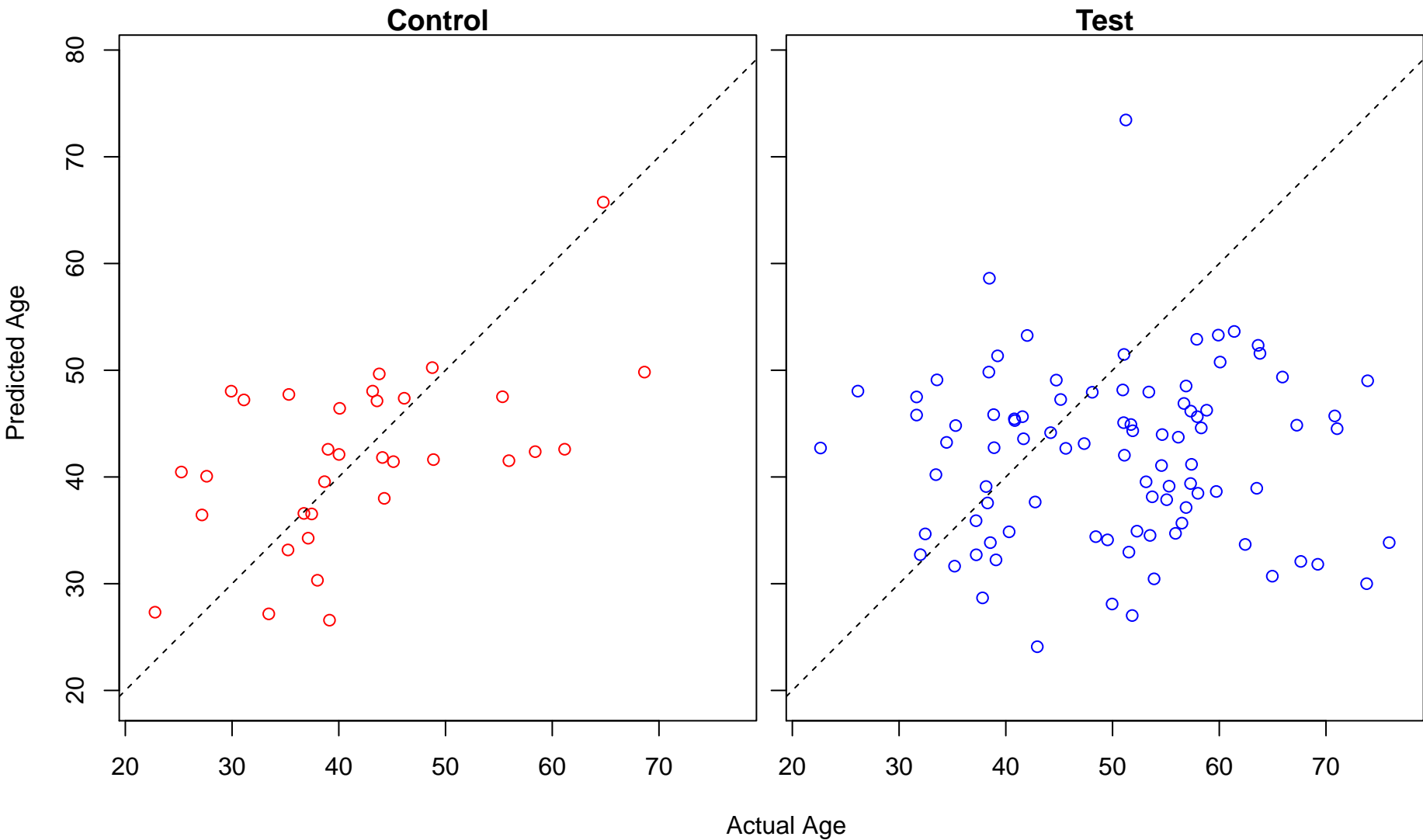
mature ribosome assembly (Score: 1.155465)



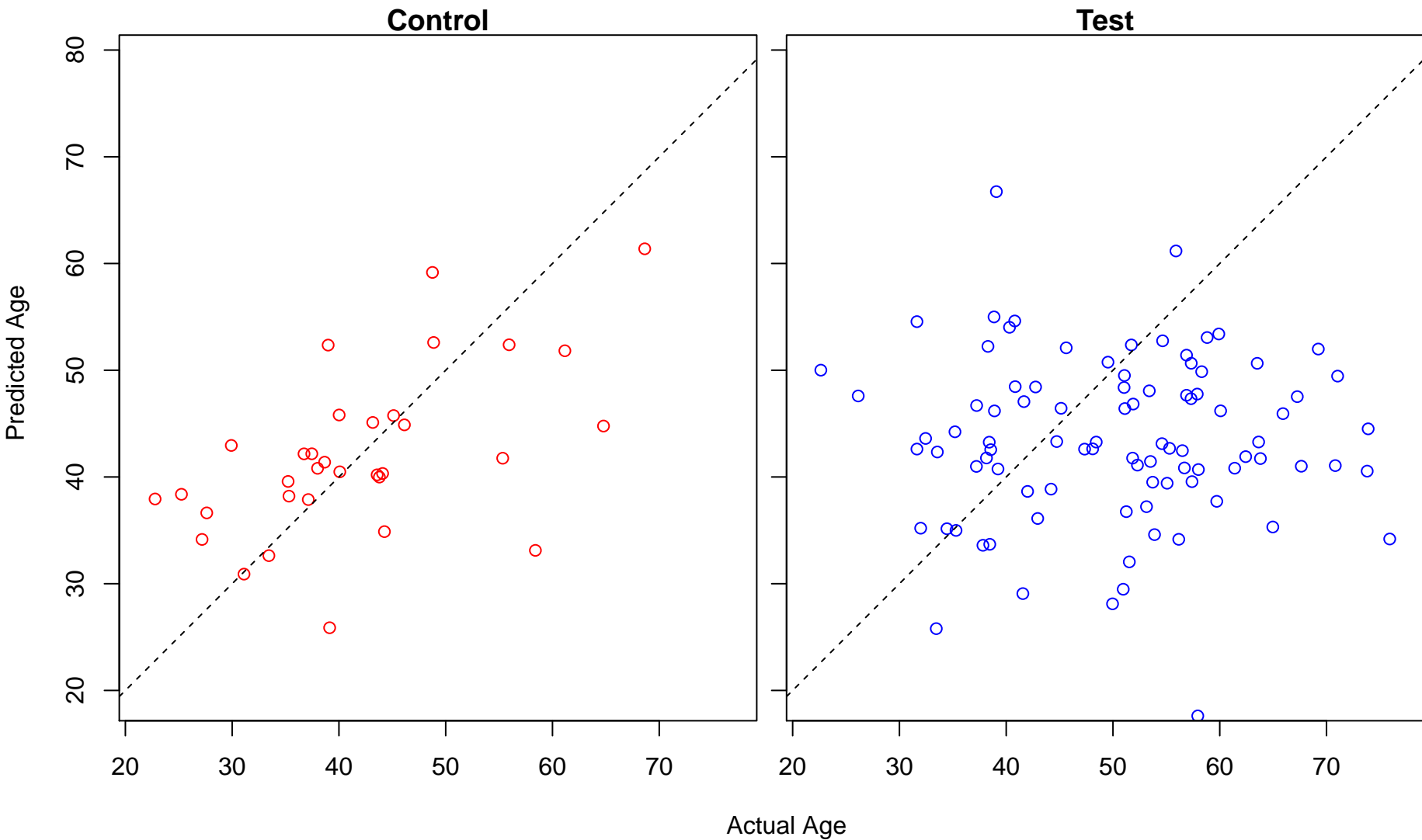
negative regulation of cell-cell adhesion (Score: 1.153509)



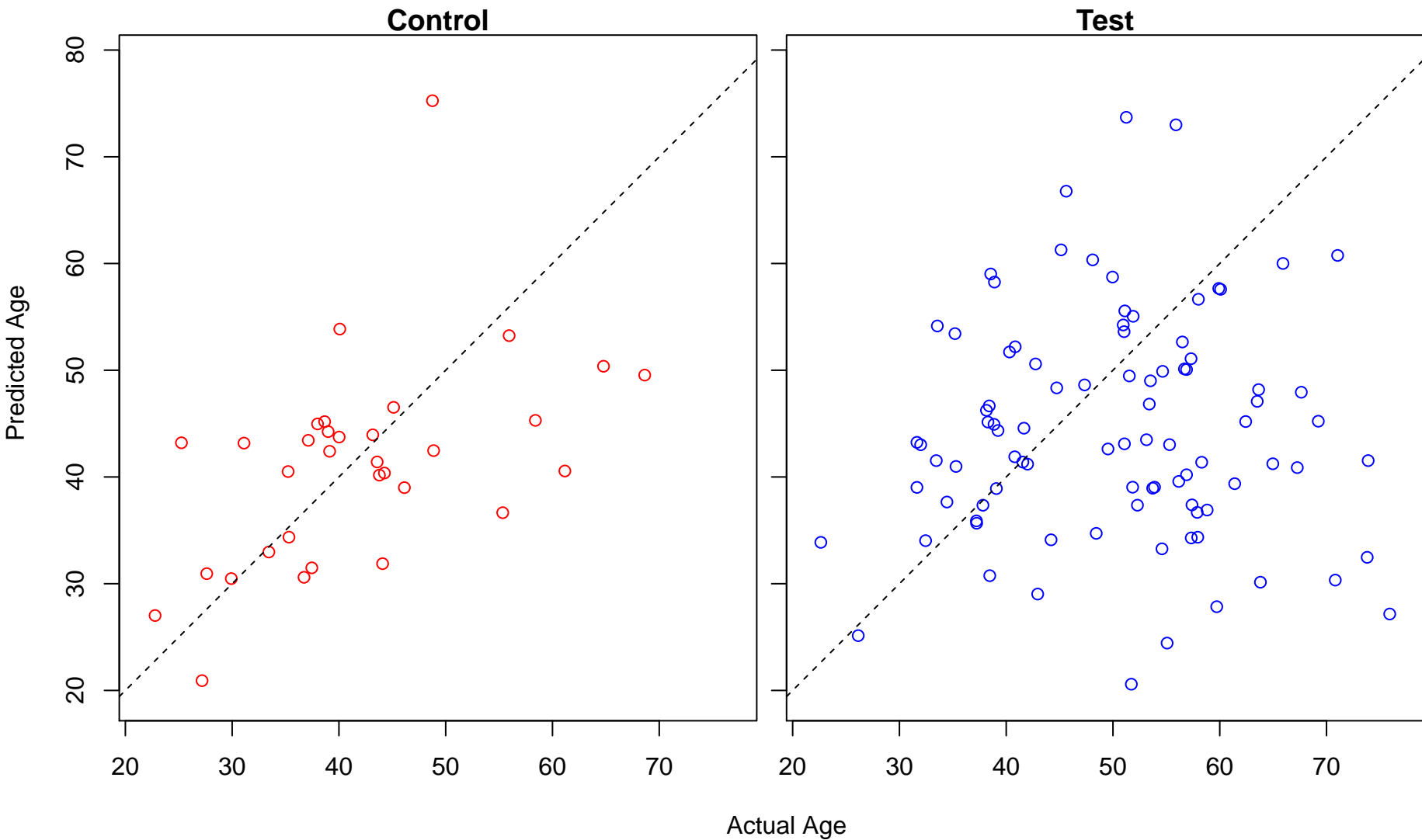
phosphatidylserine acyl-chain remodeling (Score: 1.153229)



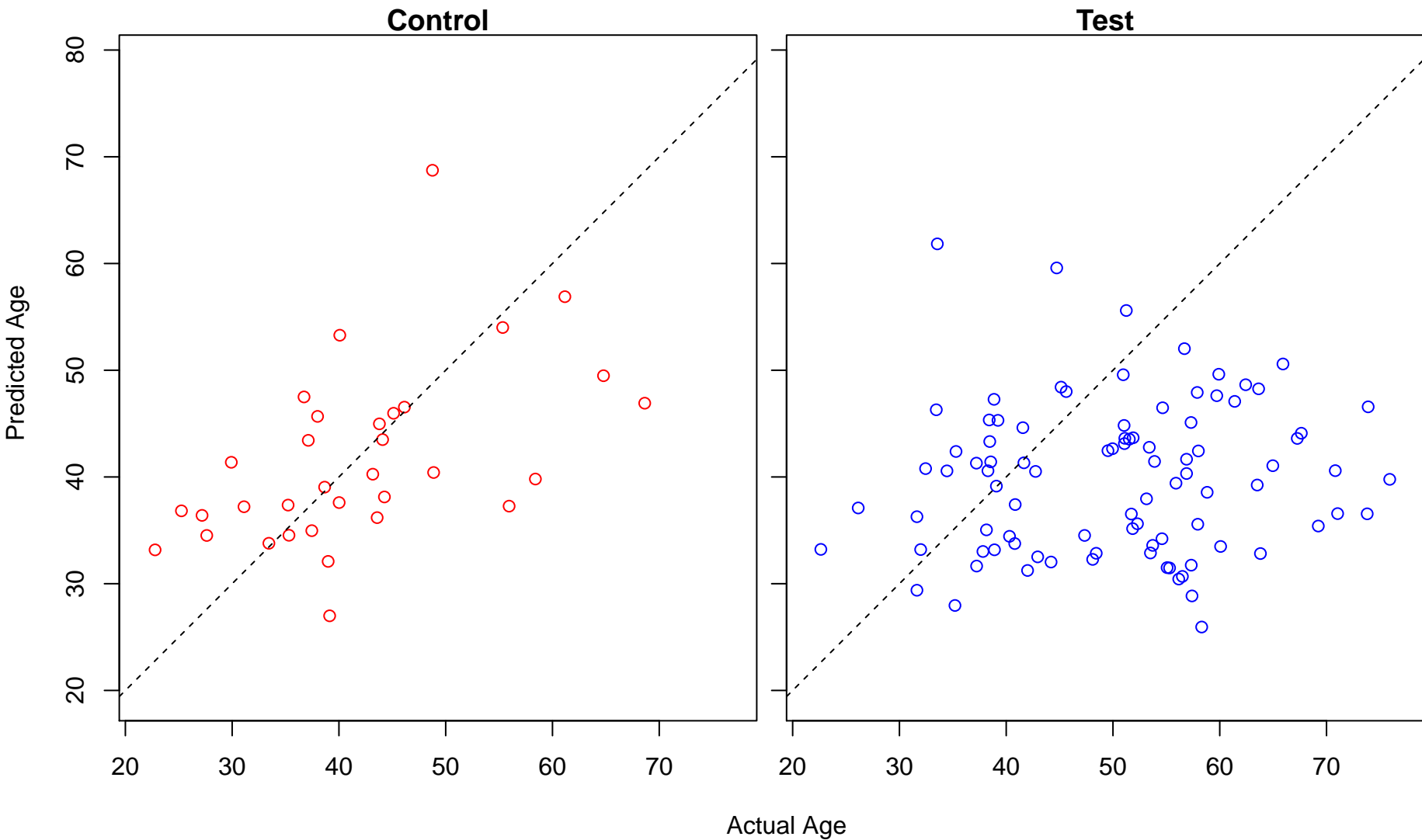
negative regulation of appetite by leptin-mediated signaling pathway (Score: 1.152840)



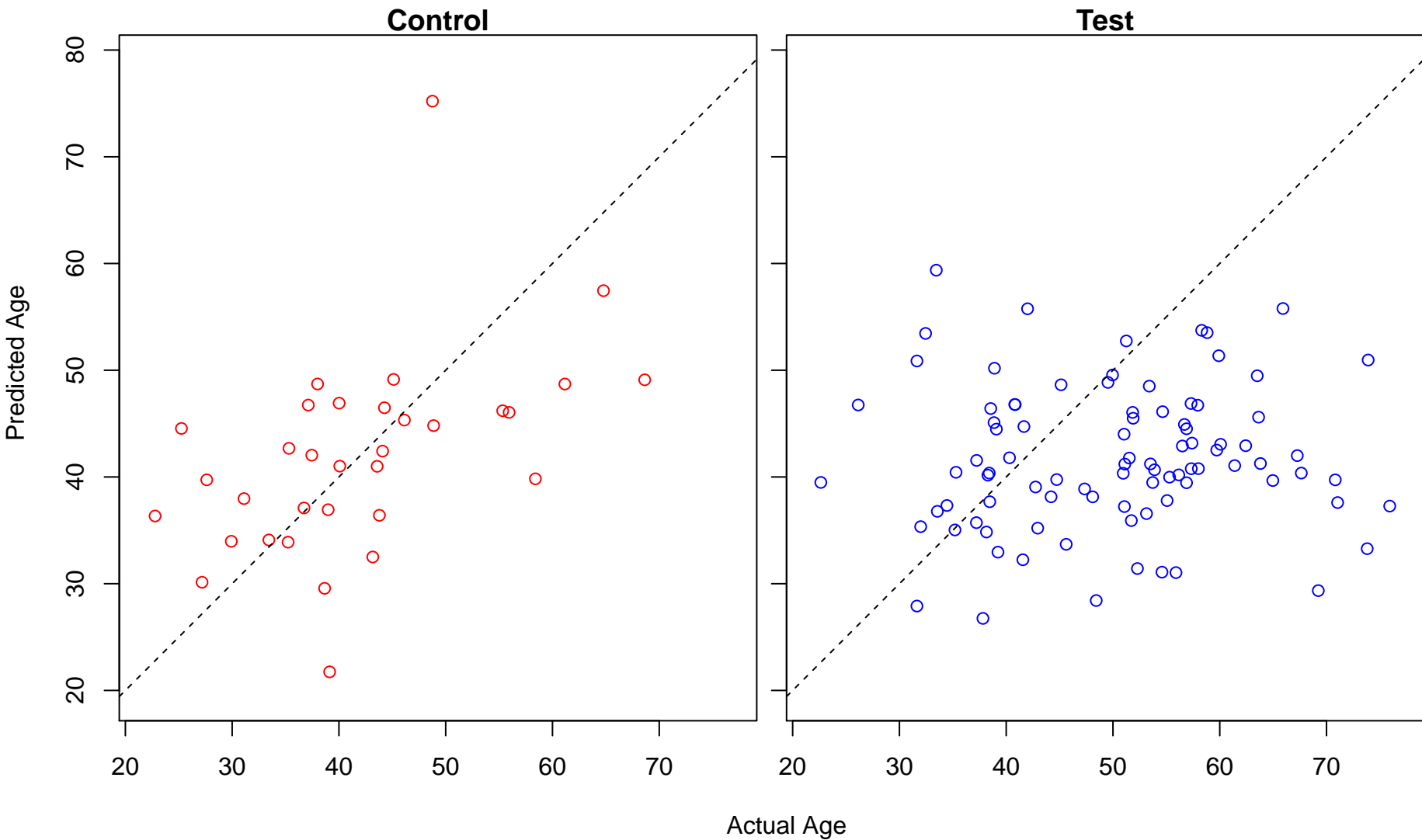
response to toxic substance (Score: 1.144271)



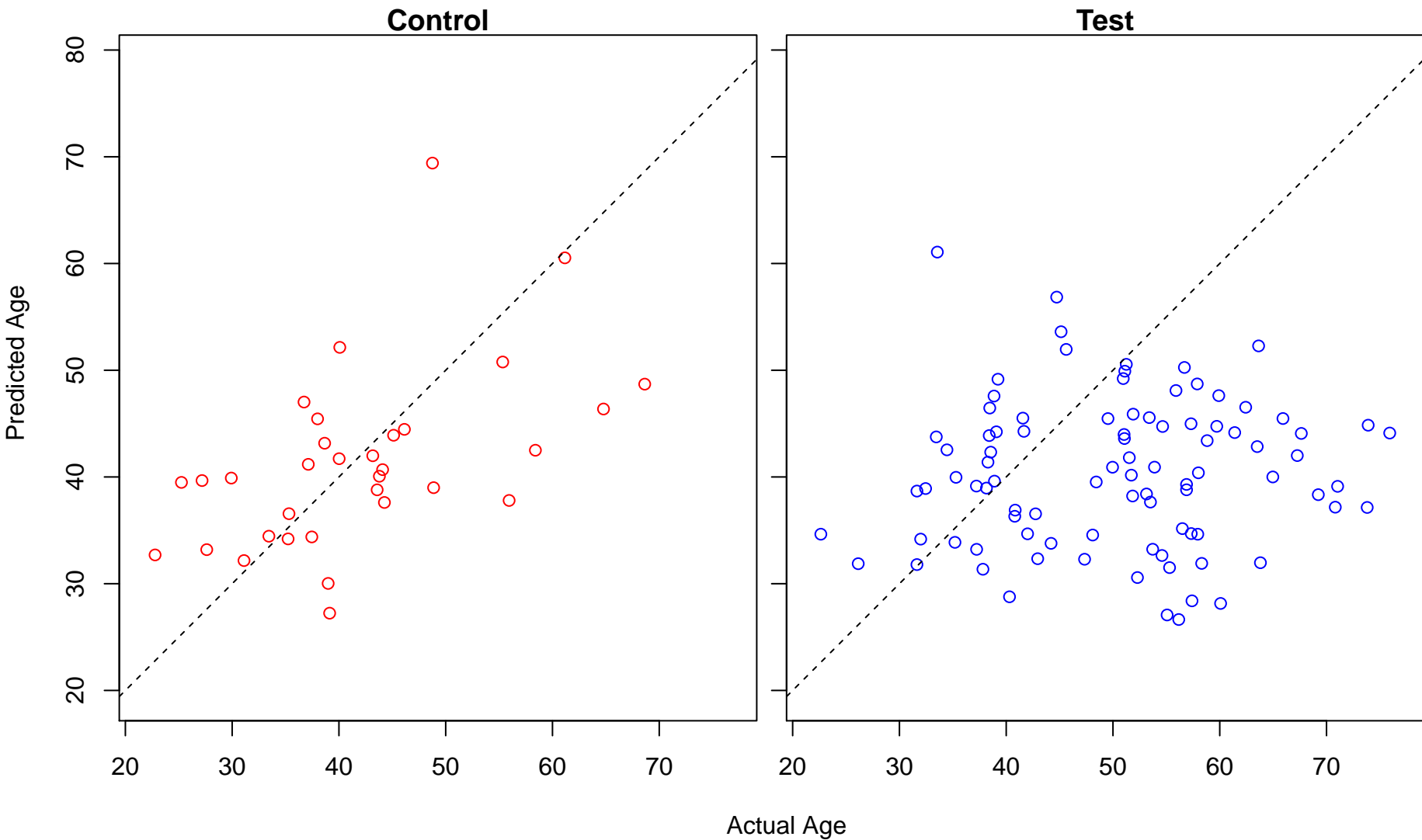
cellular response to fibroblast growth factor stimulus (Score: 1.142997)



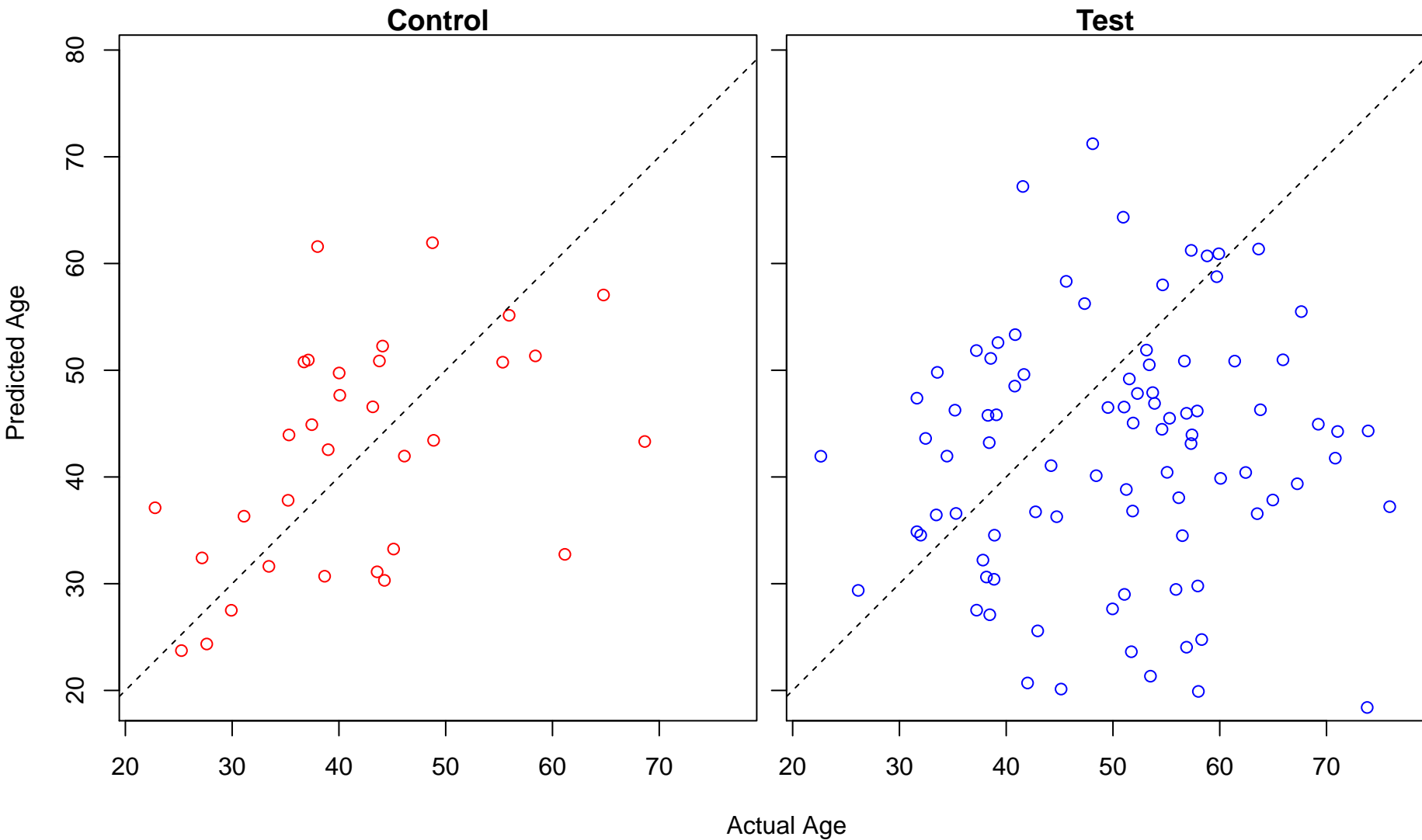
mitotic G2 DNA damage checkpoint (Score: 1.141740)



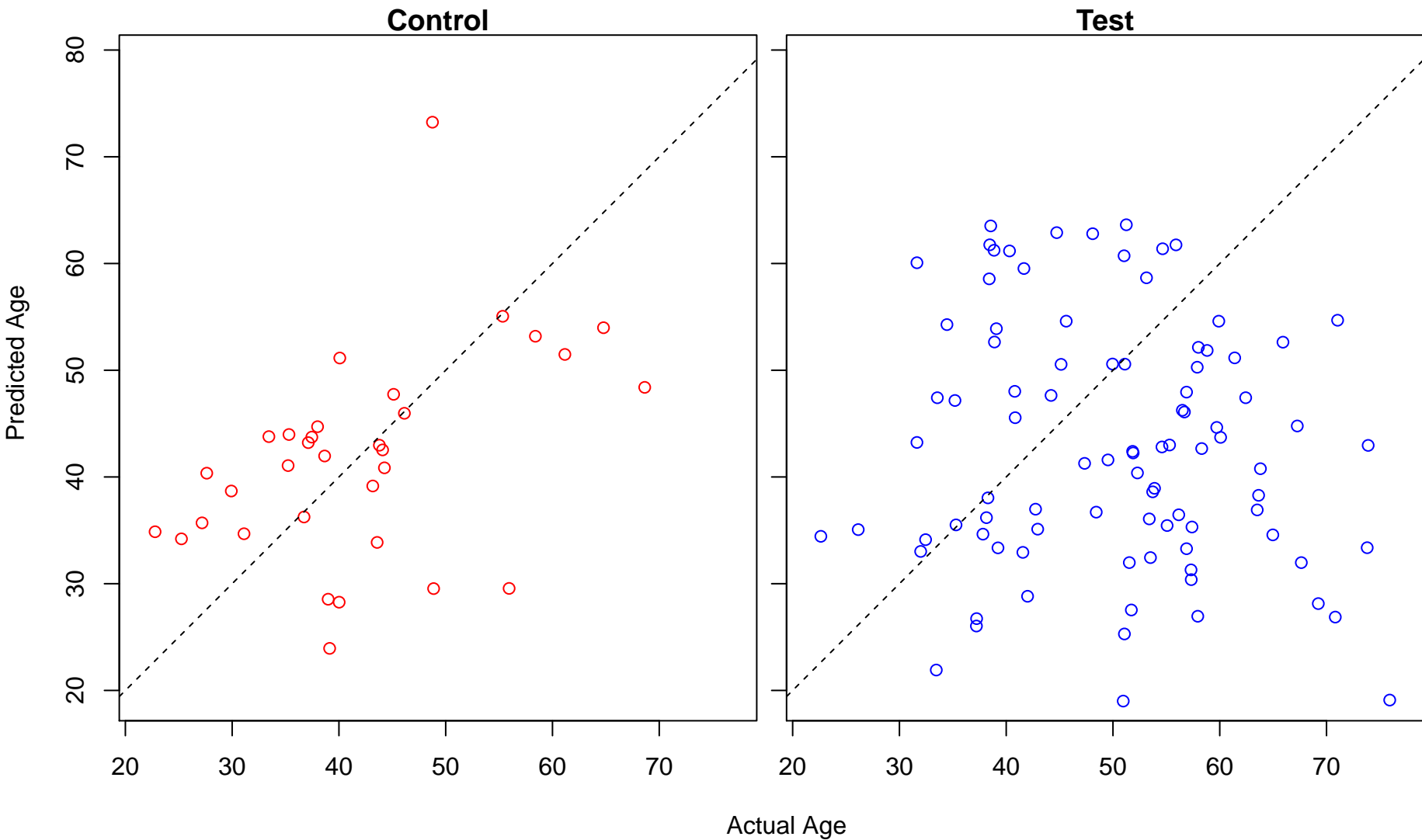
insulin receptor signaling pathway (Score: 1.139095)



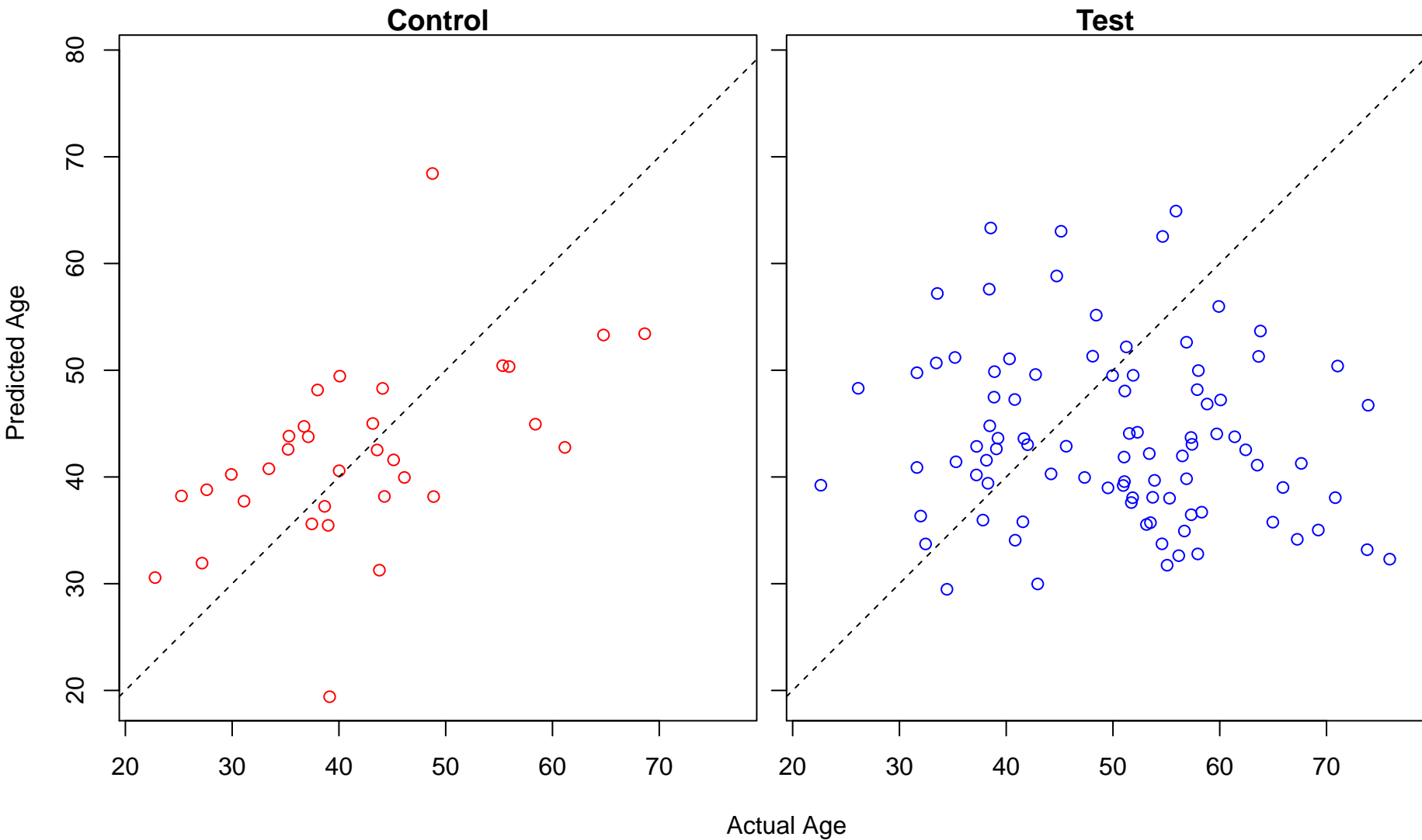
negative regulation of Notch signaling pathway (Score: 1.138975)



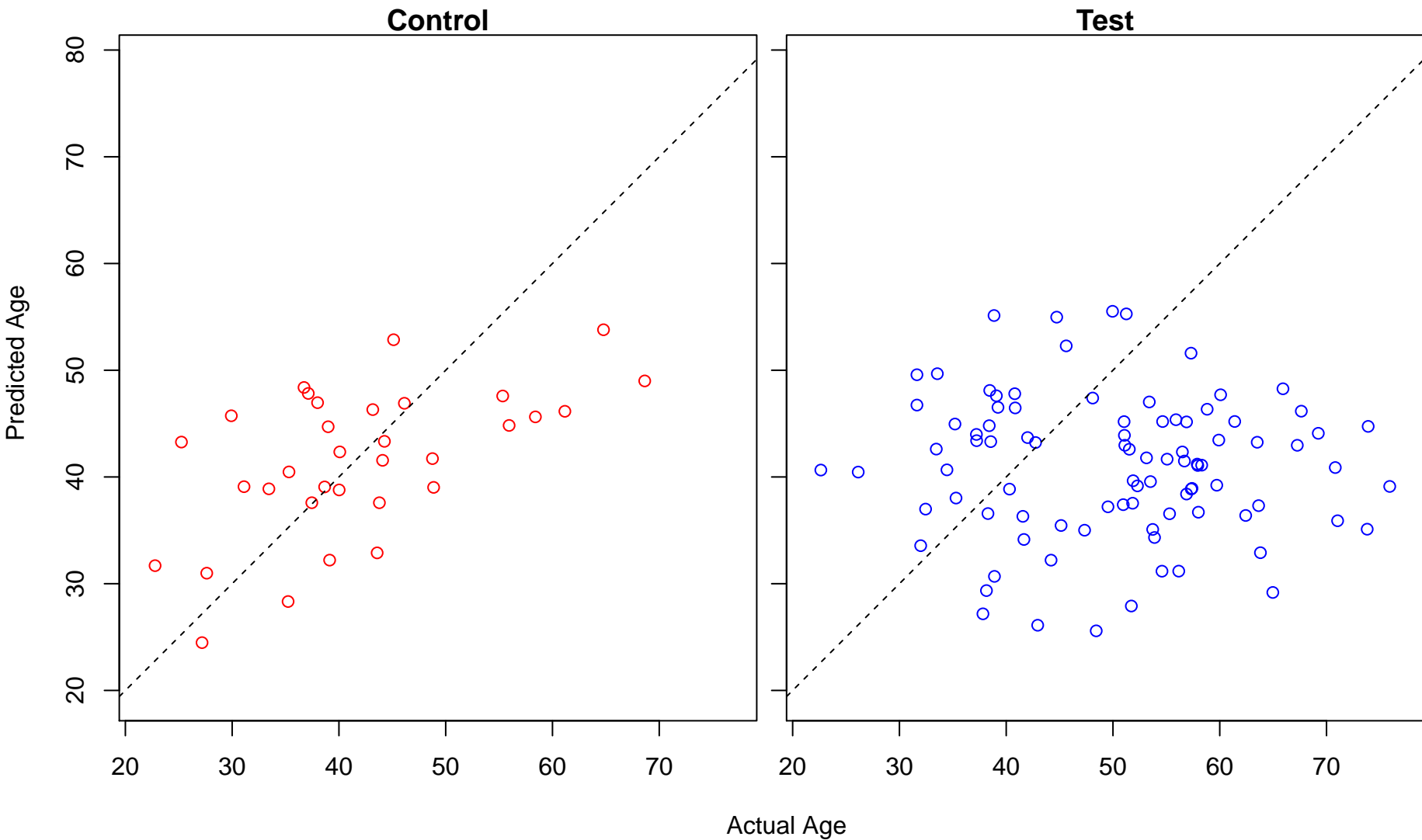
negative regulation of cell-matrix adhesion (Score: 1.138600)



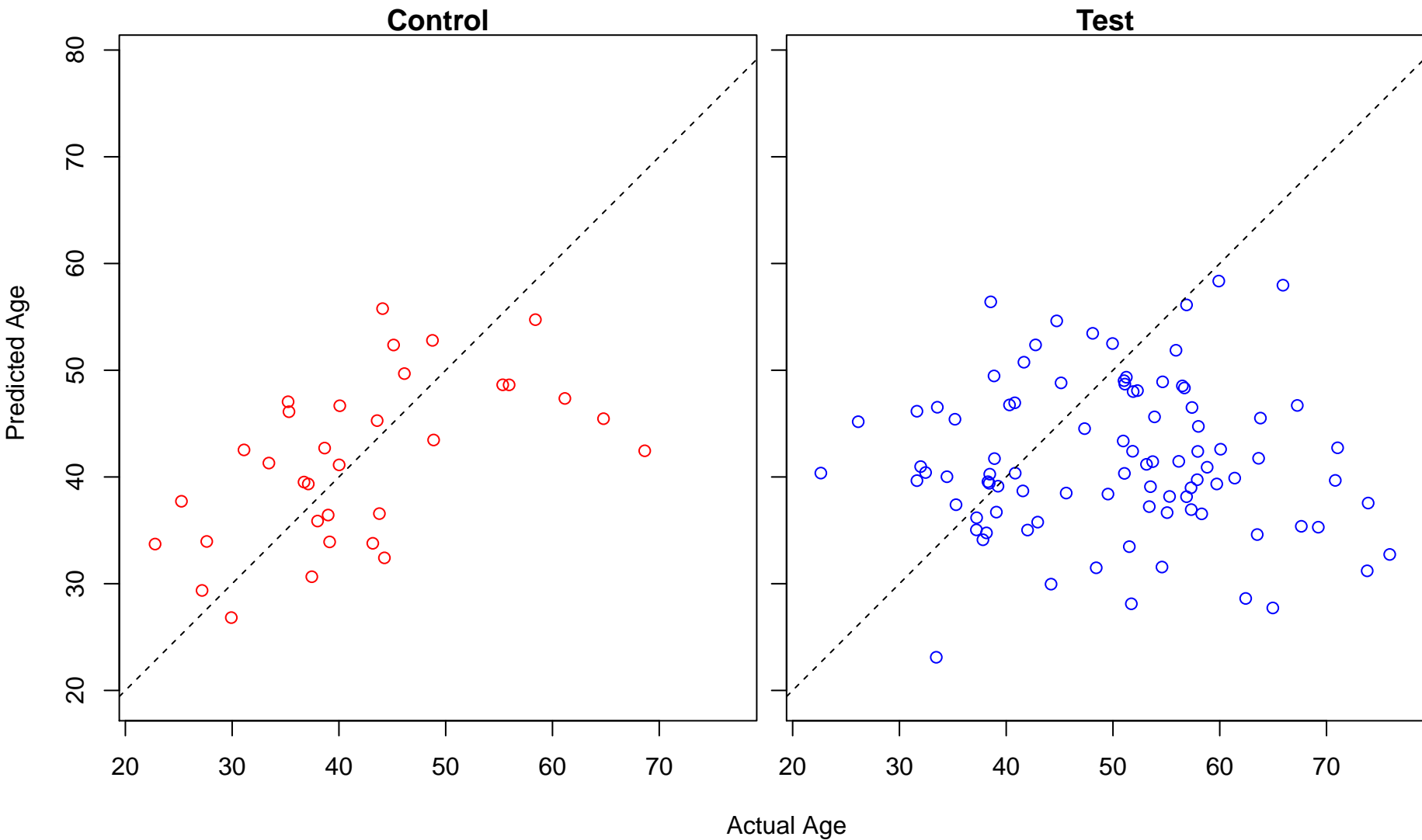
myeloid leukocyte differentiation (Score: 1.138323)



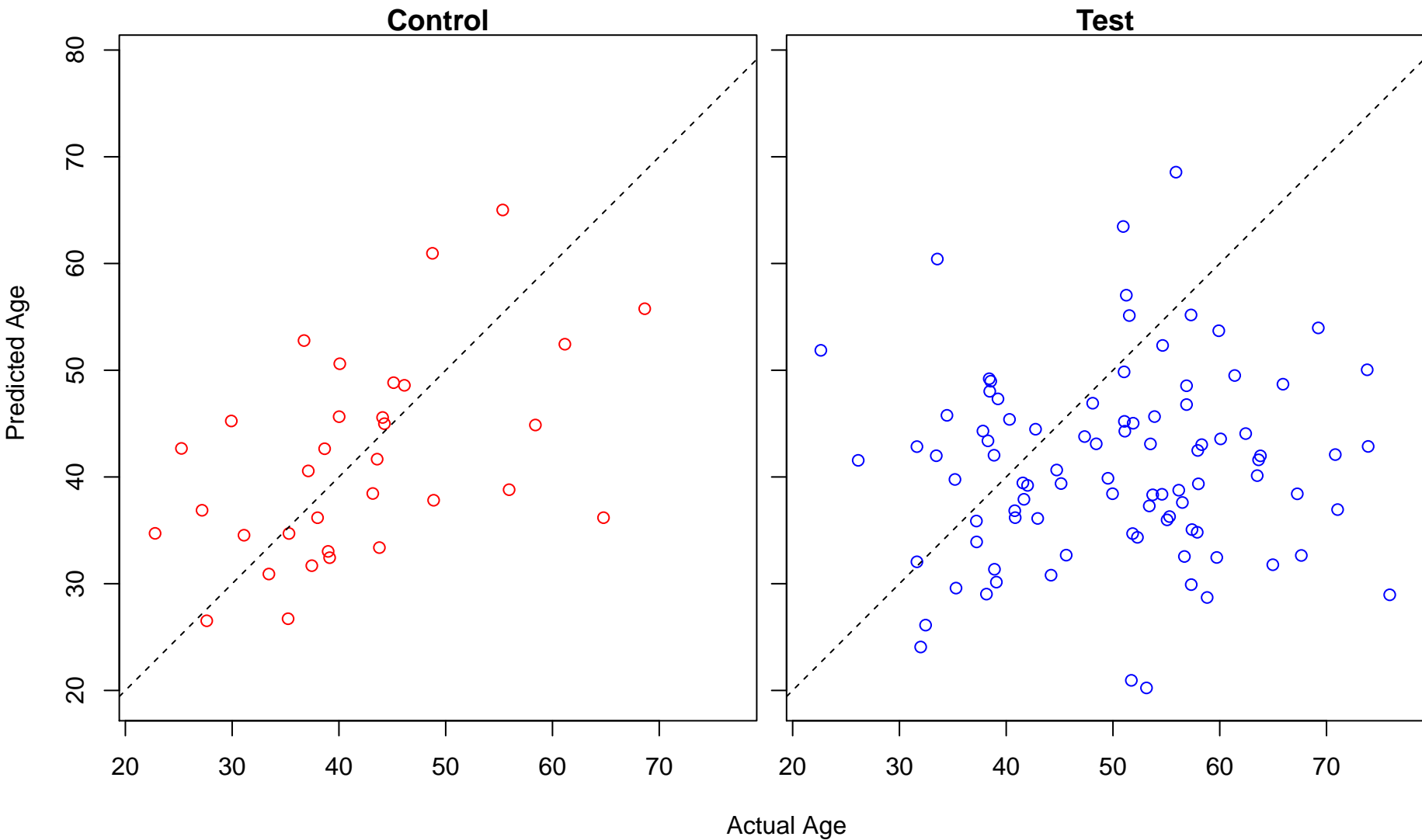
cholesterol transport (Score: 1.138032)



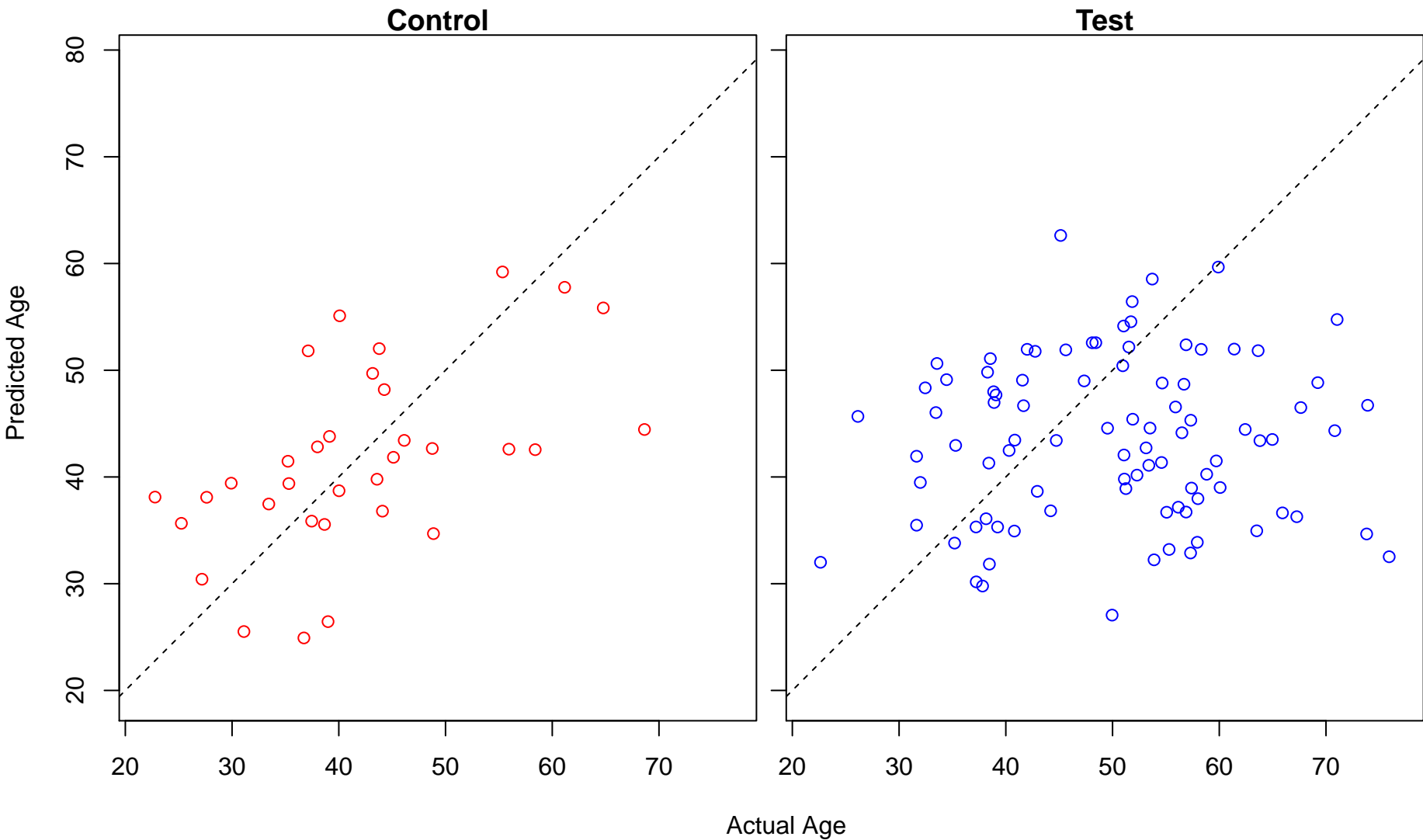
striated muscle contraction (Score: 1.137763)



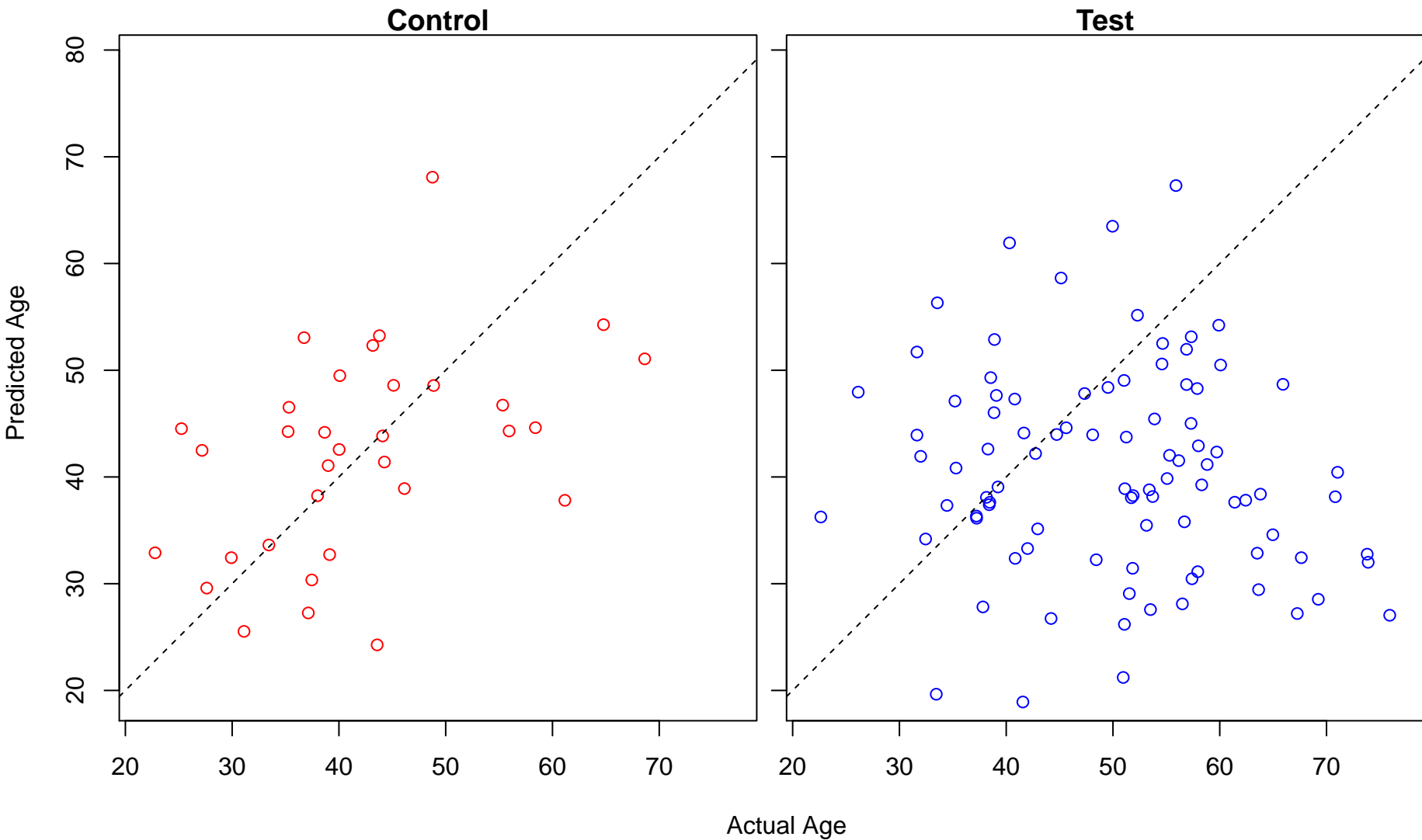
postreplication repair (Score: 1.135898)



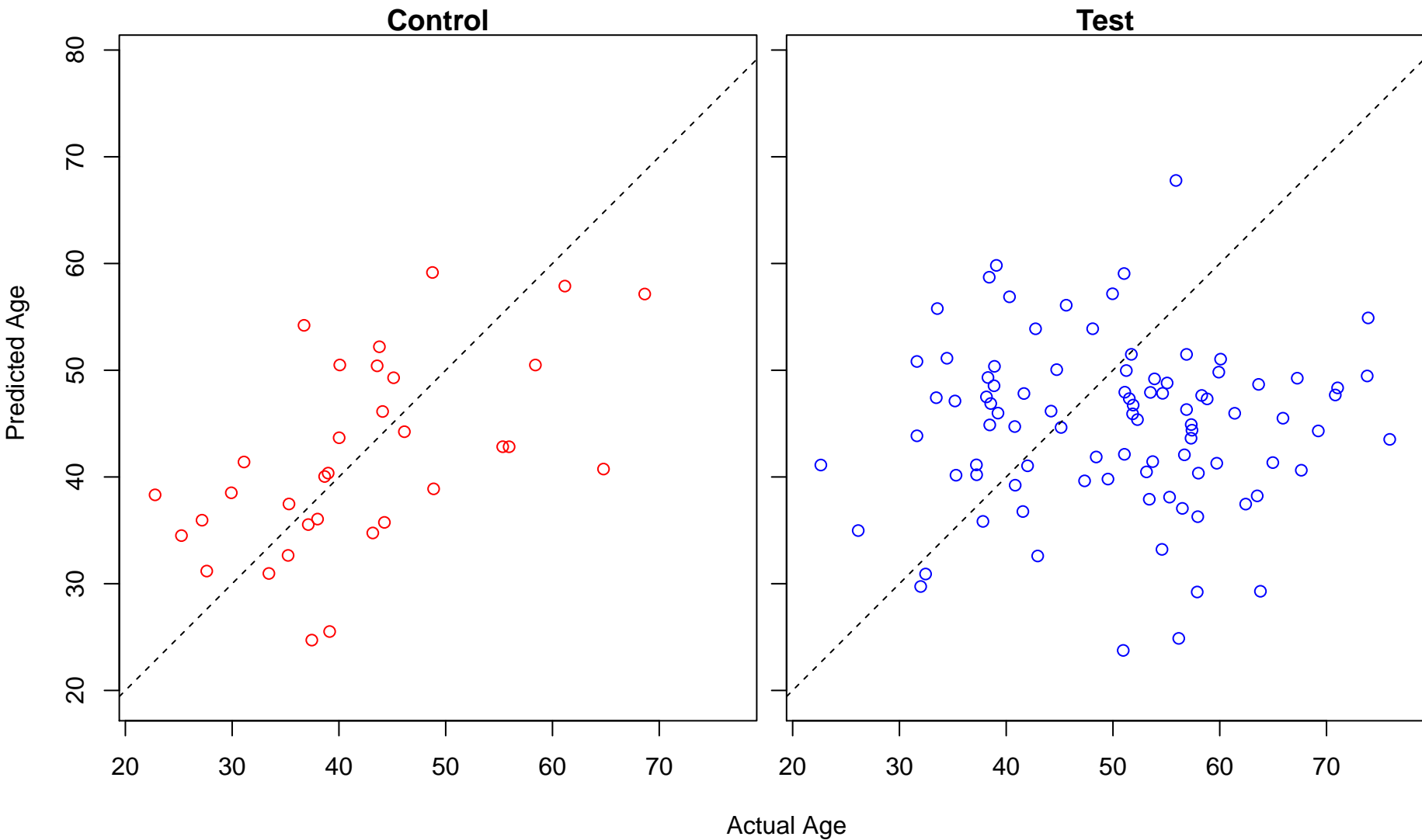
negative regulation of ryanodine-sensitive calcium-release channel activity (Score: 1.135776)



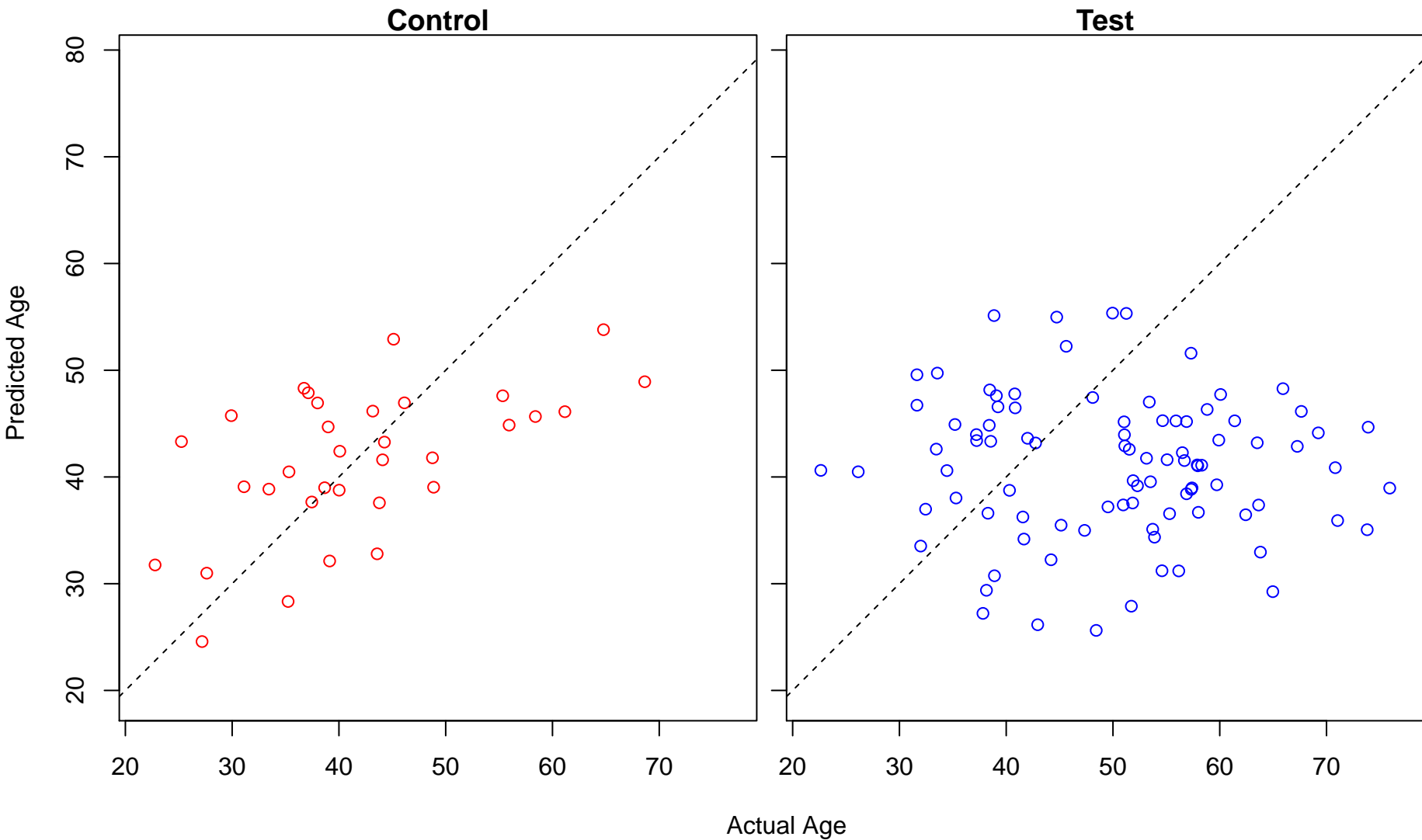
cholesterol biosynthetic process (Score: 1.135220)



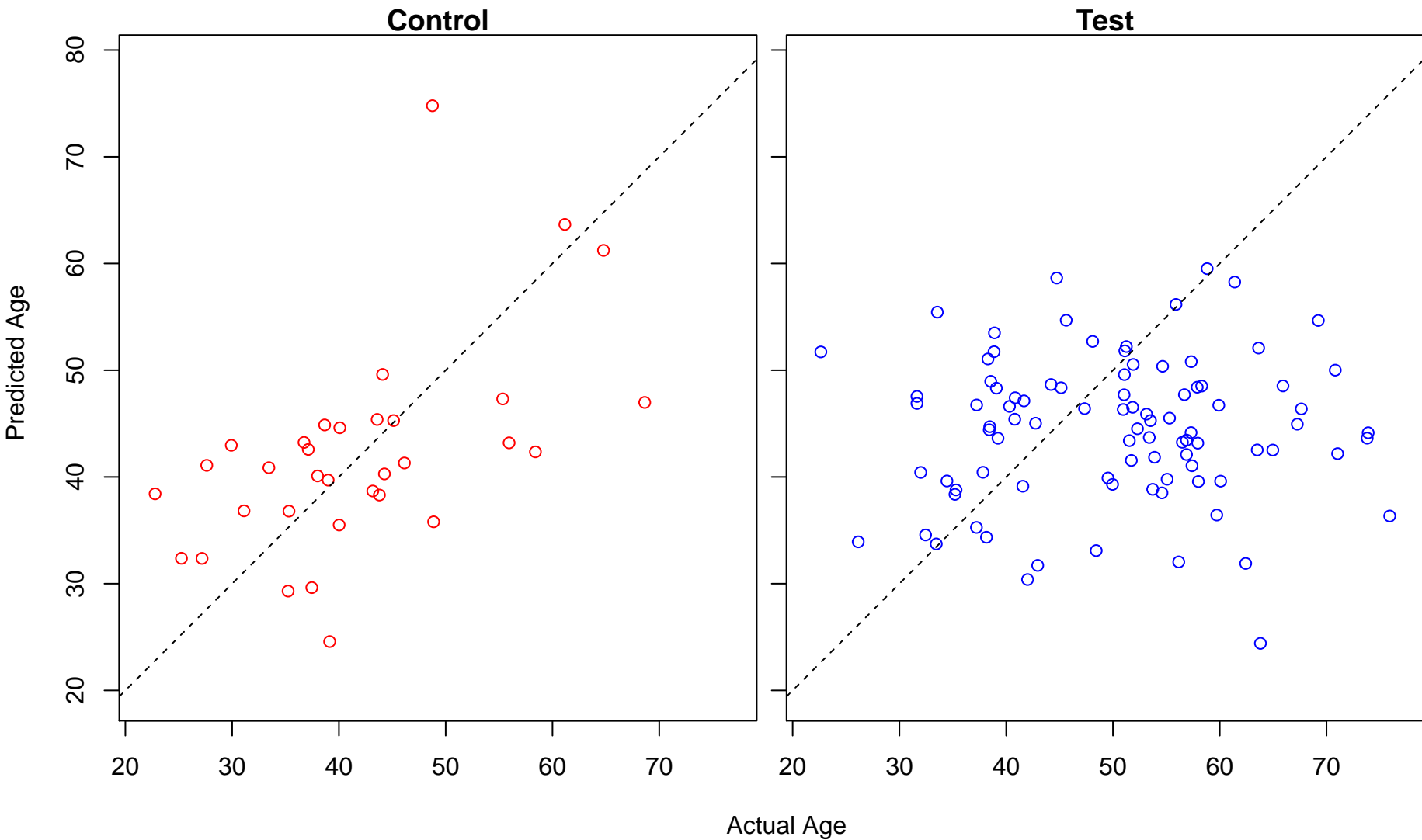
membrane assembly (Score: 1.134840)



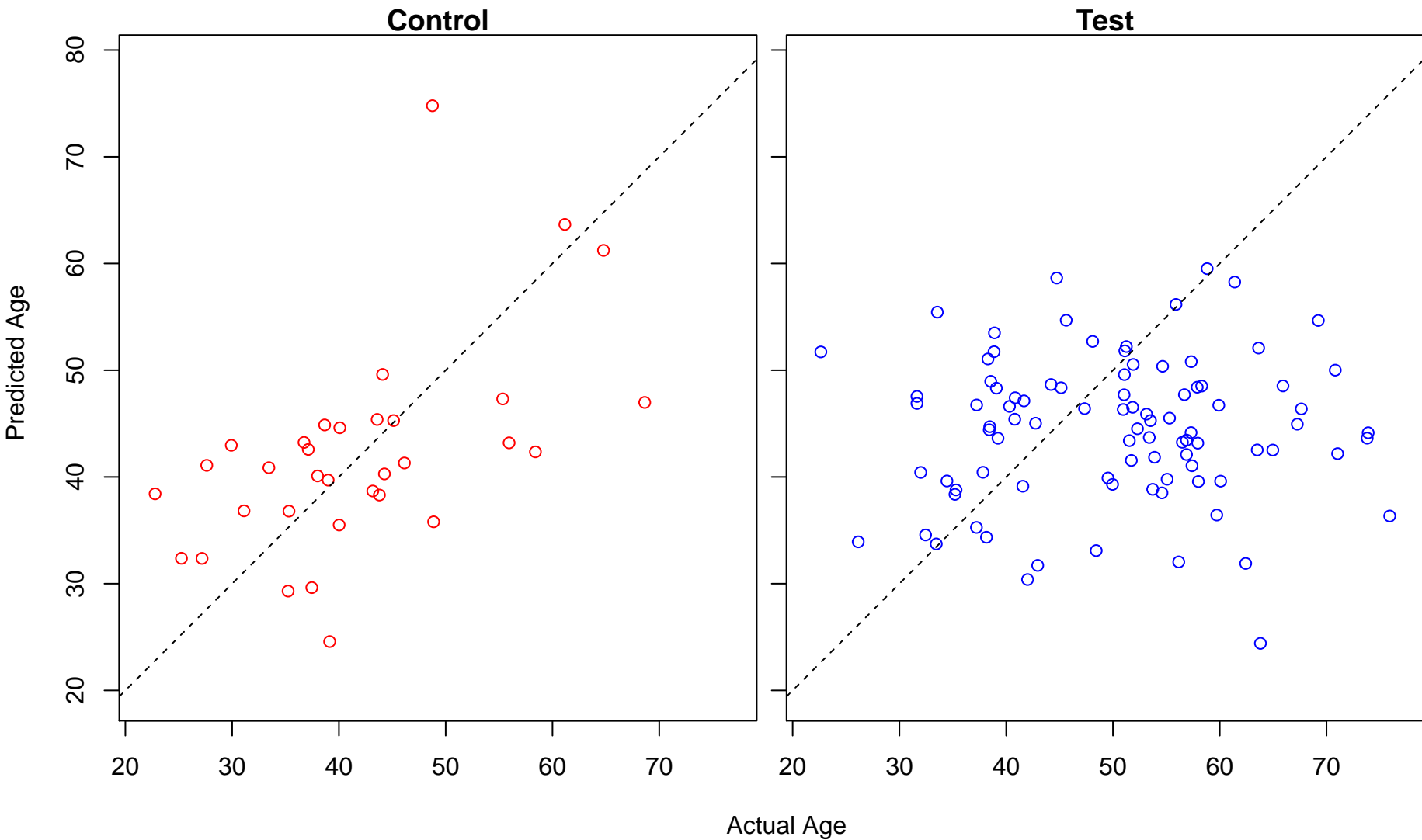
sterol transport (Score: 1.134491)



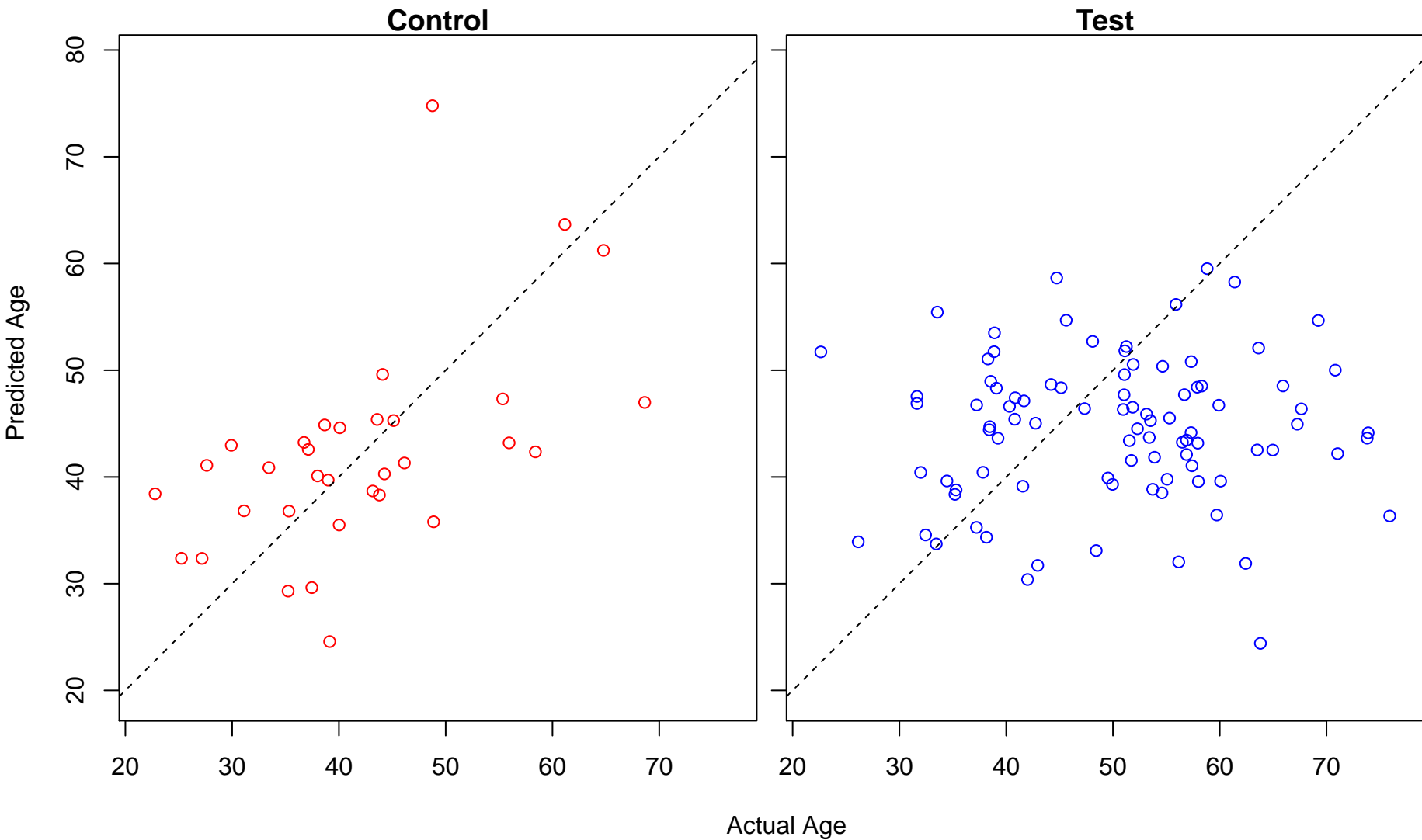
endosome to melanosome transport (Score: 1.133355)



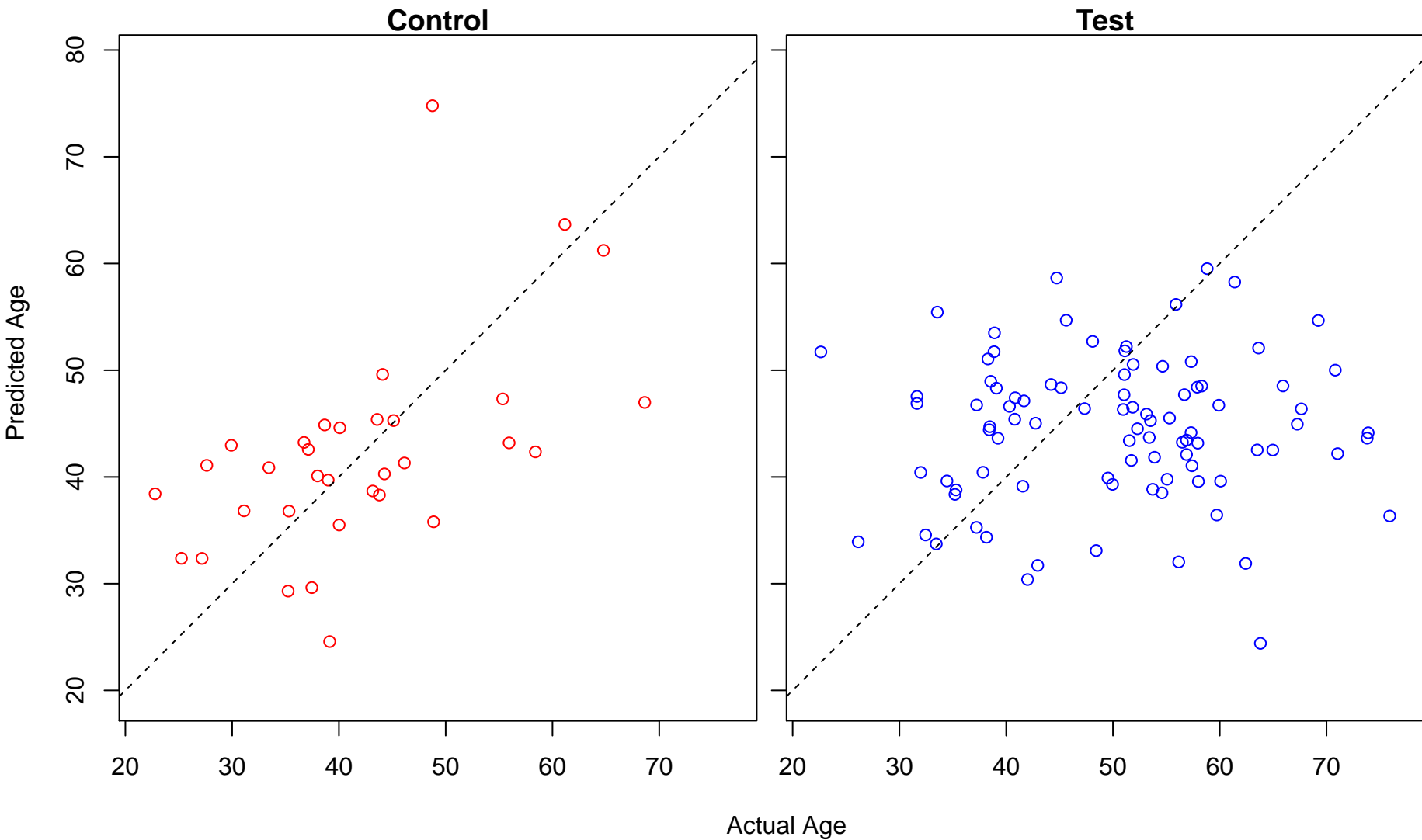
pigment accumulation (Score: 1.133355)



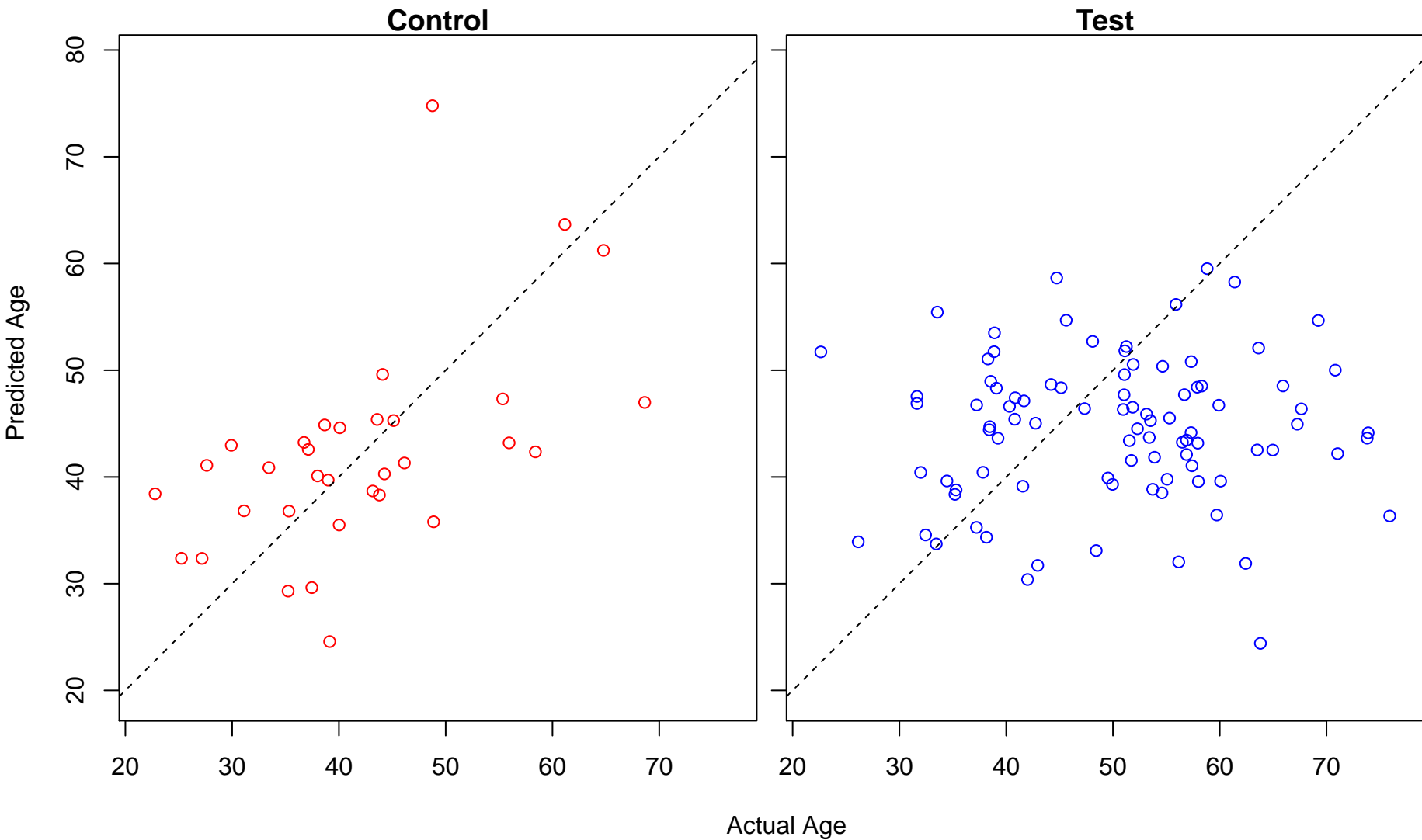
cellular pigment accumulation (Score: 1.133355)



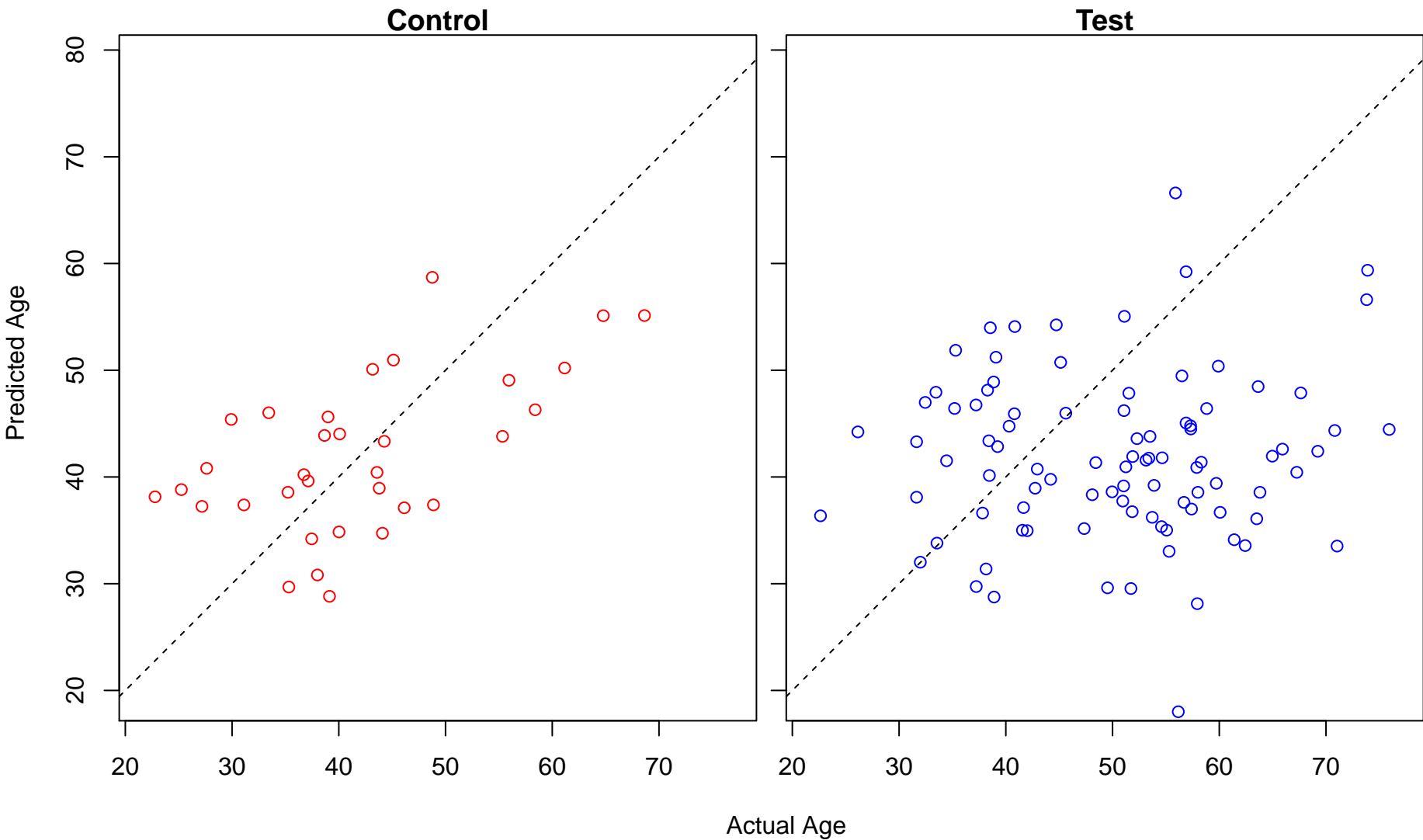
endosome to pigment granule transport (Score: 1.133355)



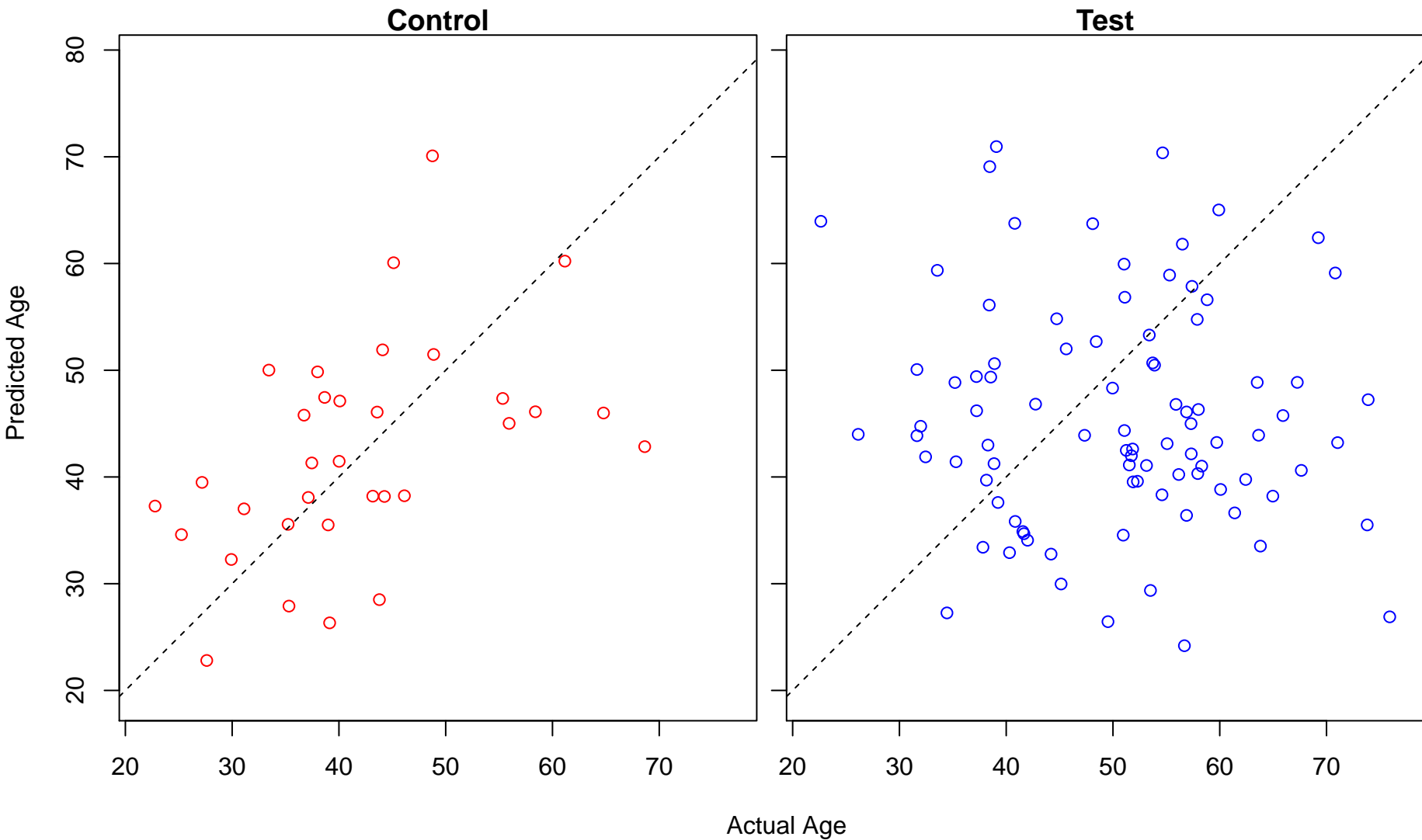
pigment granule maturation (Score: 1.133355)



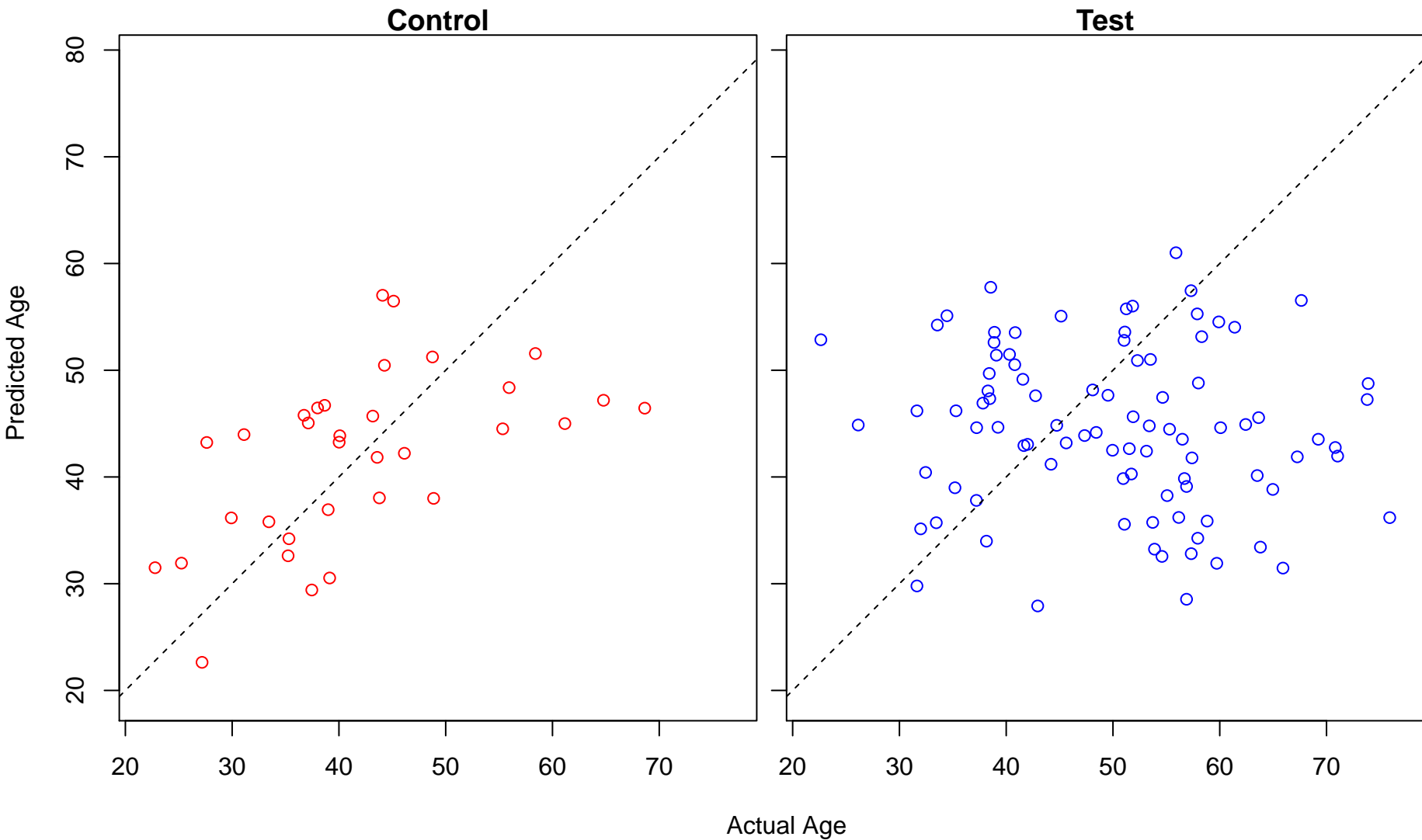
vitamin transport (Score: 1.132765)



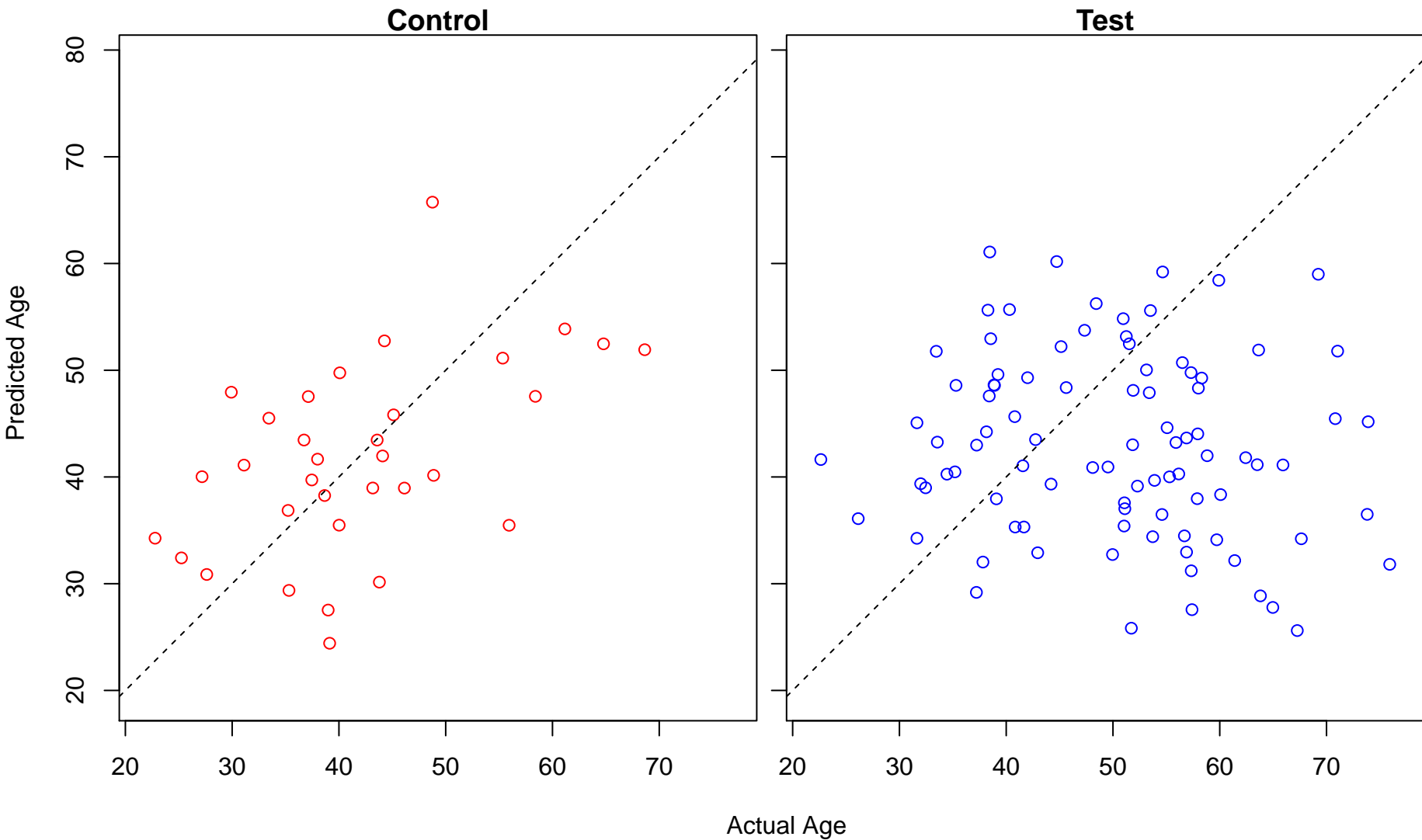
positive regulation of alpha-beta T cell proliferation (Score: 1.132730)



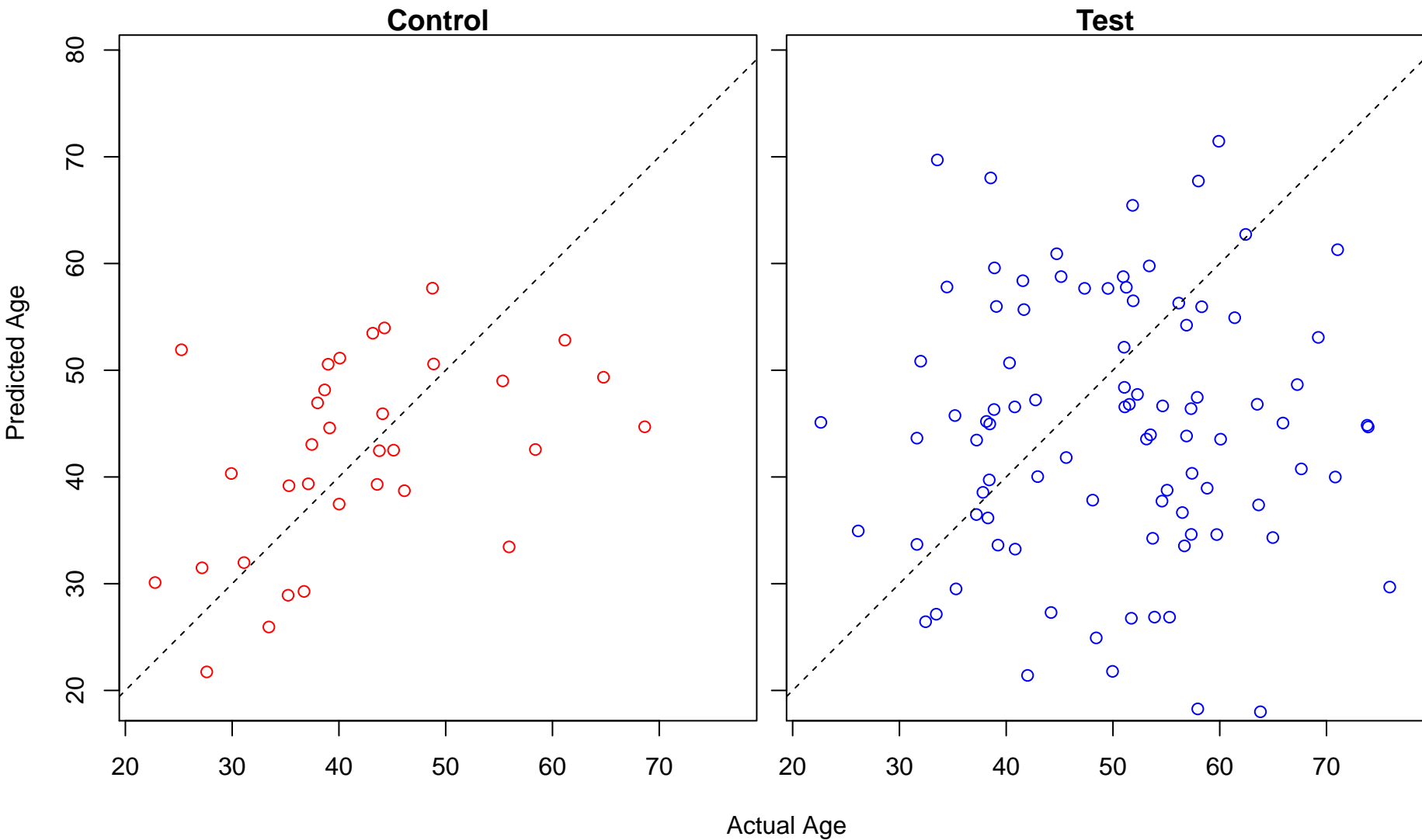
vascular smooth muscle contraction (Score: 1.132507)



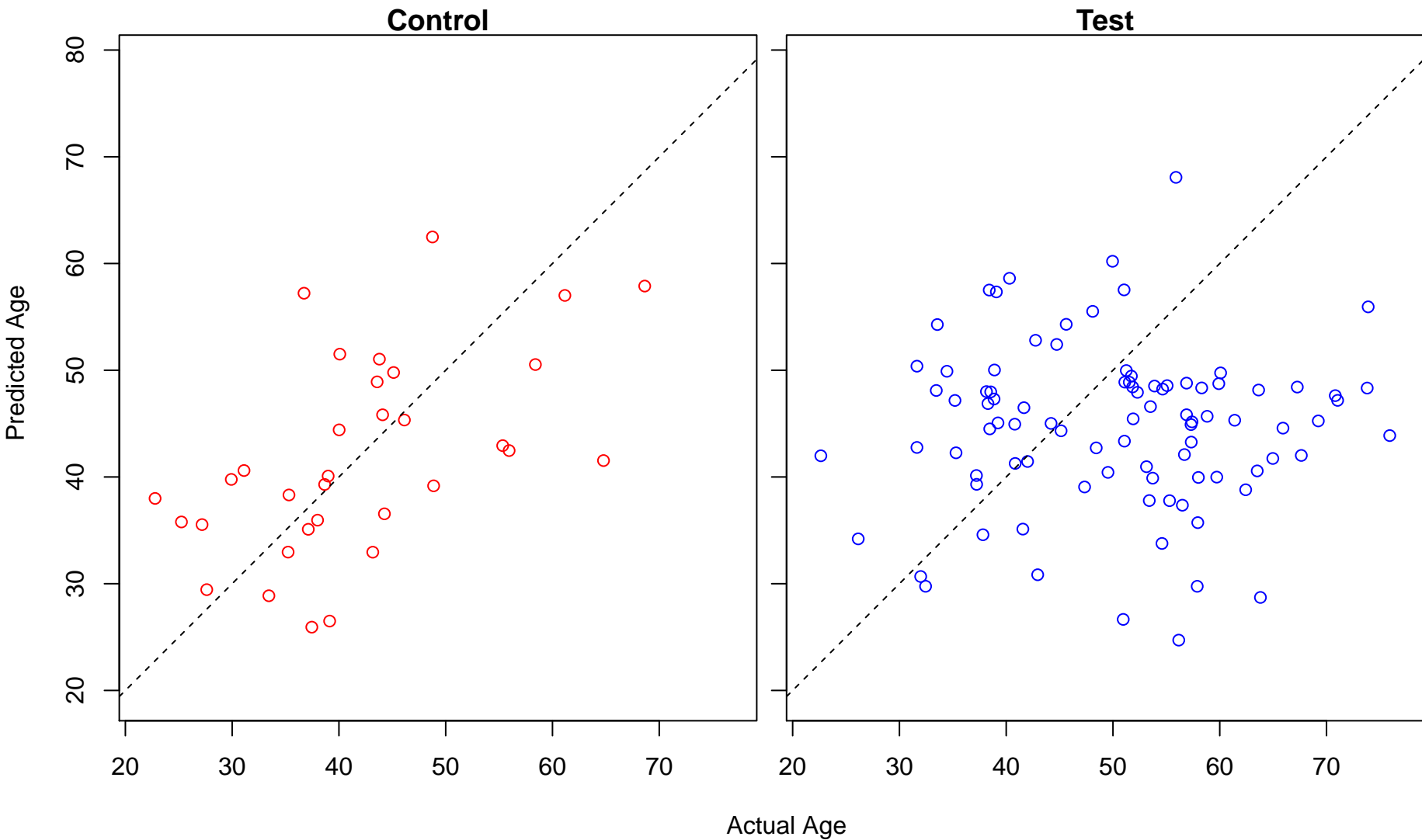
negative regulation of epidermal growth factor receptor signaling pathway (Score: 1.130201)



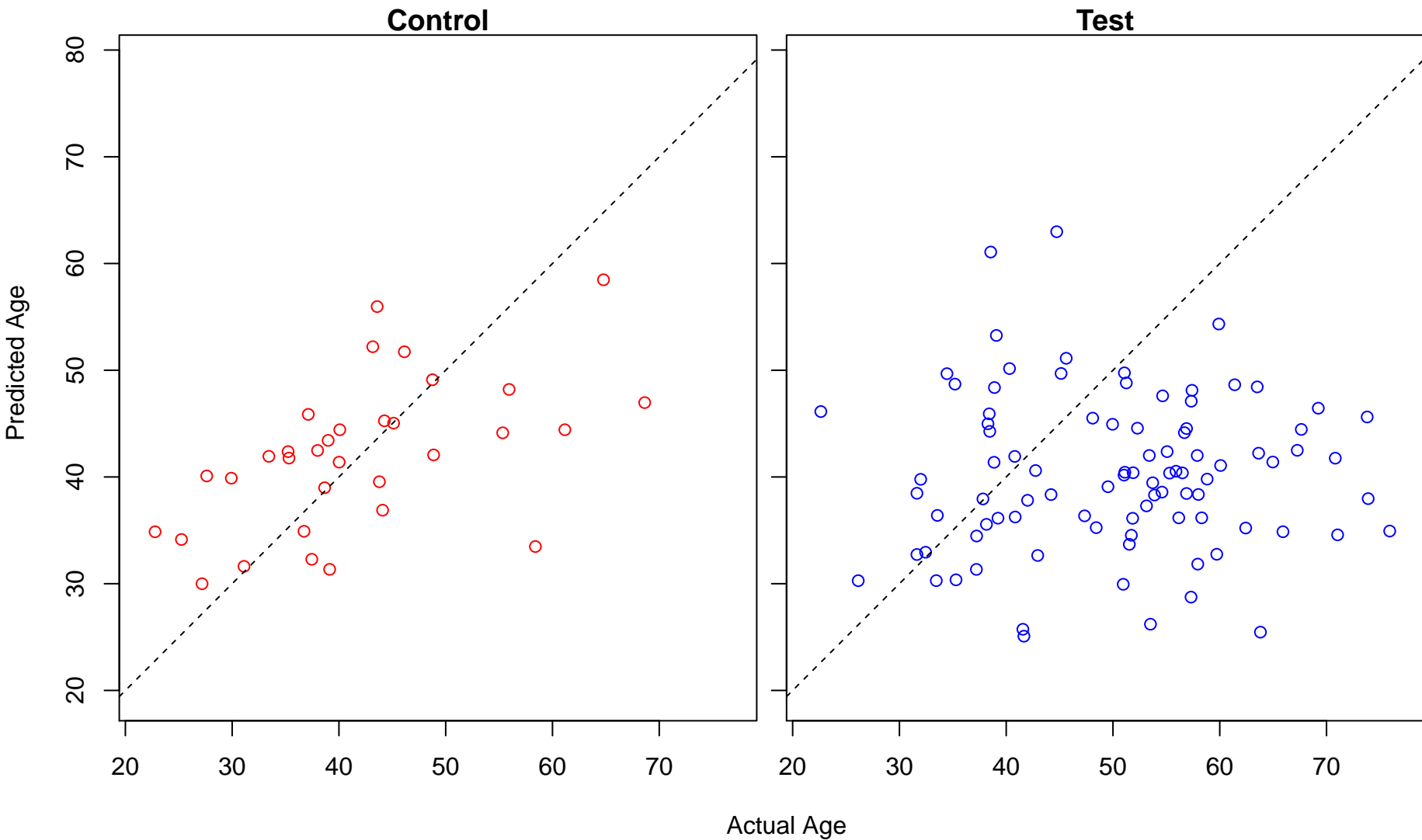
stem cell division (Score: 1.124983)



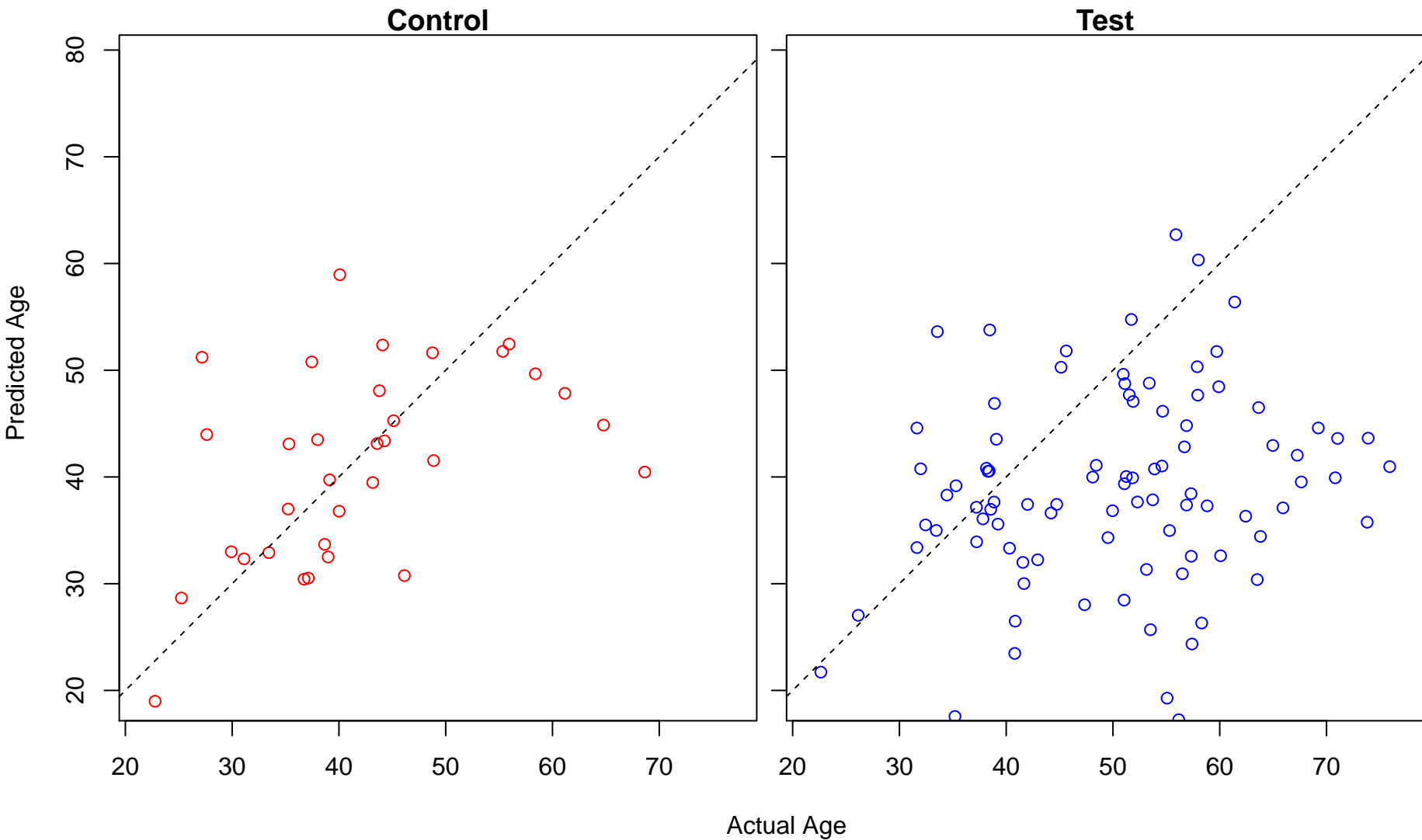
membrane biogenesis (Score: 1.124762)



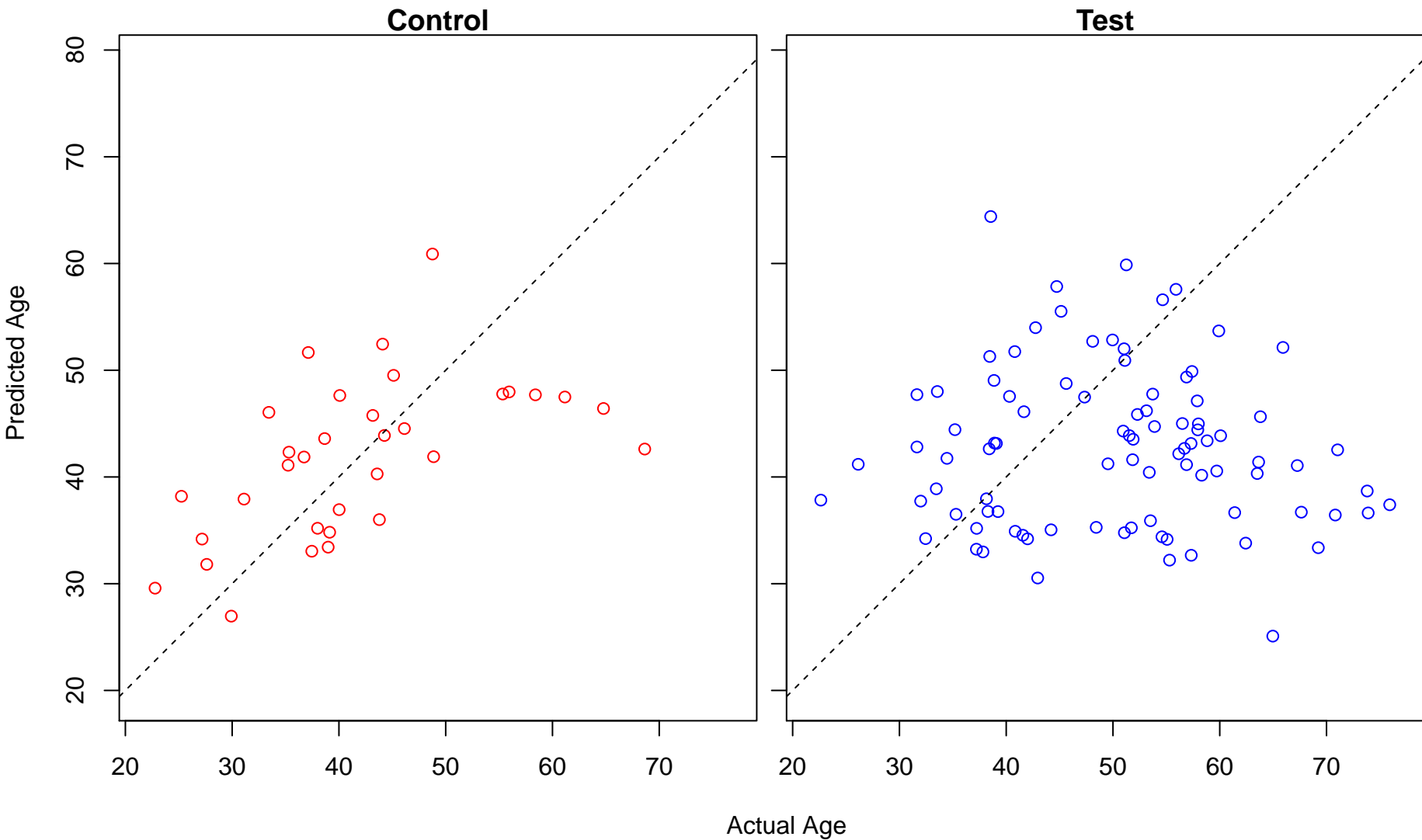
receptor guanylyl cyclase signaling pathway (Score: 1.123853)



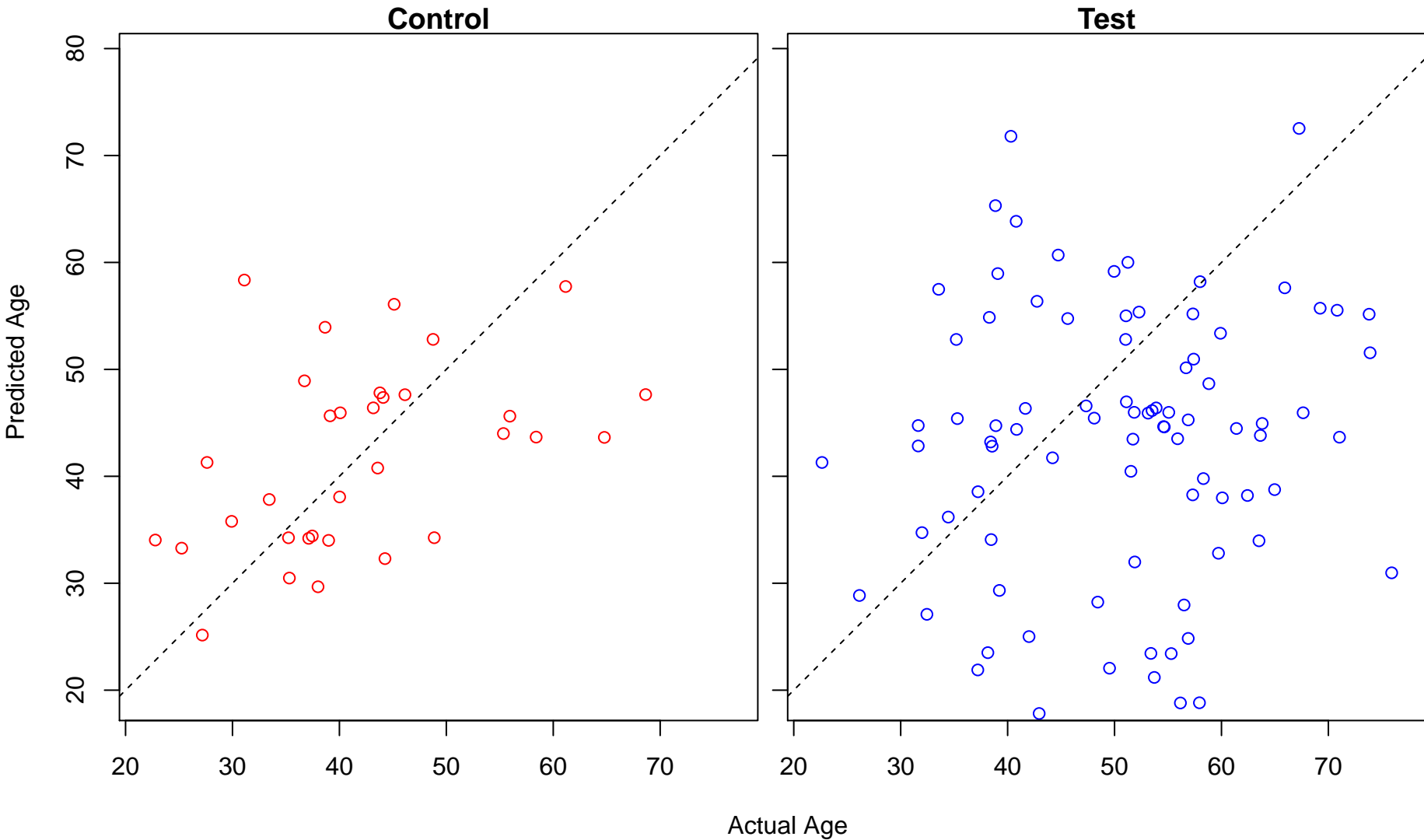
positive regulation of phosphatidylinositol 3-kinase activity (Score: 1.121055)



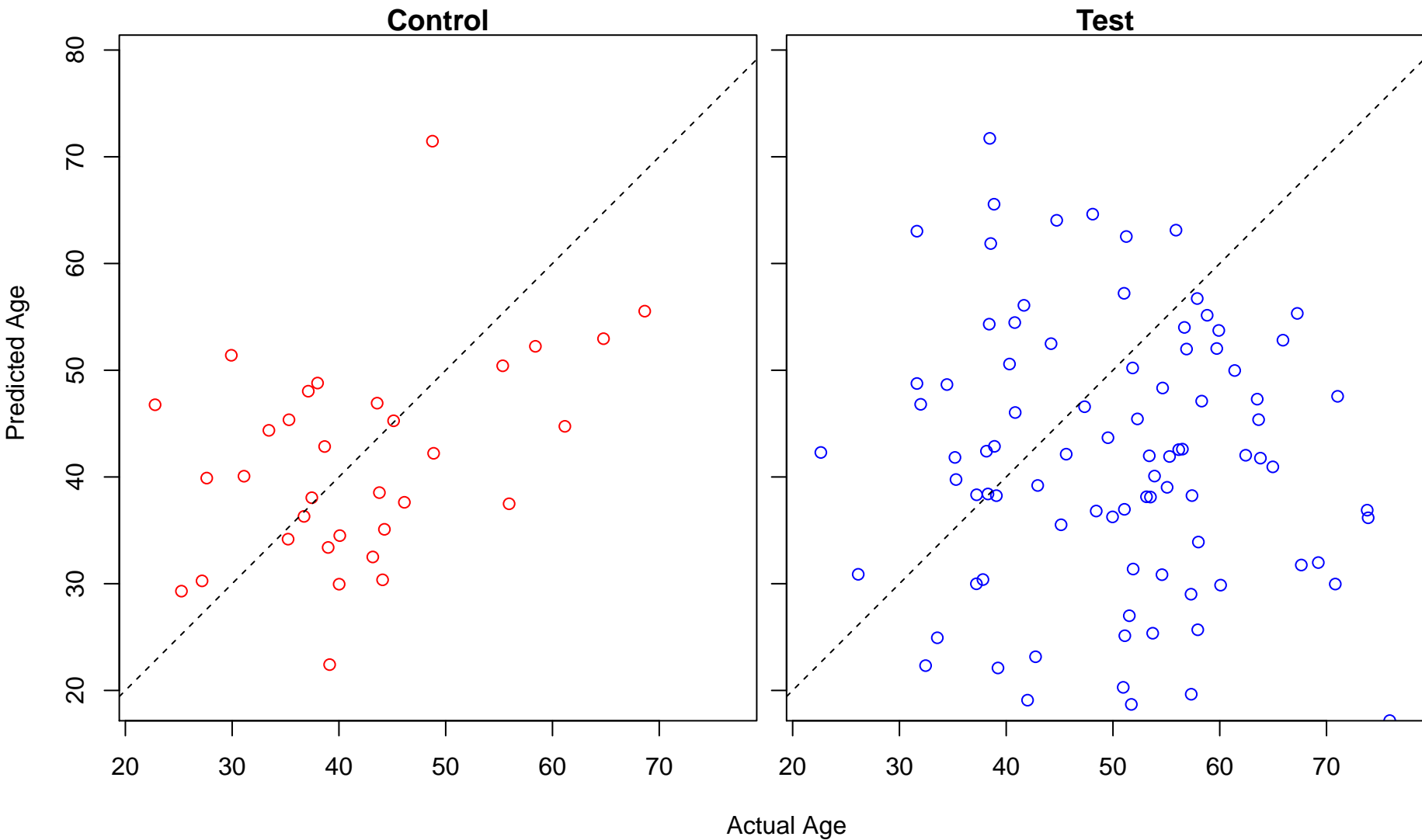
muscle contraction (Score: 1.119825)



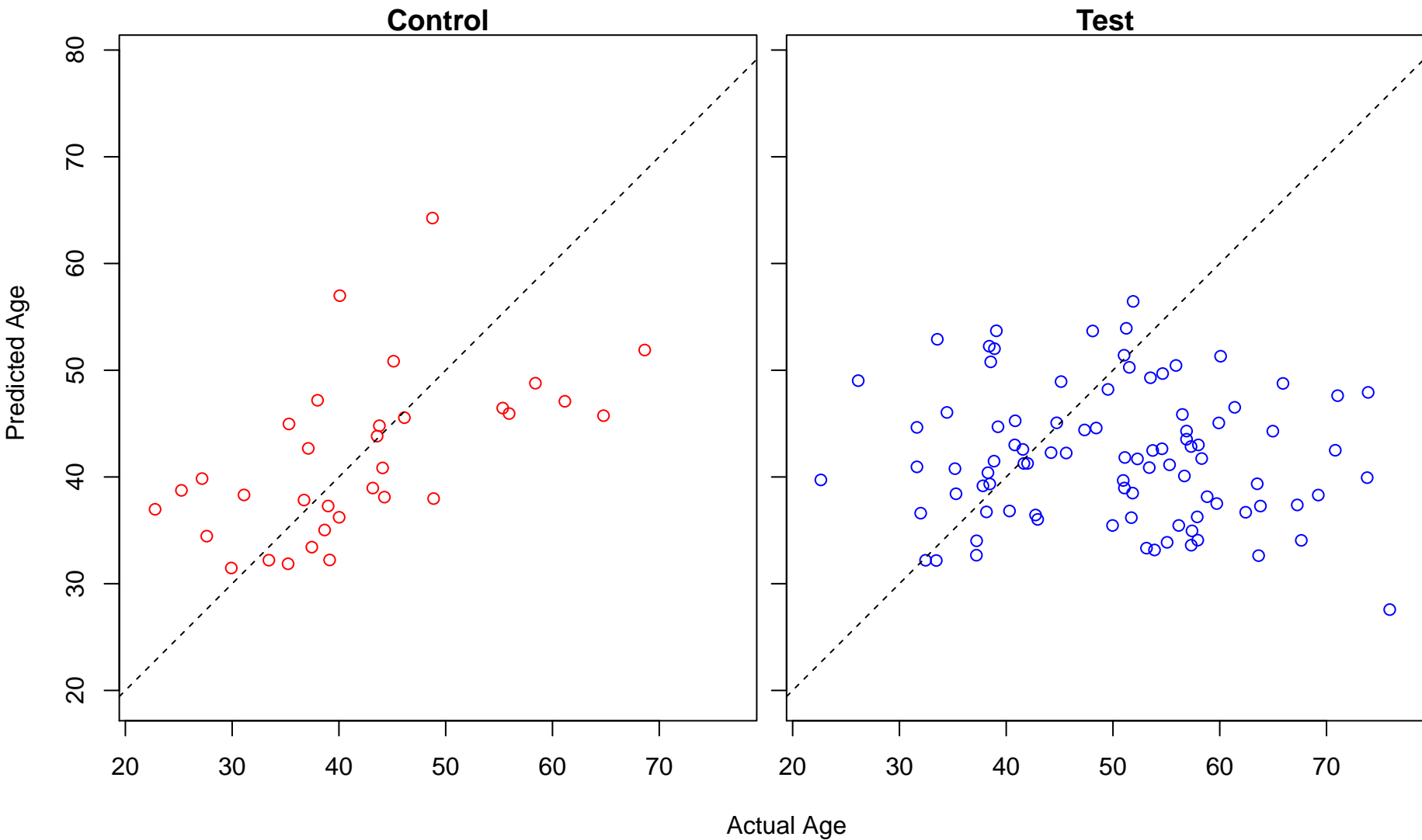
regulation of cardiac muscle cell action potential (Score: 1.119004)



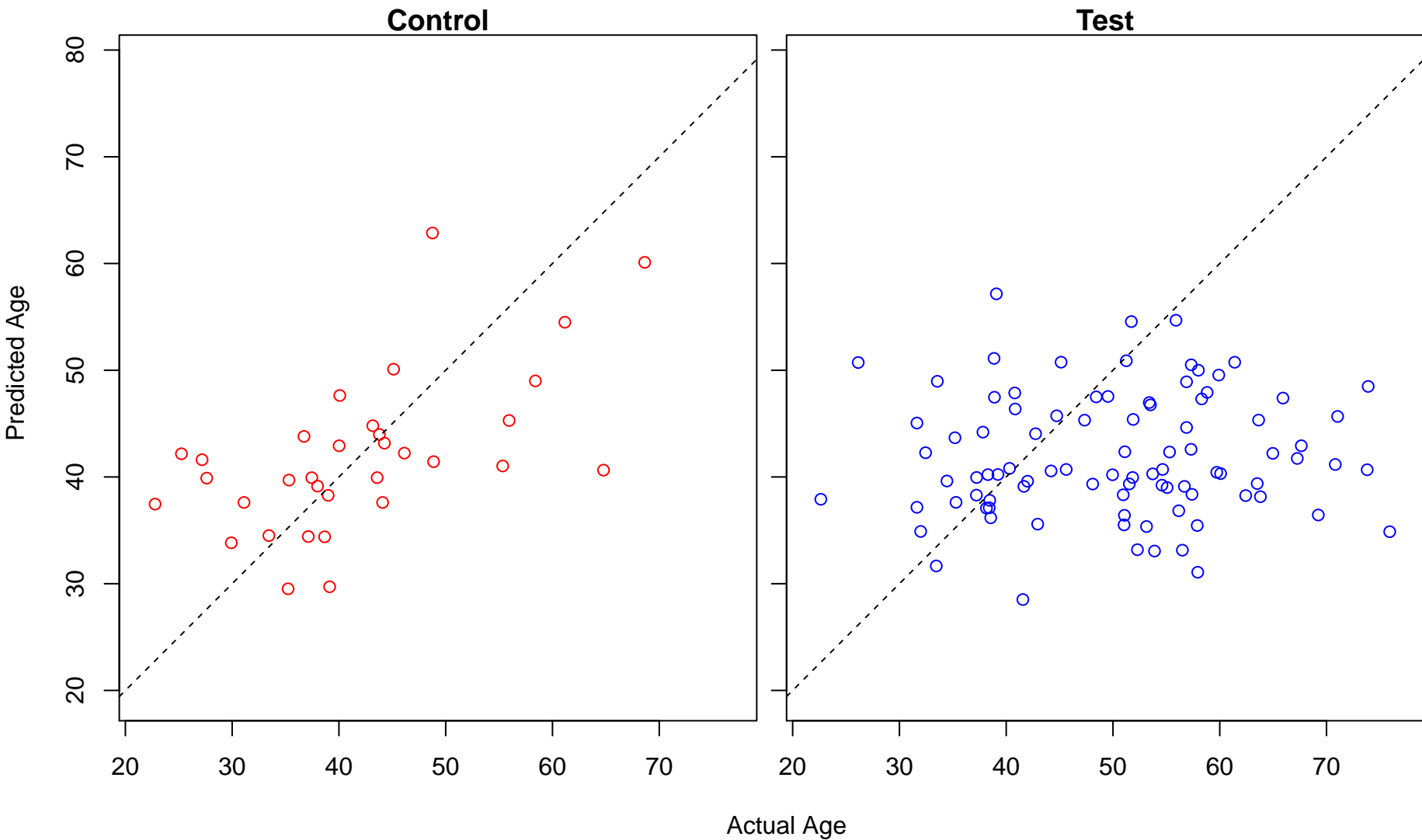
negative regulation of focal adhesion assembly (Score: 1.118622)



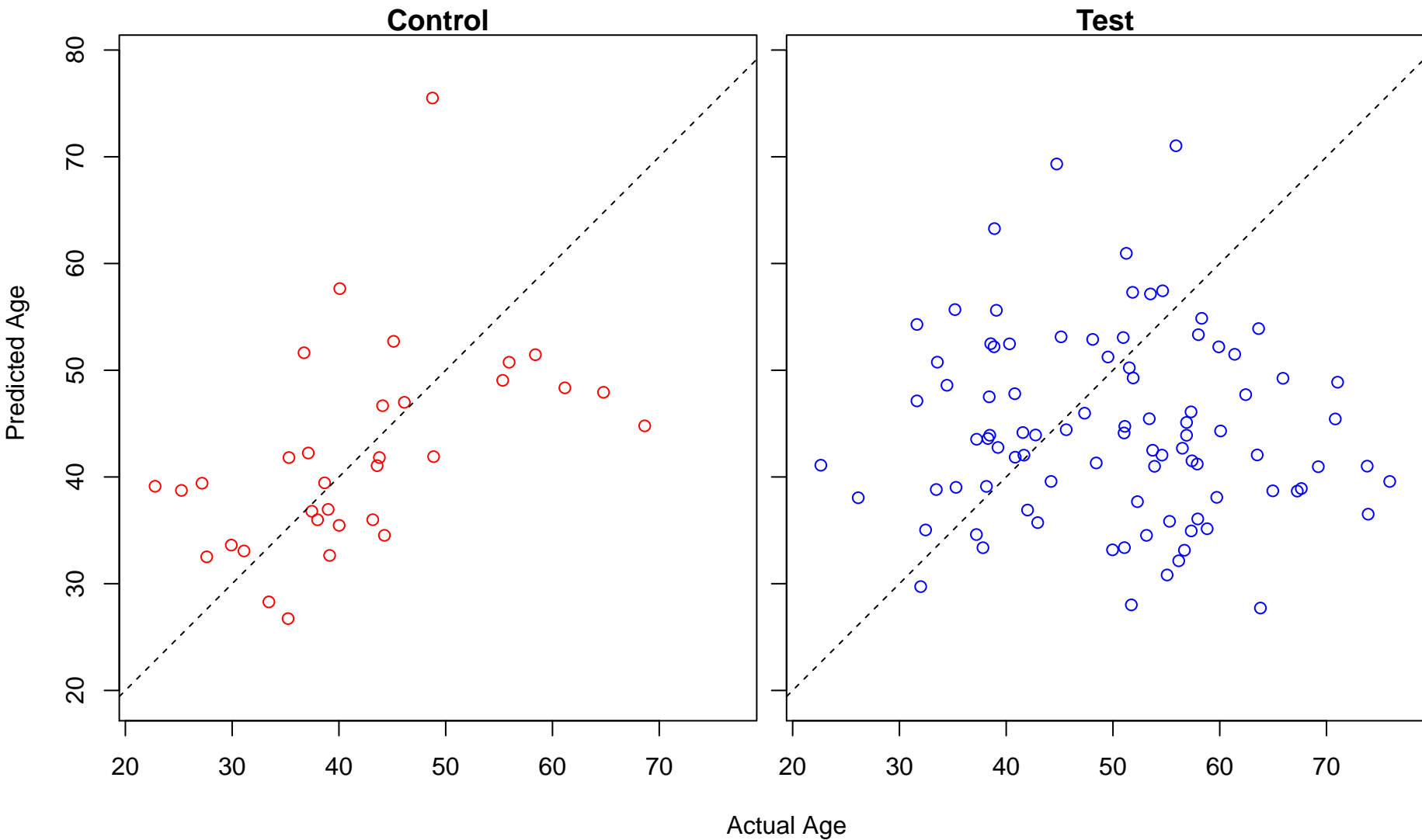
snRNA transcription (Score: 1.118396)



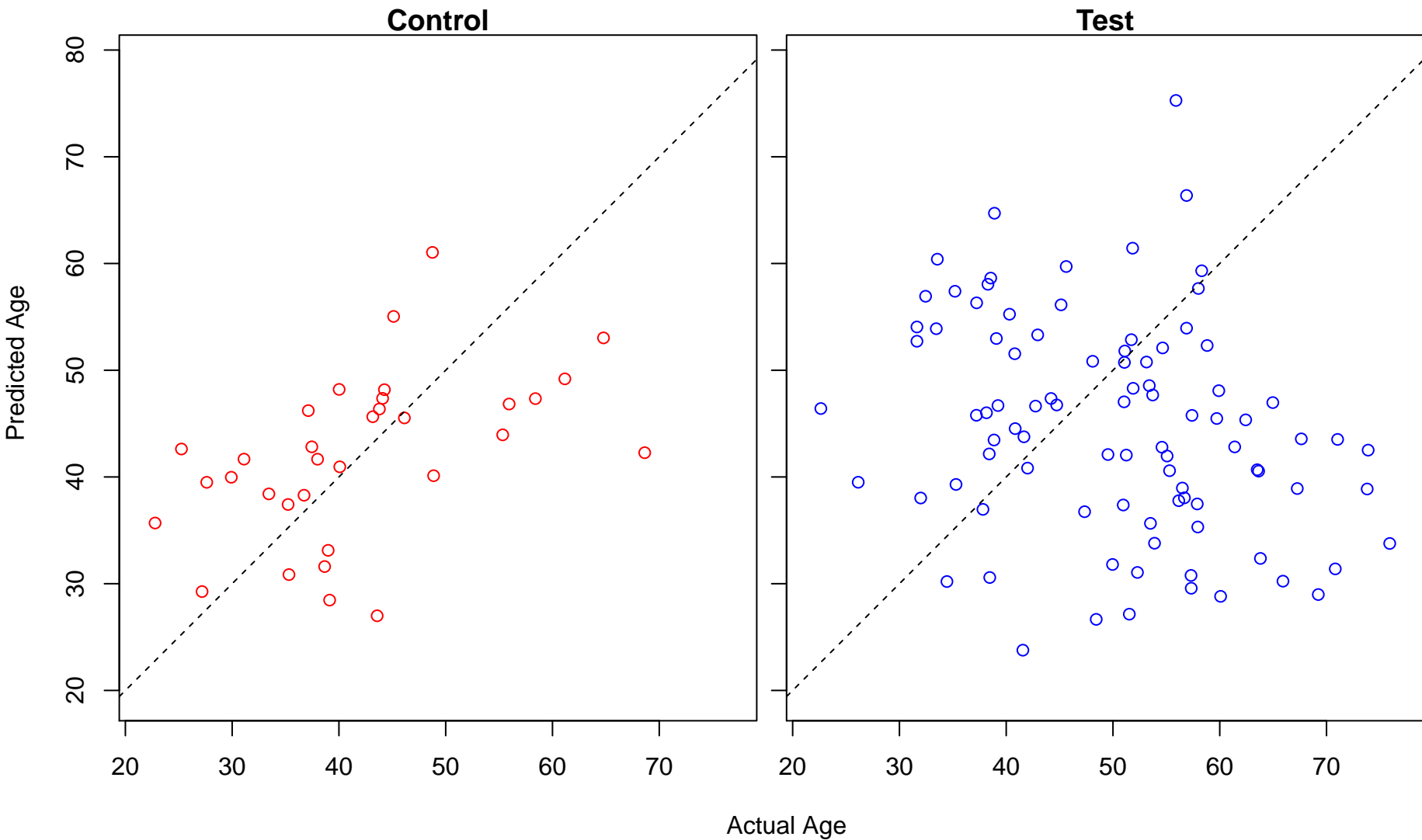
maintenance of DNA methylation (Score: 1.118013)



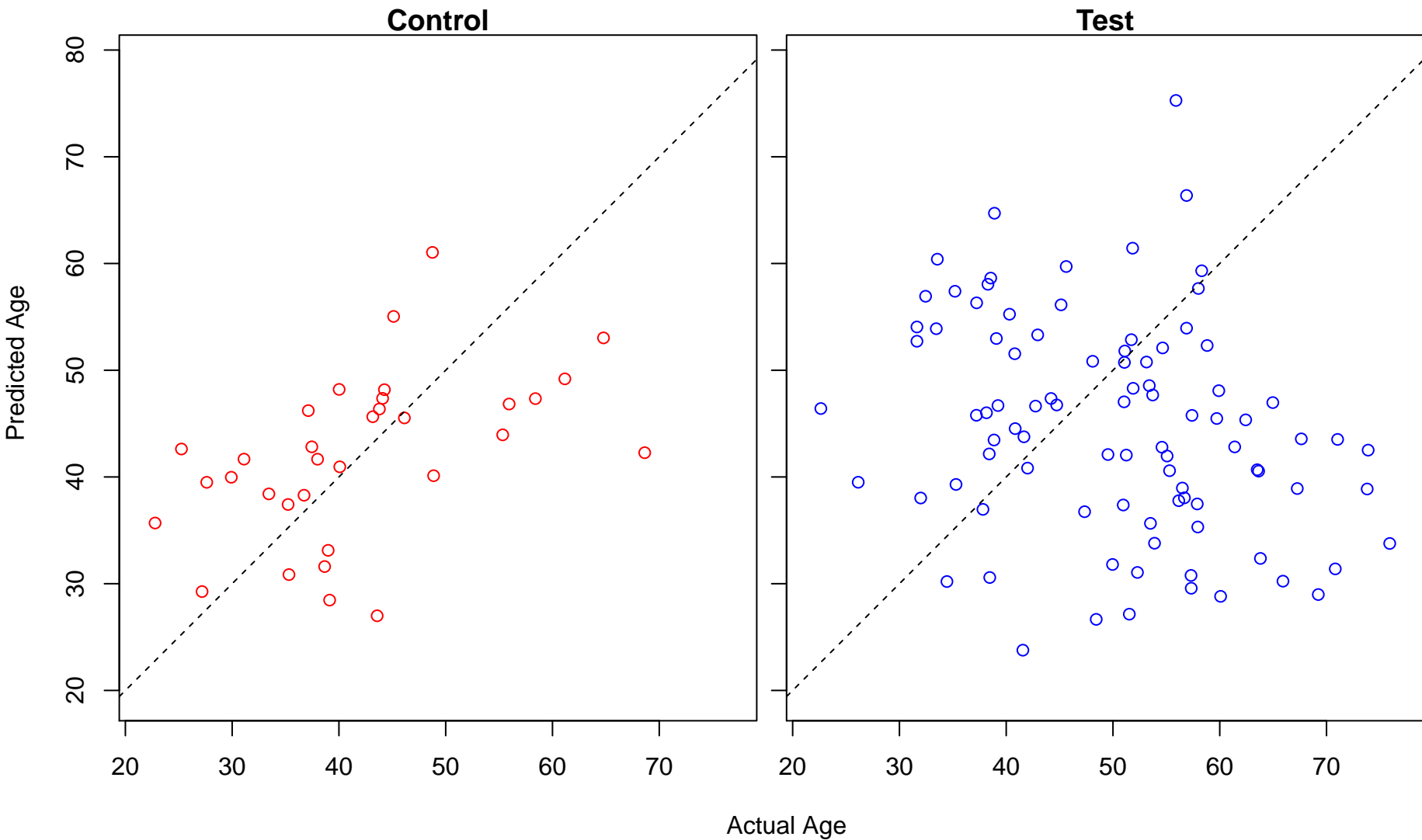
regulation of mast cell activation involved in immune response (Score: 1.117645)



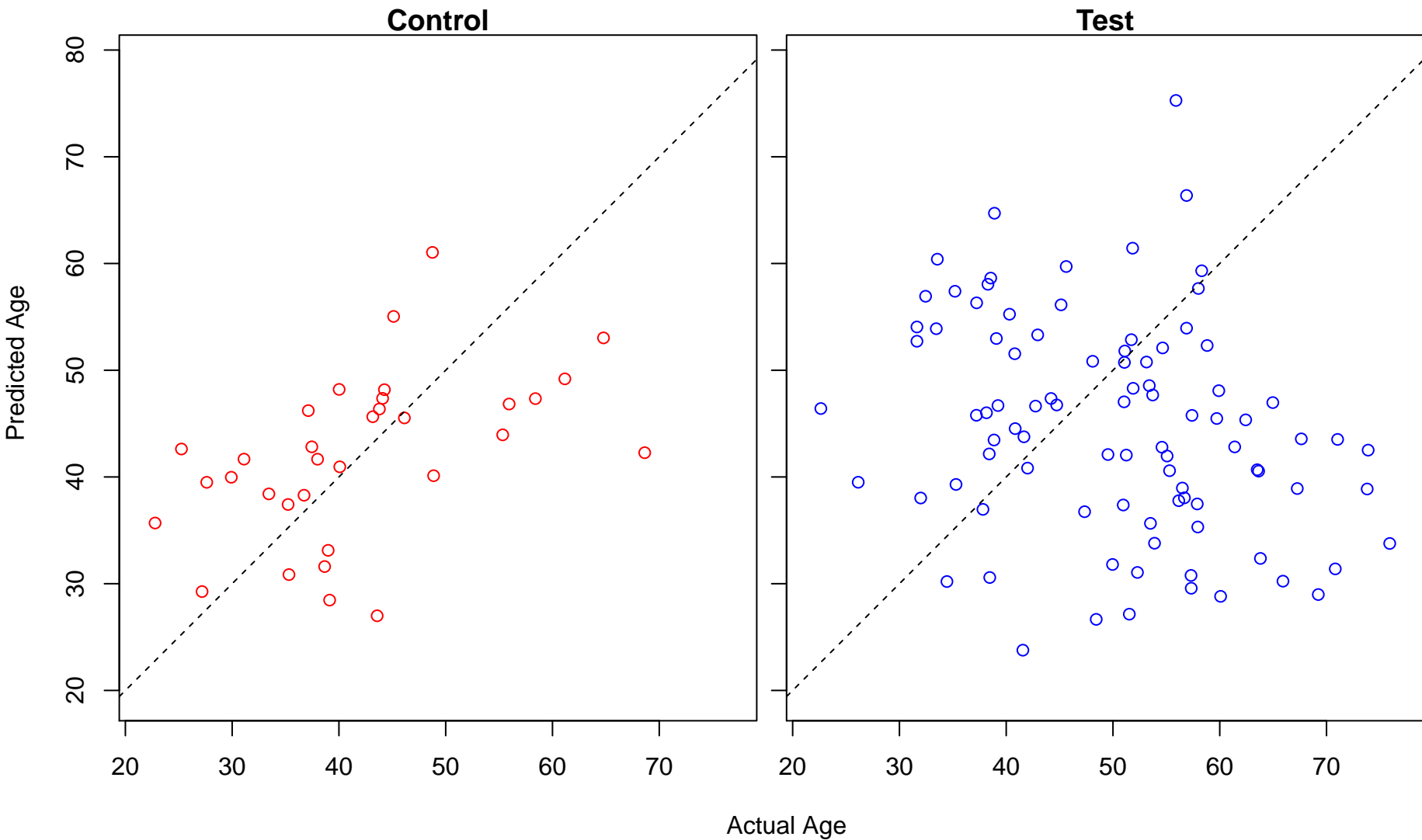
regulation of immature T cell proliferation (Score: 1.116417)



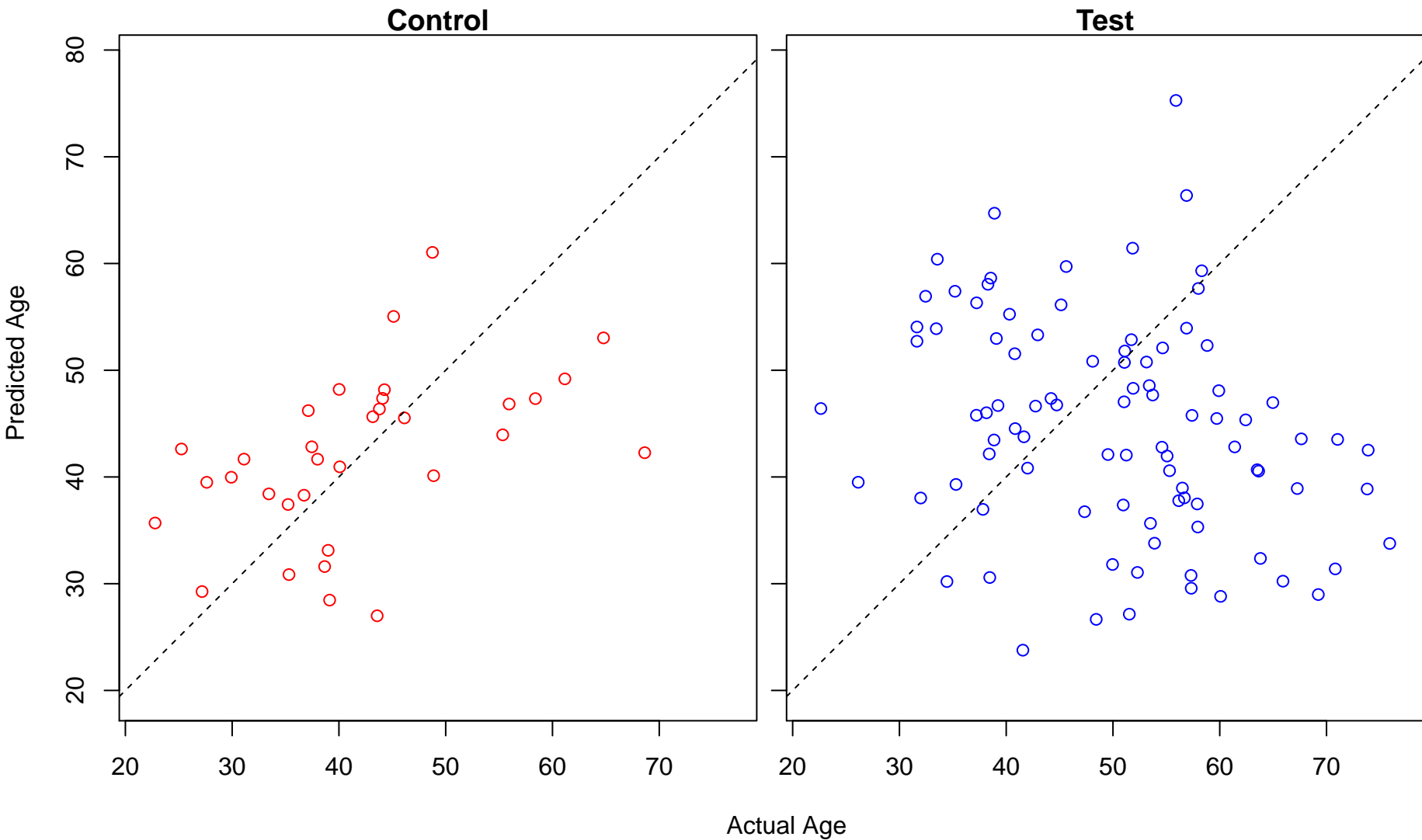
regulation of immature T cell proliferation in thymus (Score: 1.116417)



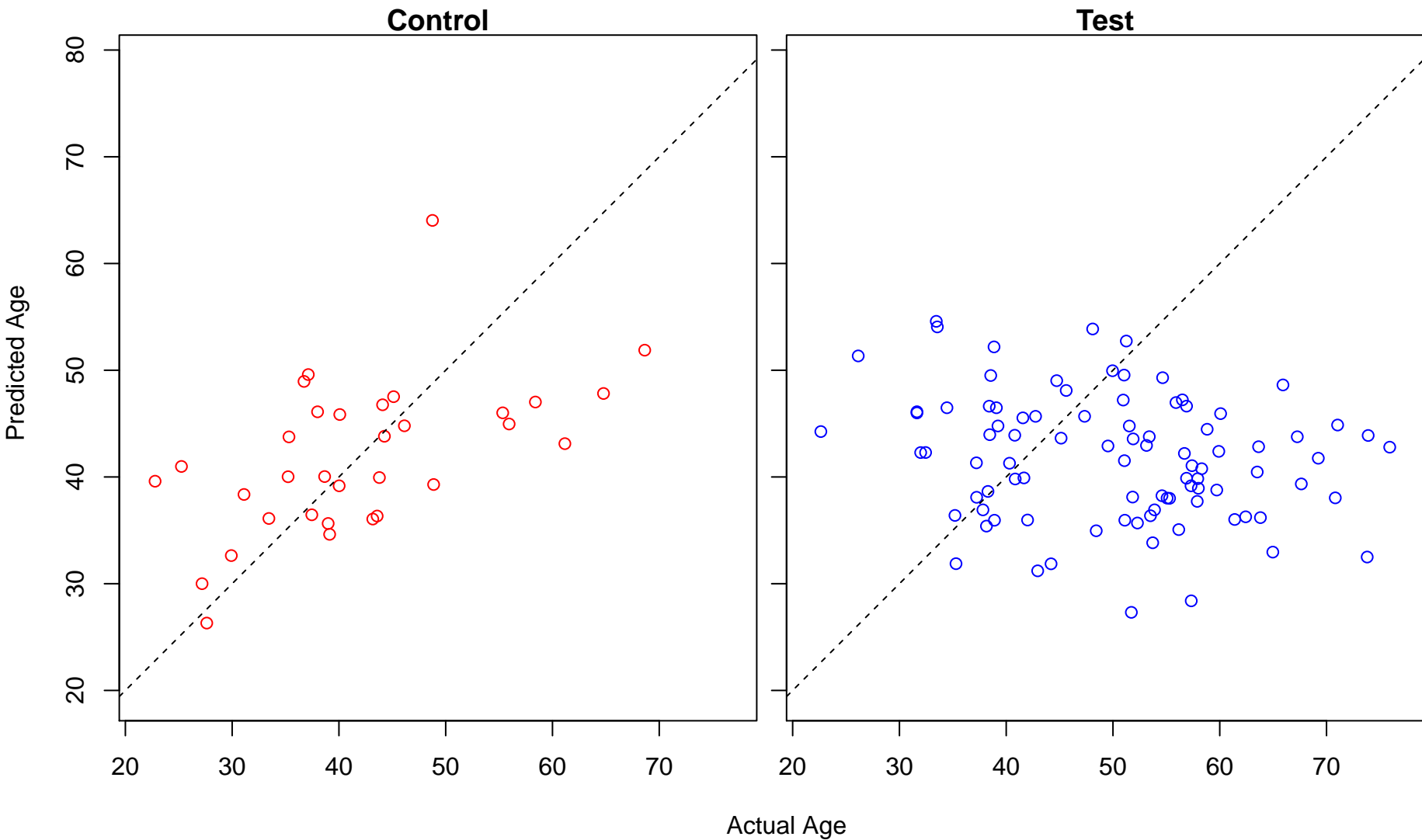
negative regulation of immature T cell proliferation (Score: 1.116417)



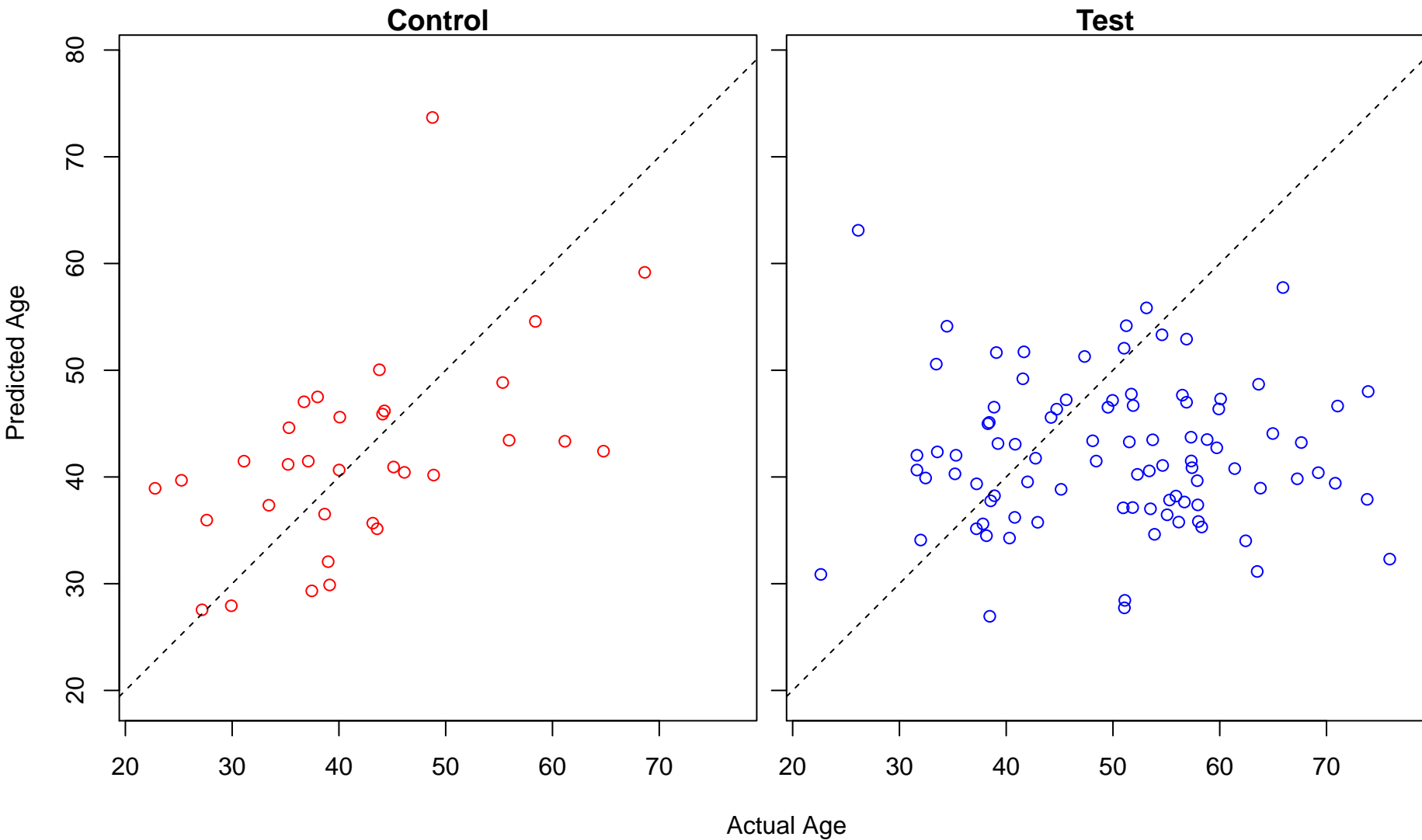
negative regulation of immature T cell proliferation in thymus (Score: 1.116417)



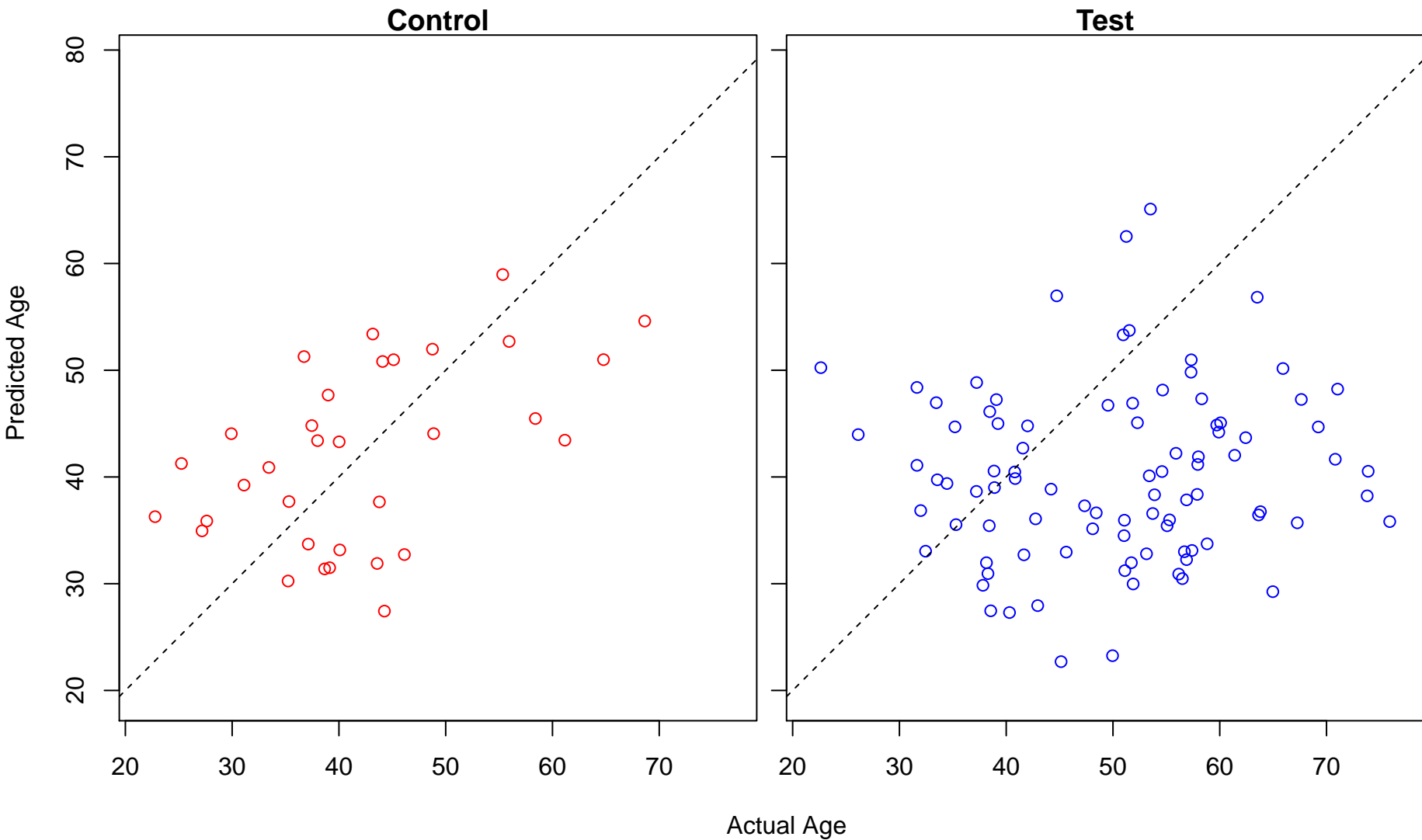
negative regulation of protein oligomerization (Score: 1.115755)



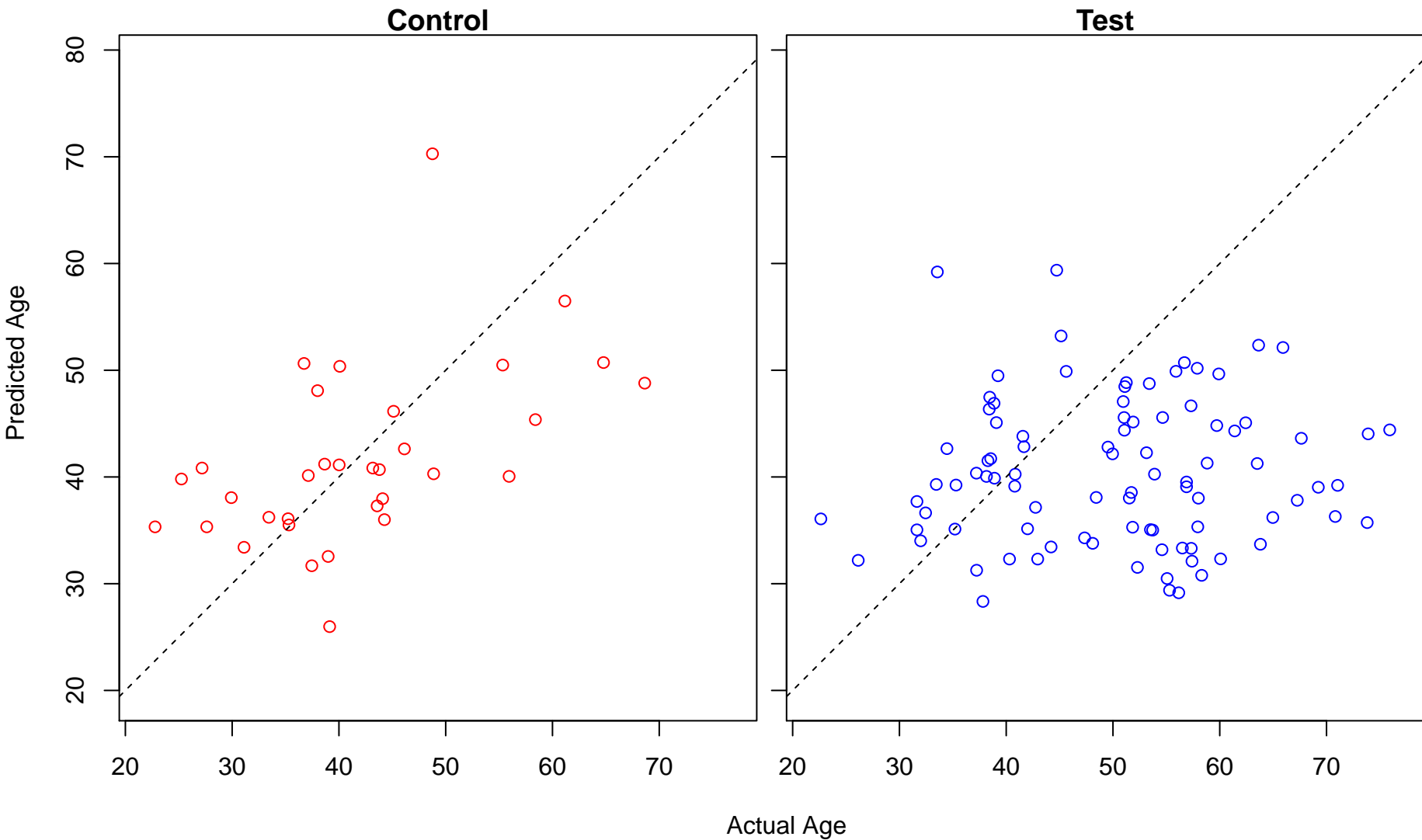
negative regulation of transcription regulatory region DNA binding (Score: 1.114994)



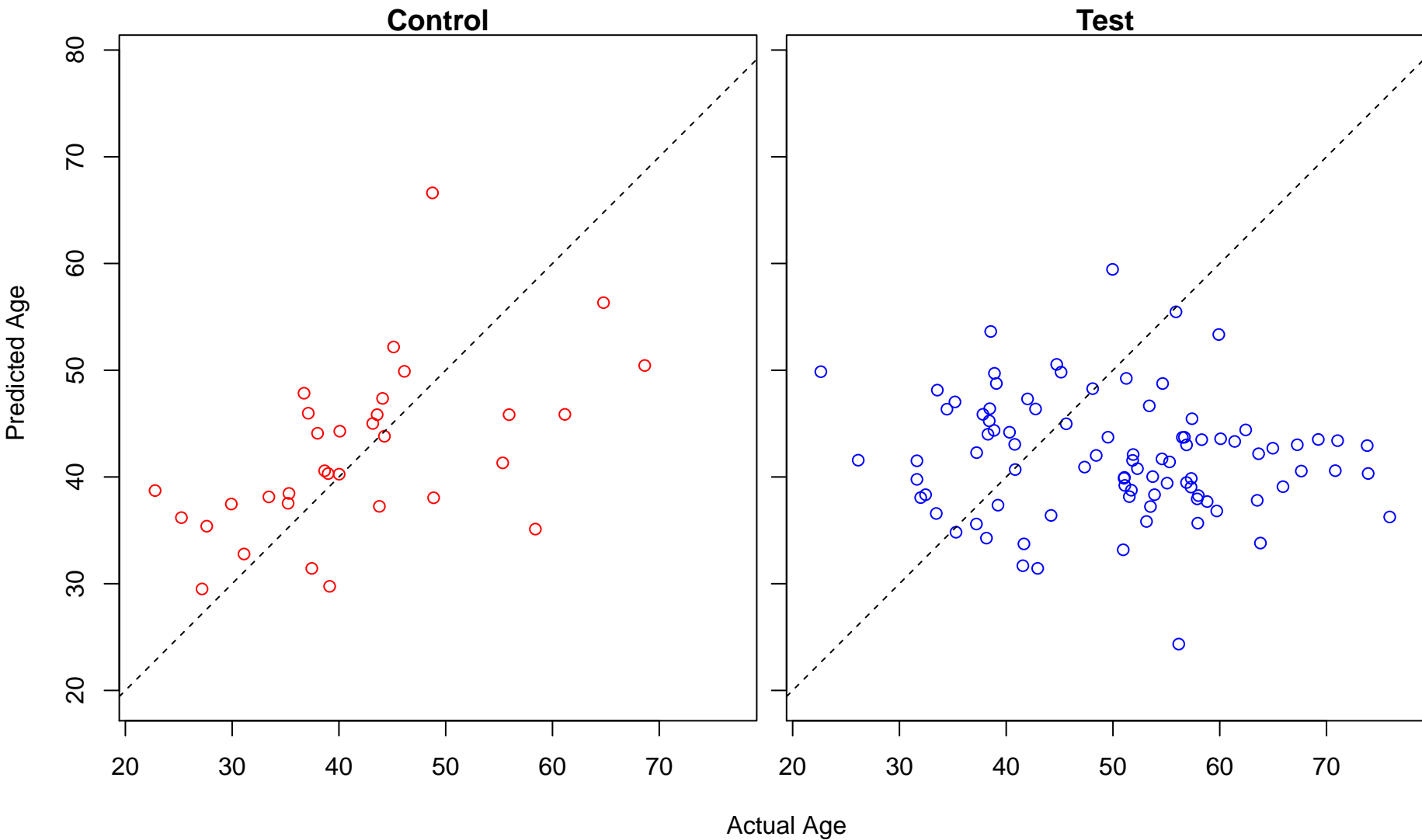
retinal metabolic process (Score: 1.114849)



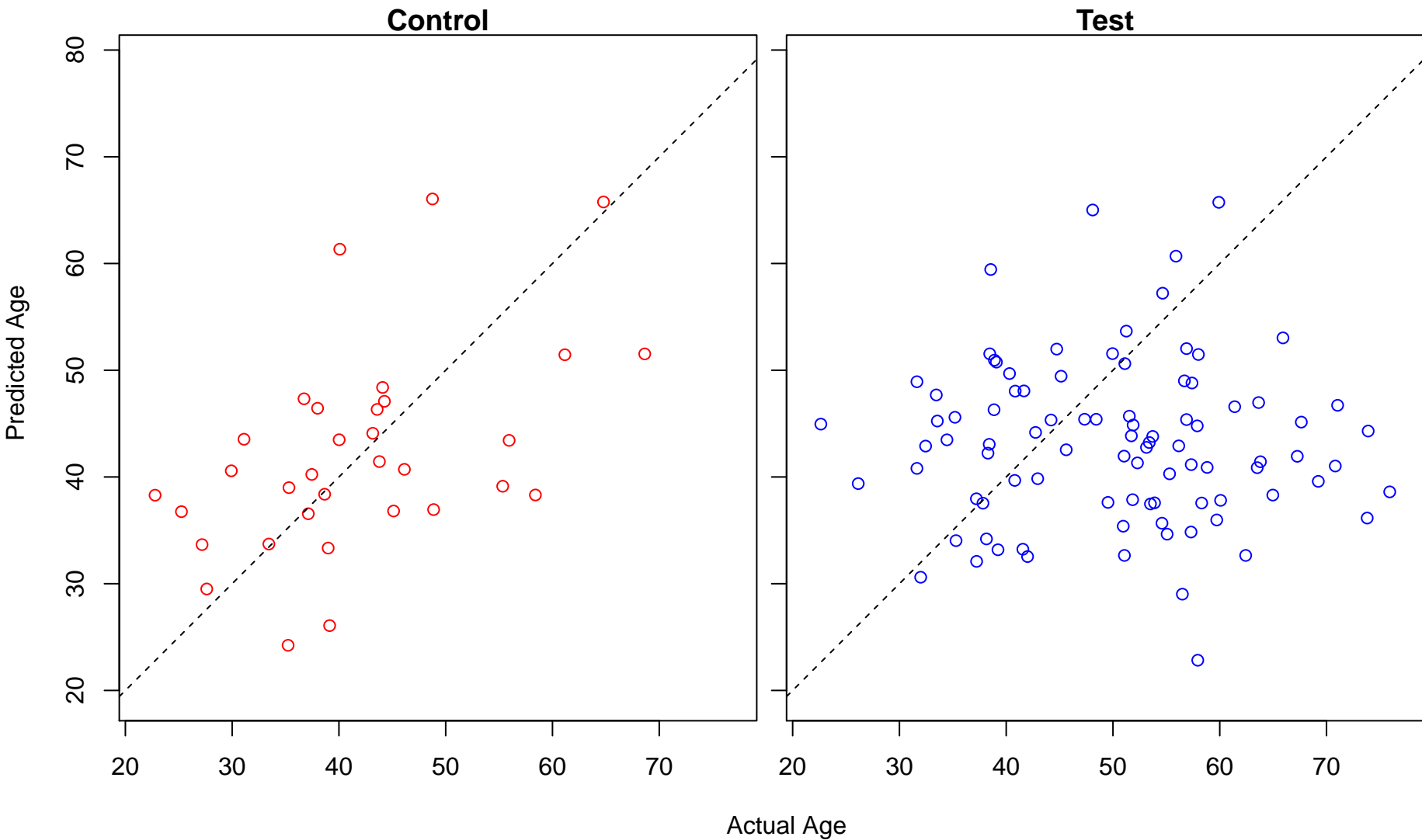
cellular response to insulin stimulus (Score: 1.113179)



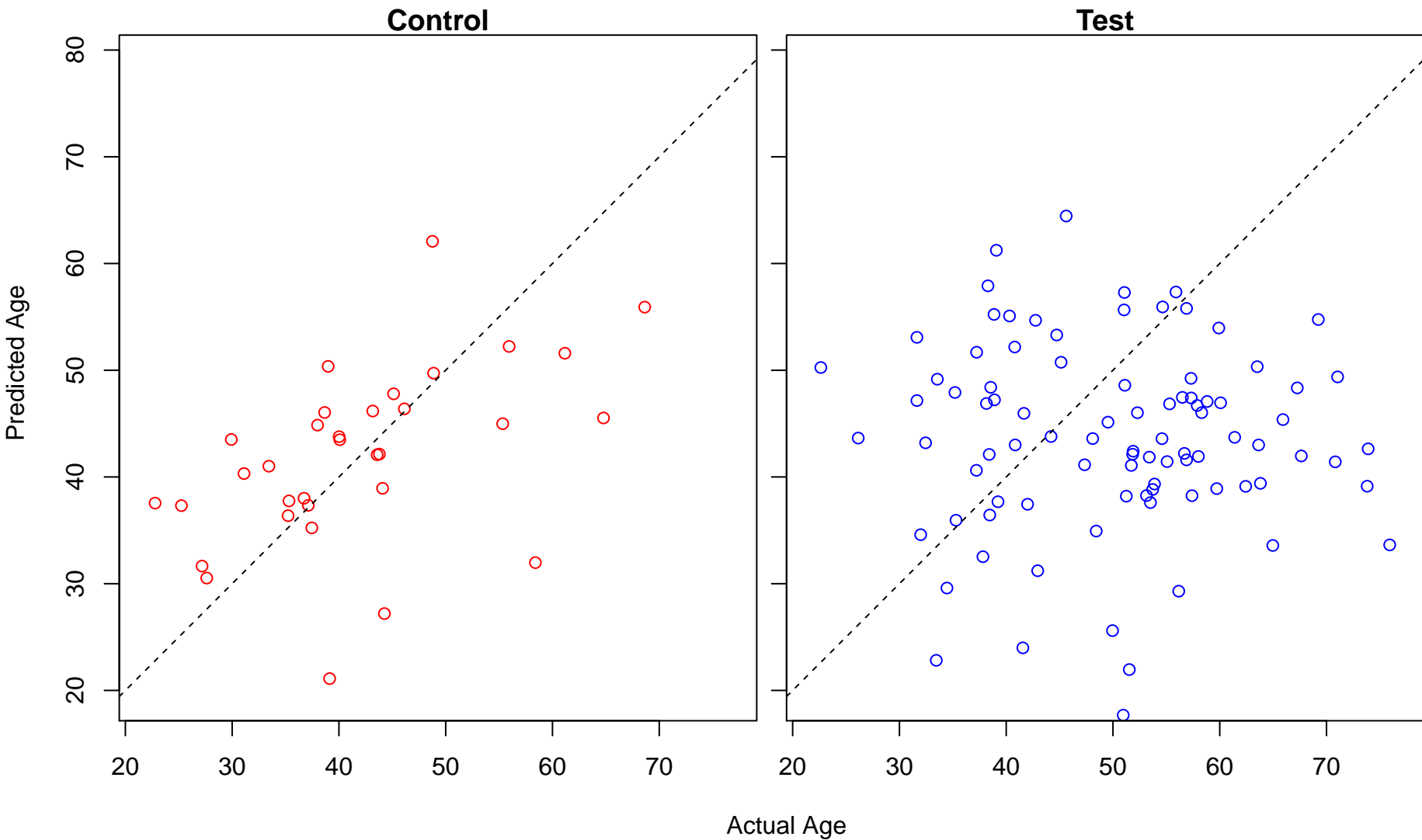
cGMP biosynthetic process (Score: 1.108762)



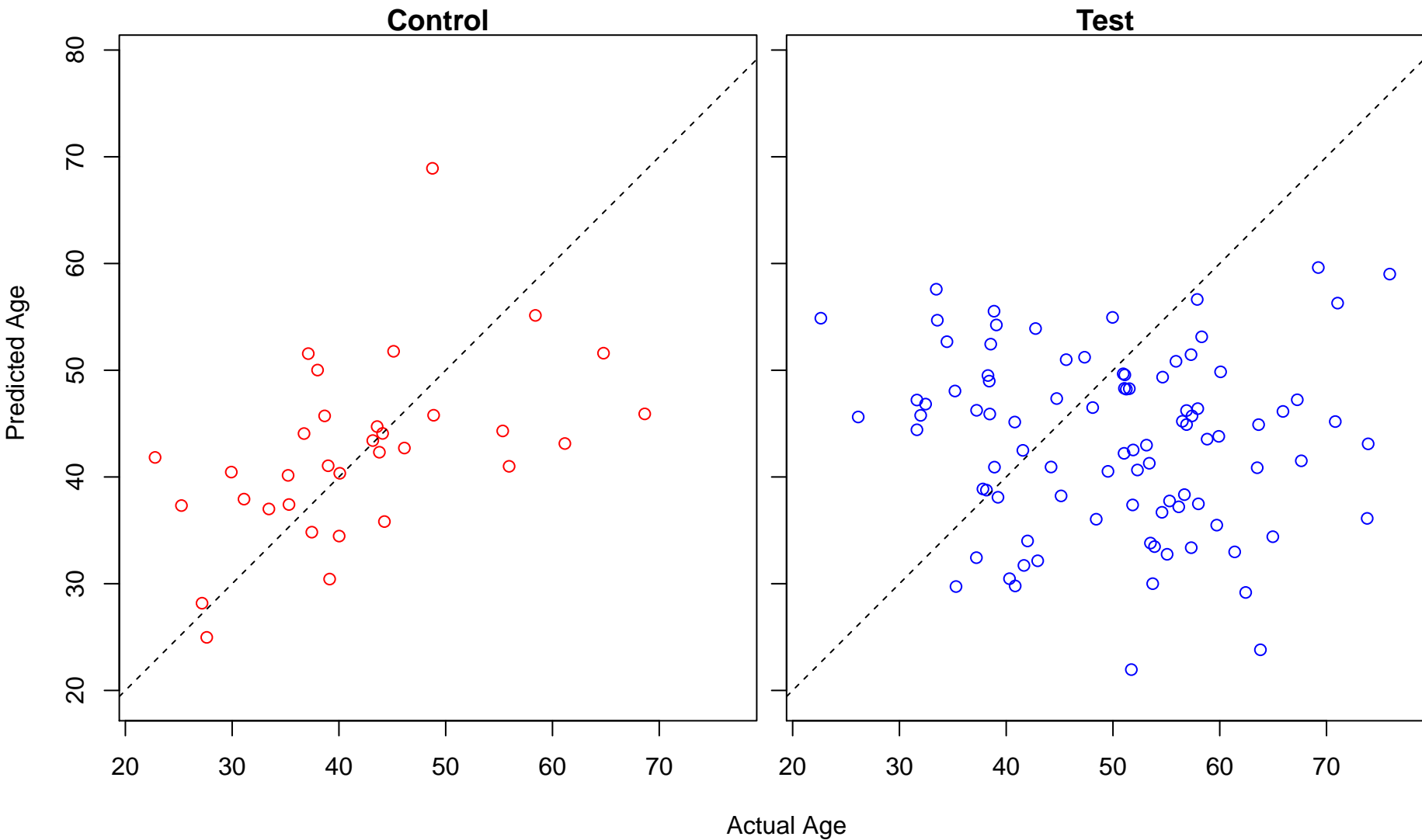
mitochondrial fission (Score: 1.107269)



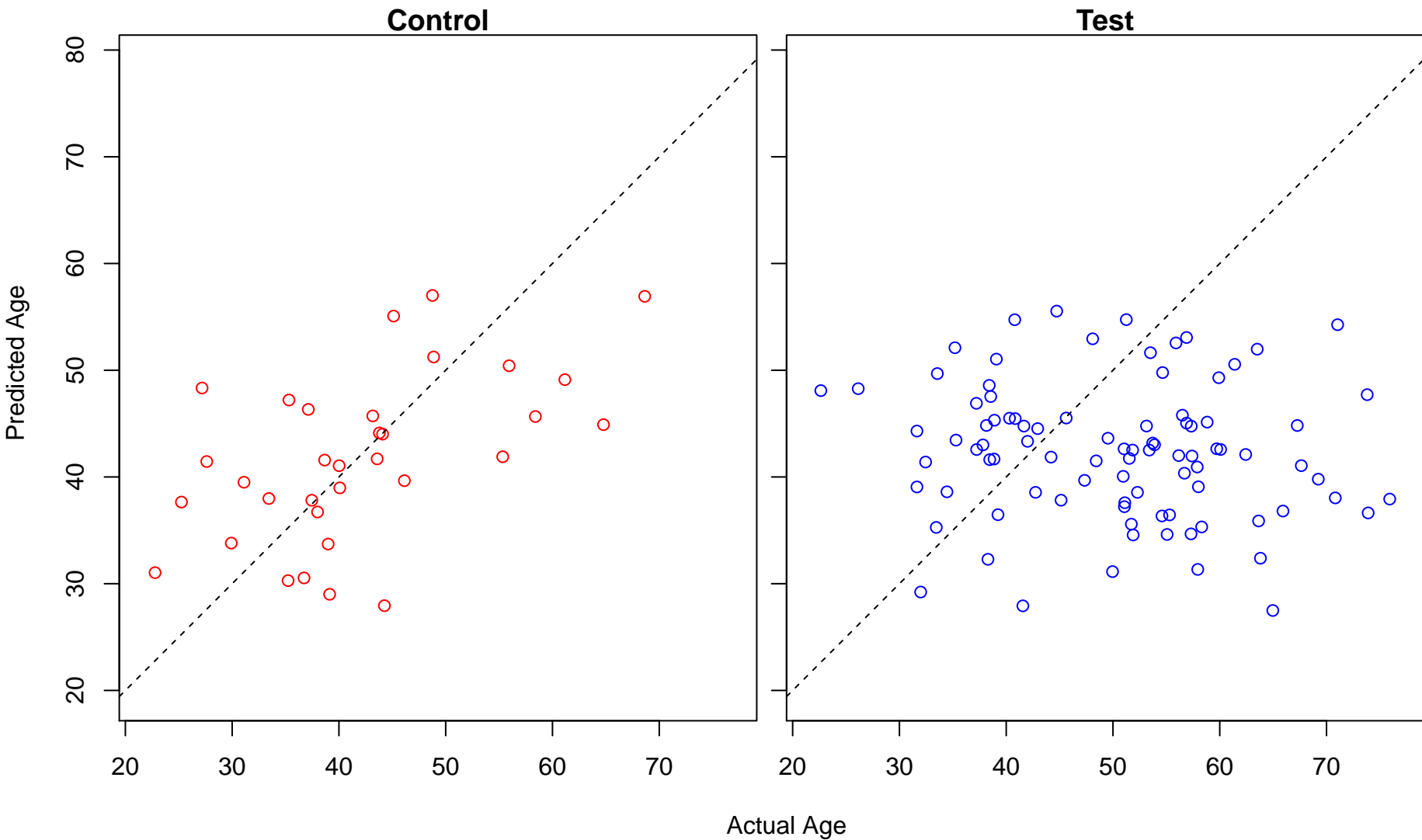
cellular response to leptin stimulus (Score: 1.105252)



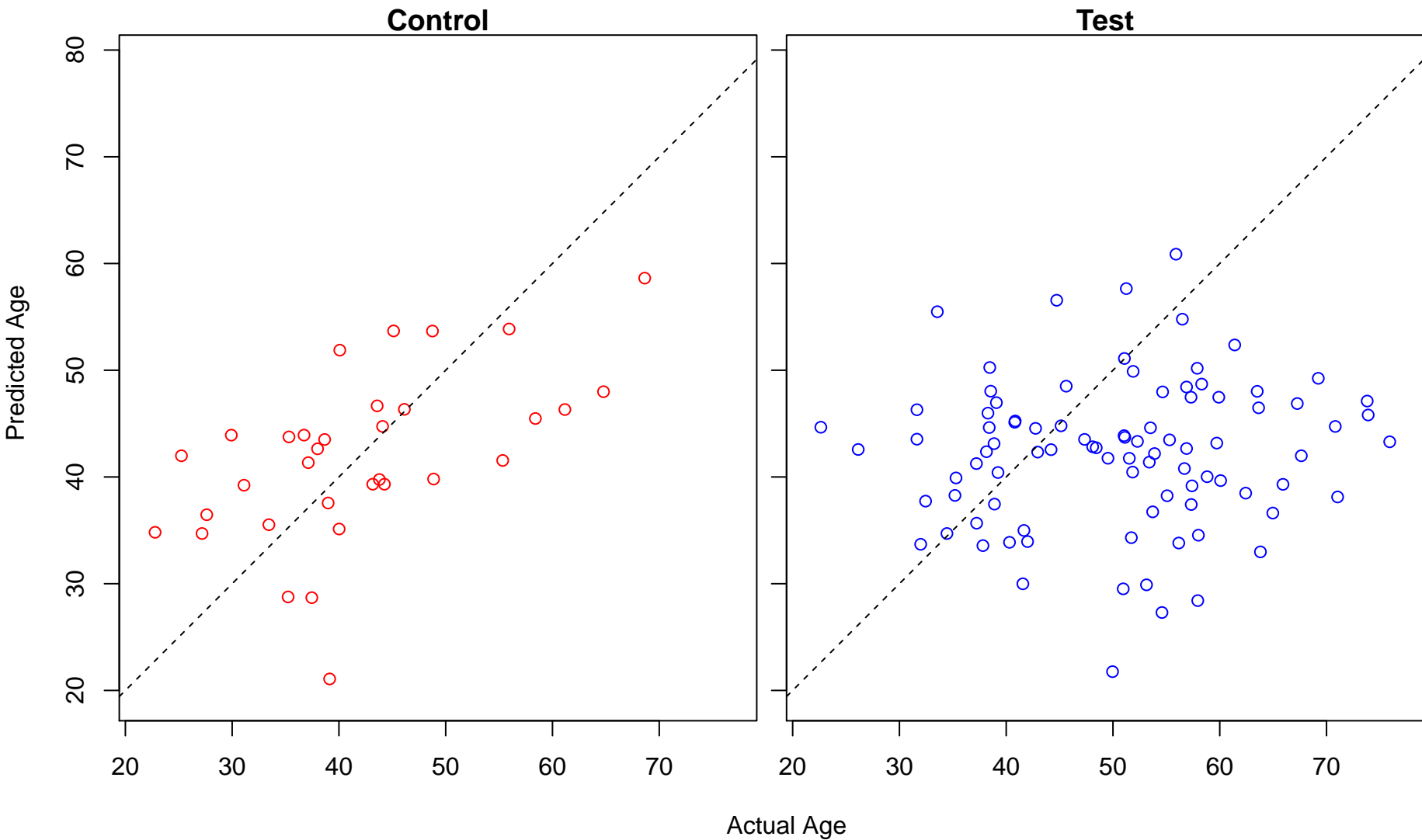
oligodendrocyte differentiation (Score: 1.105042)



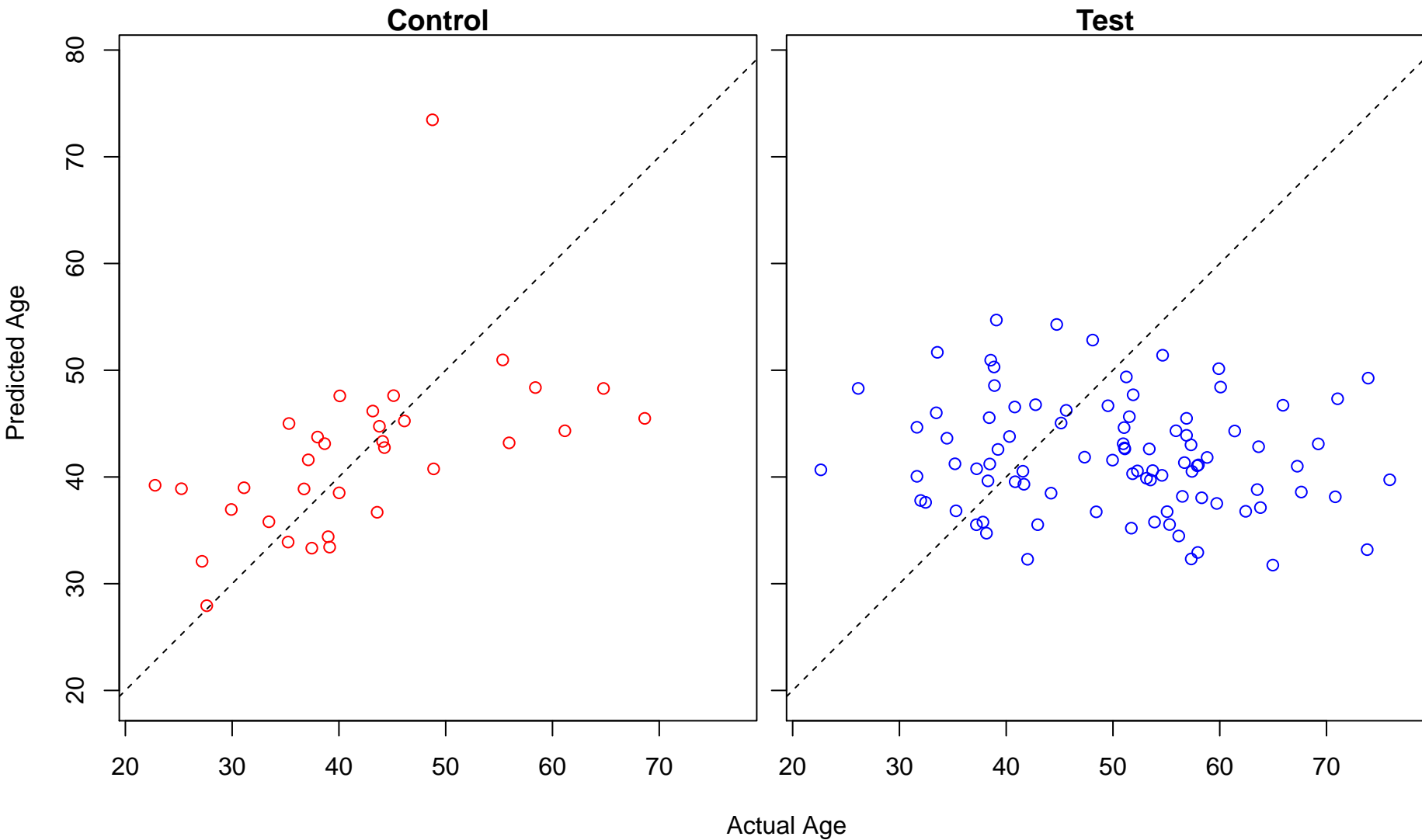
locomotory behavior (Score: 1.103121)



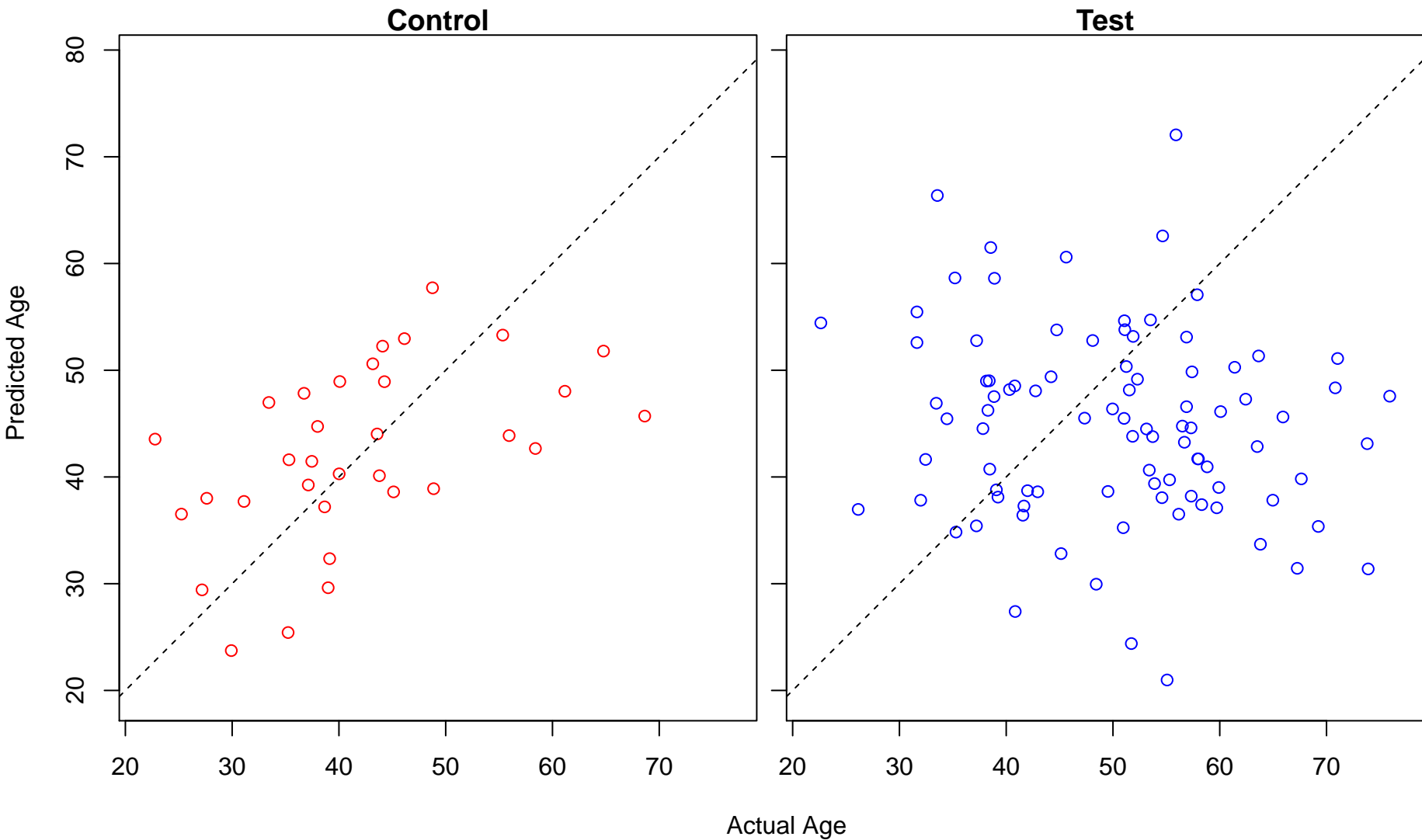
glutamine metabolic process (Score: 1.101166)



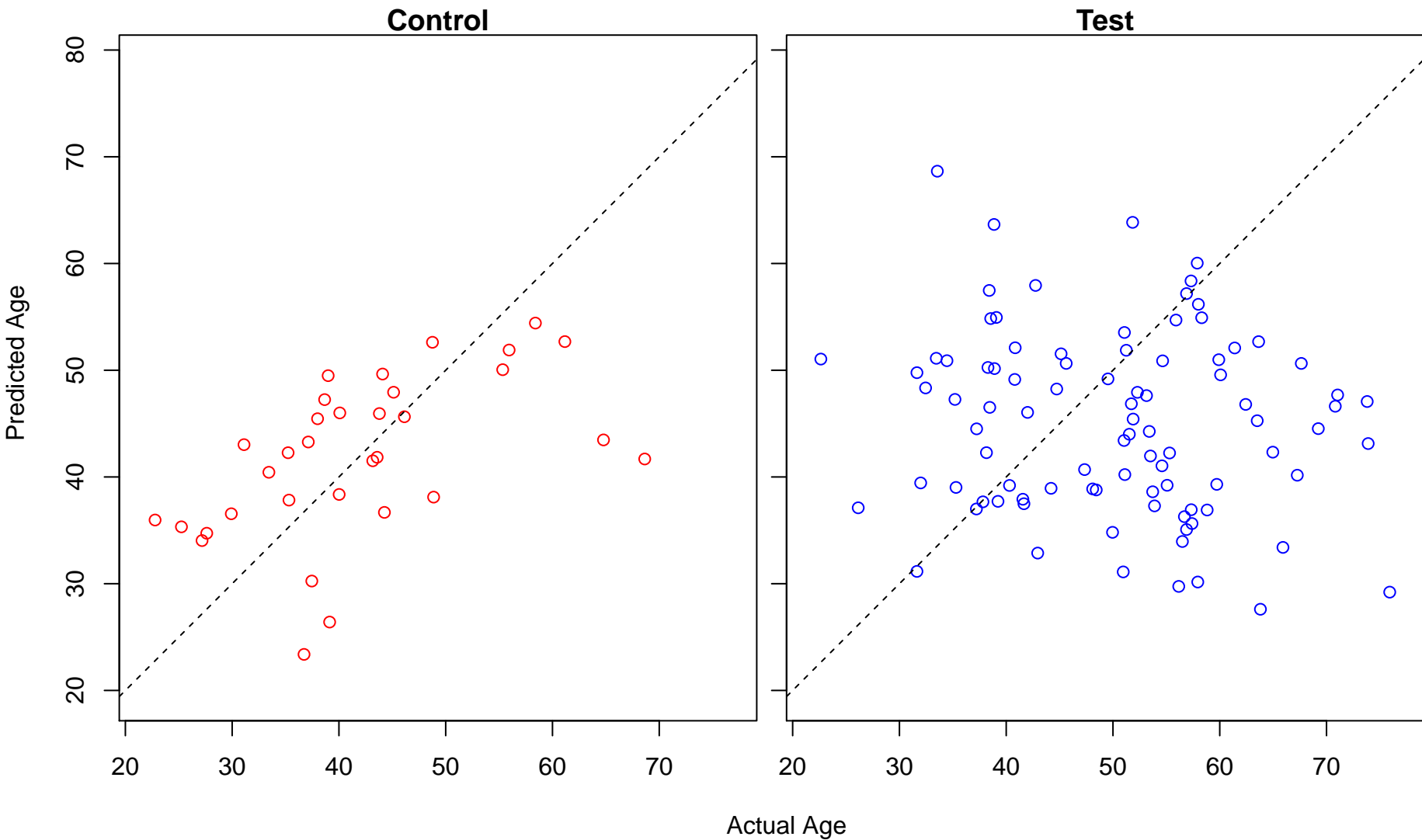
negative regulation of response to DNA damage stimulus (Score: 1.097708)



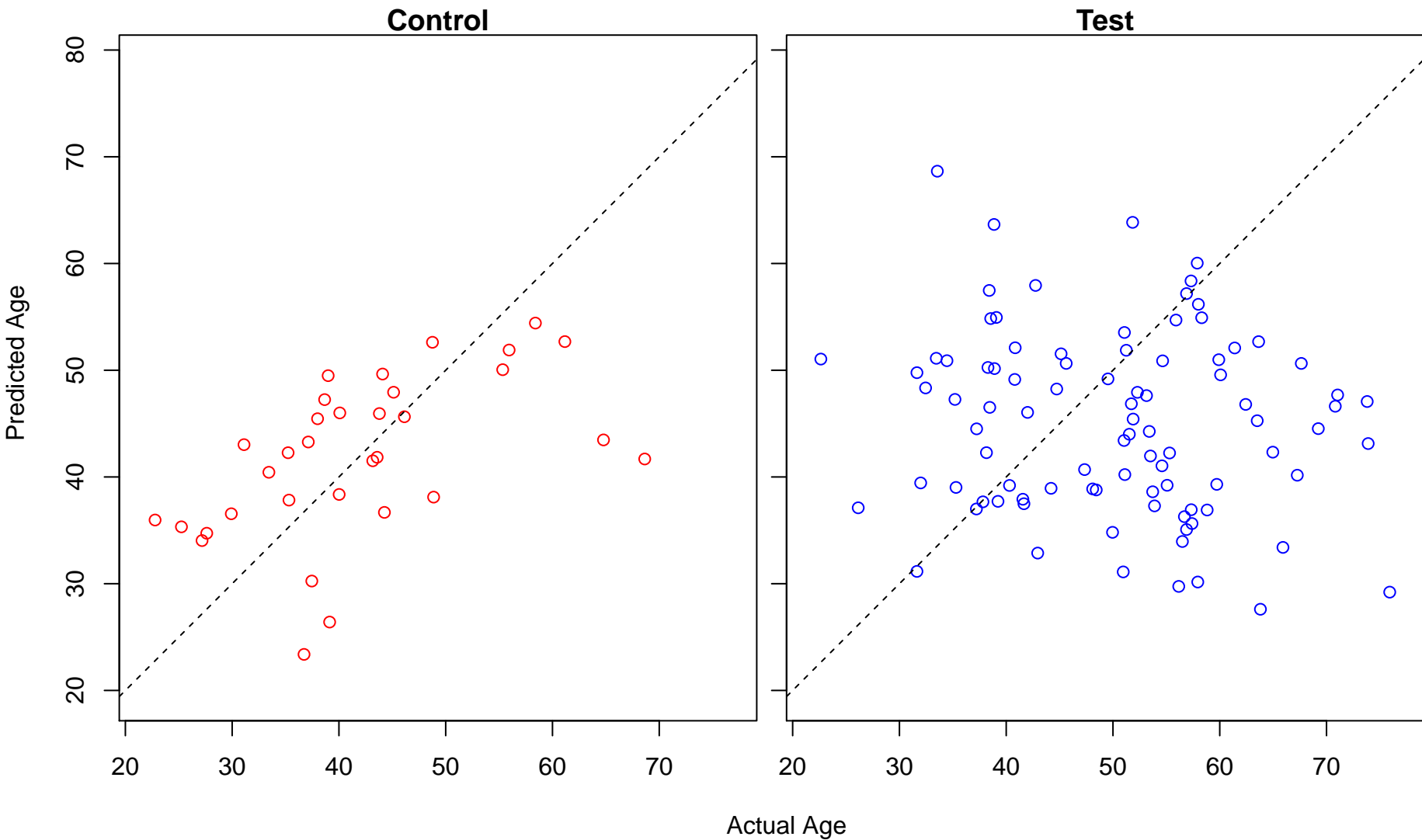
epithelial cell development (Score: 1.096491)



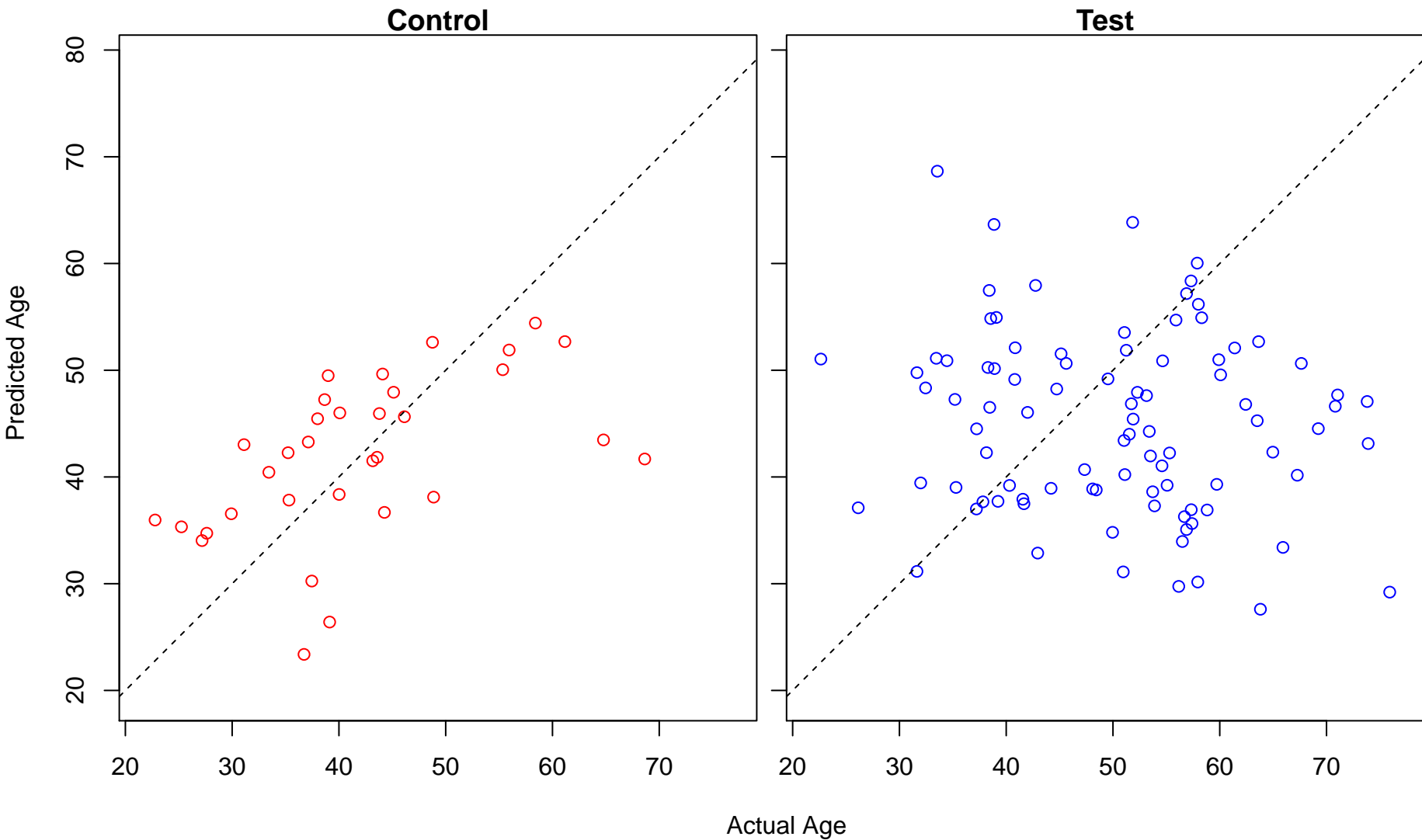
response to caffeine (Score: 1.091812)



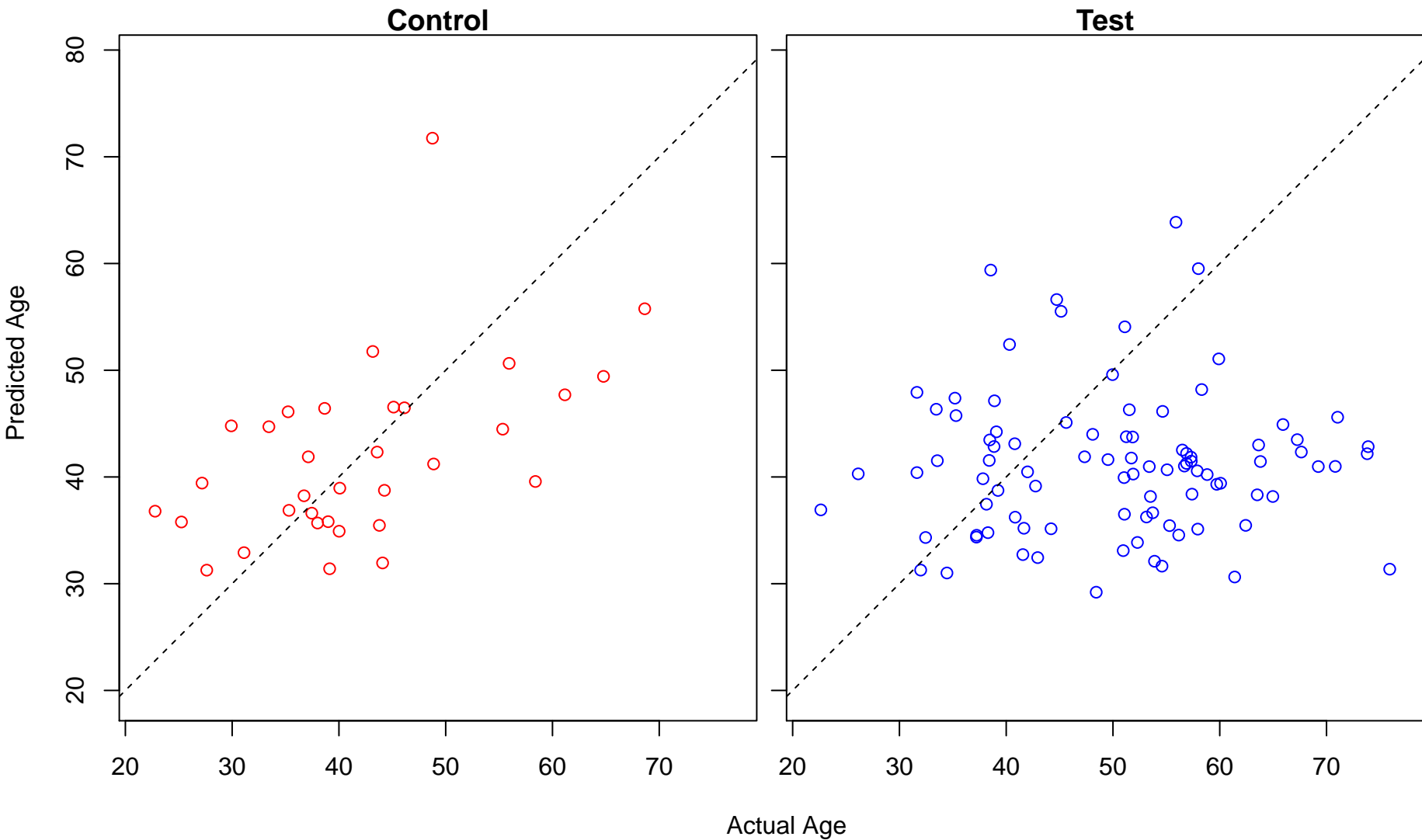
cellular response to caffeine (Score: 1.091812)



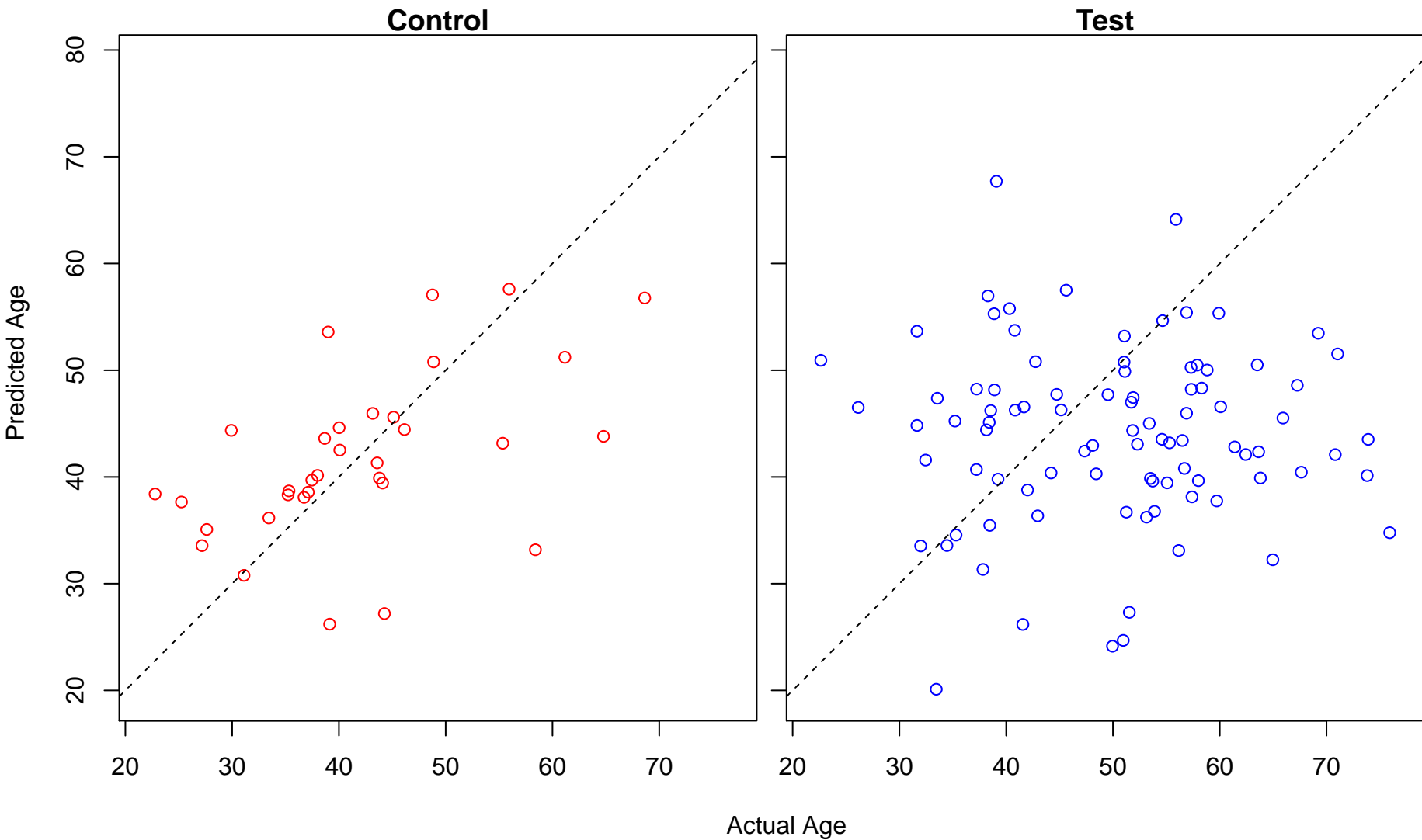
cellular response to purine-containing compound (Score: 1.091812)



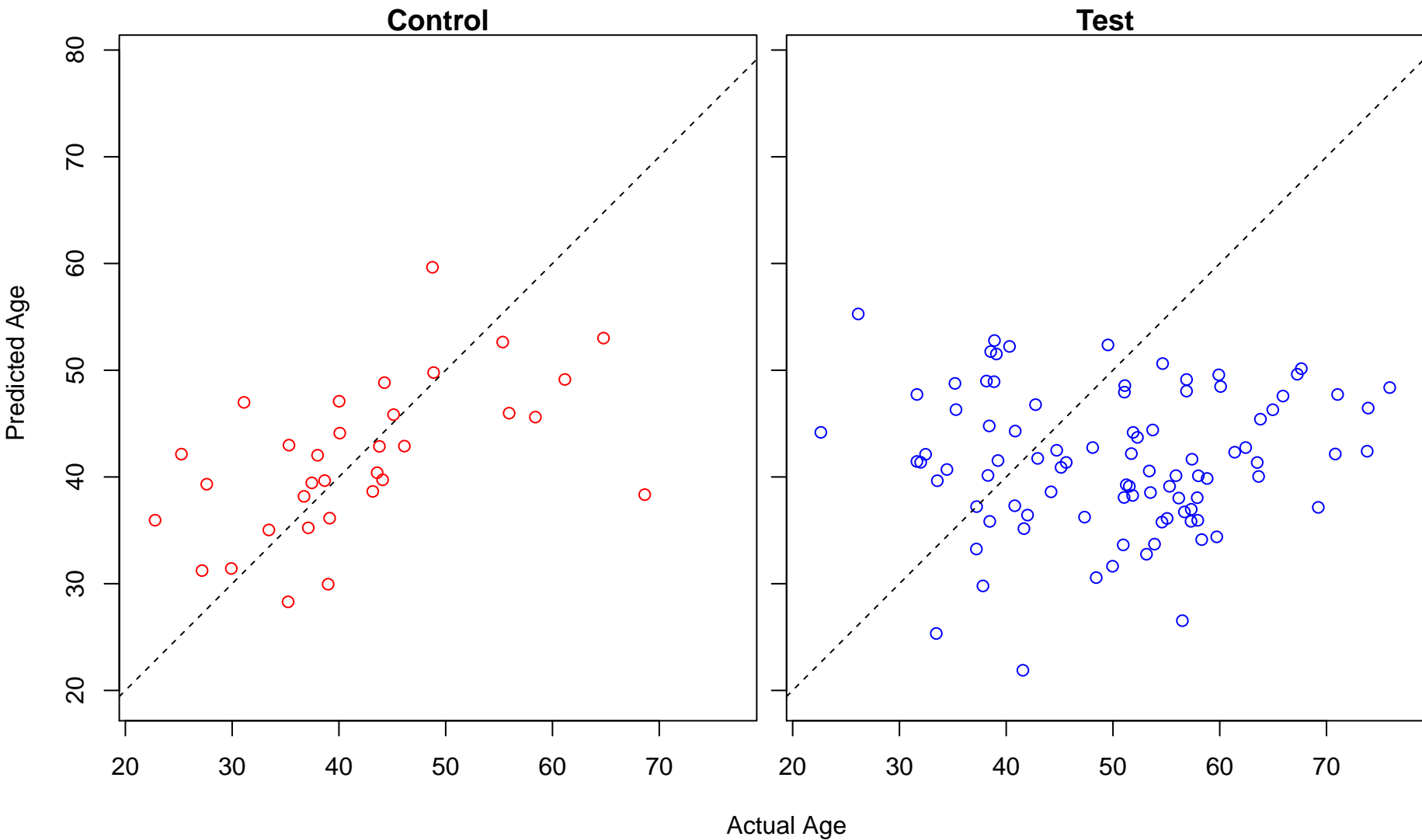
negative regulation of production of molecular mediator of immune response (Score: 1.091717)



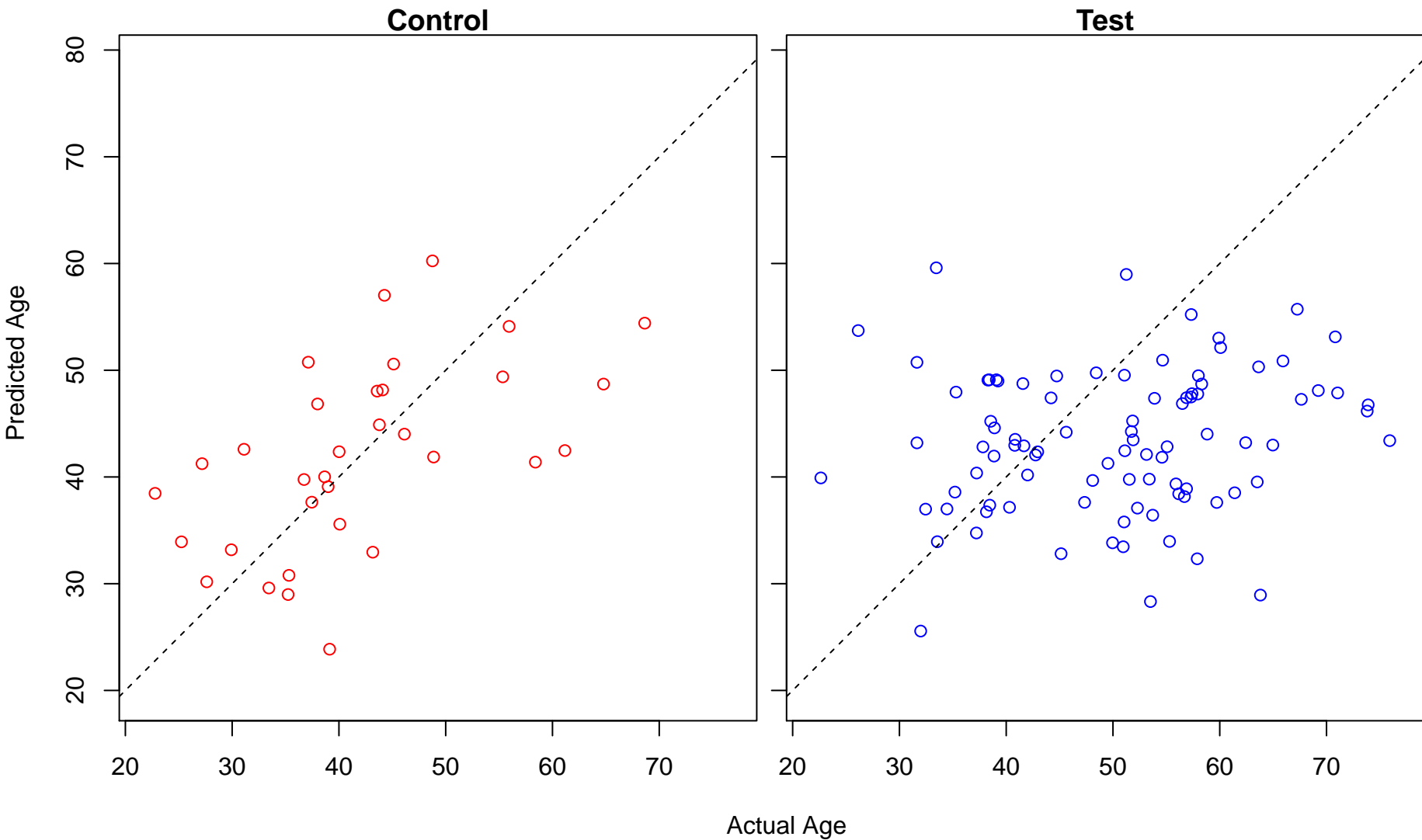
leptin-mediated signaling pathway (Score: 1.091180)



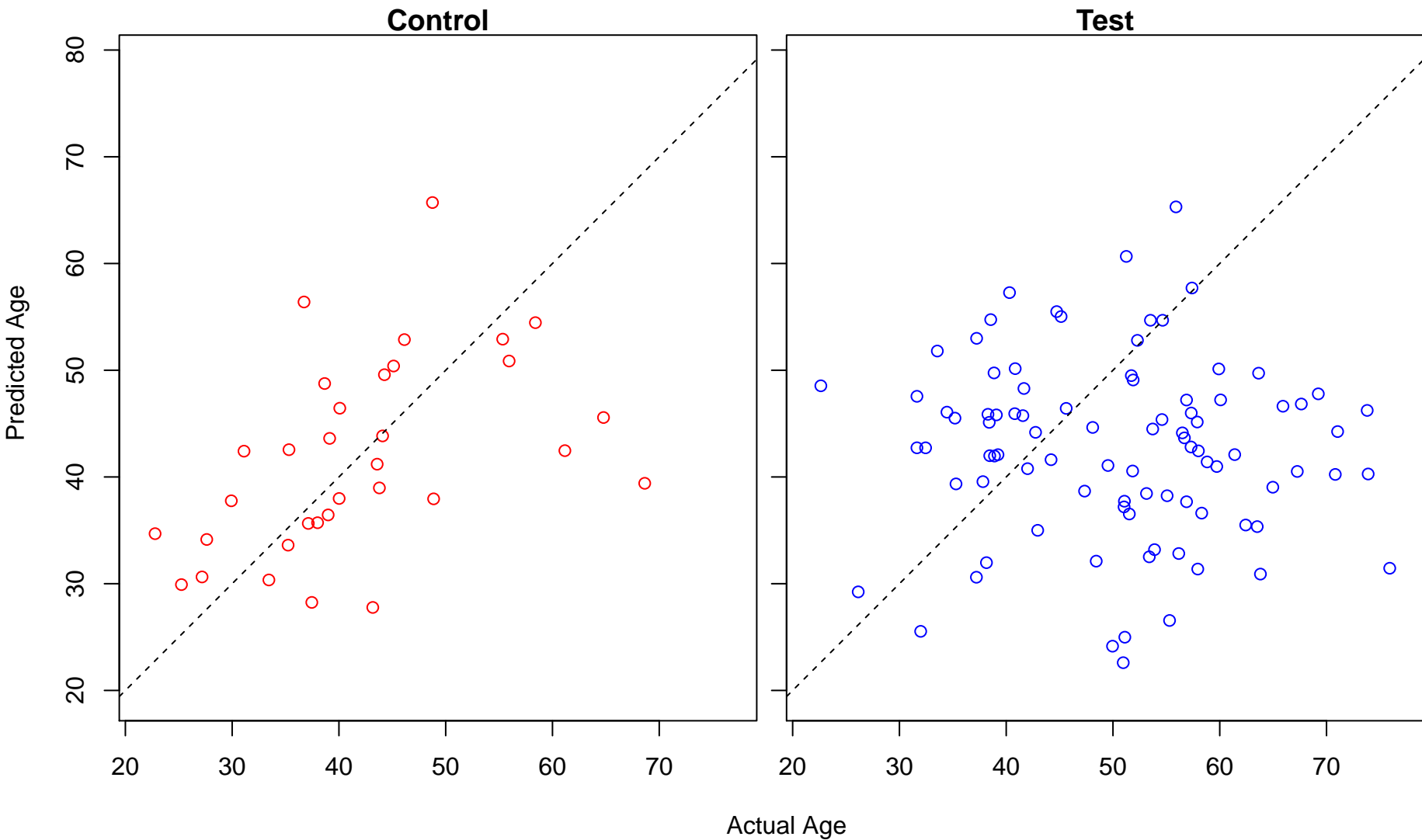
mesoderm development (Score: 1.090830)



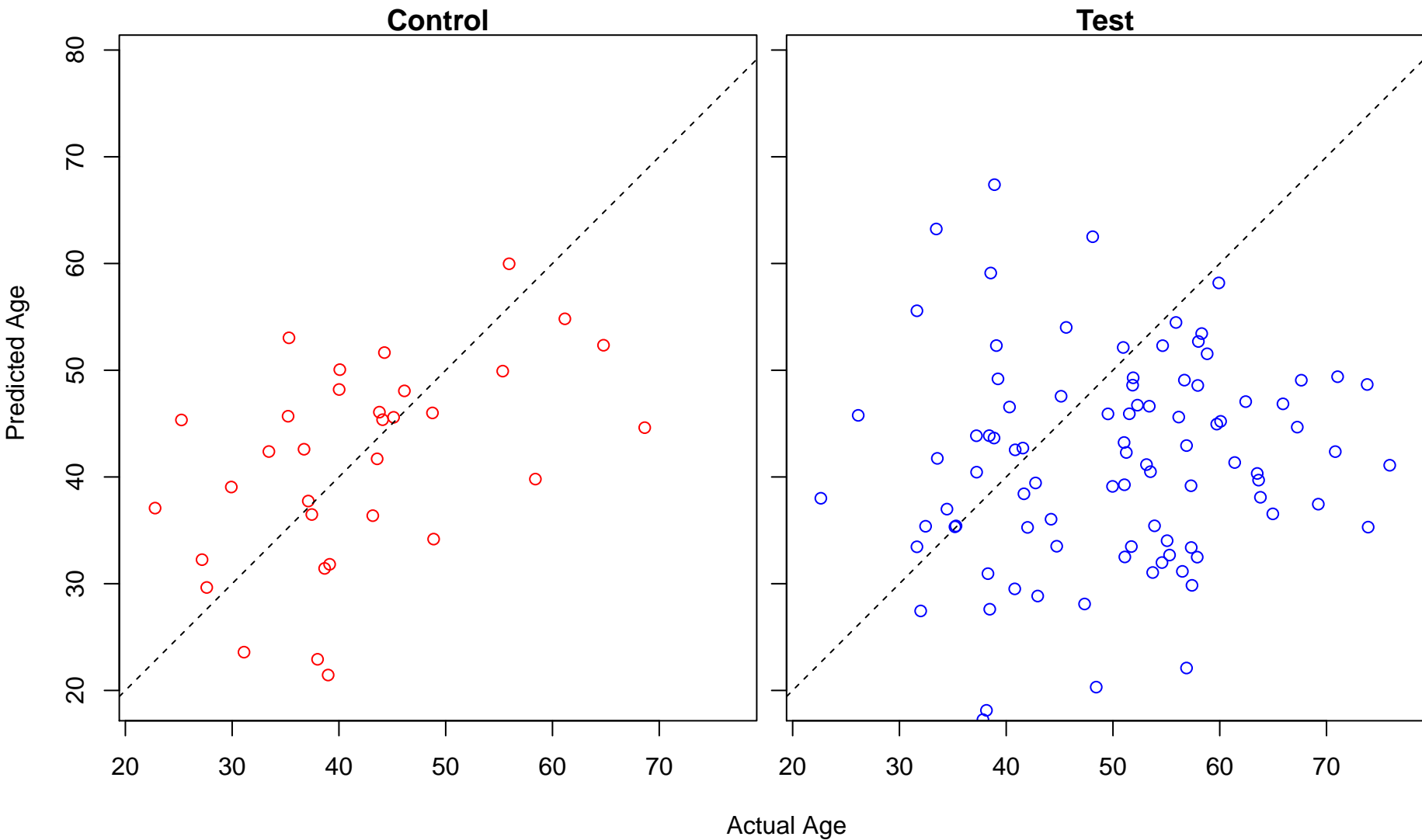
negative regulation of BMP signaling pathway (Score: 1.089549)



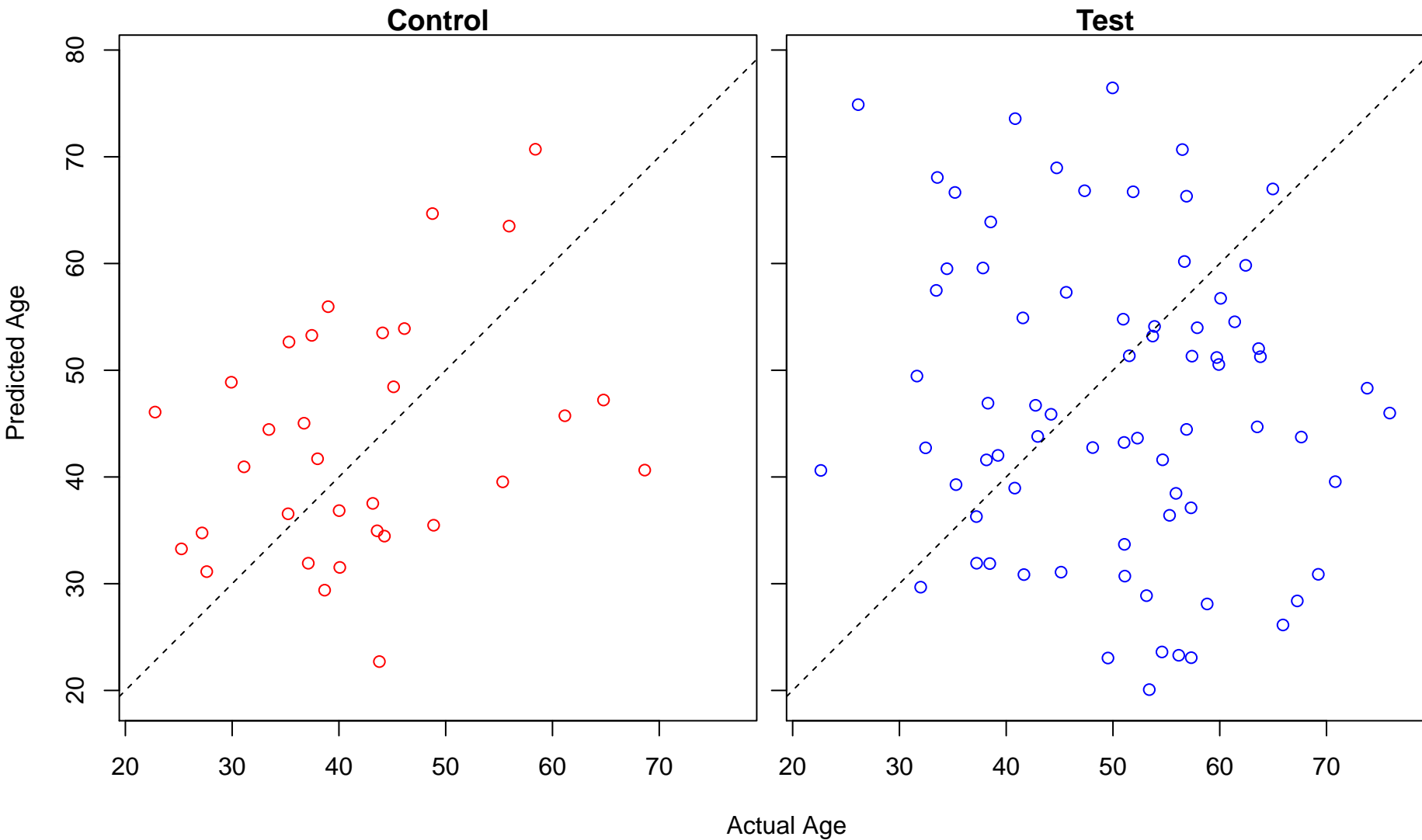
negative regulation of endopeptidase activity (Score: 1.088538)



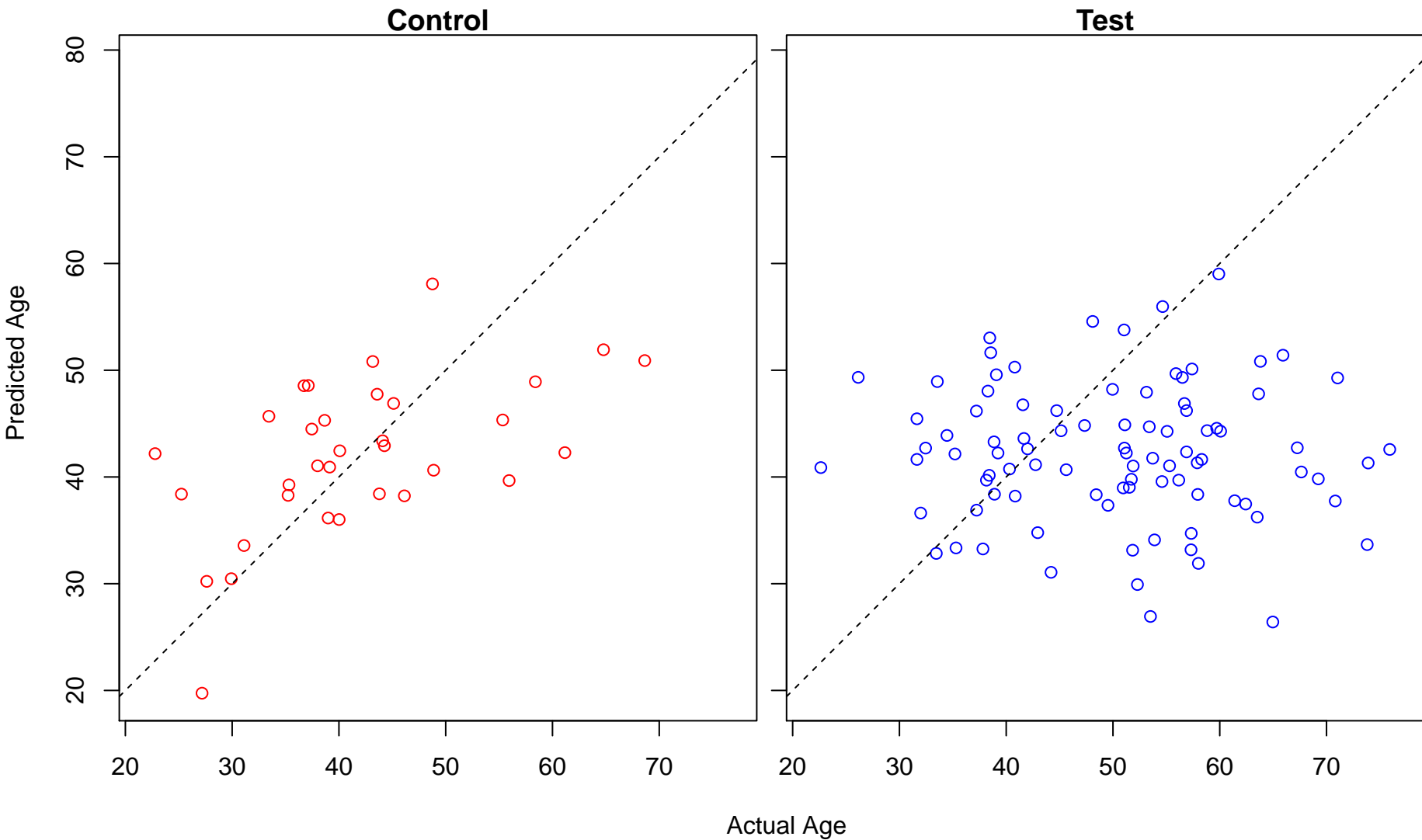
response to osmotic stress (Score: 1.086624)



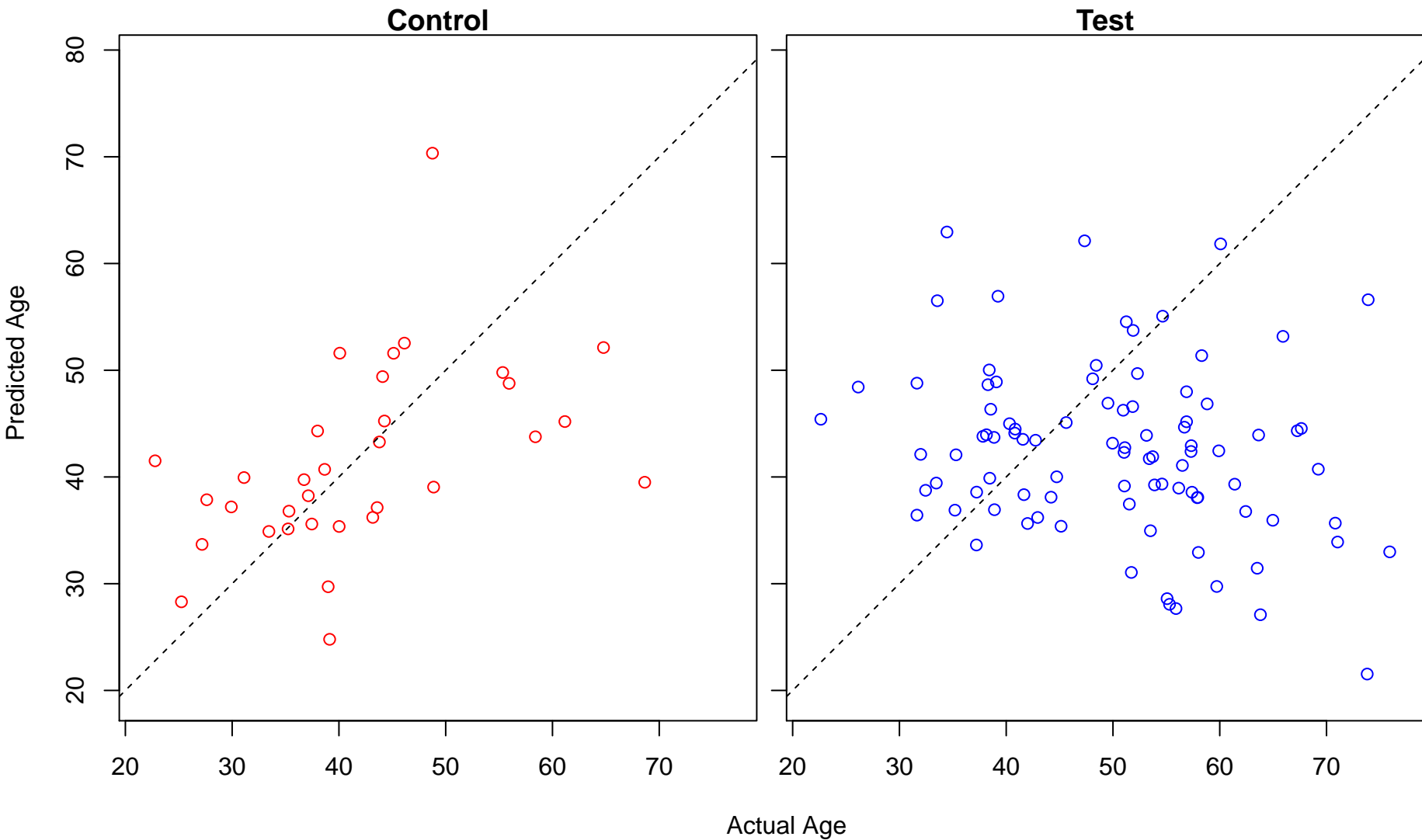
regulation of osteoclast differentiation (Score: 1.086294)



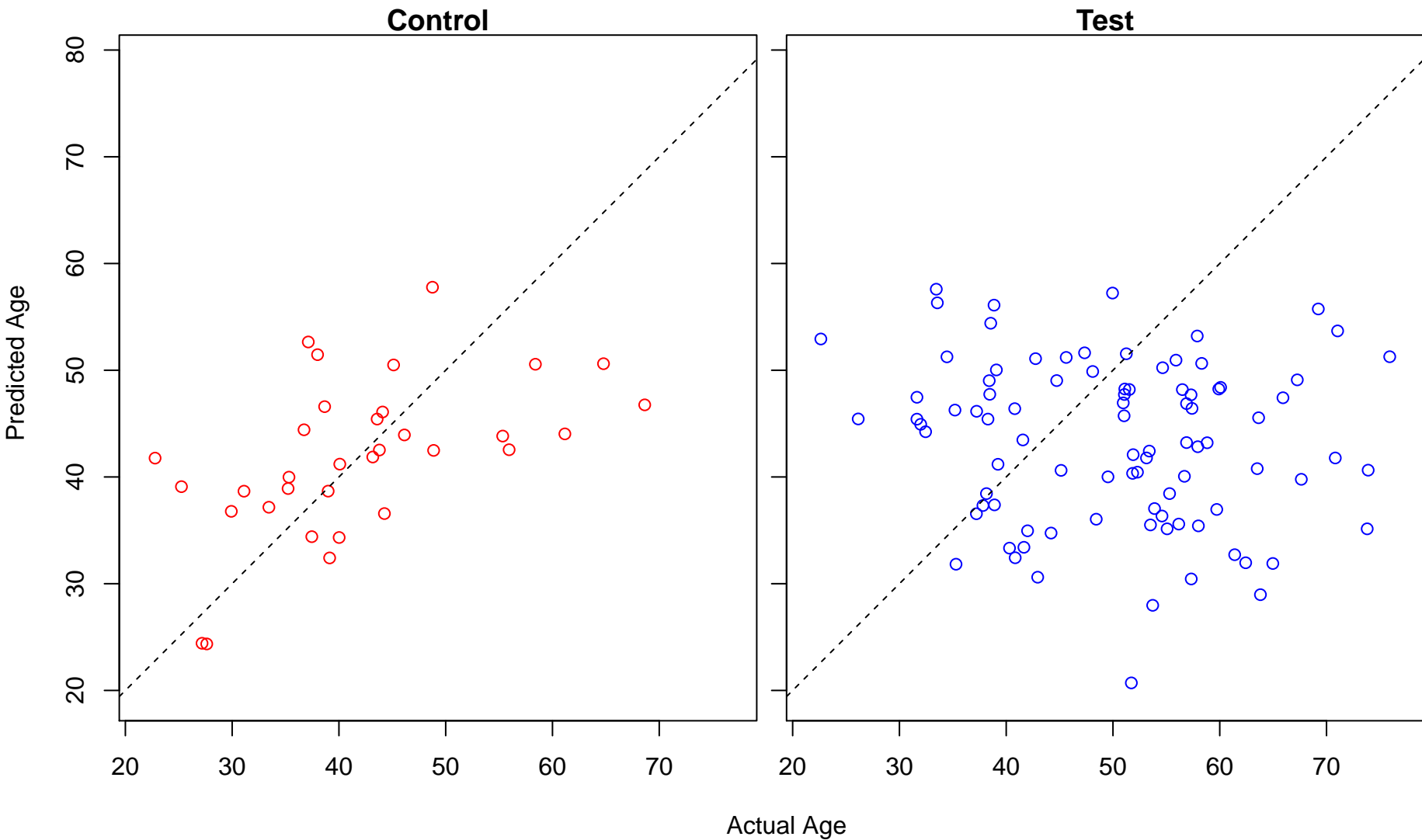
response to nematode (Score: 1.083826)



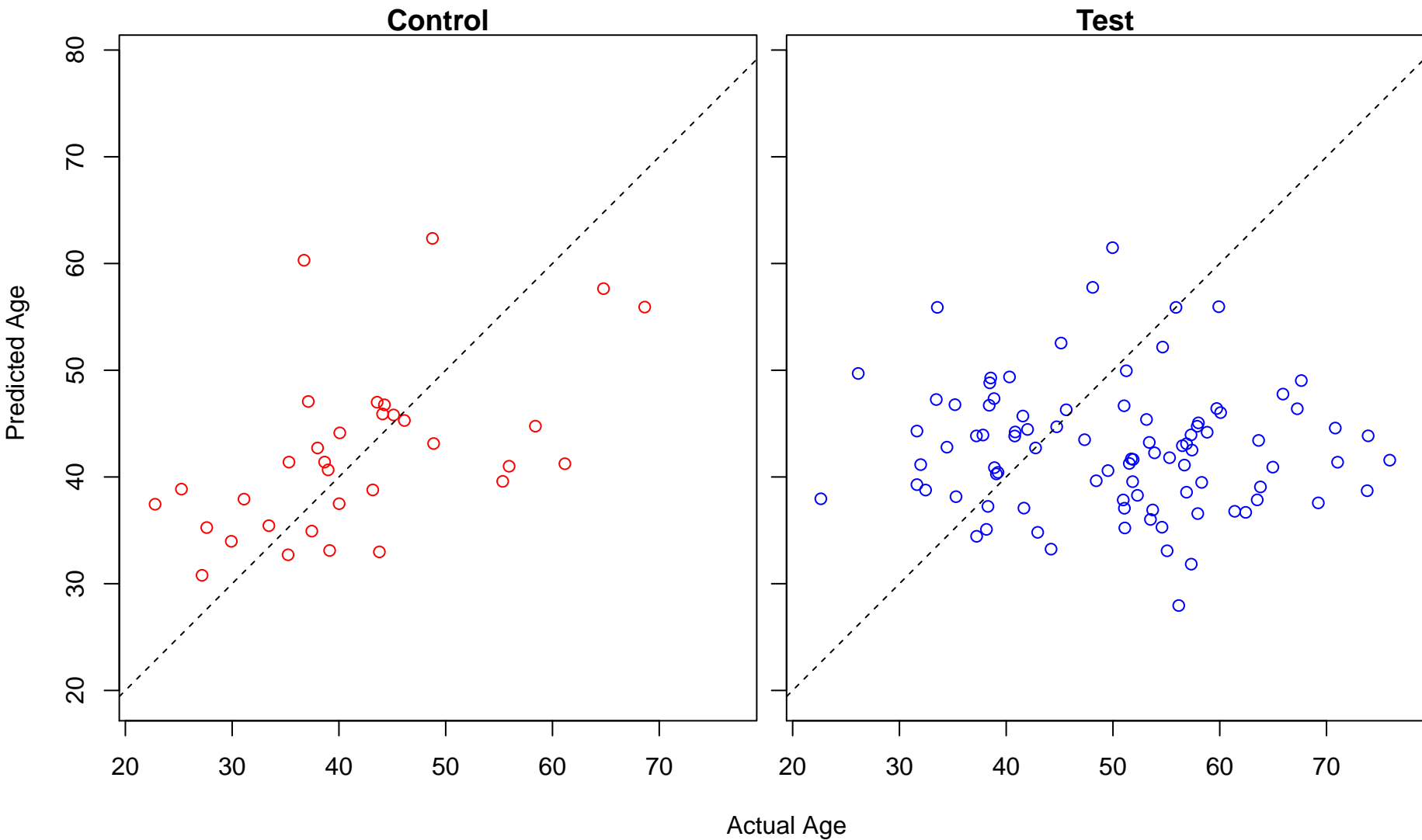
regulation of actin nucleation (Score: 1.083739)



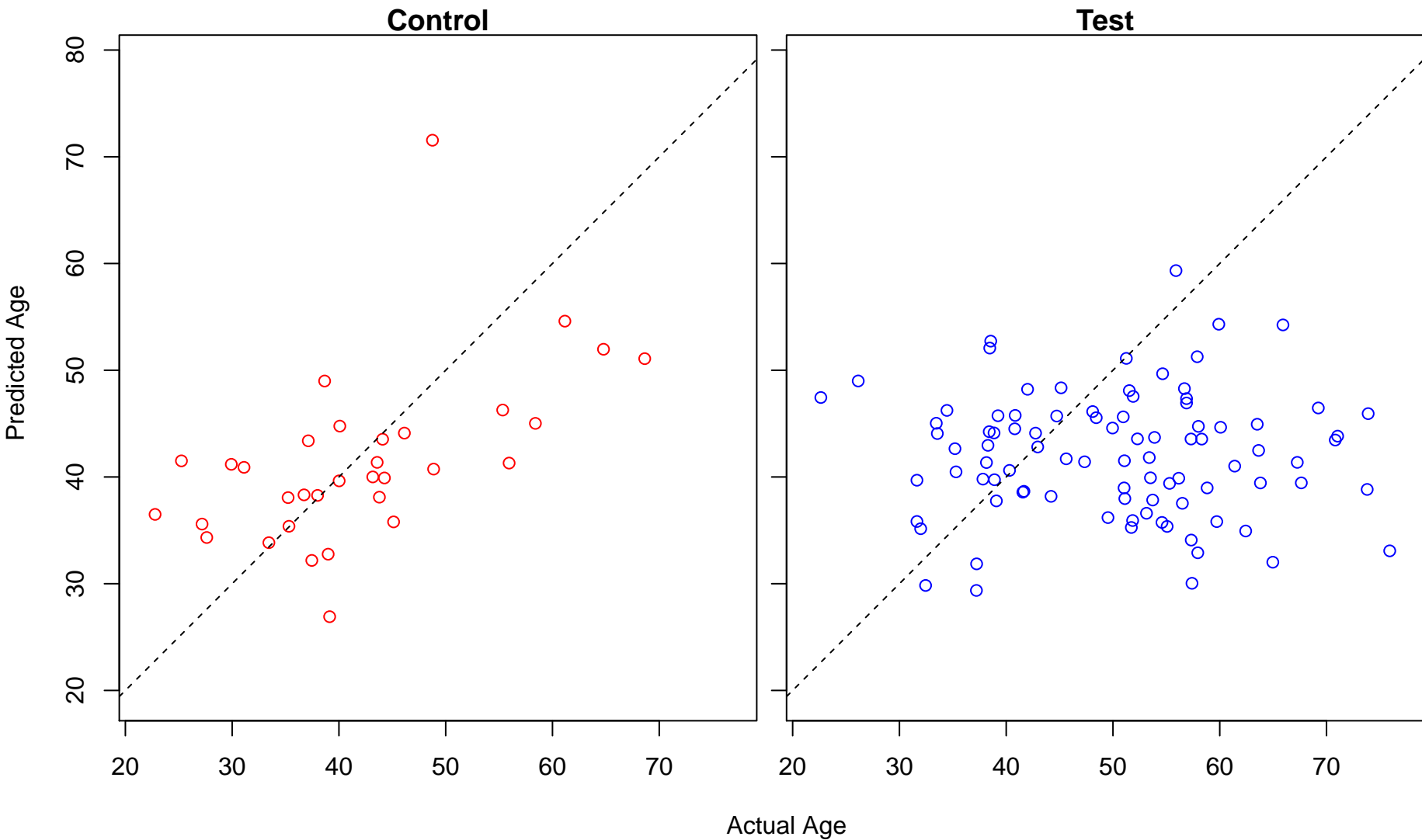
oligodendrocyte development (Score: 1.083415)



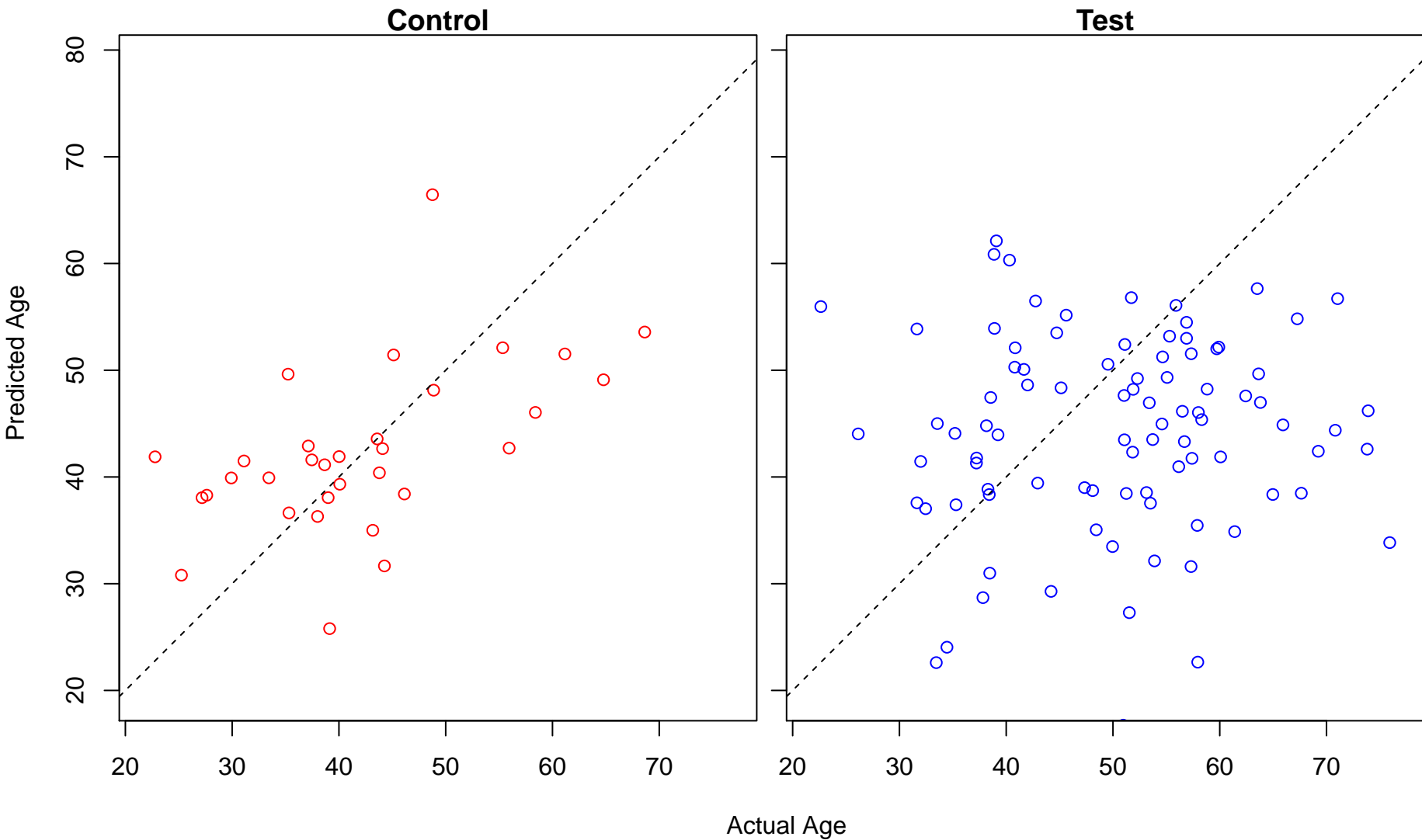
cellular response to nitric oxide (Score: 1.082675)



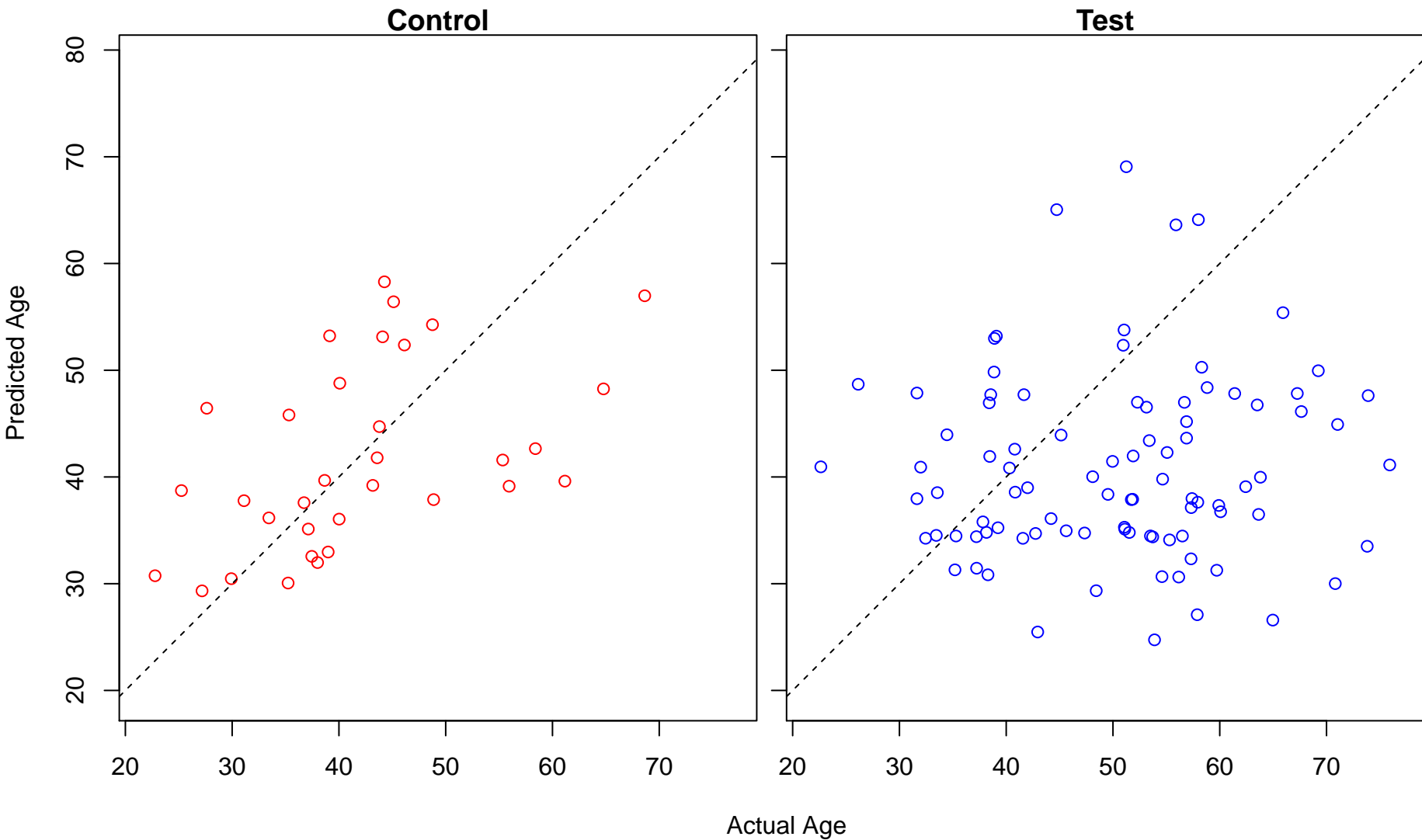
negative regulation of type I interferon production (Score: 1.082630)



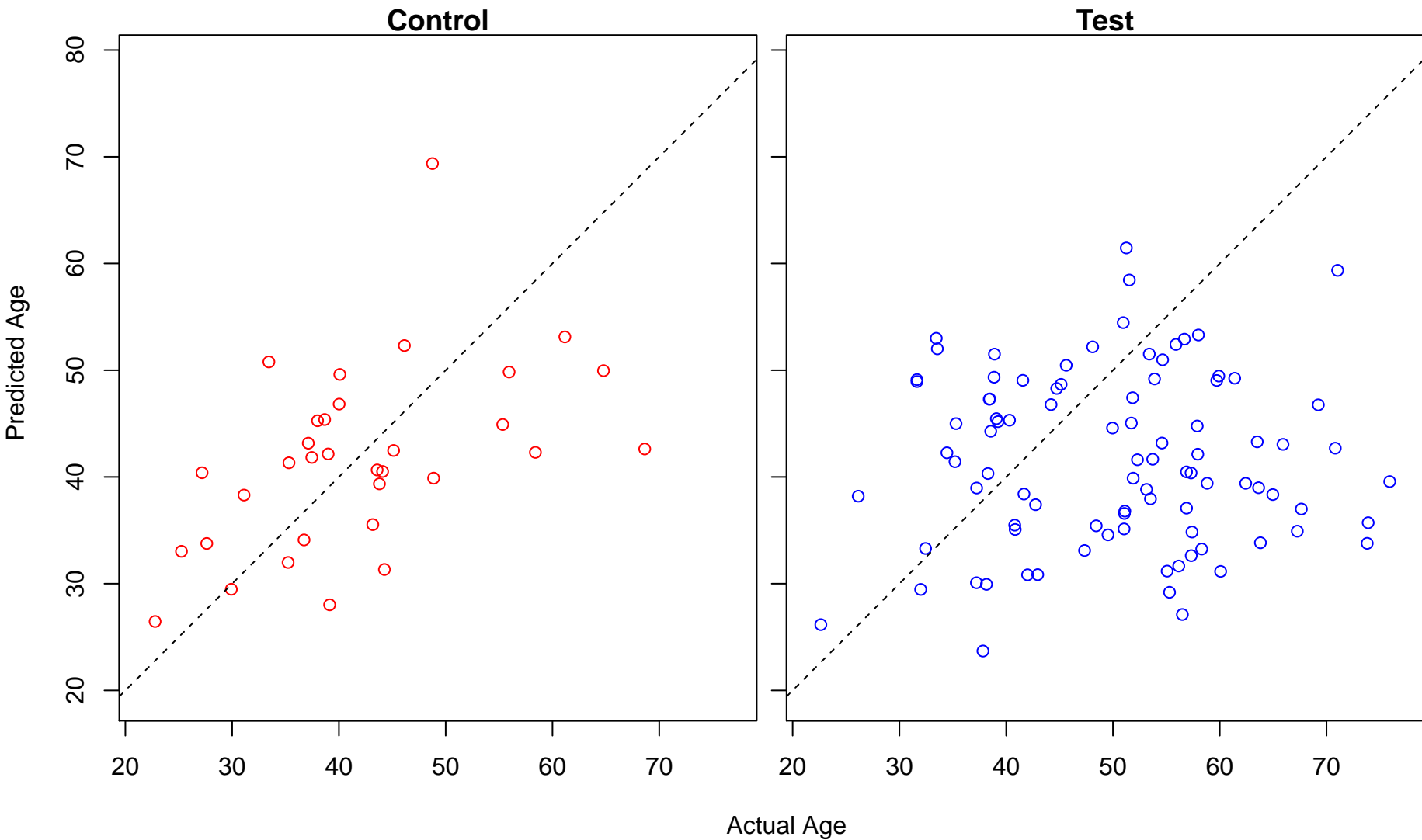
detection of mechanical stimulus involved in sensory perception (Score: 1.079113)



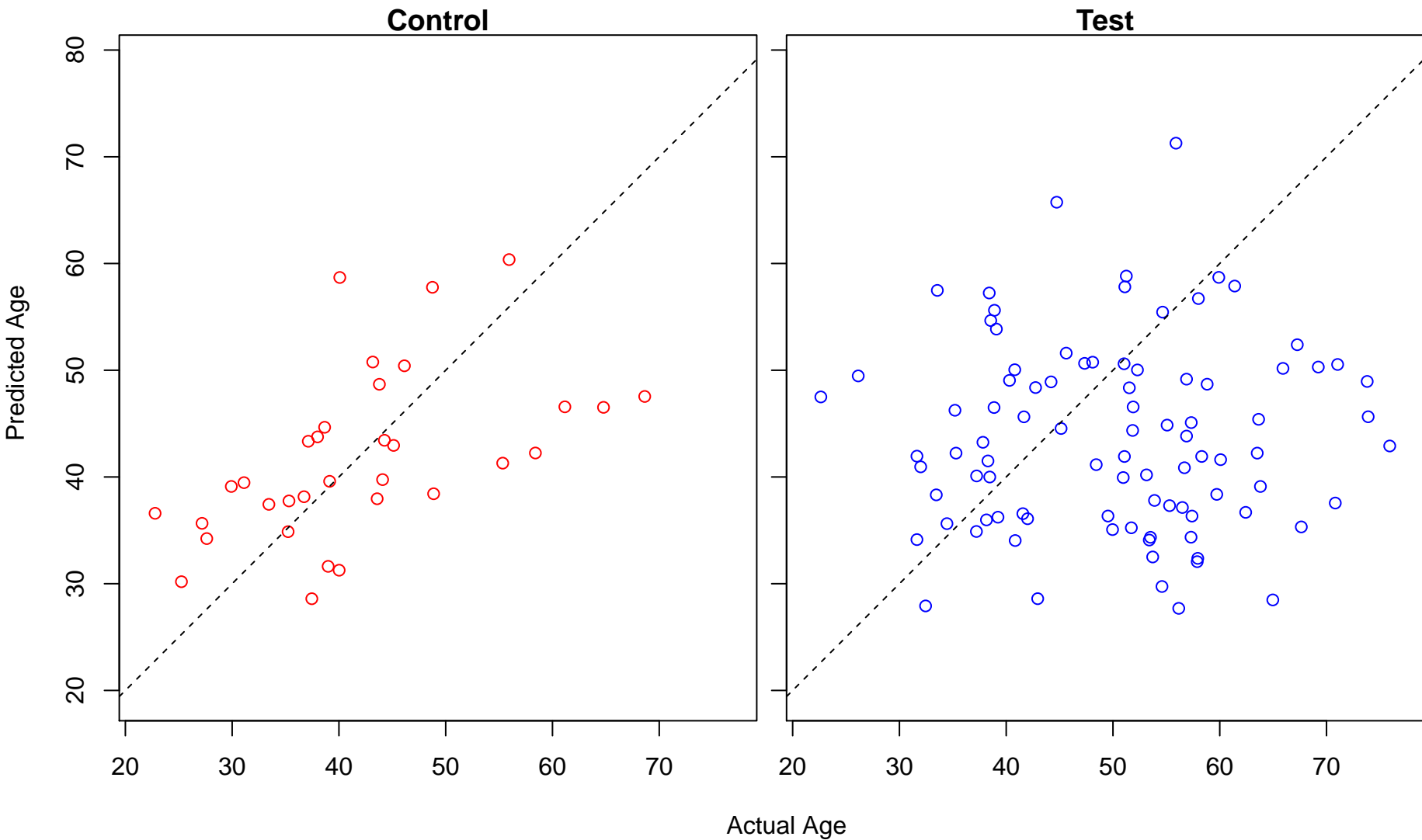
positive regulation of heart contraction (Score: 1.078422)



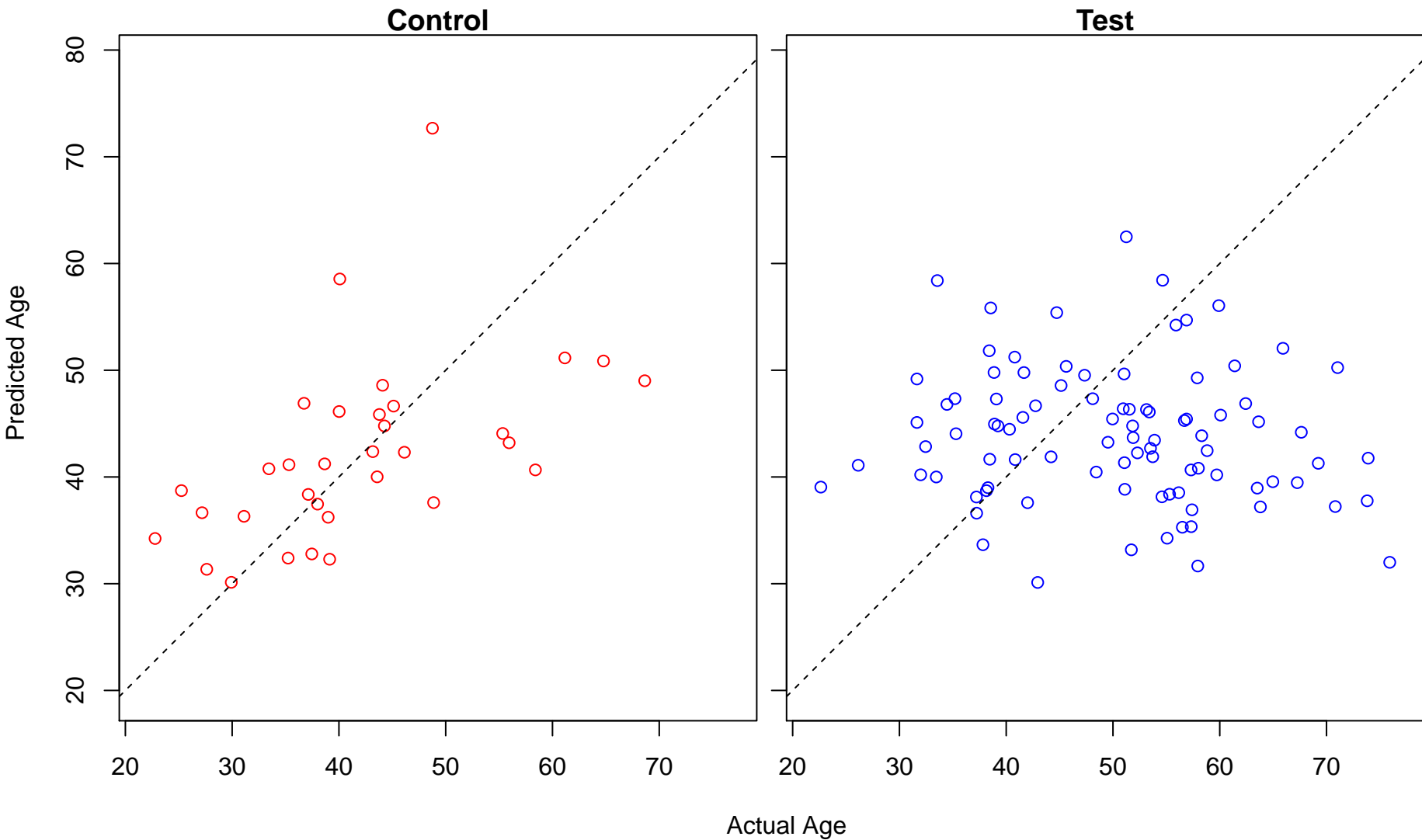
blood vessel morphogenesis (Score: 1.078004)



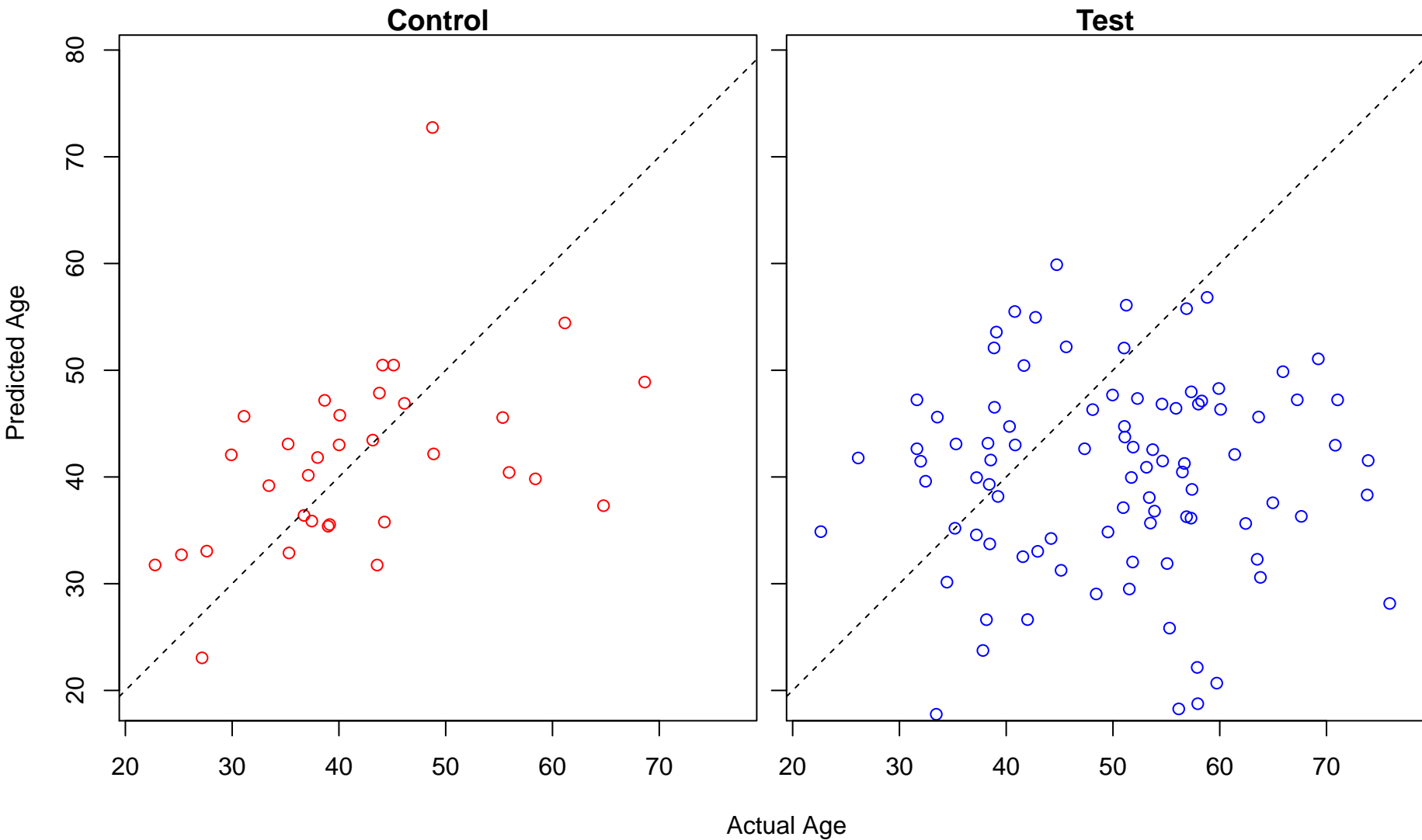
negative regulation of transporter activity (Score: 1.076594)



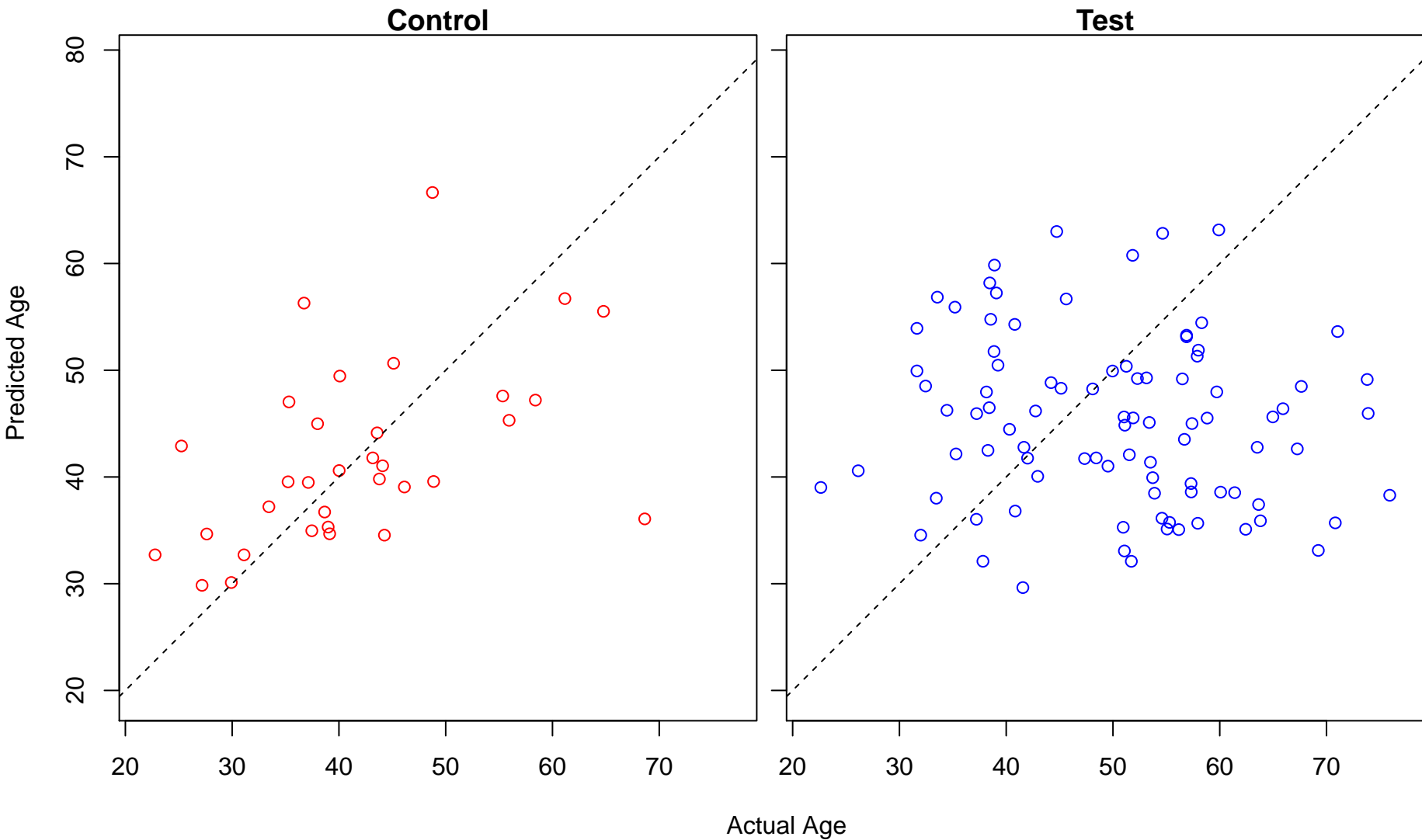
positive regulation of transcription from RNA polymerase II promoter (Score: 1.076212)



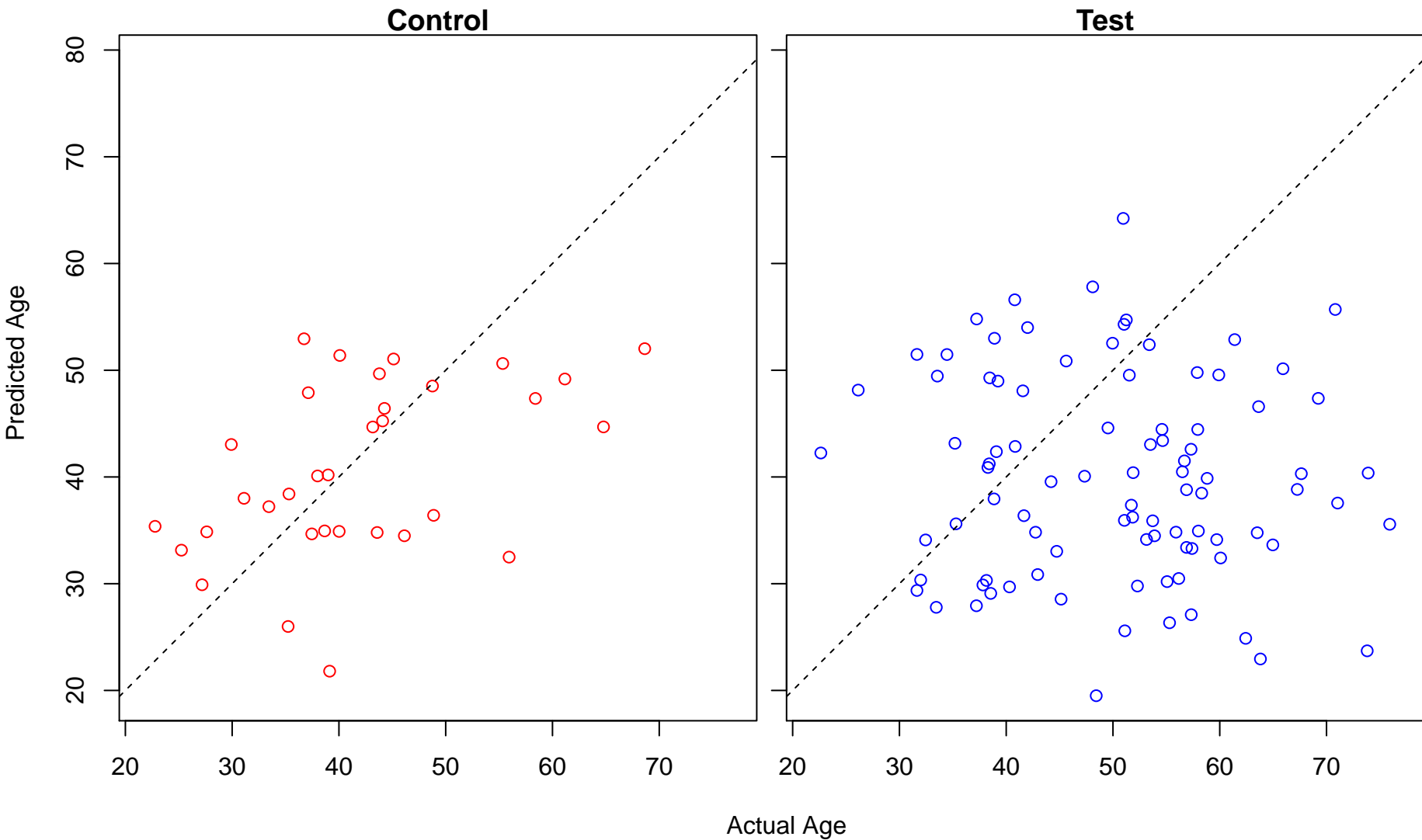
regulation of cardiac muscle contraction (Score: 1.075344)



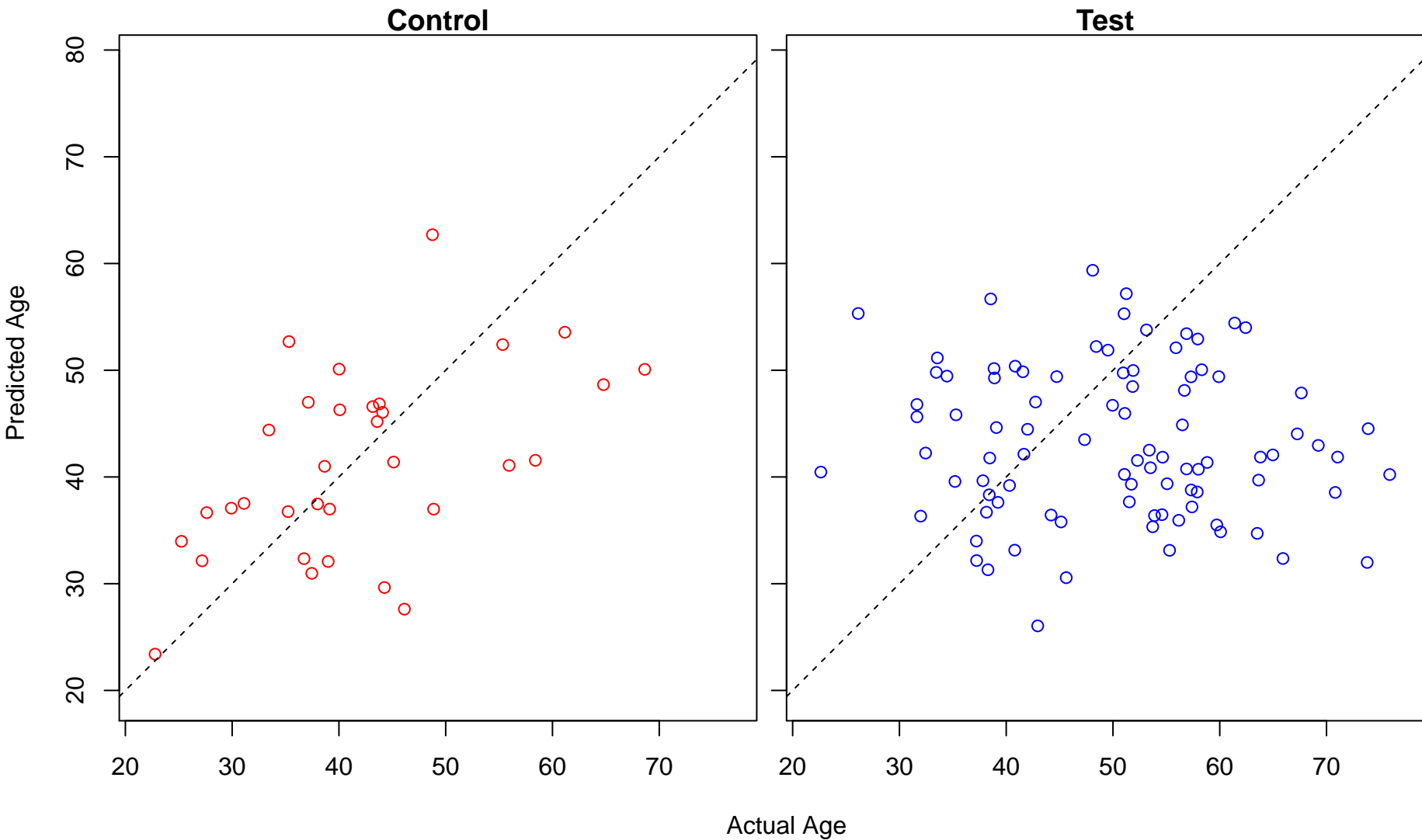
negative regulation of cell adhesion (Score: 1.074692)



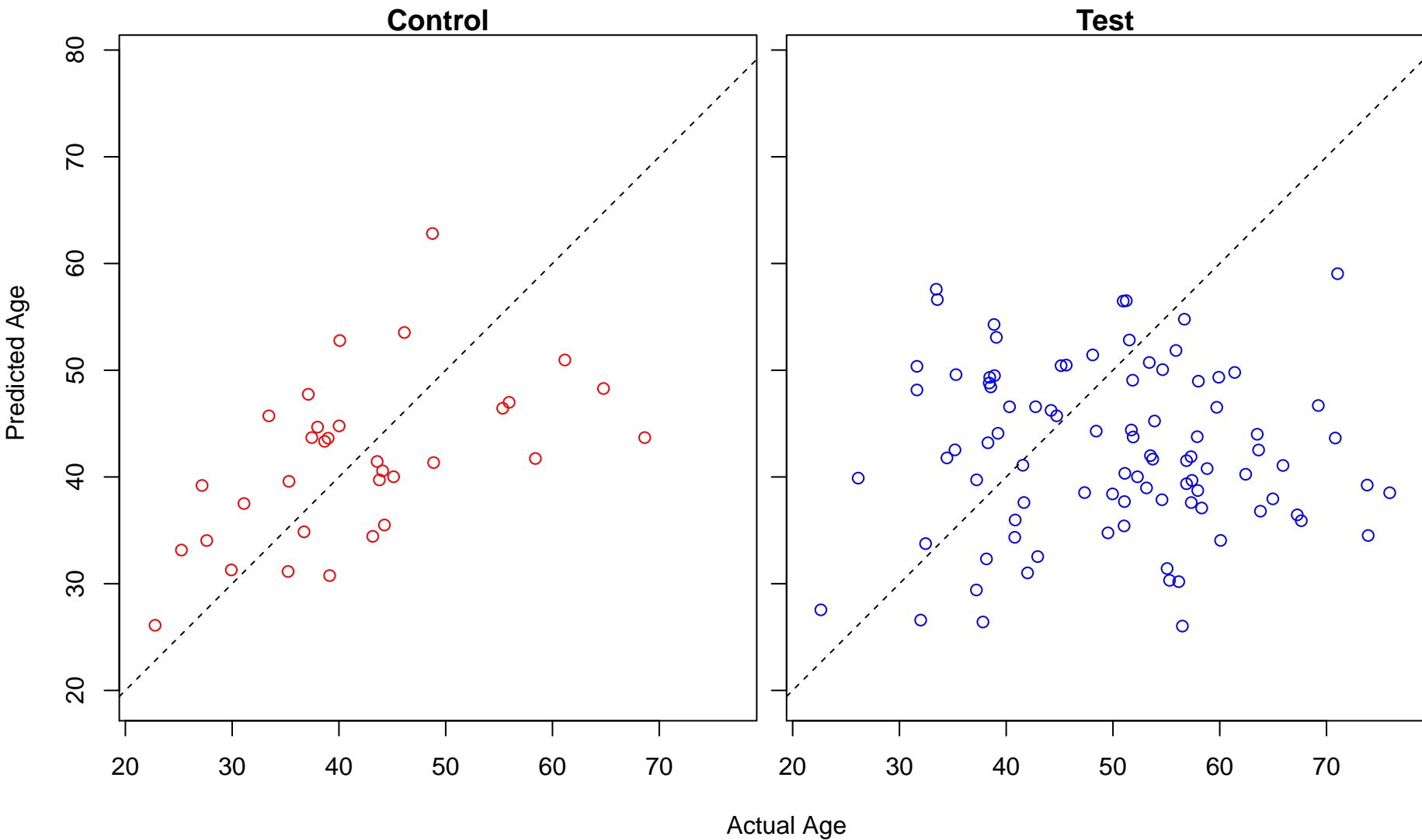
protein homooligomerization (Score: 1.074139)



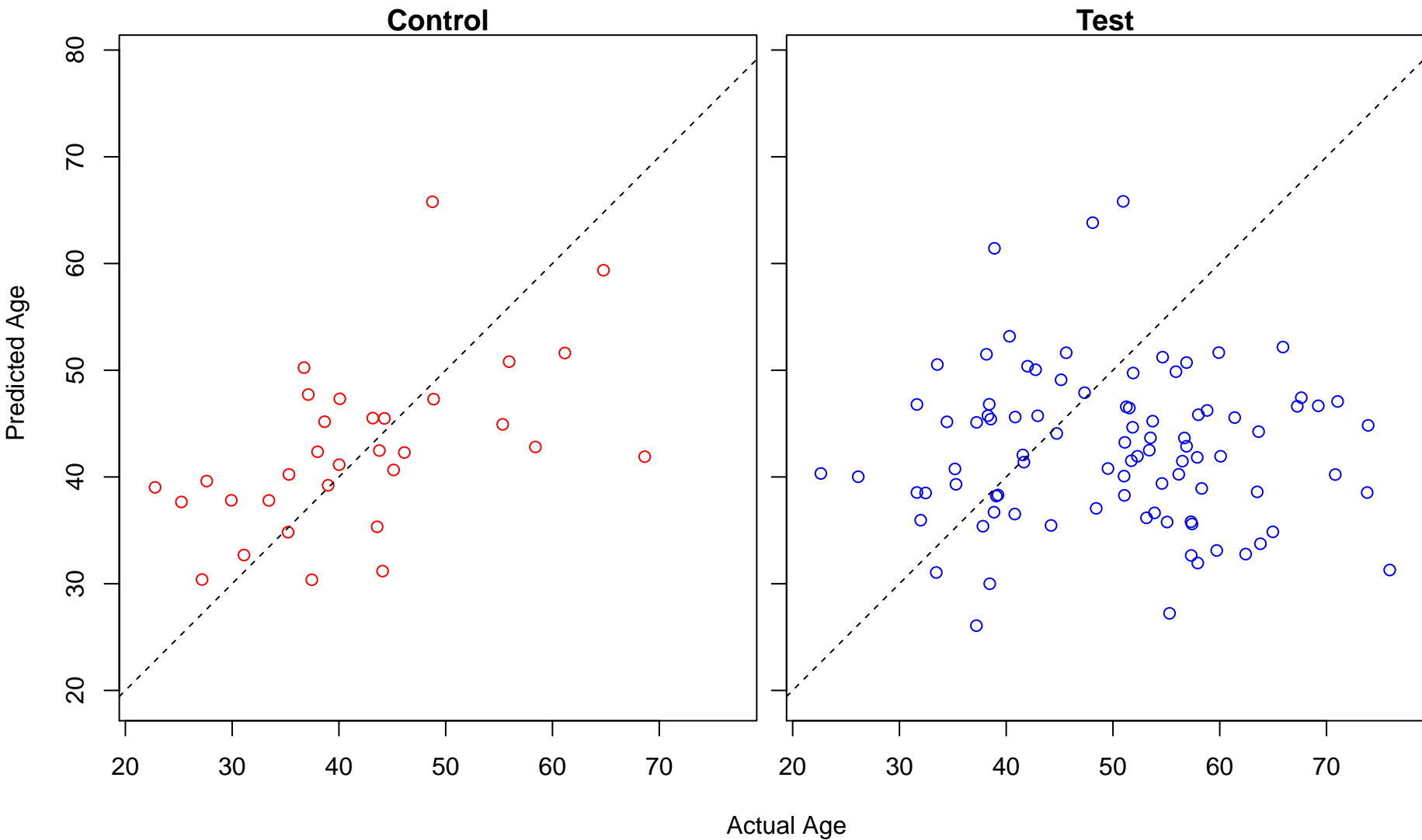
signal release (Score: 1.072775)



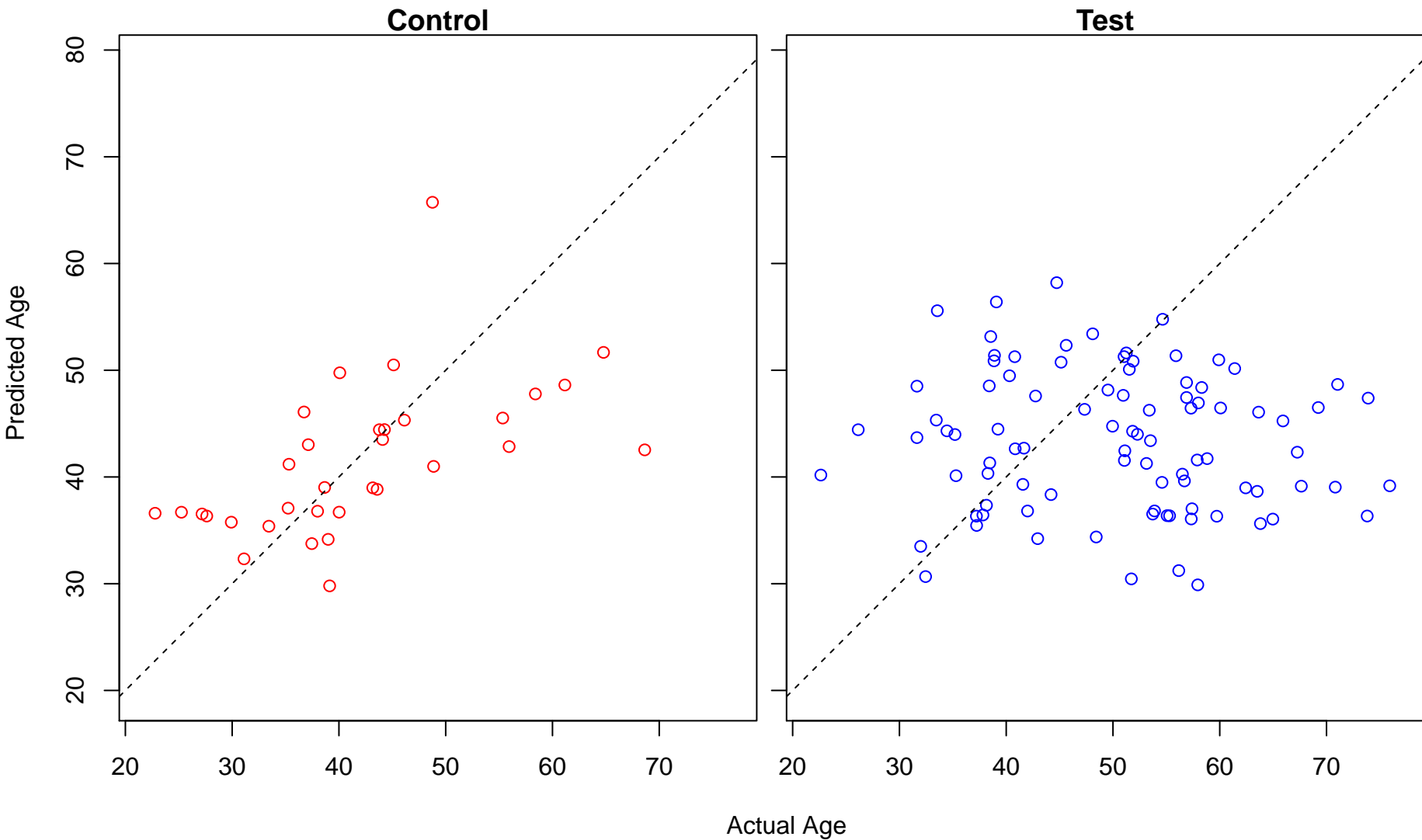
vasculature development (Score: 1.070614)



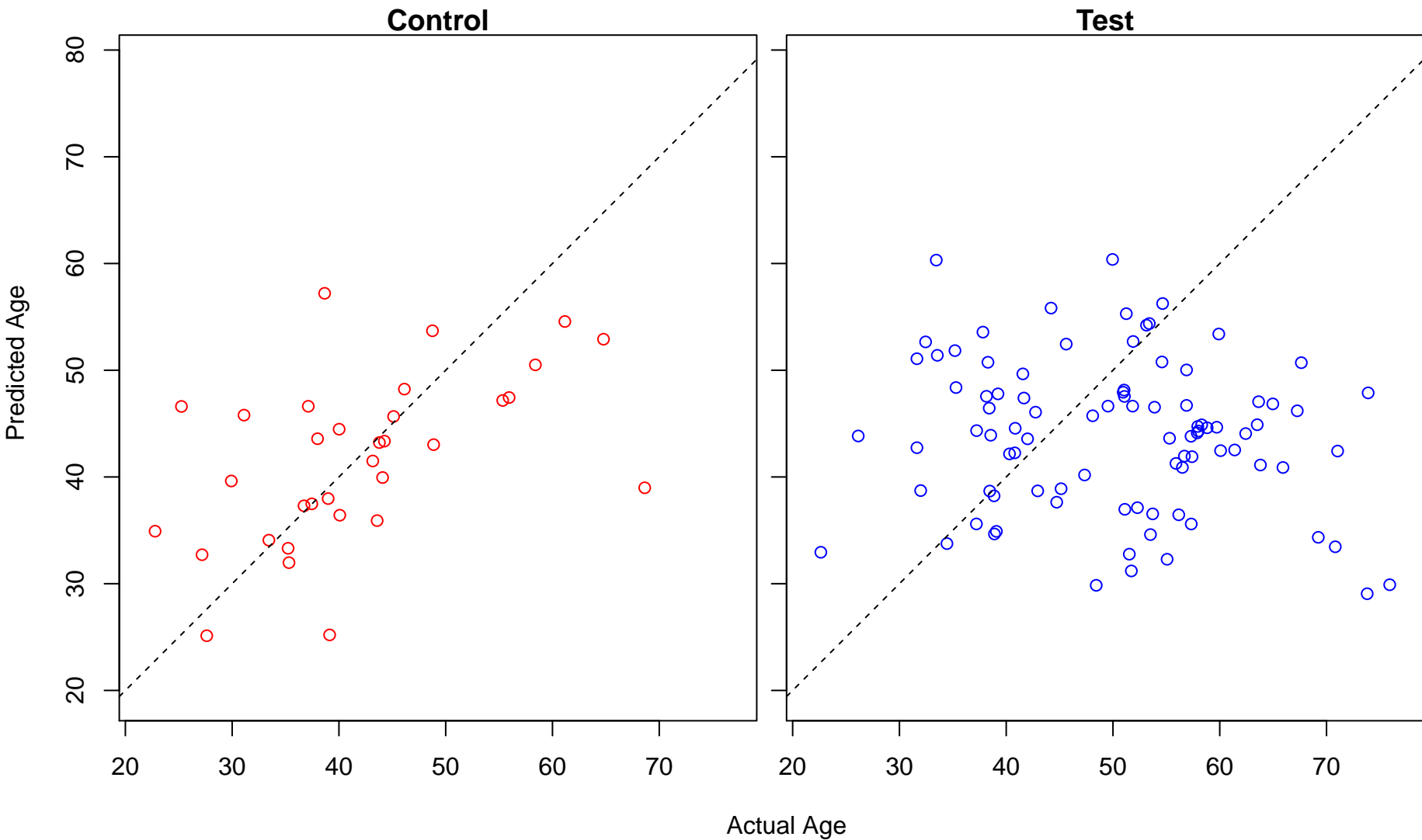
macropinocytosis (Score: 1.069633)



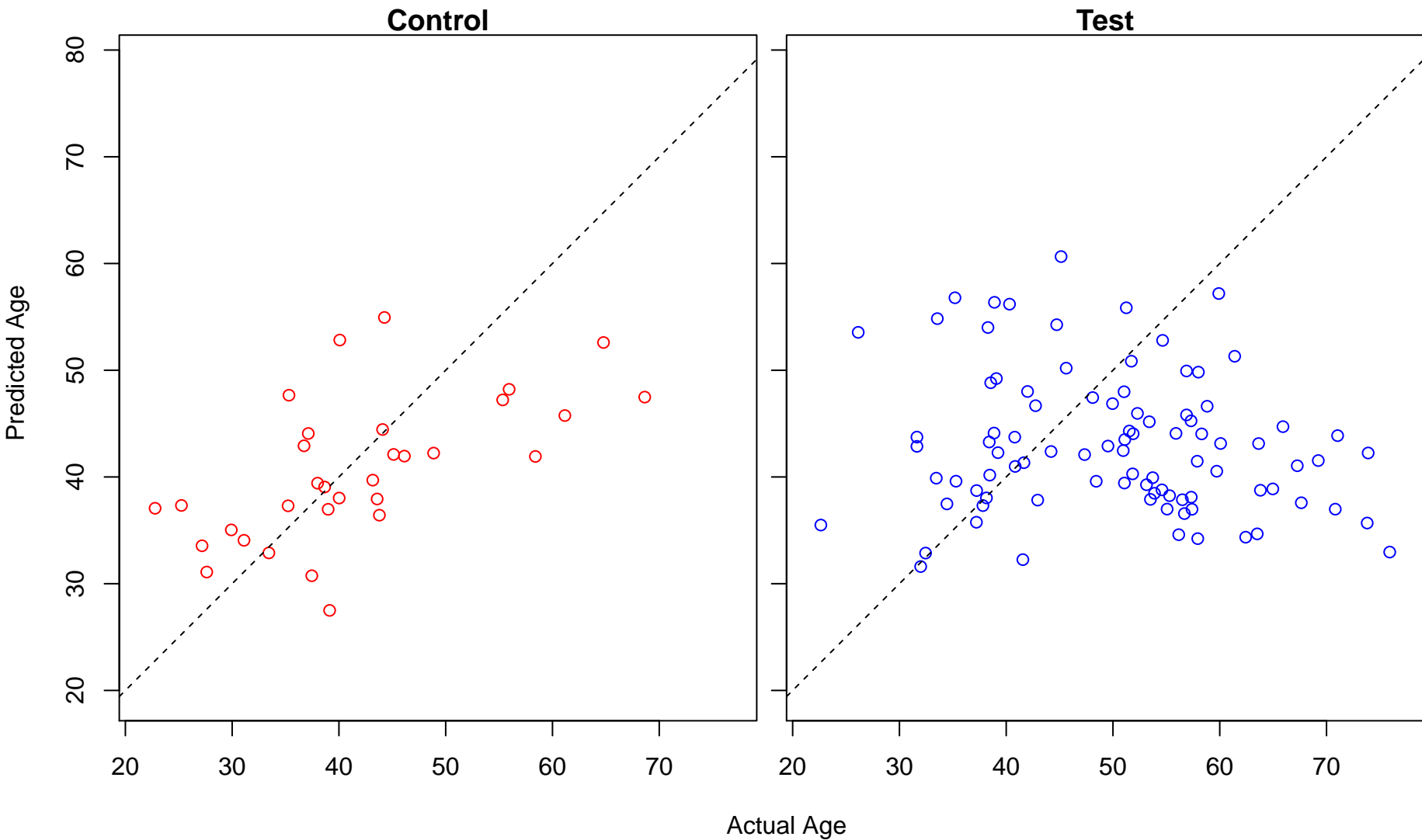
protein folding (Score: 1.068807)



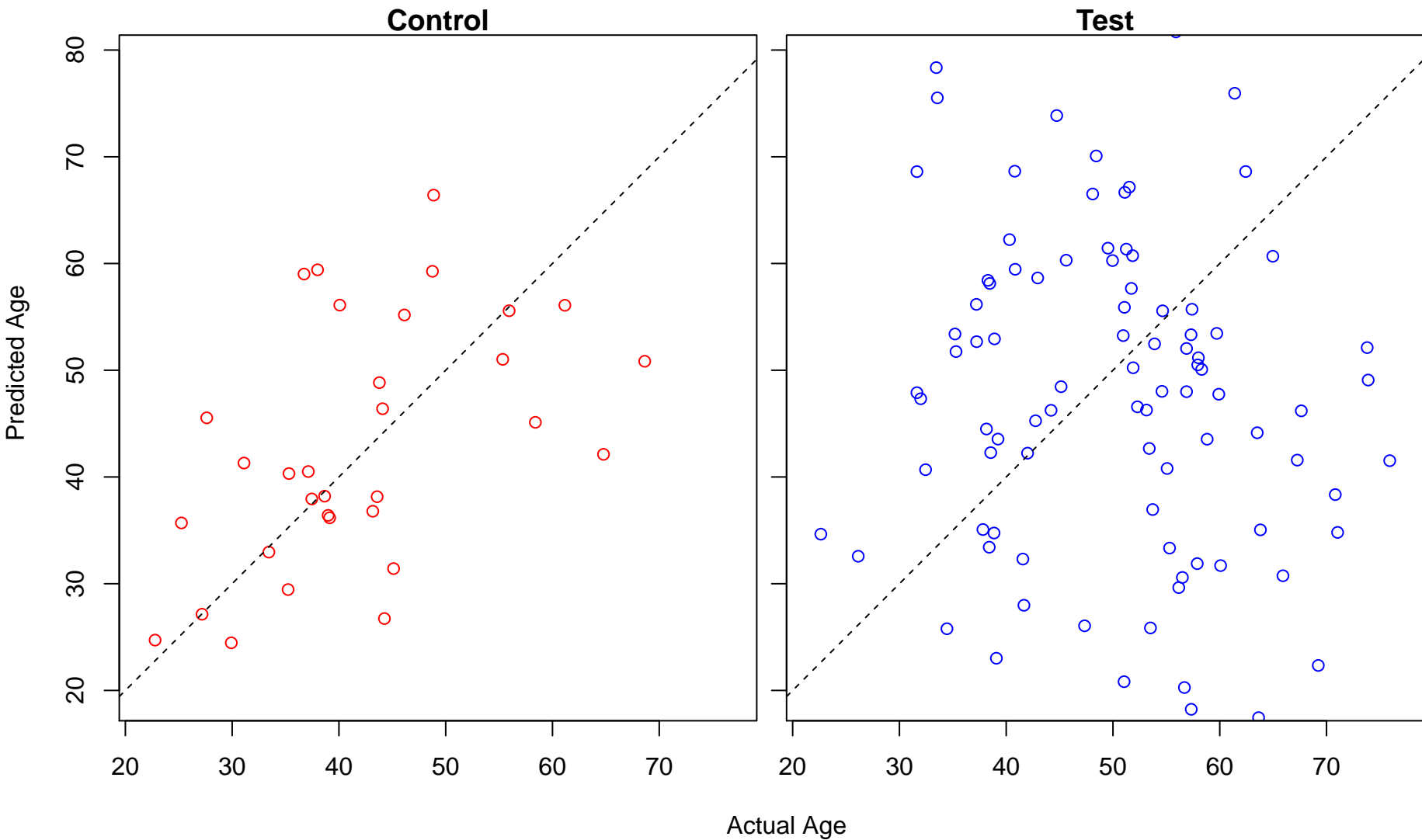
pancreas development (Score: 1.067965)



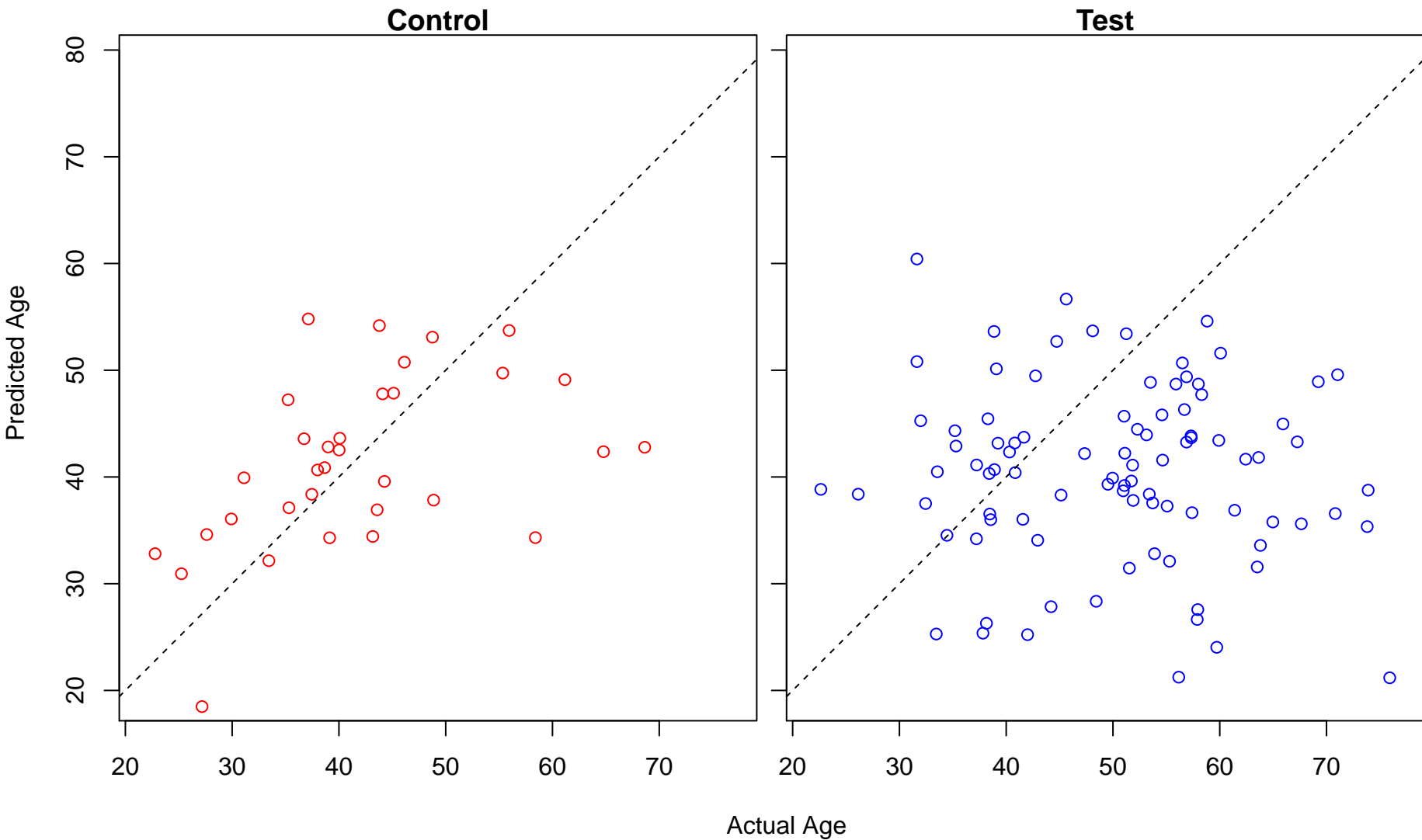
negative regulation of histone acetylation (Score: 1.067835)



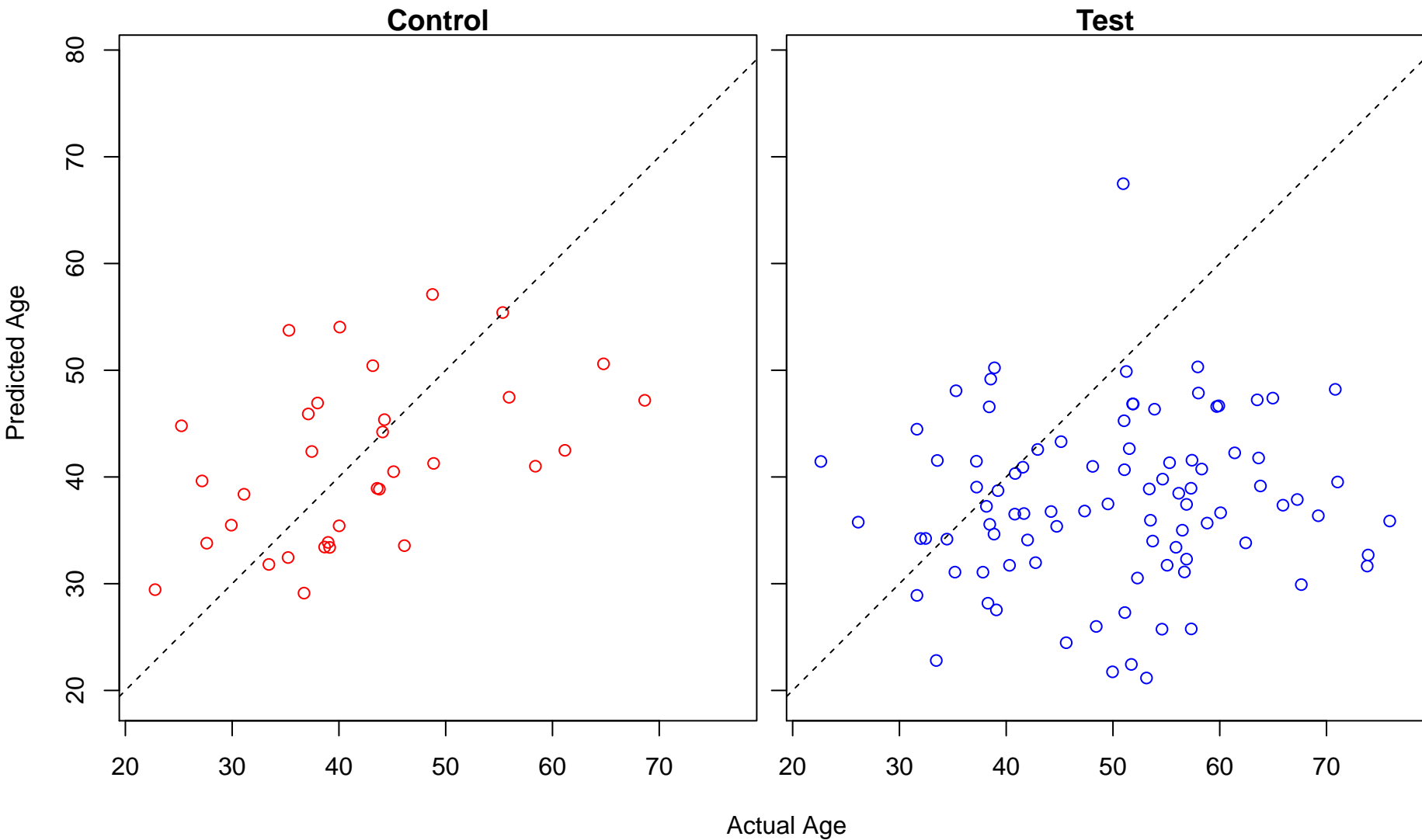
epithelial cell proliferation (Score: 1.065879)



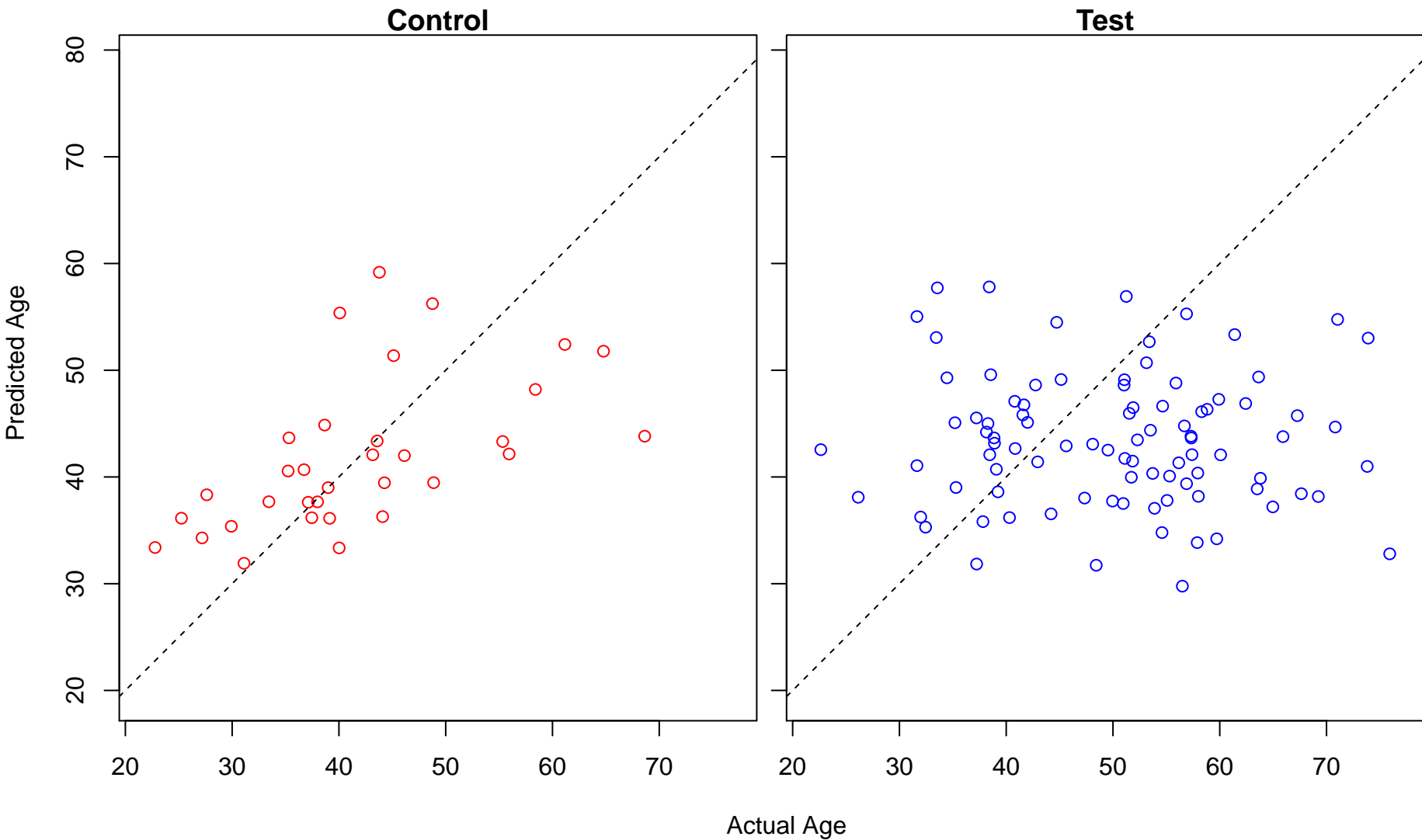
regulation of striated muscle contraction (Score: 1.065566)



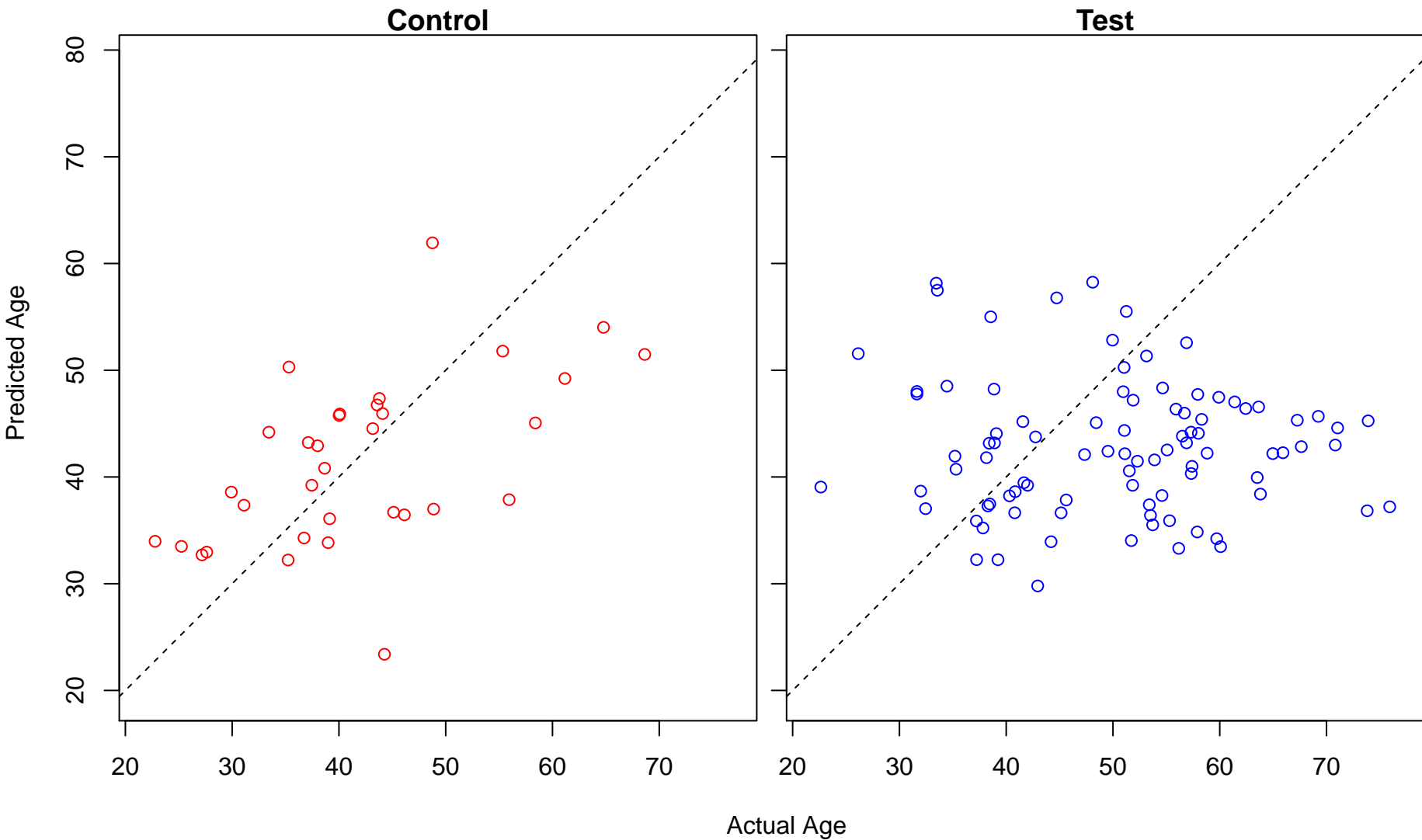
response to X-ray (Score: 1.064935)



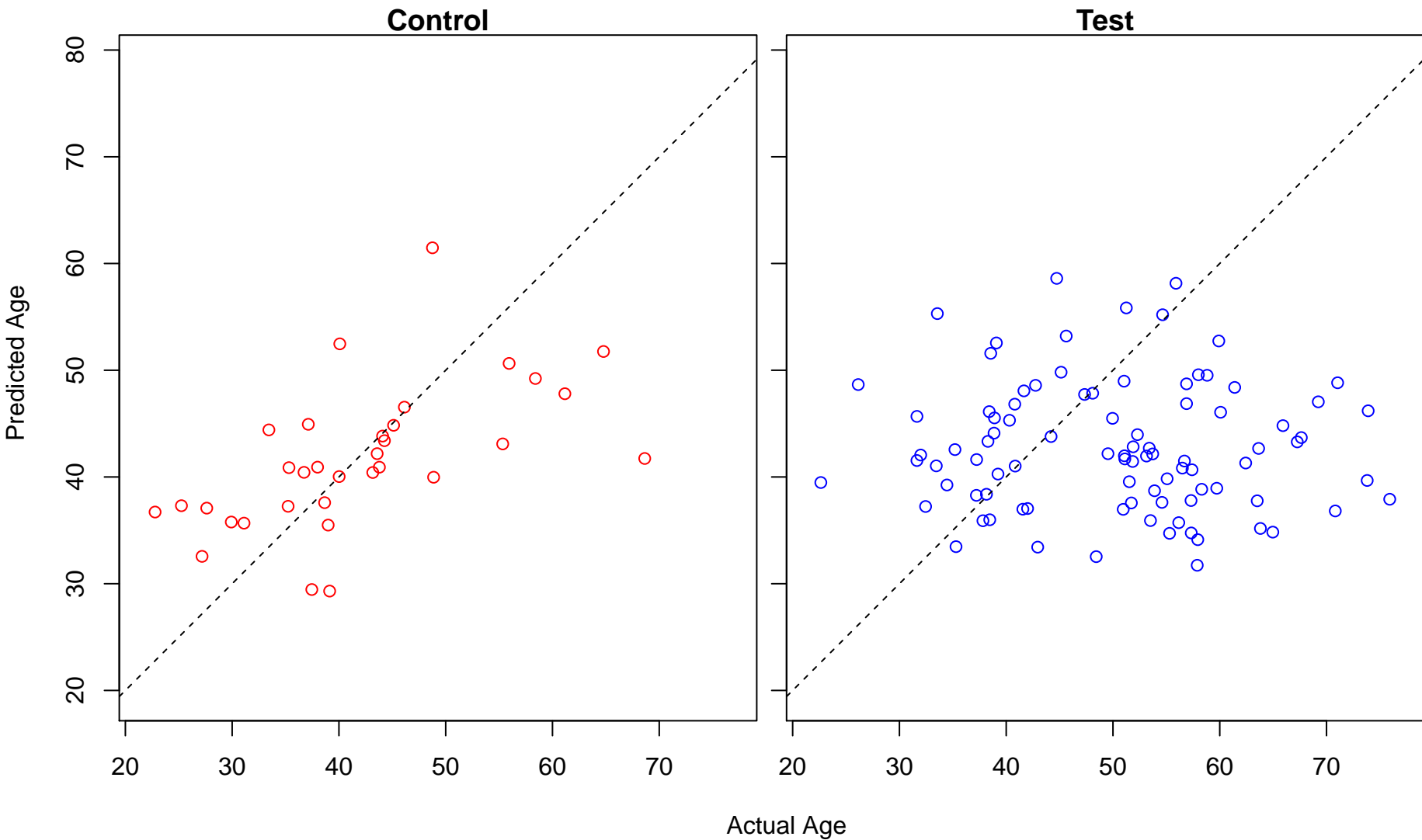
ethanolamine-containing compound metabolic process (Score: 1.063369)



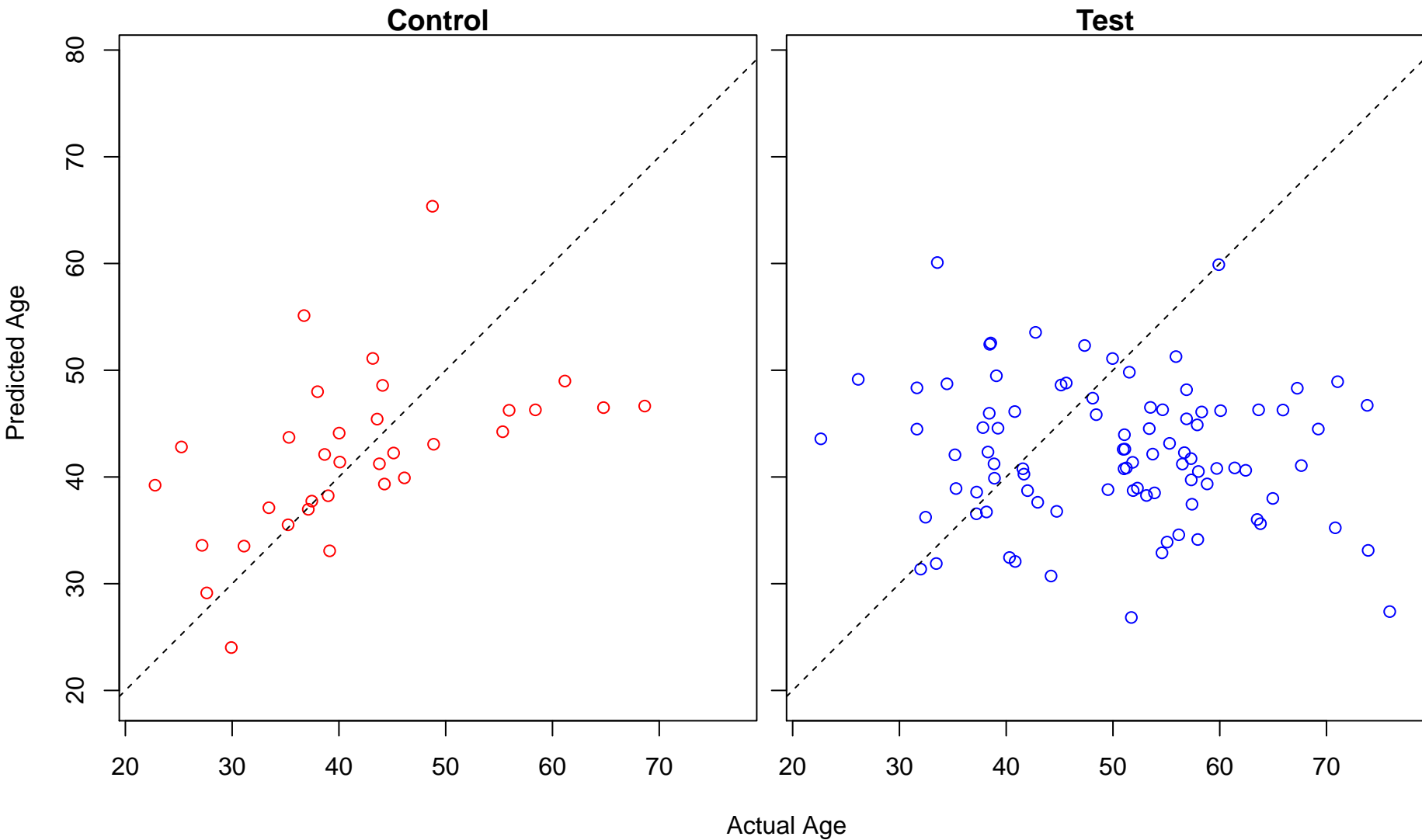
neurotransmitter secretion (Score: 1.061904)



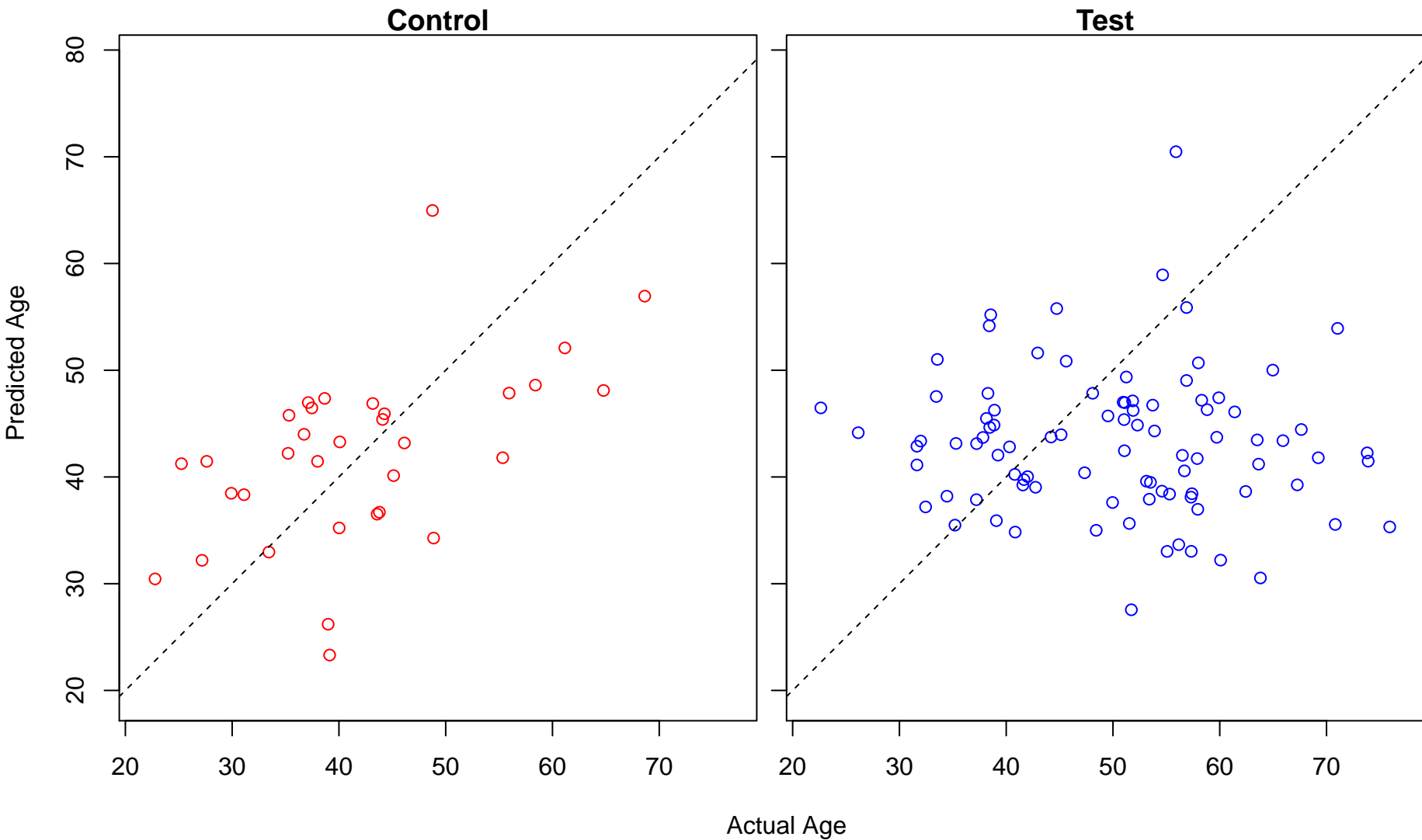
regulation of ion transmembrane transporter activity (Score: 1.061893)



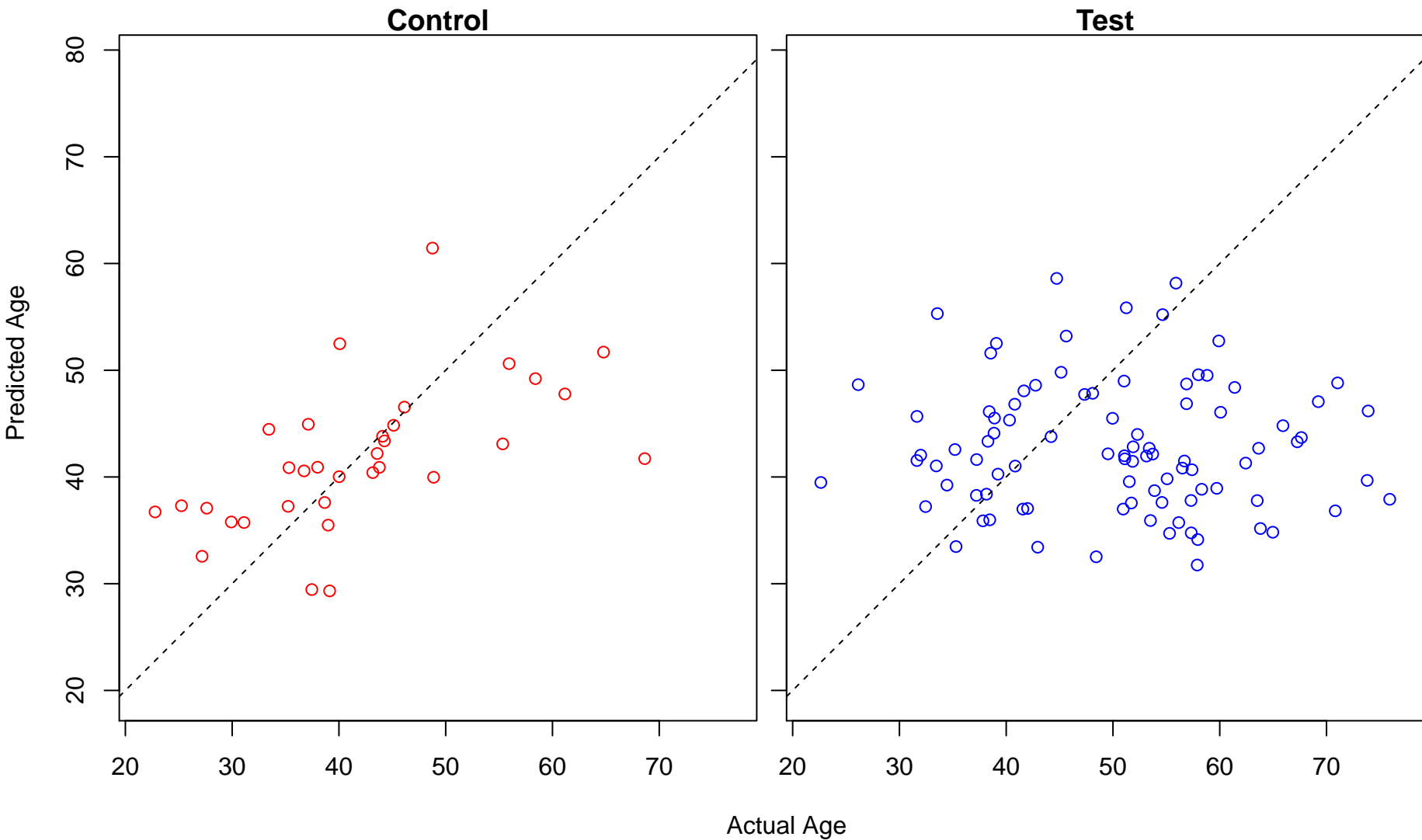
negative regulation of regulatory T cell differentiation (Score: 1.059625)



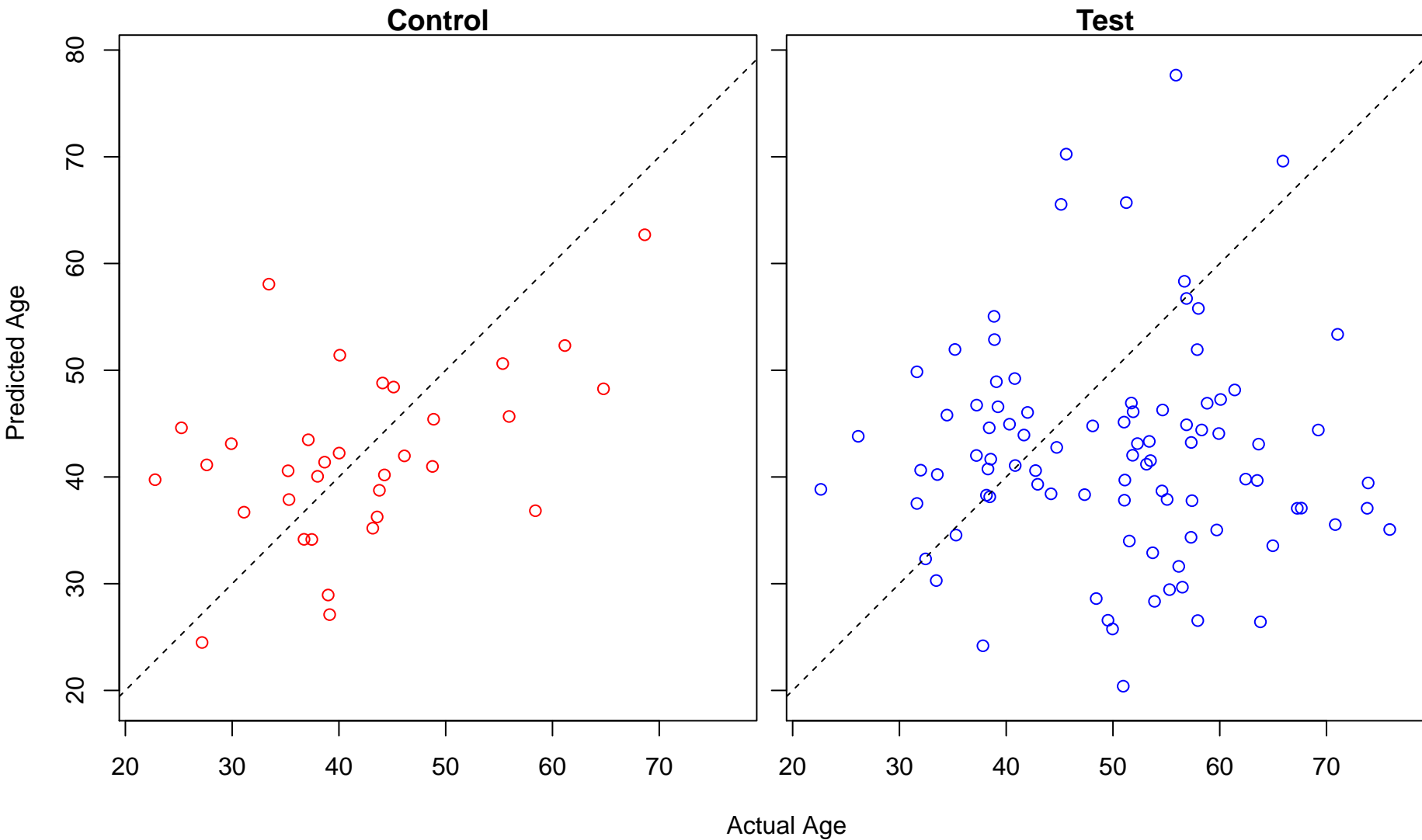
negative regulation of kidney development (Score: 1.059595)



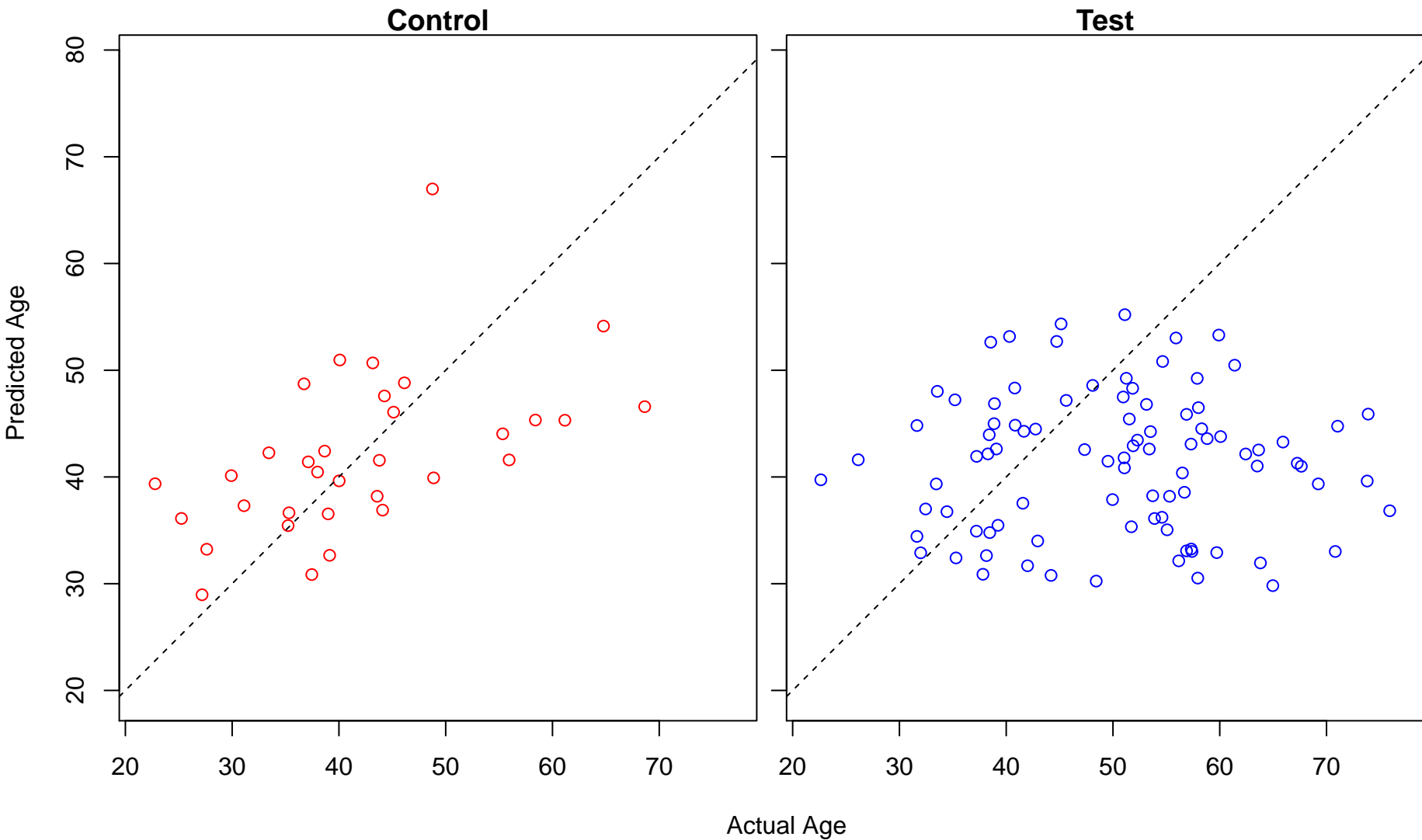
regulation of transmembrane transporter activity (Score: 1.057323)



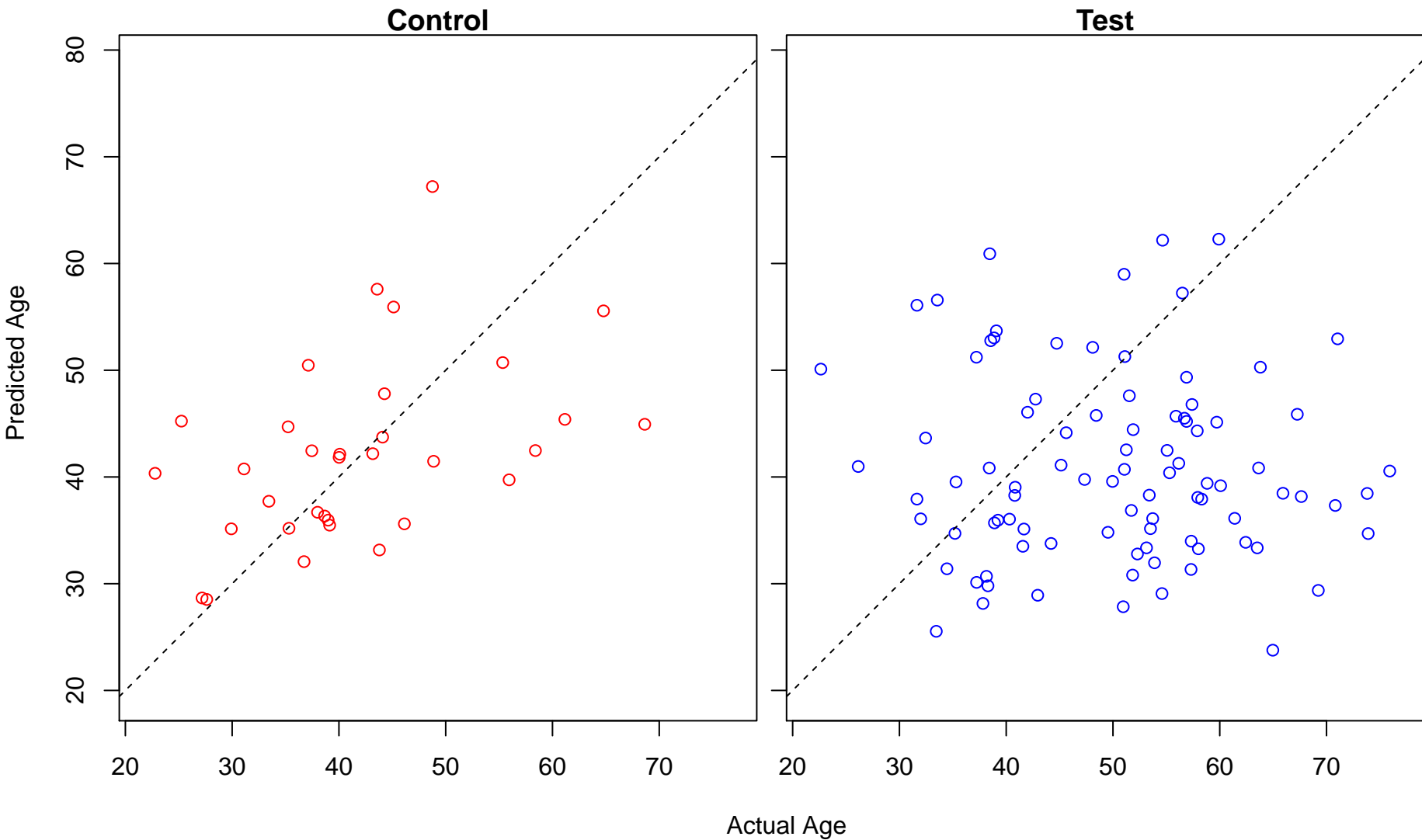
positive regulation of calcium ion import (Score: 1.051366)



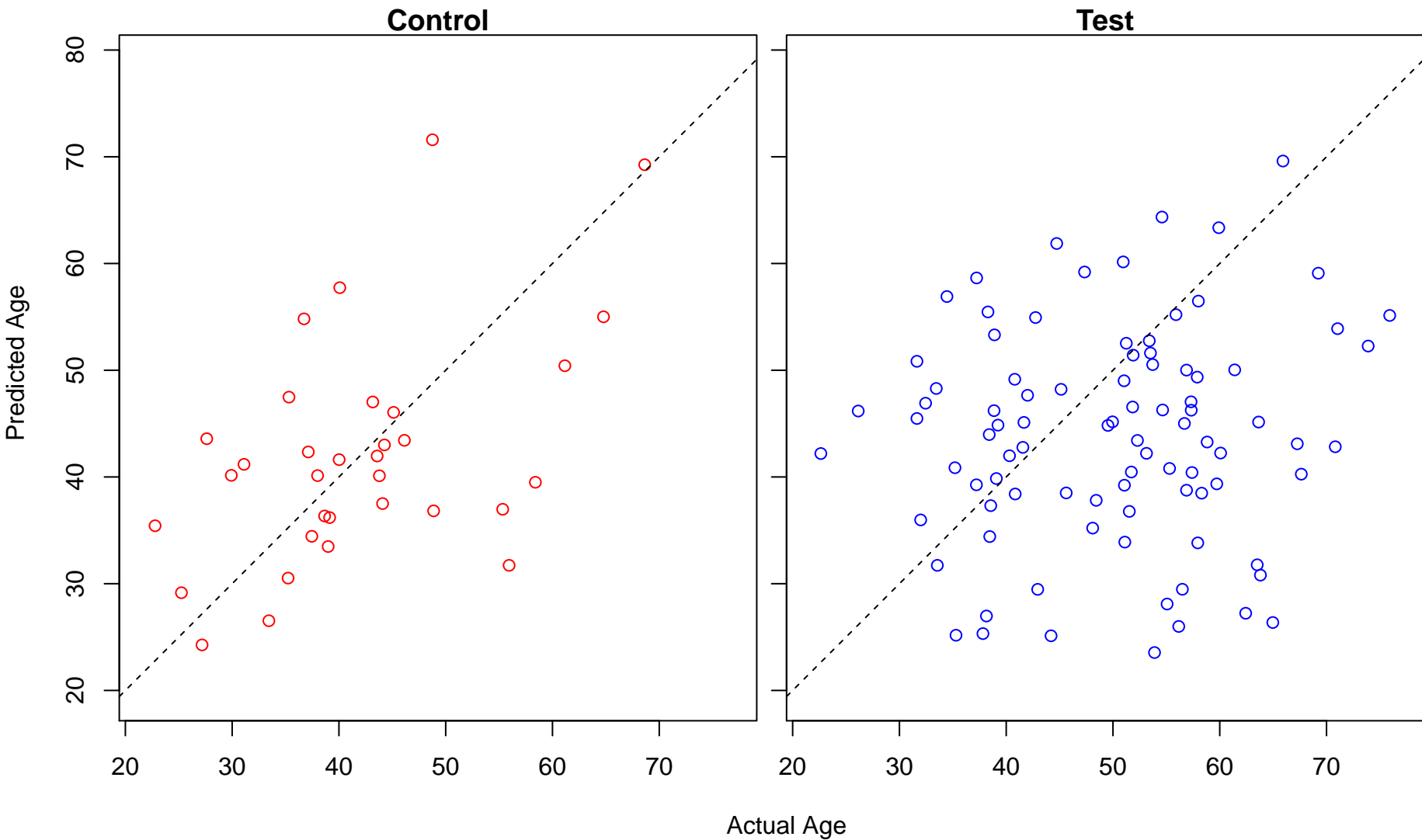
purine deoxyribonucleotide catabolic process (Score: 1.050703)



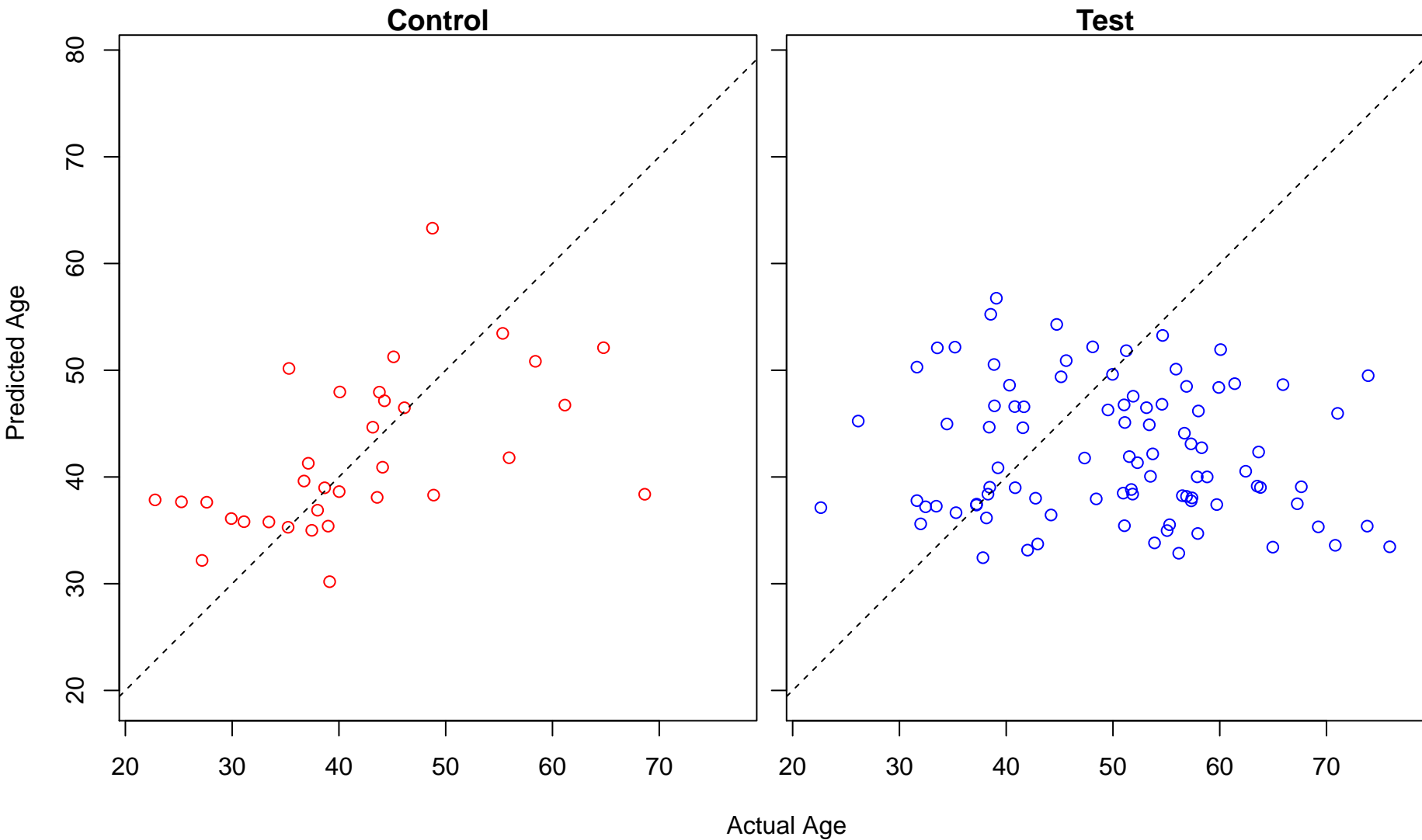
cellular response to prostaglandin E stimulus (Score: 1.050026)



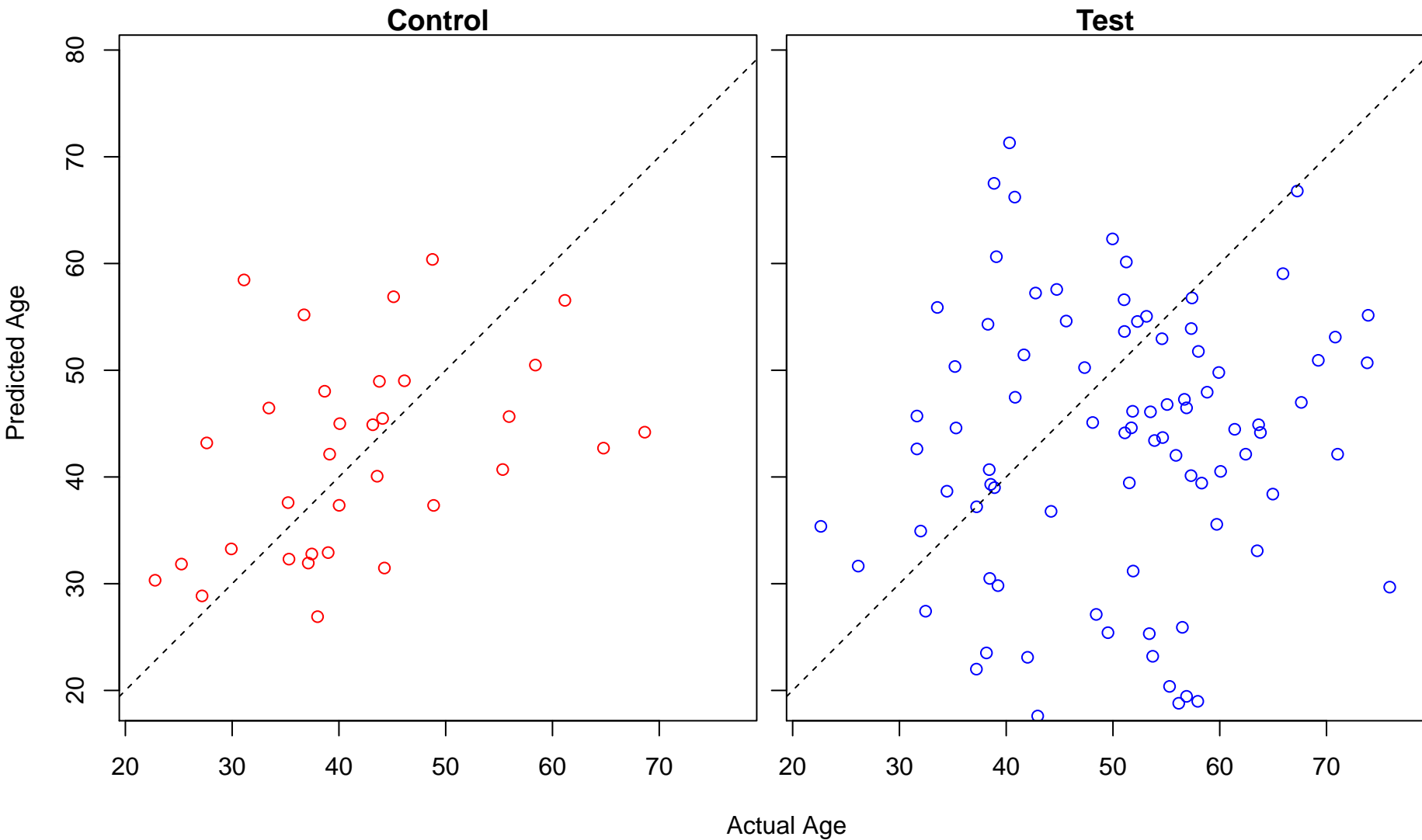
regulation of dephosphorylation (Score: 1.049062)



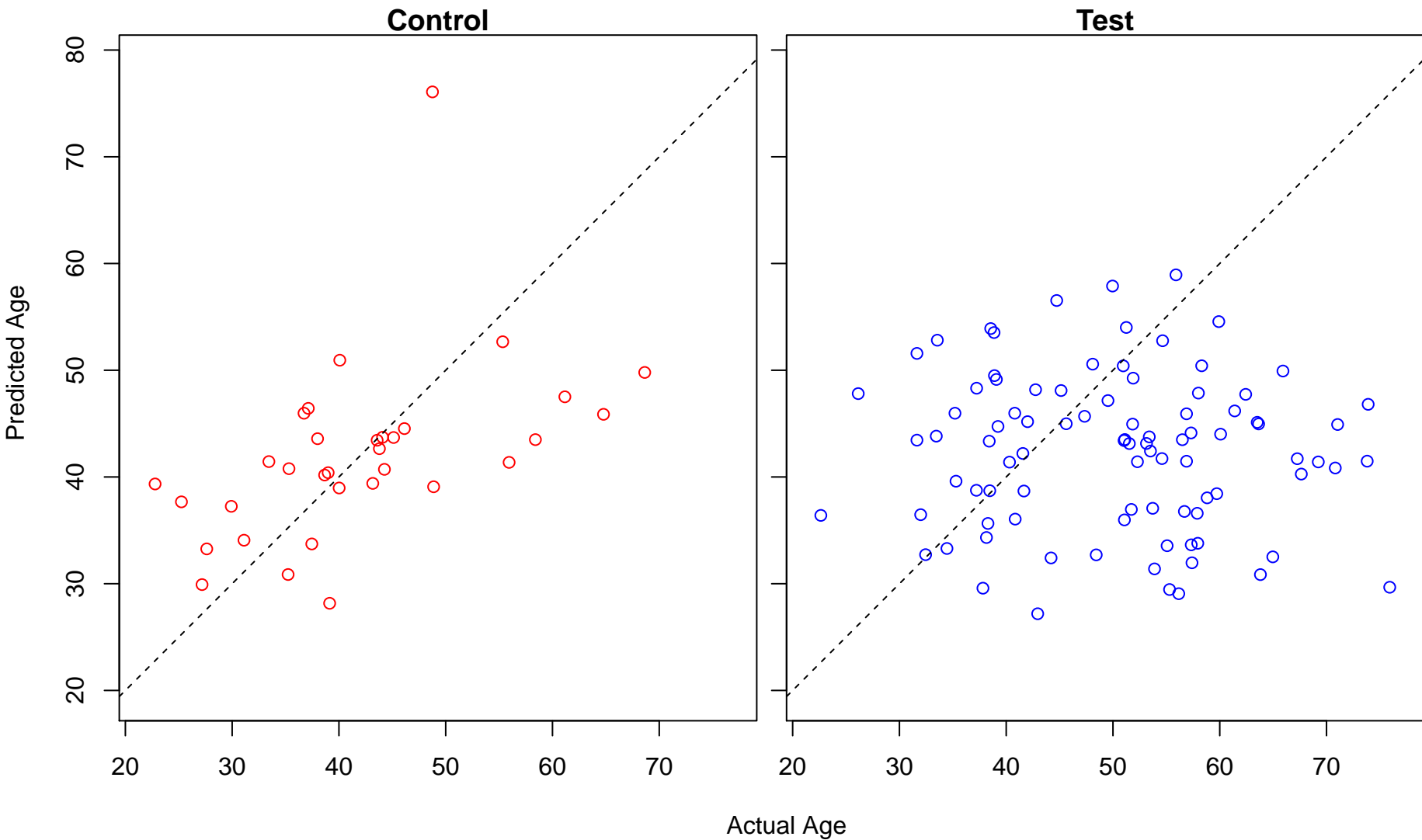
positive regulation of angiogenesis (Score: 1.048971)



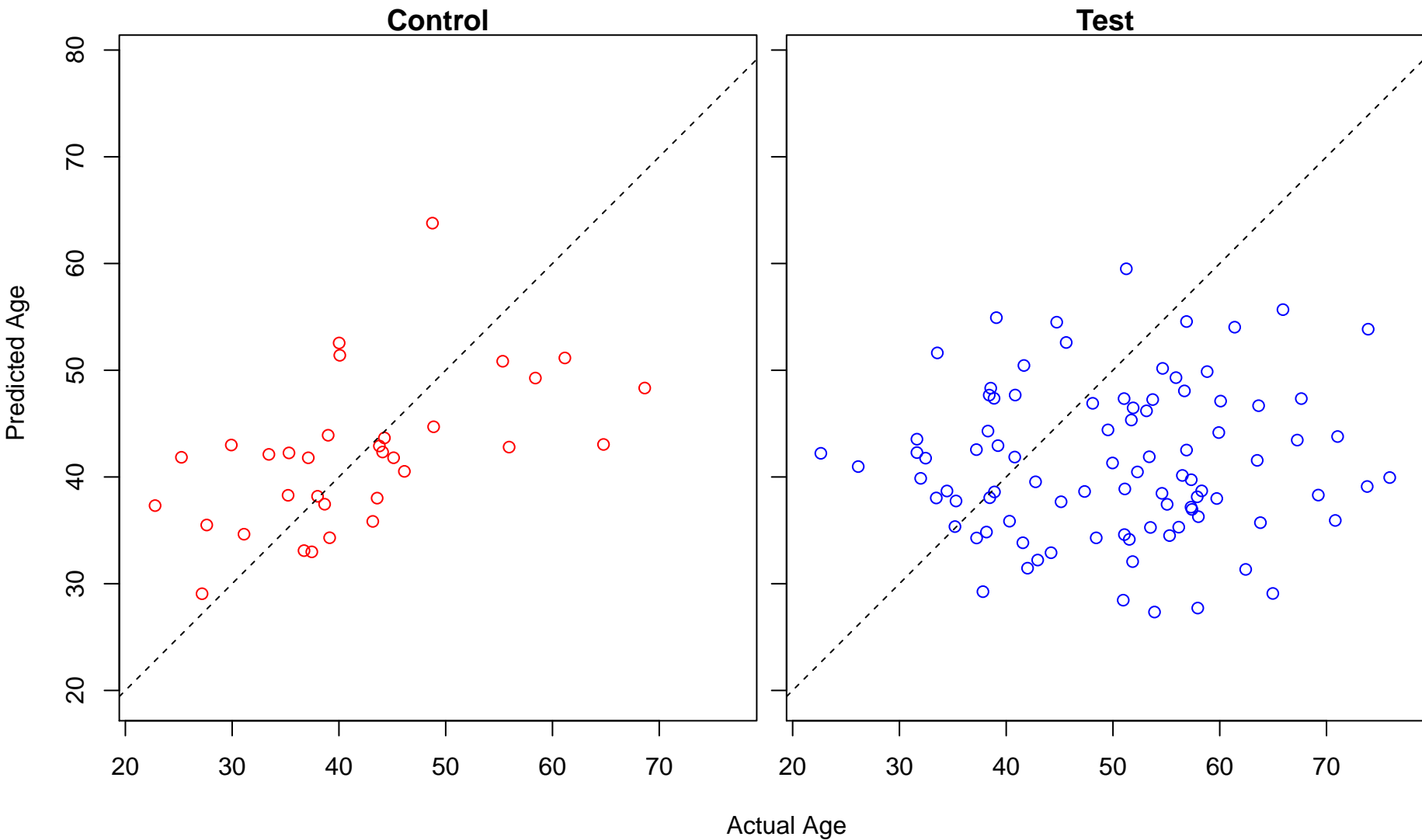
regulation of action potential (Score: 1.048086)



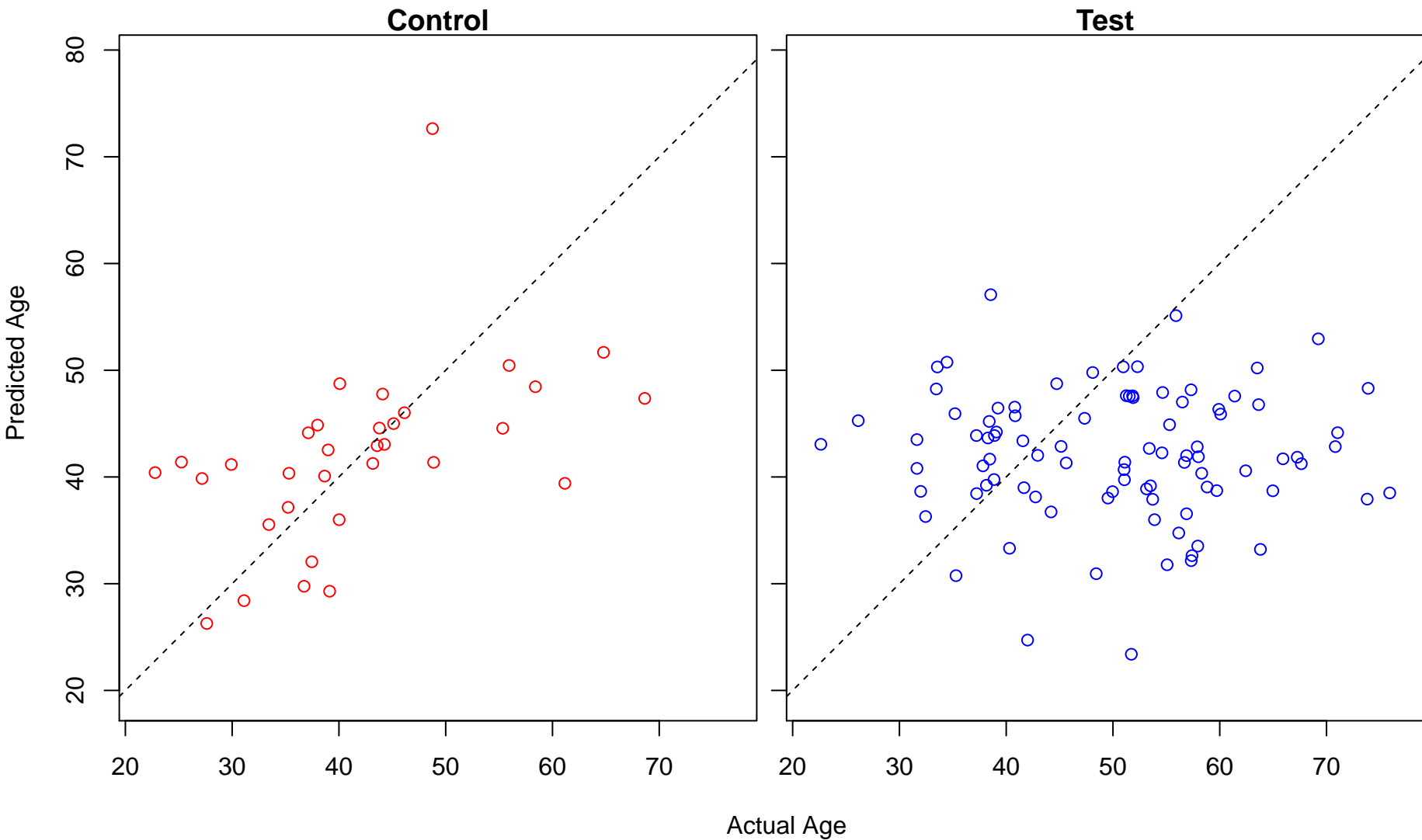
response to abiotic stimulus (Score: 1.045185)



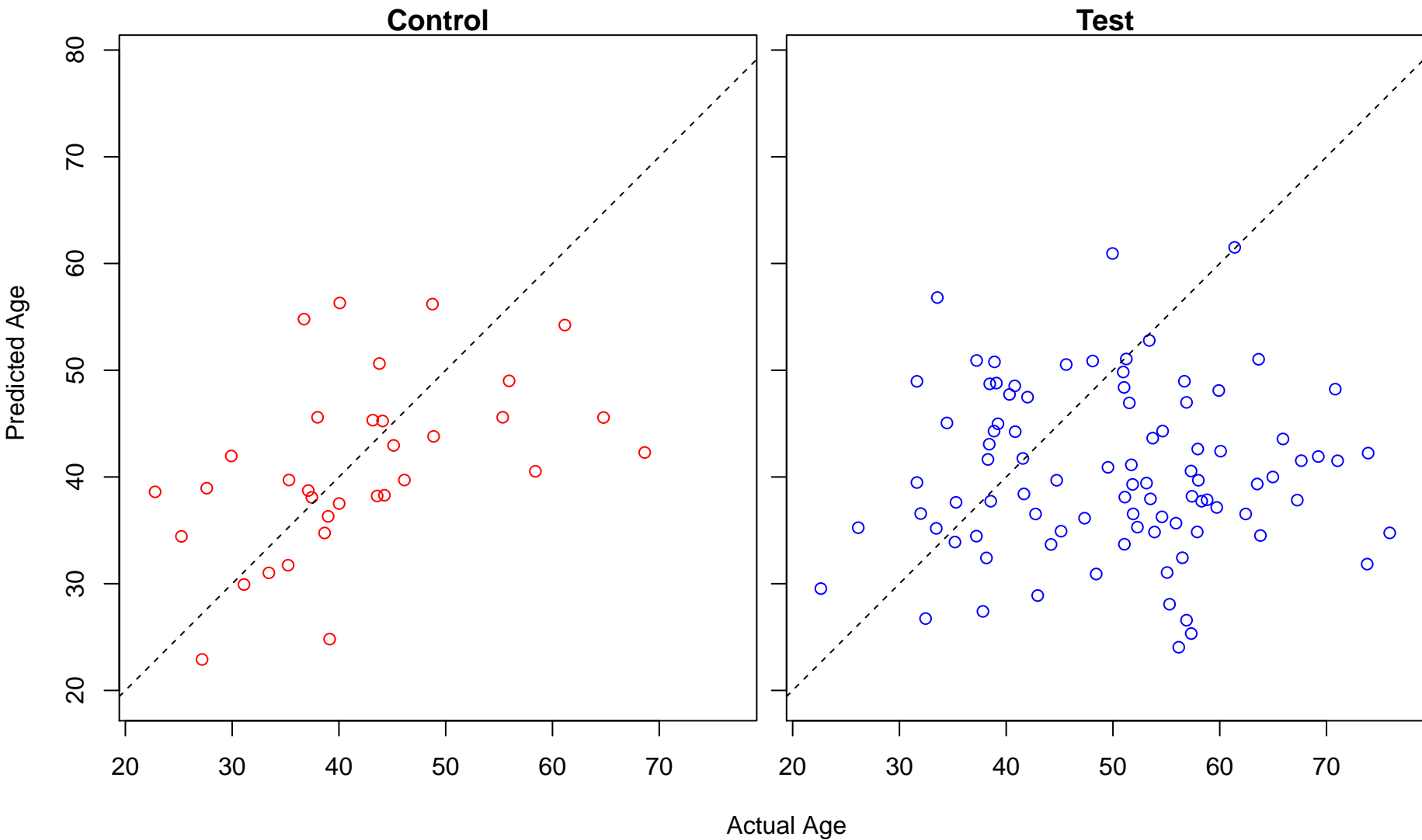
intra-Golgi vesicle-mediated transport (Score: 1.040611)



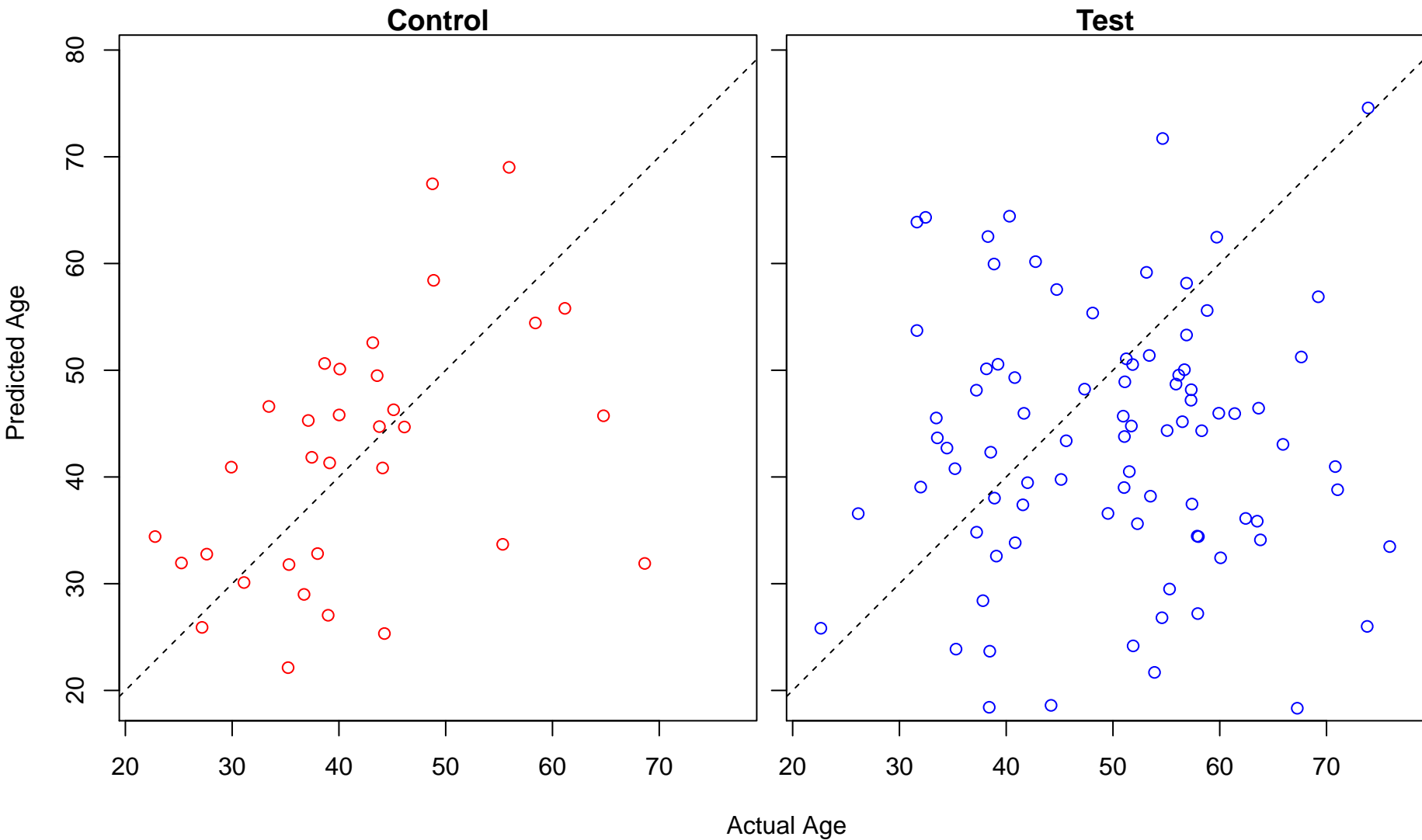
positive regulation of hormone biosynthetic process (Score: 1.037750)



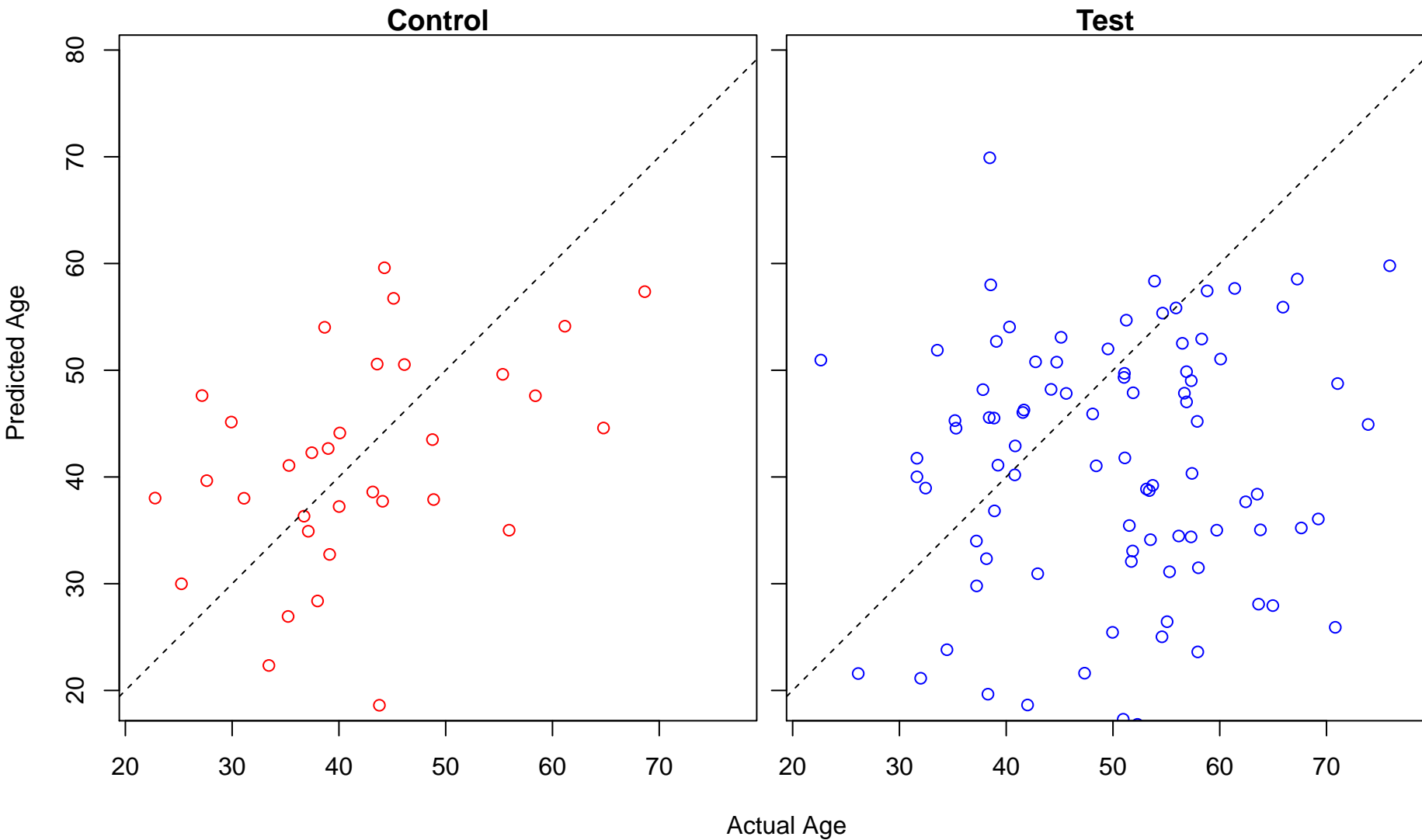
protein oligomerization (Score: 1.037088)



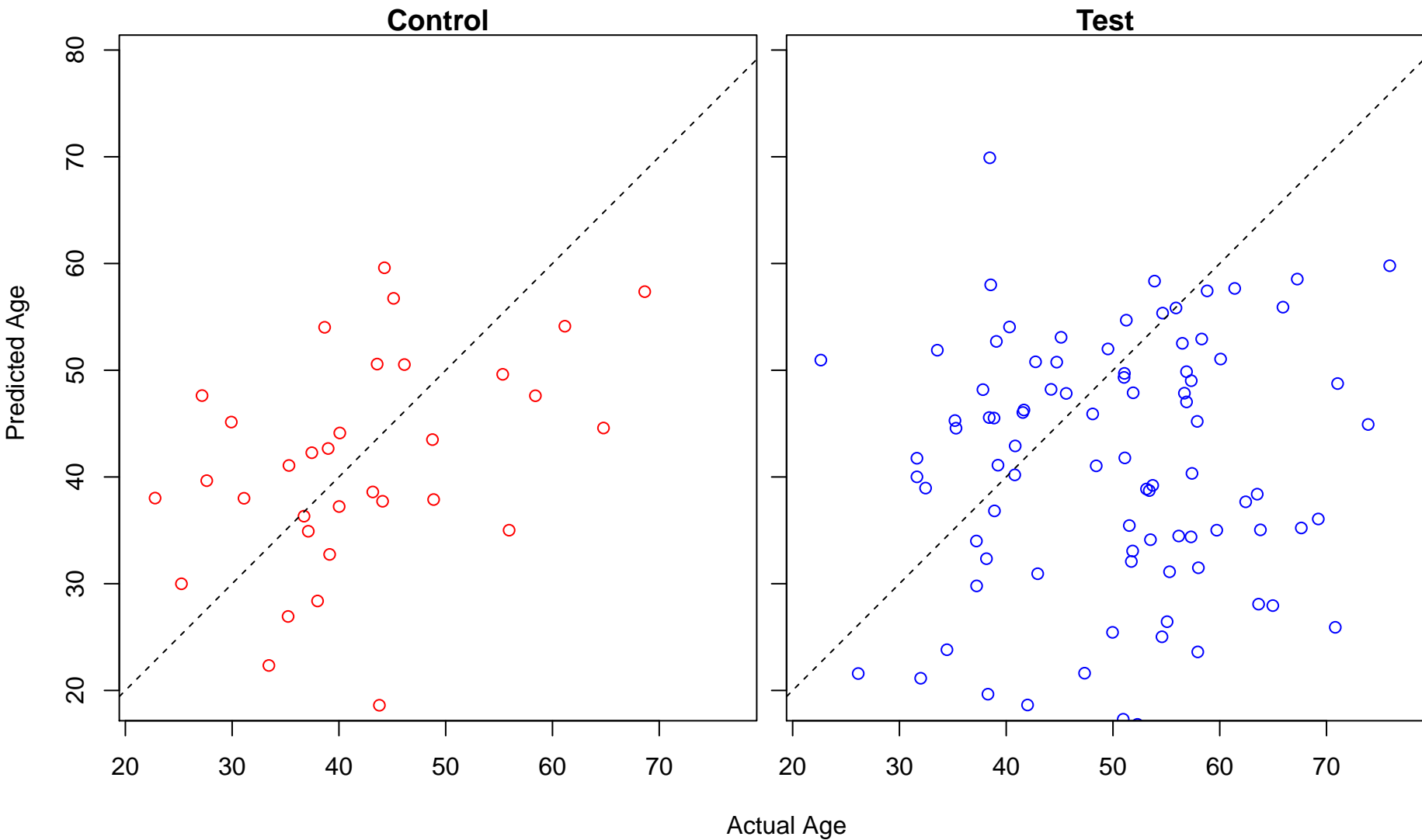
regulation of platelet activation (Score: 1.036978)



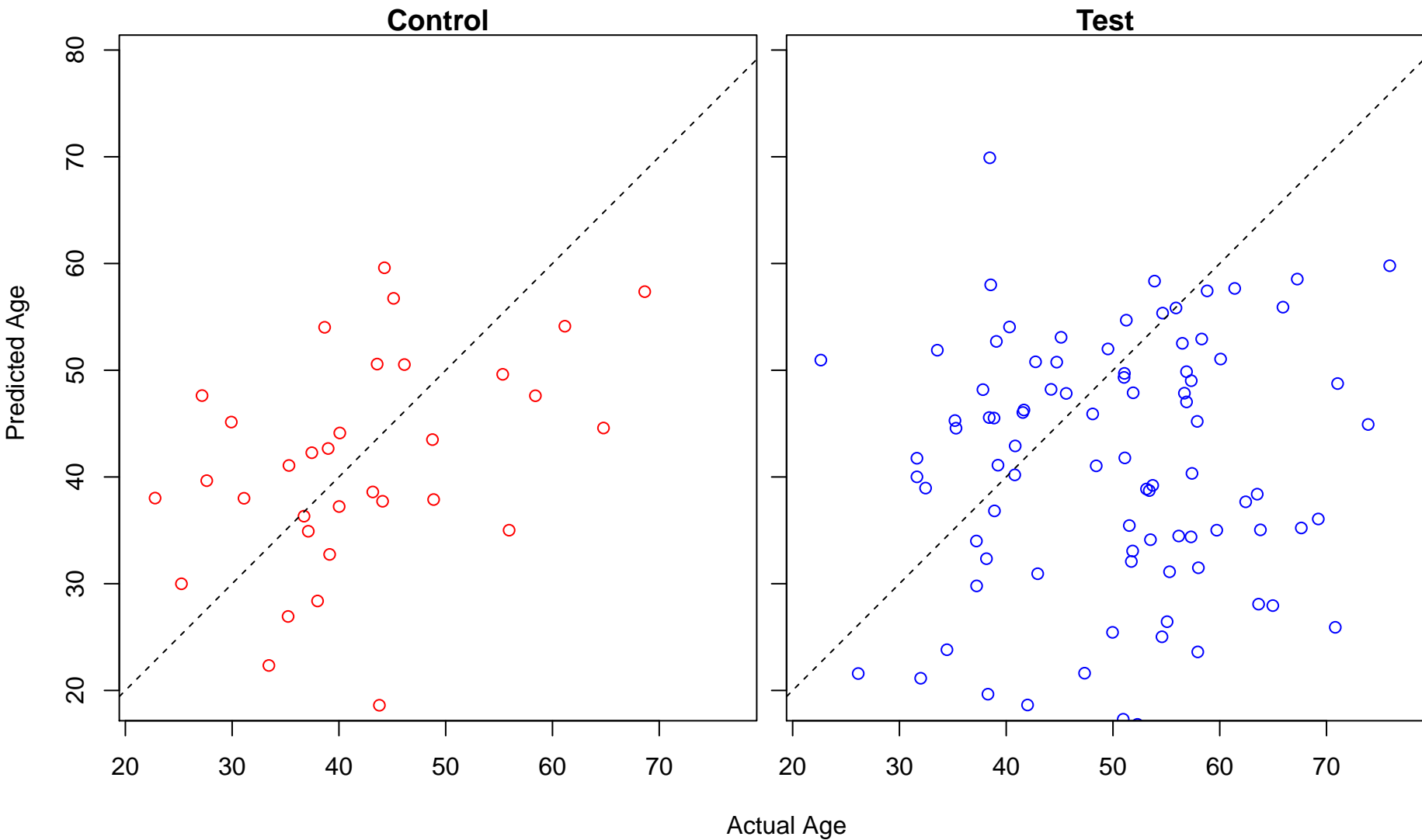
alpha-beta T cell activation involved in immune response (Score: 1.032813)



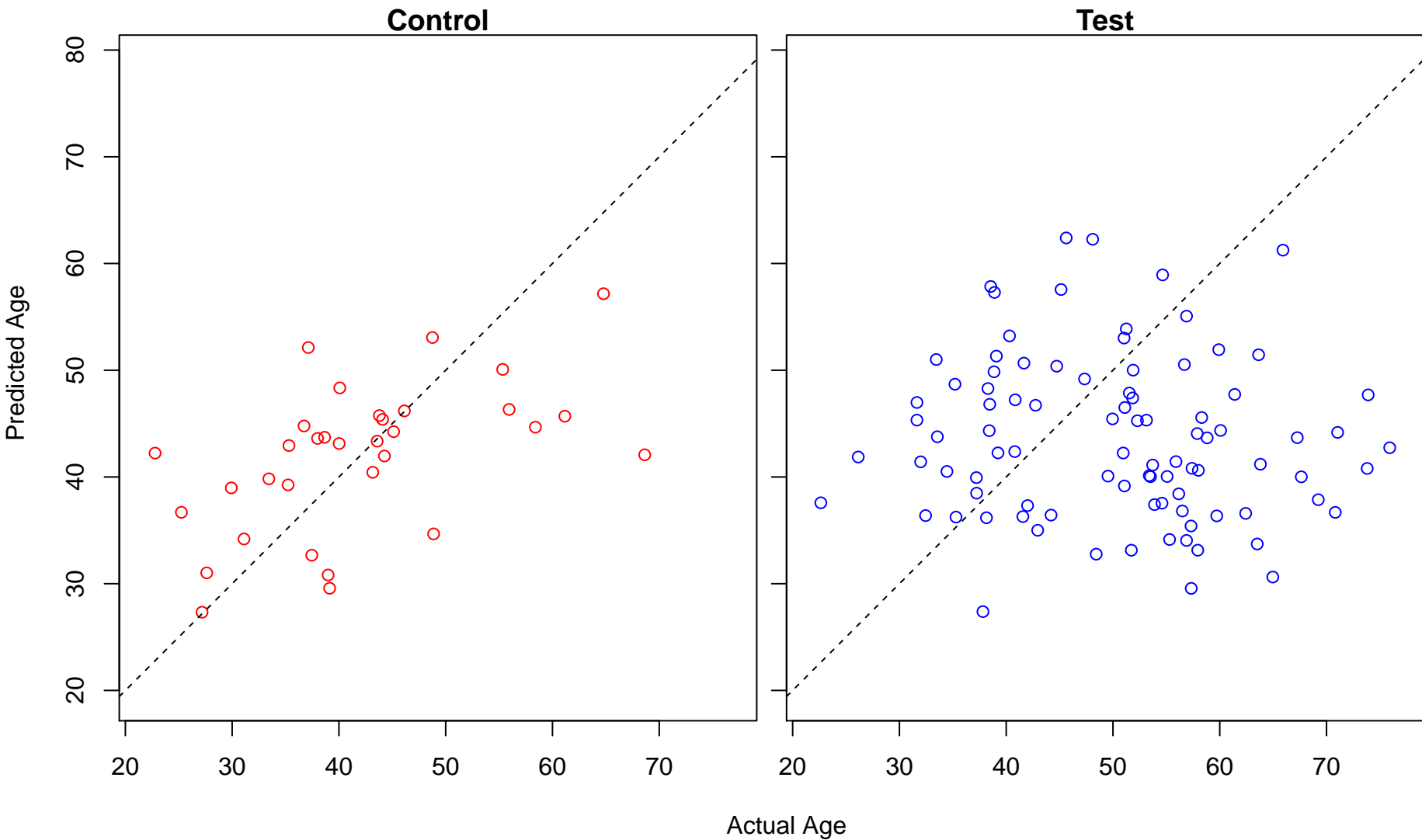
T cell differentiation involved in immune response (Score: 1.032813)



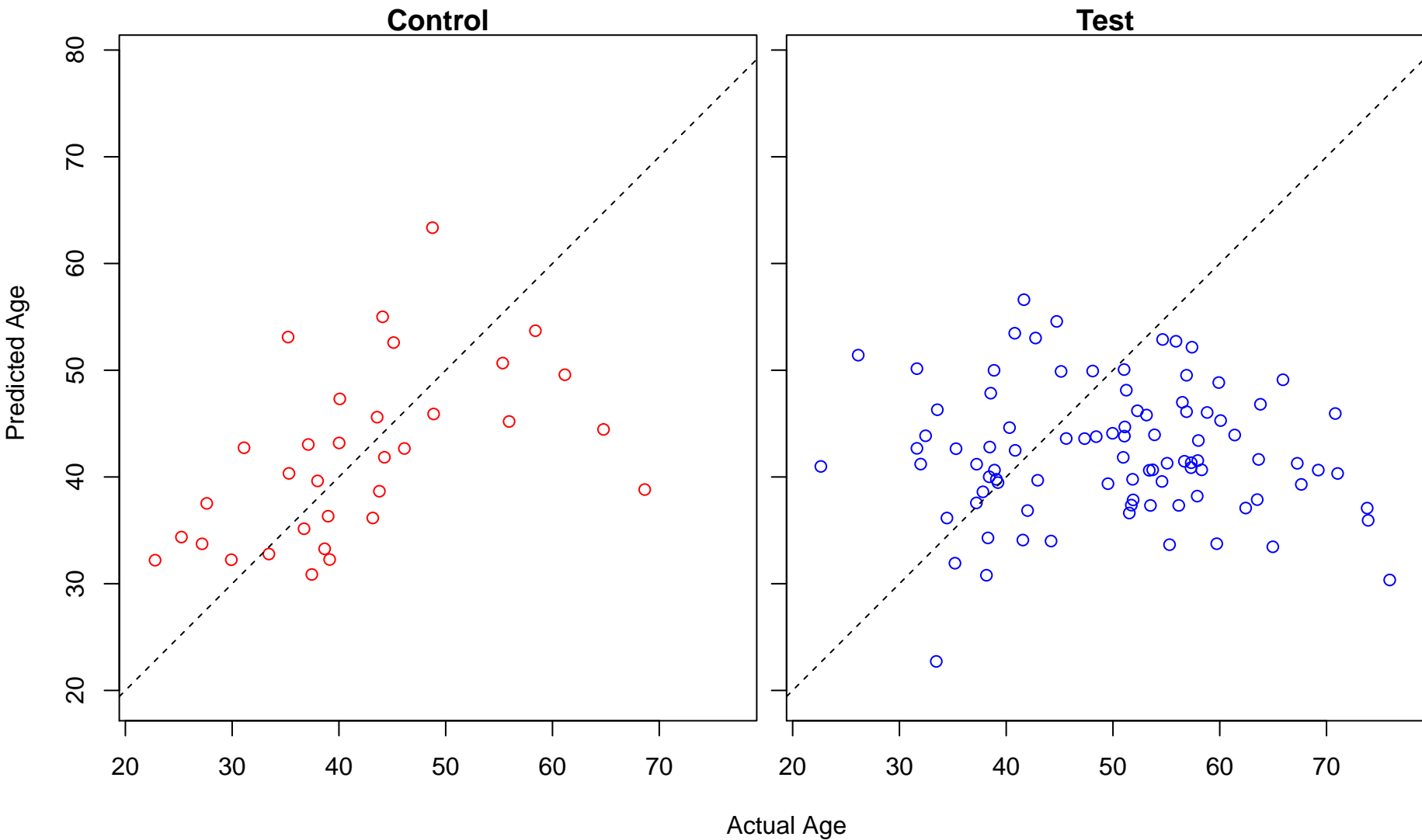
alpha-beta T cell differentiation involved in immune response (Score: 1.032813)



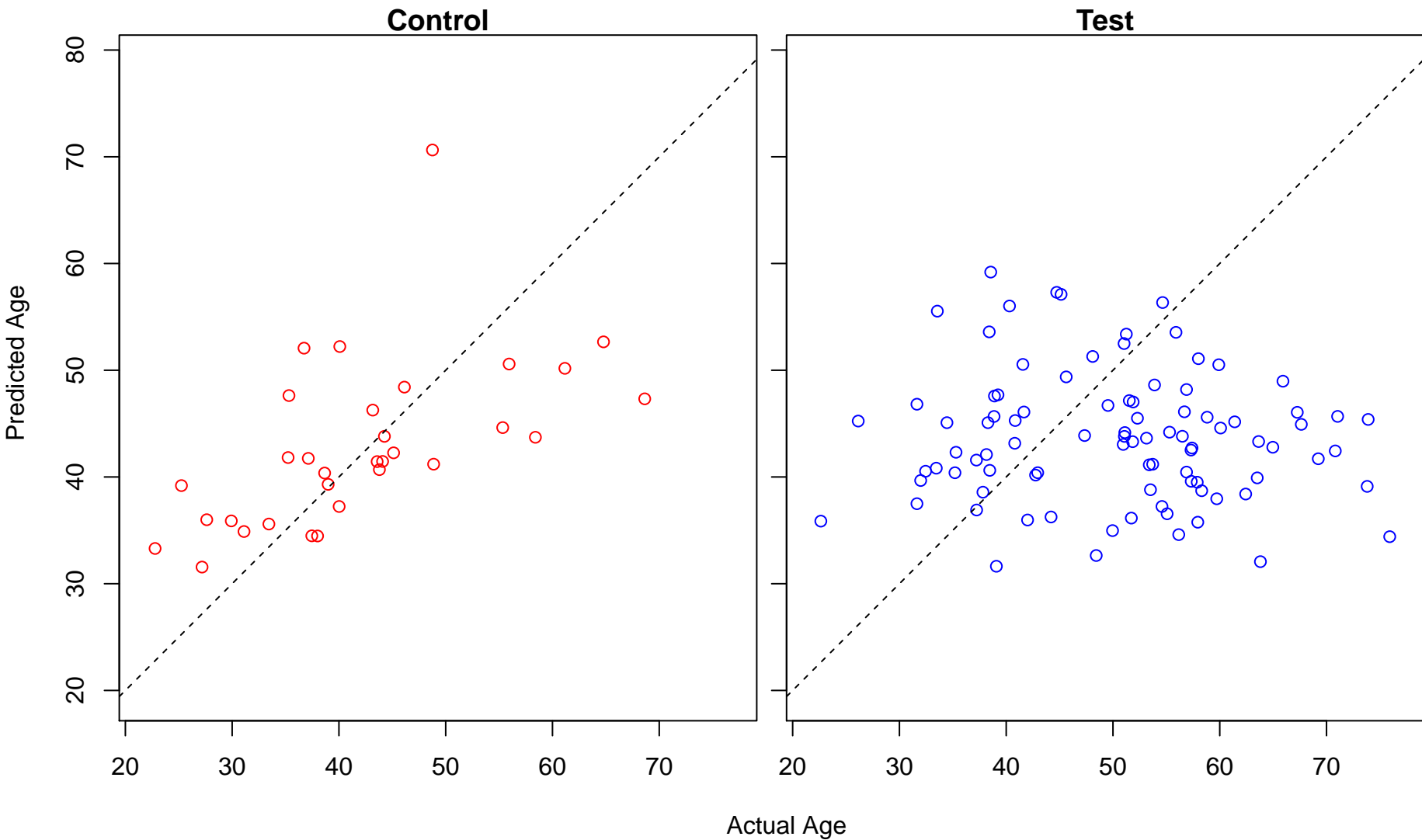
cytoplasmic sequestering of transcription factor (Score: 1.032734)



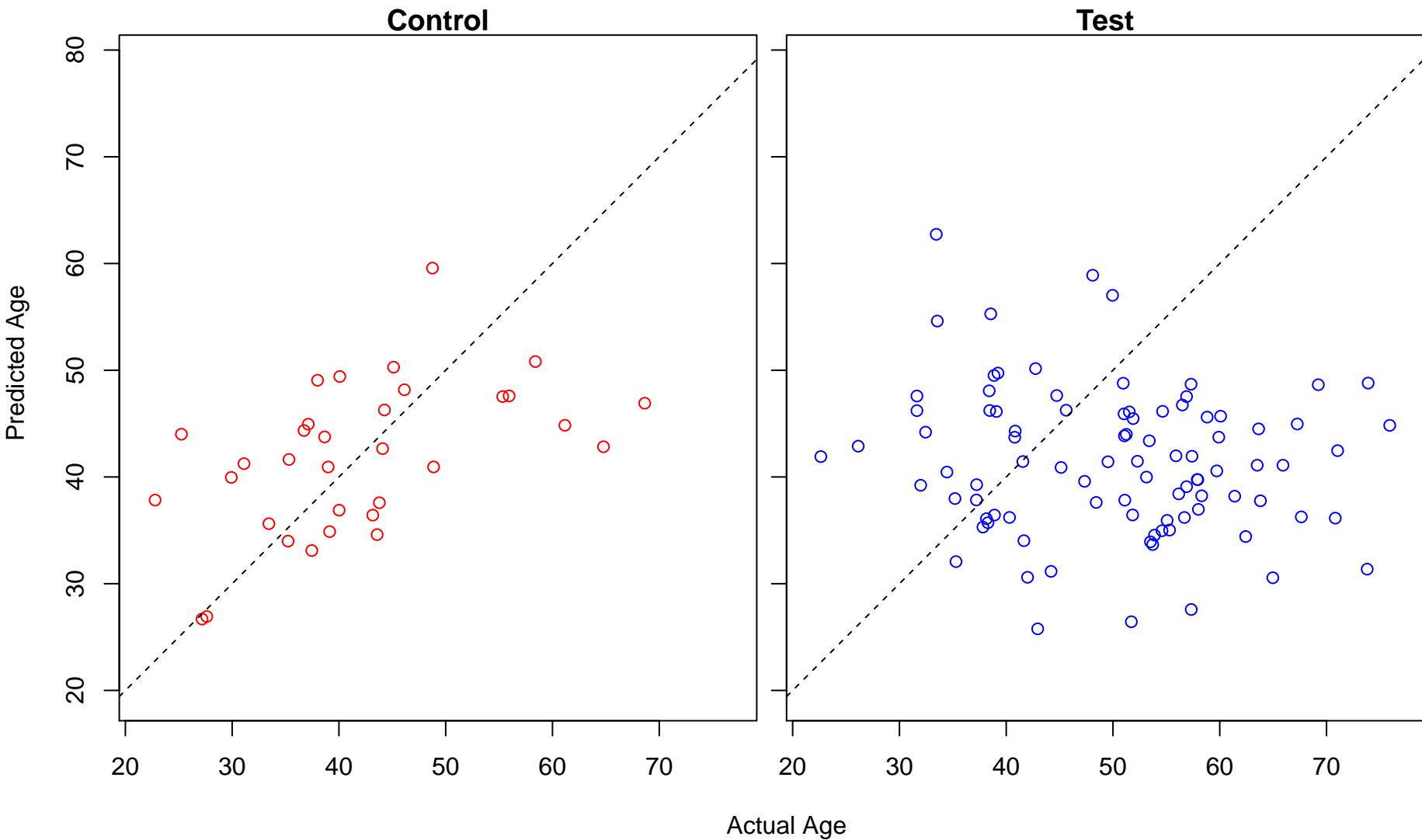
regulation of heart rate (Score: 1.030557)



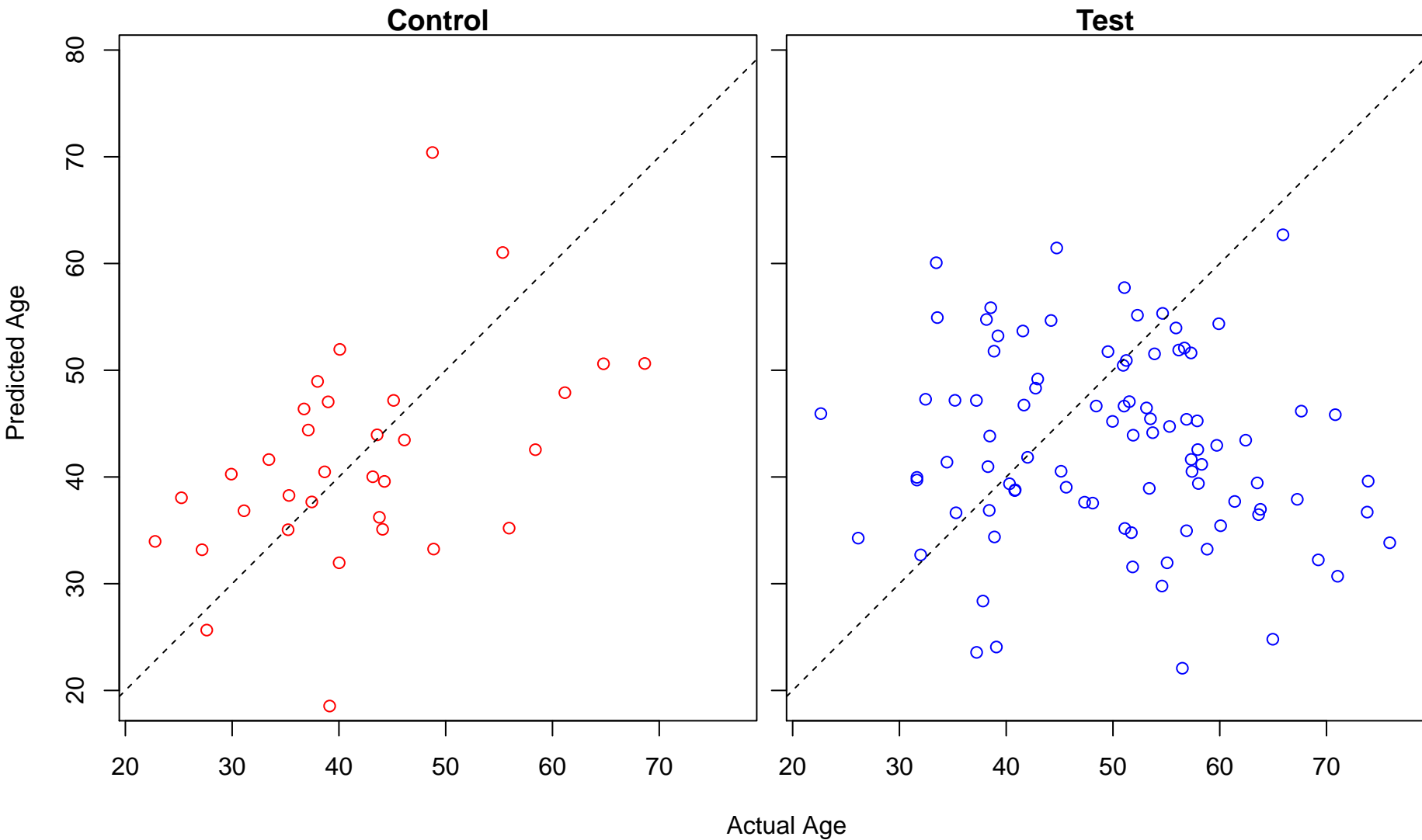
regulation of energy homeostasis (Score: 1.030397)



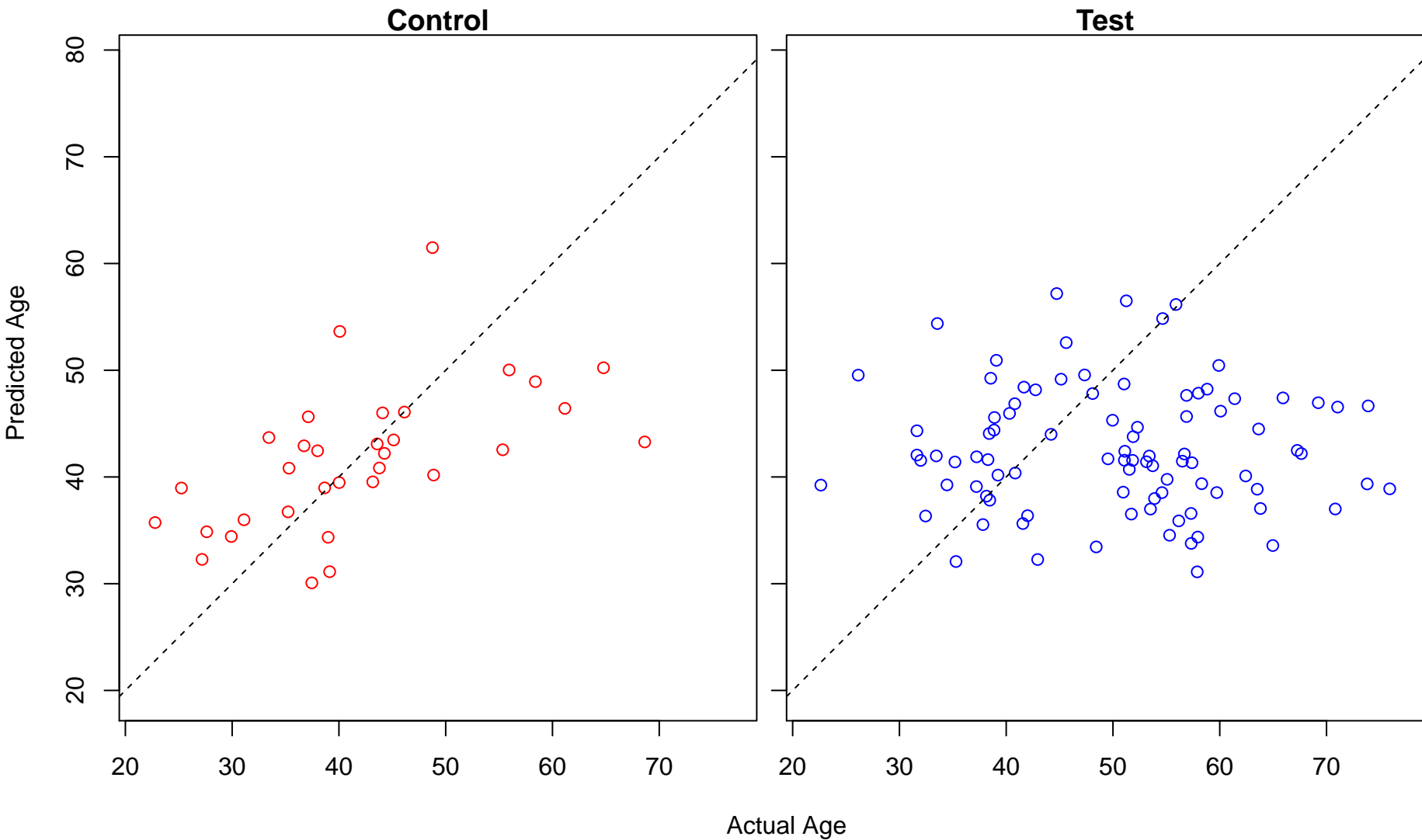
regulation of inclusion body assembly (Score: 1.030108)



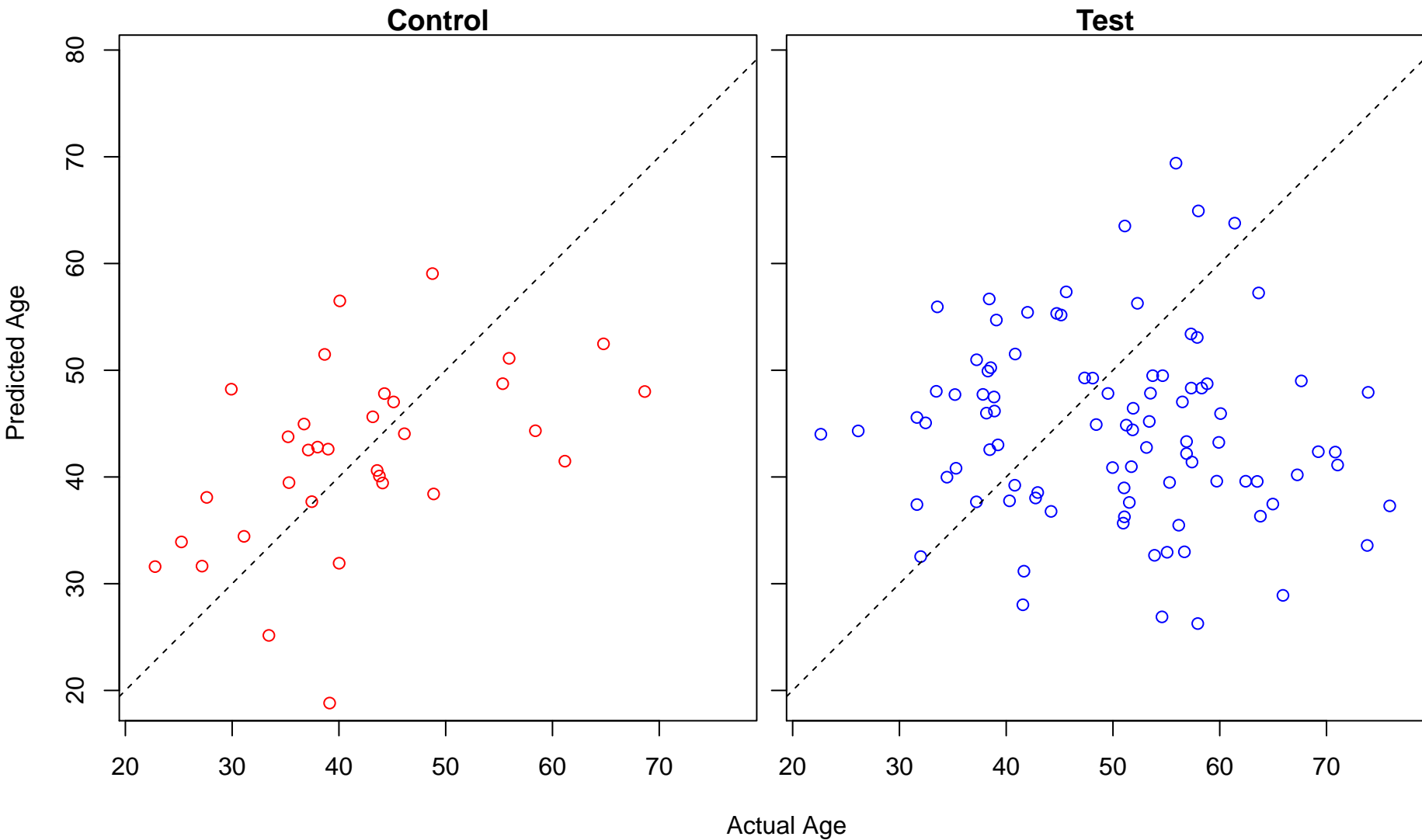
signal transduction involved in mitotic cell cycle checkpoint (Score: 1.029155)



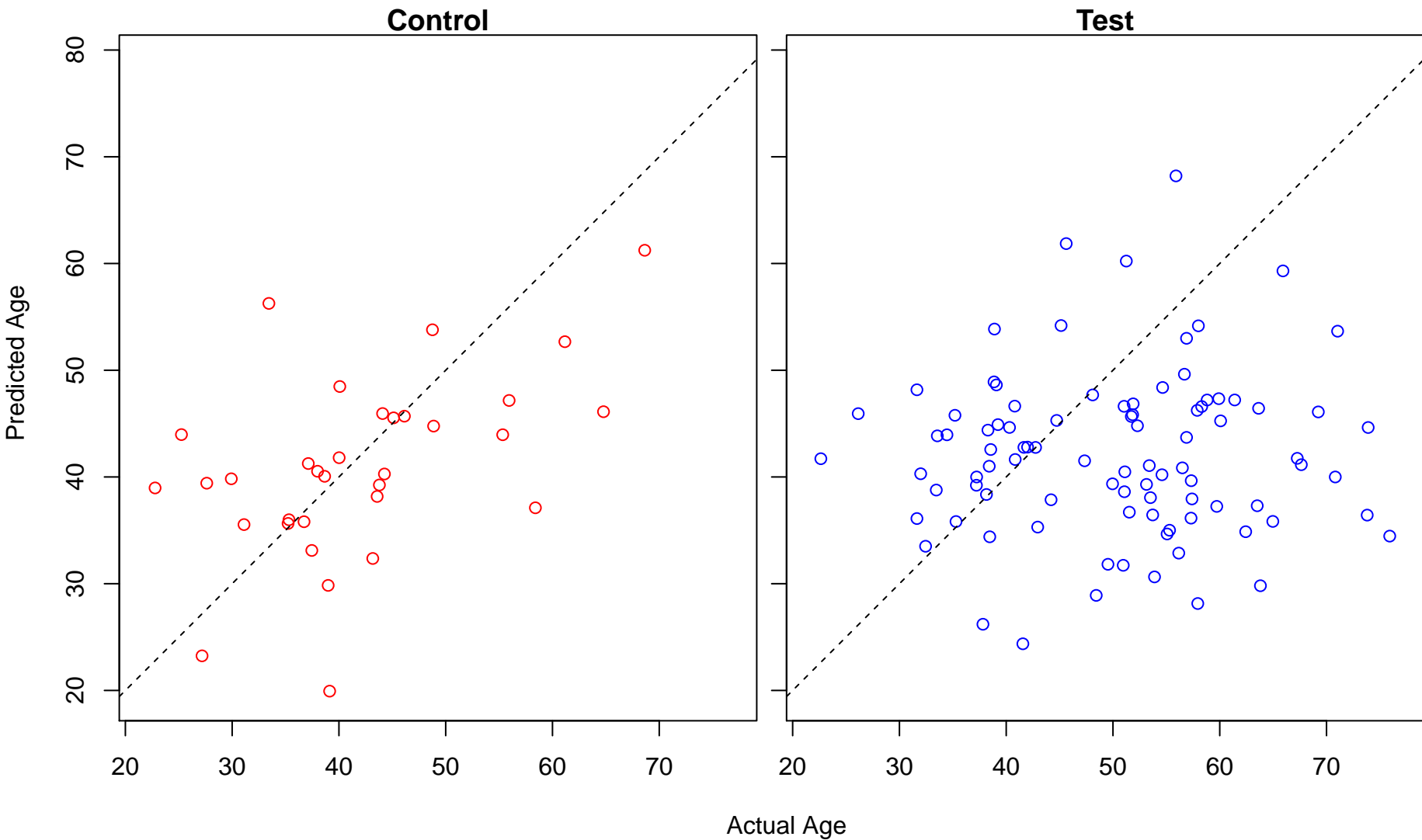
regulation of transporter activity (Score: 1.027964)



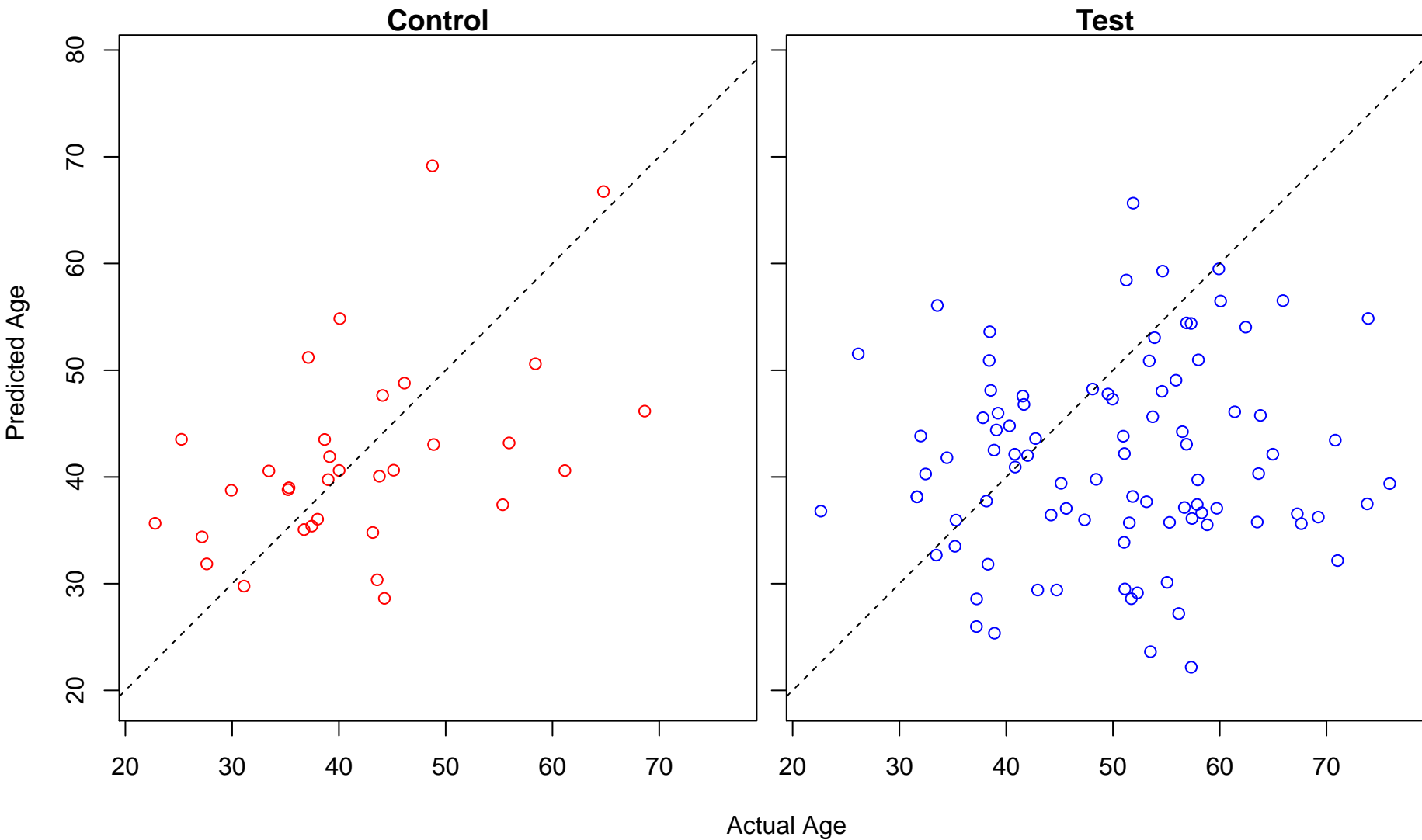
negative regulation of interleukin-6 production (Score: 1.022873)



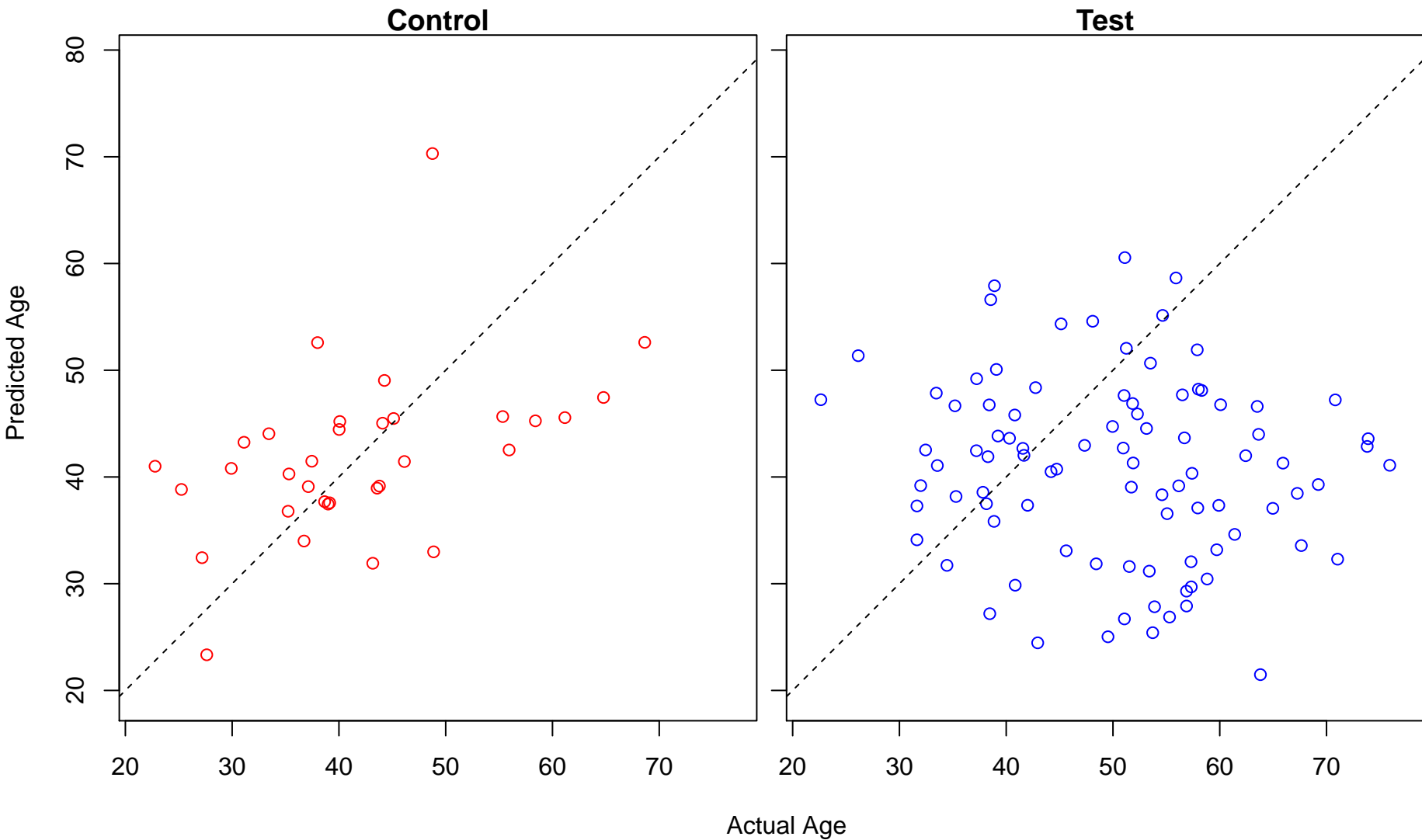
regulation of calcium ion import (Score: 1.020313)



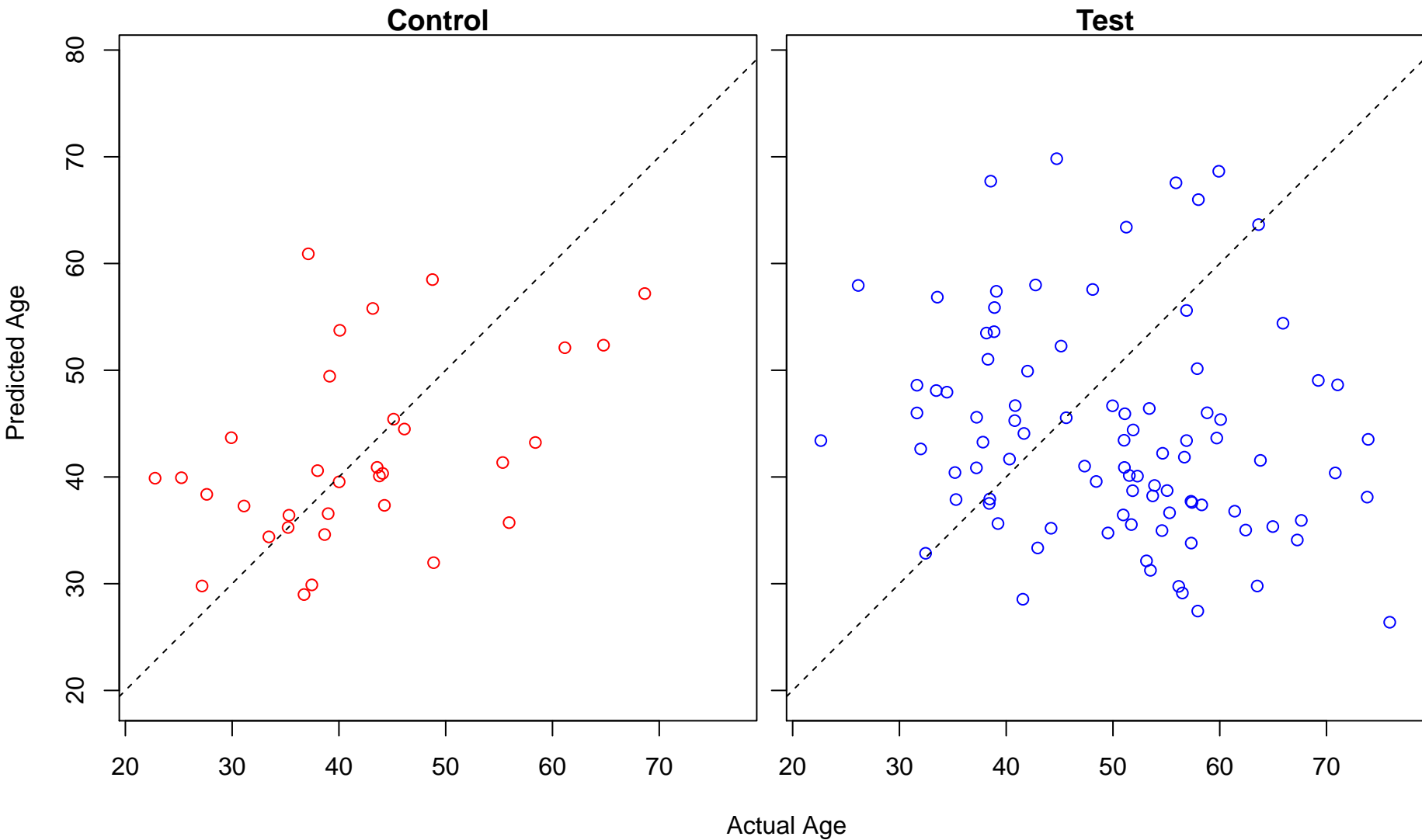
regulation of acute inflammatory response (Score: 1.020214)



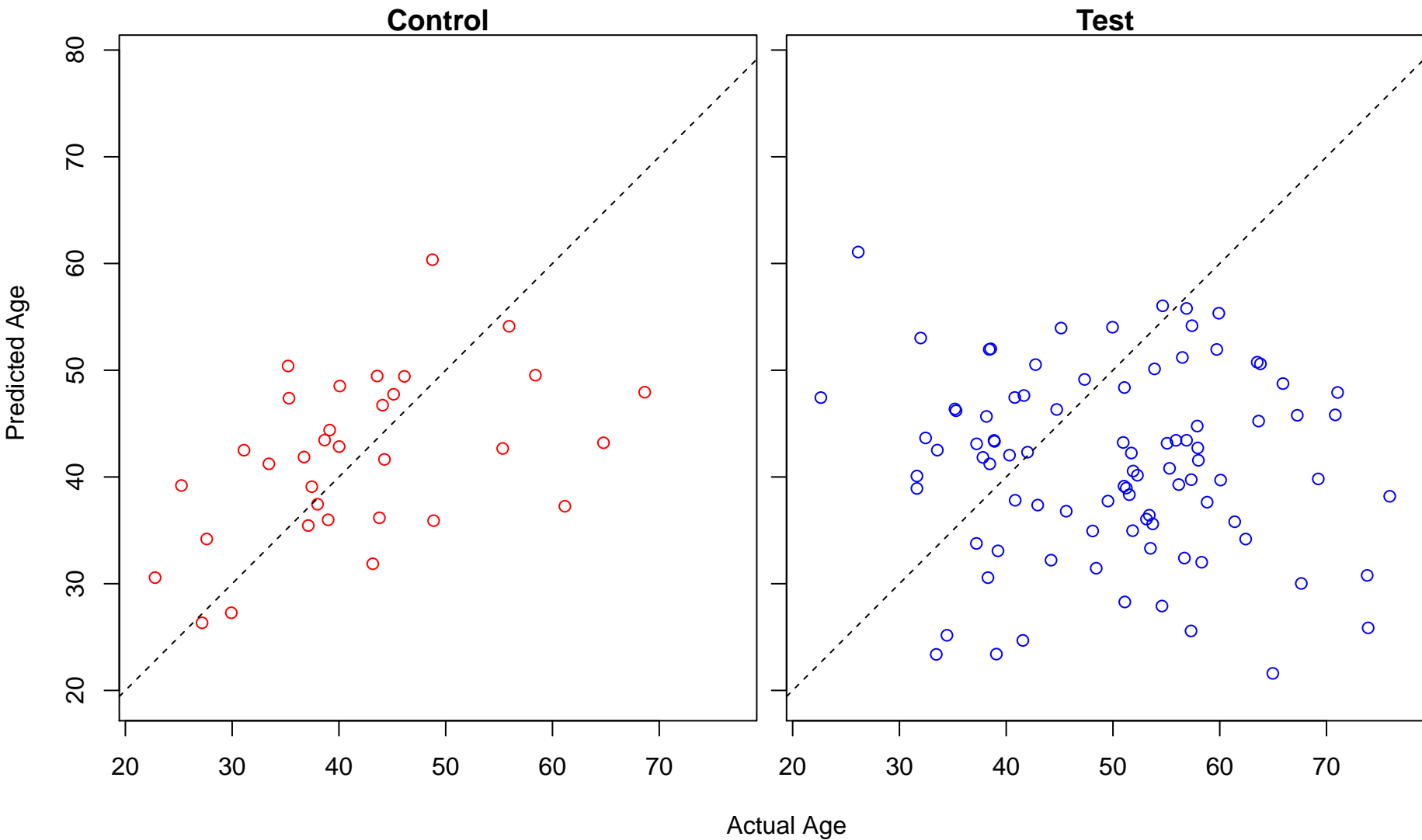
regulation of protein import into nucleus, translocation (Score: 1.019883)



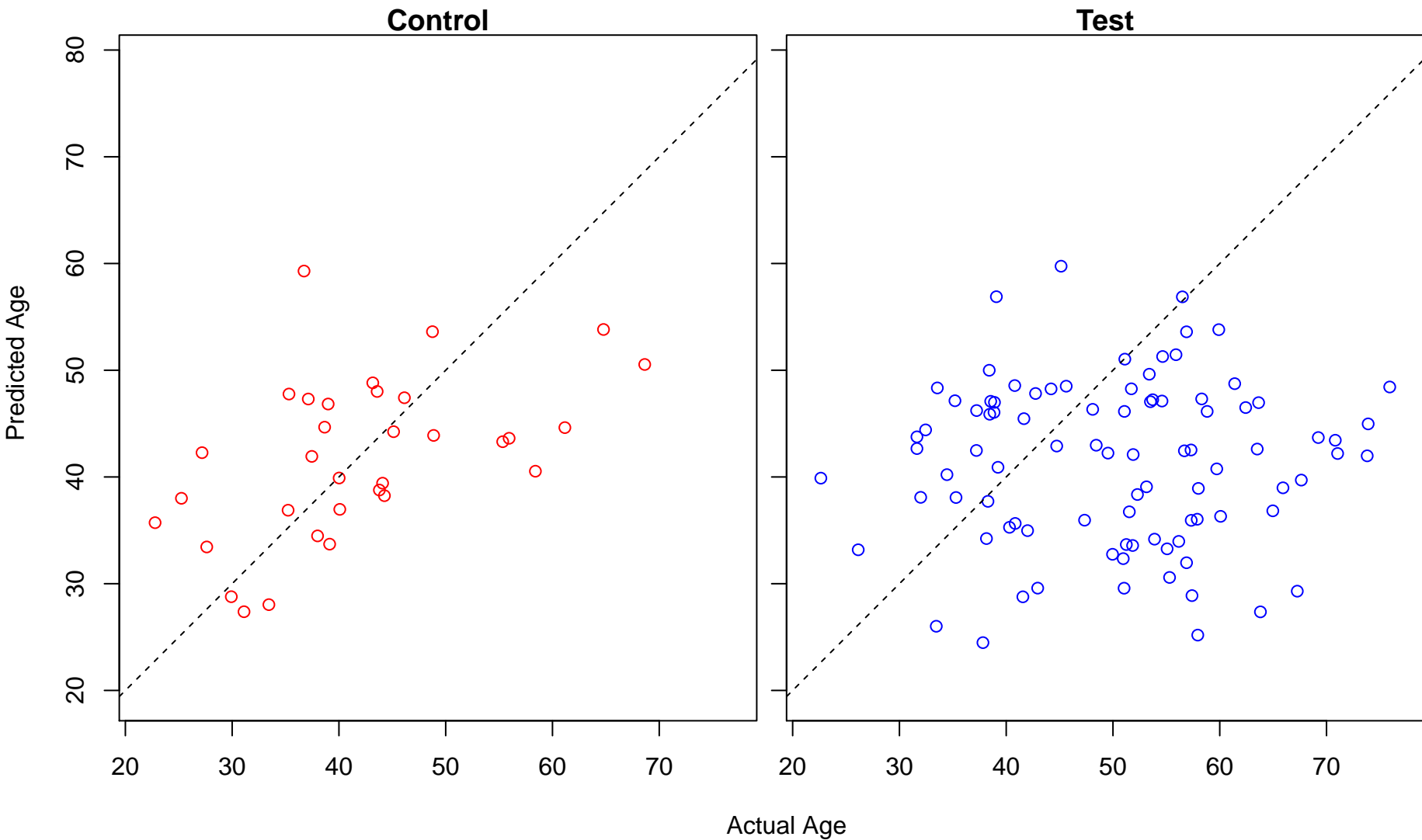
drug transport (Score: 1.019820)



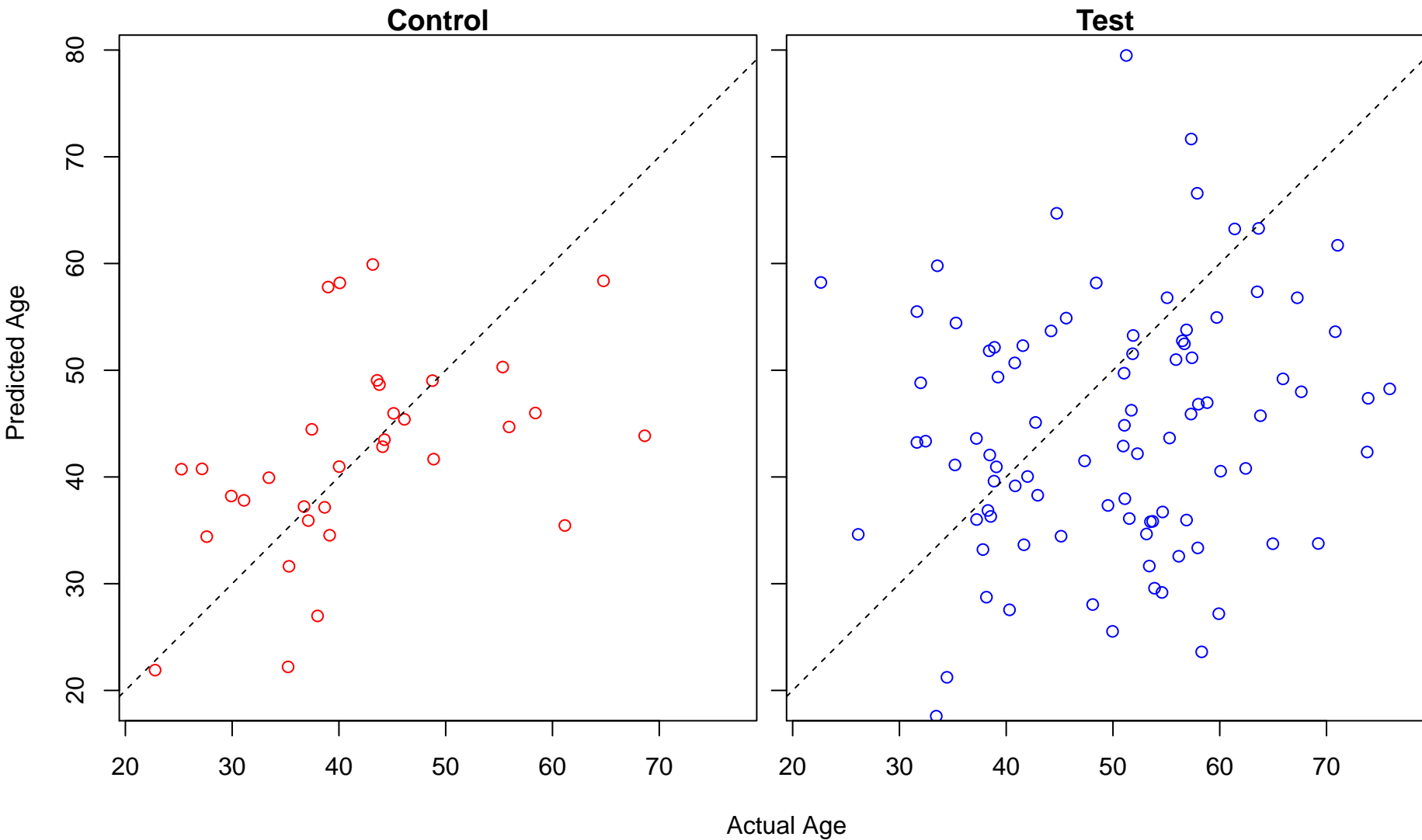
membrane repolarization (Score: 1.019461)



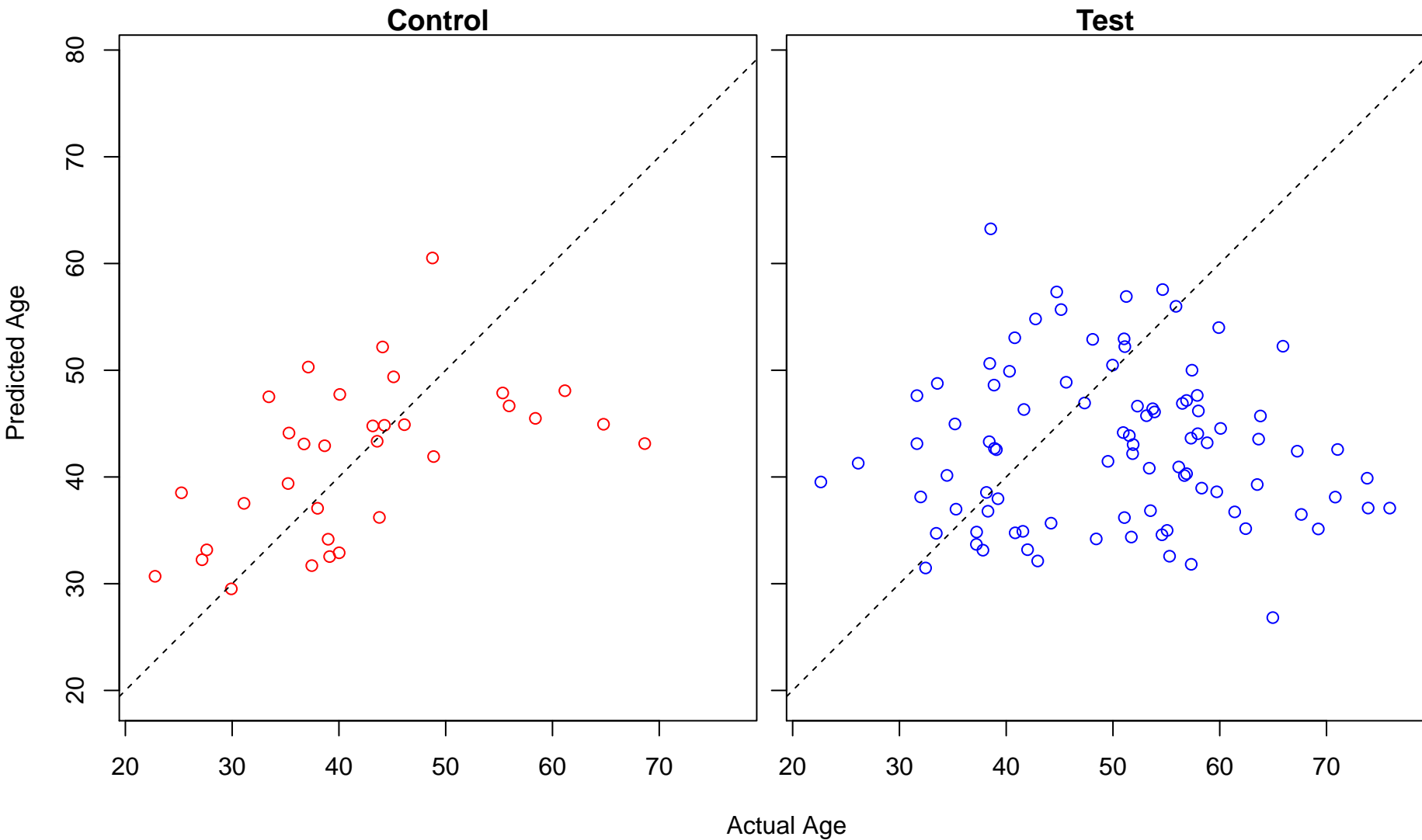
chromatin silencing (Score: 1.018269)



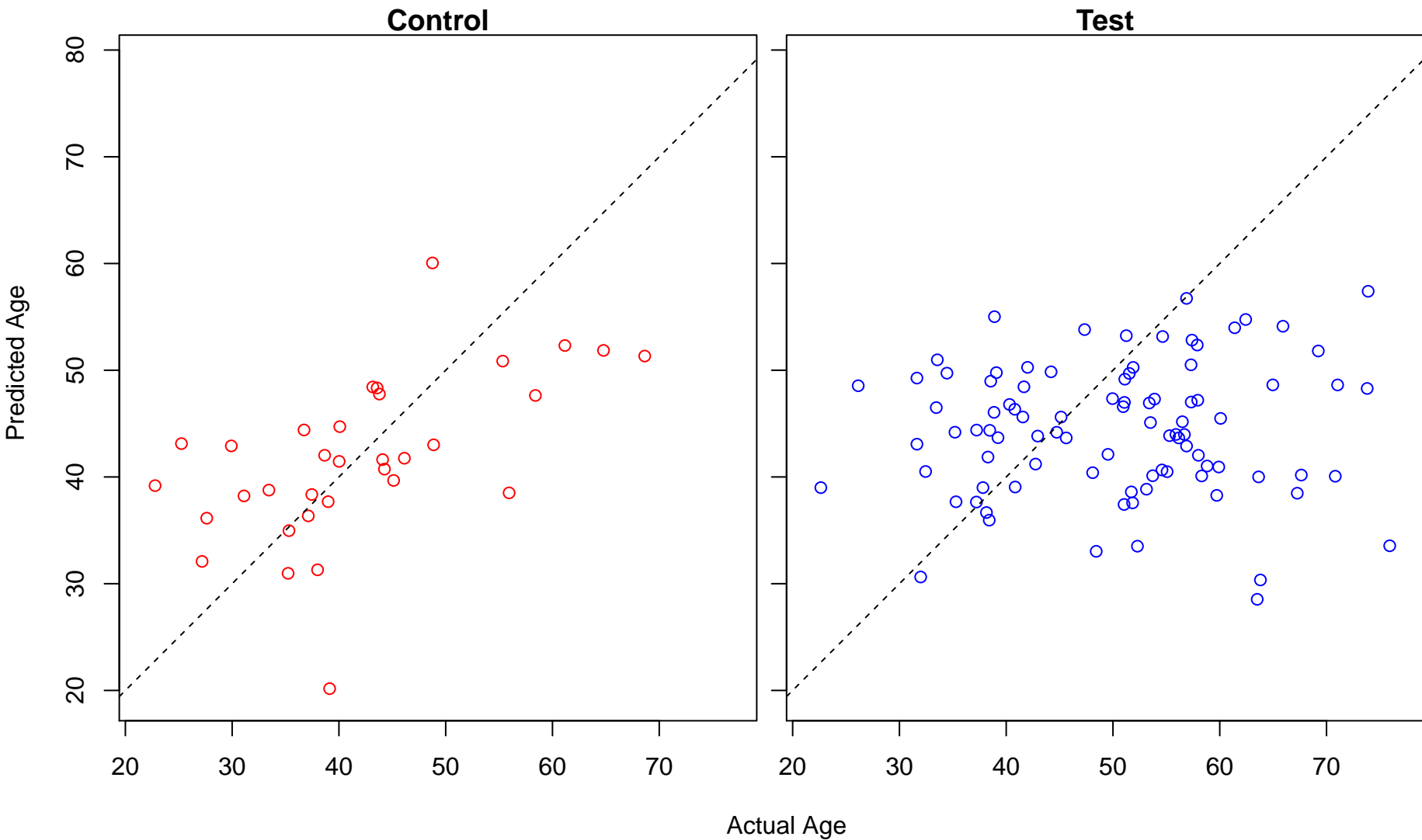
axis specification (Score: 1.018135)



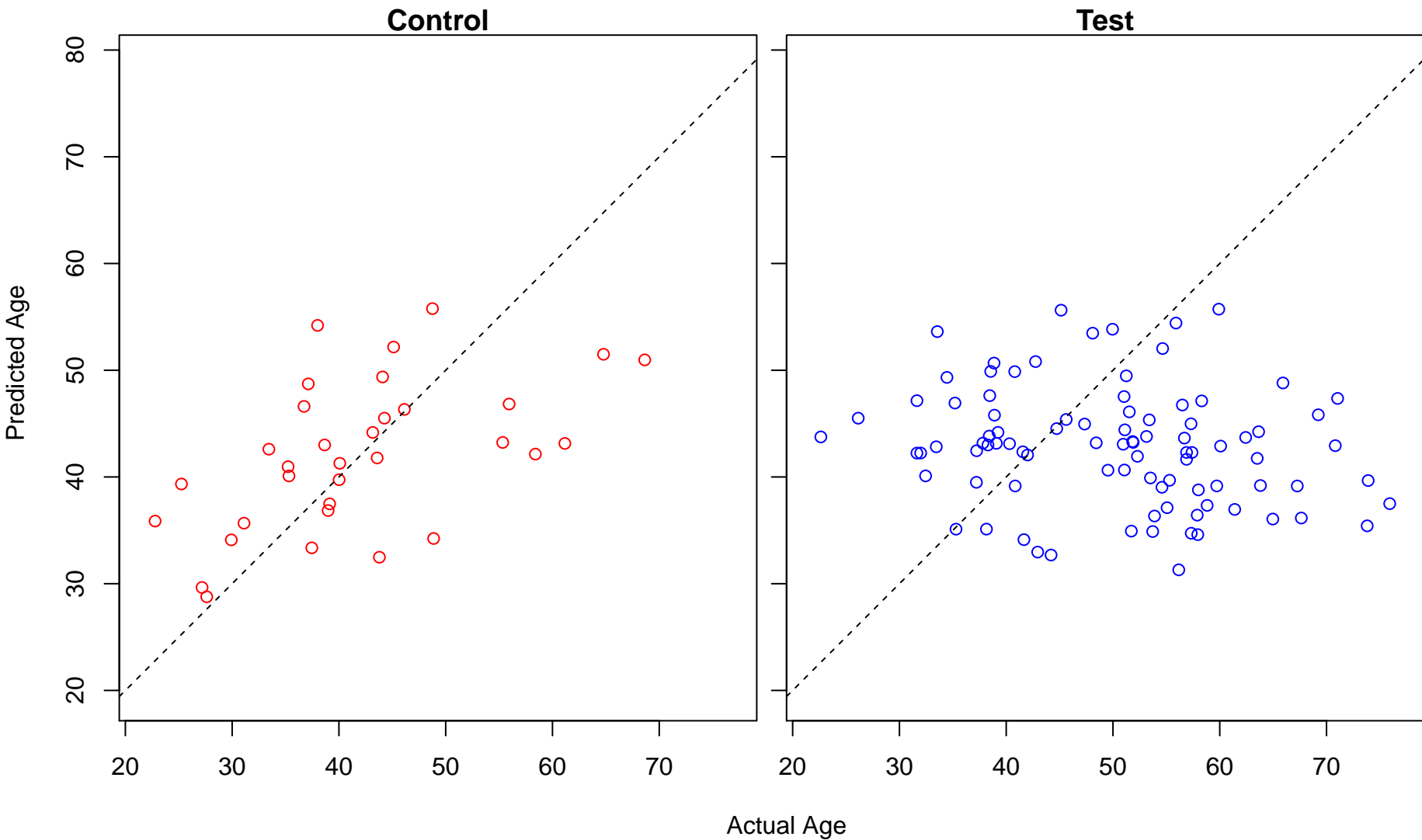
muscle system process (Score: 1.017389)



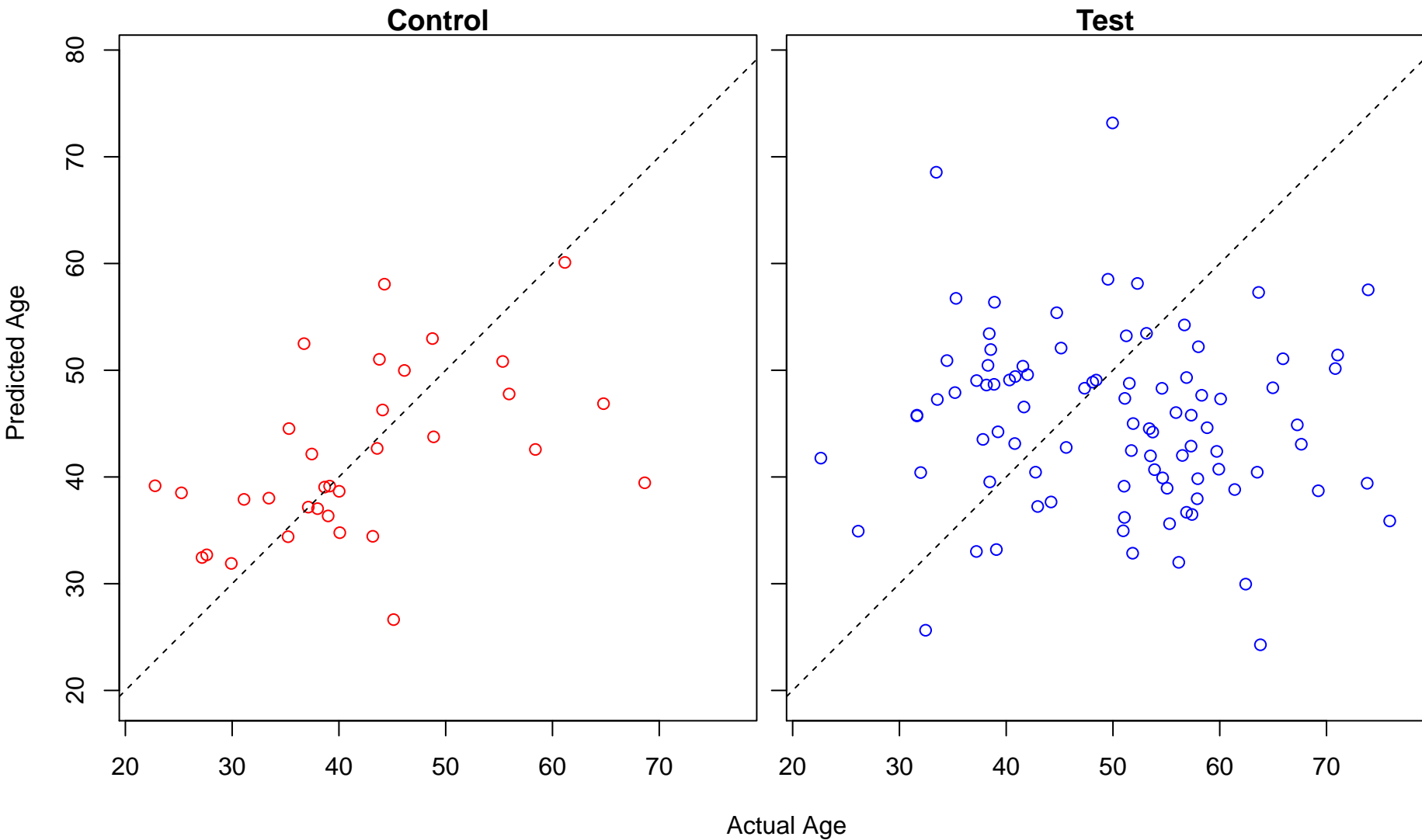
lymphocyte mediated immunity (Score: 1.015113)



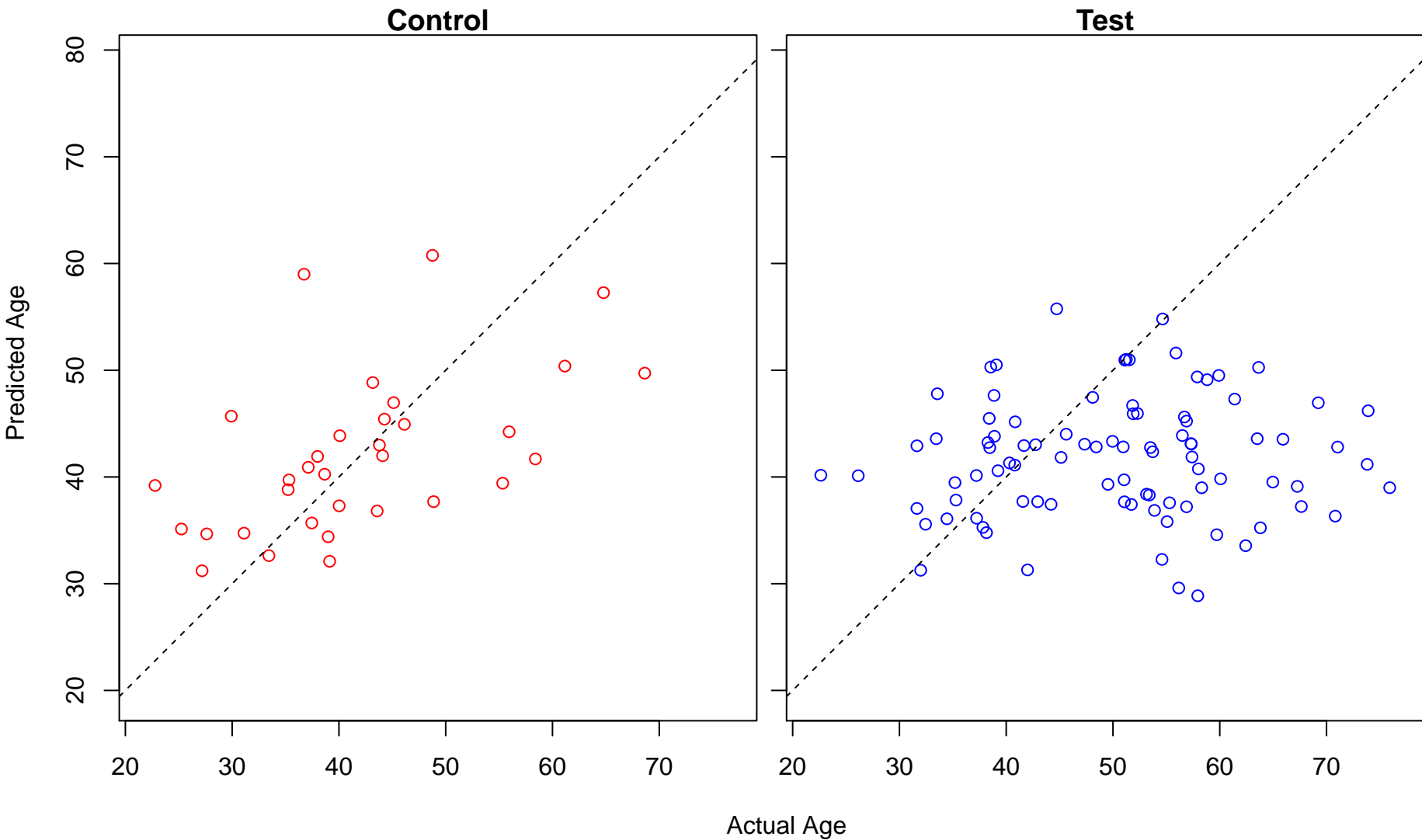
cGMP metabolic process (Score: 1.014708)



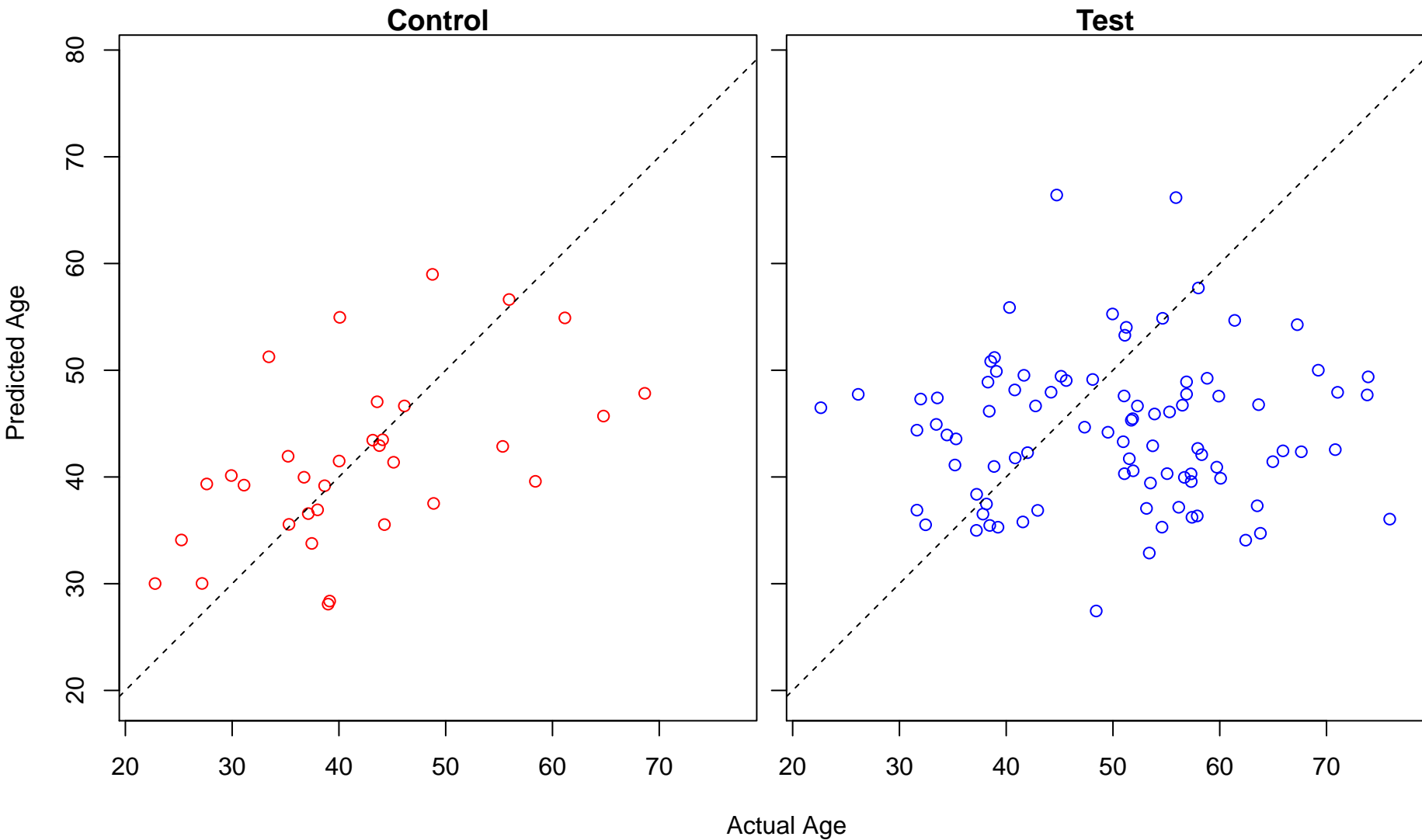
negative regulation of nitric oxide biosynthetic process (Score: 1.013955)



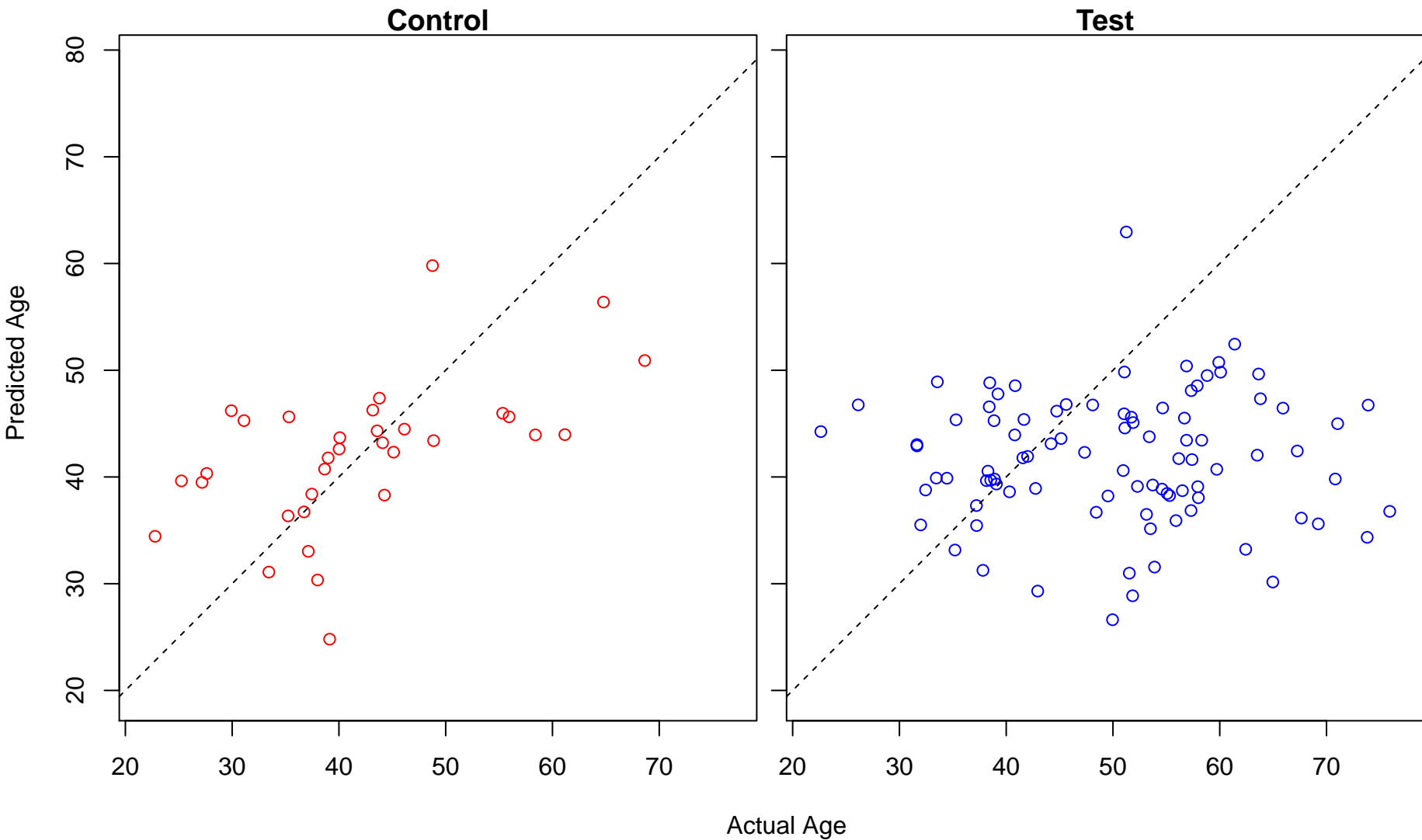
neuron apoptotic process (Score: 1.013799)



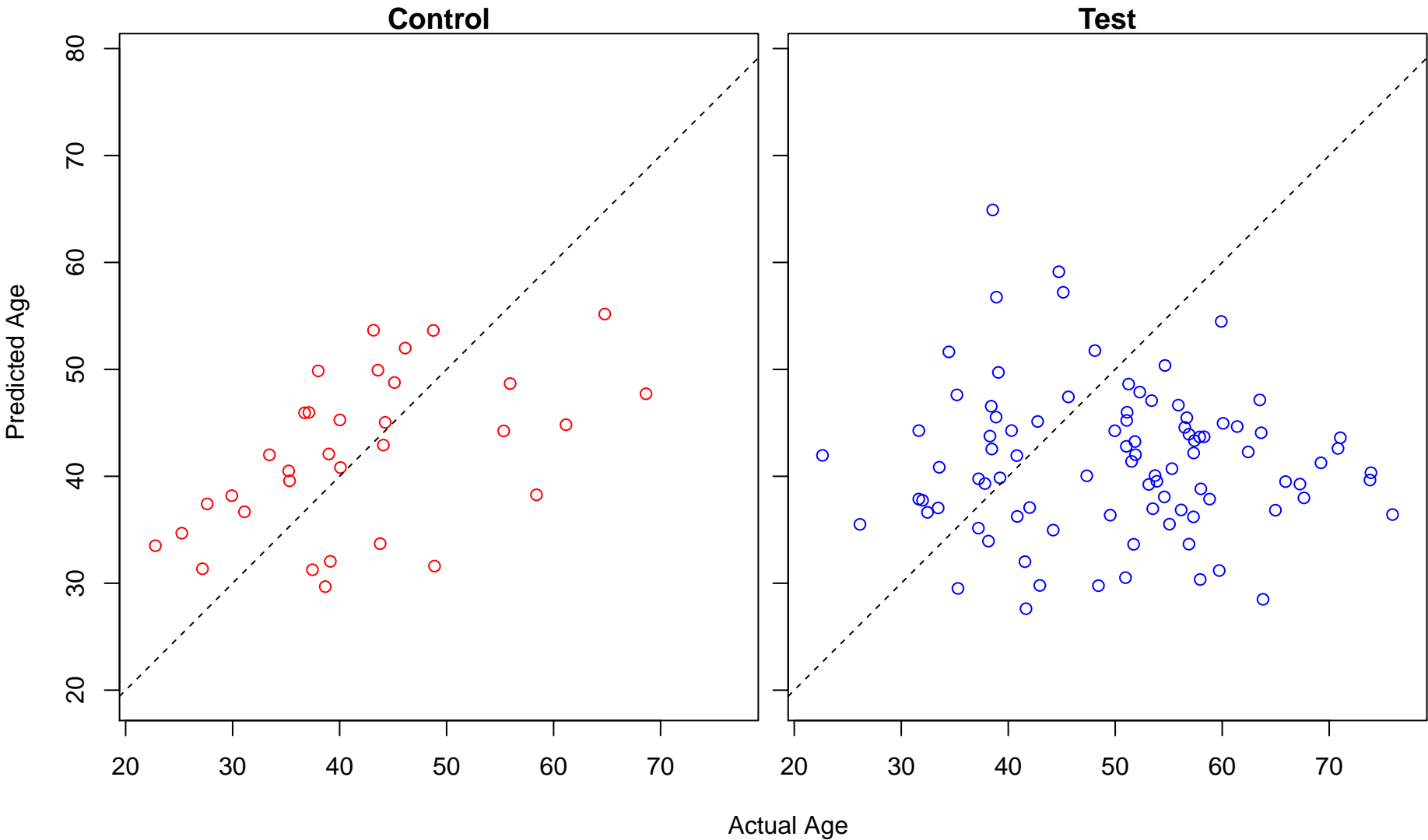
regulation of cation channel activity (Score: 1.012486)



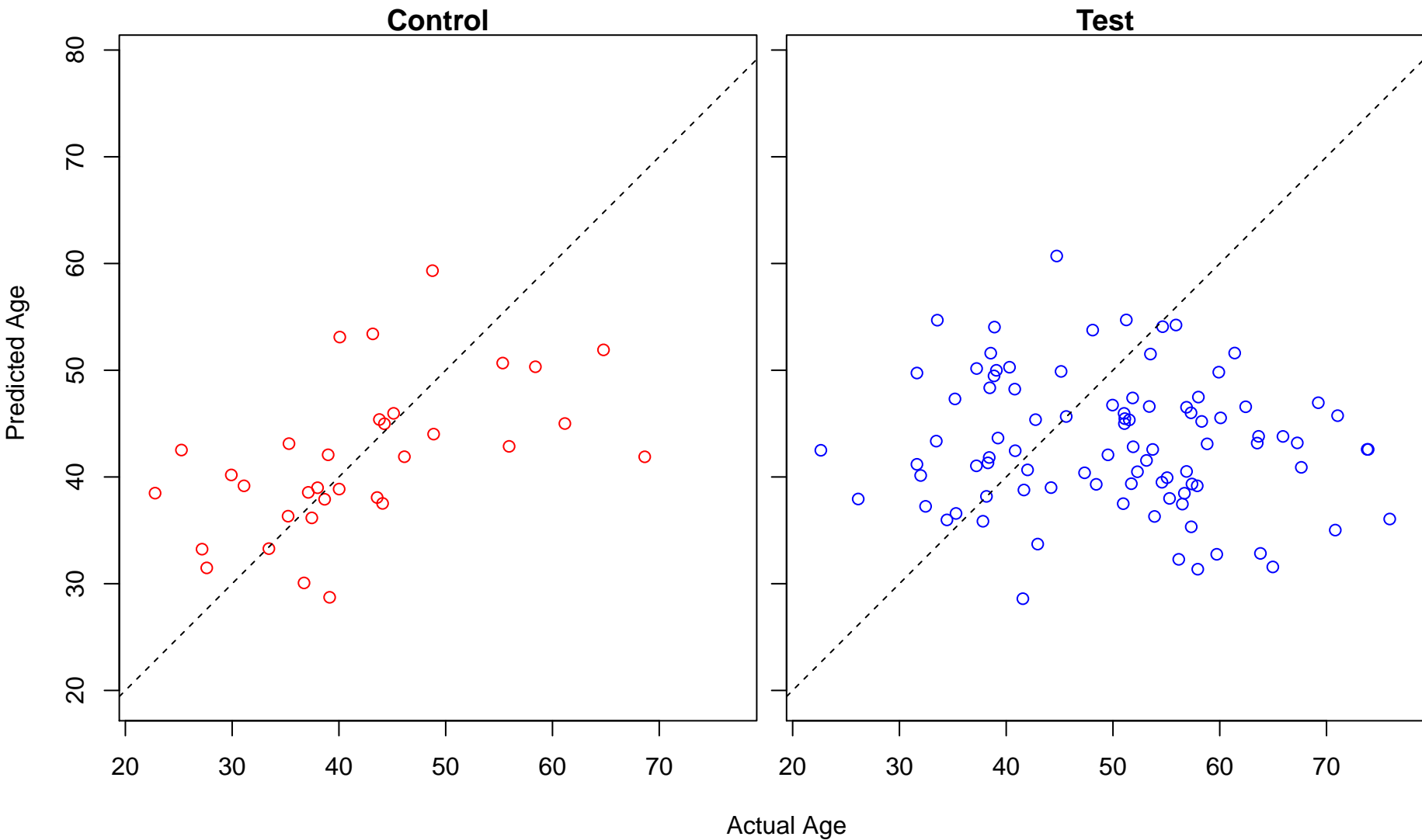
phosphatidylglycerol acyl-chain remodeling (Score: 1.008184)



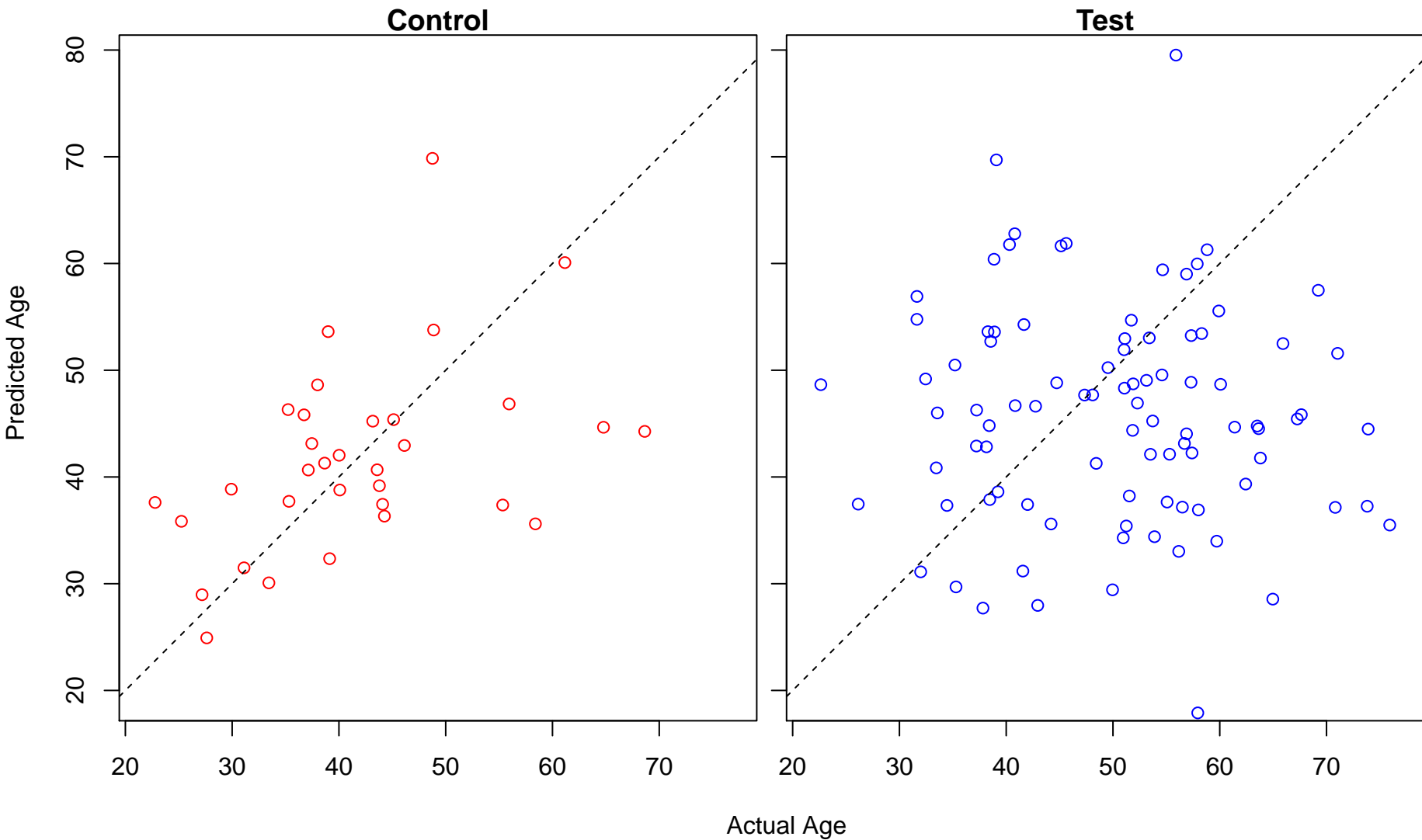
cellular response to granulocyte macrophage colony-stimulating factor stimulus (Score: 1.008122)



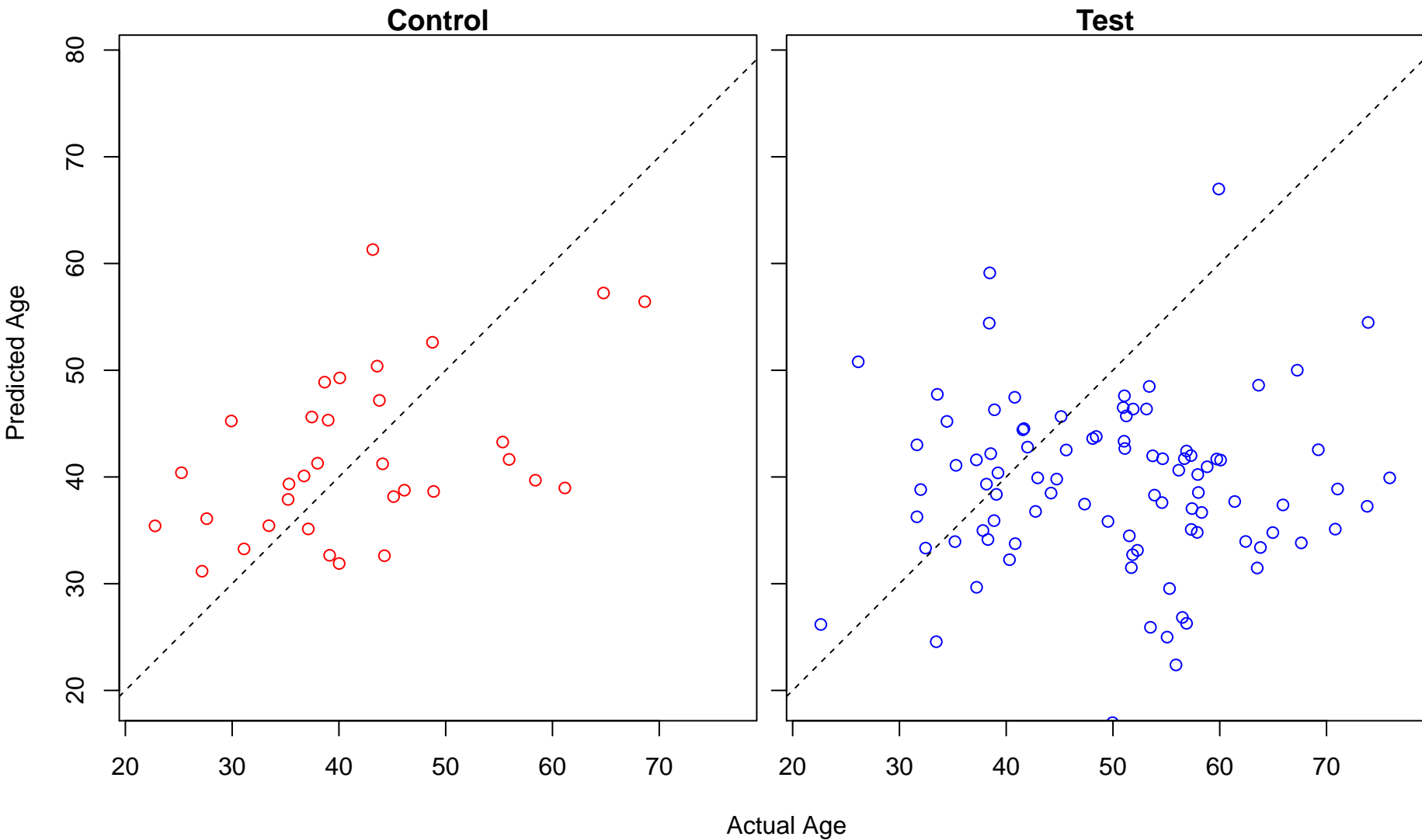
monocarboxylic acid transport (Score: 1.006478)



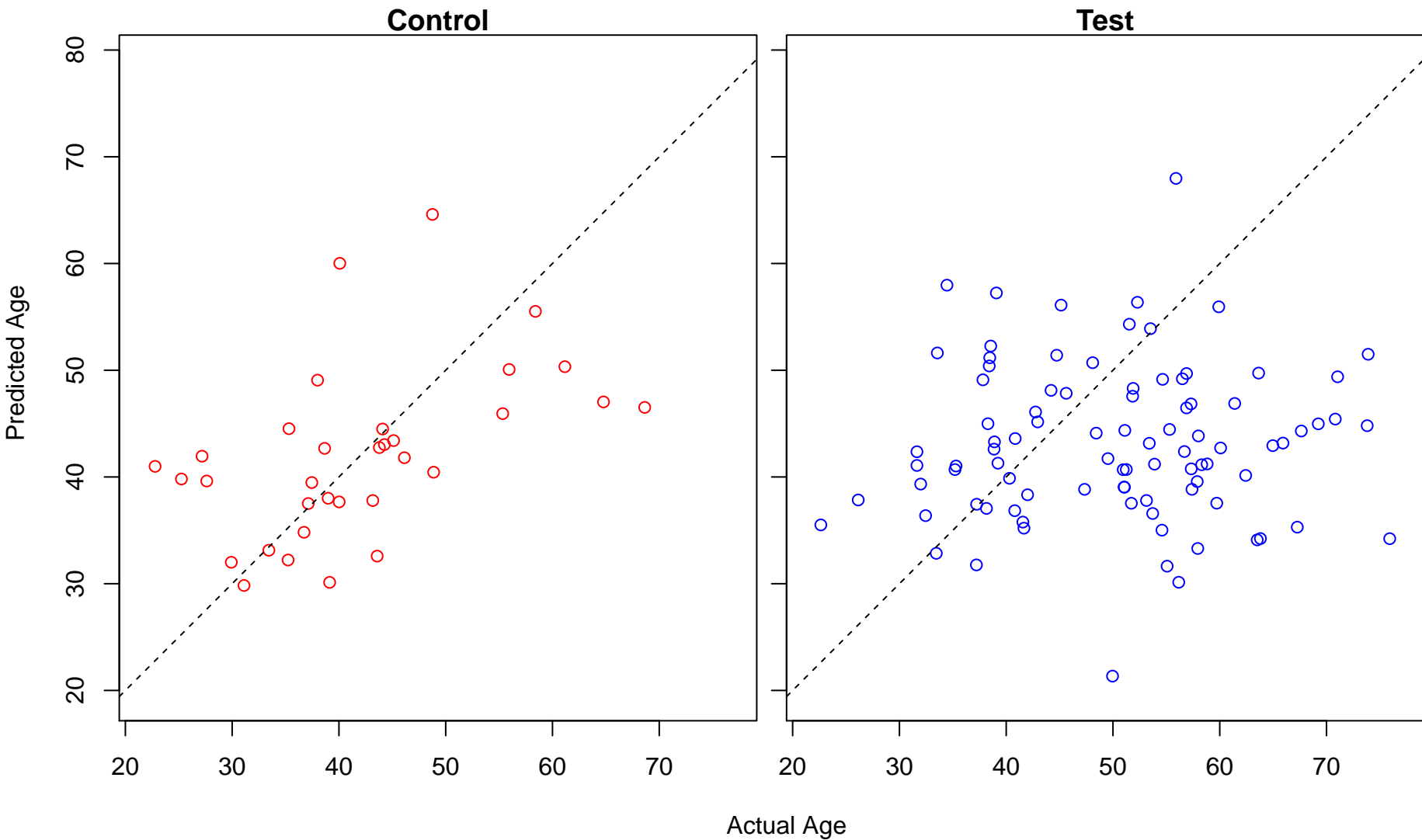
regulation of appetite (Score: 1.005047)



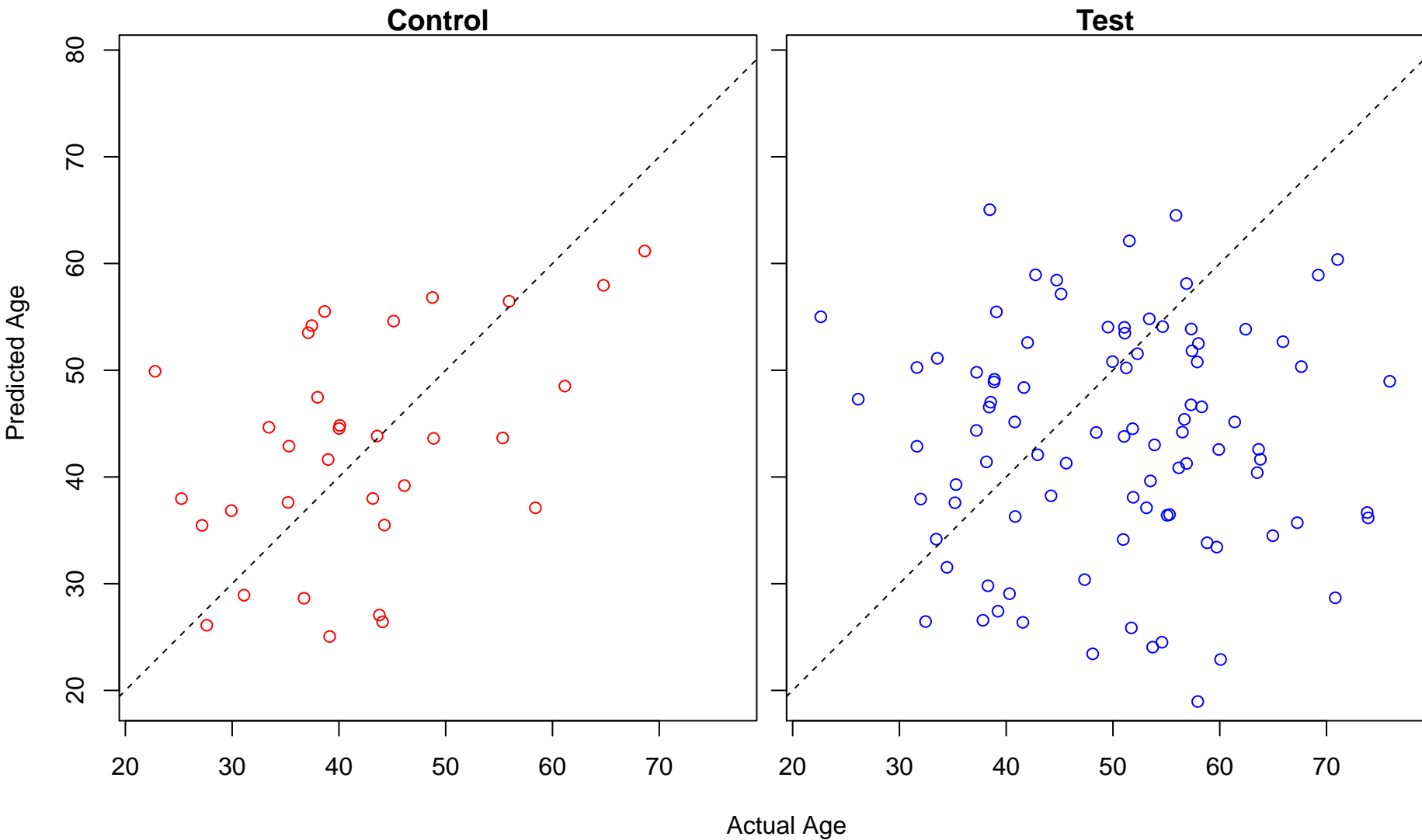
glycerophospholipid catabolic process (Score: 1.004140)



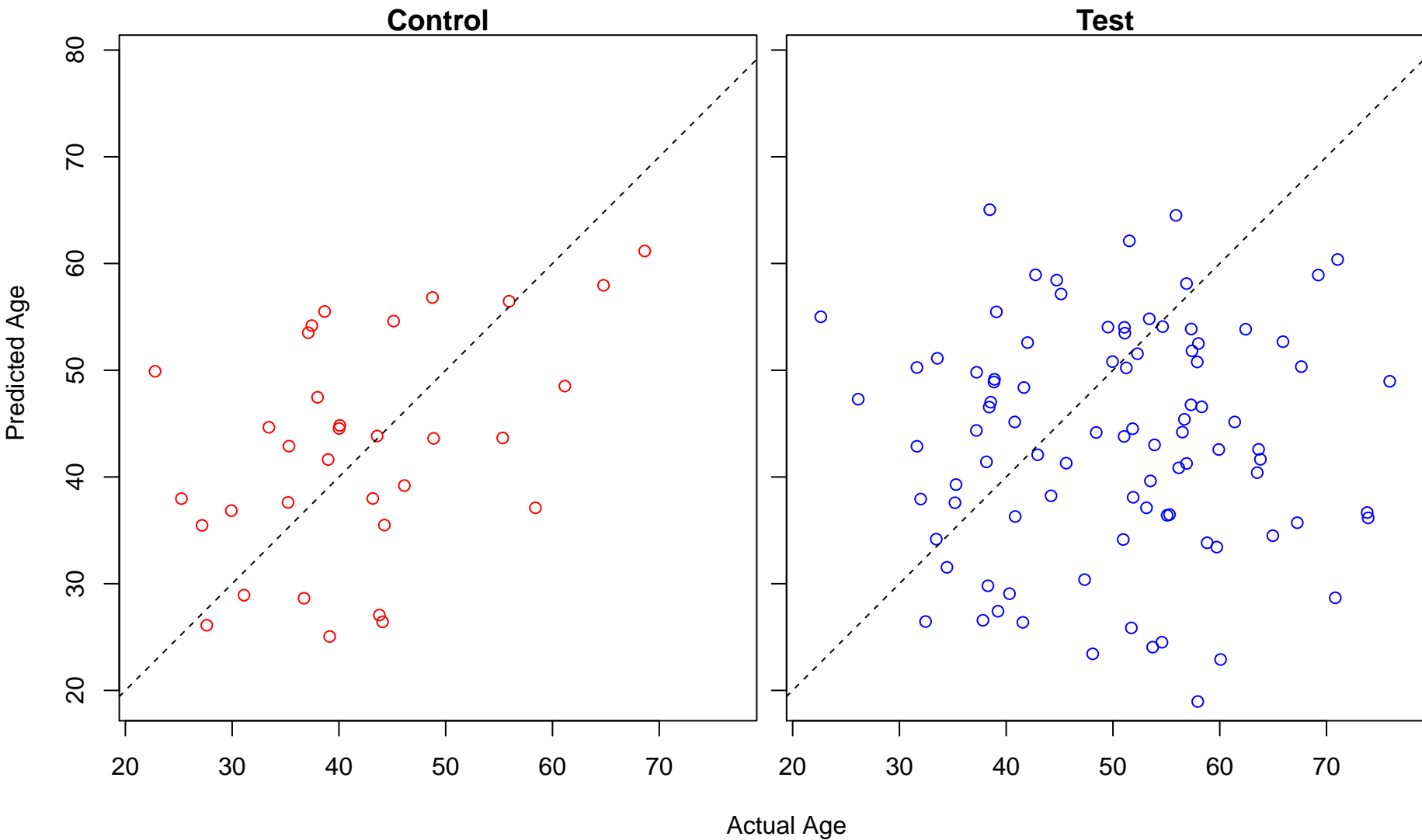
neural tube patterning (Score: 0.999842)



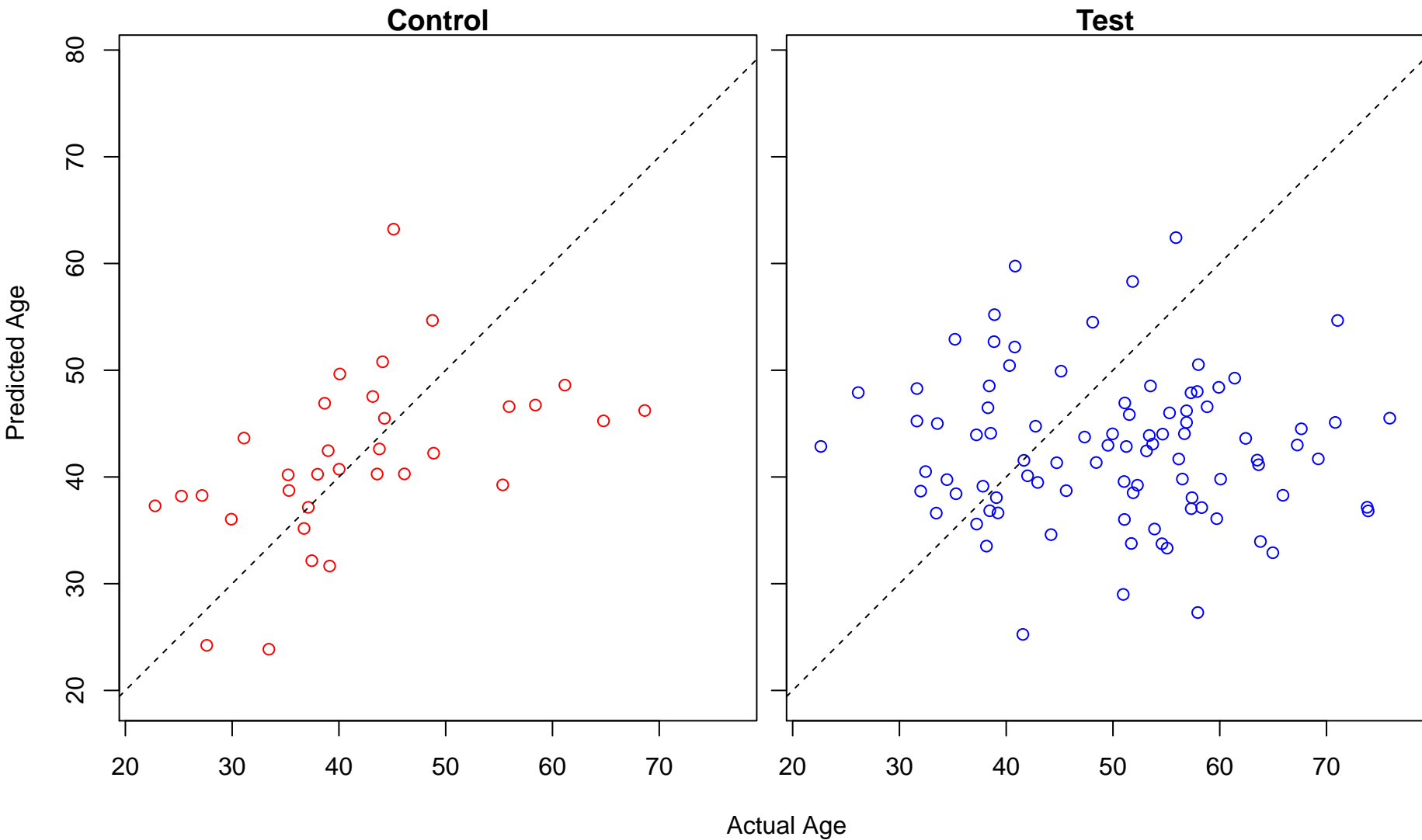
molting cycle (Score: 0.999088)



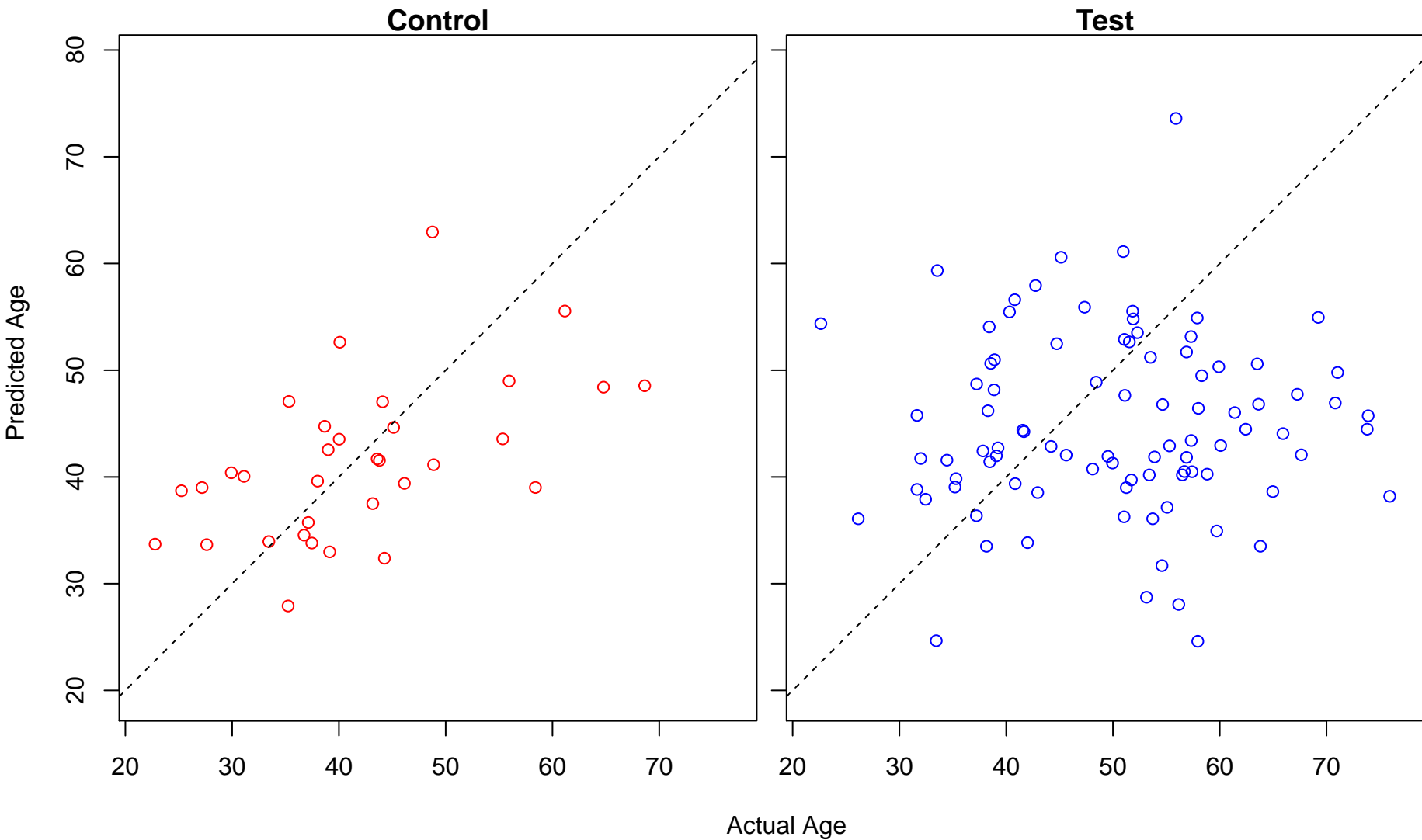
hair cycle (Score: 0.999088)



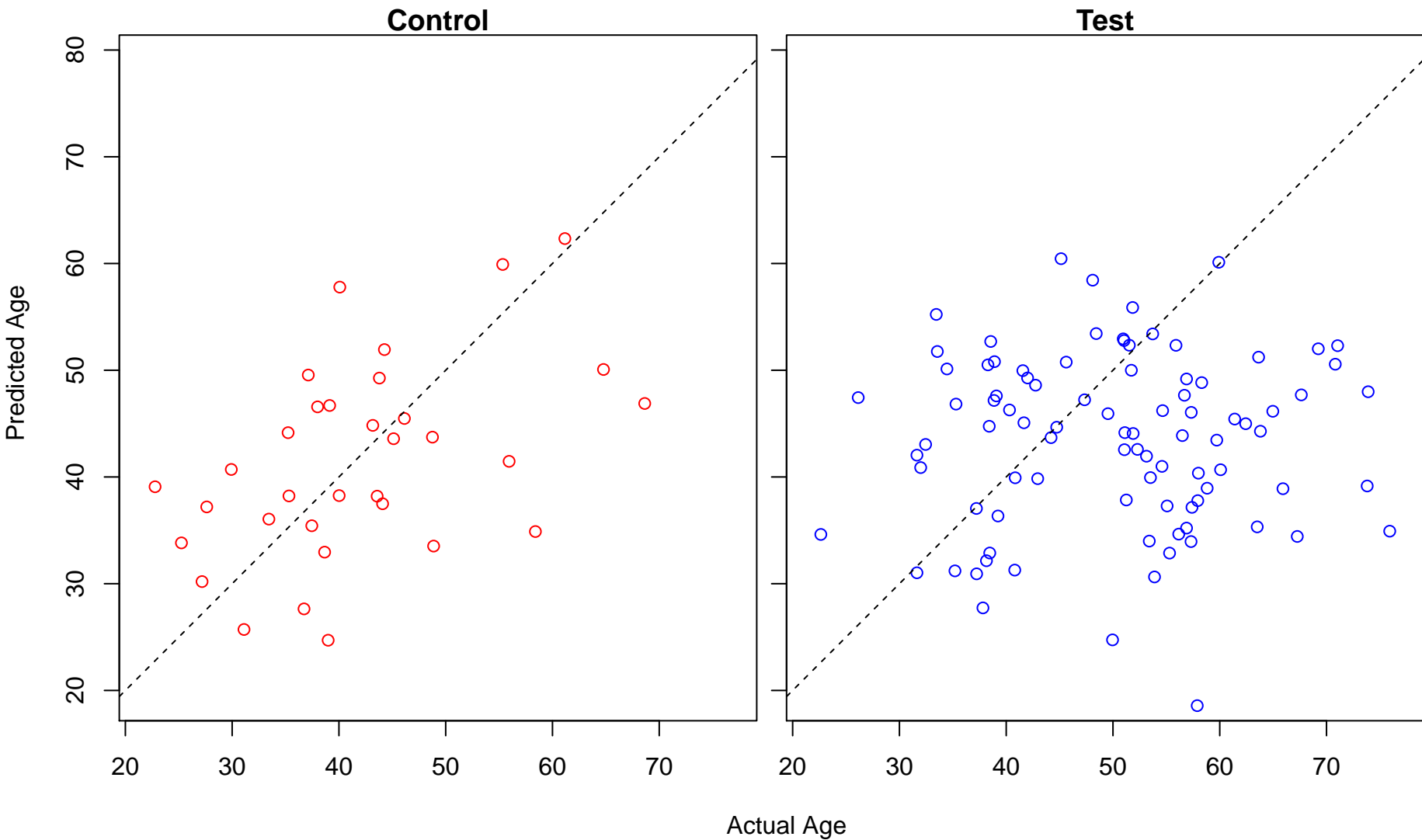
protein K29-linked ubiquitination (Score: 0.999030)



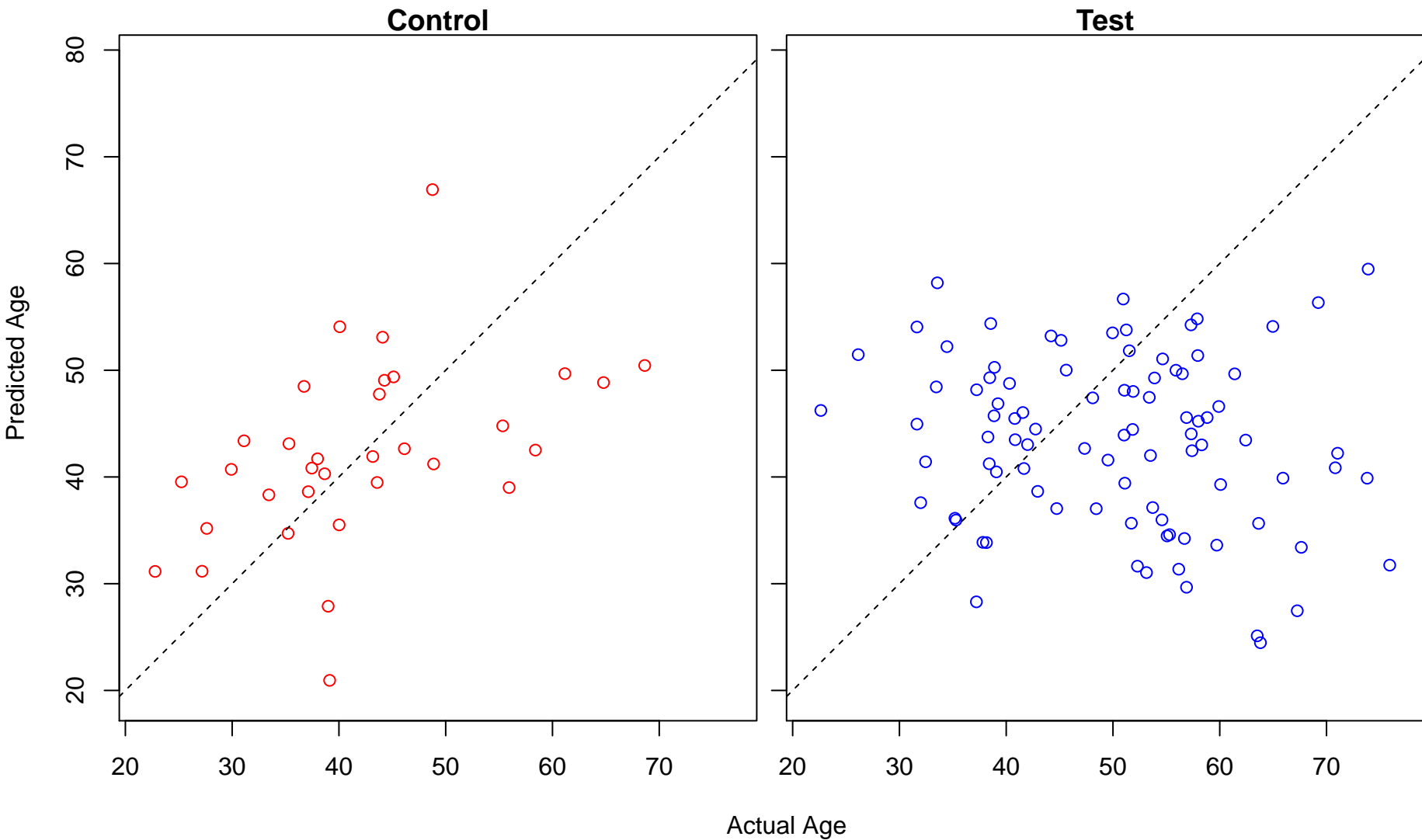
monoubiquitinated protein deubiquitination (Score: 0.998908)



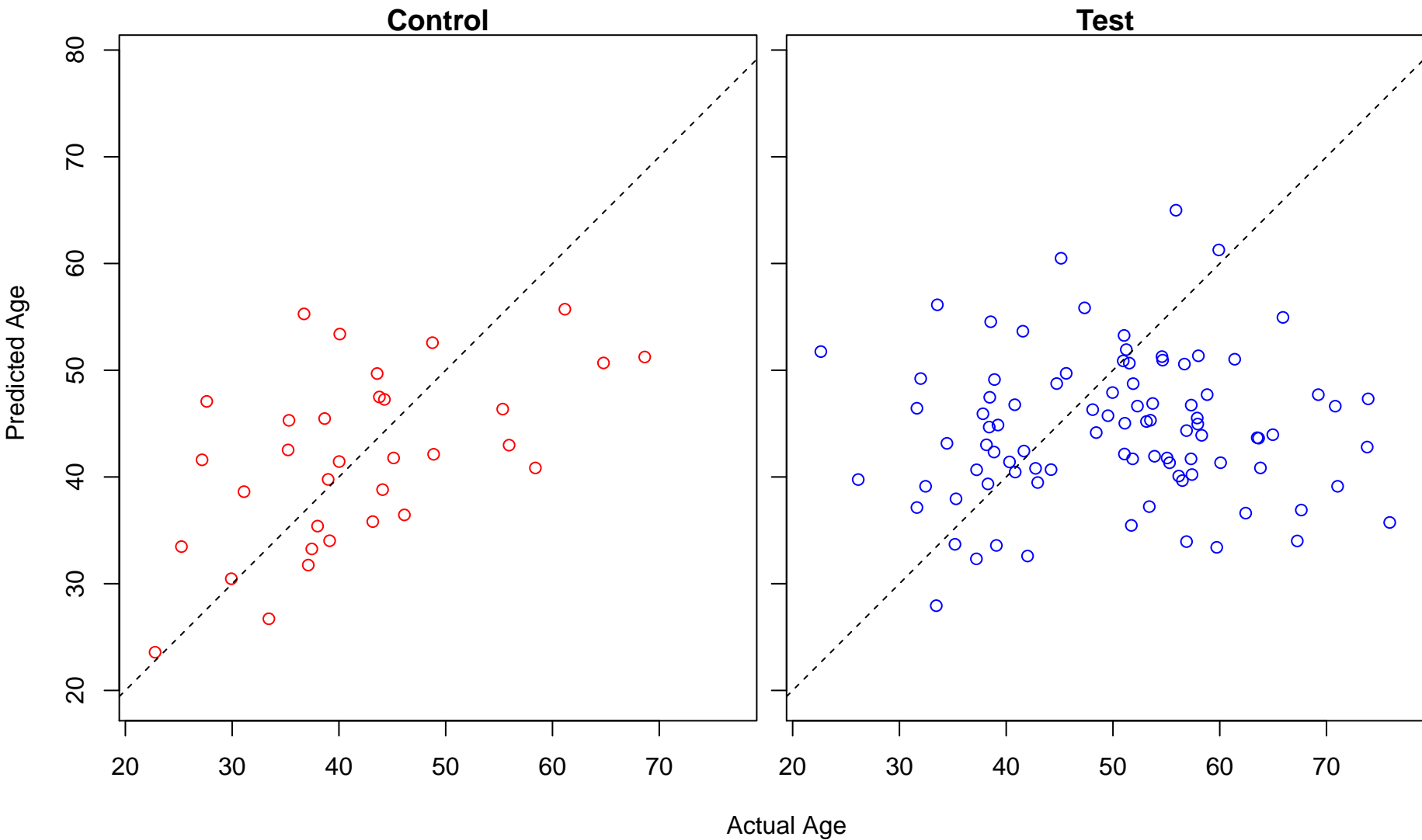
negative regulation of calcium ion transport into cytosol (Score: 0.998330)



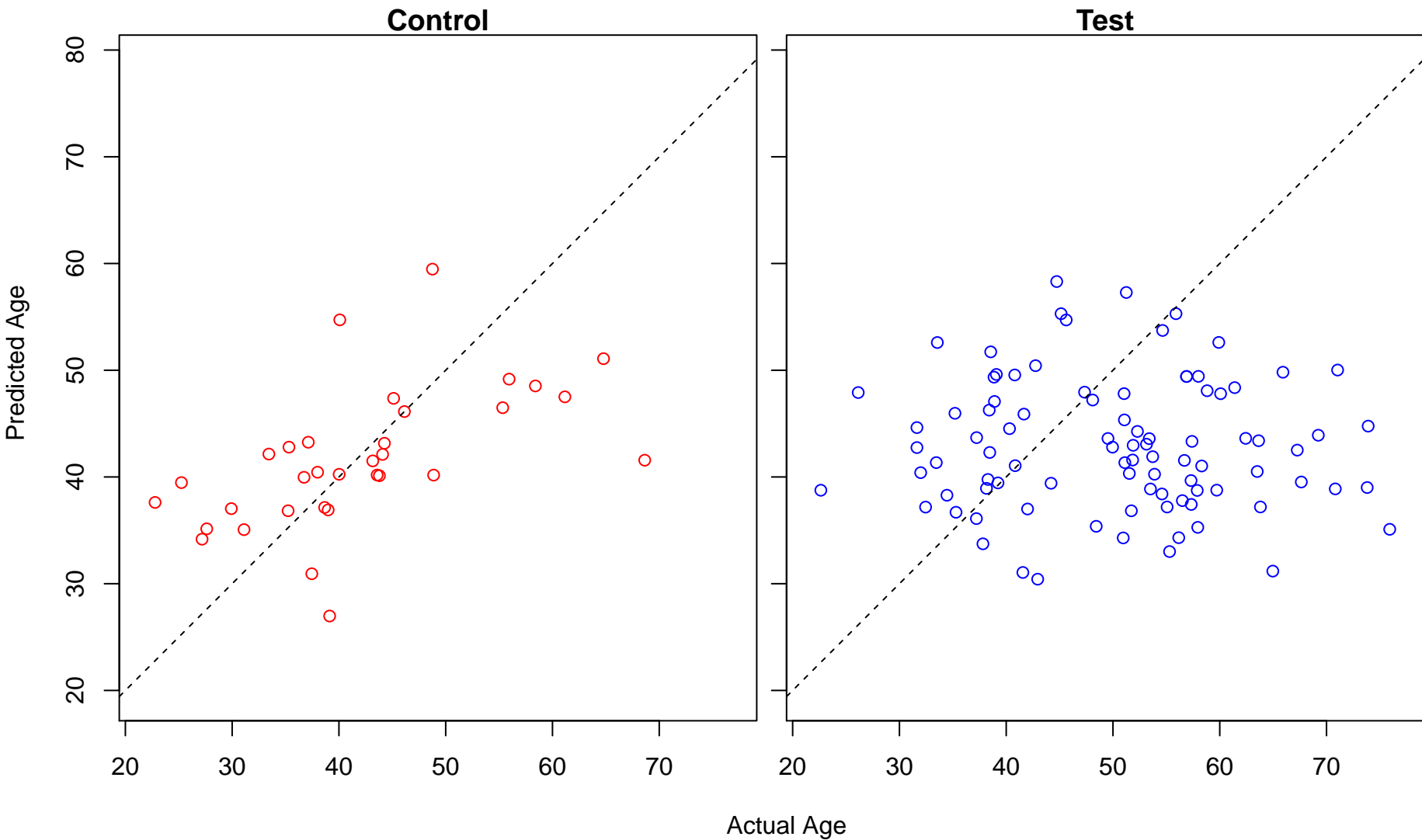
humoral immune response (Score: 0.997178)



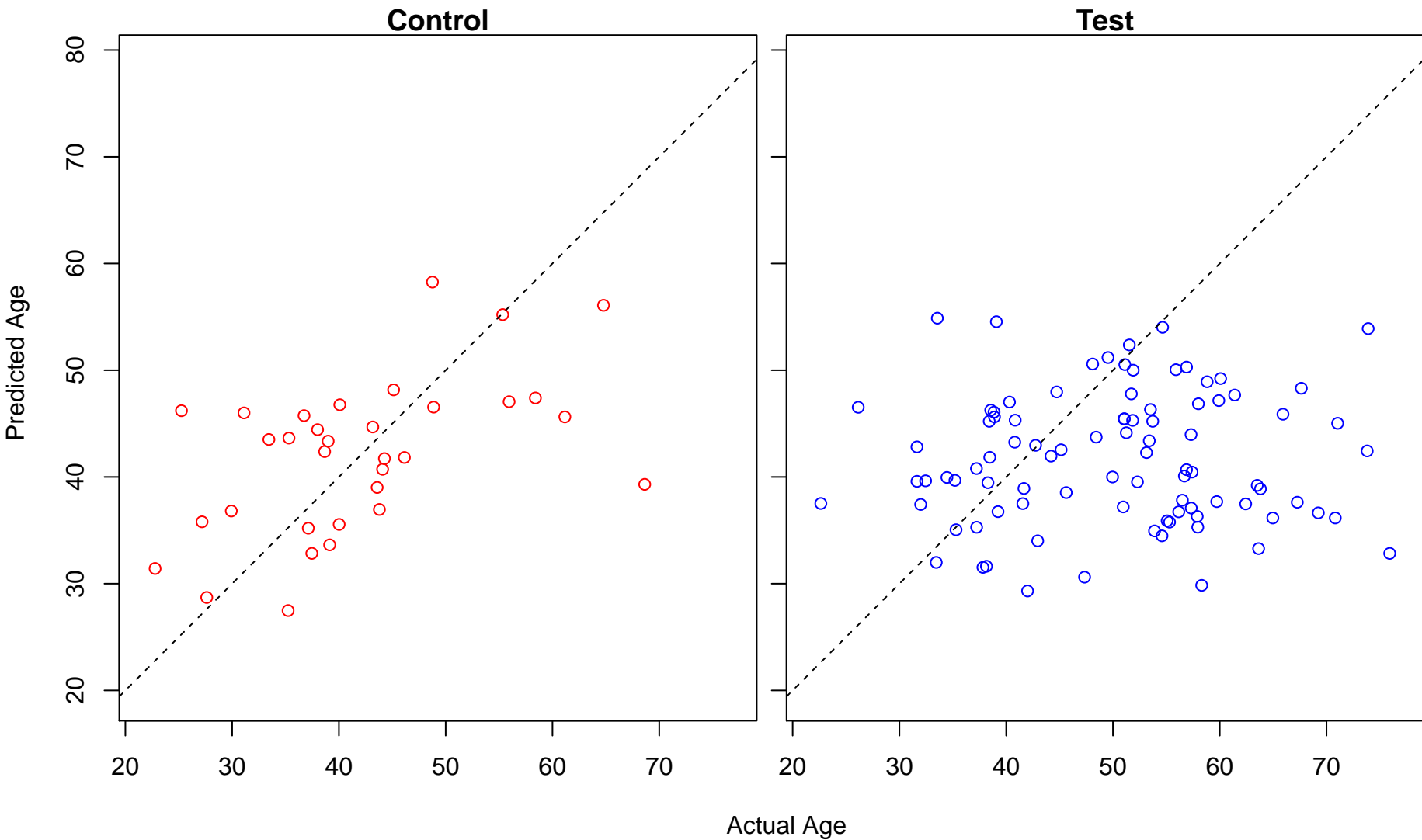
regulation of protein exit from endoplasmic reticulum (Score: 0.996825)



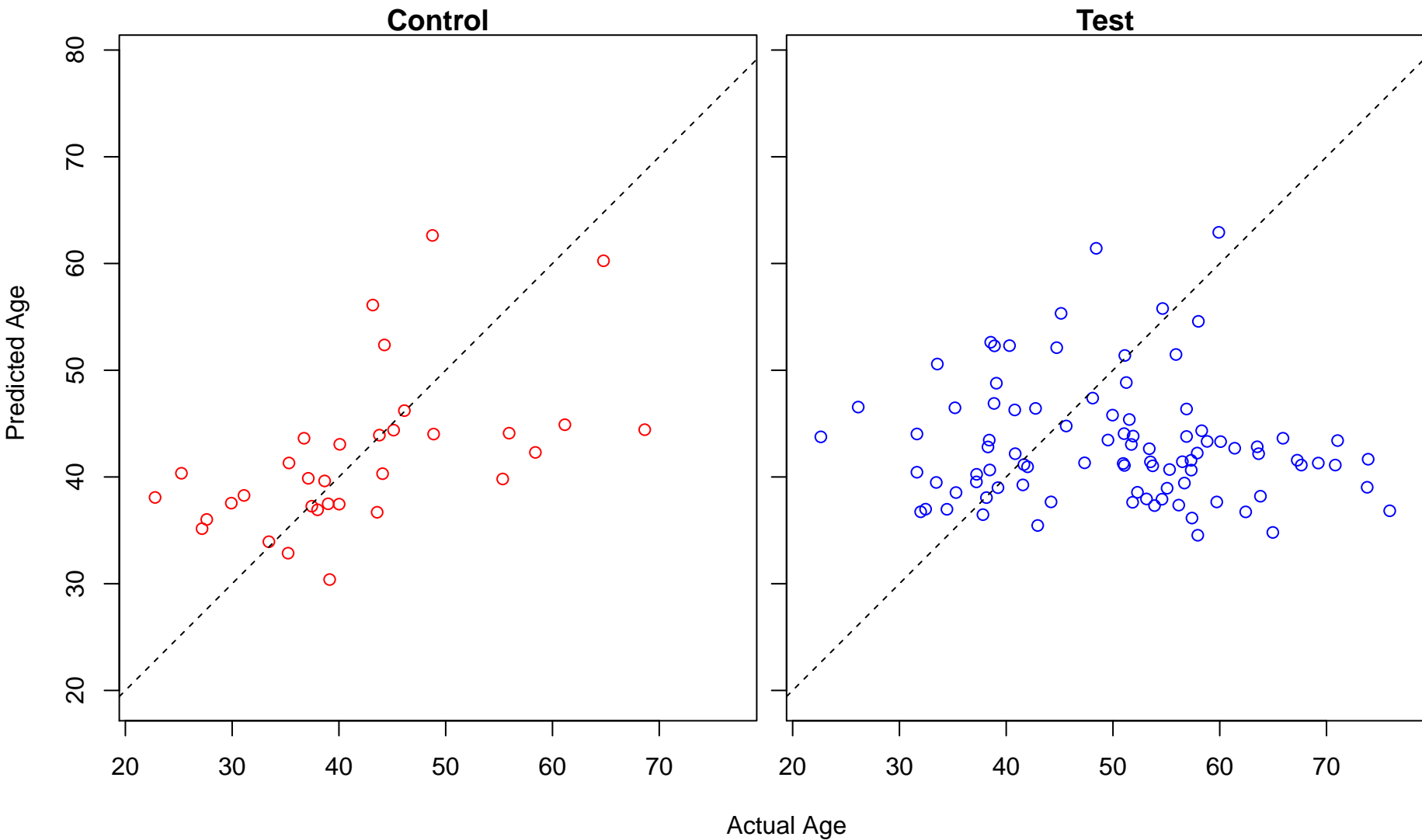
regulation of transmembrane transport (Score: 0.996298)



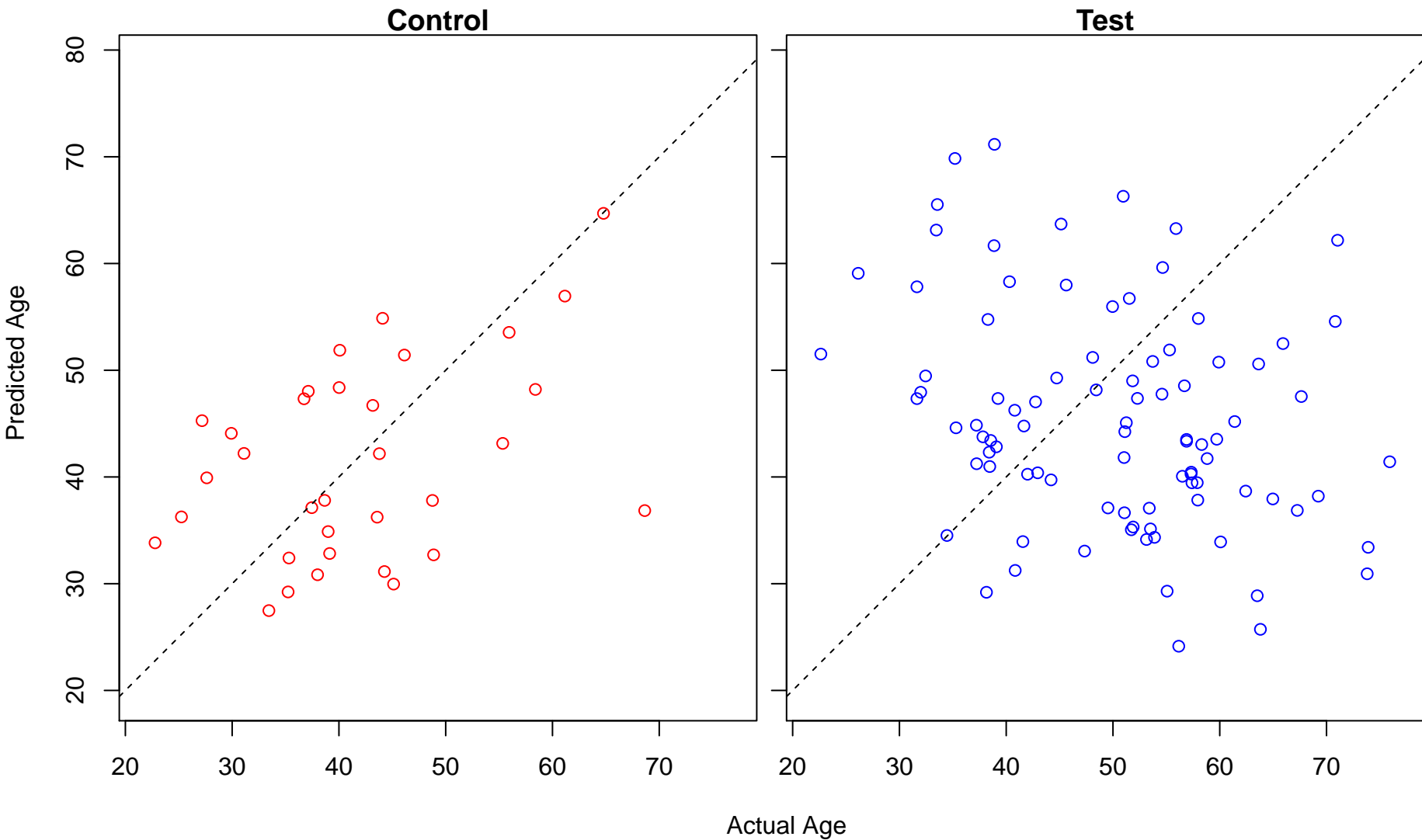
stem cell differentiation (Score: 0.996281)



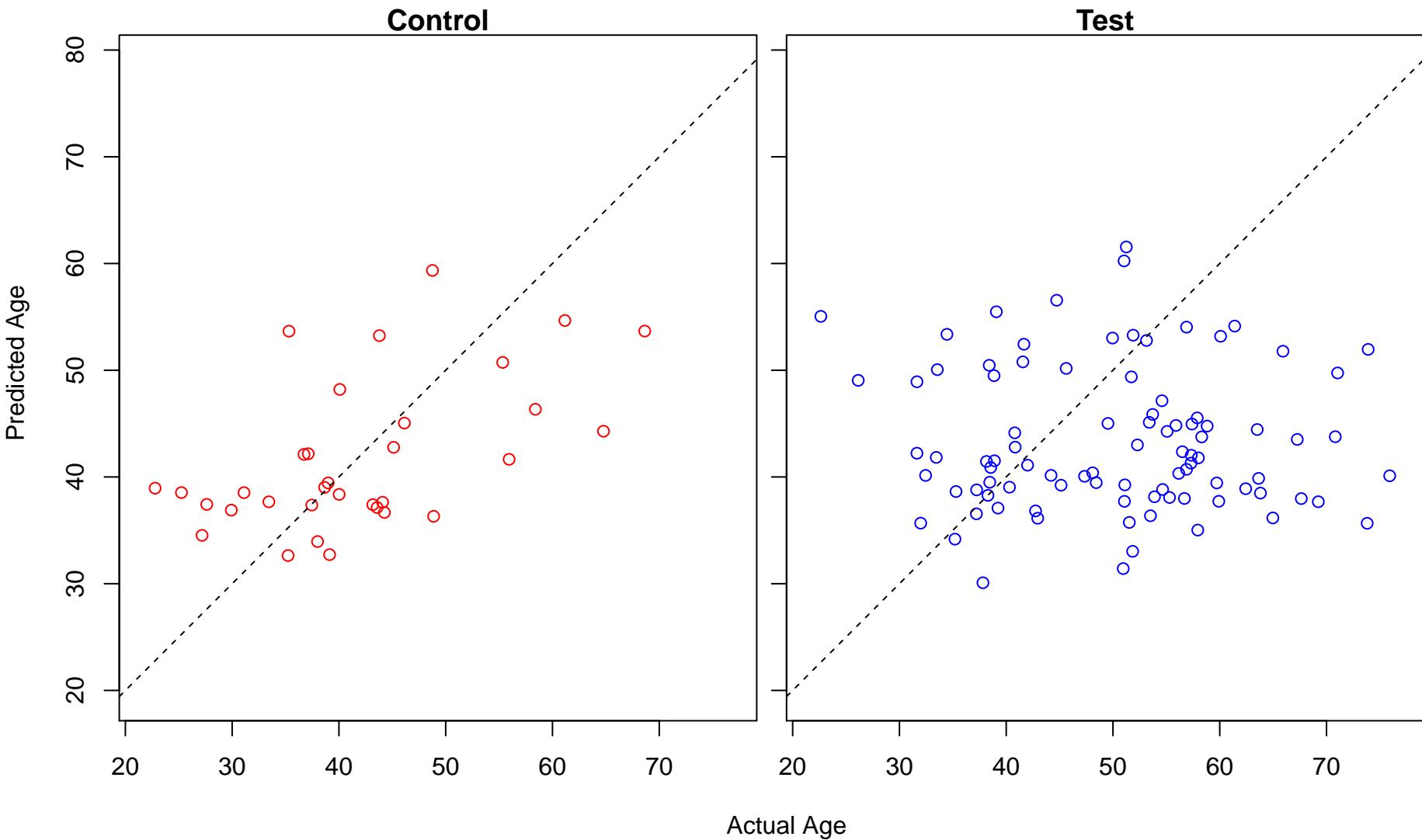
UV-damage excision repair (Score: 0.995178)



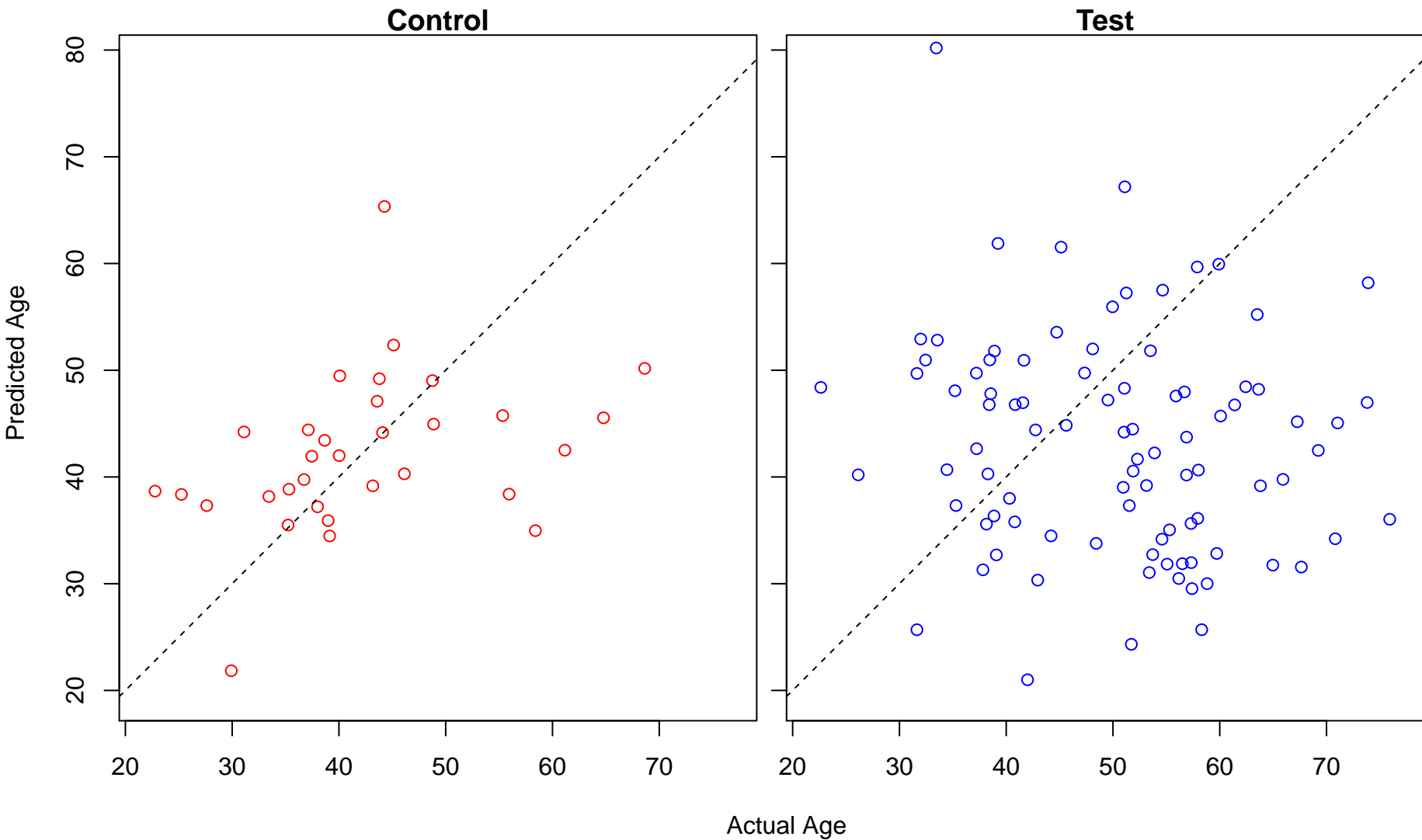
renal system development (Score: 0.994740)



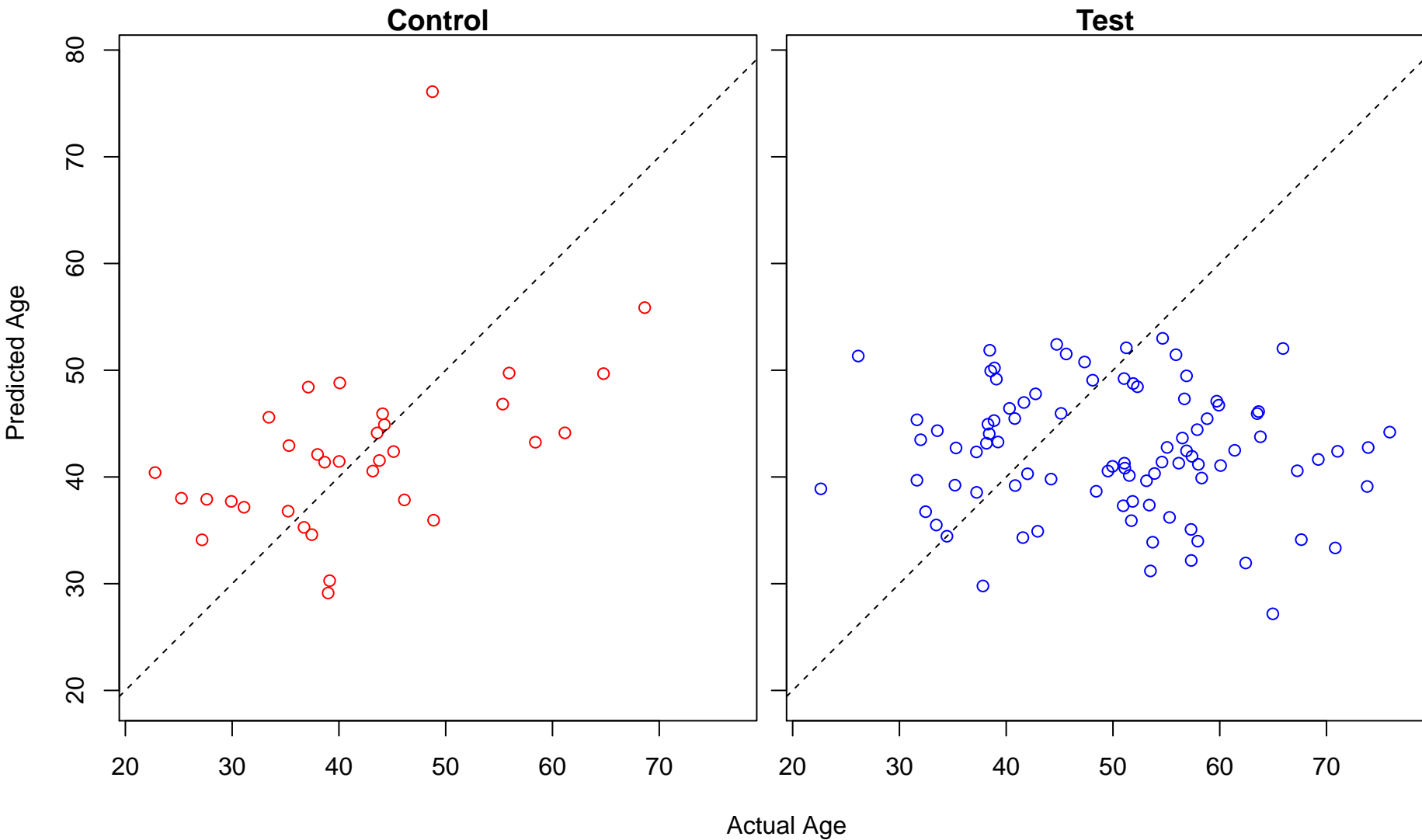
stress granule assembly (Score: 0.993161)



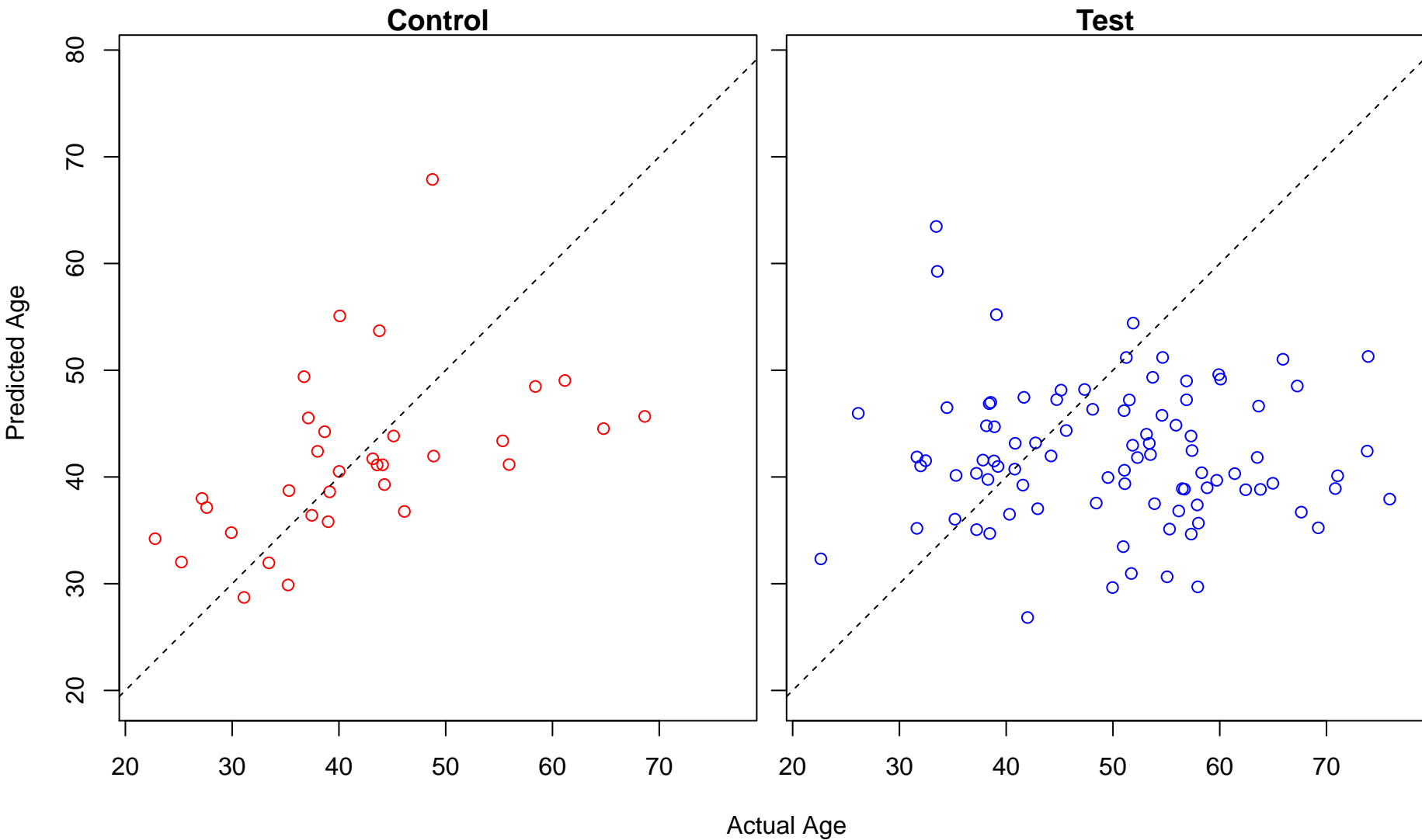
male sex differentiation (Score: 0.990675)



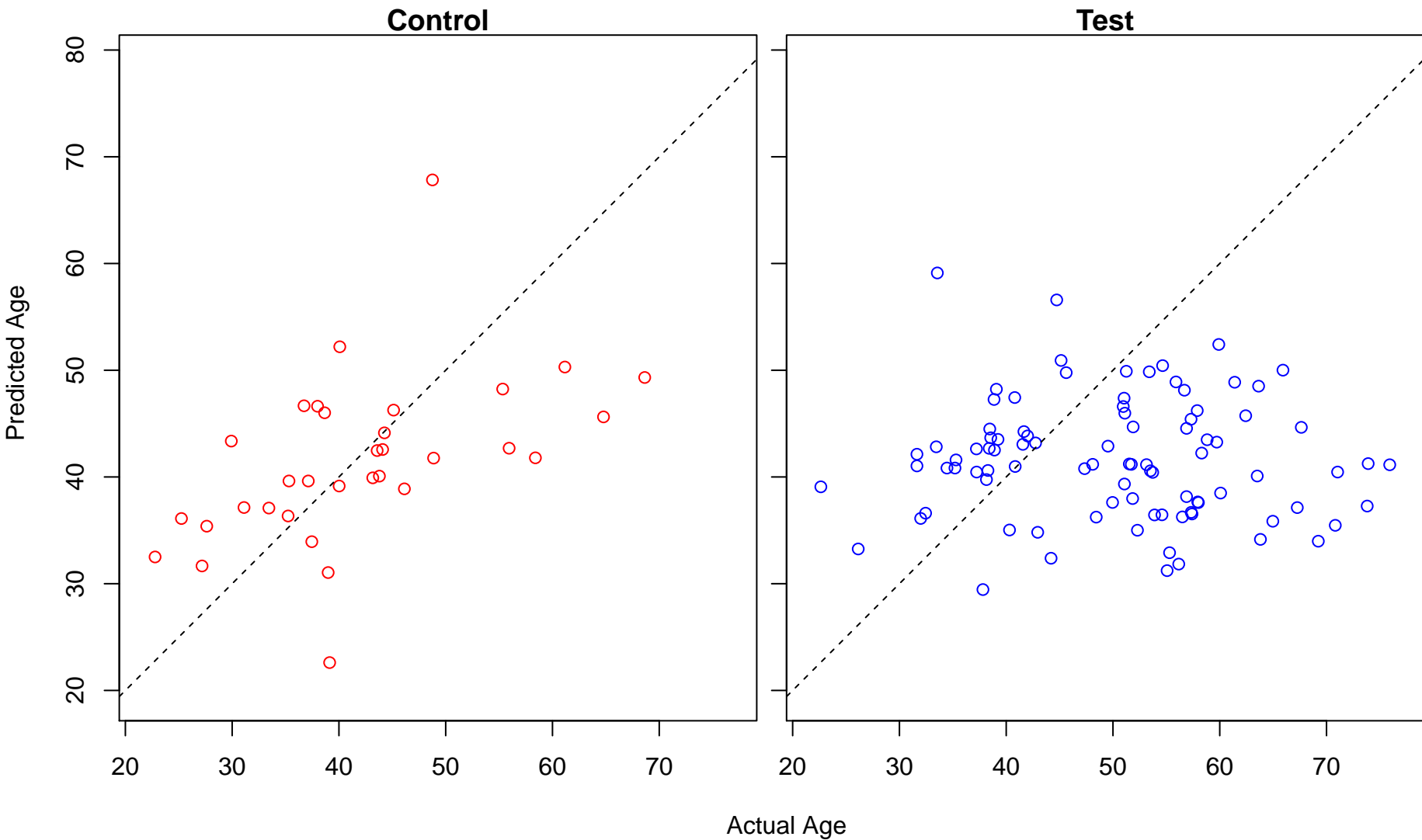
erythrocyte differentiation (Score: 0.990609)



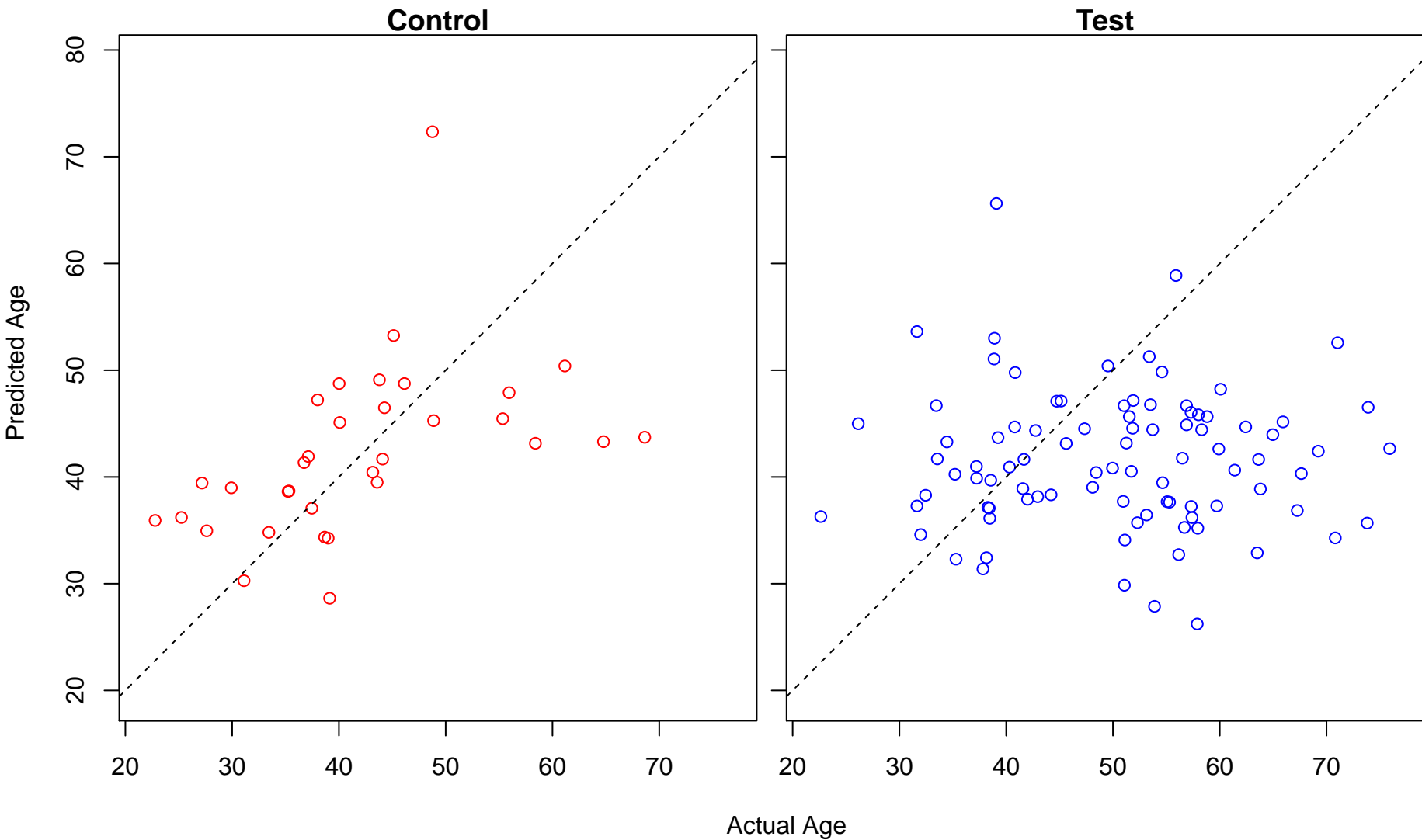
glycosphingolipid metabolic process (Score: 0.990189)



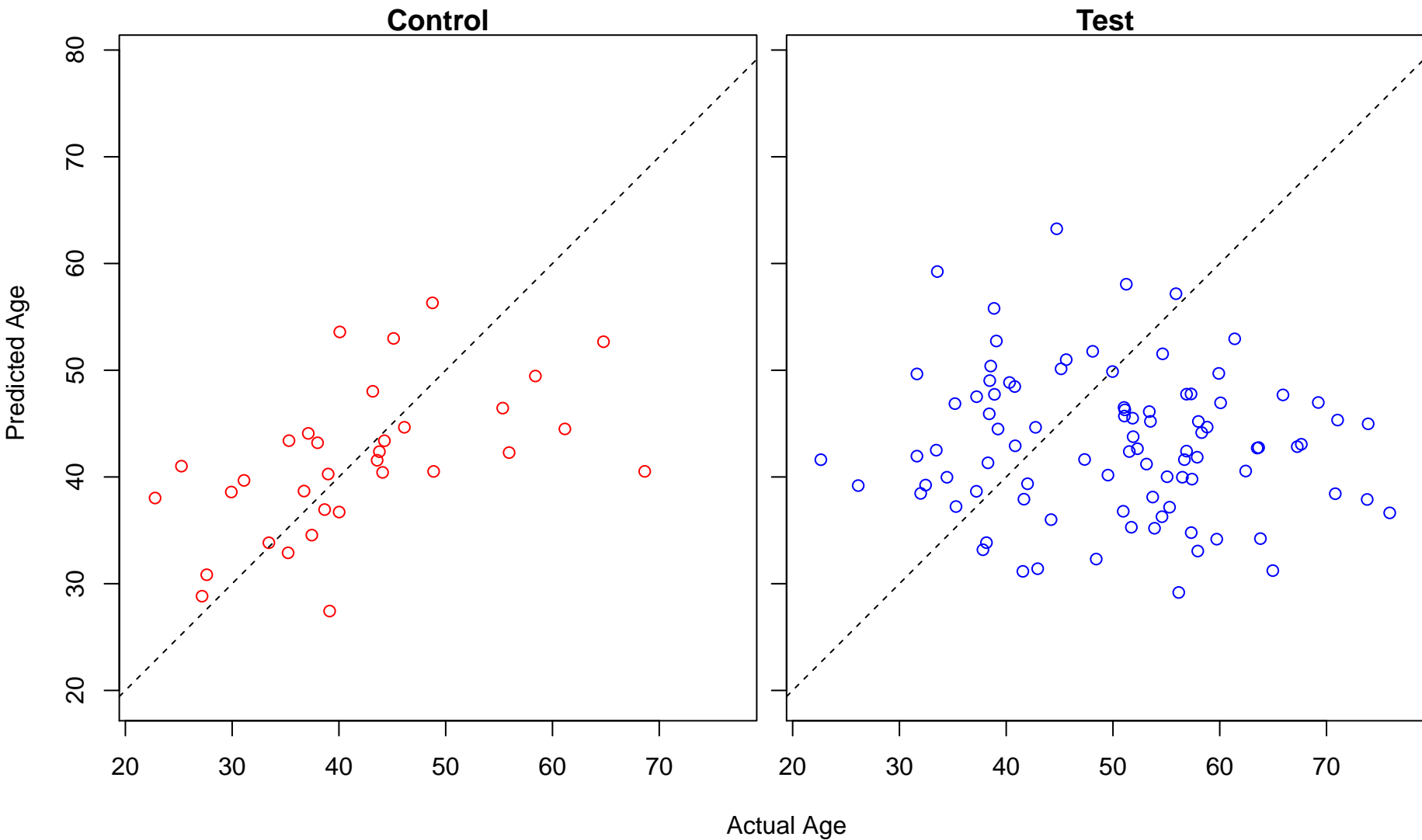
cellular response to hormone stimulus (Score: 0.989296)



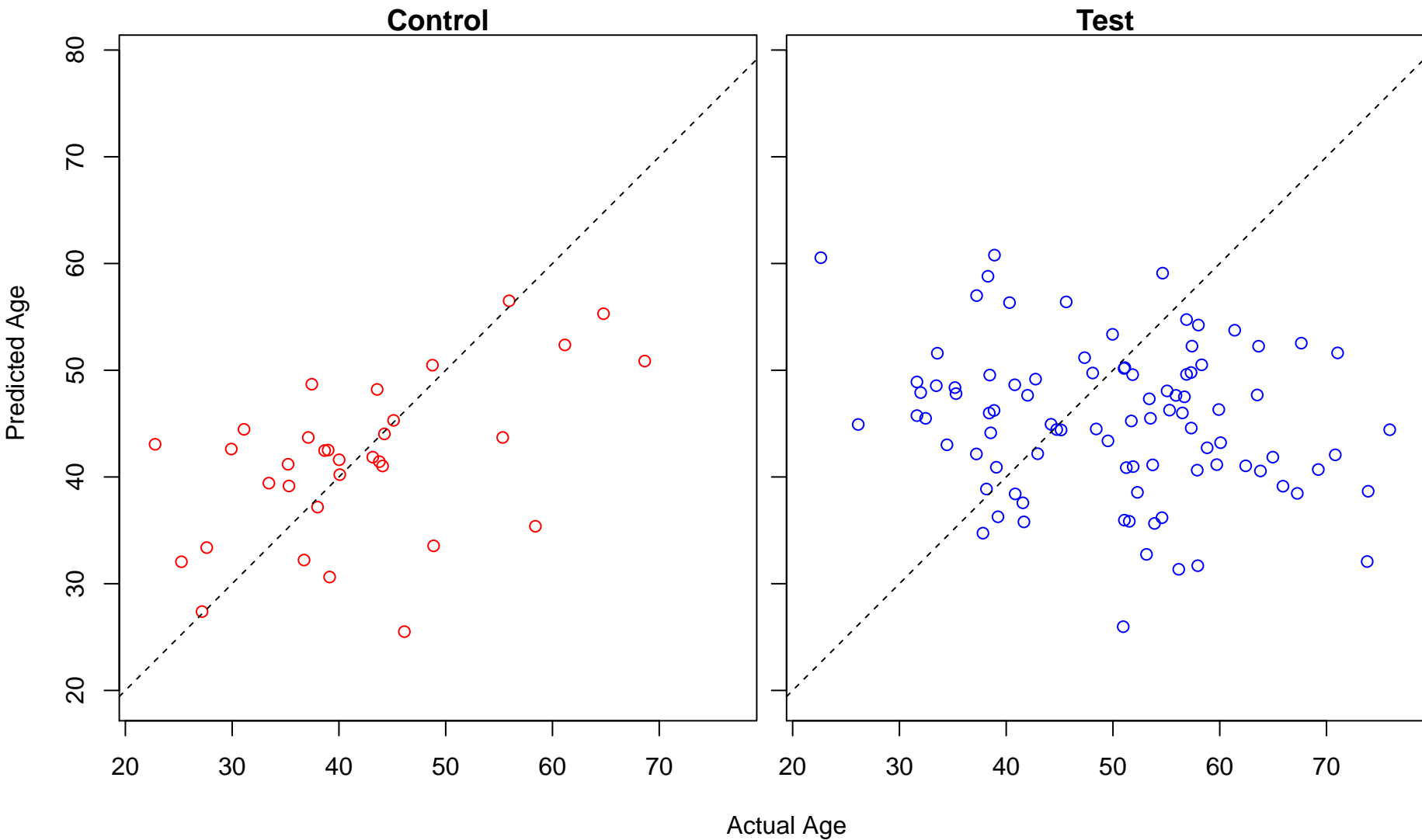
positive regulation of mitochondrial translation (Score: 0.989284)



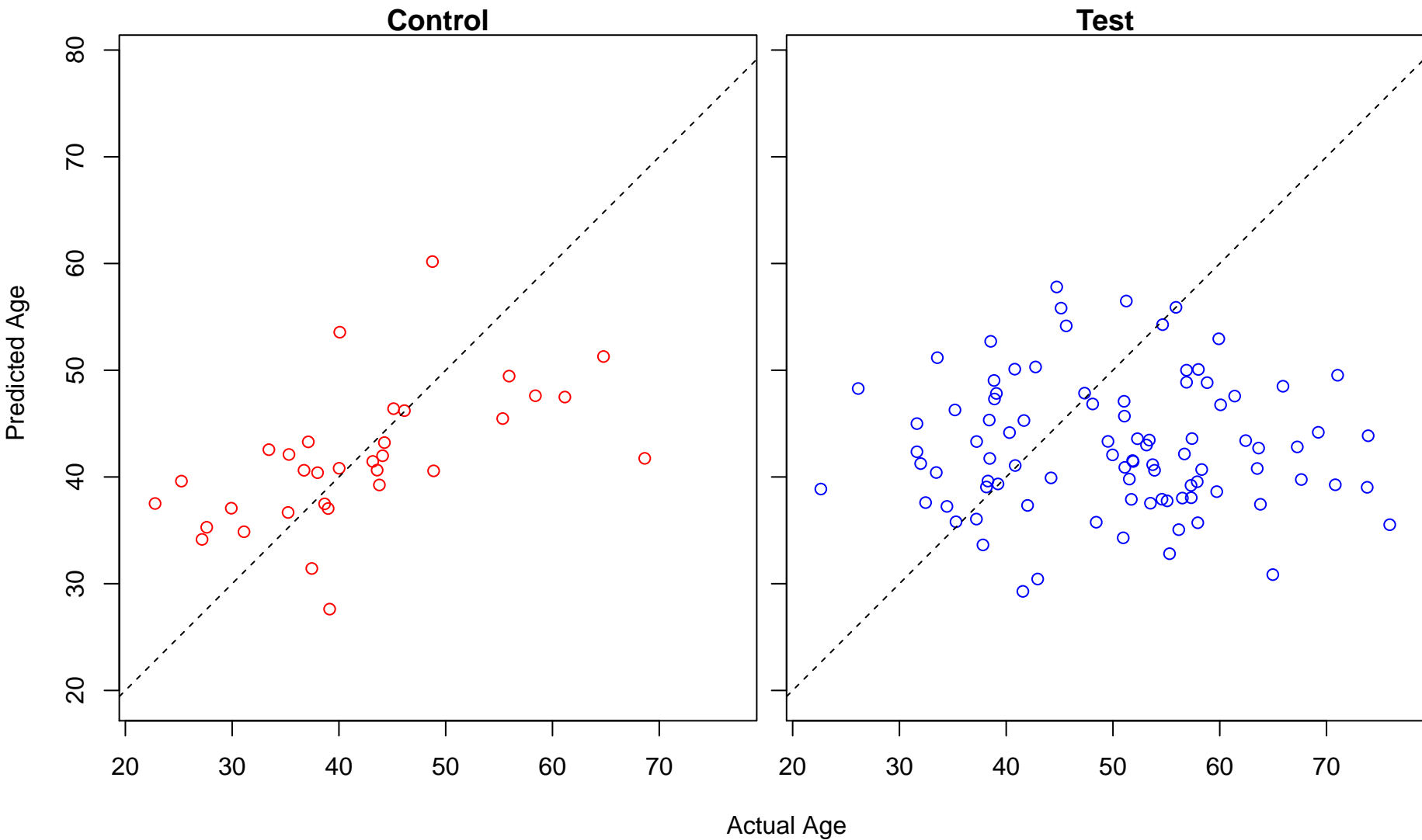
lipid transport (Score: 0.988714)



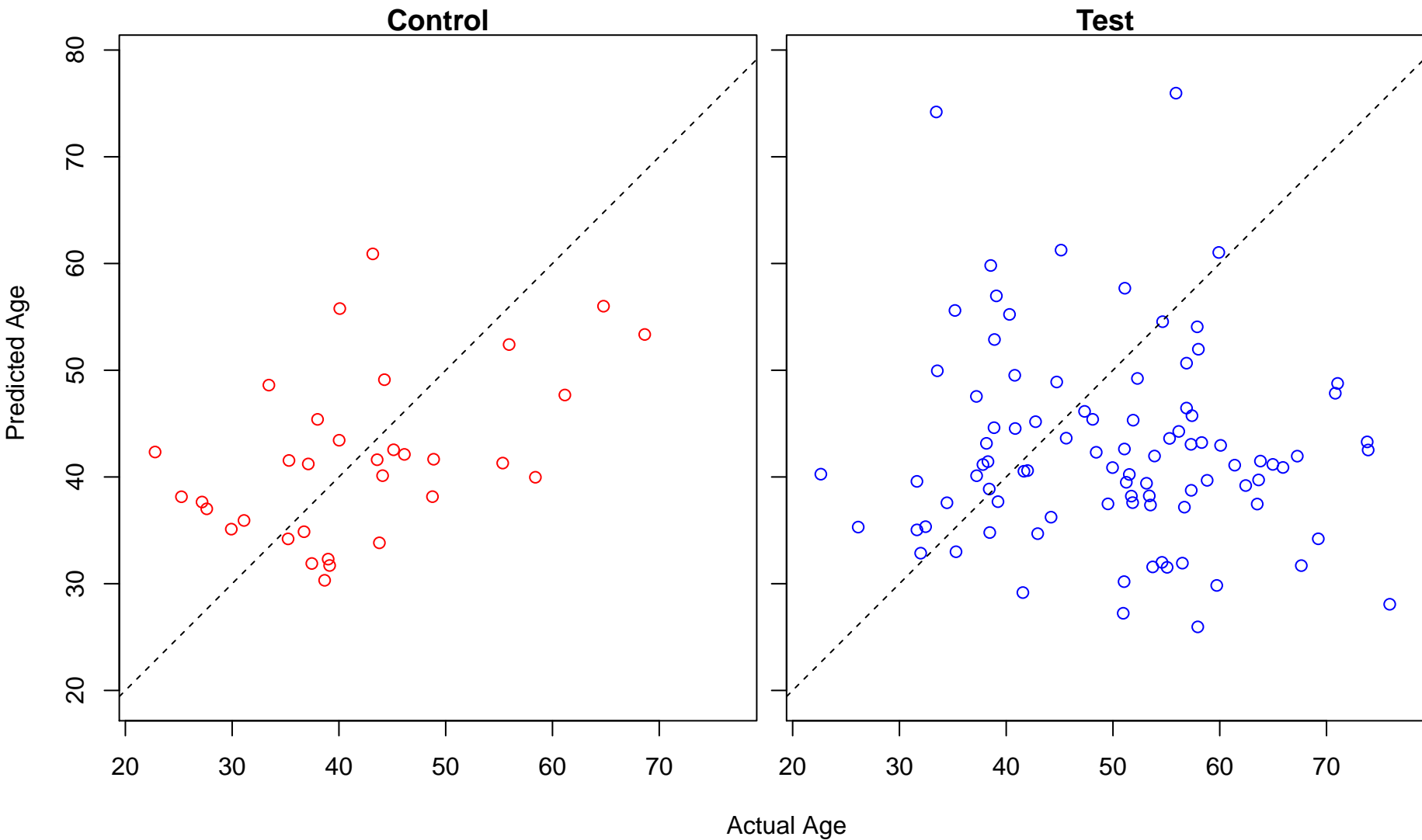
SMAD protein signal transduction (Score: 0.988633)



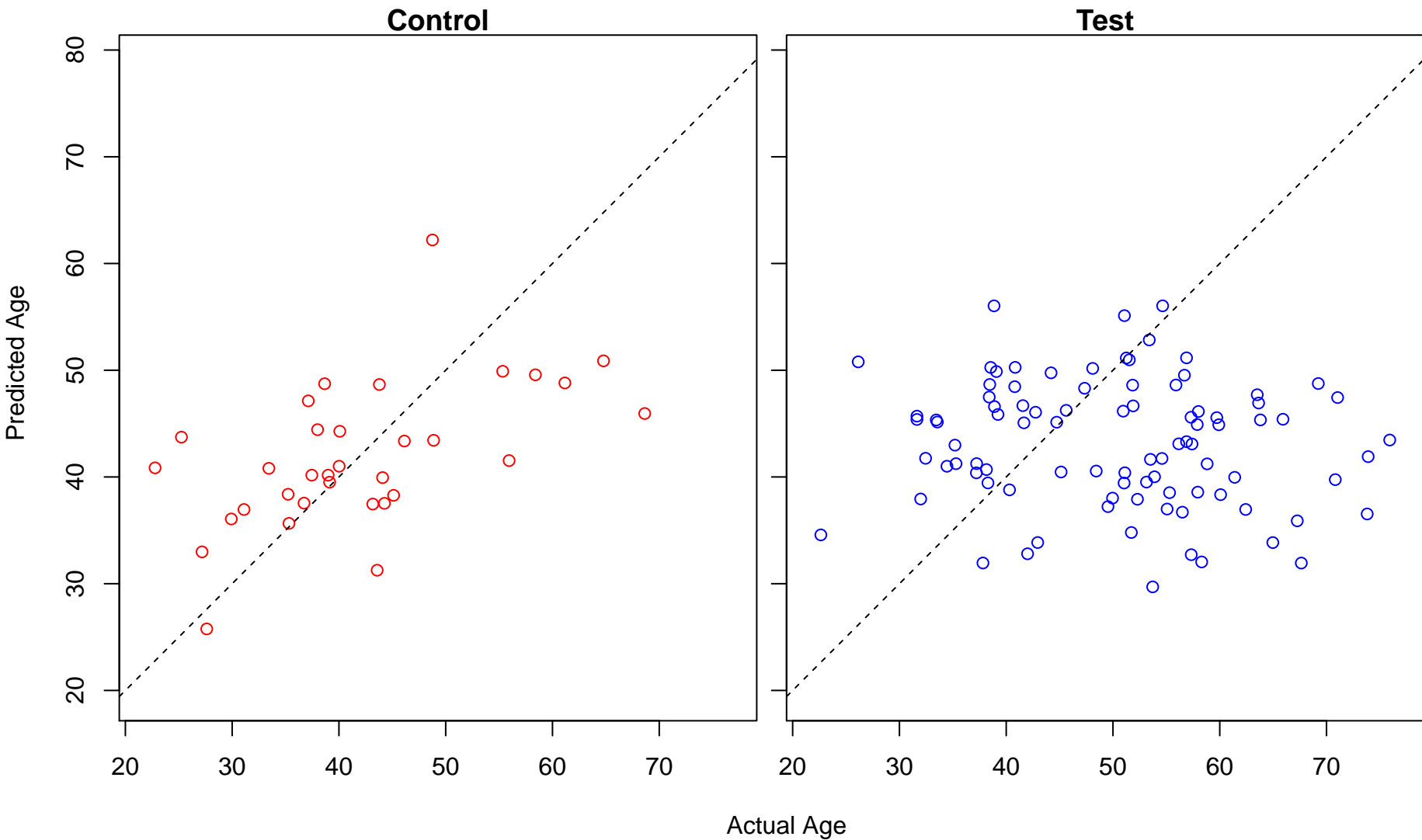
regulation of ion transmembrane transport (Score: 0.988300)



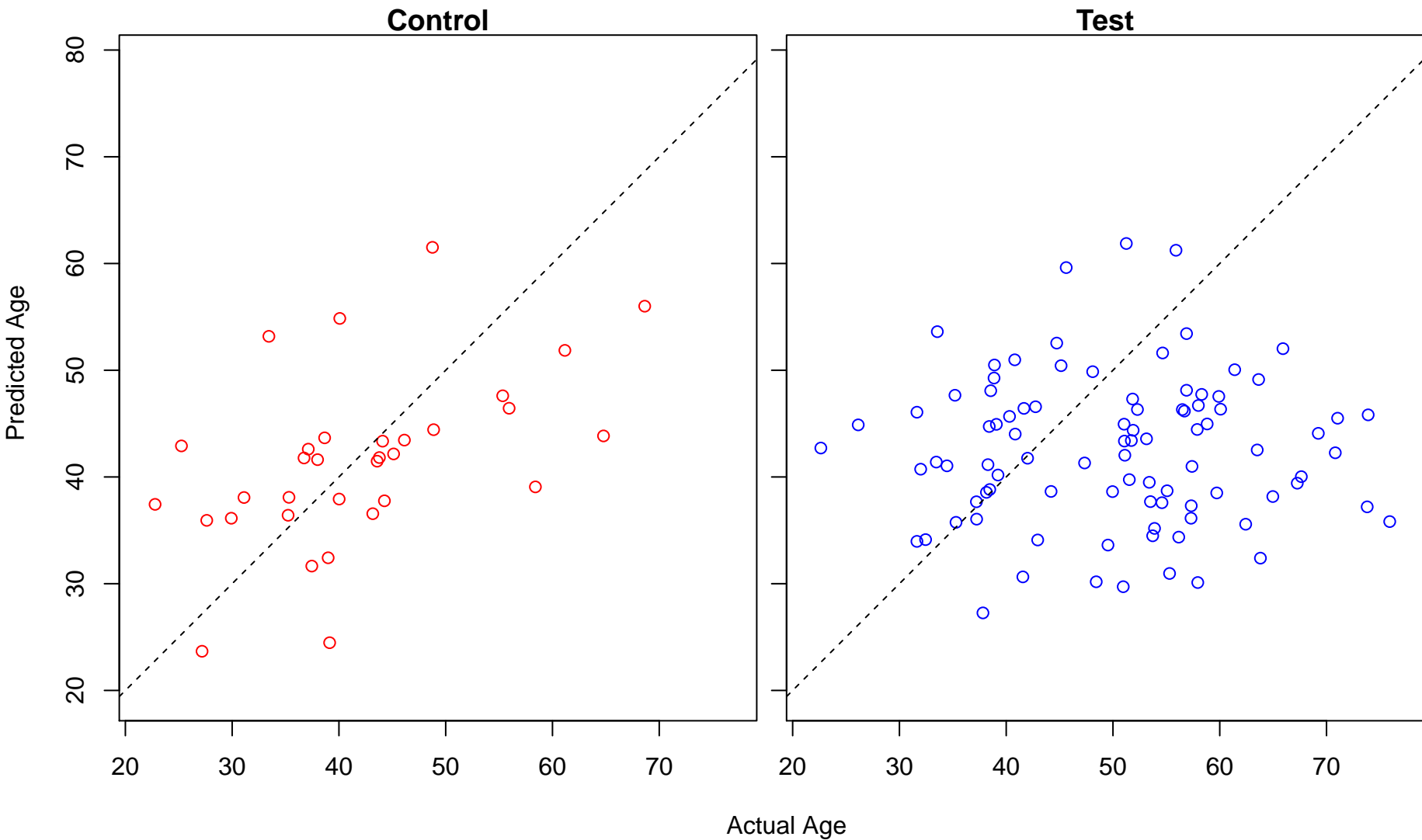
heterochromatin organization (Score: 0.987487)



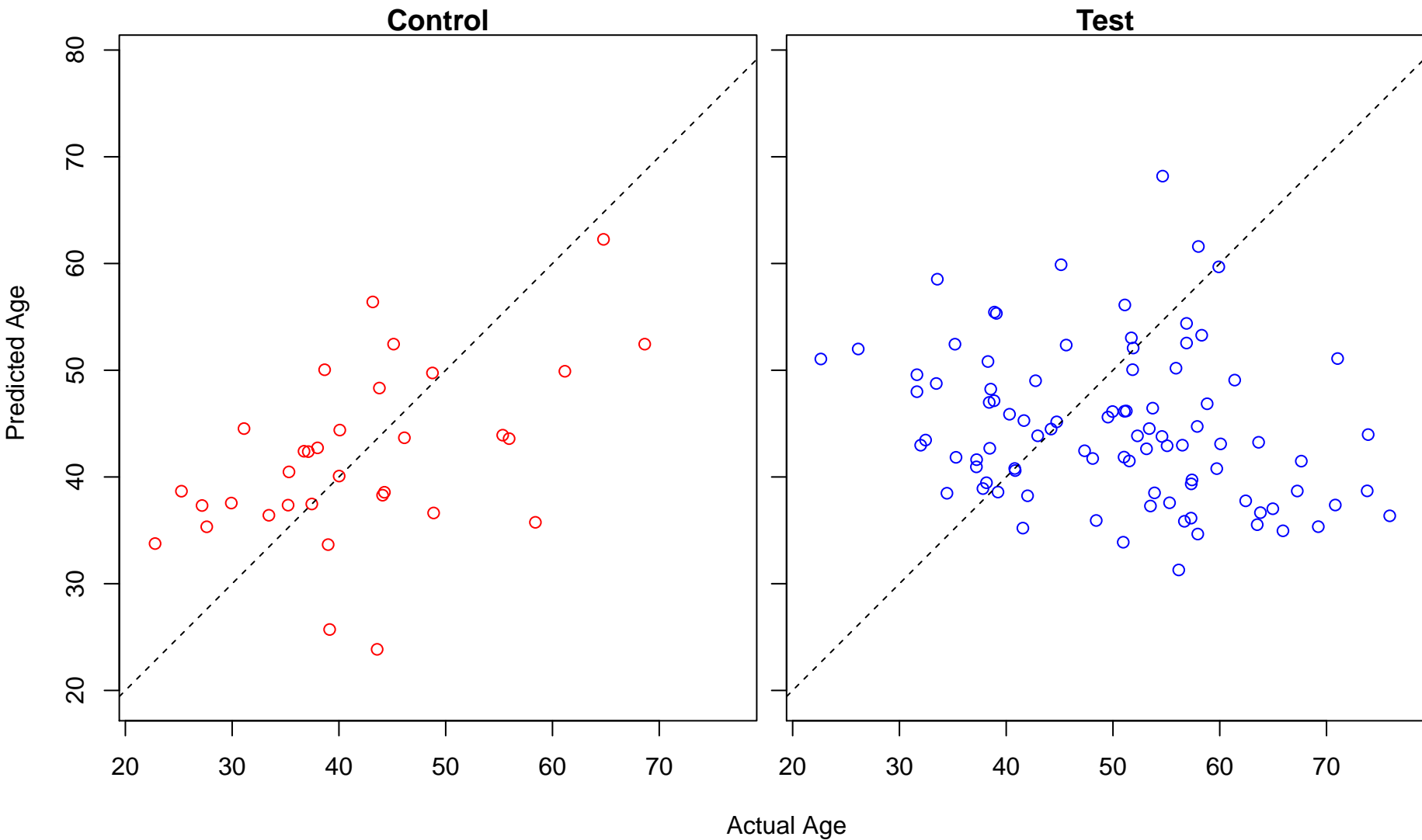
outflow tract morphogenesis (Score: 0.987297)



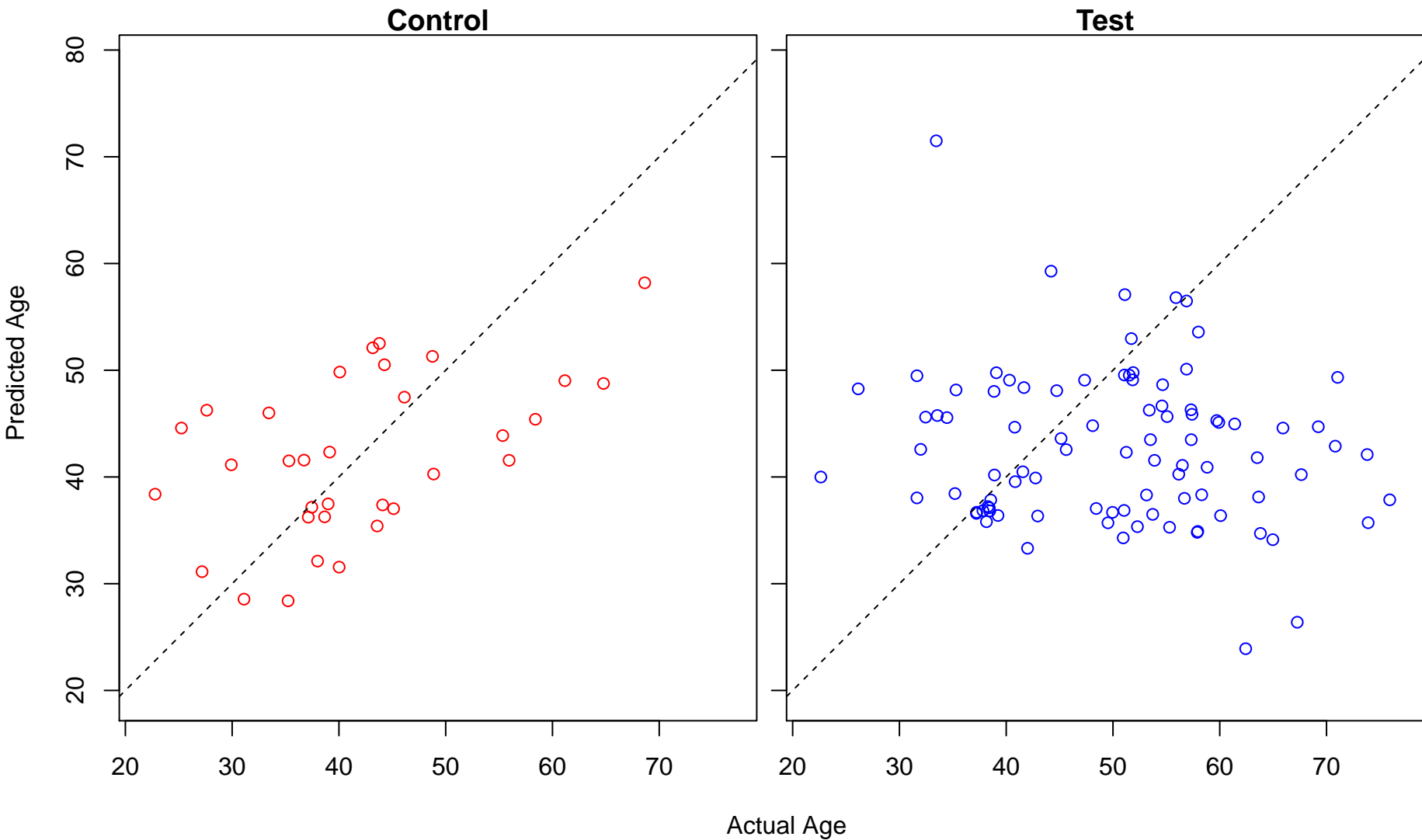
regulation of sequestering of calcium ion (Score: 0.987075)



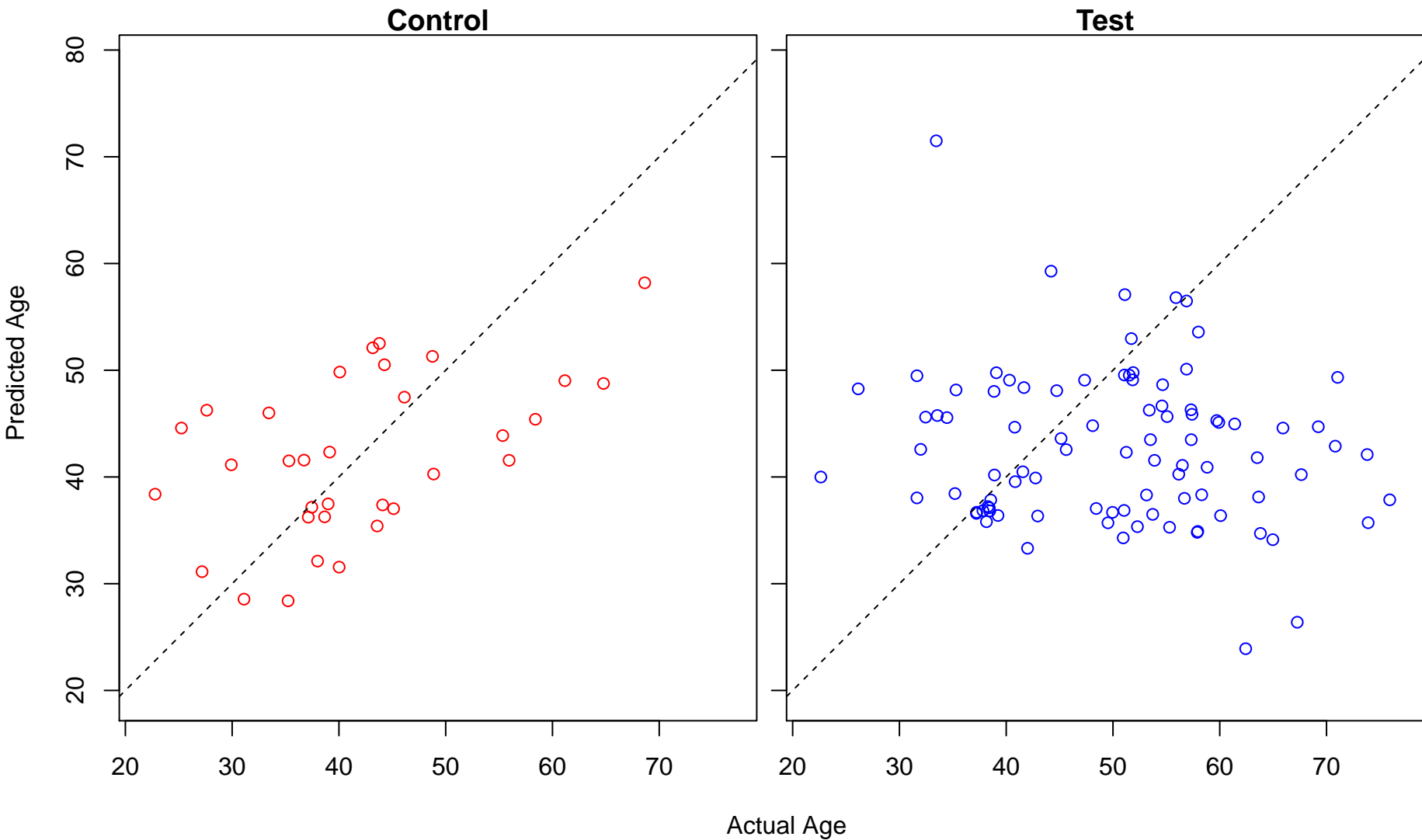
positive regulation of DNA-dependent DNA replication (Score: 0.986965)



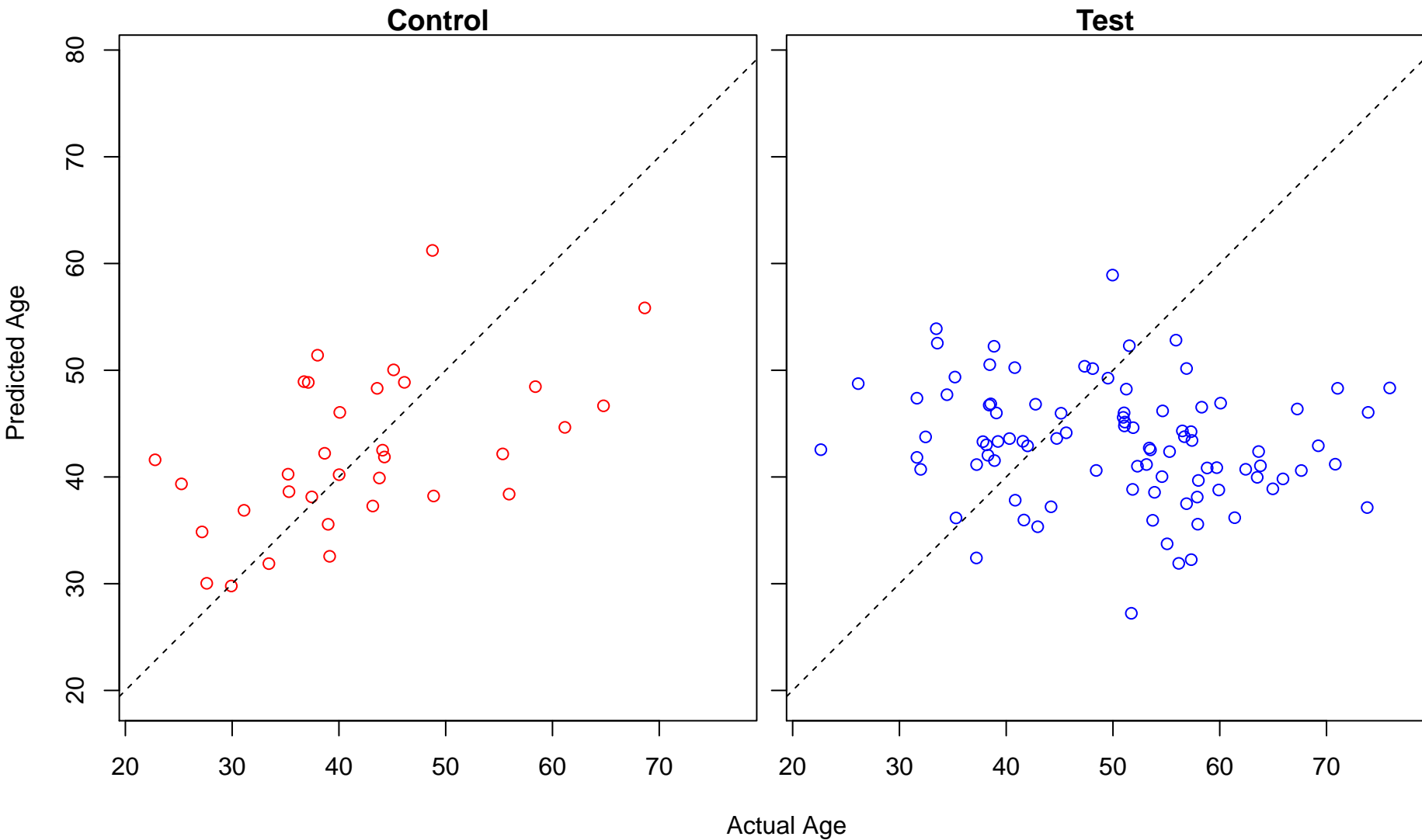
pulmonary valve development (Score: 0.985572)



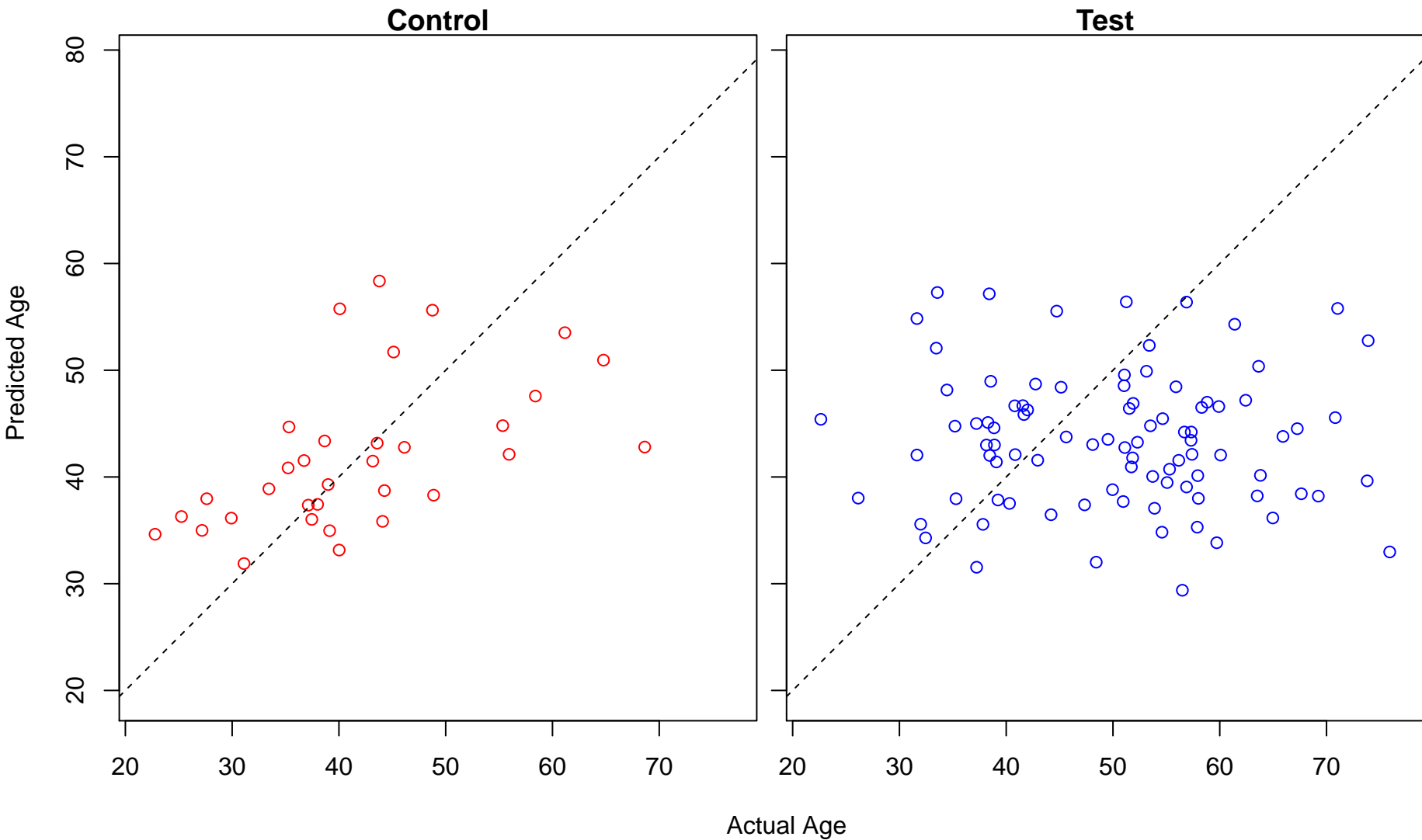
pulmonary valve morphogenesis (Score: 0.985572)



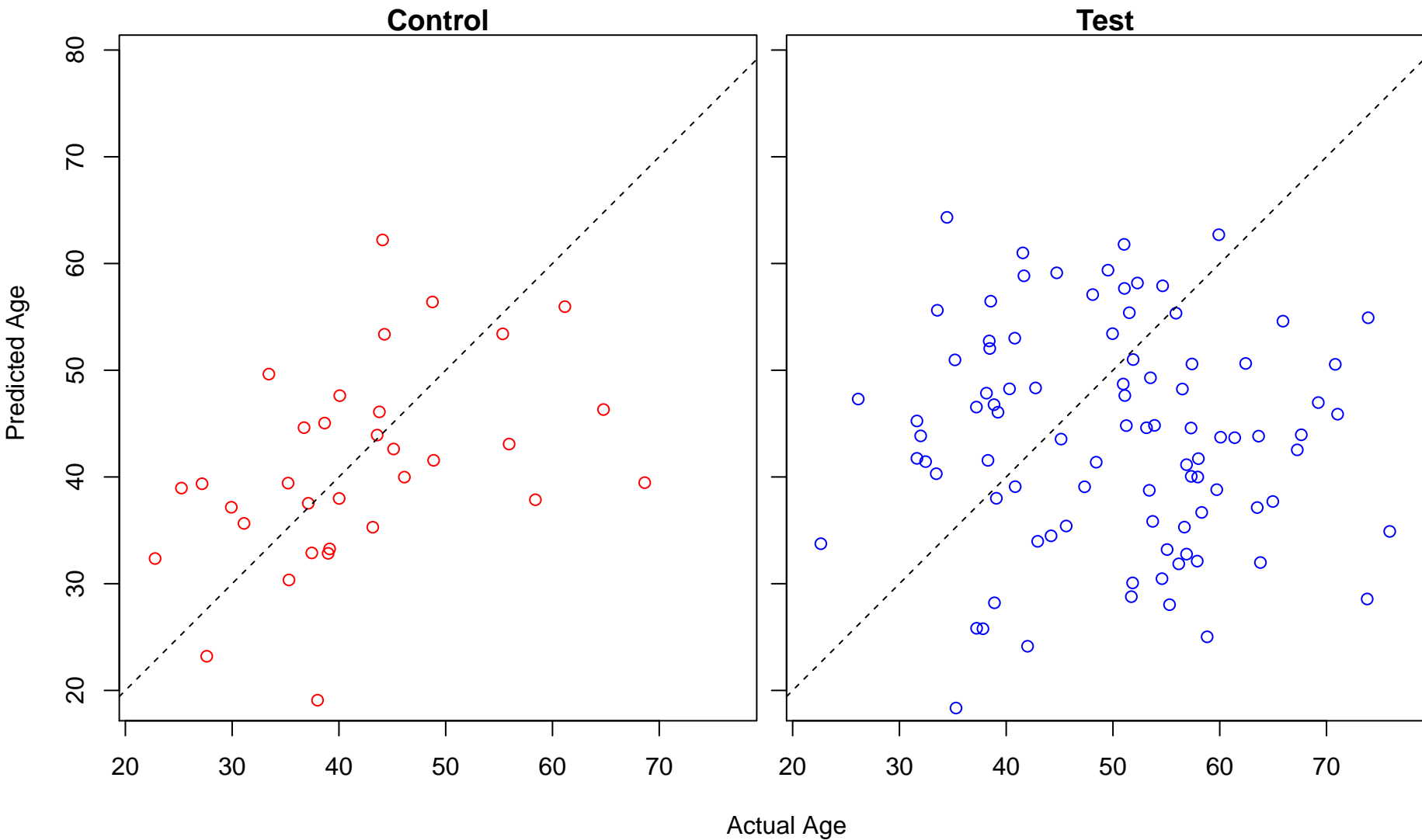
chaperone-mediated protein complex assembly (Score: 0.984685)



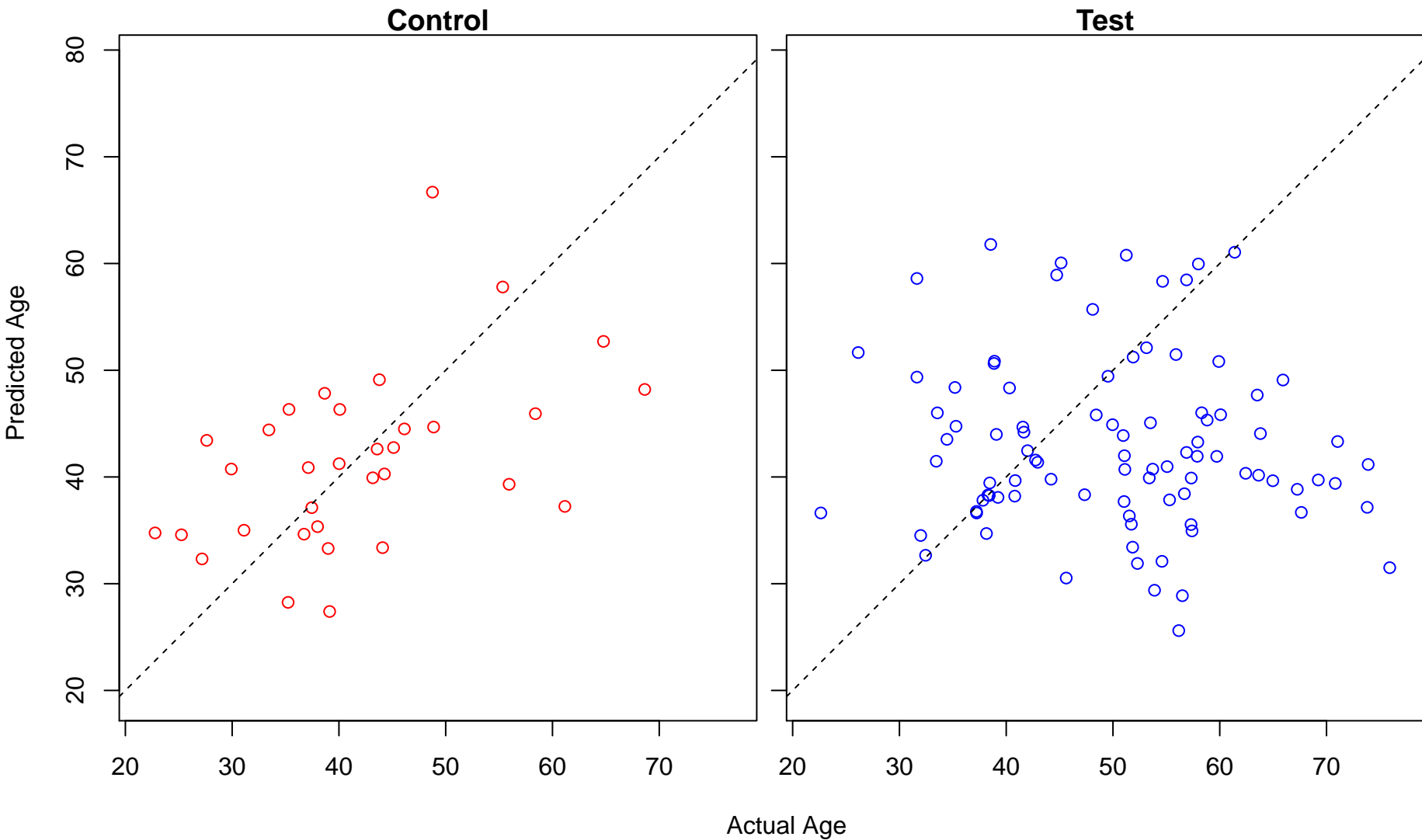
phosphatidylcholine metabolic process (Score: 0.979683)



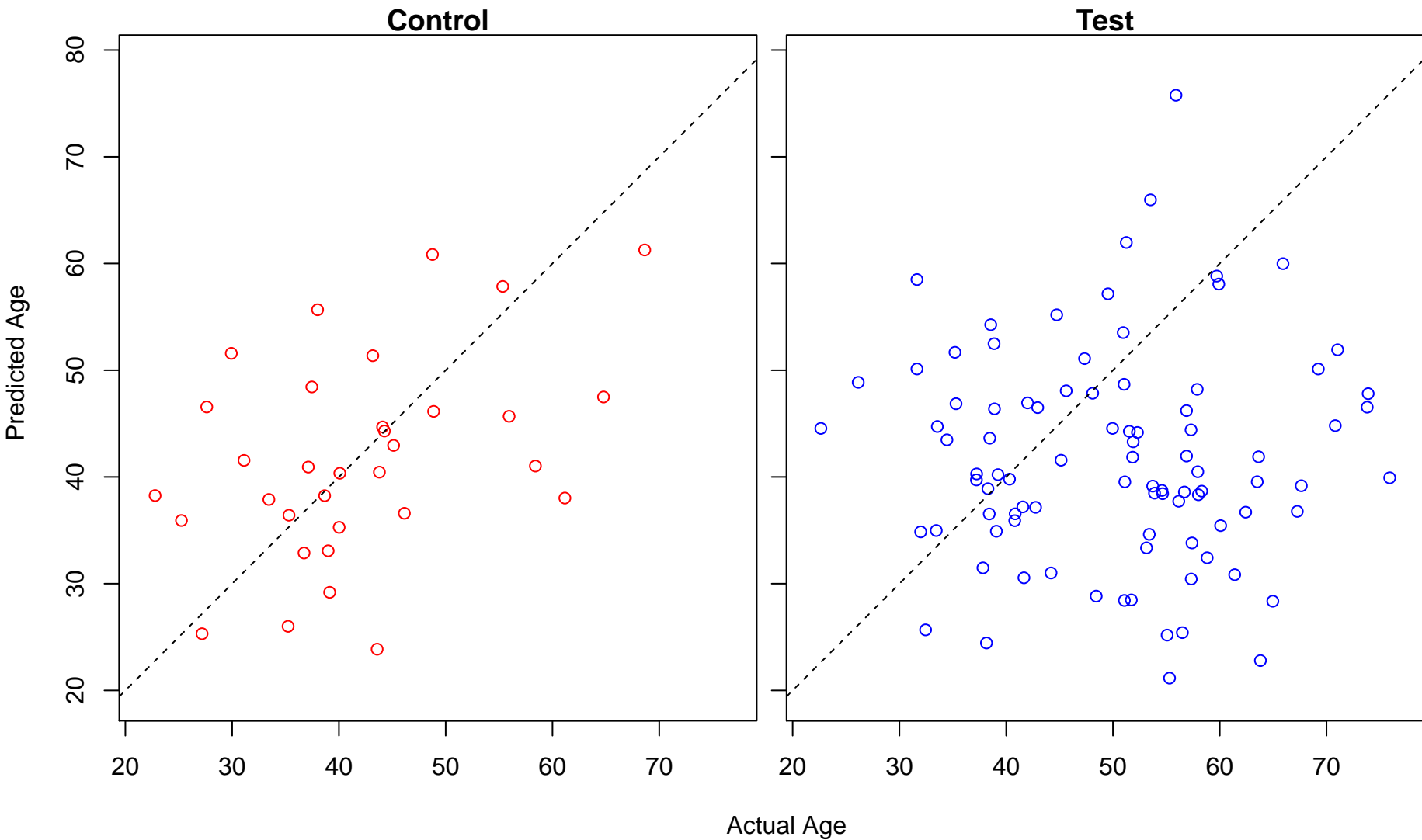
protein O-linked glycosylation (Score: 0.979022)



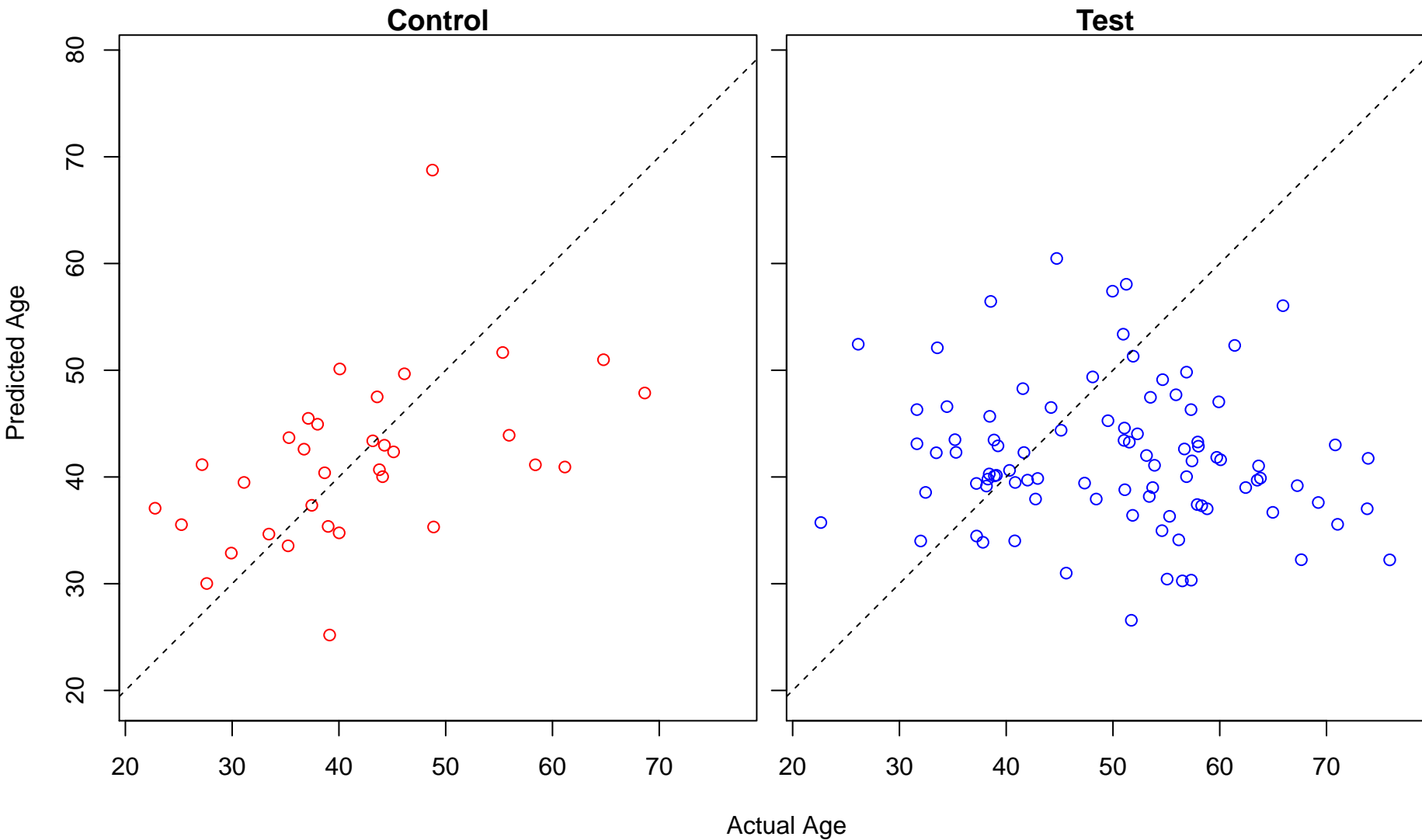
centrosome cycle (Score: 0.977662)



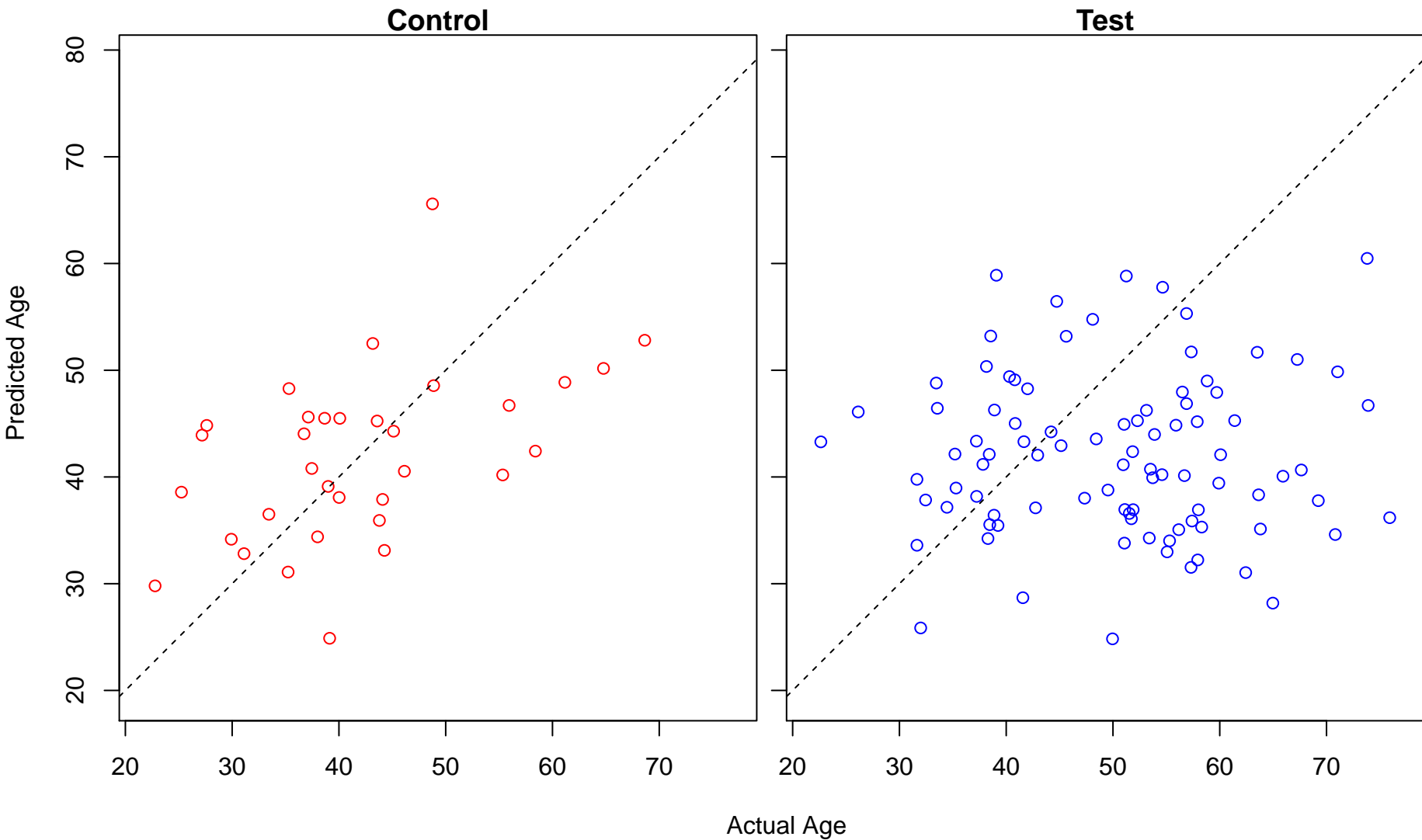
isoprenoid metabolic process (Score: 0.975854)



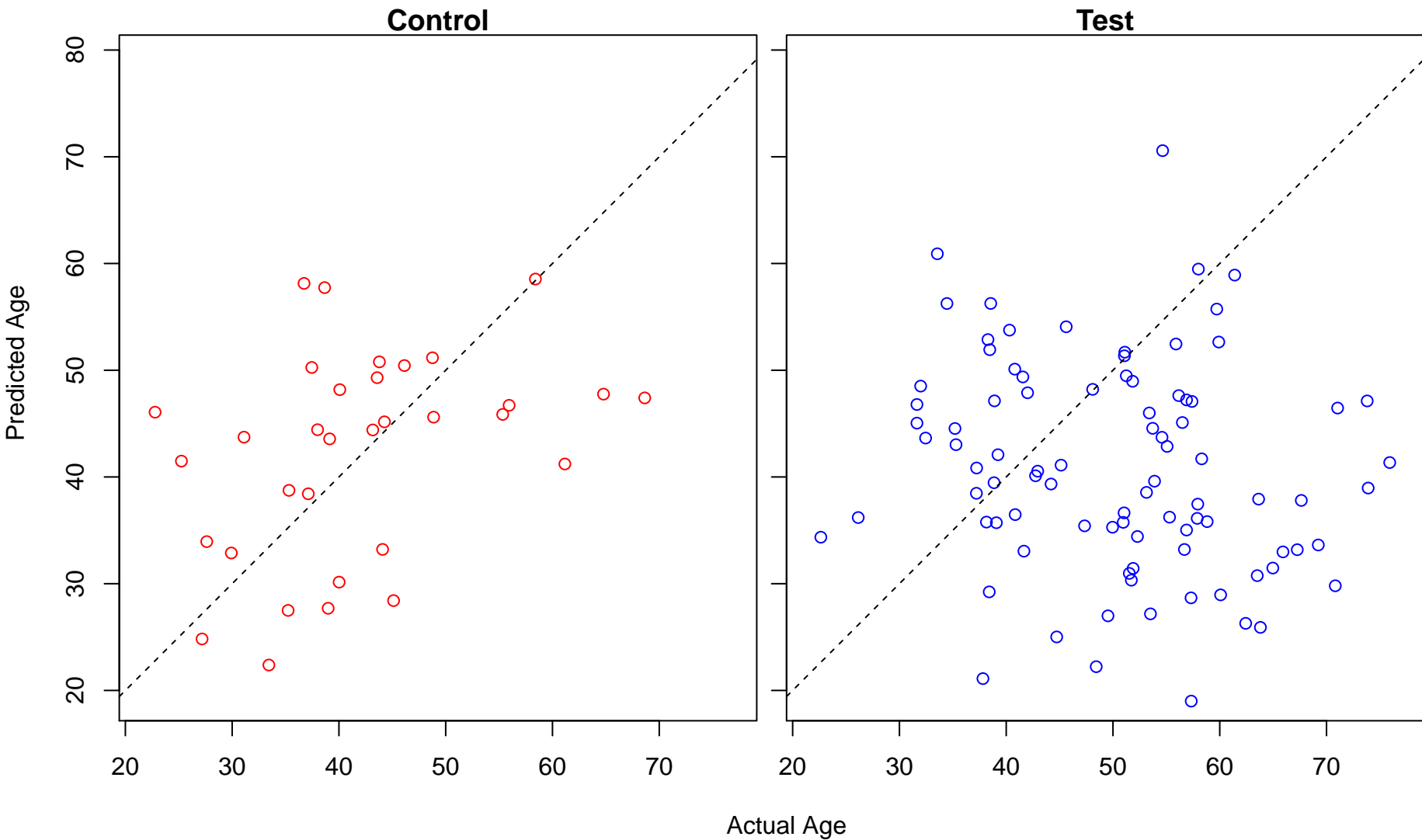
DNA damage checkpoint (Score: 0.975819)



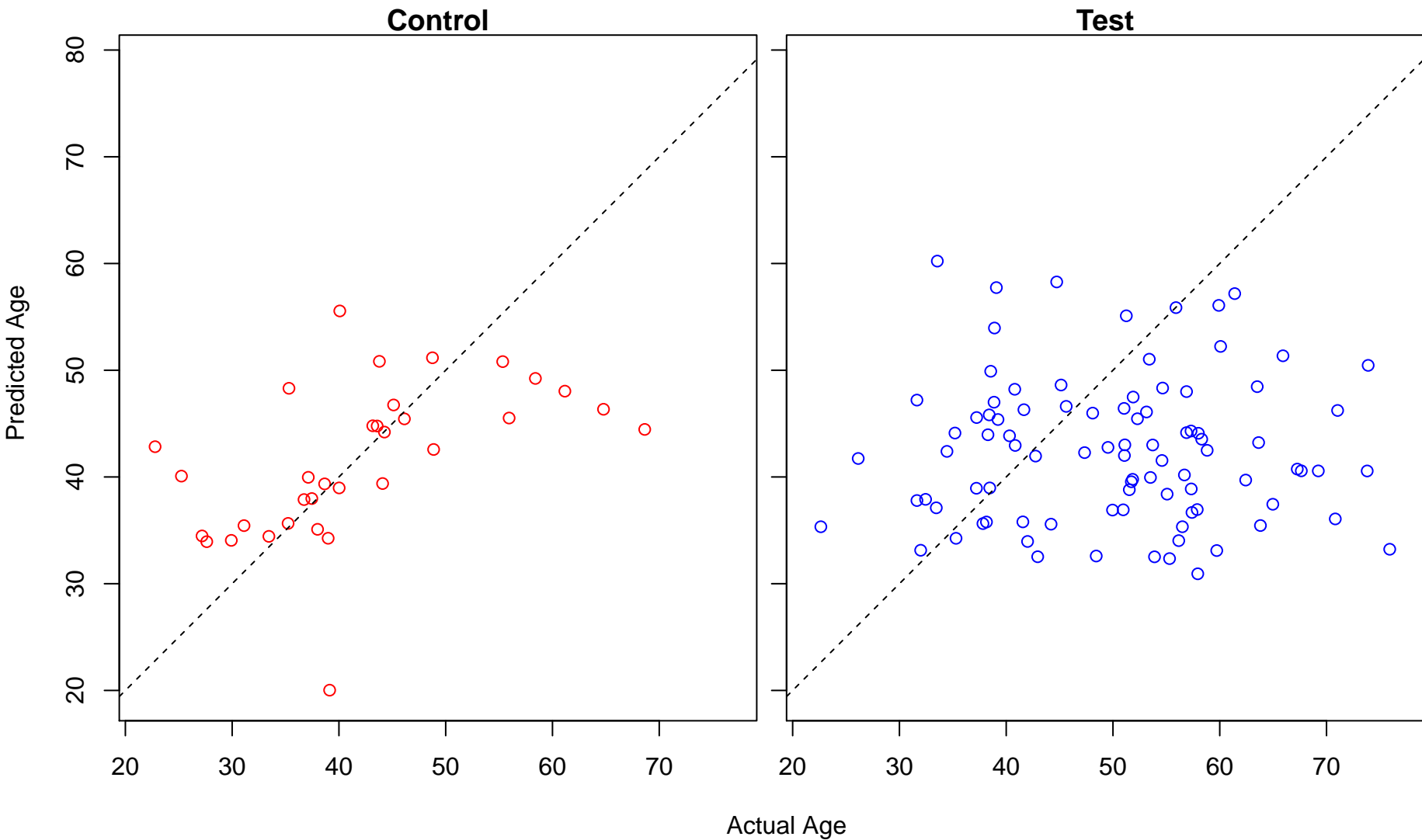
circadian regulation of gene expression (Score: 0.975751)



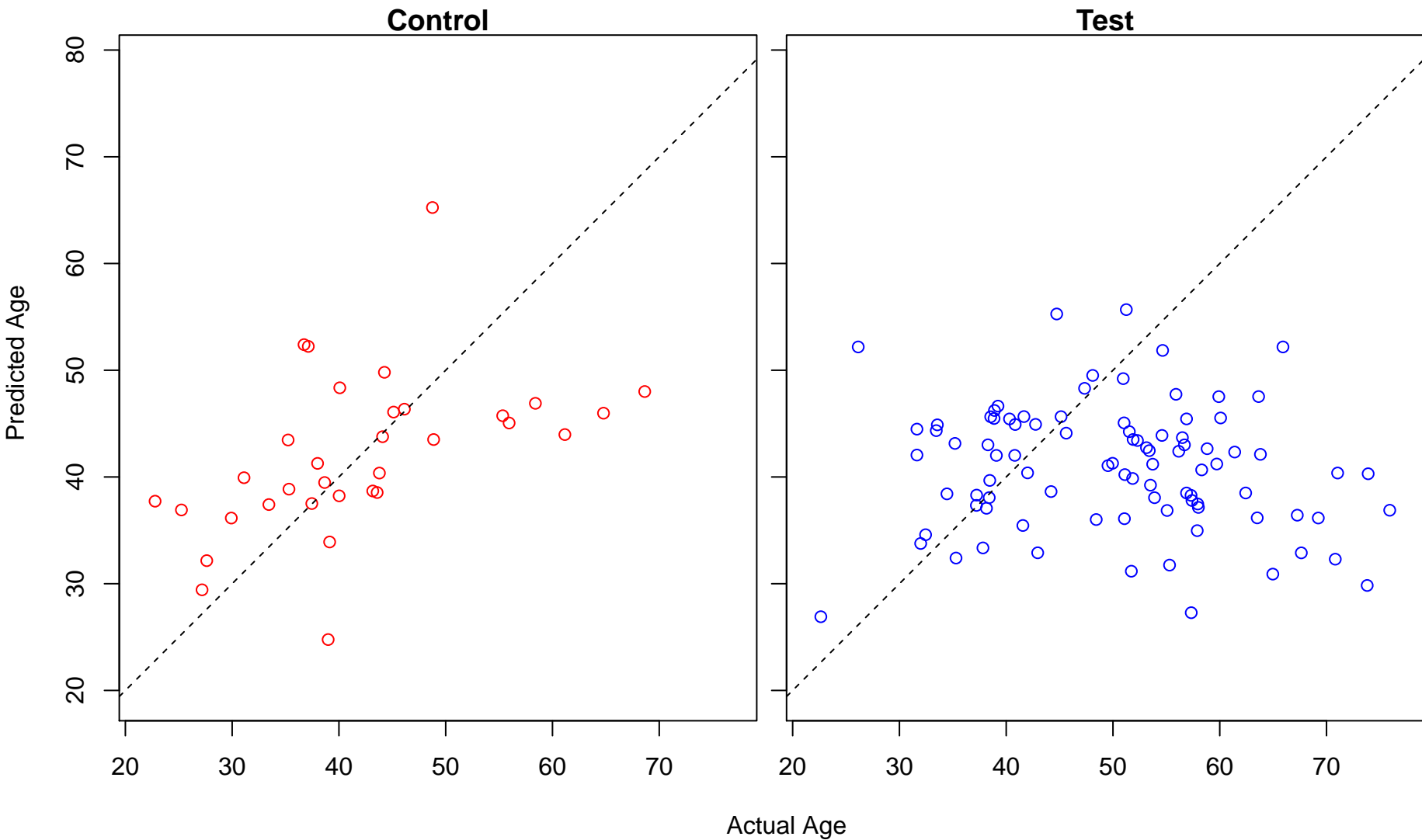
endocardial cushion development (Score: 0.975135)



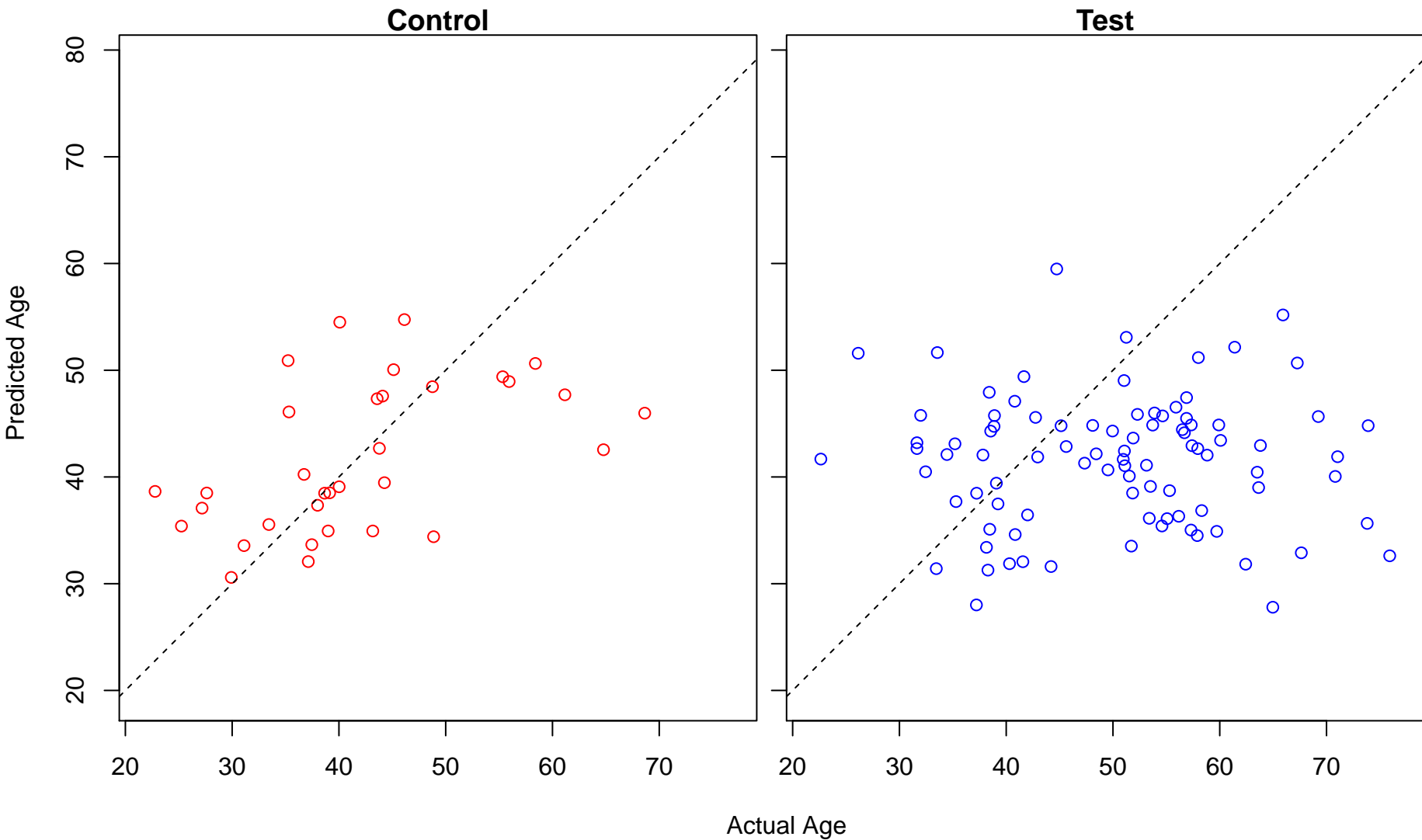
cortical cytoskeleton organization (Score: 0.974369)



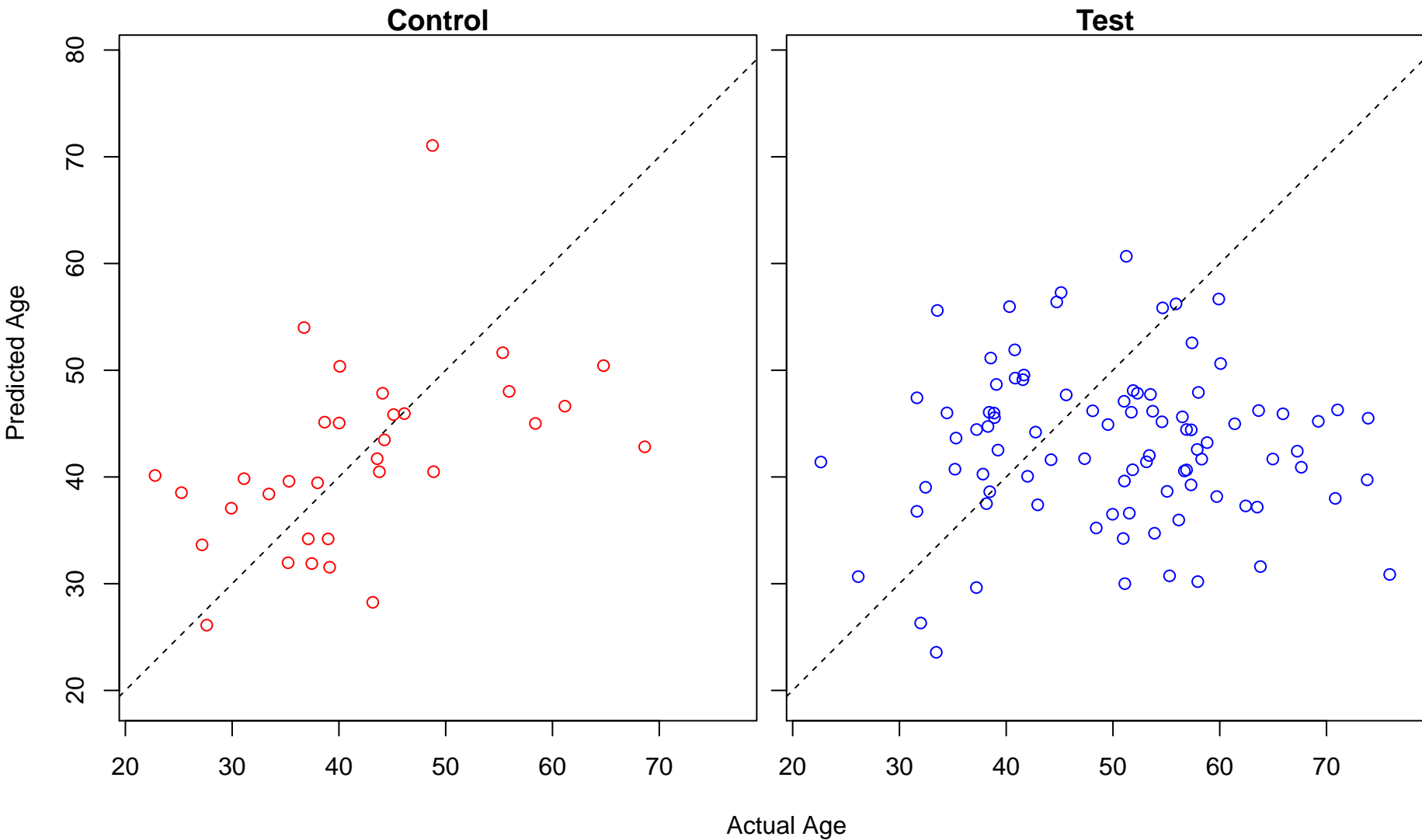
erythrocyte development (Score: 0.972795)



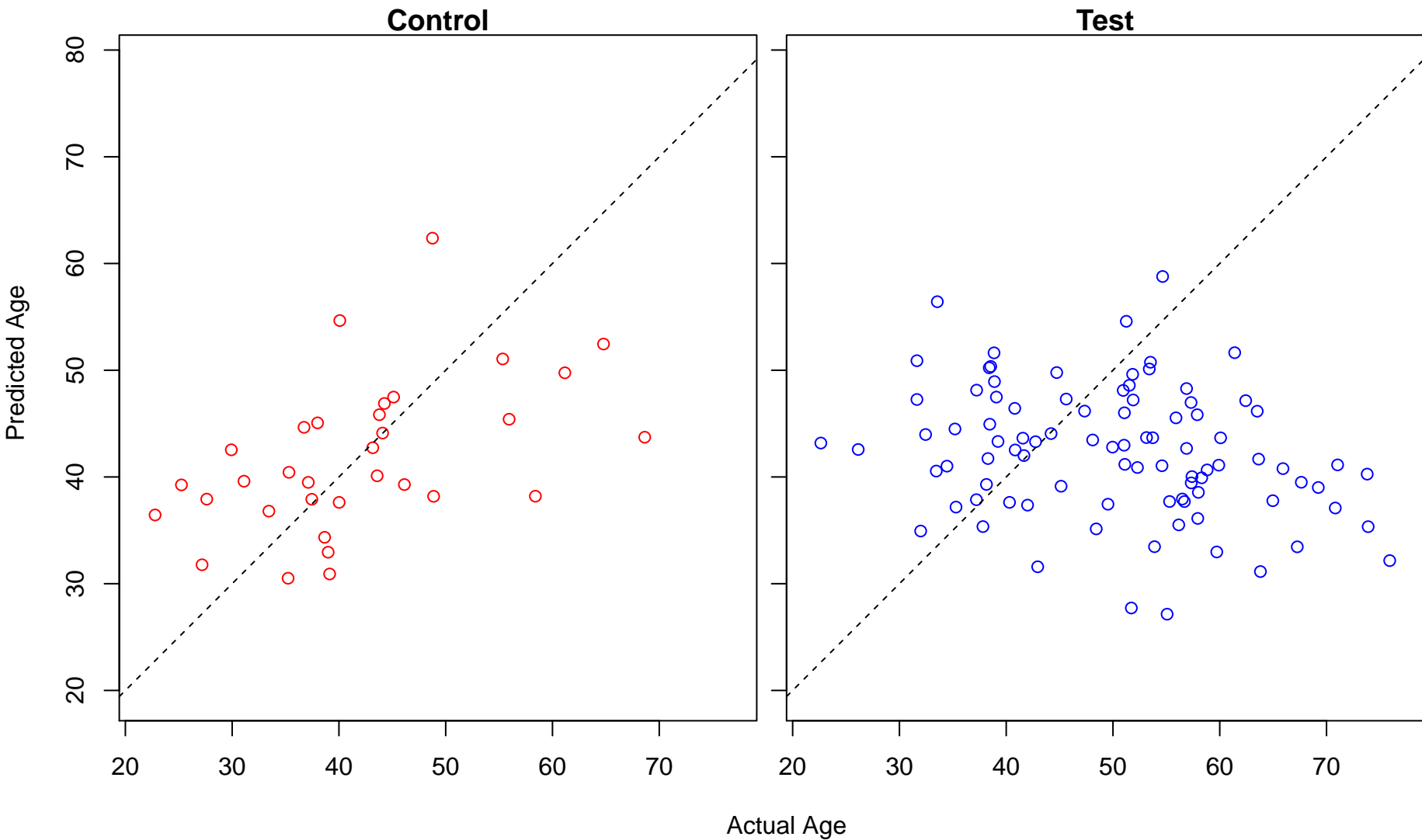
regulation of membrane repolarization (Score: 0.970575)



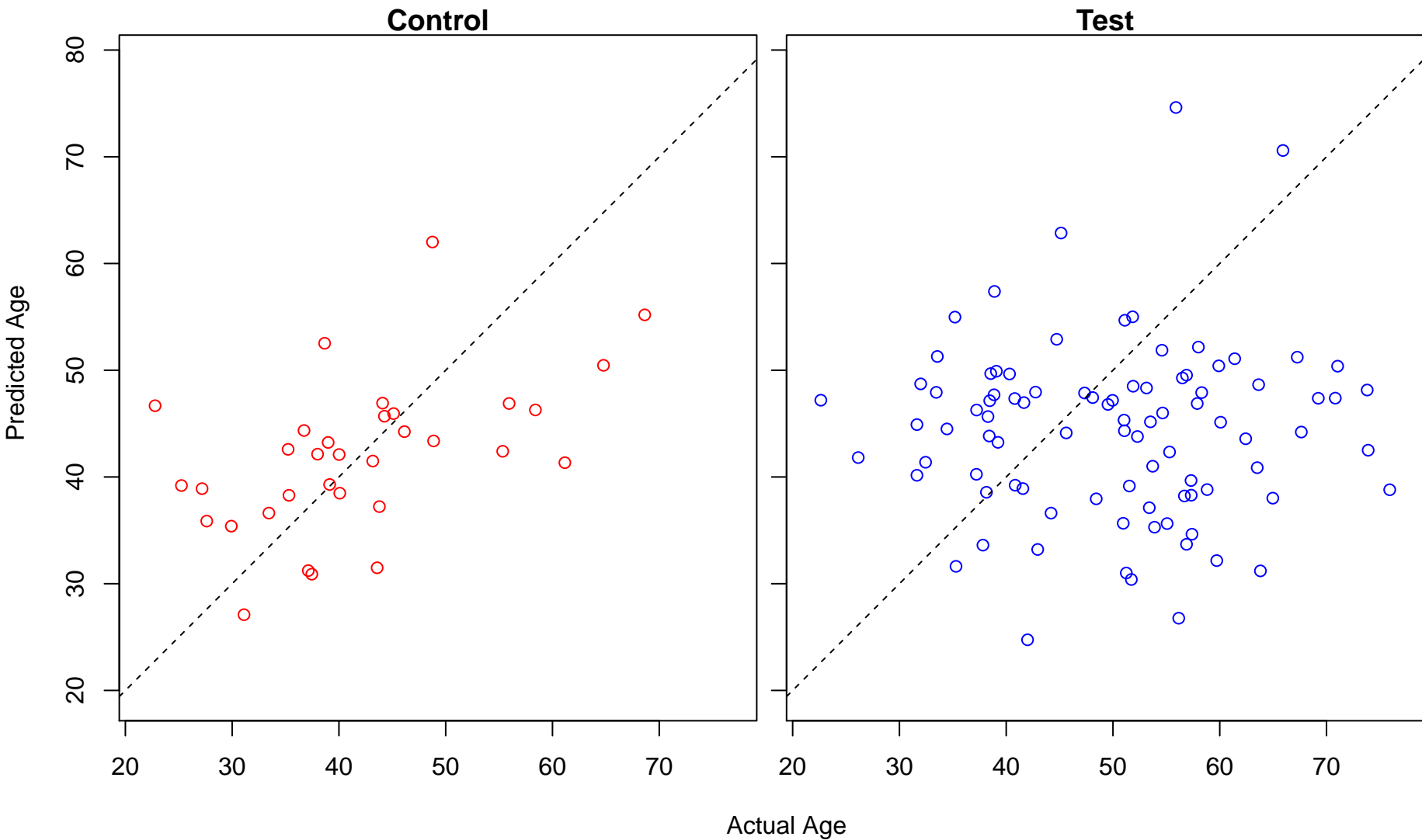
regulation of endopeptidase activity (Score: 0.968245)



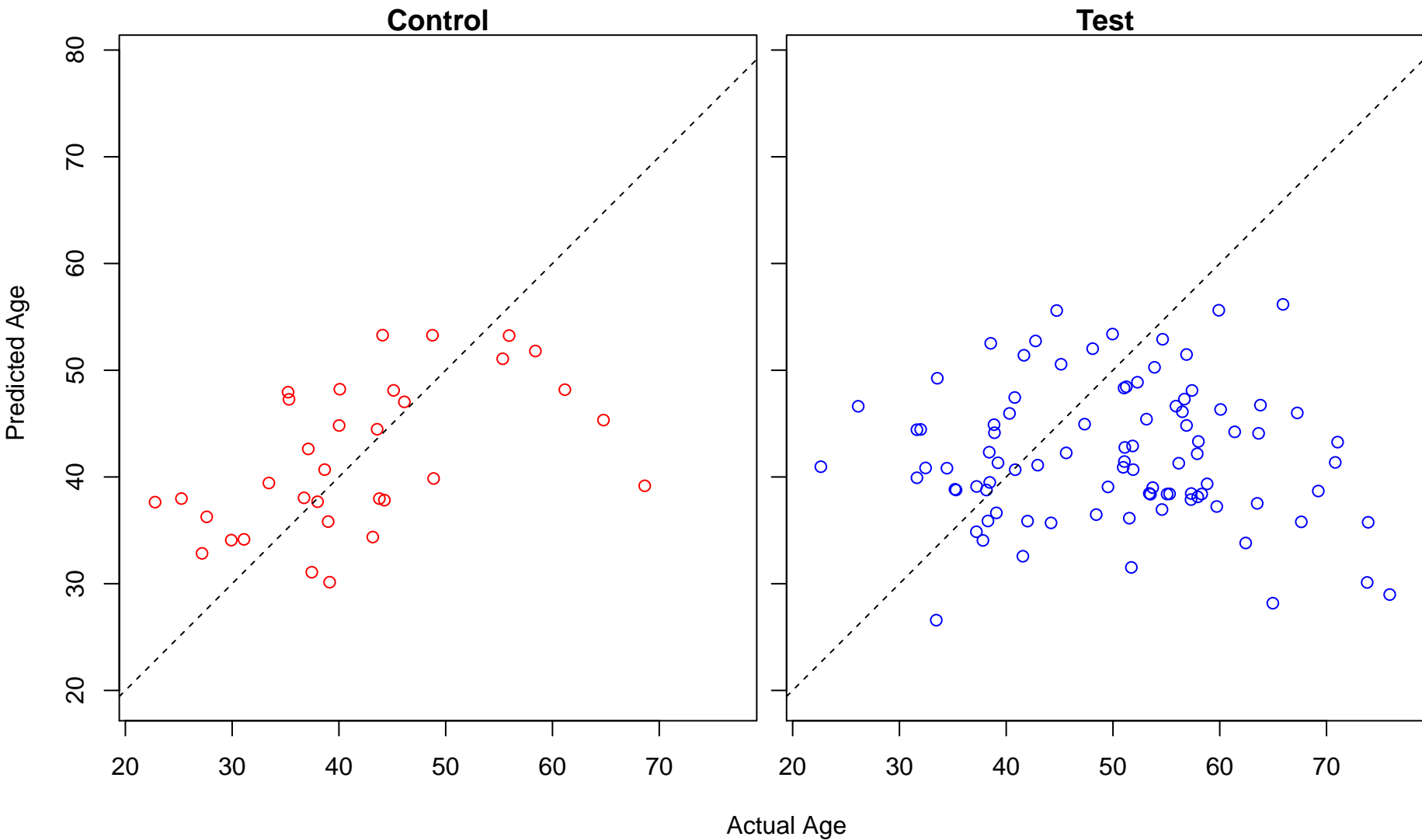
epithelium development (Score: 0.965377)



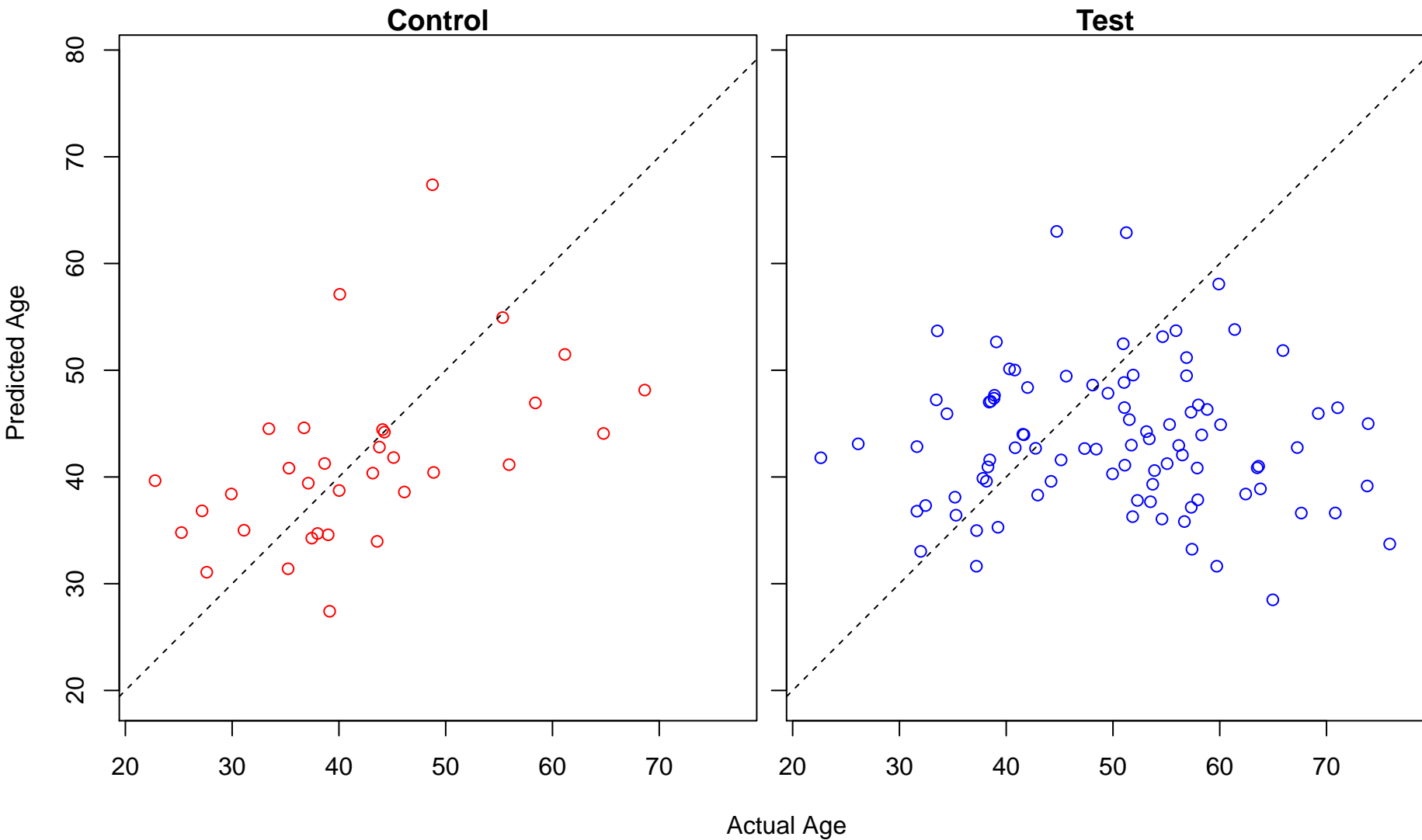
glucosylceramide metabolic process (Score: 0.964837)



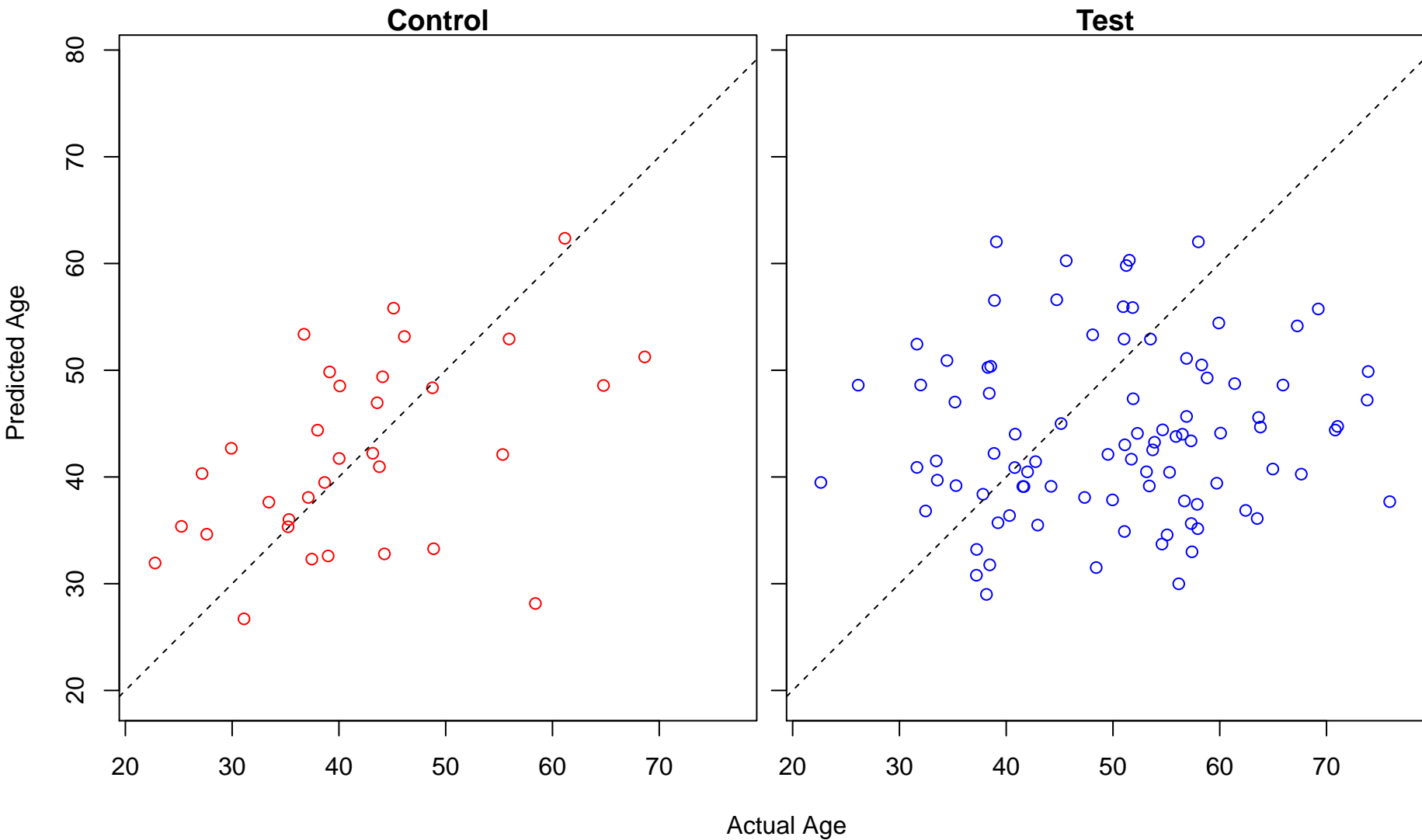
cardiac muscle contraction (Score: 0.964366)



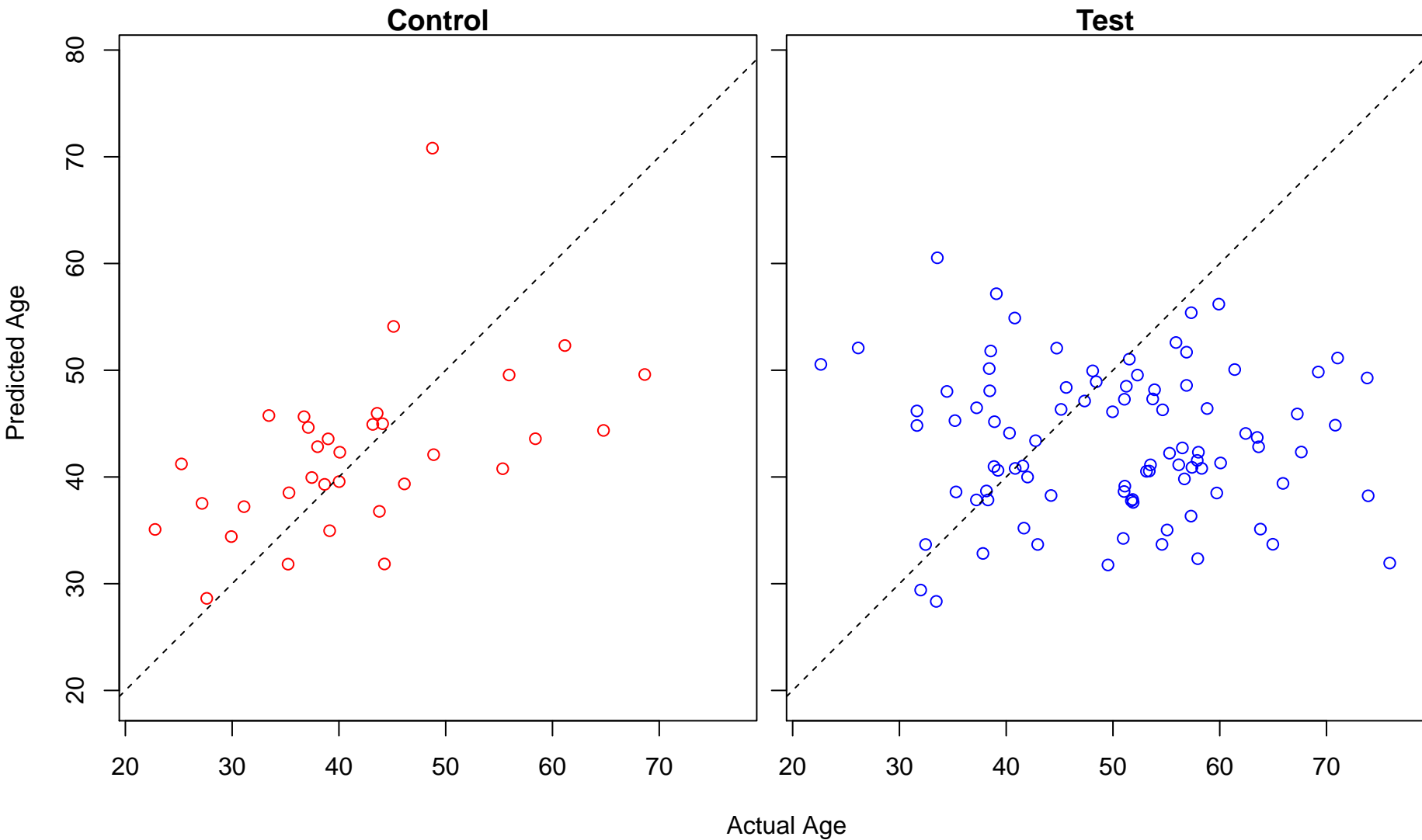
TRIF-dependent toll-like receptor signaling pathway (Score: 0.964015)



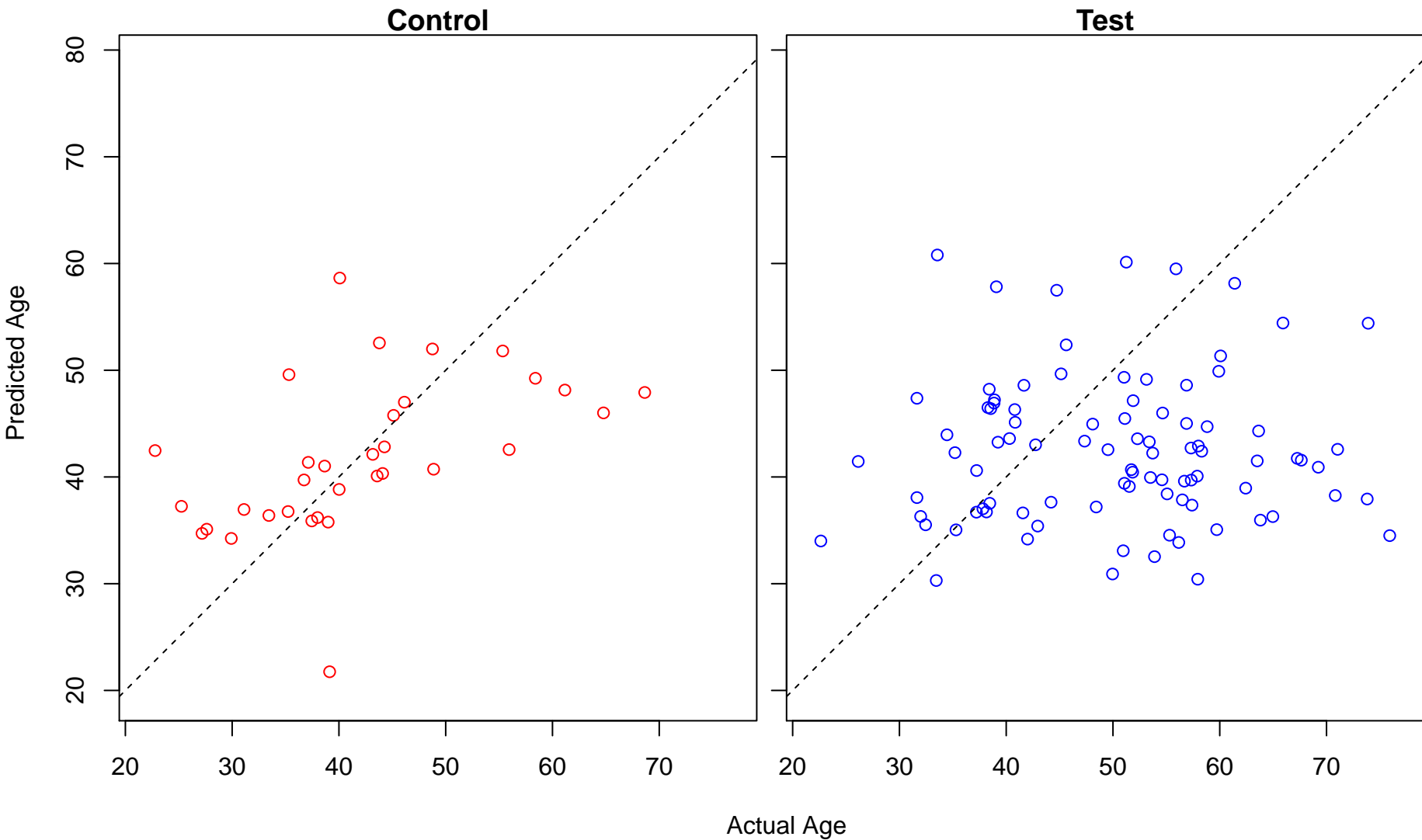
positive regulation of cation channel activity (Score: 0.962245)



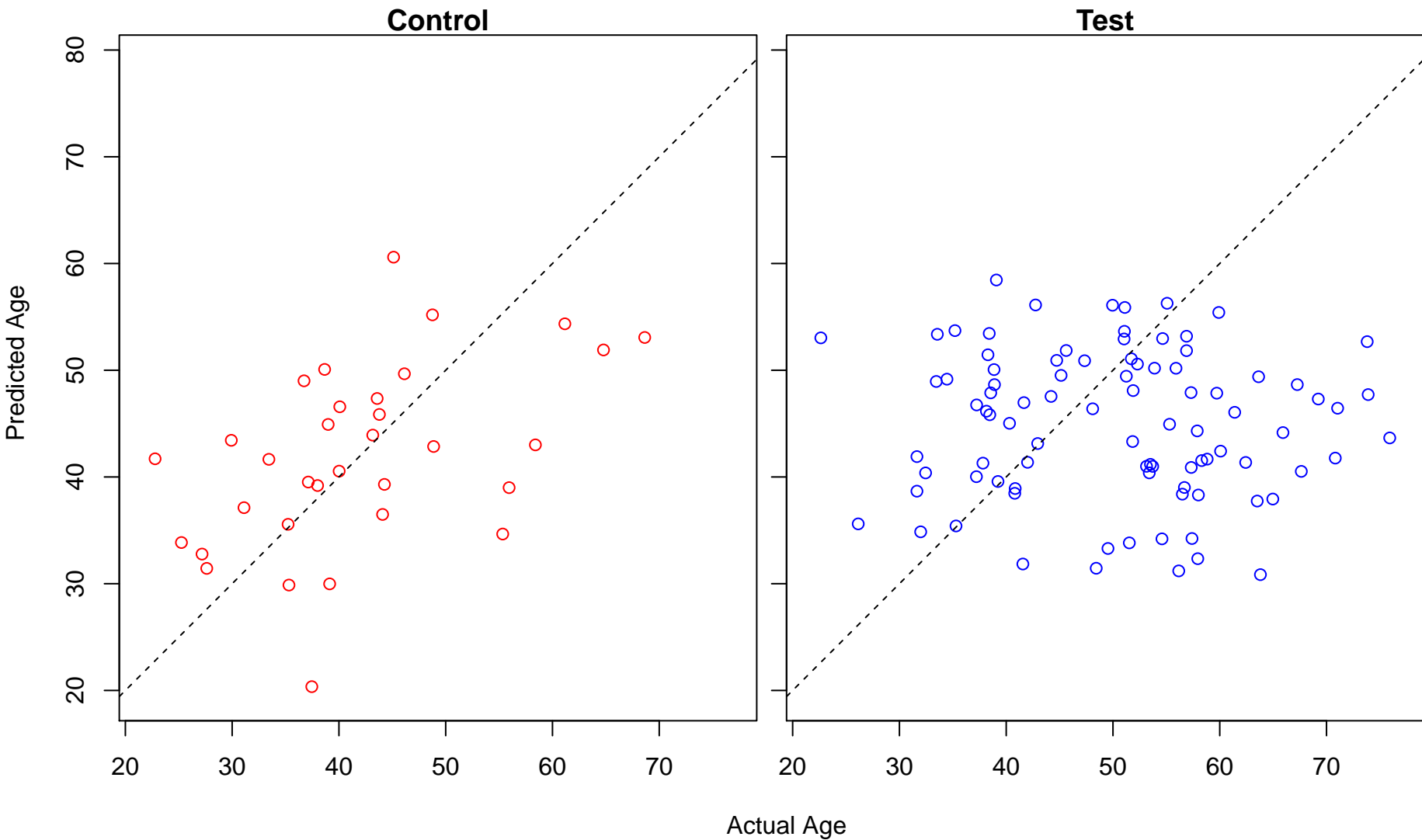
regulation of alpha-beta T cell proliferation (Score: 0.961838)



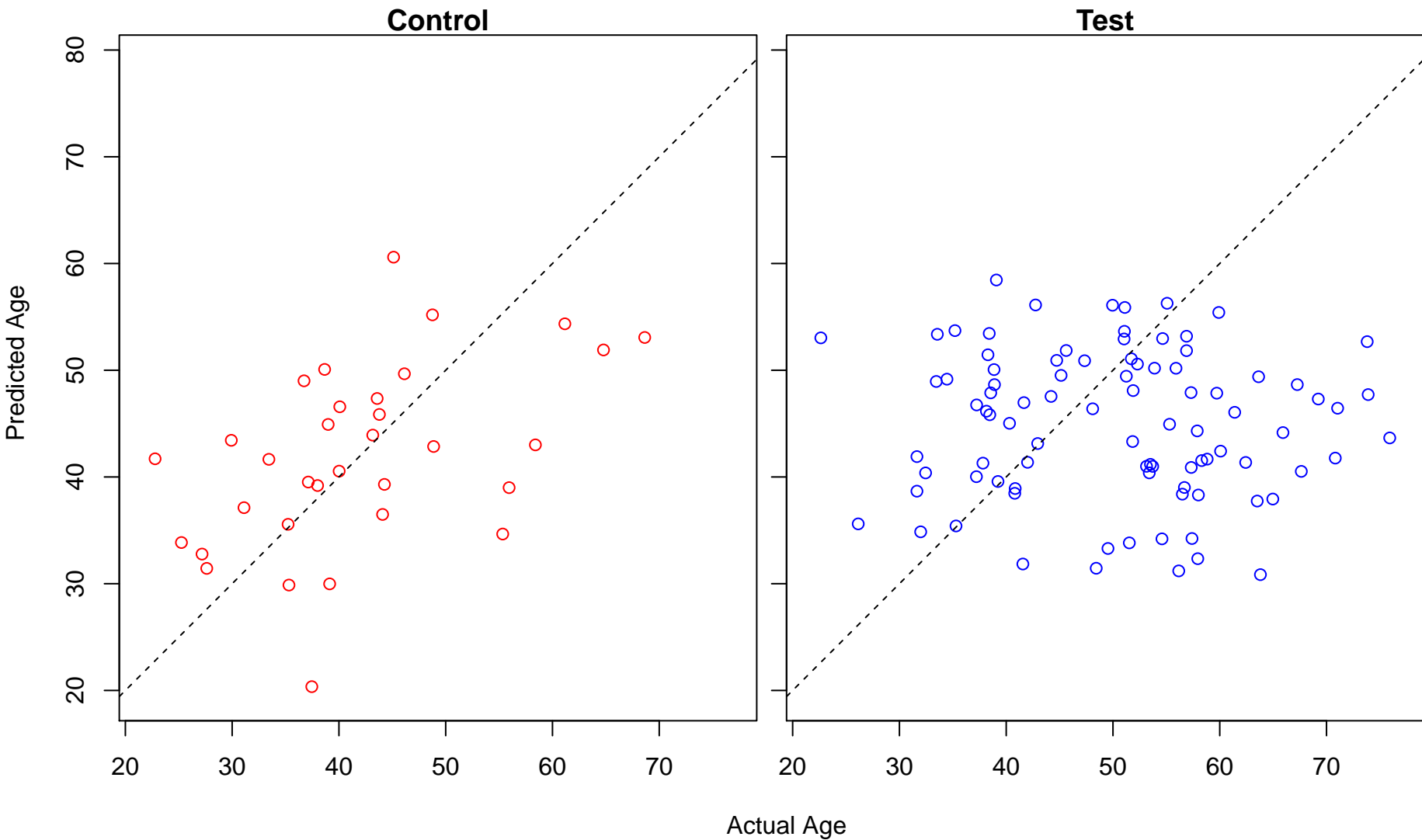
cortical actin cytoskeleton organization (Score: 0.961558)



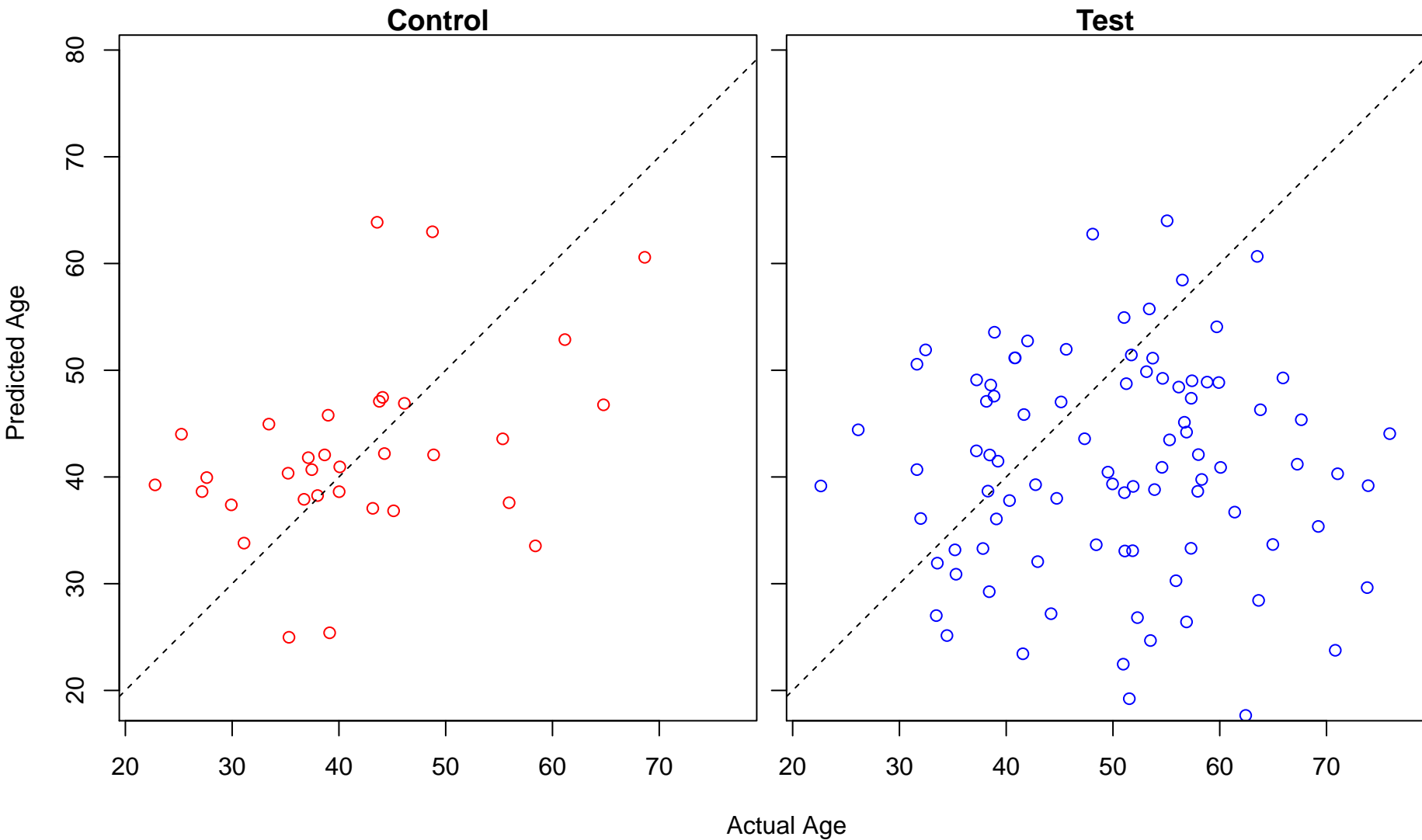
postsynaptic density organization (Score: 0.959393)



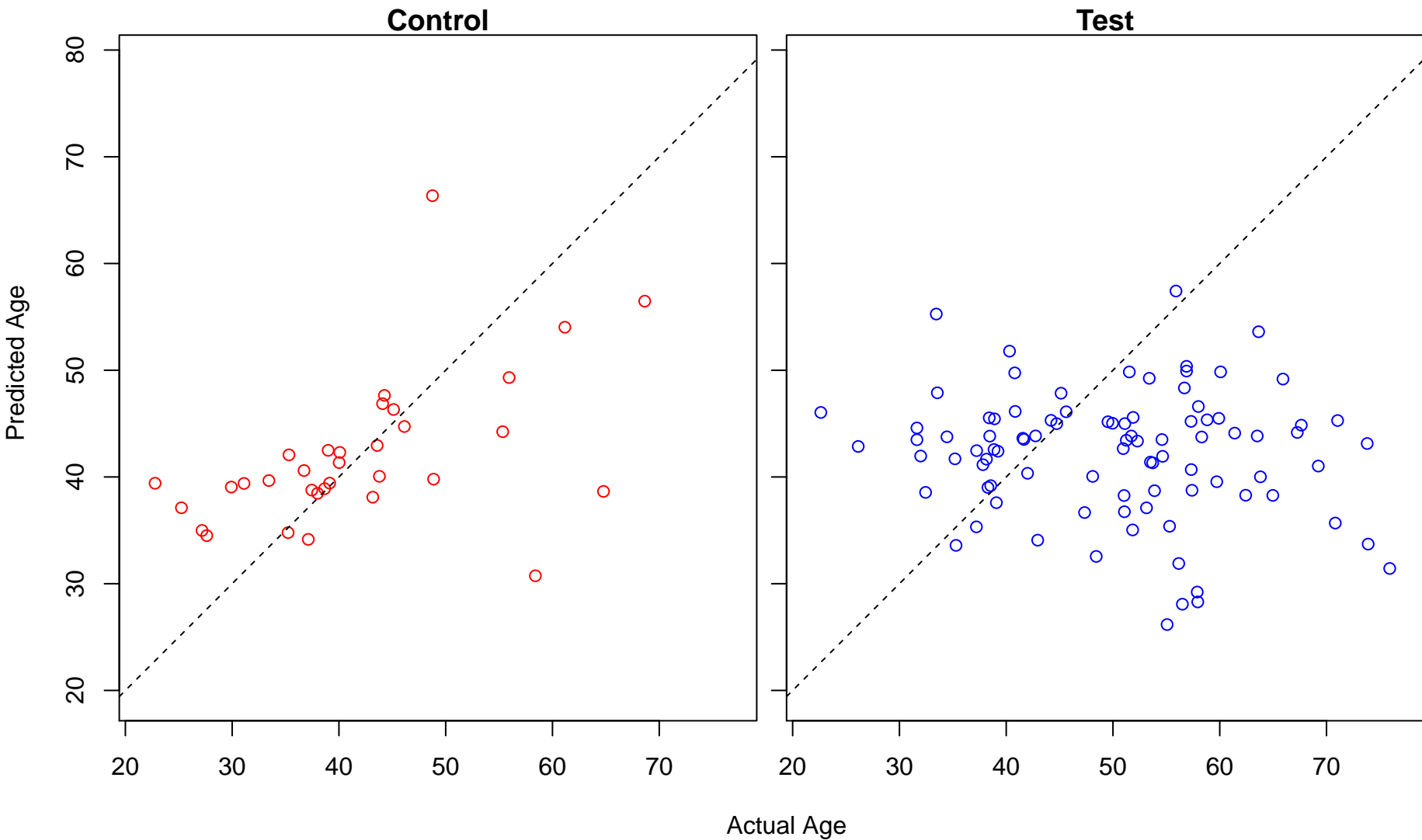
postsynaptic density assembly (Score: 0.959393)



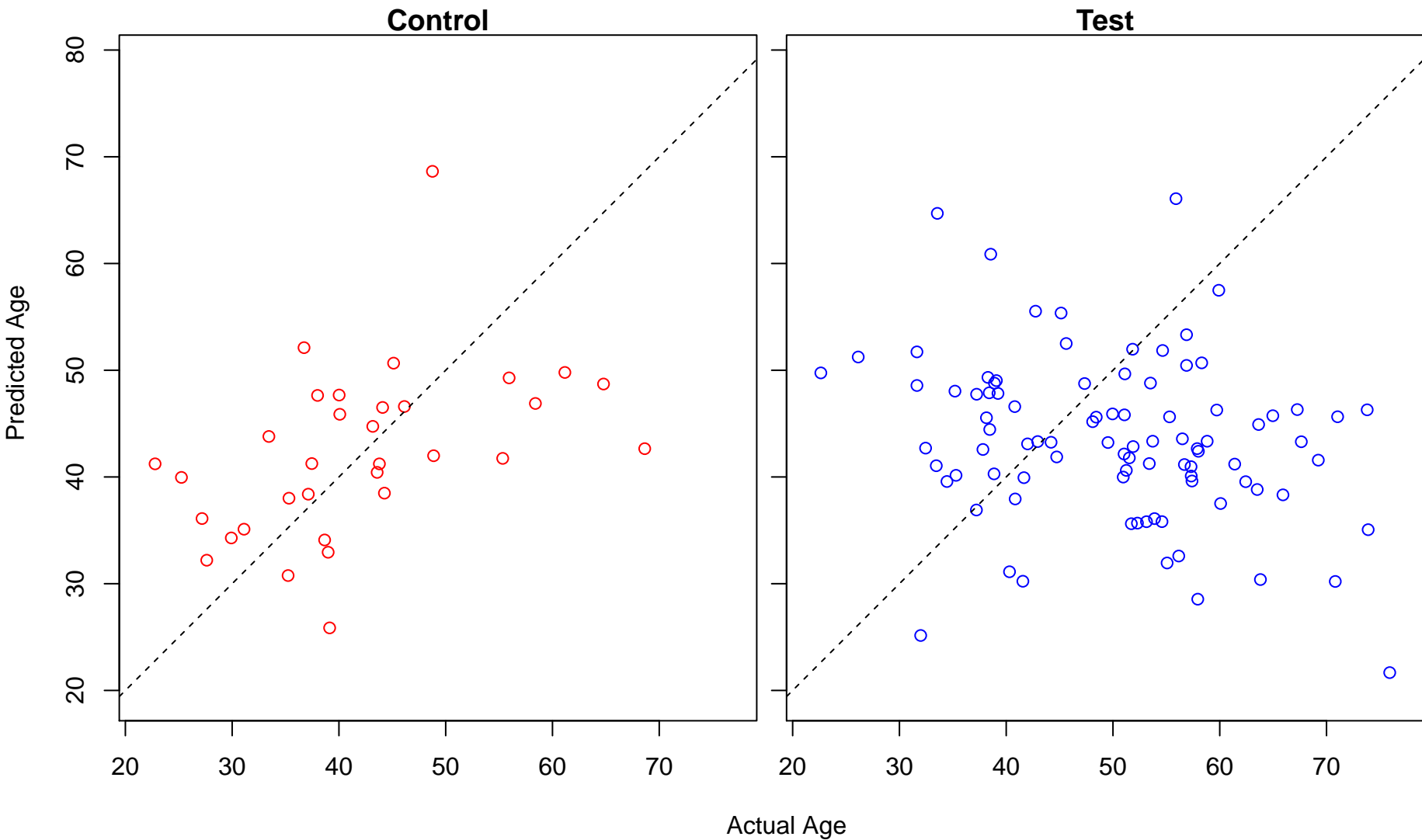
oogenesis (Score: 0.955953)



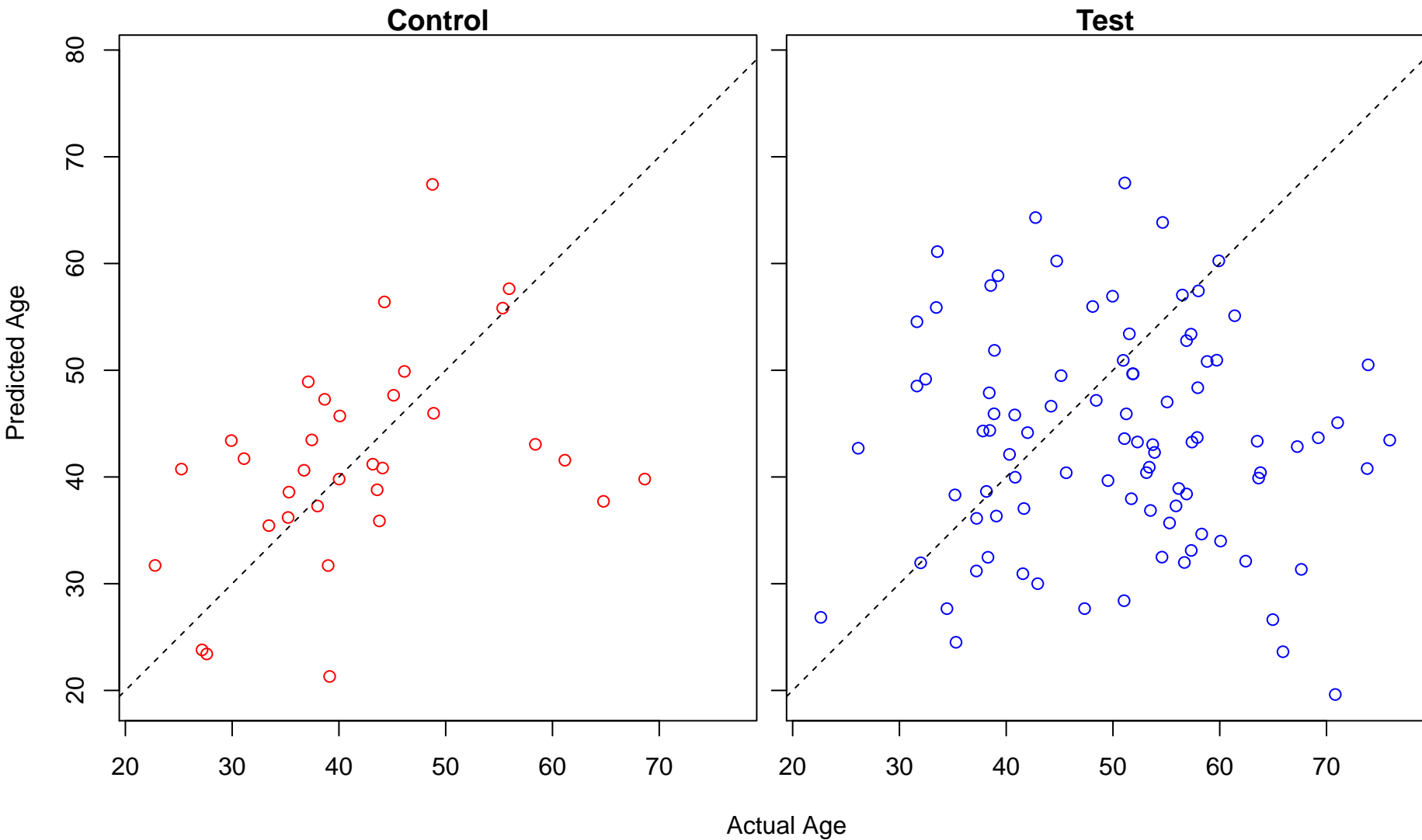
lagging strand elongation (Score: 0.951672)



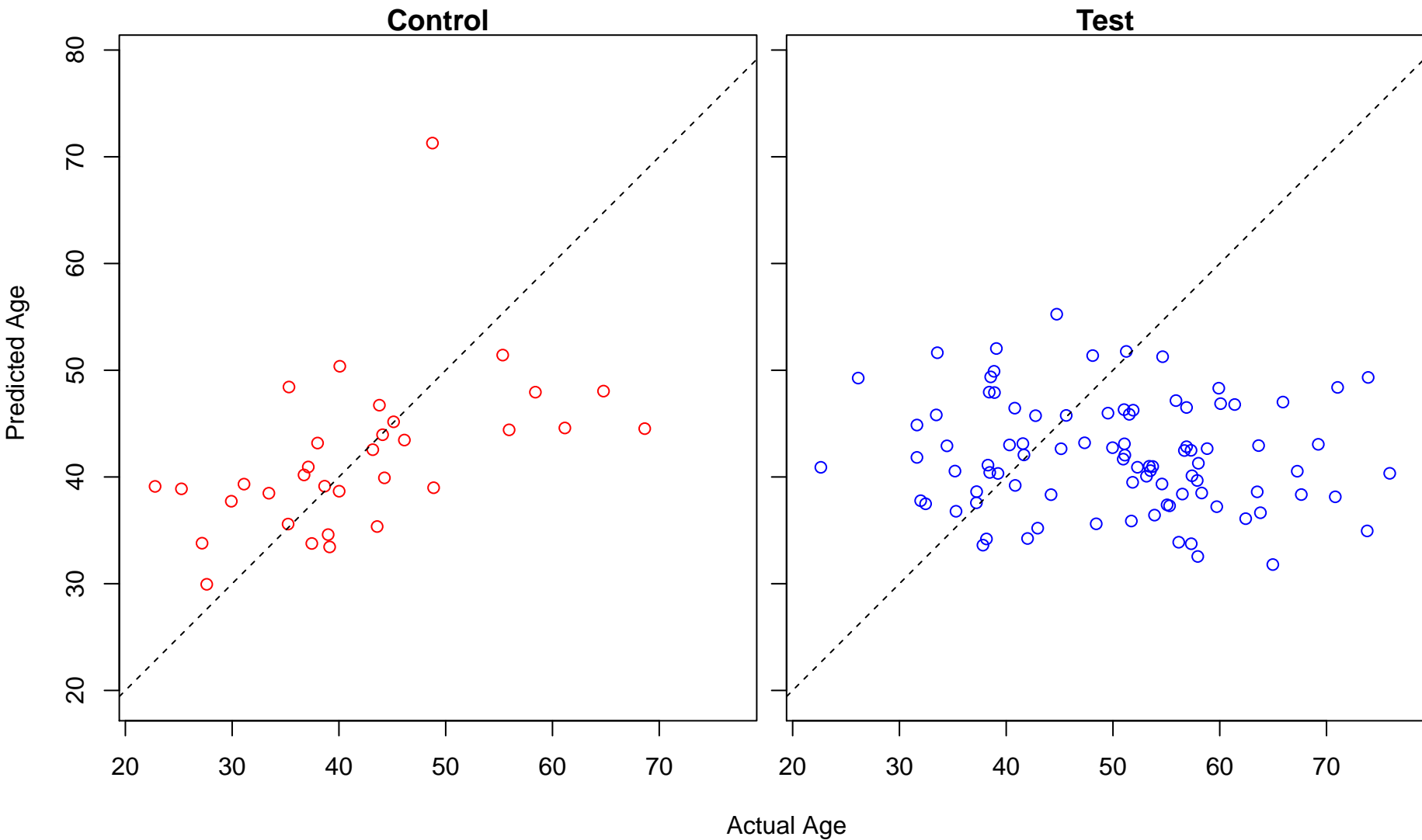
negative regulation of lymphocyte differentiation (Score: 0.951609)



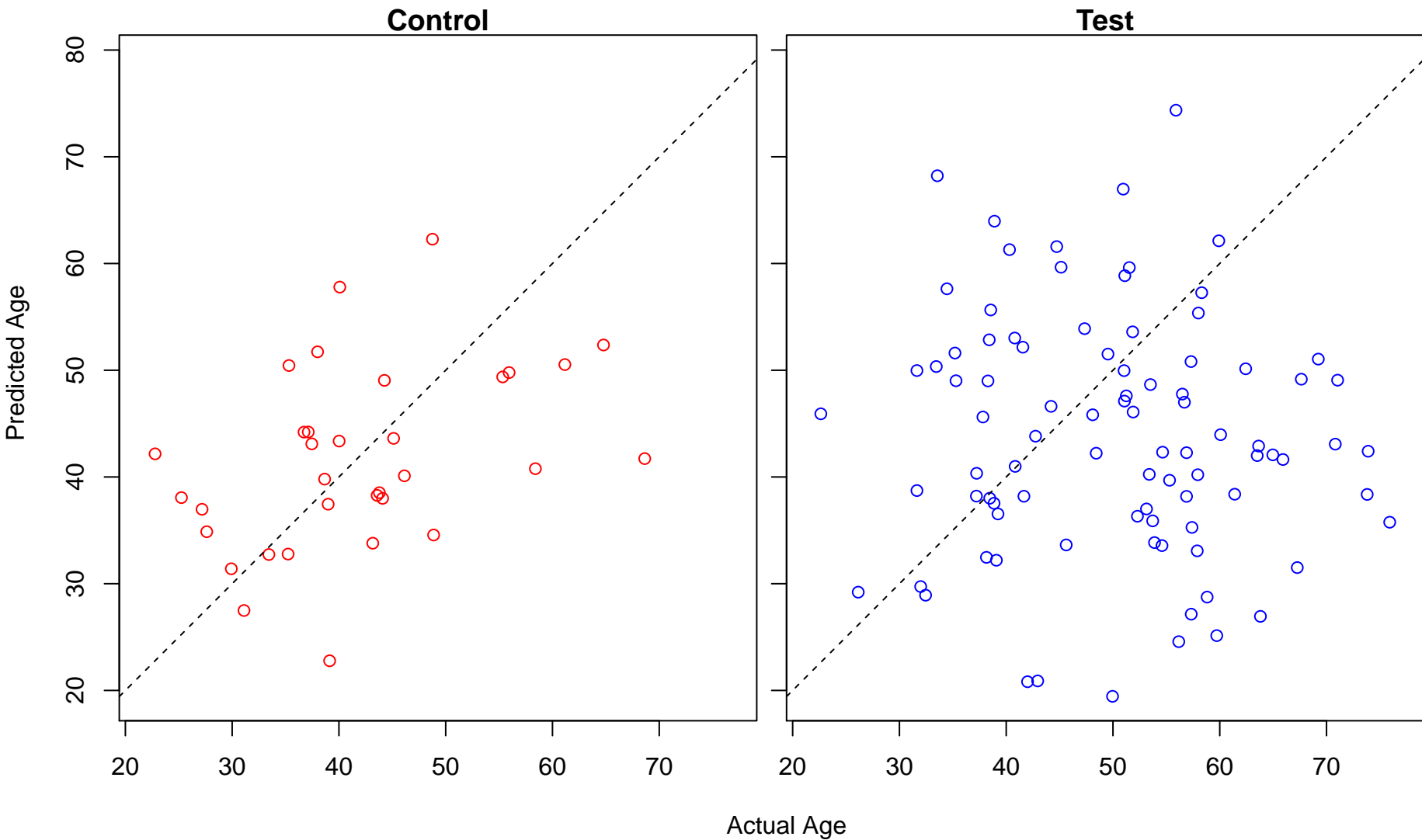
negative regulation of lipid transport (Score: 0.951308)



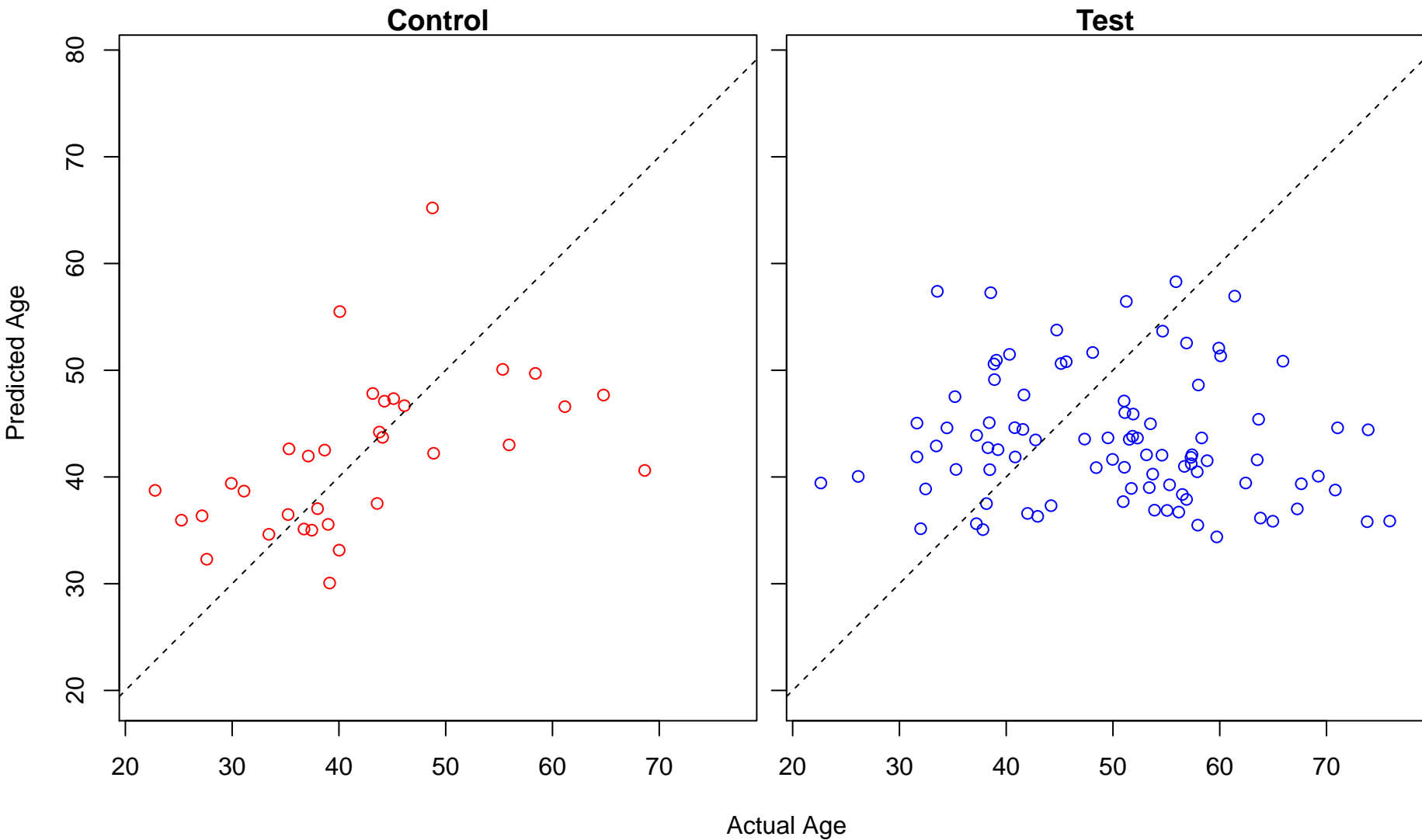
negative regulation of intrinsic apoptotic signaling pathway (Score: 0.950289)



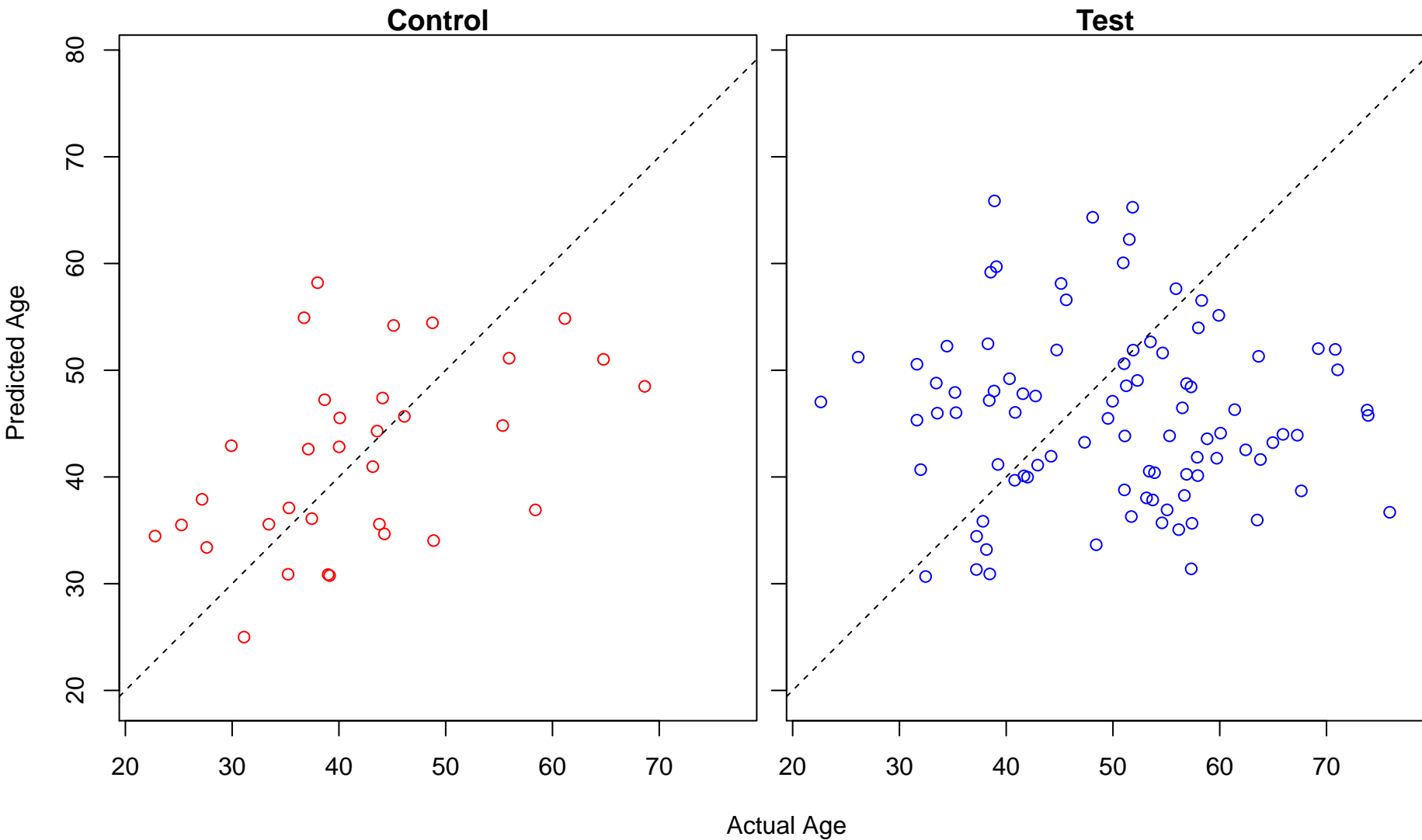
cellular response to misfolded protein (Score: 0.948942)



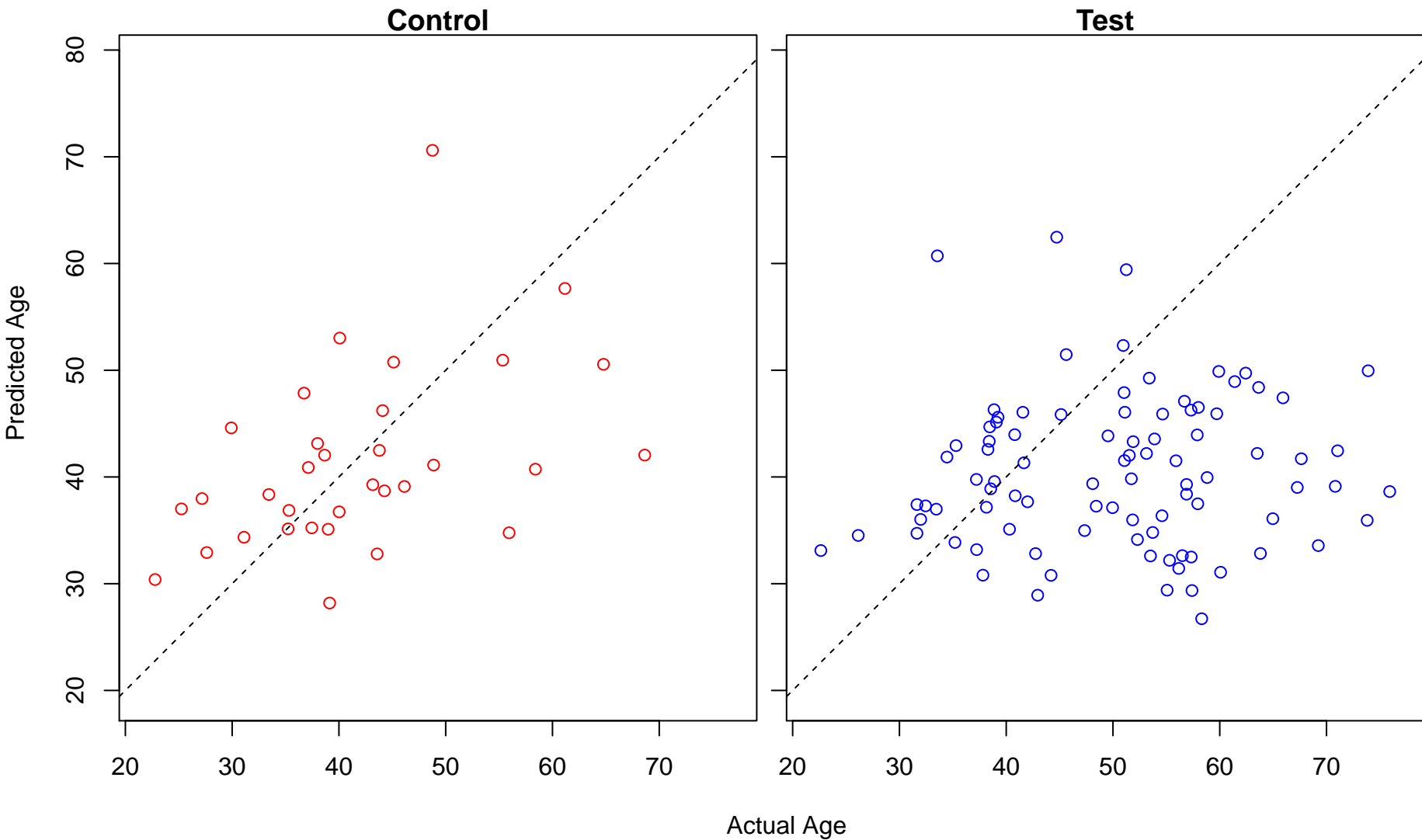
negative regulation of protein catabolic process (Score: 0.948277)



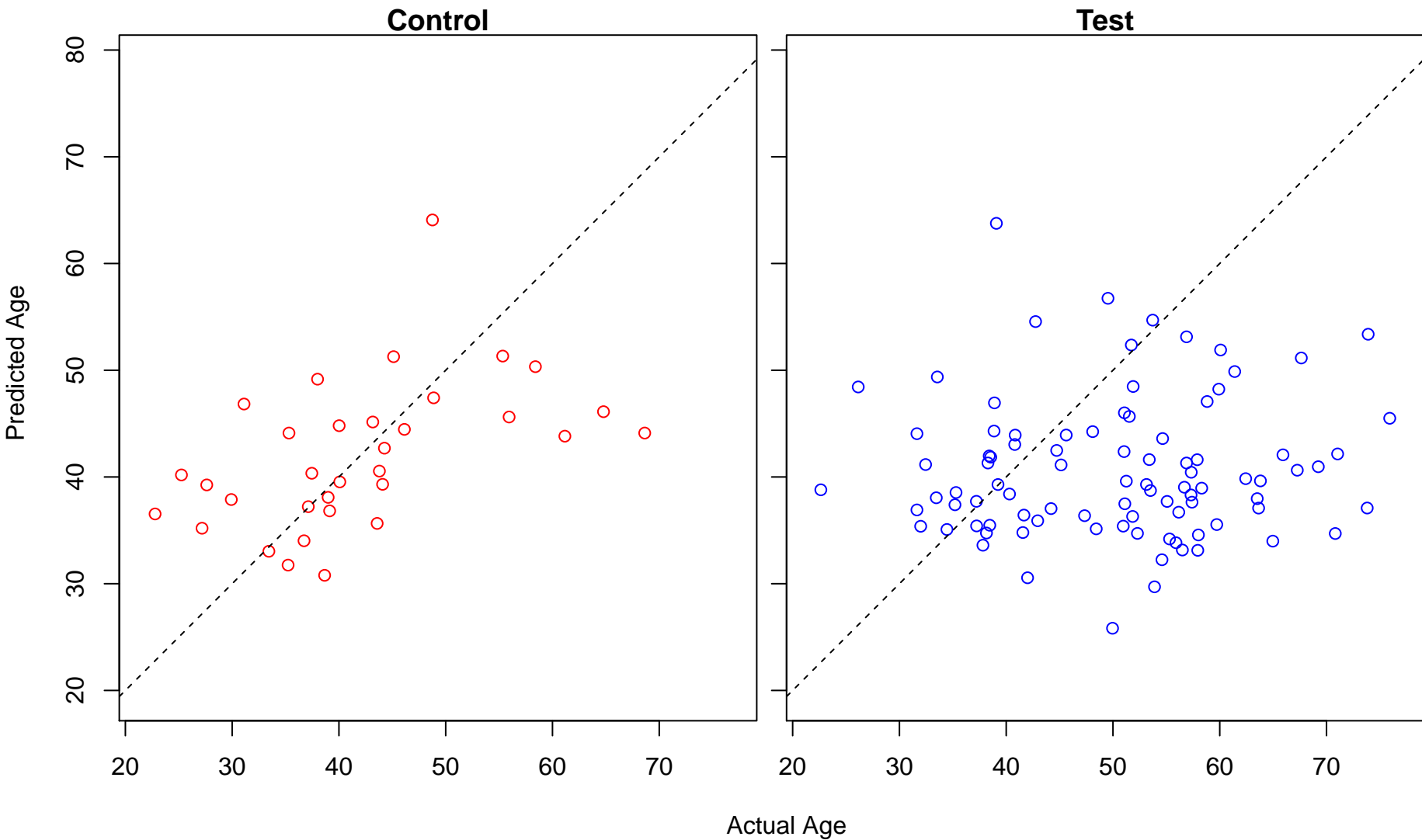
positive regulation of calcium ion transmembrane transporter activity (Score: 0.947631)



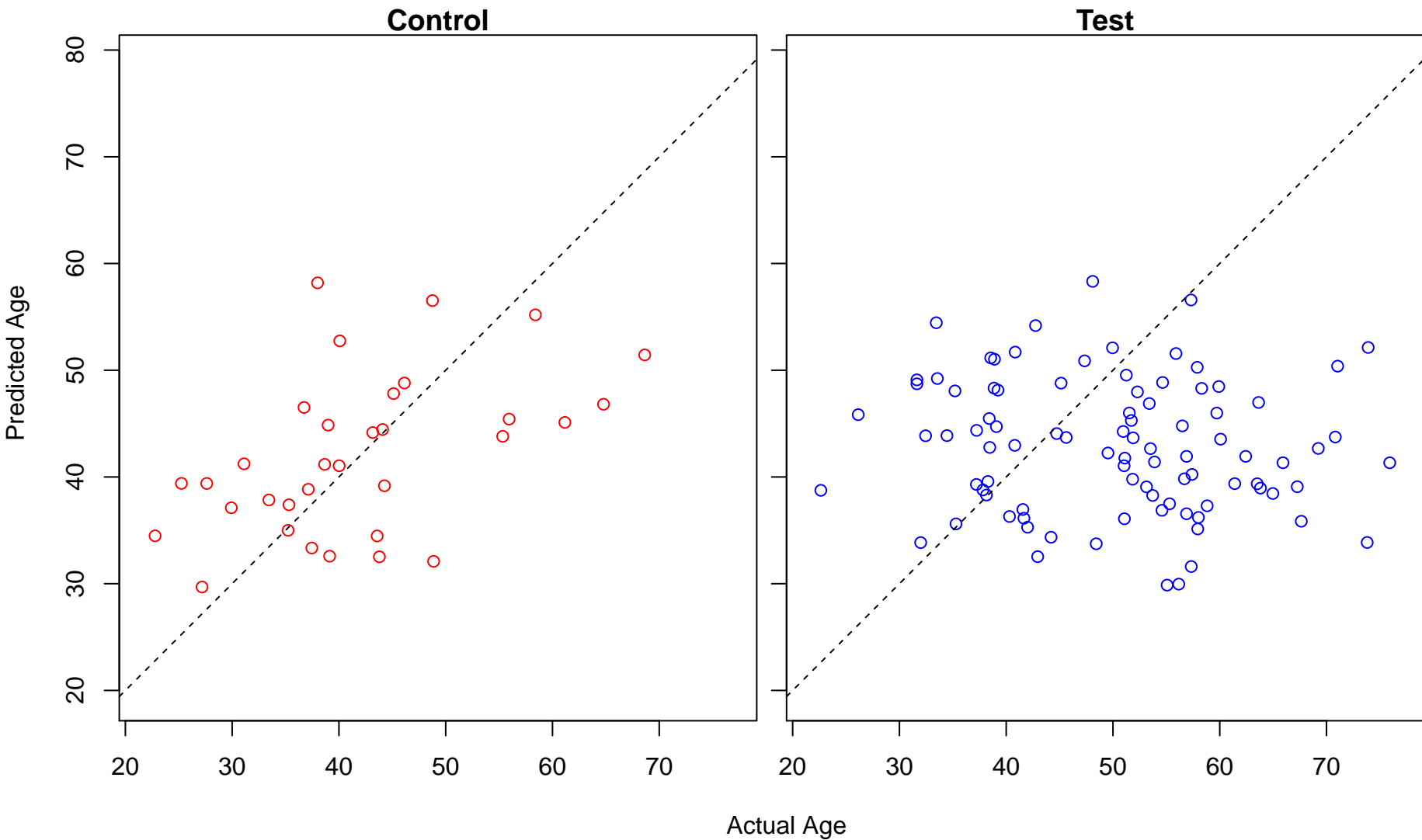
MAPK cascade (Score: 0.946985)



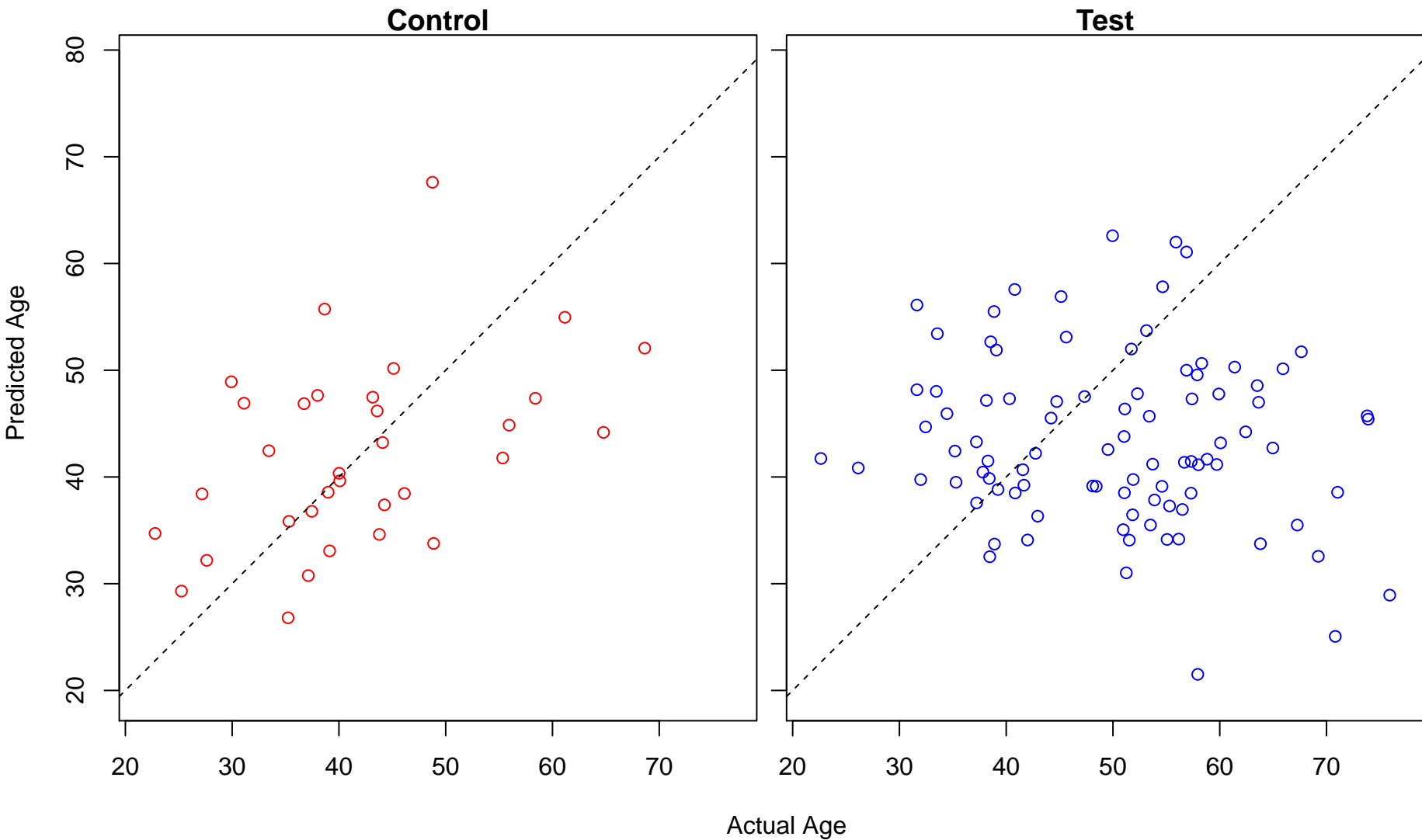
negative regulation of DNA damage response, signal transduction by p53 class mediator (Score: 0.946)



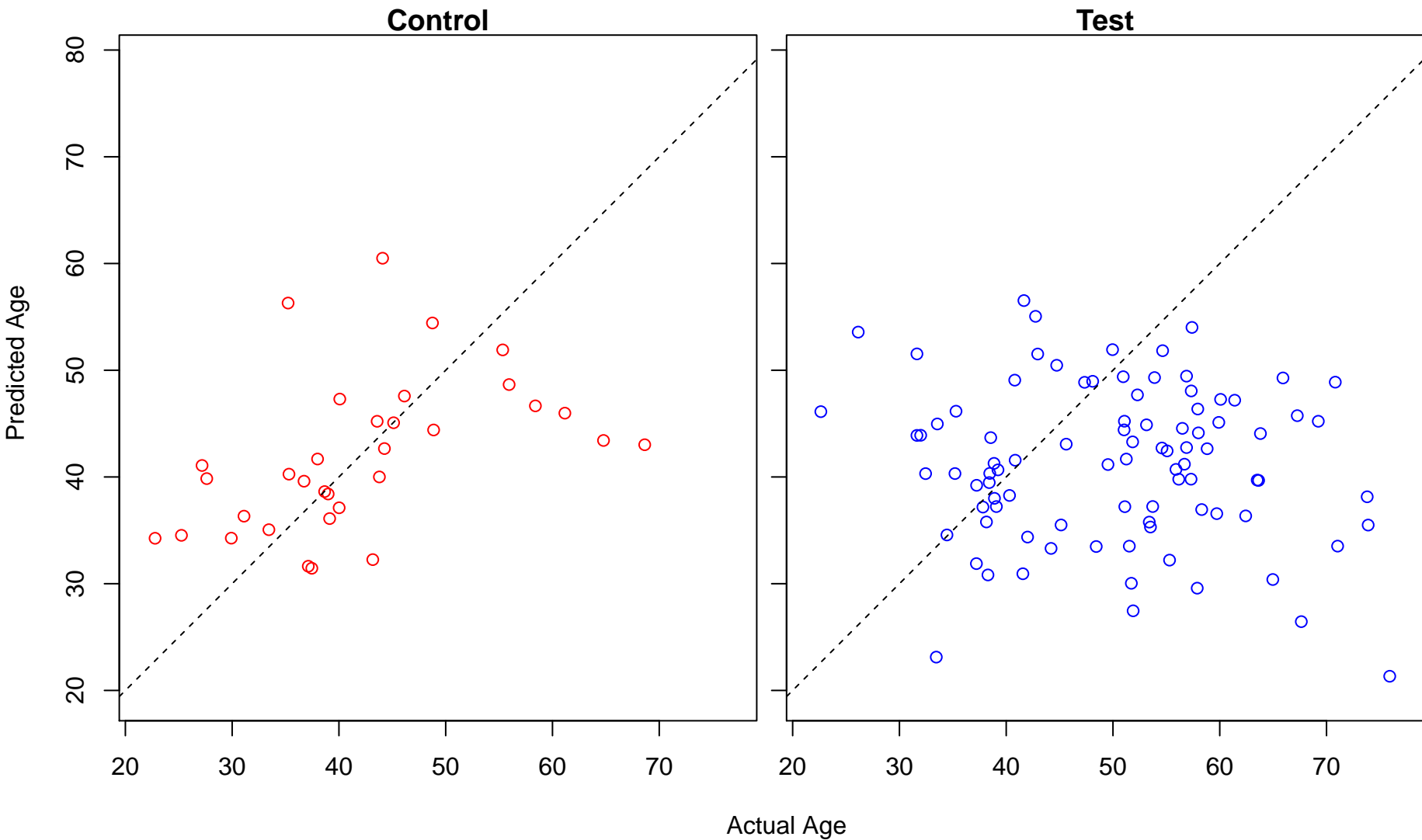
cGMP-mediated signaling (Score: 0.944892)



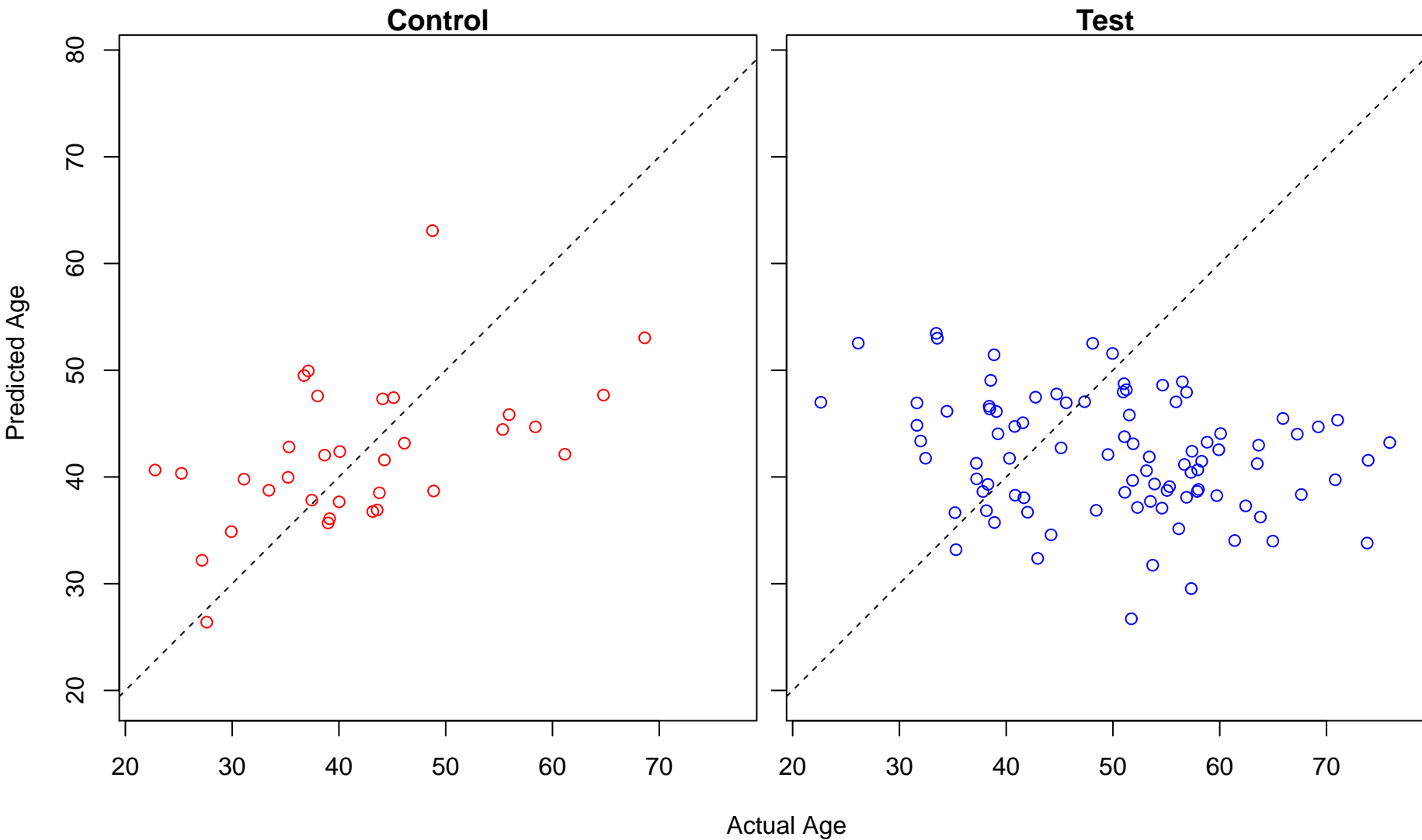
steroid hormone mediated signaling pathway (Score: 0.944694)



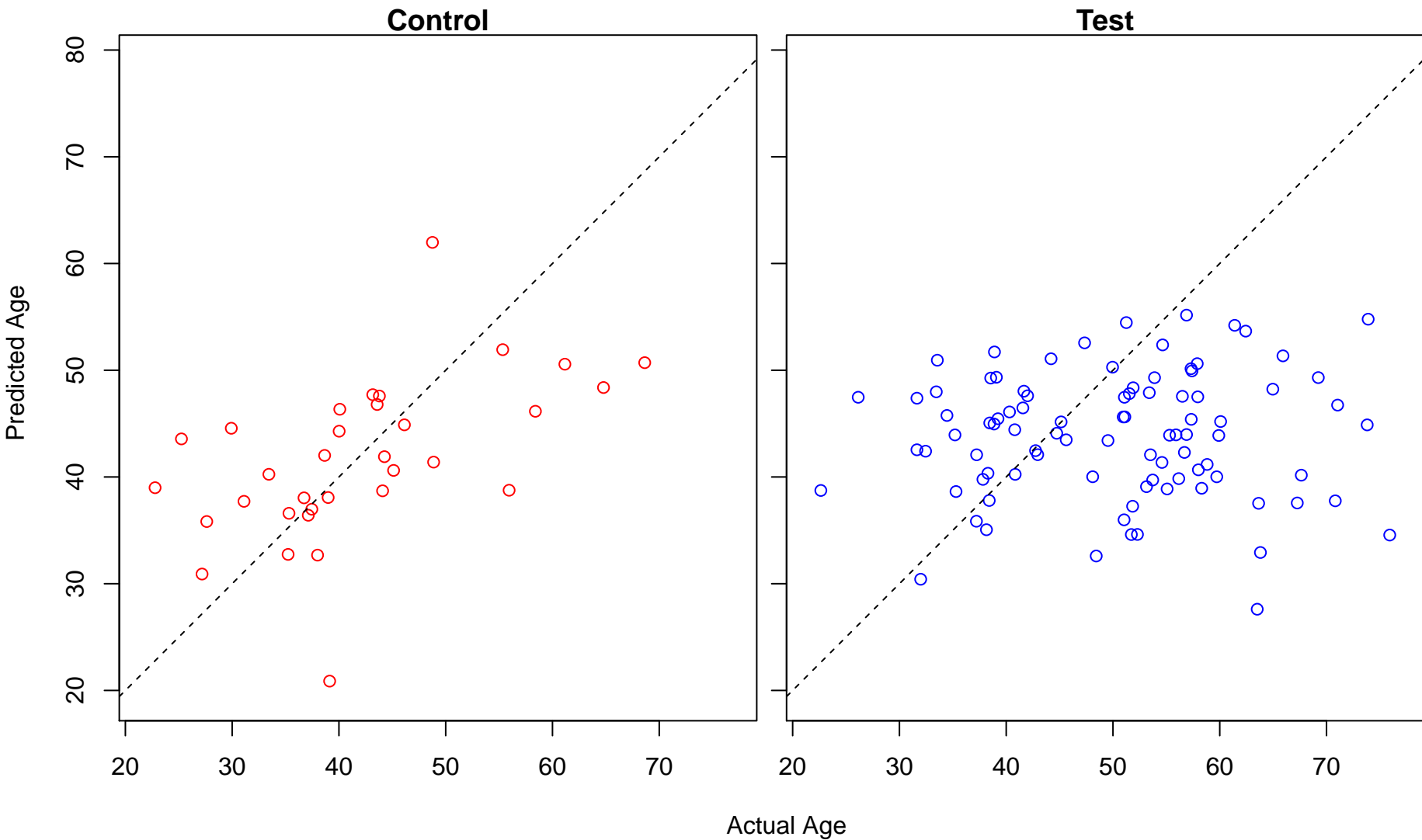
regulation of heart rate by cardiac conduction (Score: 0.944686)



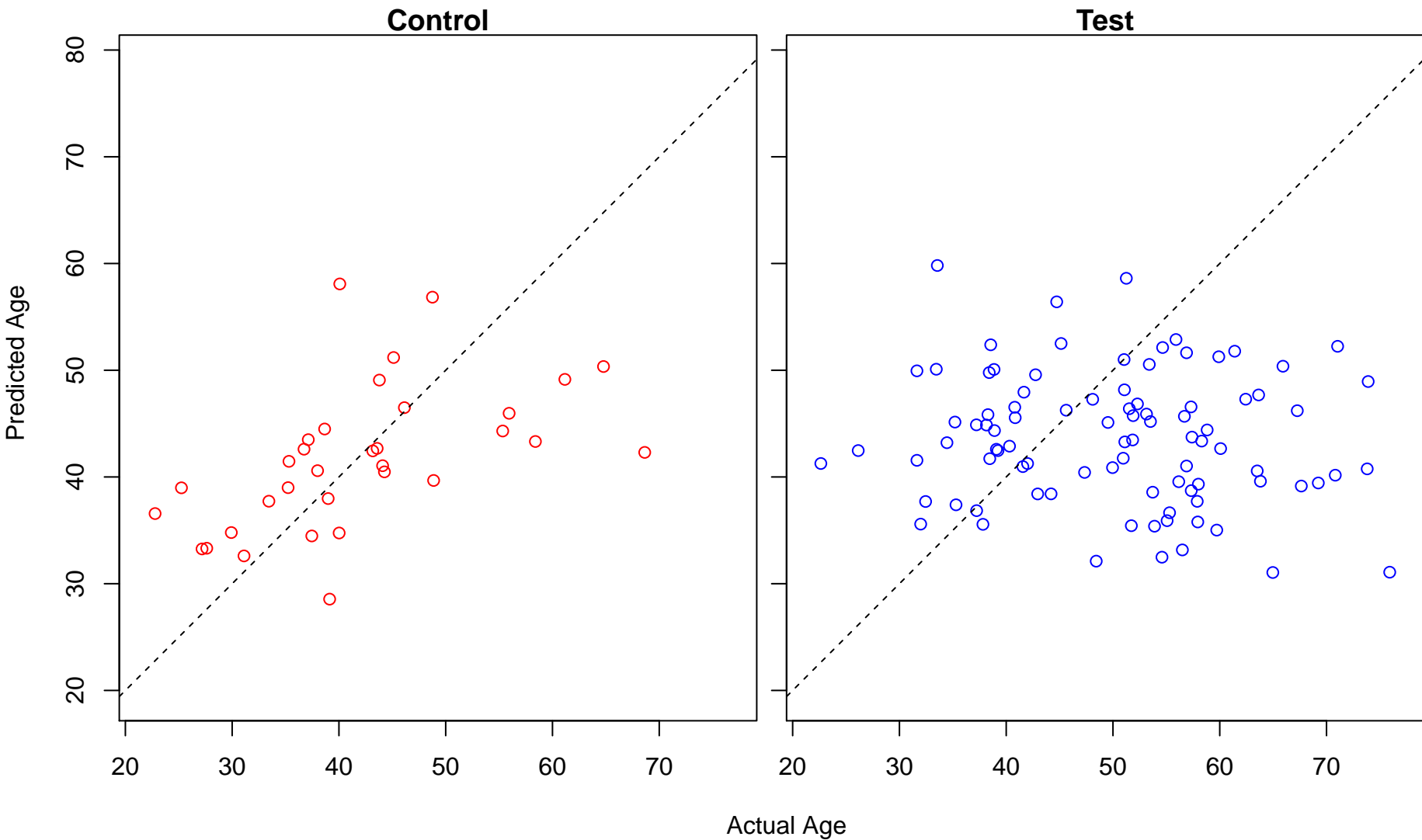
negative regulation of protein homooligomerization (Score: 0.944491)



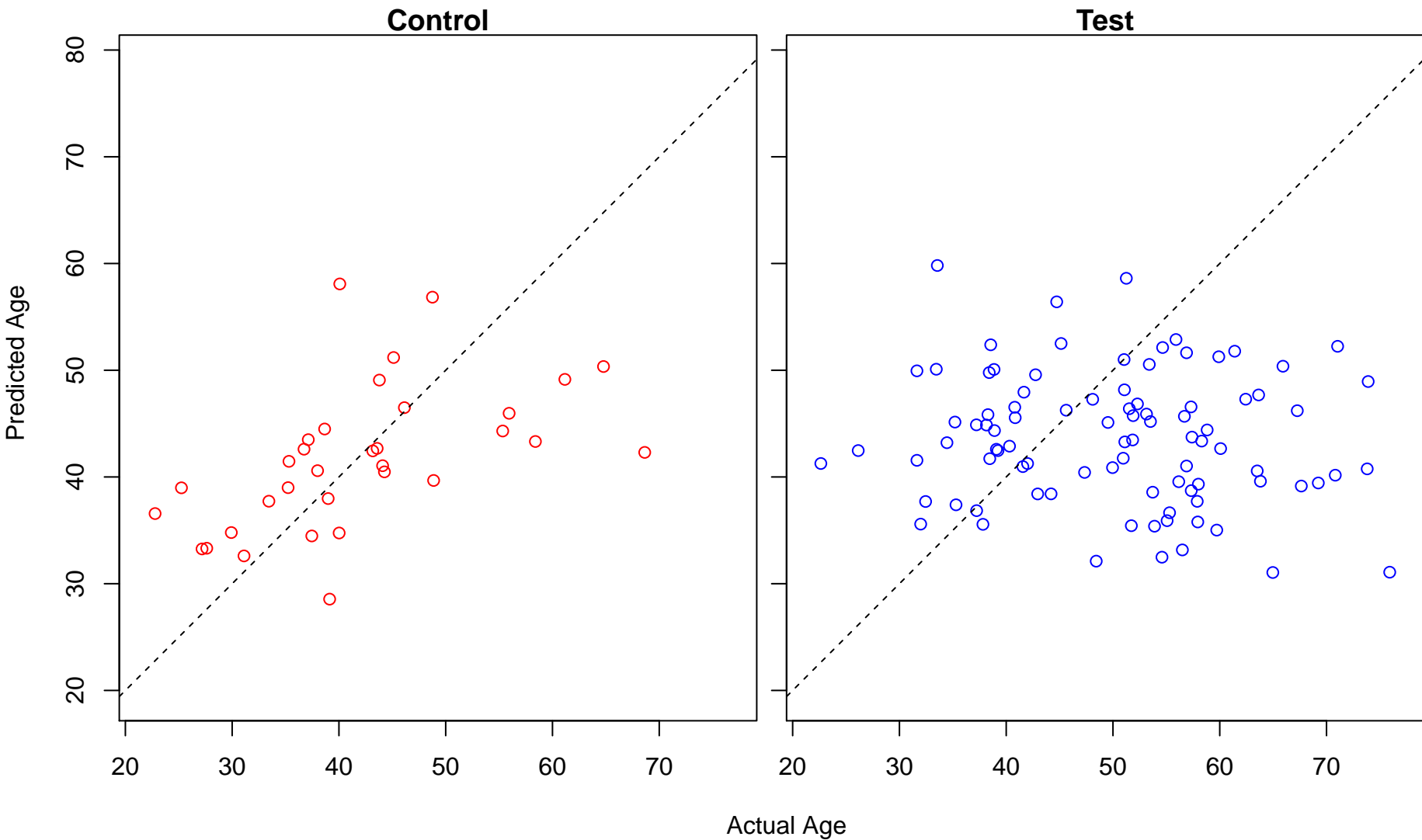
leukocyte mediated immunity (Score: 0.943175)



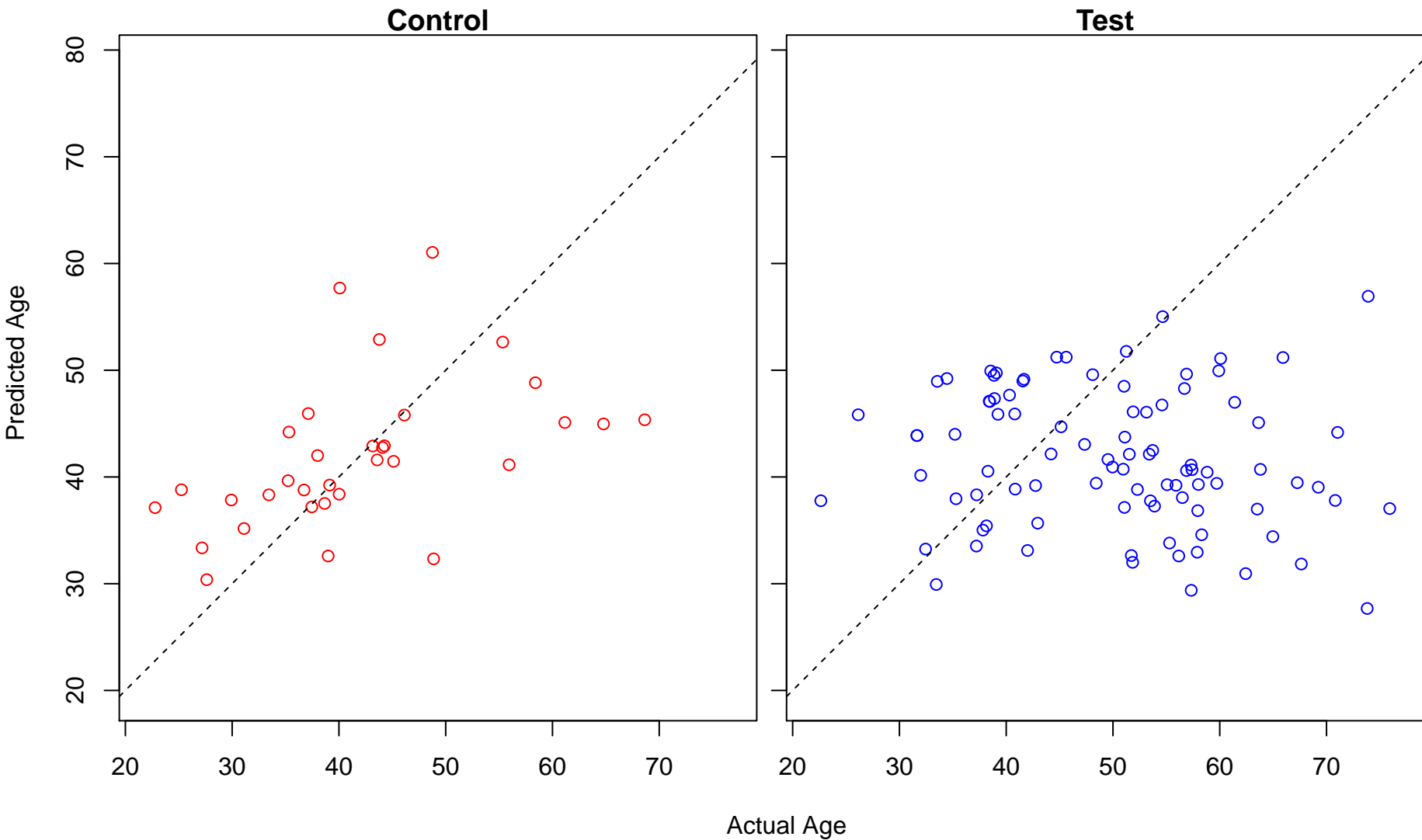
cellular biogenic amine metabolic process (Score: 0.943025)



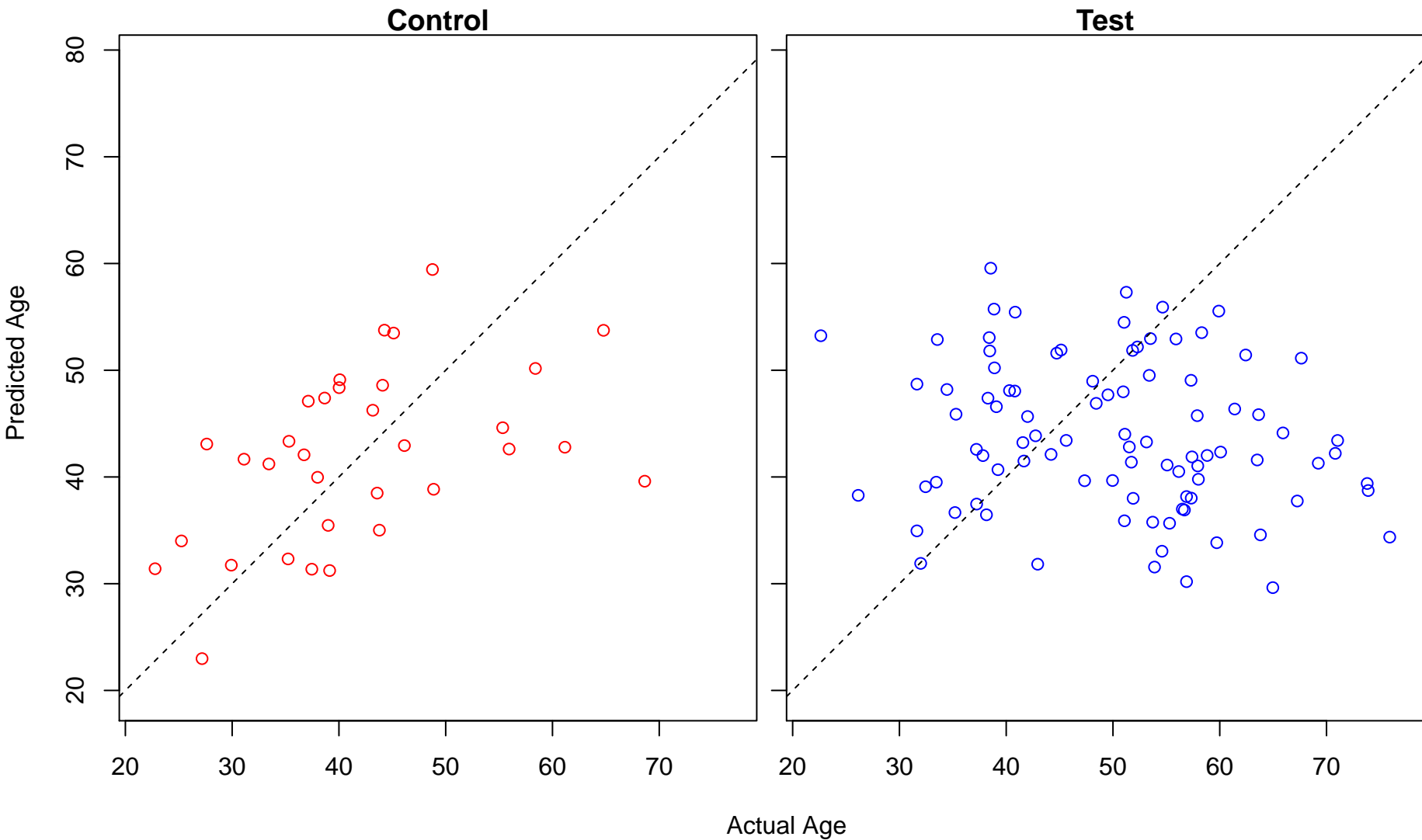
cellular amine metabolic process (Score: 0.943025)



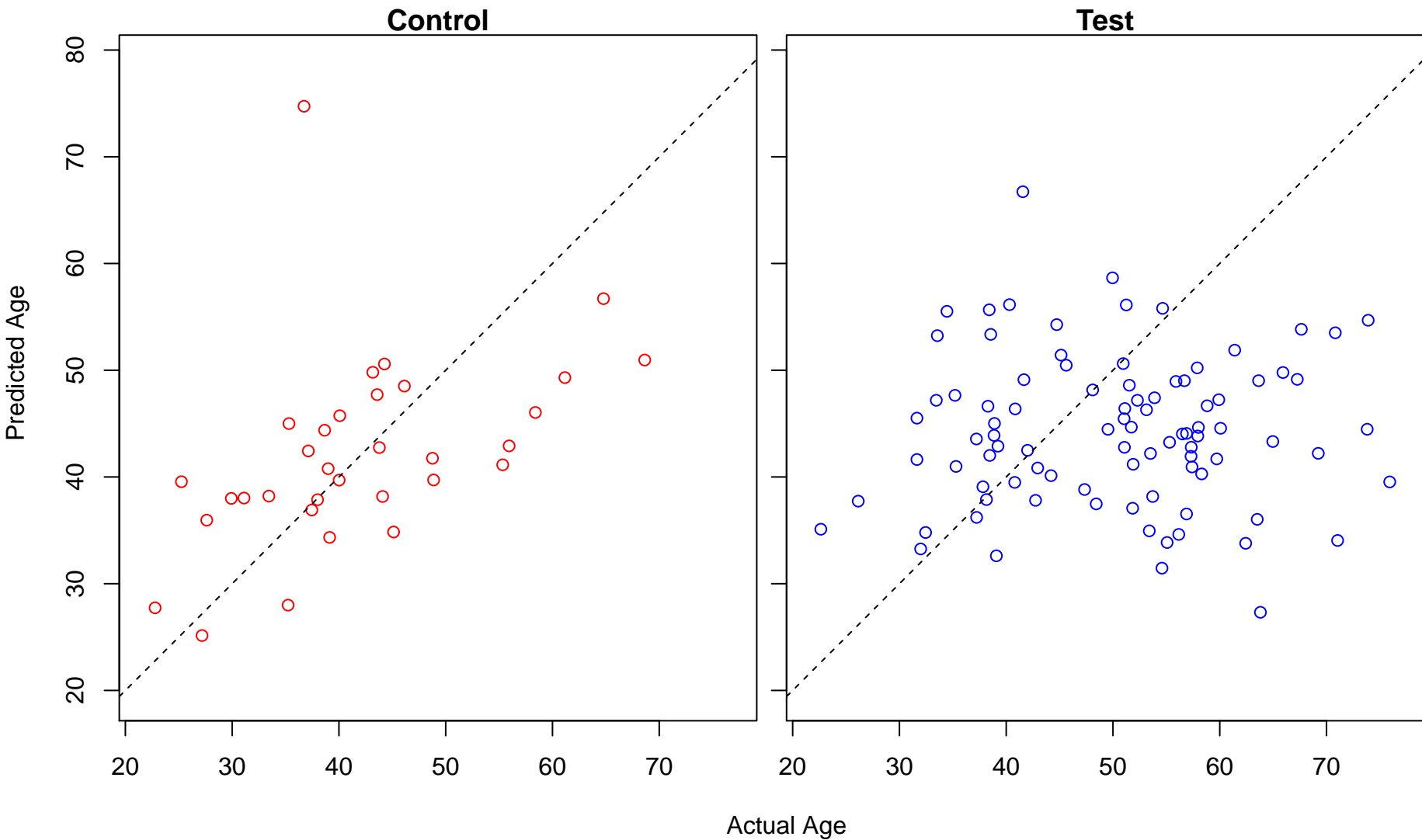
negative regulation of peptidyl-tyrosine phosphorylation (Score: 0.942836)



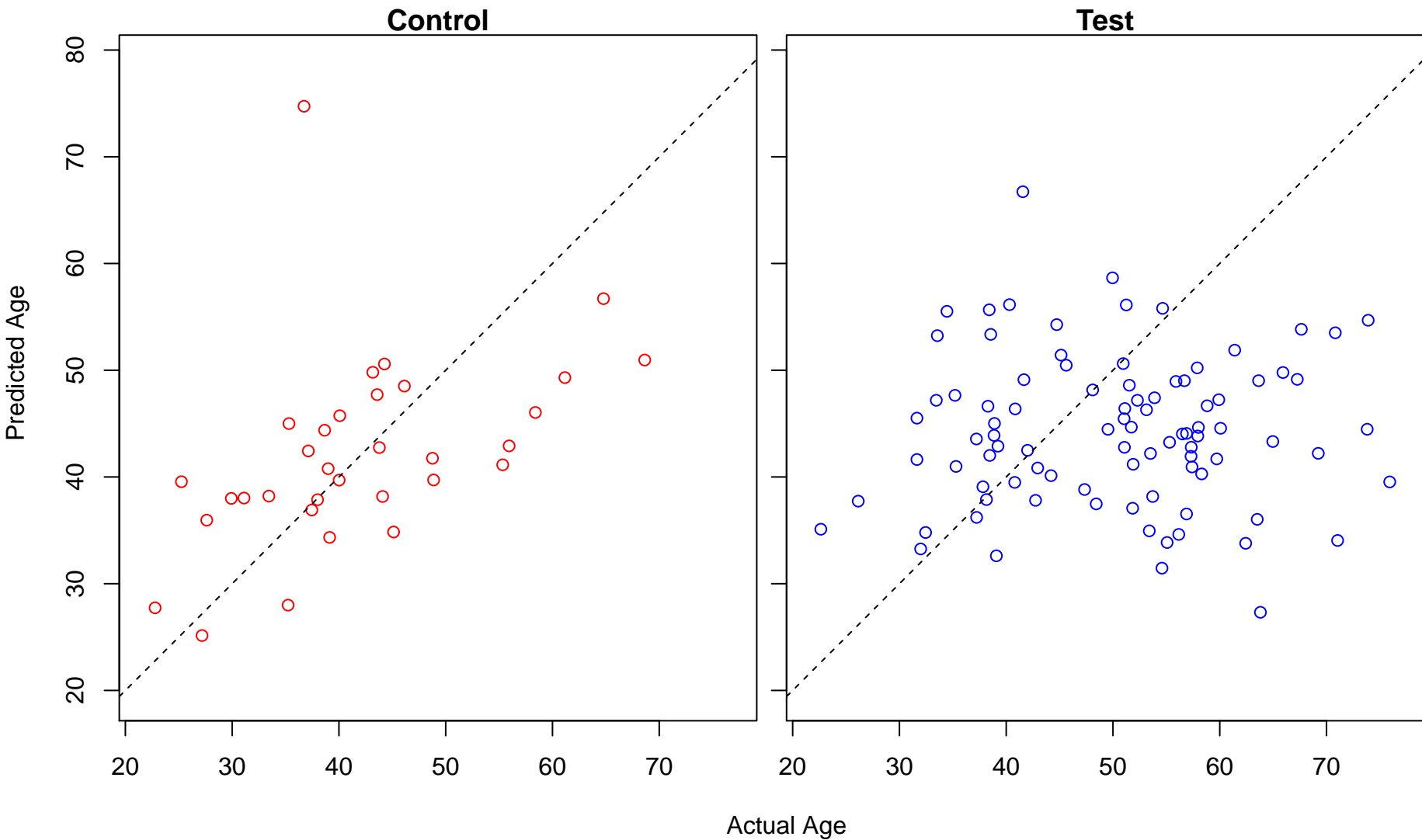
smooth muscle contraction (Score: 0.942144)



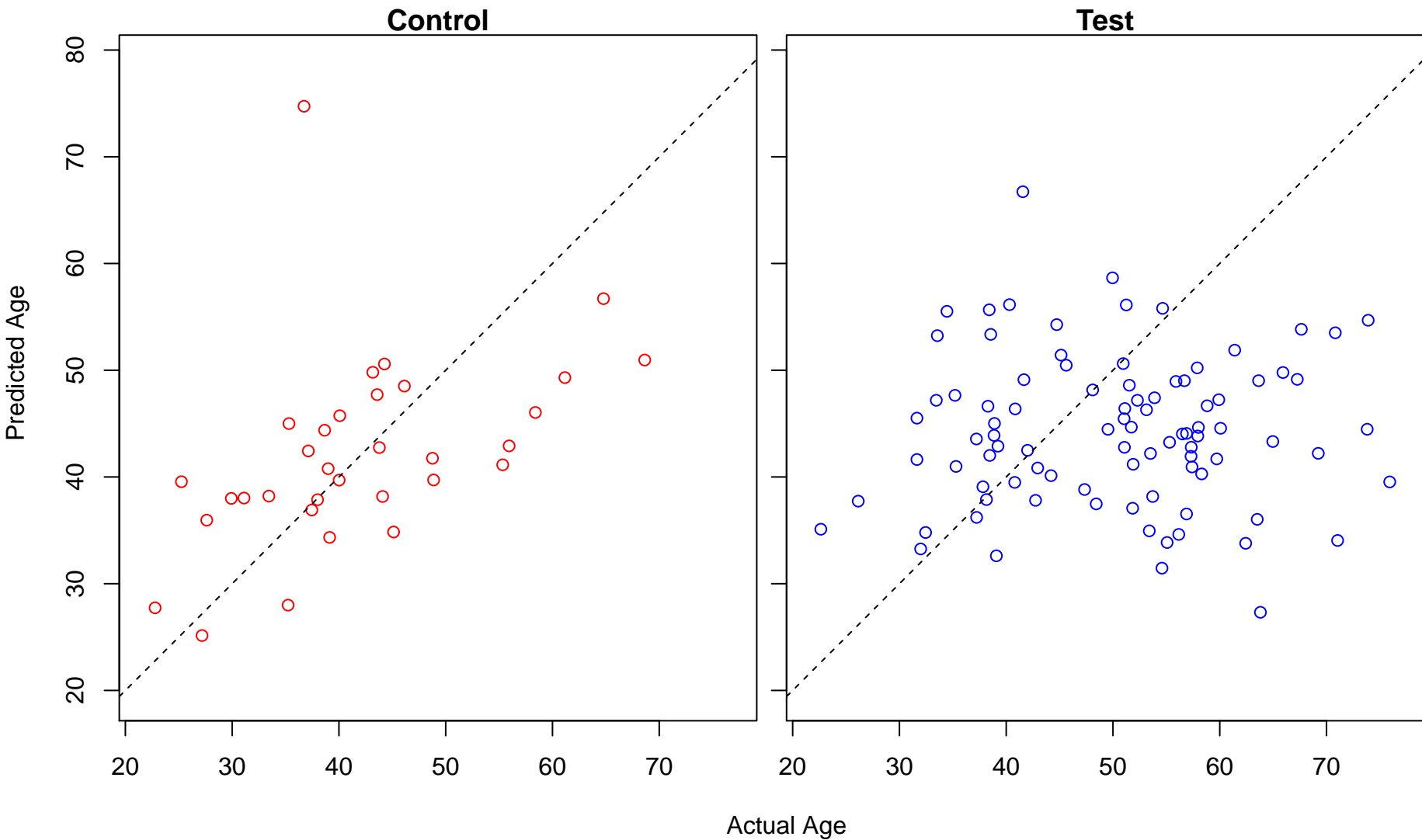
cellular response to increased oxygen levels (Score: 0.941700)



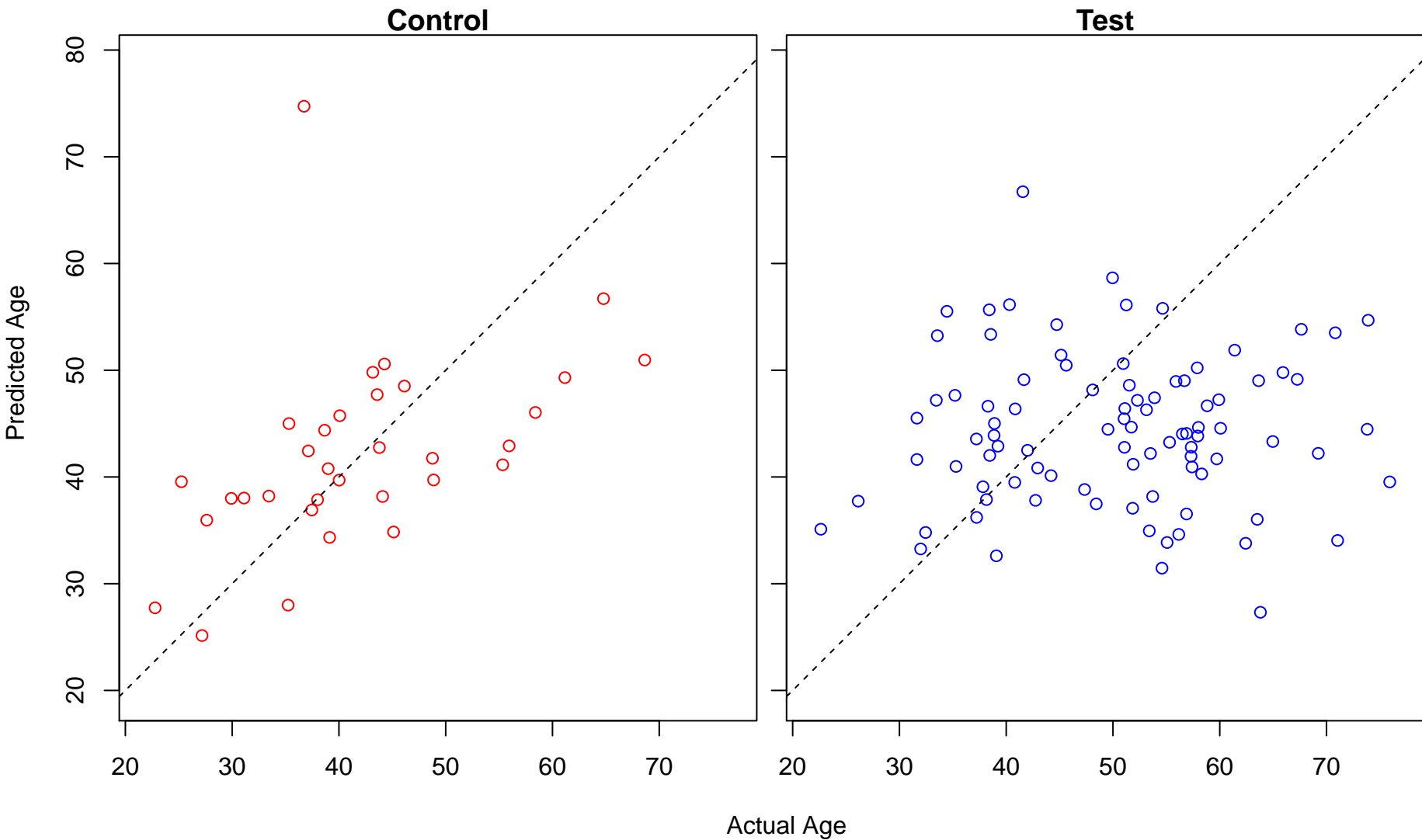
response to increased oxygen levels (Score: 0.941700)



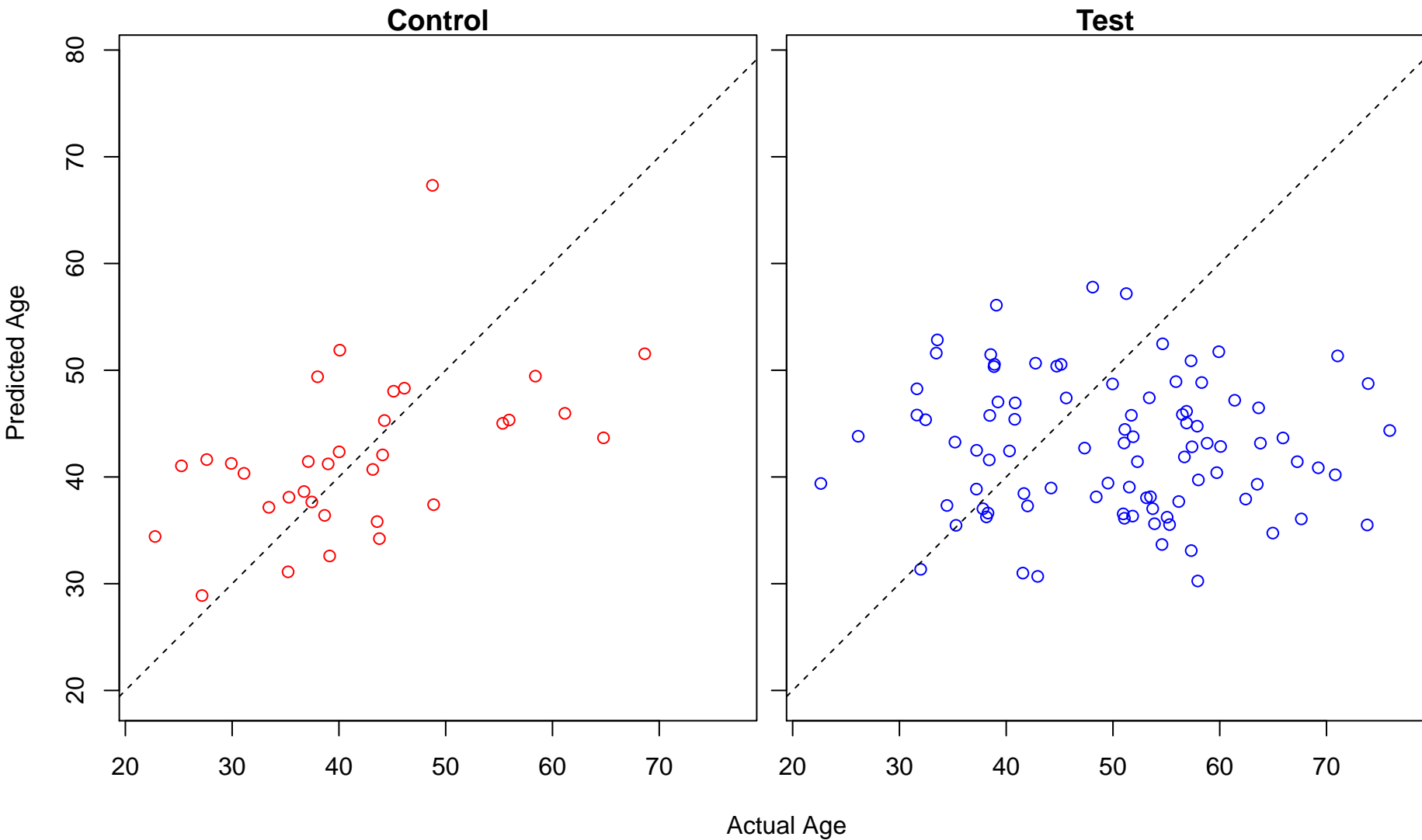
response to hyperoxia (Score: 0.941700)



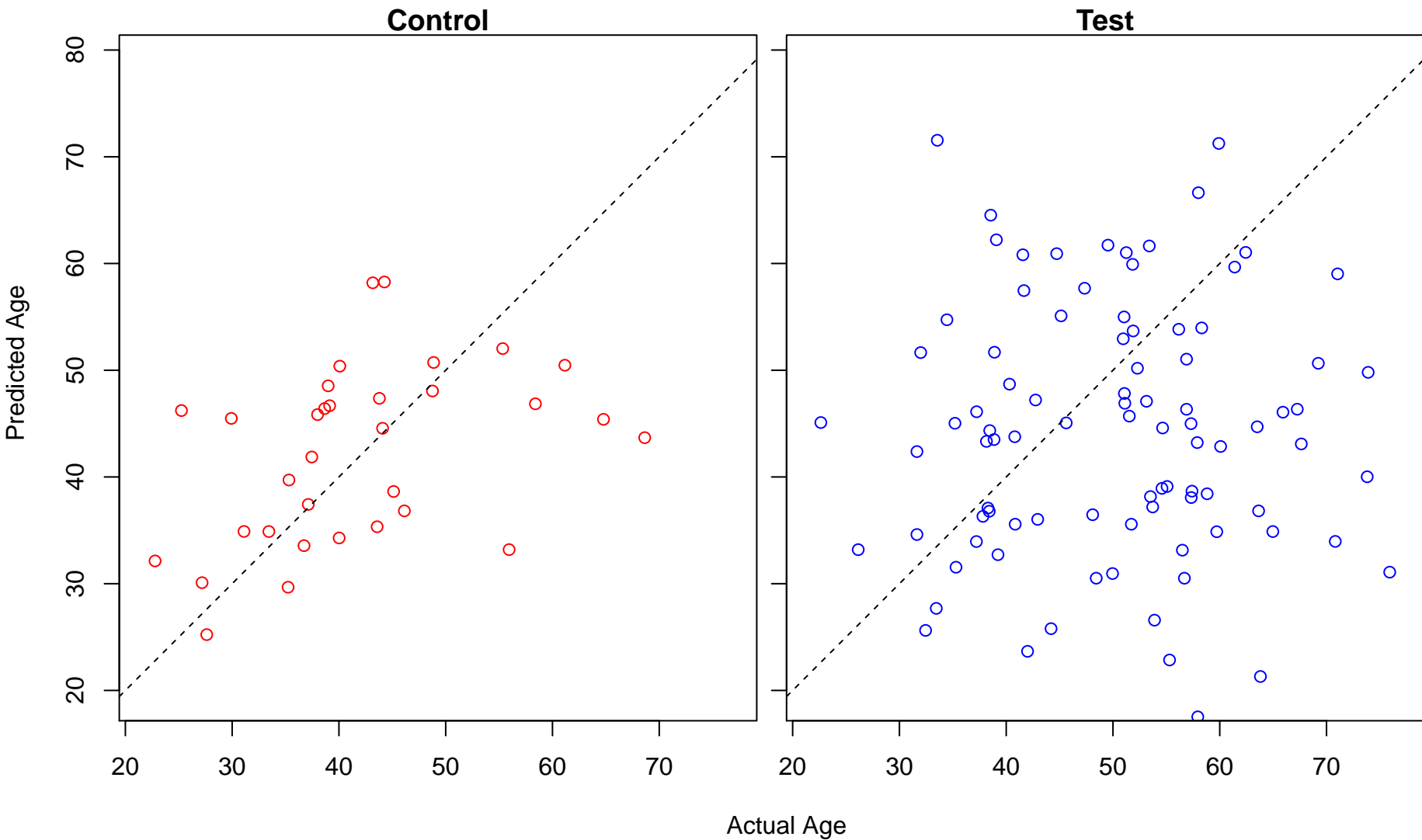
cellular response to hyperoxia (Score: 0.941700)



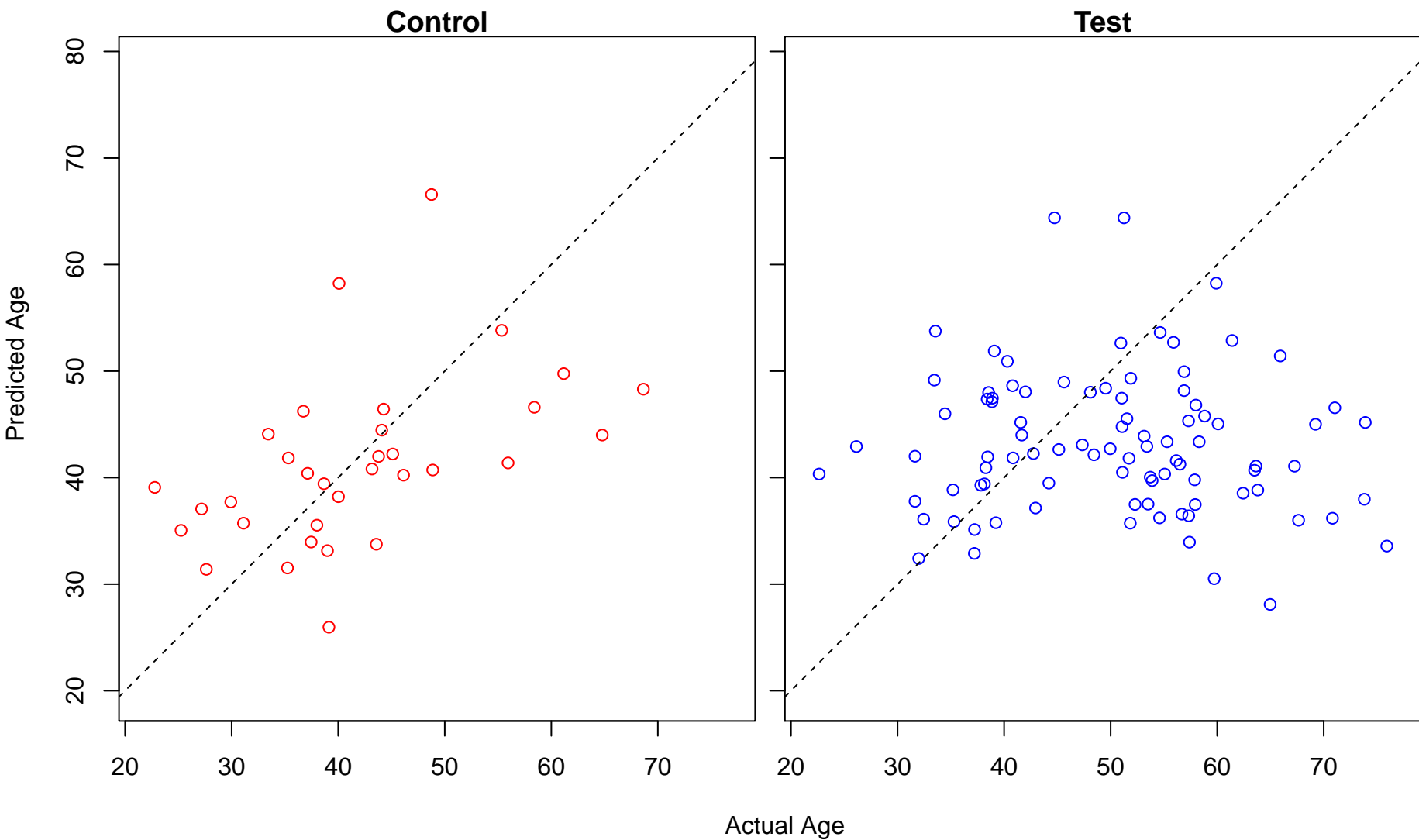
cyclic-nucleotide-mediated signaling (Score: 0.940955)



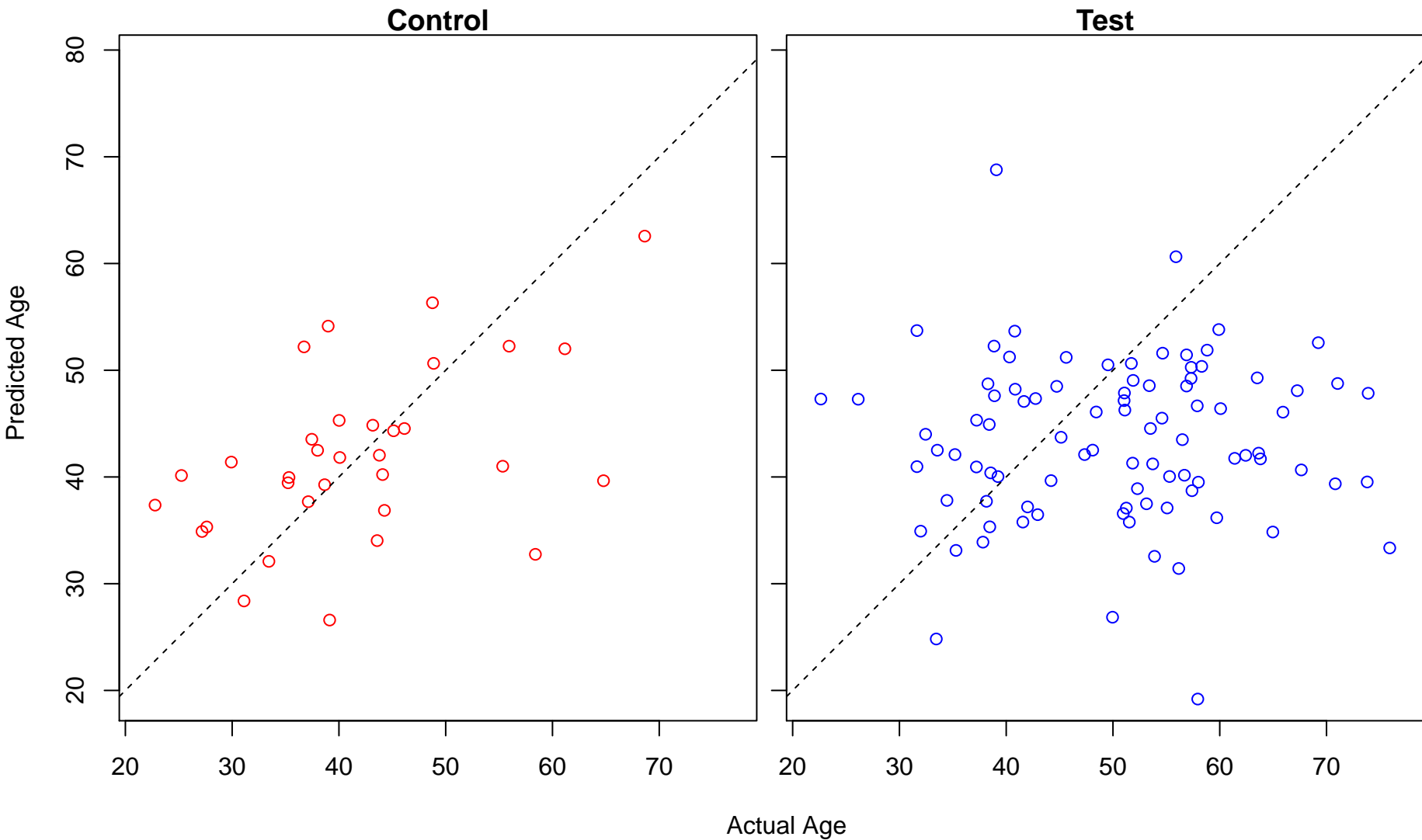
somatic stem cell division (Score: 0.940343)



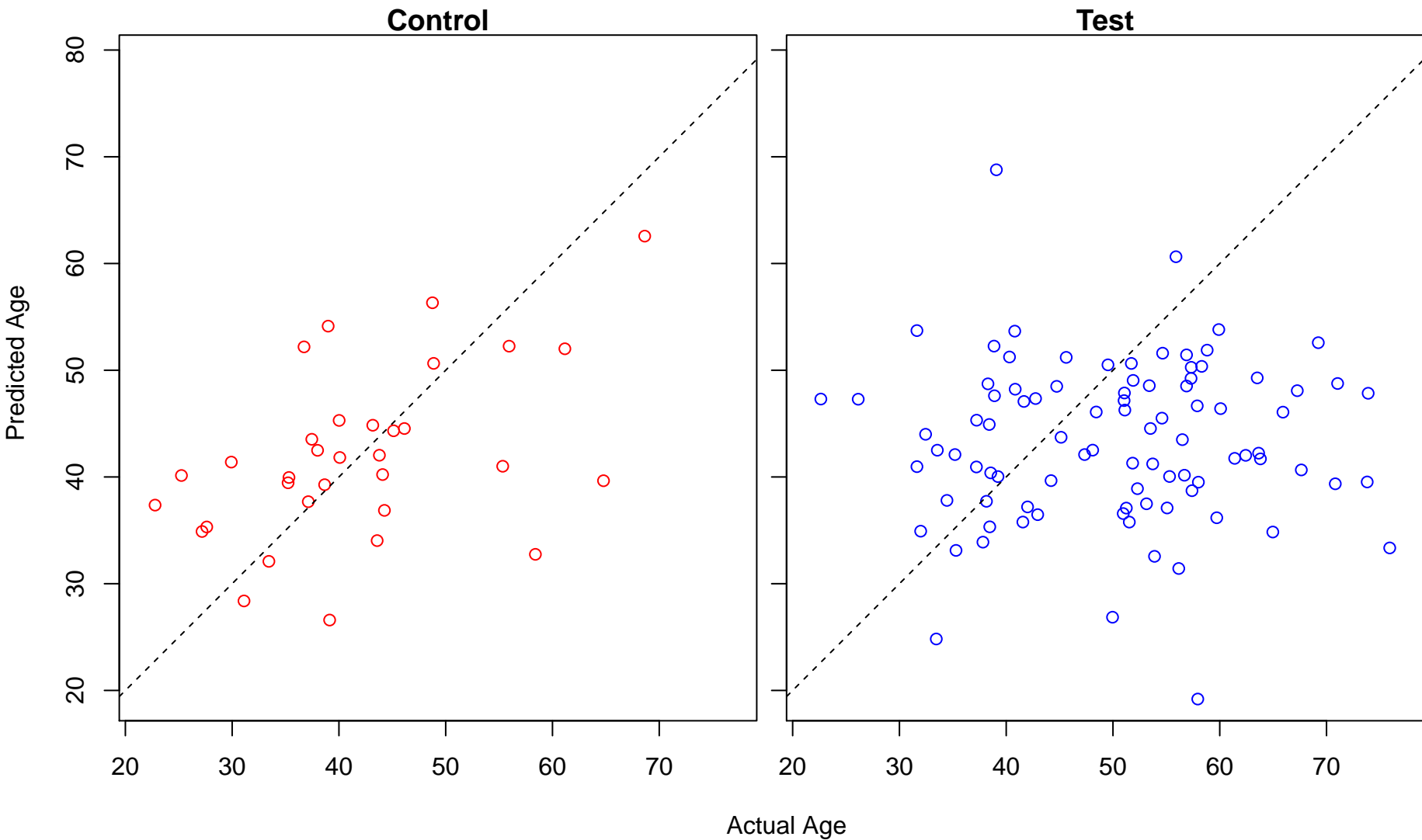
toll-like receptor 4 signaling pathway (Score: 0.938158)



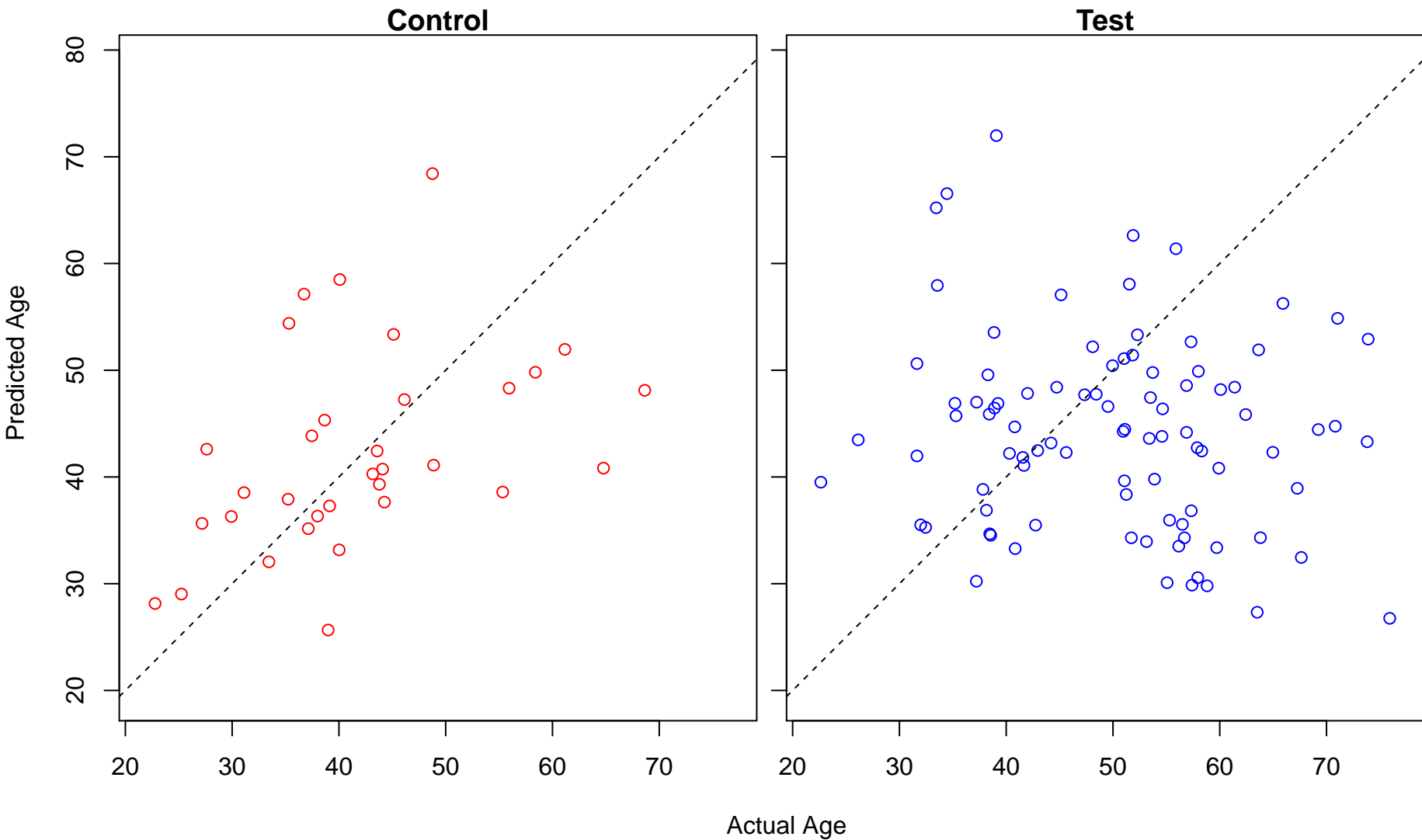
regulation of cilium movement involved in cell motility (Score: 0.937363)



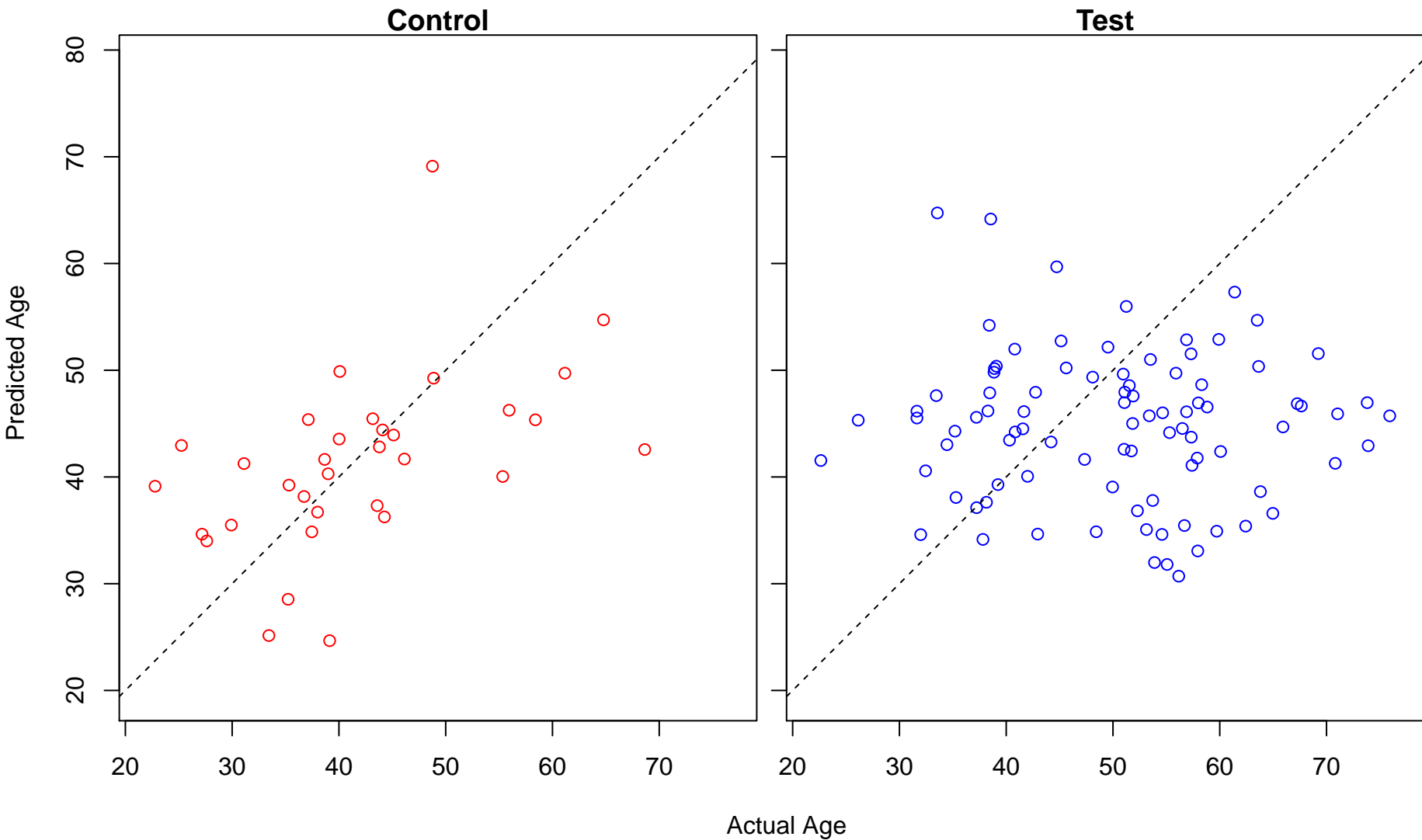
regulation of cilium beat frequency involved in ciliary motility (Score: 0.937363)



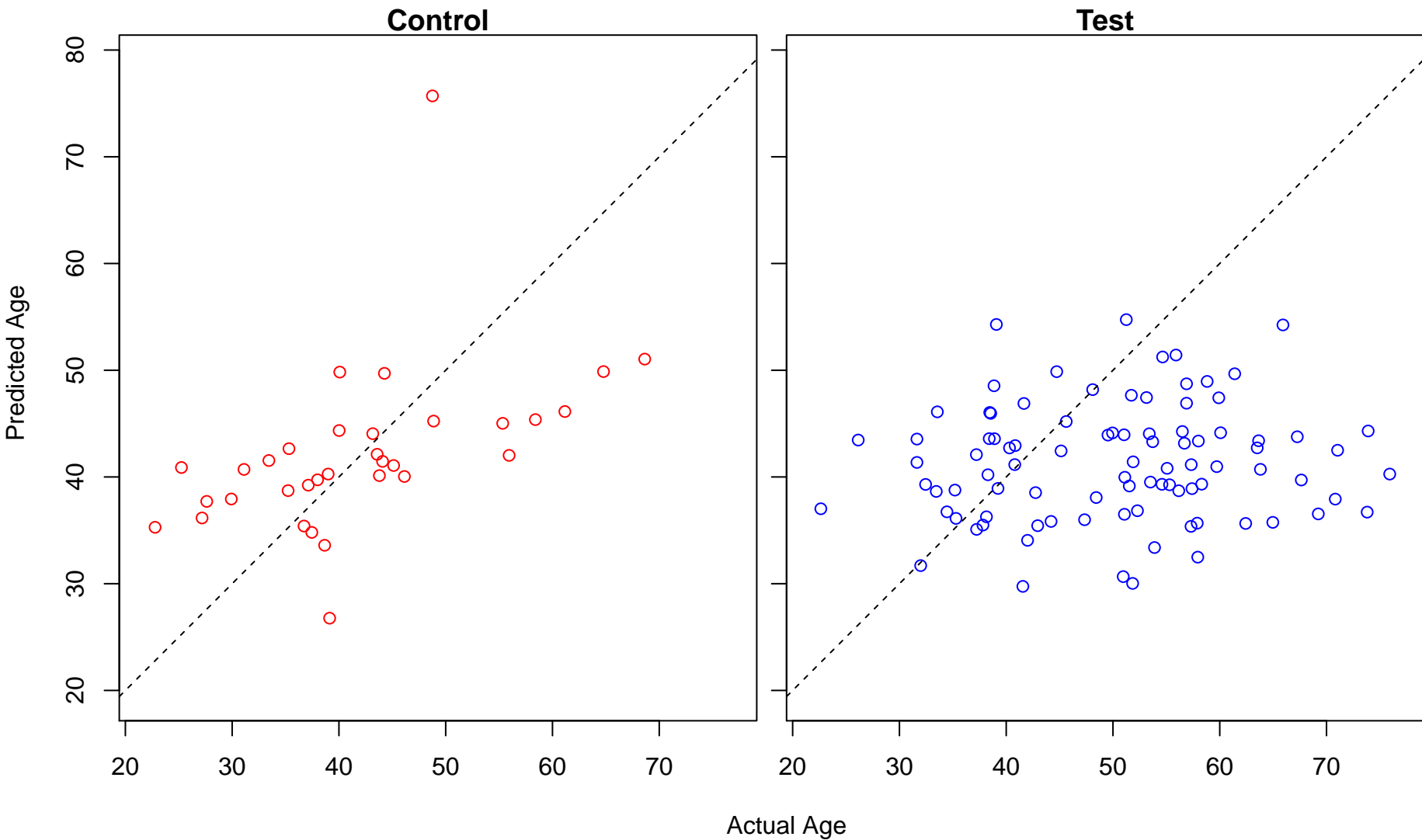
intracellular estrogen receptor signaling pathway (Score: 0.936805)



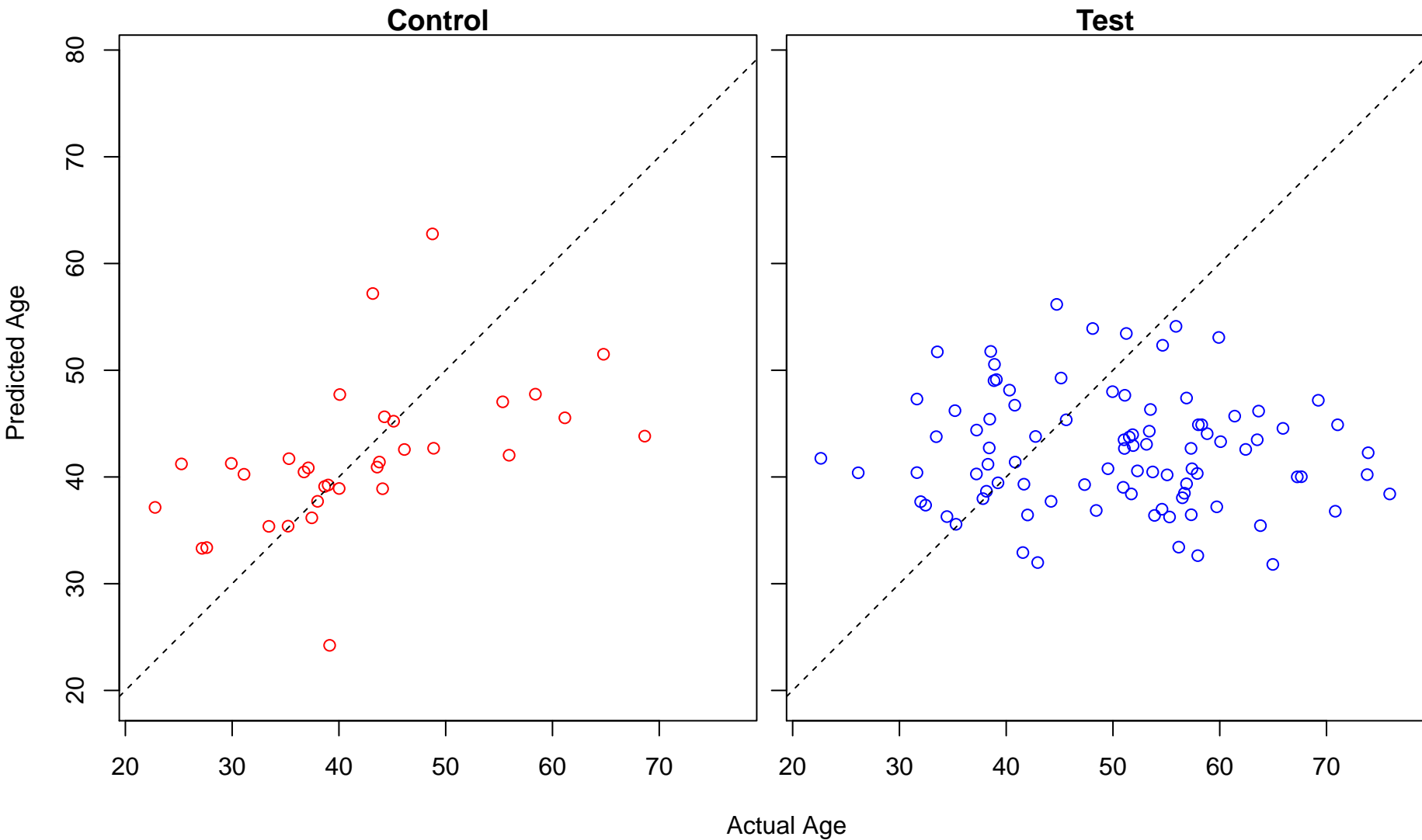
positive regulation of triglyceride metabolic process (Score: 0.936292)



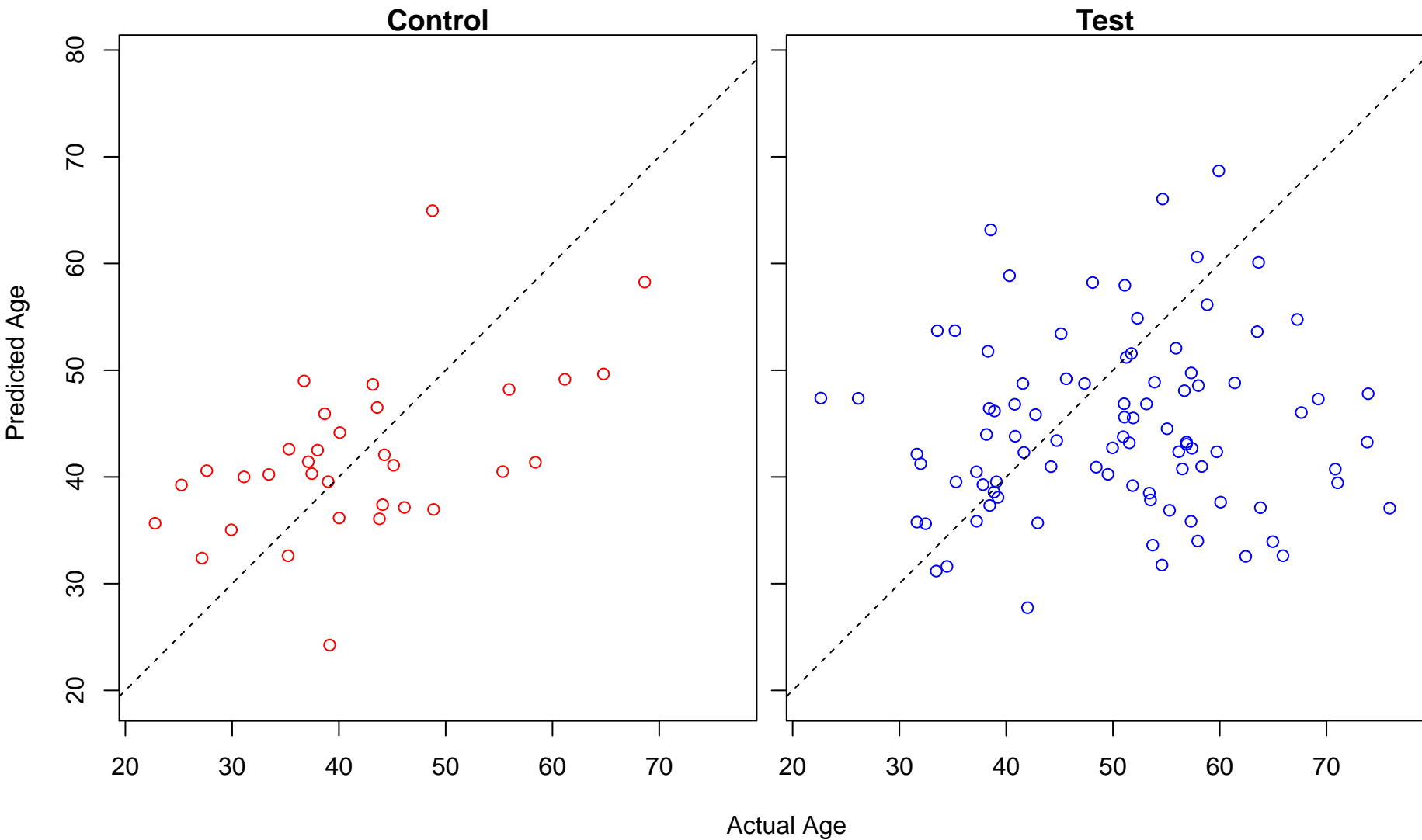
establishment of protein localization to Golgi (Score: 0.935394)



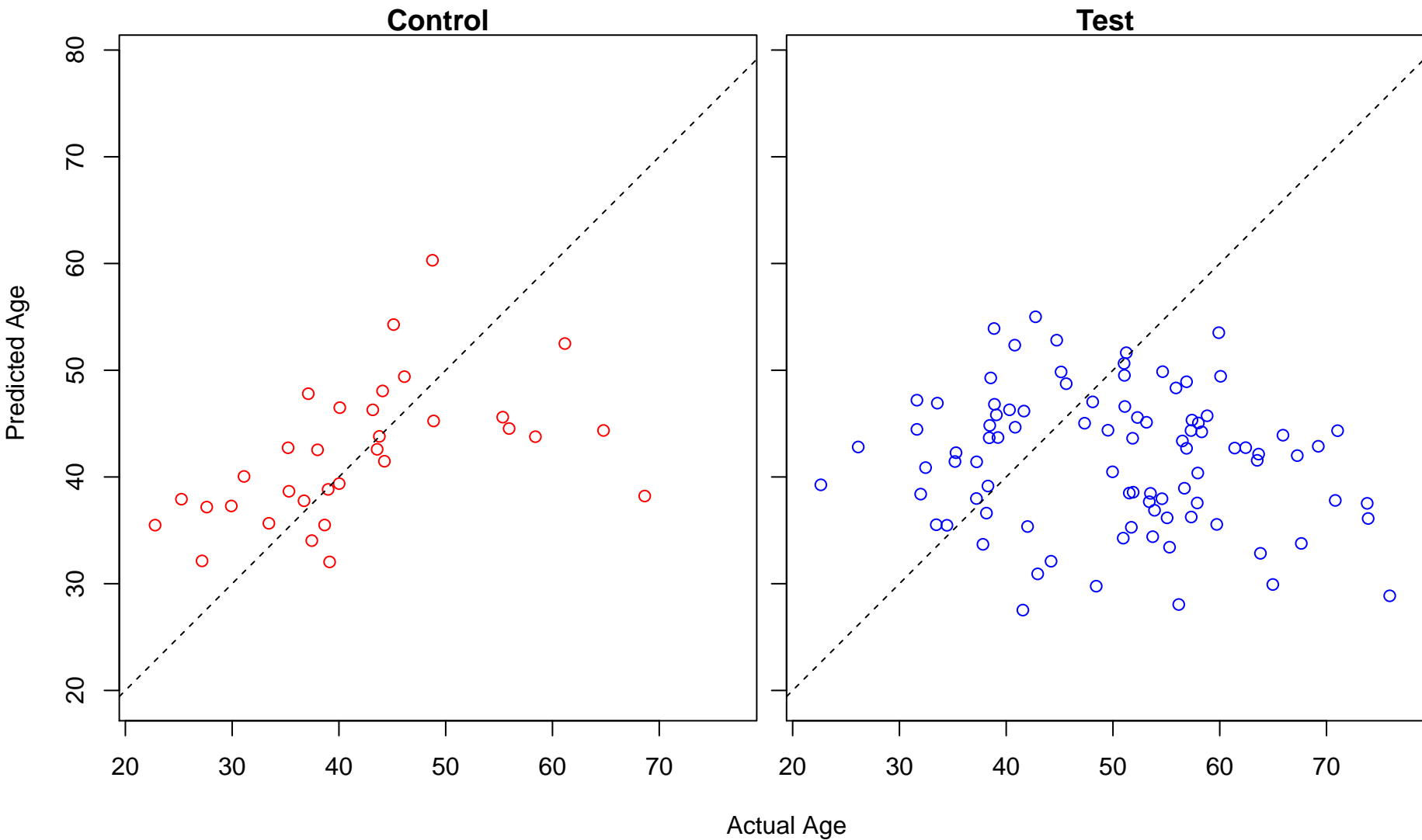
carboxylic acid transport (Score: 0.933540)



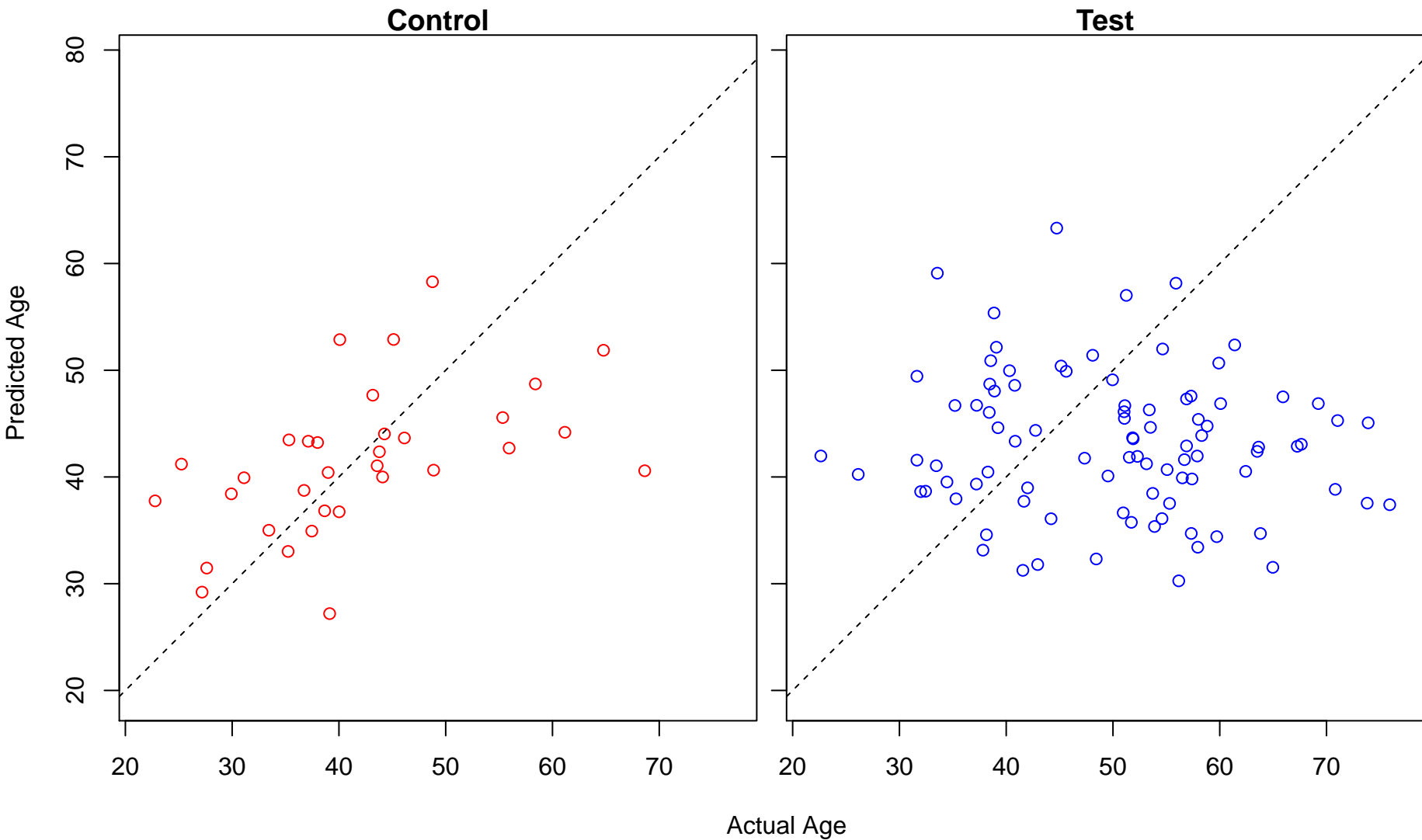
PML body organization (Score: 0.932980)



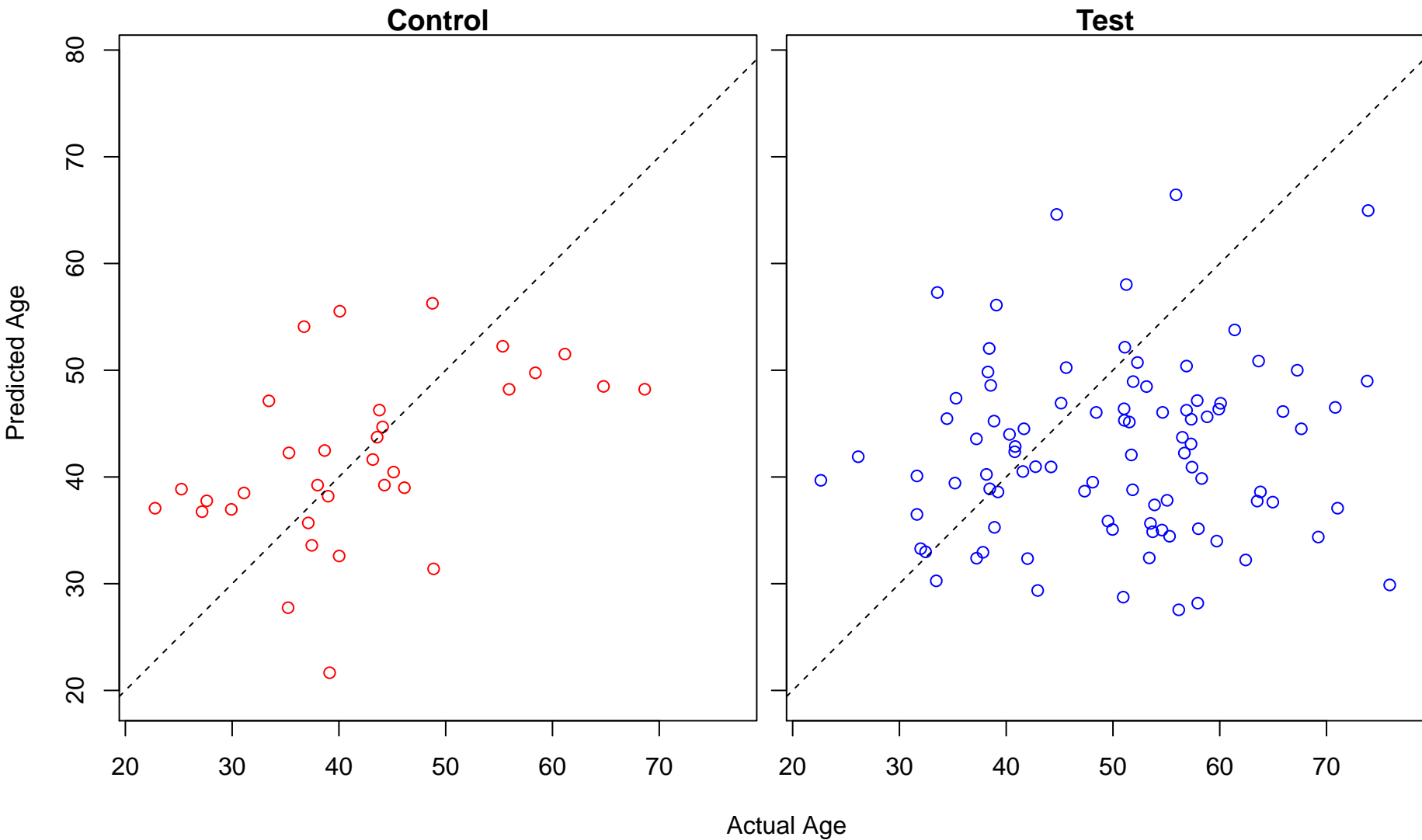
regulation of heart contraction (Score: 0.932321)



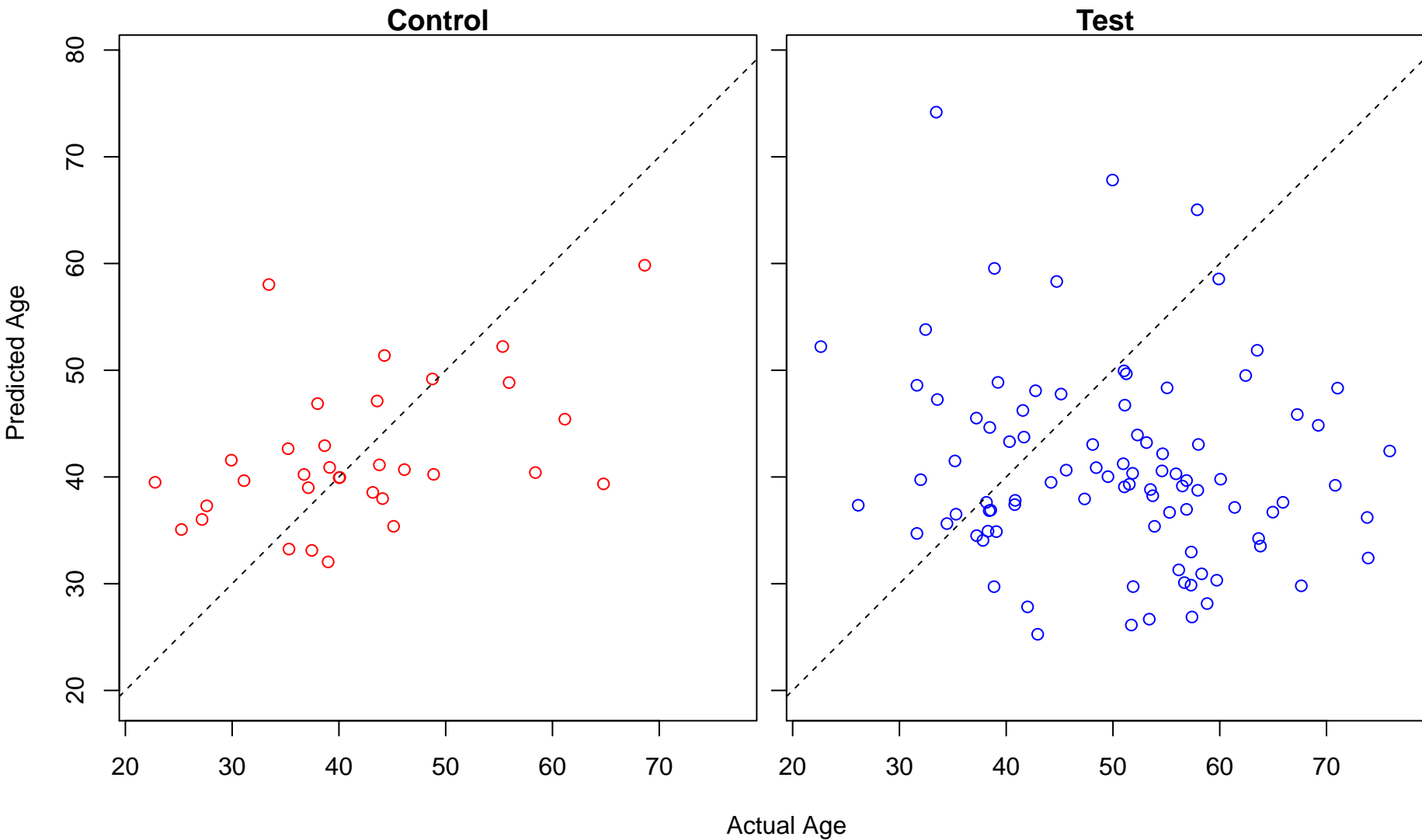
lipid localization (Score: 0.932109)



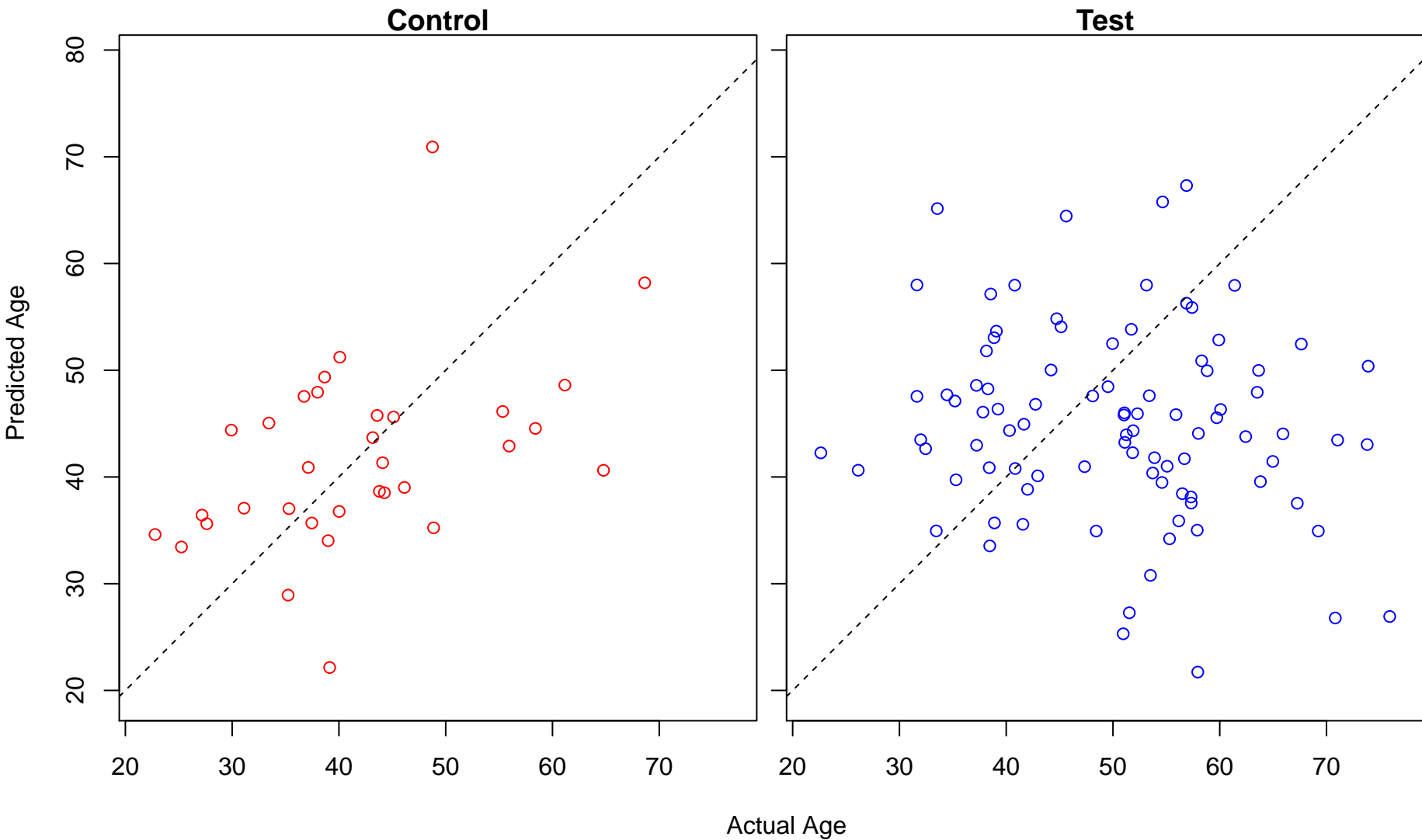
Golgi to plasma membrane transport (Score: 0.931860)



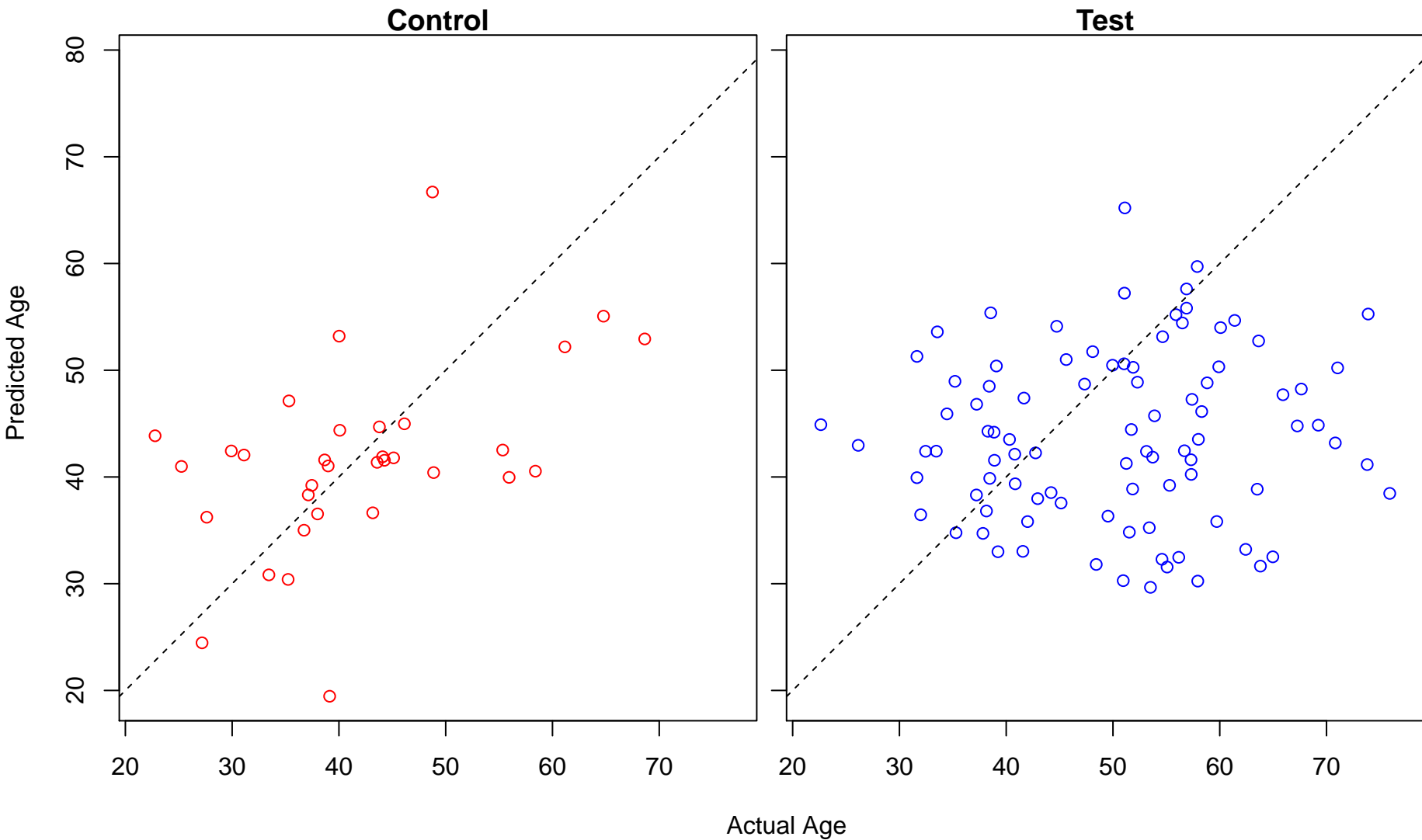
regulation of G0 to G1 transition (Score: 0.931779)



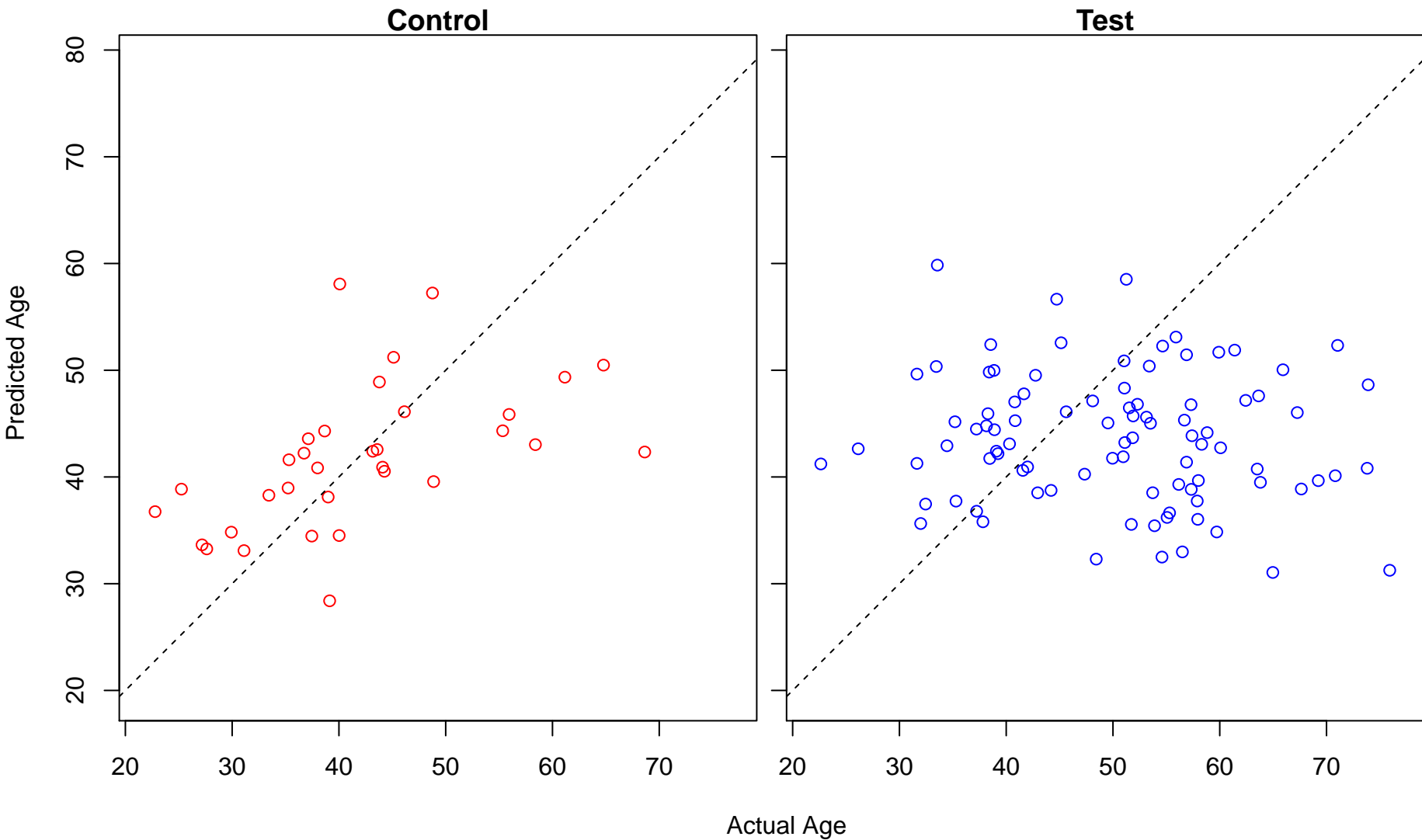
hormone-mediated signaling pathway (Score: 0.929783)



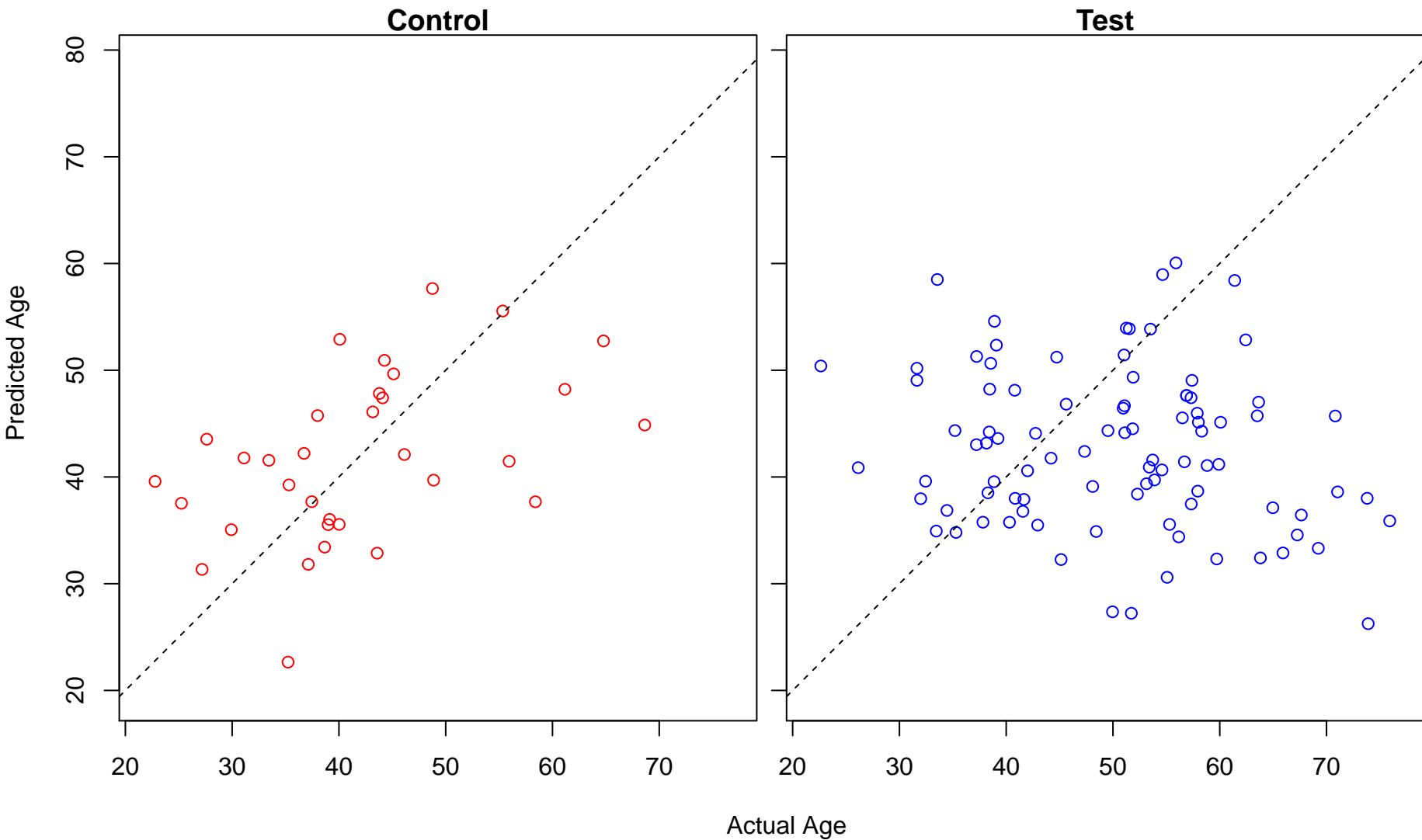
dermatan sulfate metabolic process (Score: 0.928657)



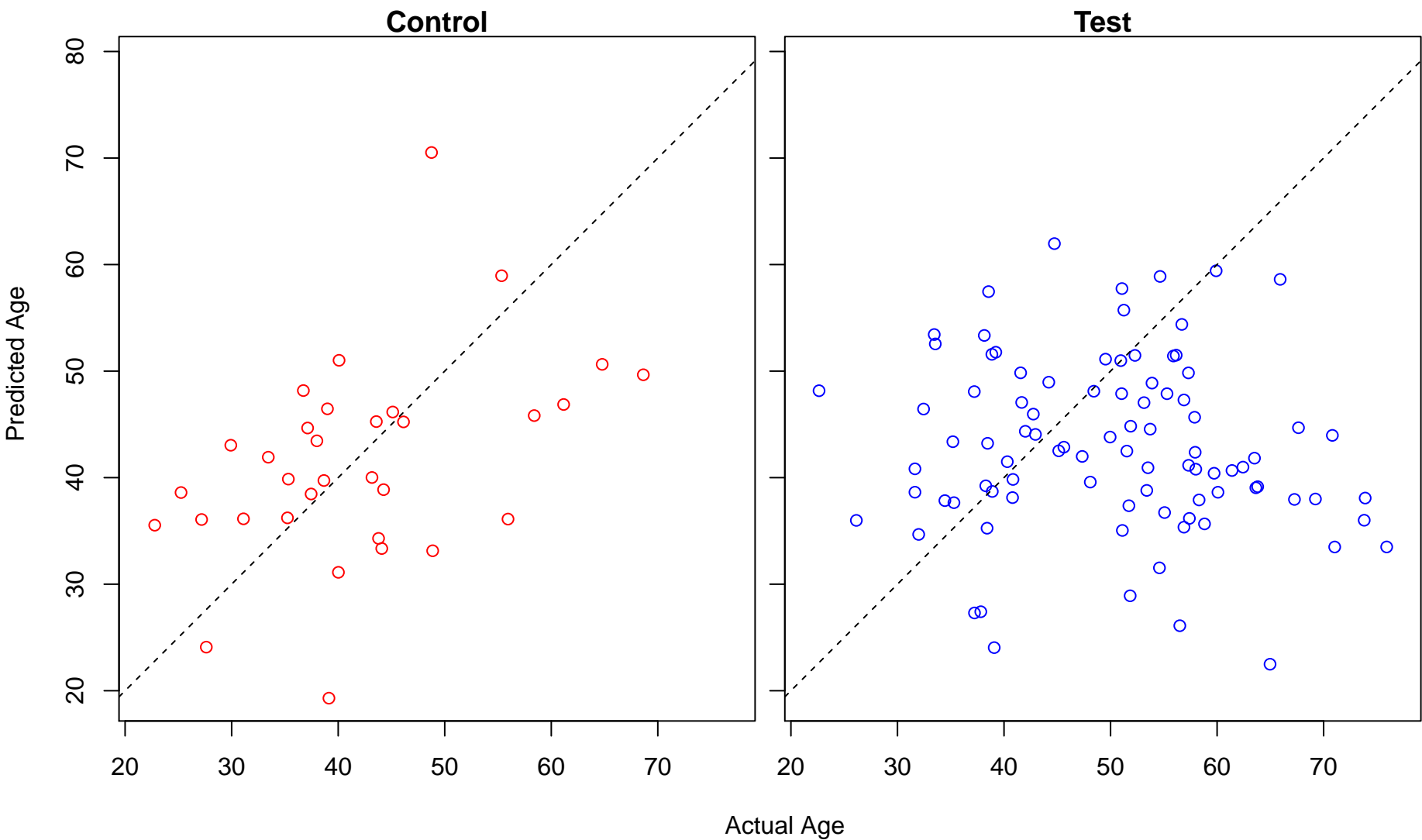
amine metabolic process (Score: 0.928547)



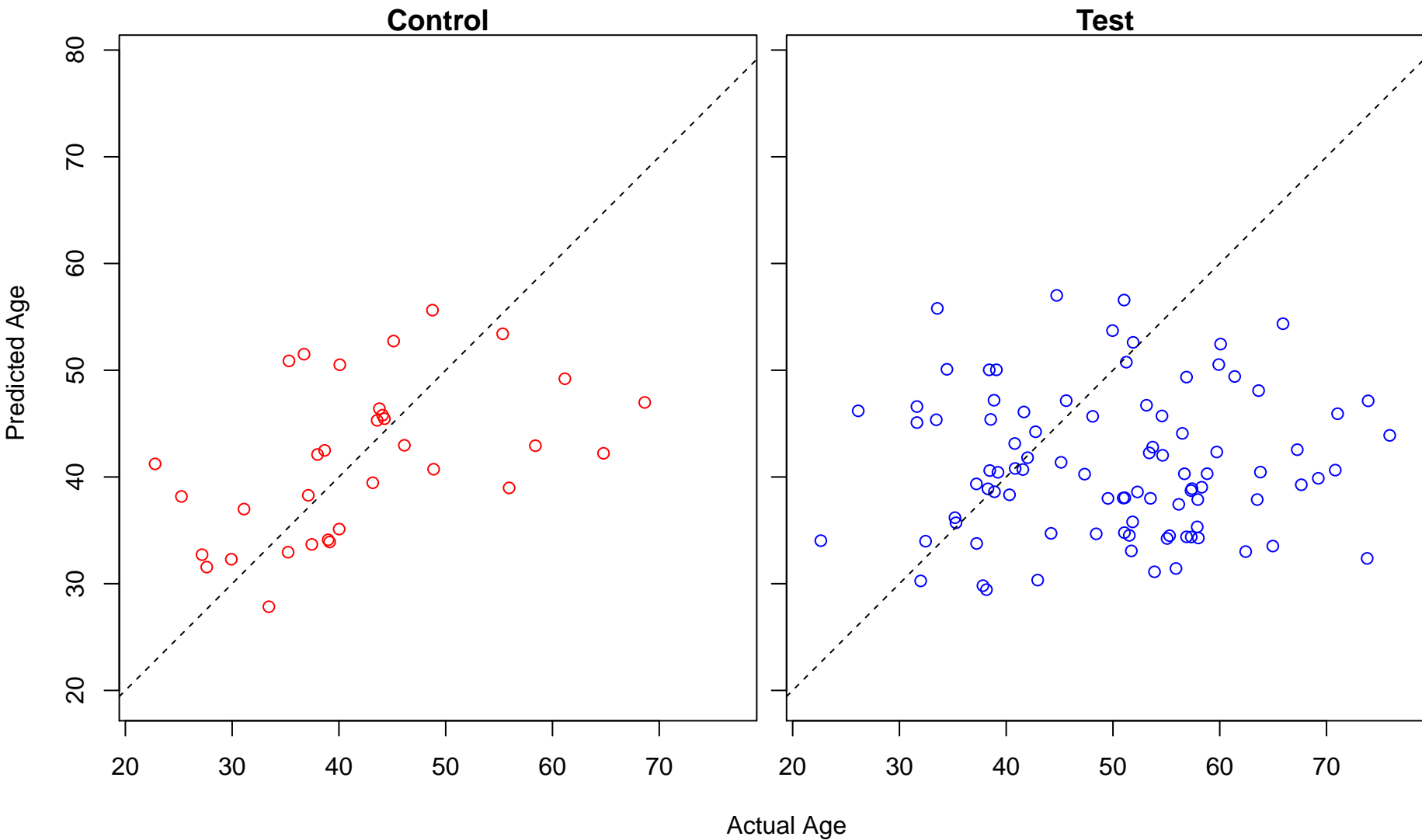
epithelial cell differentiation (Score: 0.927714)



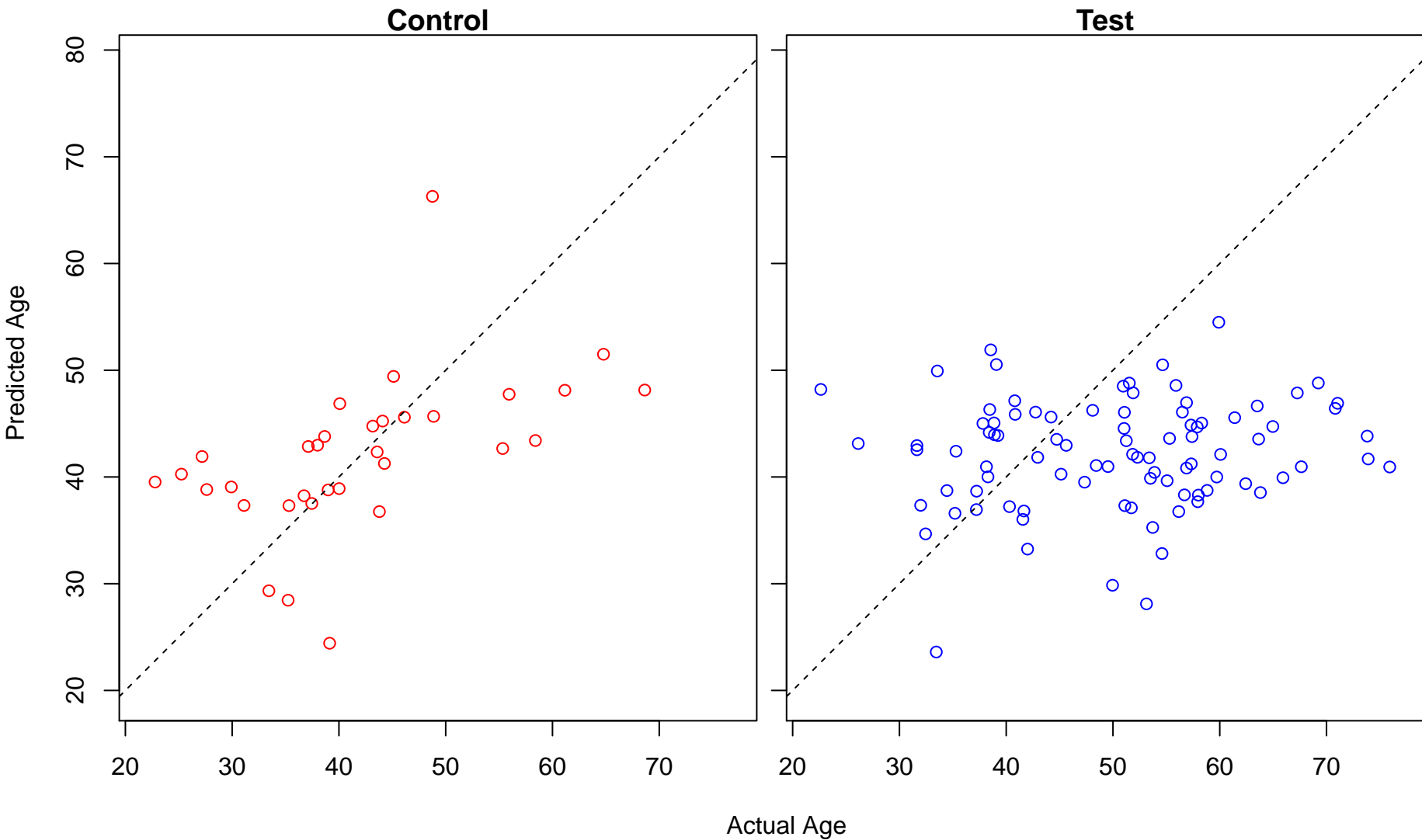
DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (Score: 0.



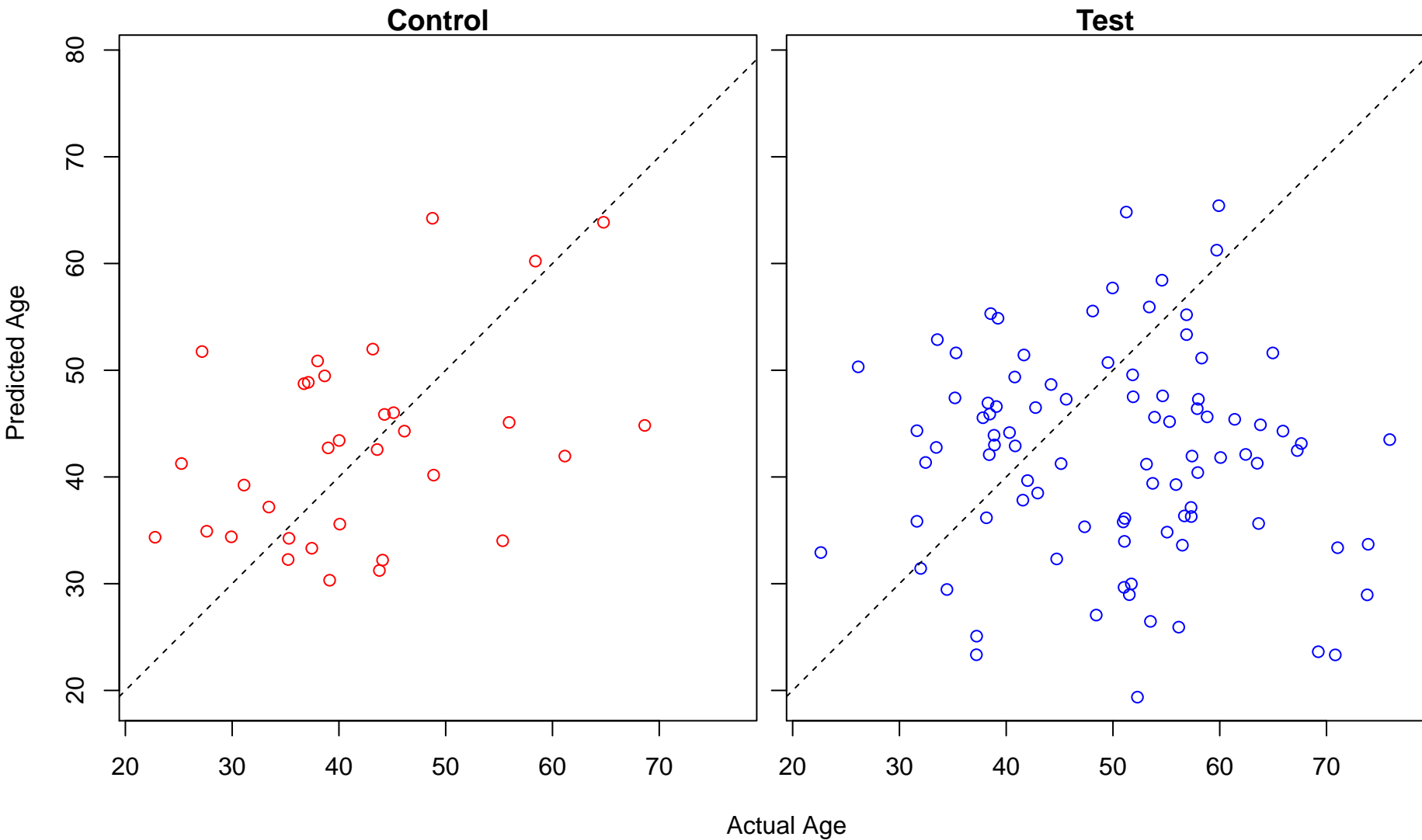
regulation of DNA recombination (Score: 0.926734)



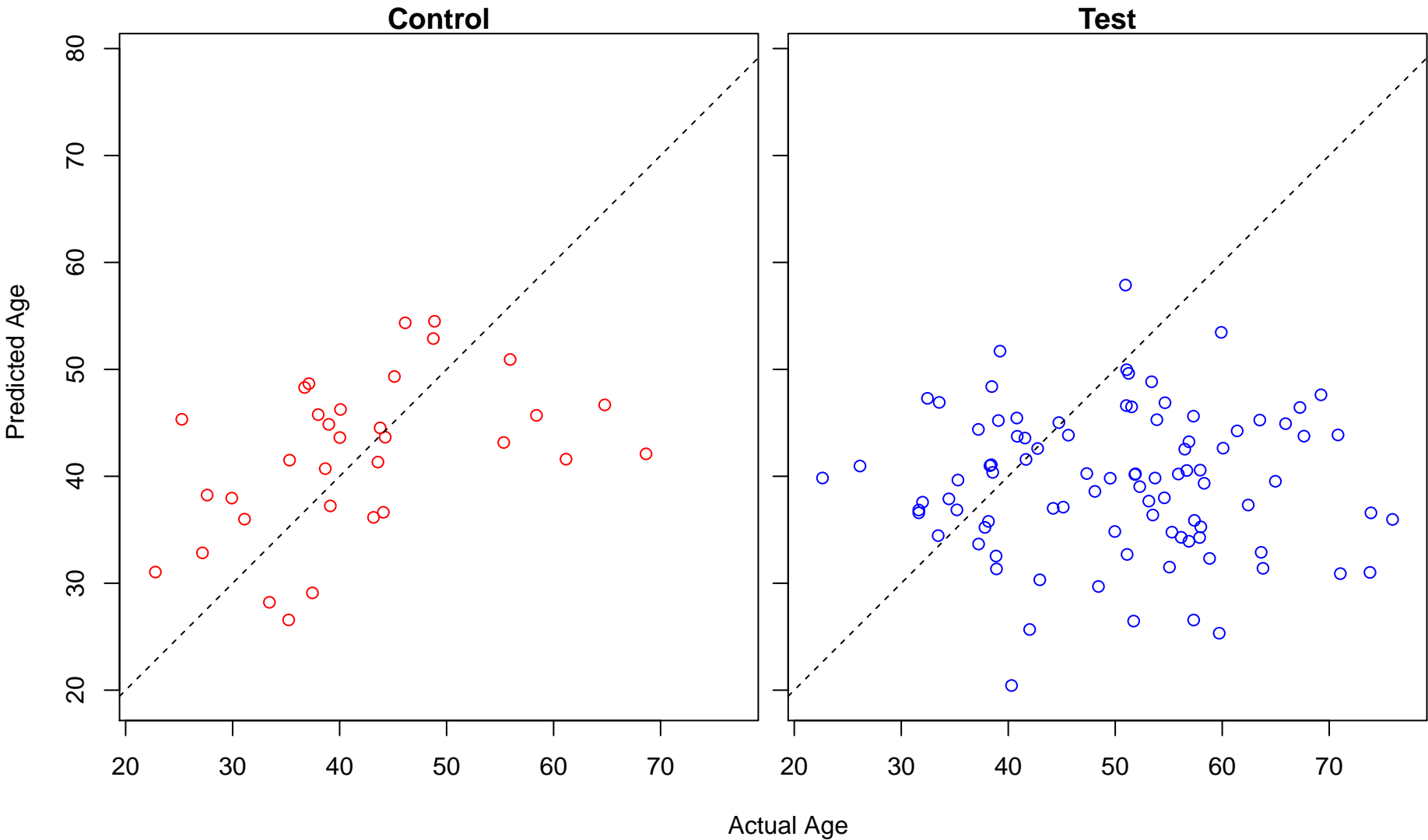
negative regulation of interleukin-23 production (Score: 0.926400)



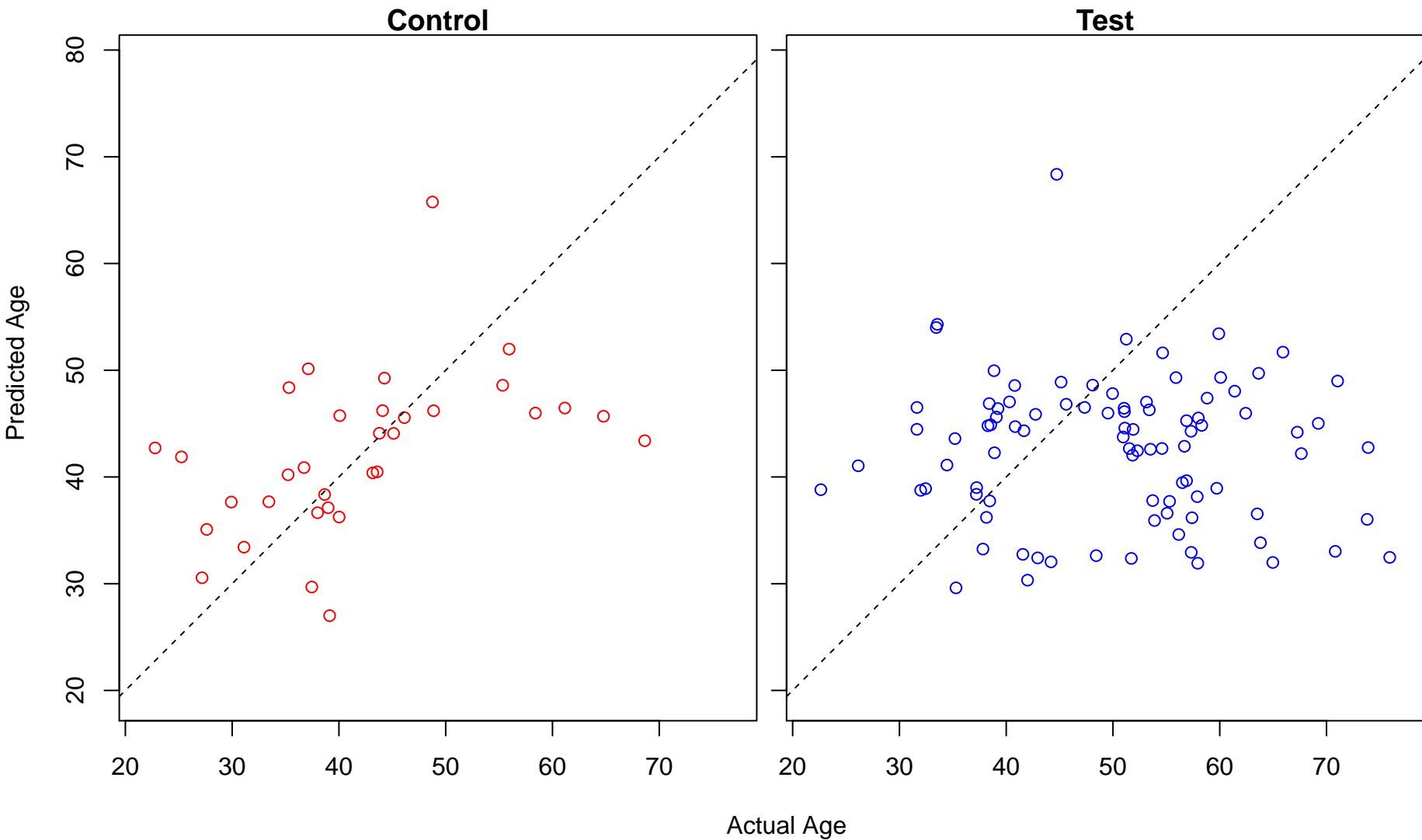
regulation of collagen biosynthetic process (Score: 0.925725)



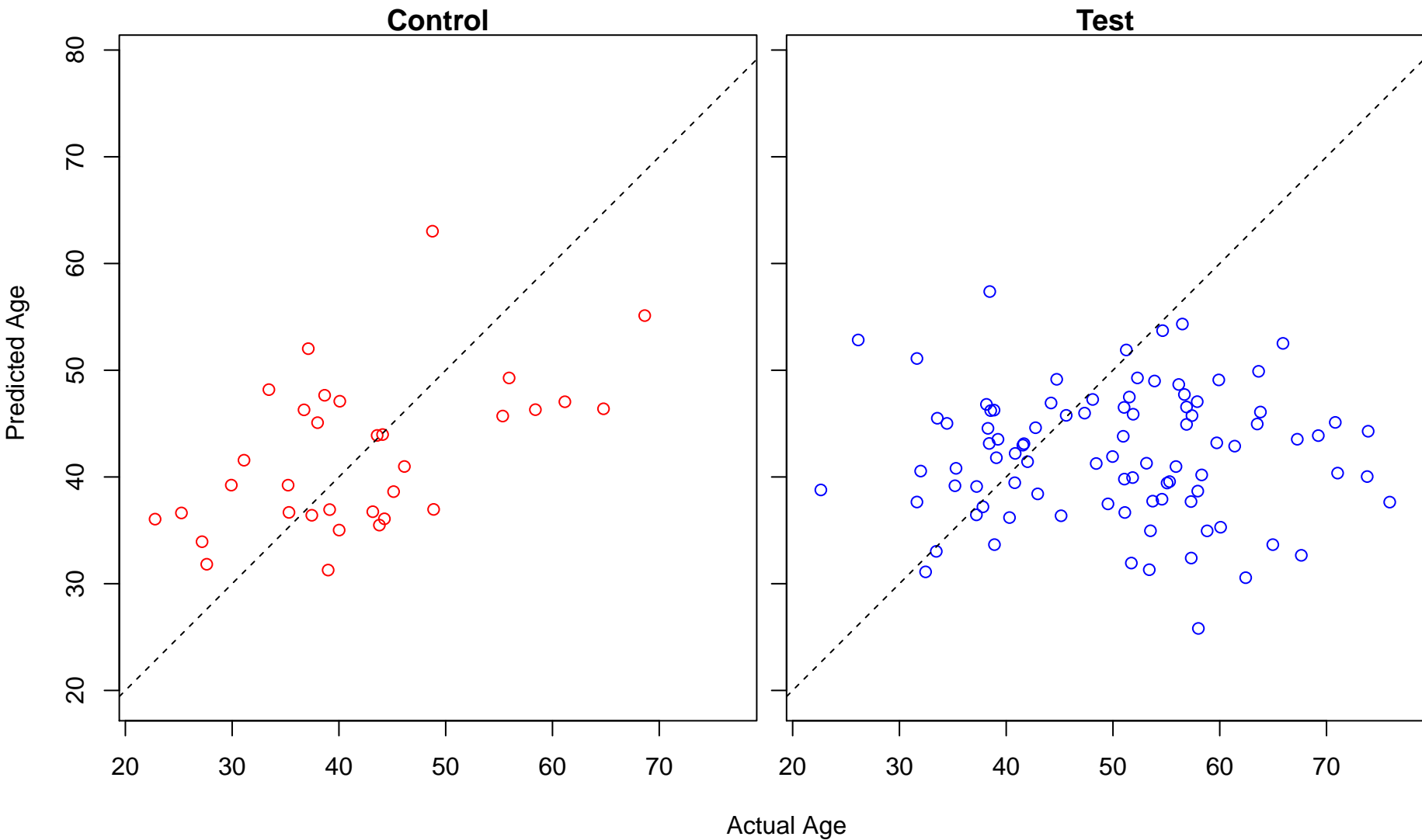
positive regulation of myeloid leukocyte cytokine production involved in immune response (Score: 0.92)



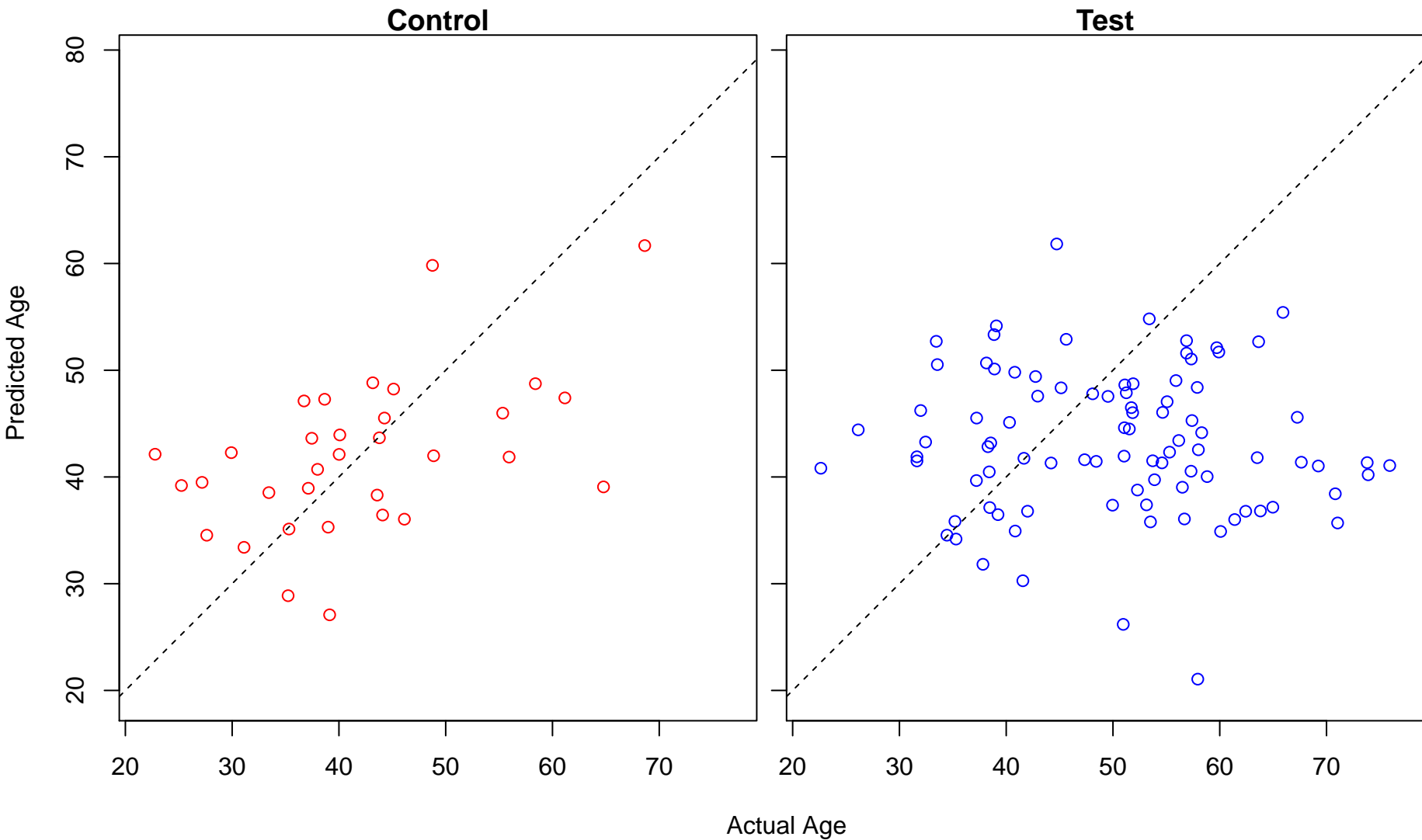
long-term synaptic potentiation (Score: 0.923390)



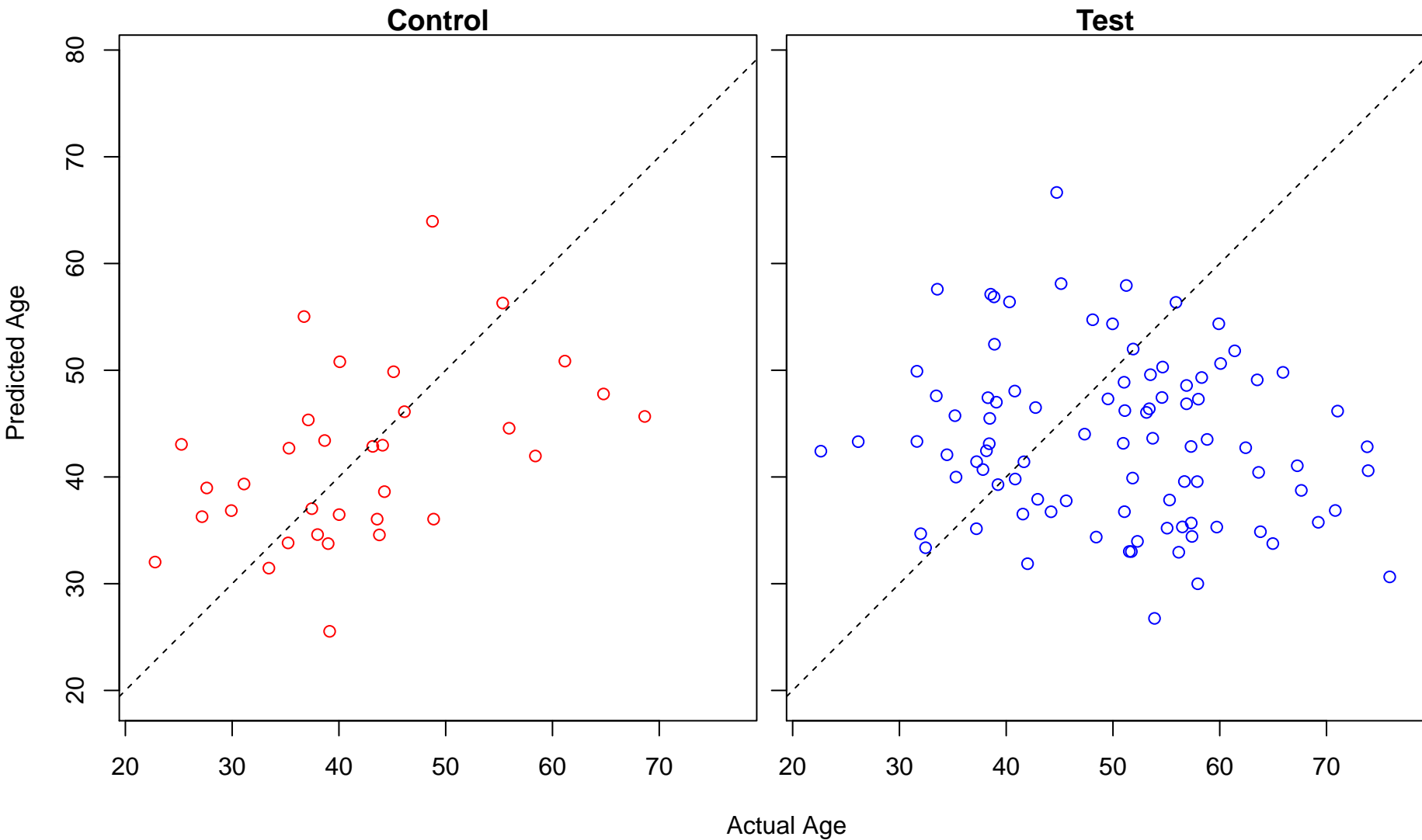
endosome transport via multivesicular body sorting pathway (Score: 0.923189)



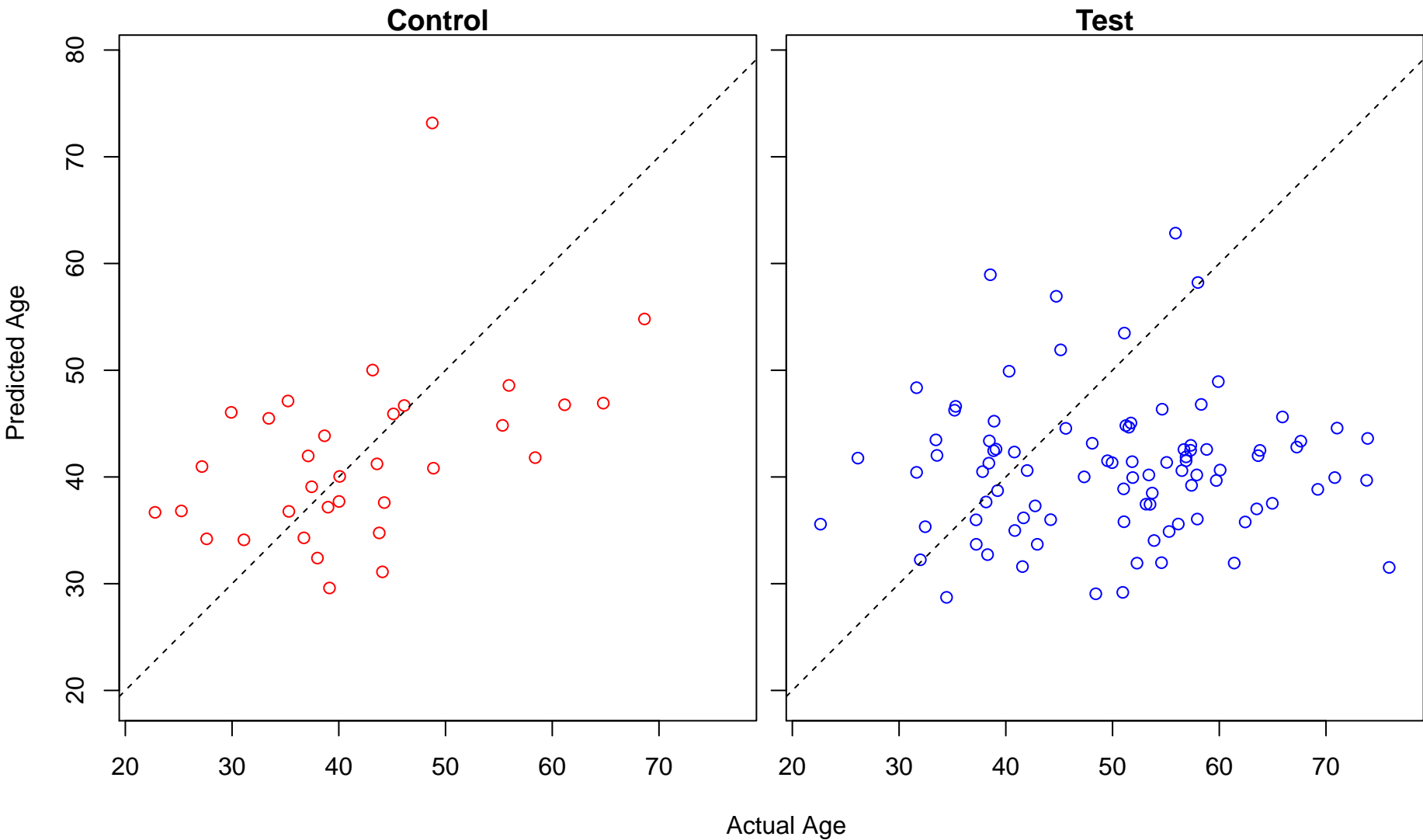
glycosphingolipid biosynthetic process (Score: 0.921823)



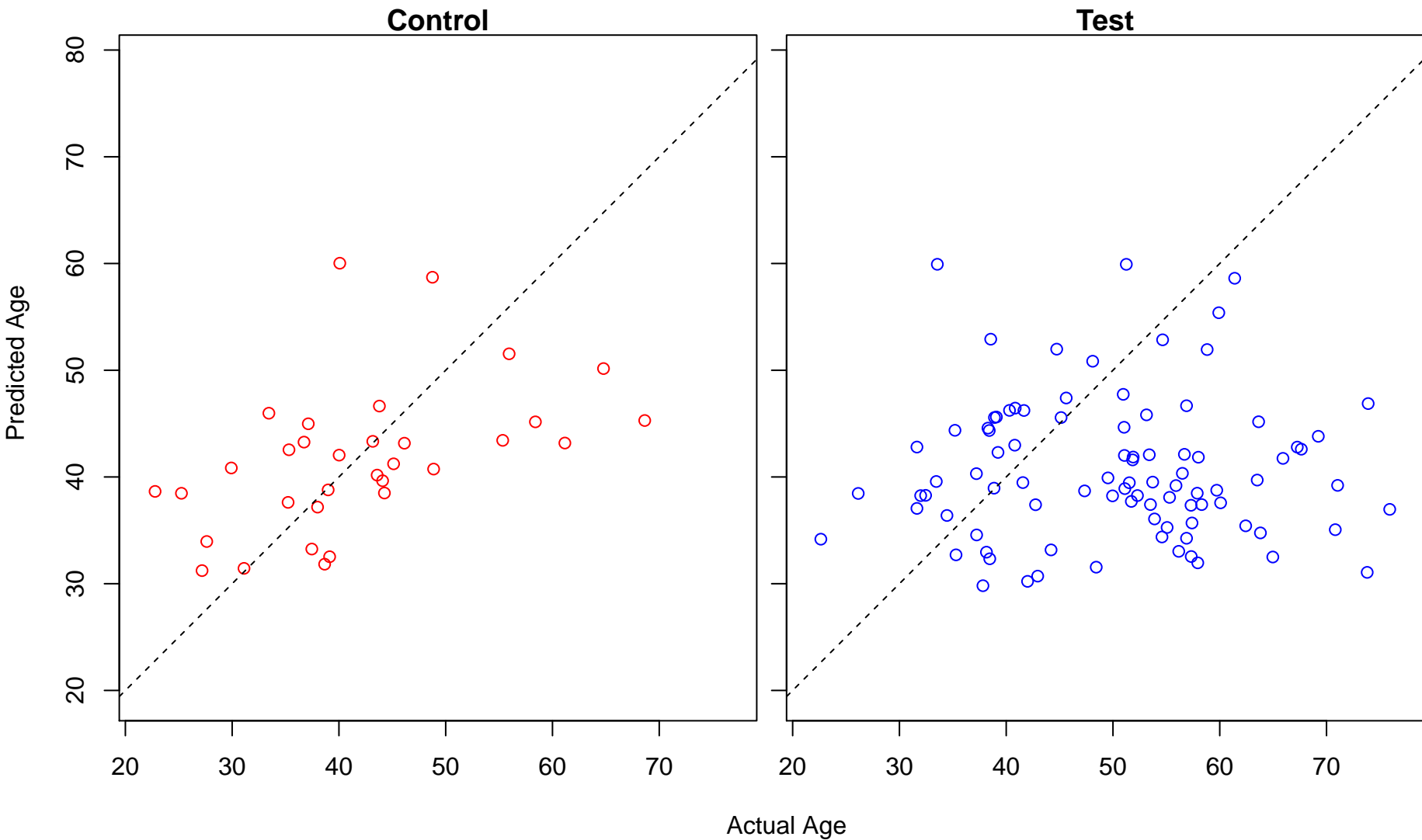
microtubule-based process (Score: 0.921277)



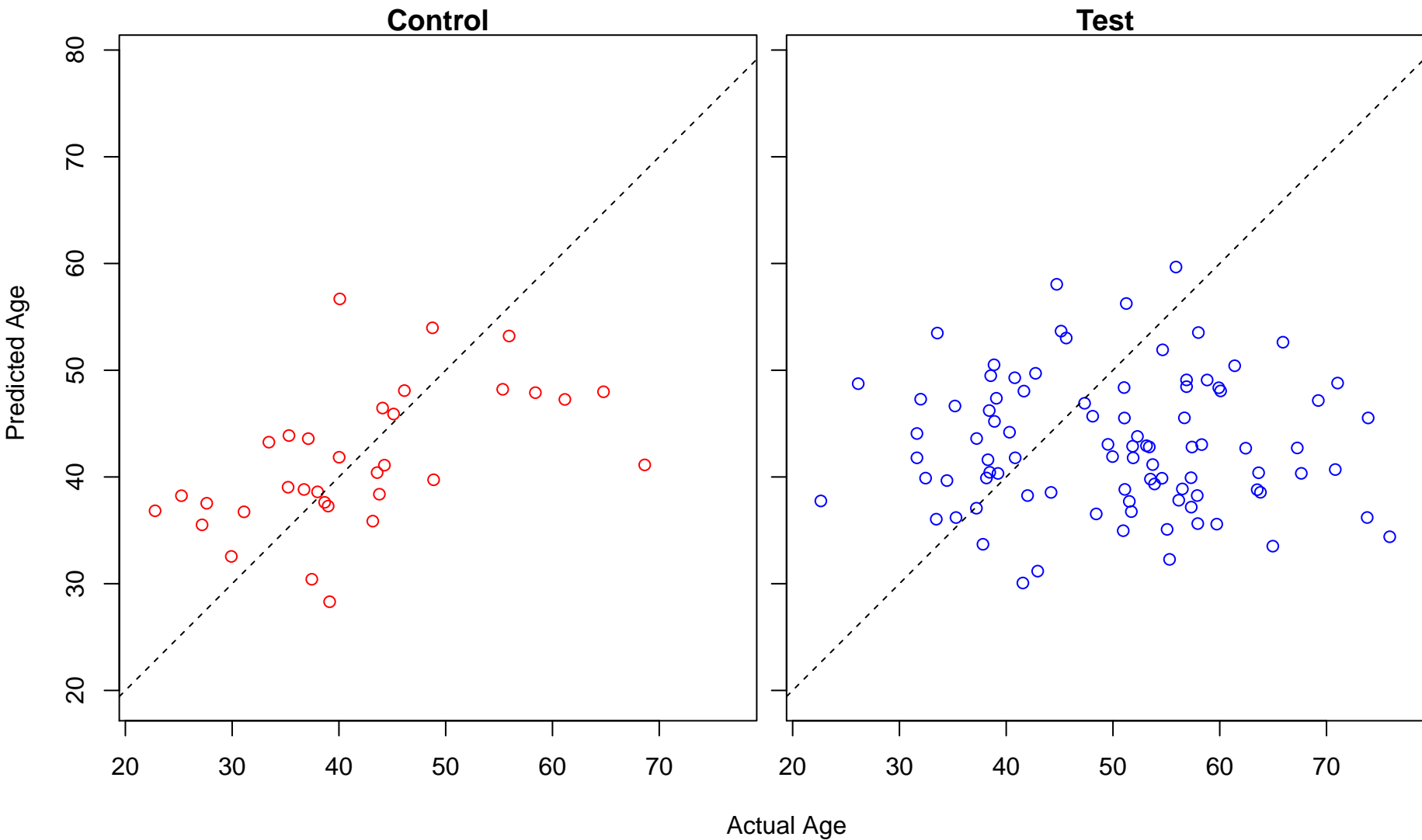
negative regulation of cytokine production involved in immune response (Score: 0.921102)



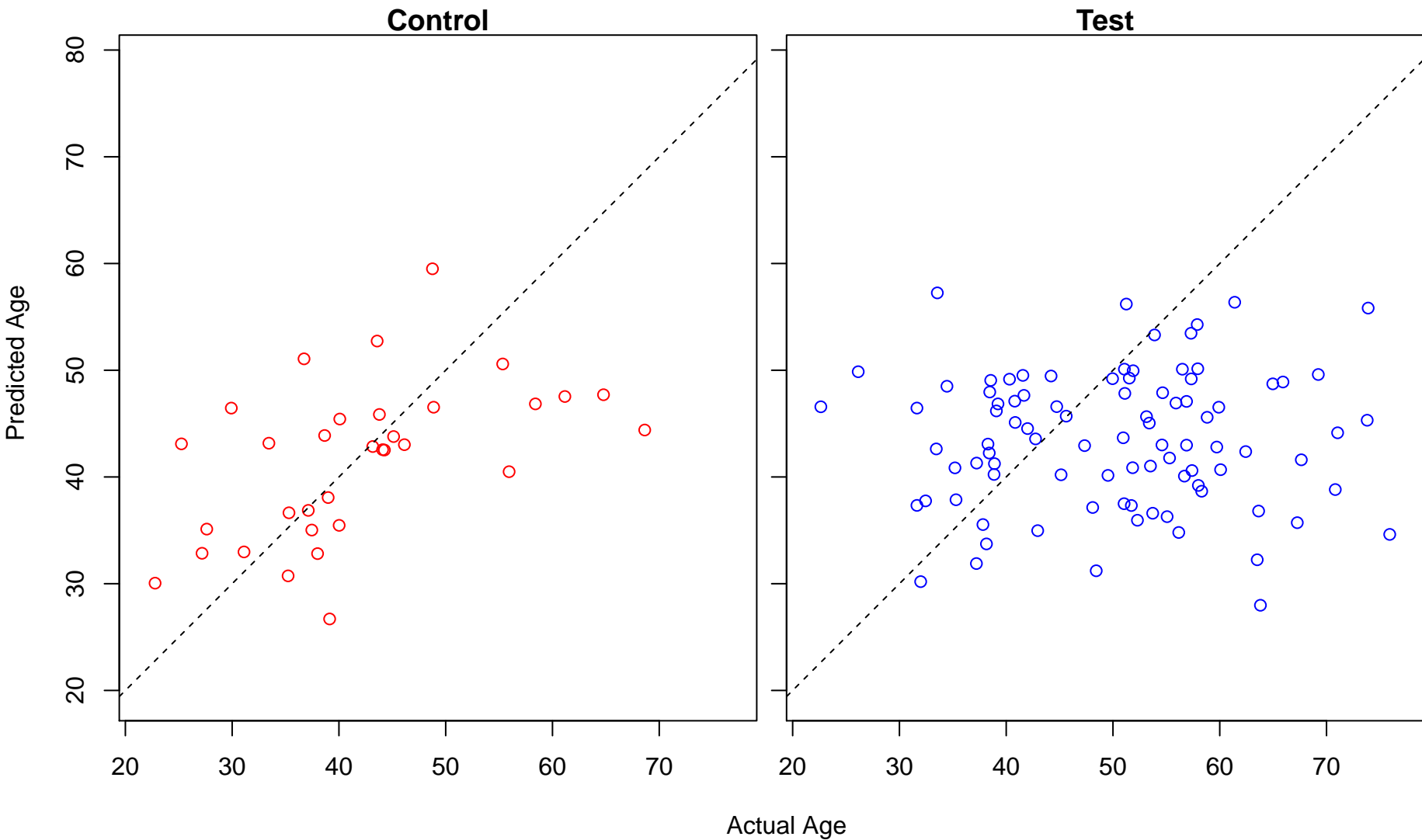
adenosine to inosine editing (Score: 0.920983)



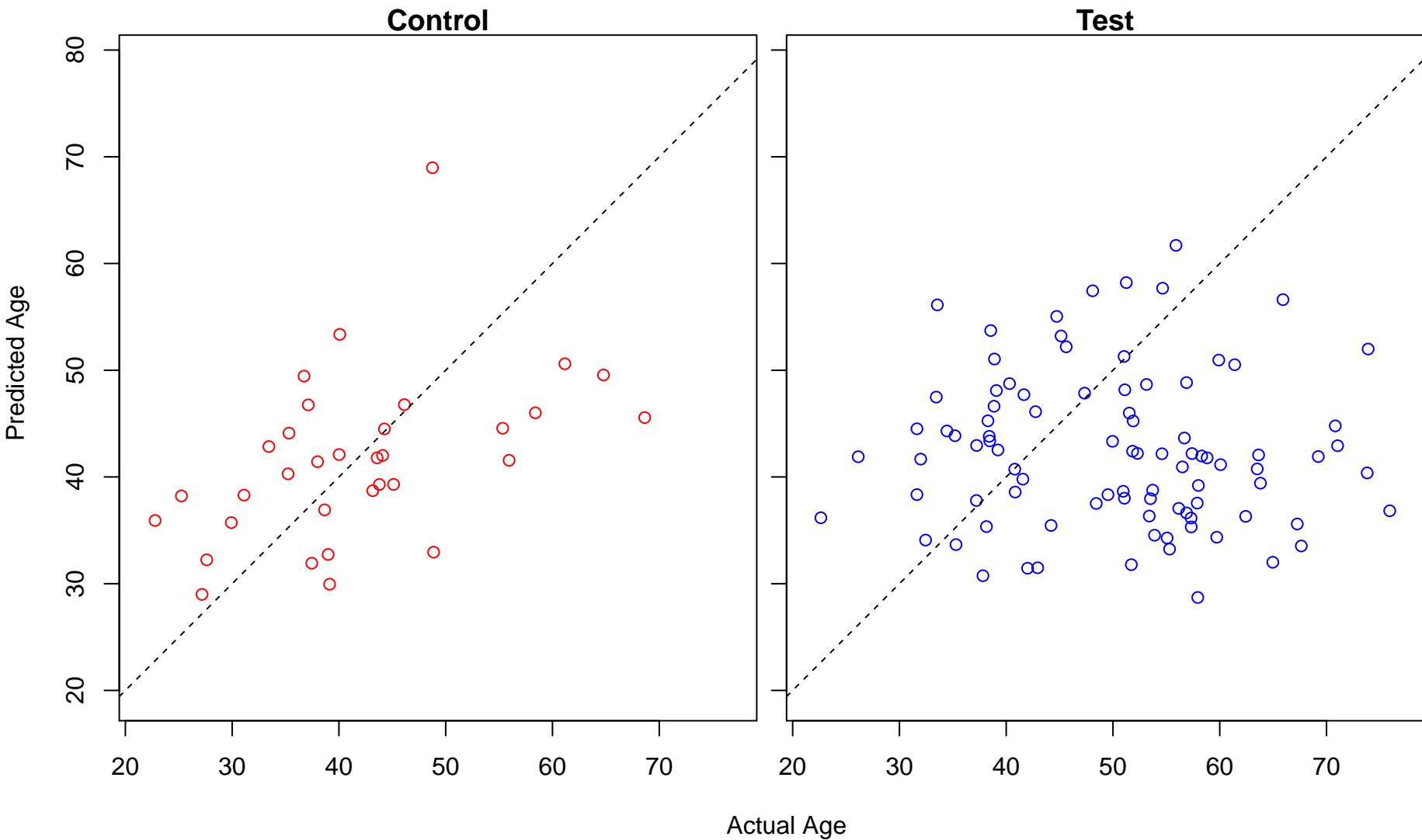
regulation of metal ion transport (Score: 0.919597)



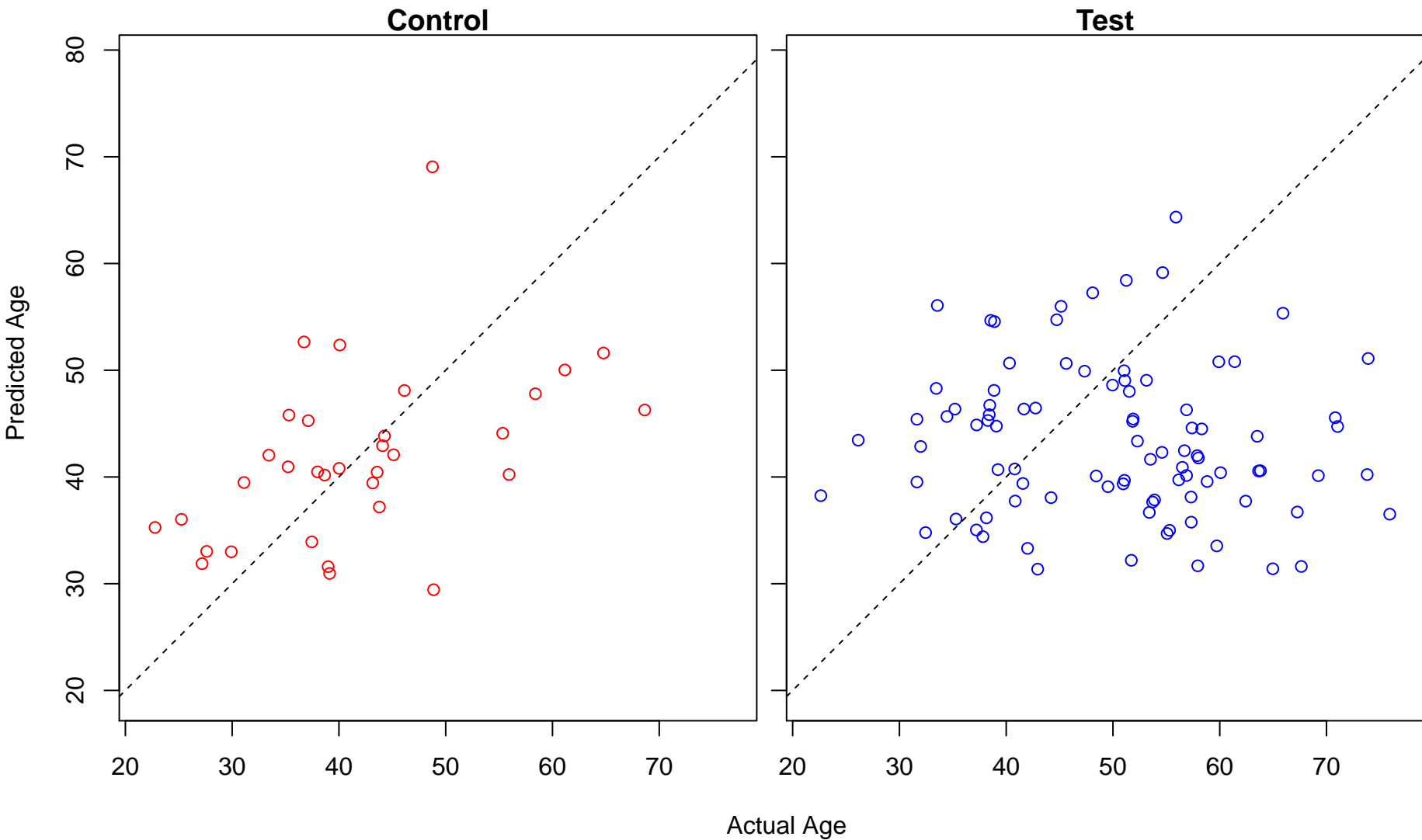
adaptive immune response (Score: 0.919241)



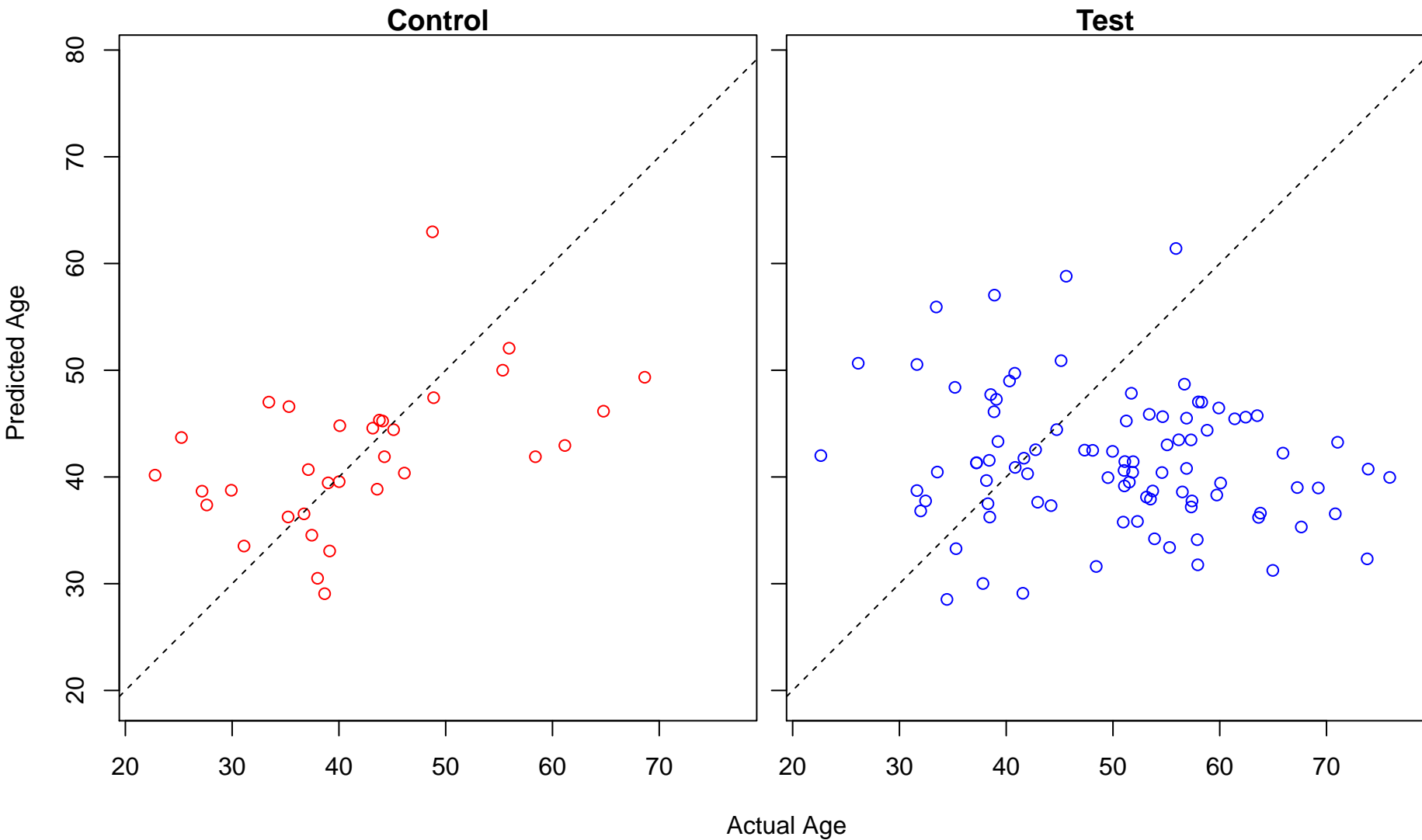
negative regulation of intracellular transport (Score: 0.919234)



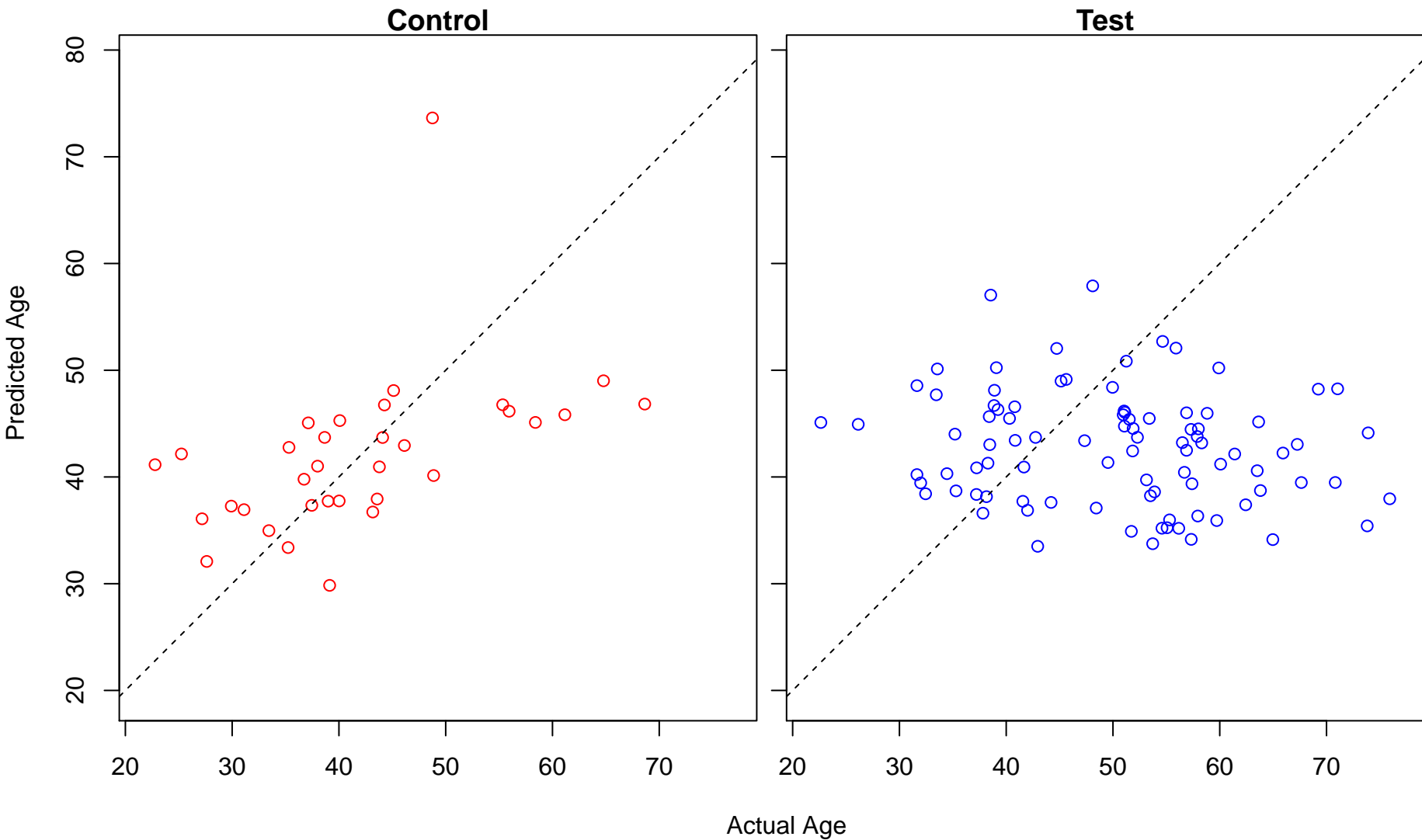
negative regulation of intracellular protein transport (Score: 0.918955)



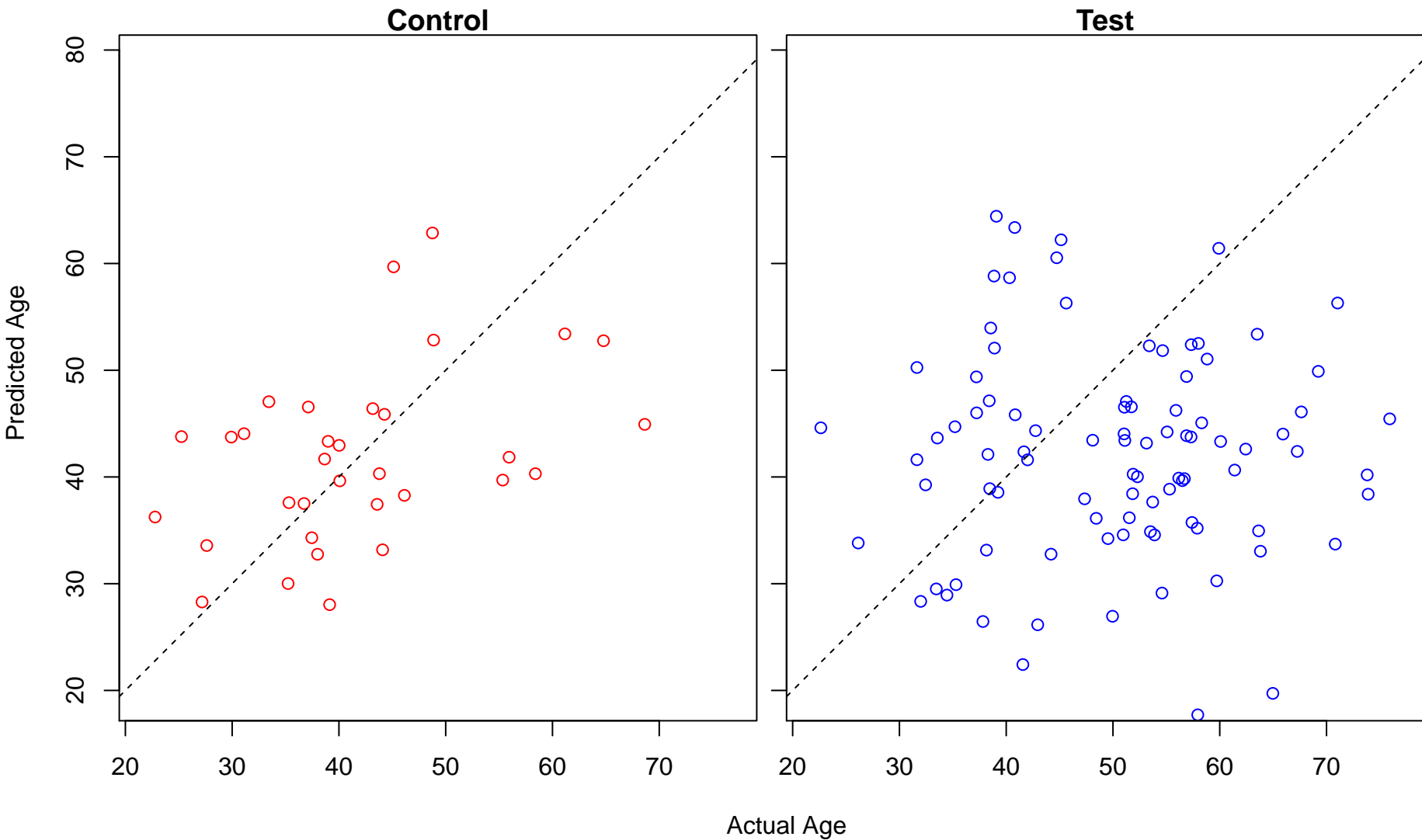
regulation of protein sumoylation (Score: 0.918472)



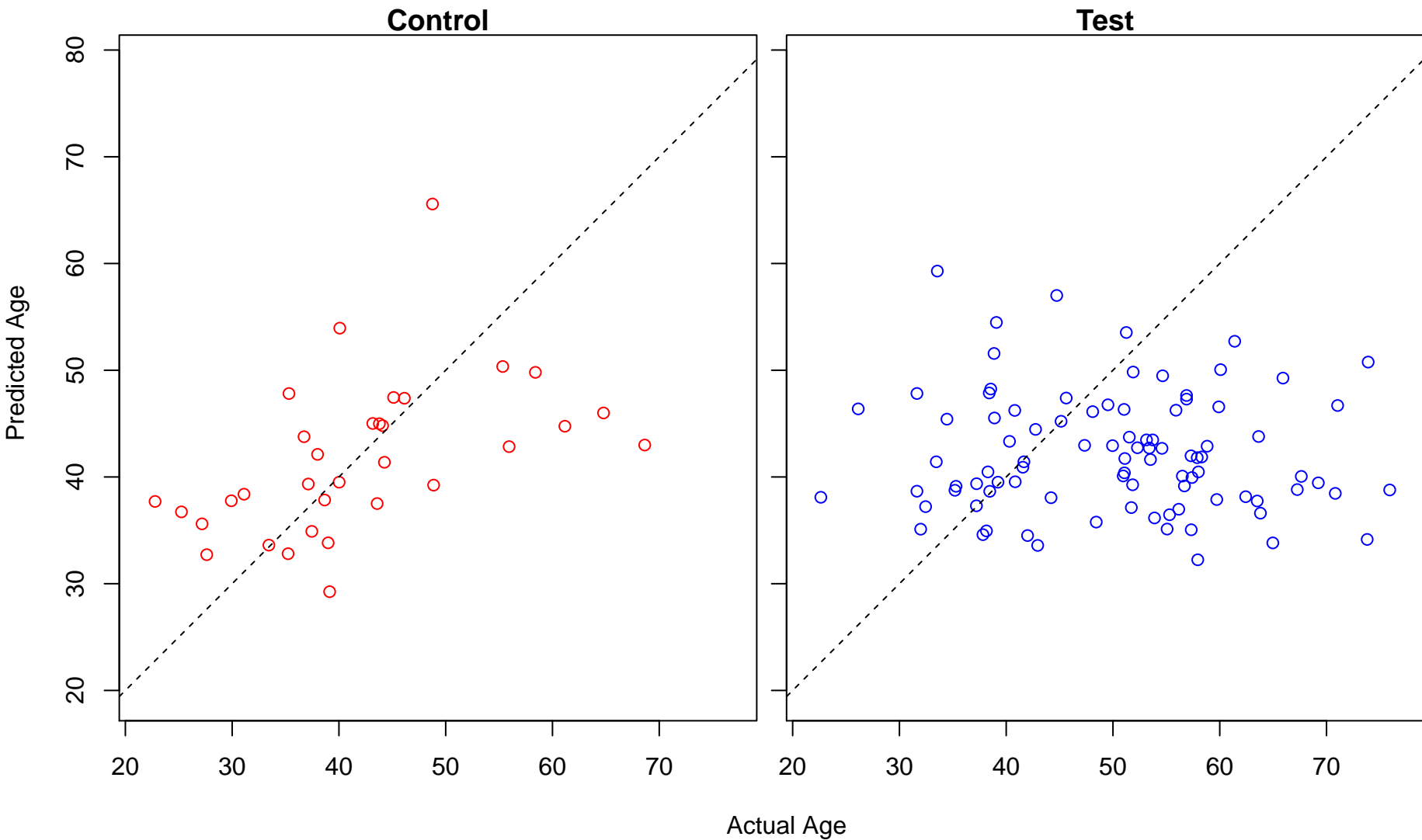
protein import (Score: 0.918403)



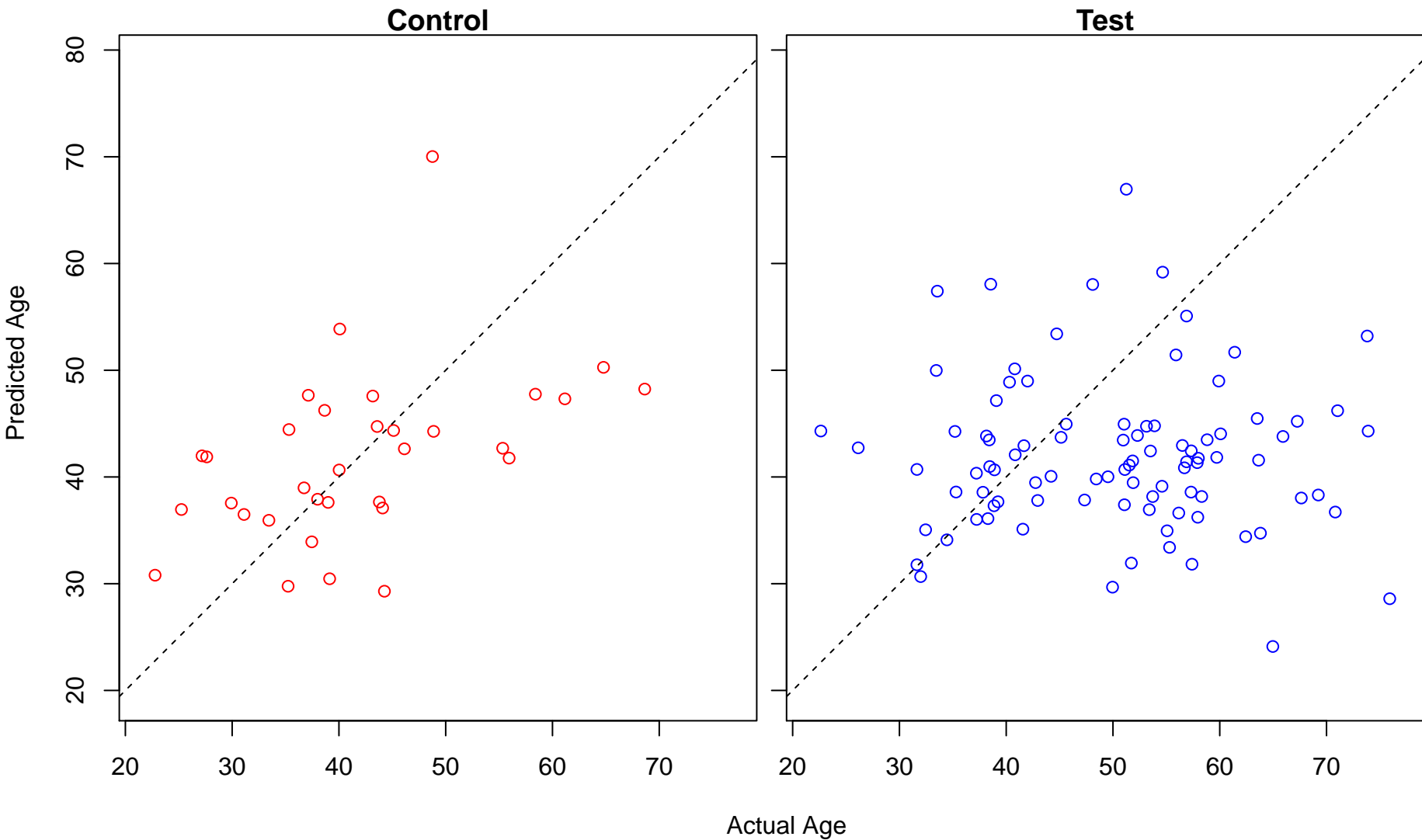
lipopolysaccharide-mediated signaling pathway (Score: 0.918058)



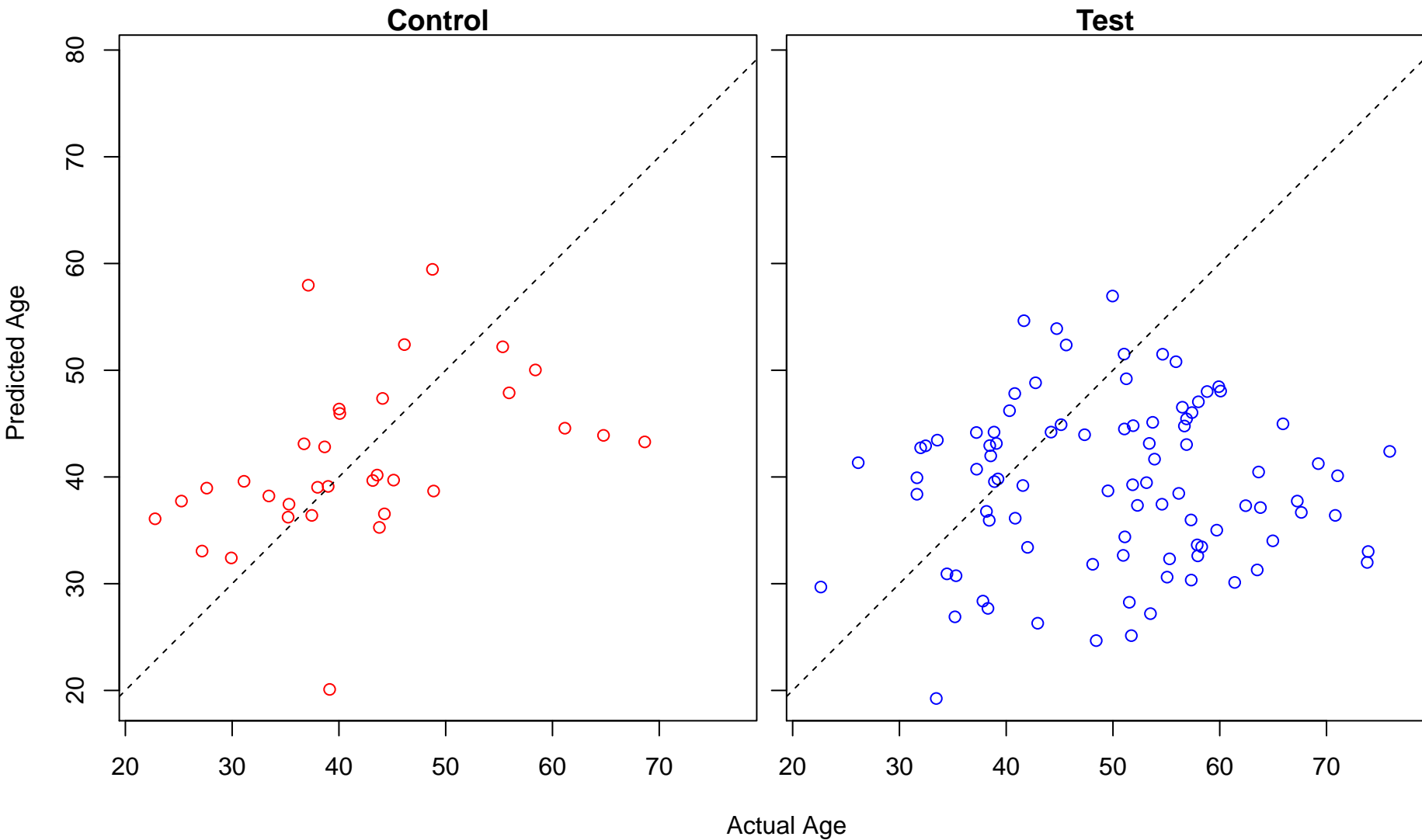
regulation of response to DNA damage stimulus (Score: 0.916179)



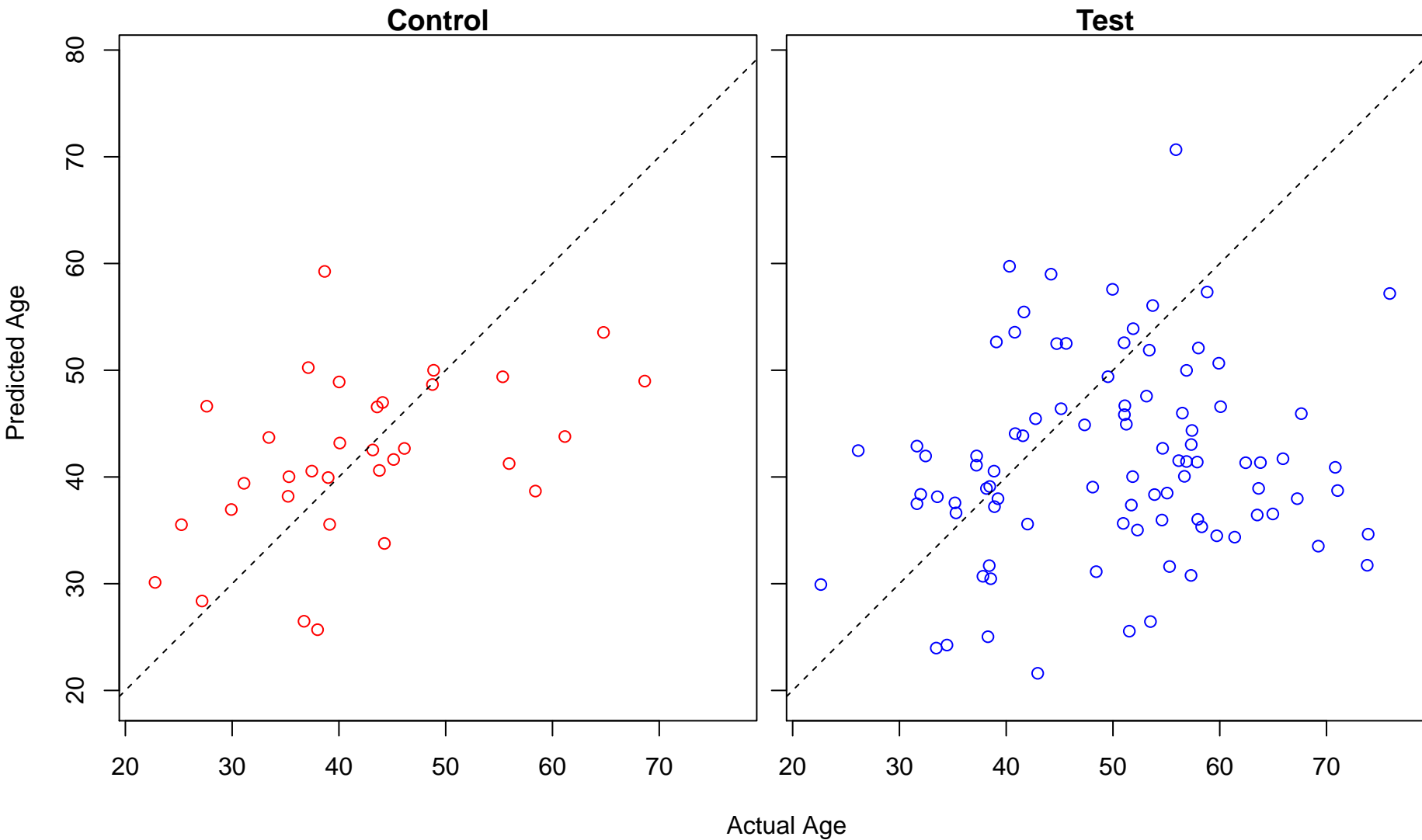
circadian rhythm (Score: 0.916031)



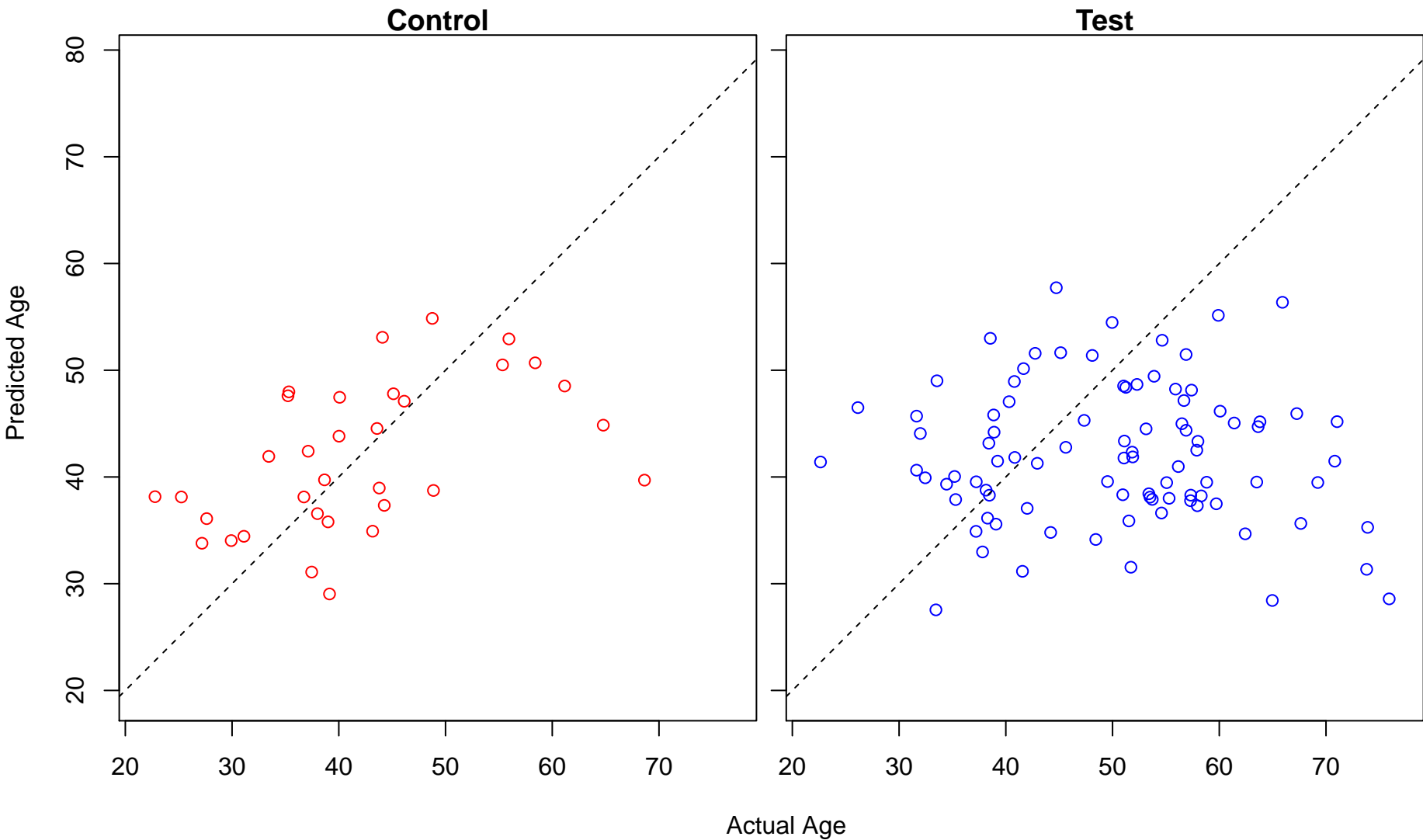
regulation of sodium ion transport (Score: 0.914362)



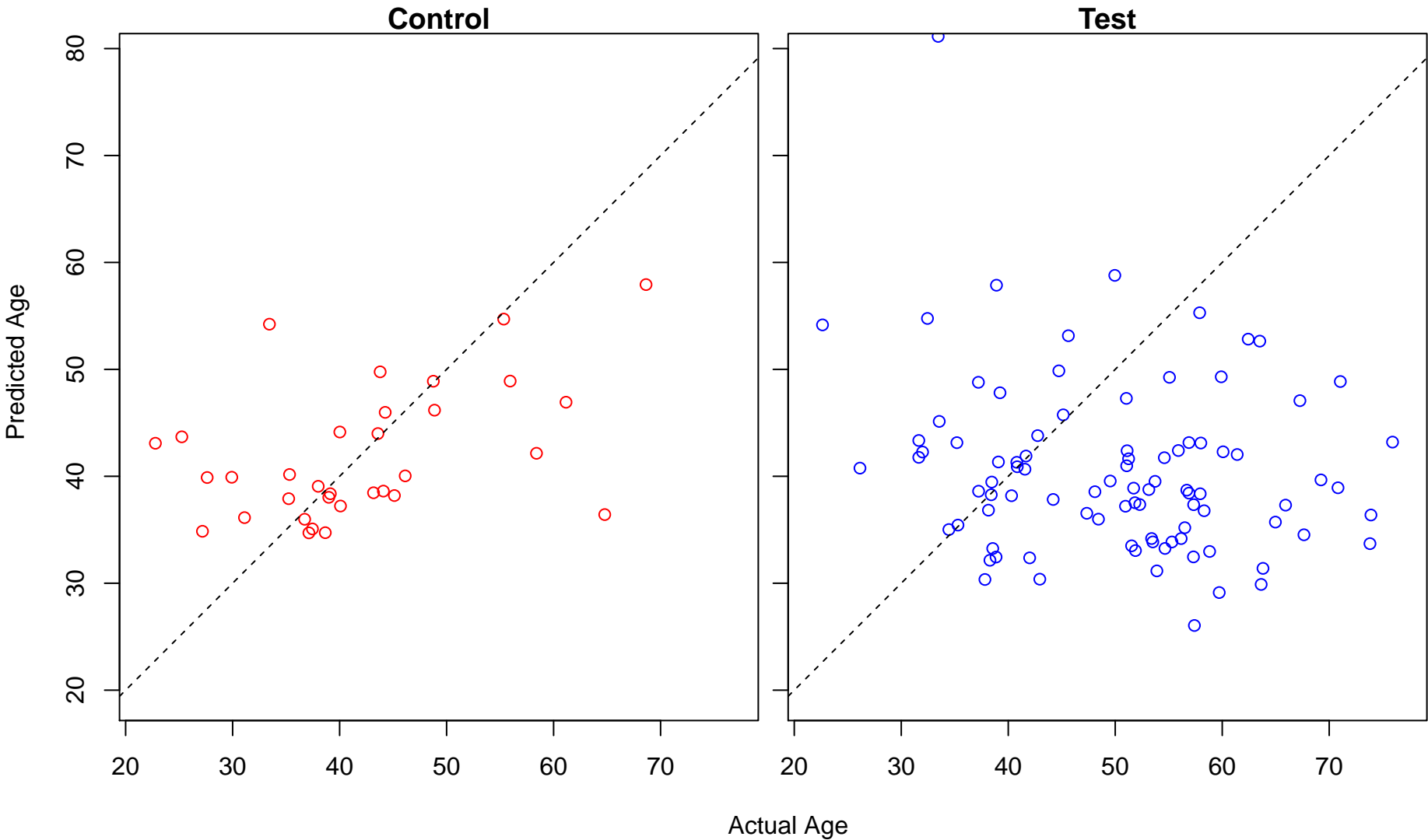
positive regulation of sodium ion transmembrane transporter activity (Score: 0.912885)



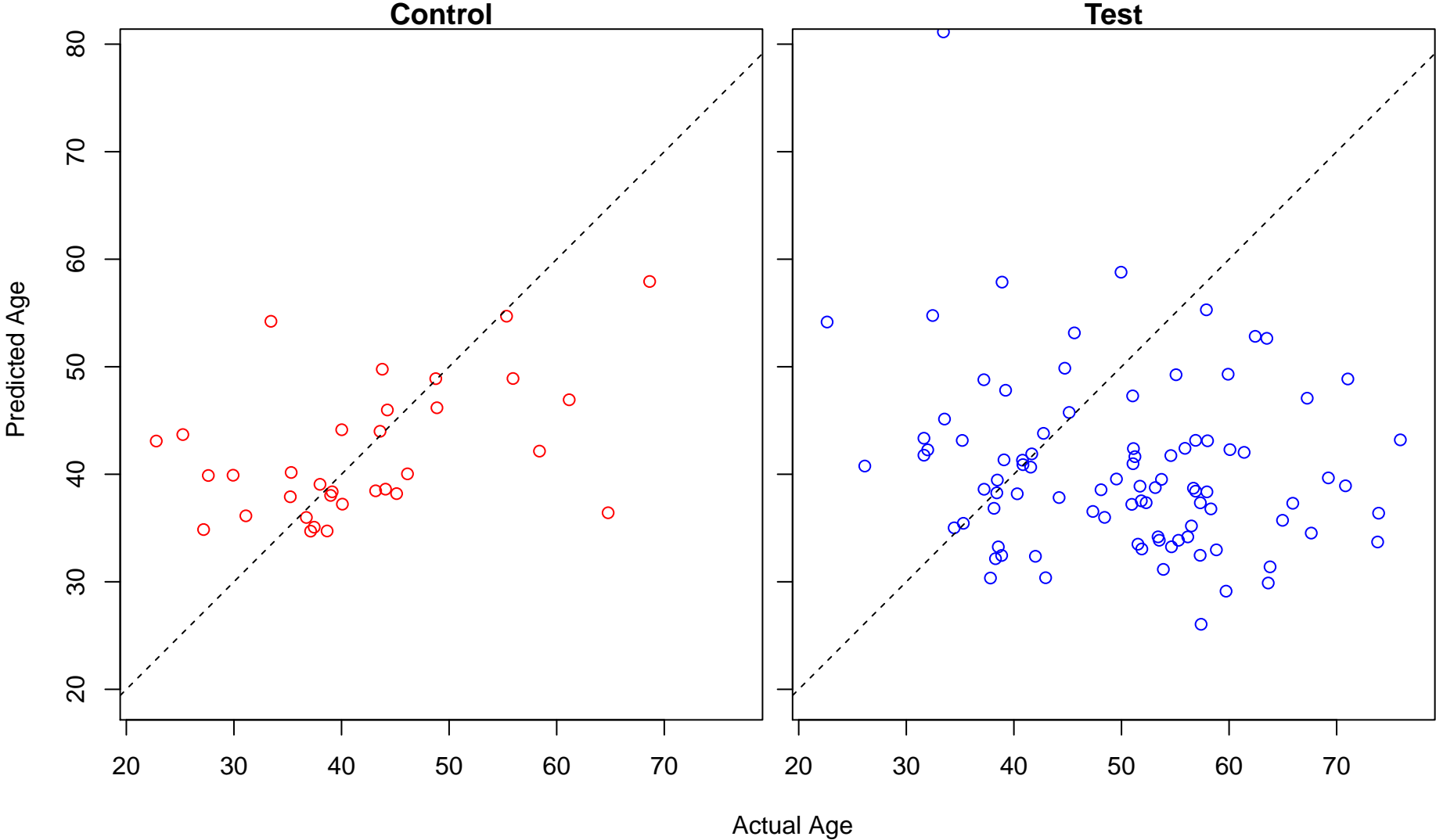
heart contraction (Score: 0.911443)



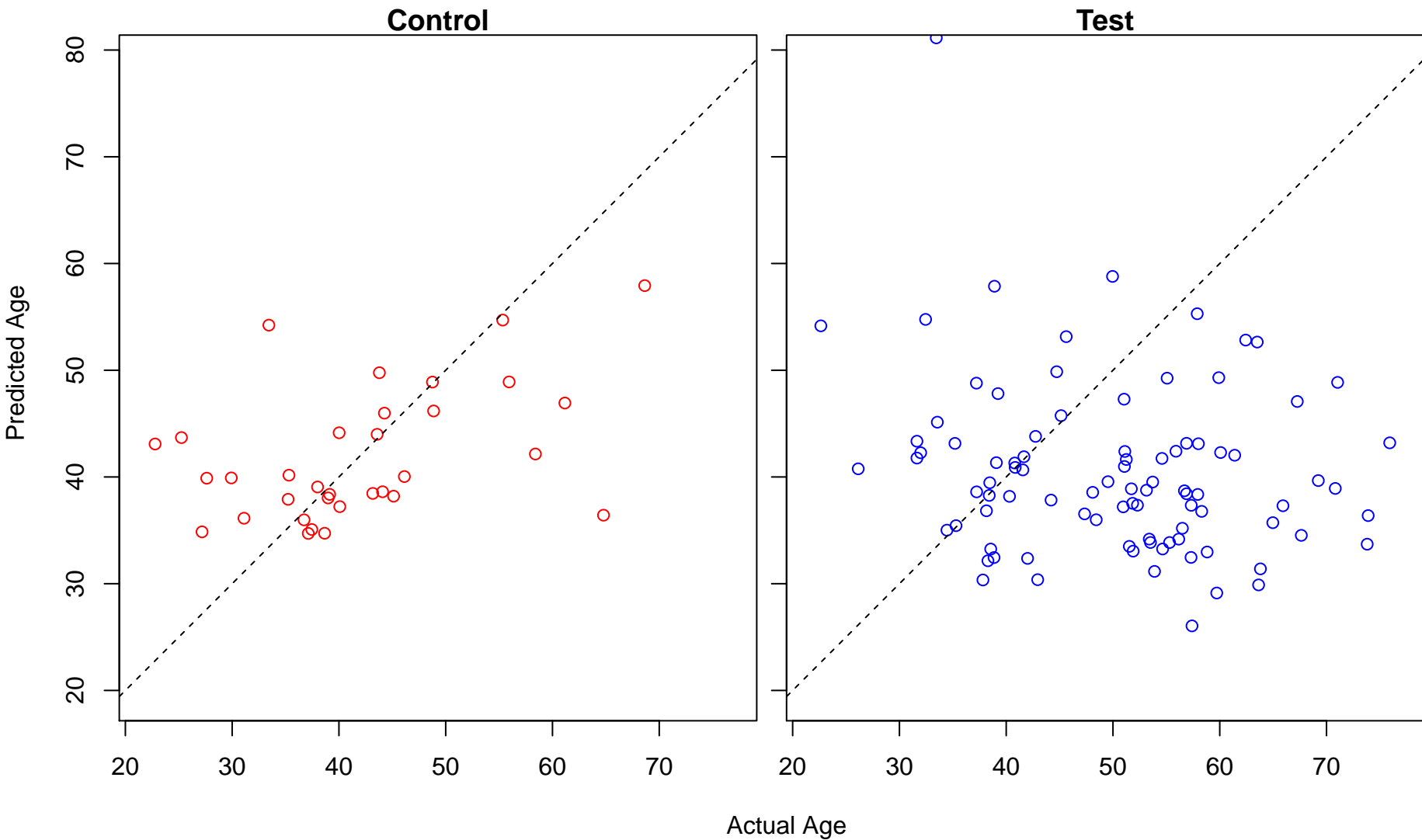
regulation of satellite cell activation involved in skeletal muscle regeneration (Score: 0.910627)



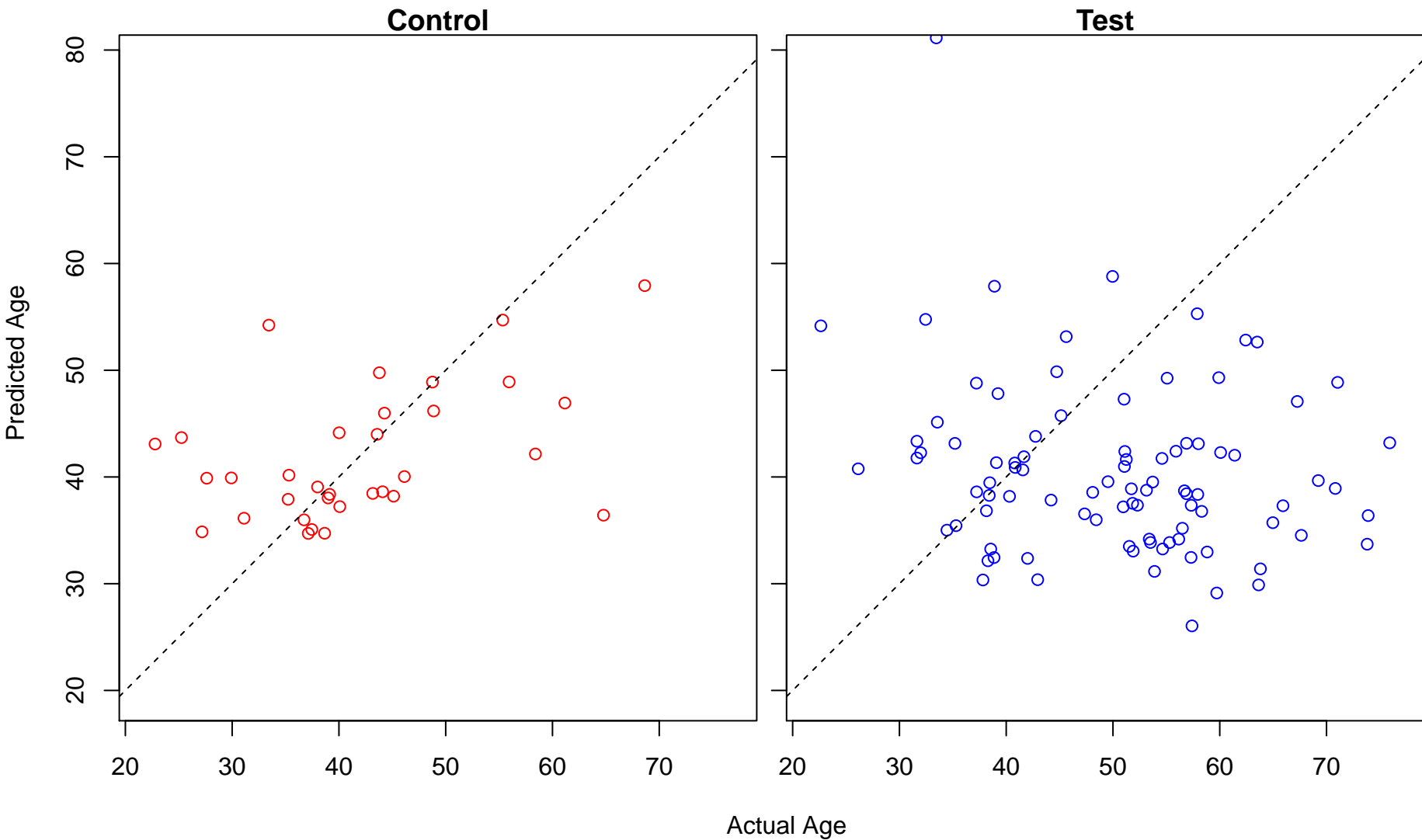
positive regulation of satellite cell activation involved in skeletal muscle regeneration (Score: 0.9106)



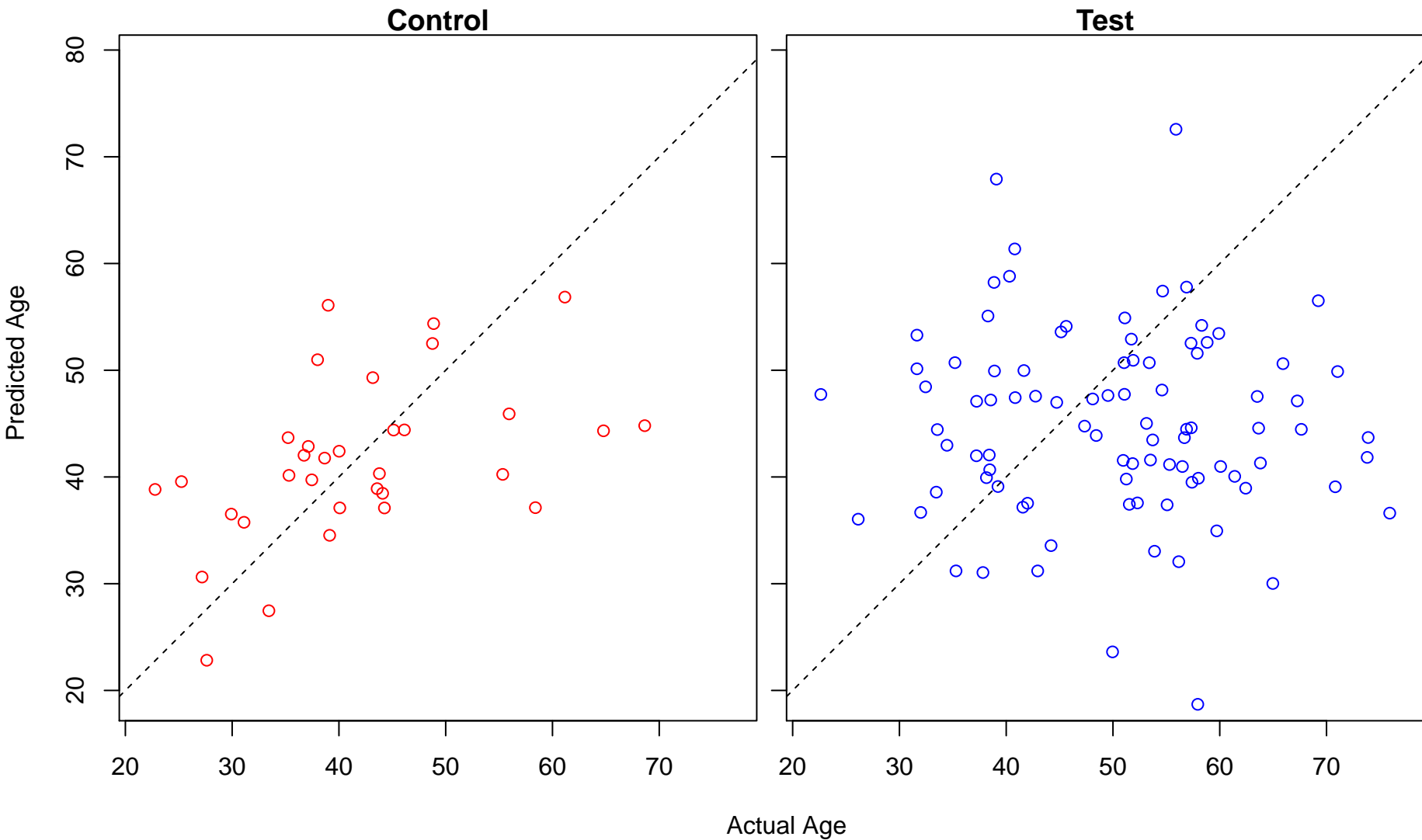
positive regulation of skeletal muscle tissue regeneration (Score: 0.910627)



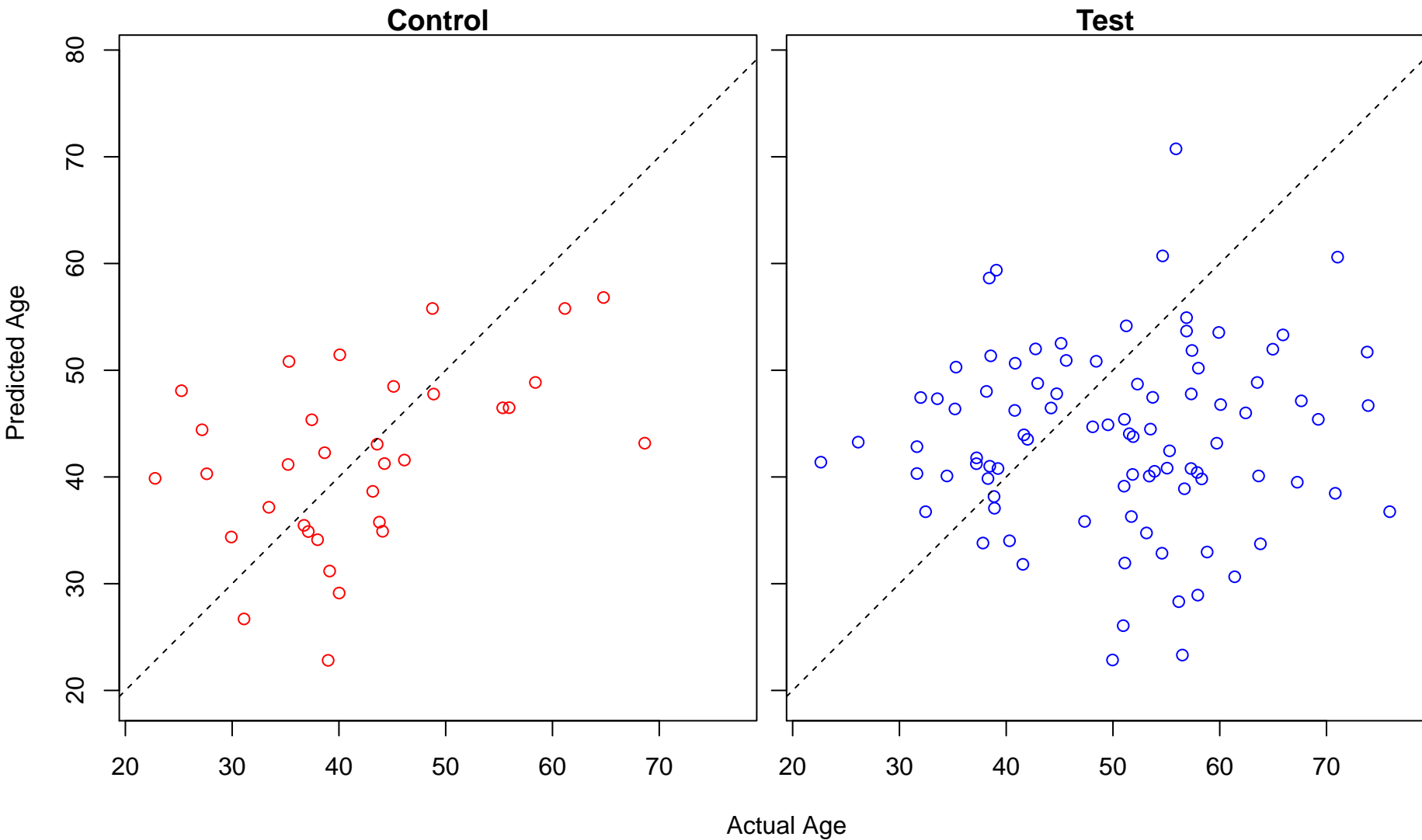
regulation of skeletal muscle tissue regeneration (Score: 0.910627)



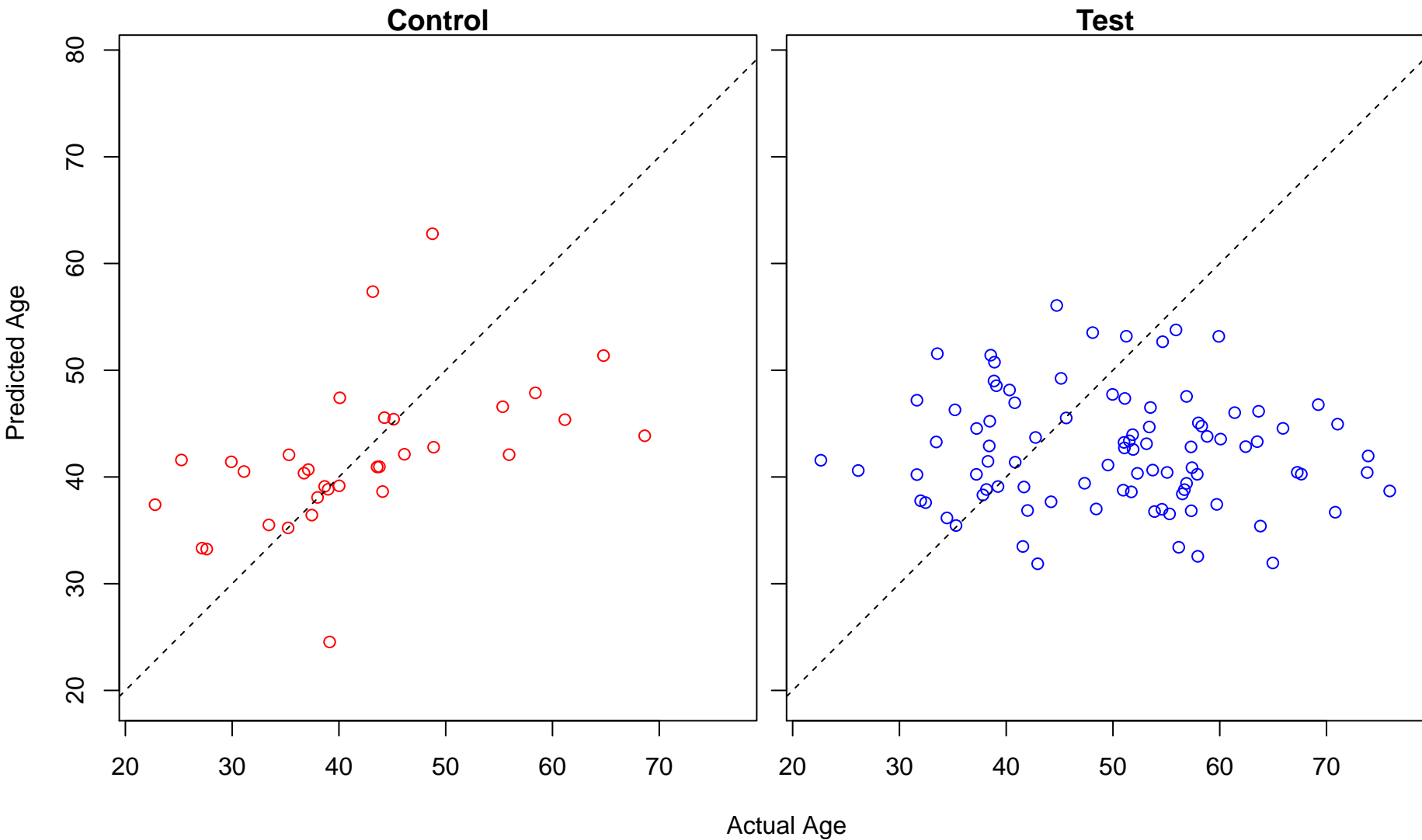
regulation of response to food (Score: 0.909021)



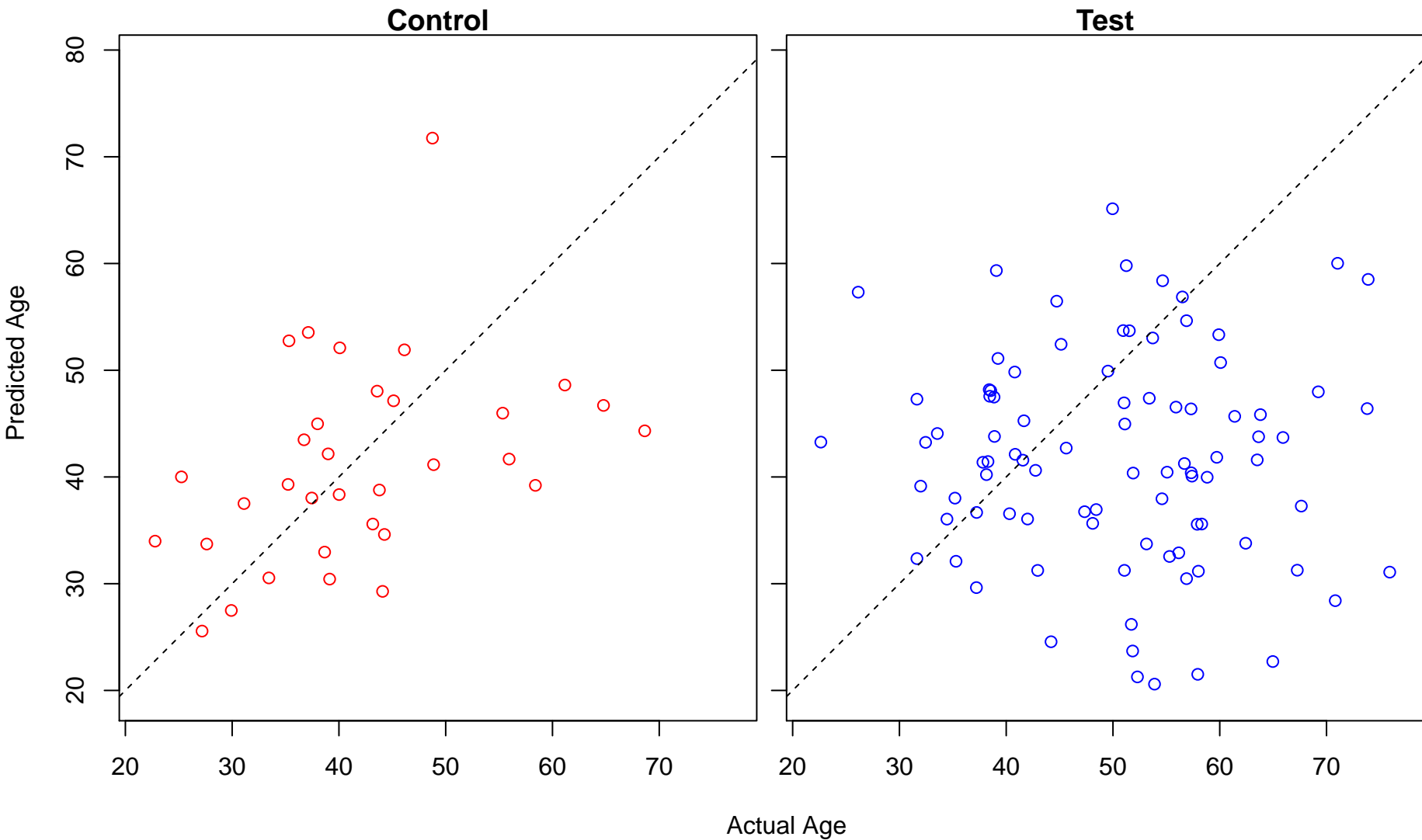
regulation of monocyte chemotaxis (Score: 0.906351)



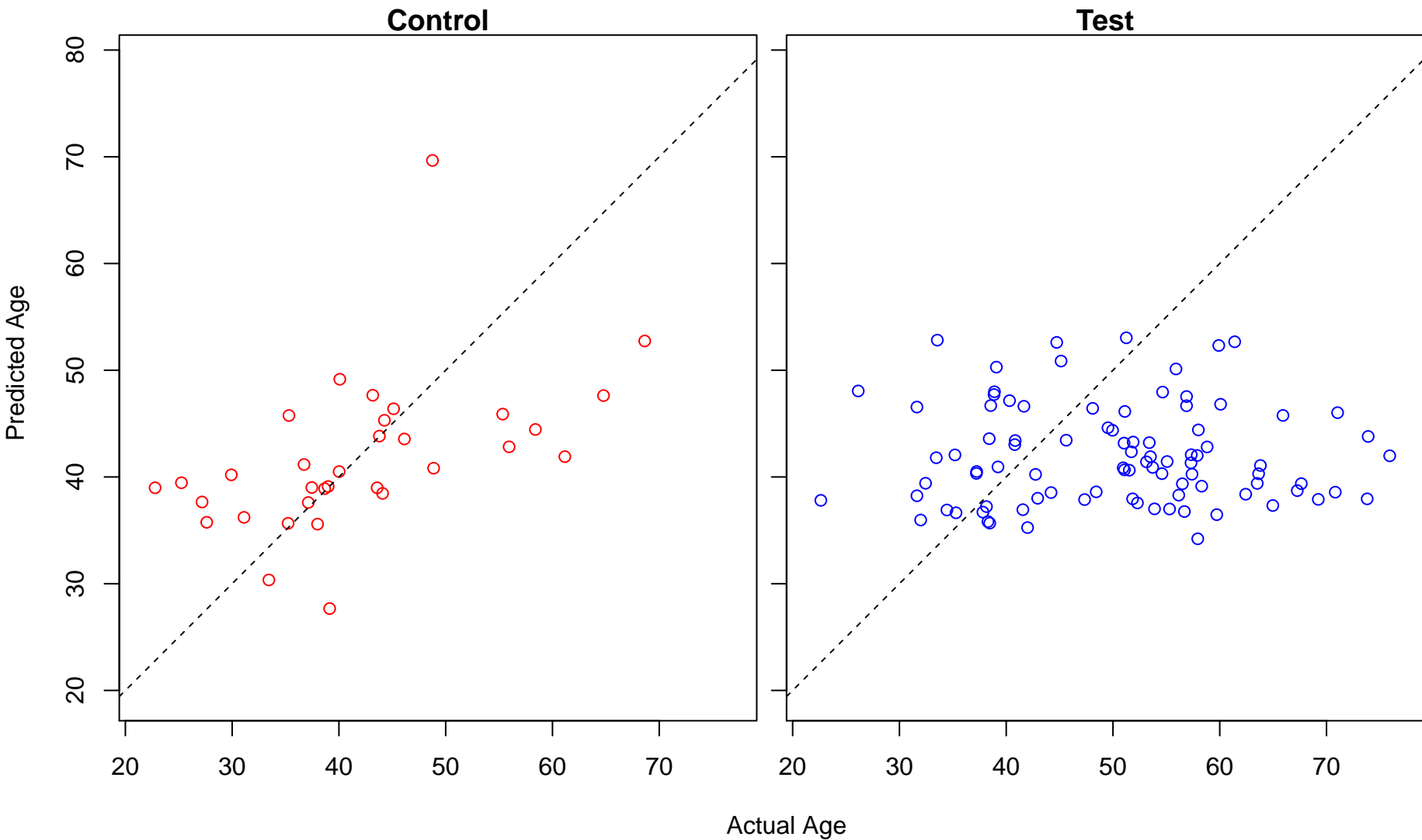
organic acid transport (Score: 0.905744)



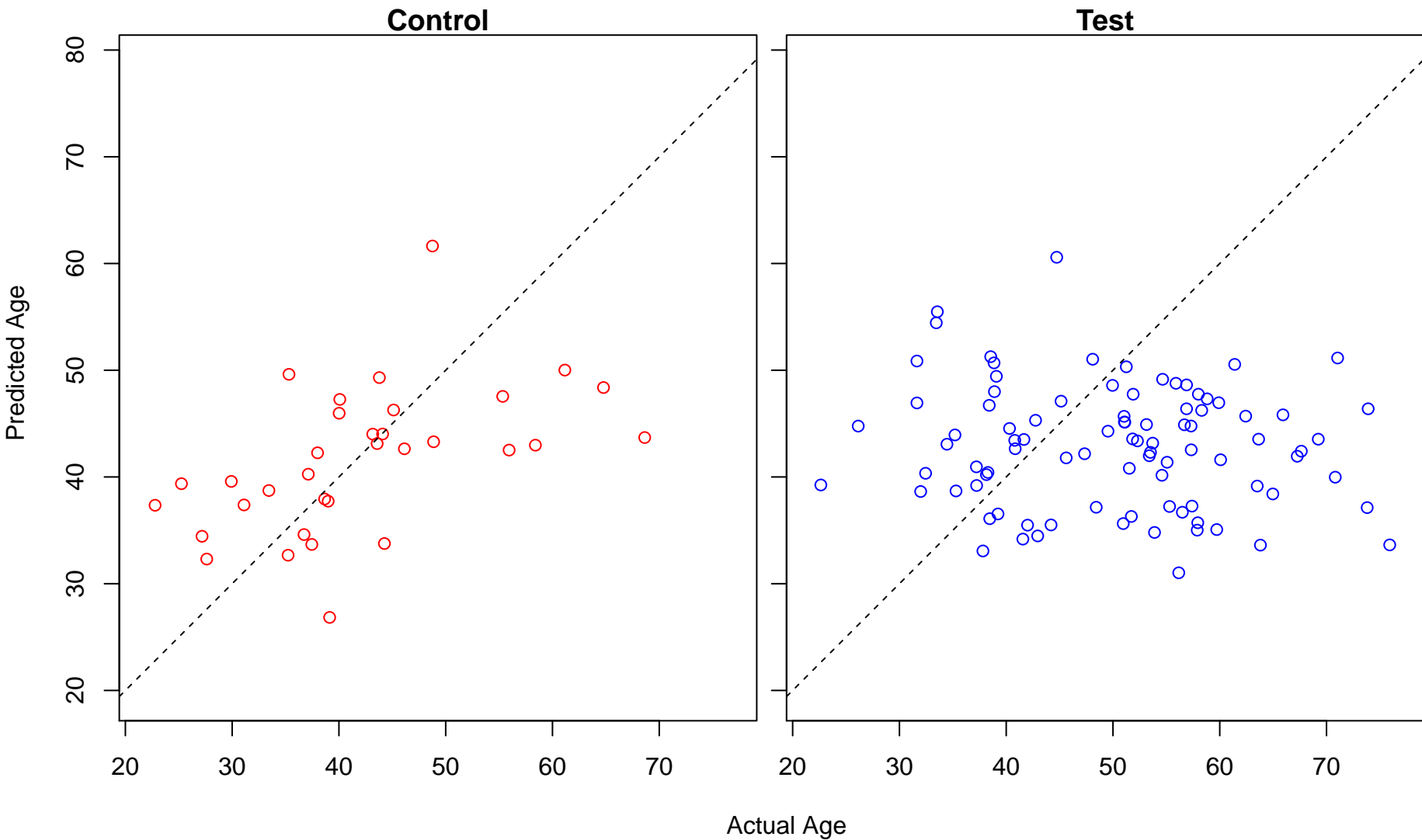
cellular metabolic compound salvage (Score: 0.903411)



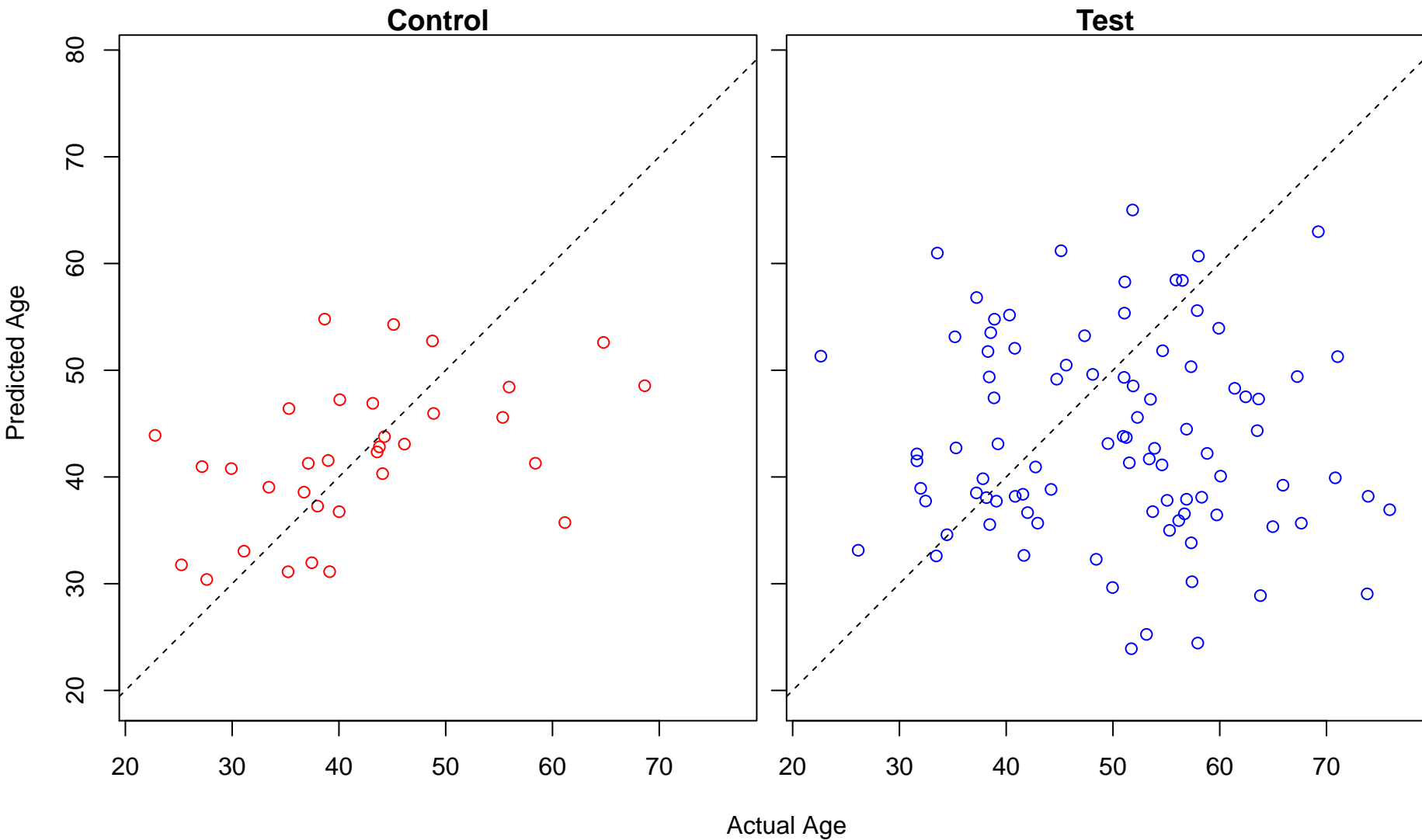
nuclear-transcribed mRNA poly(A) tail shortening (Score: 0.900884)



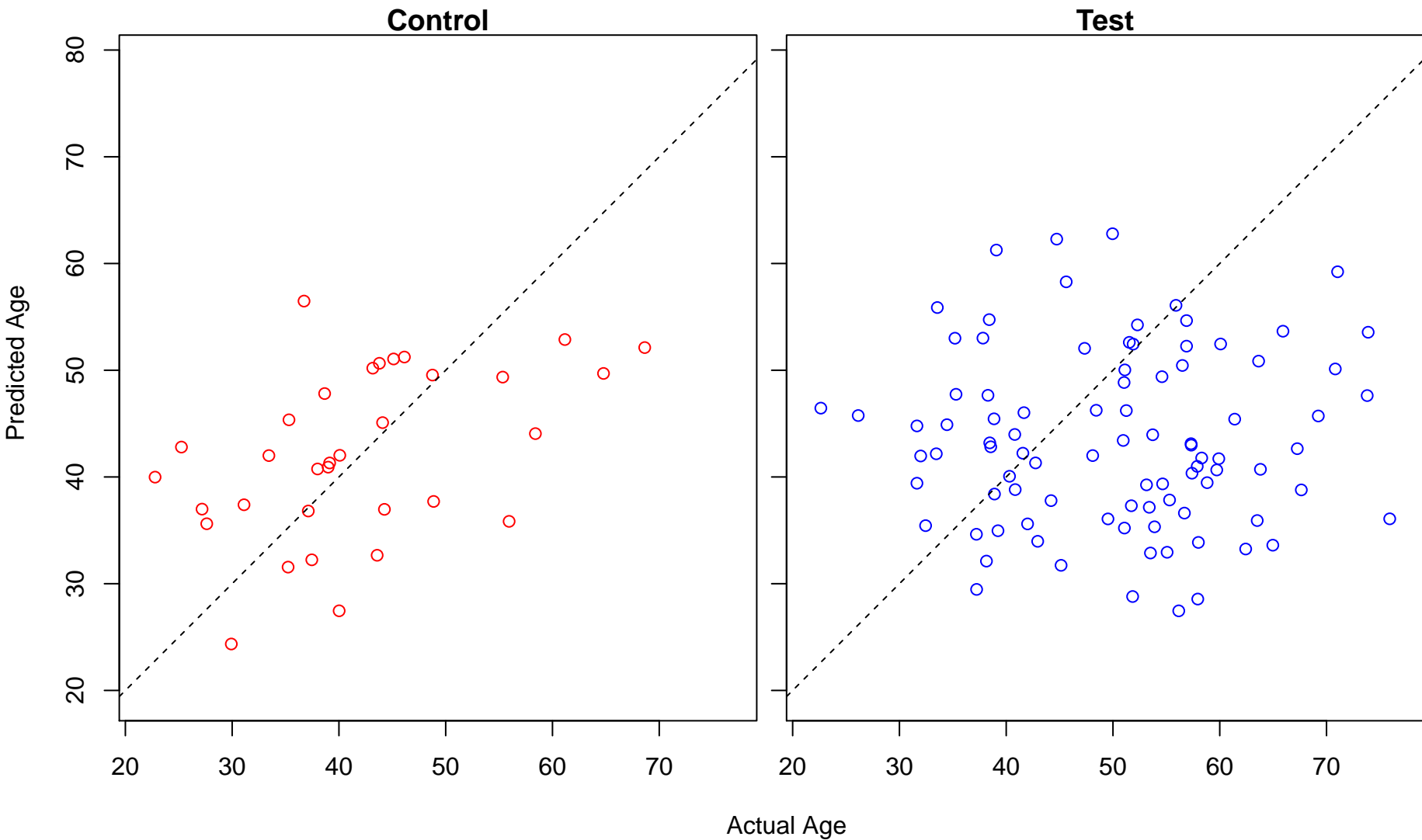
regulation of neurotransmitter levels (Score: 0.899536)



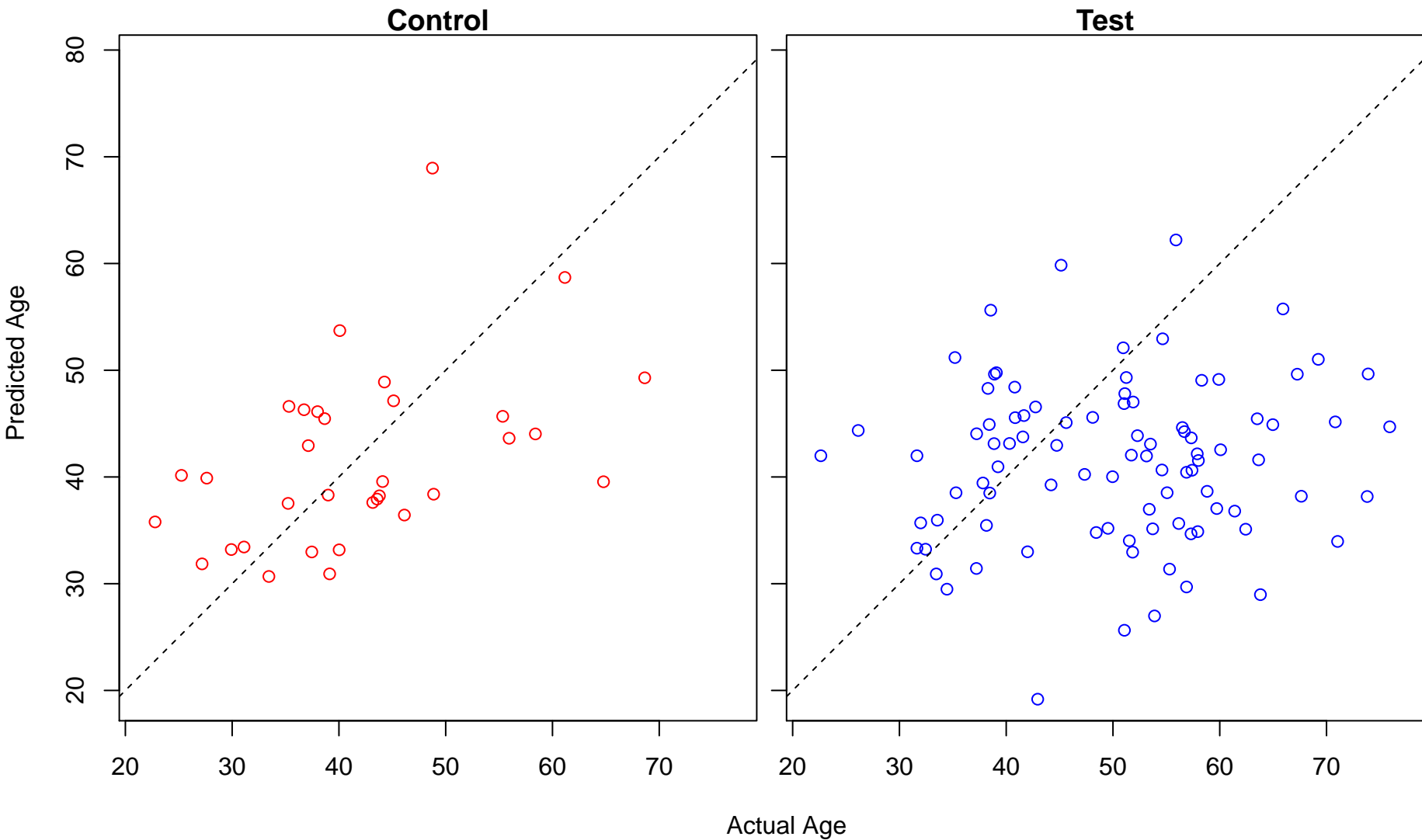
bone marrow development (Score: 0.899322)



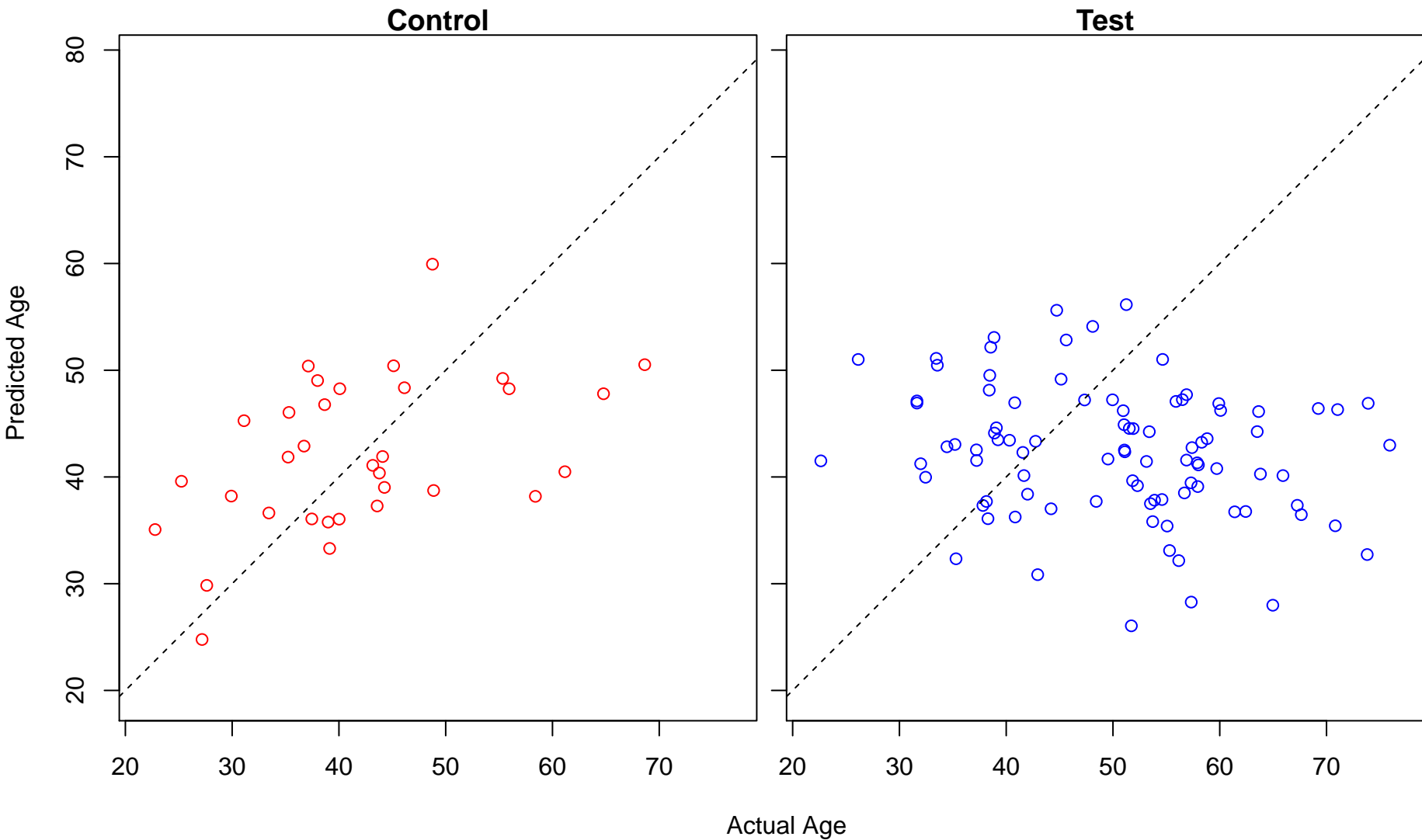
regulation of cell-cell adhesion mediated by integrin (Score: 0.898838)



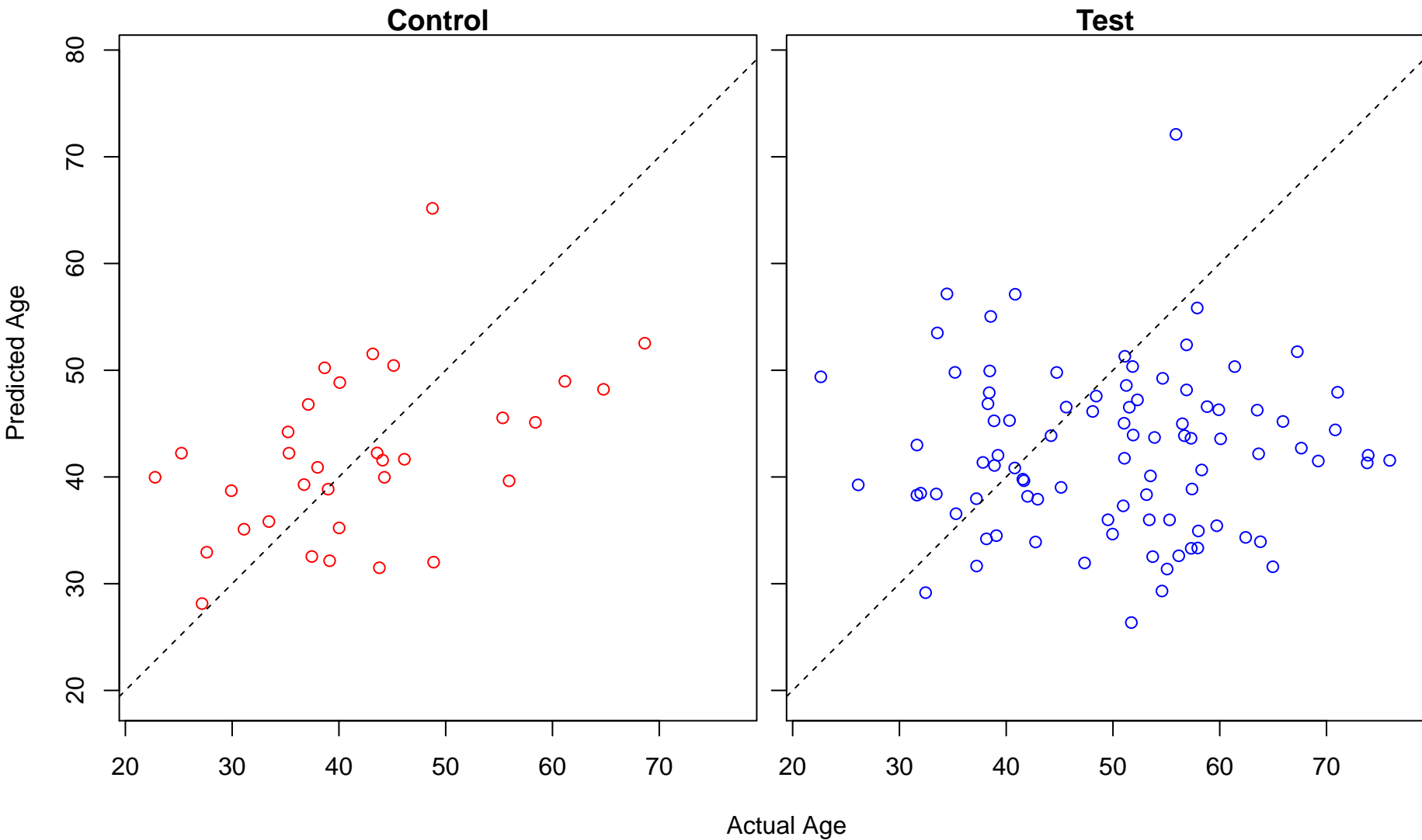
nucleobase-containing small molecule metabolic process (Score: 0.898503)



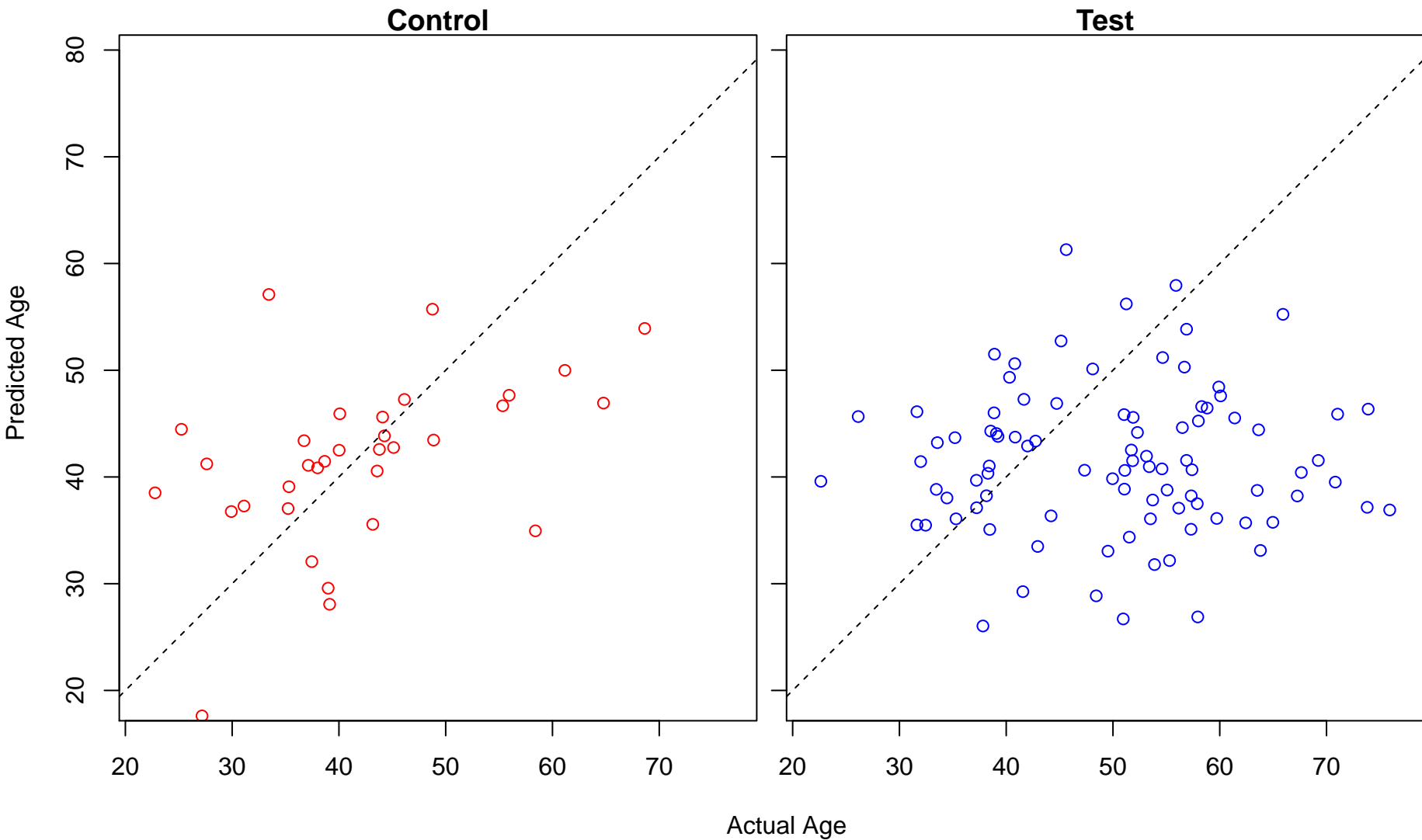
macrophage activation (Score: 0.894538)



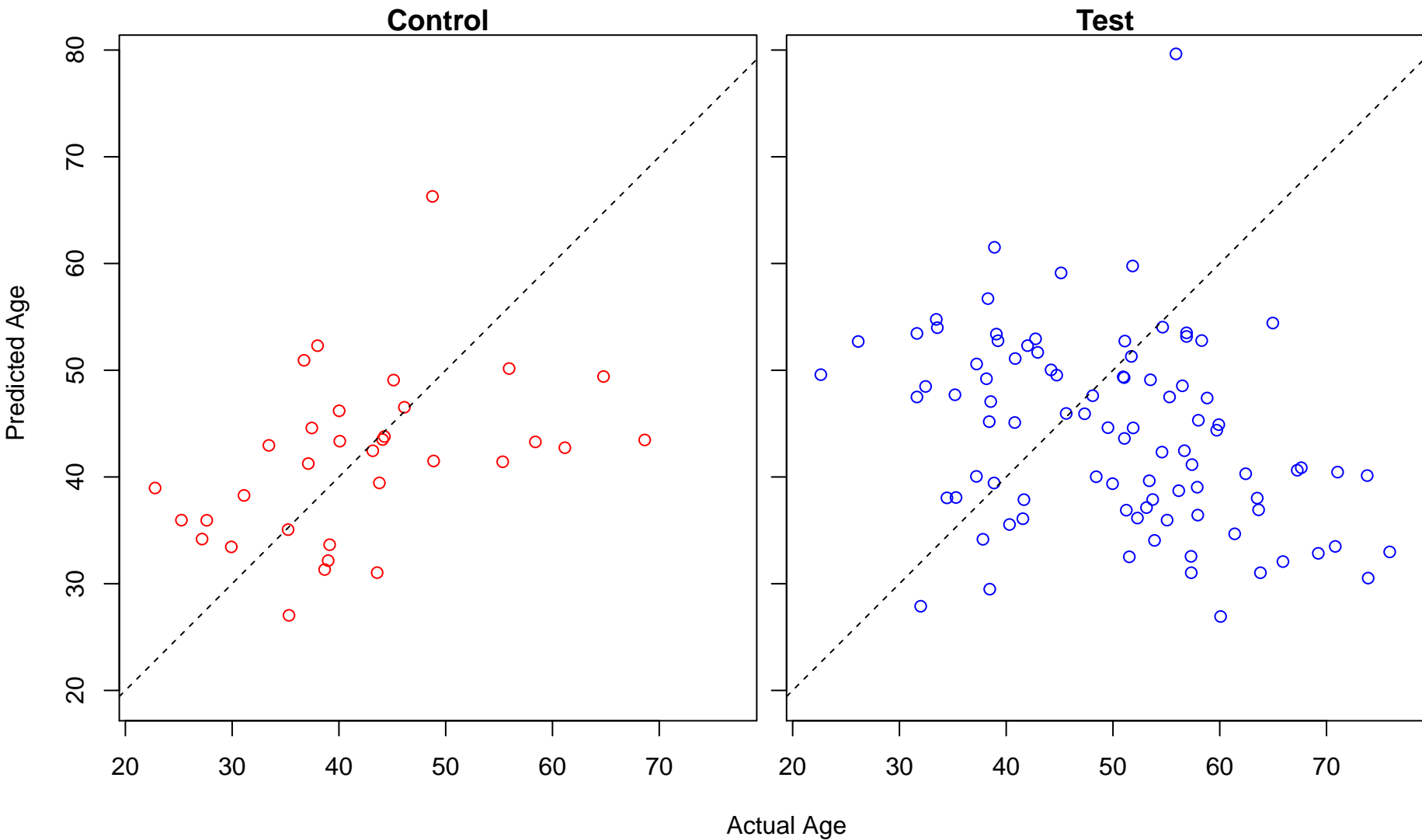
regulation of protein deubiquitination (Score: 0.893402)



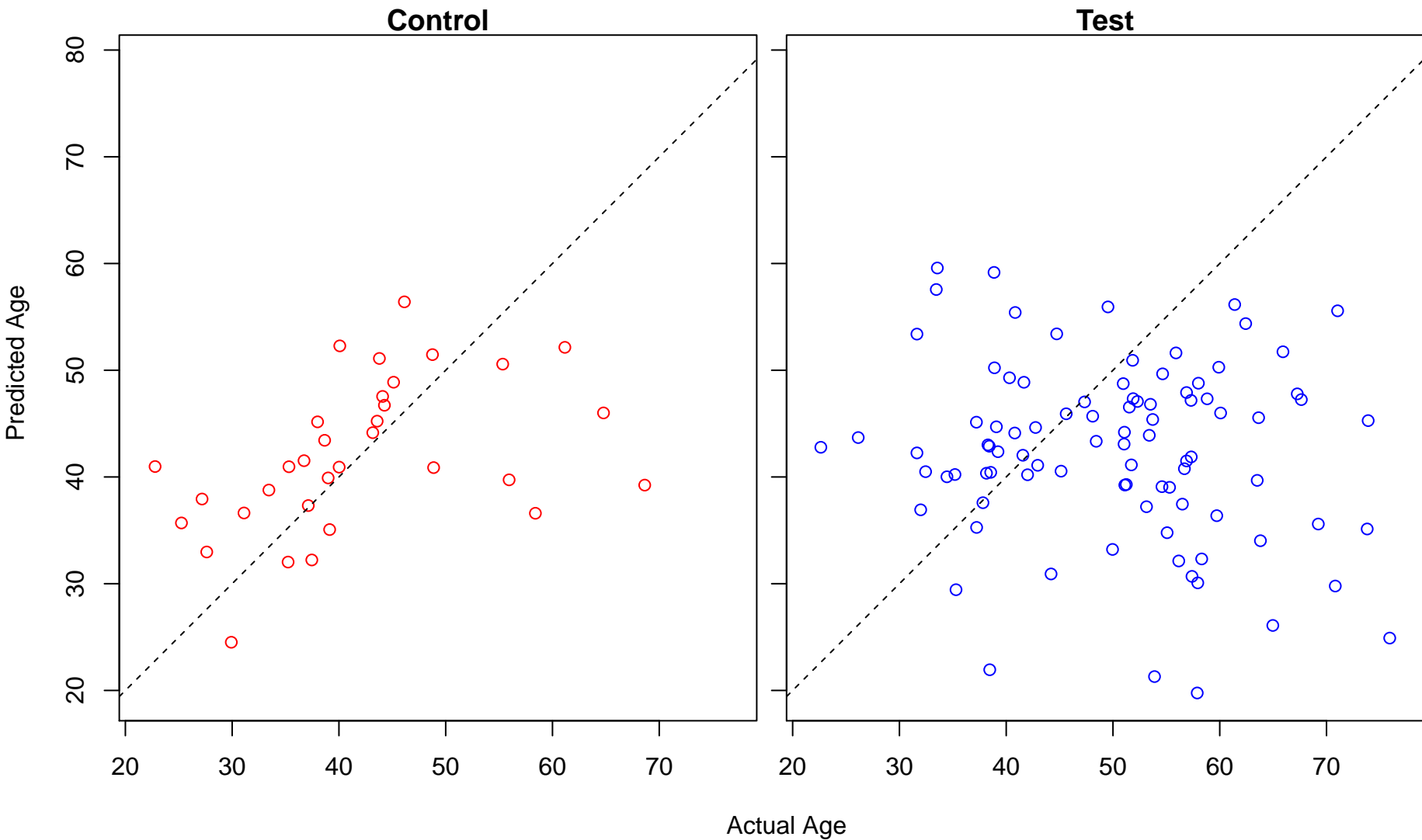
regulation of release of sequestered calcium ion into cytosol (Score: 0.893327)



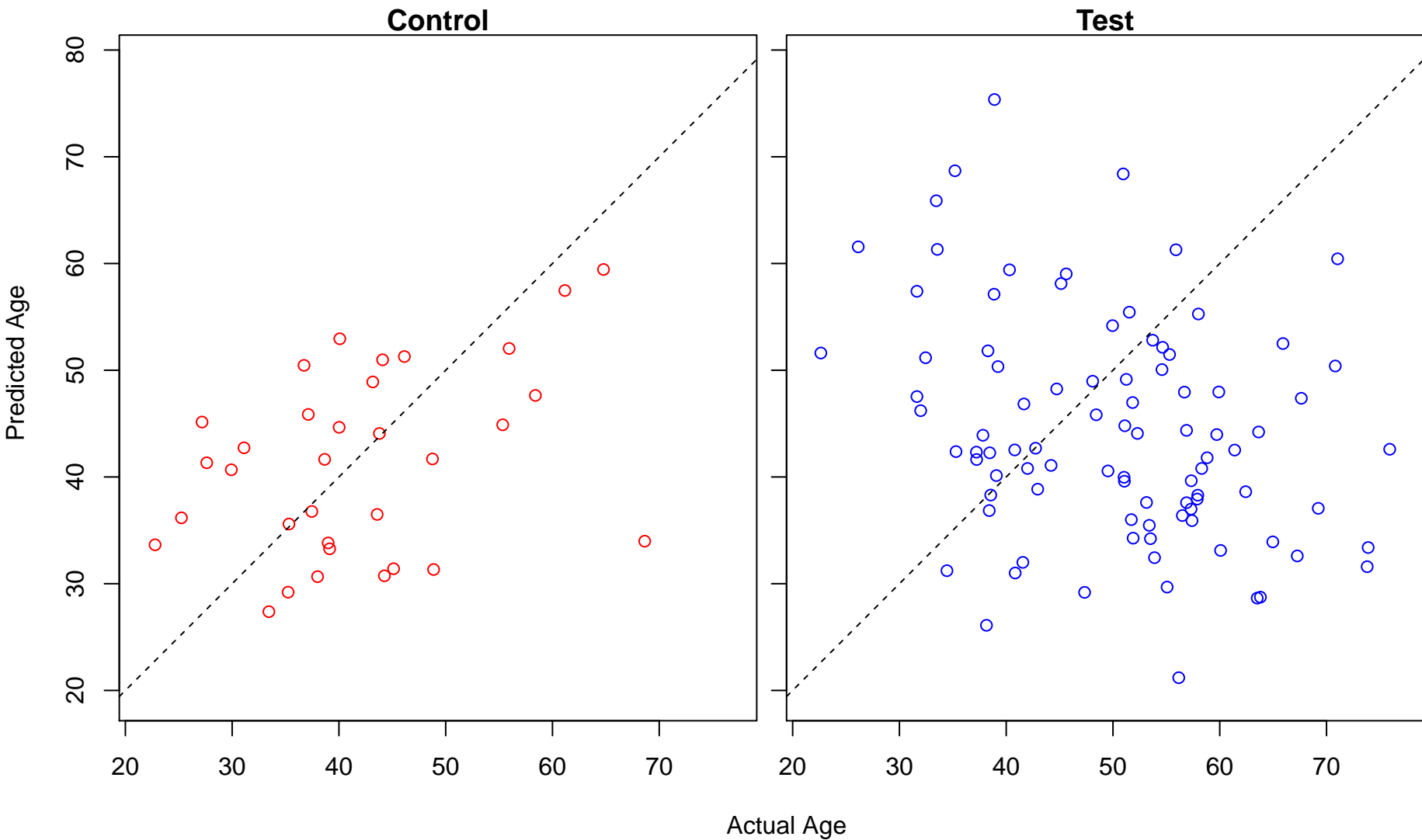
regulation of T cell differentiation in thymus (Score: 0.893083)



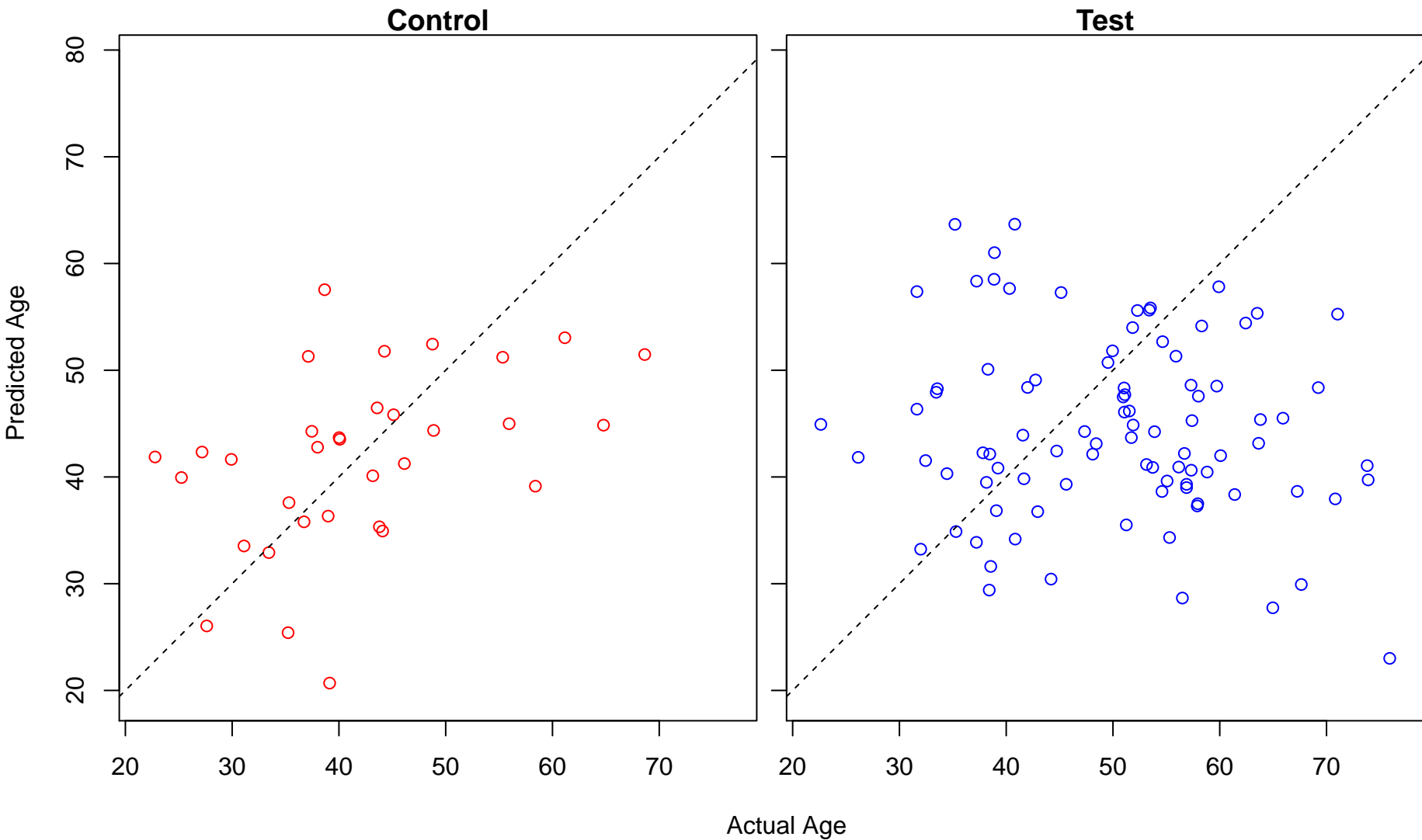
neurotransmitter biosynthetic process (Score: 0.892263)



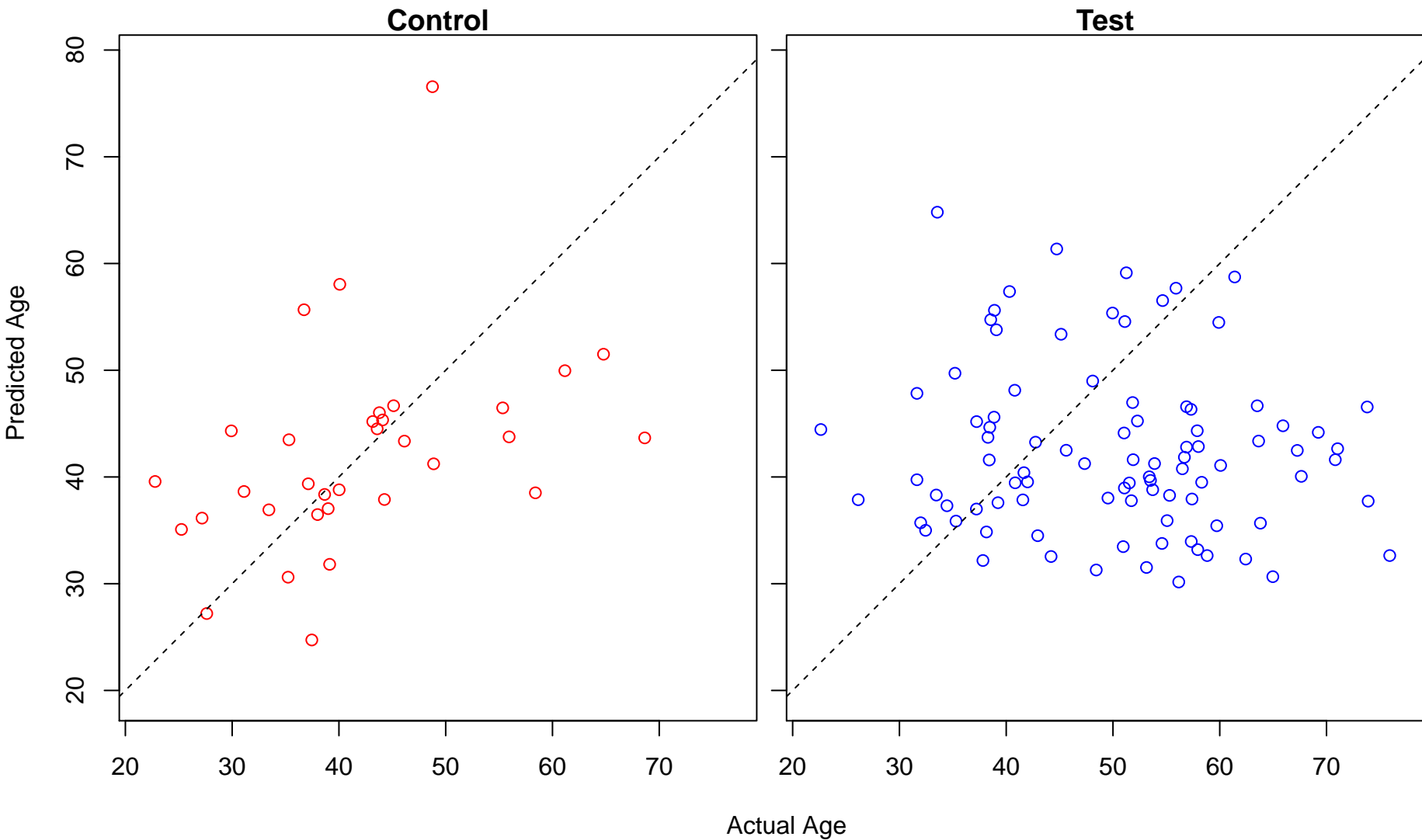
urogenital system development (Score: 0.890450)



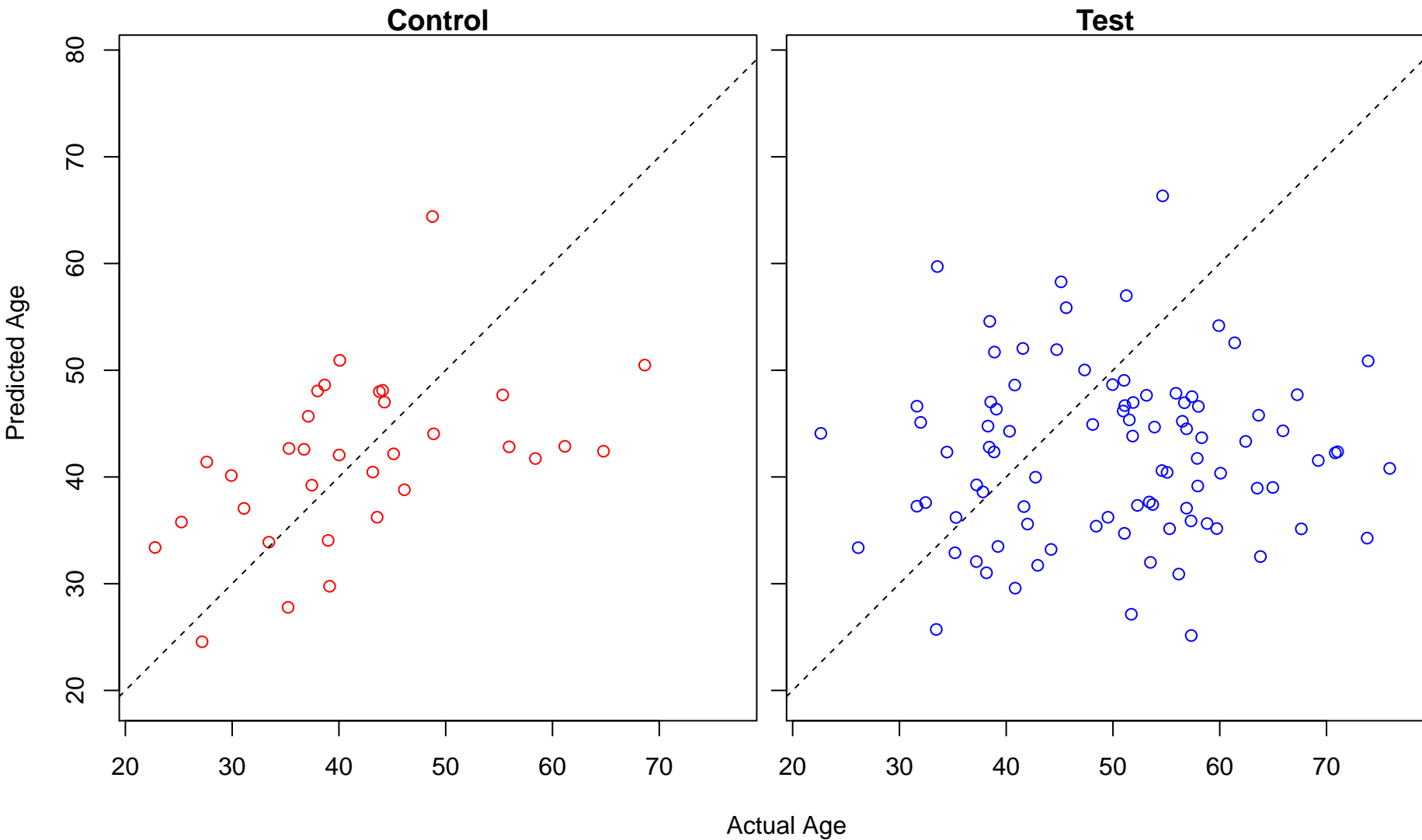
cell volume homeostasis (Score: 0.889474)



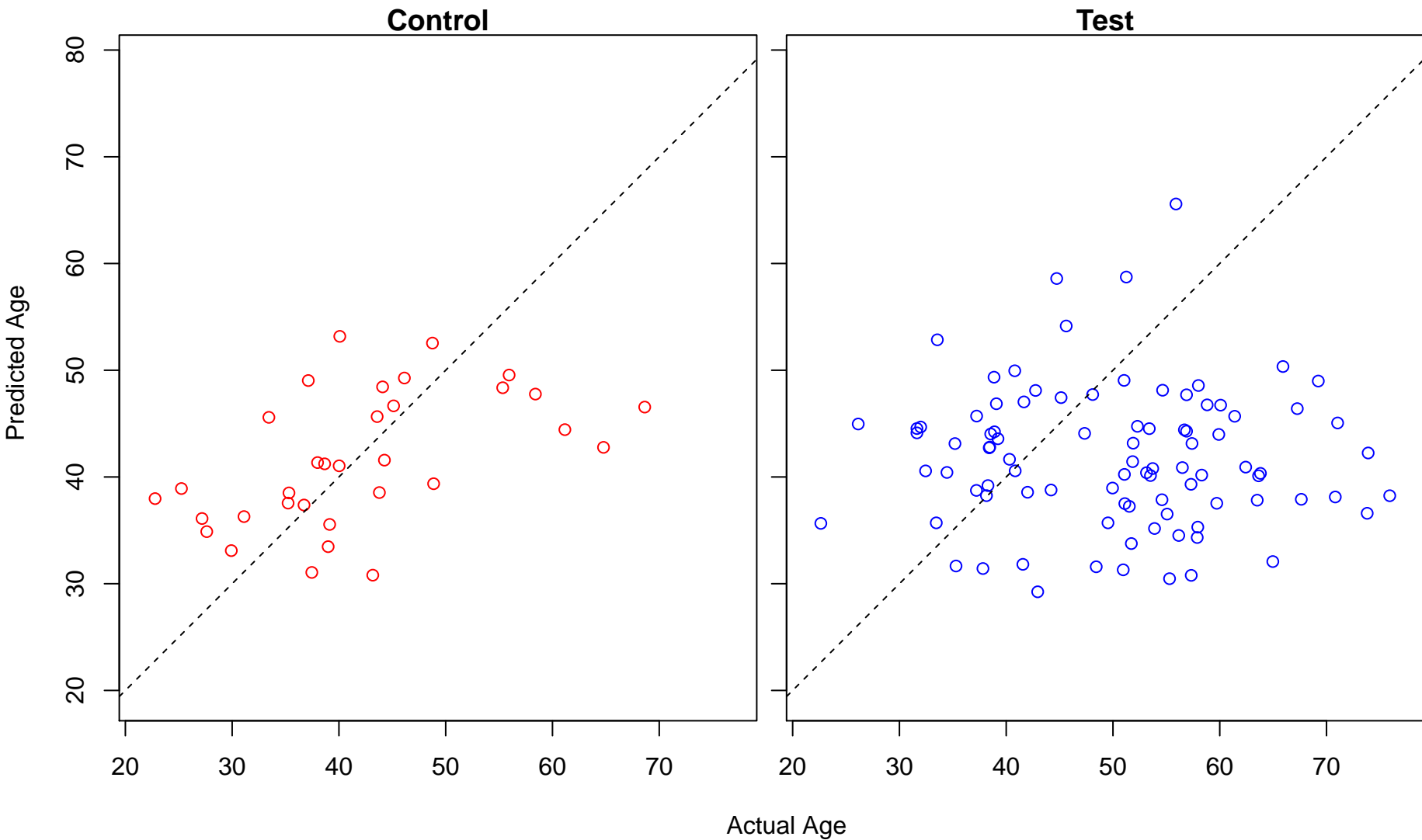
endosome organization (Score: 0.888323)



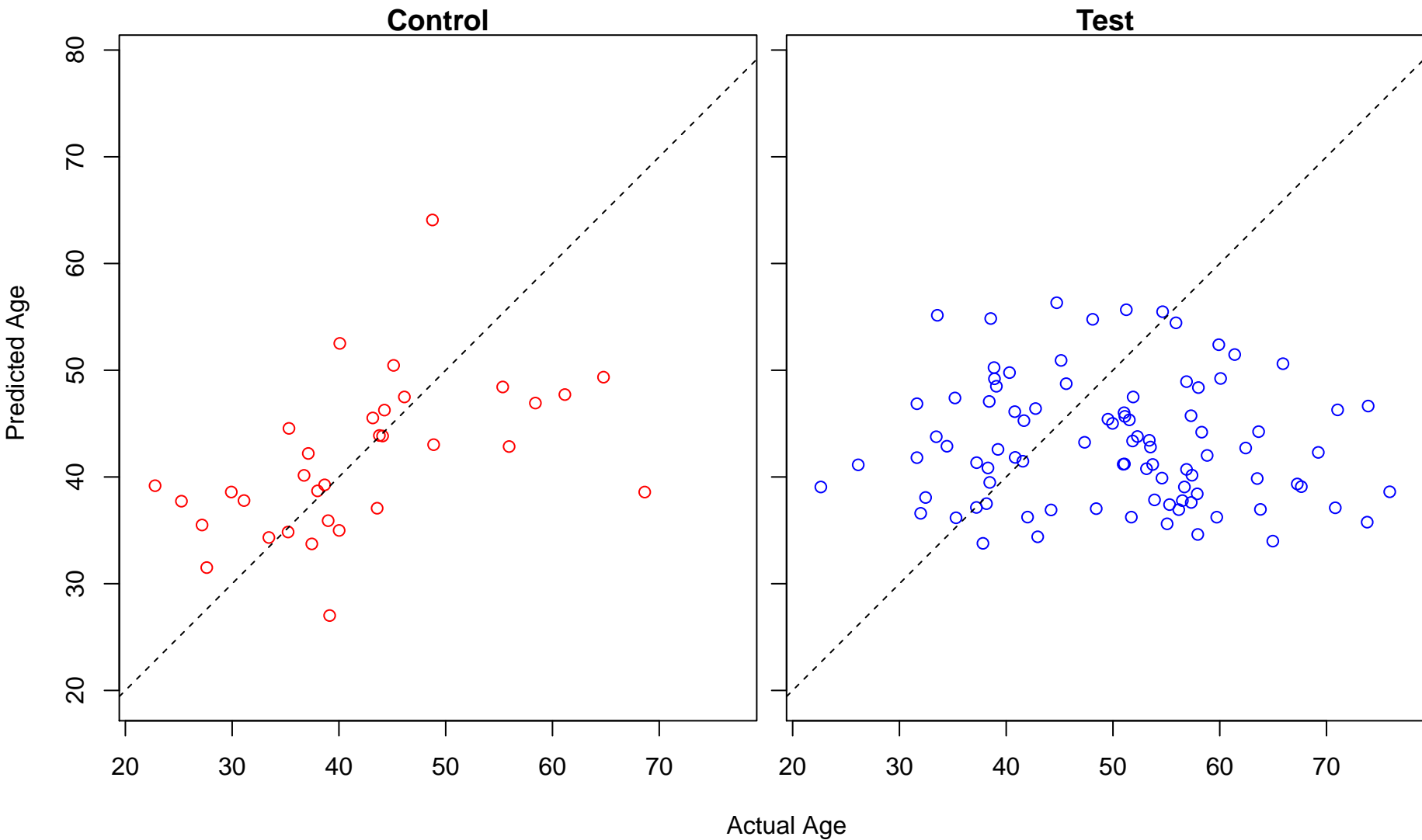
cell proliferation (Score: 0.888080)



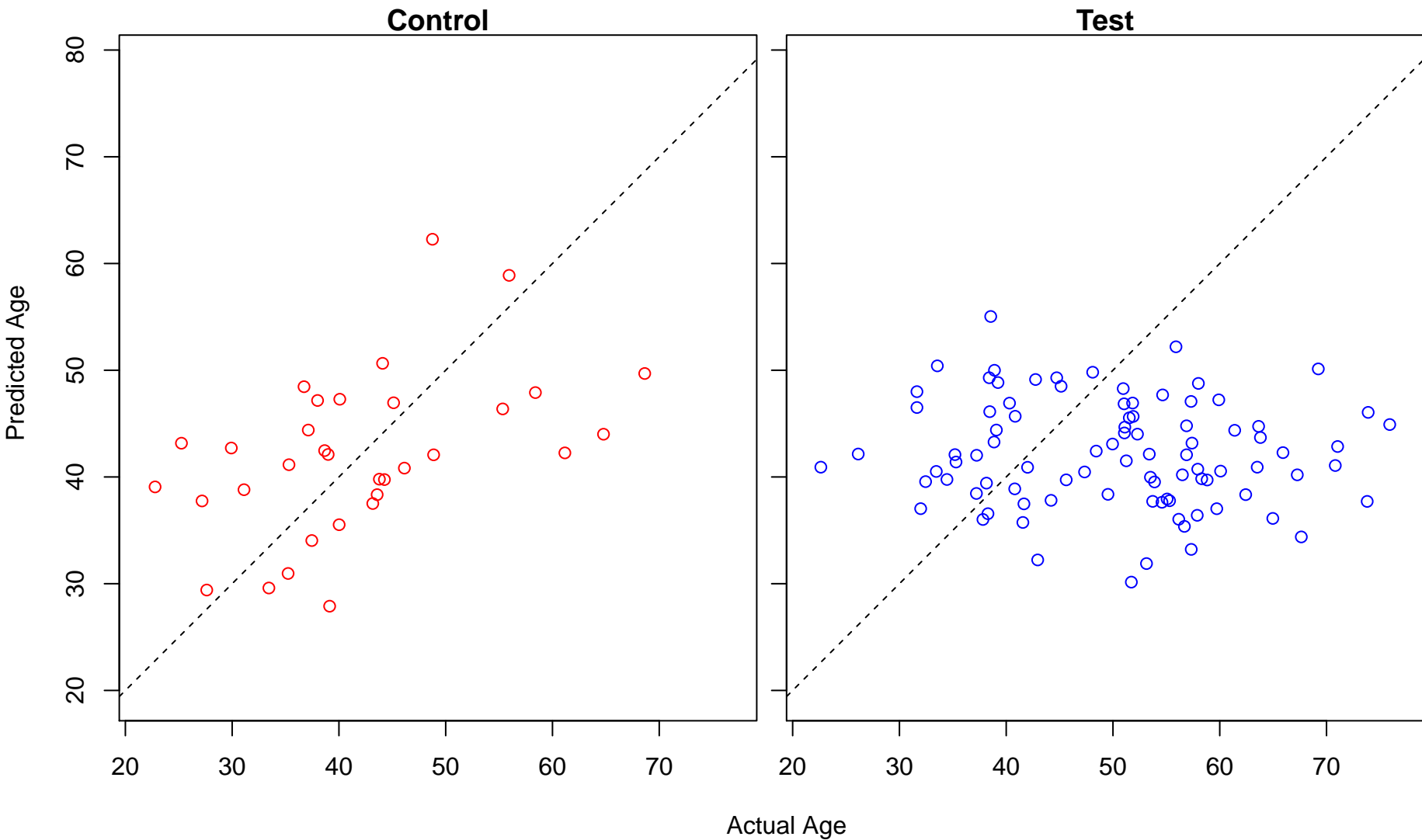
positive regulation of ion transport (Score: 0.887988)



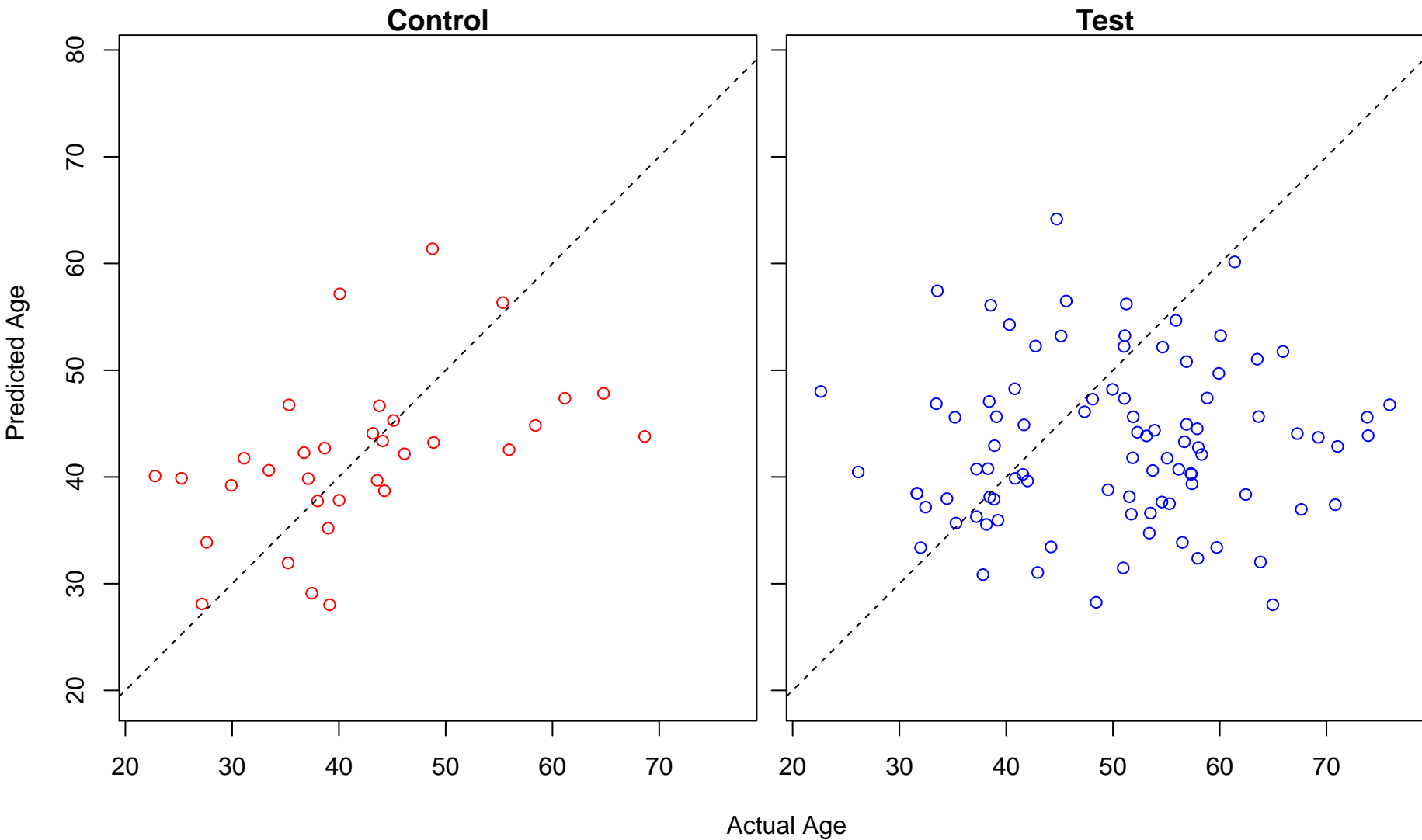
regulation of protein catabolic process (Score: 0.887222)



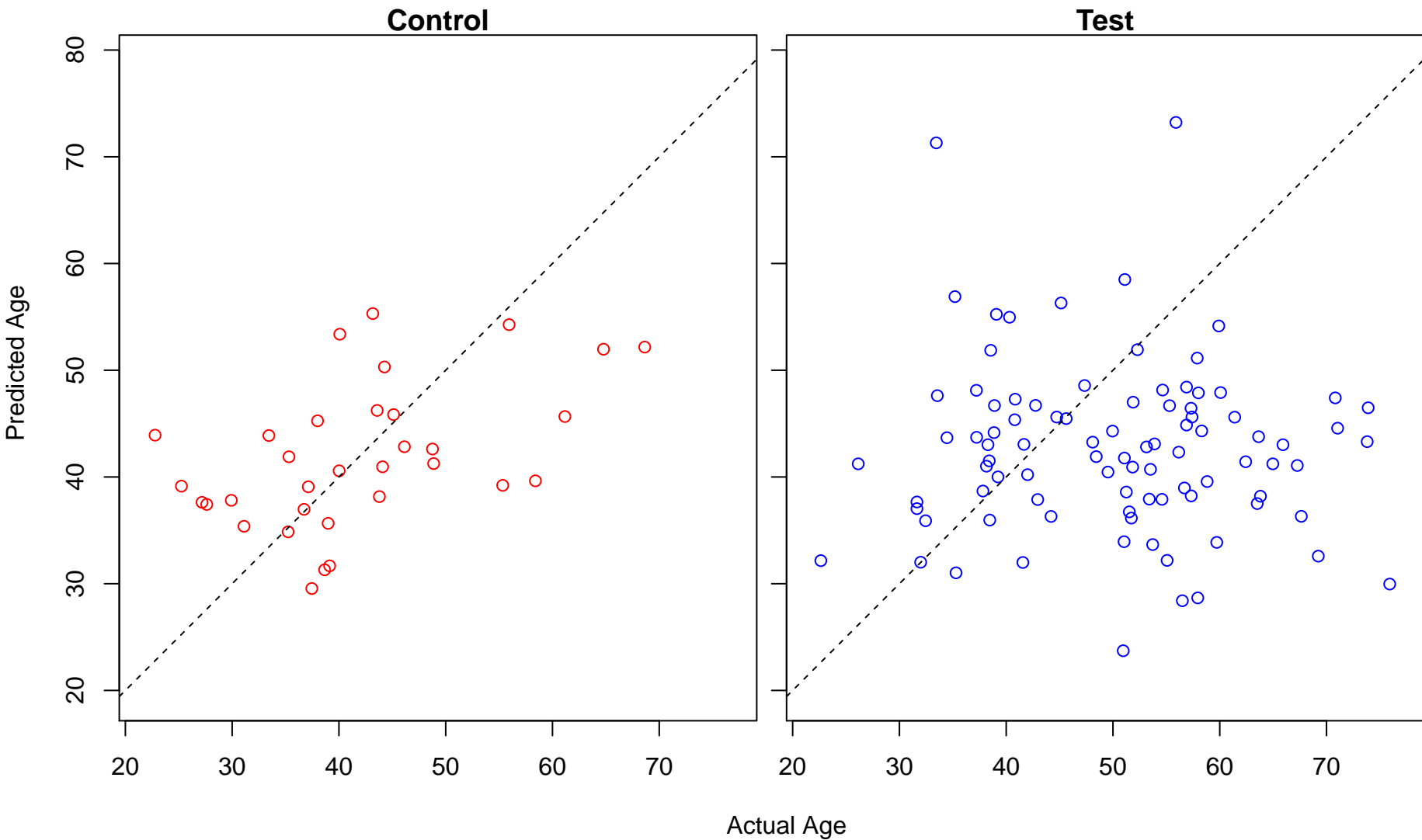
regulation of receptor catabolic process (Score: 0.886504)



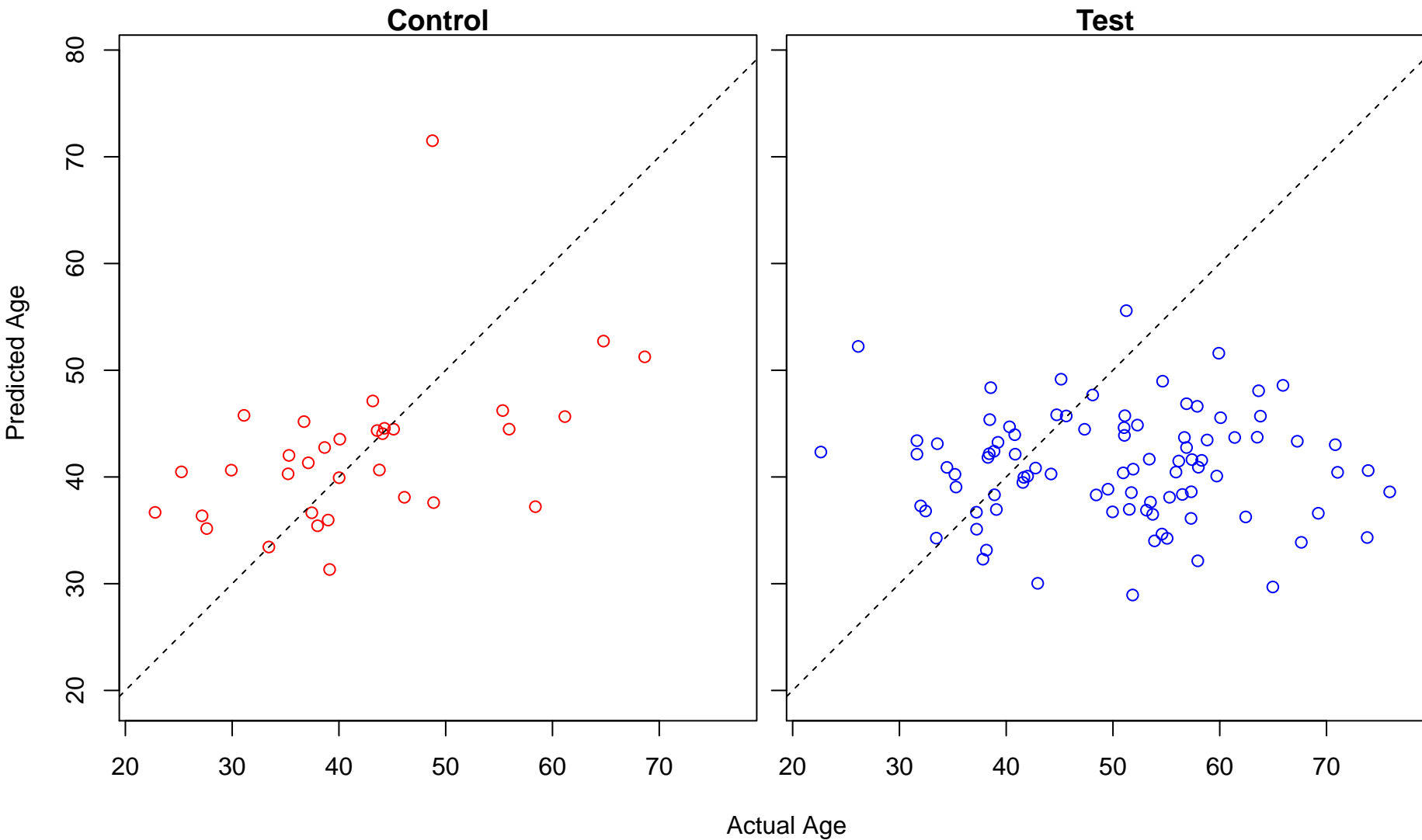
B cell proliferation (Score: 0.883582)



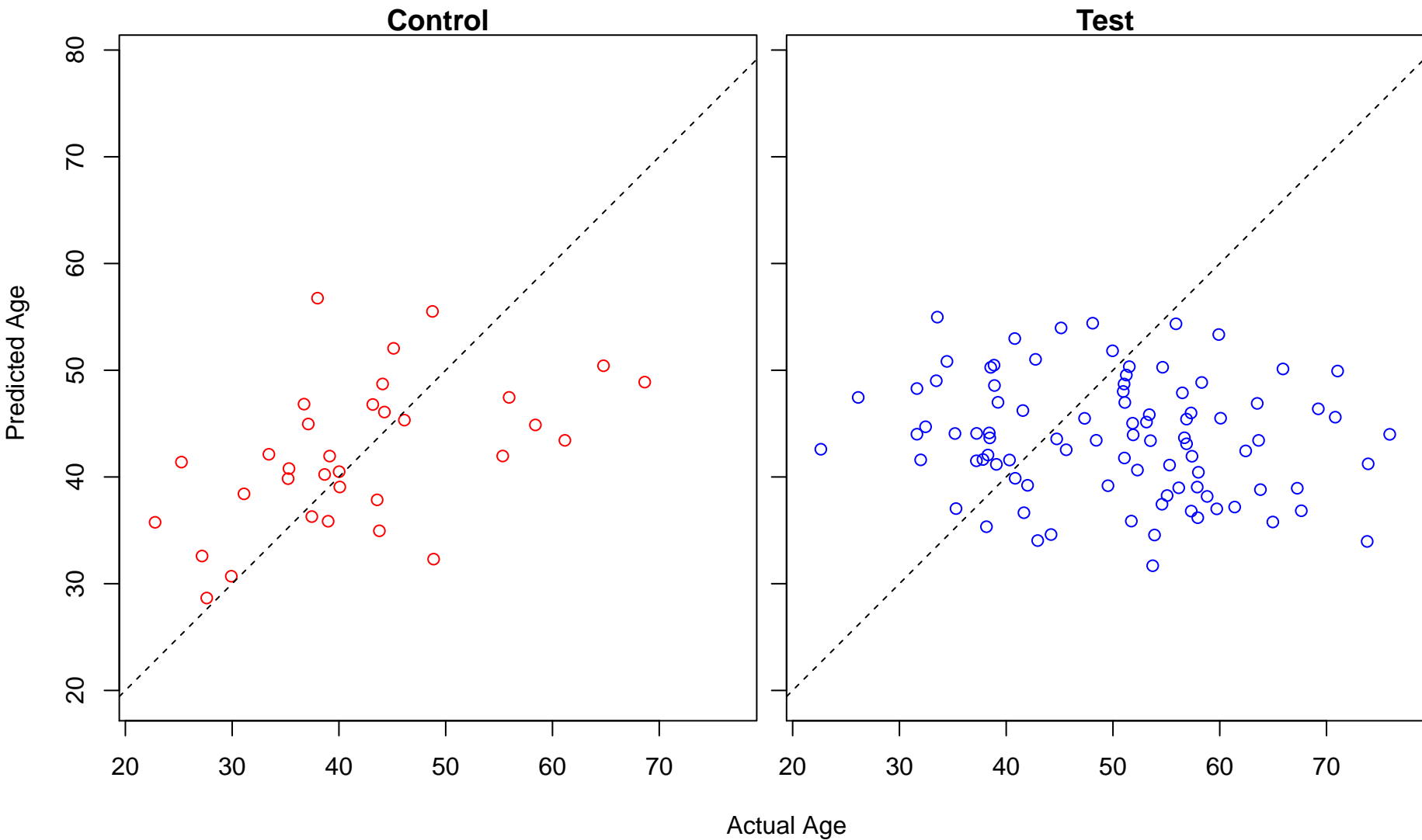
heterochromatin assembly (Score: 0.882246)



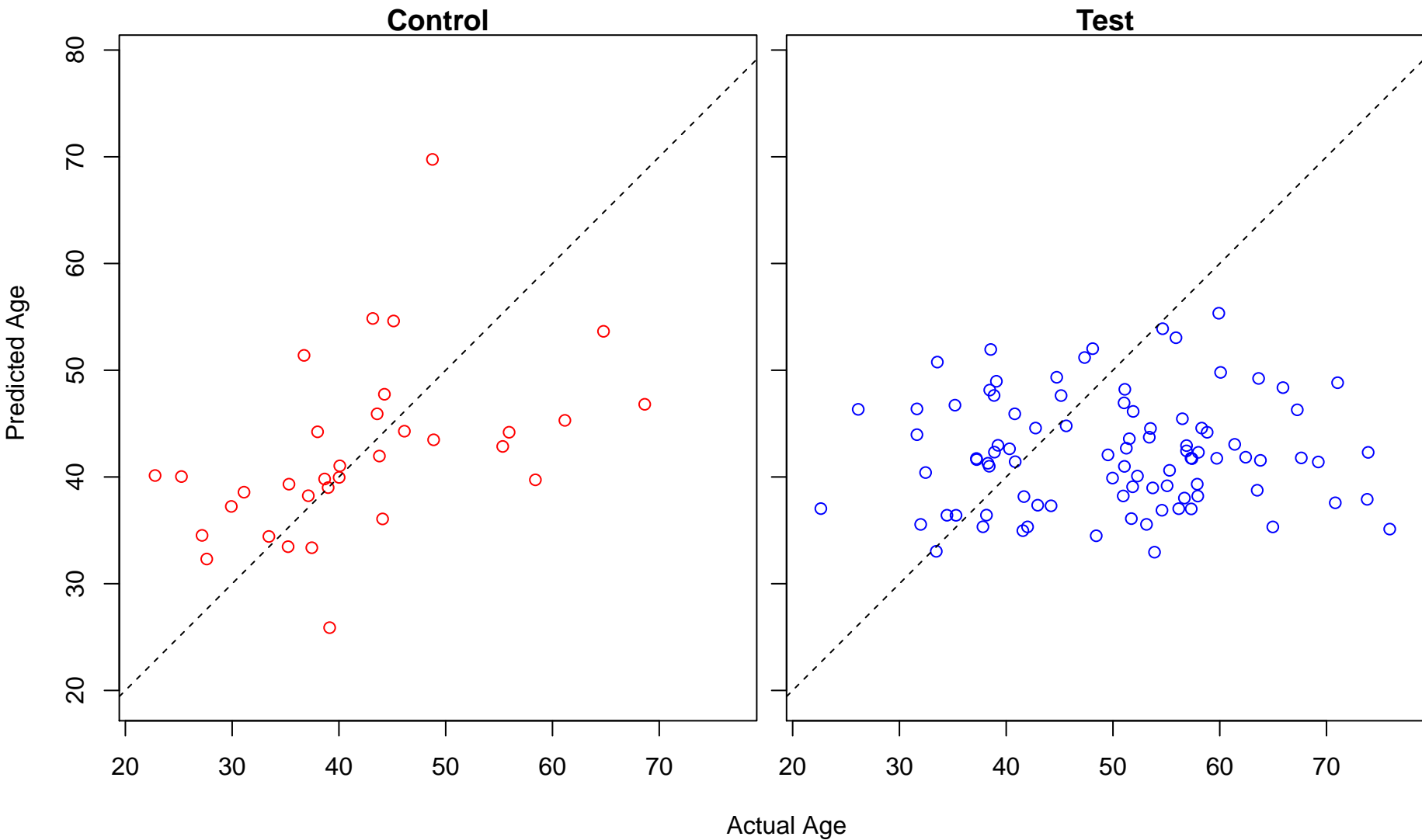
phosphatidylglycerol metabolic process (Score: 0.882244)



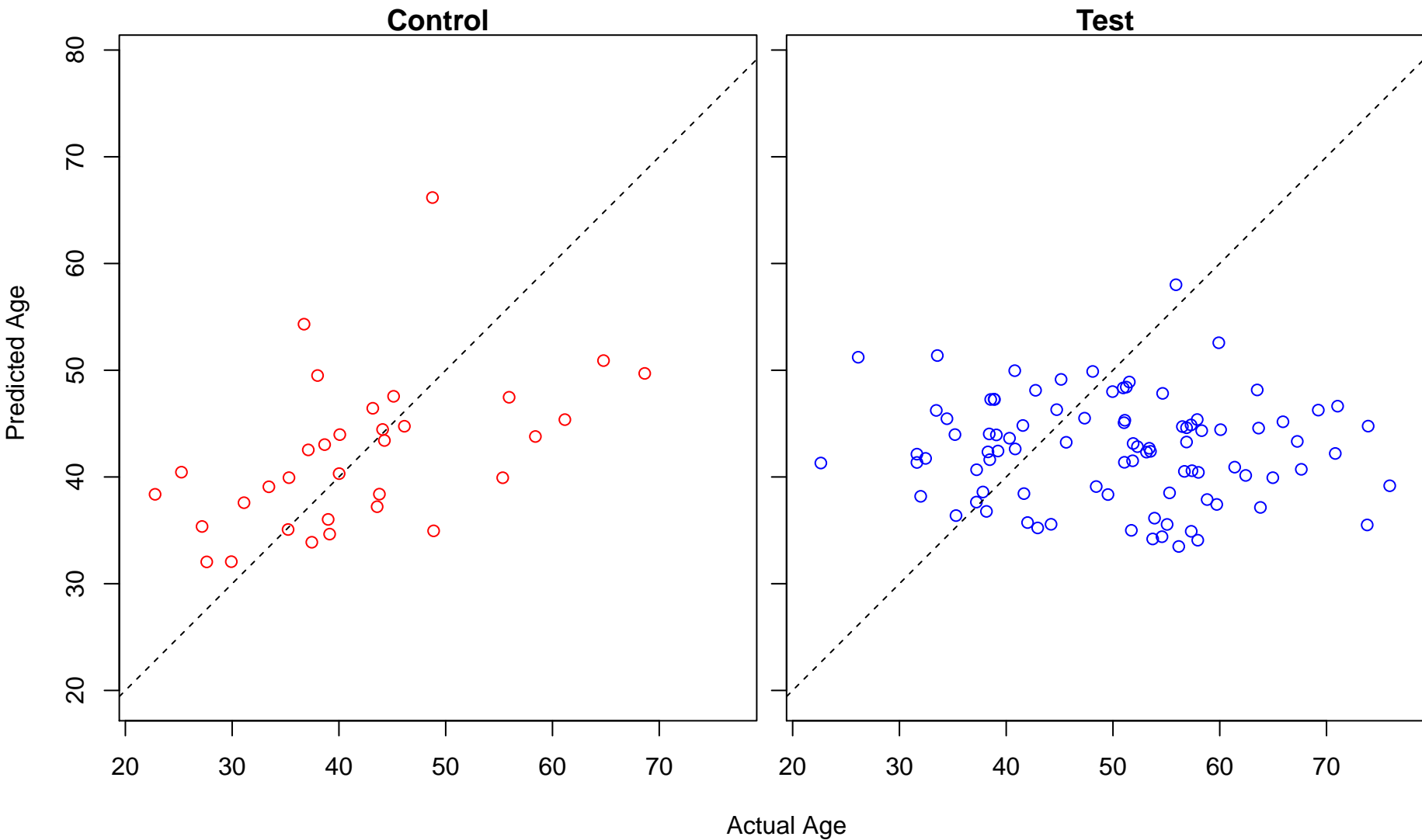
cGMP catabolic process (Score: 0.881195)



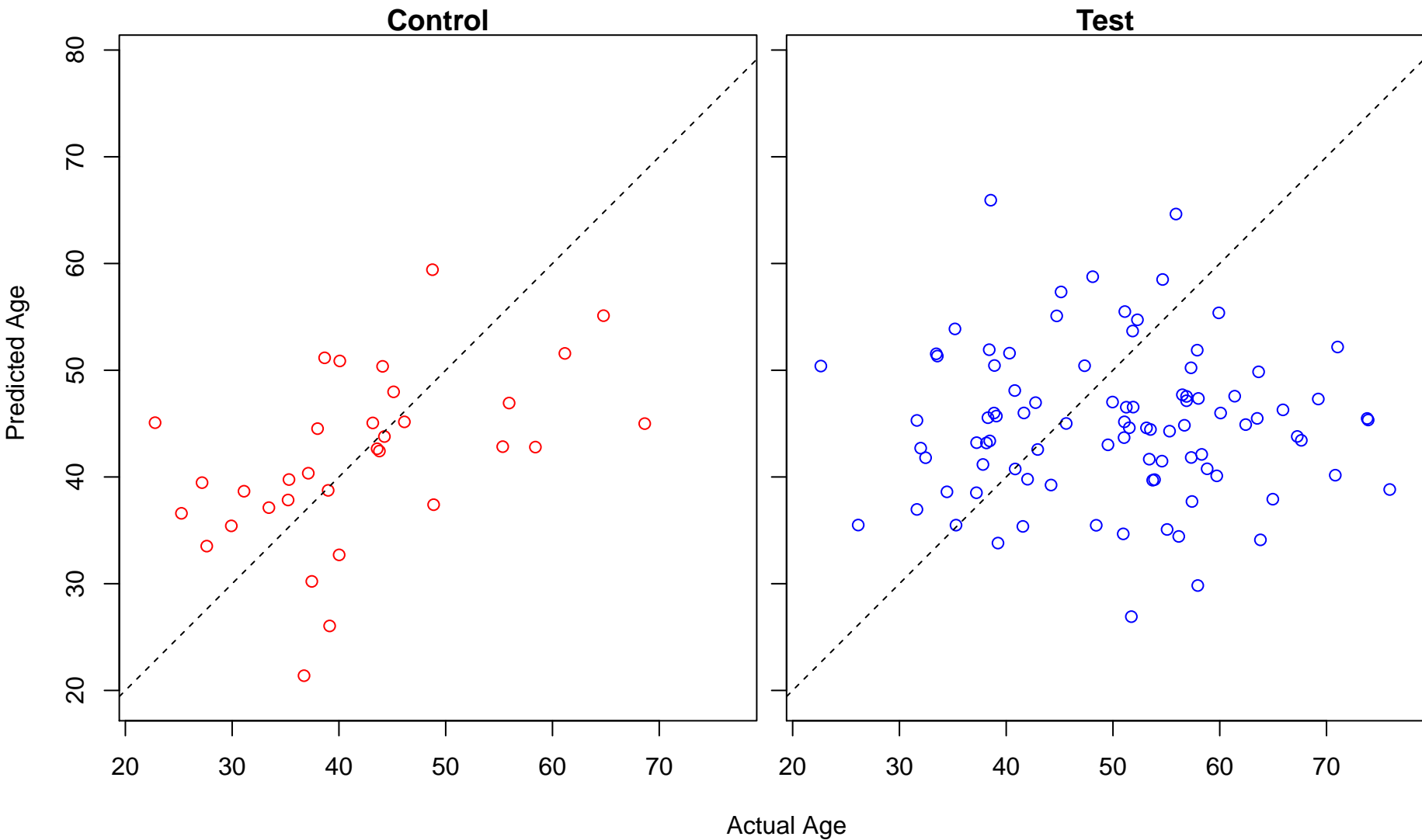
negative regulation of interleukin-17 production (Score: 0.880256)



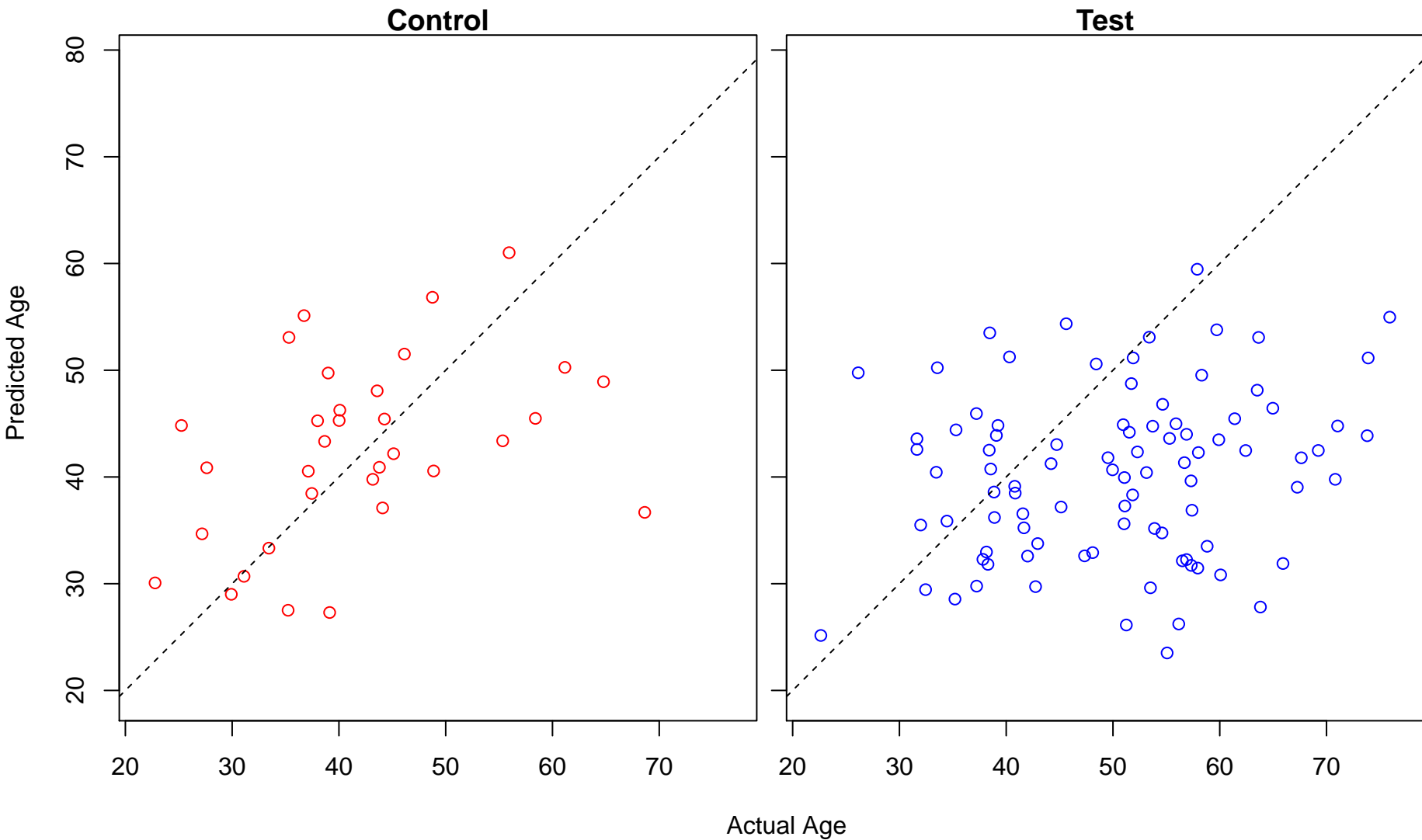
purine nucleotide catabolic process (Score: 0.880094)



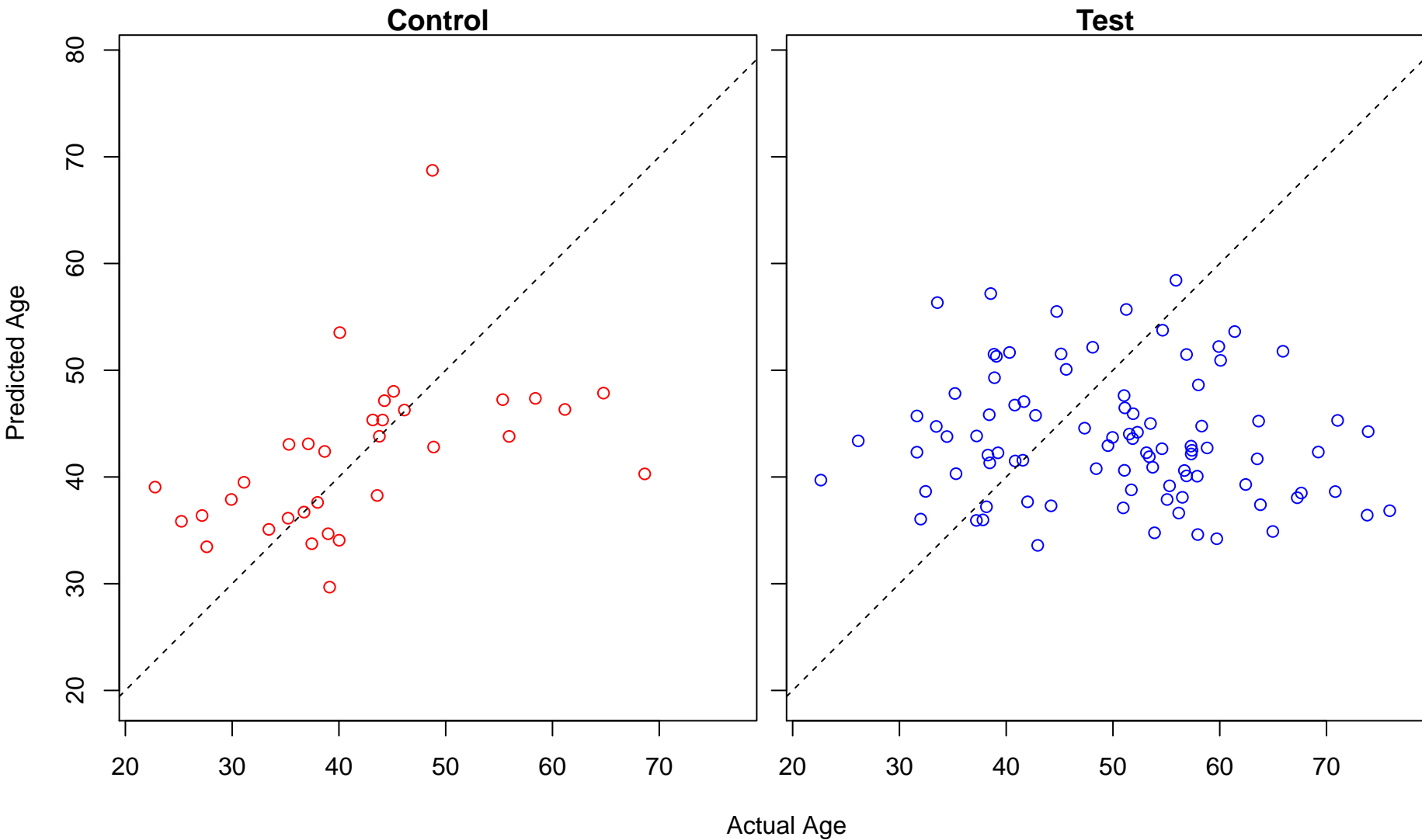
positive regulation of hormone metabolic process (Score: 0.879635)



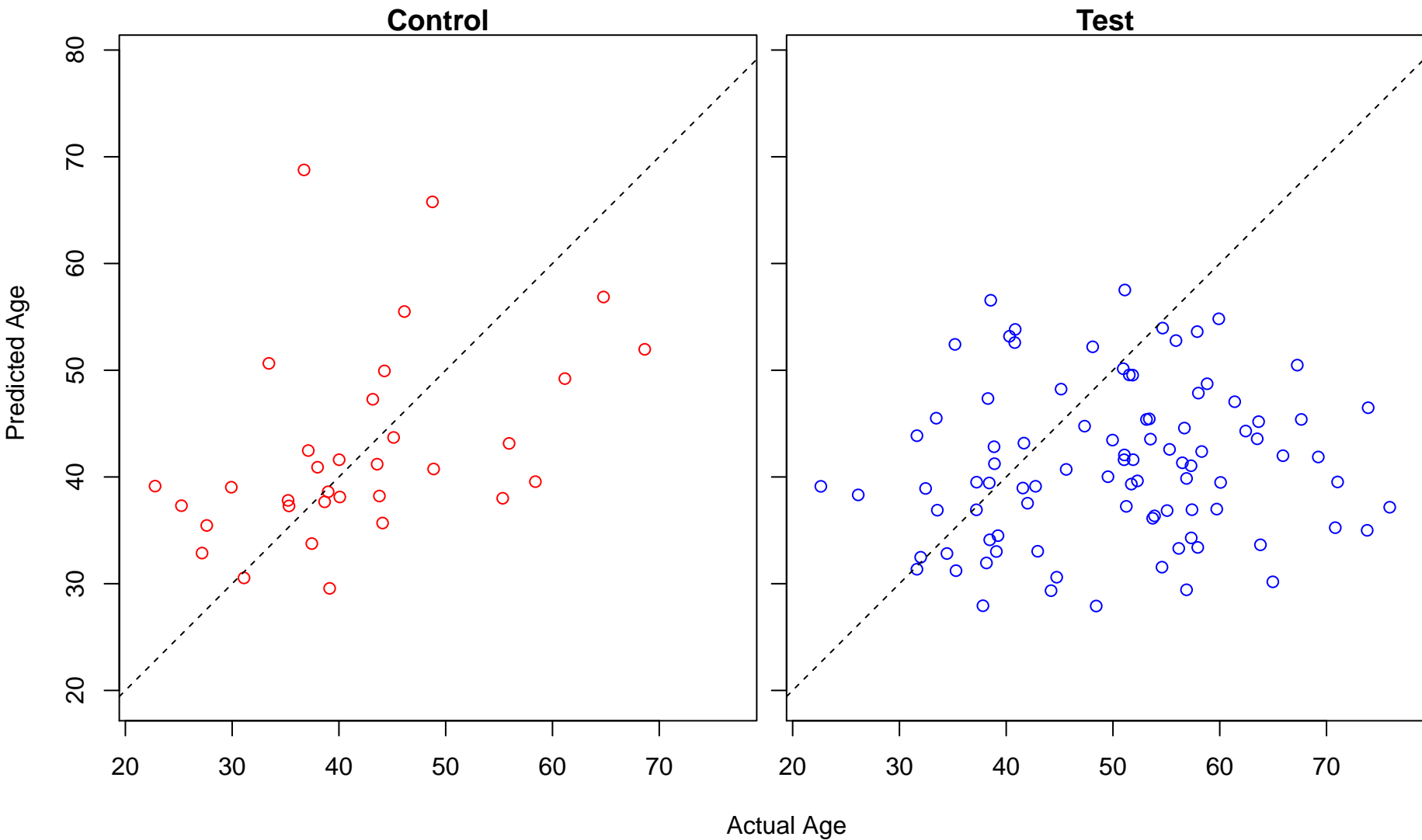
substrate adhesion-dependent cell spreading (Score: 0.878884)



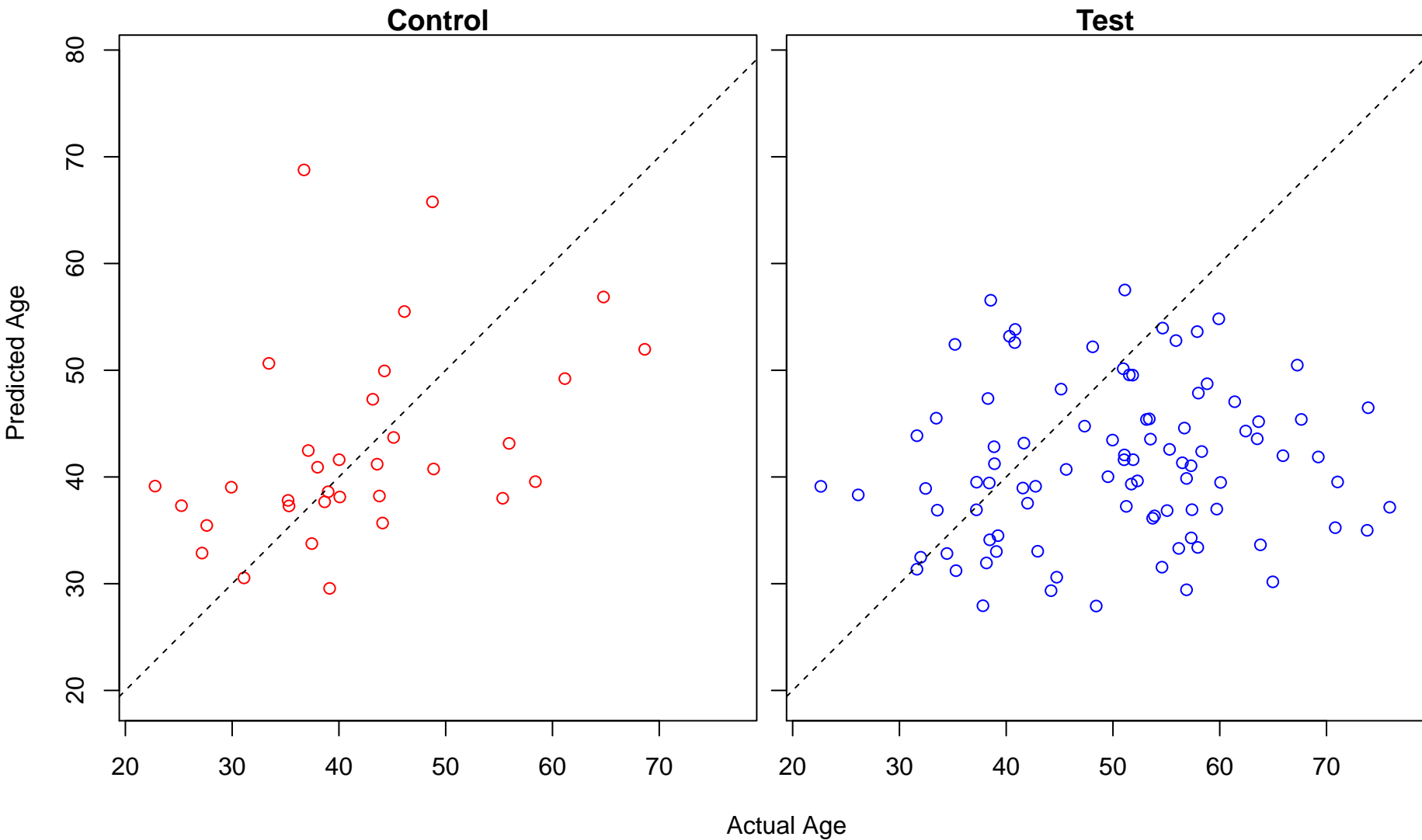
negative regulation of catabolic process (Score: 0.878782)



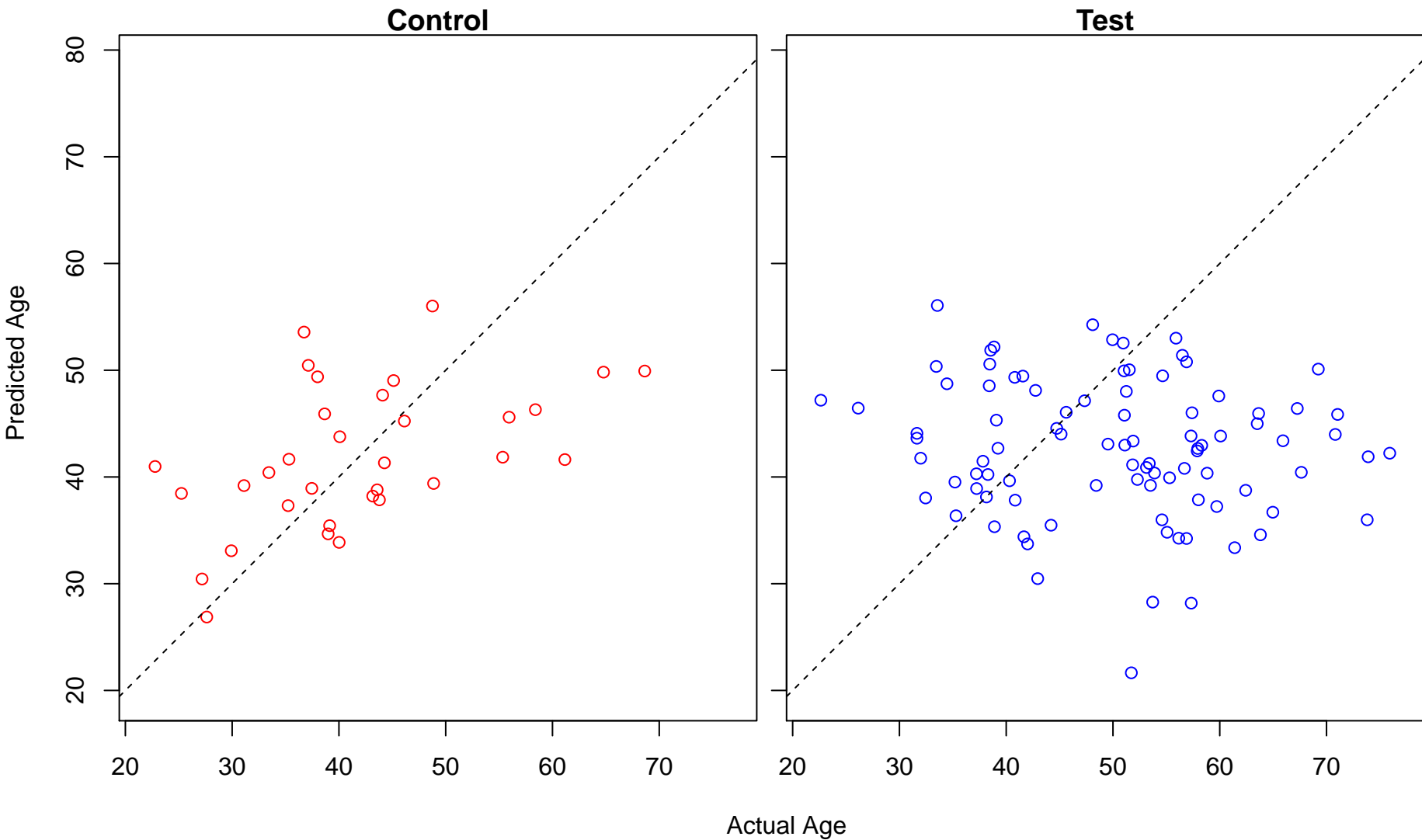
deoxyribonucleoside triphosphate metabolic process (Score: 0.878716)



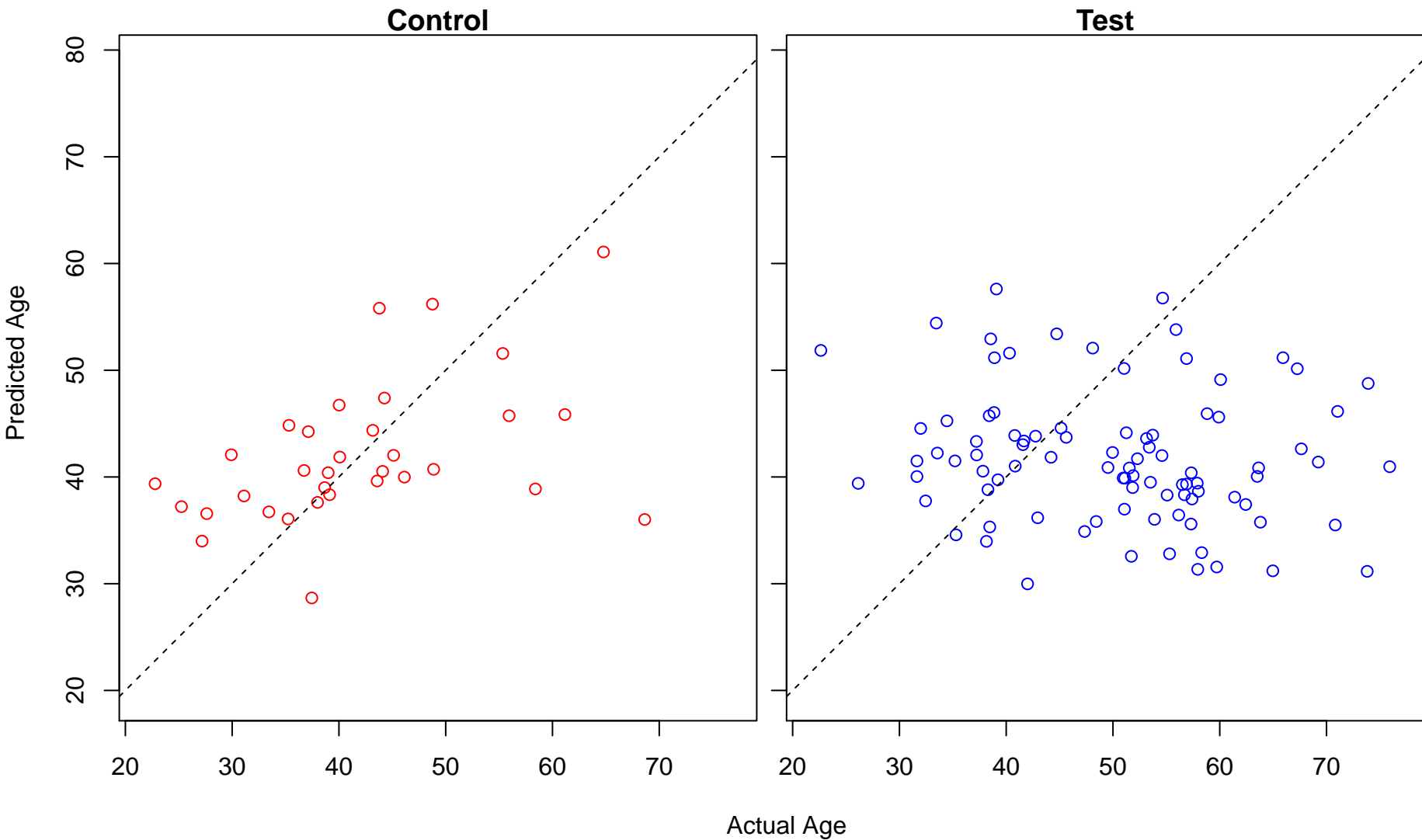
purine deoxyribonucleoside triphosphate metabolic process (Score: 0.878716)



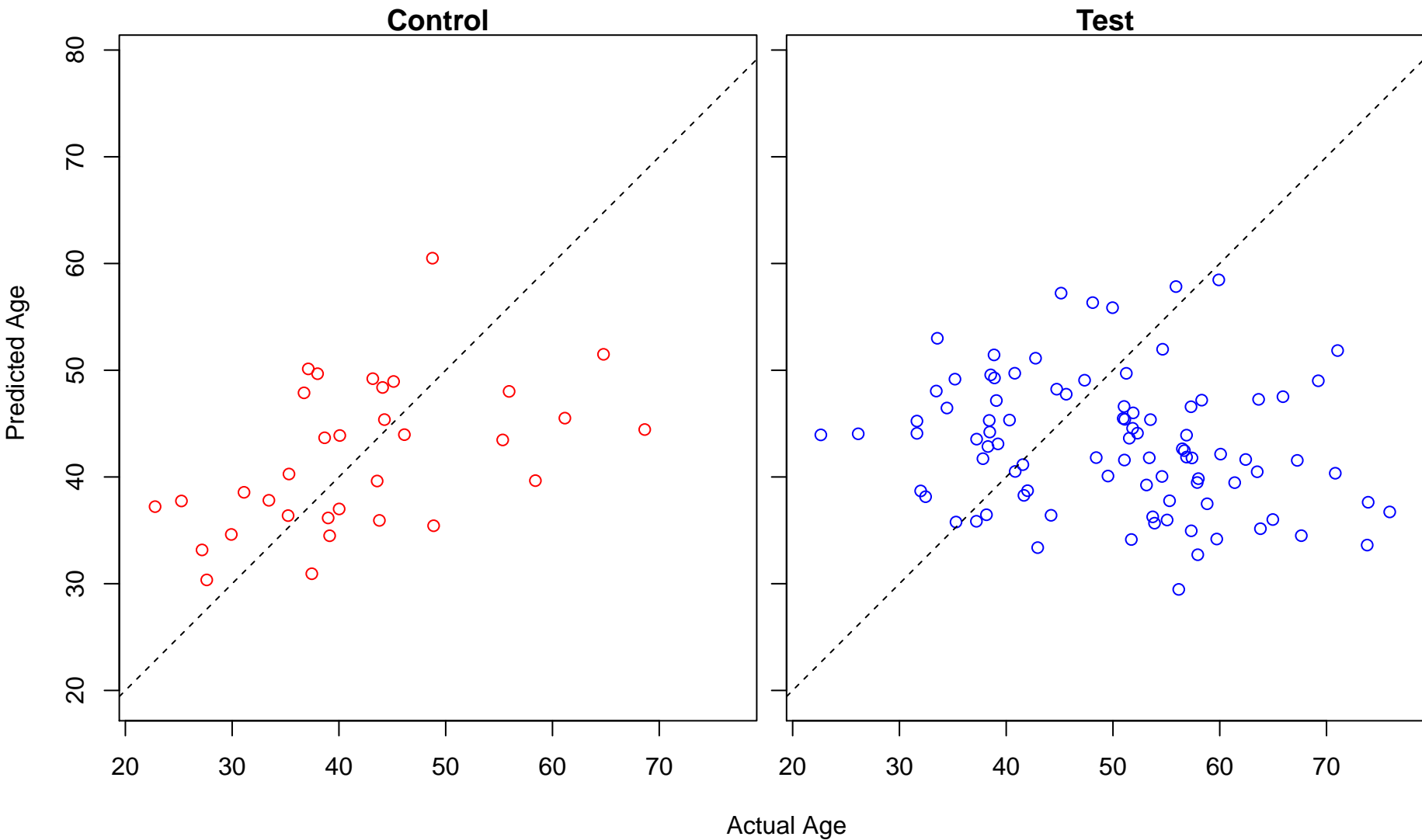
response to misfolded protein (Score: 0.878298)



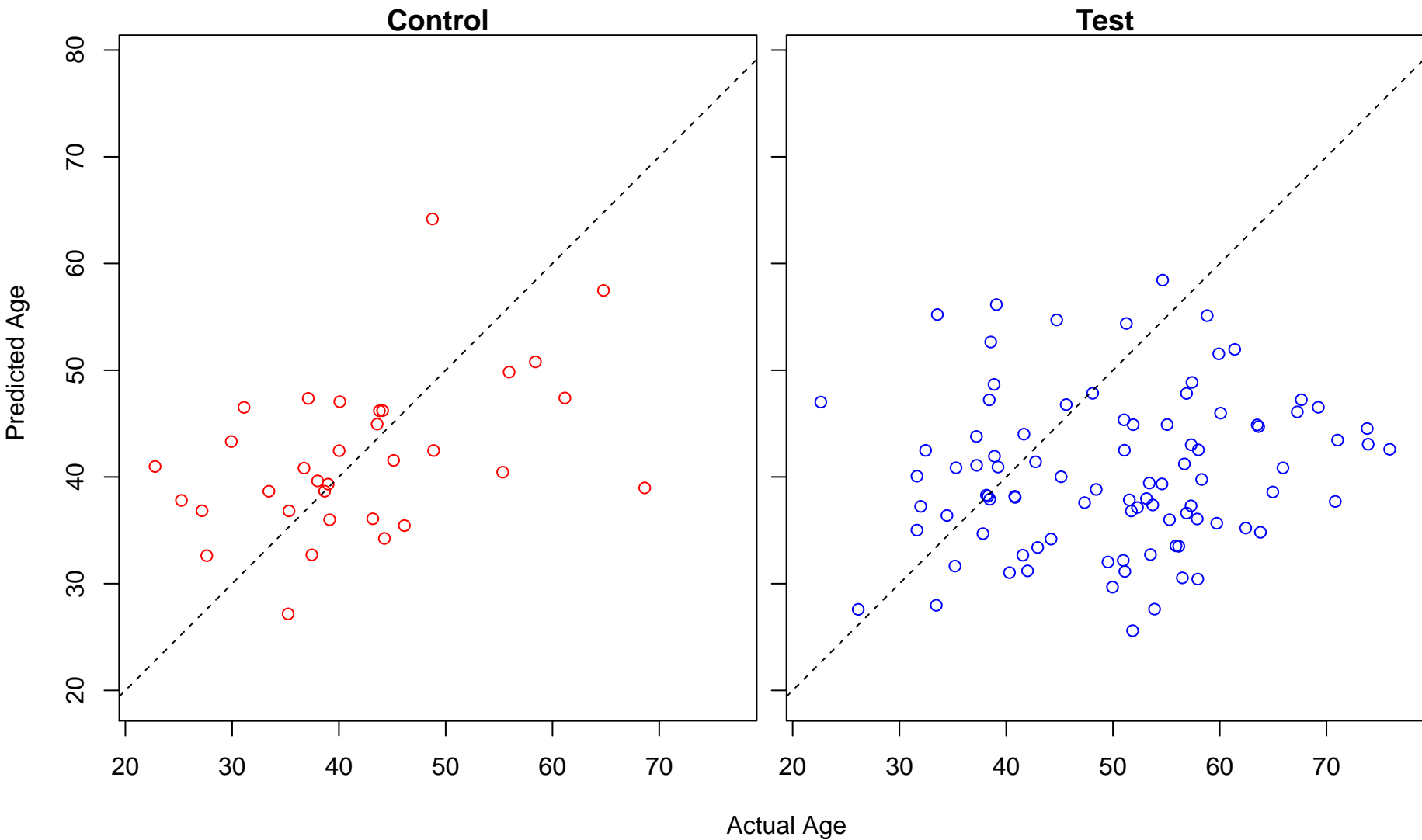
cartilage condensation (Score: 0.877299)



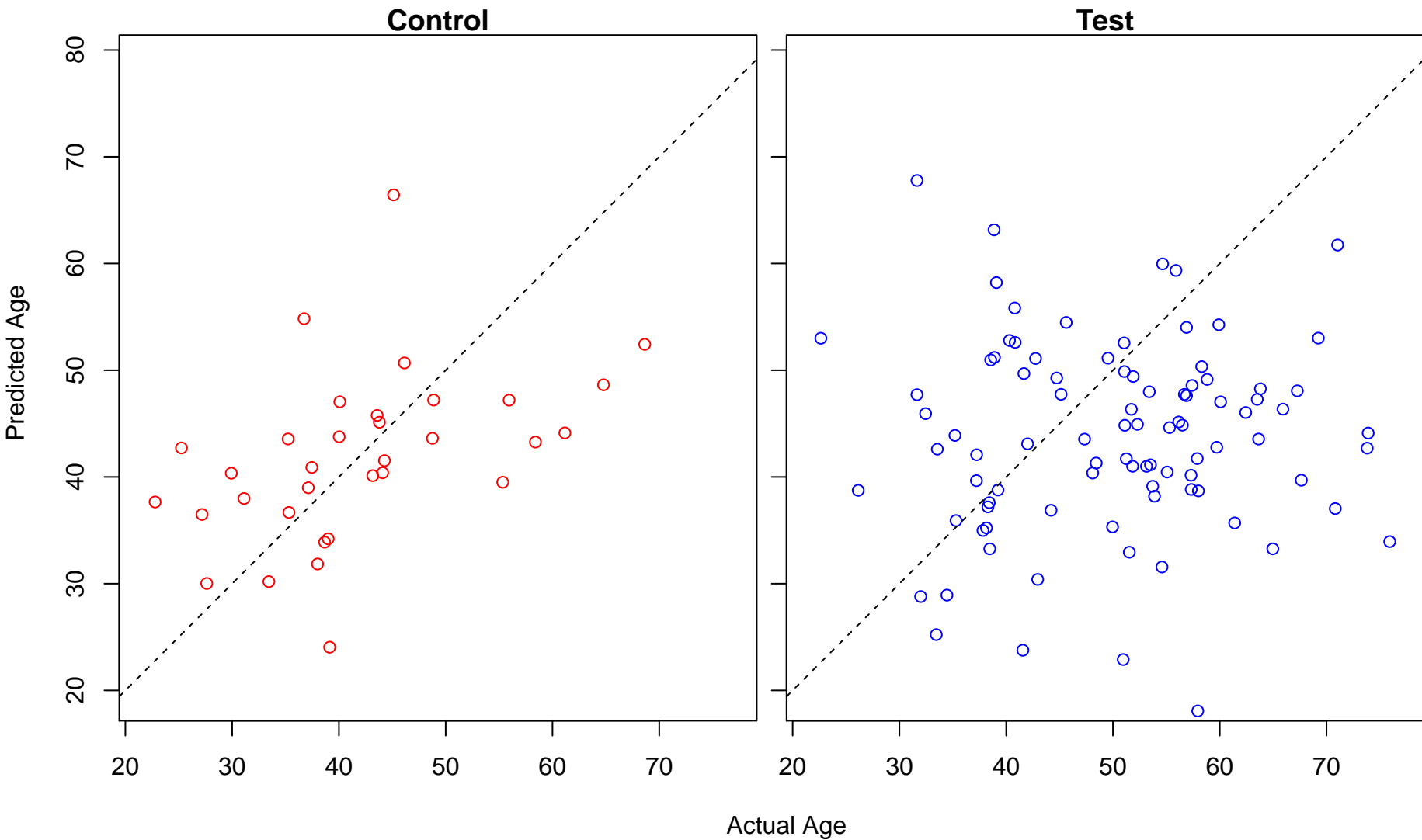
cyclic nucleotide metabolic process (Score: 0.876838)



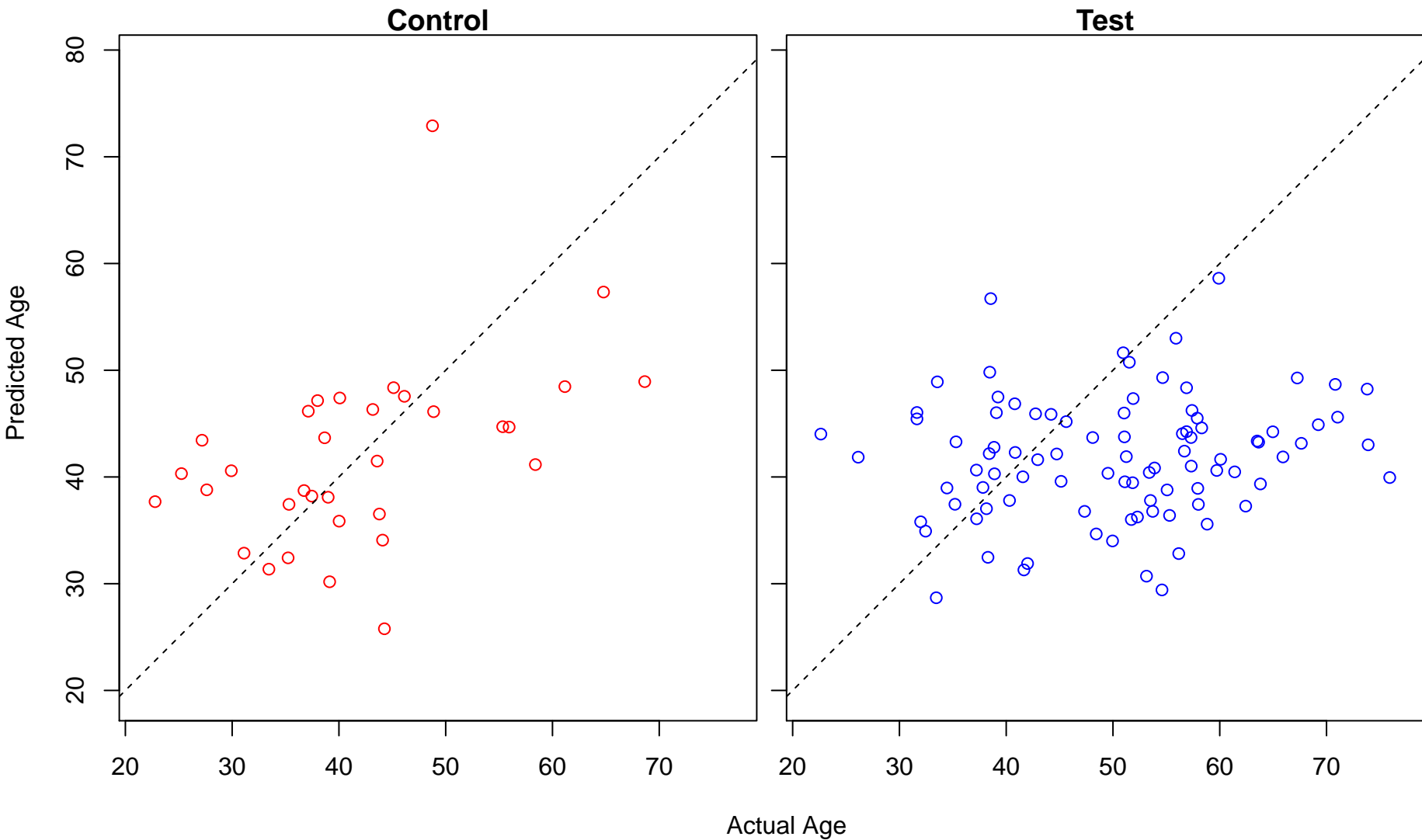
regulation of transcription by glucose (Score: 0.871223)



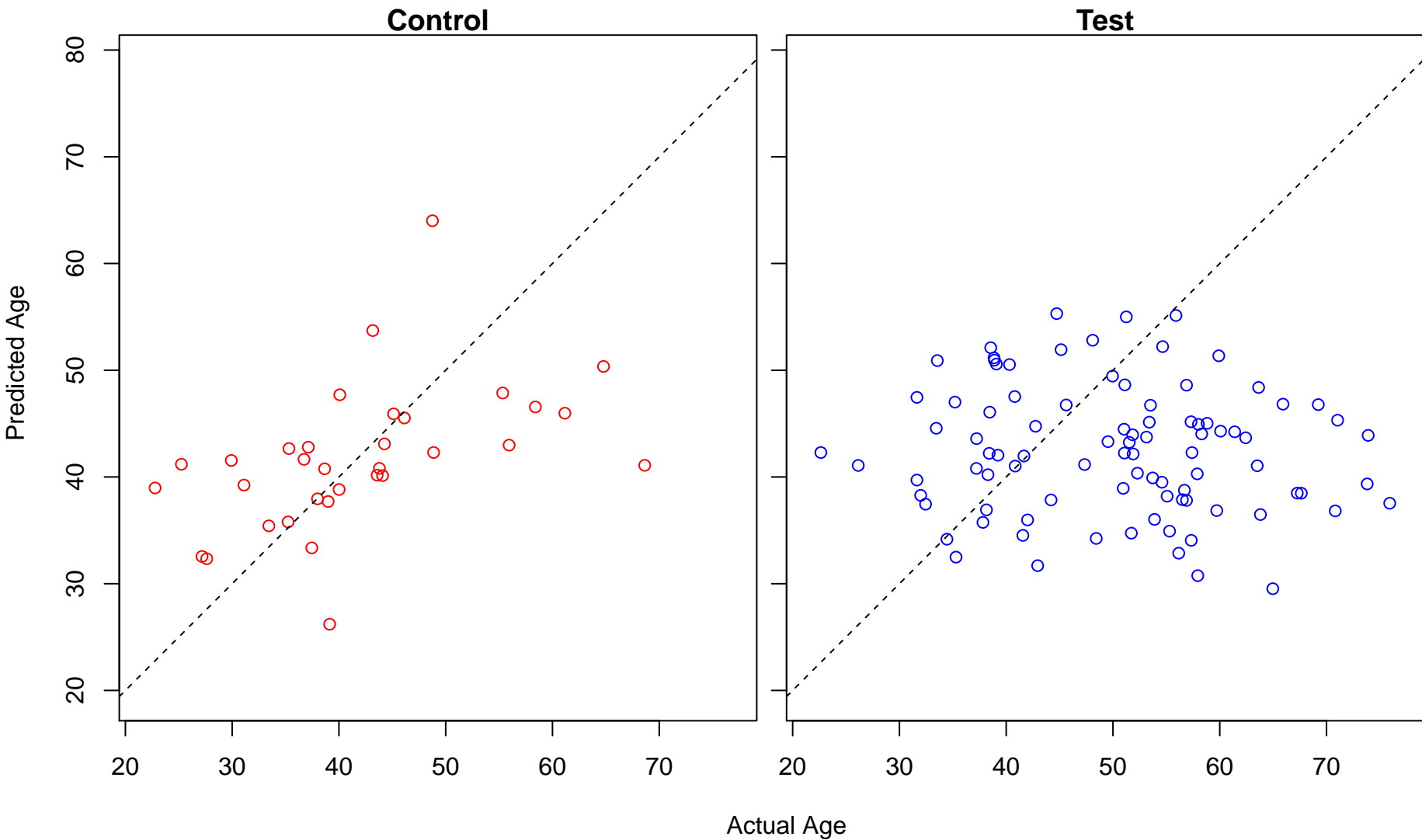
sensory perception of smell (Score: 0.870560)



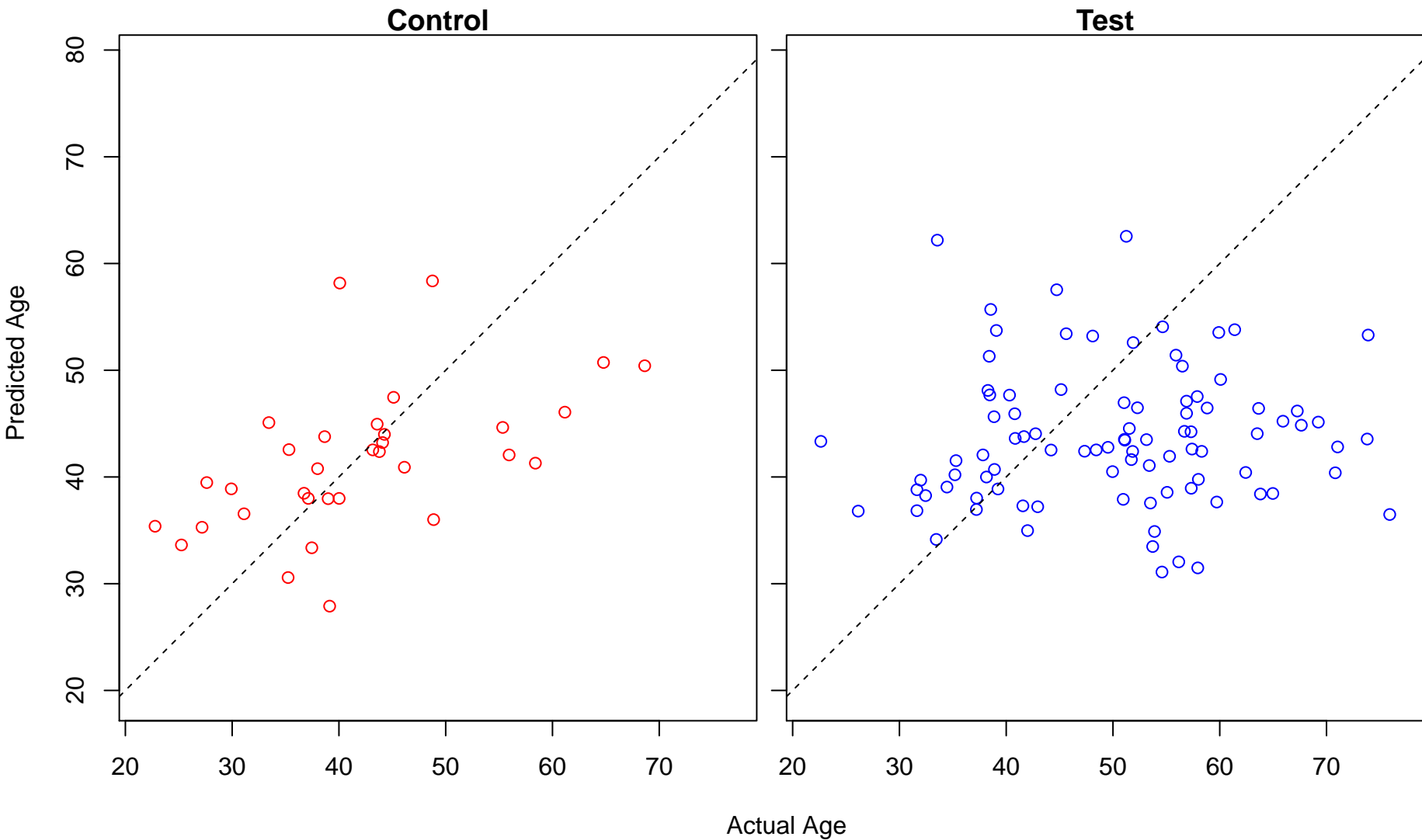
positive regulation of Rho protein signal transduction (Score: 0.870007)



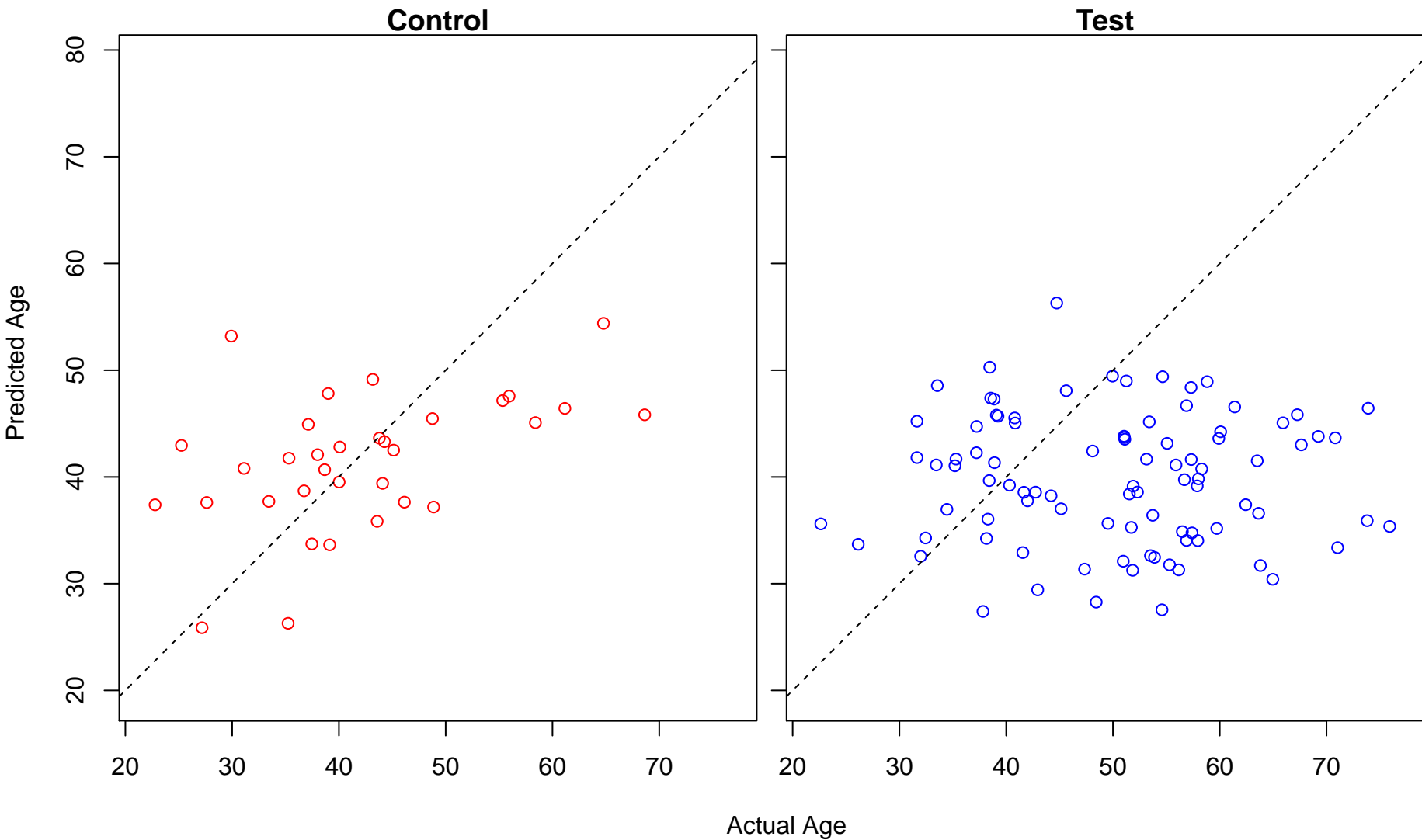
organic anion transport (Score: 0.869039)



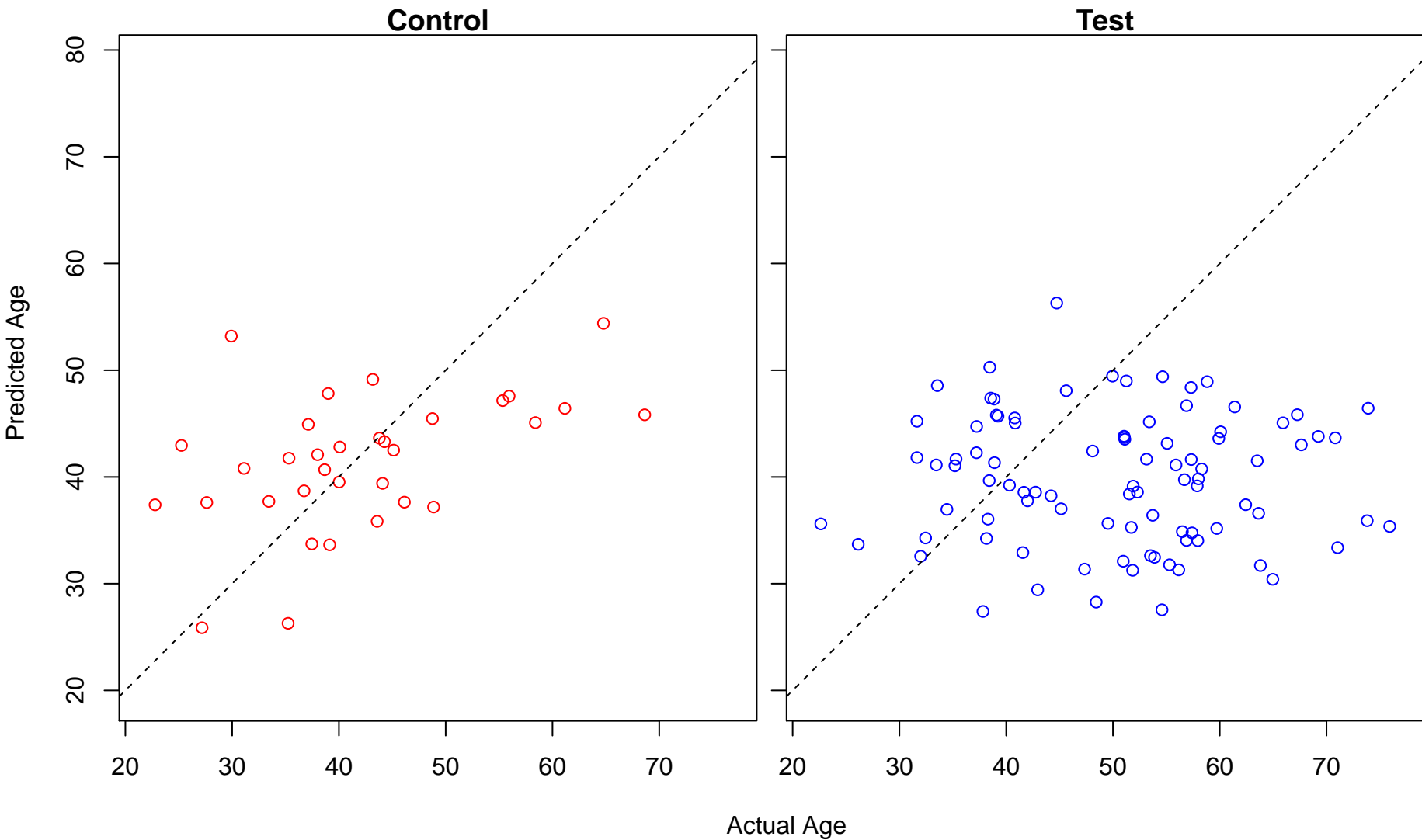
lamellipodium assembly (Score: 0.868439)



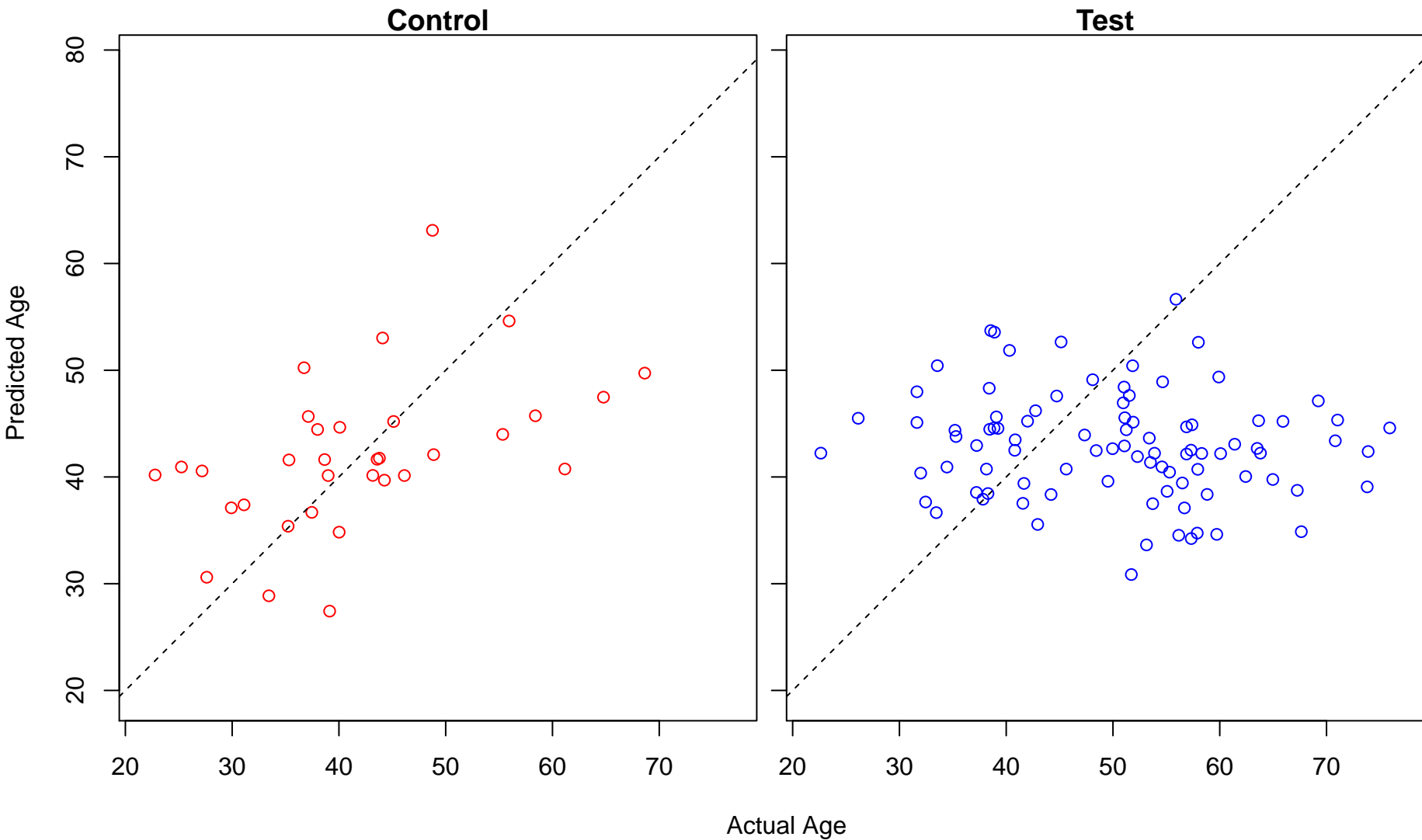
cholesterol homeostasis (Score: 0.868089)



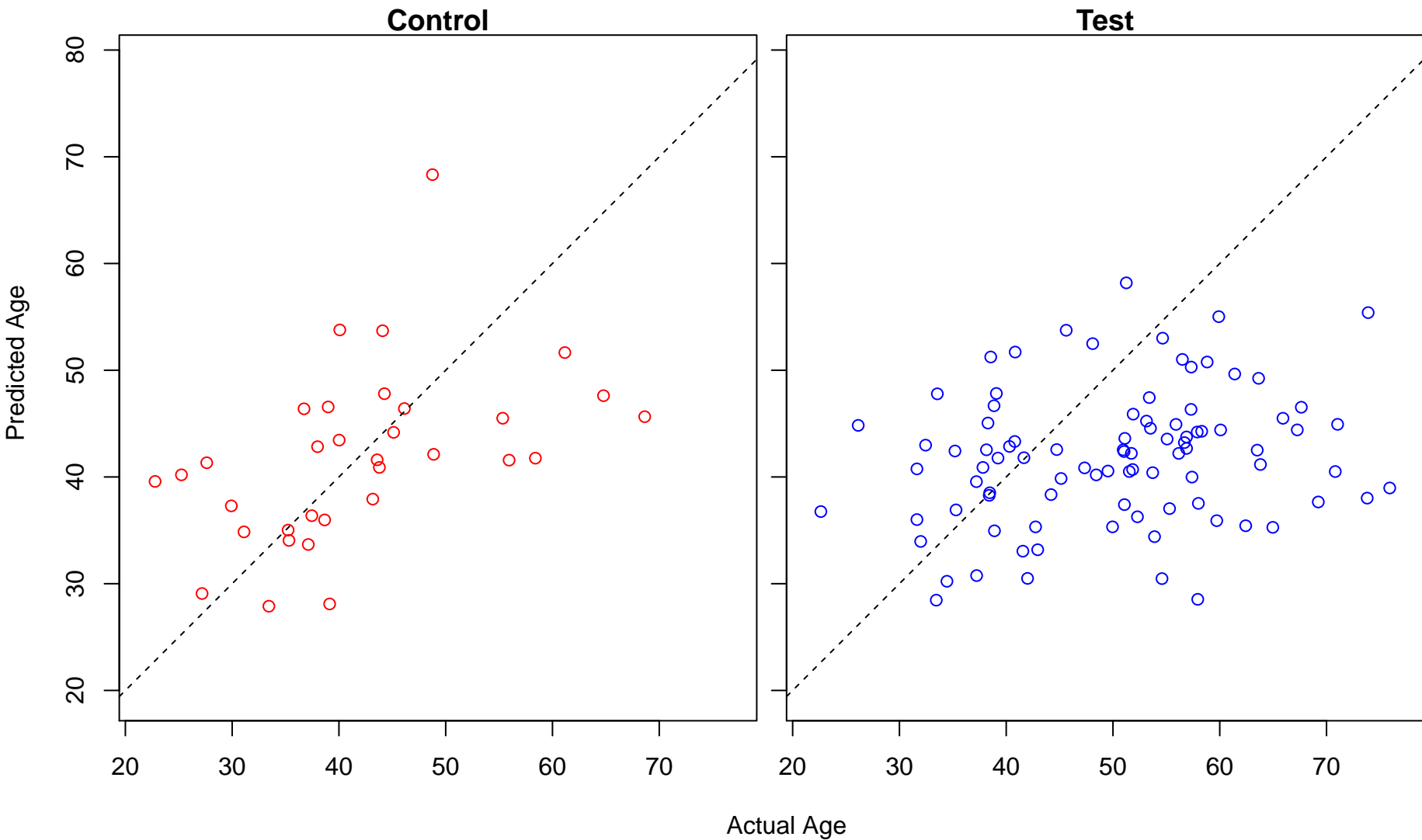
sterol homeostasis (Score: 0.868089)



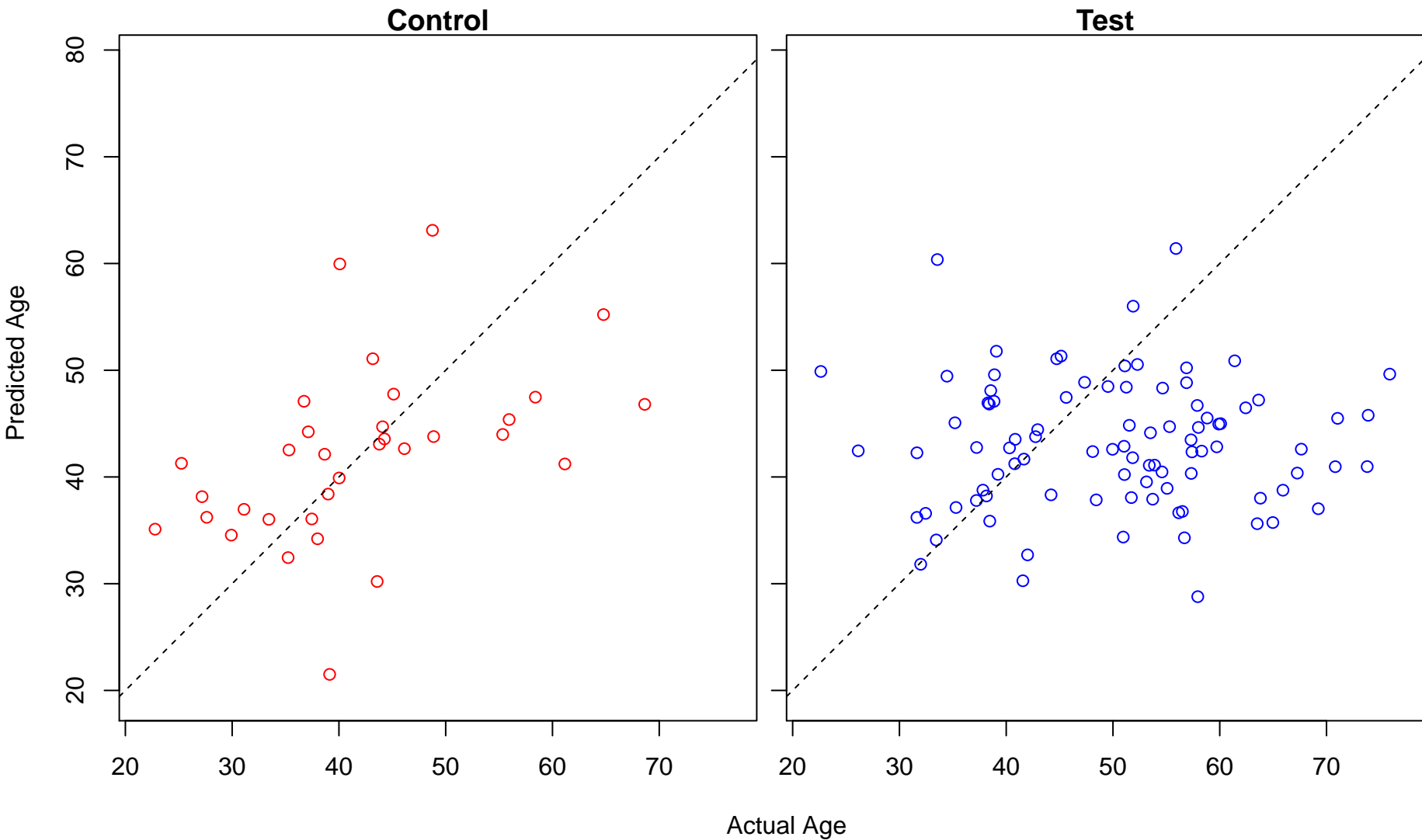
negative regulation of receptor catabolic process (Score: 0.868055)



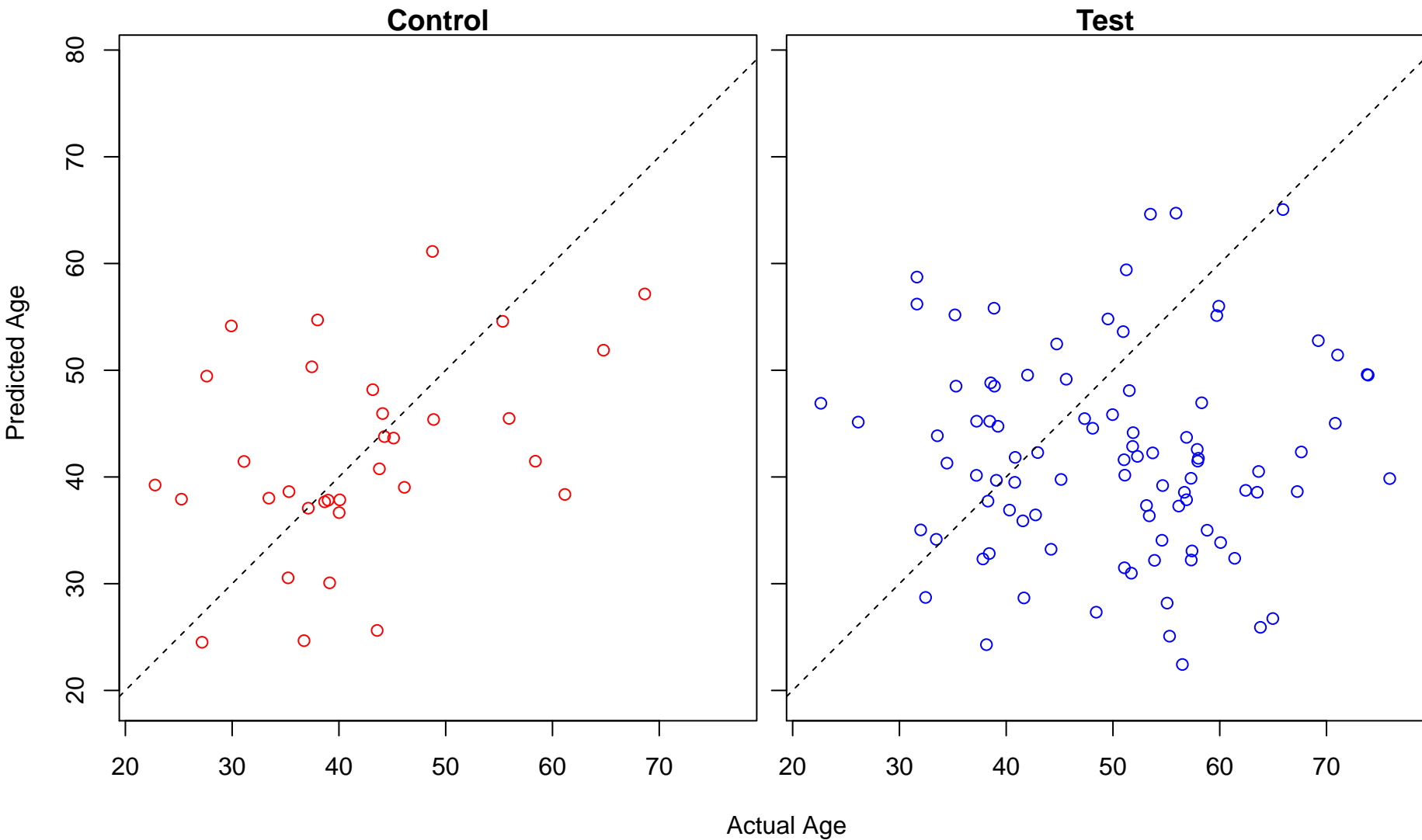
dicarboxylic acid biosynthetic process (Score: 0.866071)



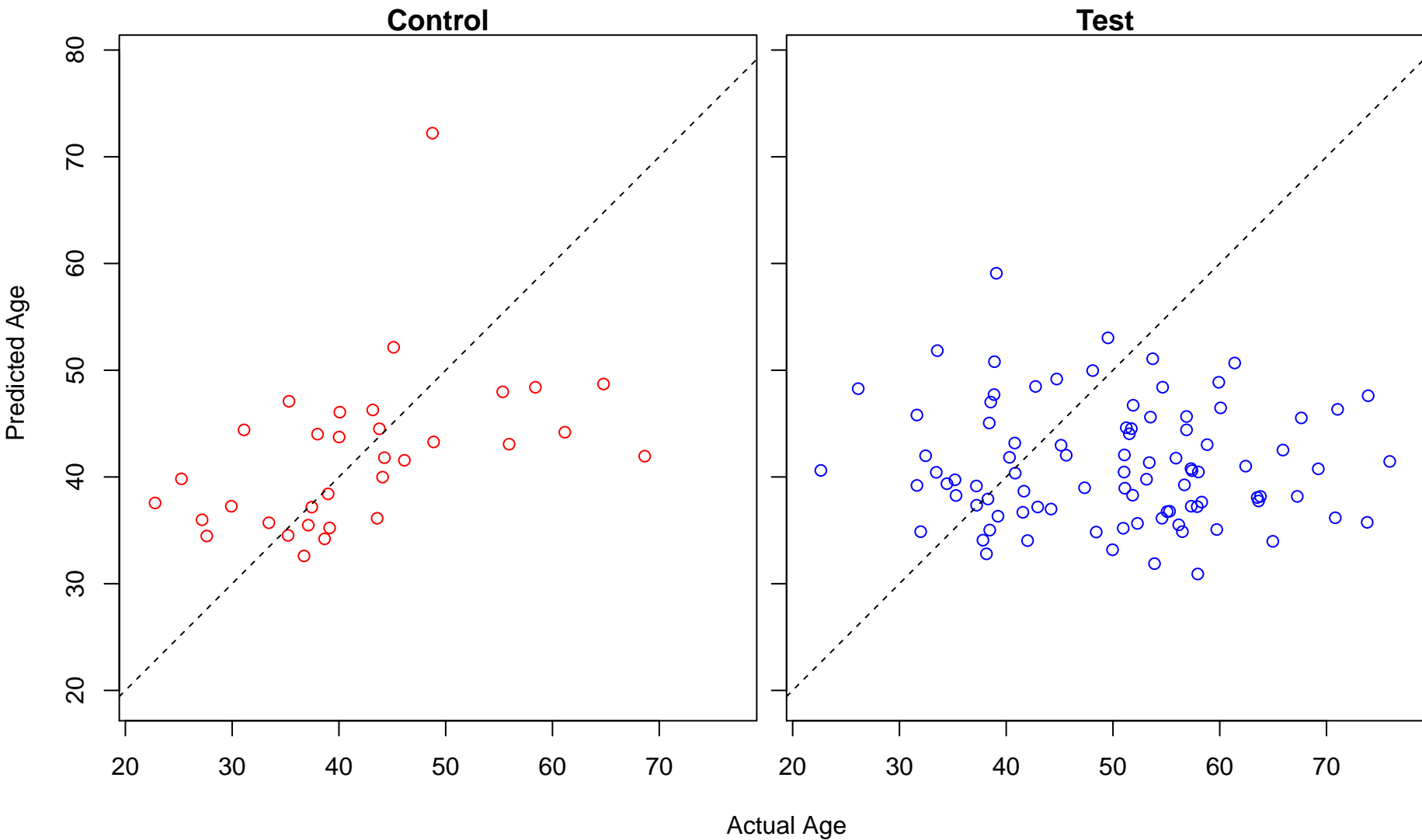
positive regulation of double-strand break repair (Score: 0.864854)



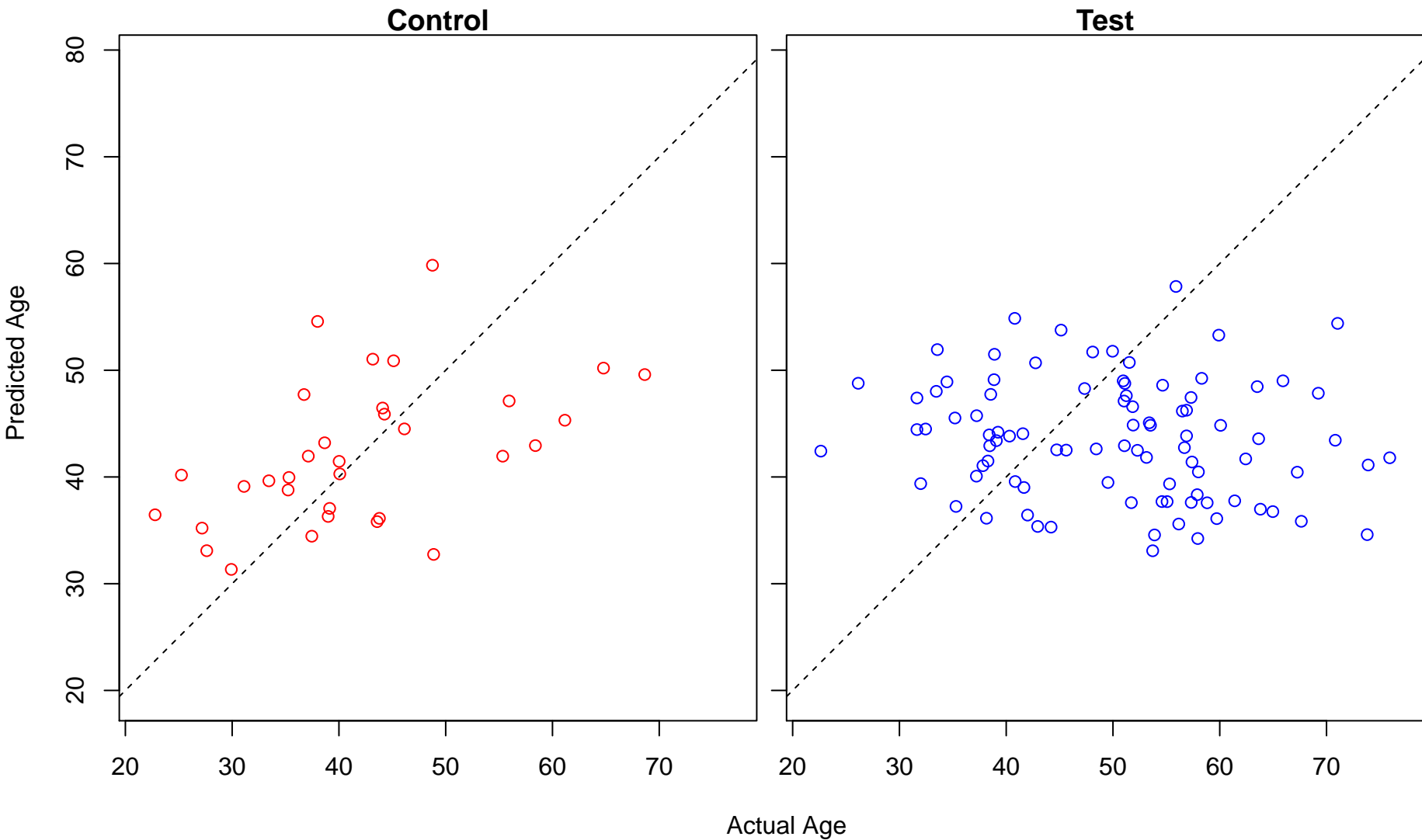
terpenoid metabolic process (Score: 0.864008)



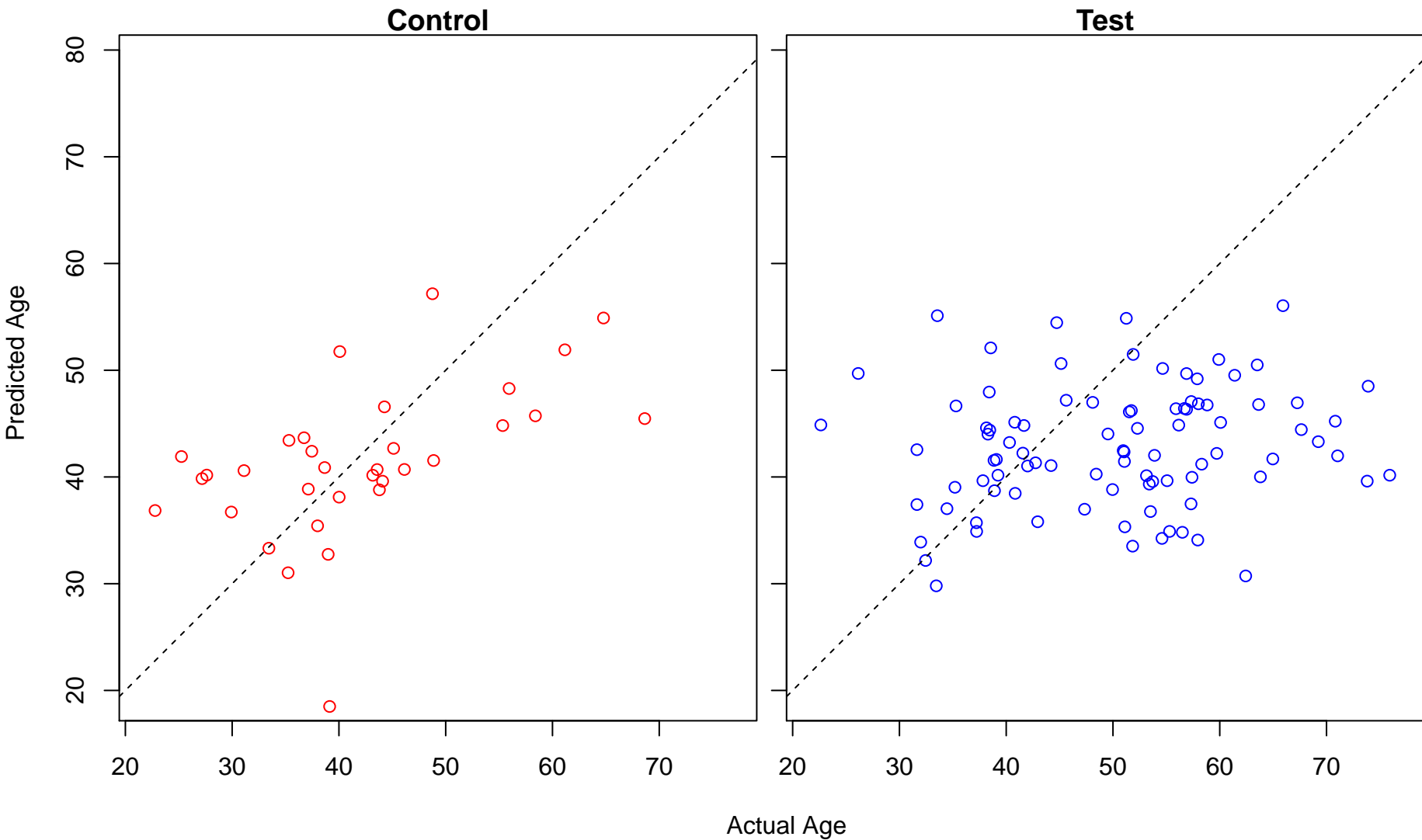
negative regulation of signal transduction by p53 class mediator (Score: 0.863028)



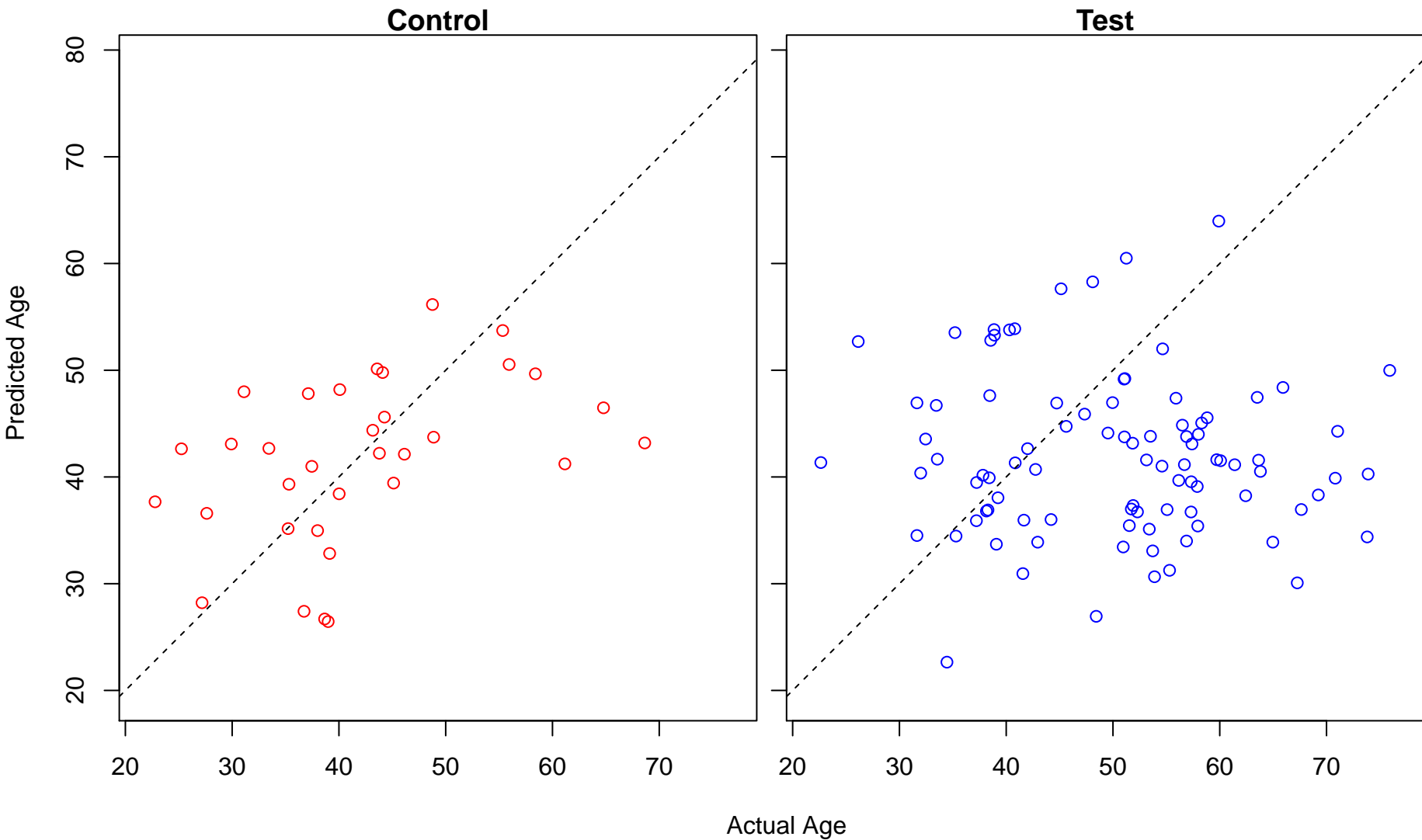
cyclic nucleotide catabolic process (Score: 0.861572)



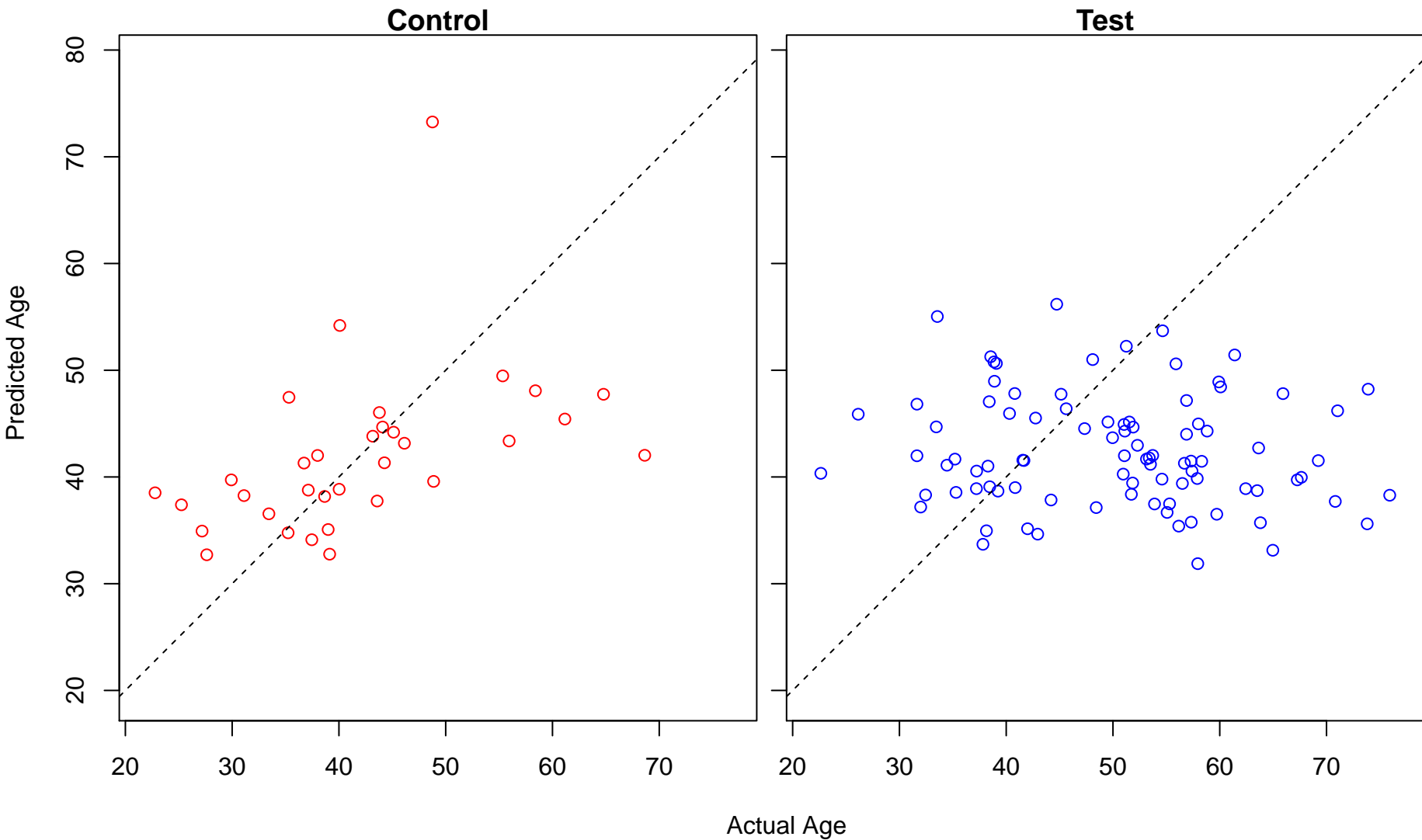
nuclear body organization (Score: 0.861009)



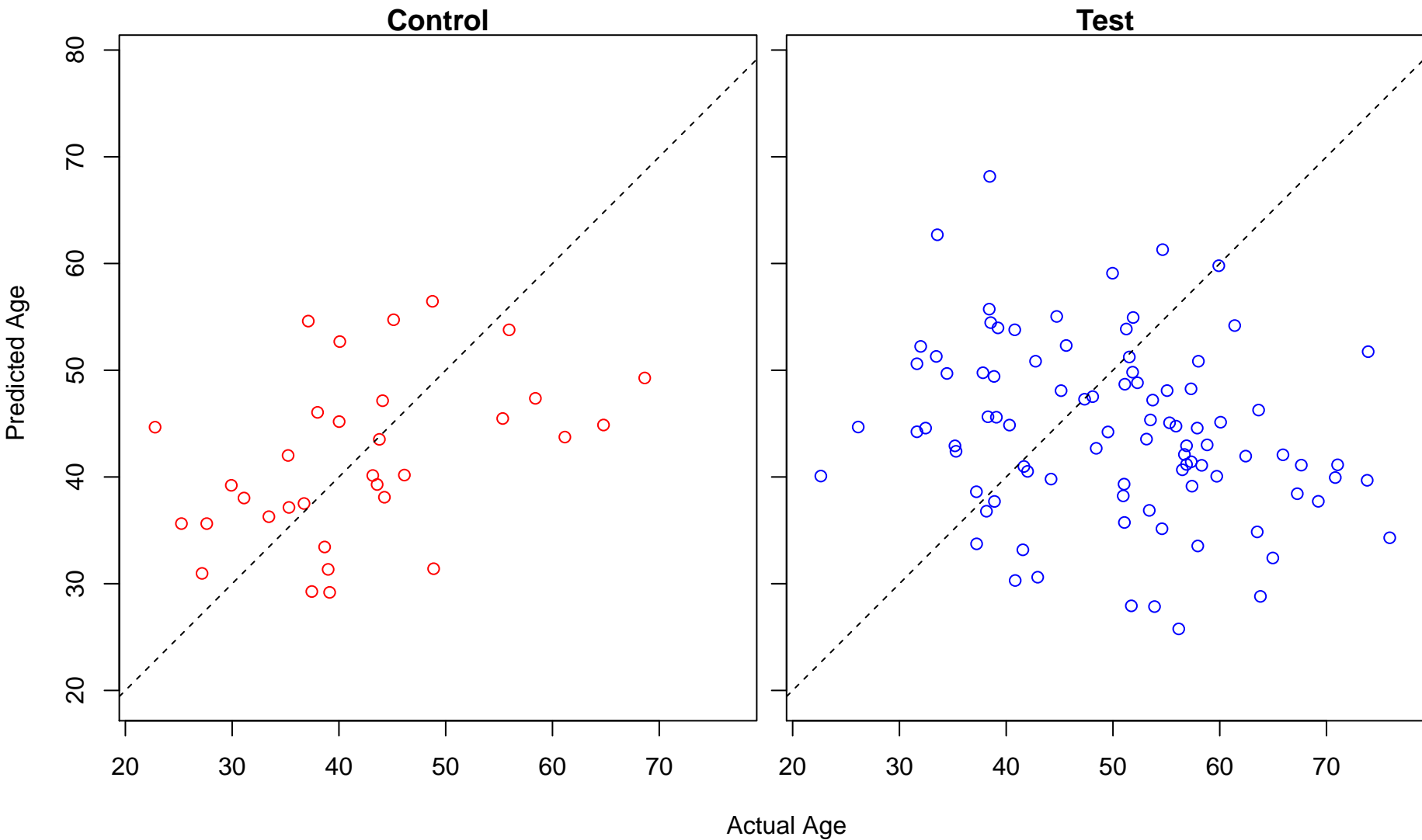
motile cilium assembly (Score: 0.860636)



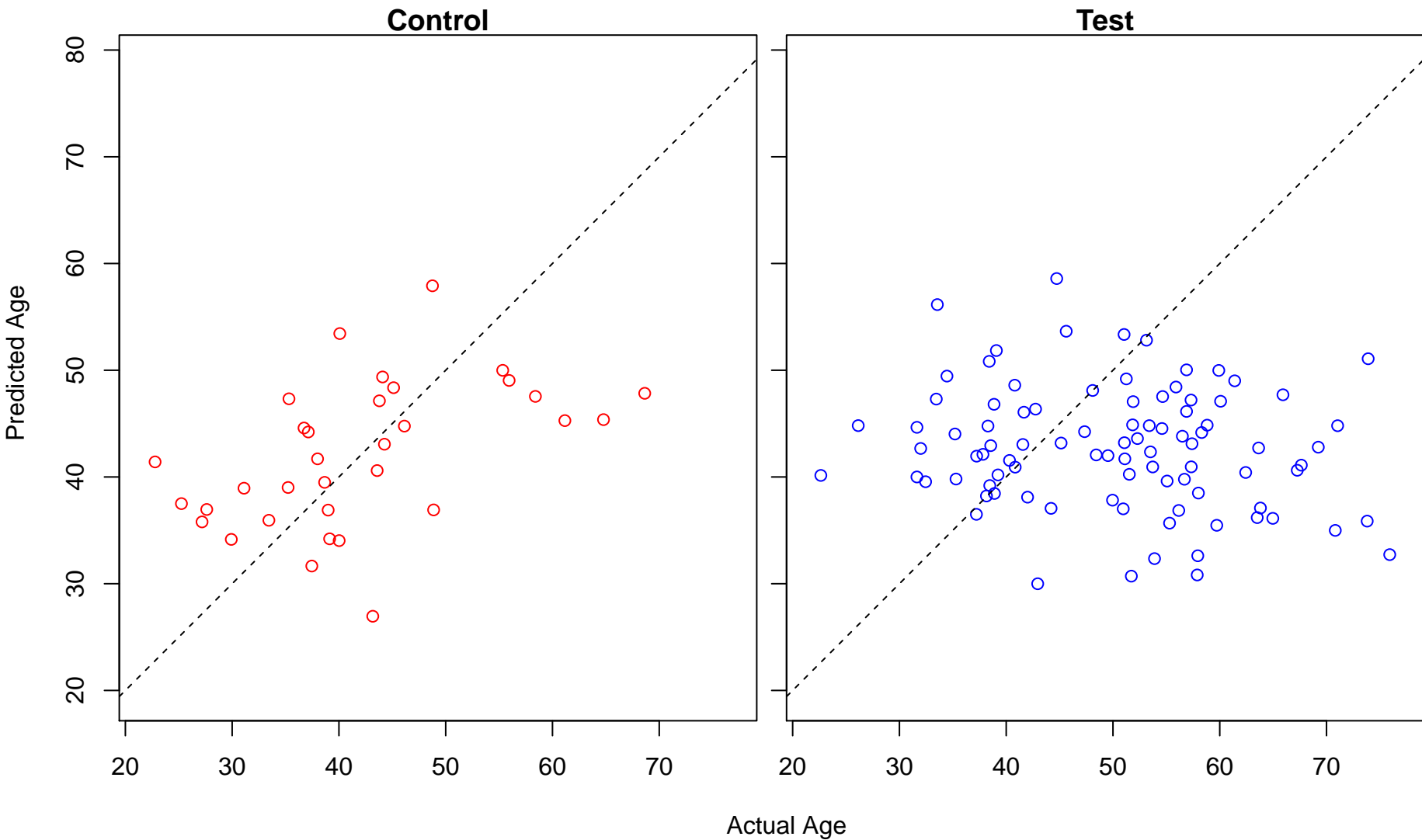
regulation of intrinsic apoptotic signaling pathway (Score: 0.858666)



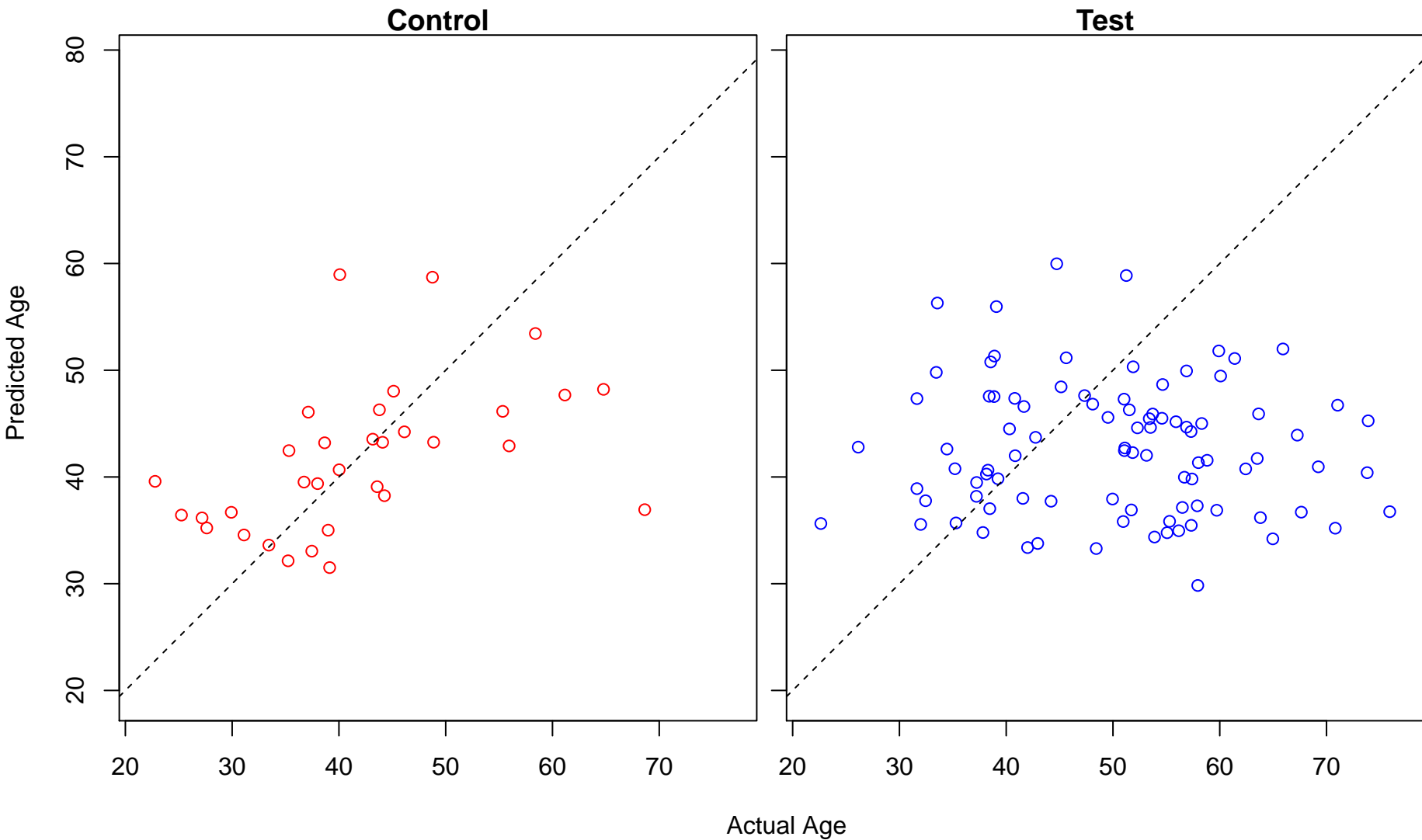
very long-chain fatty acid metabolic process (Score: 0.857131)



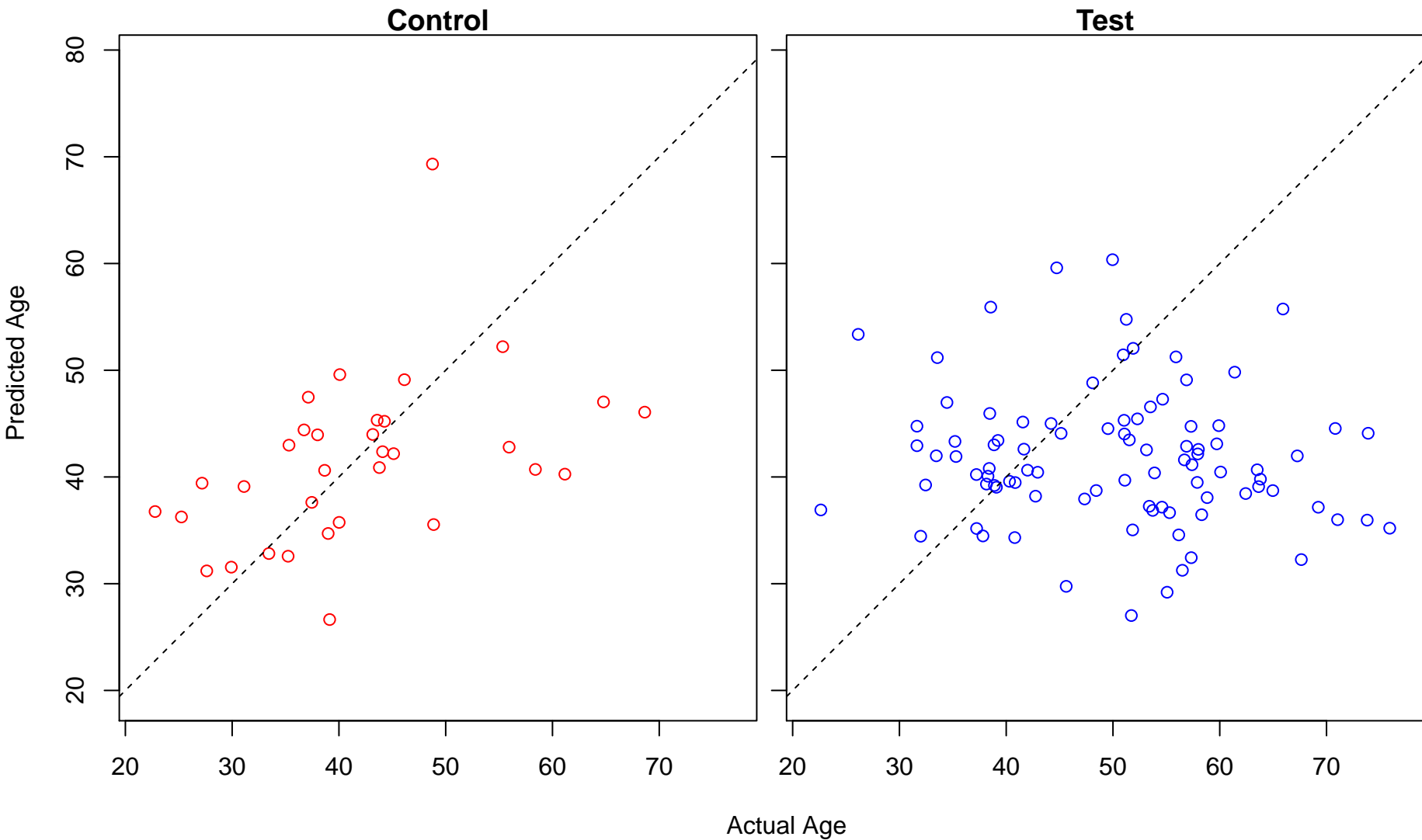
regulation of epidermal growth factor-activated receptor activity (Score: 0.855877)



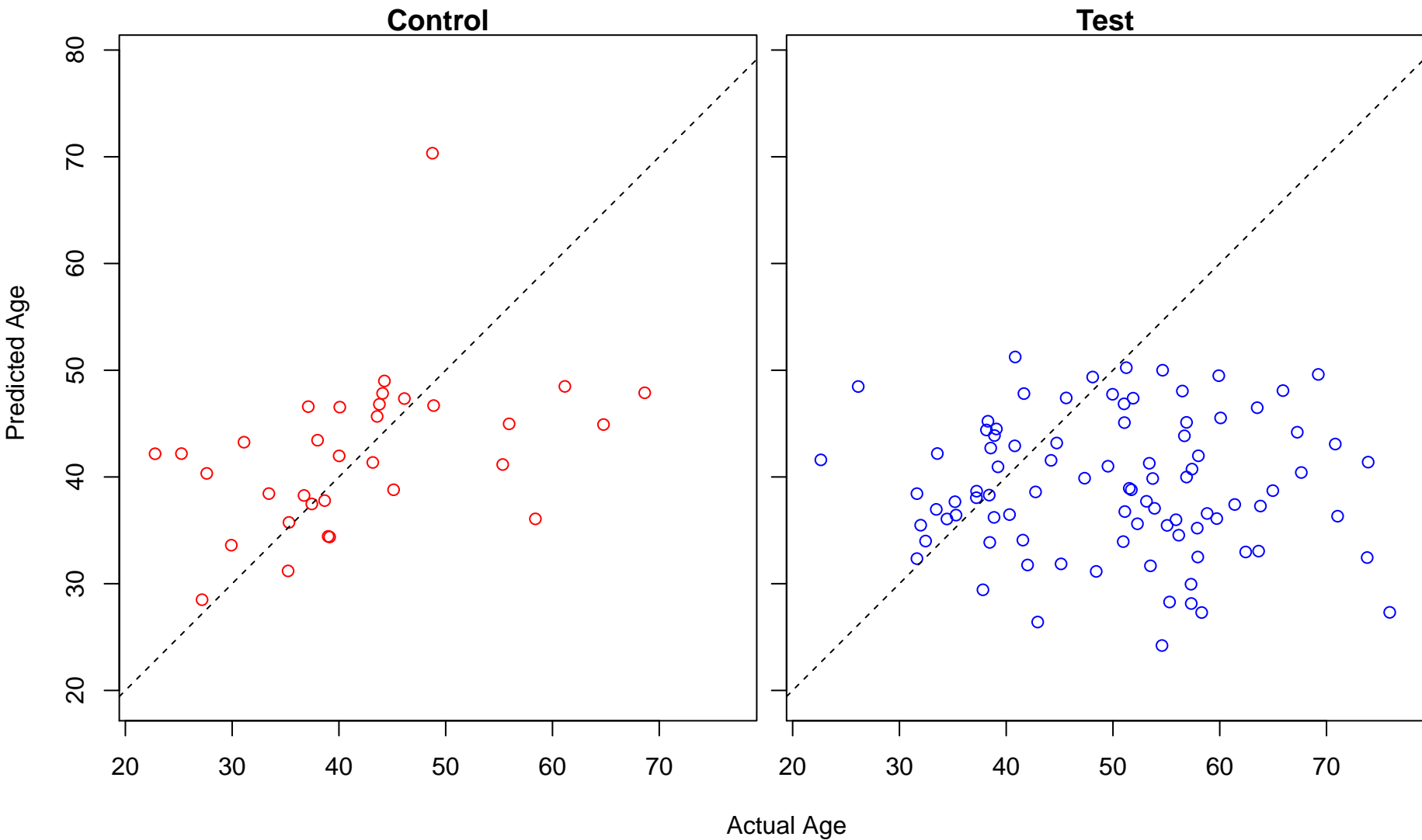
glycolipid metabolic process (Score: 0.855121)



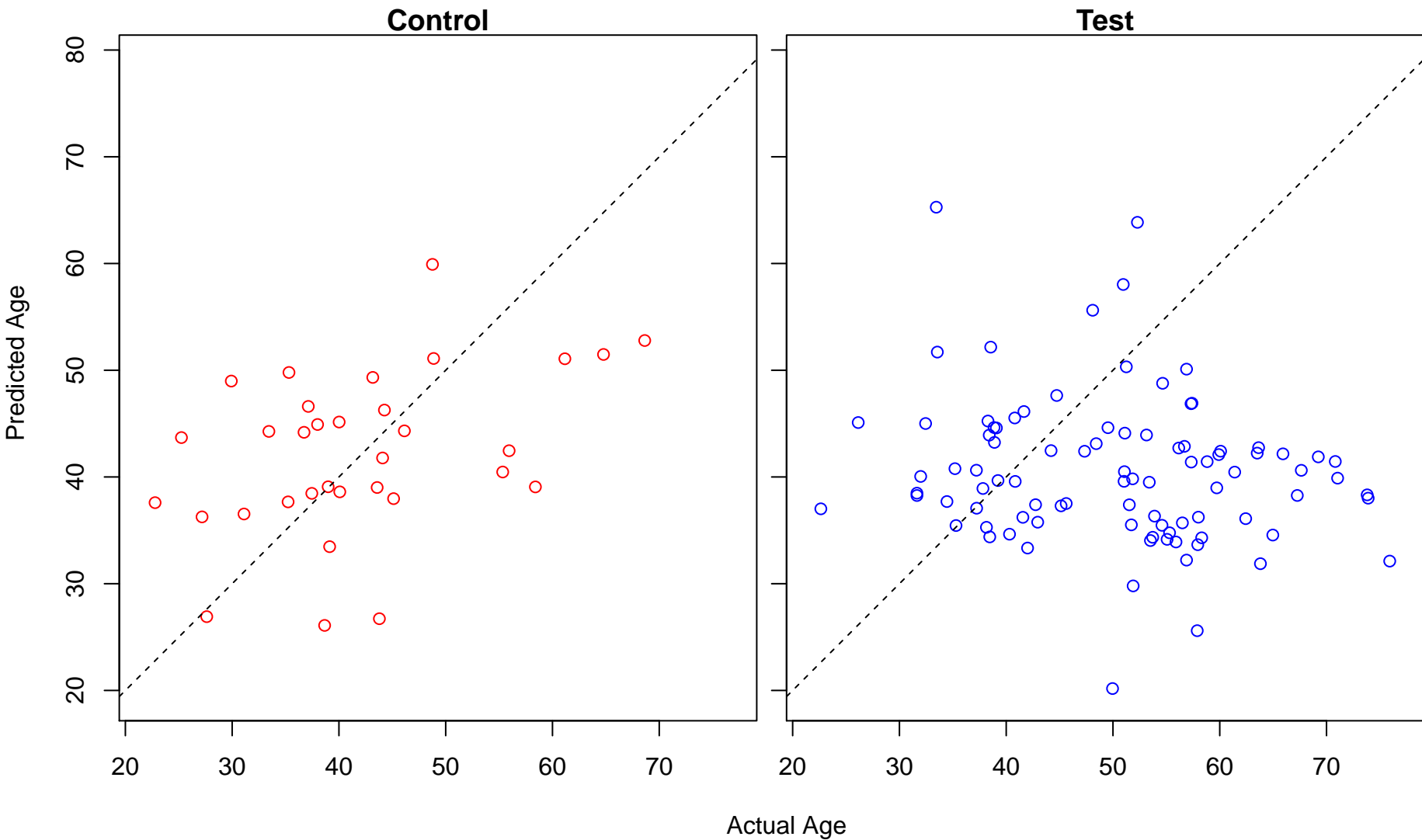
DNA integrity checkpoint (Score: 0.854144)



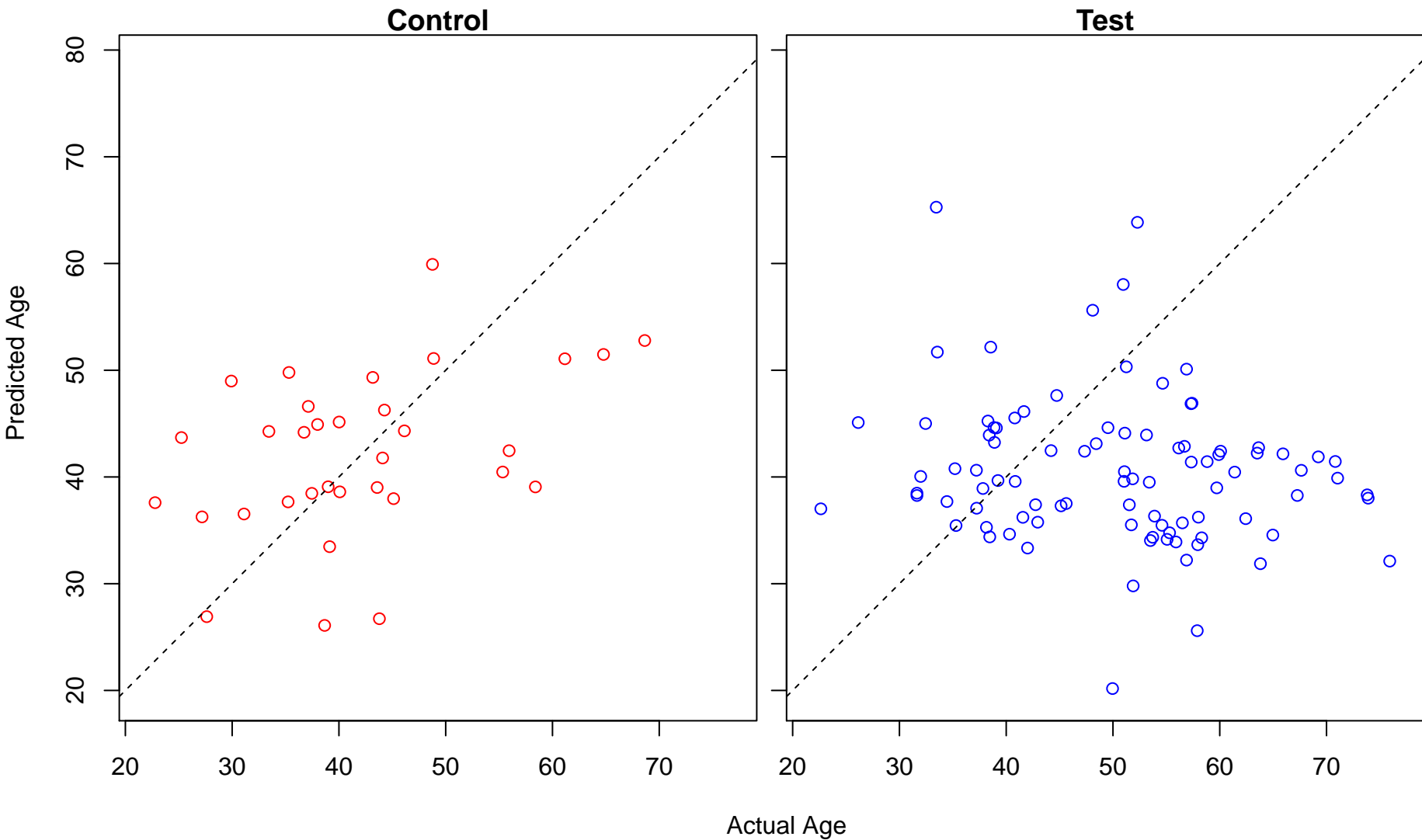
UV protection (Score: 0.853802)



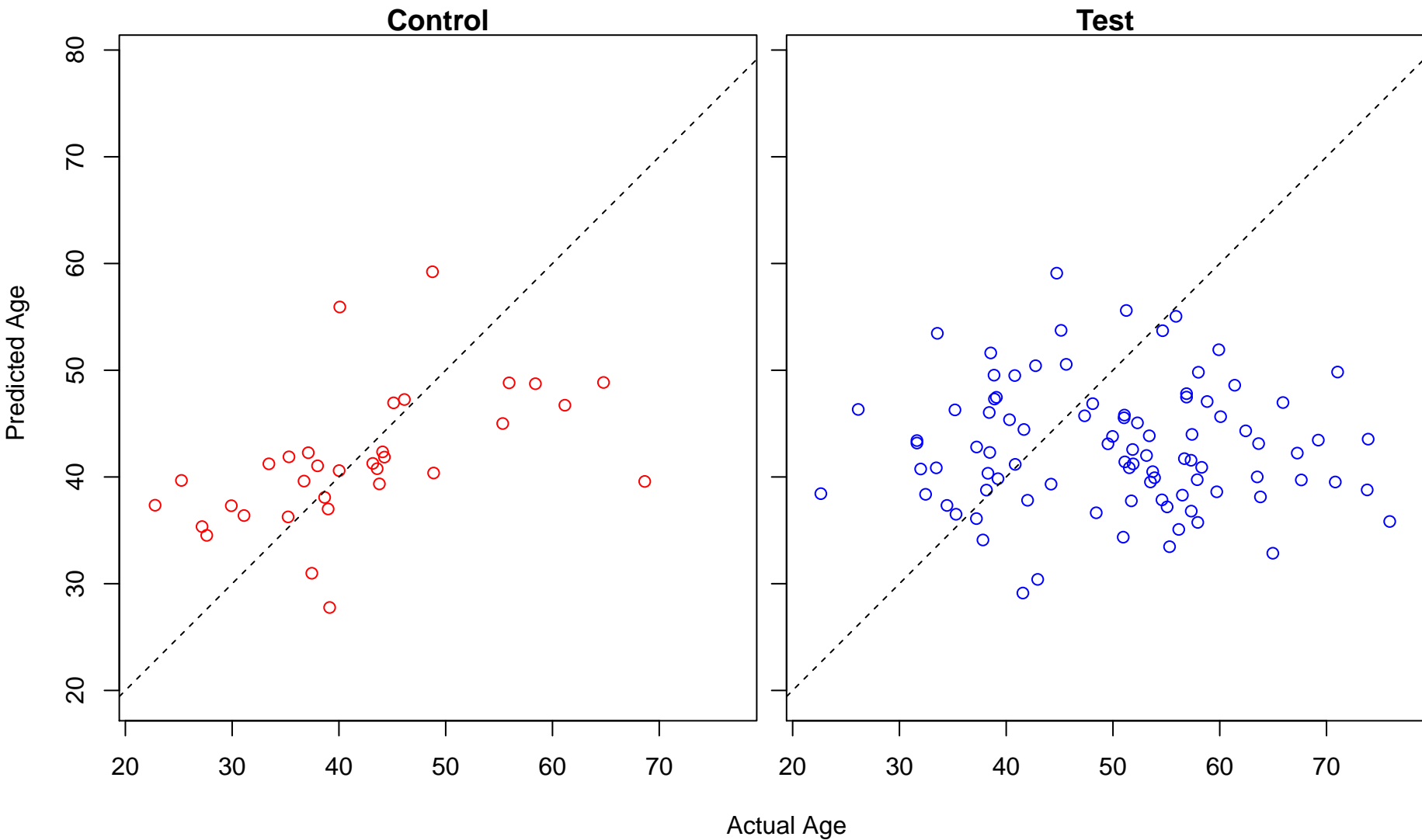
dolichyl diphosphate biosynthetic process (Score: 0.853700)



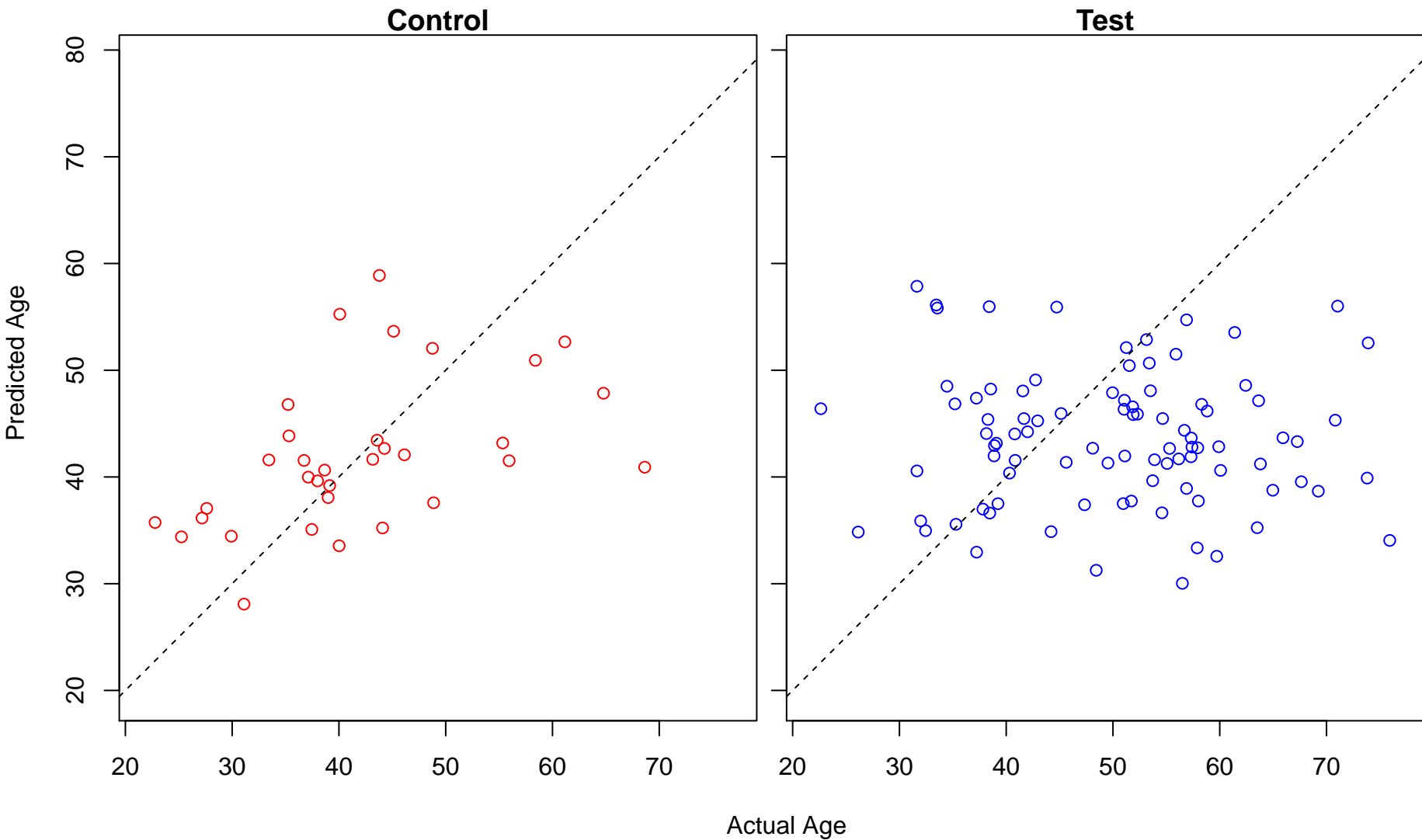
dolichyl diphosphate metabolic process (Score: 0.853700)



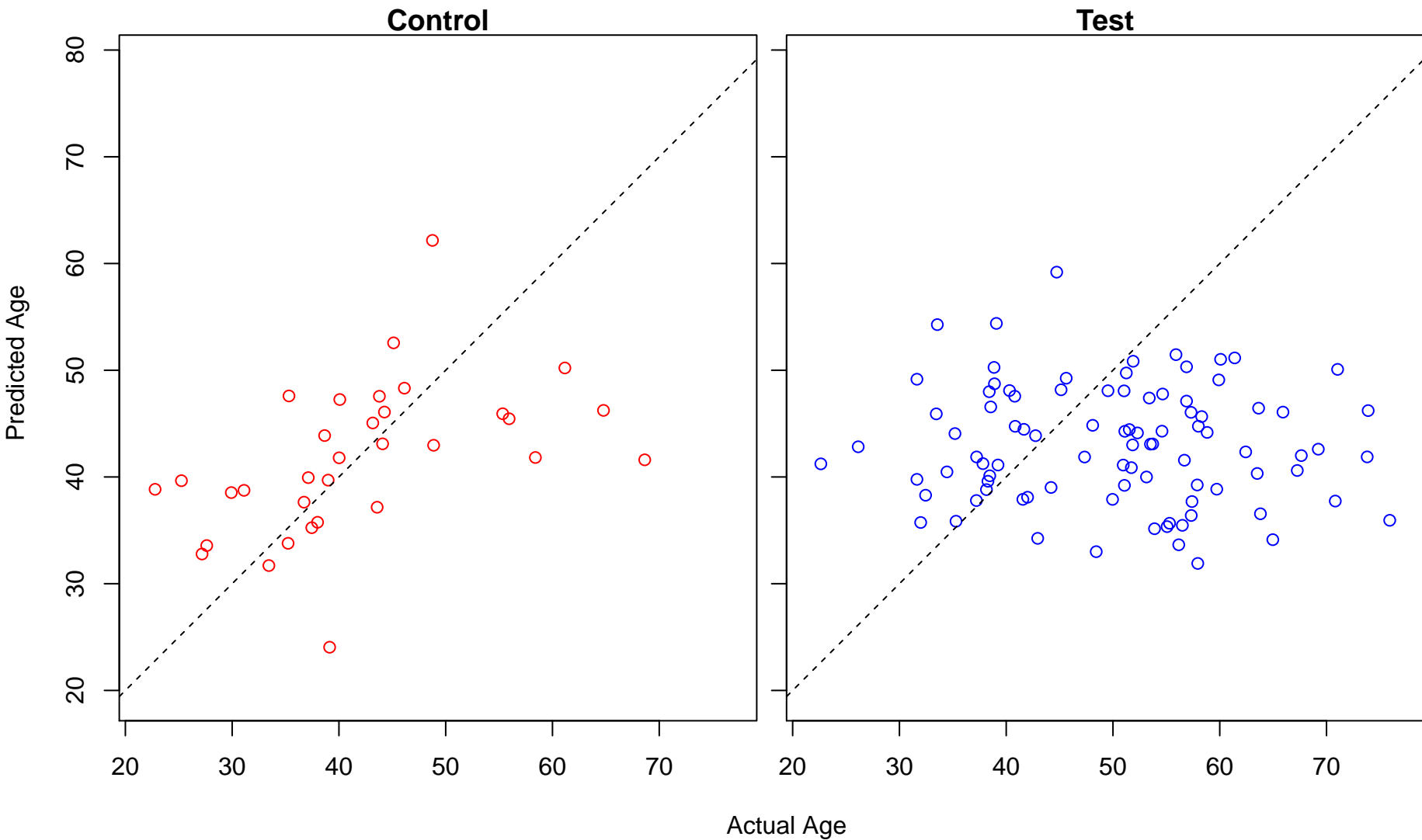
regulation of ion transport (Score: 0.853475)



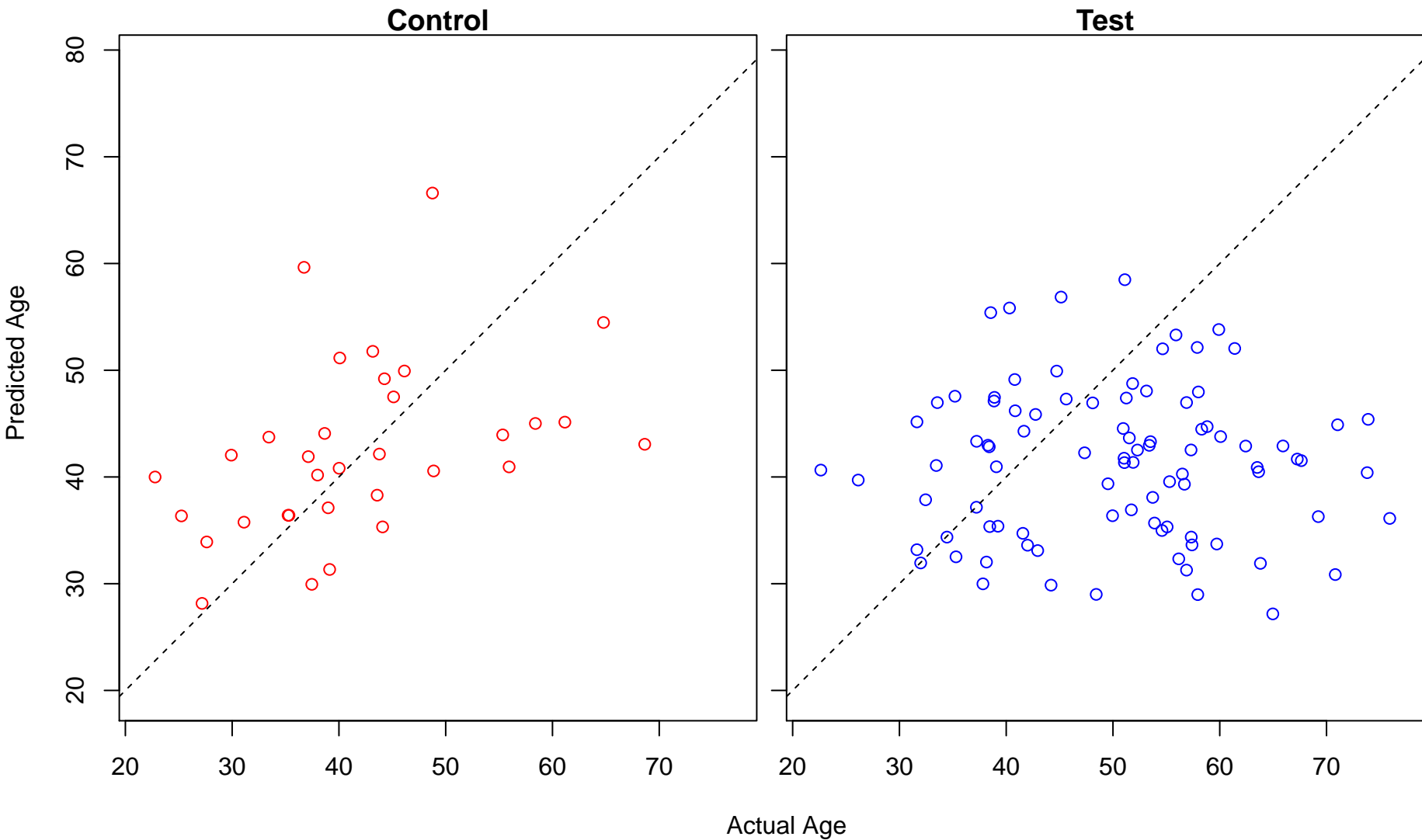
phosphatidylcholine biosynthetic process (Score: 0.852817)



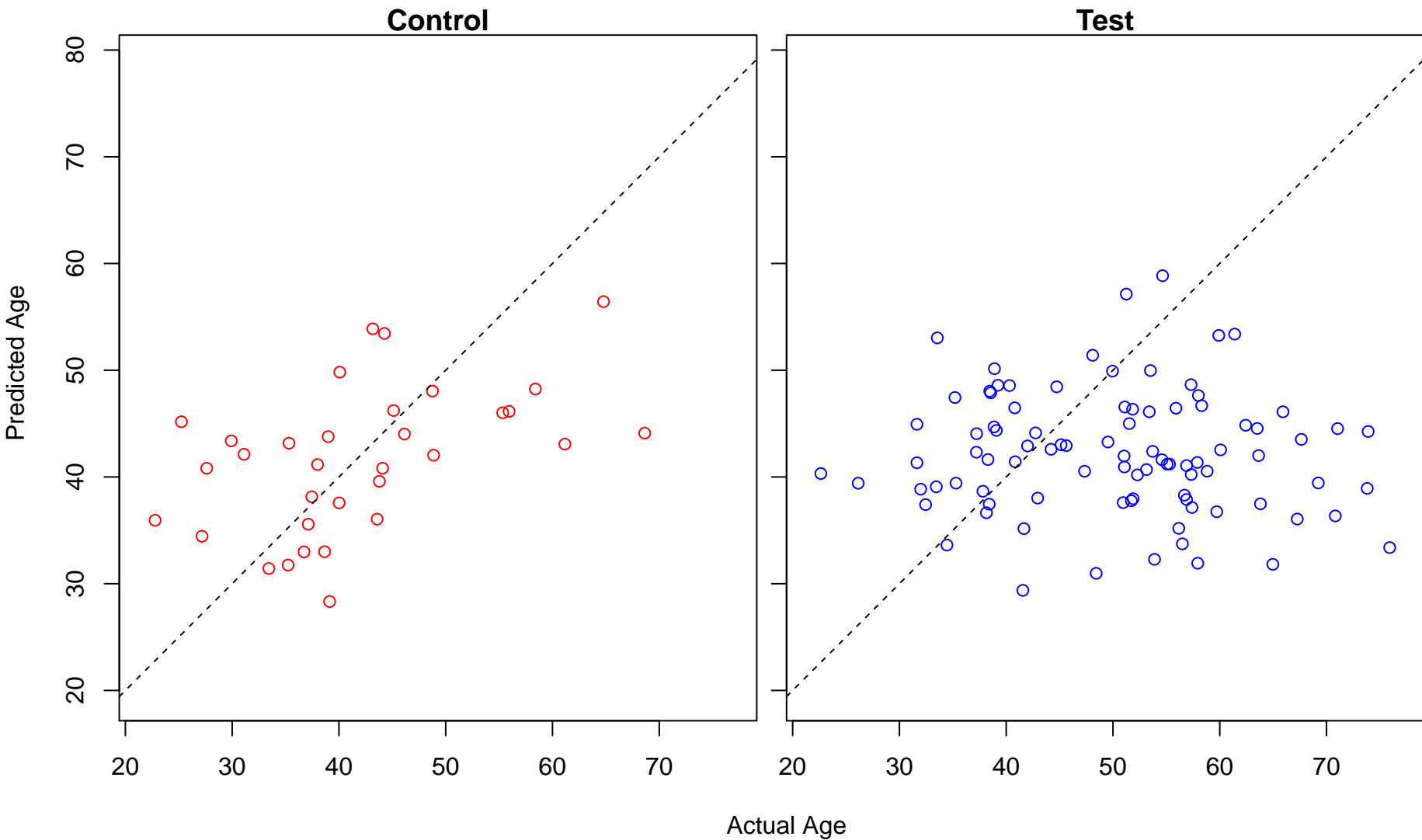
telomere maintenance via semi-conservative replication (Score: 0.852572)



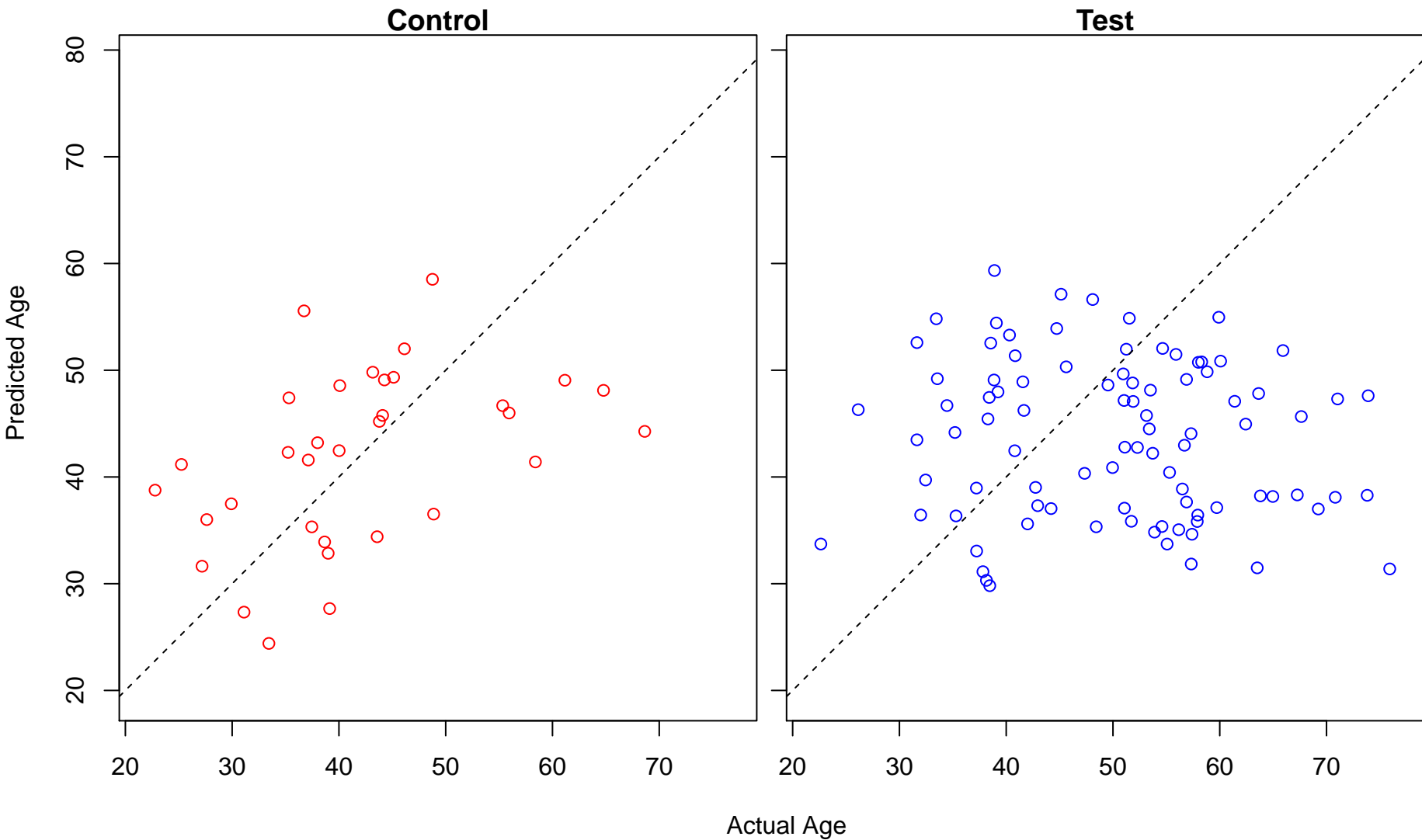
purine deoxyribonucleotide metabolic process (Score: 0.851558)



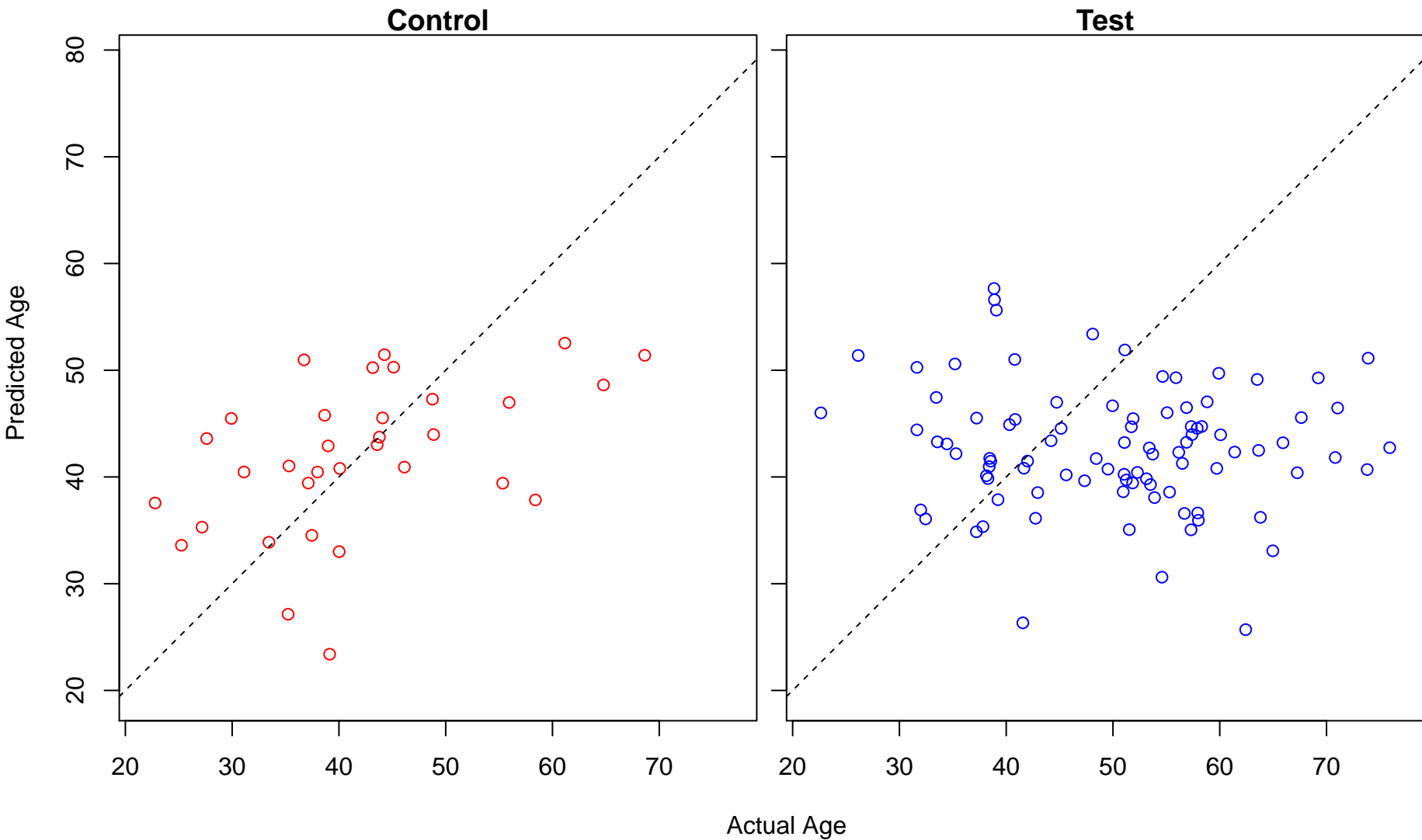
bile acid metabolic process (Score: 0.851287)



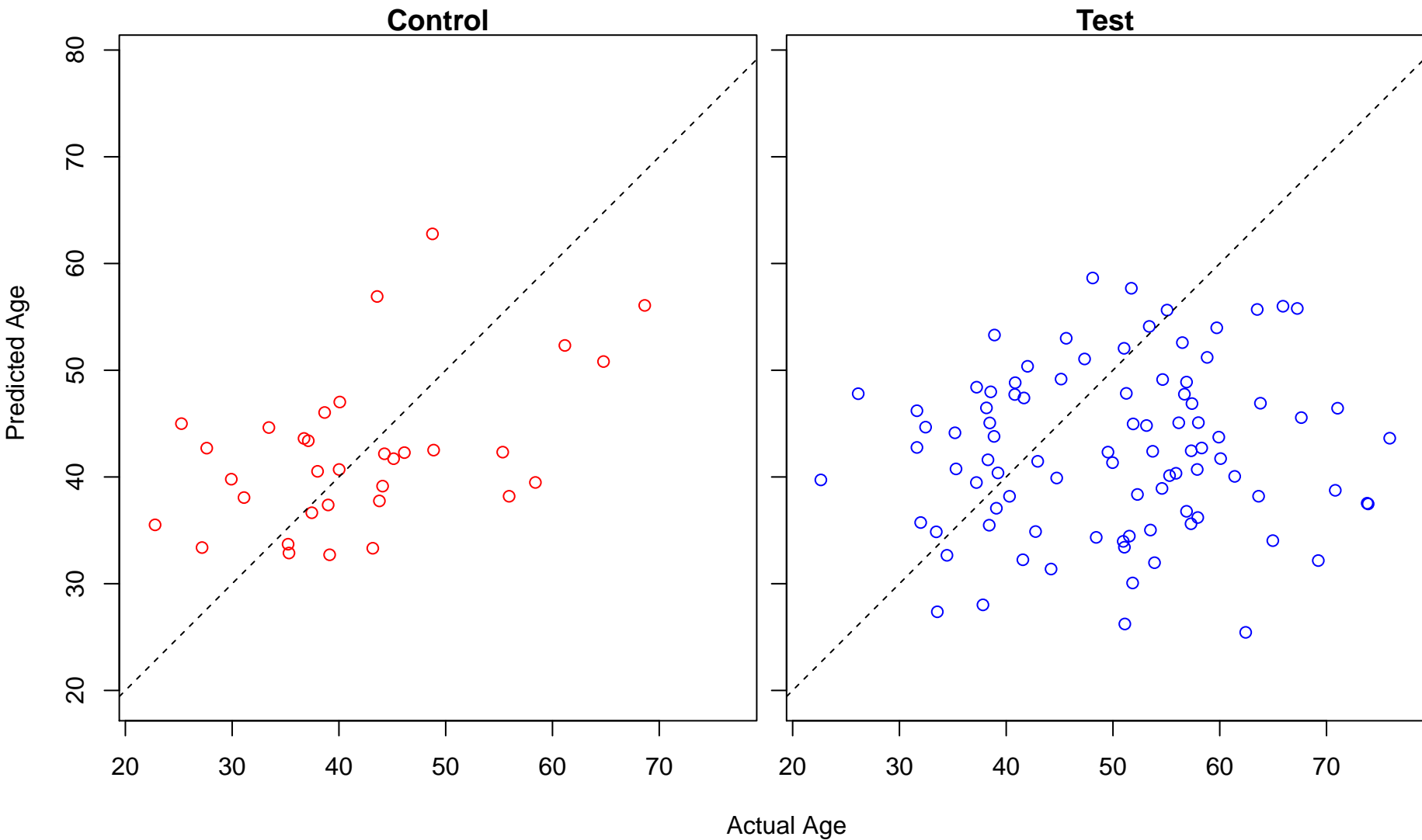
cellular response to fluid shear stress (Score: 0.850996)



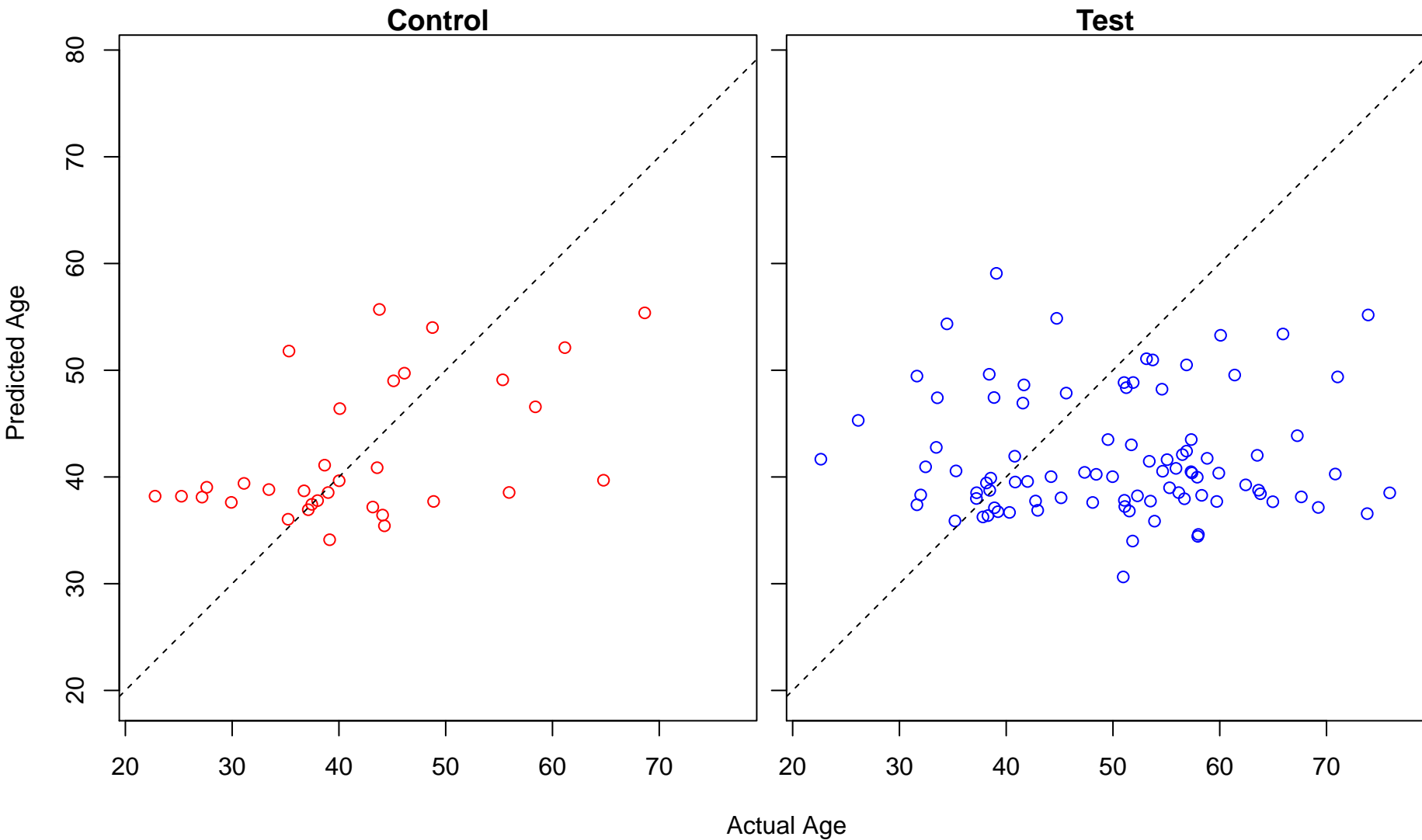
alkaloid metabolic process (Score: 0.849455)



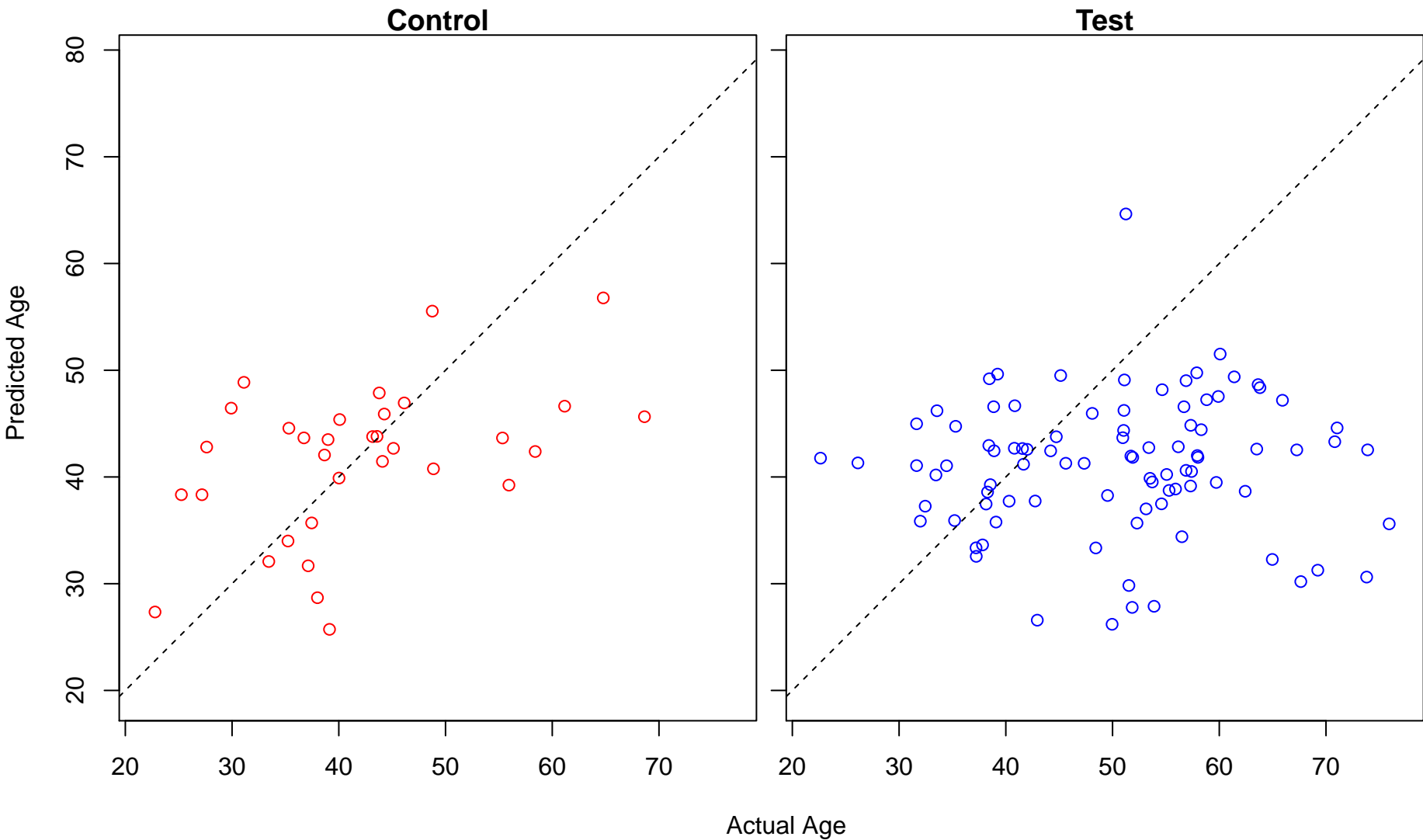
positive regulation of intracellular estrogen receptor signaling pathway (Score: 0.849290)



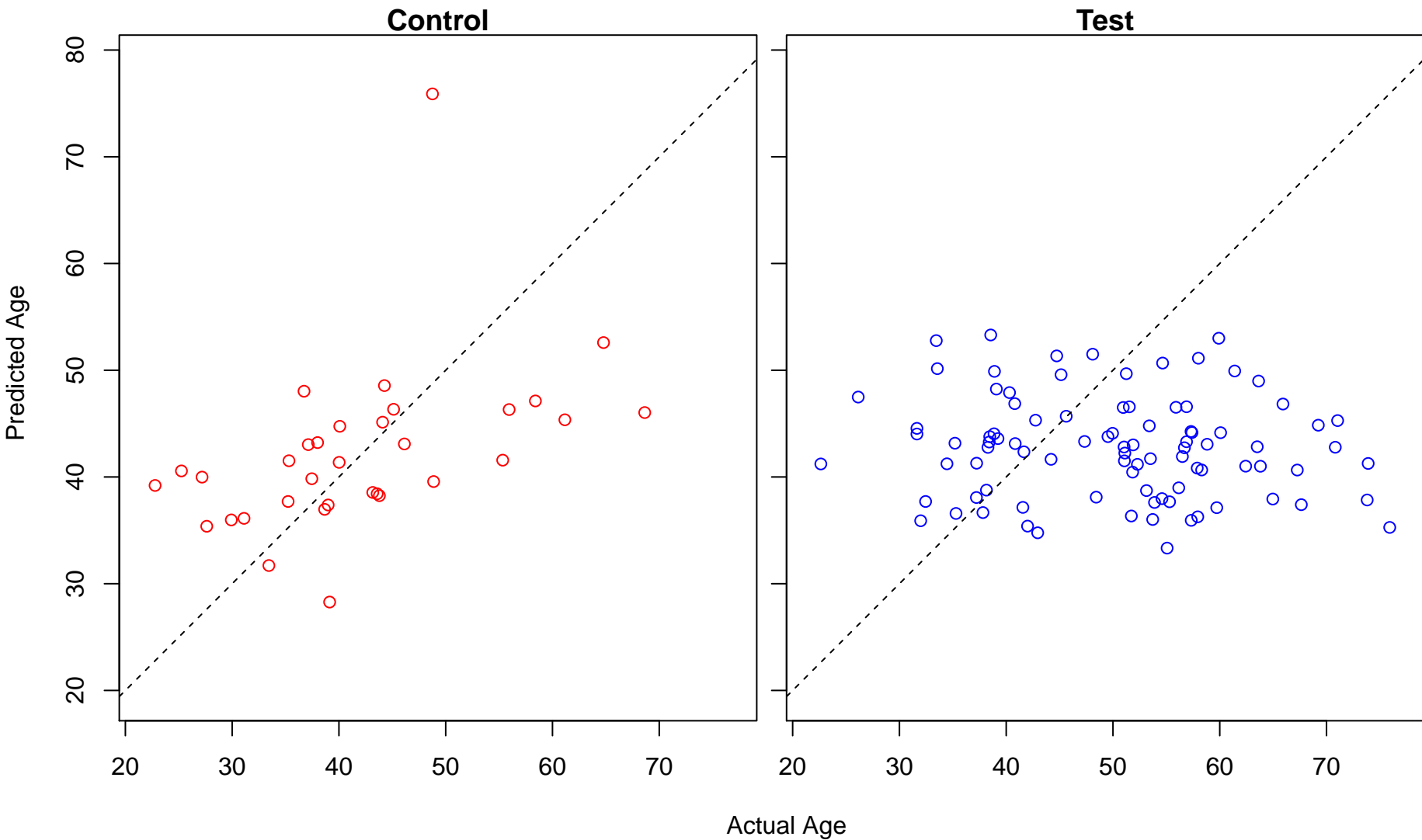
regulation of cytoplasmic mRNA processing body assembly (Score: 0.848532)



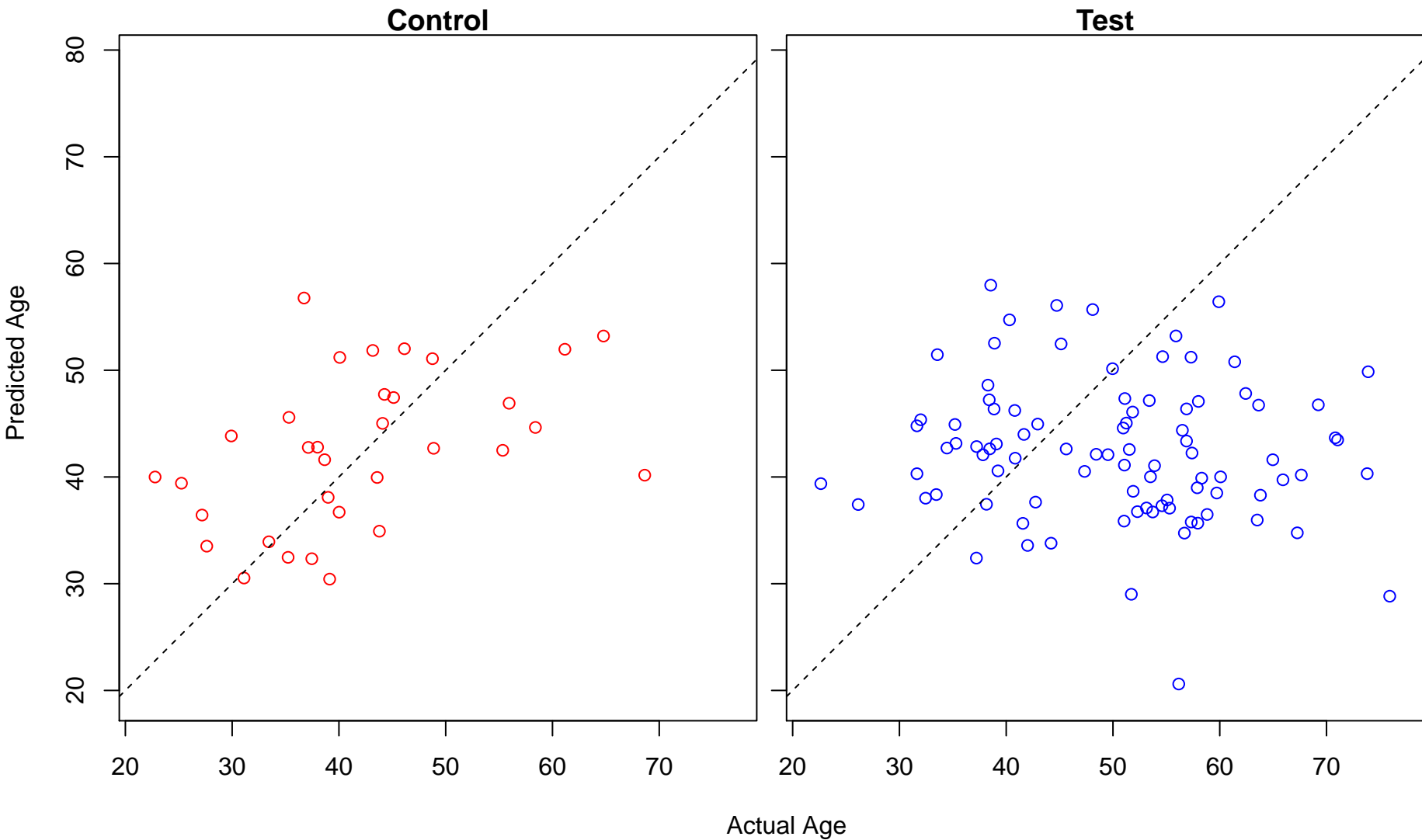
phosphatidylserine metabolic process (Score: 0.848438)



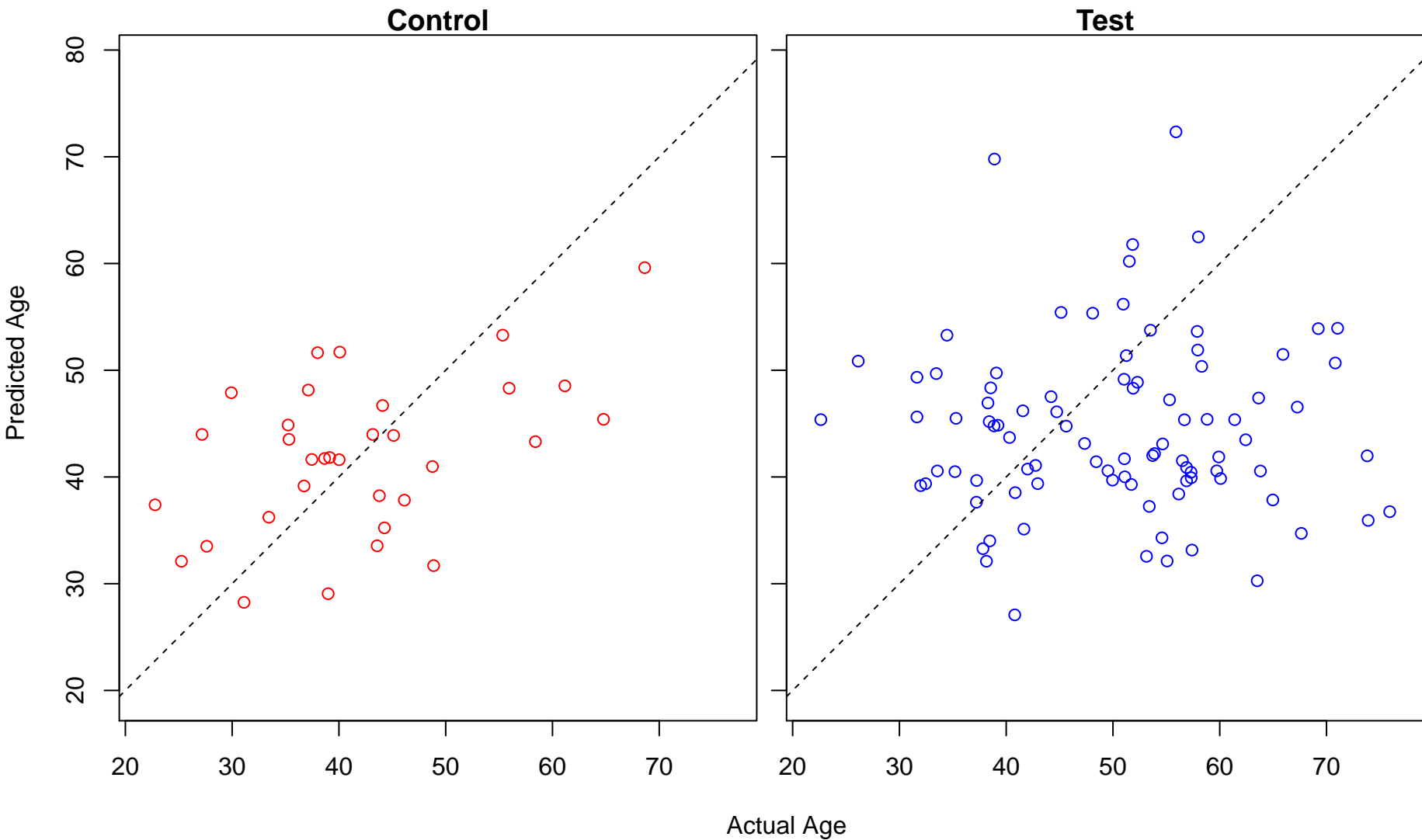
protein targeting to mitochondrion (Score: 0.848095)



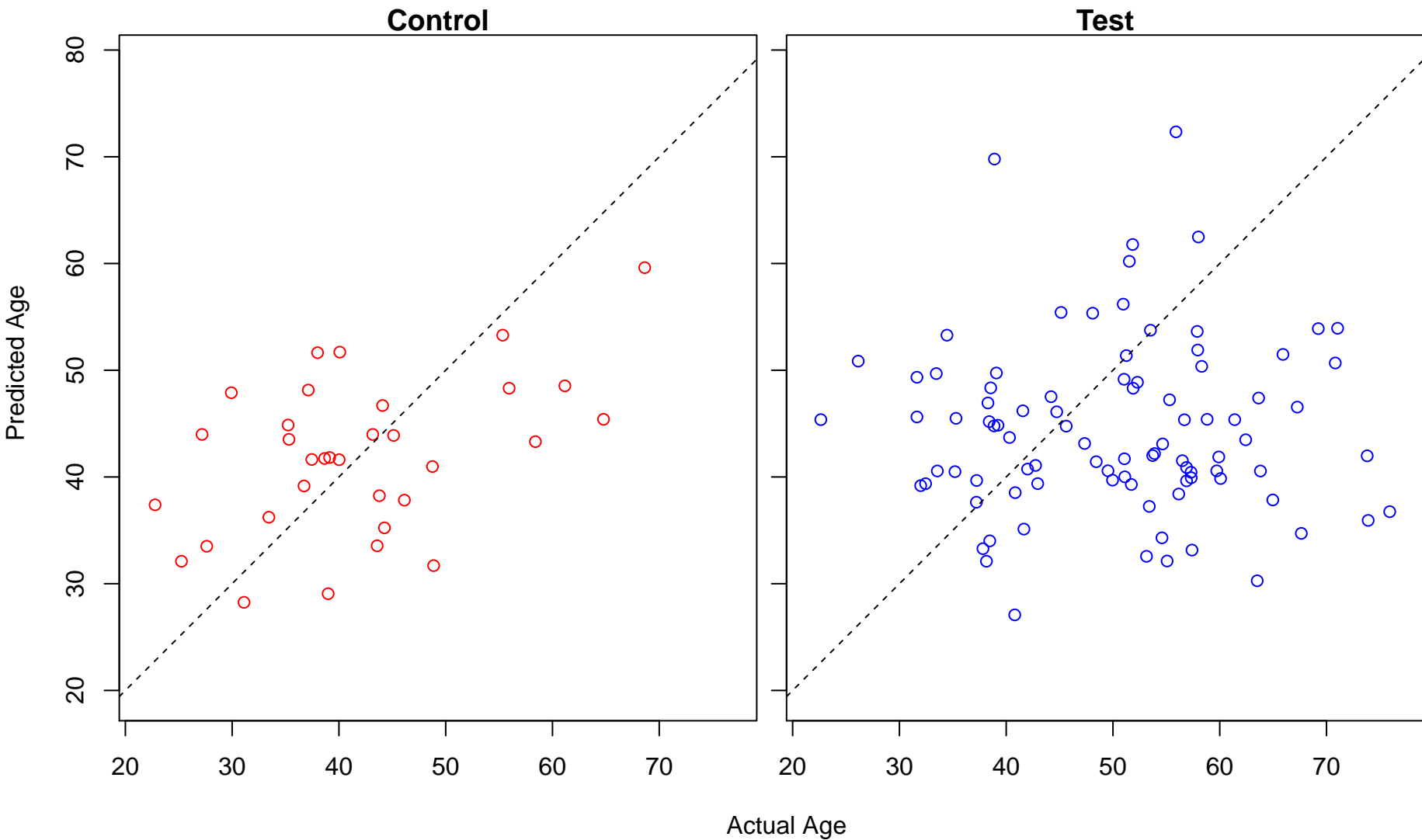
N-acetylglucosamine metabolic process (Score: 0.846416)



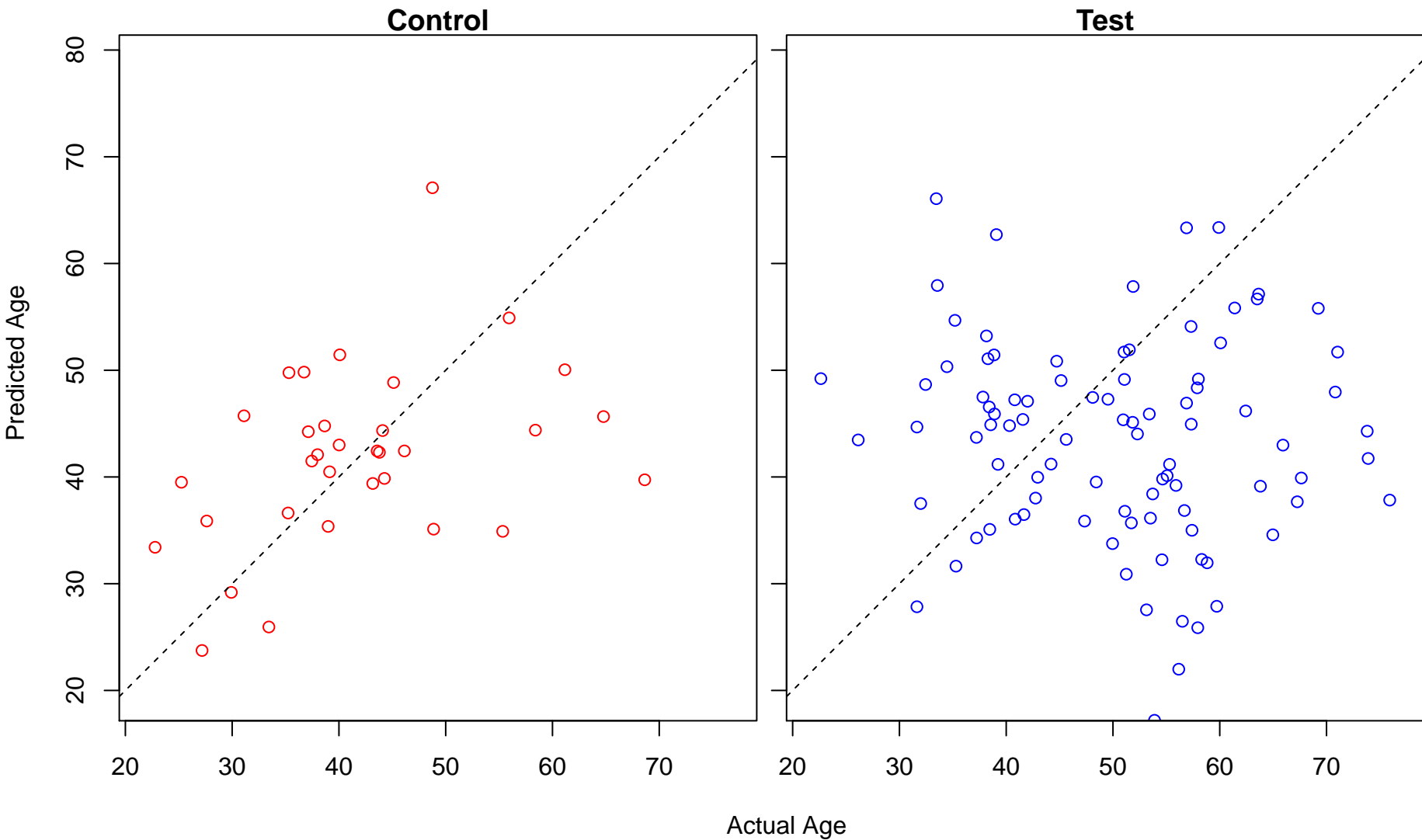
renal system vasculature morphogenesis (Score: 0.846259)



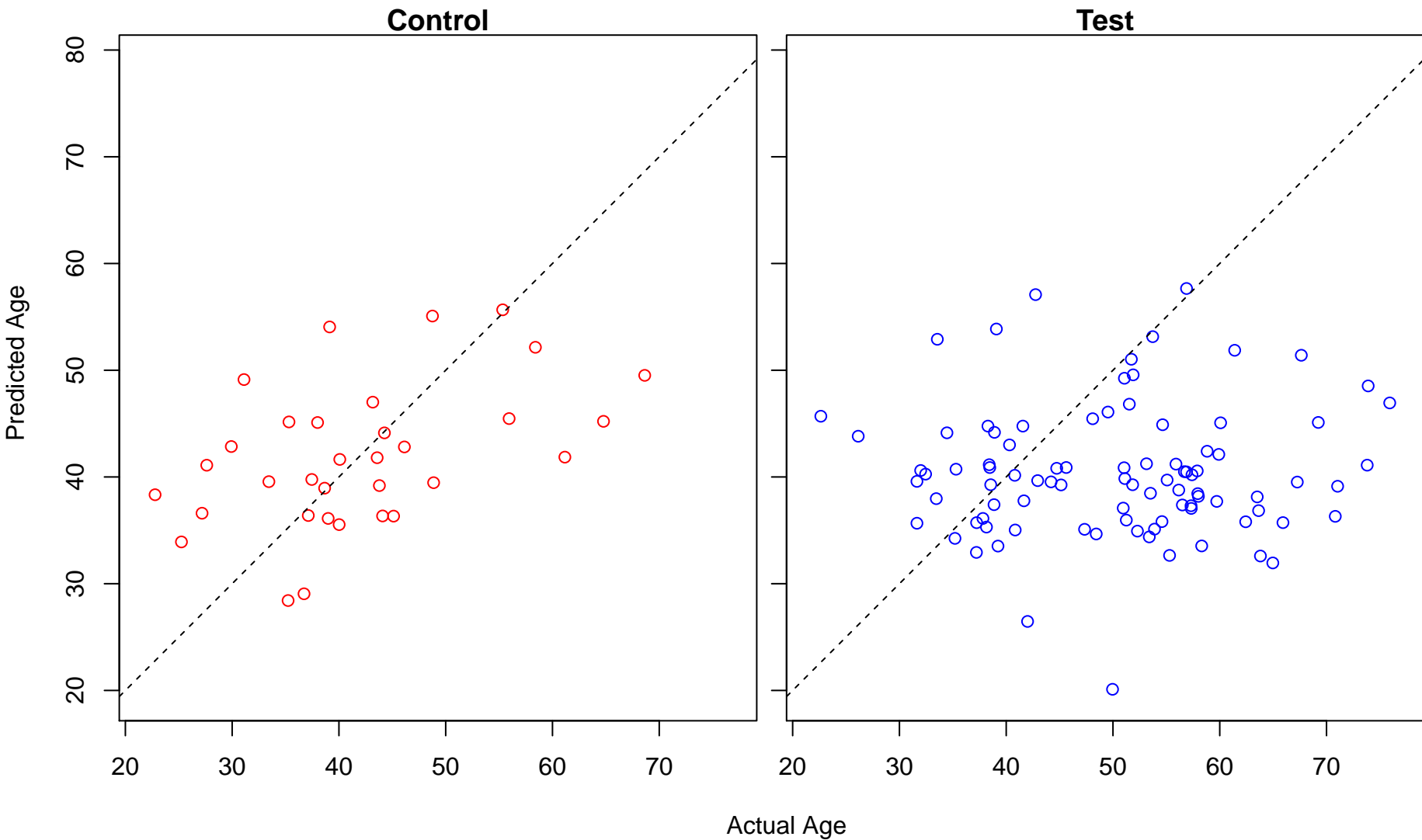
kidney vasculature morphogenesis (Score: 0.846259)



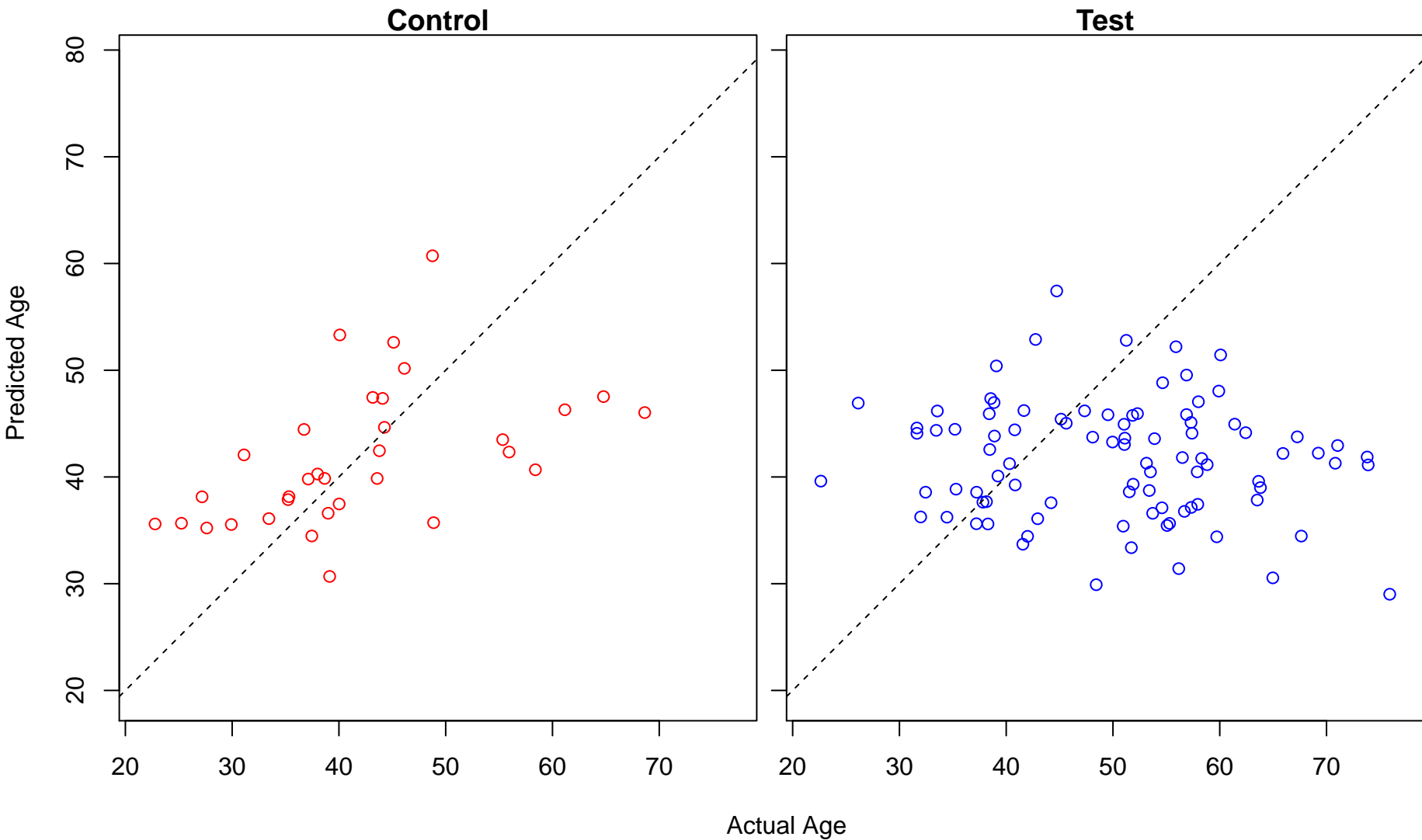
xenobiotic metabolic process (Score: 0.845519)



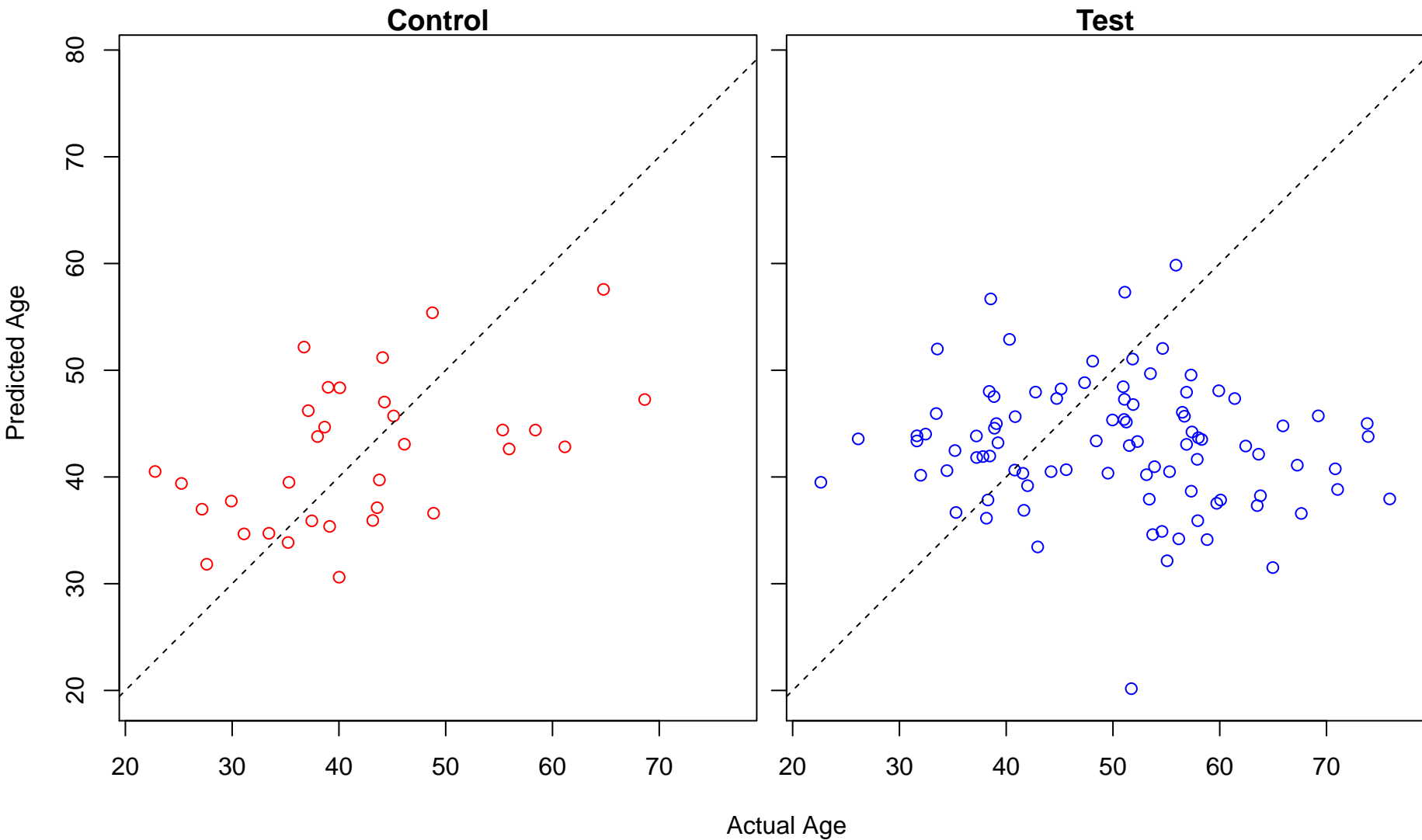
Notch signaling involved in heart development (Score: 0.844705)



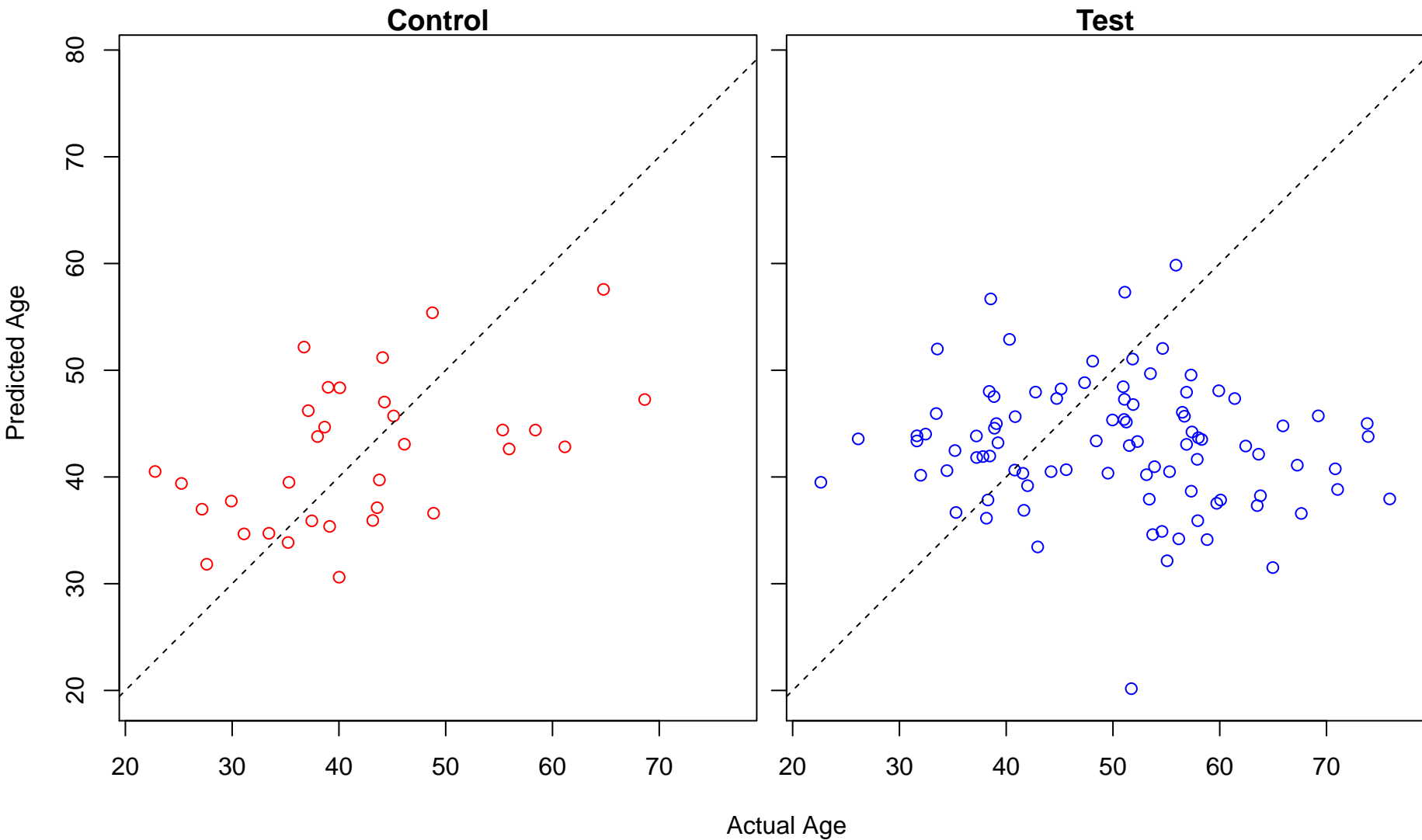
regulation of membrane potential (Score: 0.844622)



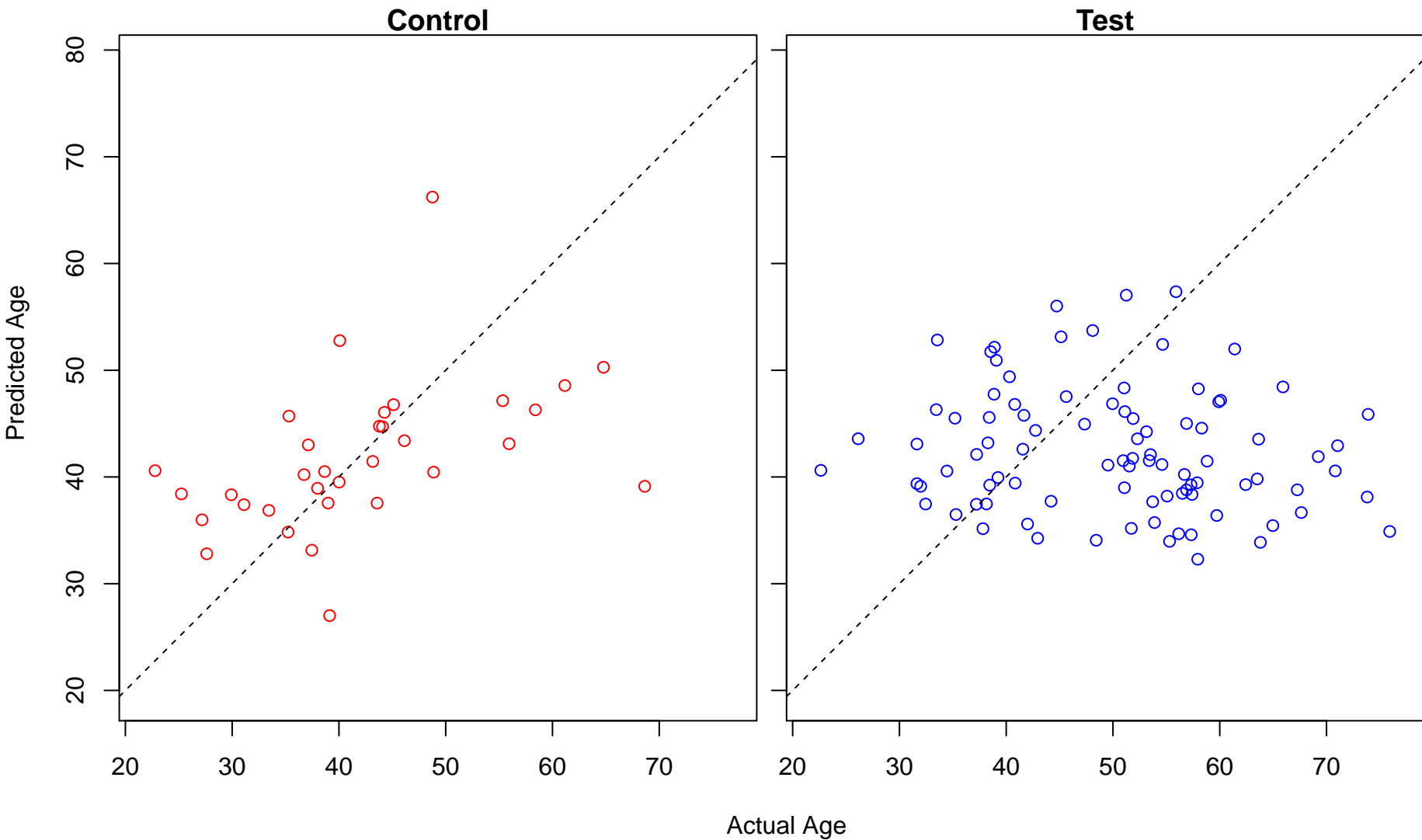
negative regulation of transforming growth factor beta1 production (Score: 0.84325)



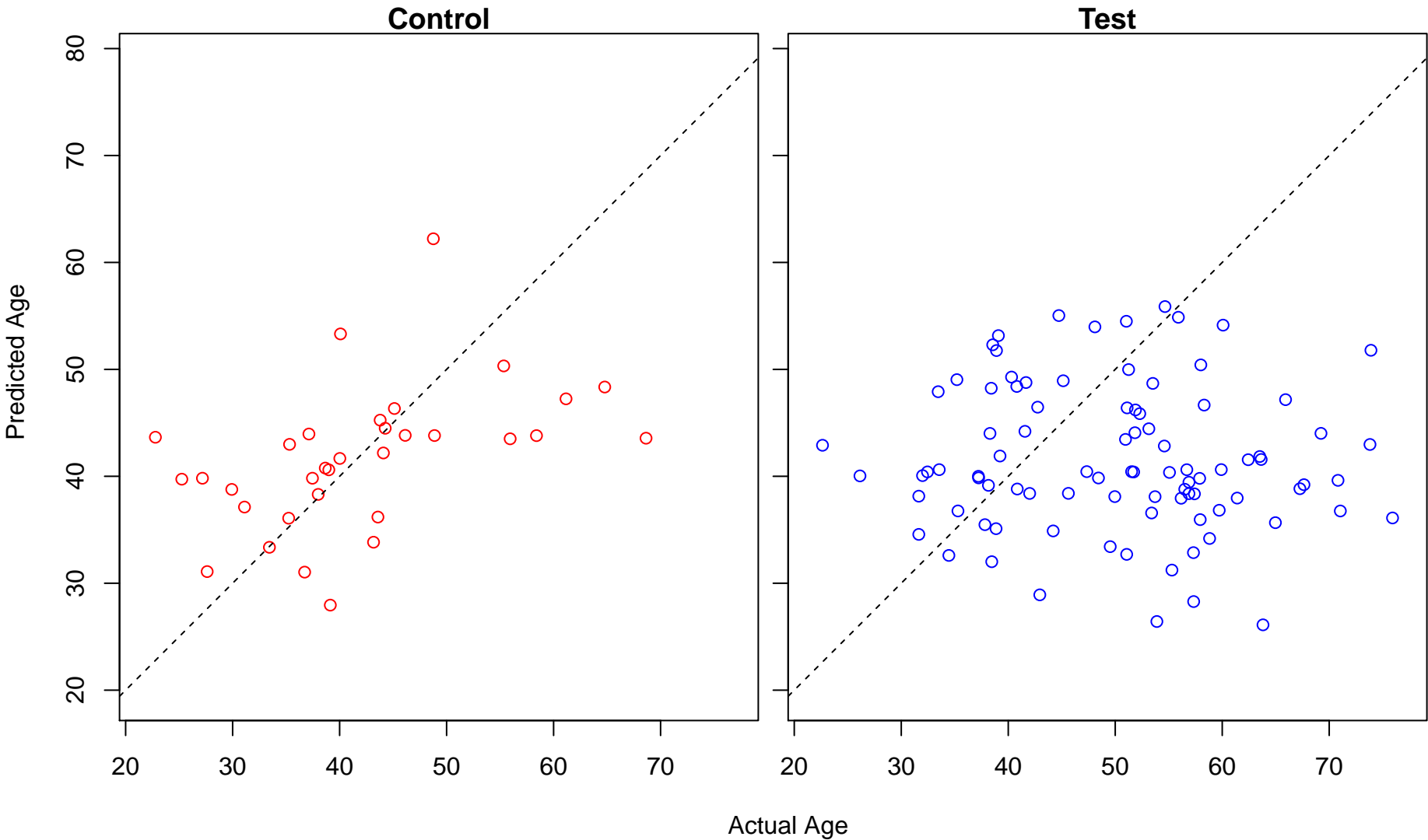
negative regulation of transforming growth factor beta production (Score: 0.843325)



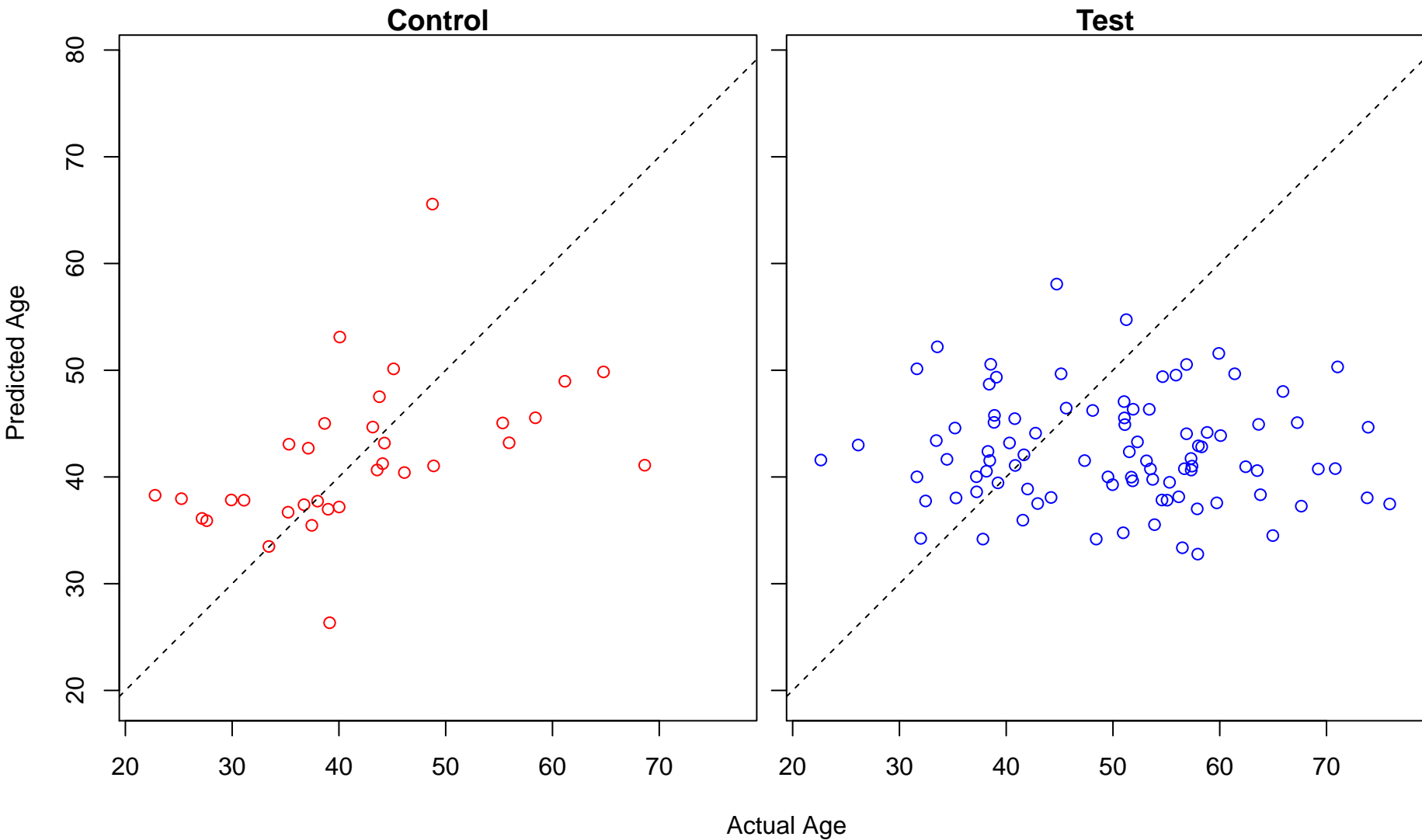
regulation of intracellular protein transport (Score: 0.843164)



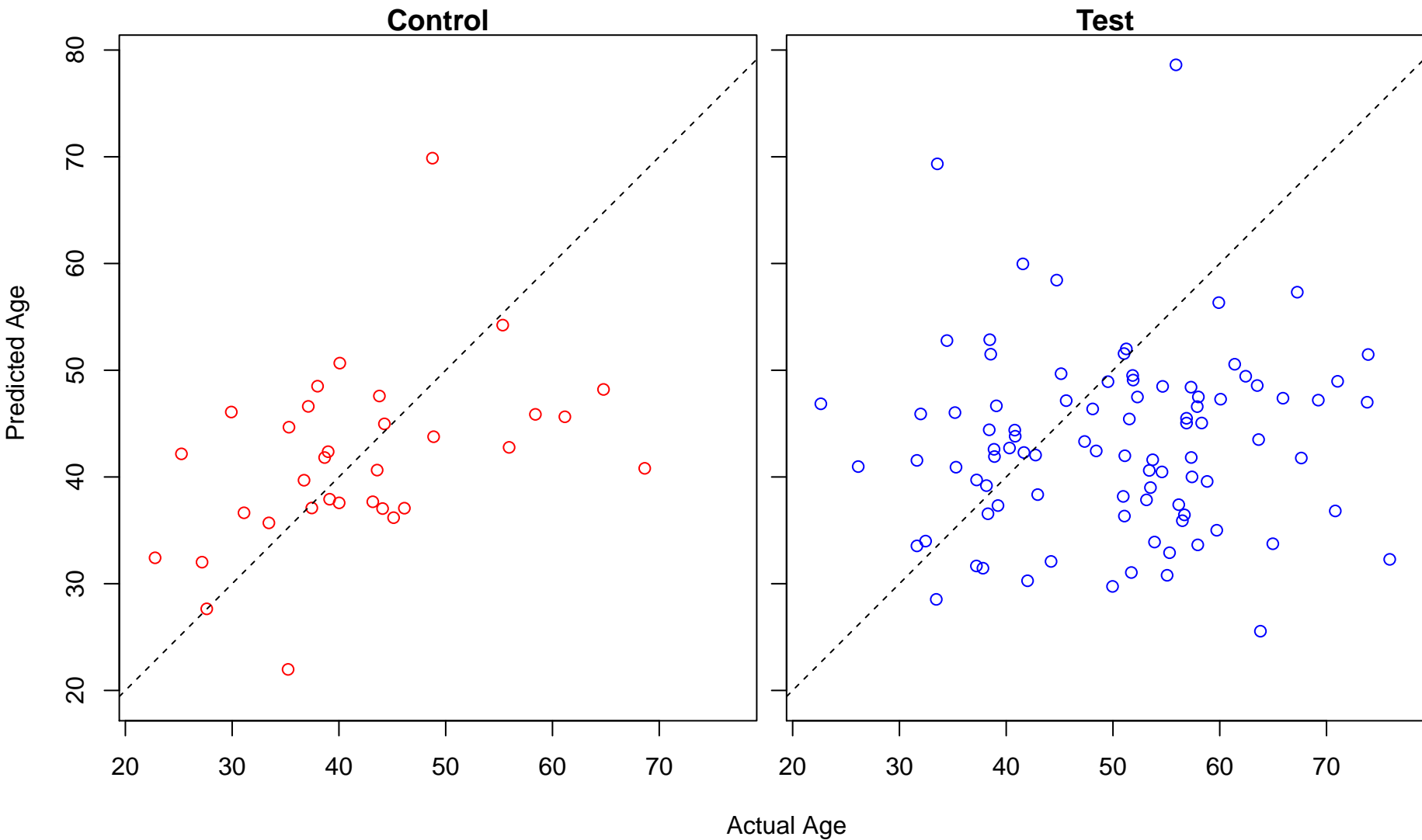
nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway (Score: 0.8423)



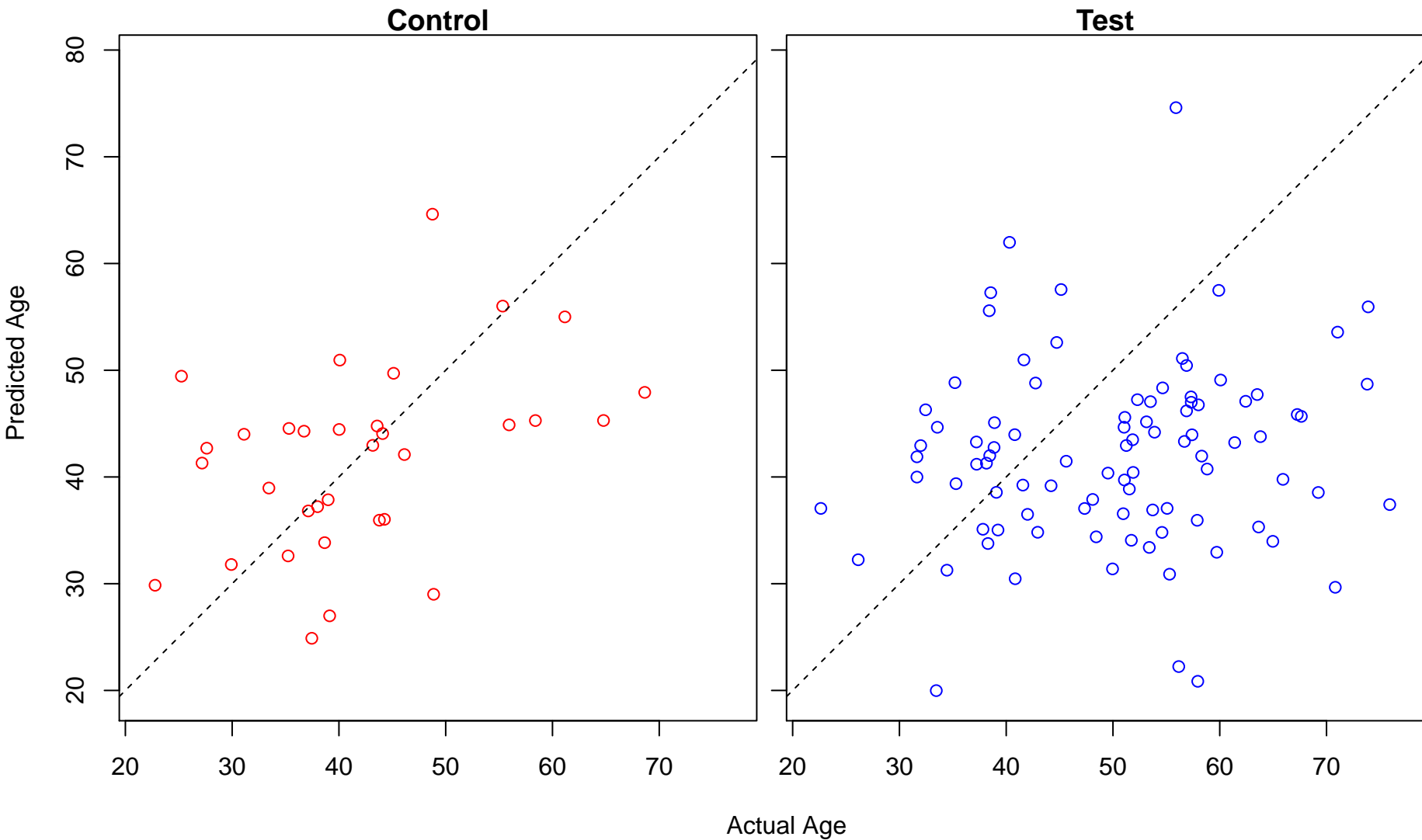
glycerophospholipid metabolic process (Score: 0.841444)



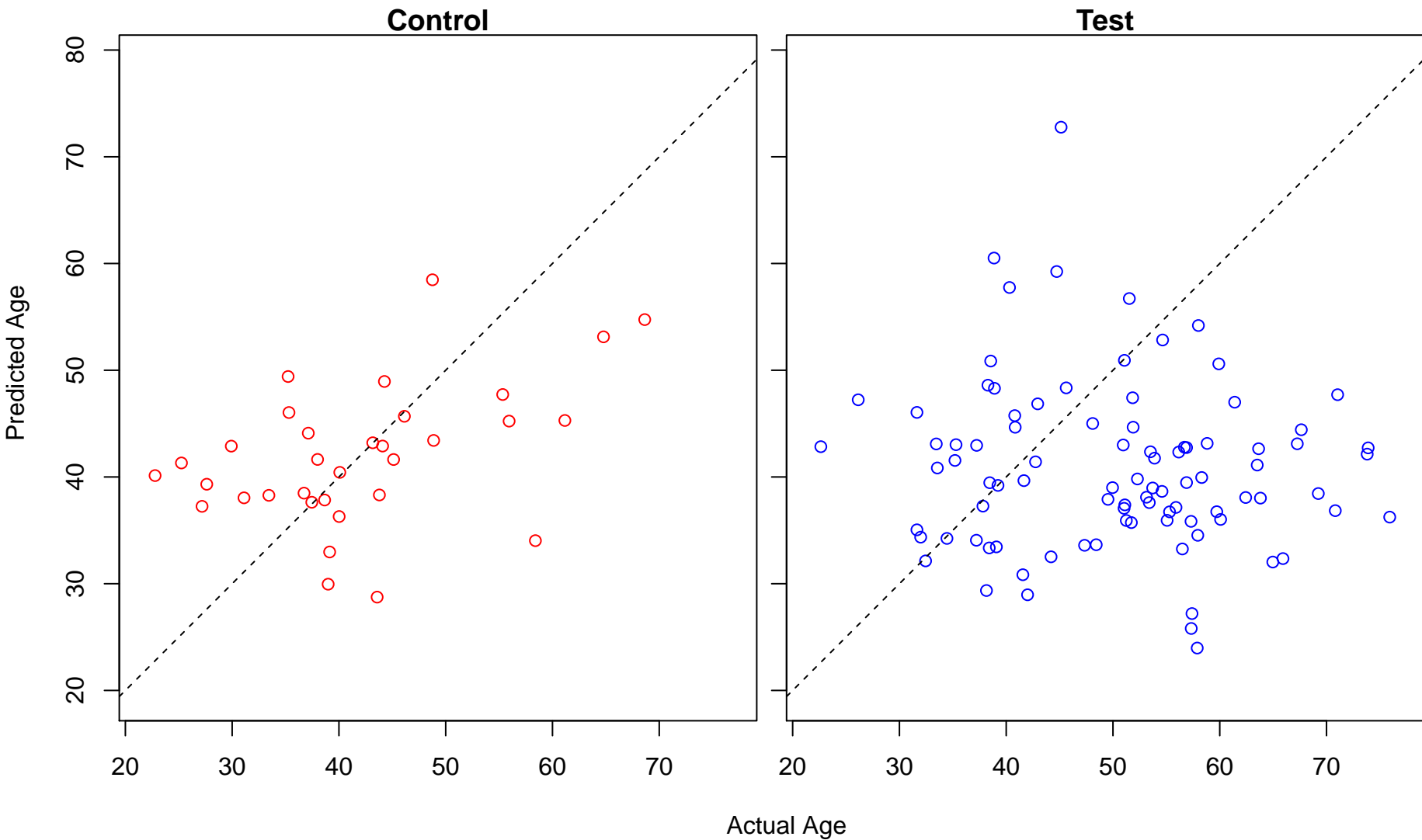
cell proliferation in forebrain (Score: 0.840462)



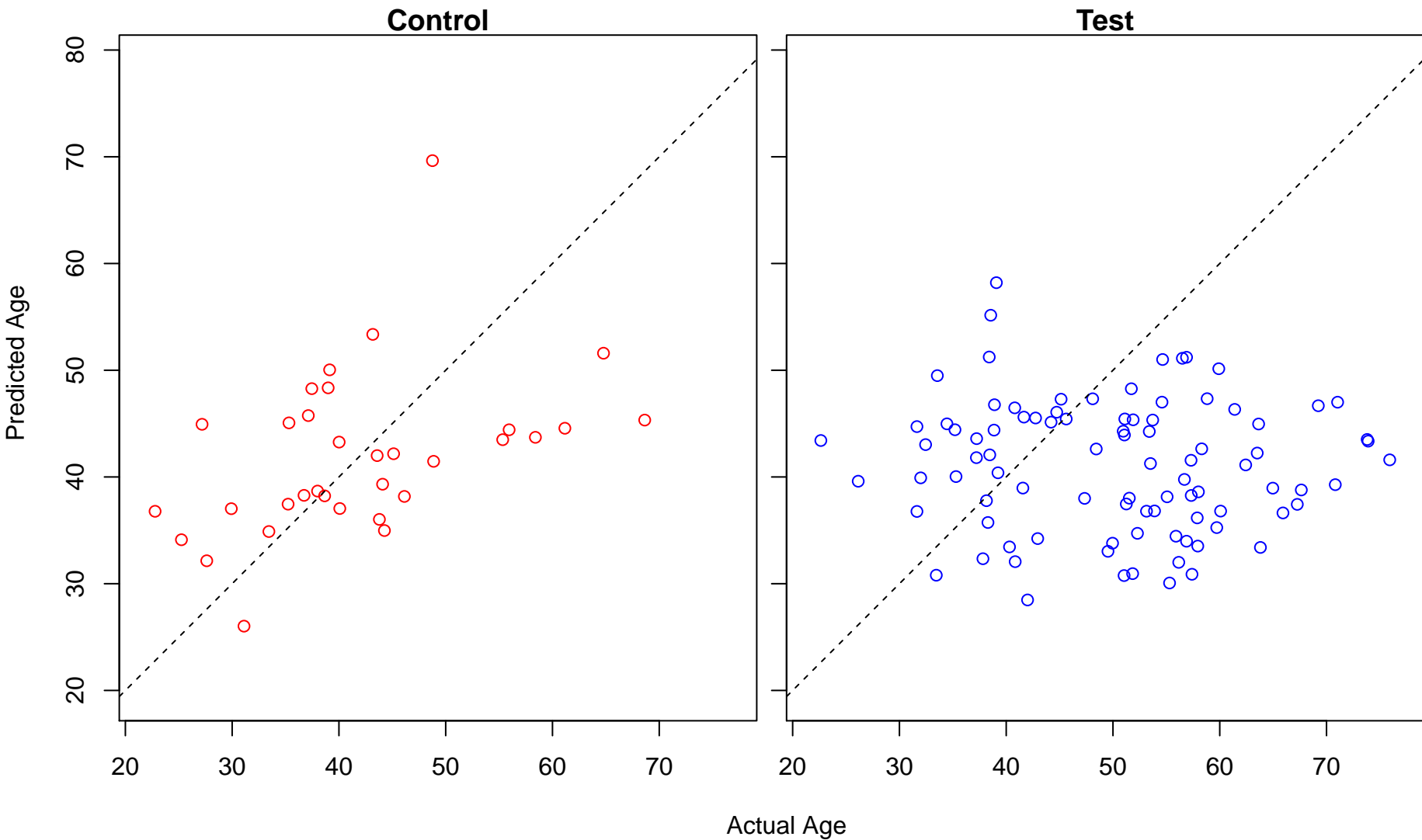
positive regulation of interleukin-2 production (Score: 0.839450)



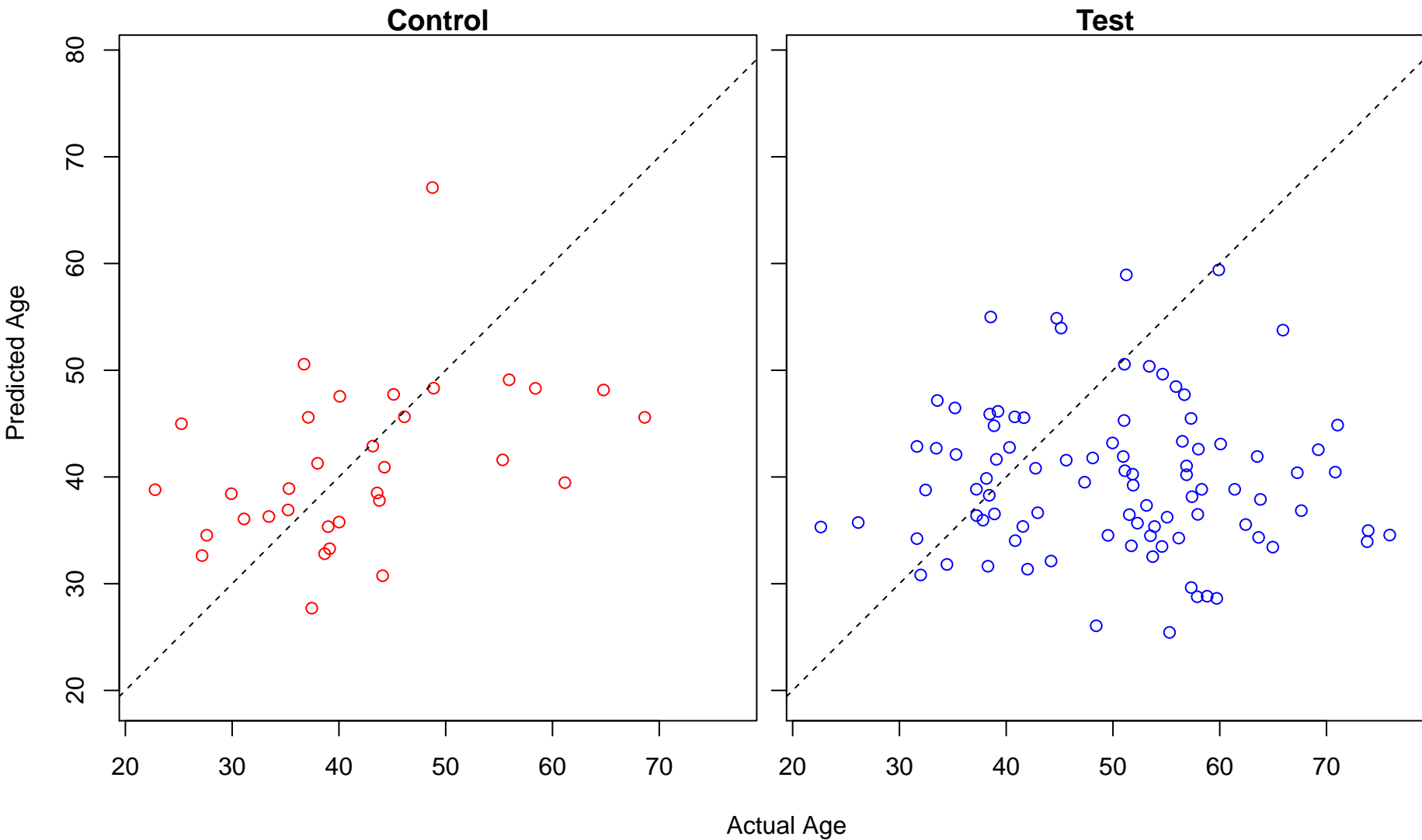
inner ear receptor stereocilium organization (Score: 0.838669)



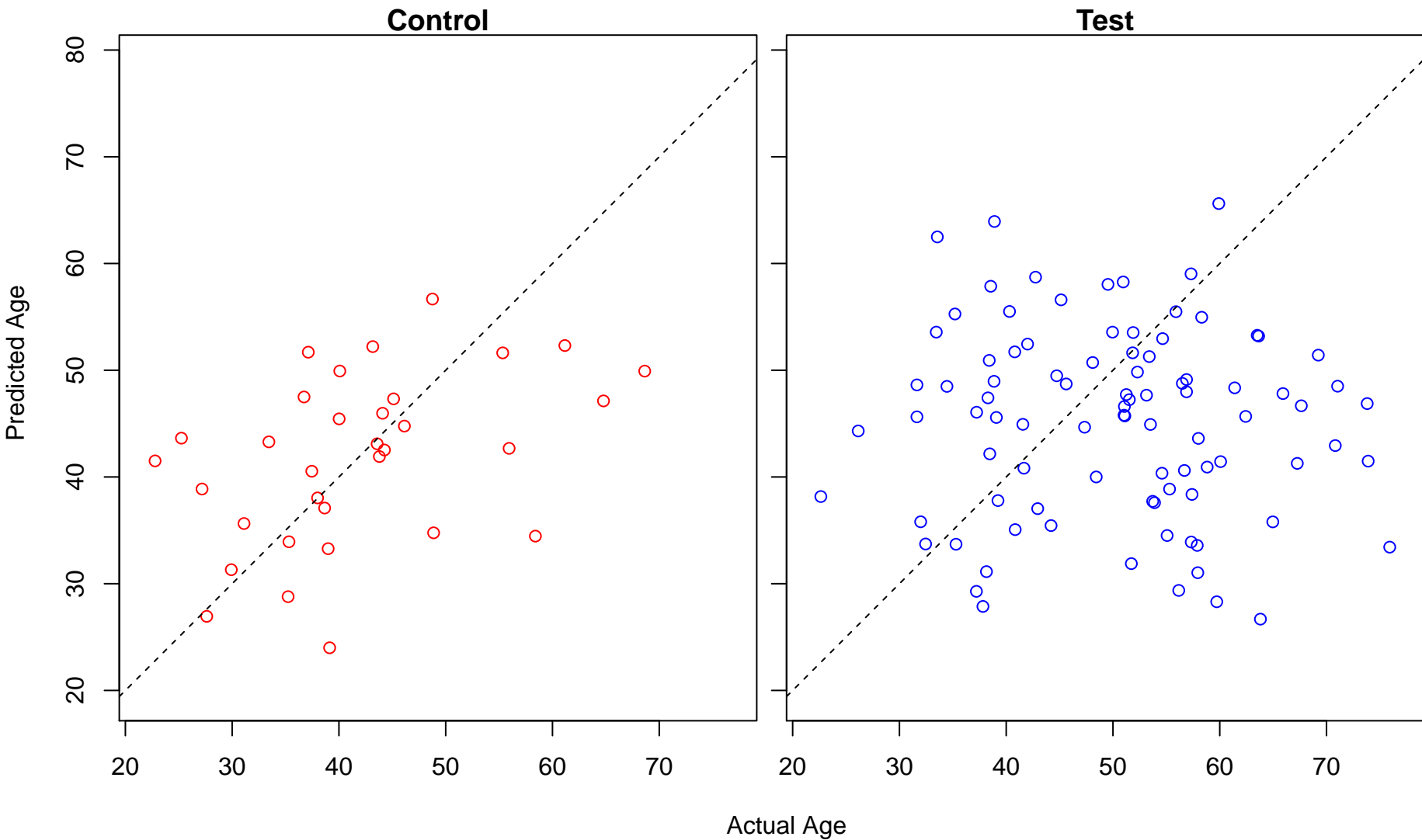
chromatin silencing at rDNA (Score: 0.837654)



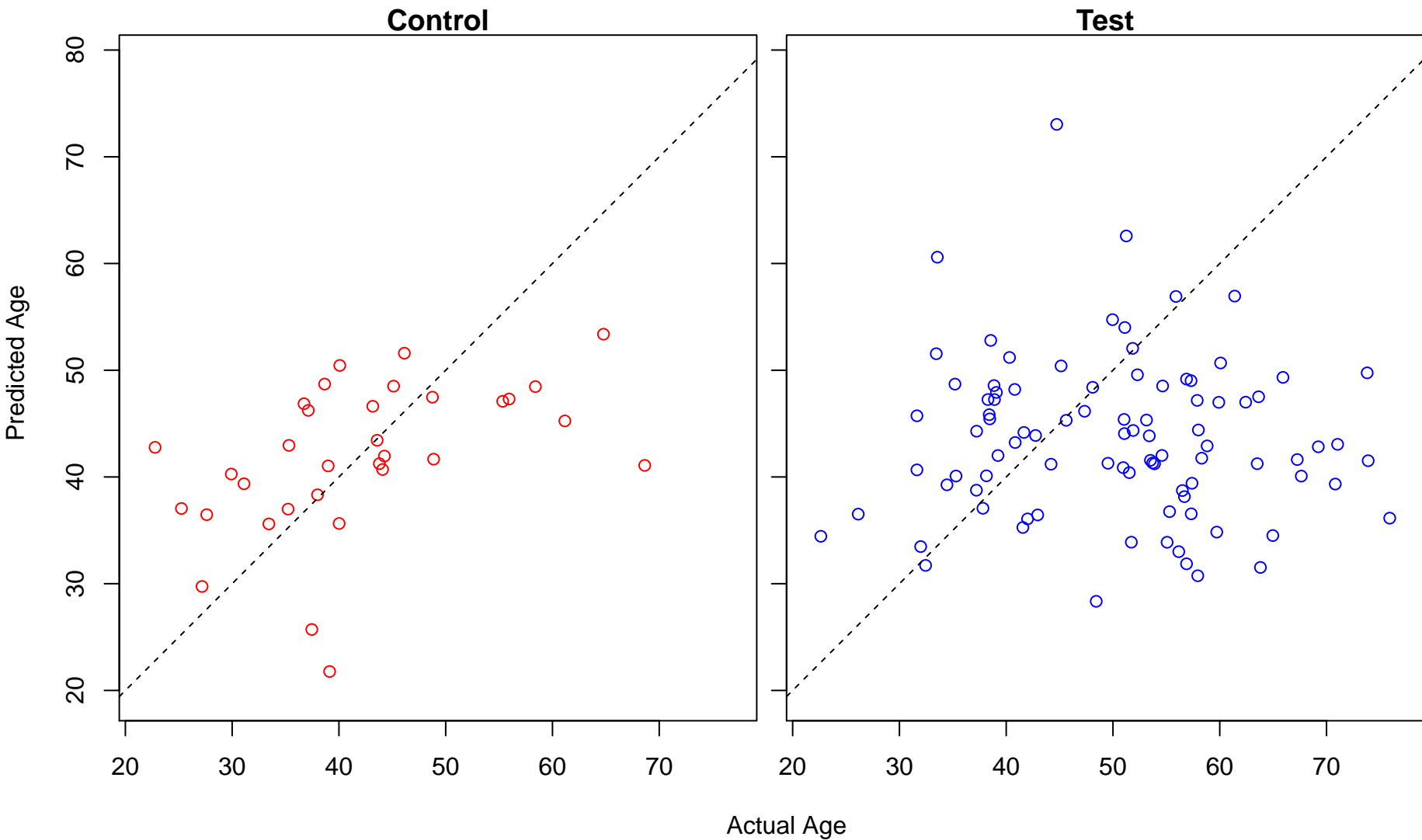
regulation of cytokine production involved in immune response (Score: 0.837558)



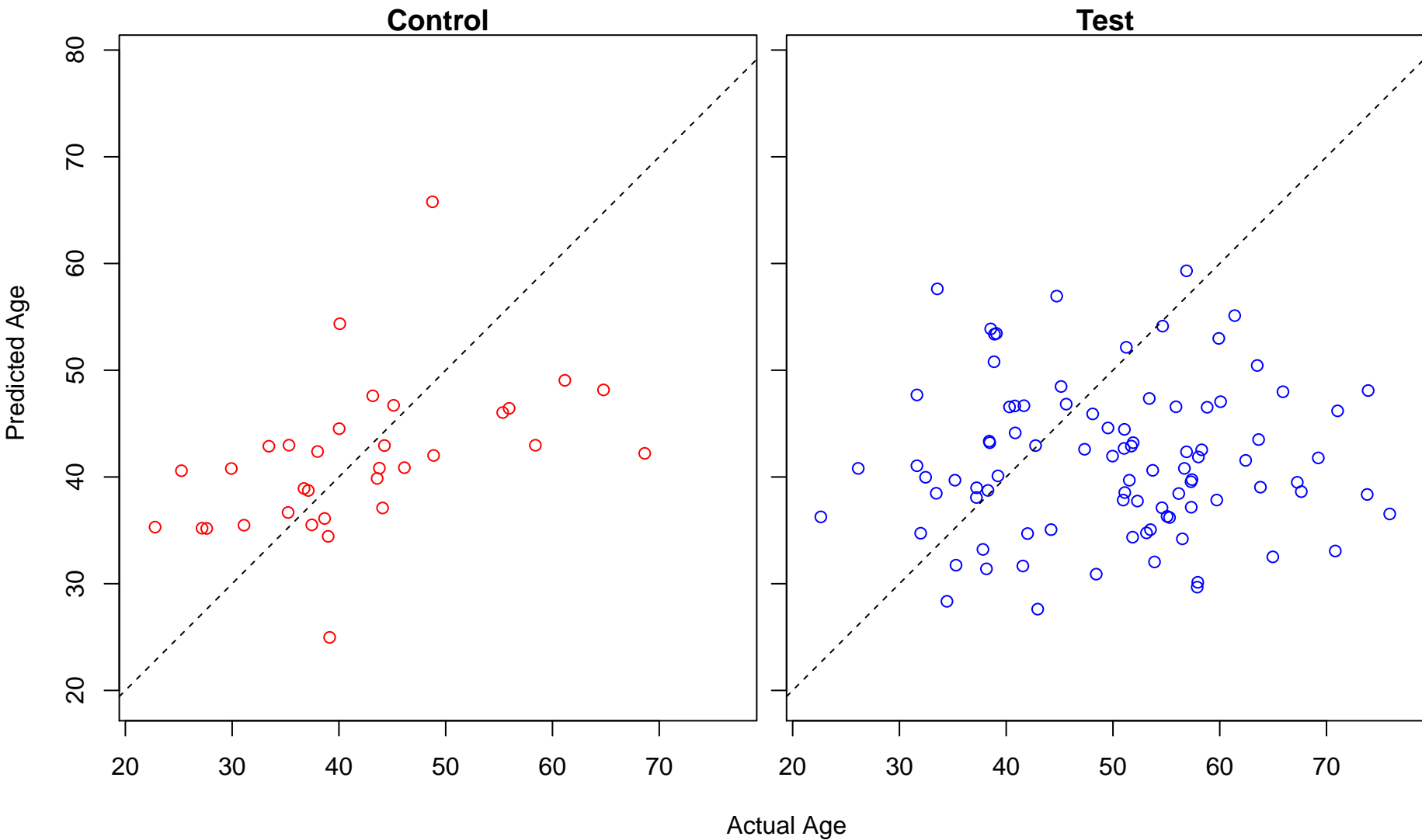
cellular response to abiotic stimulus (Score: 0.837276)



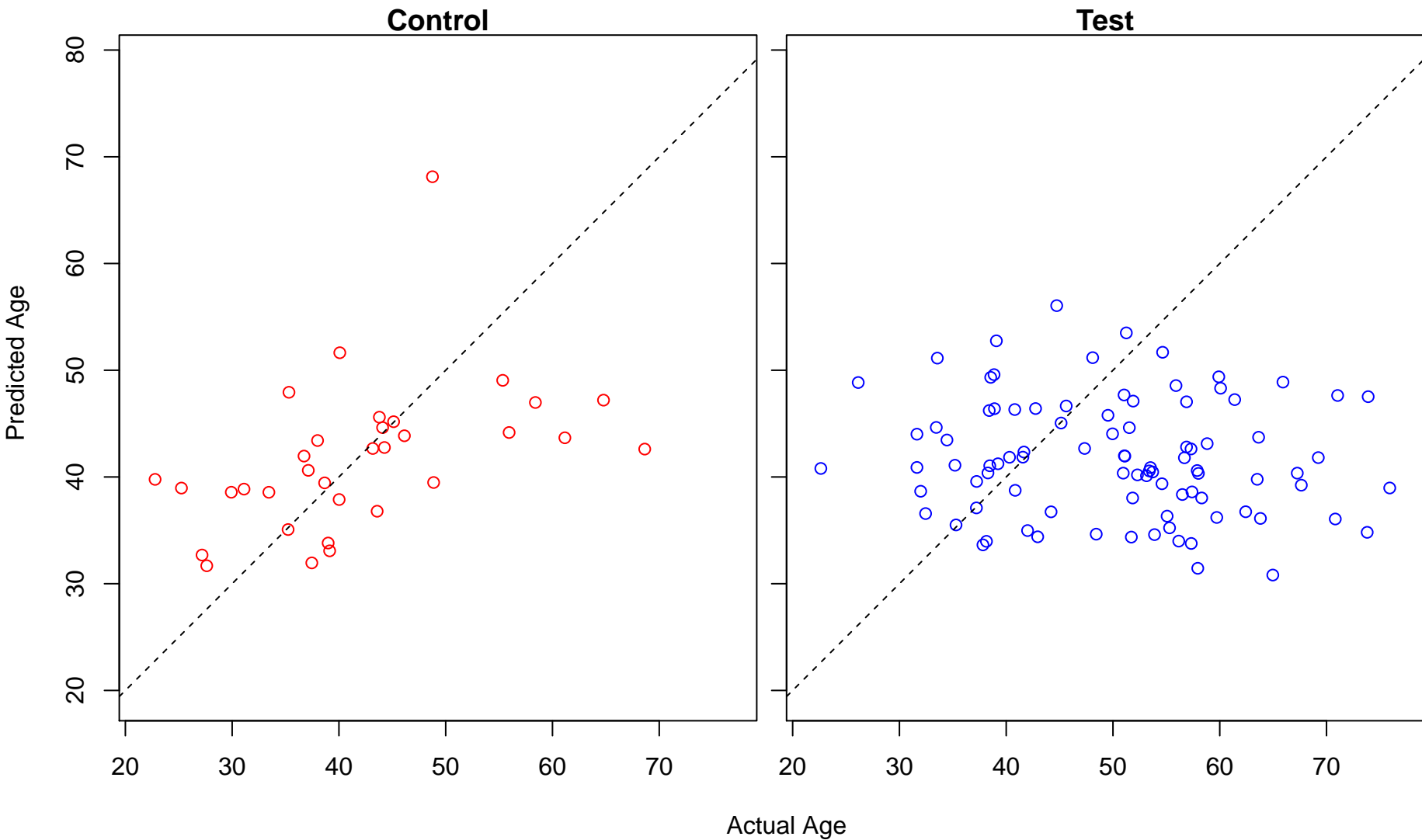
regulation of Rac protein signal transduction (Score: 0.836033)



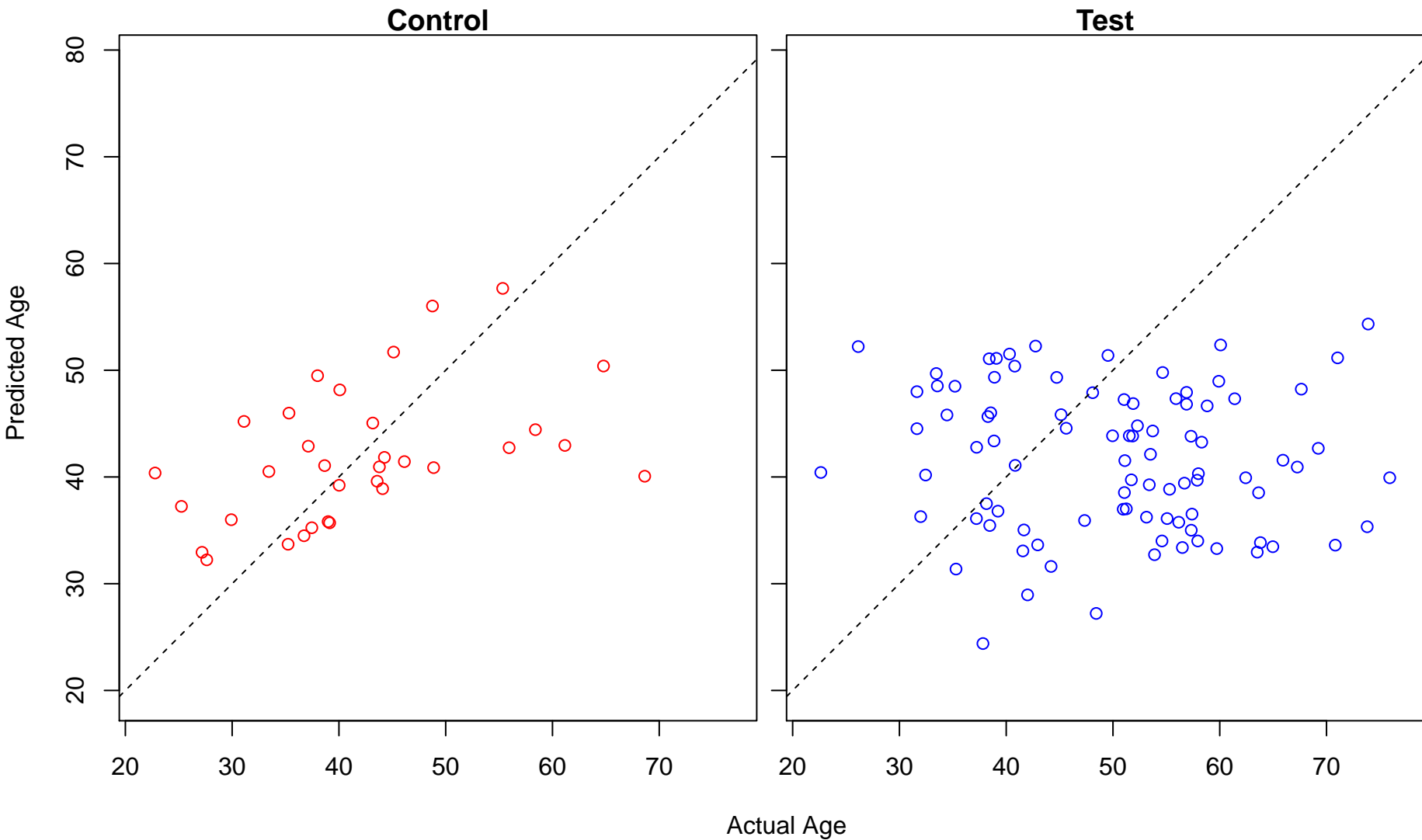
actin cytoskeleton reorganization (Score: 0.835822)



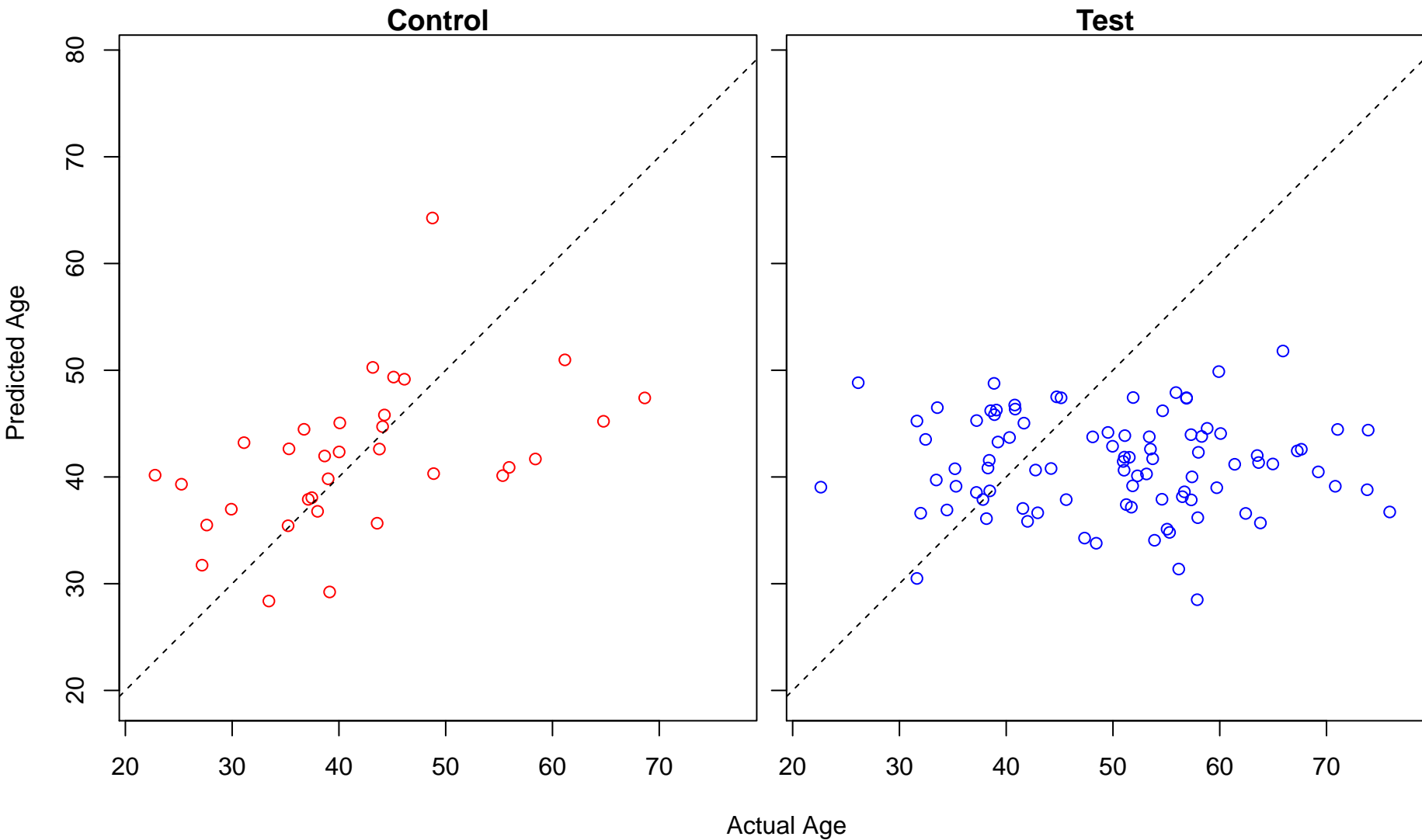
negative regulation of apoptotic signaling pathway (Score: 0.833941)



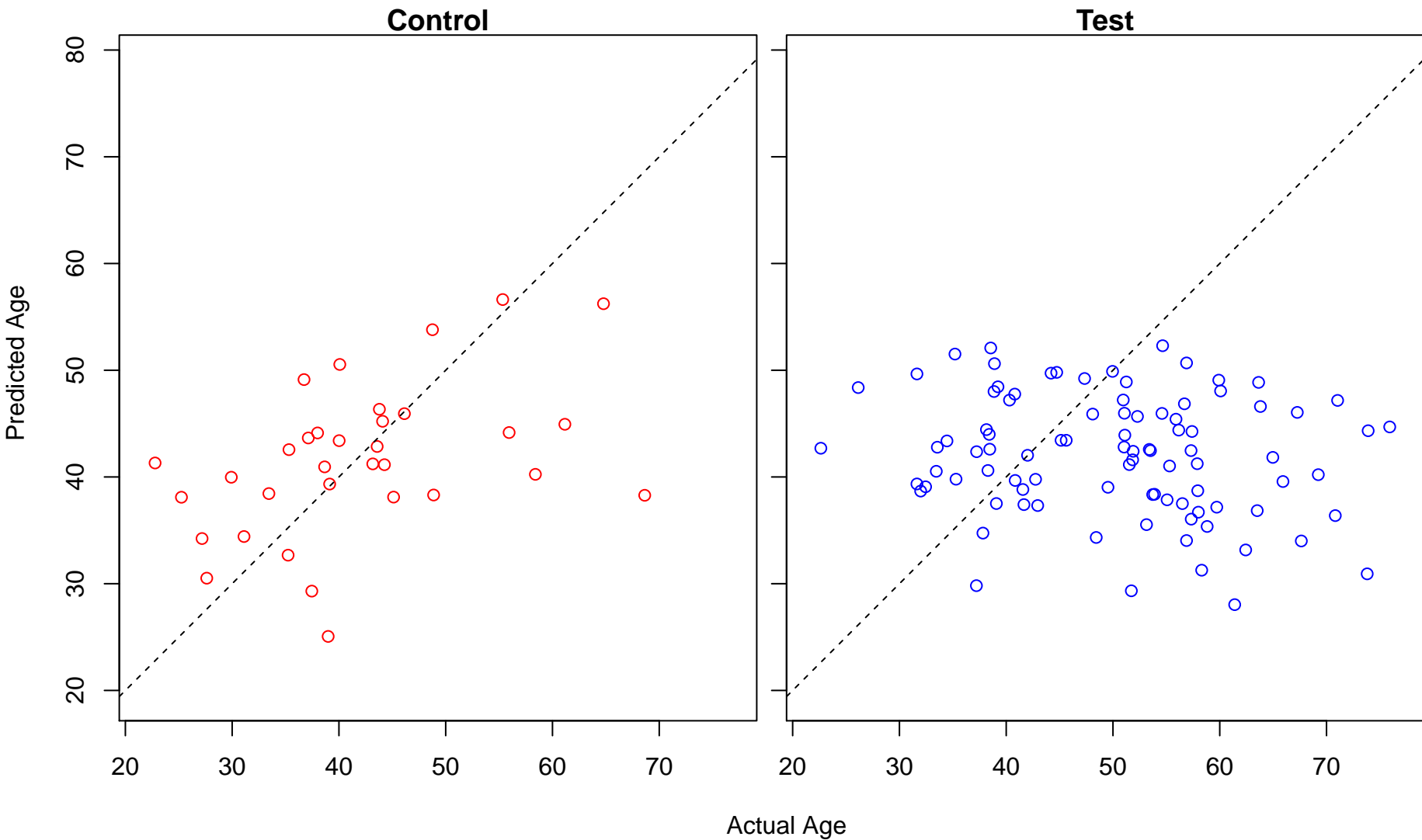
positive regulation of epithelial to mesenchymal transition (Score: 0.833864)



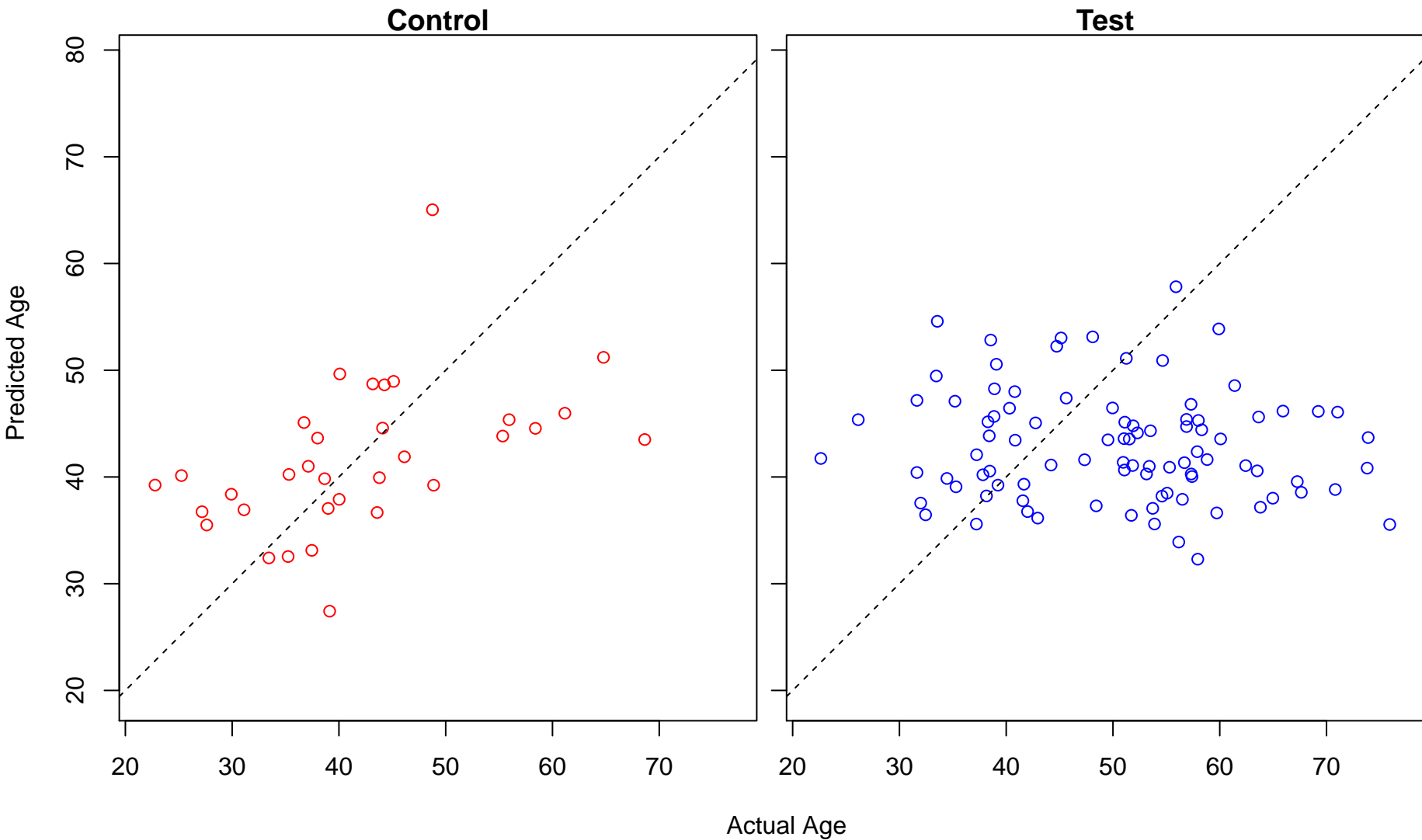
DNA strand elongation involved in DNA replication (Score: 0.831073)



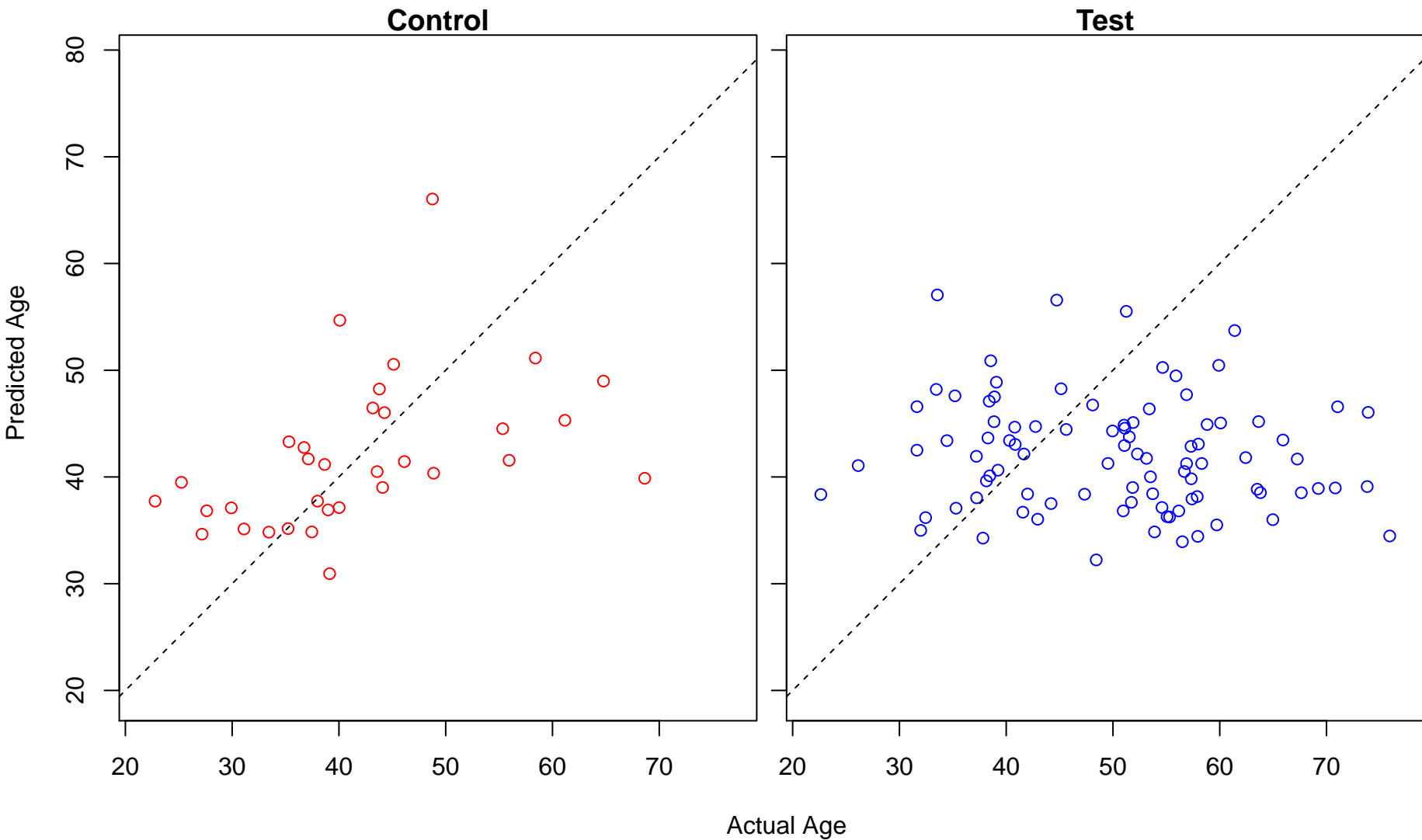
somite development (Score: 0.830766)



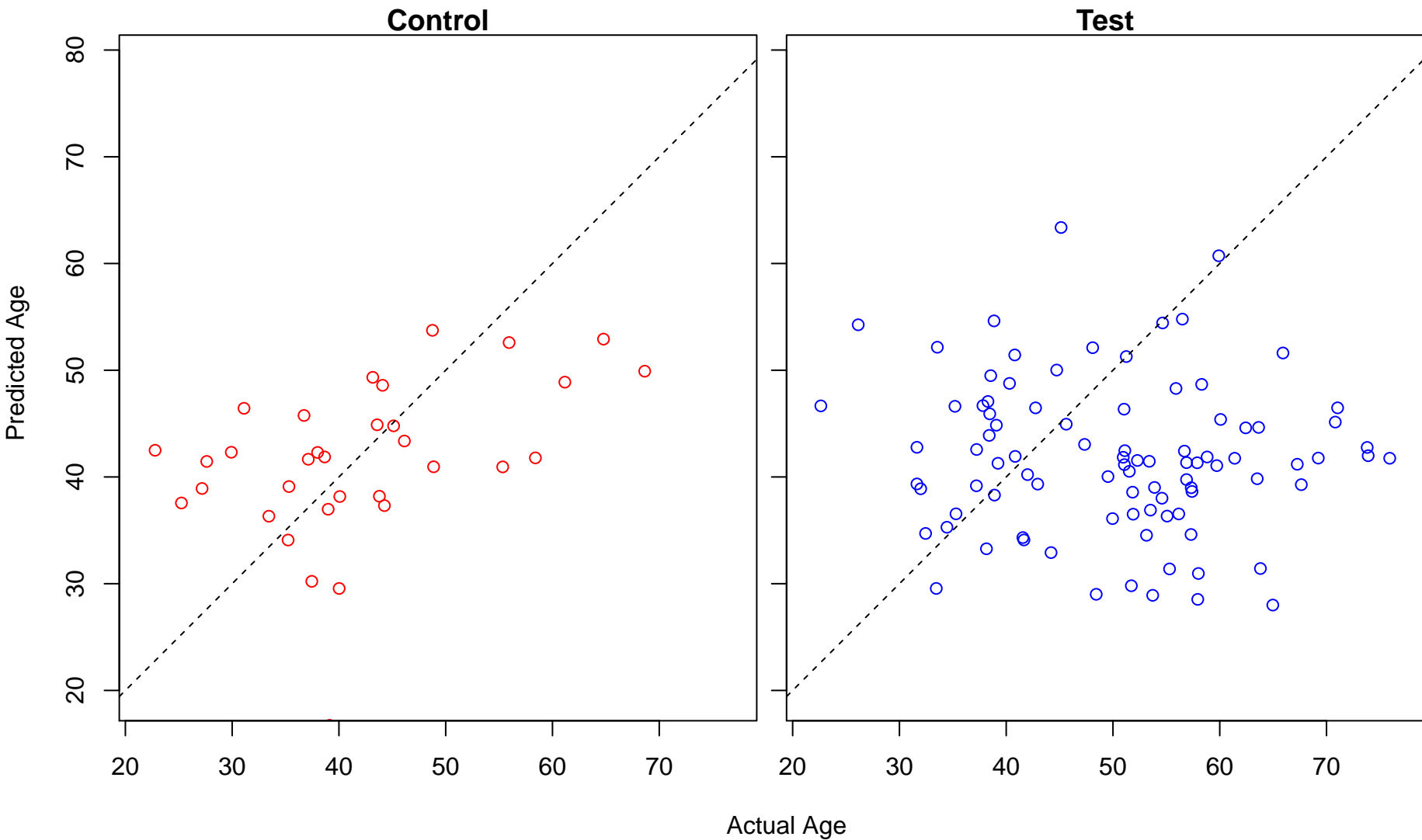
ribonucleotide metabolic process (Score: 0.829402)



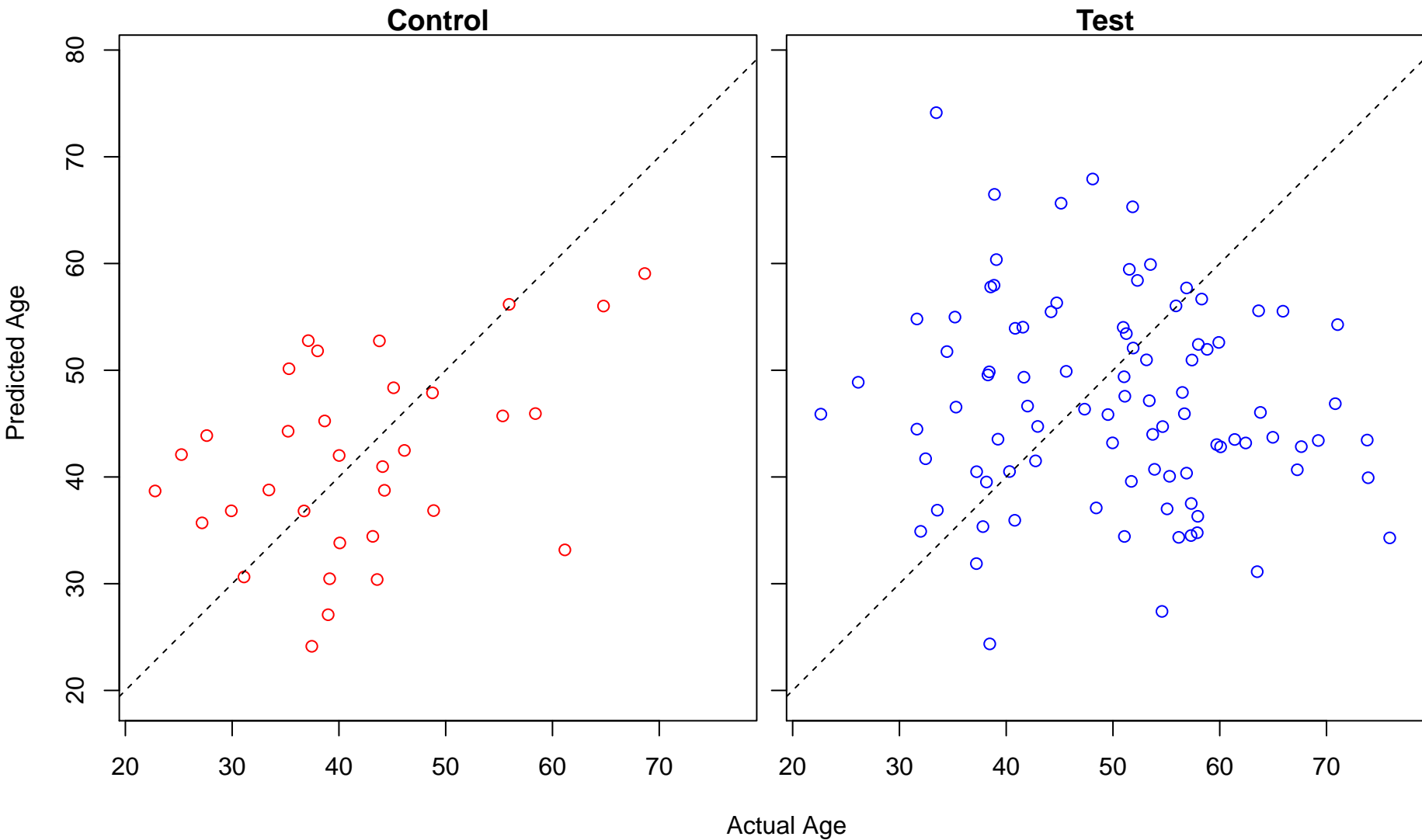
alcohol metabolic process (Score: 0.829350)



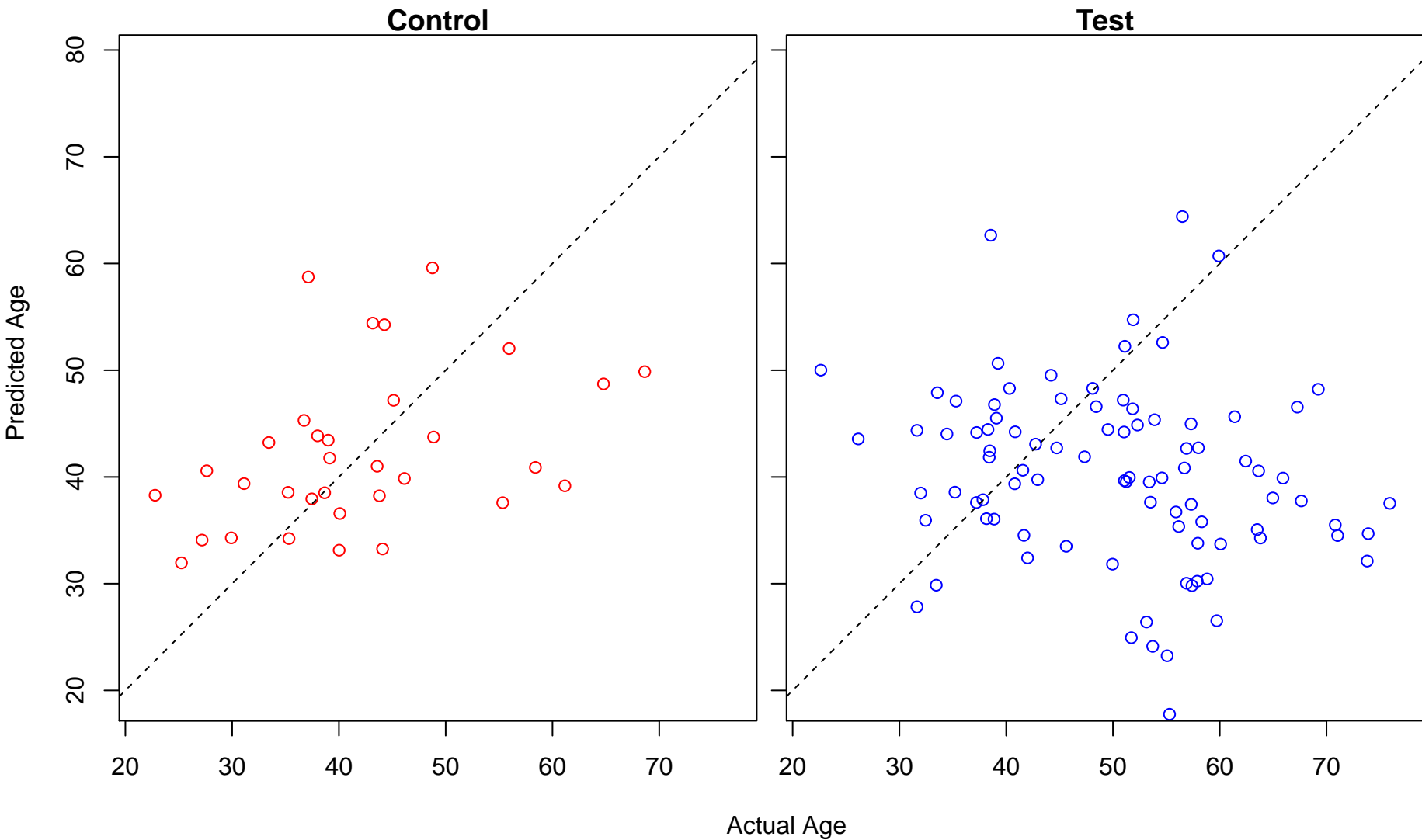
axoneme assembly (Score: 0.829184)



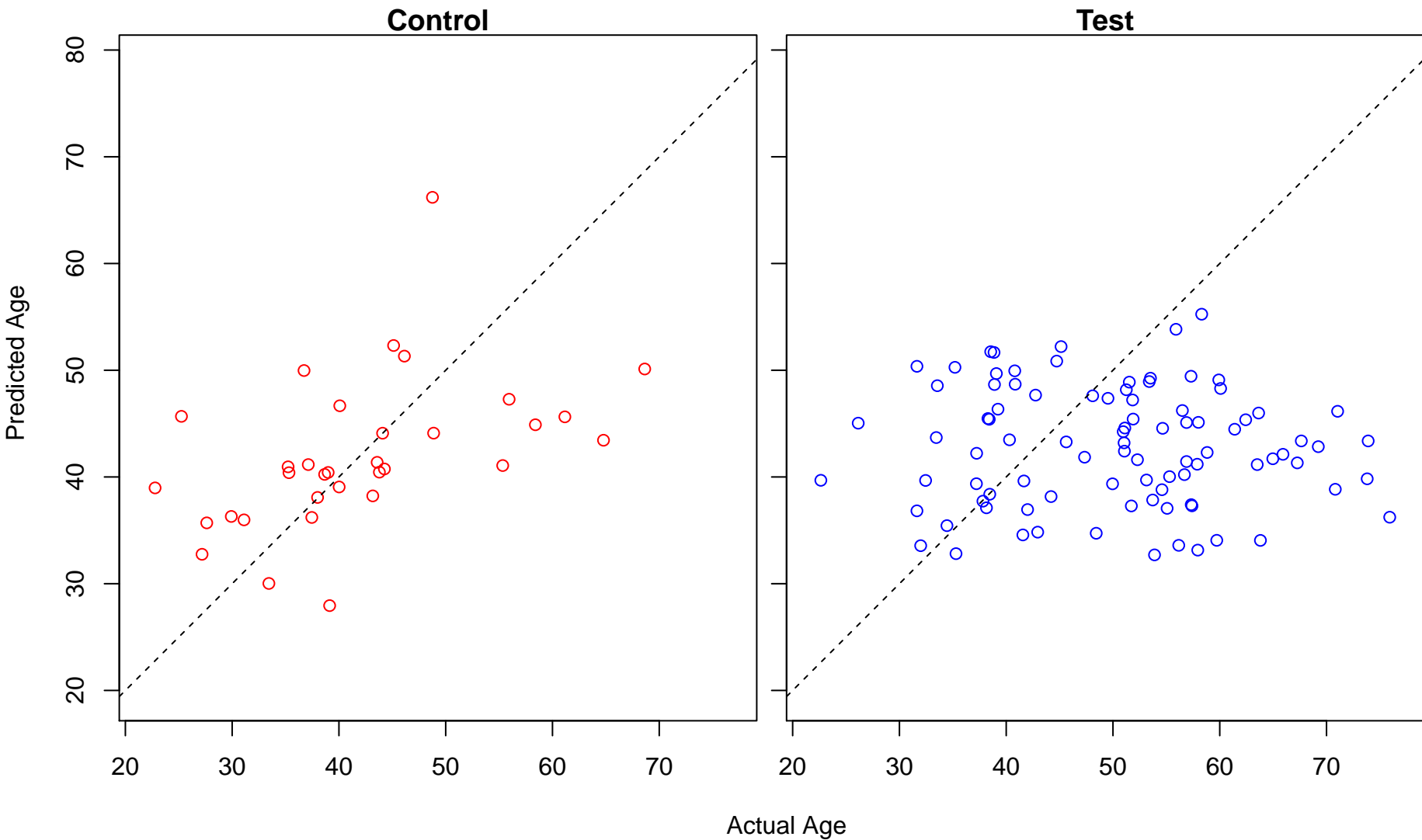
embryonic placenta development (Score: 0.829033)



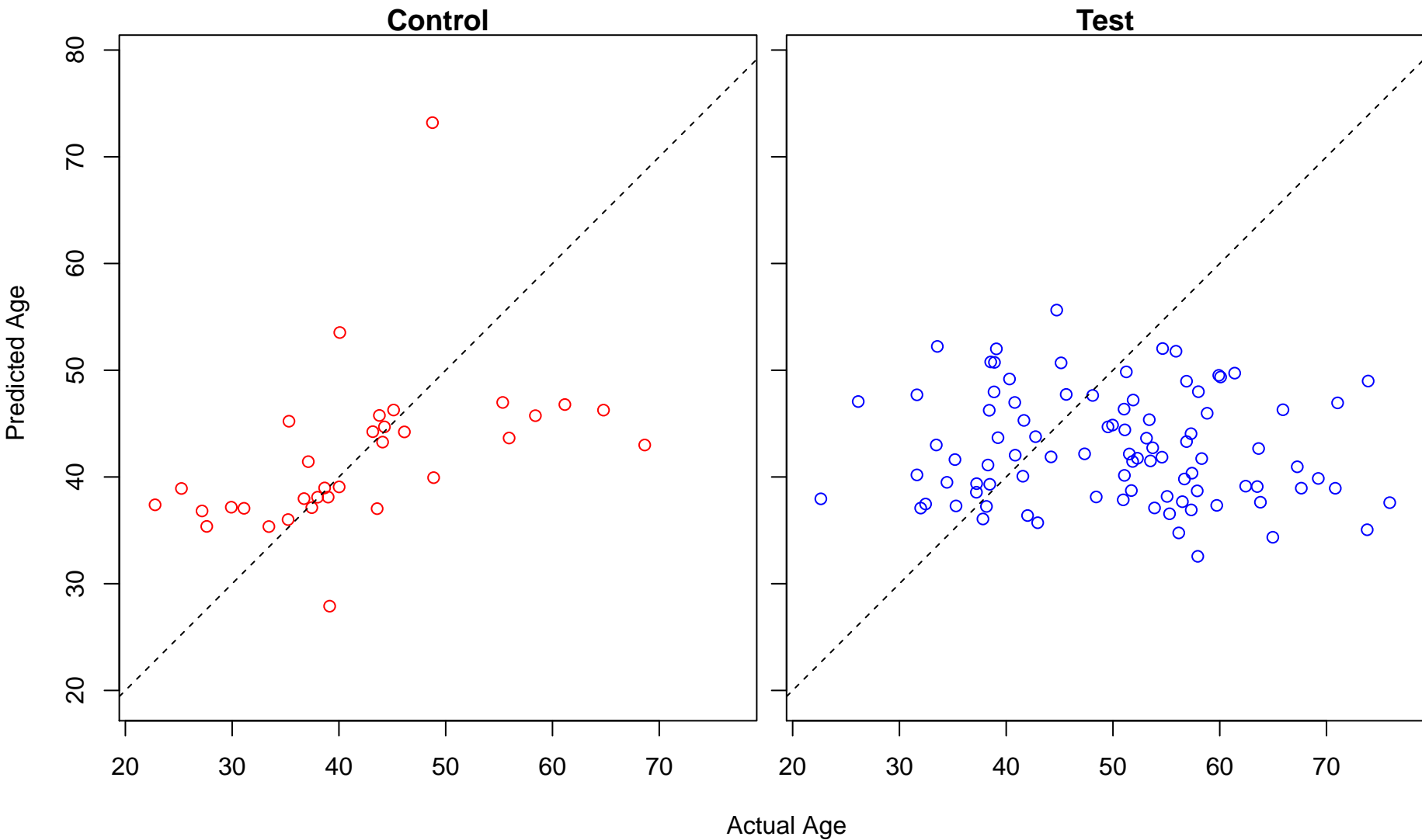
spindle stabilization (Score: 0.828939)



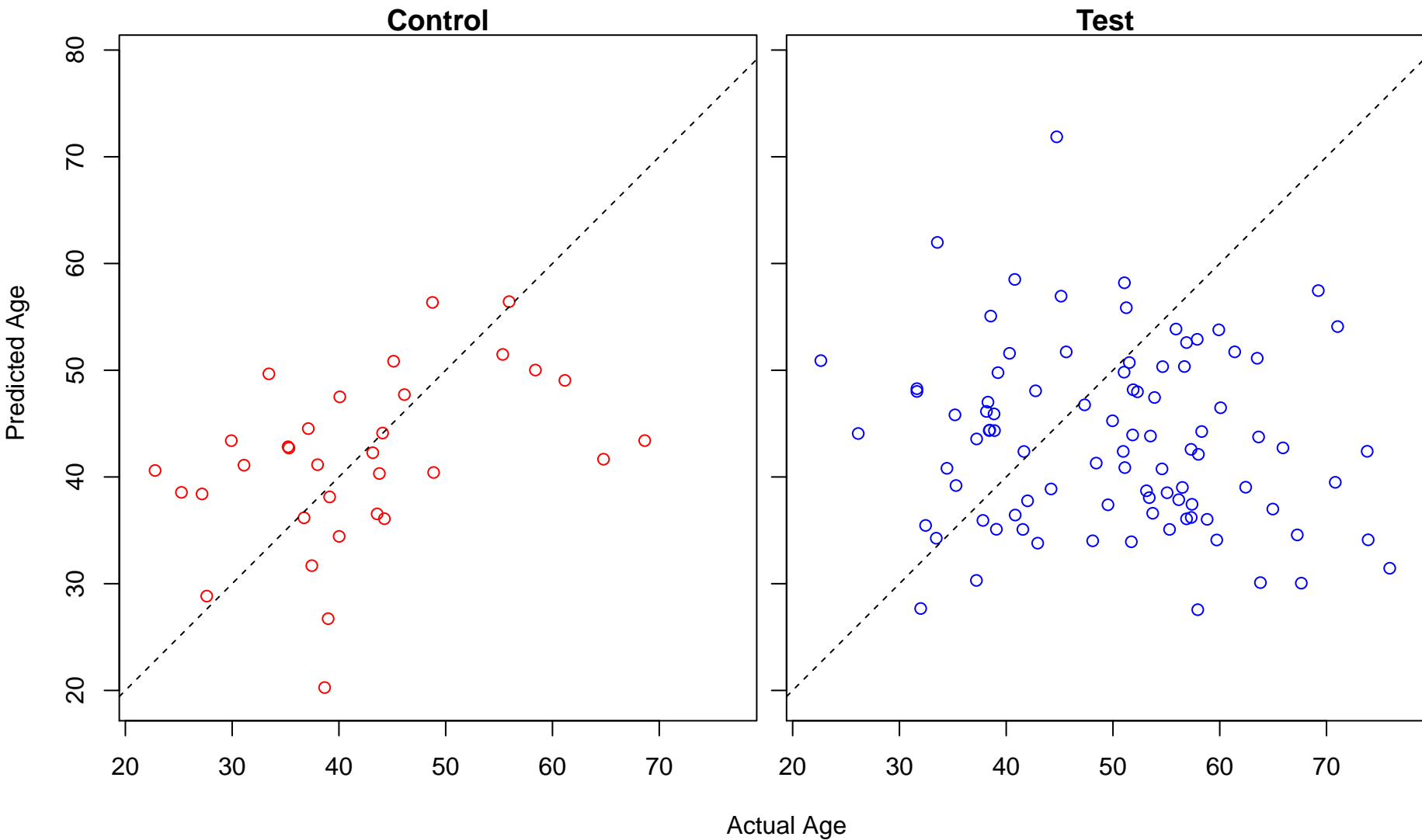
negative regulation of interleukin-12 production (Score: 0.828729)



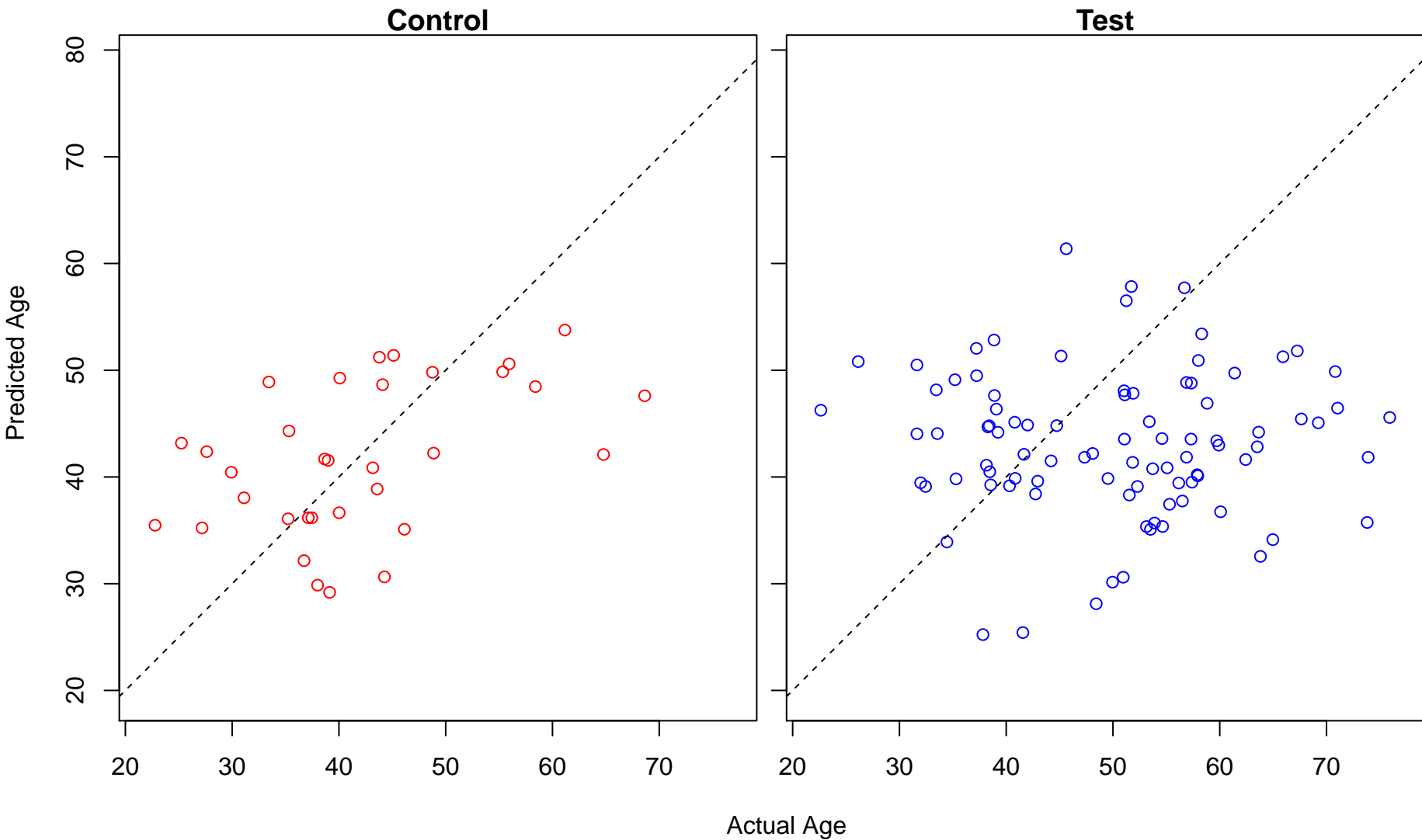
negative regulation of protein phosphorylation (Score: 0.827712)



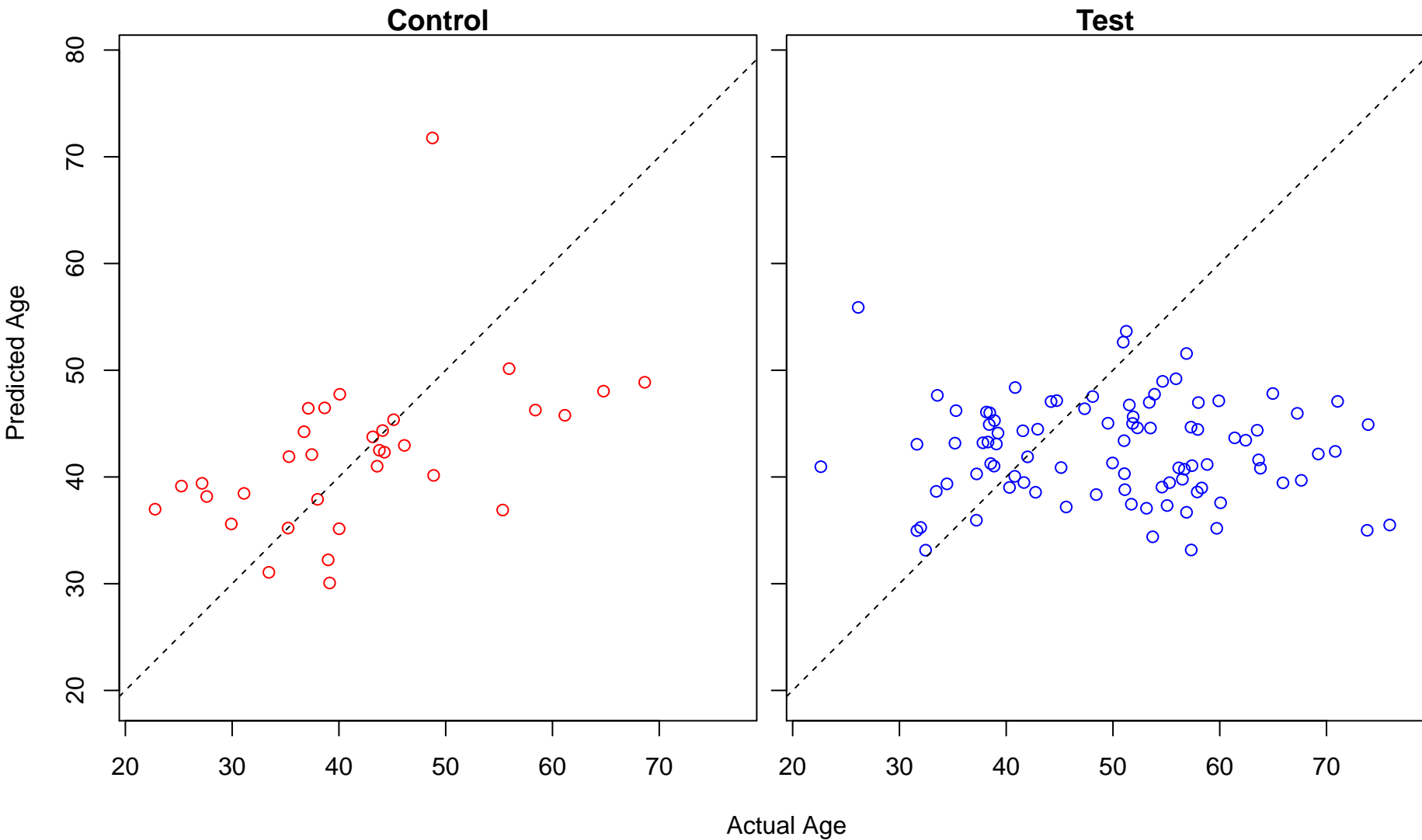
hair cell differentiation (Score: 0.827301)



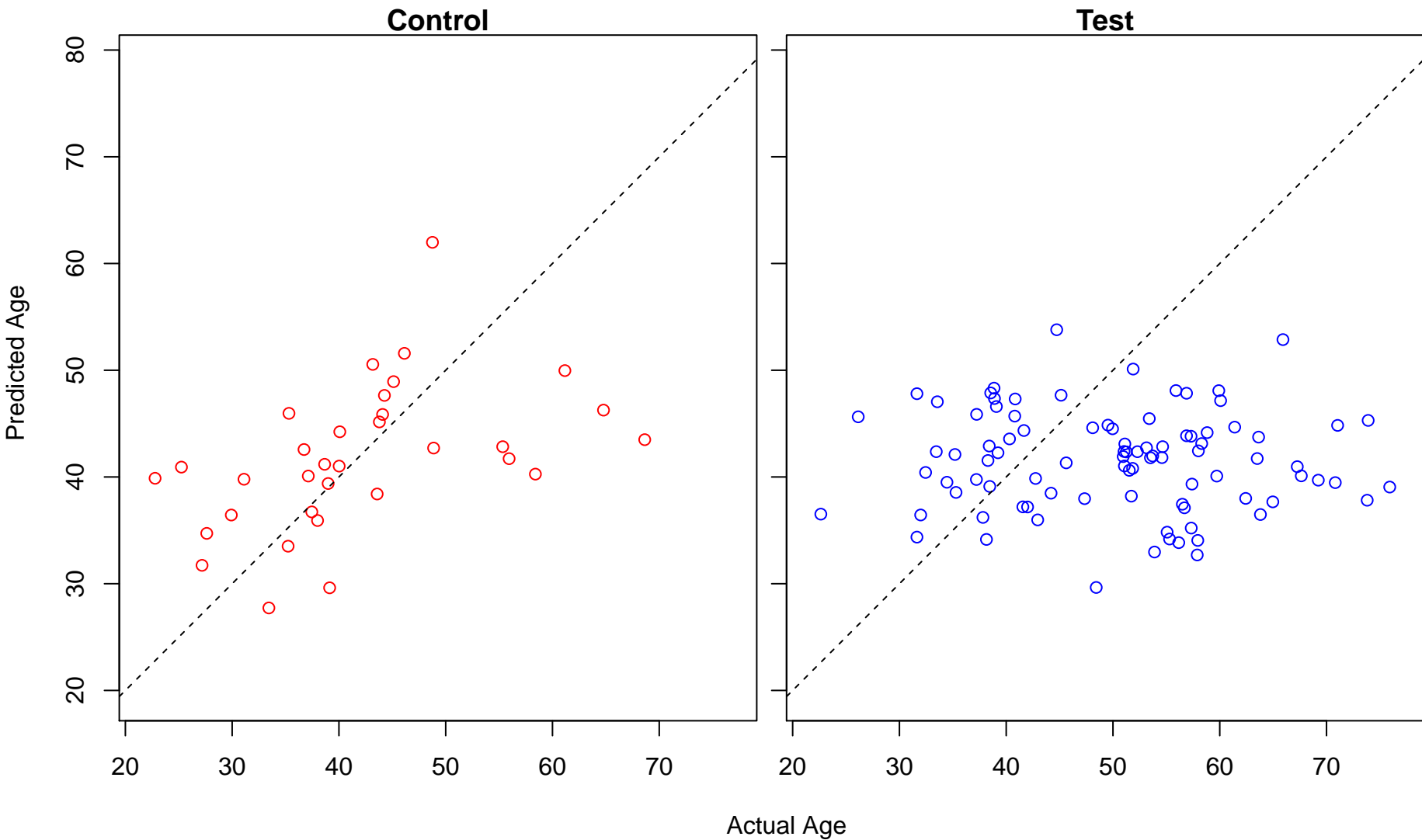
myofibril assembly (Score: 0.827119)



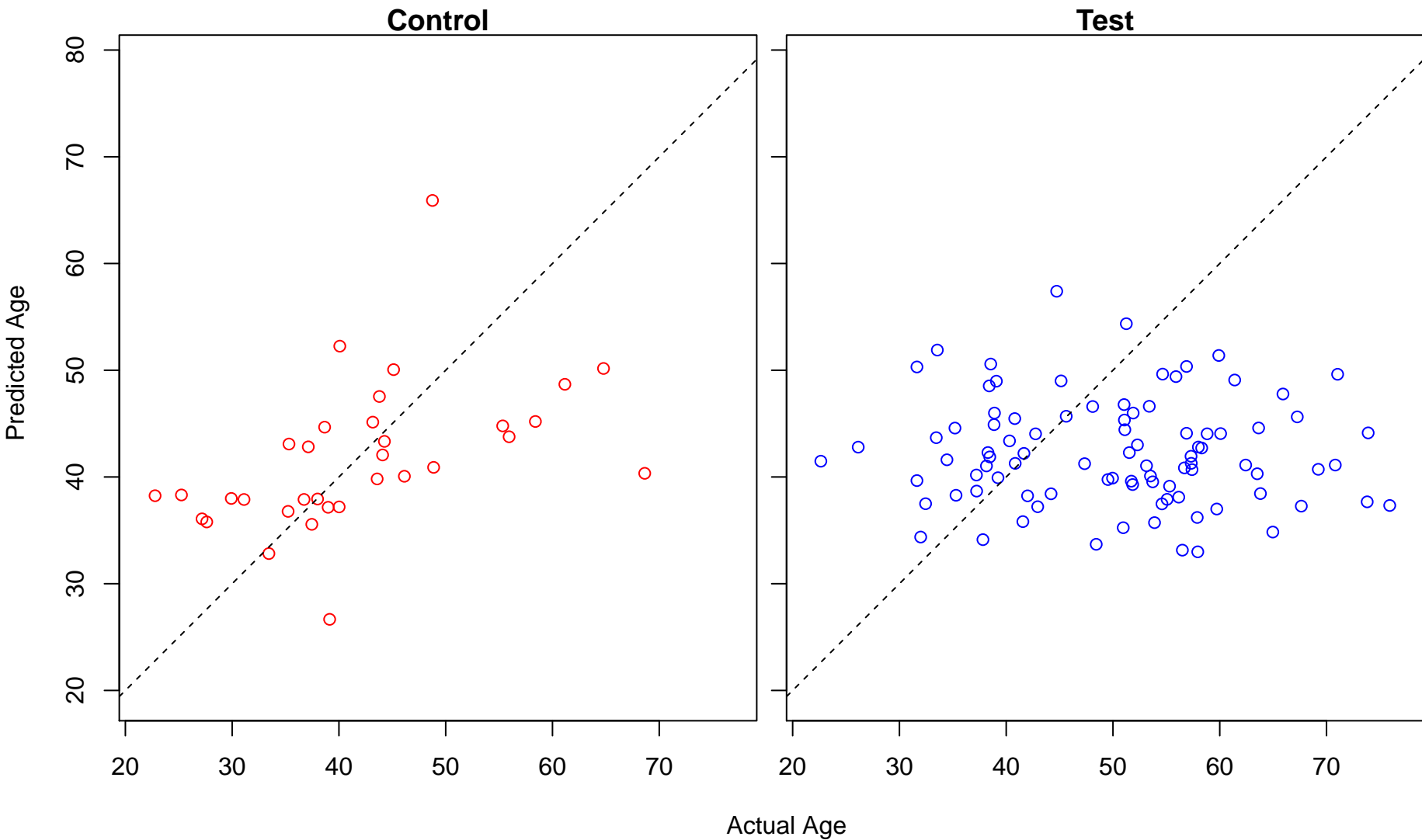
regulation of pro-B cell differentiation (Score: 0.826731)



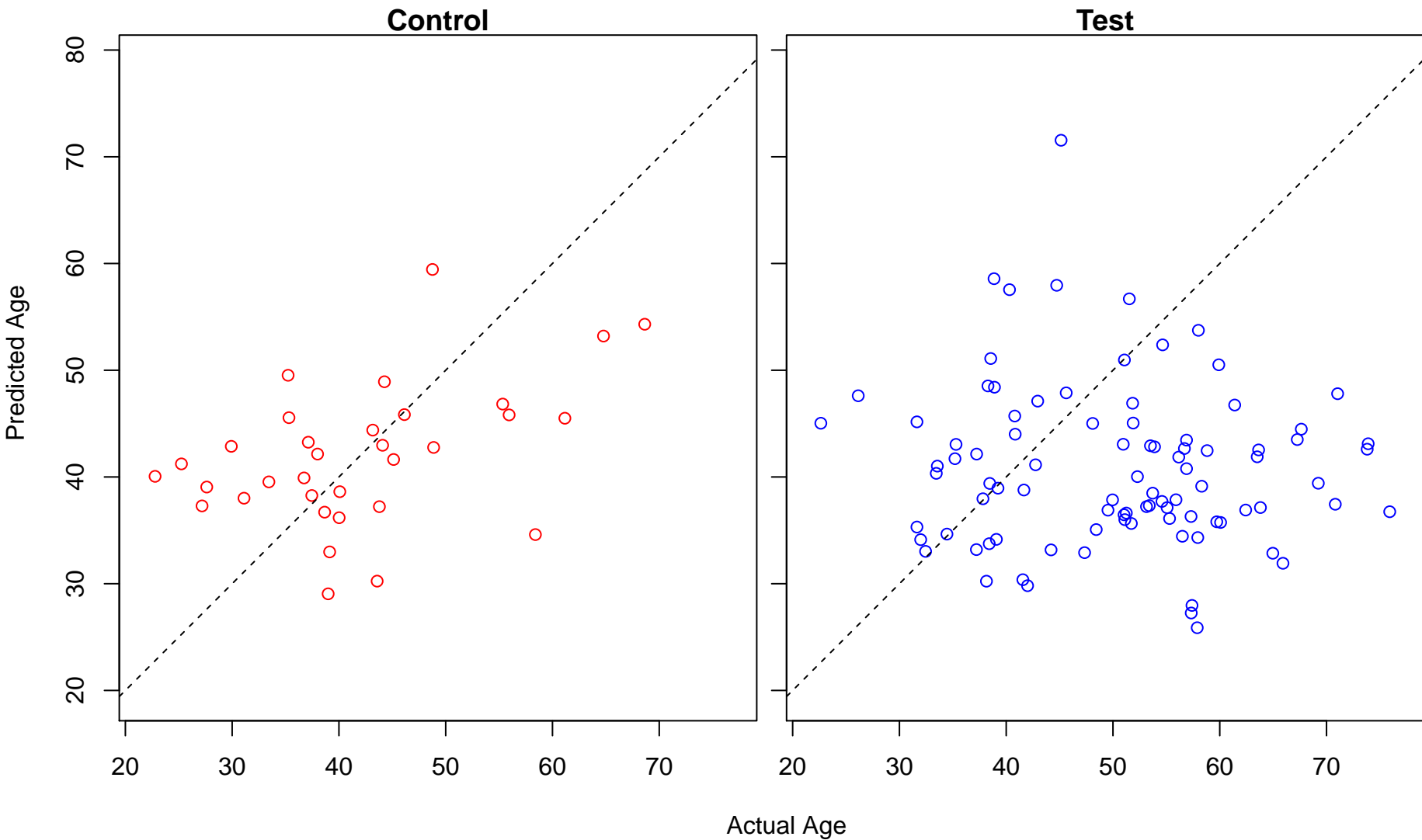
DNA-dependent DNA replication (Score: 0.826506)



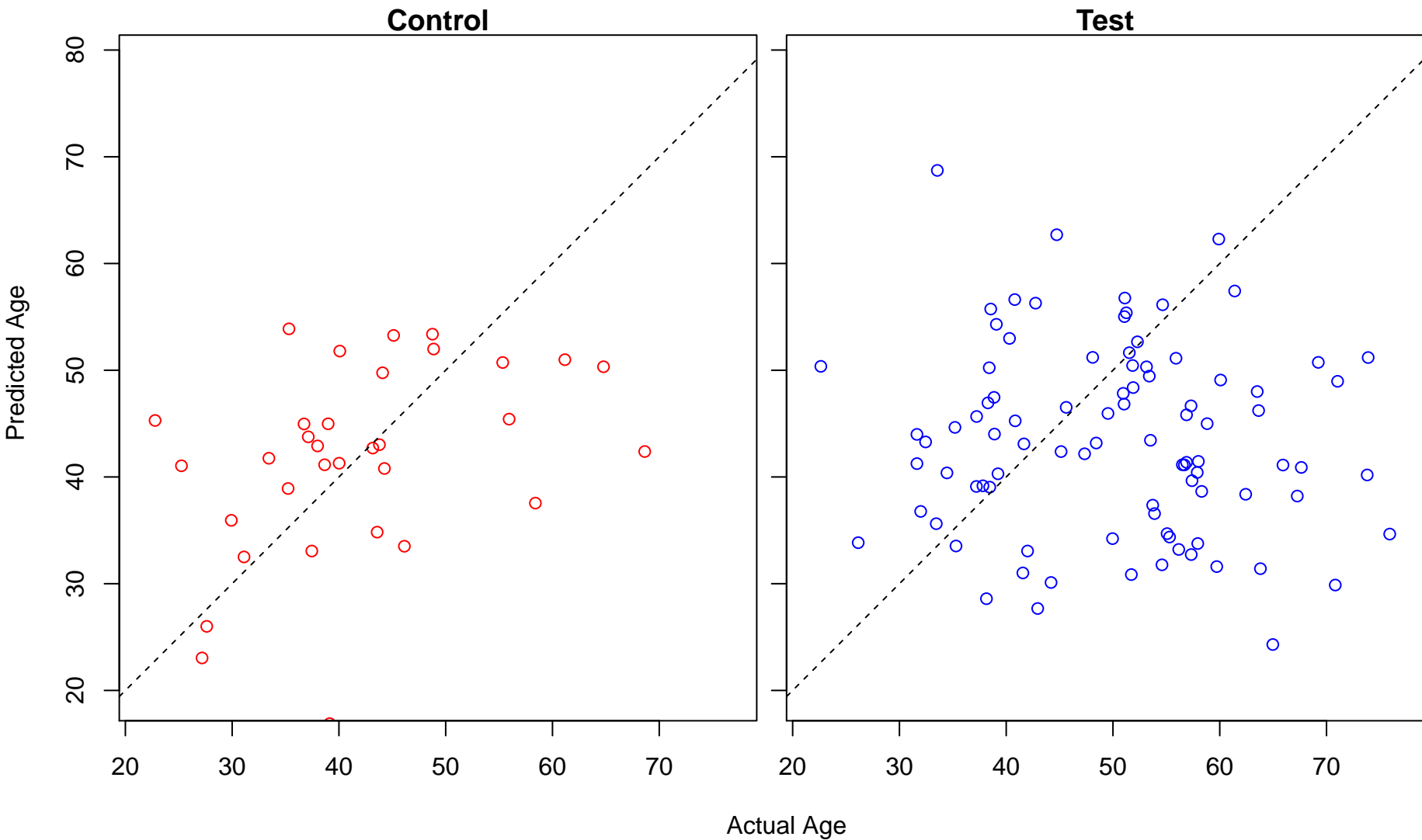
phospholipid metabolic process (Score: 0.825921)



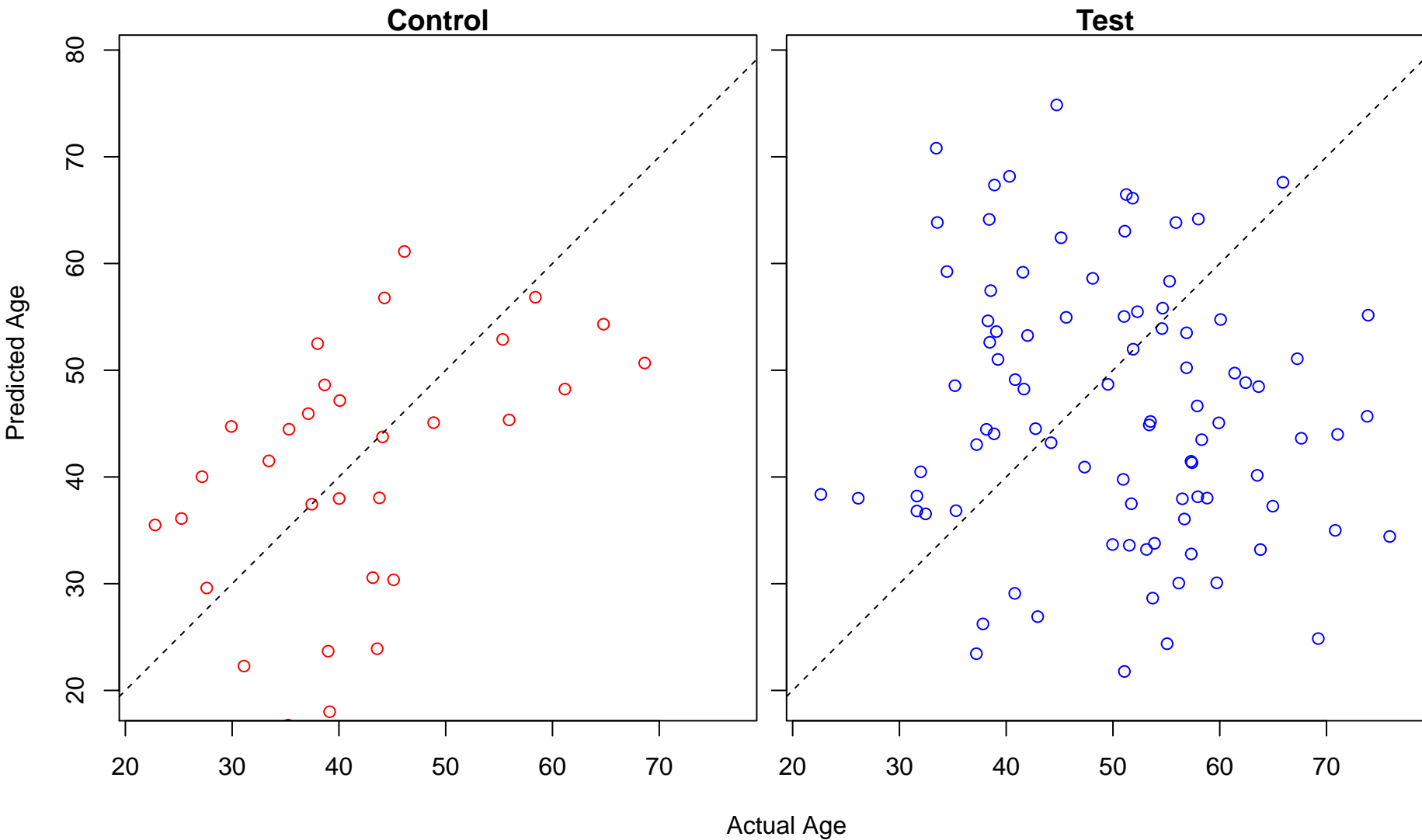
inner ear receptor cell development (Score: 0.824914)



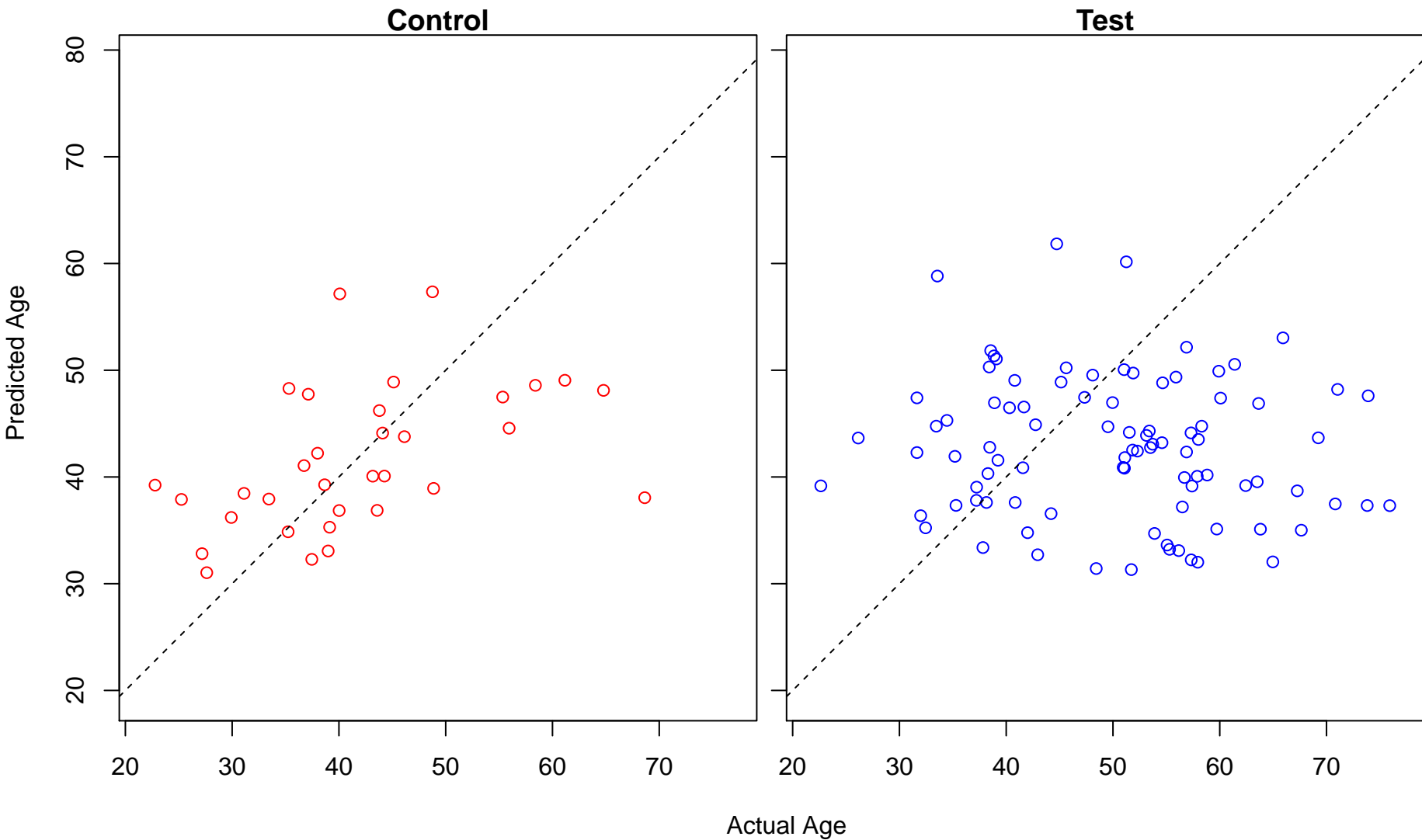
Rap protein signal transduction (Score: 0.824416)



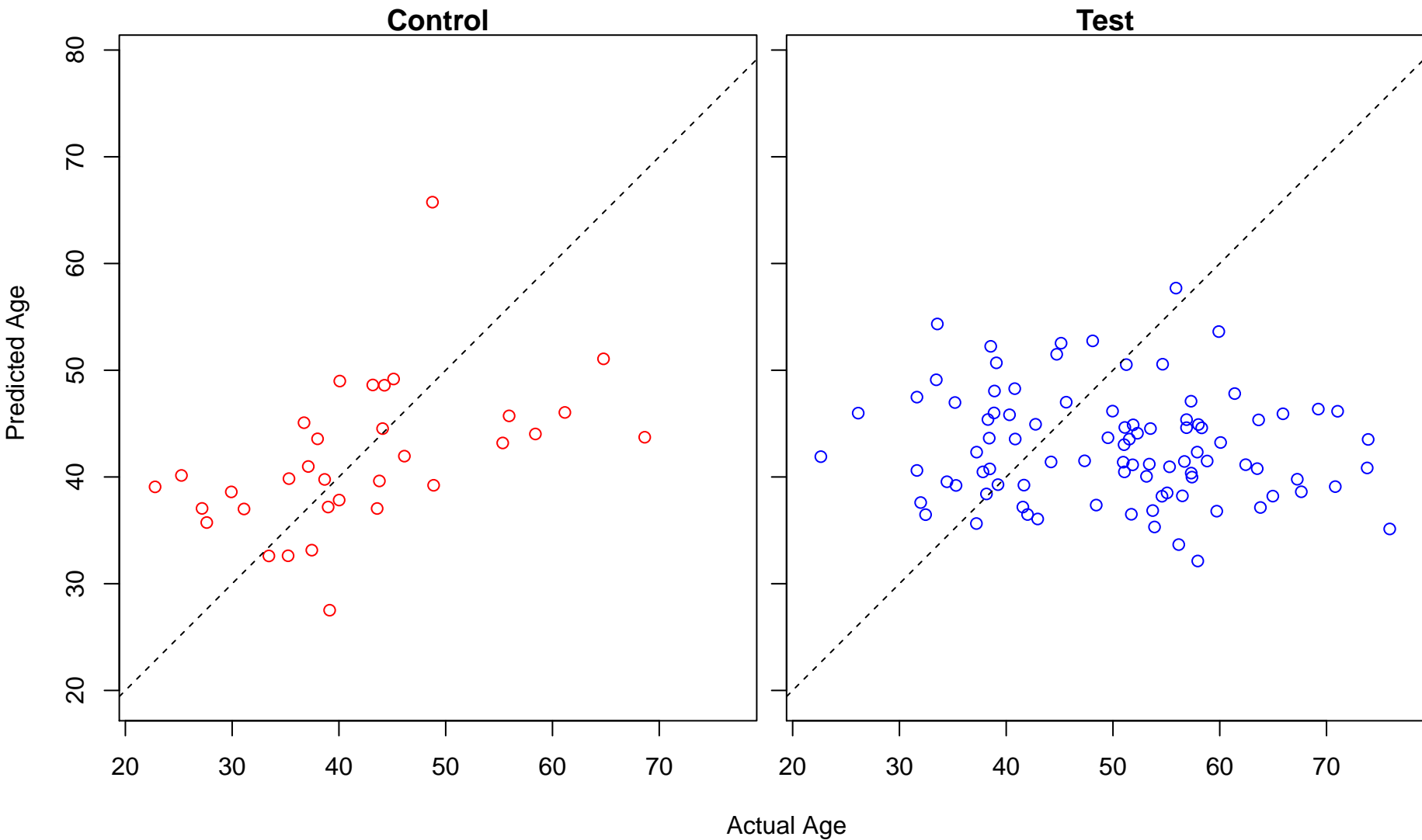
monosaccharide catabolic process (Score: 0.822592)



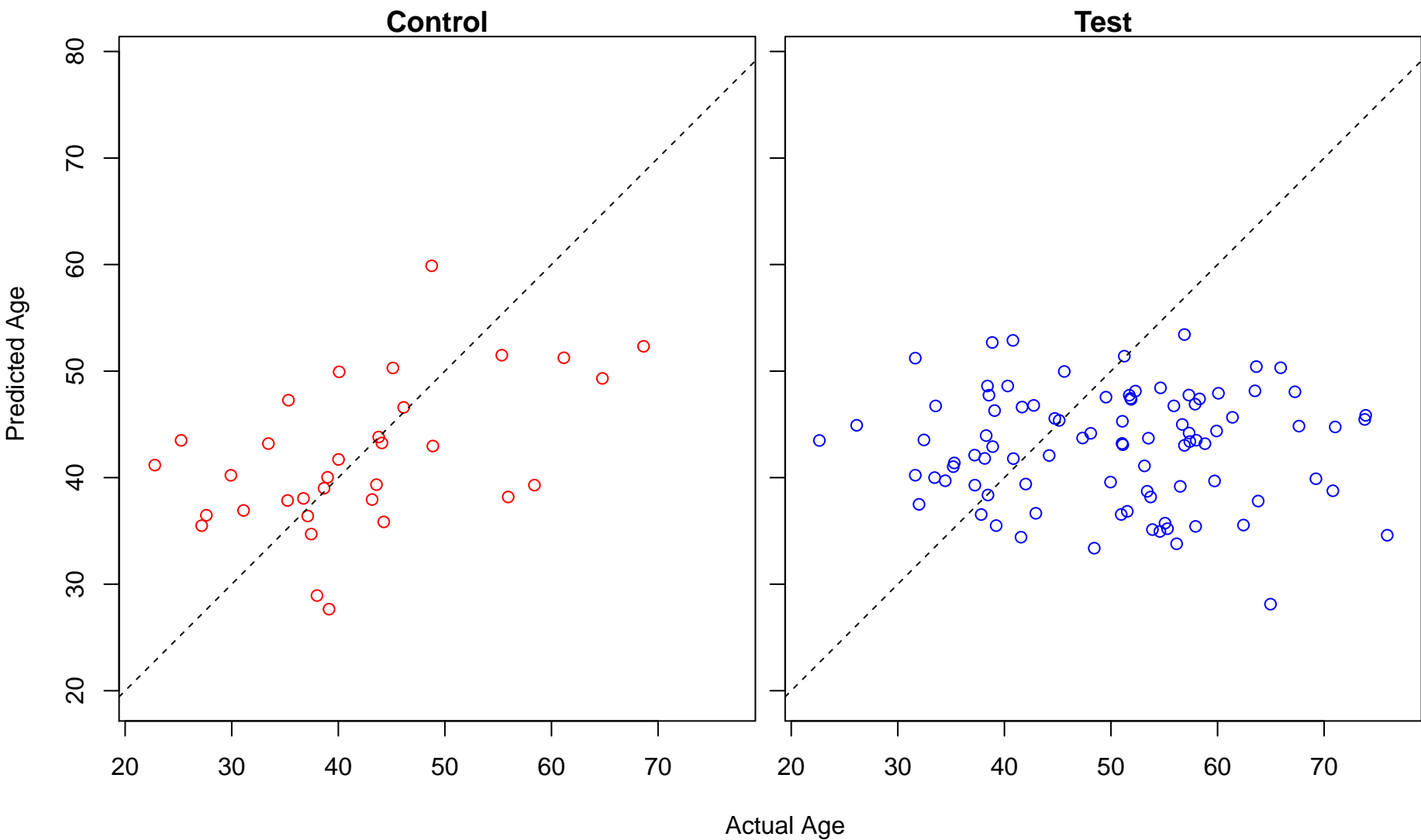
regulation of protein stability (Score: 0.822470)



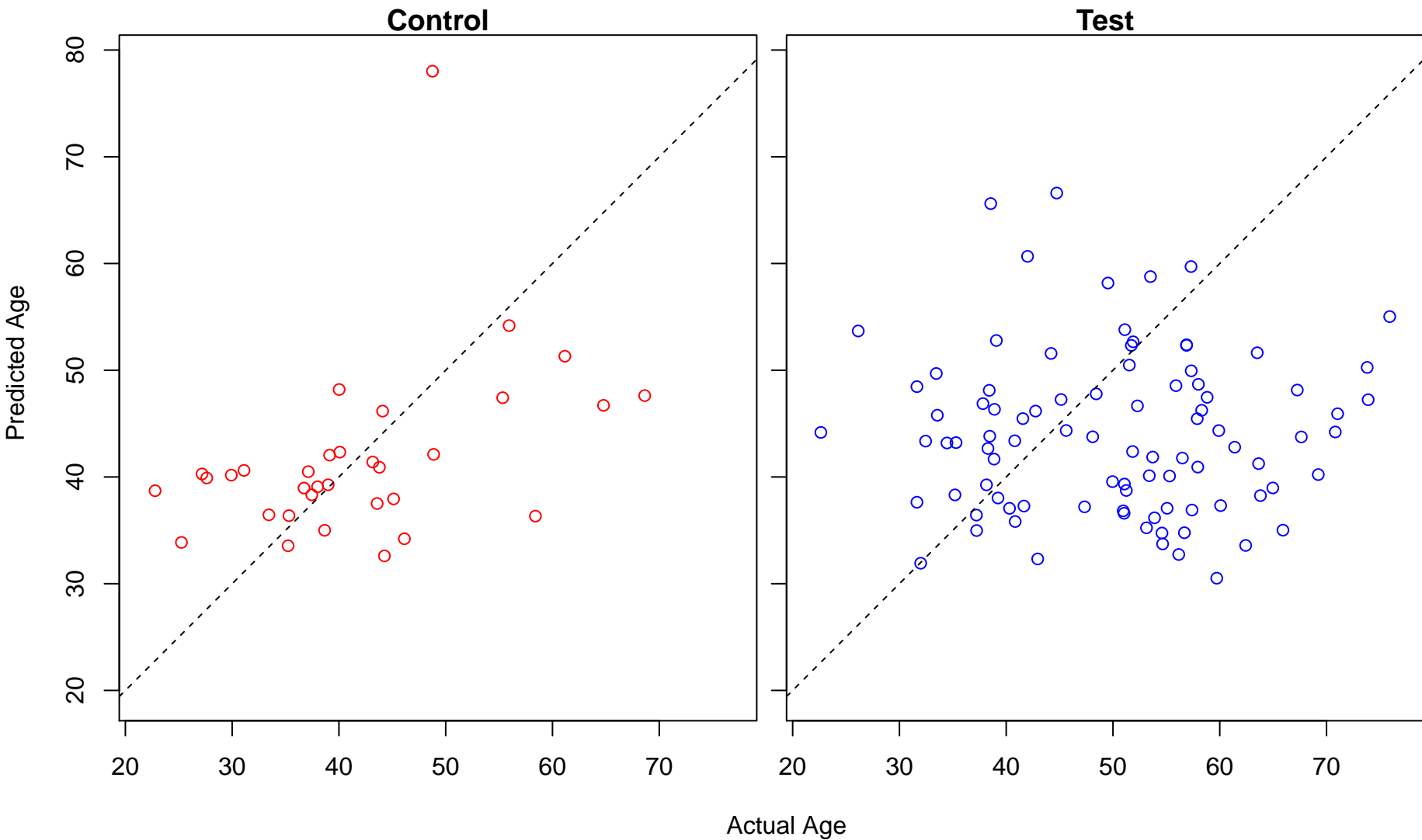
purine ribonucleotide metabolic process (Score: 0.822460)



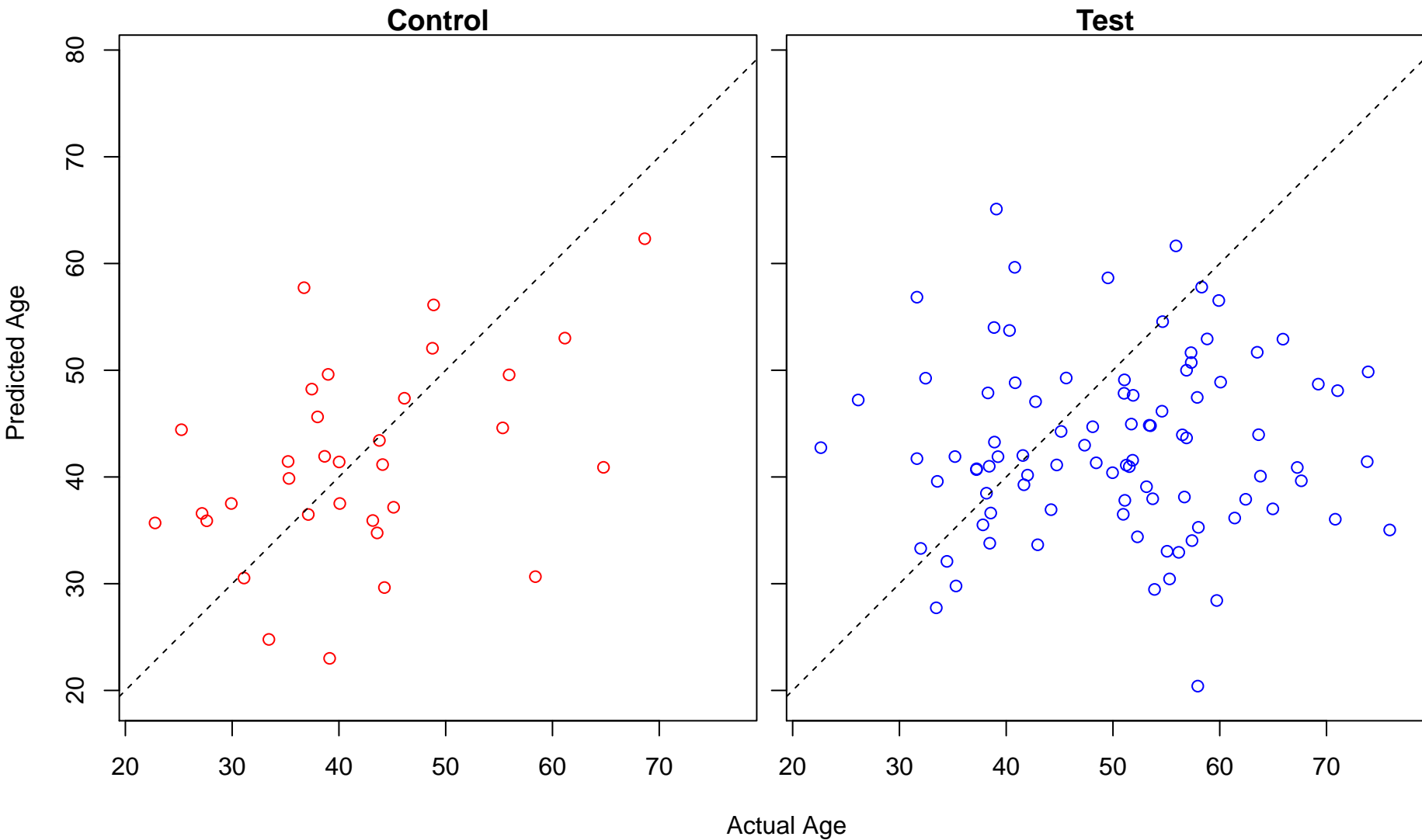
on of cellular ketone metabolic process by regulation of transcription from RNA polymerase II promoter (S



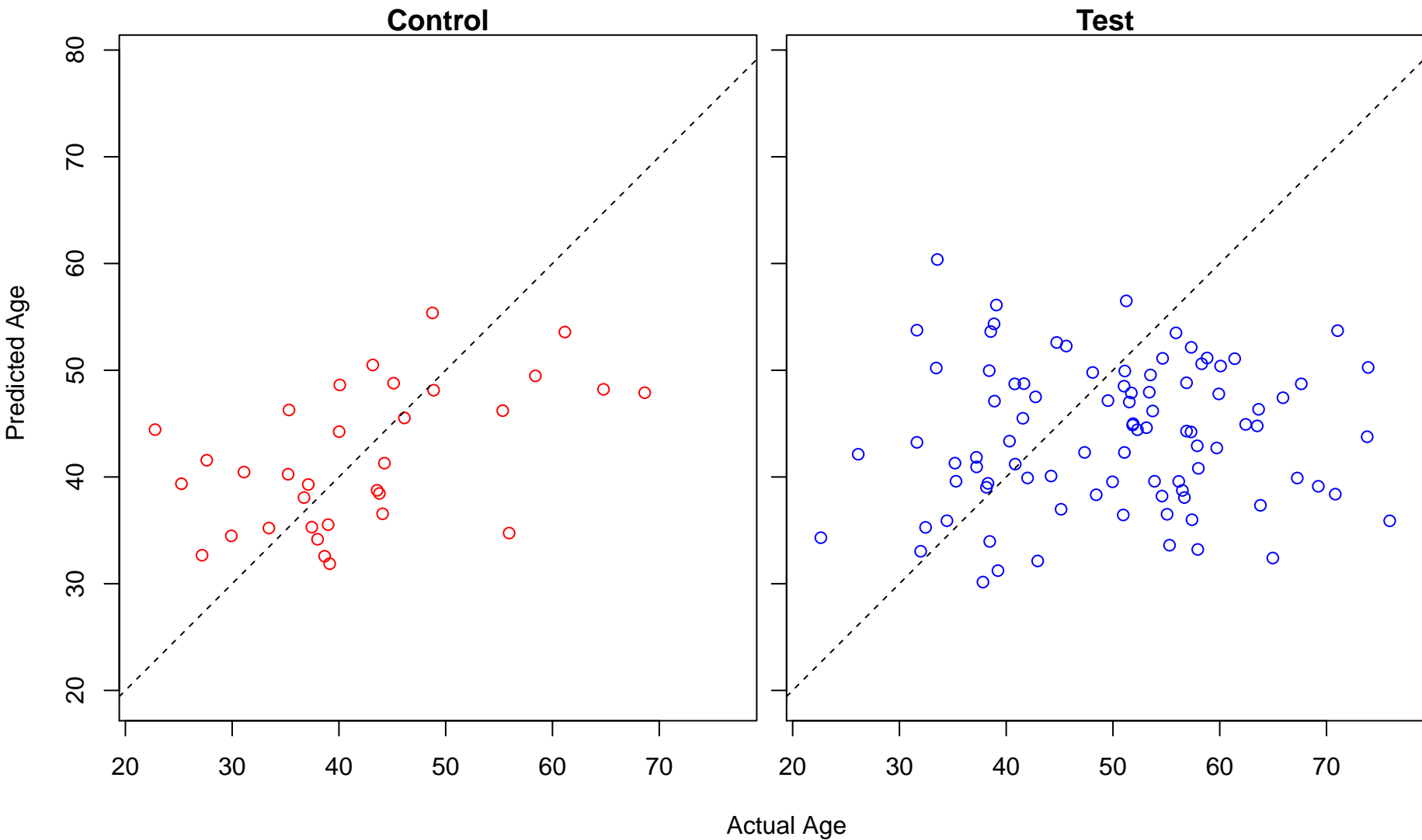
complement receptor mediated signaling pathway (Score: 0.821644)



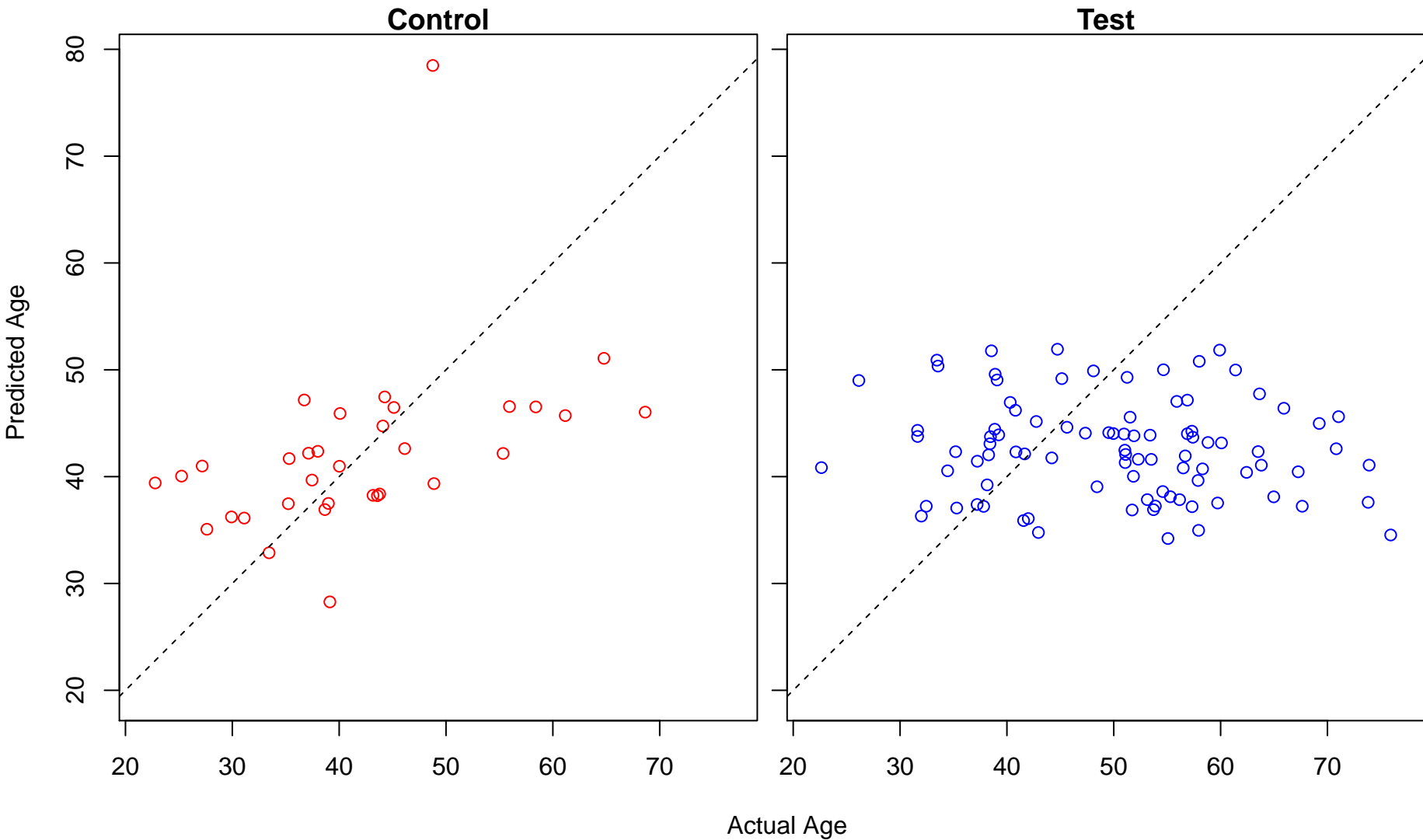
regulation of cilium movement (Score: 0.821403)



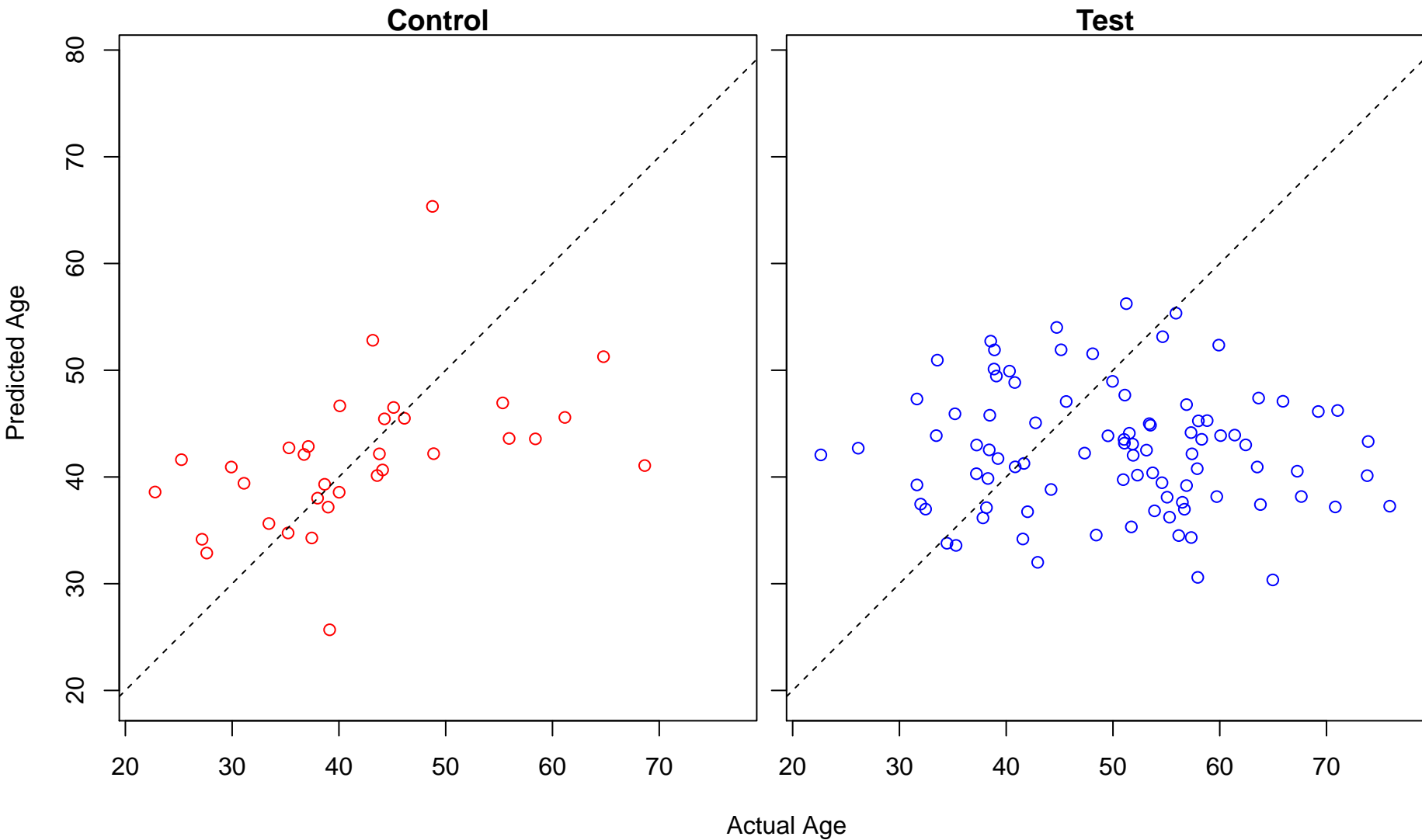
endothelial cell migration (Score: 0.821069)



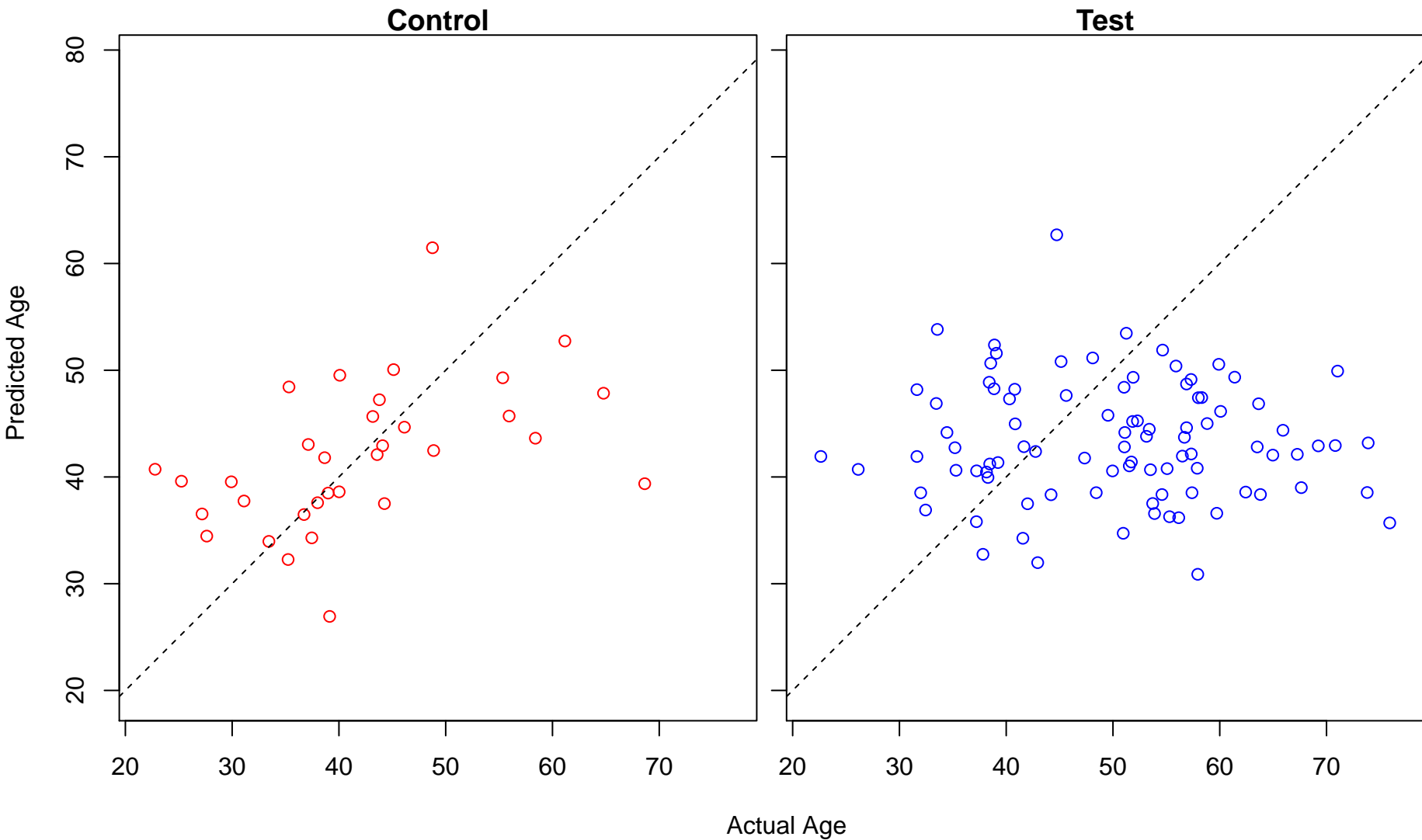
protein localization to mitochondrion (Score: 0.820916)



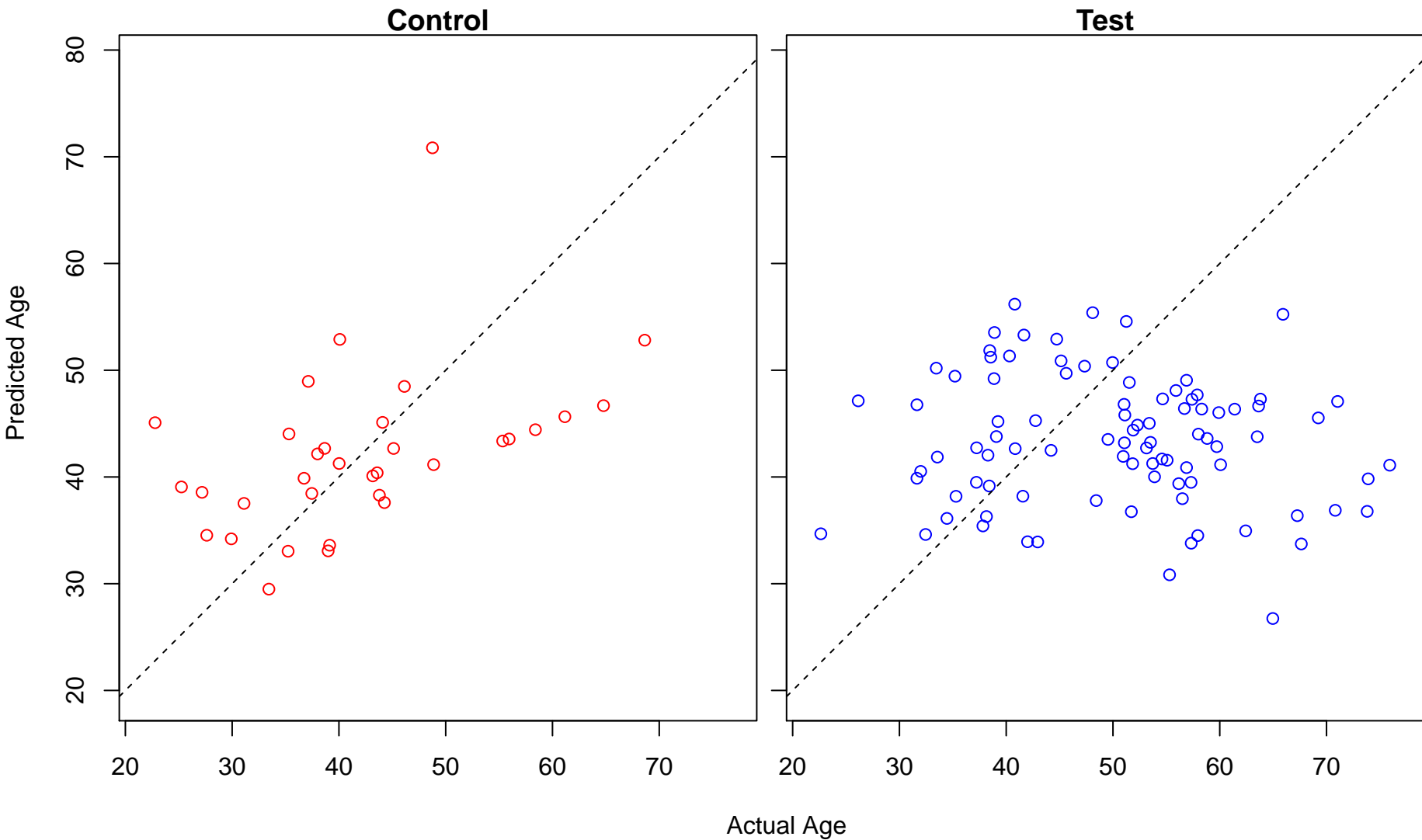
anion transport (Score: 0.820900)



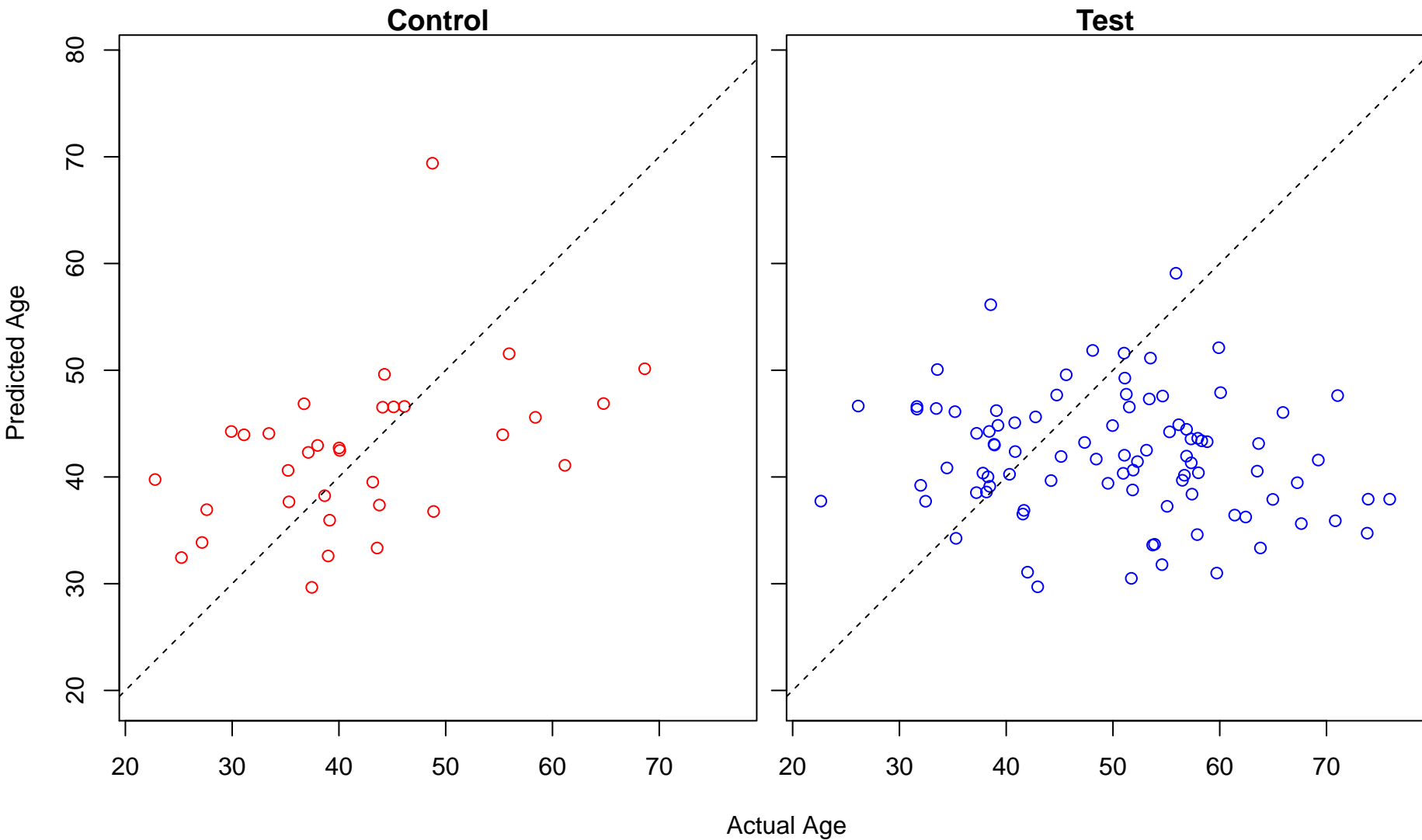
membrane fusion (Score: 0.820853)



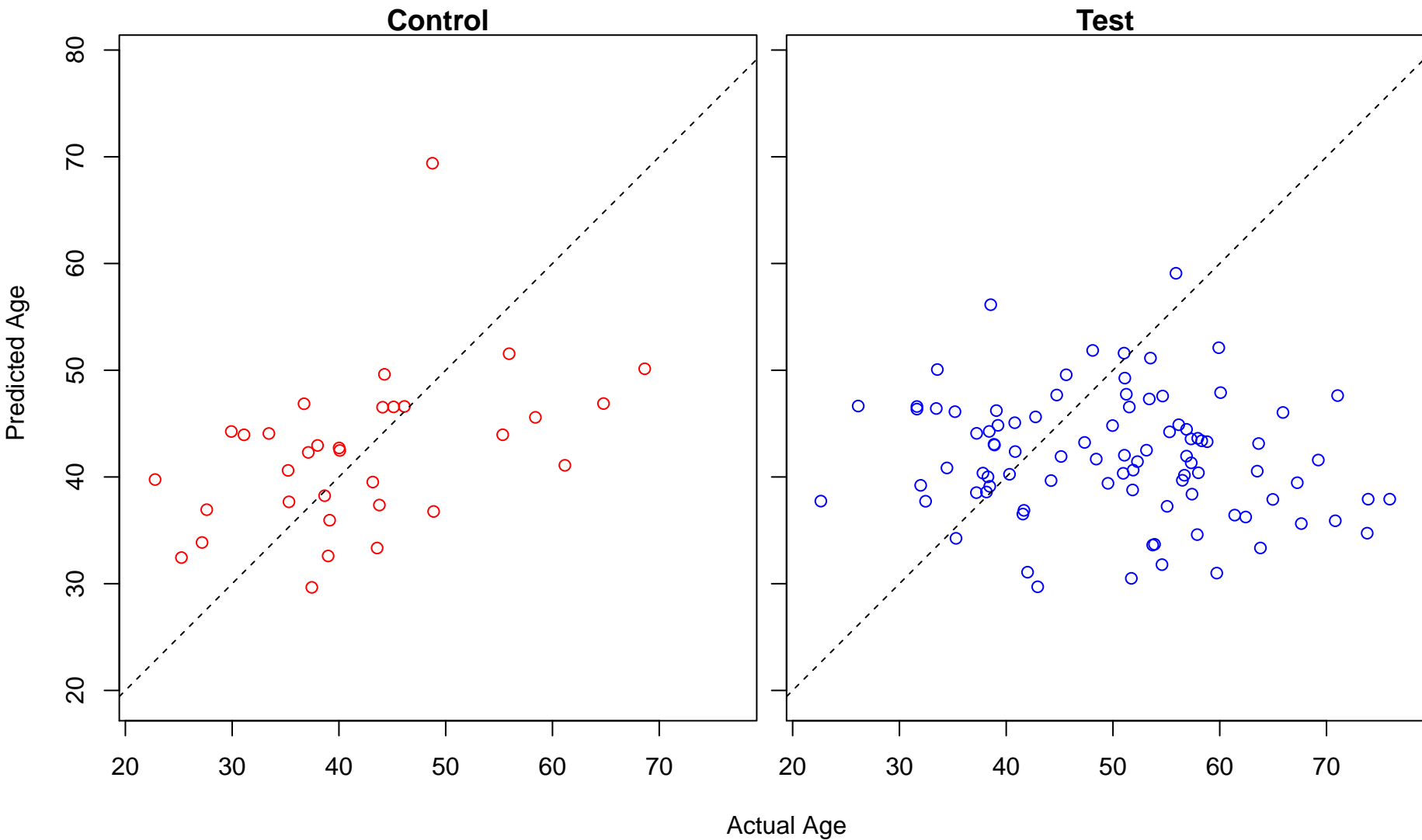
regulation of oxidative phosphorylation (Score: 0.820564)



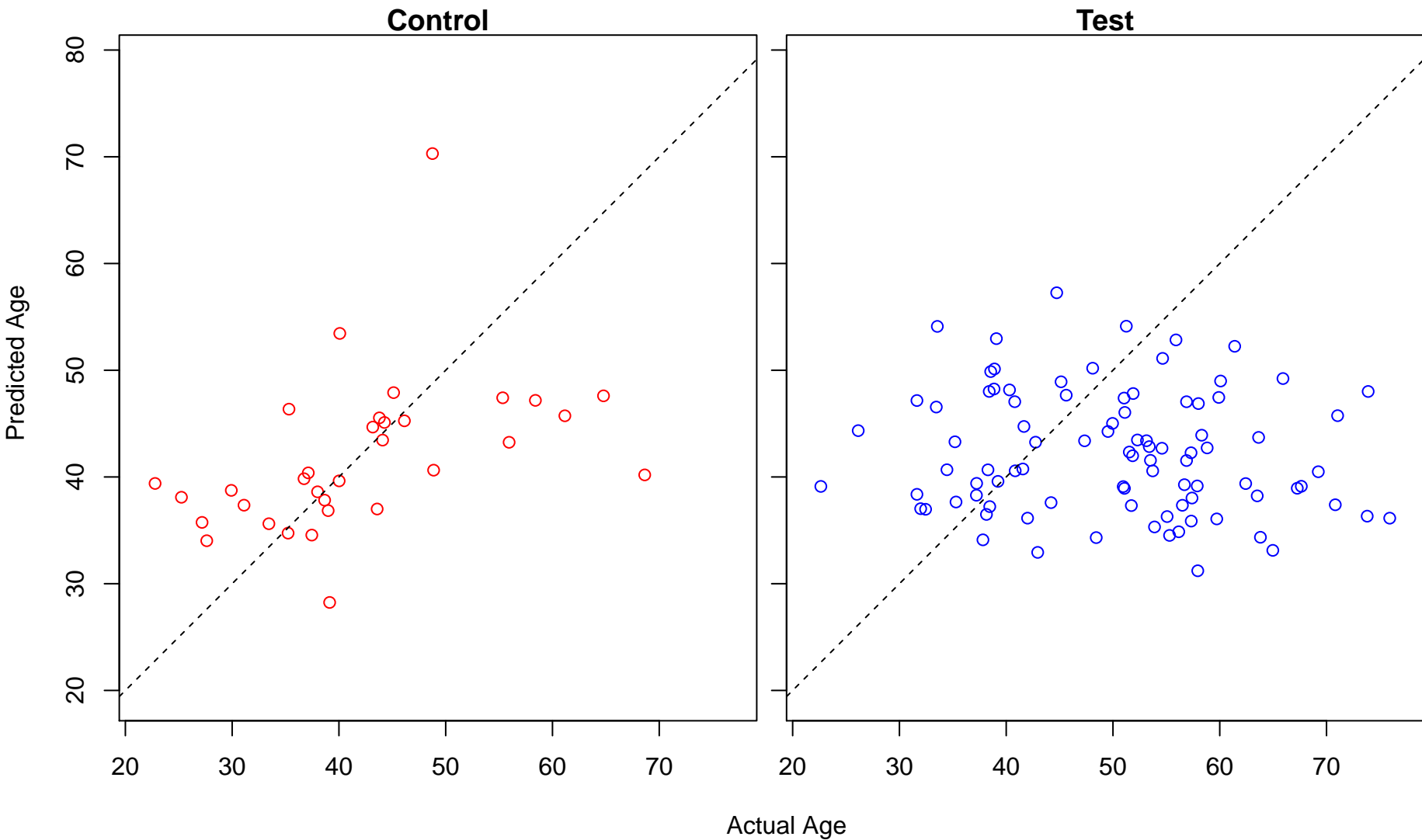
negative regulation of nucleotide biosynthetic process (Score: 0.819834)



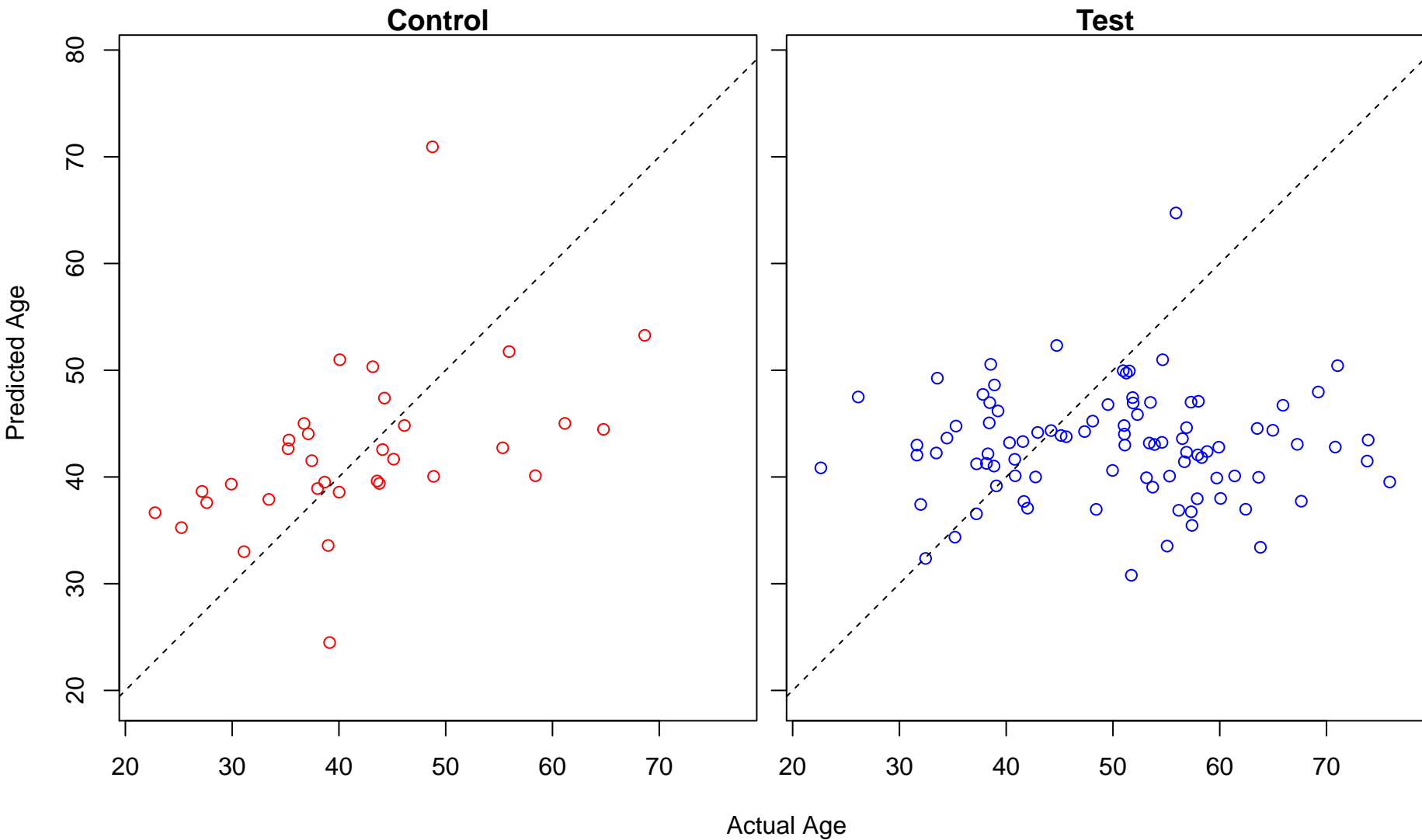
negative regulation of purine nucleotide biosynthetic process (Score: 0.819834)



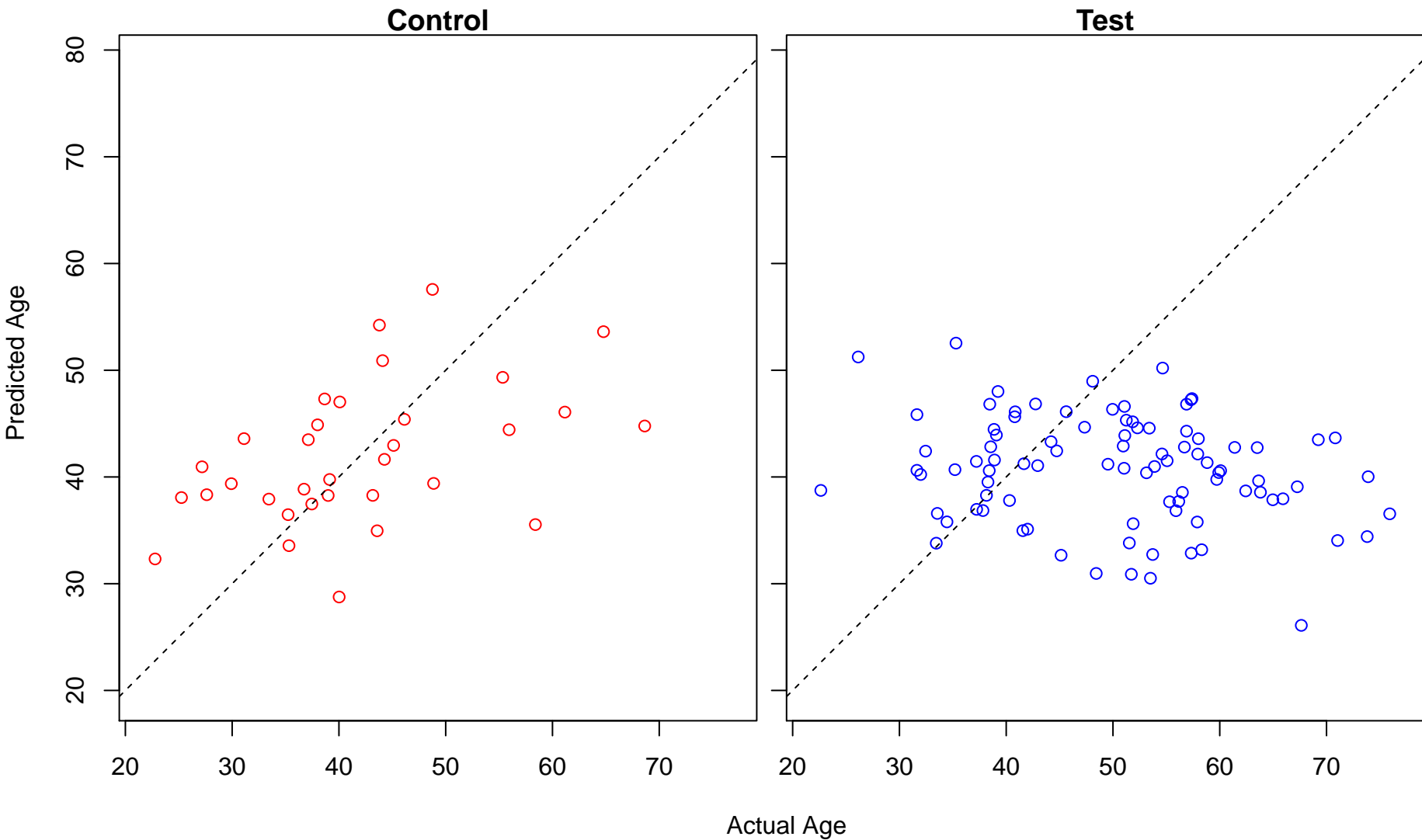
regulation of cellular response to stress (Score: 0.819478)



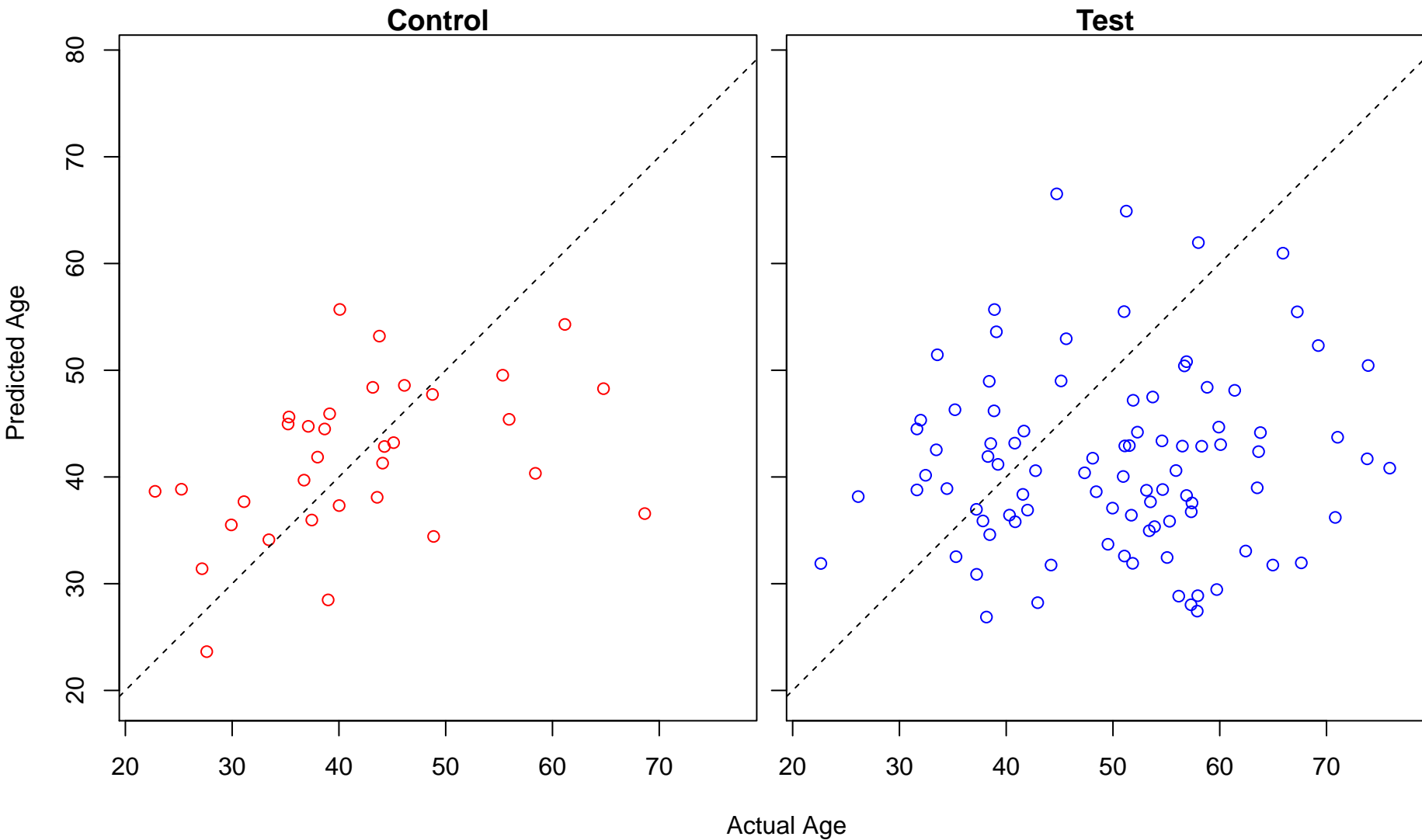
regulation of ATP biosynthetic process (Score: 0.819316)



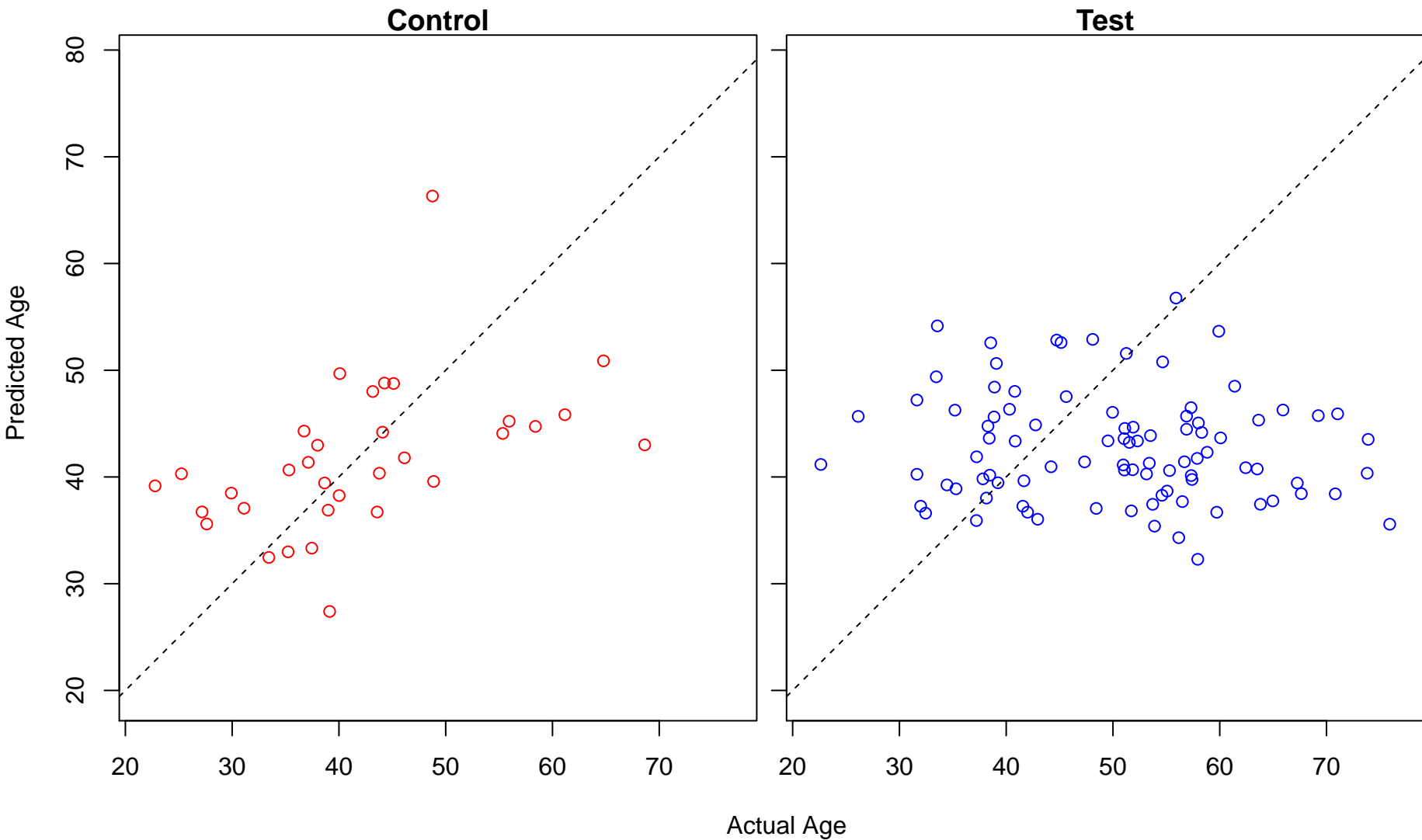
cardiac chamber development (Score: 0.818521)



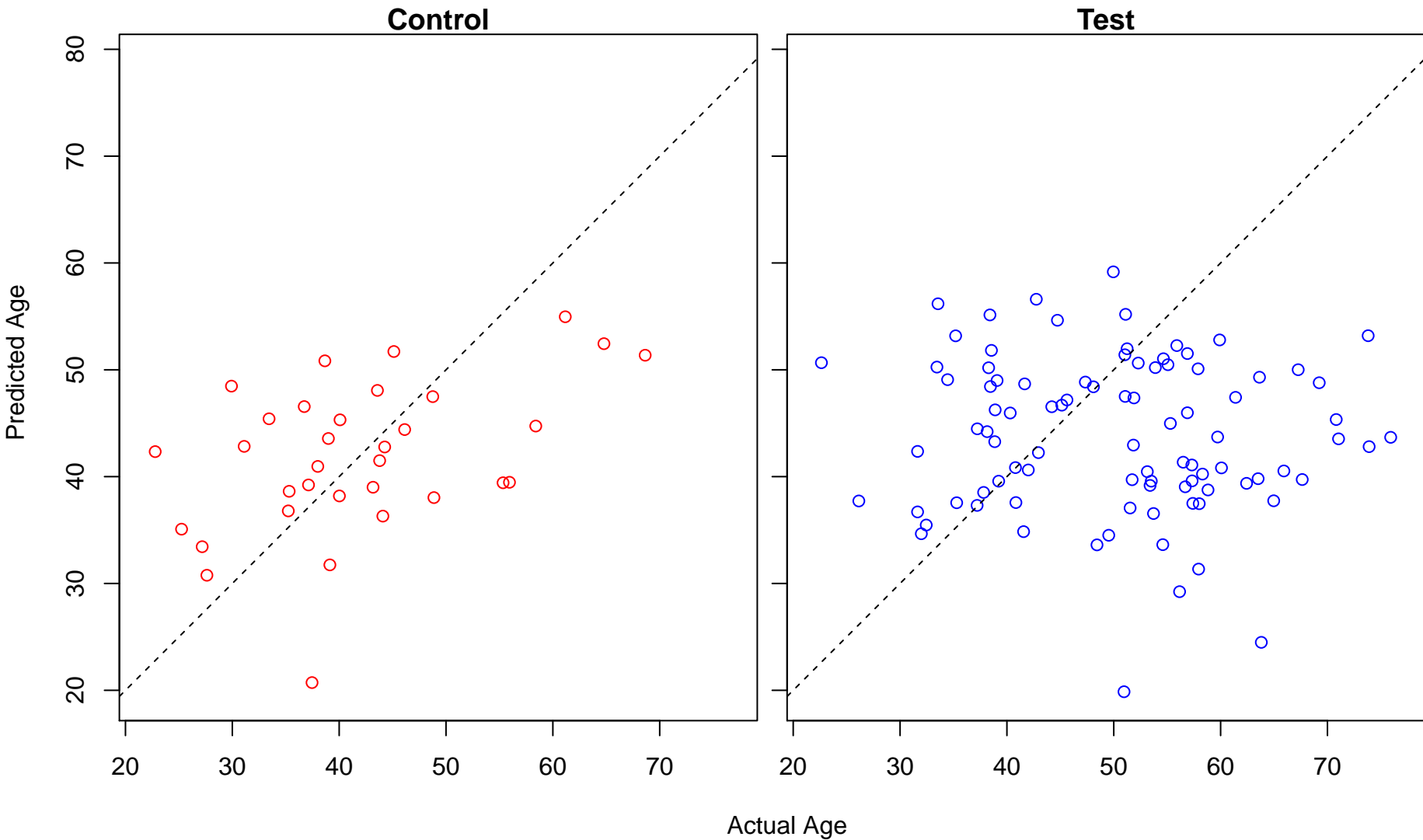
negative regulation of heart contraction (Score: 0.818501)



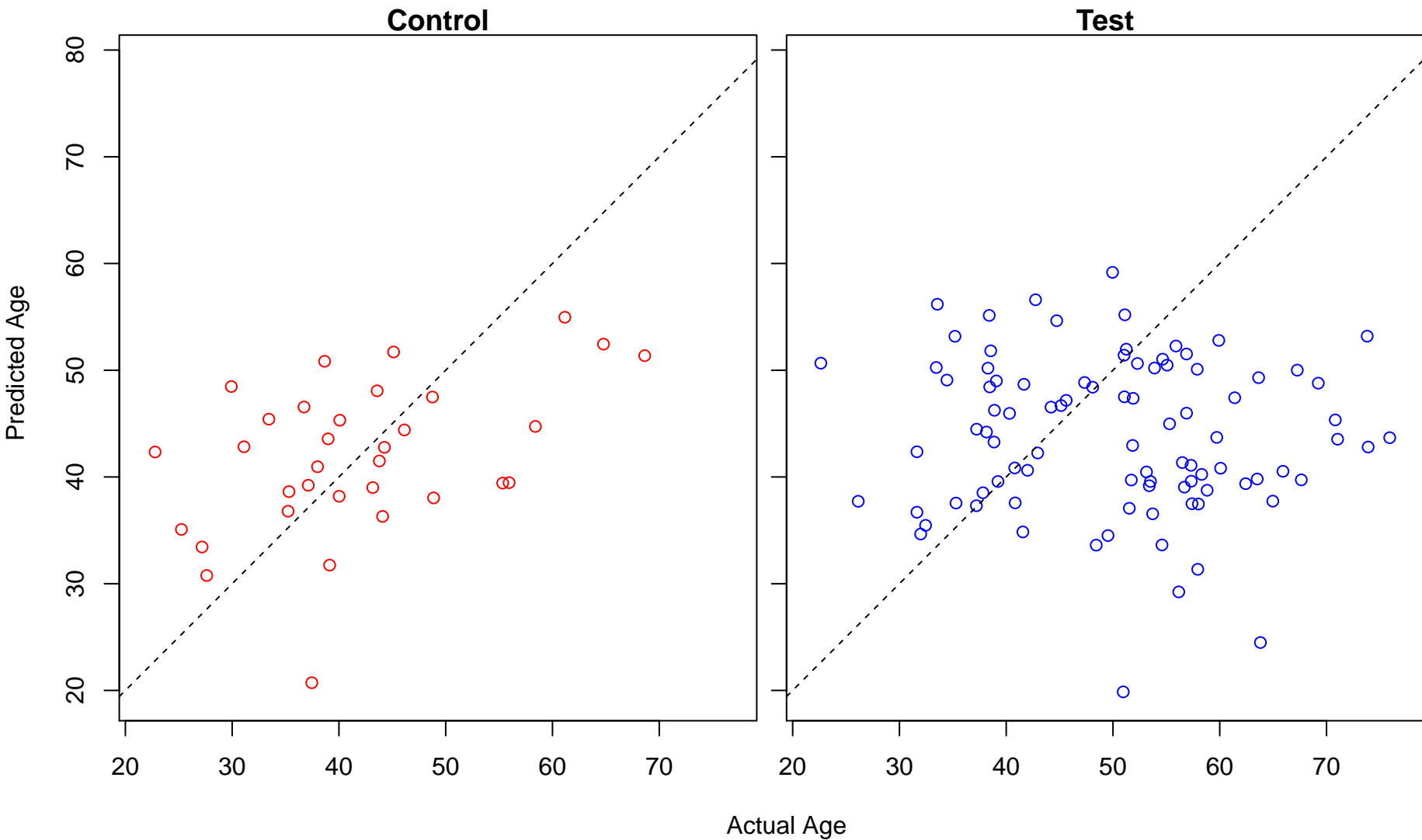
ribose phosphate metabolic process (Score: 0.818253)



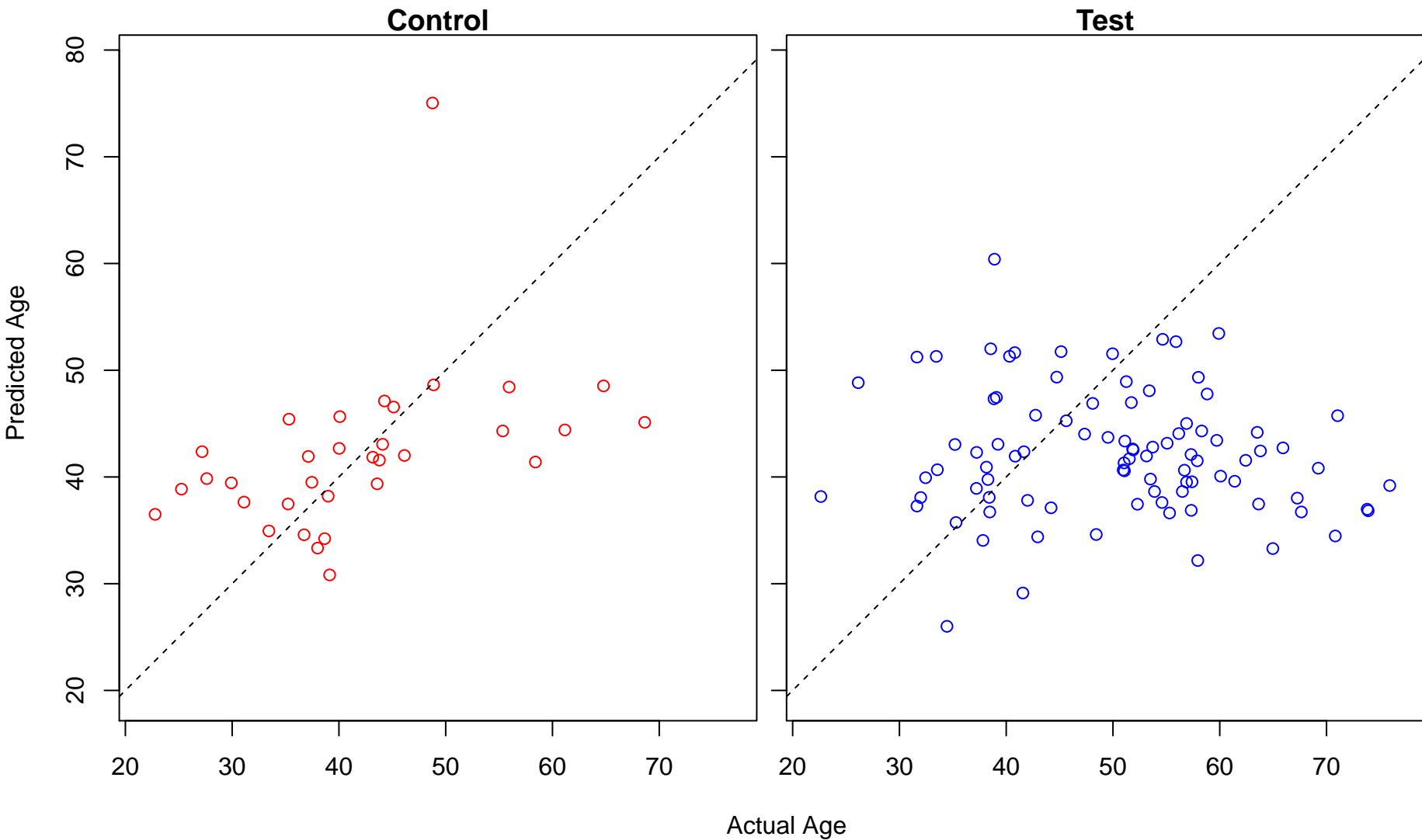
presynaptic membrane organization (Score: 0.817802)



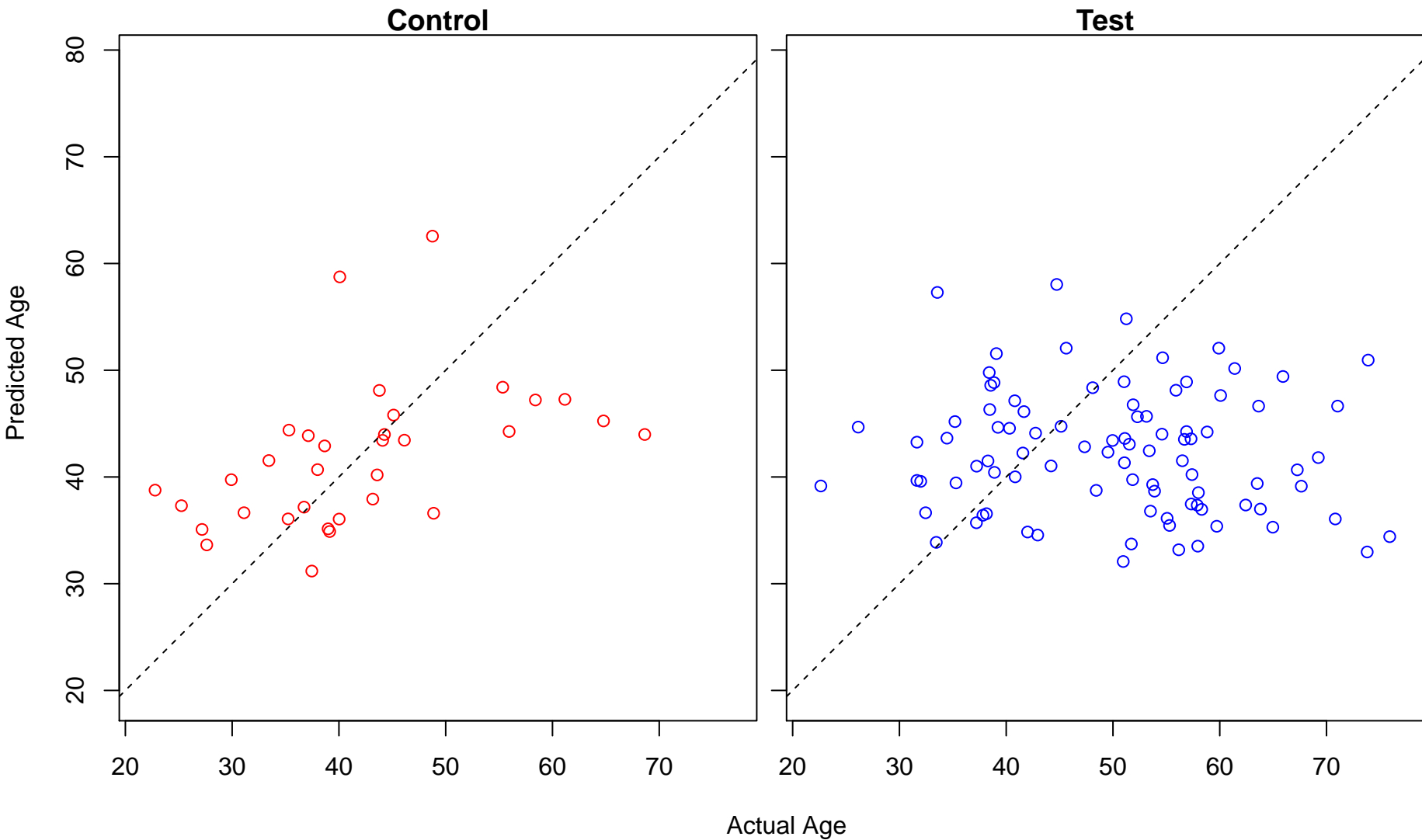
presynaptic membrane assembly (Score: 0.817802)



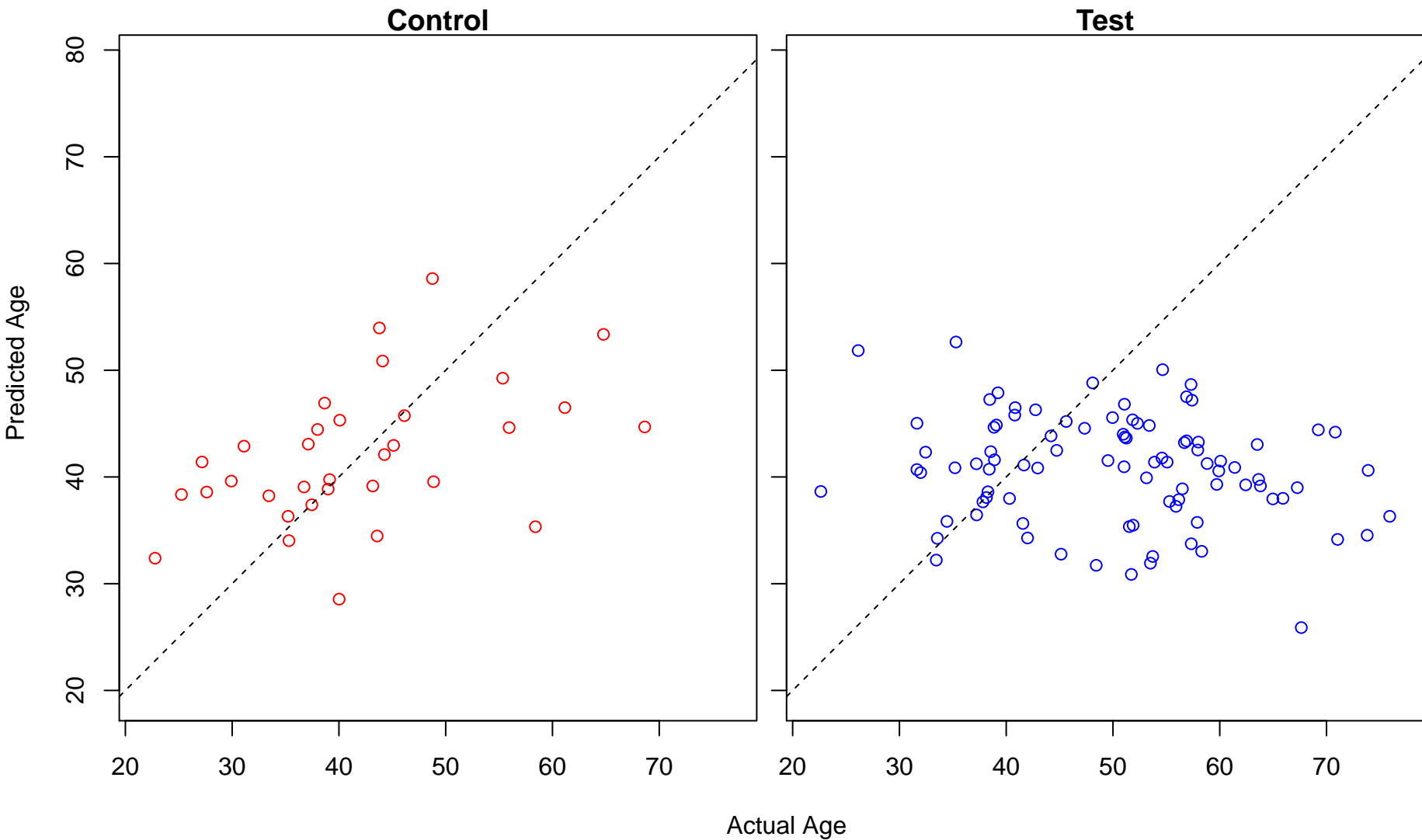
positive regulation of protein sumoylation (Score: 0.816967)



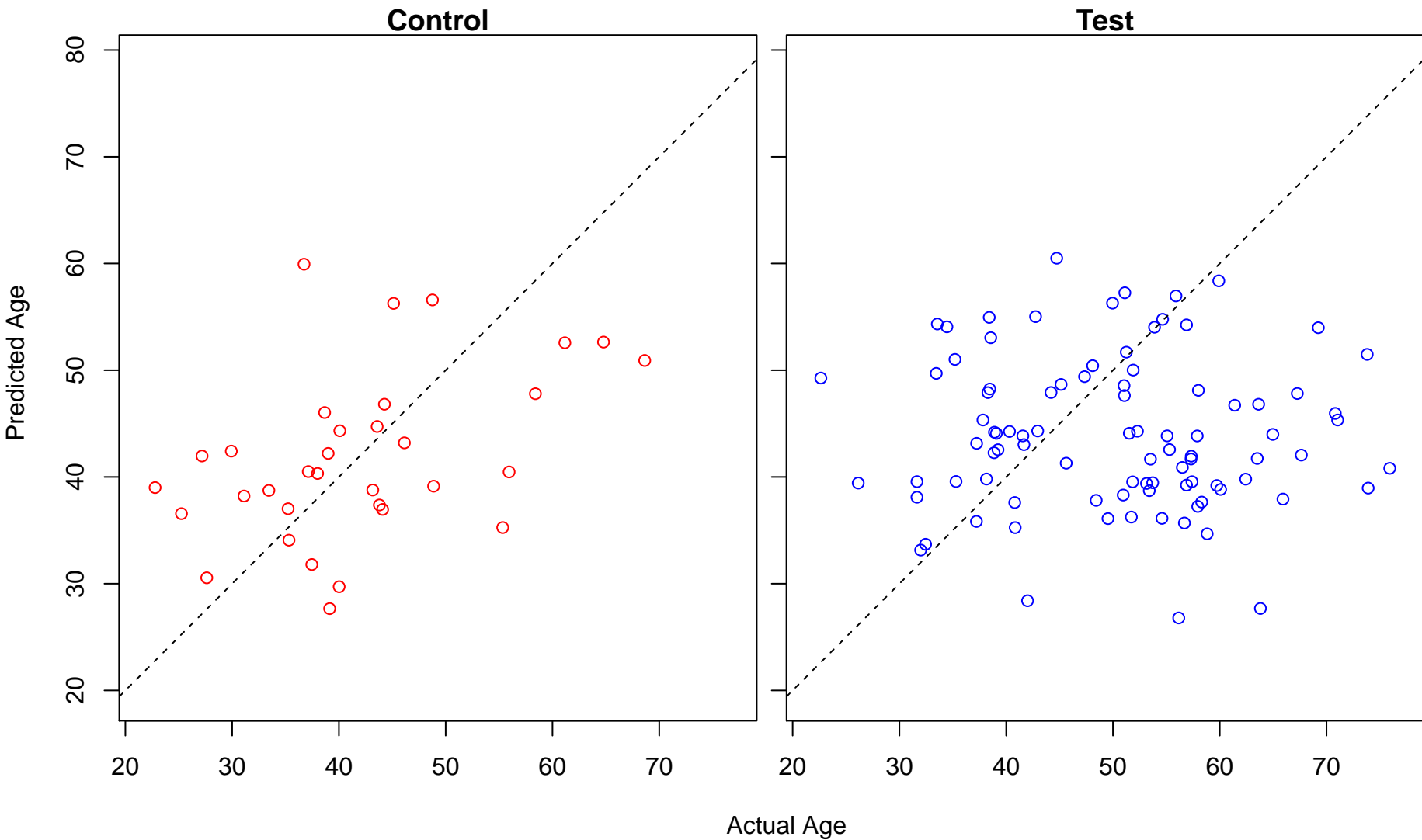
regulation of peptidyl-tyrosine phosphorylation (Score: 0.816483)



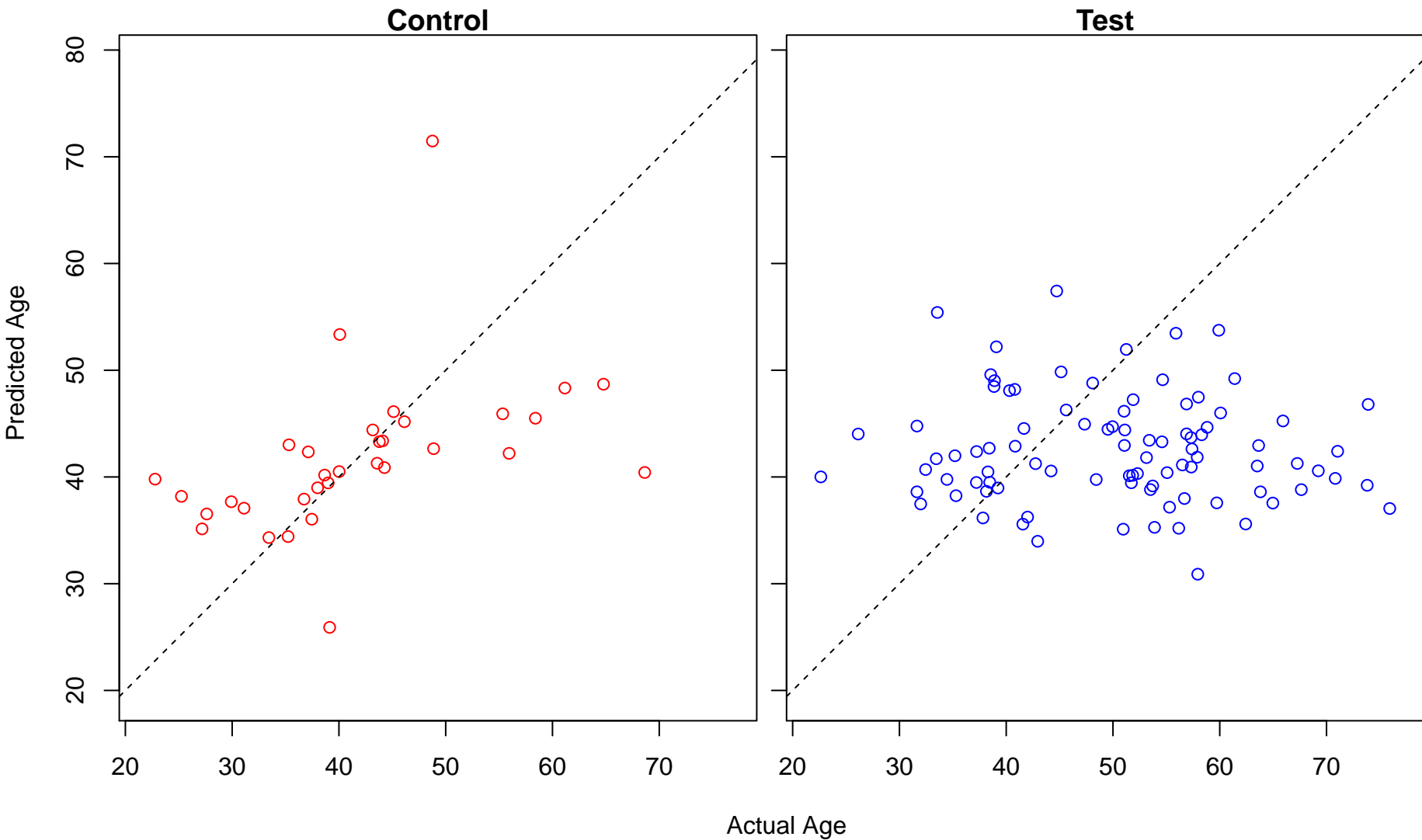
cardiac chamber morphogenesis (Score: 0.816473)



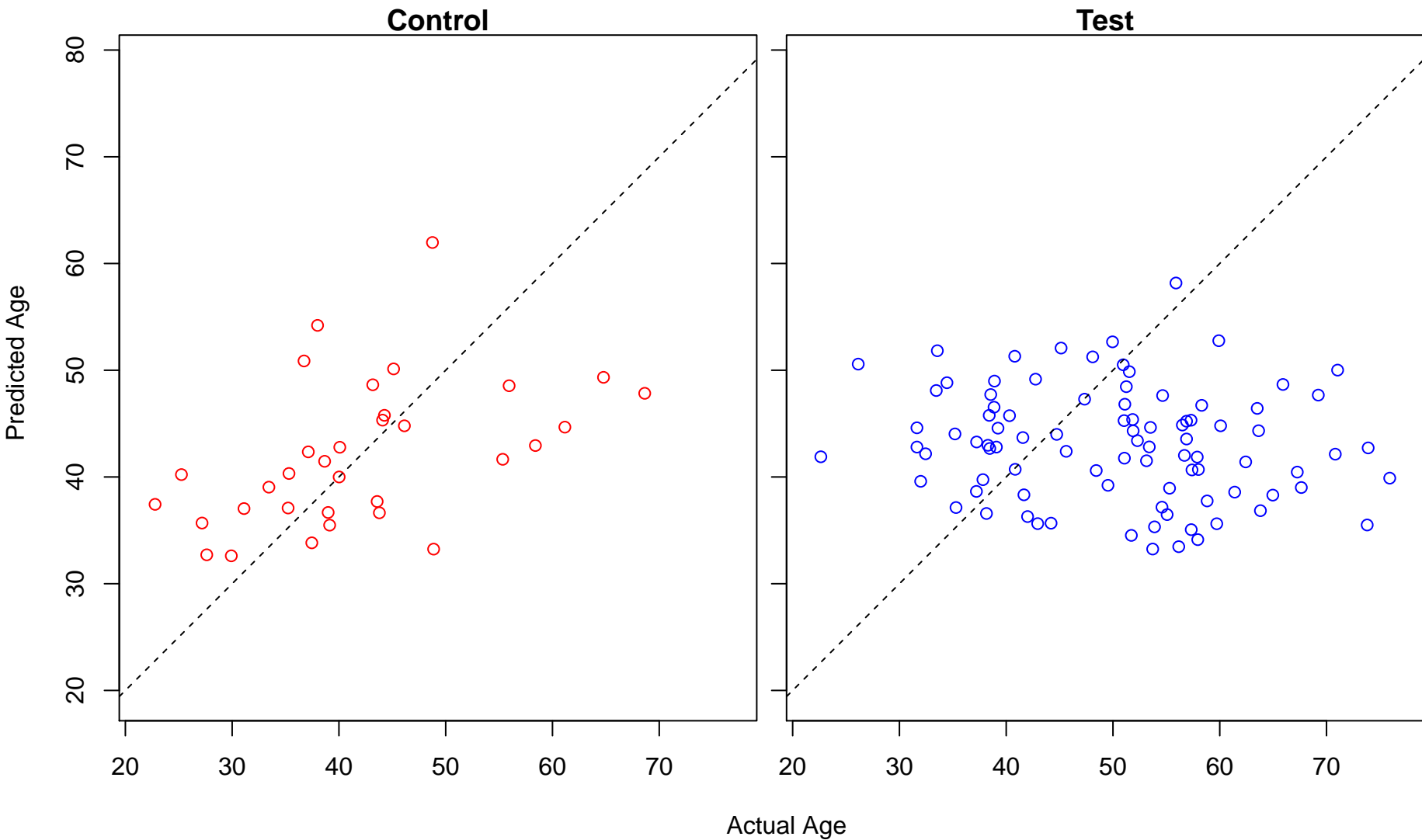
positive regulation of synaptic transmission, glutamatergic (Score: 0.815687)



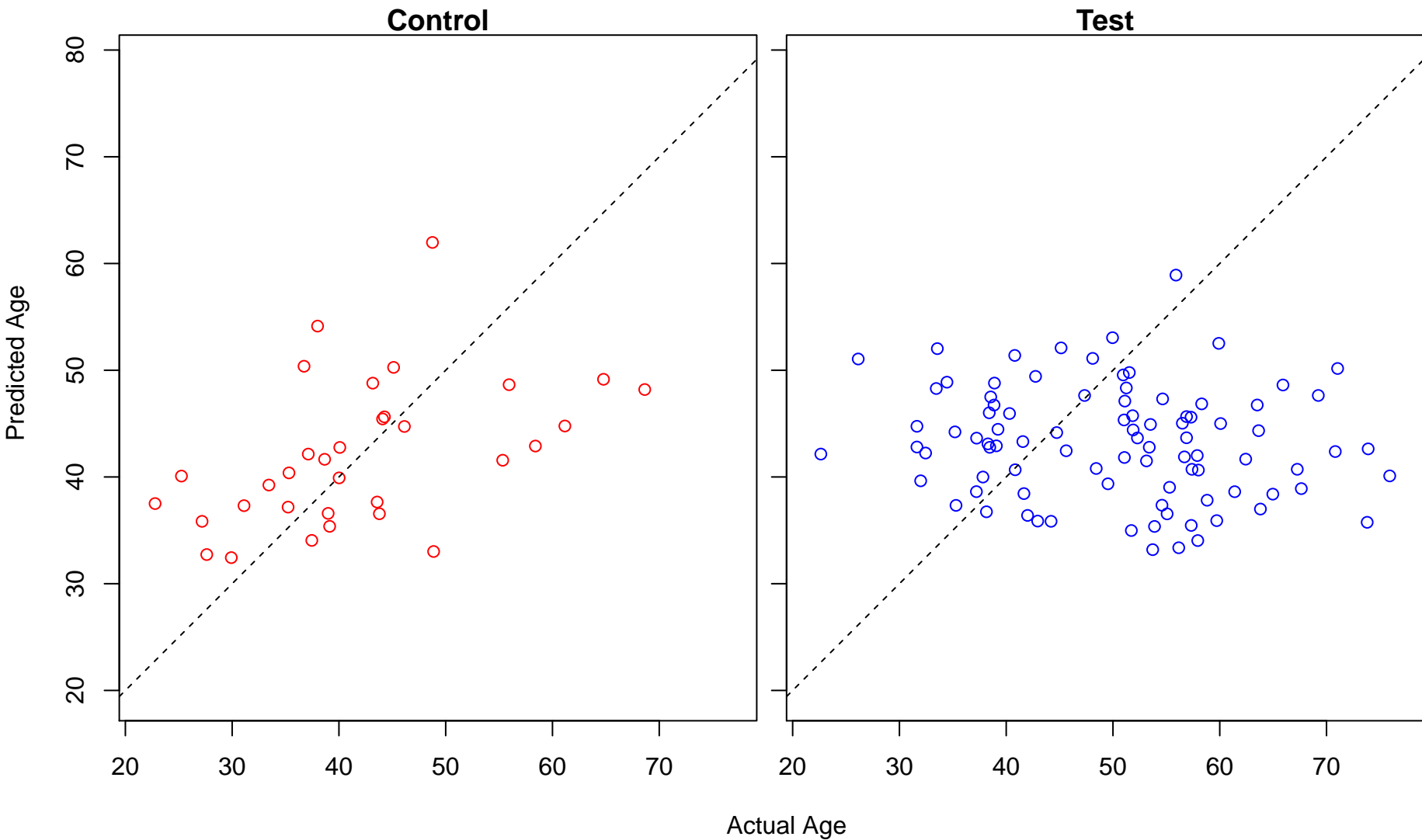
organelle localization (Score: 0.815500)



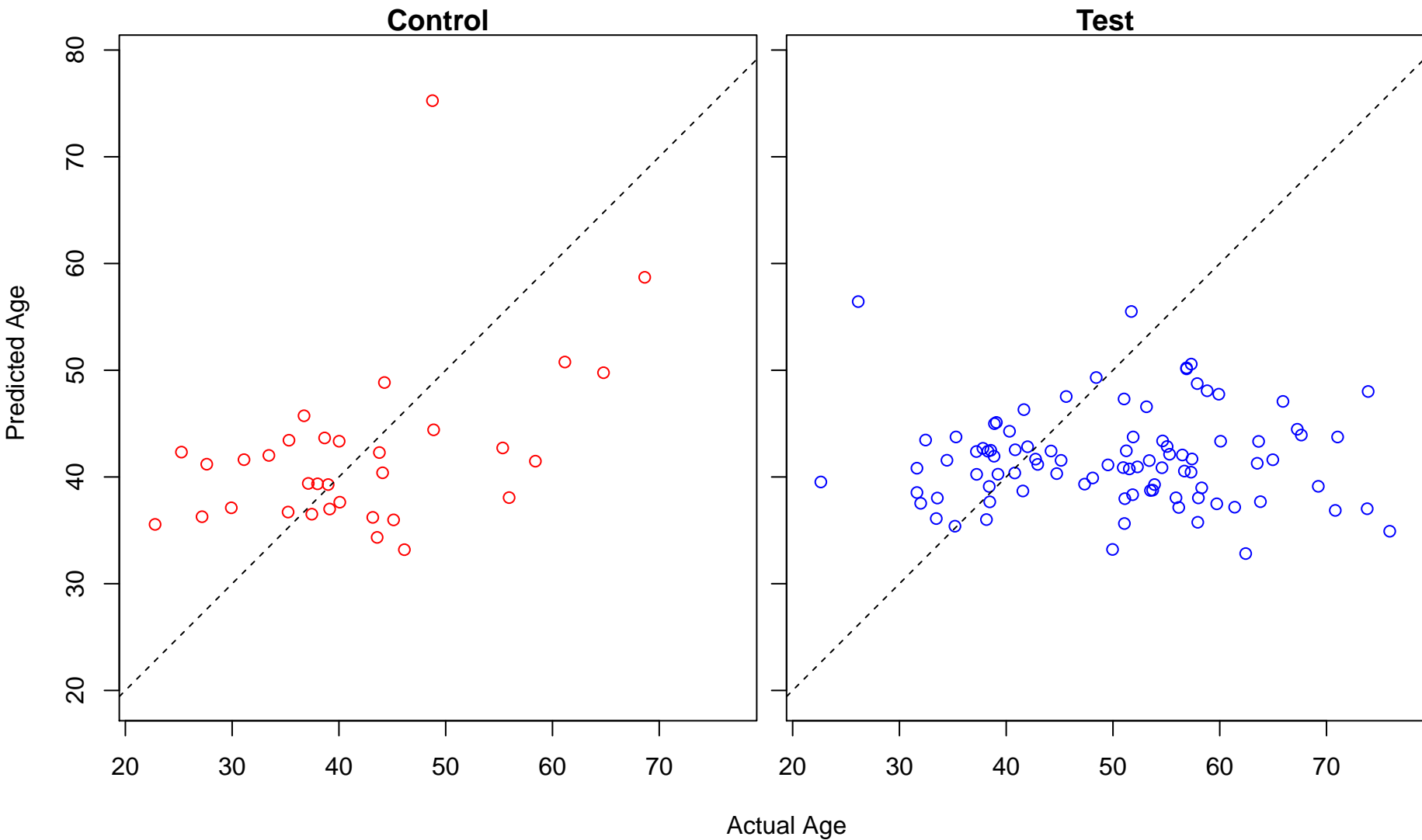
ribonucleotide catabolic process (Score: 0.815454)



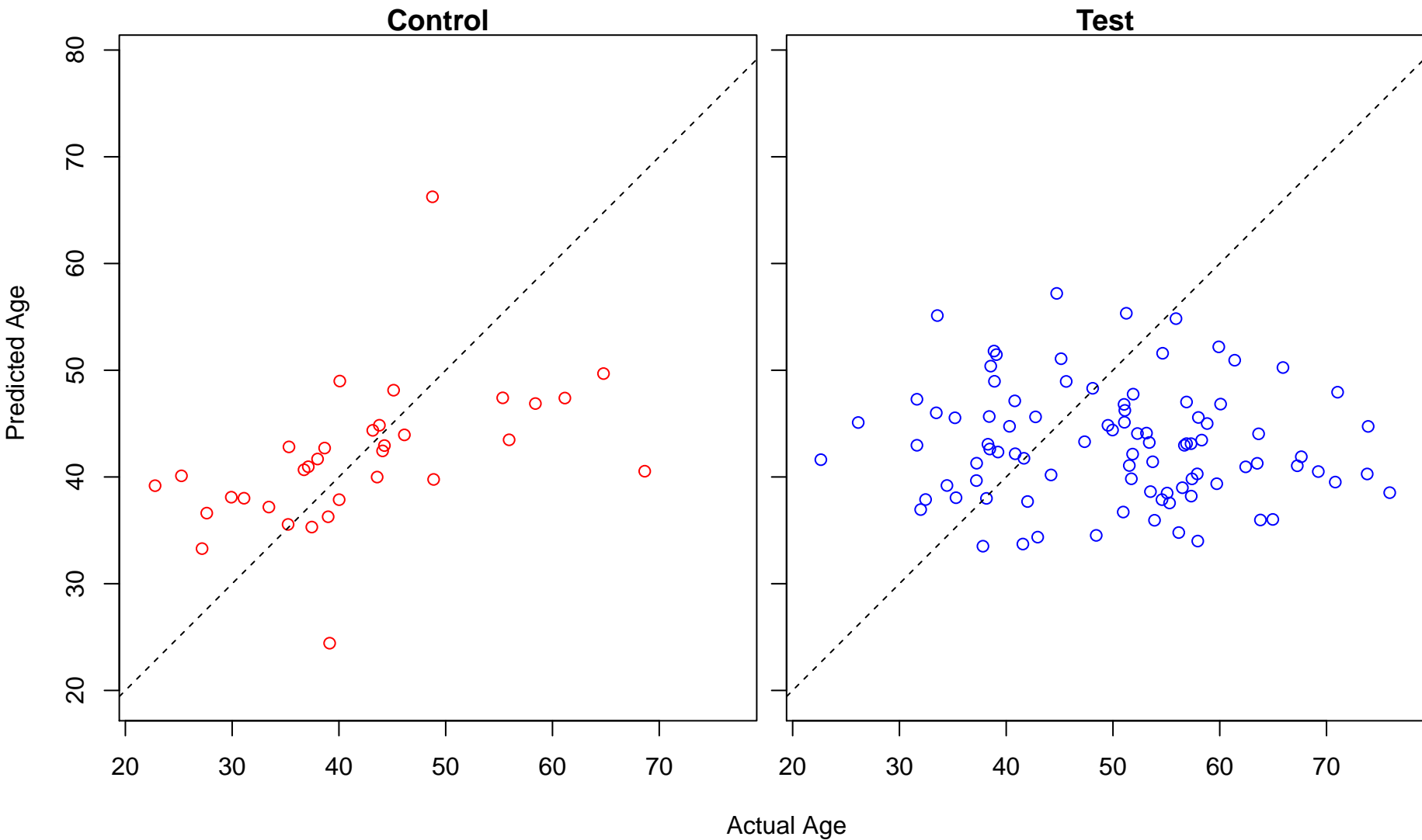
purine ribonucleotide catabolic process (Score: 0.815444)



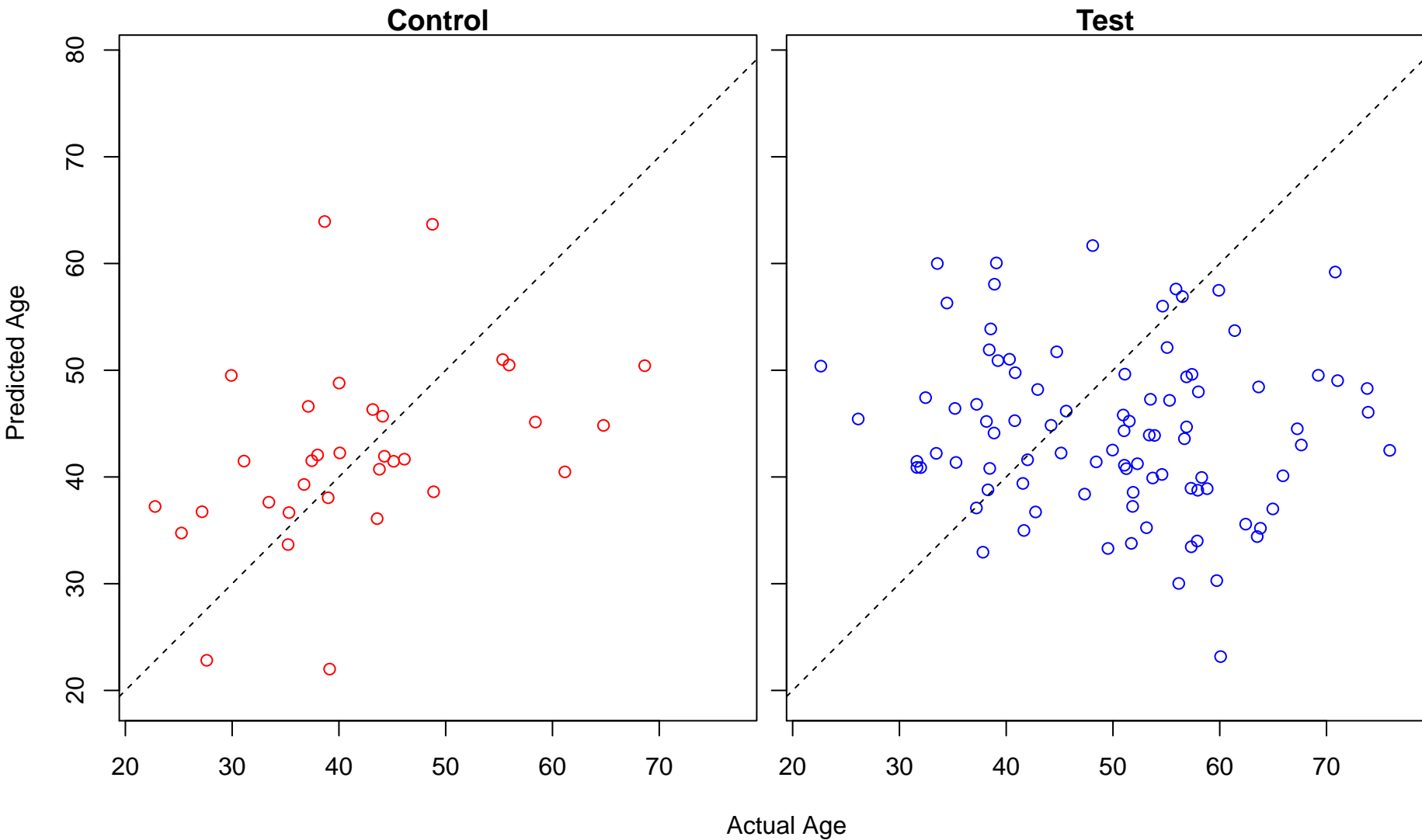
regulation of histone H3-K27 acetylation (Score: 0.815228)



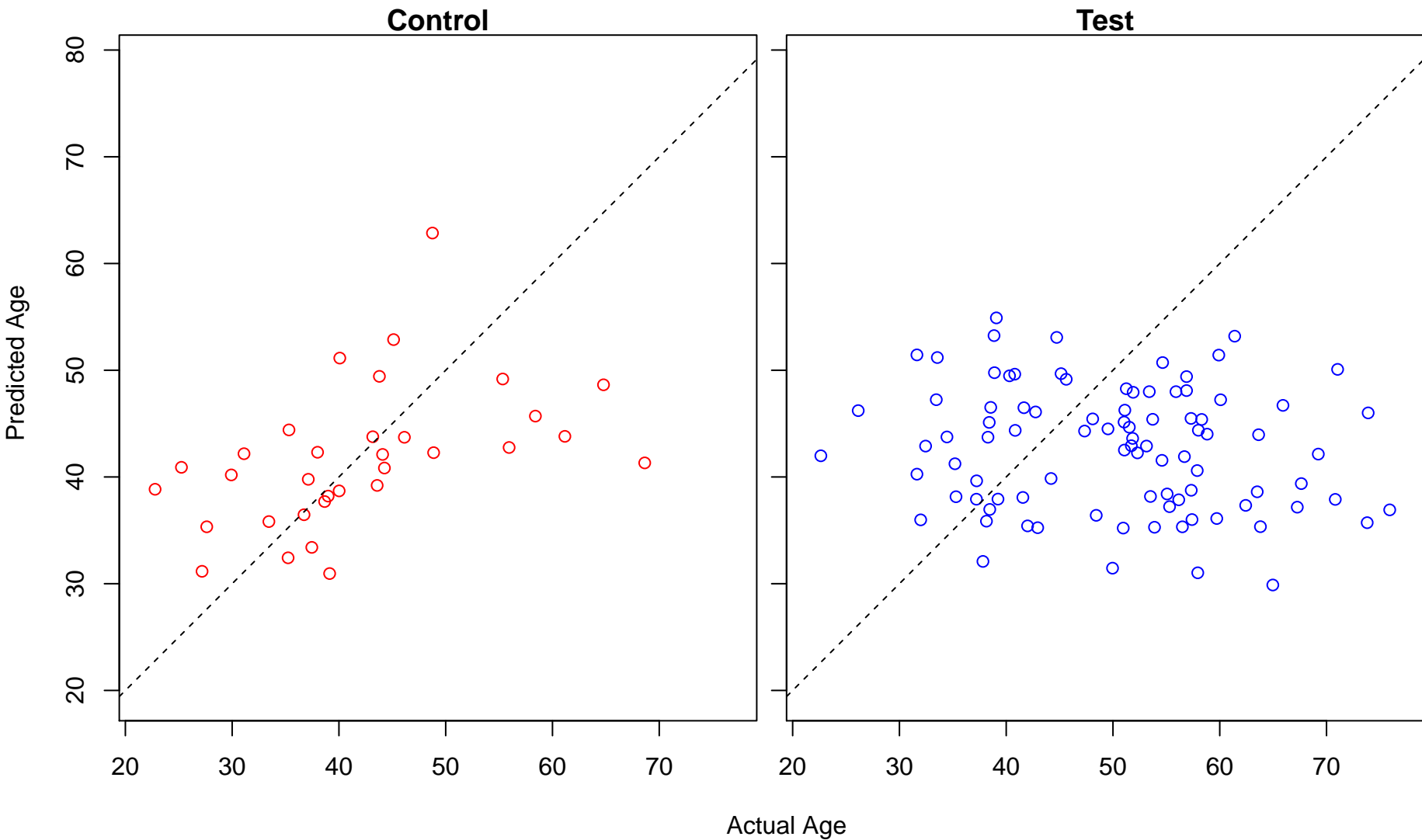
cell development (Score: 0.813490)



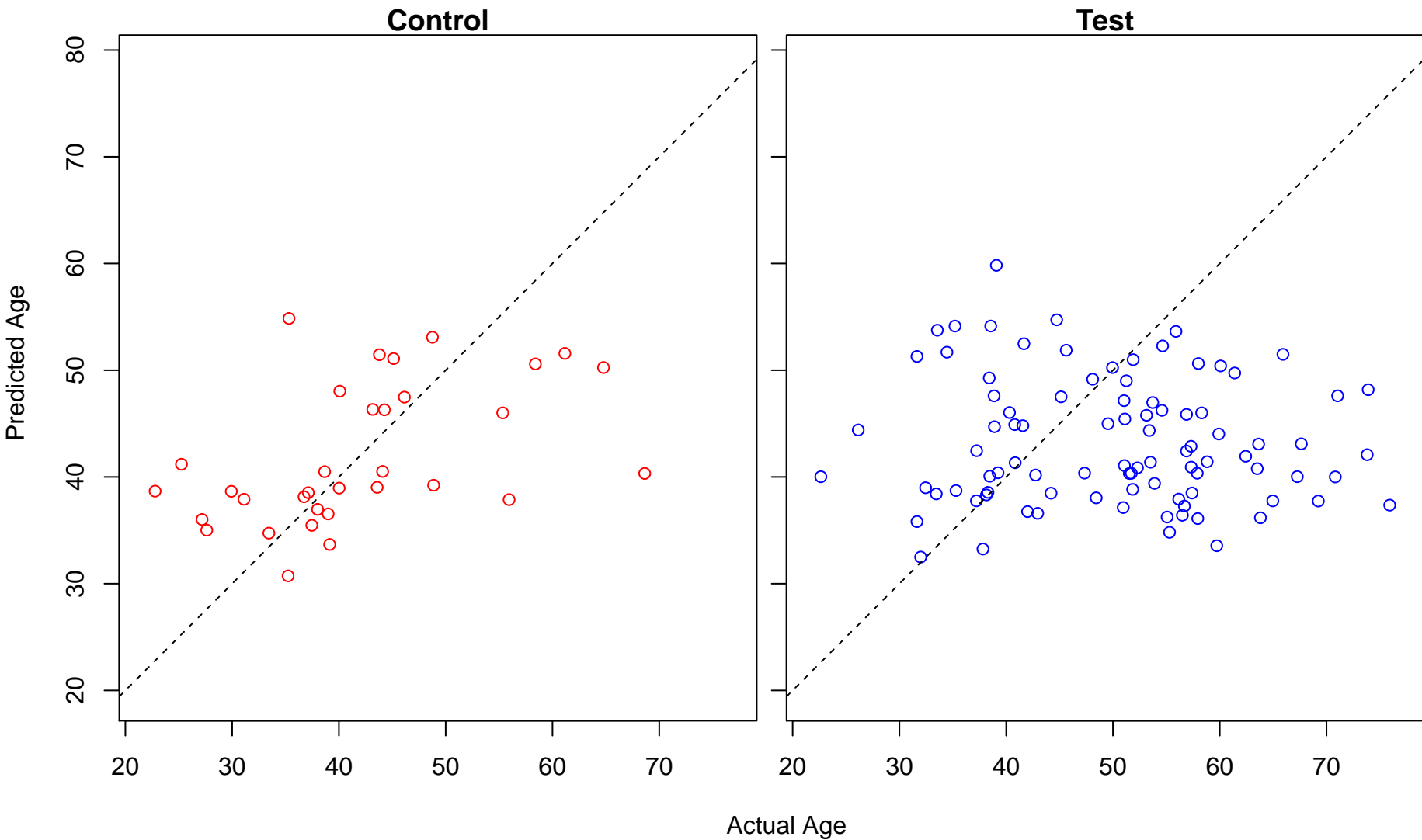
maternal process involved in female pregnancy (Score: 0.812980)



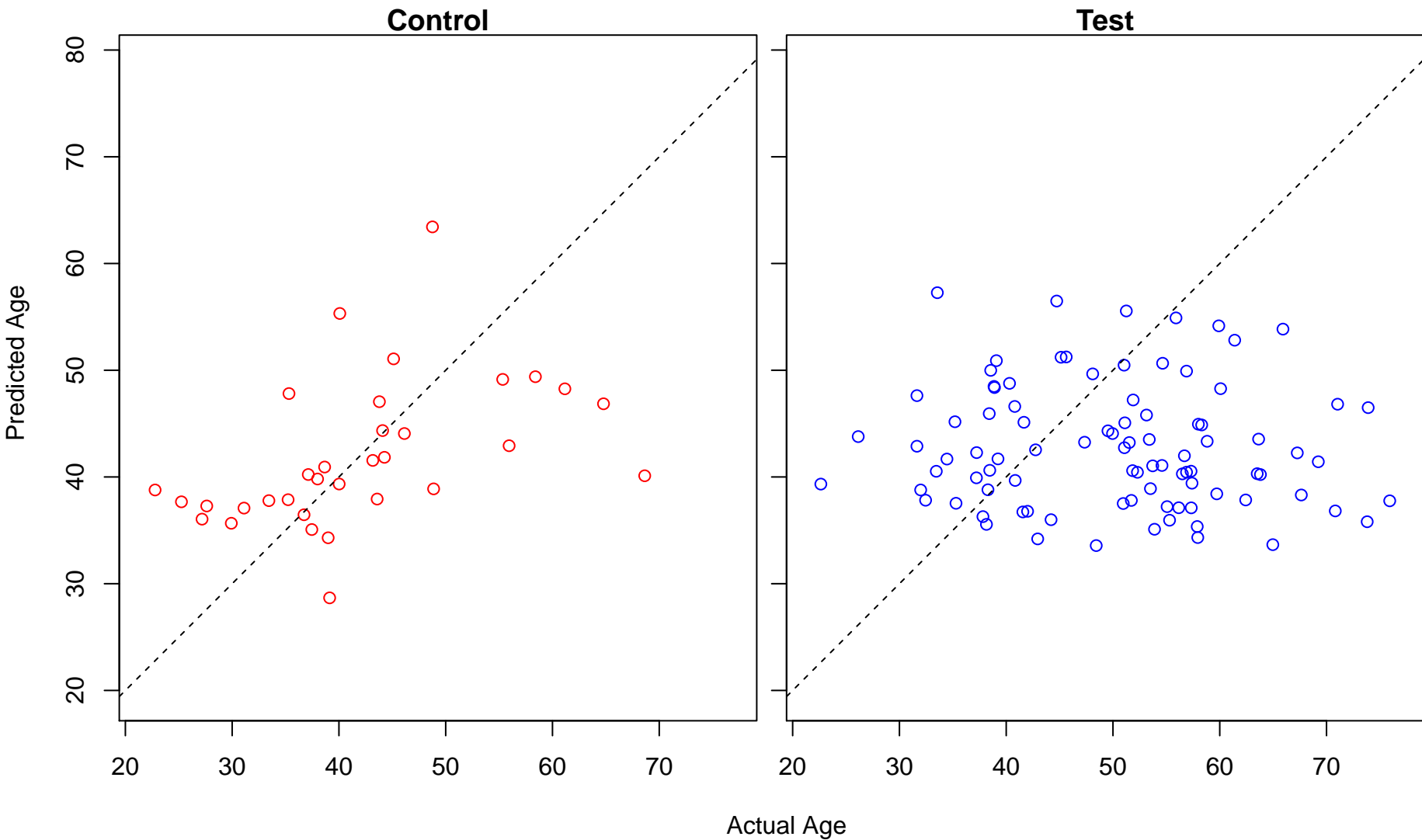
Notch signaling pathway (Score: 0.812722)



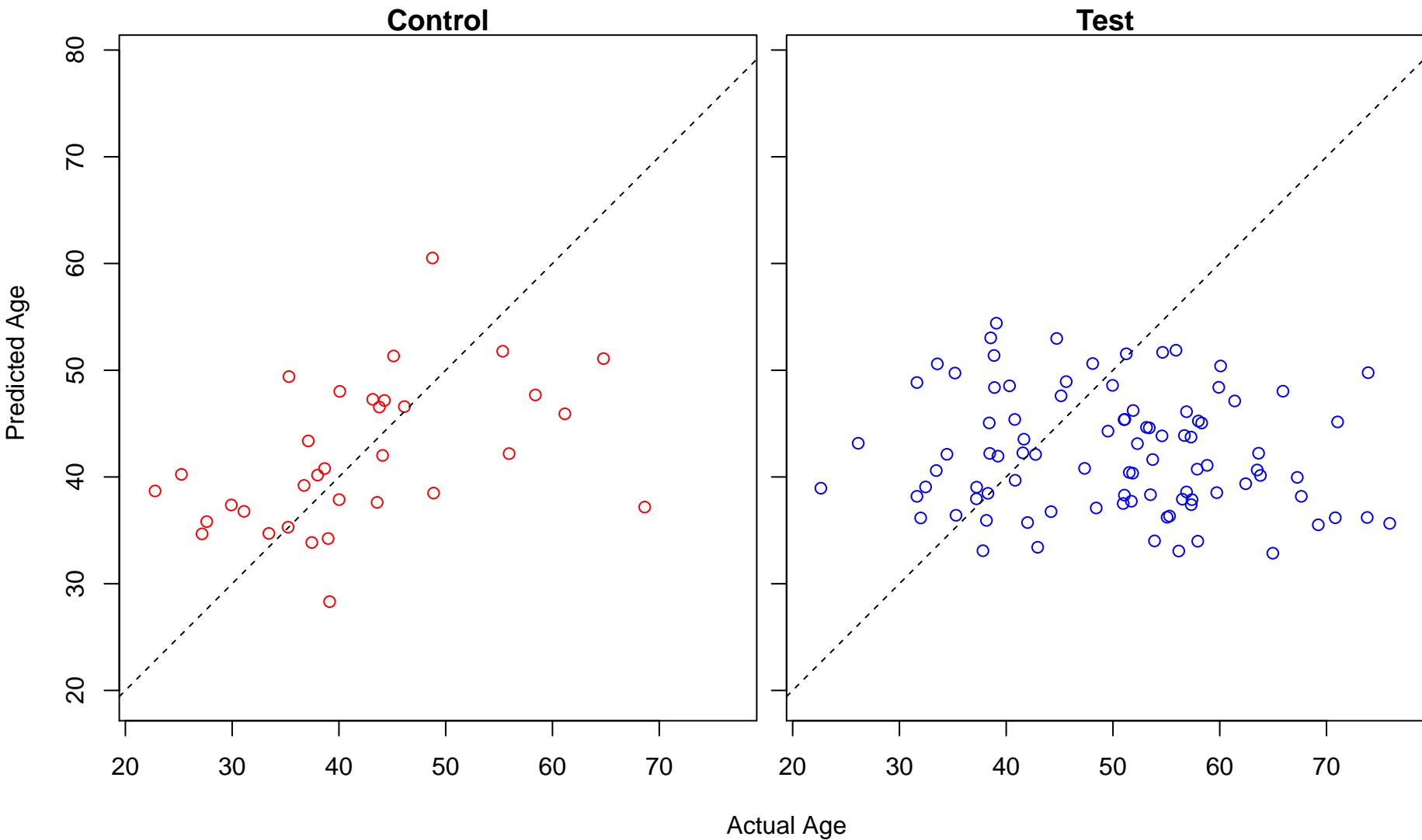
regulation of activated T cell proliferation (Score: 0.811811)



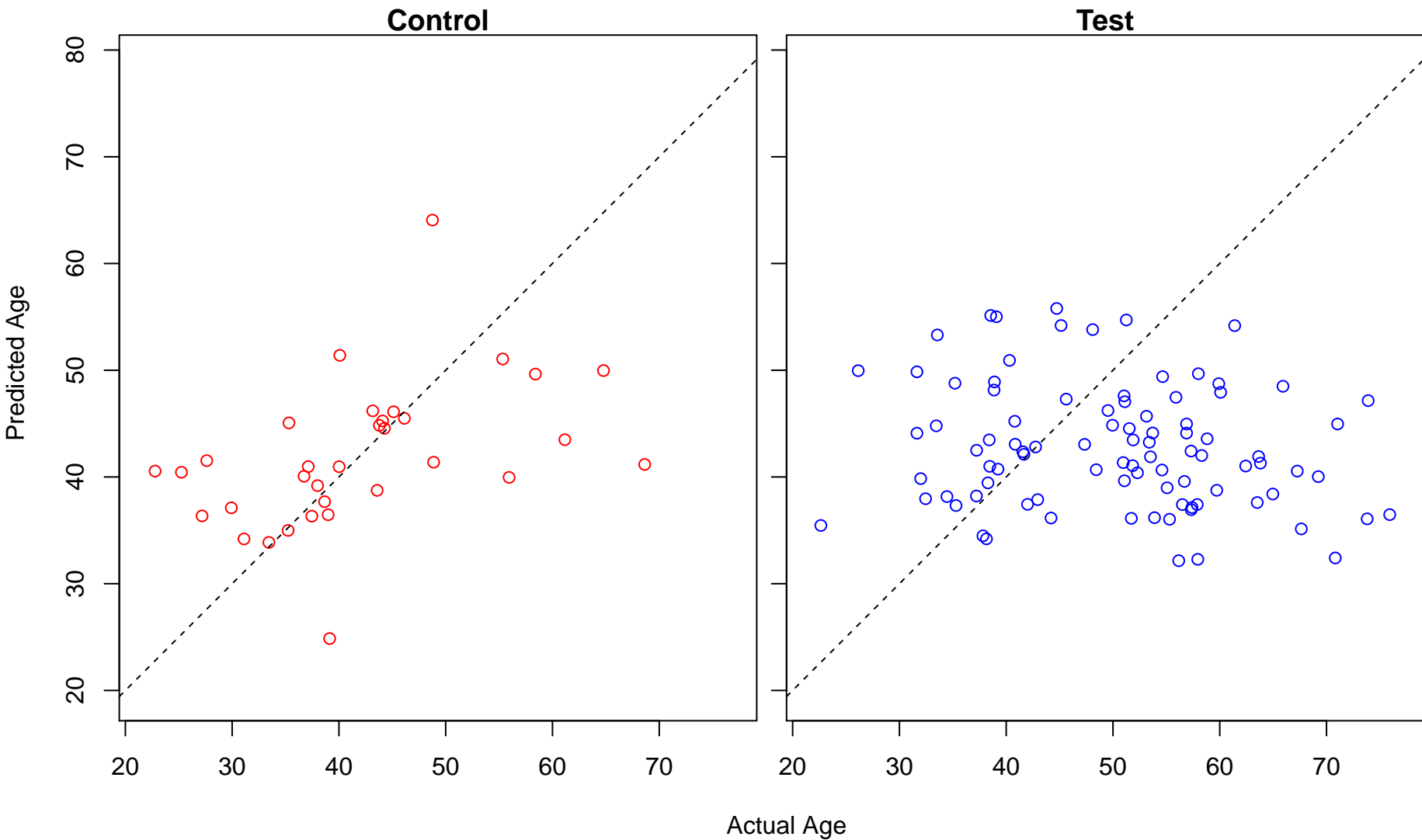
actin filament-based process (Score: 0.811360)



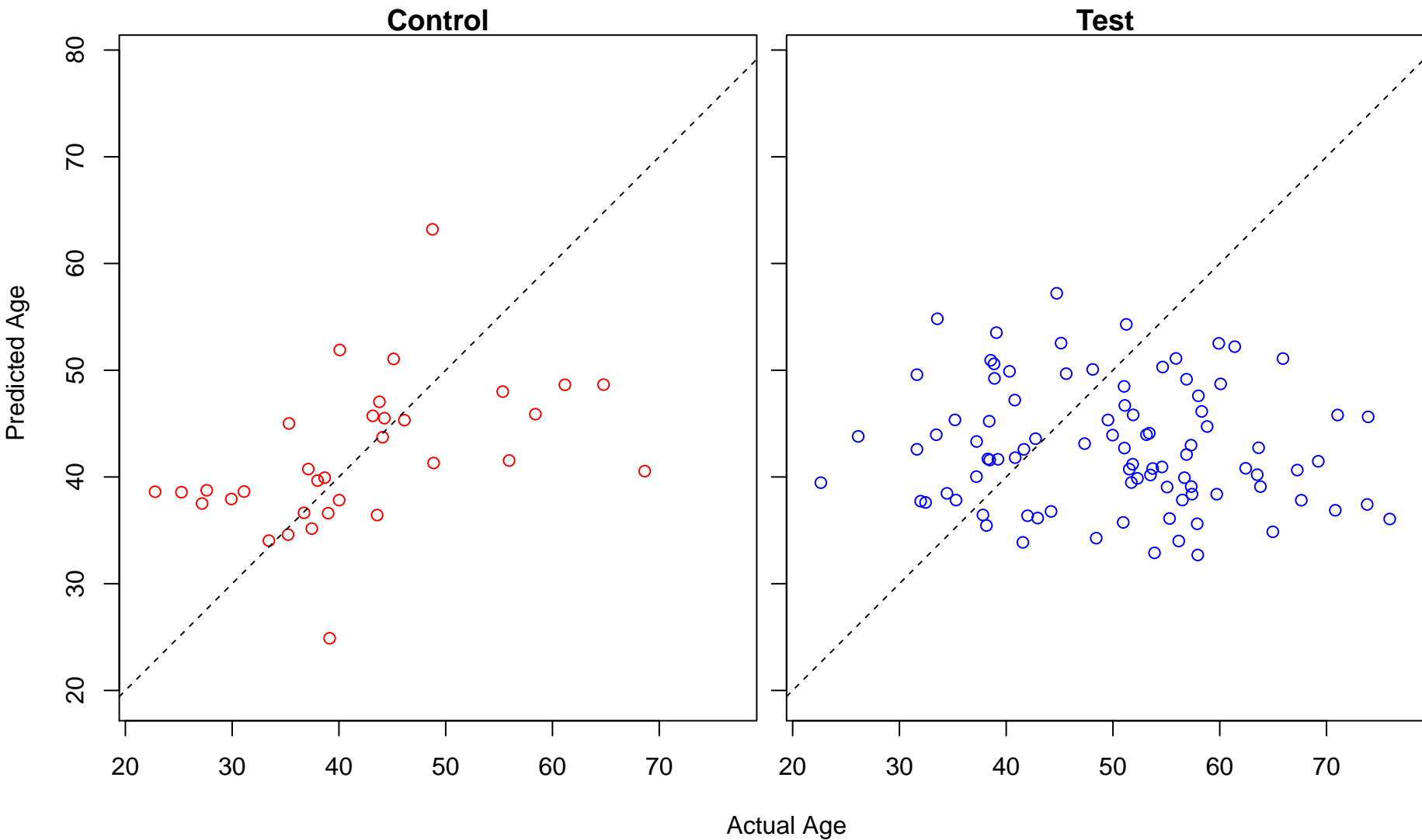
regulation of angiogenesis (Score: 0.811280)



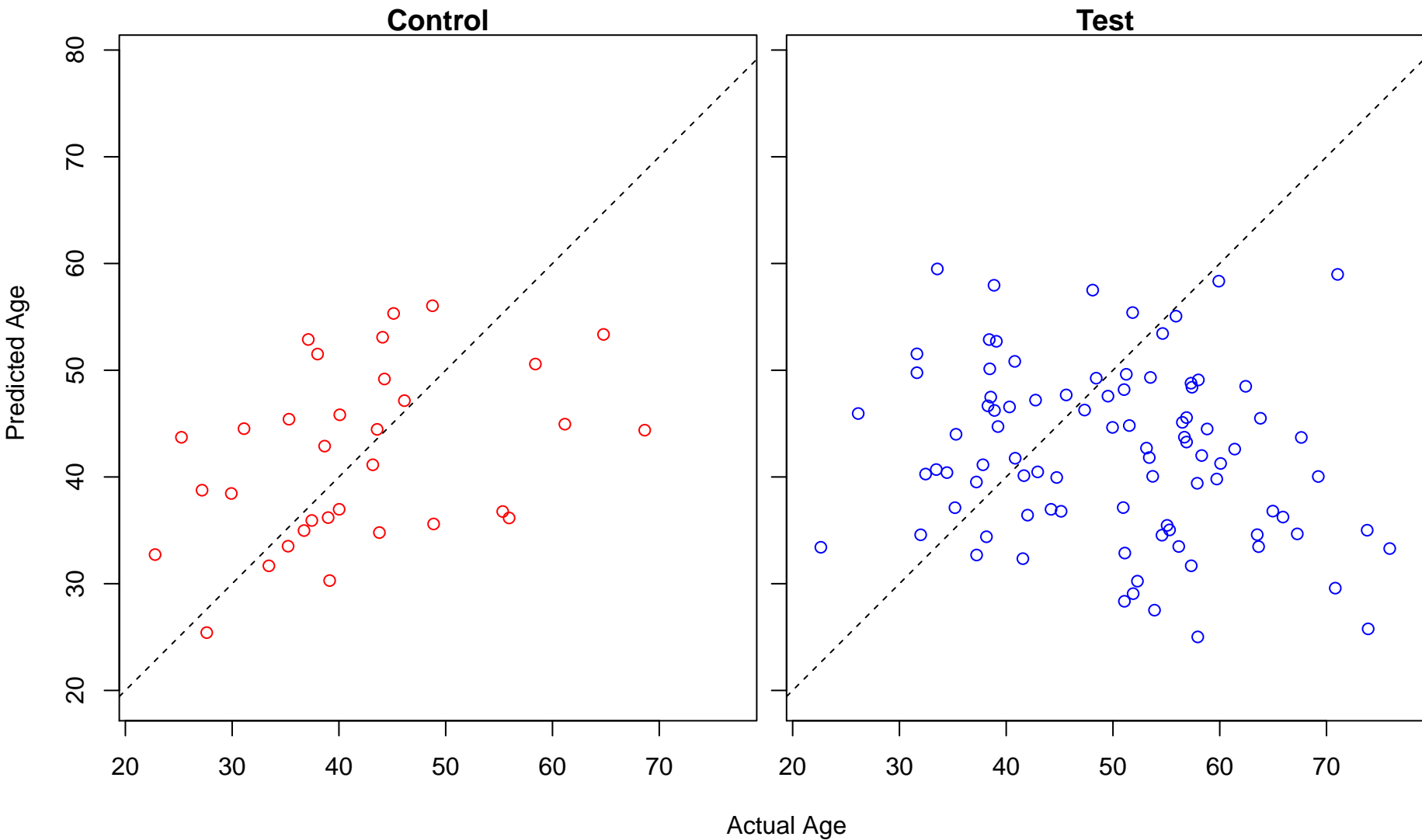
establishment or maintenance of cell polarity (Score: 0.811004)



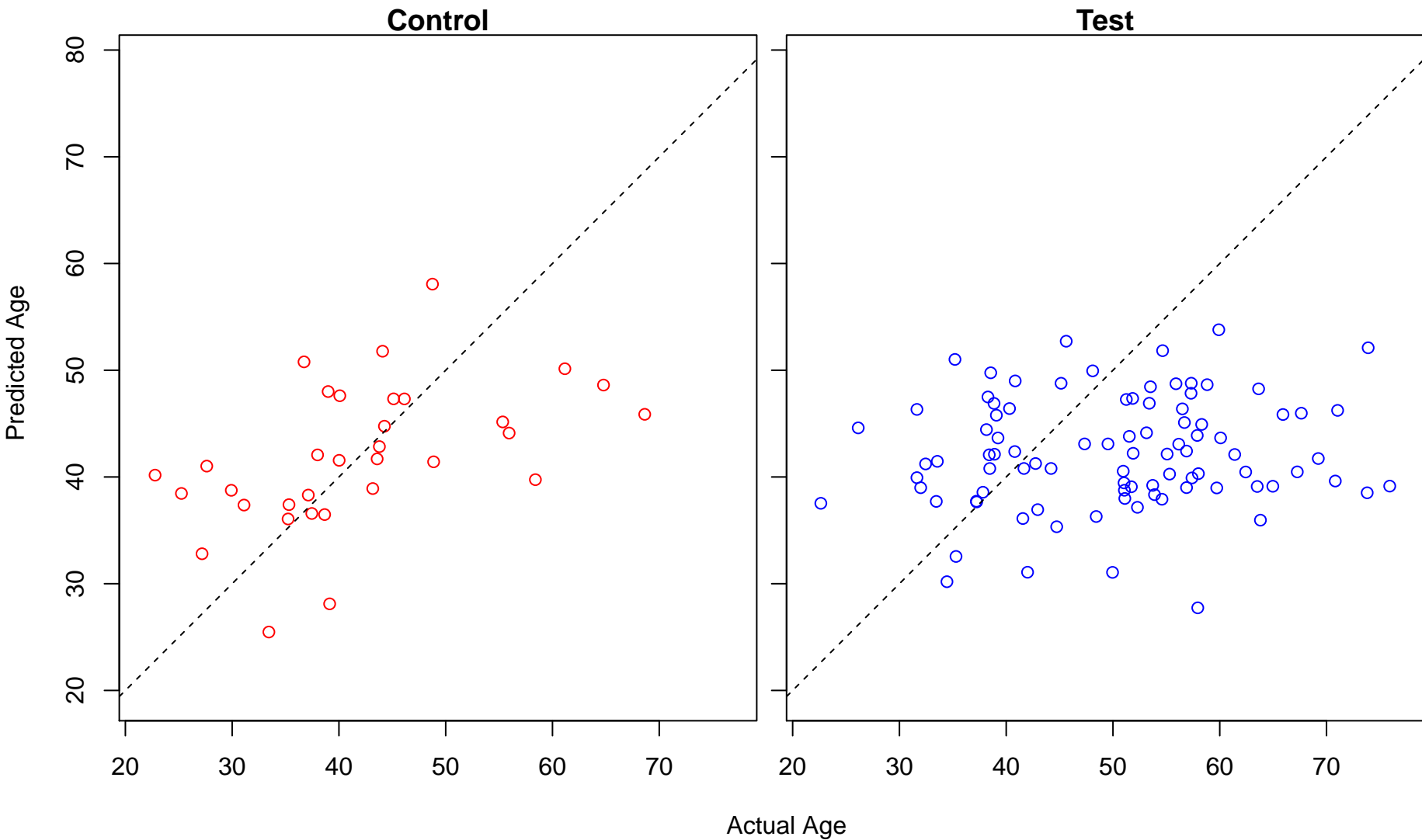
cytoskeleton organization (Score: 0.810807)



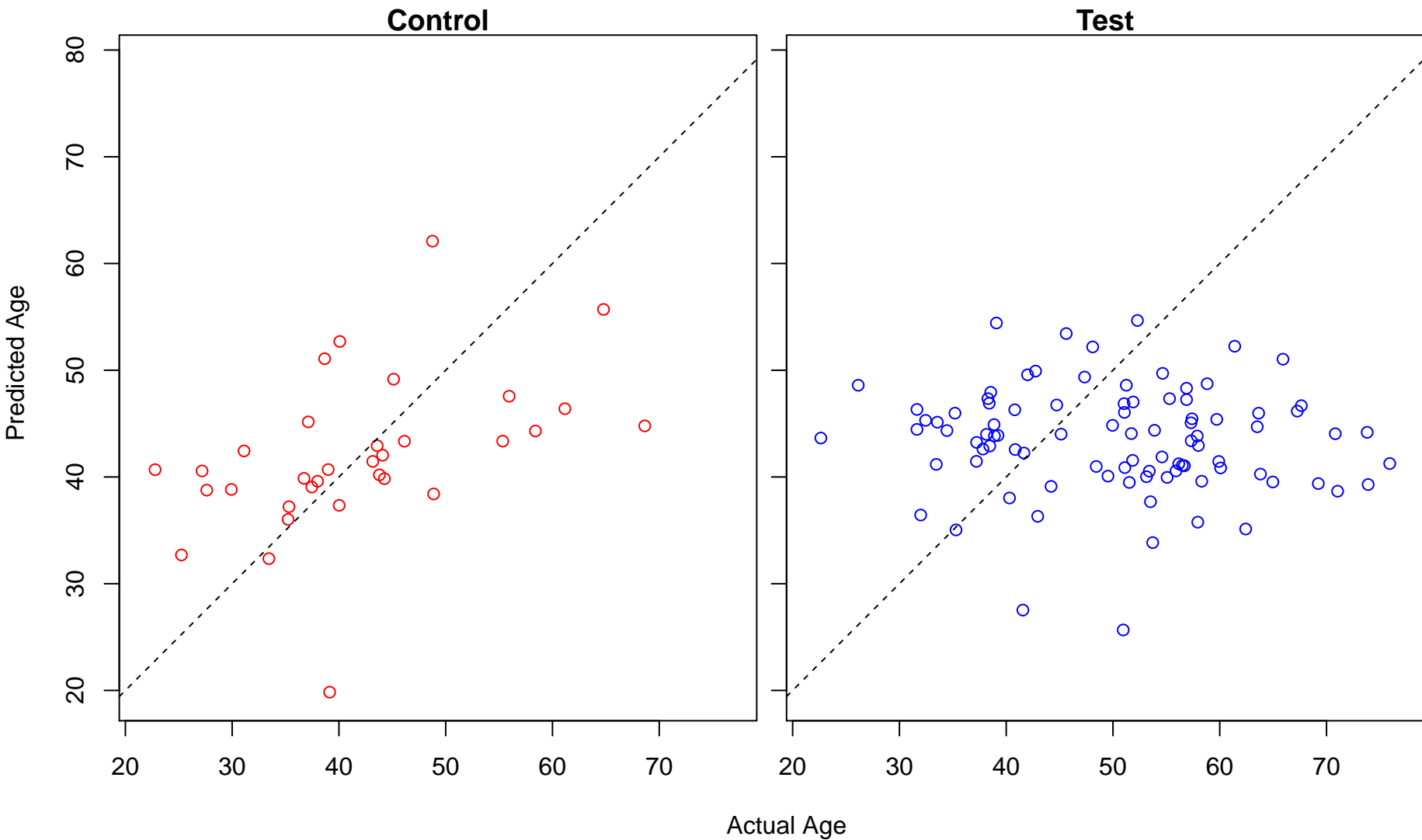
negative regulation of actin filament bundle assembly (Score: 0.810488)



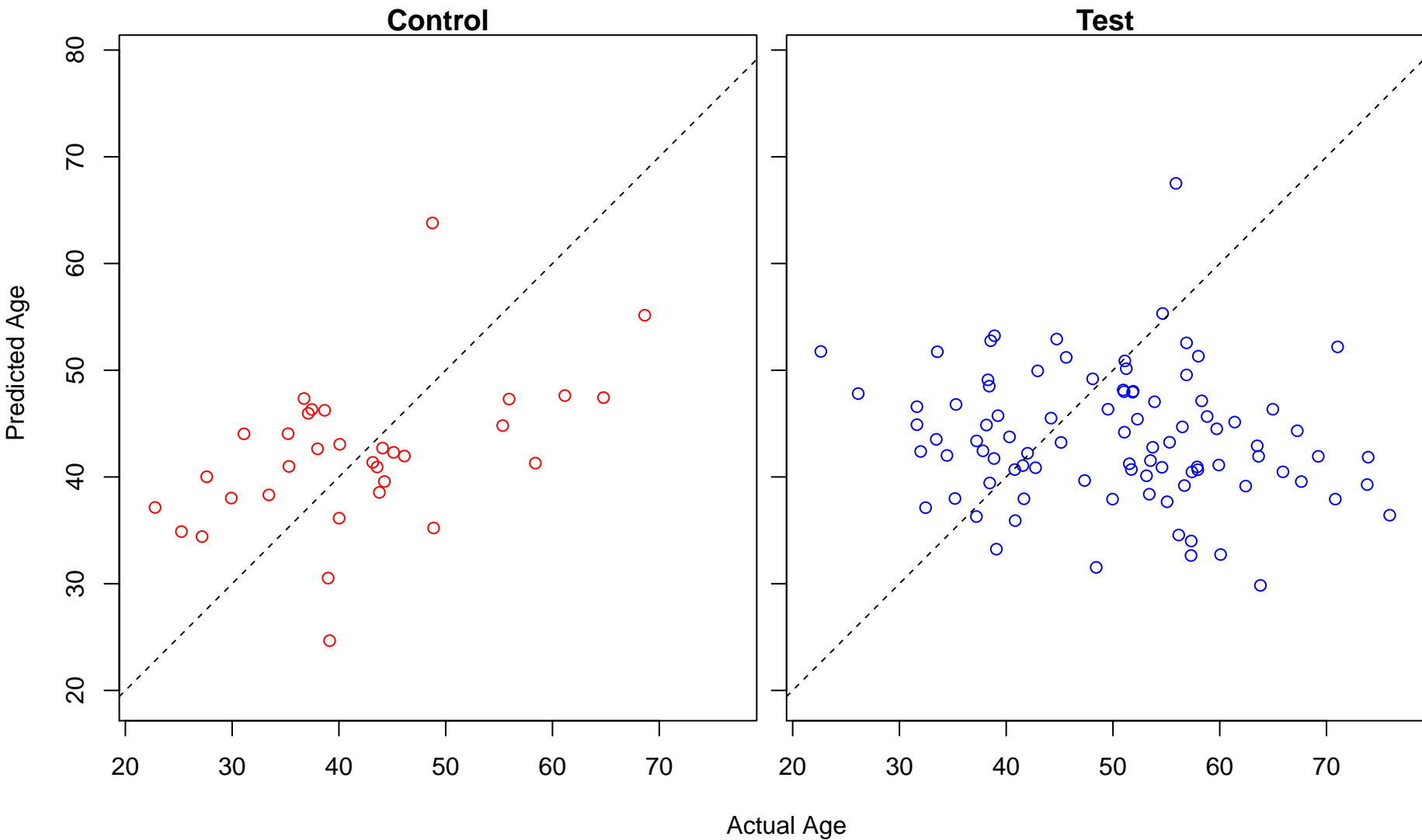
pyridine-containing compound biosynthetic process (Score: 0.809486)



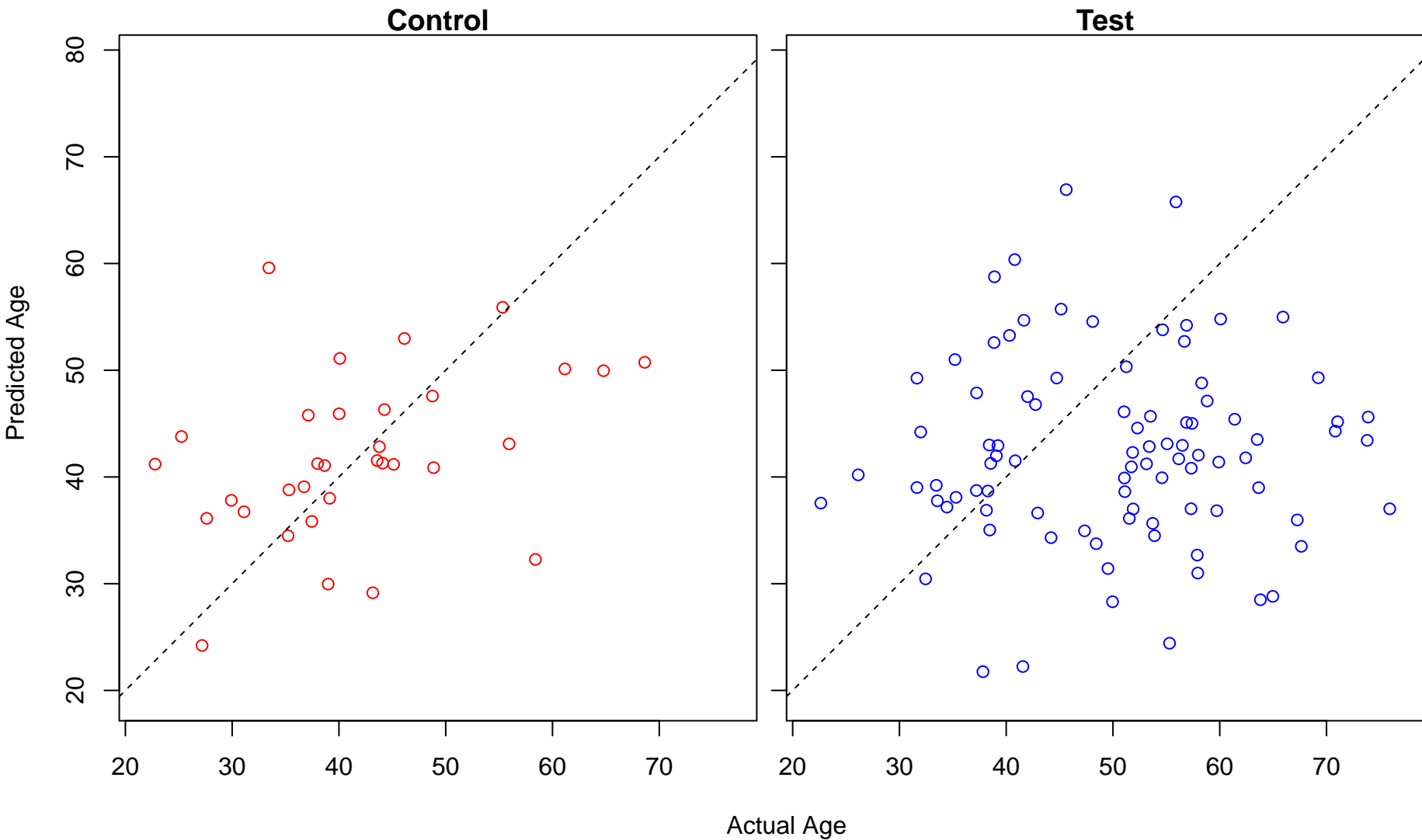
regulation of growth hormone receptor signaling pathway (Score: 0.808606)



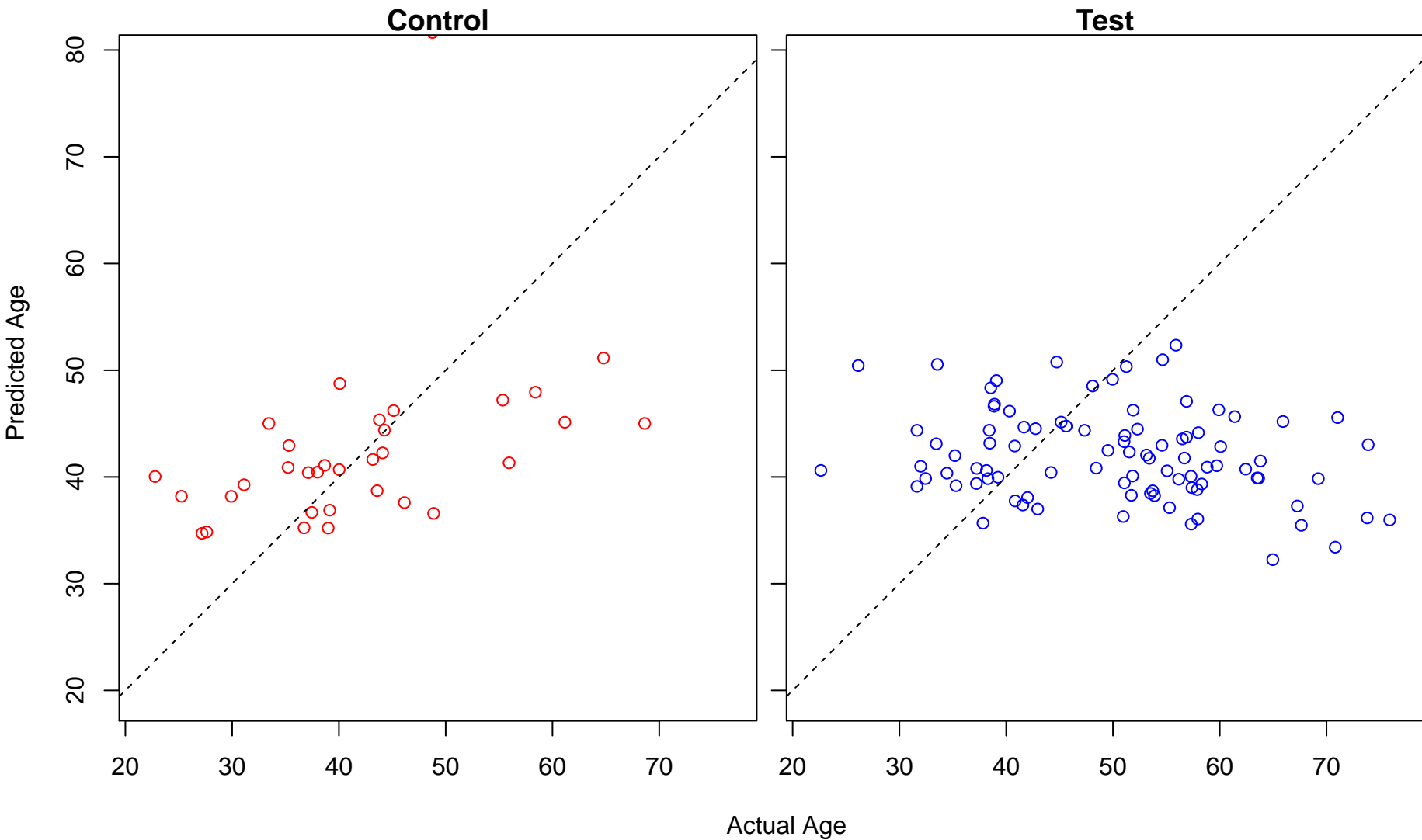
negative regulation of cell proliferation involved in kidney development (Score: 0.808402)



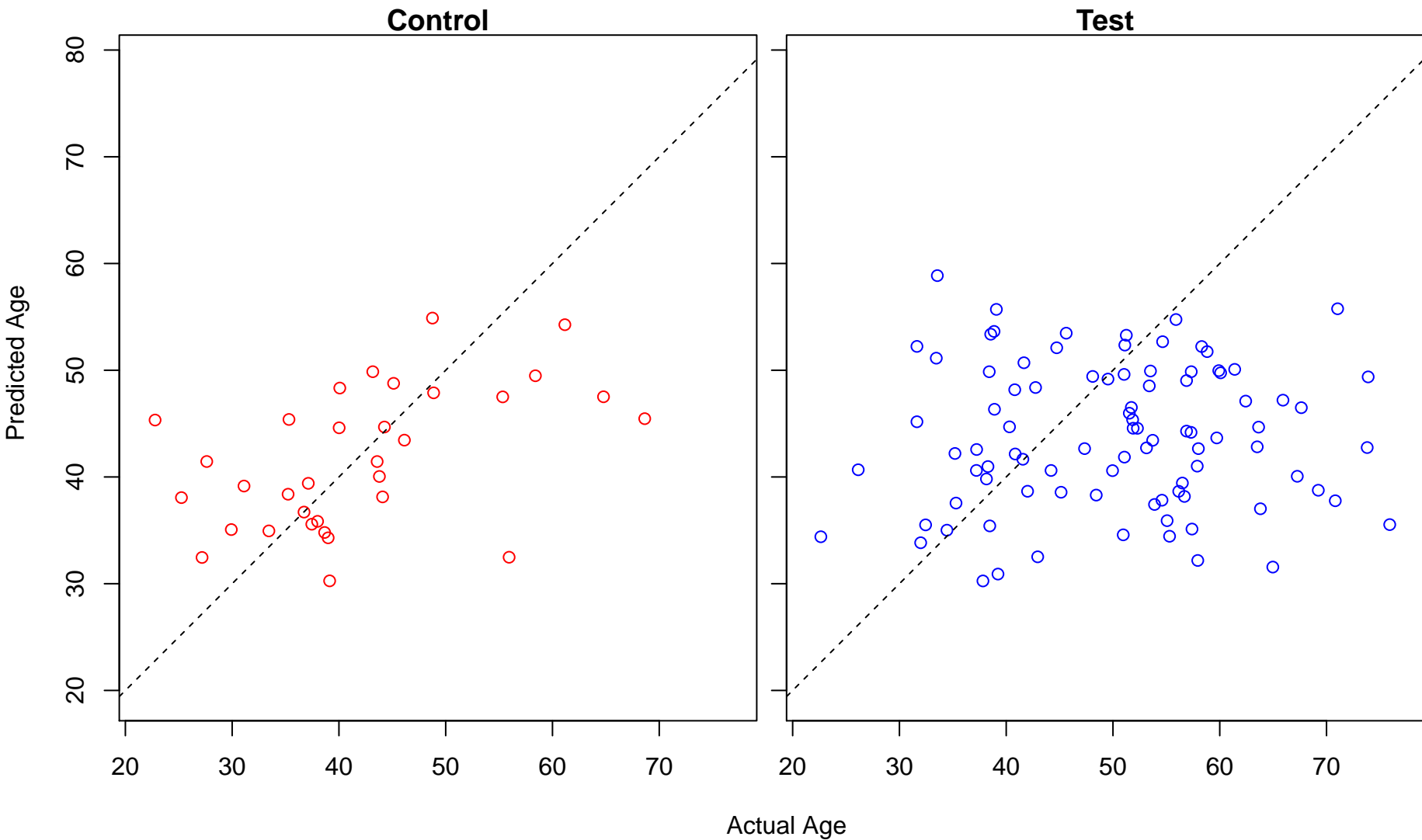
positive regulation of calcium ion transport into cytosol (Score: 0.807162)



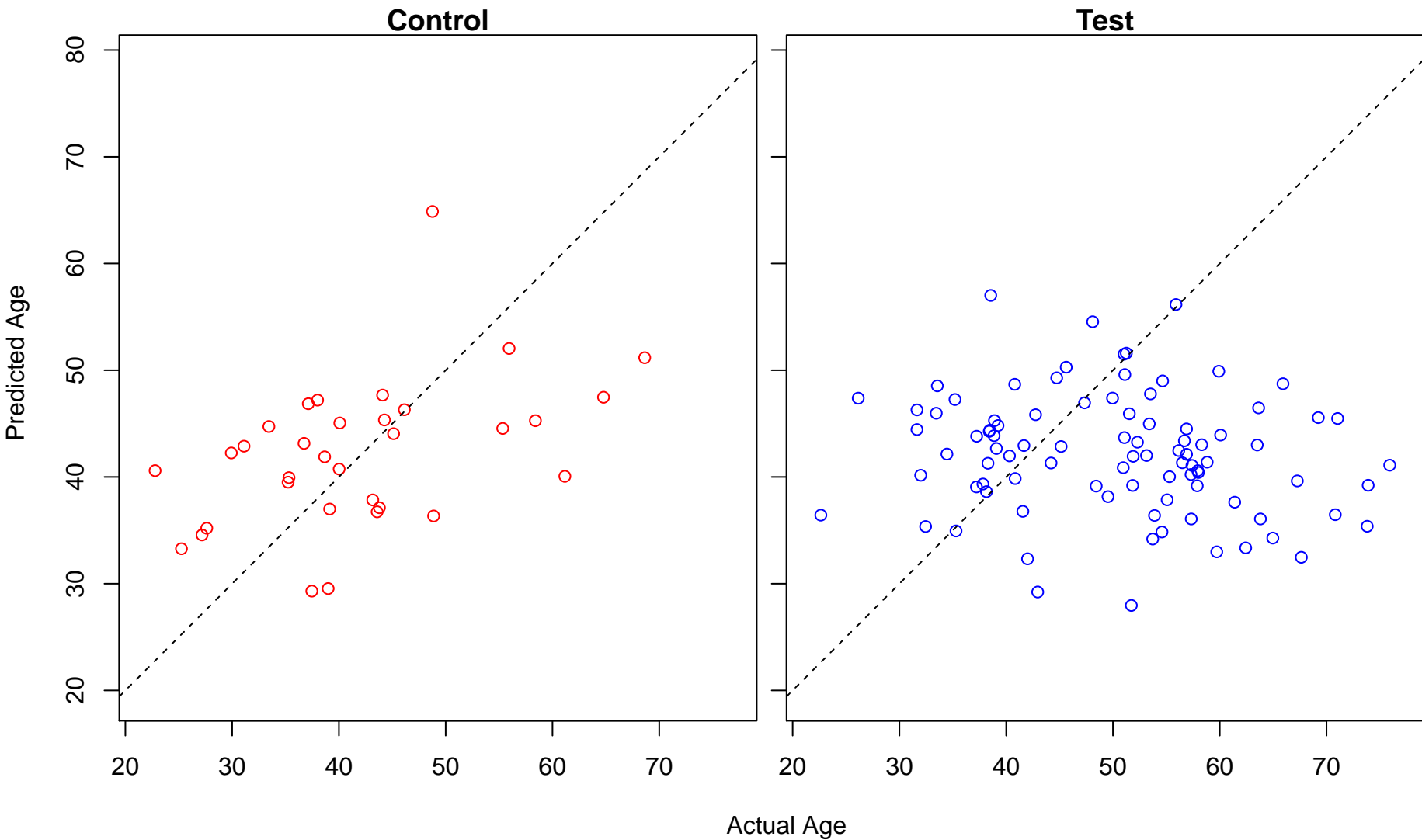
megakaryocyte differentiation (Score: 0.806512)



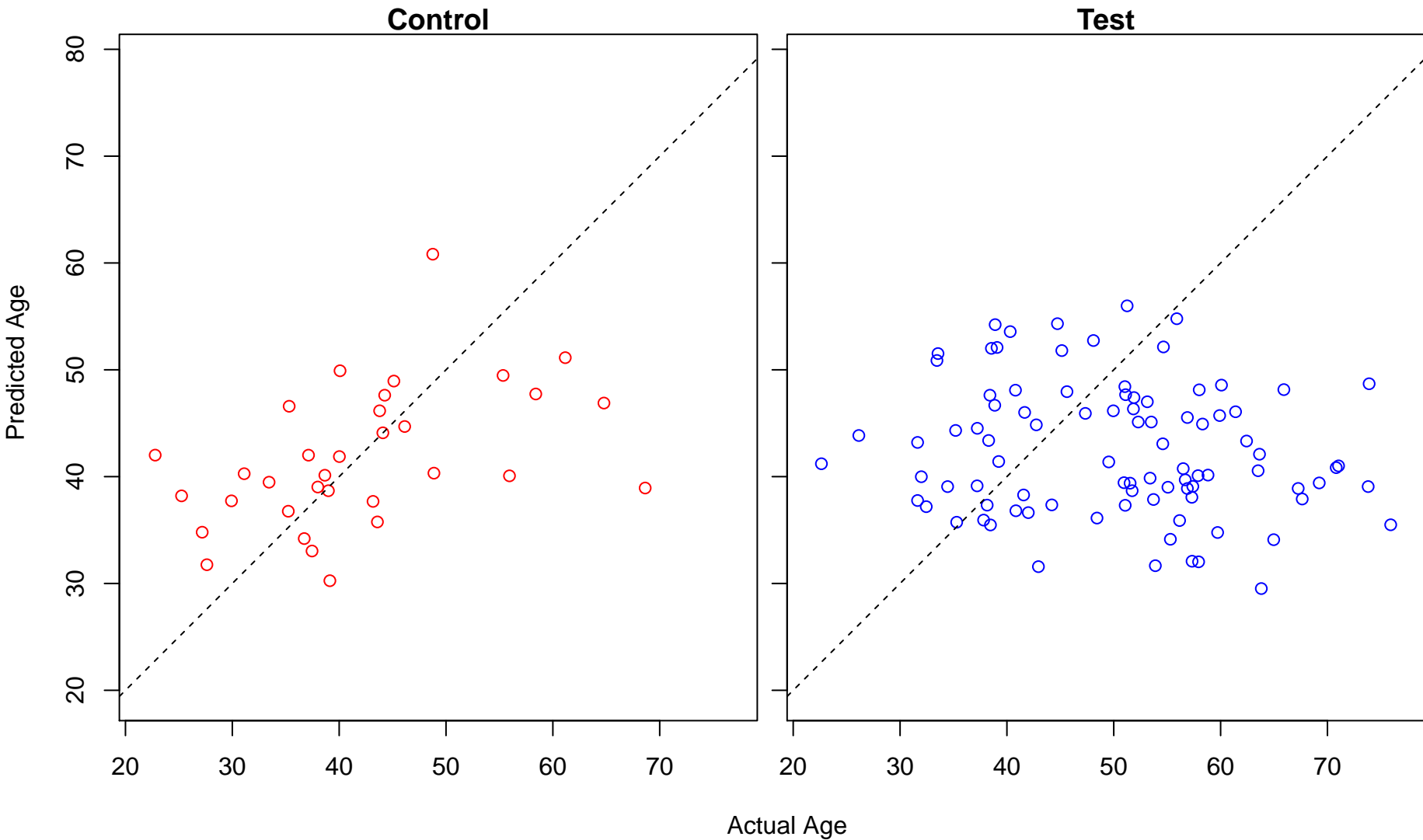
epithelial cell migration (Score: 0.806135)



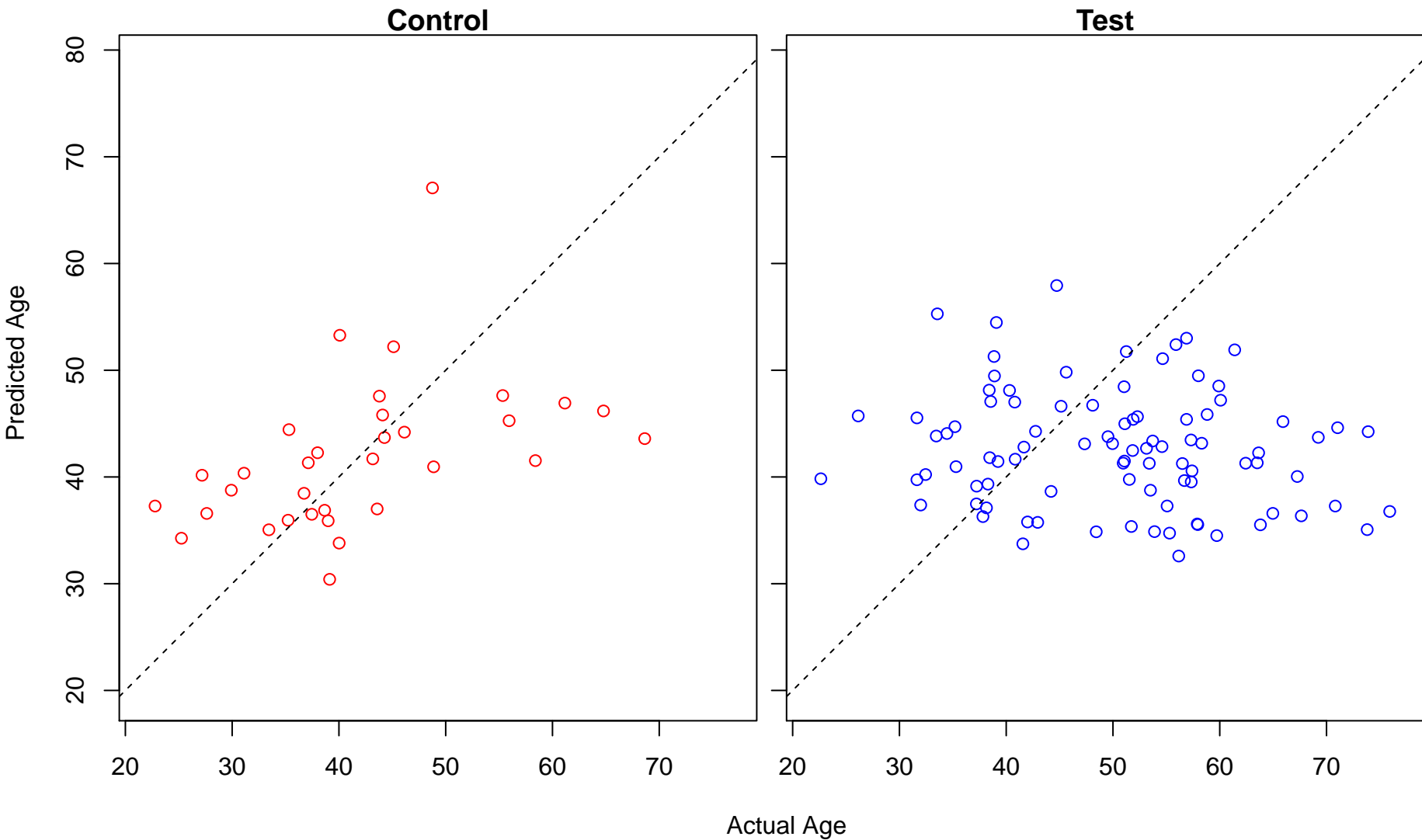
negative regulation of purine nucleotide metabolic process (Score: 0.805420)



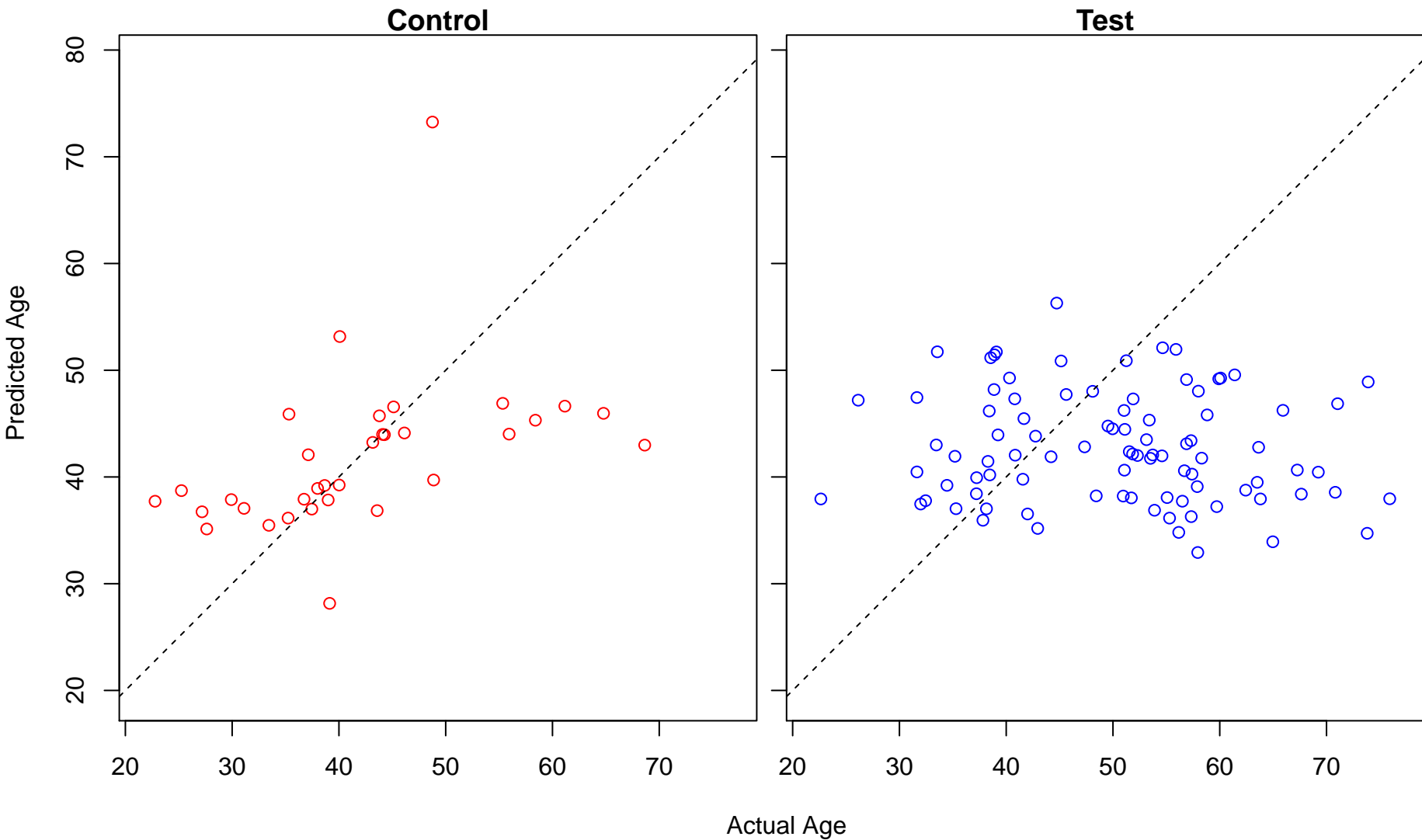
regulation of protein localization to nucleus (Score: 0.805023)



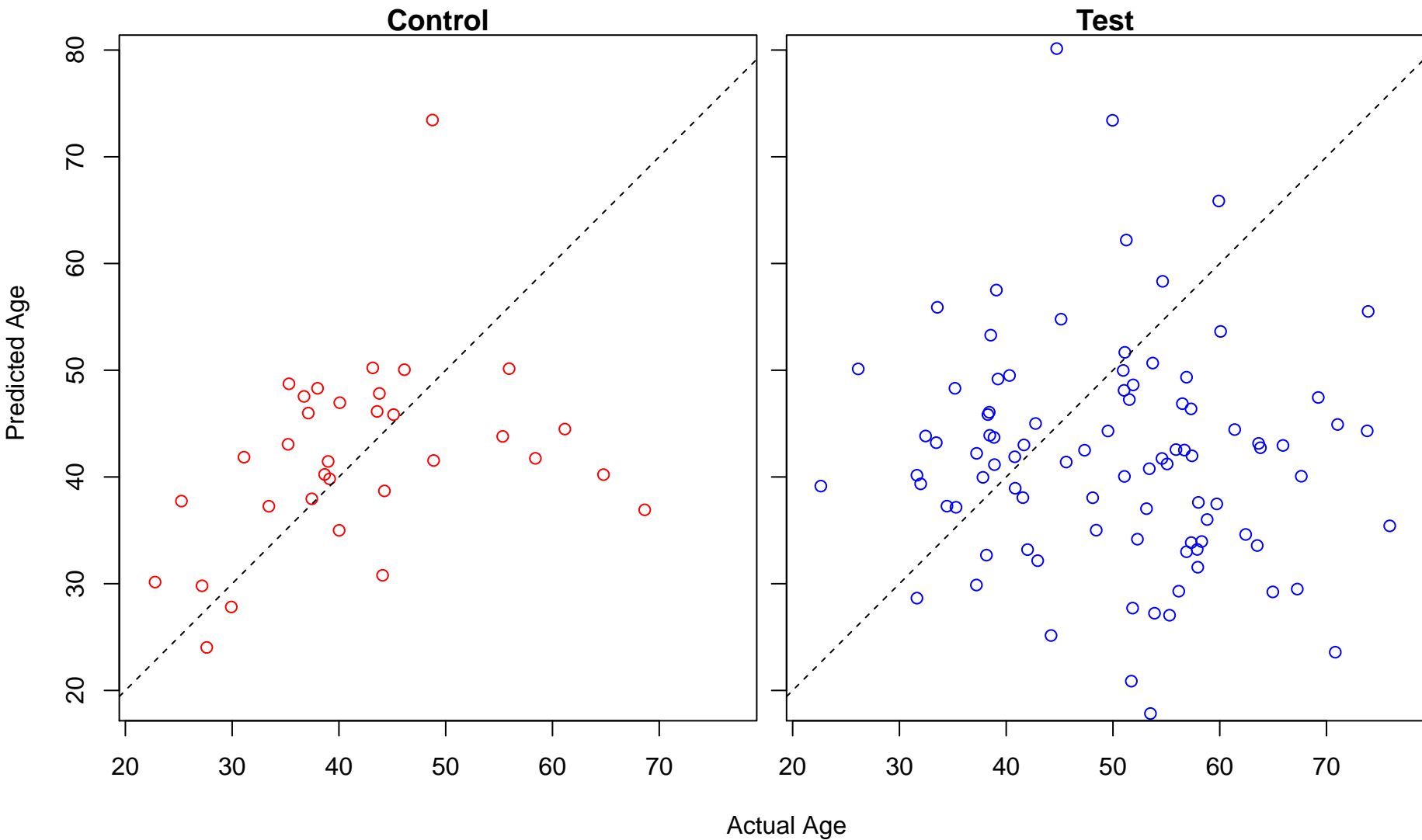
regulation of actin filament-based process (Score: 0.803941)



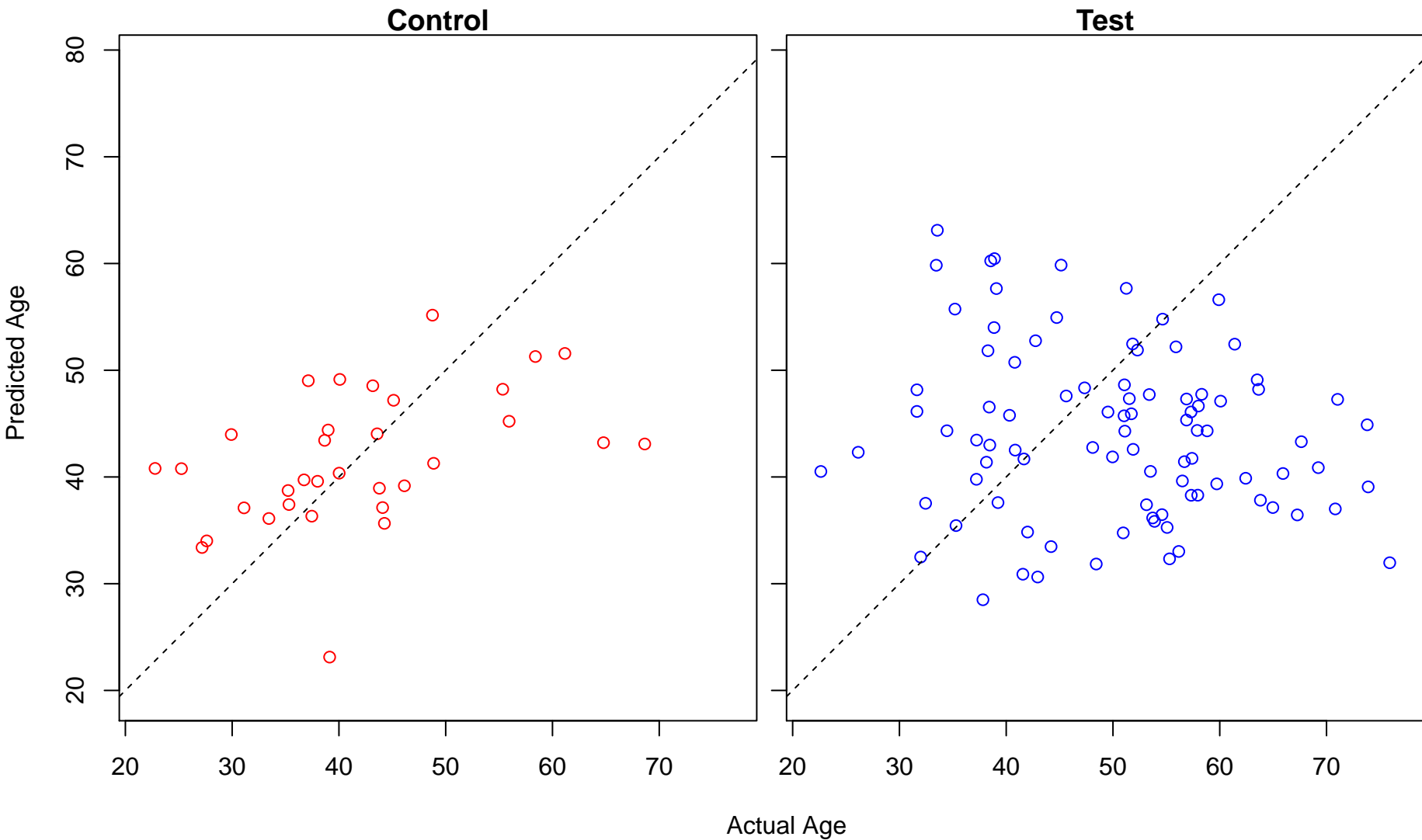
negative regulation of phosphorylation (Score: 0.803855)



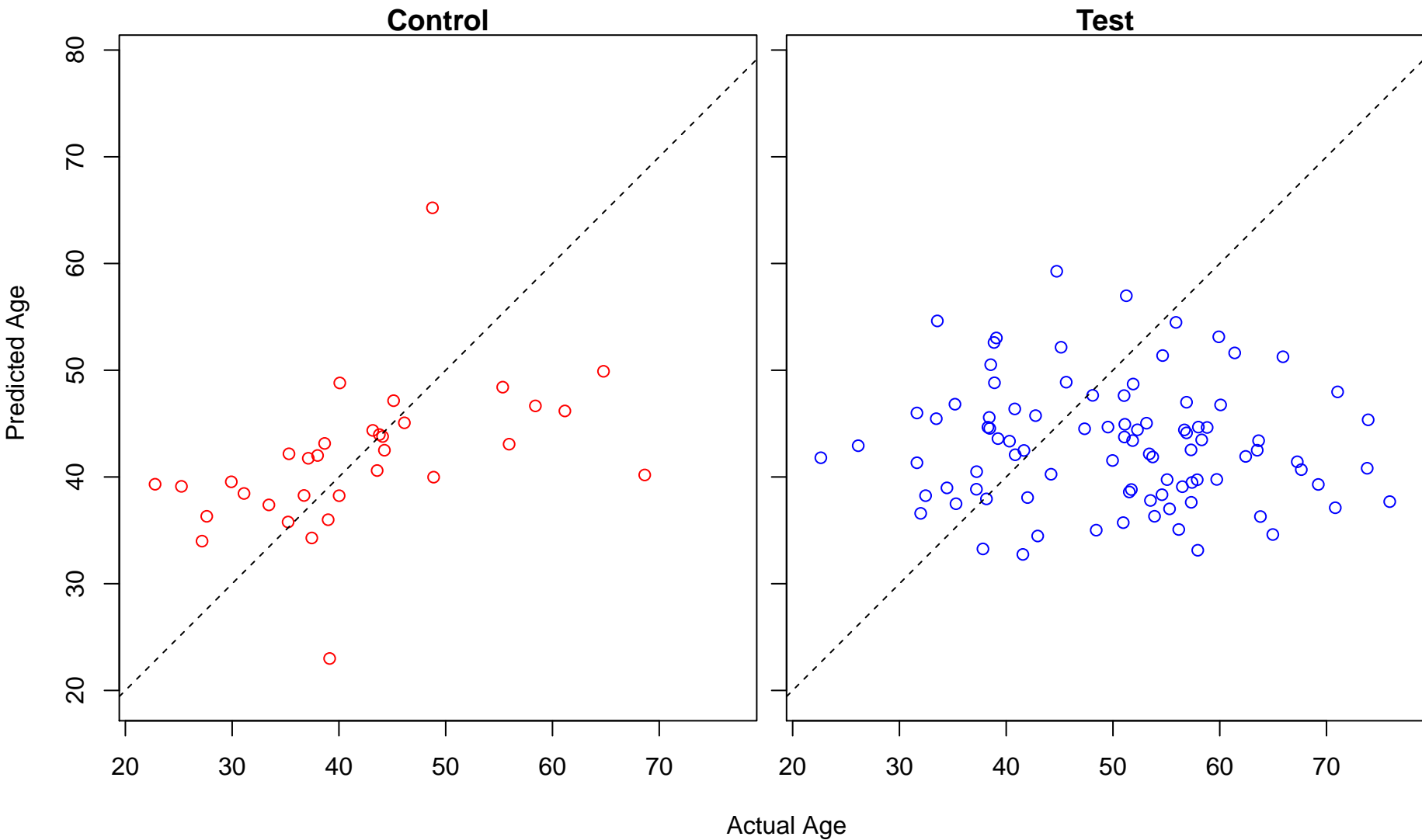
purine-containing compound salvage (Score: 0.803718)



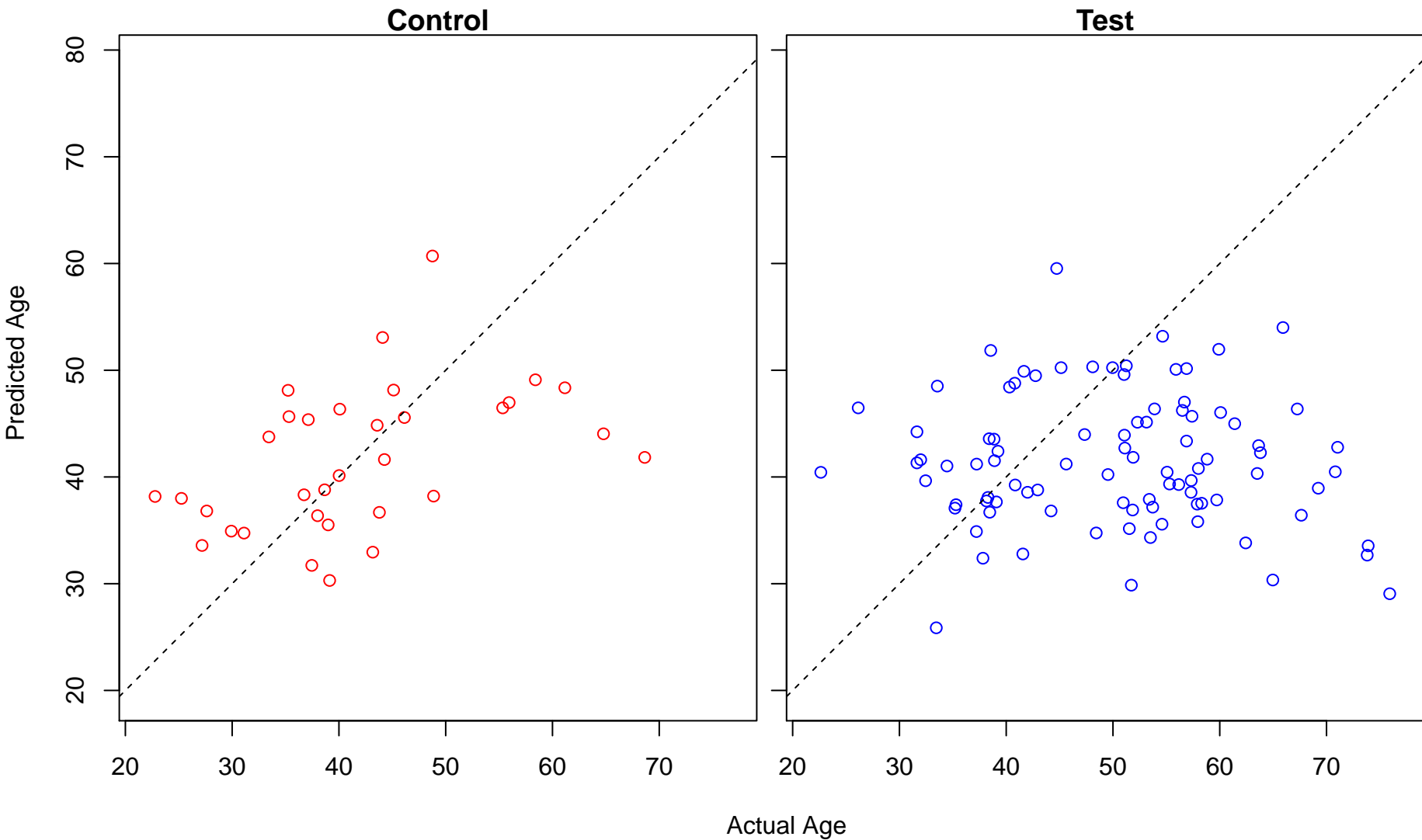
calcium ion import (Score: 0.803261)



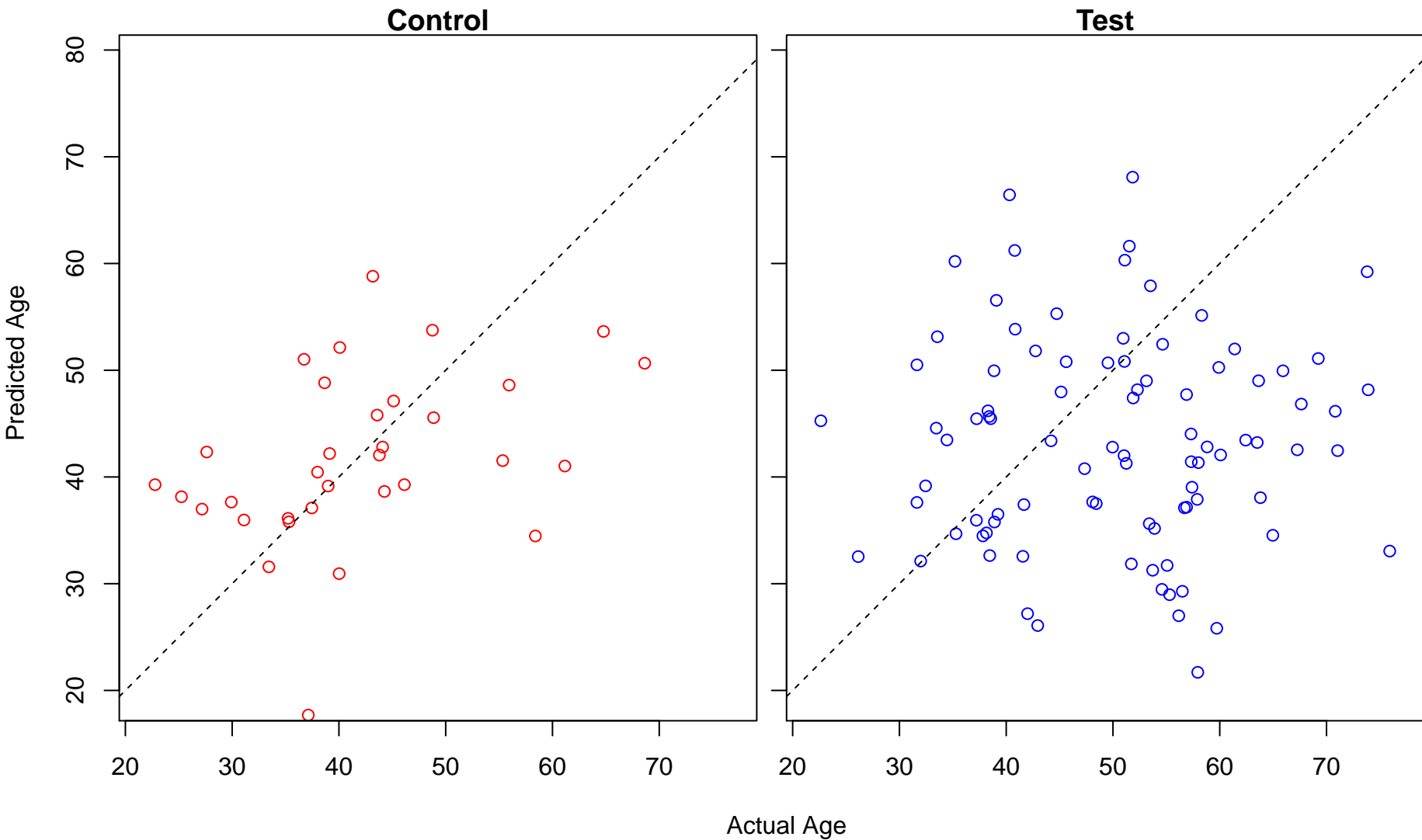
cell morphogenesis involved in neuron differentiation (Score: 0.802007)



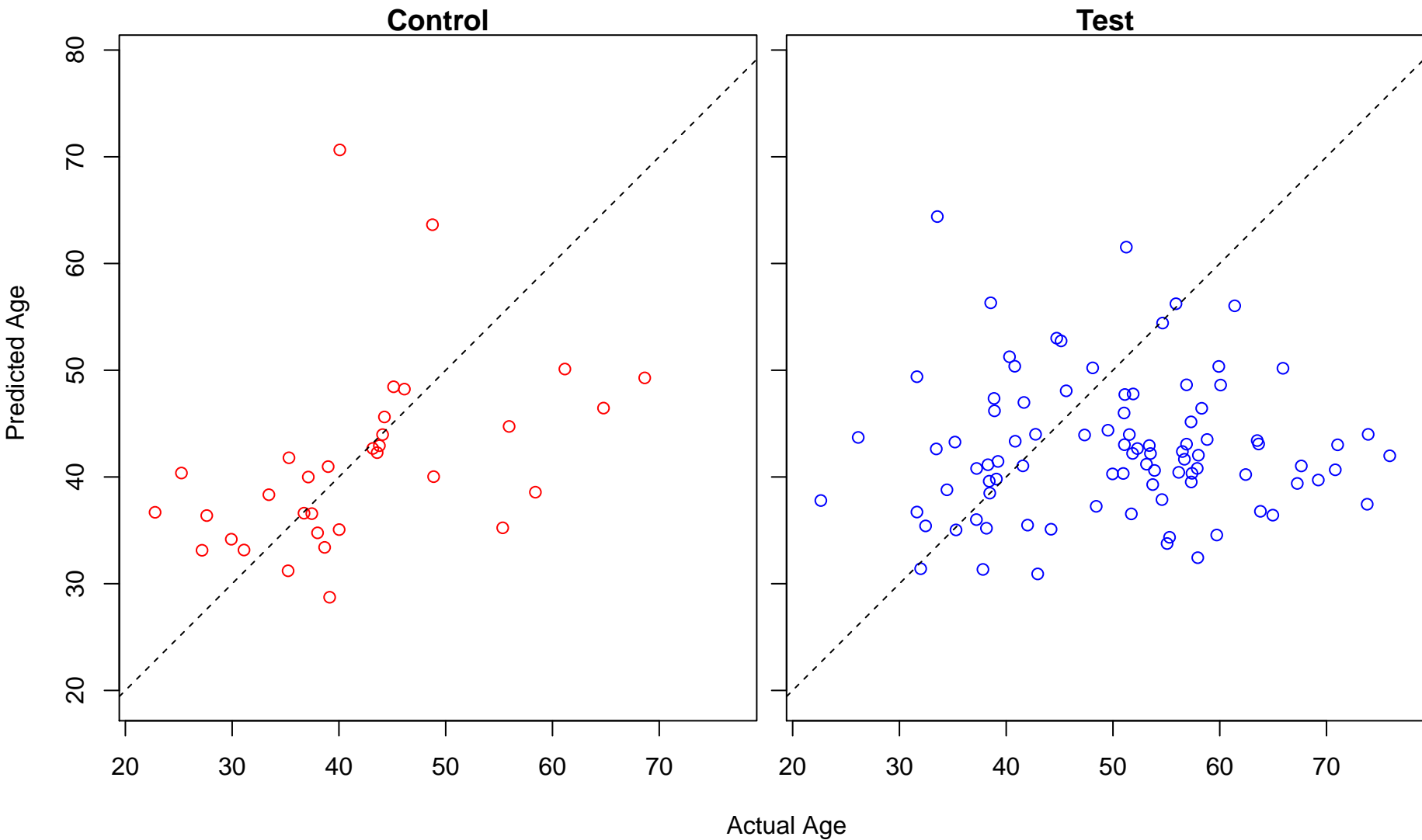
heart process (Score: 0.801484)



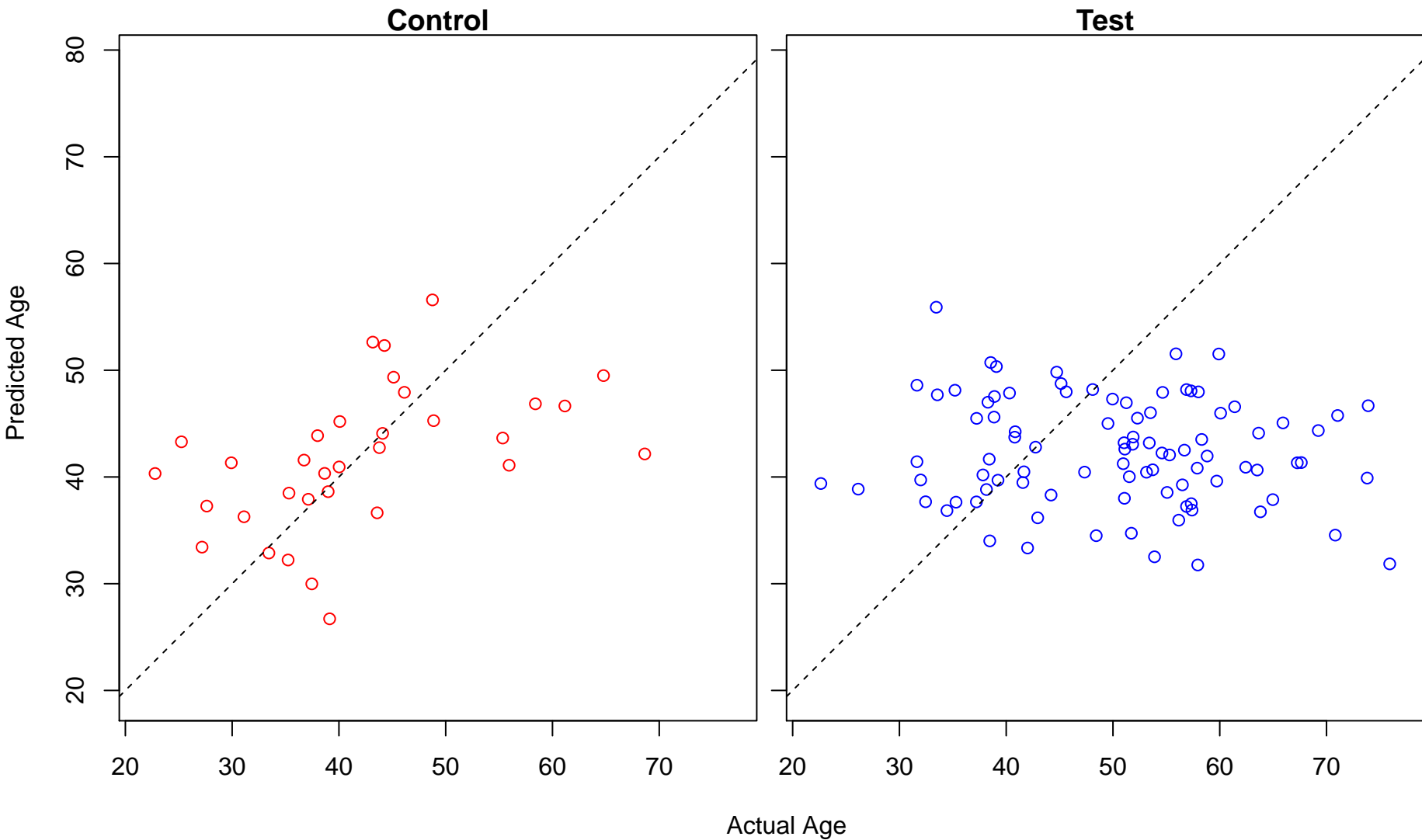
positive regulation of membrane potential (Score: 0.801291)



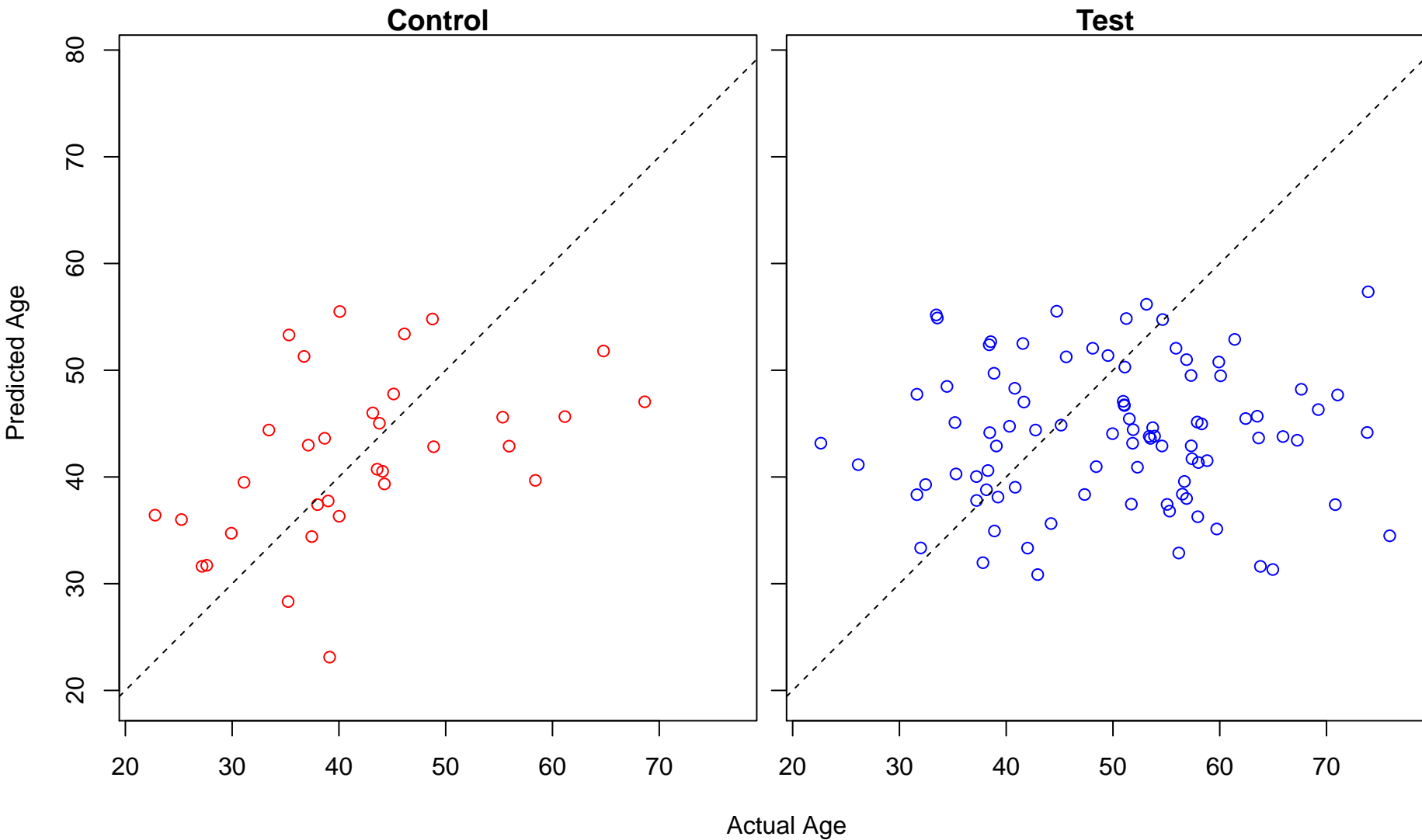
protein modification by small protein removal (Score: 0.800800)



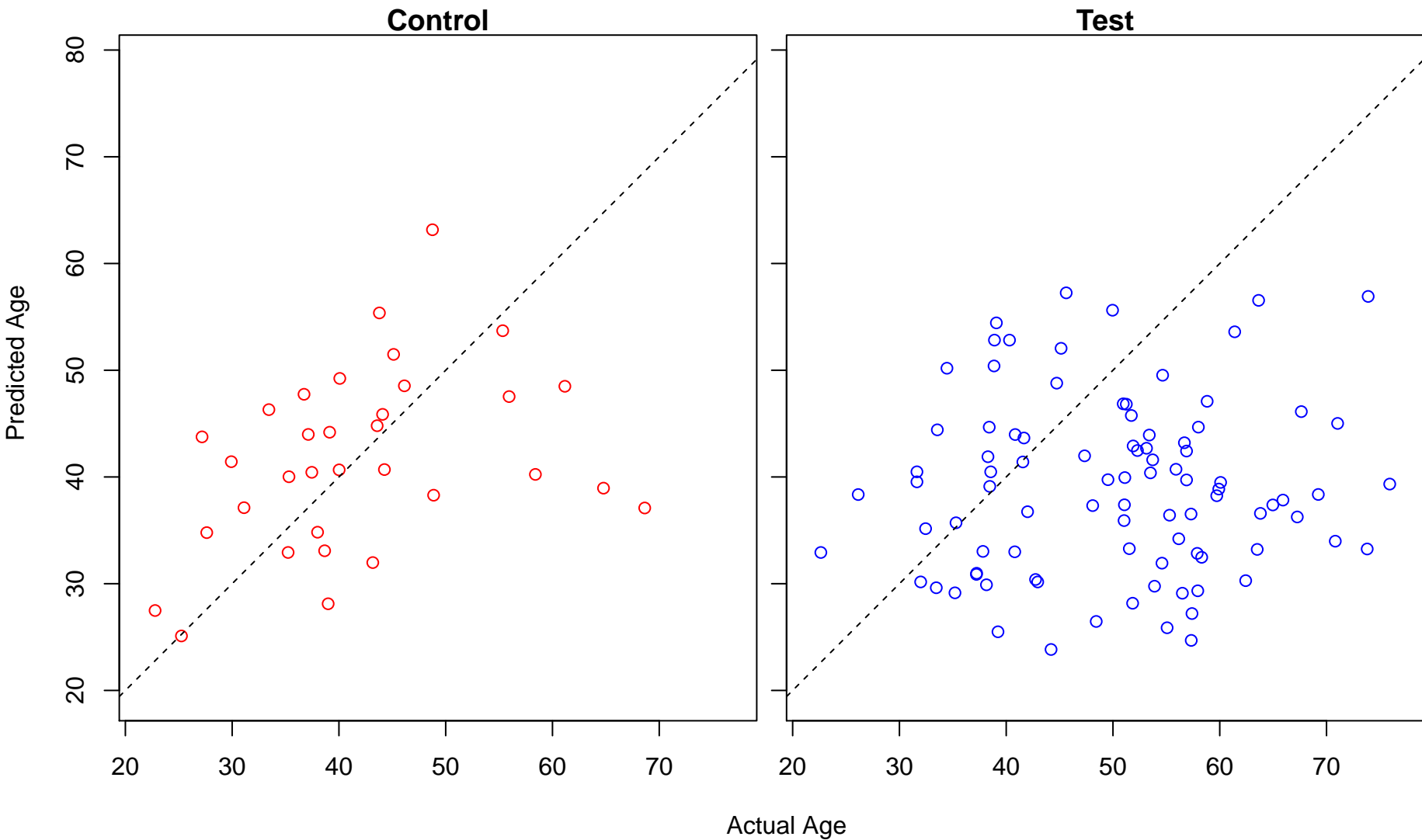
hexose catabolic process (Score: 0.800428)



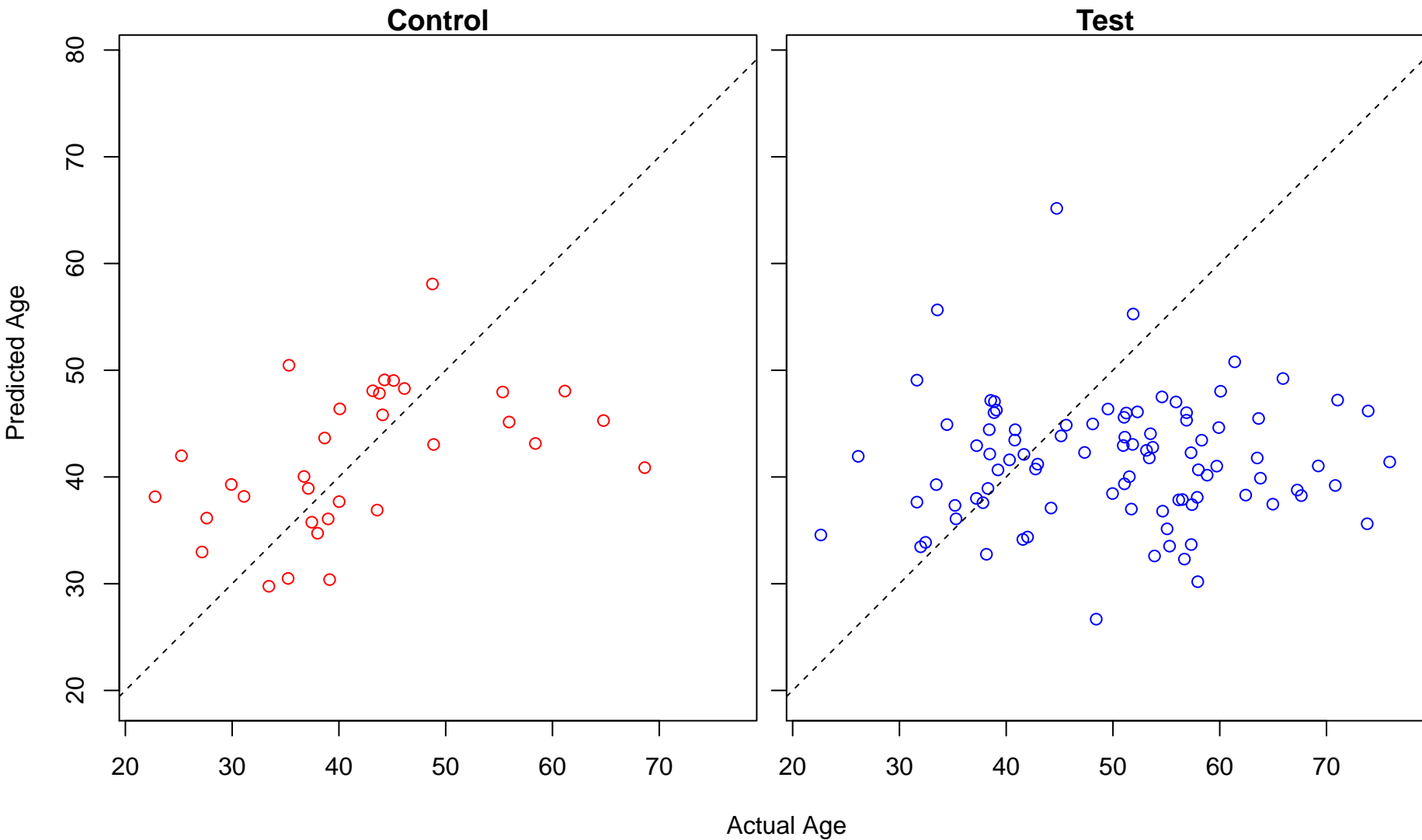
regulation of antigen processing and presentation (Score: 0.799951)



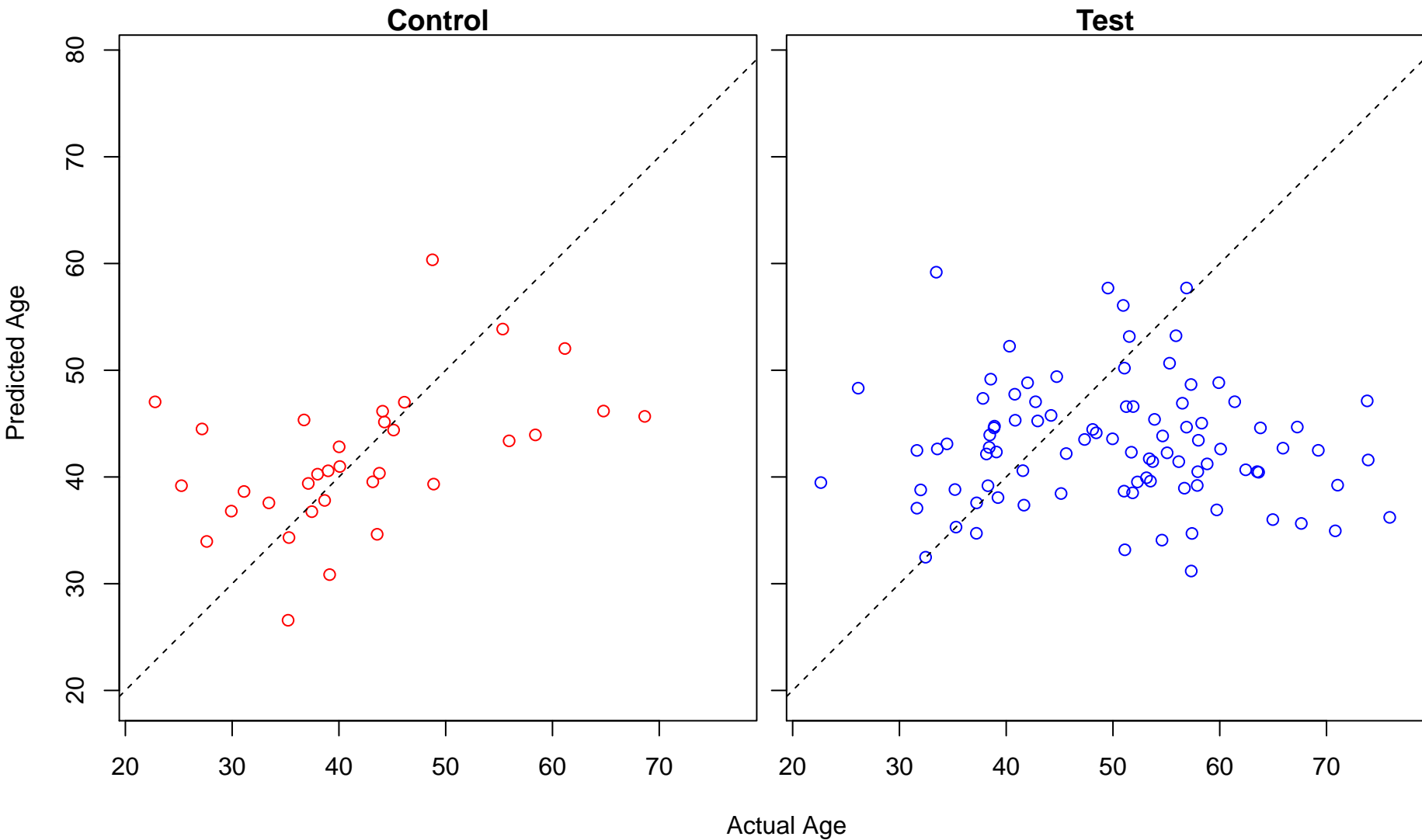
regulation of establishment or maintenance of cell polarity (Score: 0.799937)



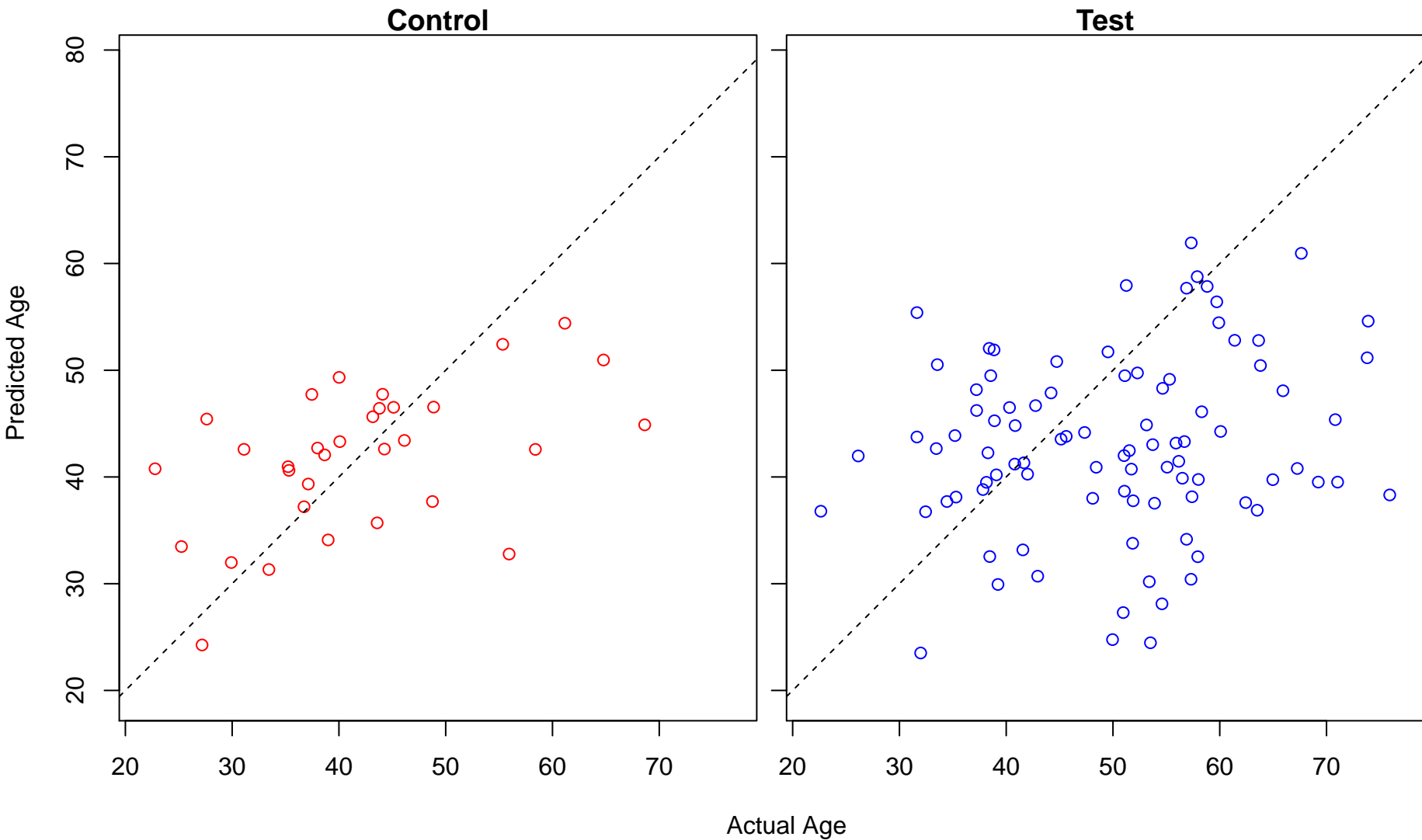
replication fork processing (Score: 0.799329)



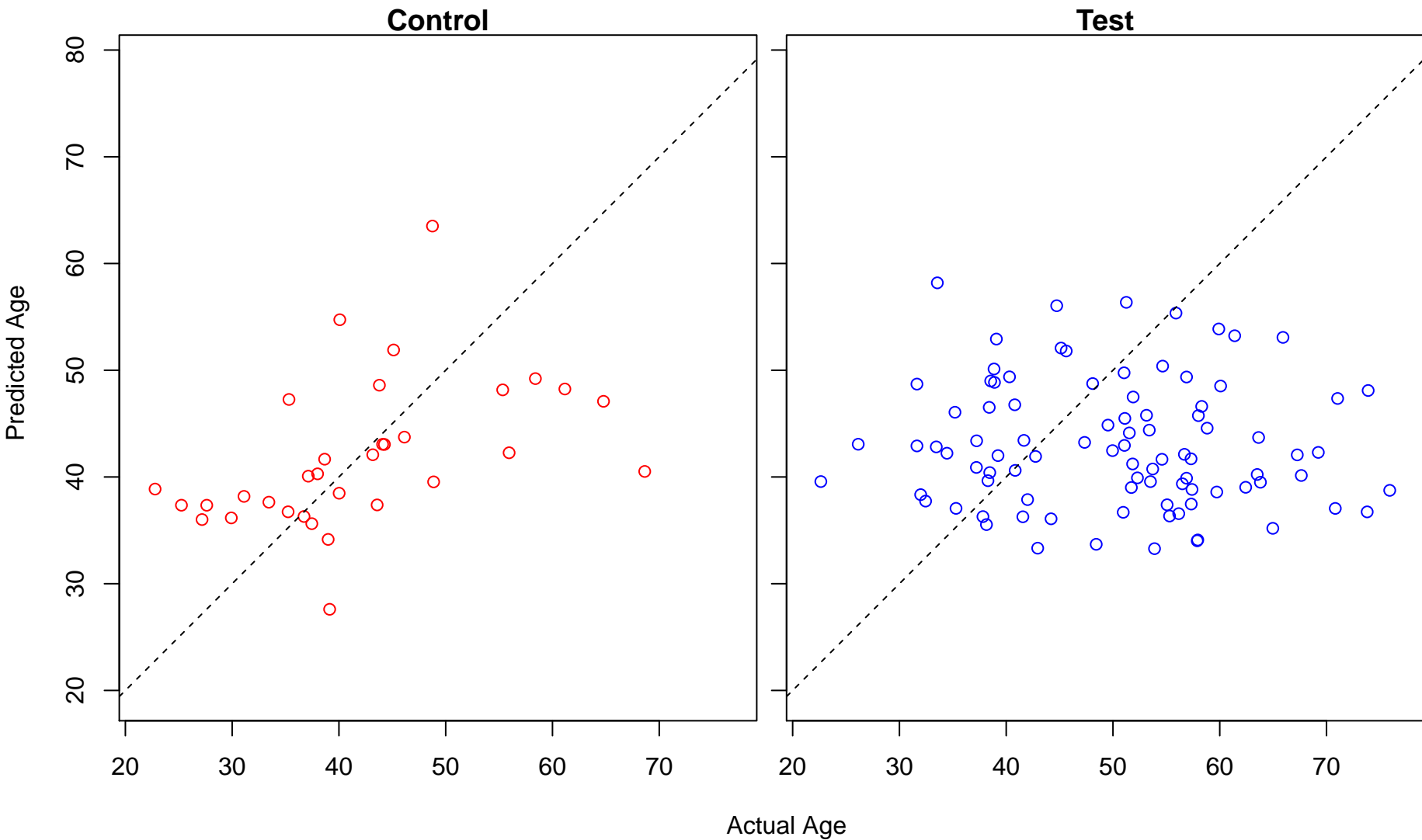
necrotic cell death (Score: 0.799134)



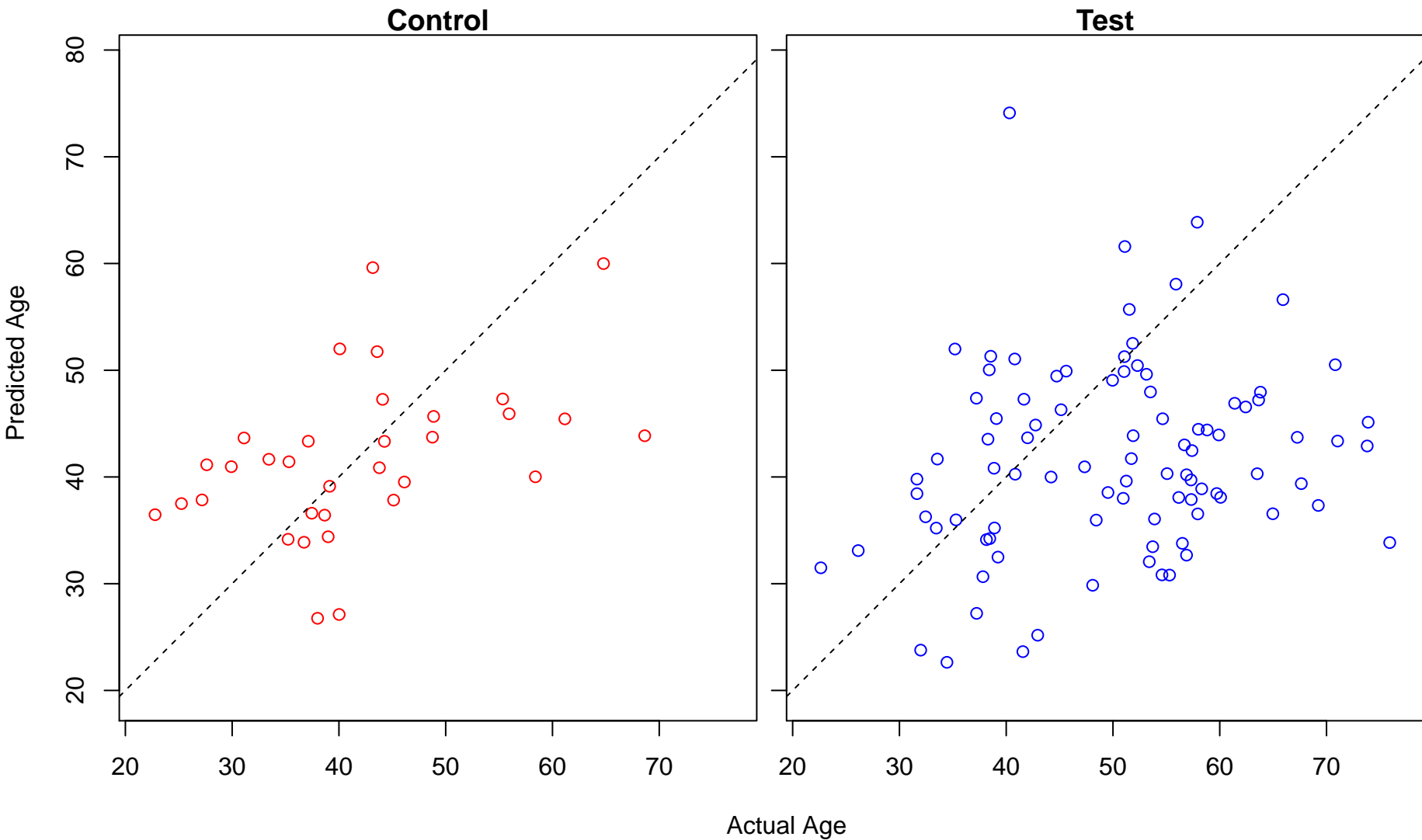
regulation of neural precursor cell proliferation (Score: 0.798630)



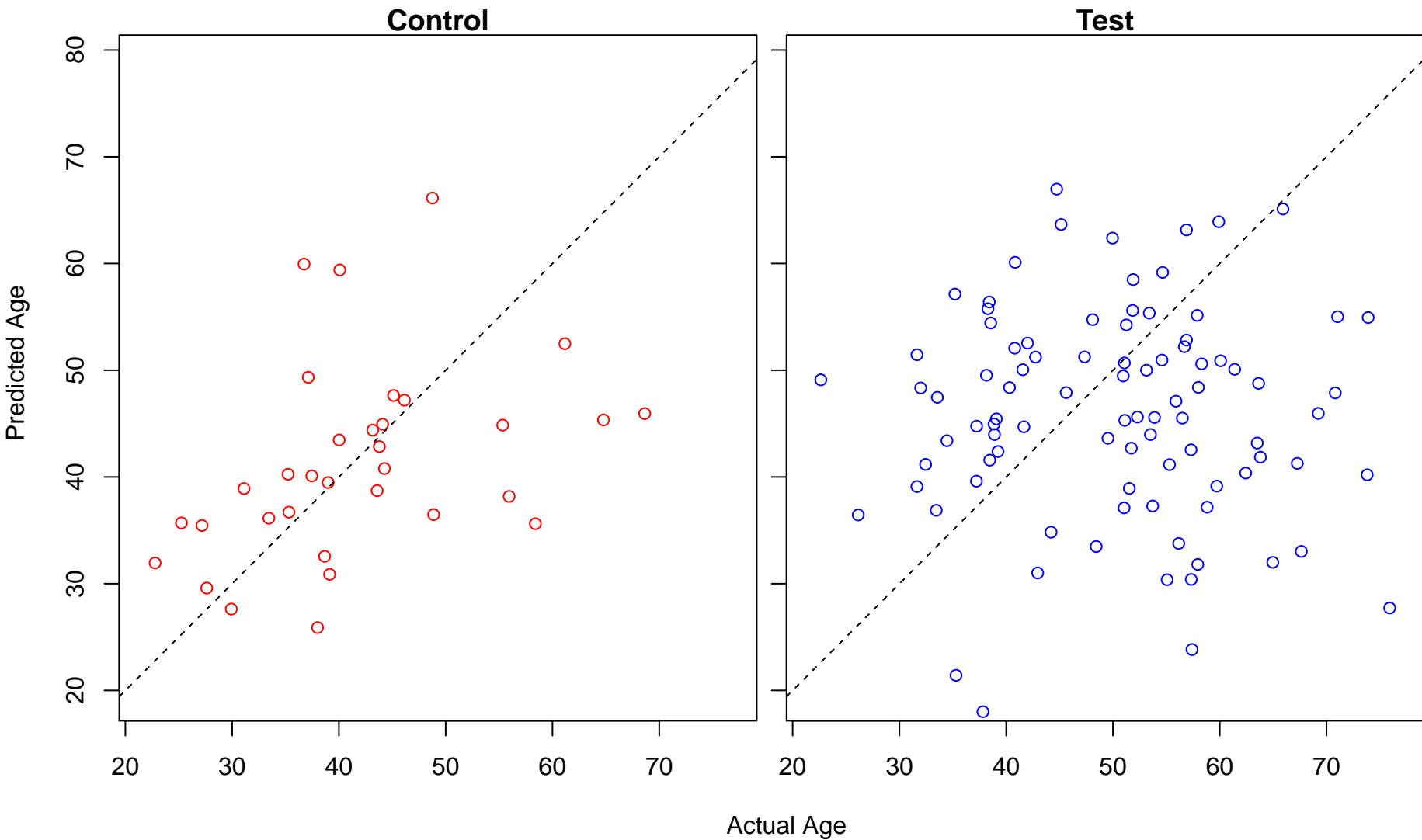
actin cytoskeleton organization (Score: 0.798341)



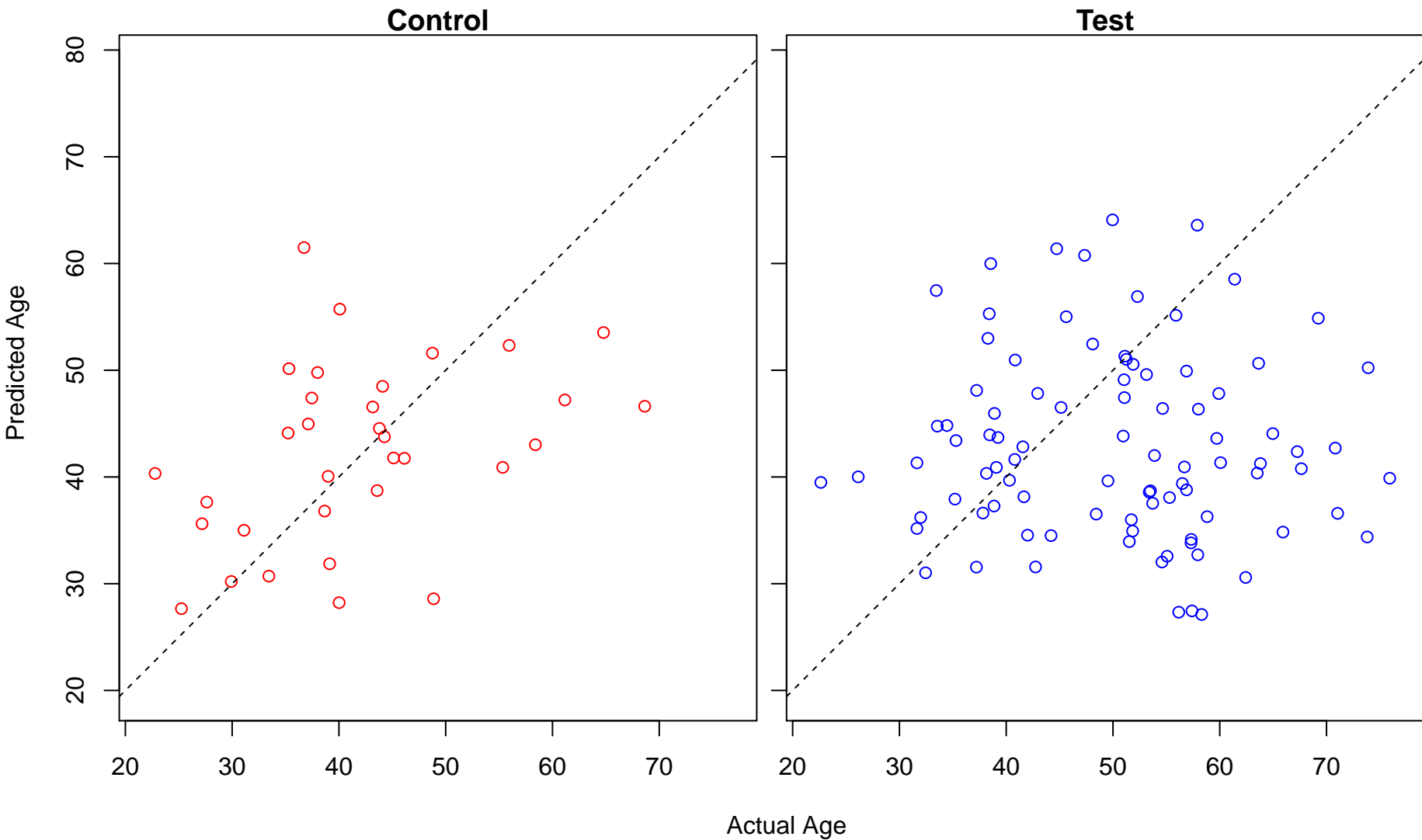
cytoskeletal anchoring at plasma membrane (Score: 0.797130)



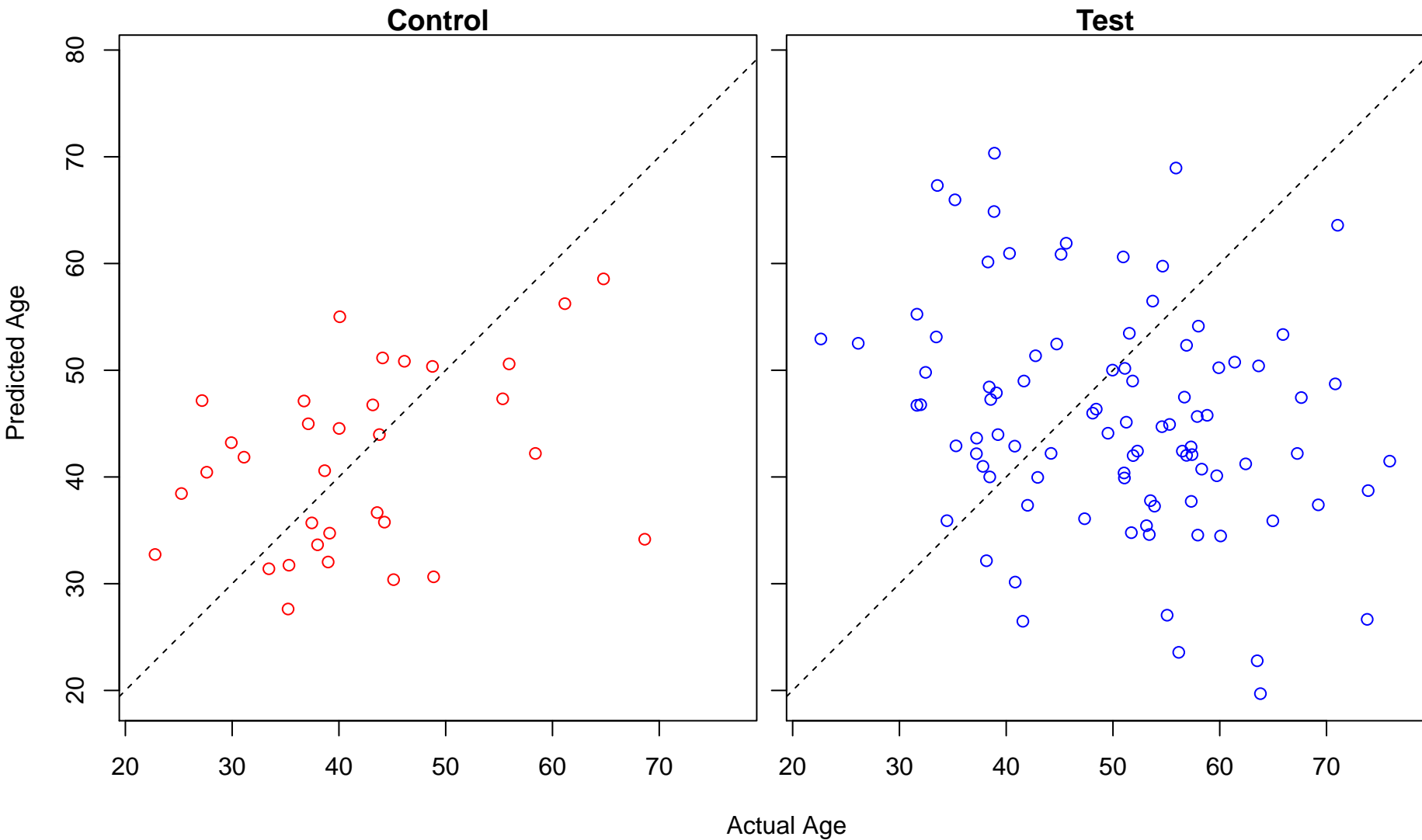
G1/S transition of mitotic cell cycle (Score: 0.796384)



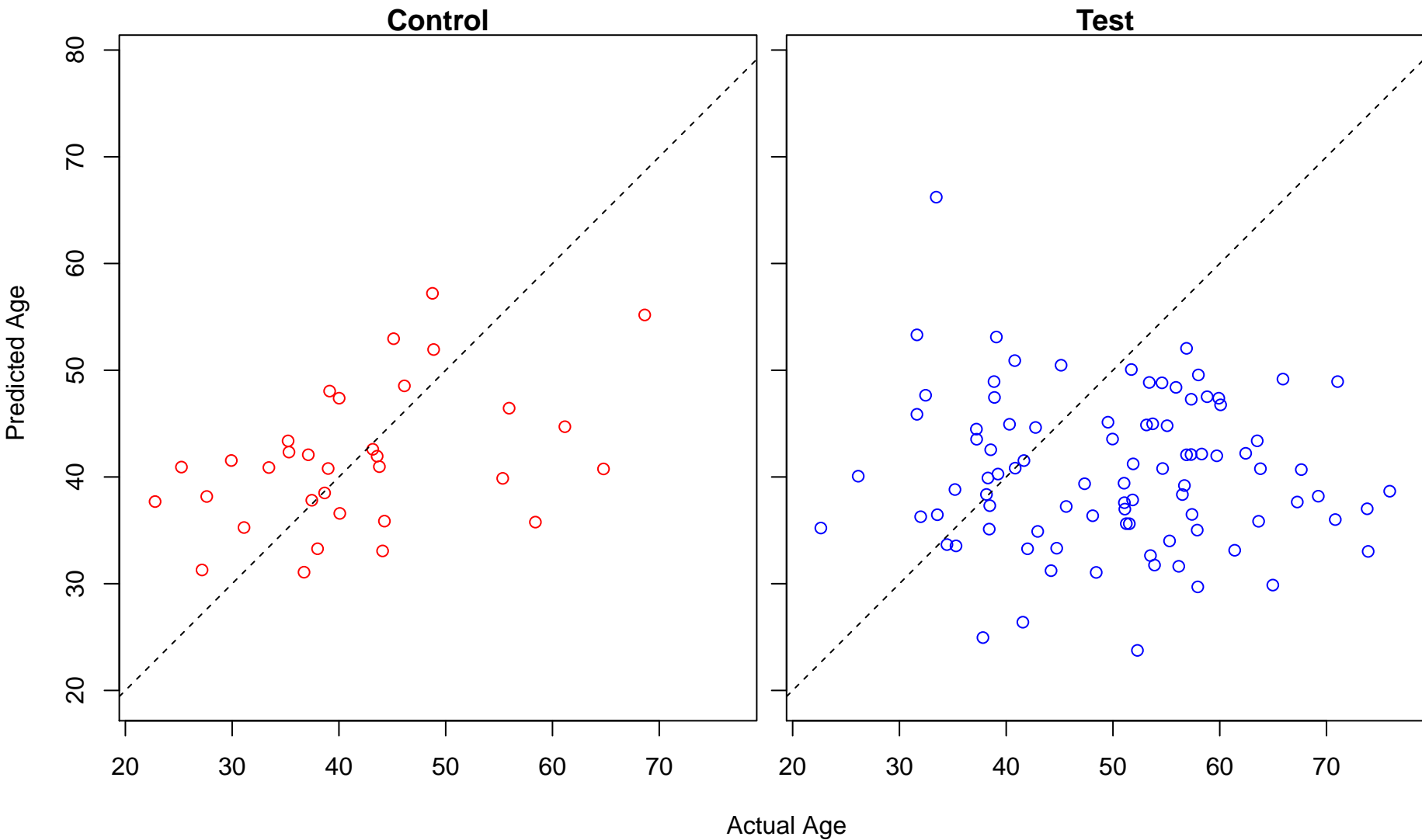
regulation of B cell differentiation (Score: 0.796357)



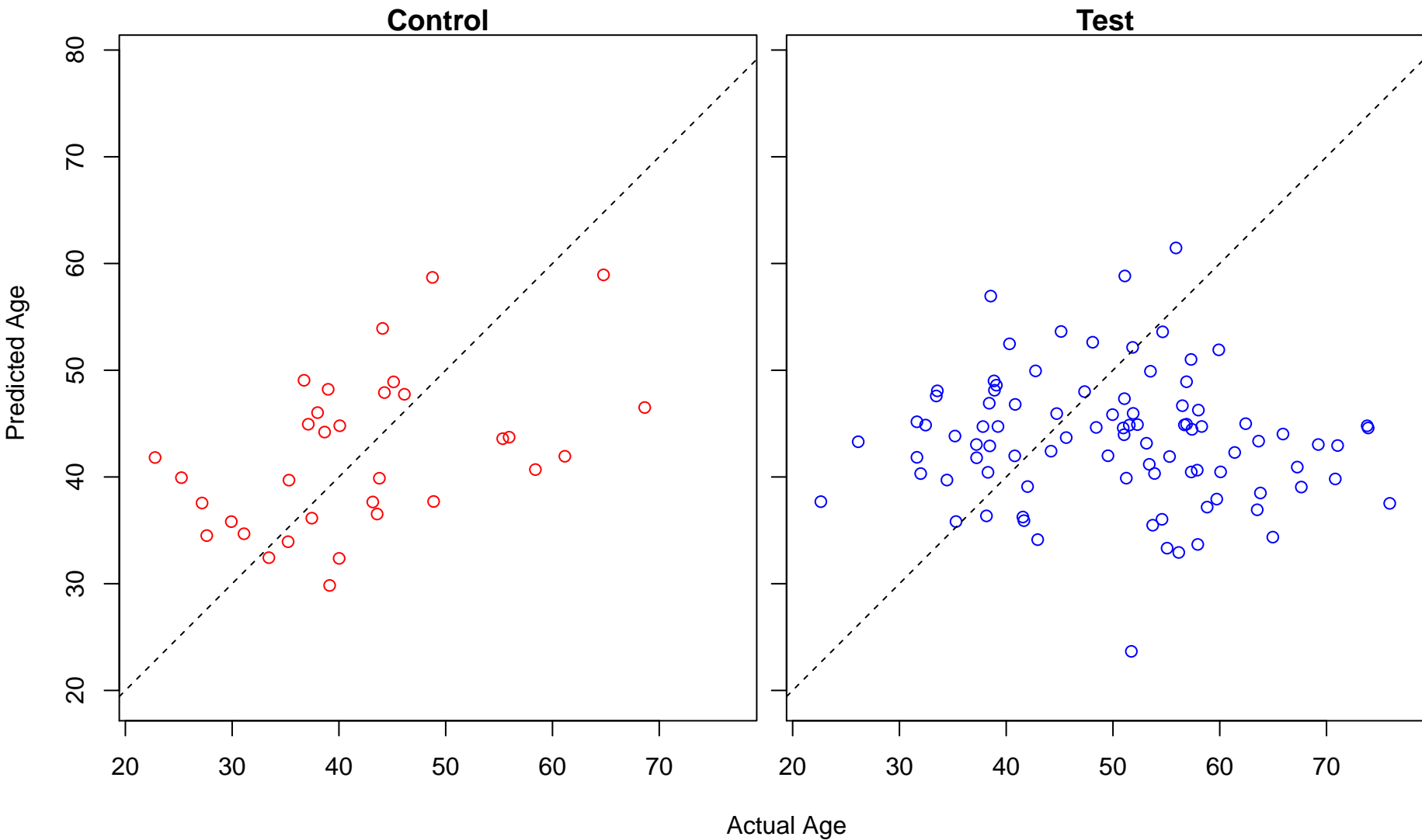
kidney development (Score: 0.795588)



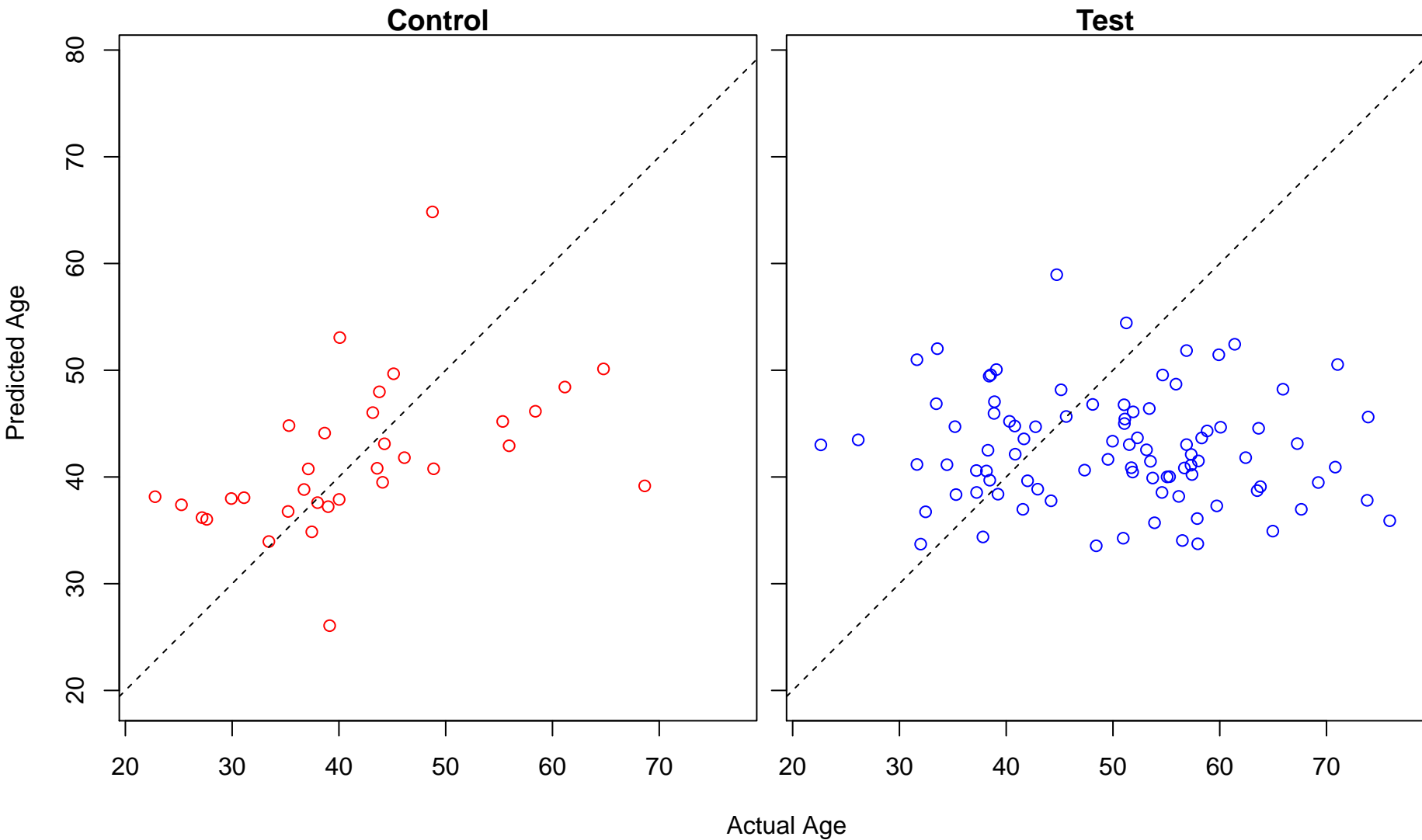
protein oxidation (Score: 0.795424)



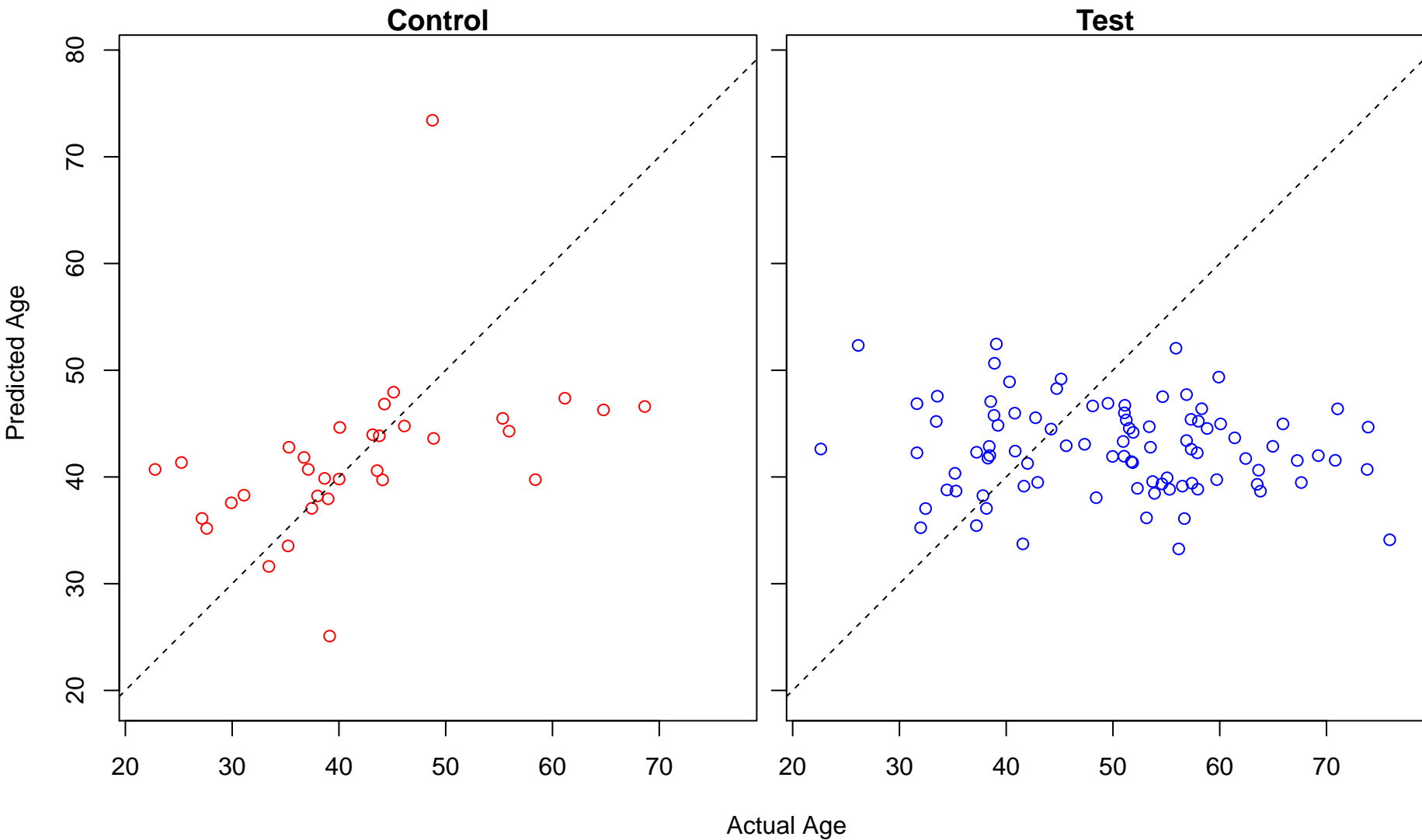
regulation of transforming growth factor beta1 production (Score: 0.794857)



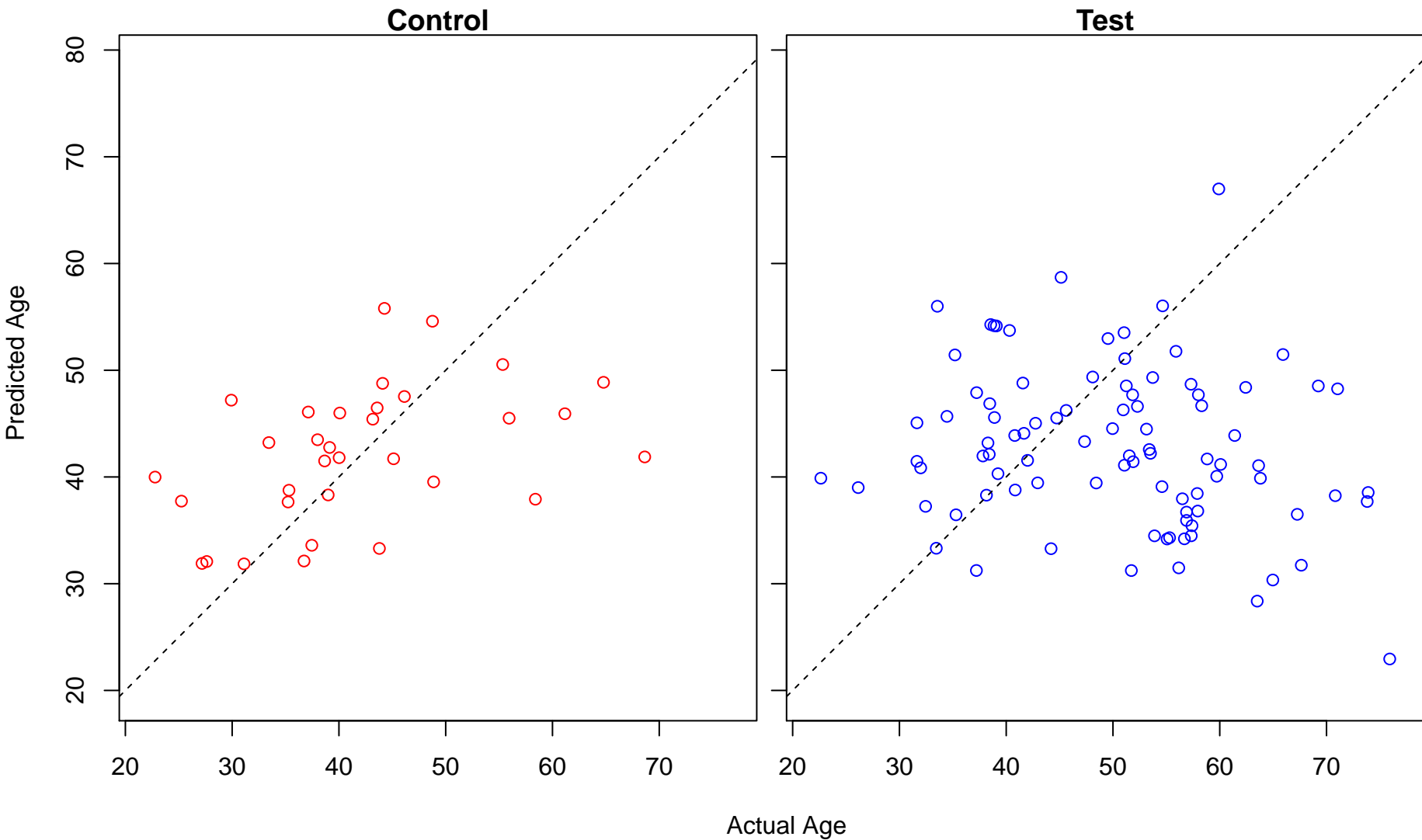
phospholipid biosynthetic process (Score: 0.794616)



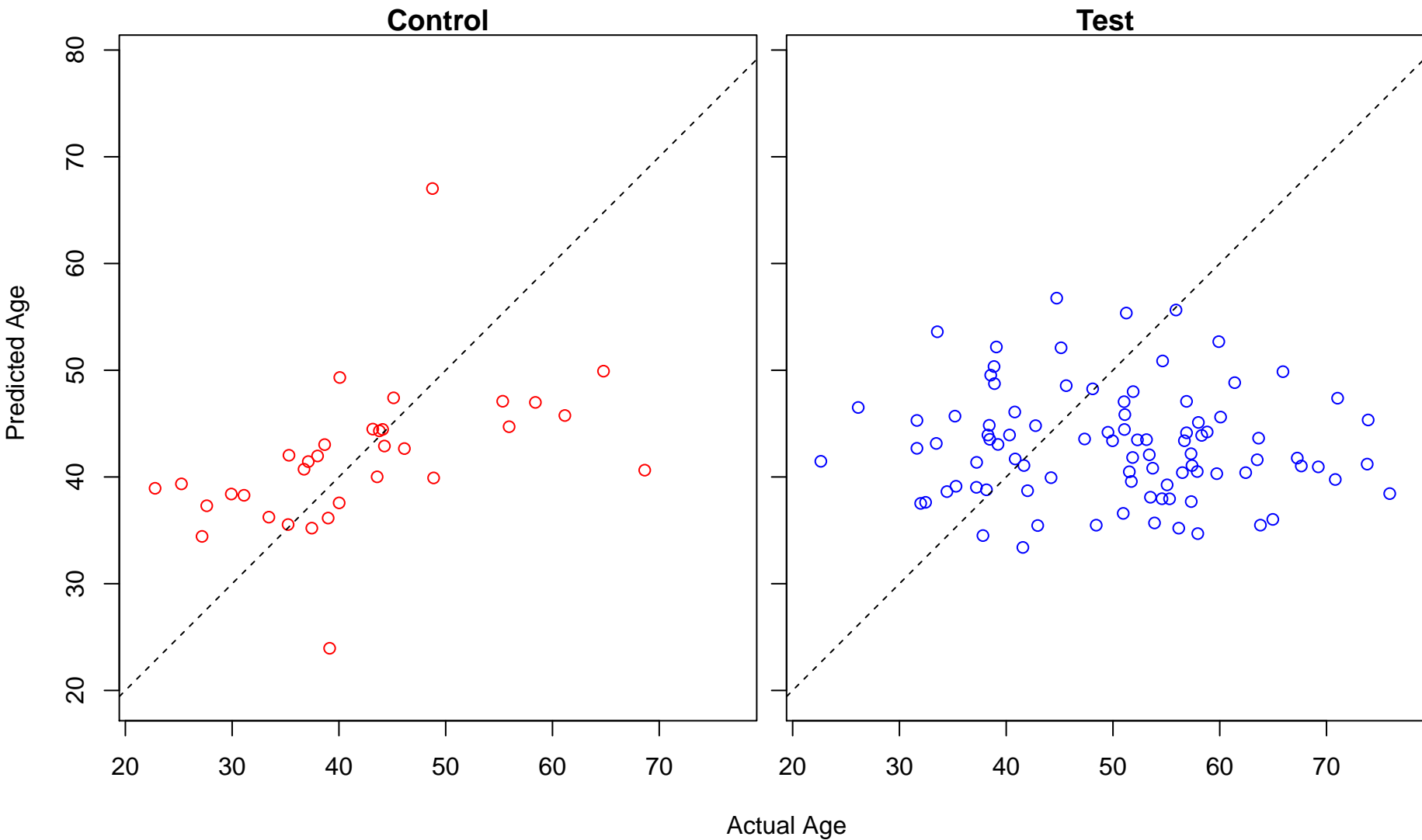
phagocytosis (Score: 0.794571)



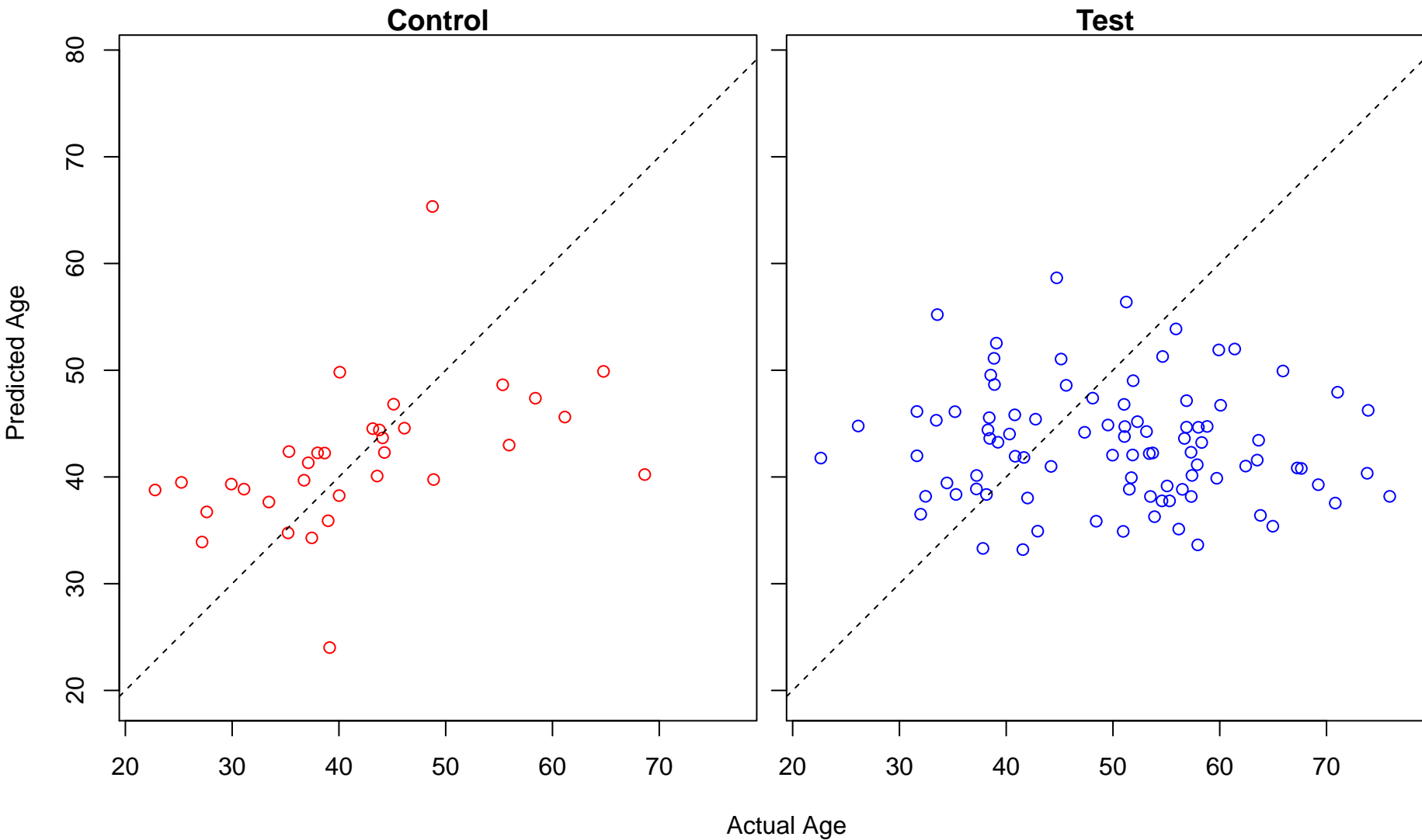
ventricular system development (Score: 0.793469)



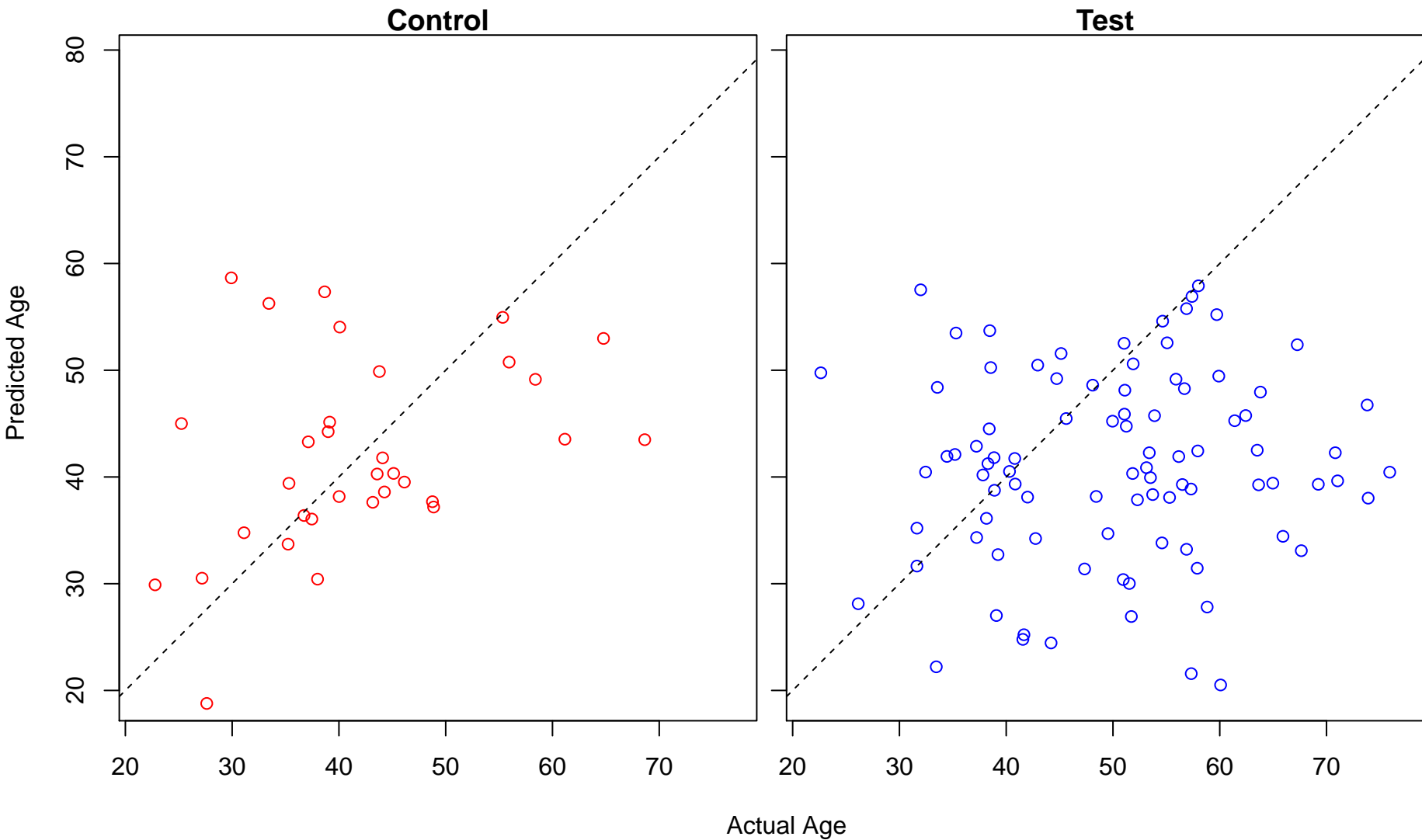
cellular component morphogenesis (Score: 0.792283)



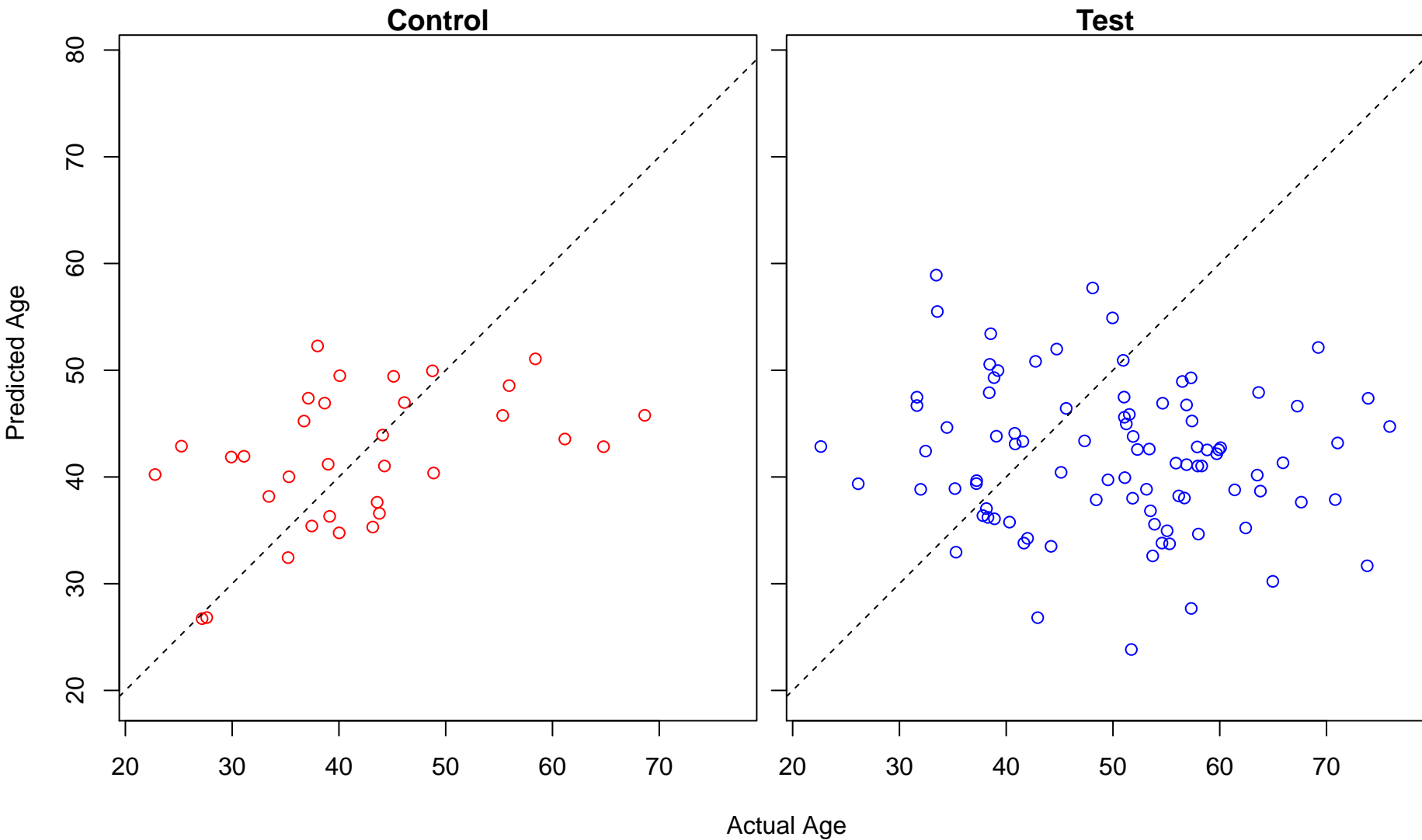
cell morphogenesis involved in differentiation (Score: 0.791625)



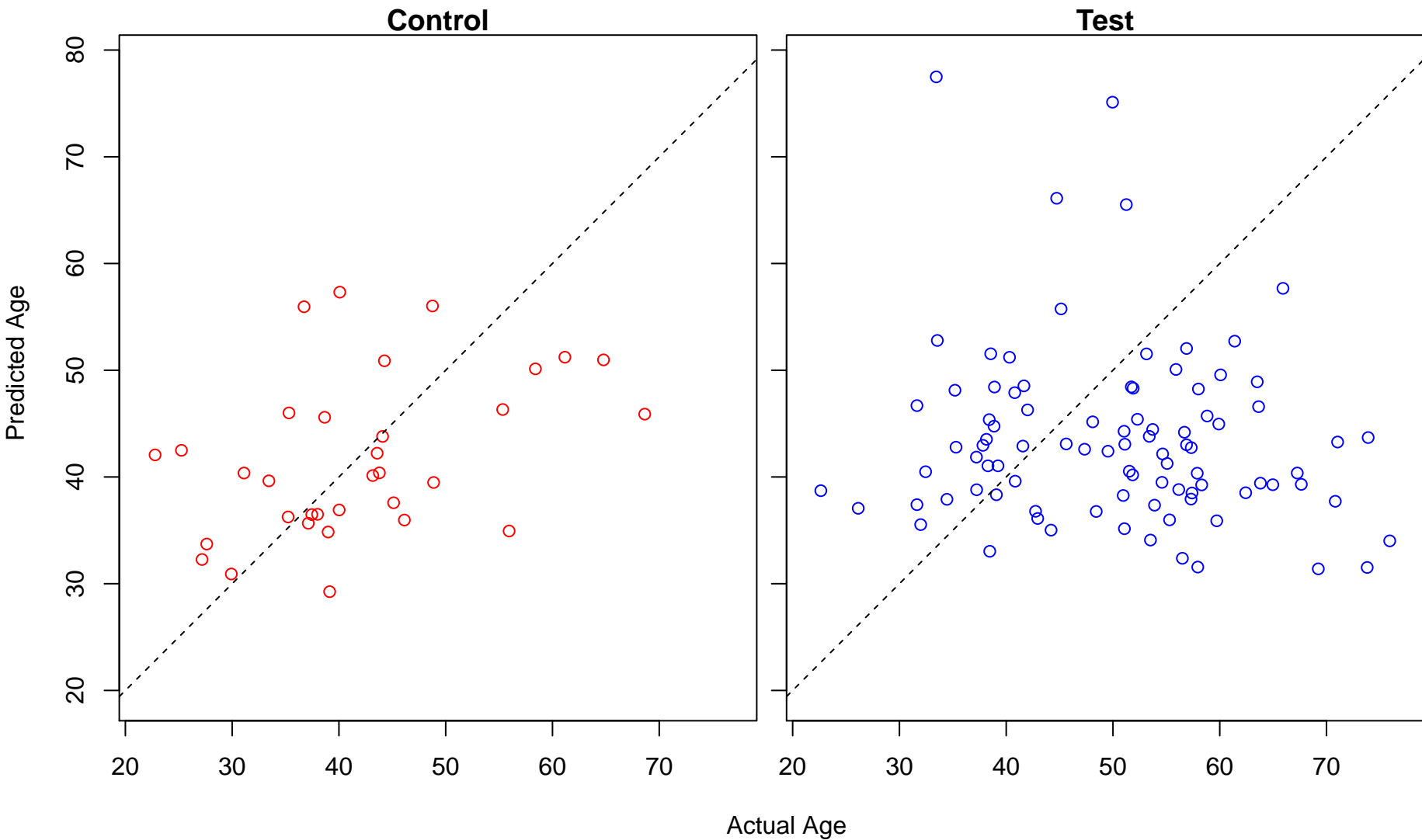
neural crest cell differentiation (Score: 0.791272)



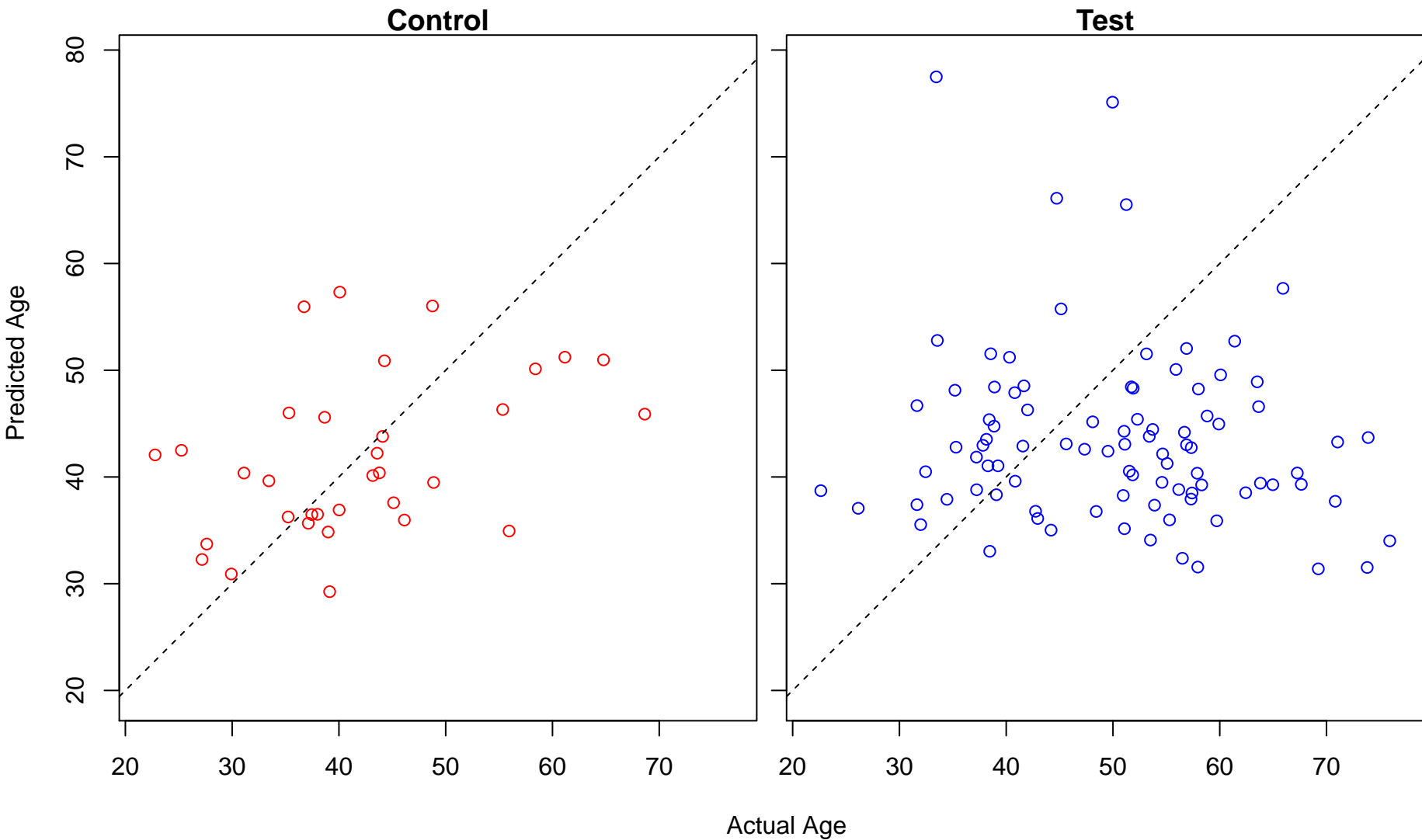
regulation of beta-amyloid clearance (Score: 0.790834)



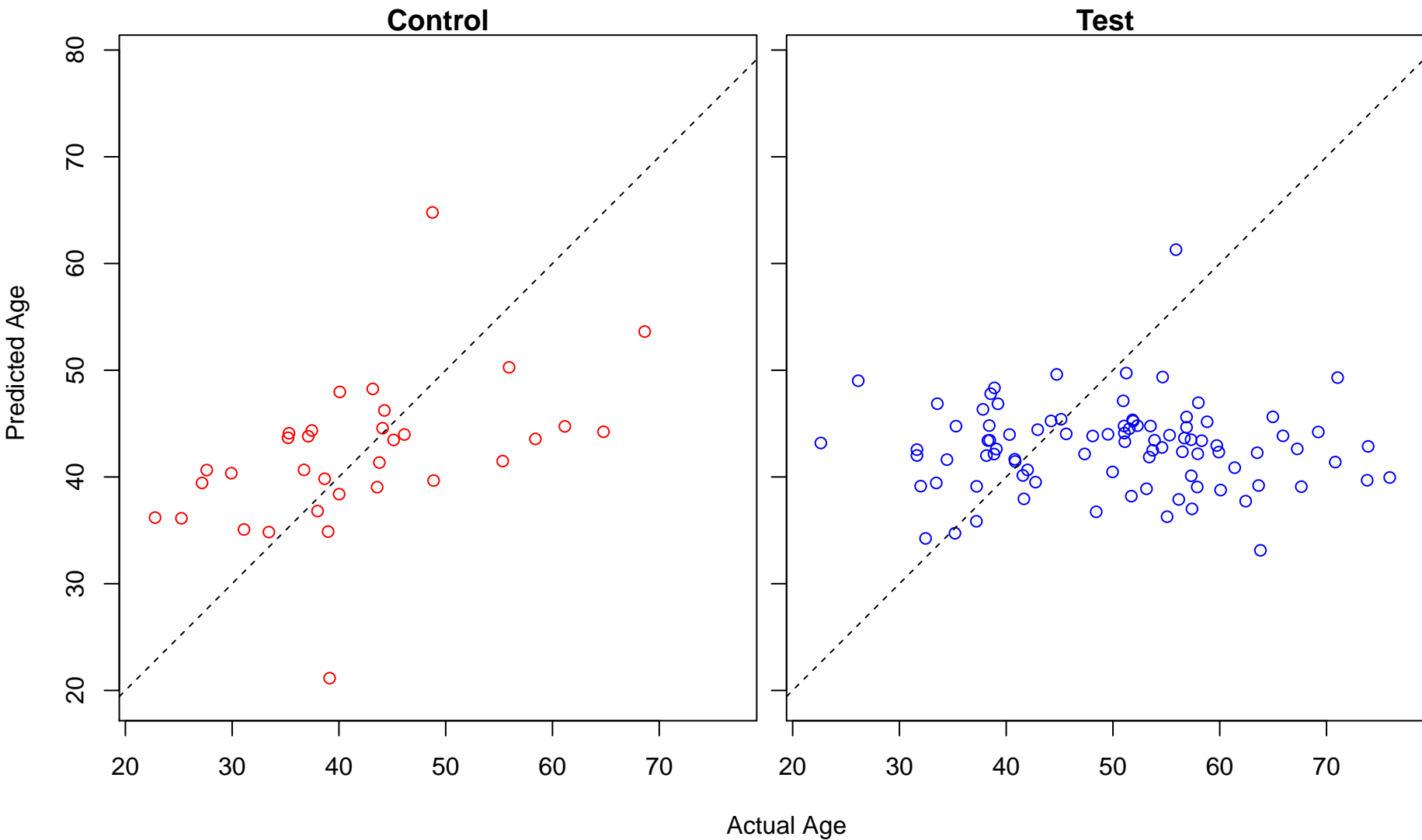
regulation of miRNA metabolic process (Score: 0.790380)



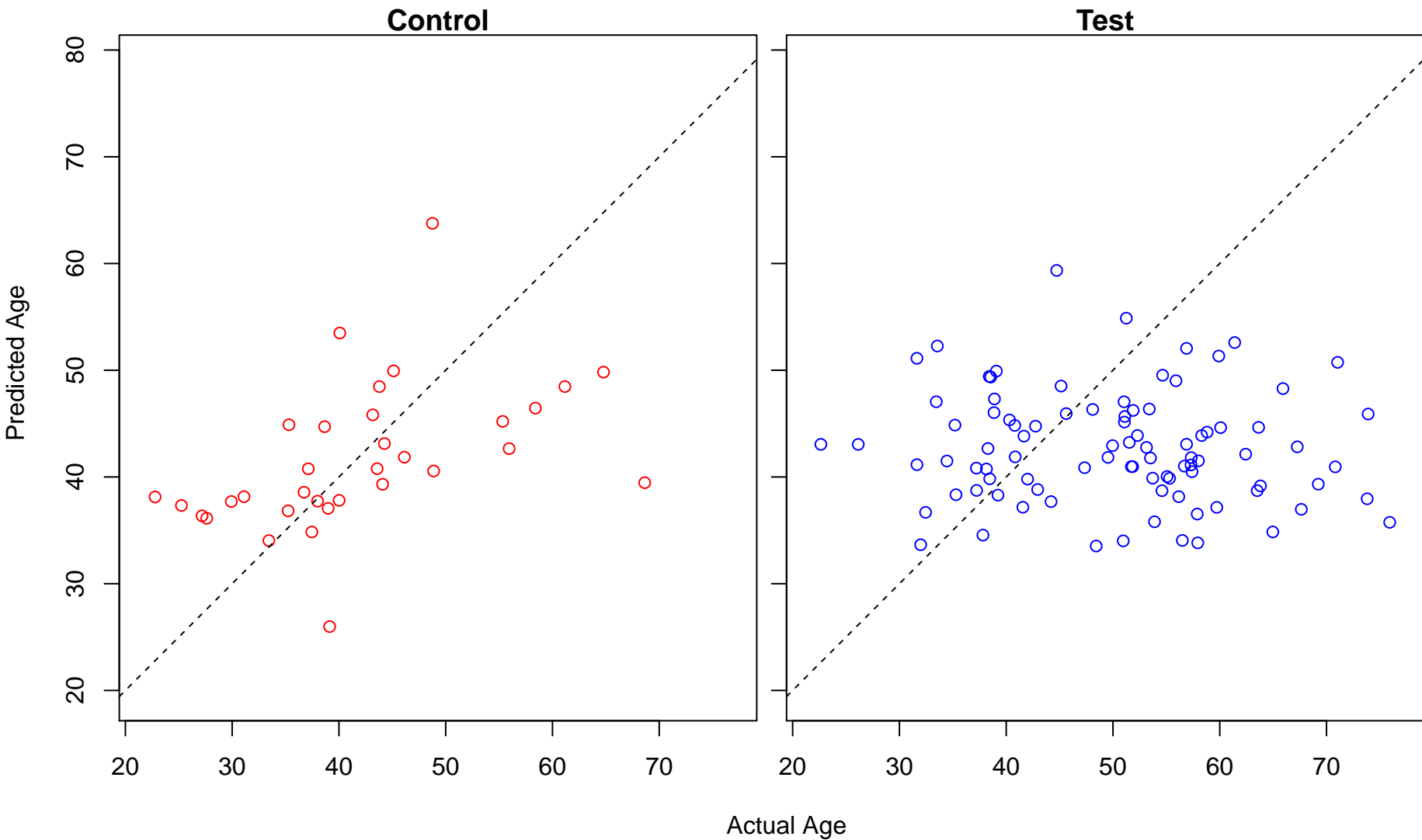
positive regulation of miRNA metabolic process (Score: 0.790380)



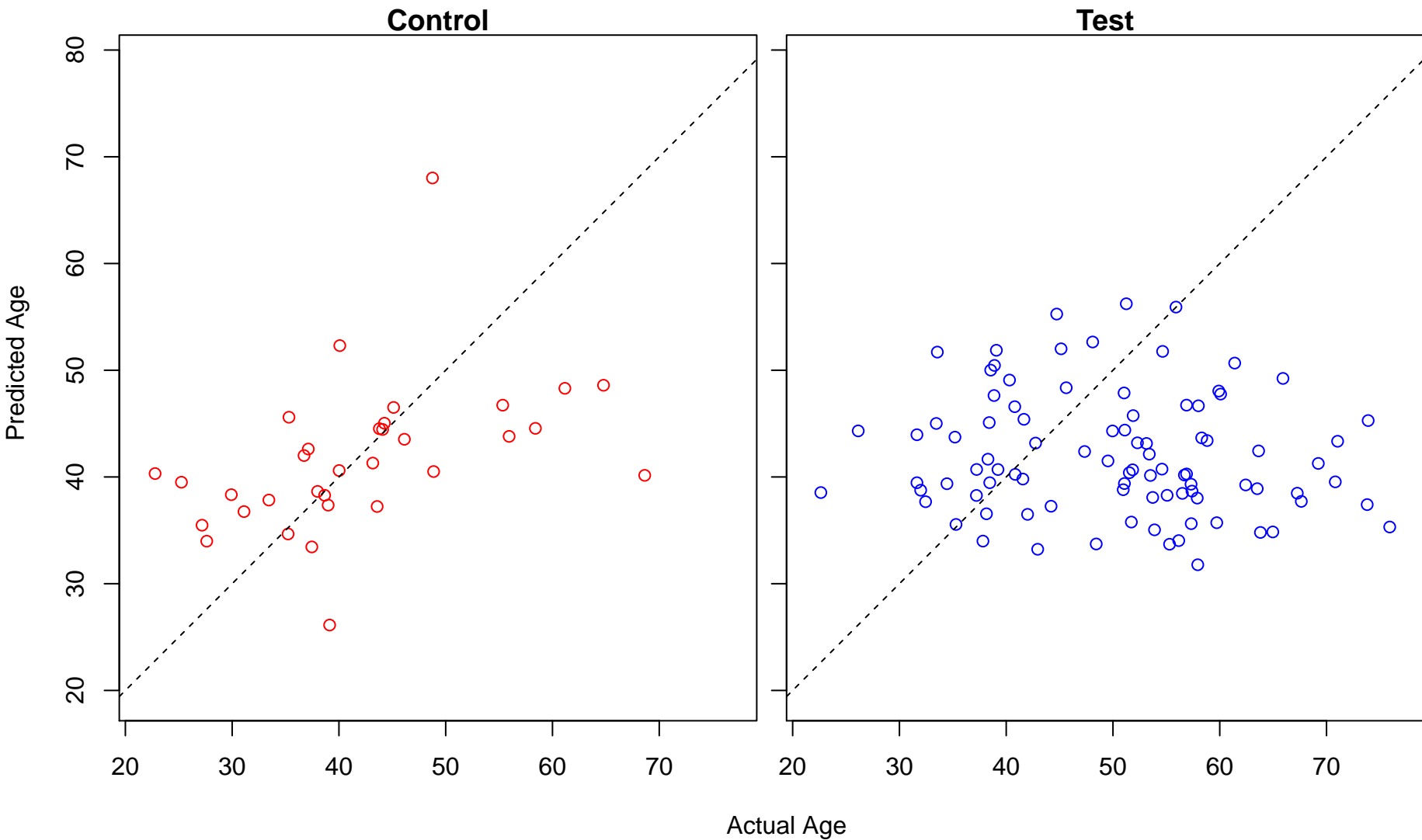
negative regulation of ATP biosynthetic process (Score: 0.790163)



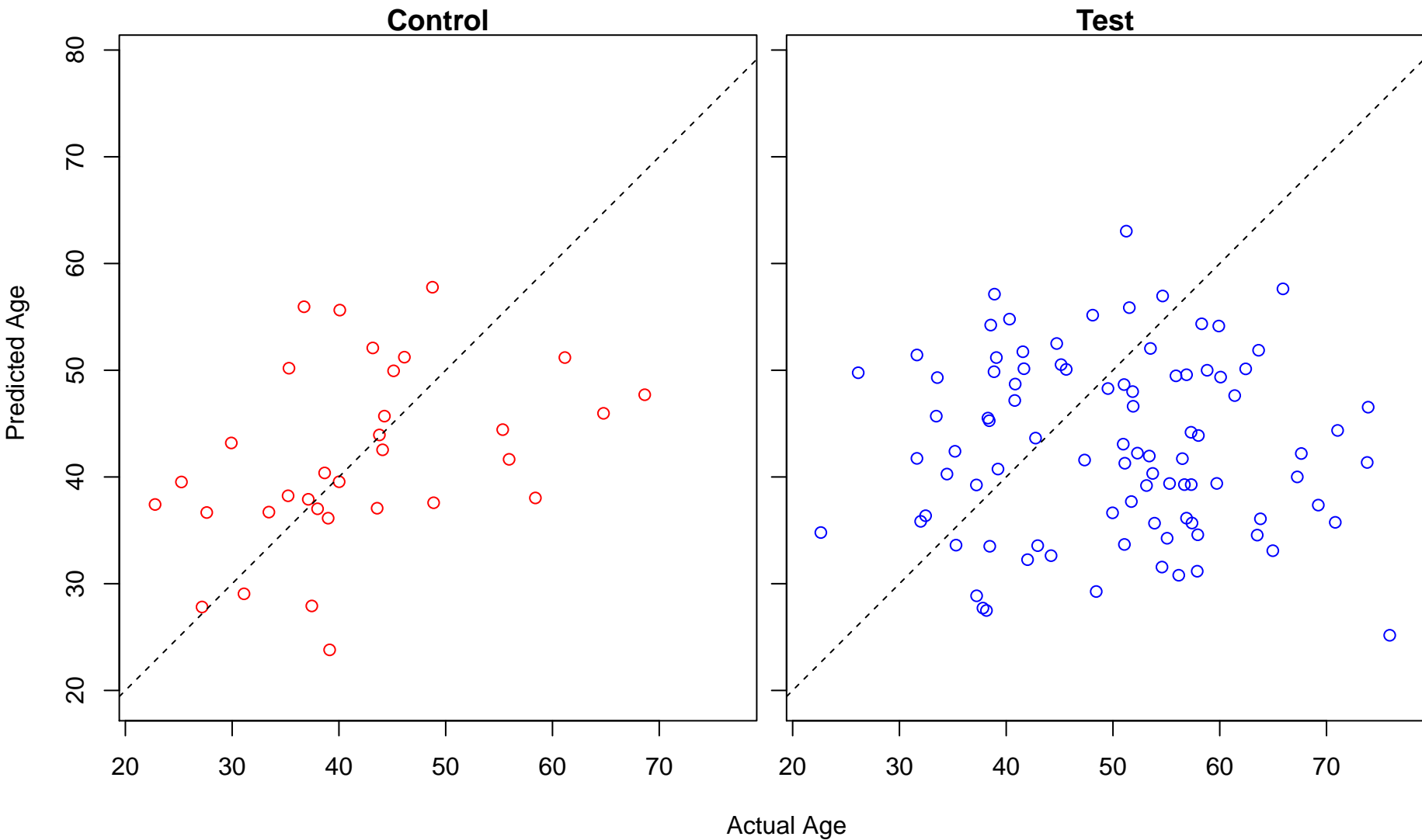
glycerophospholipid biosynthetic process (Score: 0.789654)



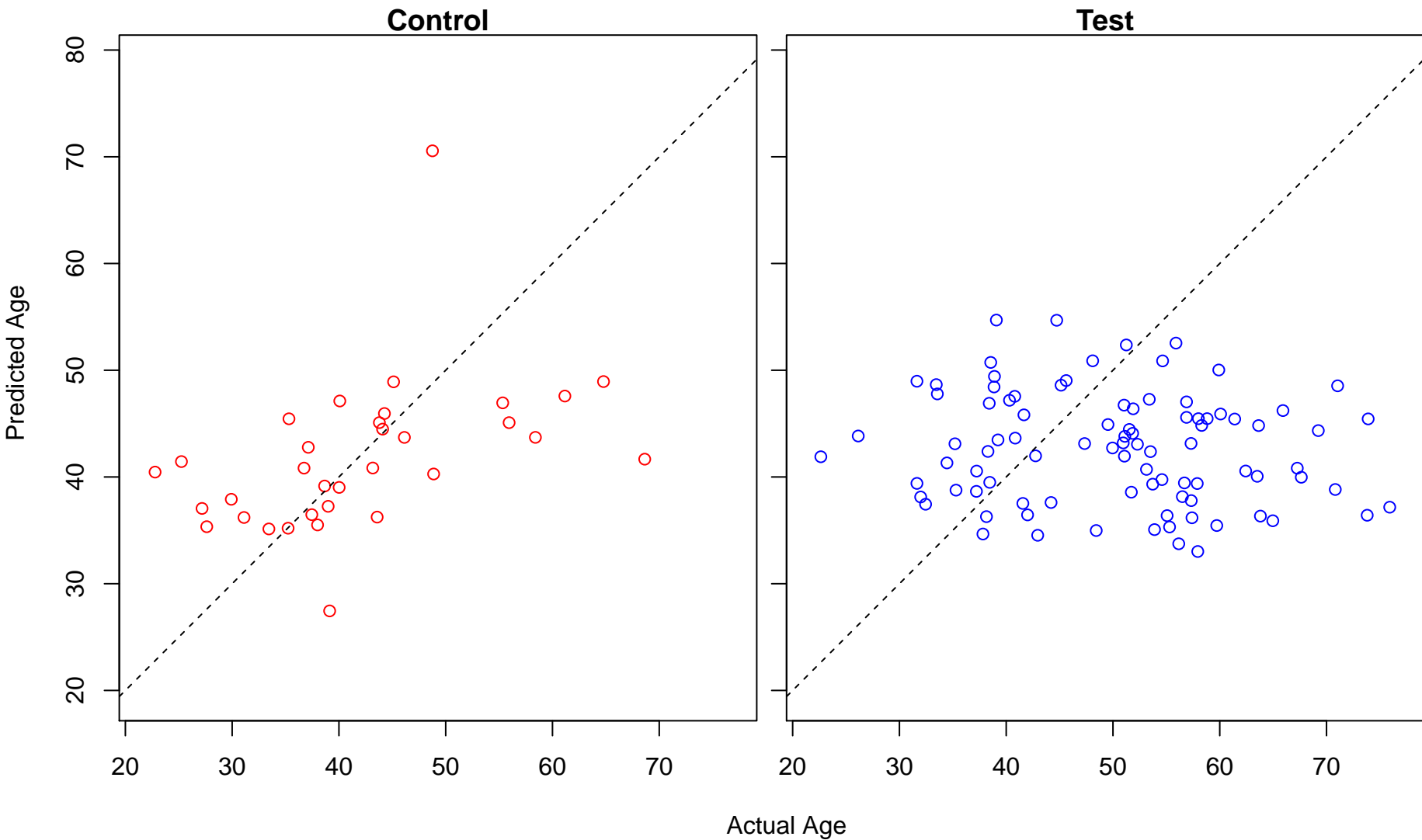
regulation of intracellular transport (Score: 0.787956)



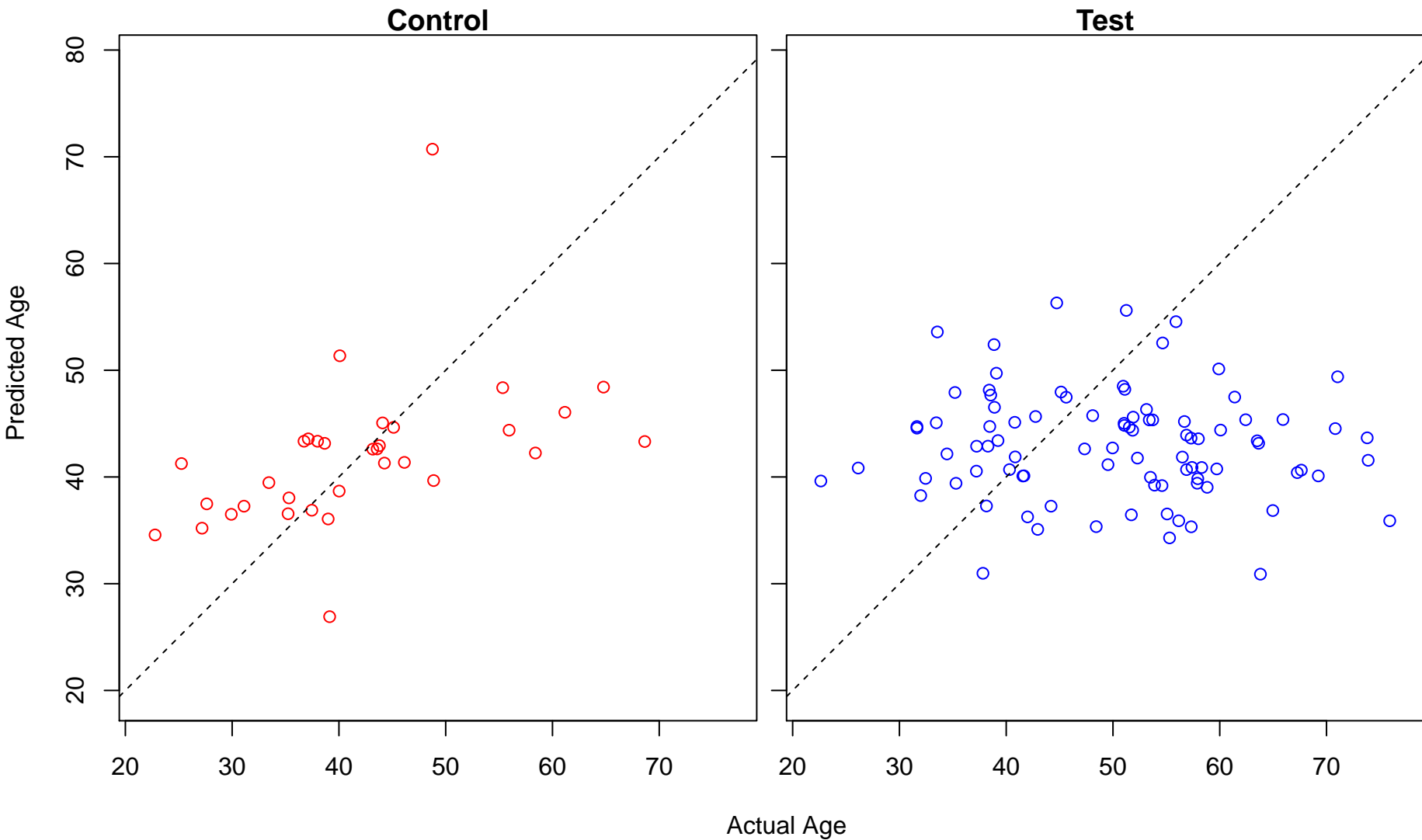
response to fluid shear stress (Score: 0.787305)



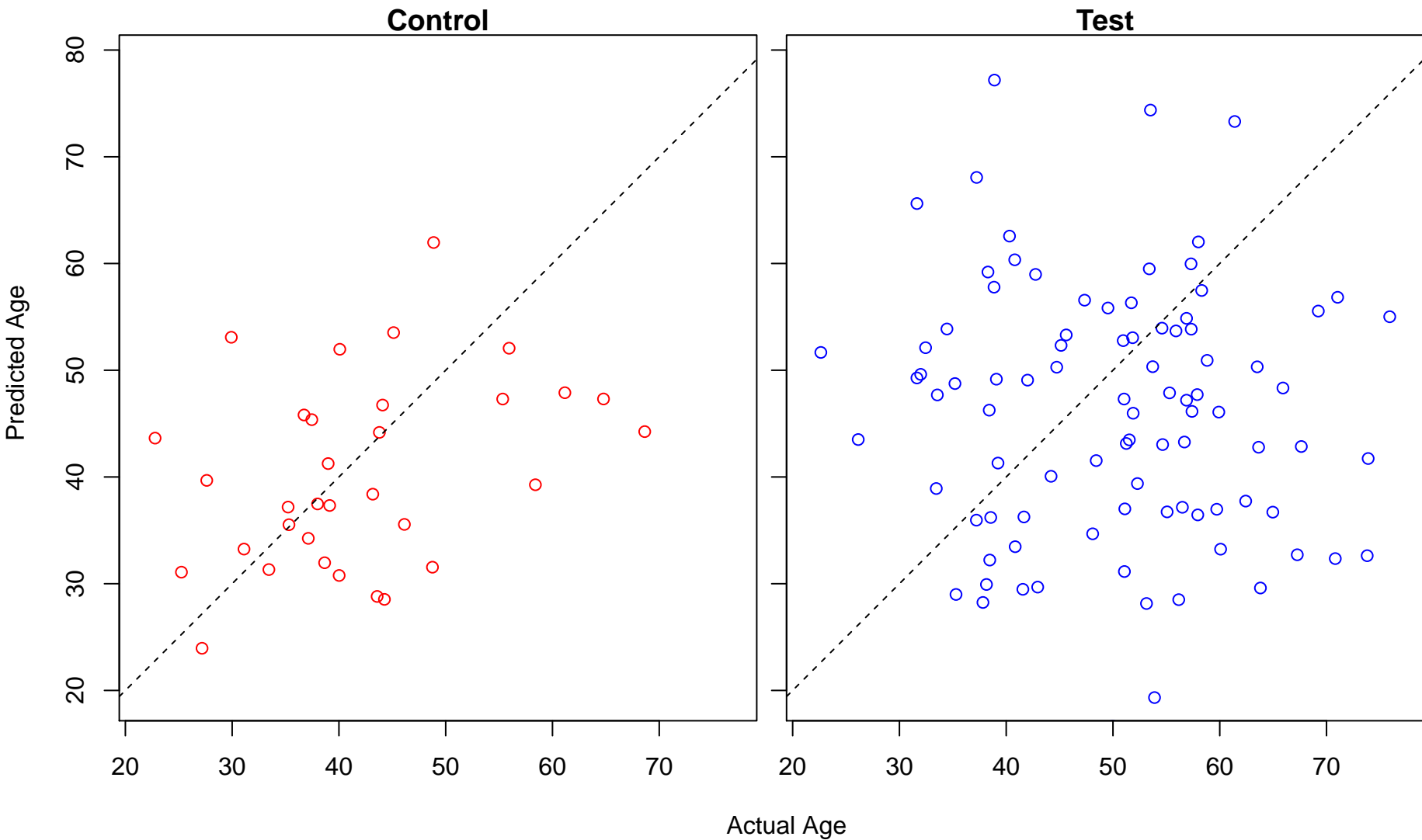
nucleocytoplasmic transport (Score: 0.786299)



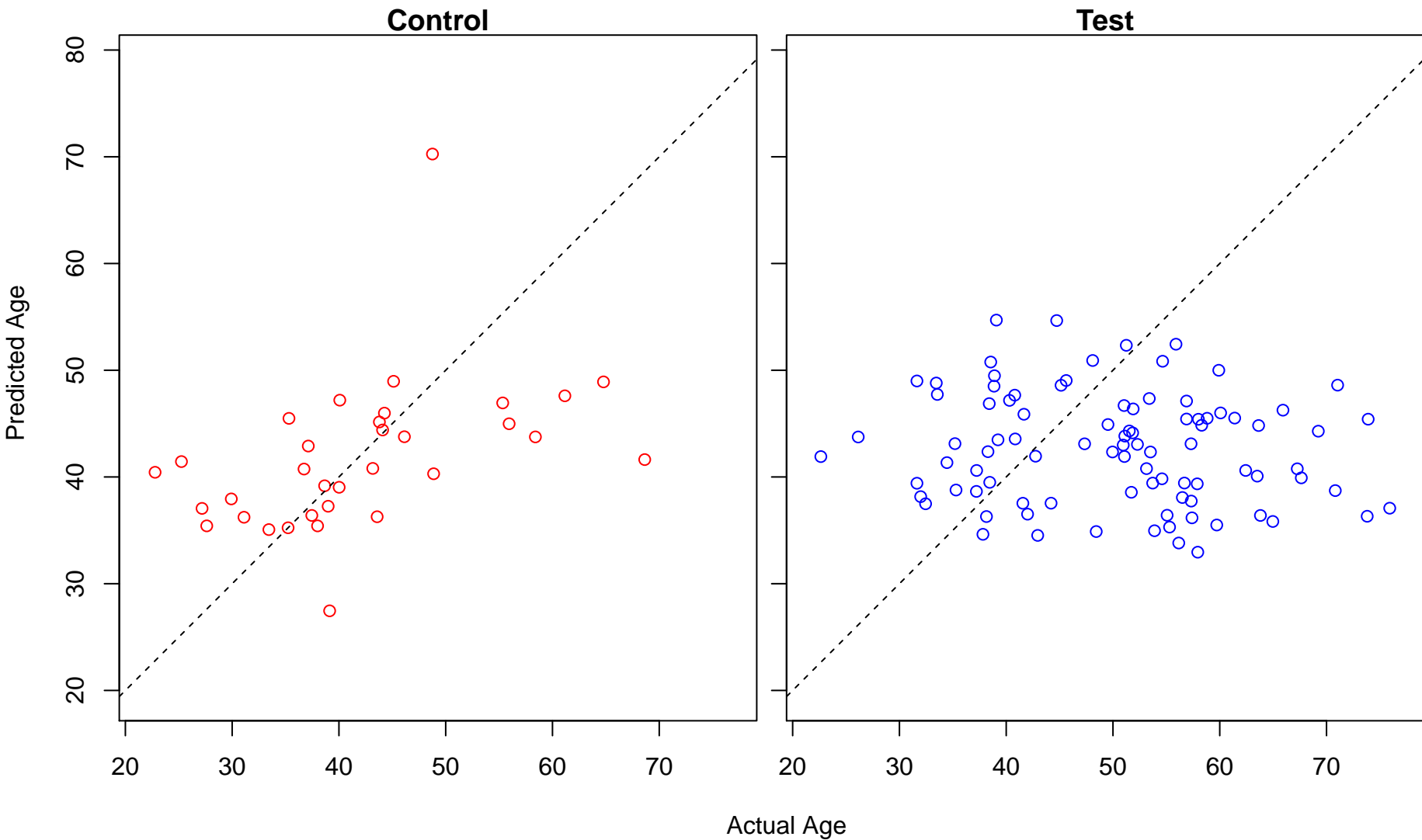
anatomical structure morphogenesis (Score: 0.785954)



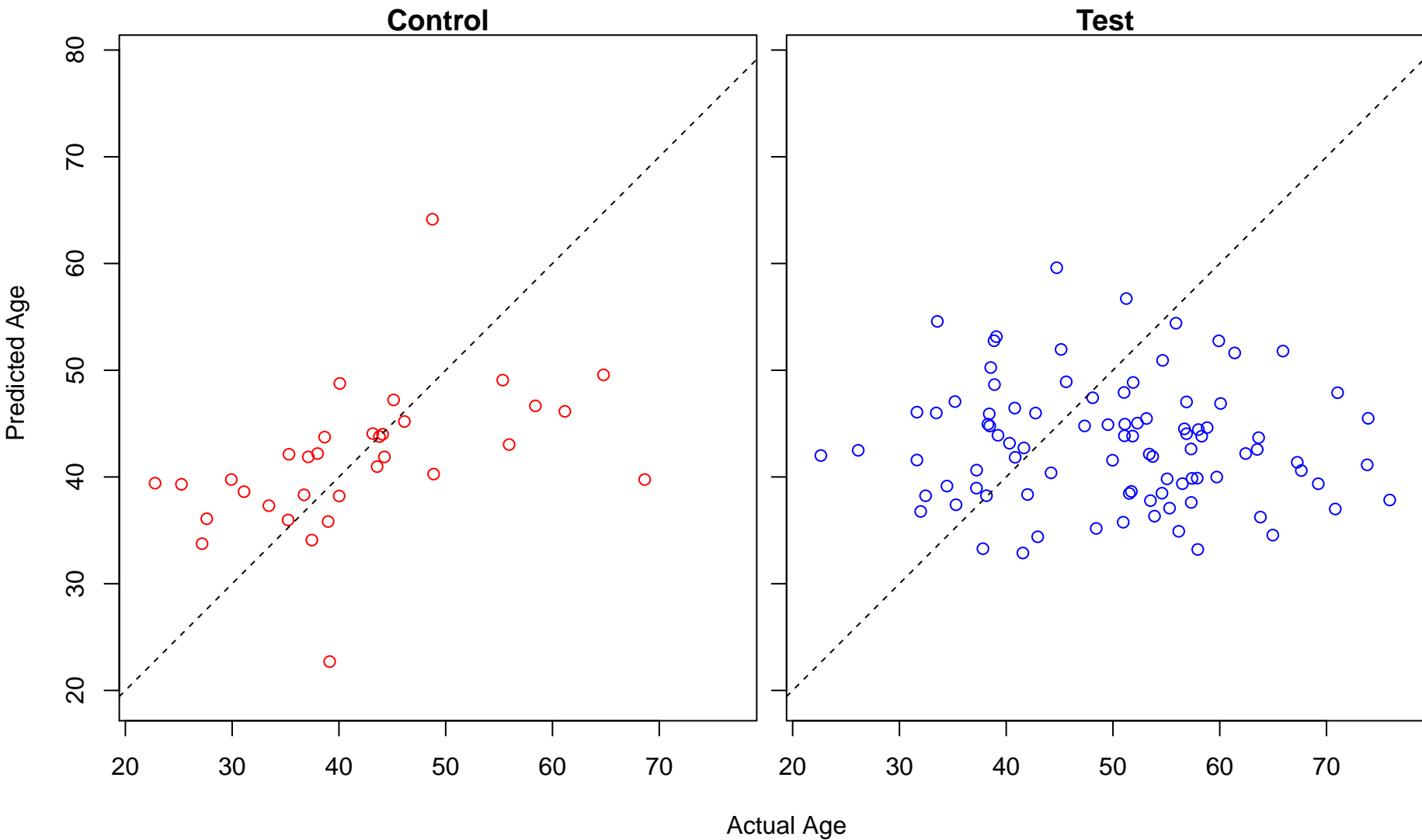
positive regulation of phosphatase activity (Score: 0.785847)



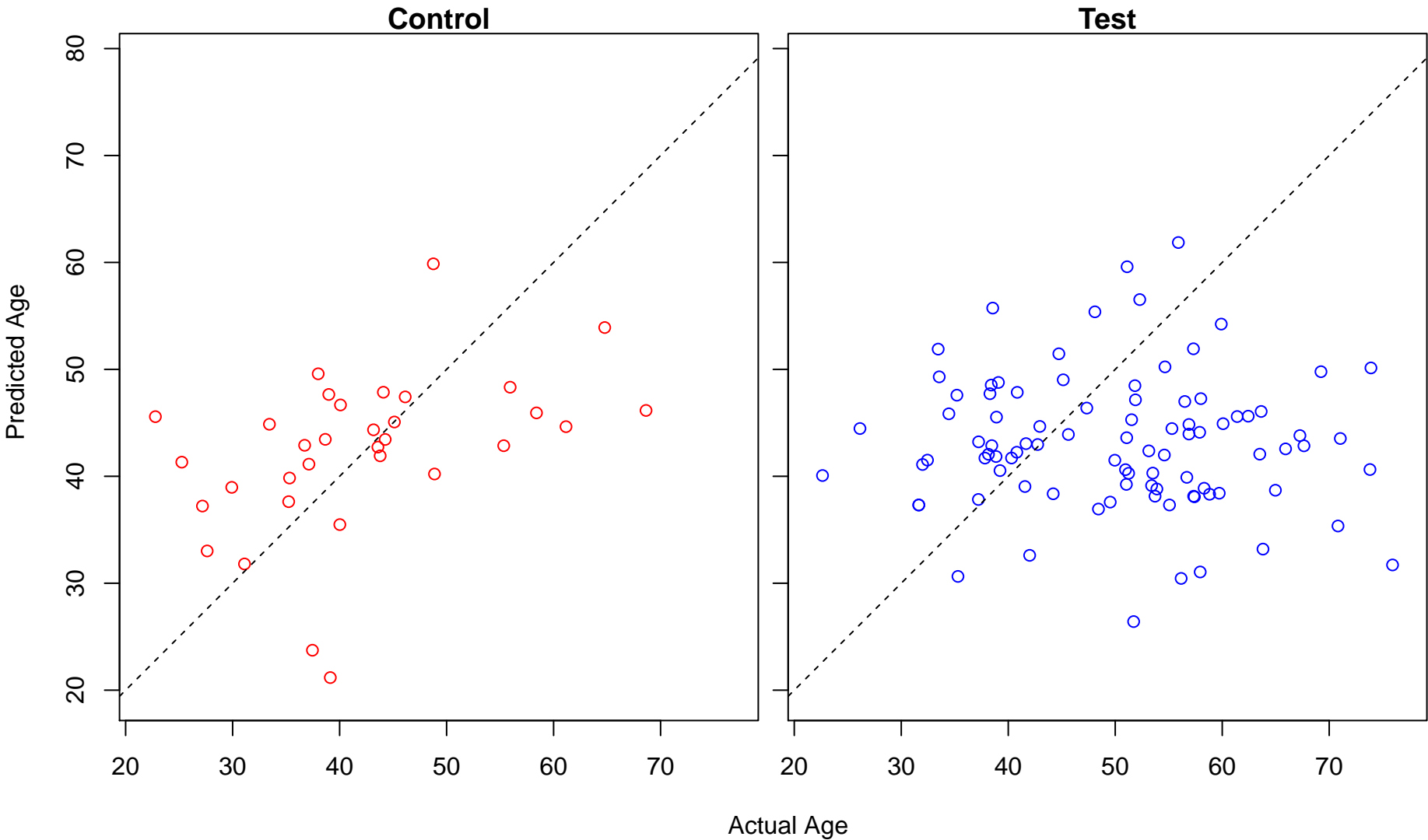
nuclear transport (Score: 0.784676)



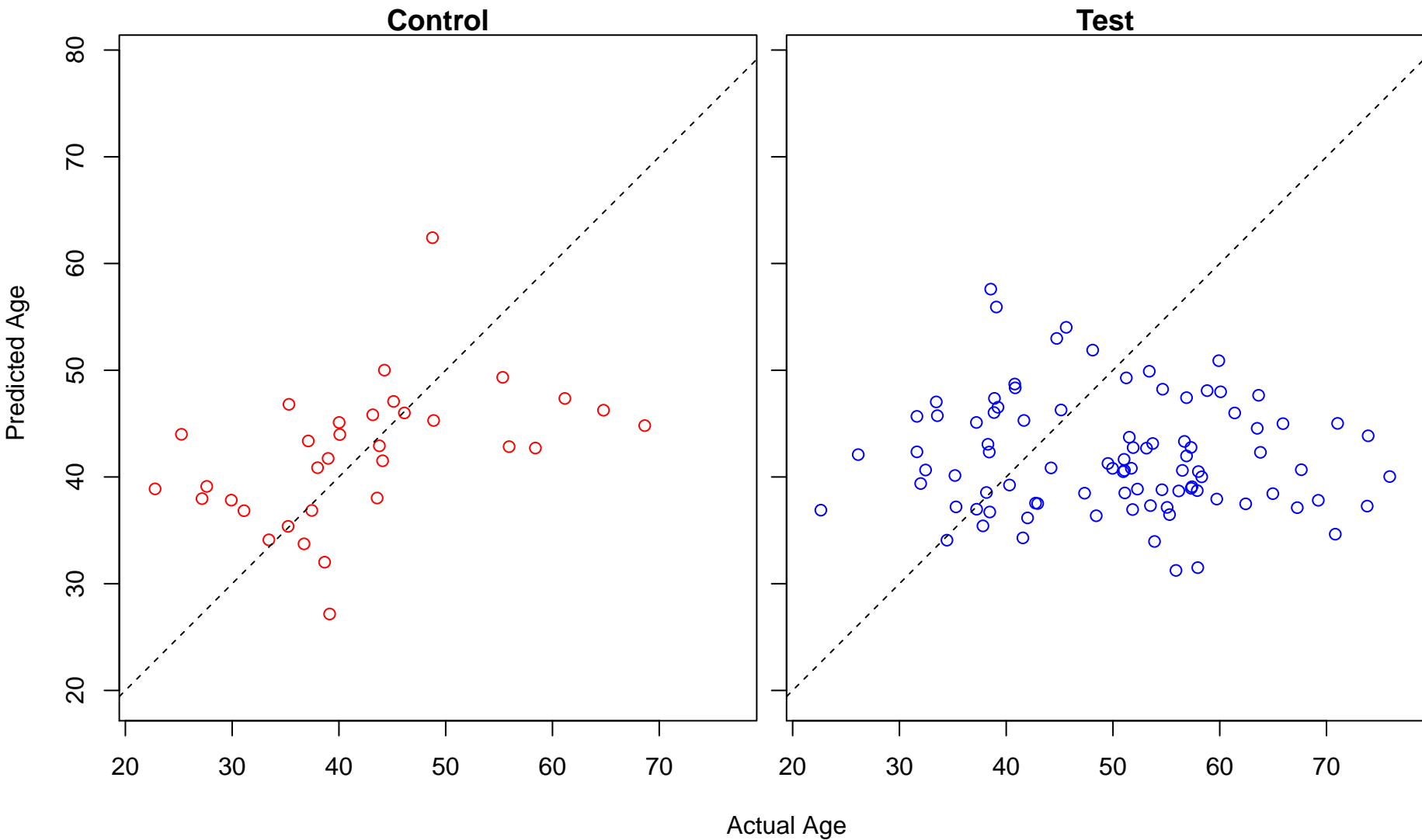
axonogenesis (Score: 0.784128)

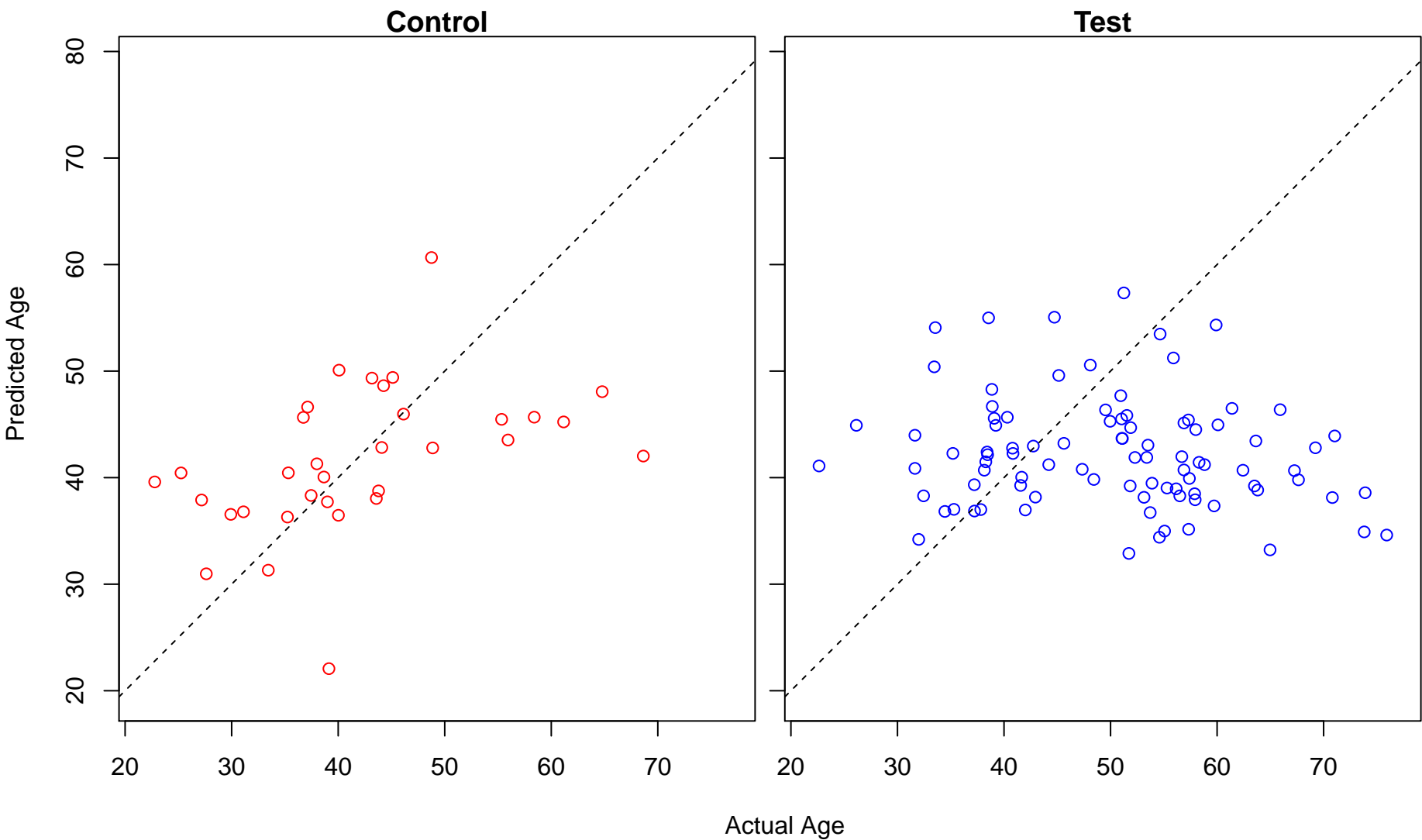


regulation of transcription from RNA polymerase II promoter in response to oxidative stress (Score: 0.7)

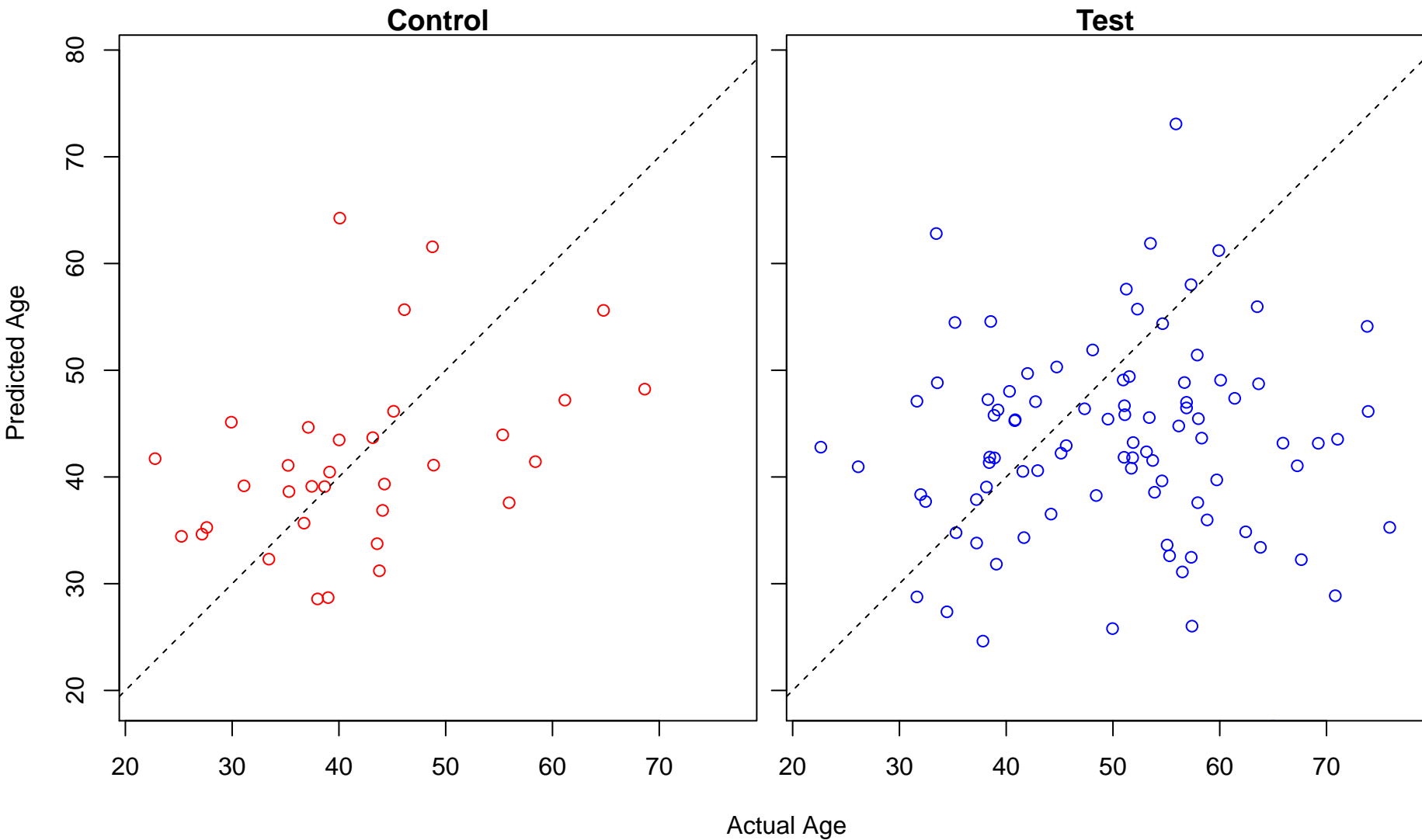


protein import into mitochondrial matrix (Score: 0.783404)

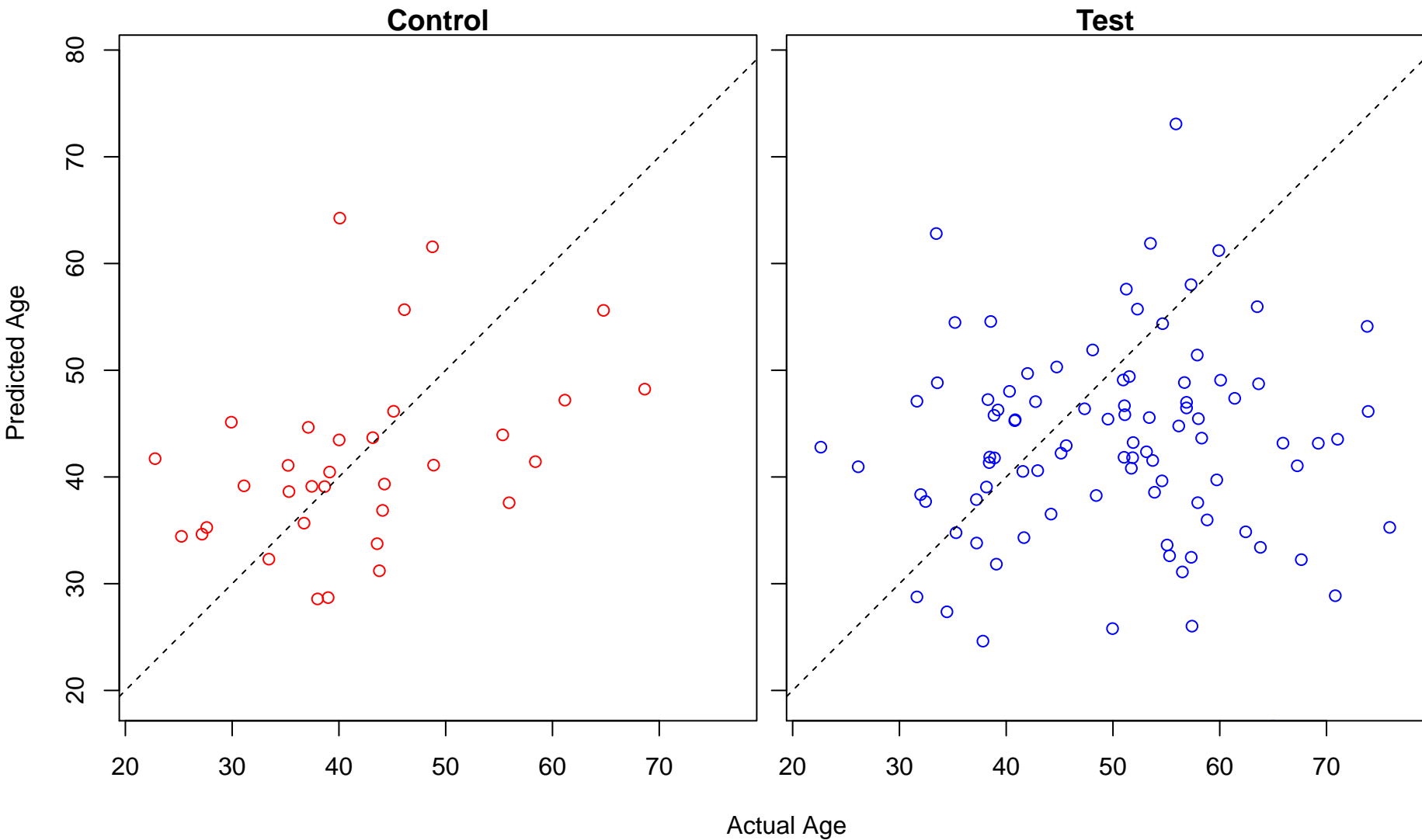




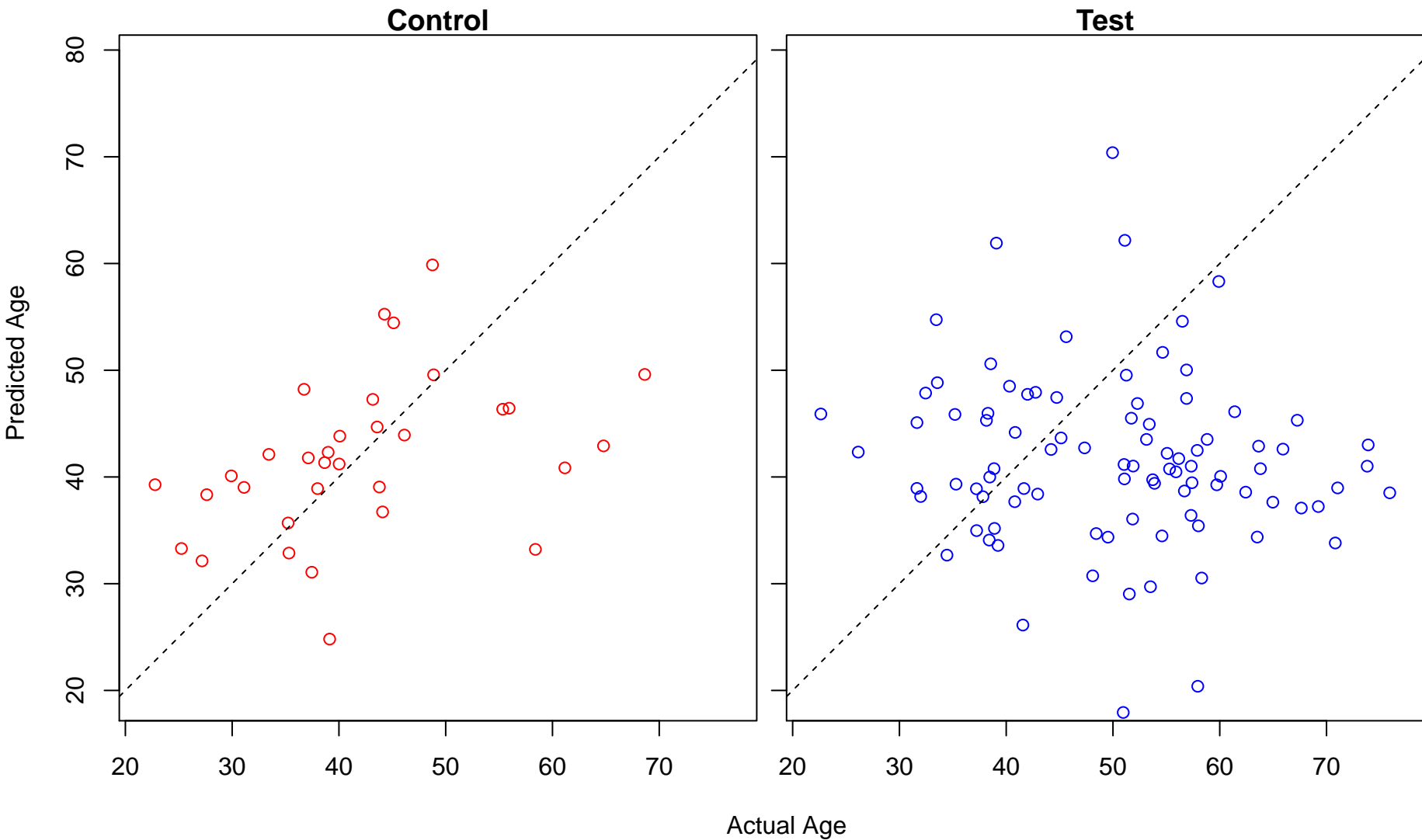
glycogen metabolic process (Score: 0.781954)



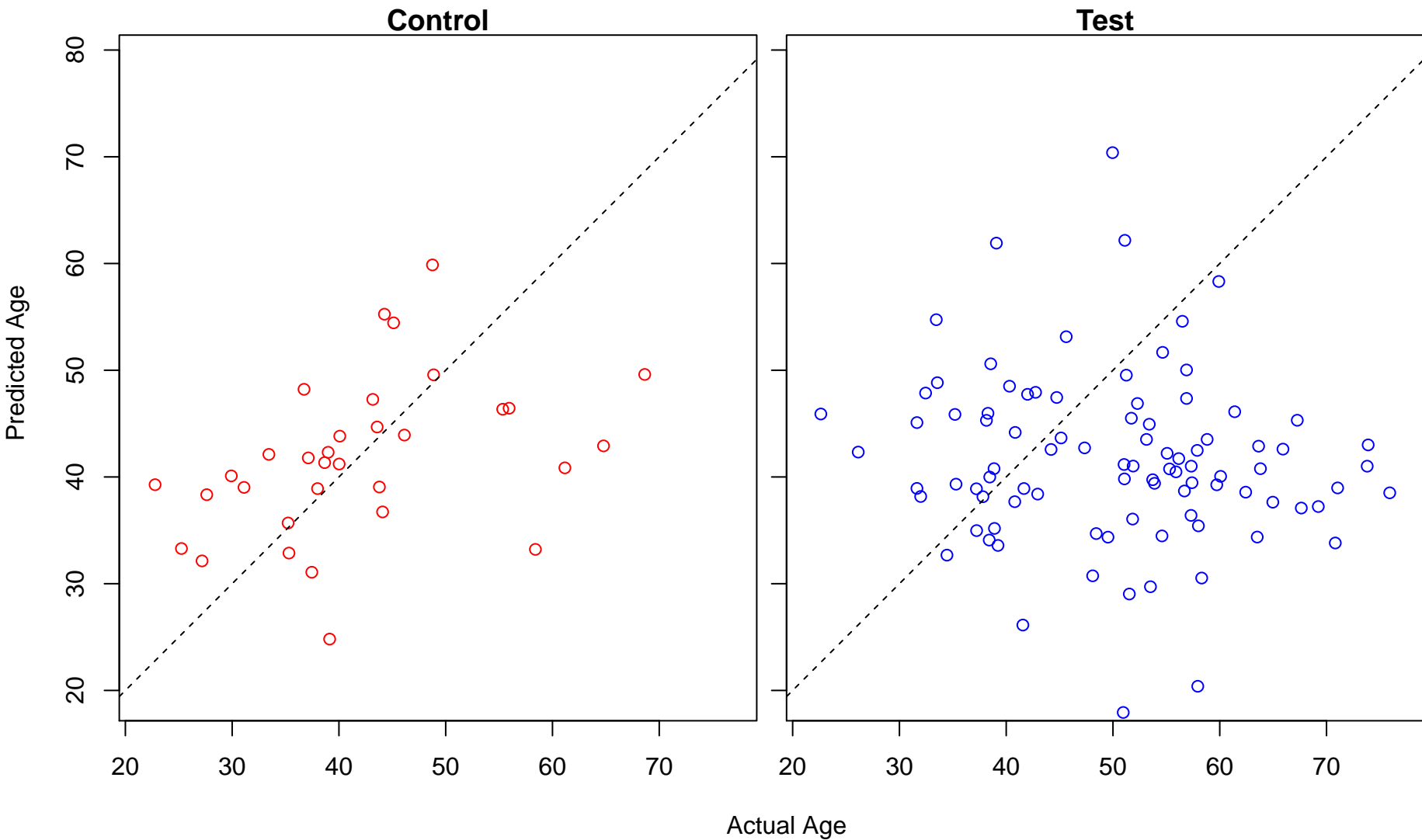
glucan metabolic process (Score: 0.781954)



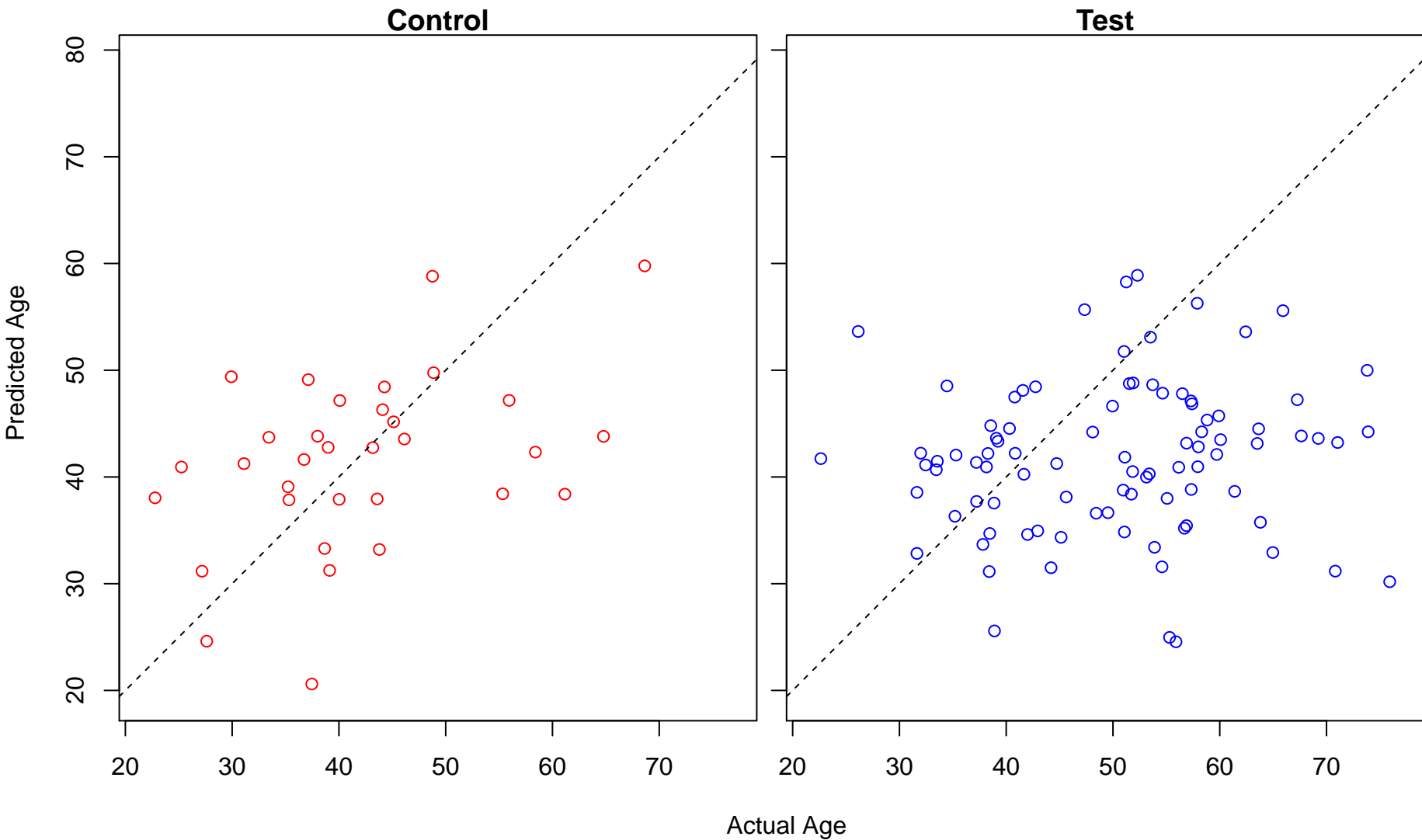
cadmium ion transport (Score: 0.781237)



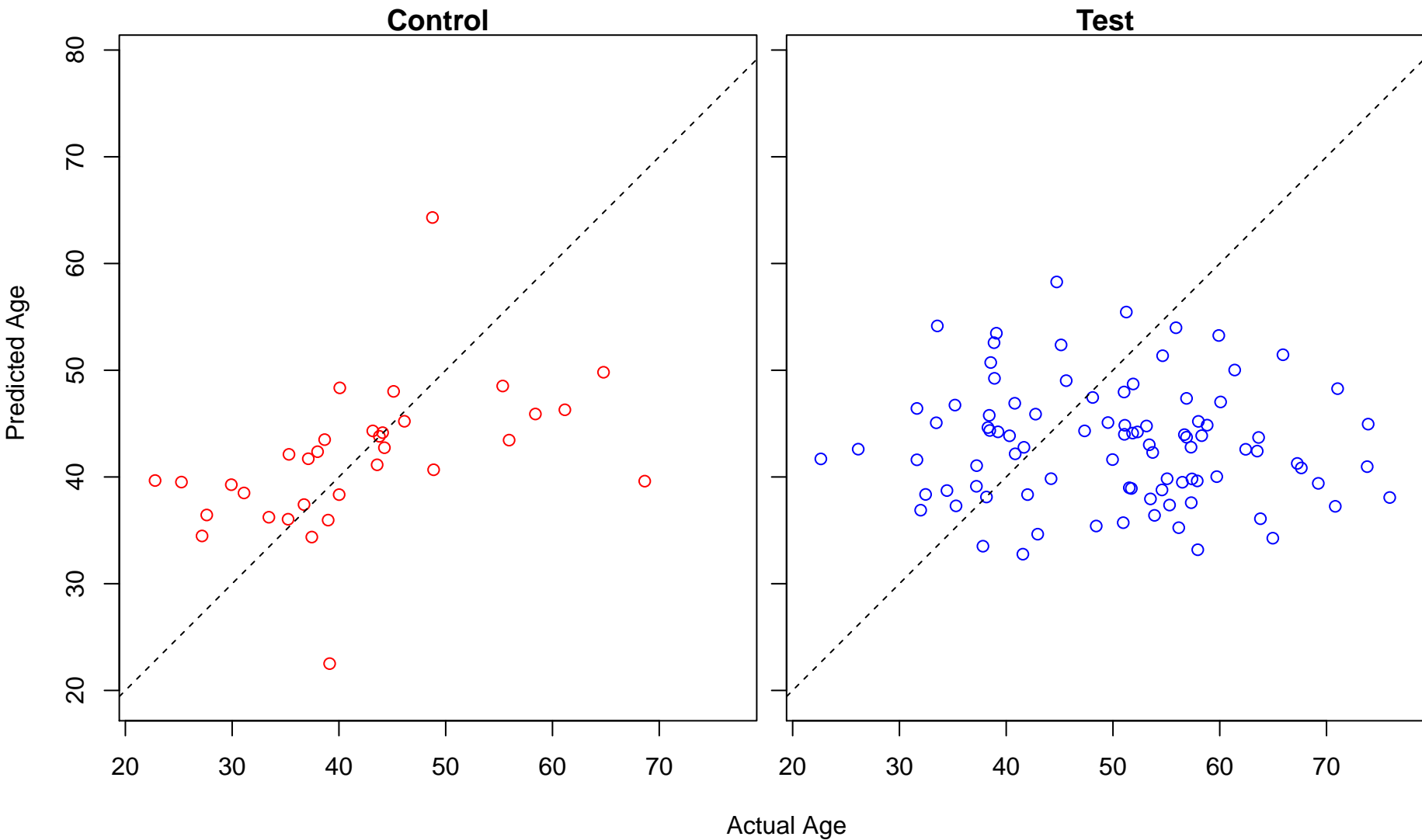
cadmium ion transmembrane transport (Score: 0.781237)



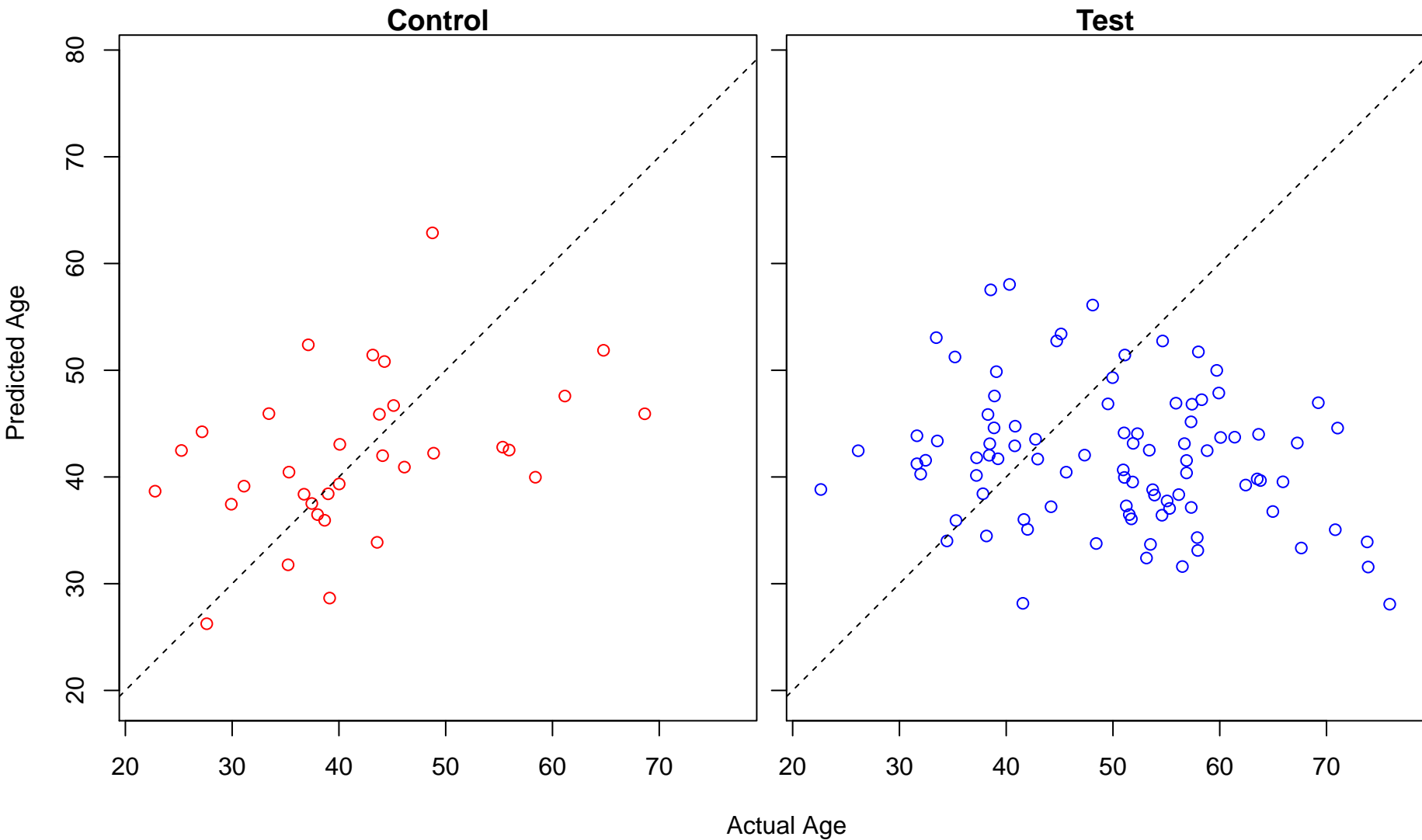
nitric oxide biosynthetic process (Score: 0.780543)



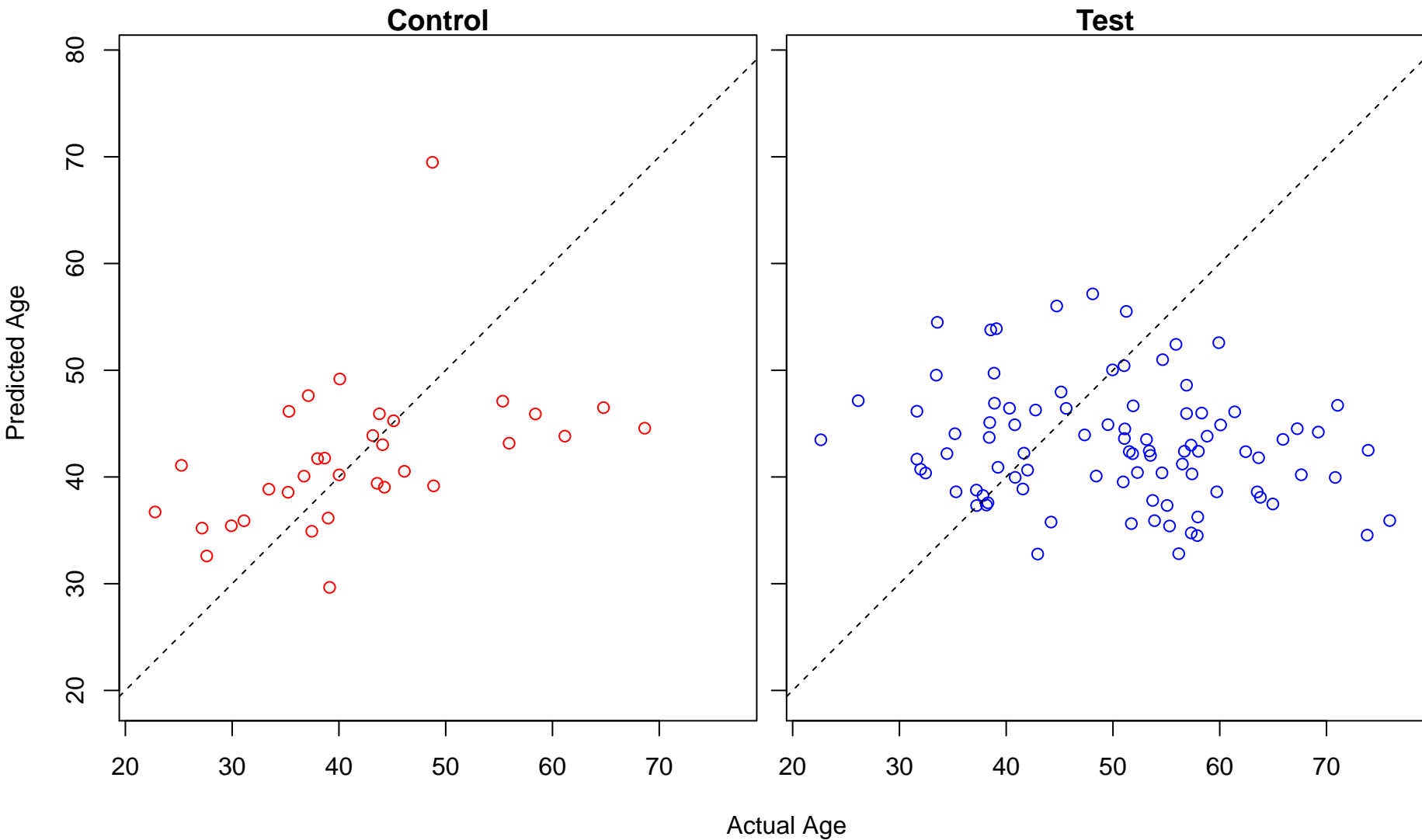
neuron projection morphogenesis (Score: 0.780499)



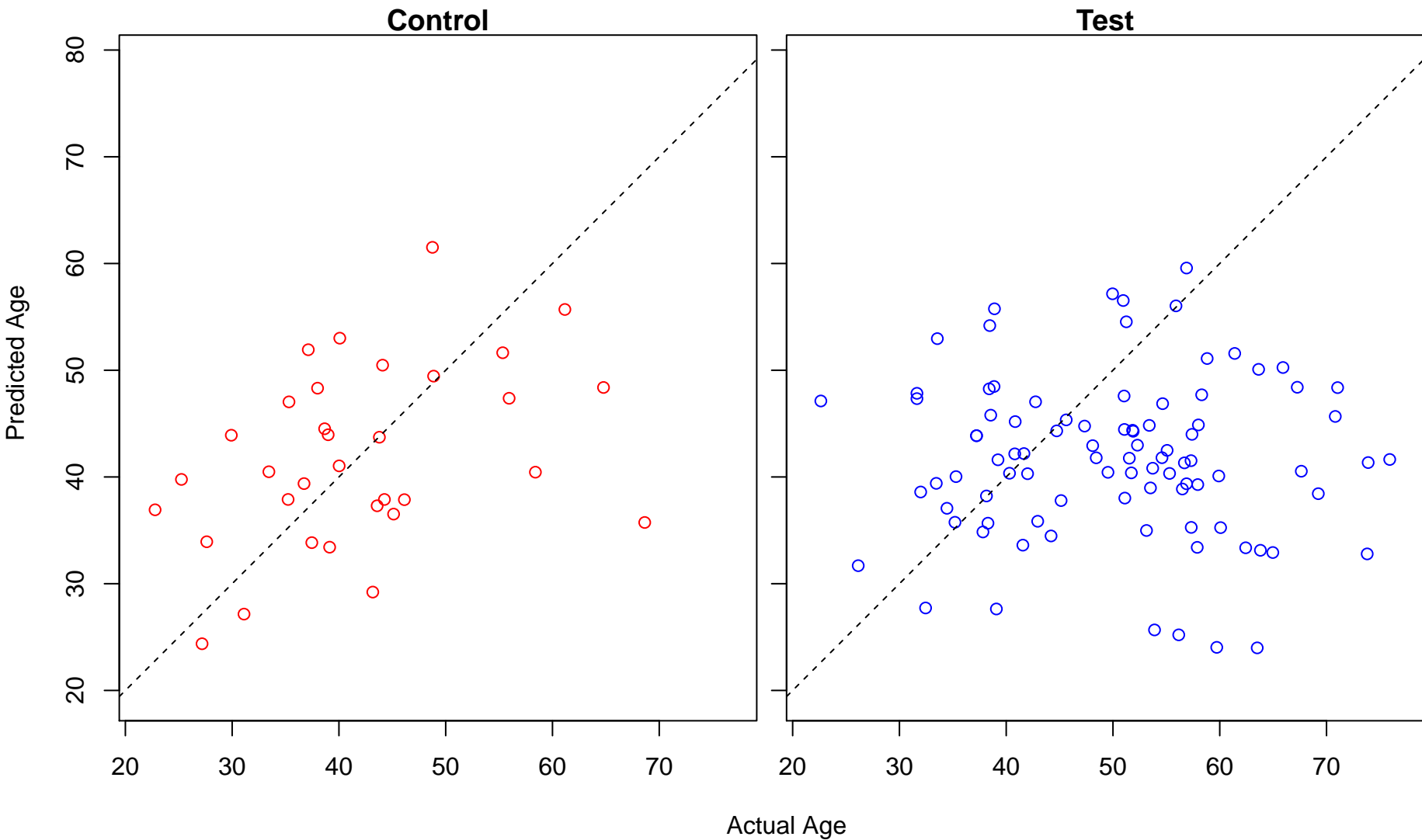
regulation of neuron migration (Score: 0.780152)



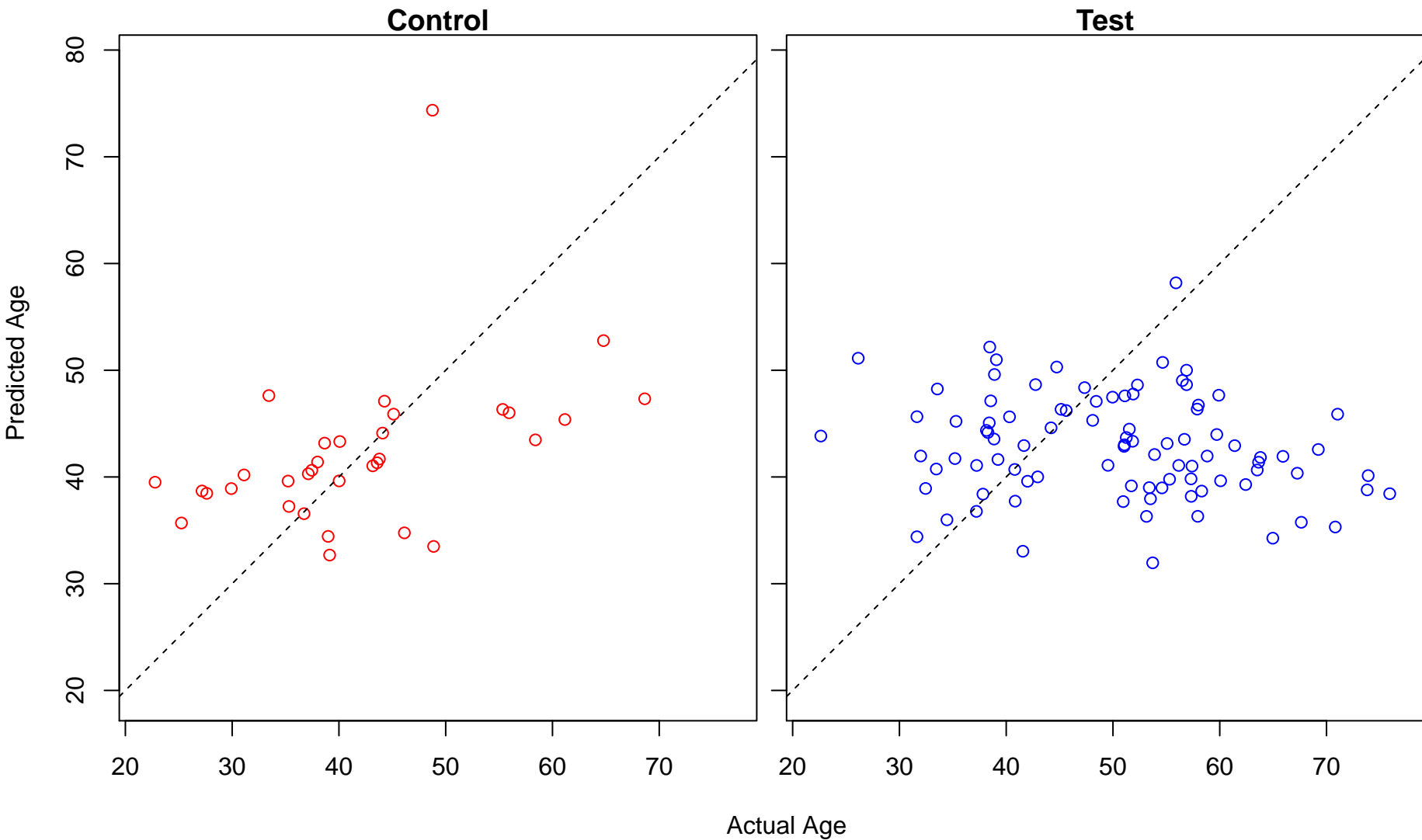
secretion (Score: 0.779816)



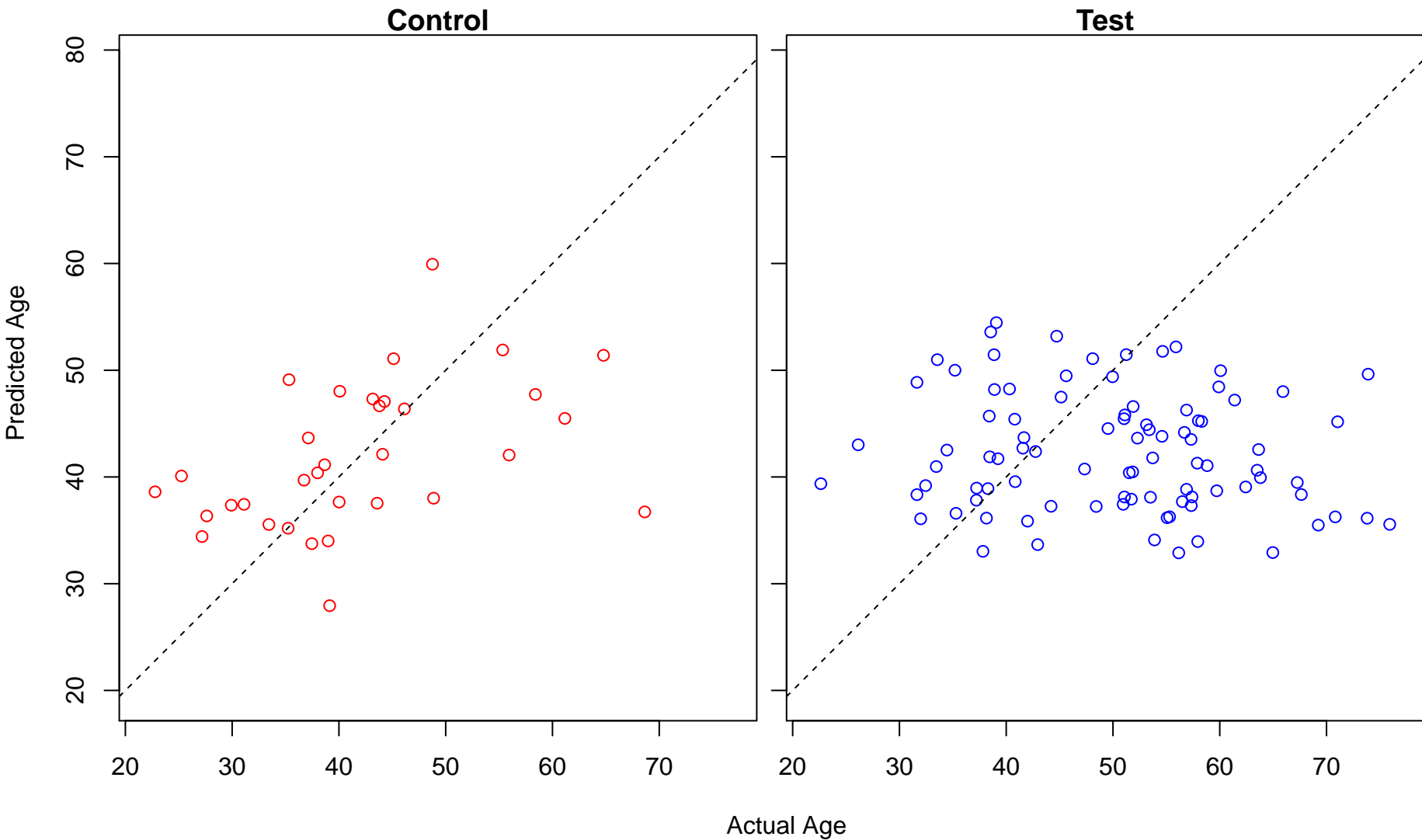
regulation of cholesterol efflux (Score: 0.779407)



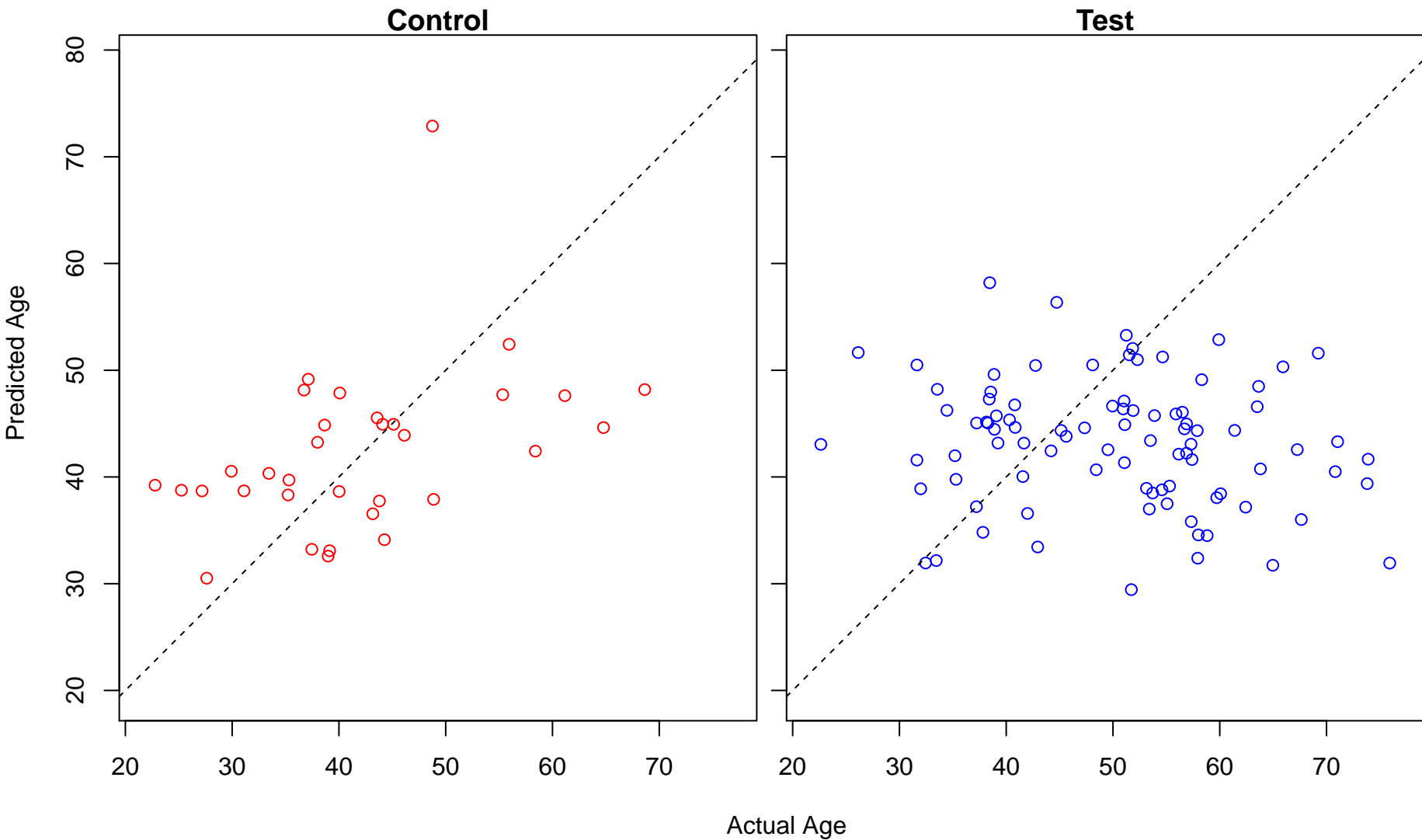
embryonic hemopoiesis (Score: 0.779322)



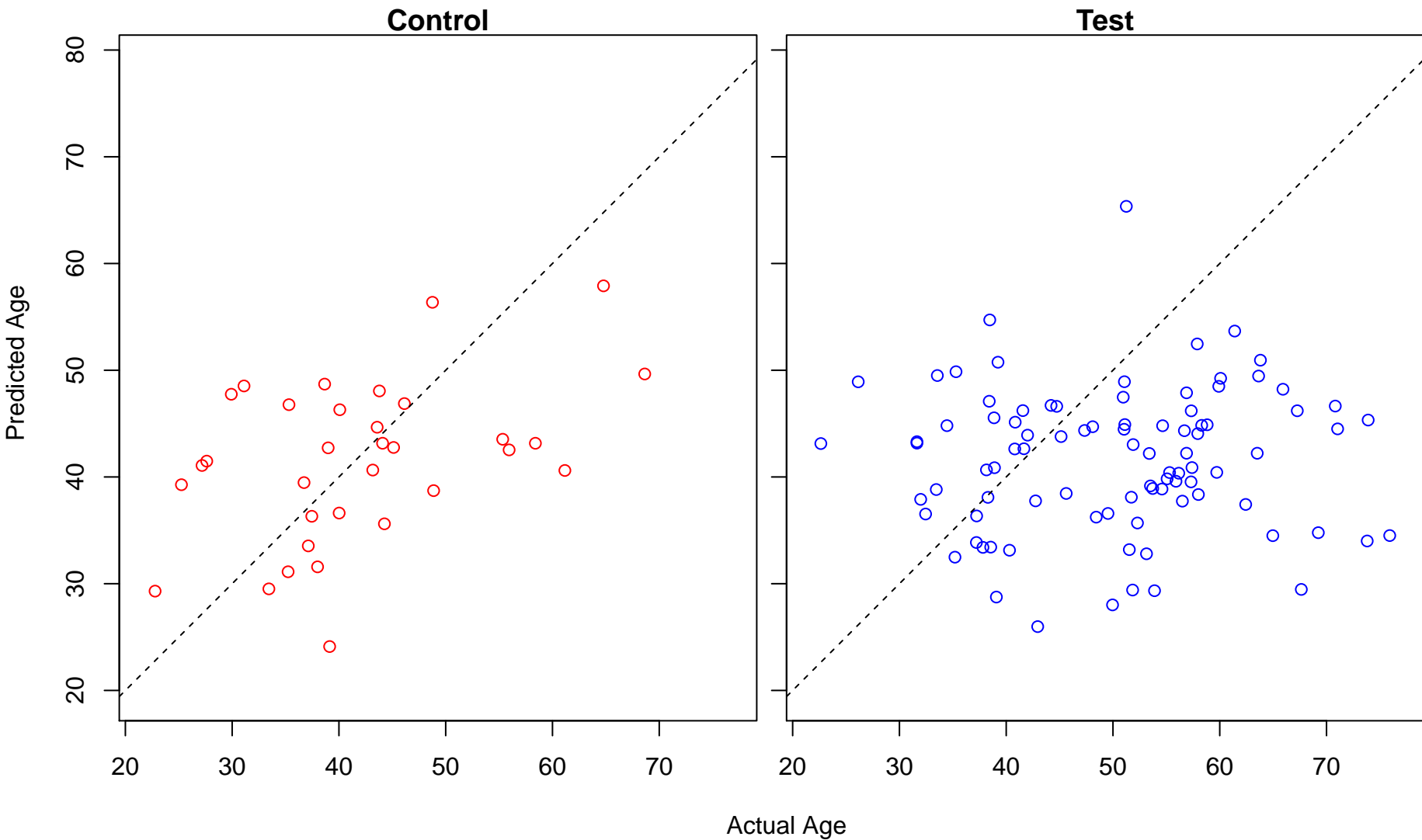
regulation of vasculature development (Score: 0.779162)



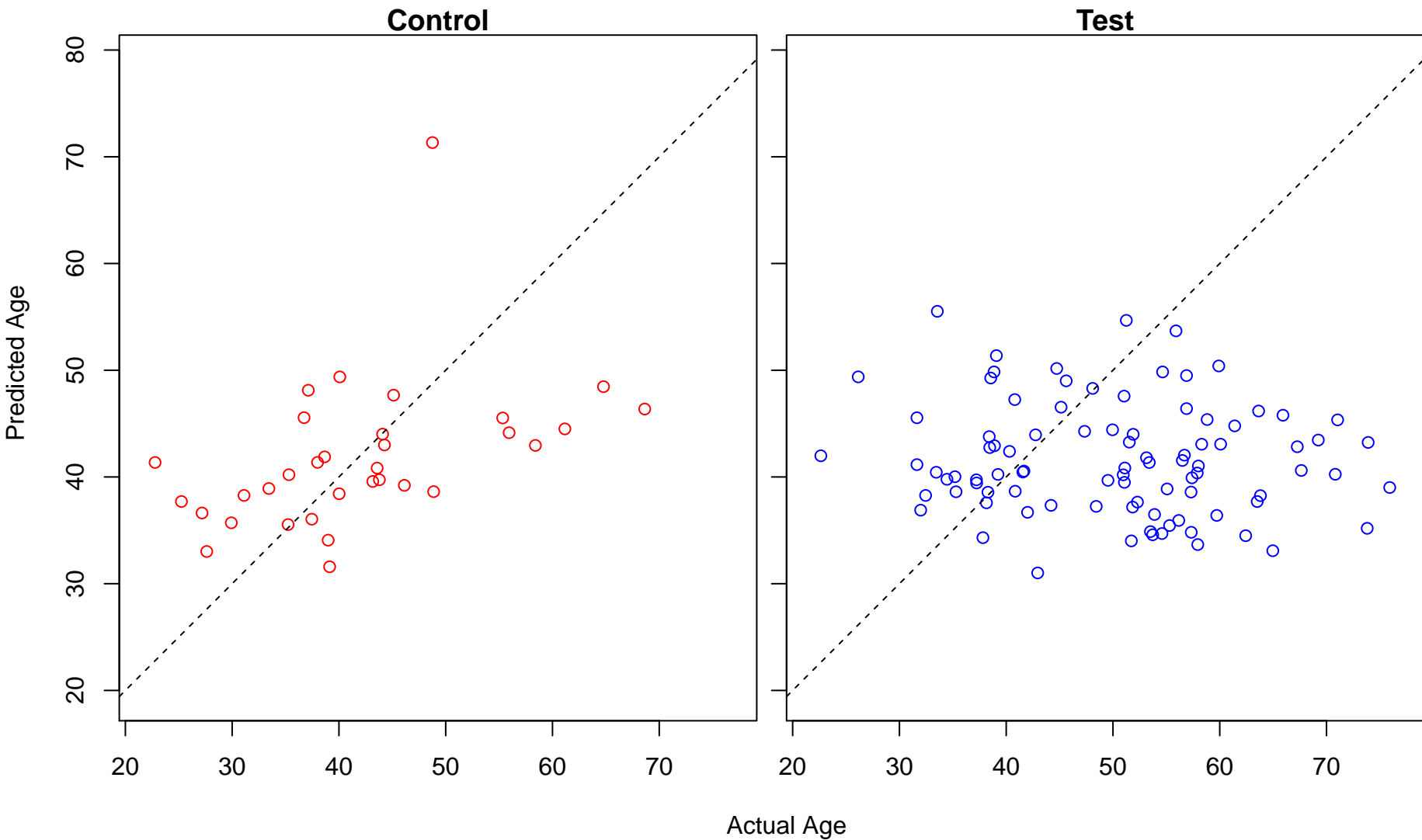
early endosome to late endosome transport (Score: 0.778960)



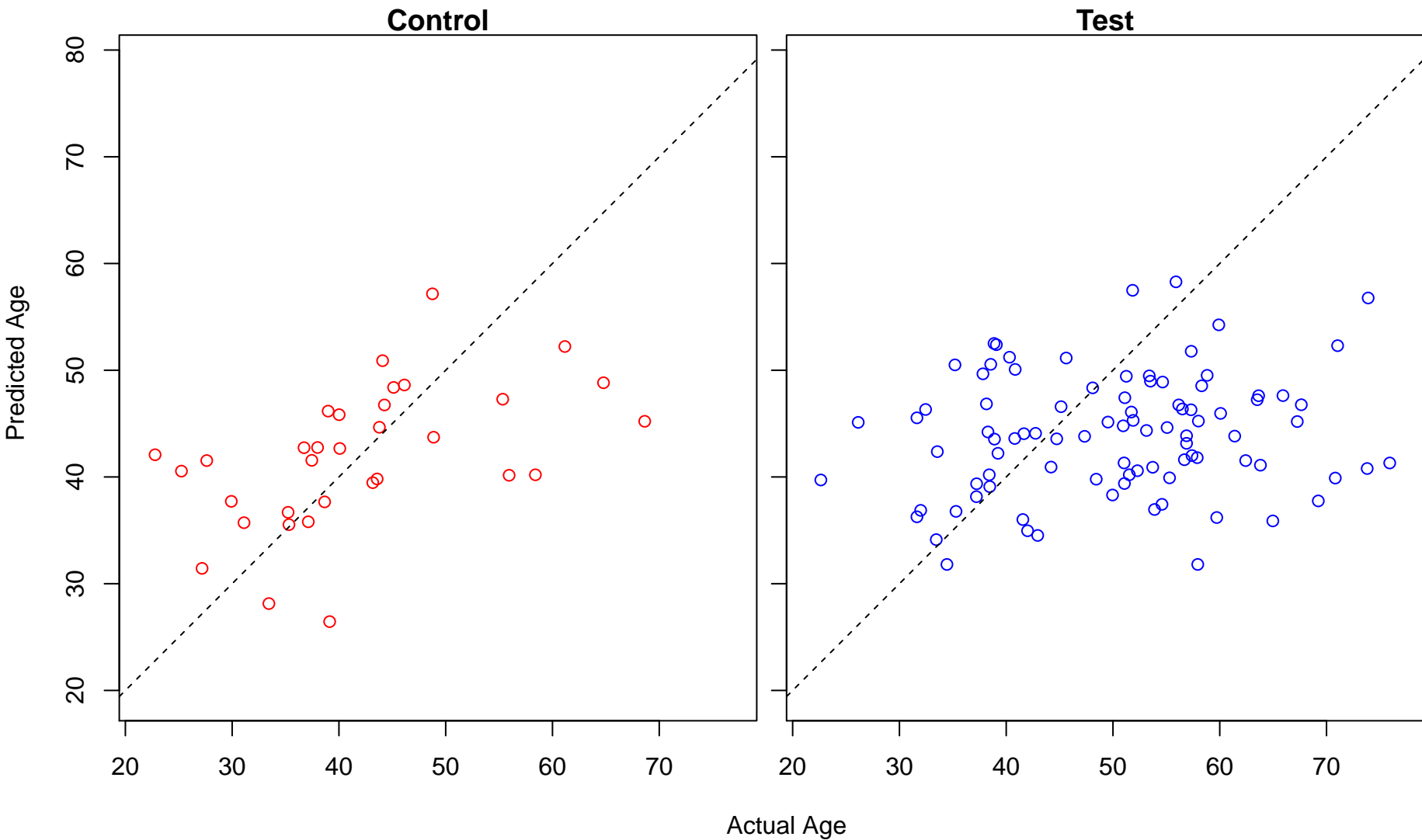
phosphatidylcholine acyl-chain remodeling (Score: 0.778486)



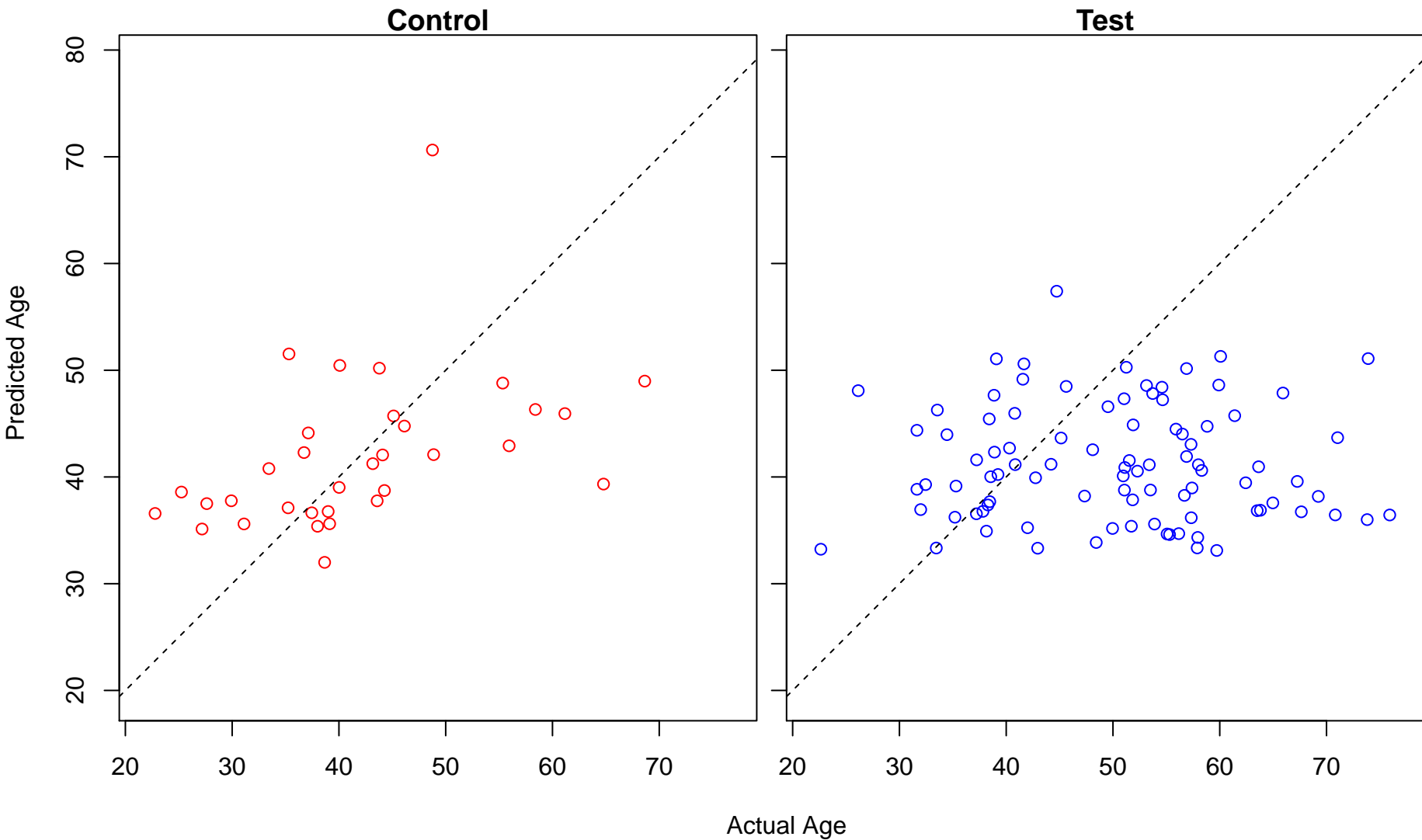
hemostasis (Score: 0.777817)



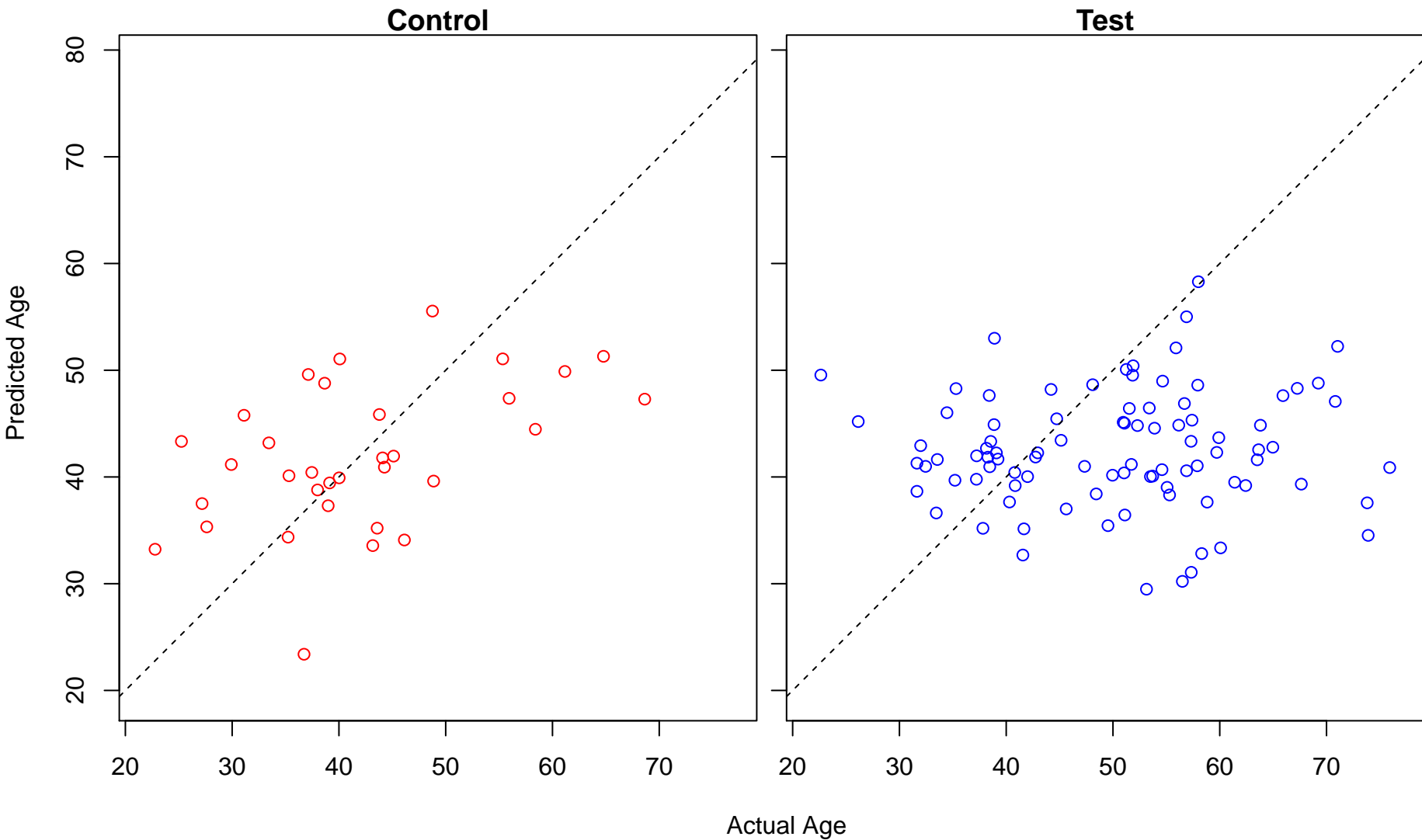
quinolinate metabolic process (Score: 0.777804)



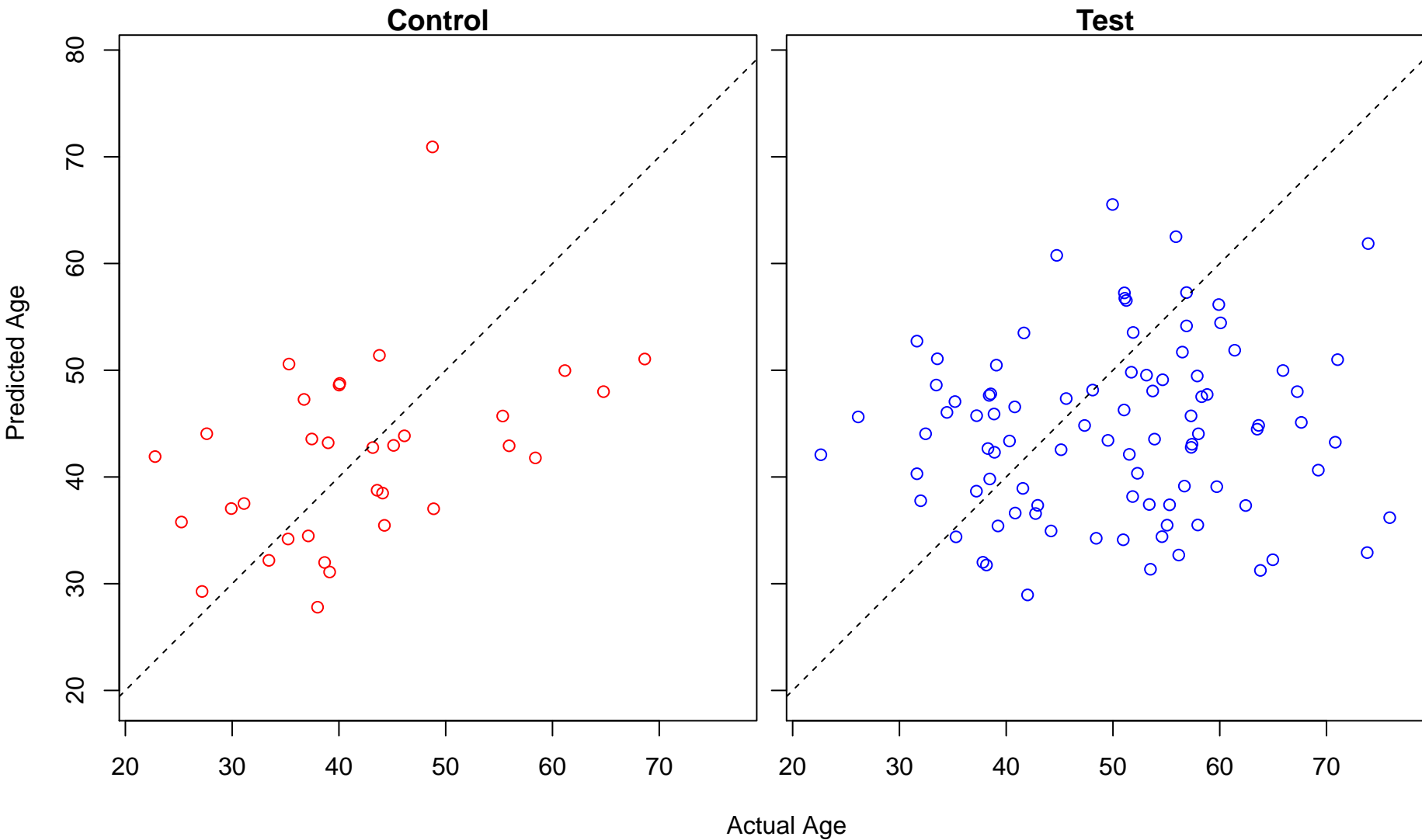
negative regulation of peptidyl-serine phosphorylation (Score: 0.777742)



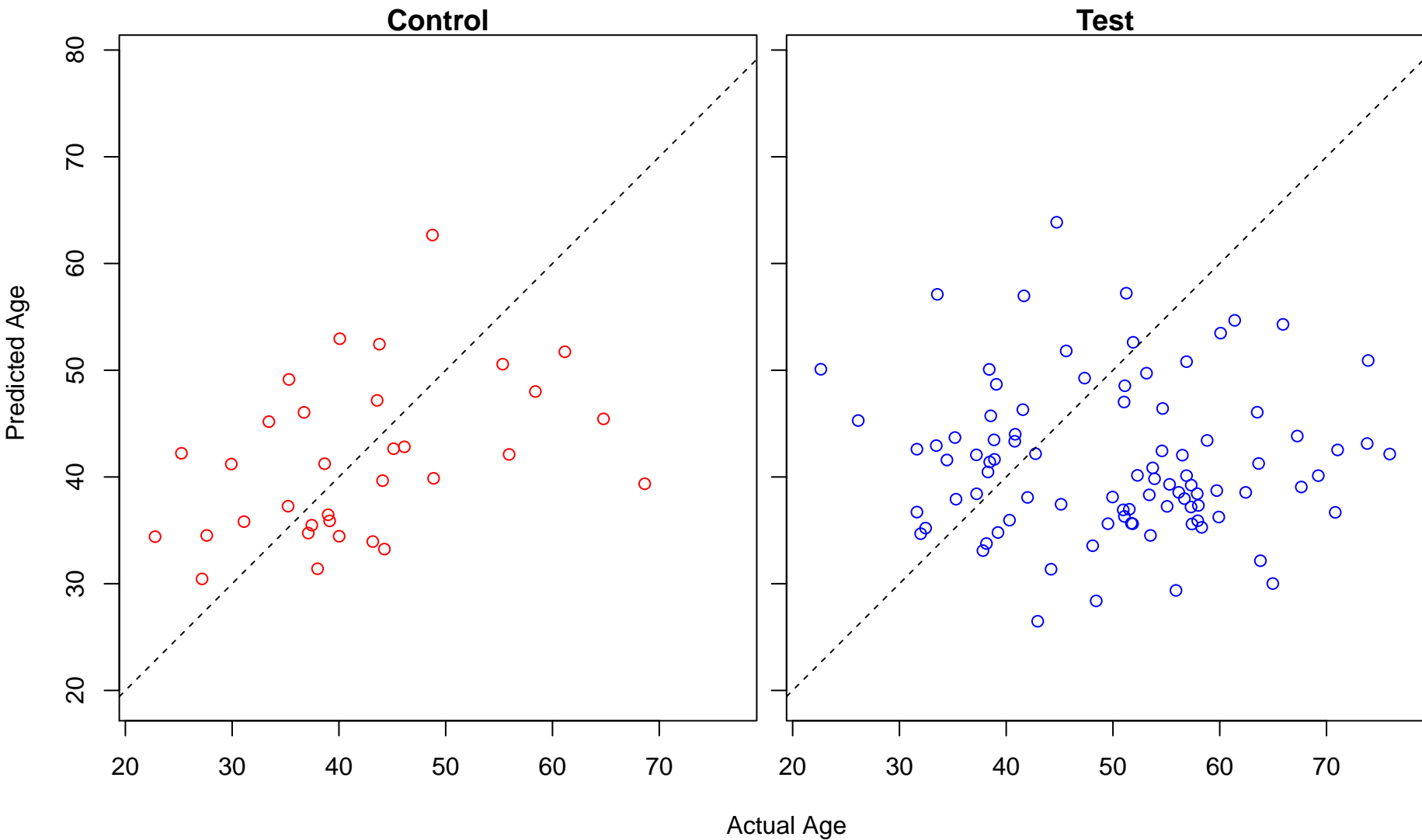
aorta development (Score: 0.777699)



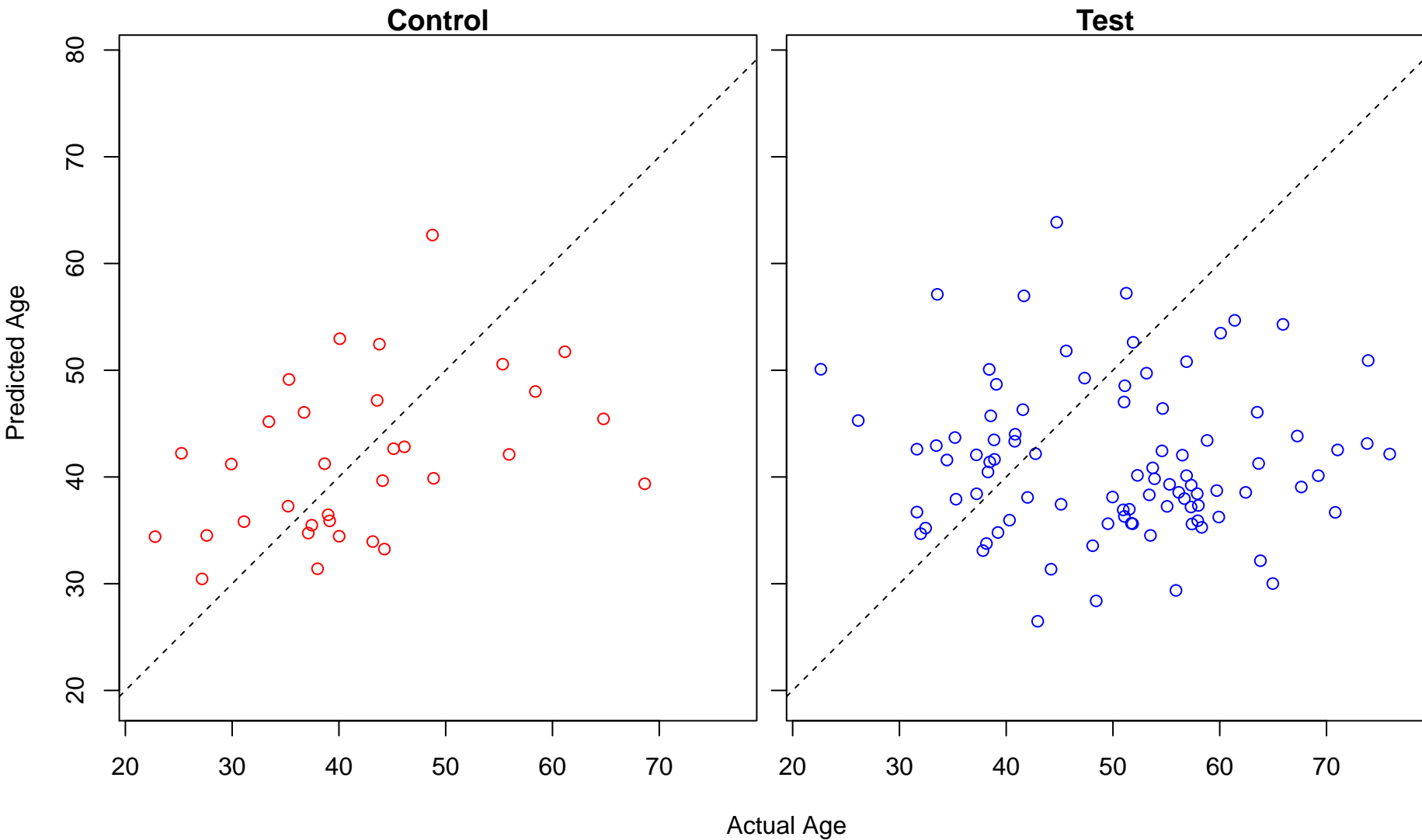
dermatan sulfate proteoglycan biosynthetic process (Score: 0.777308)



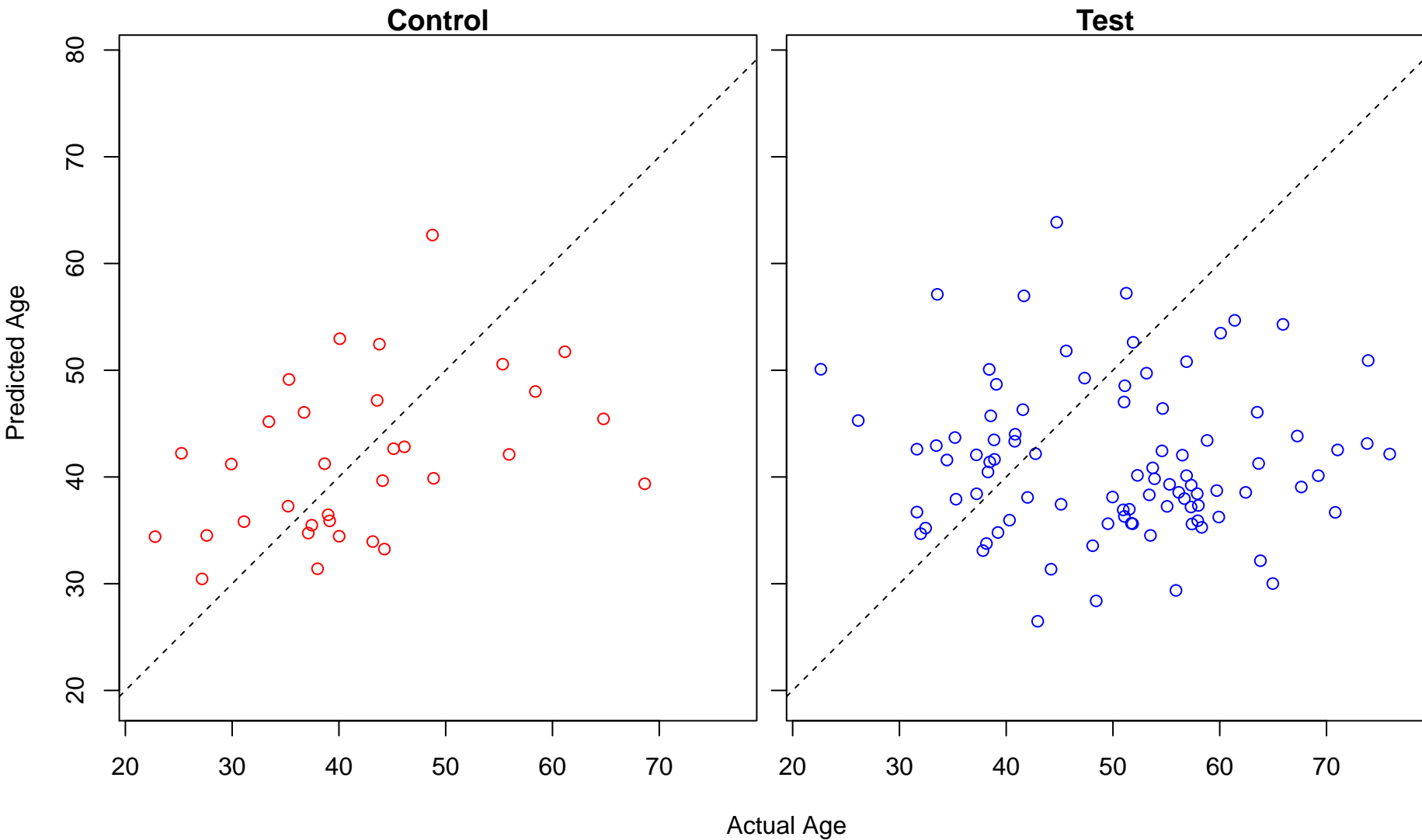
somatic recombination of immunoglobulin genes involved in immune response (Score: 0.776655)



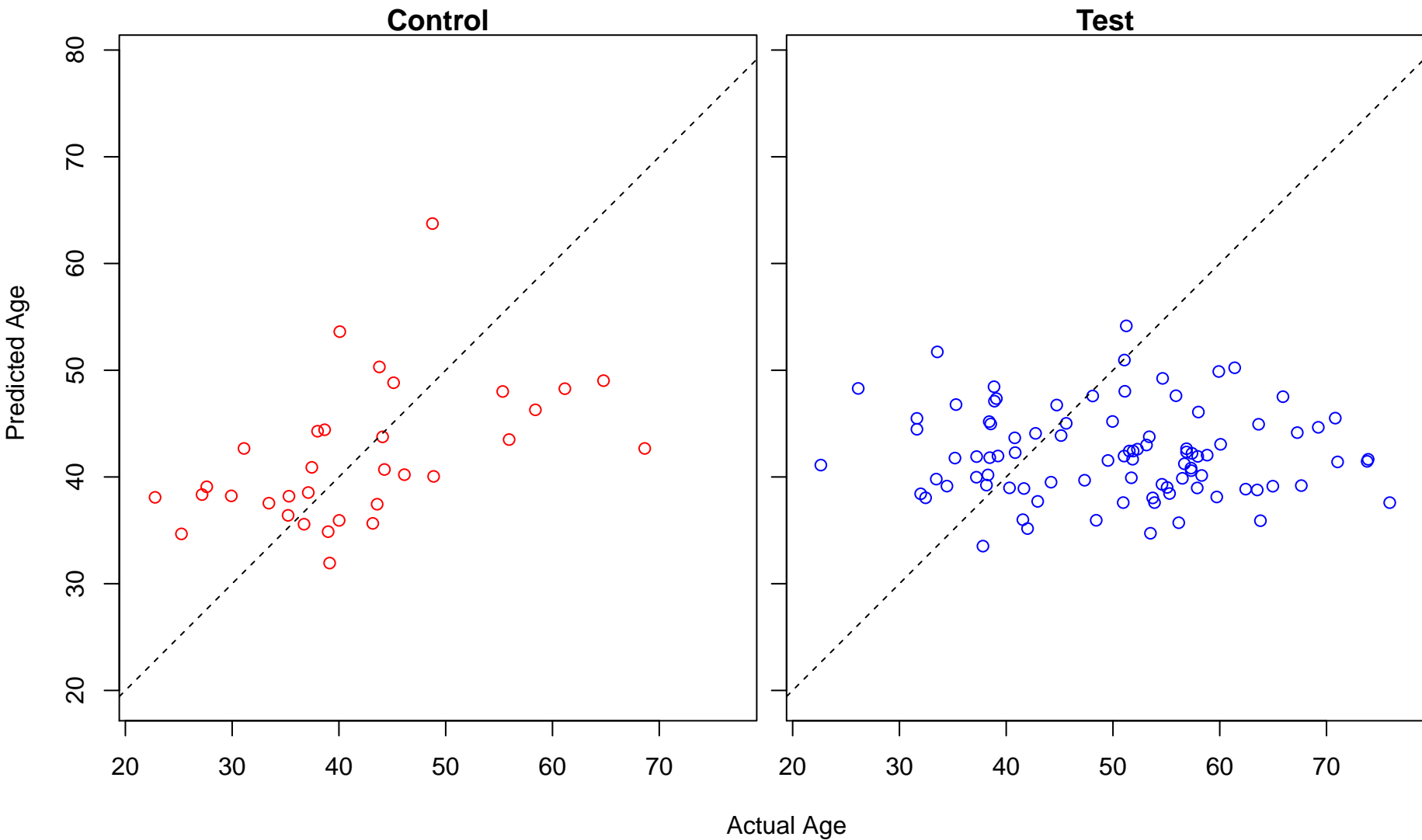
somatic diversification of immunoglobulins involved in immune response (Score: 0.776655)



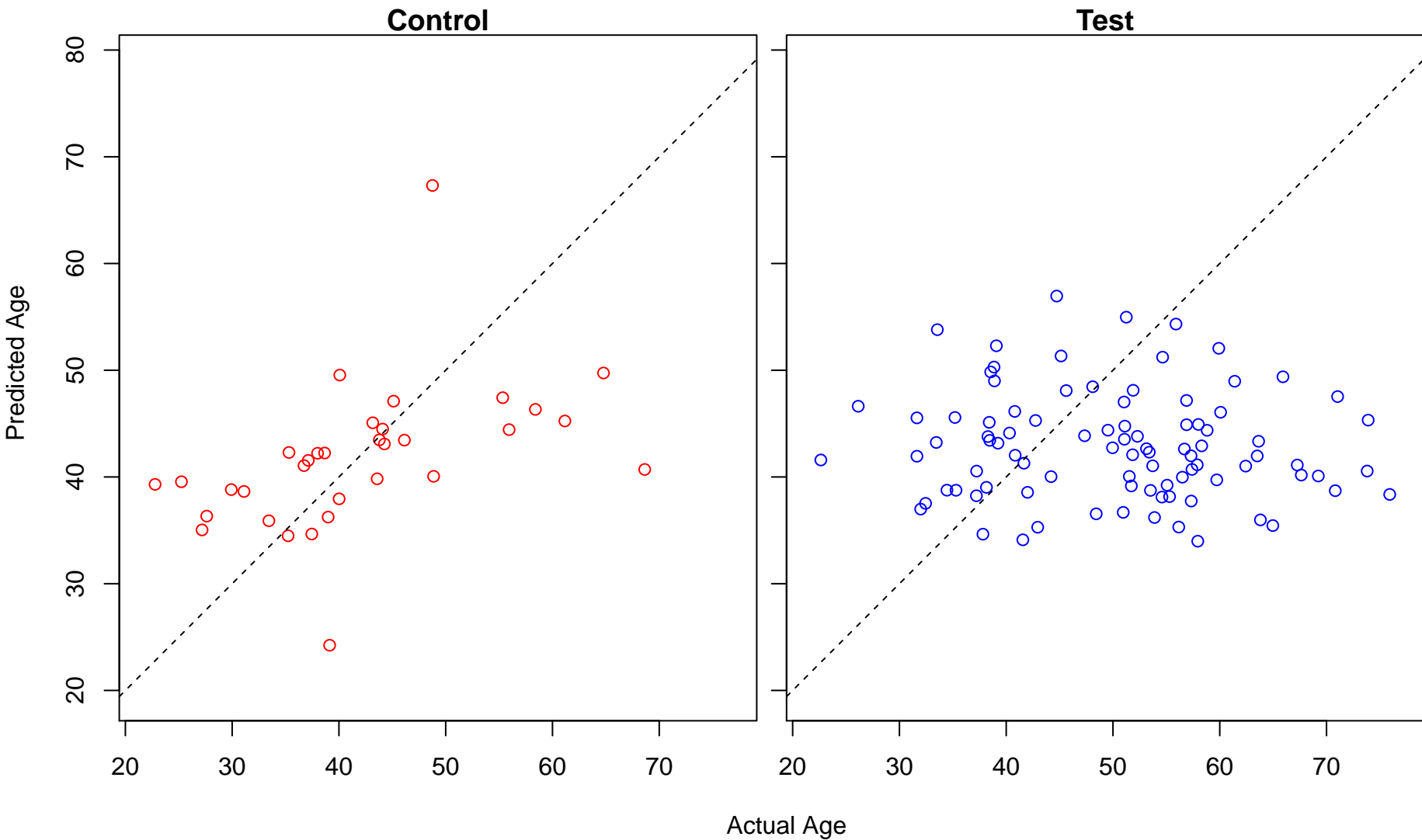
isotype switching (Score: 0.776655)



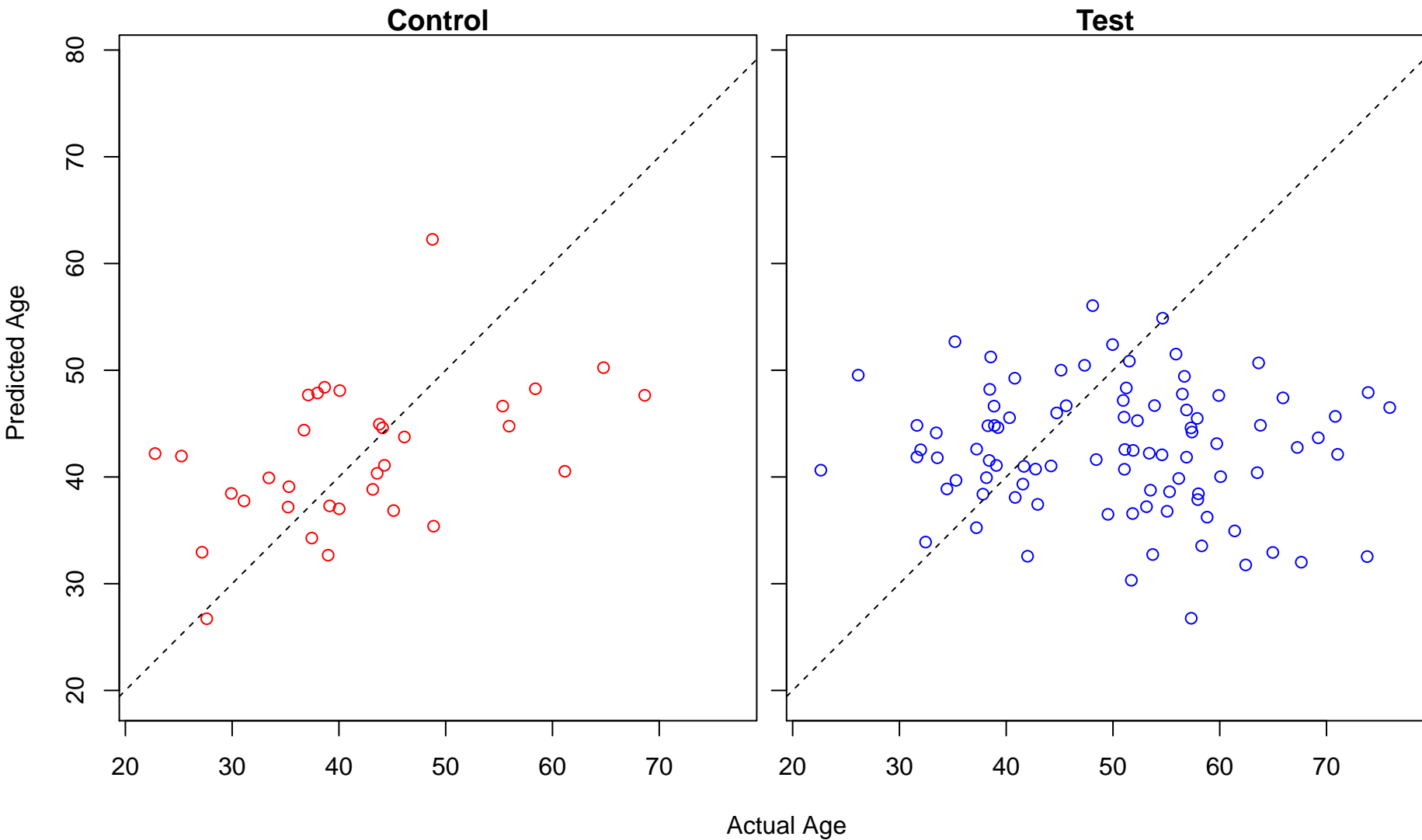
heart development (Score: 0.776458)



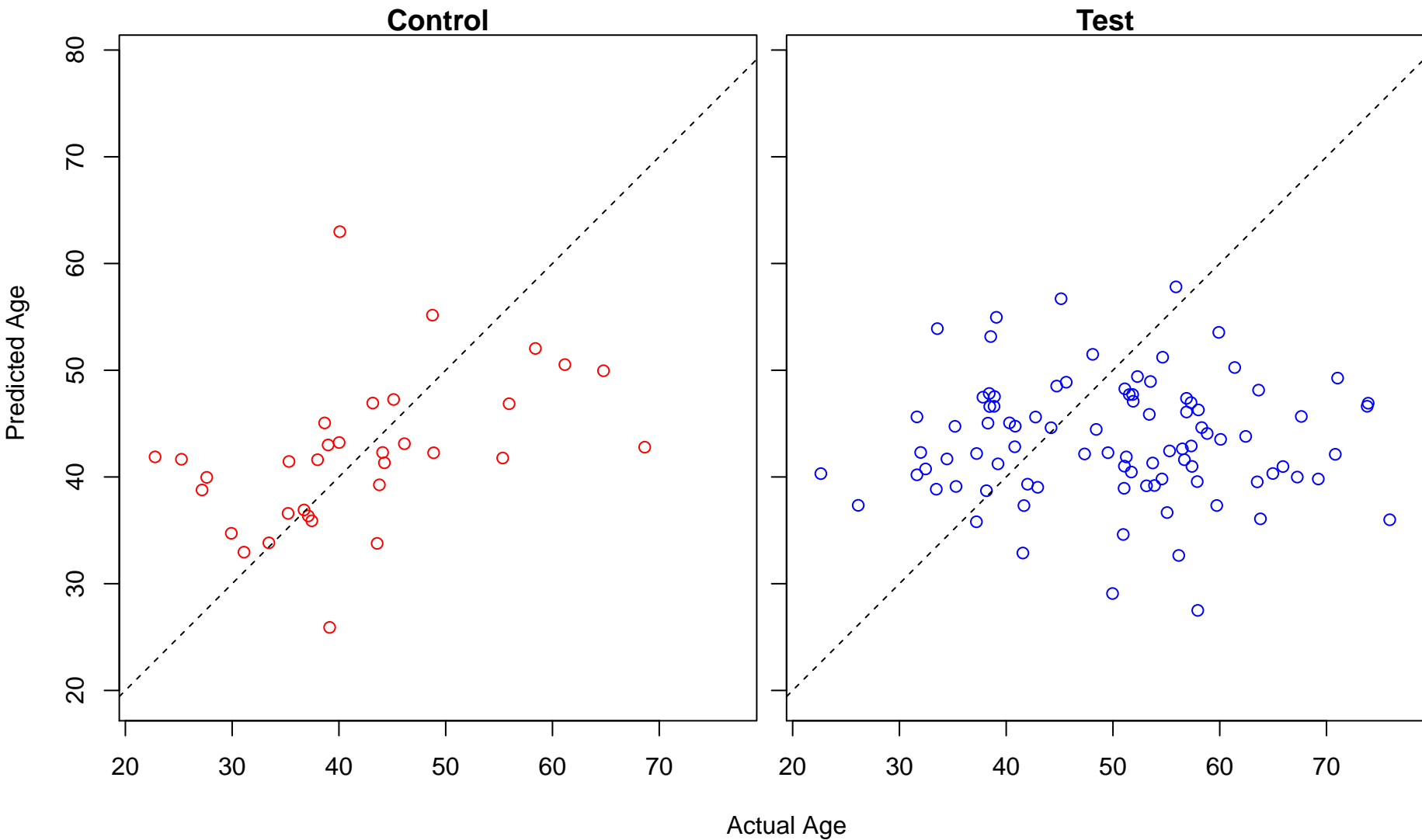
cell morphogenesis (Score: 0.775716)



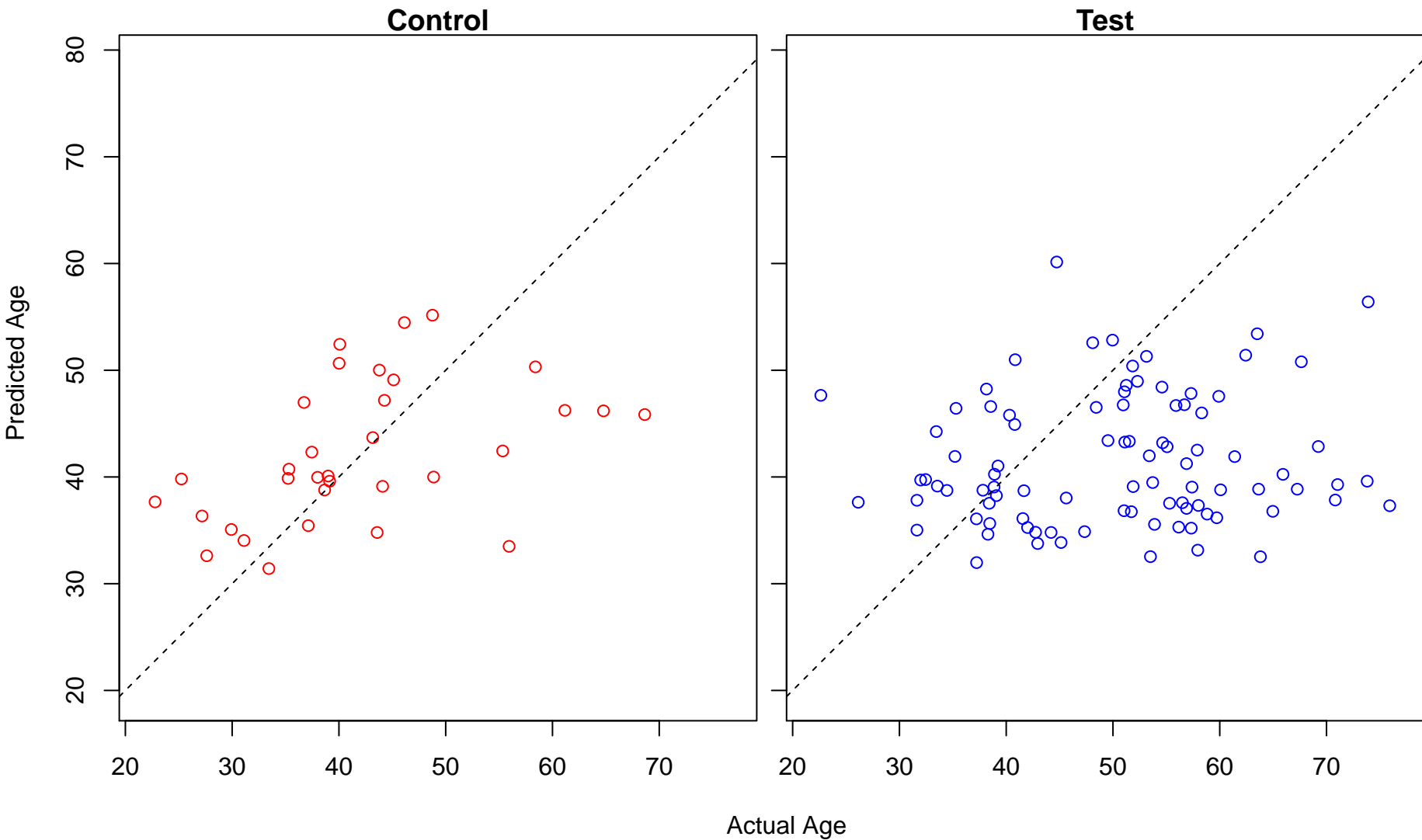
positive regulation of cell adhesion mediated by integrin (Score: 0.775574)



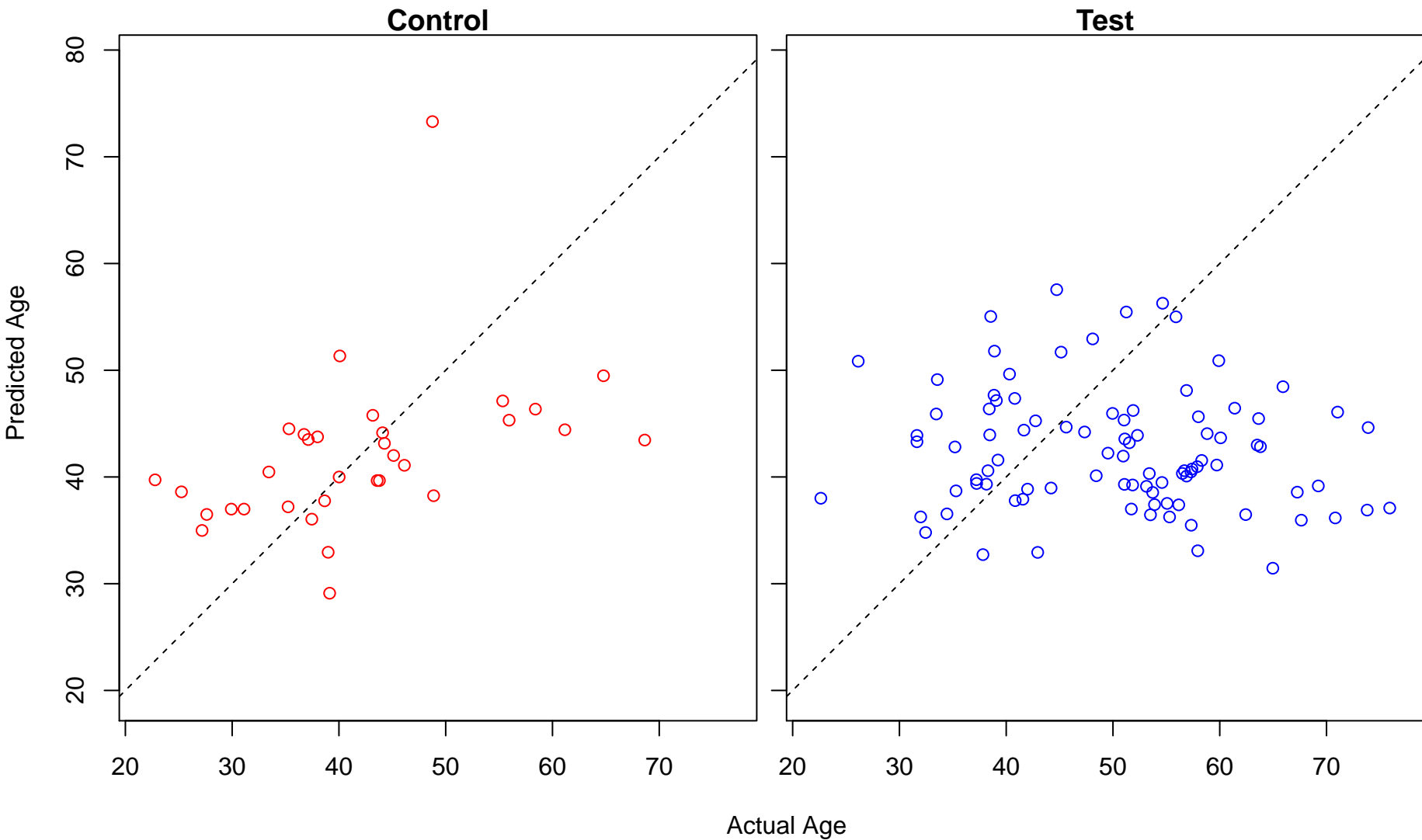
rostrocaudal neural tube patterning (Score: 0.775506)



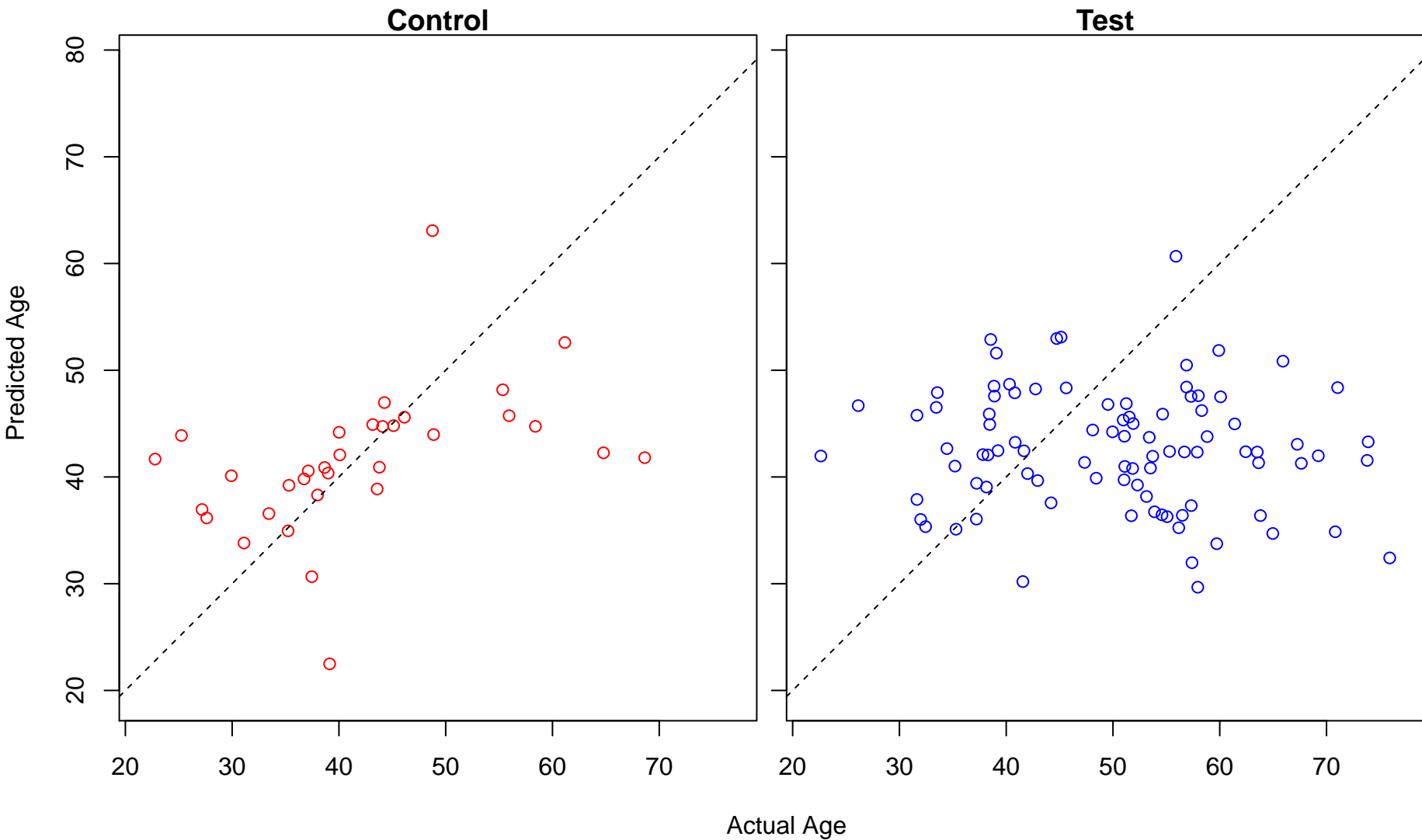
peroxisome membrane biogenesis (Score: 0.774840)



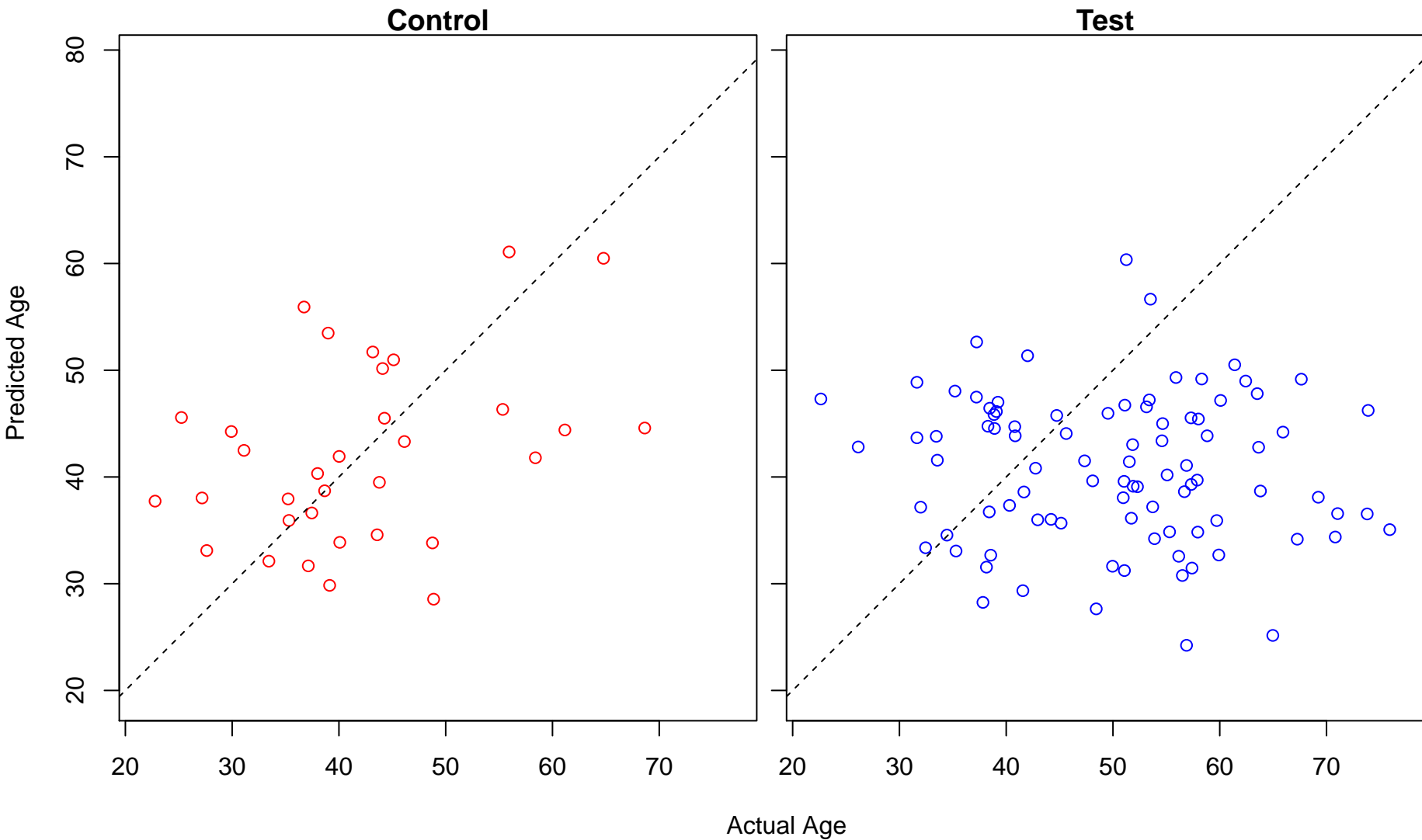
myeloid cell differentiation (Score: 0.774837)



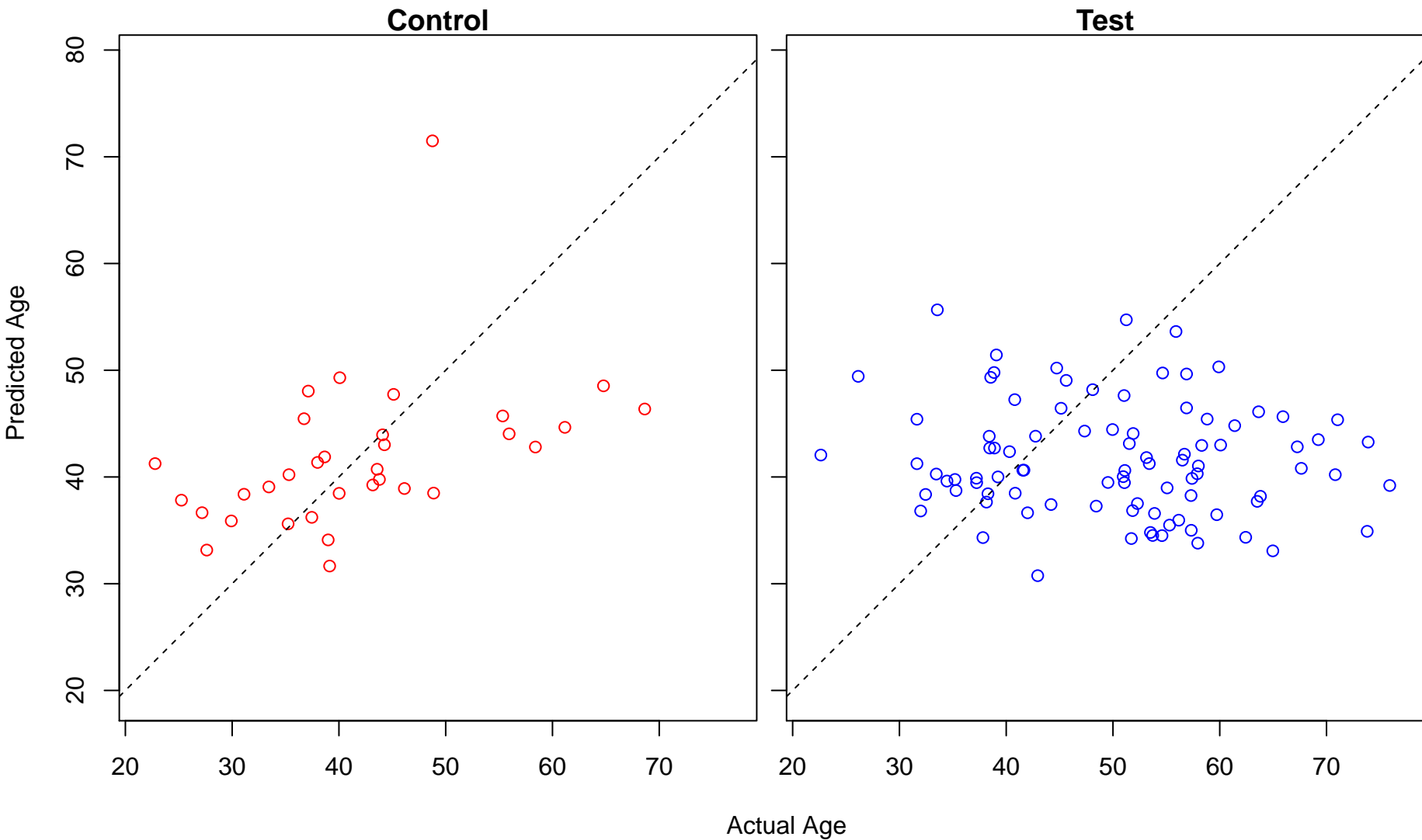
regulation of type I interferon production (Score: 0.774657)



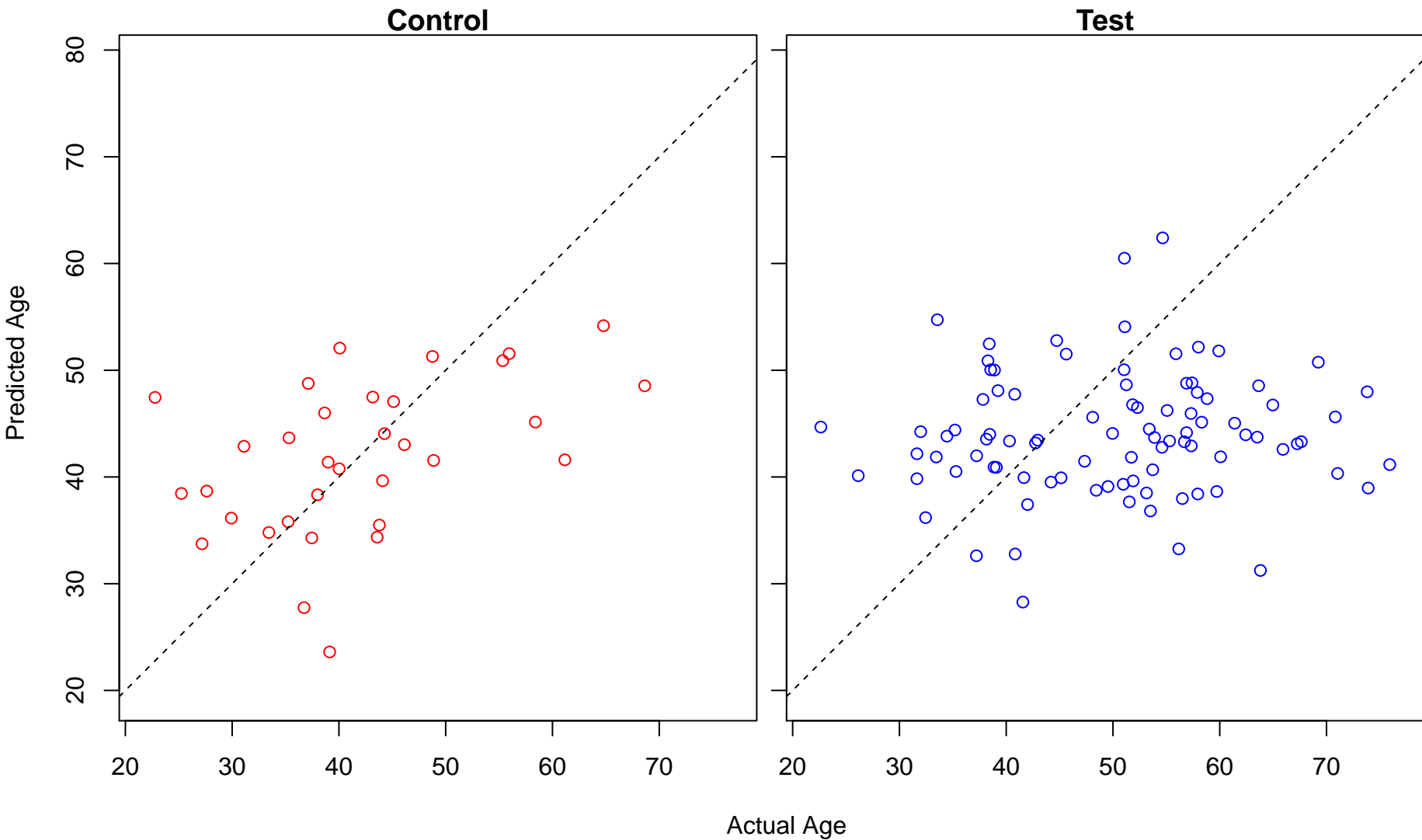
secondary metabolic process (Score: 0.773415)



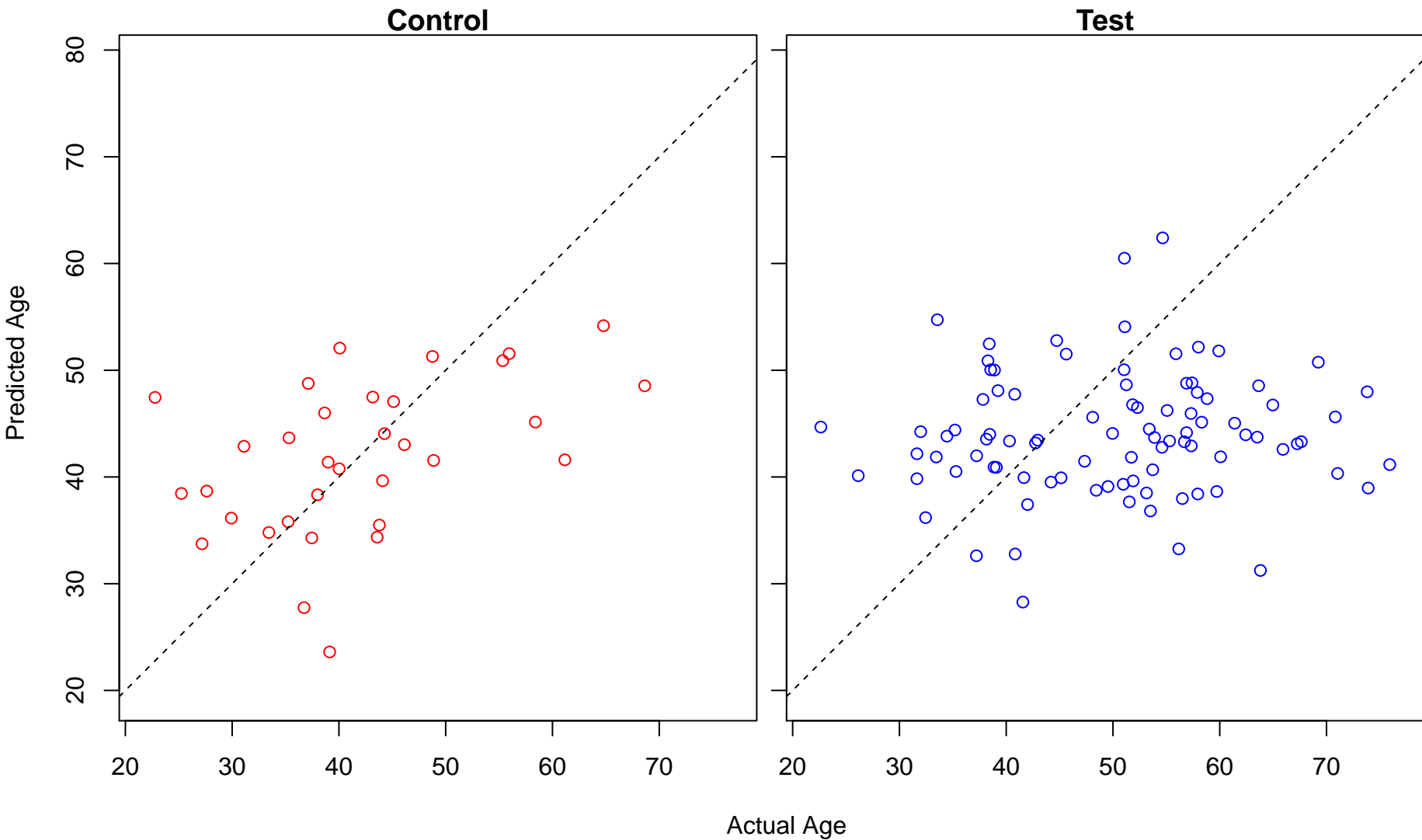
blood coagulation (Score: 0.772818)



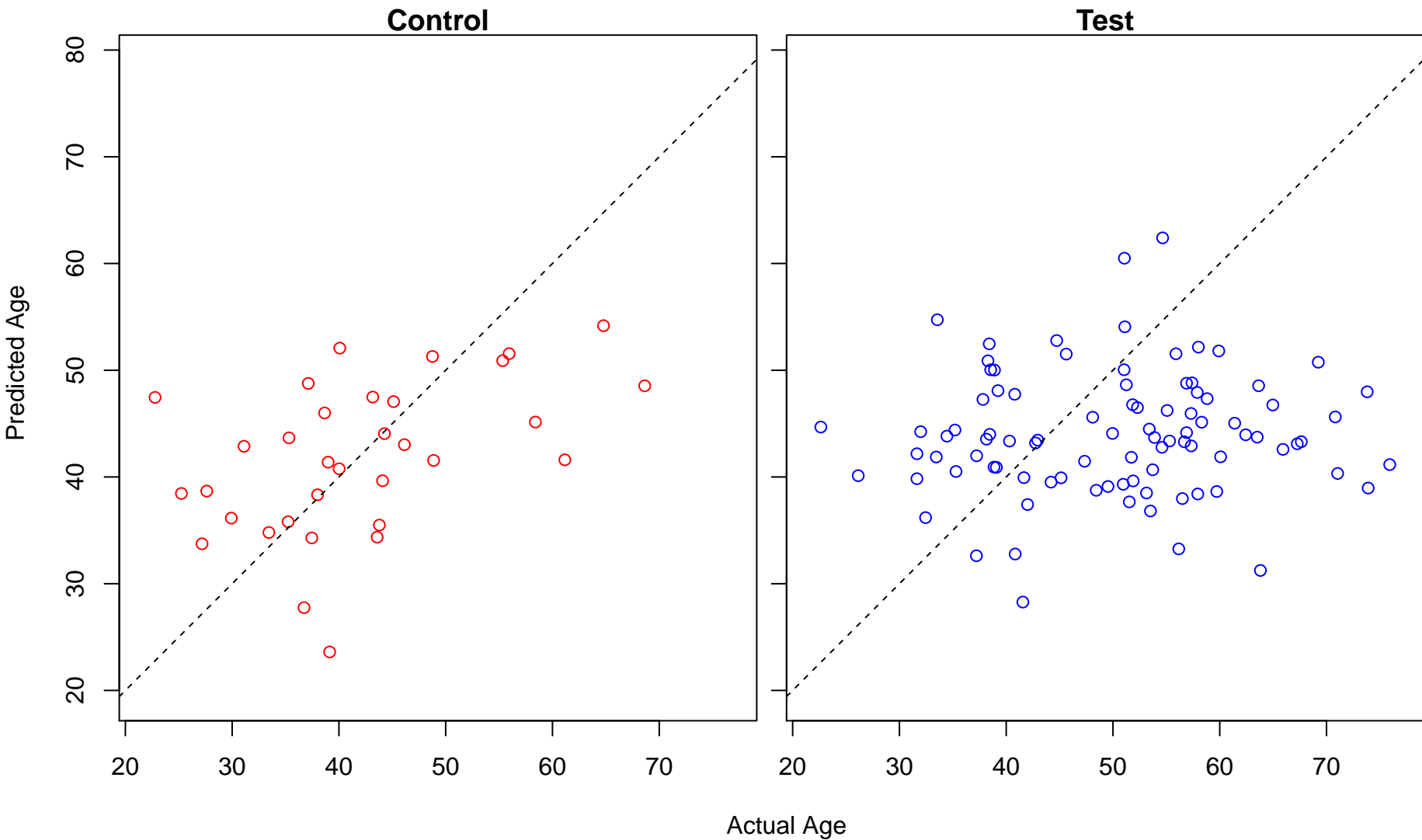
histidine metabolic process (Score: 0.772110)



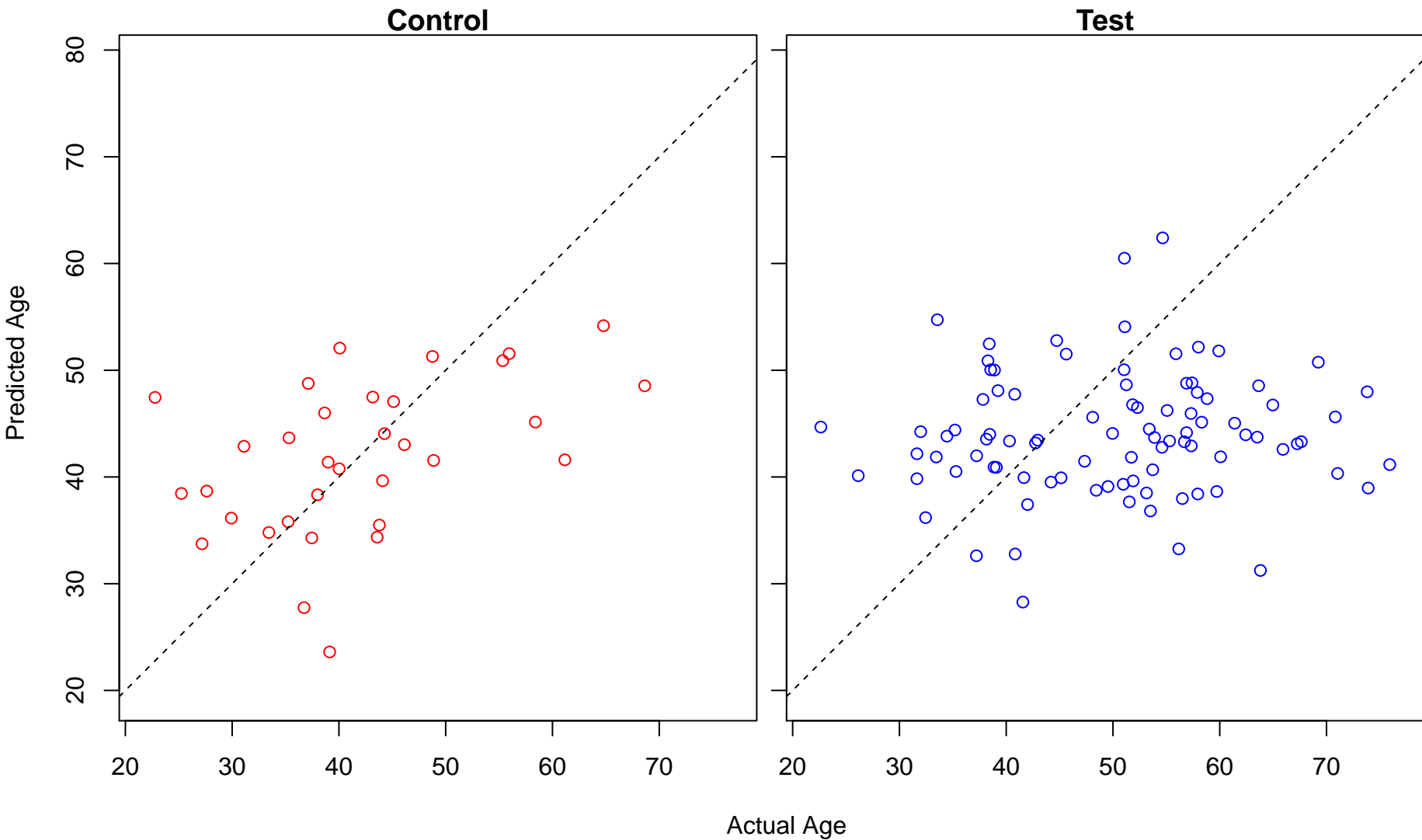
histidine catabolic process (Score: 0.772110)



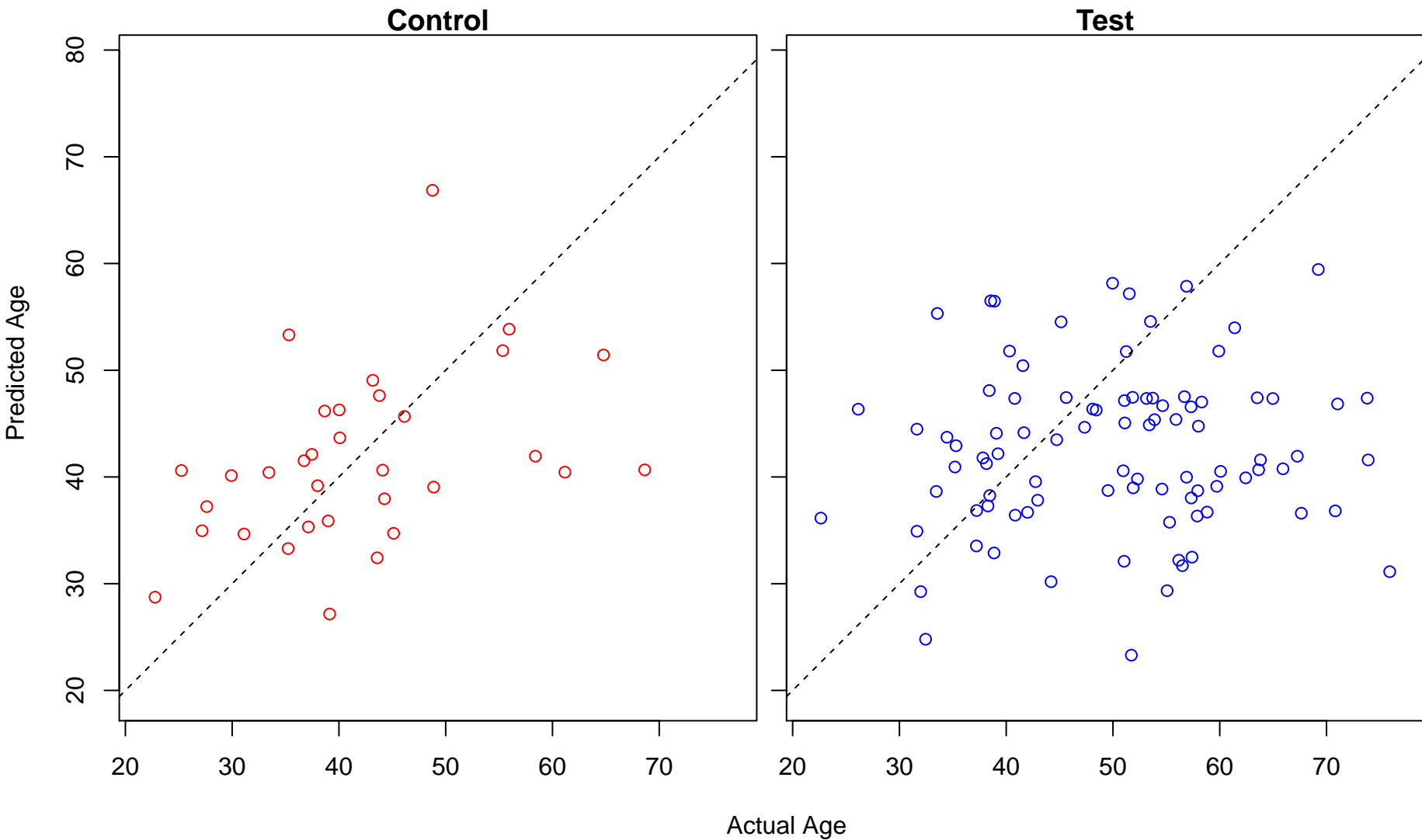
imidazole-containing compound metabolic process (Score: 0.772110)



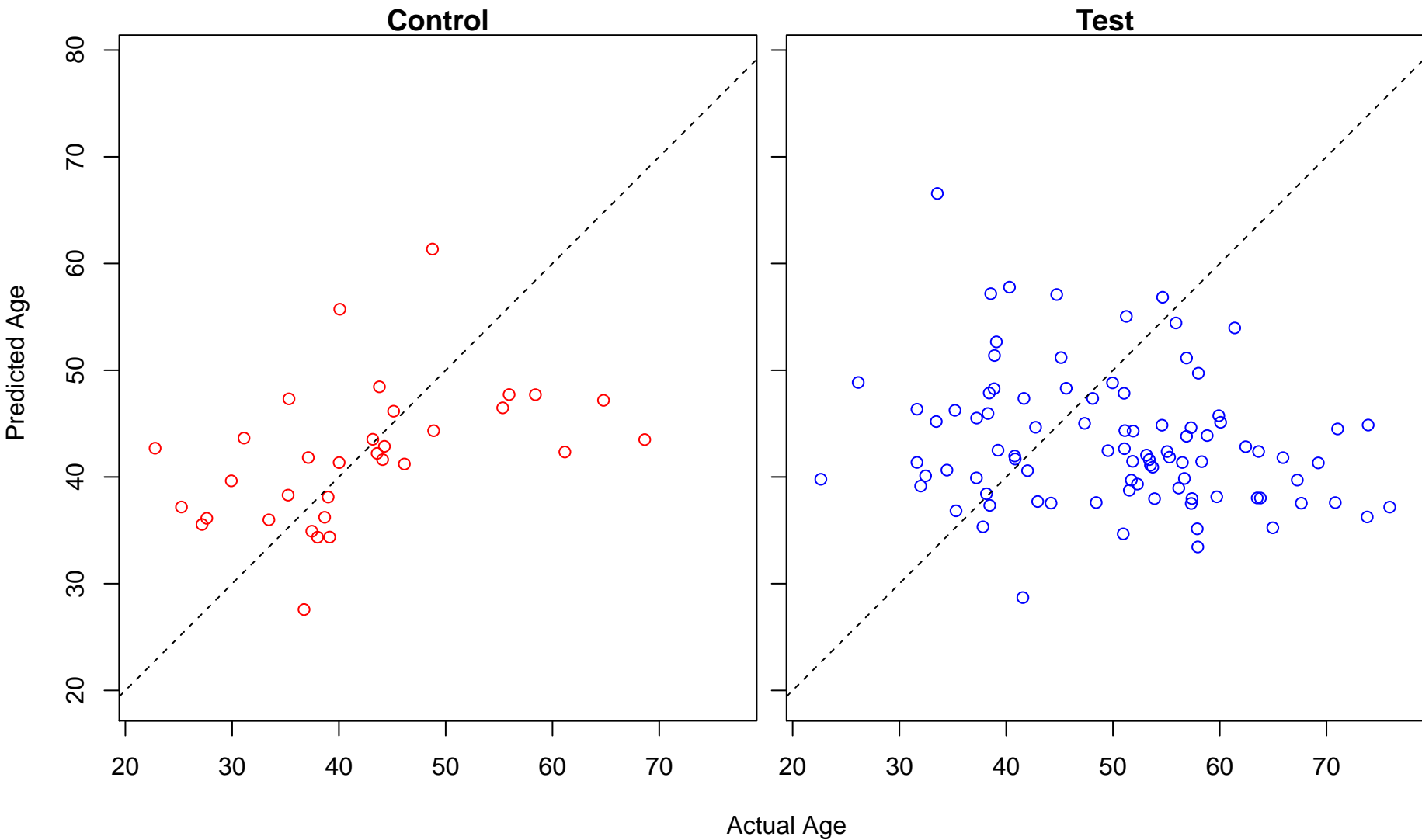
imidazole-containing compound catabolic process (Score: 0.772110)



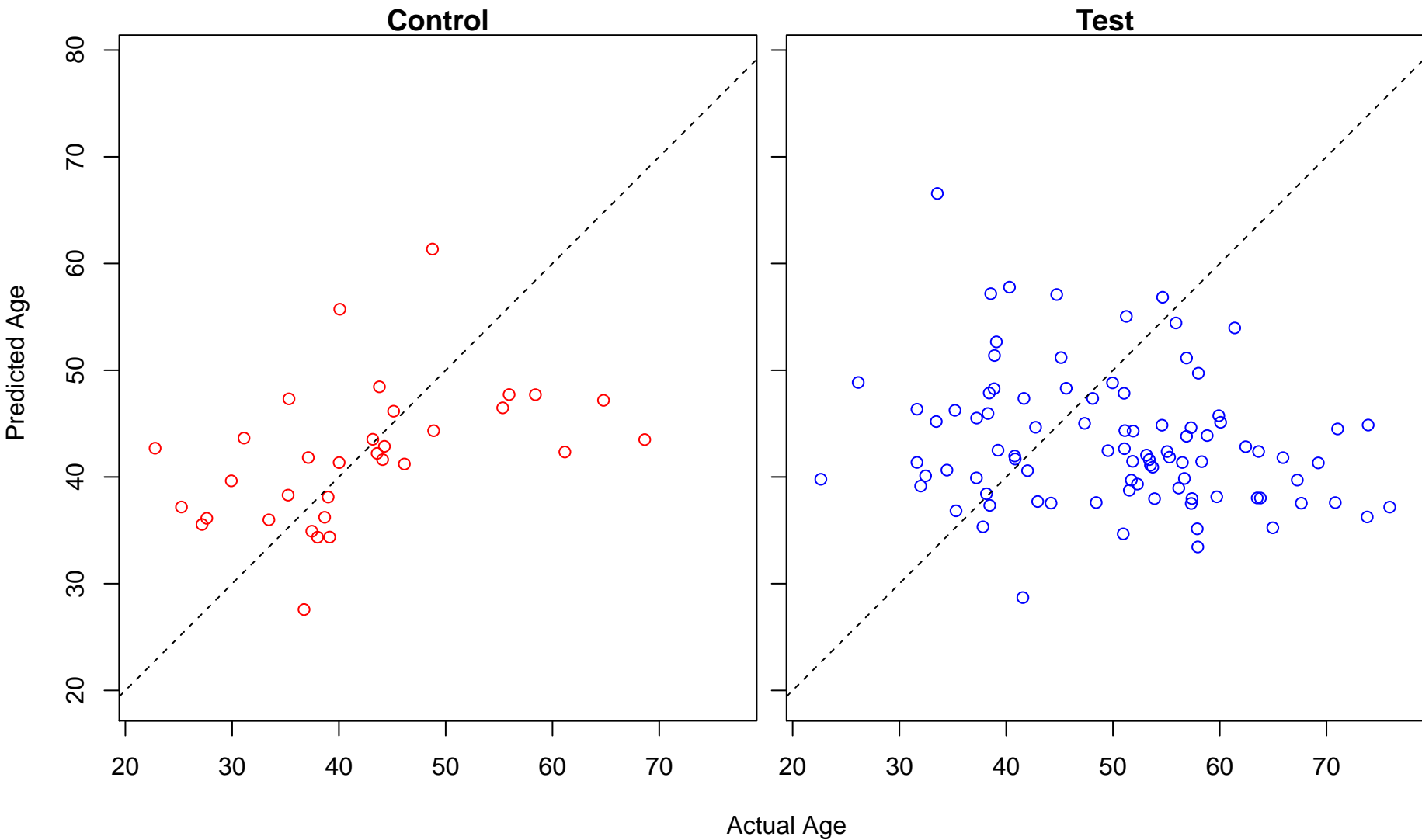
response to interferon-beta (Score: 0.771890)



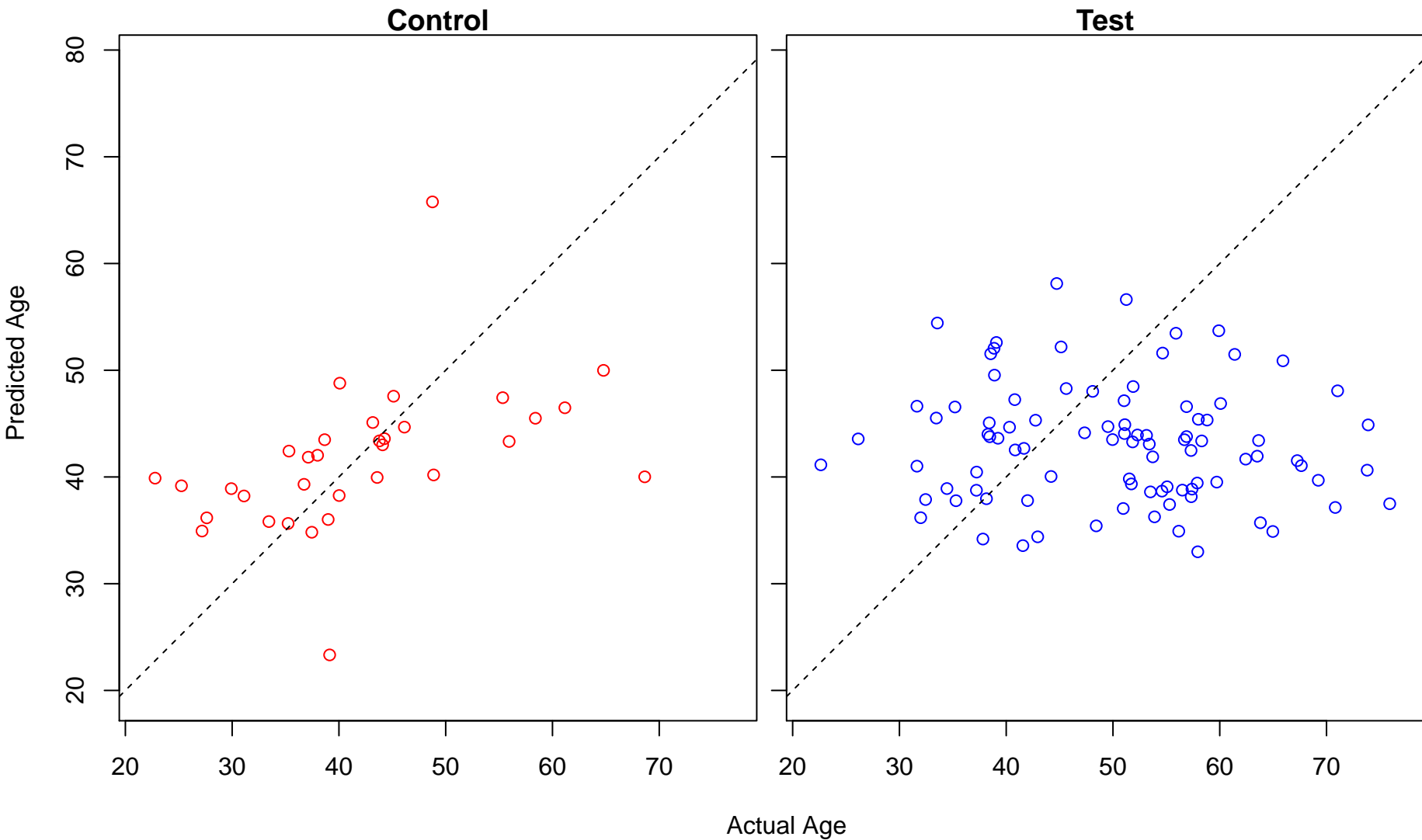
regulation of ATP citrate synthase activity (Score: 0.771149)



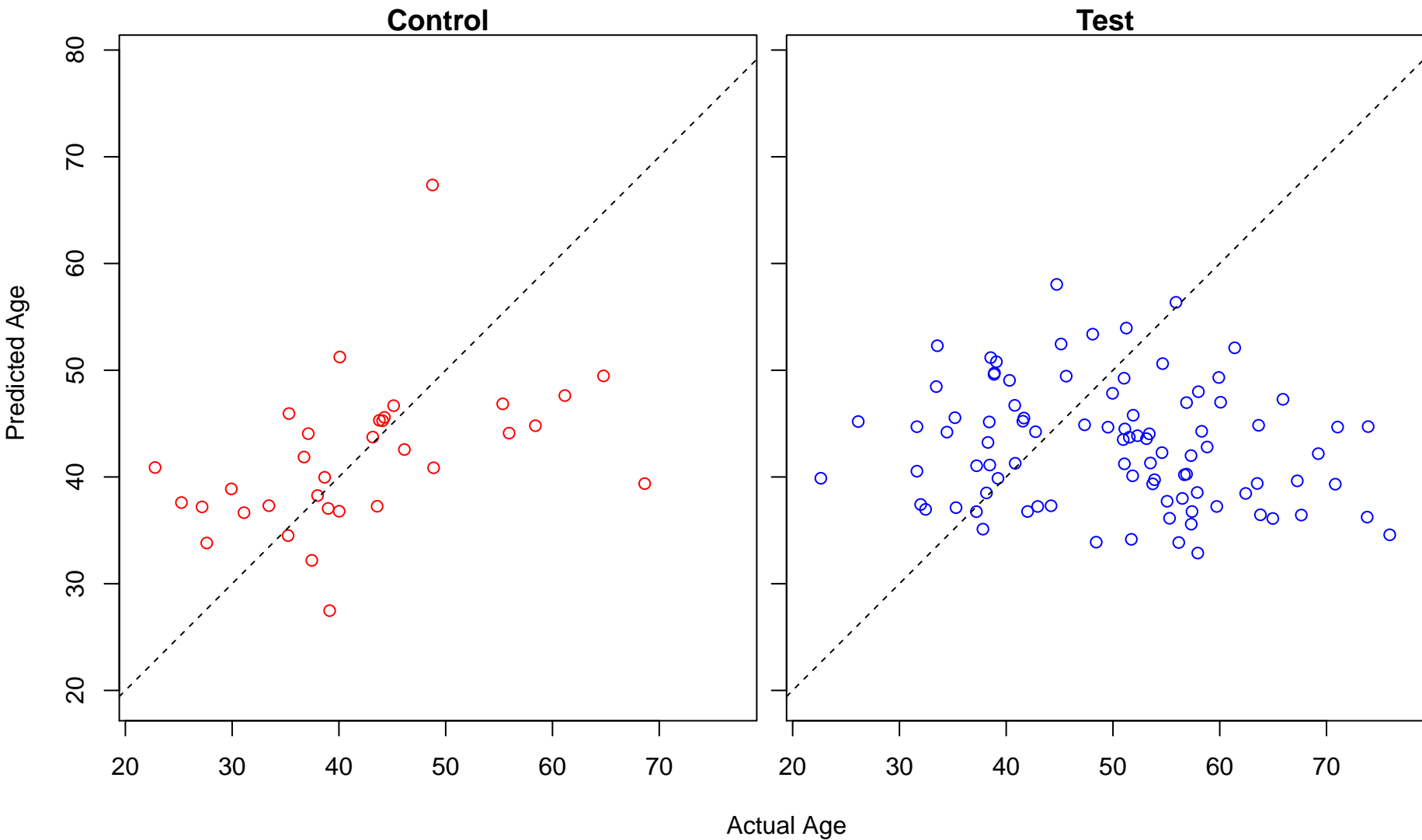
negative regulation of ATP citrate synthase activity (Score: 0.771149)



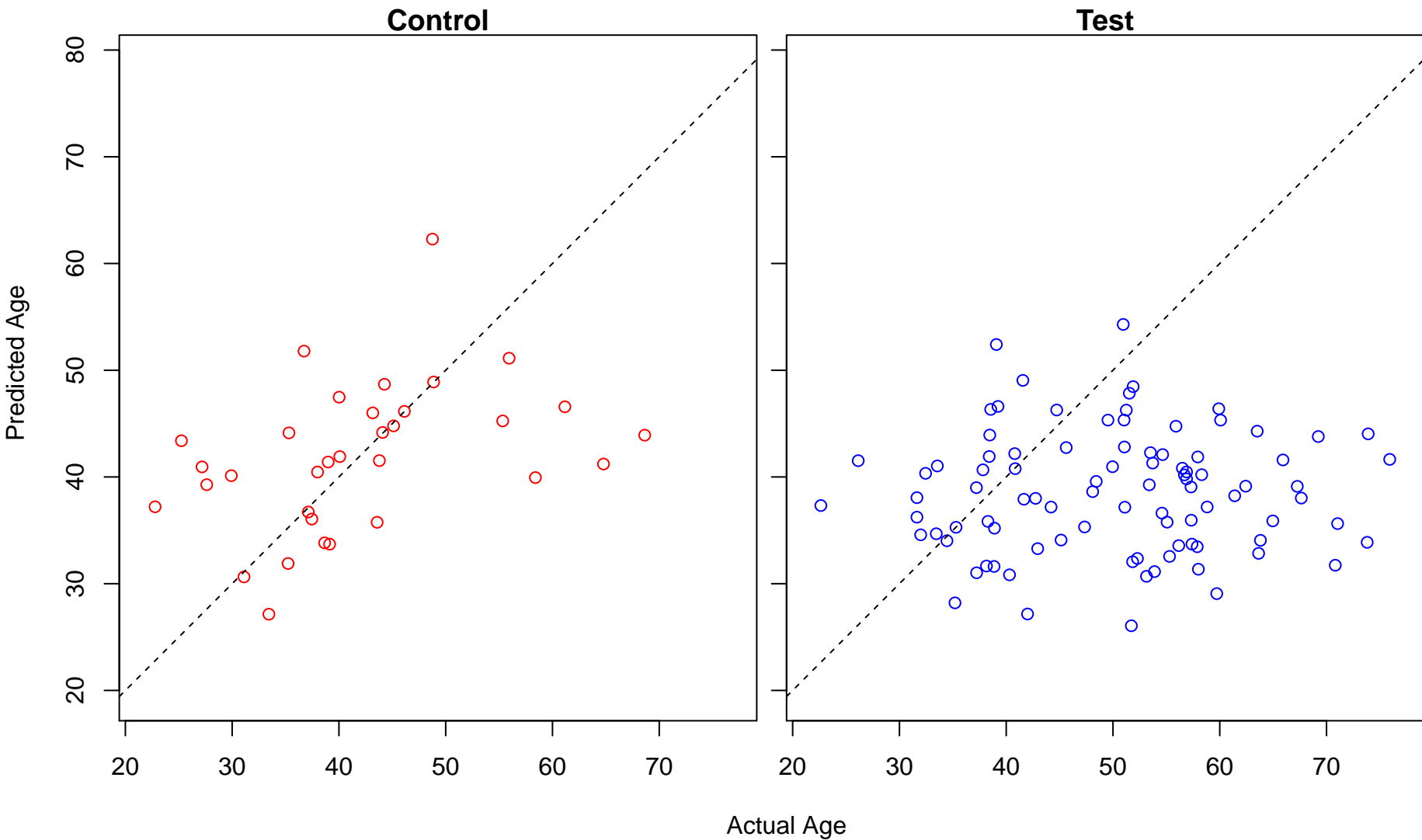
neuron development (Score: 0.770184)



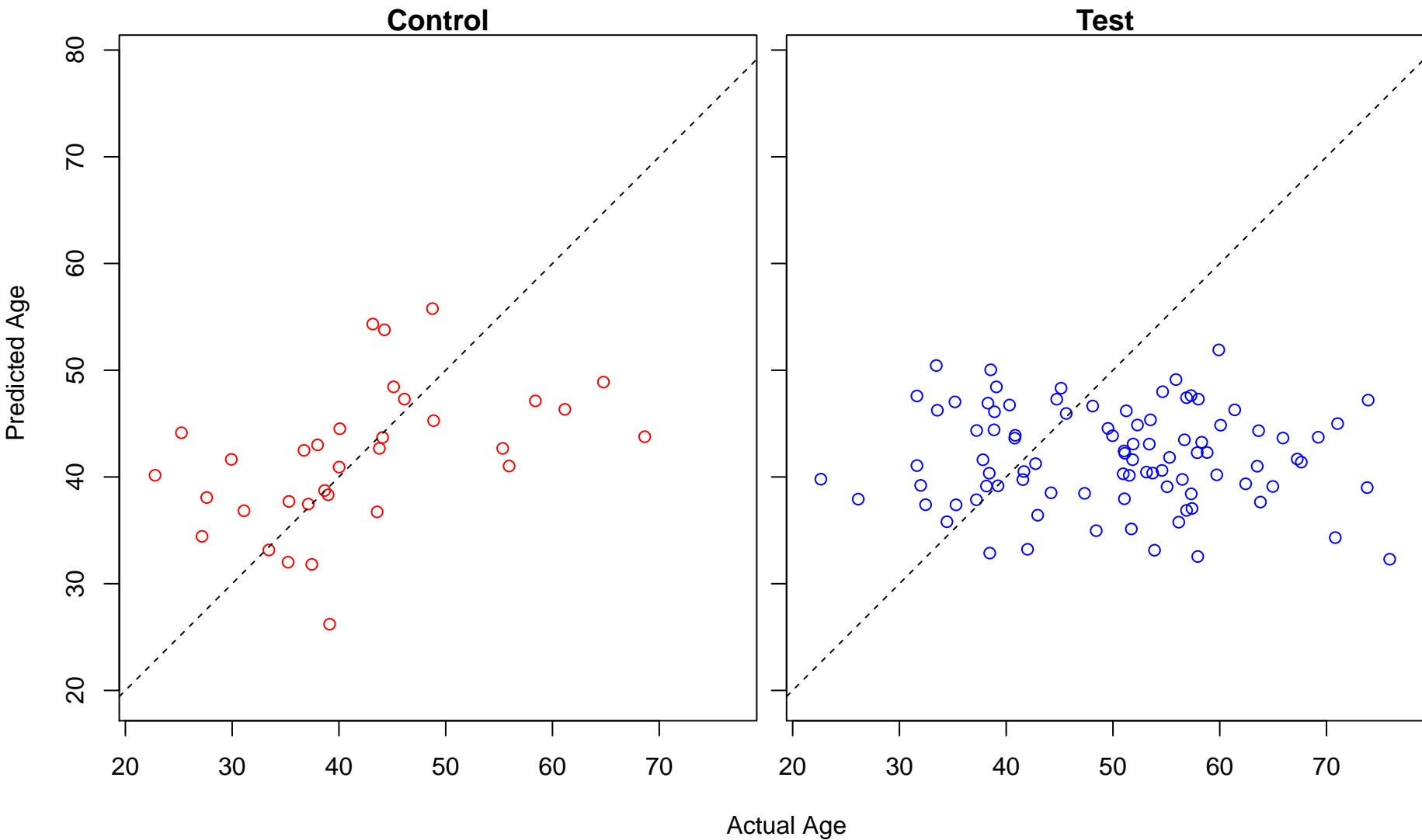
positive regulation of intracellular protein transport (Score: 0.769754)



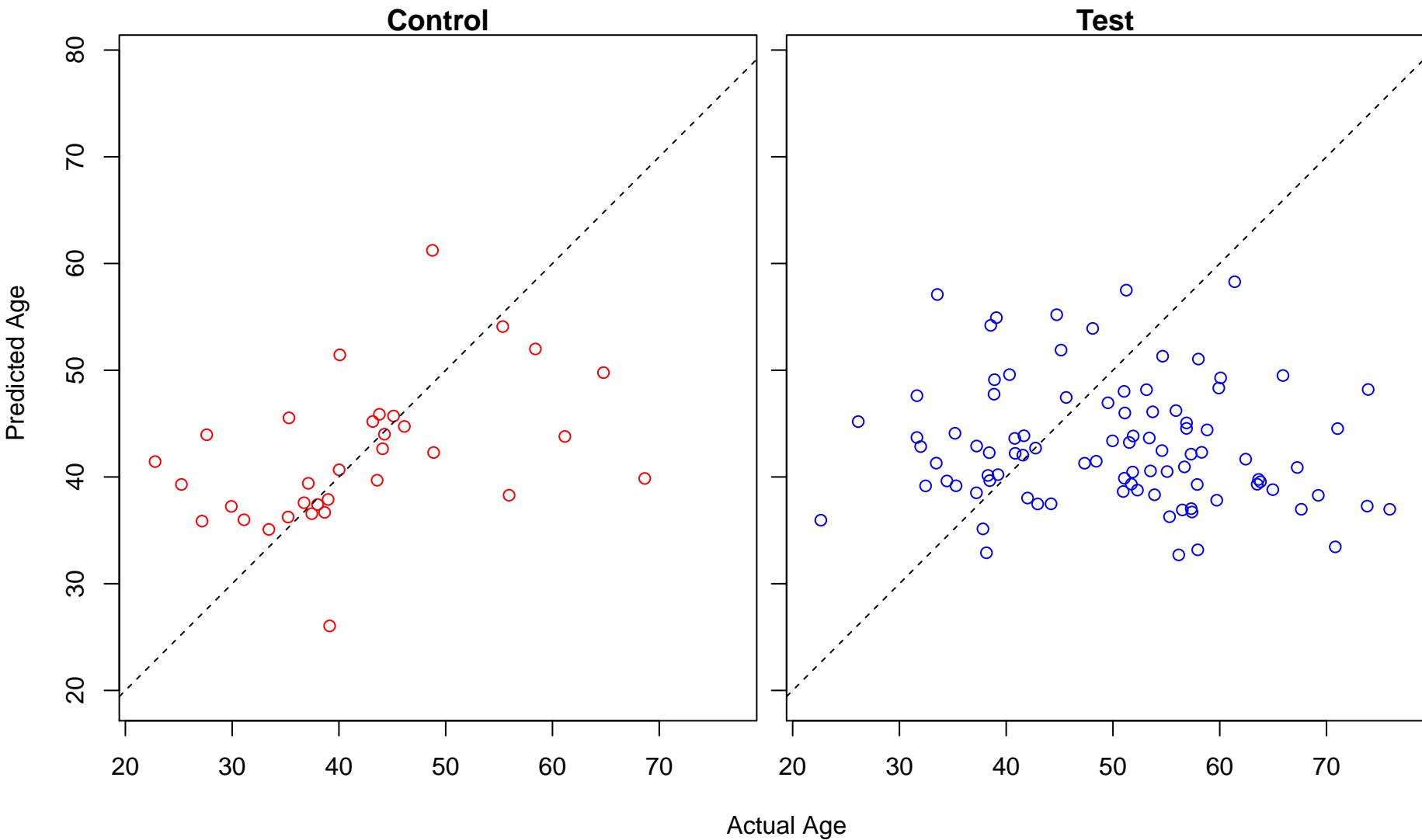
regulation of chemokine (C-X-C motif) ligand 2 production (Score: 0.768968)



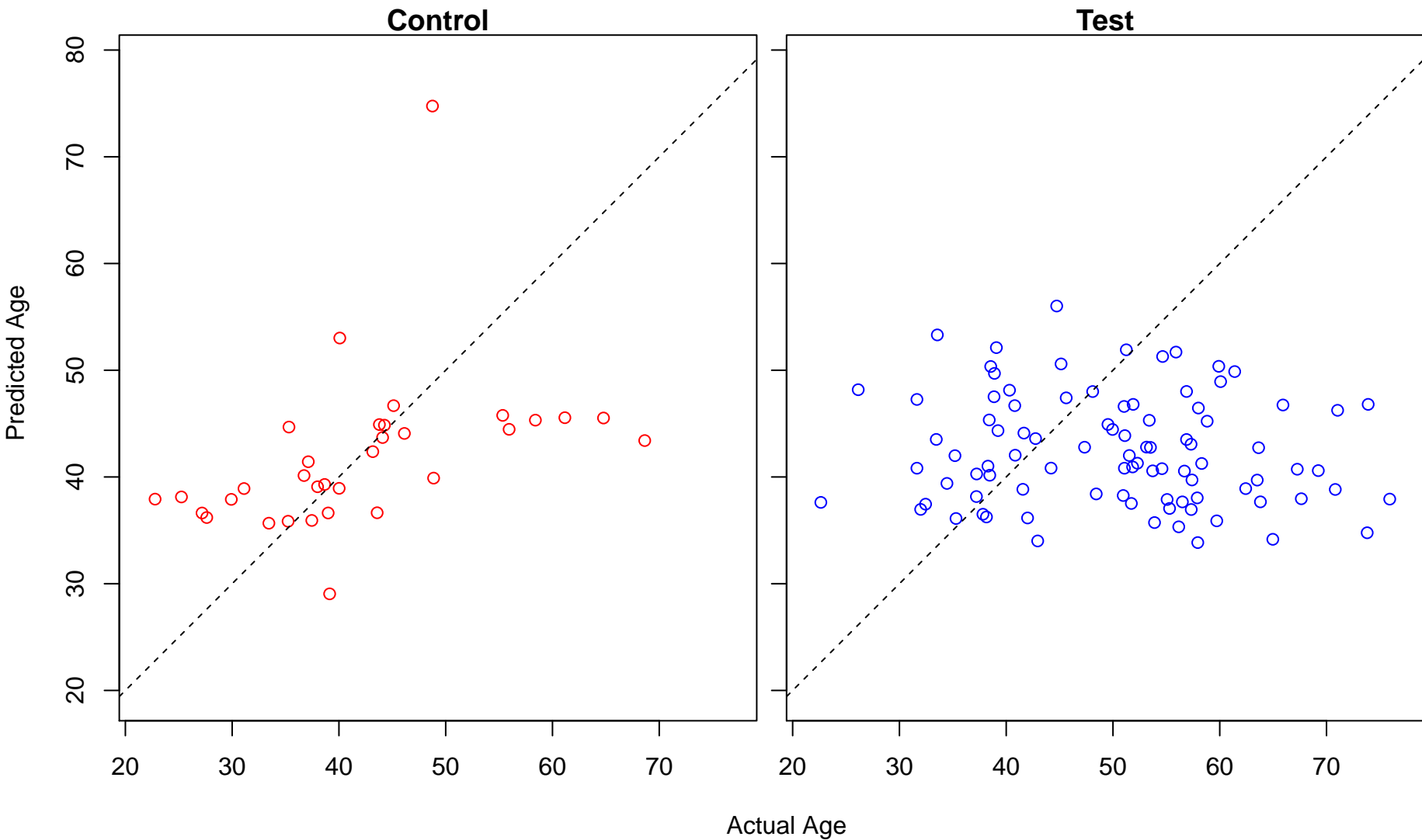
glucose catabolic process (Score: 0.768387)



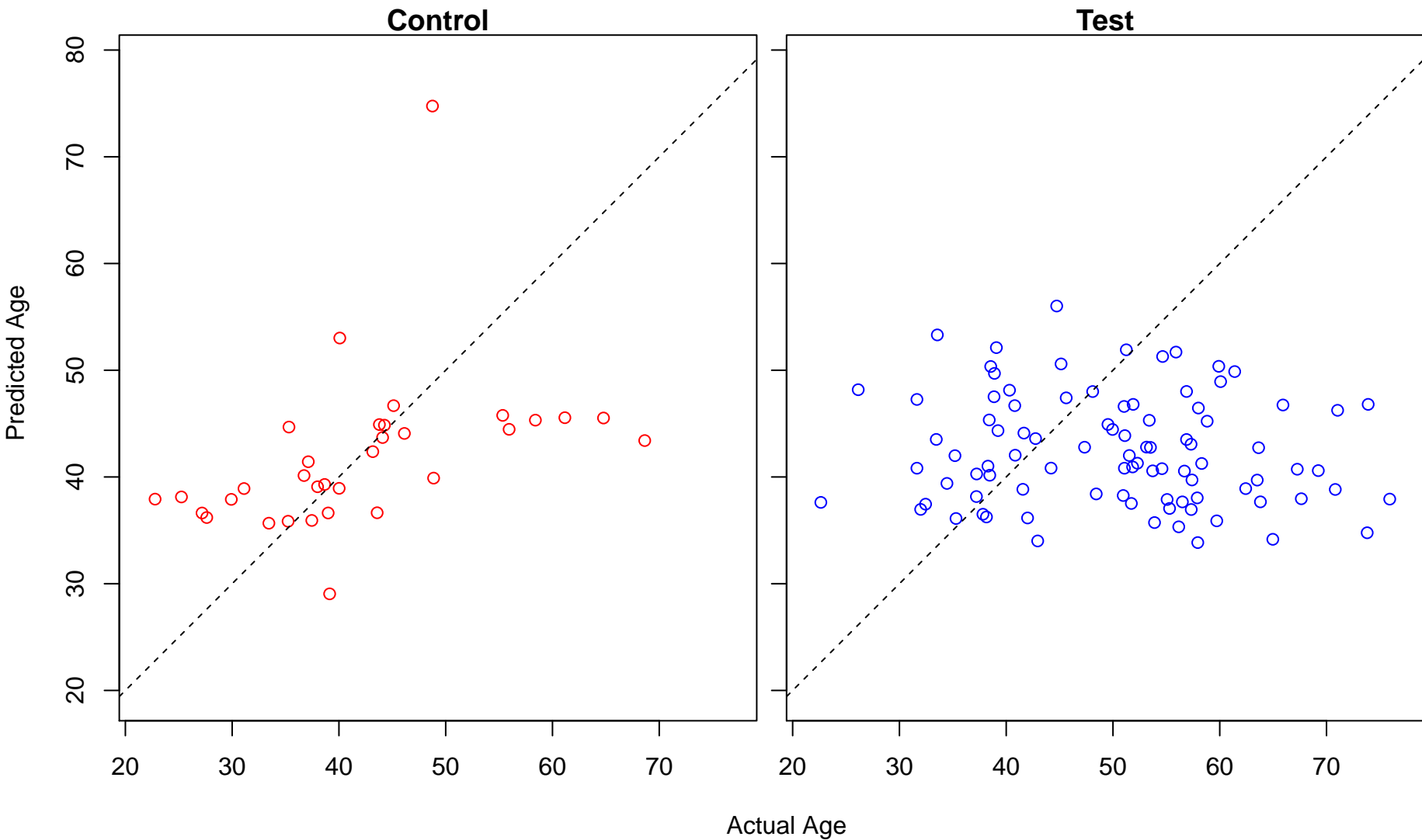
establishment of cell polarity (Score: 0.767944)



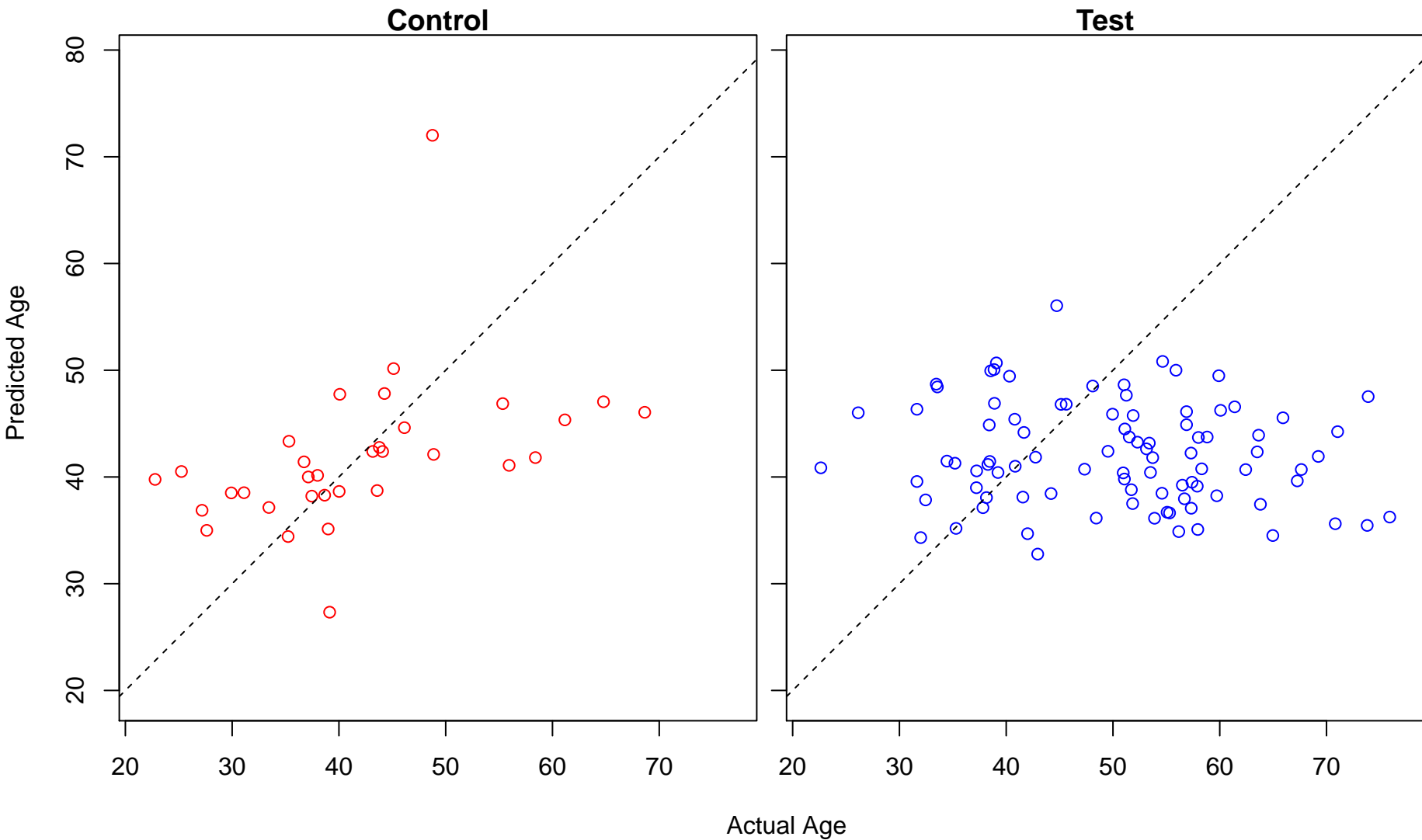
negative regulation of phosphorus metabolic process (Score: 0.765755)



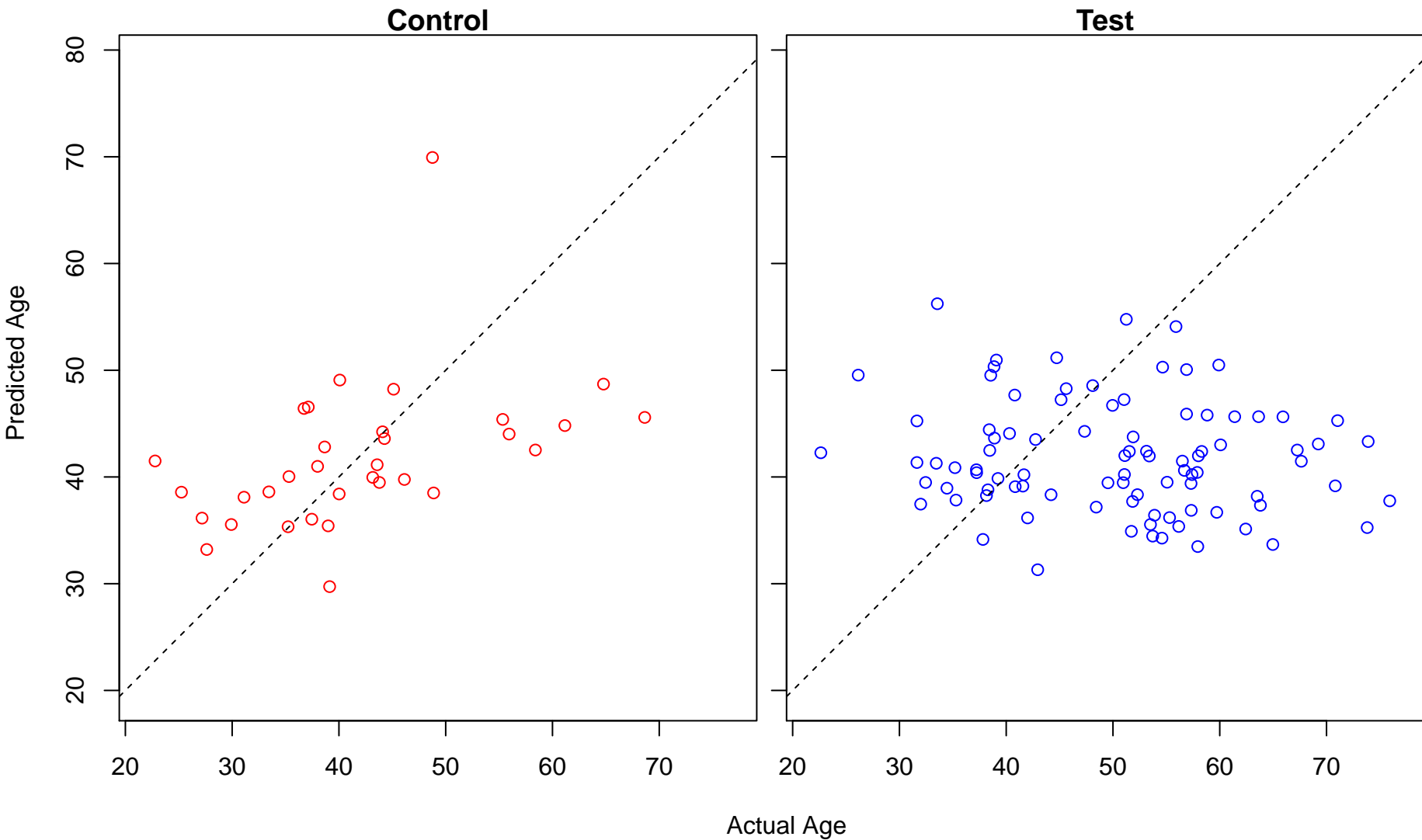
negative regulation of phosphate metabolic process (Score: 0.765755)



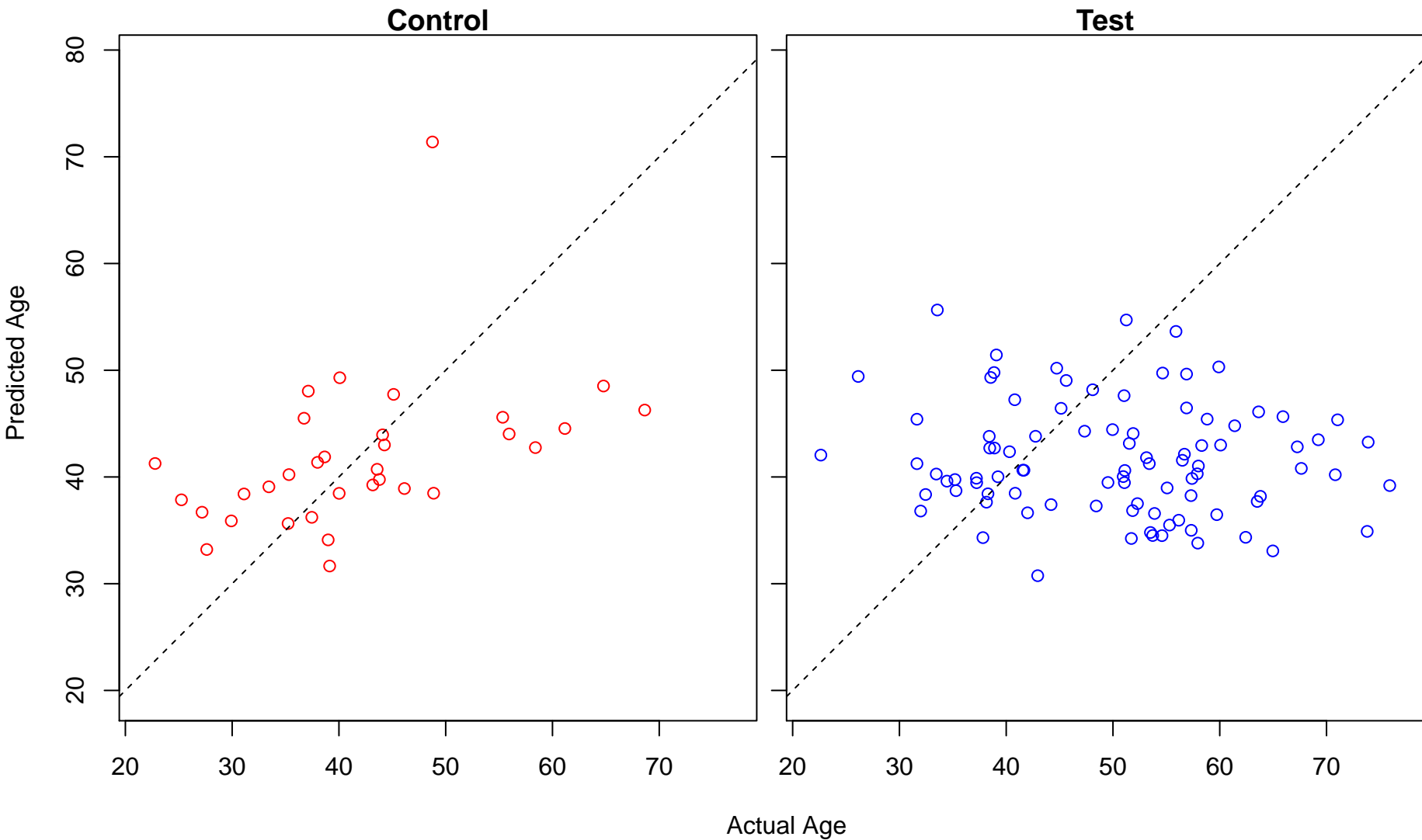
positive regulation of cellular component biogenesis (Score: 0.765433)



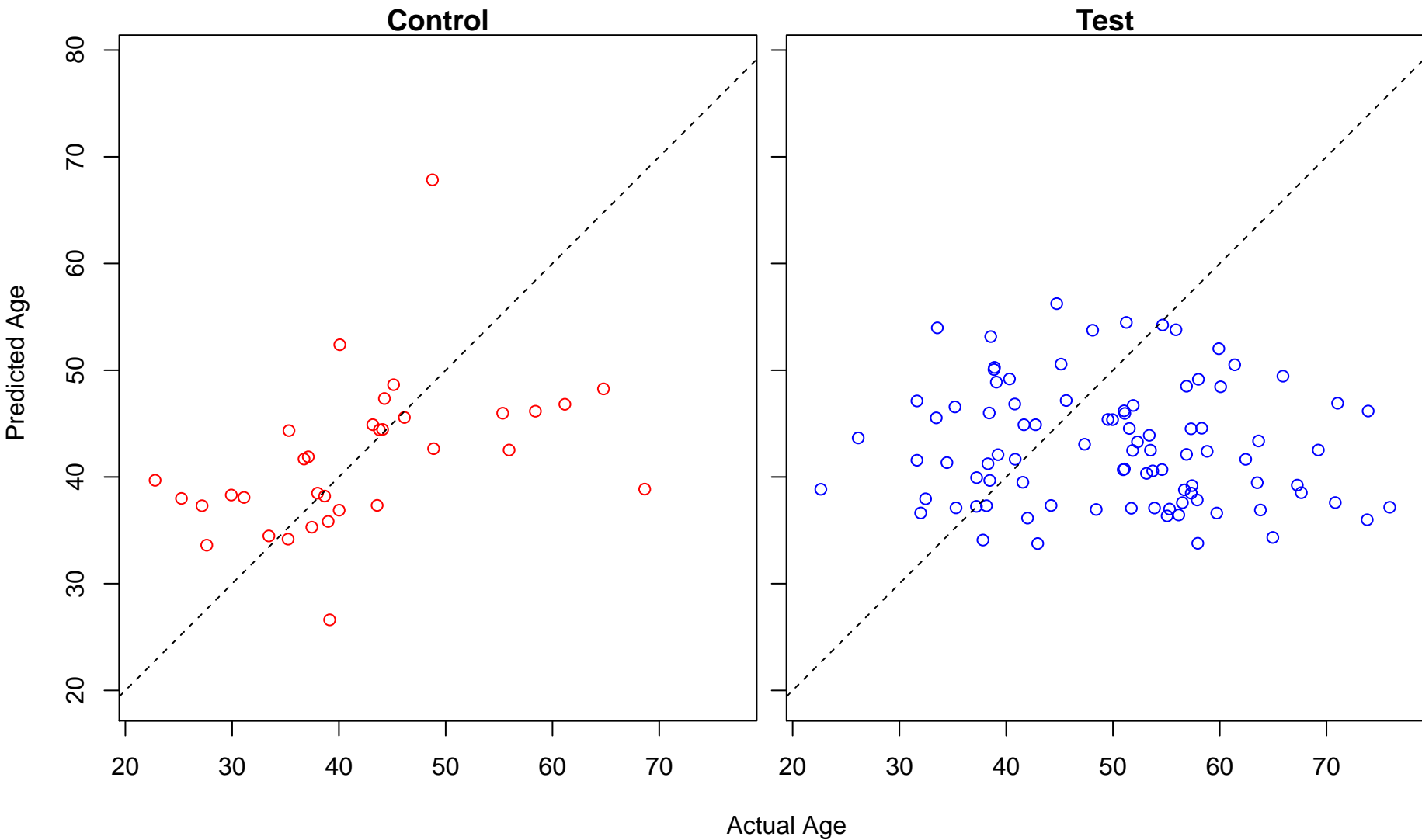
response to wounding (Score: 0.764459)



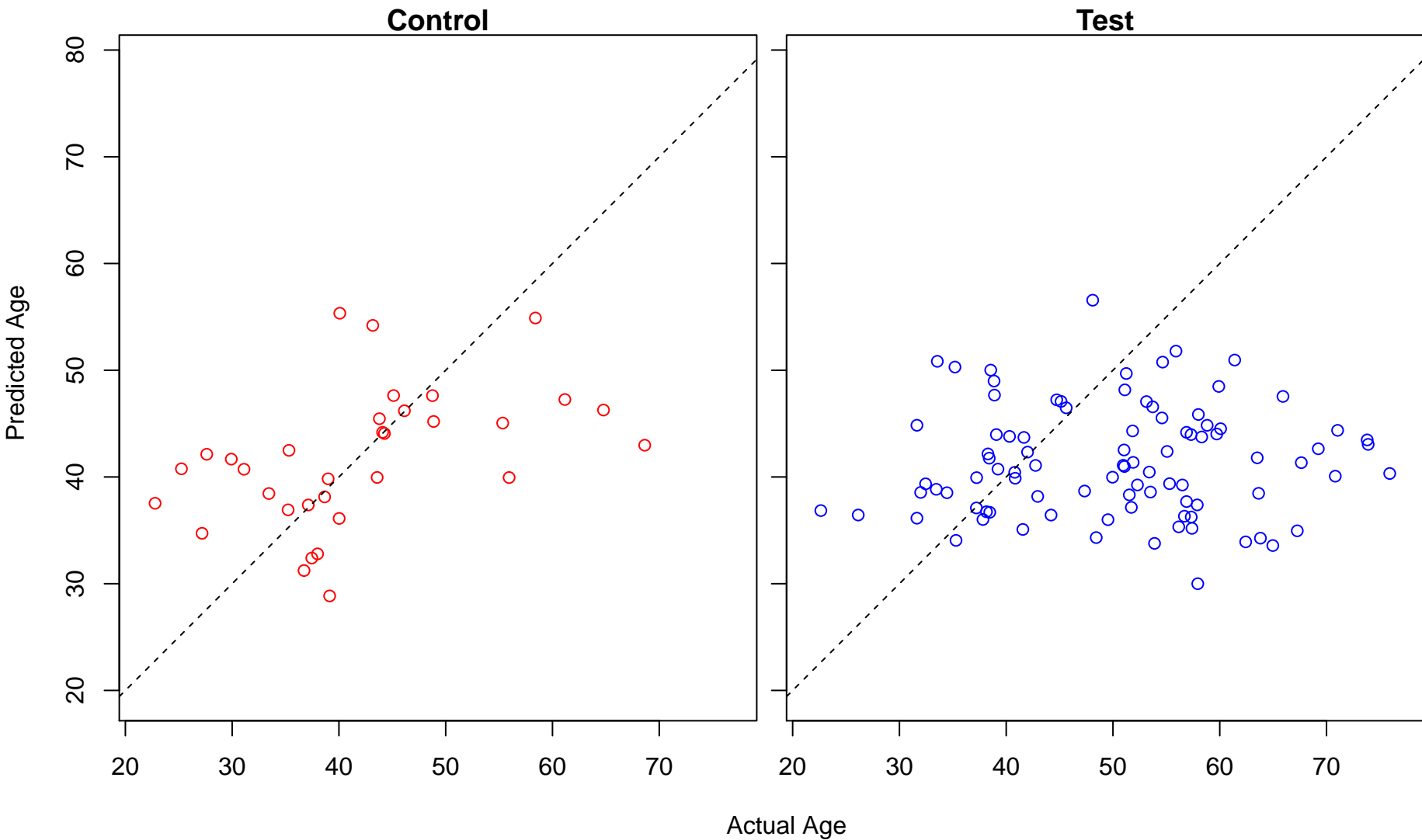
coagulation (Score: 0.763304)



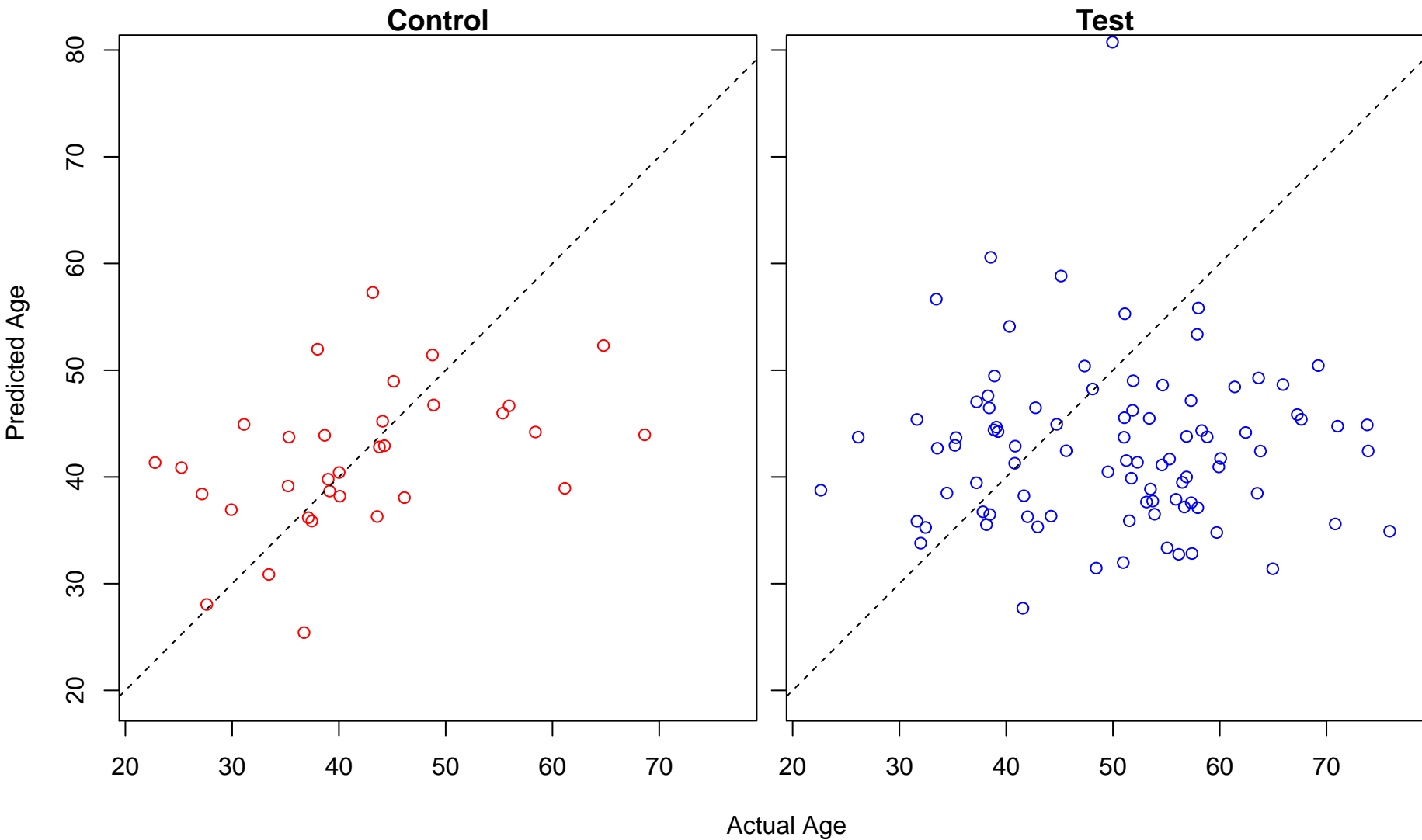
regulation of catabolic process (Score: 0.762893)



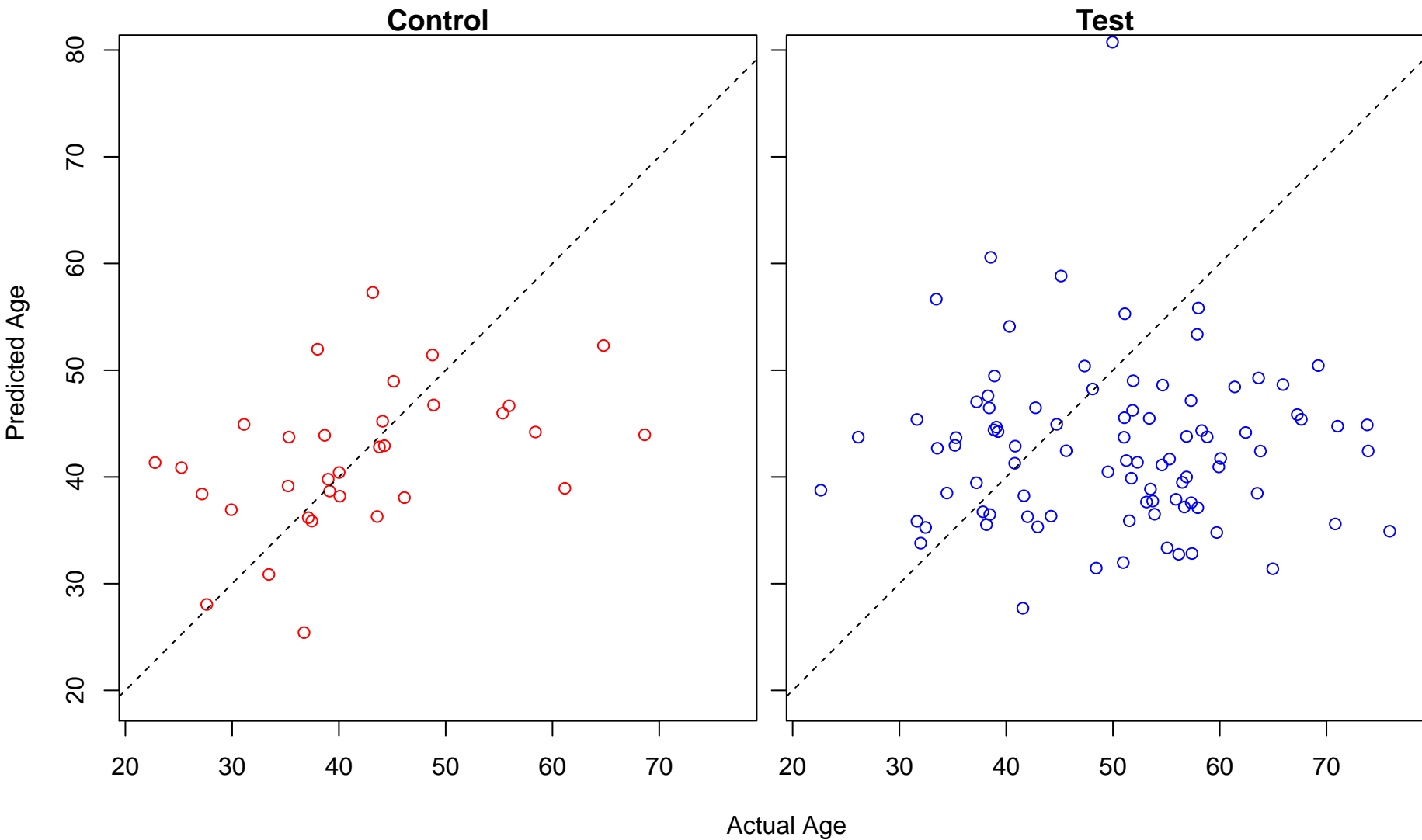
sulfur compound transport (Score: 0.762873)



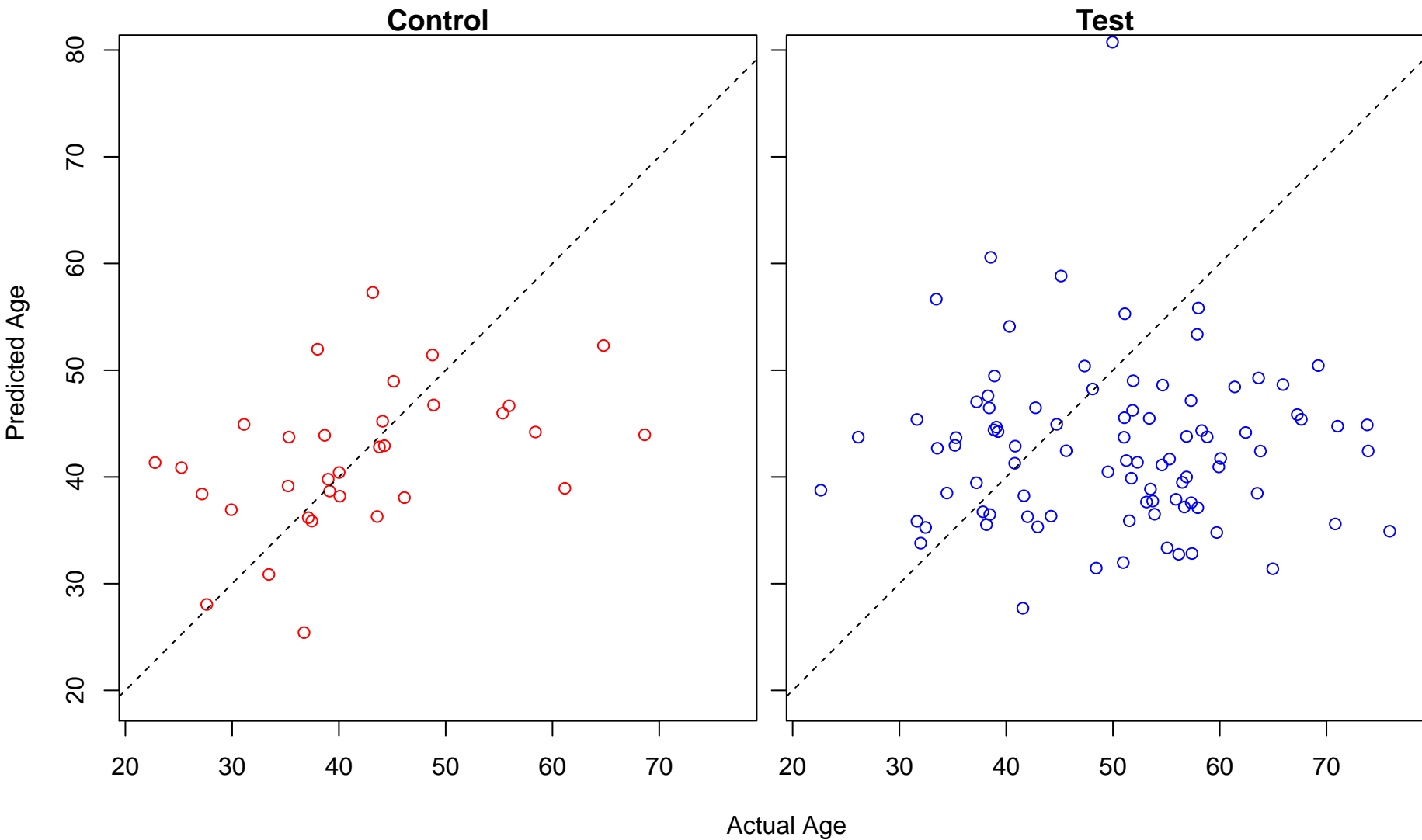
ether lipid biosynthetic process (Score: 0.762417)



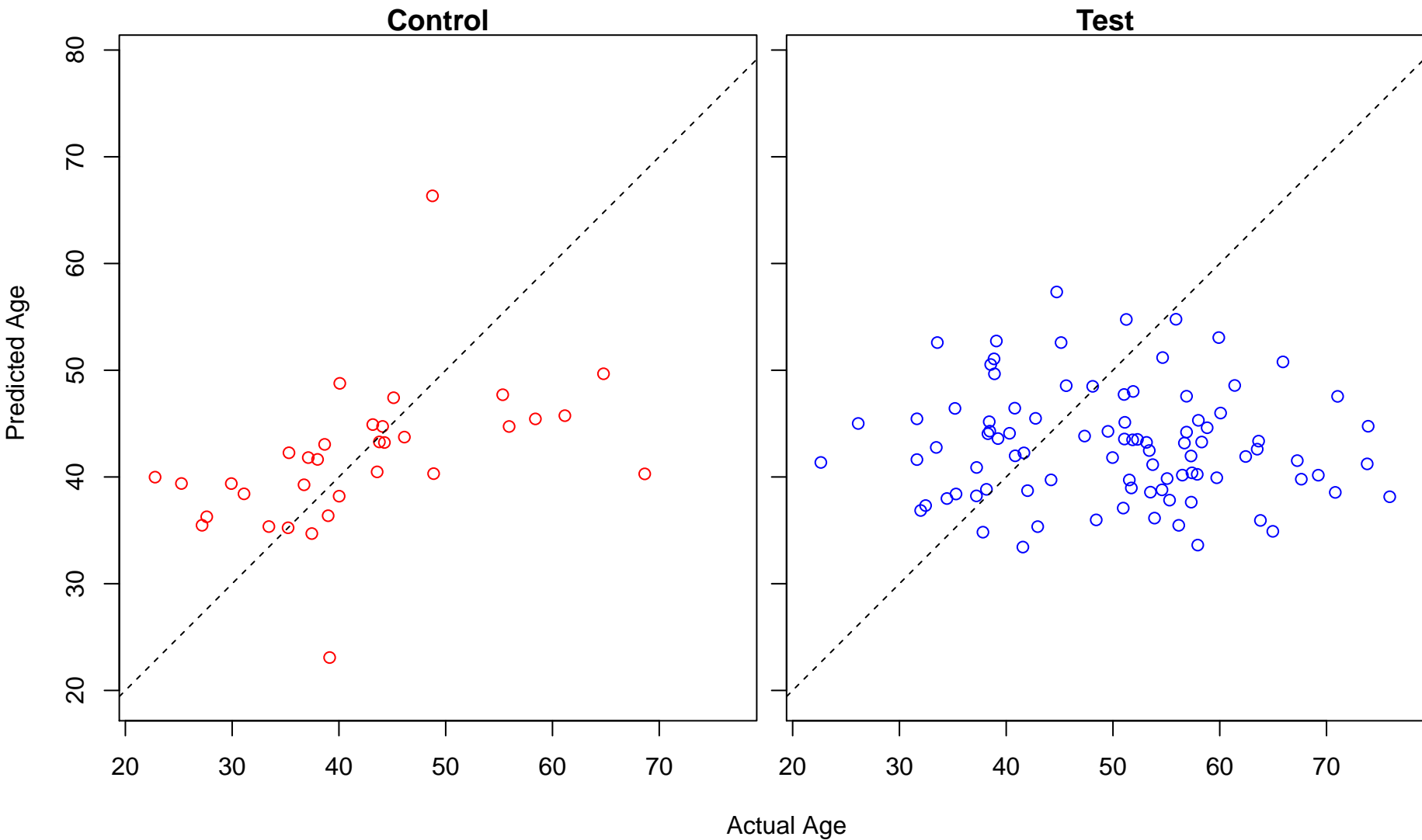
cellular lipid biosynthetic process (Score: 0.762417)



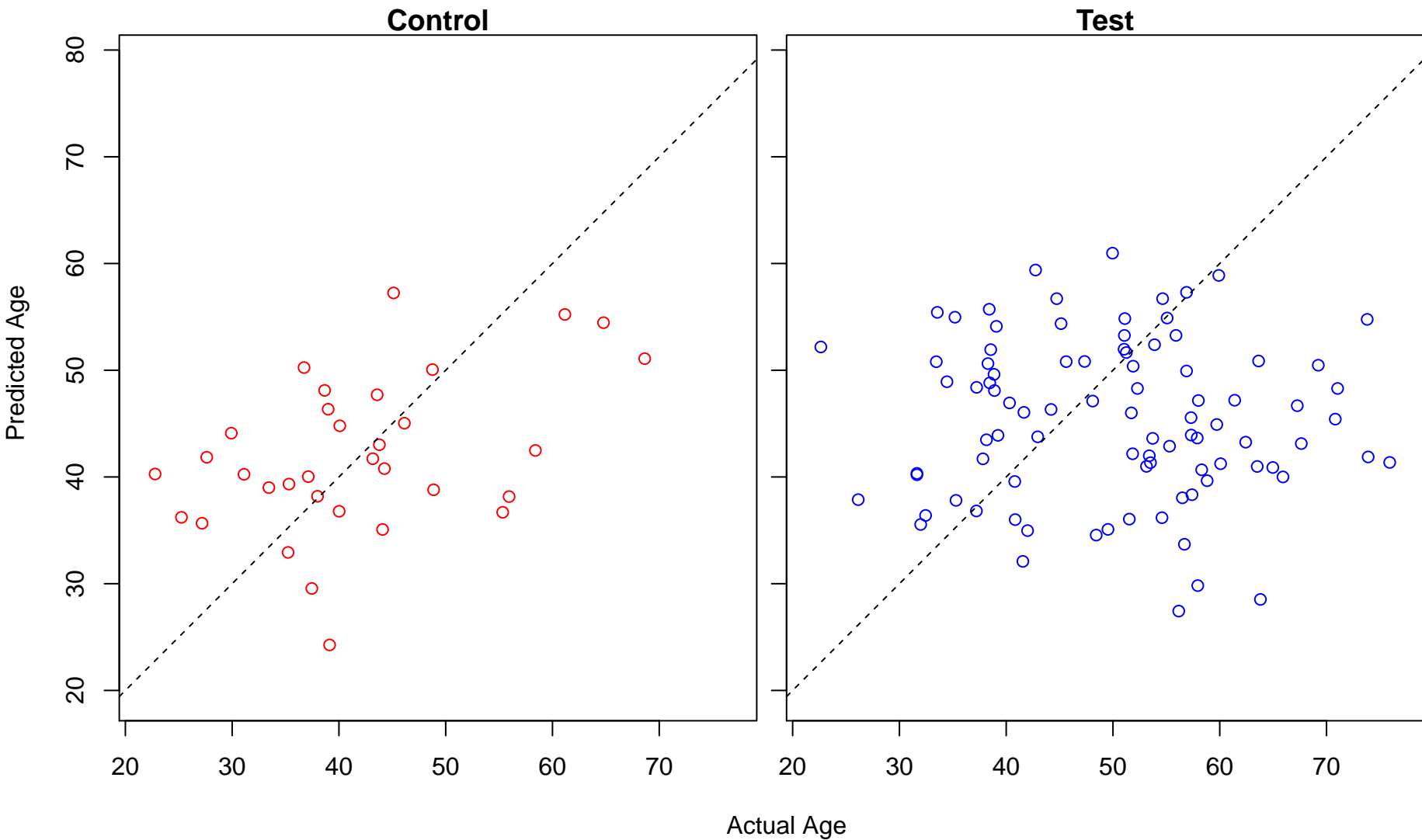
ether biosynthetic process (Score: 0.762417)



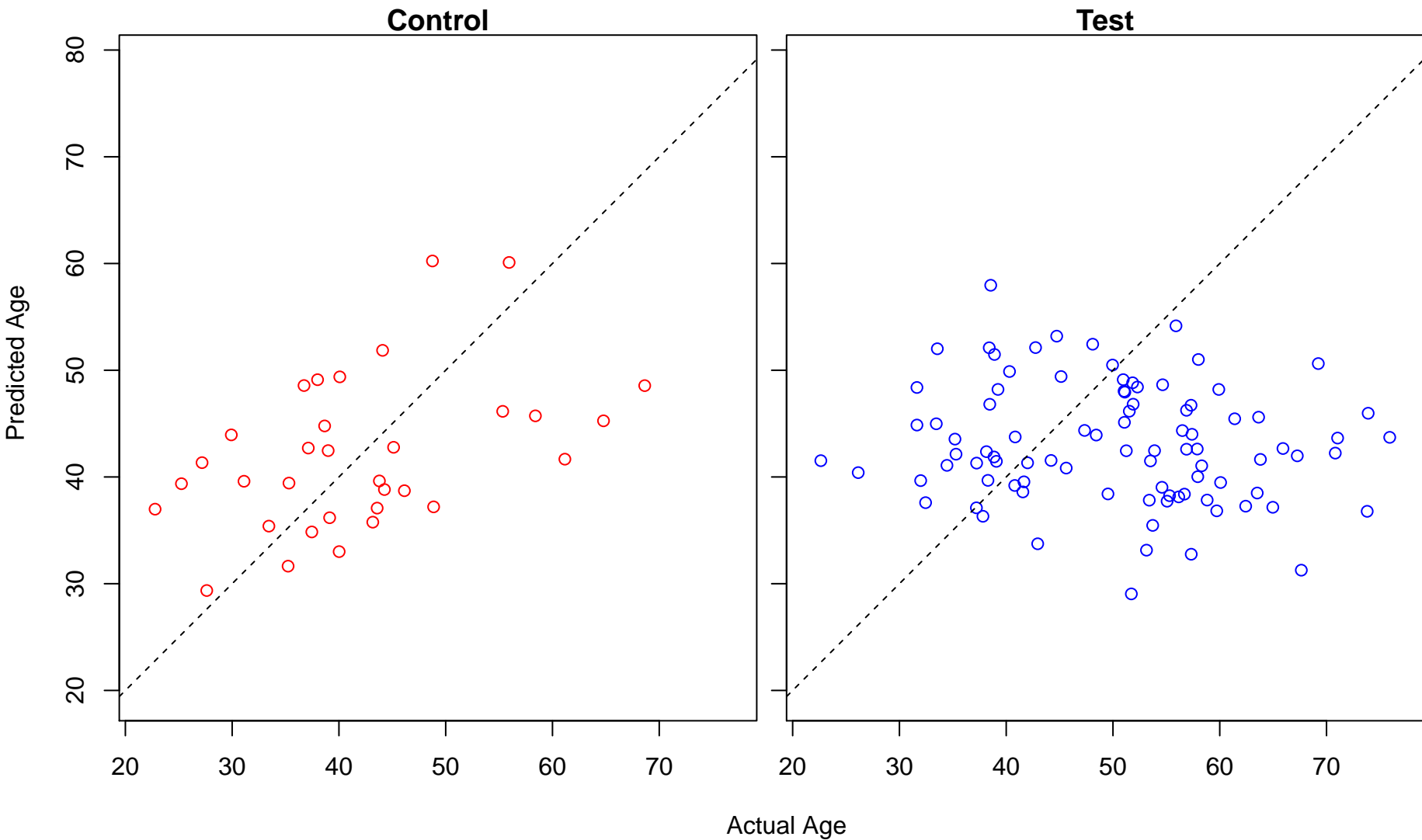
cell part morphogenesis (Score: 0.761646)



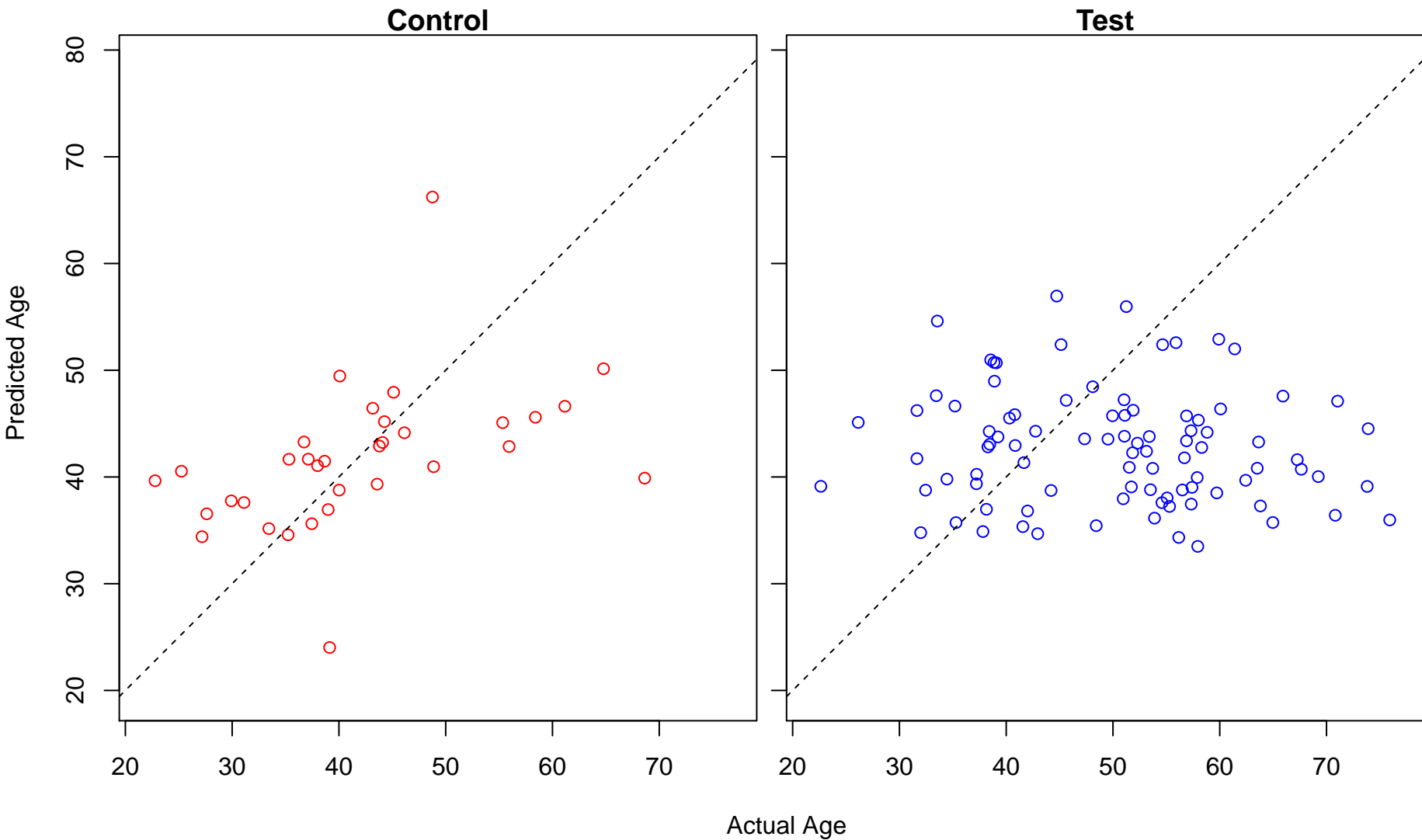
regulation of synaptic transmission, glutamatergic (Score: 0.761300)



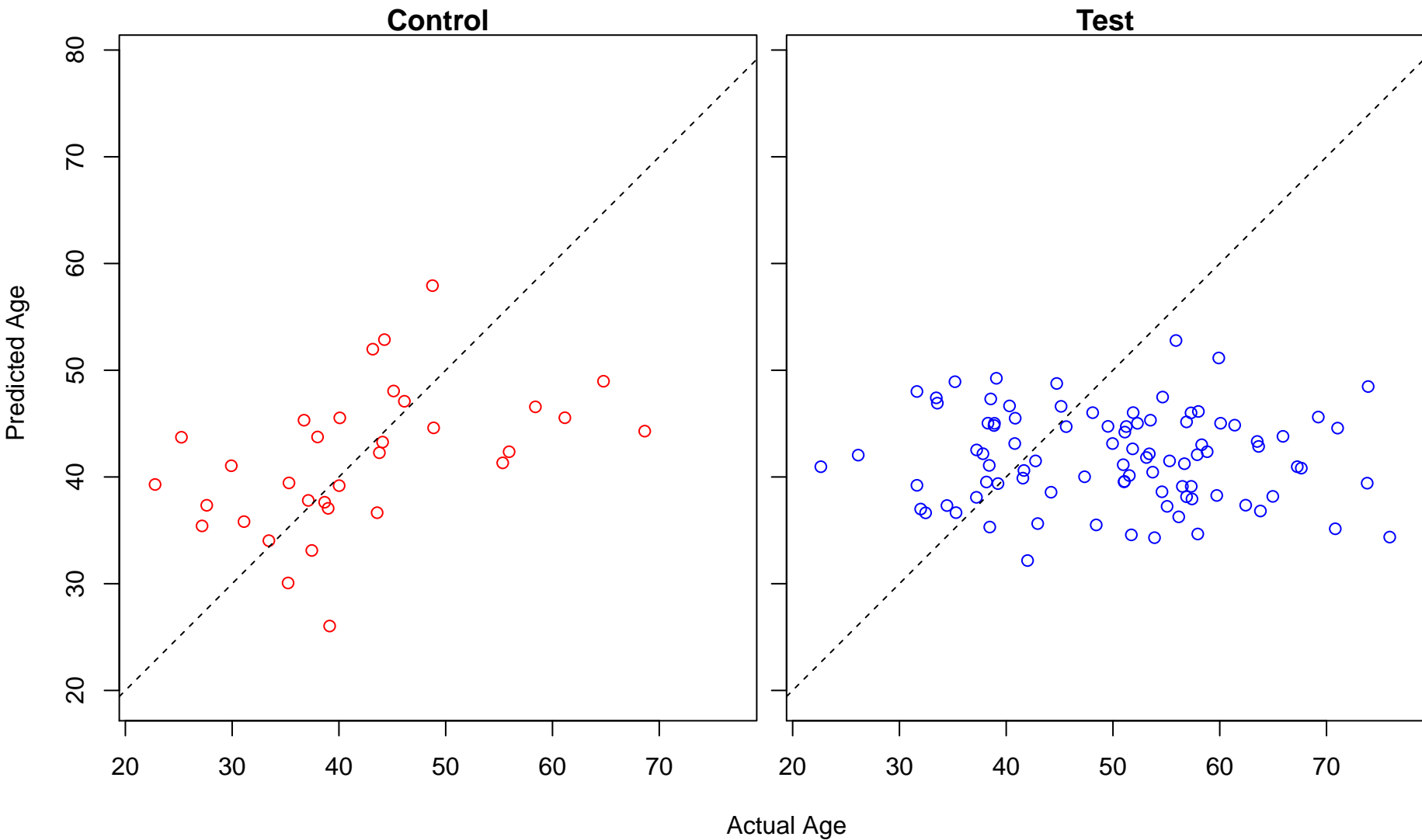
regulation of low-density lipoprotein particle receptor catabolic process (Score: 0.760937)



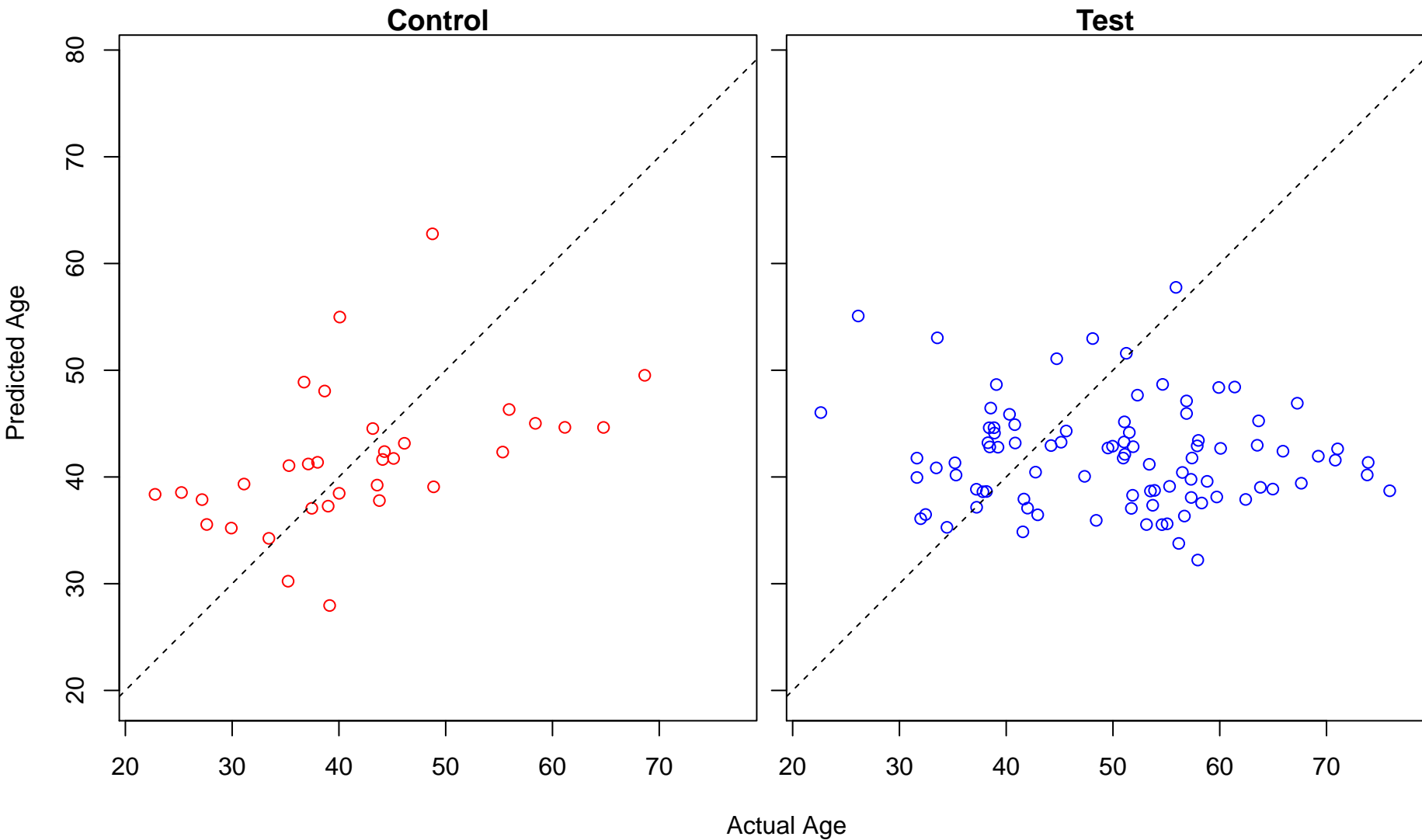
neurogenesis (Score: 0.760796)



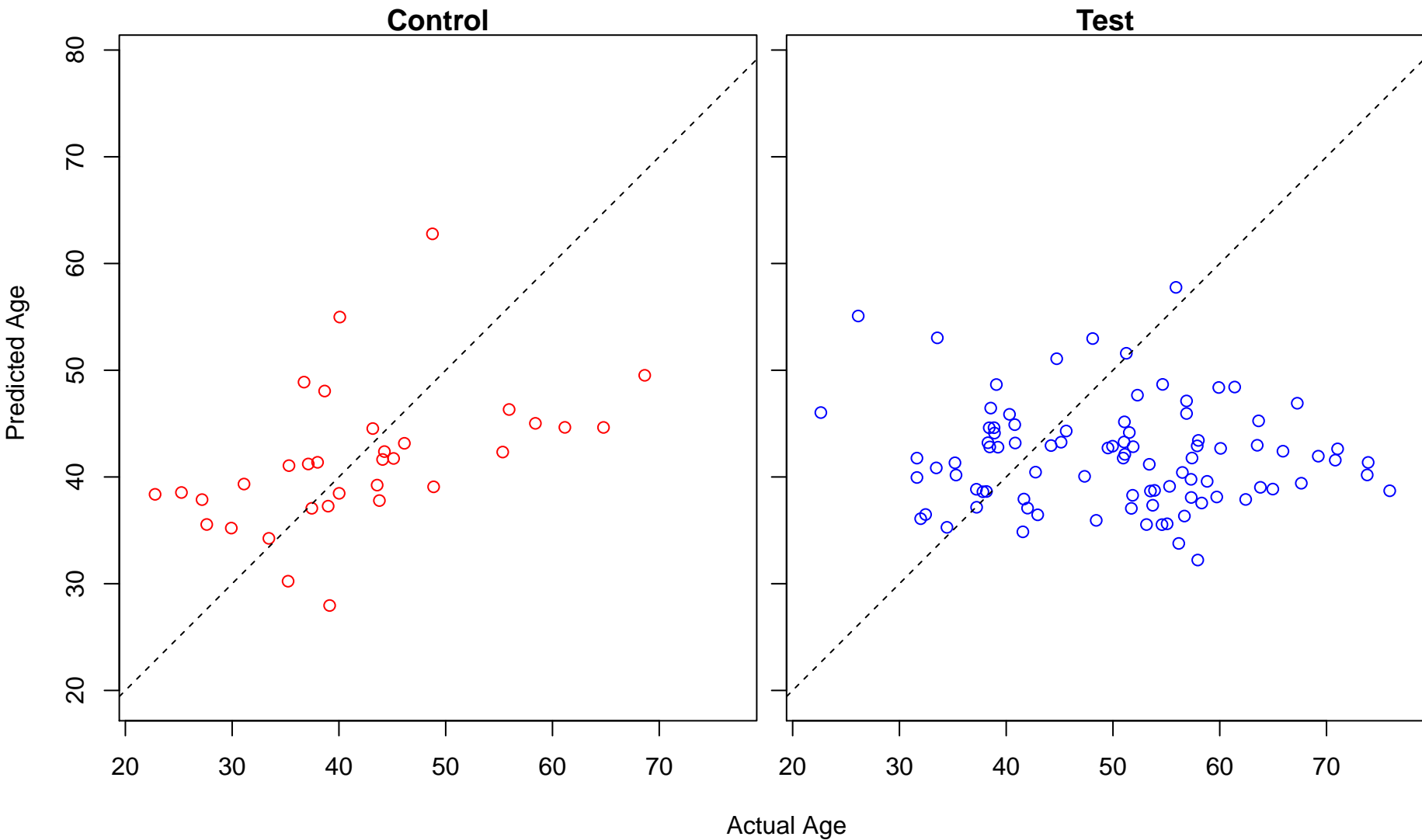
NAD metabolic process (Score: 0.760337)



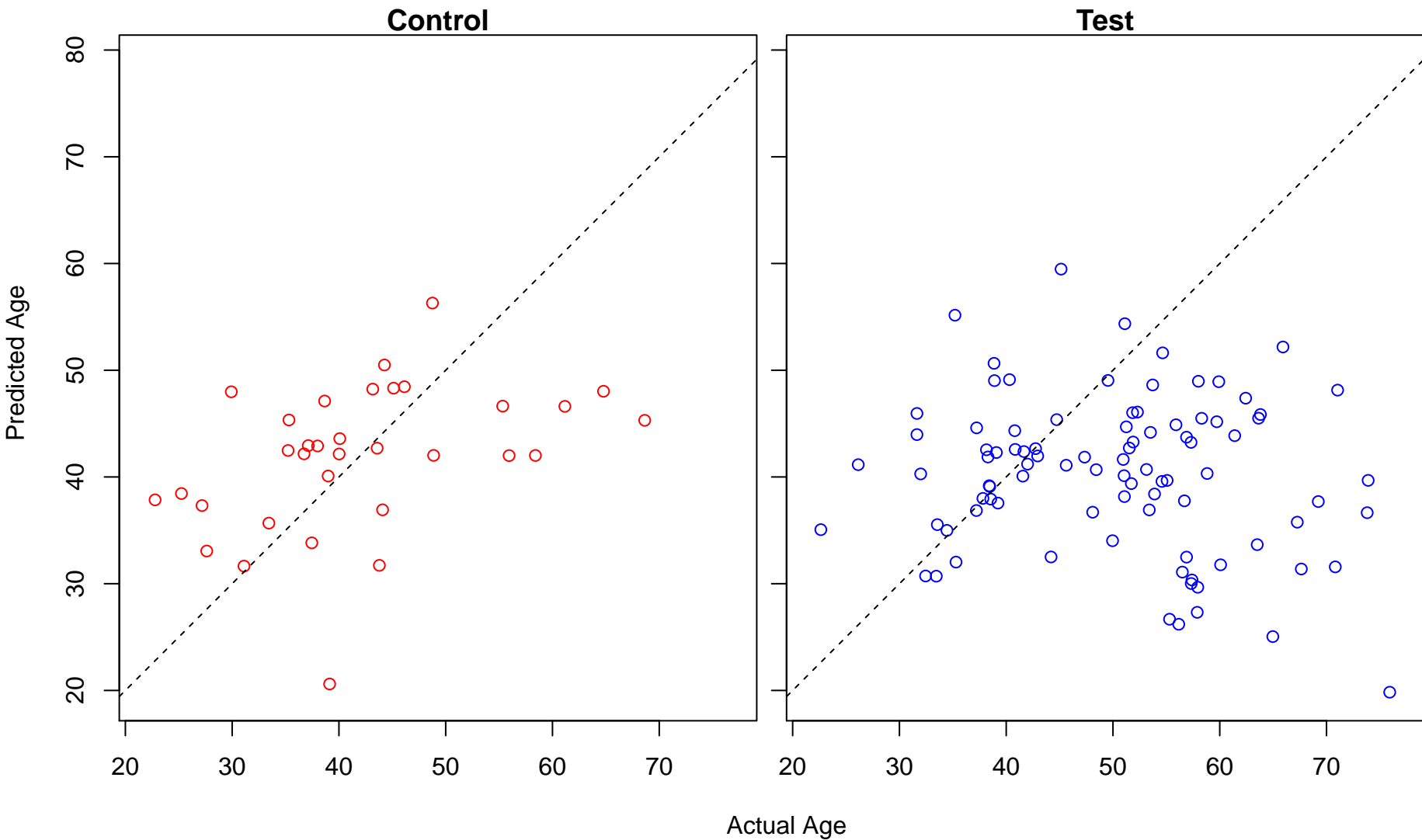
amino acid activation (Score: 0.760237)



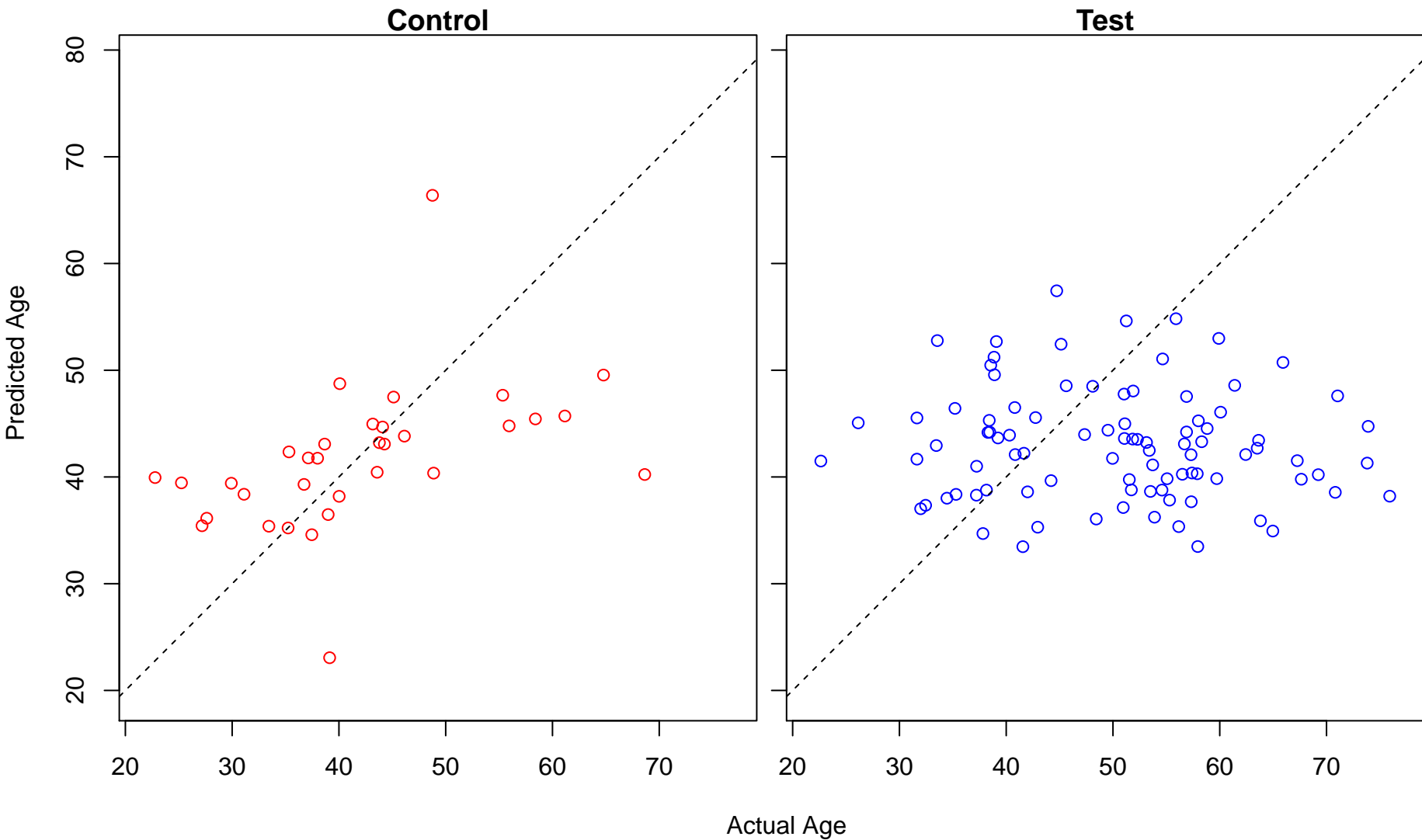
tRNA aminoacylation (Score: 0.760237)



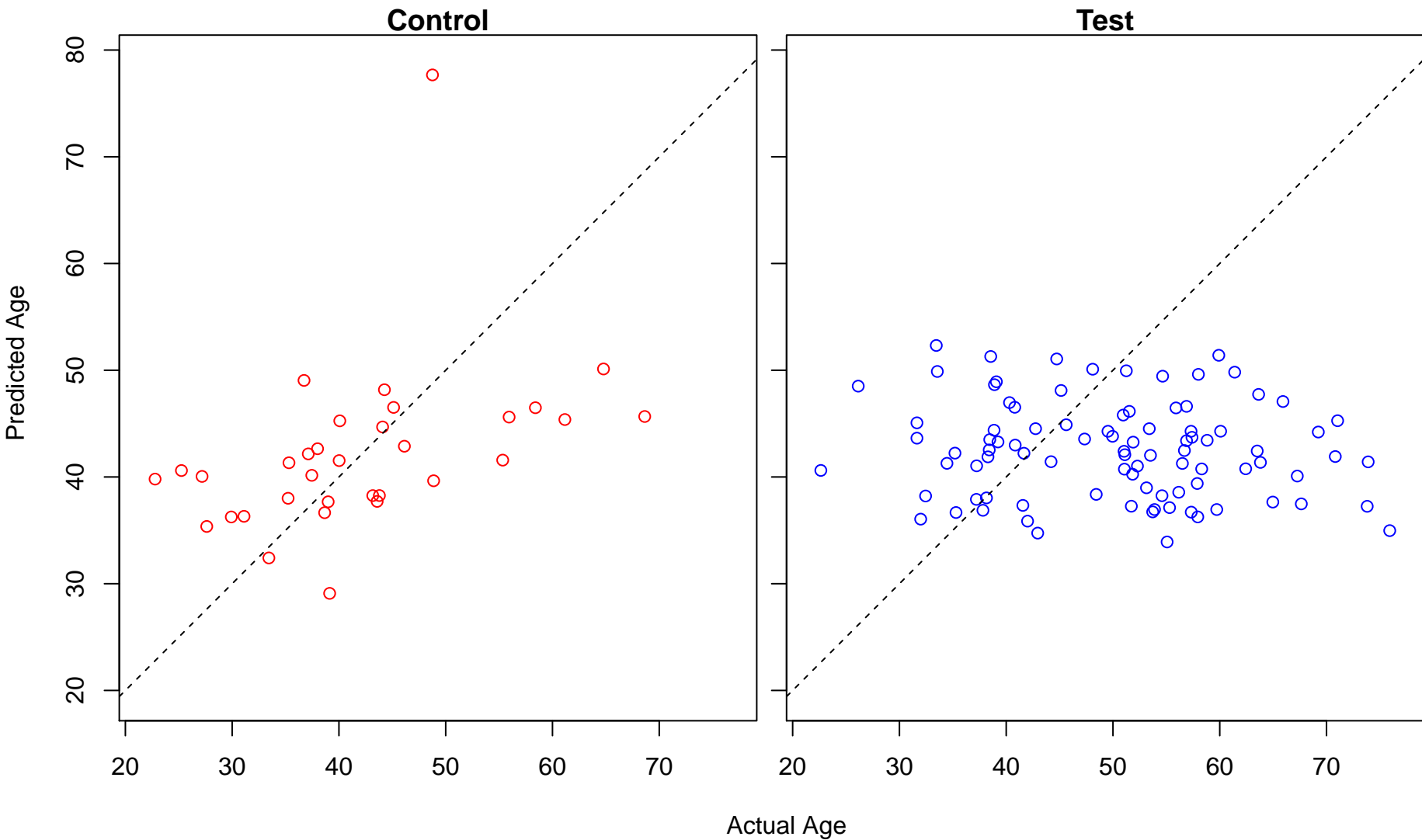
establishment or maintenance of cytoskeleton polarity (Score: 0.759151)



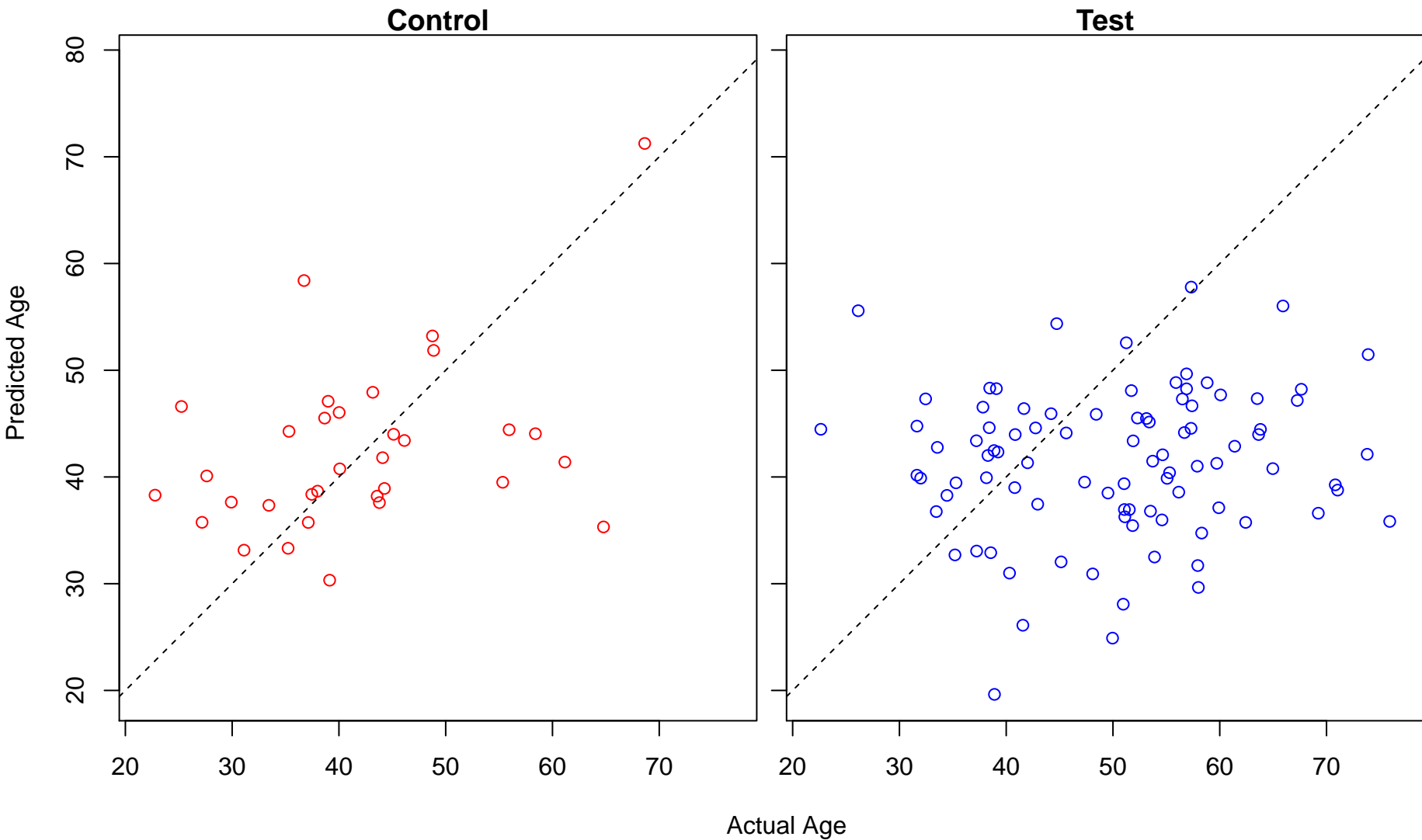
cell projection morphogenesis (Score: 0.758766)



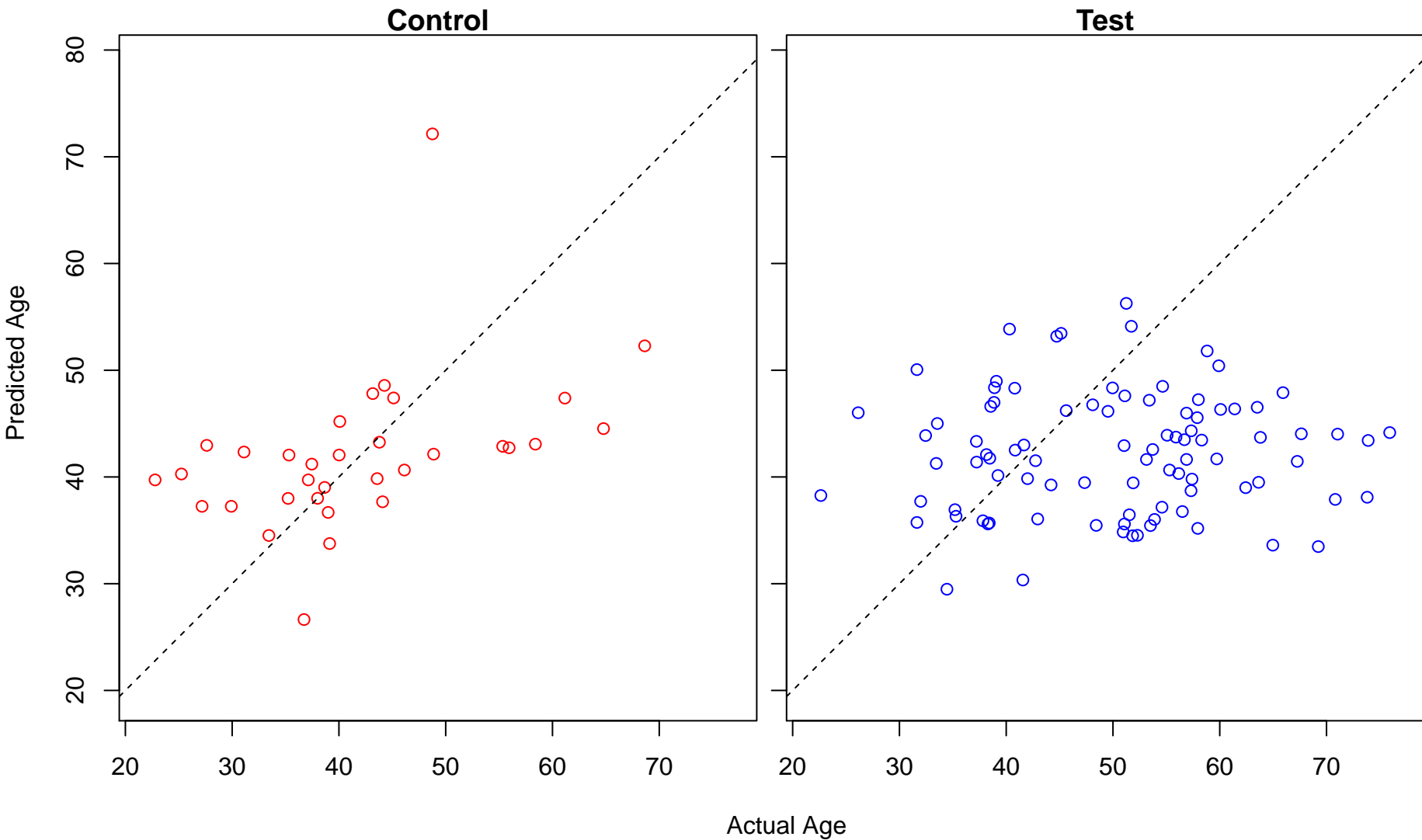
establishment of protein localization to mitochondrion (Score: 0.758644)



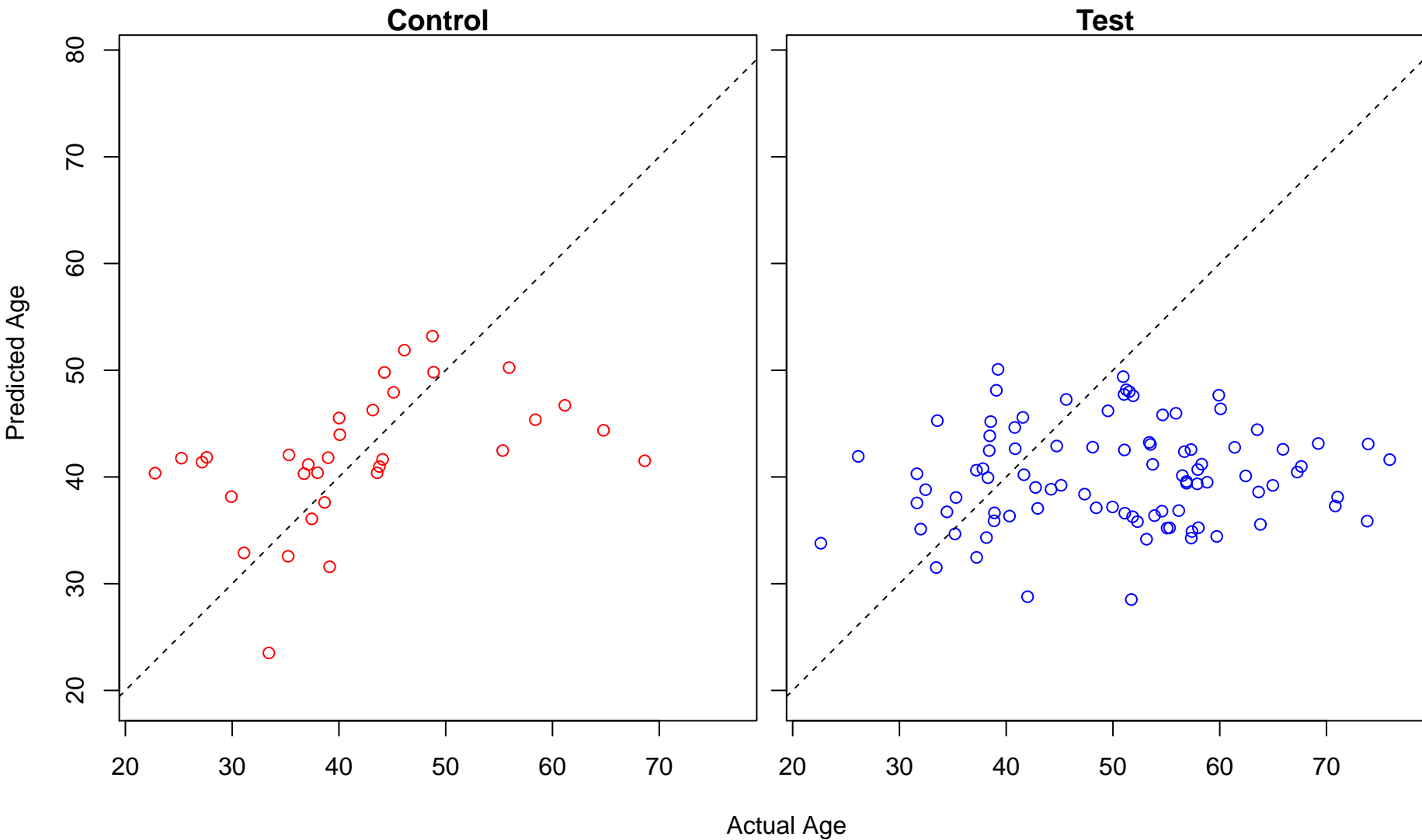
regulation of protein K63-linked ubiquitination (Score: 0.758353)



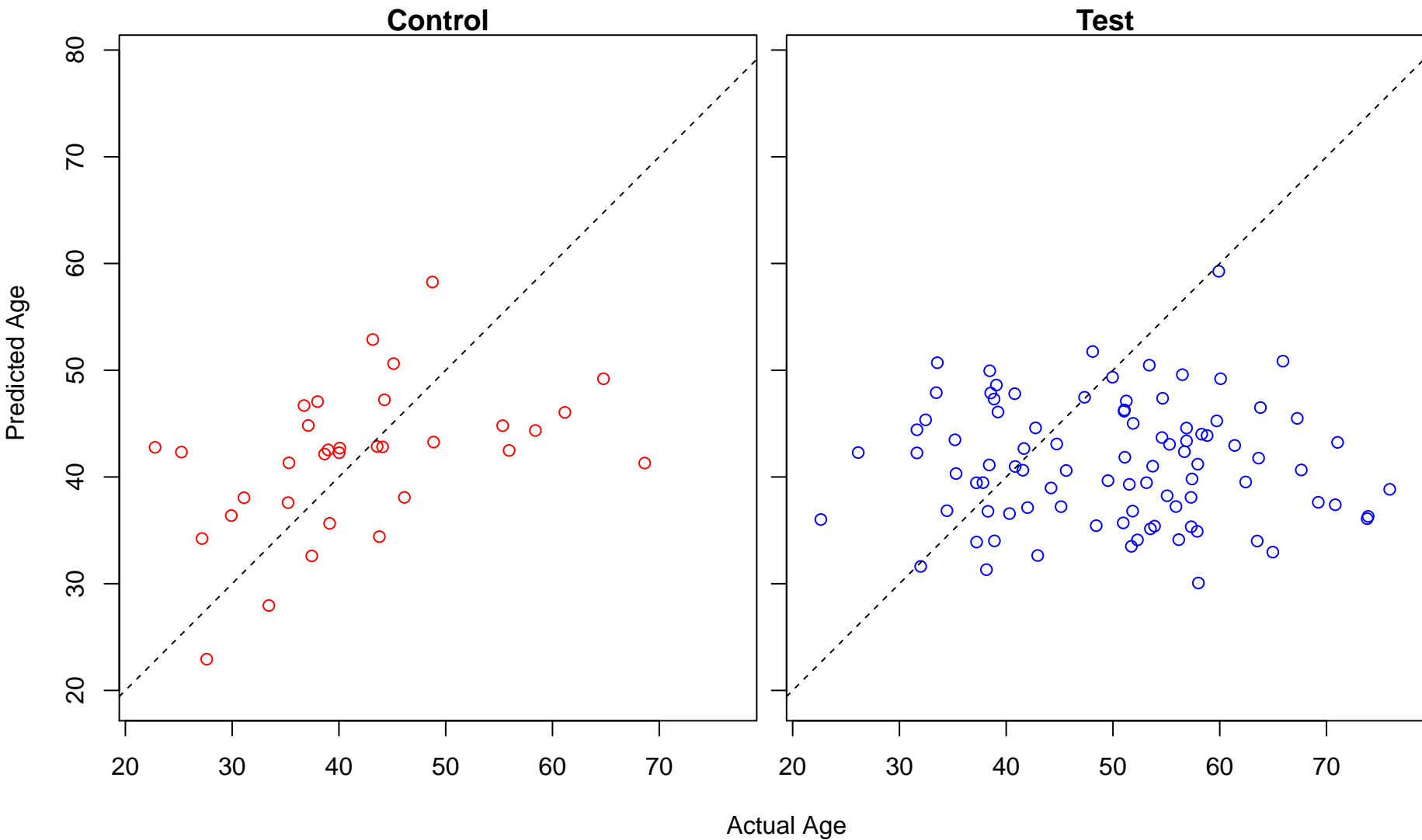
regulation of cellular response to hypoxia (Score: 0.758294)



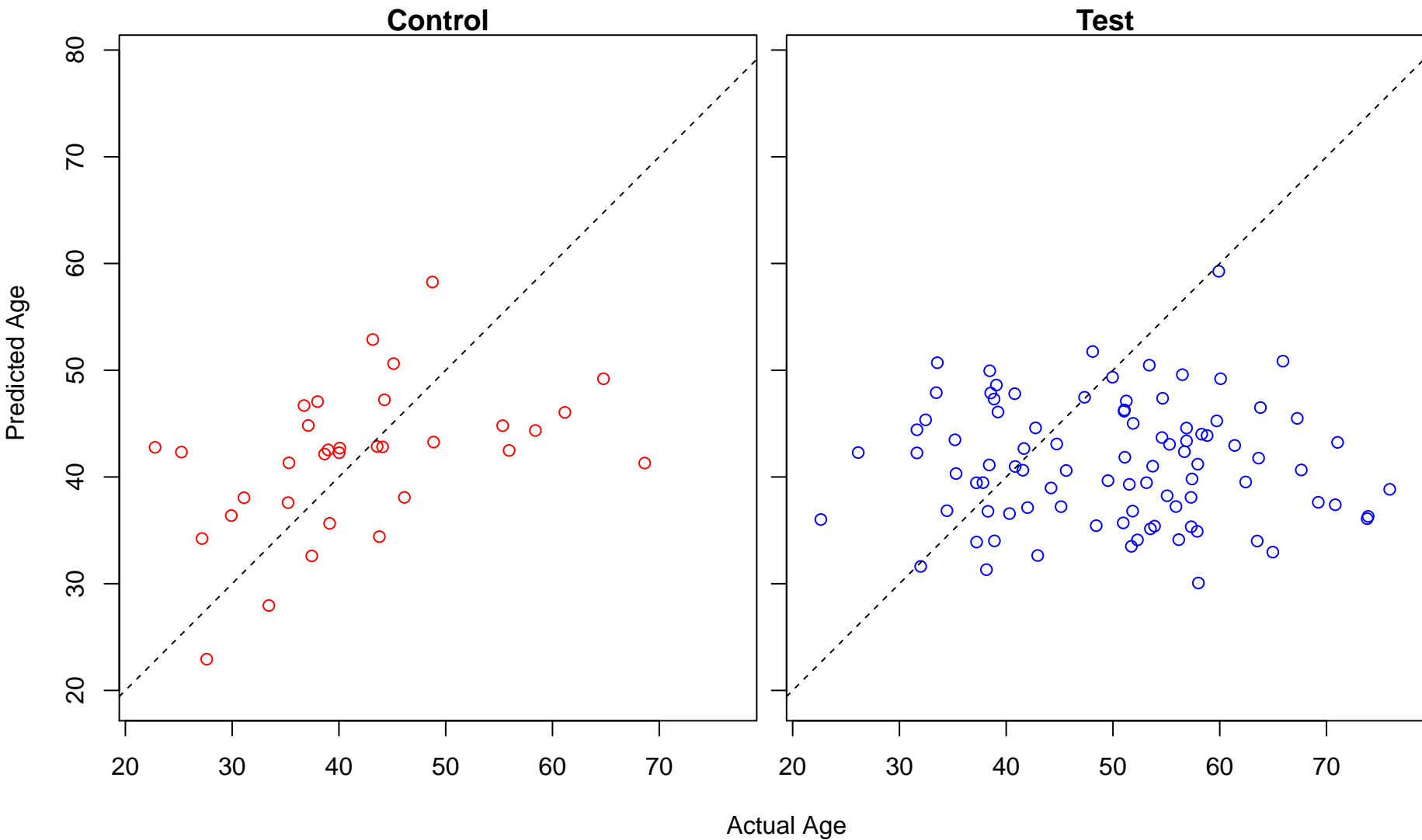
positive regulation of chemokine (C-X-C motif) ligand 2 production (Score: 0.757845)



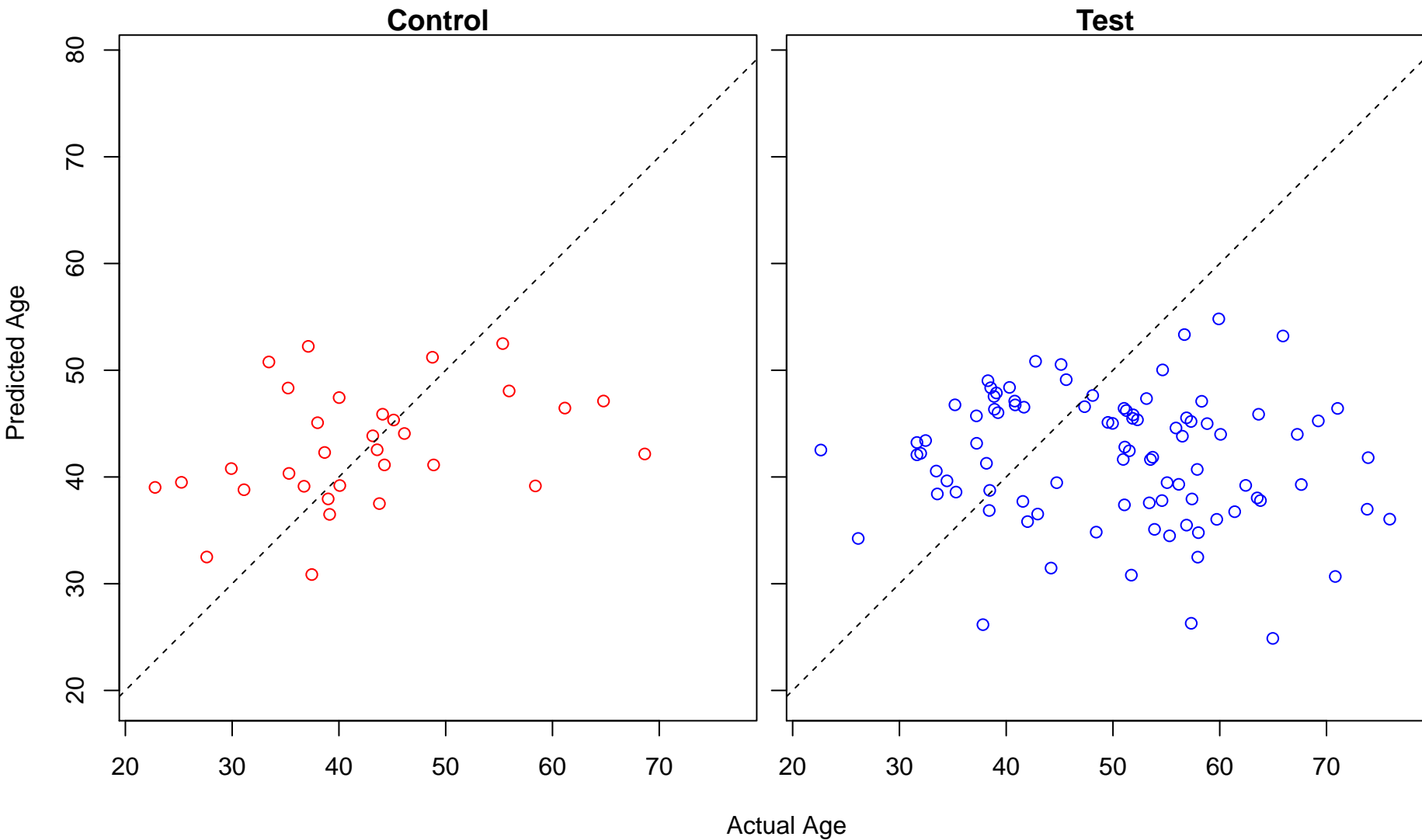
regulation of immunoglobulin secretion (Score: 0.757768)



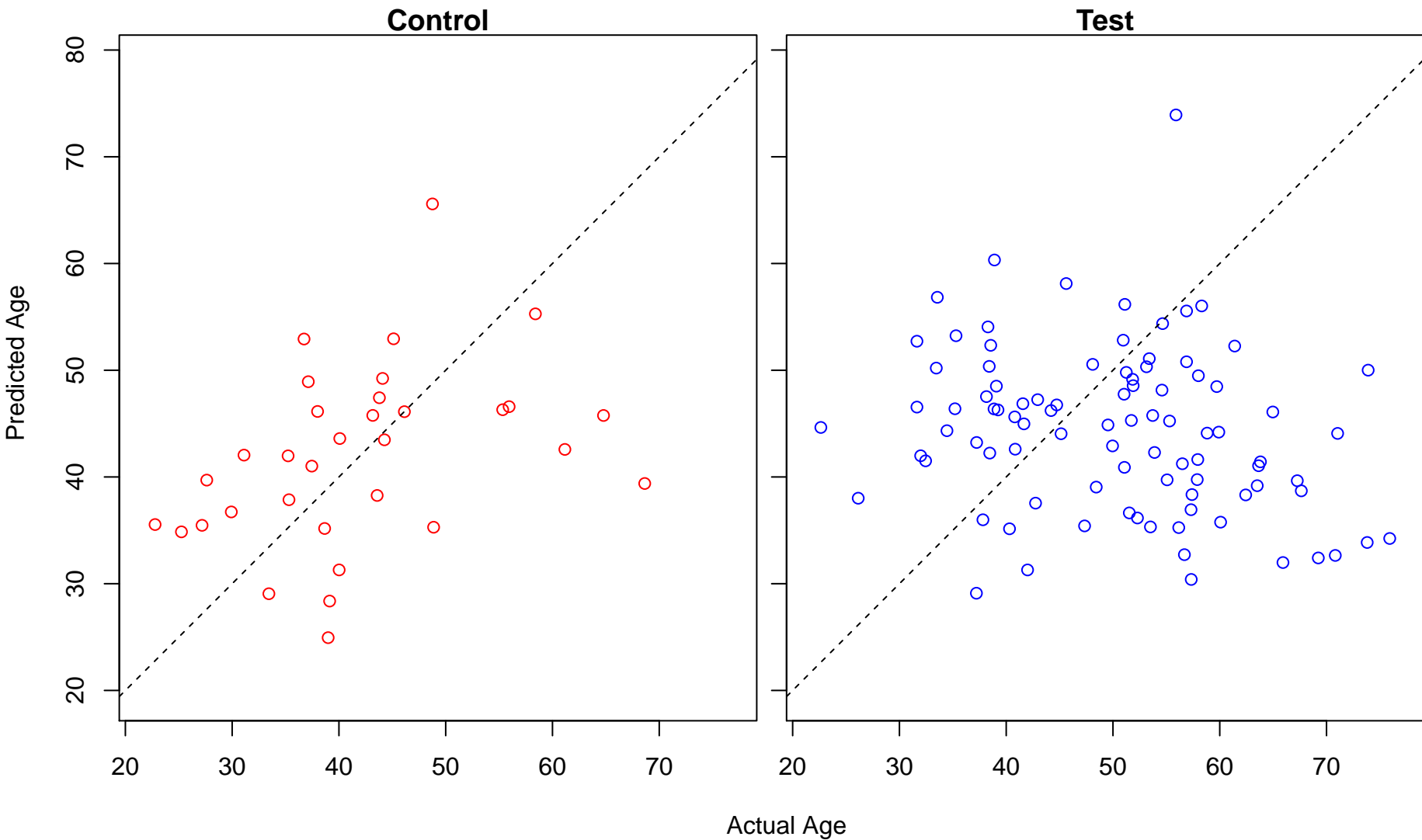
positive regulation of immunoglobulin secretion (Score: 0.757768)



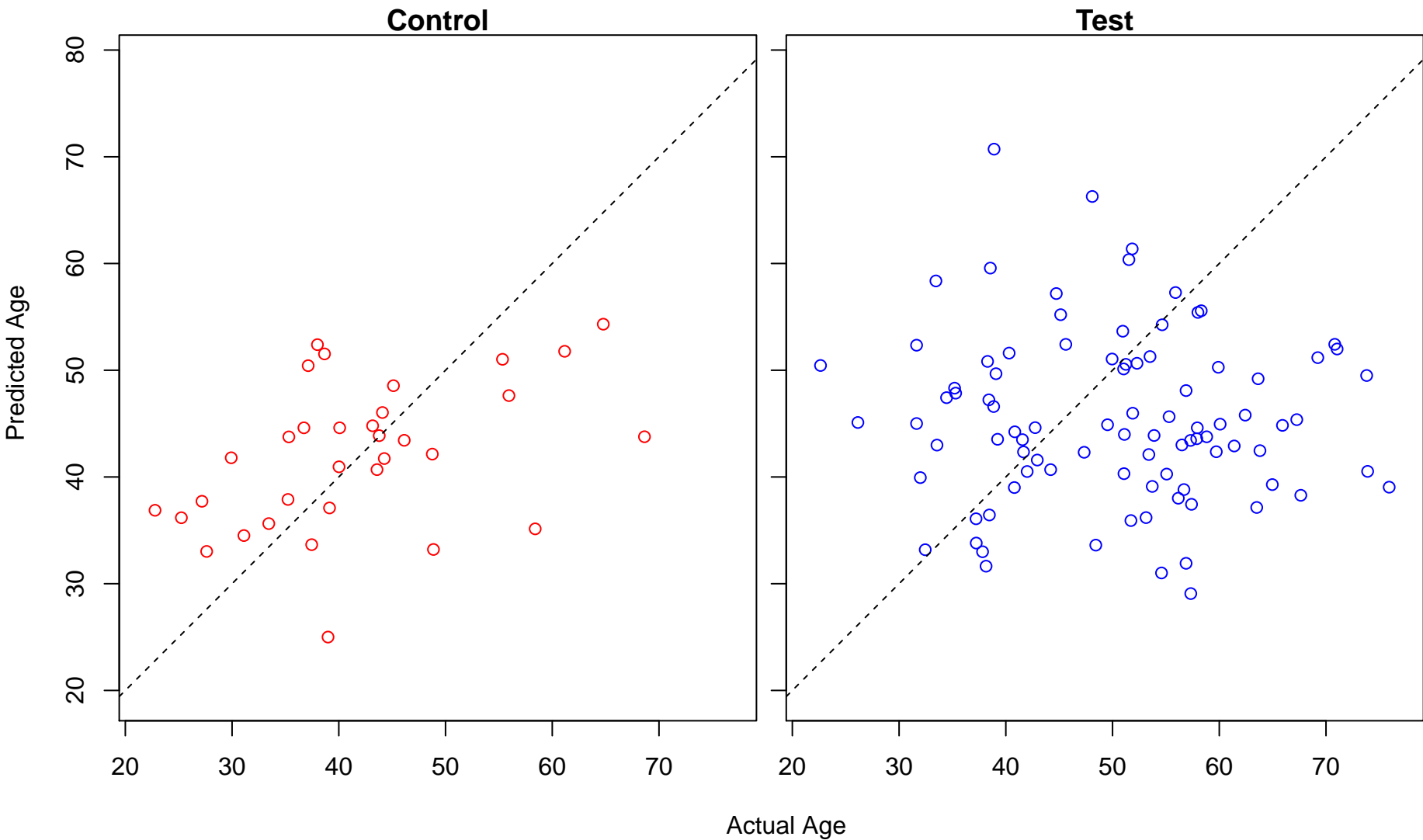
regulation of the force of heart contraction (Score: 0.756958)



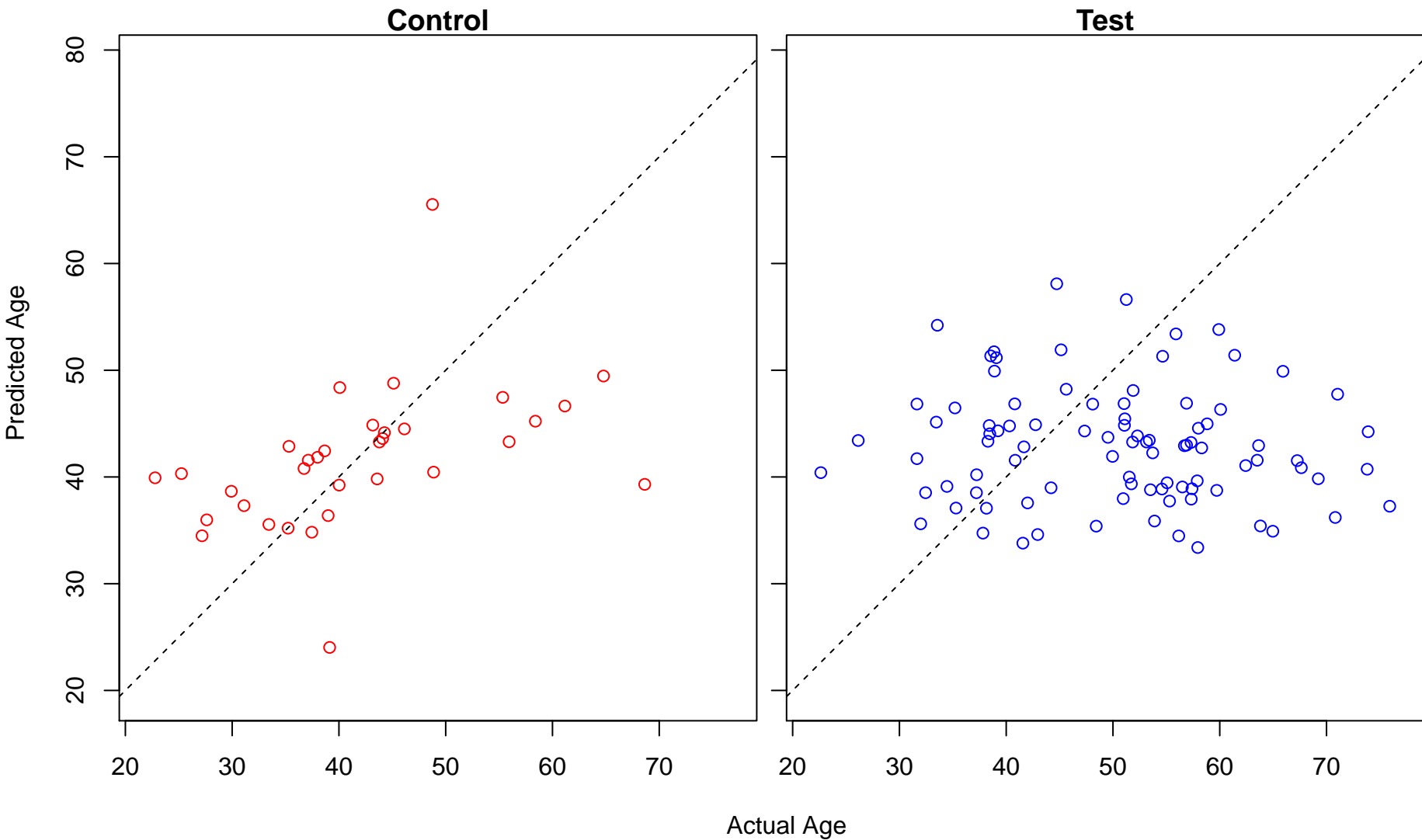
endothelial tube morphogenesis (Score: 0.756580)



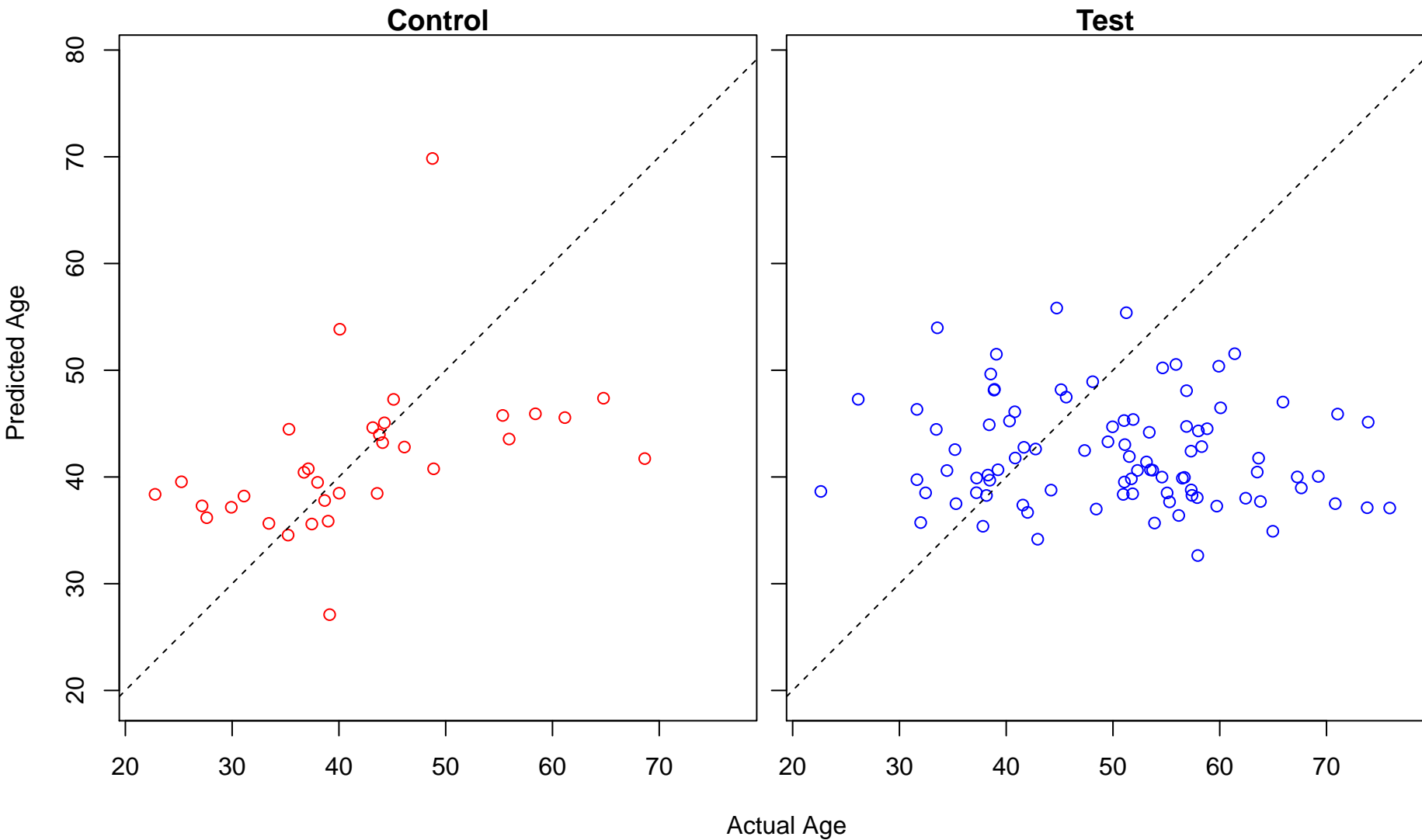
regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity (Score: 0.7565)



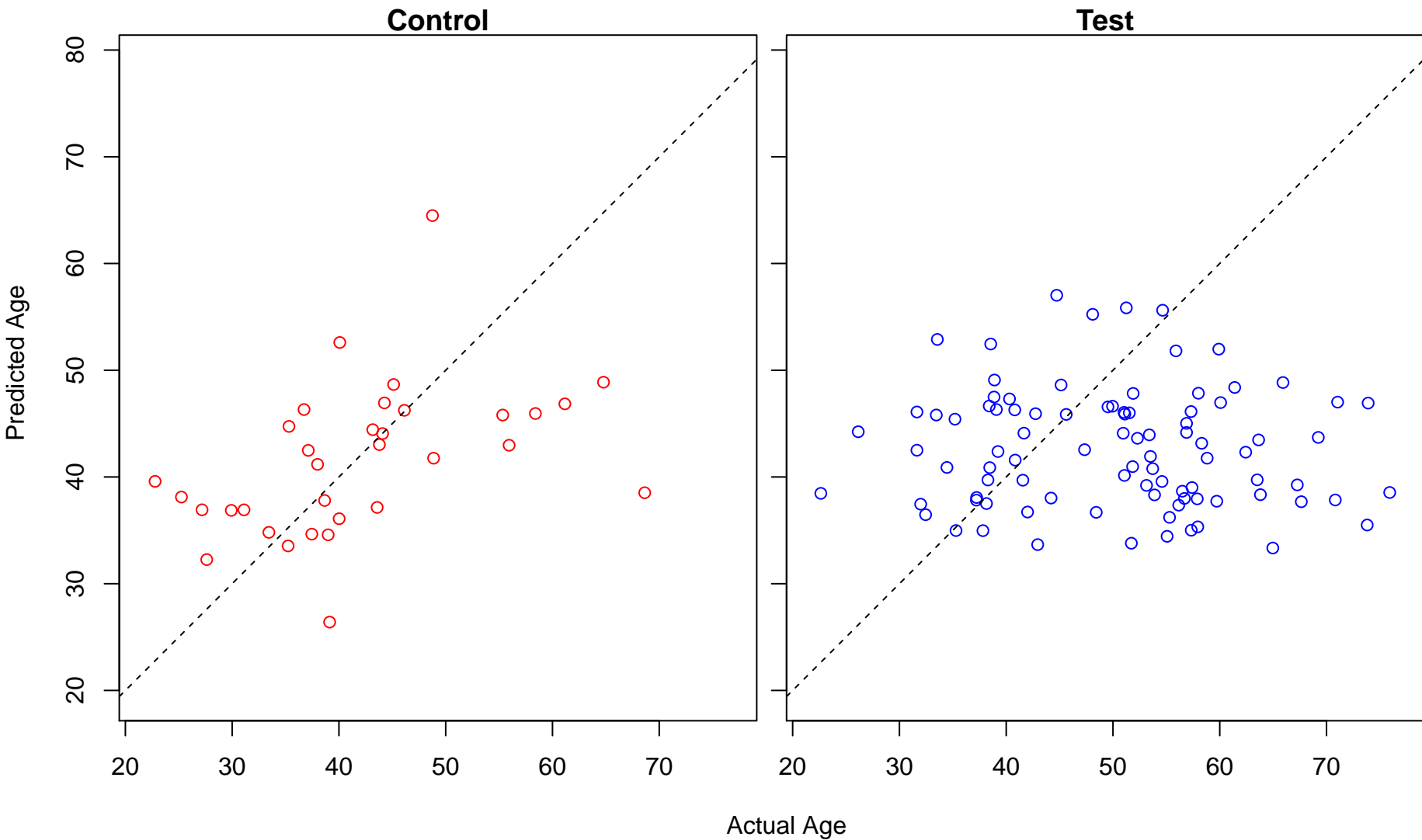
neuron differentiation (Score: 0.756086)



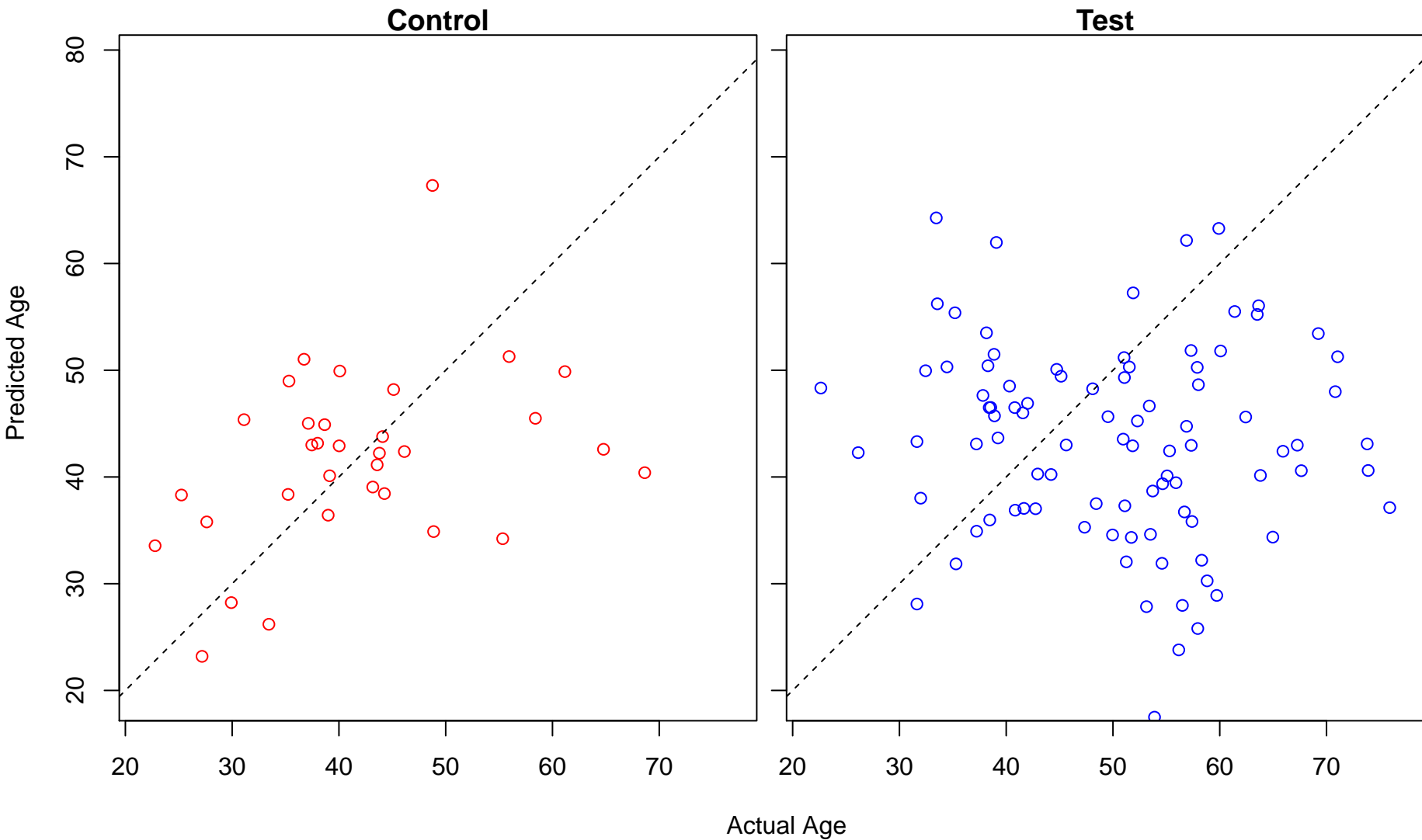
negative regulation of nitrogen compound metabolic process (Score: 0.756037)



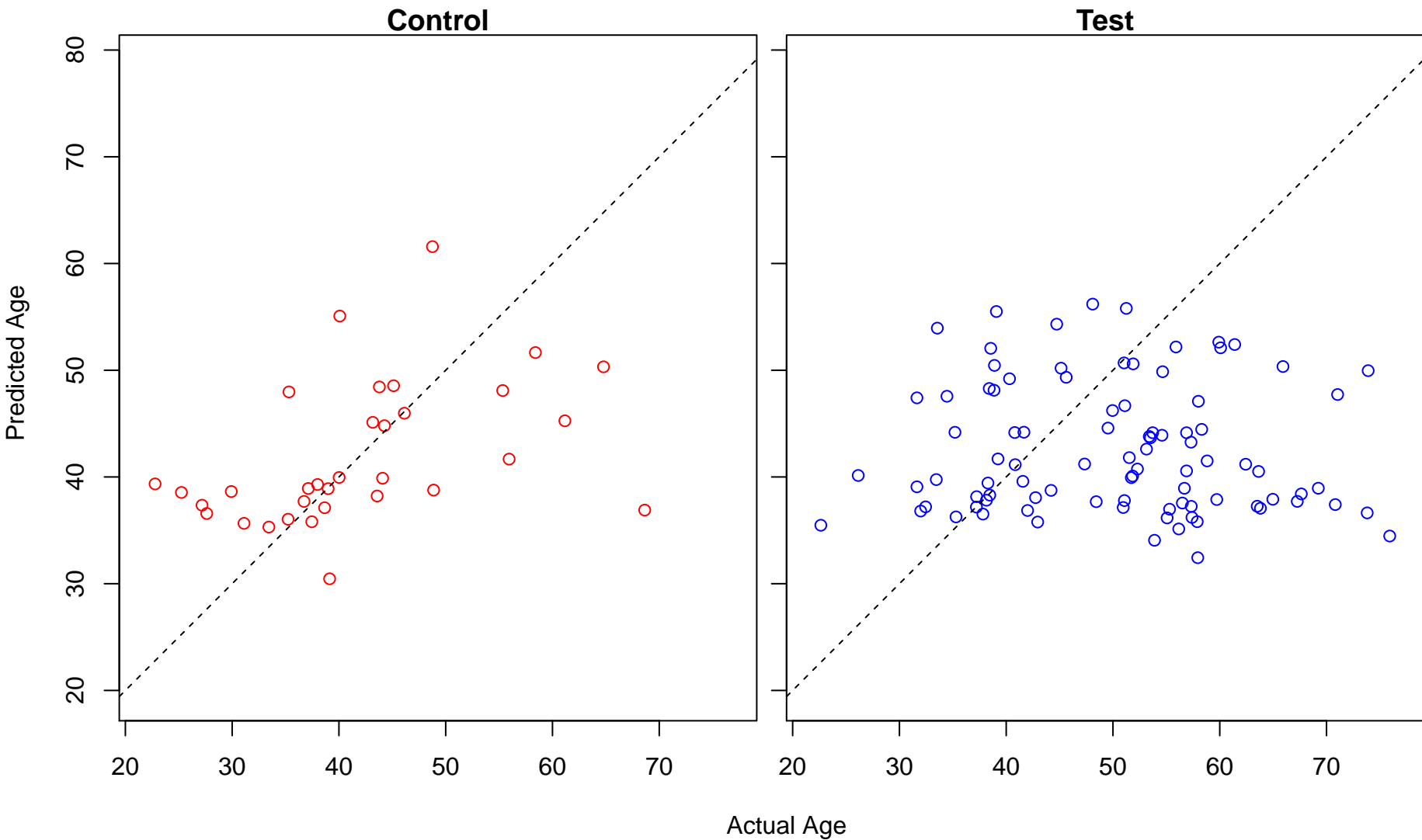
positive regulation of catabolic process (Score: 0.755930)



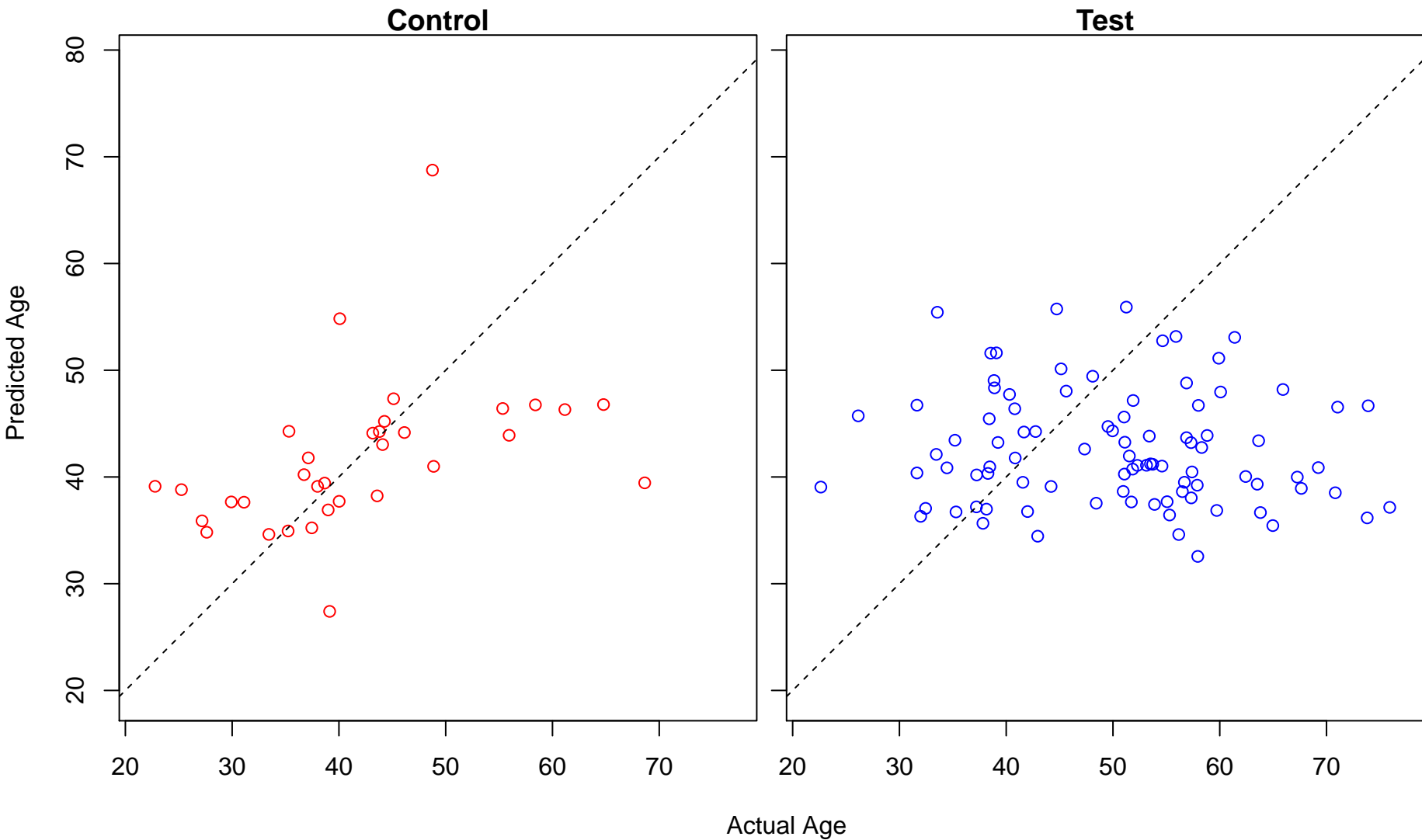
cellular response to xenobiotic stimulus (Score: 0.754204)



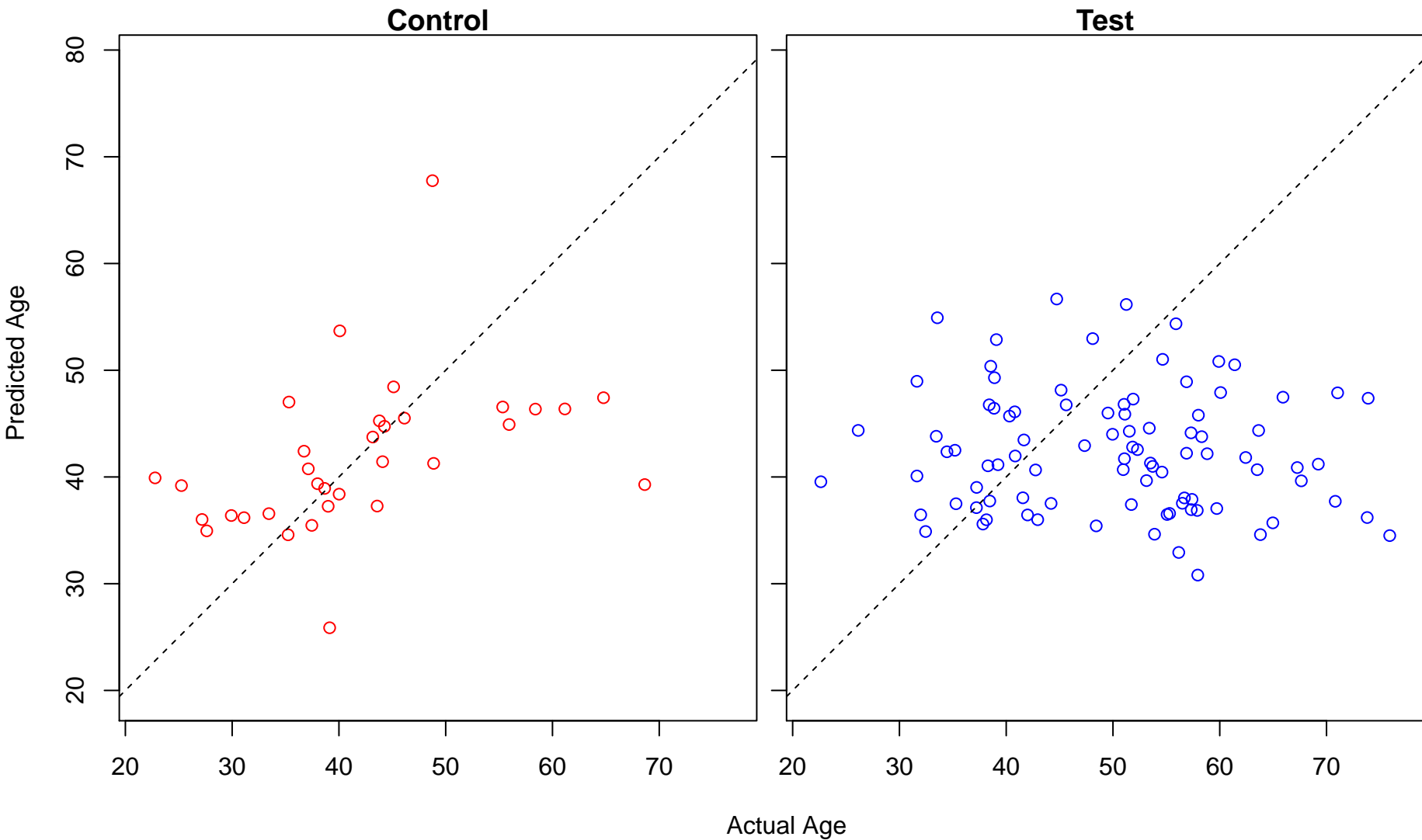
transcription from RNA polymerase III promoter (Score: 0.753972)



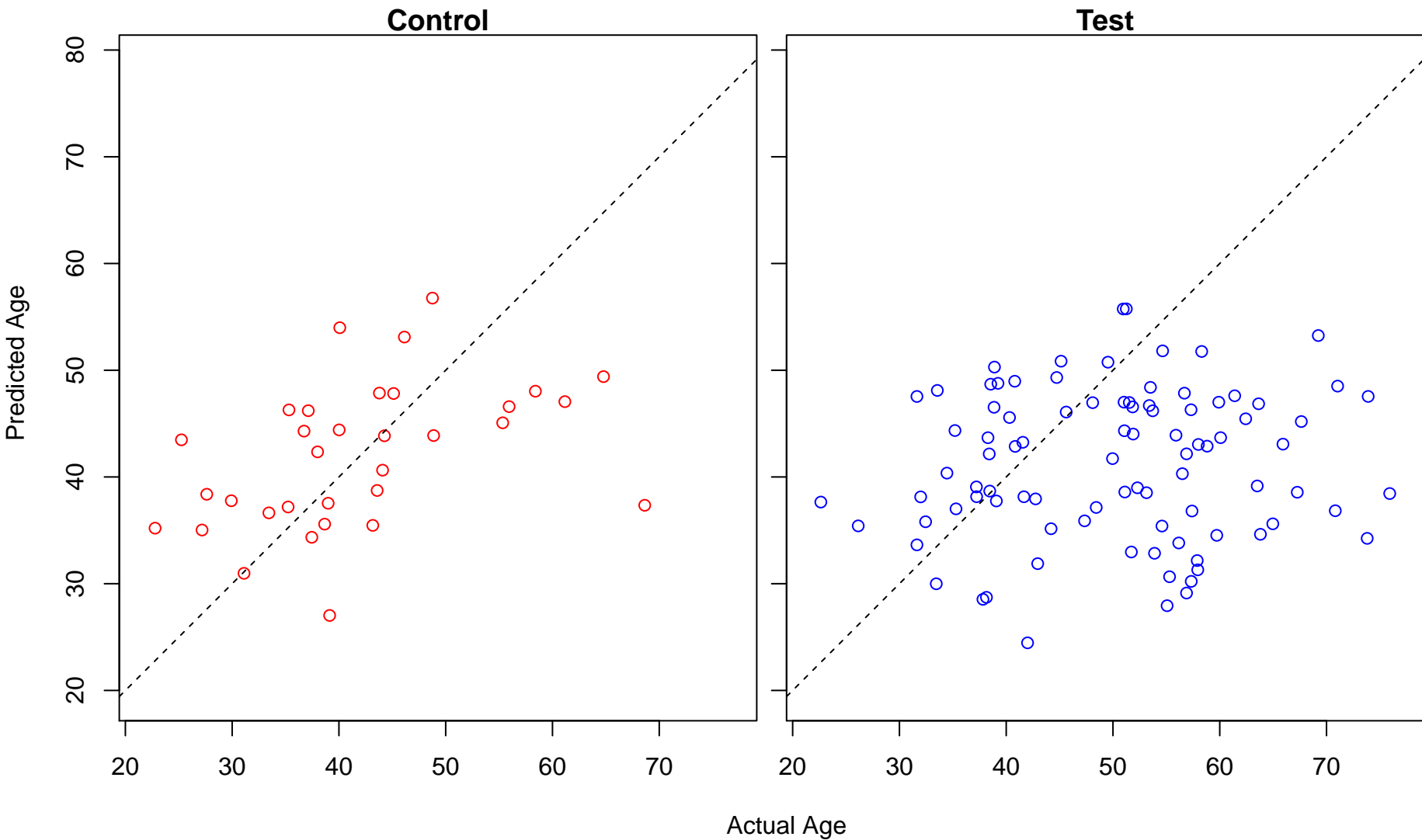
negative regulation of protein metabolic process (Score: 0.753816)



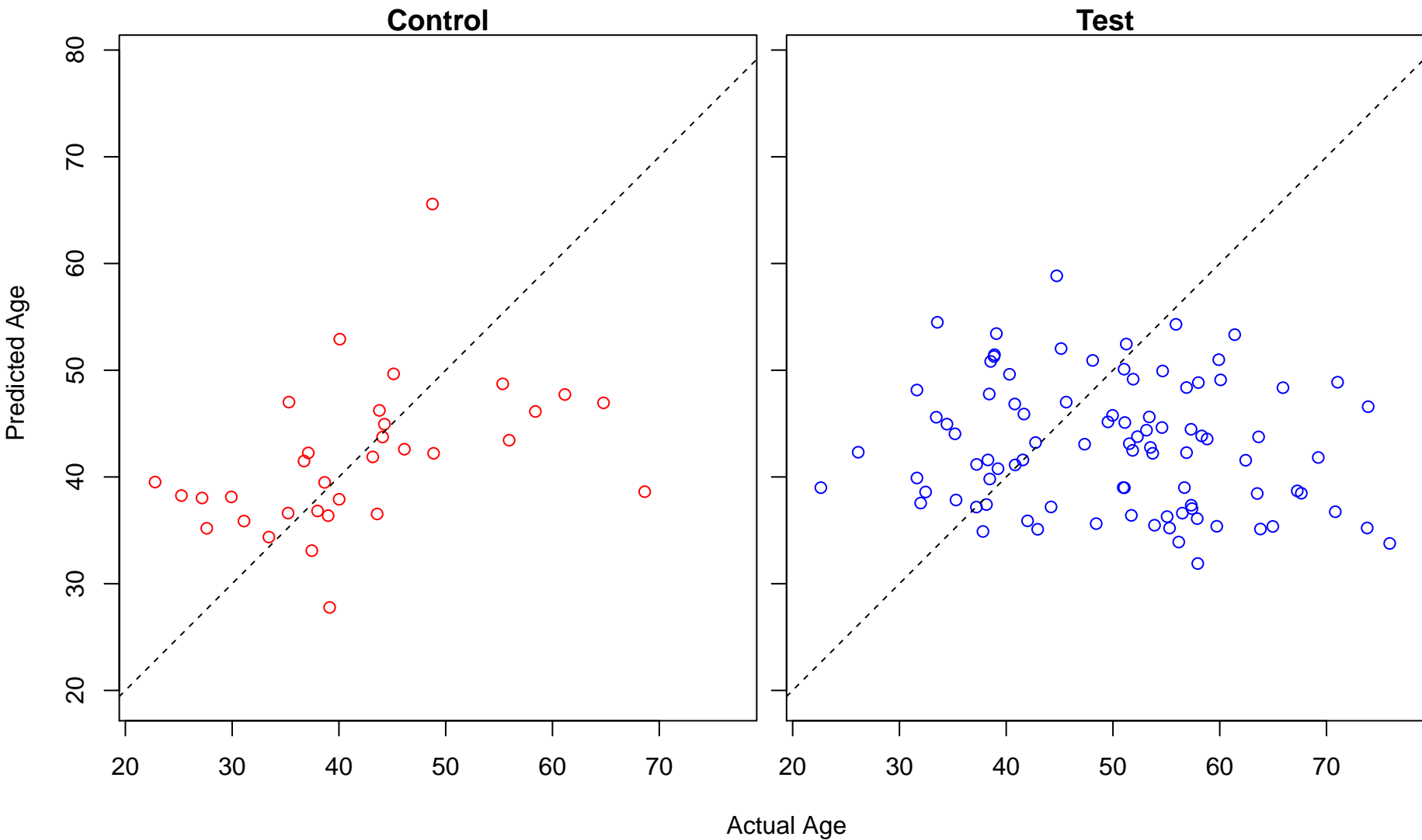
ncRNA metabolic process (Score: 0.753282)



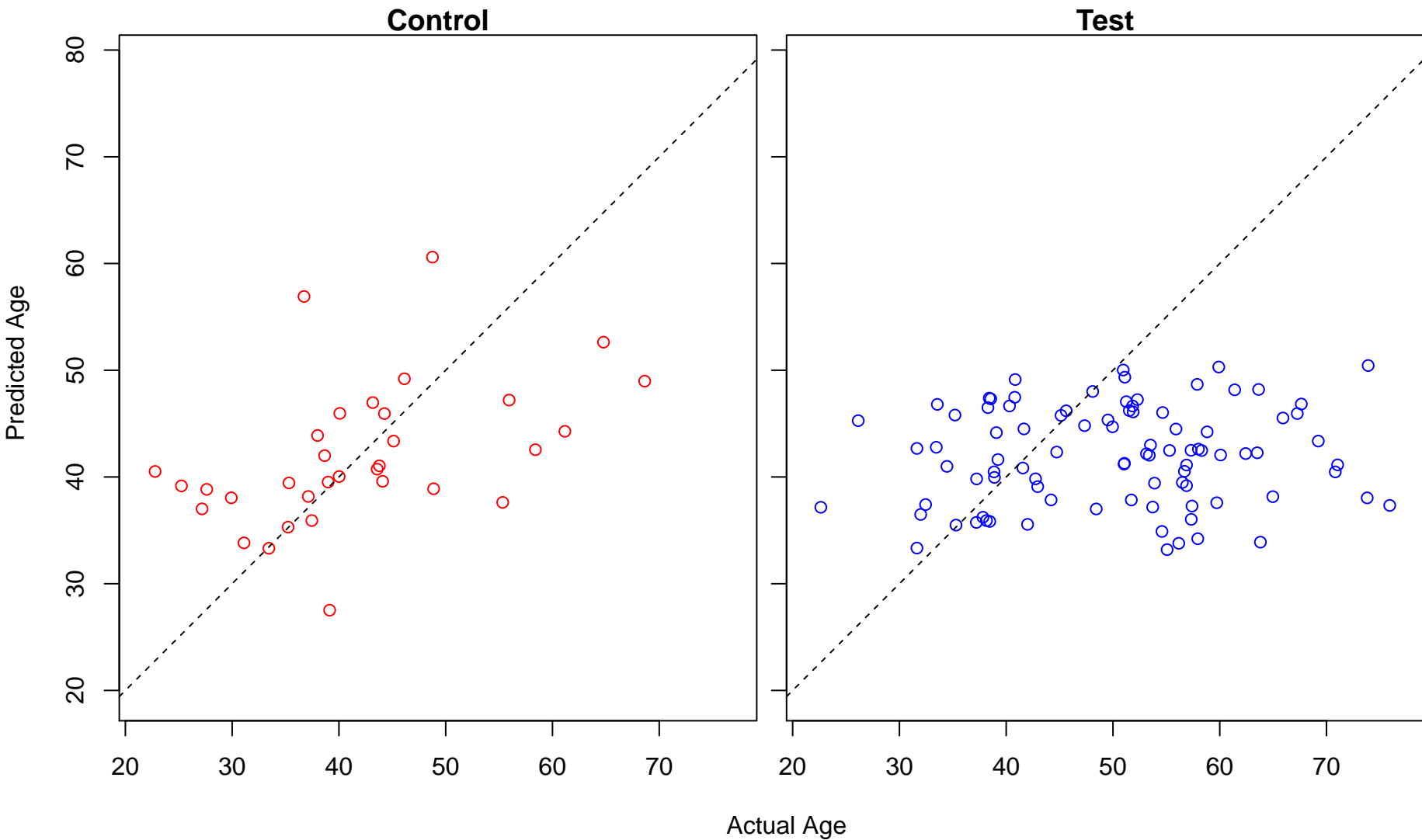
early endosome to Golgi transport (Score: 0.752822)



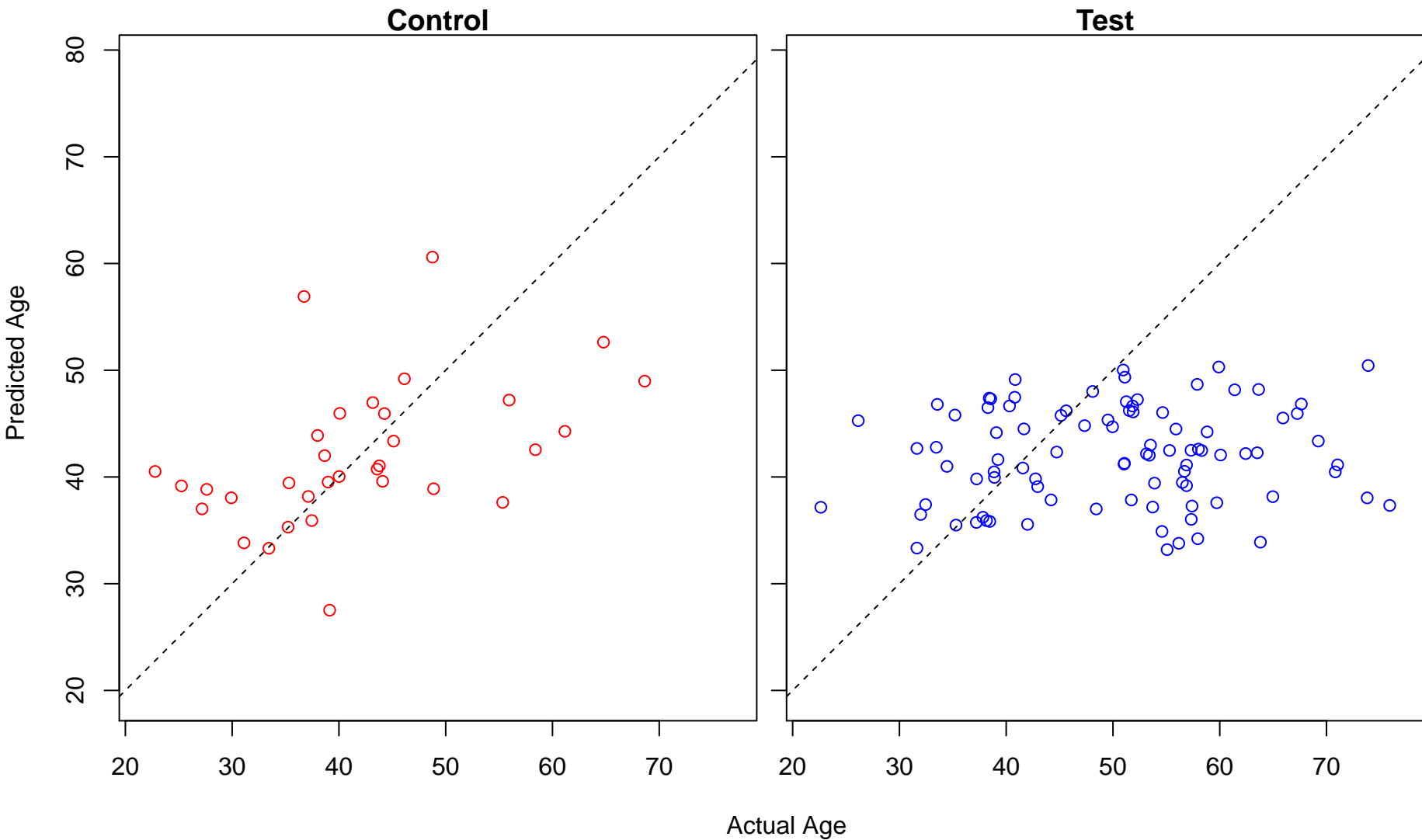
positive regulation of organelle organization (Score: 0.752811)



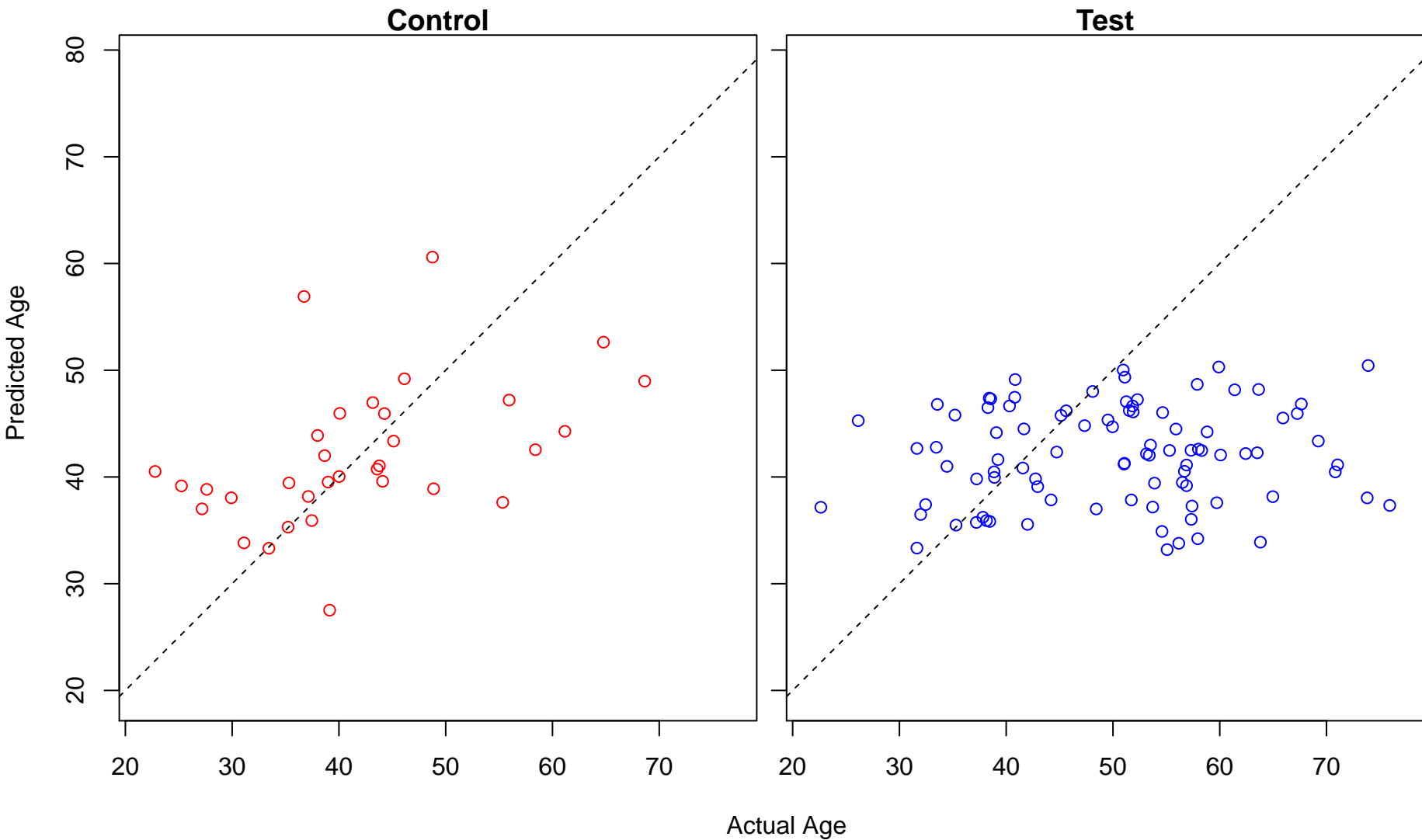
regulation of ribosome biogenesis (Score: 0.752196)



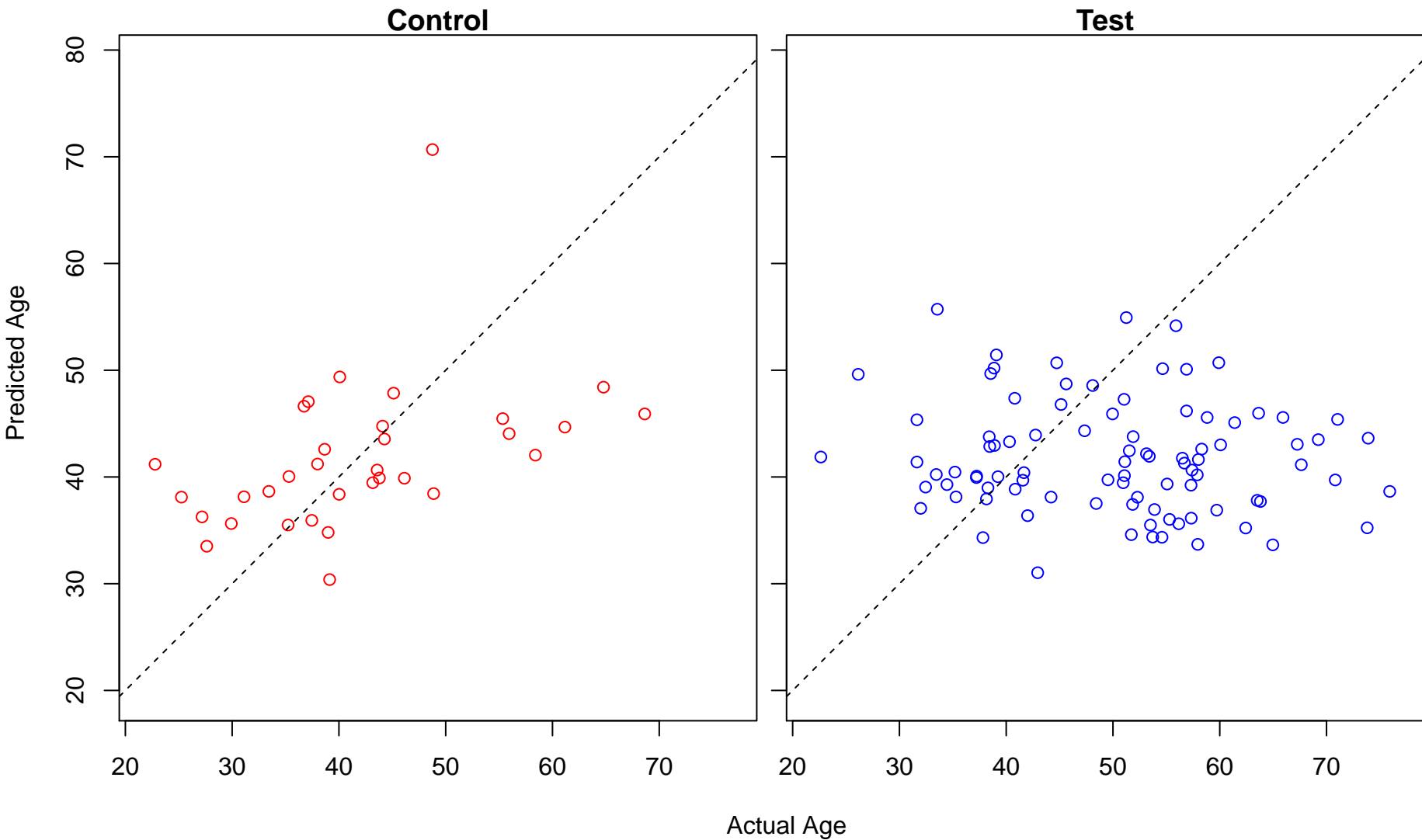
regulation of rRNA processing (Score: 0.752196)



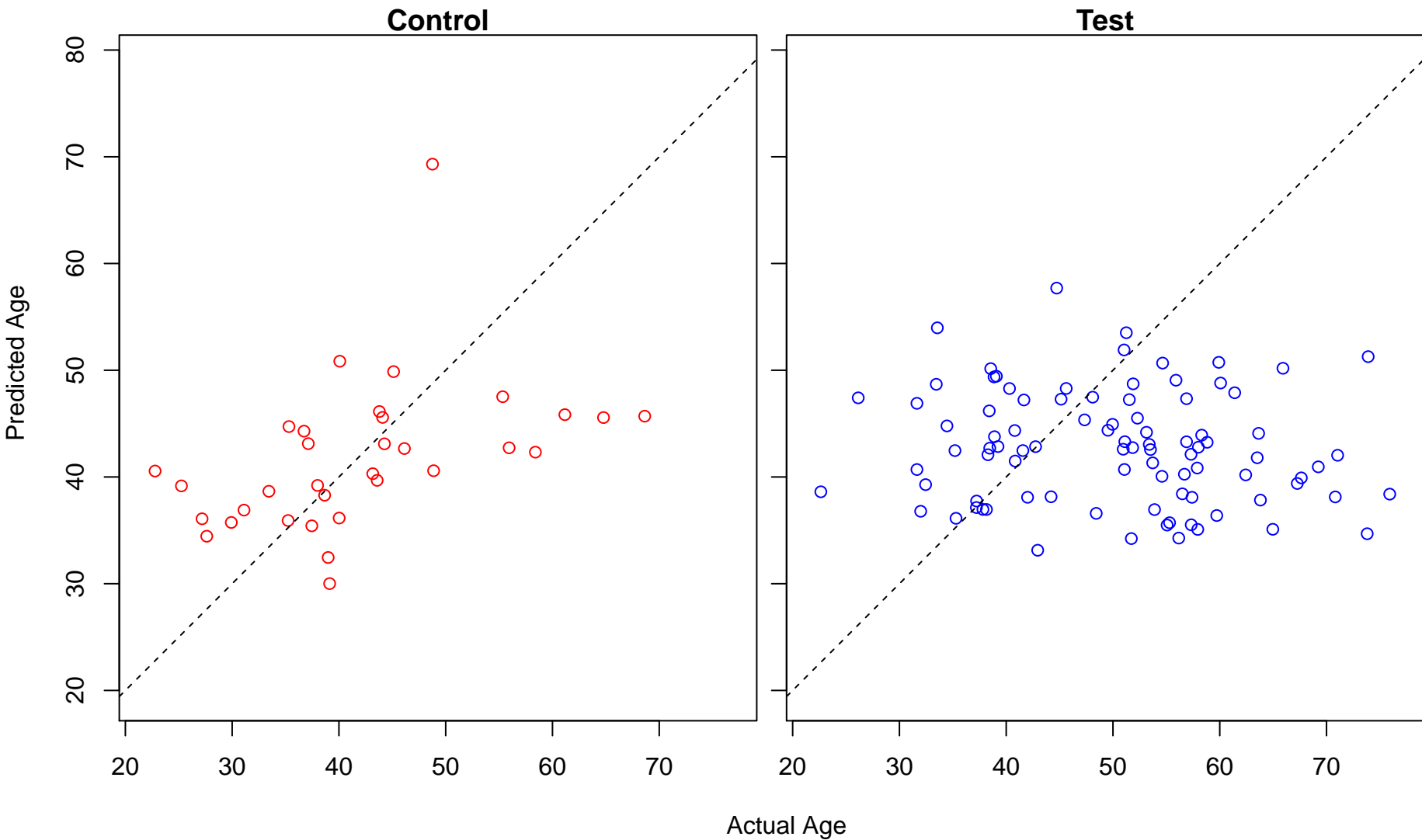
negative regulation of rRNA processing (Score: 0.752196)



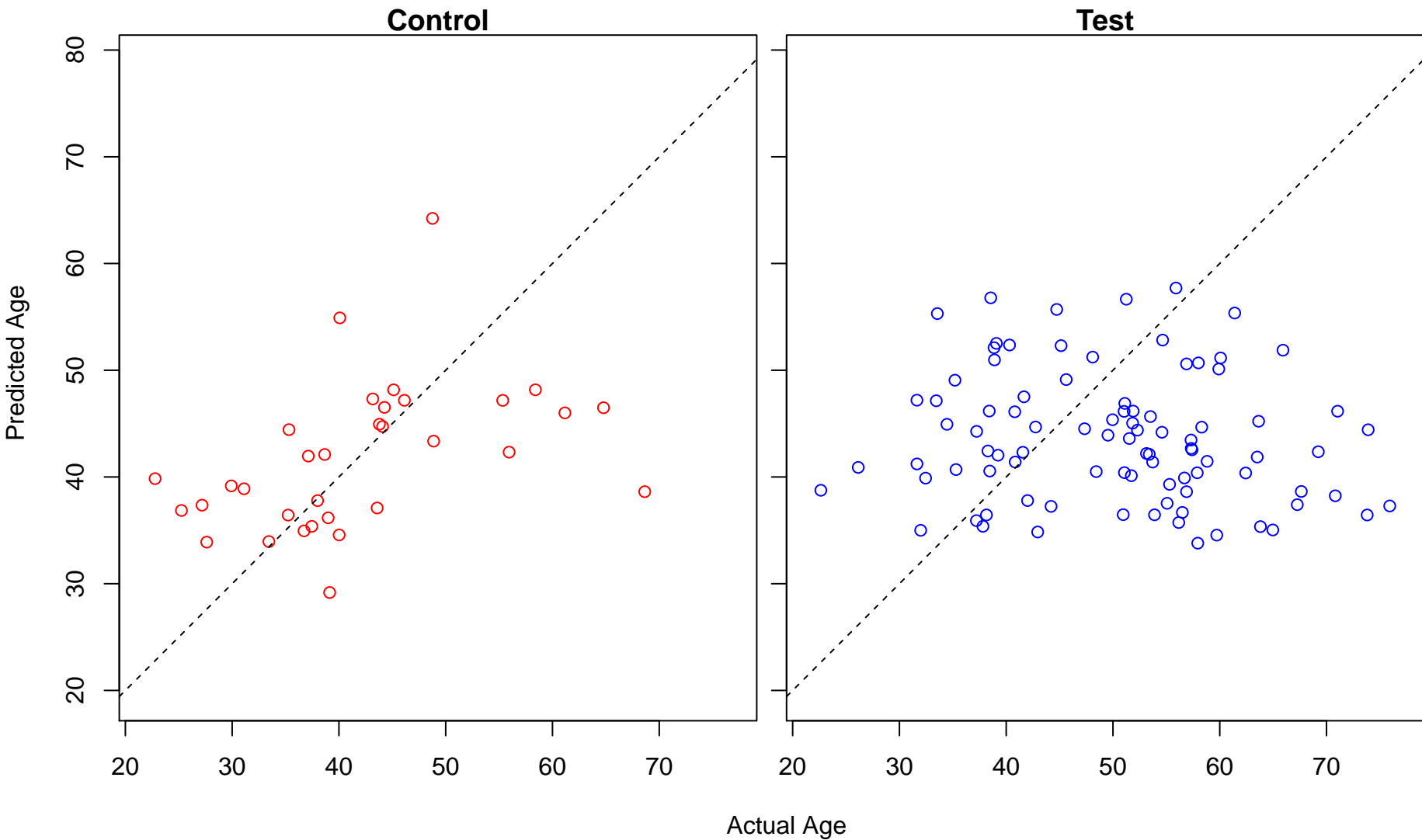
wound healing (Score: 0.751936)



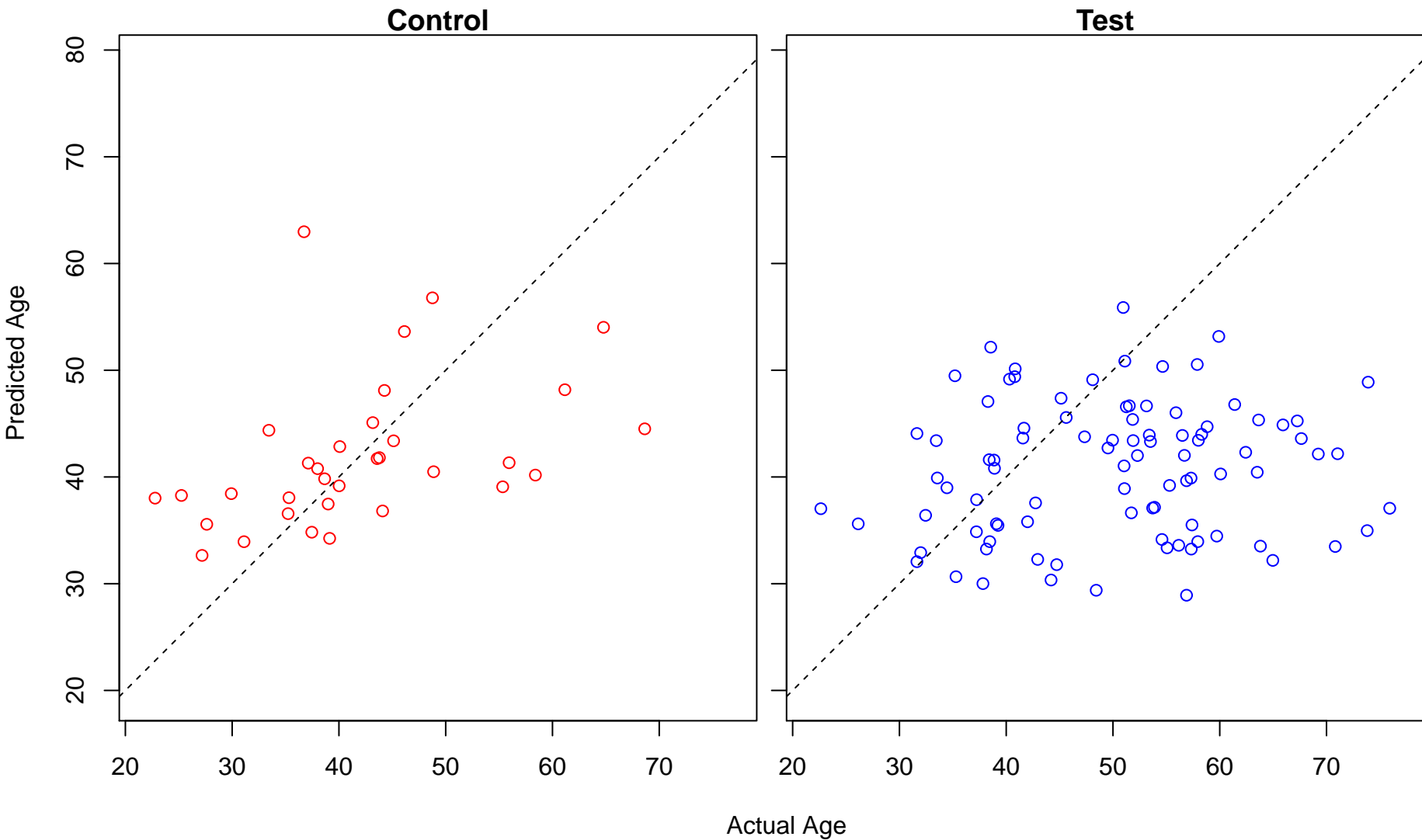
regulation of protein complex assembly (Score: 0.751791)



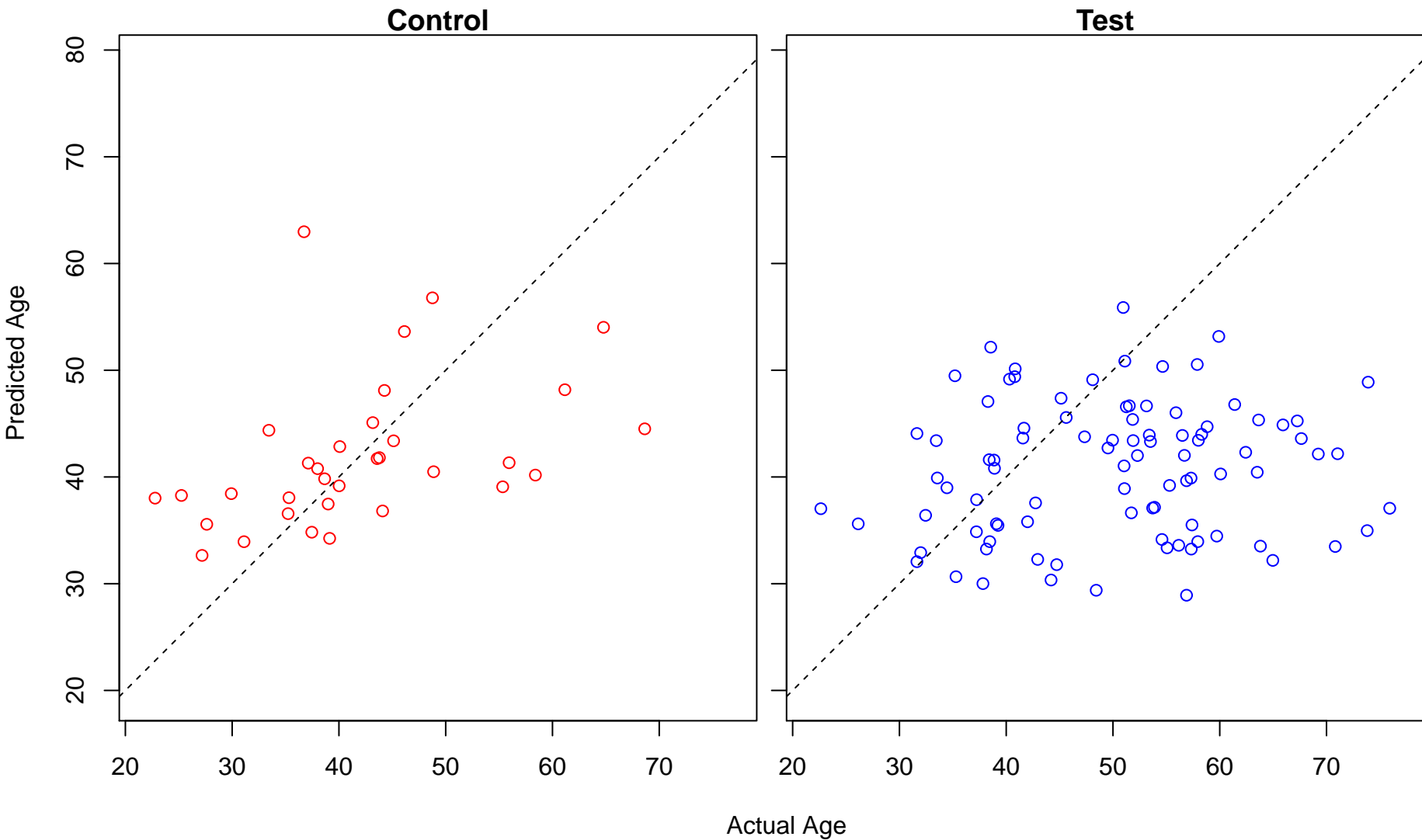
negative regulation of cellular catabolic process (Score: 0.751605)



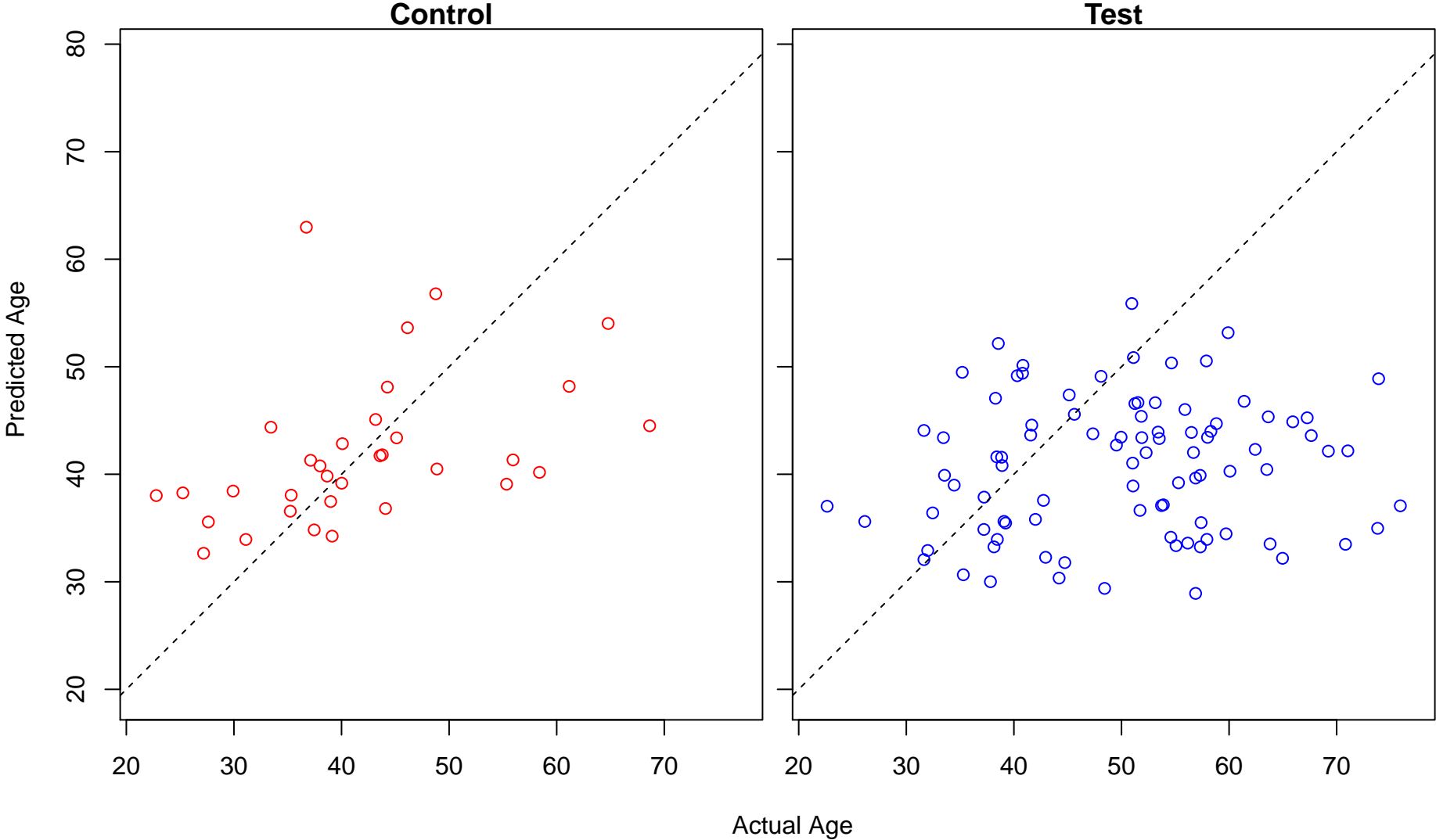
purine nucleoside triphosphate catabolic process (Score: 0.751356)



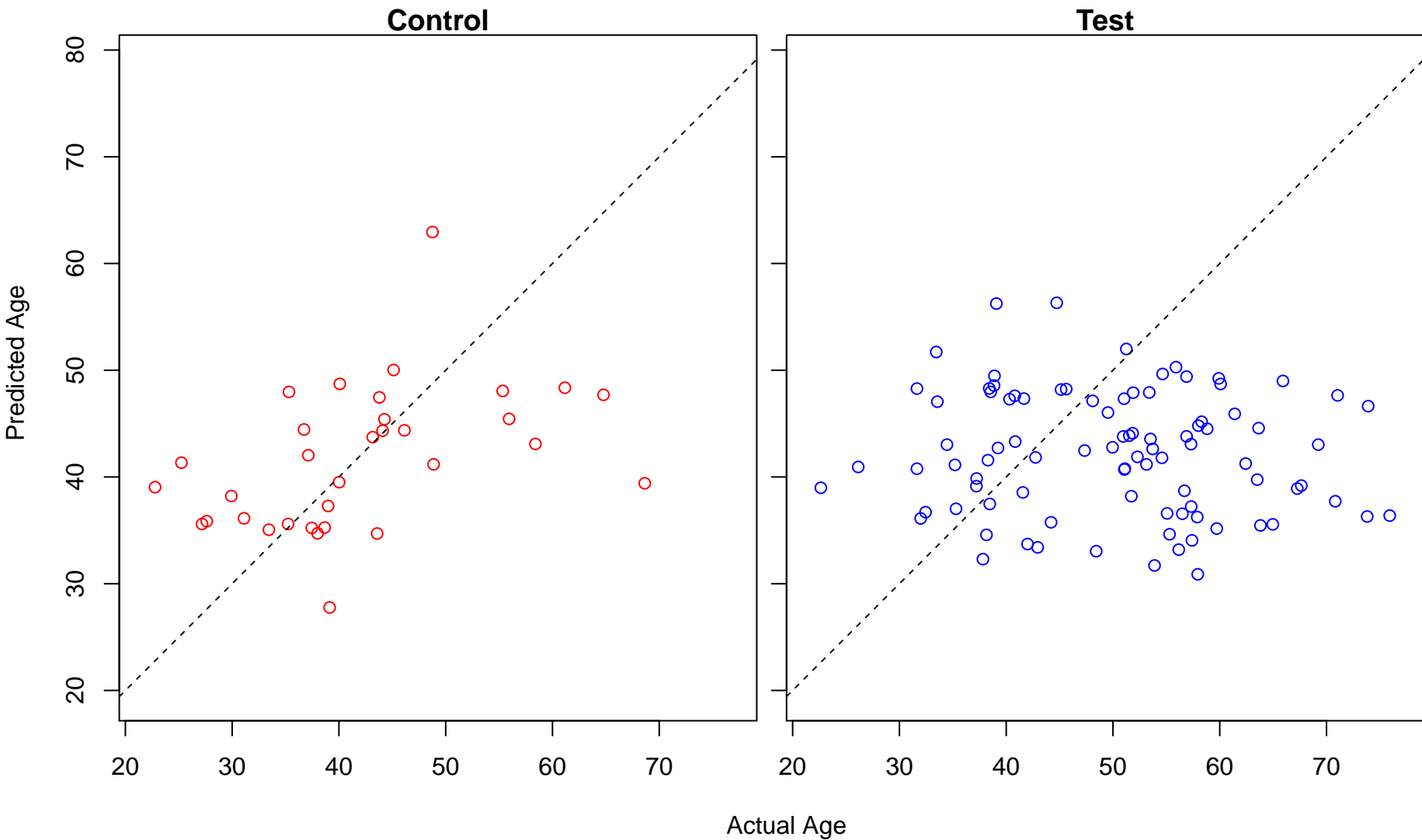
deoxyribonucleoside triphosphate catabolic process (Score: 0.751356)



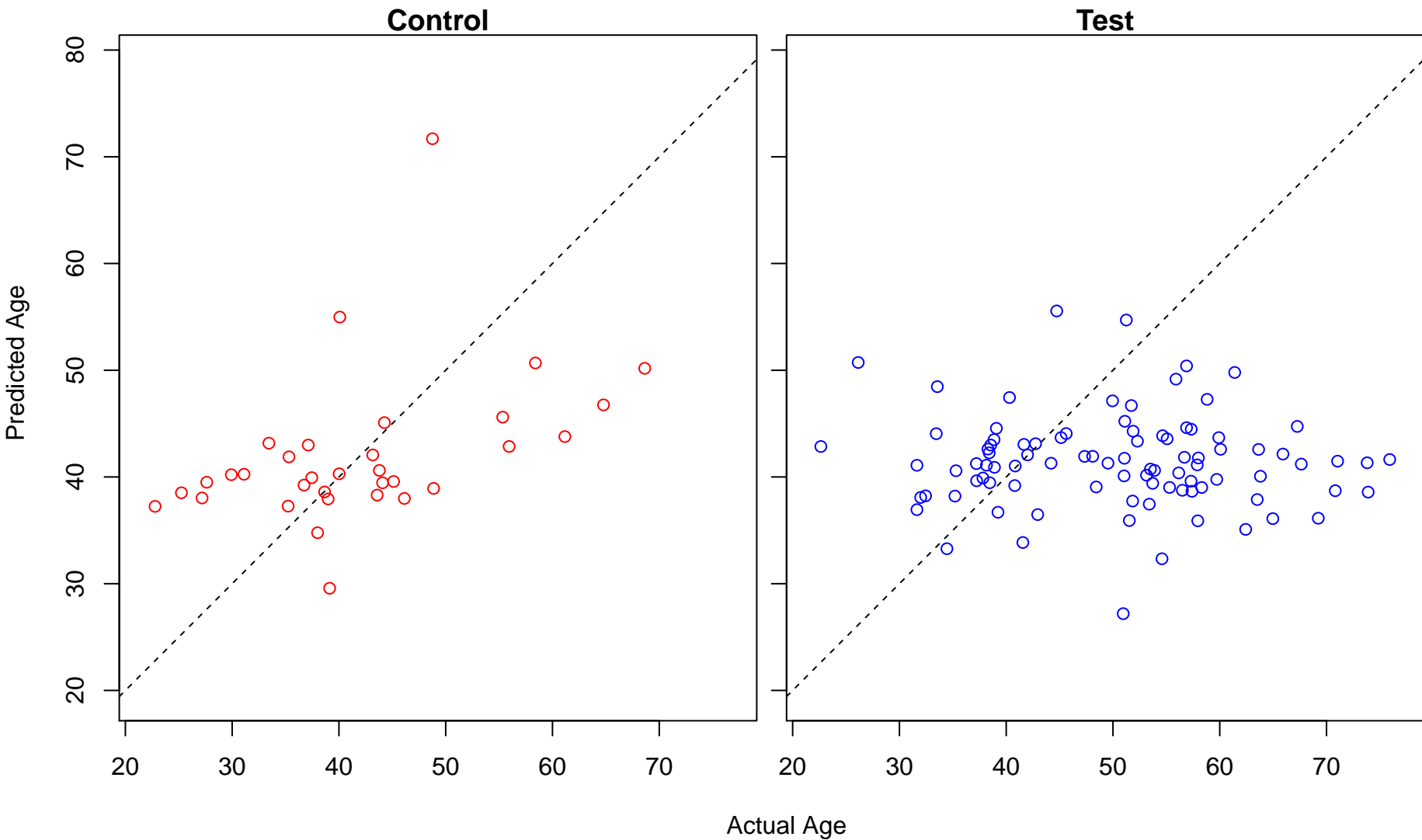
purine deoxyribonucleoside triphosphate catabolic process (Score: 0.751356)



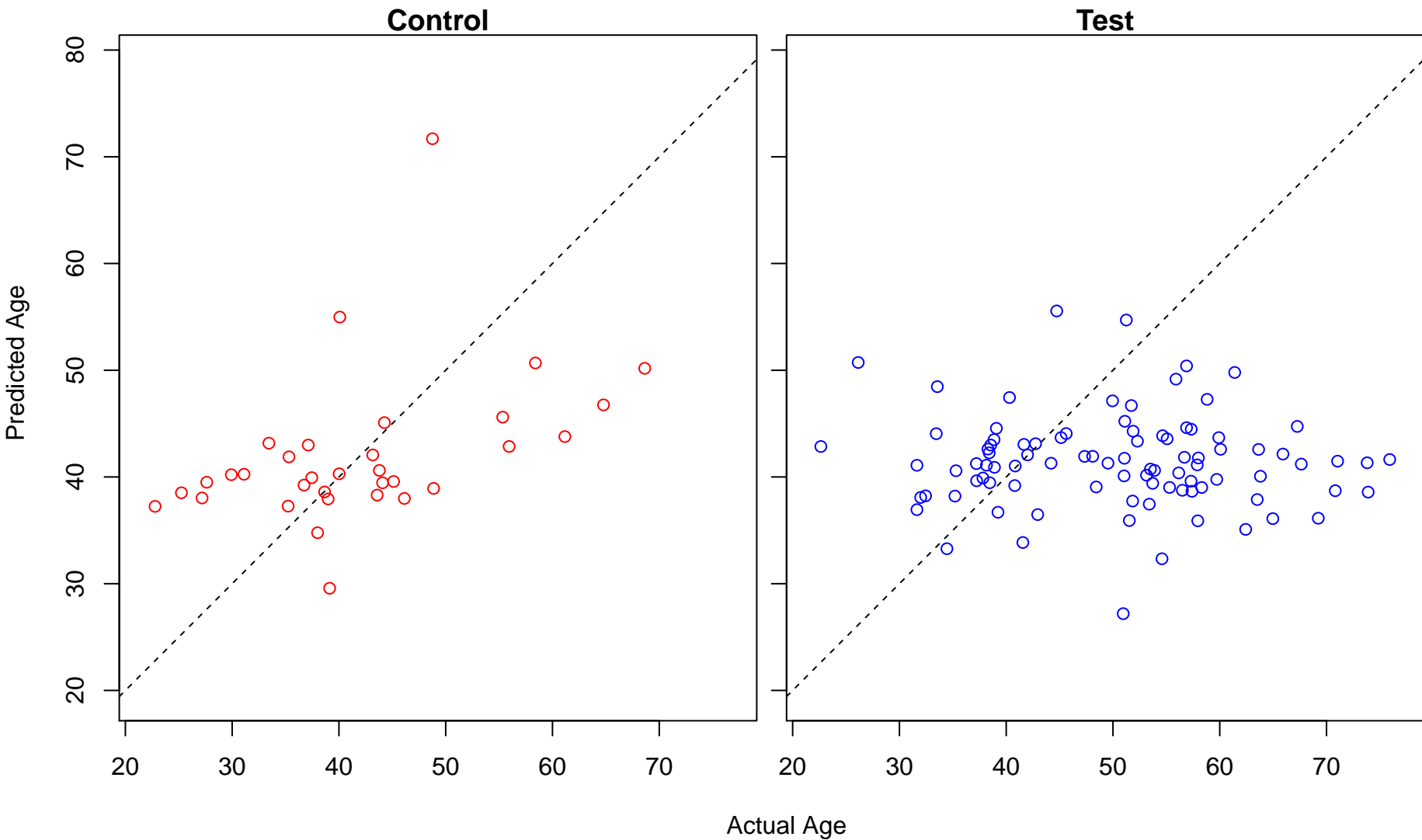
nuclear export (Score: 0.751256)



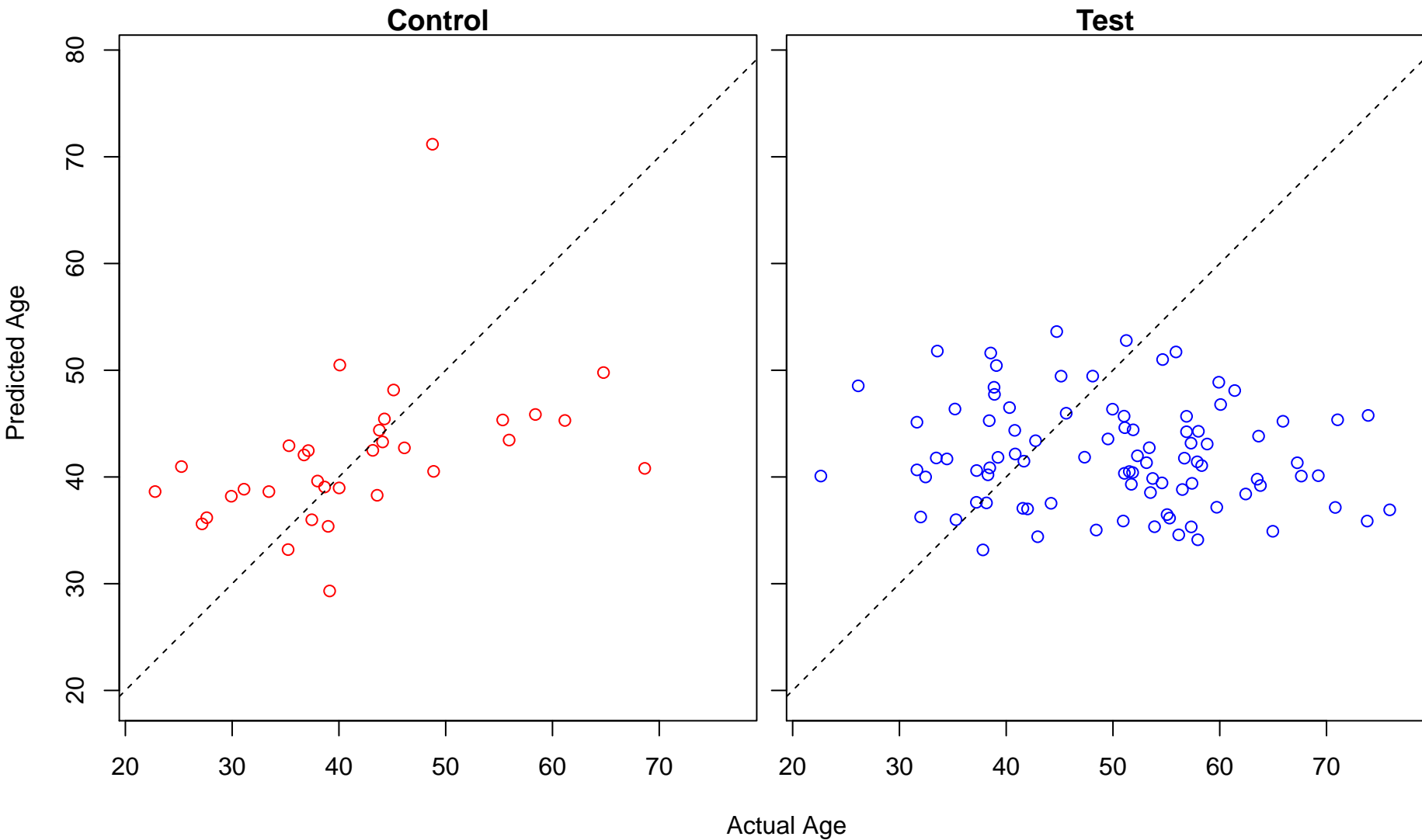
oxidative RNA demethylation (Score: 0.749890)



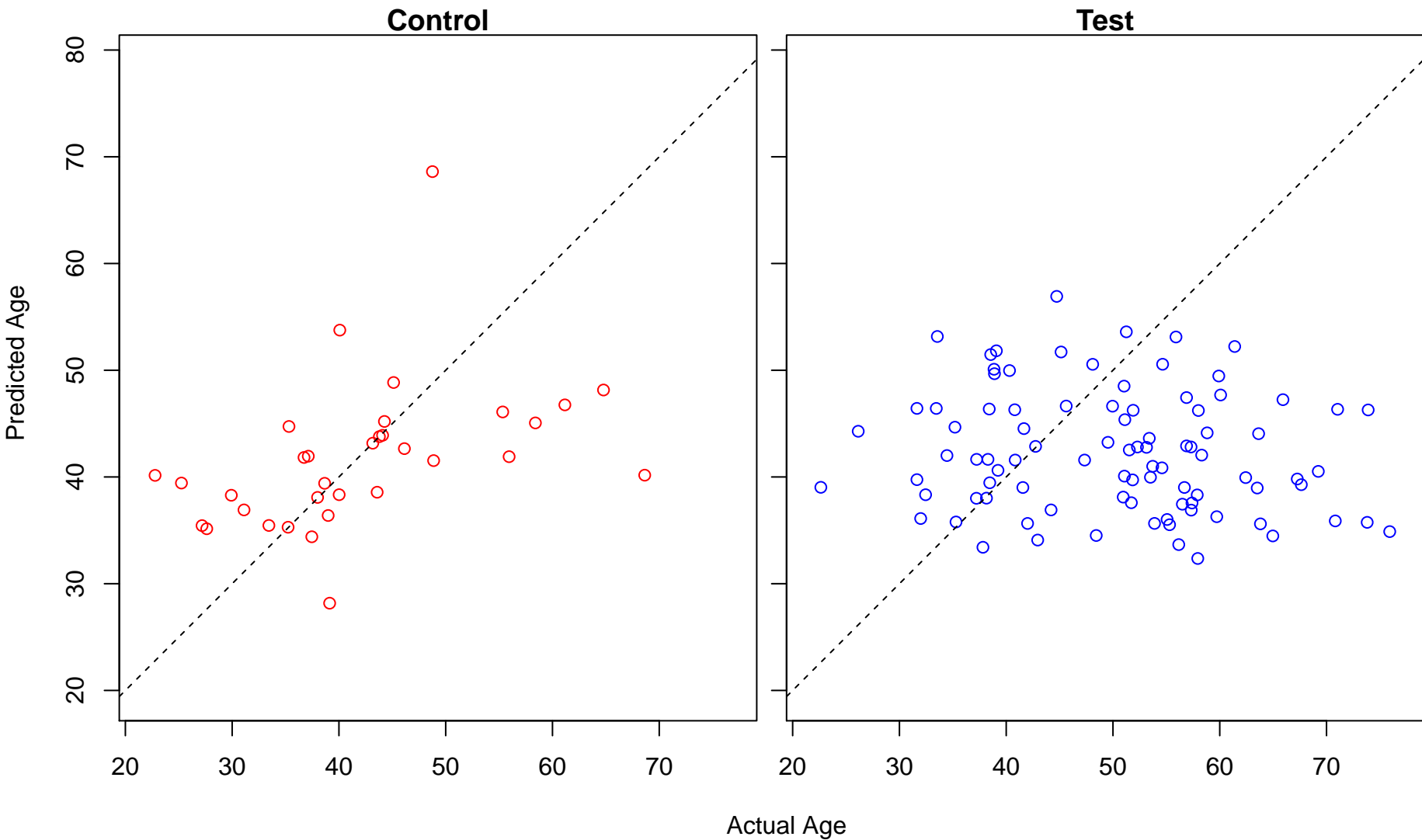
oxidative single-stranded RNA demethylation (Score: 0.749890)



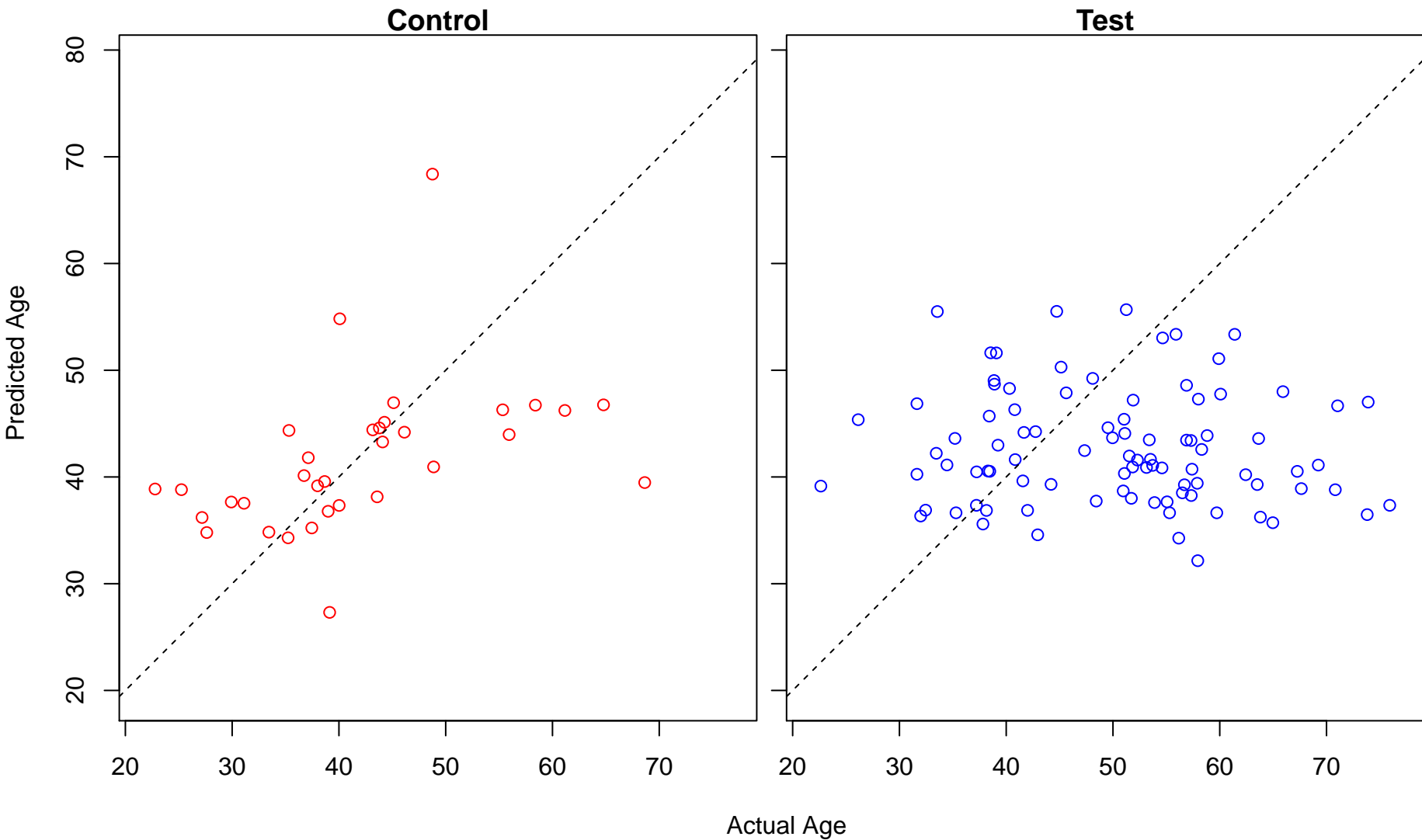
positive regulation of developmental process (Score: 0.749865)



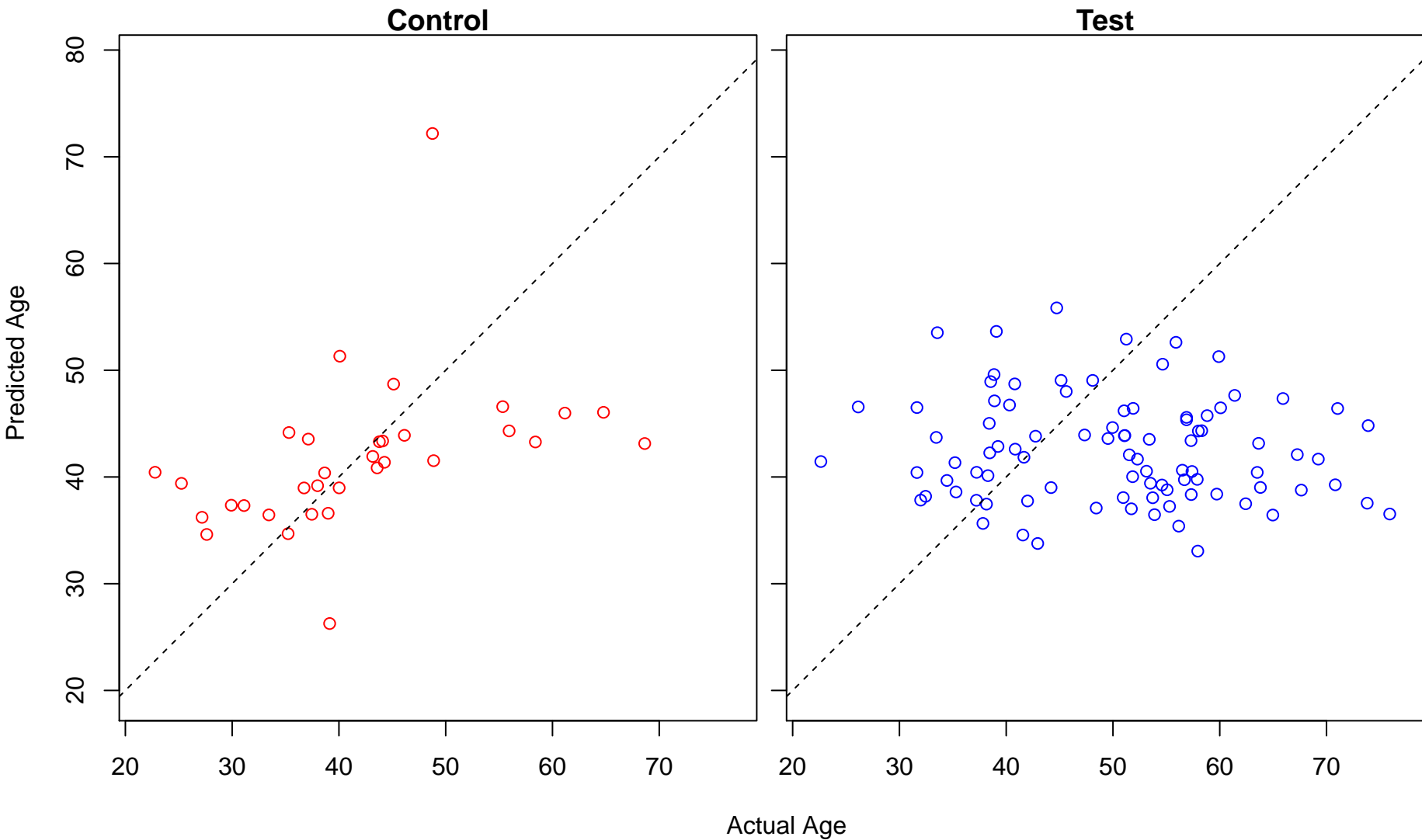
positive regulation of cellular component organization (Score: 0.749773)



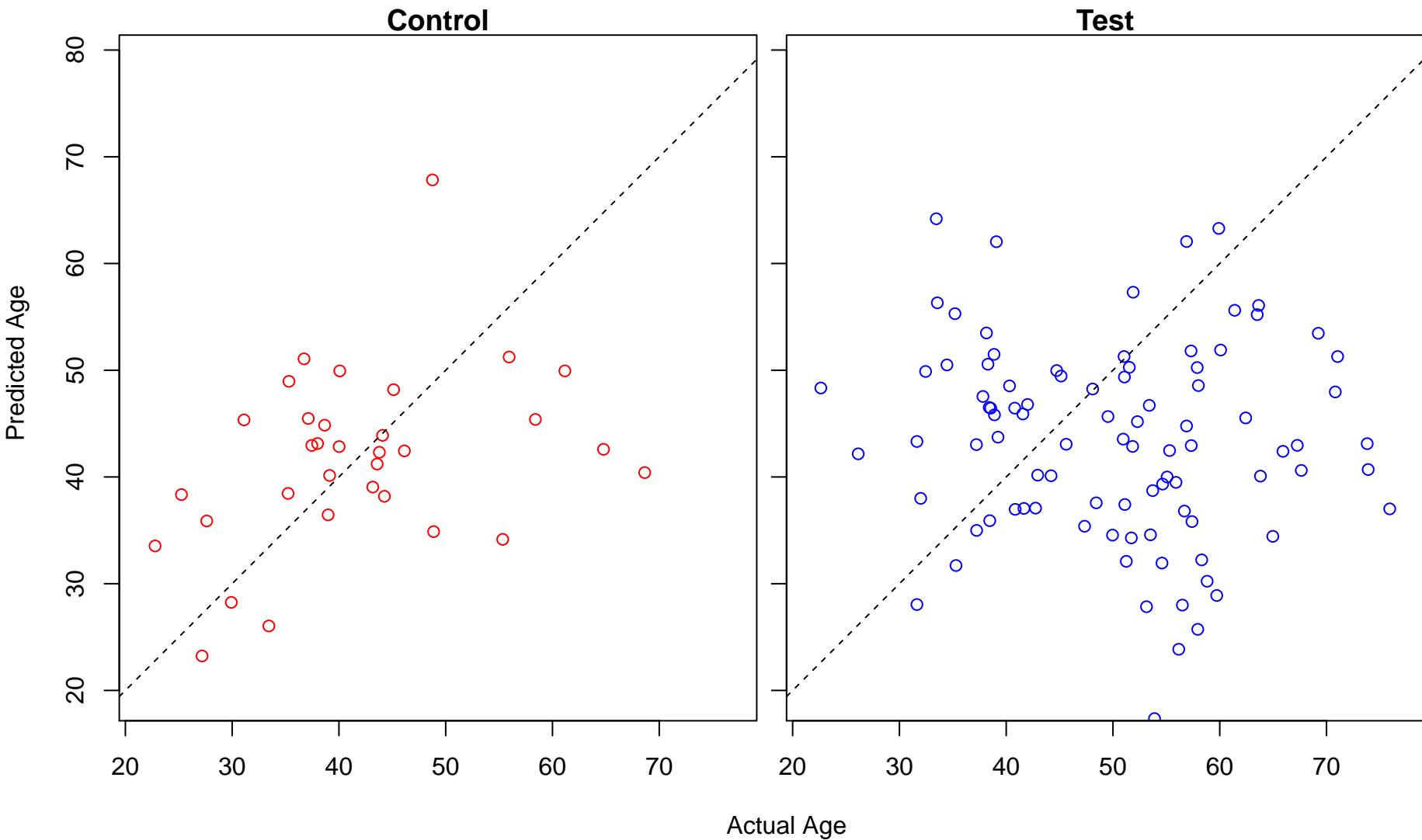
negative regulation of cellular protein metabolic process (Score: 0.749674)



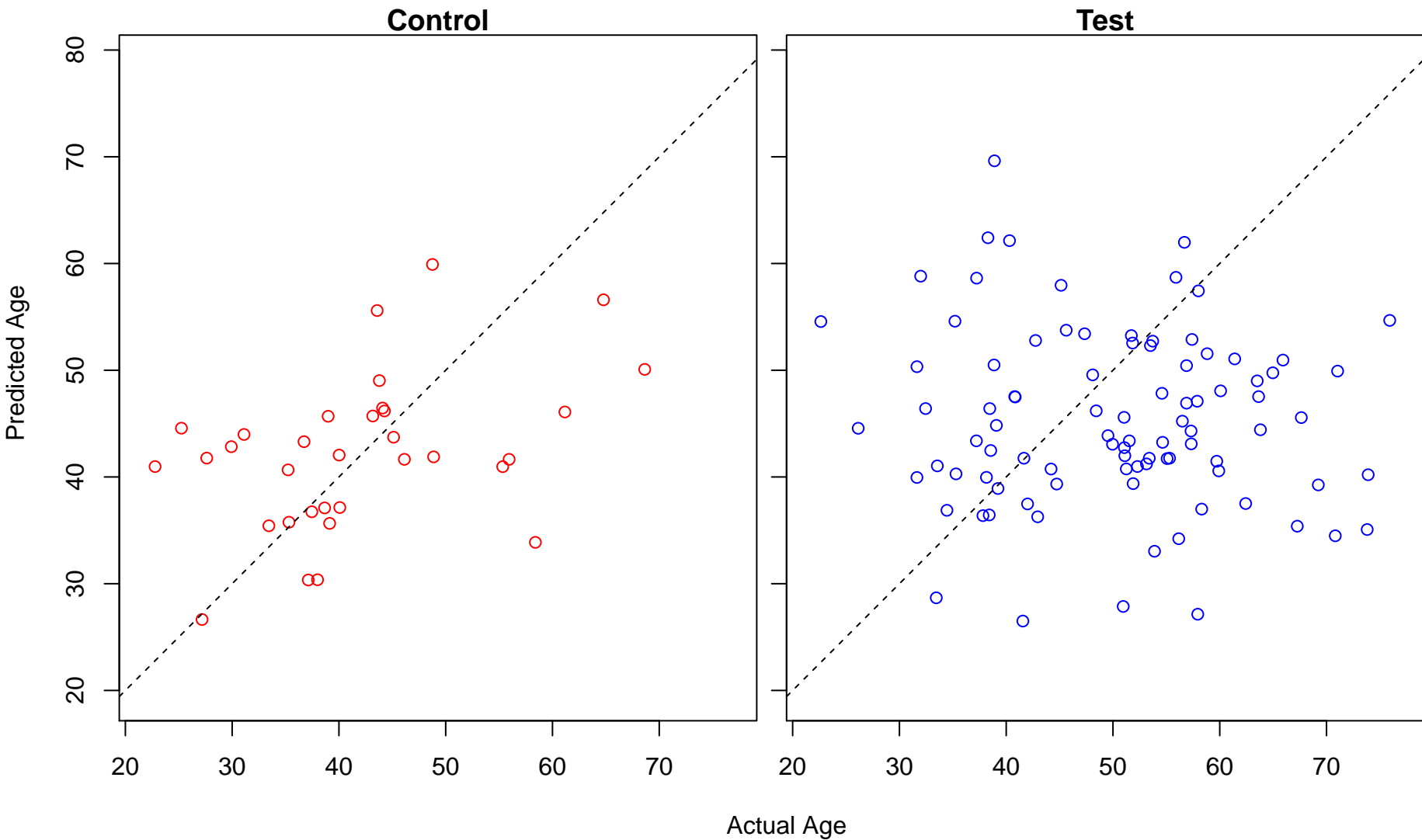
vesicle-mediated transport (Score: 0.749182)



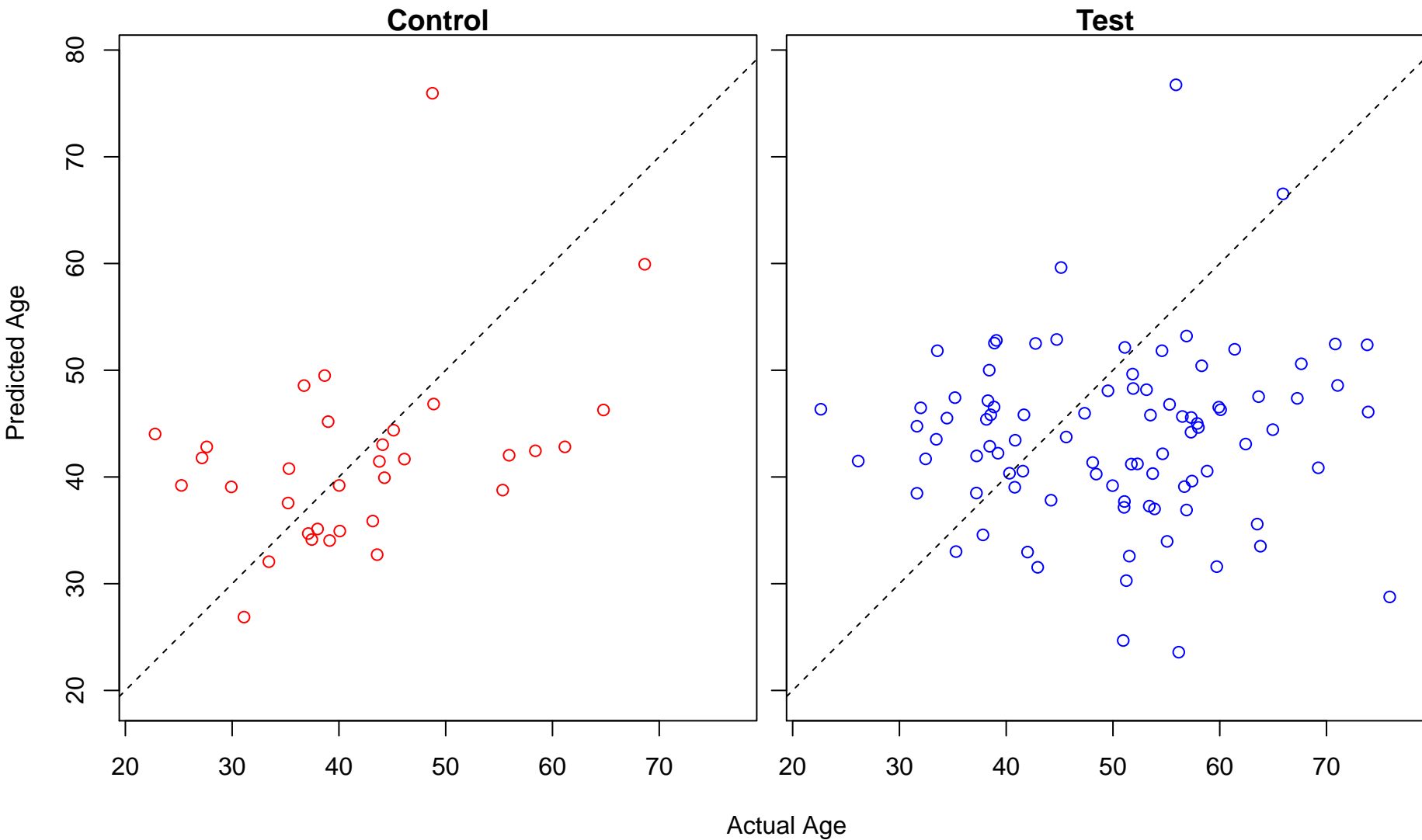
response to xenobiotic stimulus (Score: 0.748856)



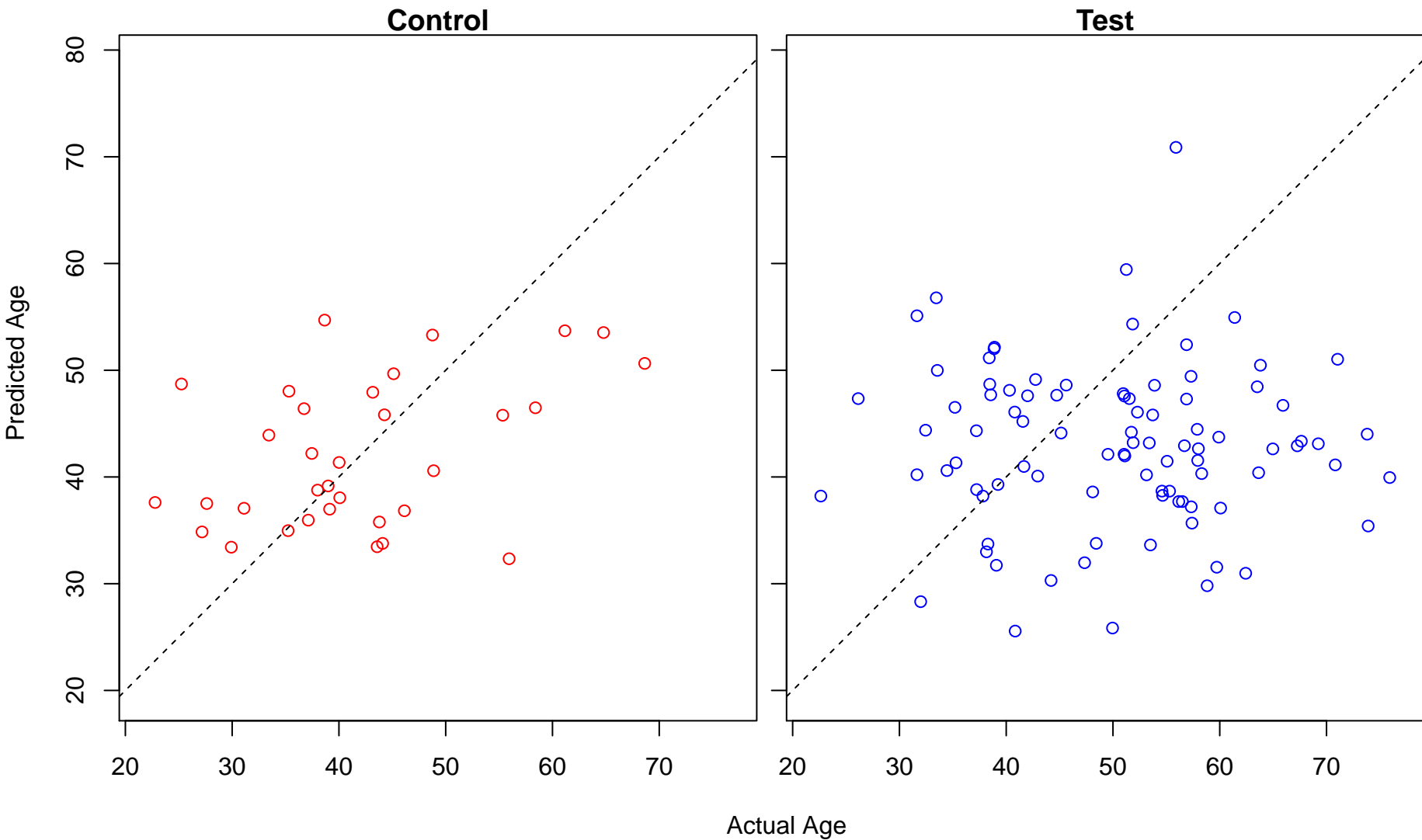
negative regulation of activin receptor signaling pathway (Score: 0.748668)



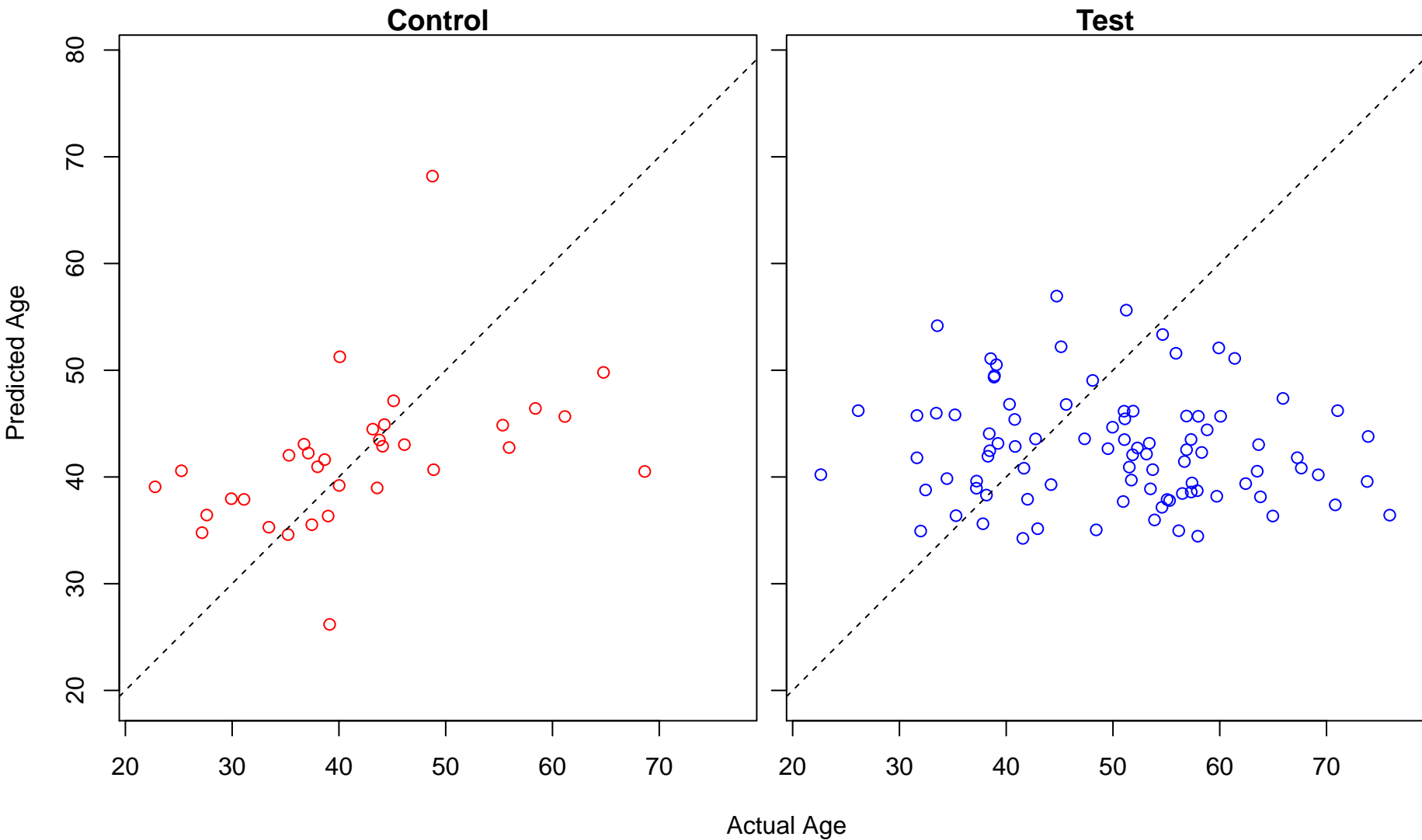
glycosylceramide metabolic process (Score: 0.747976)



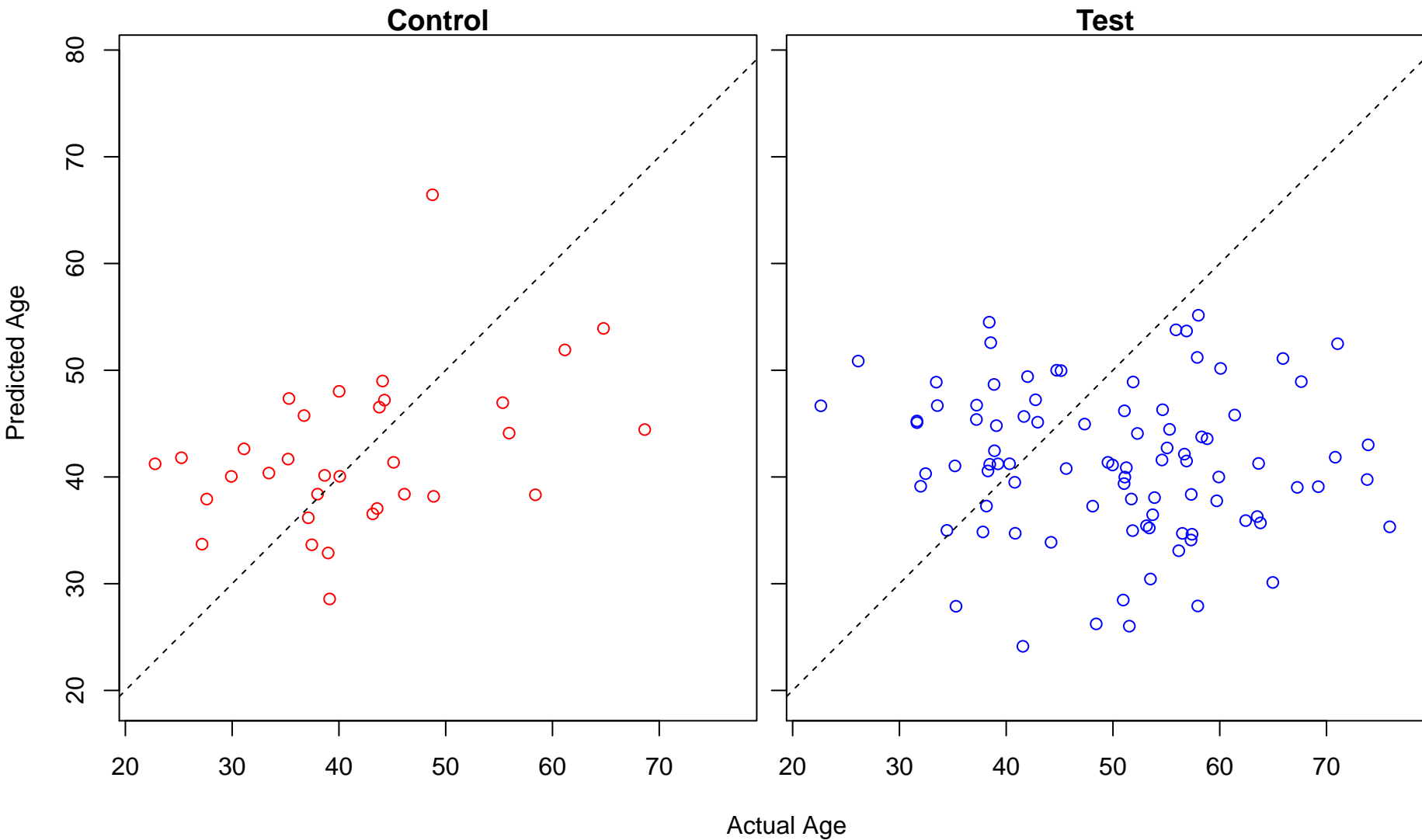
cell differentiation in spinal cord (Score: 0.747931)



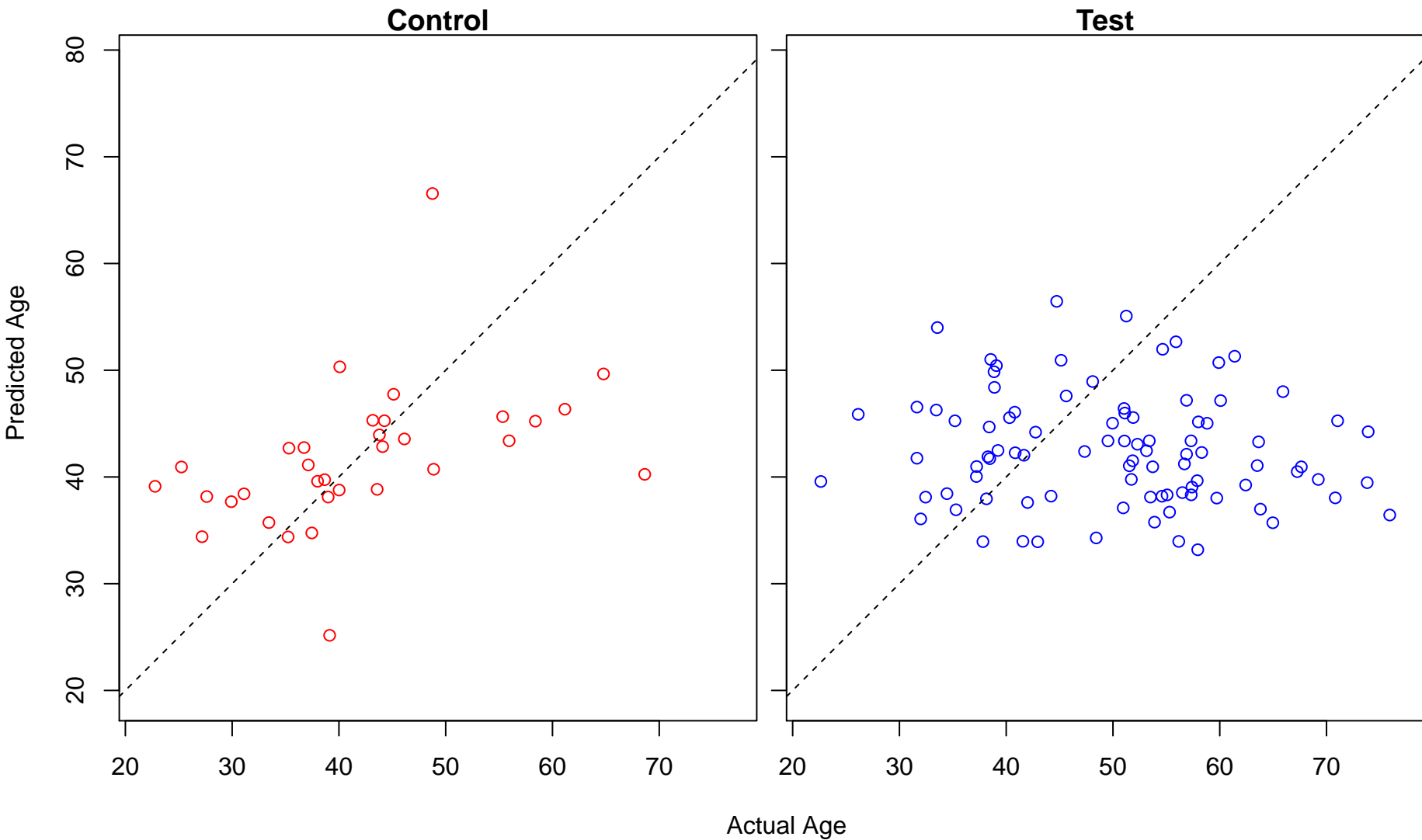
nervous system development (Score: 0.747900)



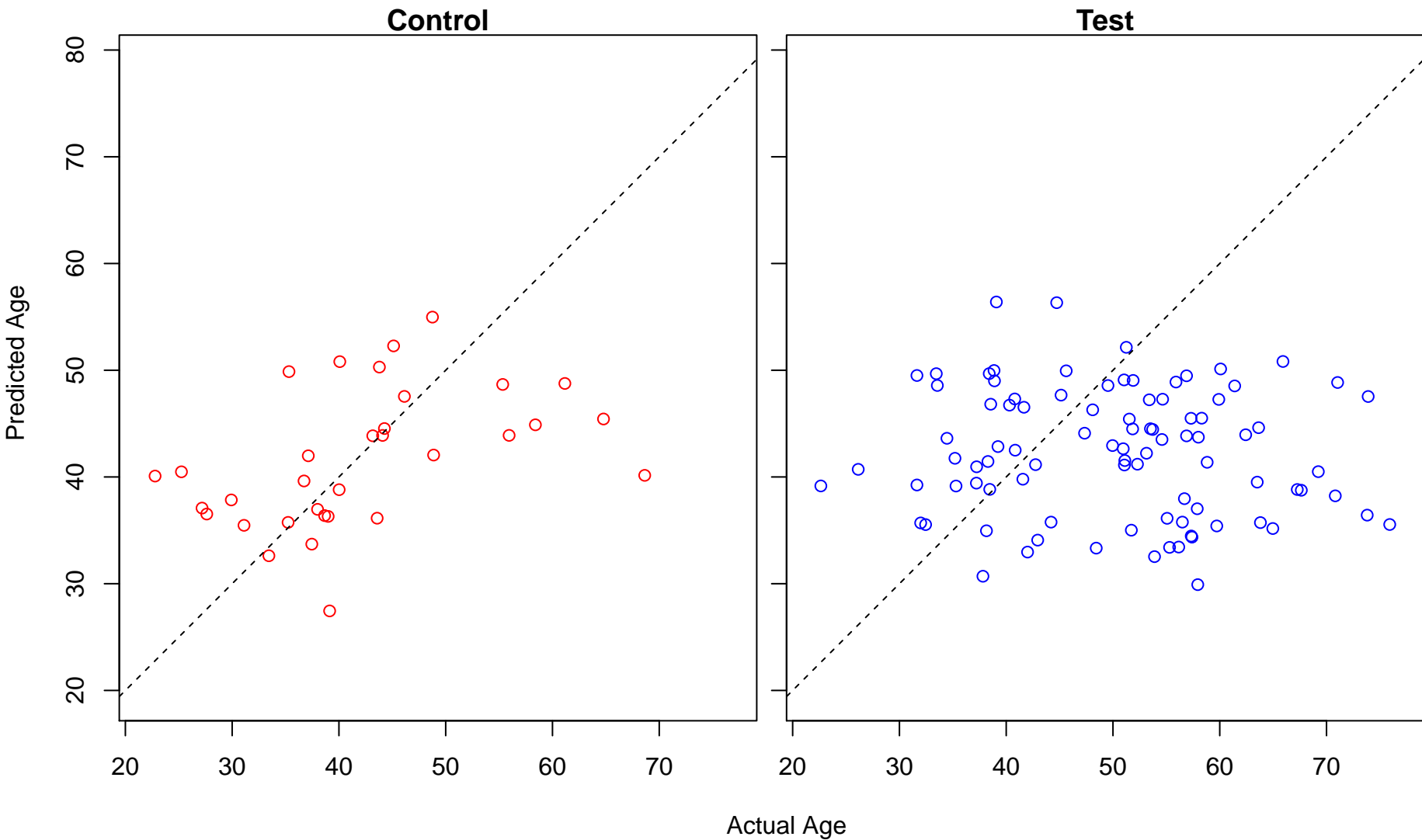
regulation of mitochondrial depolarization (Score: 0.747006)



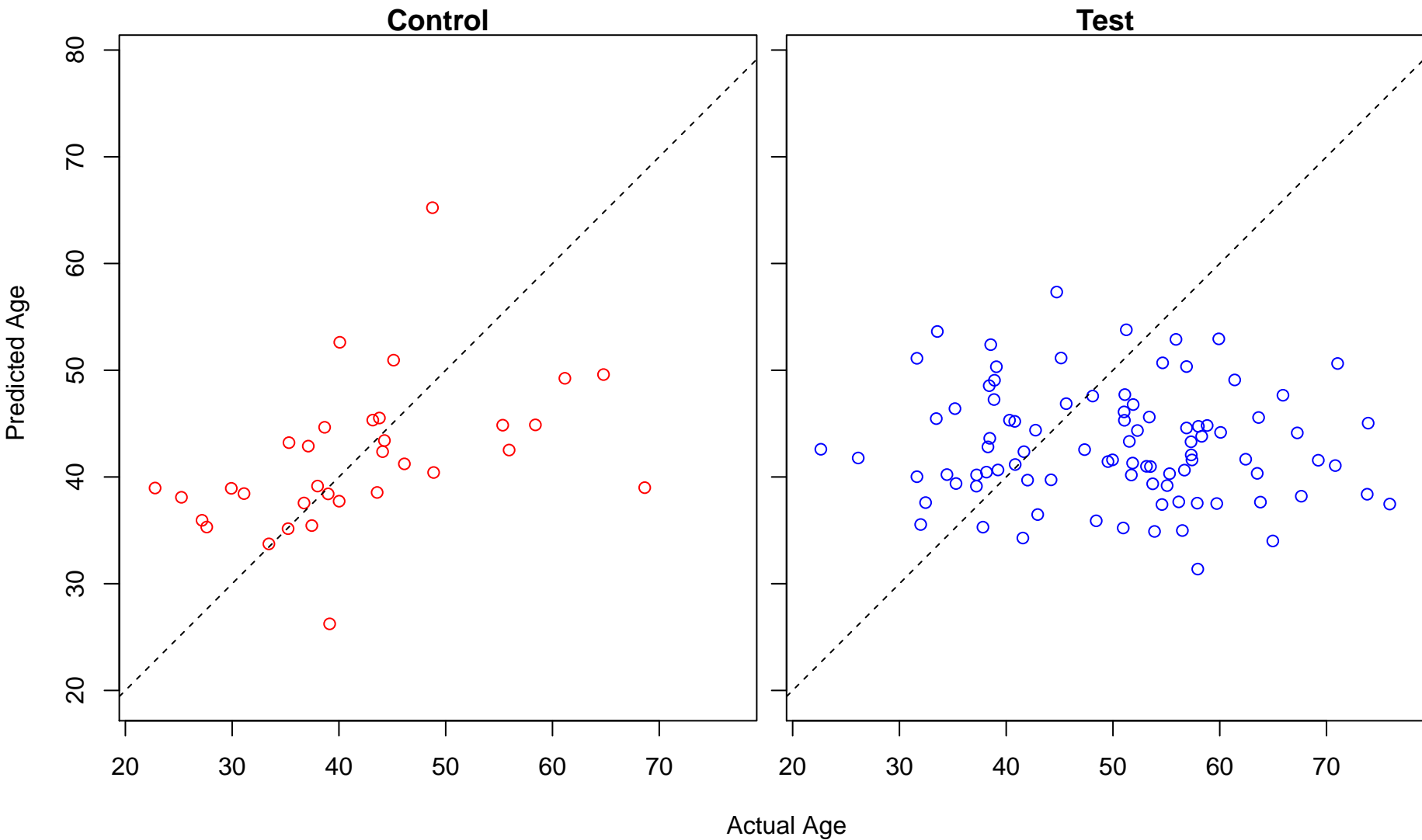
cell differentiation (Score: 0.746999)



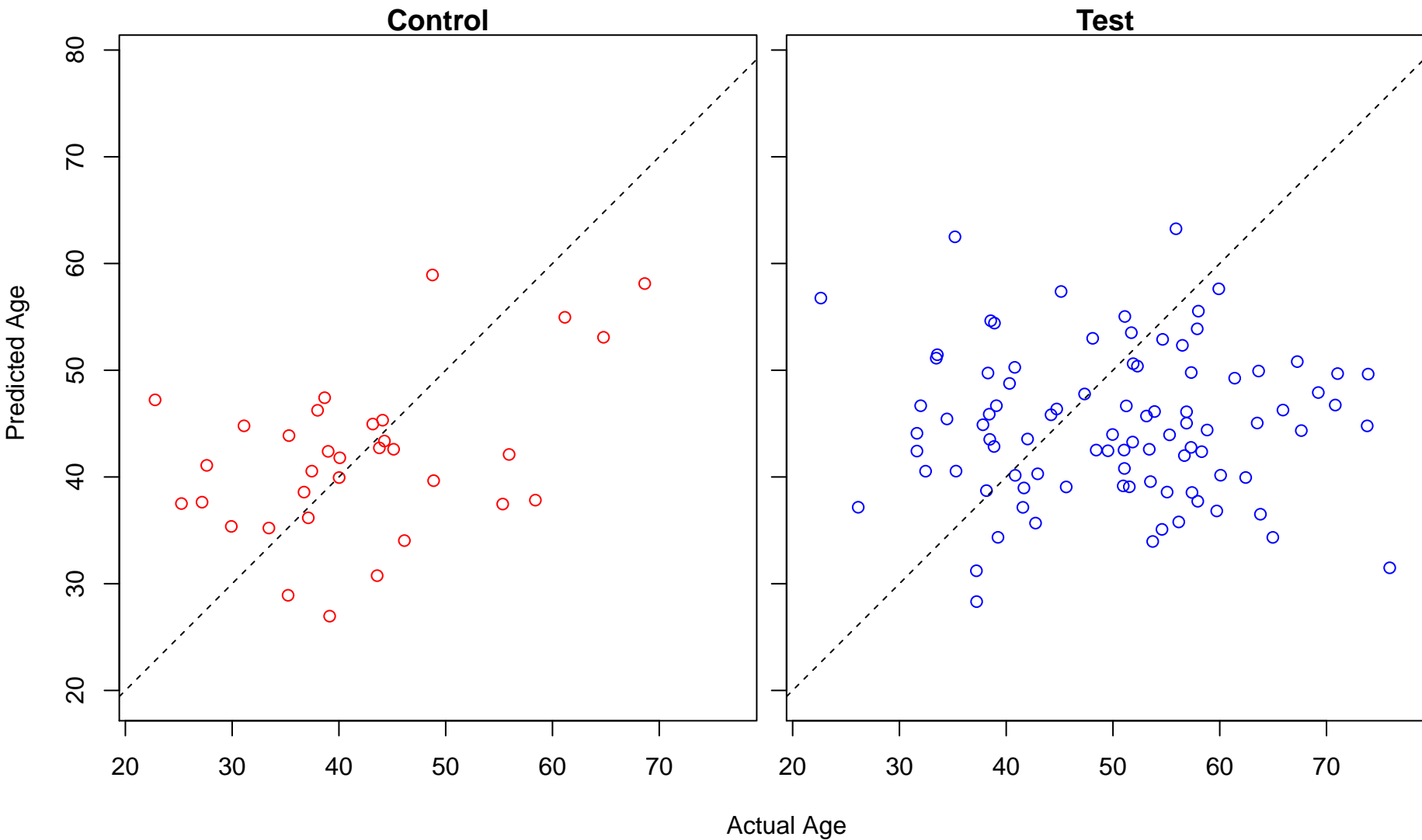
mRNA export from nucleus (Score: 0.746862)



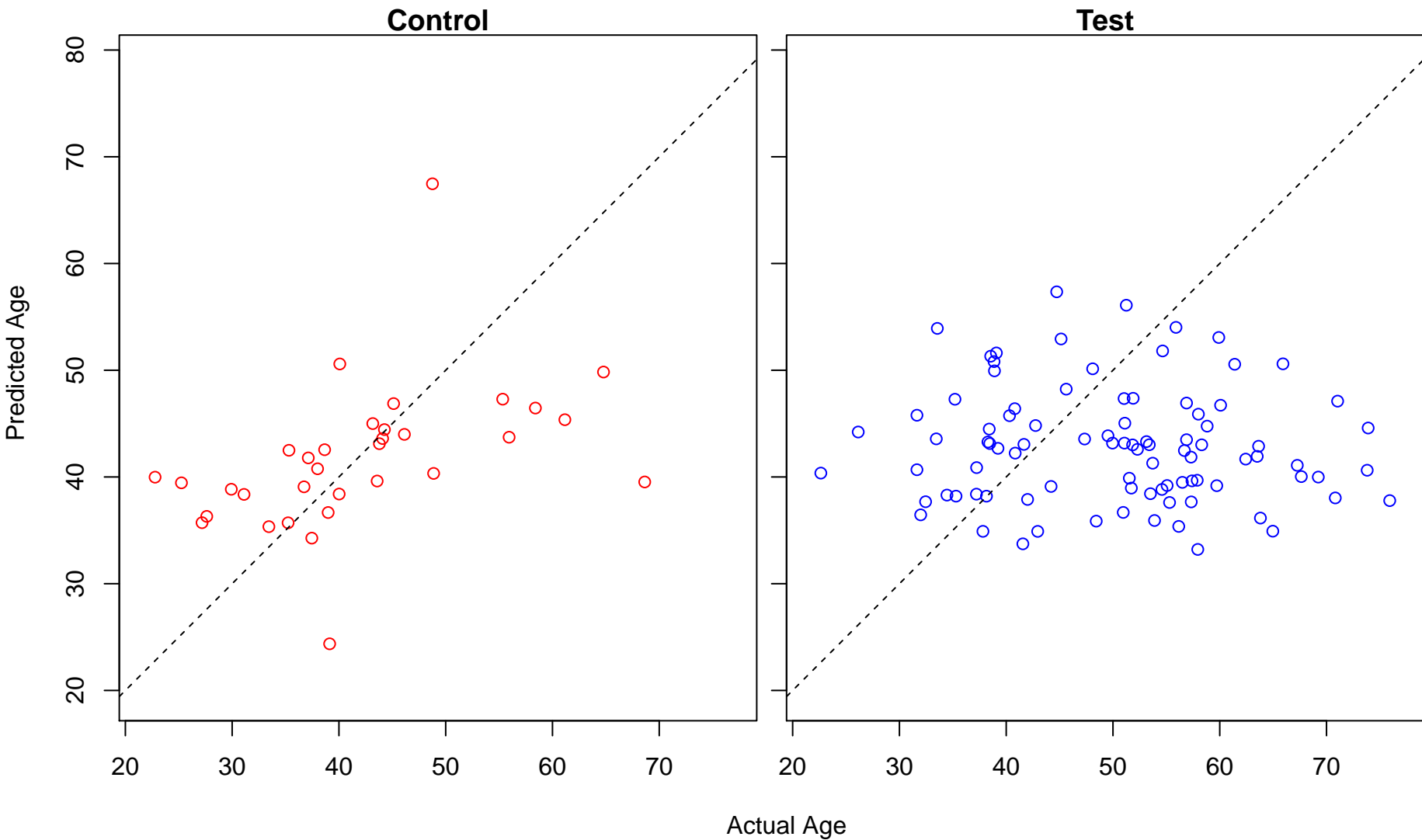
glycerolipid metabolic process (Score: 0.746091)



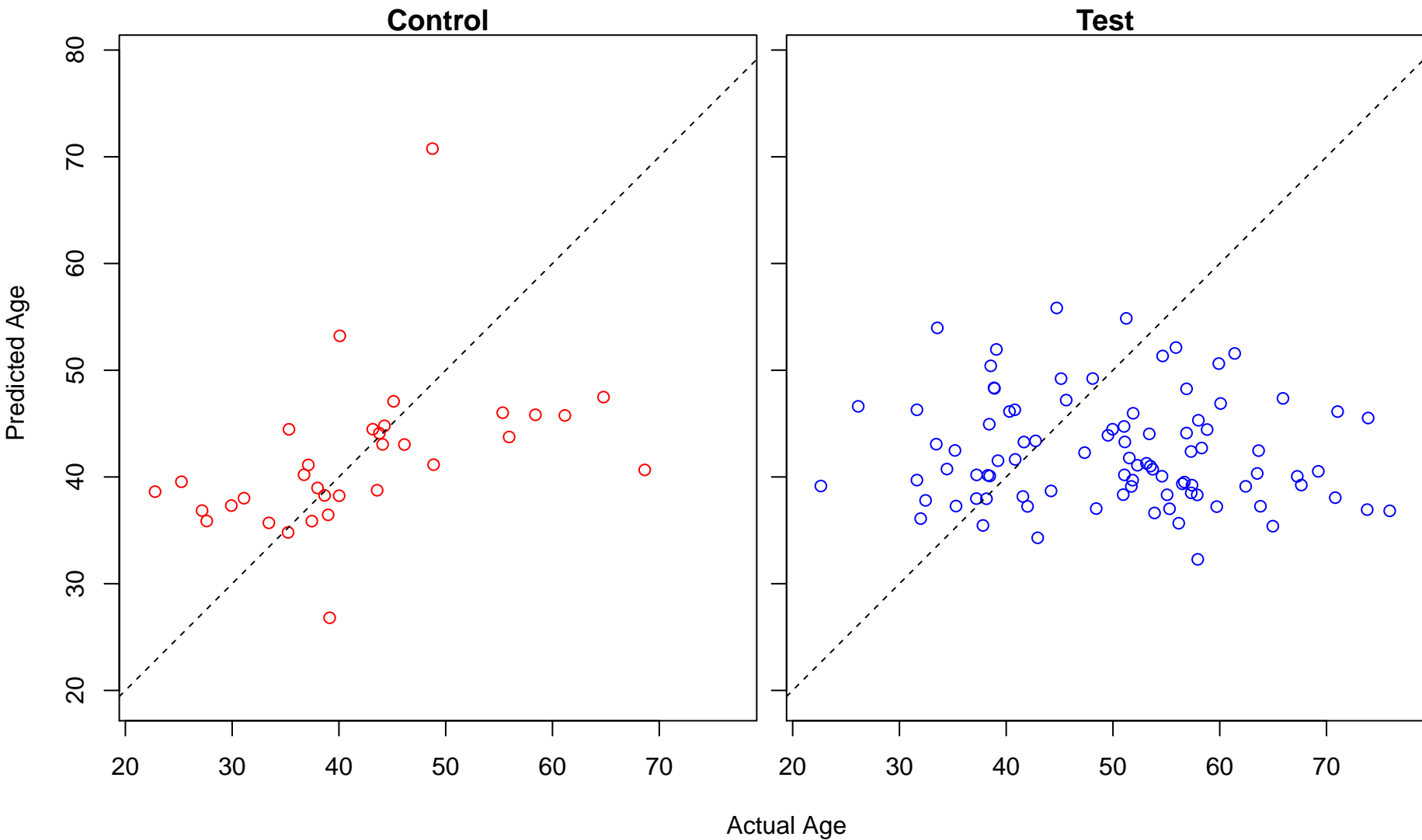
C-5 methylation of cytosine (Score: 0.746089)



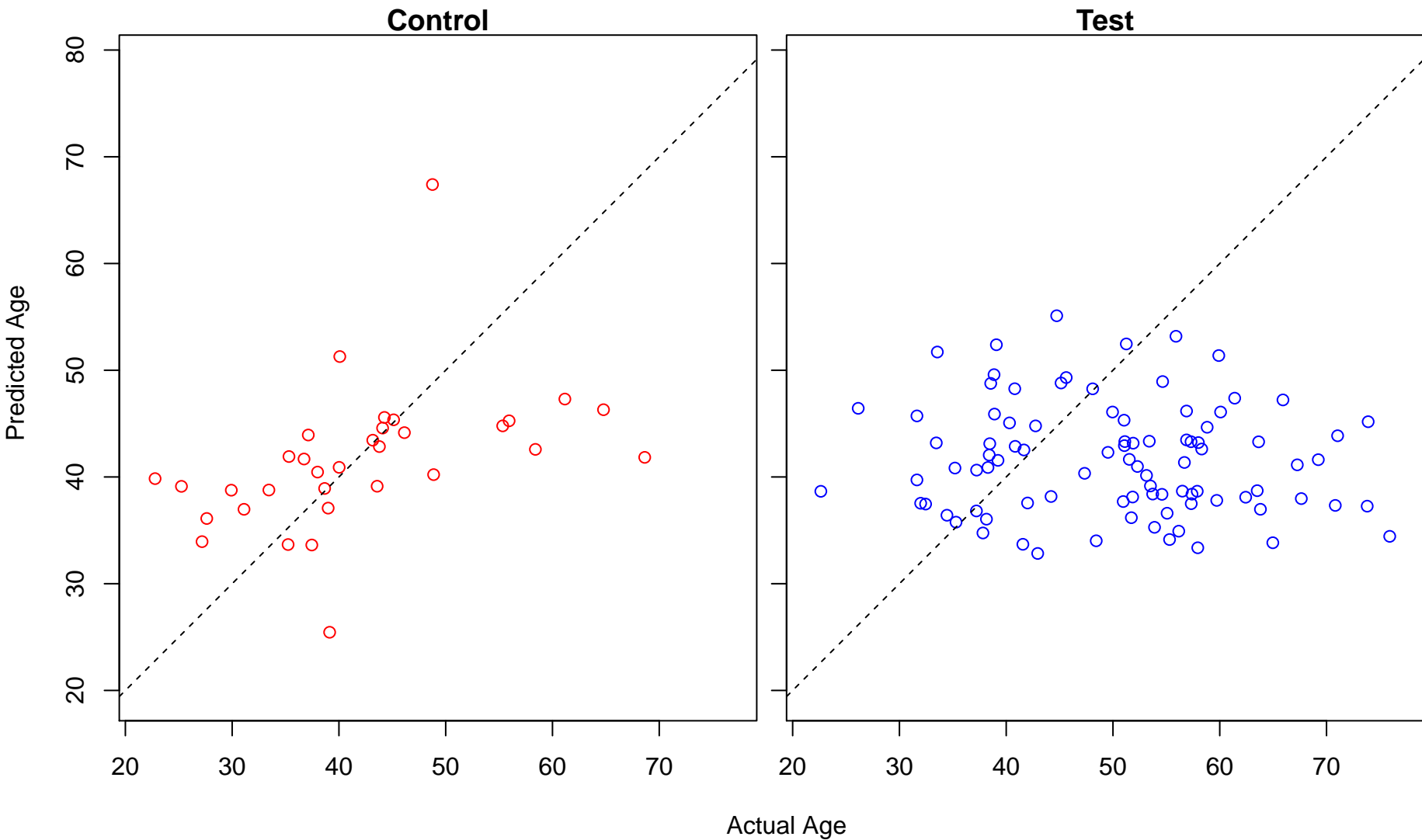
cell projection organization (Score: 0.745979)



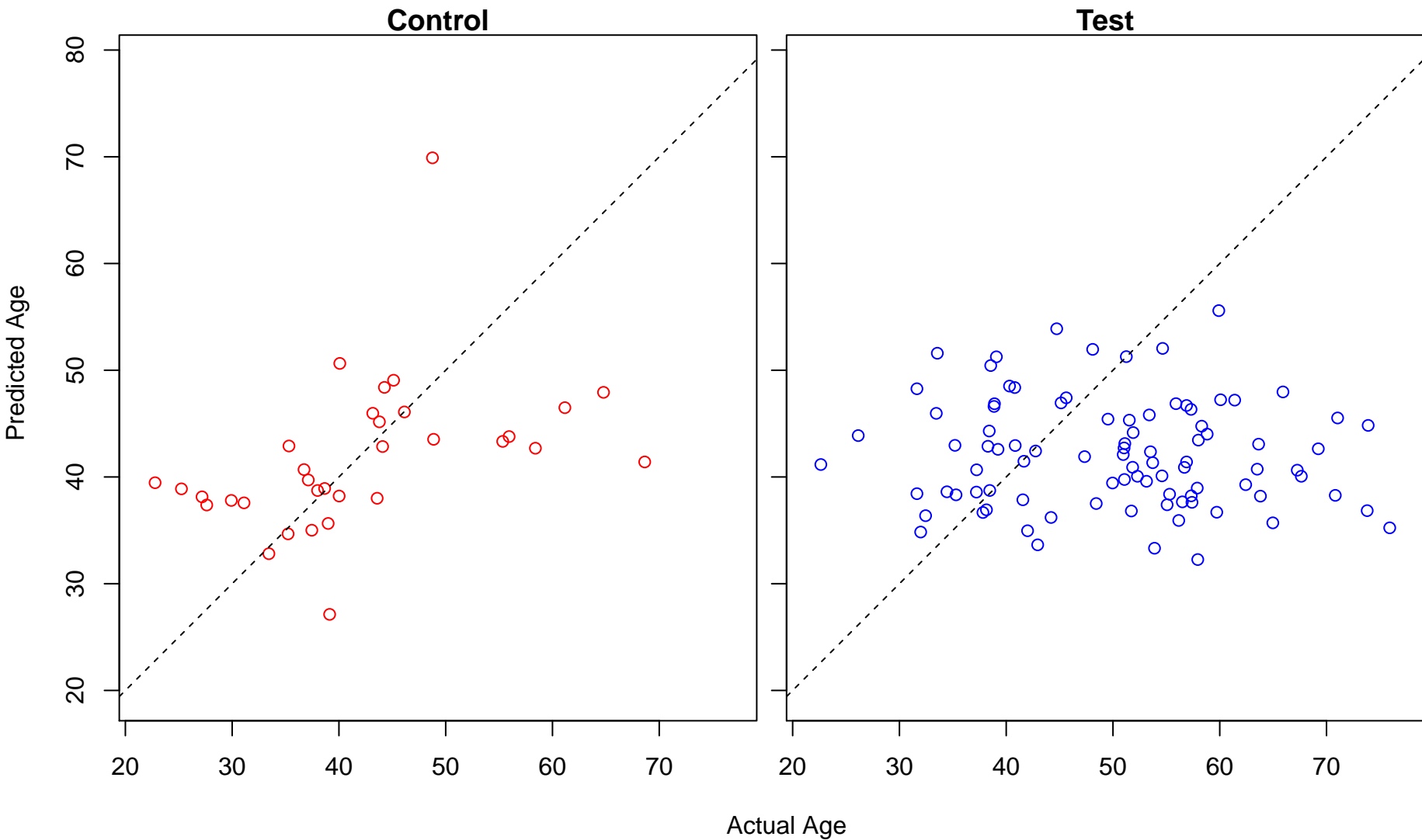
negative regulation of macromolecule metabolic process (Score: 0.745862)



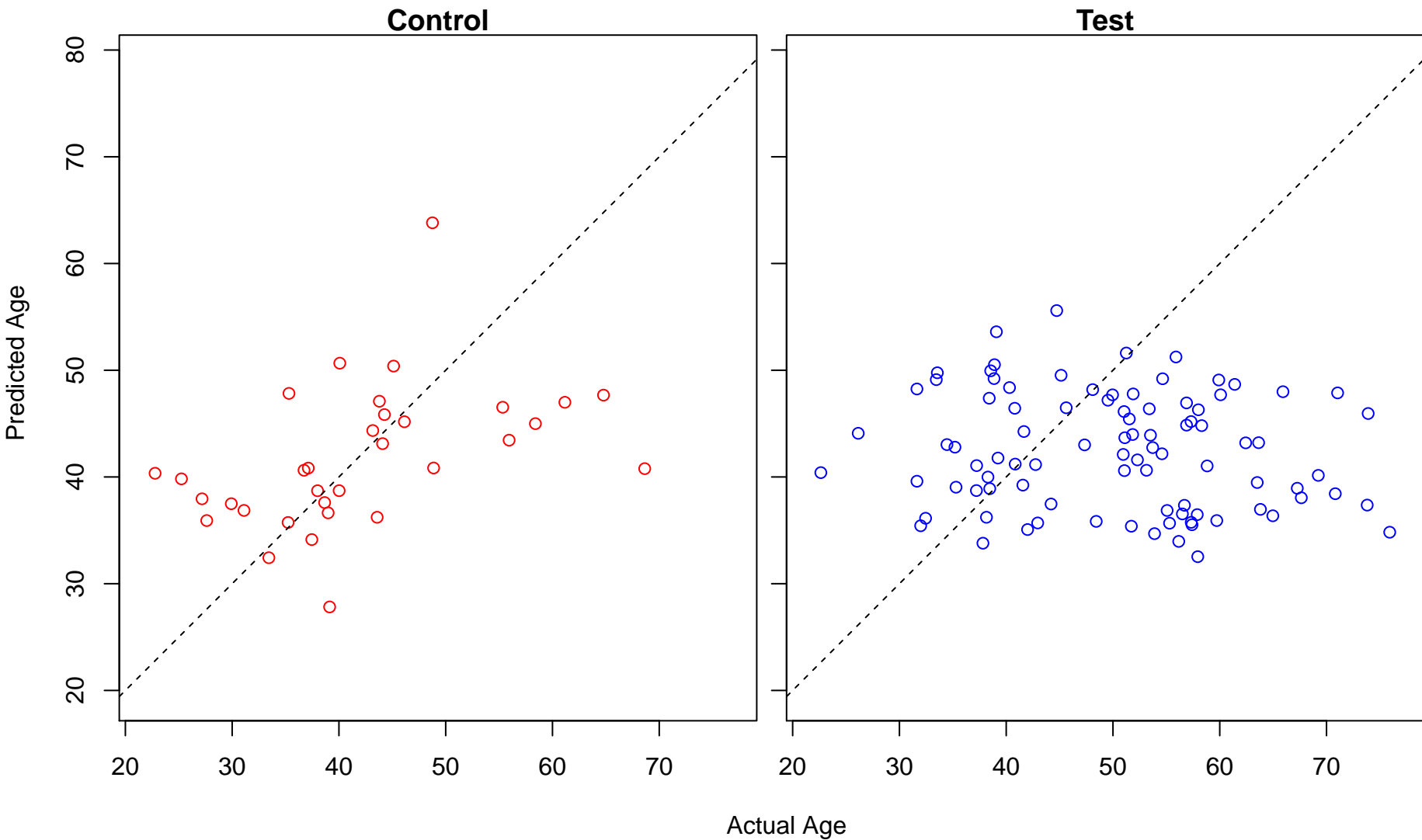
homeostatic process (Score: 0.745709)



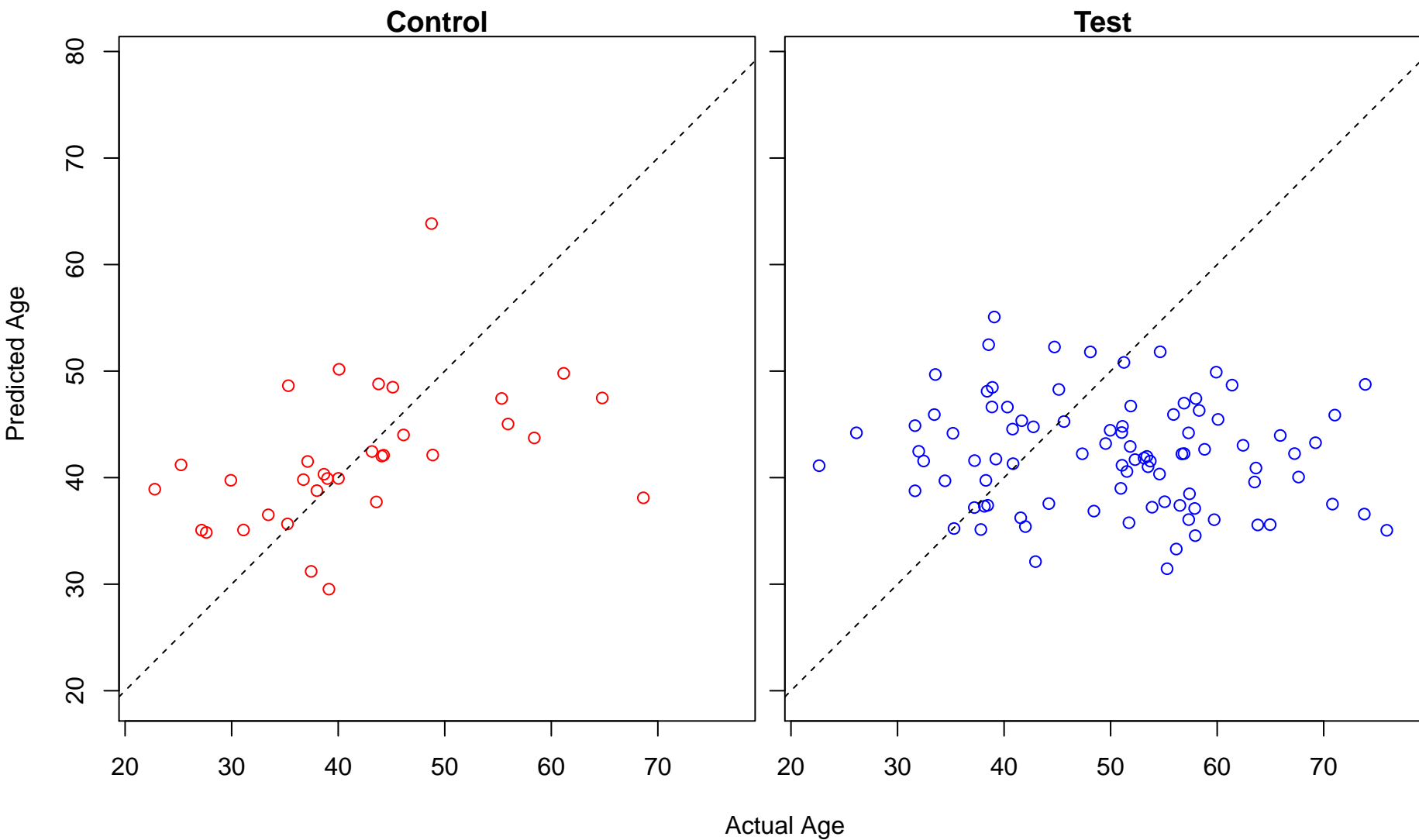
generation of precursor metabolites and energy (Score: 0.745553)



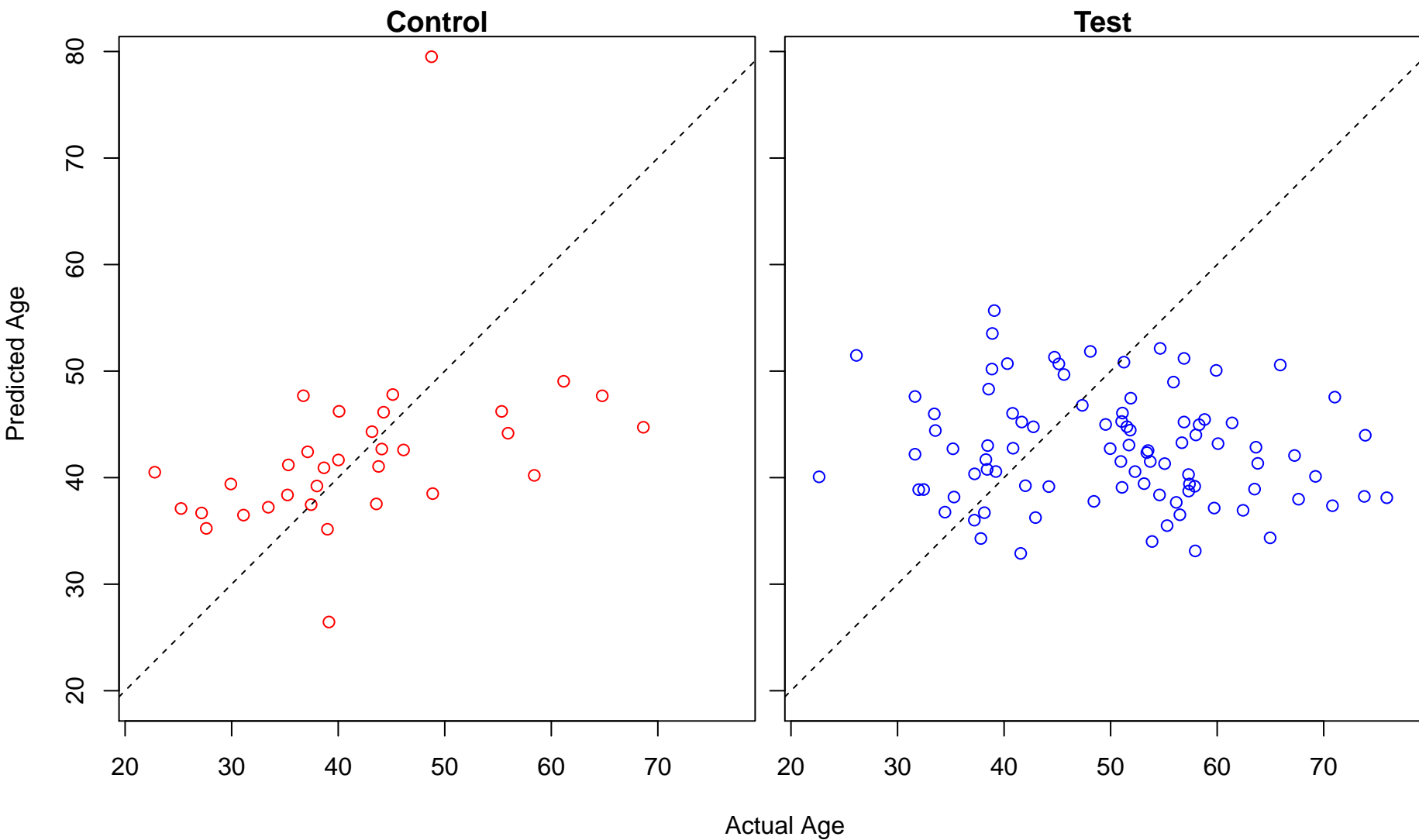
RNA localization (Score: 0.745147)



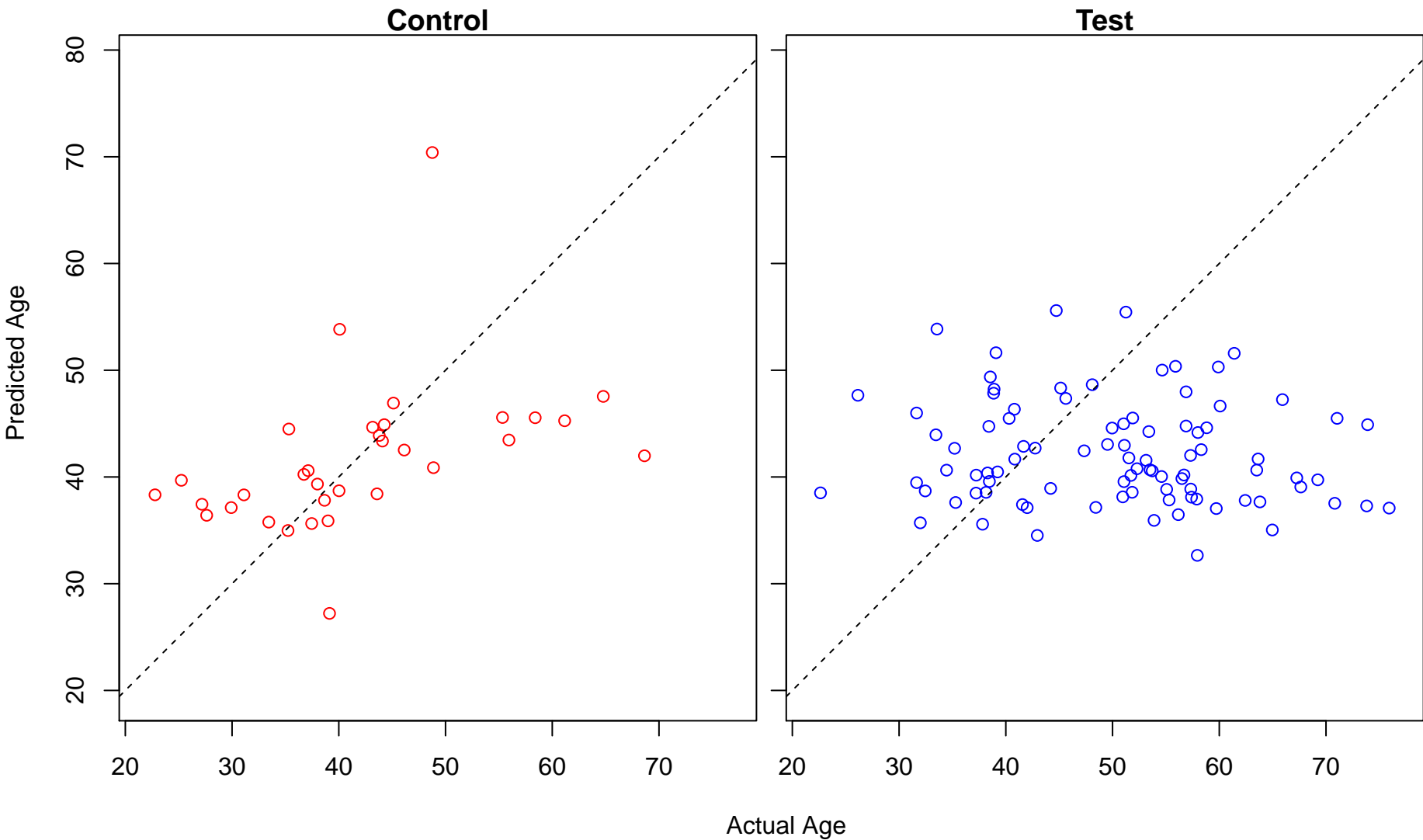
cell-cell signaling (Score: 0.745145)



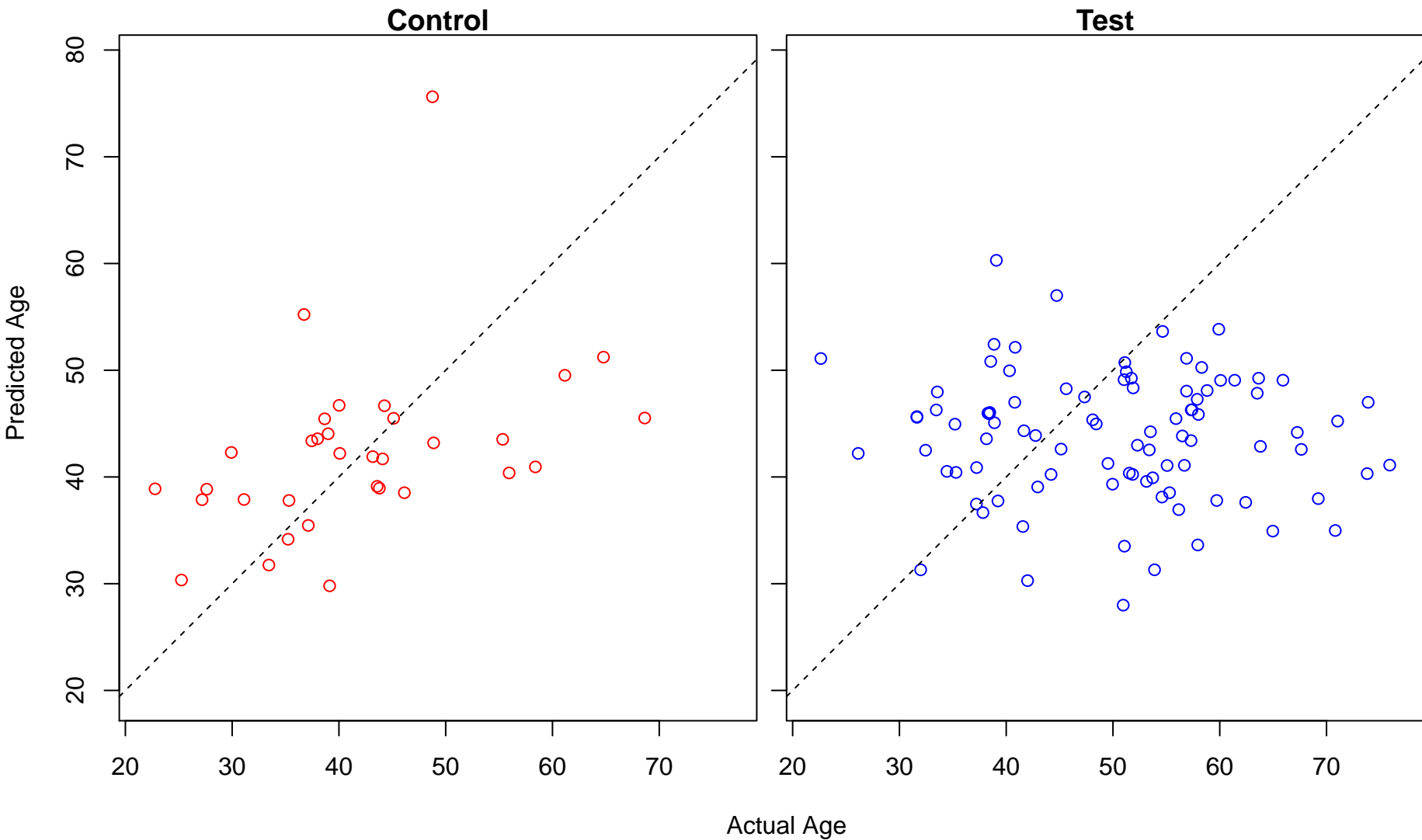
cytoplasmic sequestering of protein (Score: 0.745007)



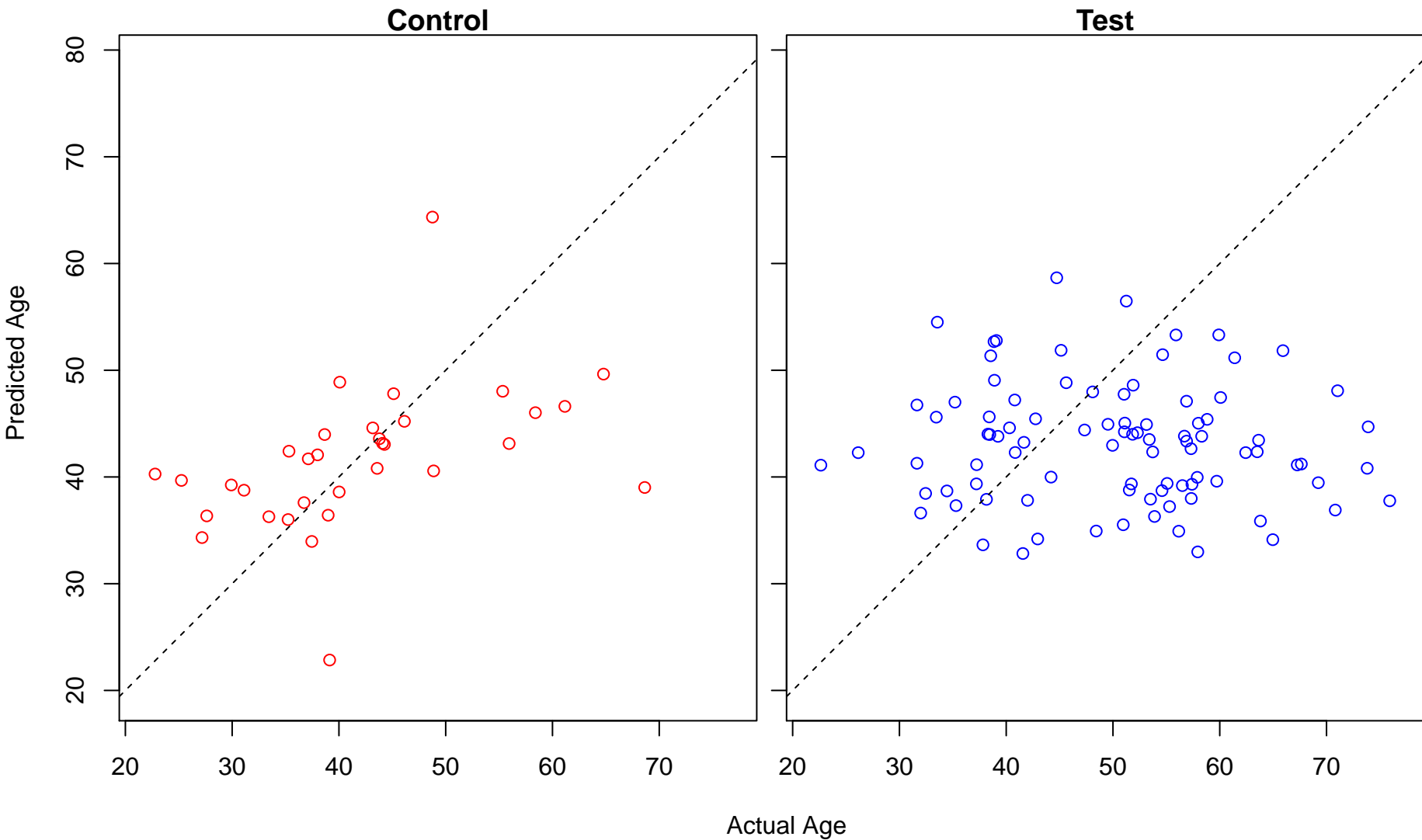
negative regulation of nucleobase-containing compound metabolic process (Score: 0.744966)



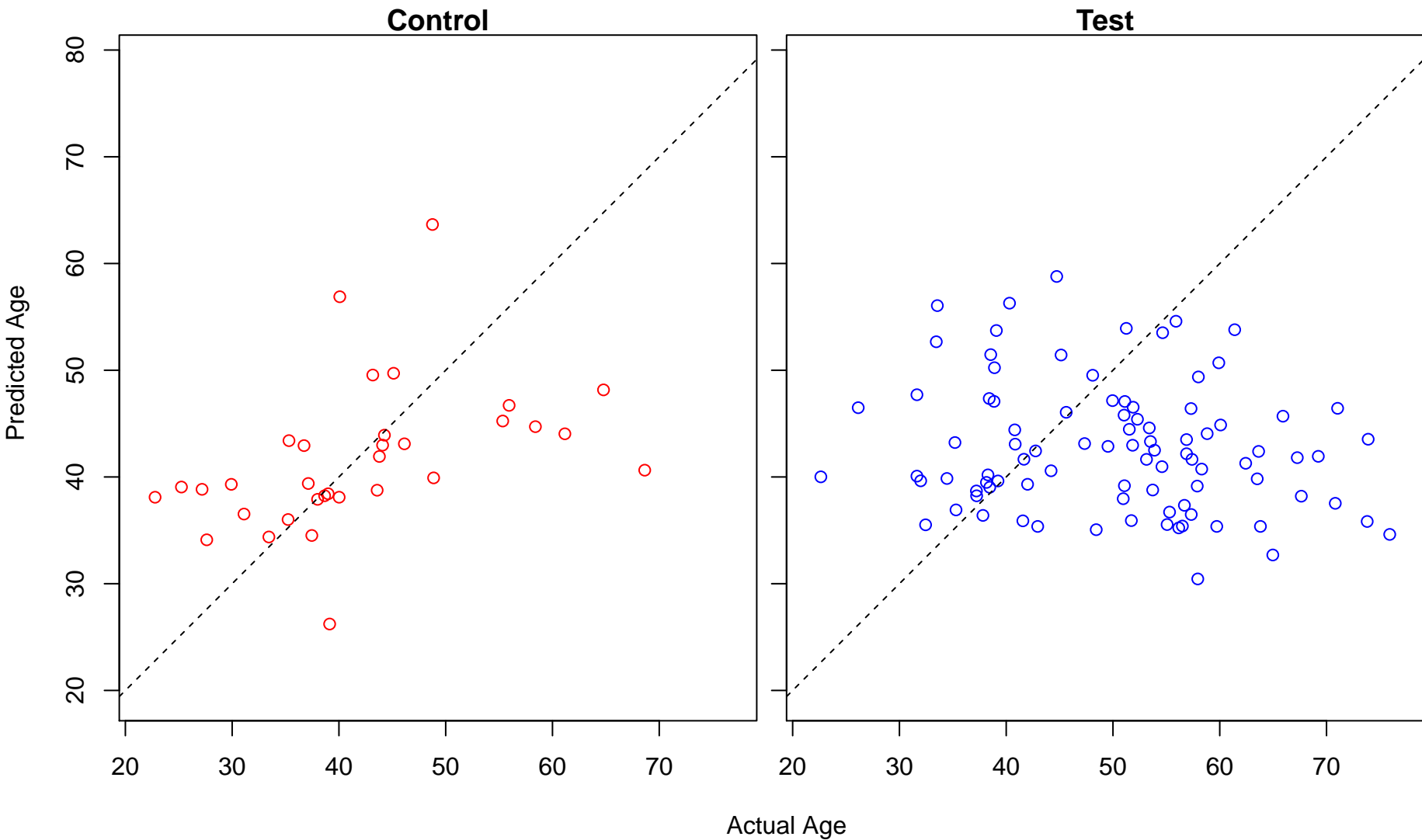
negative regulation of membrane potential (Score: 0.744957)



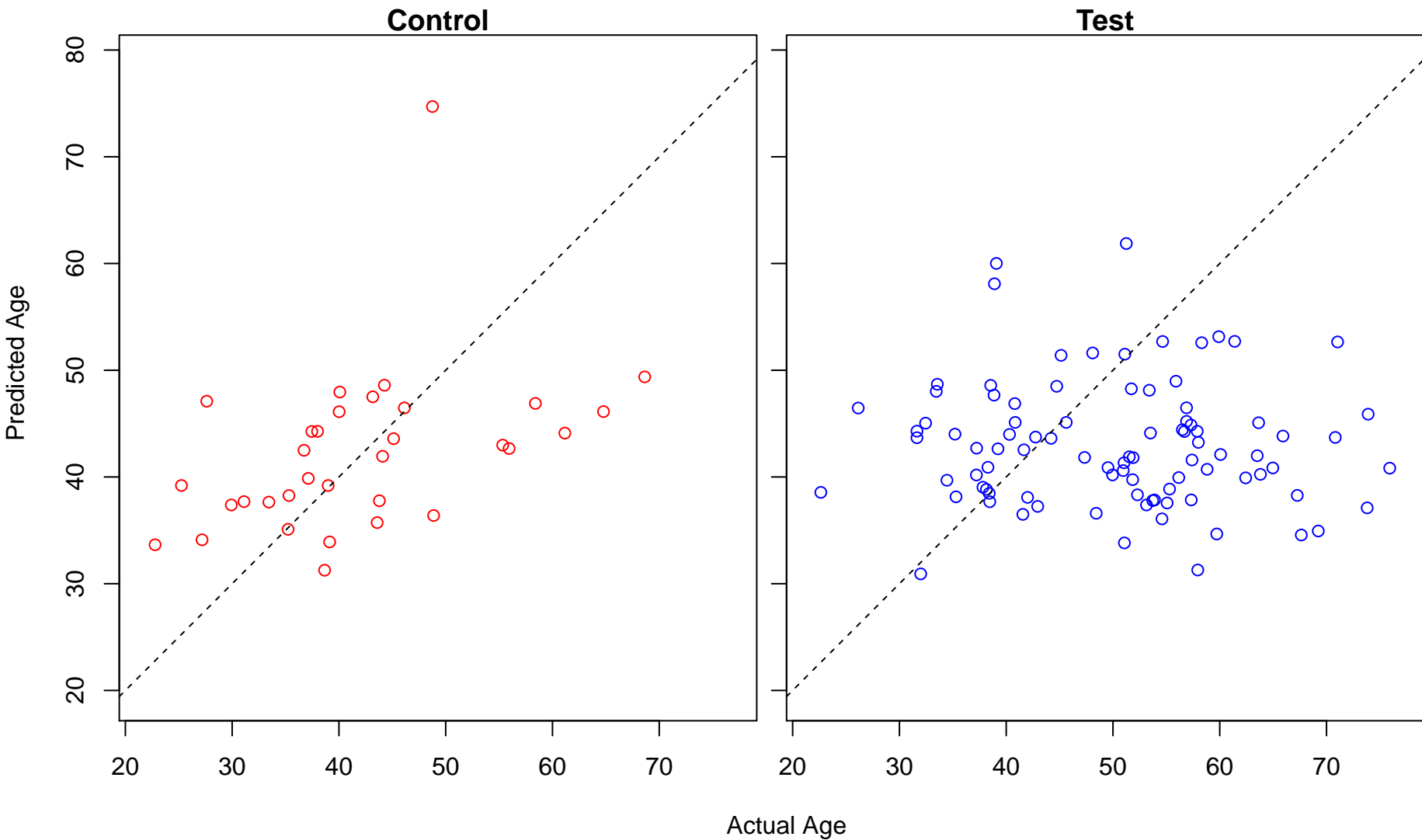
neuron projection development (Score: 0.744895)



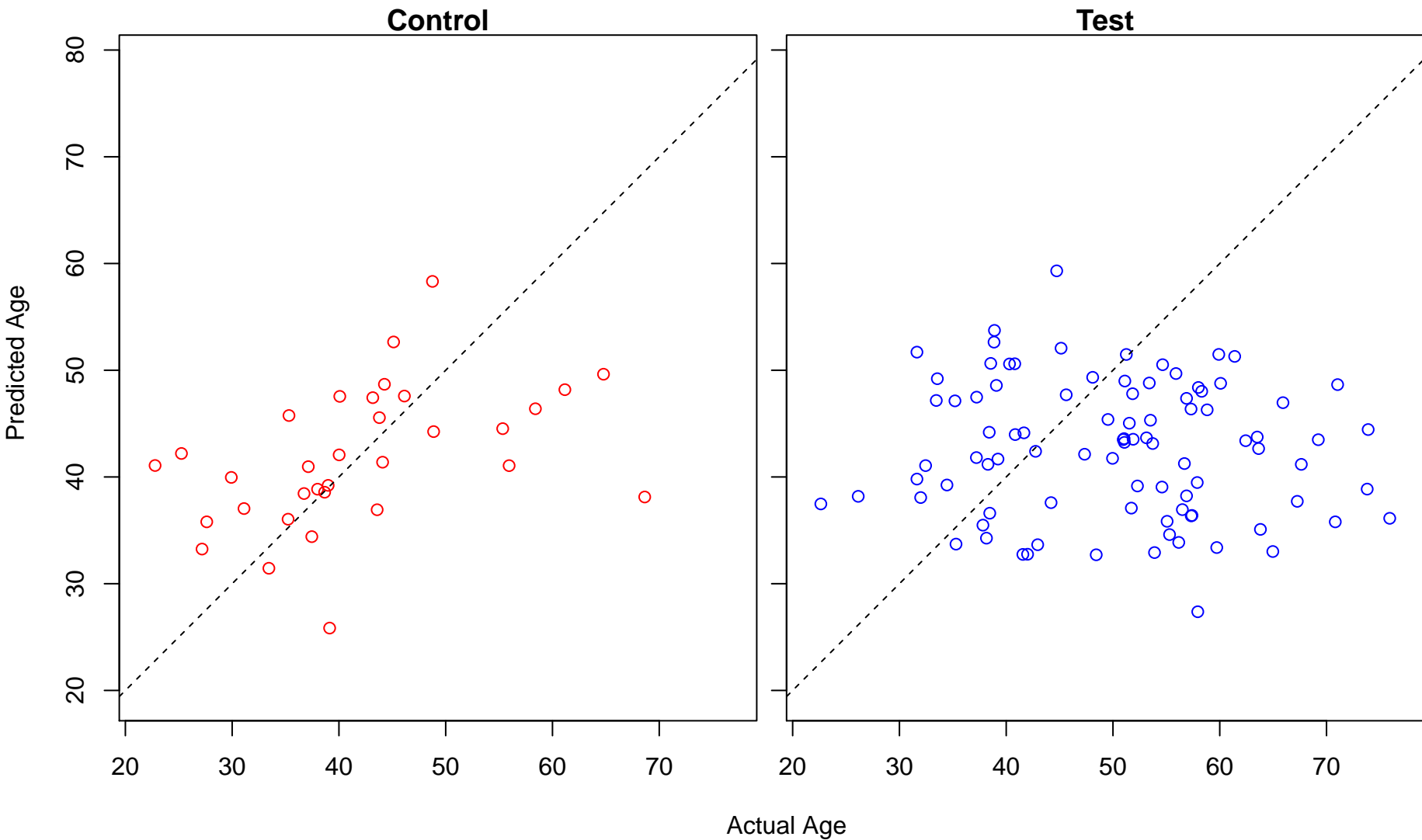
regulation of JNK cascade (Score: 0.744717)



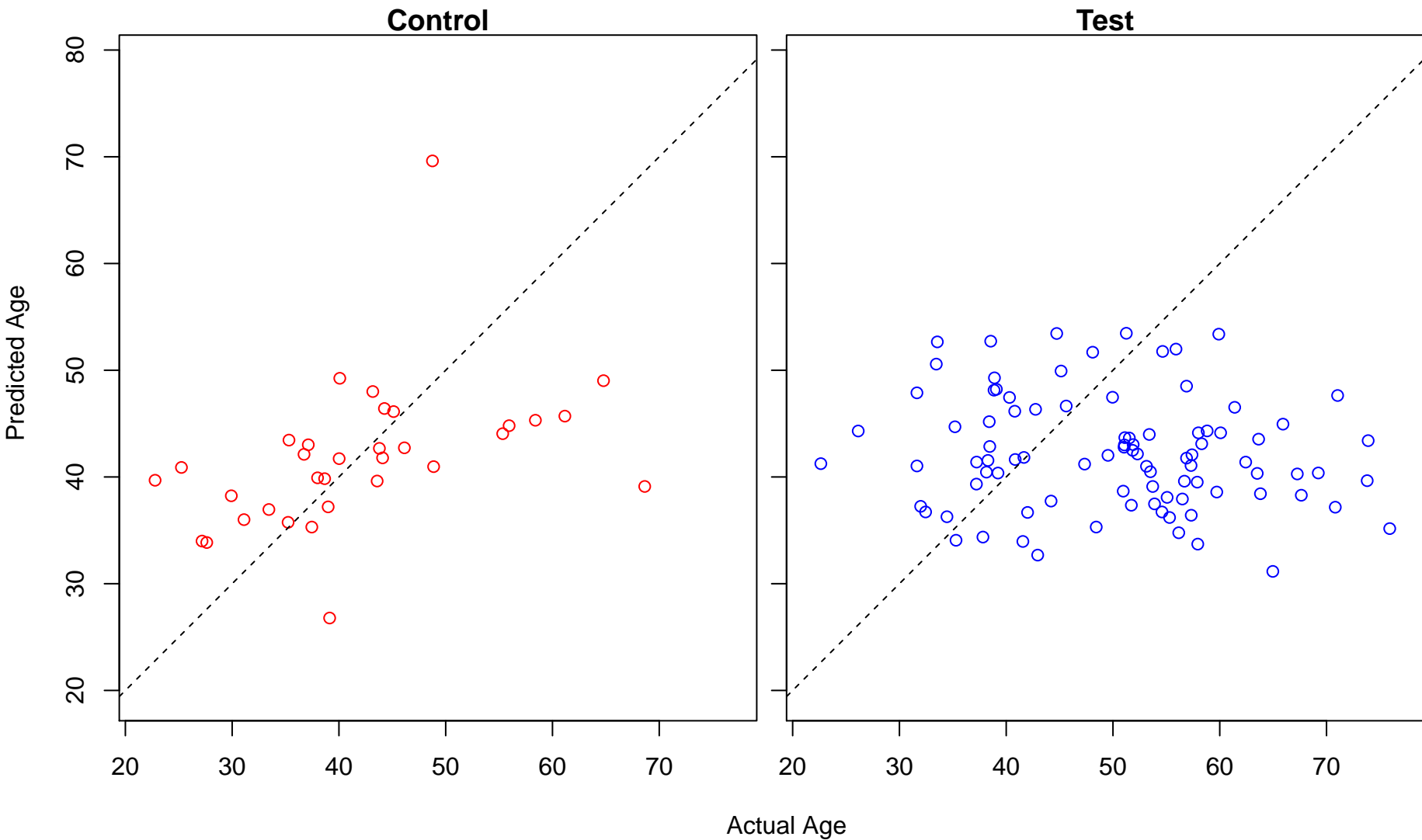
cAMP-mediated signaling (Score: 0.744105)



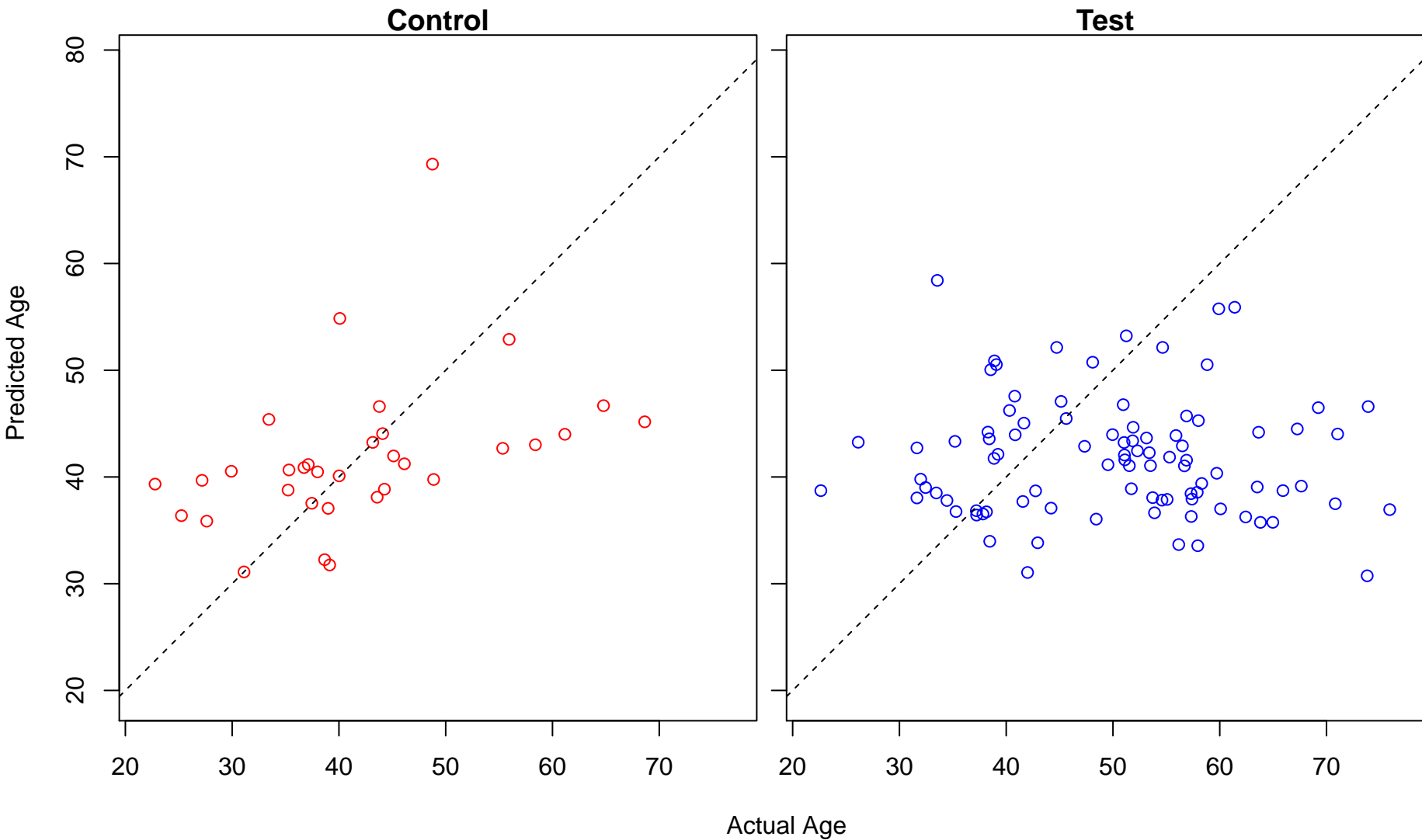
retrograde protein transport, ER to cytosol (Score: 0.744084)



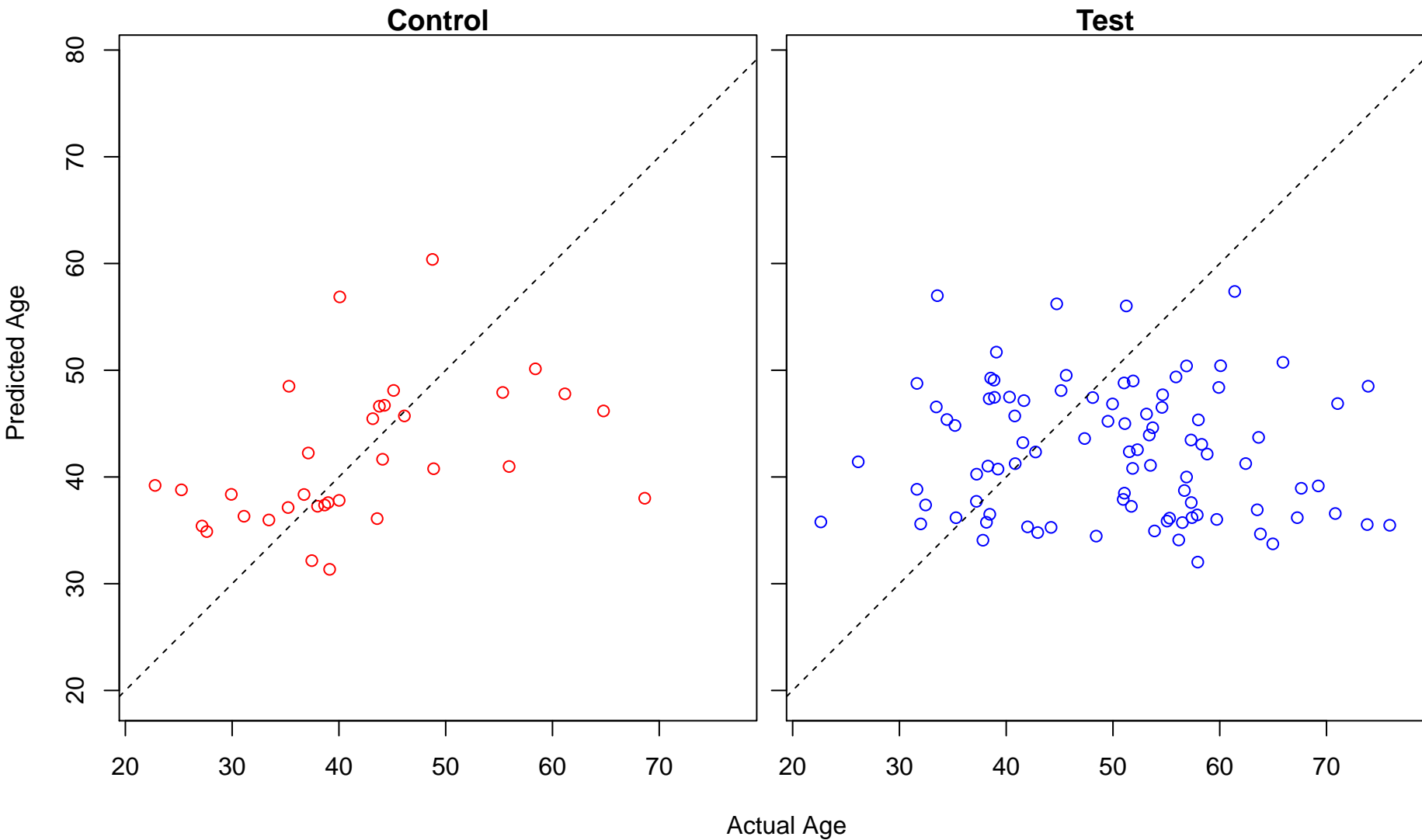
transmembrane transport (Score: 0.743618)



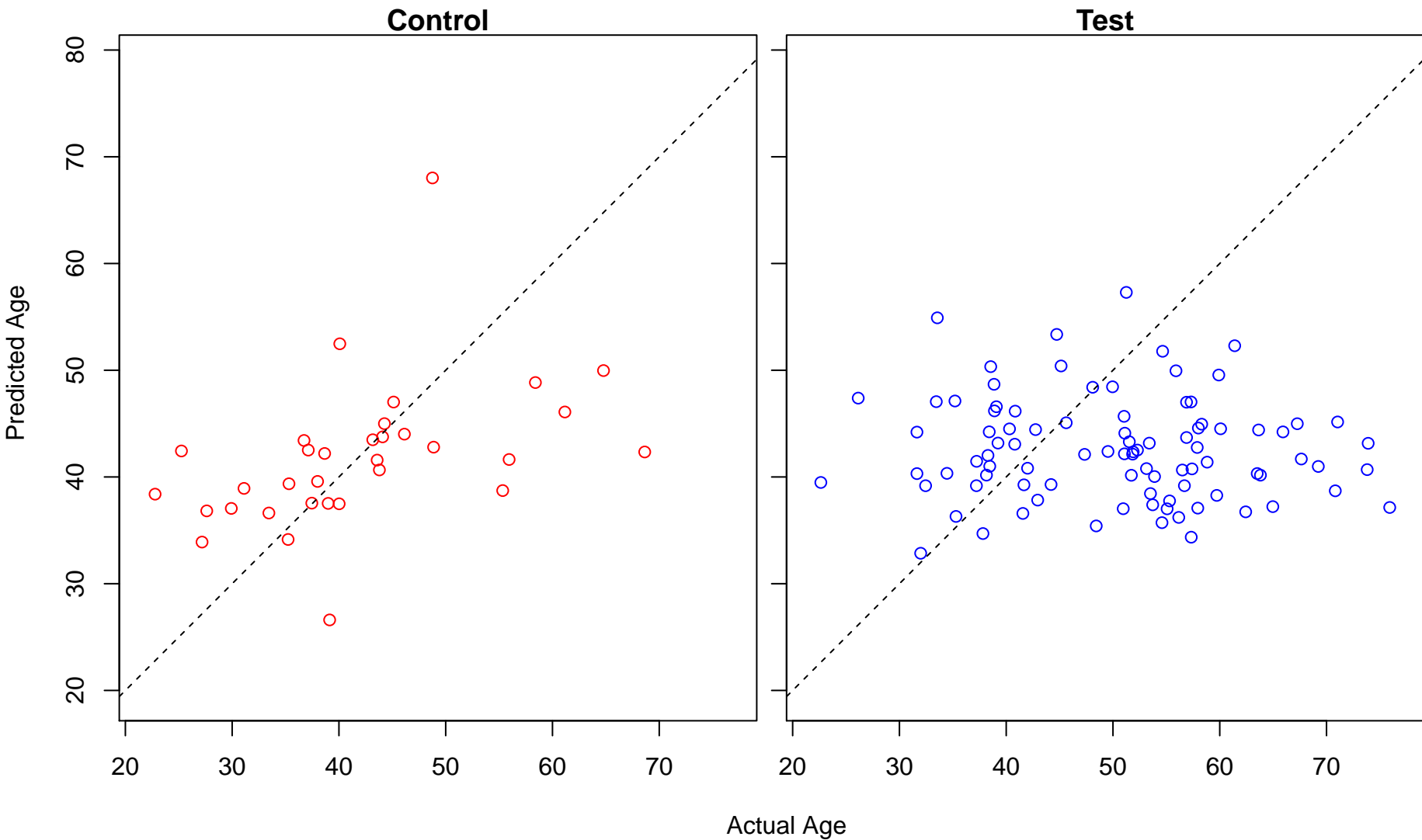
base conversion or substitution editing (Score: 0.743385)



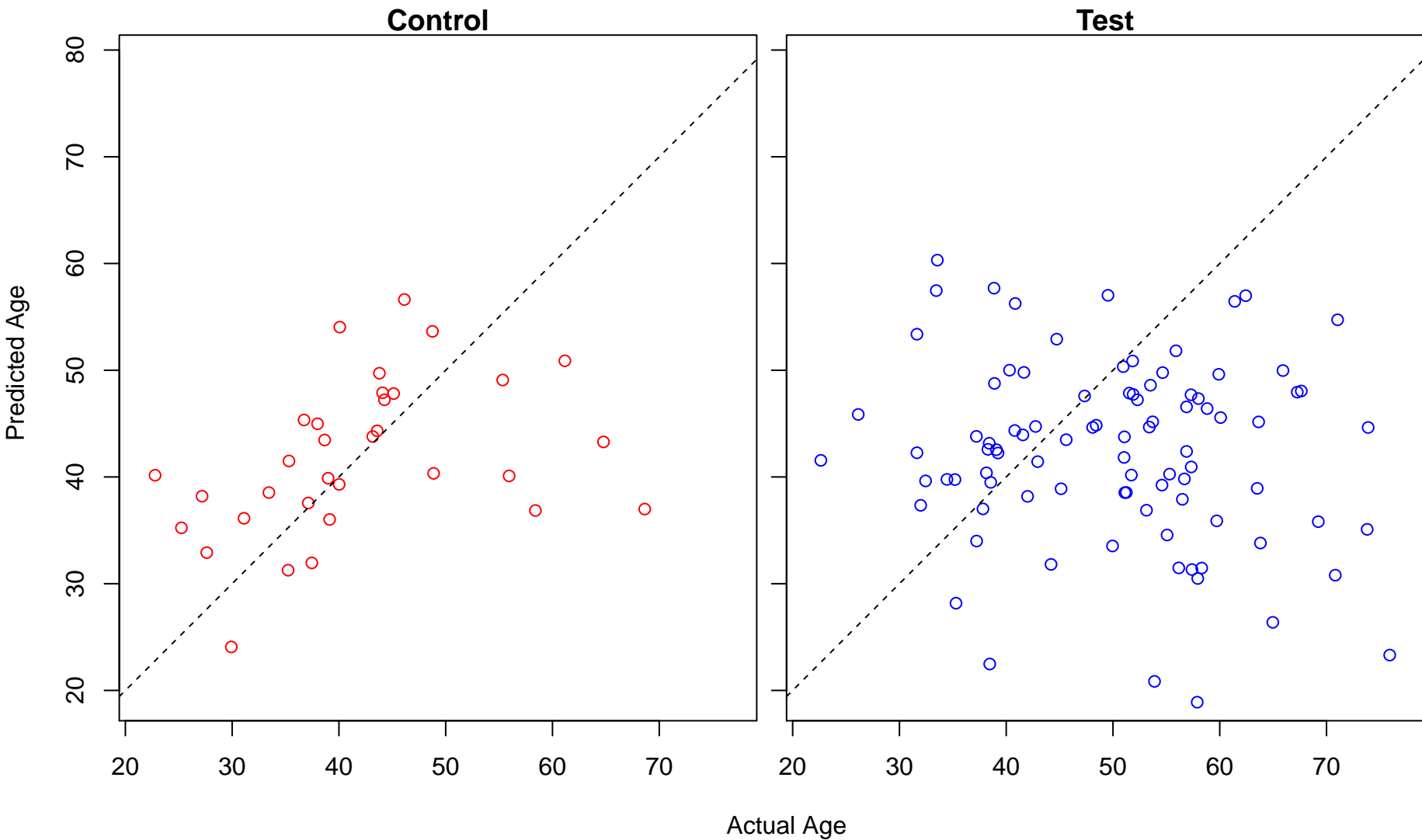
regulation of chromosome organization (Score: 0.743305)



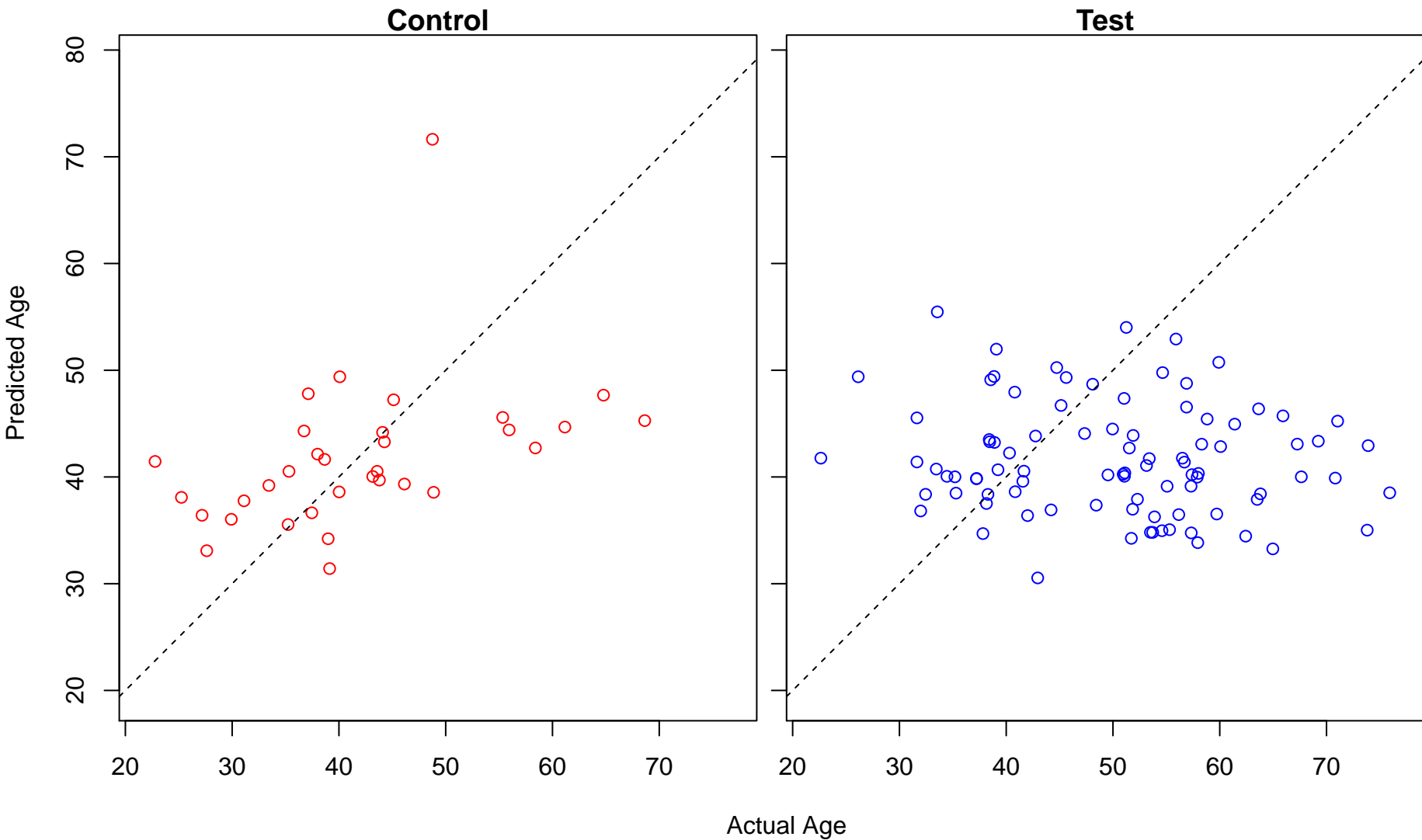
positive regulation of nervous system development (Score: 0.742919)



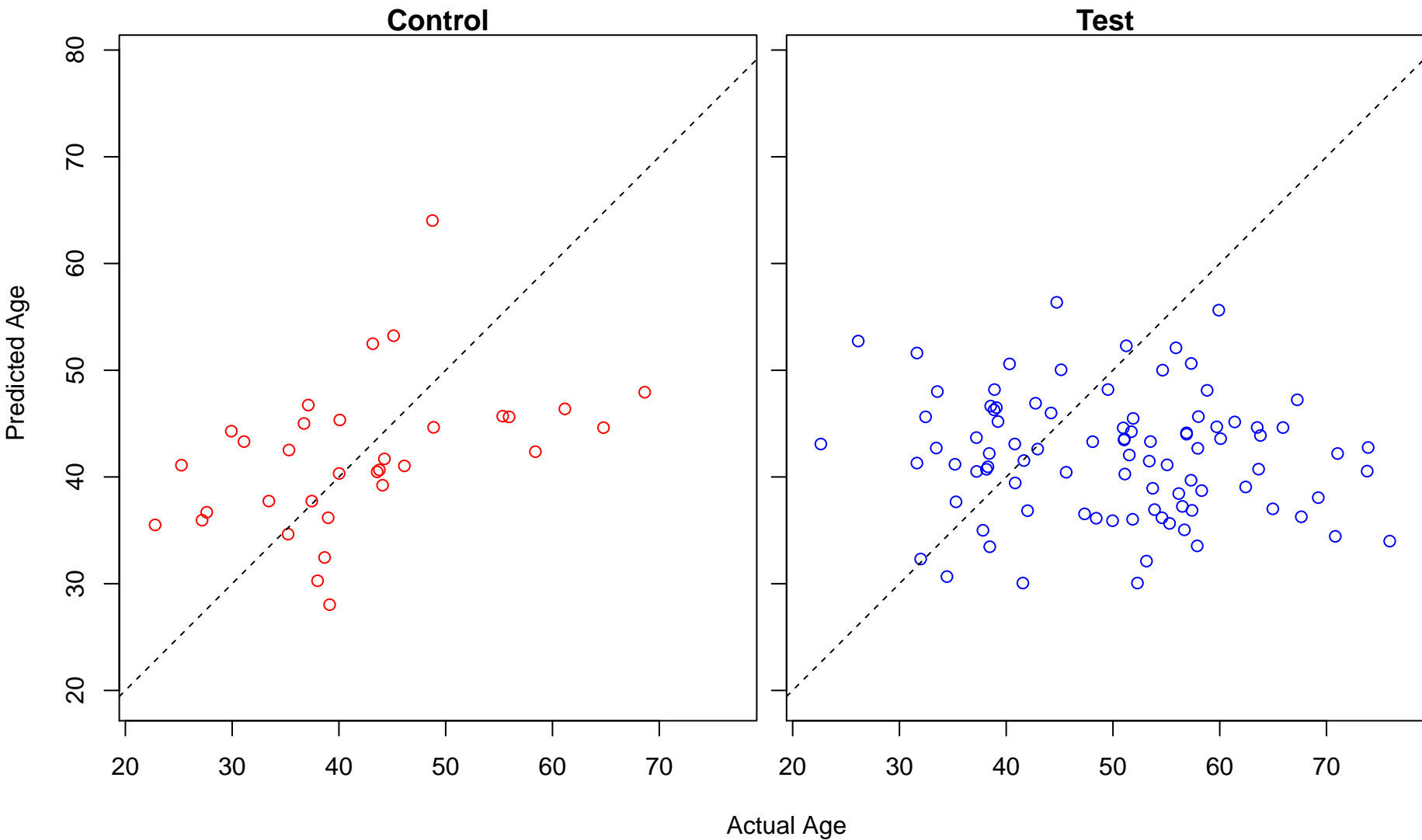
neurotransmitter metabolic process (Score: 0.742575)



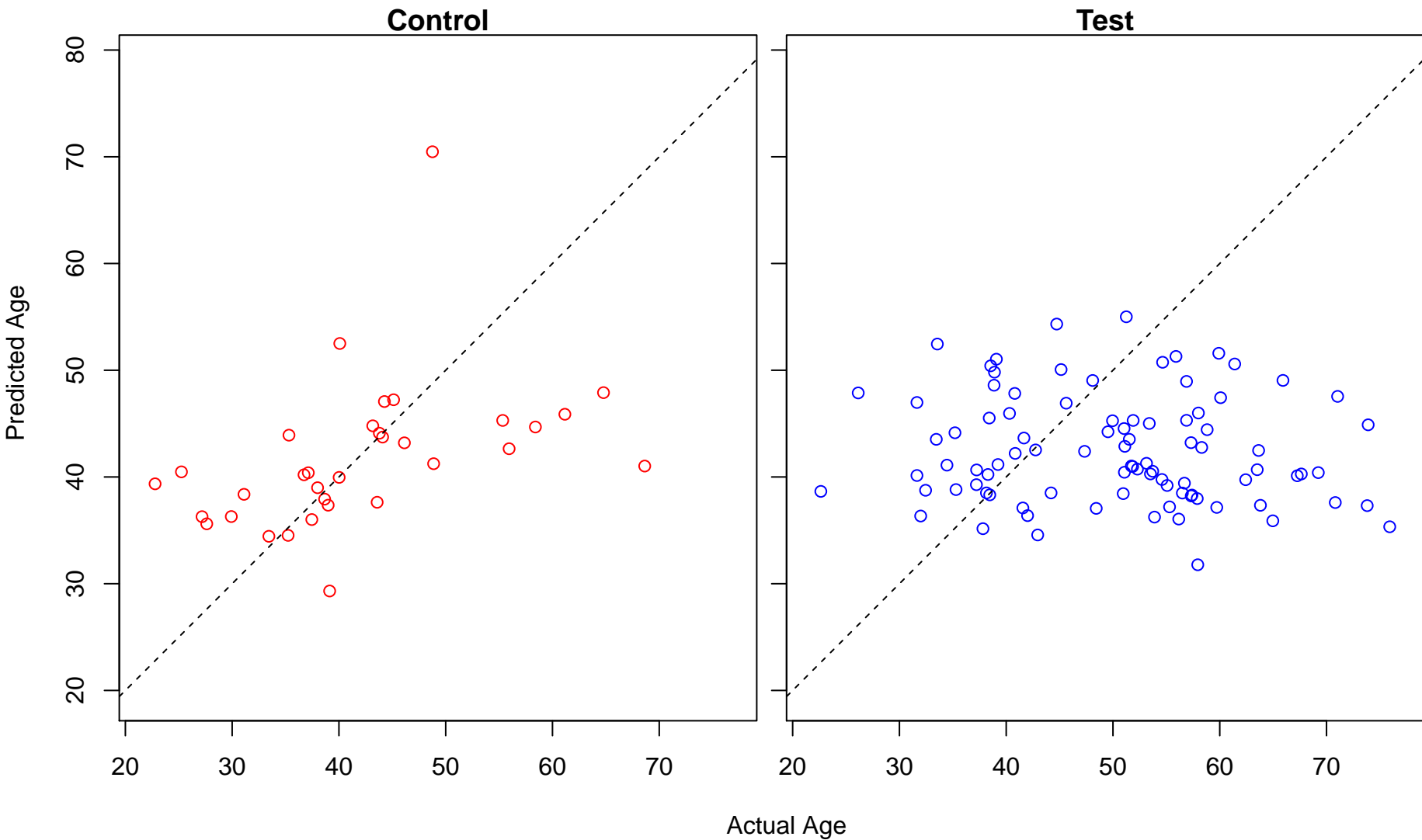
regulation of body fluid levels (Score: 0.742367)



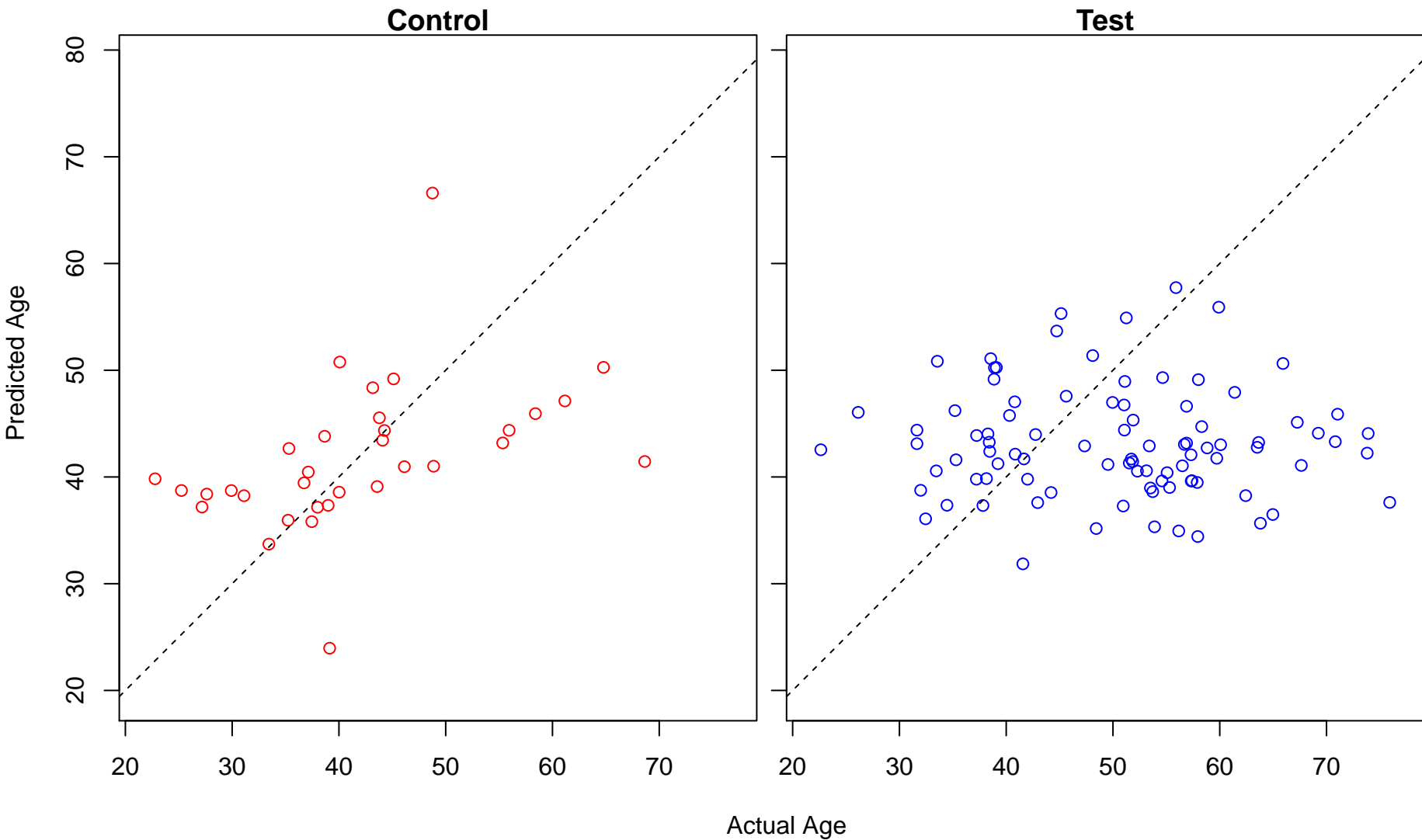
ectoderm development (Score: 0.742063)



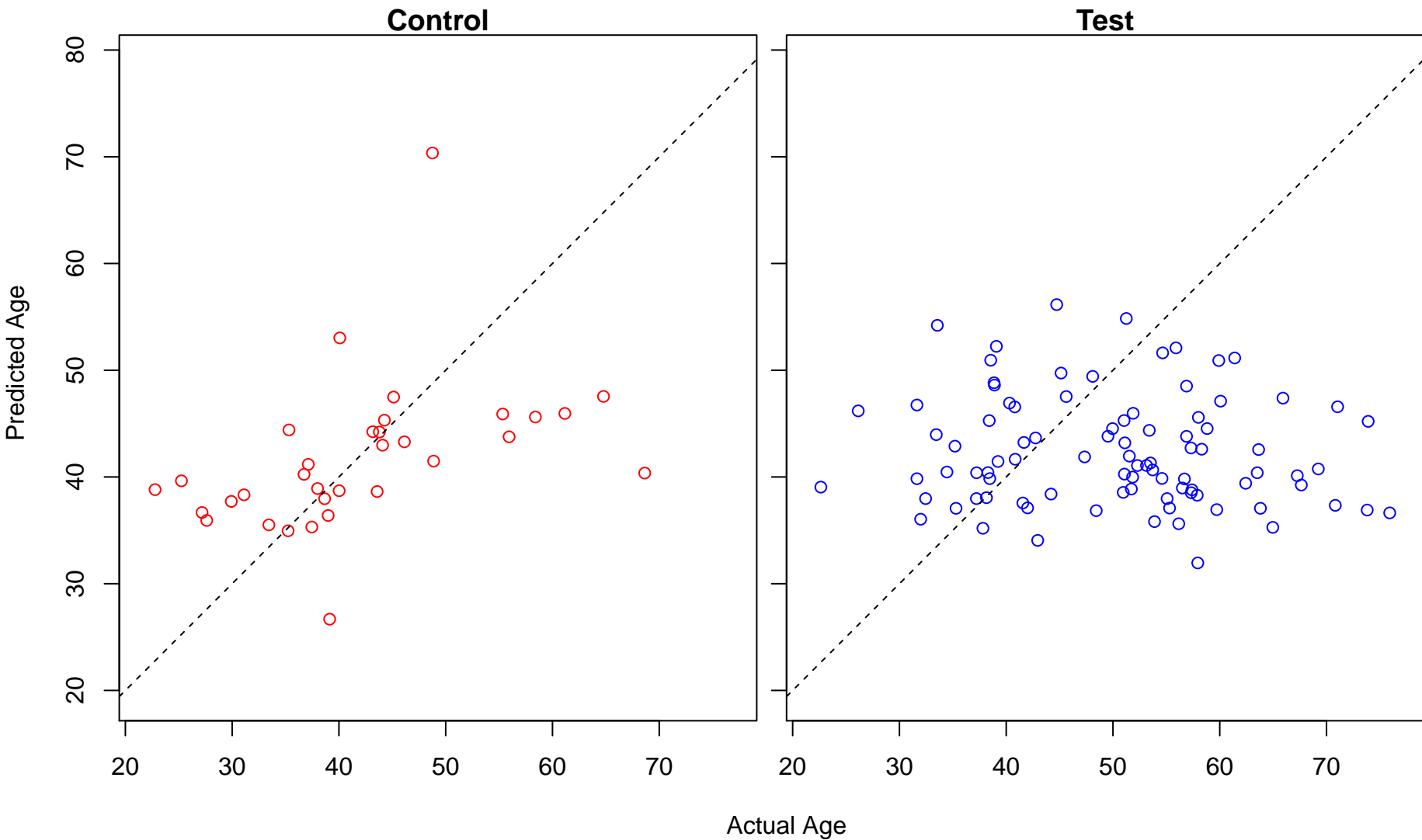
regulation of transcription from RNA polymerase II promoter (Score: 0.741660)



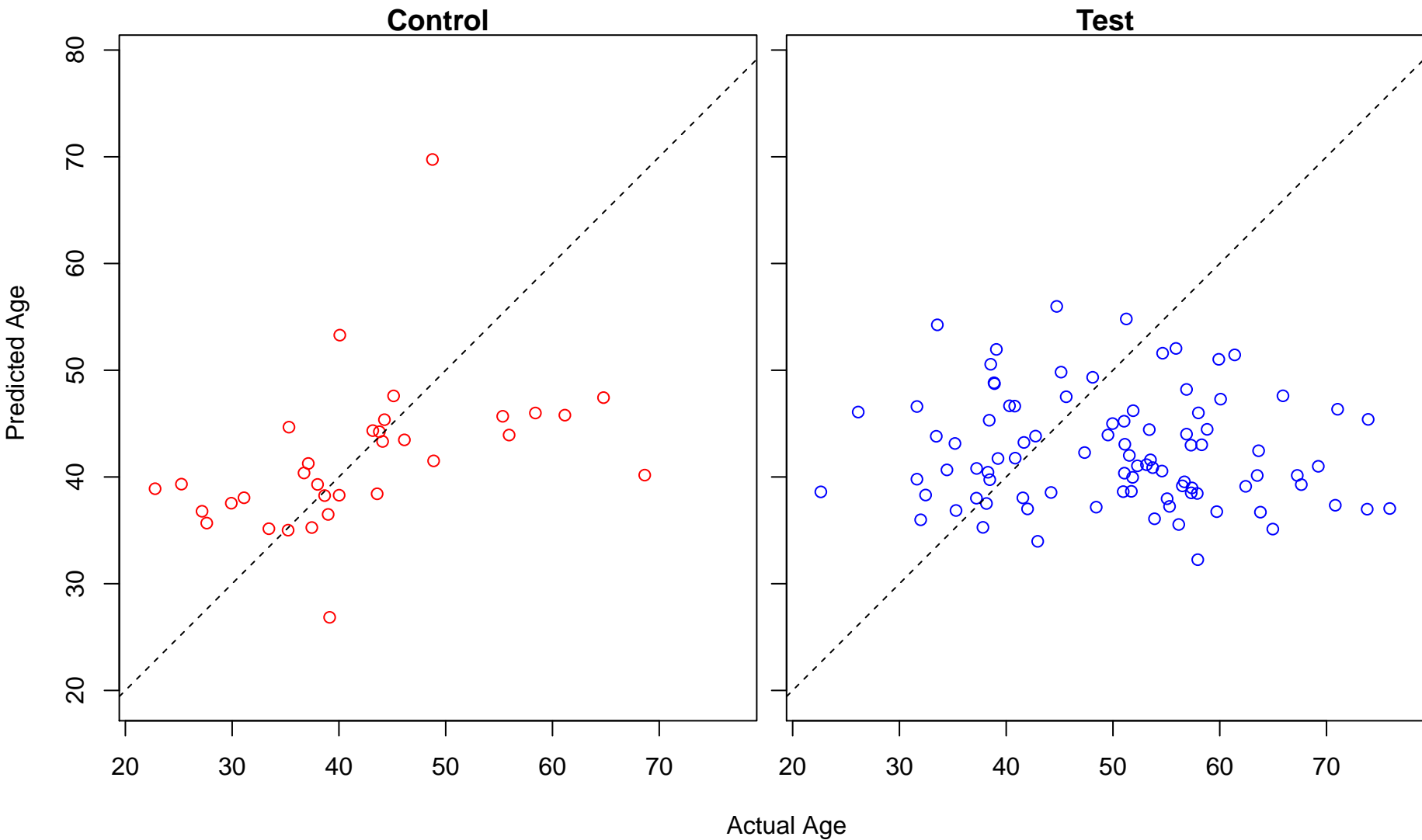
organelle assembly (Score: 0.741555)



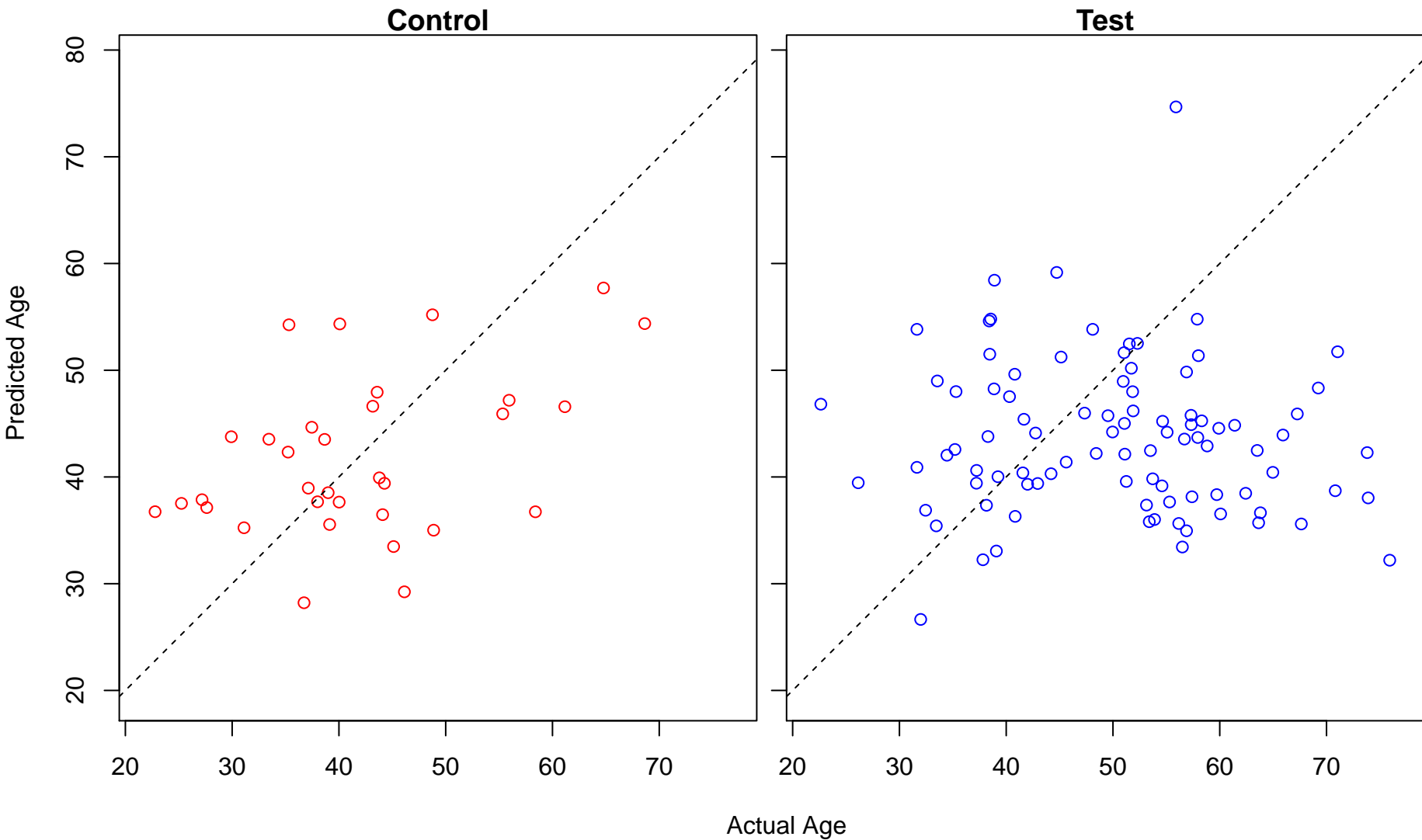
negative regulation of metabolic process (Score: 0.741461)



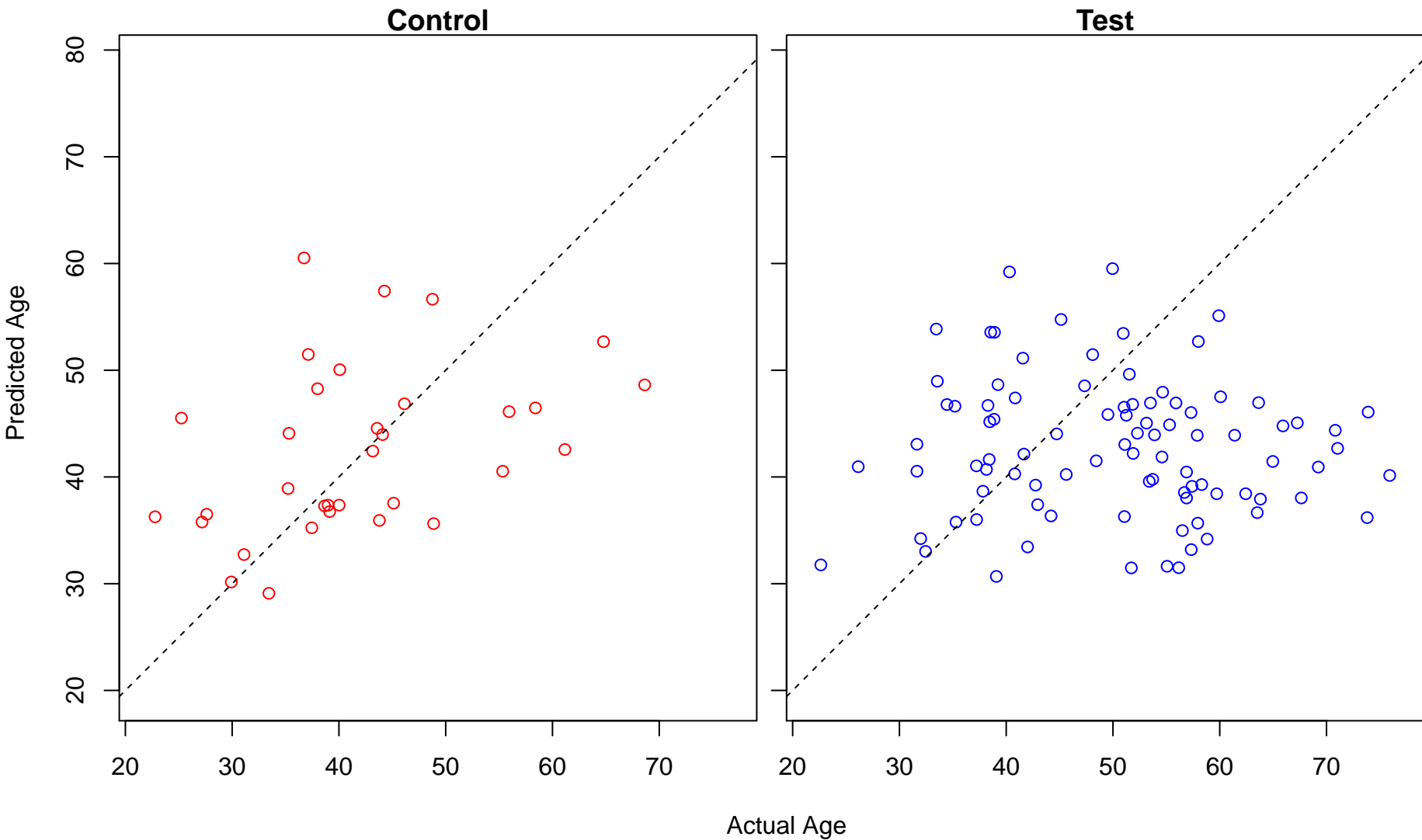
negative regulation of cellular metabolic process (Score: 0.741070)



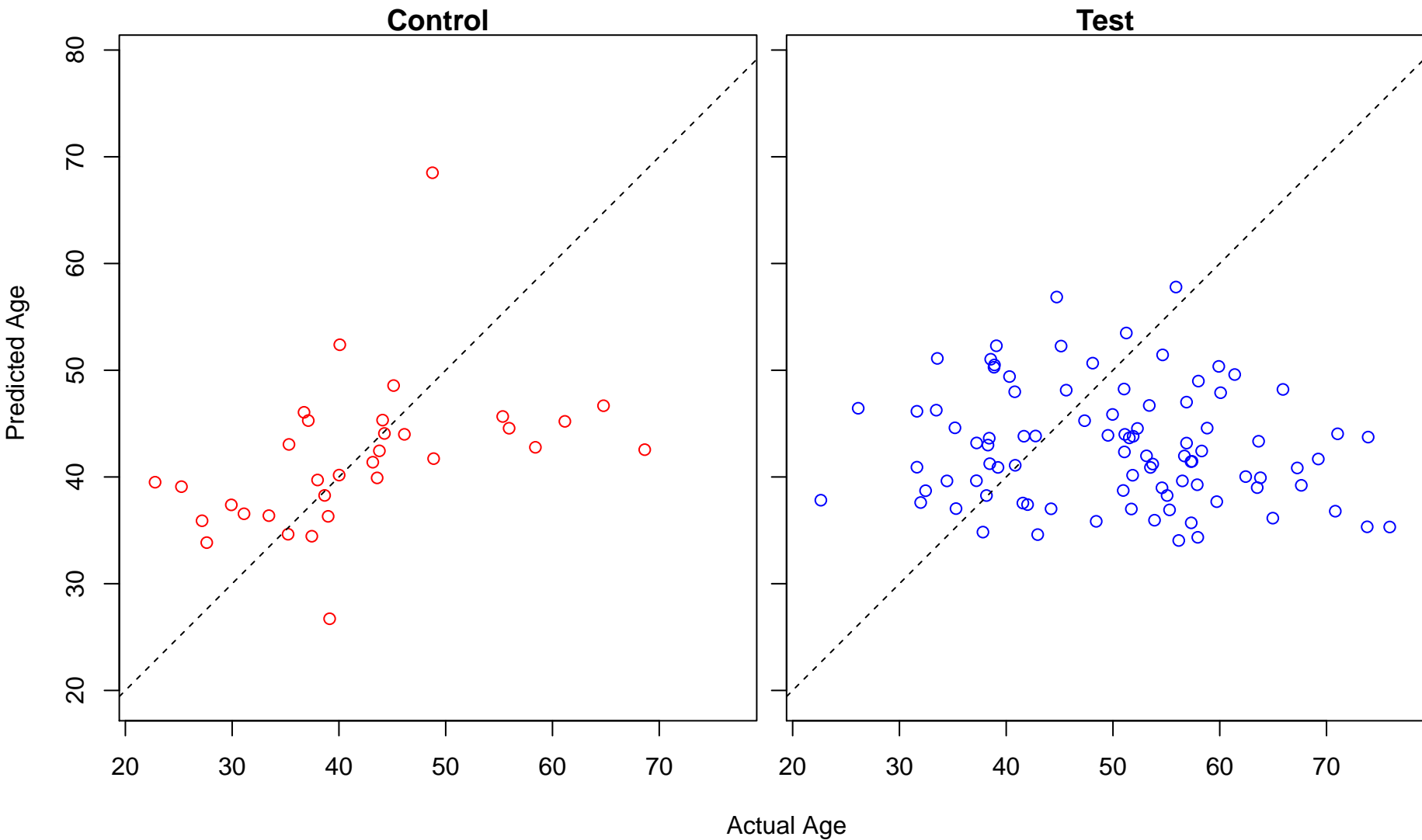
microtubule anchoring (Score: 0.740999)



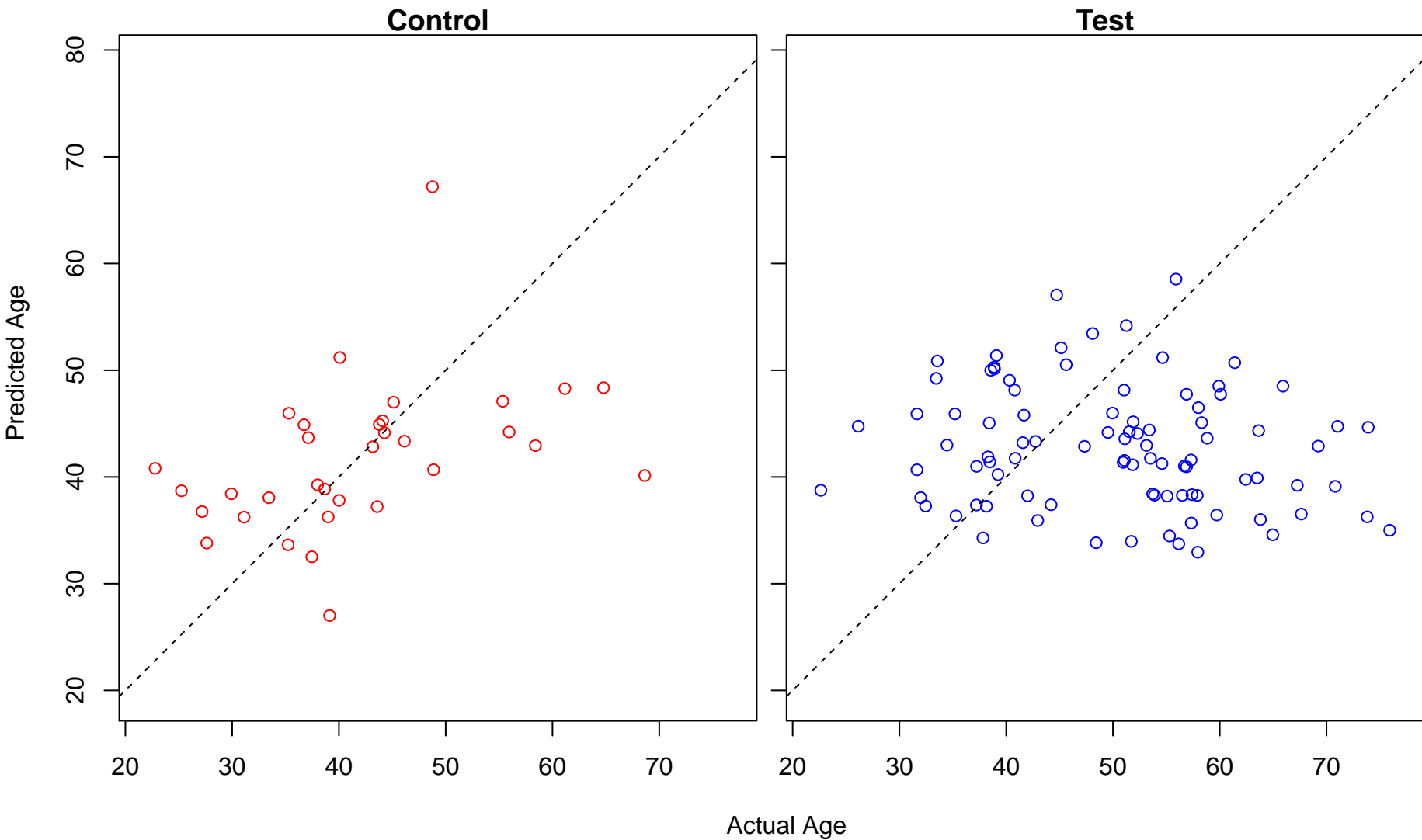
response to cold (Score: 0.740946)



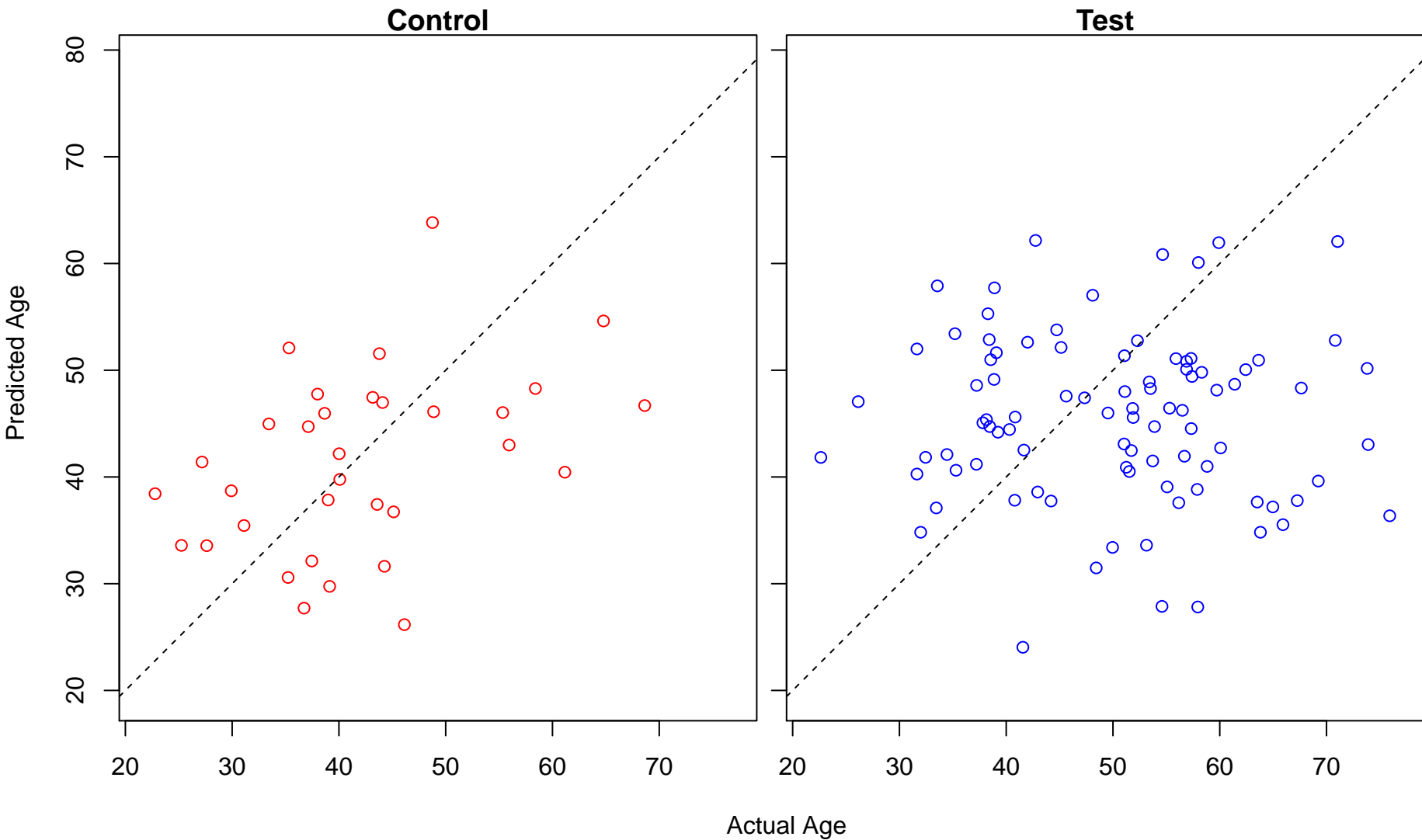
positive regulation of transport (Score: 0.740189)



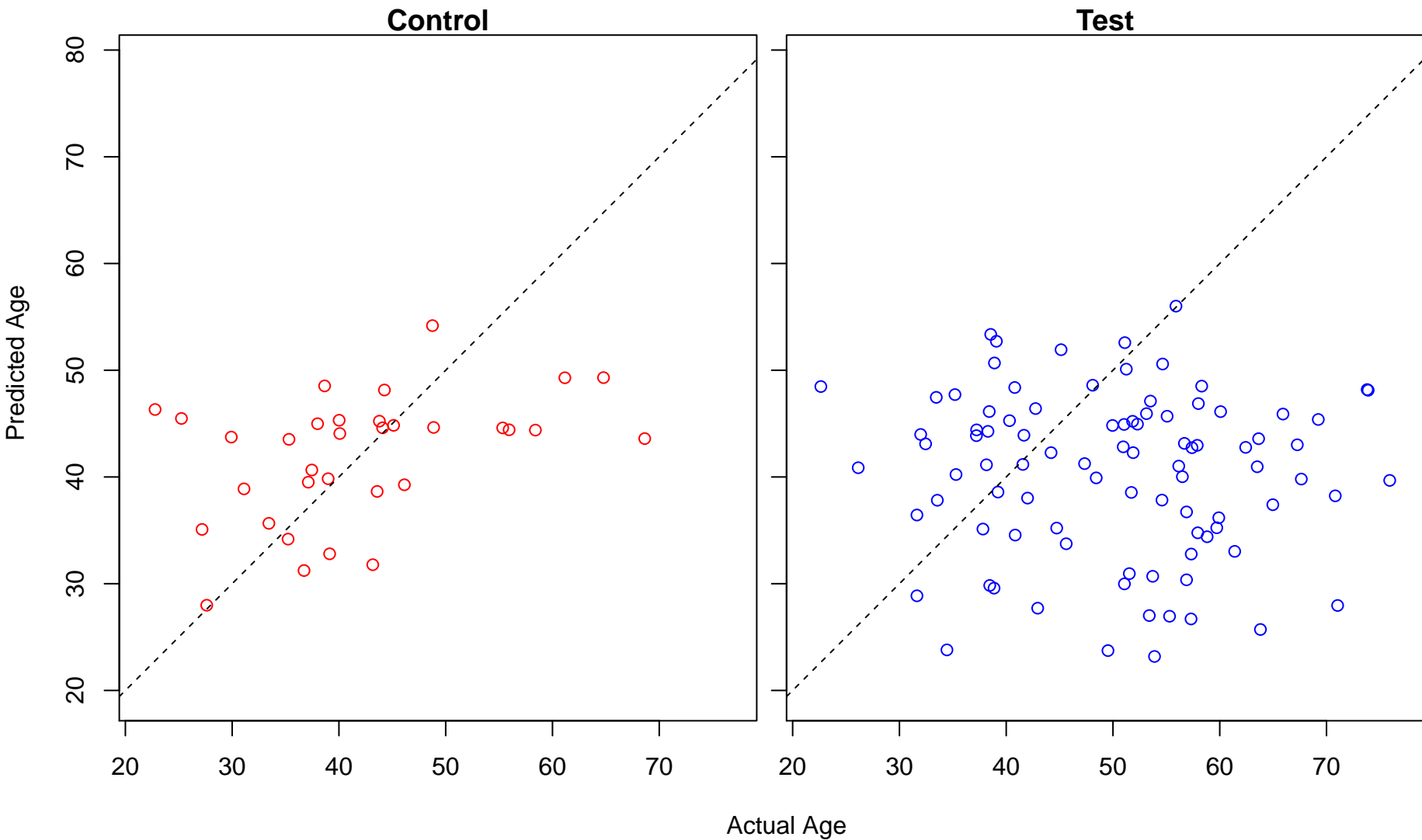
positive regulation of intracellular transport (Score: 0.739967)



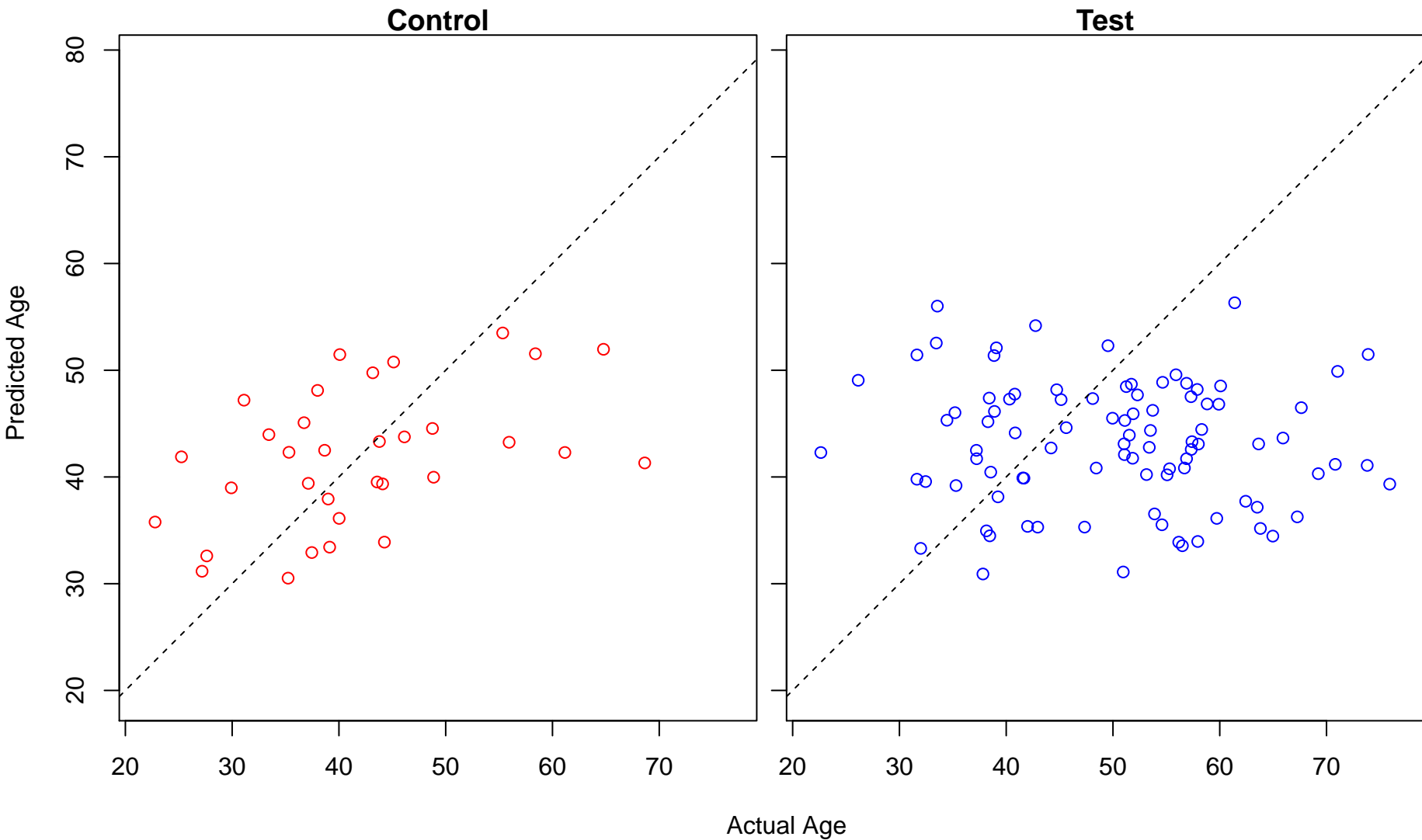
cellular response to ammonium ion (Score: 0.739916)



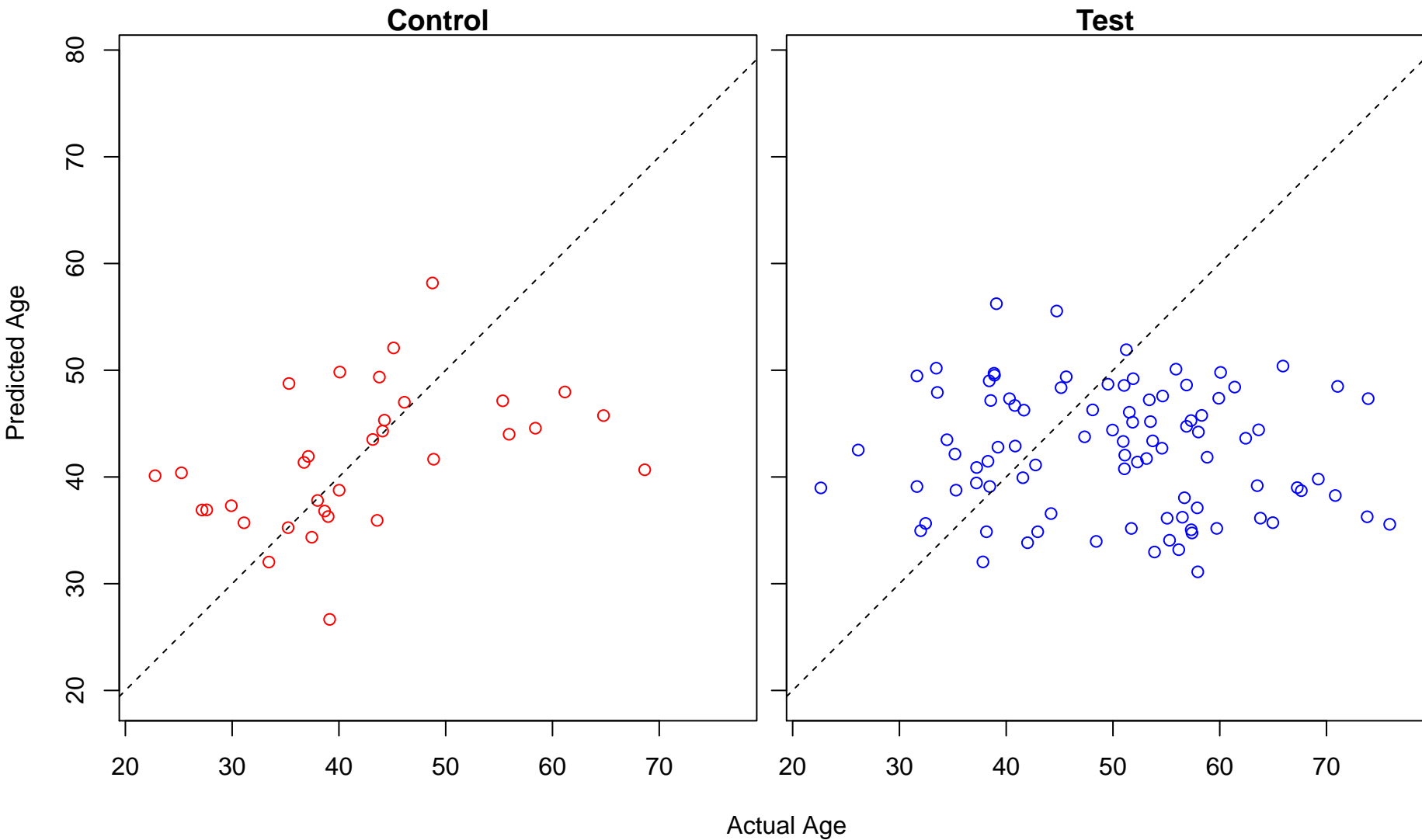
nucleobase-containing small molecule interconversion (Score: 0.739591)



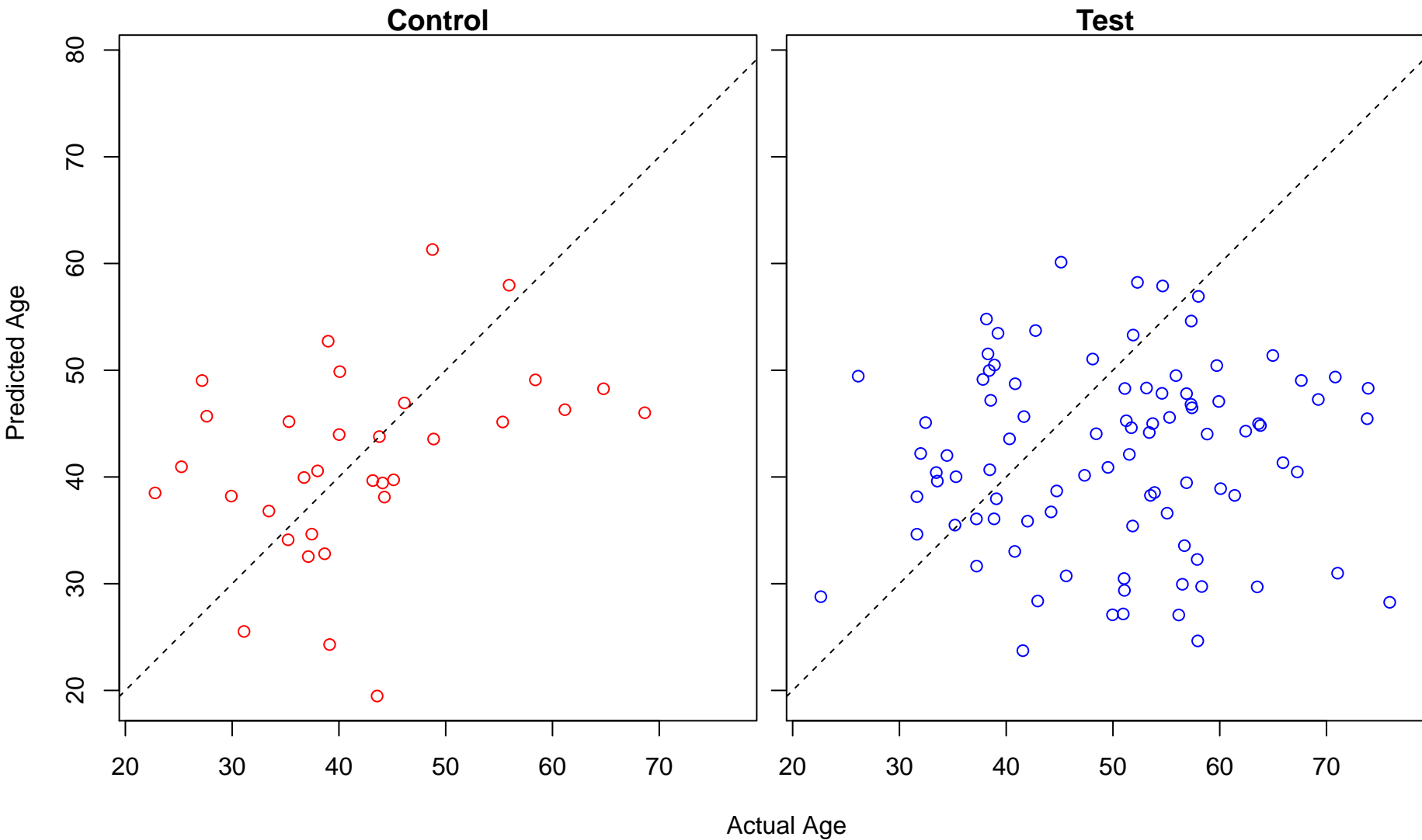
epithelial to mesenchymal transition (Score: 0.737826)



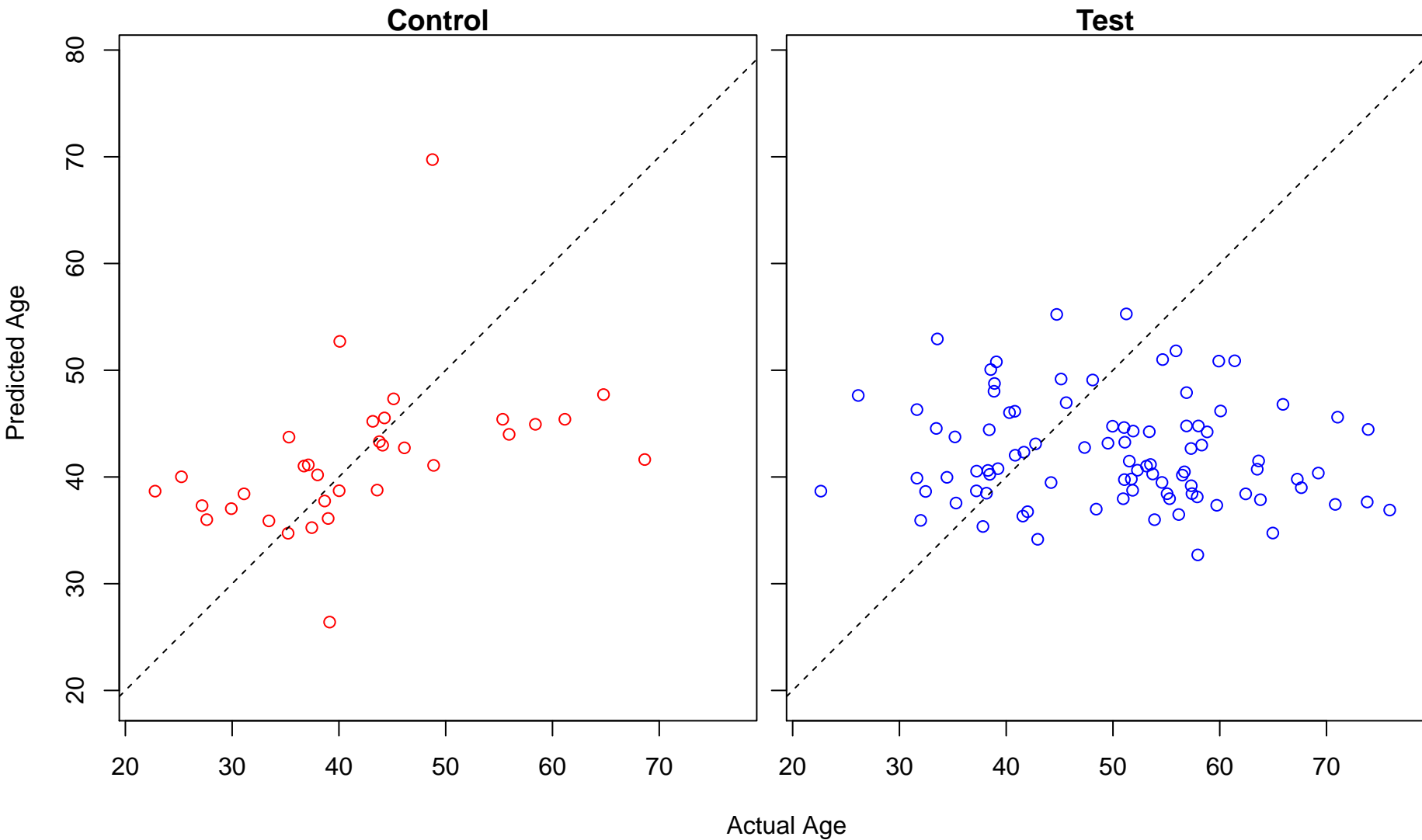
establishment of RNA localization (Score: 0.737760)



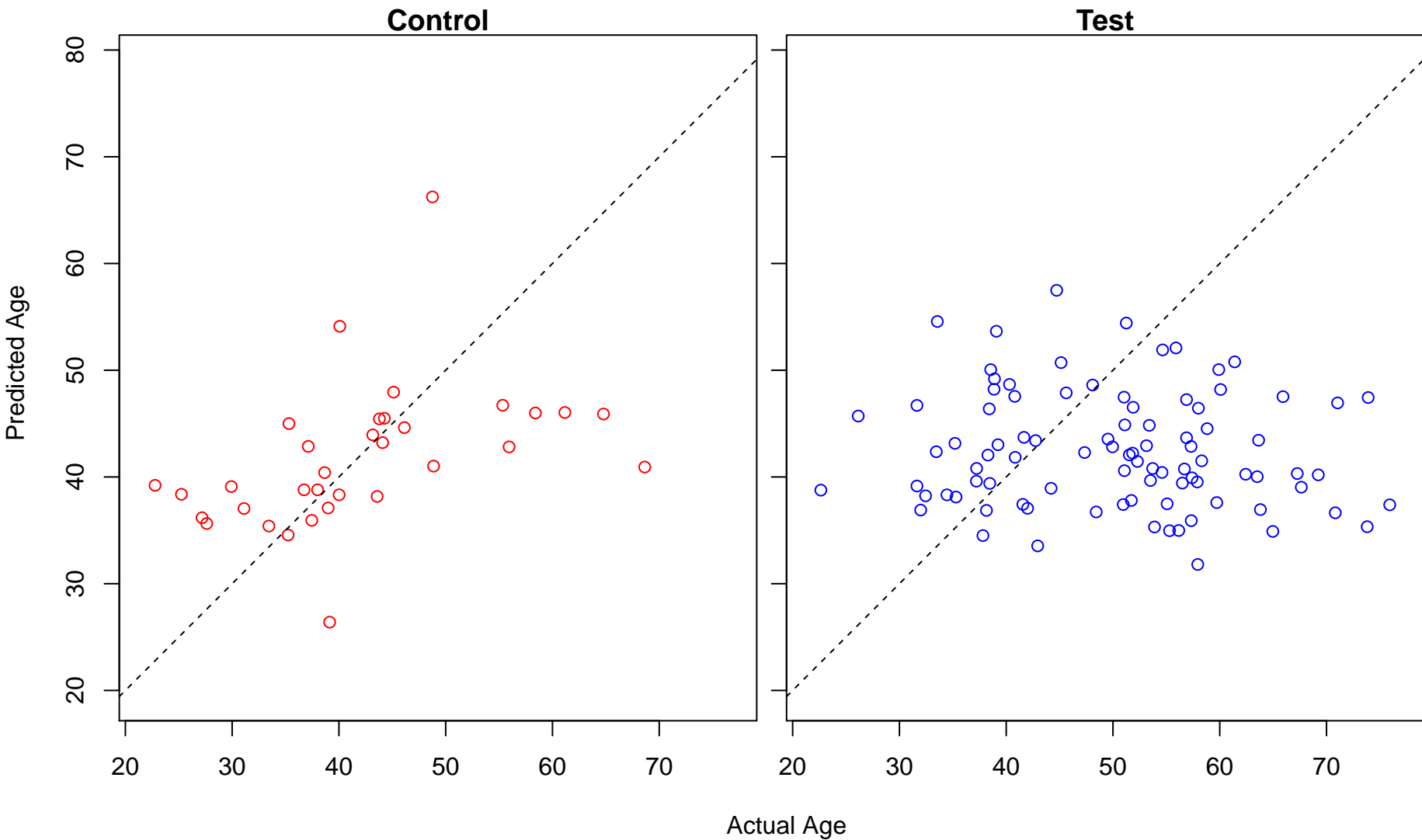
negative regulation of JUN kinase activity (Score: 0.737640)



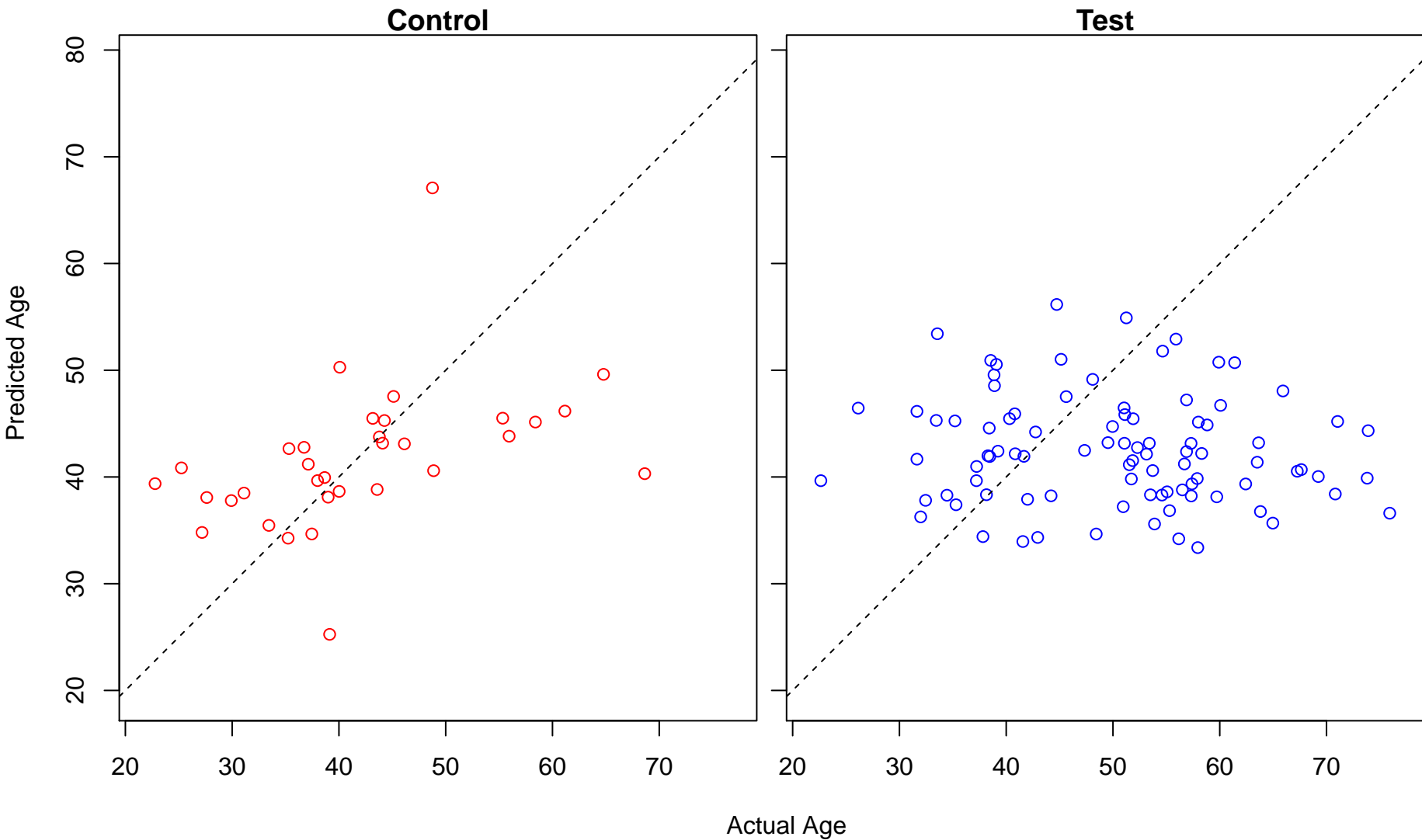
negative regulation of cellular biosynthetic process (Score: 0.737315)



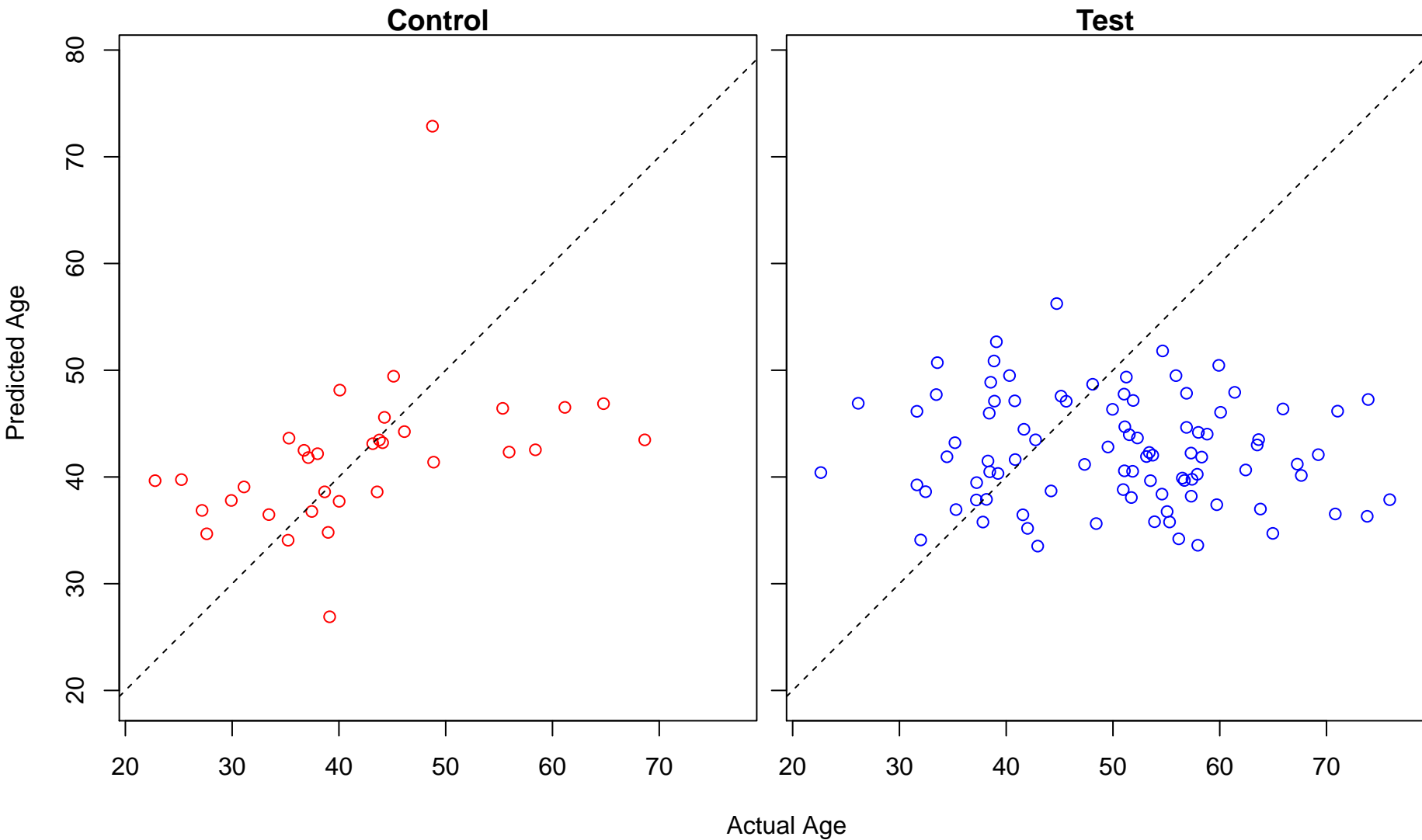
regulation of protein phosphorylation (Score: 0.736977)



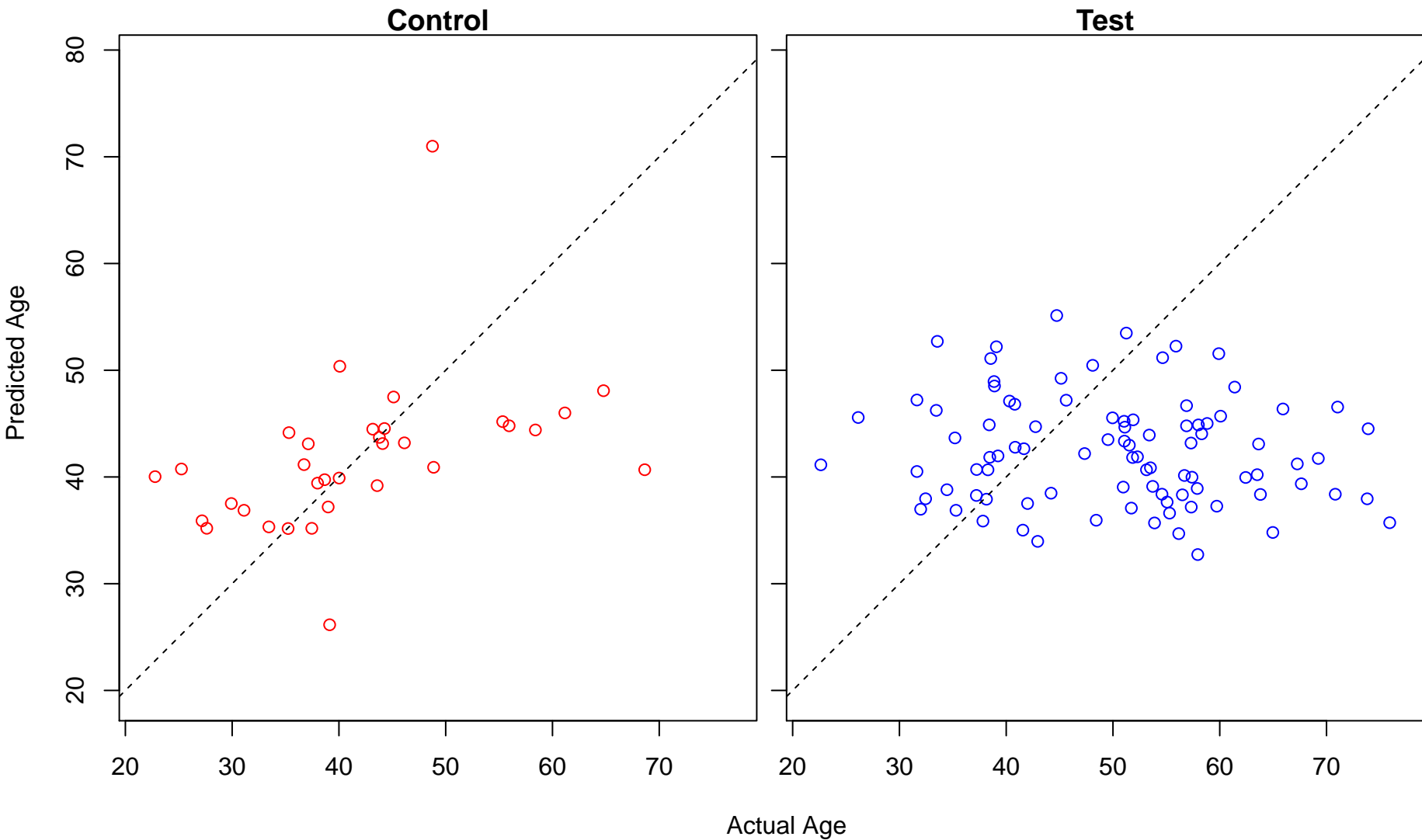
cellular developmental process (Score: 0.735584)



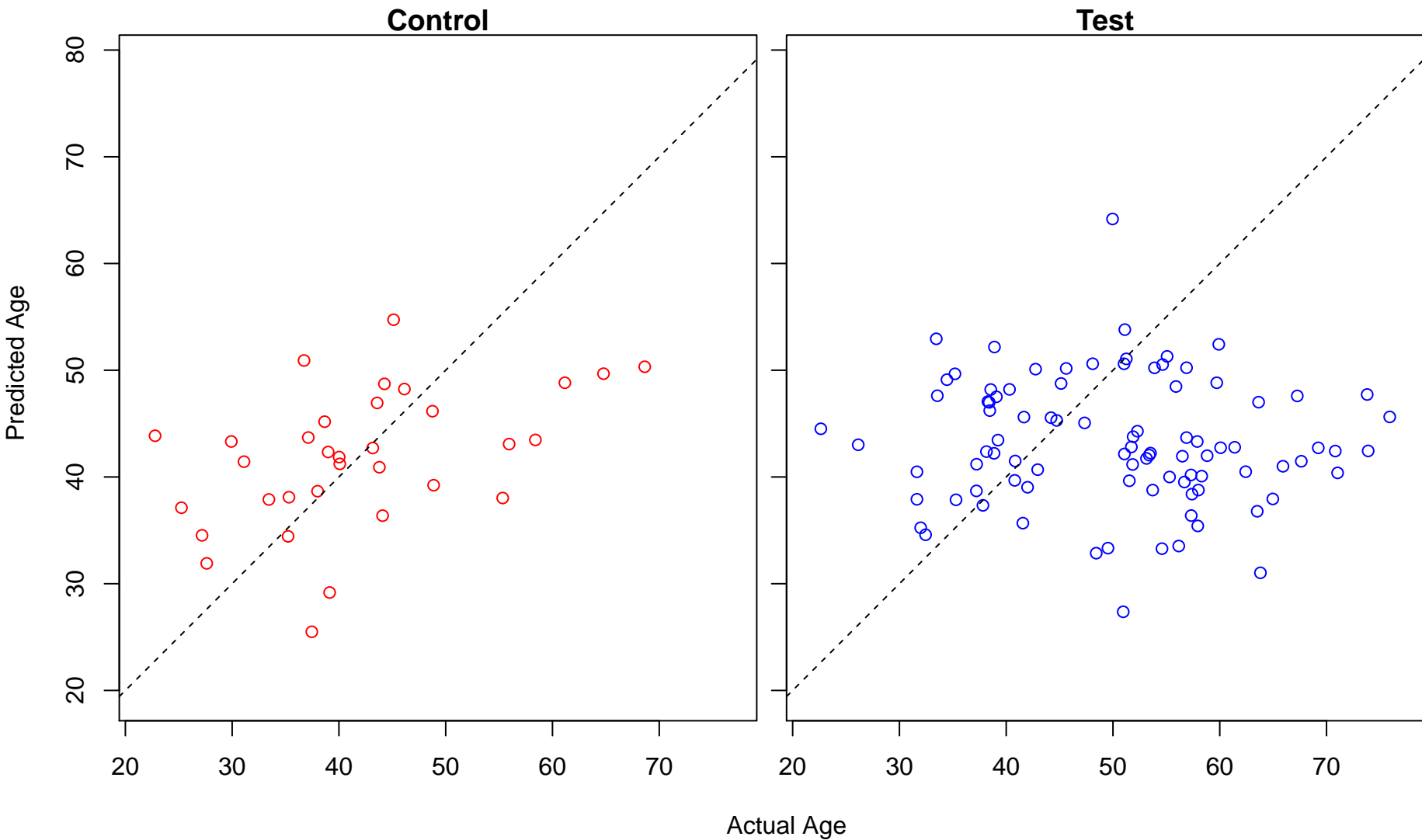
regulation of cellular component biogenesis (Score: 0.735165)



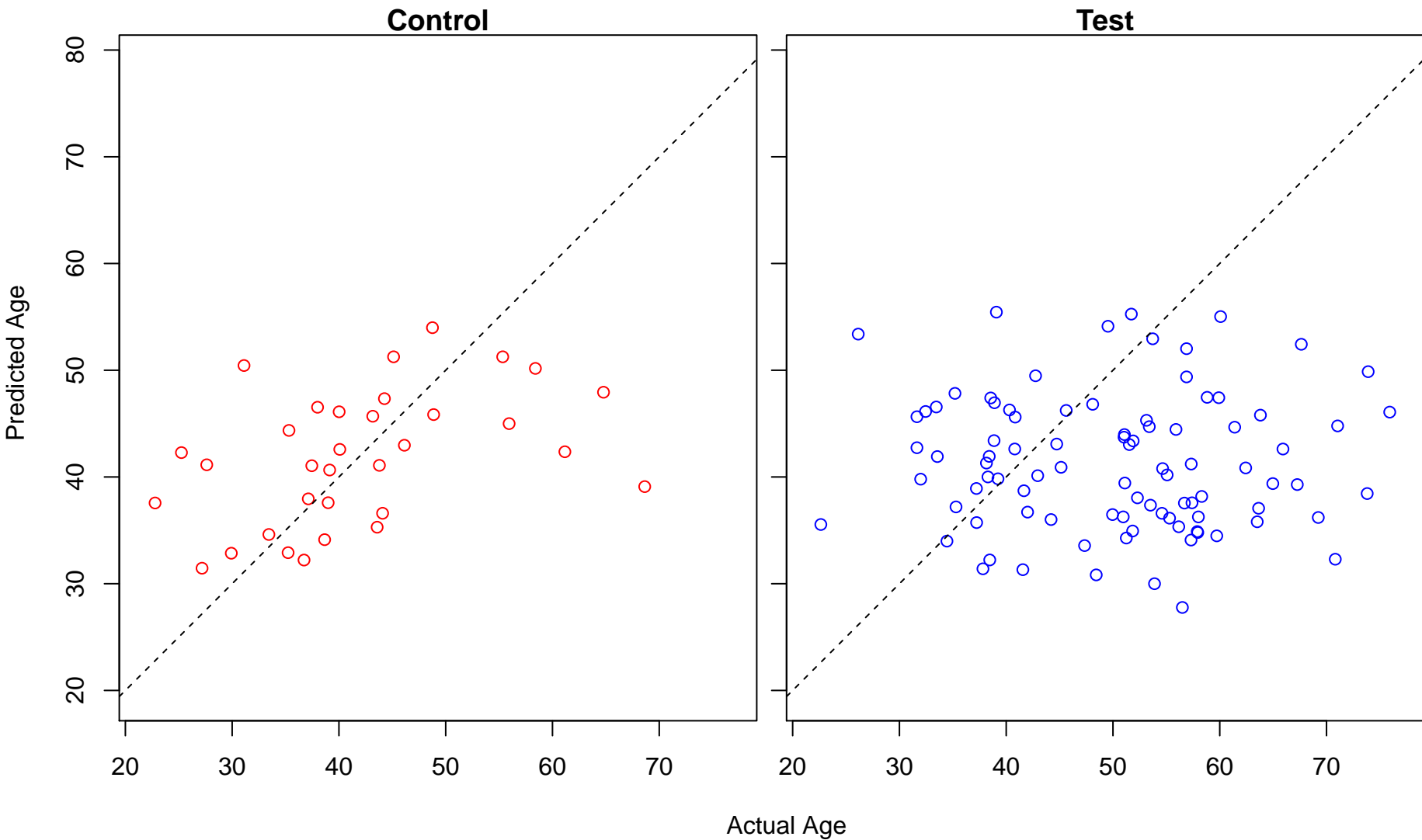
transport (Score: 0.735133)



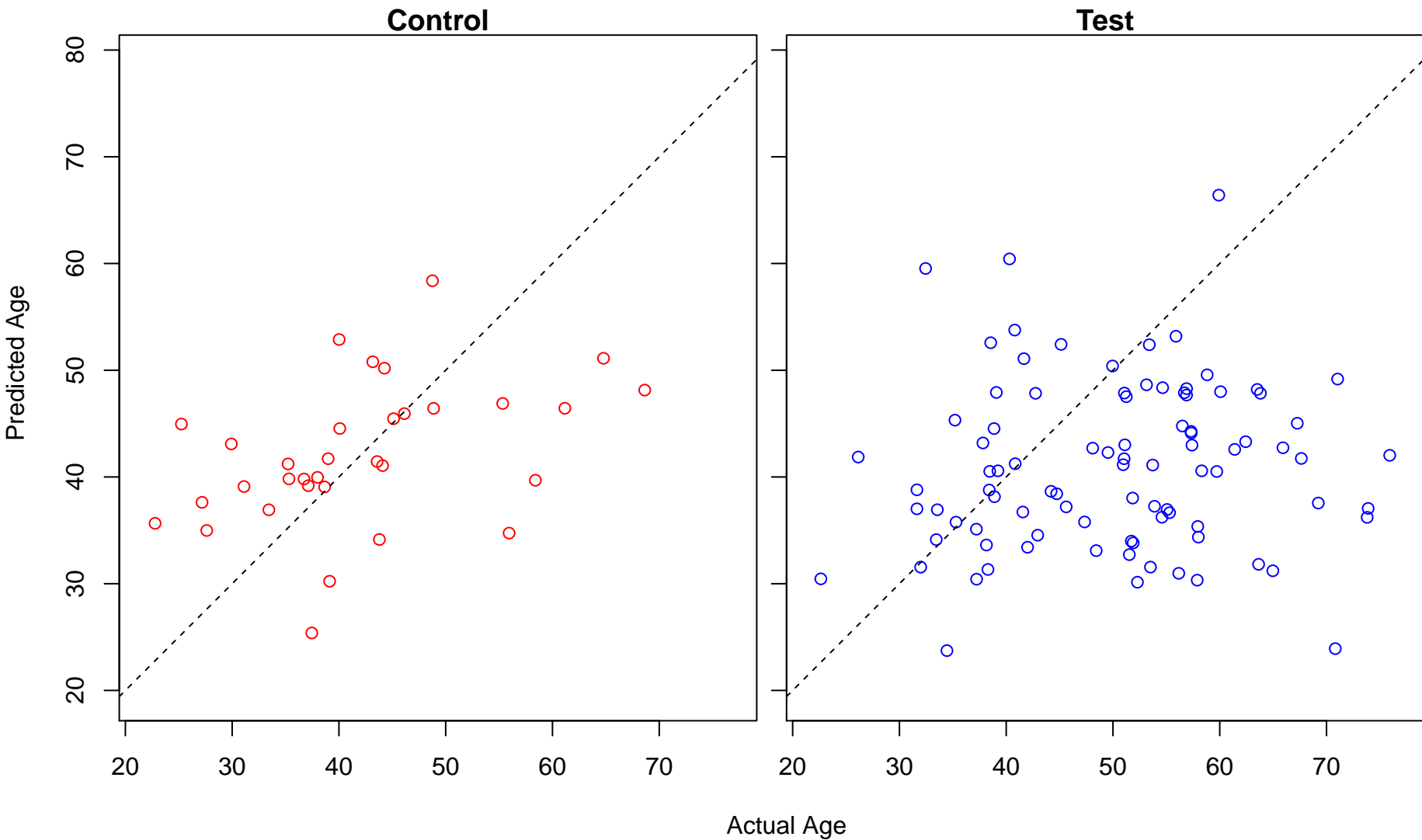
regulation of respiratory system process (Score: 0.734851)



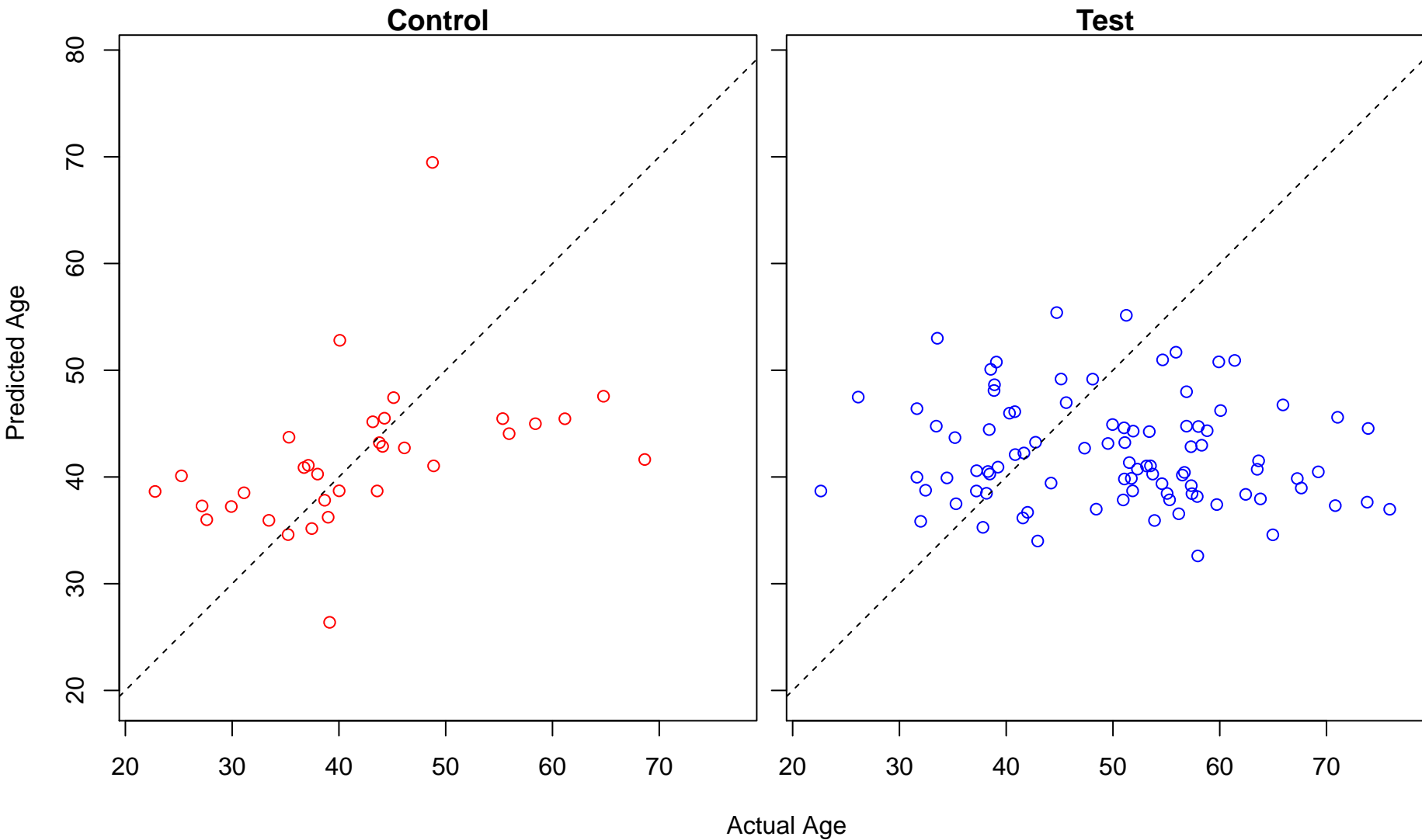
mesoderm formation (Score: 0.734822)



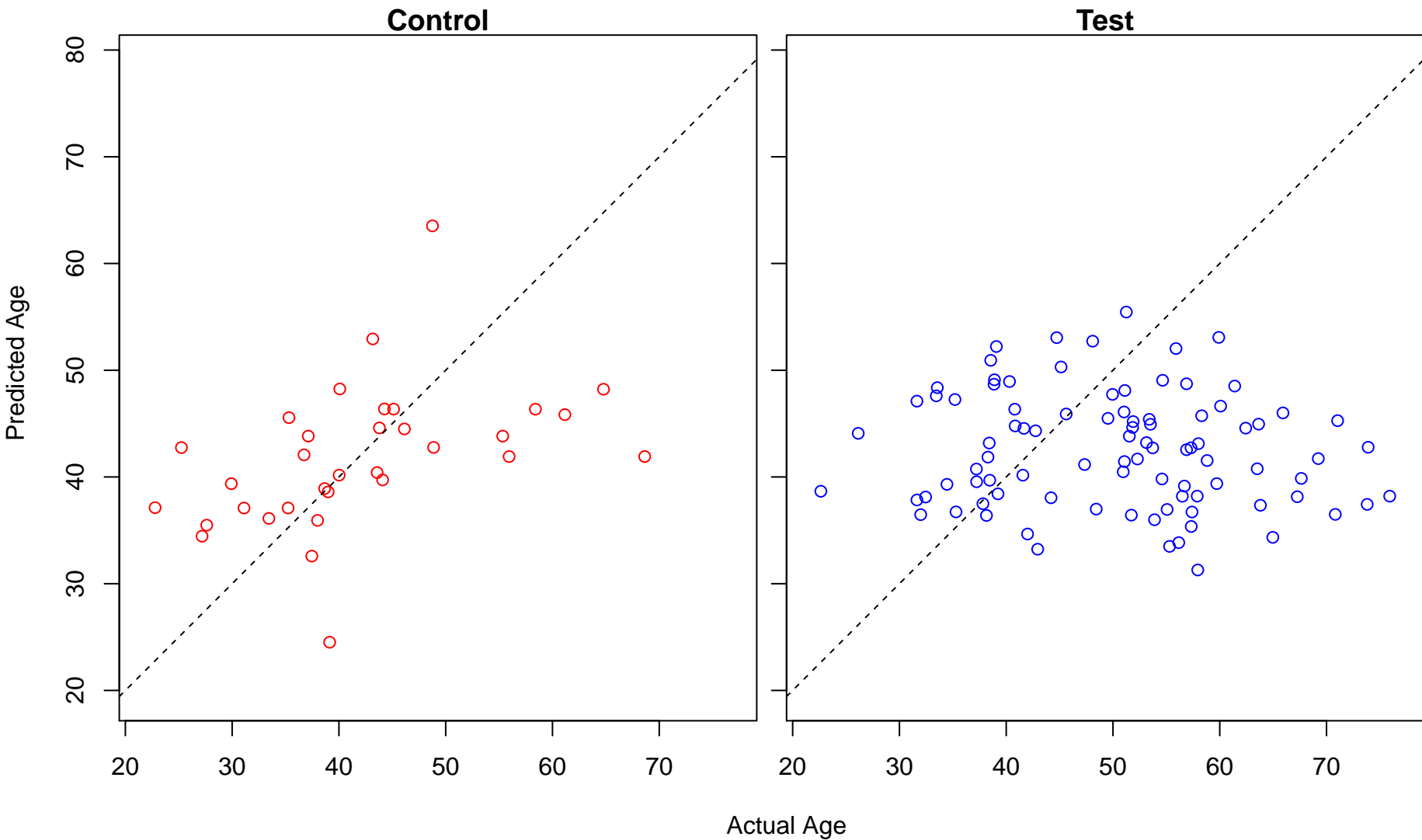
neutrophil homeostasis (Score: 0.734624)



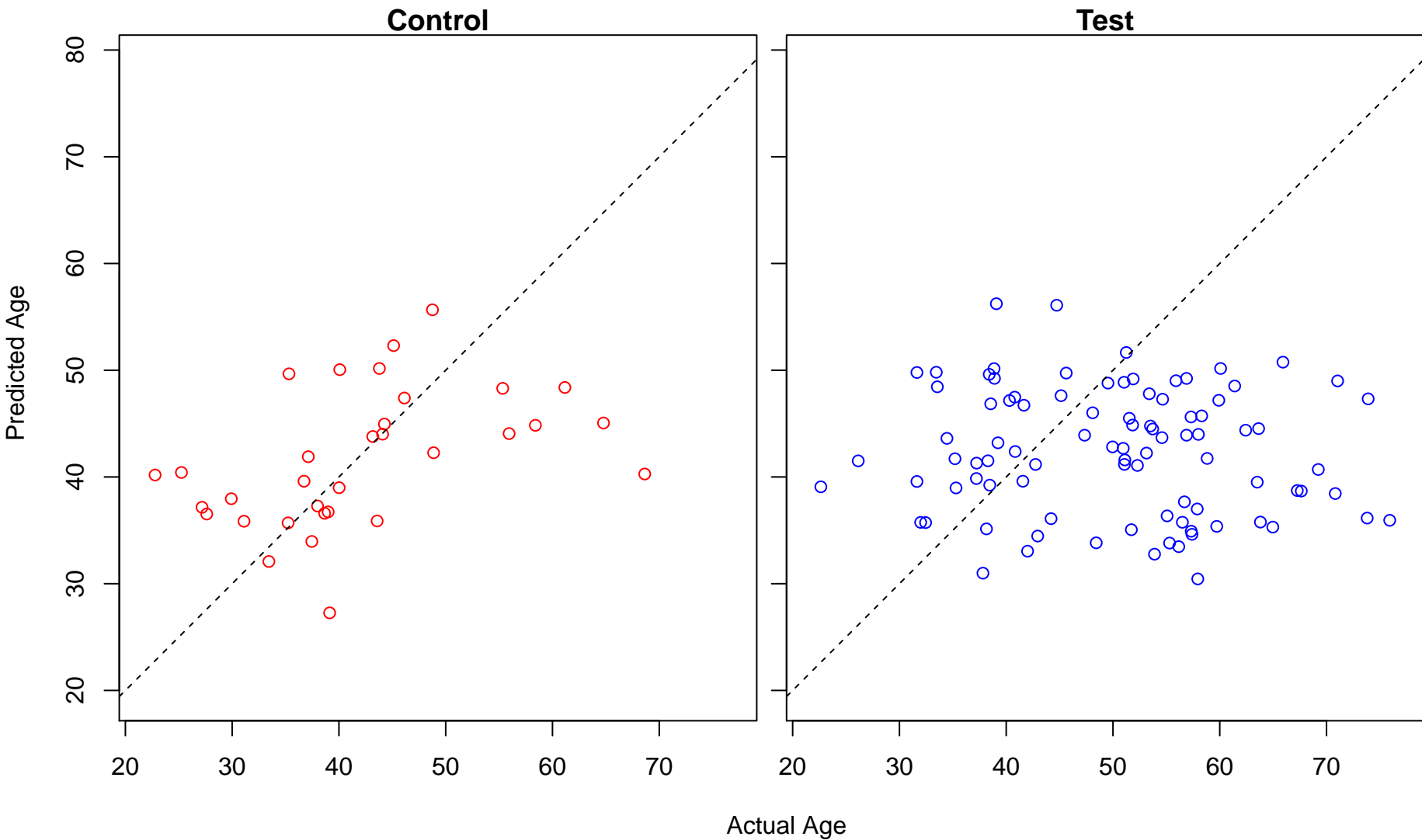
negative regulation of biosynthetic process (Score: 0.734163)



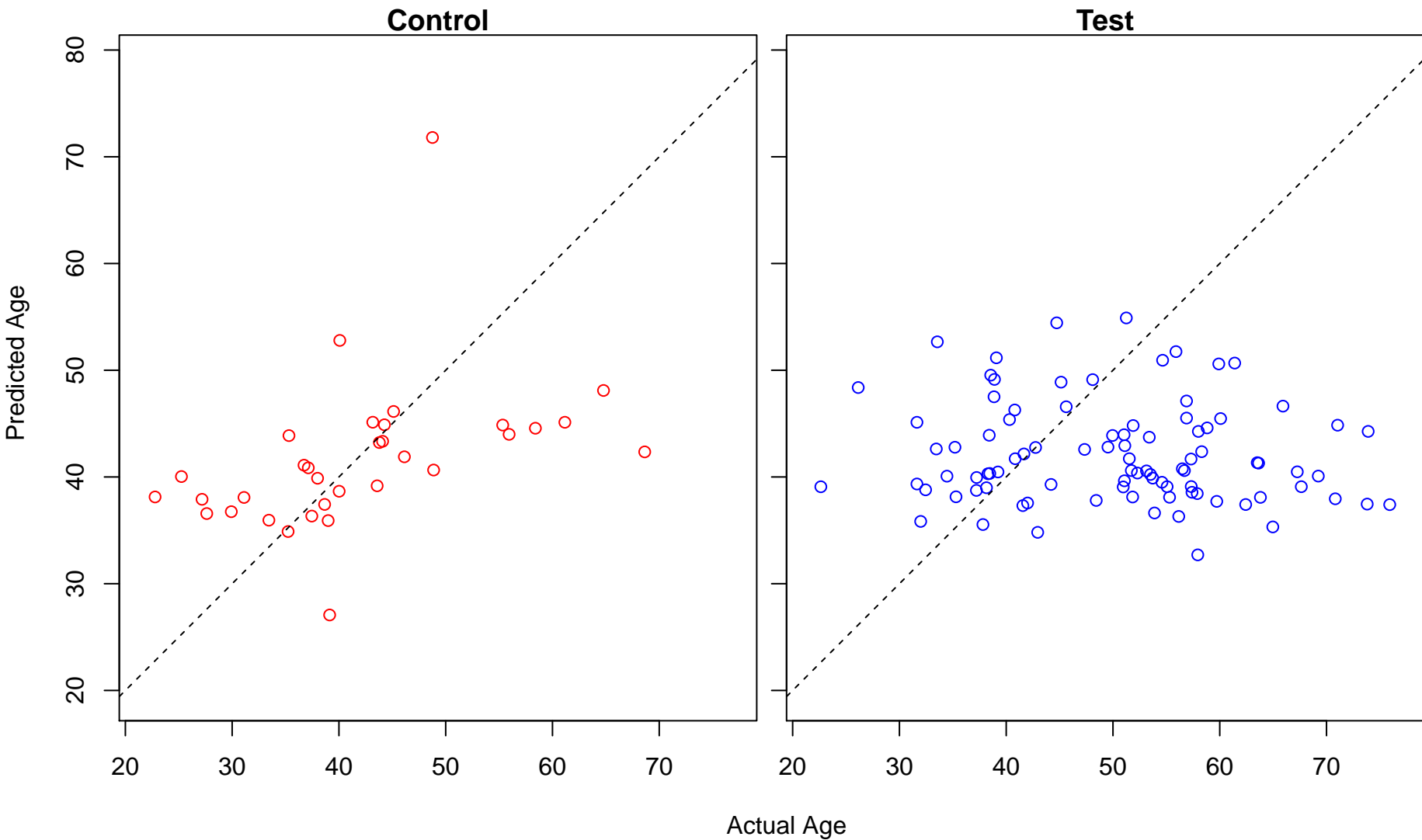
nitrogen compound transport (Score: 0.733917)



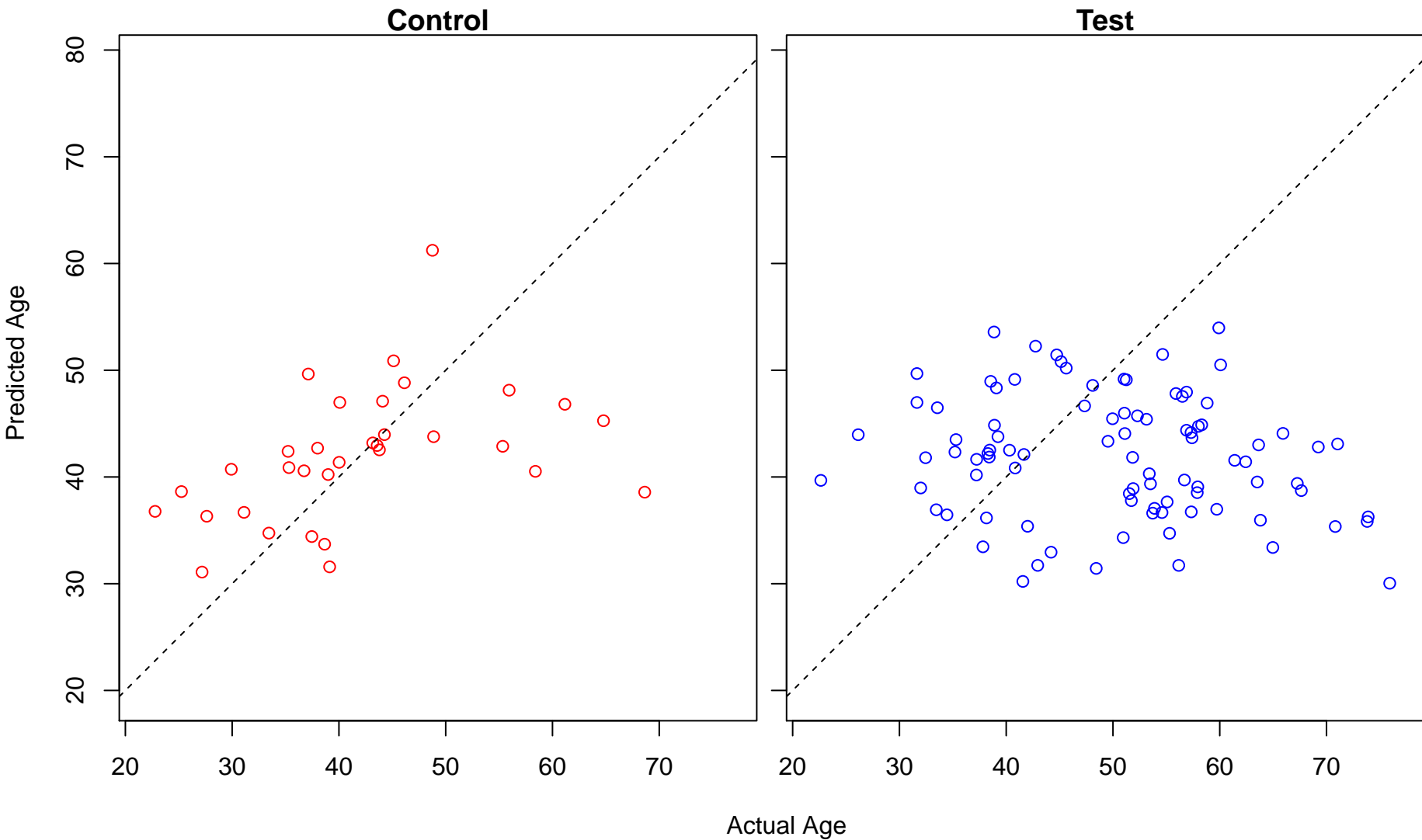
mRNA transport (Score: 0.733634)



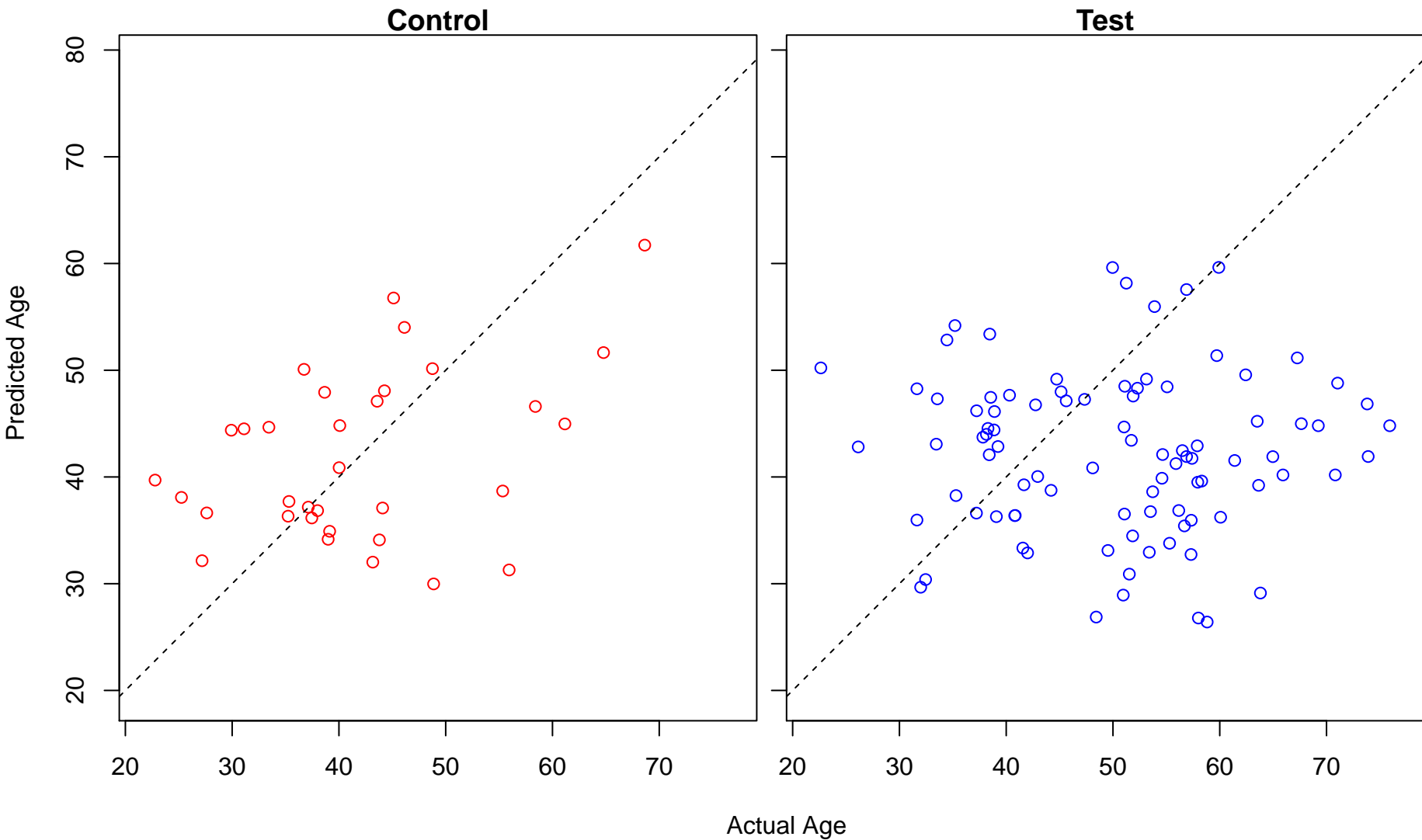
negative regulation of RNA metabolic process (Score: 0.73537)



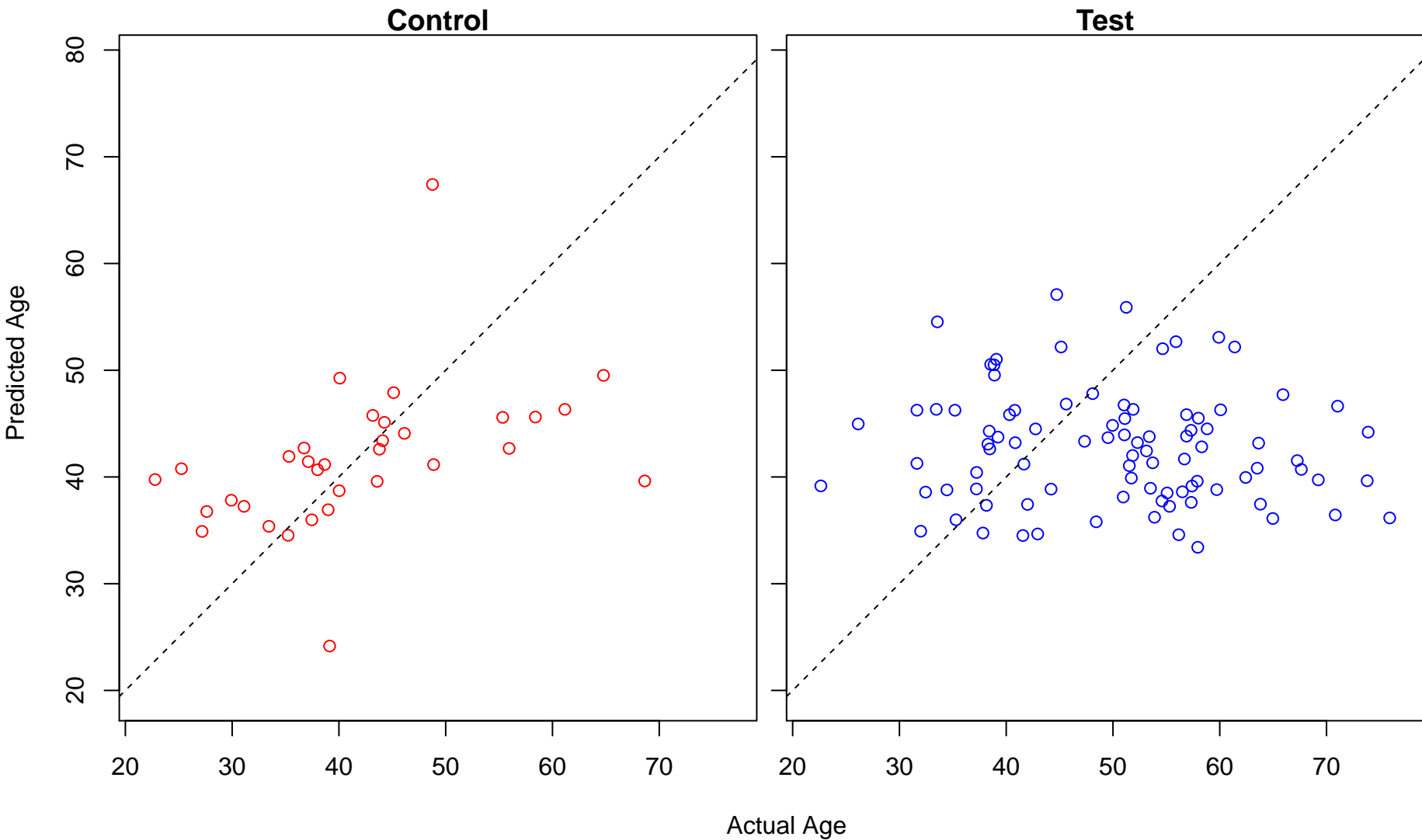
regulation of system process (Score: 0.733522)



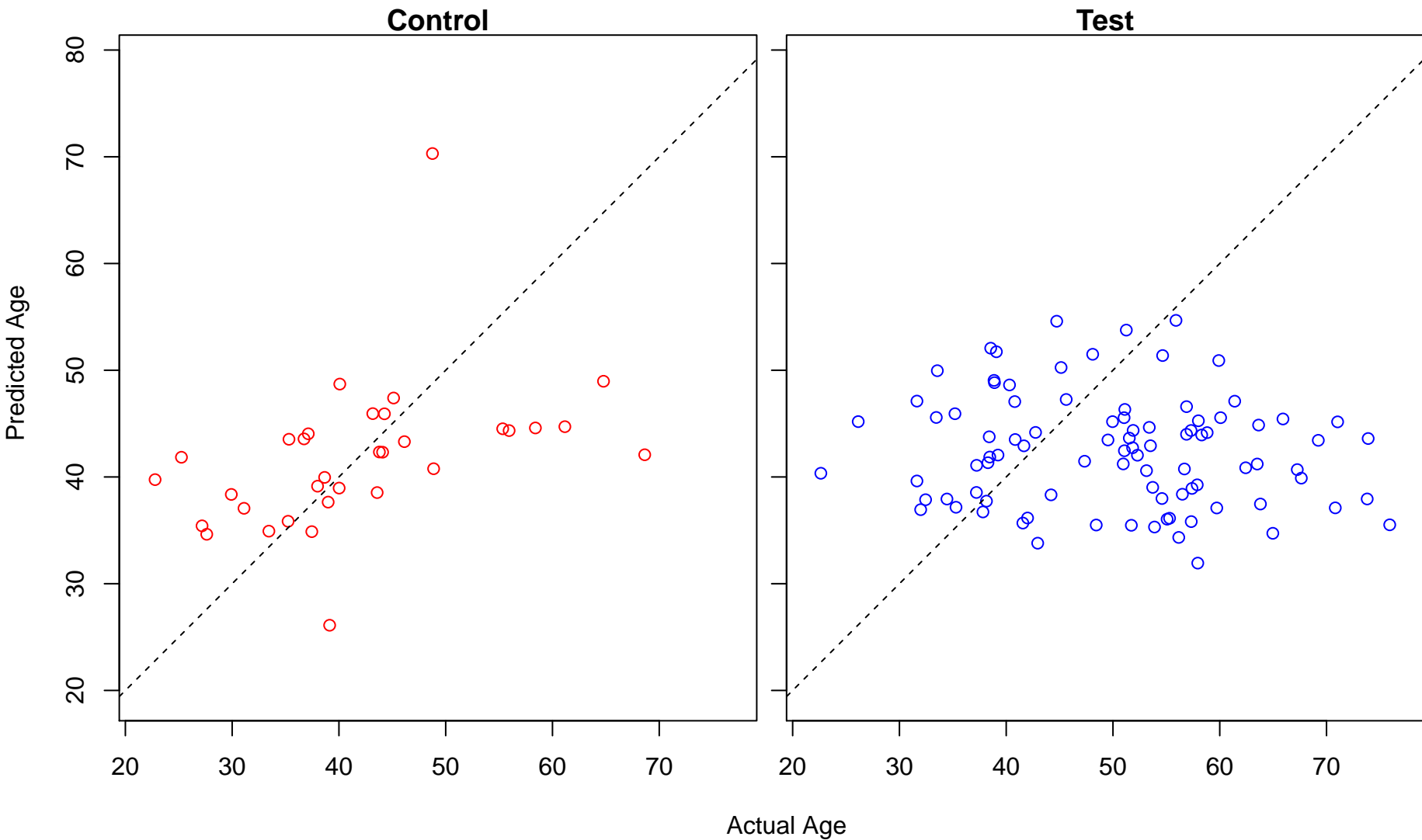
positive regulation of synapse assembly (Score: 0.733379)



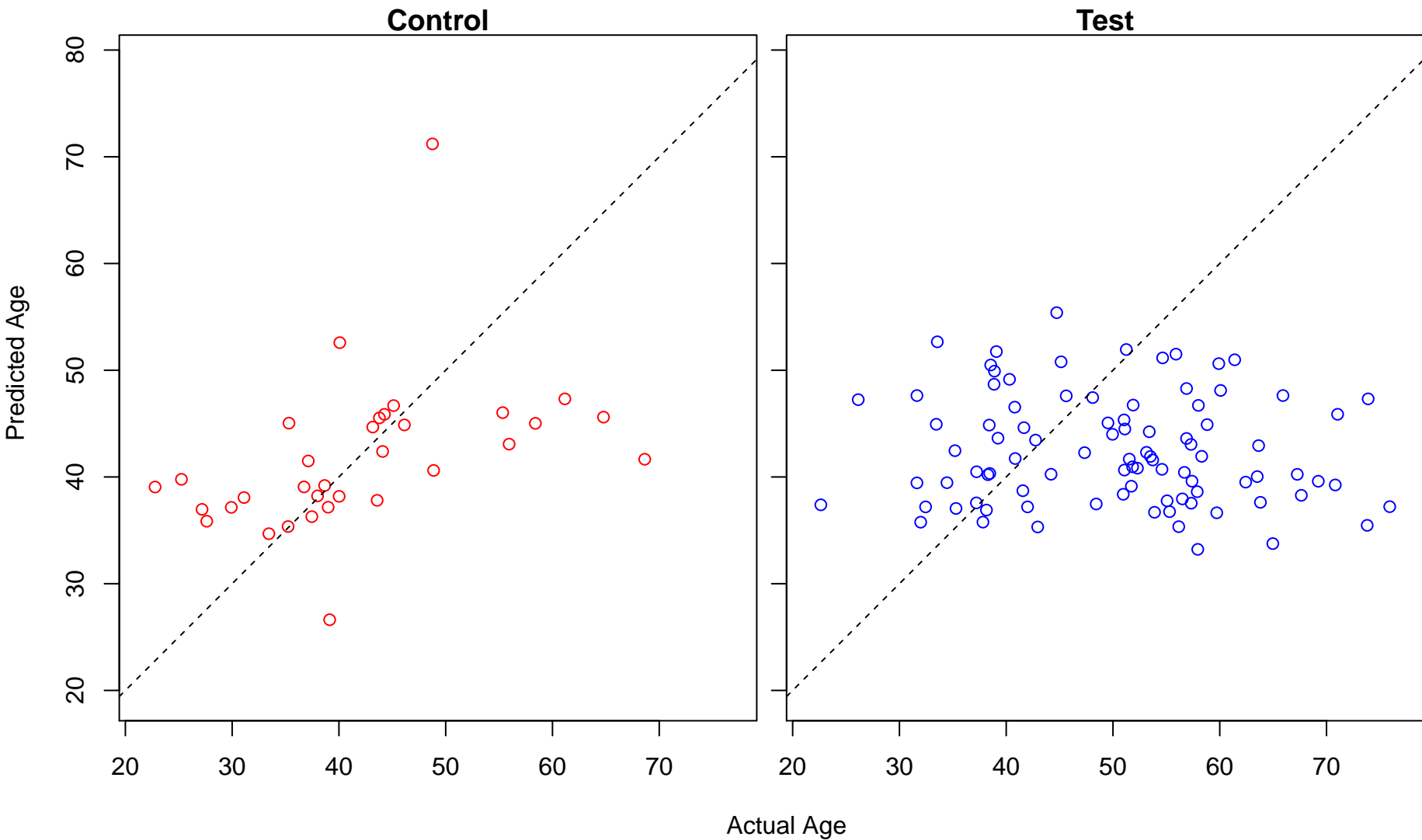
generation of neurons (Score: 0.733092)



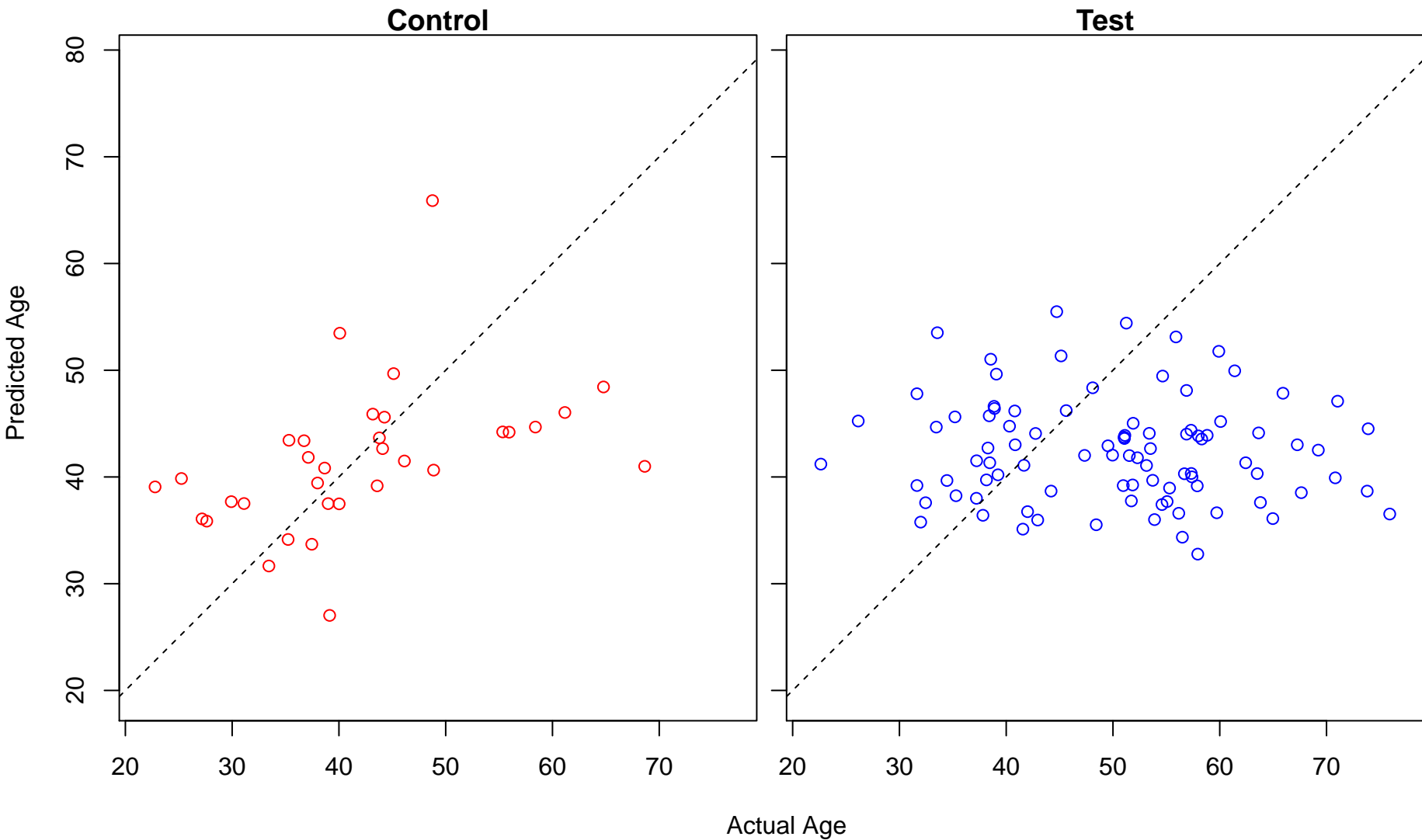
organic substance transport (Score: 0.732646)



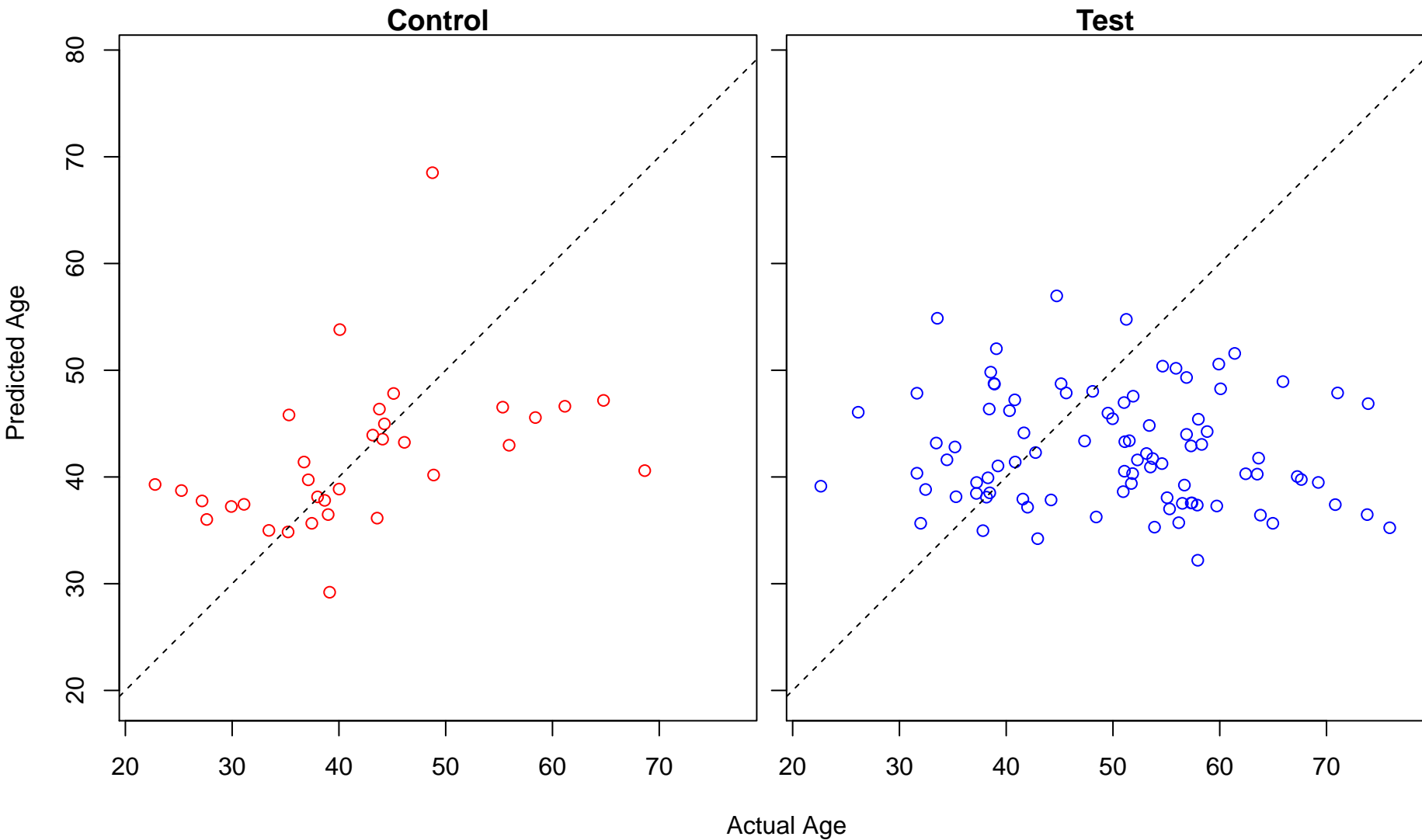
negative regulation of protein modification process (Score: 0.732608)



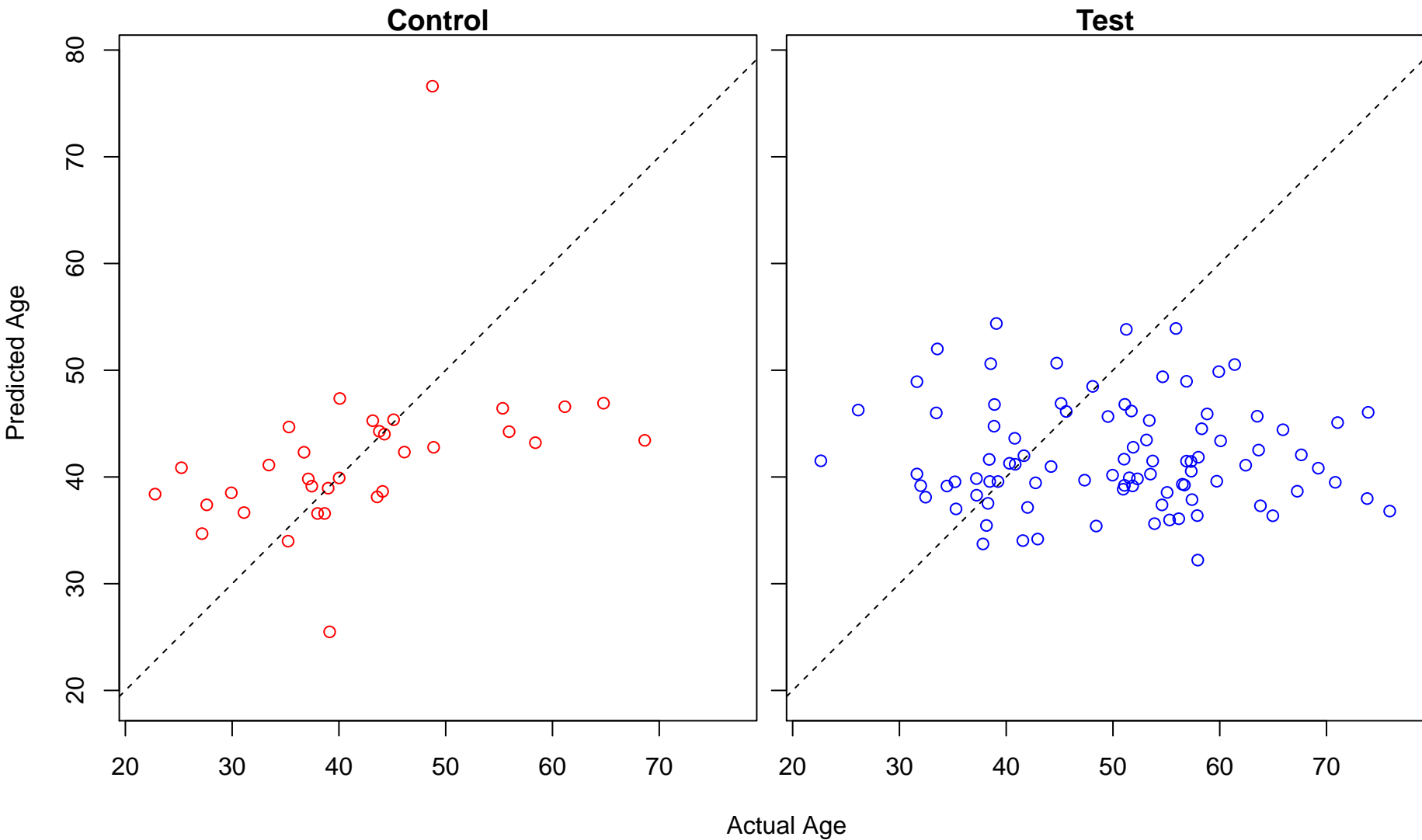
organophosphate metabolic process (Score: 0.731859)



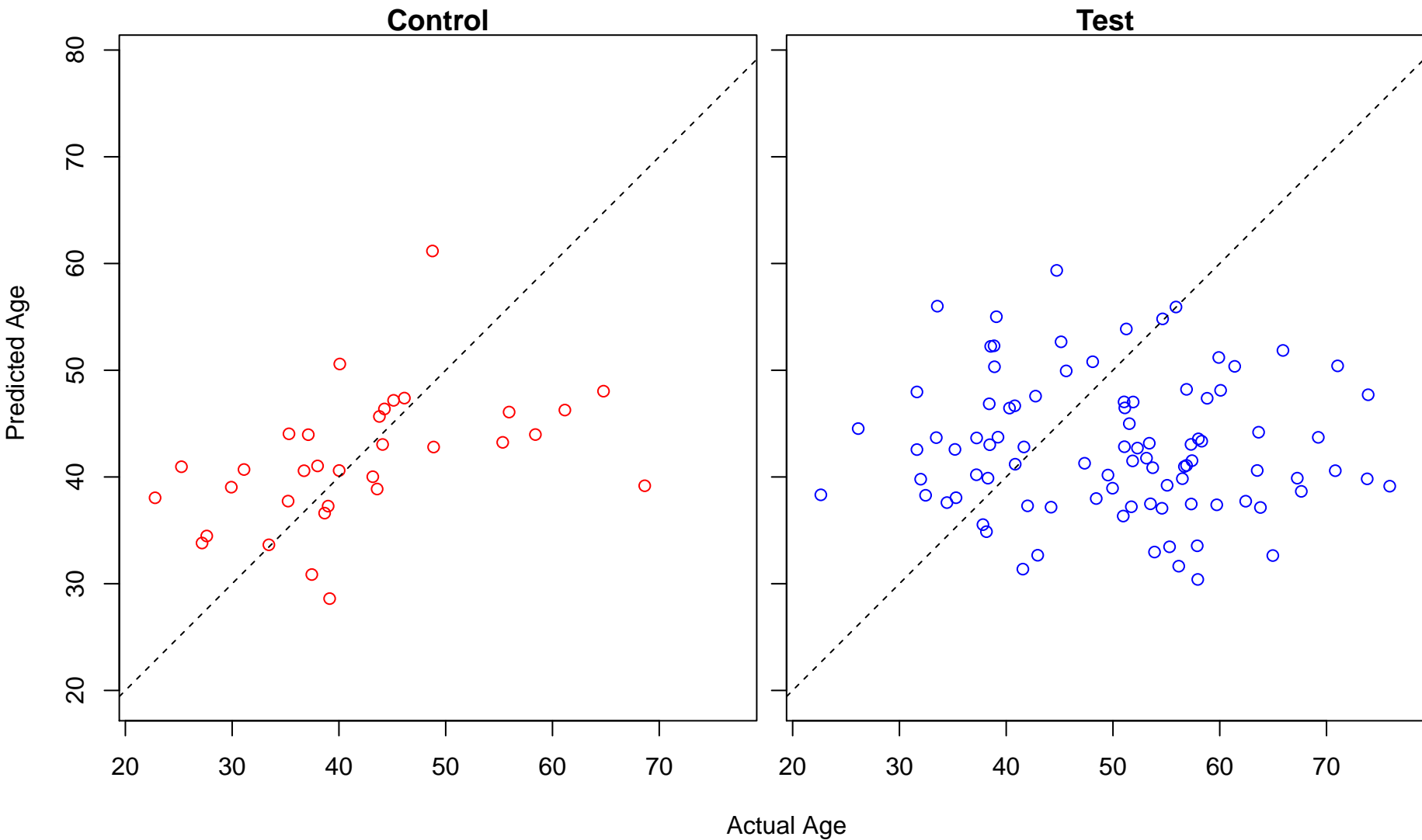
positive regulation of RNA metabolic process (Score: 0.731530)



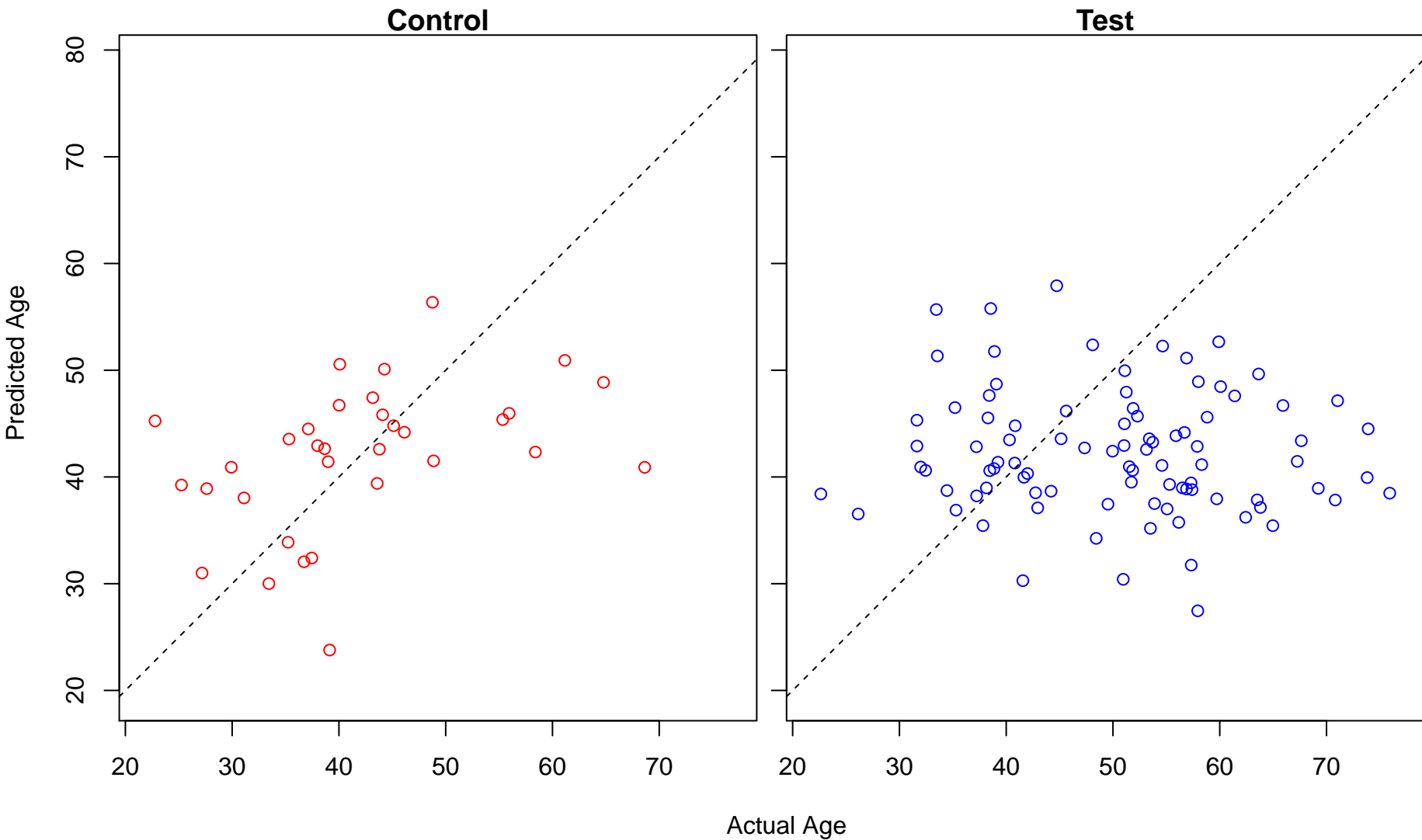
gene silencing (Score: 0.731314)



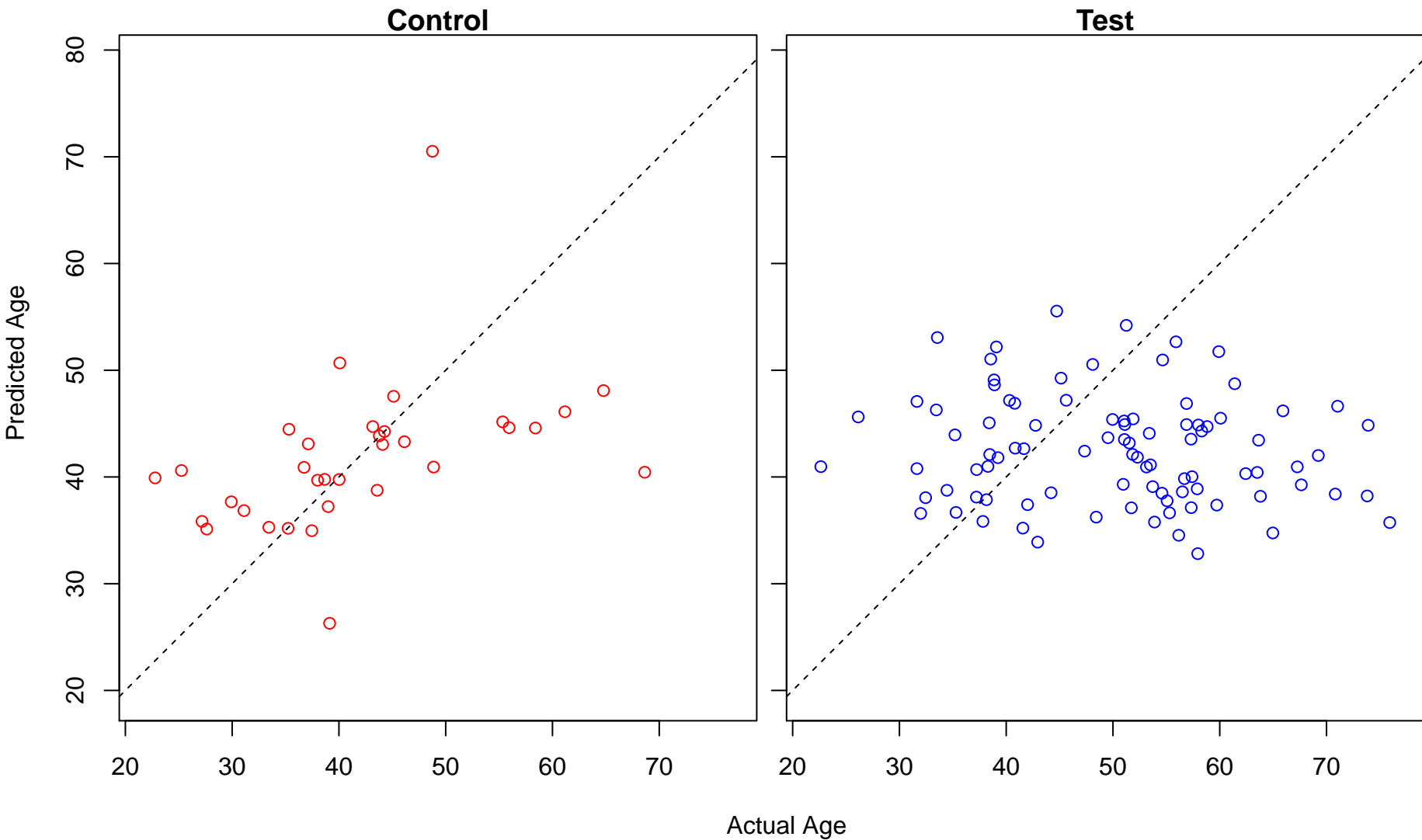
negative regulation of transport (Score: 0.730687)



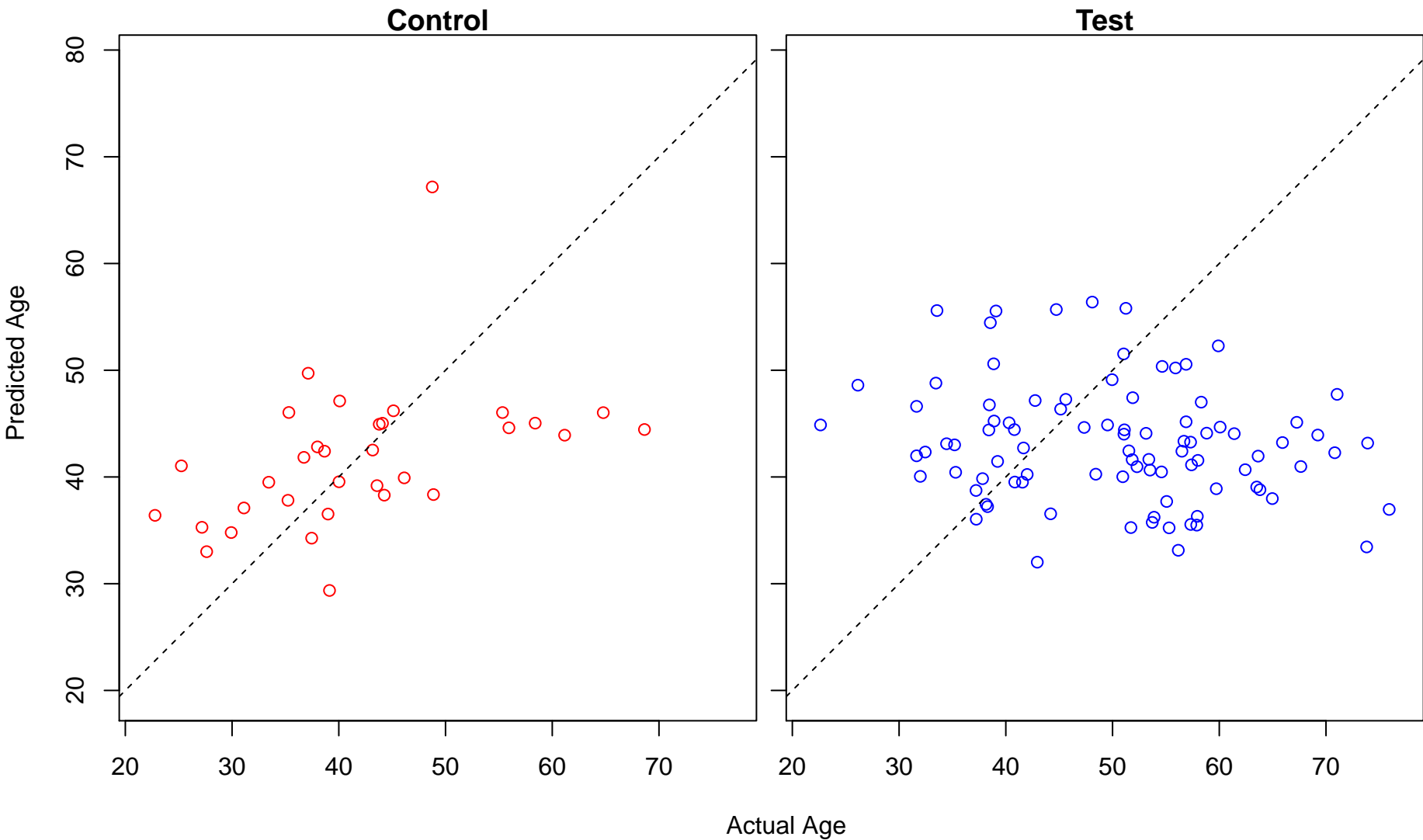
chondroitin sulfate catabolic process (Score: 0.730673)



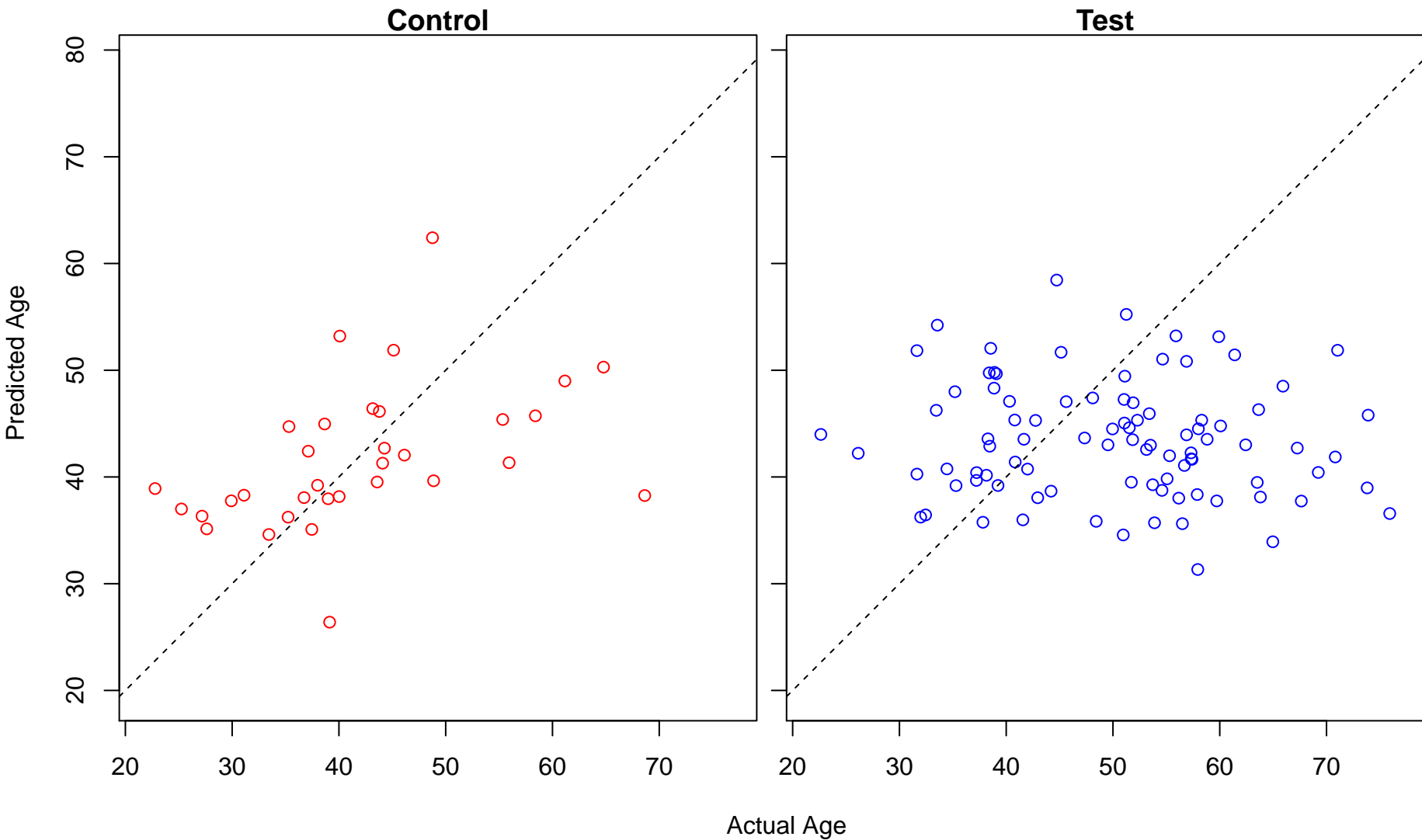
single-organism transport (Score: 0.730648)



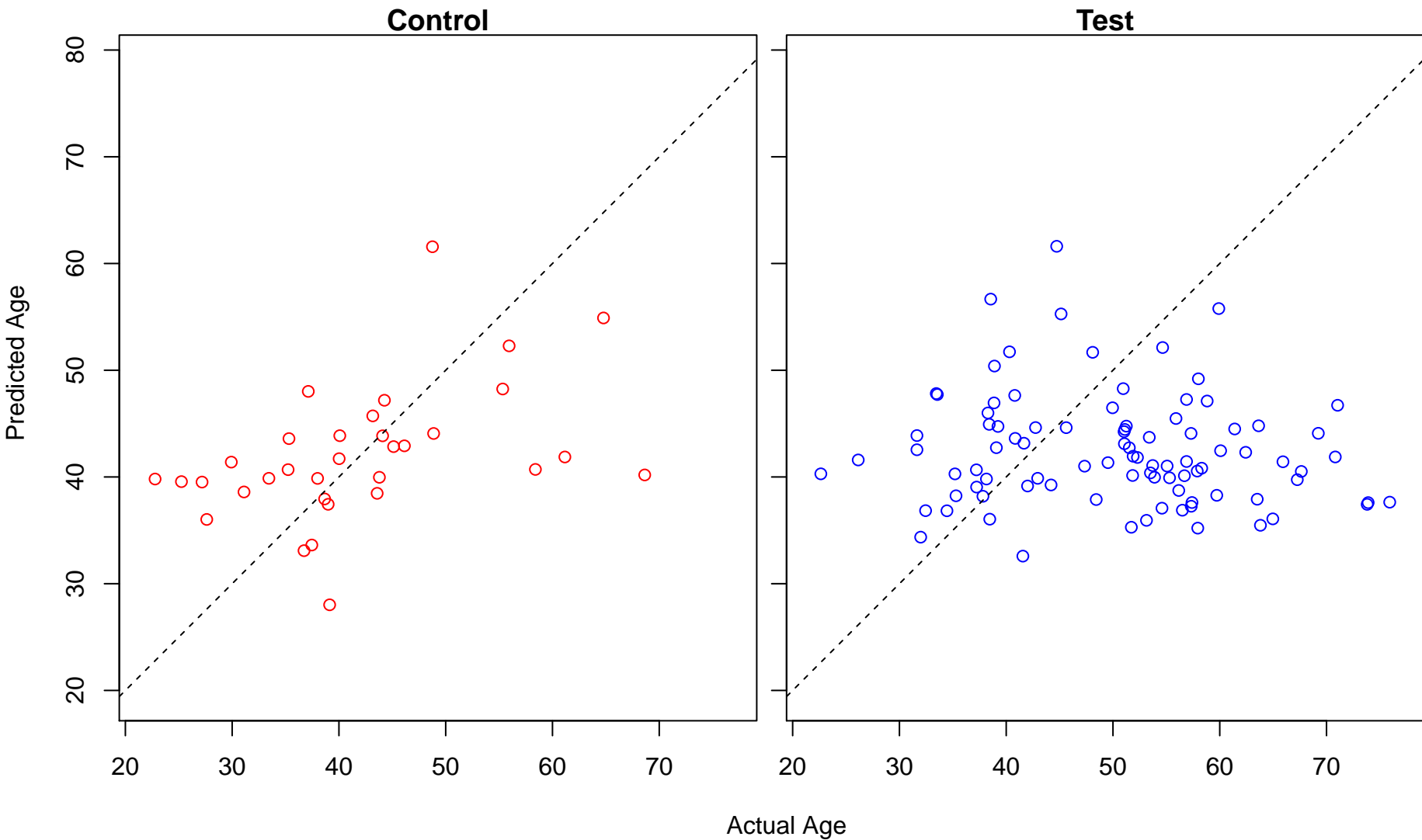
secretion by cell (Score: 0.730585)



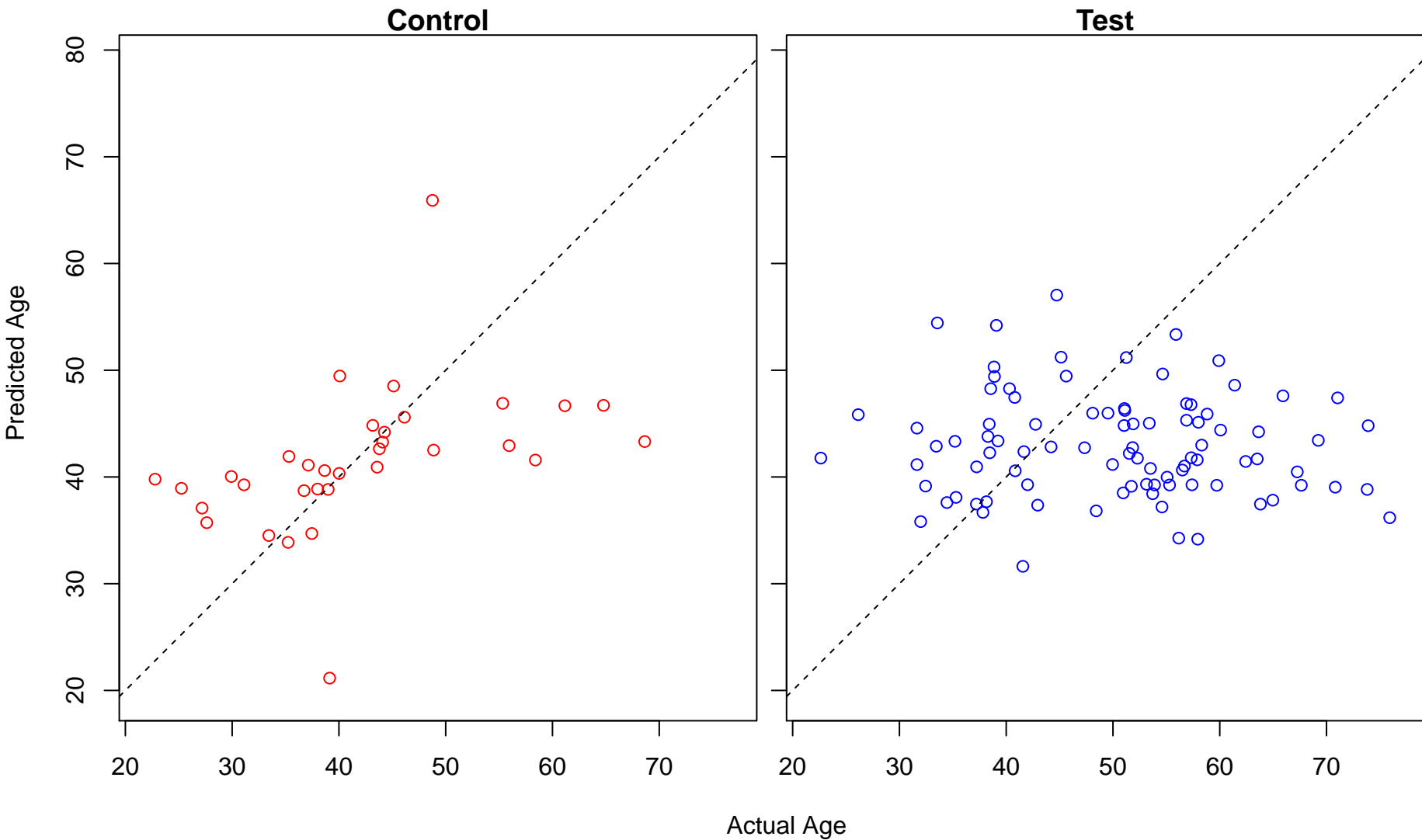
glycerolipid biosynthetic process (Score: 0.730578)



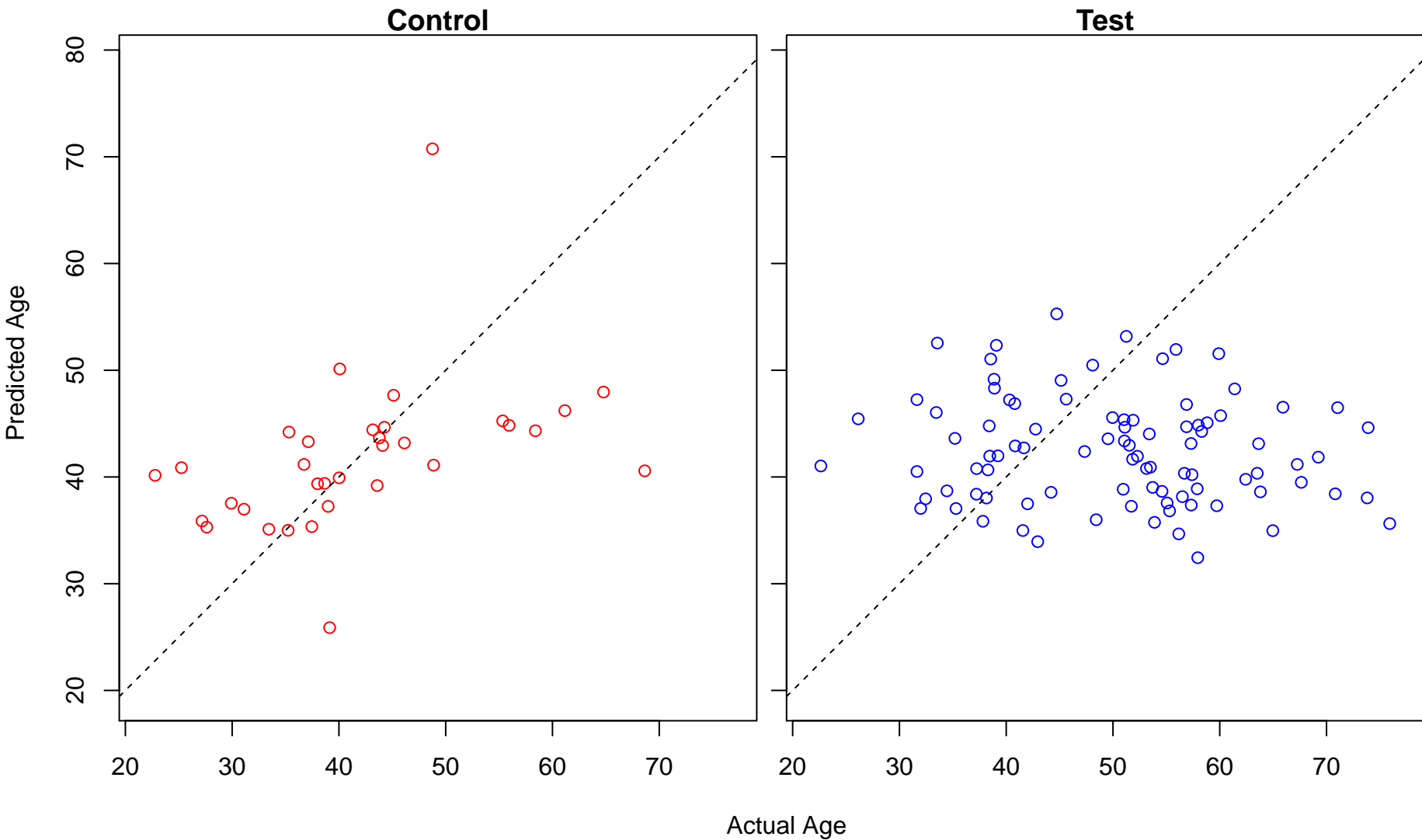
mRNA 3'-splice site recognition (Score: 0.730237)



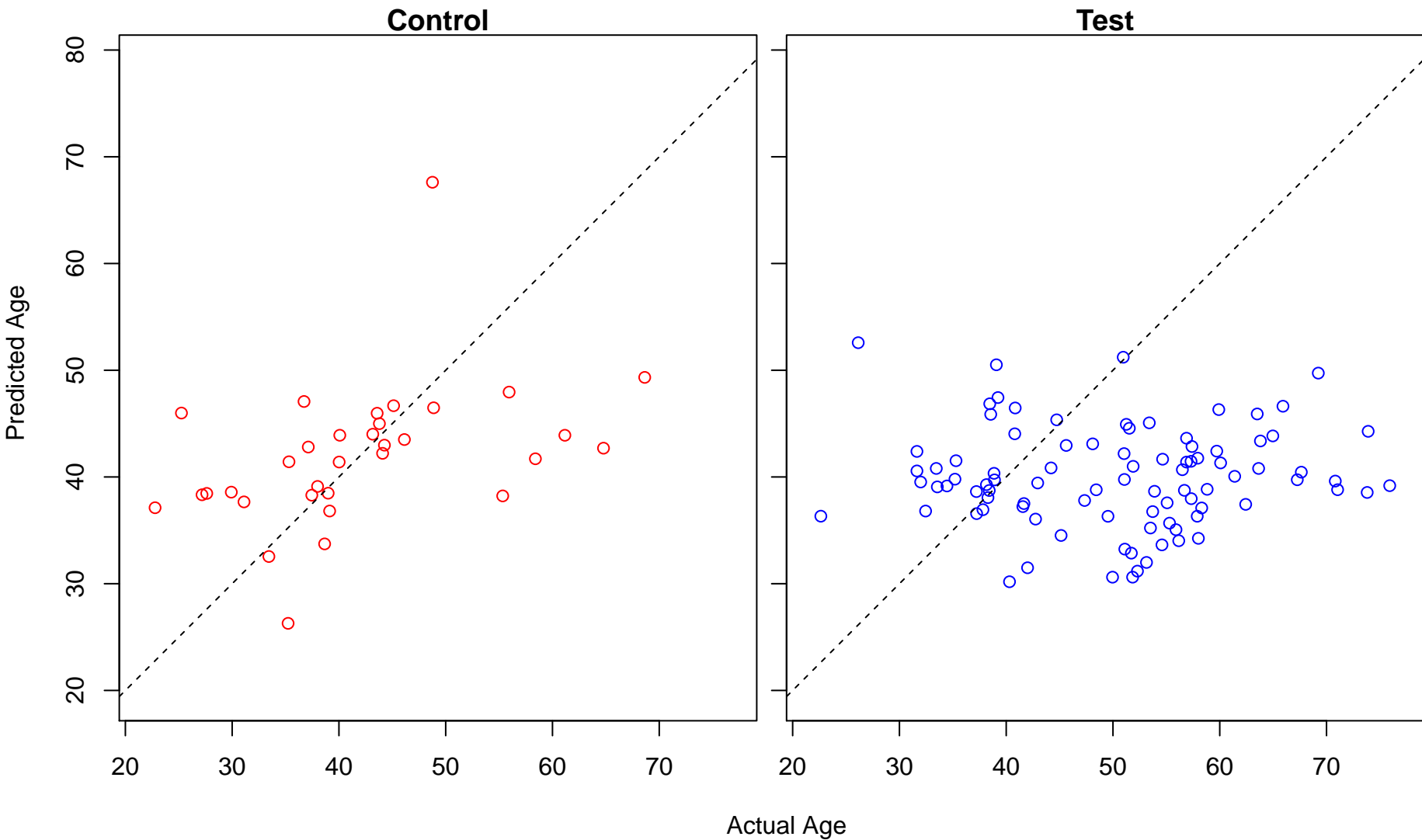
Fc receptor signaling pathway (Score: 0.730187)



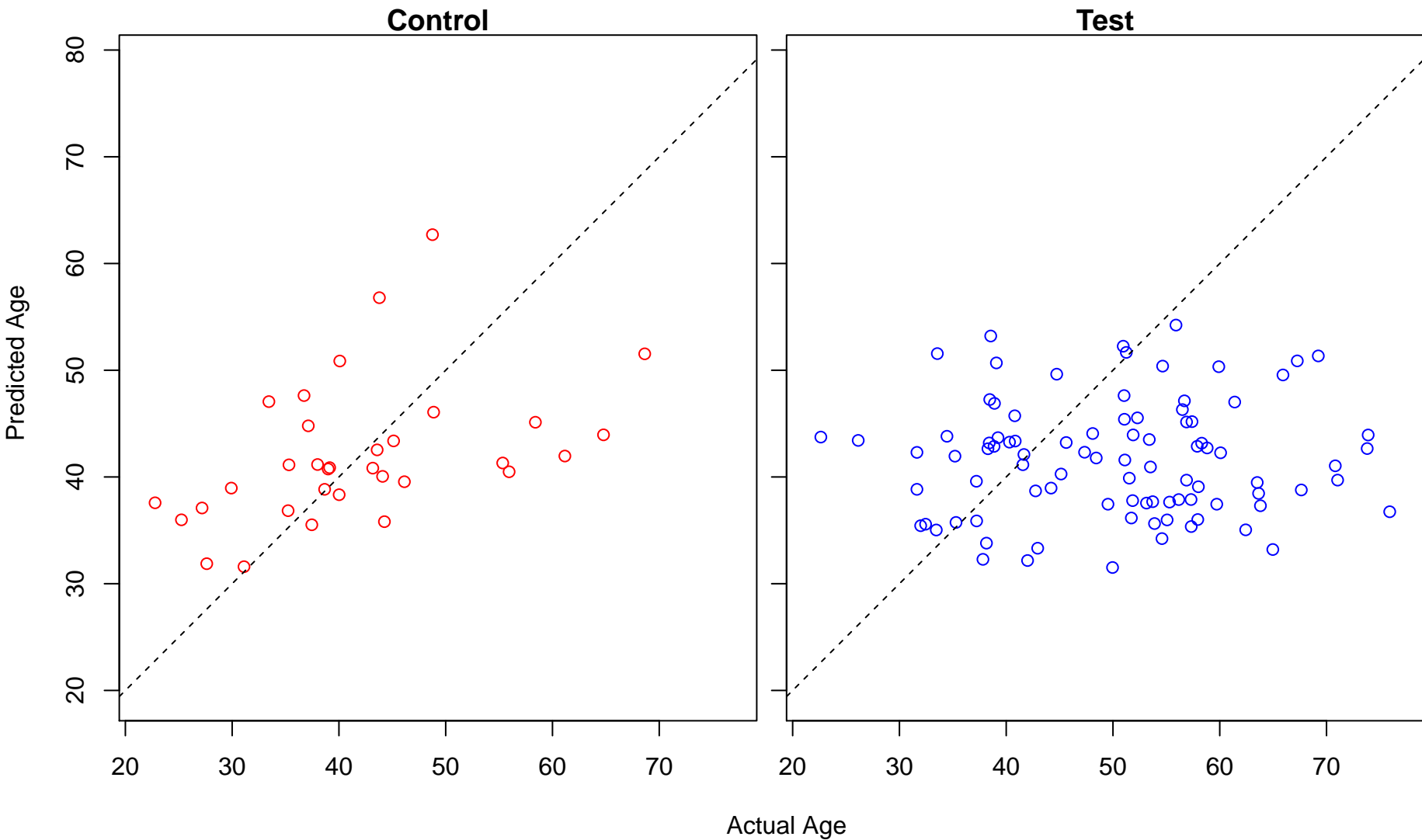
establishment of localization (Score: 0.730082)



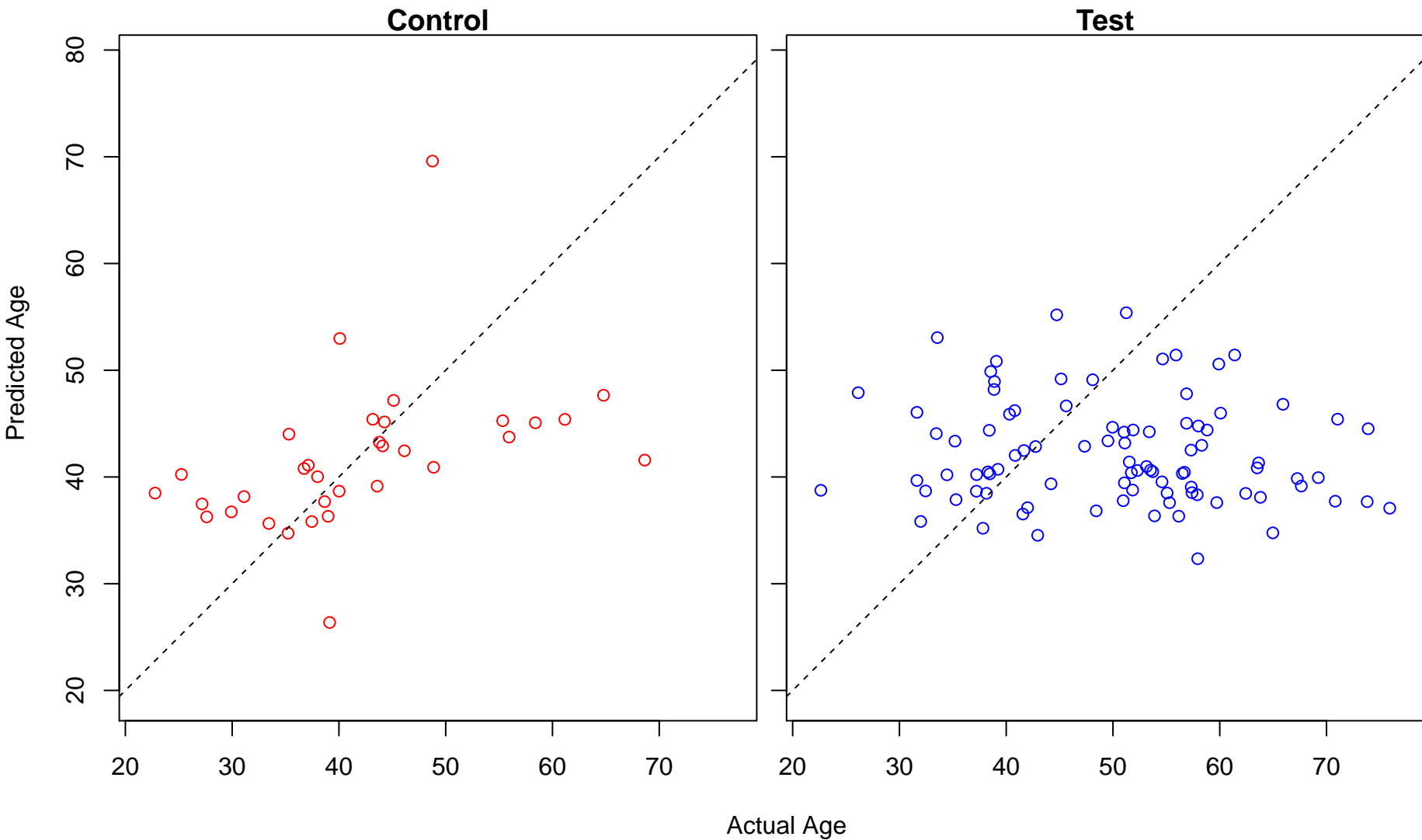
isocitrate metabolic process (Score: 0.730000)



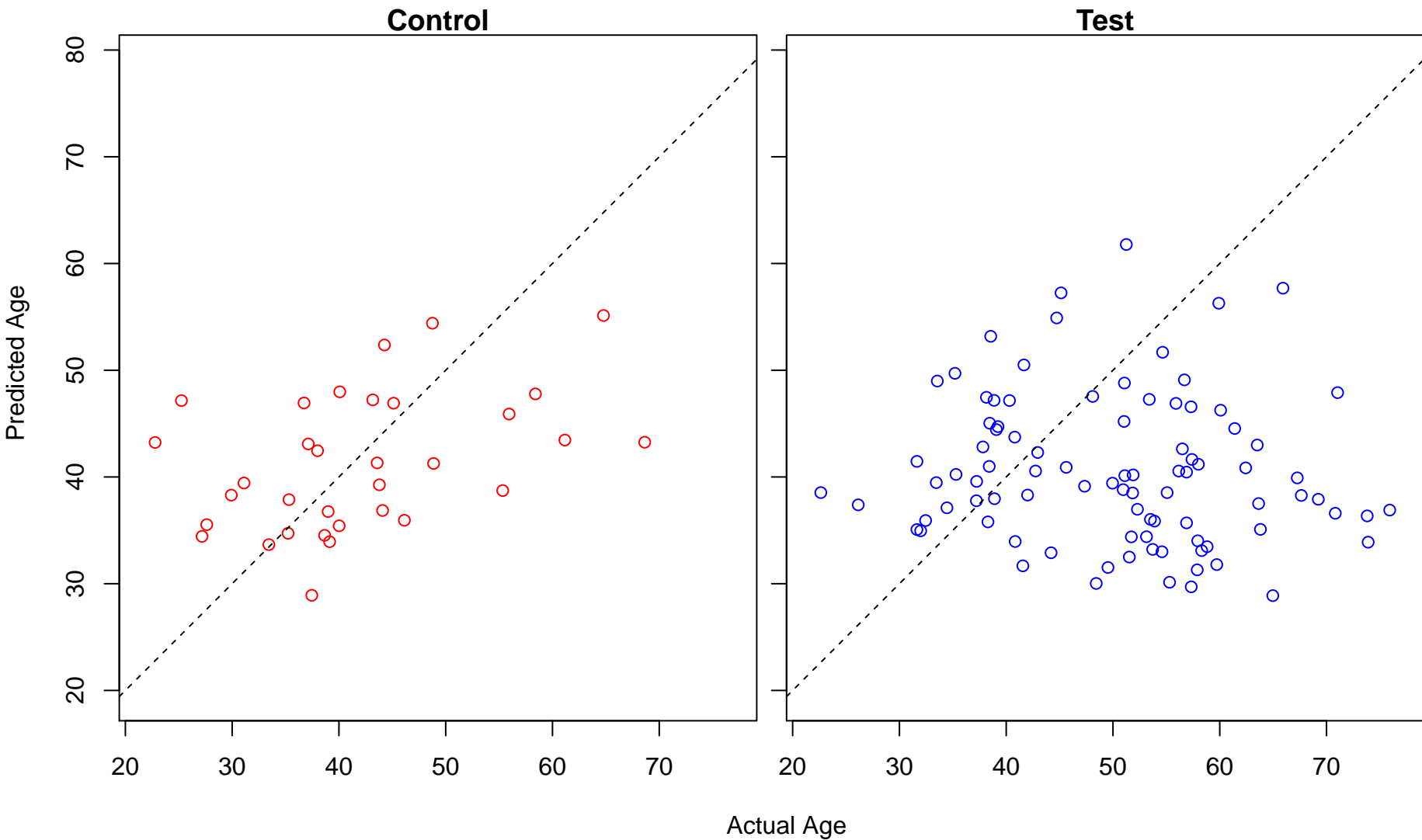
peptidyl-histidine modification (Score: 0.729422)



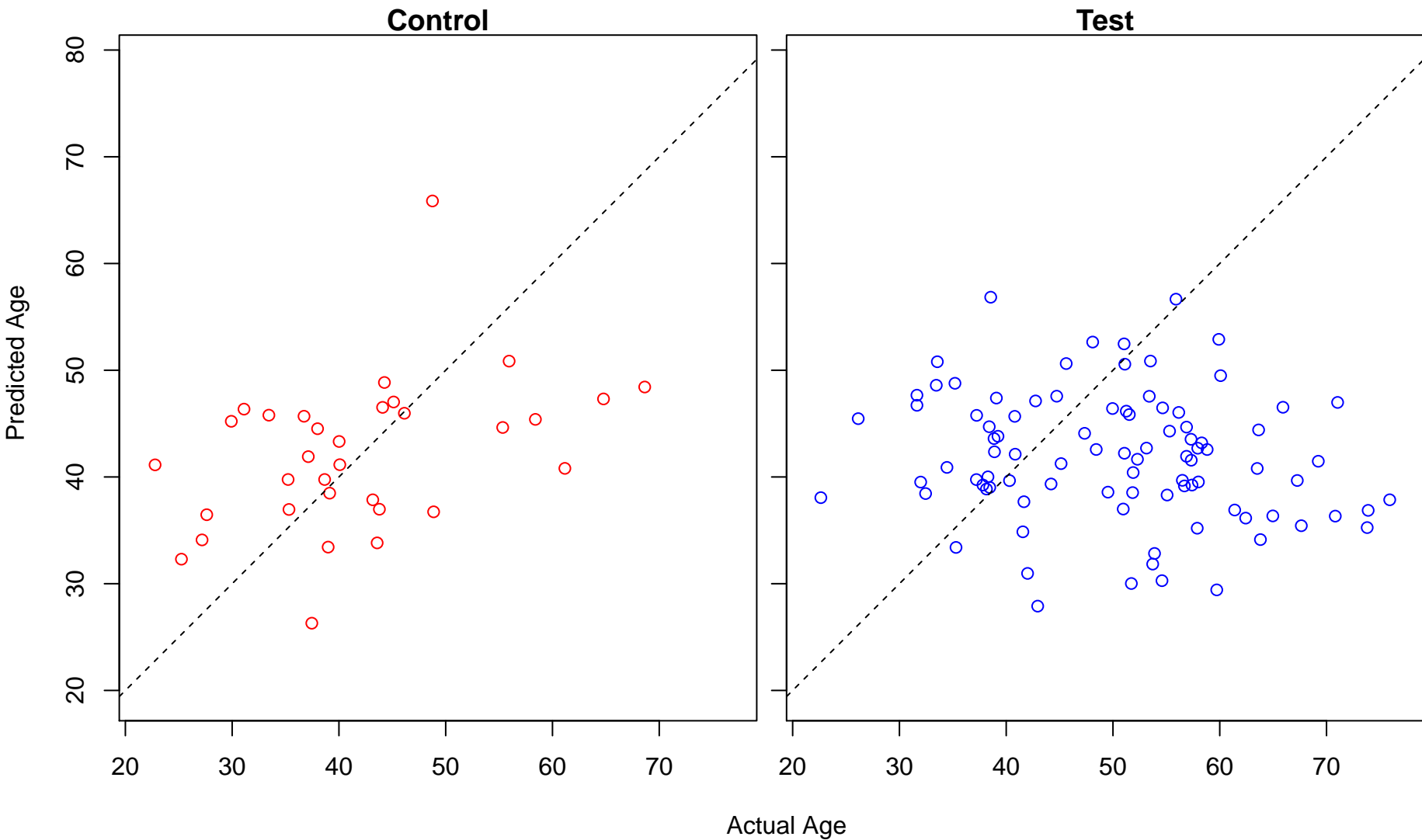
negative regulation of macromolecule biosynthetic process (Score: 0.728795)



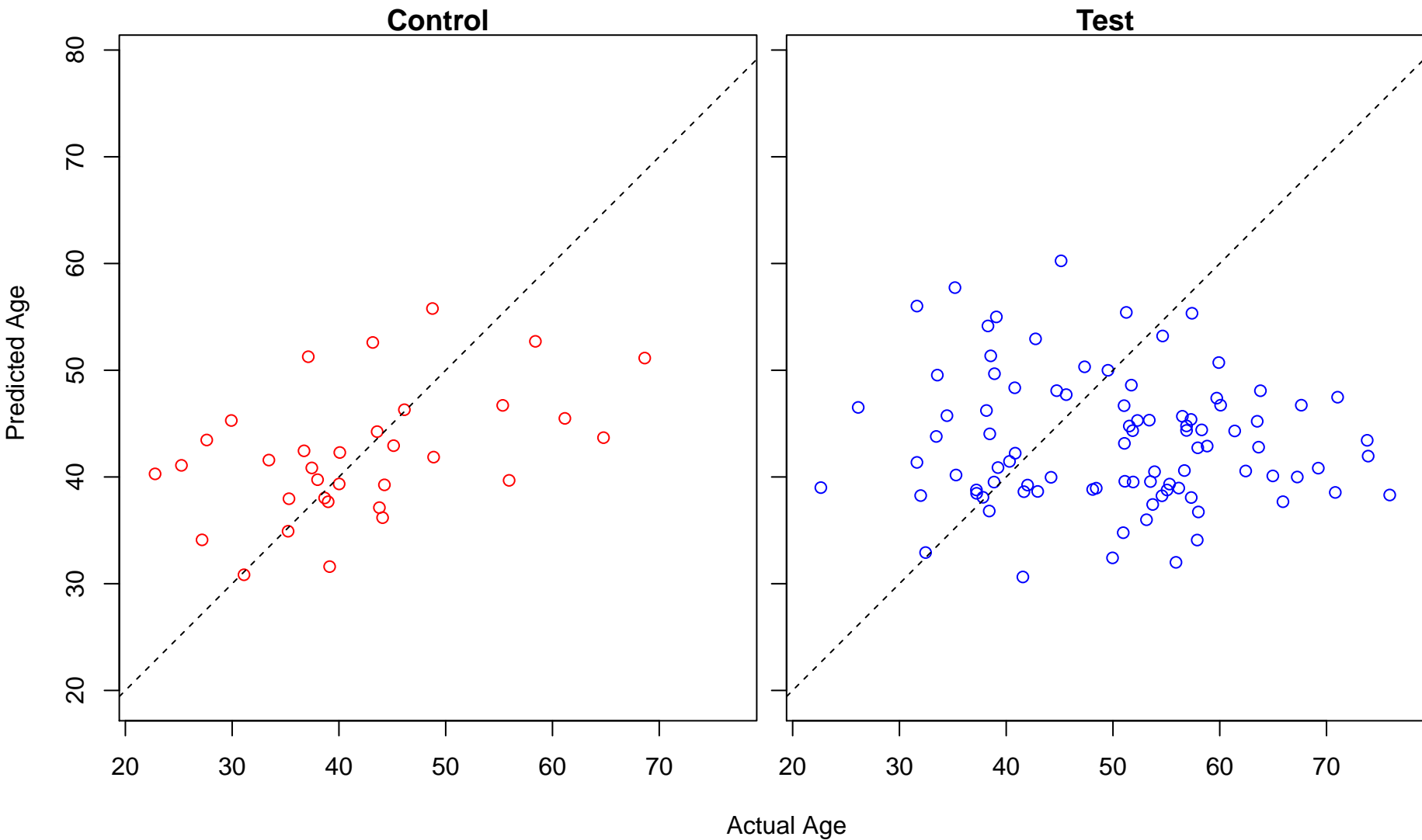
regulation of T cell cytokine production (Score: 0.728581)



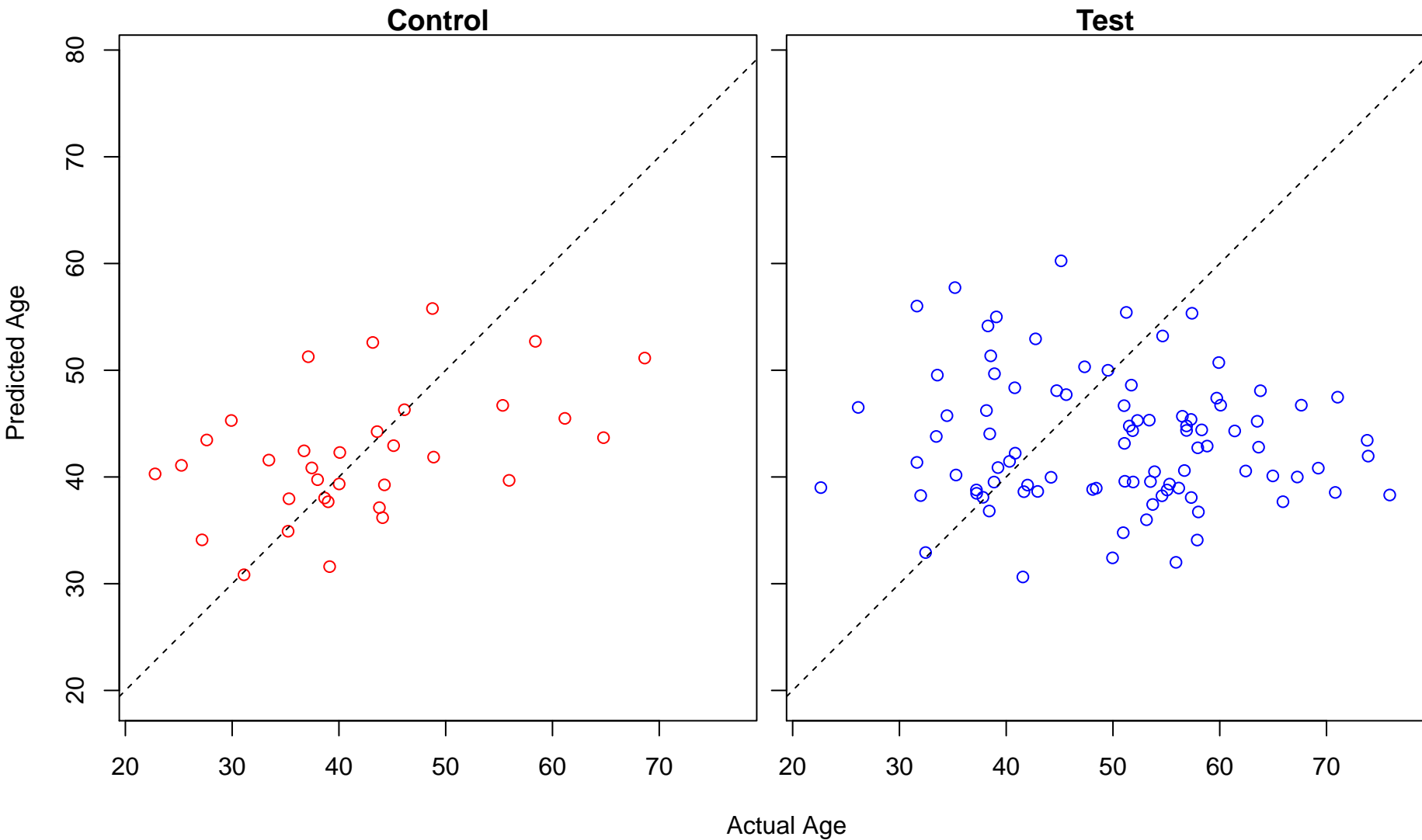
negative regulation of cyclic nucleotide metabolic process (Score: 0.728421)



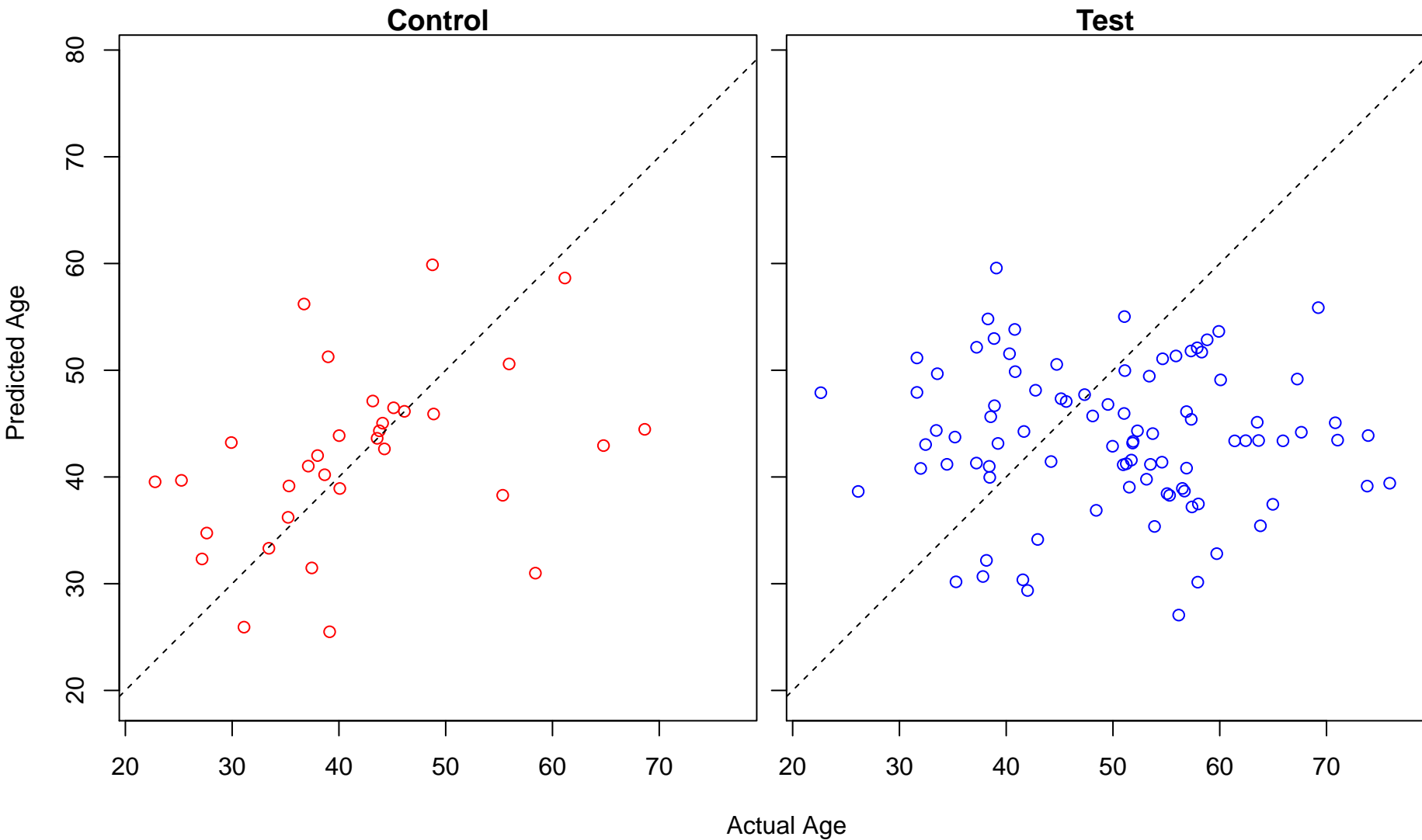
response to potassium ion (Score: 0.728051)



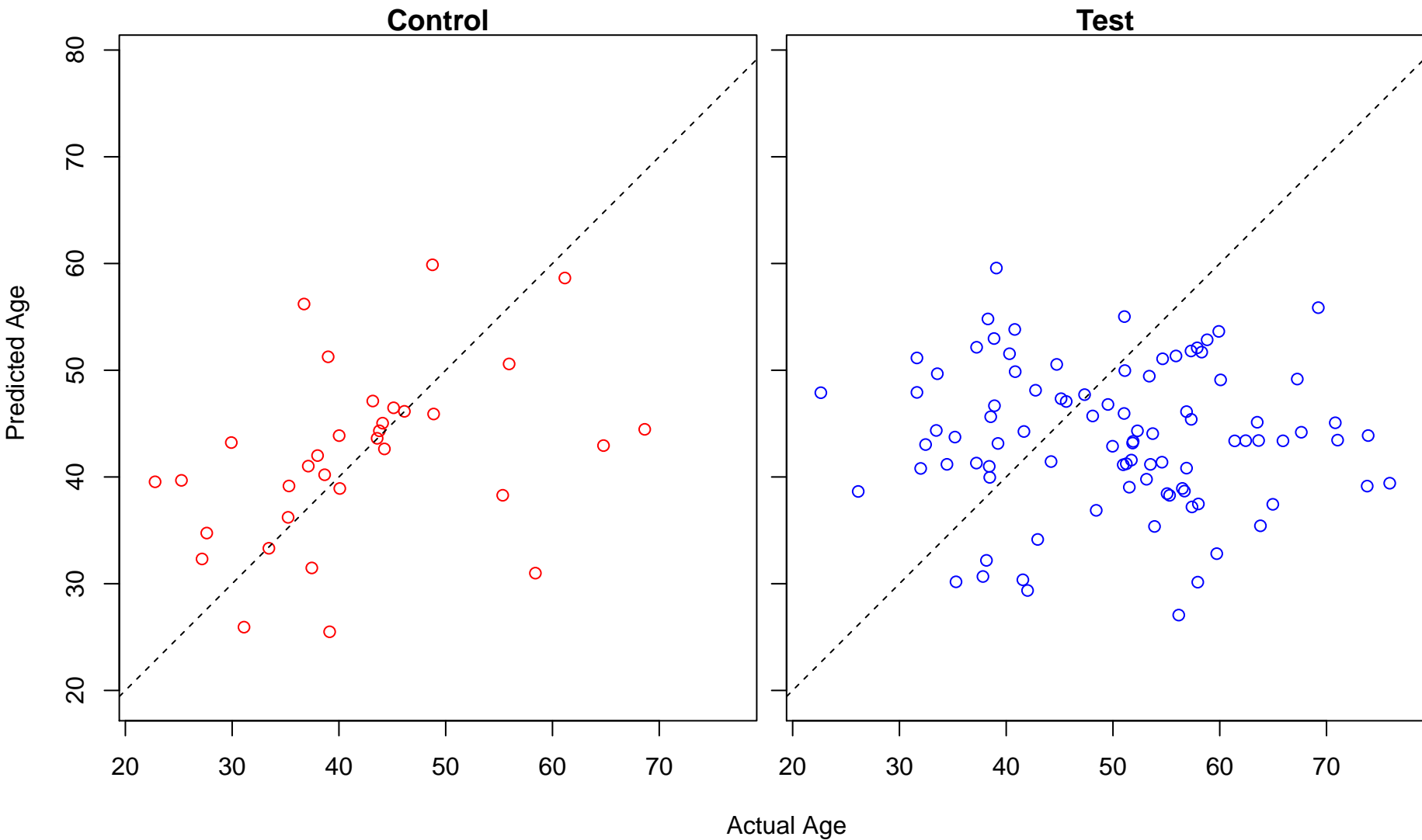
cellular response to potassium ion (Score: 0.728051)



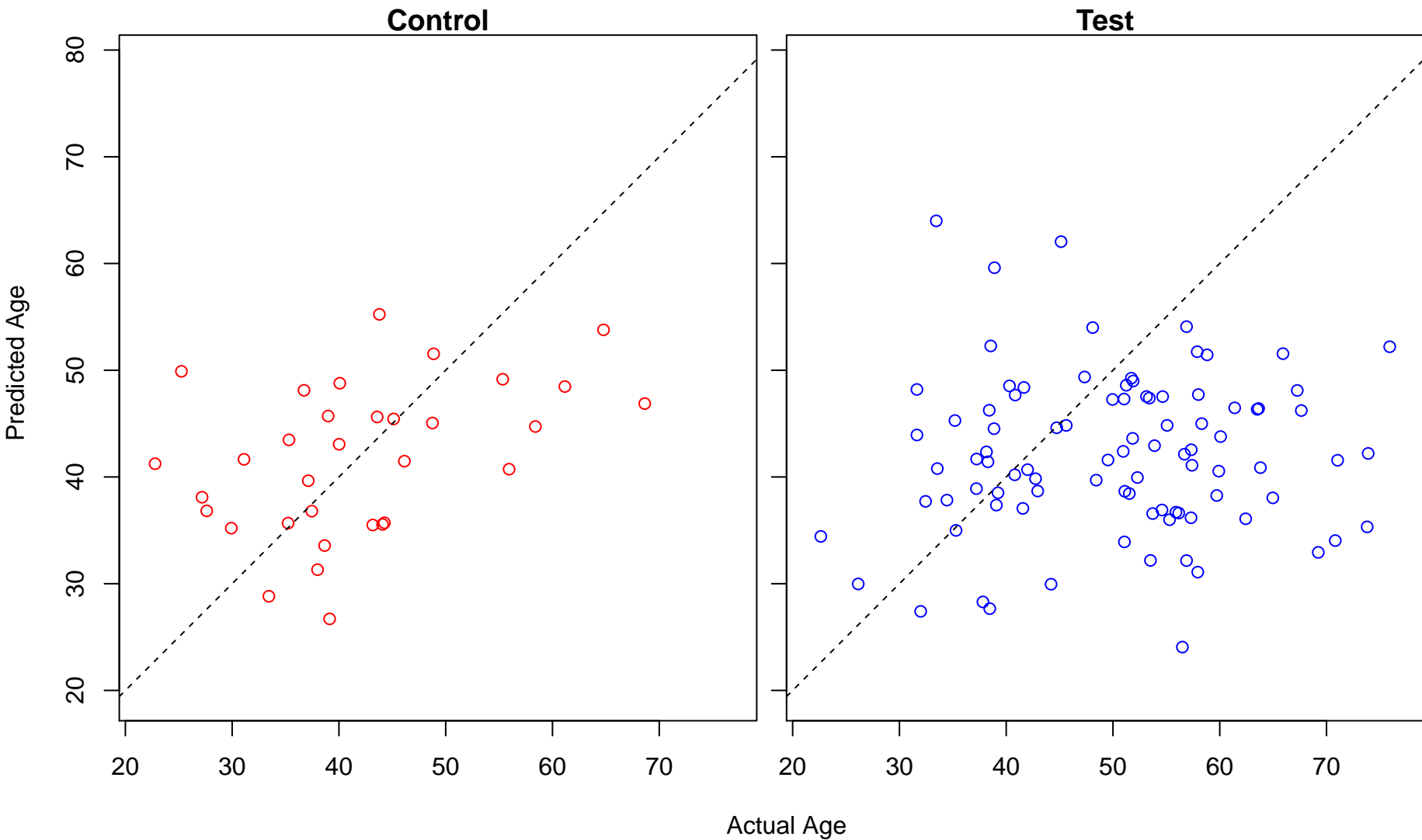
melanosome localization (Score: 0.727586)



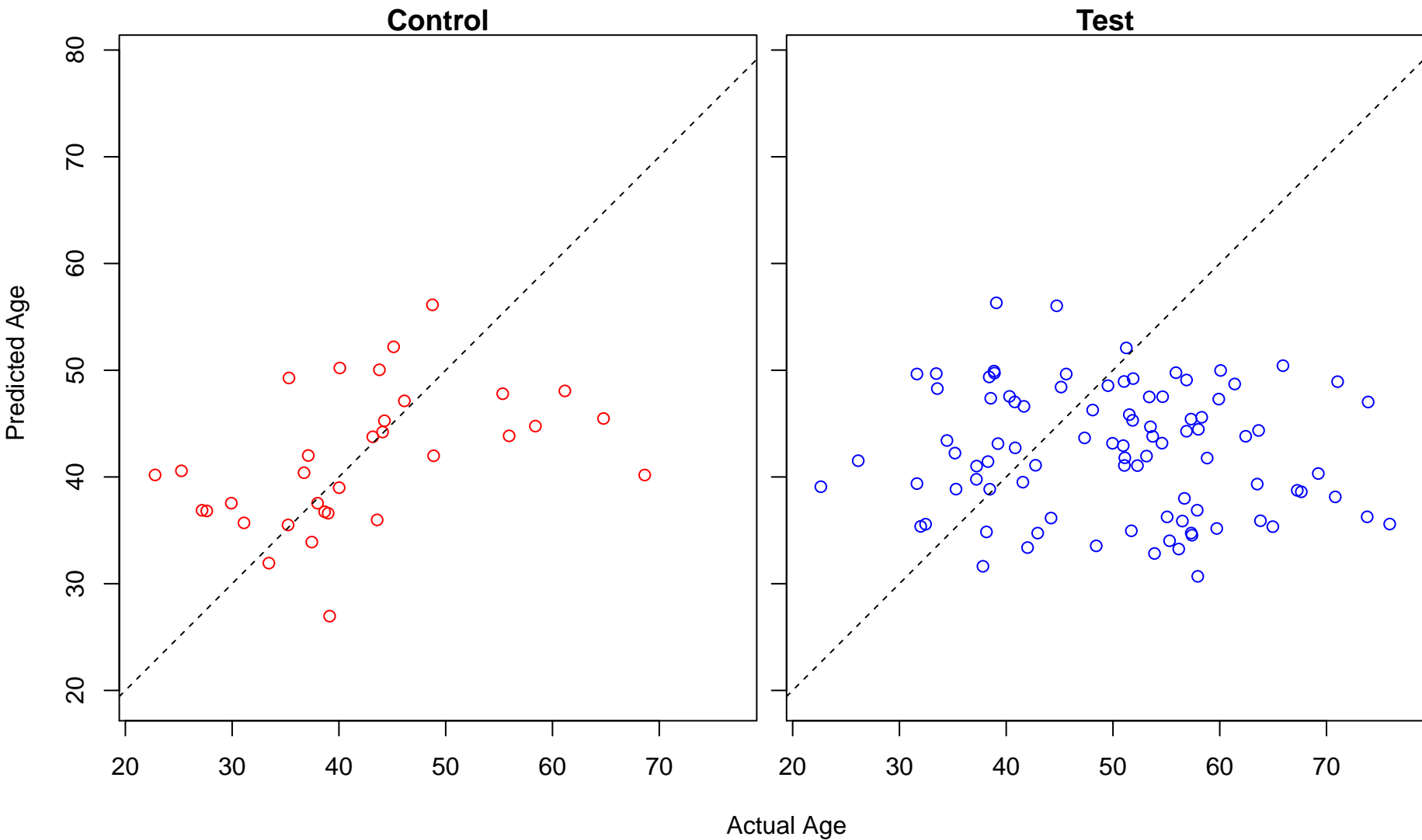
pigment granule localization (Score: 0.727586)



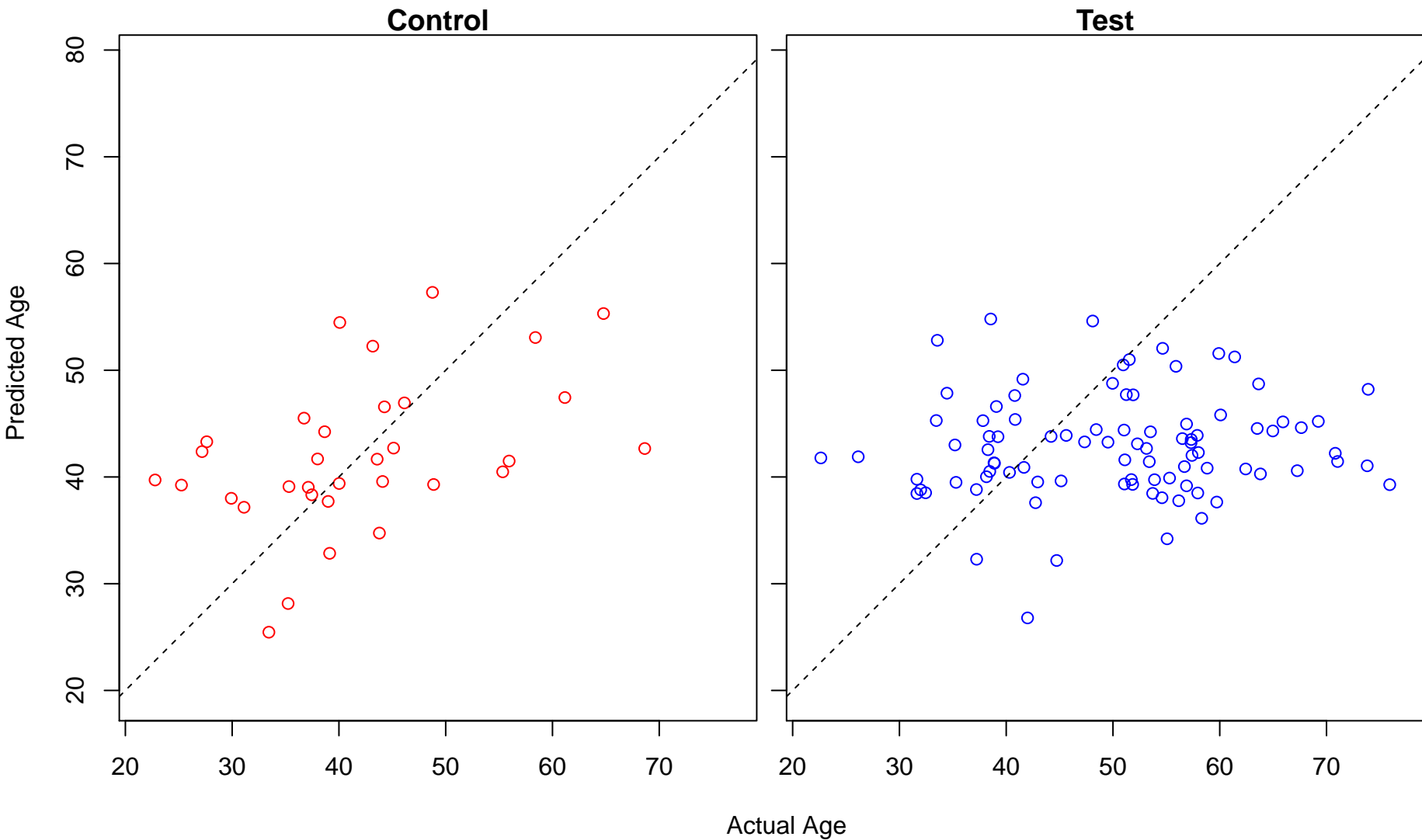
genitalia development (Score: 0.727449)



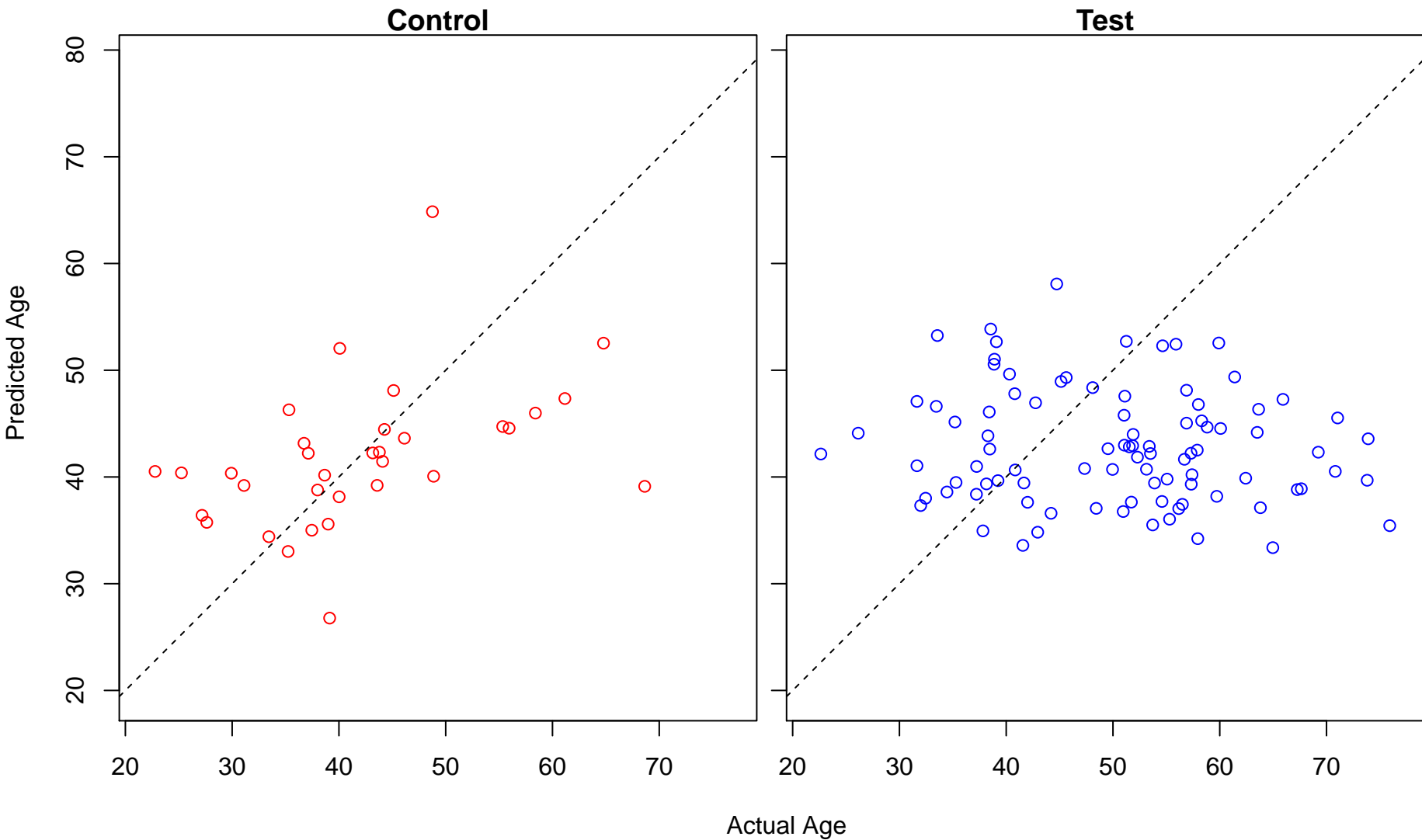
nucleic acid transport (Score: 0.727216)



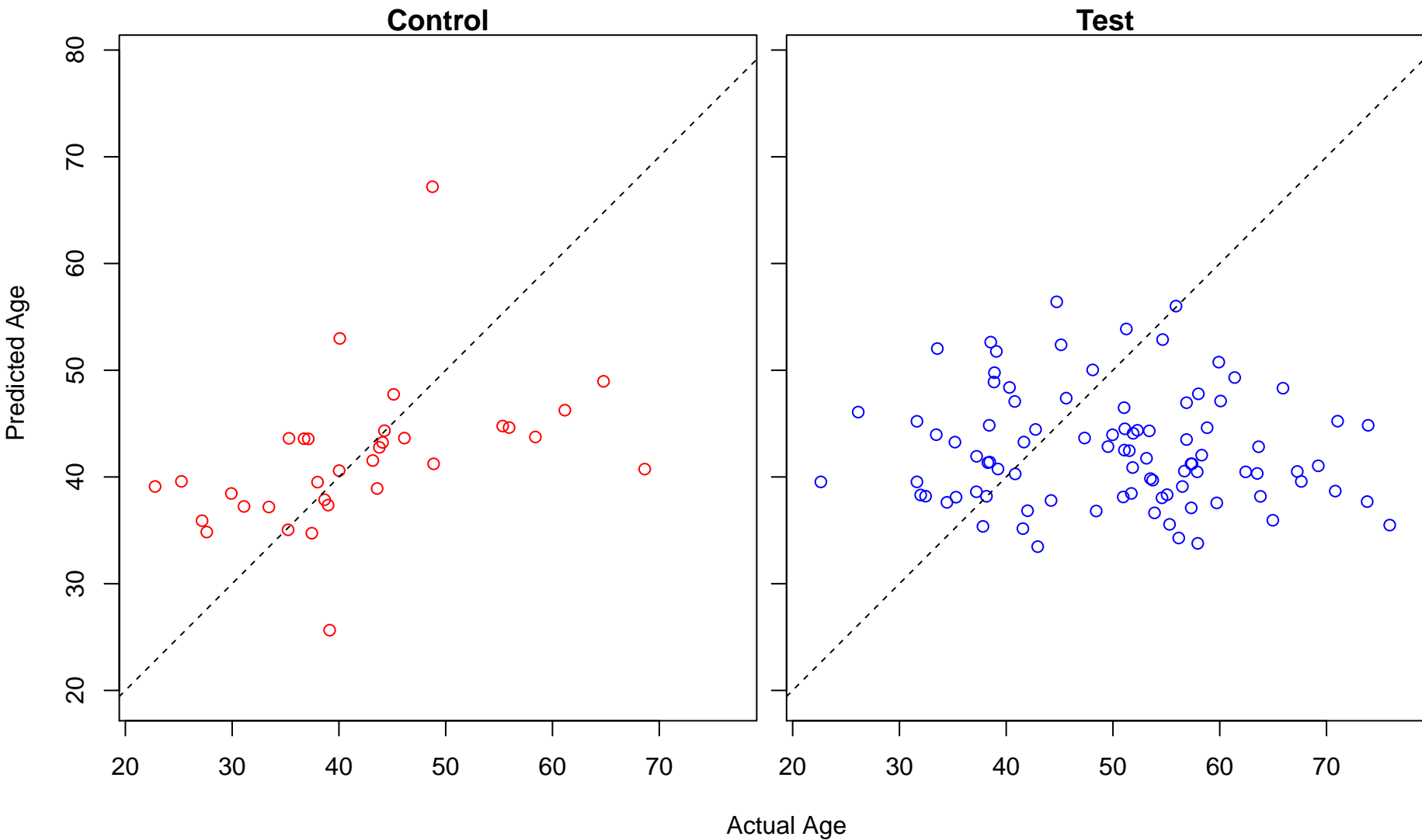
glycoside catabolic process (Score: 0.726981)



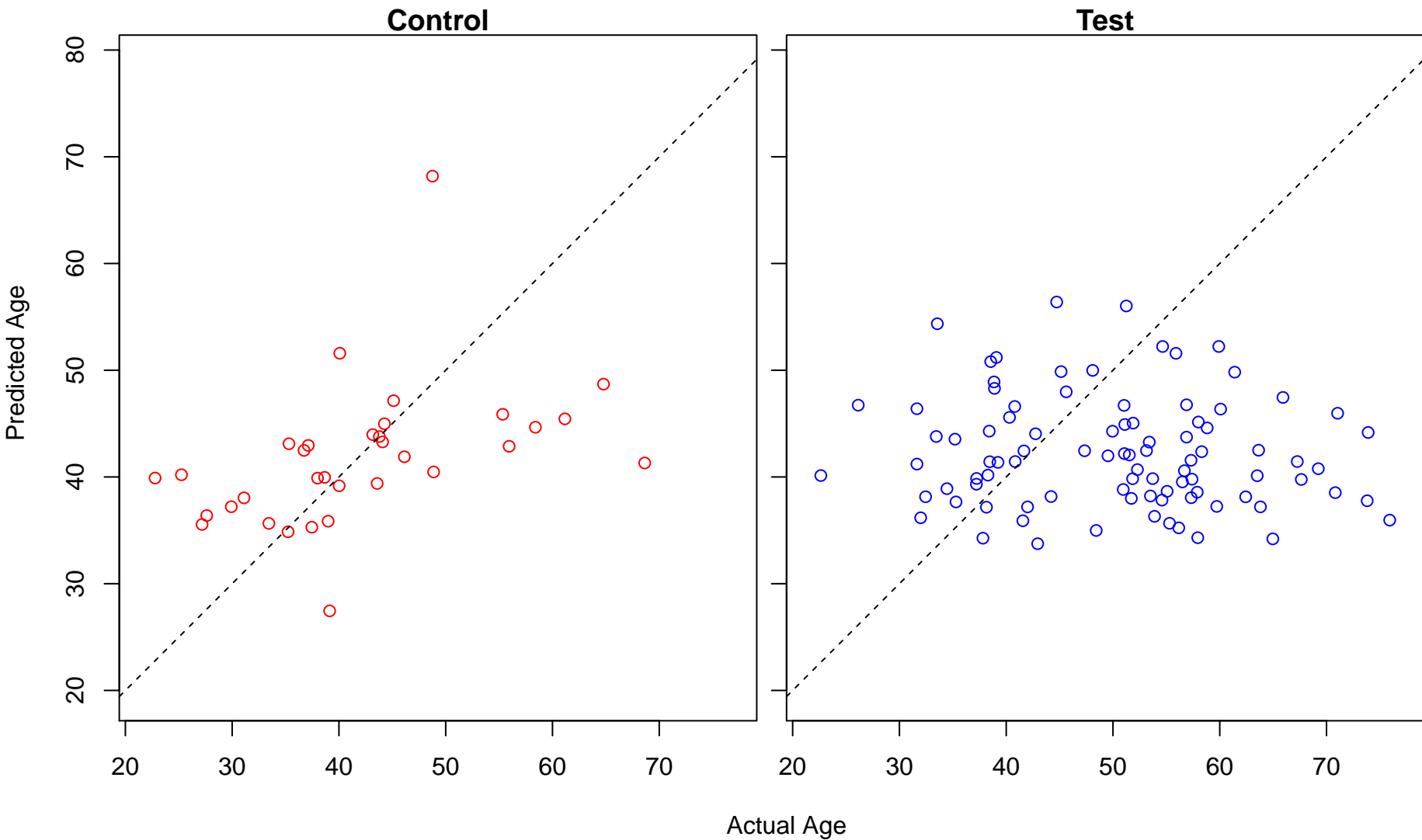
autophagy (Score: 0.726934)



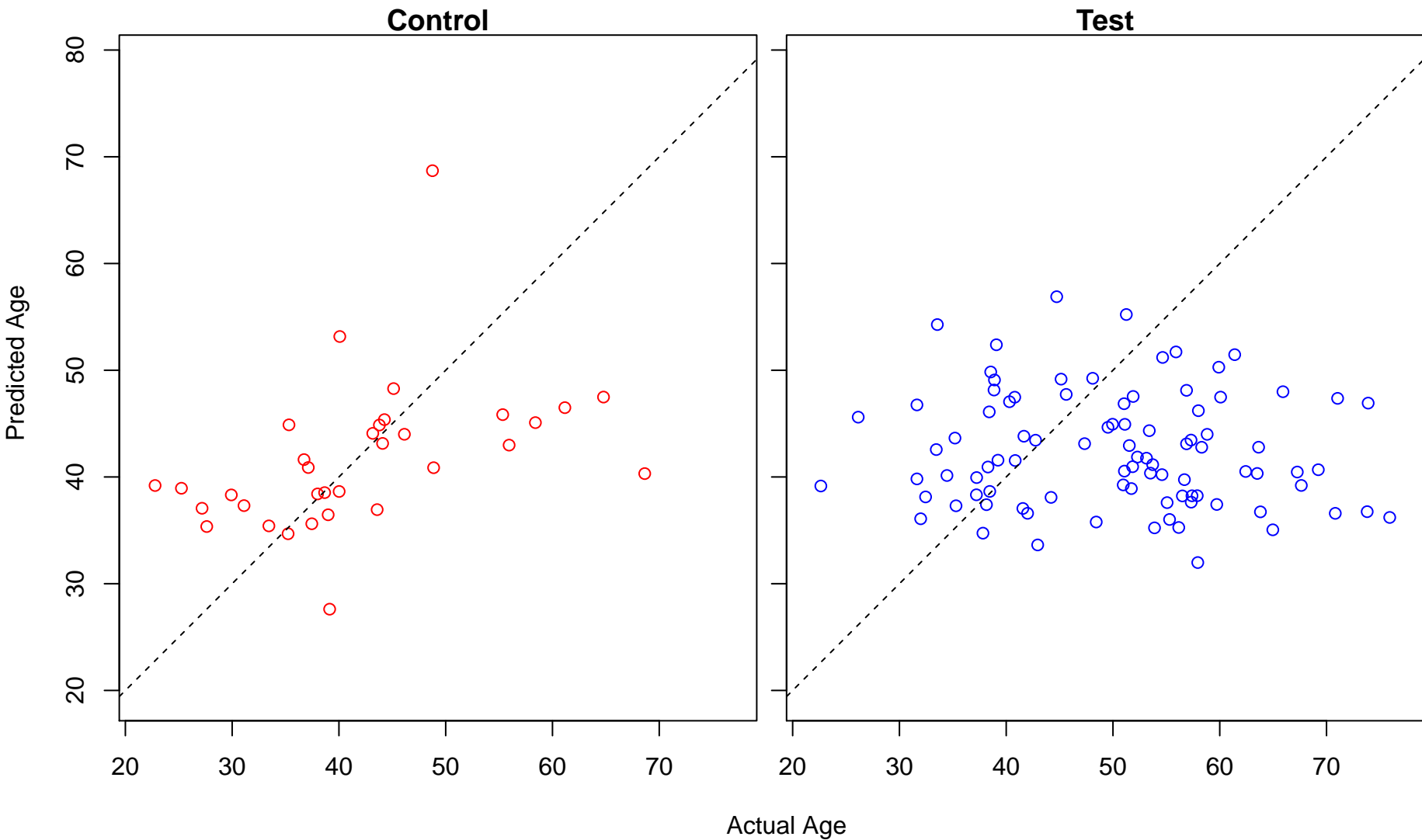
regulation of transport (Score: 0.726683)



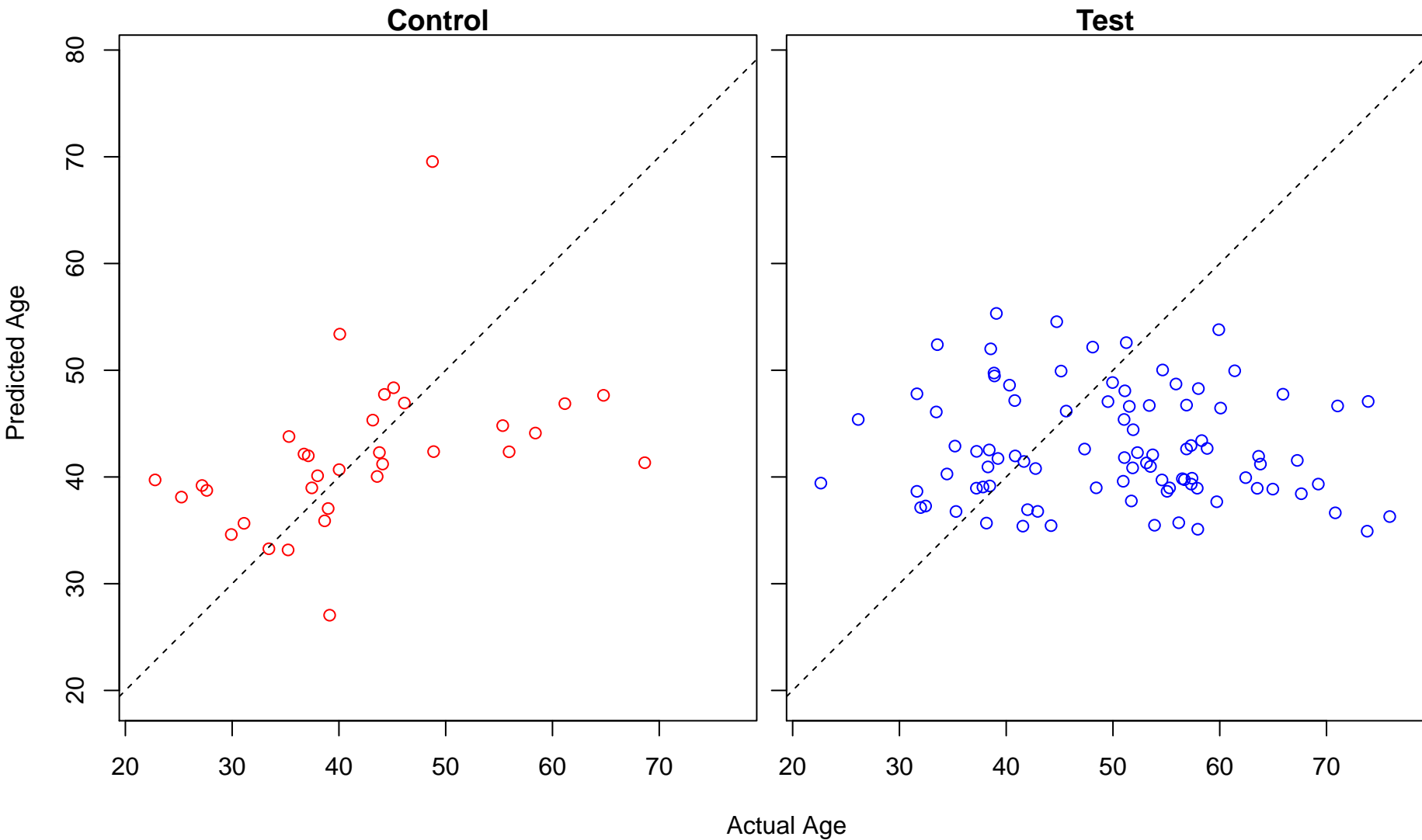
single-multicellular organism process (Score: 0.726478)



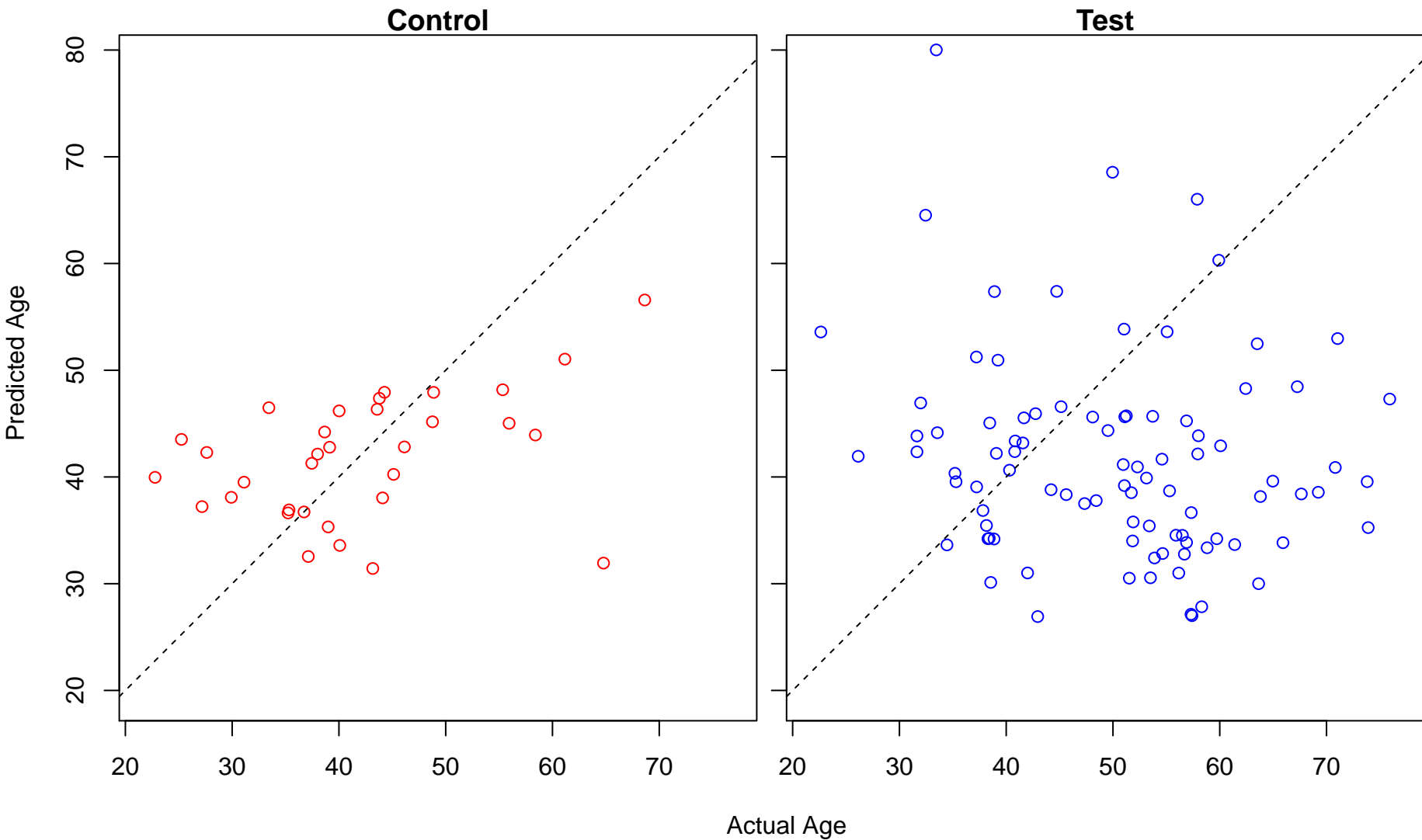
positive regulation of macromolecule metabolic process (Score: 0.725619)



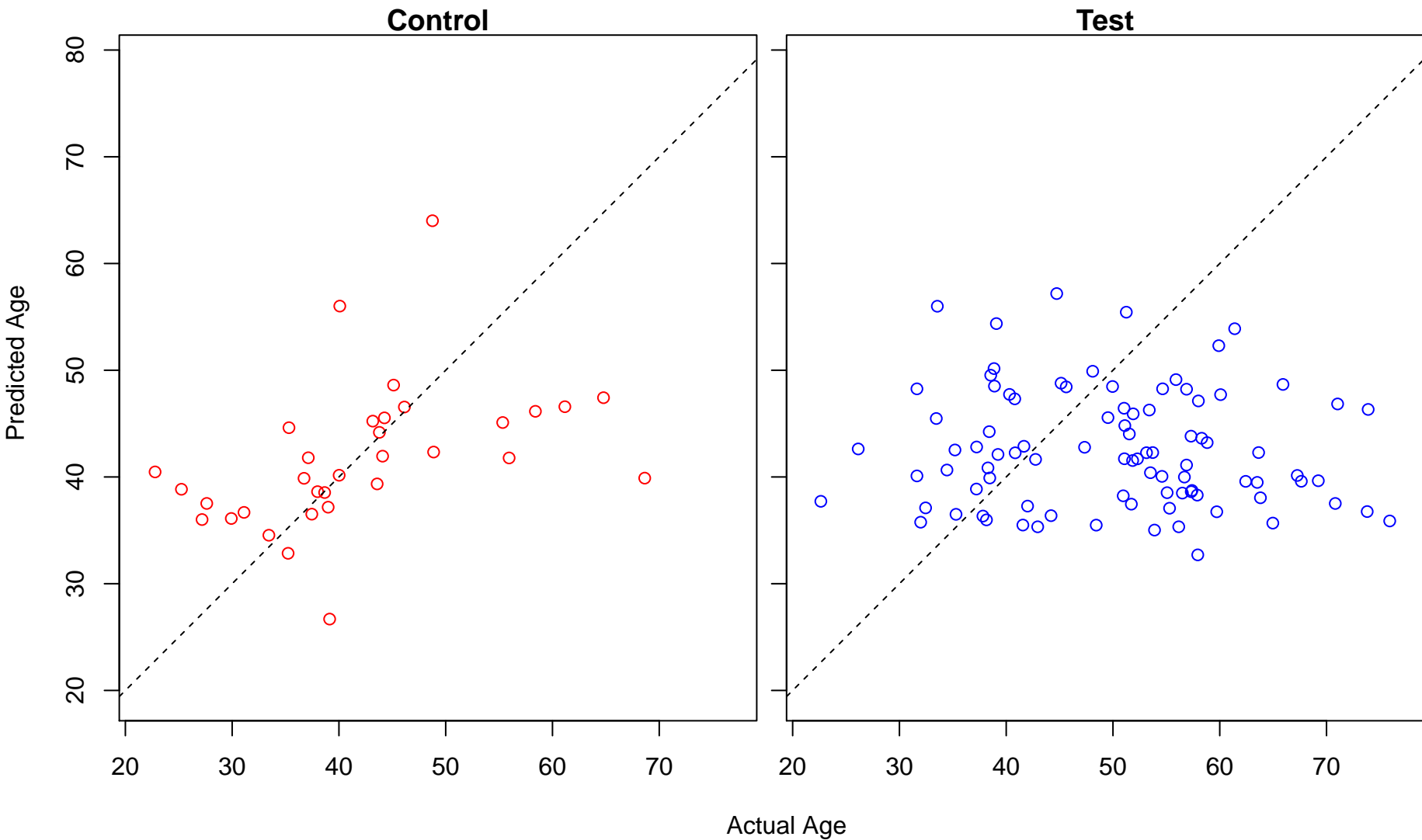
cellular macromolecular complex assembly (Score: 0.725566)



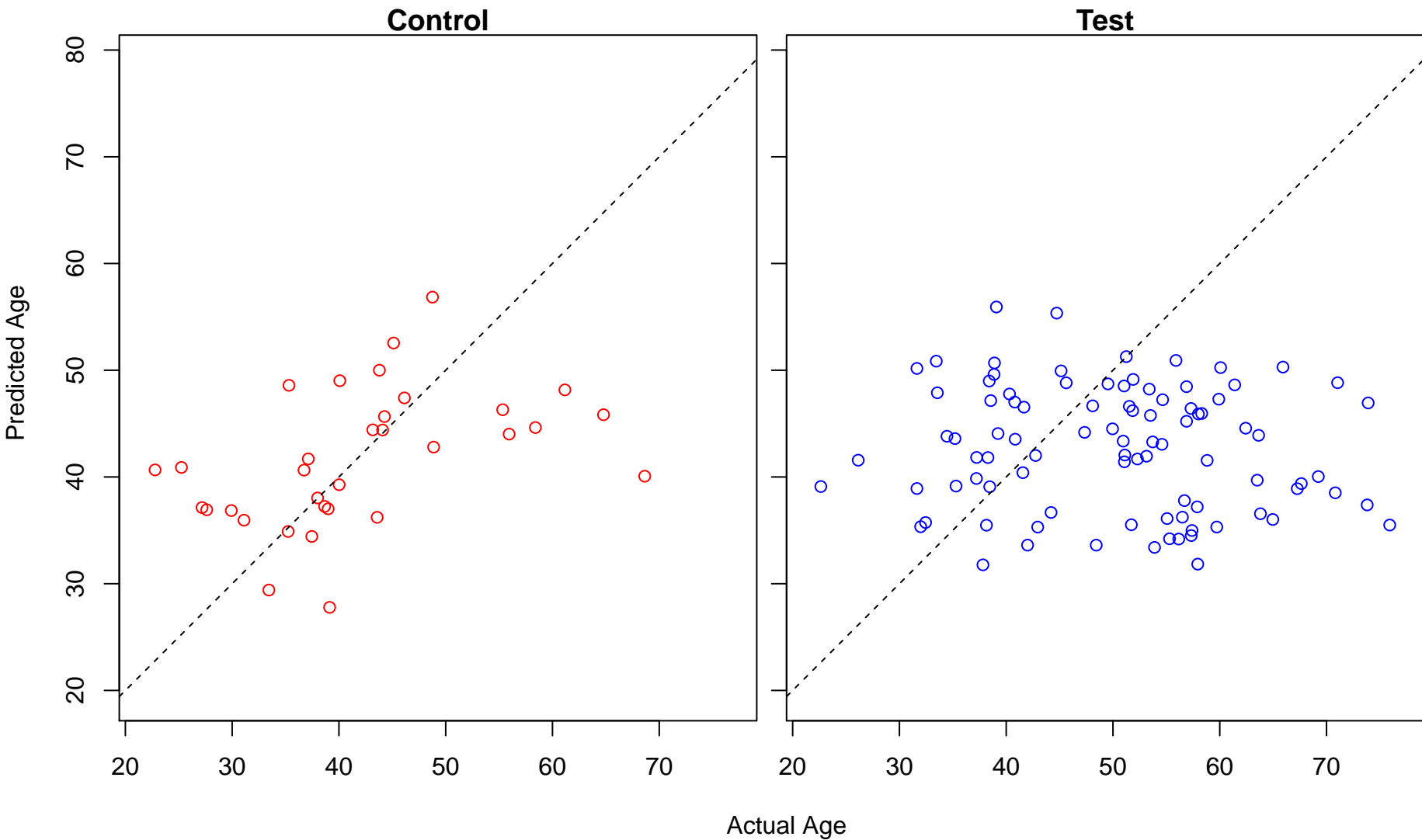
regulation of myoblast proliferation (Score: 0.725434)



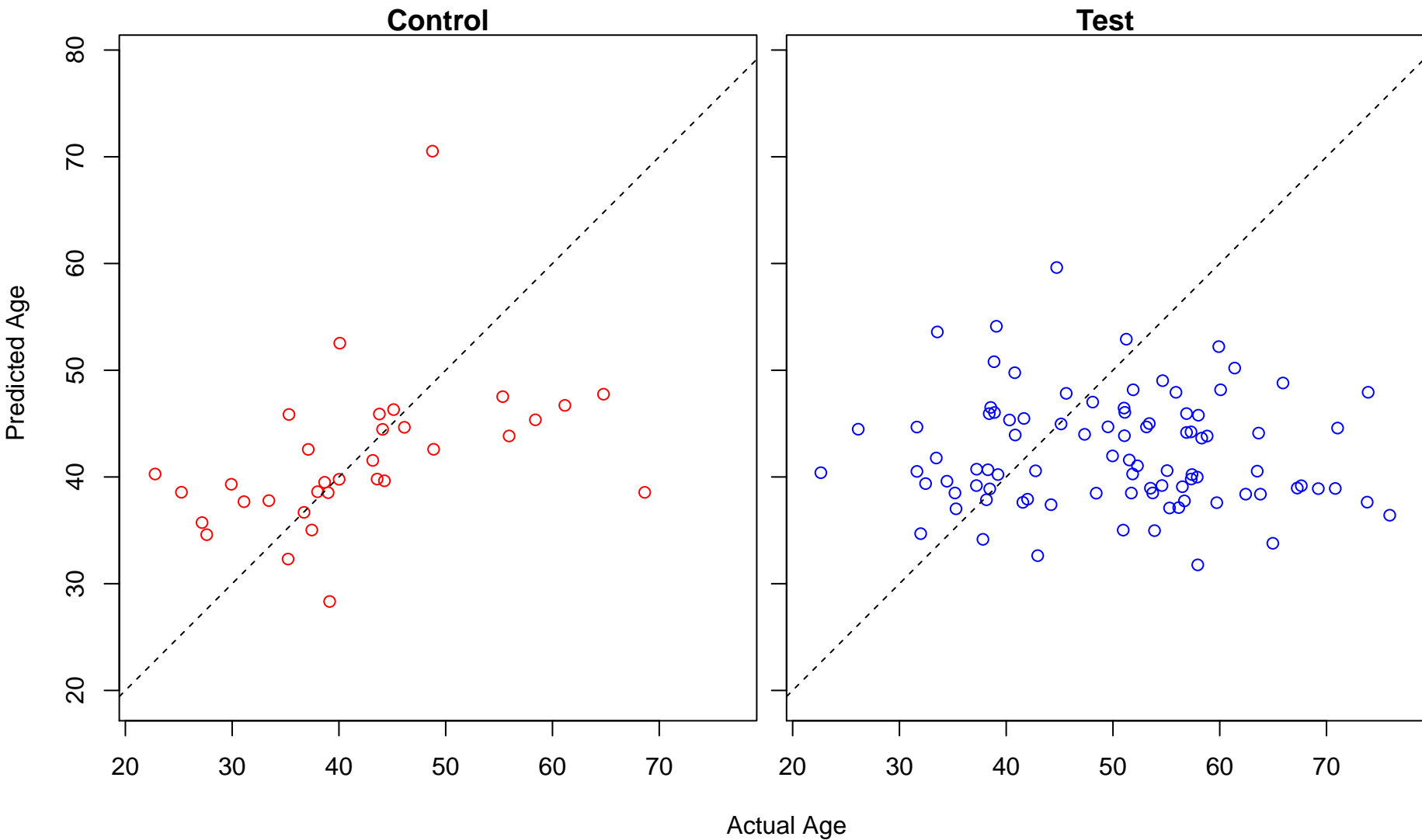
macromolecular complex assembly (Score: 0.725036)



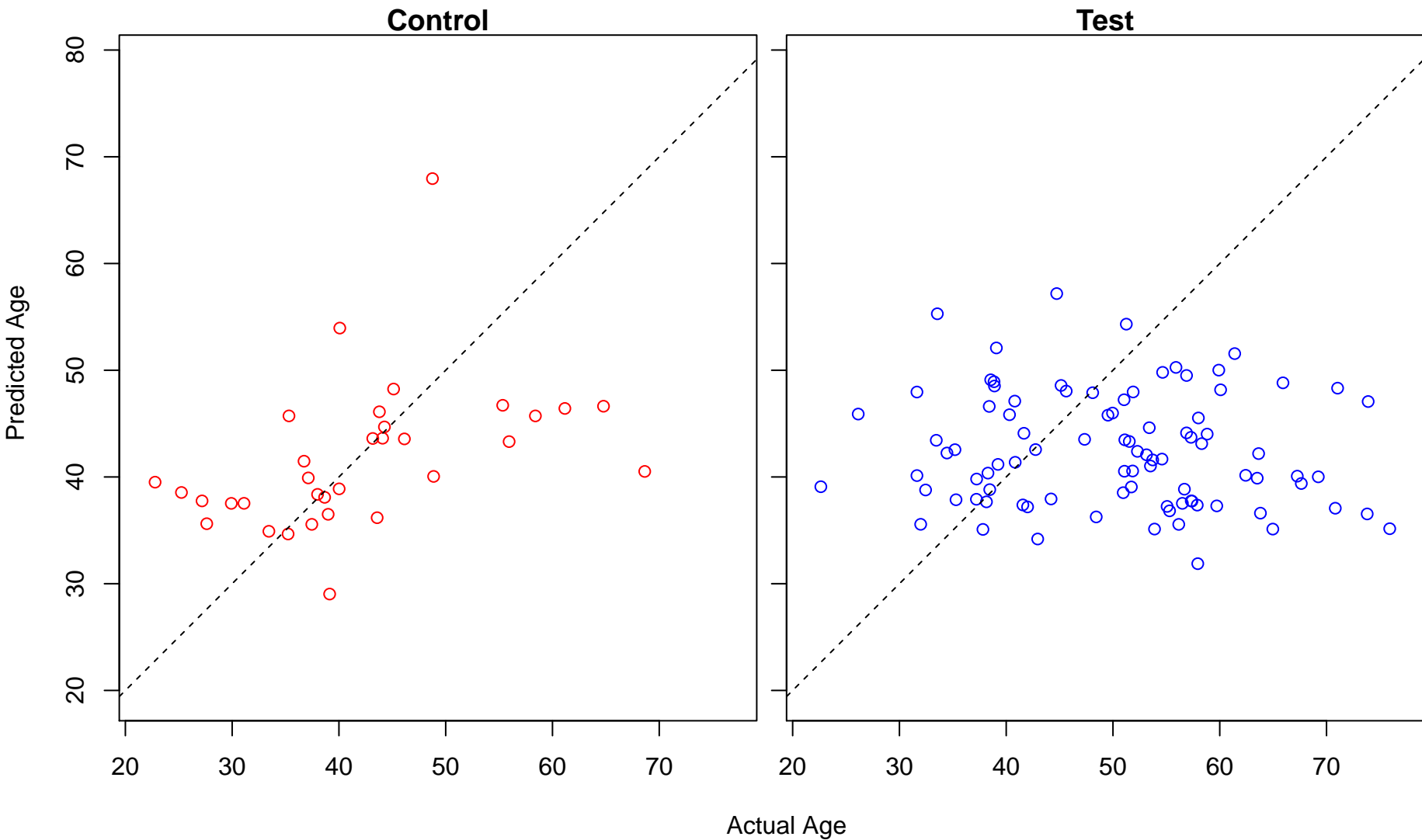
nucleobase-containing compound transport (Score: 0.724761)



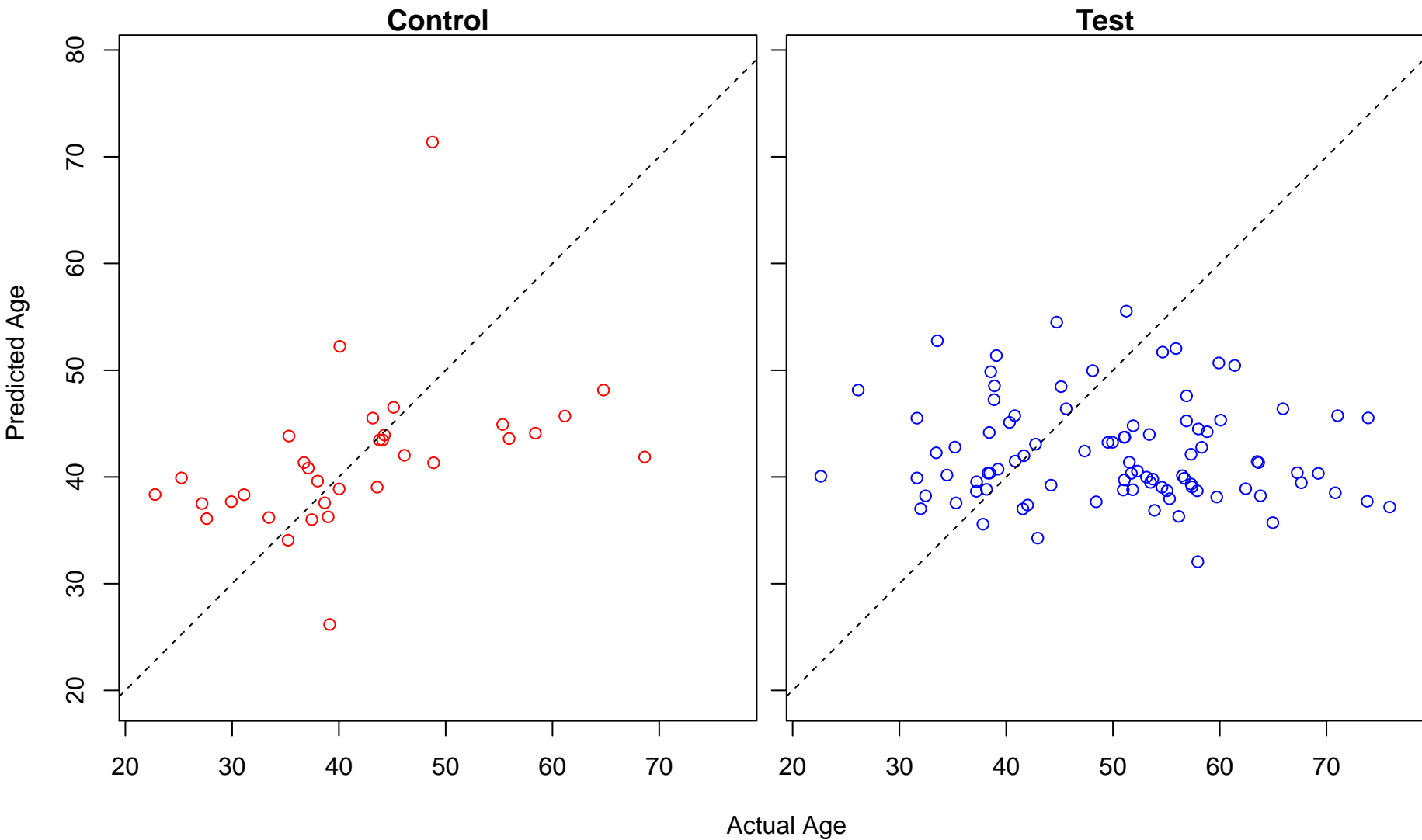
protein N-linked glycosylation (Score: 0.724663)



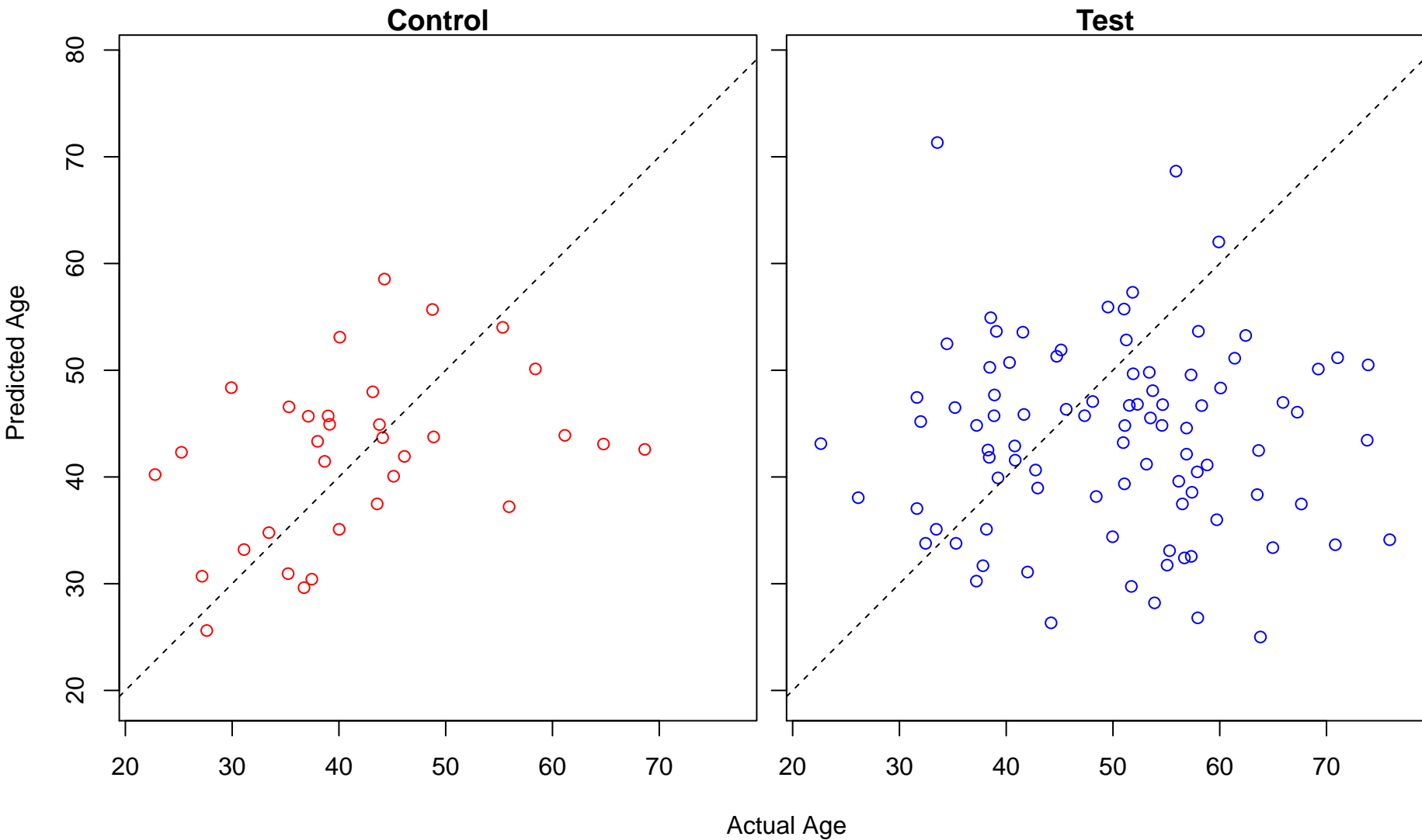
positive regulation of nucleobase-containing compound metabolic process (Score: 0.724647)



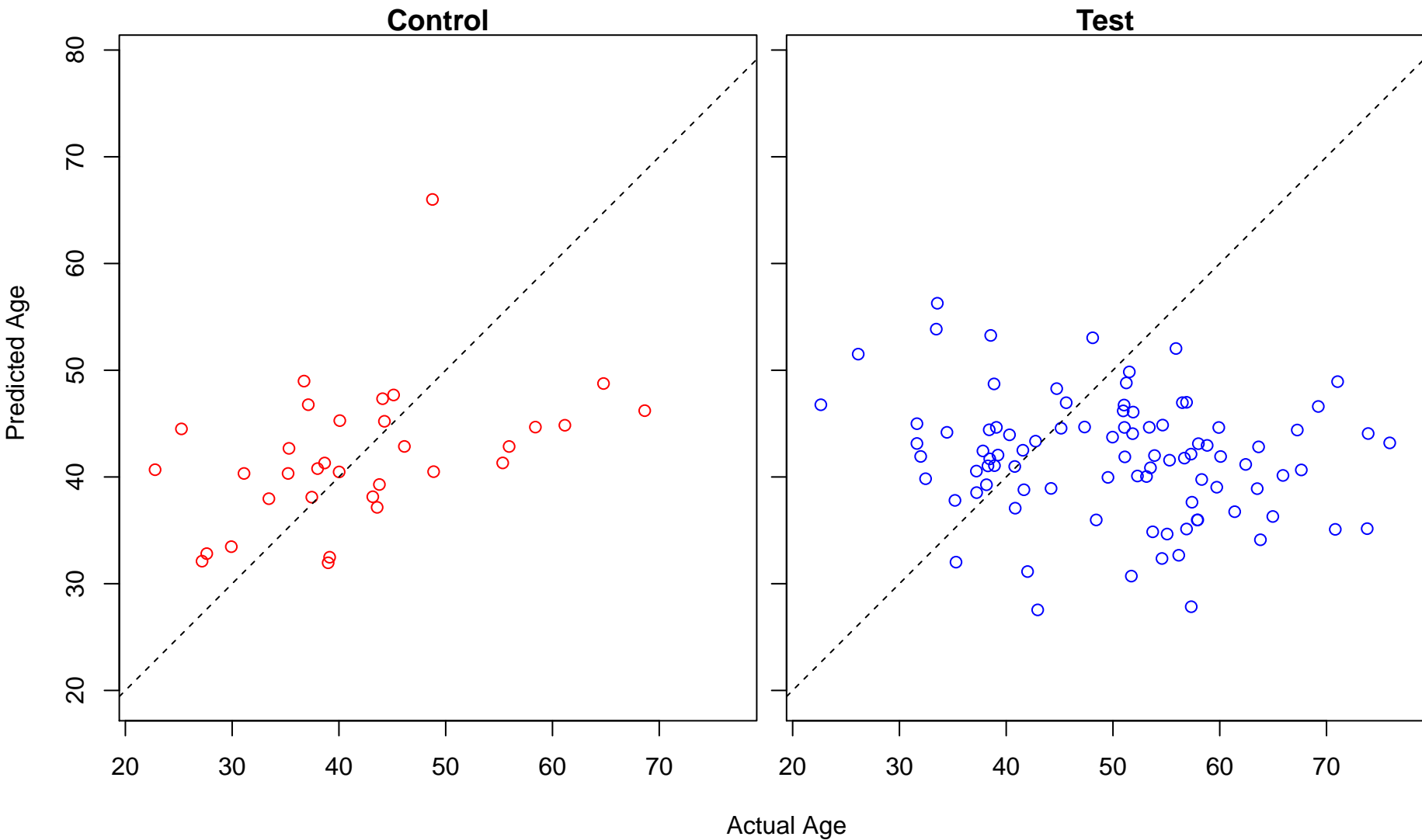
negative regulation of gene expression (Score: 0.723457)



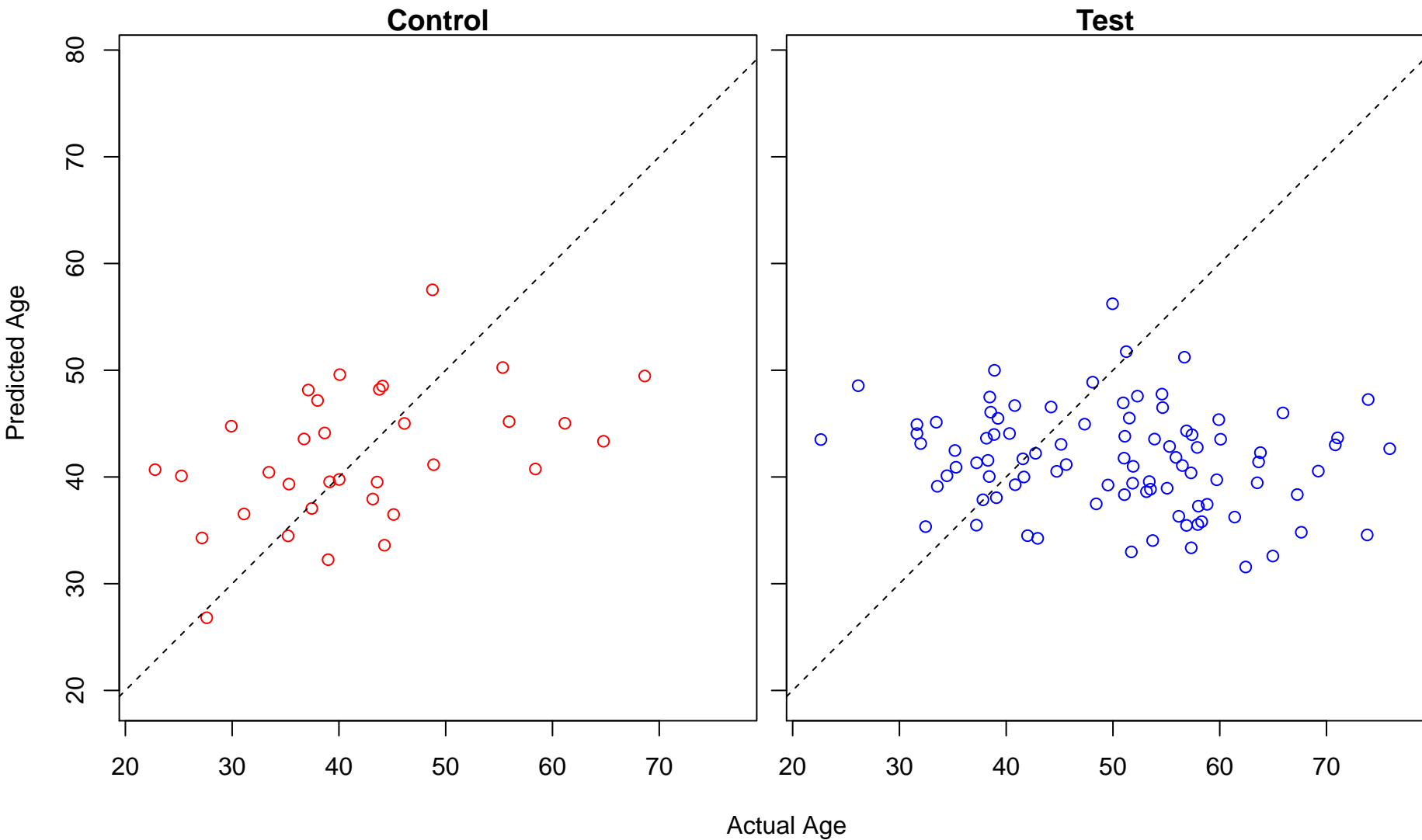
neuroblast division (Score: 0.723075)



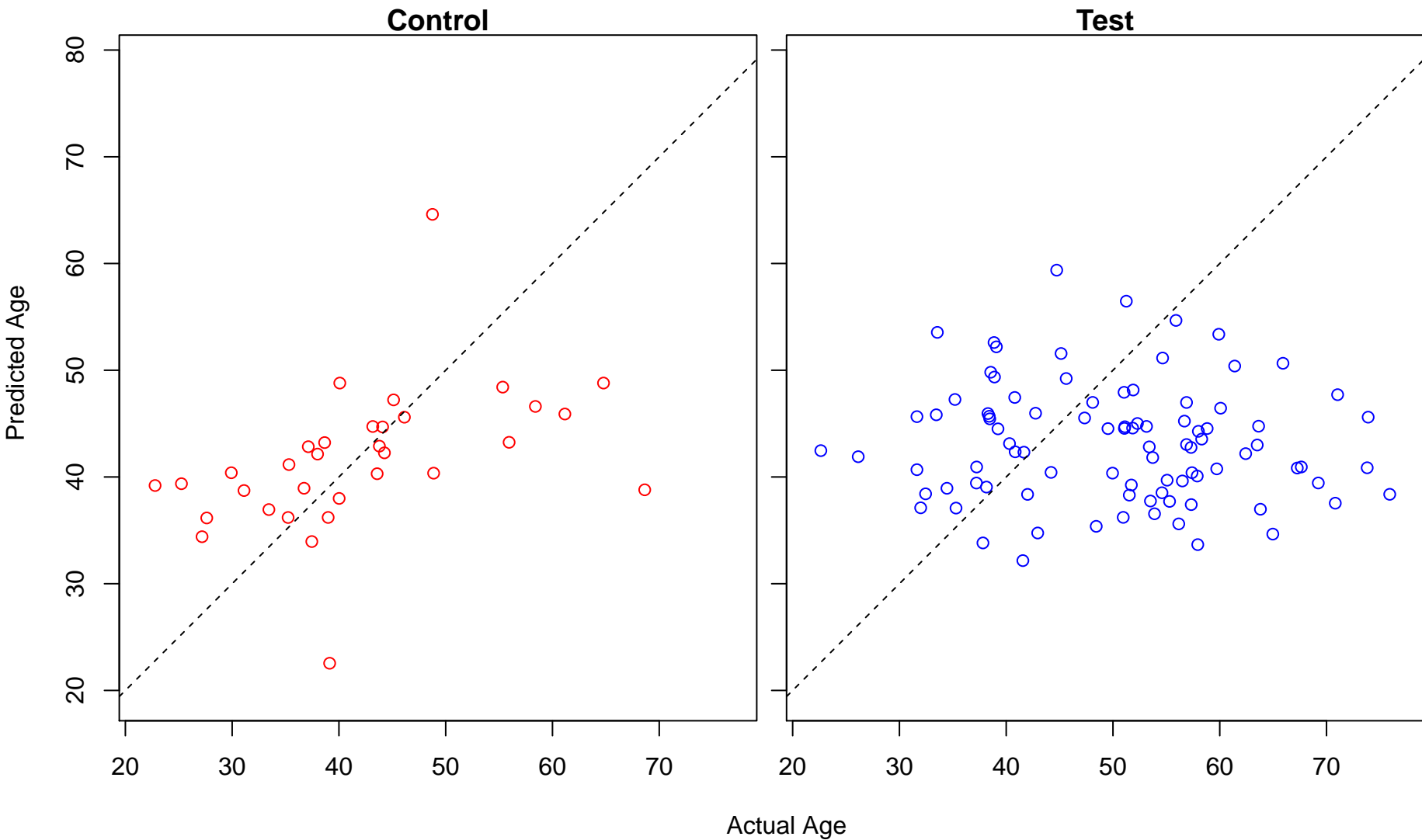
regulation of protein homooligomerization (Score: 0.722655)



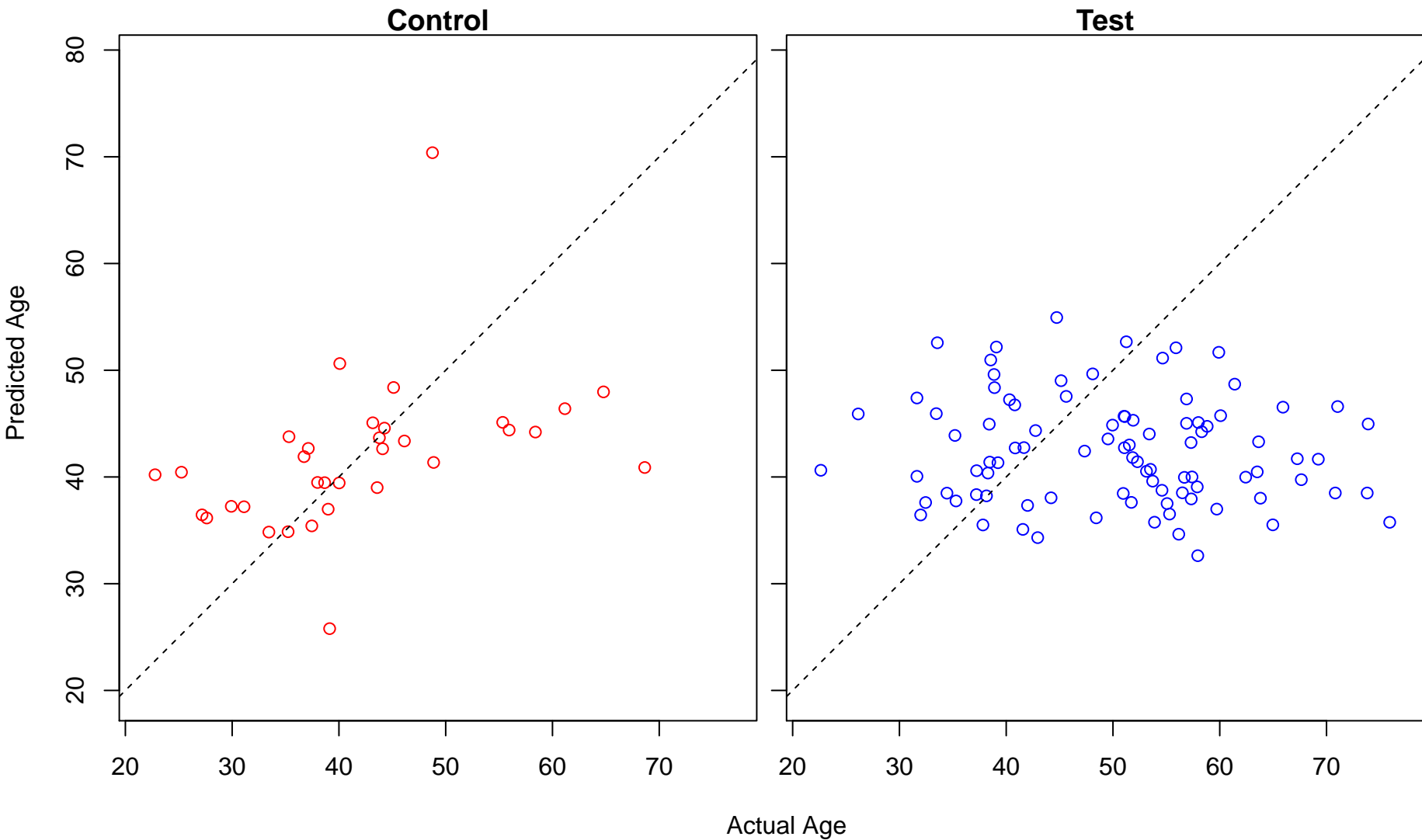
patterning of blood vessels (Score: 0.721938)



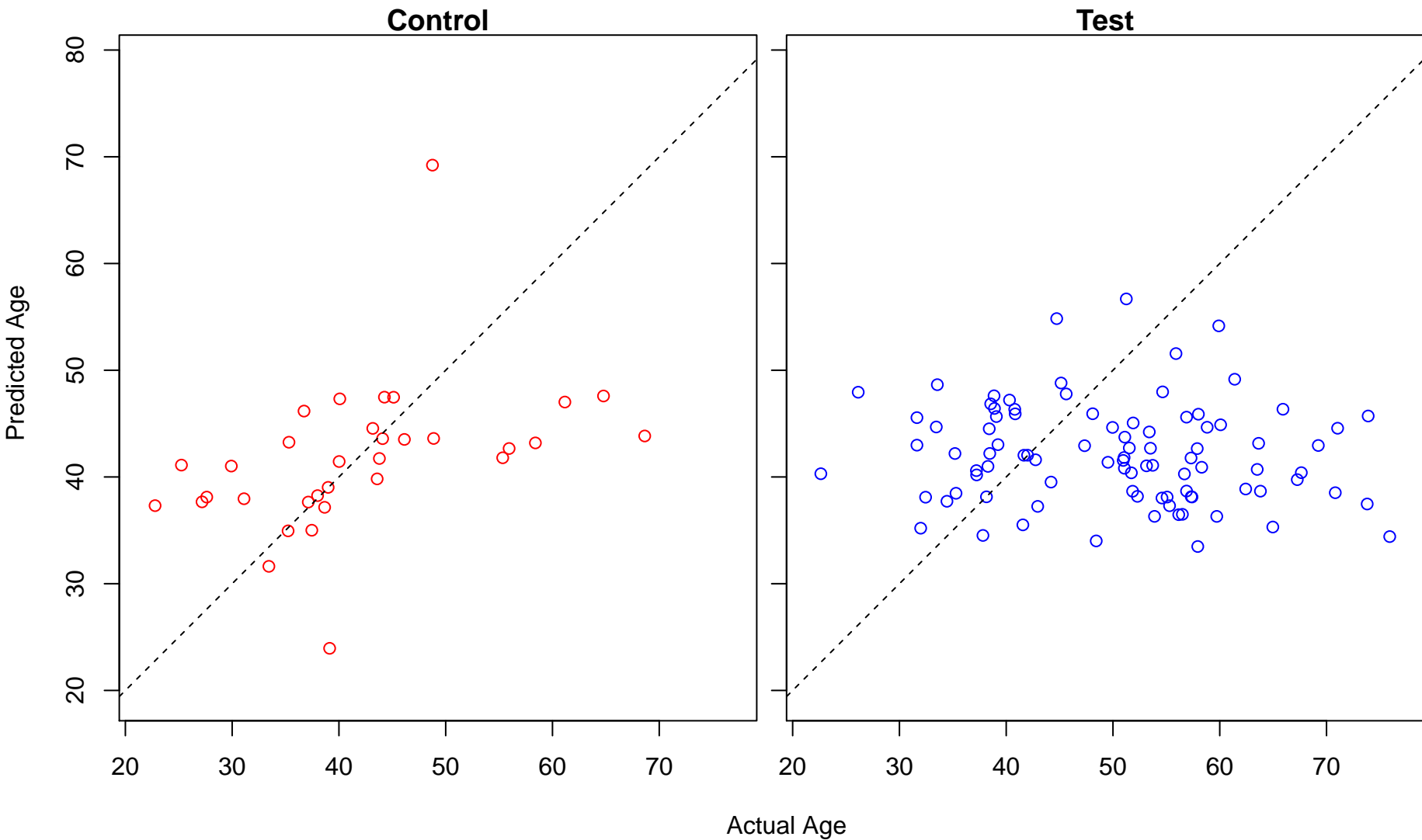
axon guidance (Score: 0.721590)



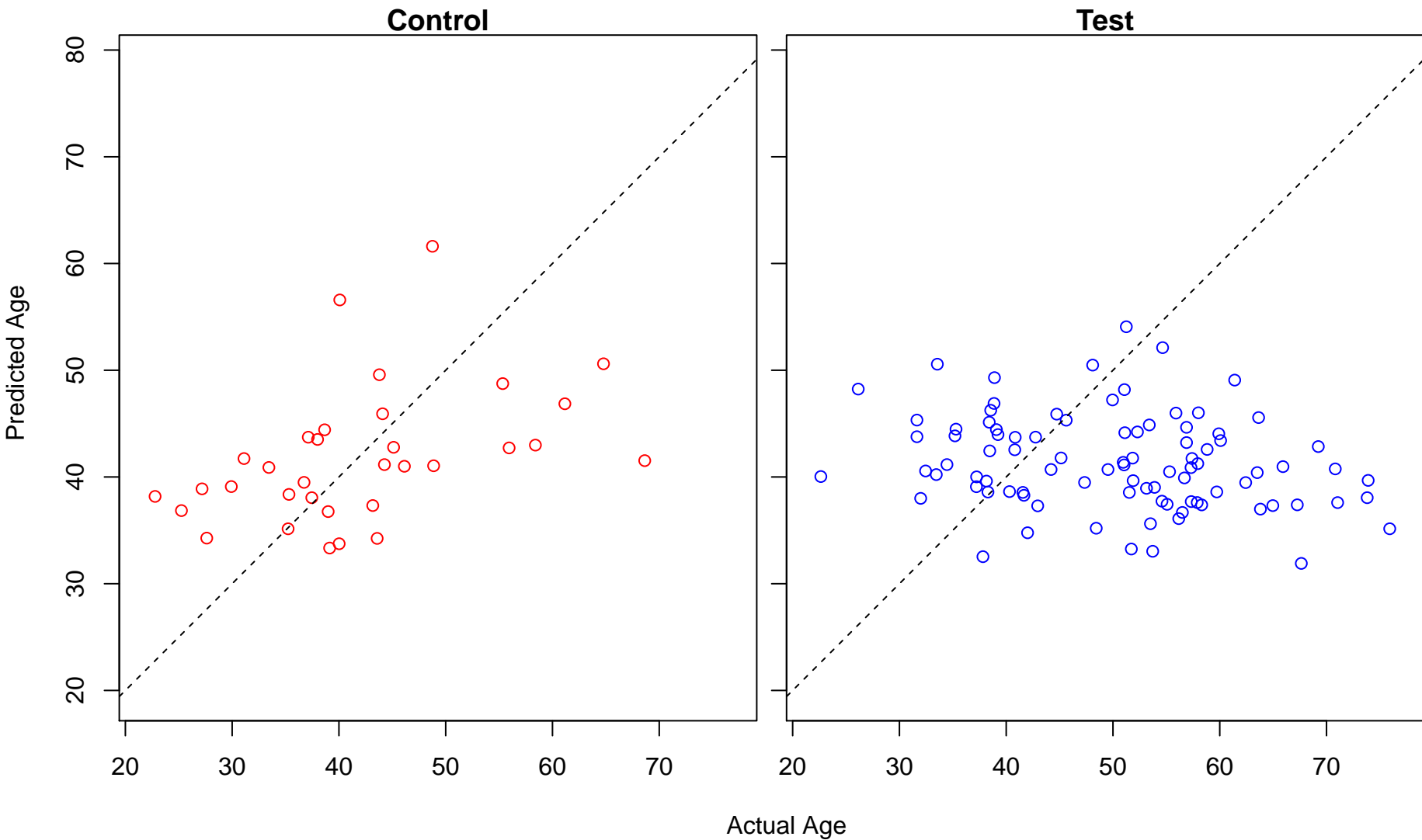
localization (Score: 0.721407)



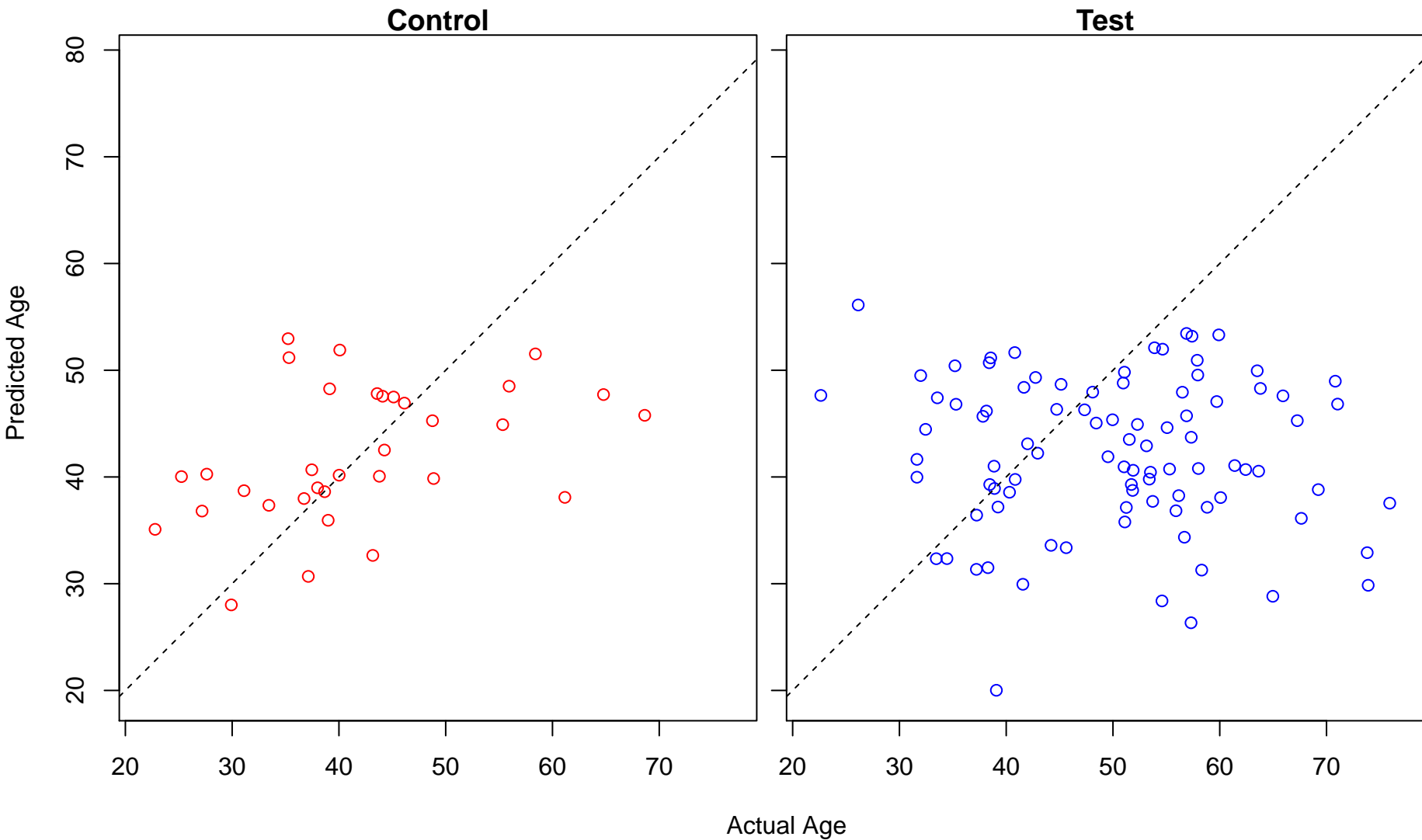
cellular response to unfolded protein (Score: 0.721242)



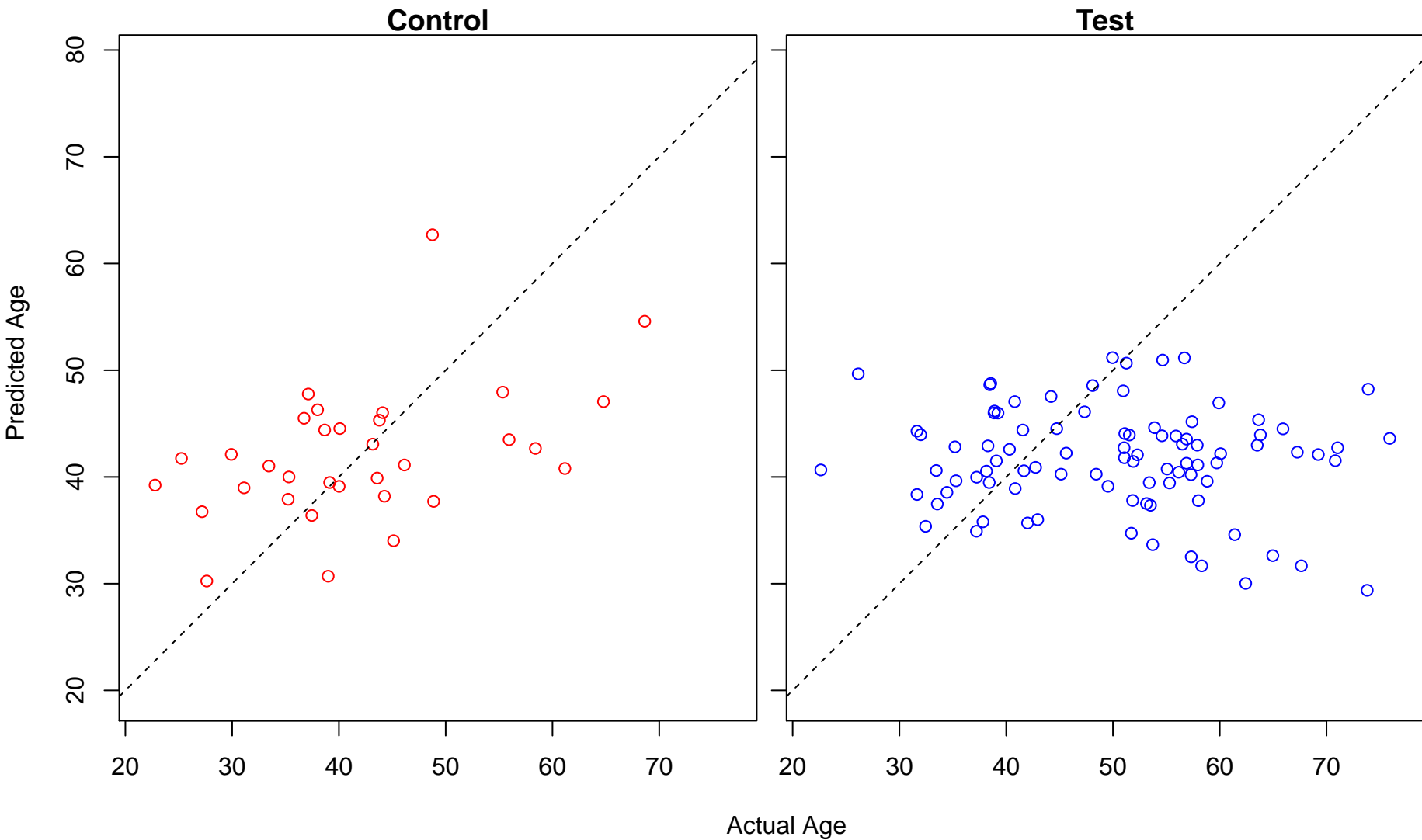
heart morphogenesis (Score: 0.721214)



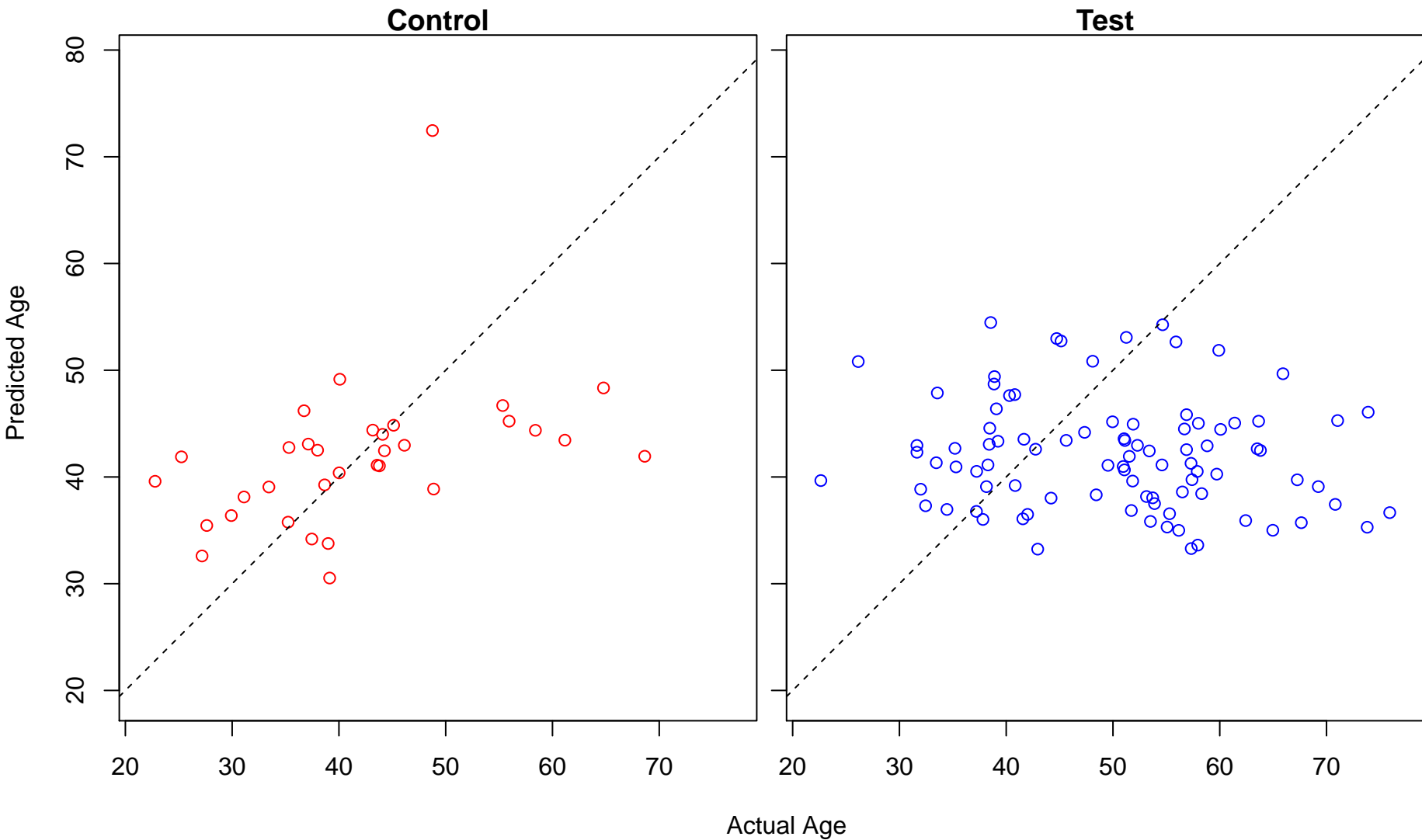
potassium ion export (Score: 0.720479)



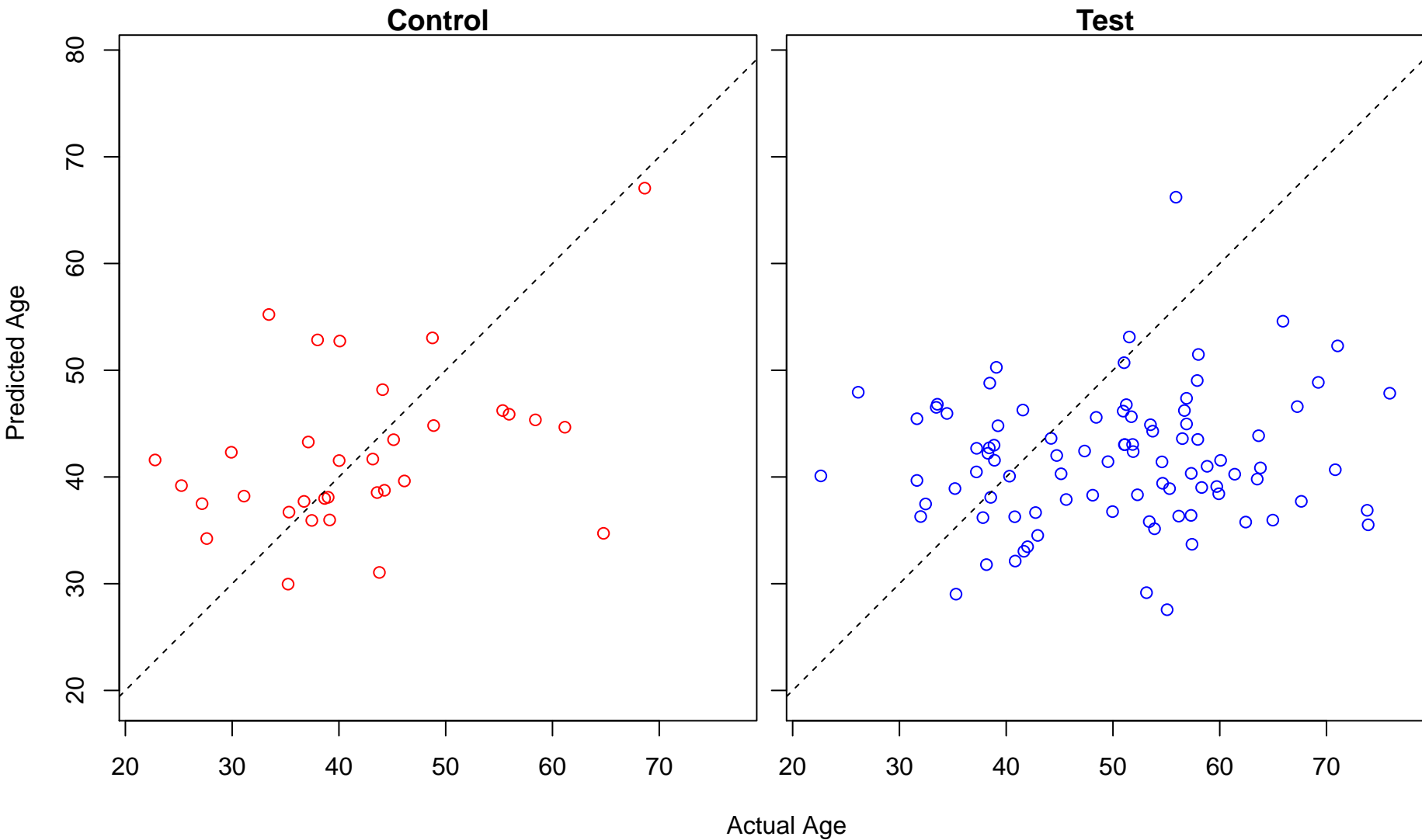
cardiac left ventricle morphogenesis (Score: 0.720065)



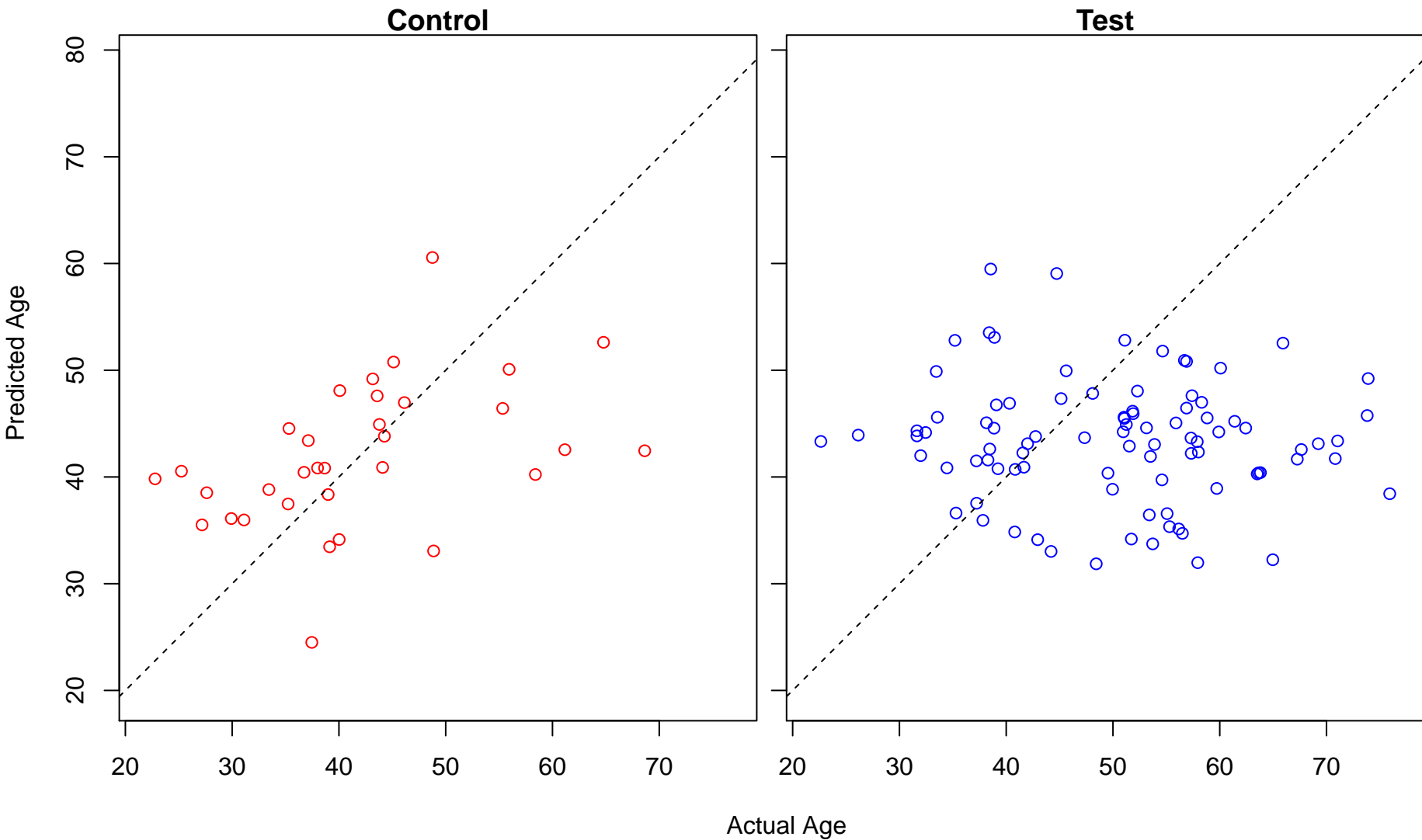
hematopoietic or lymphoid organ development (Score: 0.719896)



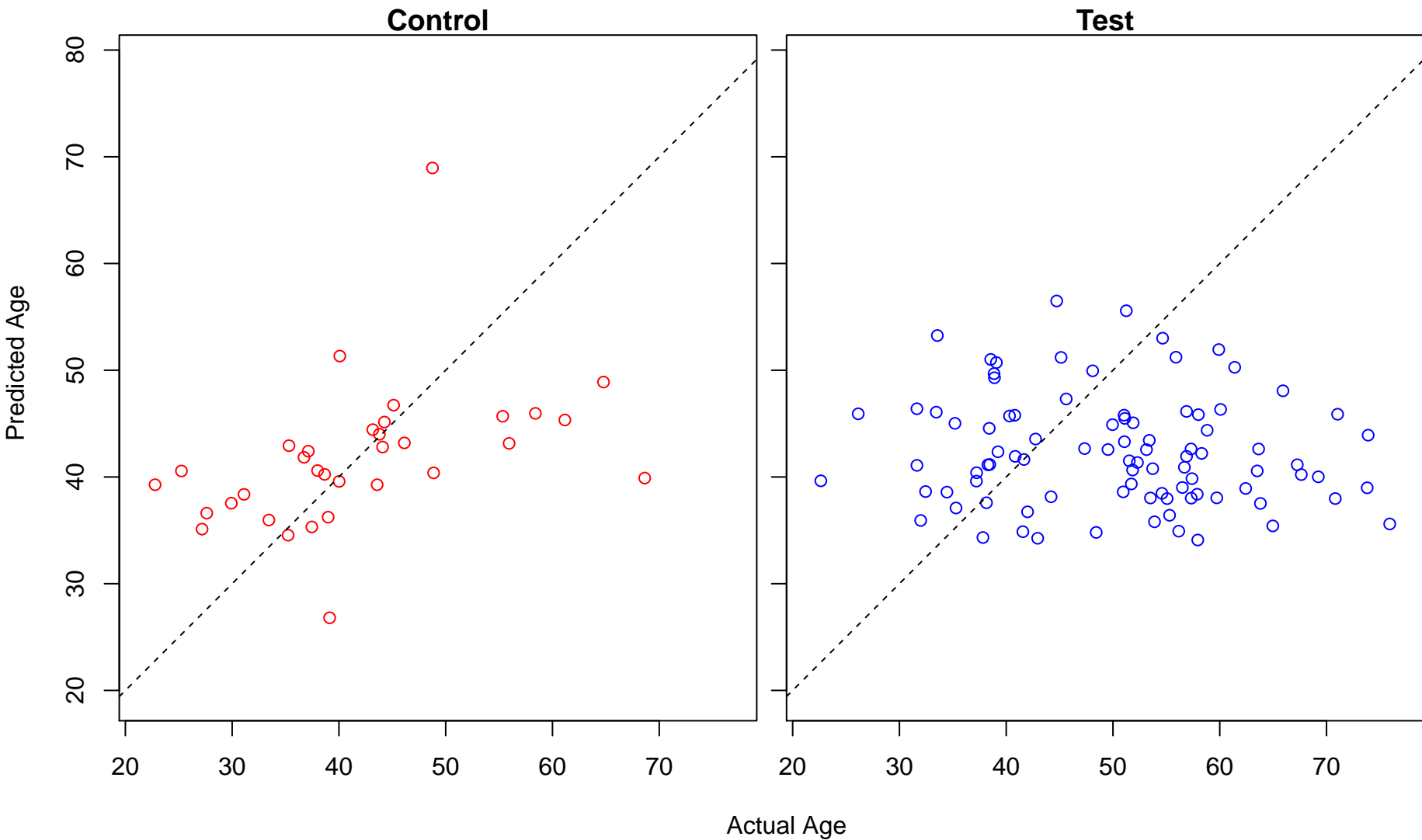
platelet-derived growth factor receptor signaling pathway (Score: 0.718879)



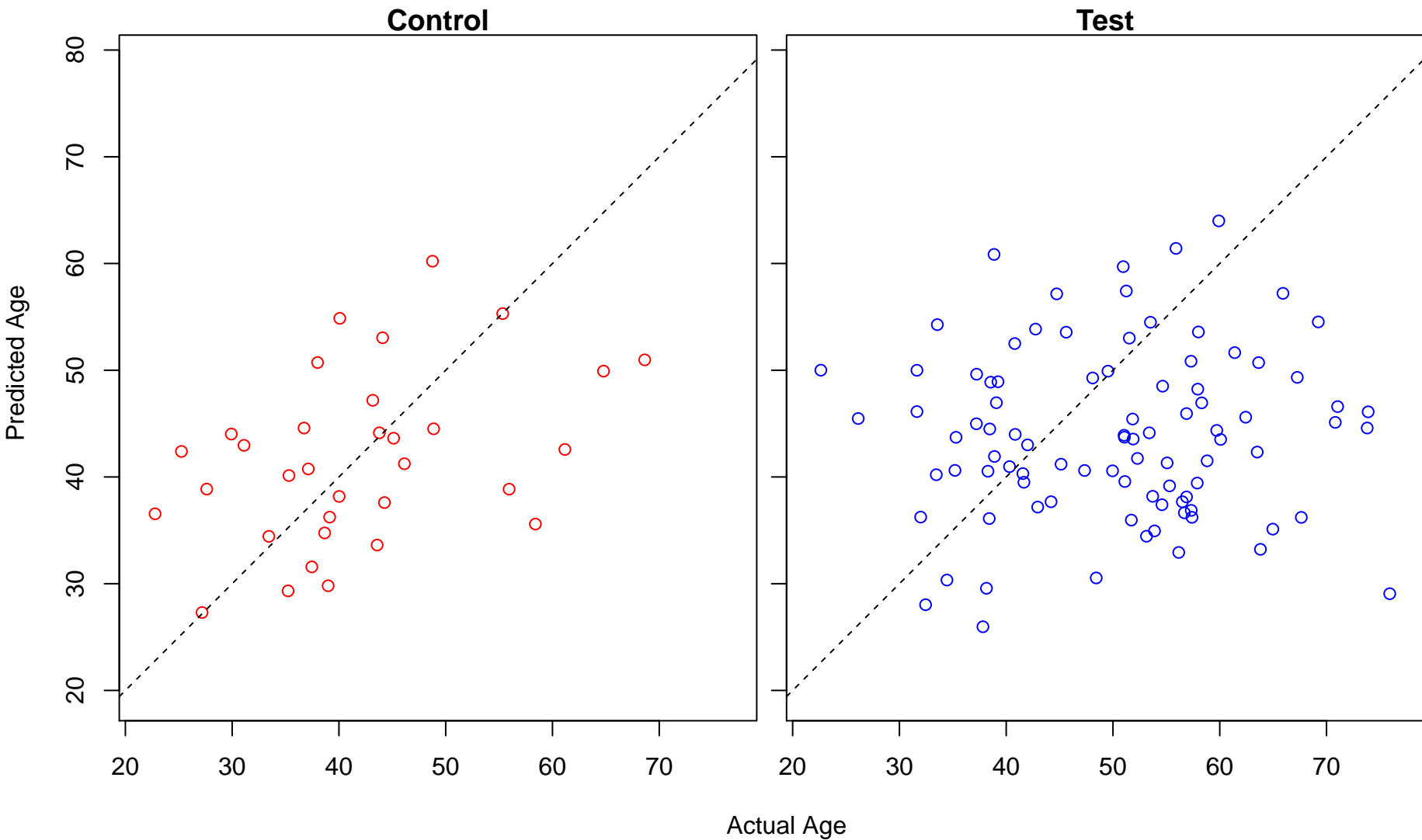
positive regulation of T cell receptor signaling pathway (Score: 0.718858)



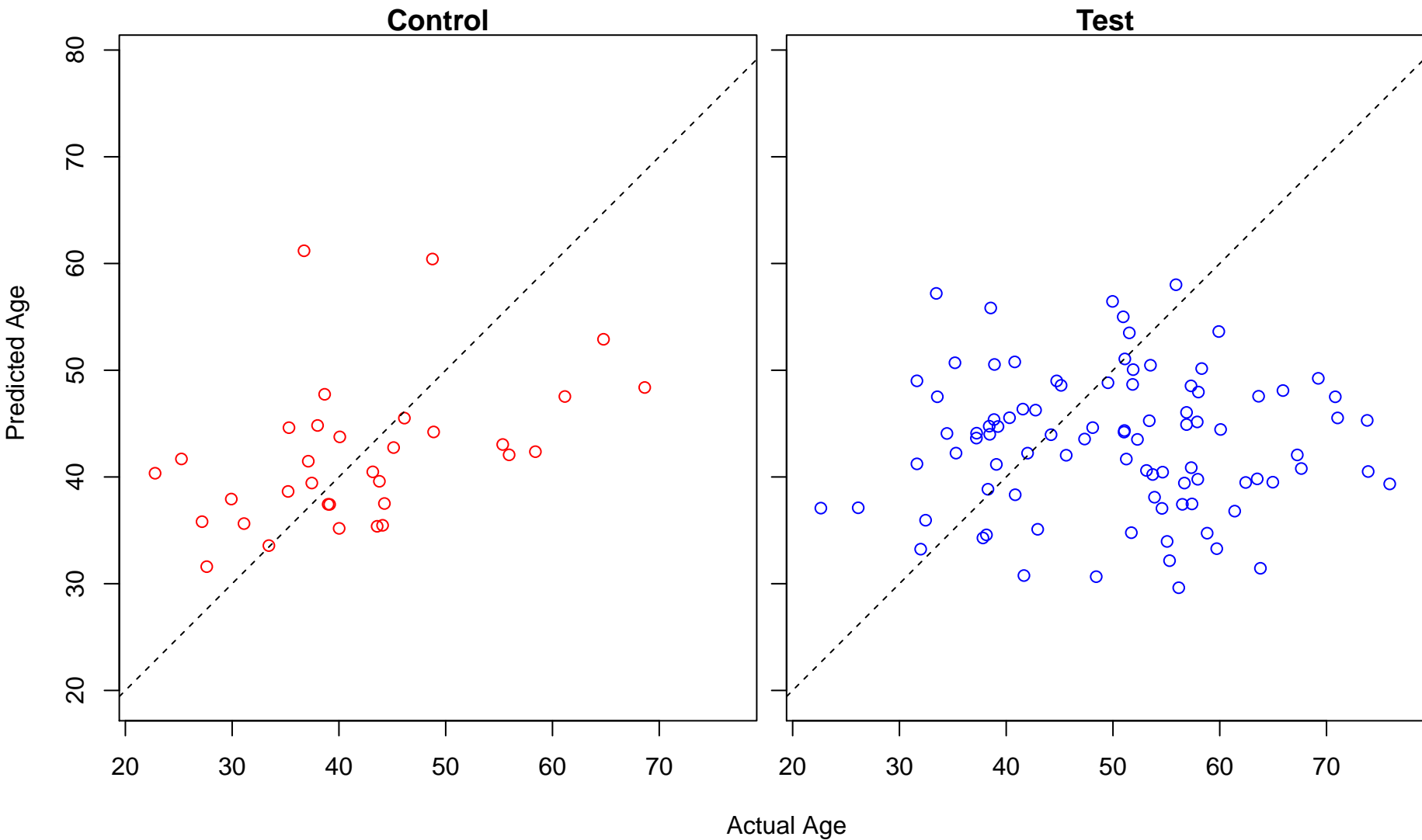
system development (Score: 0.718520)



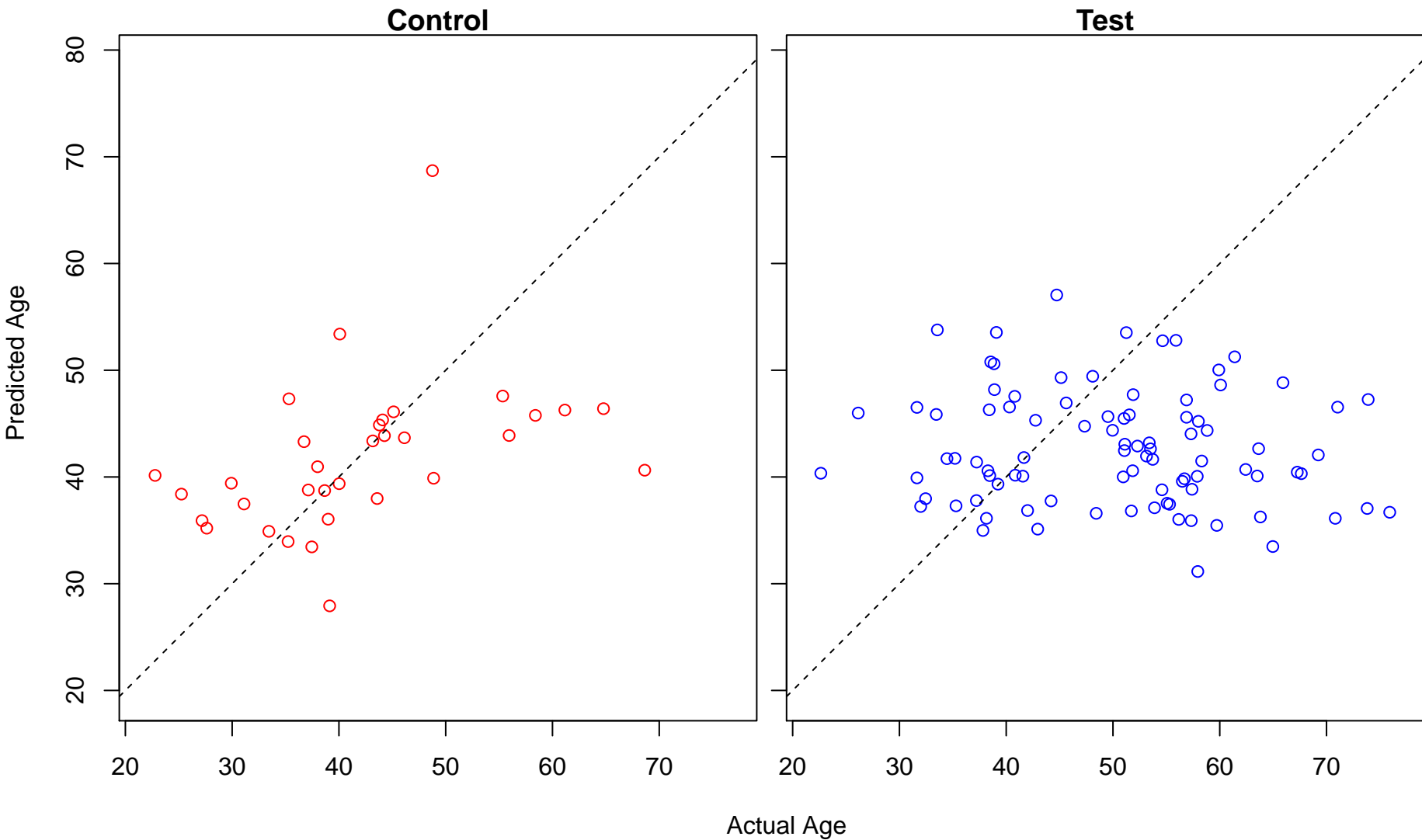
detection of stimulus (Score: 0.718356)



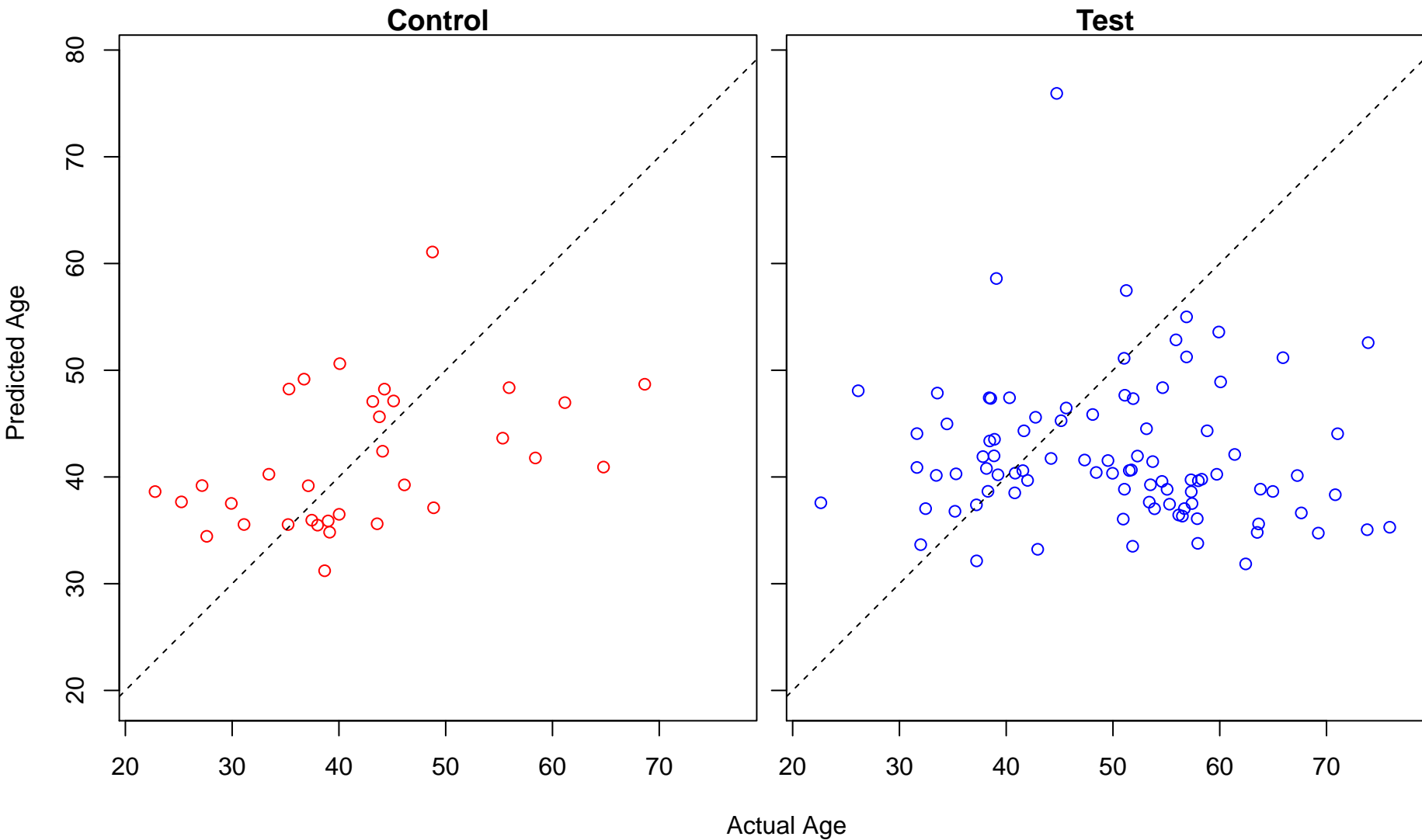
negative regulation of interleukin-1 beta production (Score: 0.718235)



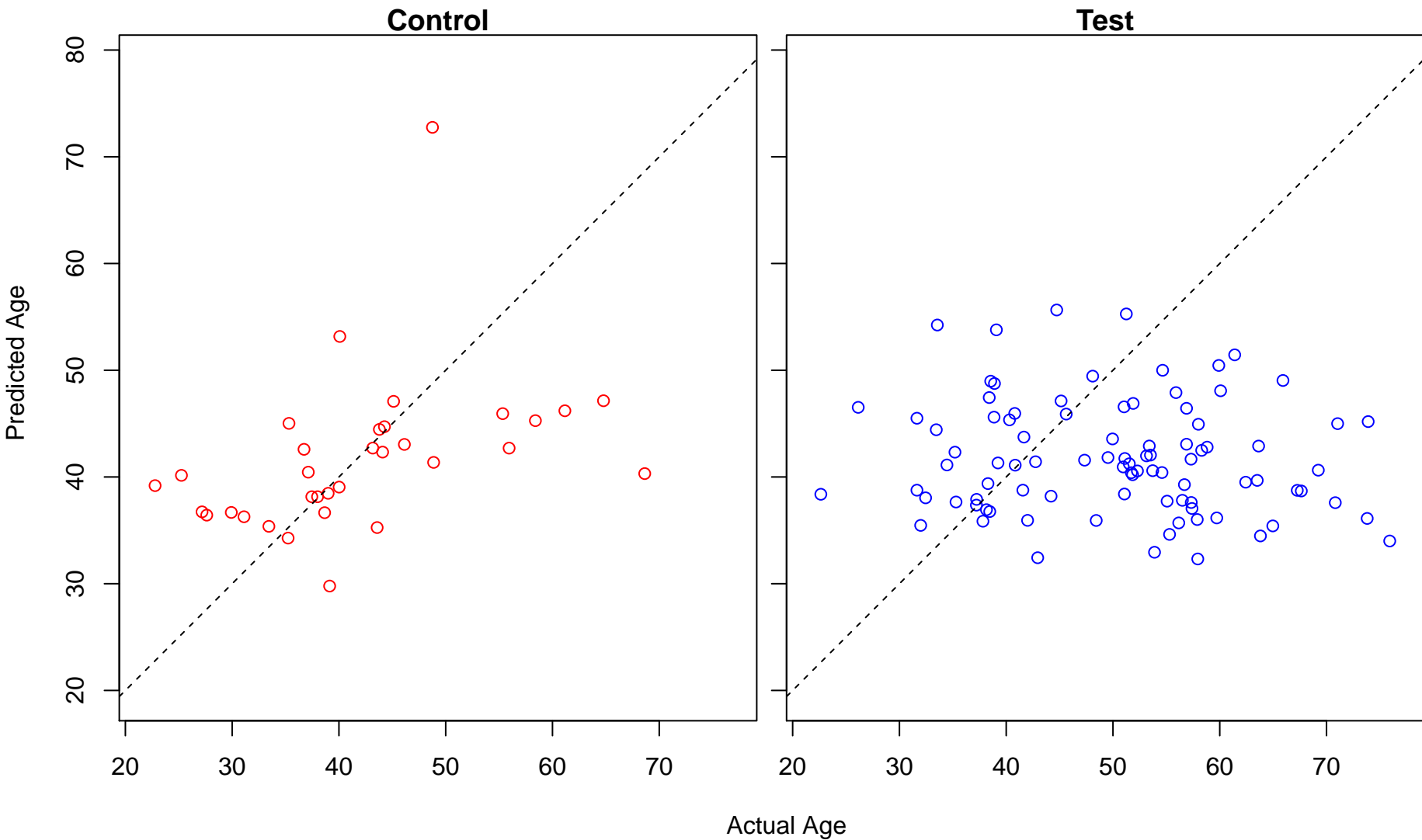
regulation of apoptotic signaling pathway (Score: 0.718123)



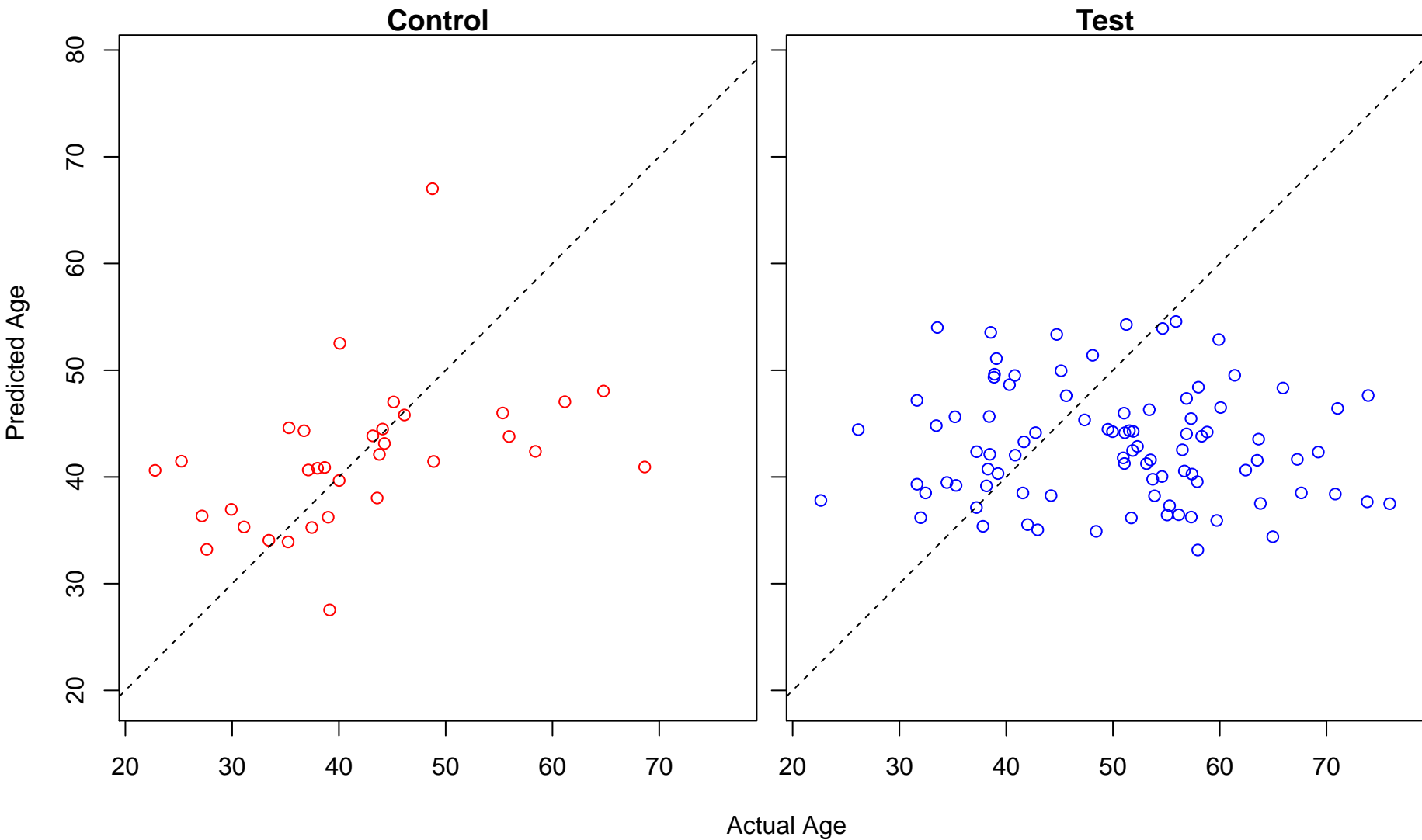
histone H4-K16 acetylation (Score: 0.717503)



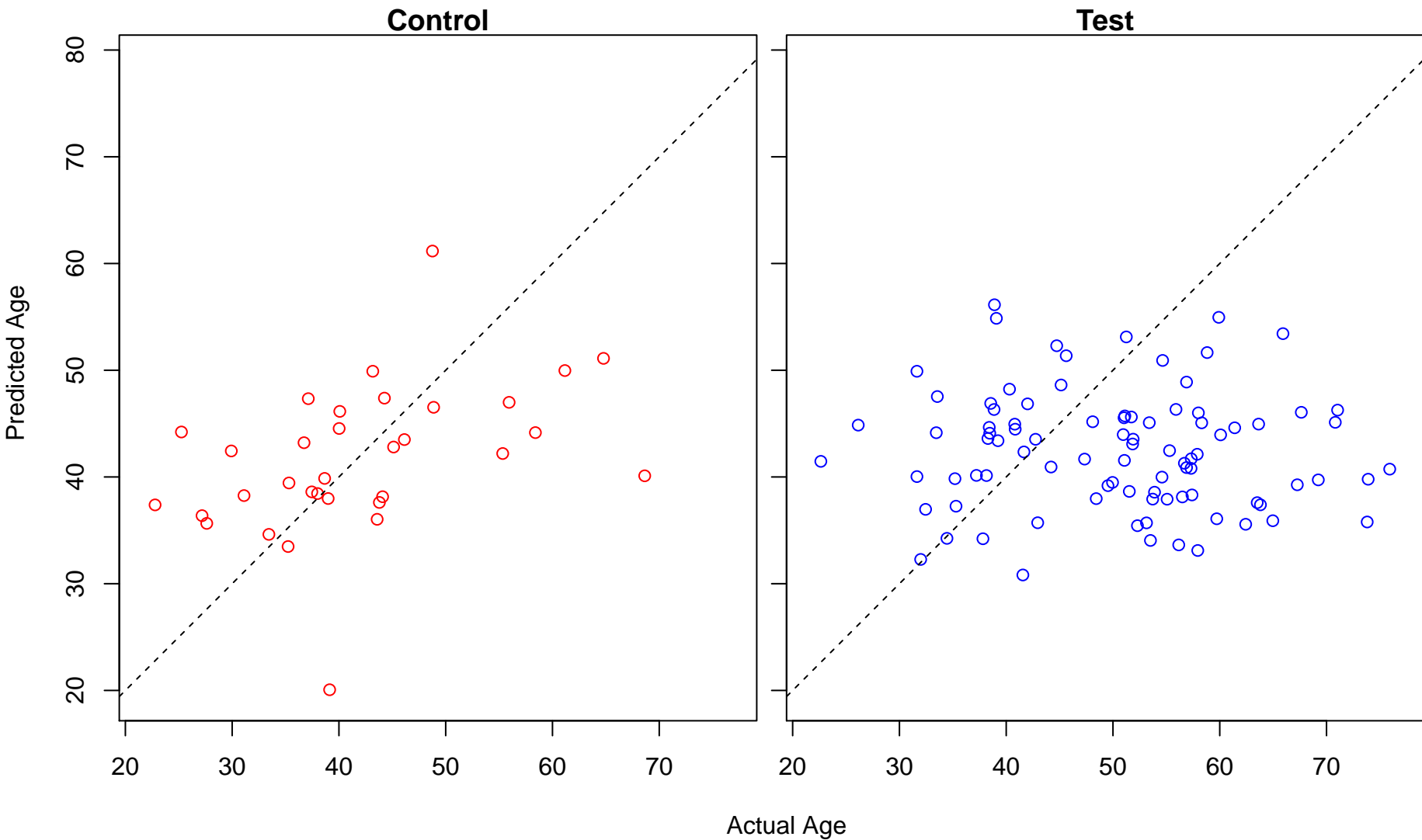
transcription from RNA polymerase II promoter (Score: 0.717431)



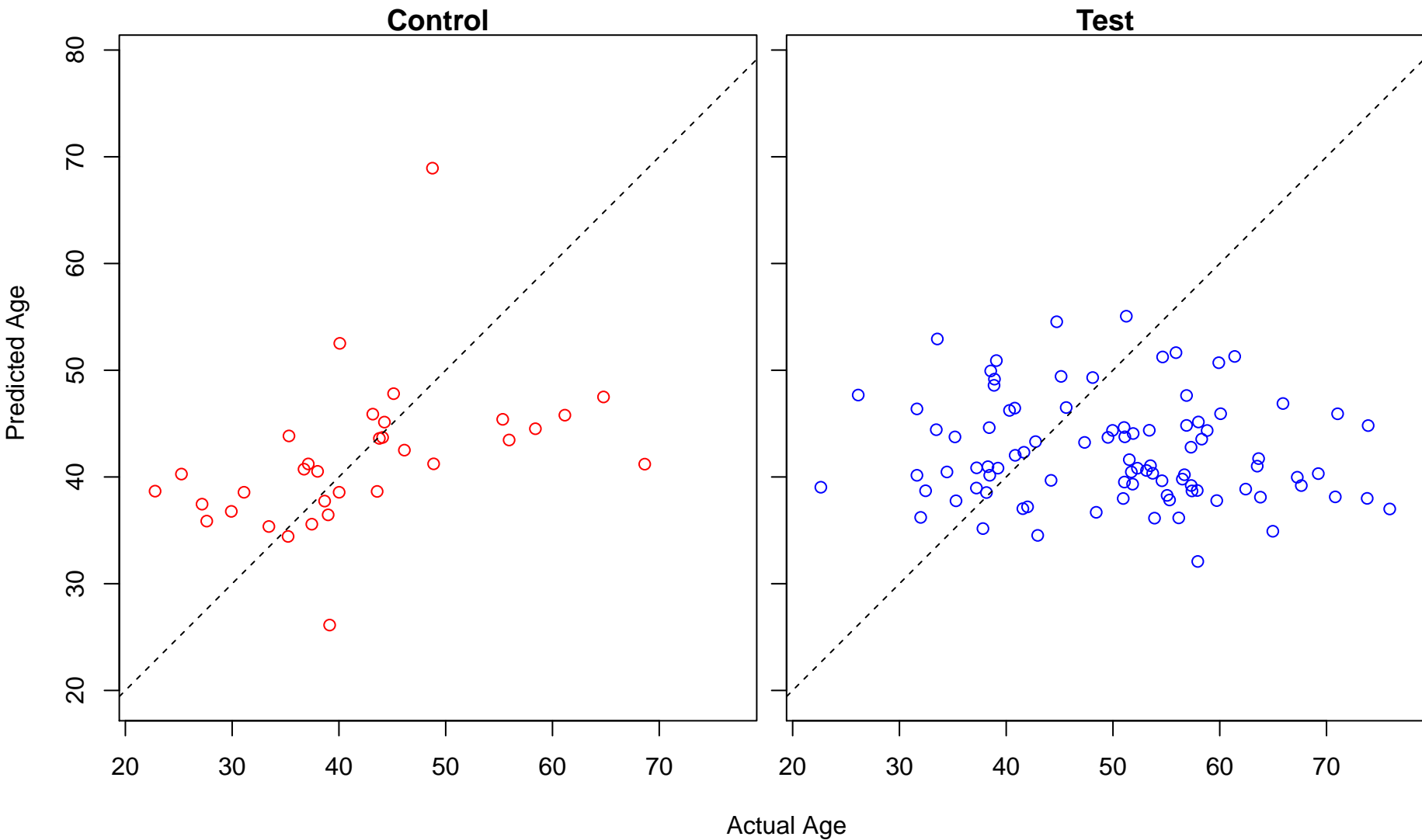
positive regulation of cell death (Score: 0.716855)



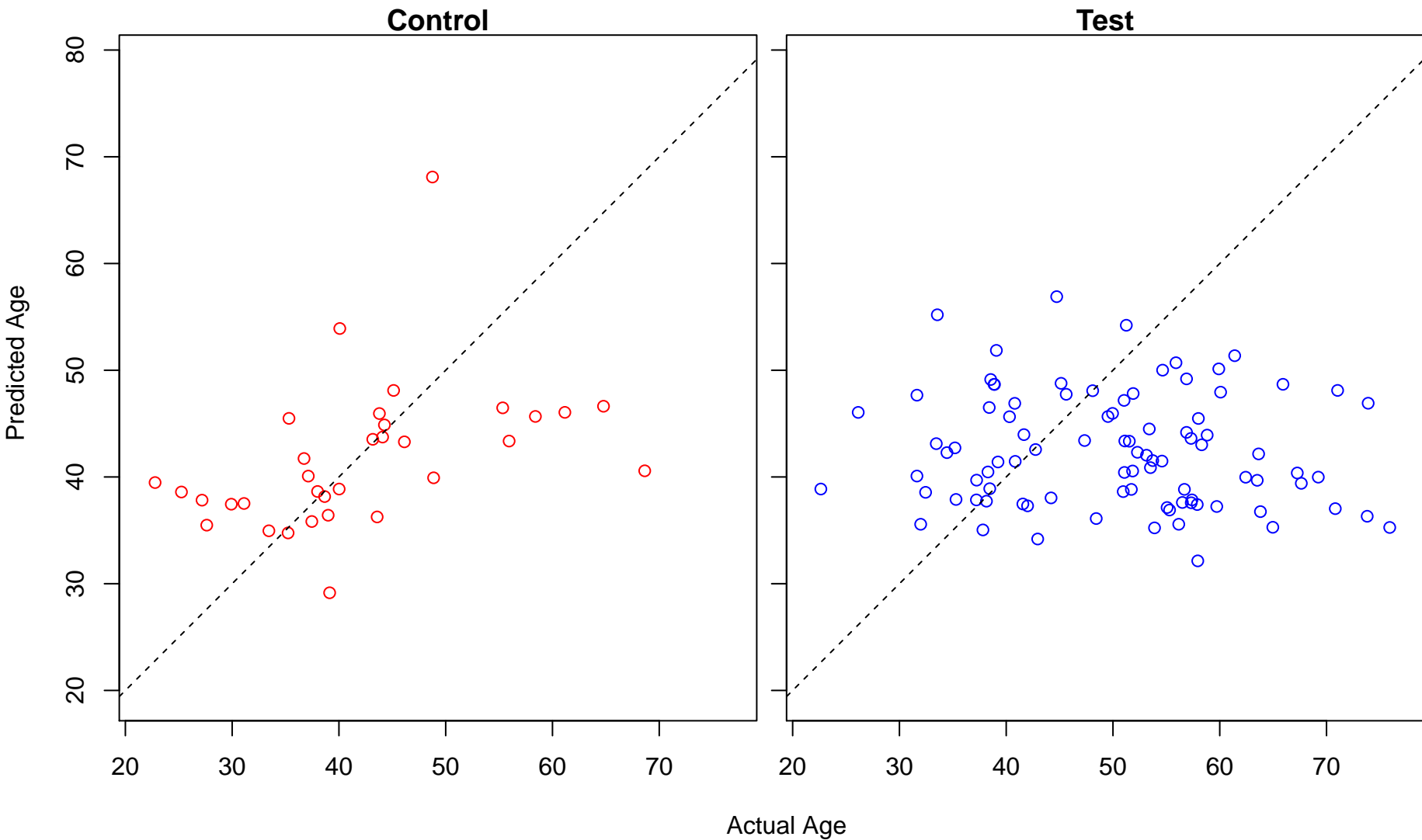
membrane invagination (Score: 0.716814)



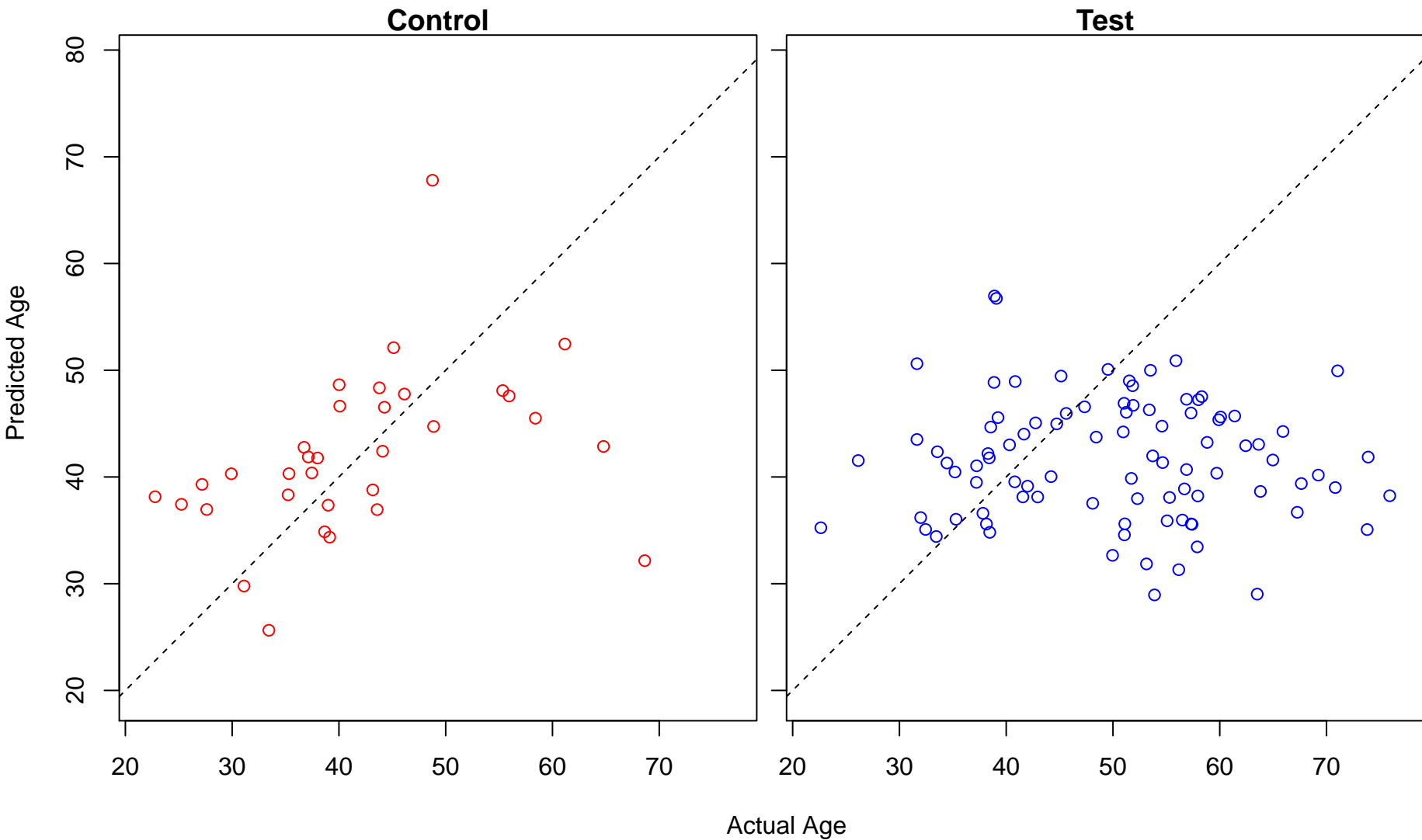
negative regulation of cellular macromolecule biosynthetic process (Score: 0.715892)



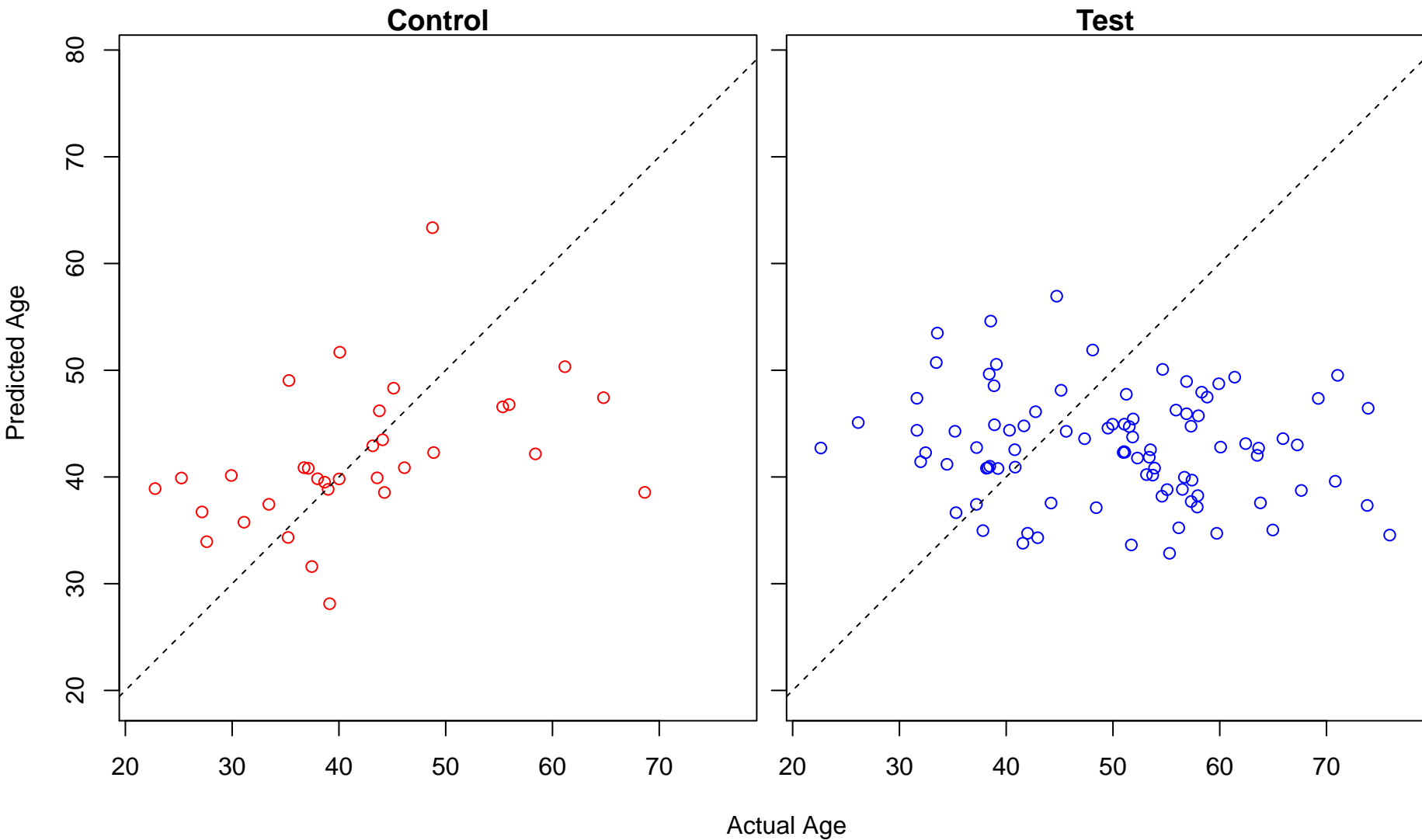
positive regulation of nitrogen compound metabolic process (Score: 0.715207)



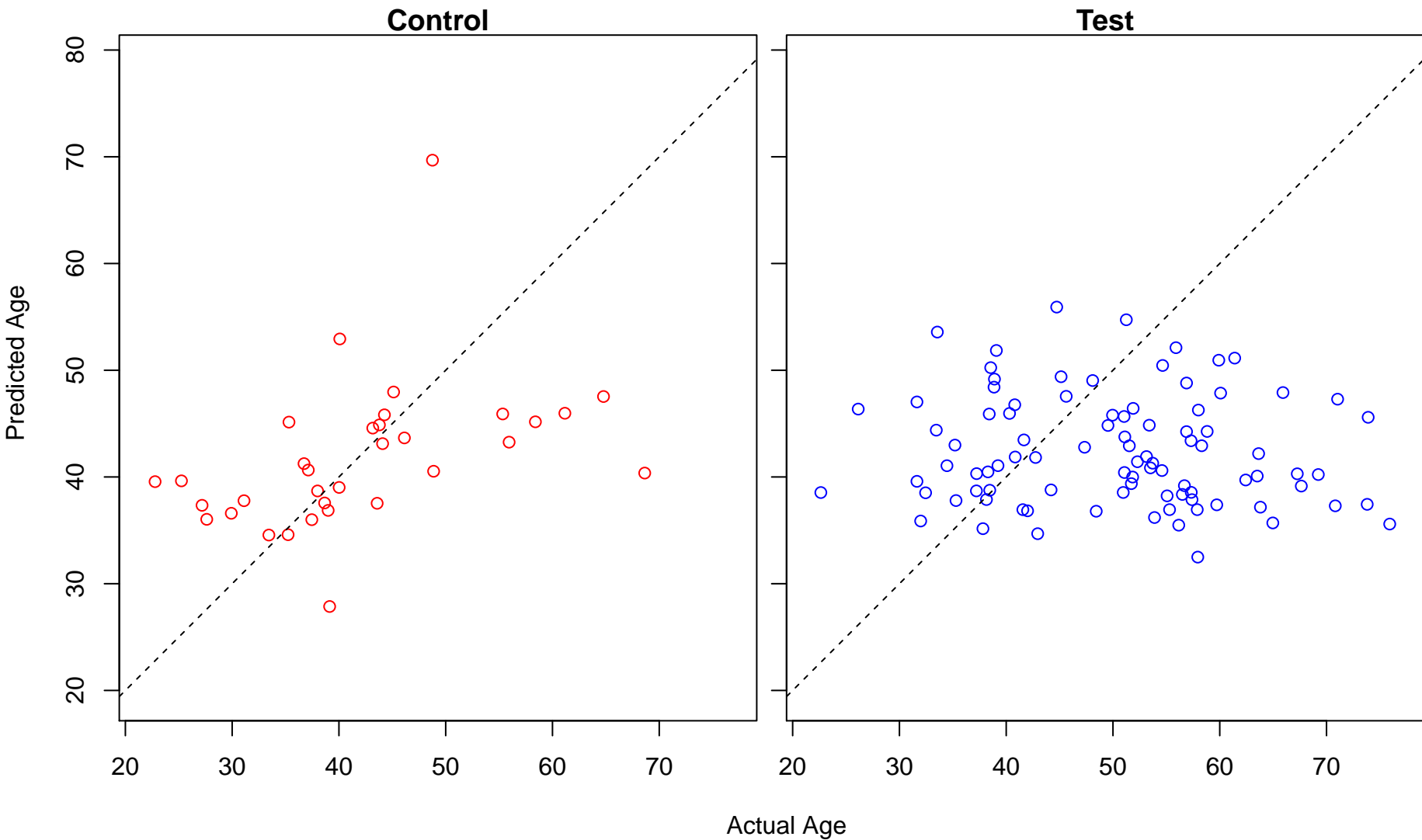
negative regulation of RIG-I signaling pathway (Score: 0.714784)



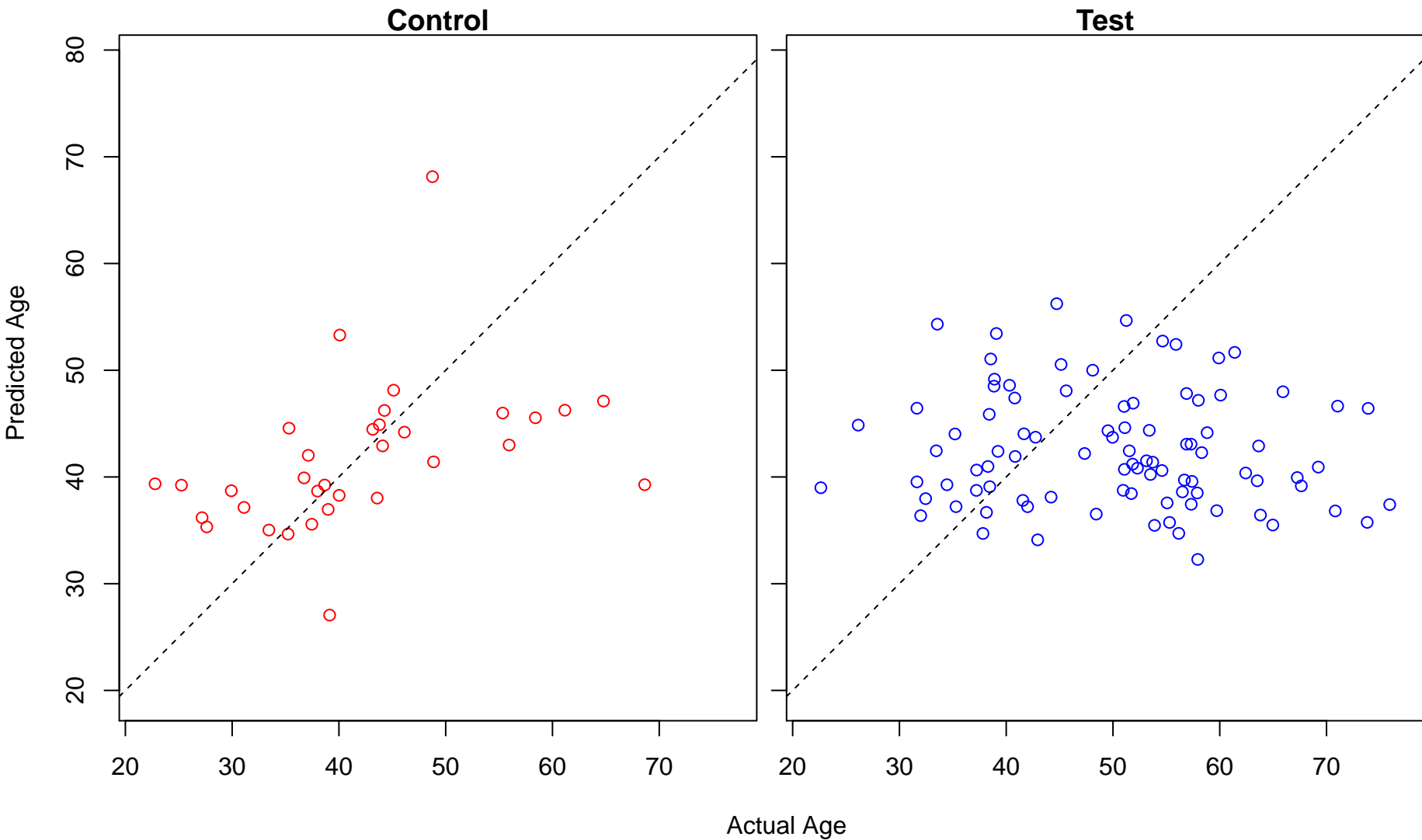
synaptic transmission (Score: 0.714222)



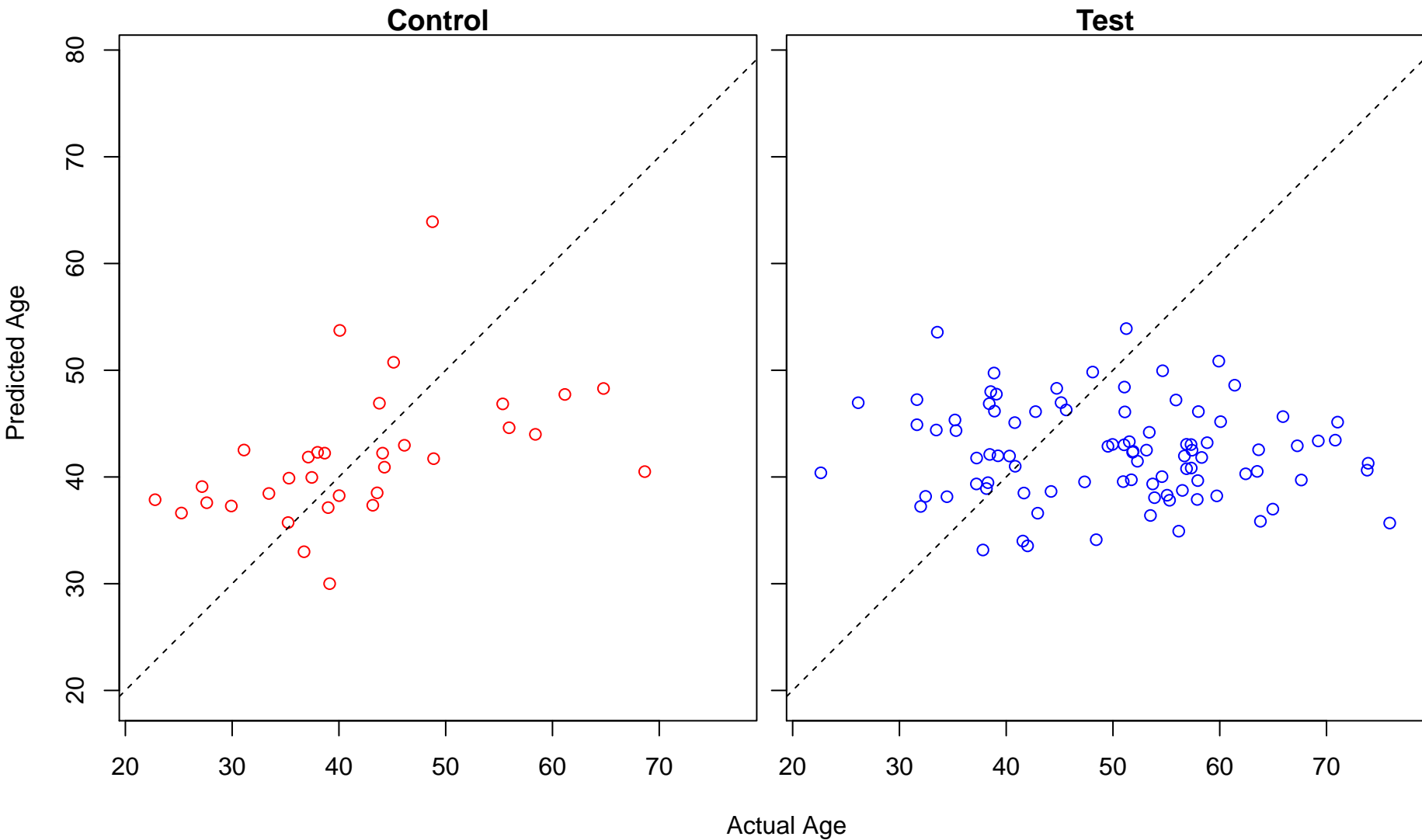
regulation of macromolecule biosynthetic process (Score: 0.714181)



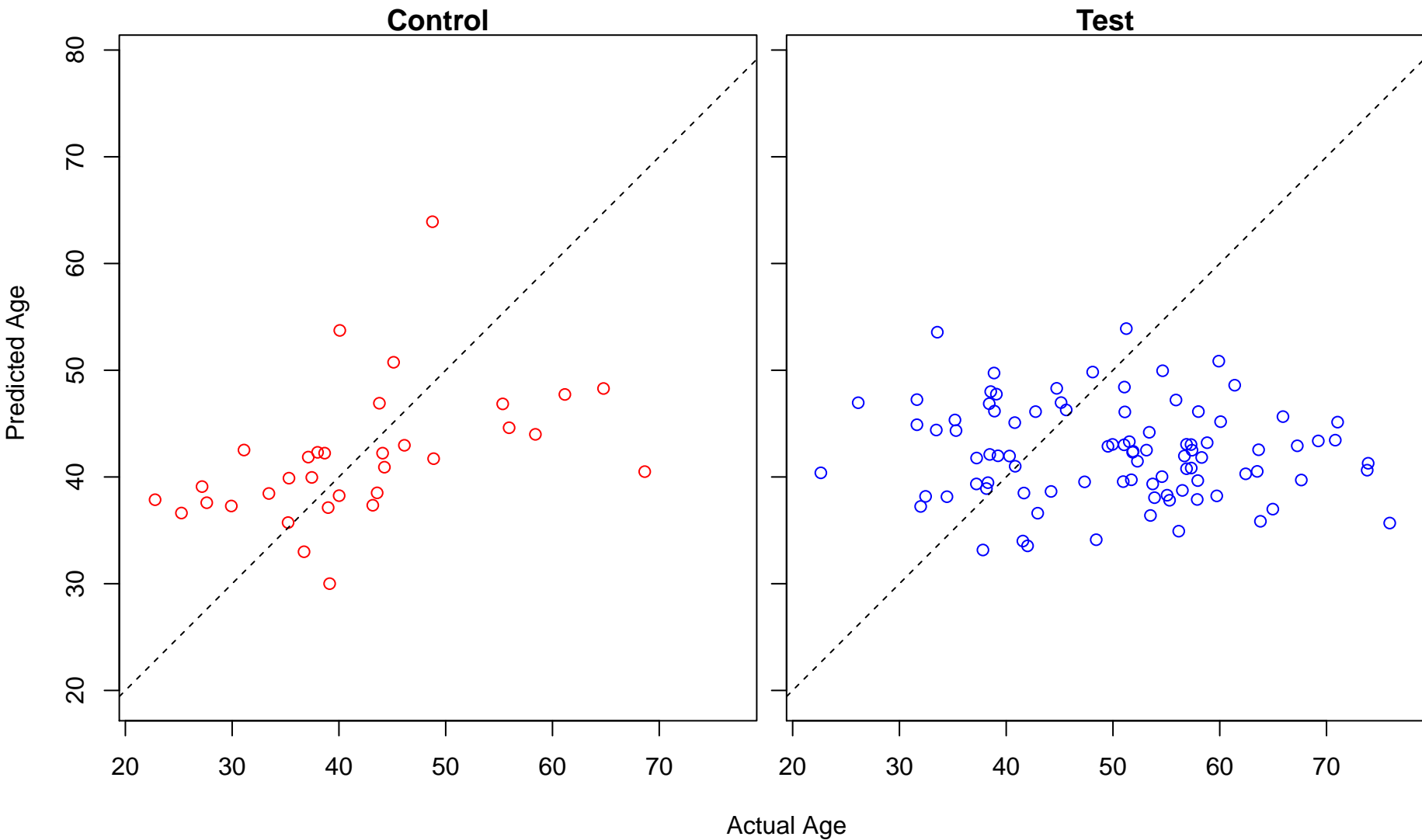
regulation of cellular protein metabolic process (Score: 0.713800)



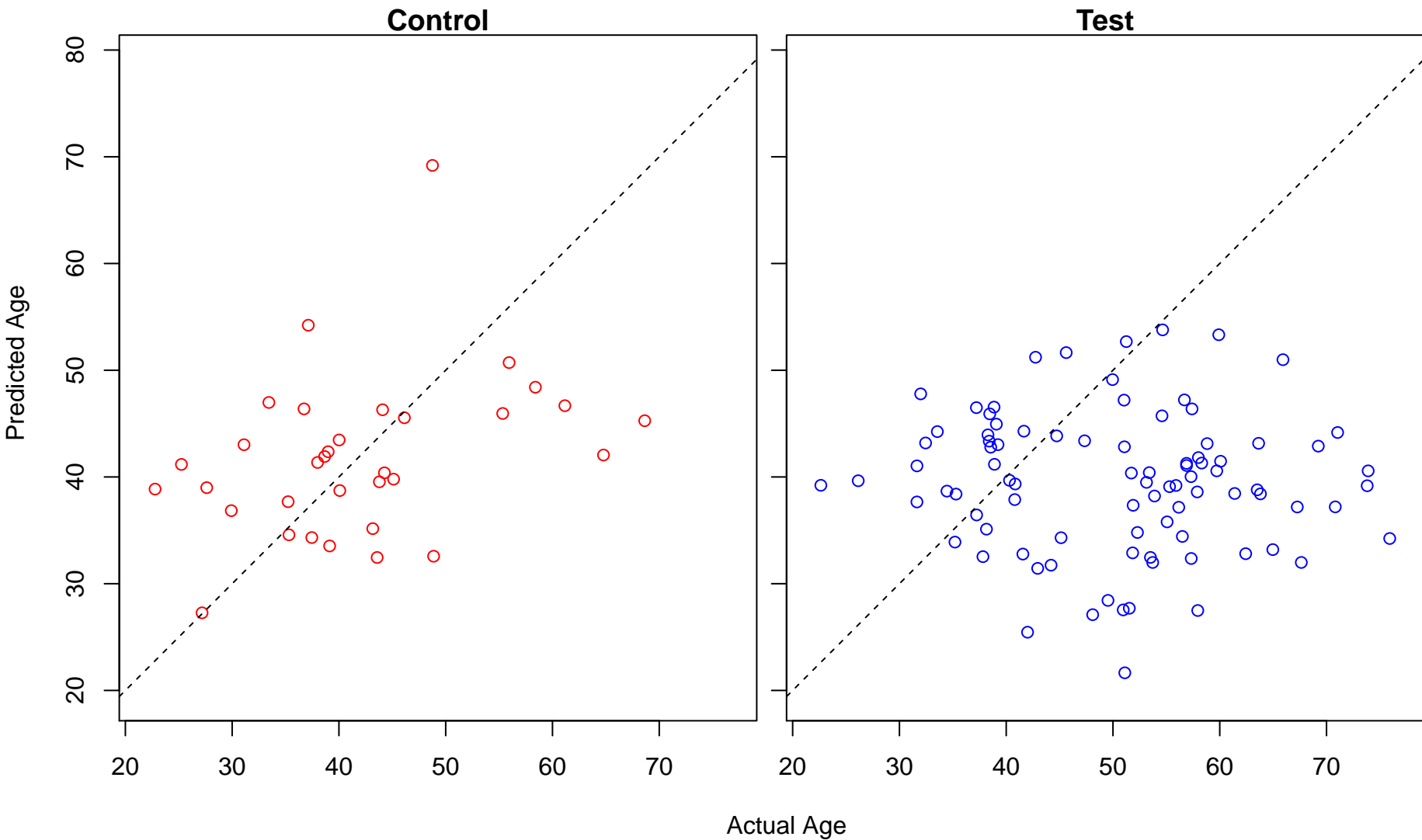
cardiovascular system development (Score: 0.713535)



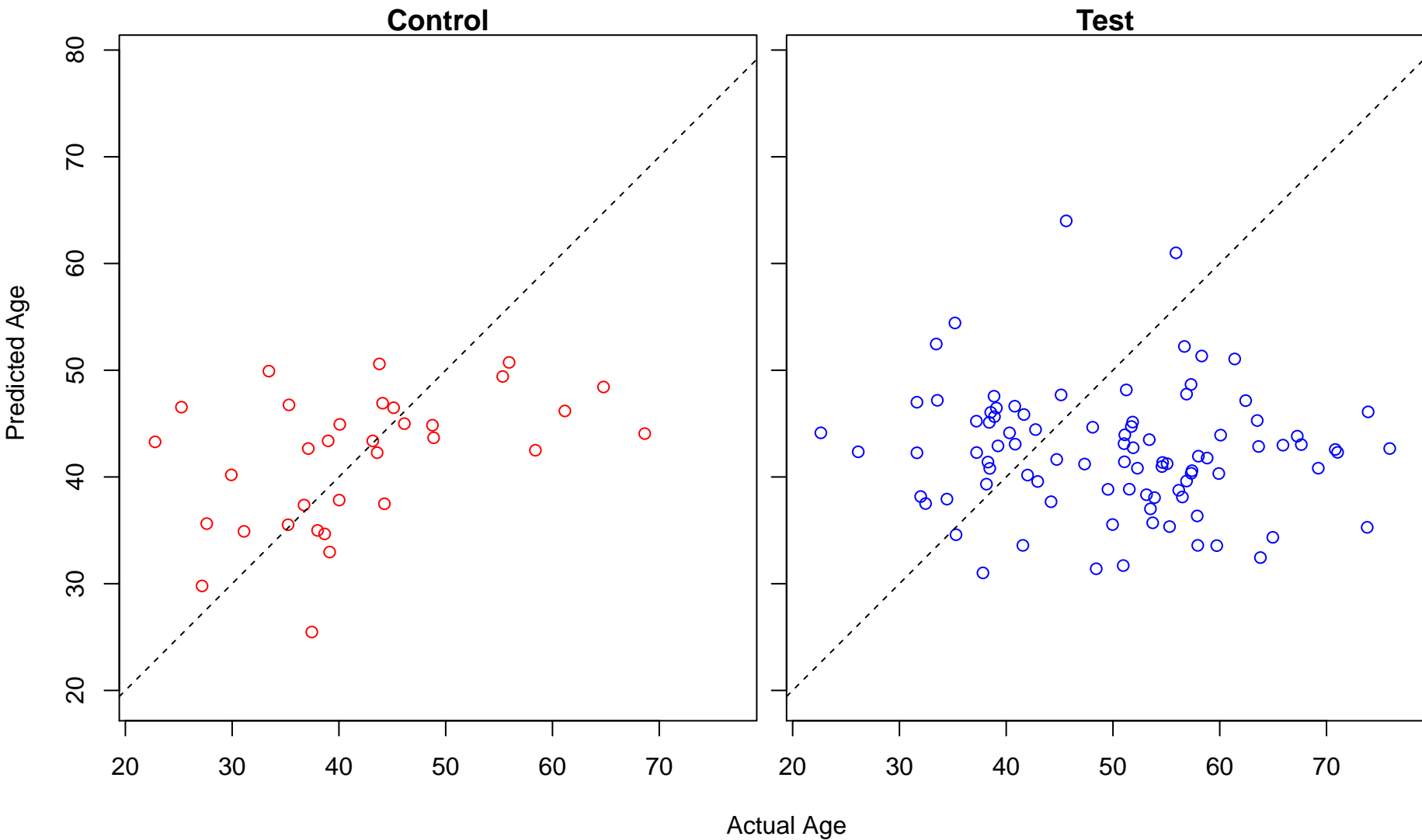
circulatory system development (Score: 0.713535)



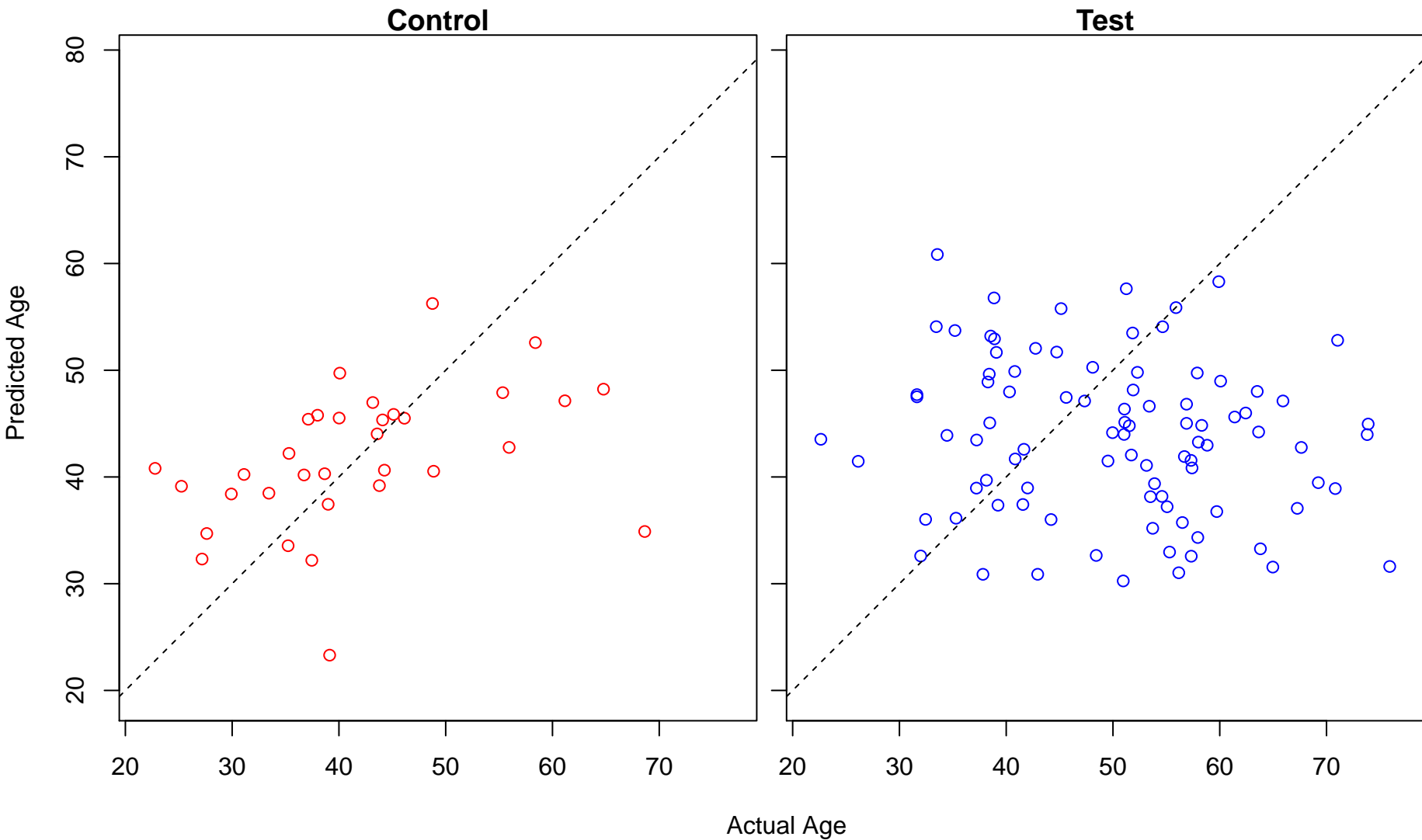
cell communication by electrical coupling (Score: 0.713115)



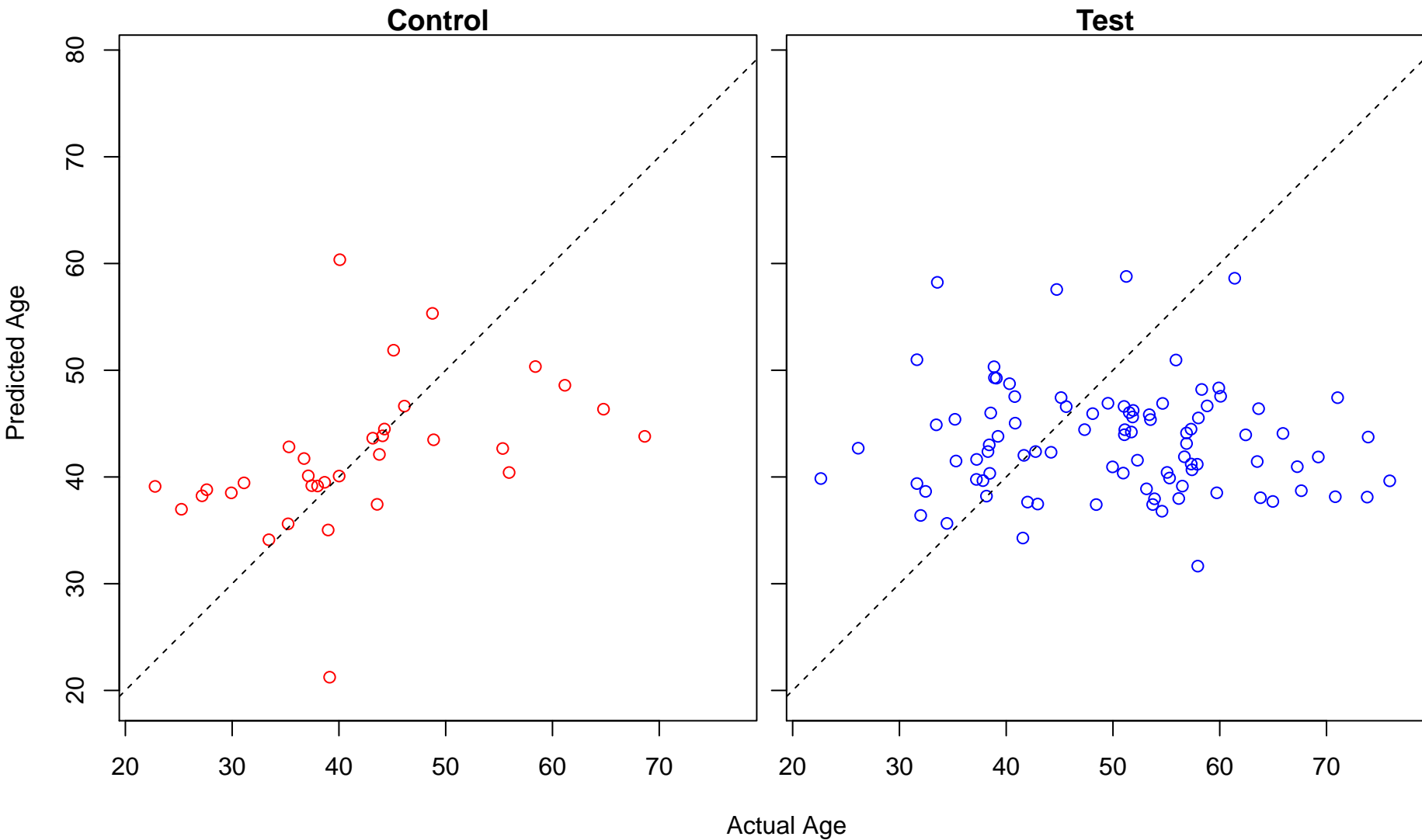
sarcomere organization (Score: 0.713089)



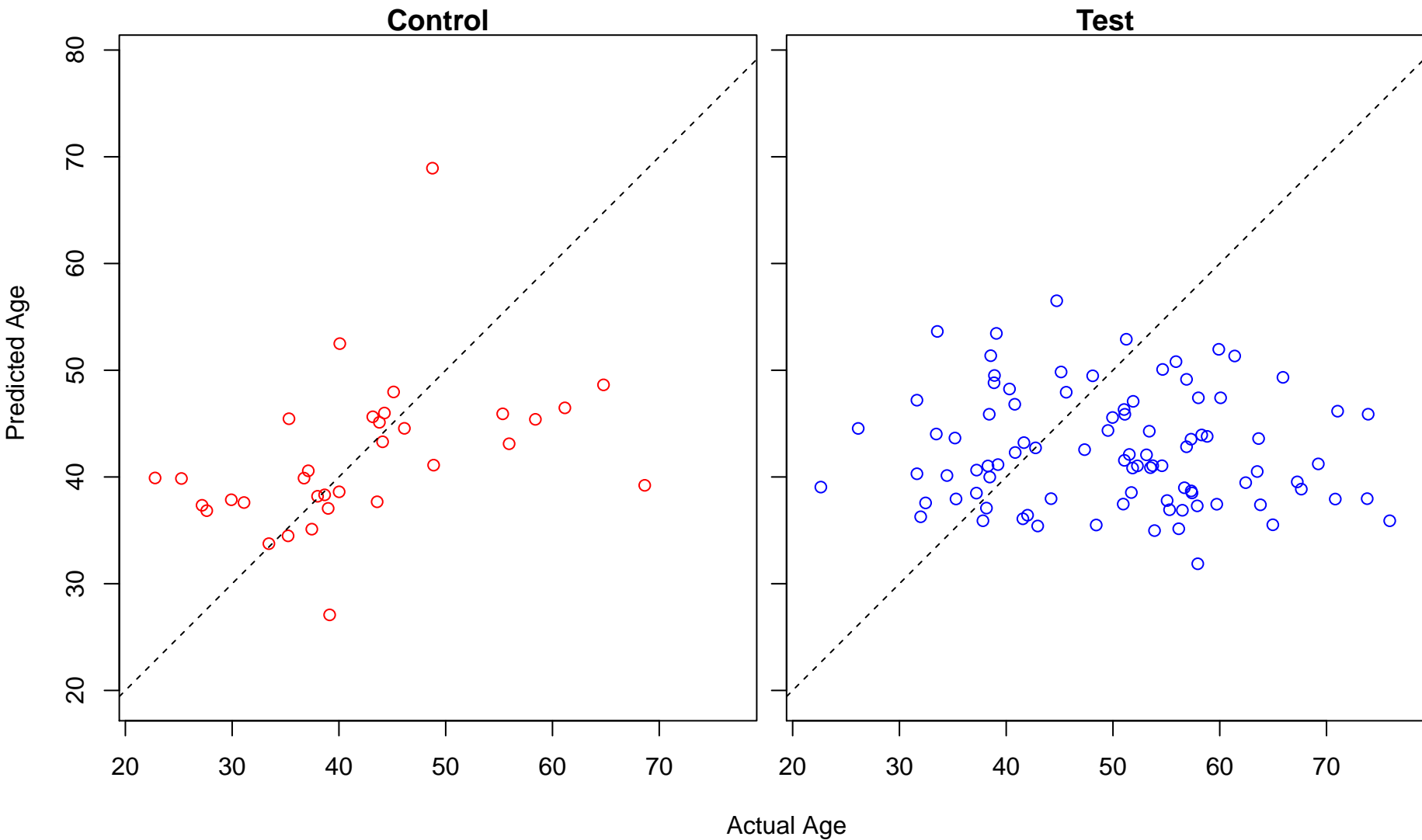
calcium ion transmembrane transport (Score: 0.713088)



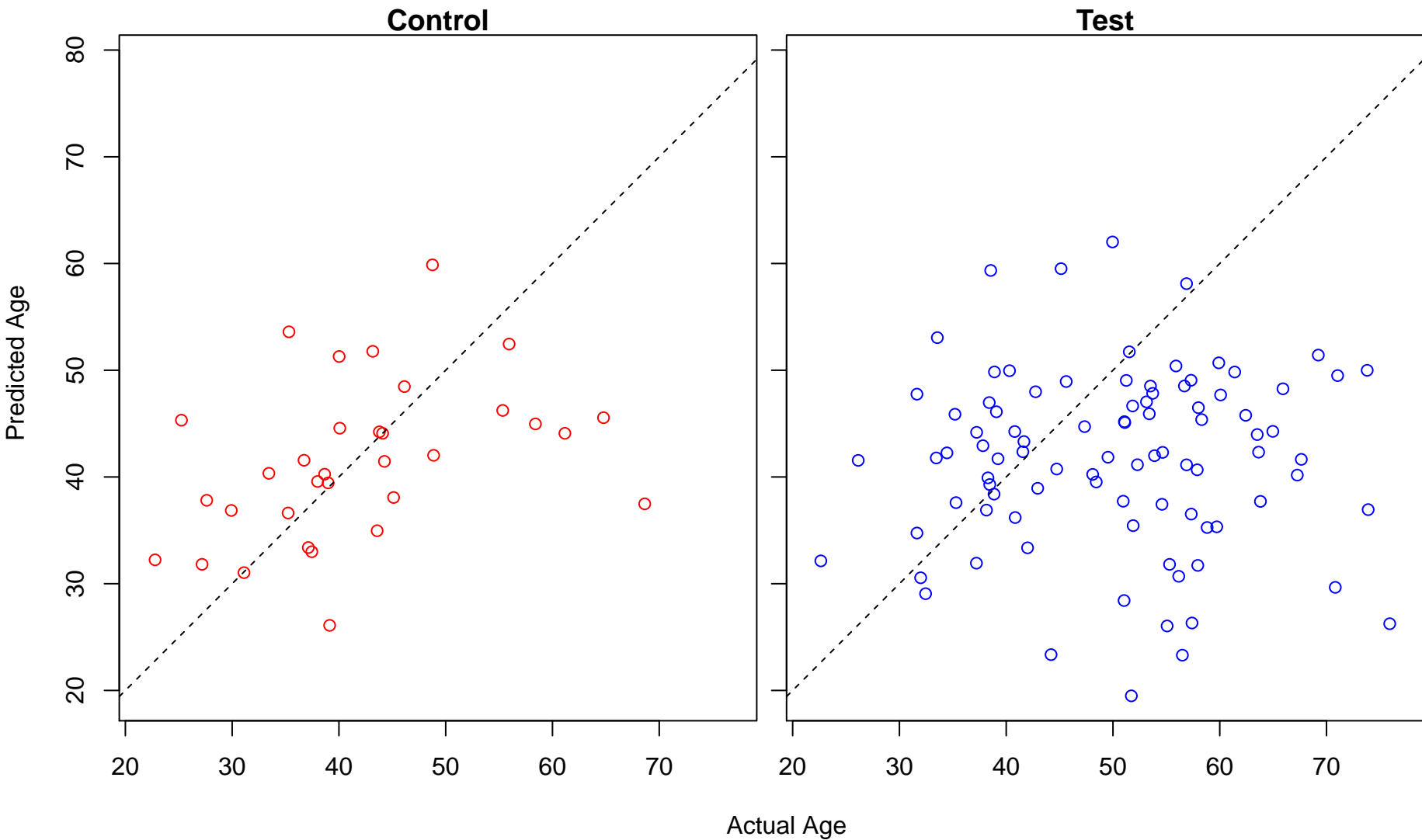
rRNA transcription (Score: 0.712737)



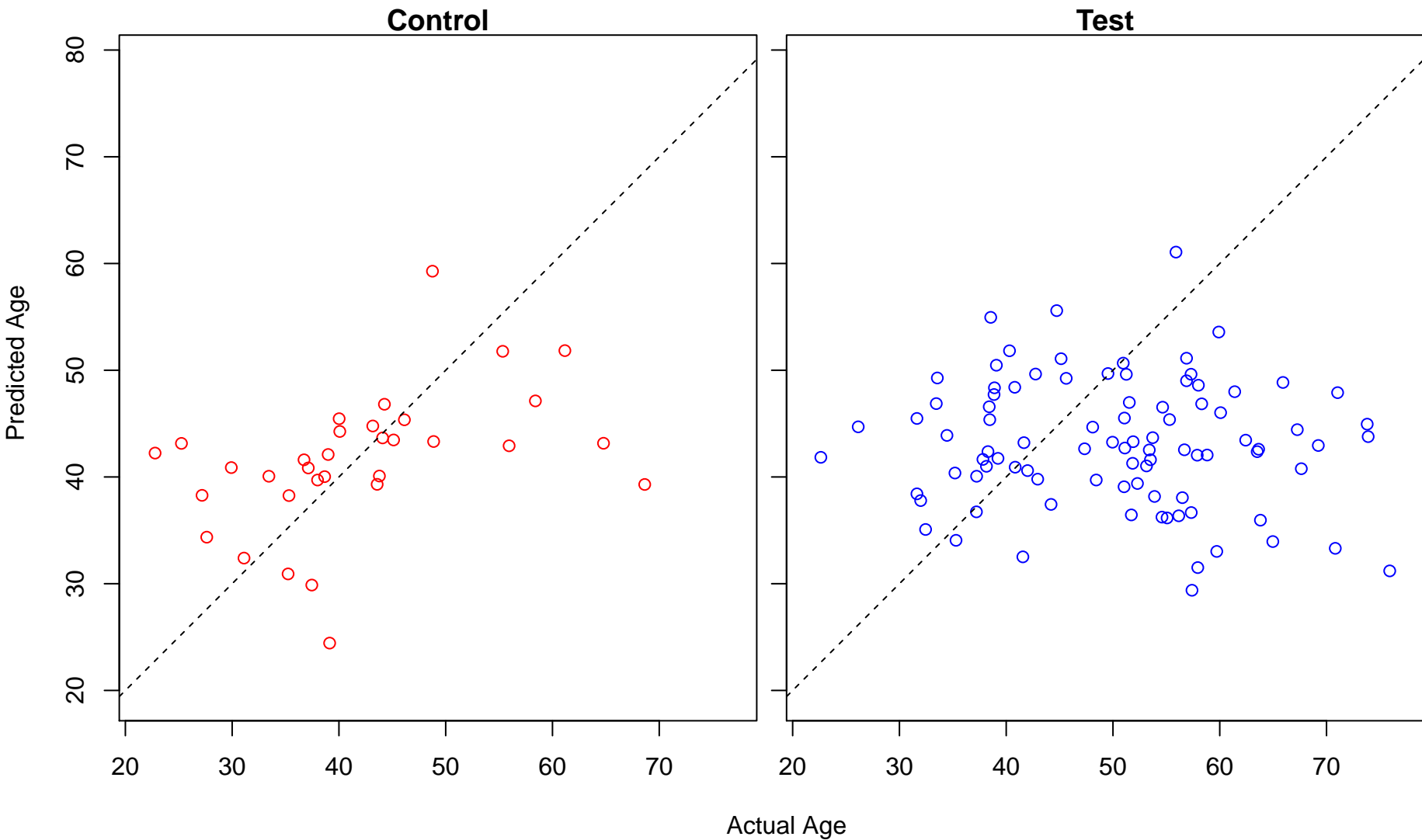
organelle organization (Score: 0.712685)



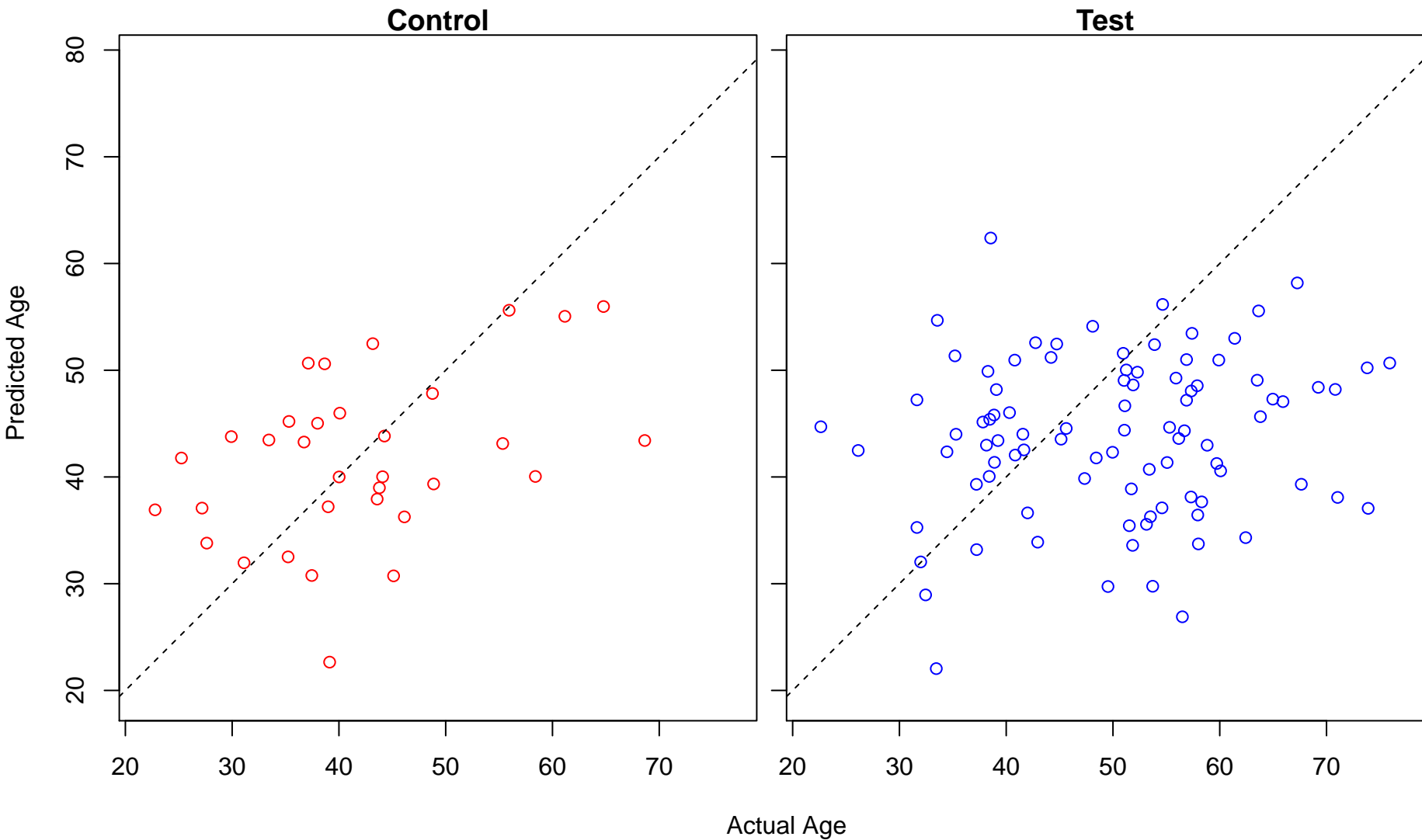
cellular response to interferon-beta (Score: 0.712194)



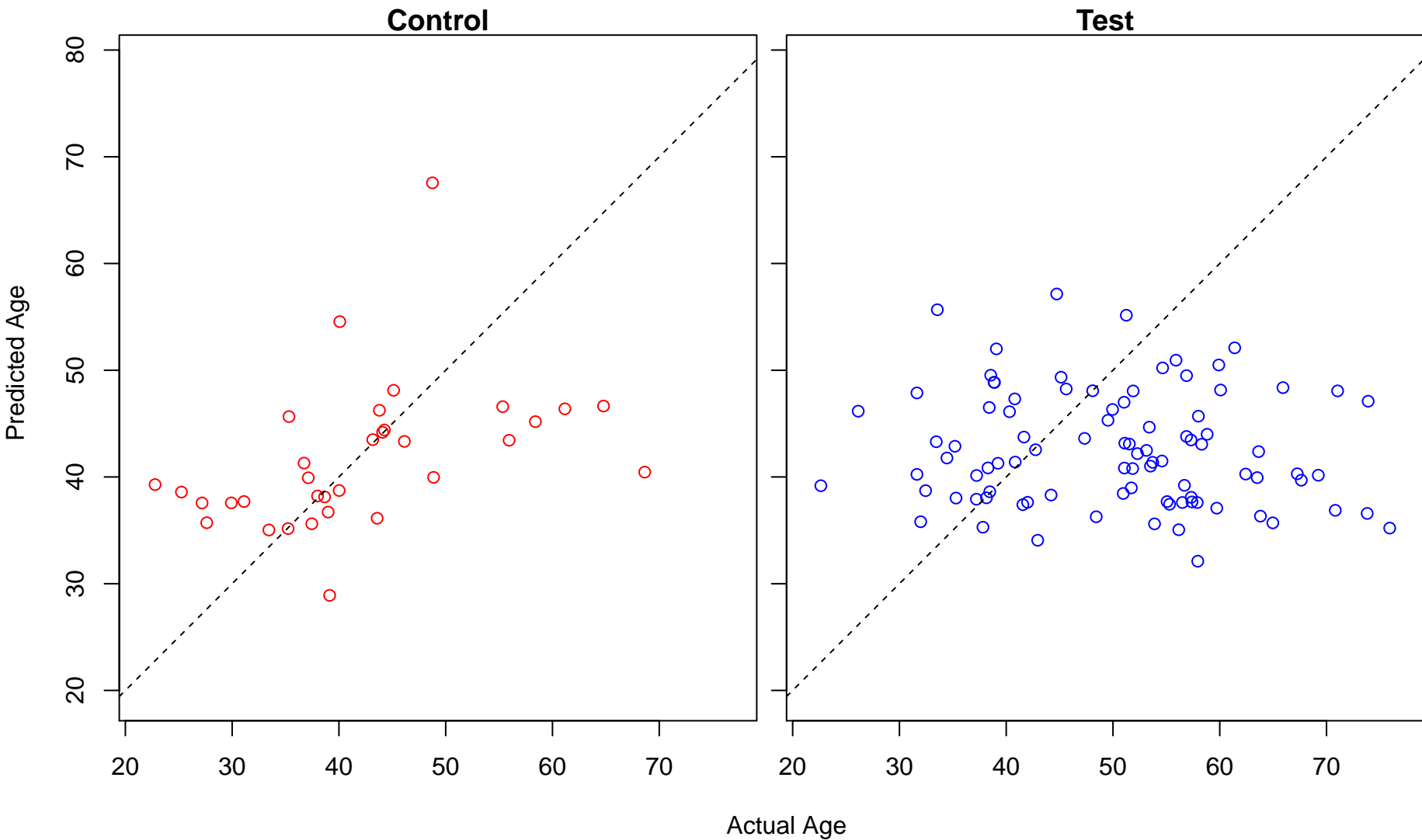
positive regulation of type I interferon production (Score: 0.711456)



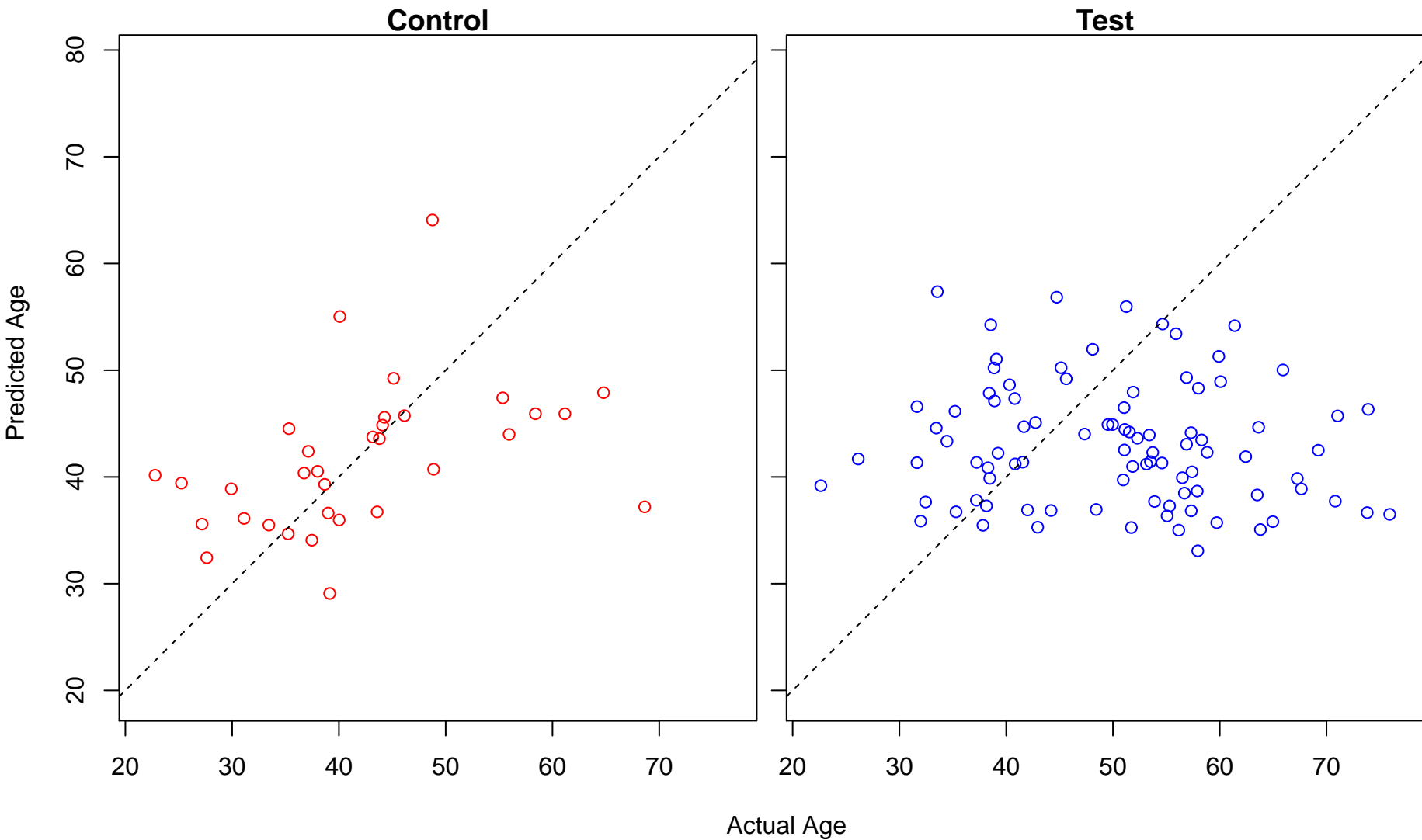
response to redox state (Score: 0.711399)



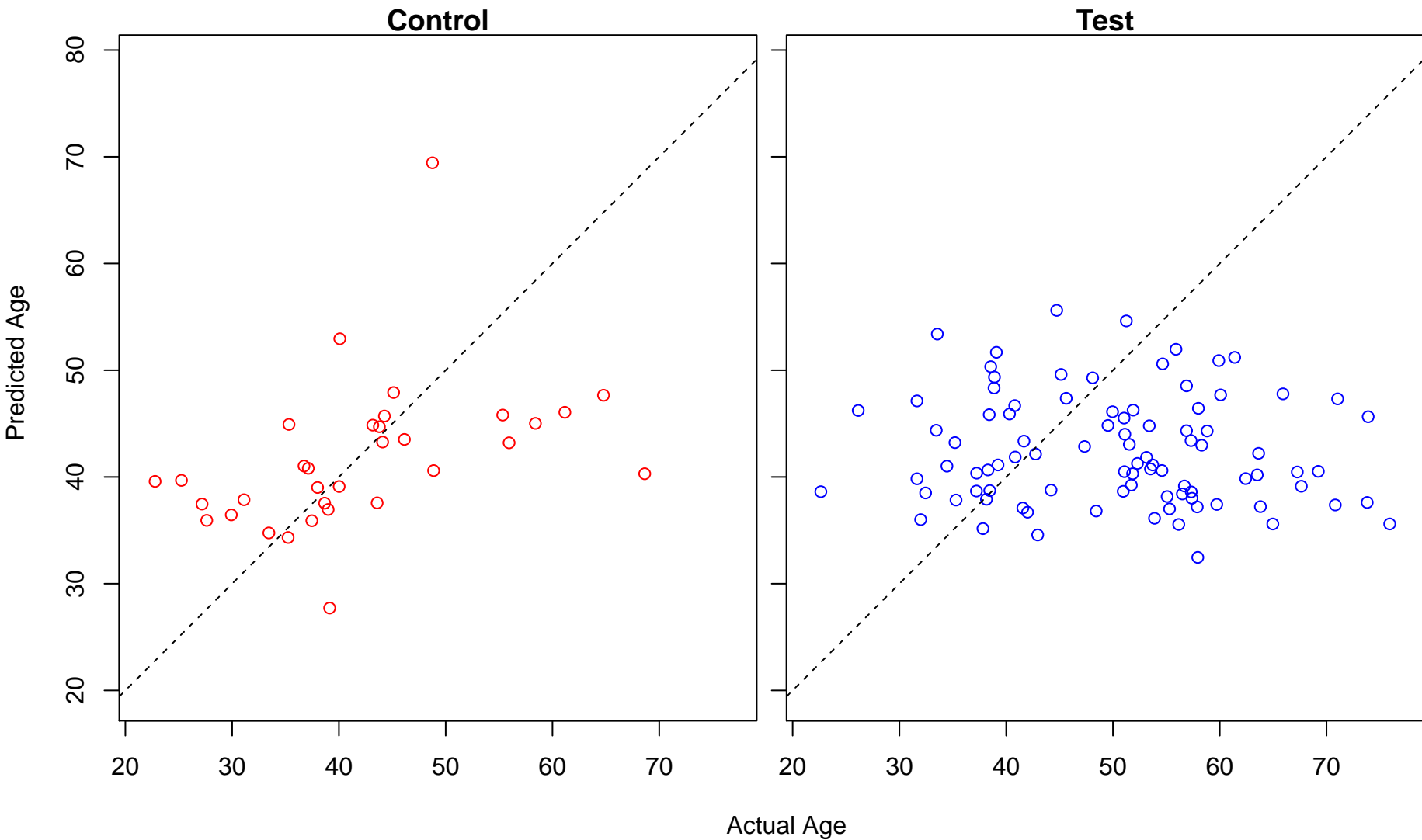
positive regulation of macromolecule biosynthetic process (Score: 0.711368)



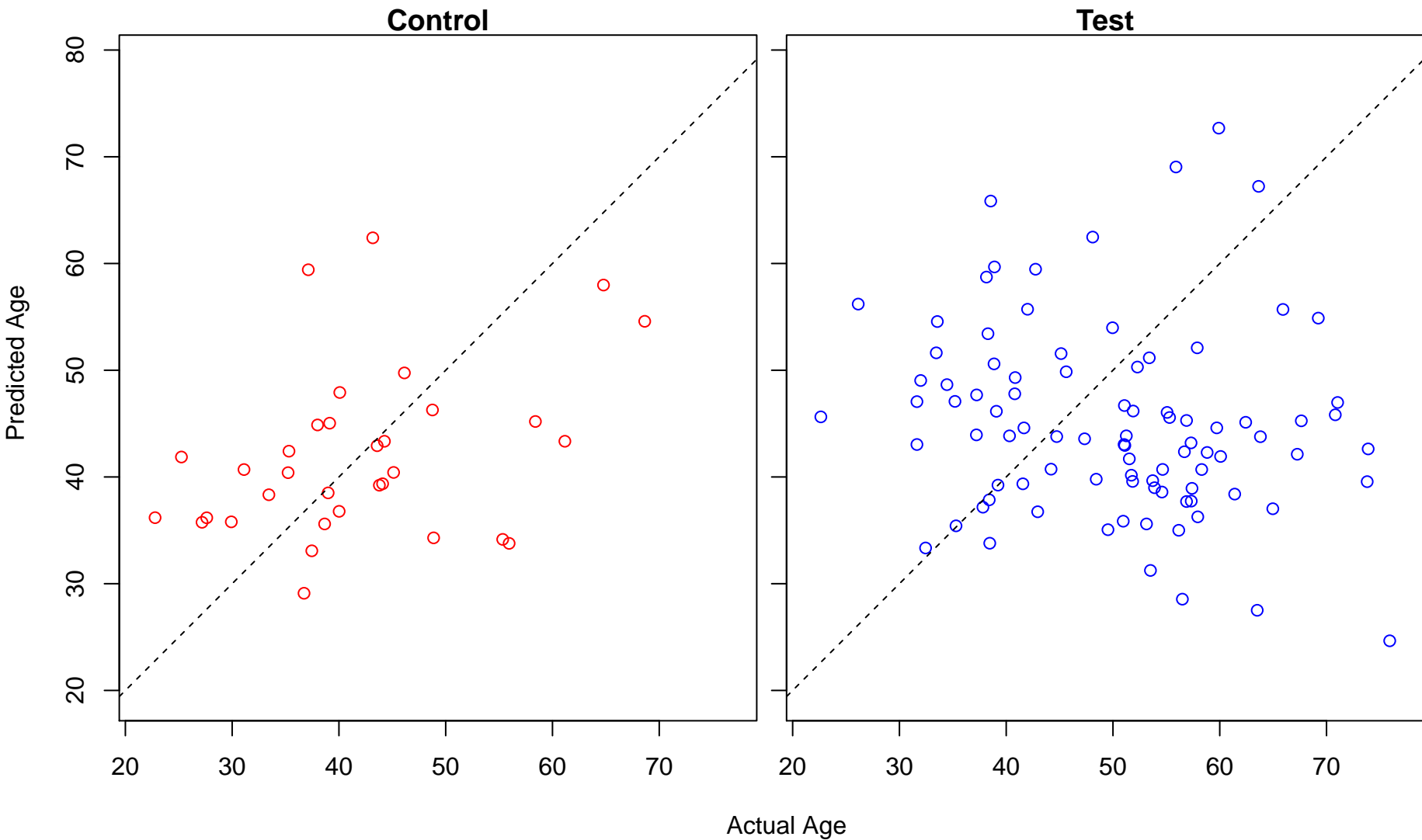
regulation of proteolysis (Score: 0.711270)



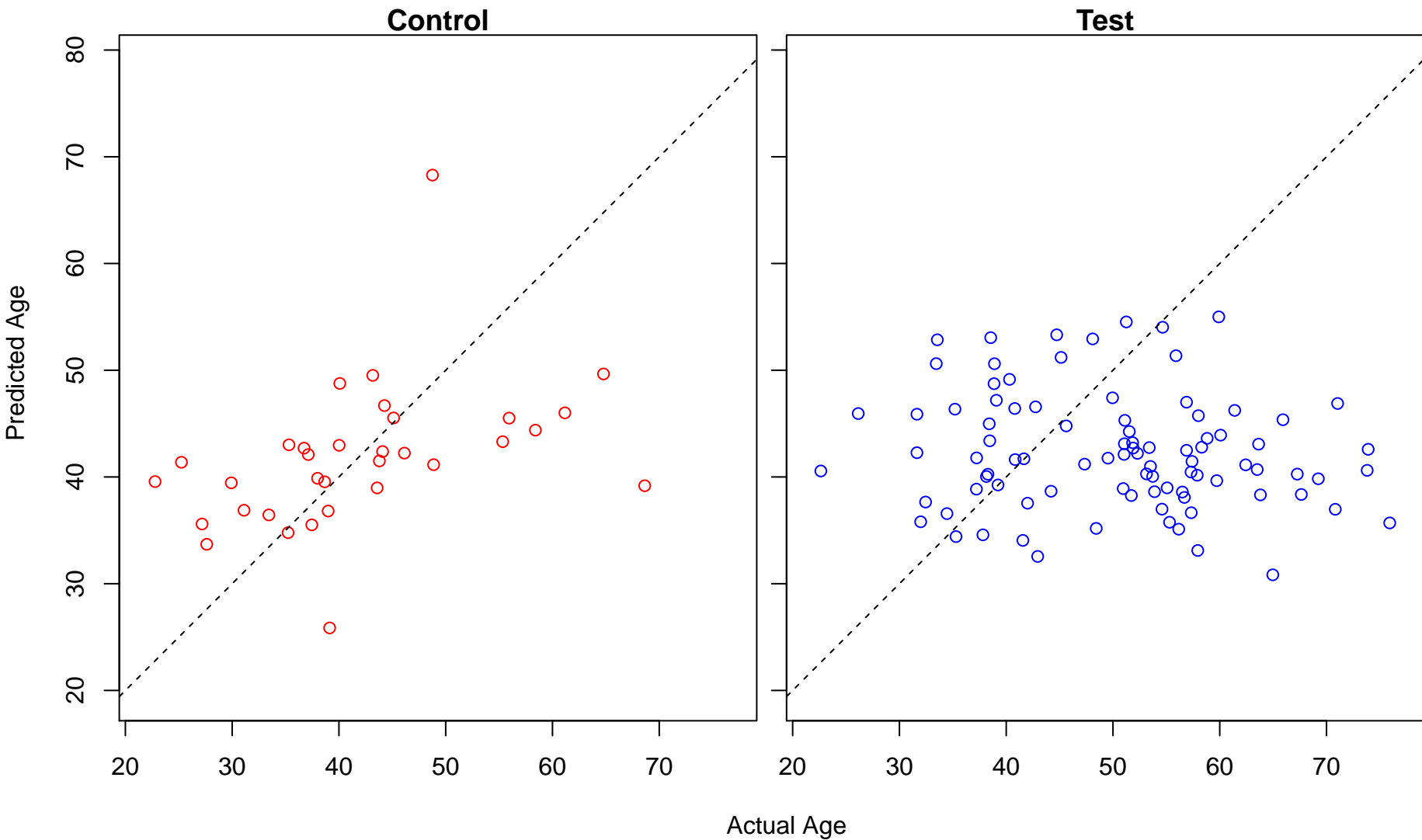
regulation of cellular macromolecule biosynthetic process (Score: 0.710626)



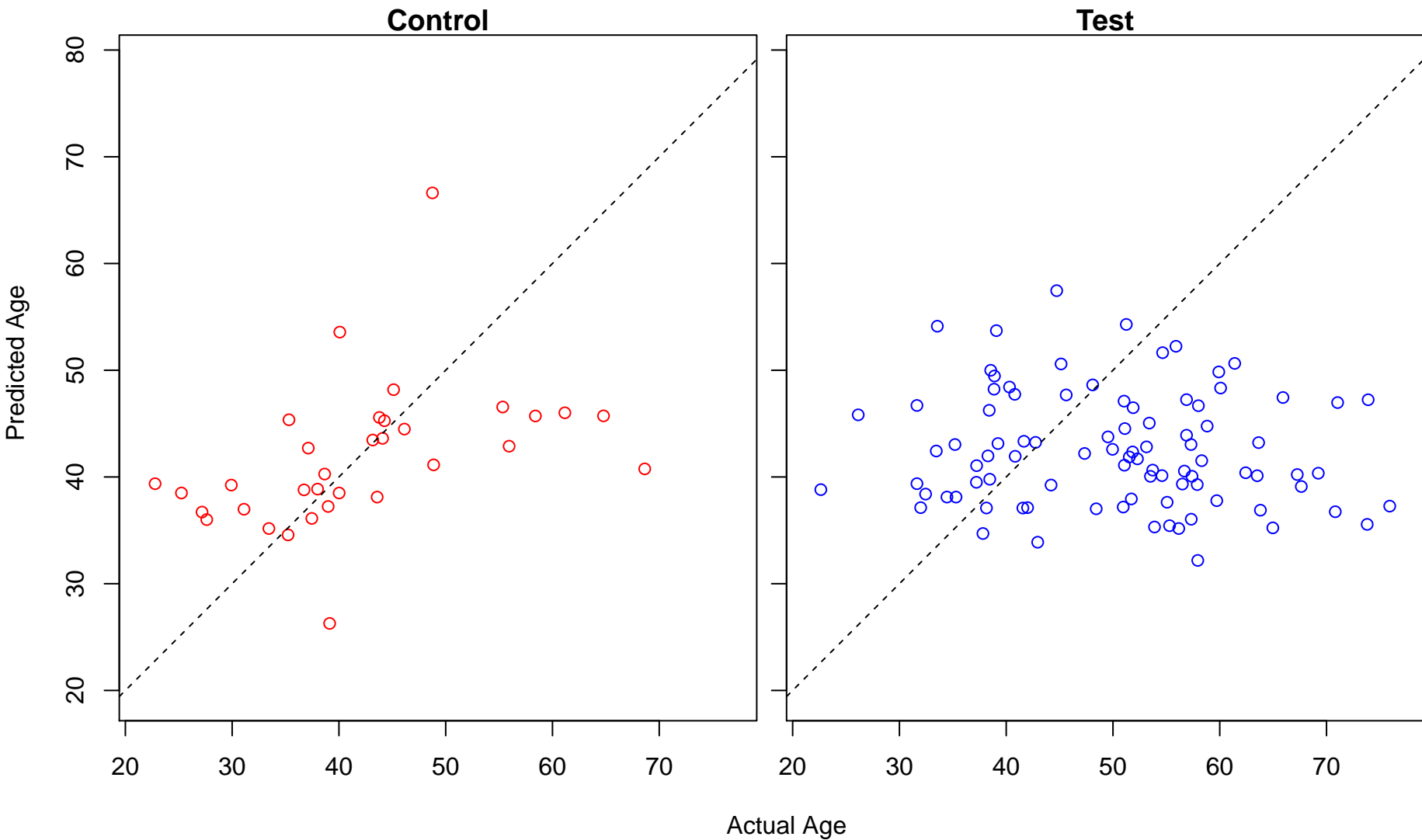
drug transmembrane transport (Score: 0.710550)



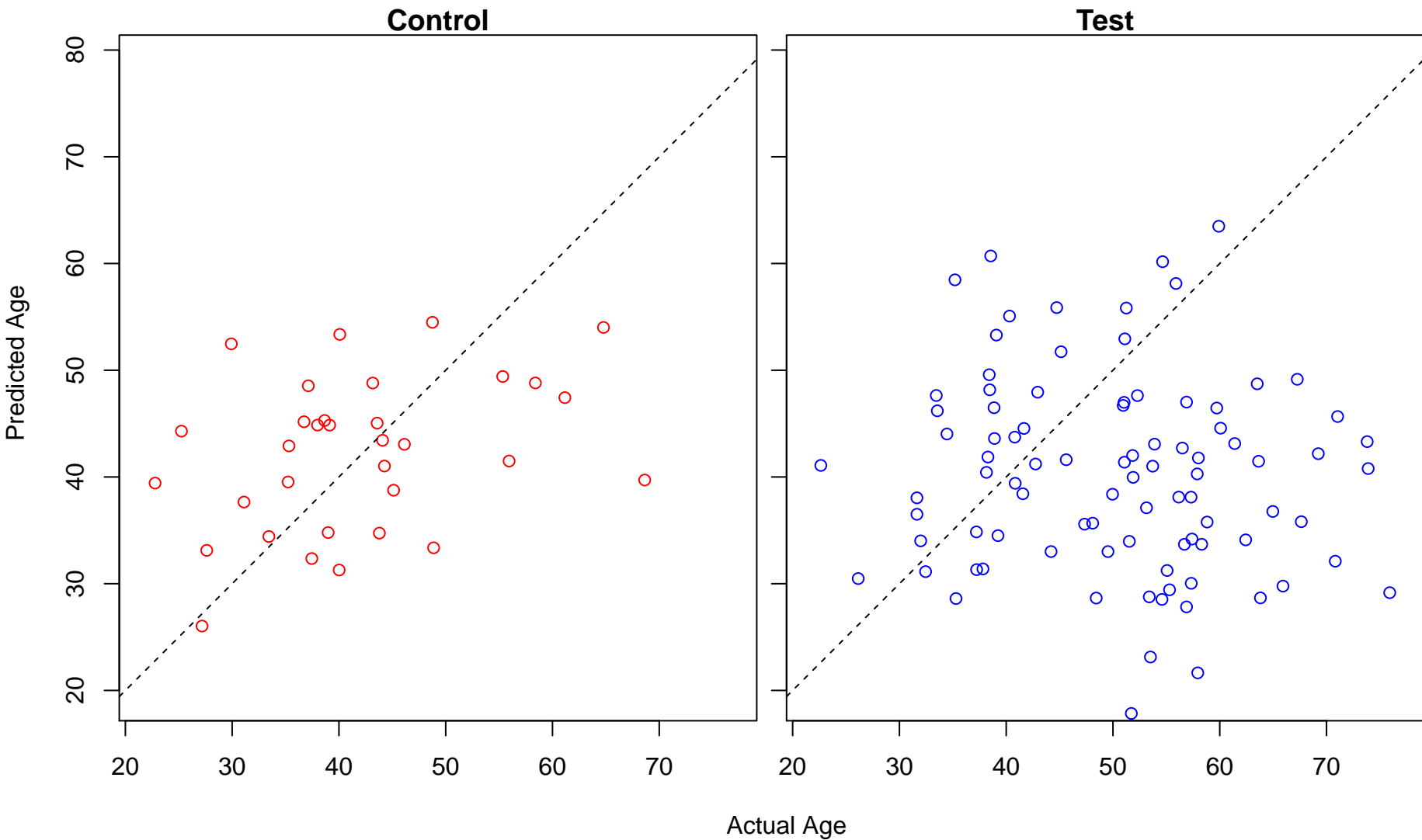
ion transmembrane transport (Score: 0.710015)



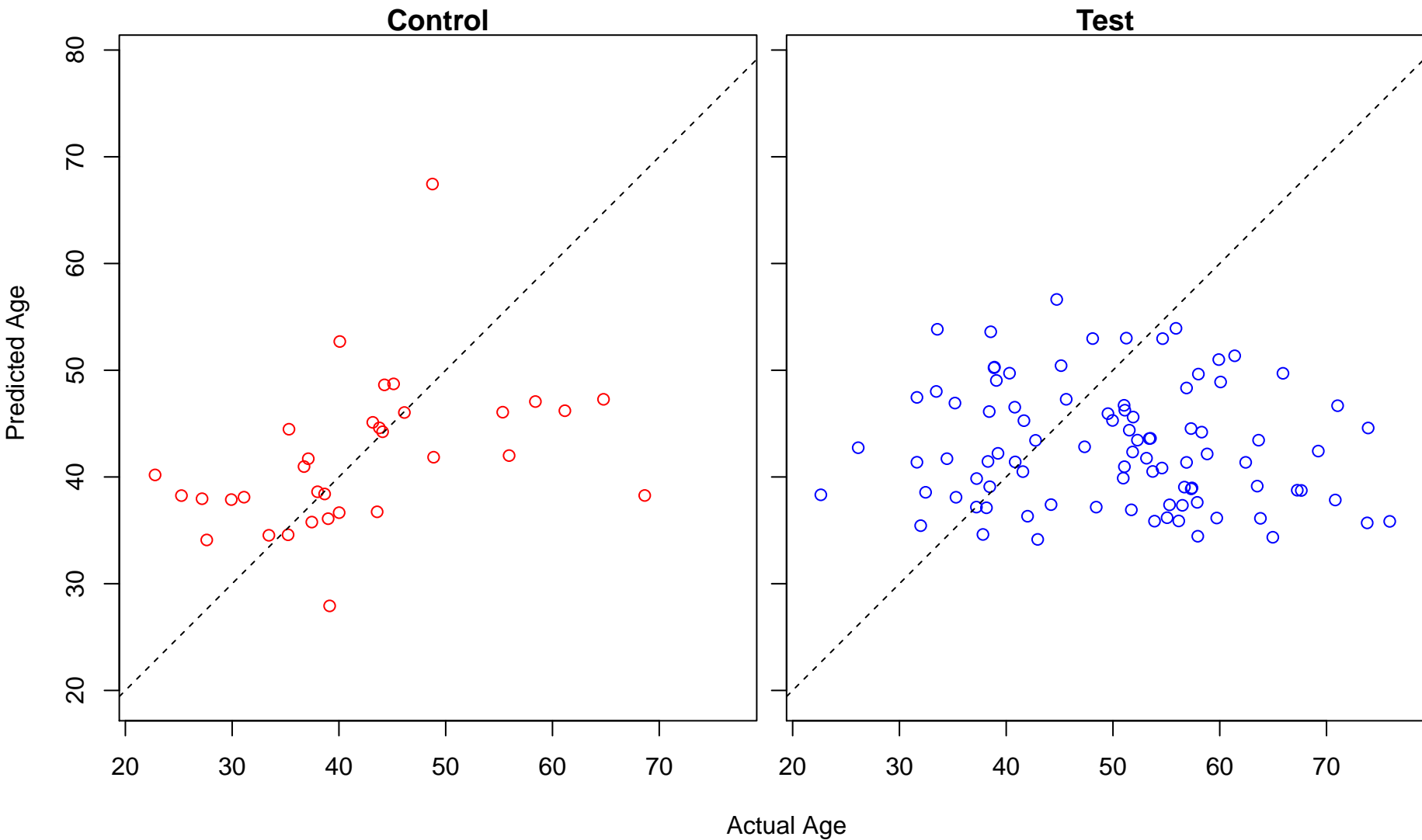
regulation of phosphorylation (Score: 0.709701)



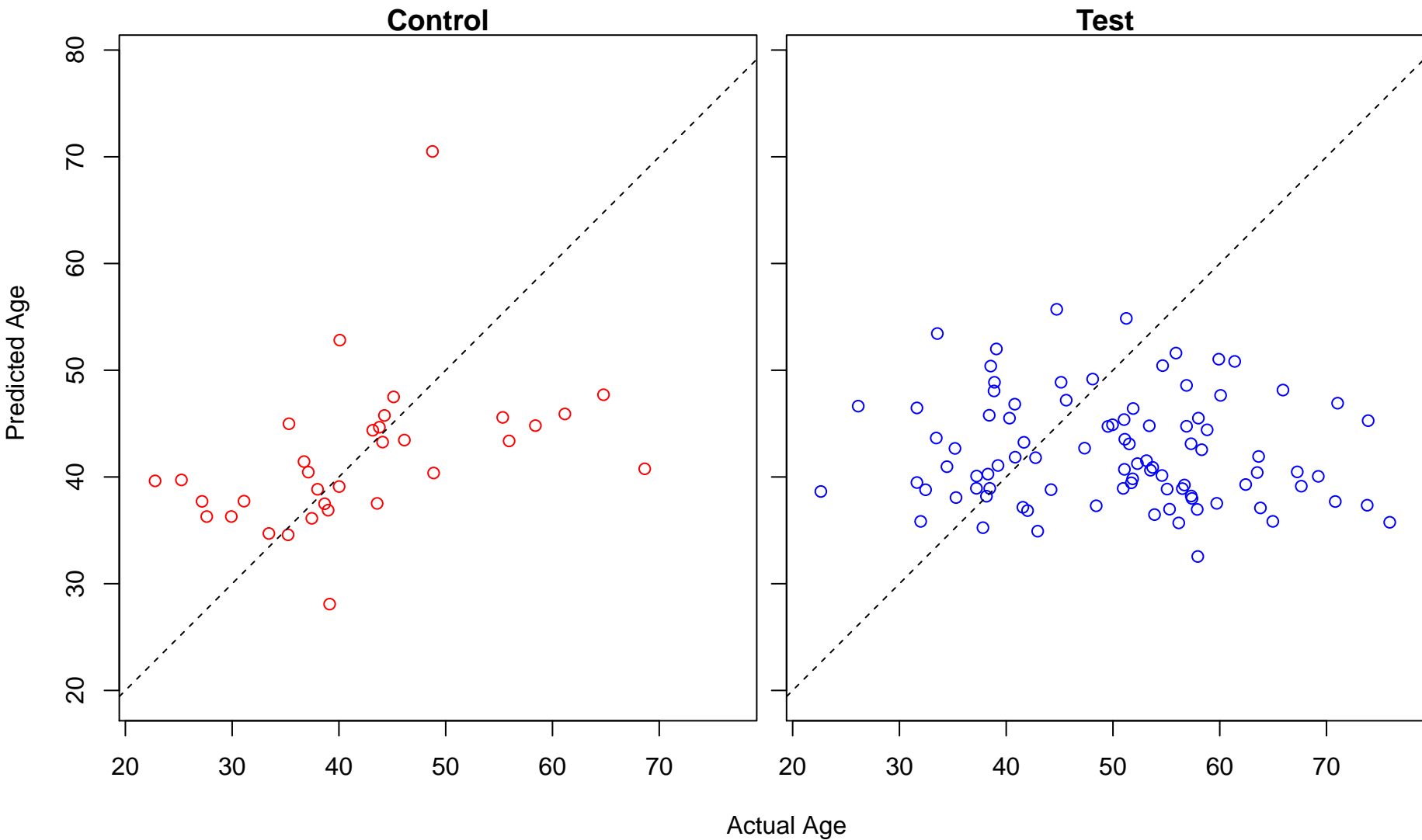
negative regulation of substrate adhesion-dependent cell spreading (Score: 0.709221)



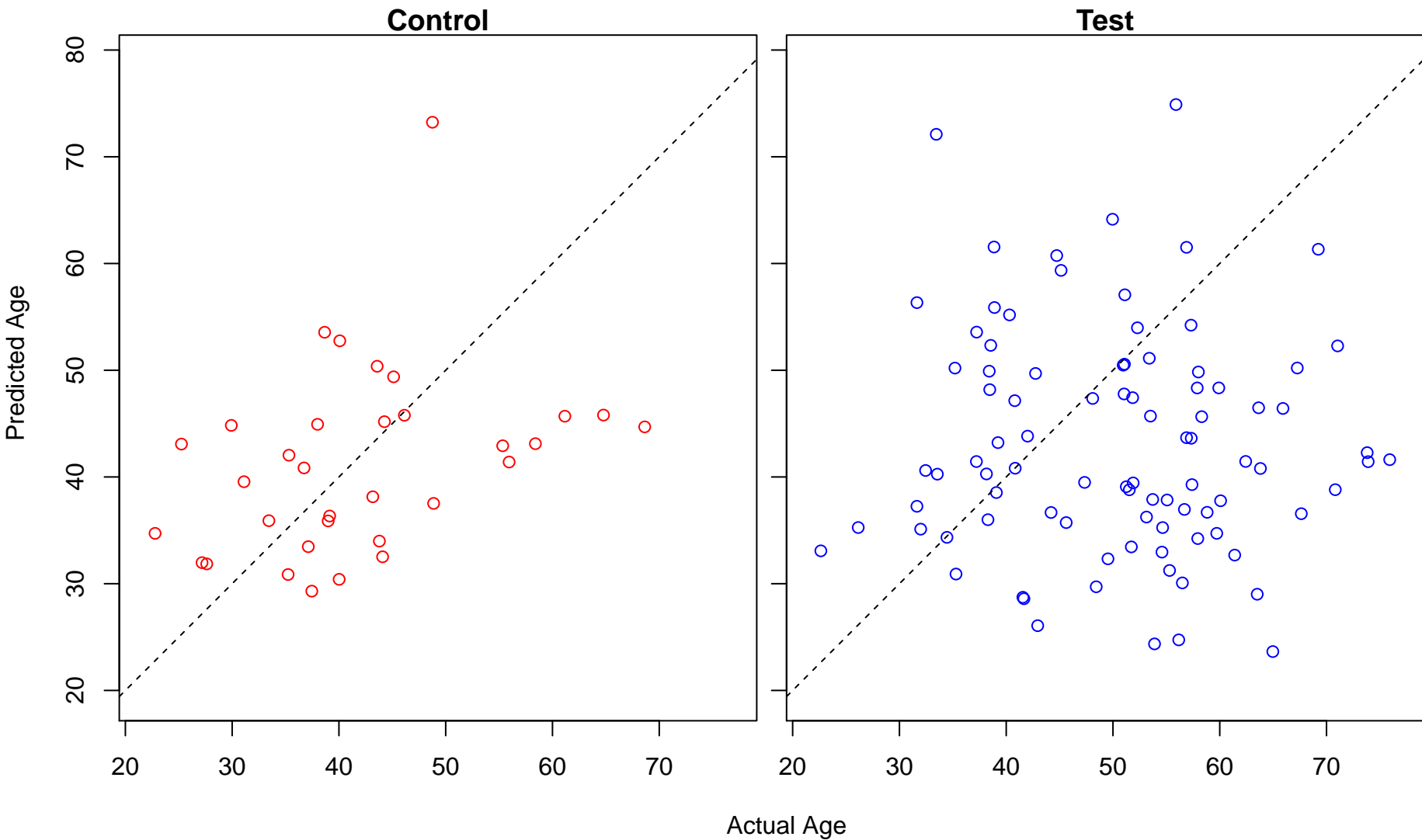
regulation of cellular catabolic process (Score: 0.708894)



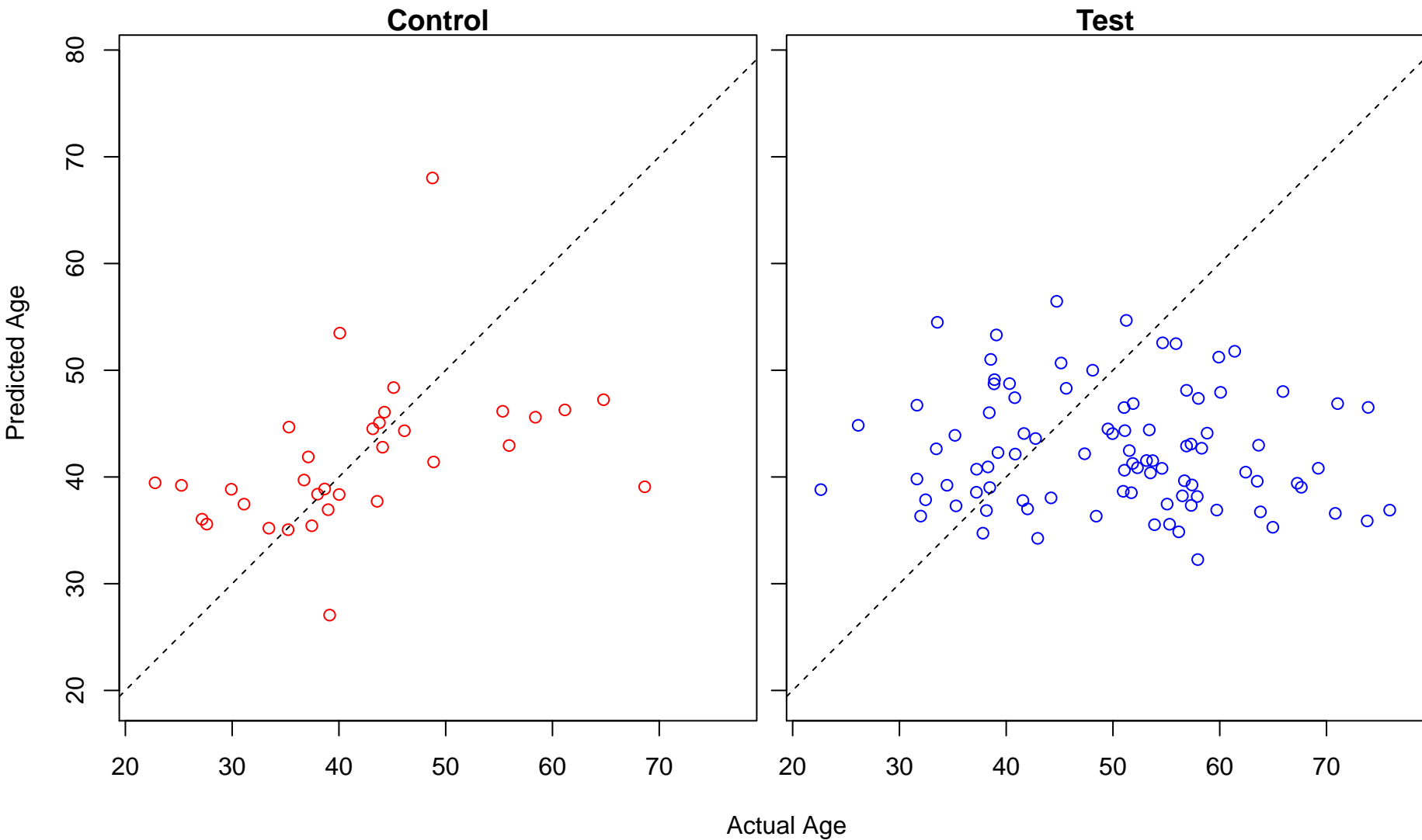
regulation of RNA biosynthetic process (Score: 0.708882)



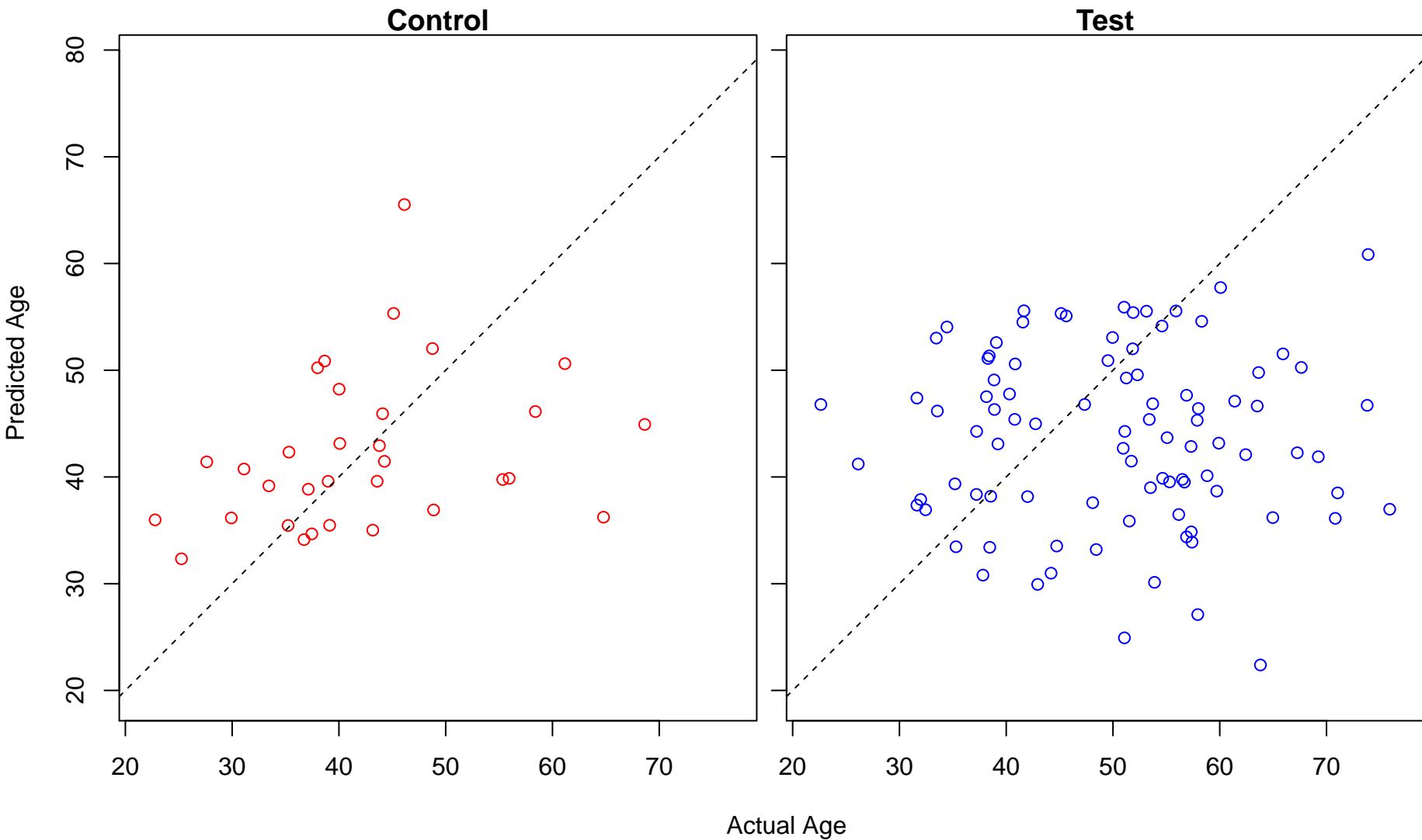
phospholipid transport (Score: 0.708732)



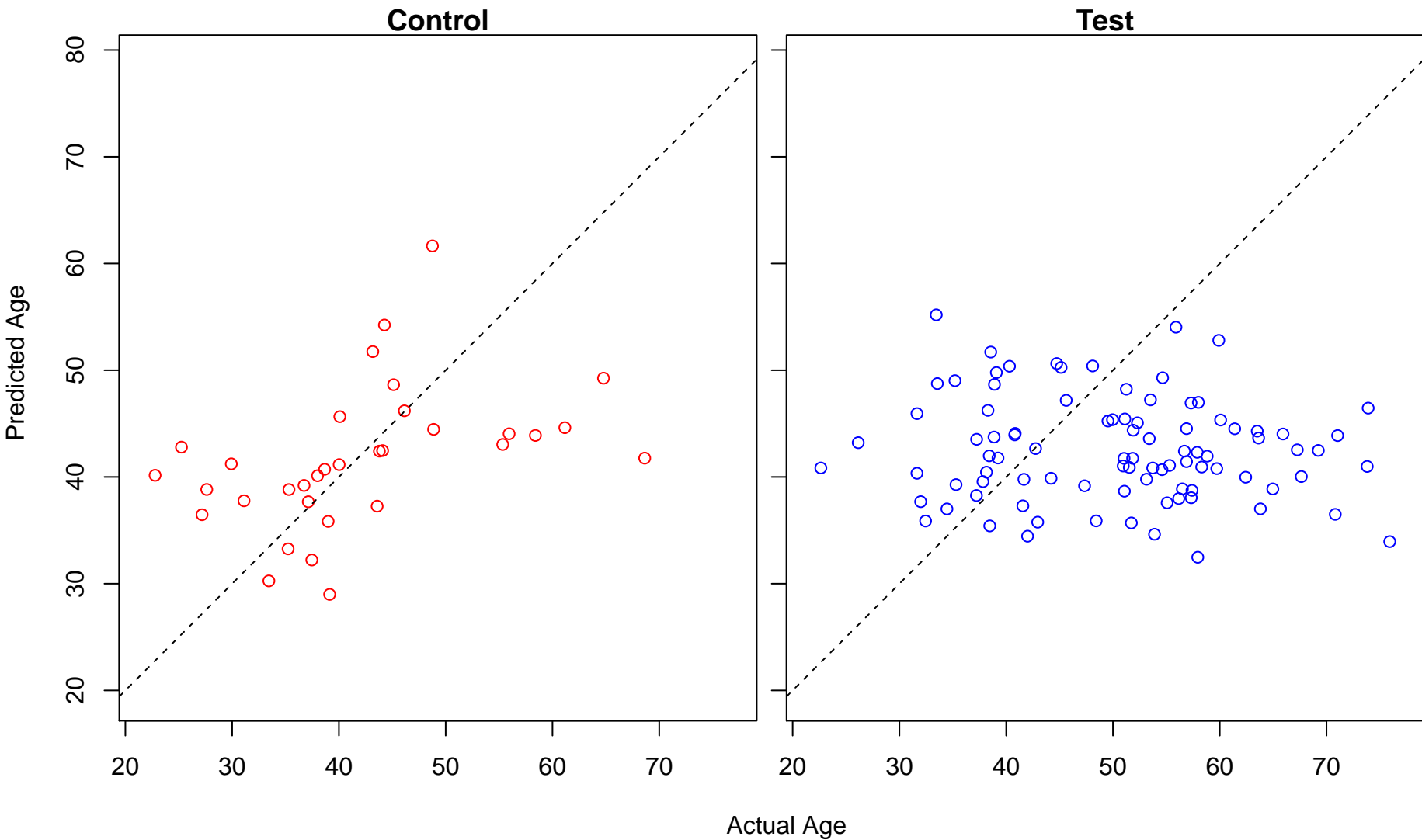
regulation of protein metabolic process (Score: 0.708257)



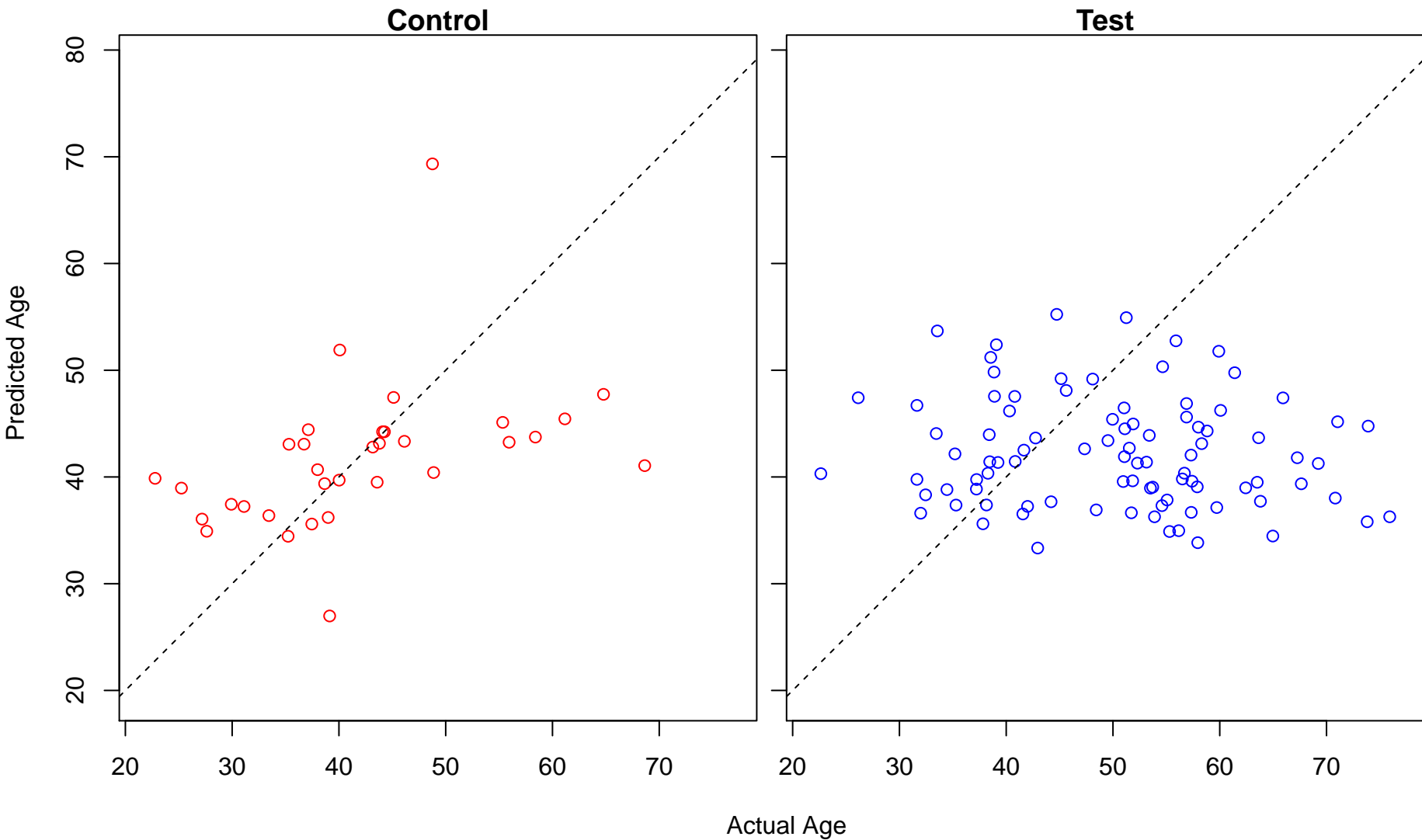
relaxation of cardiac muscle (Score: 0.708106)



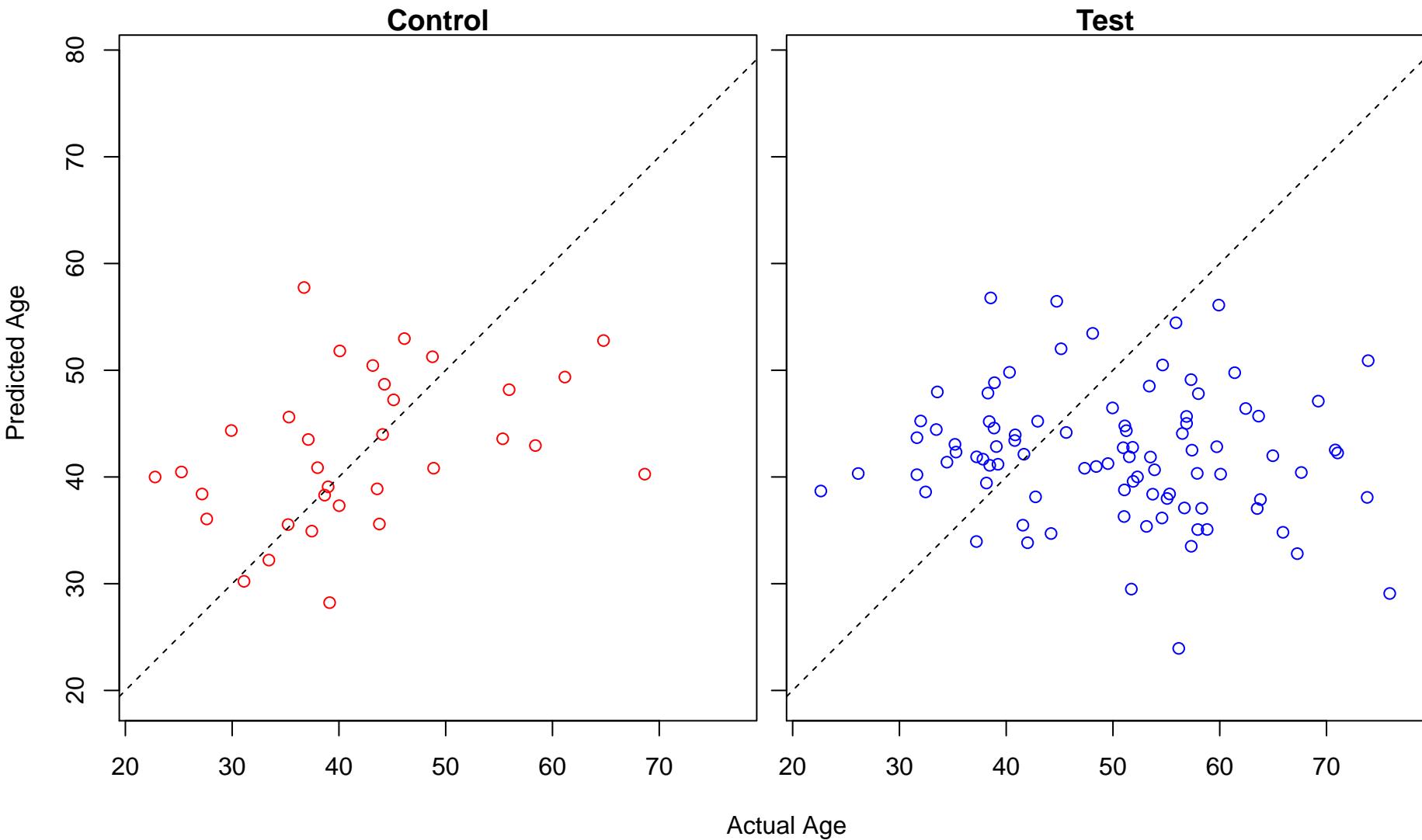
single-organism carbohydrate catabolic process (Score: 0.707487)



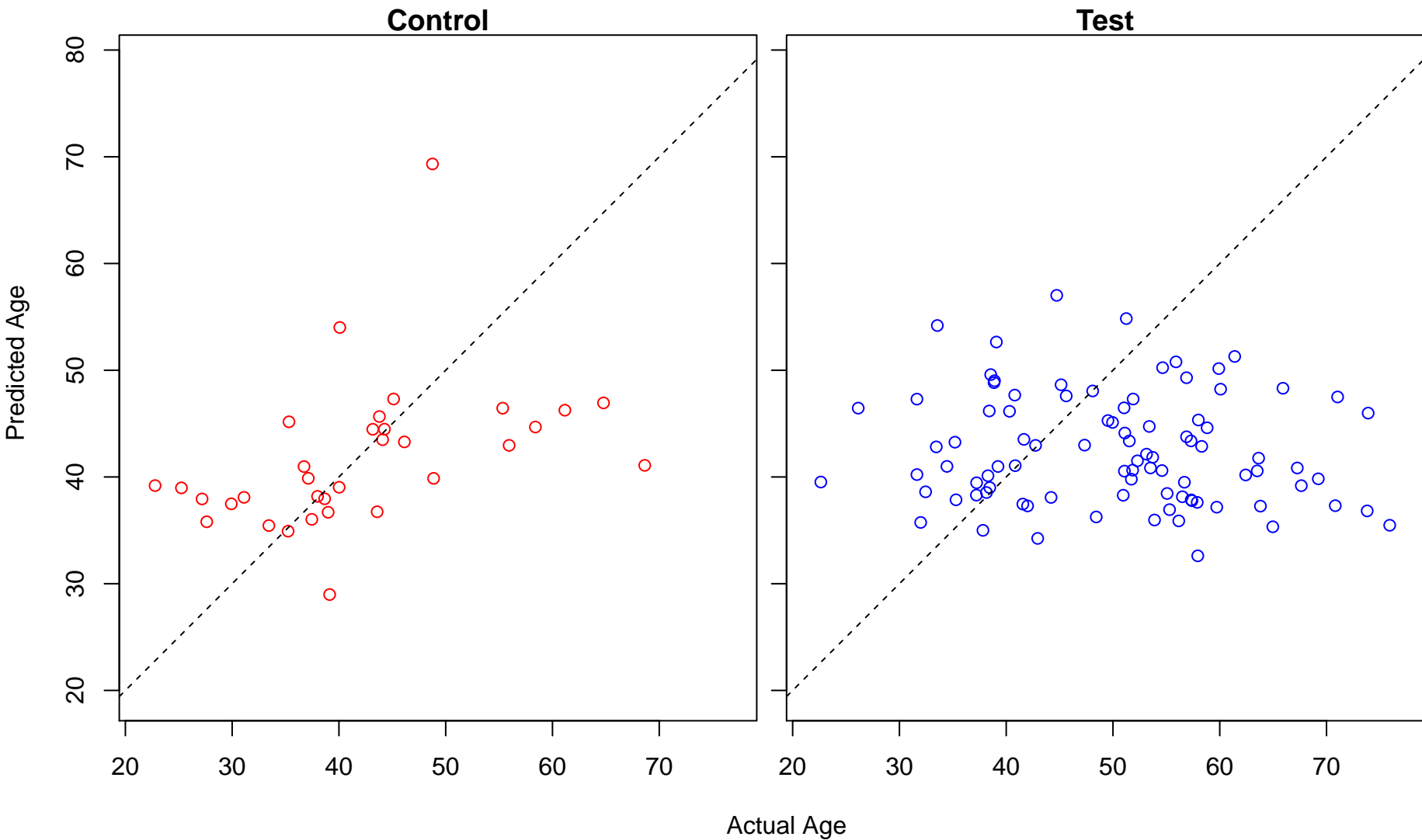
regulation of biological quality (Score: 0.707106)



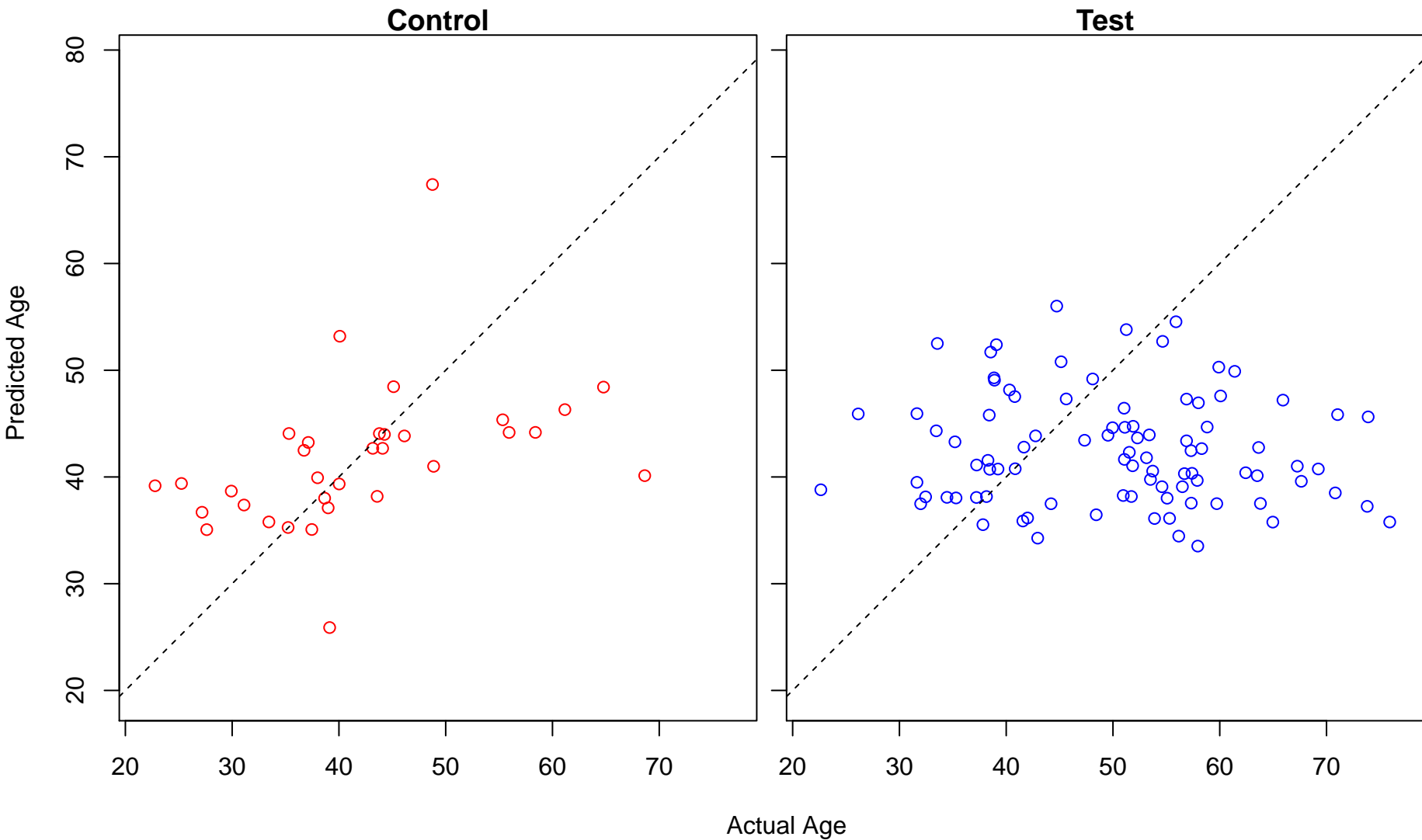
glucosamine-containing compound metabolic process (Score: 0.706874)



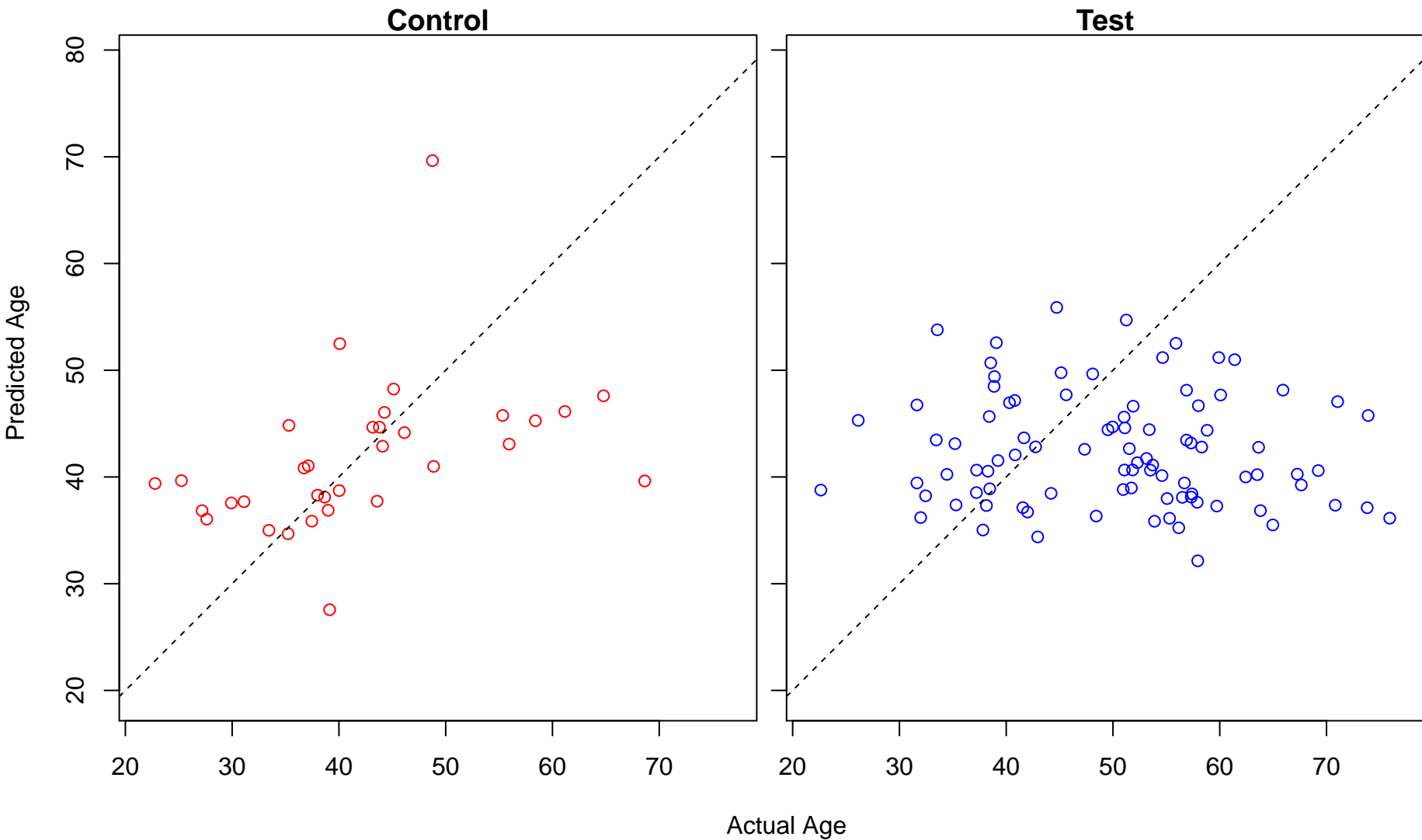
positive regulation of gene expression (Score: 0.706761)



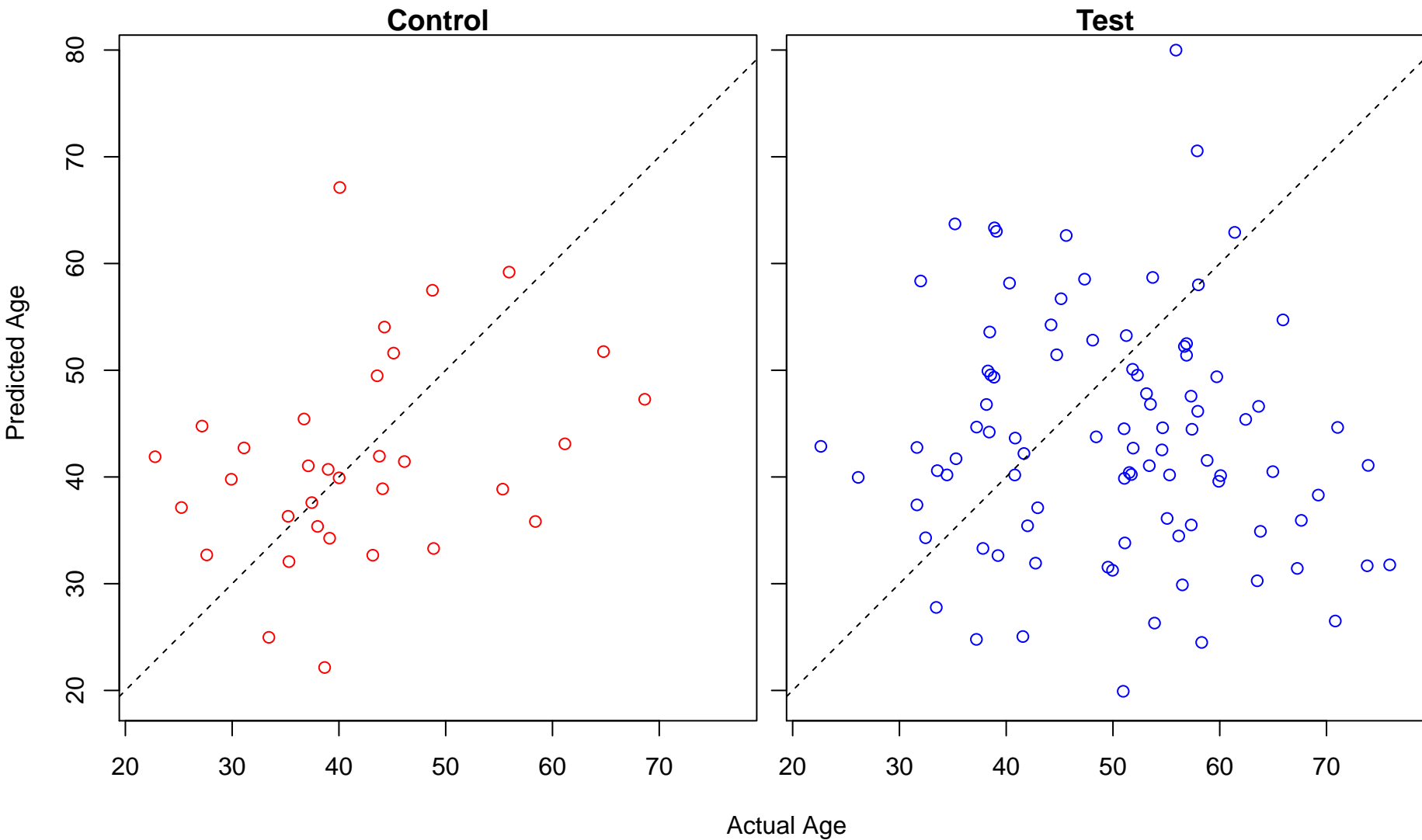
regulation of localization (Score: 0.706709)



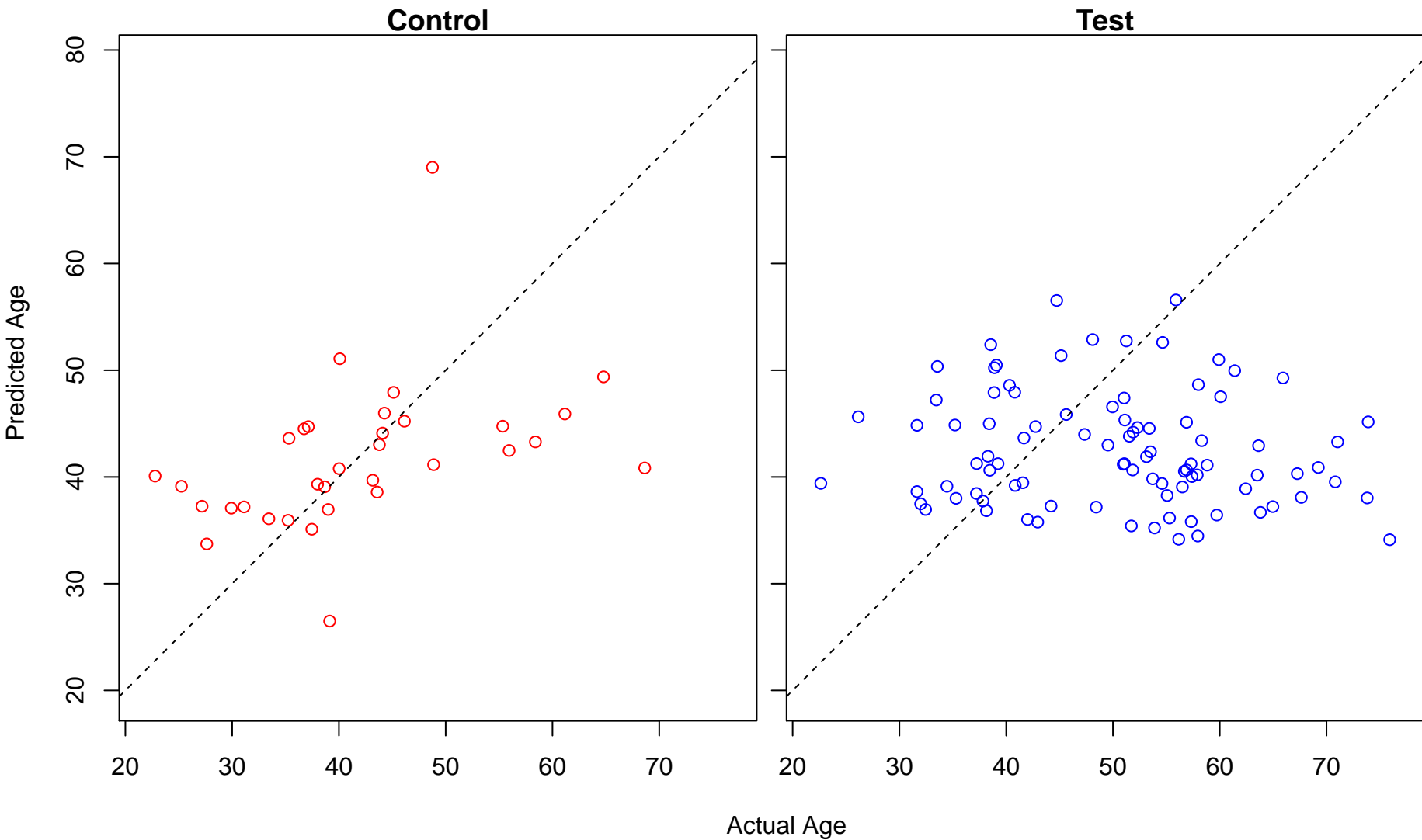
regulation of macromolecule metabolic process (Score: 0.706699)



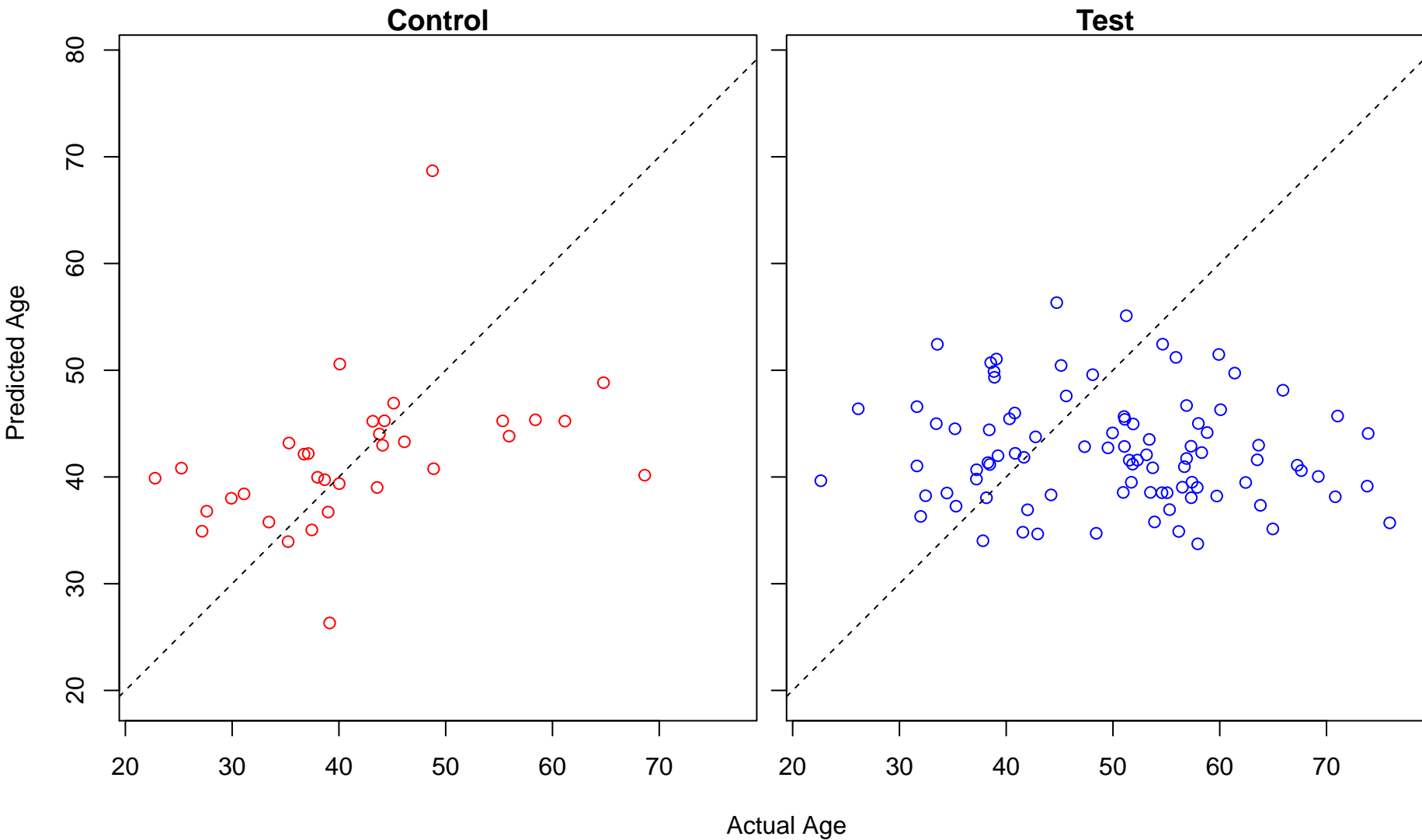
positive regulation of receptor-mediated endocytosis (Score: 0.706155)



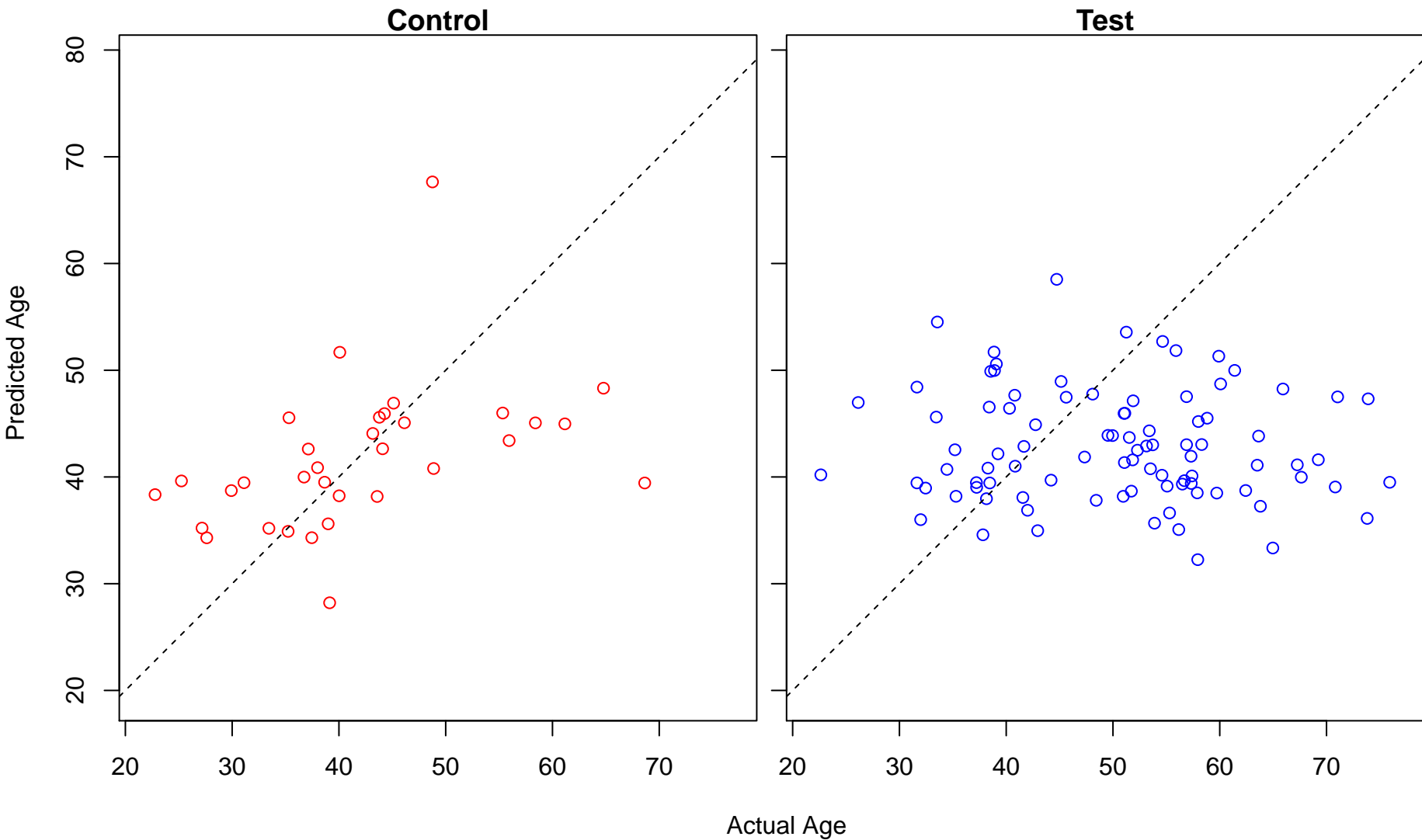
regulation of protein transport (Score: 0.705805)



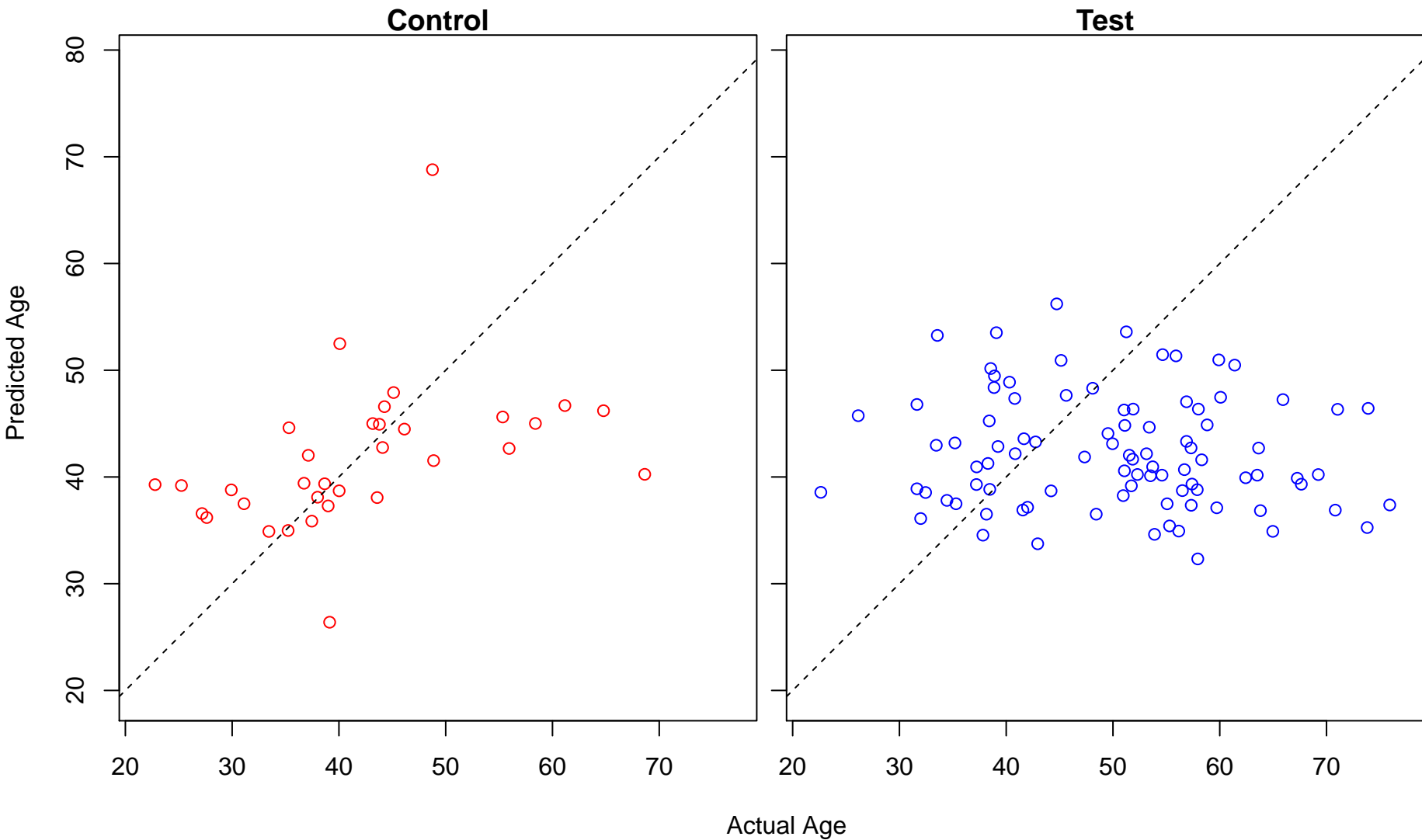
anatomical structure development (Score: 0.705321)



negative regulation of signaling (Score: 0.705245)



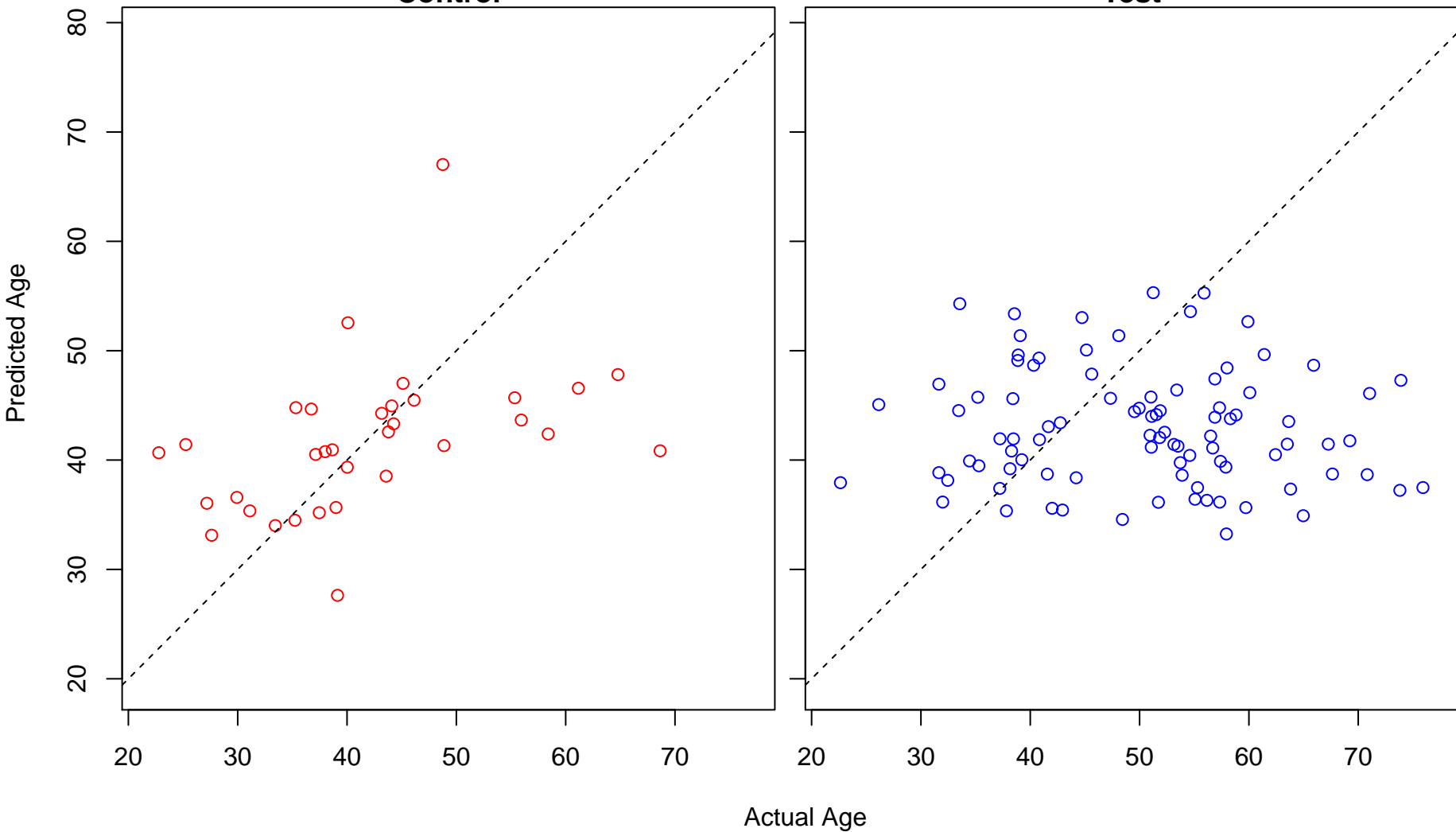
regulation of protein modification process (Score: 0.705075)



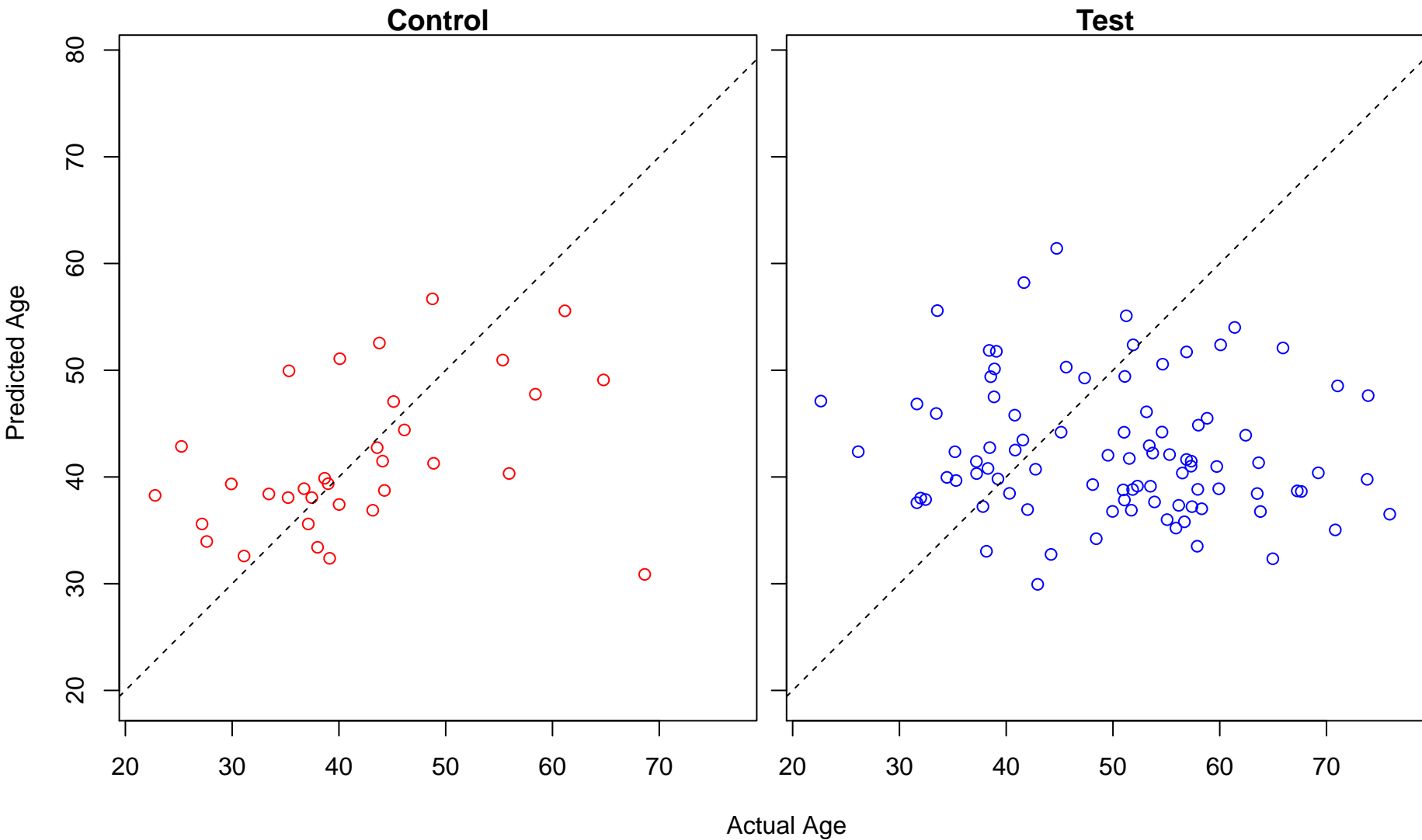
positive regulation of apoptotic process (Score: 0.704364)

Control

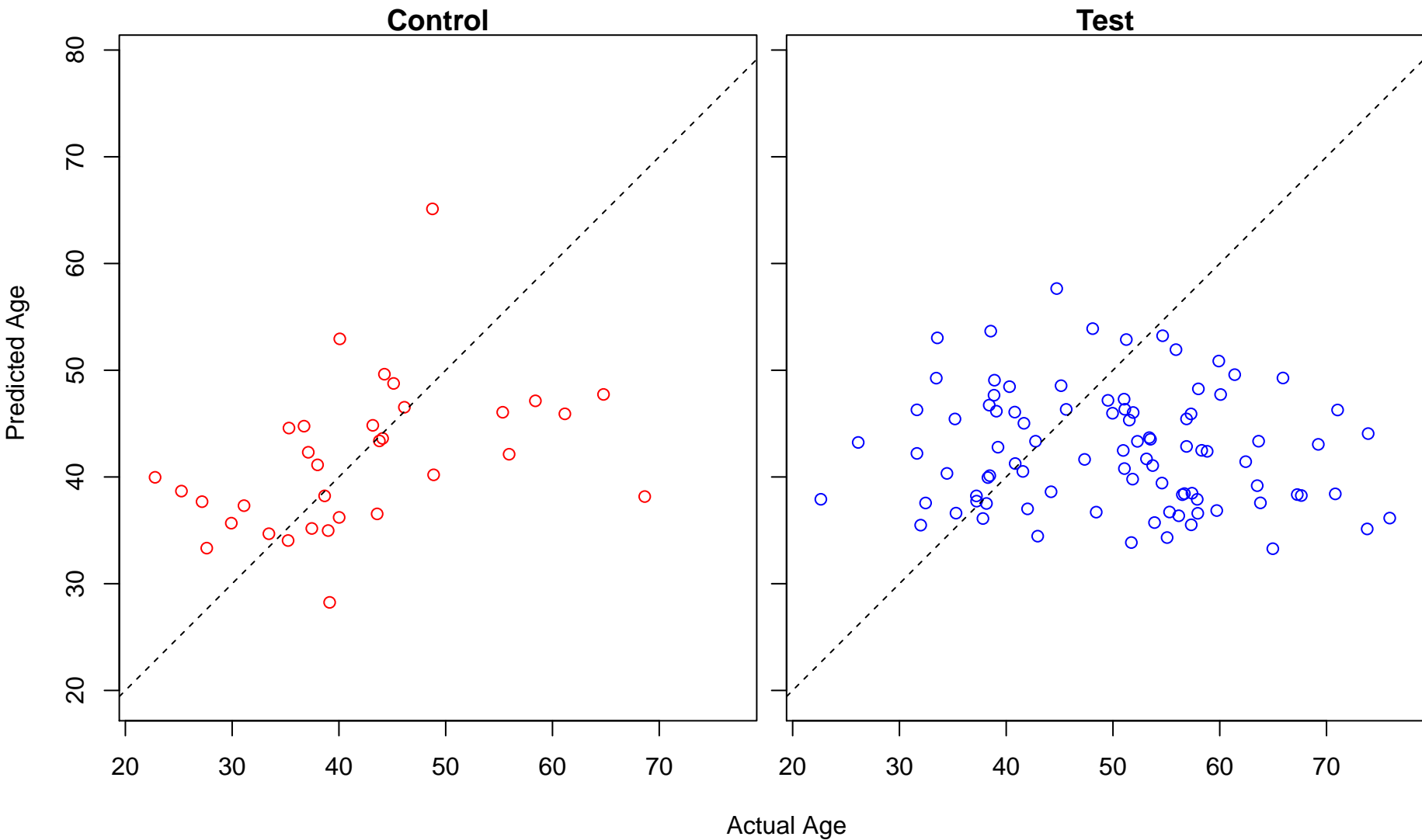
Test



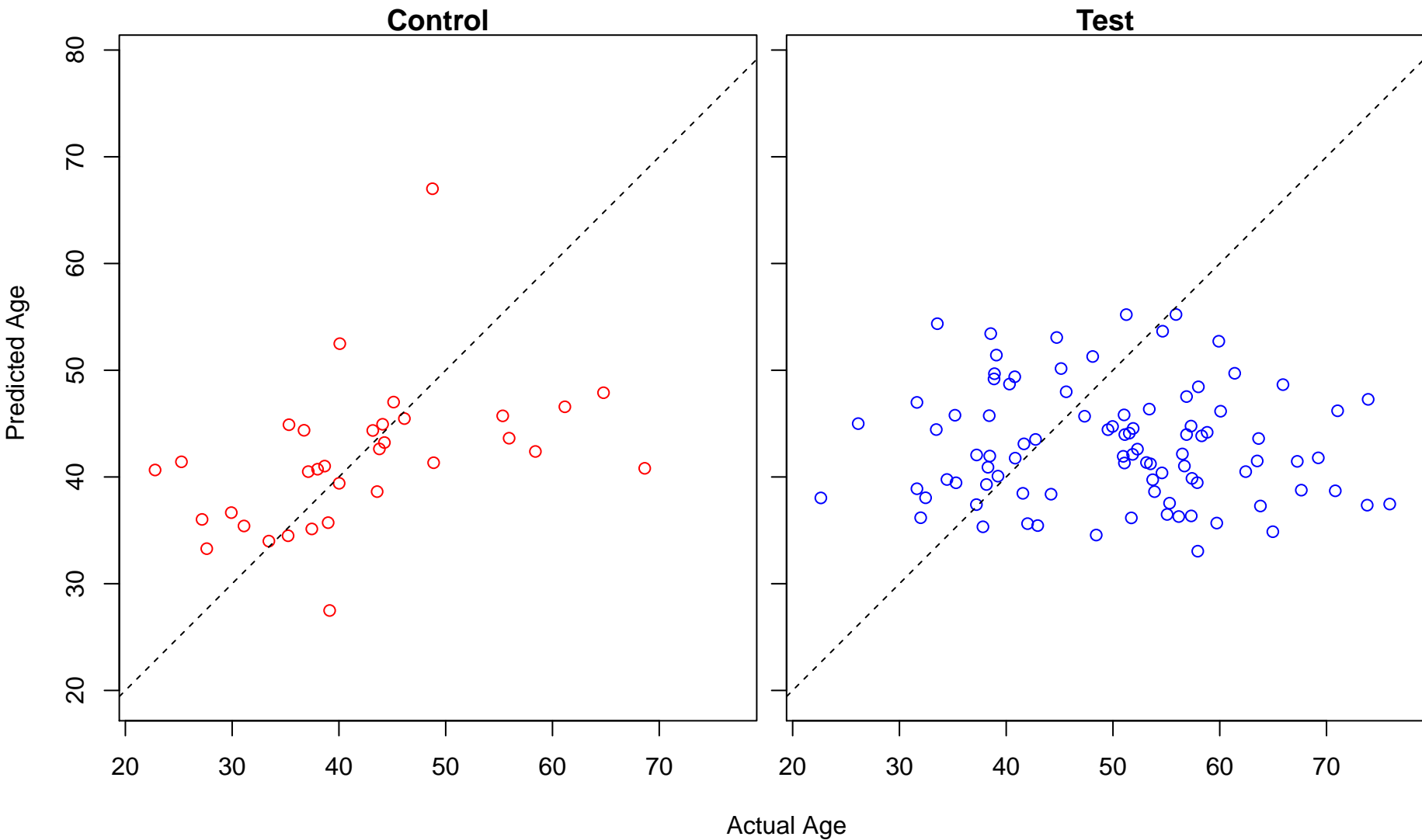
B cell activation involved in immune response (Score: 0.704349)



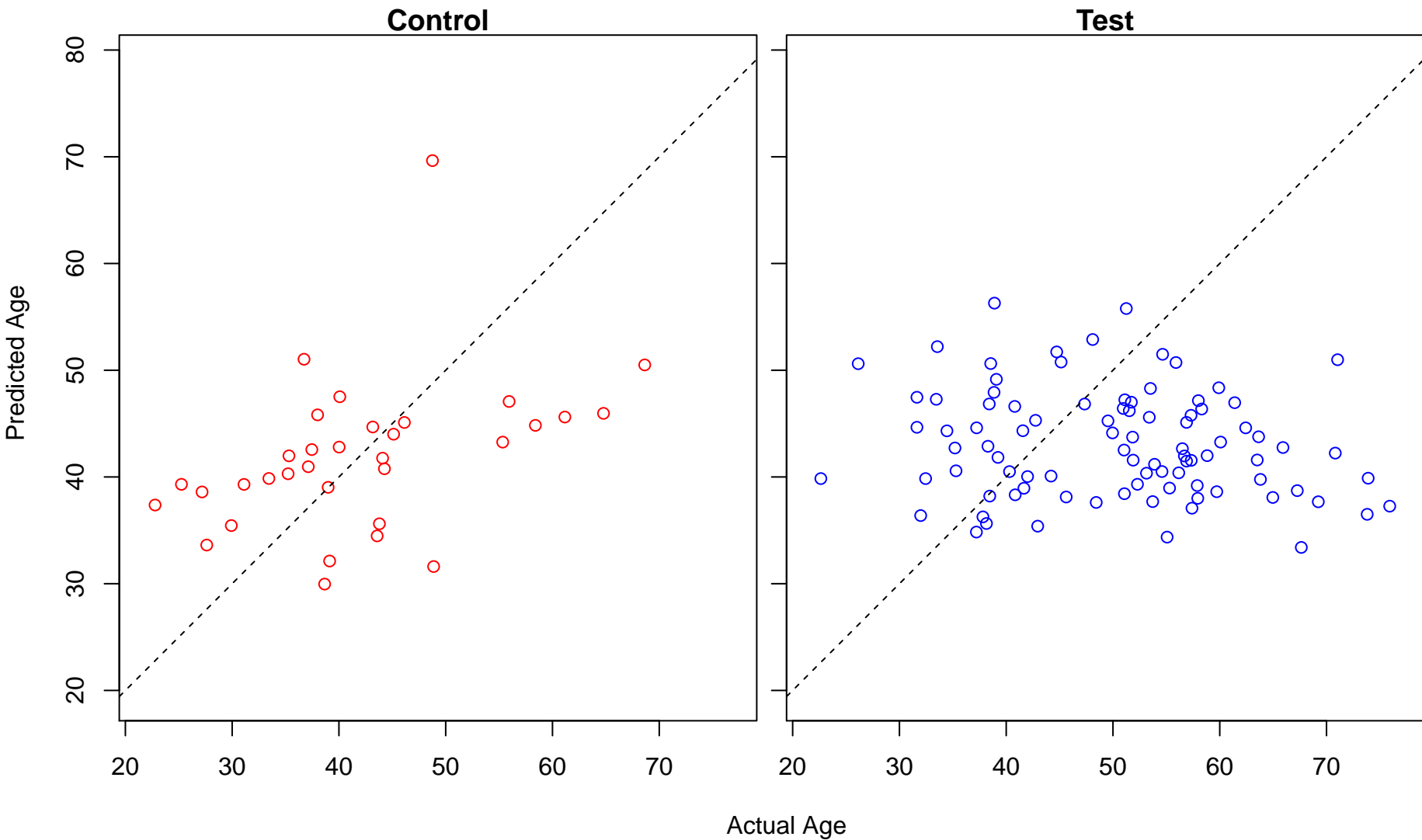
positive regulation of cellular catabolic process (Score: 0.704166)



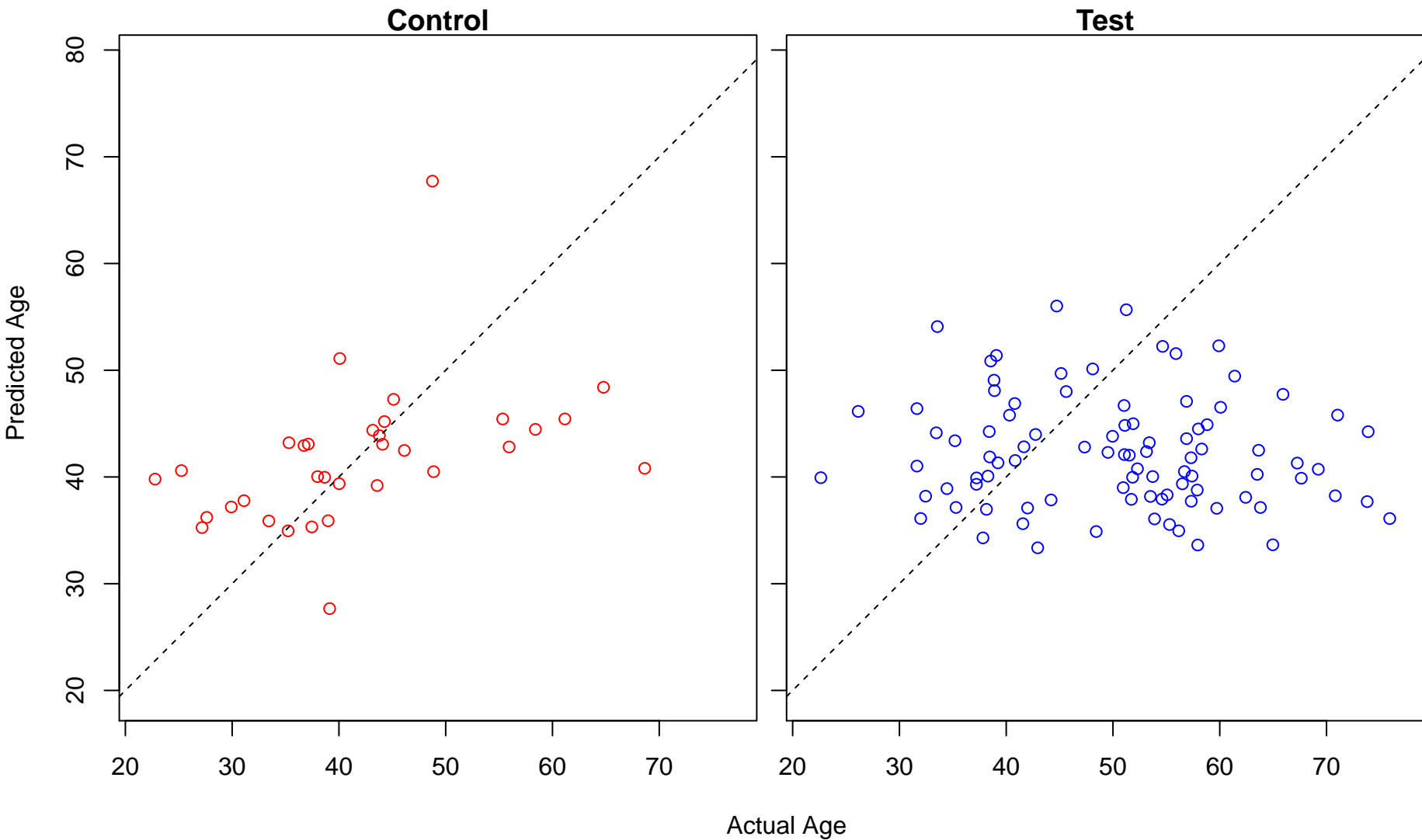
positive regulation of programmed cell death (Score: 0.704109)



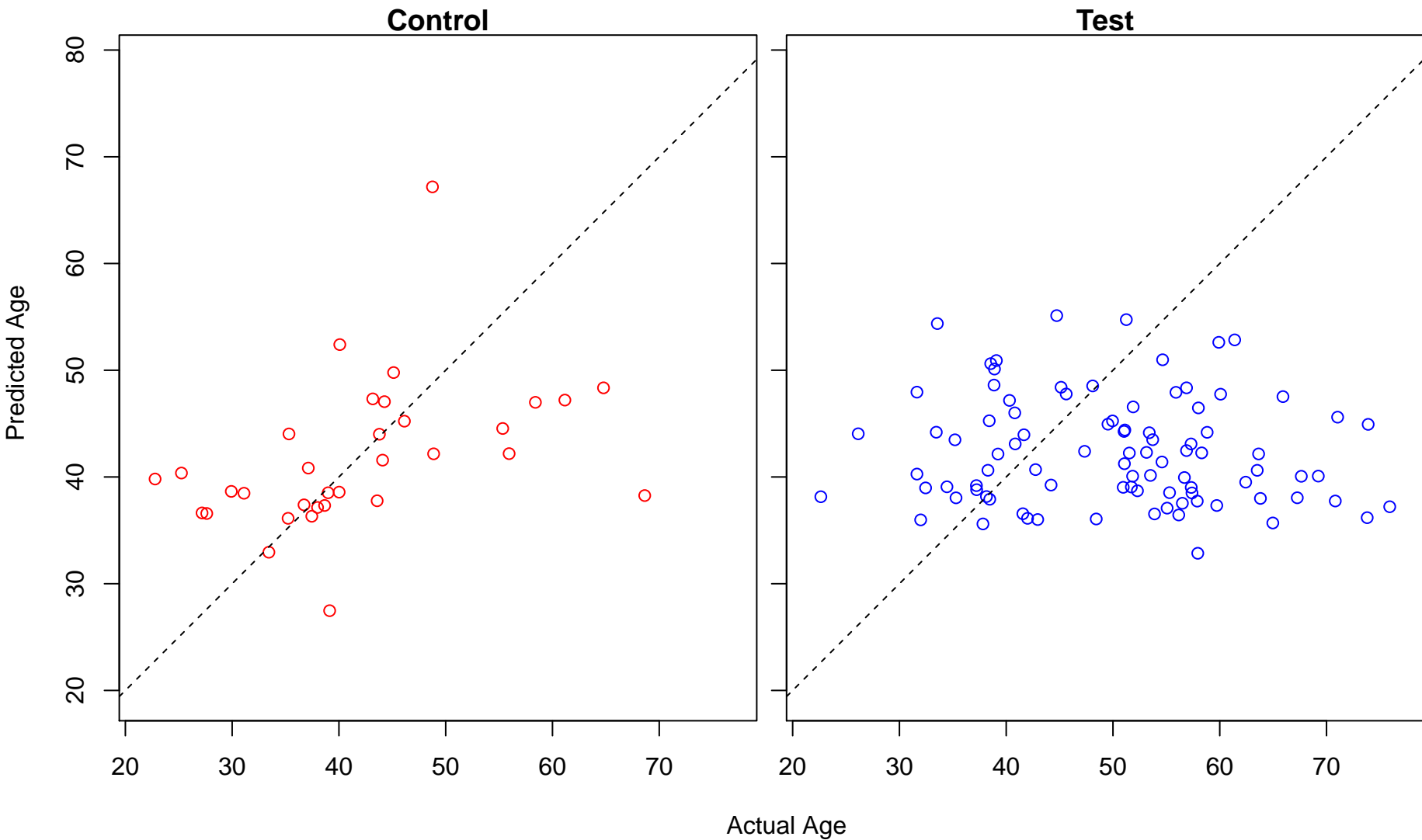
monocyte differentiation (Score: 0.703996)



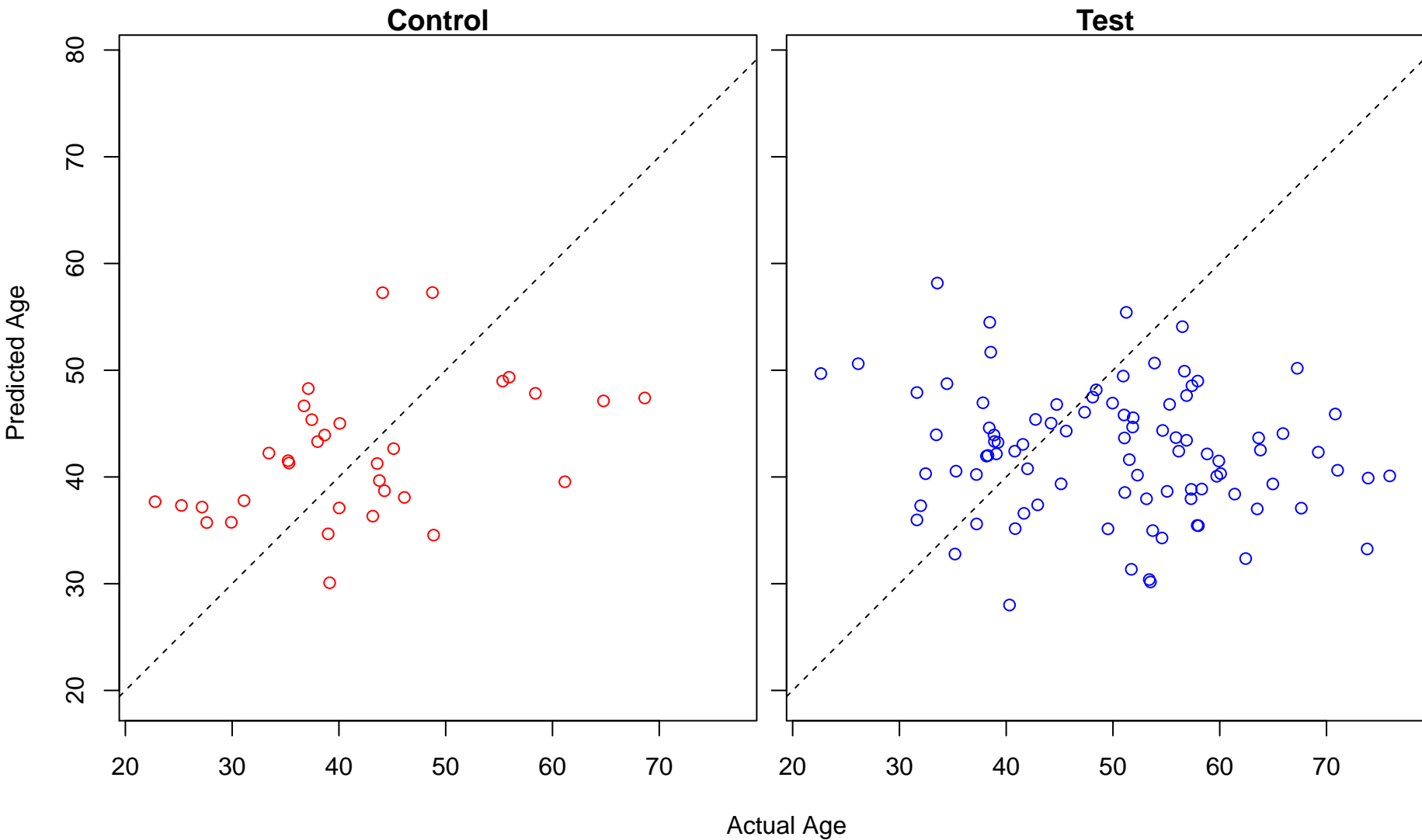
multicellular organismal process (Score: 0.703894)



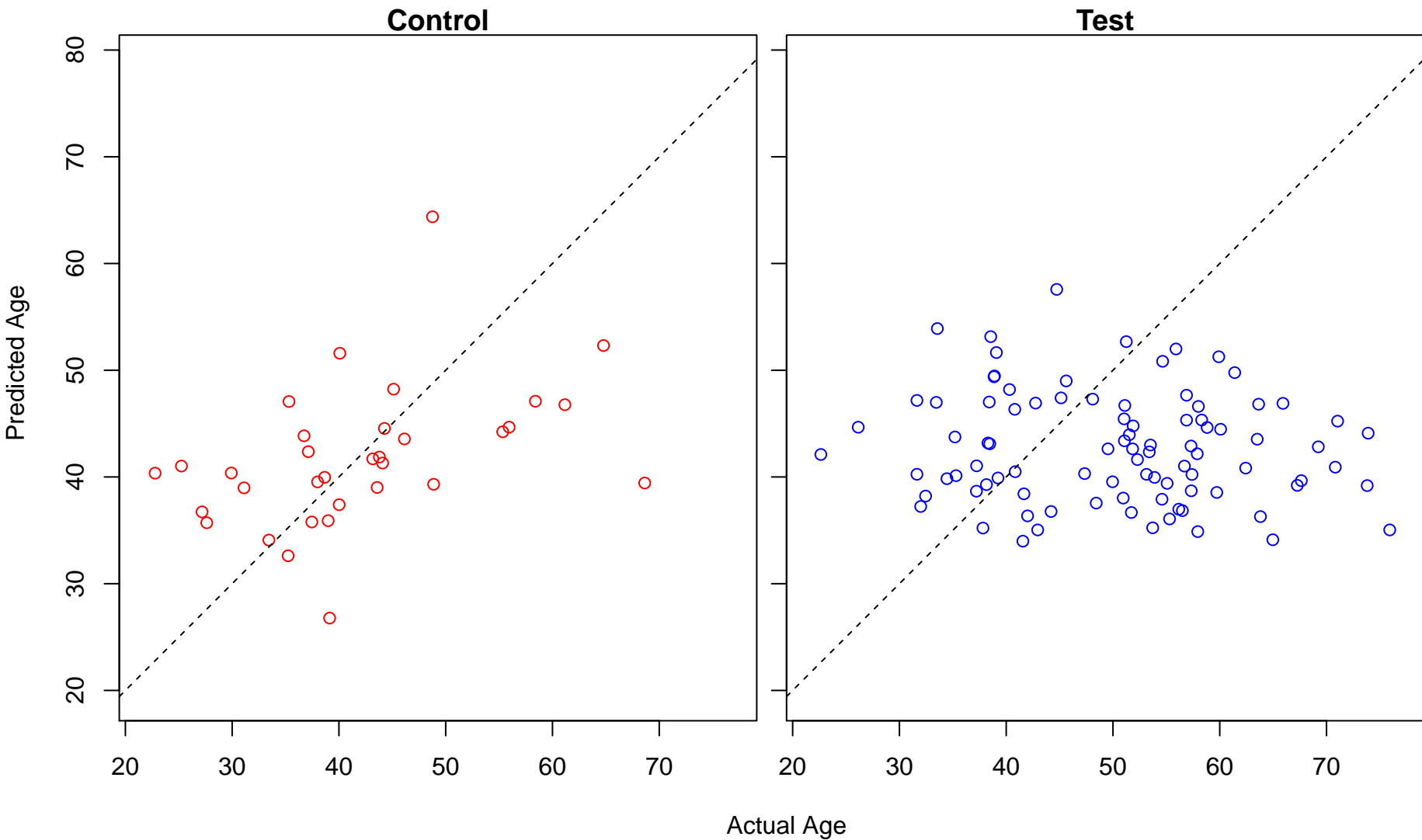
ubiquitin-dependent protein catabolic process (Score: 0.703822)



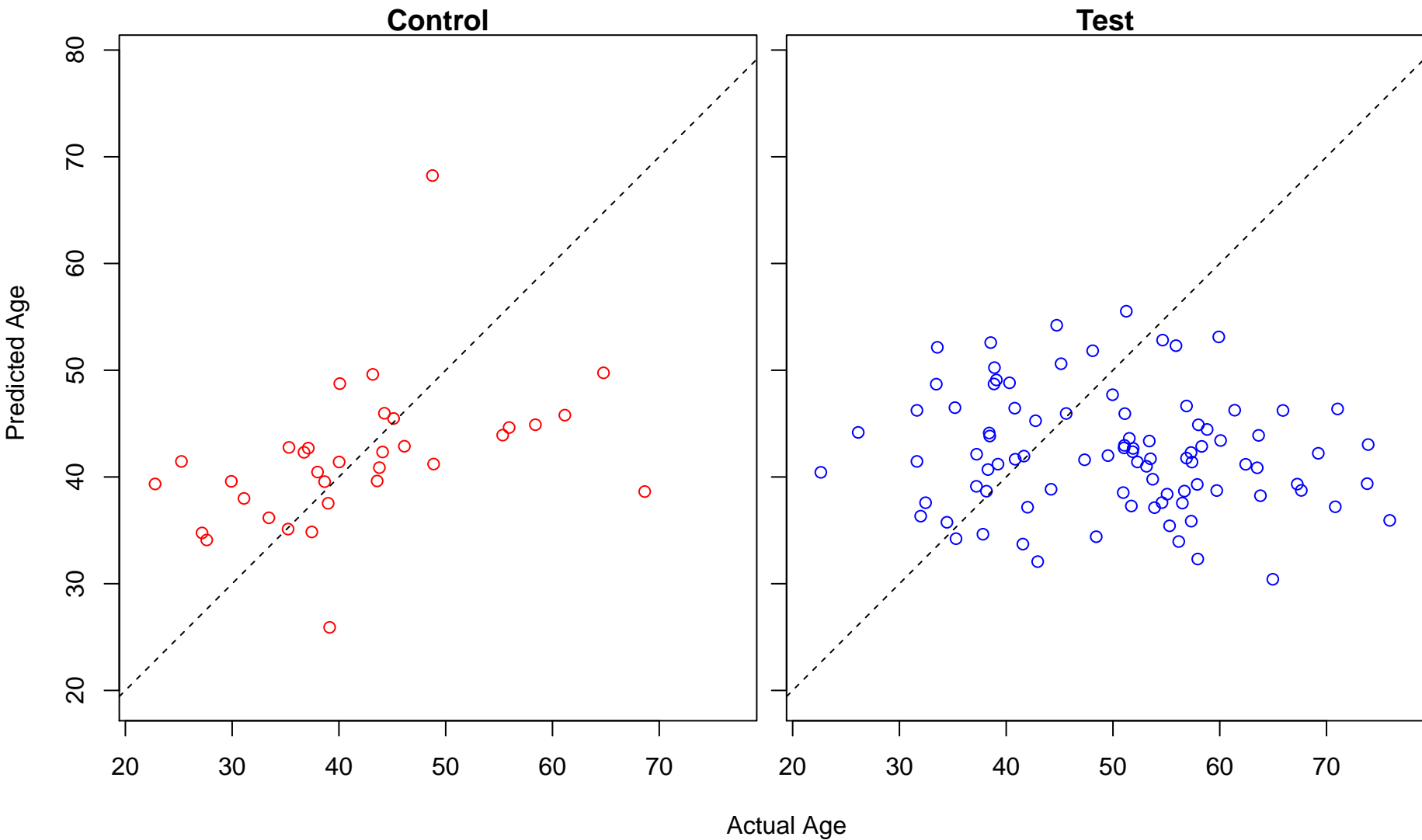
corticospinal tract morphogenesis (Score: 0.703803)



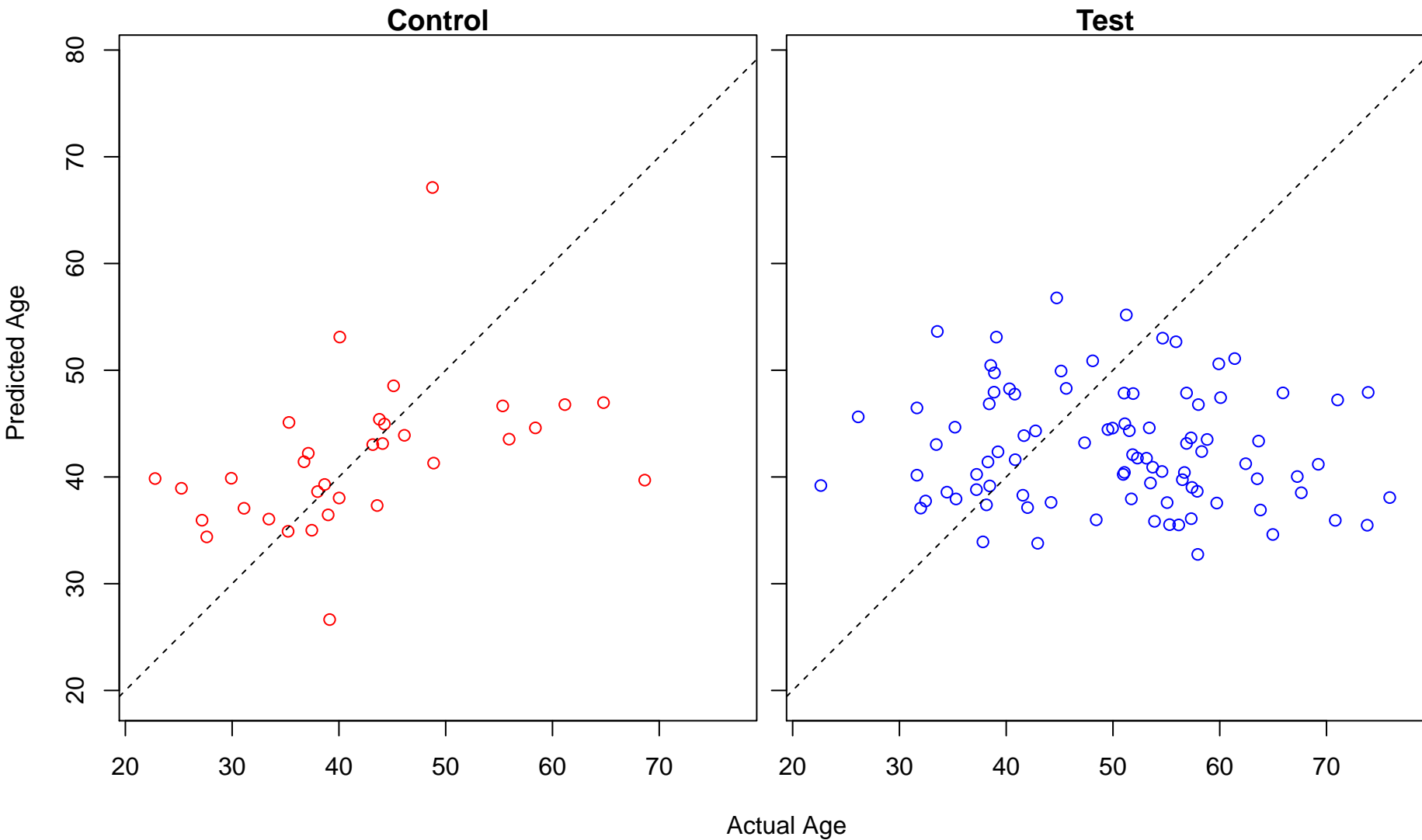
macroautophagy (Score: 0.703366)



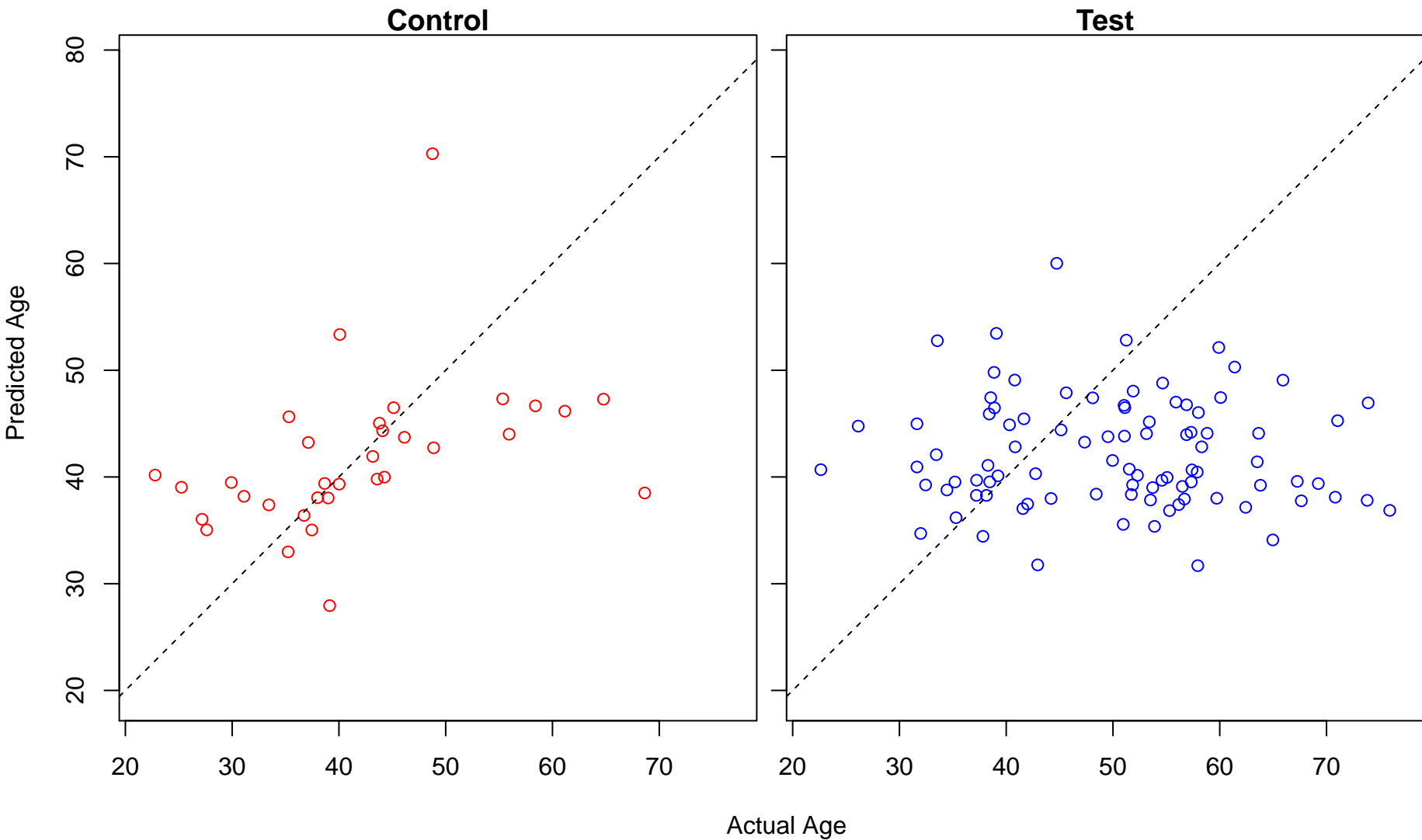
ion transport (Score: 0.703282)



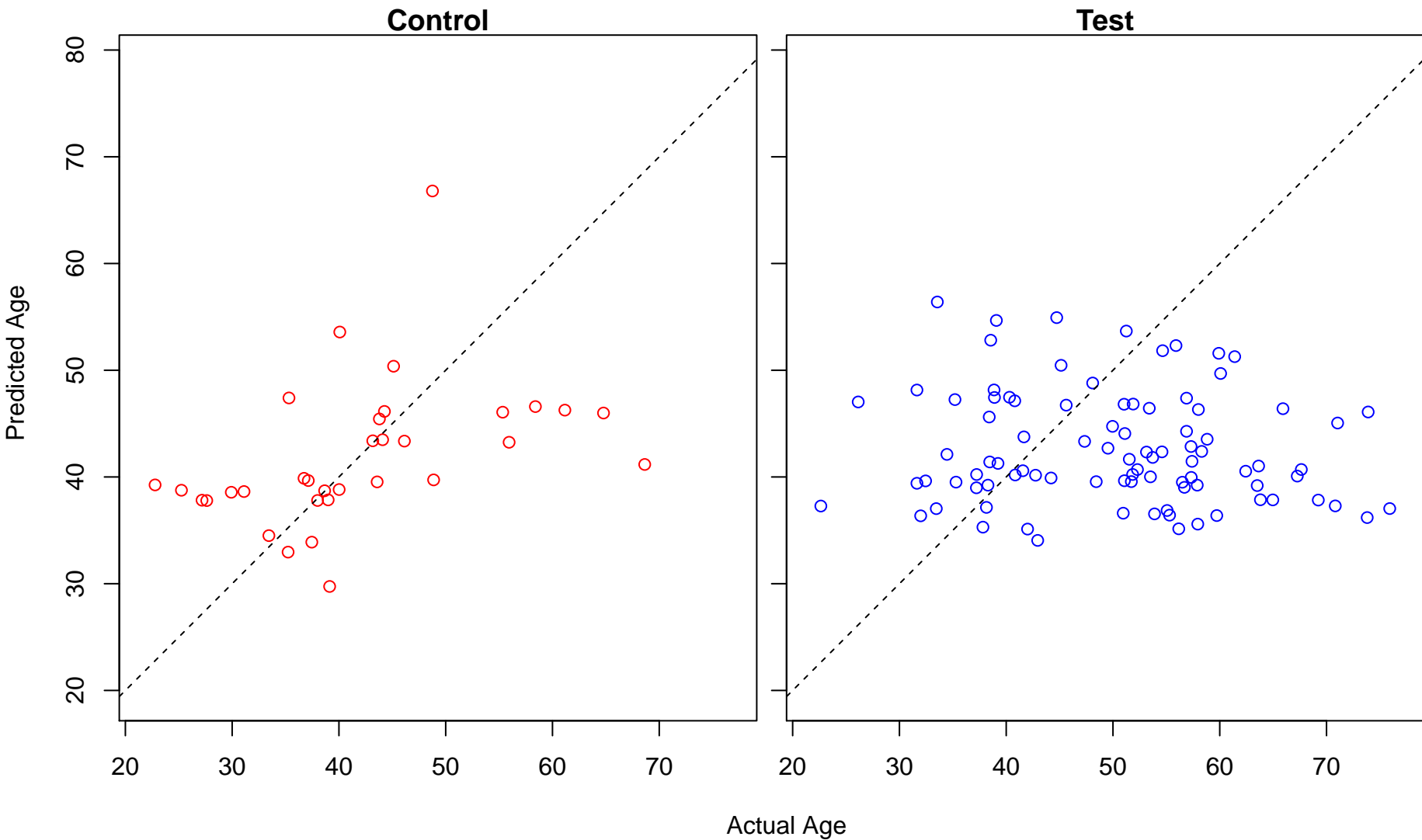
positive regulation of protein metabolic process (Score: 0.703258)



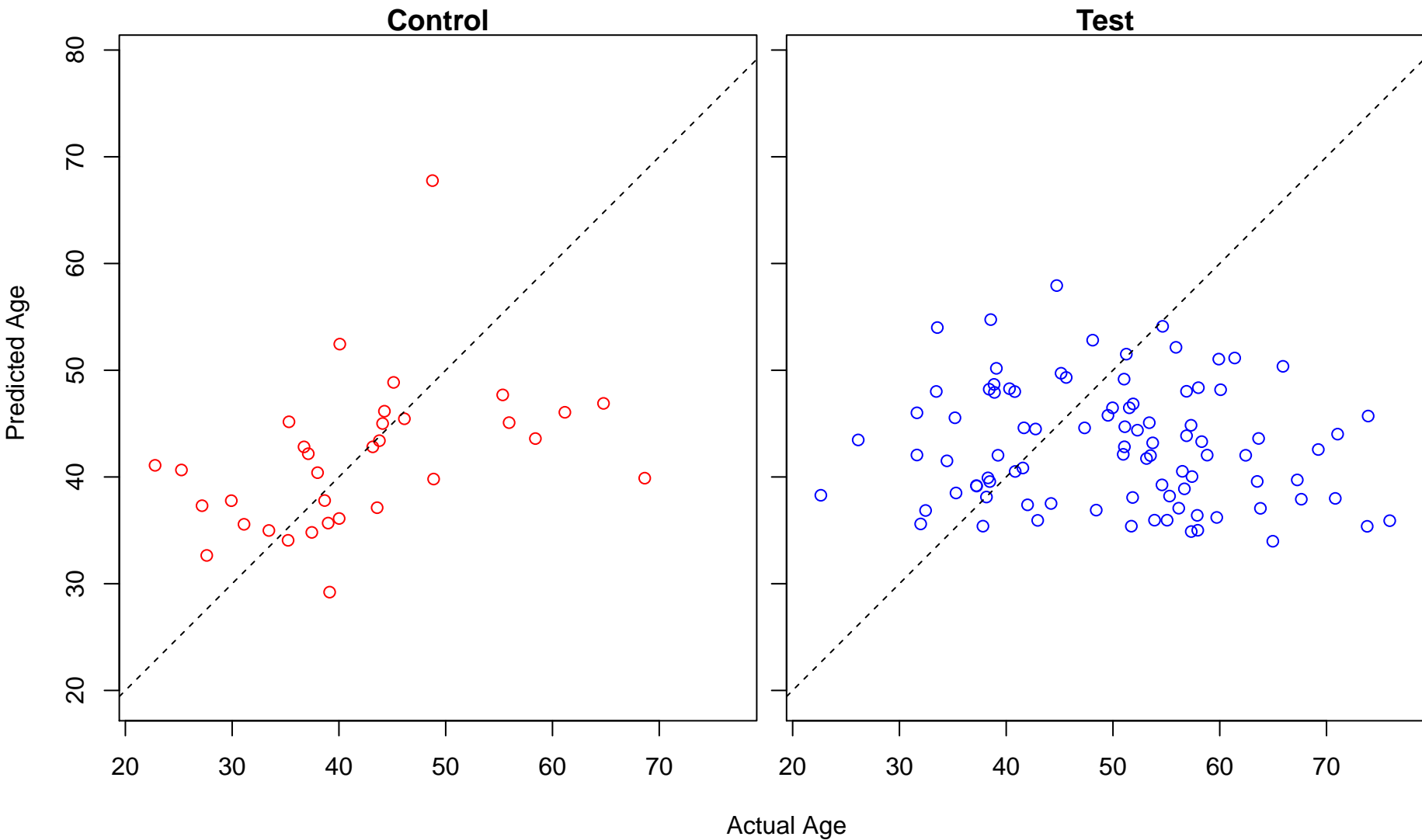
protein N-linked glycosylation via asparagine (Score: 0.703201)



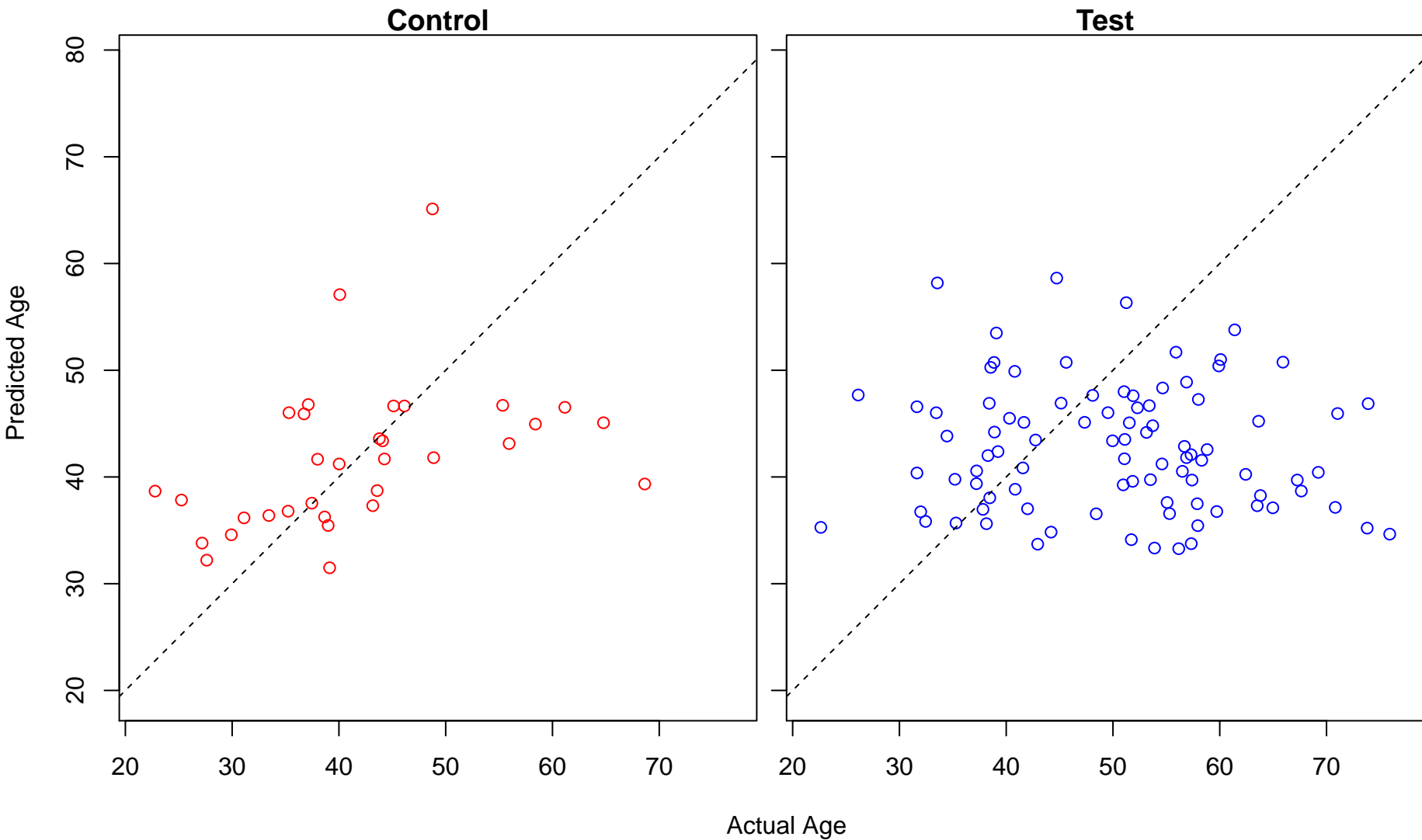
positive regulation of cell proliferation (Score: 0.703068)



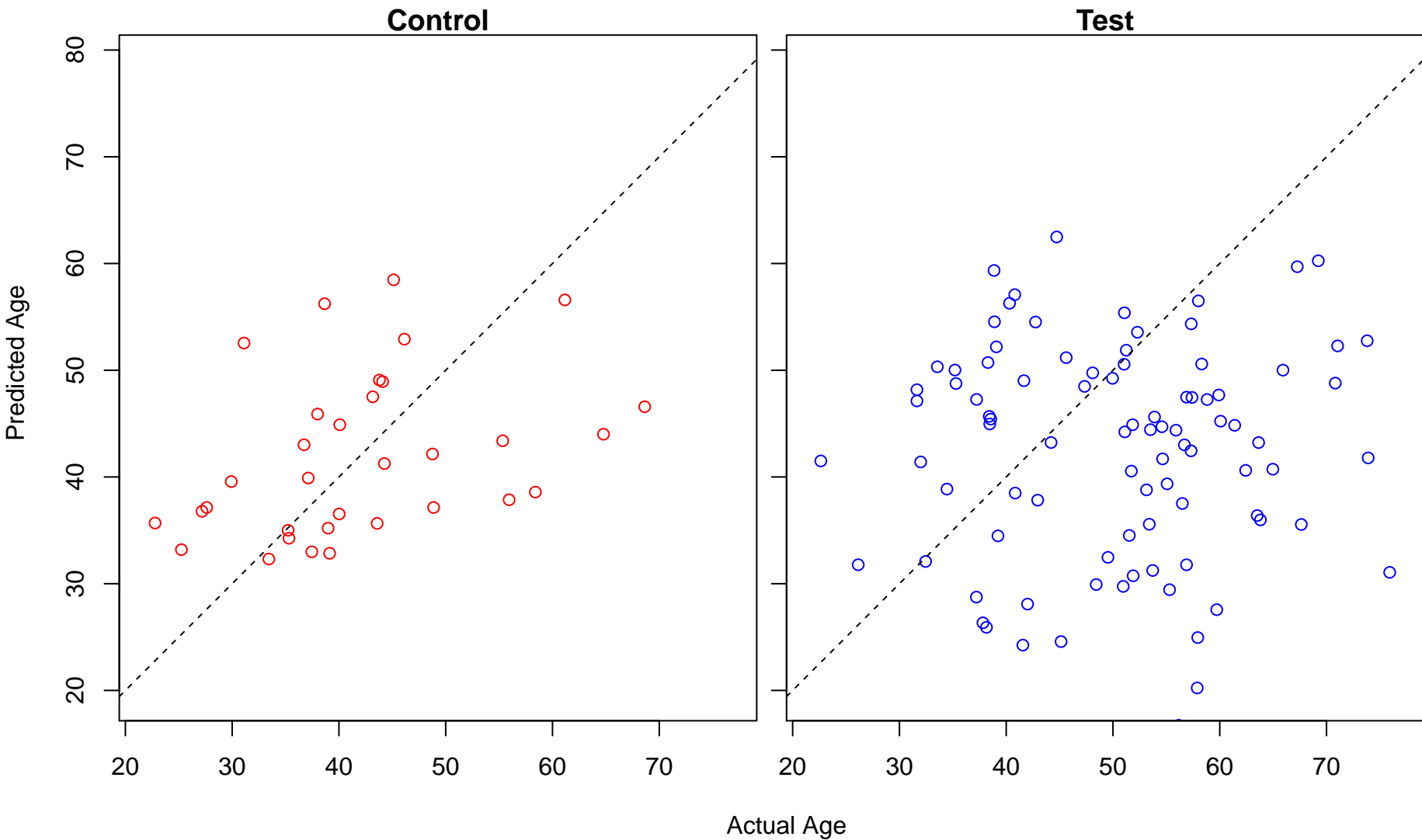
positive regulation of proteolysis (Score: 0.702994)



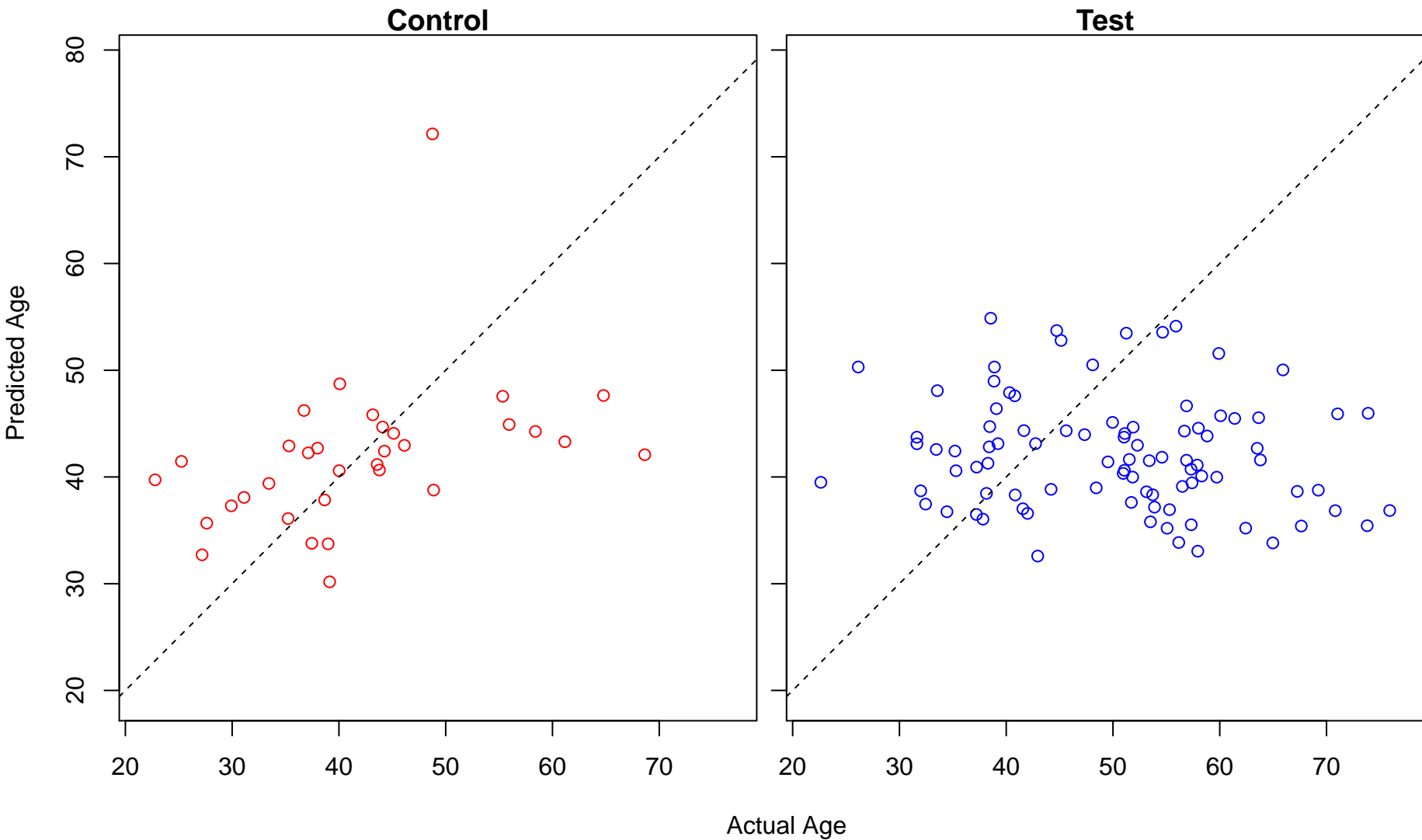
regulation of homeostatic process (Score: 0.702777)



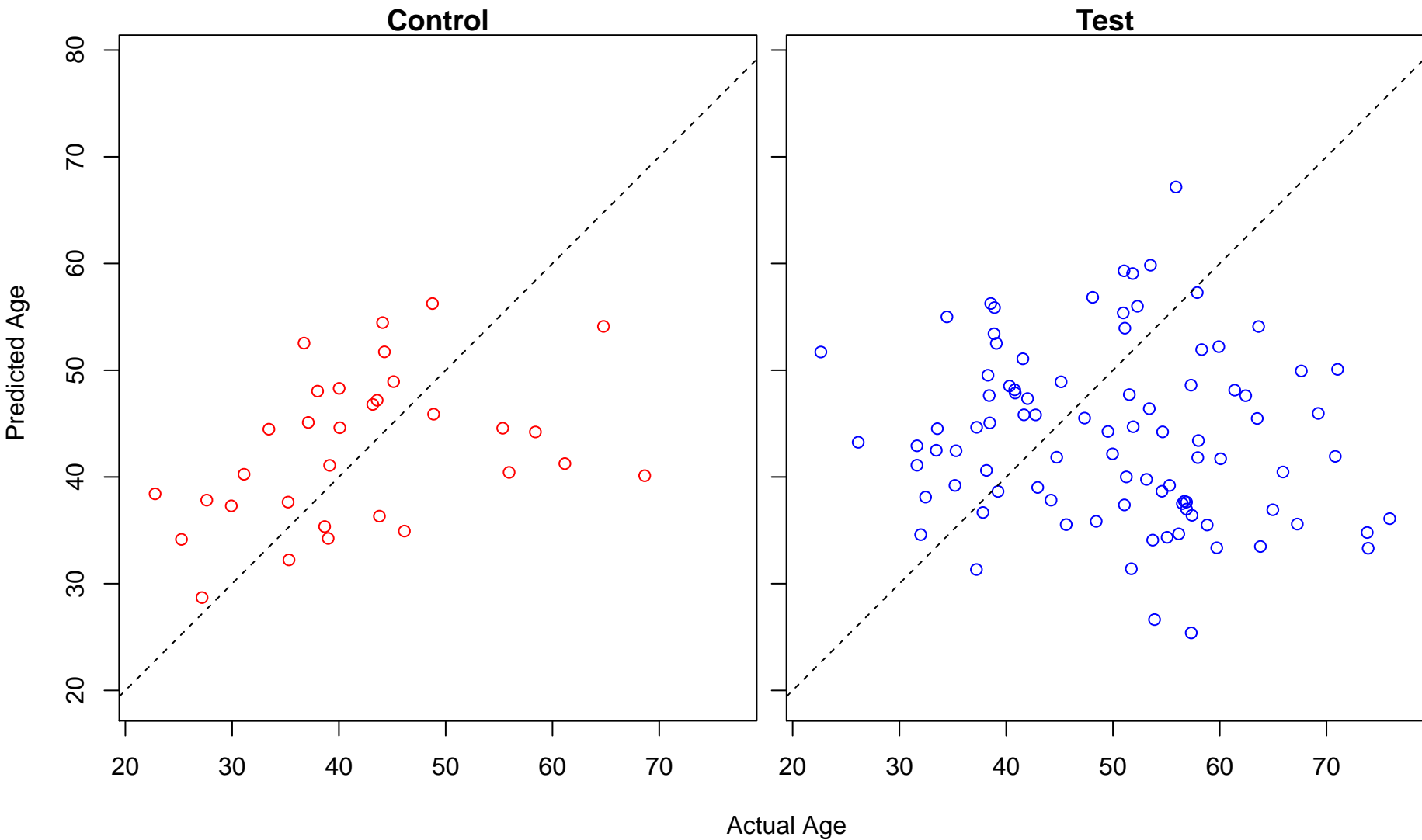
regulation of cardiac muscle cell contraction (Score: 0.702540)



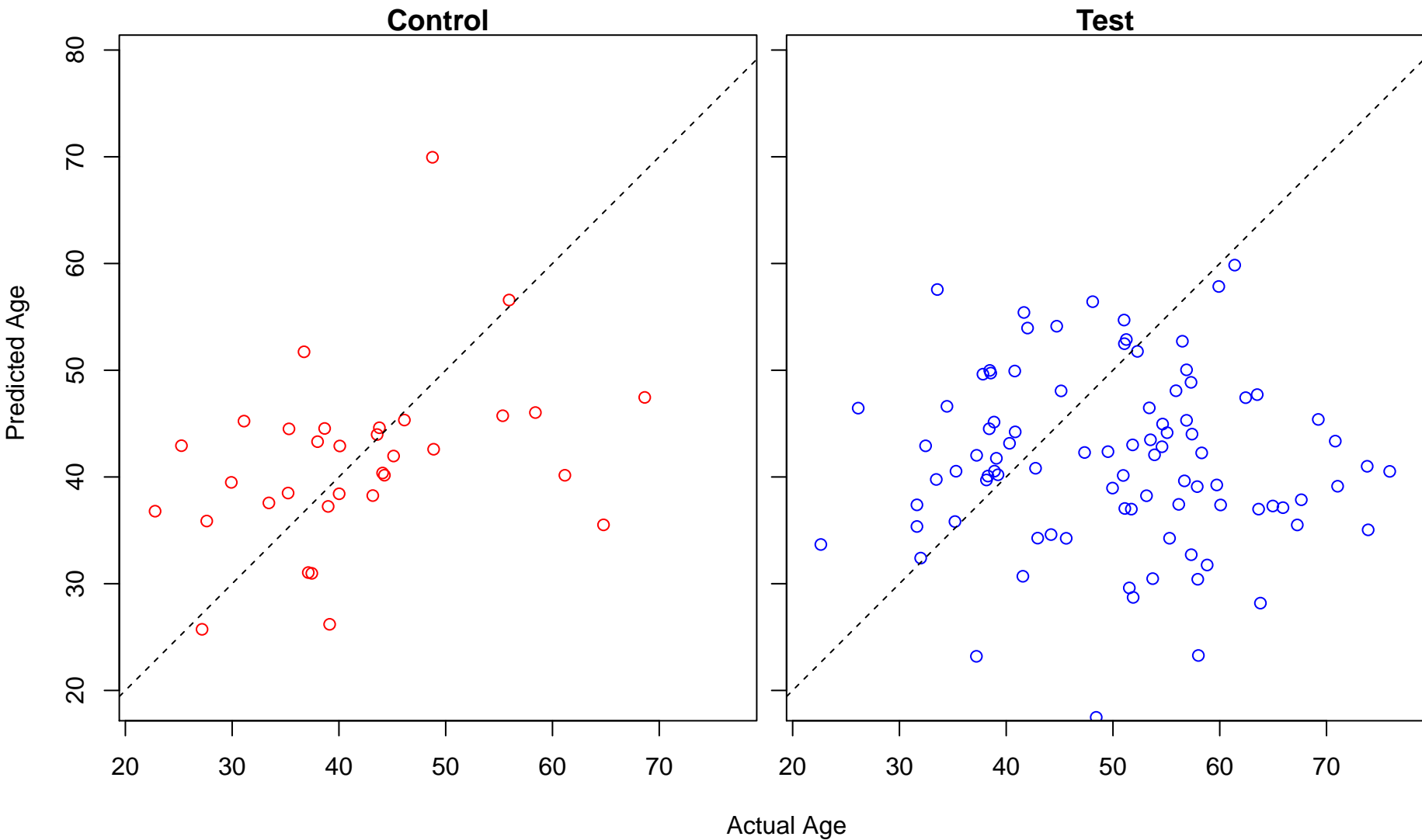
hemopoiesis (Score: 0.702001)



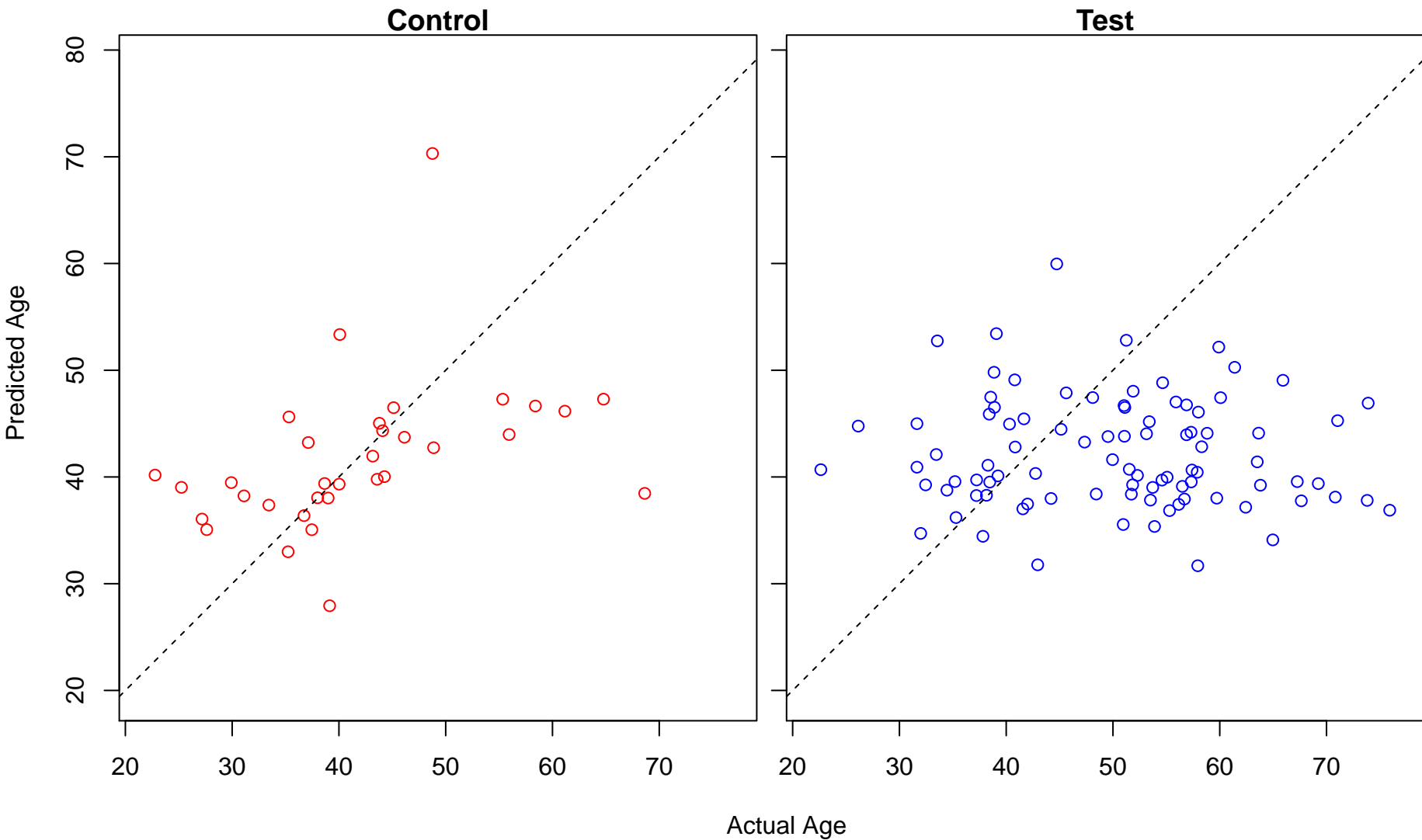
inositol phosphate-mediated signaling (Score: 0.701827)



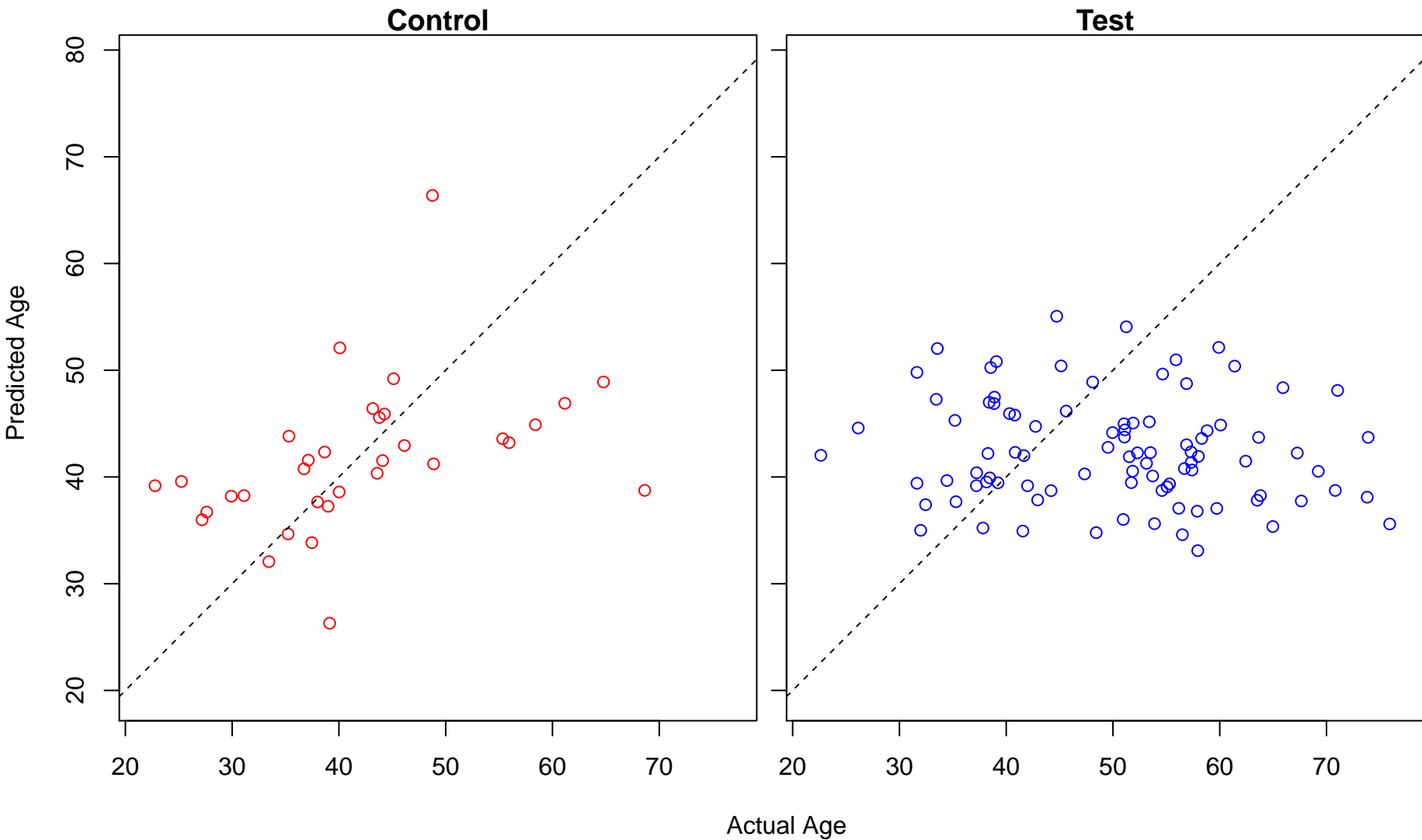
multicellular organism reproduction (Score: 0.701323)



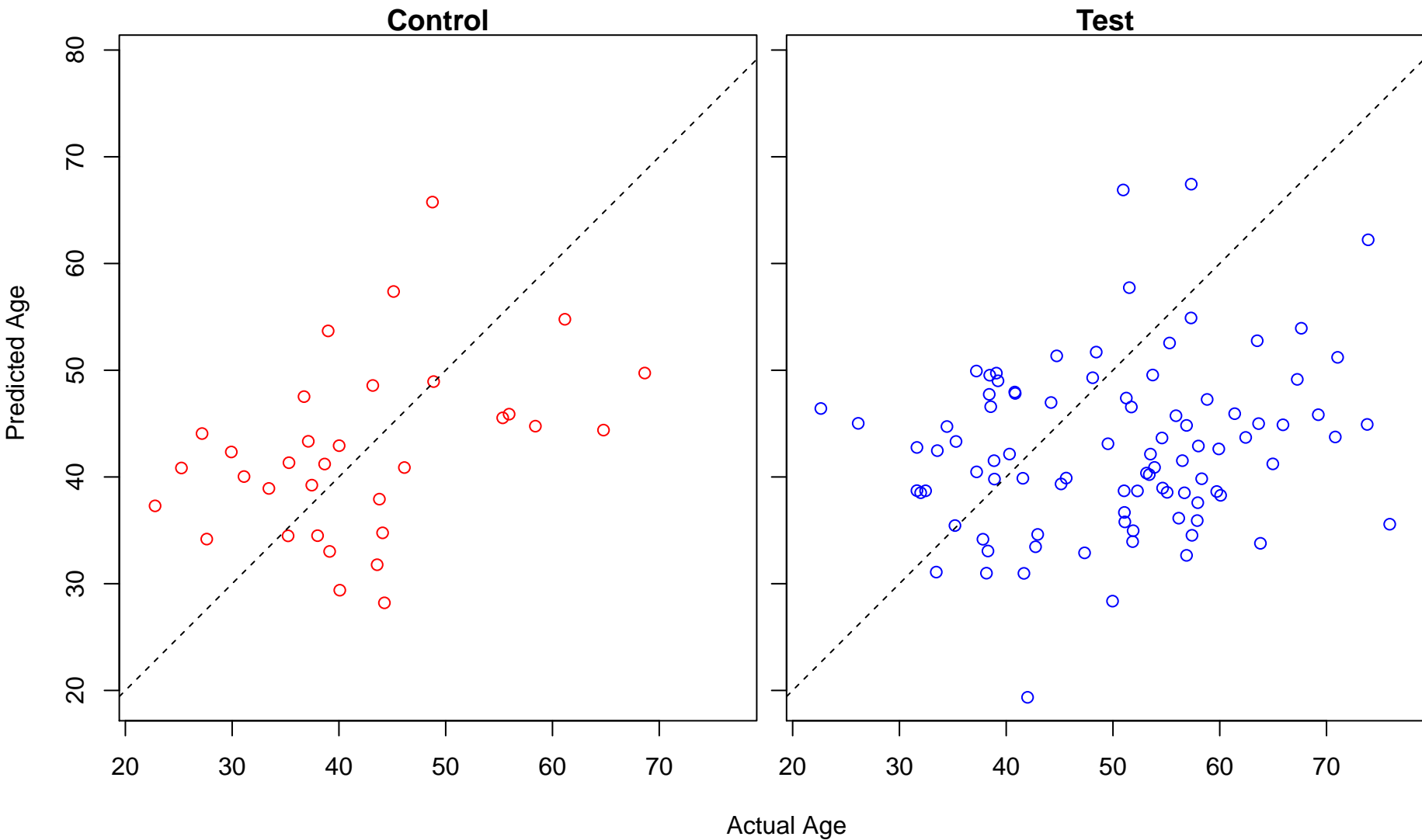
peptidyl-asparagine modification (Score: 0.701154)



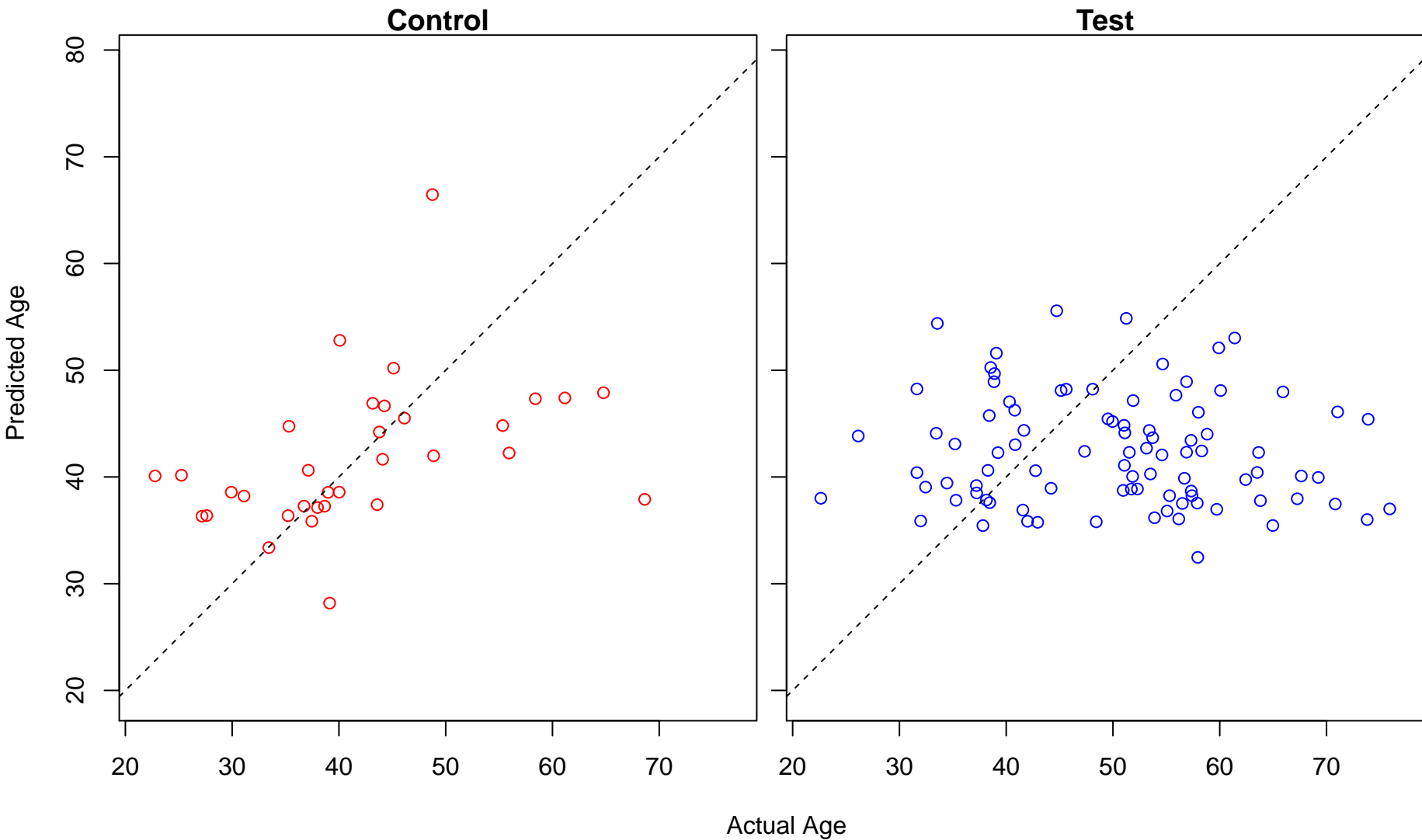
organophosphate biosynthetic process (Score: 0.701118)



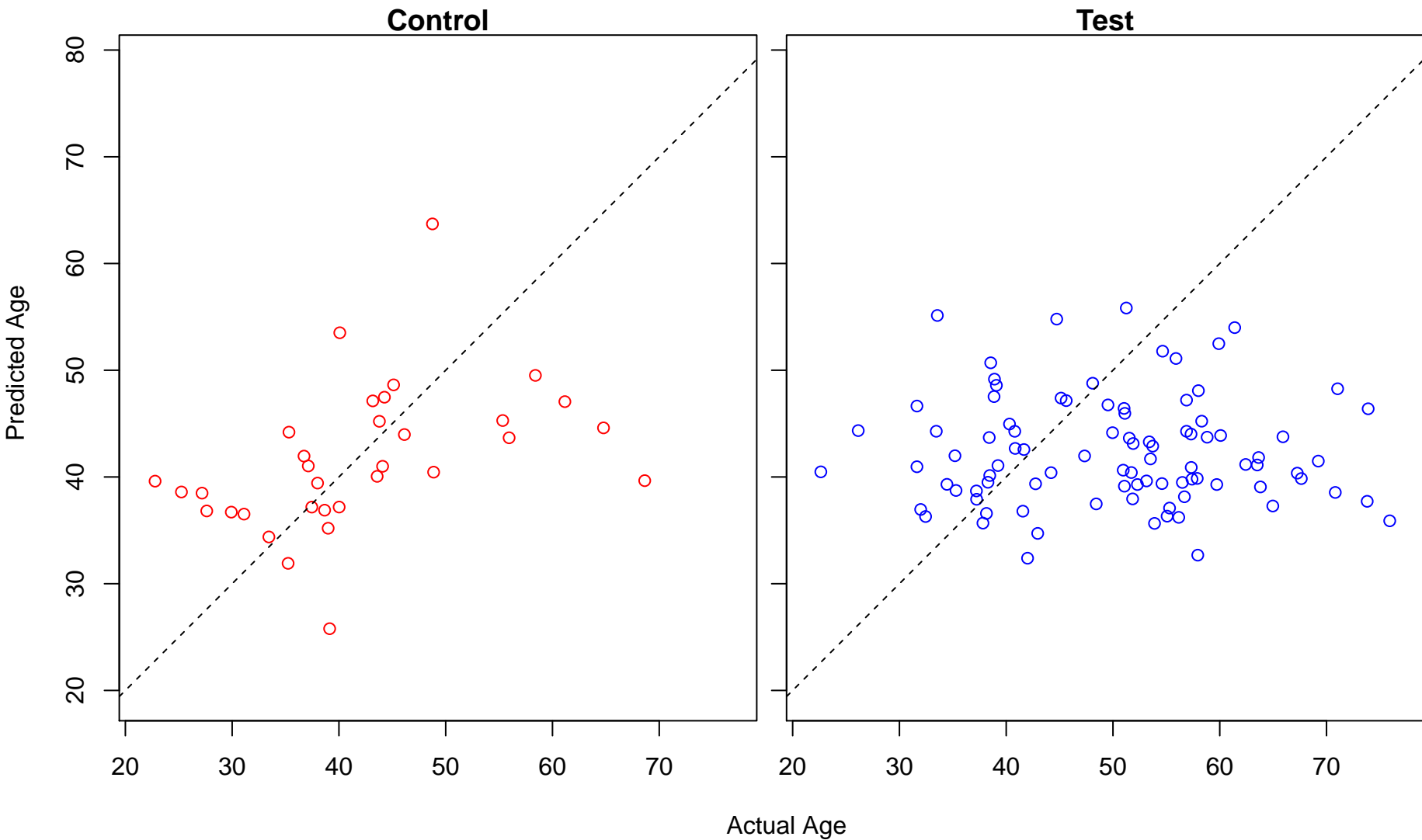
regulation of natural killer cell activation (Score: 0.700387)



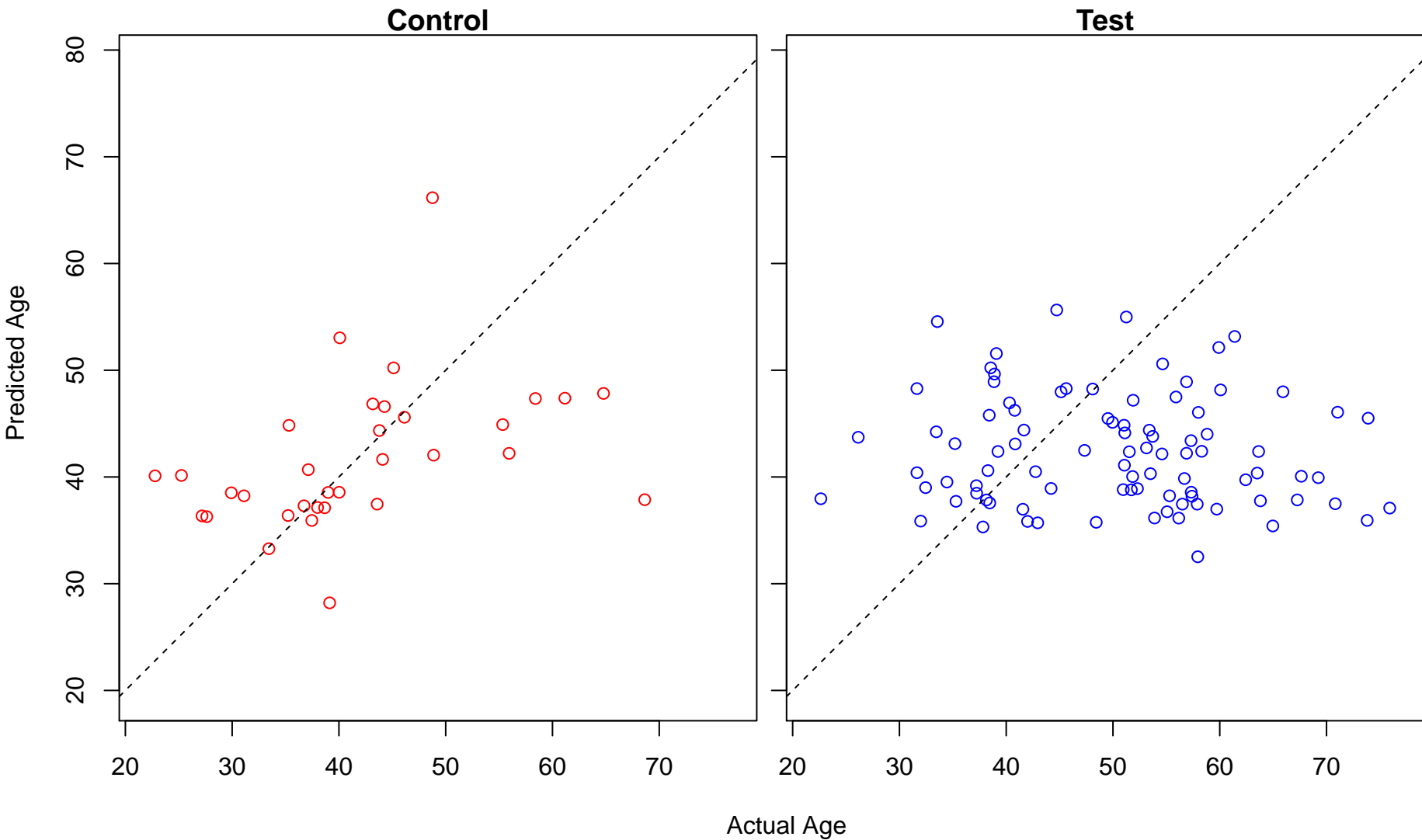
modification-dependent macromolecule catabolic process (Score: 0.700088)



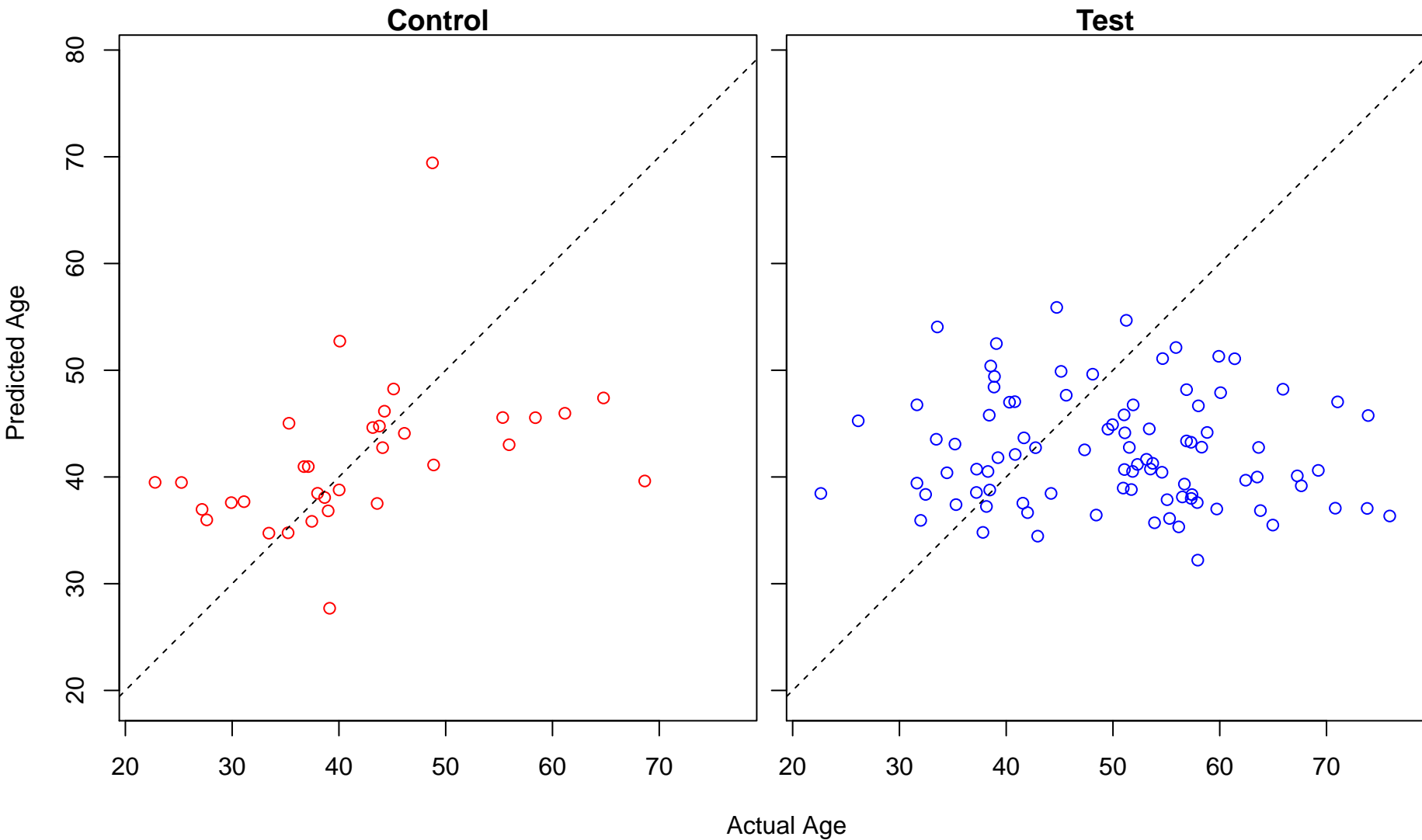
negative regulation of translation (Score: 0.700086)



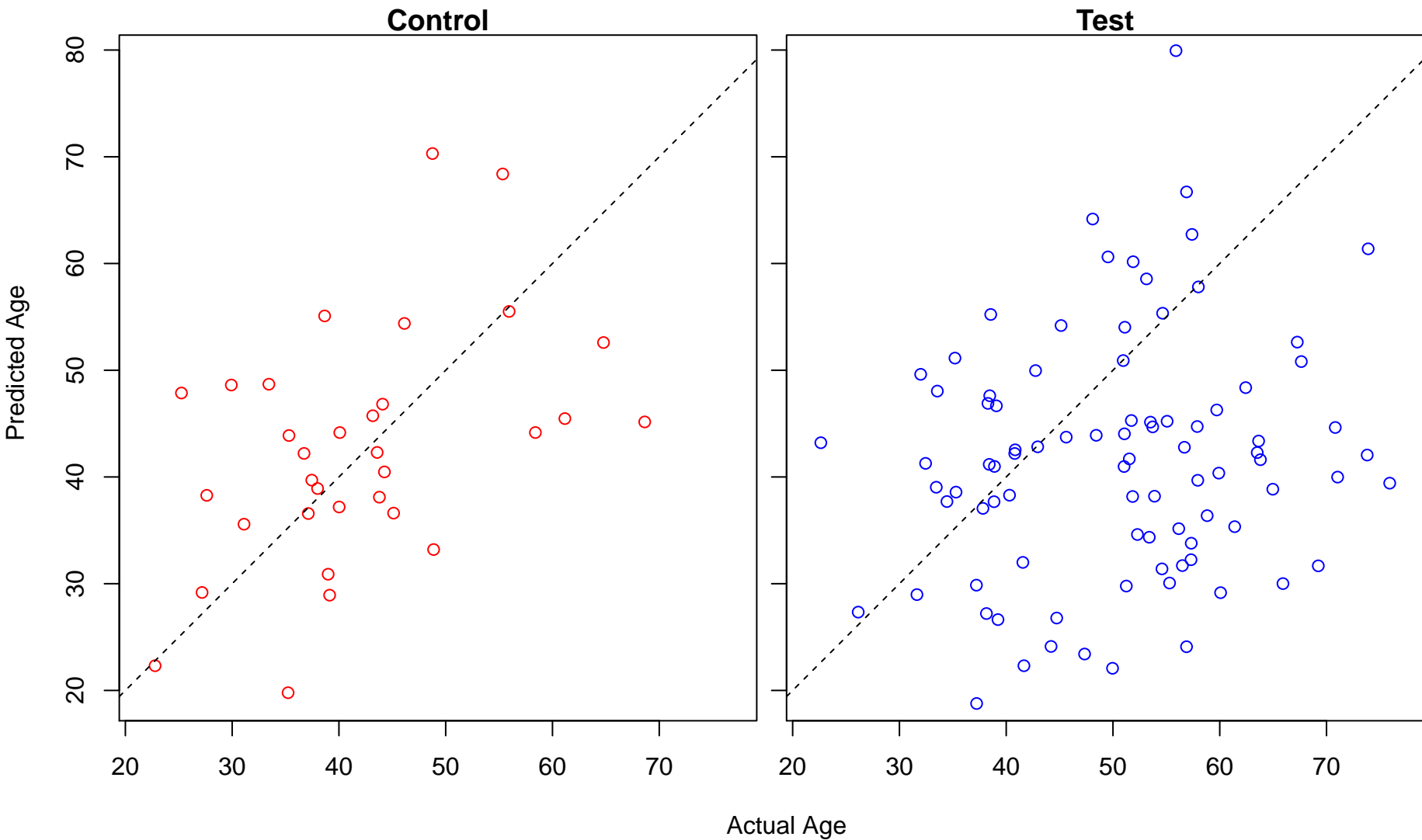
modification-dependent protein catabolic process (Score: 0.700074)



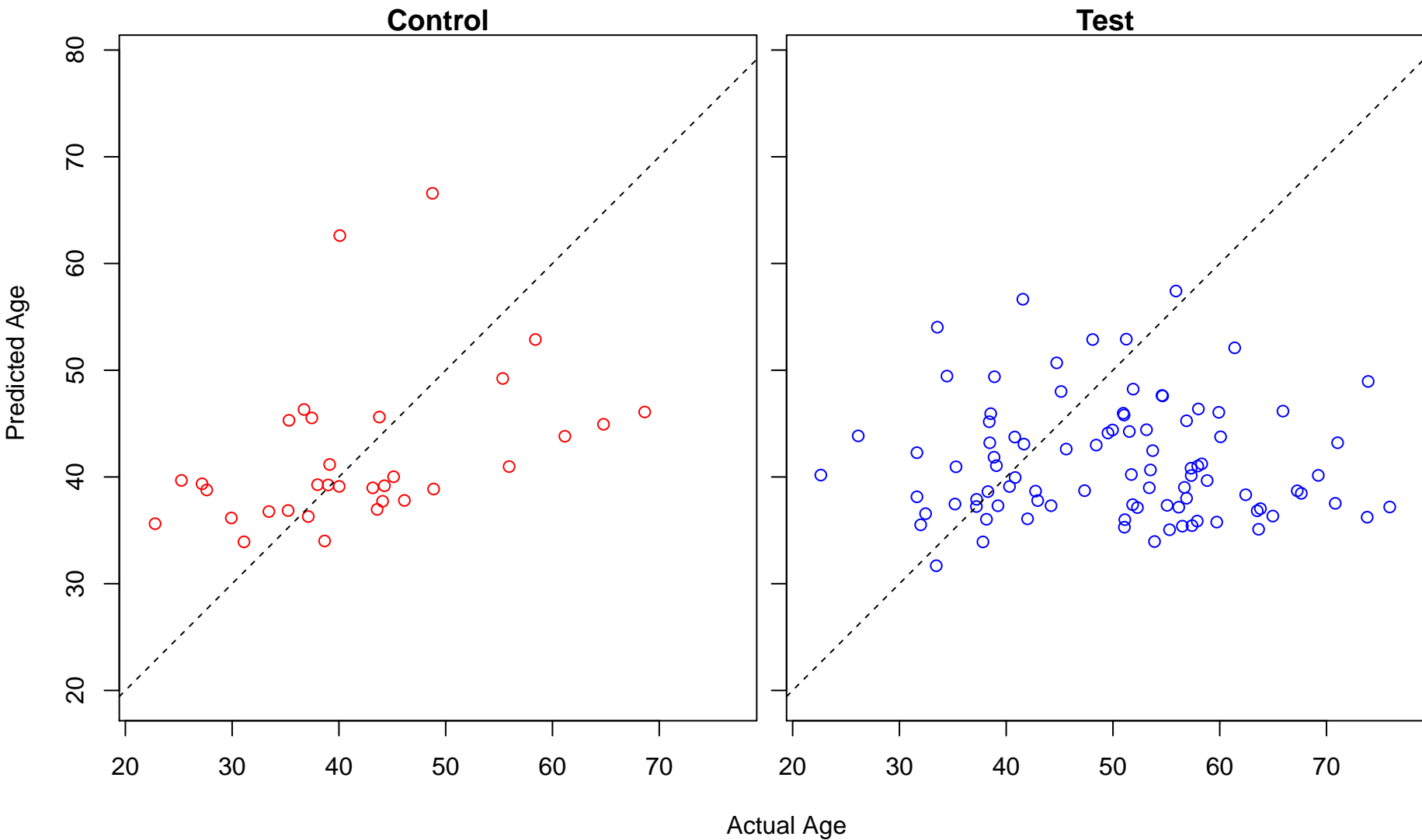
regulation of primary metabolic process (Score: 0.700011)



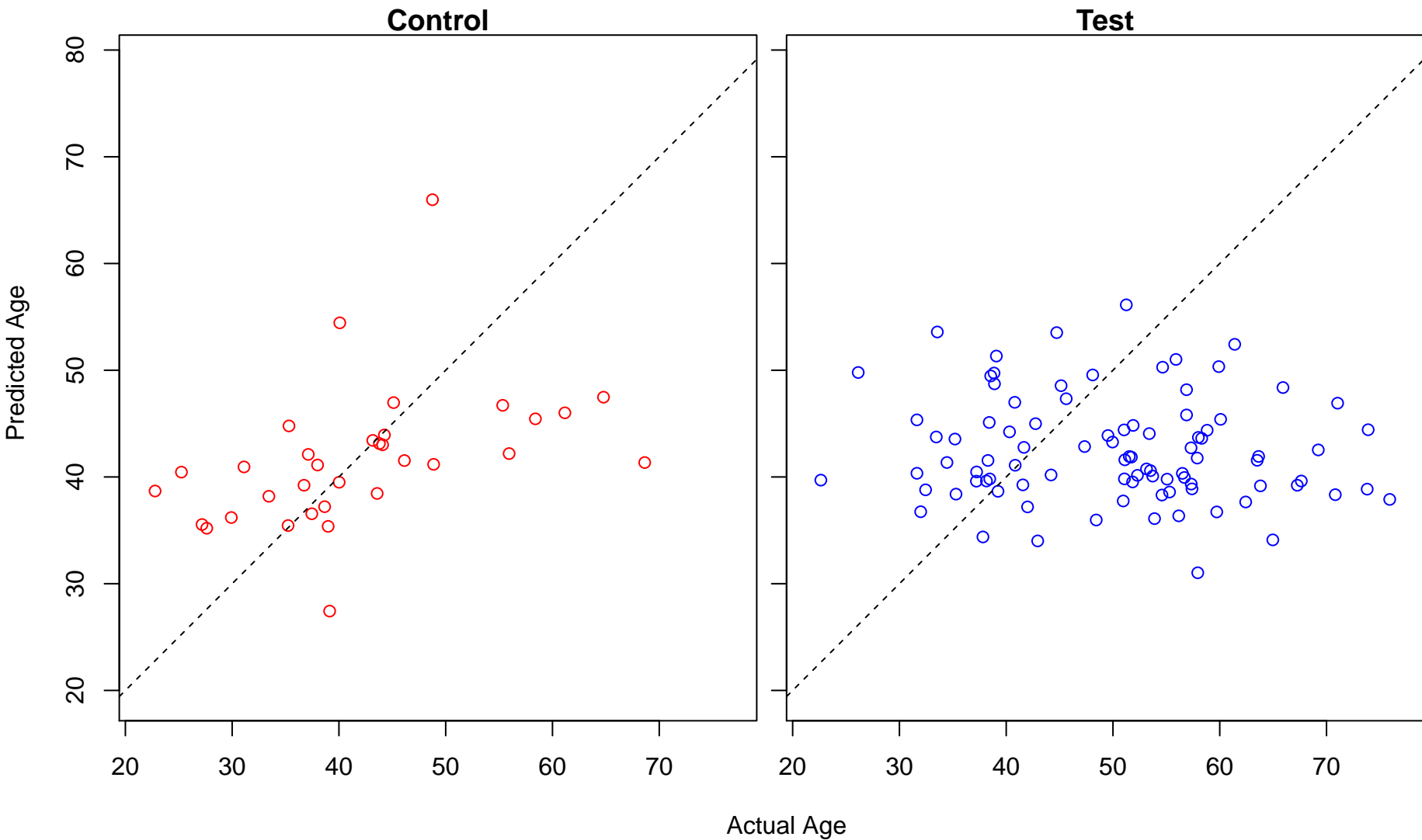
mesenchymal cell differentiation (Score: 0.699829)



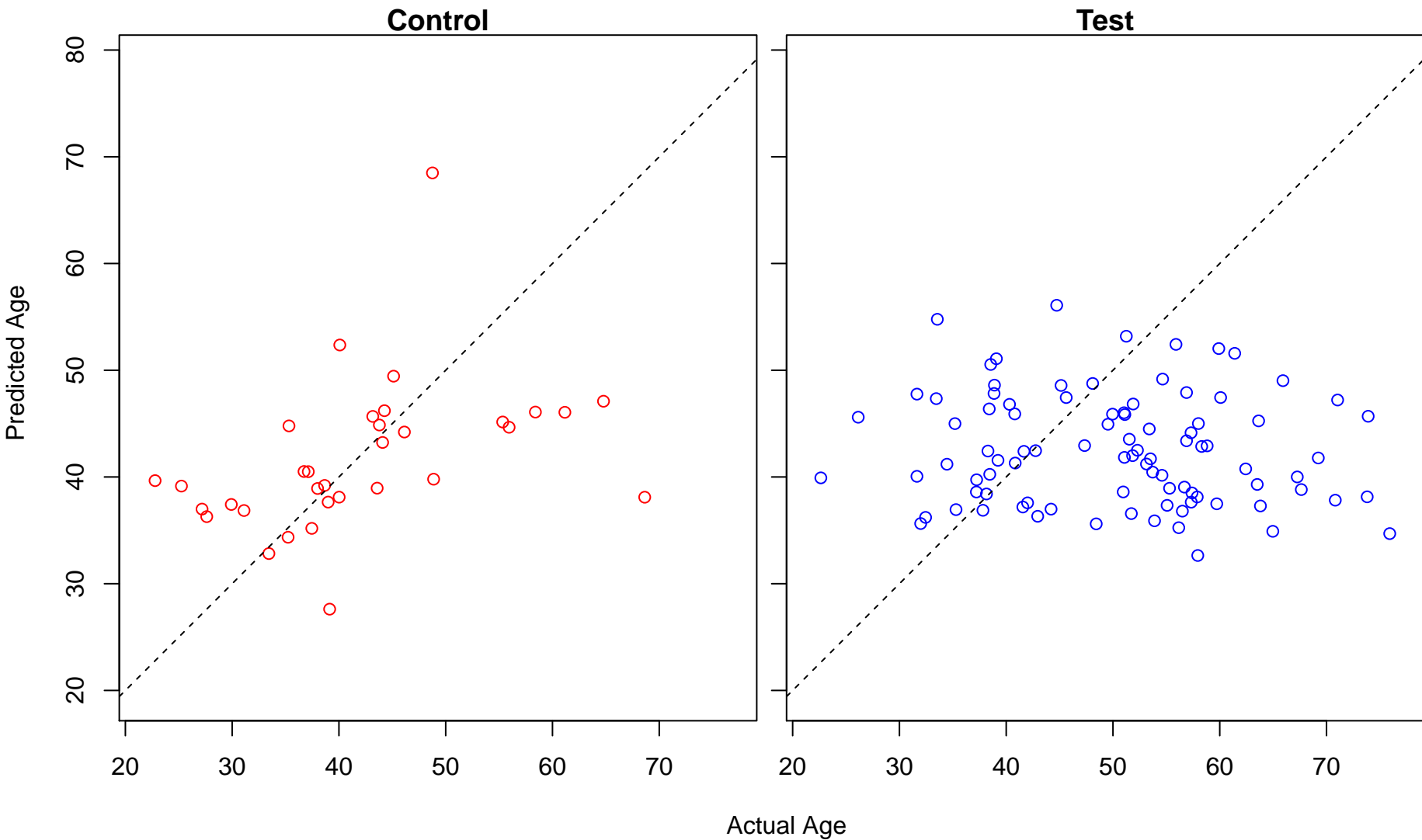
nucleus localization (Score: 0.699539)



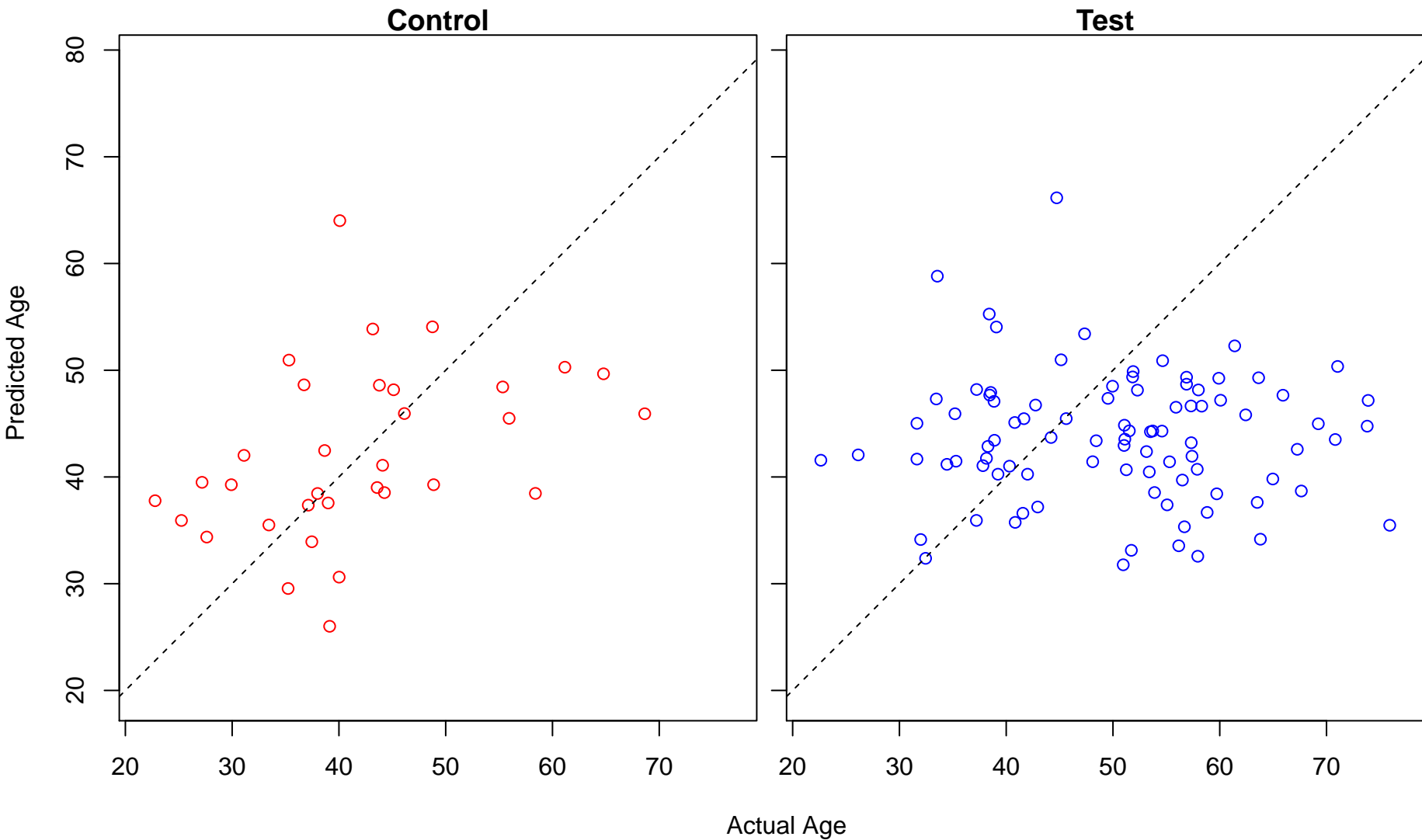
negative regulation of transcription from RNA polymerase II promoter (Score: 0.699134)



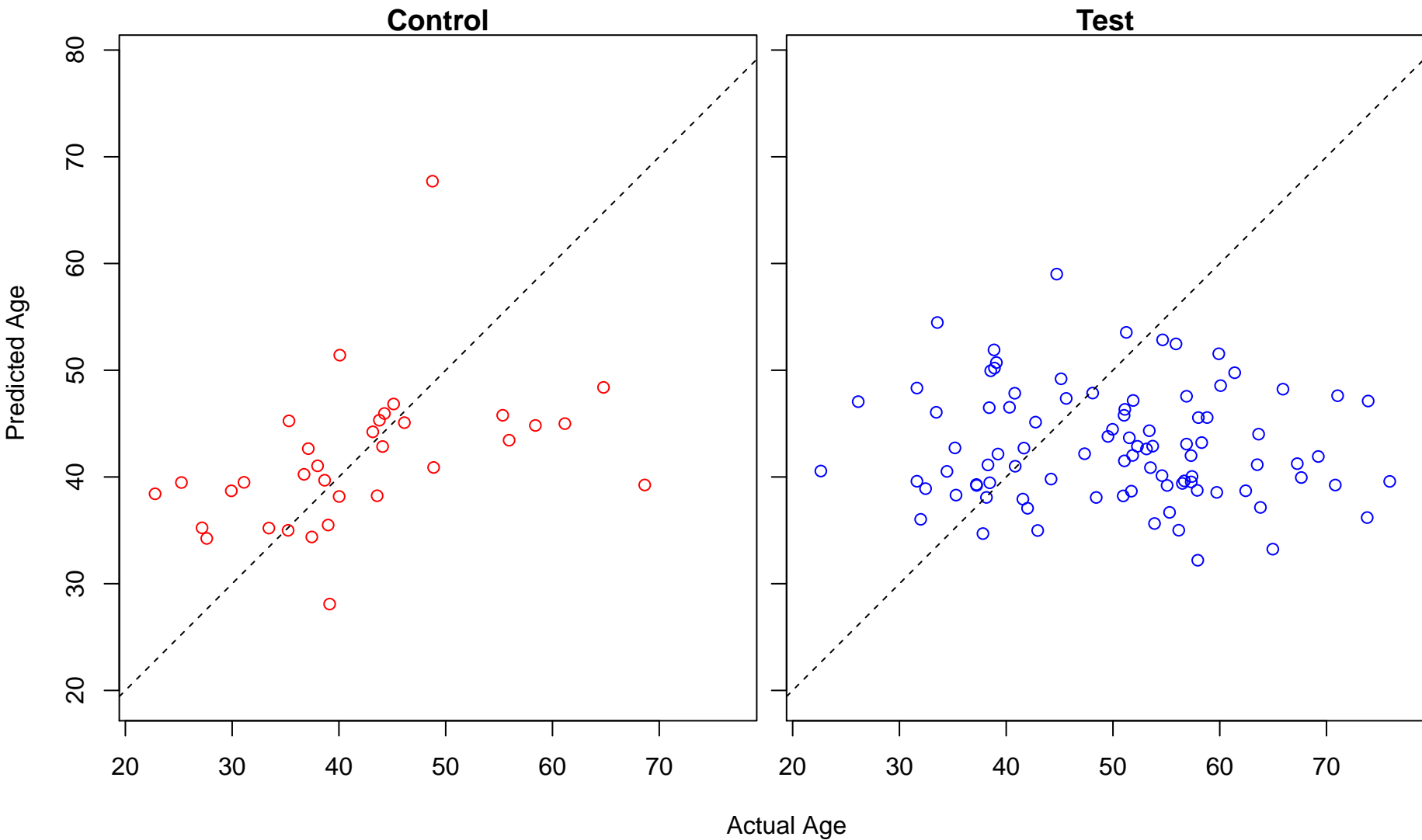
single-organism biosynthetic process (Score: 0.698903)



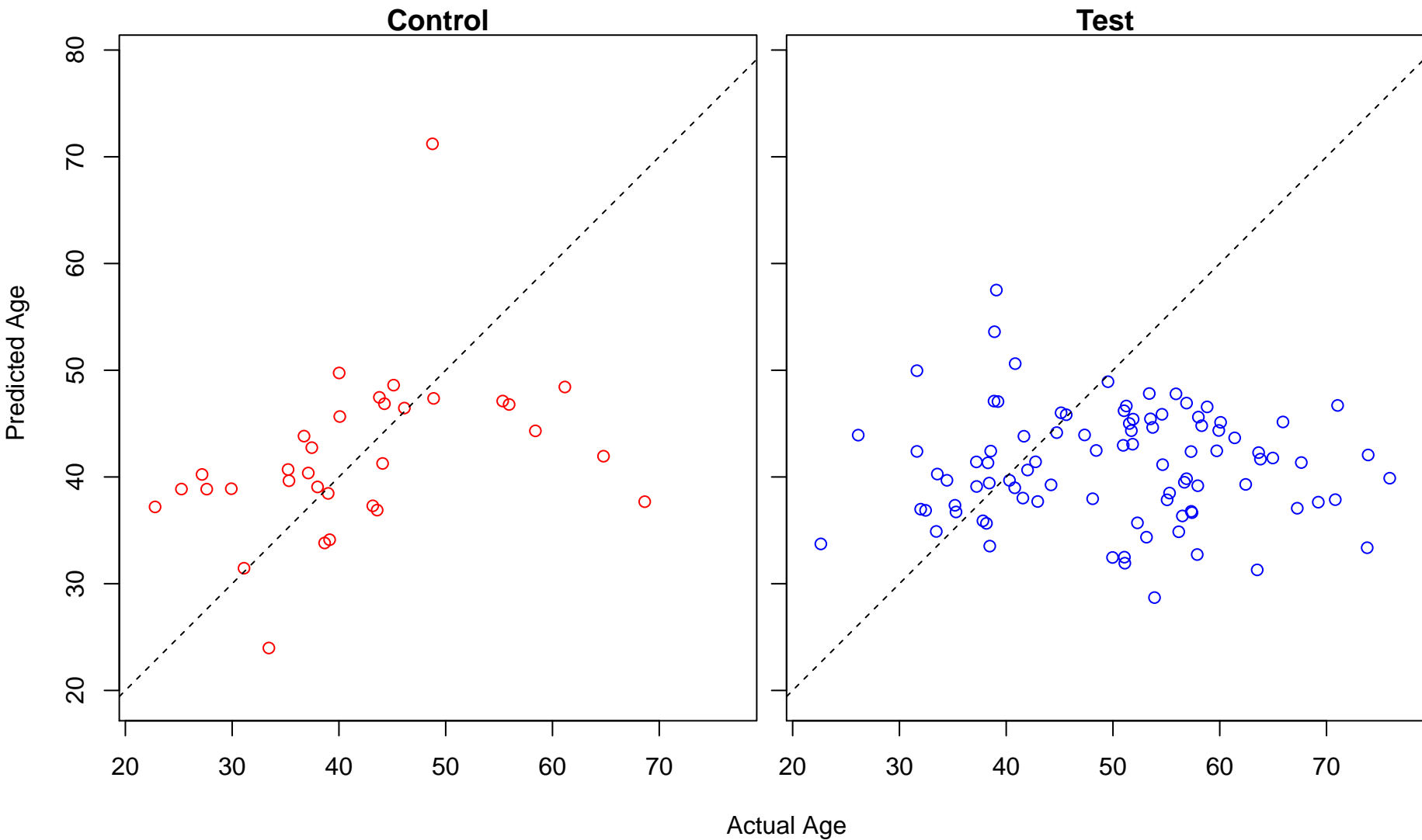
regulation of lysosomal lumen pH (Score: 0.698581)



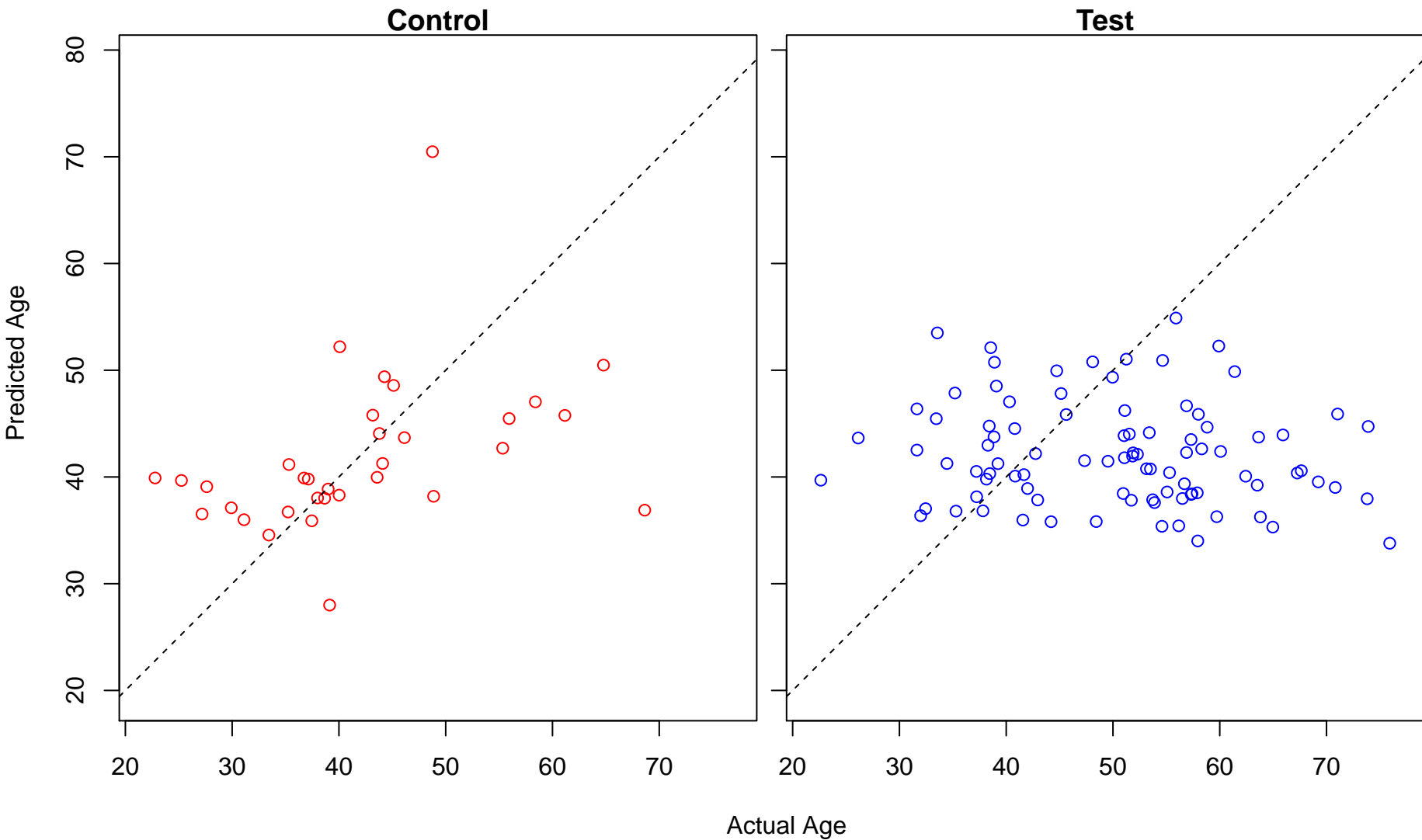
negative regulation of cell communication (Score: 0.698529)



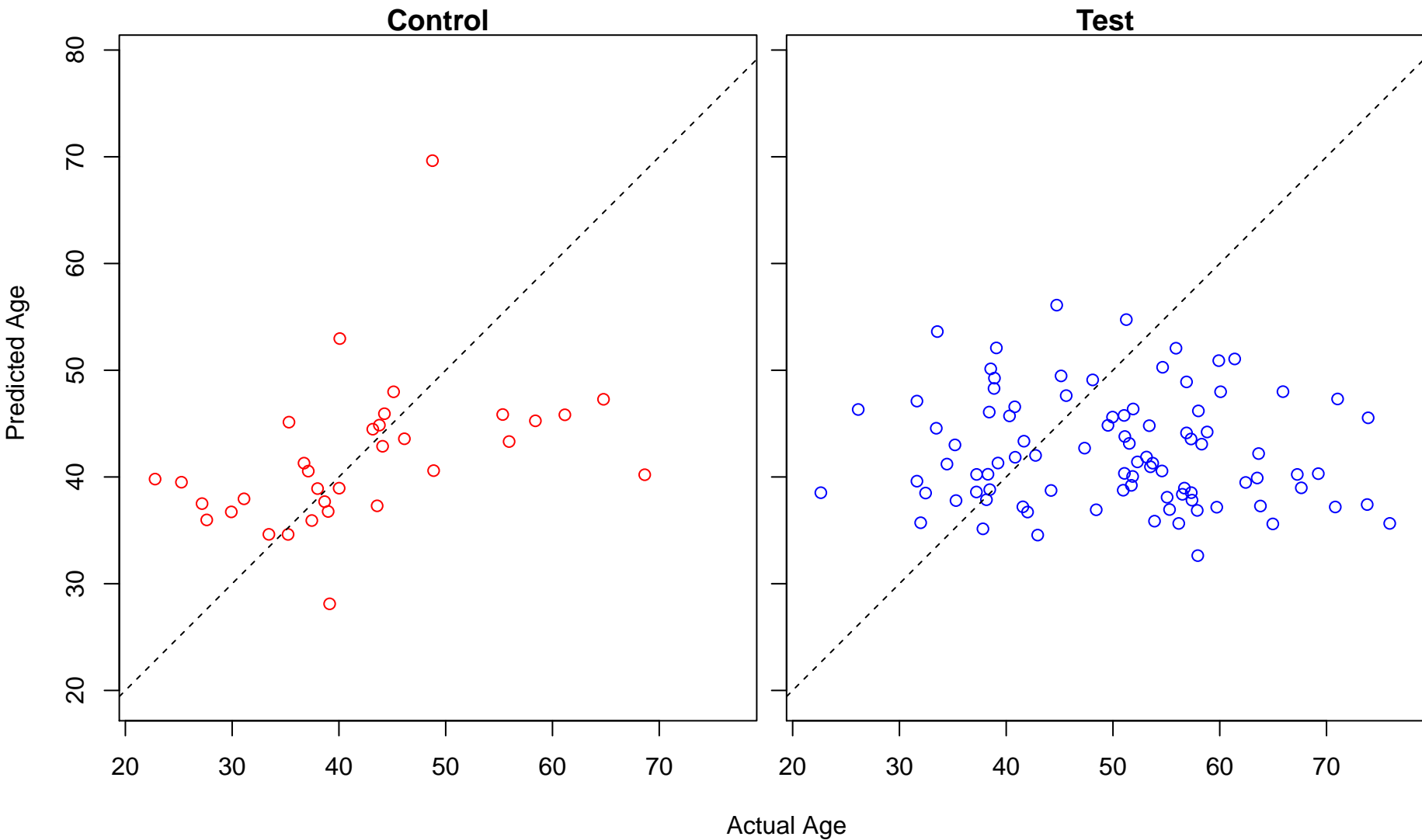
negative regulation of MDA-5 signaling pathway (Score: 0.697887)



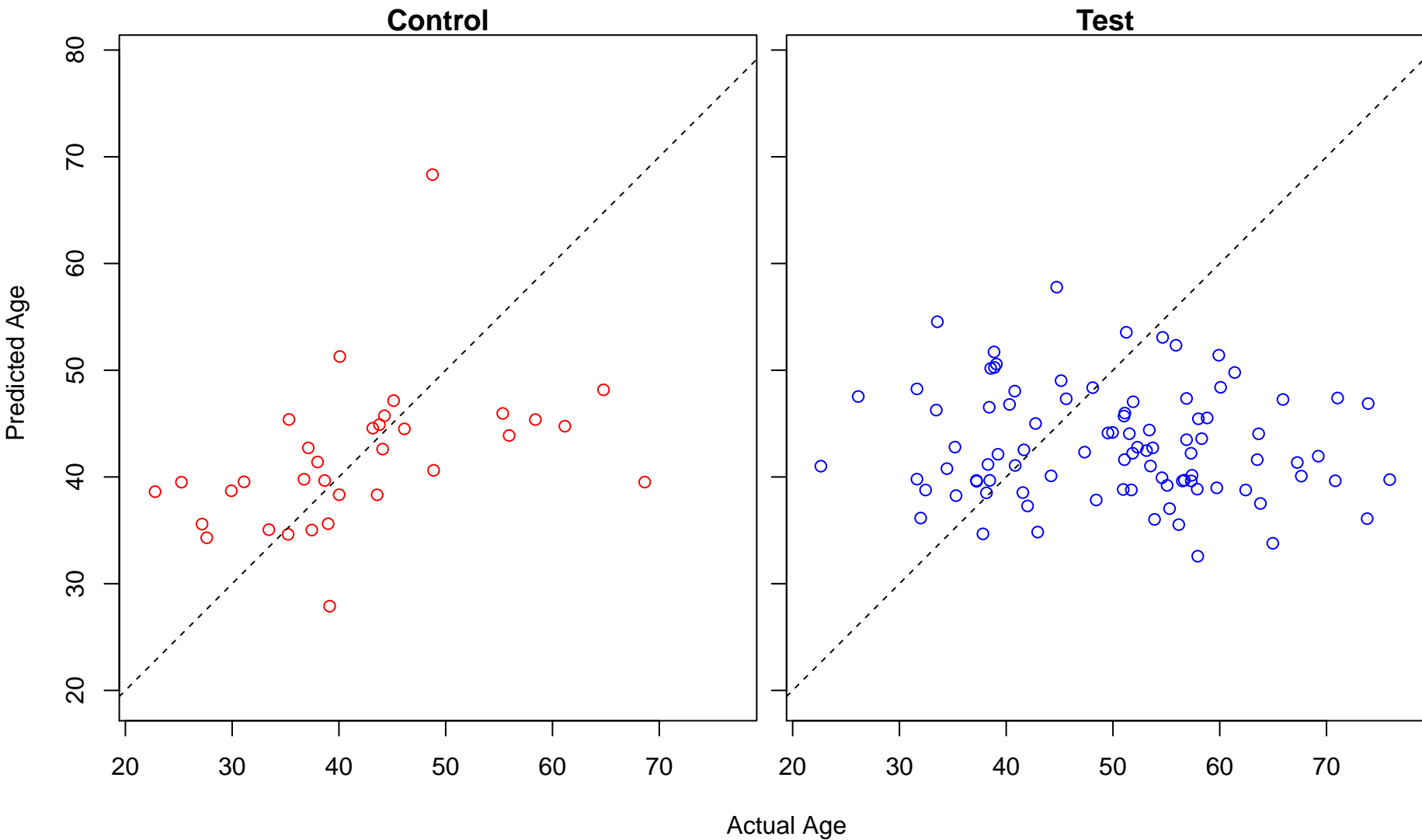
small molecule biosynthetic process (Score: 0.697484)



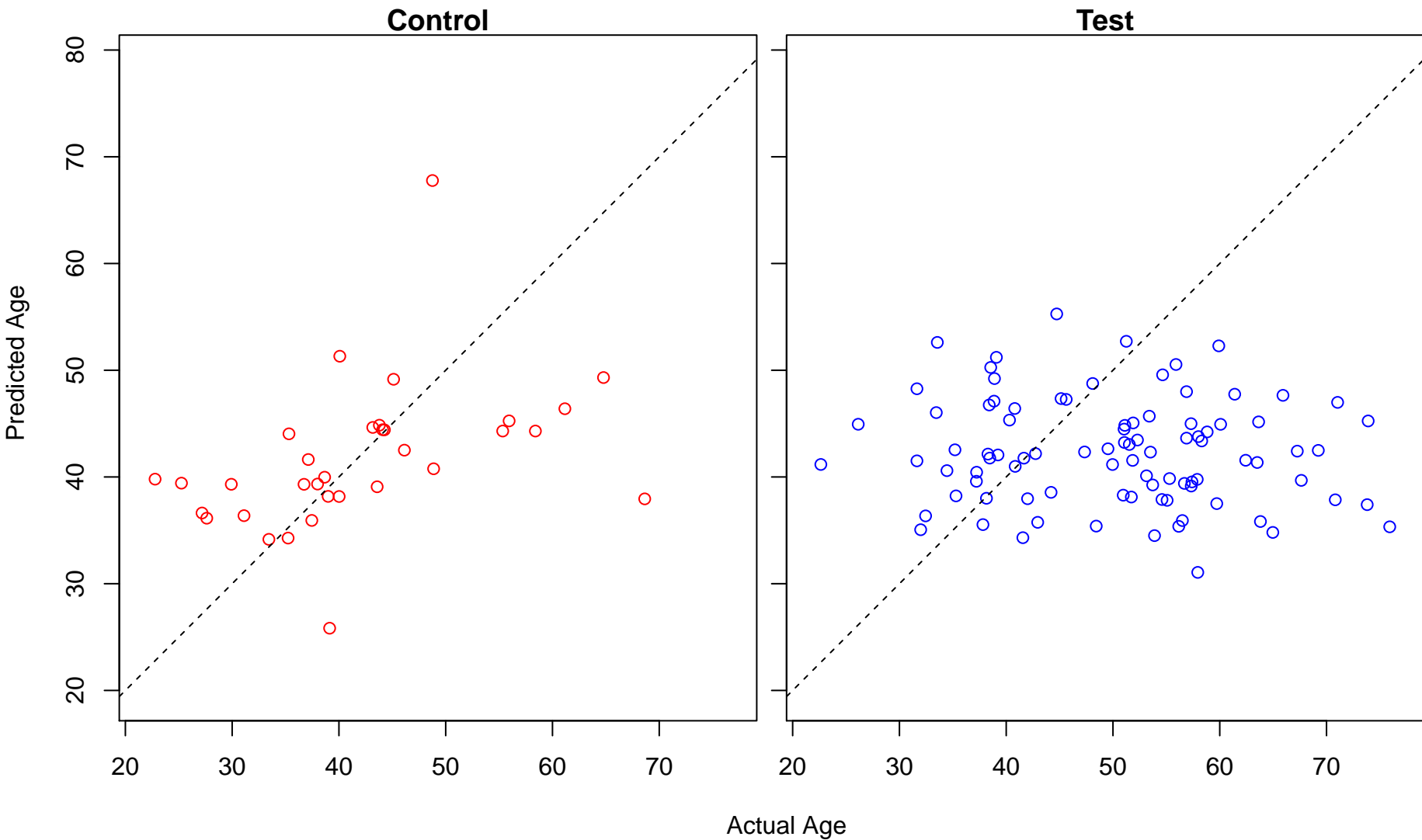
regulation of cellular biosynthetic process (Score: 0.697334)



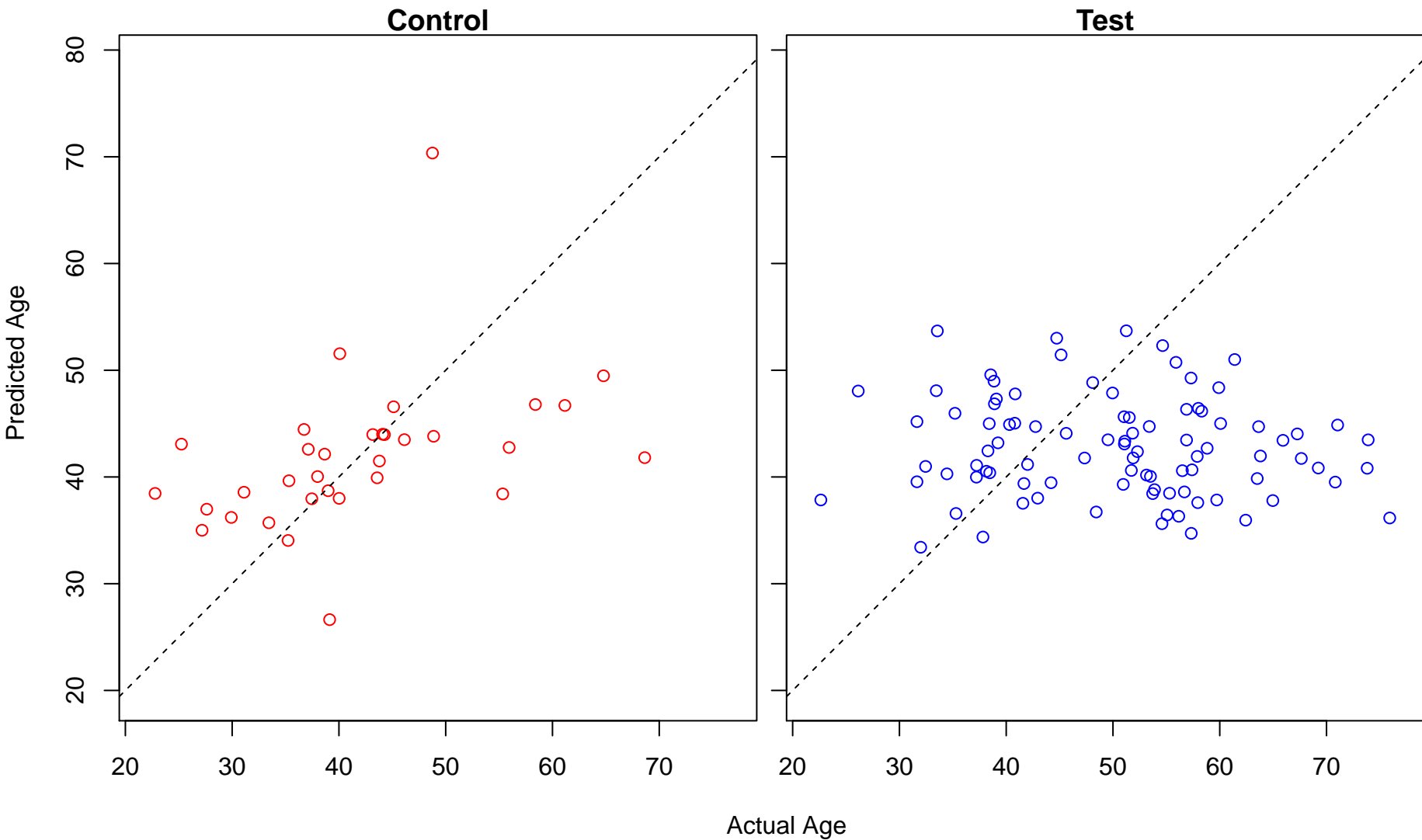
negative regulation of signal transduction (Score: 0.697277)



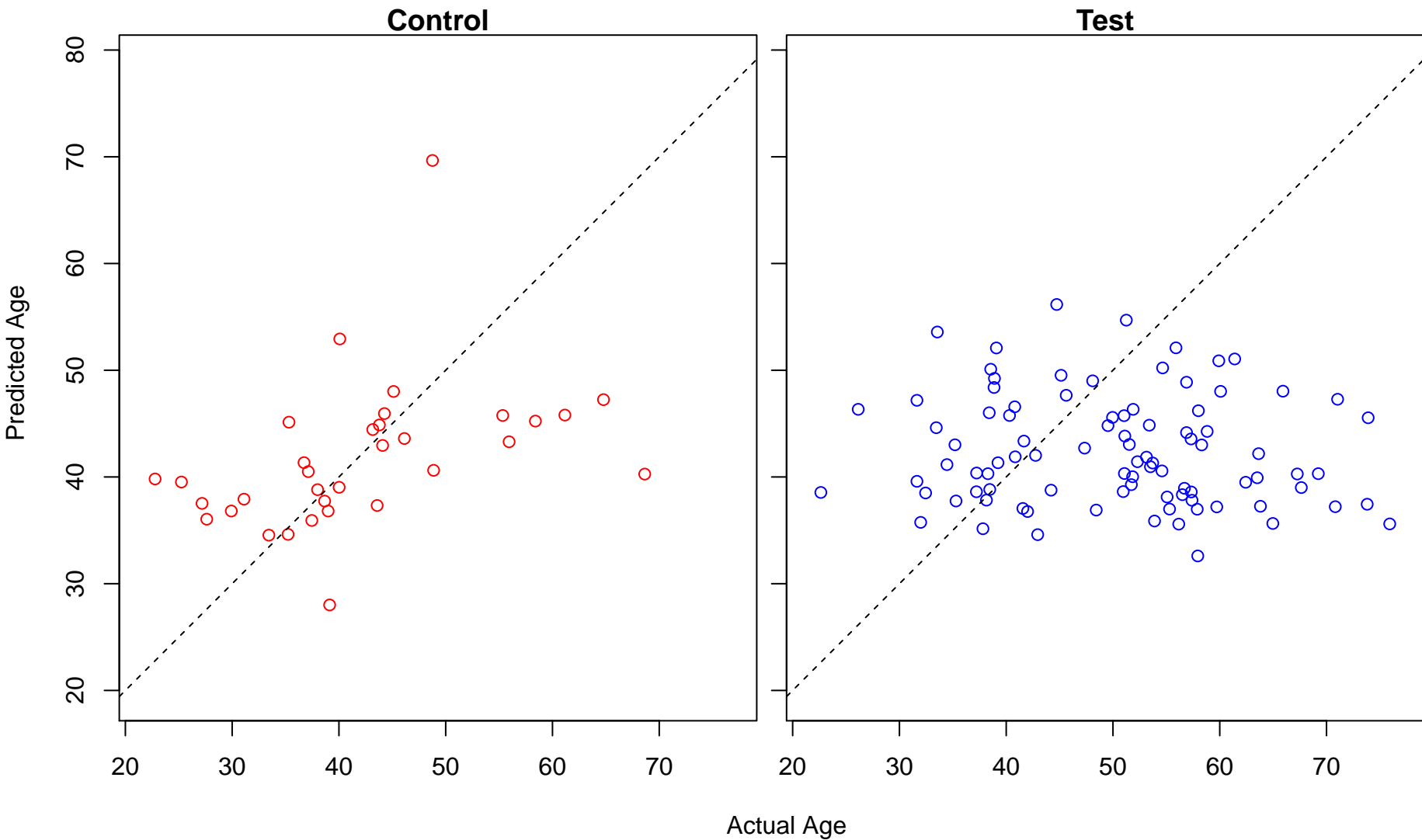
cellular lipid metabolic process (Score: 0.696997)



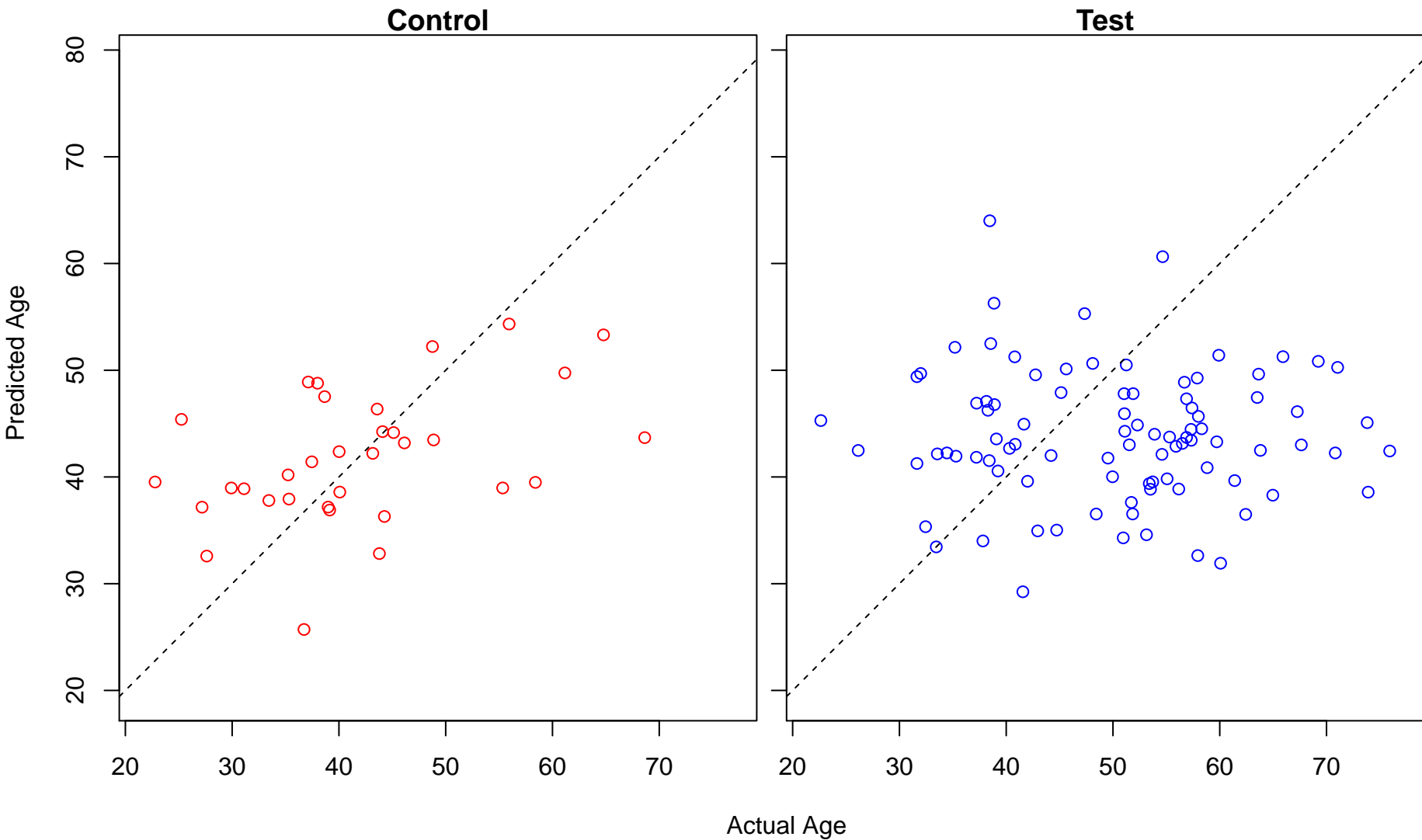
positive regulation of neurogenesis (Score: 0.695743)



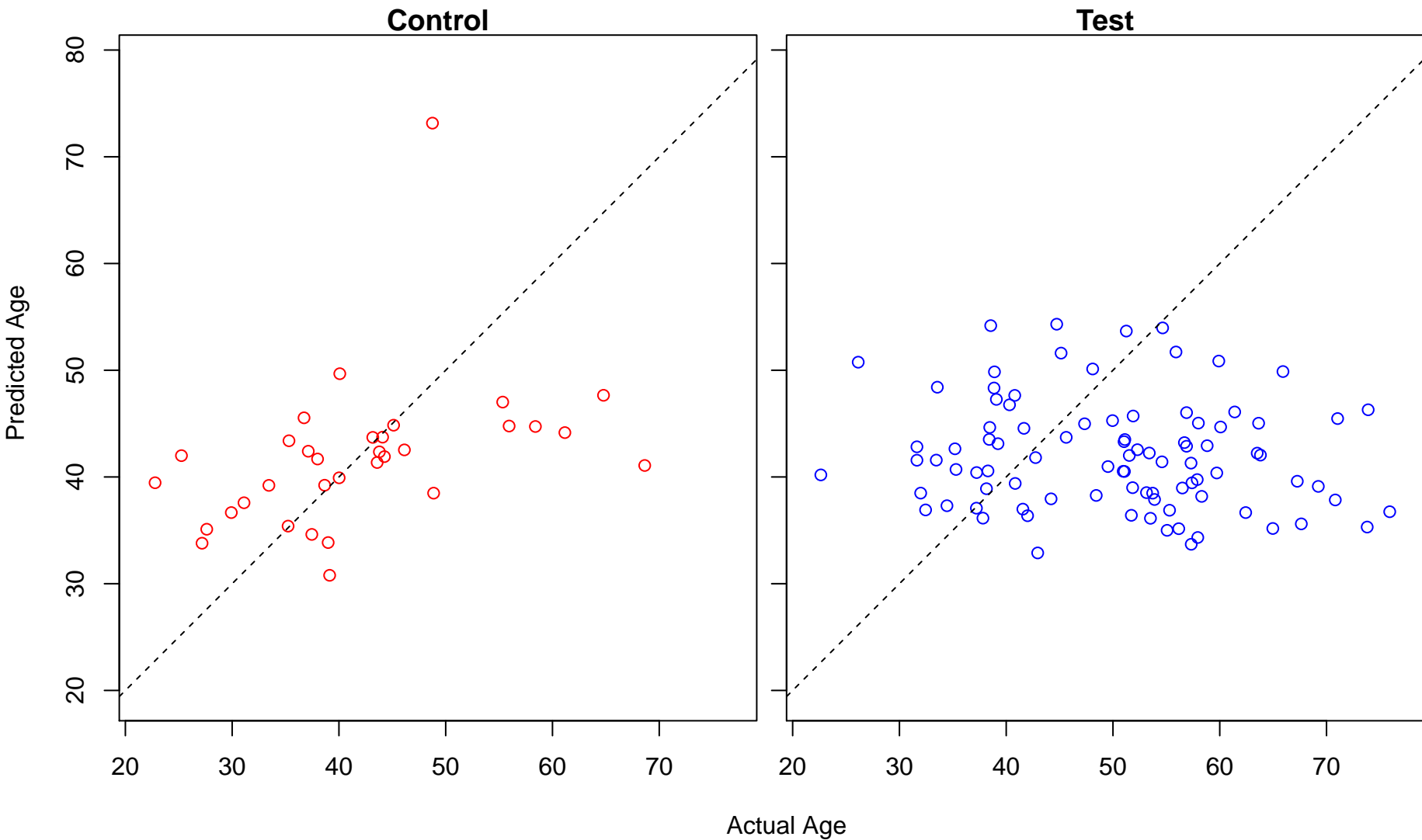
regulation of biosynthetic process (Score: 0.695705)



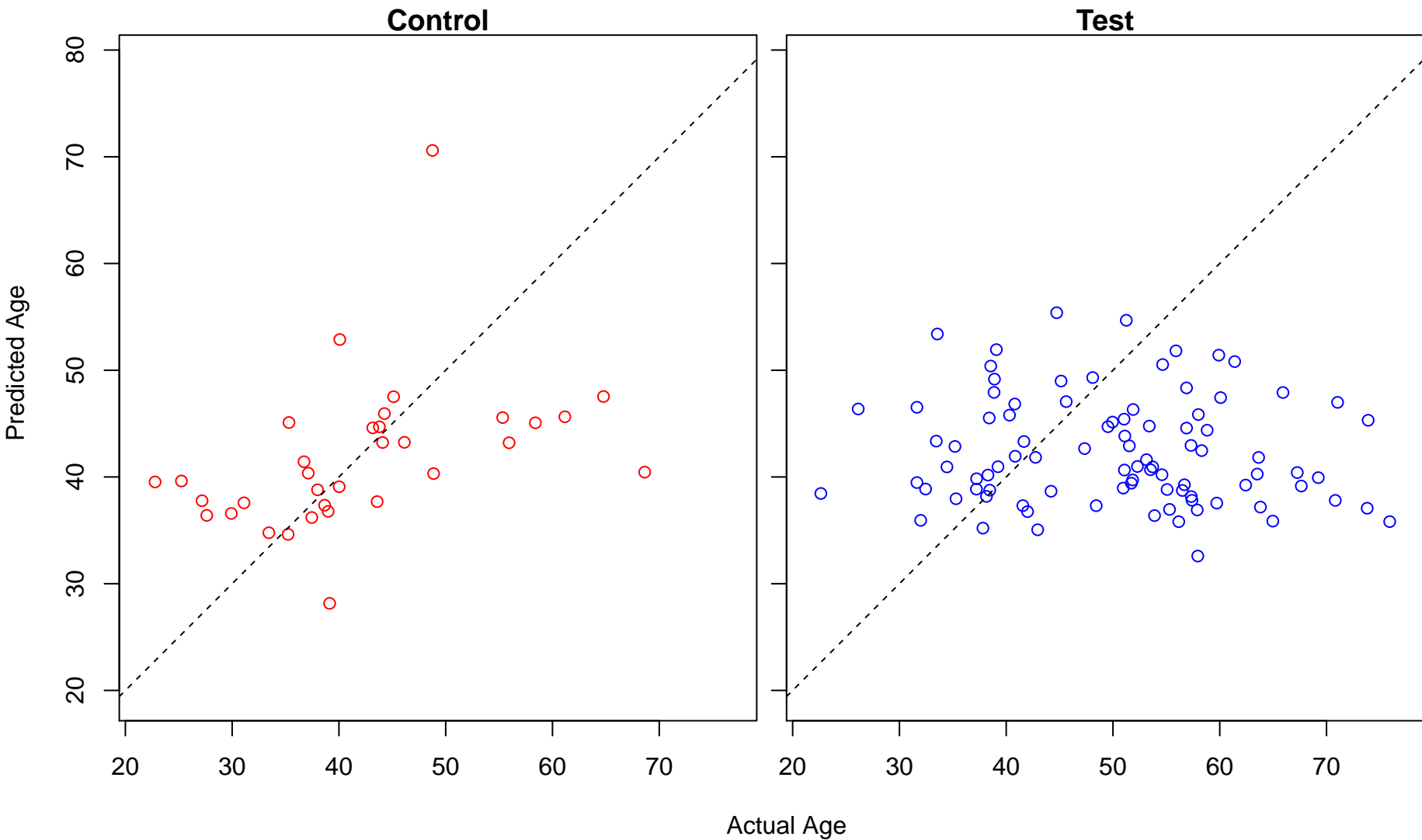
platelet activating factor metabolic process (Score: 0.695184)



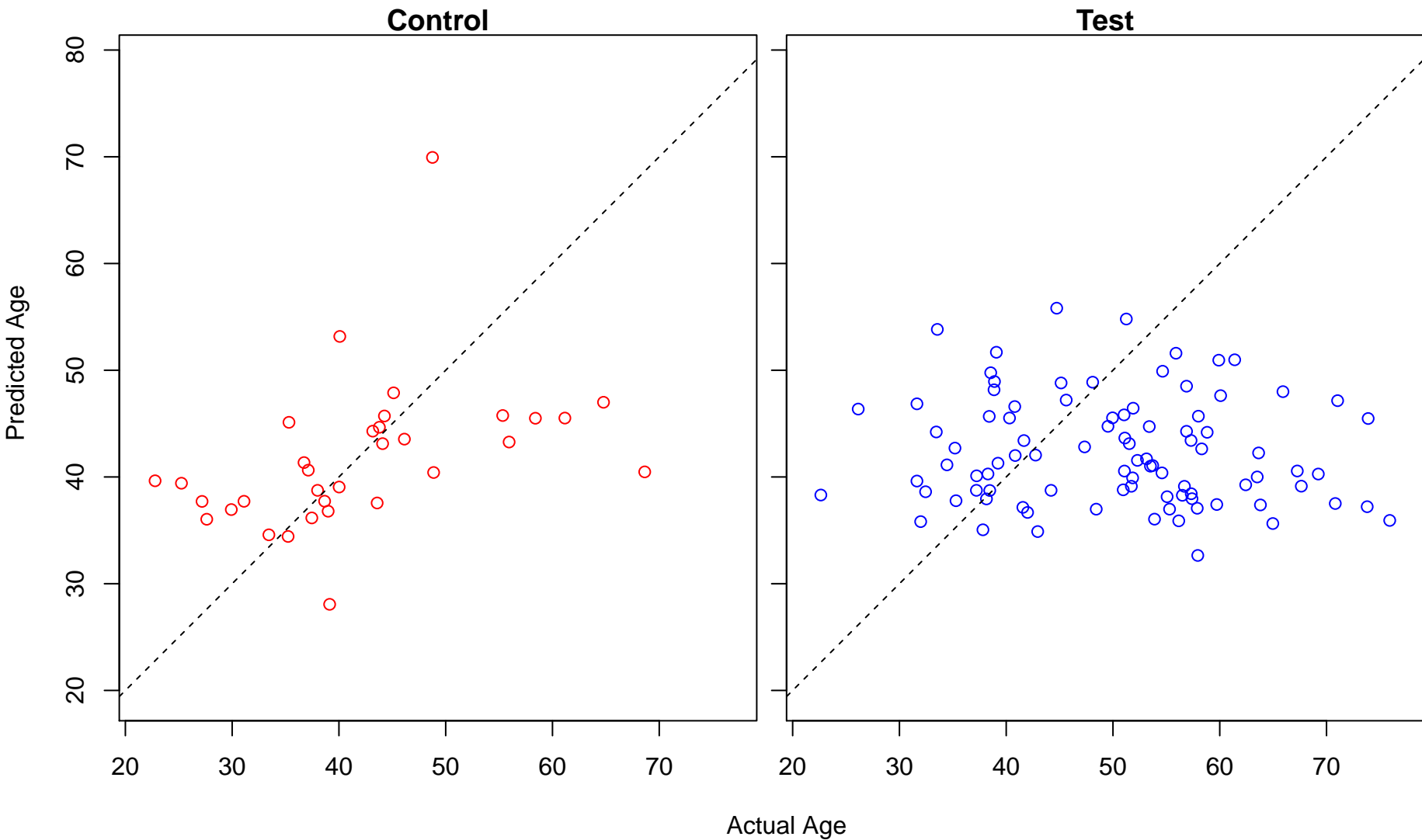
immune system development (Score: 0.694949)



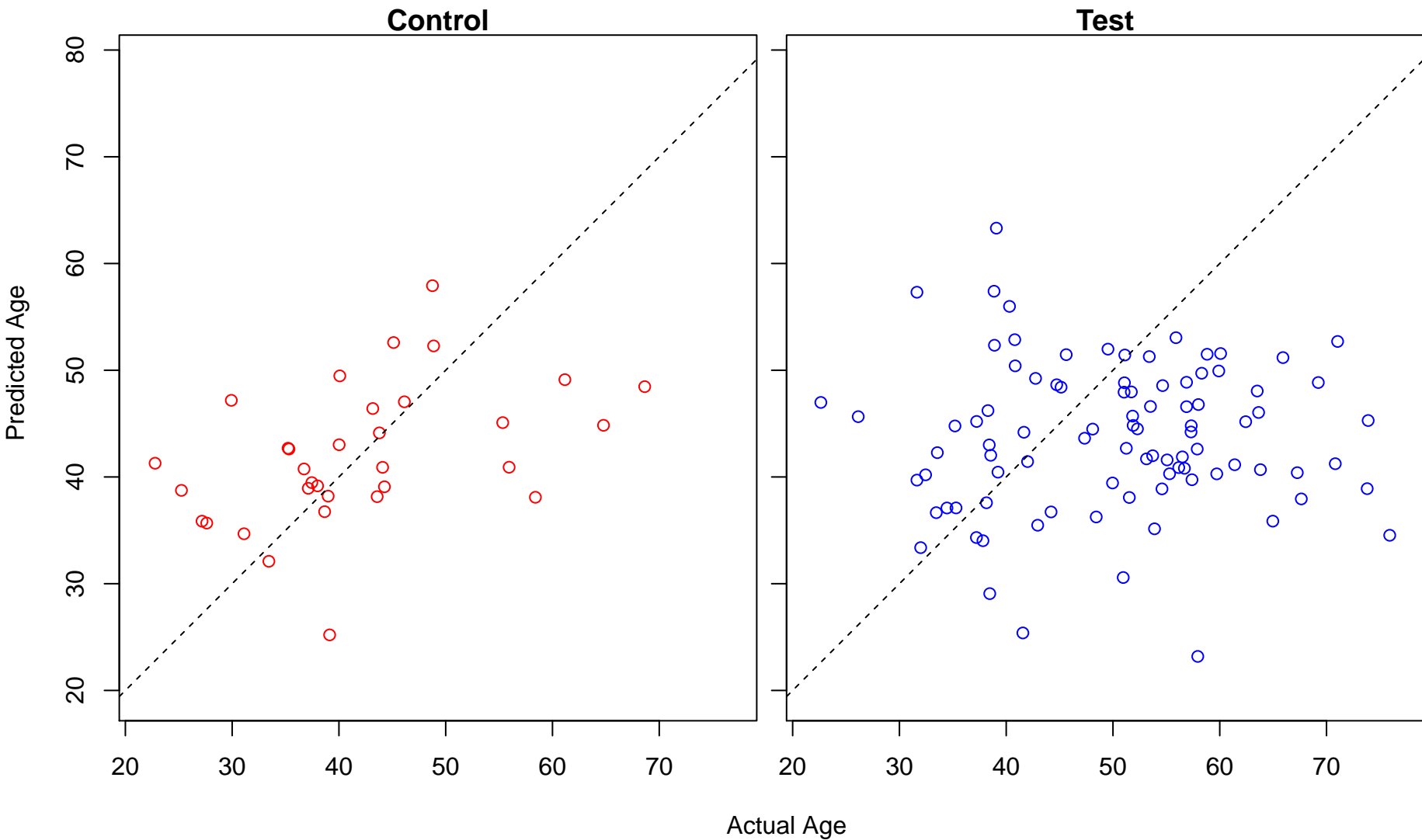
regulation of RNA metabolic process (Score: 0.693598)



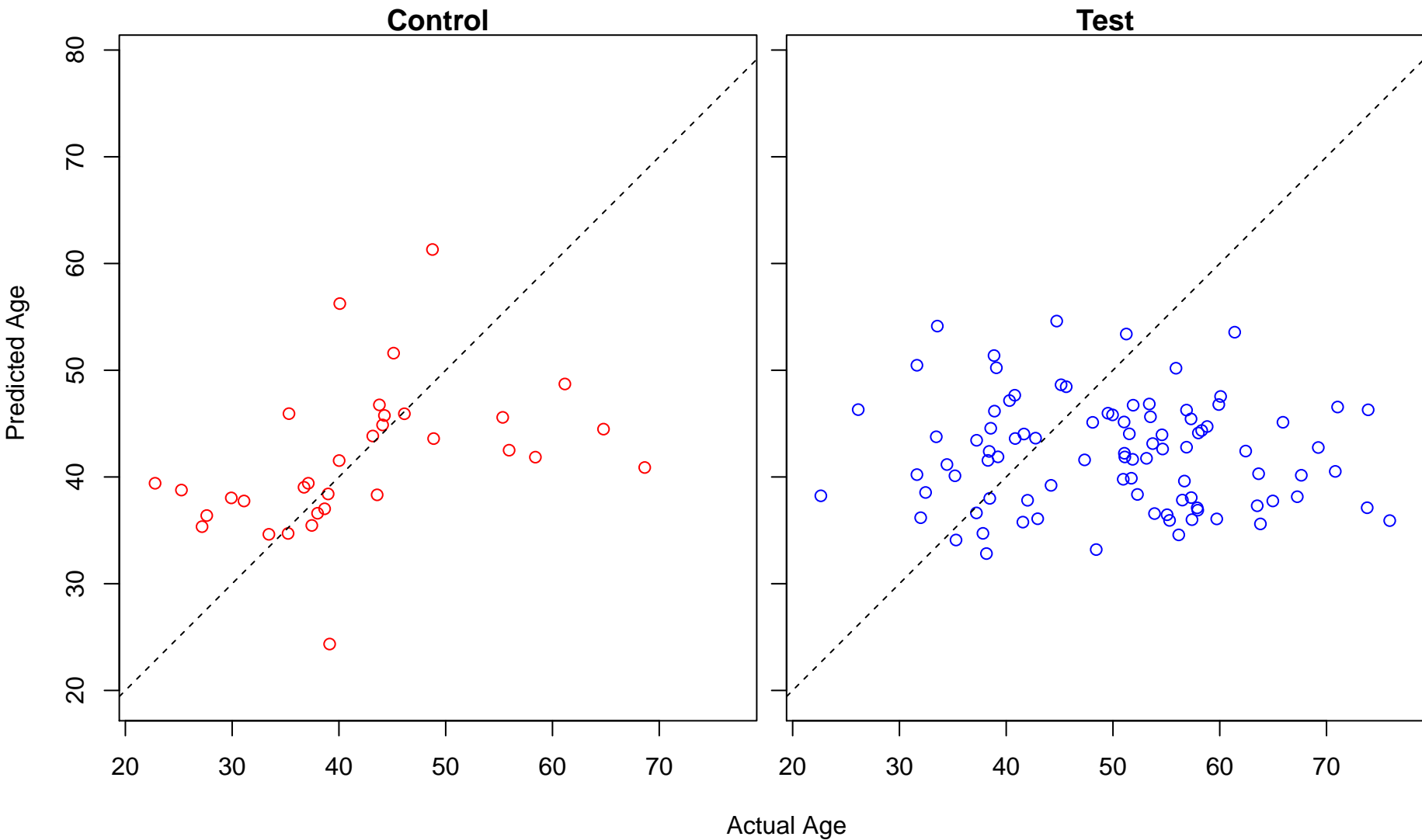
regulation of nitrogen compound metabolic process (Score: 0.693397)



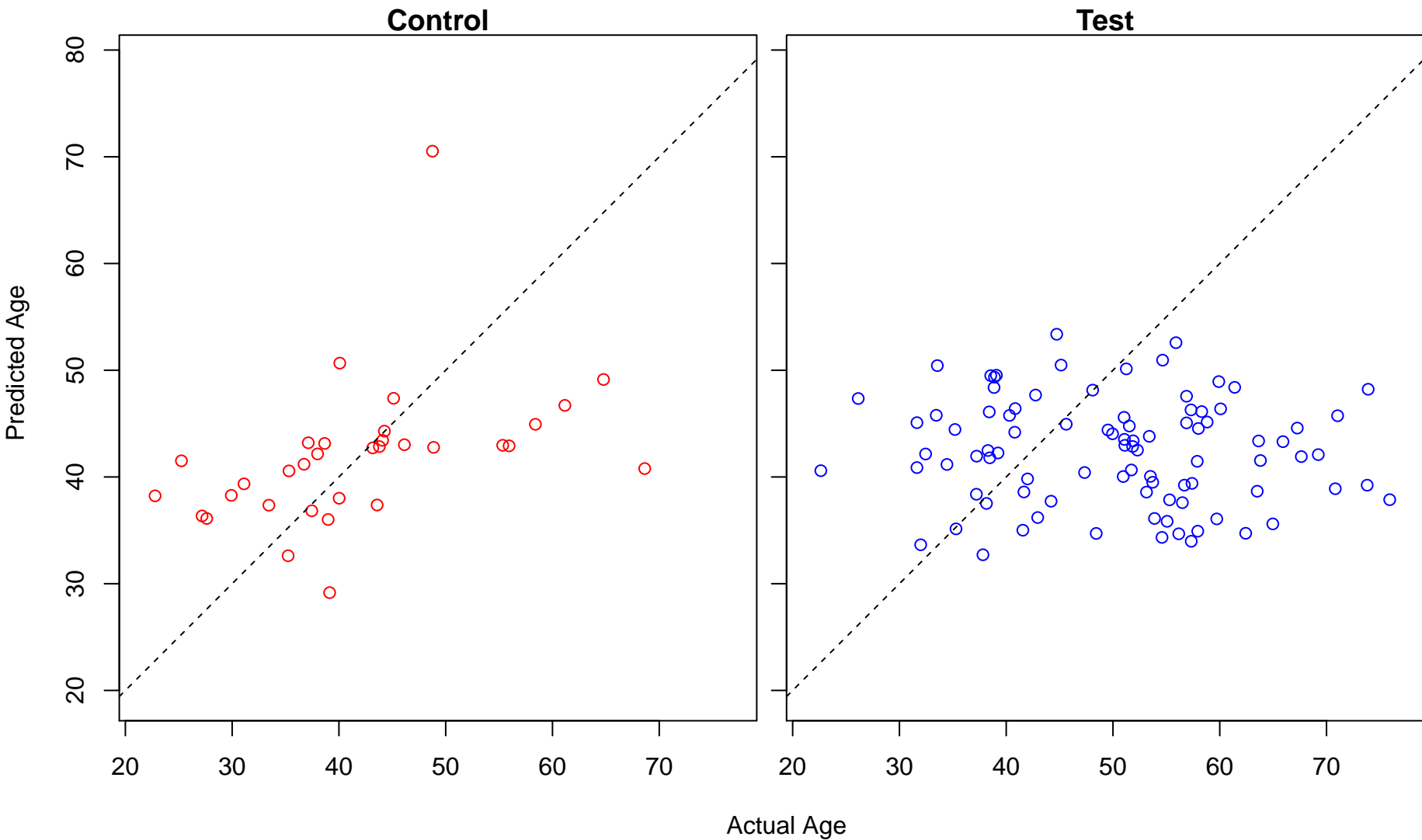
convergent extension involved in gastrulation (Score: 0.693253)



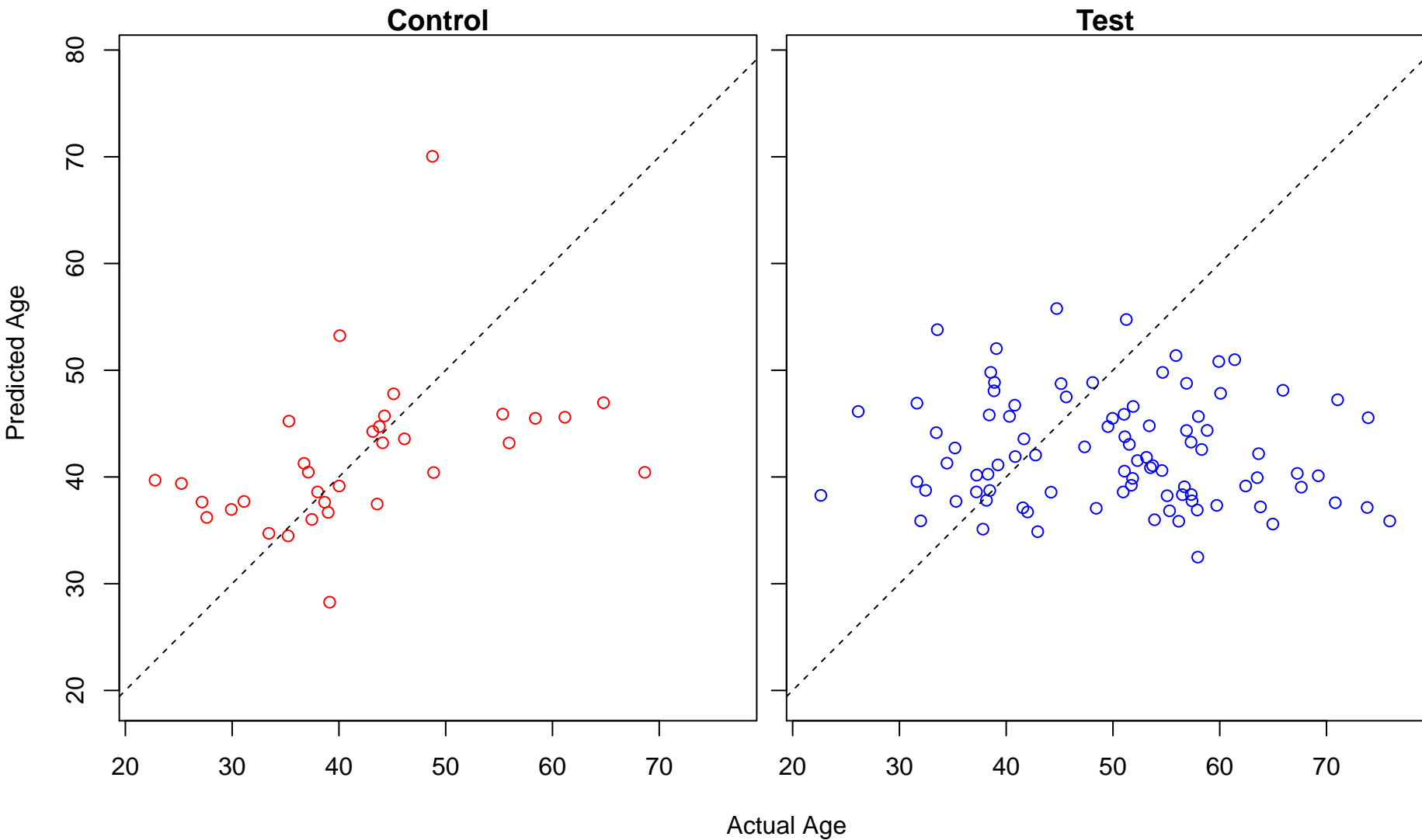
anatomical structure homeostasis (Score: 0.693168)



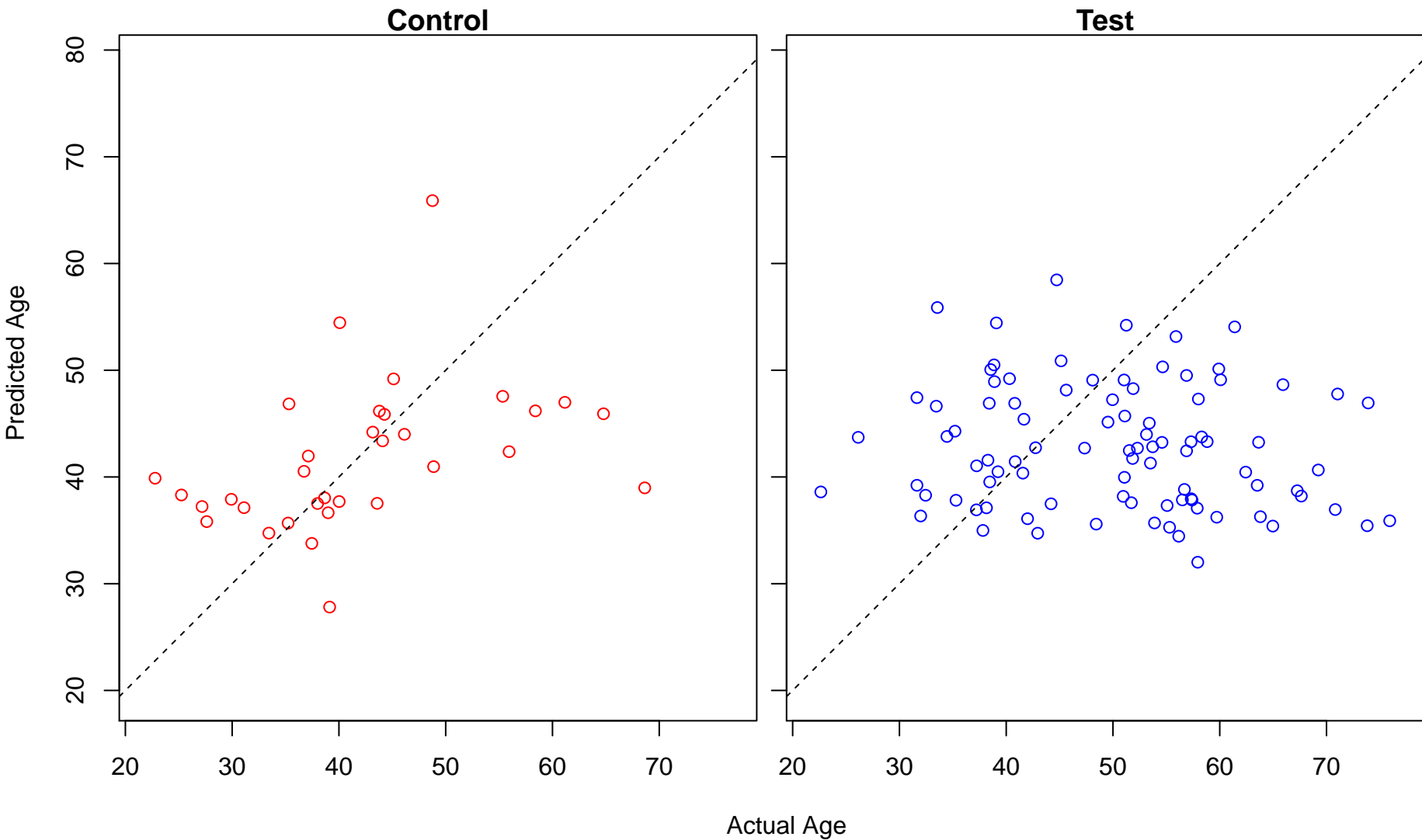
positive regulation of cell development (Score: 0.693124)



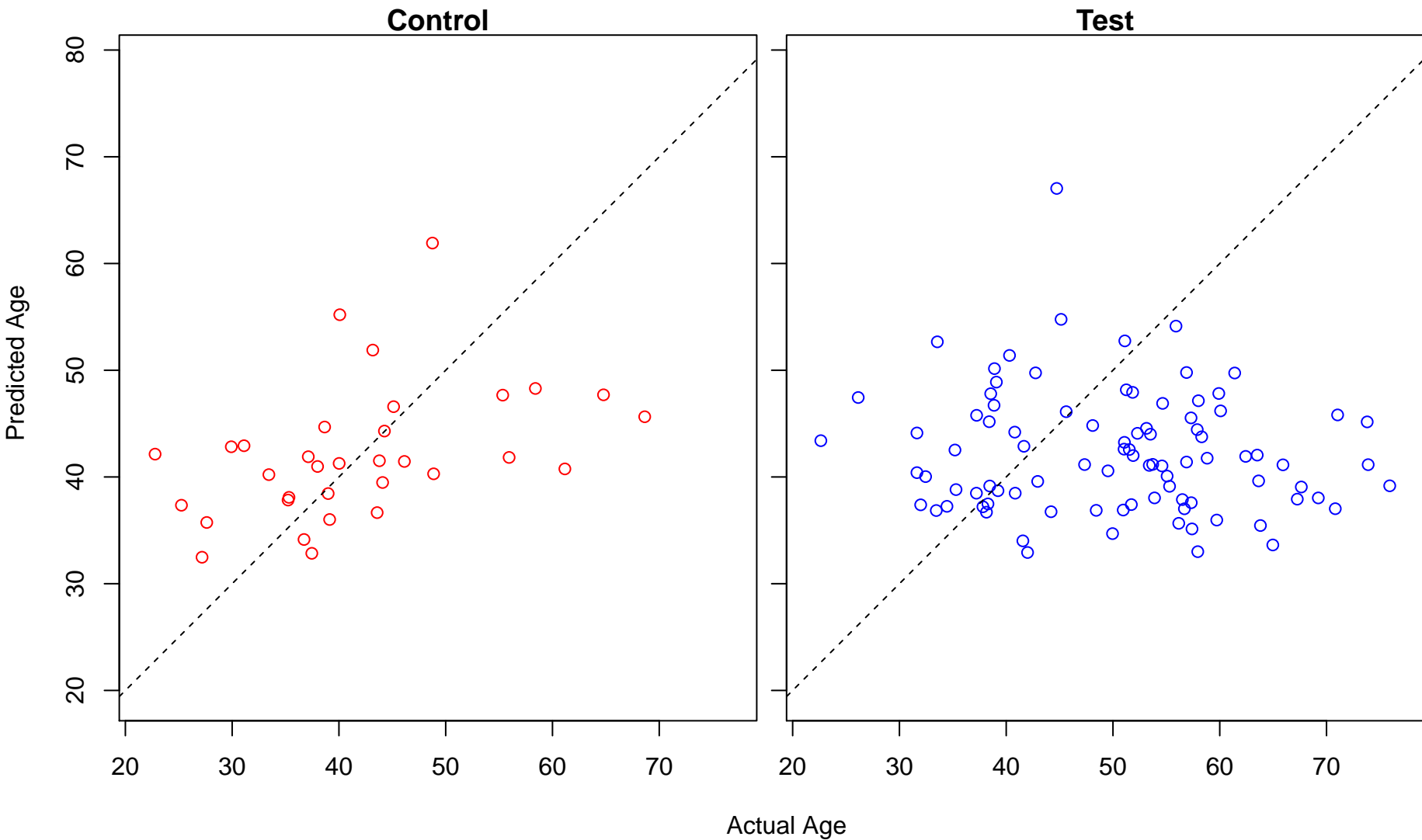
regulation of nucleobase-containing compound metabolic process (Score: 0.692888)



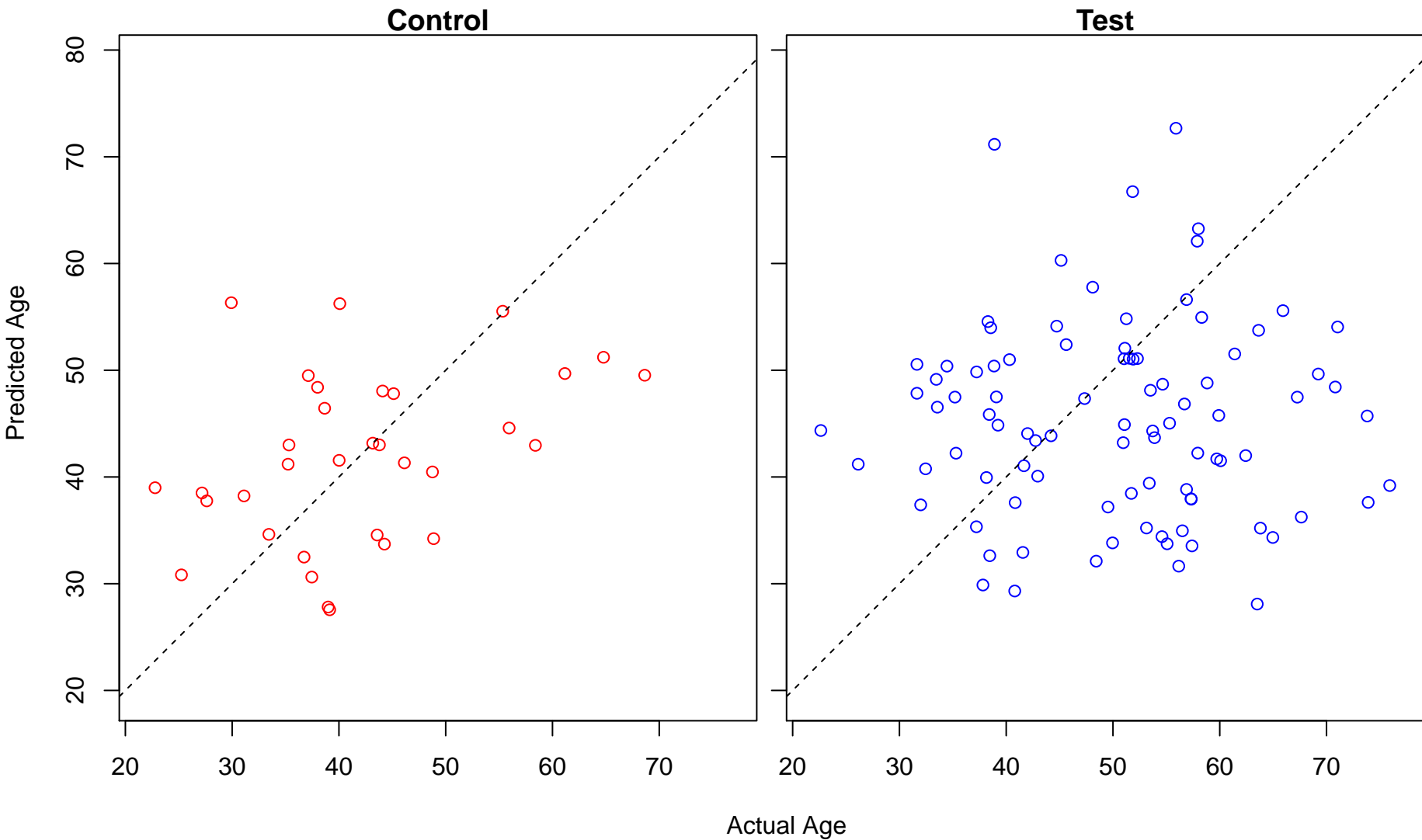
regulation of organelle organization (Score: 0.692880)



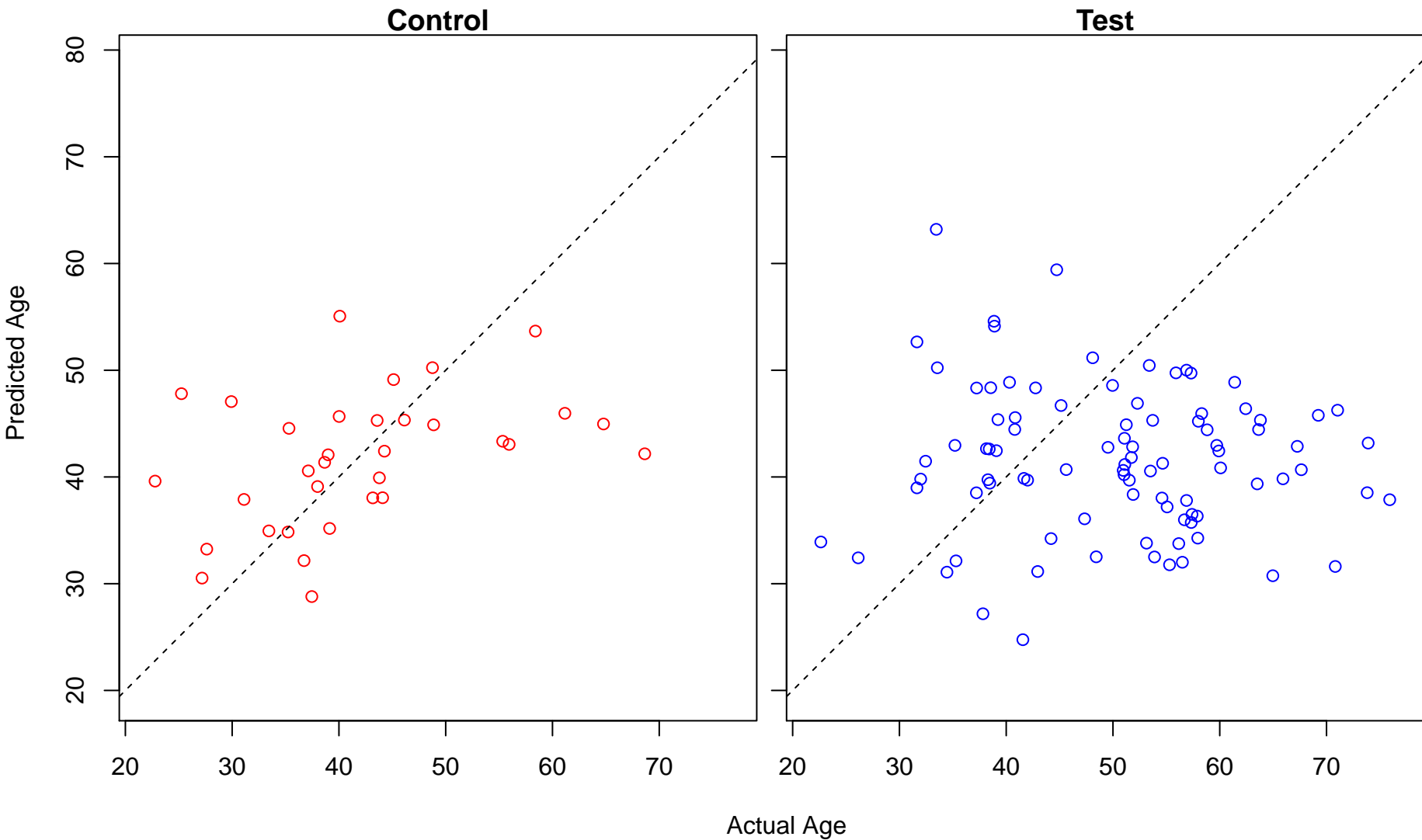
depurination (Score: 0.692795)



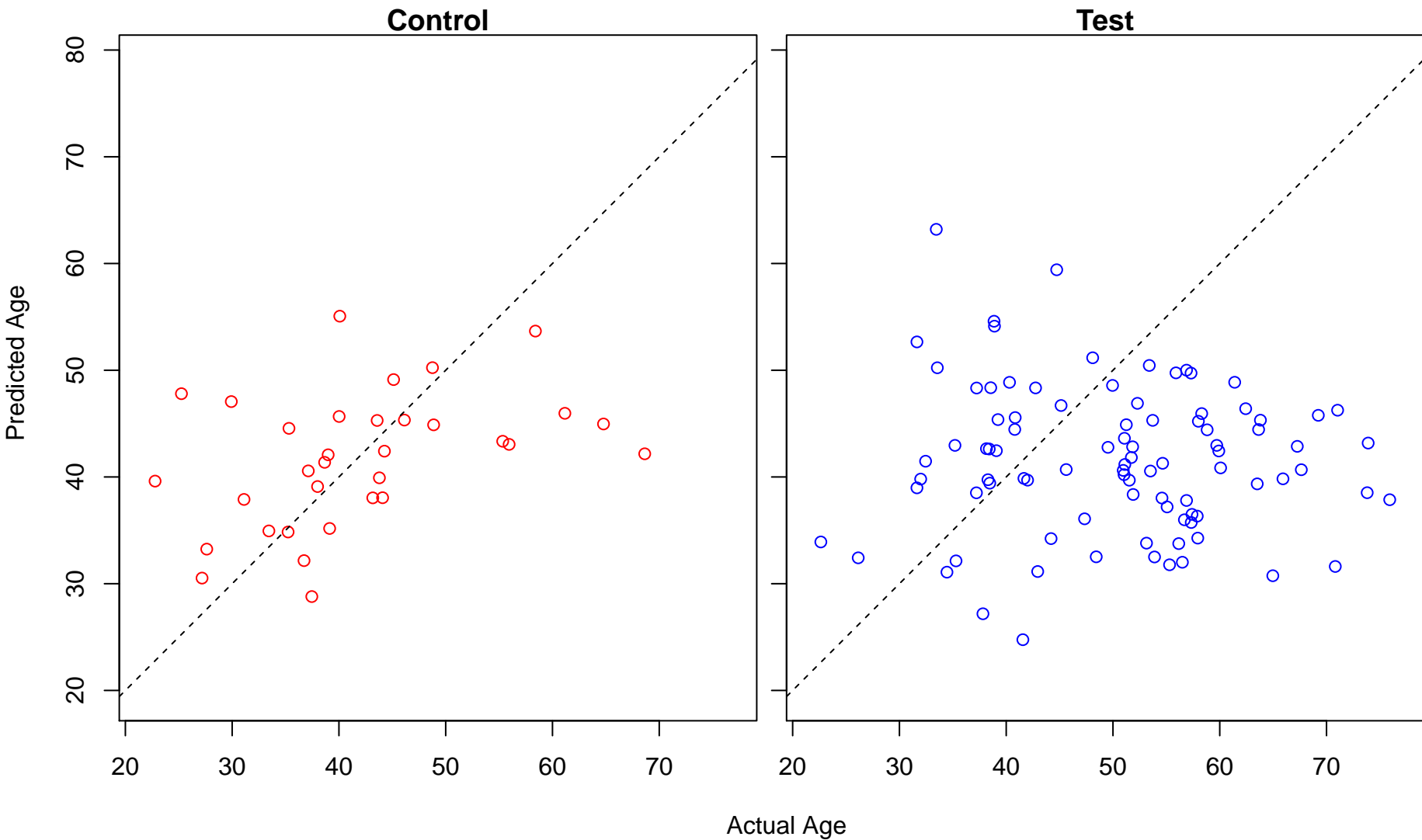
metanephric nephron development (Score: 0.692059)



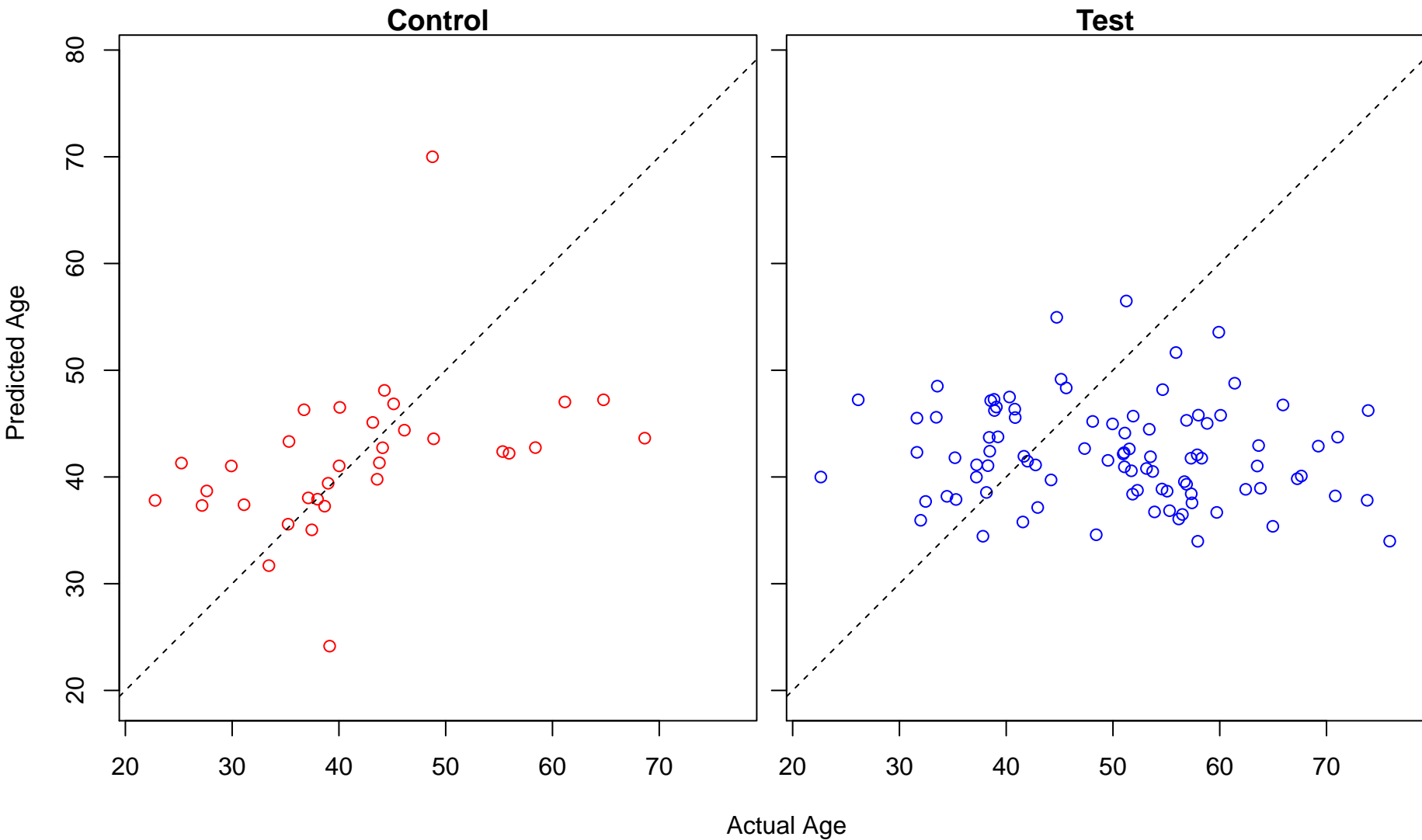
positive regulation of sterol transport (Score: 0.691976)



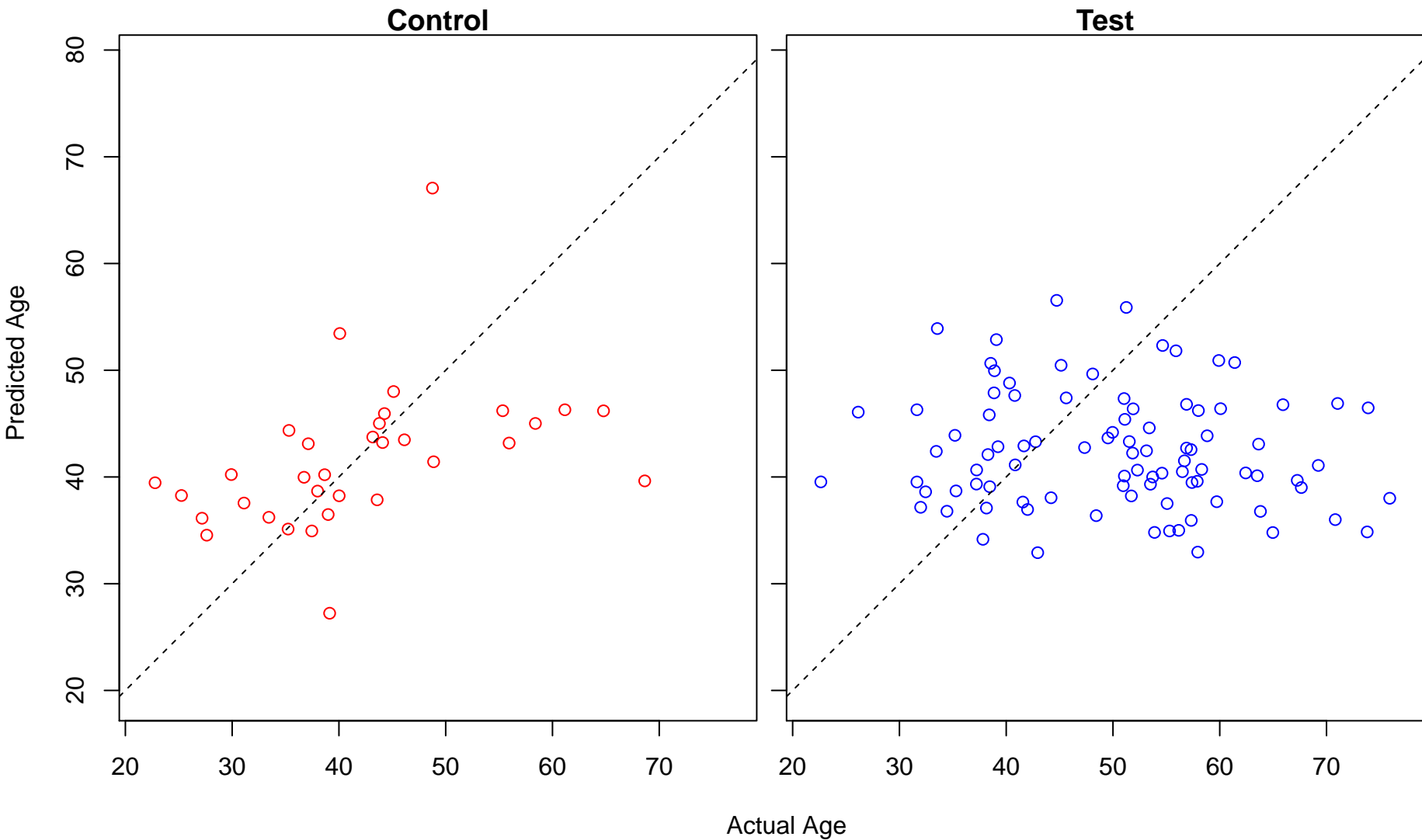
positive regulation of cholesterol transport (Score: 0.691976)



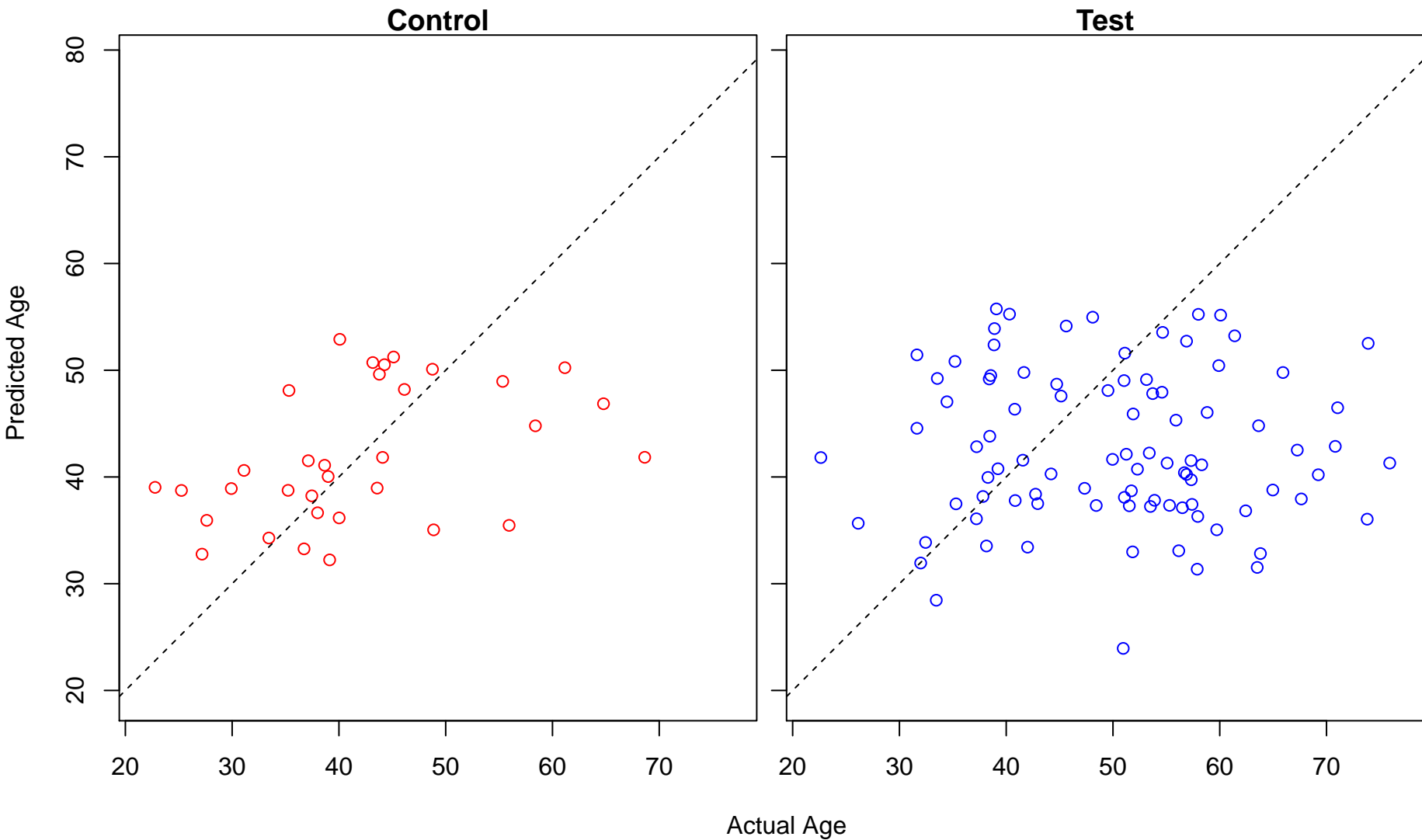
endoplasmic reticulum unfolded protein response (Score: 0.691932)



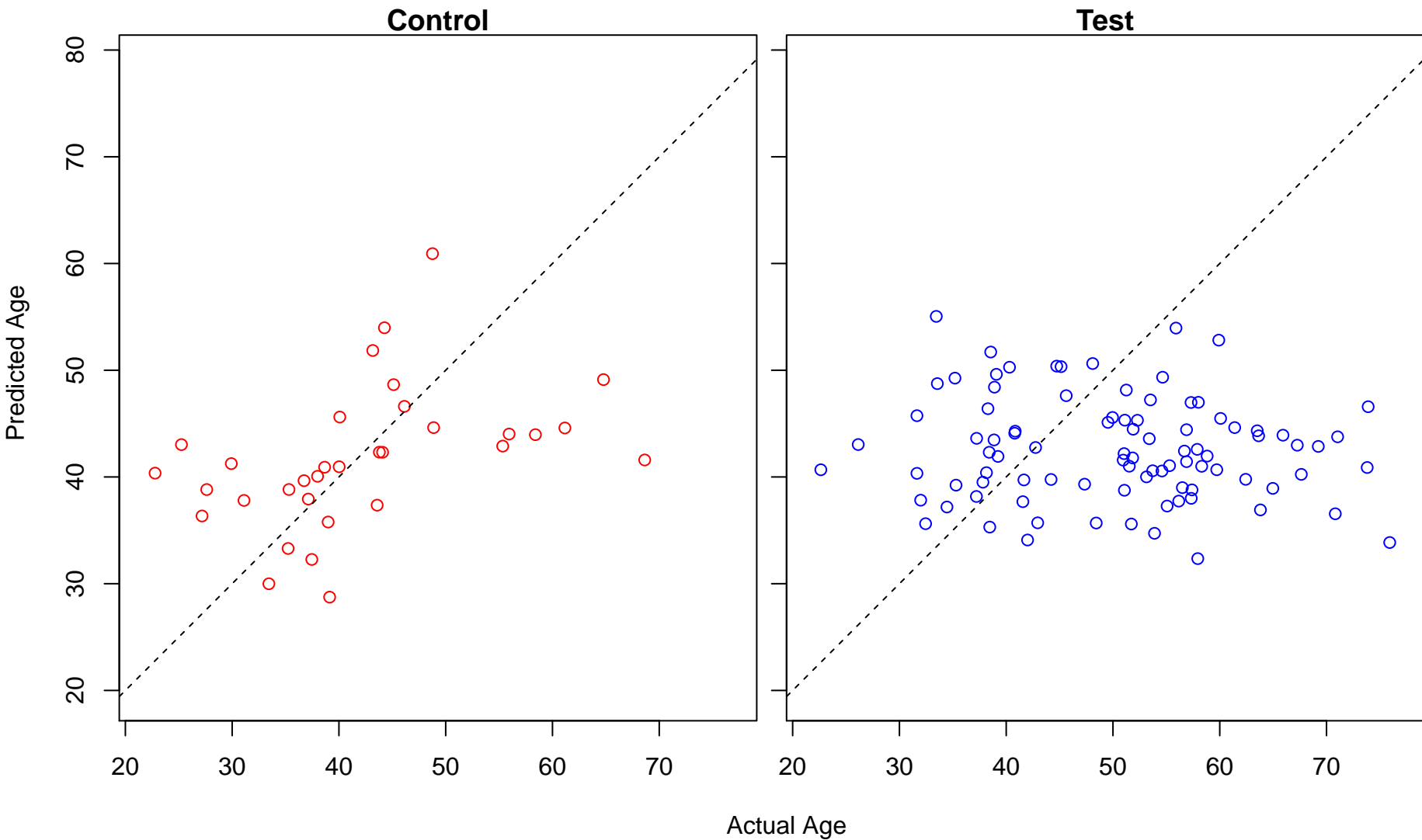
positive regulation of protein modification process (Score: 0.691165)



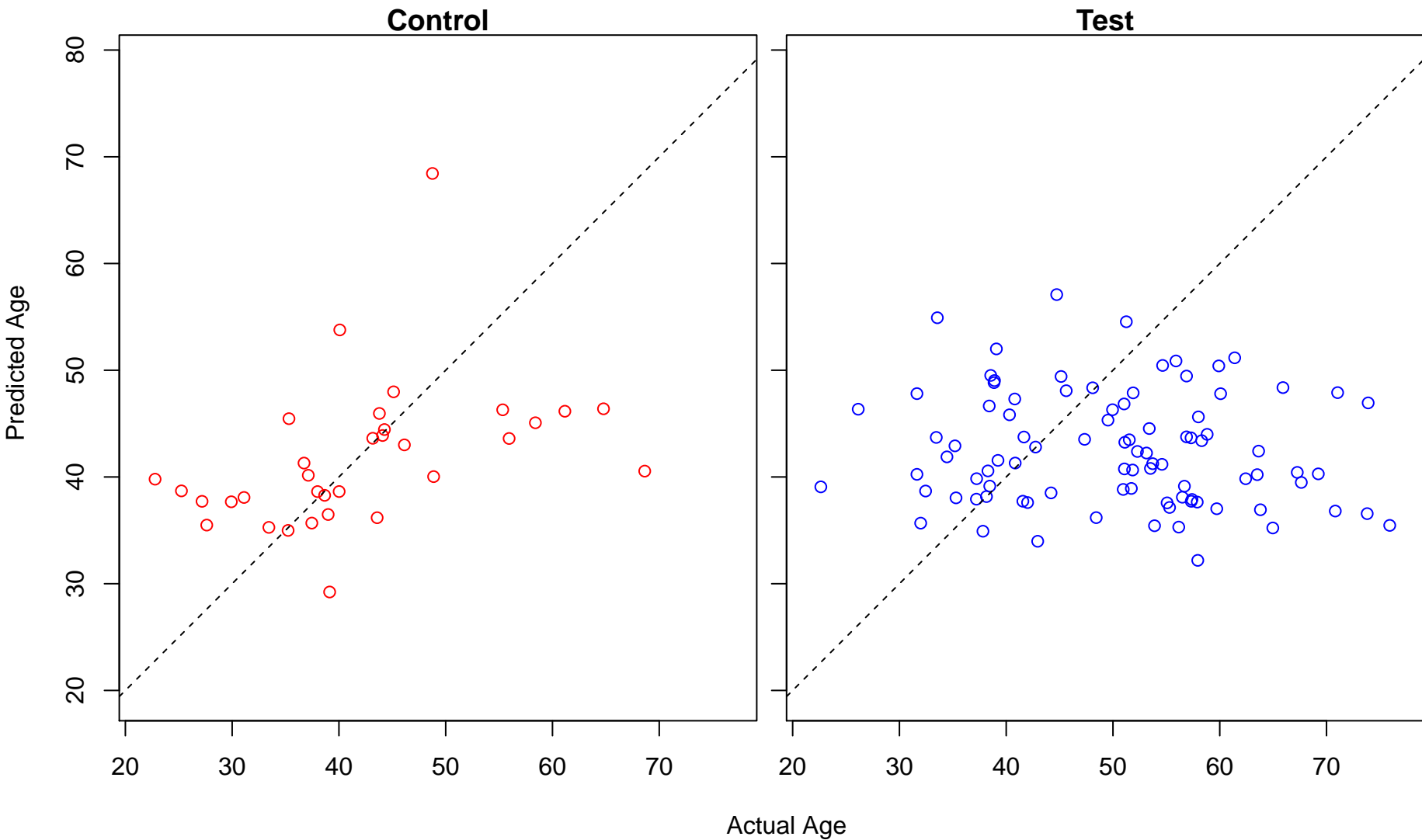
negative regulation of JAK-STAT cascade (Score: 0.691070)



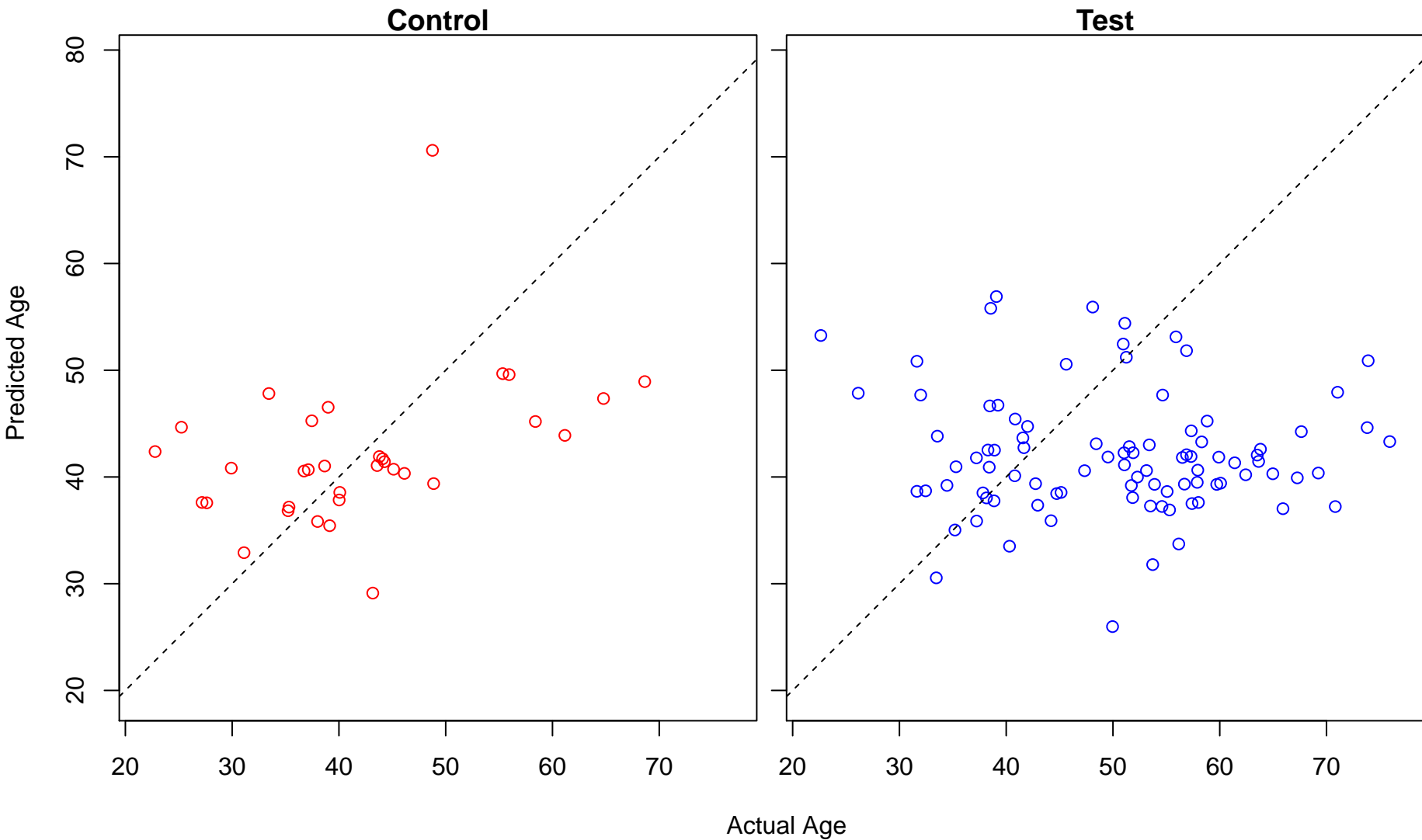
carbohydrate catabolic process (Score: 0.690931)



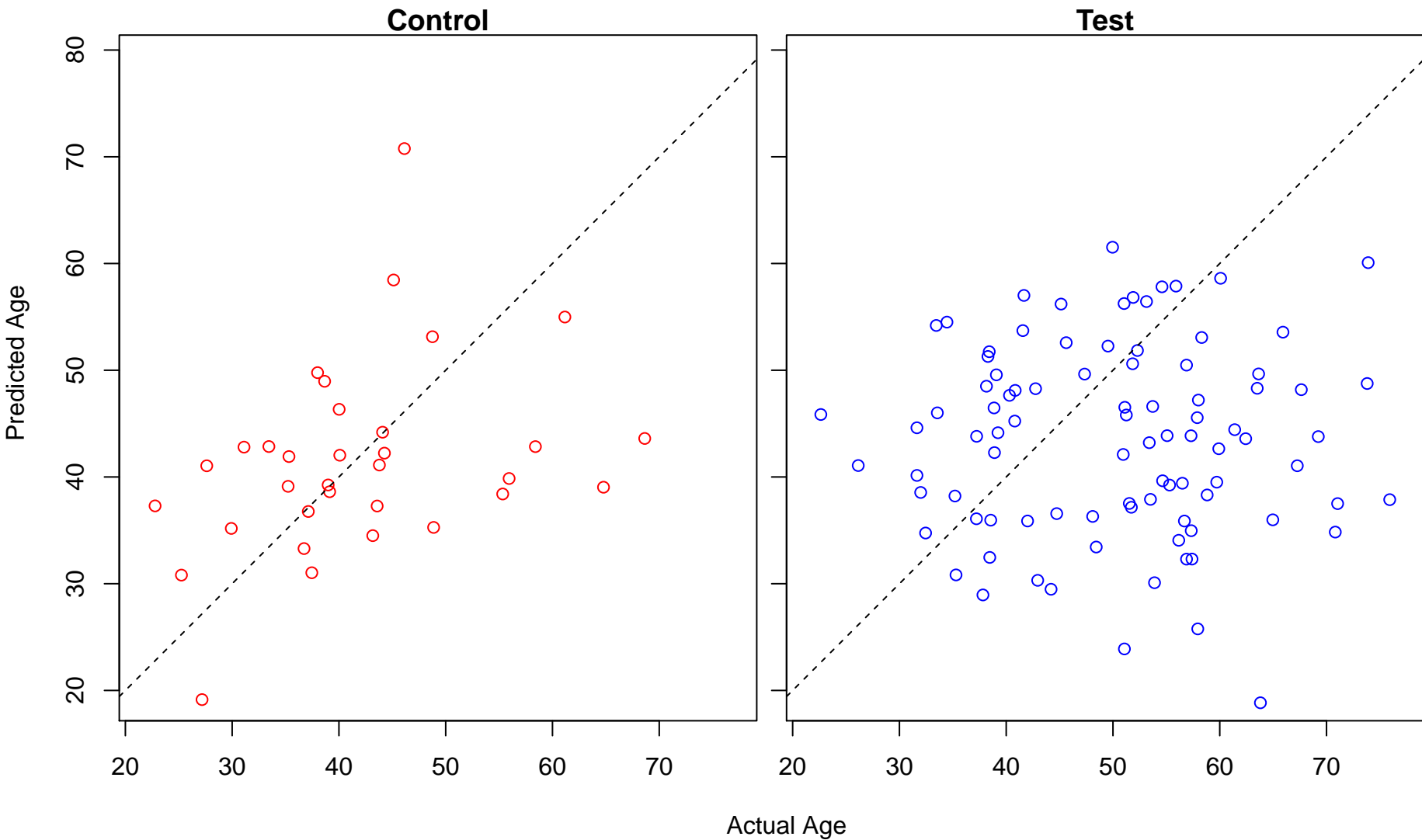
positive regulation of cellular biosynthetic process (Score: 0.689917)



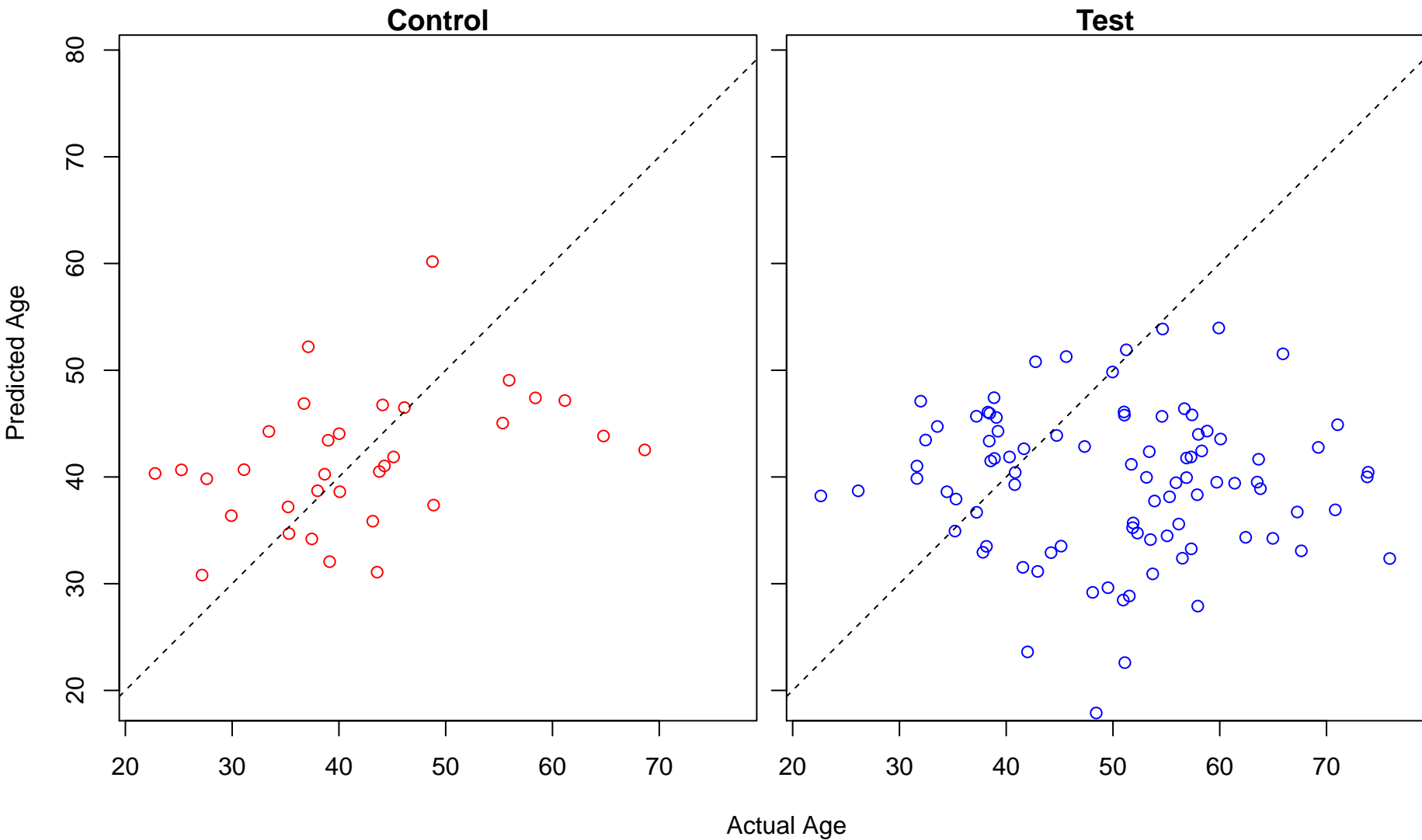
nuclear pore complex assembly (Score: 0.689759)



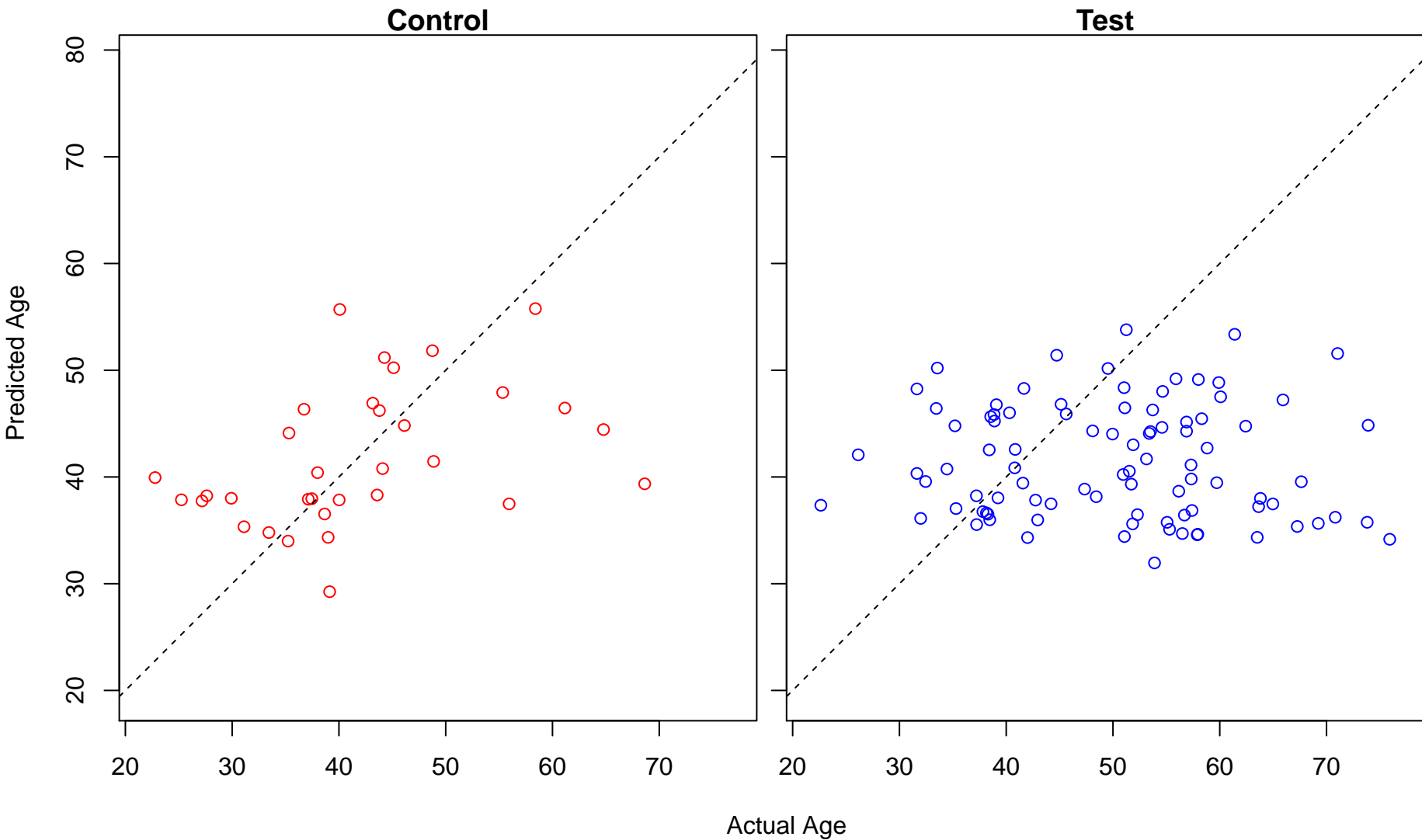
relaxation of muscle (Score: 0.689566)



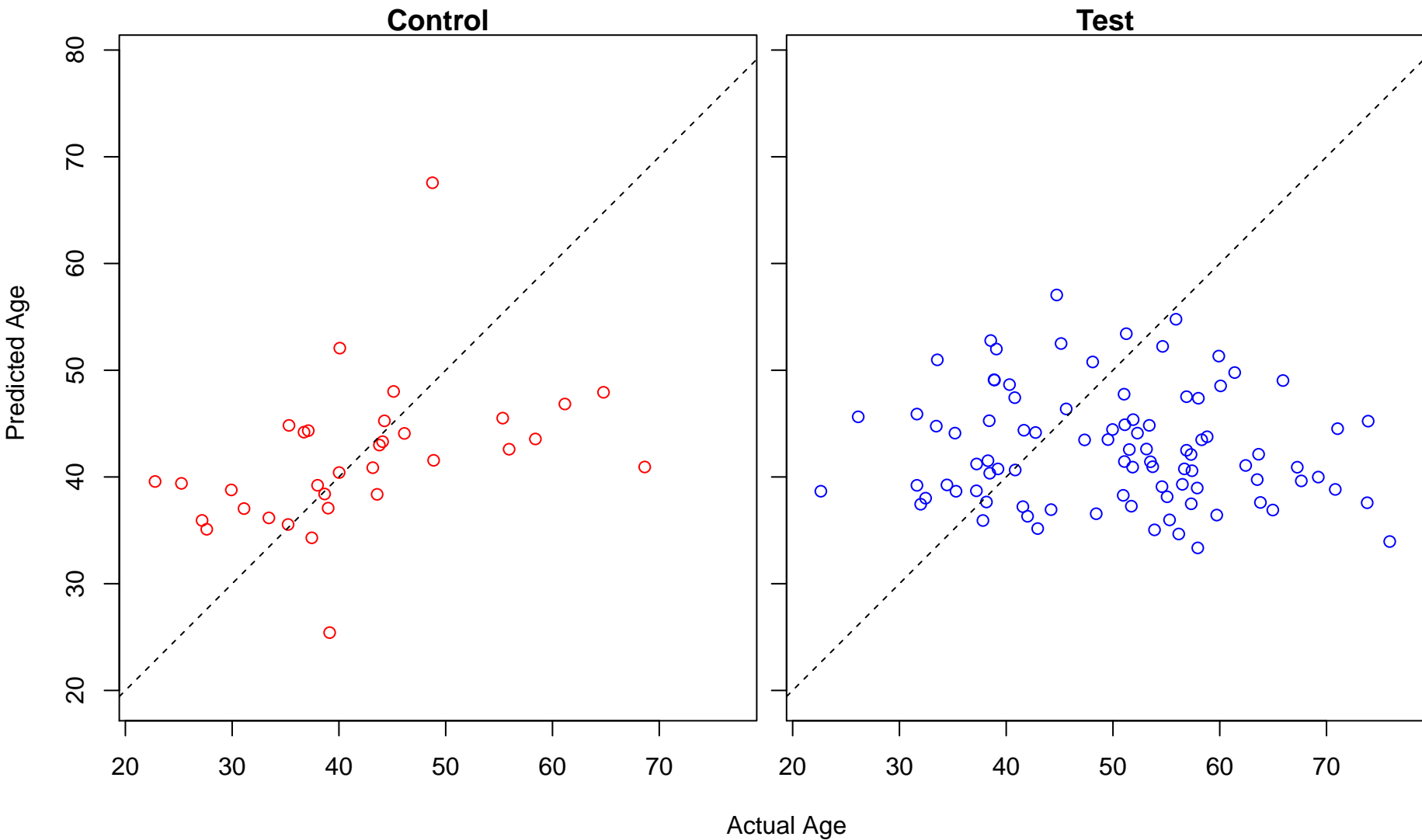
cell communication by electrical coupling involved in cardiac conduction (Score: 0.689523)



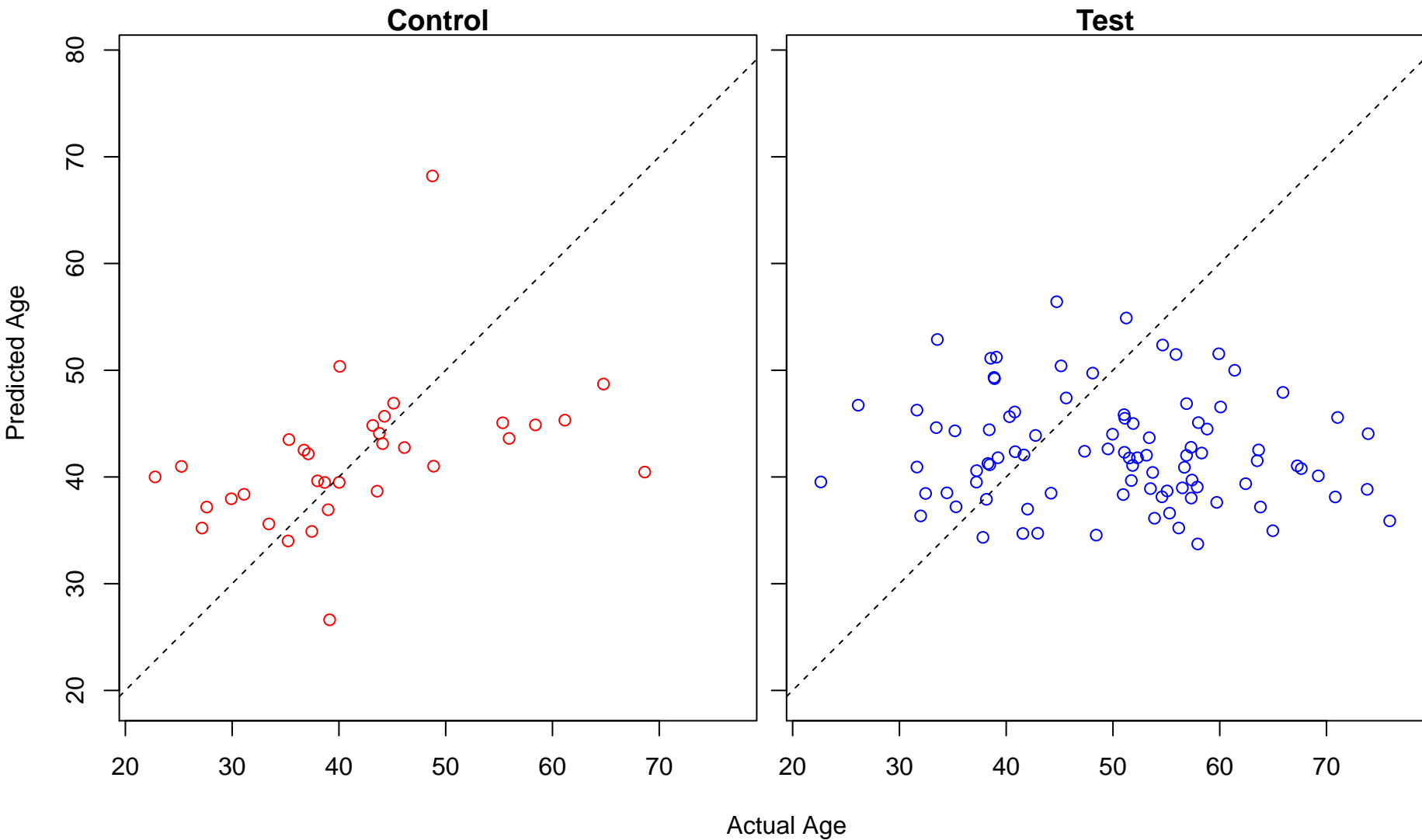
positive regulation of mRNA catabolic process (Score: 0.688751)



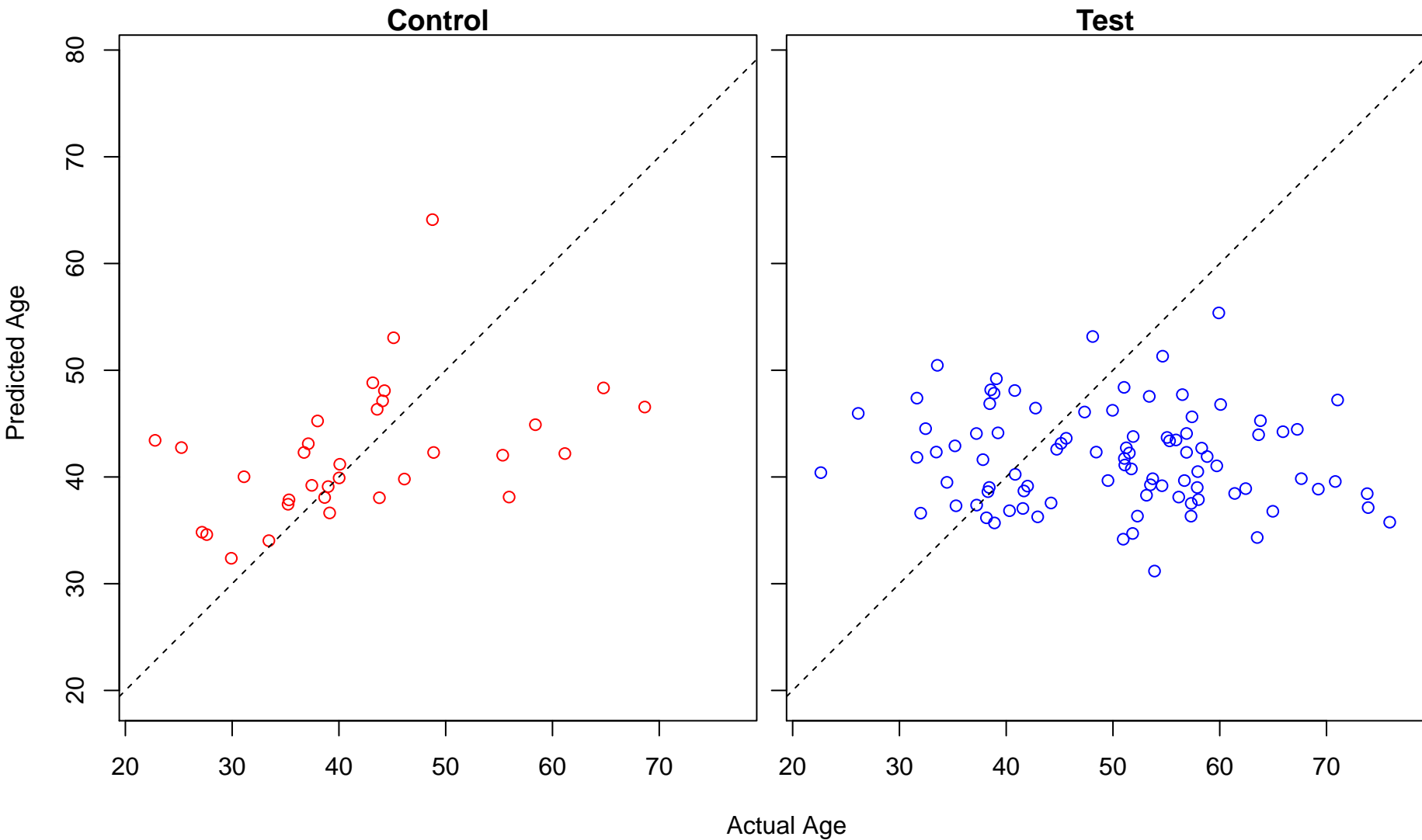
regulation of cellular localization (Score: 0.688726)



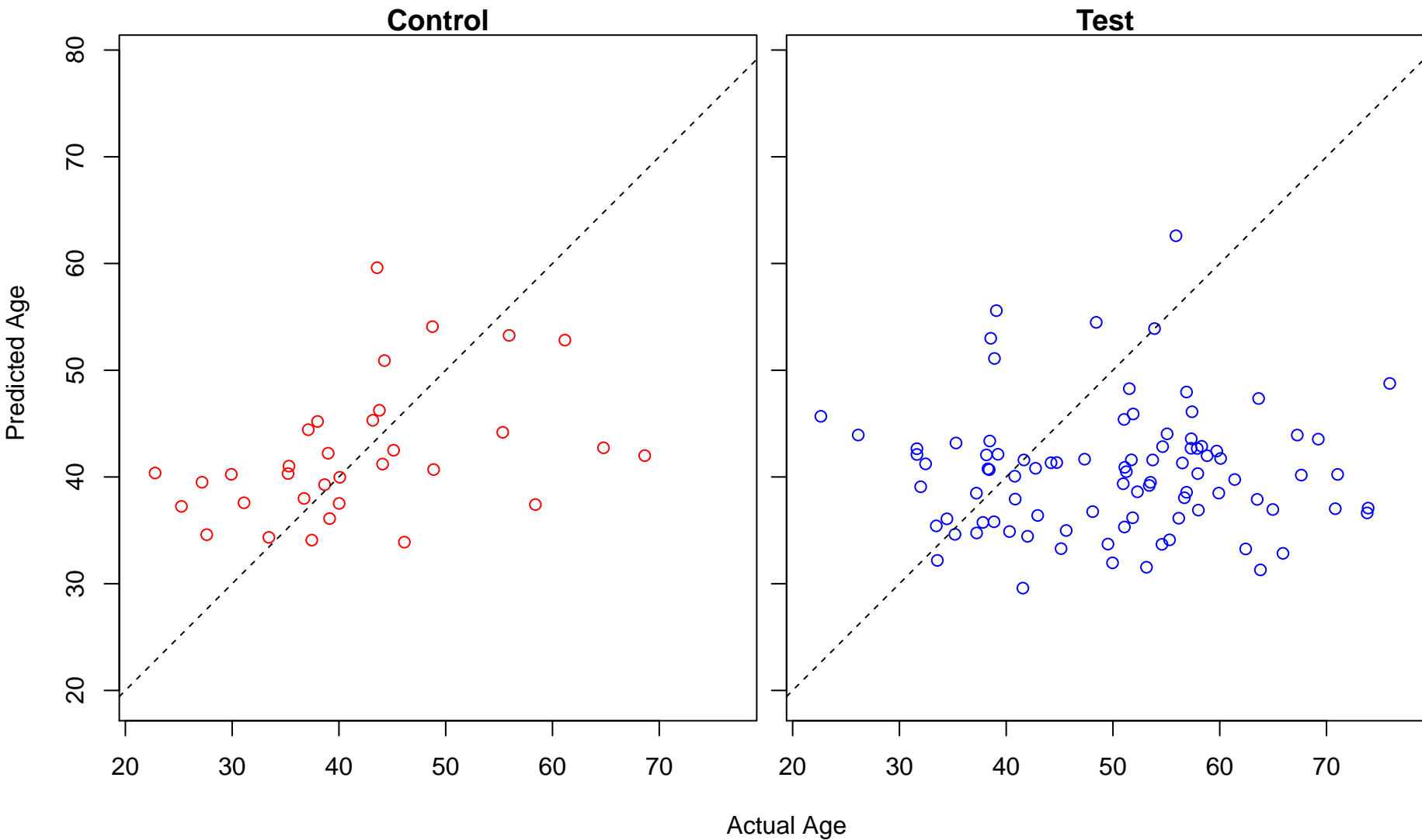
developmental process (Score: 0.688424)



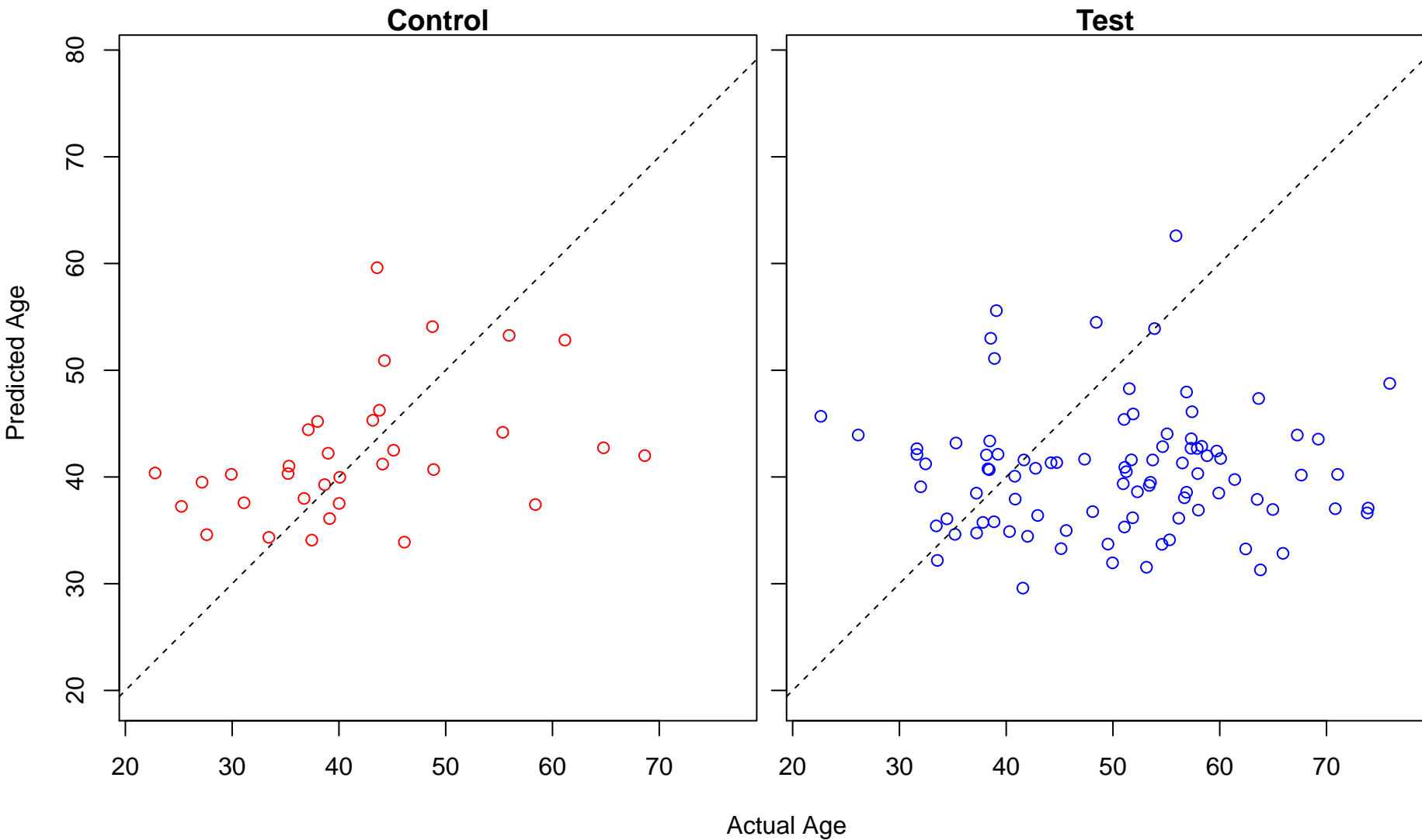
negative regulation of T-helper 1 cell differentiation (Score: 0.688402)



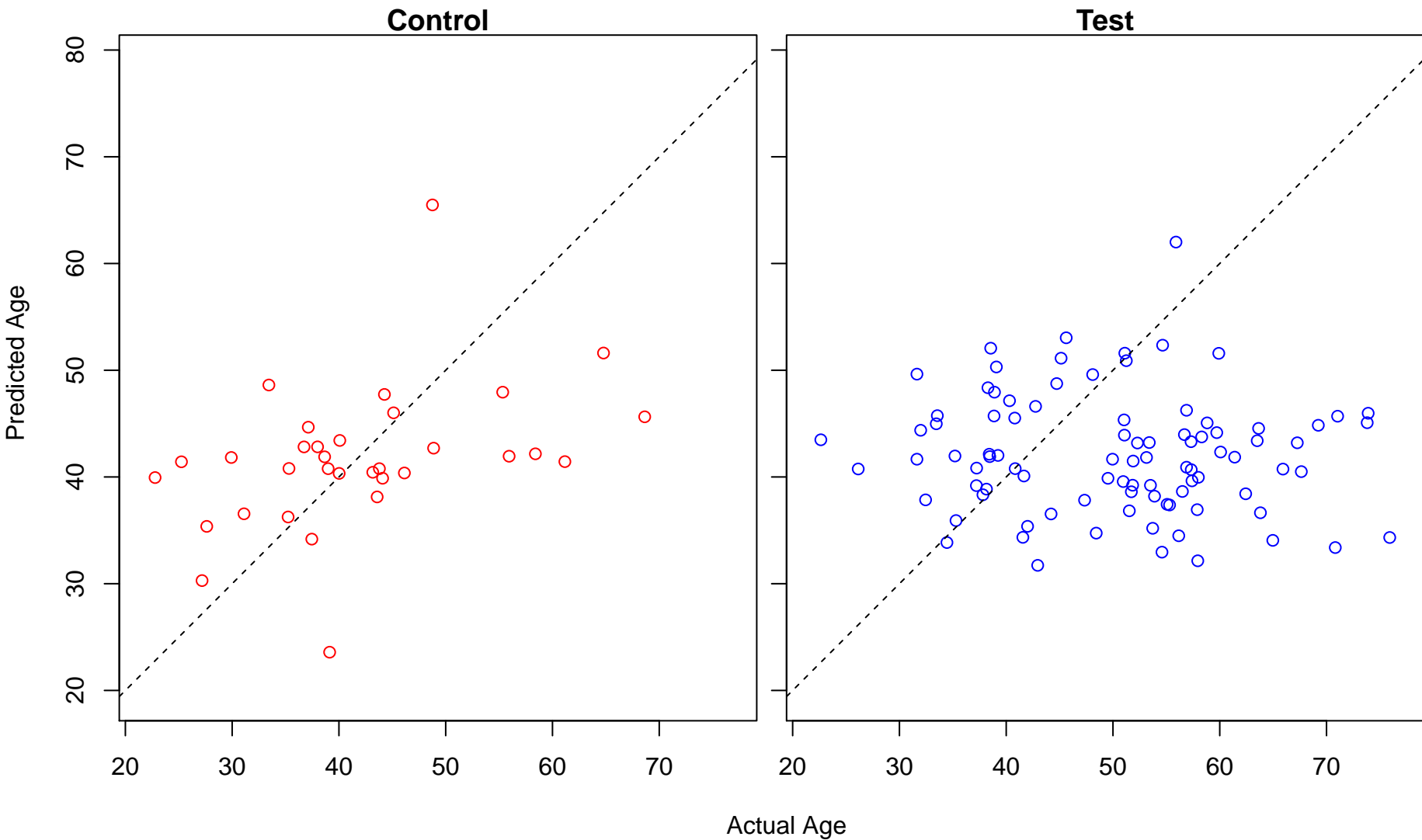
cell envelope organization (Score: 0.687946)



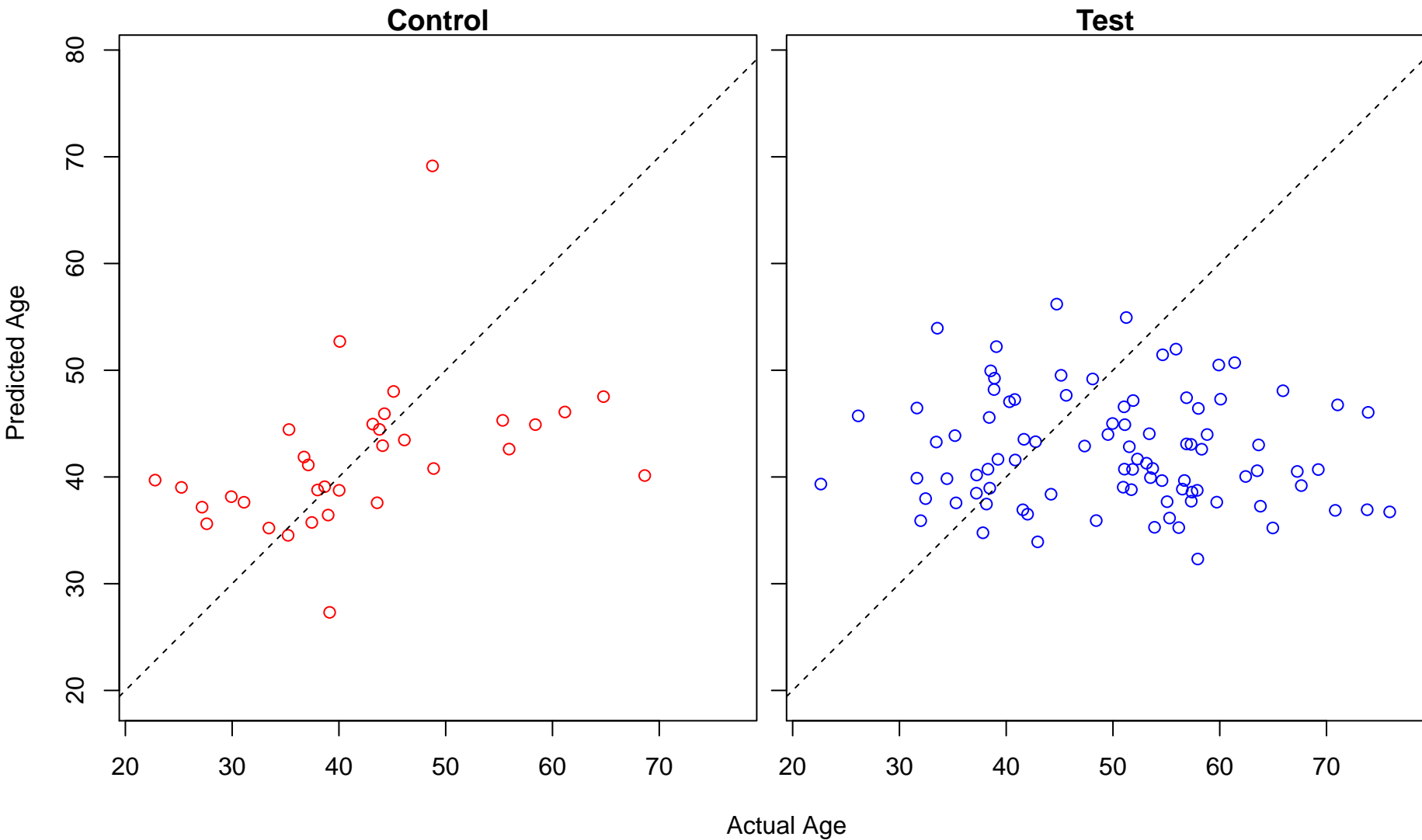
external encapsulating structure organization (Score: 0.687946)



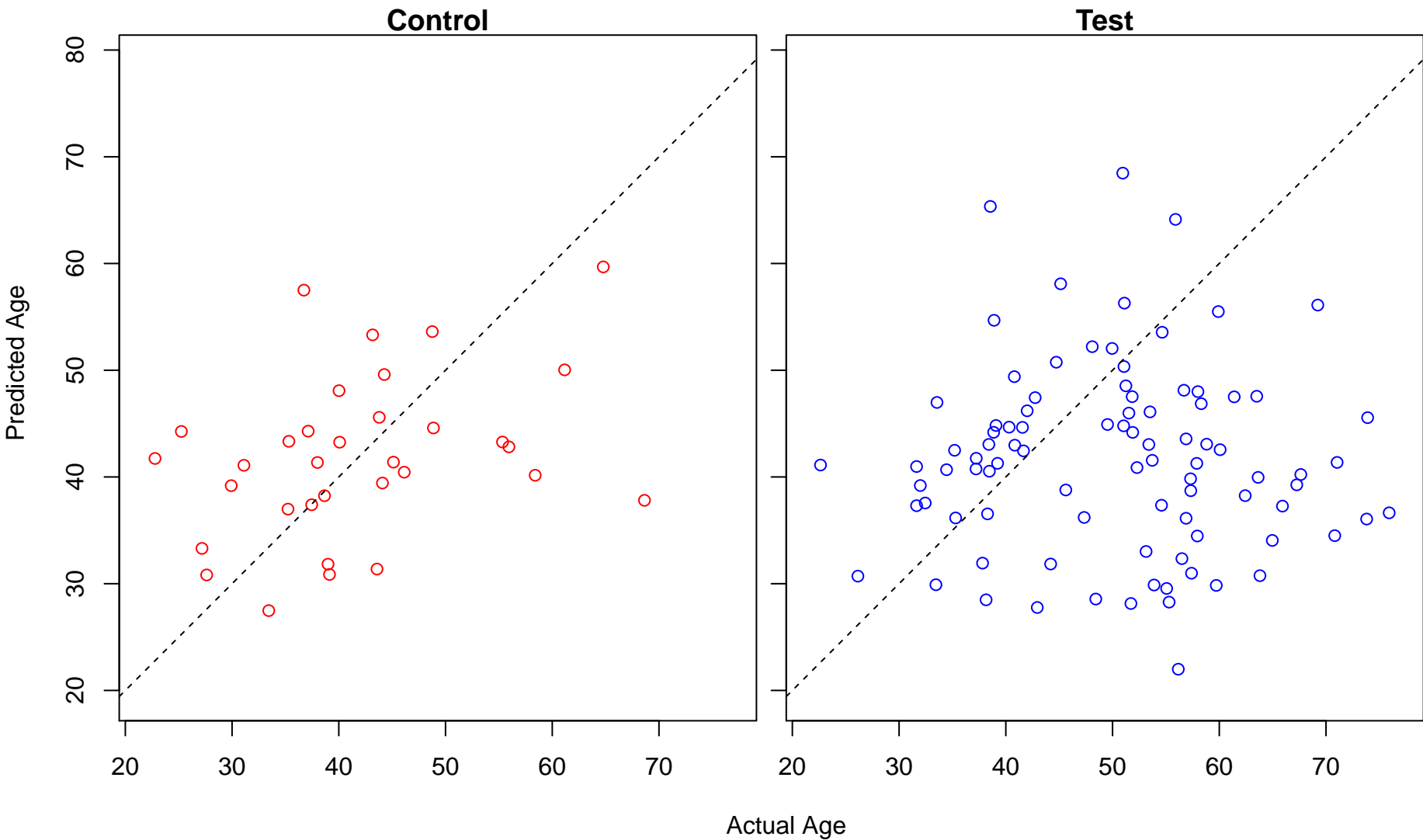
carbohydrate transport (Score: 0.687096)



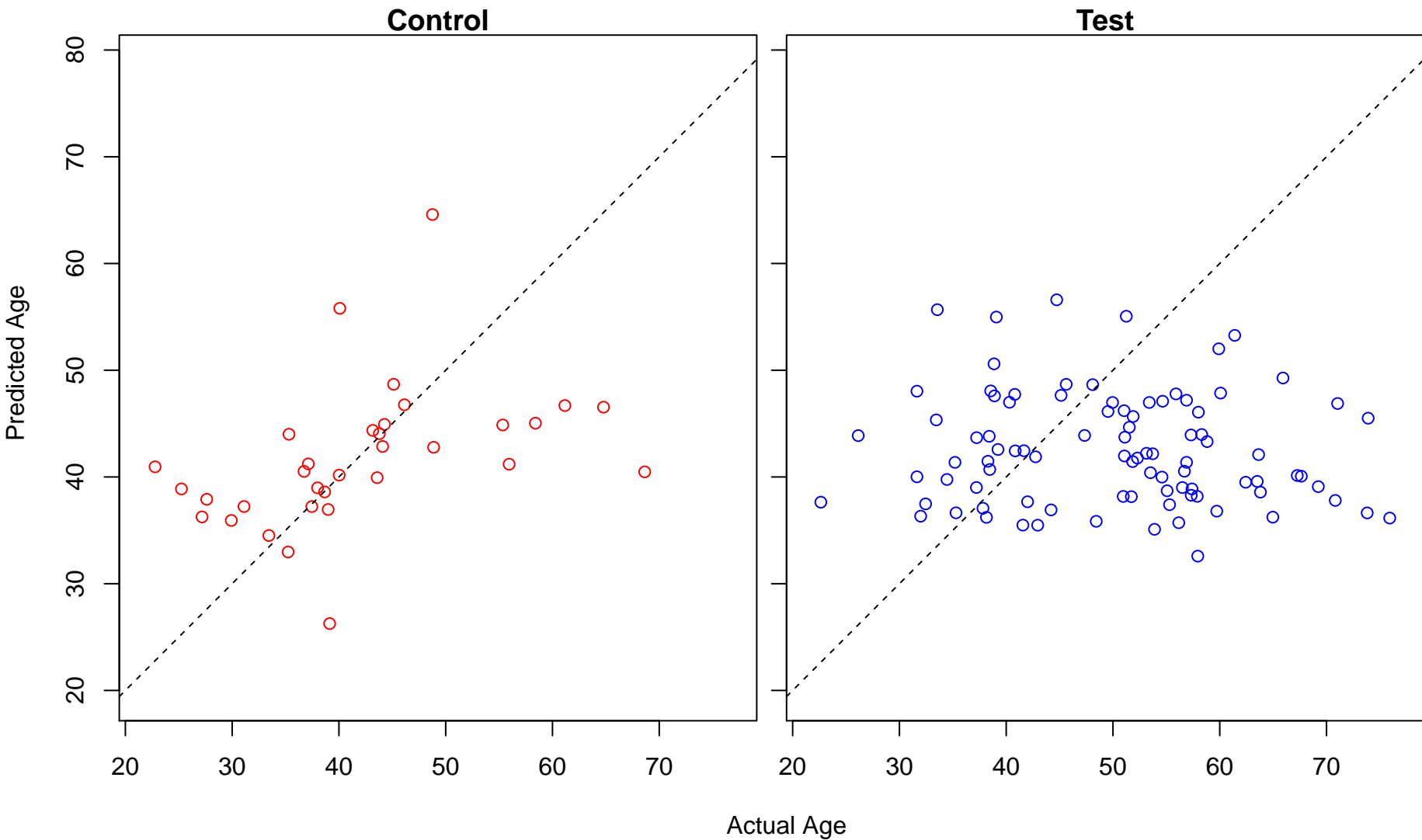
positive regulation of metabolic process (Score: 0.686523)



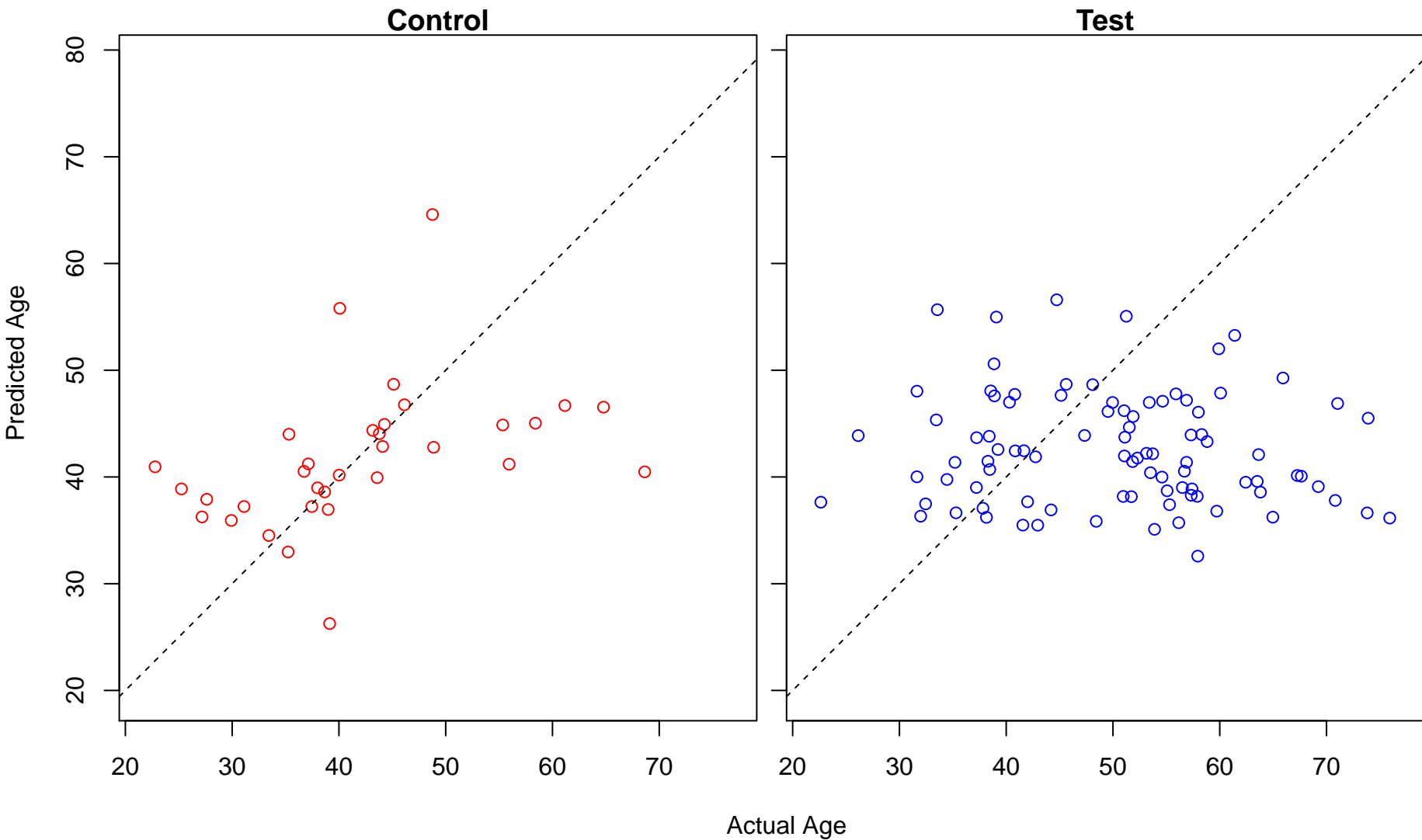
negative regulation of vascular endothelial growth factor receptor signaling pathway (Score: 0.68617)



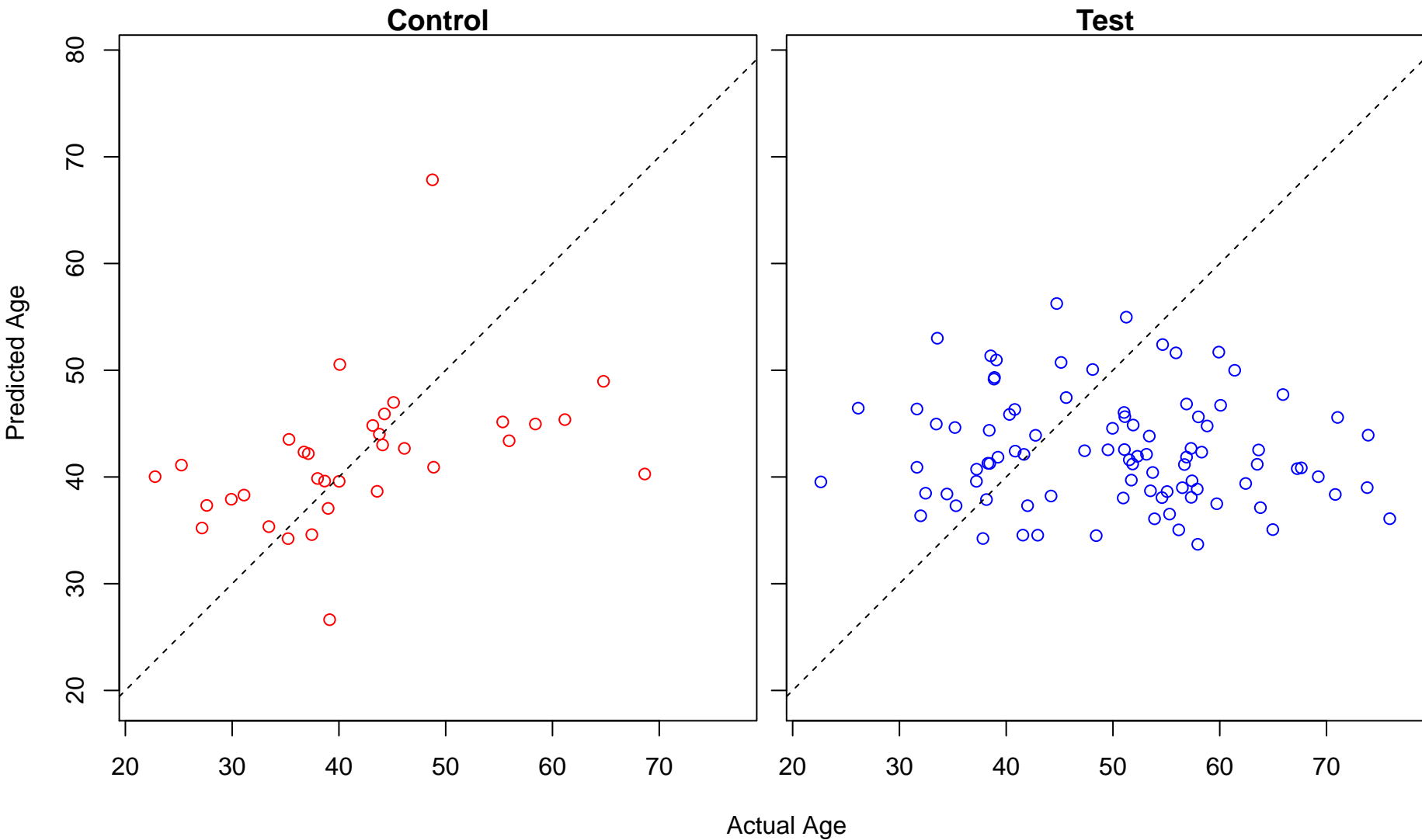
protein complex assembly (Score: 0.685684)



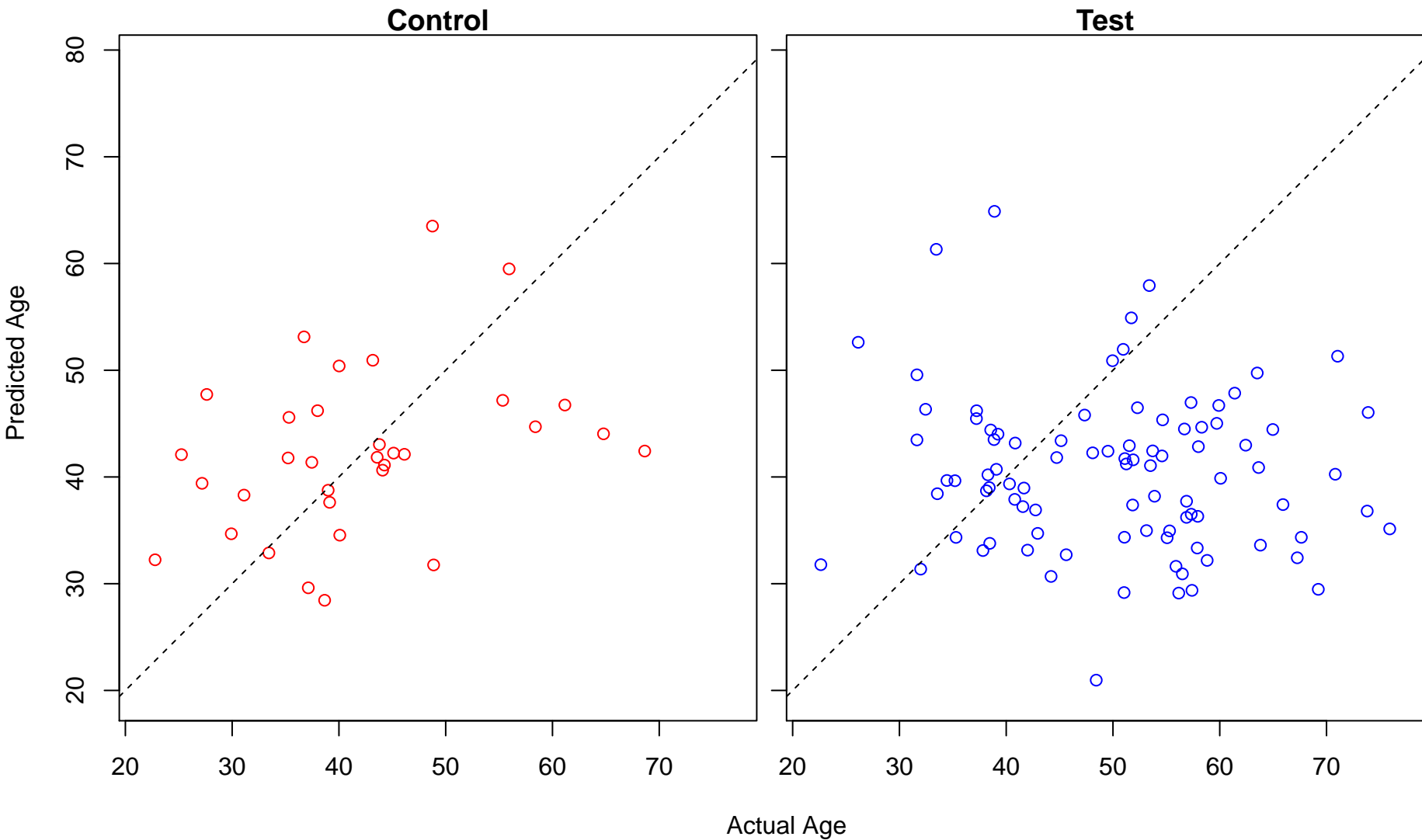
protein complex biogenesis (Score: 0.685684)



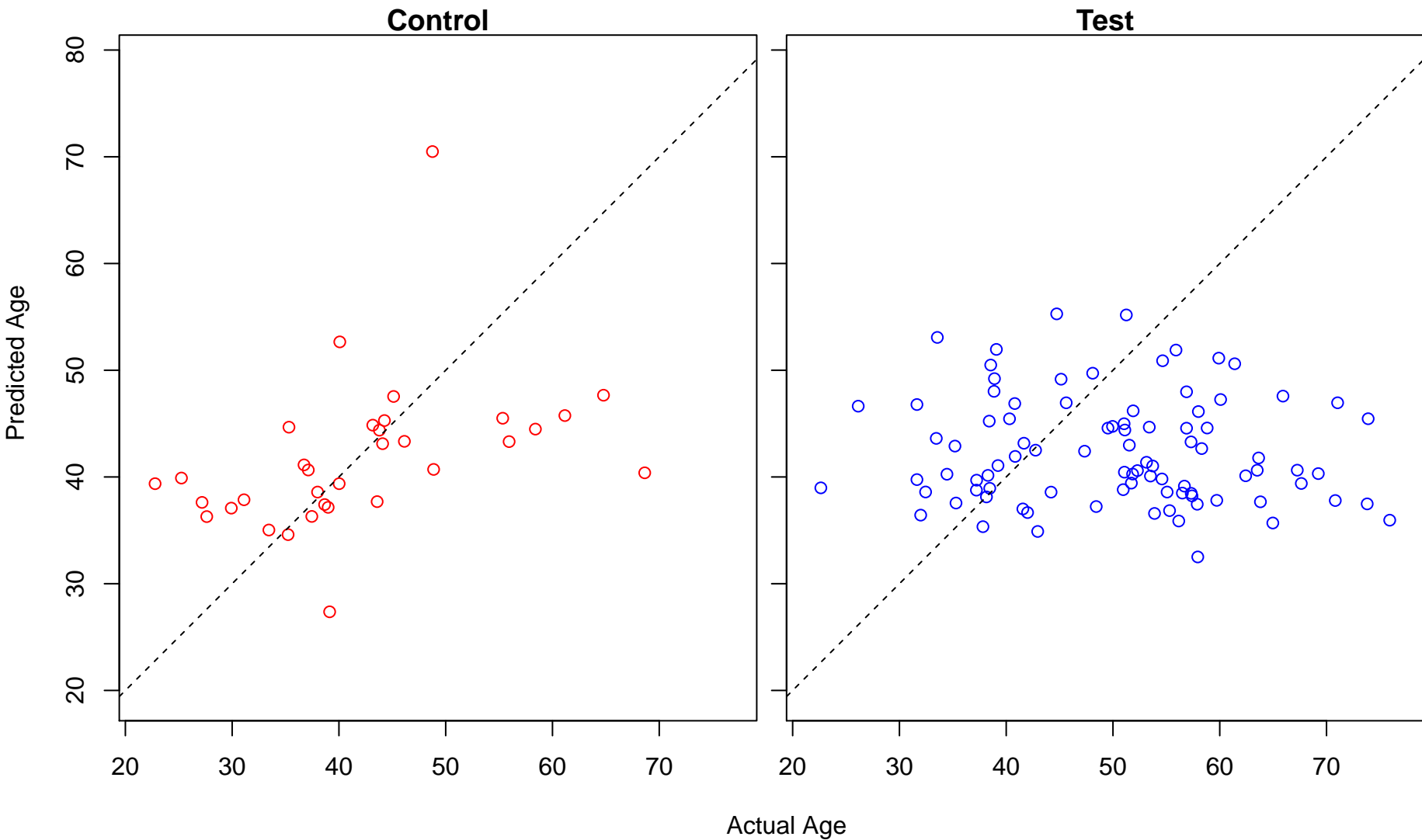
single-organism developmental process (Score: 0.685583)



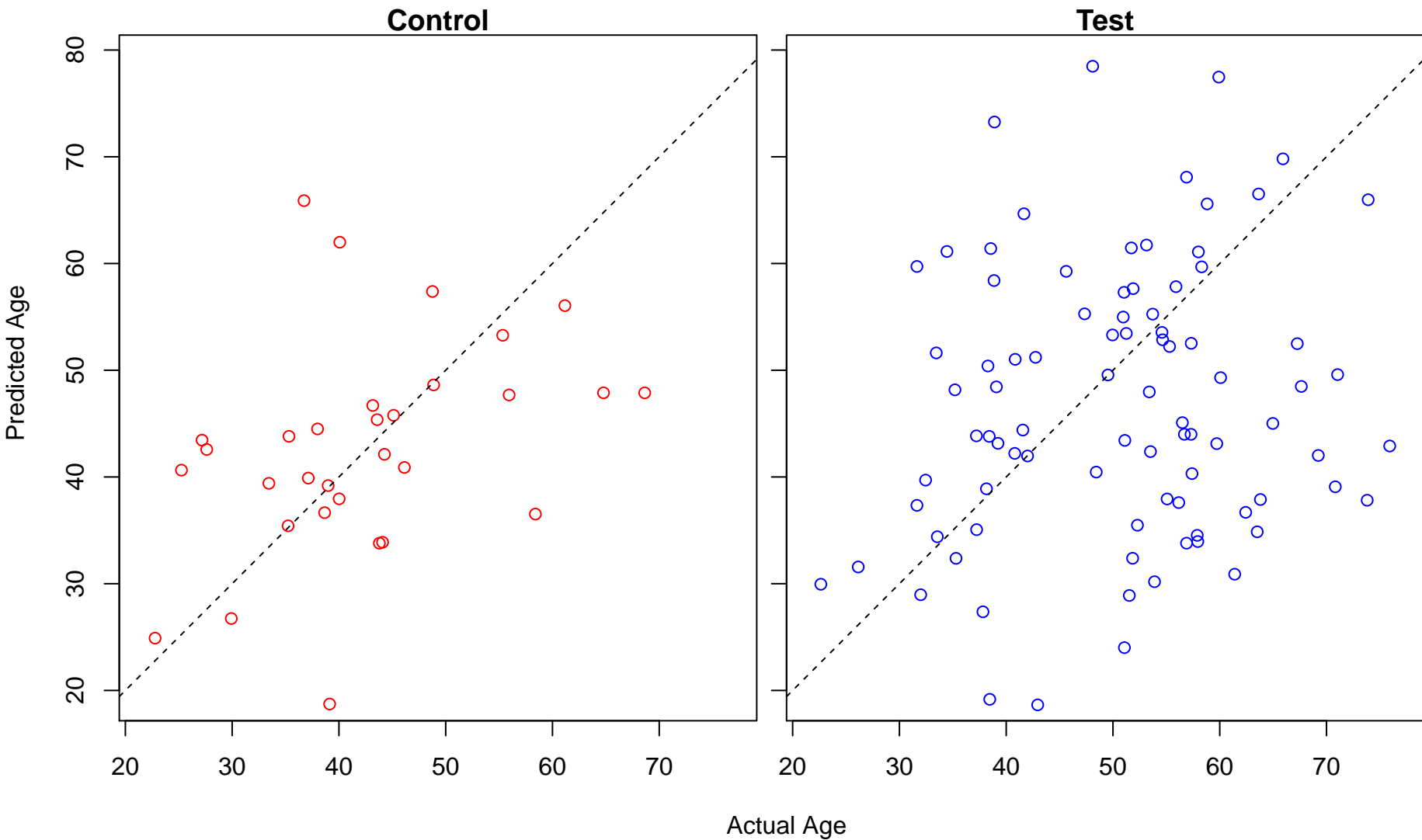
regulation of vascular permeability (Score: 0.685536)



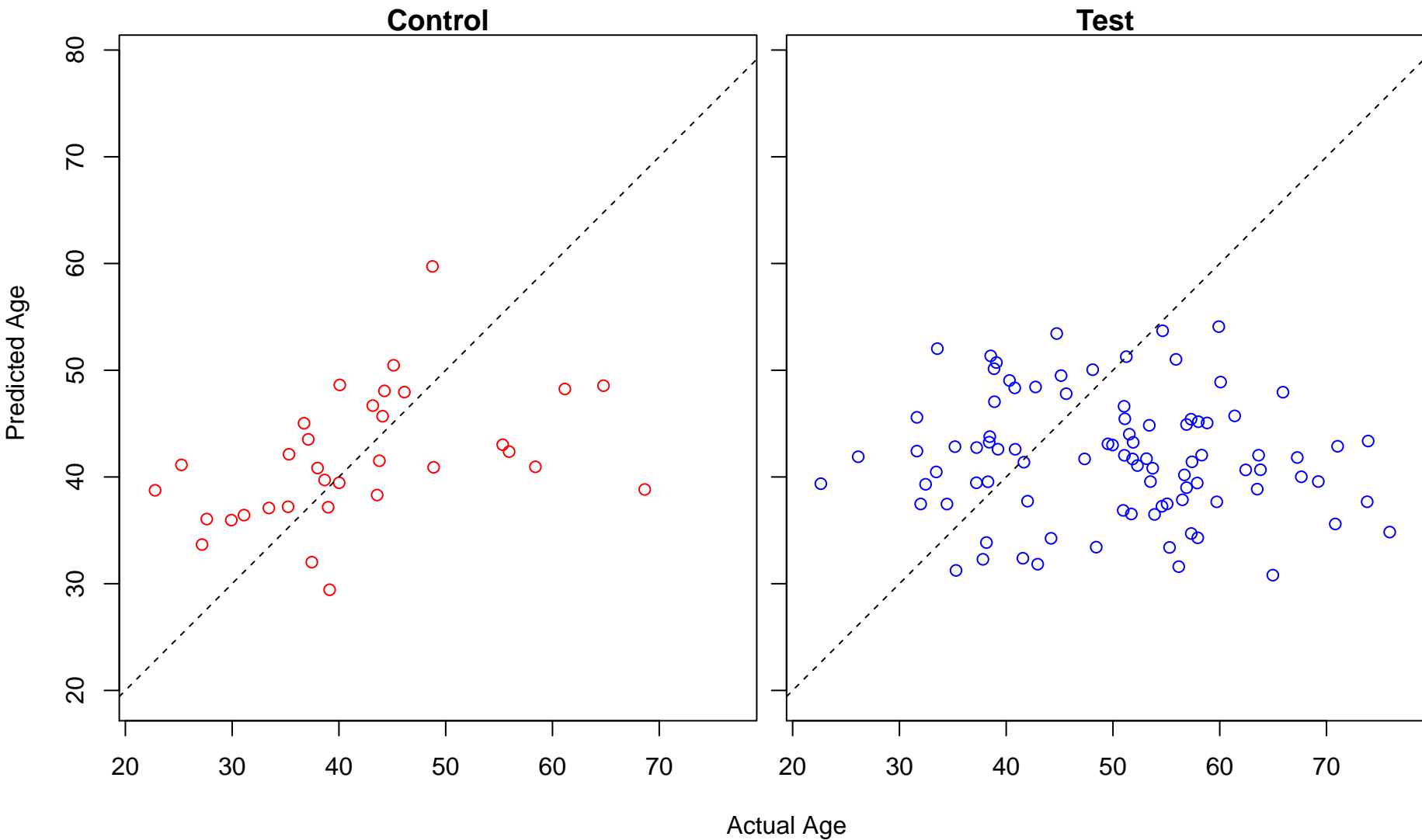
regulation of gene expression (Score: 0.685160)



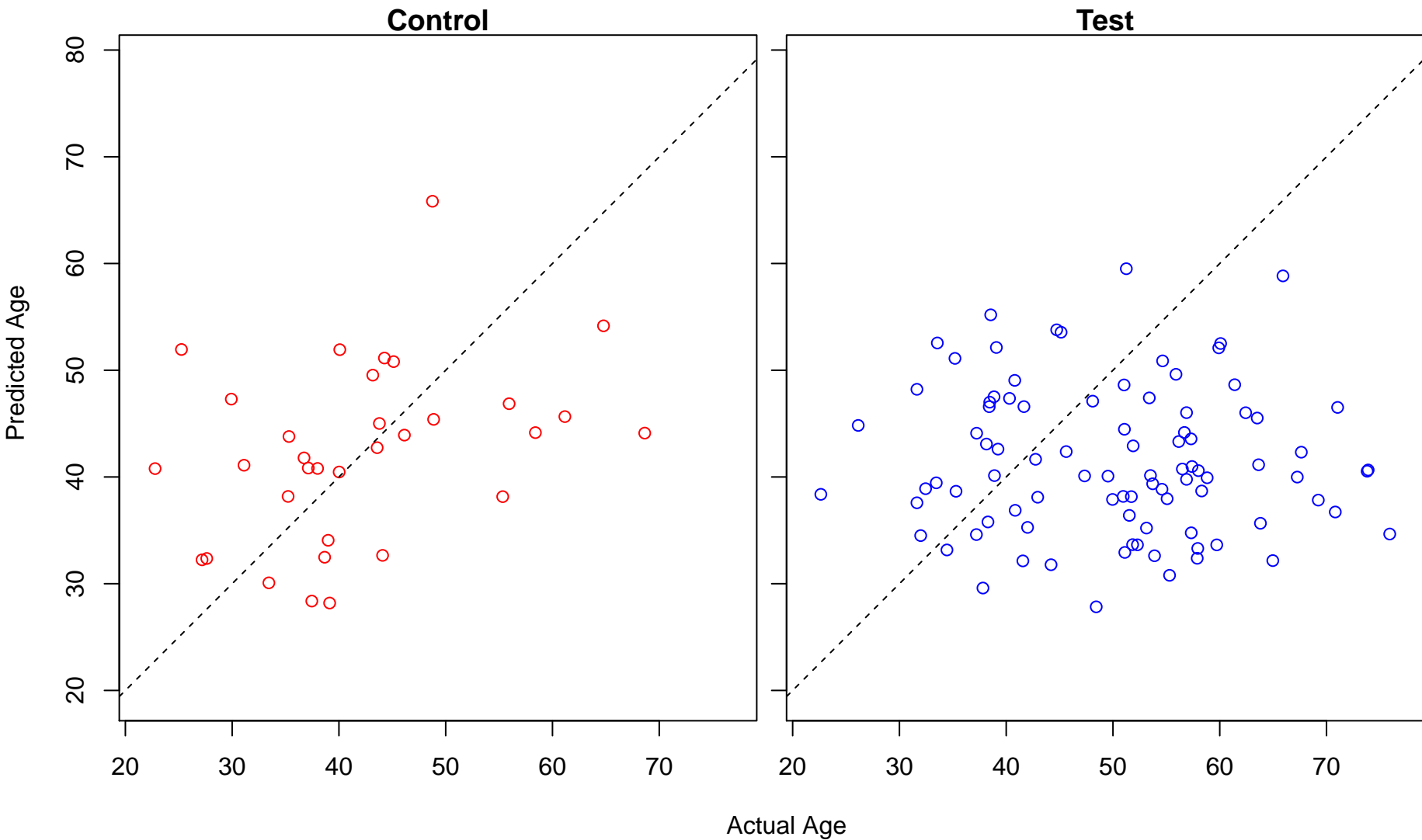
spliceosomal complex assembly (Score: 0.684885)



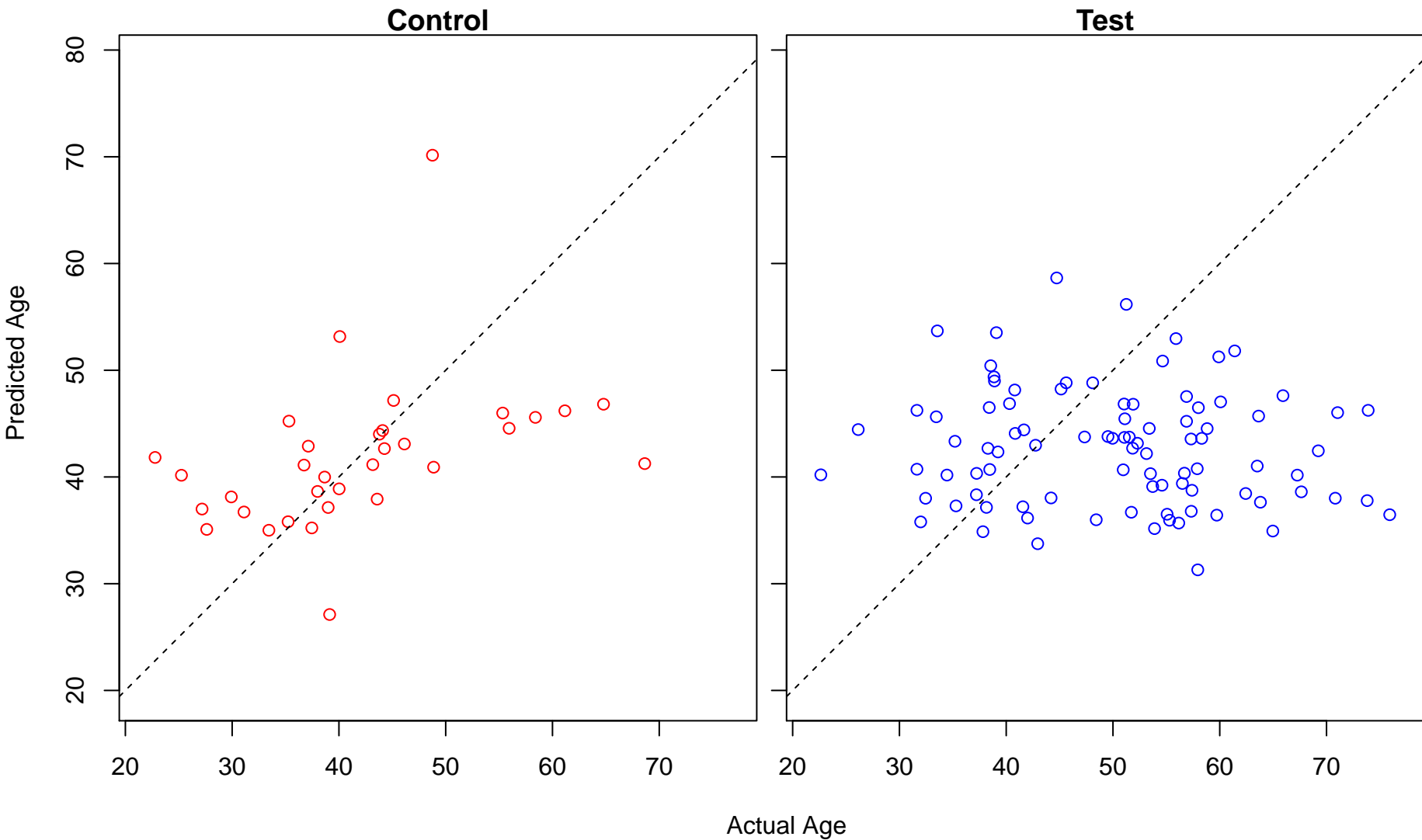
system process (Score: 0.684811)



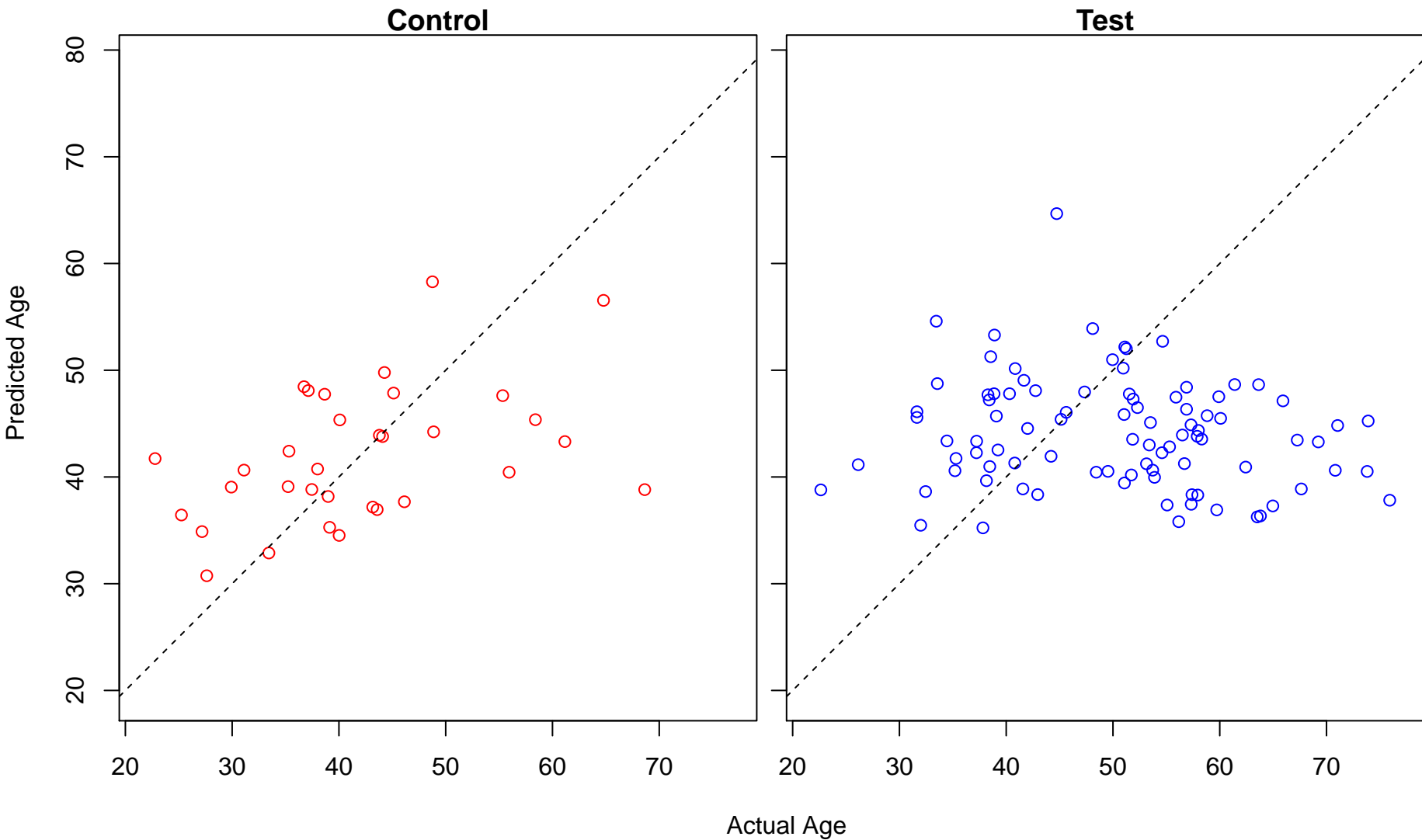
regulation of T cell mediated immunity (Score: 0.684684)



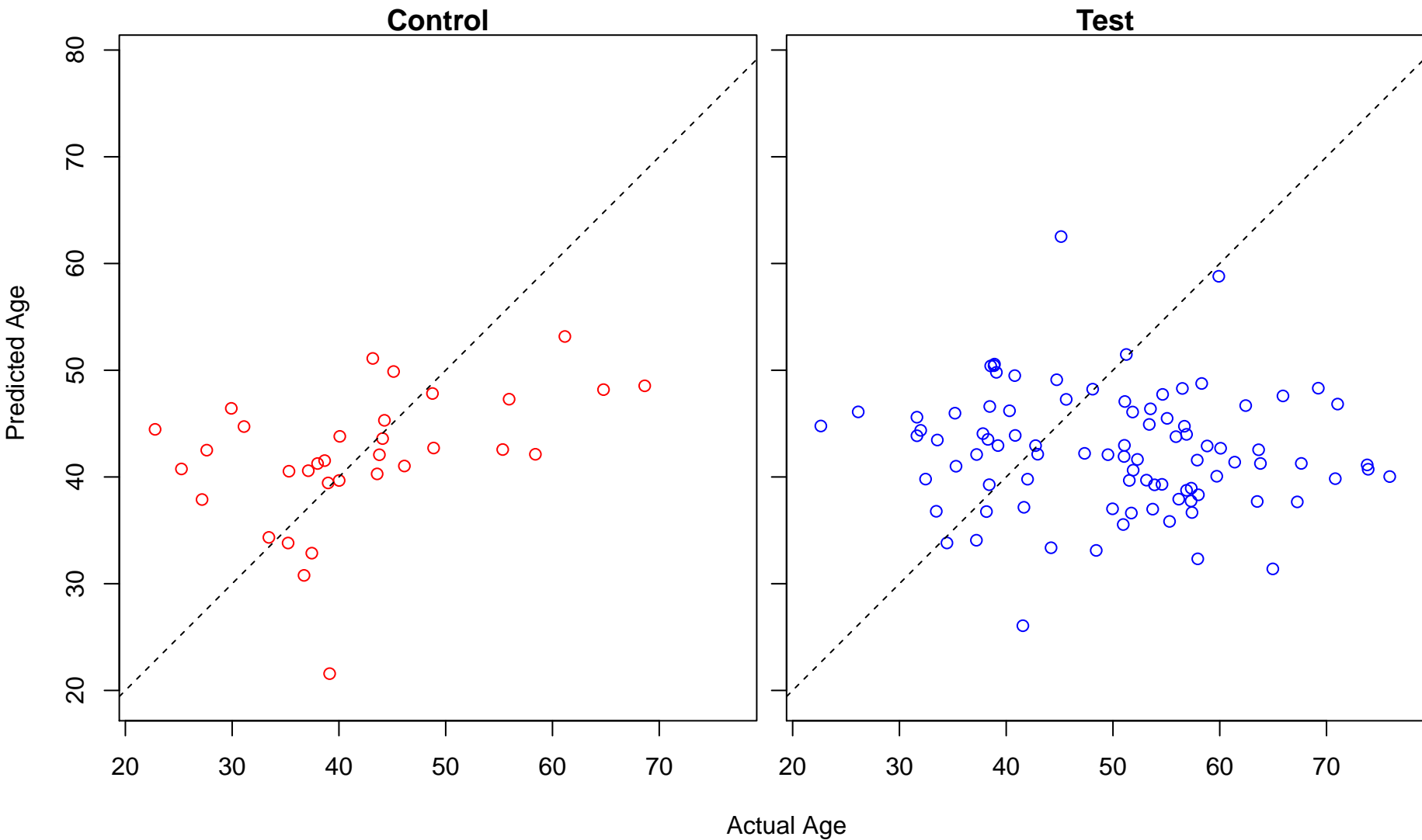
cytoplasmic transport (Score: 0.684325)



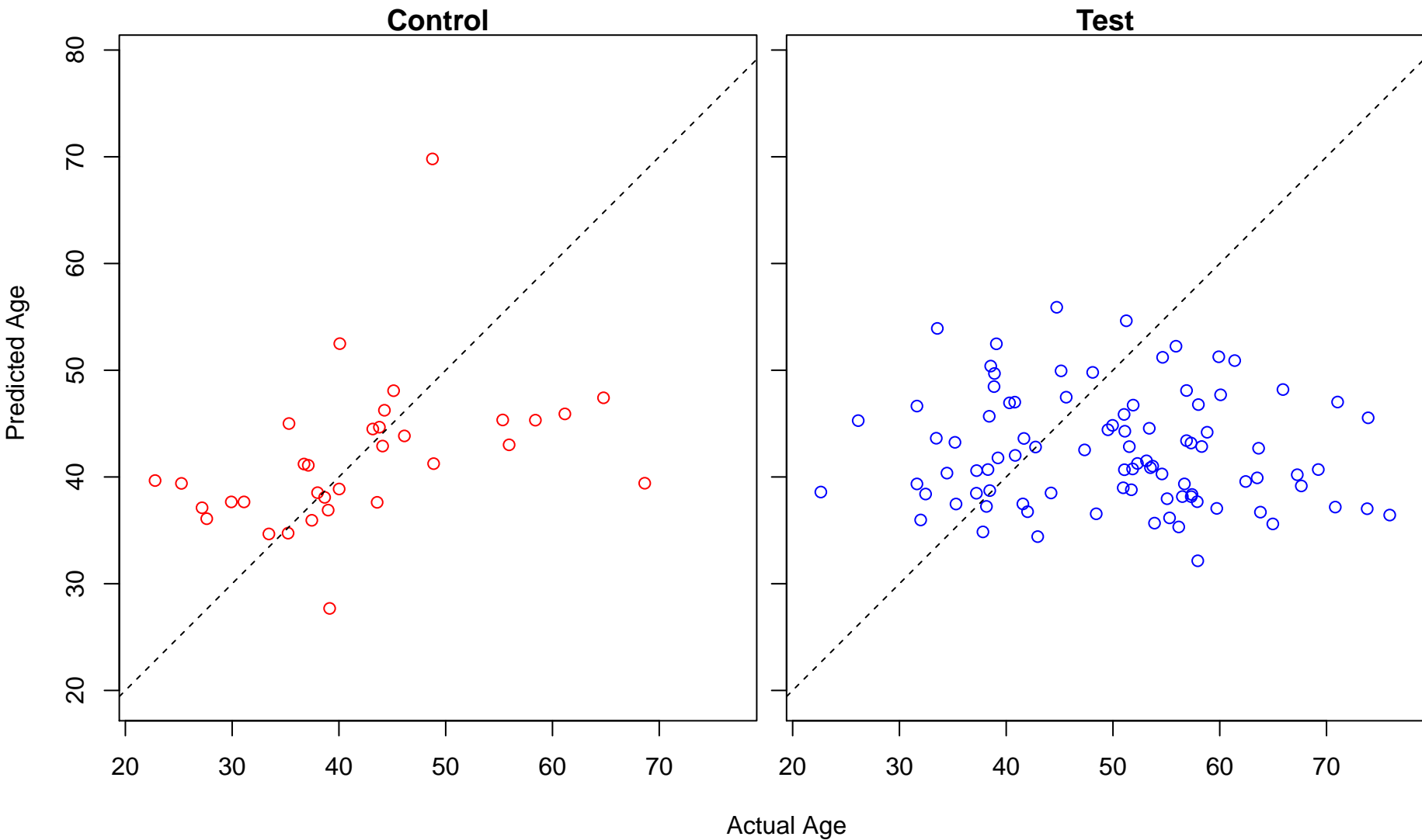
pentose-phosphate shunt, oxidative branch (Score: 0.683451)



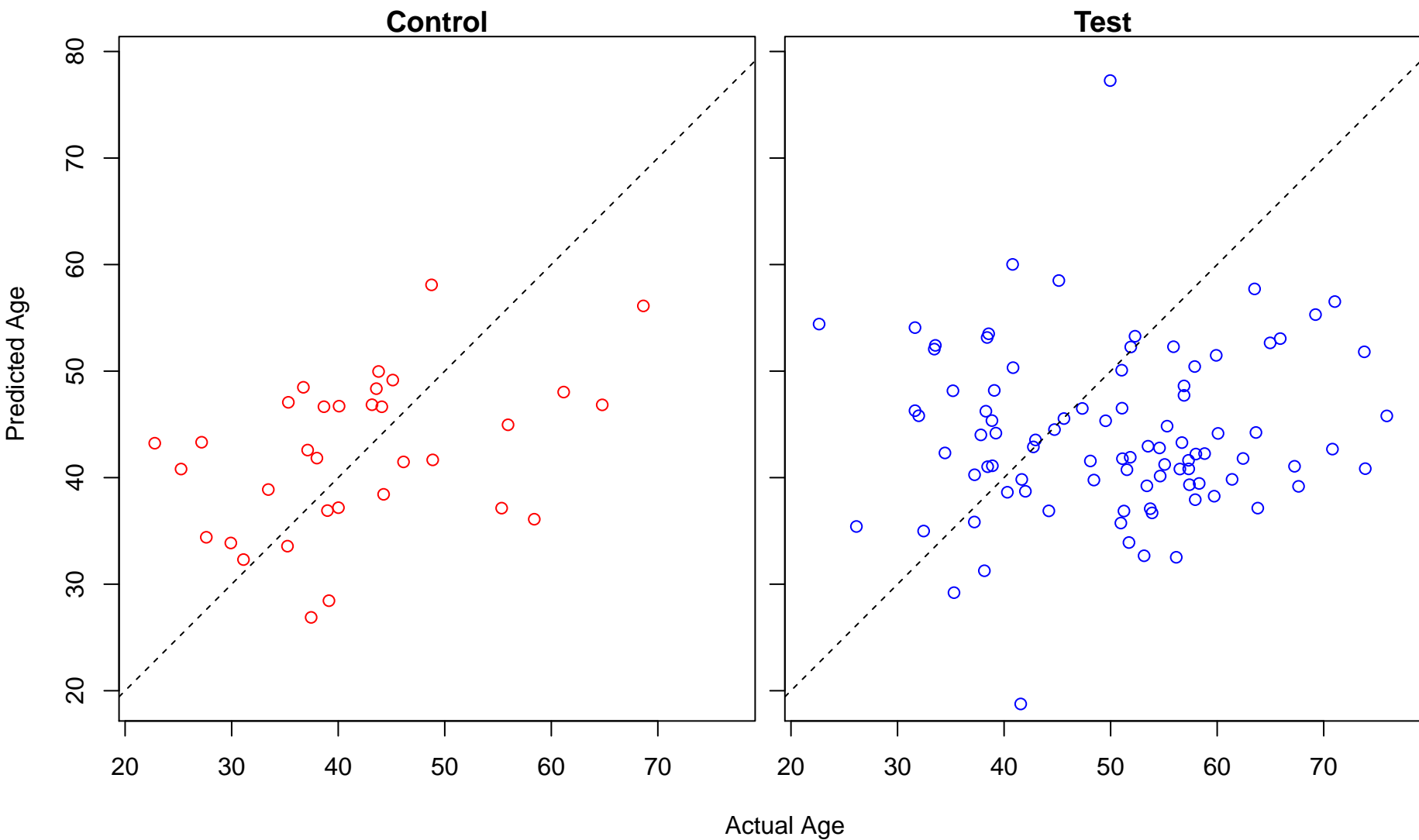
outer dynein arm assembly (Score: 0.683294)



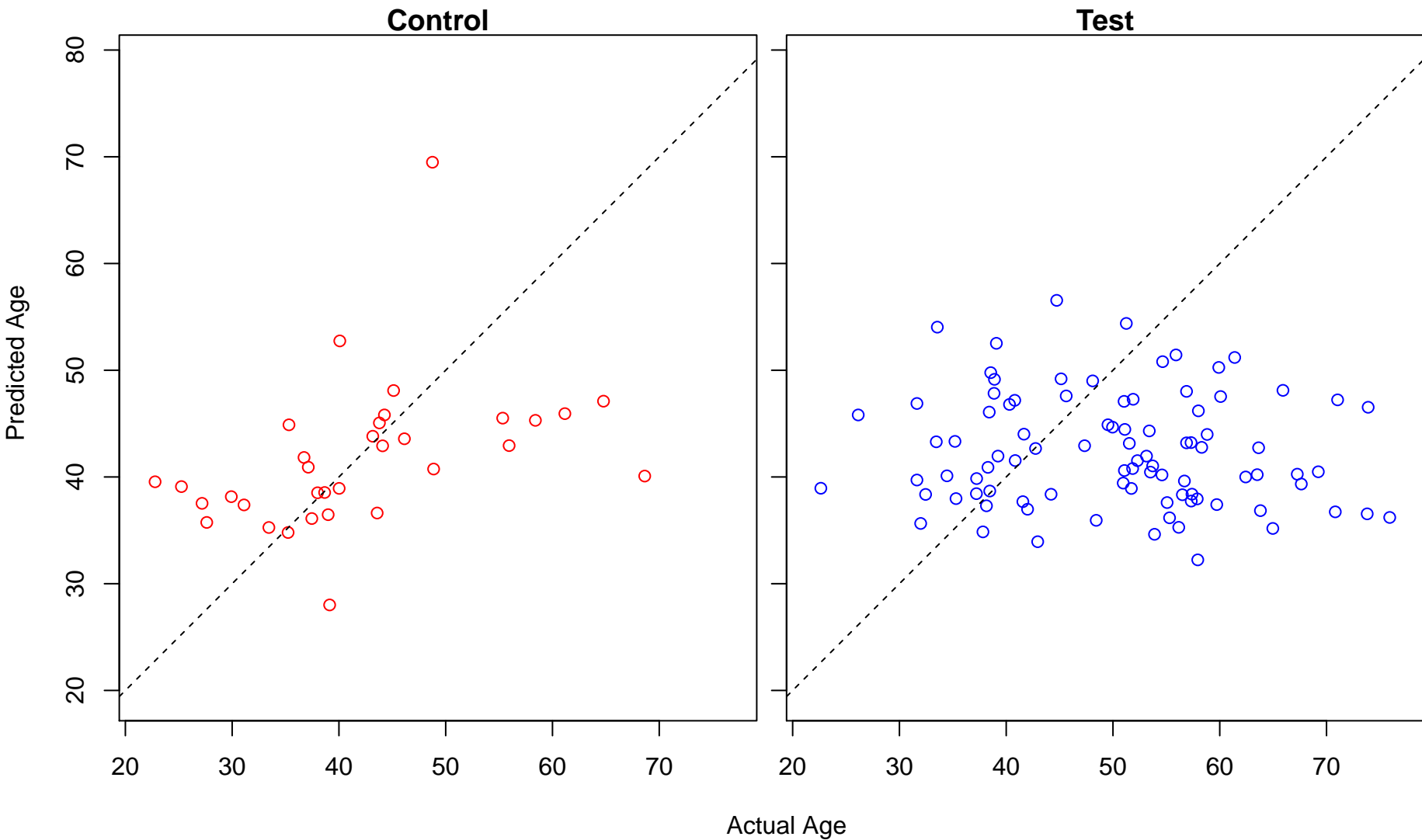
regulation of cellular metabolic process (Score: 0.683165)



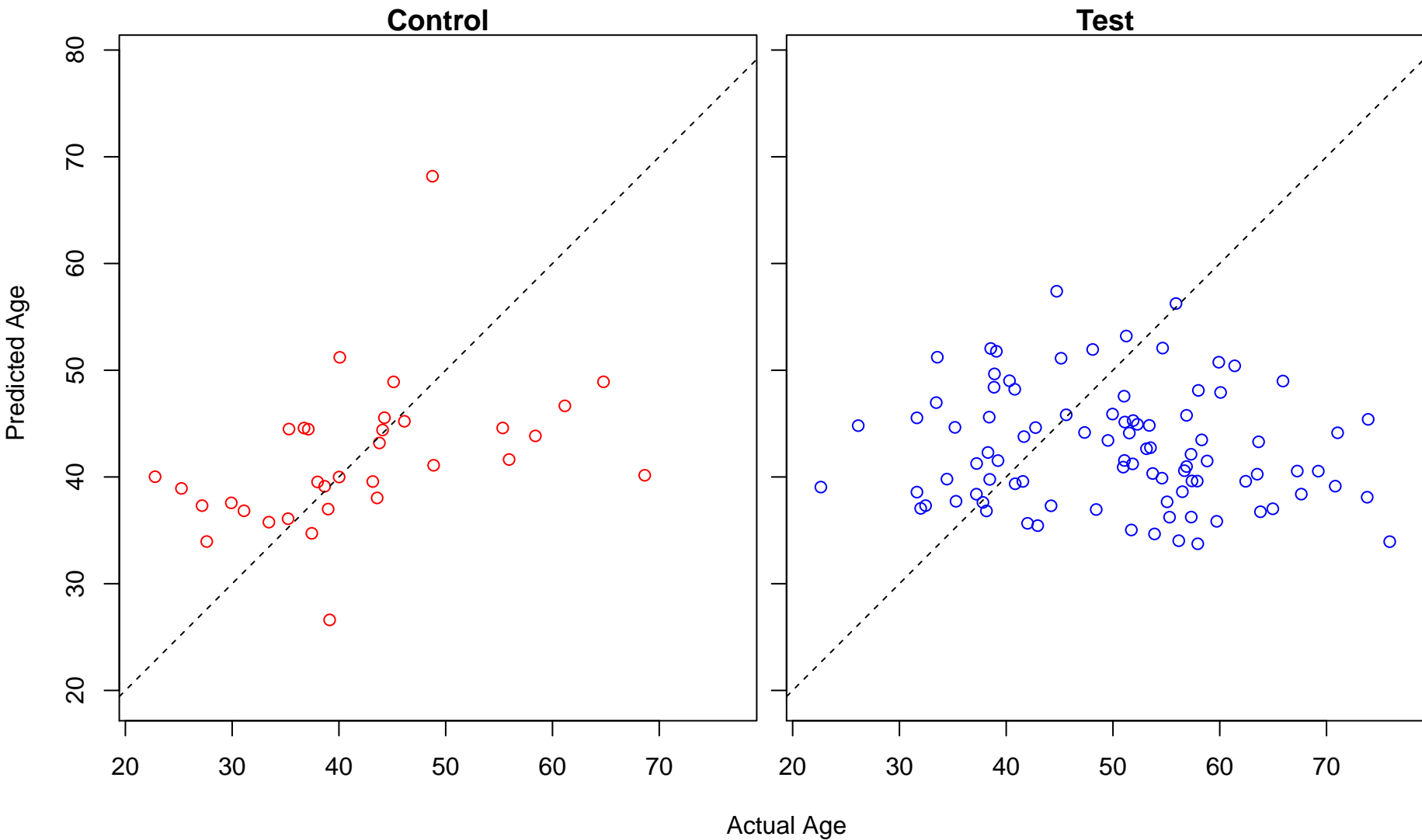
positive regulation of protein autophosphorylation (Score: 0.683099)



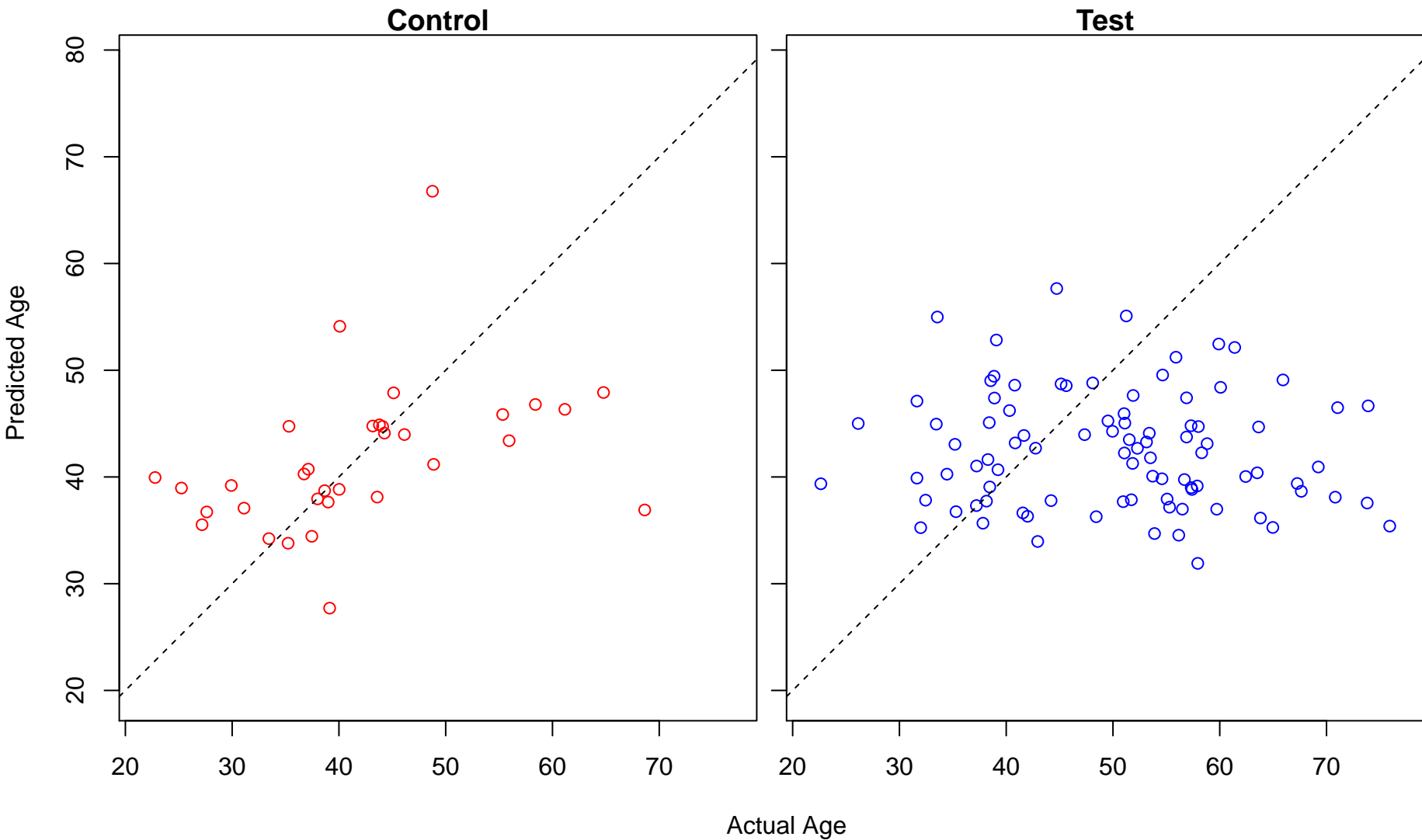
positive regulation of cellular metabolic process (Score: 0.682747)



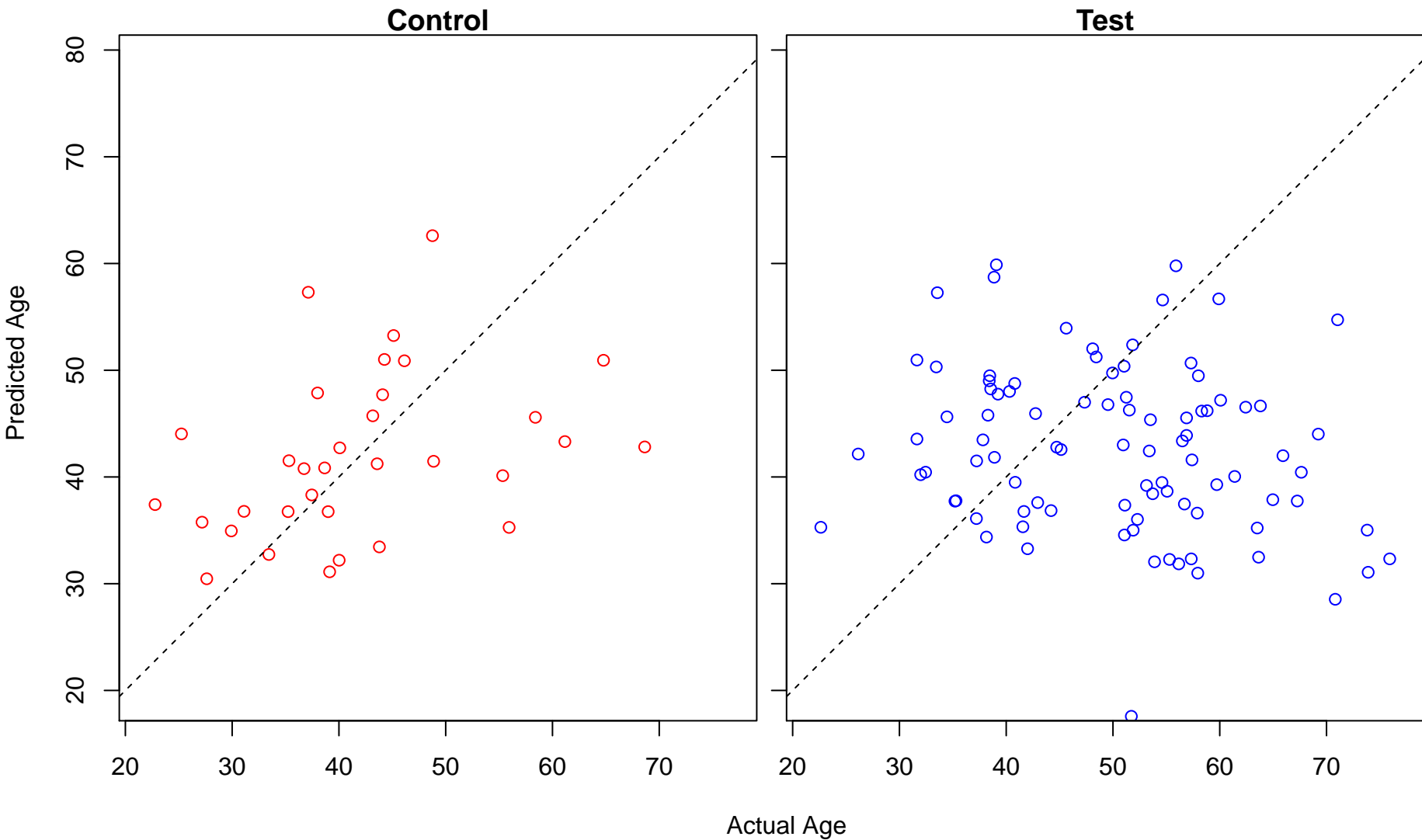
regulation of establishment of protein localization (Score: 0.682628)



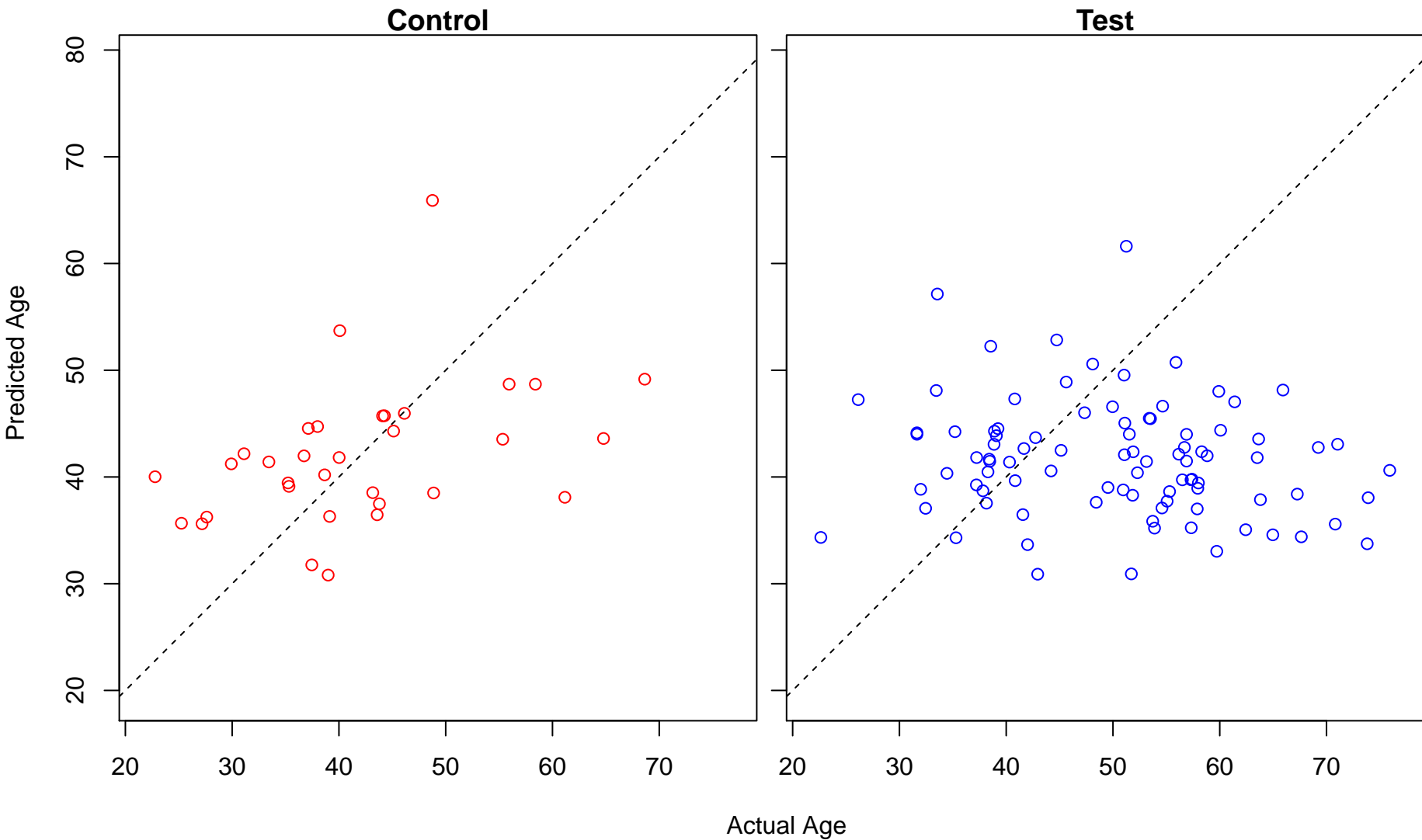
carbohydrate derivative metabolic process (Score: 0.682208)



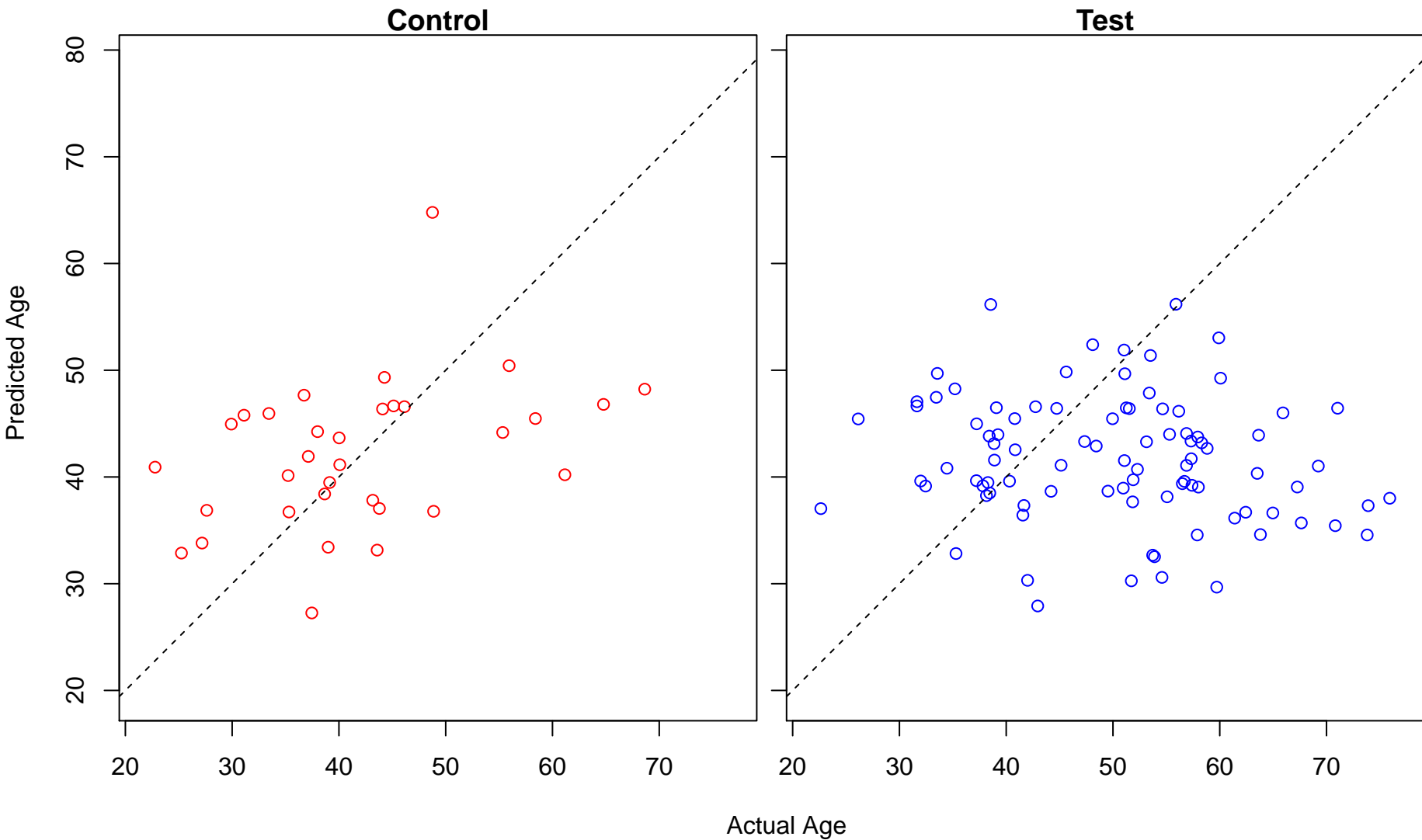
negative regulation of stress fiber assembly (Score: 0.682142)



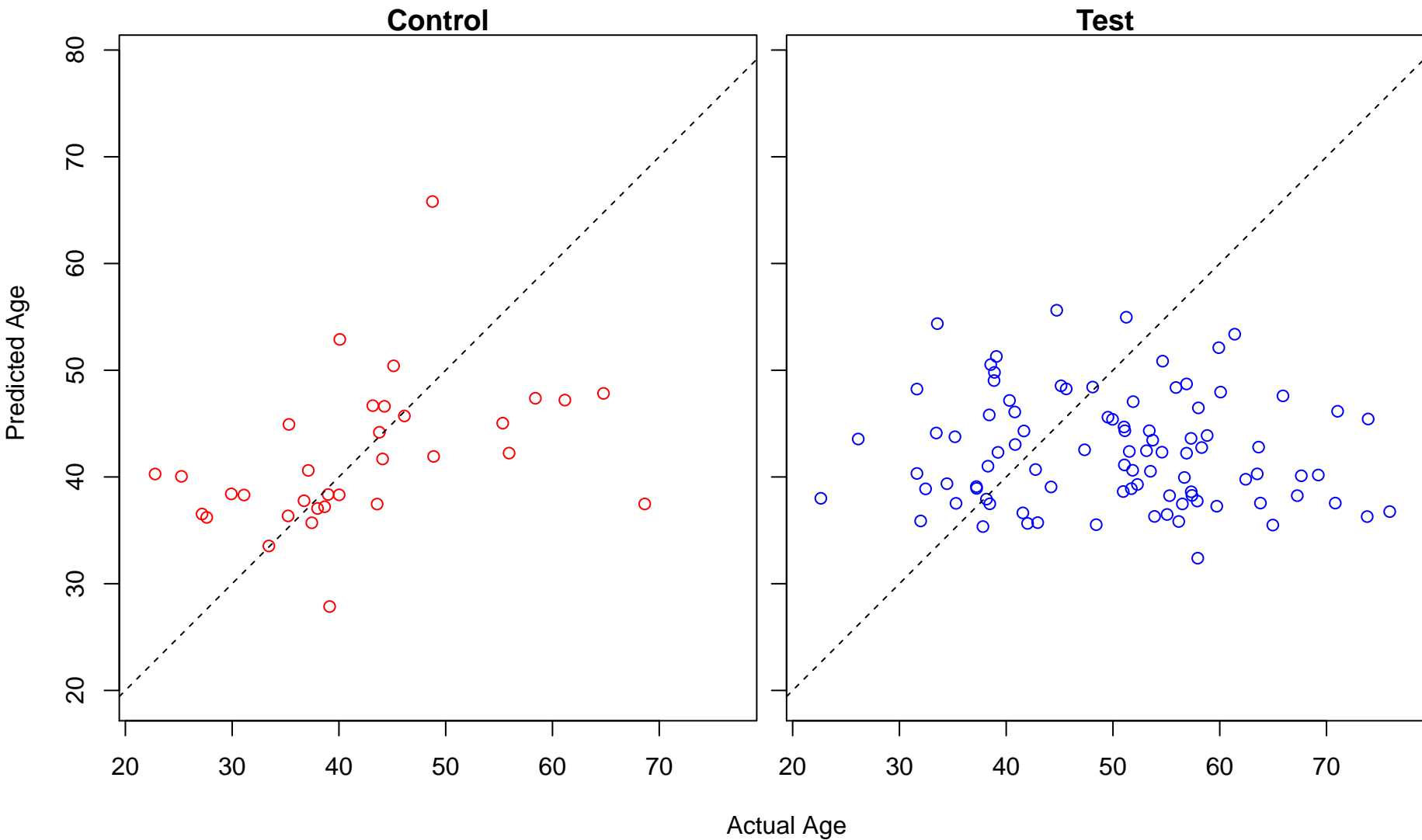
negative regulation of nucleotide metabolic process (Score: 0.681856)



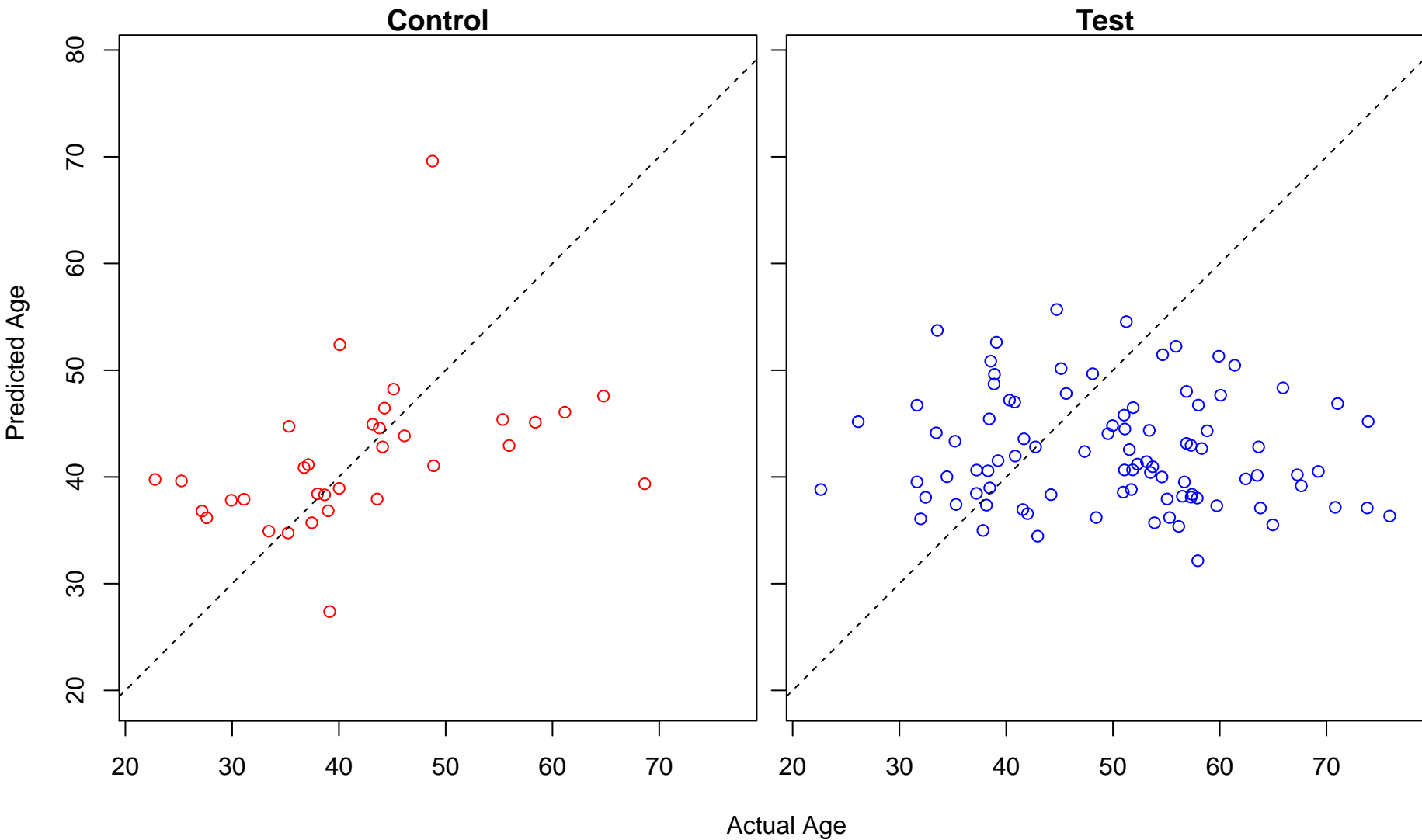
negative regulation of cyclic nucleotide biosynthetic process (Score: 0.681818)



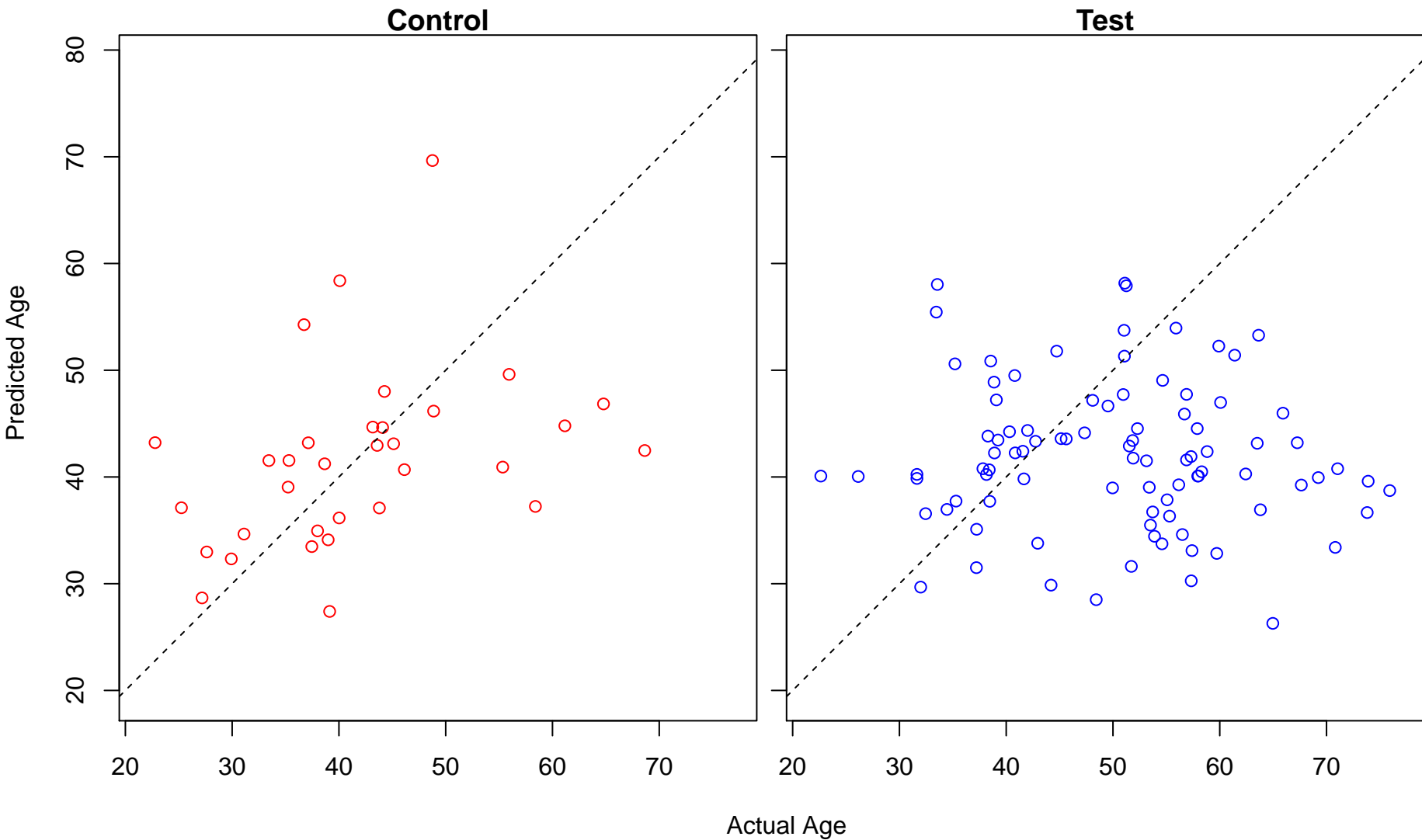
proteolysis involved in cellular protein catabolic process (Score: 0.681728)



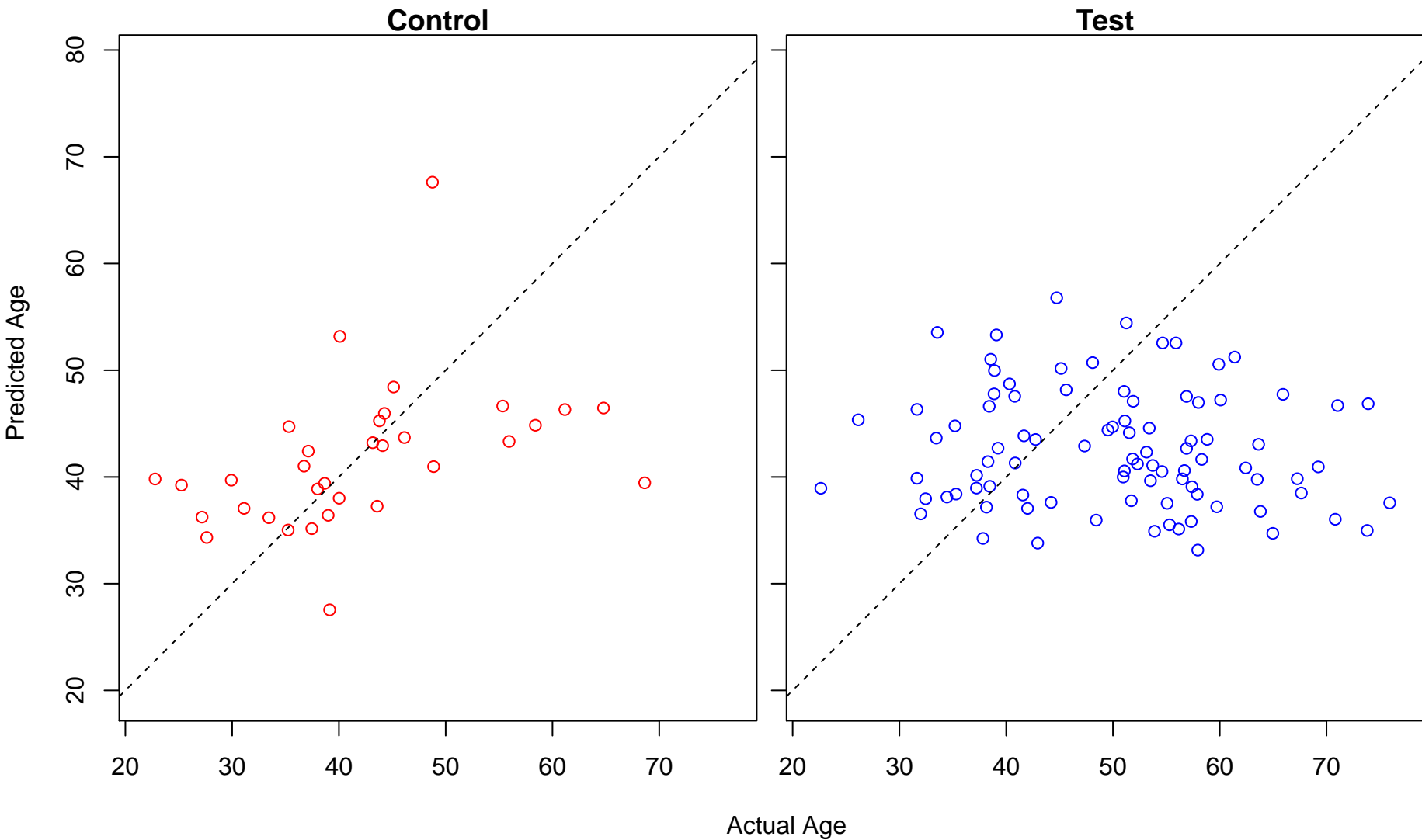
regulation of metabolic process (Score: 0.681661)



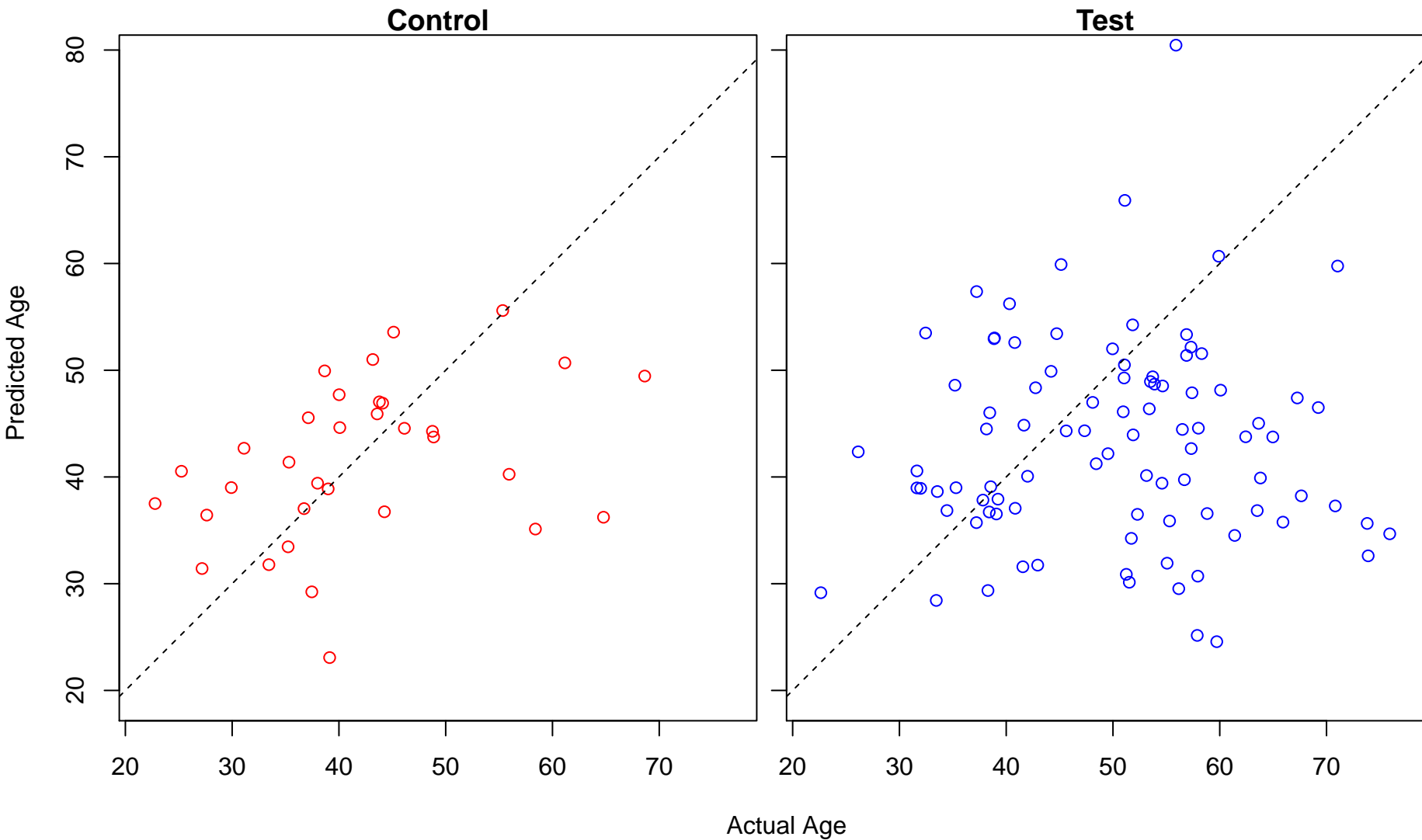
cellular modified amino acid metabolic process (Score: 0.681558)



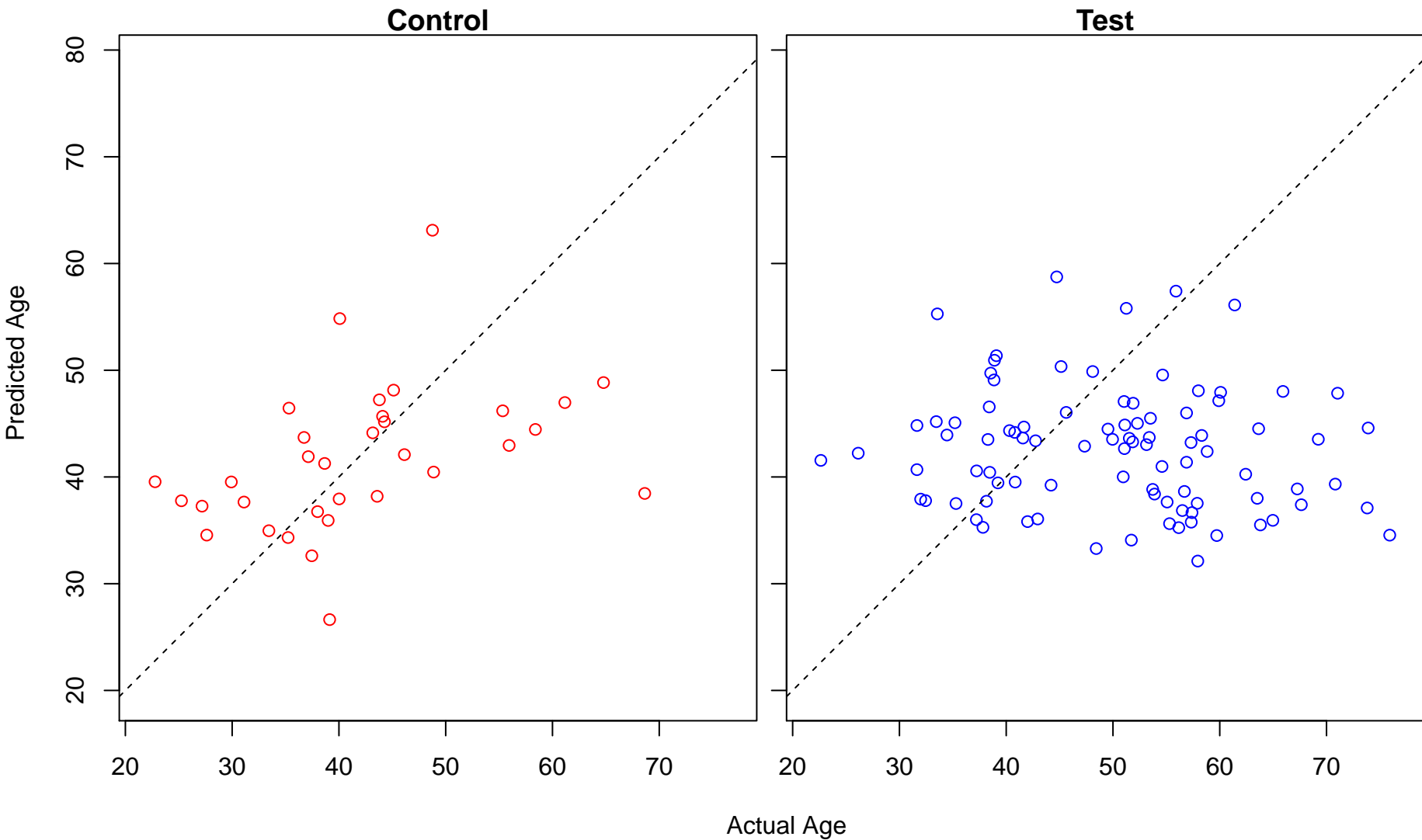
positive regulation of cellular protein metabolic process (Score: 0.680806)



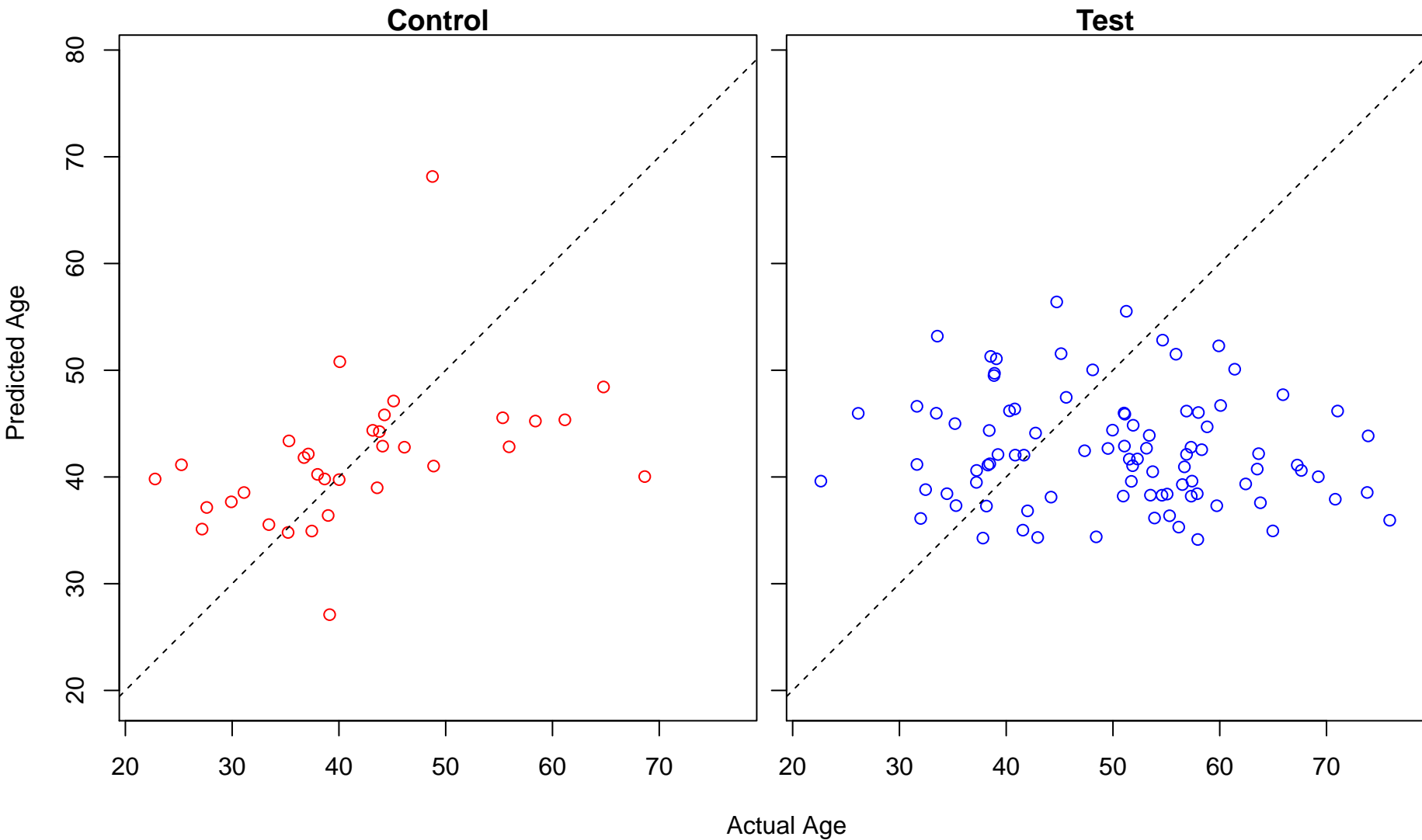
regulation of voltage-gated calcium channel activity (Score: 0.680733)



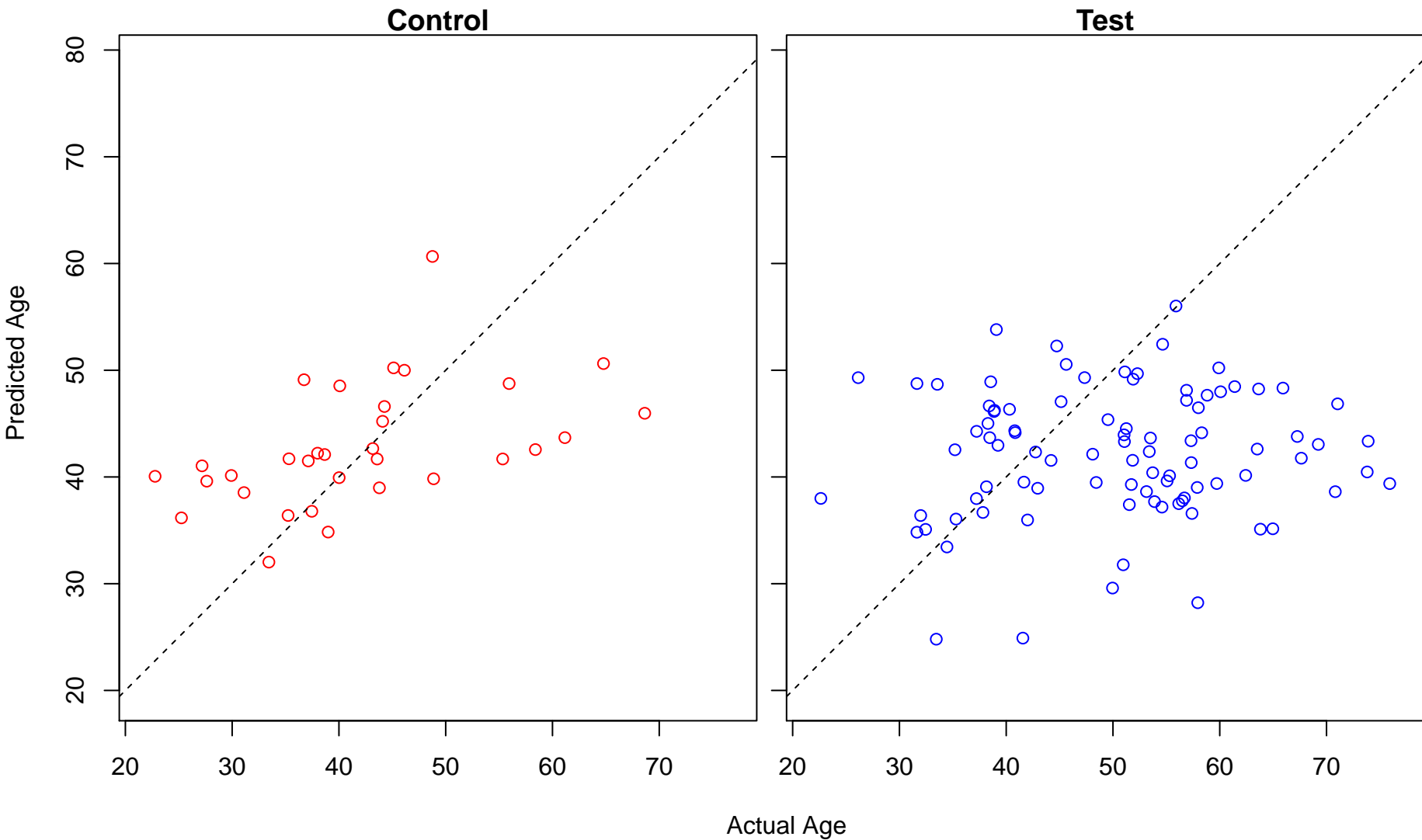
regulation of mitochondrion organization (Score: 0.680717)



multicellular organismal development (Score: 0.680703)

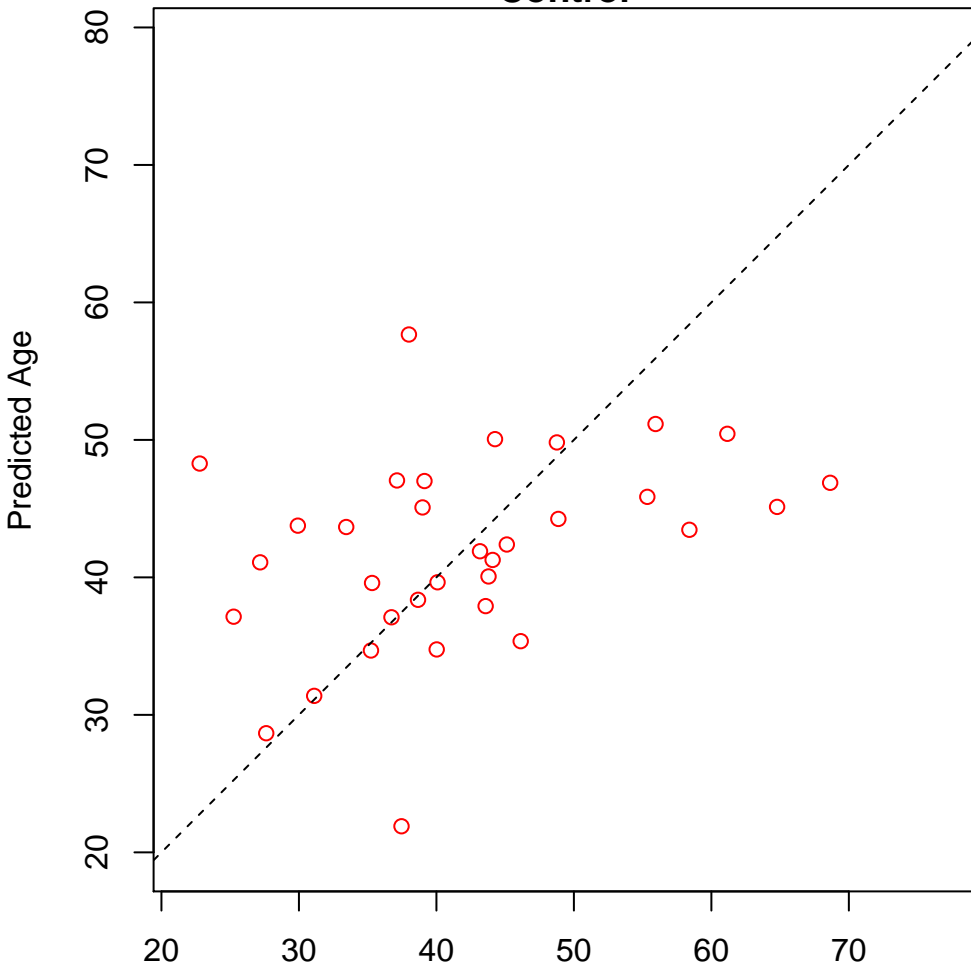


regulation of myosin-light-chain-phosphatase activity (Score: 0.680646)

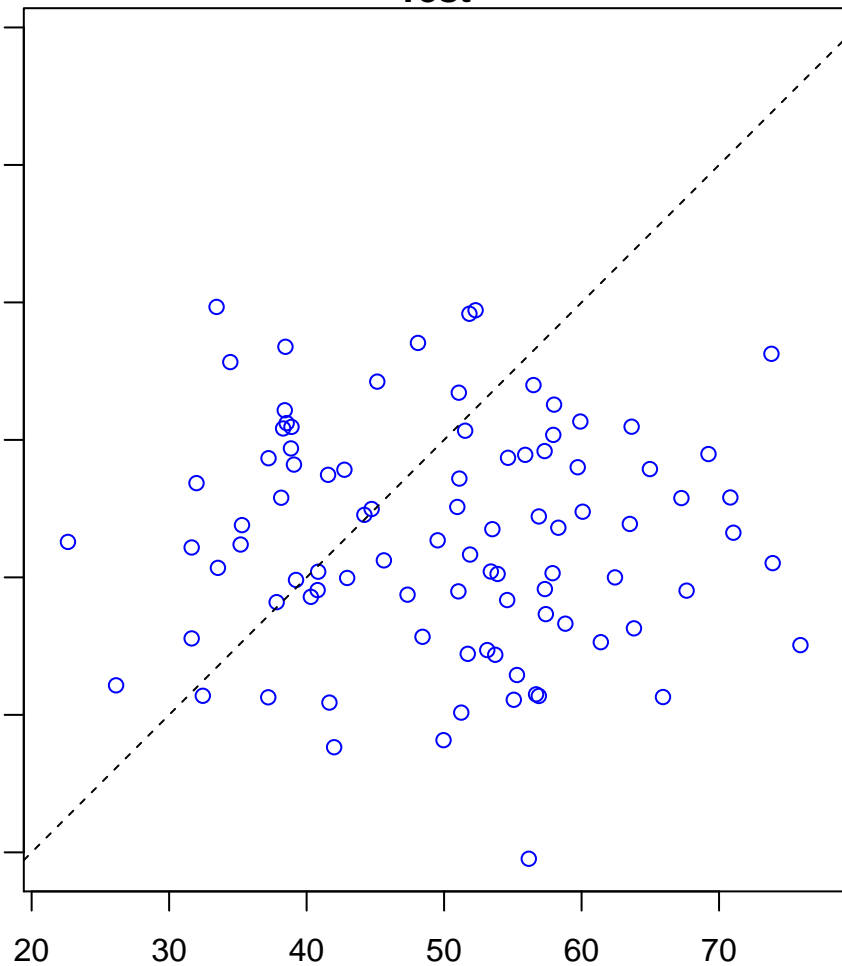


ossification involved in bone maturation (Score: 0.679772)

Control

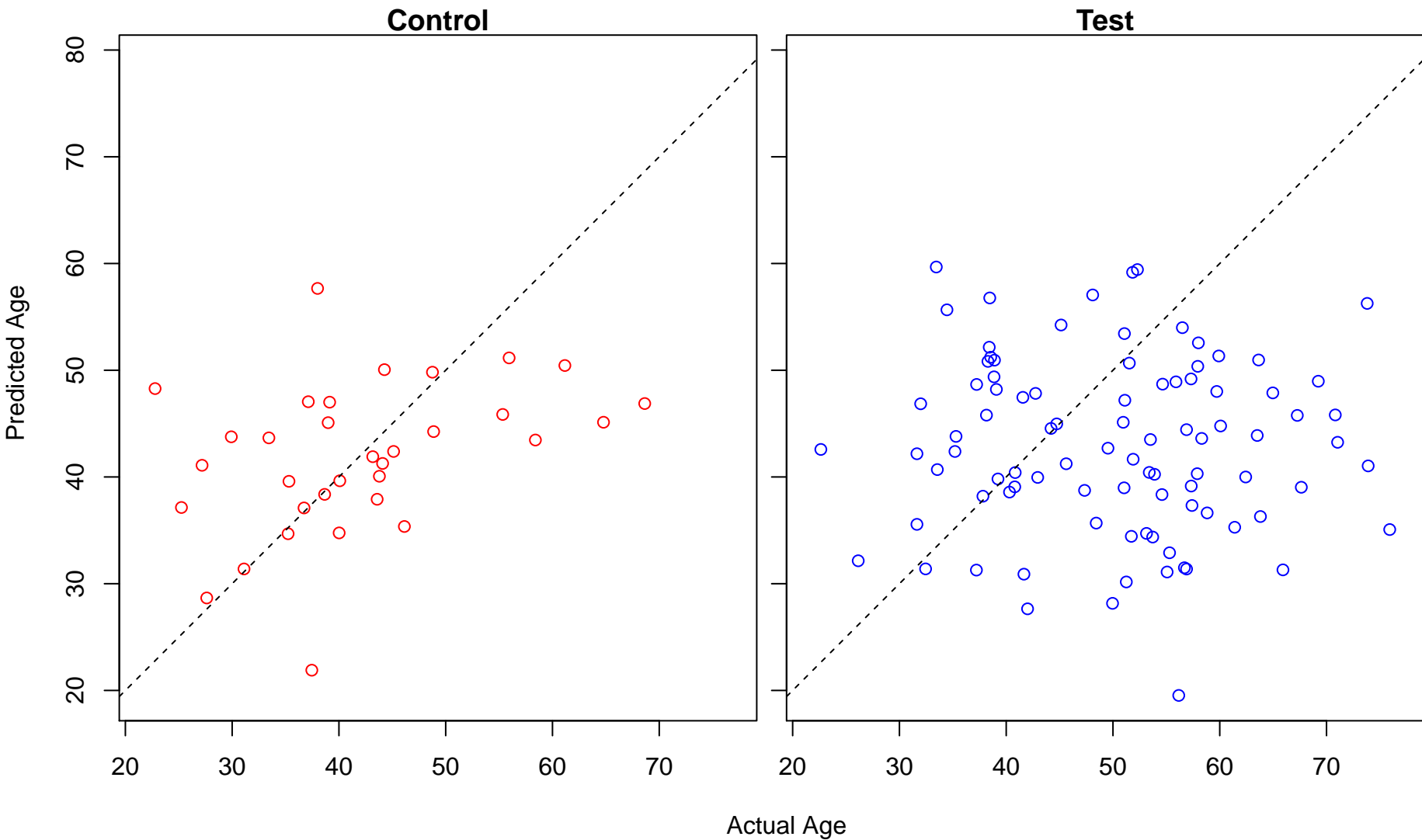


Test

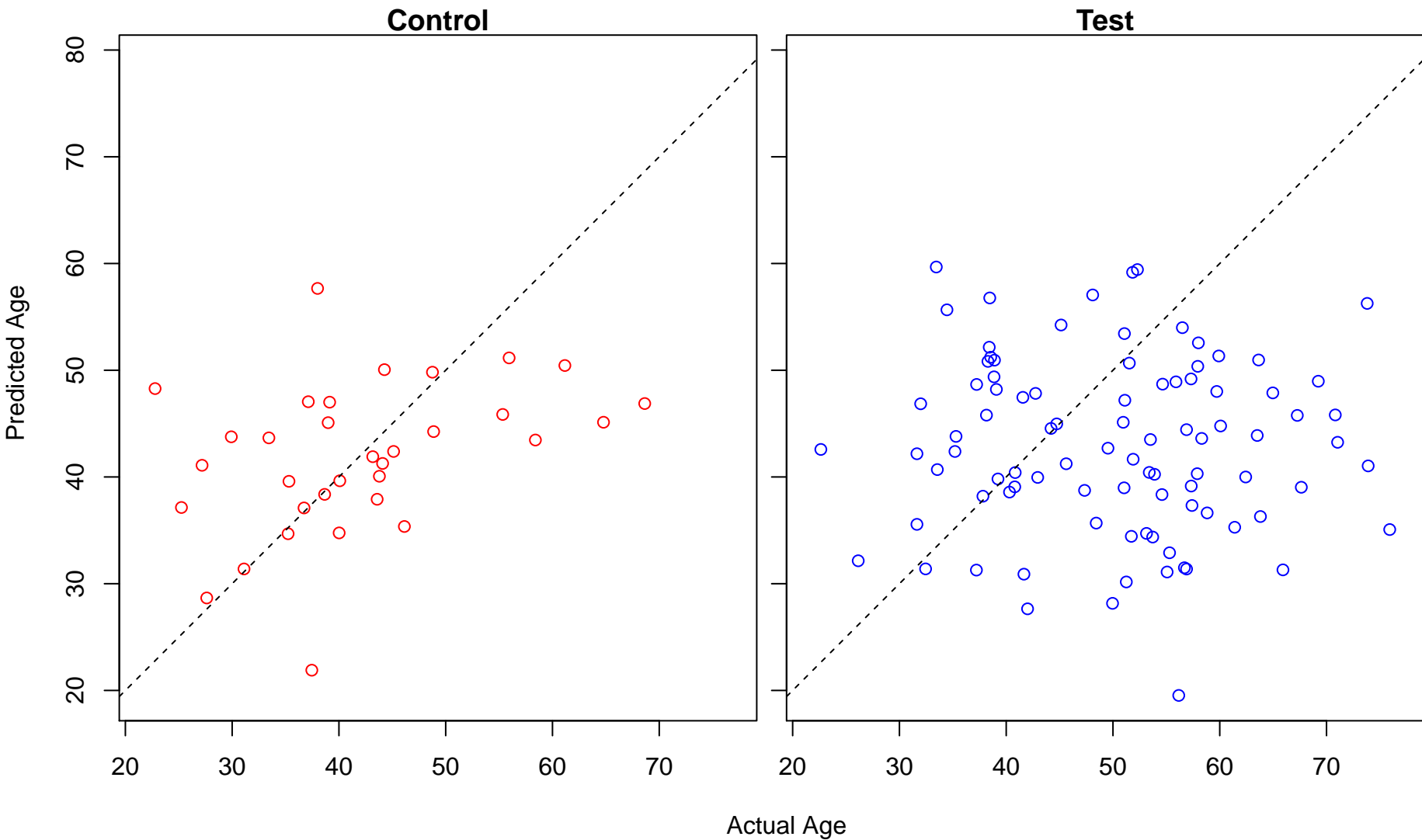


Actual Age

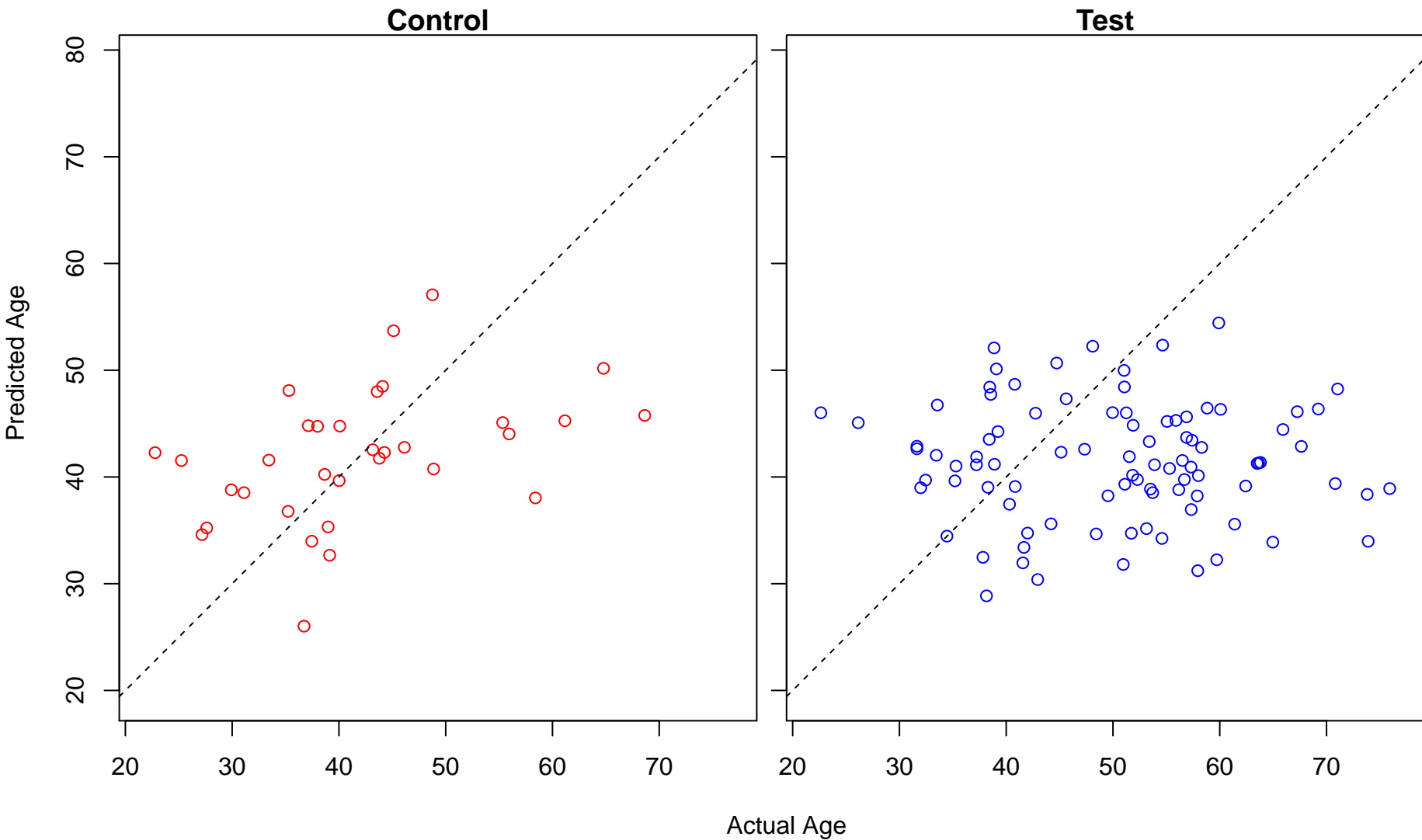
organ maturation (Score: 0.679772)



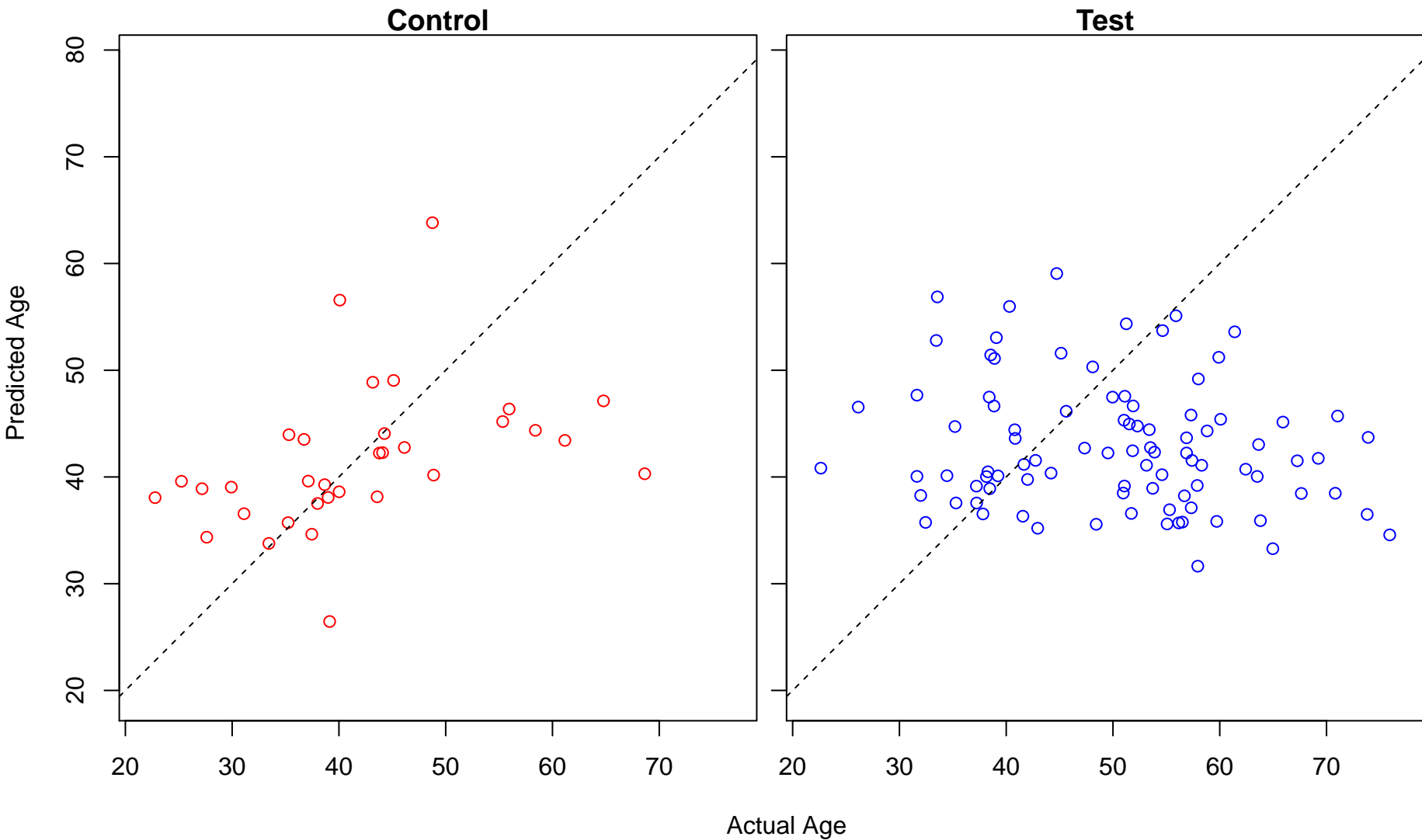
bone maturation (Score: 0.679772)



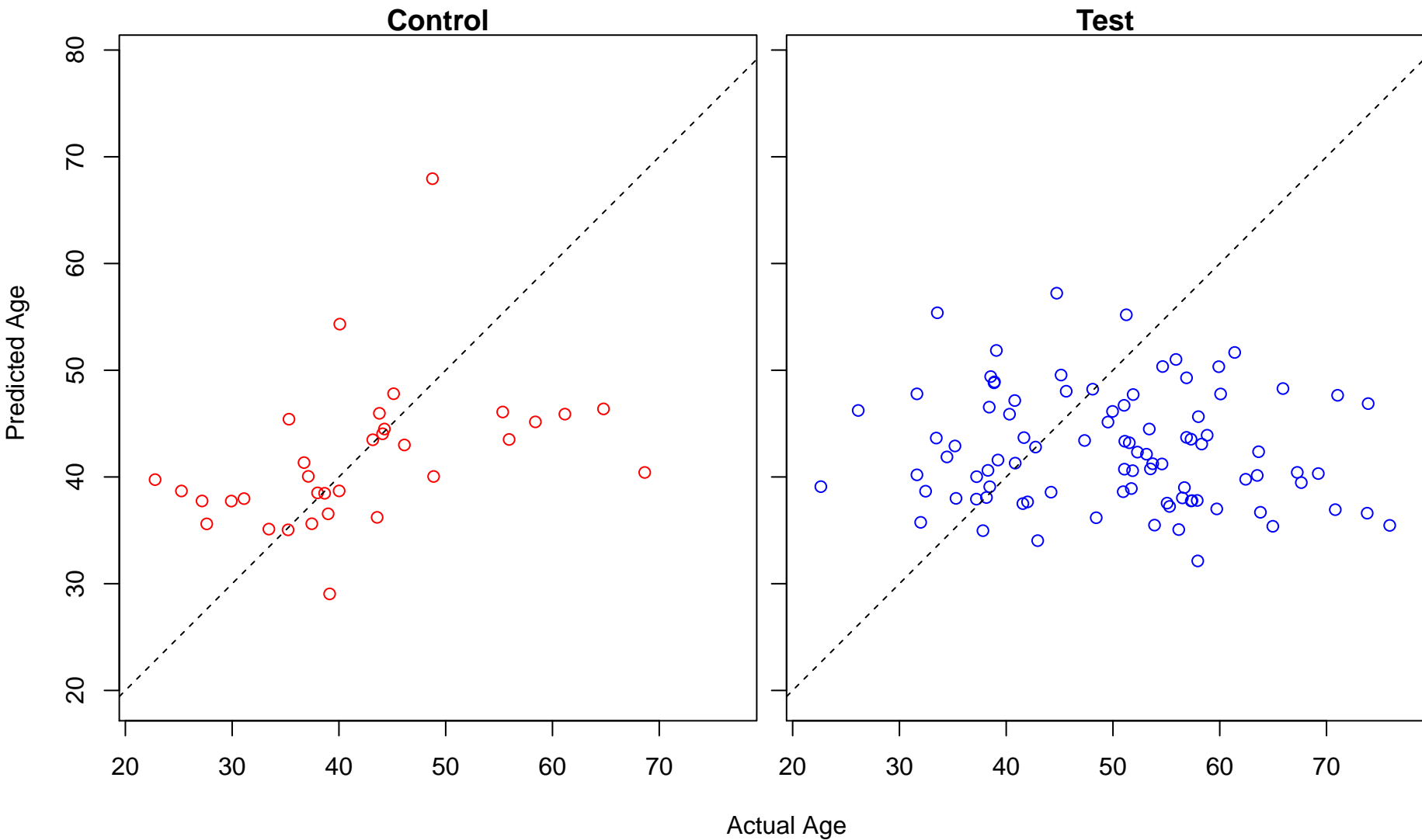
multivesicular body sorting pathway (Score: 0.679768)



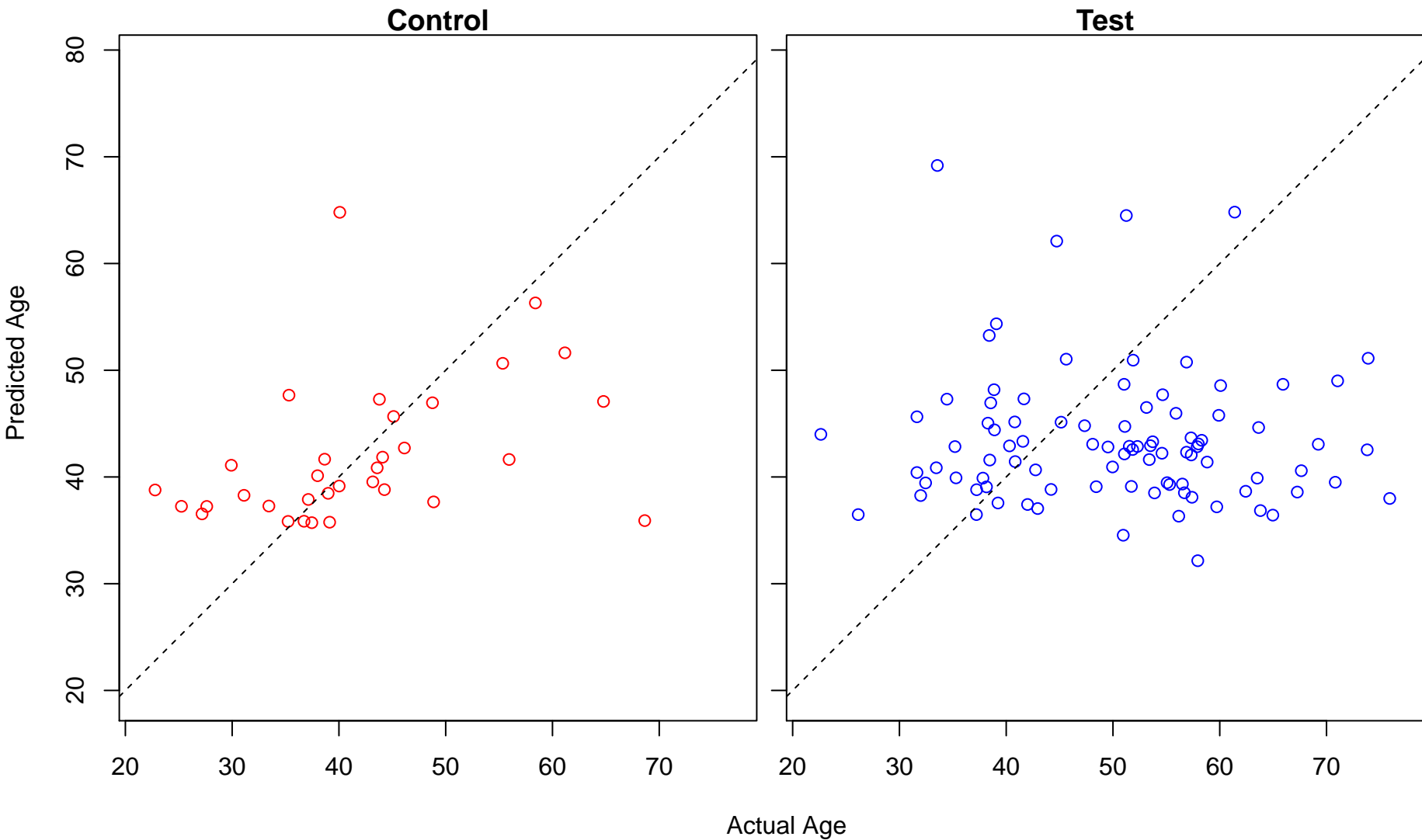
regulation of stress-activated MAPK cascade (Score: 0.679646)



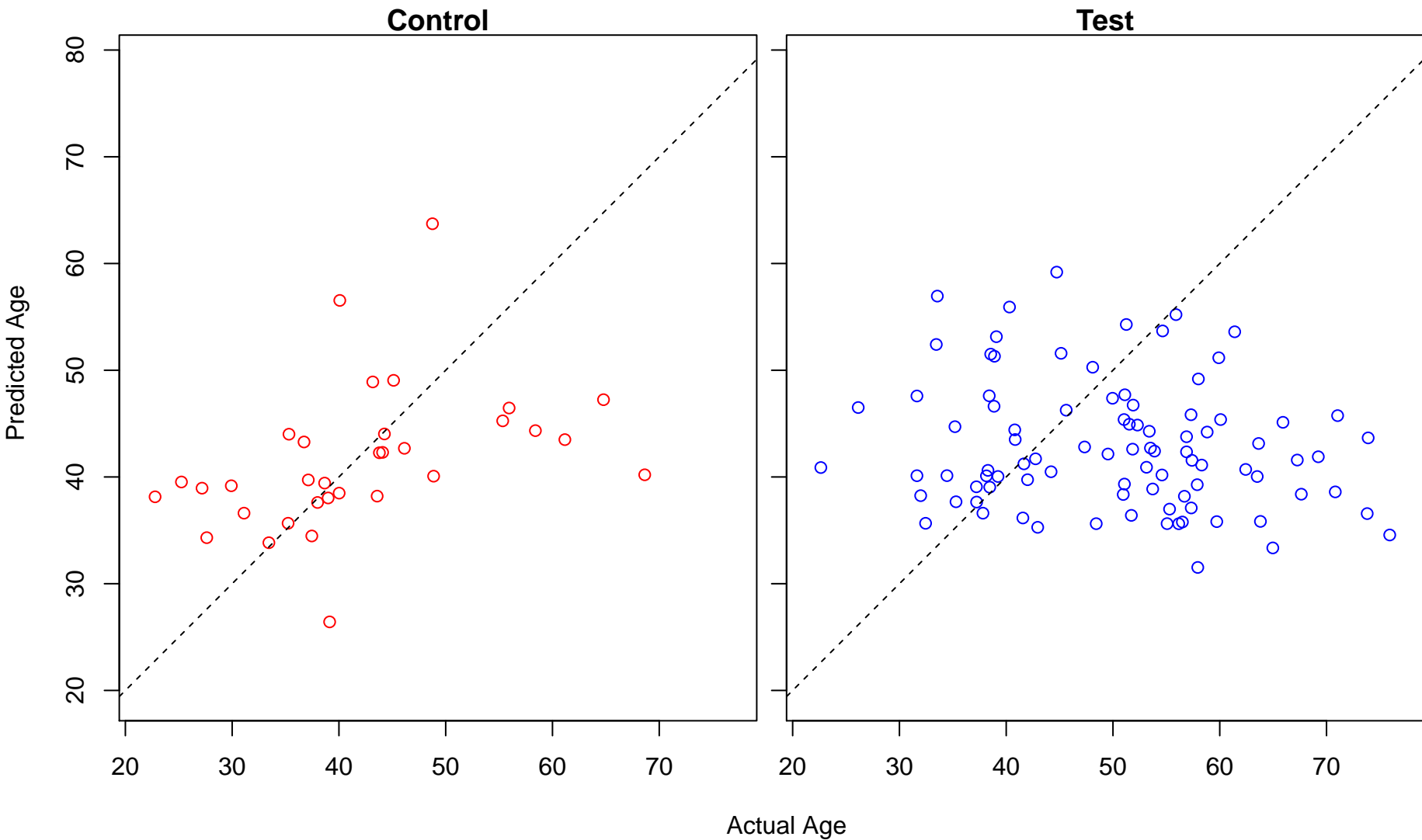
positive regulation of biosynthetic process (Score: 0.679333)



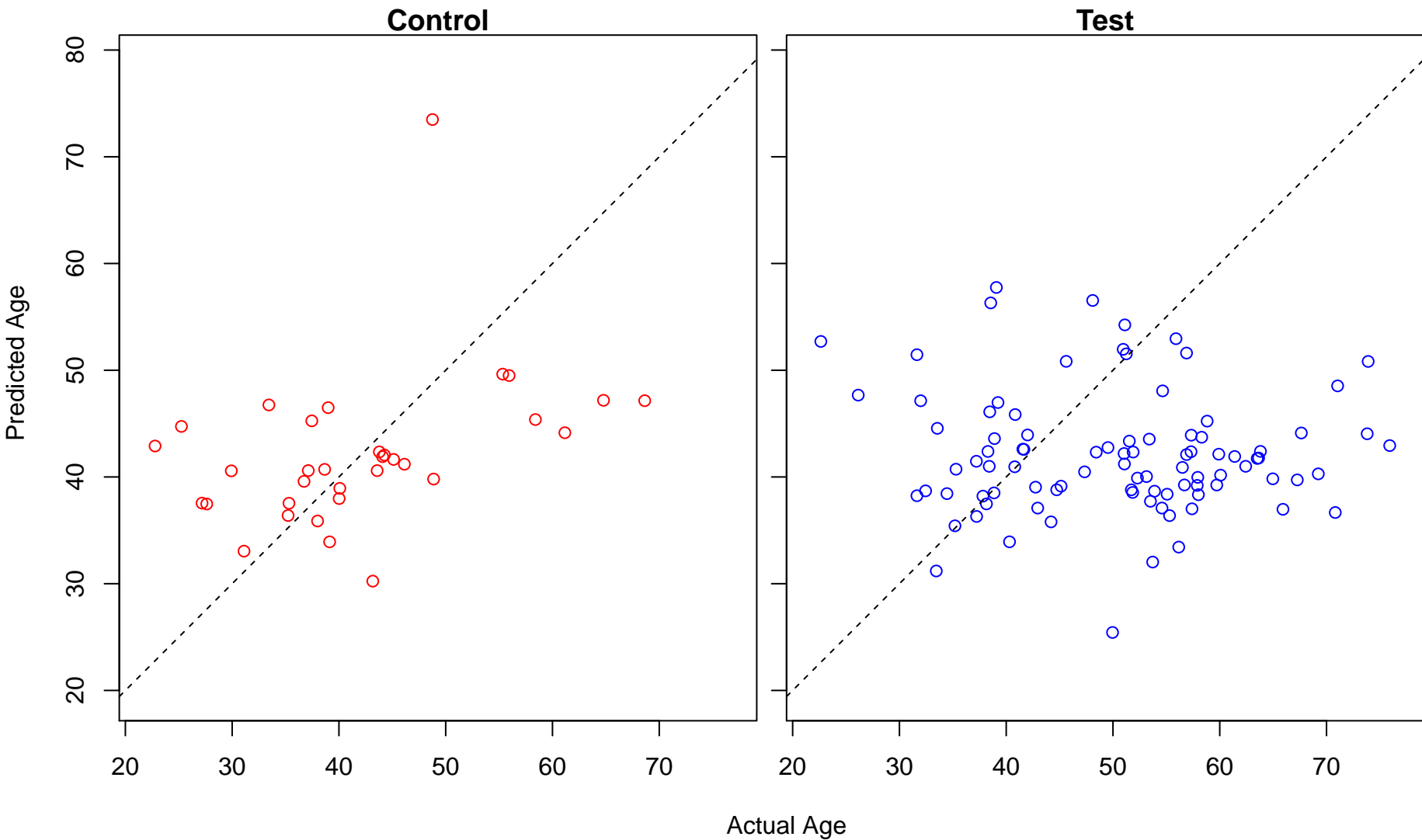
histone H2A ubiquitination (Score: 0.678929)



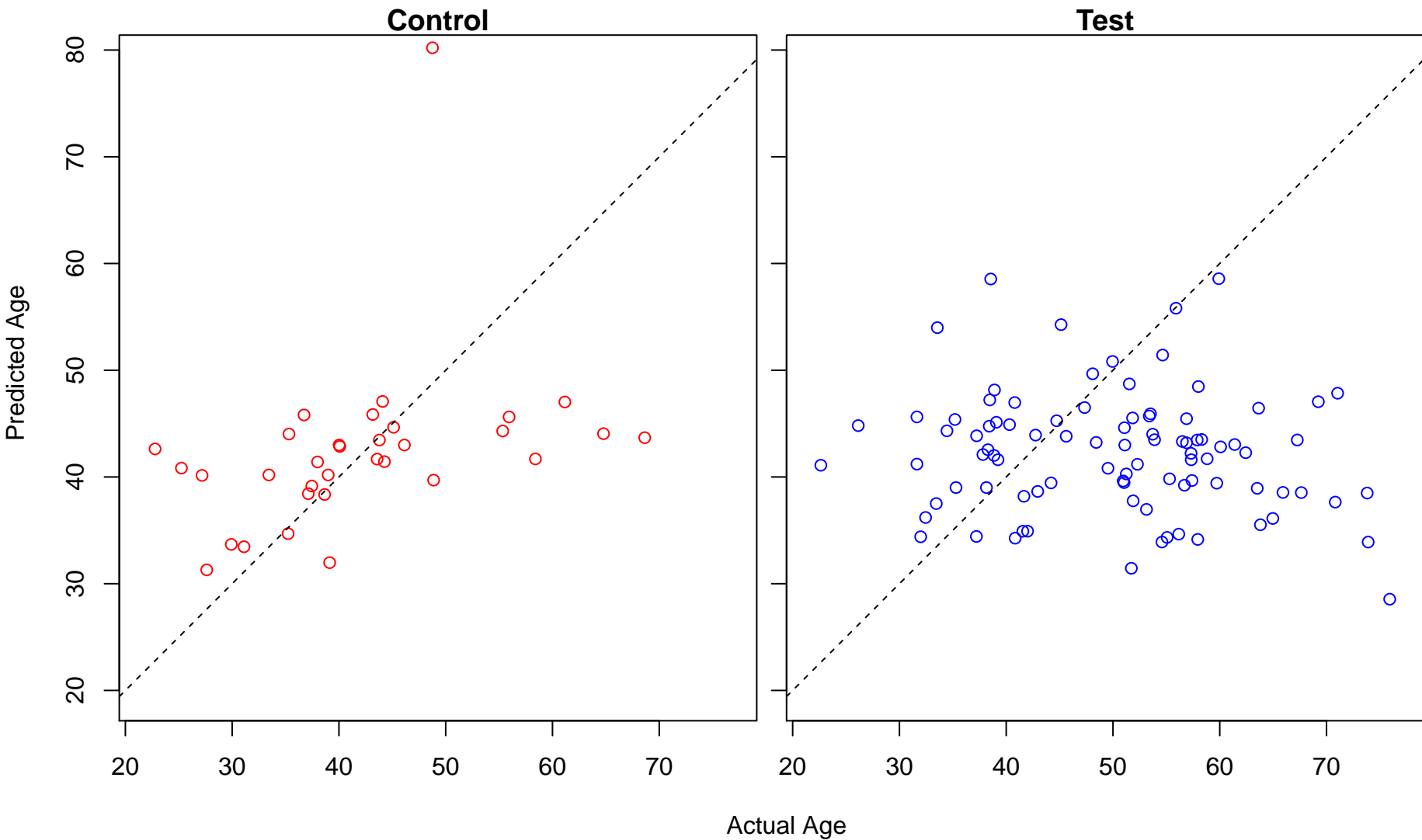
regulation of stress-activated protein kinase signaling cascade (Score: 0.678845)



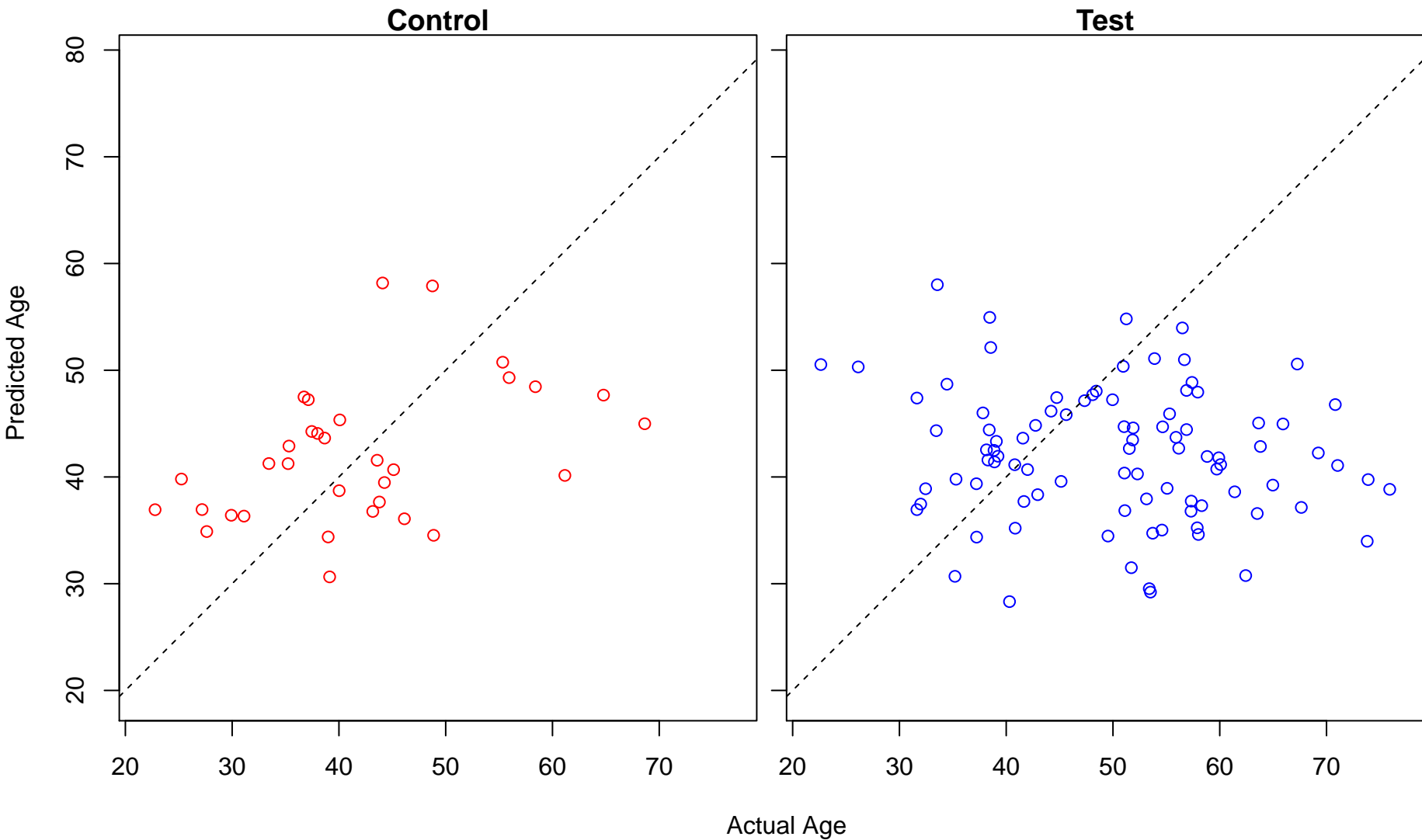
nuclear pore organization (Score: 0.678455)



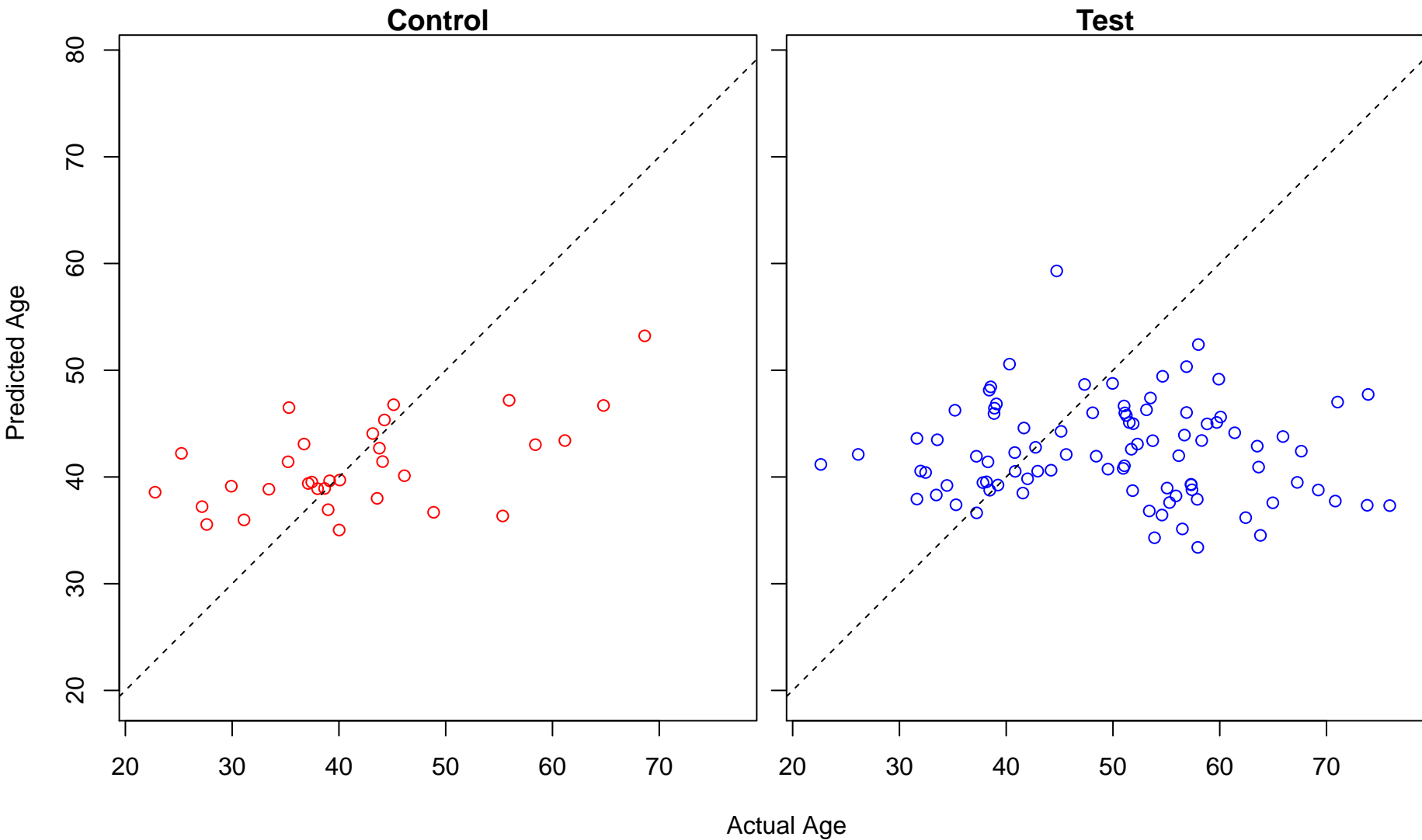
regulation of regulatory T cell differentiation (Score: 0.677519)



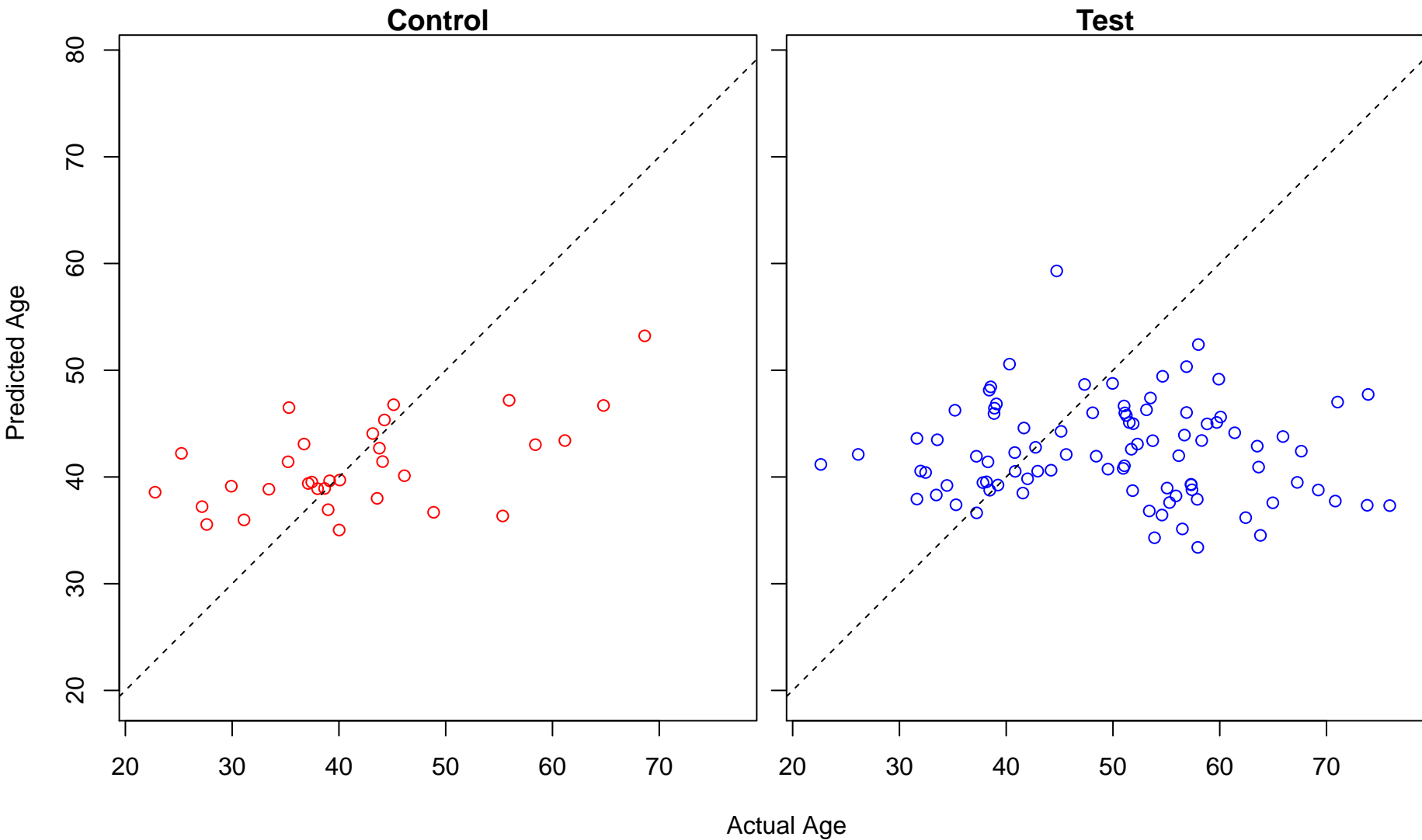
regulation of atrial cardiac muscle cell membrane depolarization (Score: 0.677211)



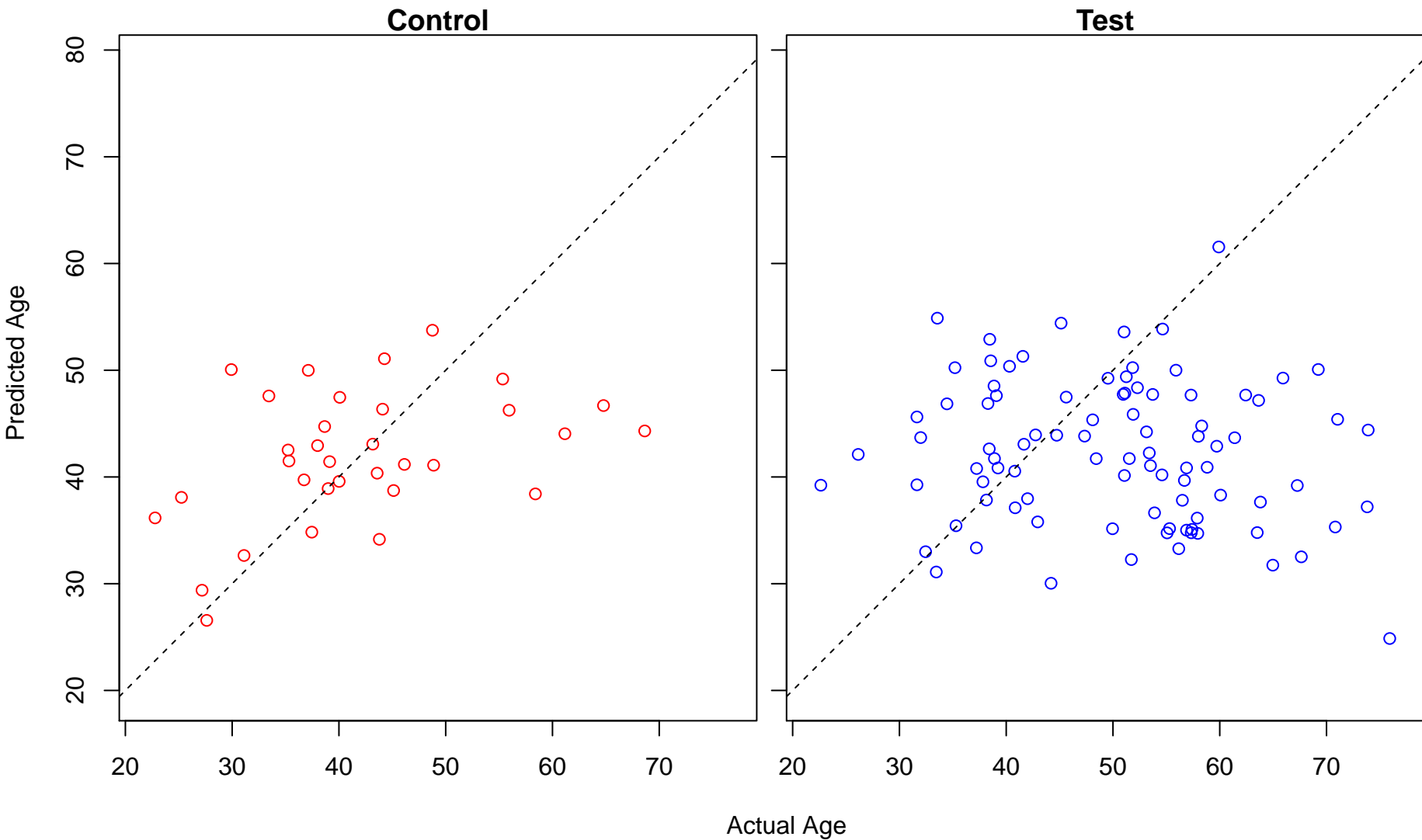
histone H4-K5 acetylation (Score: 0.677181)



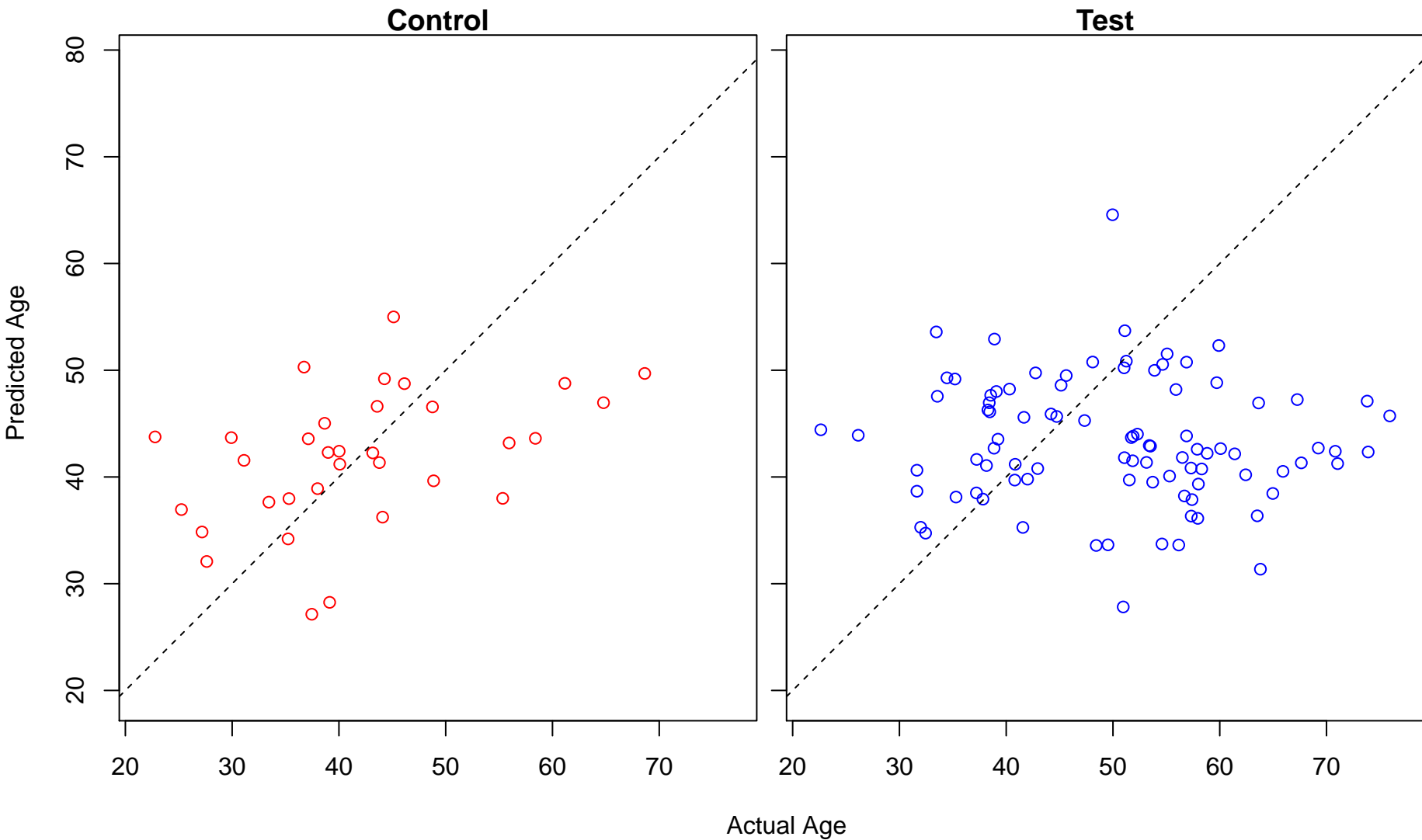
histone H4-K8 acetylation (Score: 0.677181)



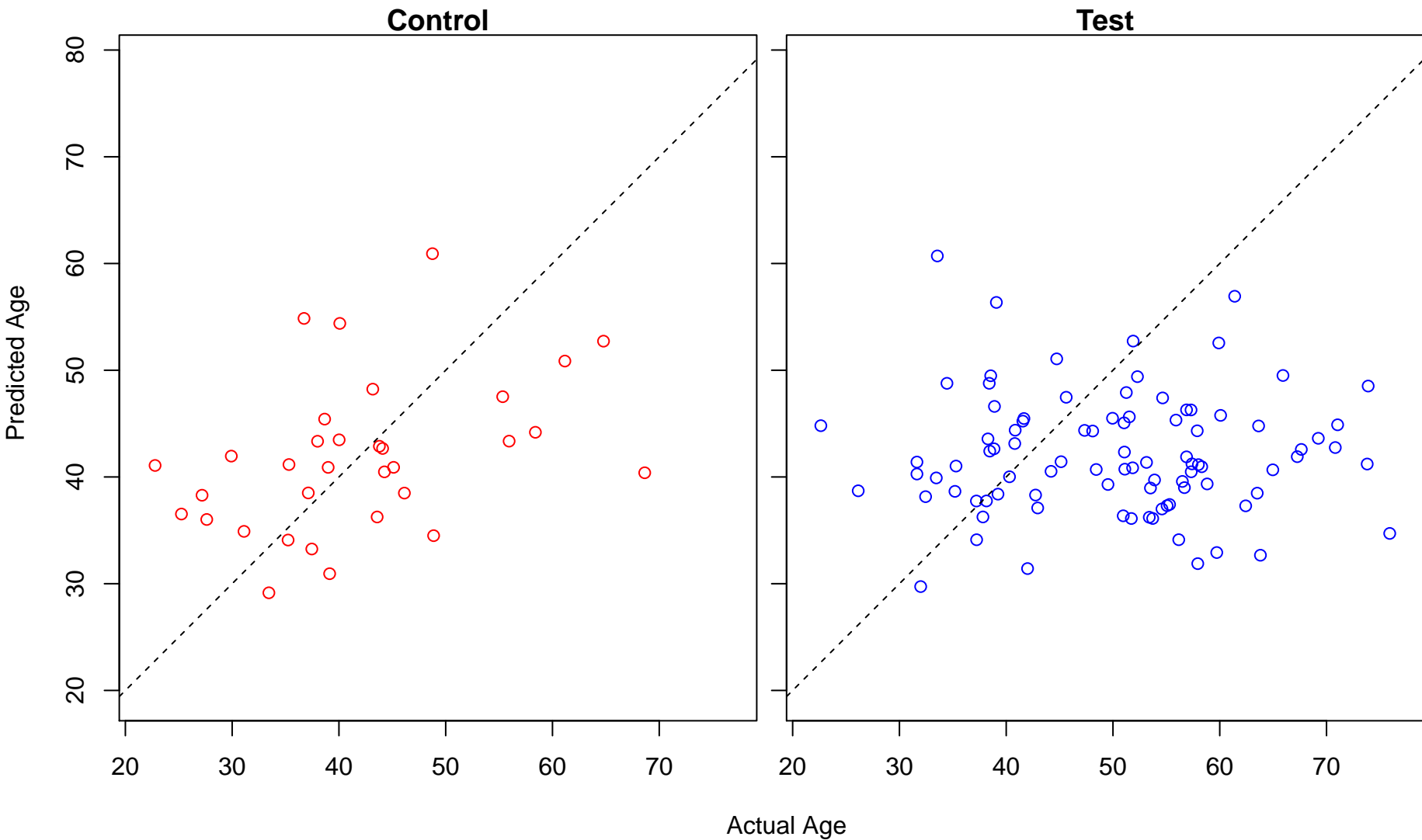
lateral ventricle development (Score: 0.677176)



regulation of respiratory gaseous exchange (Score: 0.677137)

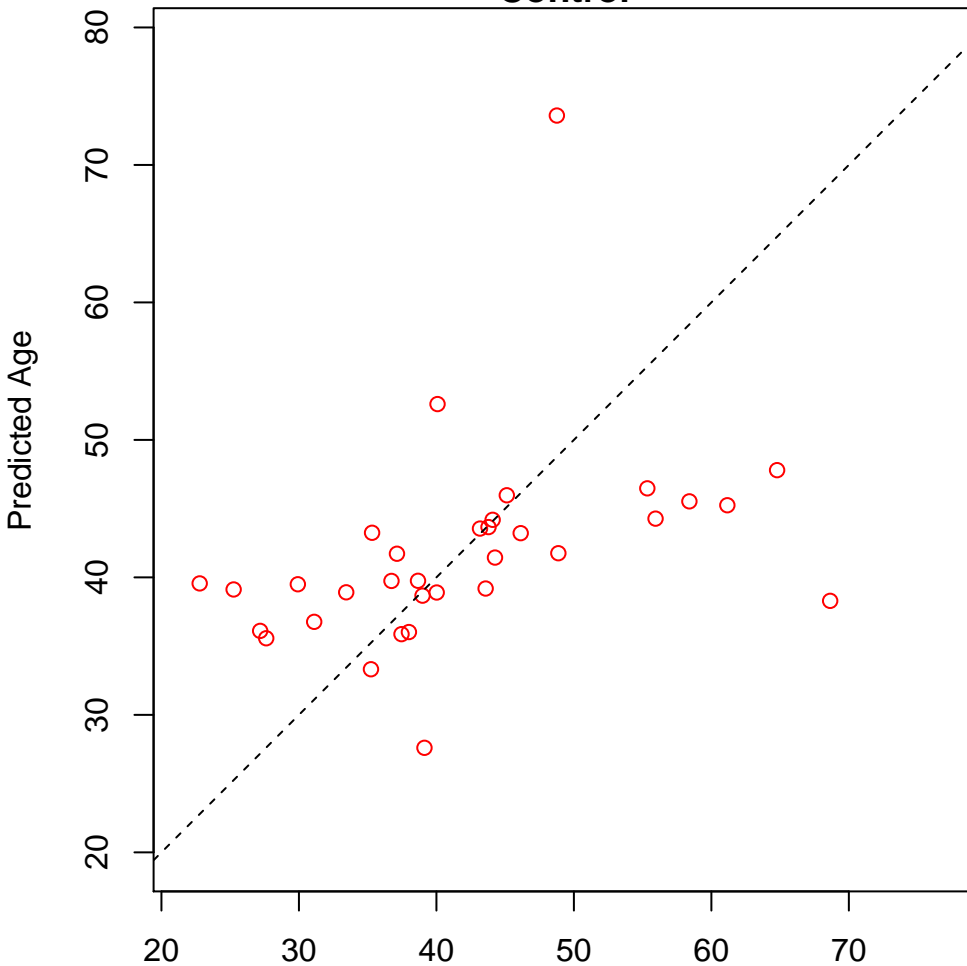


negative regulation of cAMP-mediated signaling (Score: 0.676973)

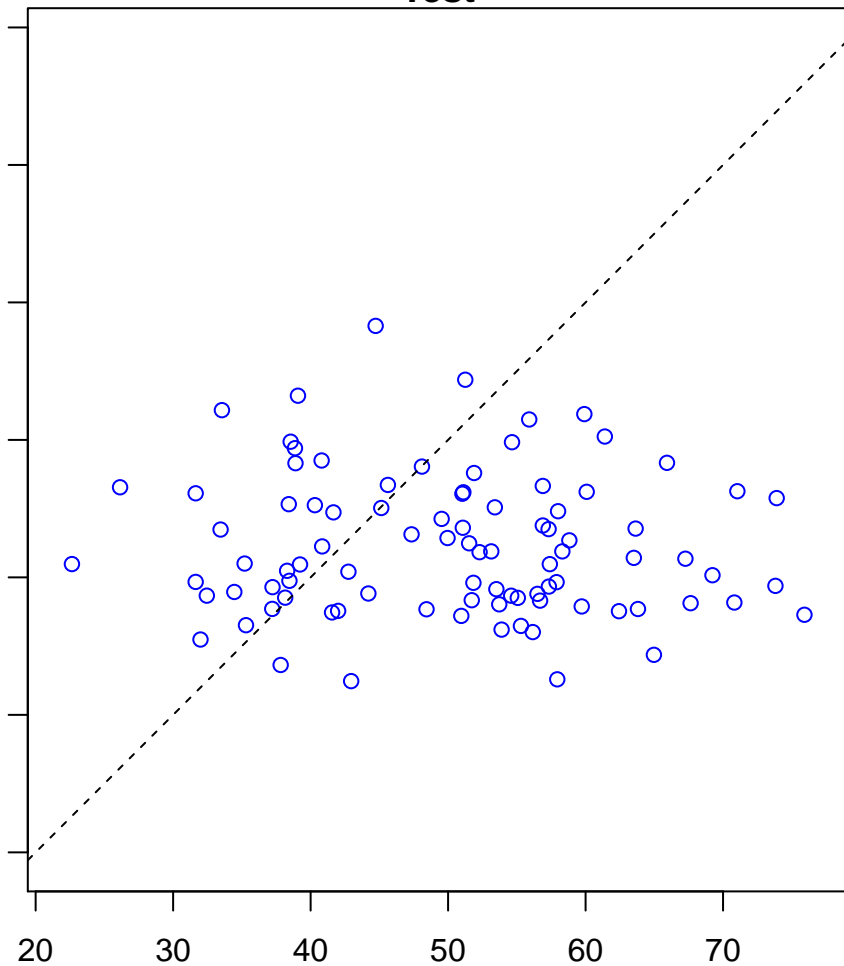


post-translational protein modification (Score: 0.676827)

Control

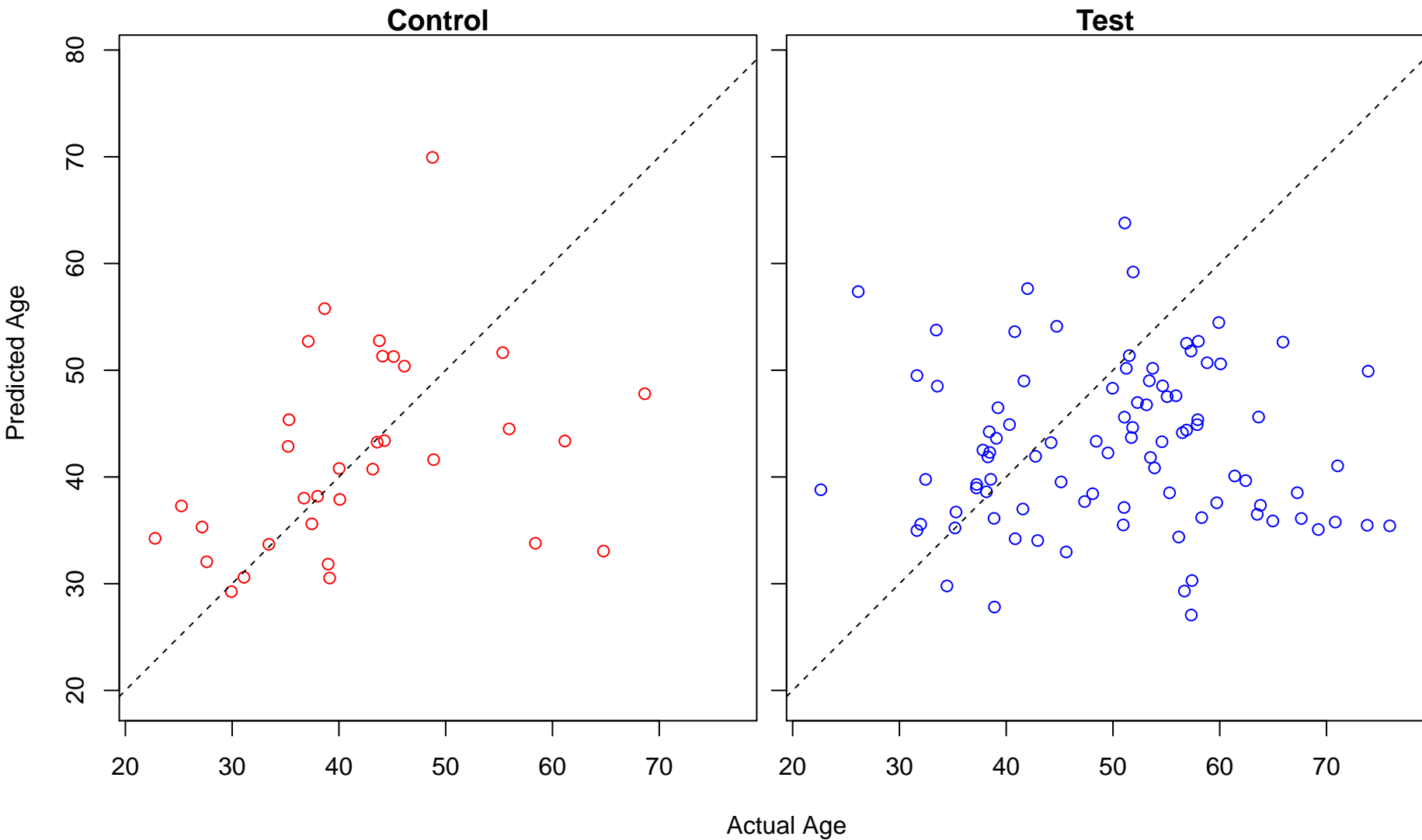


Test

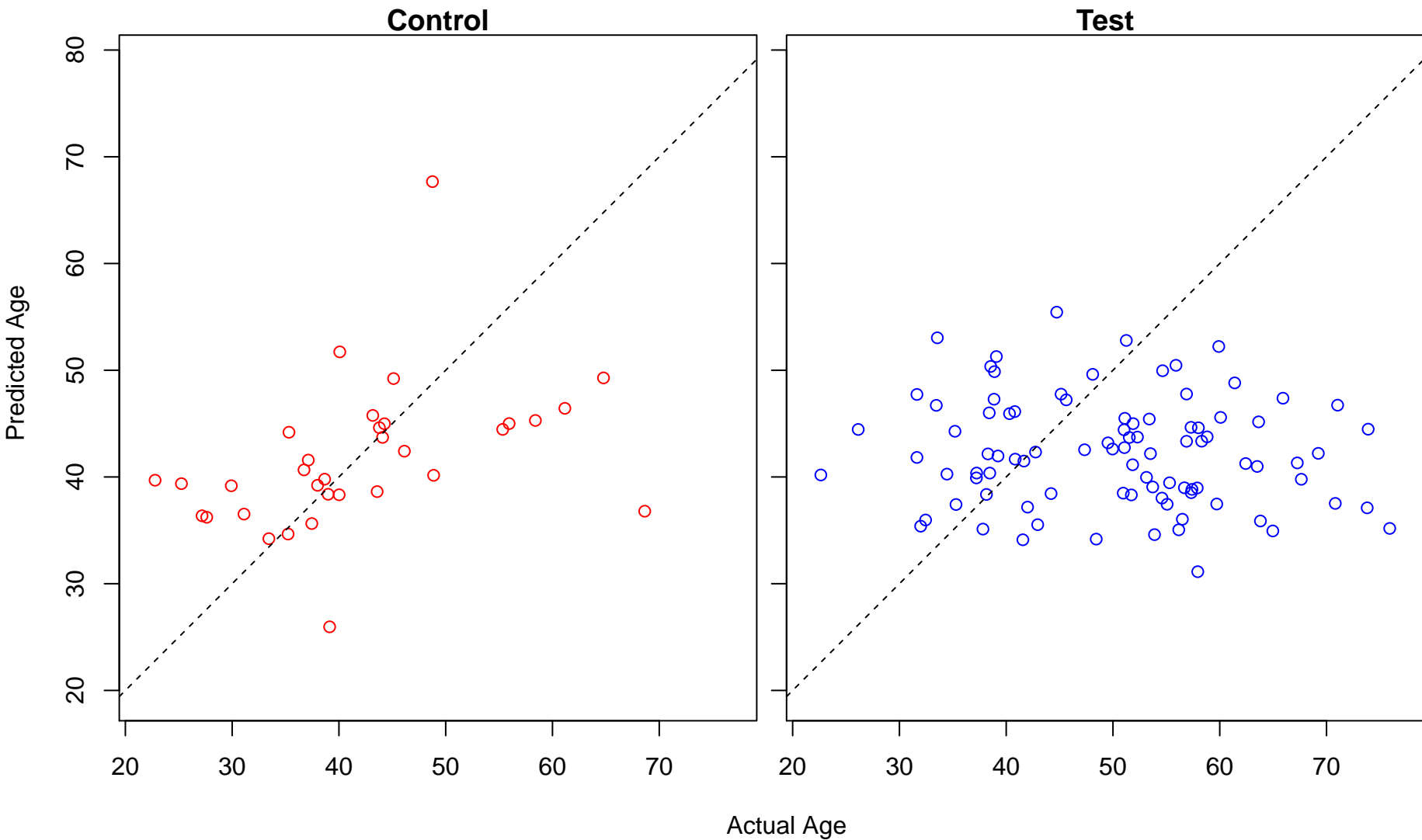


Actual Age

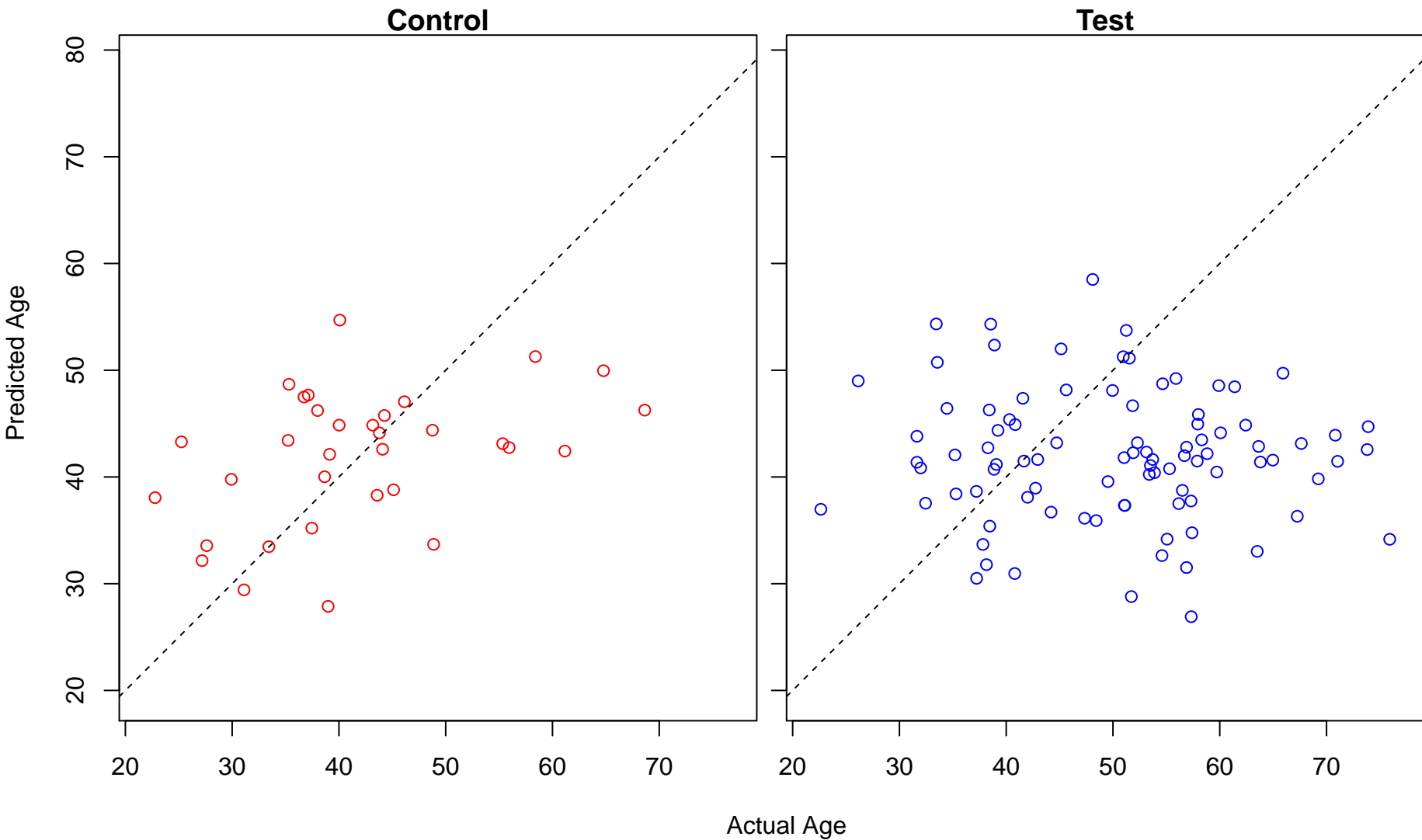
regulation of fatty acid transport (Score: 0.676516)



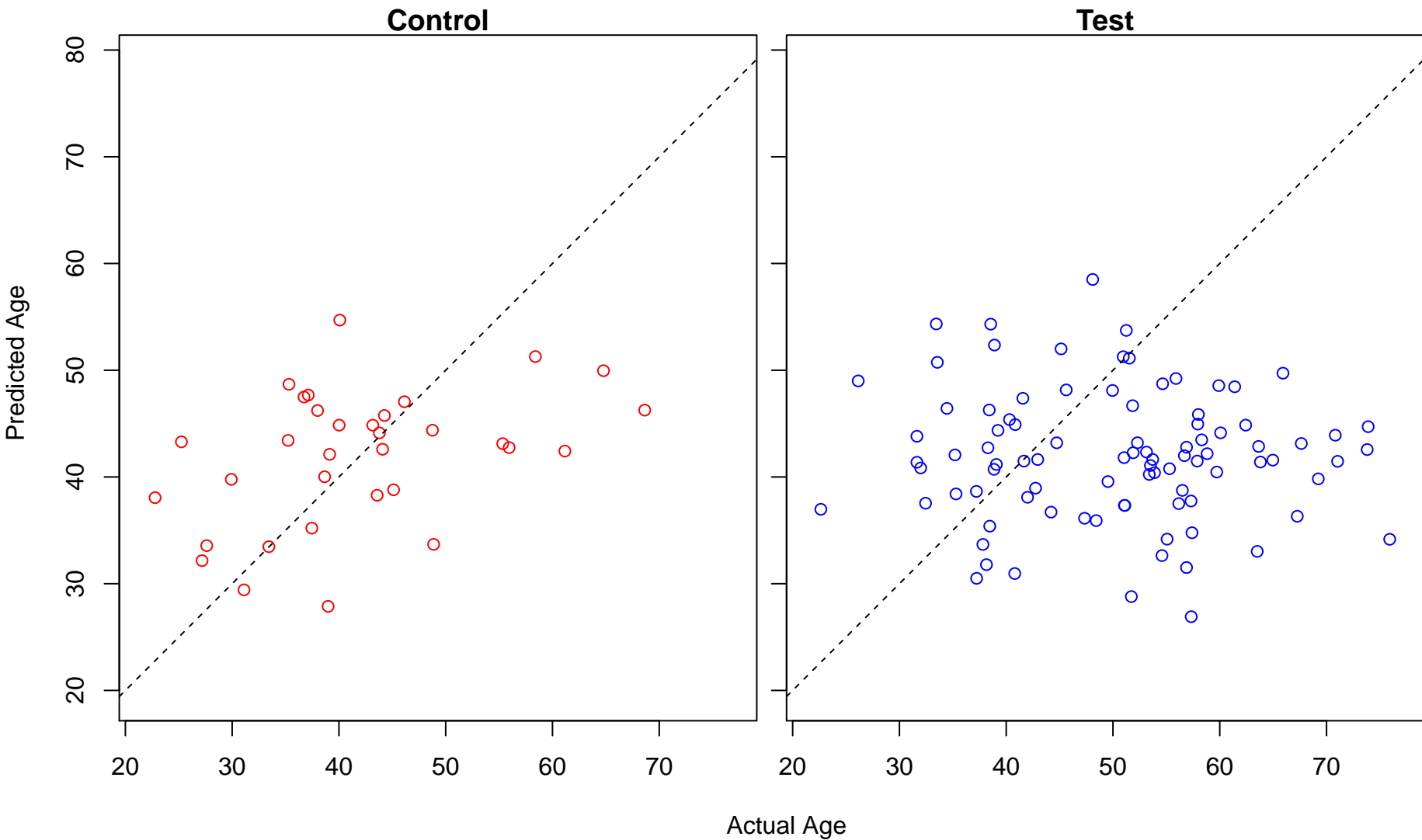
lipid metabolic process (Score: 0.676342)



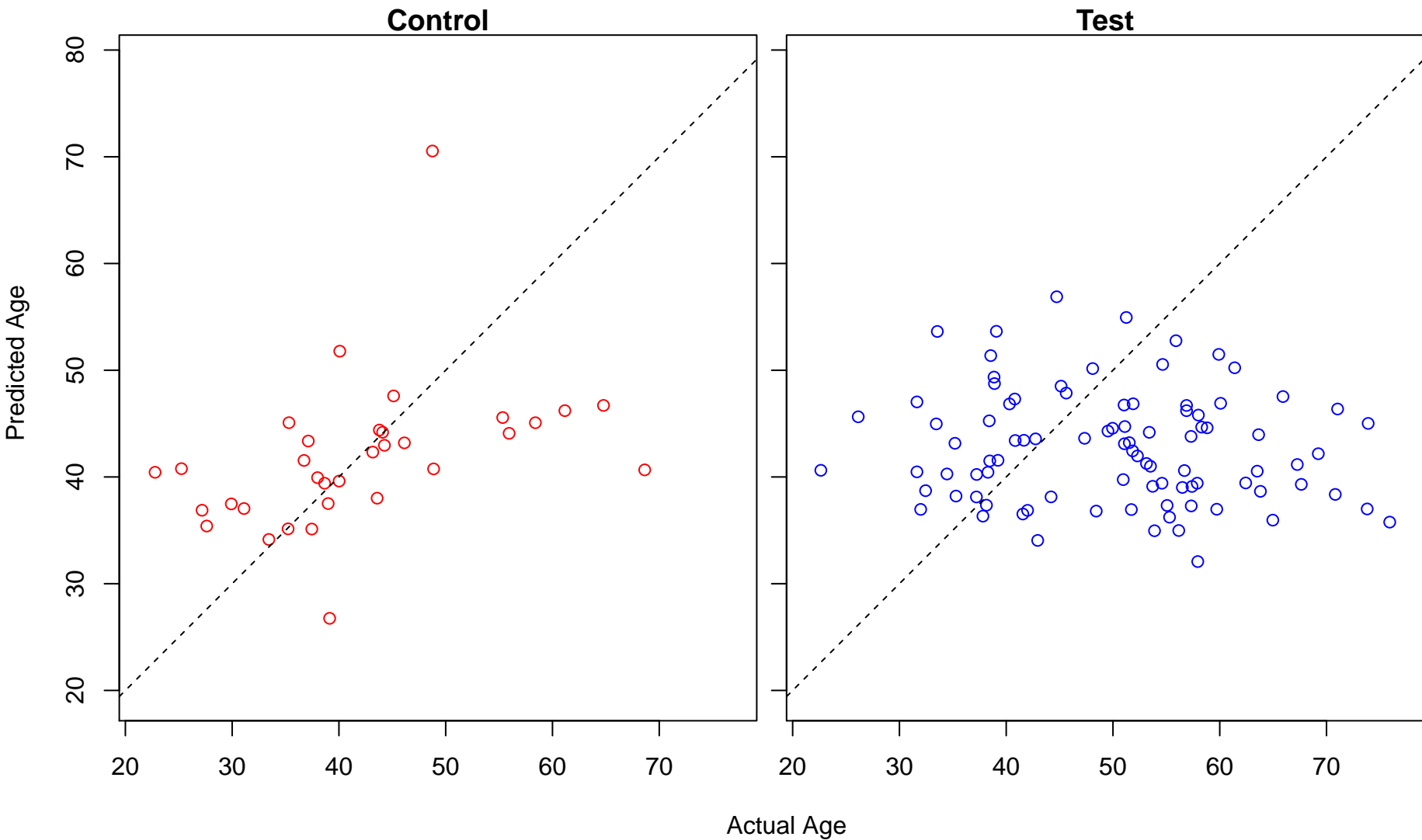
kidney mesenchyme development (Score: 0.676257)



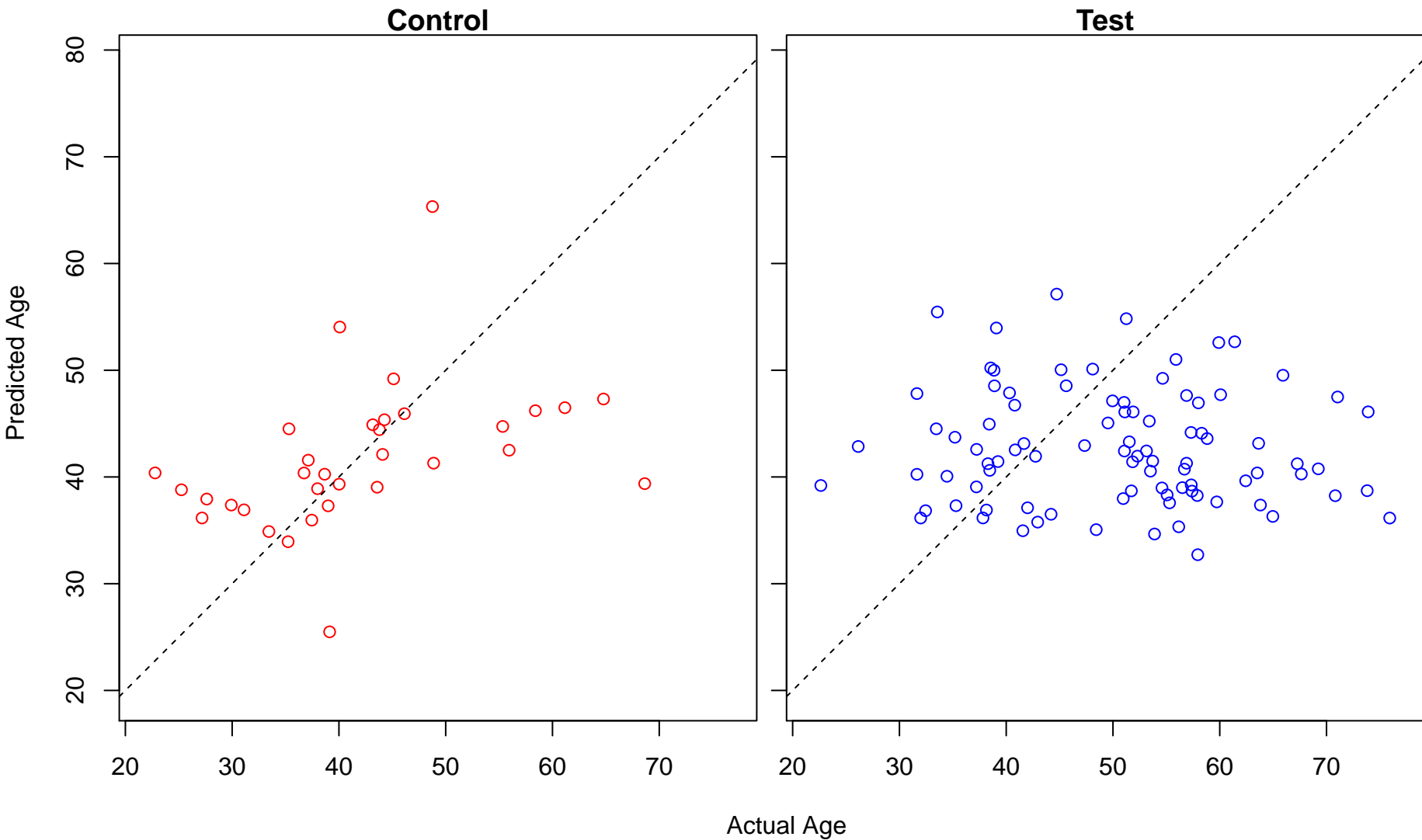
metanephric mesenchyme development (Score: 0.676257)



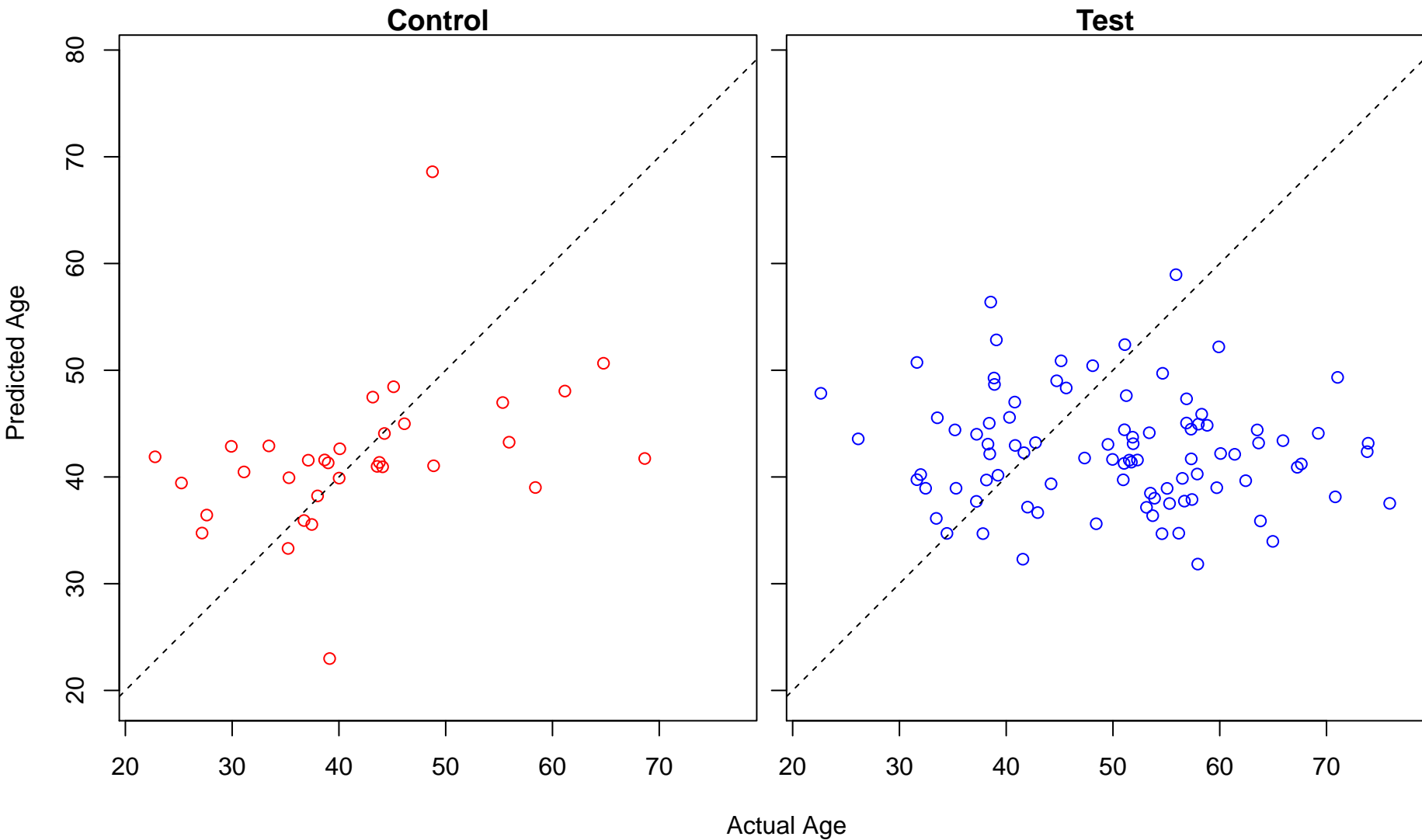
establishment of localization in cell (Score: 0.676043)



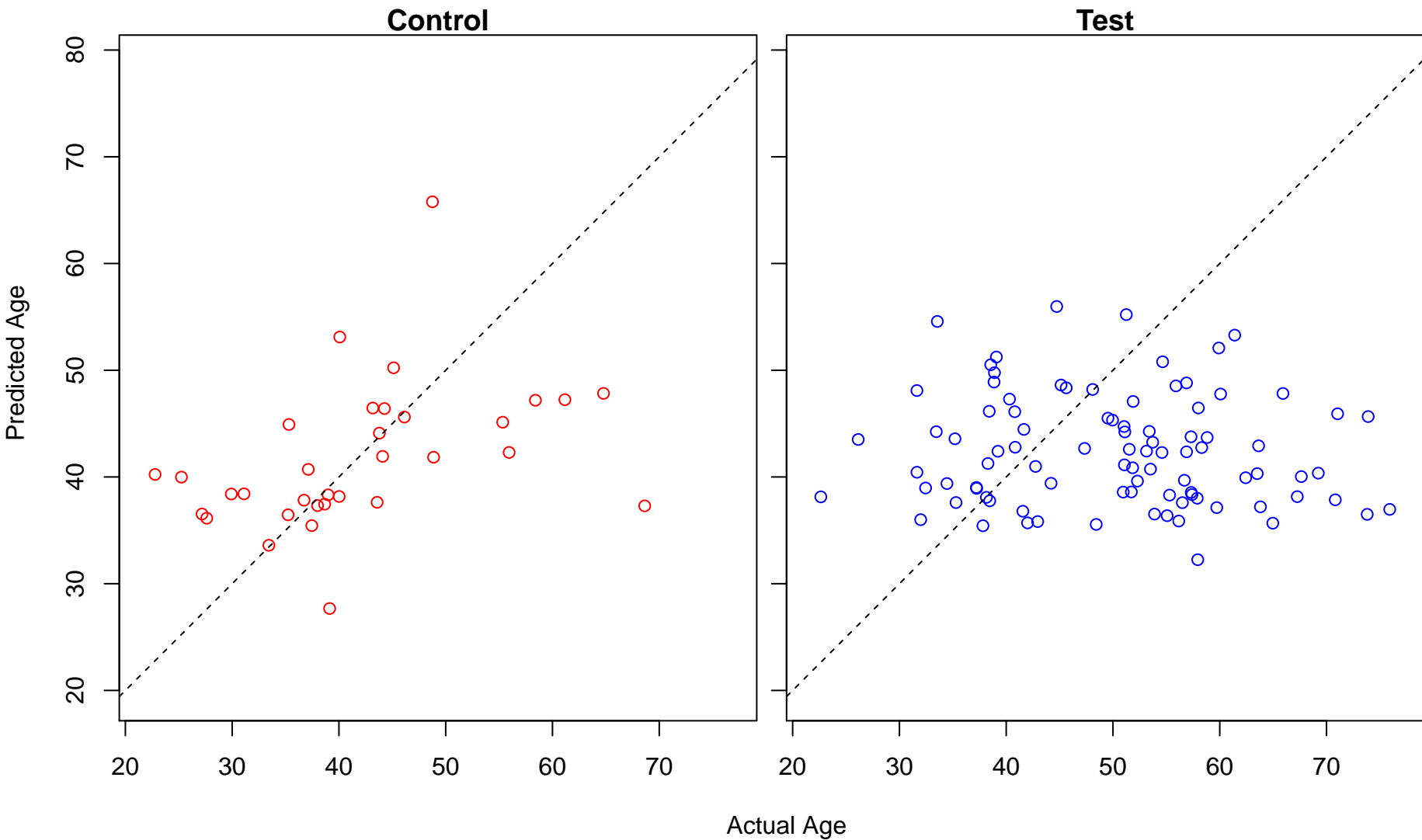
cellular component assembly (Score: 0.675709)



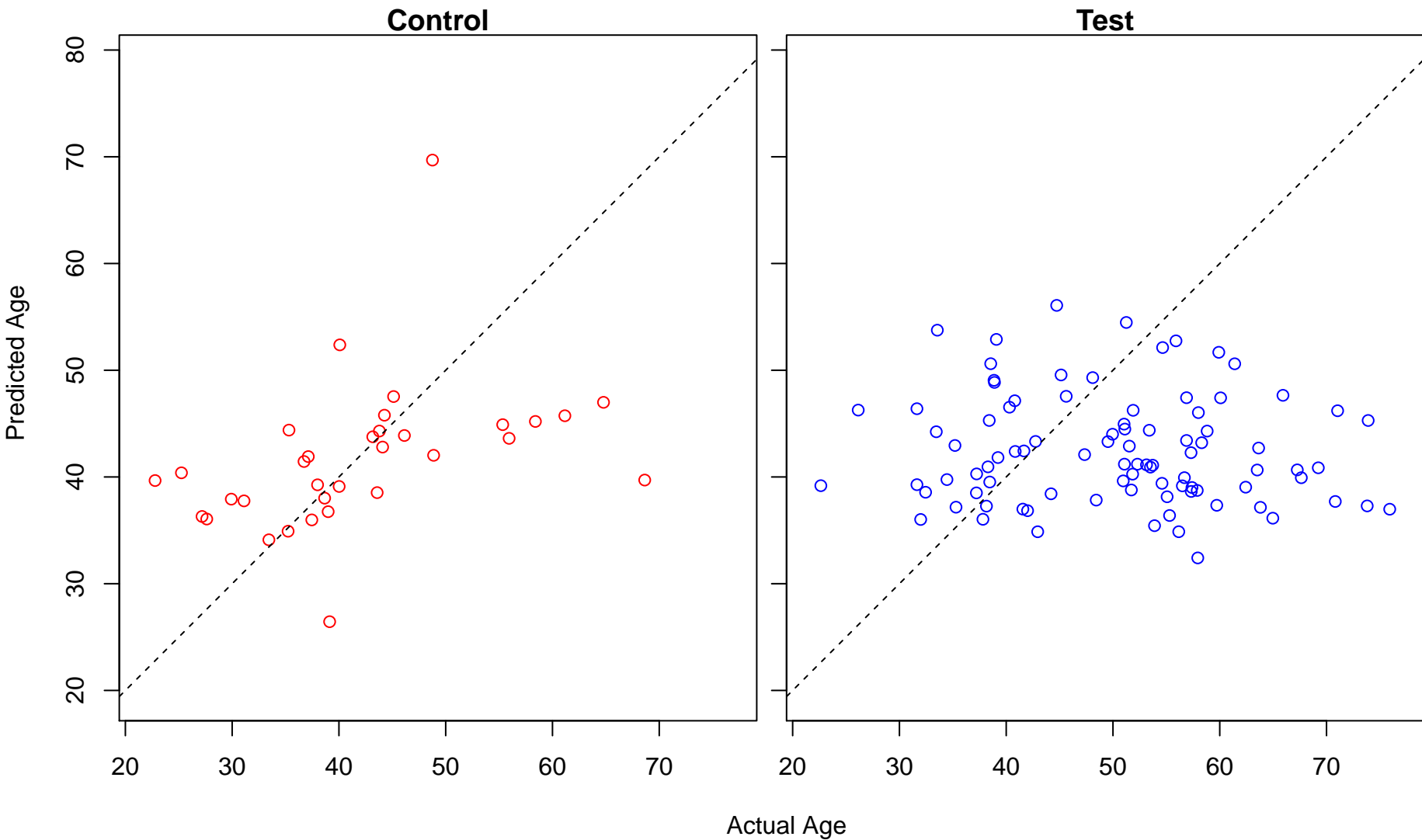
nuclear envelope organization (Score: 0.675503)



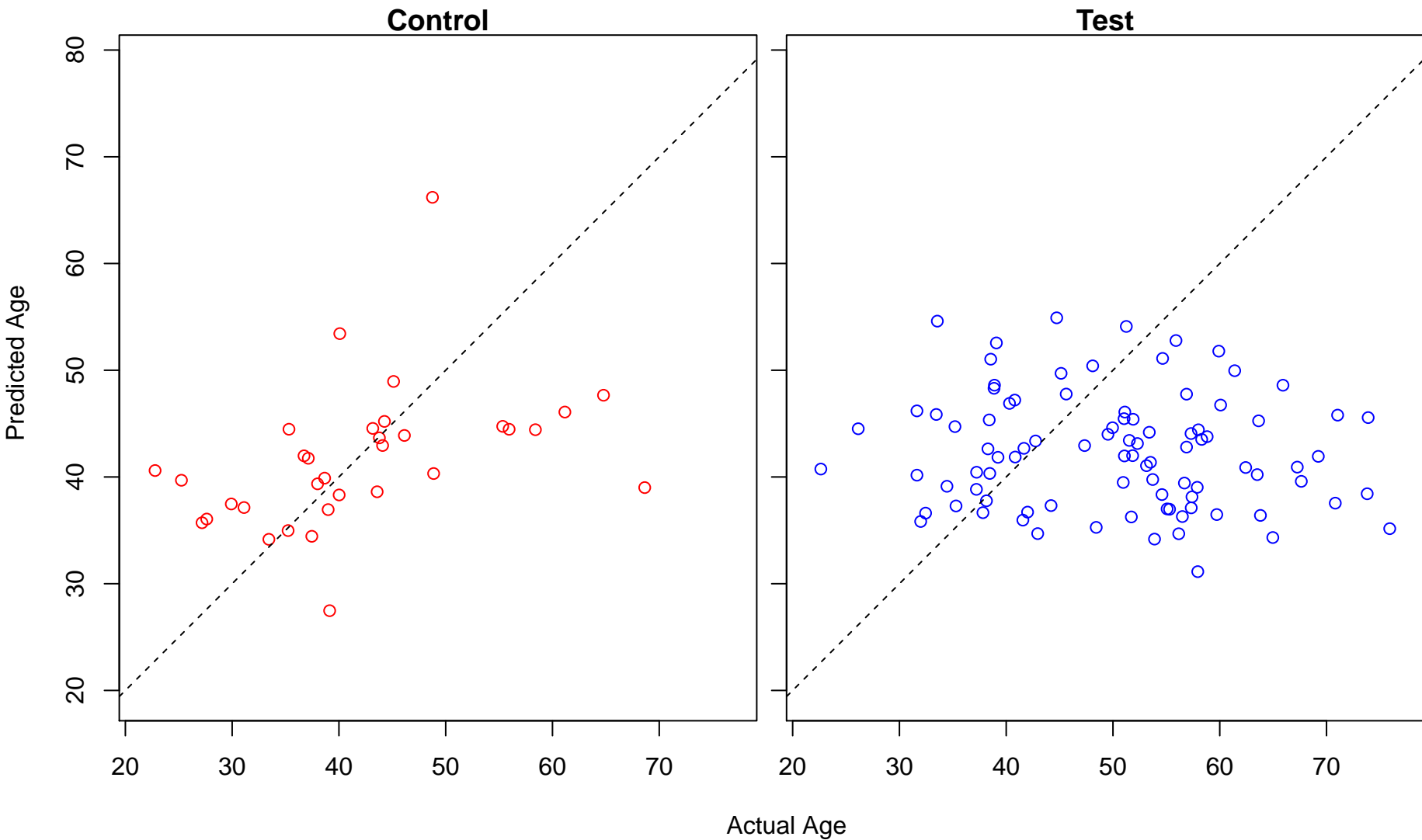
cellular protein catabolic process (Score: 0.675123)



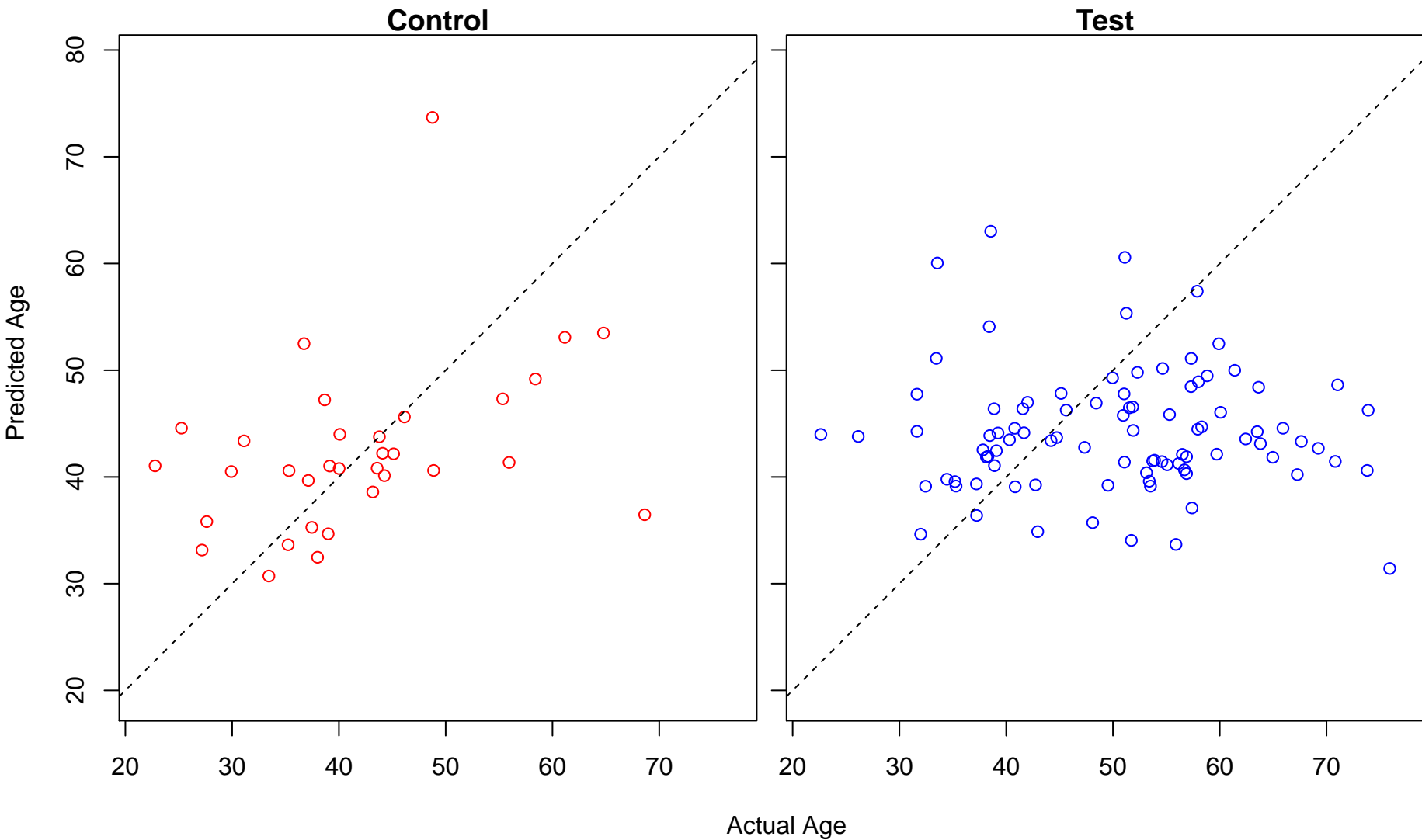
negative regulation of cellular process (Score: 0.674816)



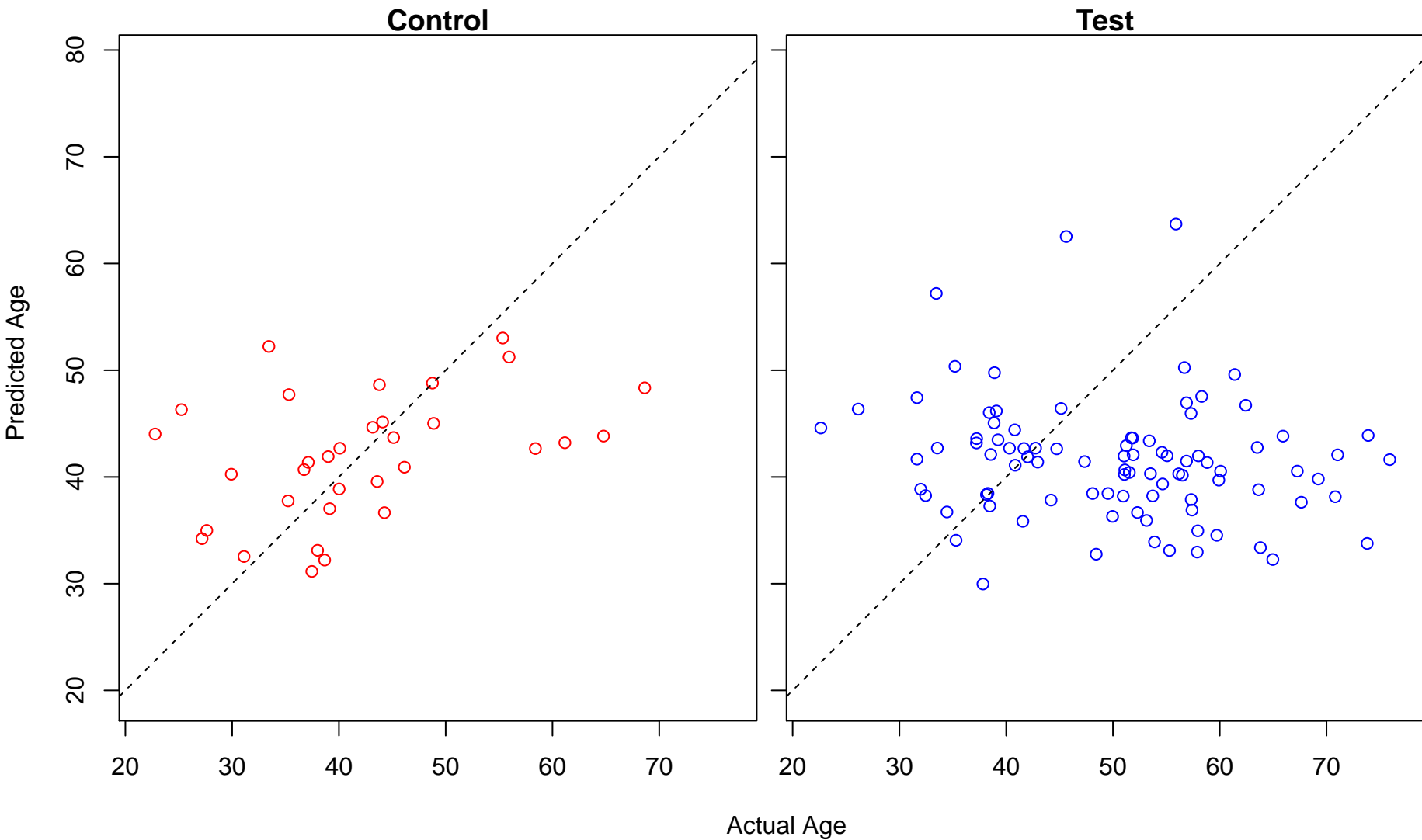
small molecule metabolic process (Score: 0.674129)



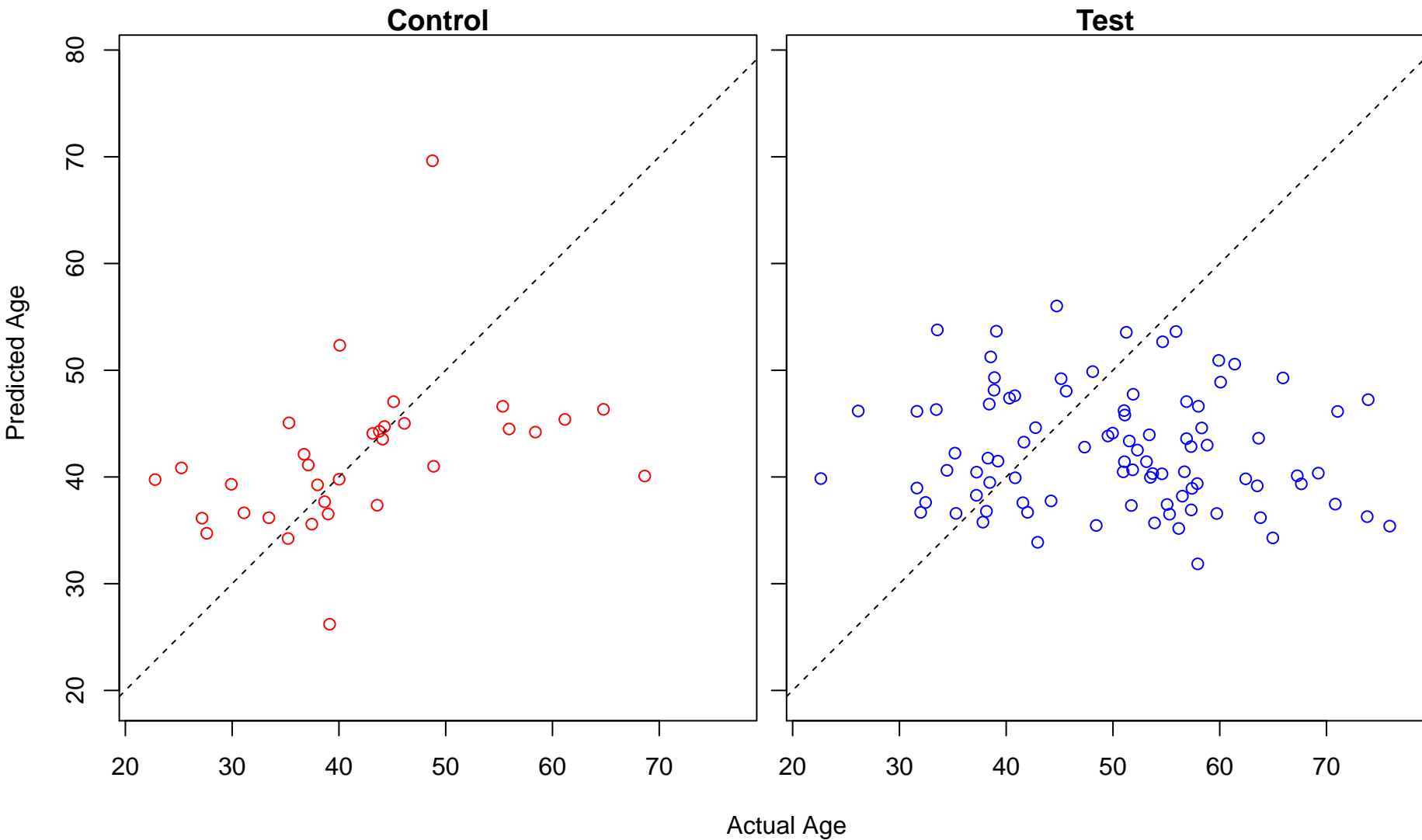
astrocyte development (Score: 0.674025)



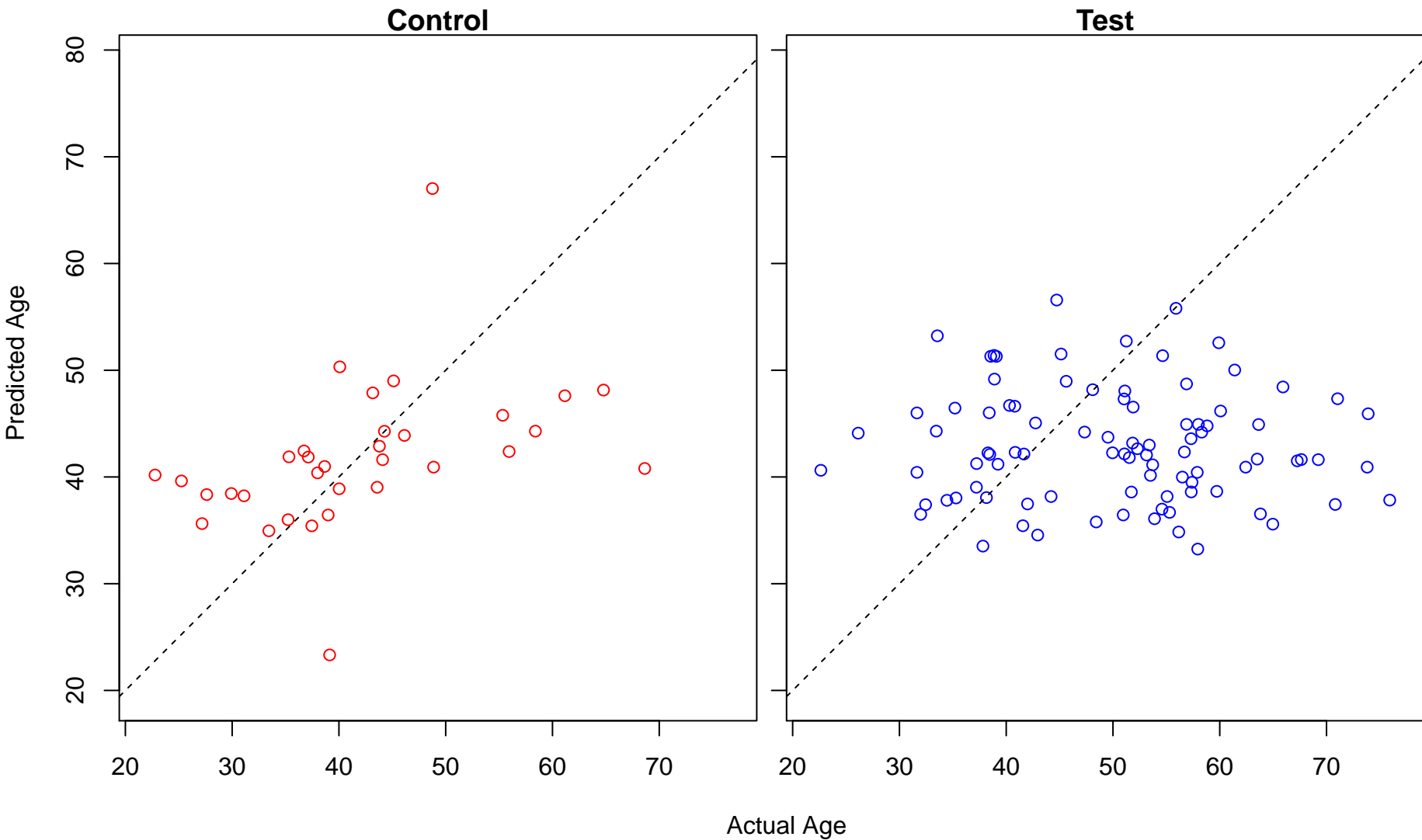
negative regulation of protein sumoylation (Score: 0.673833)



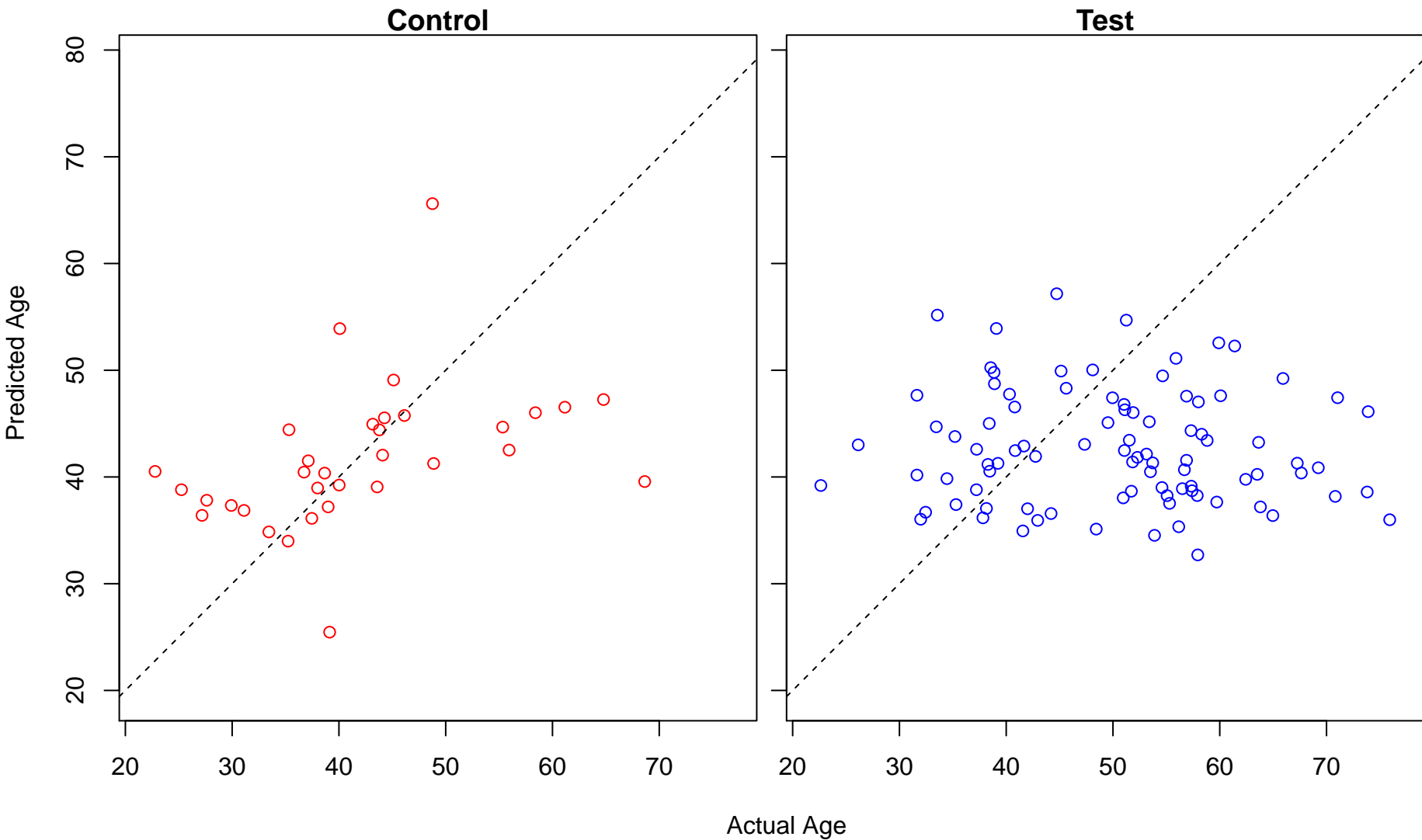
regulation of response to stress (Score: 0.673793)



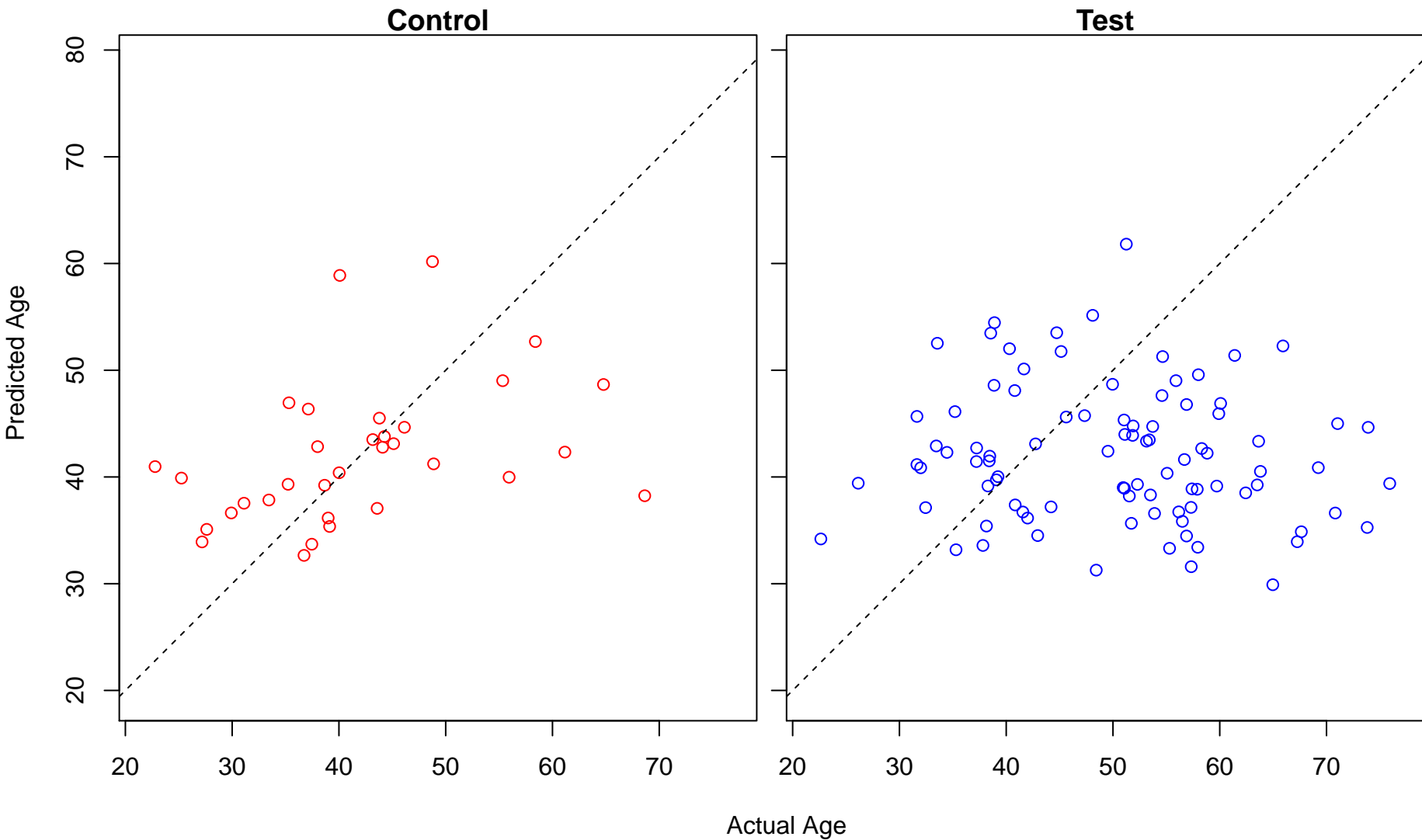
locomotion (Score: 0.673685)



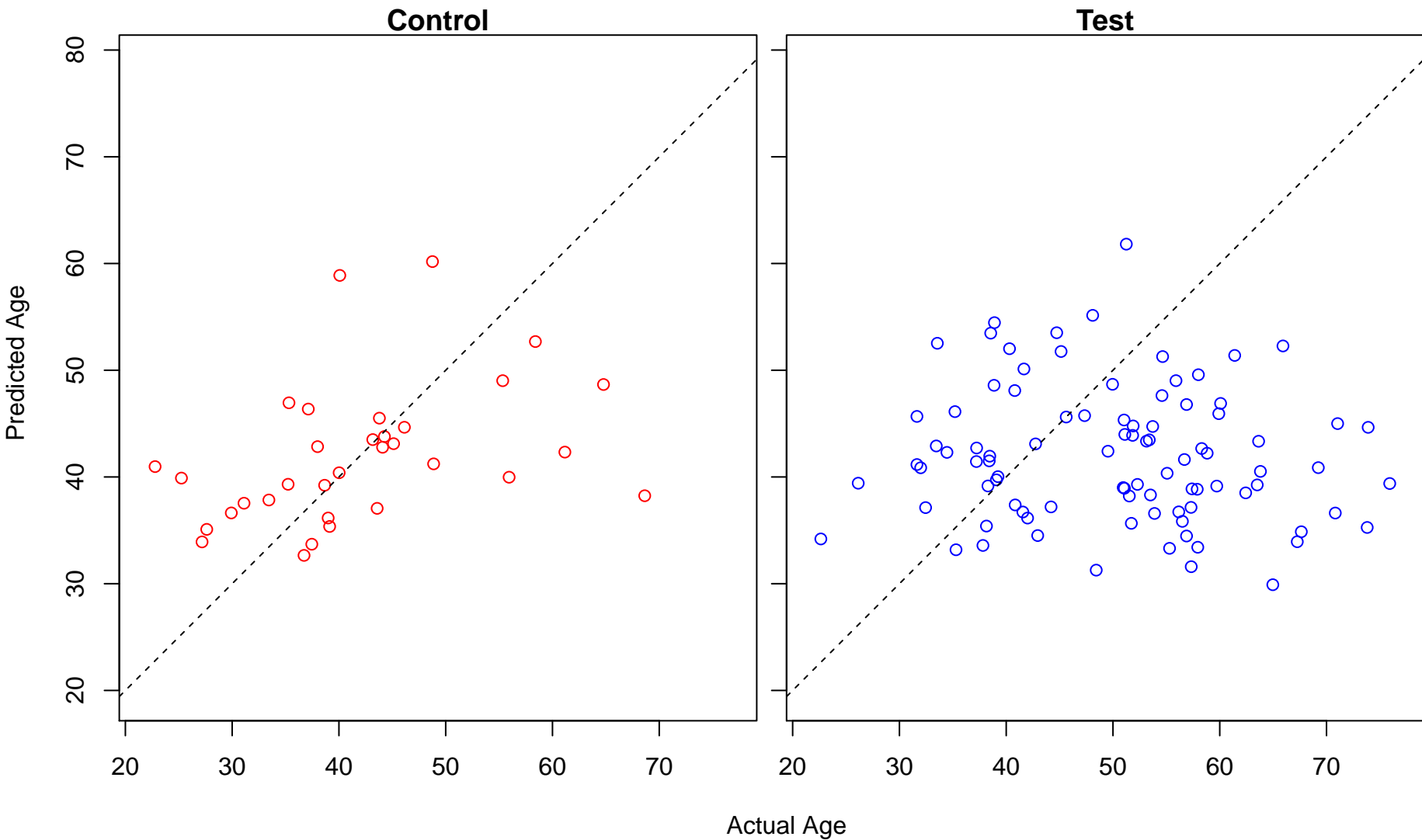
cellular component biogenesis (Score: 0.673520)



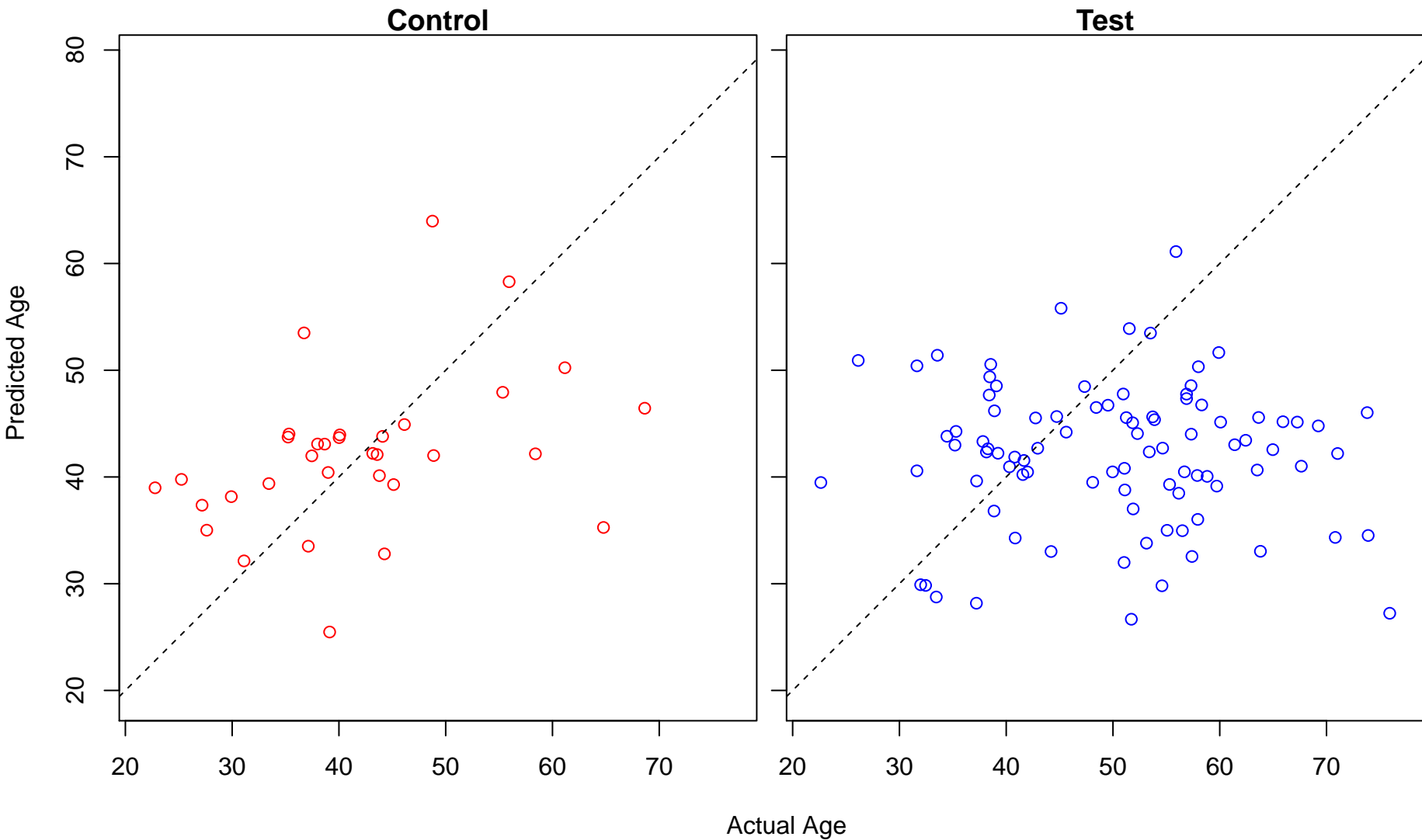
regulation of platelet-derived growth factor receptor signaling pathway (Score: 0.673086)



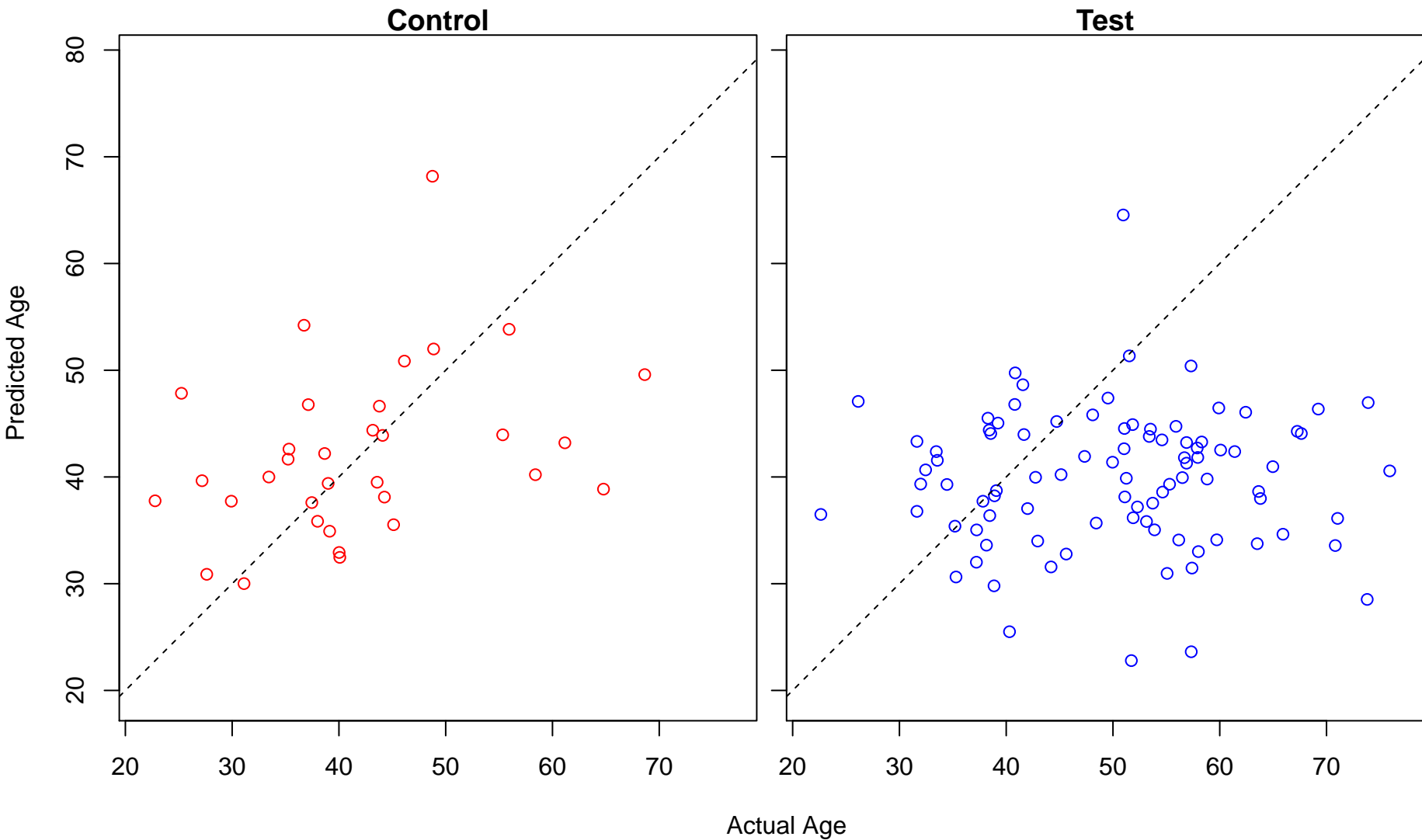
negative regulation of platelet-derived growth factor receptor signaling pathway (Score: 0.673086)



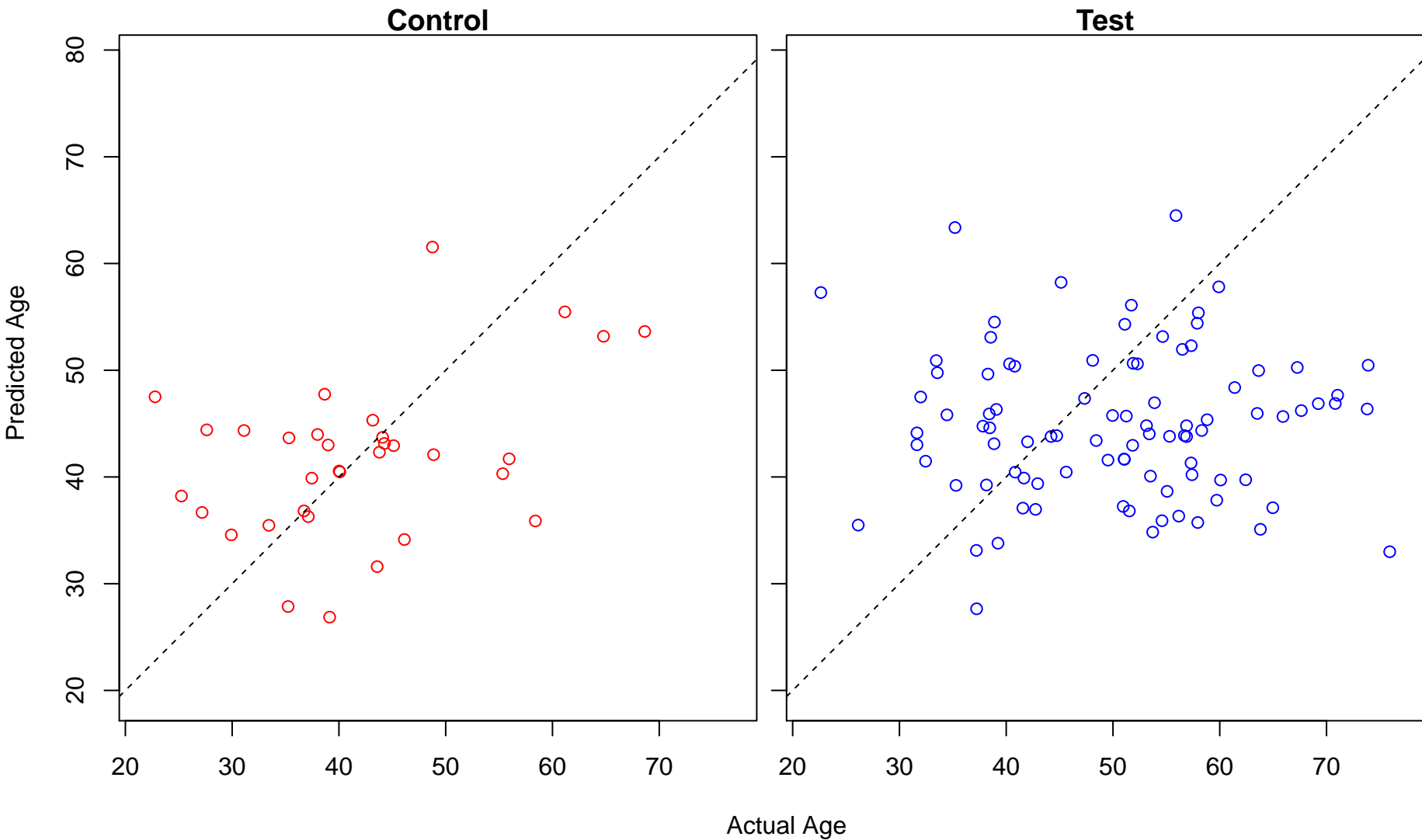
regulation of CD8-positive, alpha-beta T cell activation (Score: 0.673000)



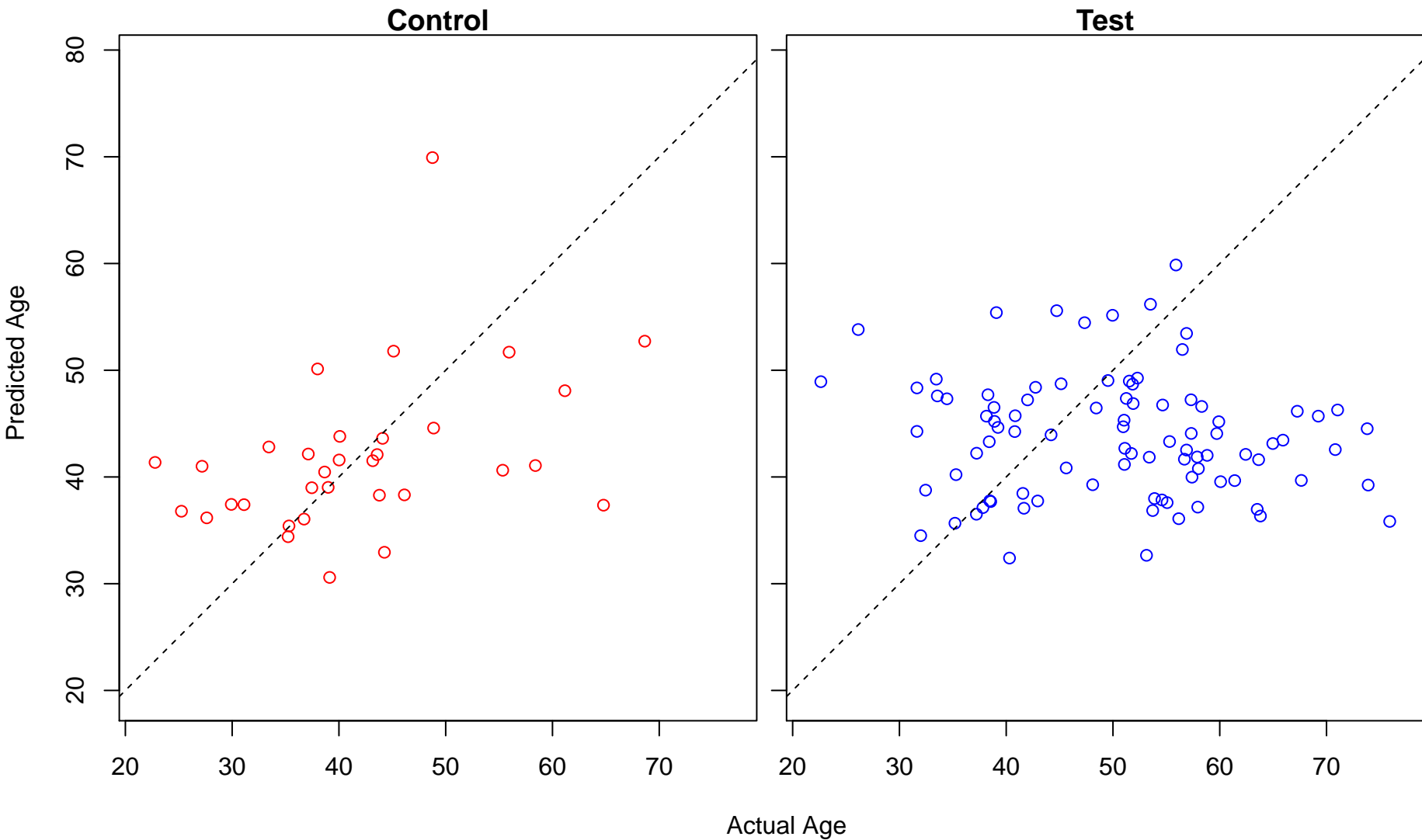
binding of sperm to zona pellucida (Score: 0.672987)



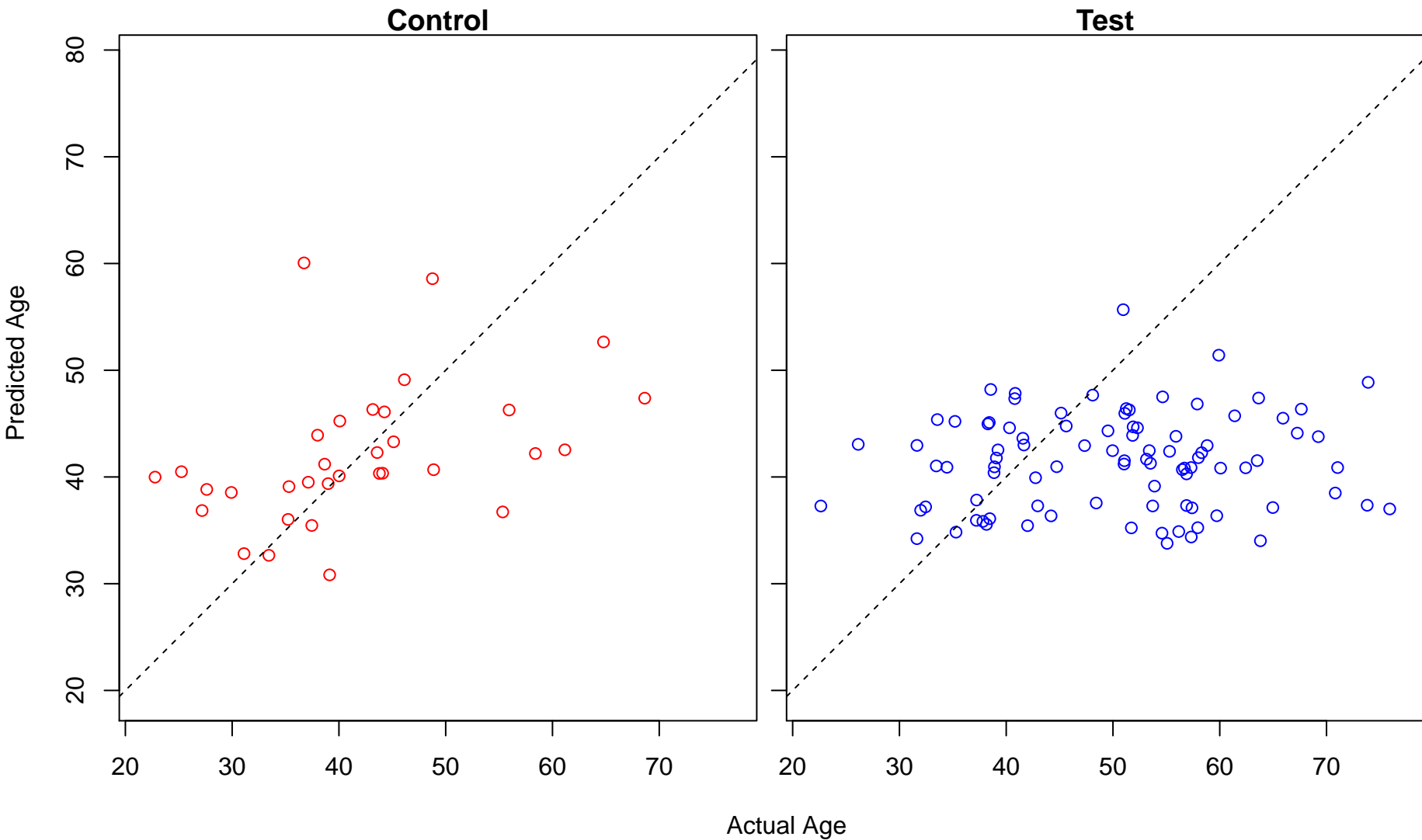
DNA methylation on cytosine (Score: 0.672839)



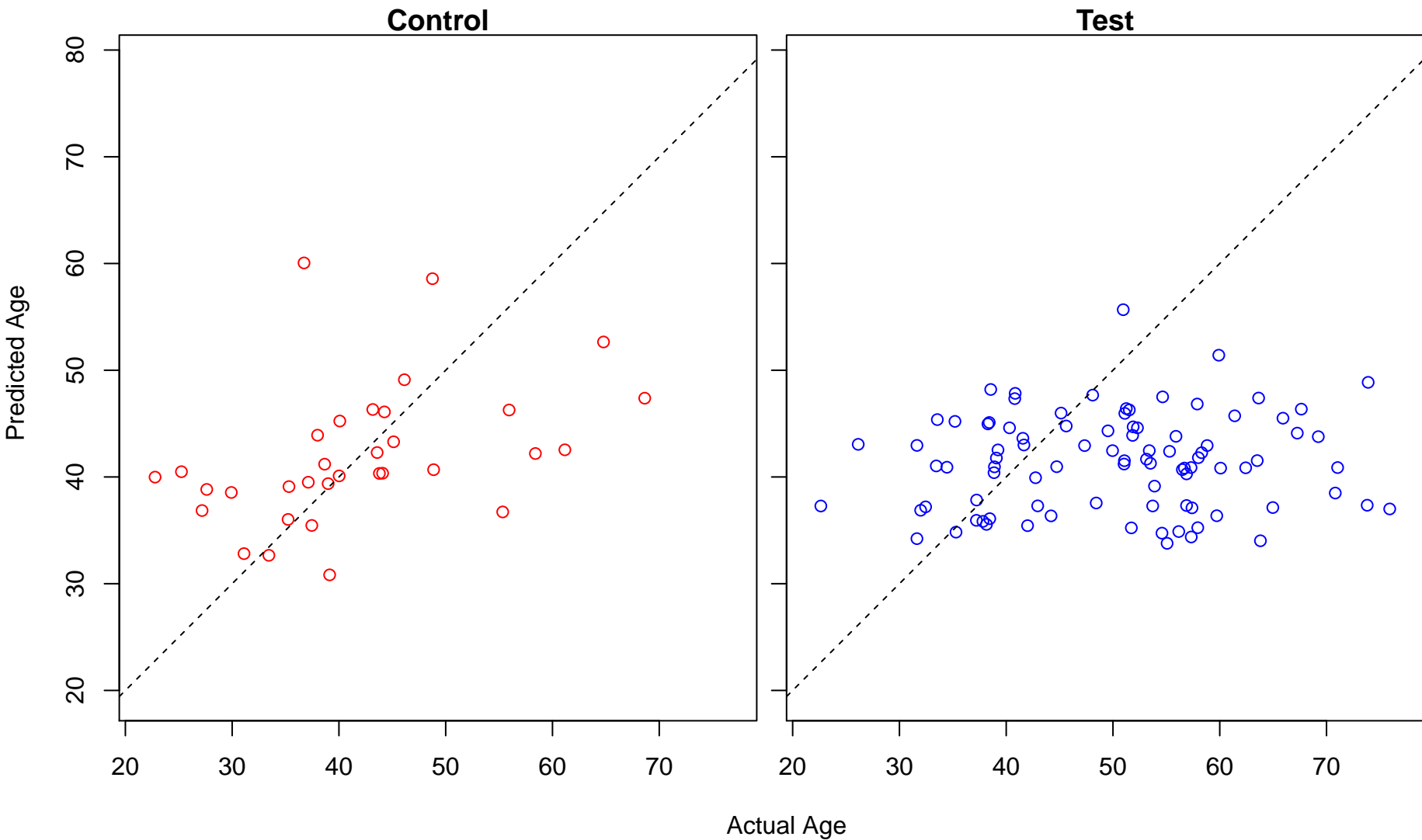
positive regulation of transcription from RNA polymerase III promoter (Score: 0.672749)



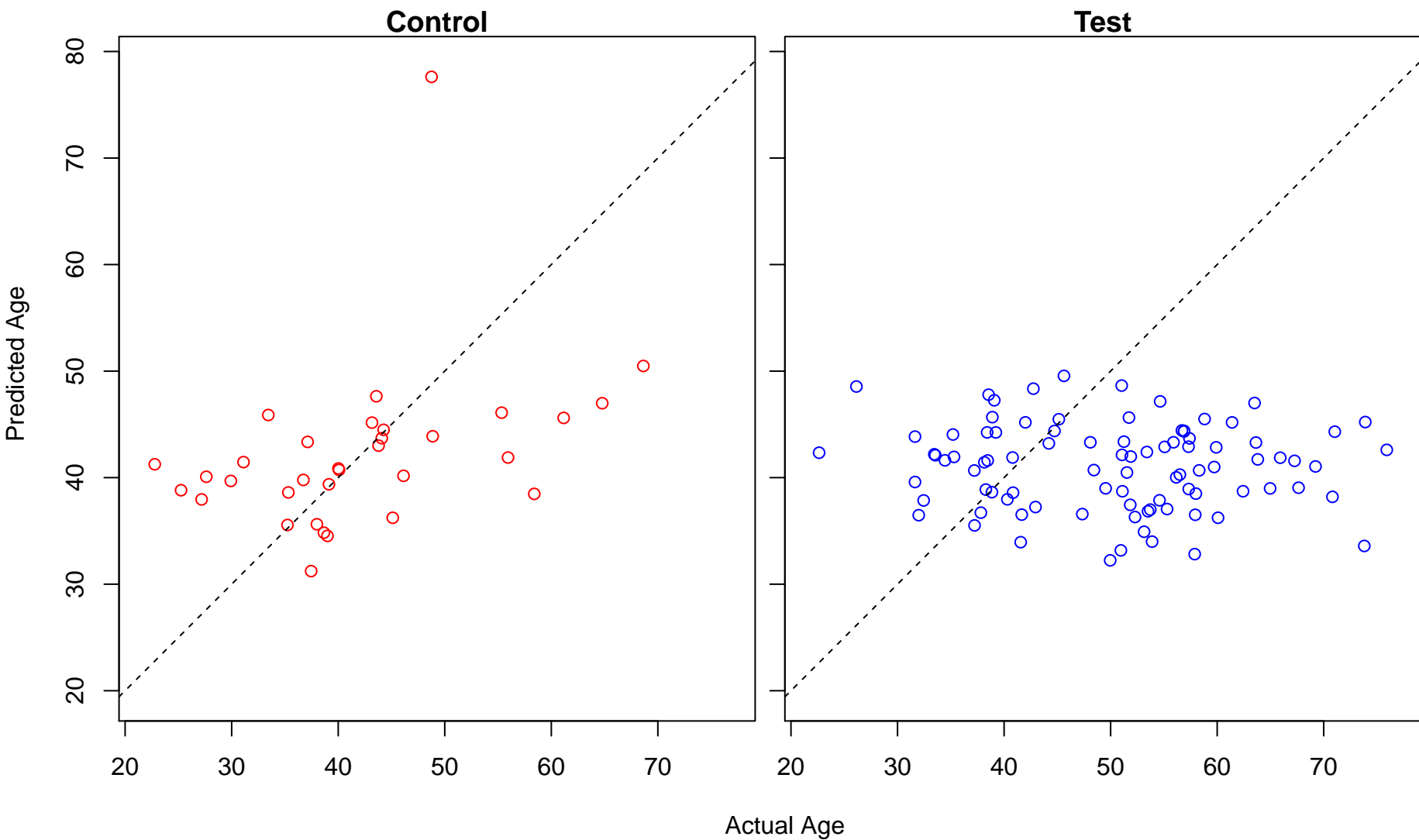
nucleoside diphosphate catabolic process (Score: 0.672737)



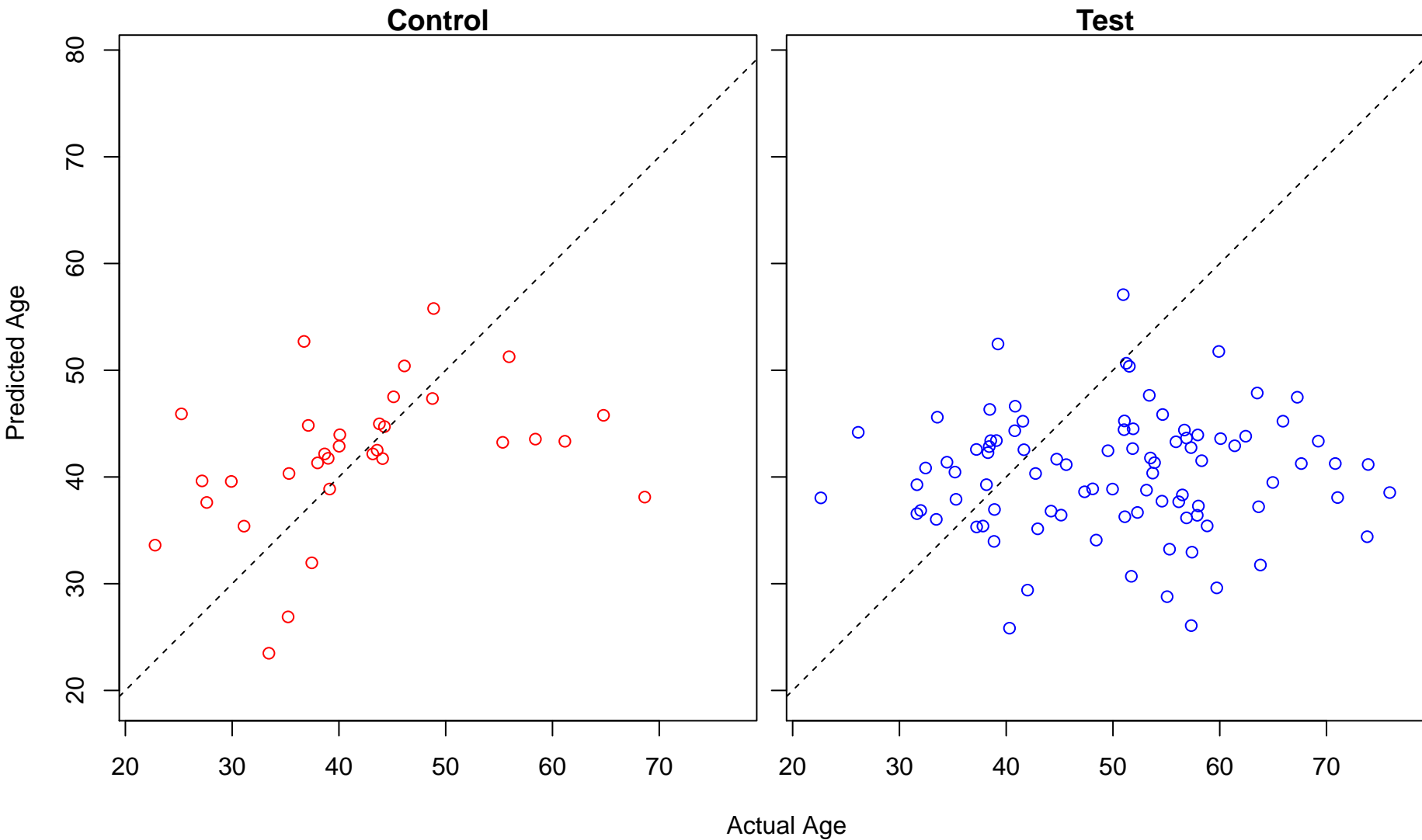
ribonucleoside diphosphate catabolic process (Score: 0.672737)



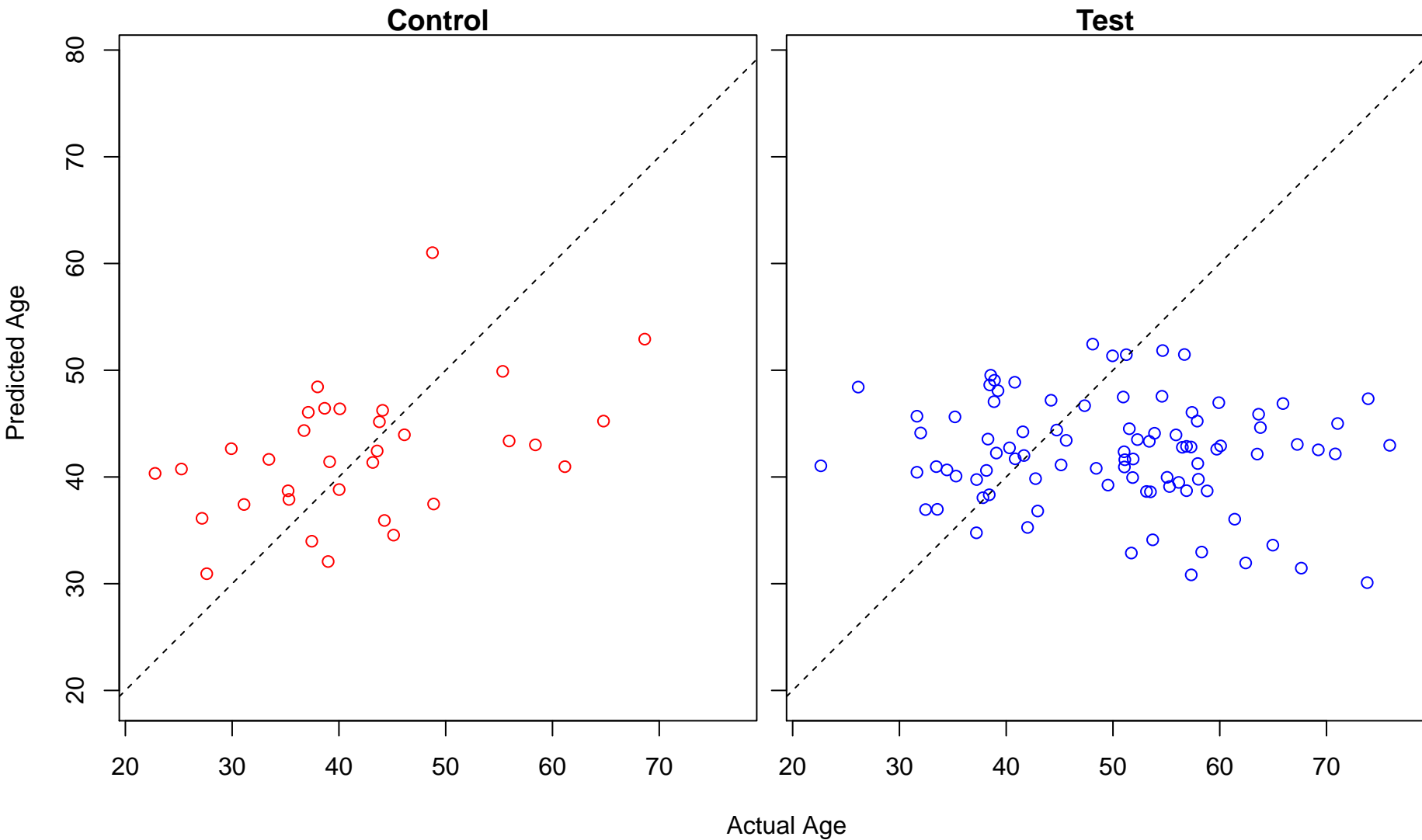
cellular response to calcium ion (Score: 0.672511)



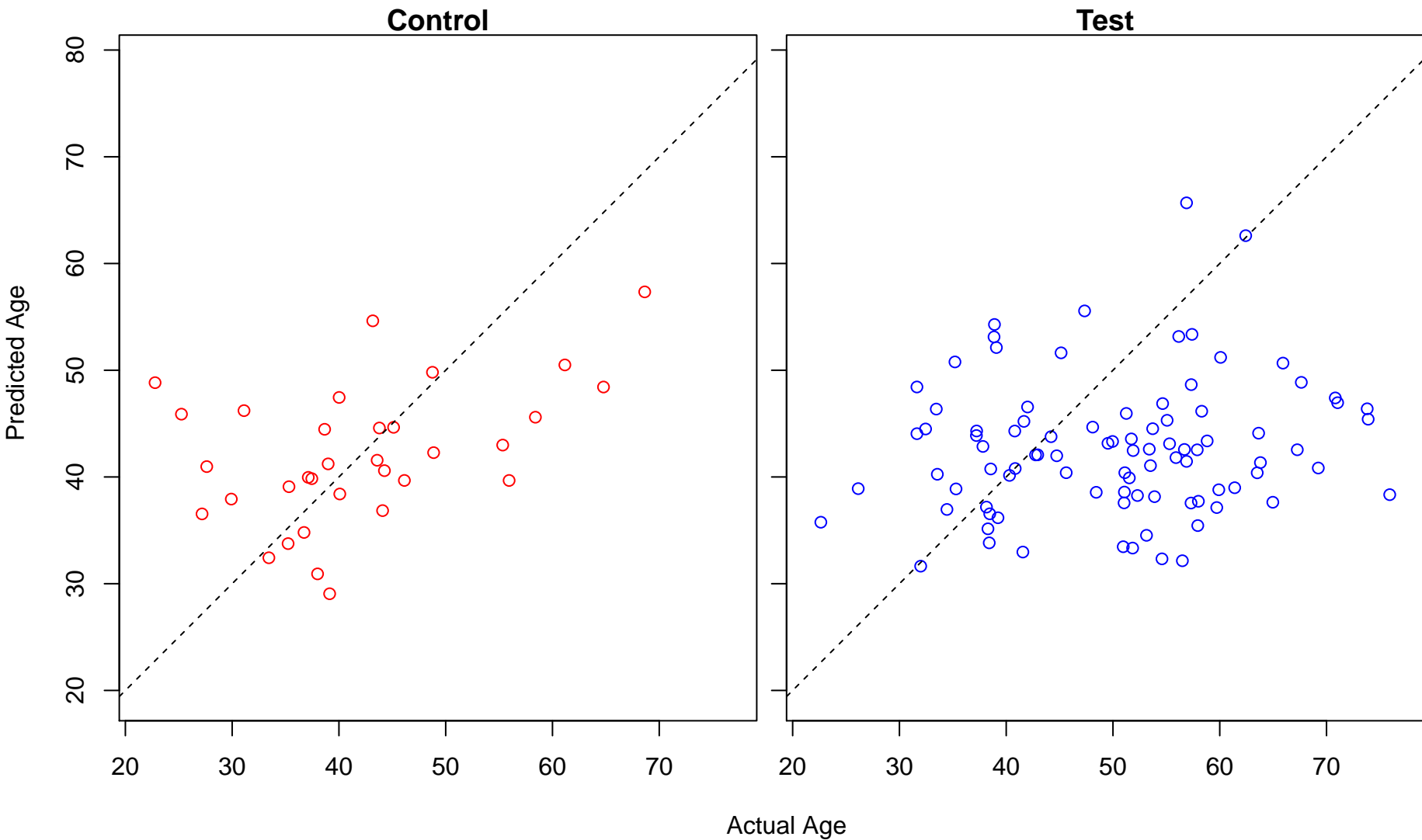
positive regulation of macrophage cytokine production (Score: 0.672250)



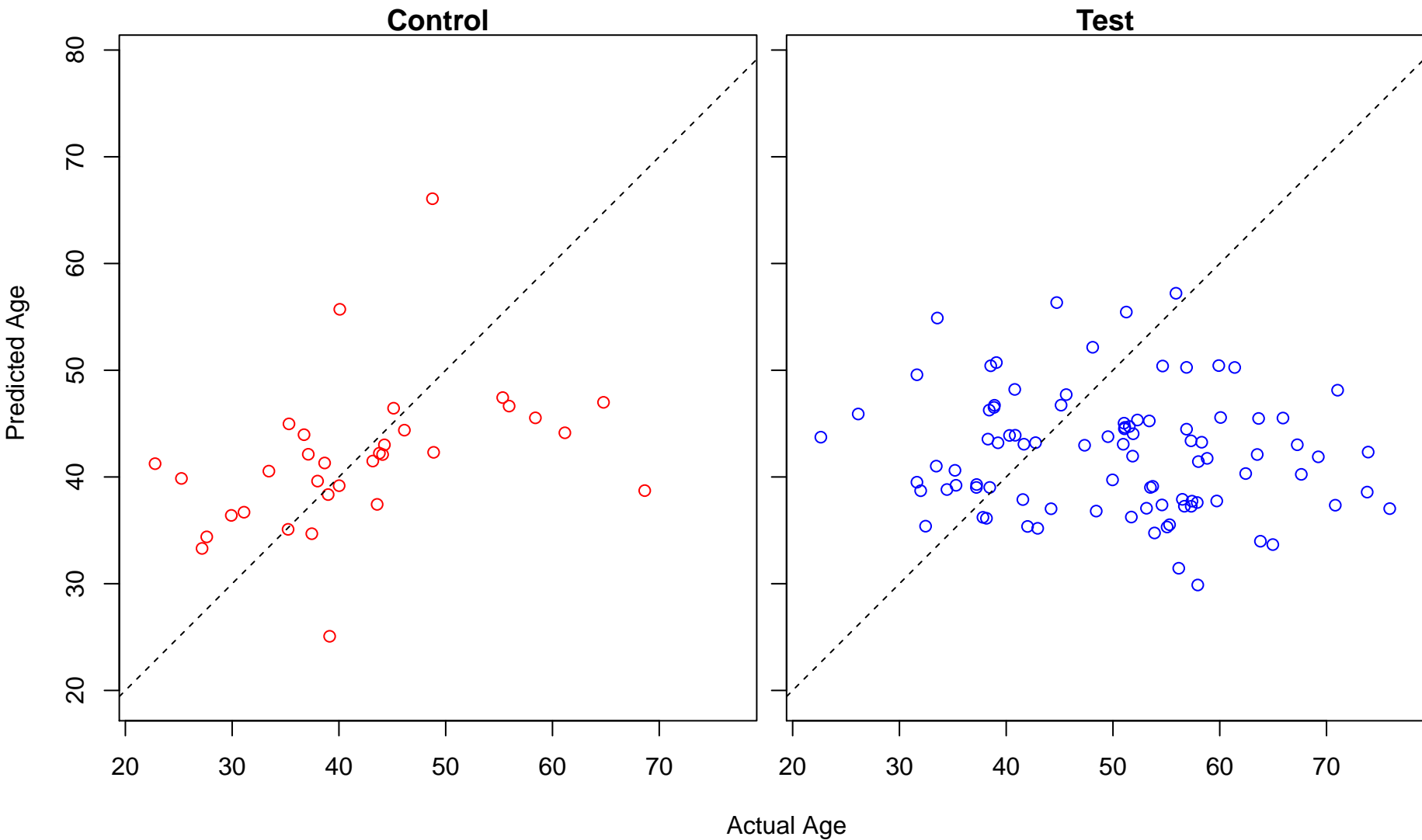
hematopoietic stem cell proliferation (Score: 0.672016)



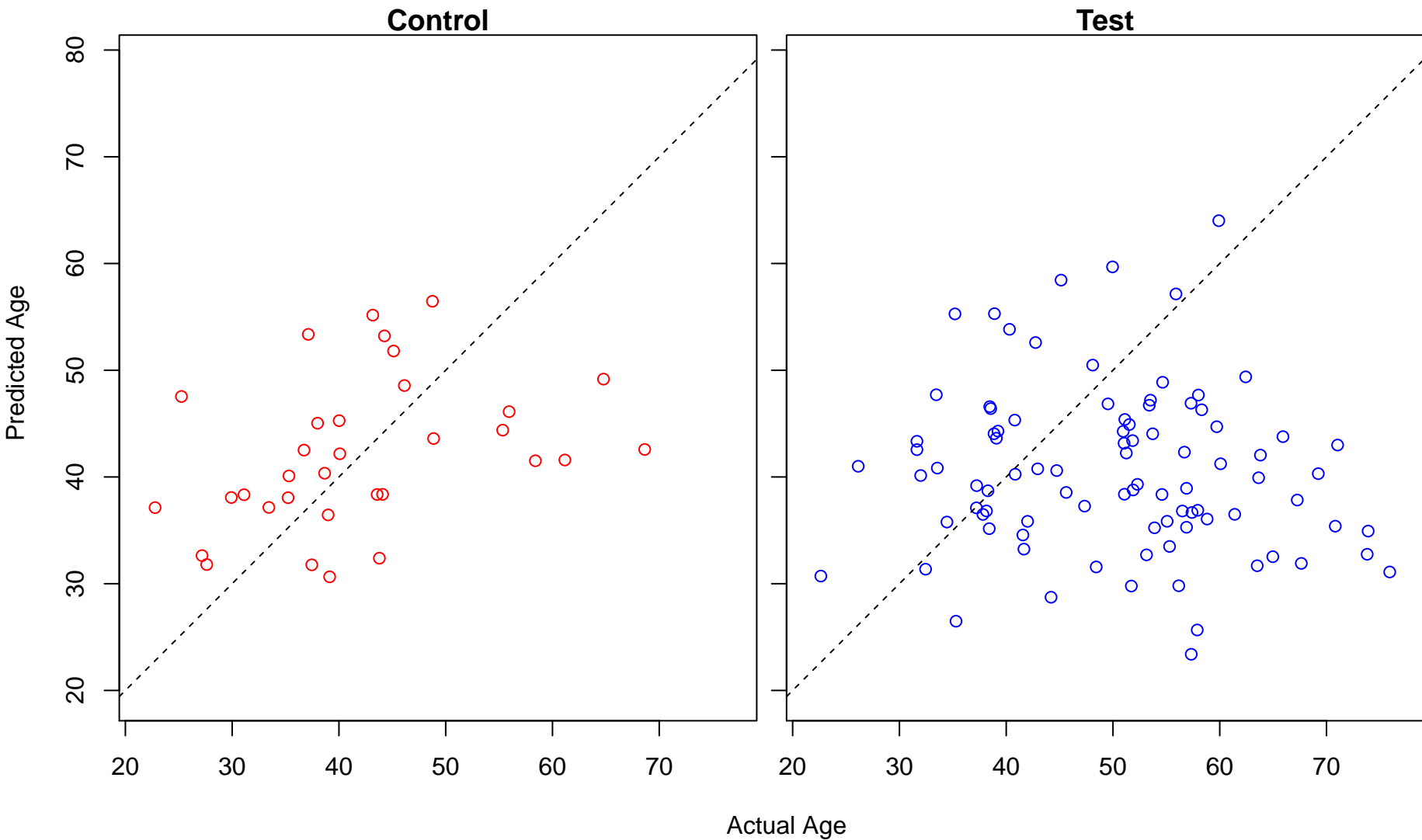
natural killer cell mediated immunity (Score: 0.671742)



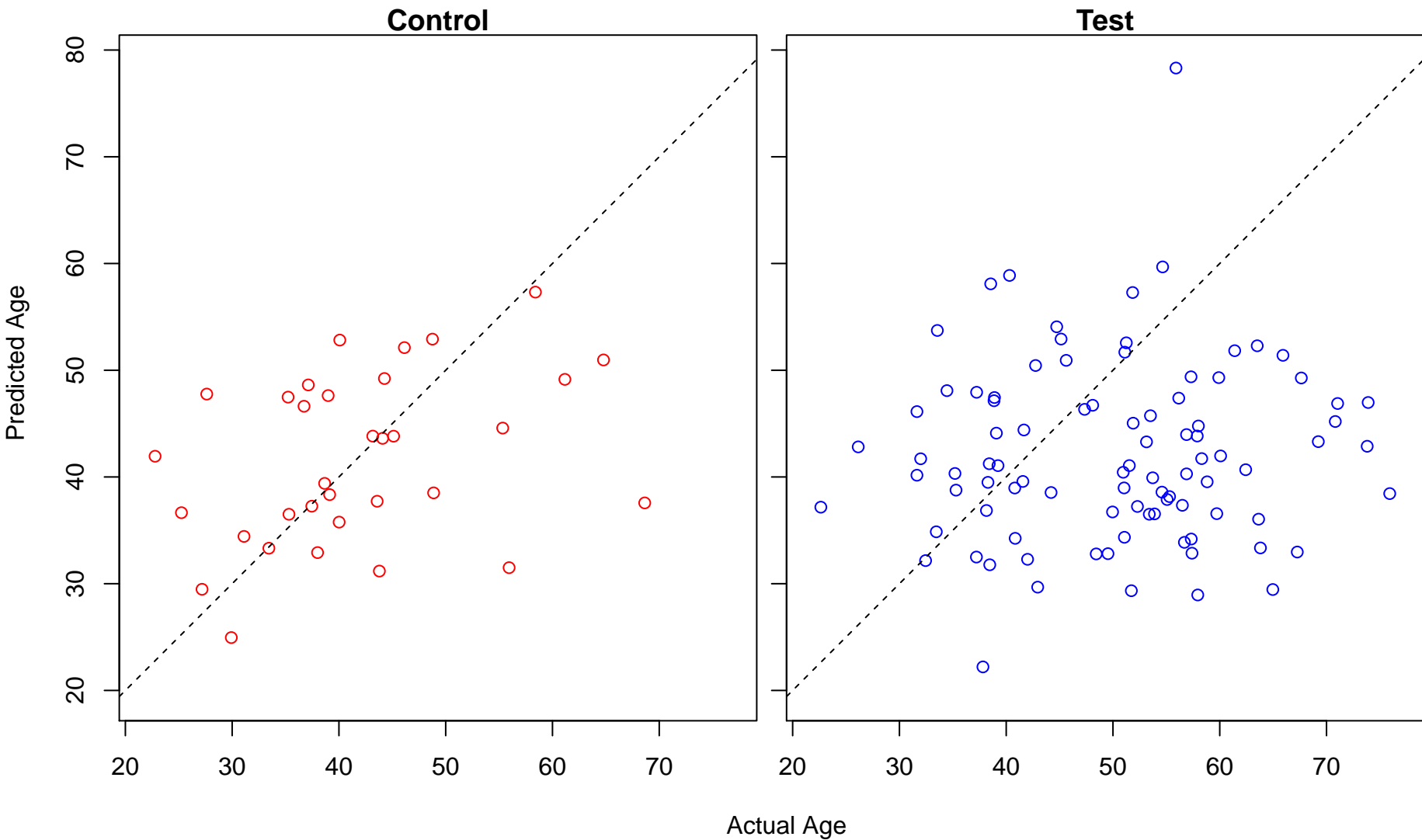
tRNA metabolic process (Score: 0.671610)



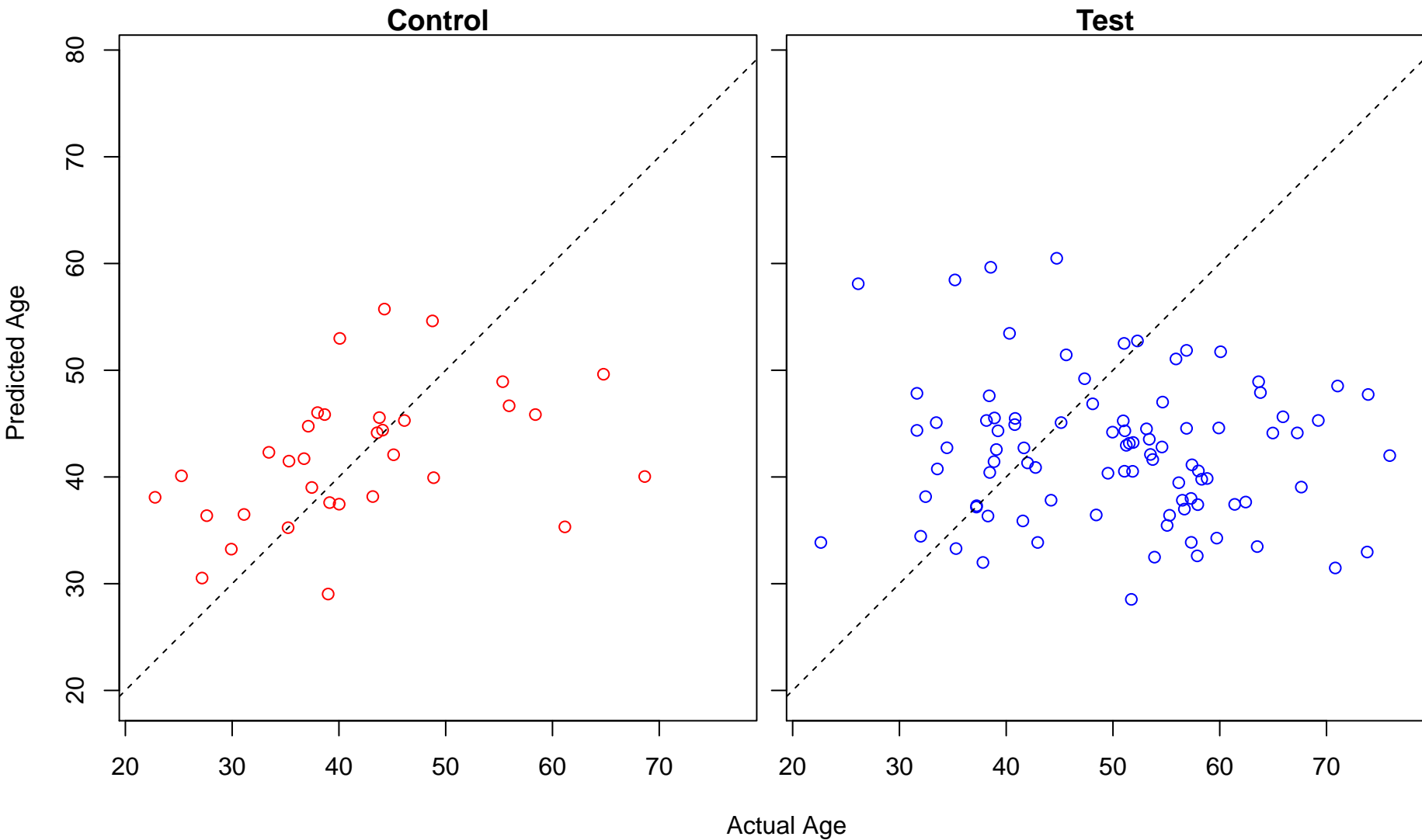
polyol transport (Score: 0.671075)



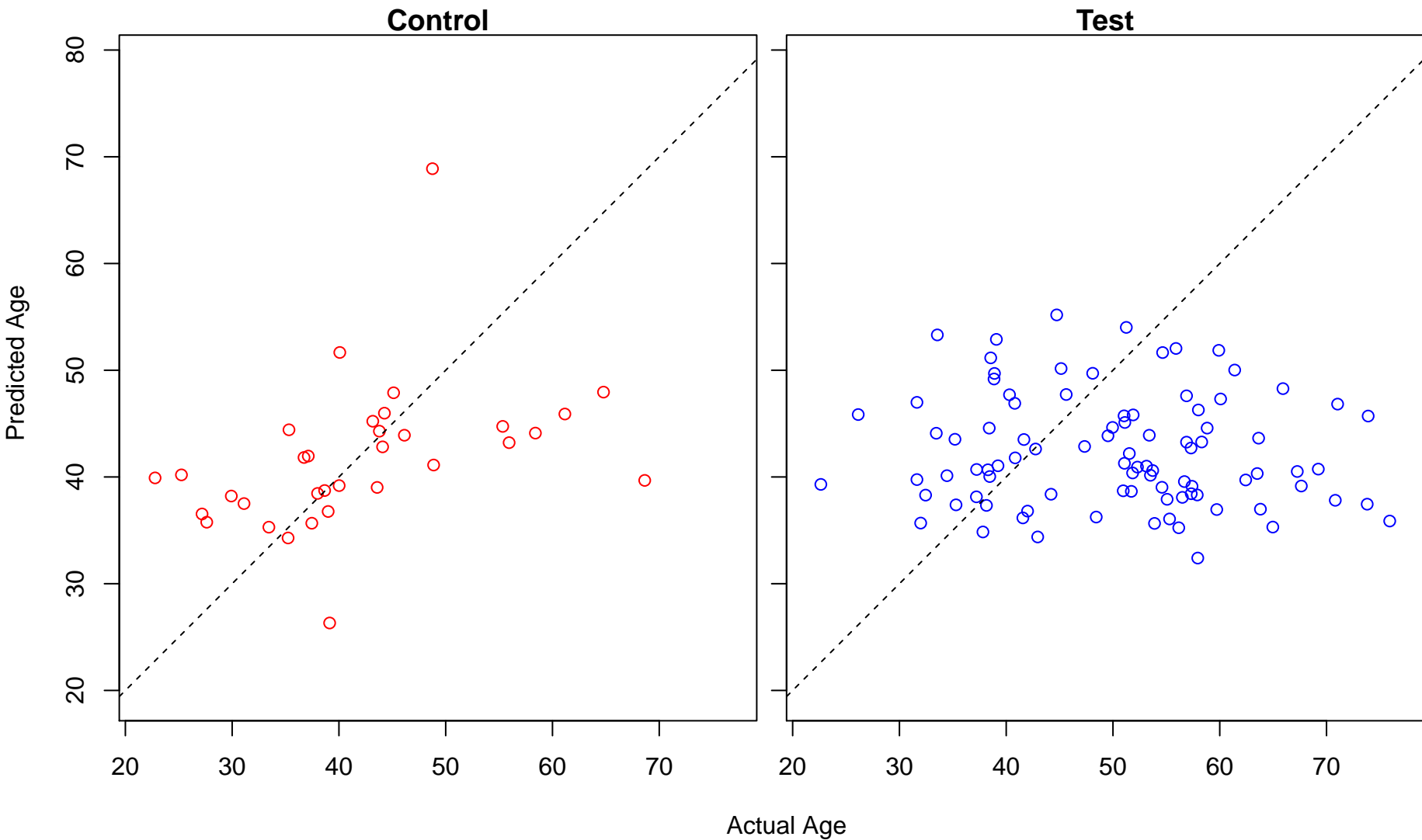
negative regulation of catenin import into nucleus (Score: 0.670723)



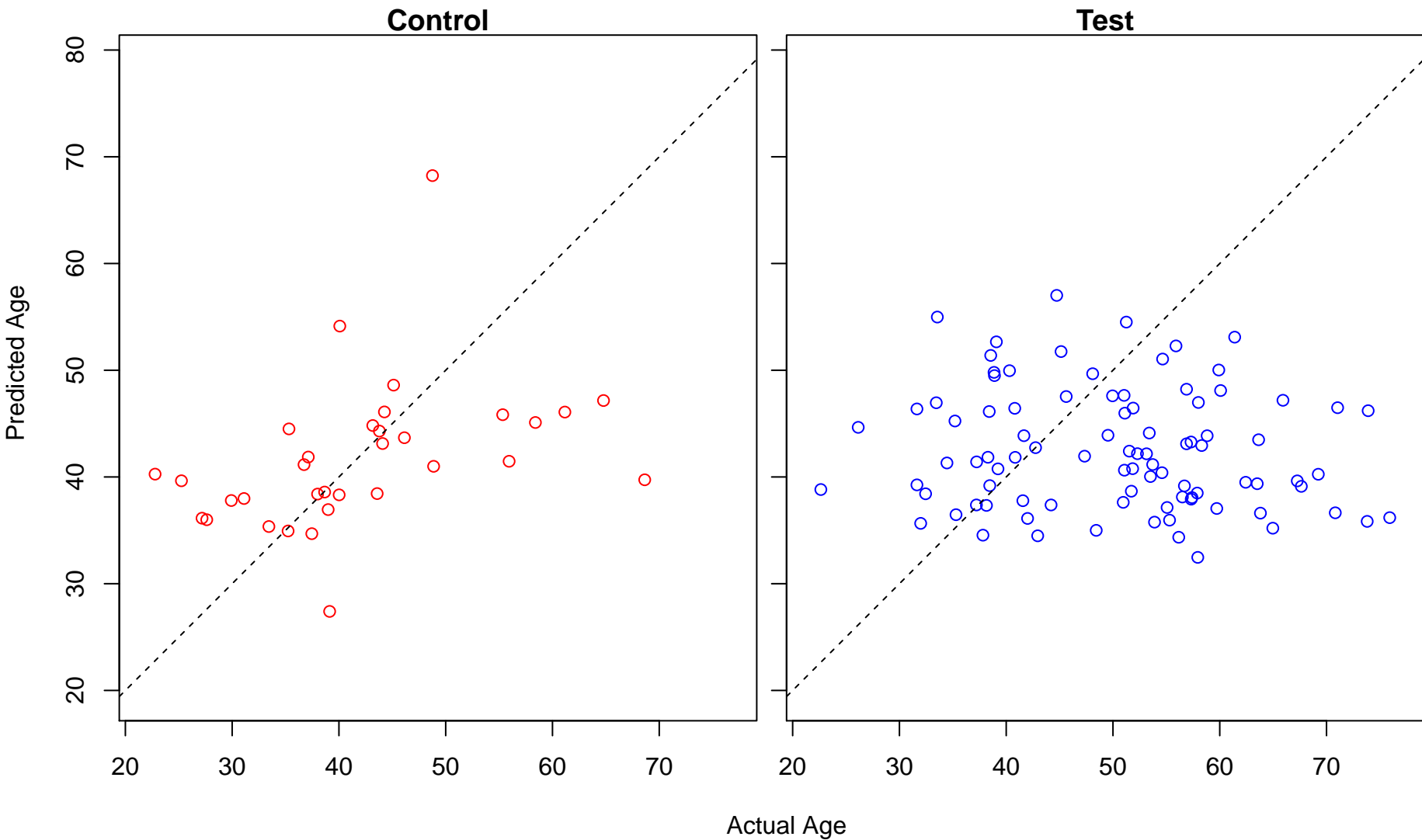
maintenance of cell polarity (Score: 0.670577)



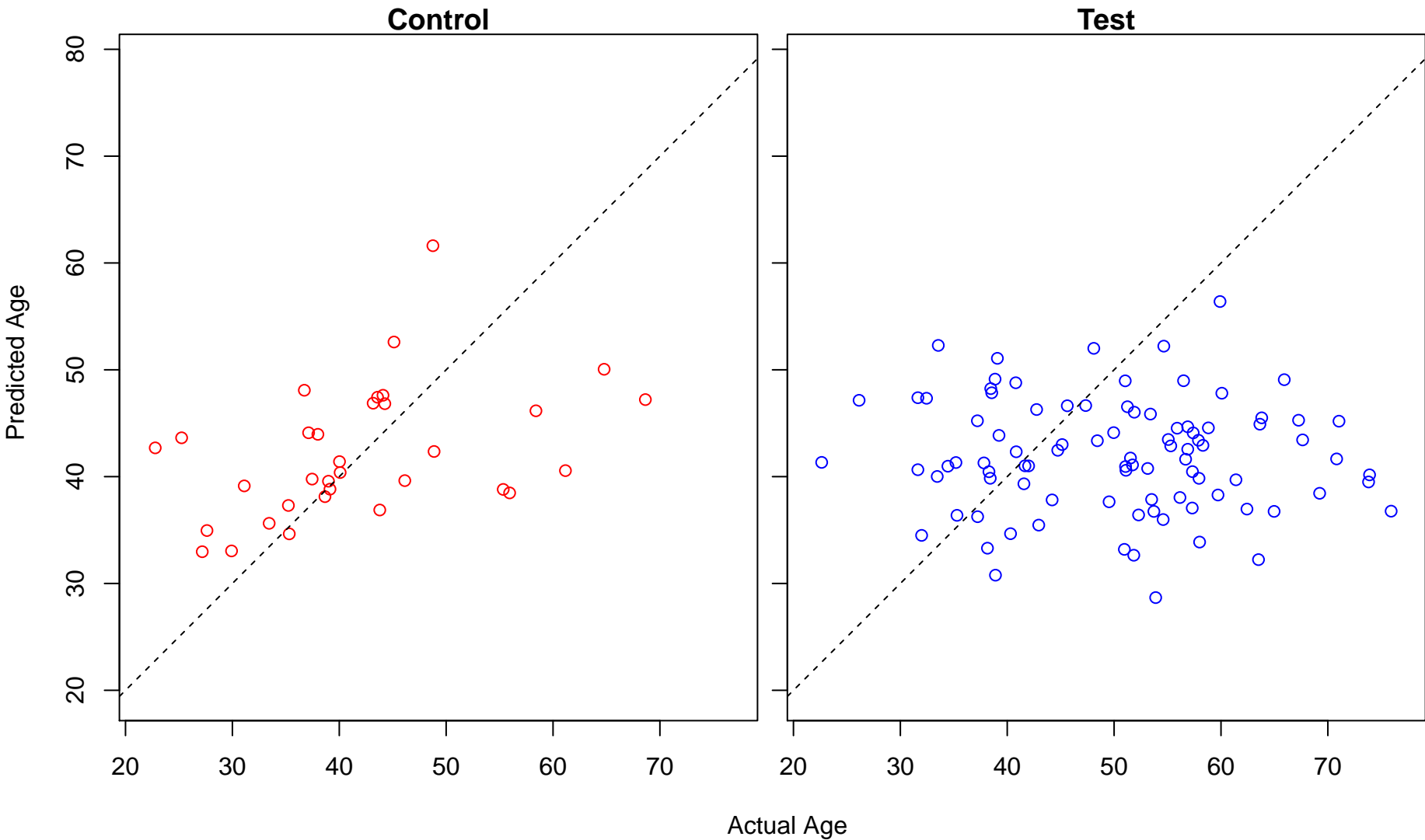
biological regulation (Score: 0.669027)



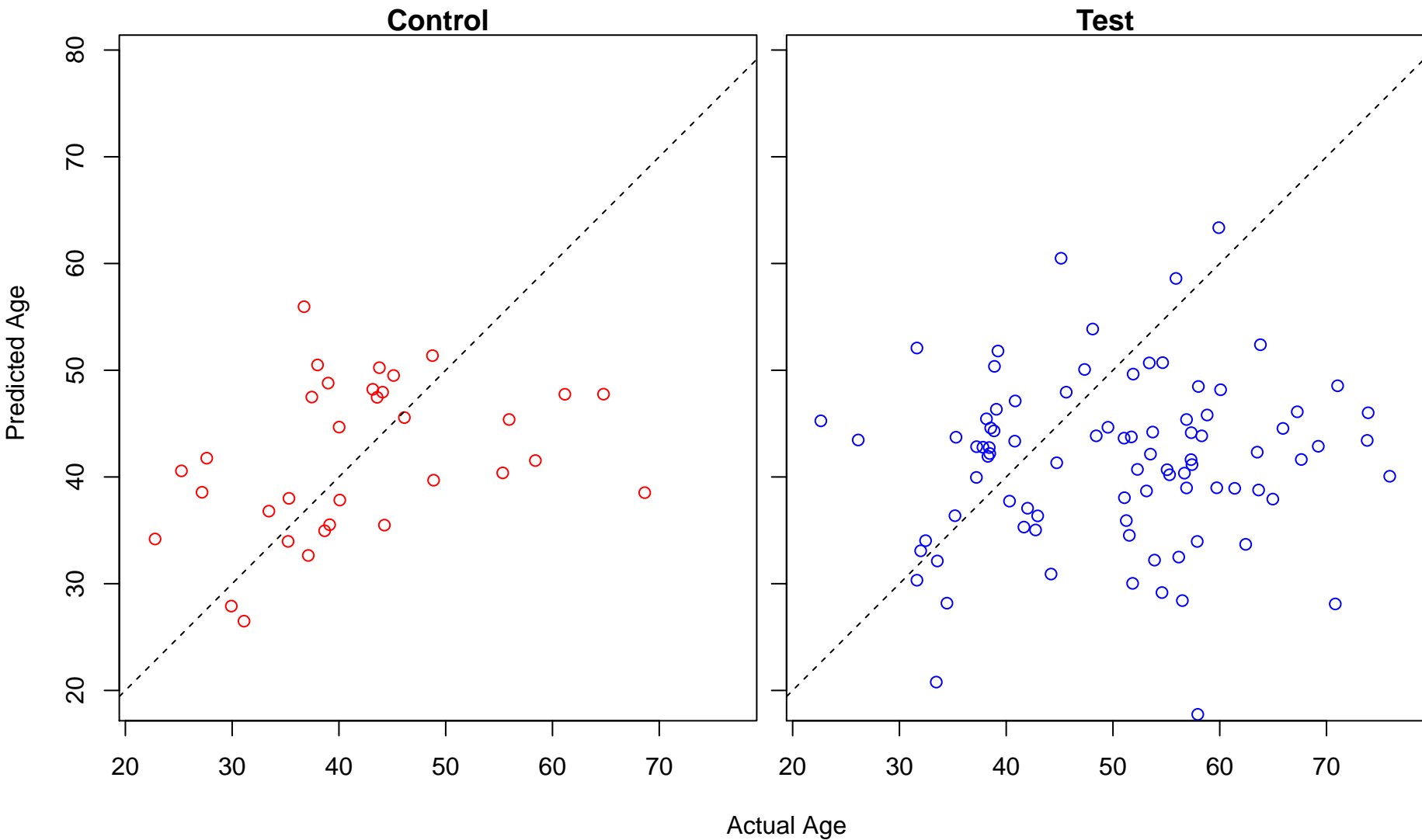
regulation of cellular component organization (Score: 0.667729)



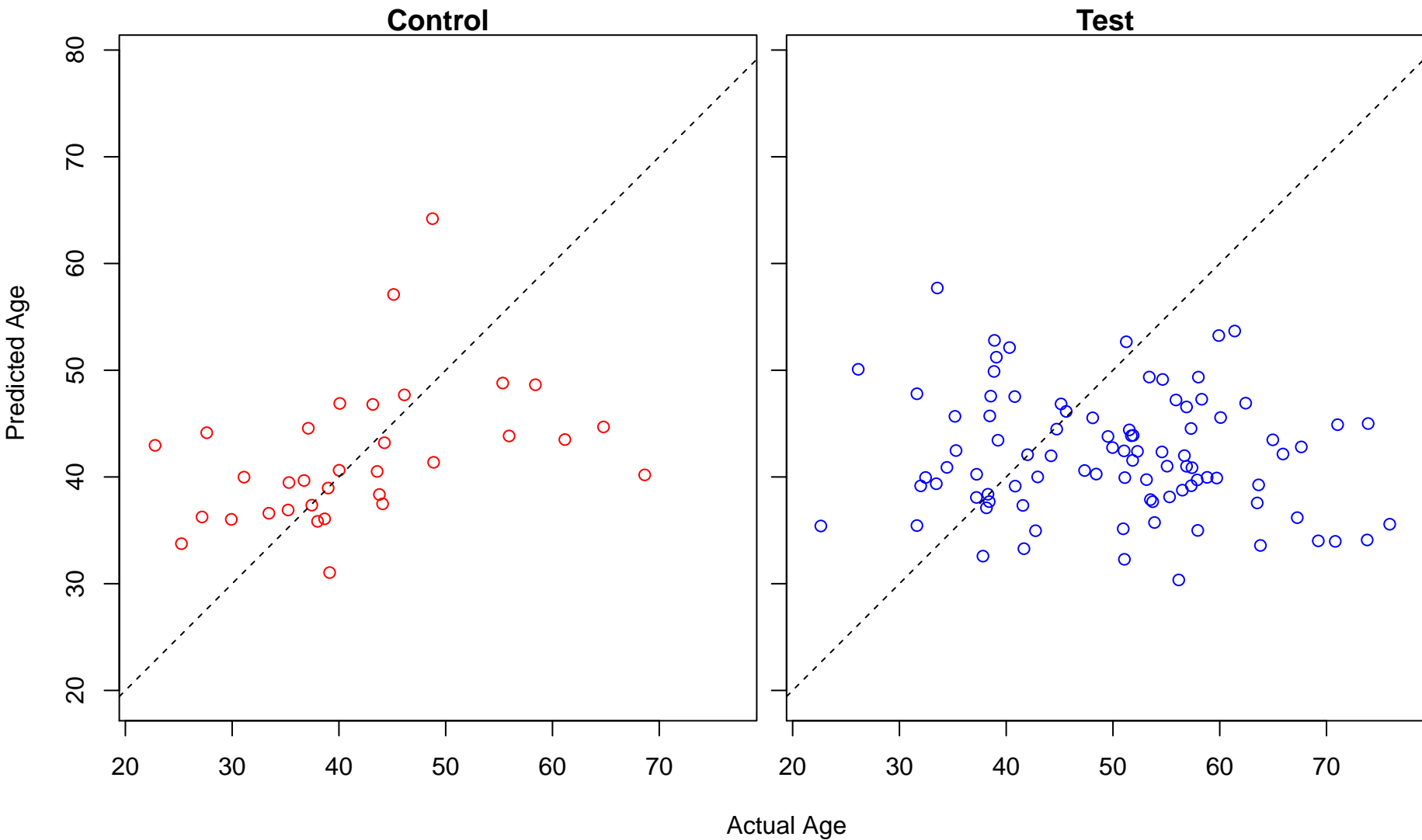
regulation of T-helper 1 cell differentiation (Score: 0.667582)



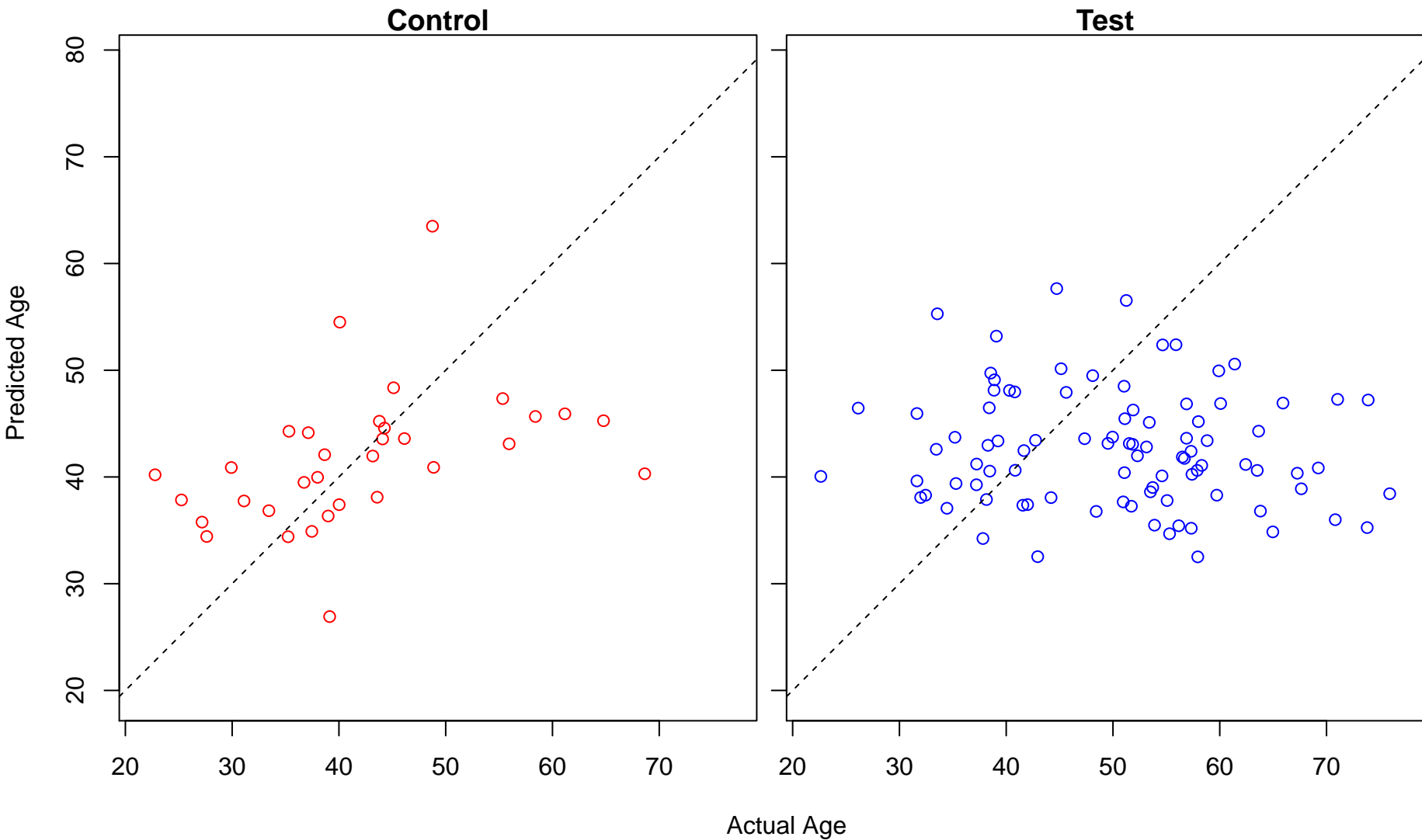
protein geranylgeranylation (Score: 0.66897)



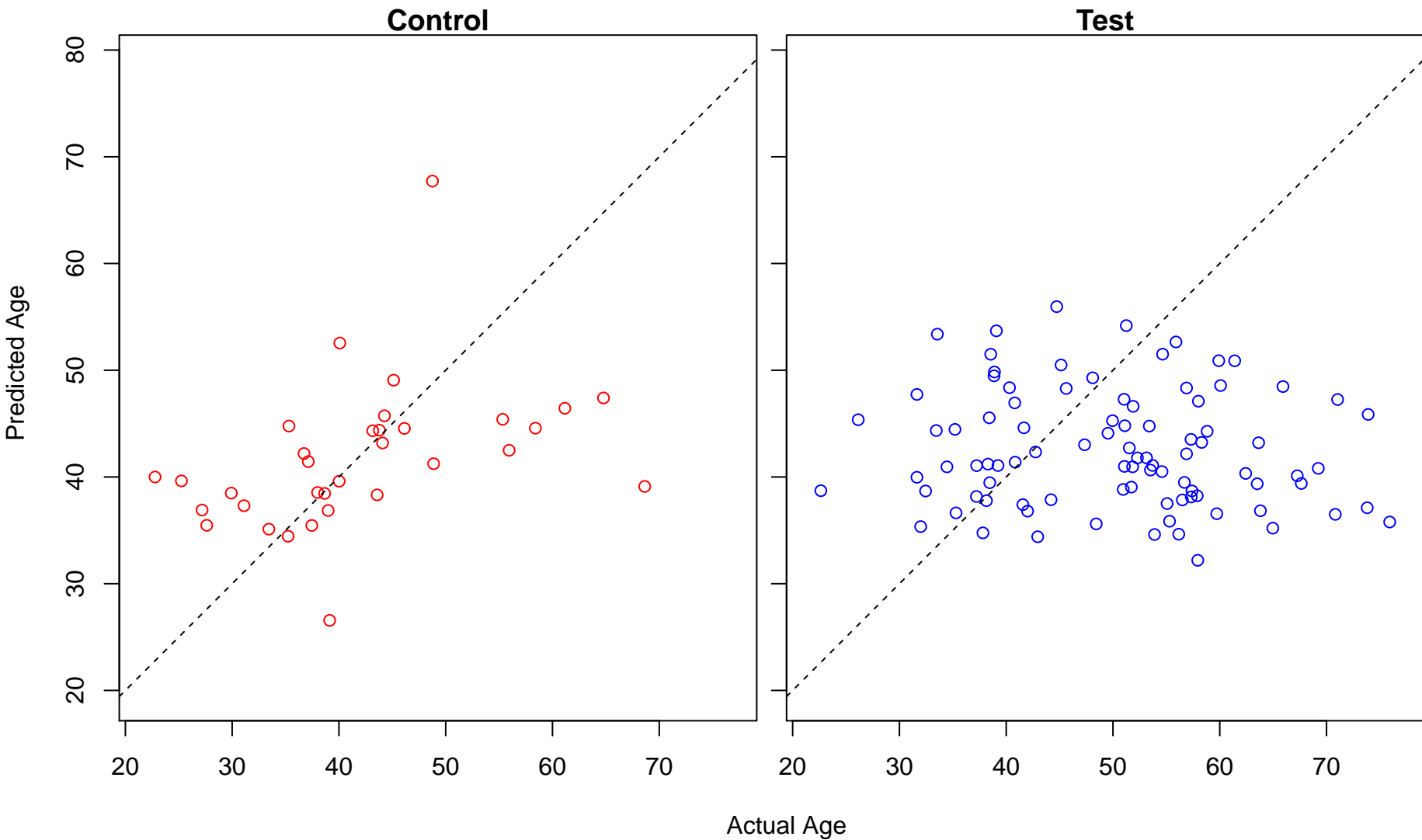
positive regulation of endothelial cell proliferation (Score: 0.666490)



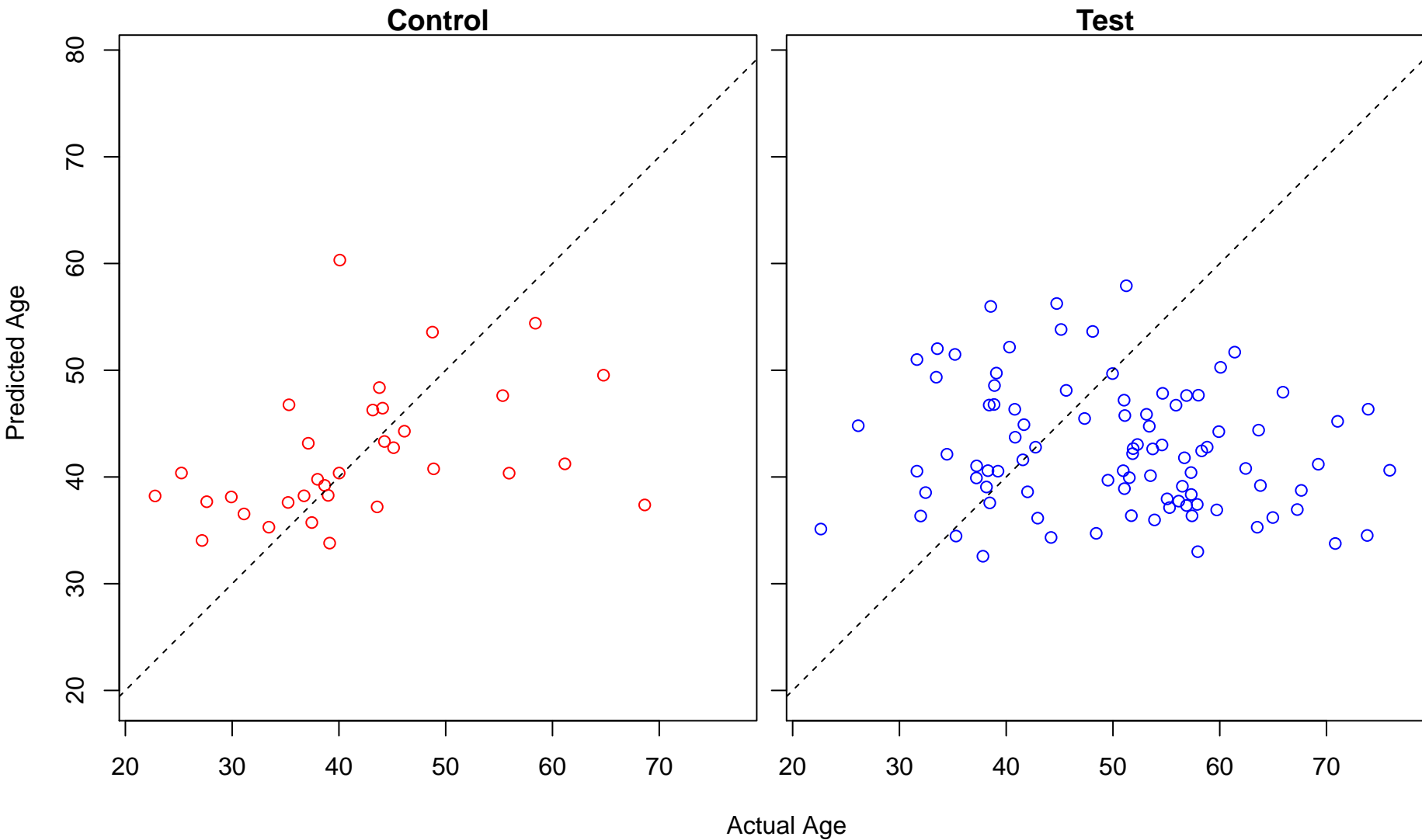
positive regulation of protein phosphorylation (Score: 0.666052)



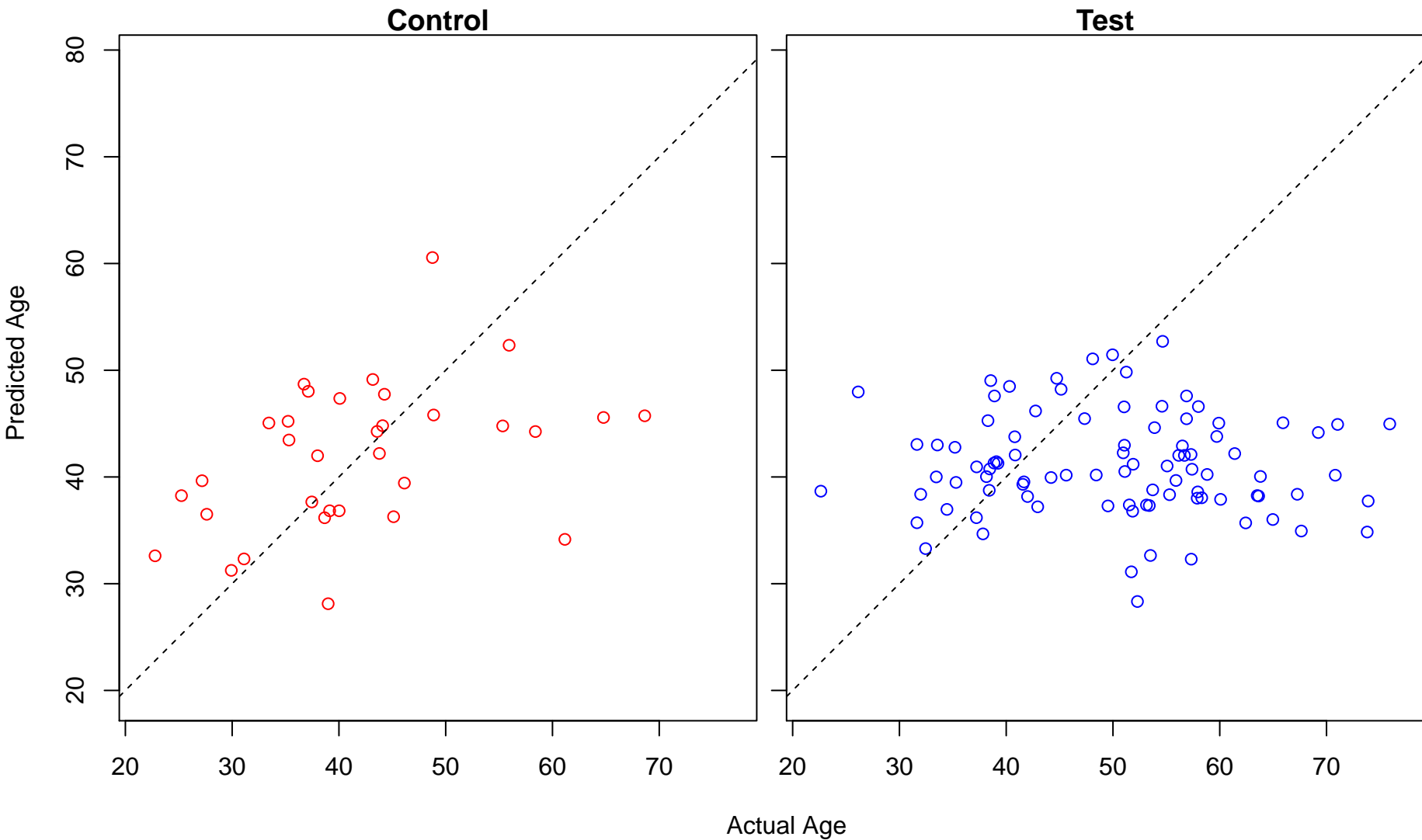
positive regulation of cellular process (Score: 0.665849)



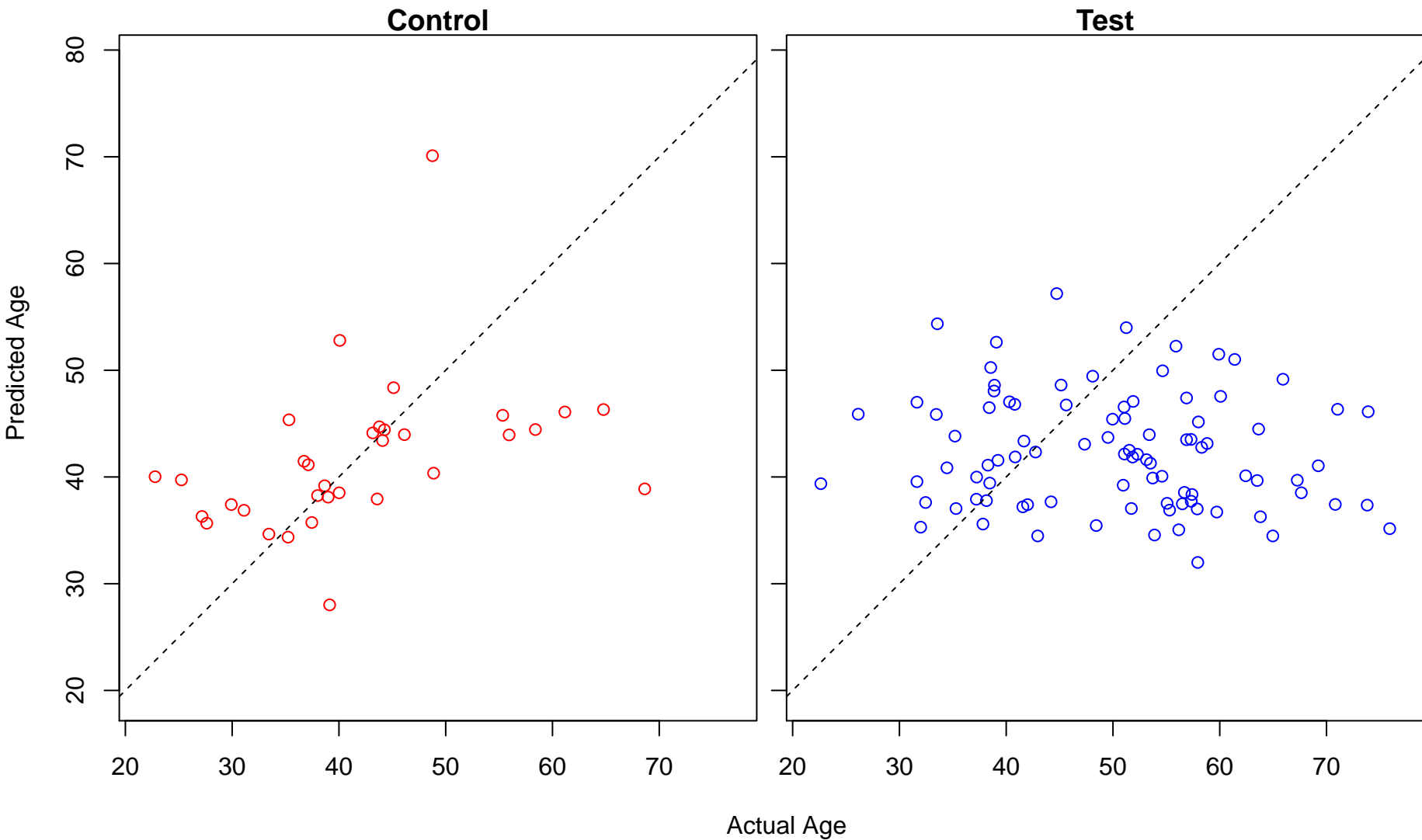
establishment or maintenance of epithelial cell apical/basal polarity (Score: 0.665618)



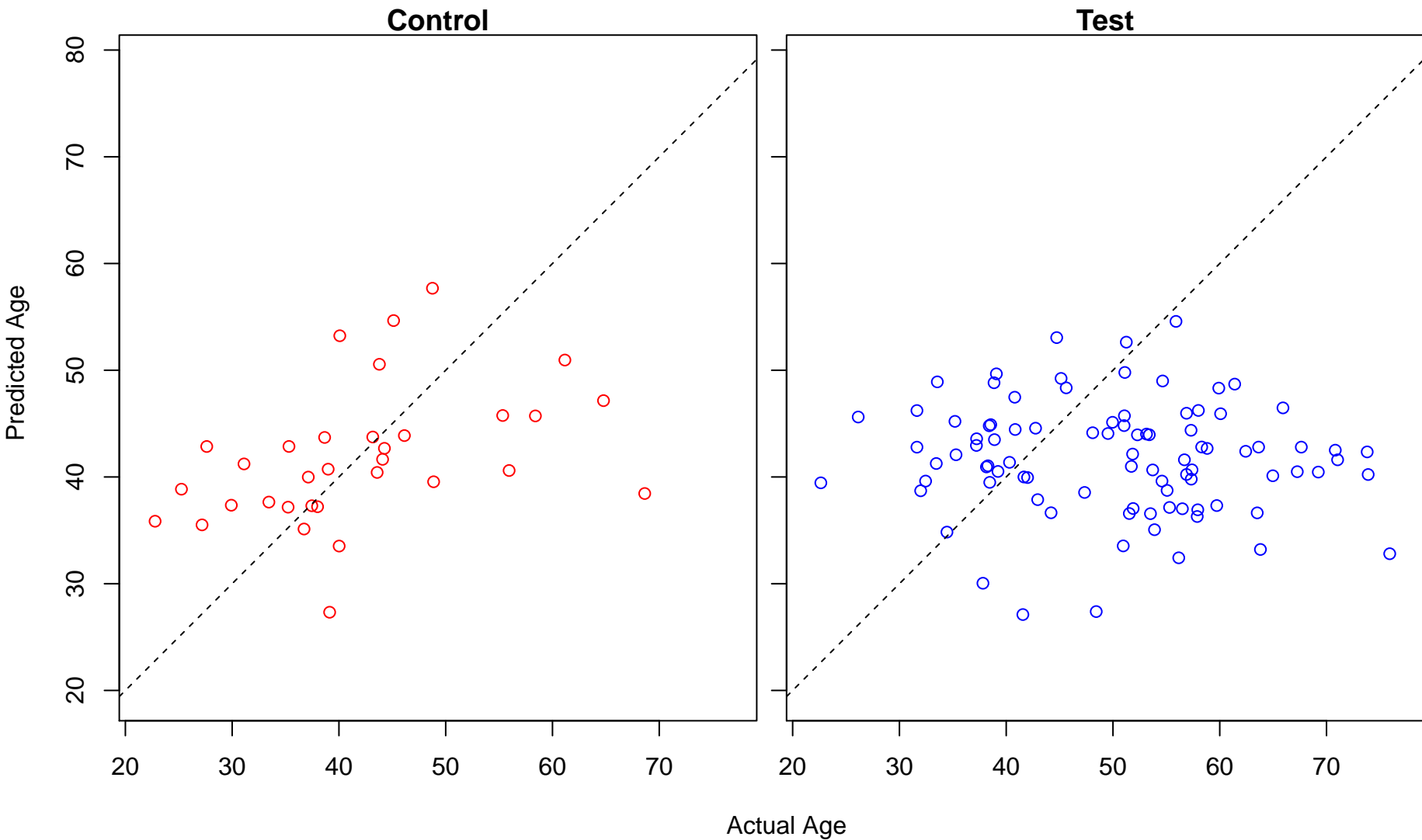
regulation of response to alcohol (Score: 0.665533)



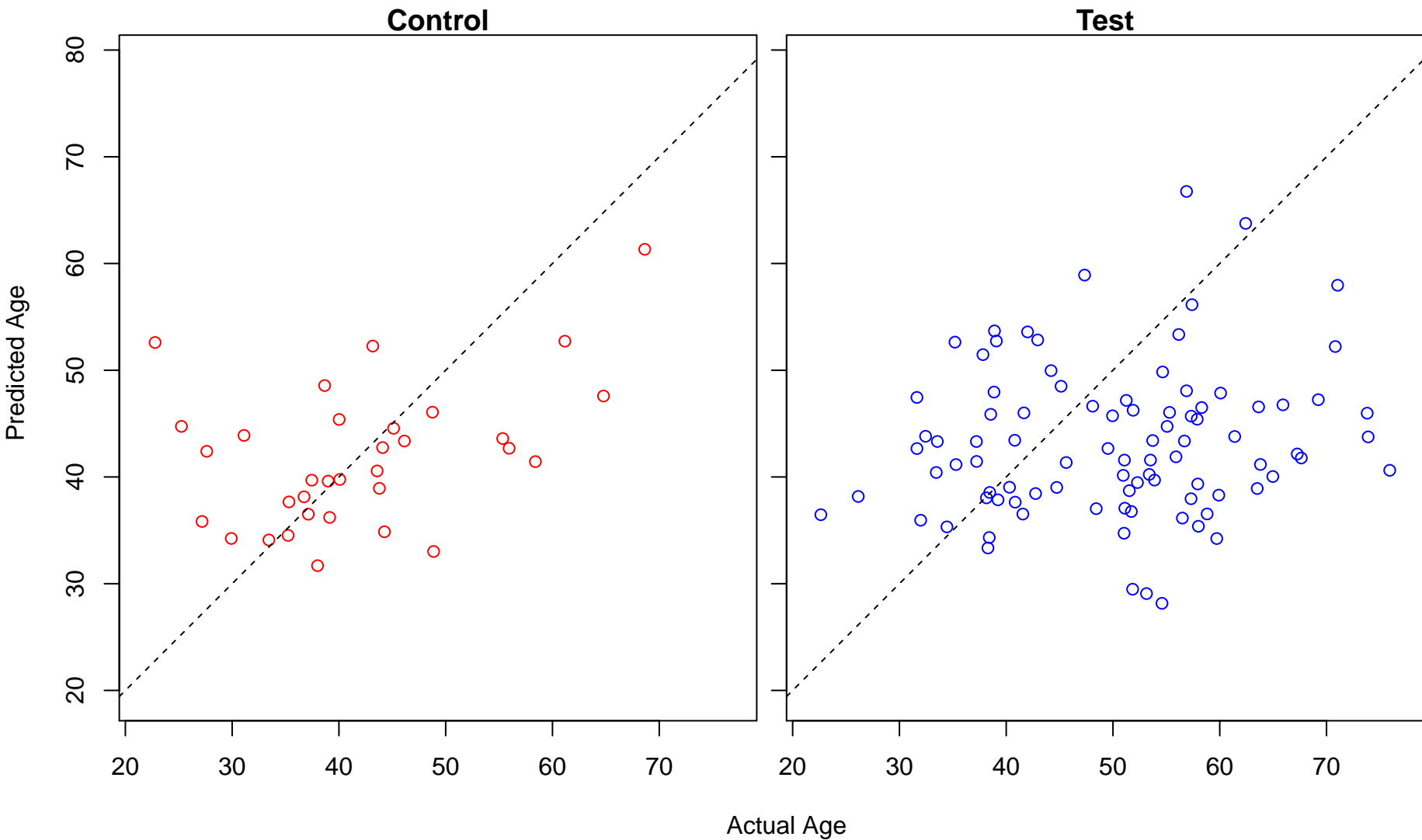
cellular biosynthetic process (Score: 0.665459)



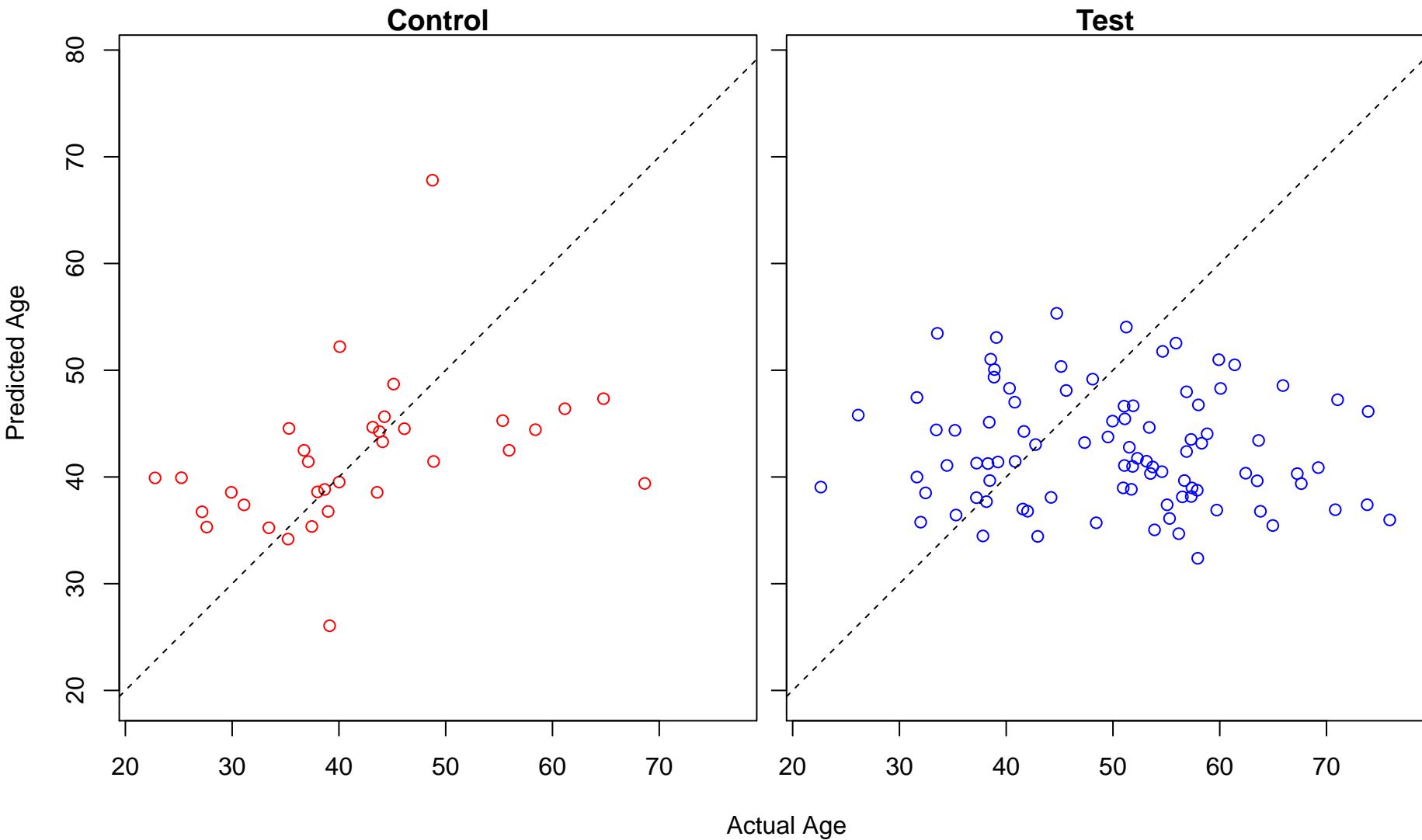
muscle structure development (Score: 0.665312)



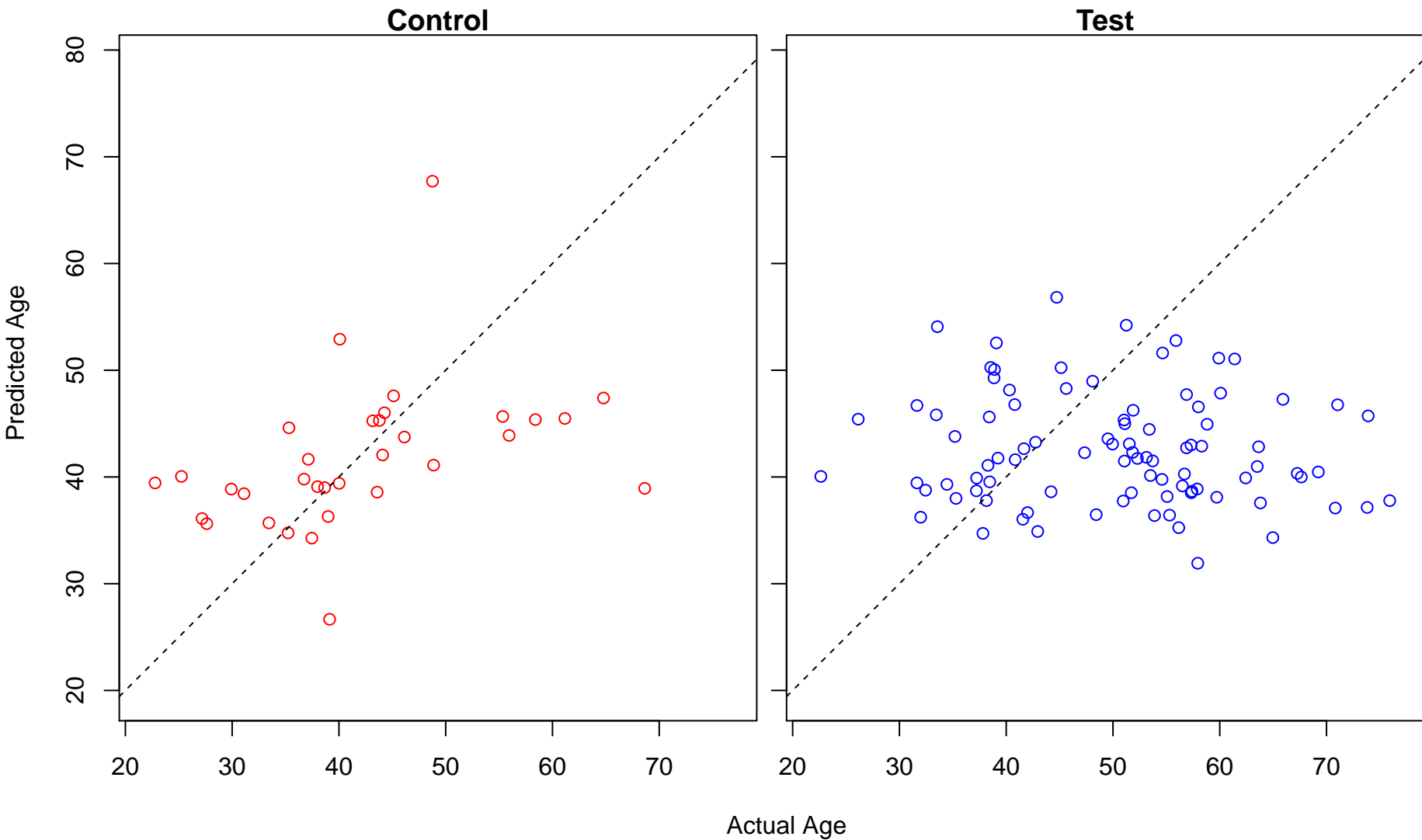
natural killer cell mediated cytotoxicity (Score: 0.665172)



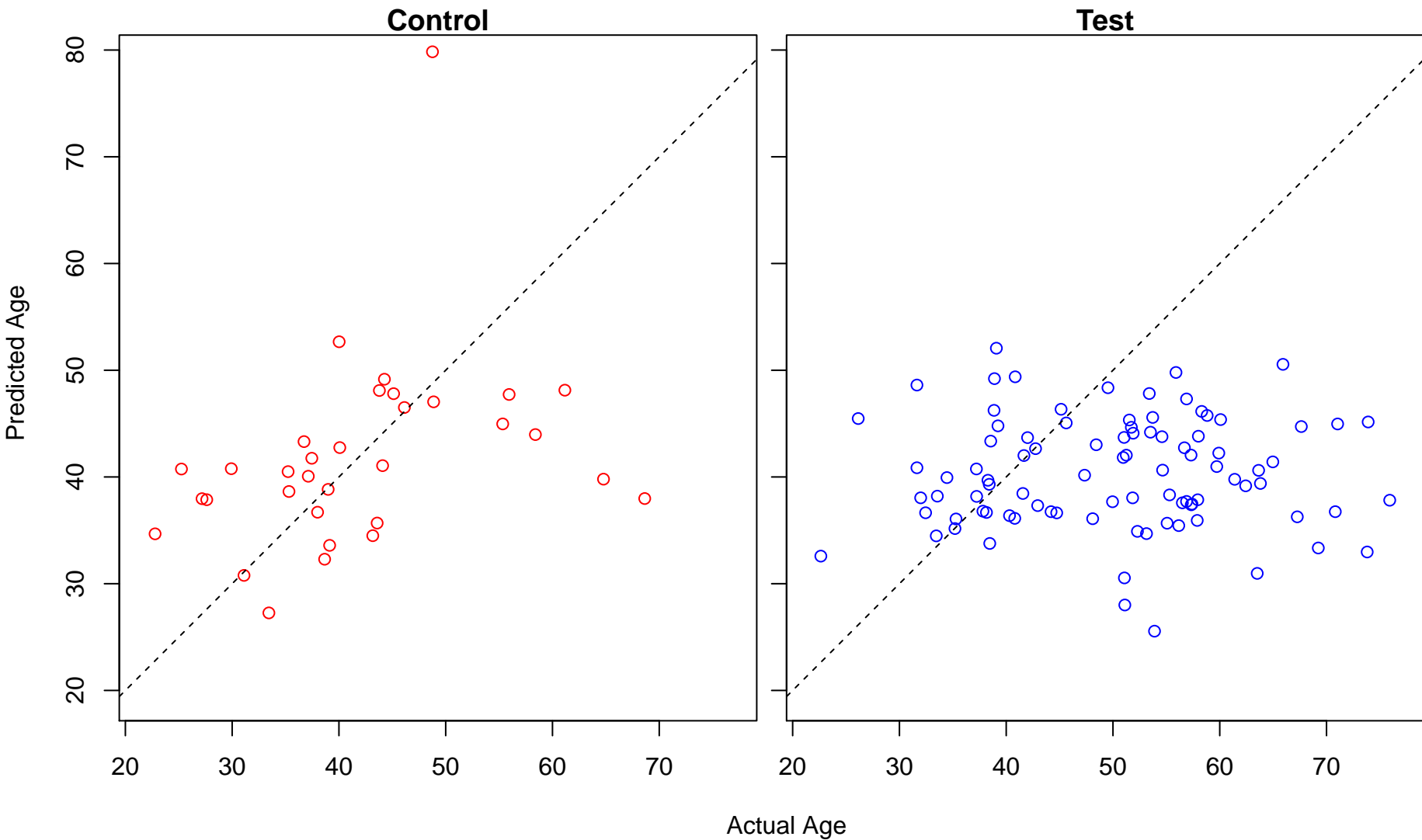
positive regulation of biological process (Score: 0.665158)



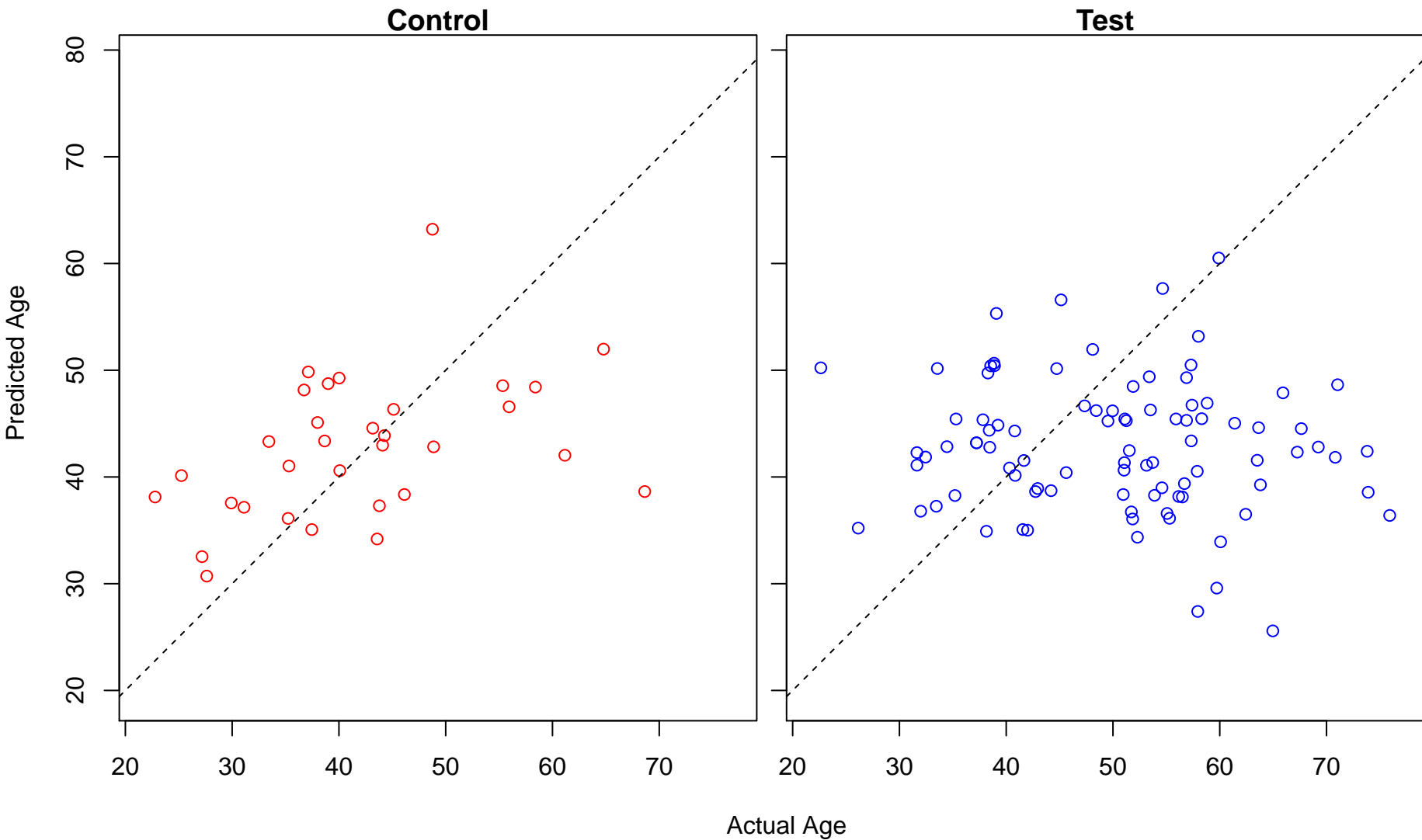
regulation of signal transduction (Score: 0.665140)



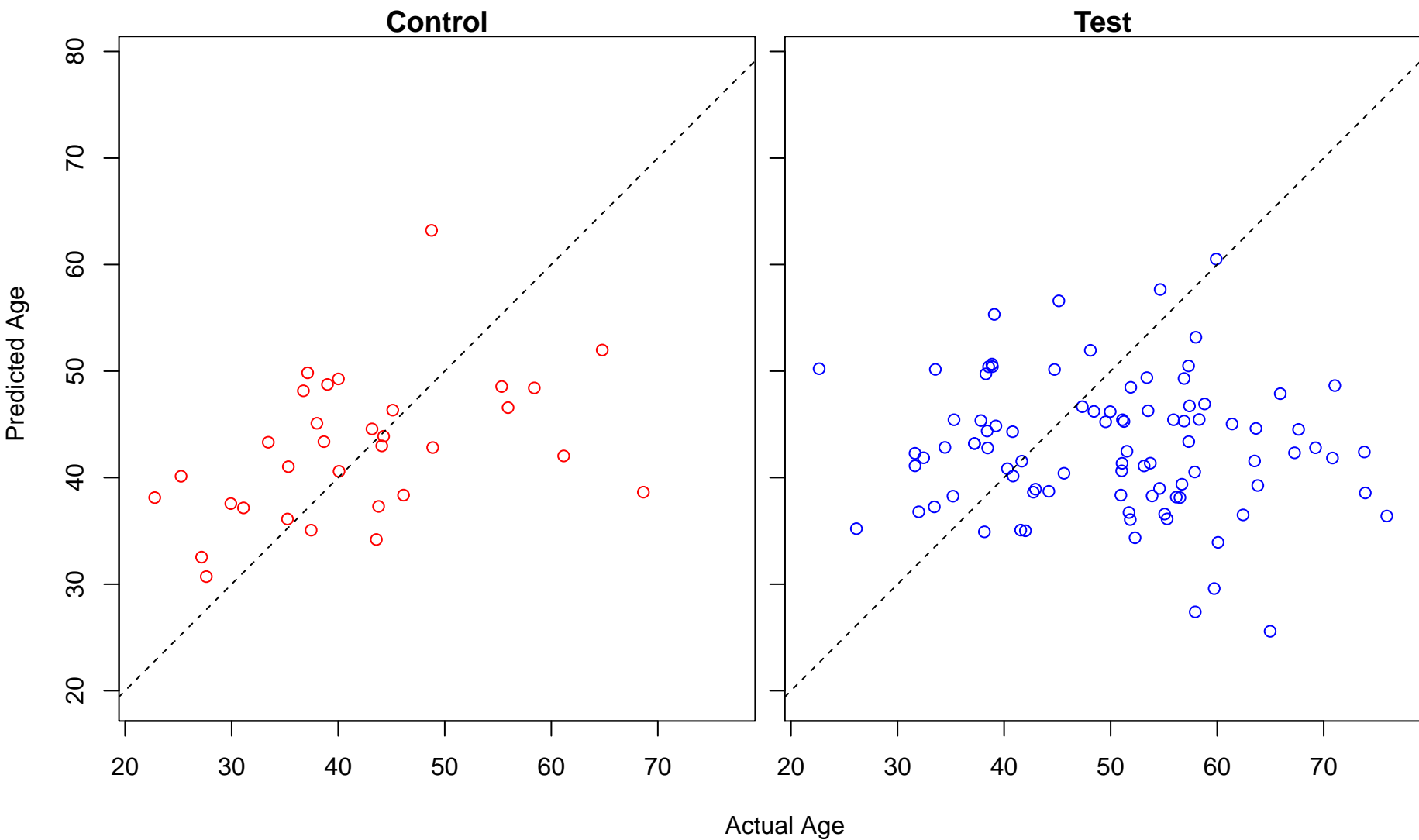
regulation of MDA-5 signaling pathway (Score: 0.665082)



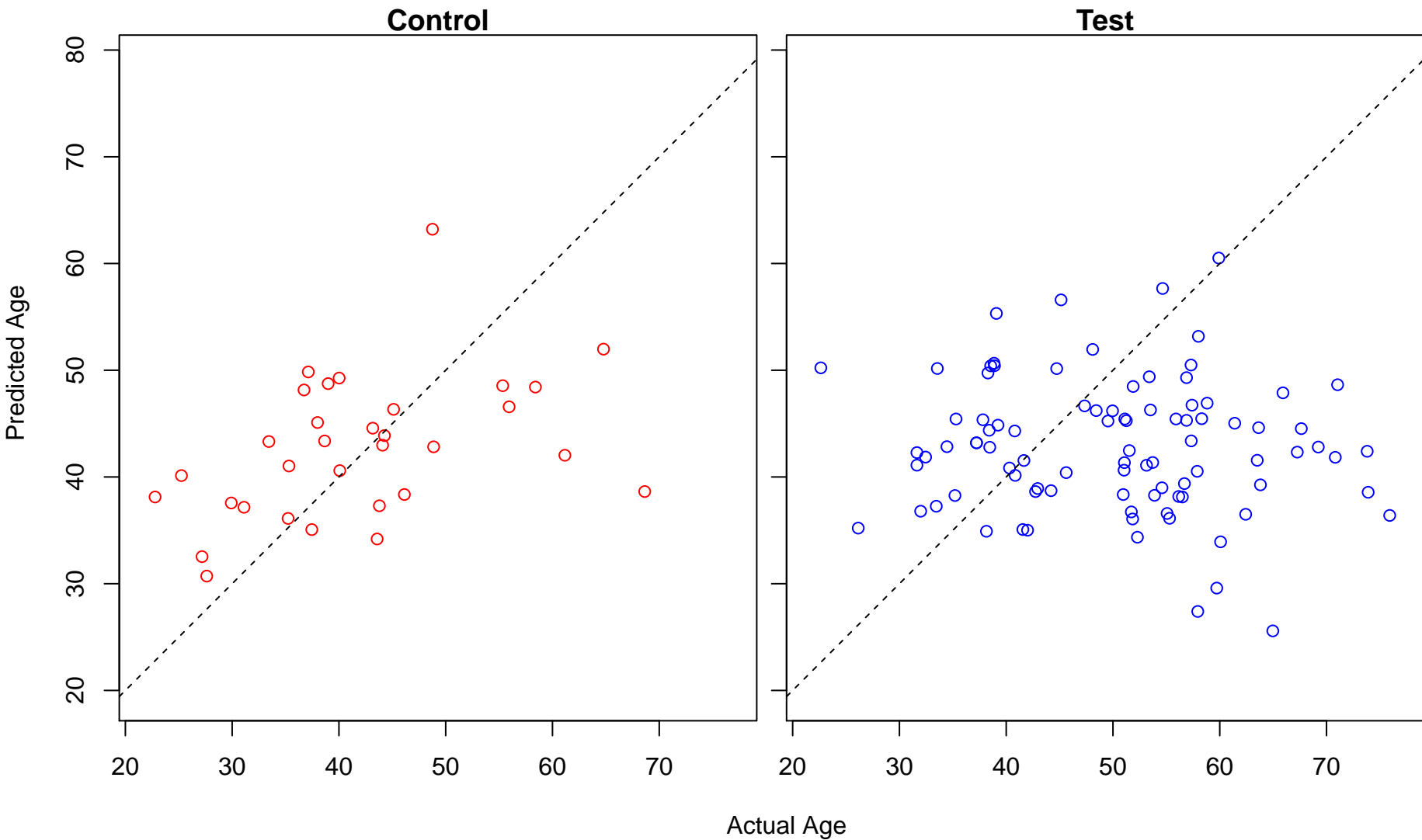
positive regulation of maintenance of sister chromatid cohesion (Score: 0.664349)



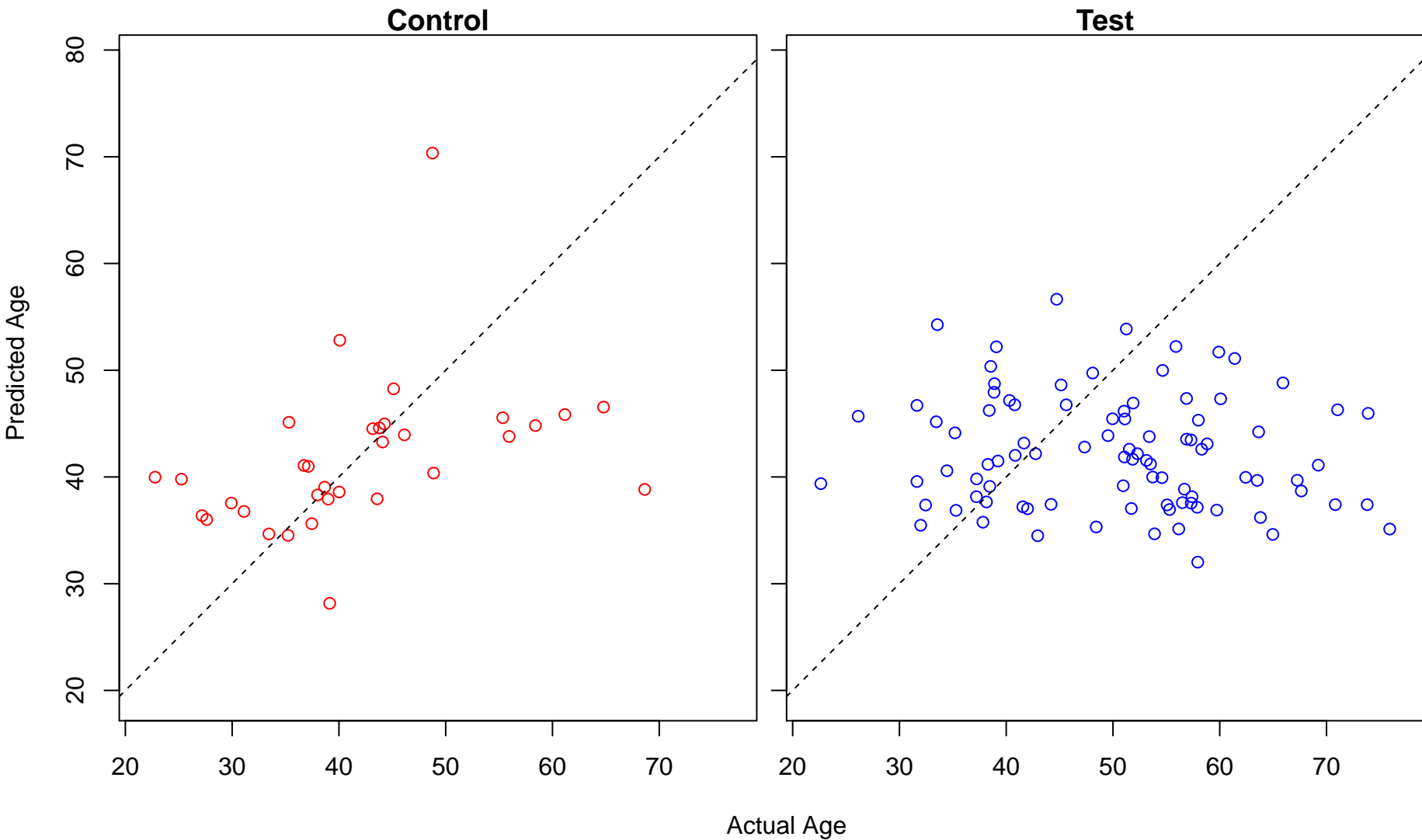
positive regulation of maintenance of mitotic sister chromatid cohesion (Score: 0.664349)



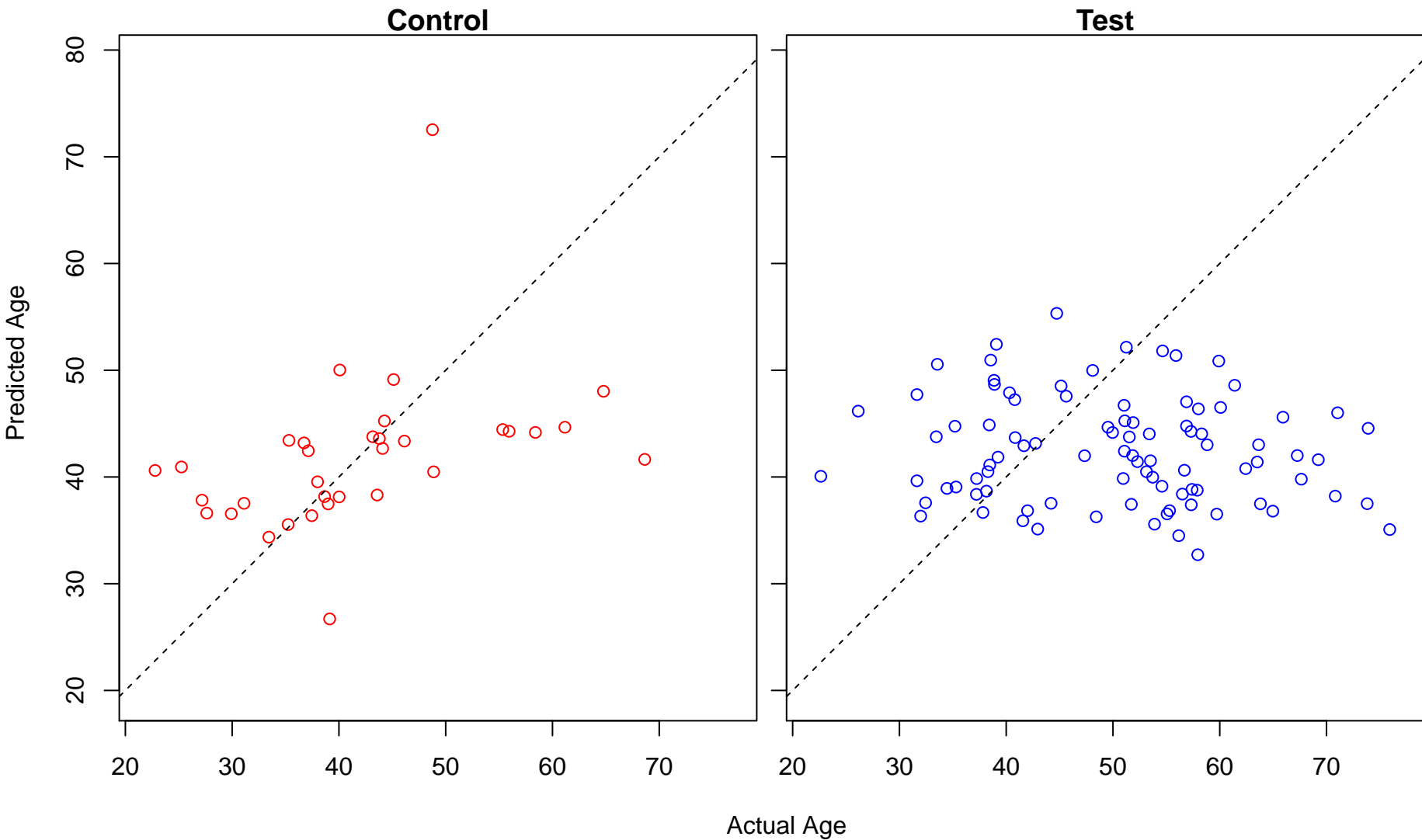
positive regulation of sister chromatid cohesion (Score: 0.664349)



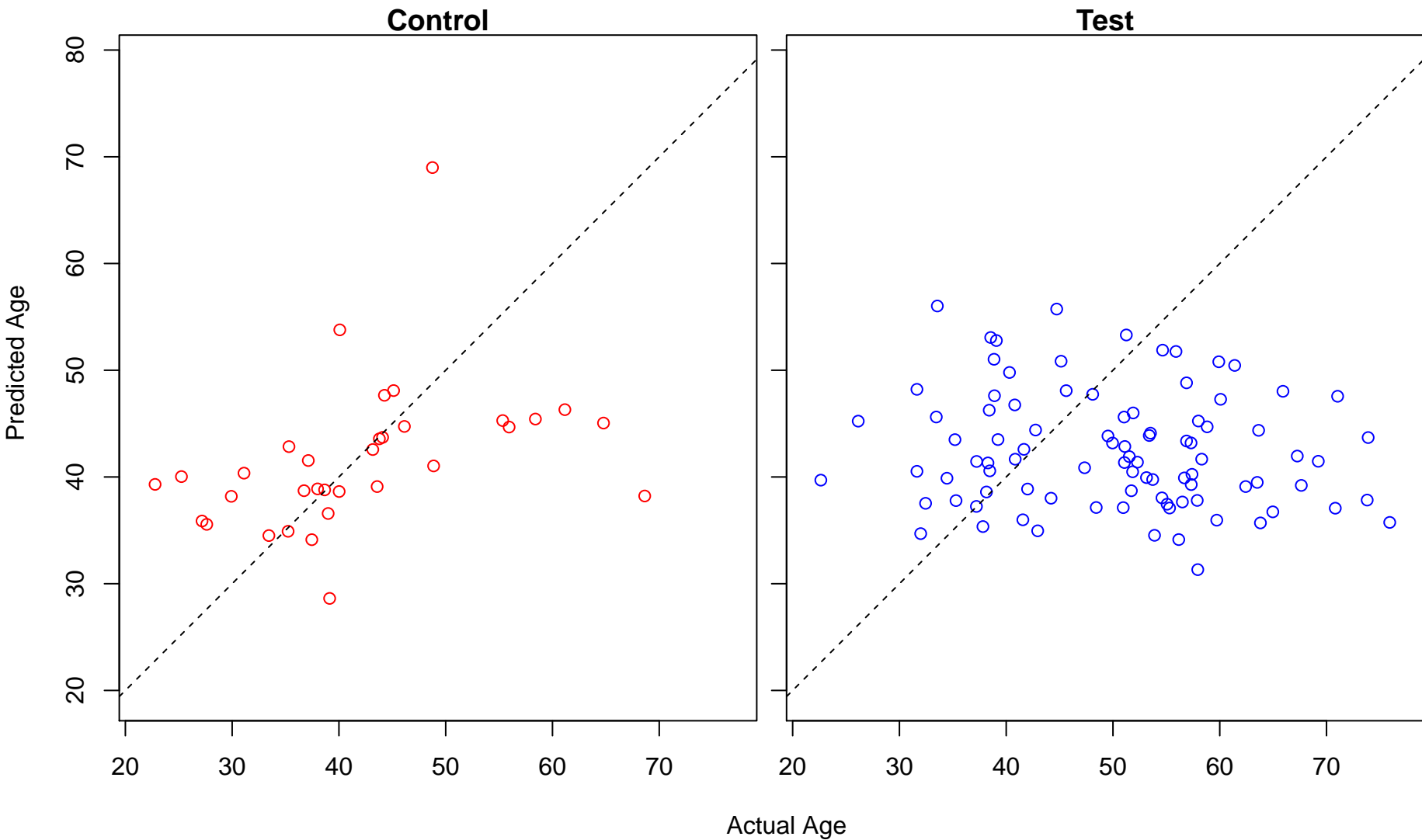
biosynthetic process (Score: 0.664187)



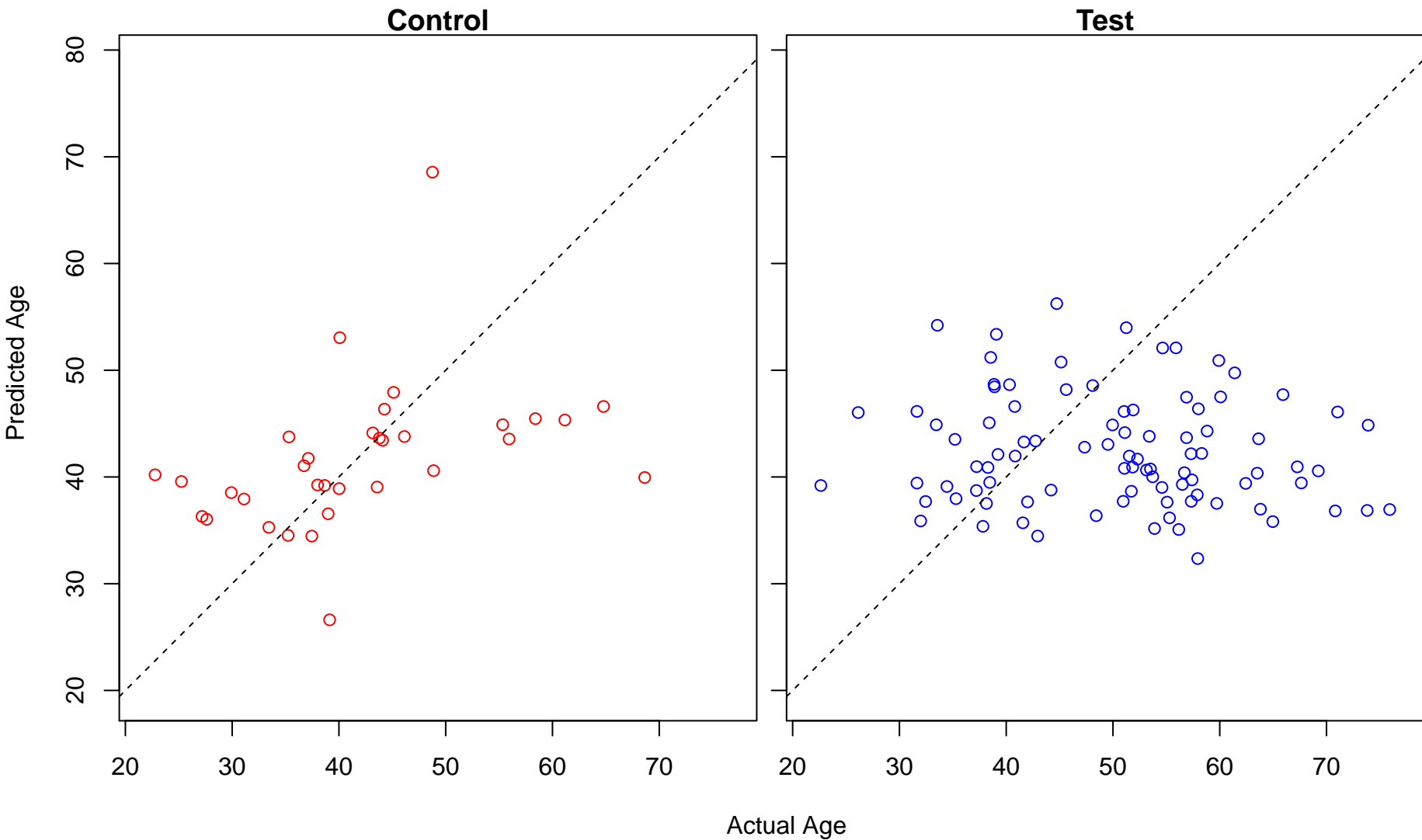
macromolecule localization (Score: 0.664045)



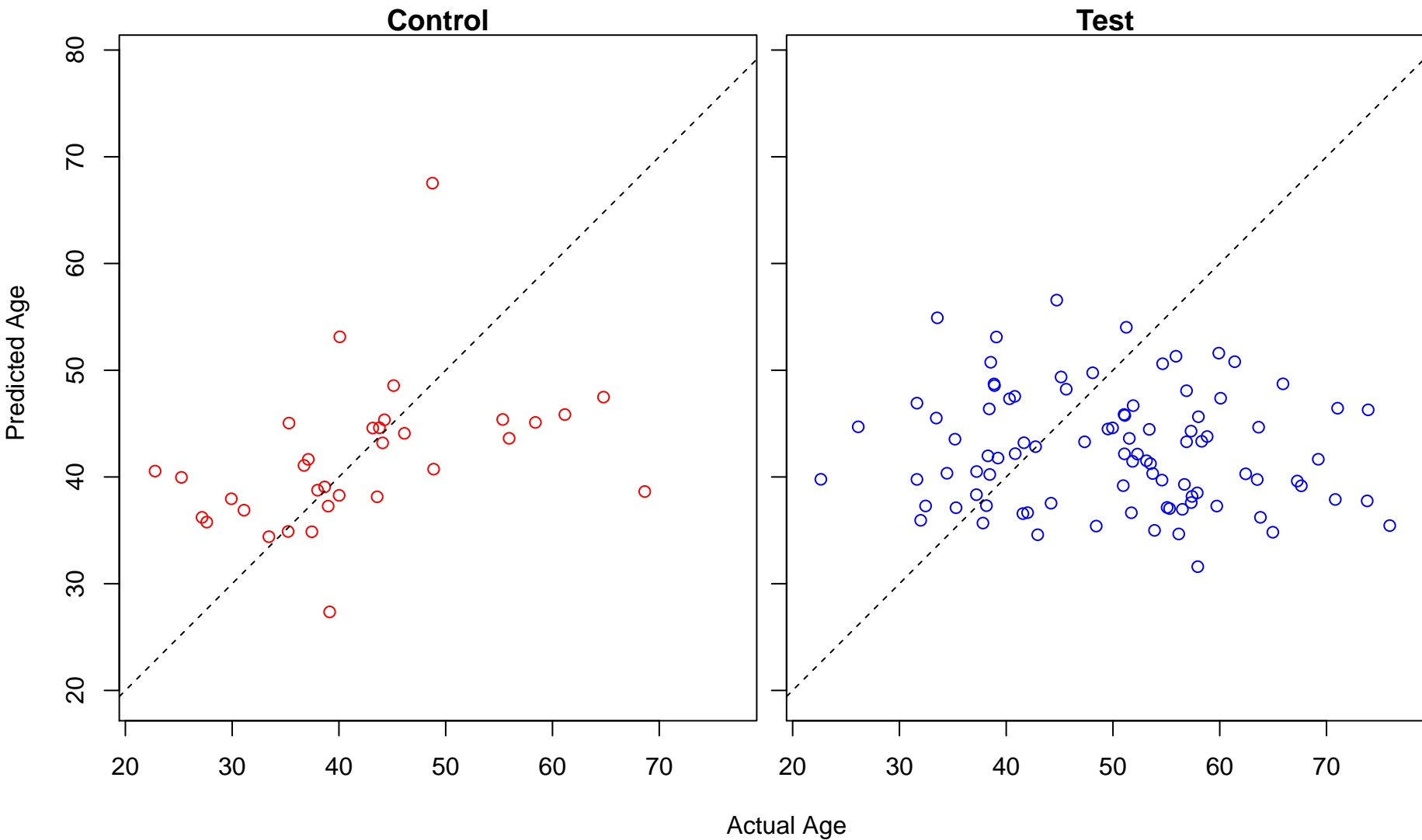
negative regulation of catalytic activity (Score: 0.663740)



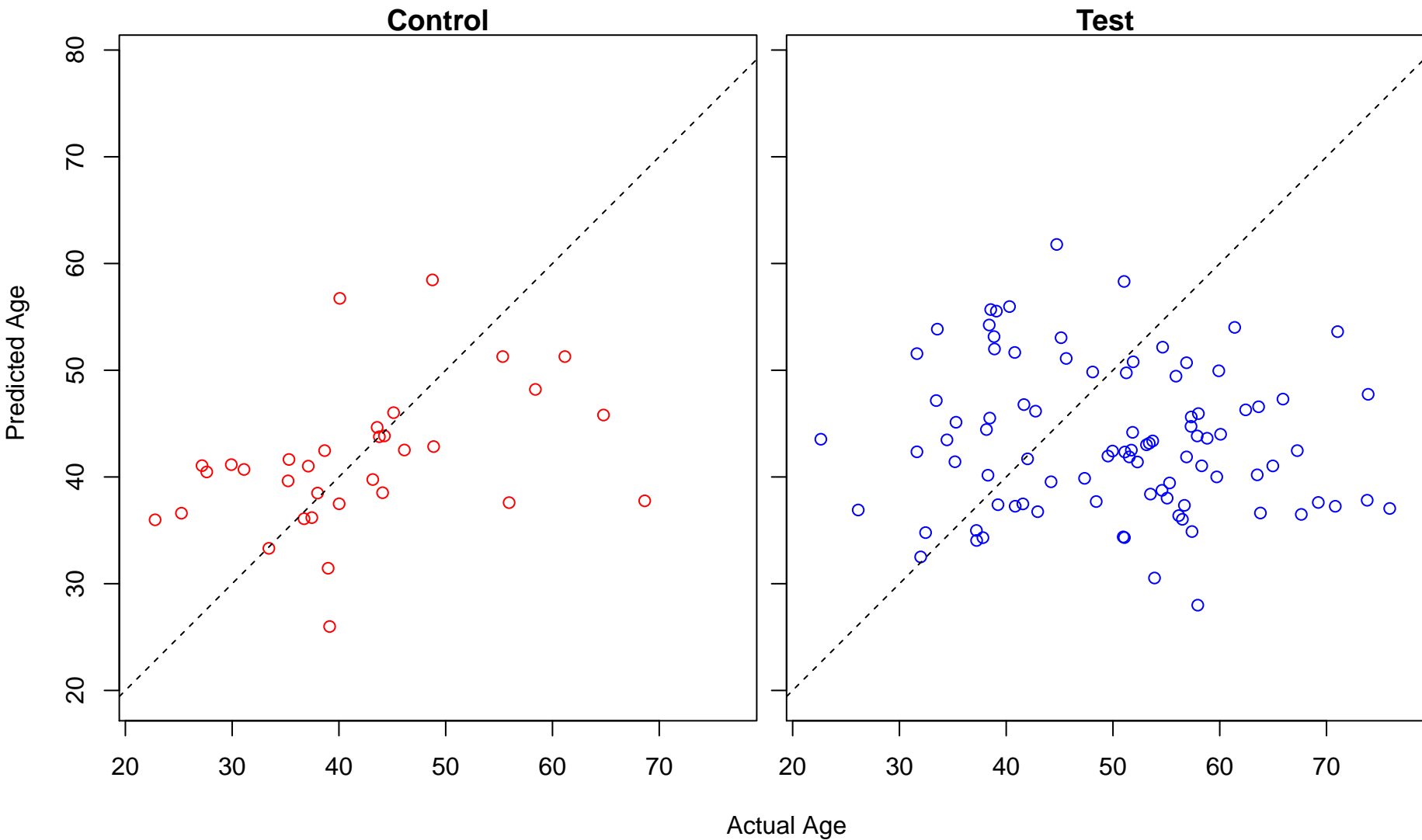
regulation of molecular function (Score: 0.663592)



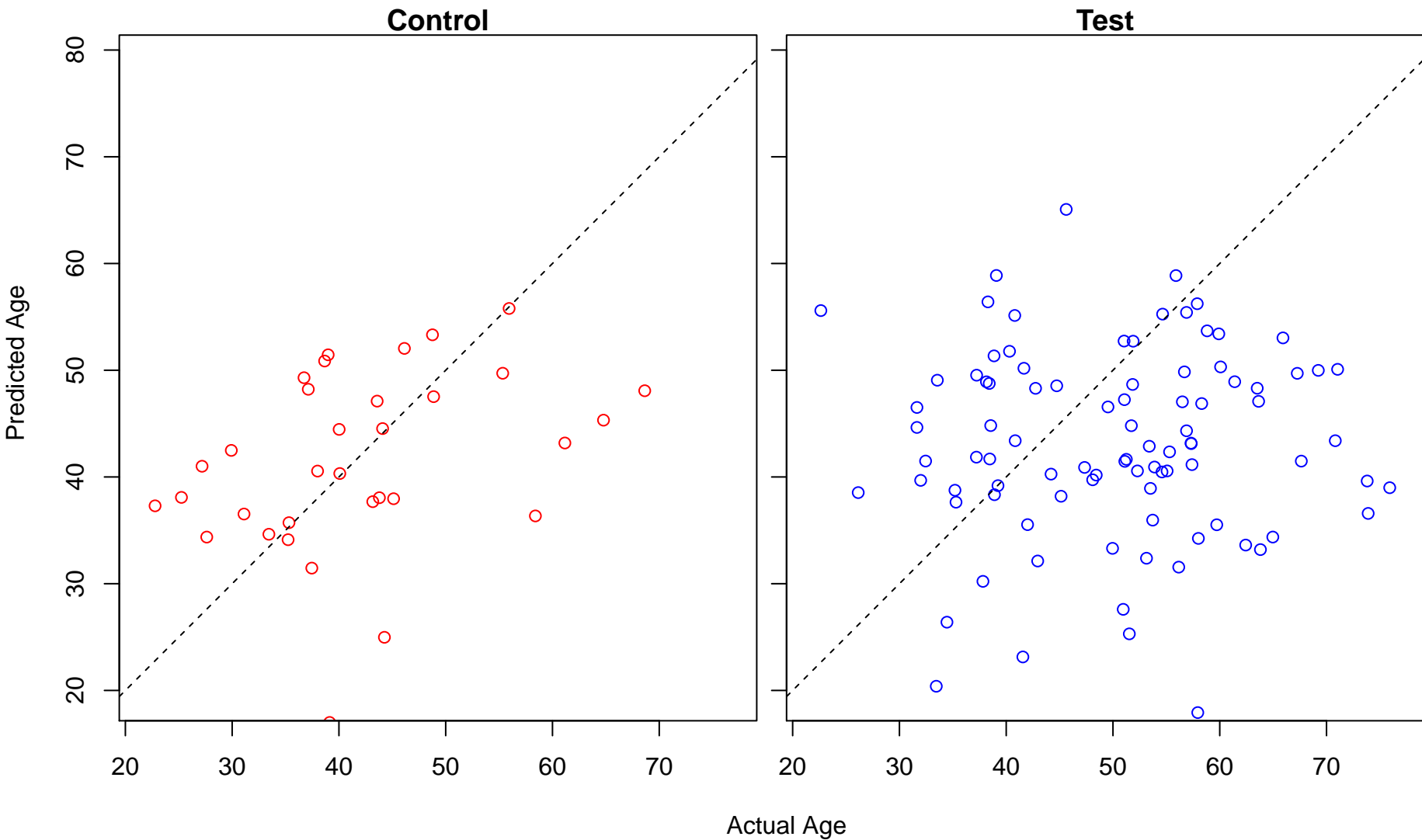
single-organism metabolic process (Score: 0.662966)



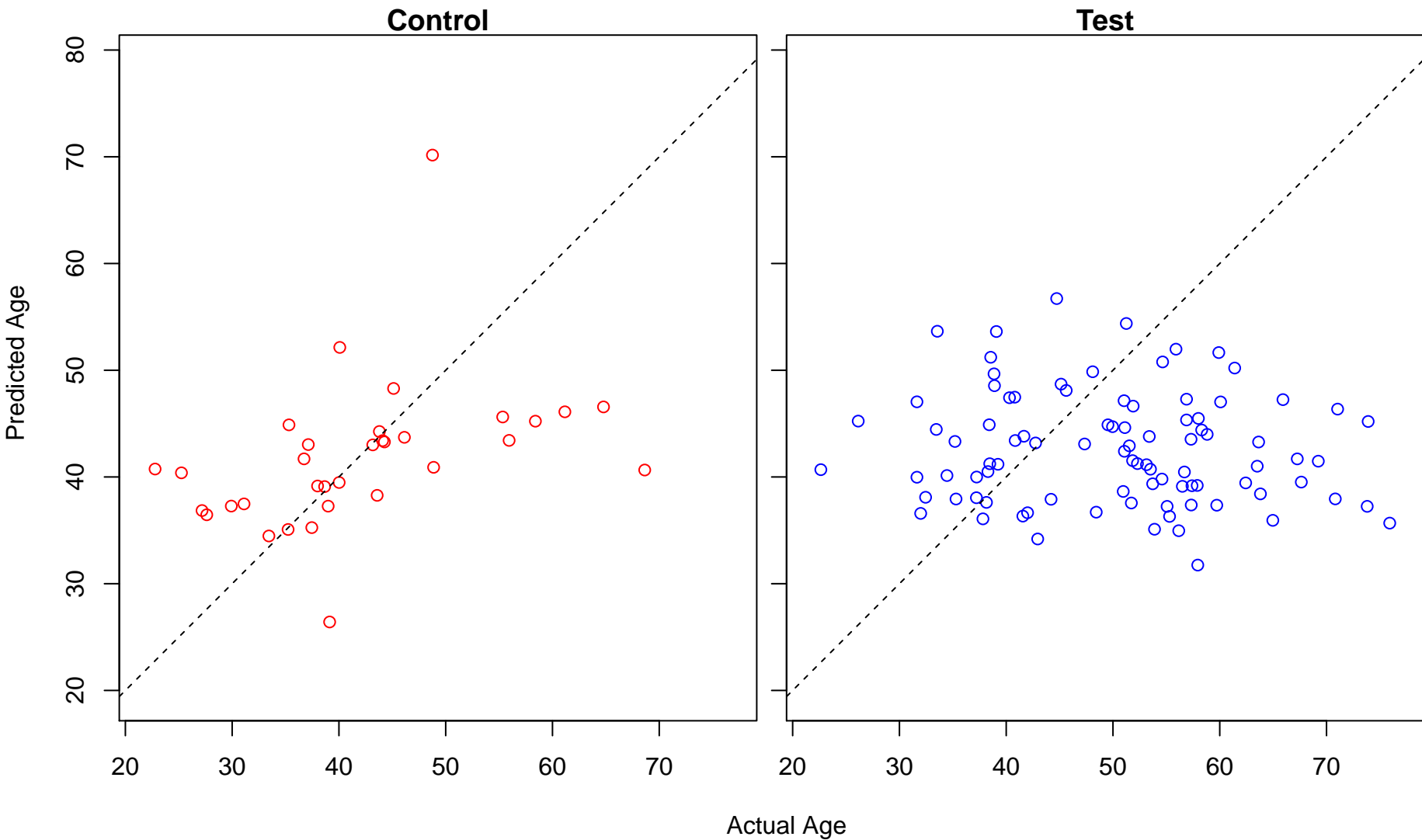
negative regulation of GTPase activity (Score: 0.662710)



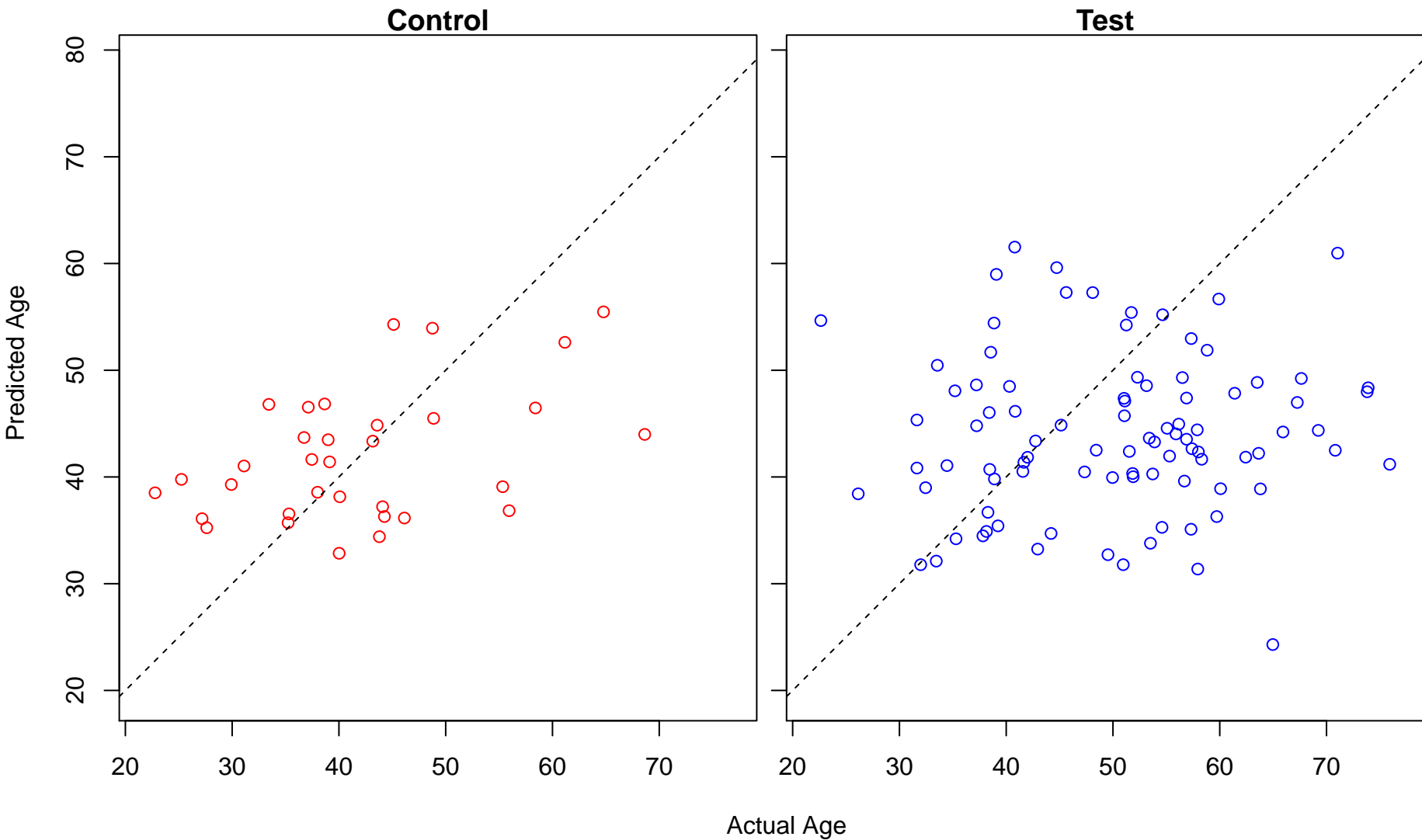
photoreceptor cell maintenance (Score: 0.662257)



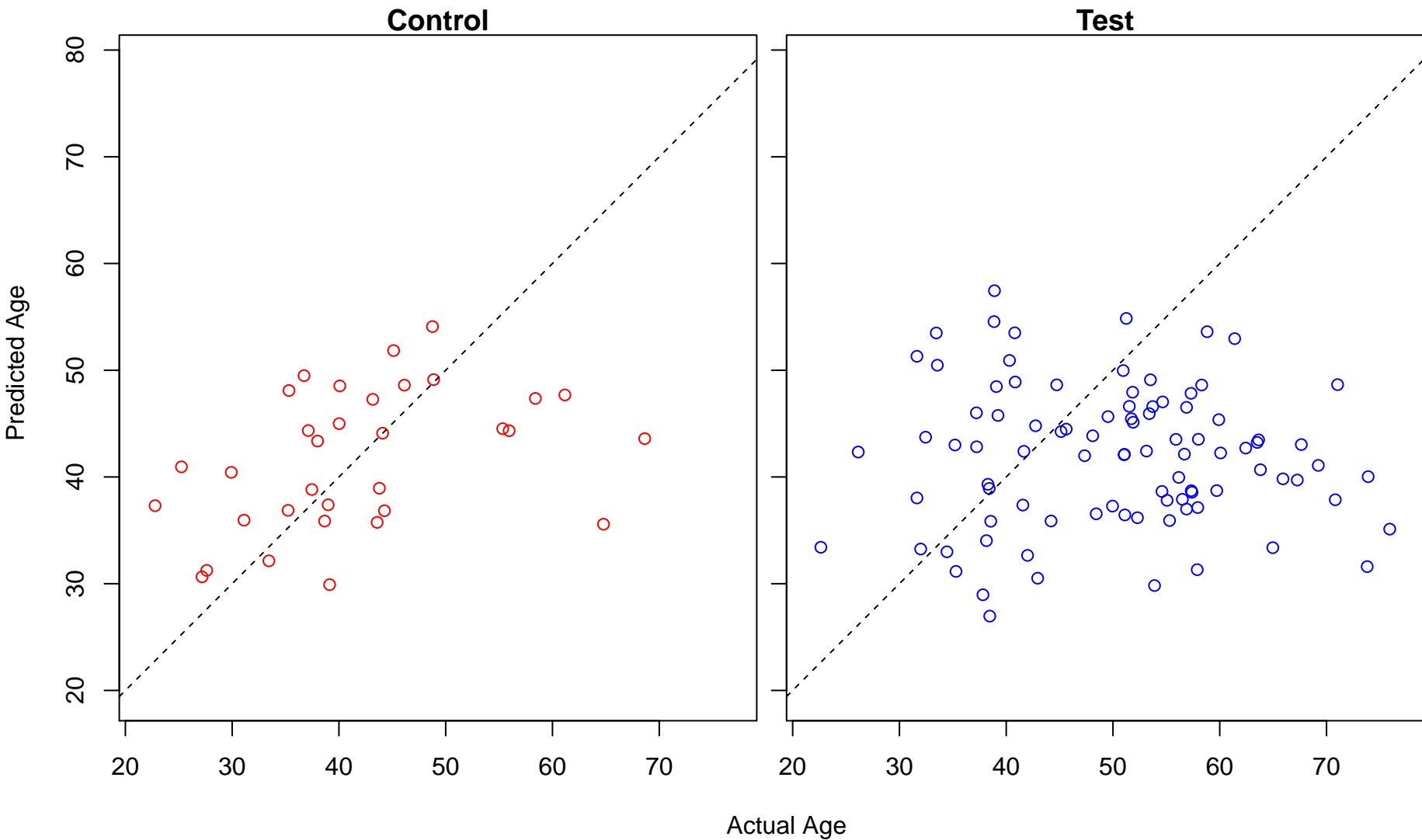
cellular localization (Score: 0.661961)



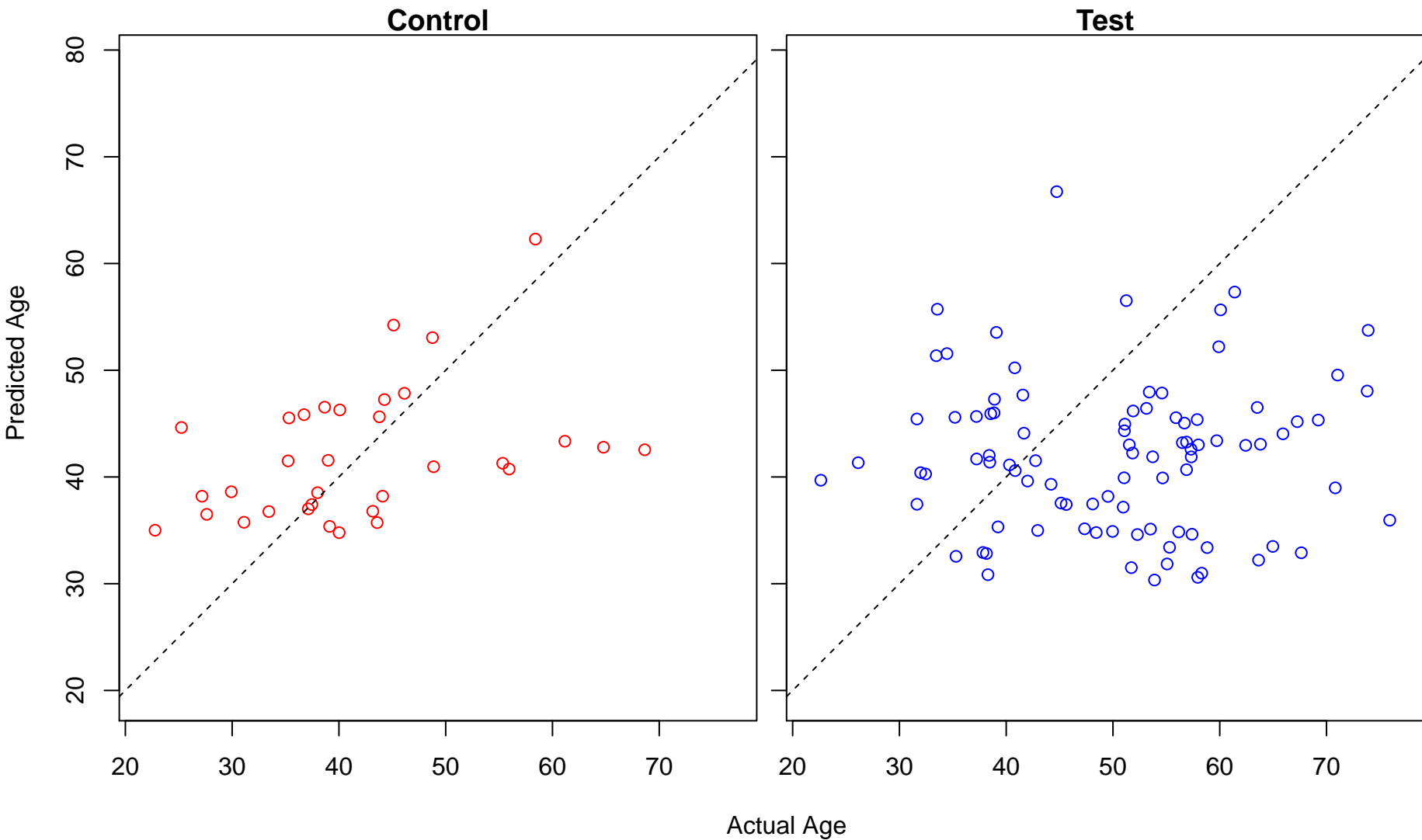
chemokine production (Score: 0.661260)



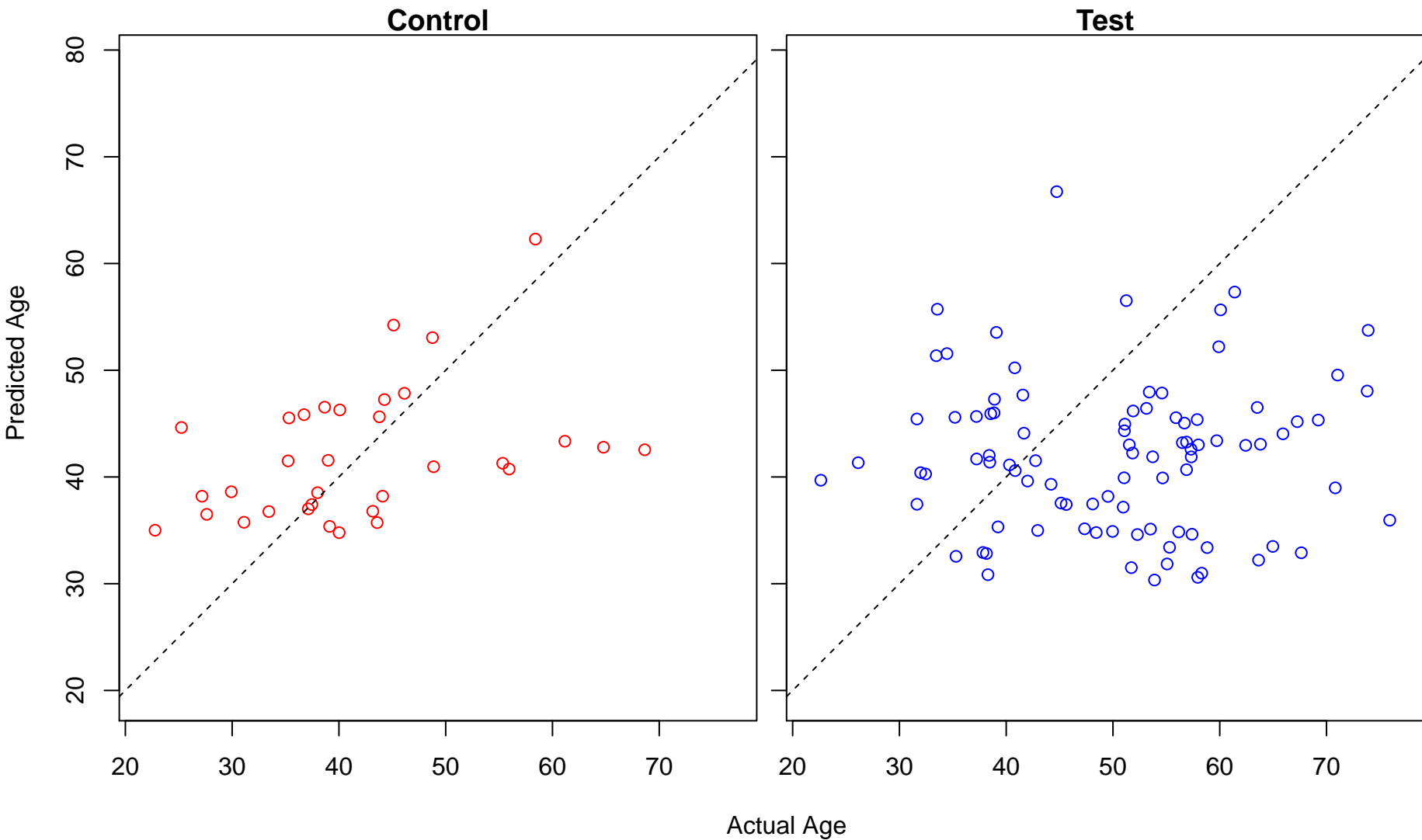
lens morphogenesis in camera-type eye (Score: 0.660330)



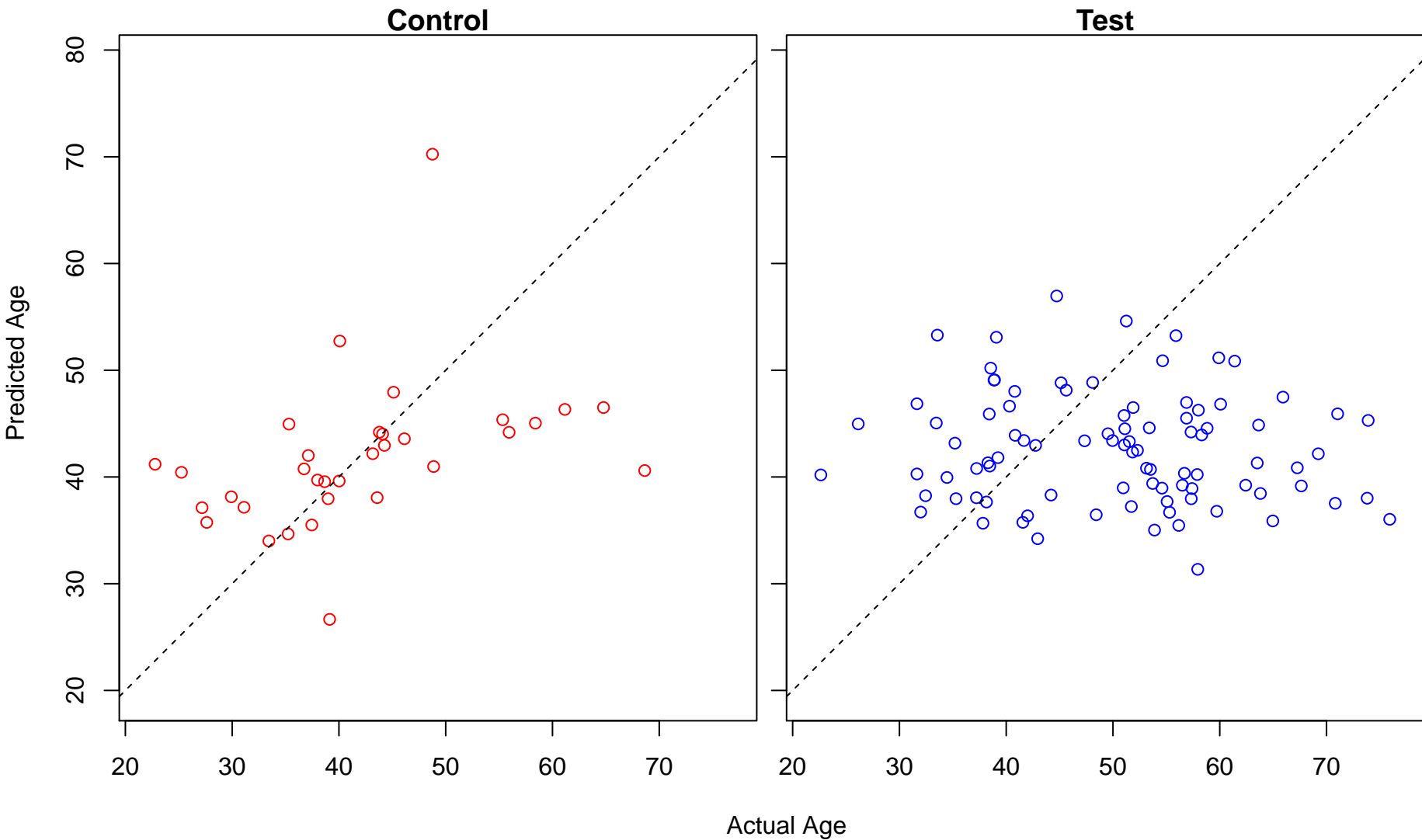
ethanol metabolic process (Score: 0.660309)



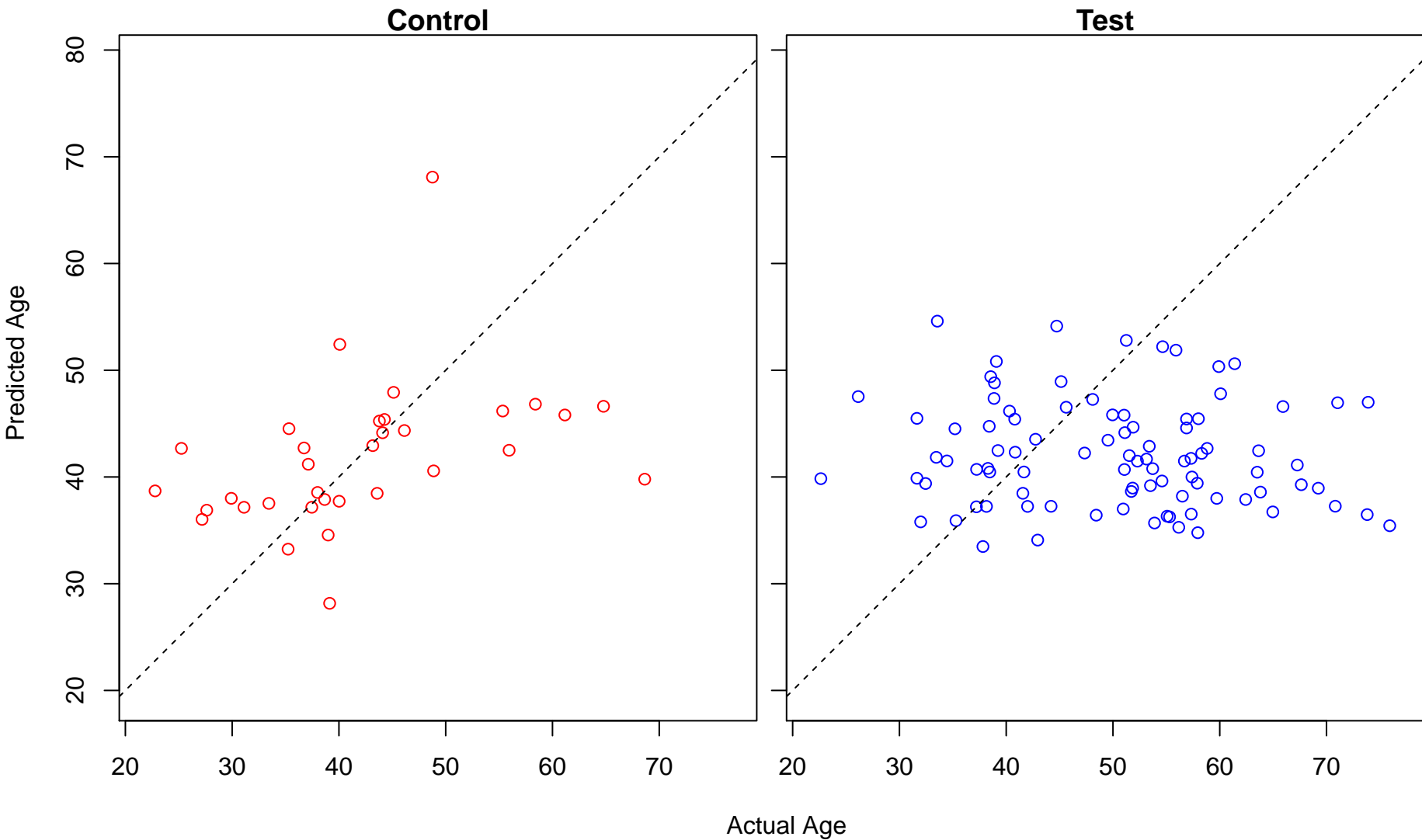
ethanol oxidation (Score: 0.660309)



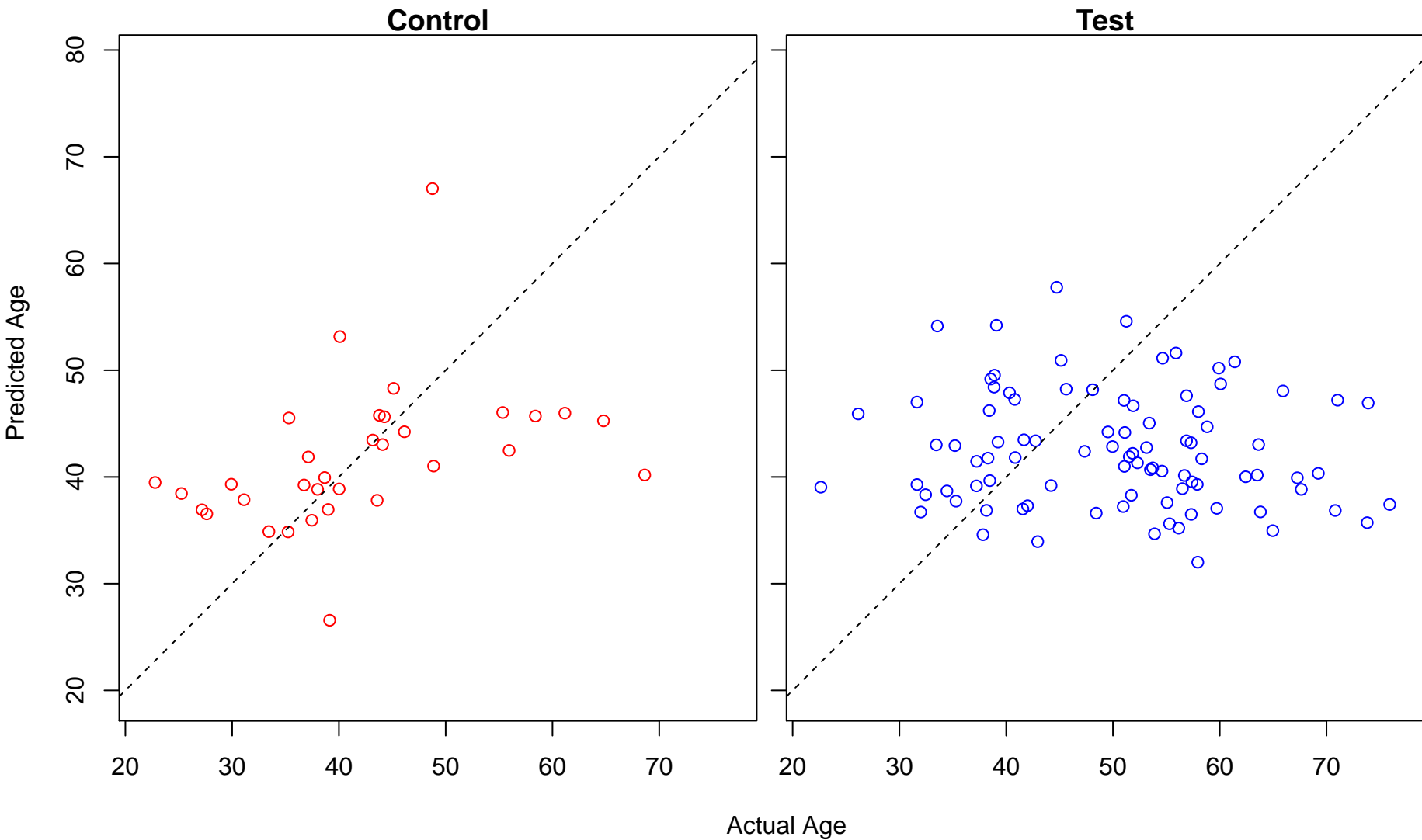
intracellular transport (Score: 0.660014)



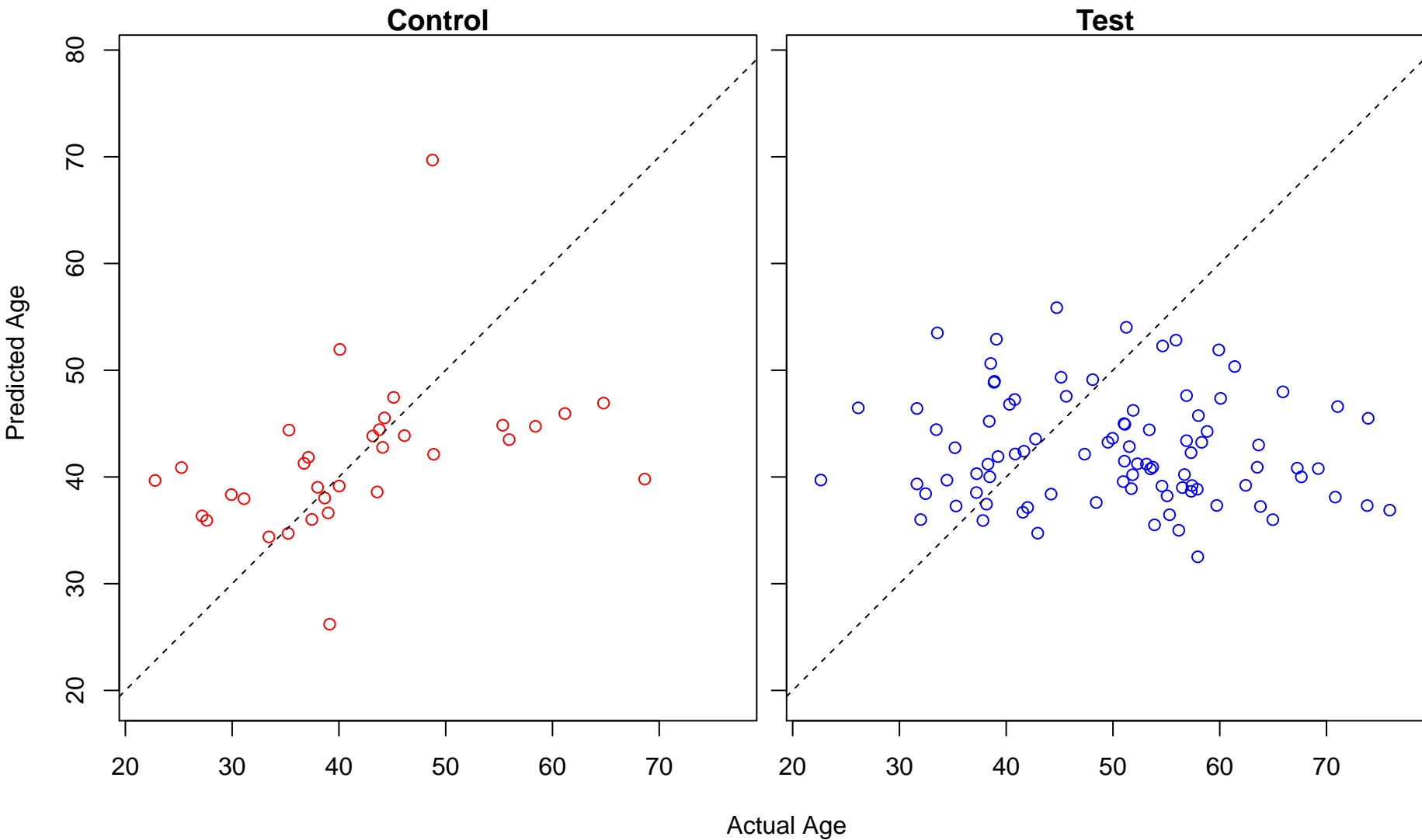
regulation of multicellular organismal development (Score: 0.659277)



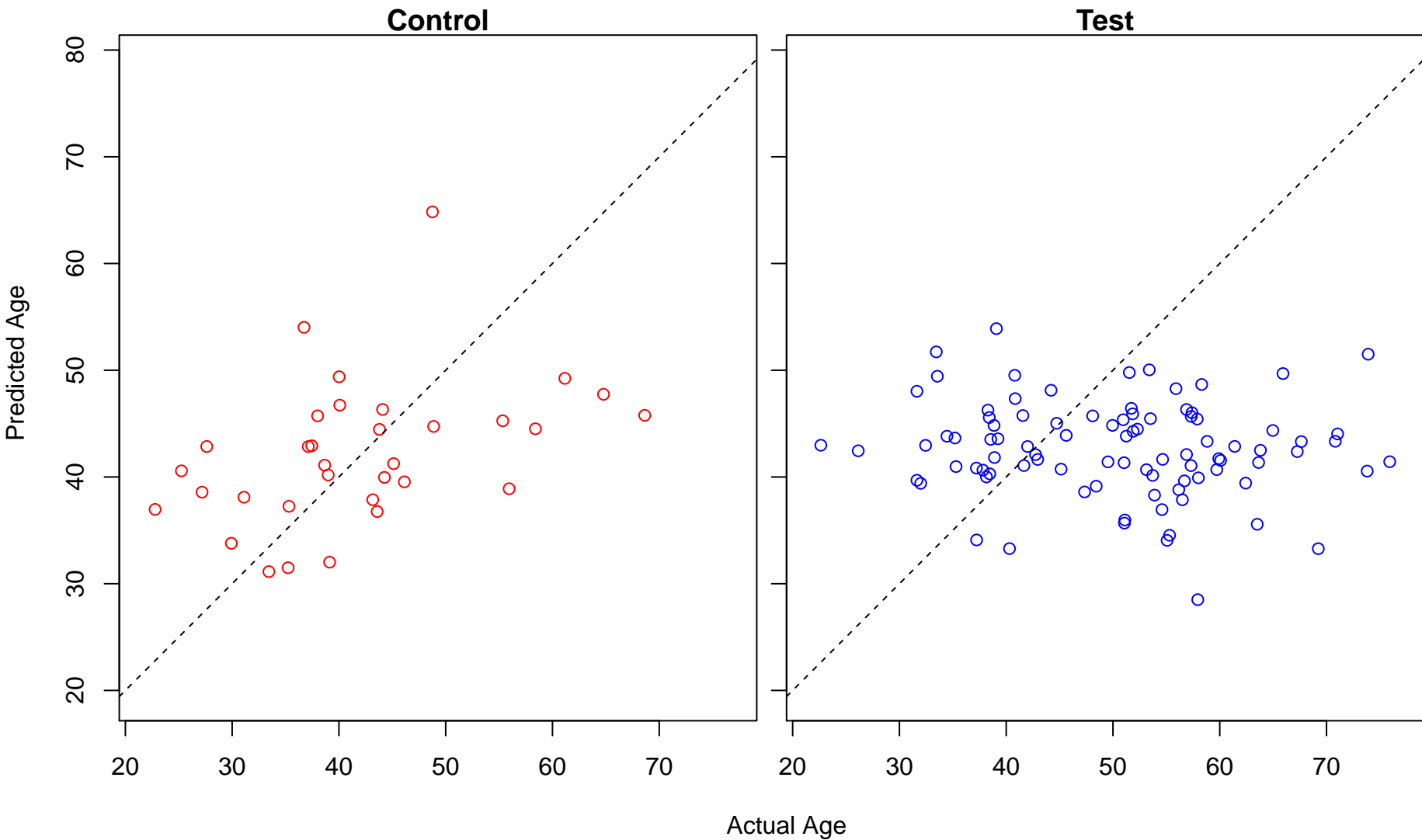
regulation of phosphorus metabolic process (Score: 0.659213)



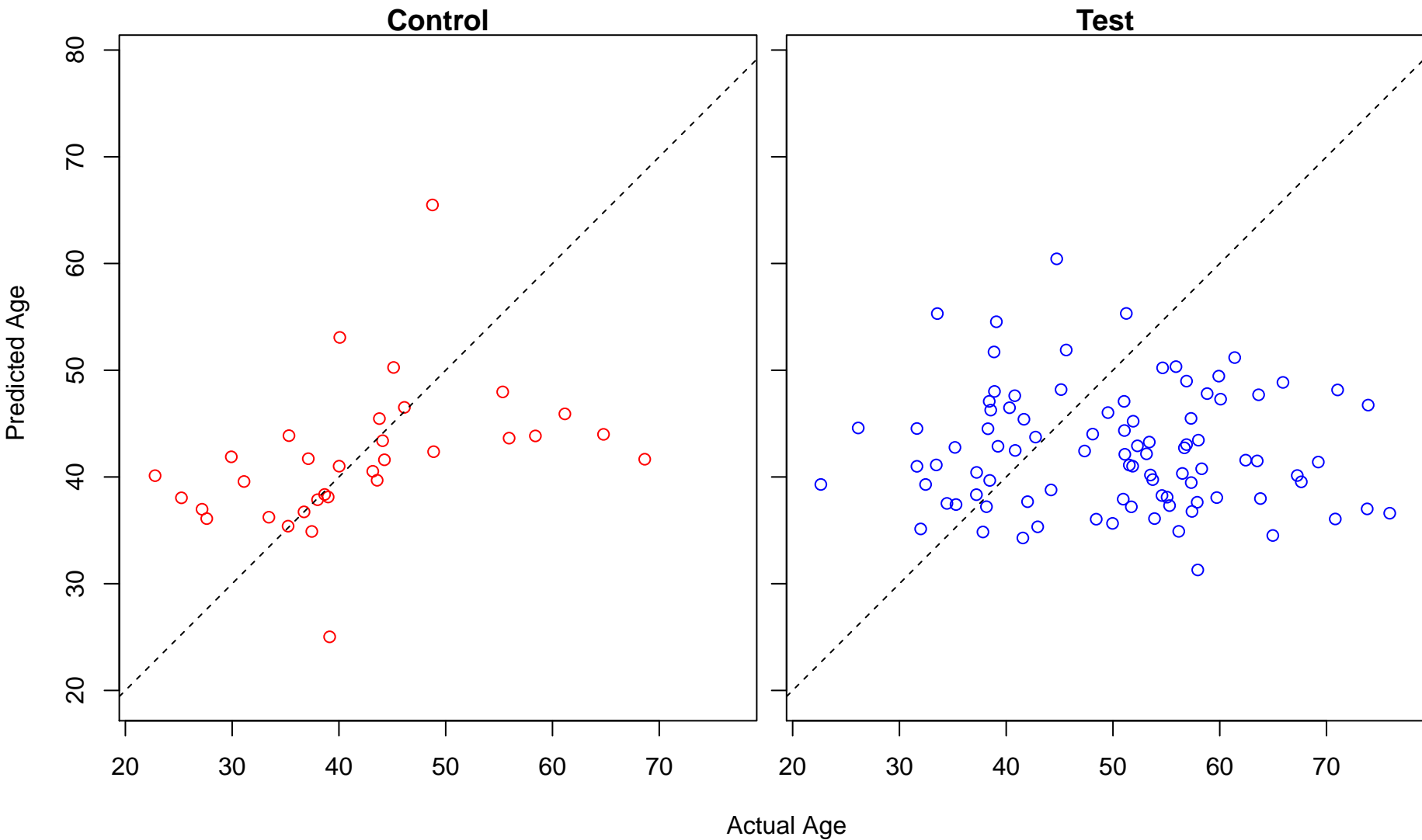
negative regulation of biological process (Score: 0.659103)



replicative cell aging (Score: 0.658988)

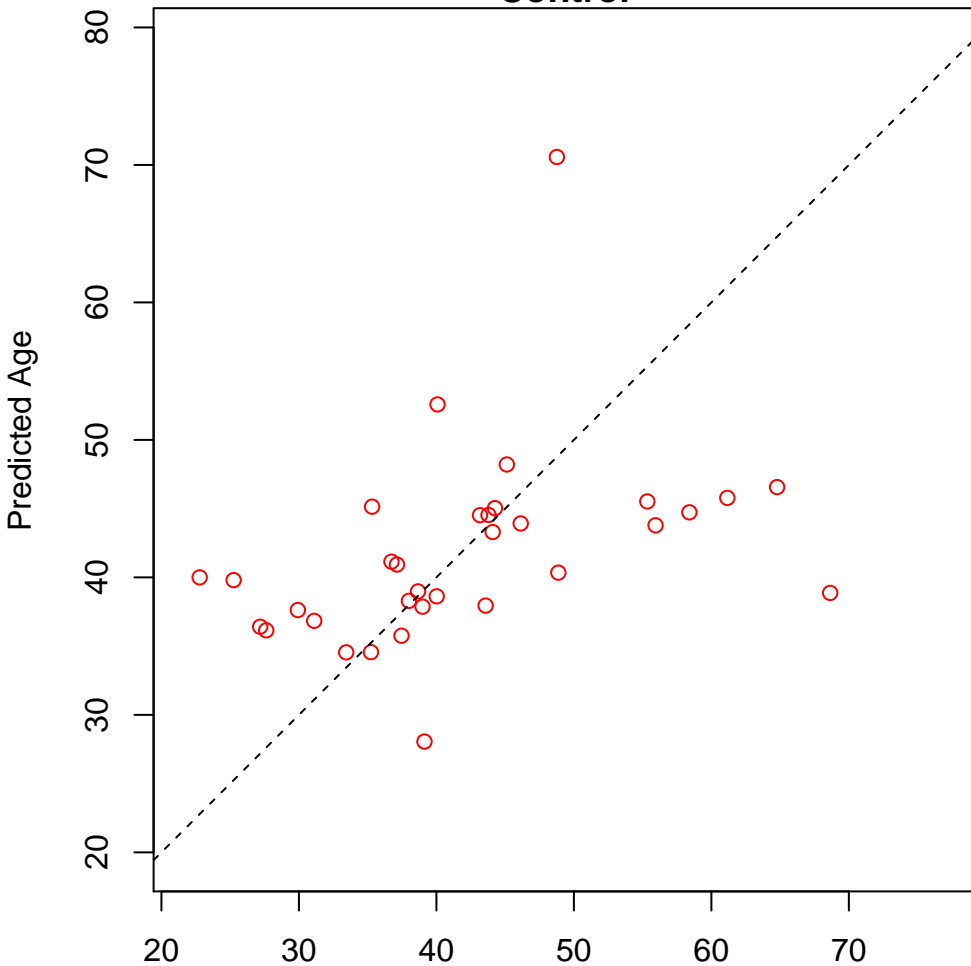


vascular endothelial growth factor receptor signaling pathway (Score: 0.658966)

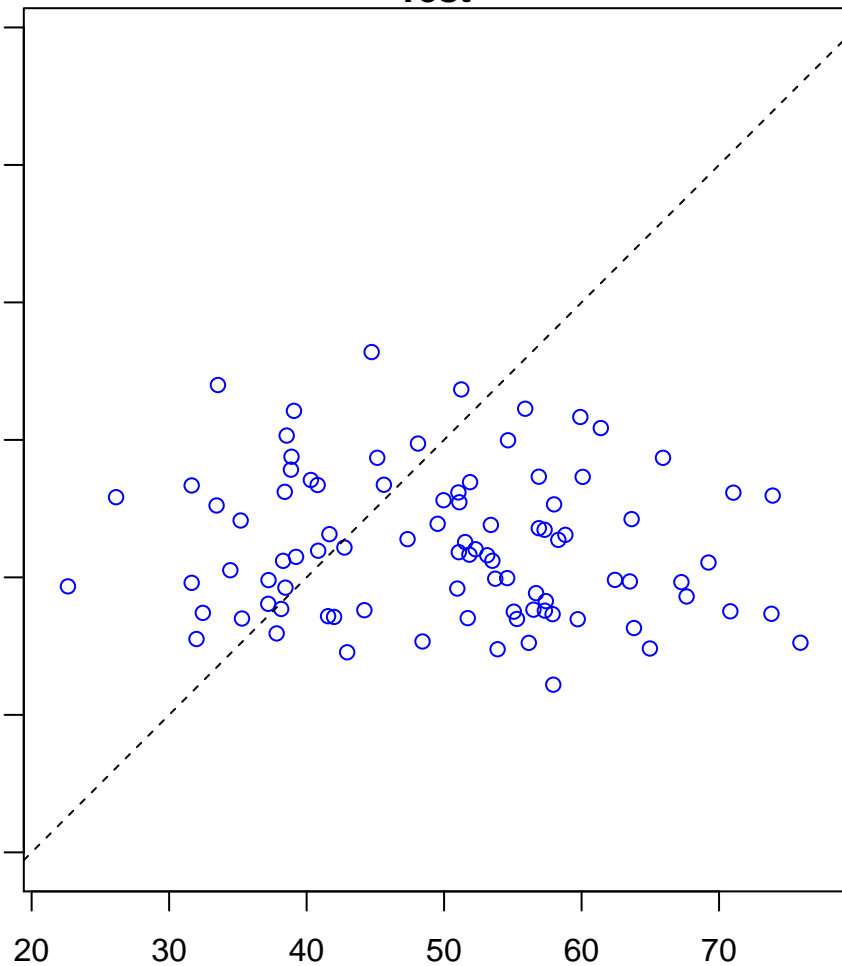


organic substance biosynthetic process (Score: 0.658706)

Control

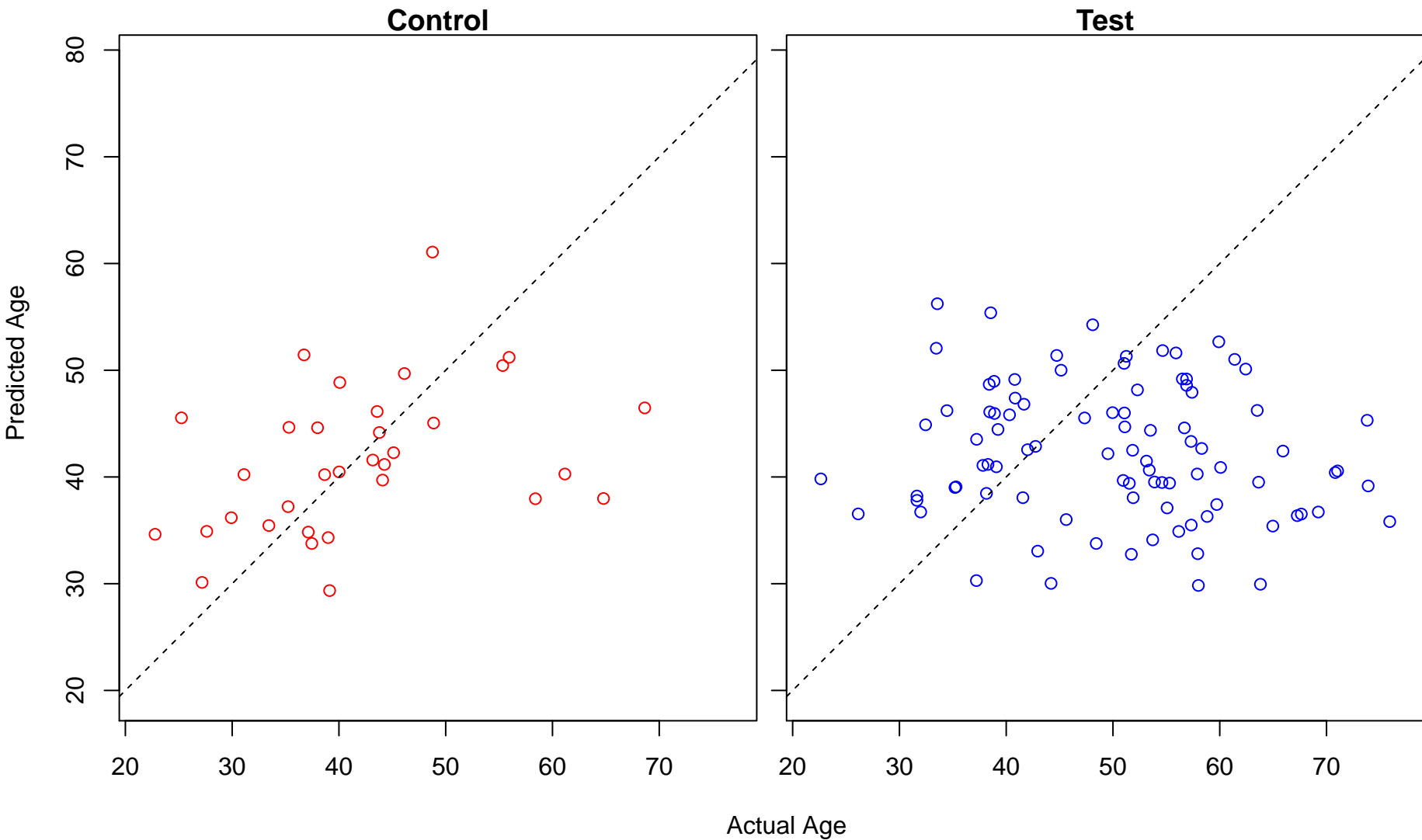


Test

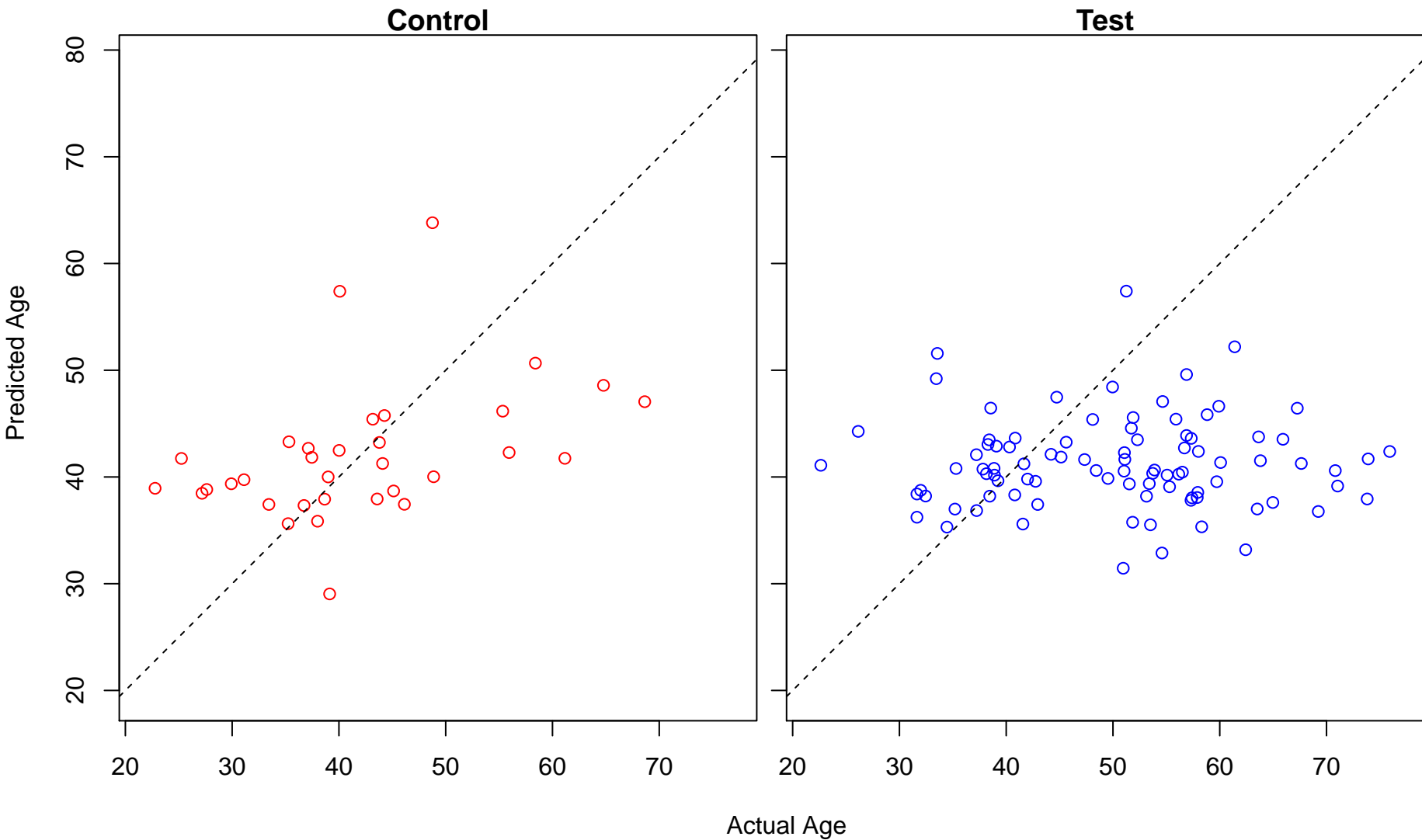


Actual Age

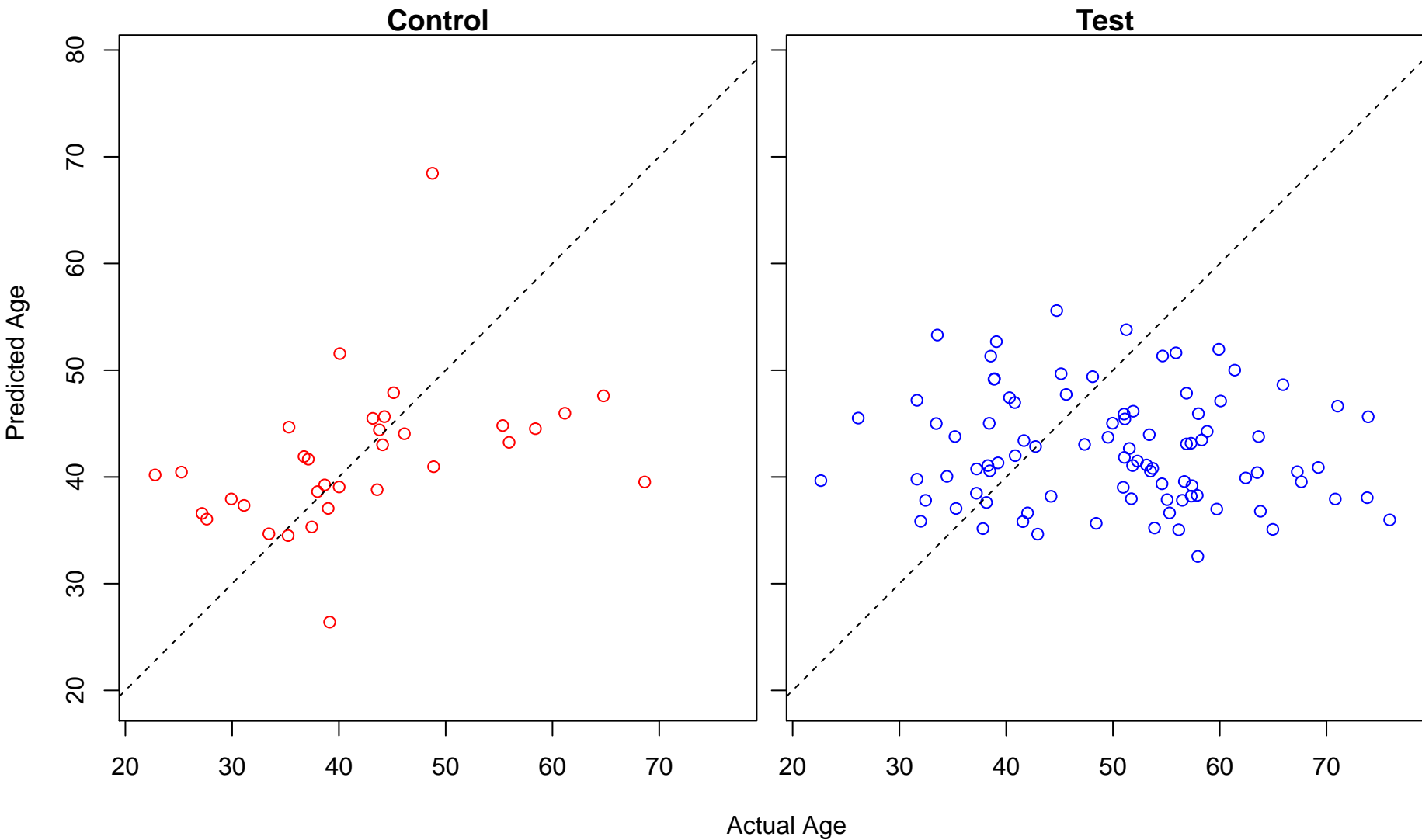
single organism reproductive process (Score: 0.658525)



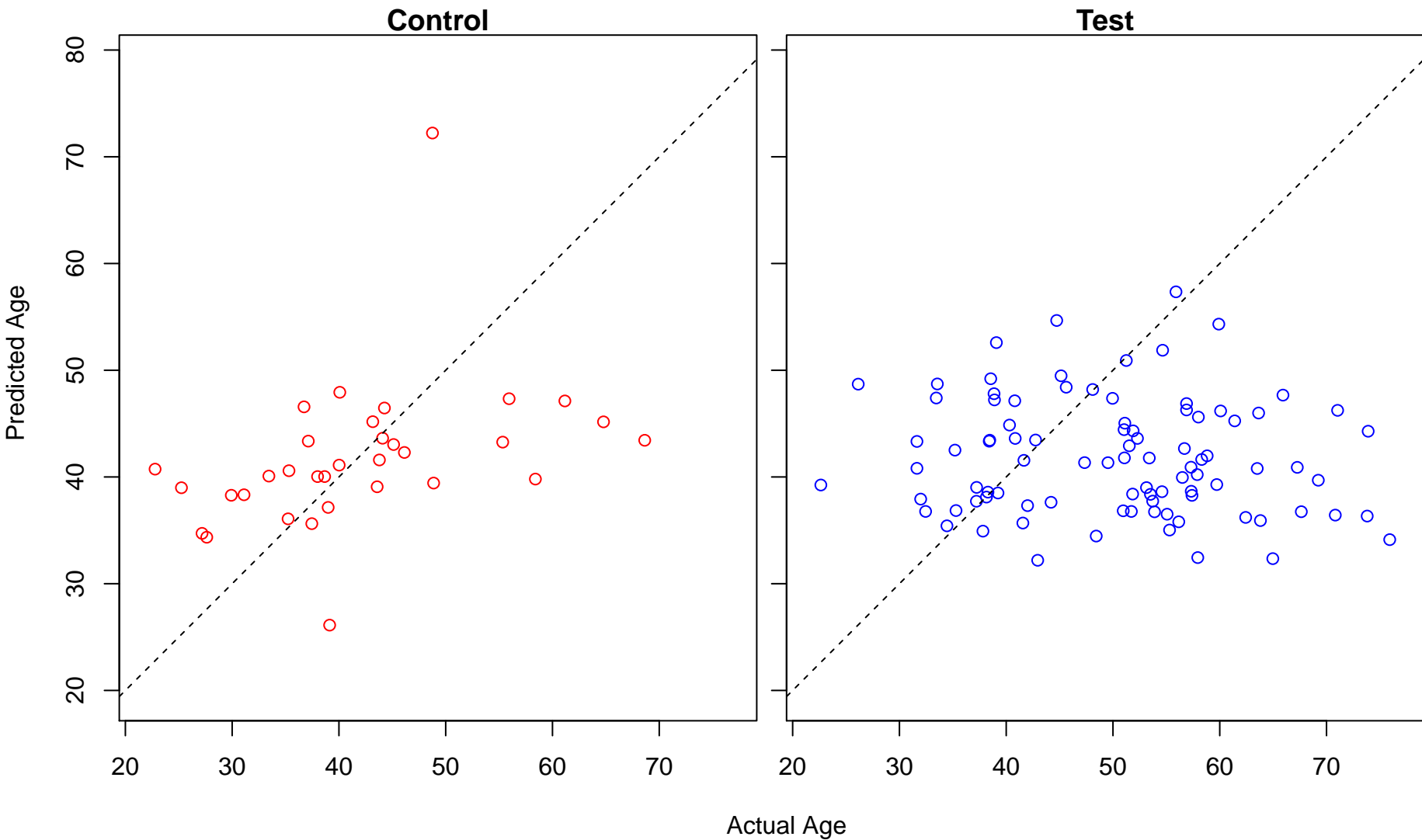
RNA repair (Score: 0.658316)



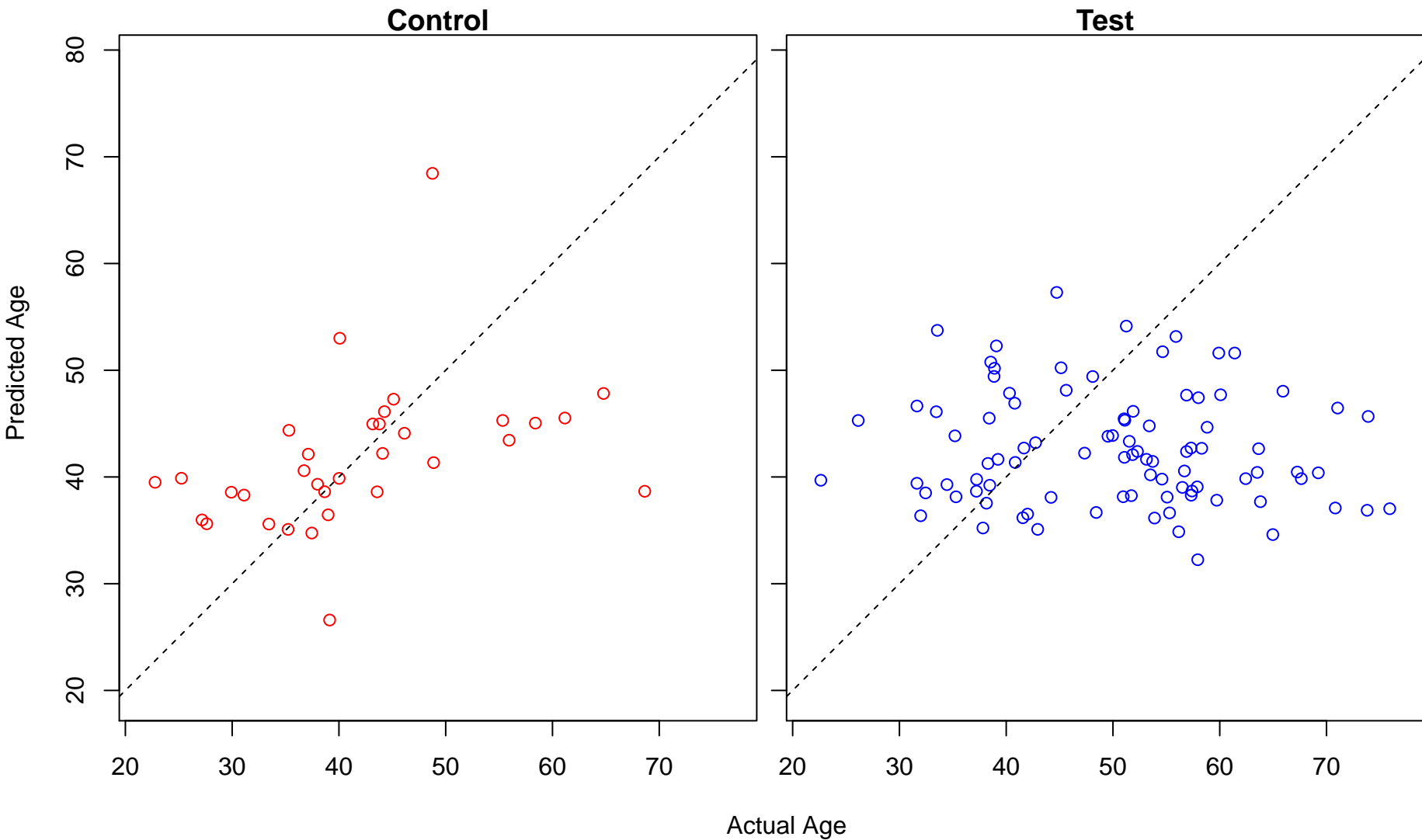
single-organism process (Score: 0.658243)



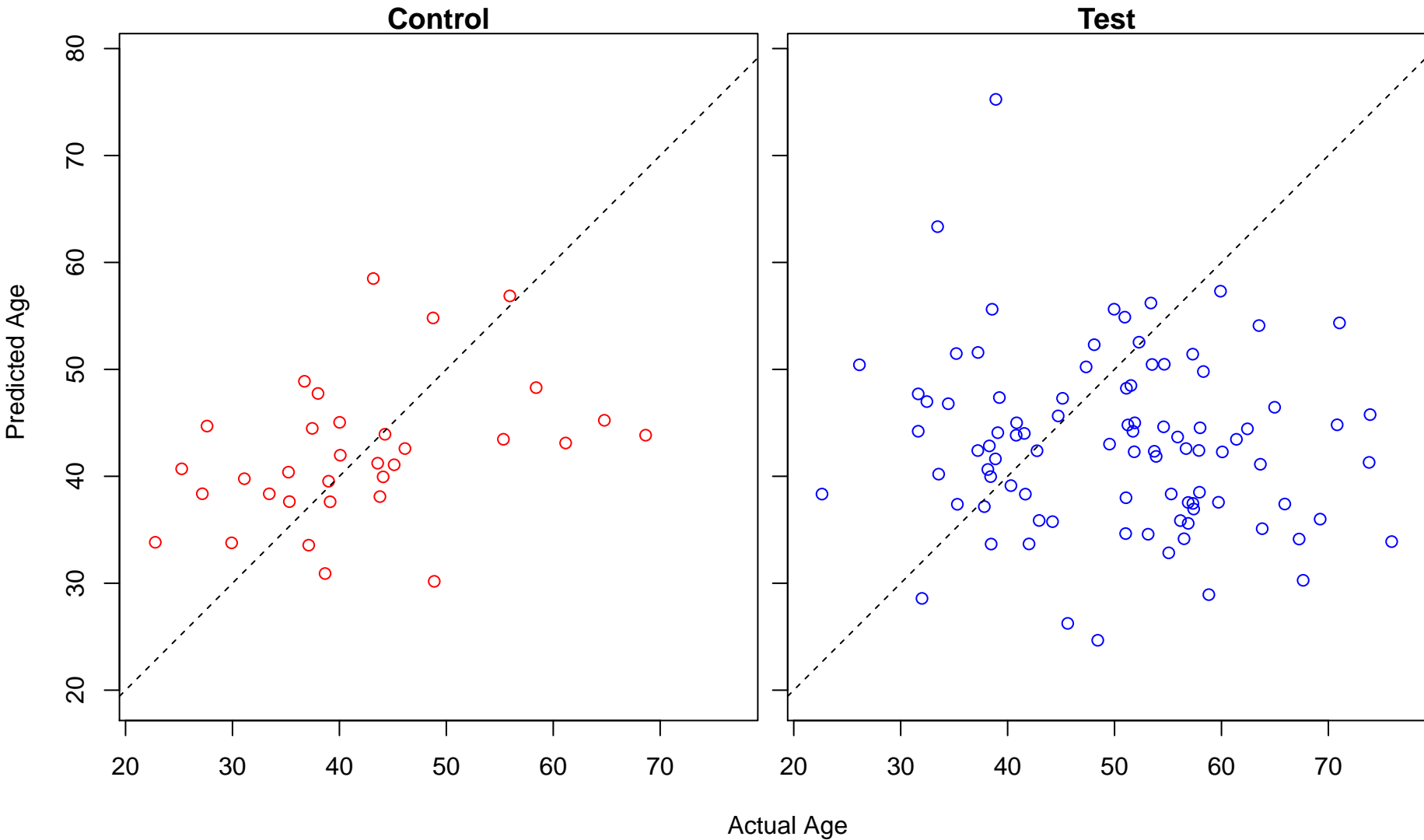
cellular homeostasis (Score: 0.658113)



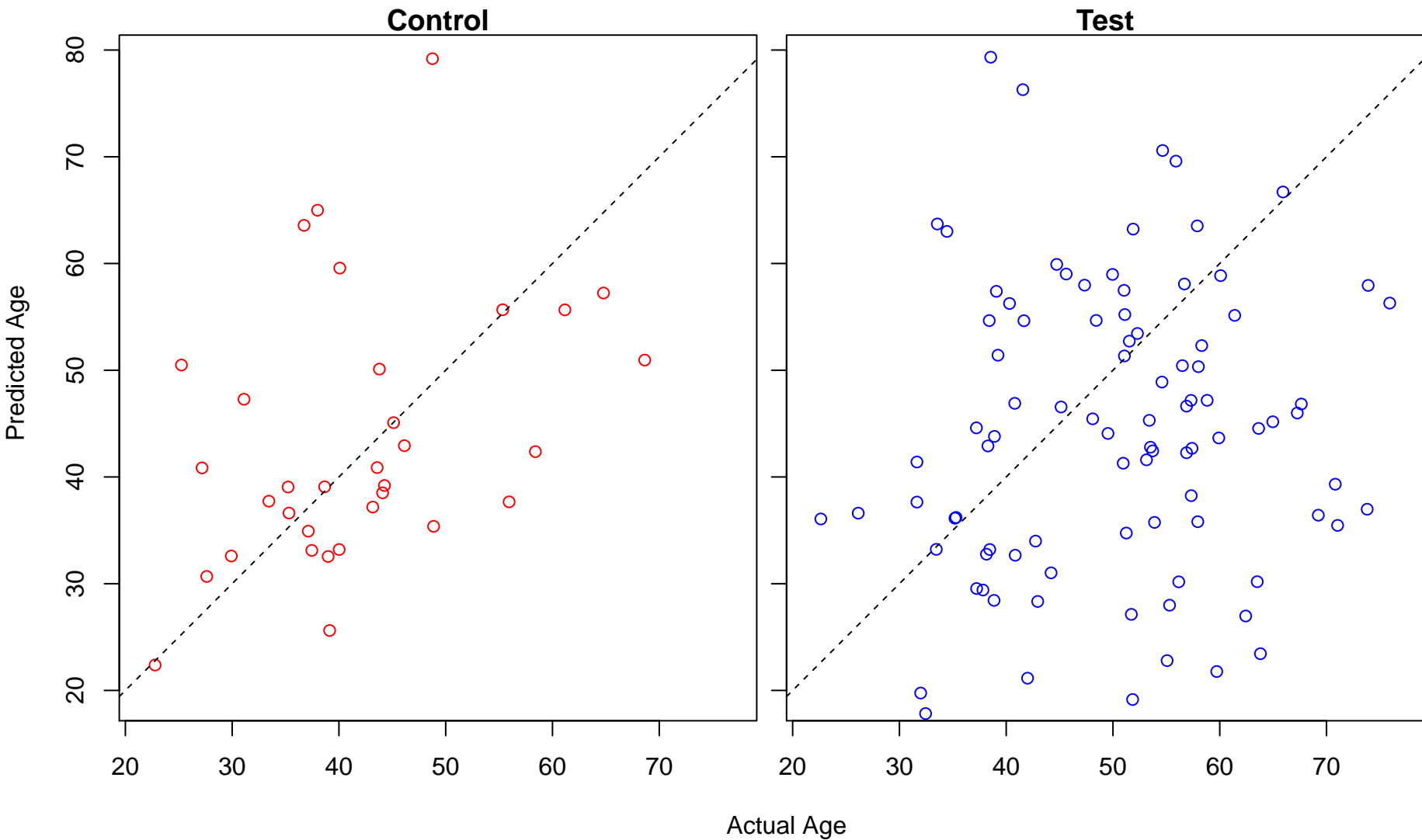
regulation of cell communication (Score: 0.658068)



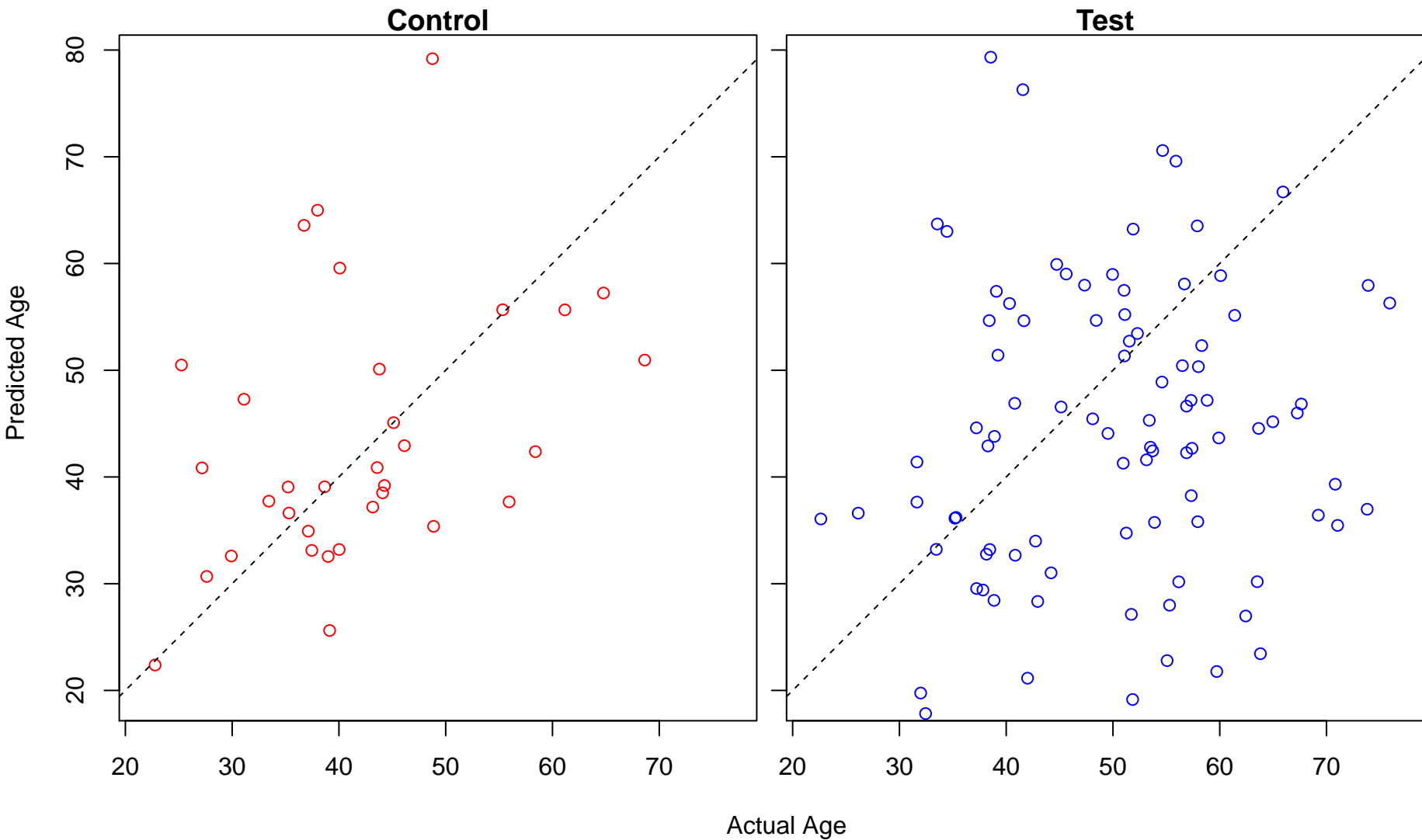
positive regulation of vascular permeability (Score: 0.657657)



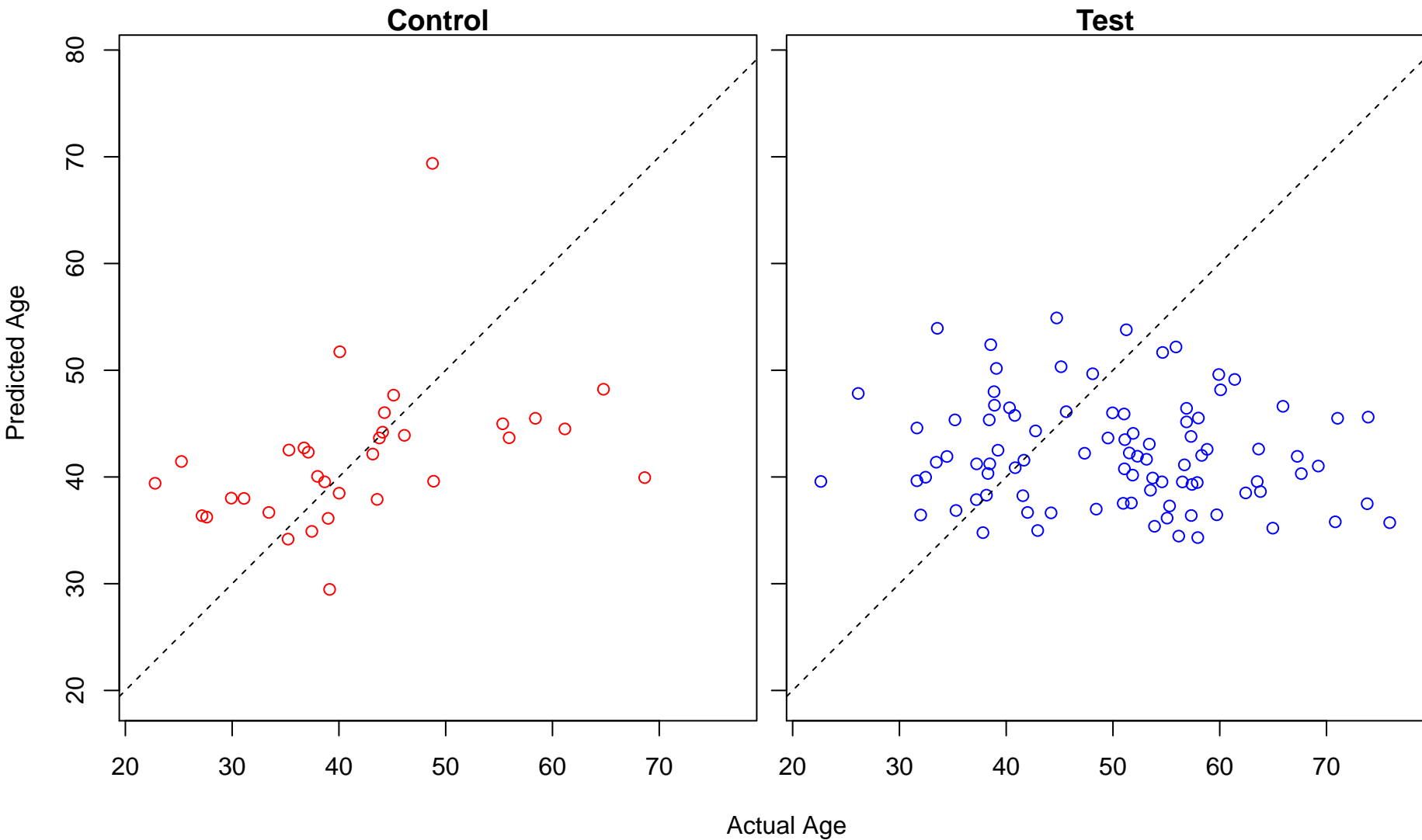
lymphocyte costimulation (Score: 0.656122)



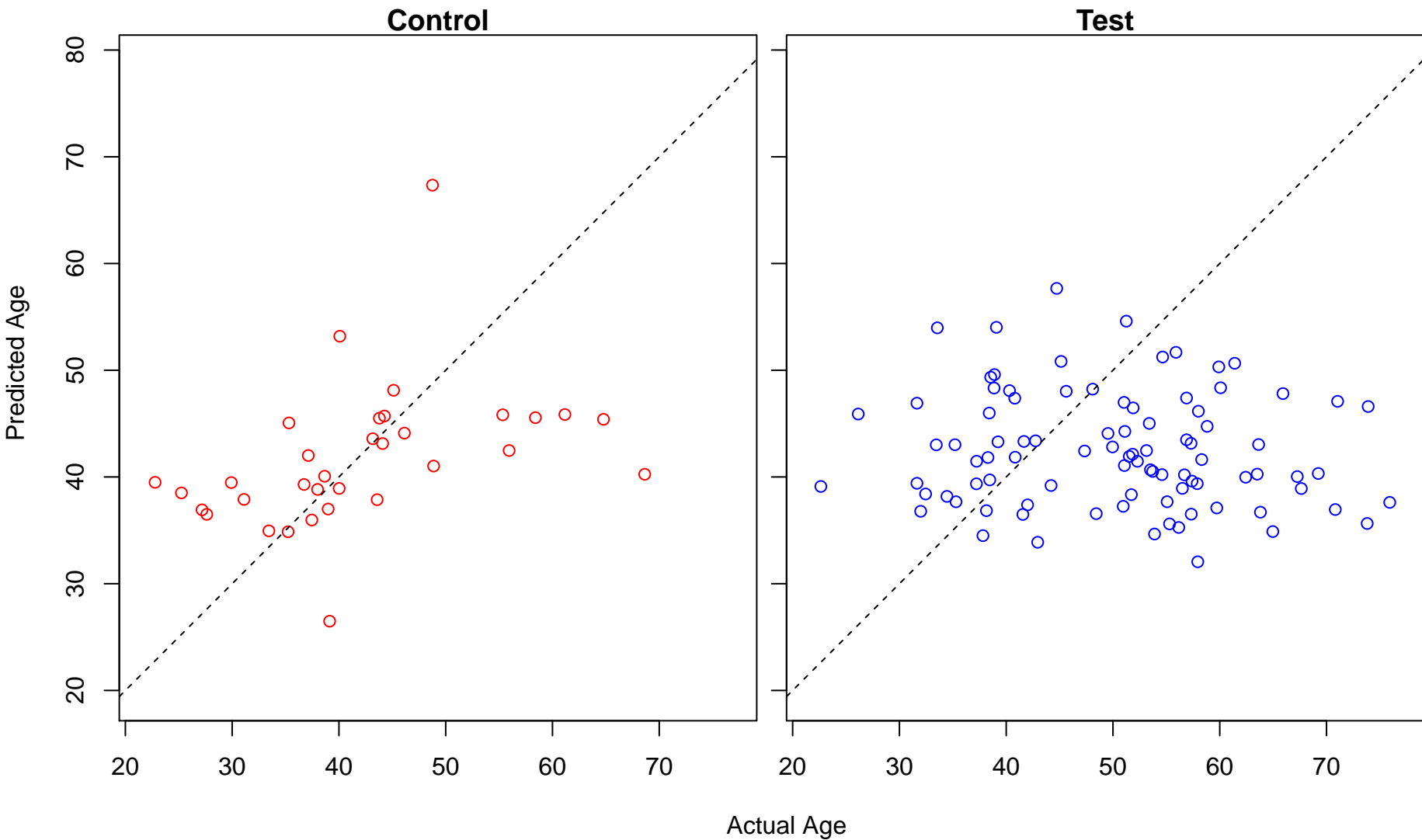
T cell costimulation (Score: 0.656122)



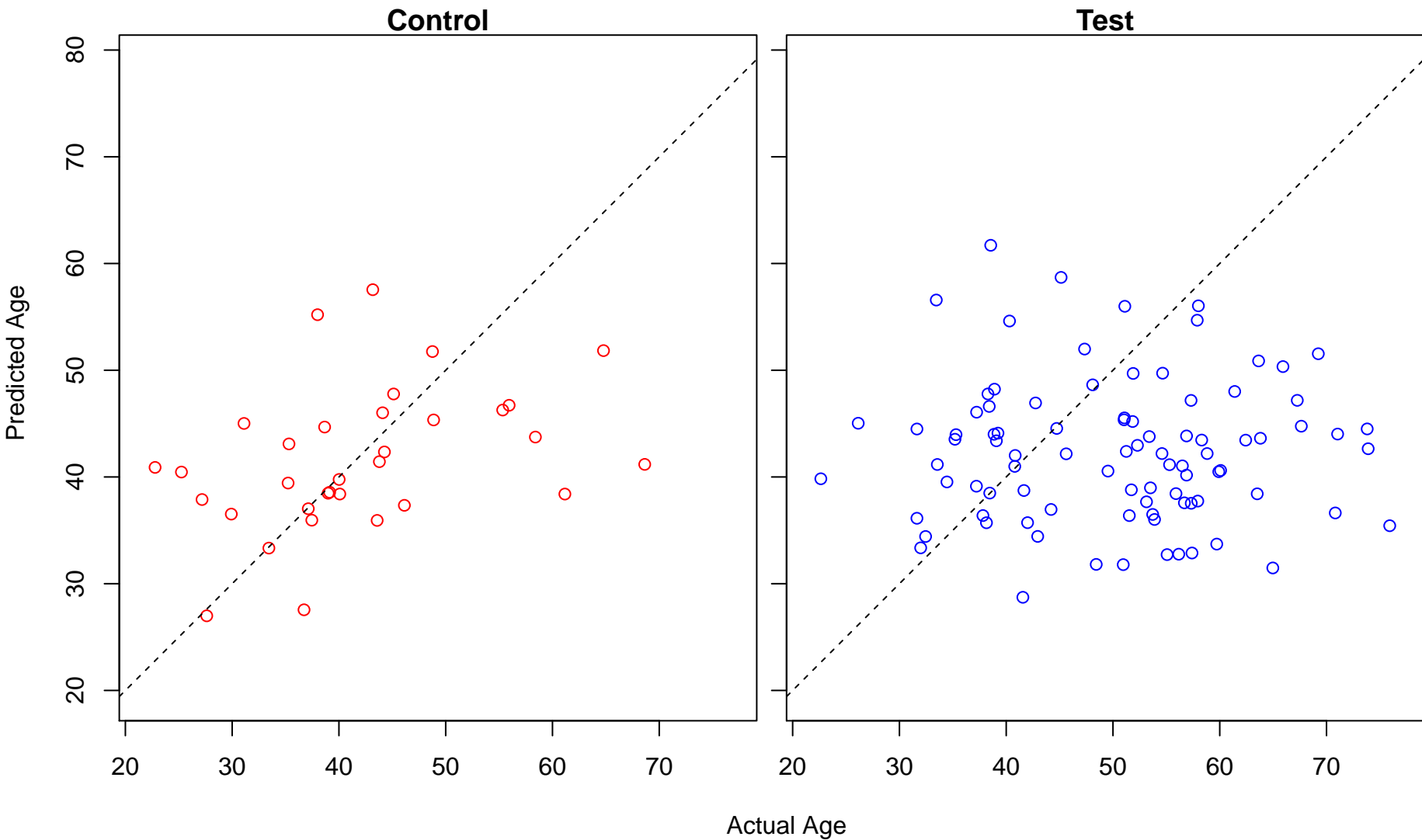
positive regulation of multicellular organismal process (Score: 0.656101)



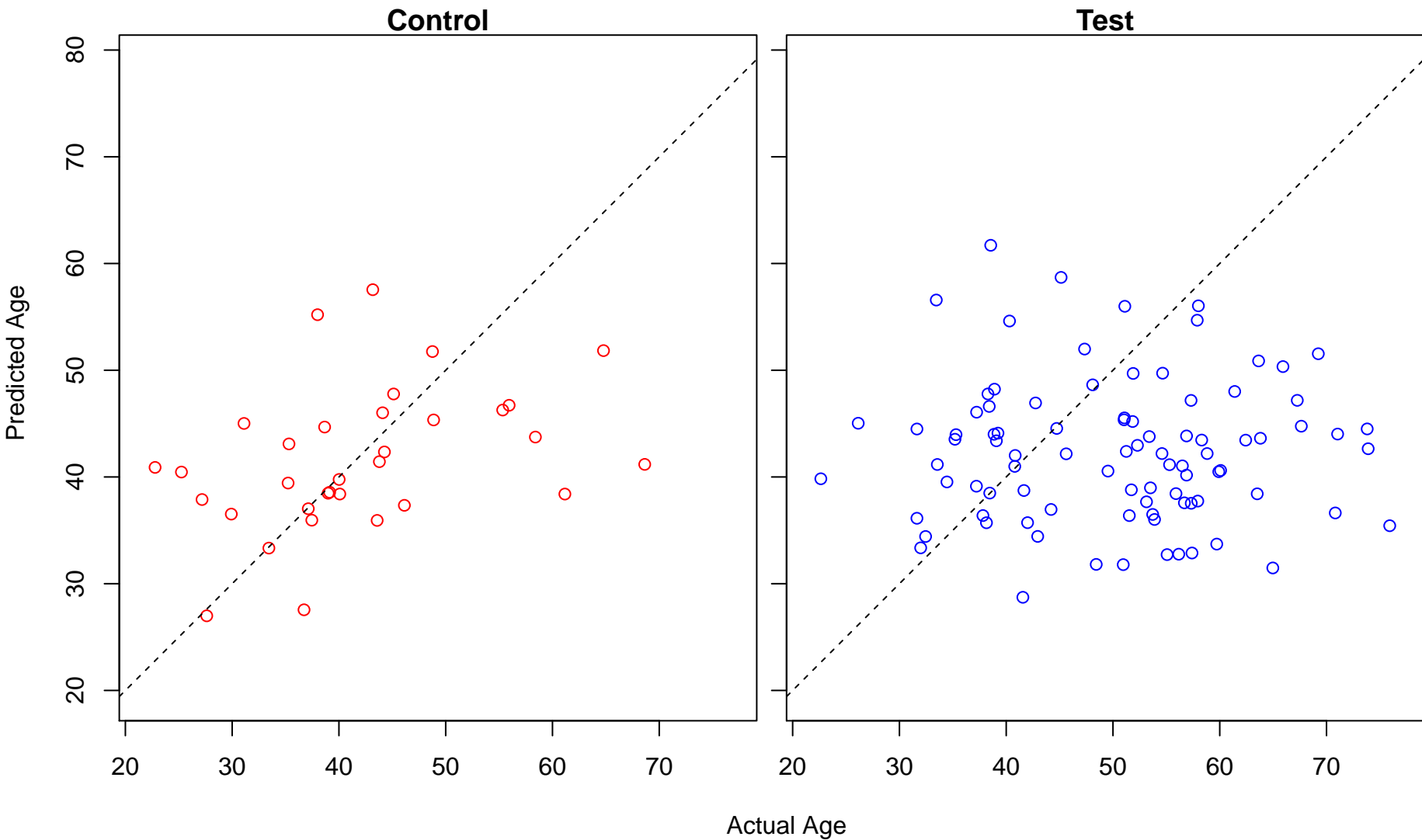
regulation of phosphate metabolic process (Score: 0.656015)



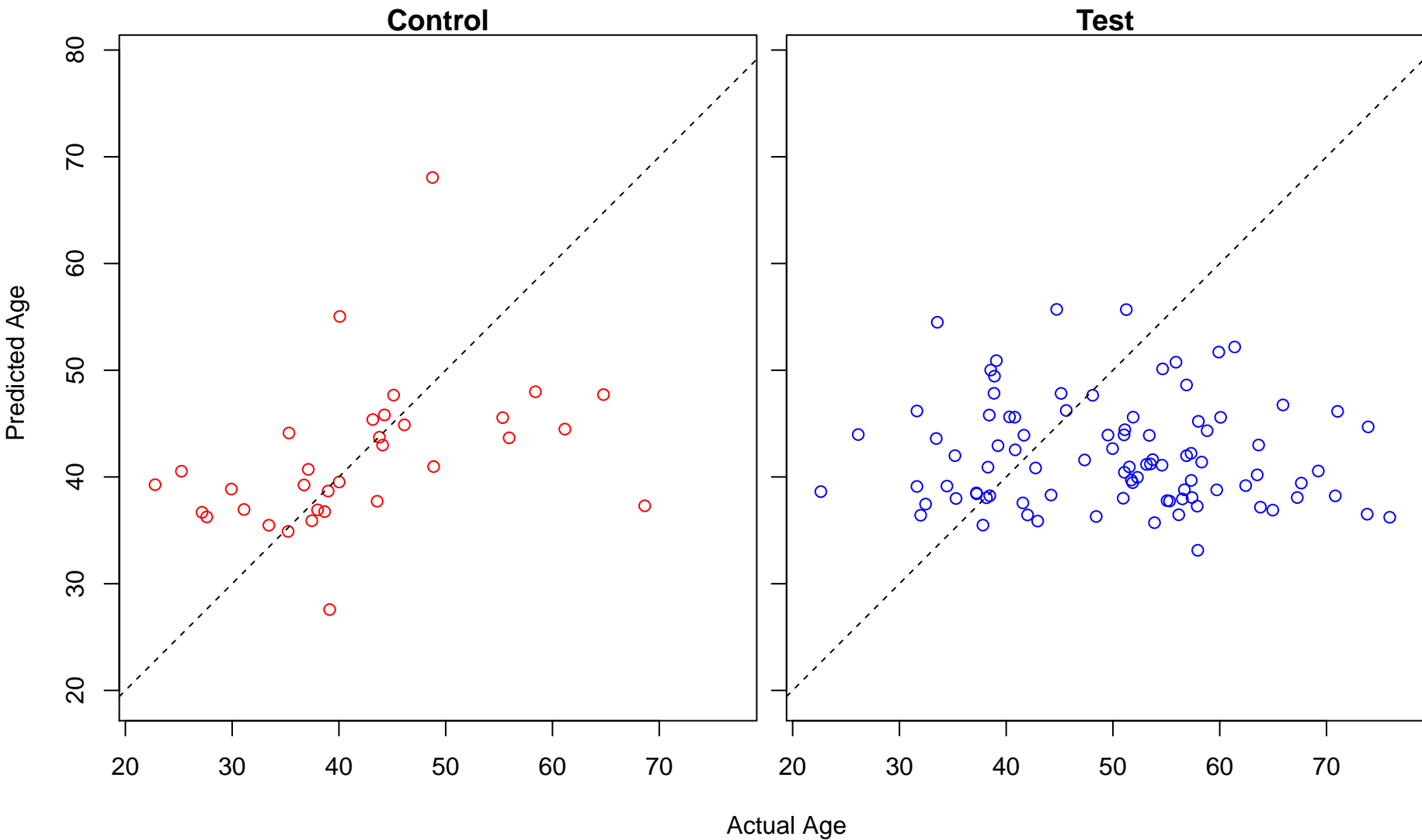
ether metabolic process (Score: 0.654745)



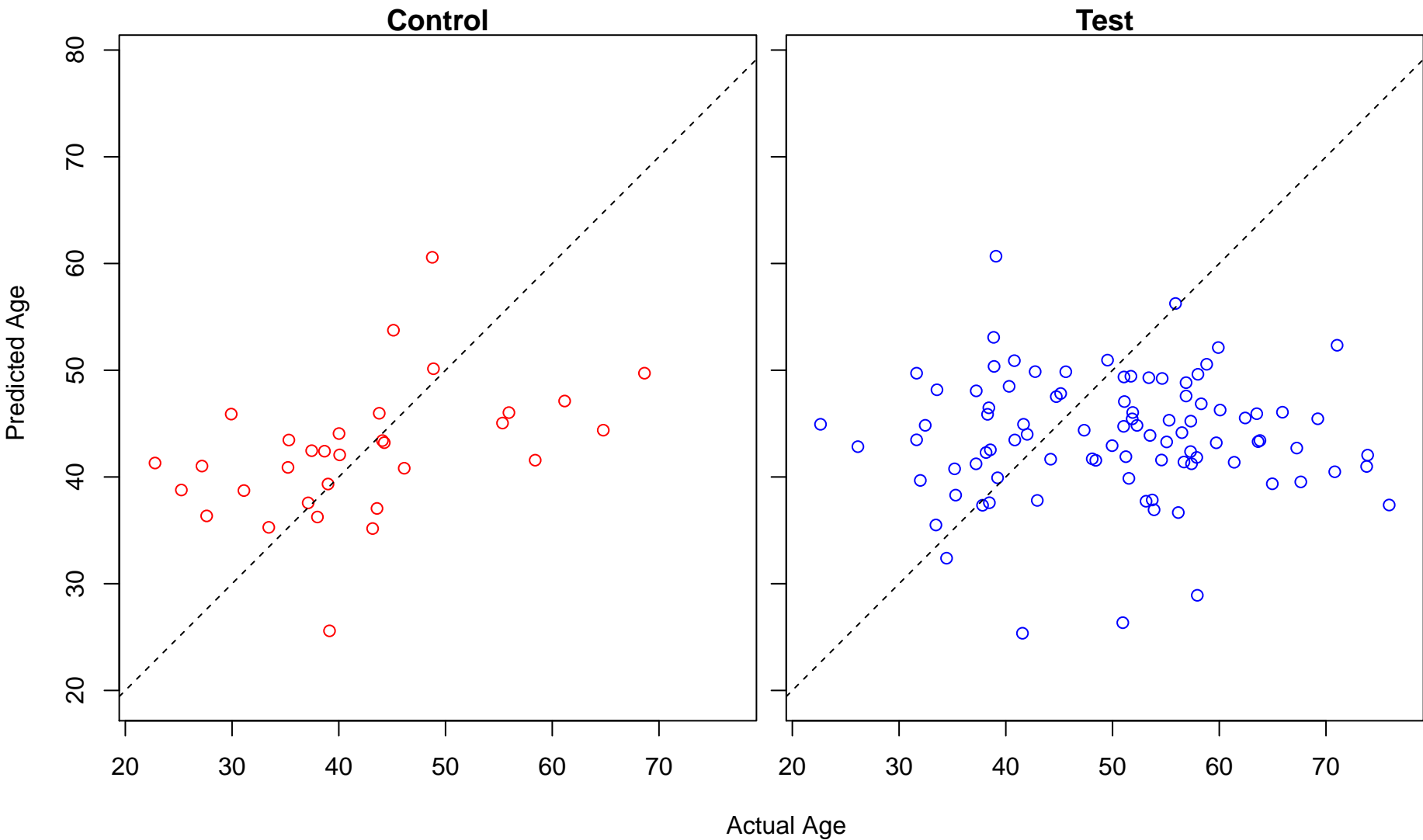
ether lipid metabolic process (Score: 0.654745)



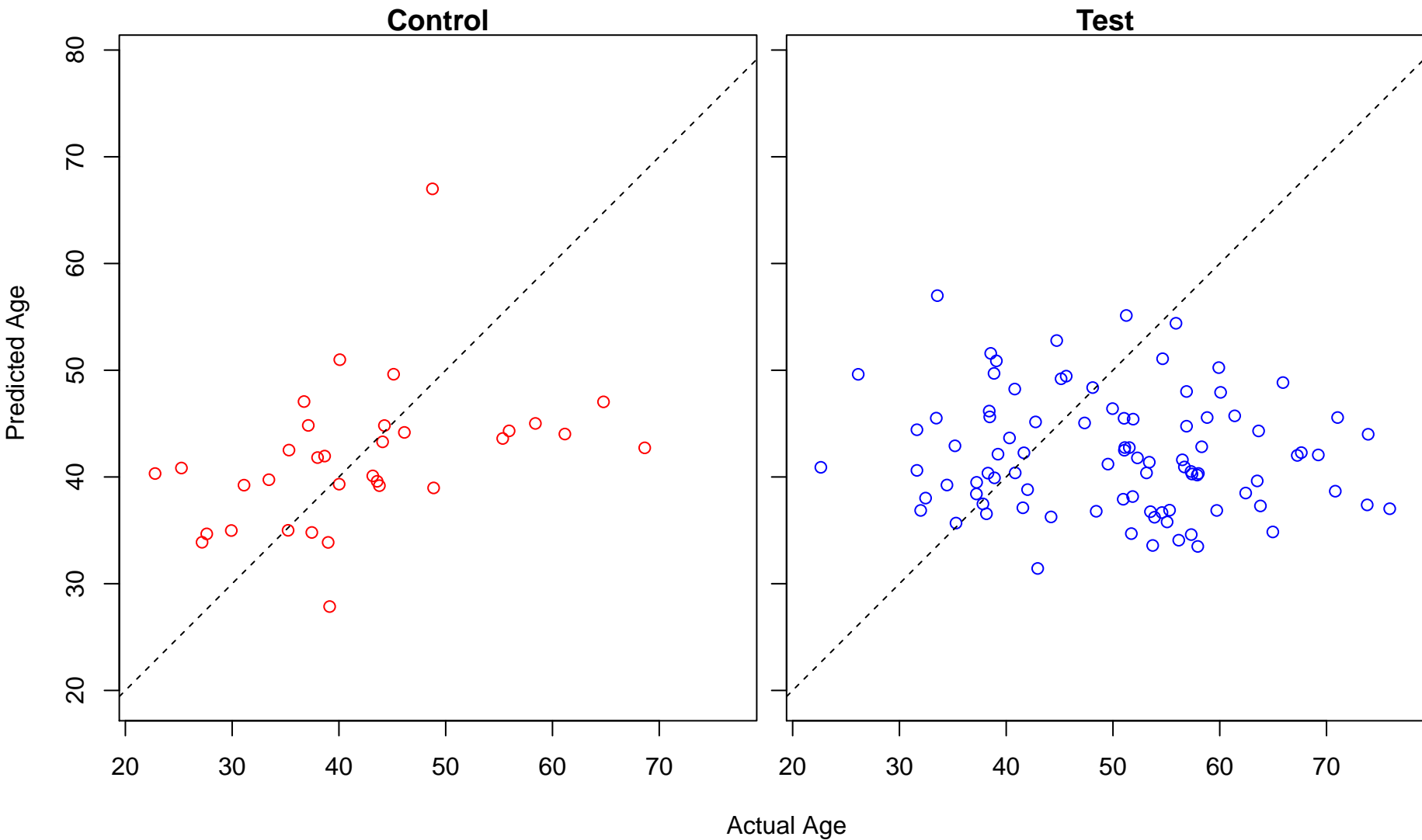
protein modification by small protein conjugation (Score: 0.654690)



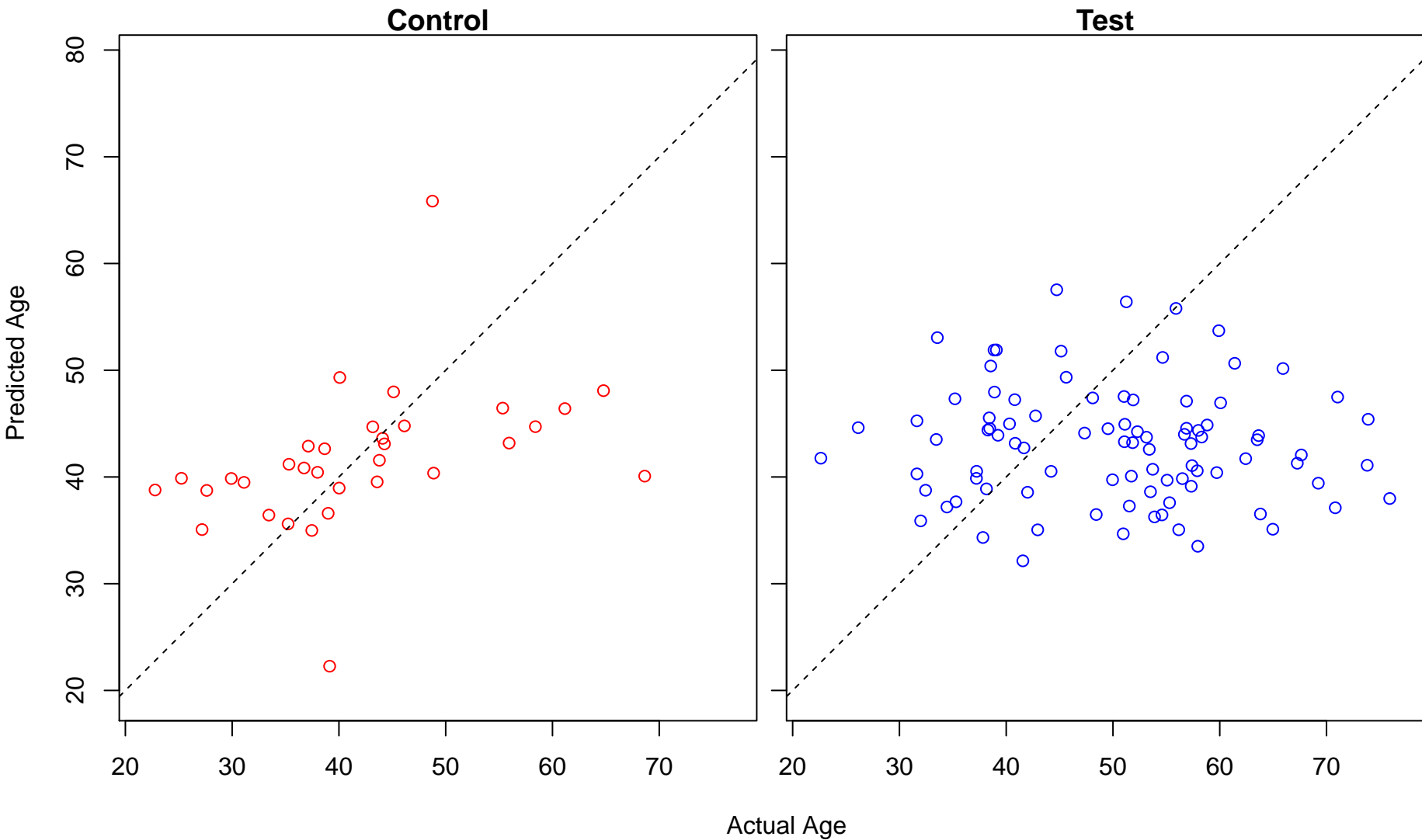
detection of mechanical stimulus involved in sensory perception of sound (Score: 0.654652)



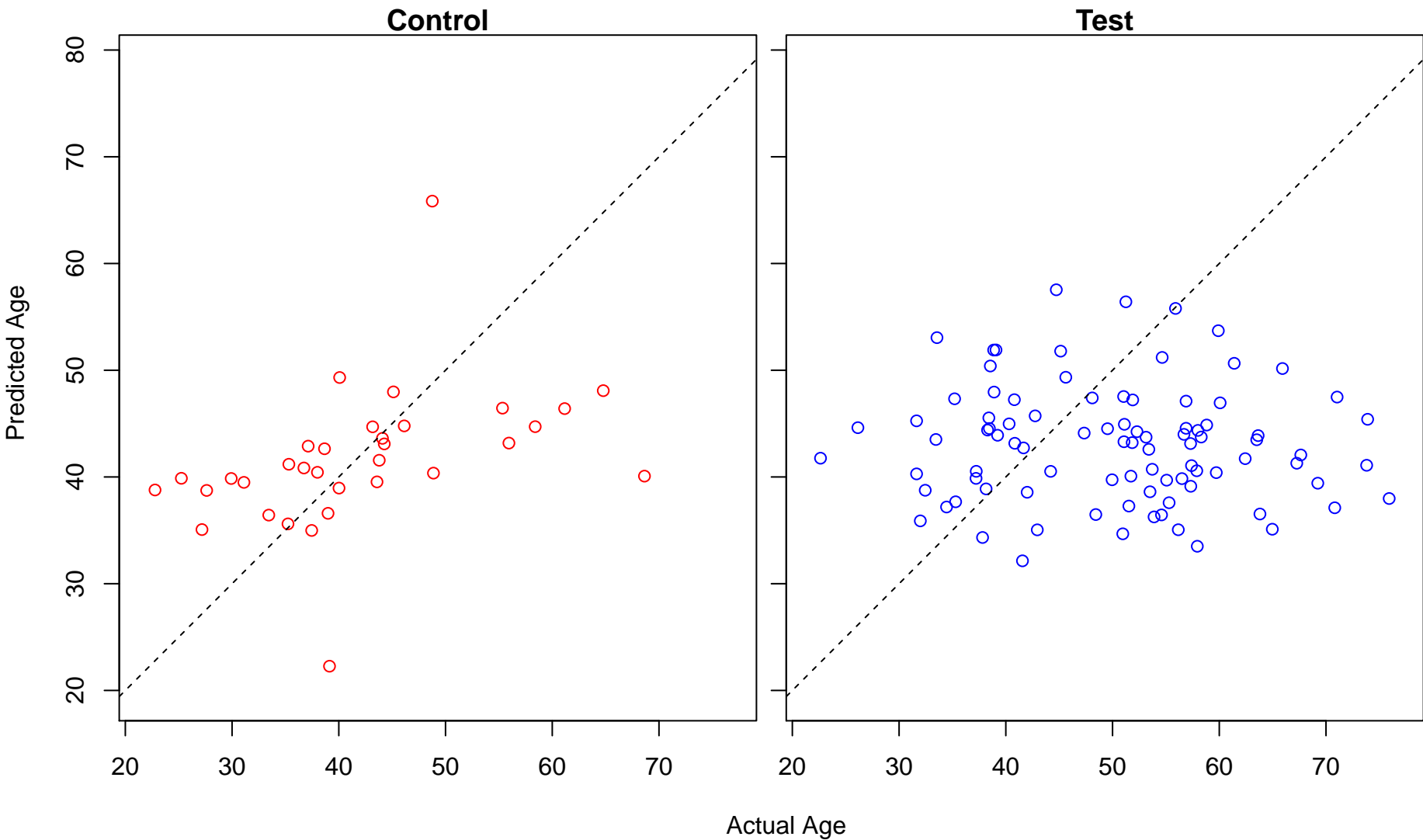
cell activation (Score: 0.654489)



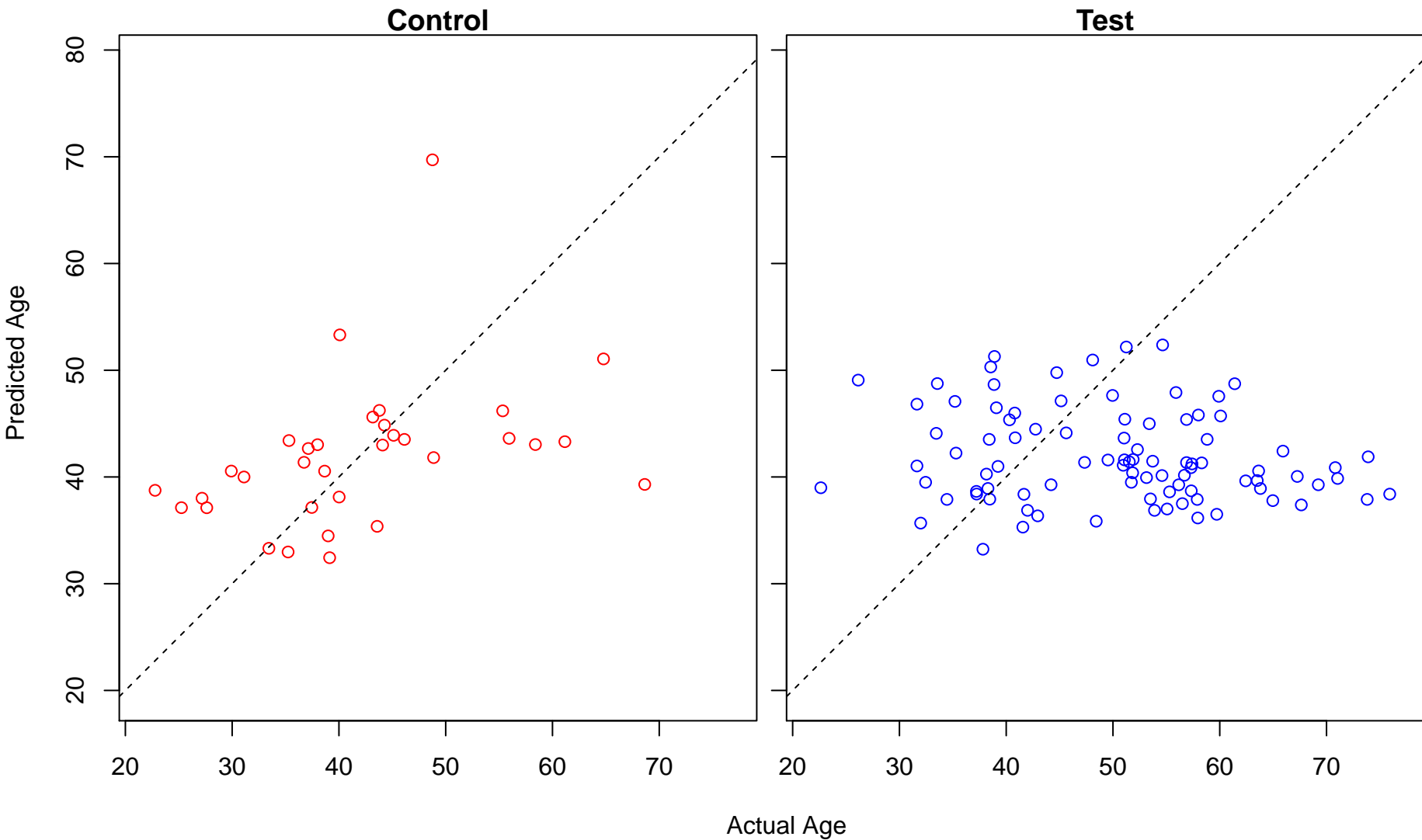
chemotaxis (Score: 0.654371)



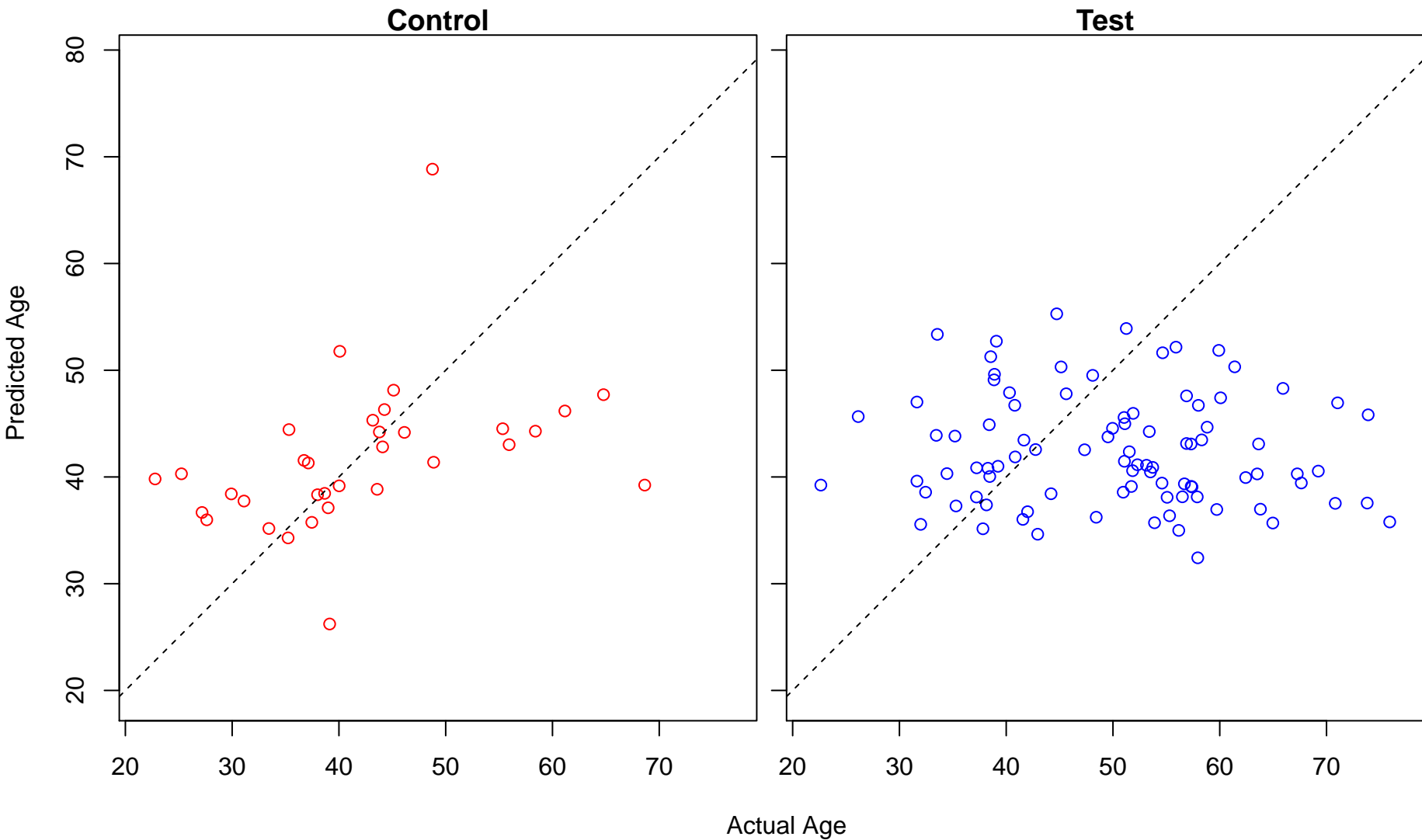
taxis (Score: 0.654371)



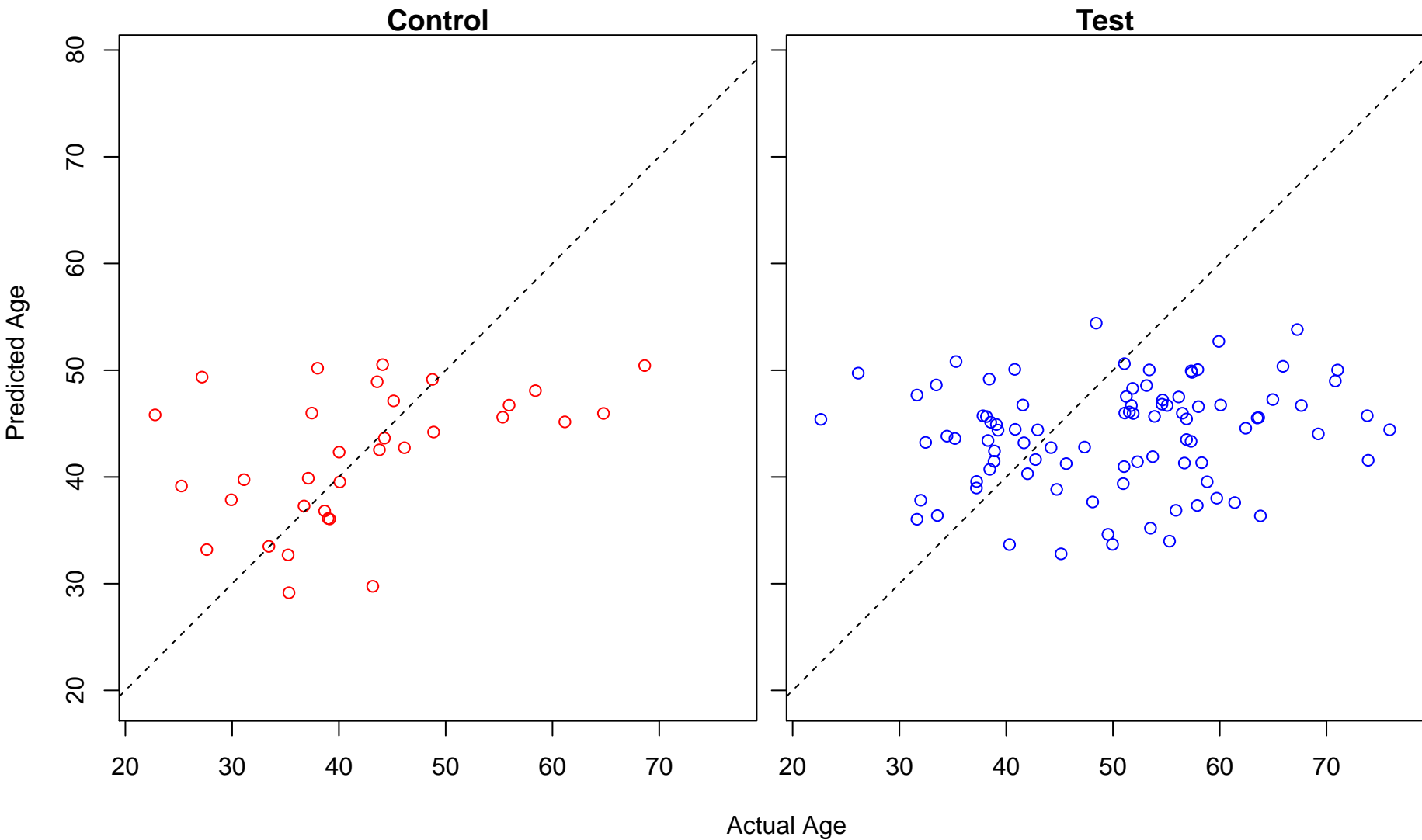
tissue morphogenesis (Score: 0.654066)



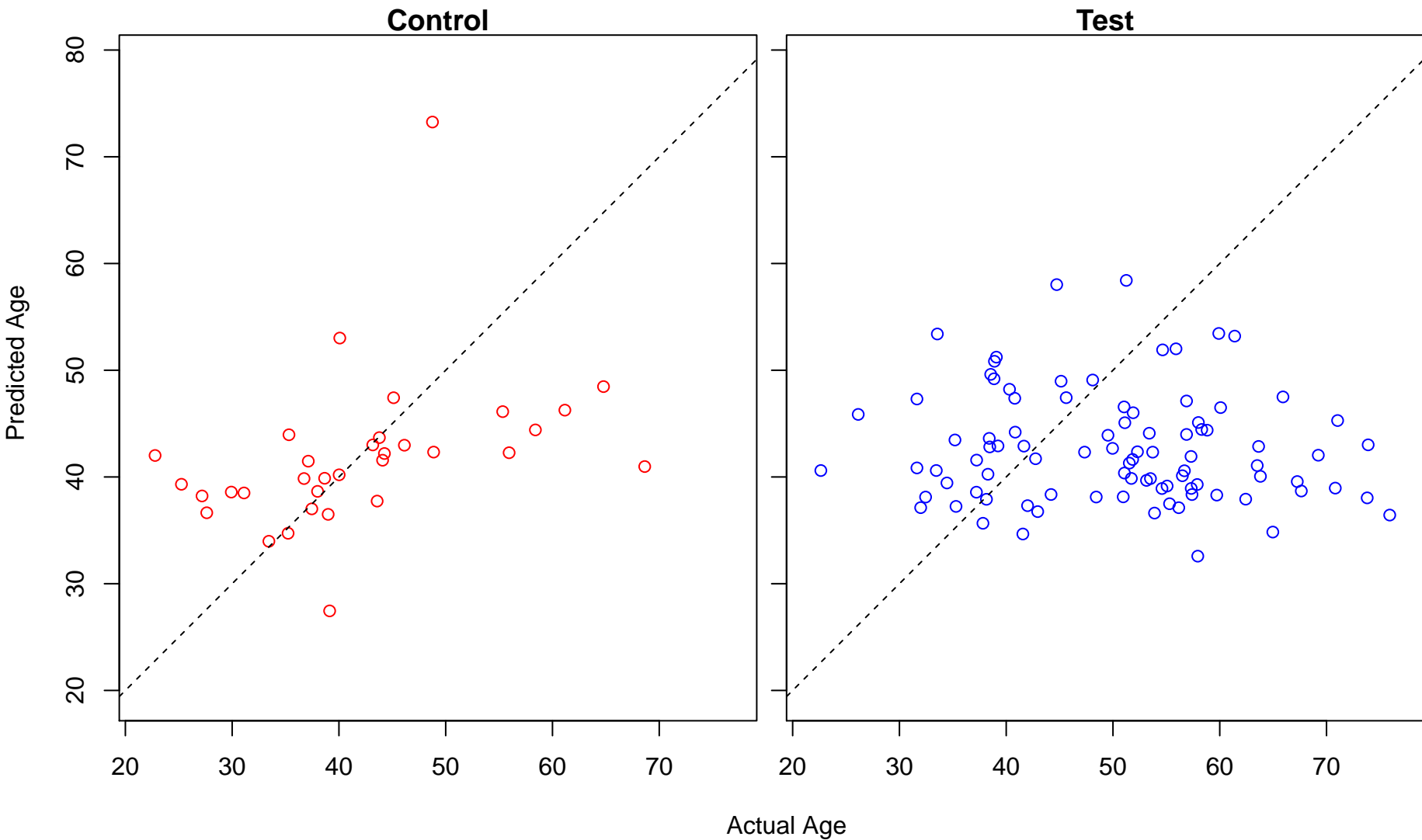
regulation of cellular process (Score: 0.653877)



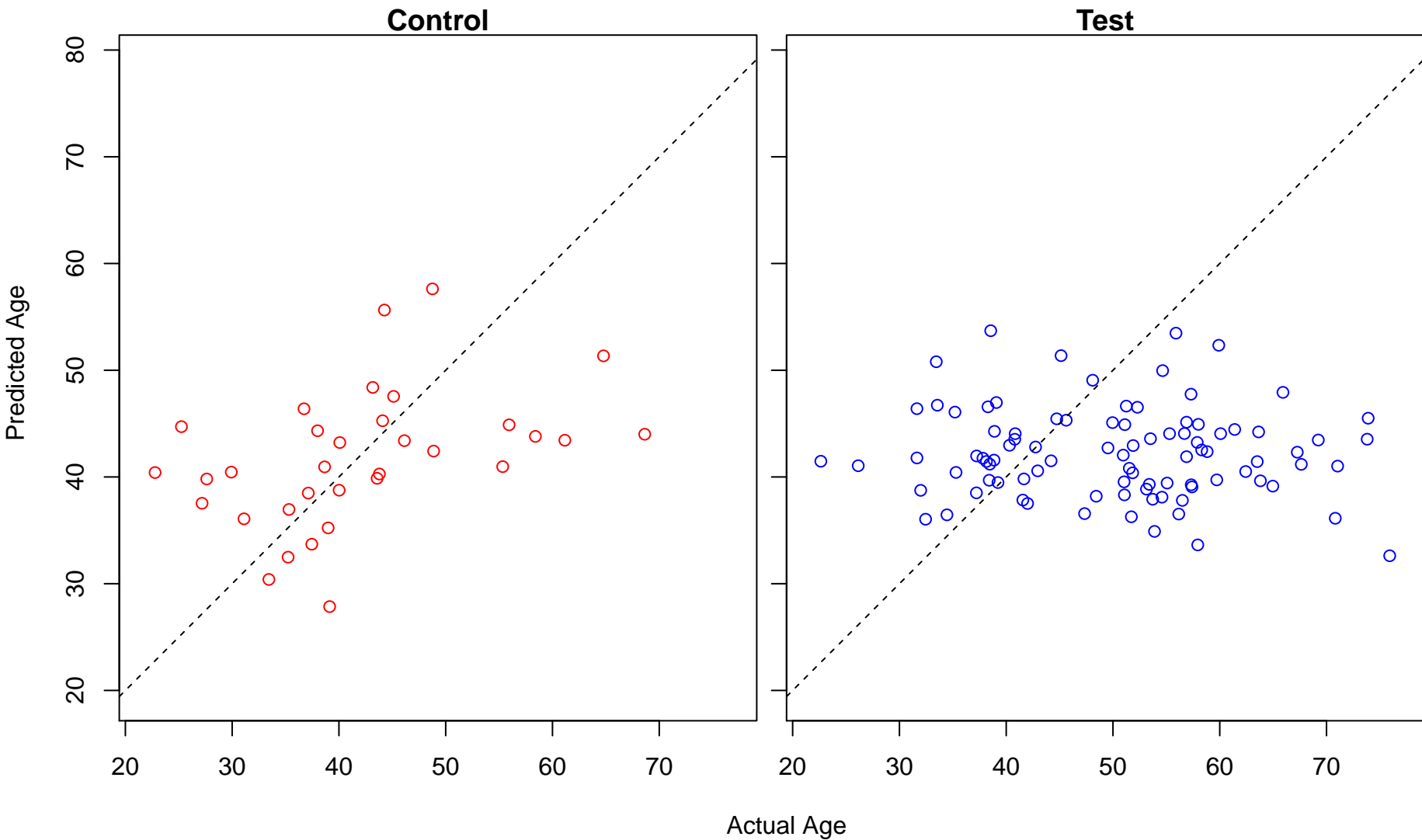
sequestering of BMP in extracellular matrix (Score: 0.653525)



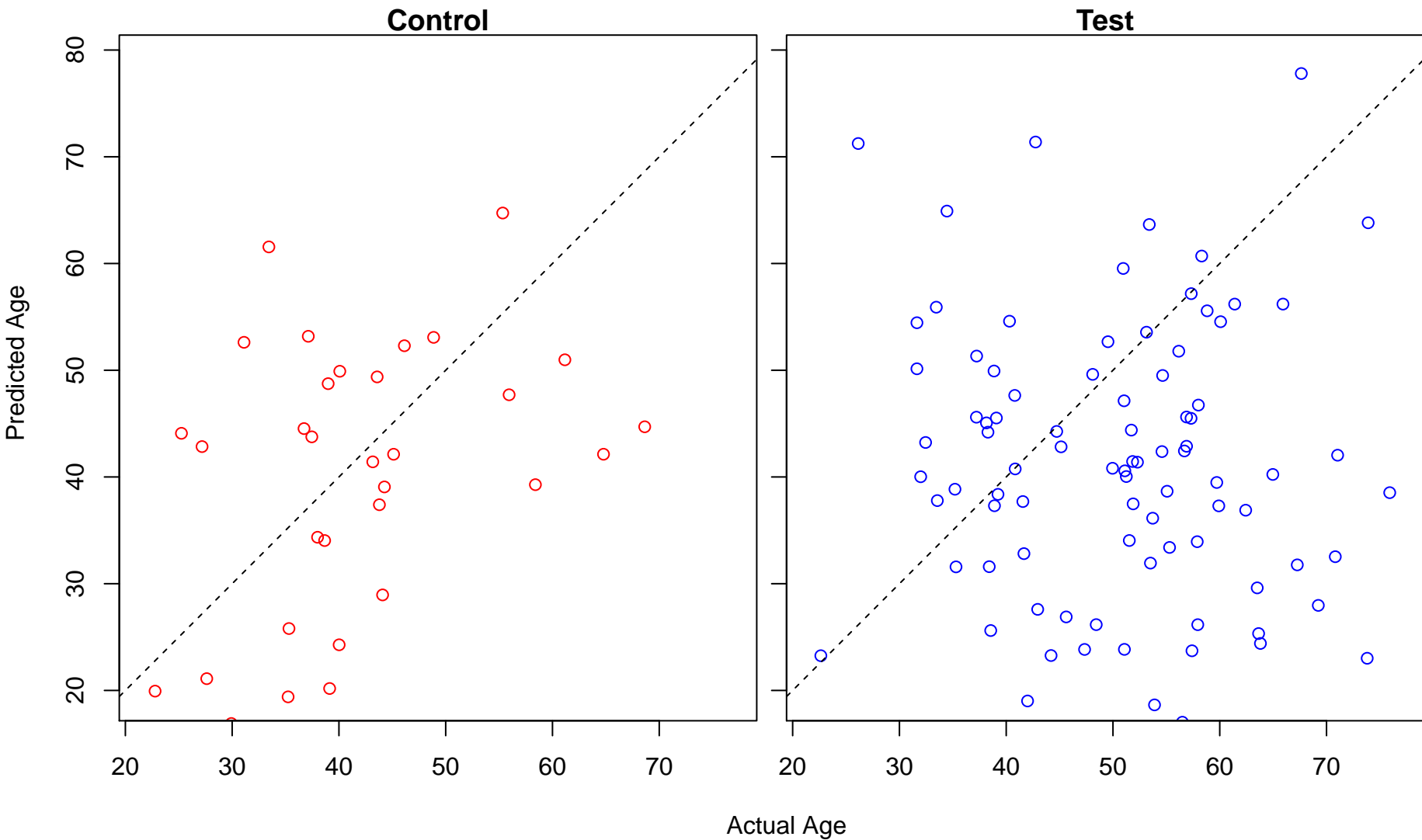
endosomal transport (Score: 0.653473)



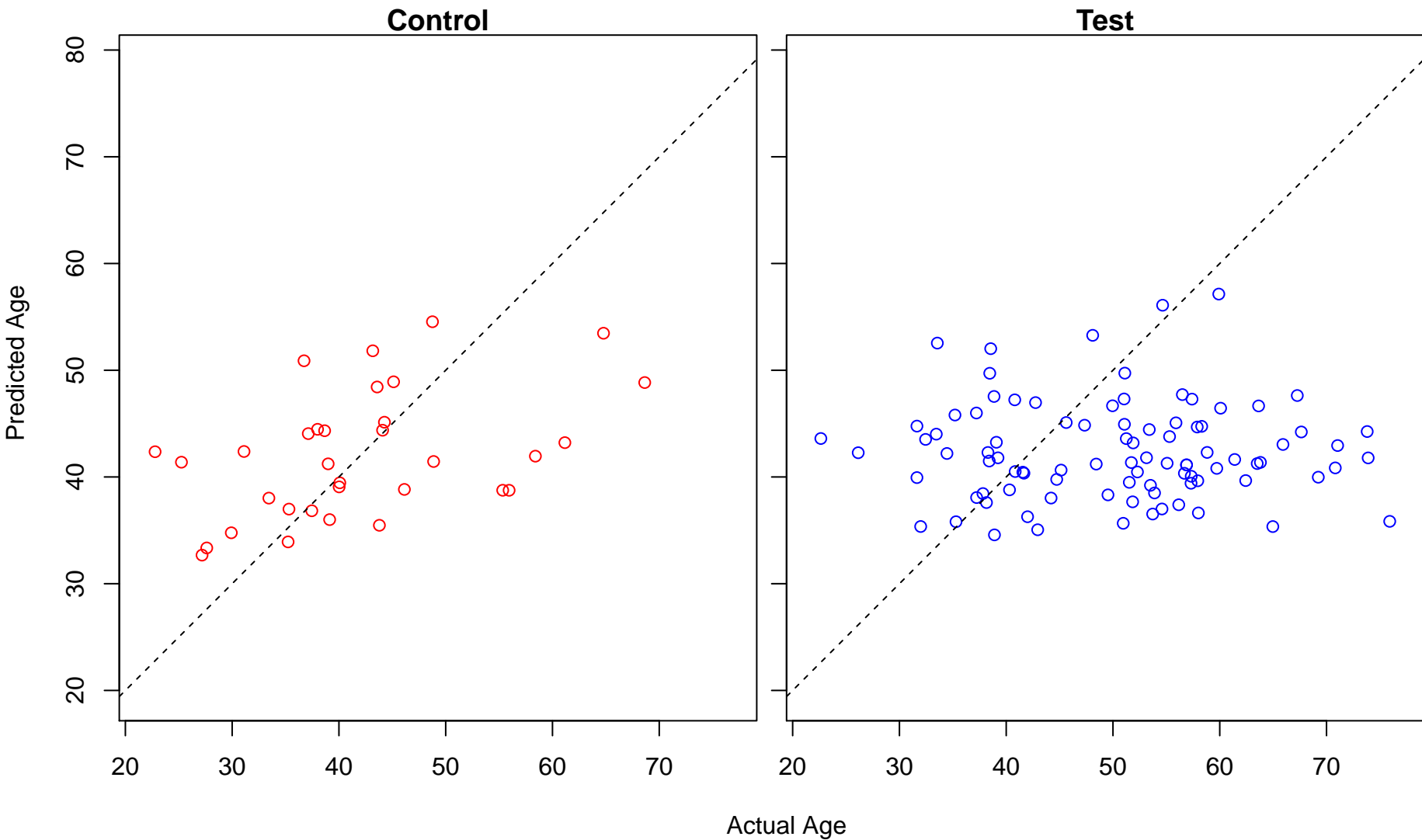
nucleoside diphosphate metabolic process (Score: 0.653263)



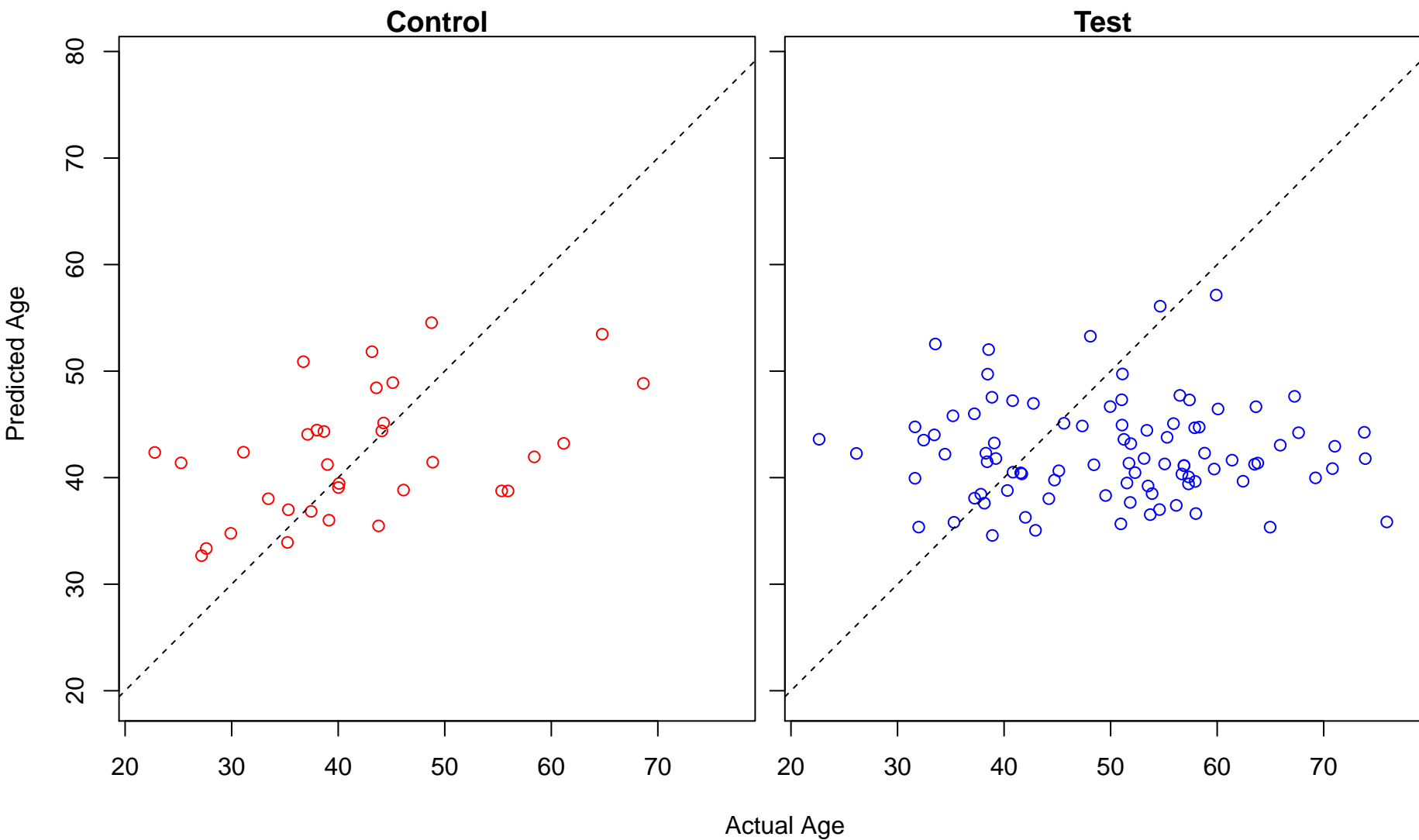
positive regulation of stem cell differentiation (Score: 0.653008)



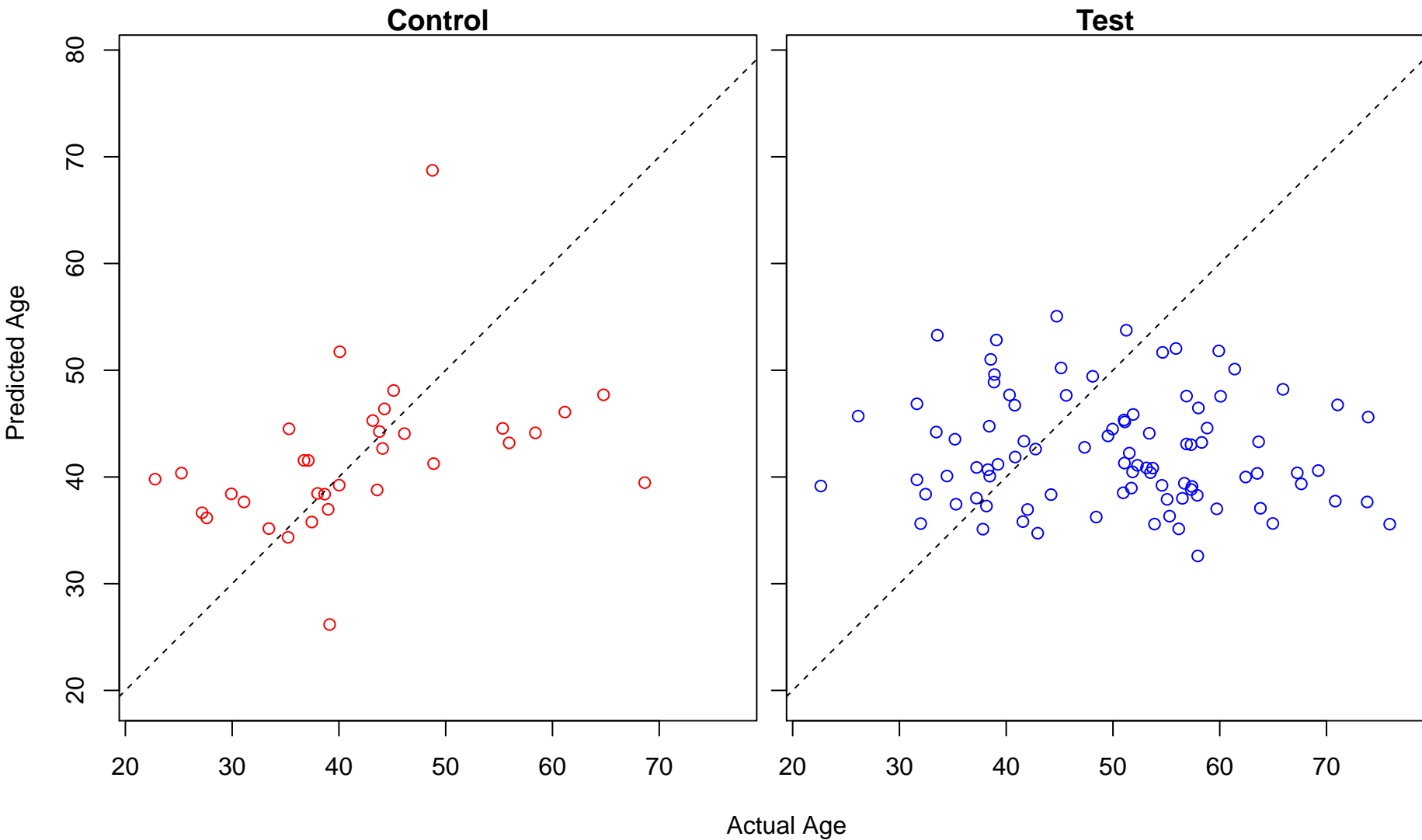
regulation of T cell costimulation (Score: 0.653004)



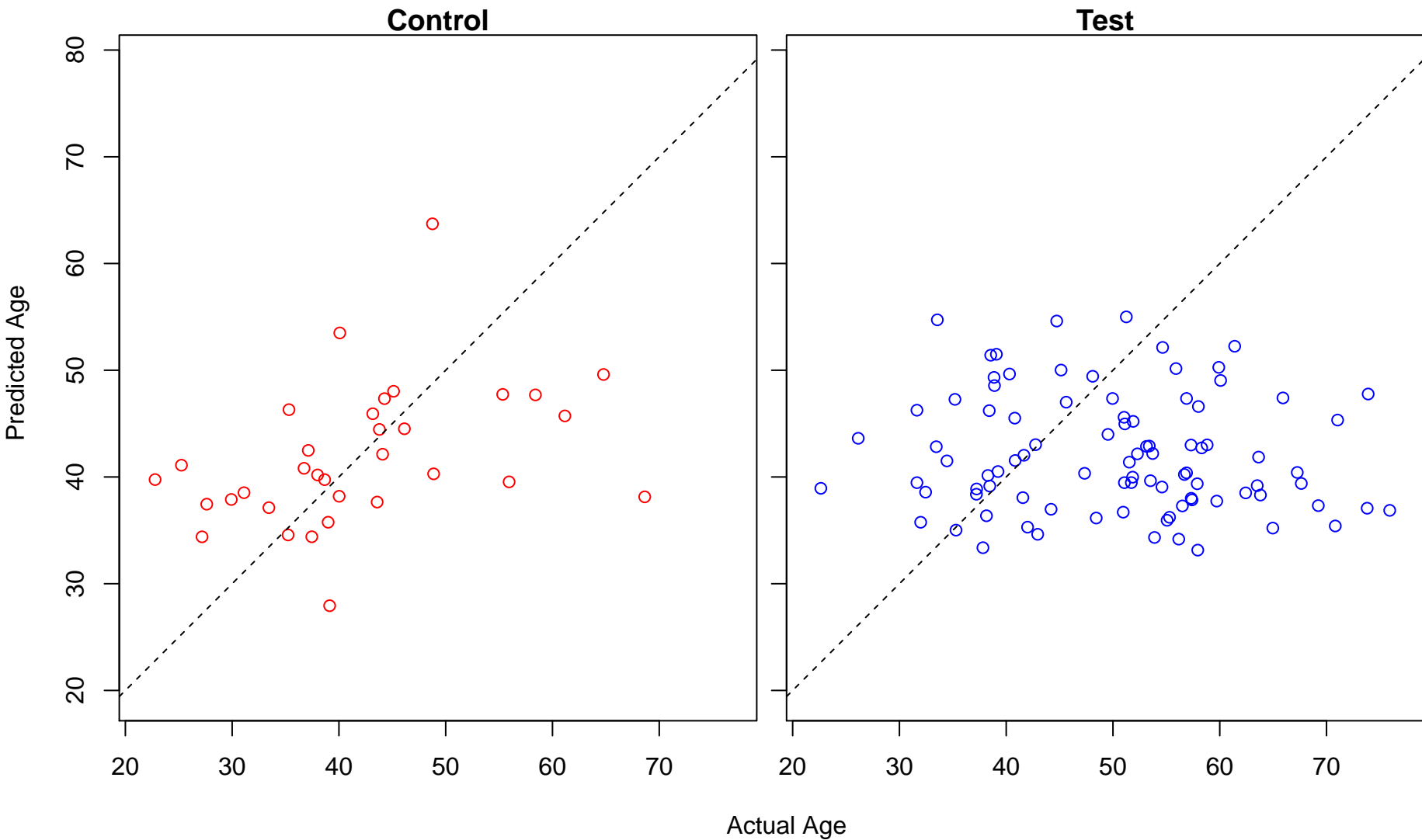
positive regulation of T cell costimulation (Score: 0.653004)



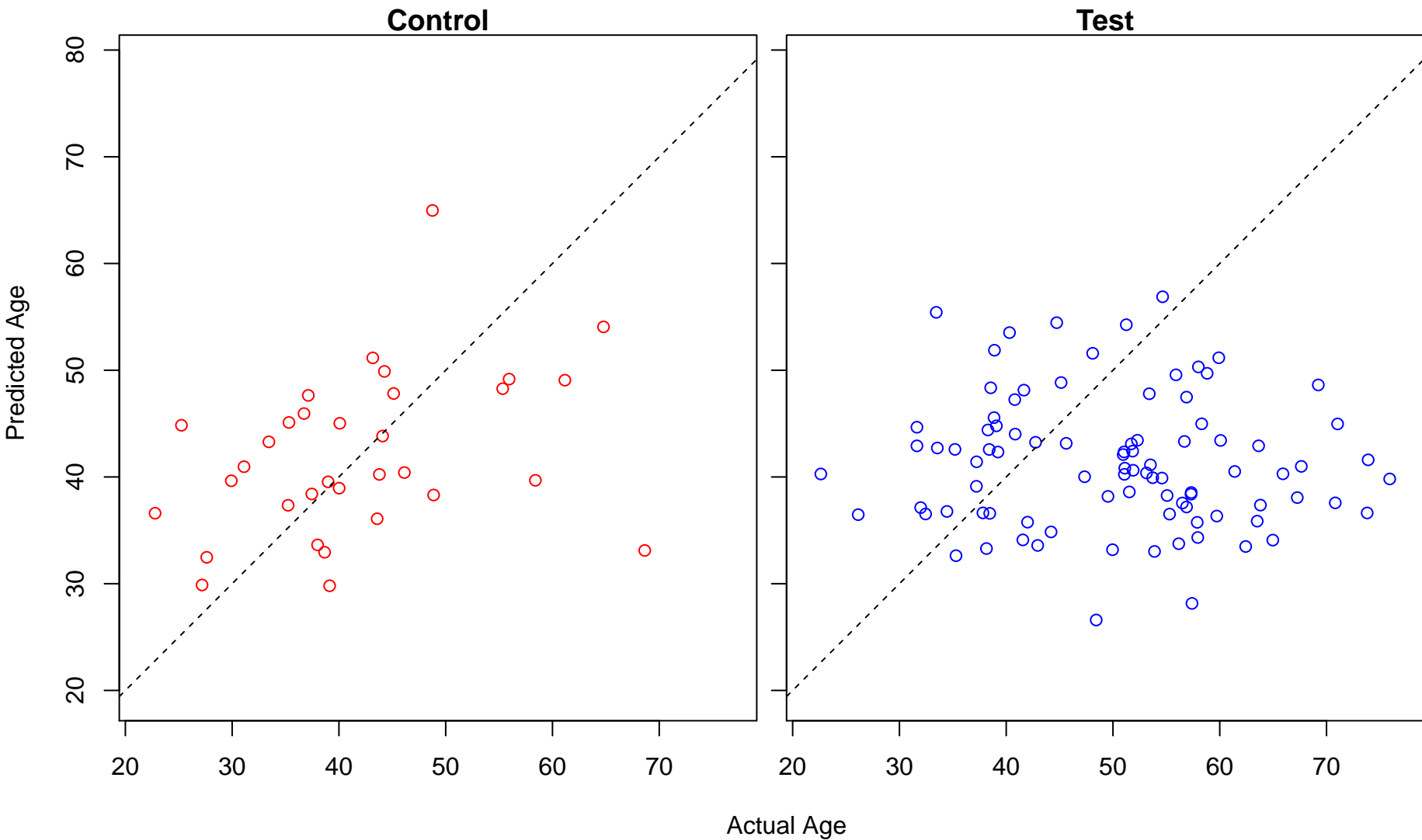
regulation of biological process (Score: 0.652653)



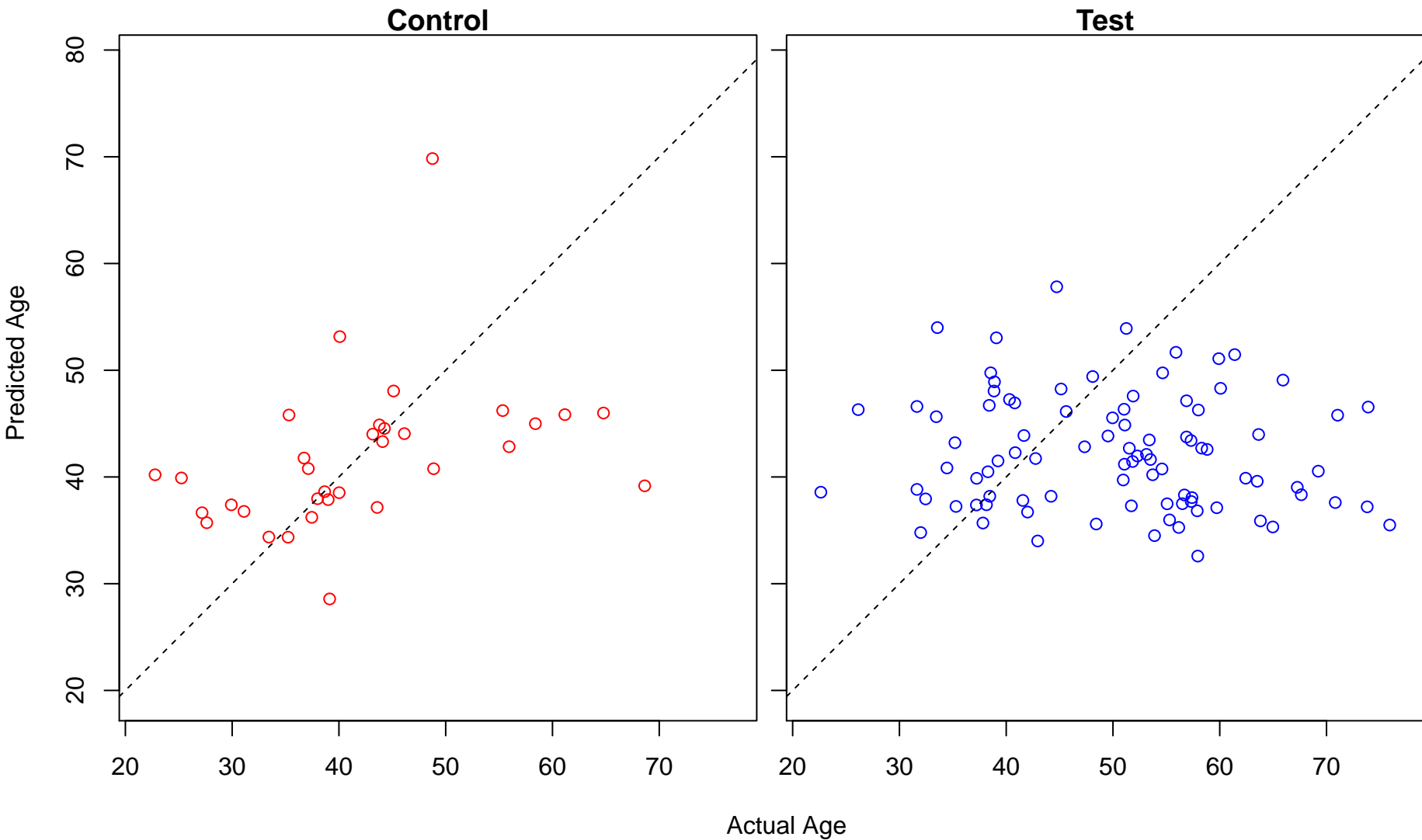
regulation of anatomical structure morphogenesis (Score: 0.652261)



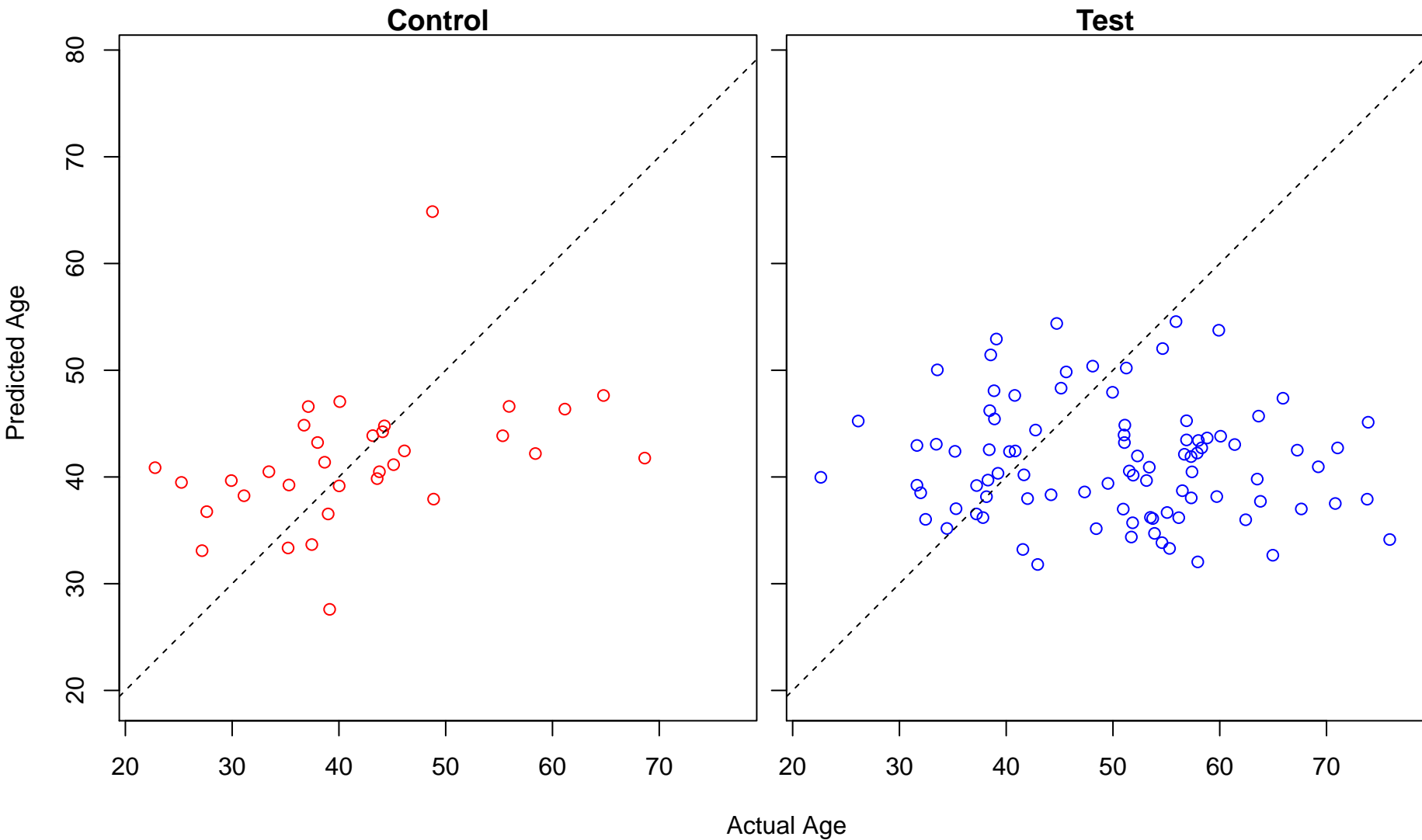
protein export from nucleus (Score: 0.651983)



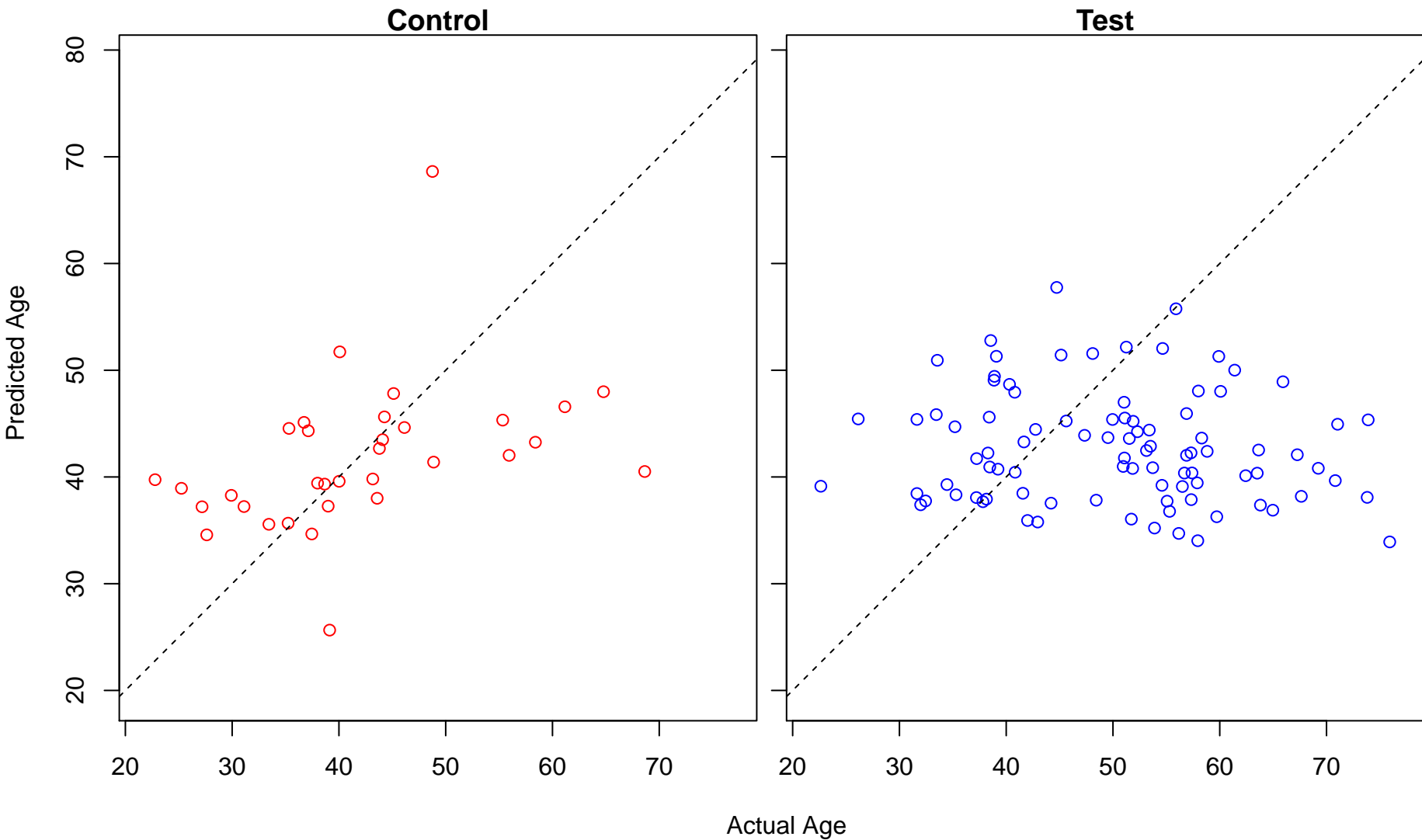
cellular macromolecule biosynthetic process (Score: 0.651851)



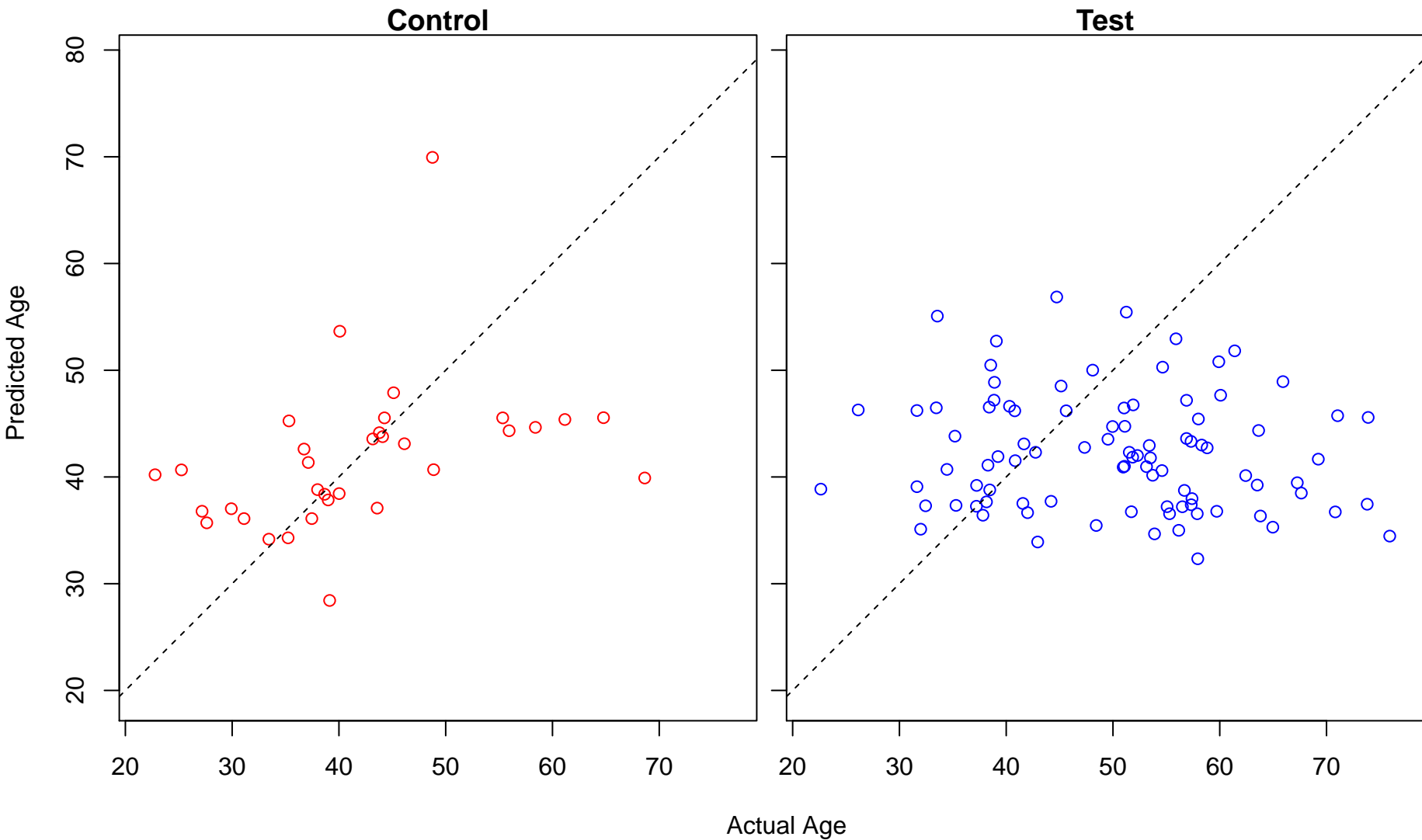
chemical homeostasis (Score: 0.651202)



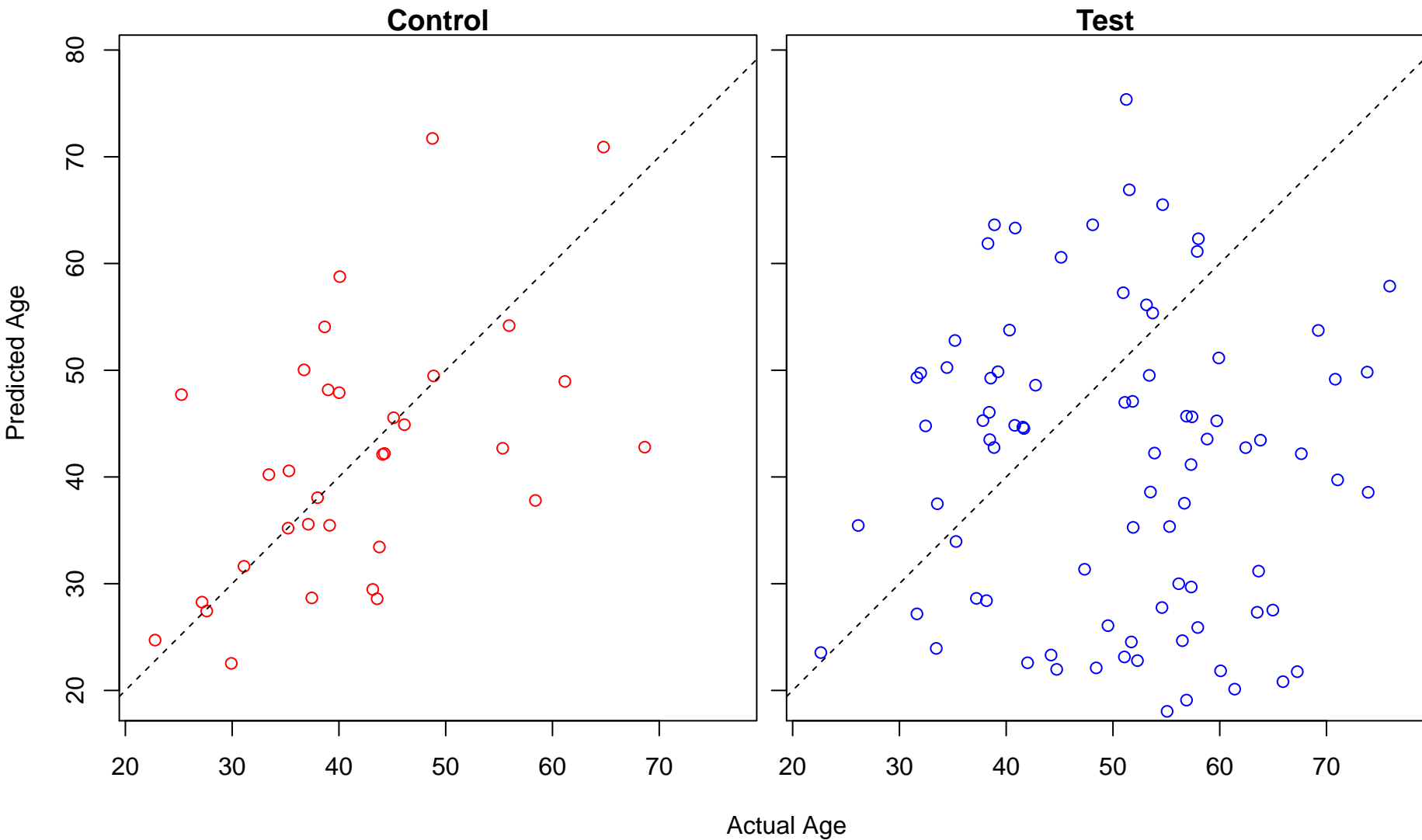
regulation of protein localization (Score: 0.651031)



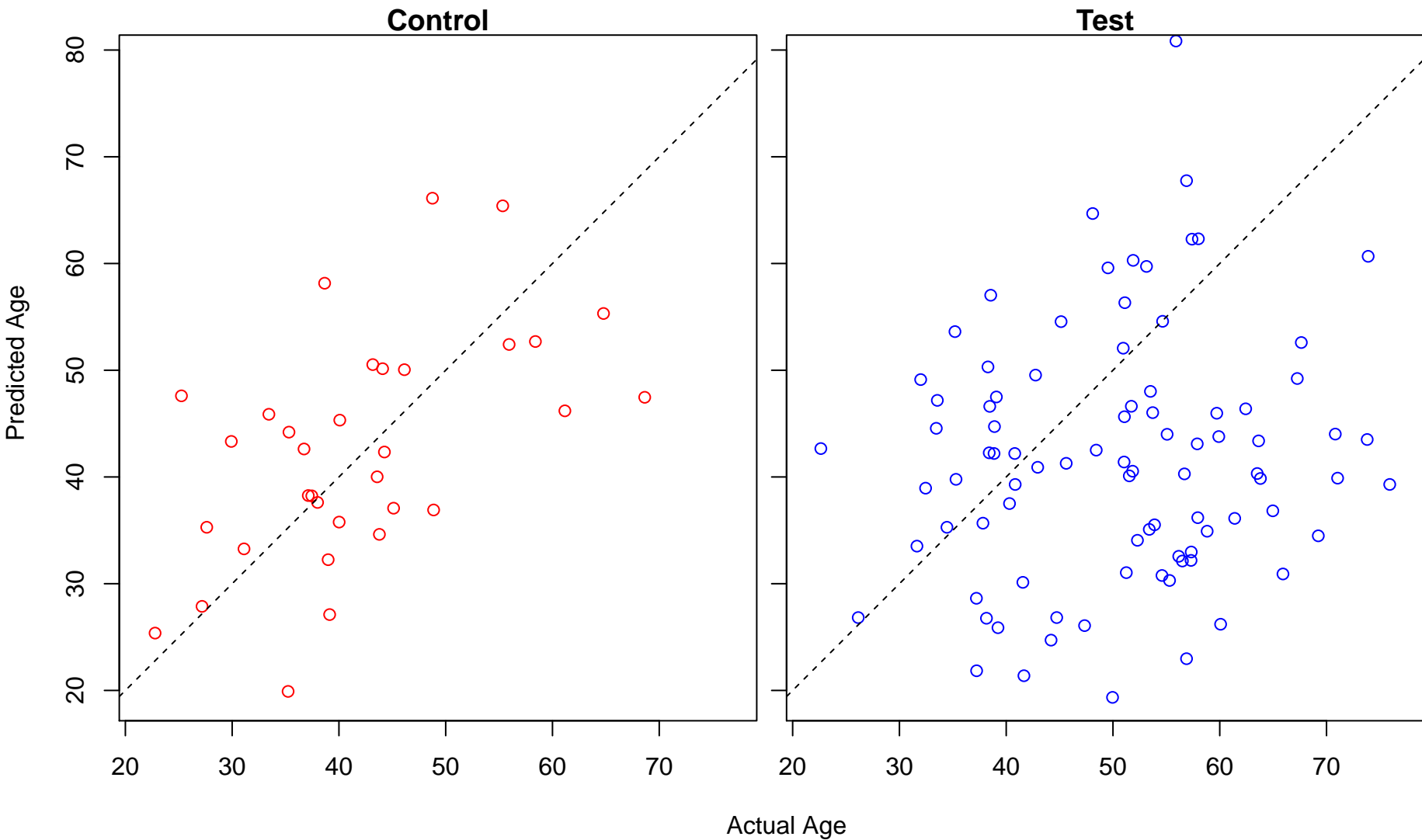
cellular nitrogen compound biosynthetic process (Score: 0.650200)



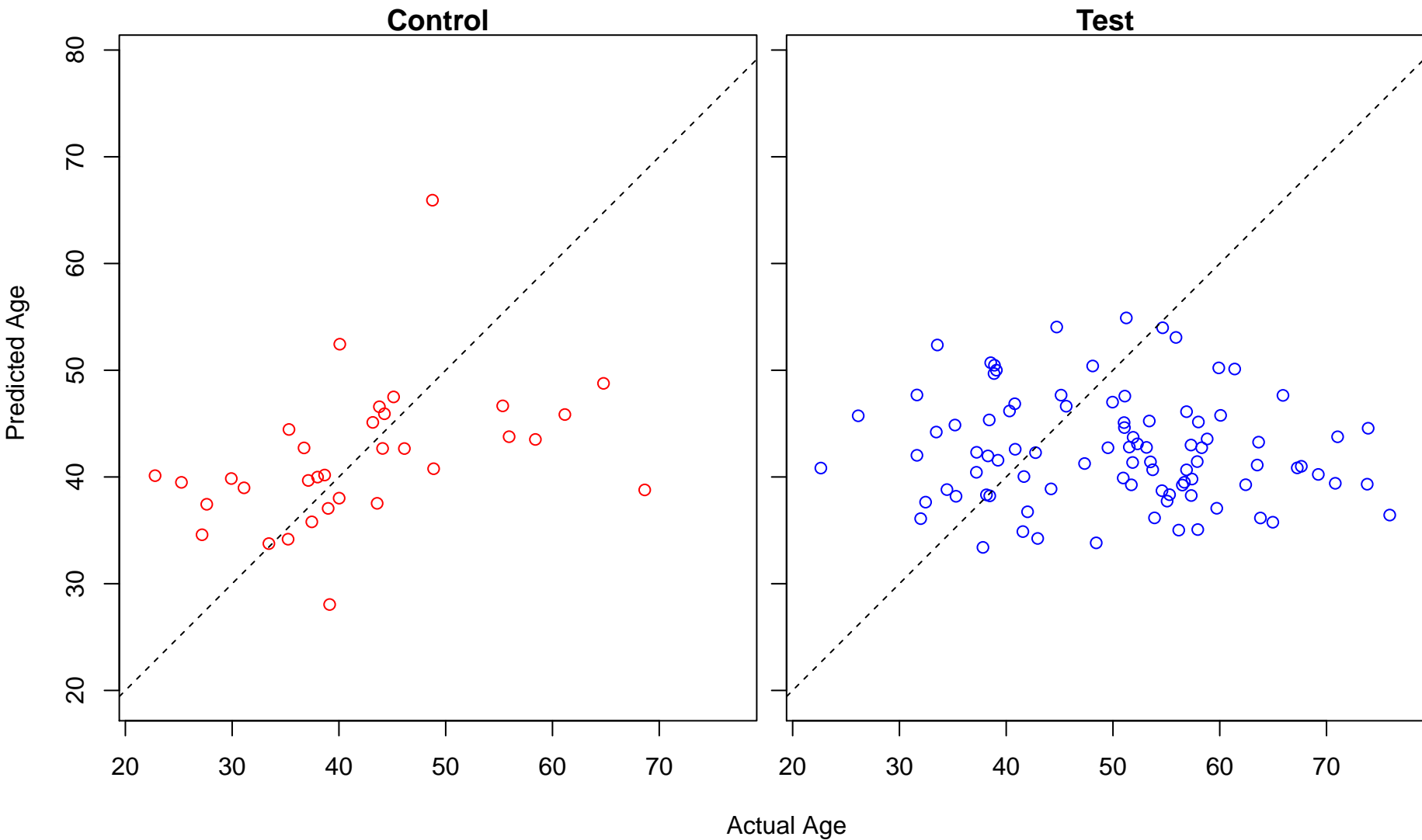
negative regulation of JNK cascade (Score: 0.650094)



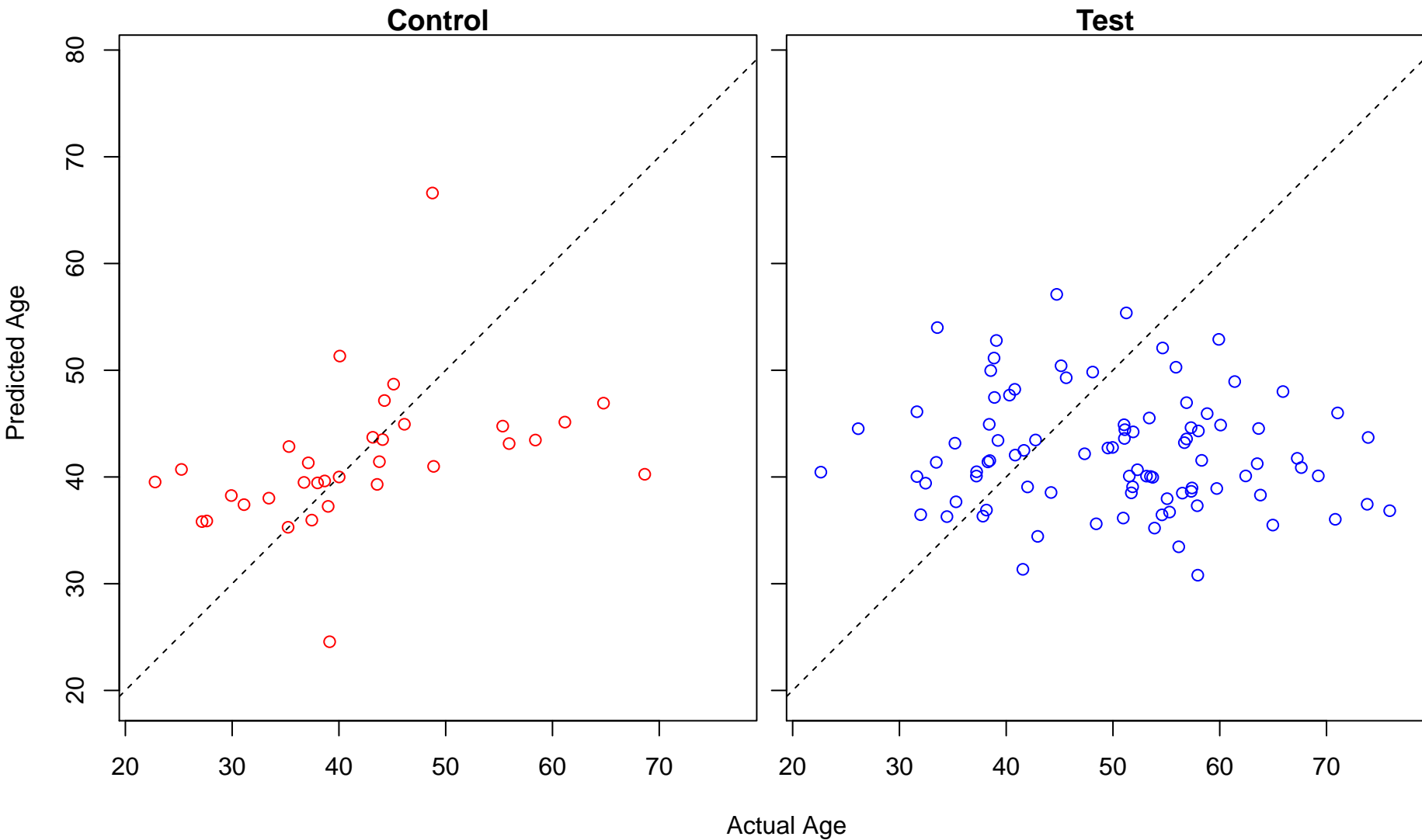
stem cell development (Score: 0.649397)



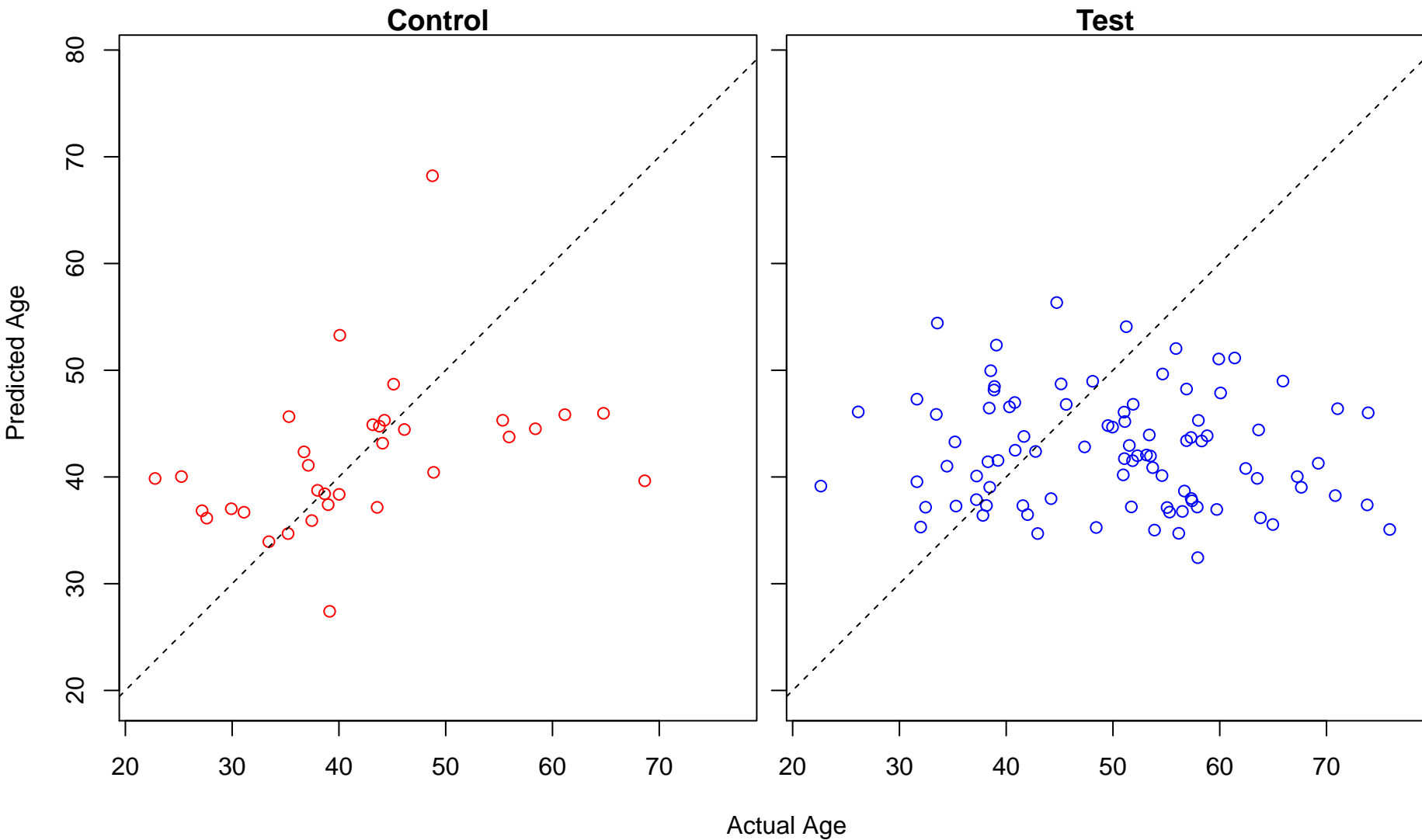
tissue development (Score: 0.649208)



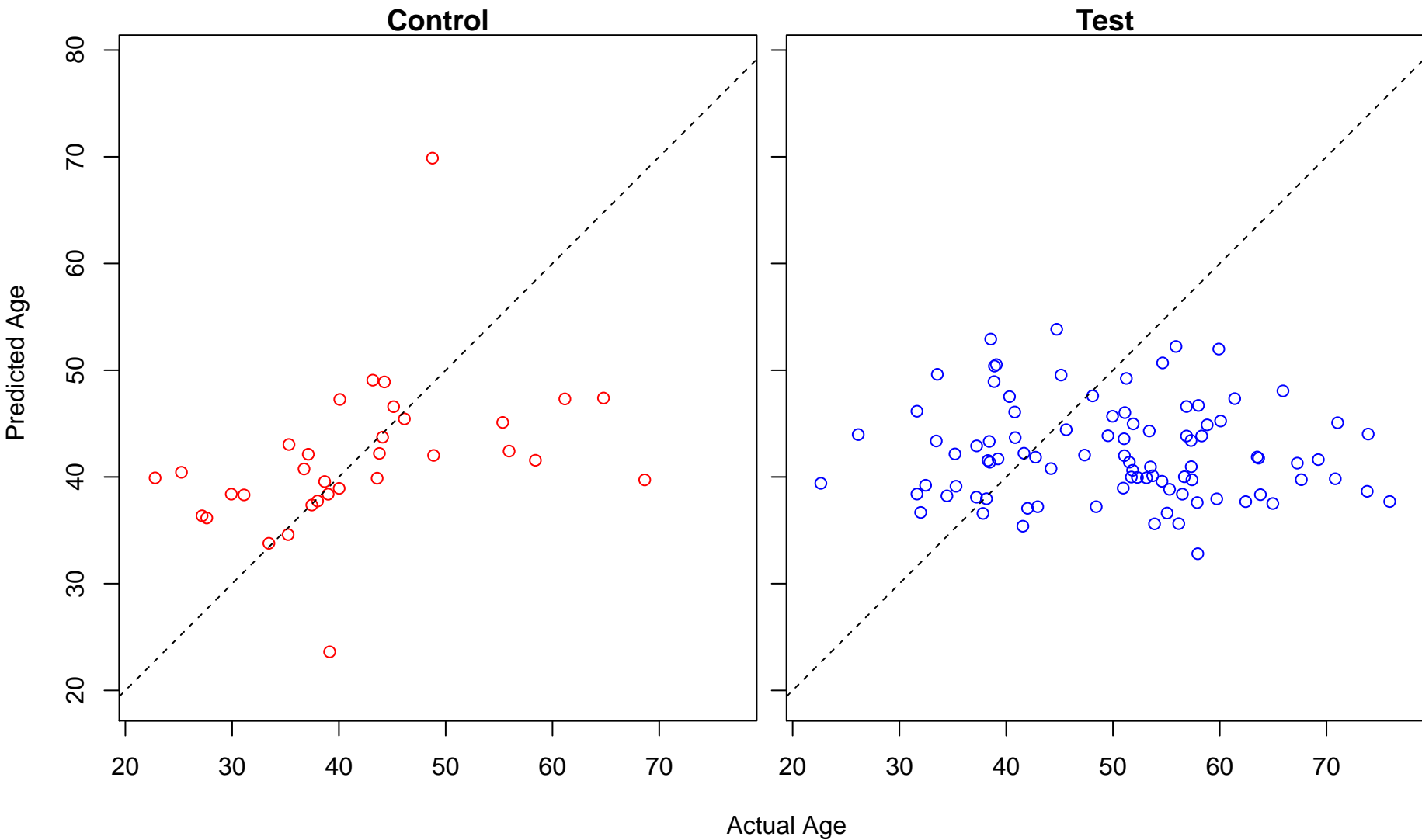
cellular response to oxygen-containing compound (Score: 0.648228)



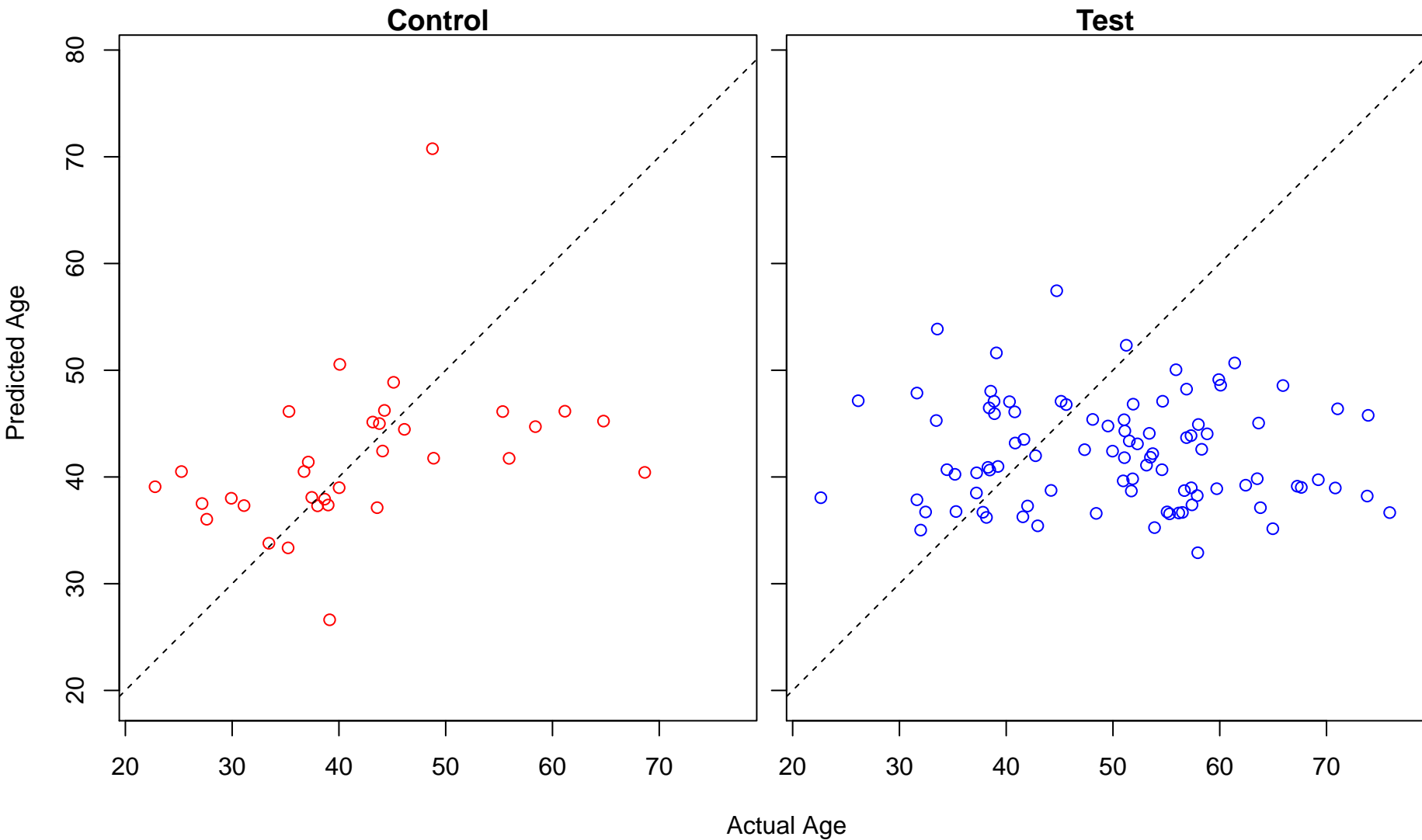
nitrogen compound metabolic process (Score: 0.648015)



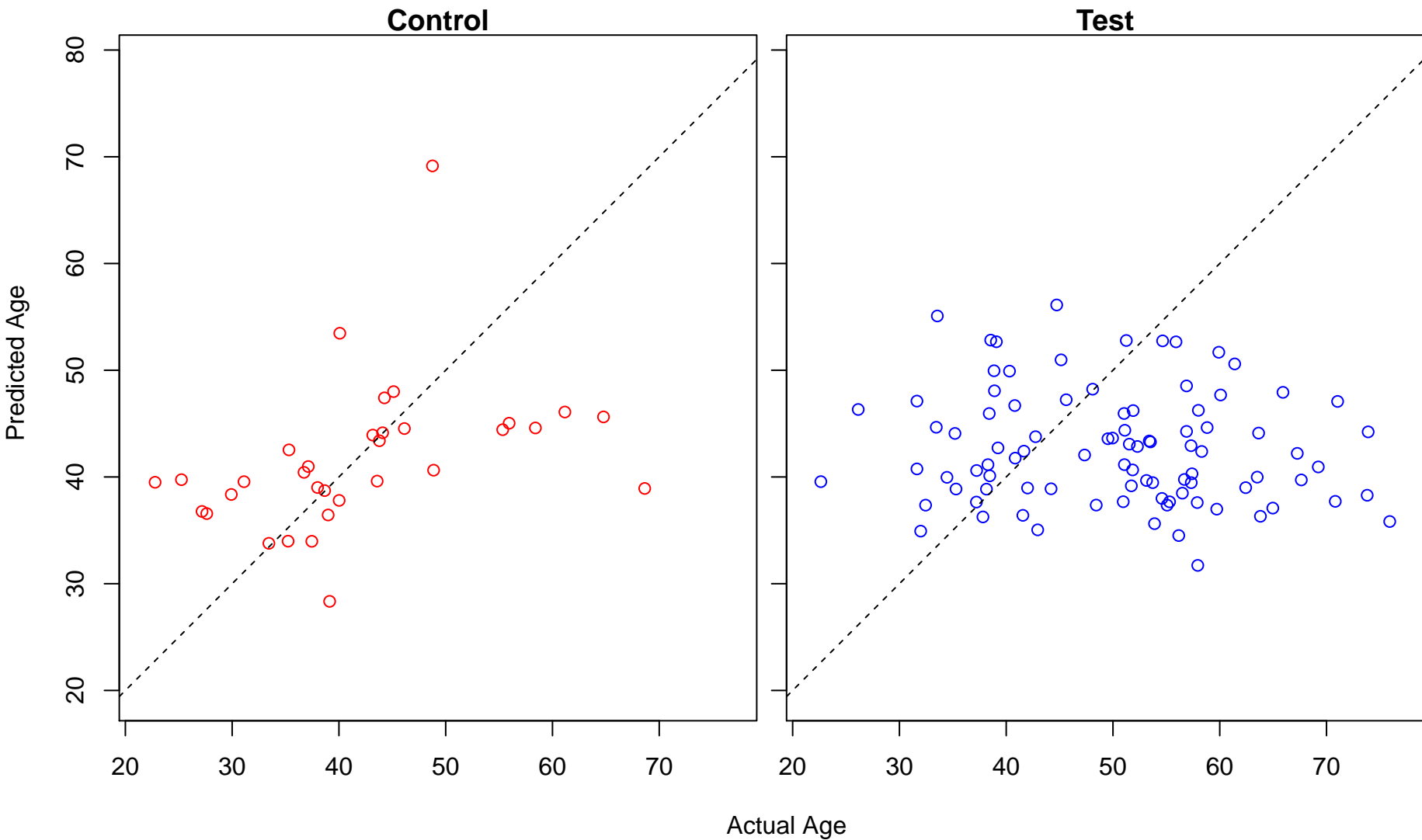
mitotic cell cycle (Score: 0.647976)



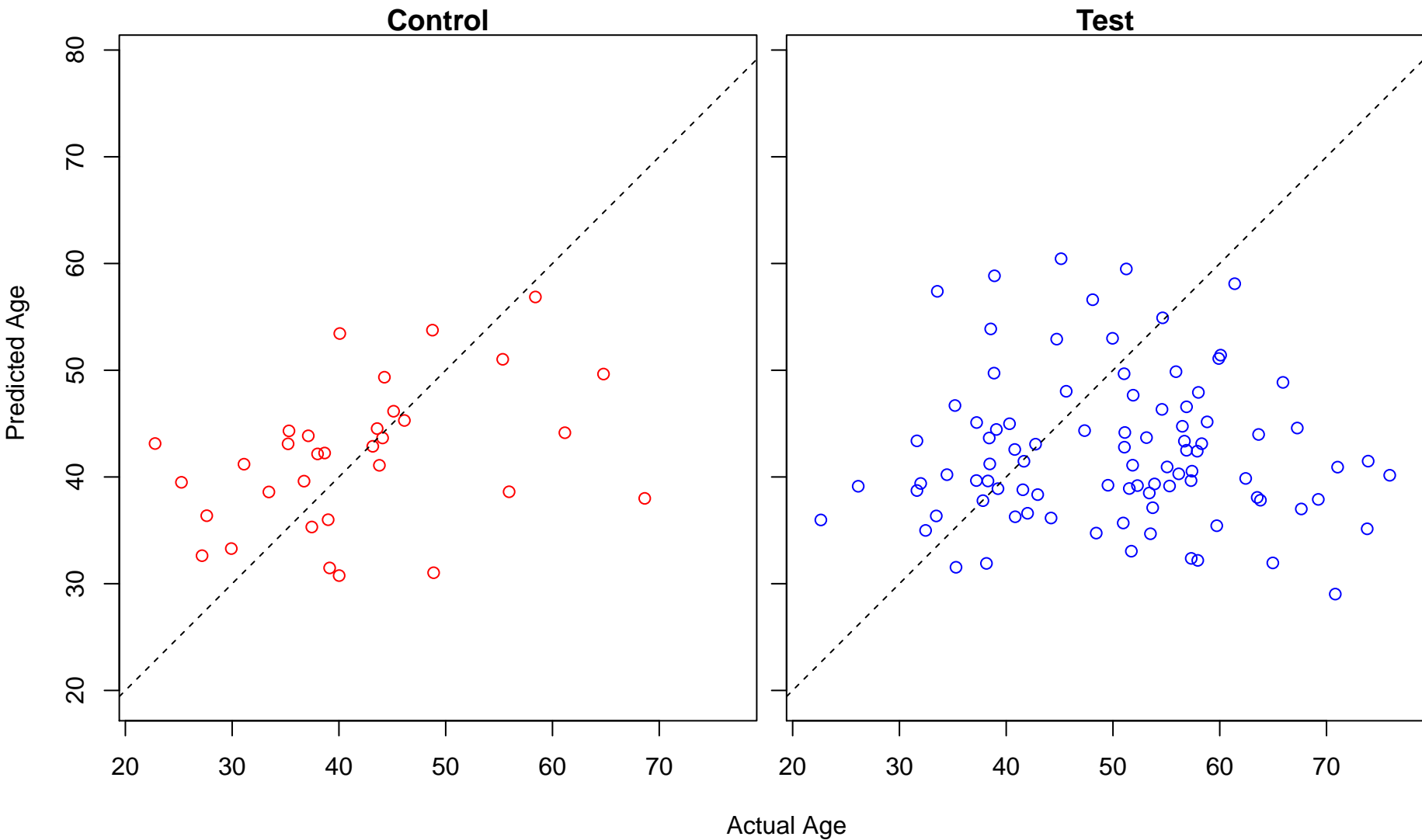
DNA repair (Score: 0.647473)



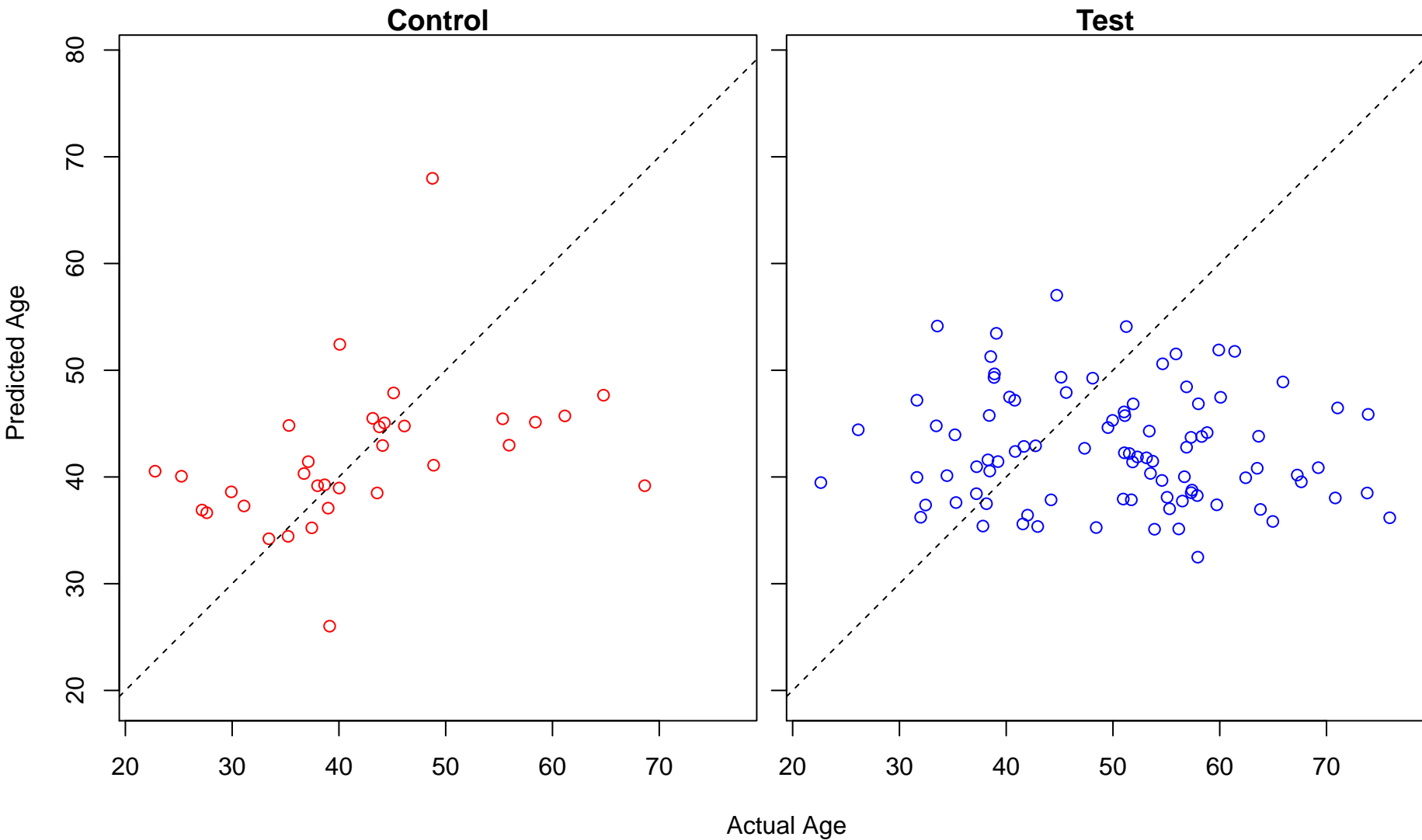
negative regulation of molecular function (Score: 0.647247)



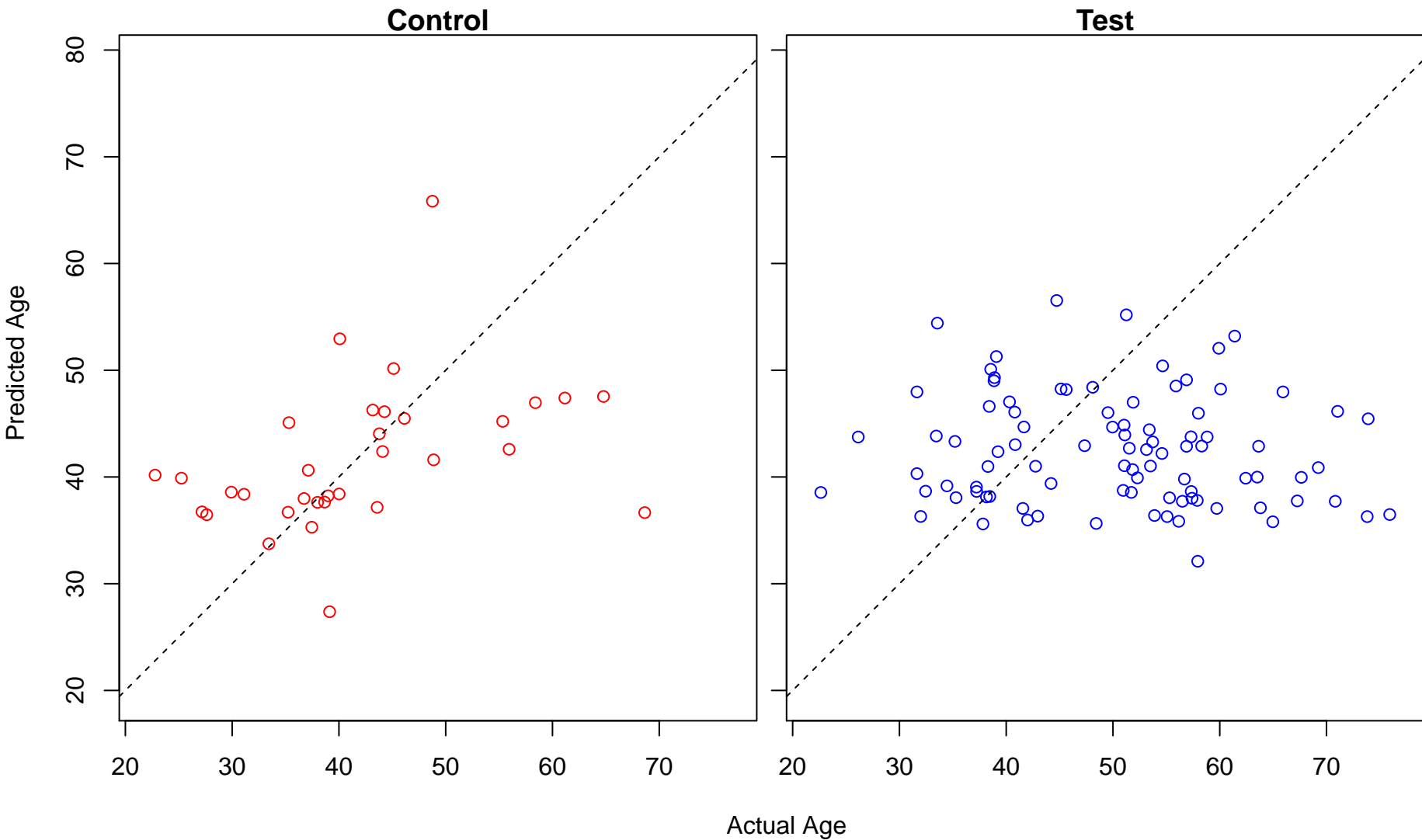
establishment of epithelial cell polarity (Score: 0.647098)



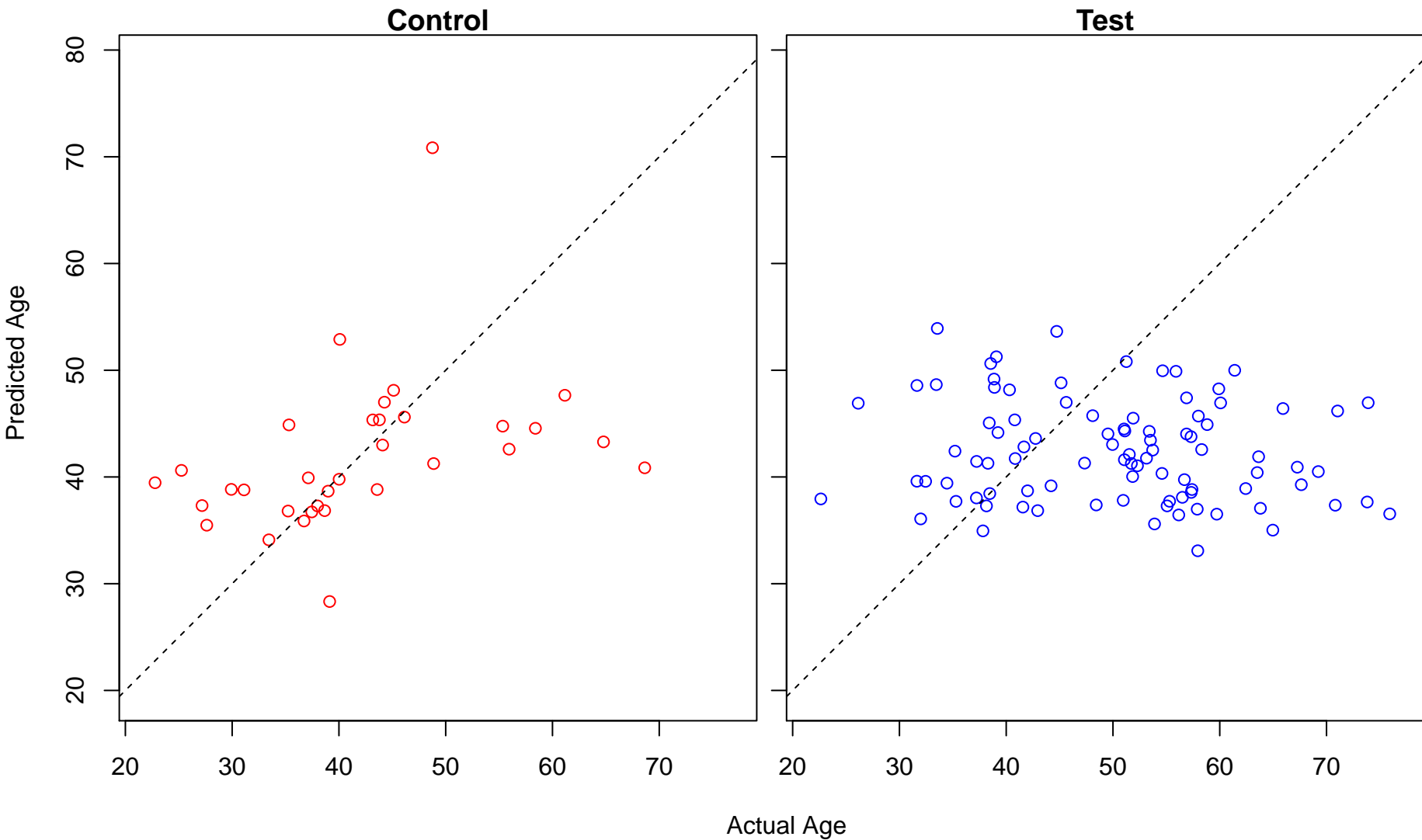
cellular component organization (Score: 0.646977)



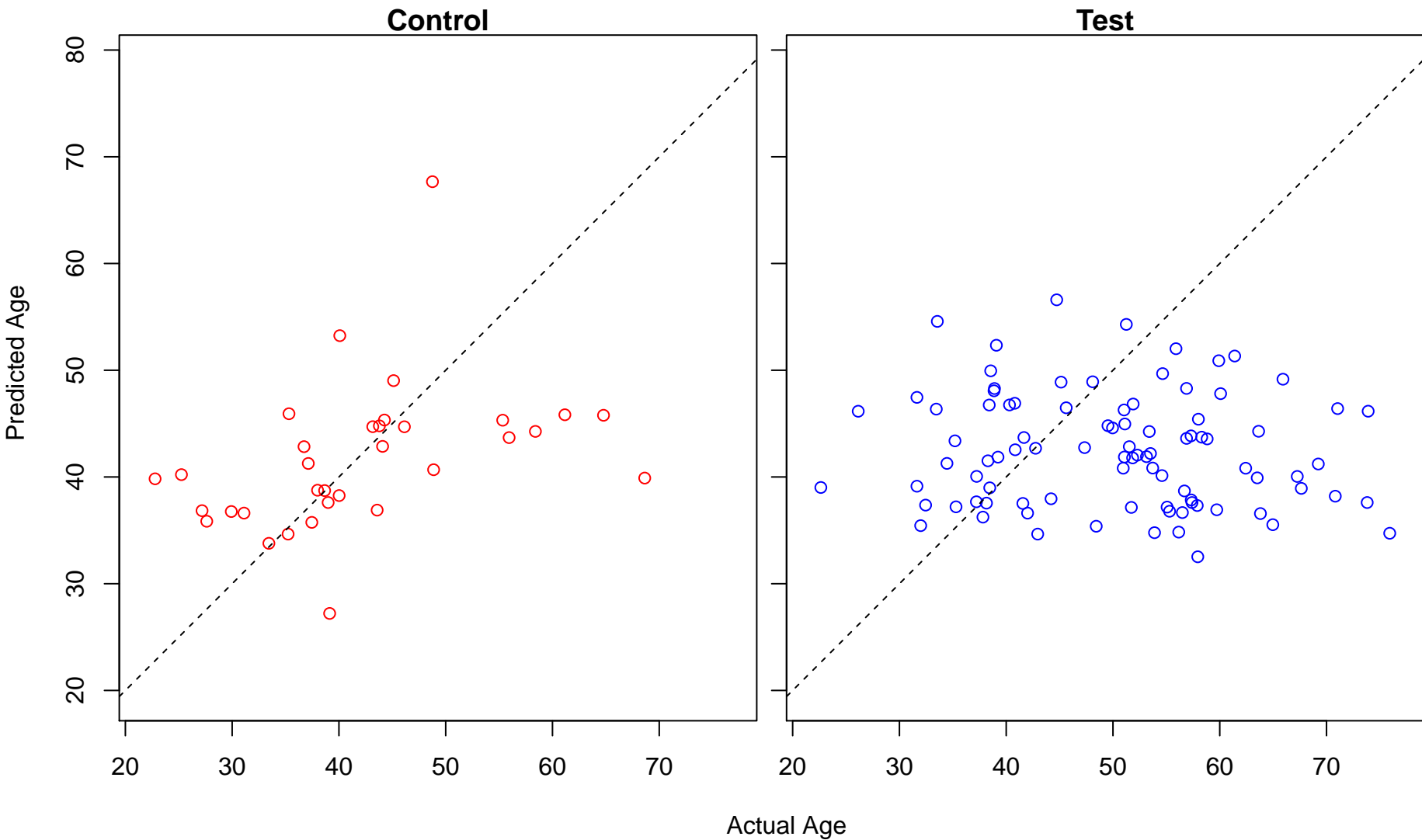
protein catabolic process (Score: 0.646908)



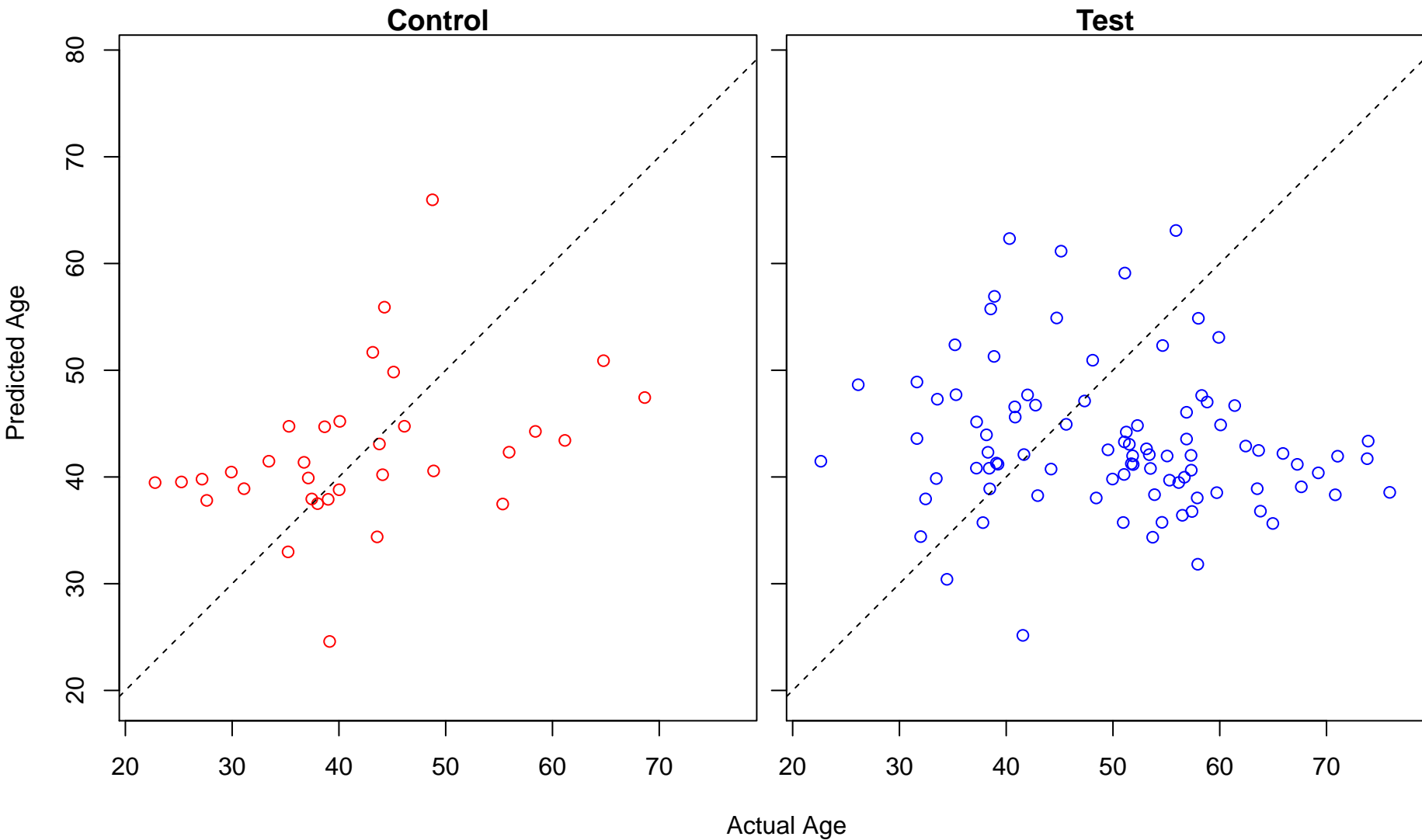
negative regulation of transferase activity (Score: 0.646839)



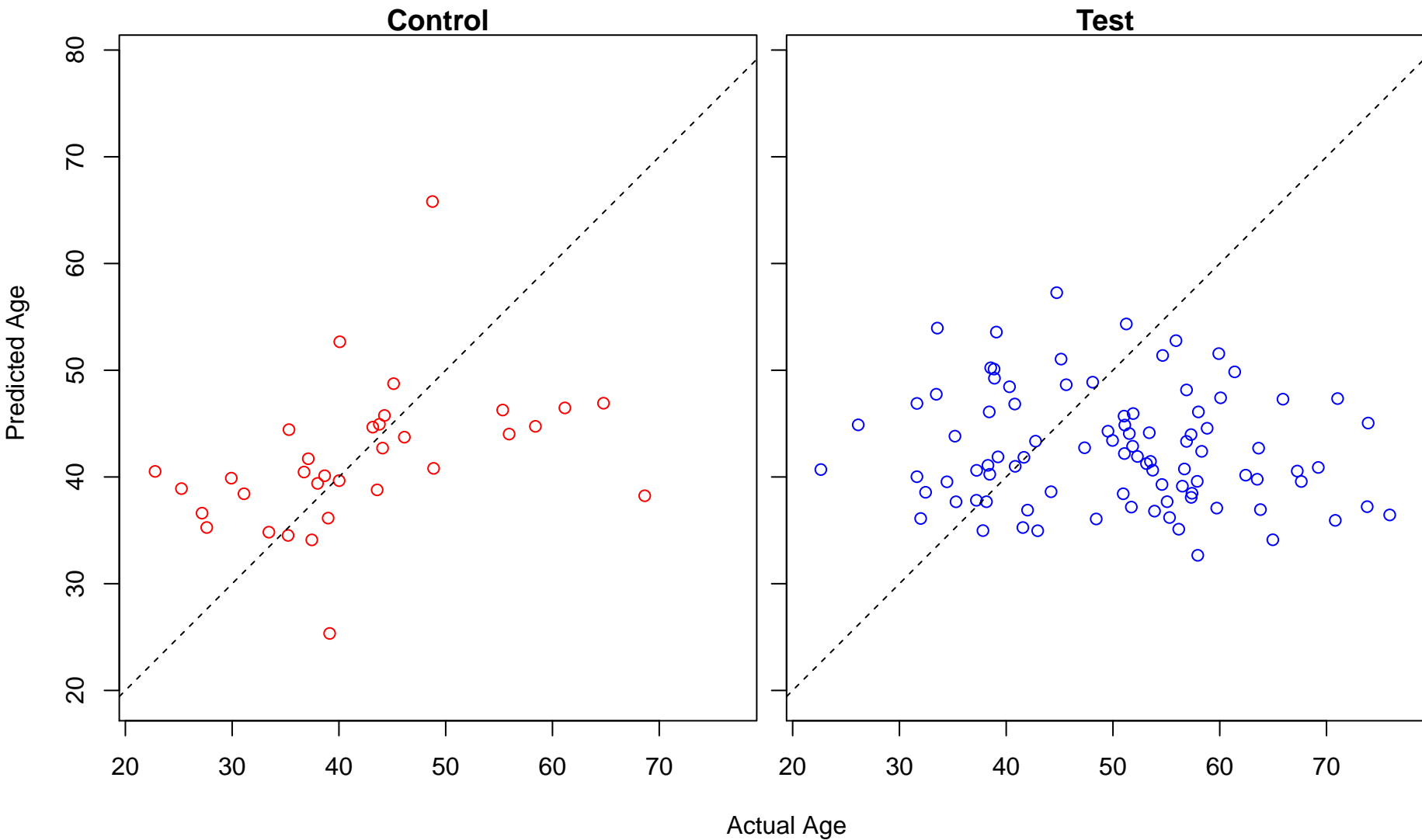
cellular nitrogen compound metabolic process (Score: 0.646695)



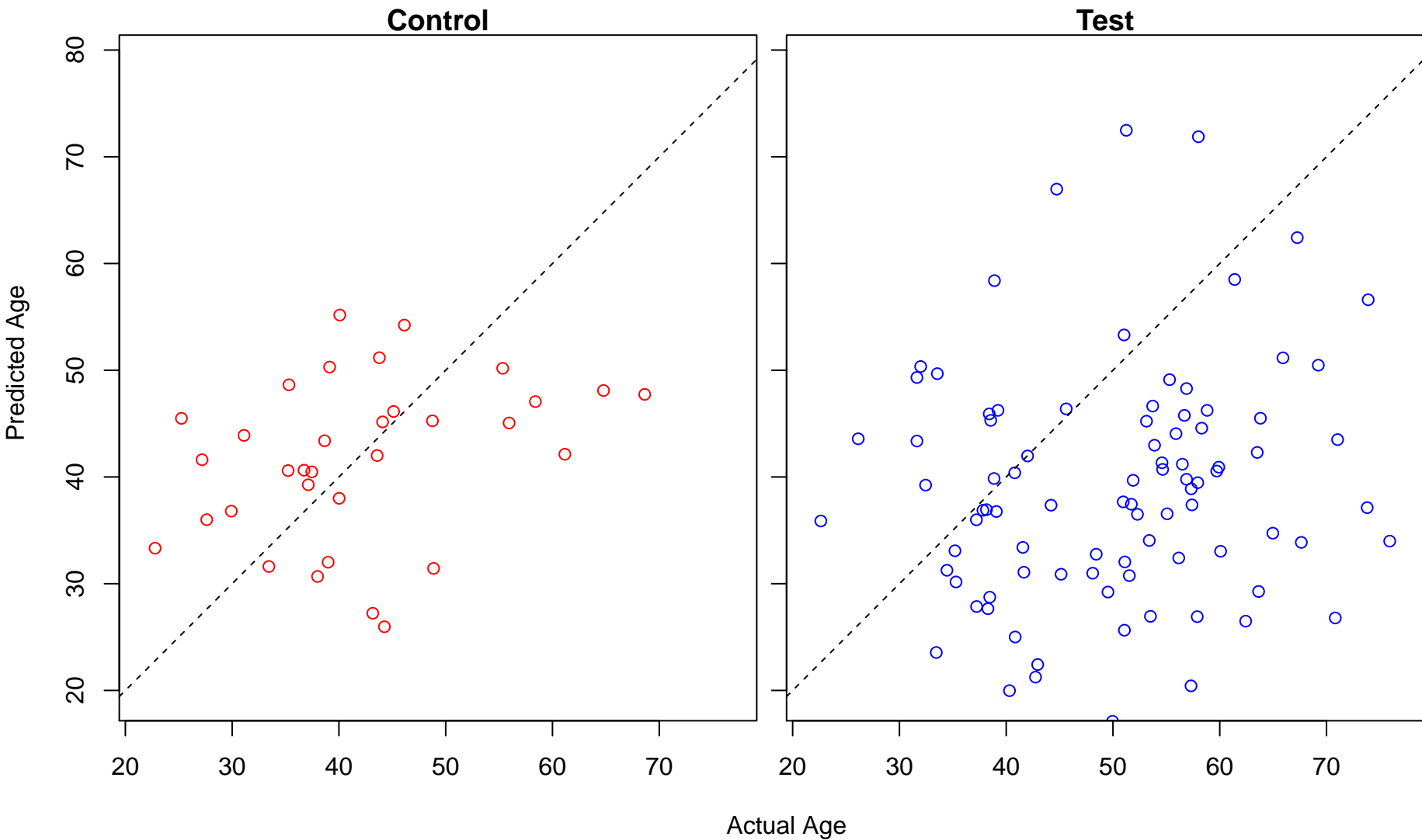
lipid particle organization (Score: 0.646660)



positive regulation of signal transduction (Score: 0.646525)

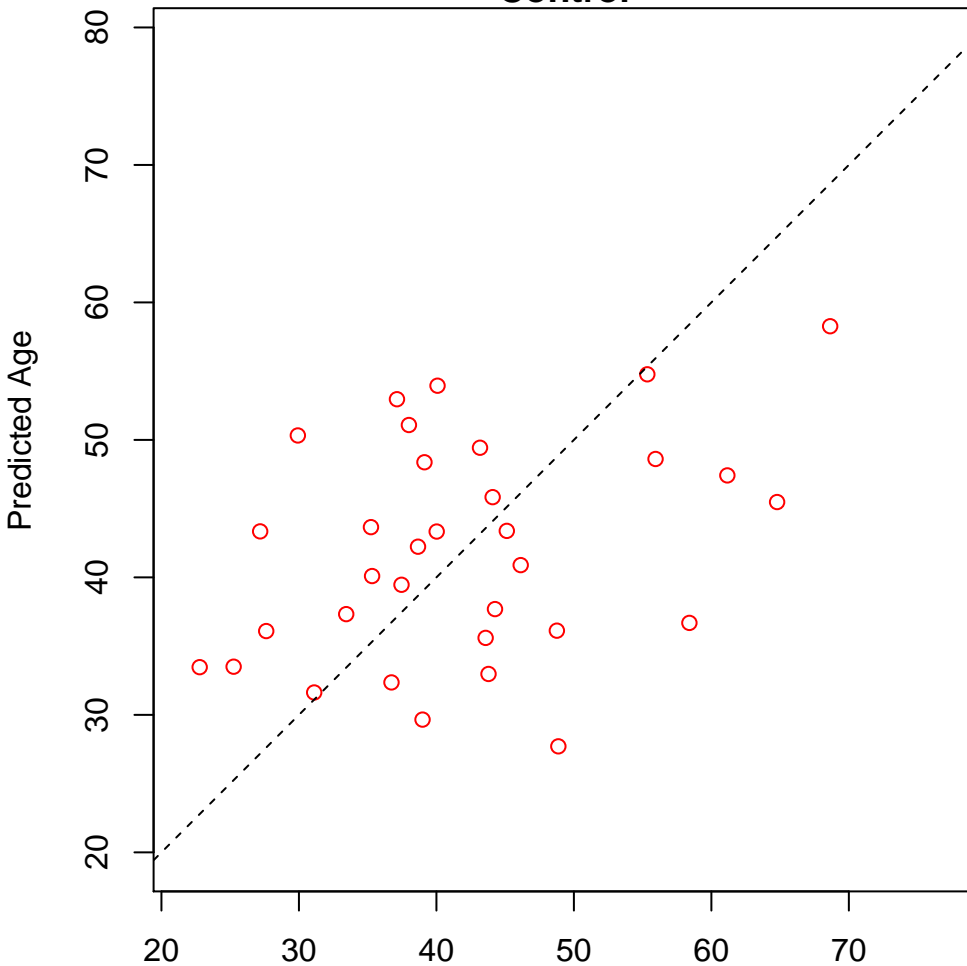


regulation of heart morphogenesis (Score: 0.646413)

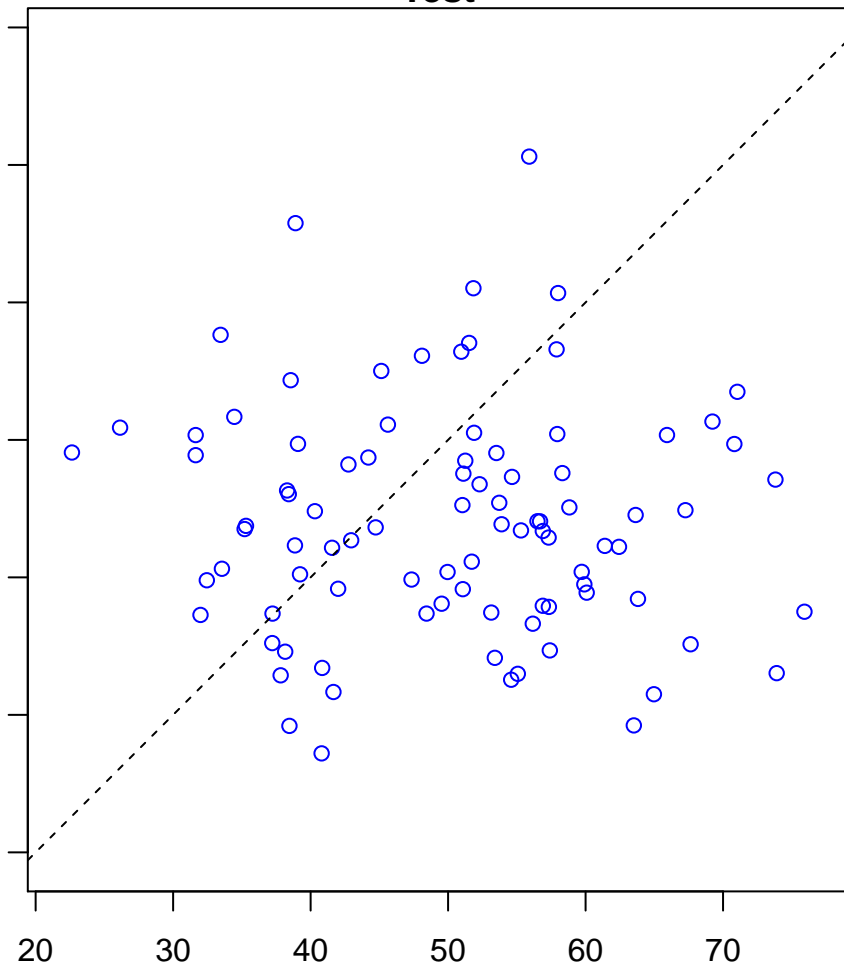


renal system vasculature development (Score: 0.646267)

Control

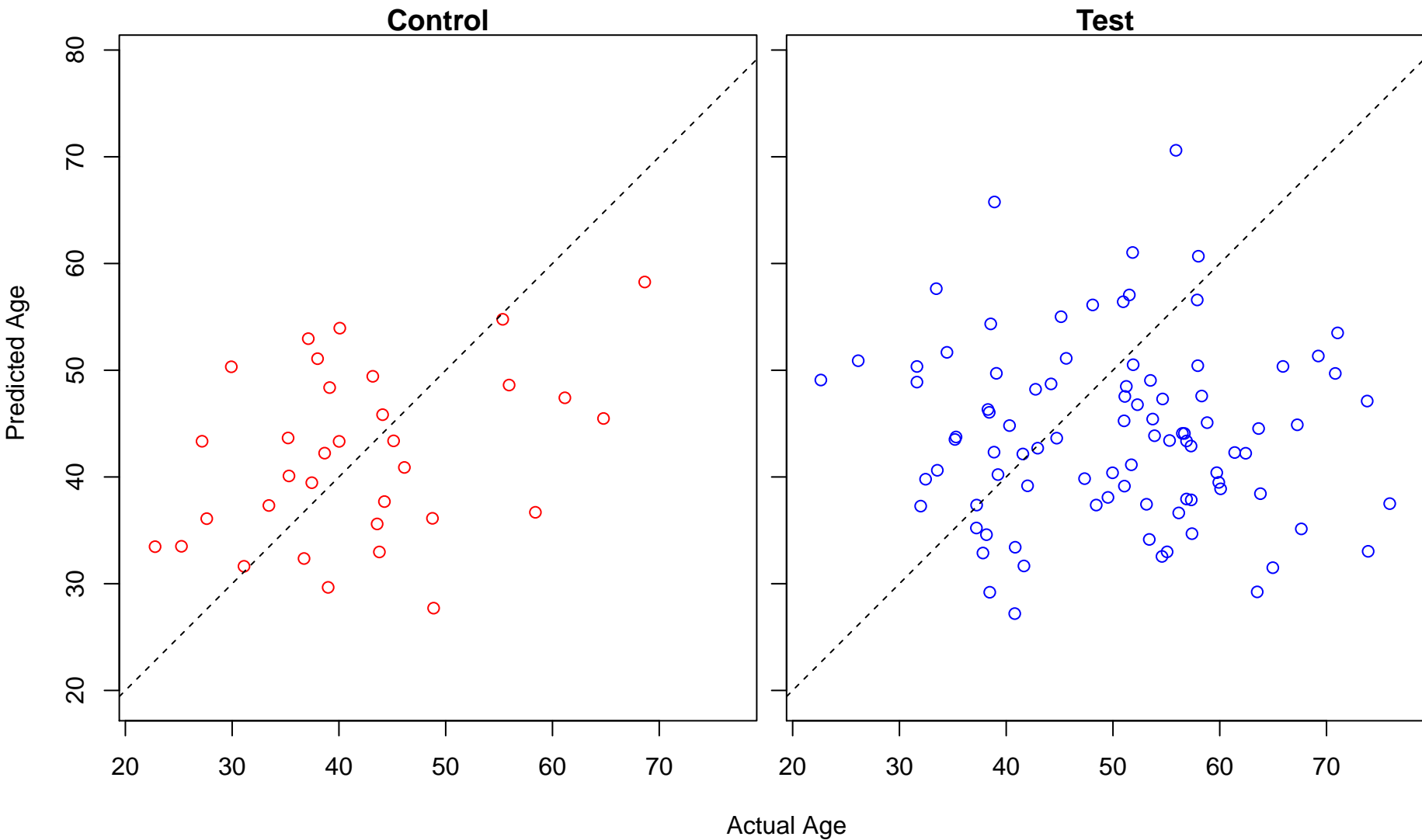


Test

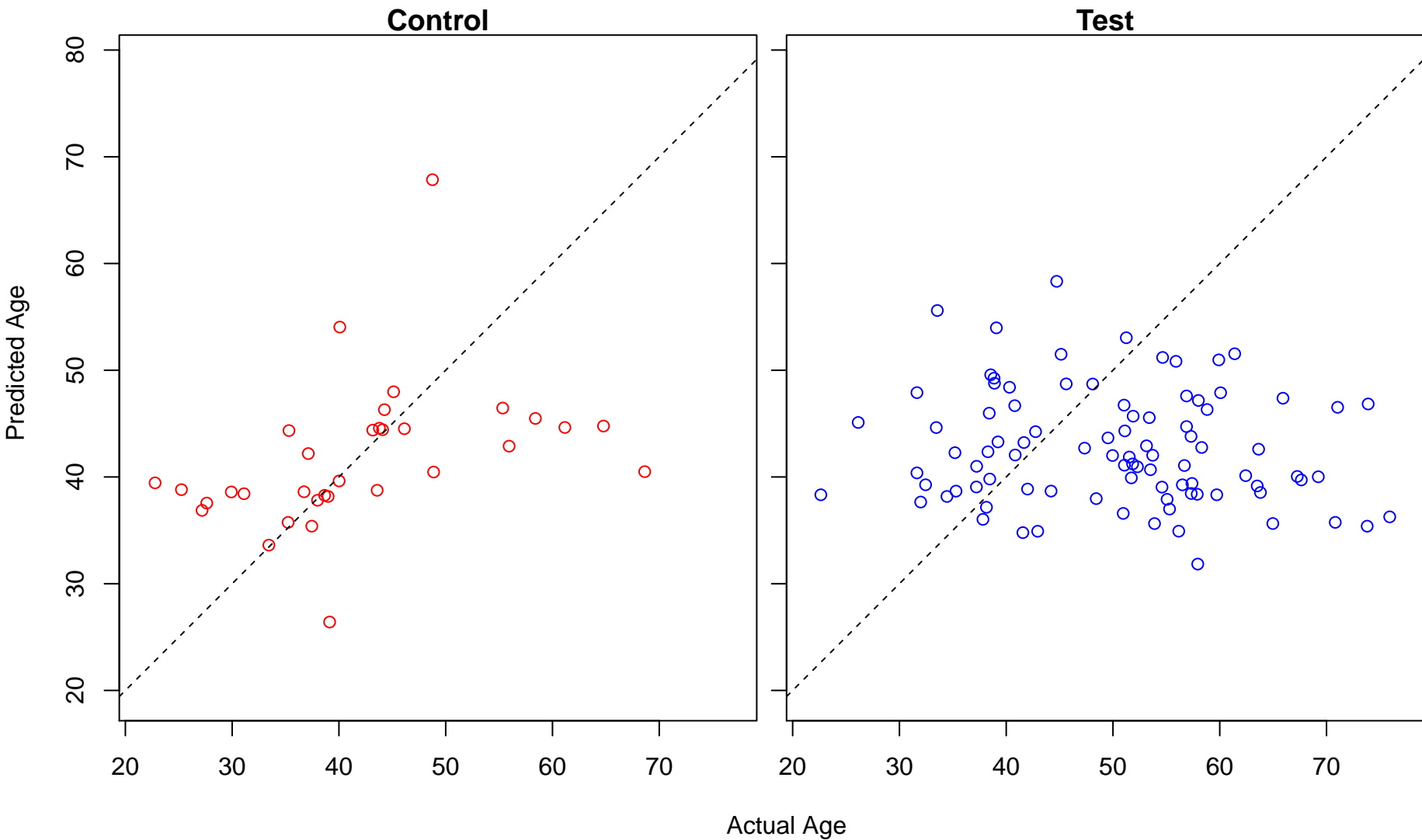


Actual Age

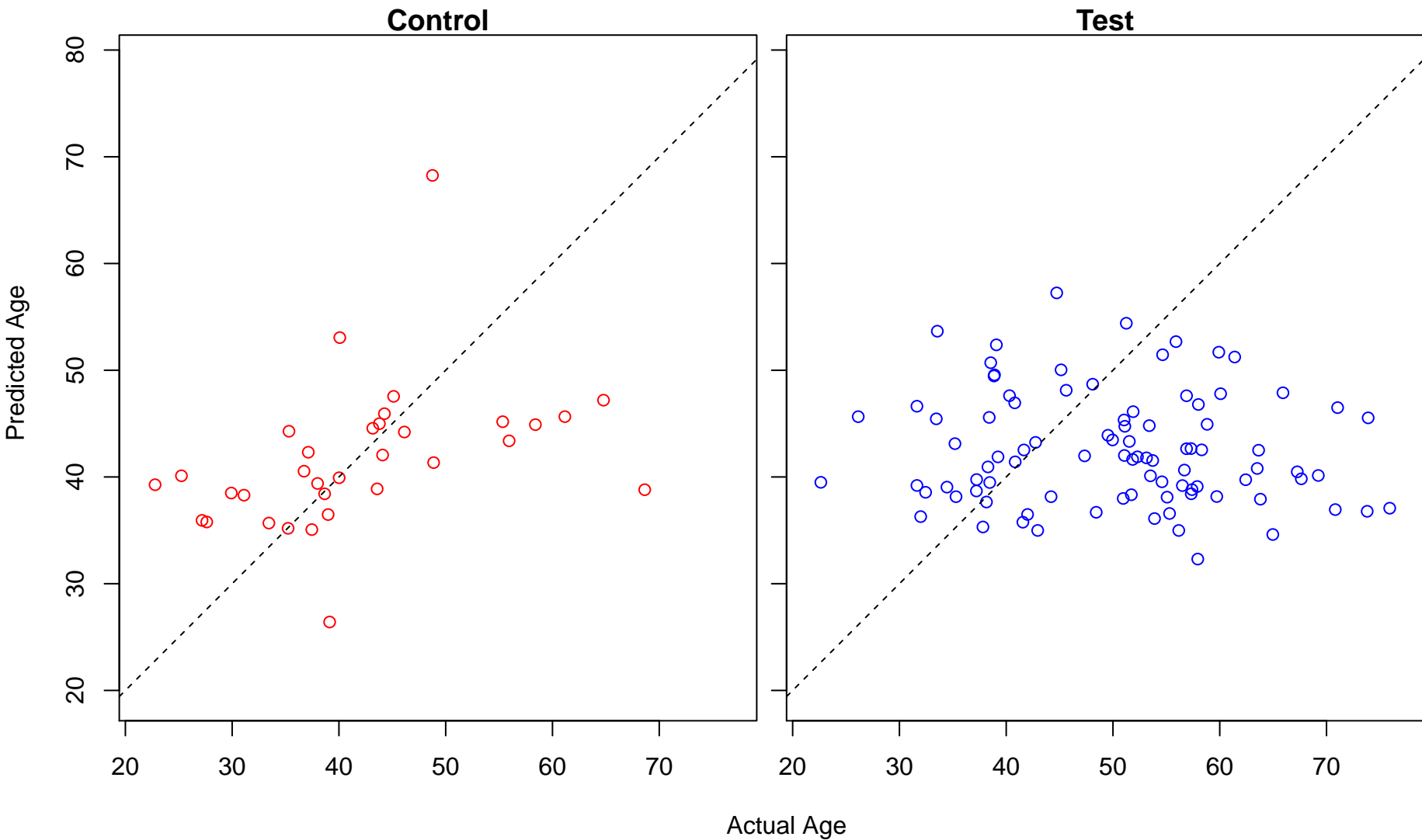
kidney vasculature development (Score: 0.646267)



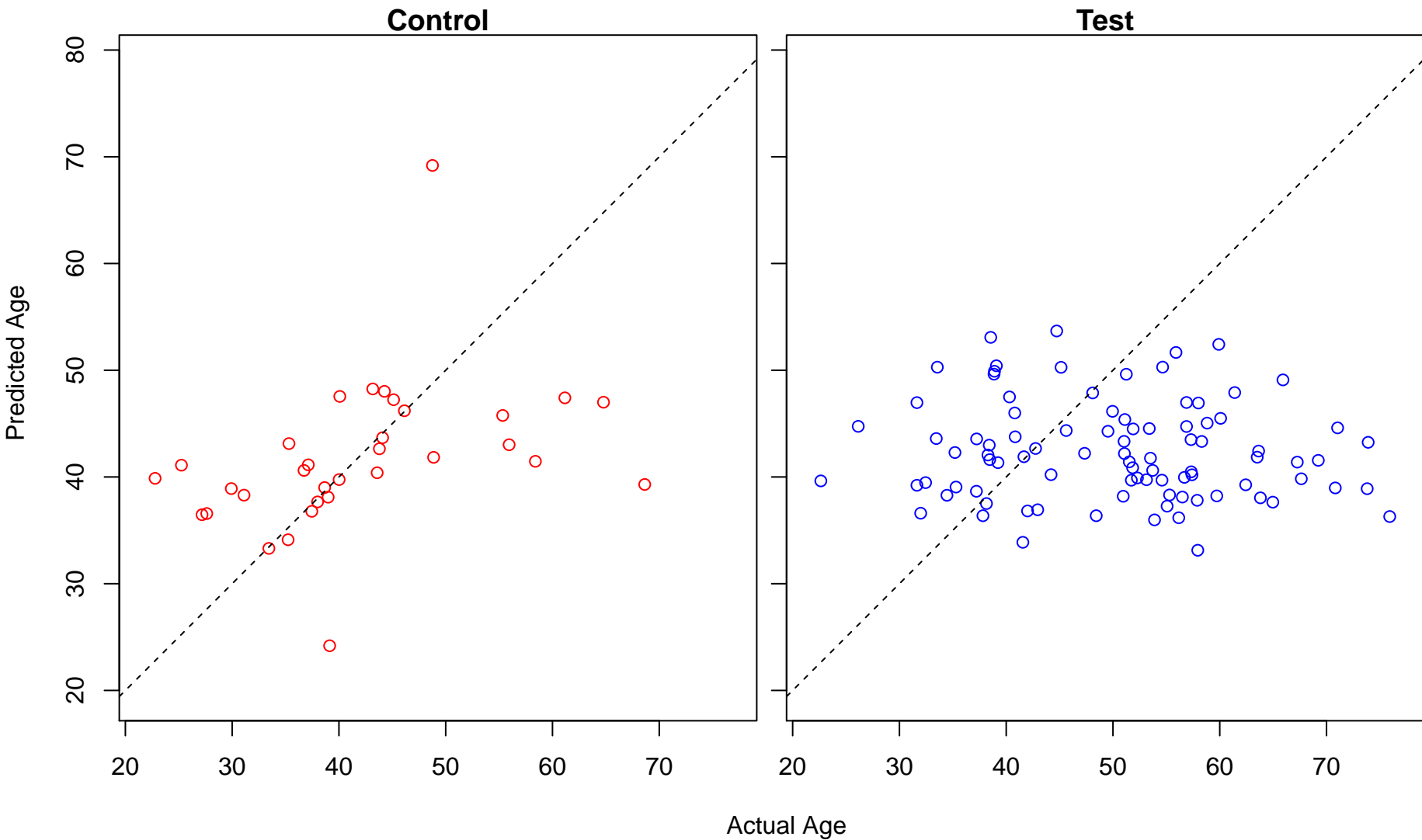
regulation of protein kinase activity (Score: 0.646242)



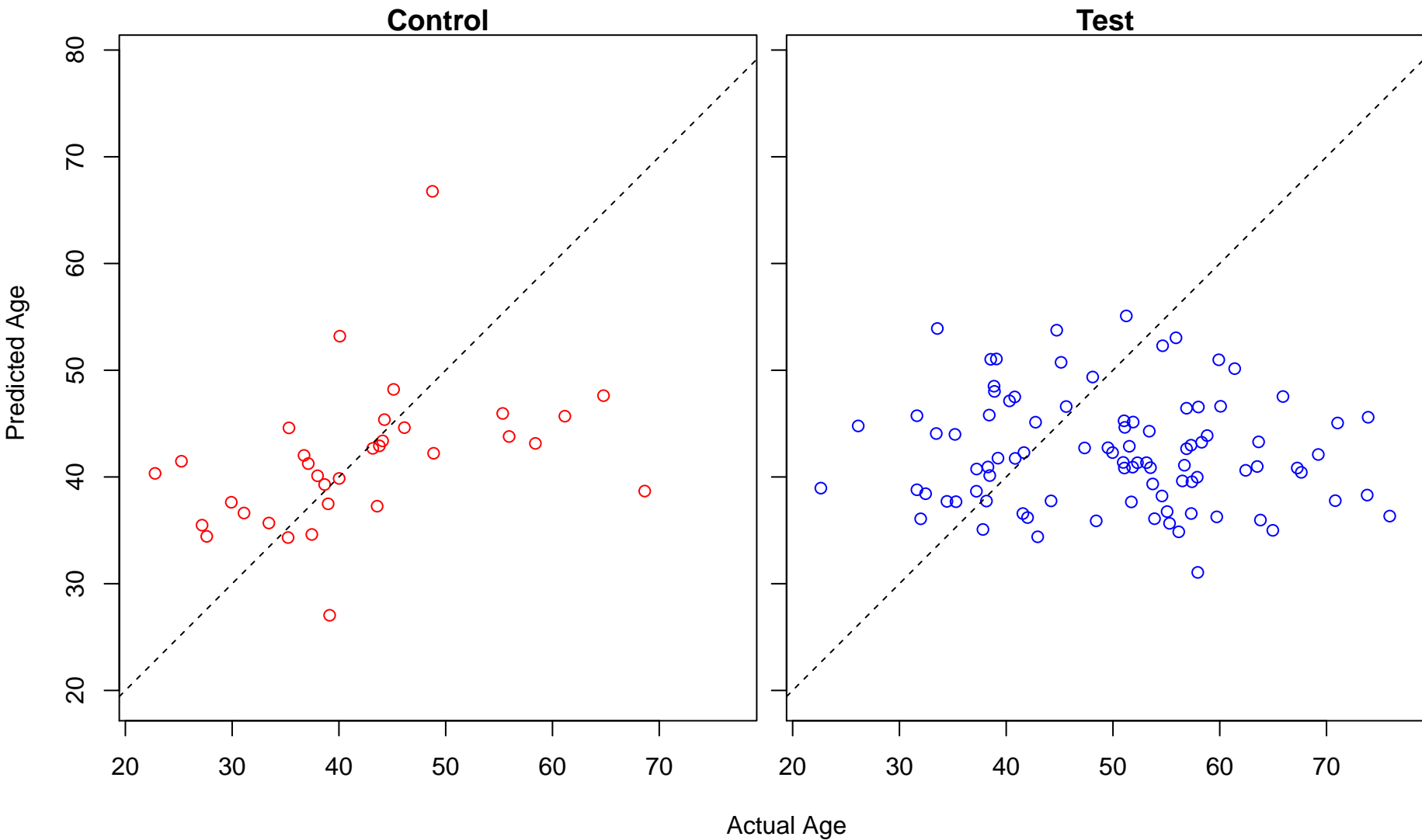
regulation of signaling (Score: 0.646205)



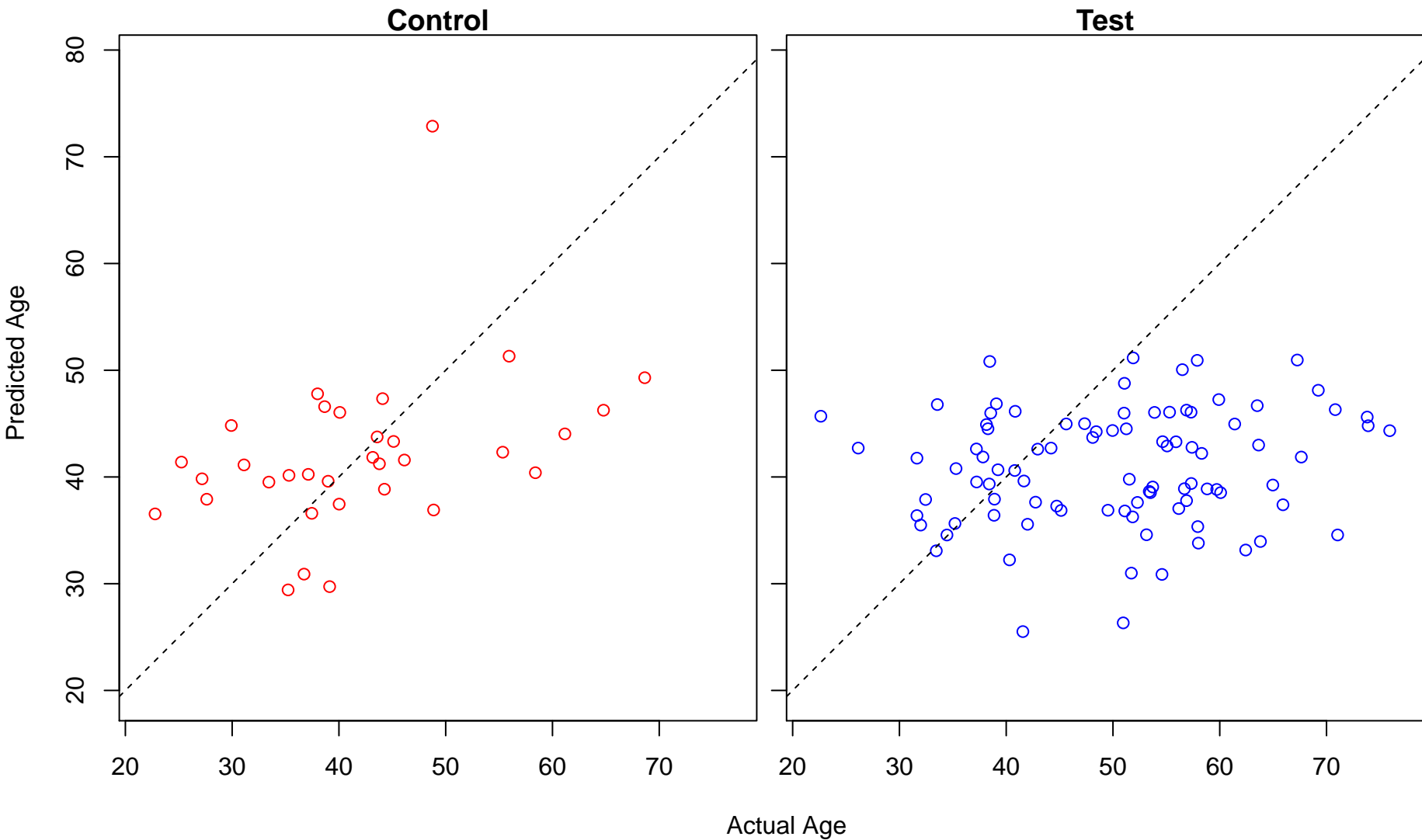
cell cycle (Score: 0.646152)



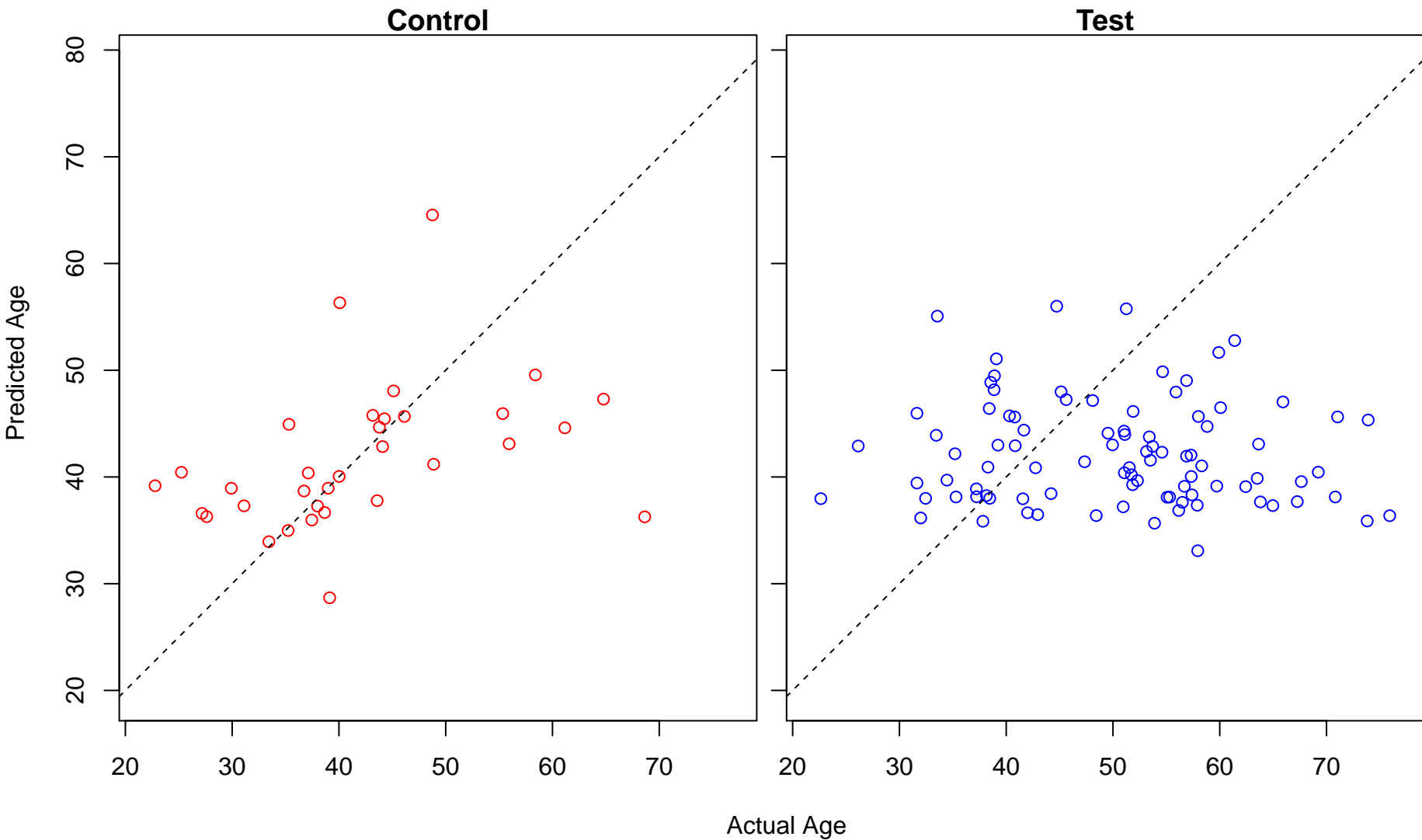
regulation of cell death (Score: 0.646074)



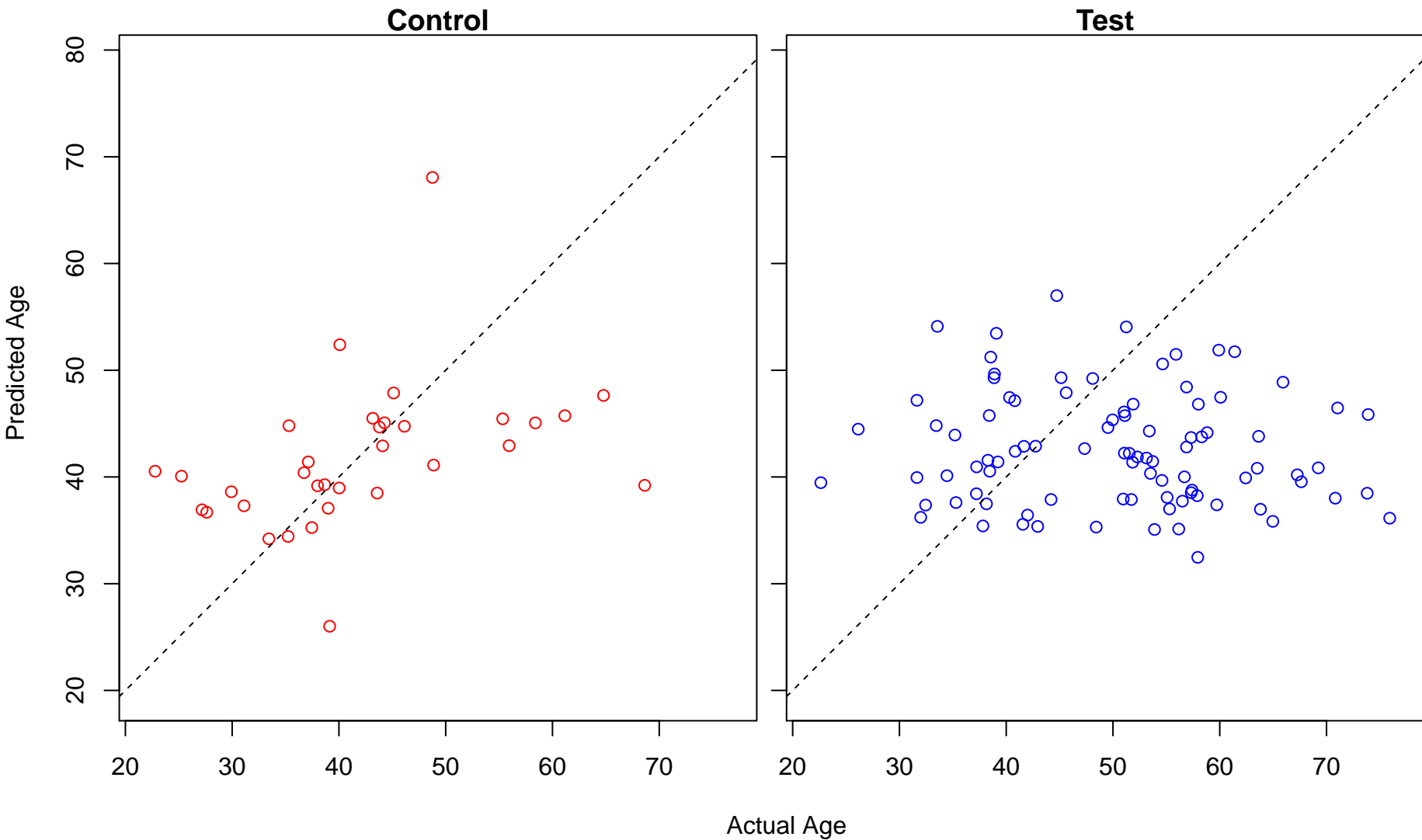
glutamate catabolic process (Score: 0.645948)



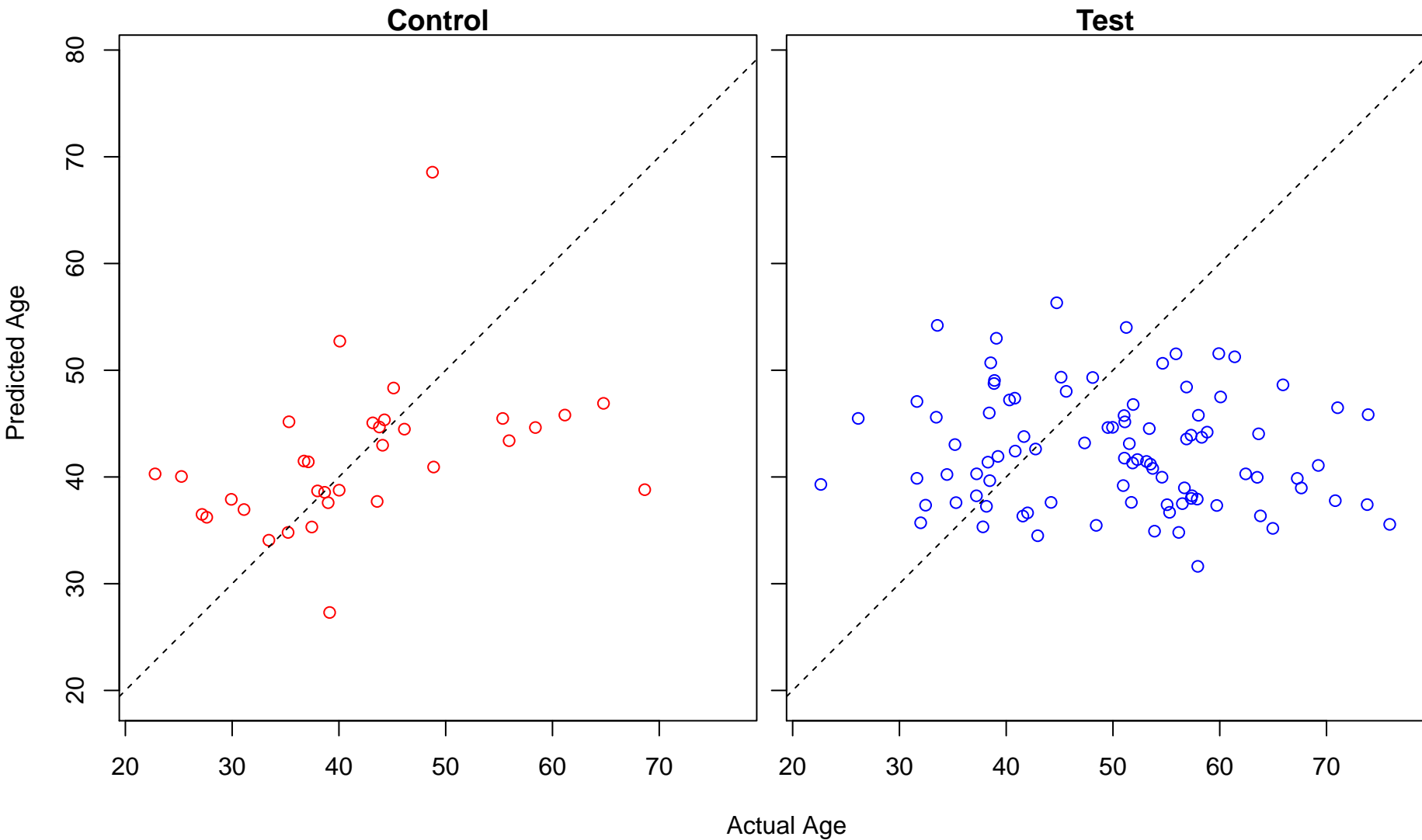
protein ubiquitination (Score: 0.645895)



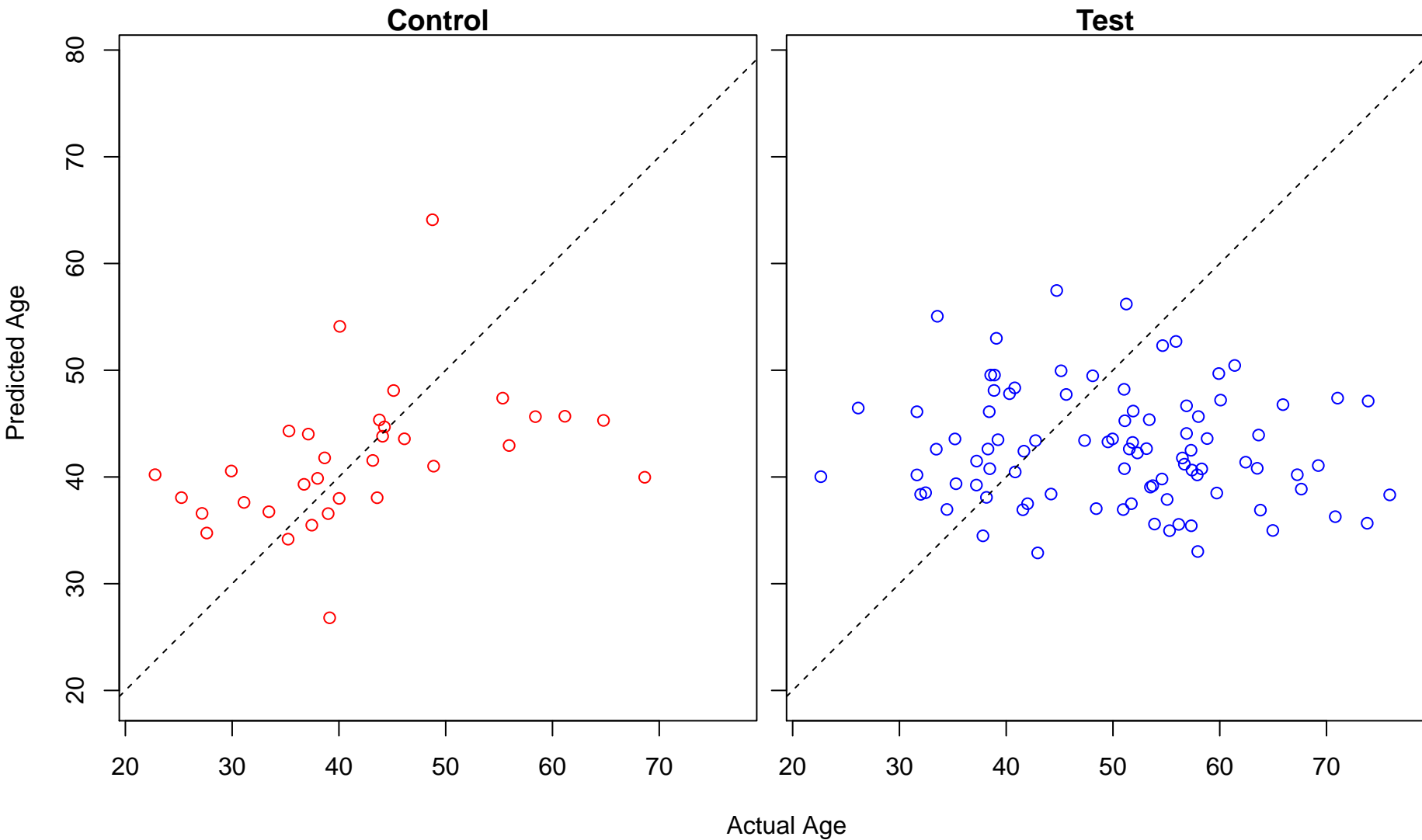
cellular component organization or biogenesis (Score: 0.645099)



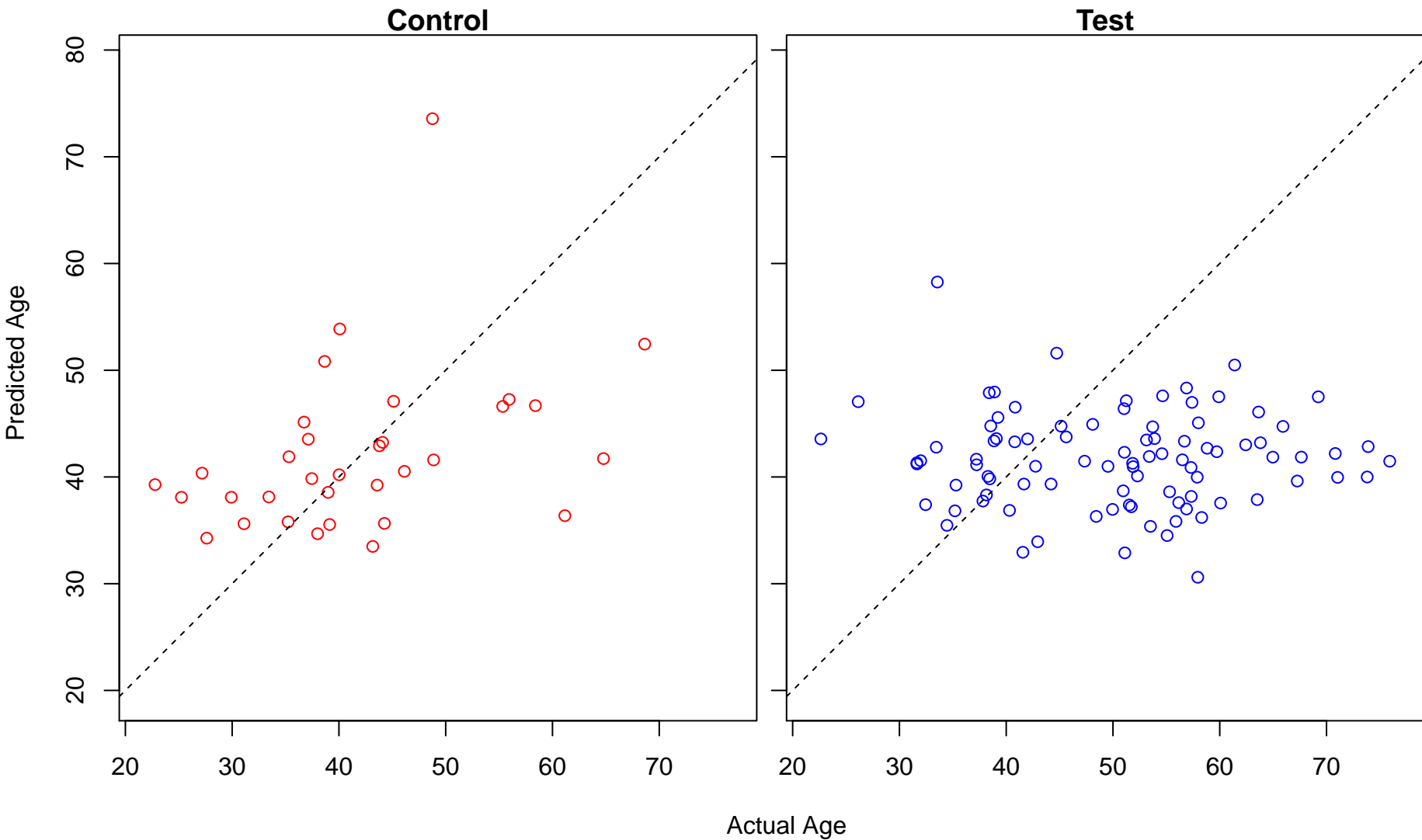
metabolic process (Score: 0.644751)



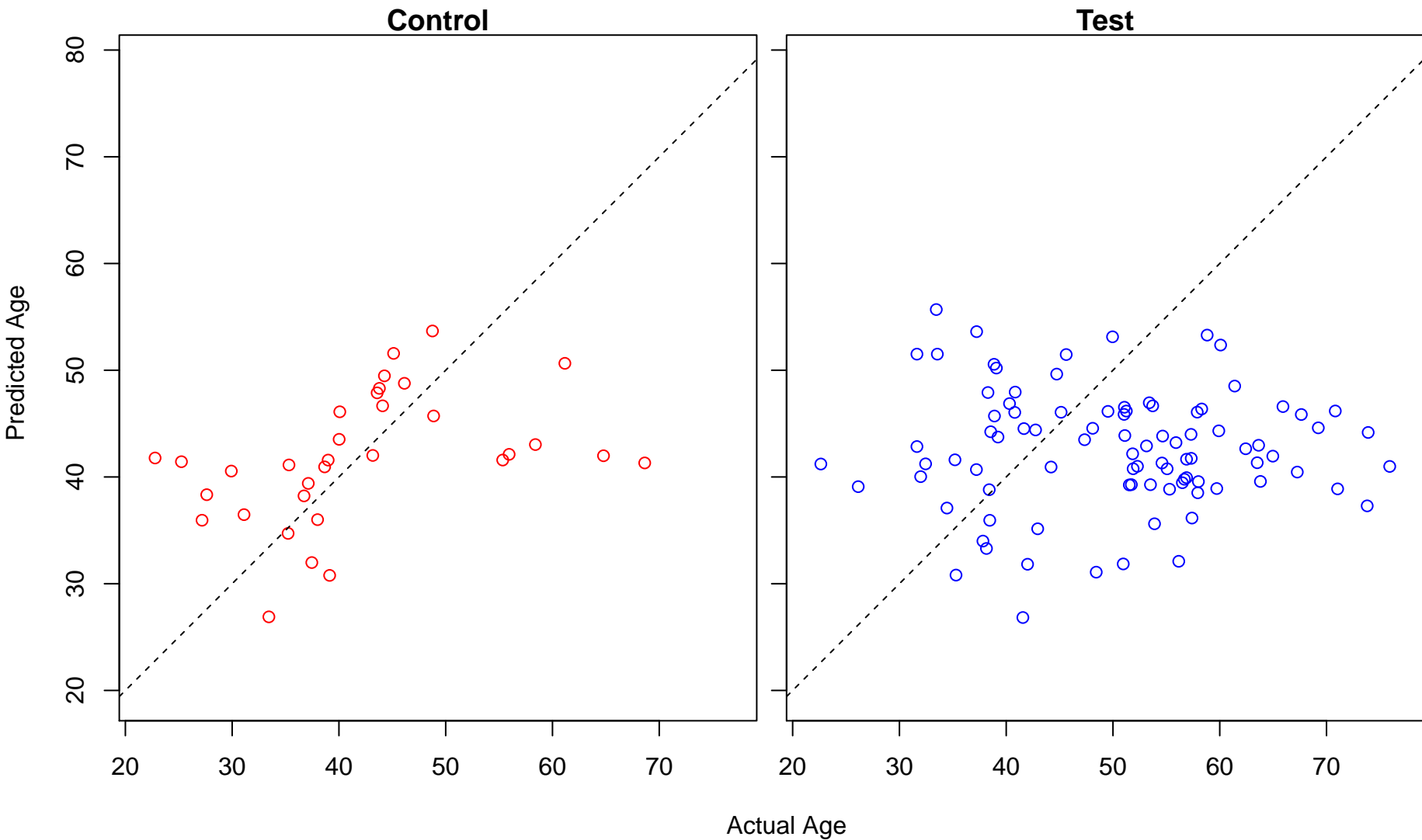
positive regulation of phosphorylation (Score: 0.644662)



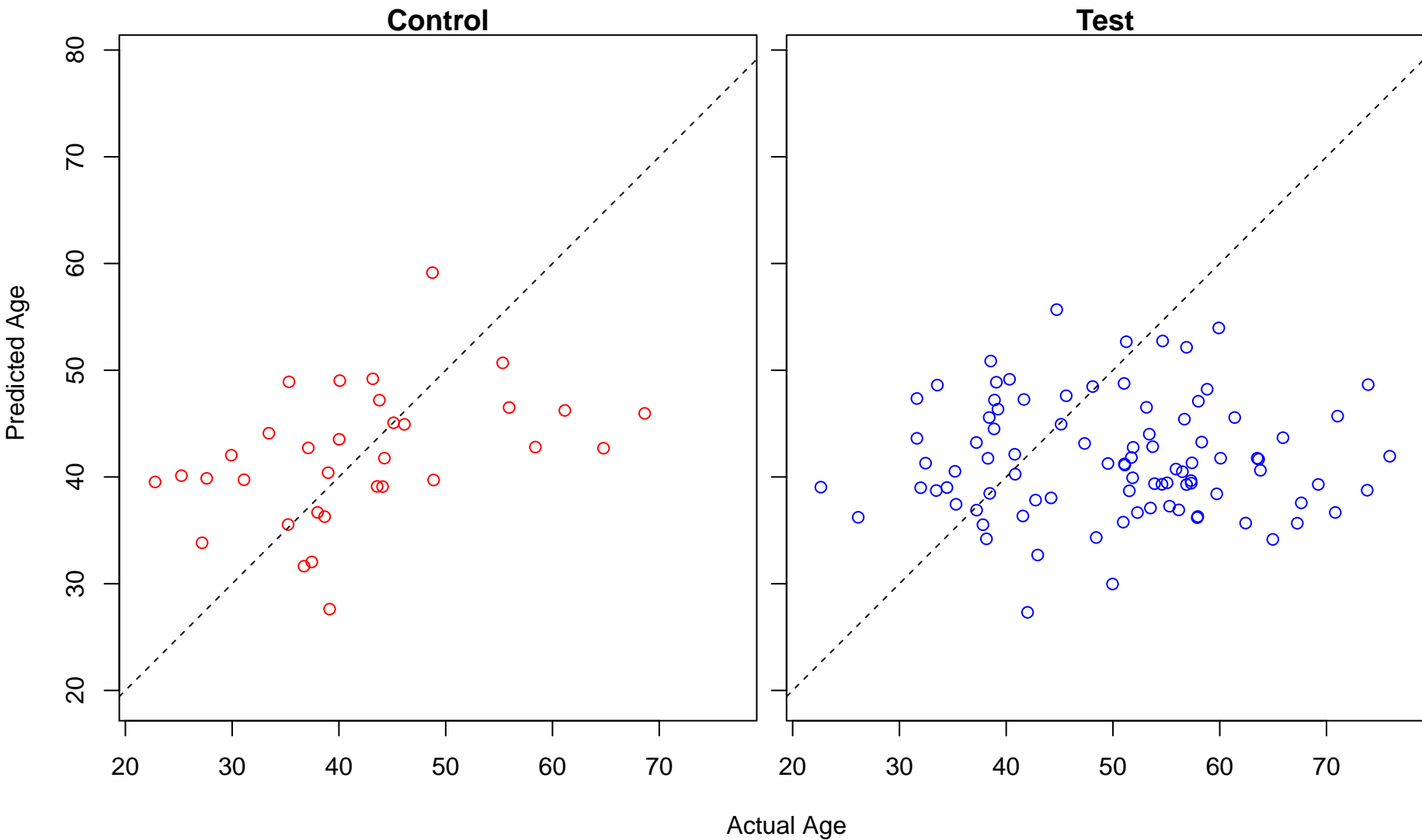
mRNA methylation (Score: 0.644594)



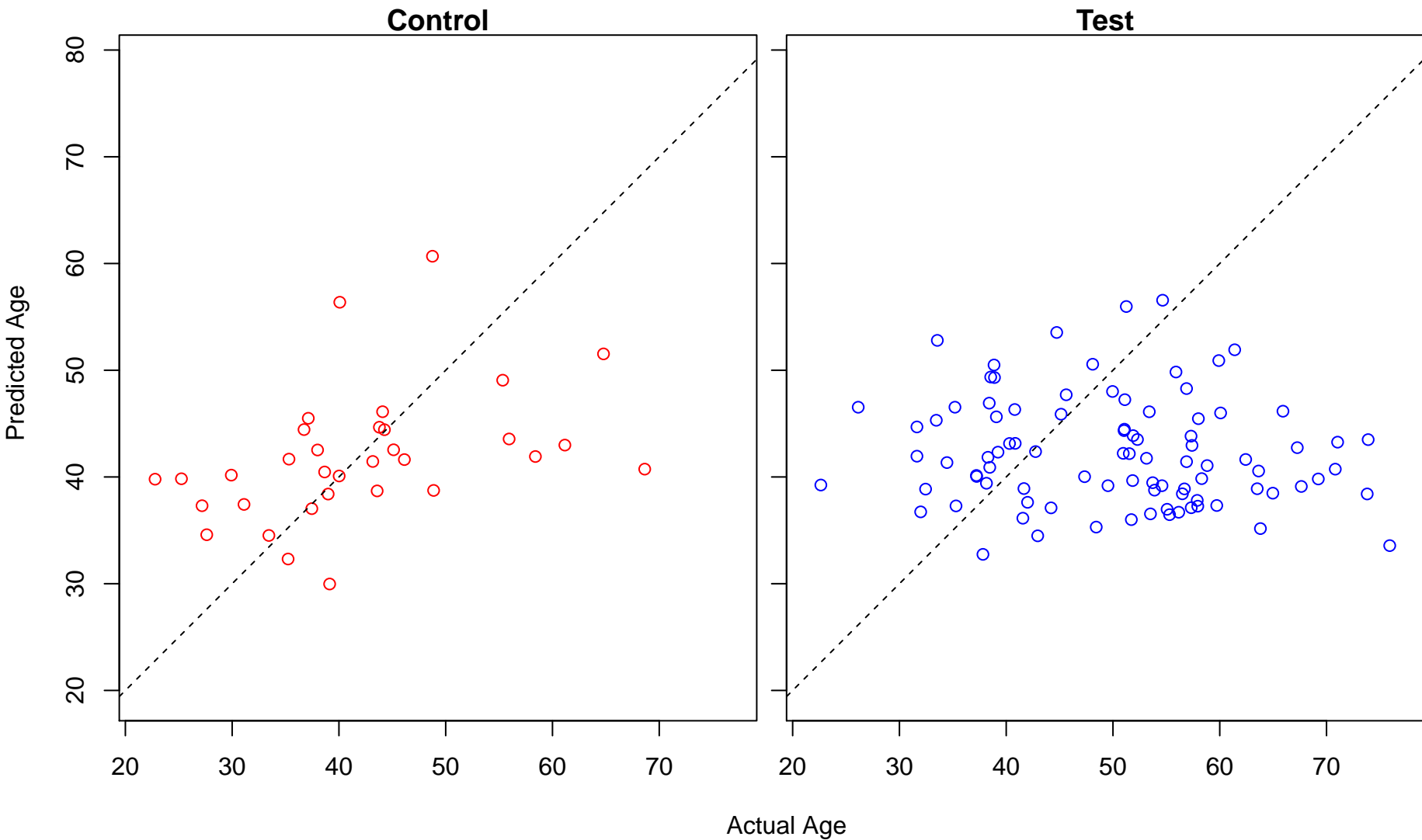
regulation of developmental pigmentation (Score: 0.644387)



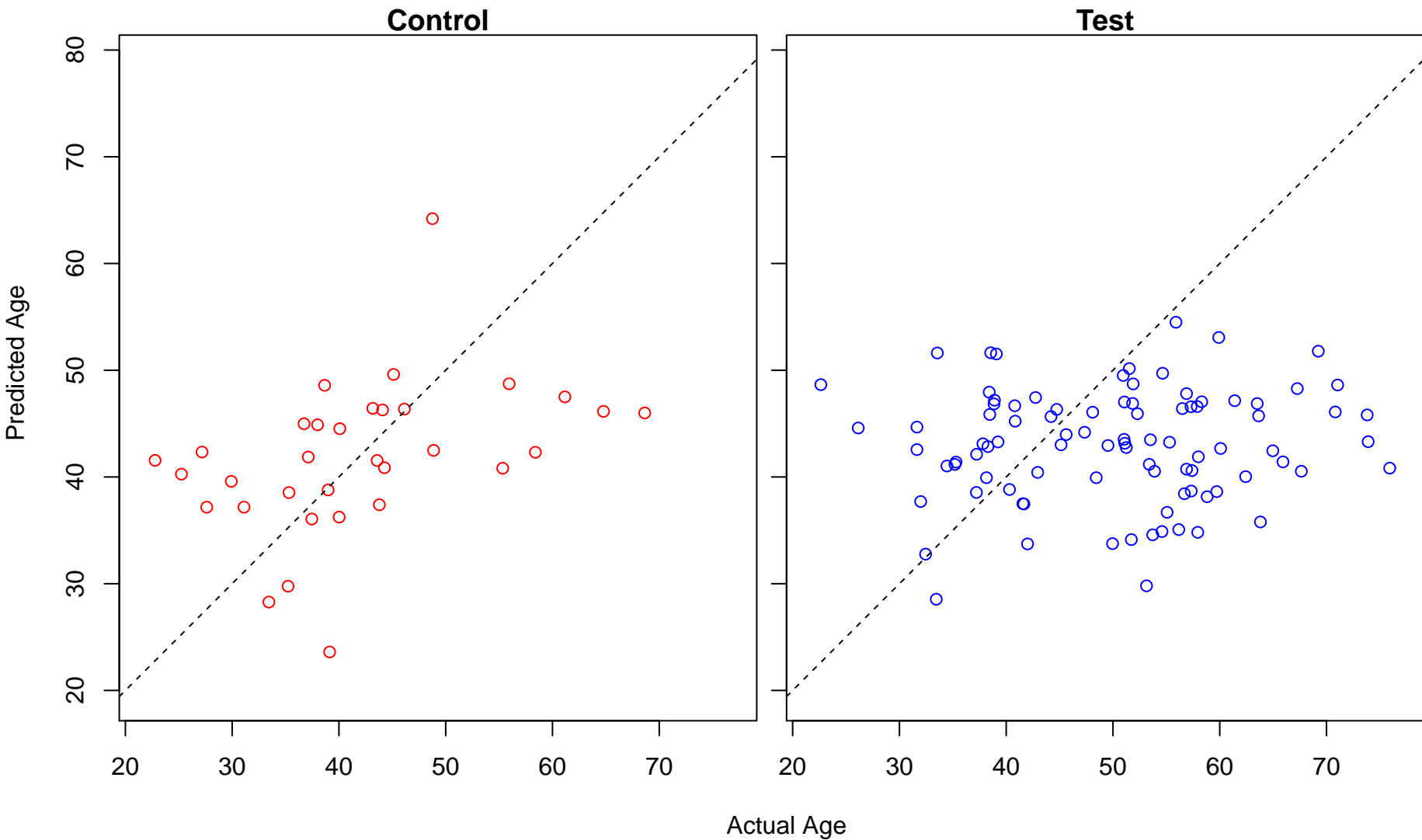
small RNA loading onto RISC (Score: 0.644077)



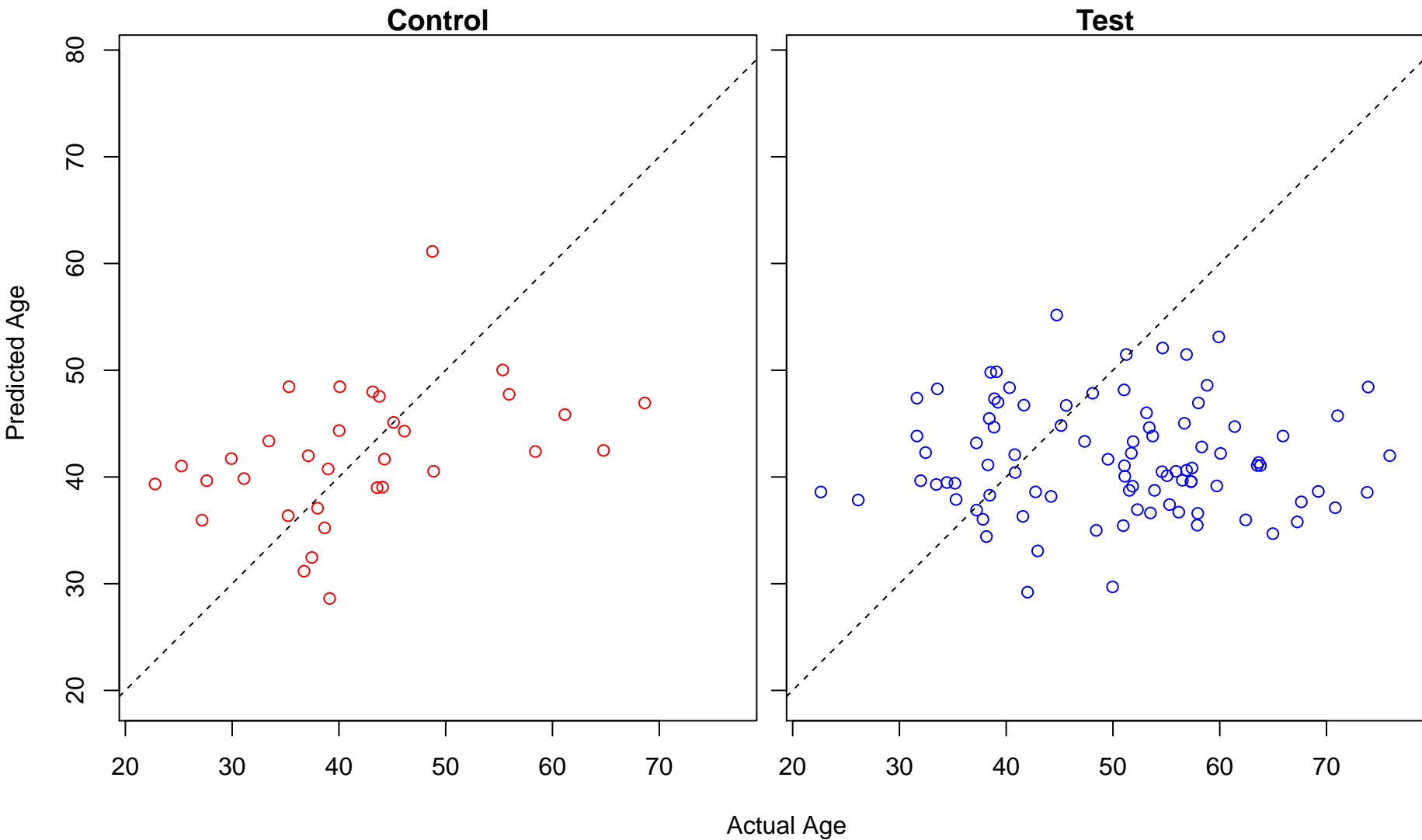
organ morphogenesis (Score: 0.643977)



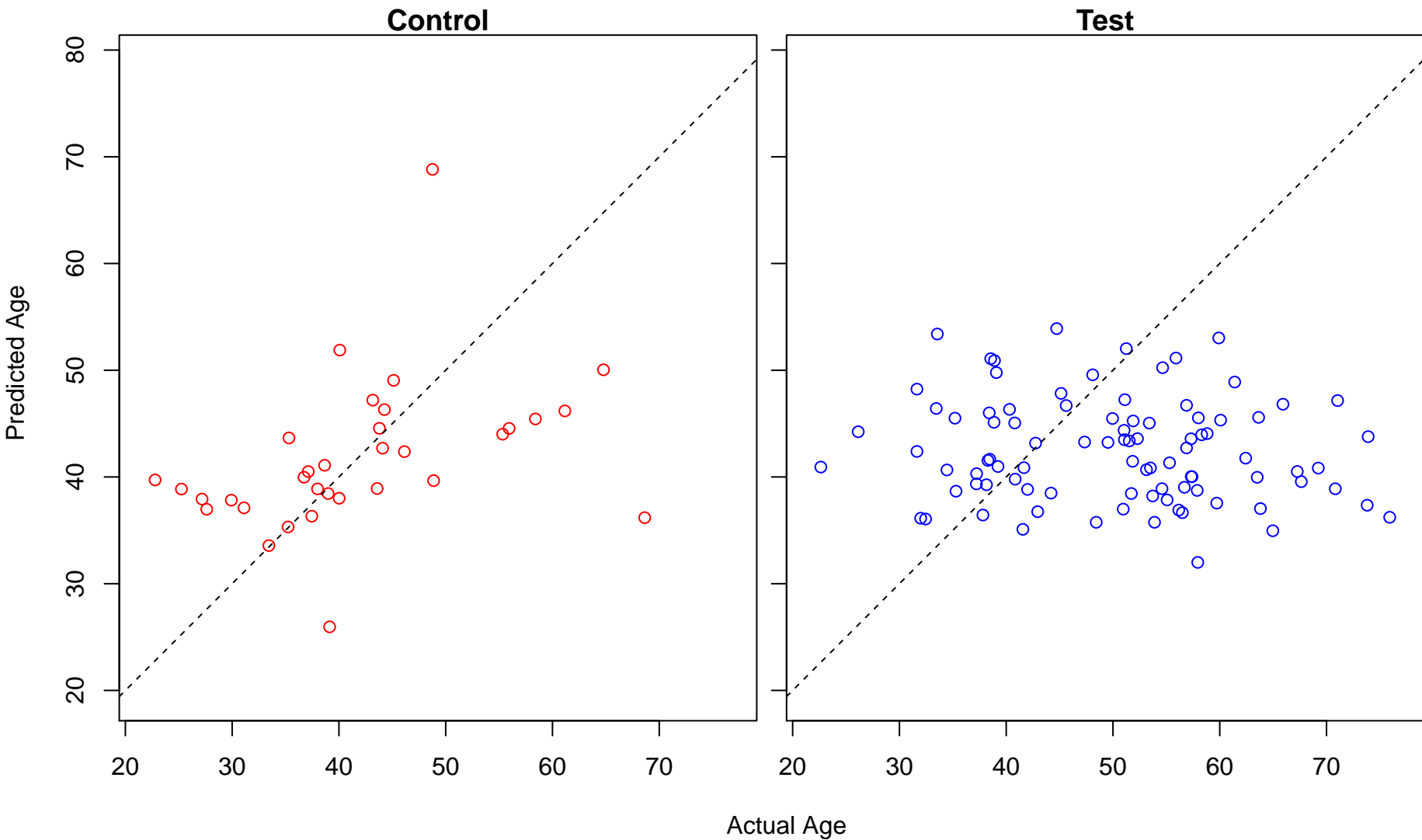
regulation of interleukin-23 production (Score: 0.643964)



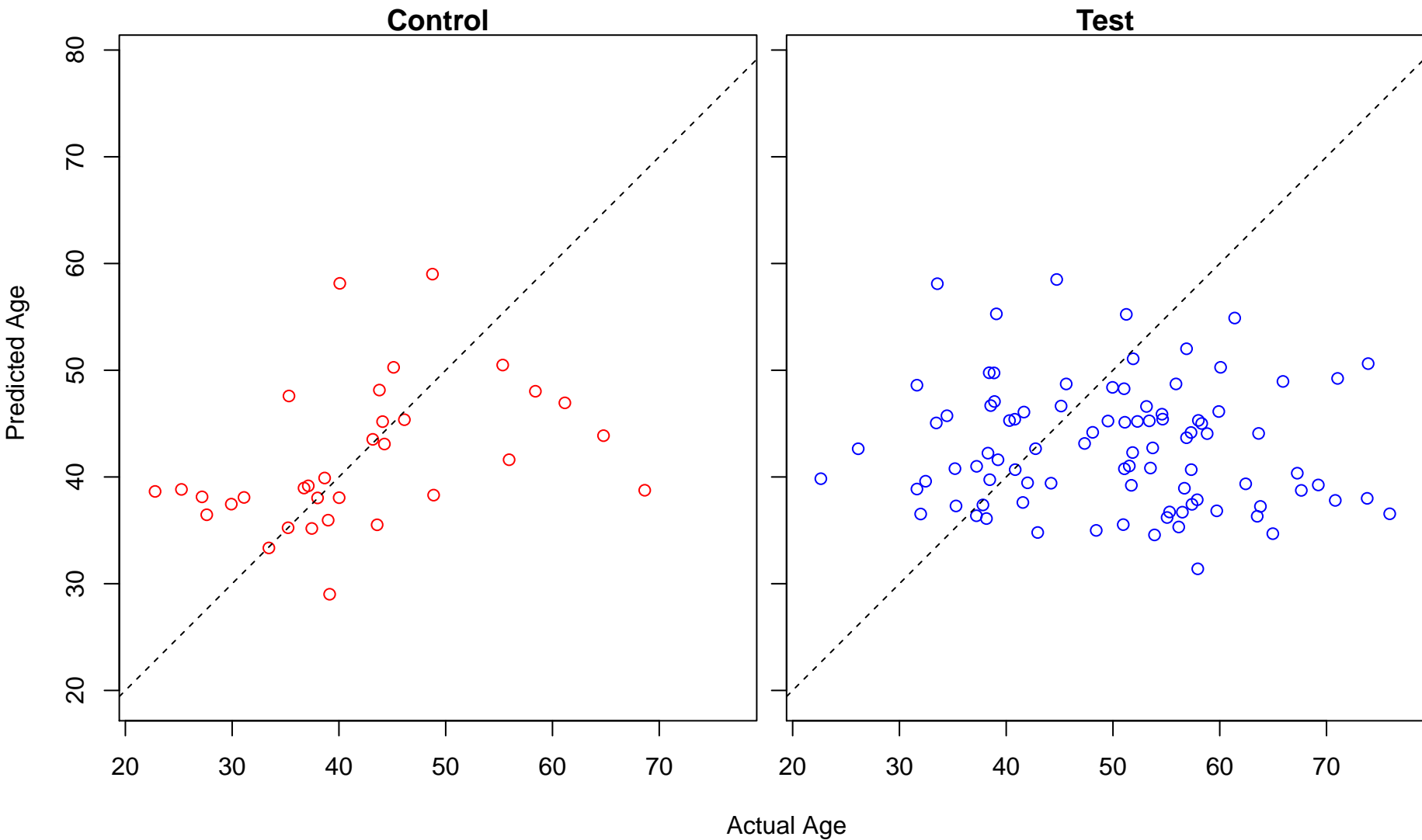
pre-miRNA processing (Score: 0.643729)



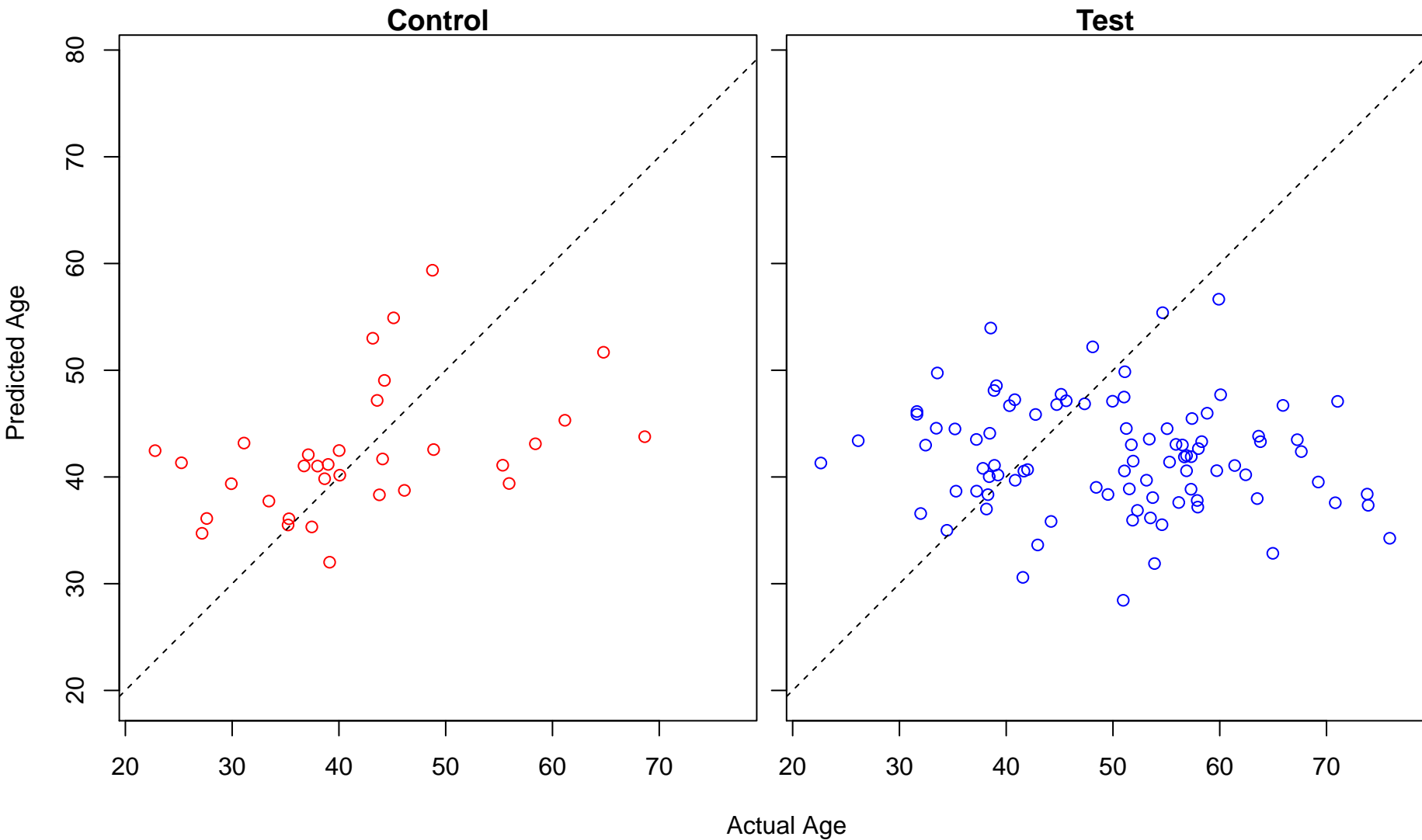
lipid biosynthetic process (Score: 0.643717)



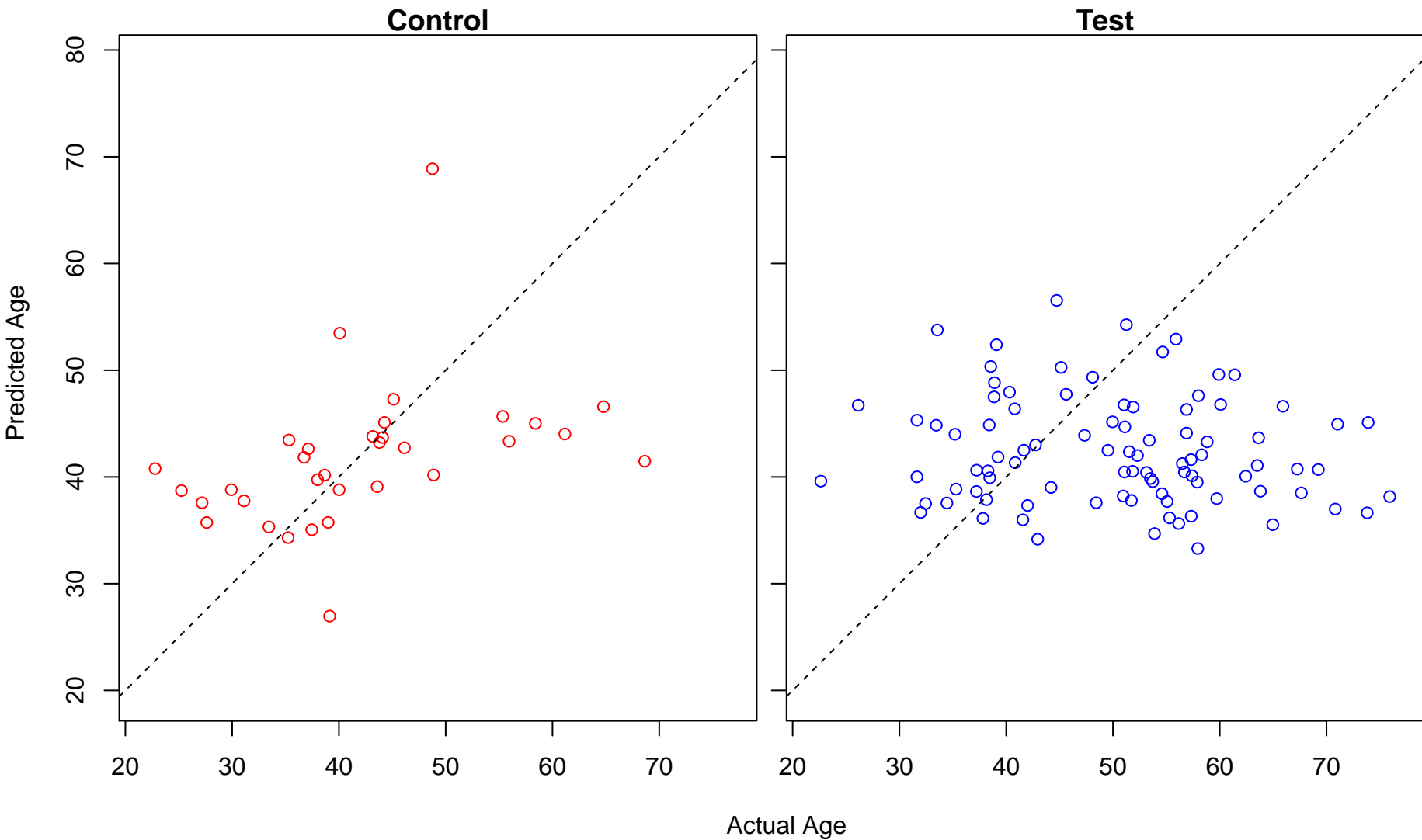
regulation of DNA metabolic process (Score: 0.643565)



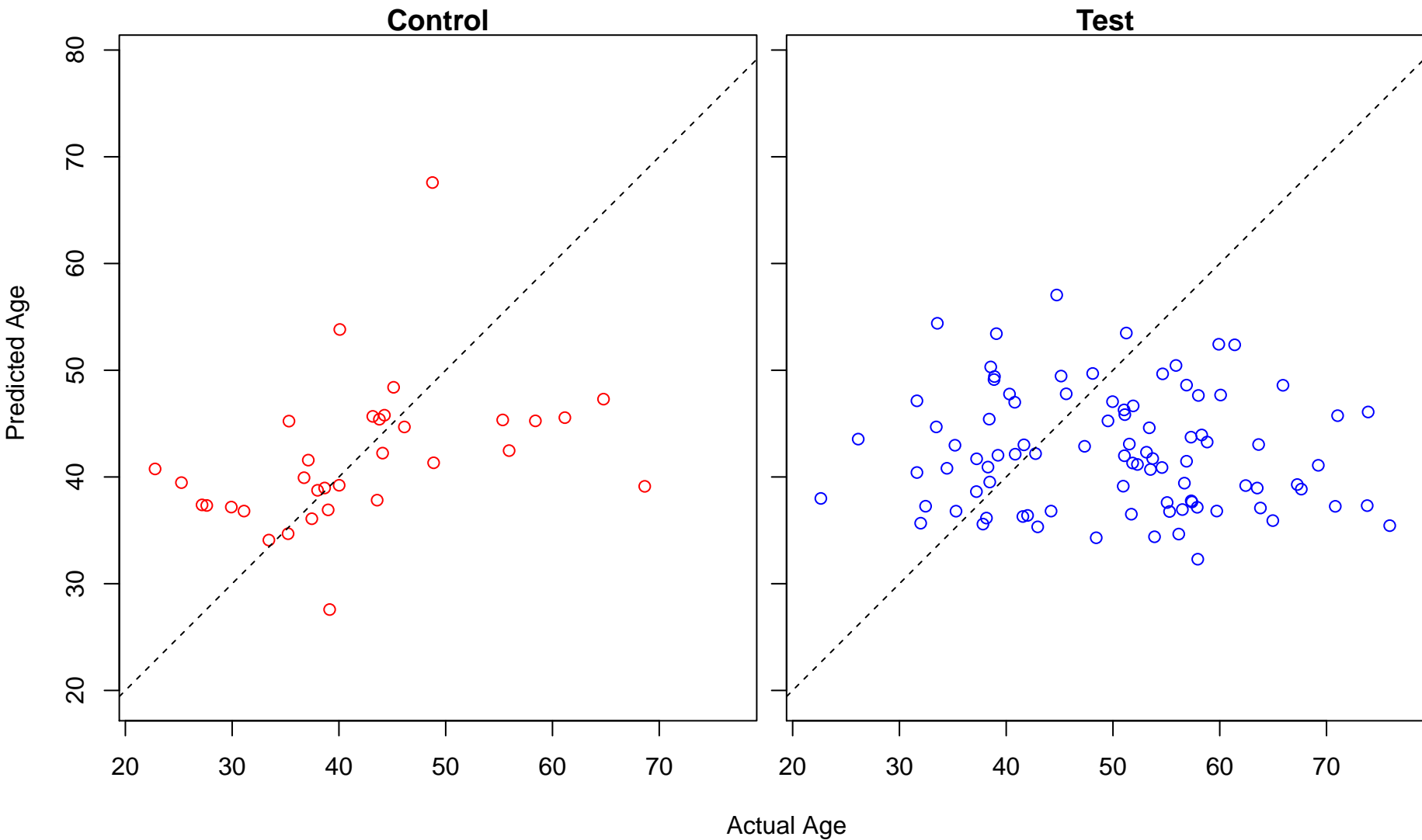
negative regulation of T-helper cell differentiation (Score: 0.643443)



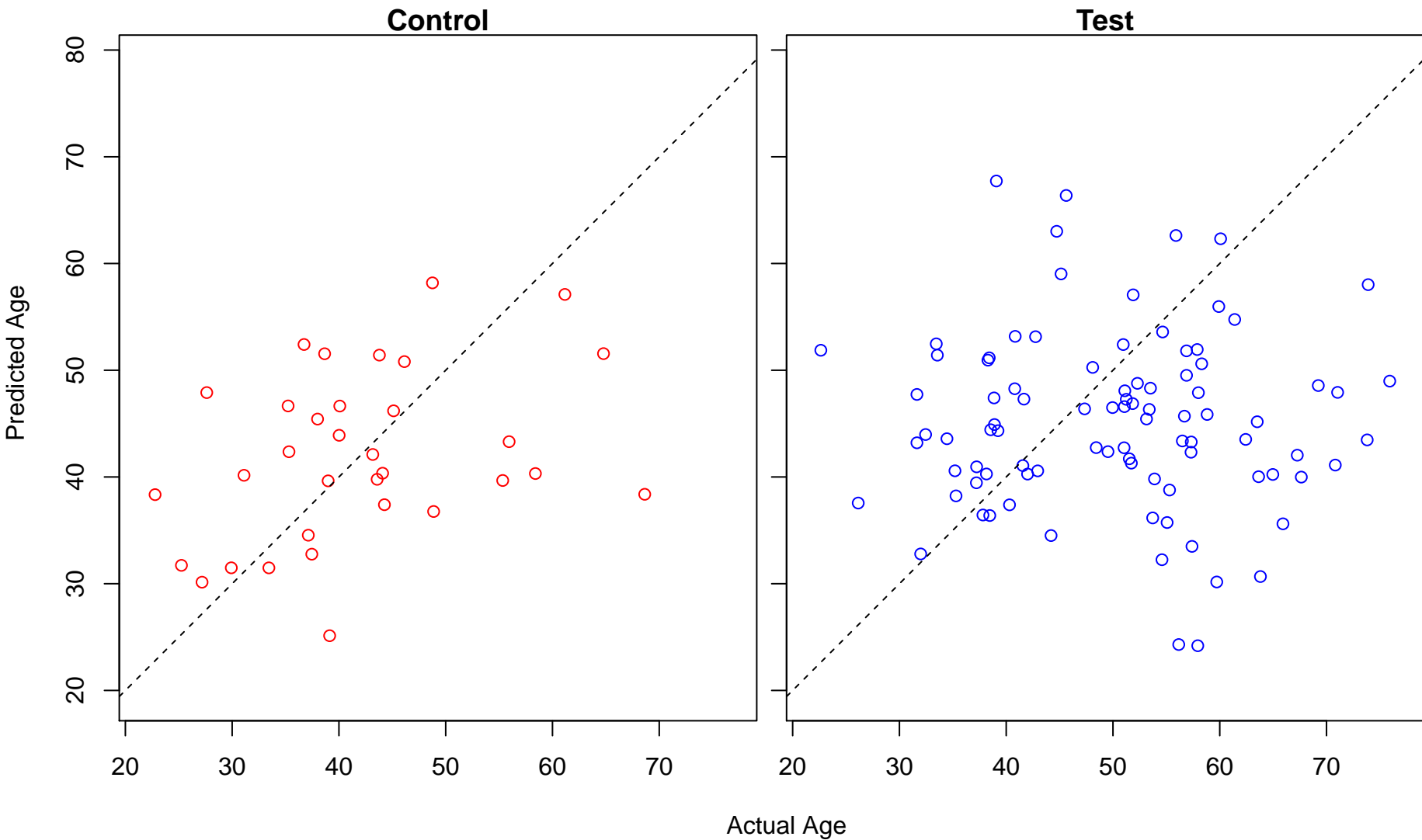
positive regulation of molecular function (Score: 0.642711)



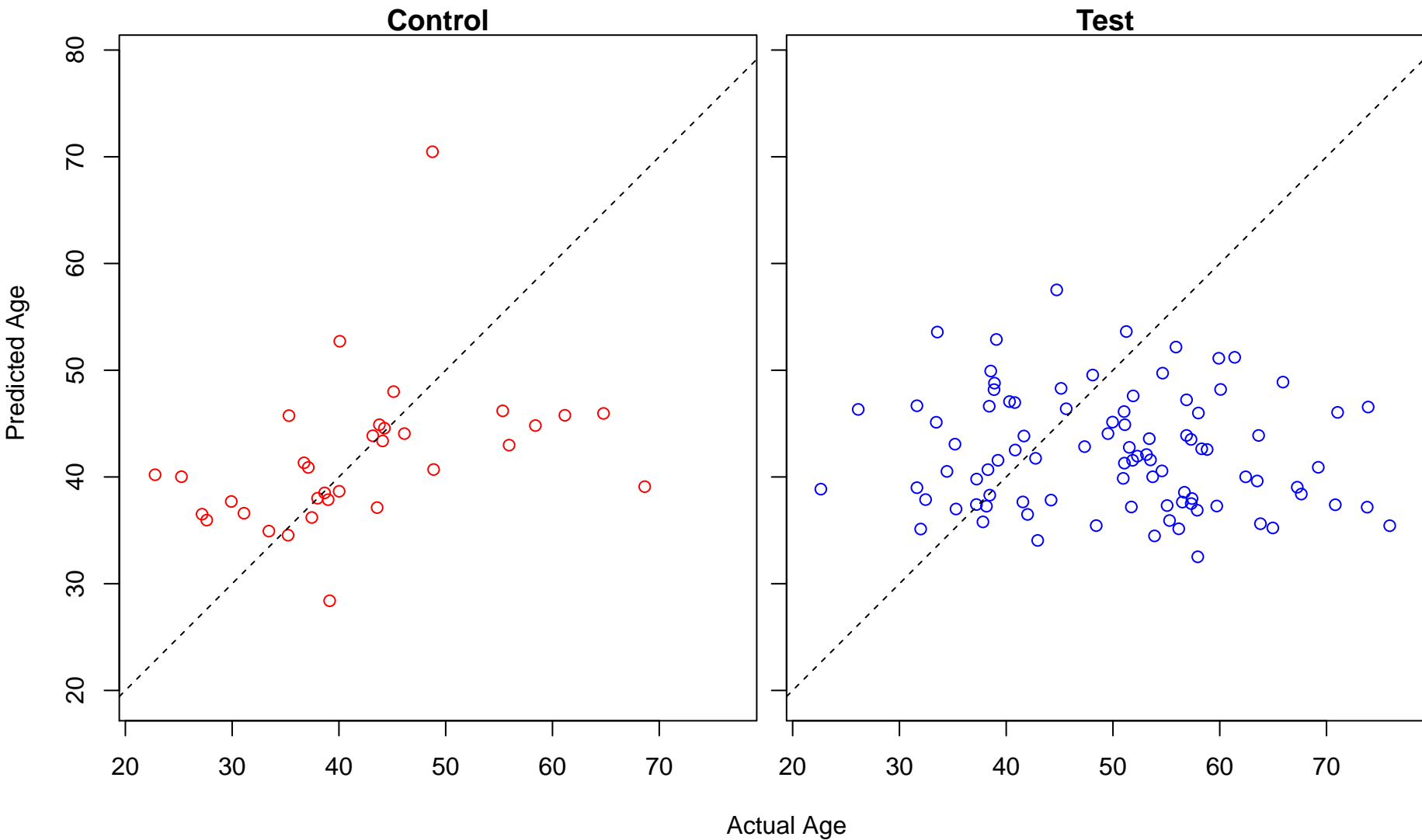
macromolecular complex subunit organization (Score: 0.642501)



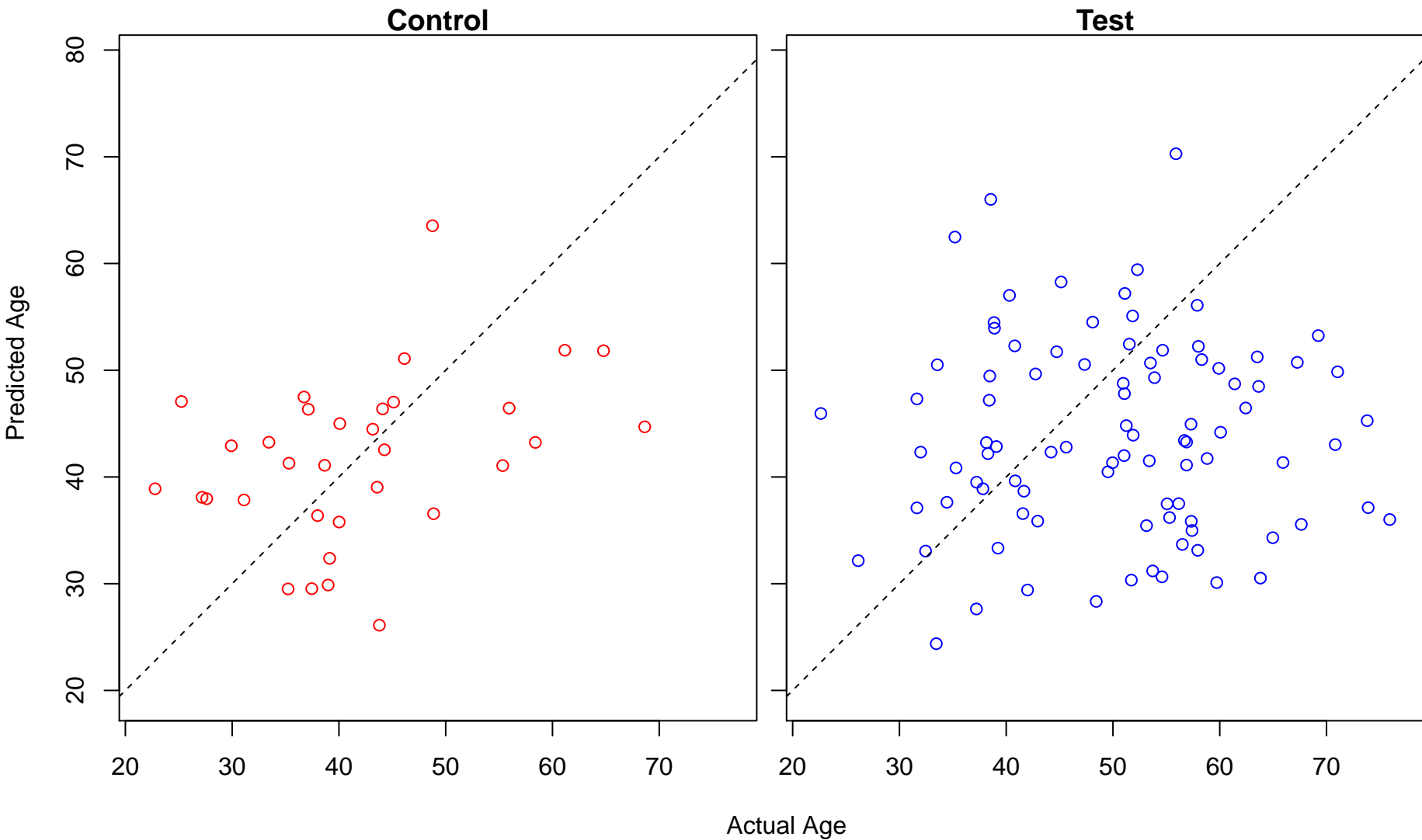
response to fungus (Score: 0.642422)



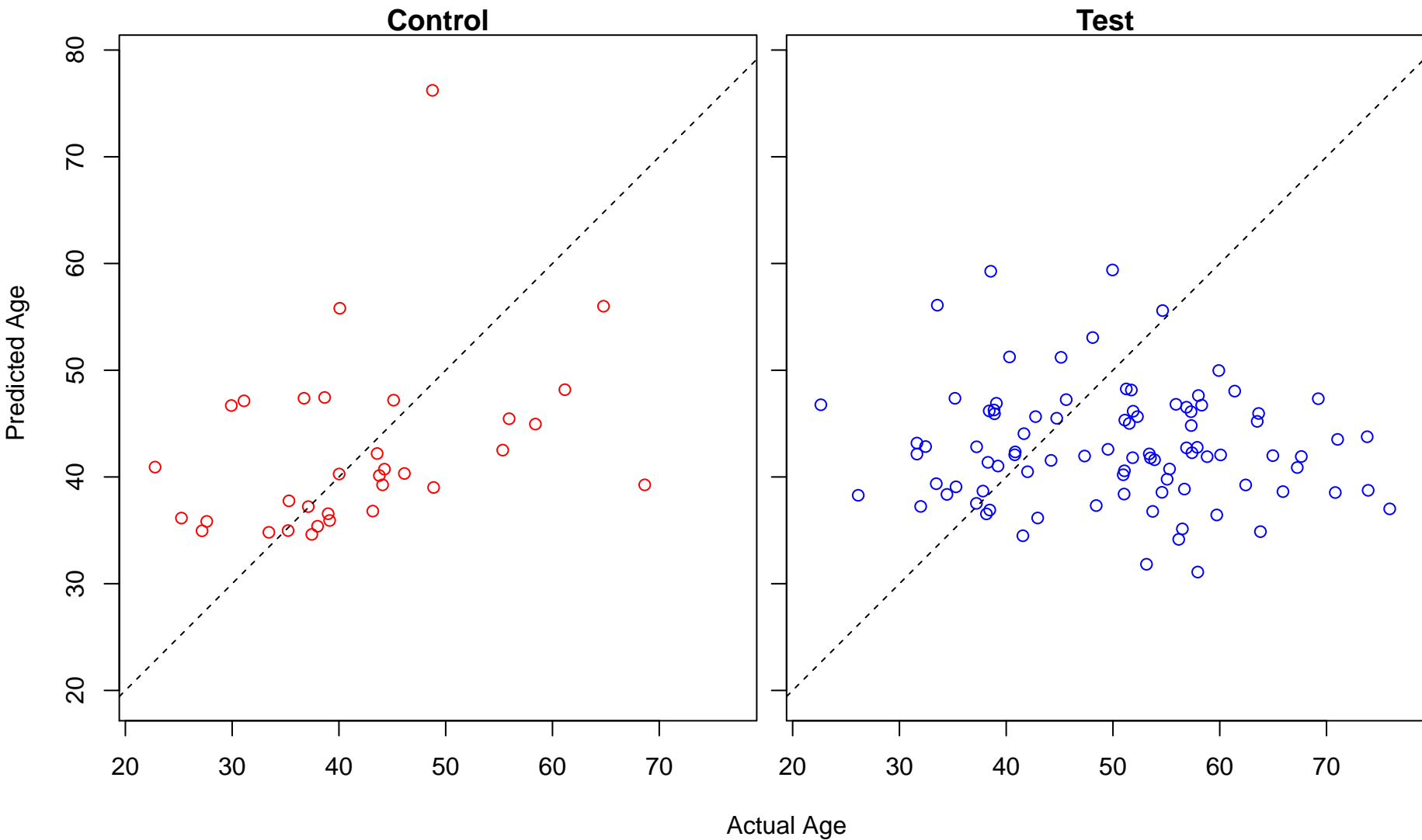
macromolecule biosynthetic process (Score: 0.642118)



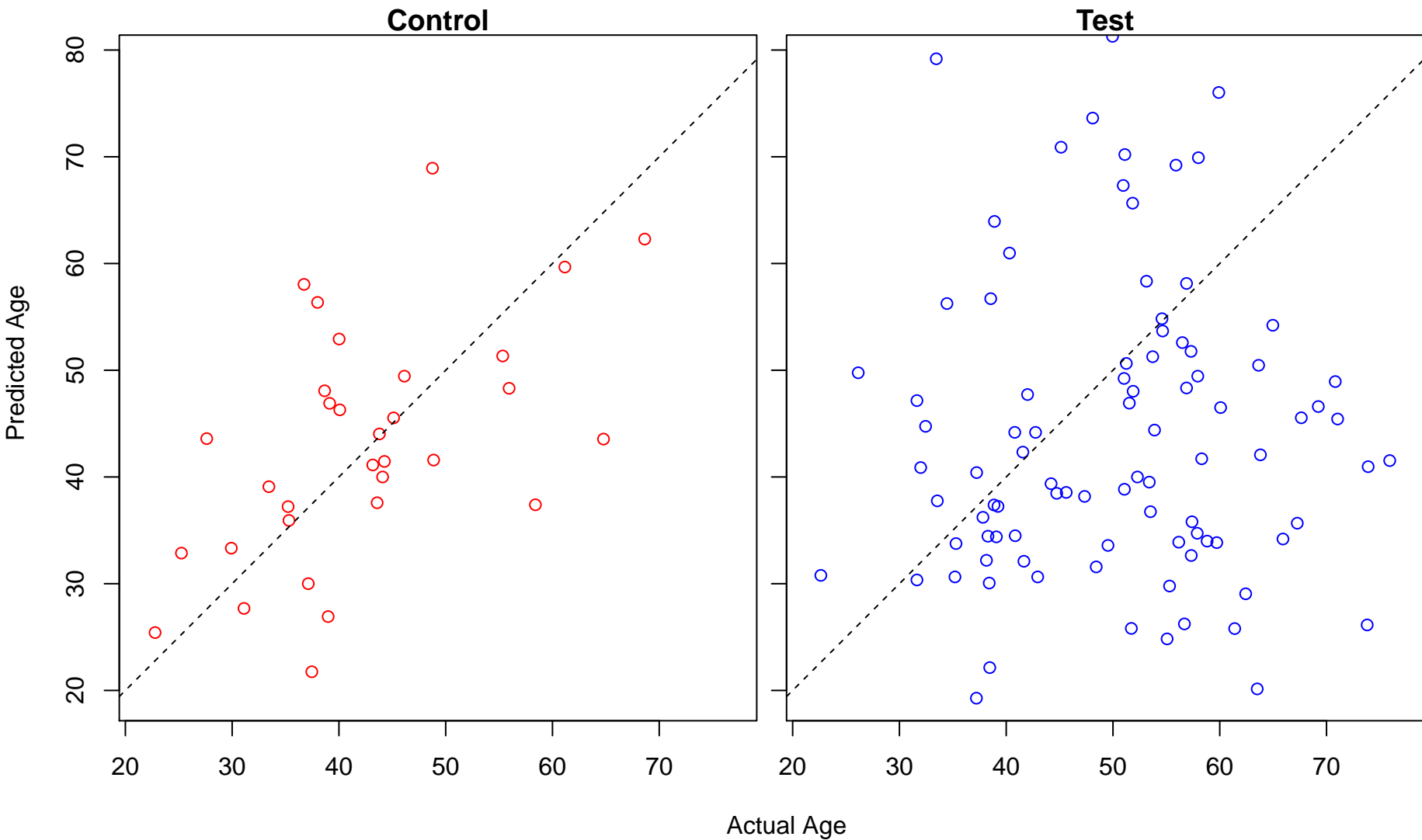
positive regulation of circadian rhythm (Score: 0.642116)



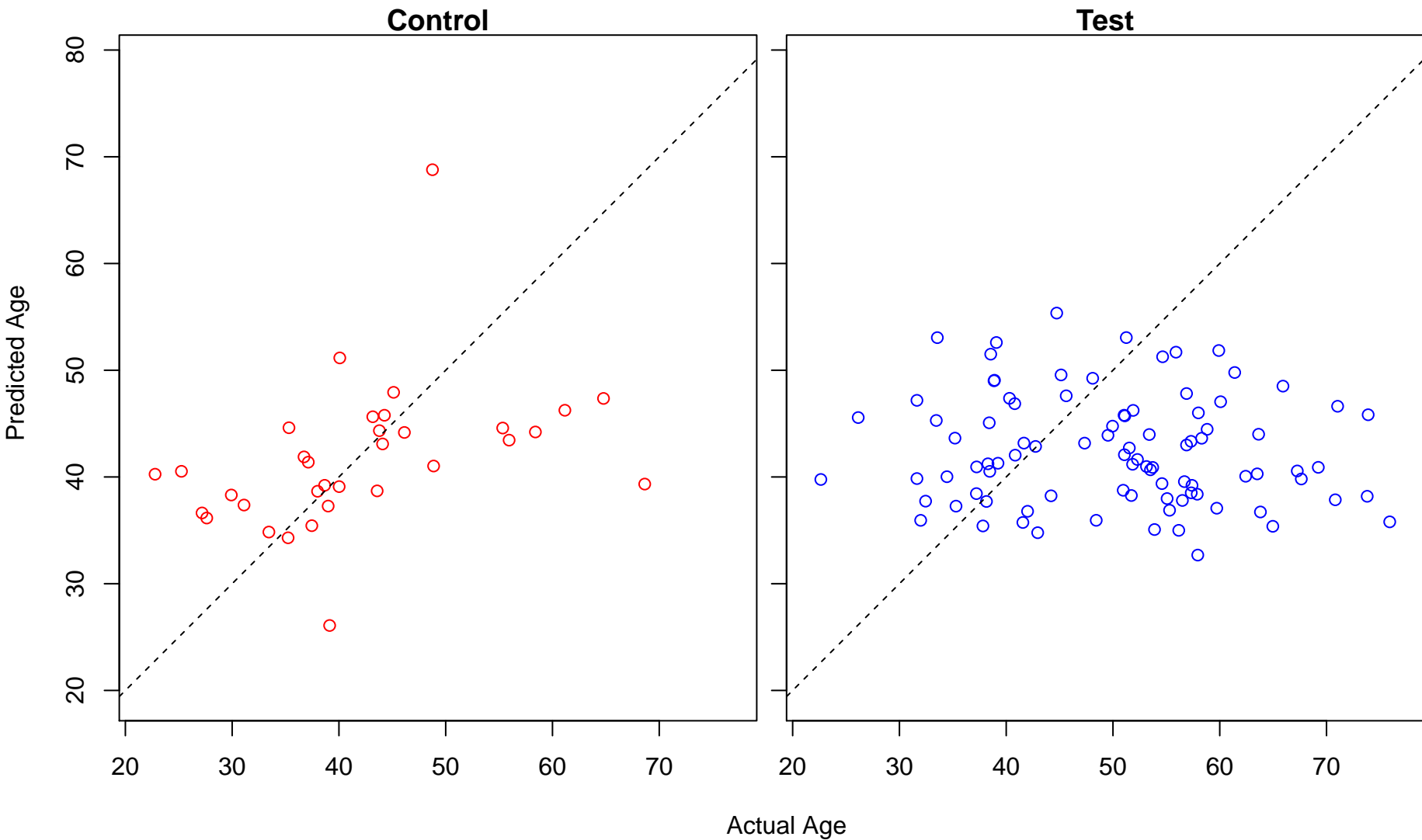
histone-threonine phosphorylation (Score: 0.641956)



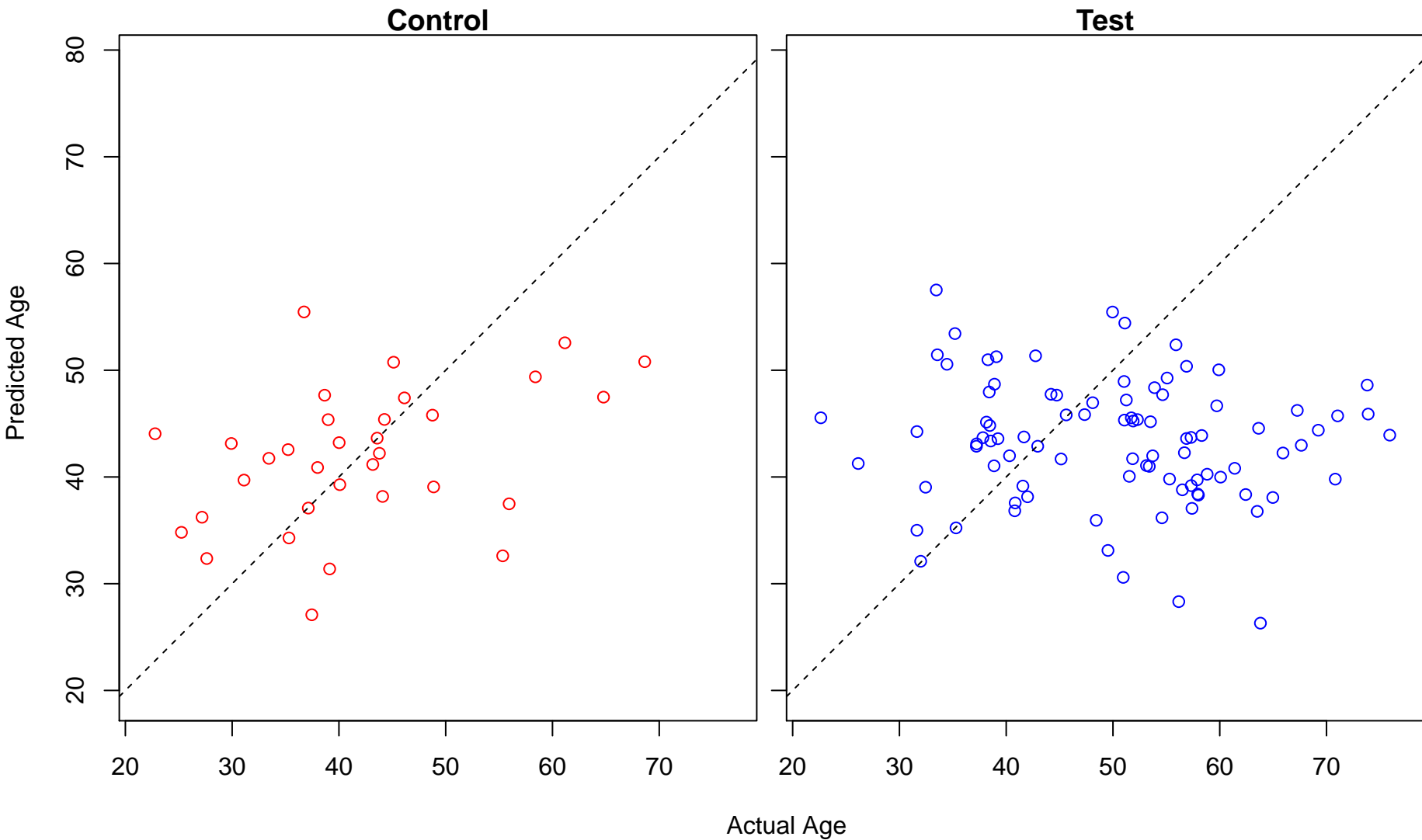
regulation of calcium ion transmembrane transporter activity (Score: 0.641942)



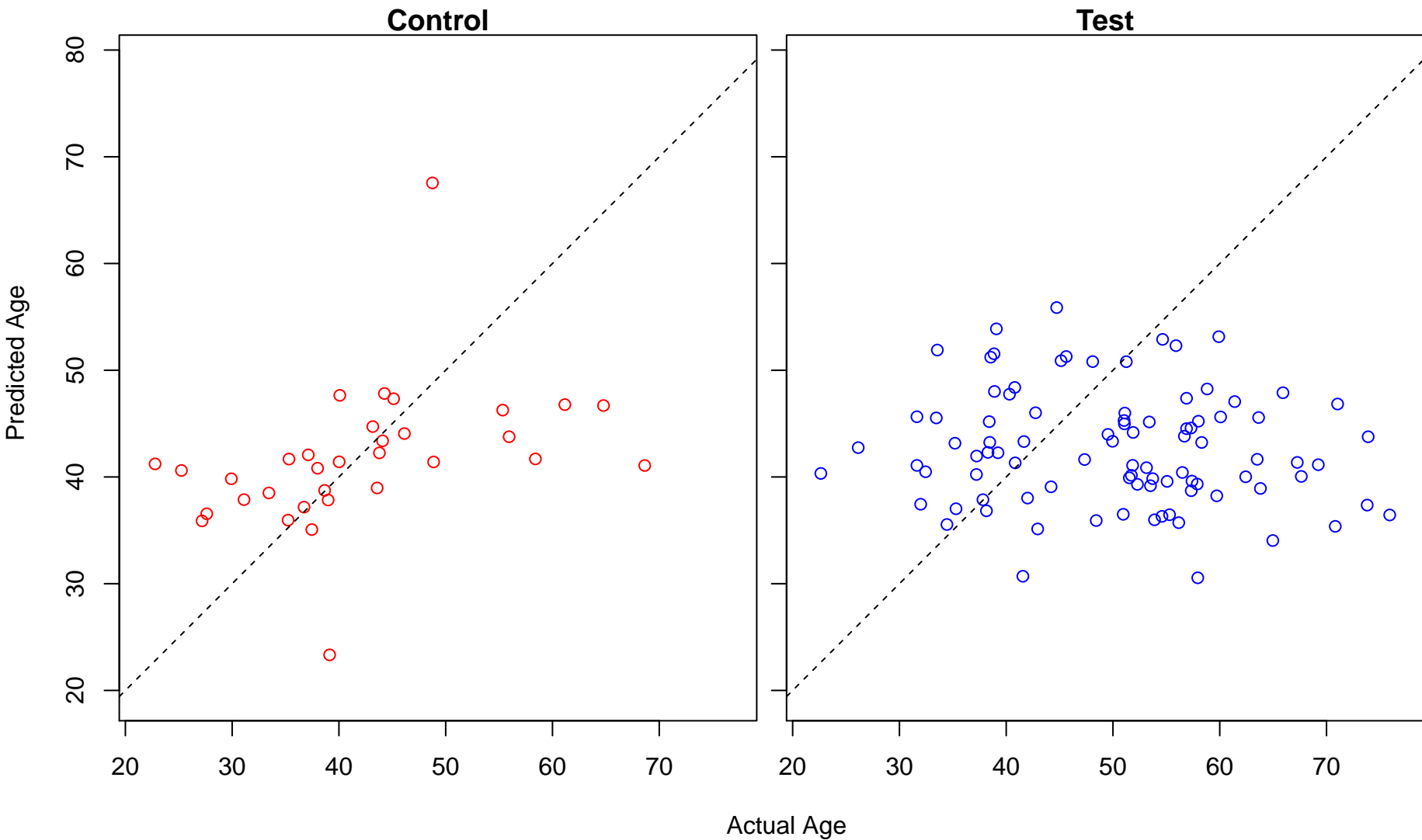
single-organism cellular process (Score: 0.641824)



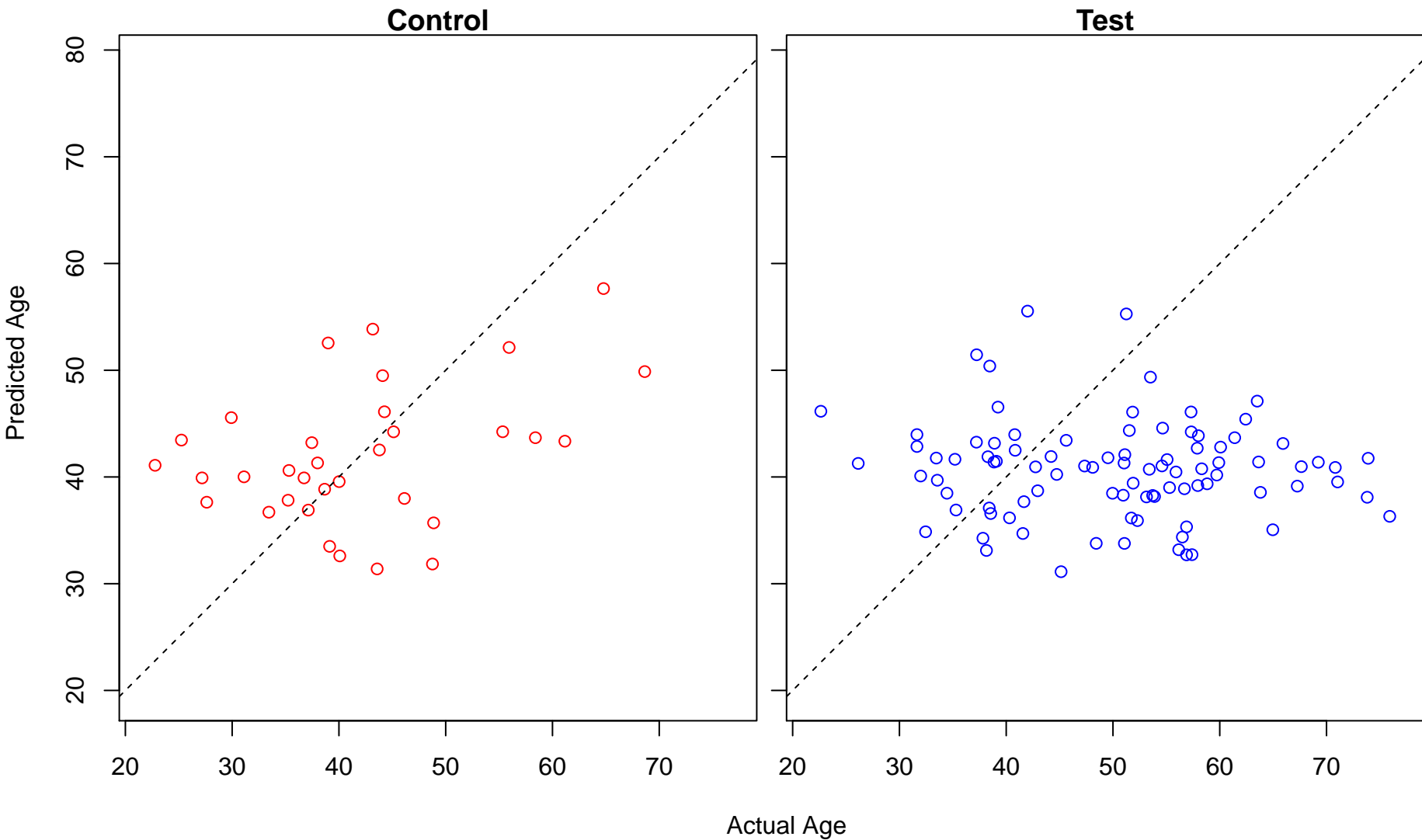
postsynaptic membrane assembly (Score: 0.641038)



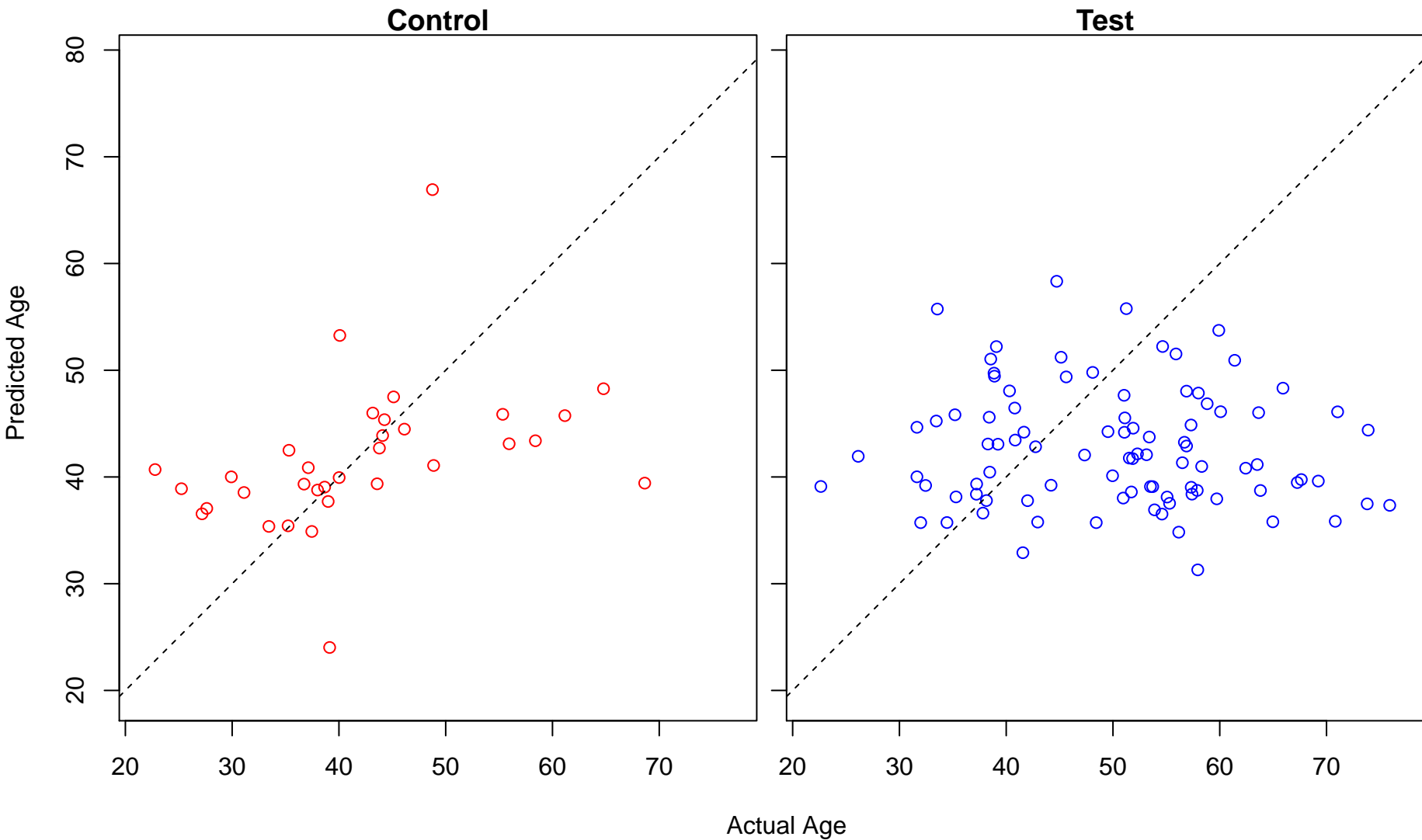
response to nitrogen compound (Score: 0.640937)



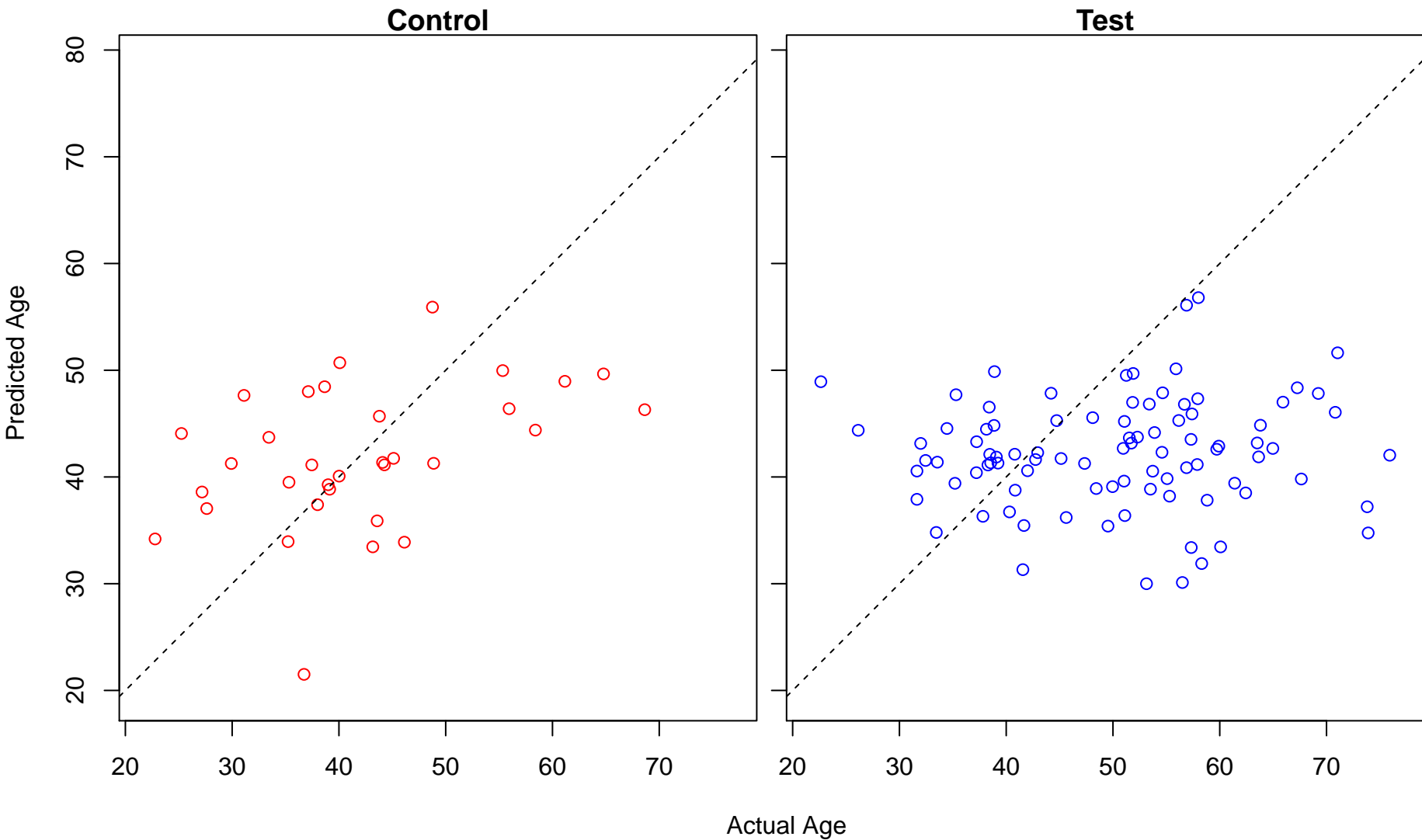
cellular response to jasmonic acid stimulus (Score: 0.640779)



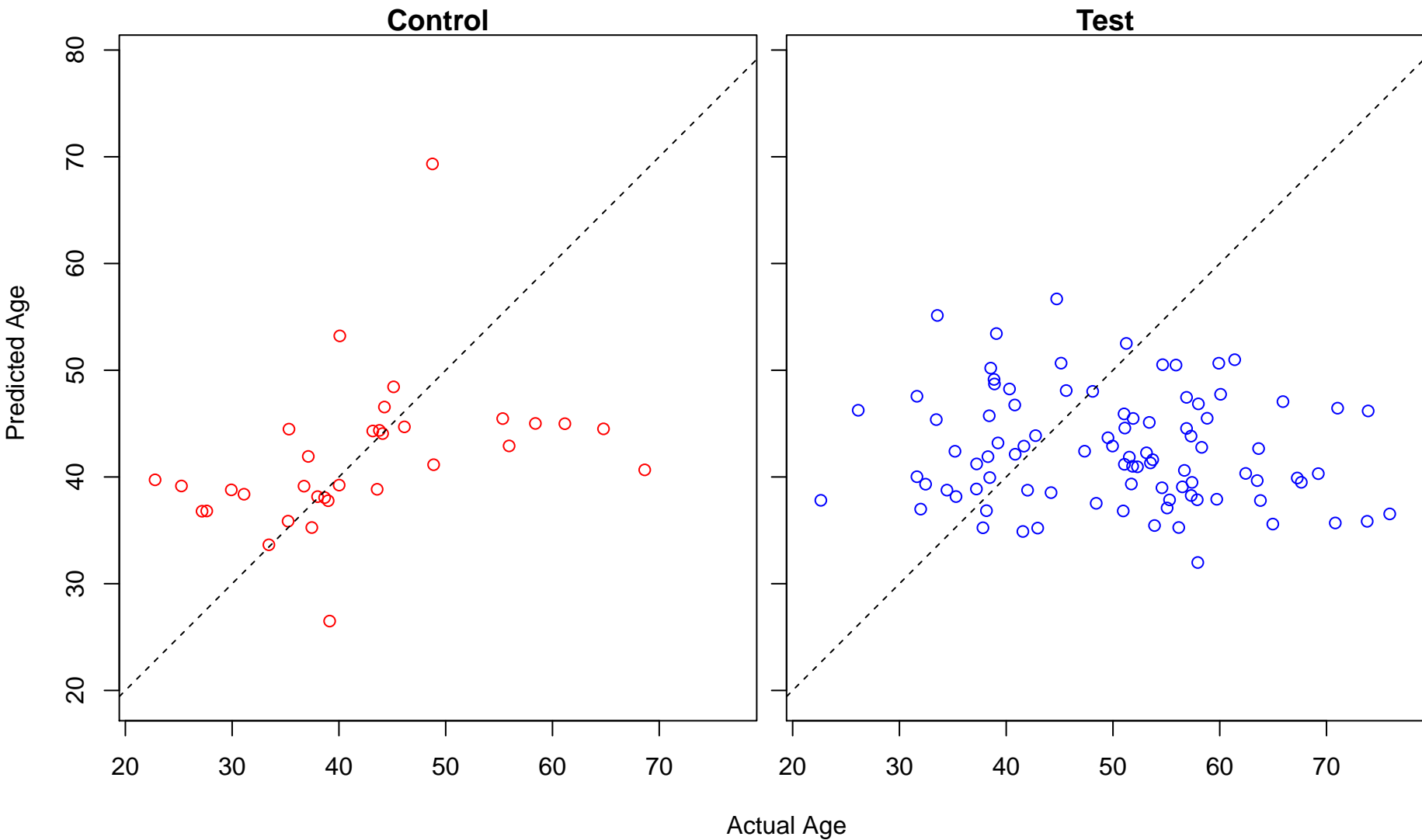
neurotrophin signaling pathway (Score: 0.640595)



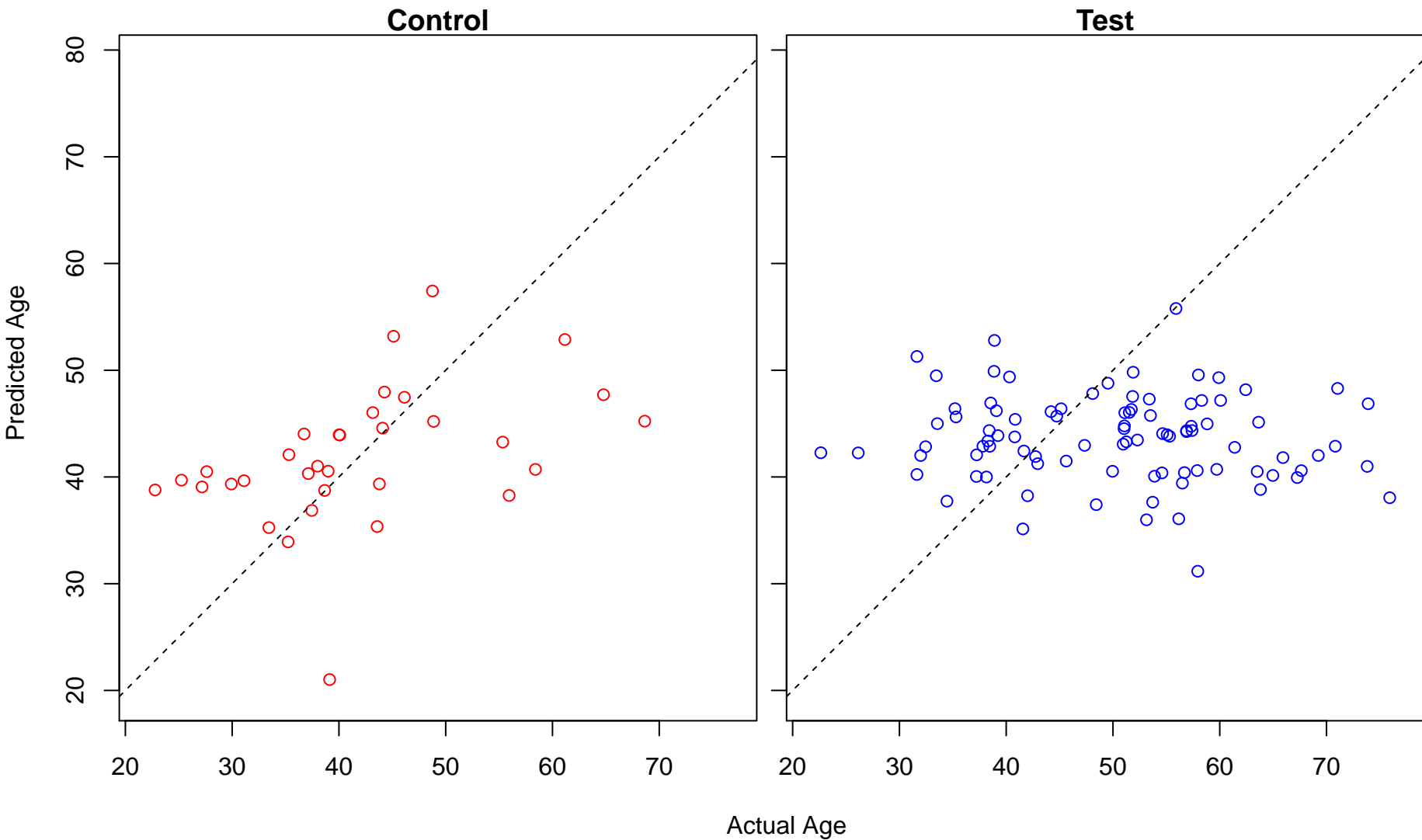
aorta morphogenesis (Score: 0.639646)



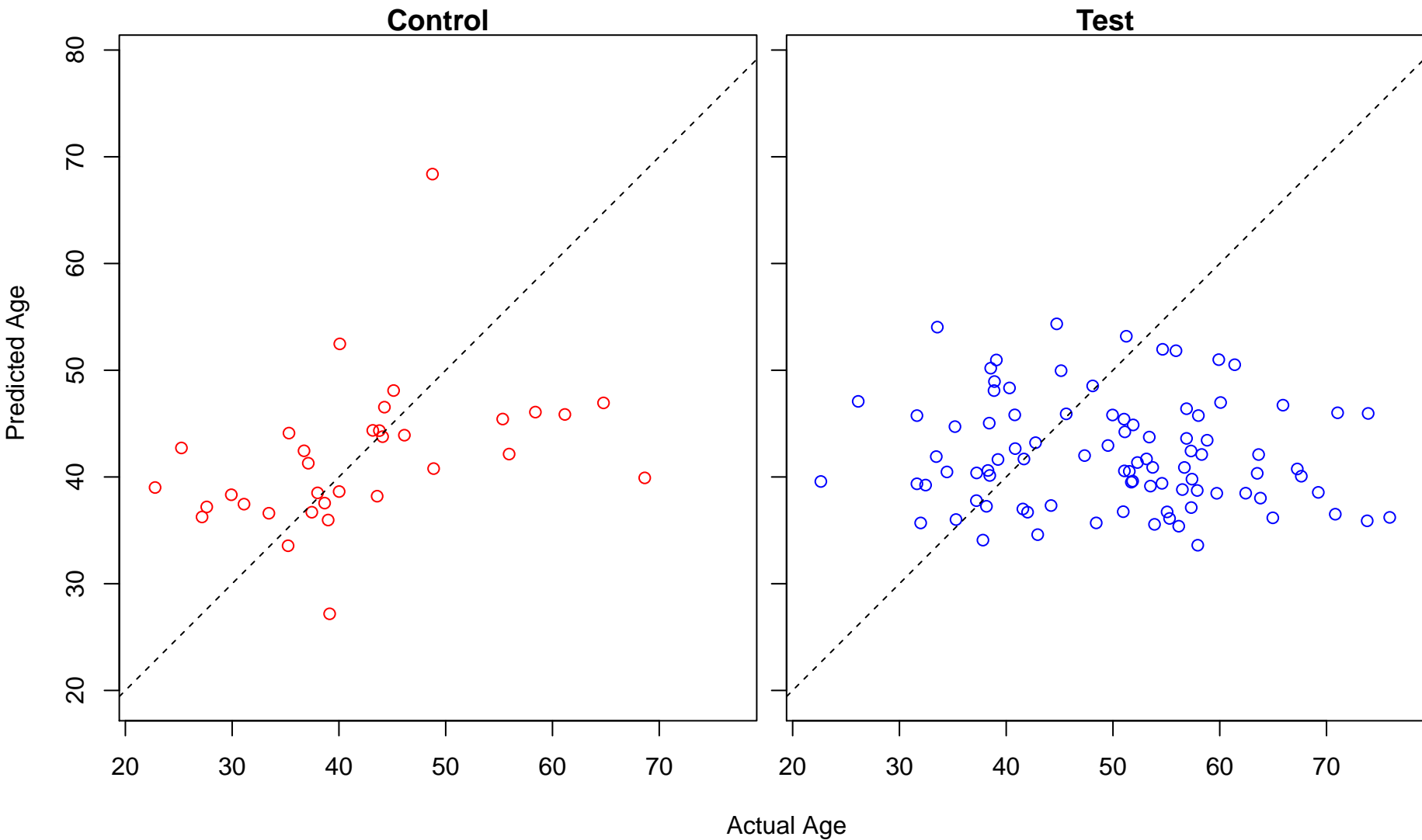
regulation of transferase activity (Score: 0.639251)



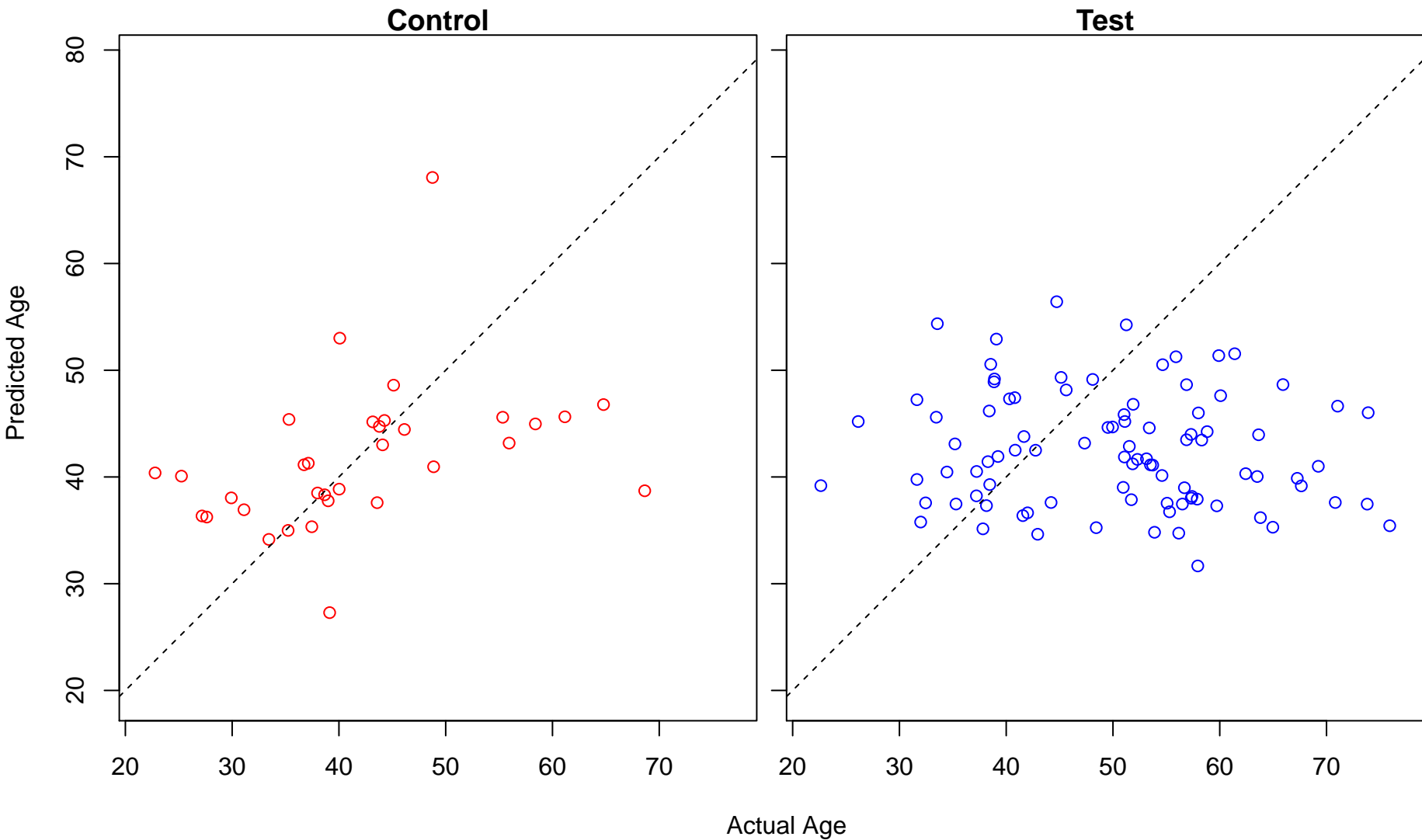
regulation of phospholipase A2 activity (Score: 0.638867)



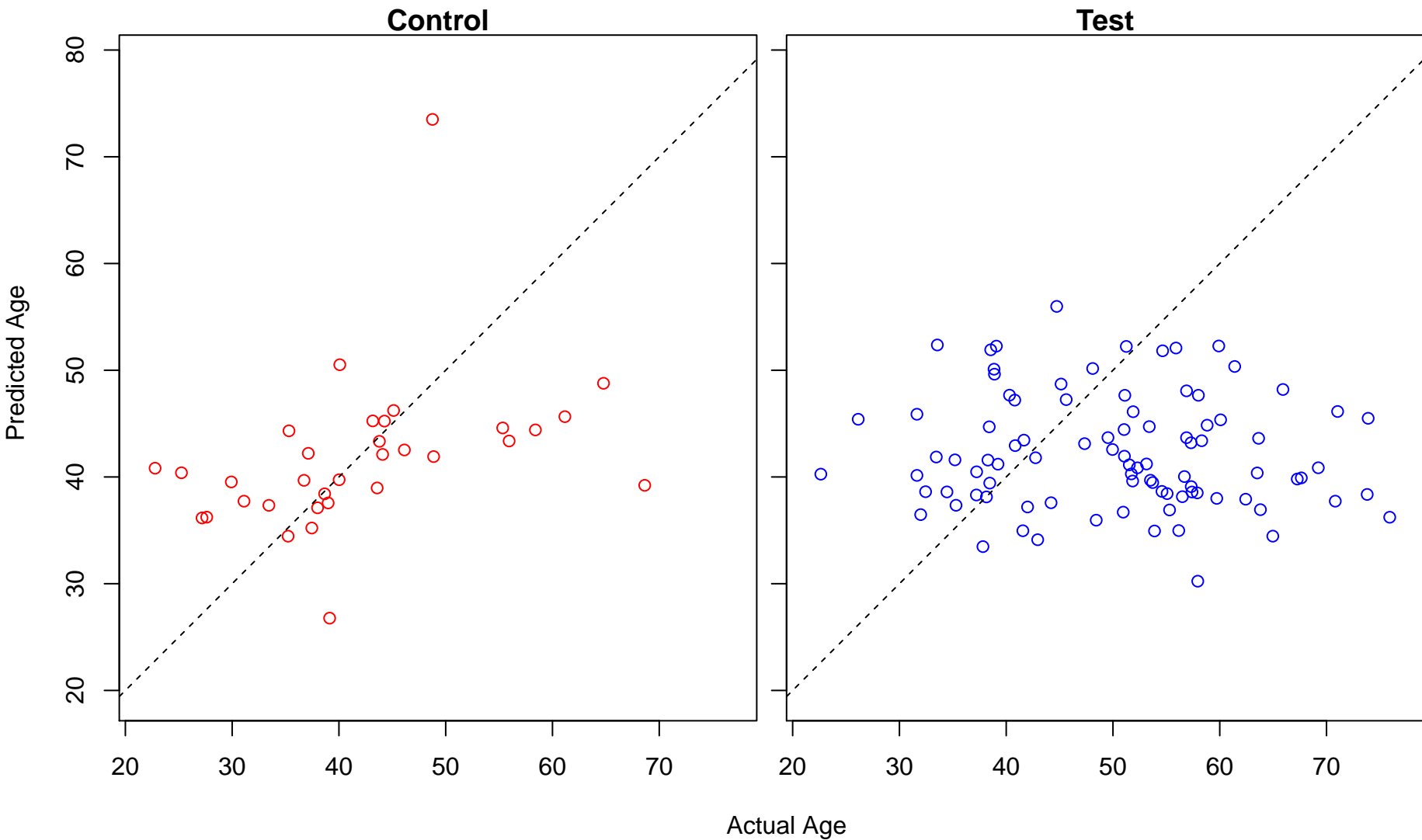
regulation of developmental process (Score: 0.638782)



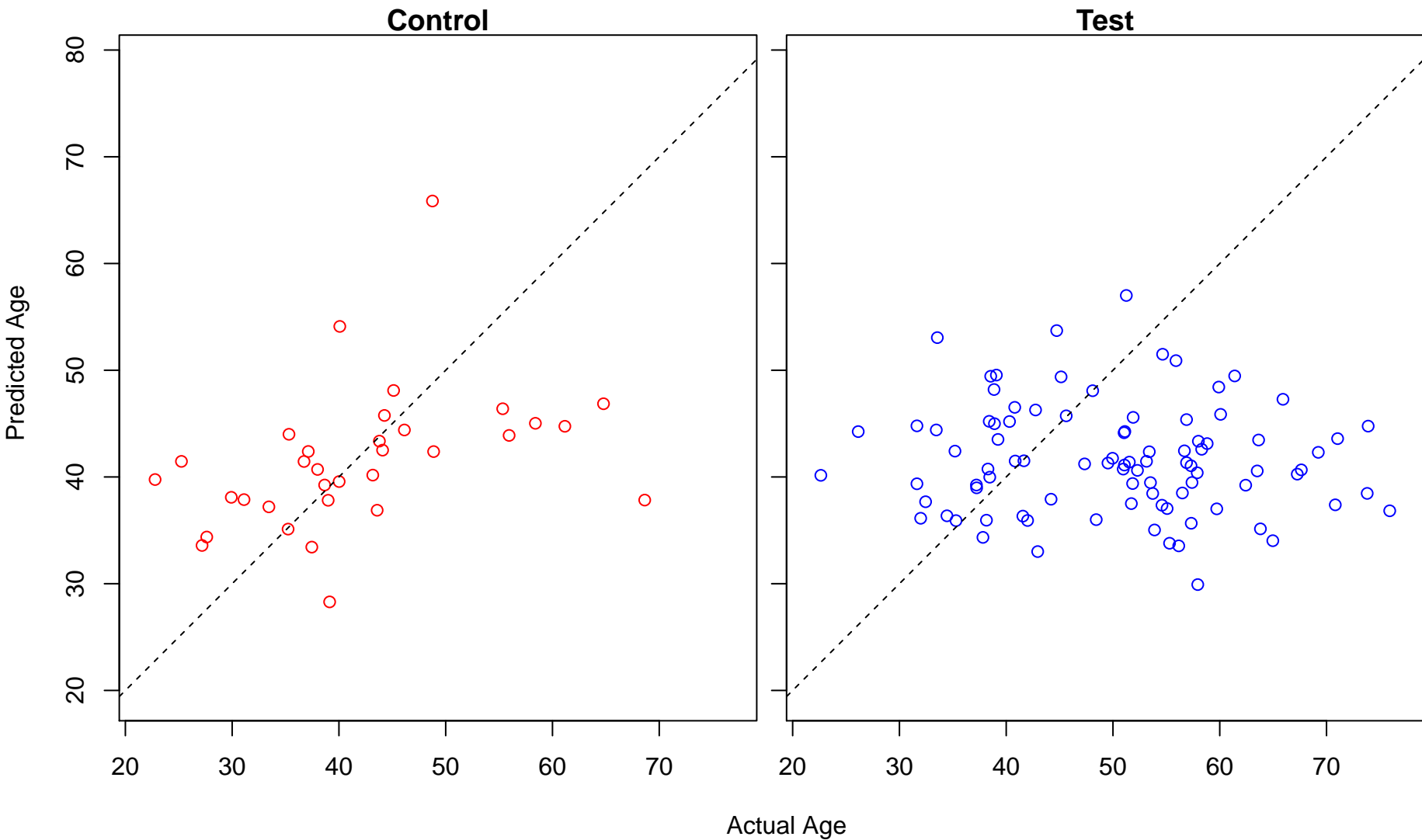
organic substance metabolic process (Score: 0.638211)



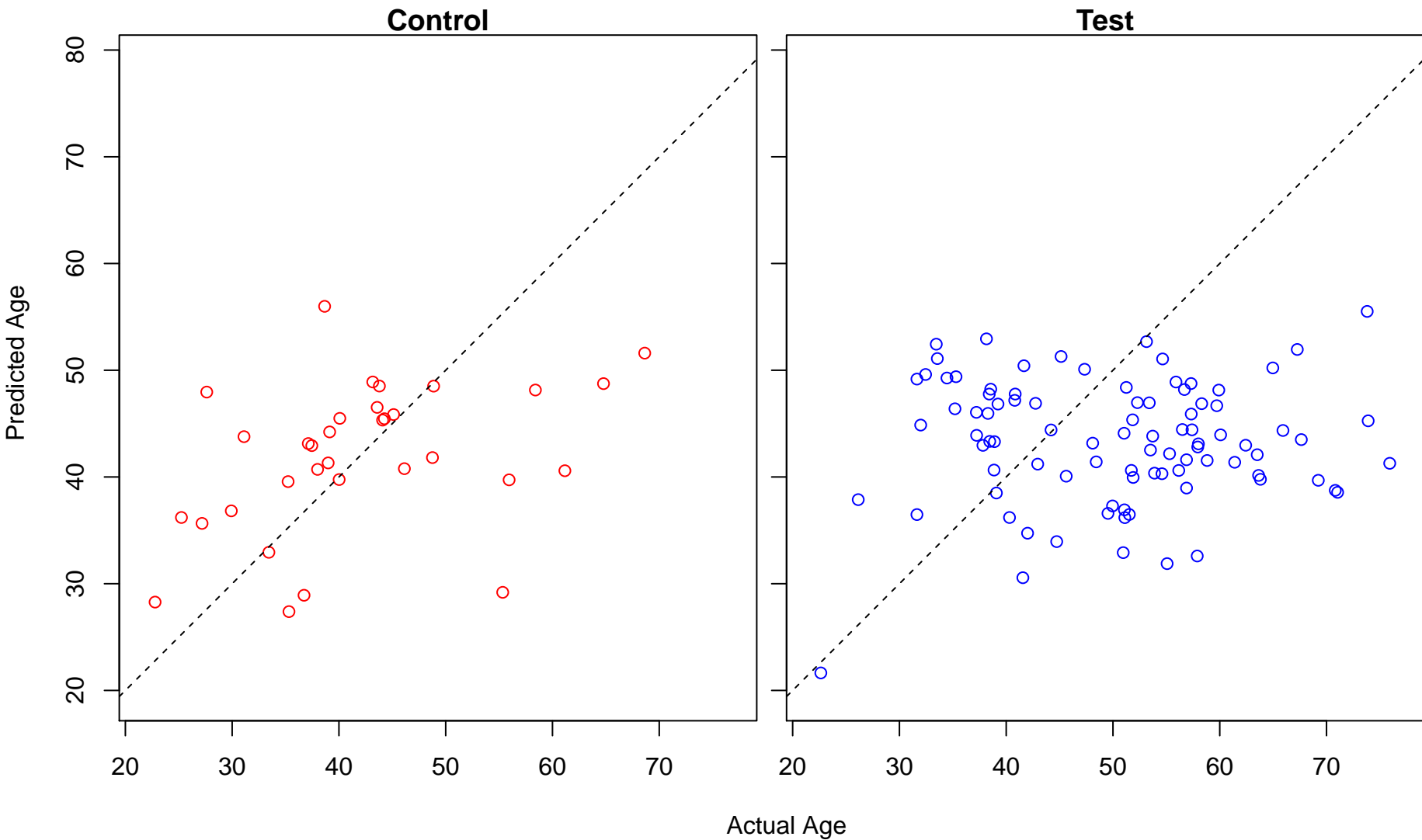
peptidyl-amino acid modification (Score: 0.638012)



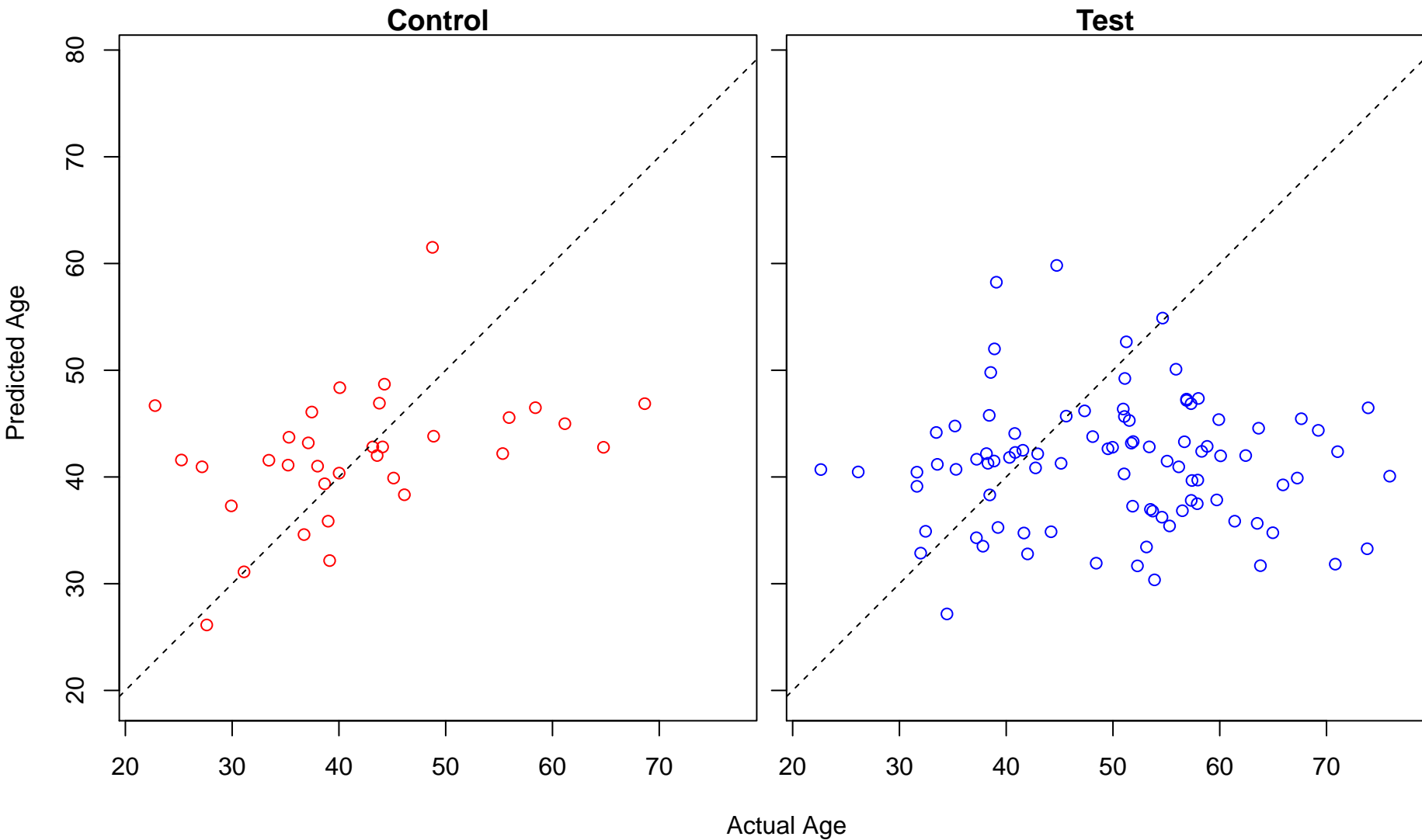
negative regulation of cell death (Score: 0.637705)



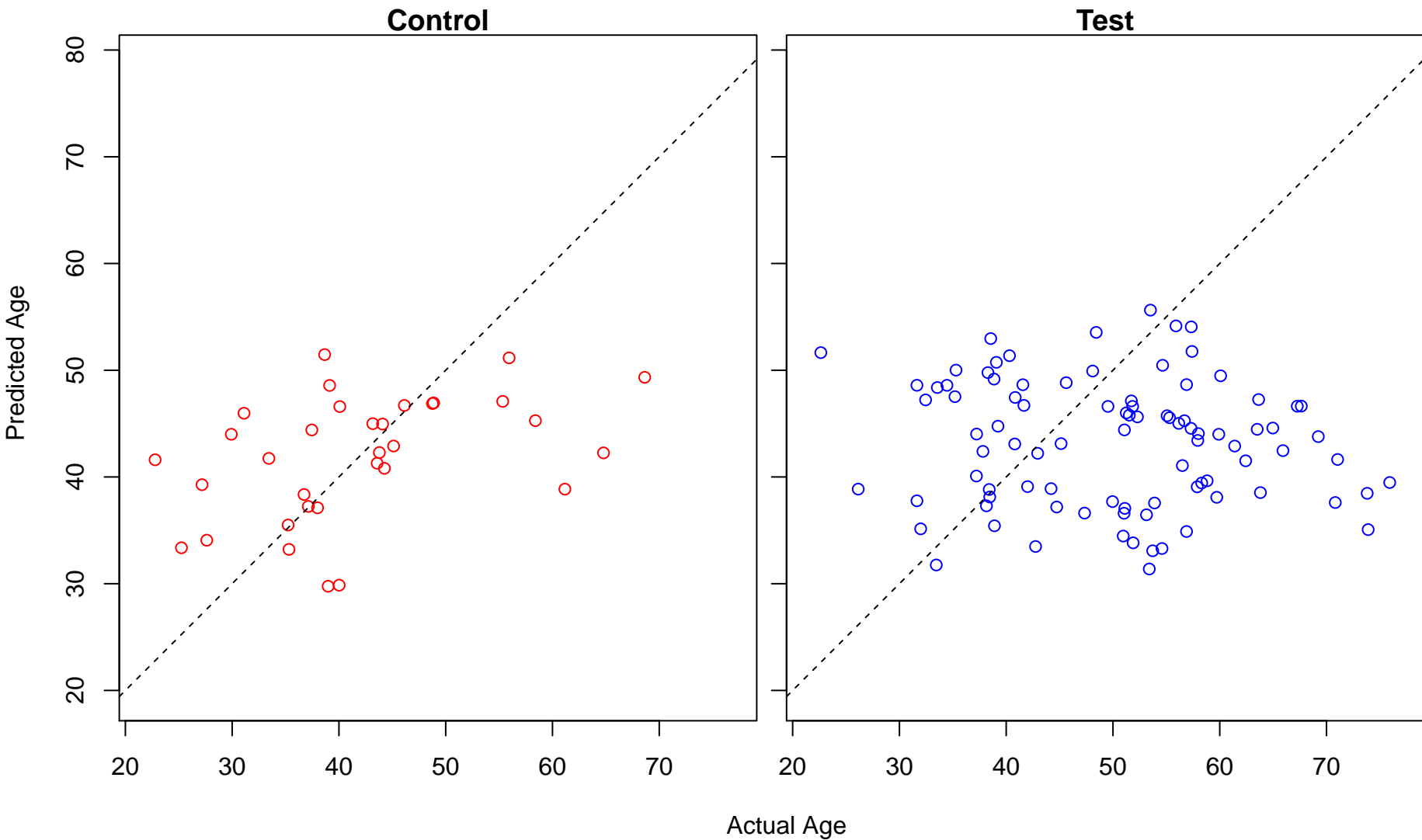
sphingomyelin metabolic process (Score: 0.637368)



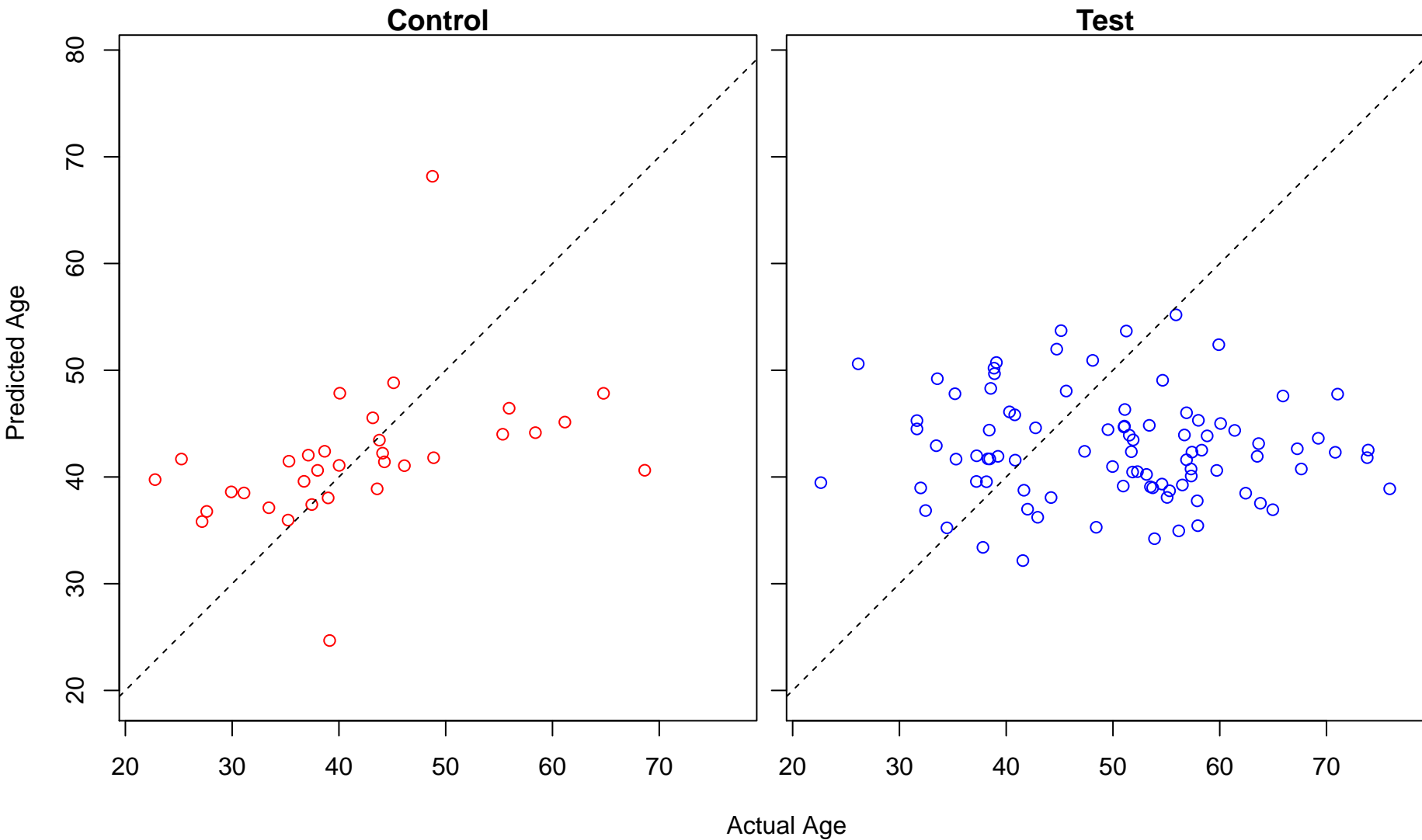
ribosomal small subunit biogenesis (Score: 0.637301)



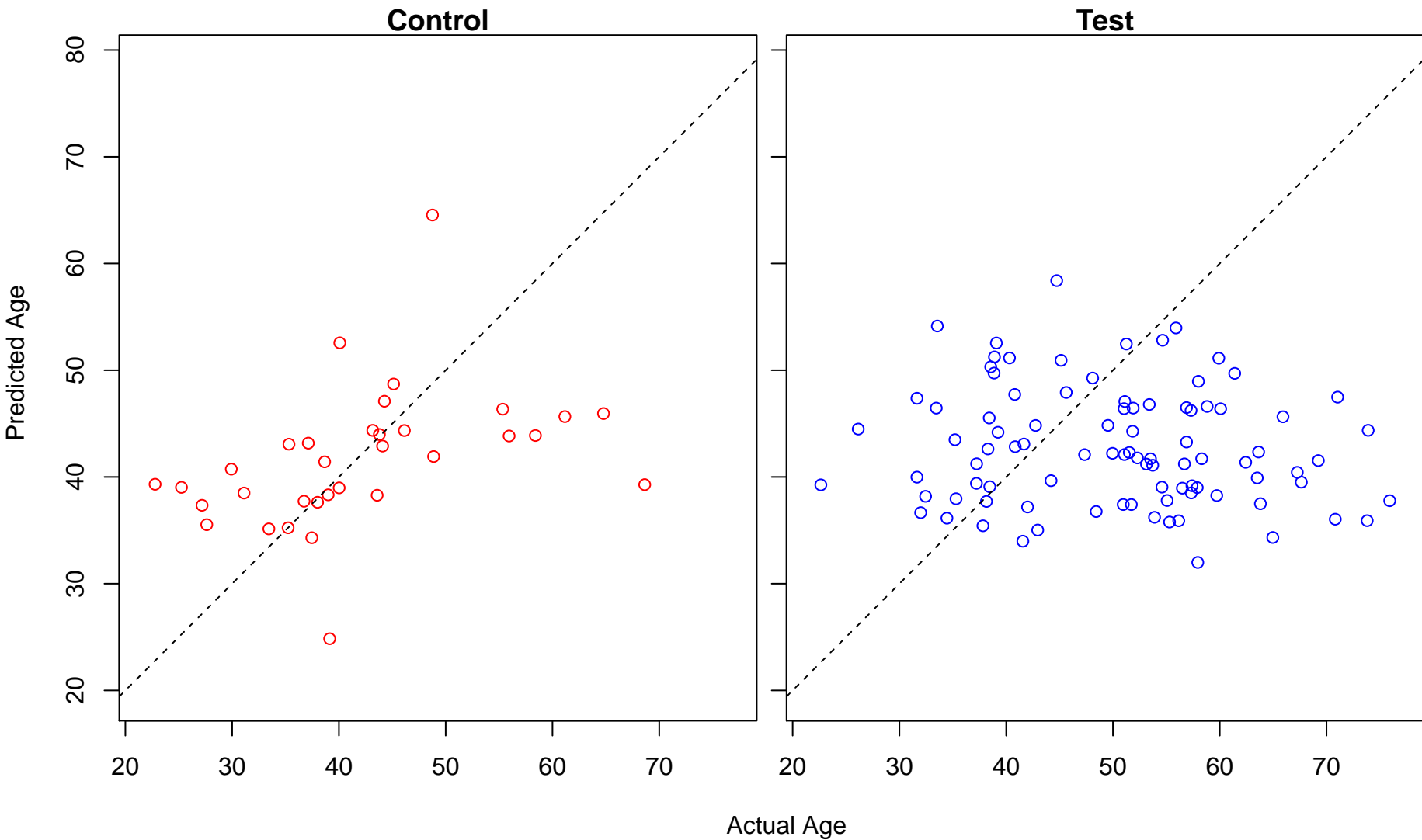
negative regulation of membrane protein ectodomain proteolysis (Score: 0.637061)



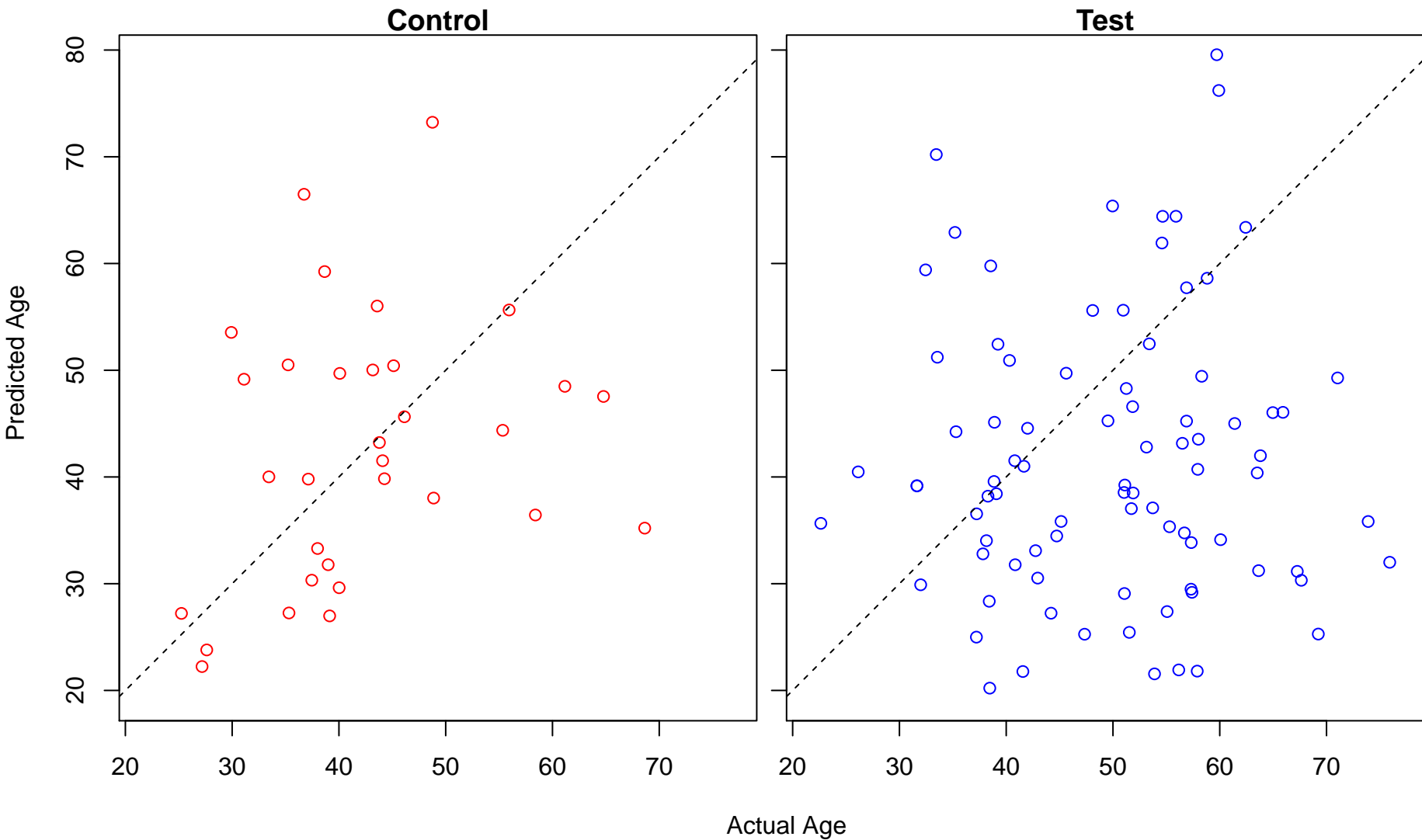
anatomical structure formation involved in morphogenesis (Score: 0.637039)



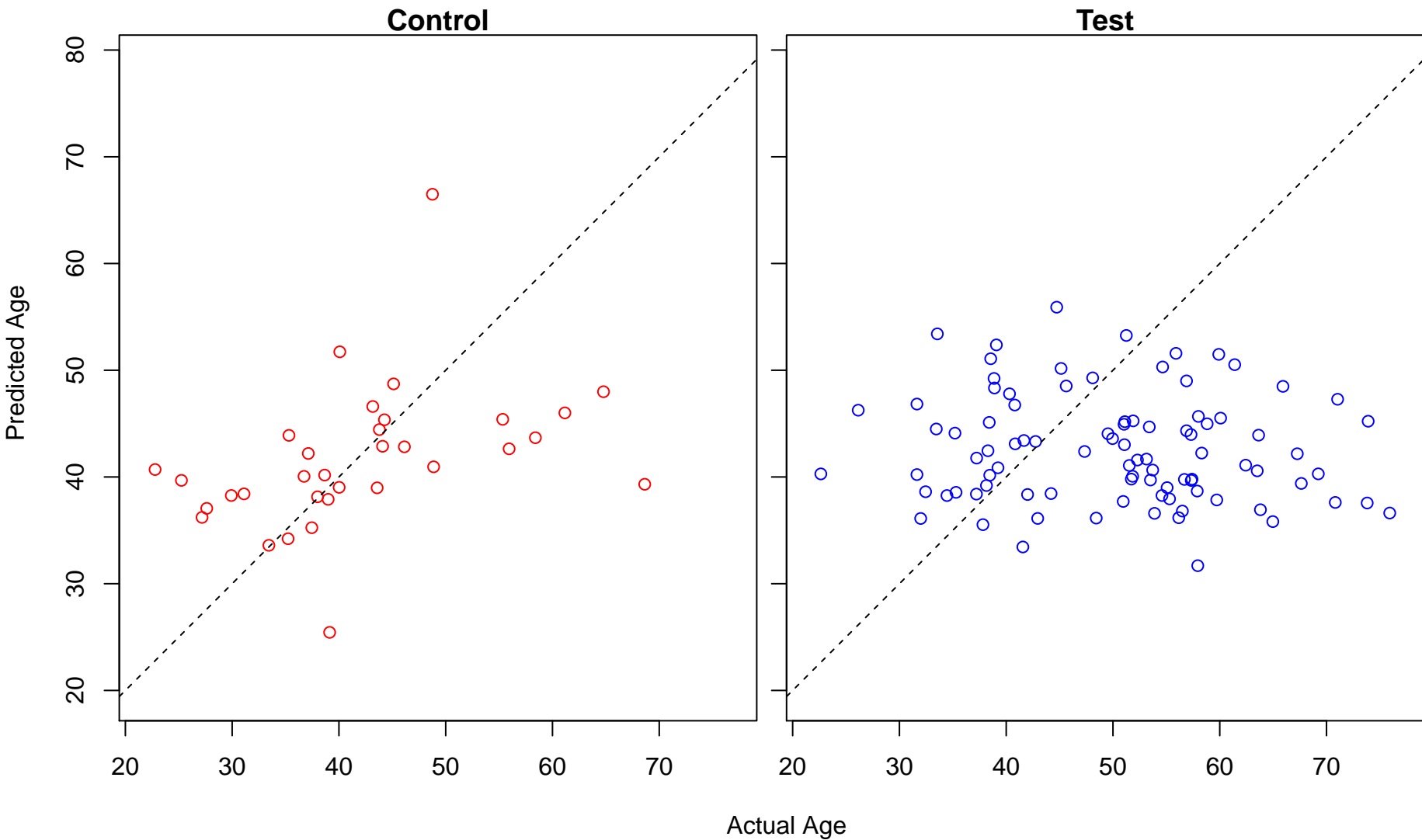
regulation of MAPK cascade (Score: 0.637028)



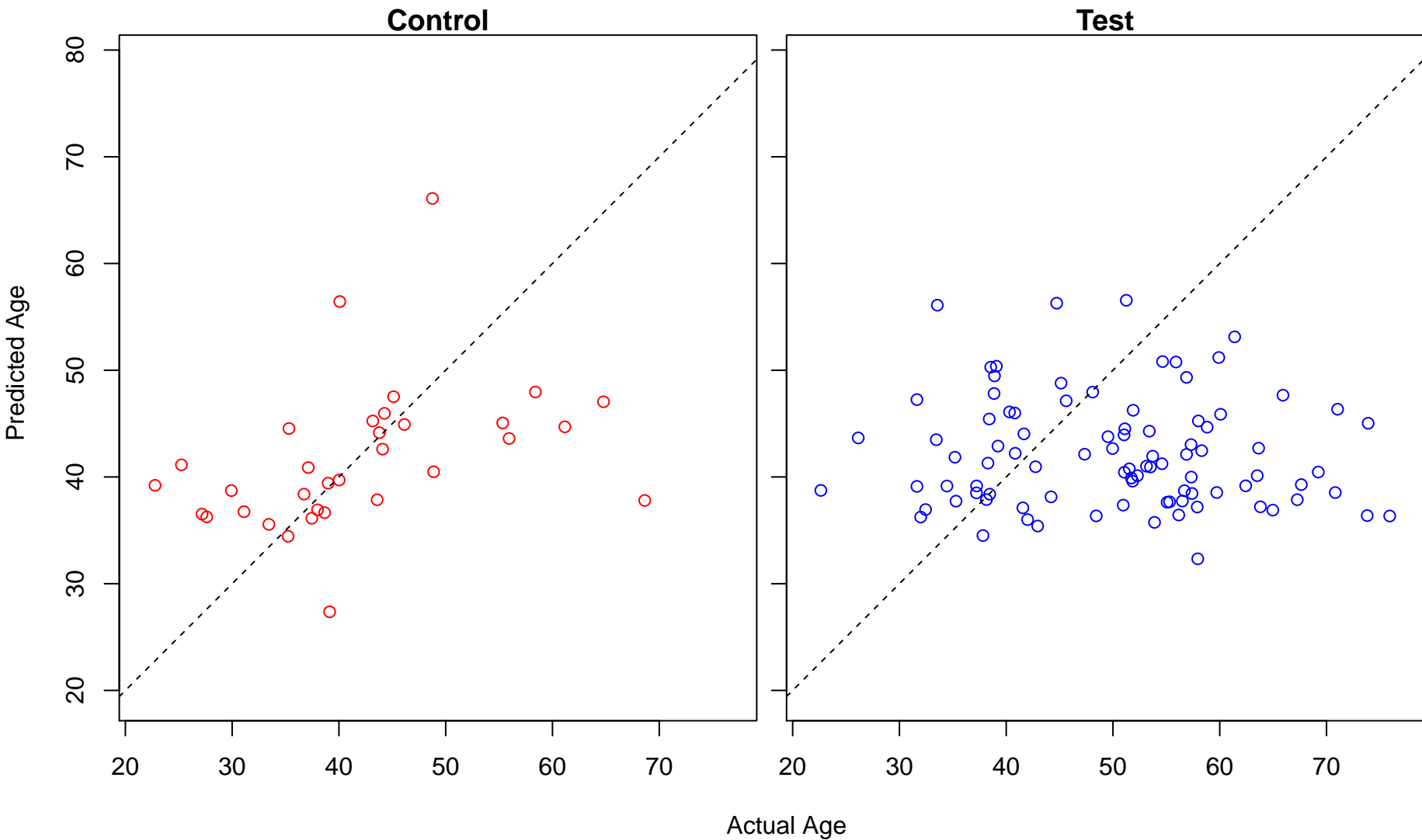
positive regulation of osteoblast differentiation (Score: 0.636906)



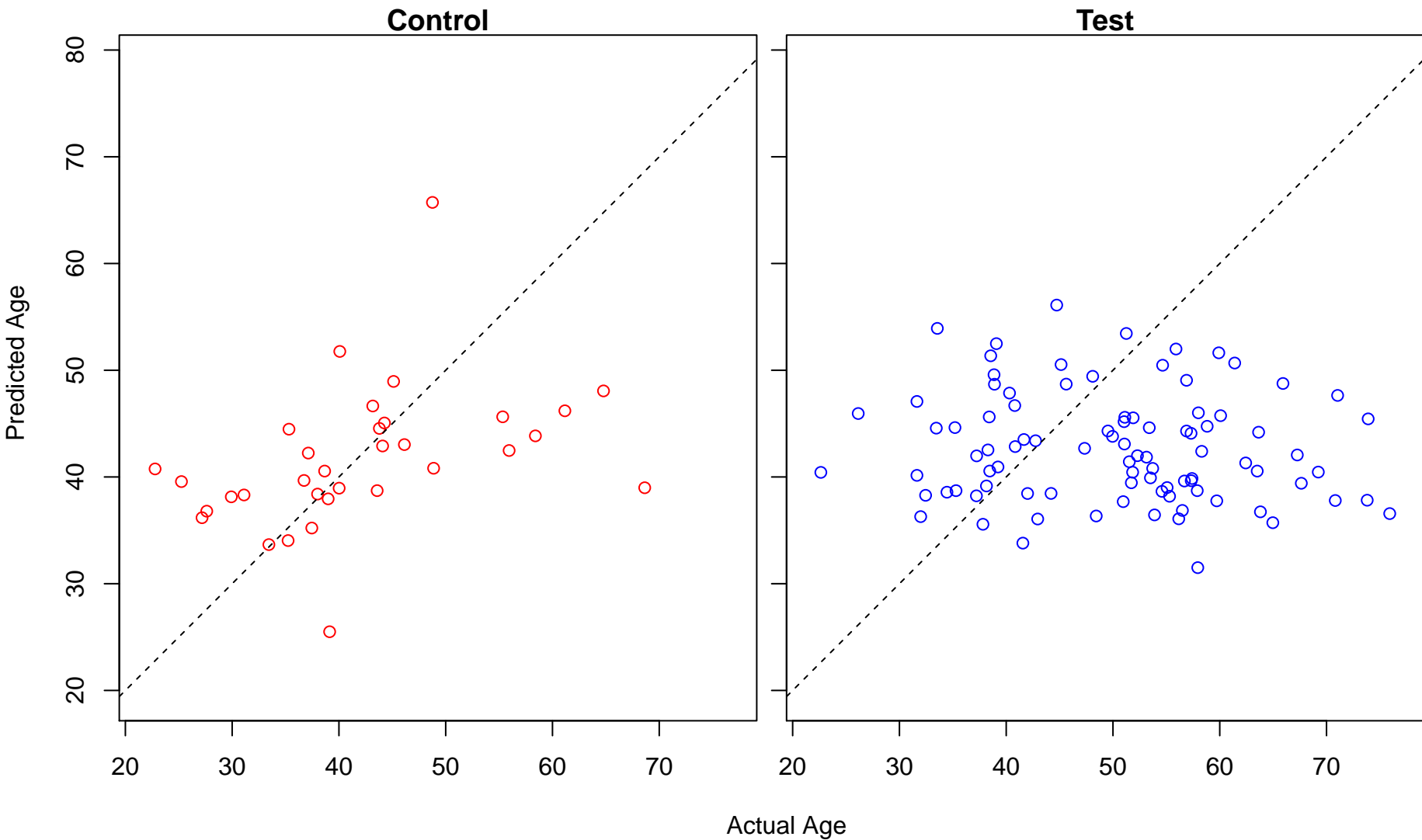
phosphate-containing compound metabolic process (Score: 0.636788)



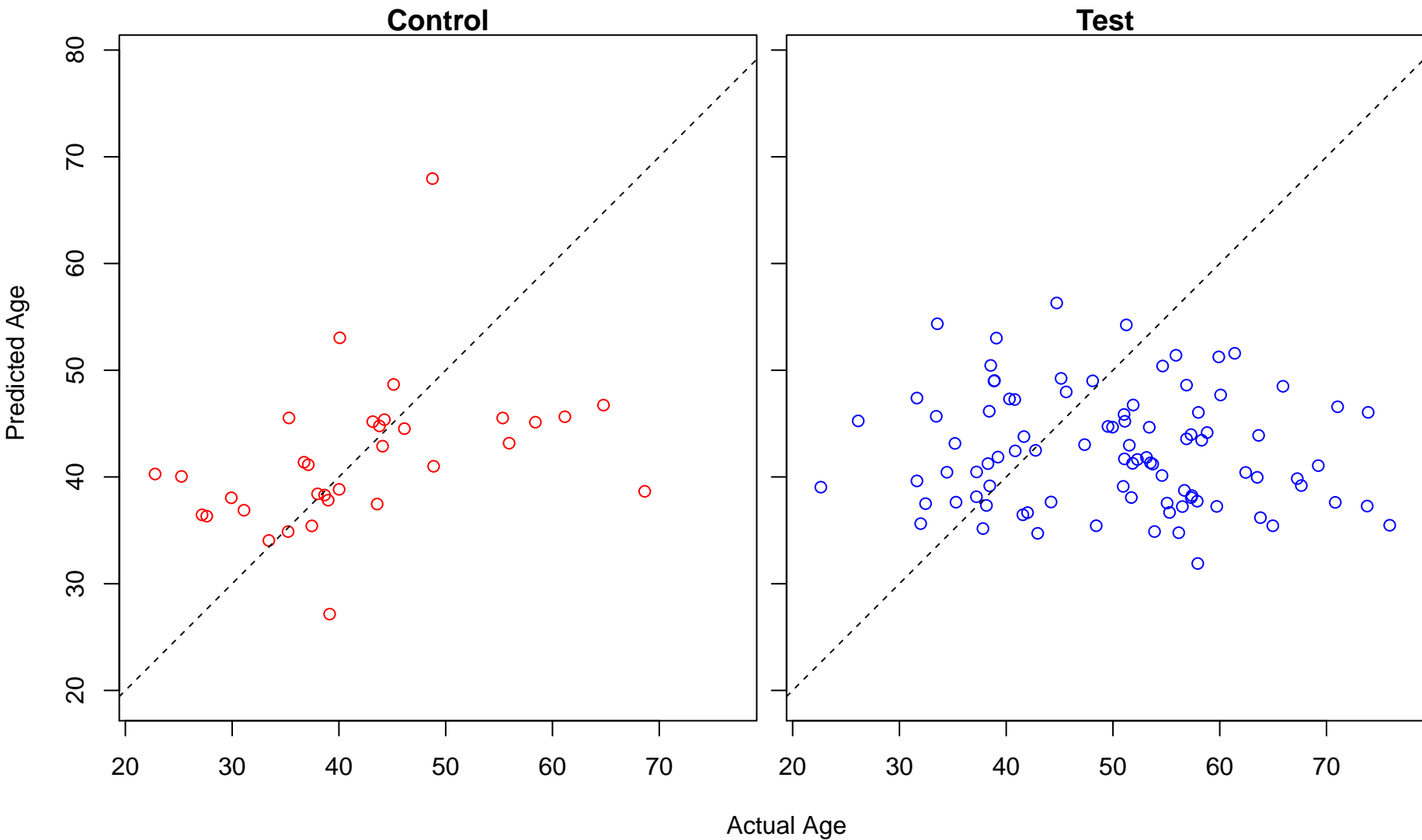
protein modification by small protein conjugation or removal (Score: 0.636629)



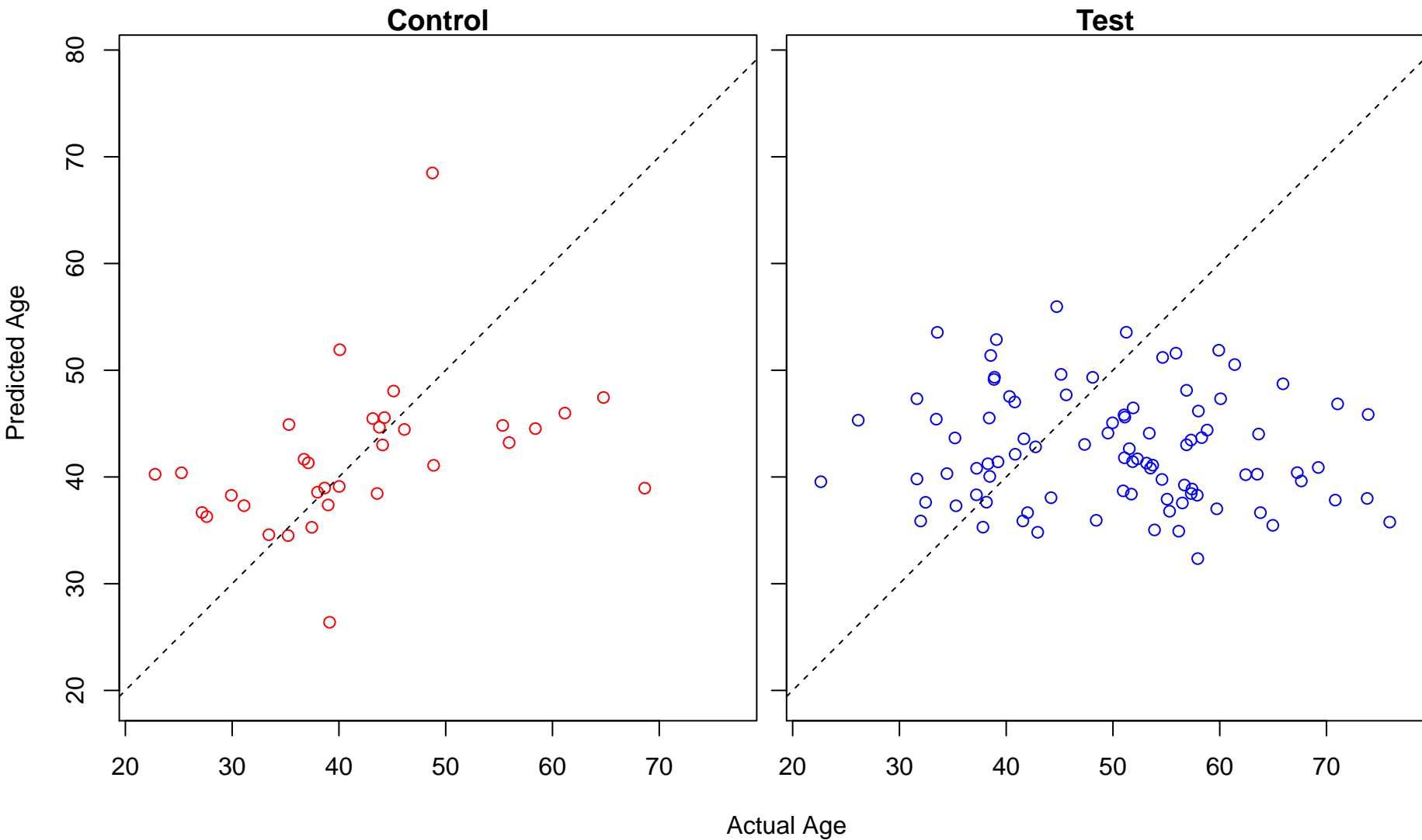
phosphorus metabolic process (Score: 0.636484)



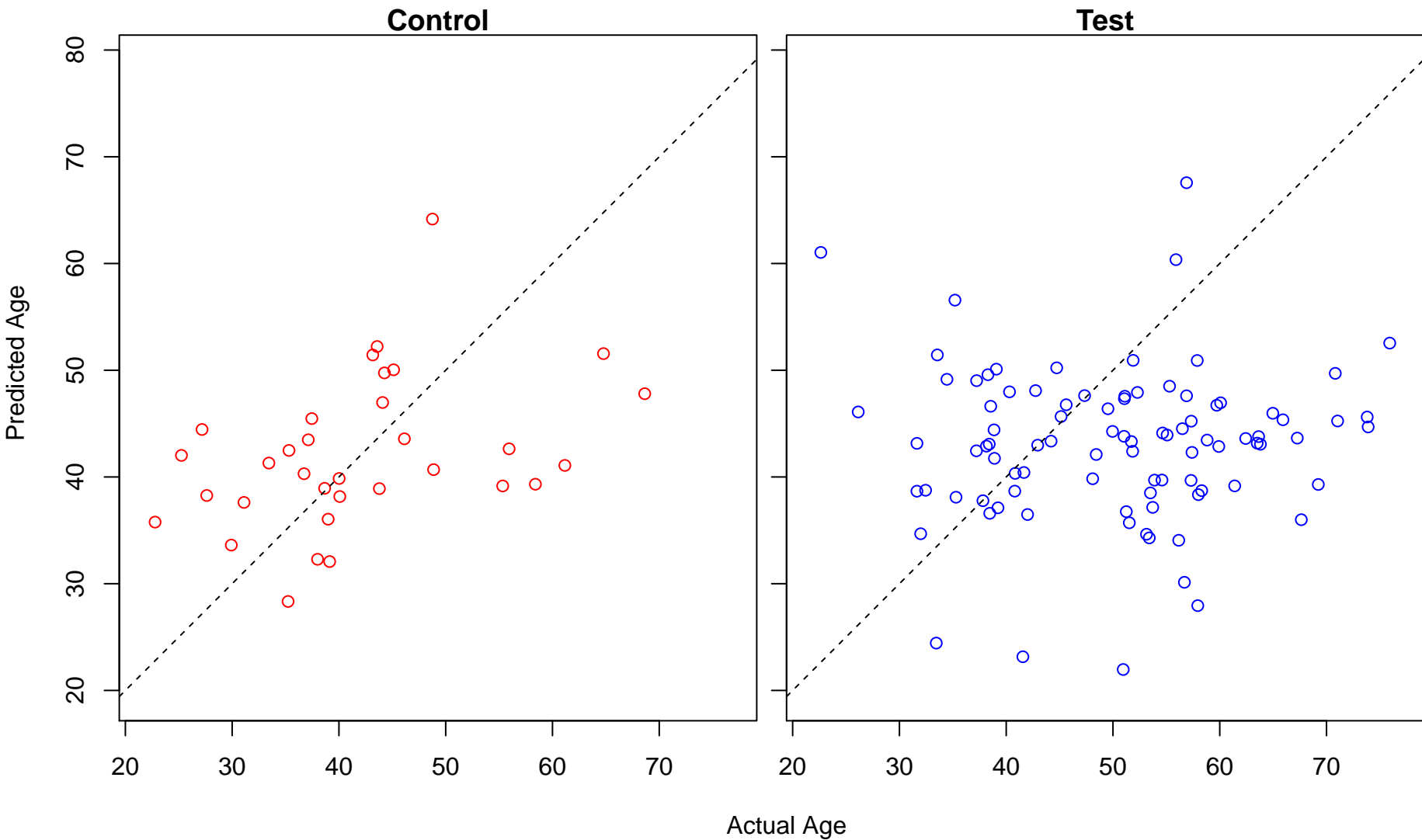
primary metabolic process (Score: 0.636407)



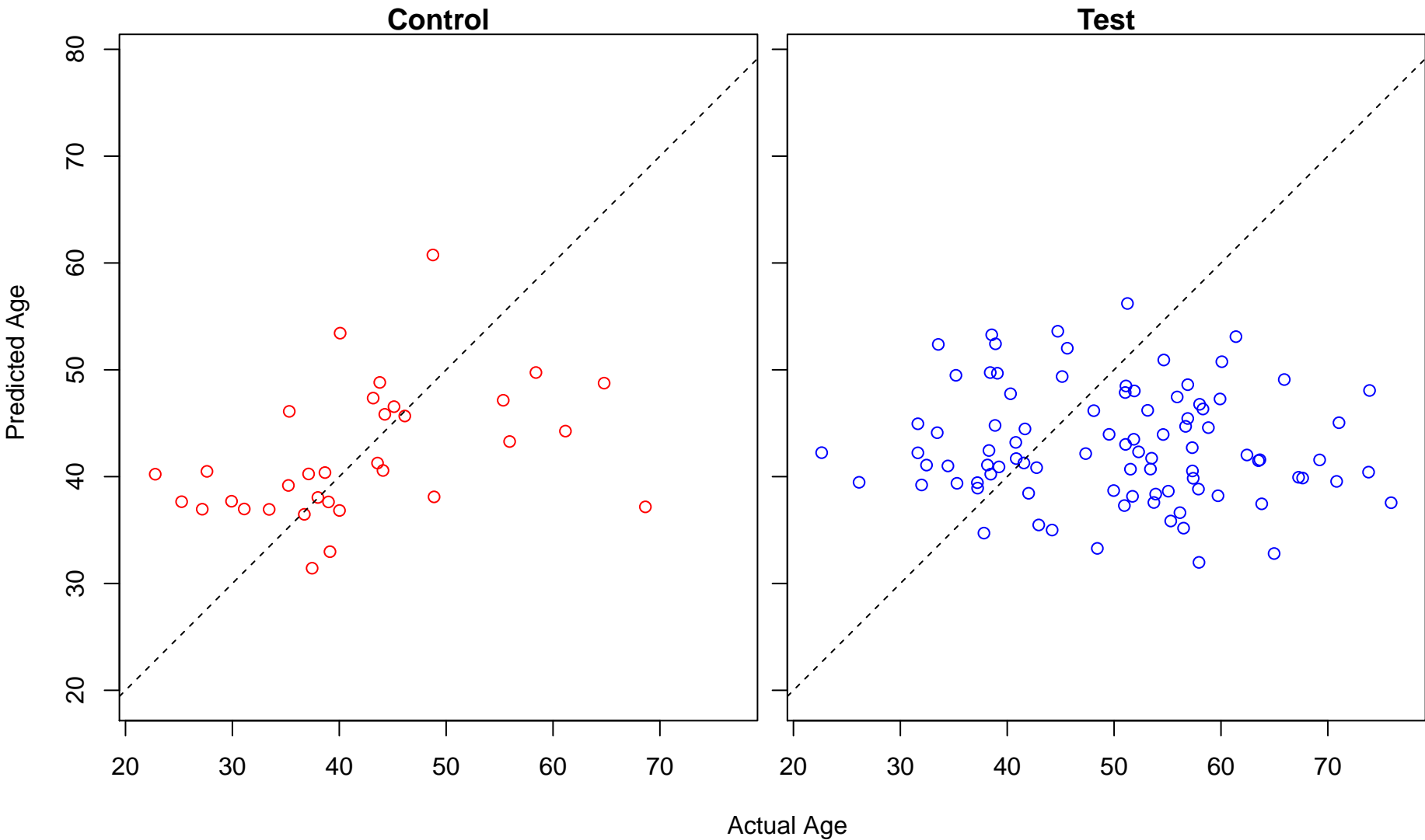
cellular process (Score: 0.636200)



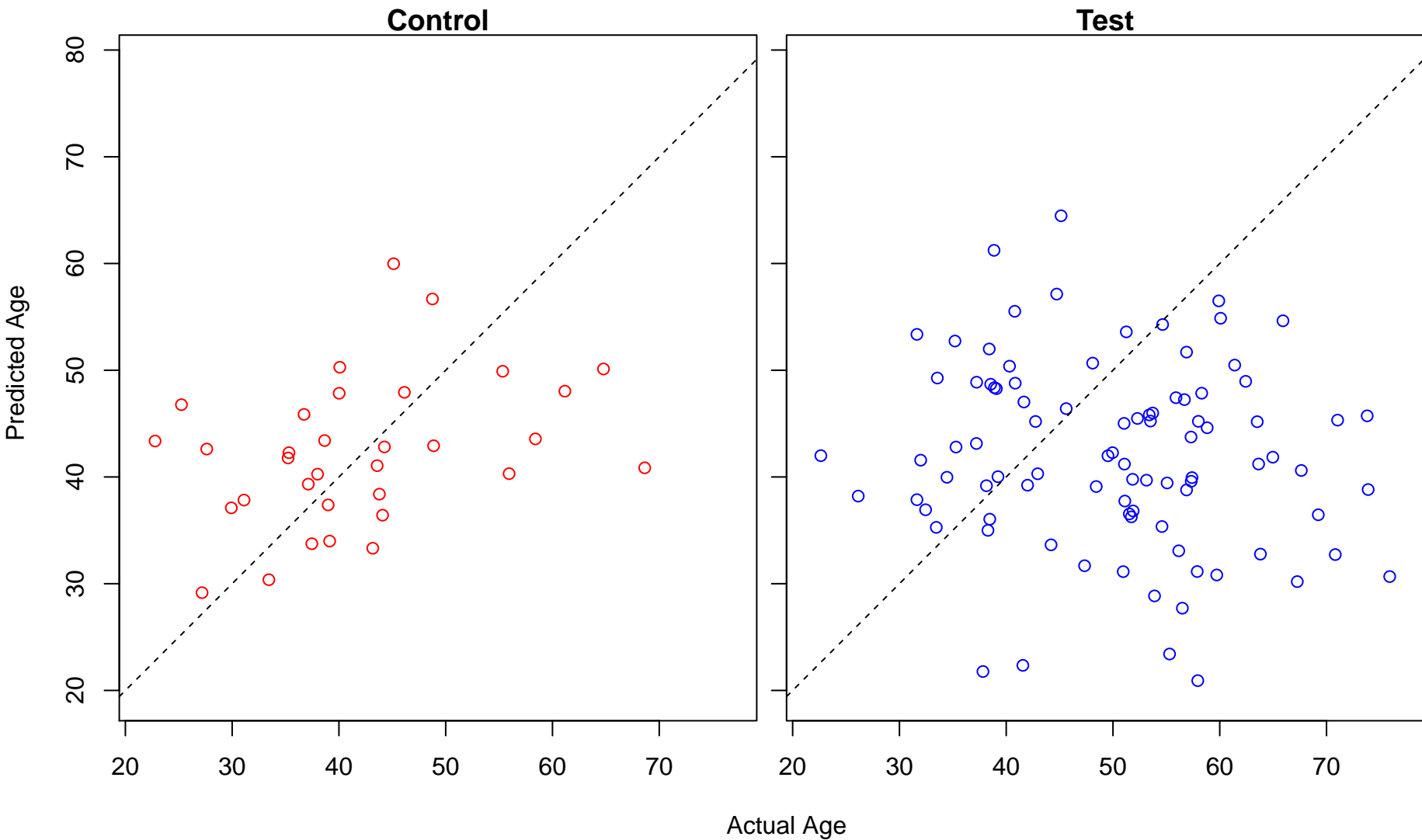
negative regulation of cell cycle arrest (Score: 0.636033)



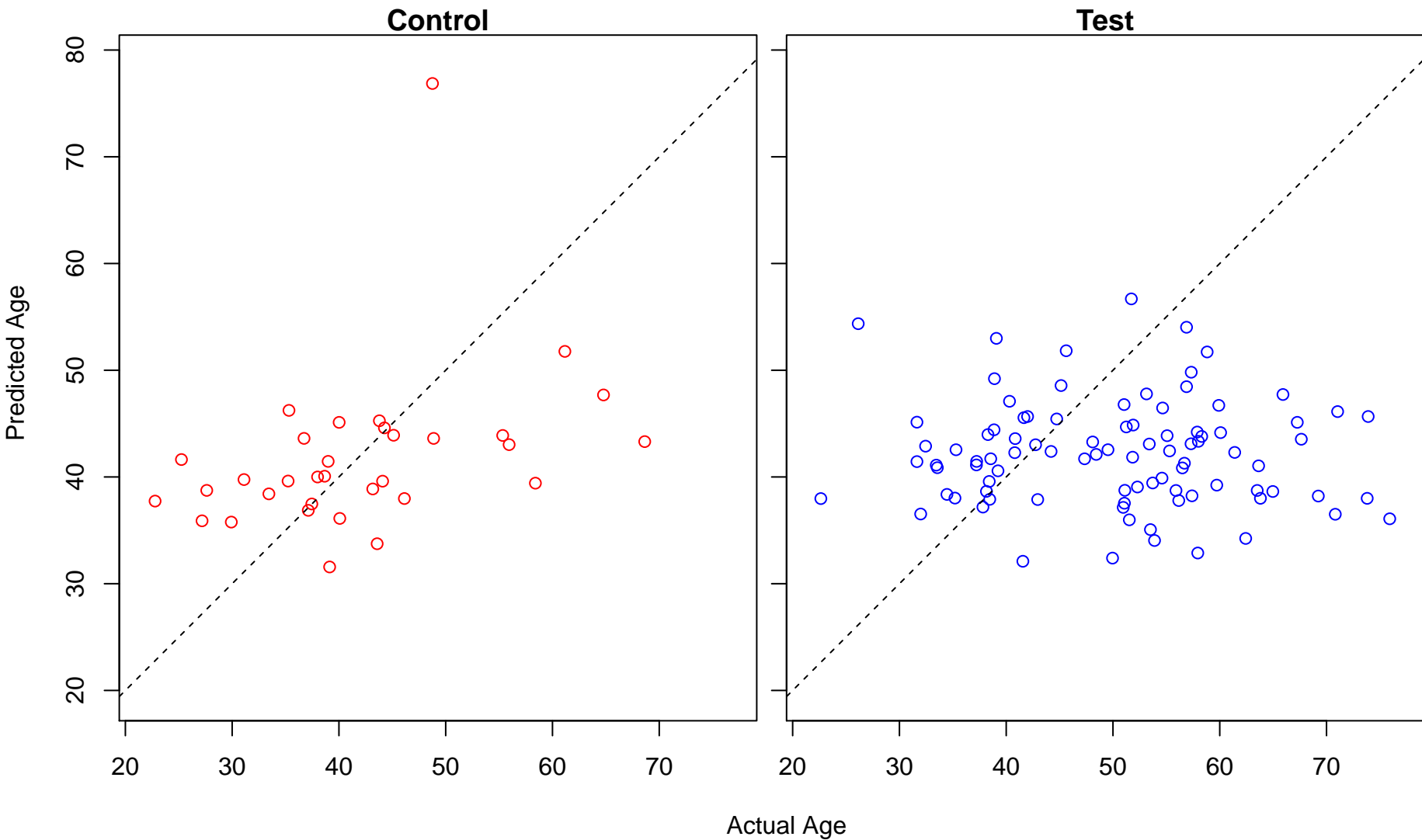
positive regulation of antigen receptor-mediated signaling pathway (Score: 0.635155)



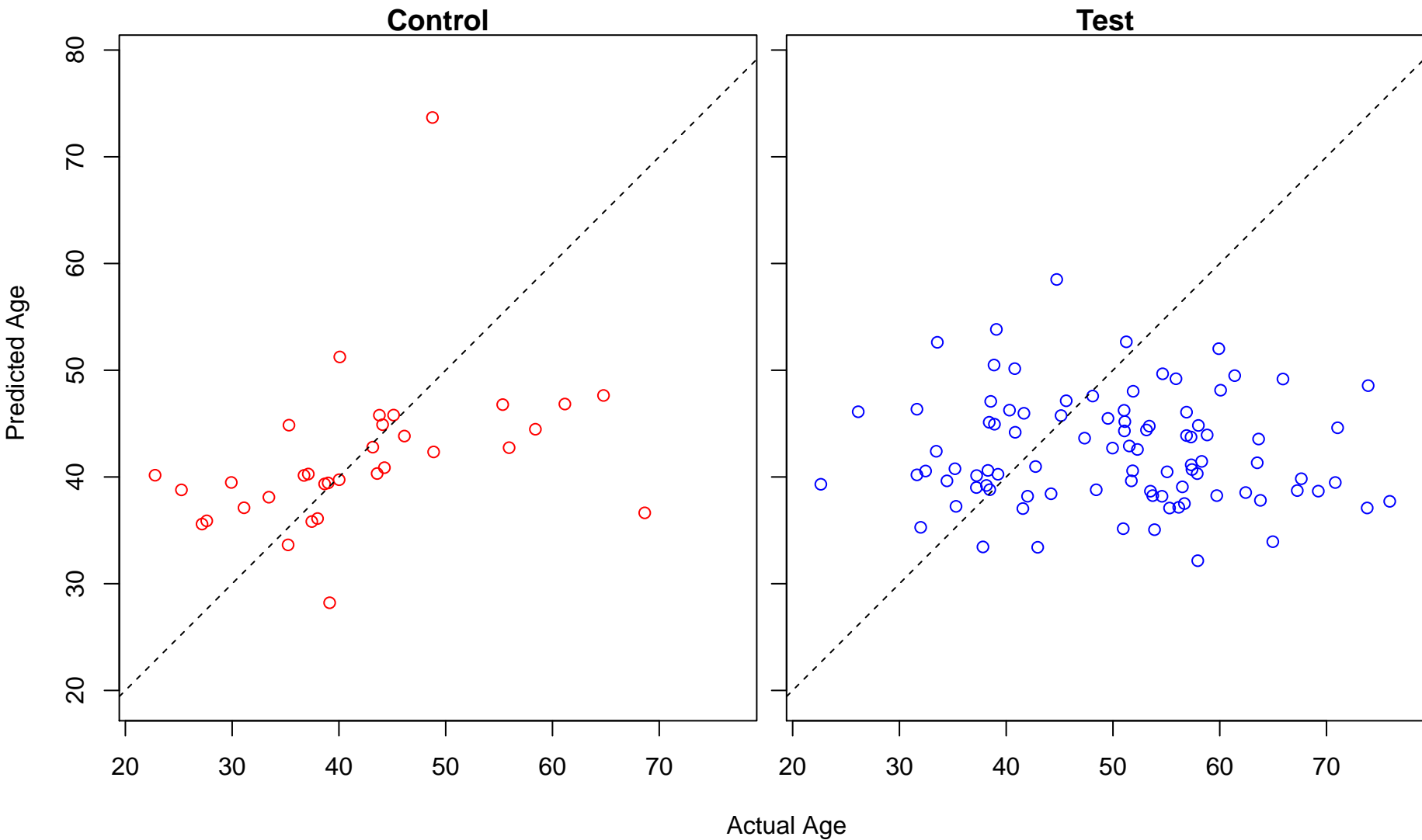
regulation of T cell chemotaxis (Score: 0.635018)



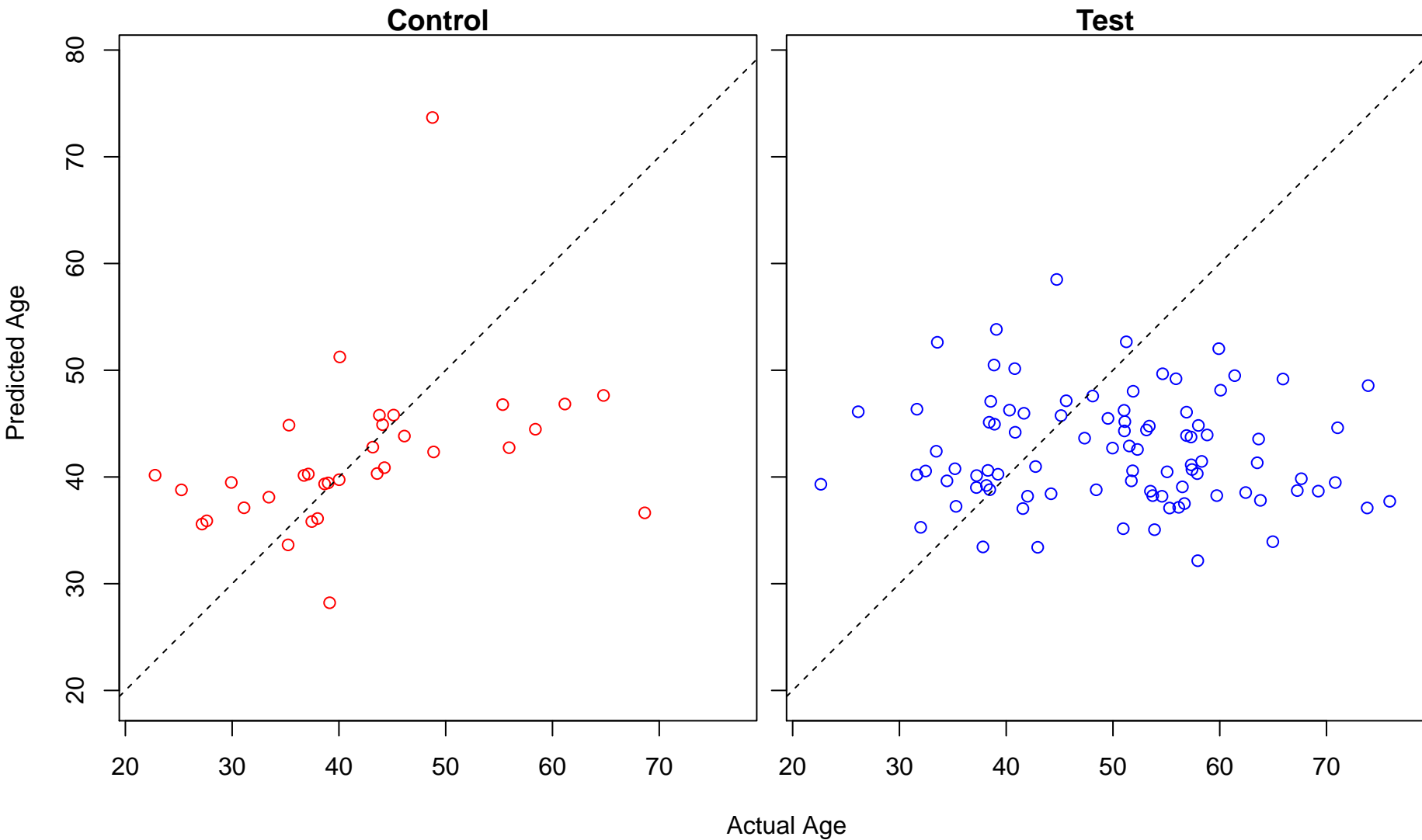
positive regulation of chromatin silencing (Score: 0.634673)



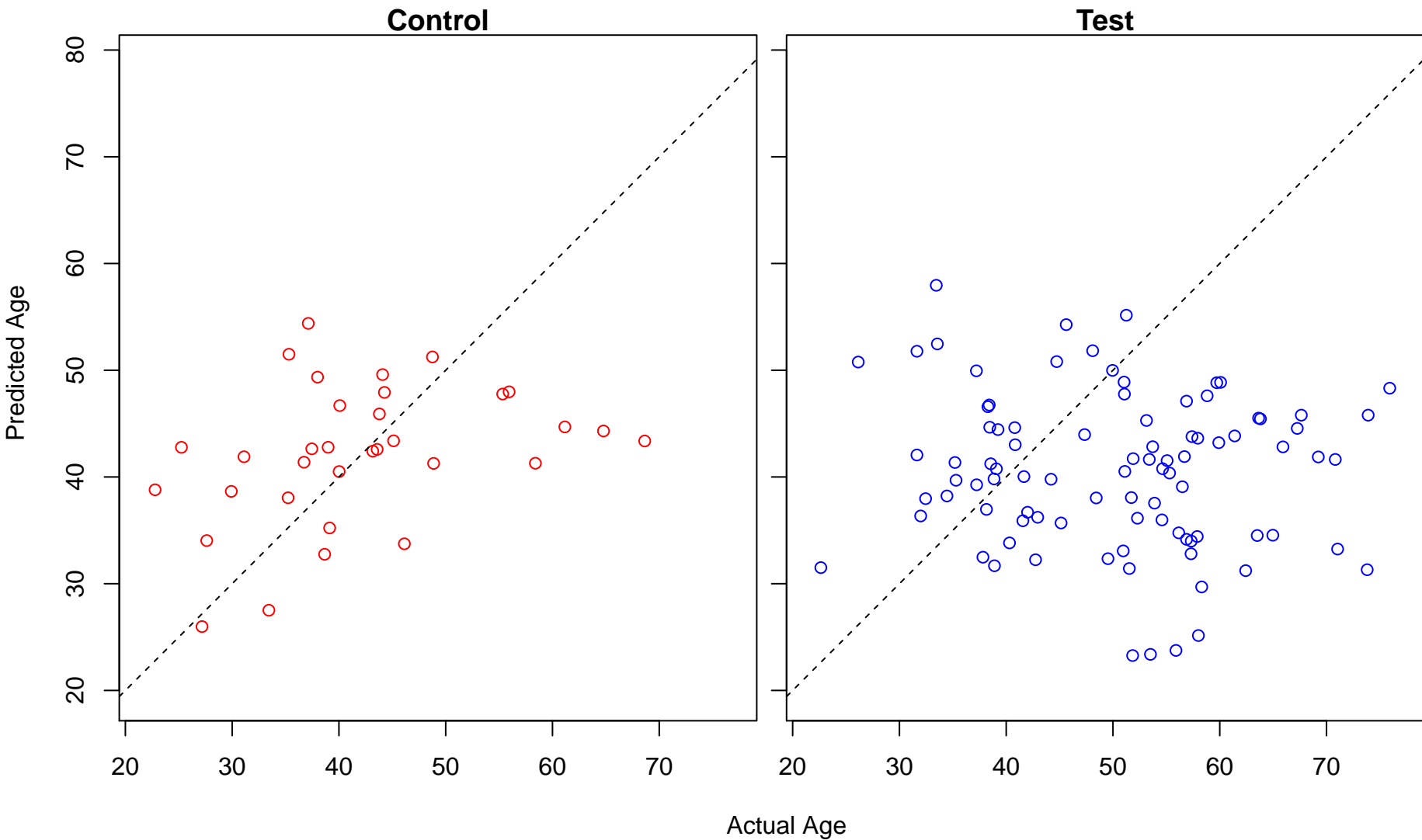
protein glycosylation (Score: 0.634022)



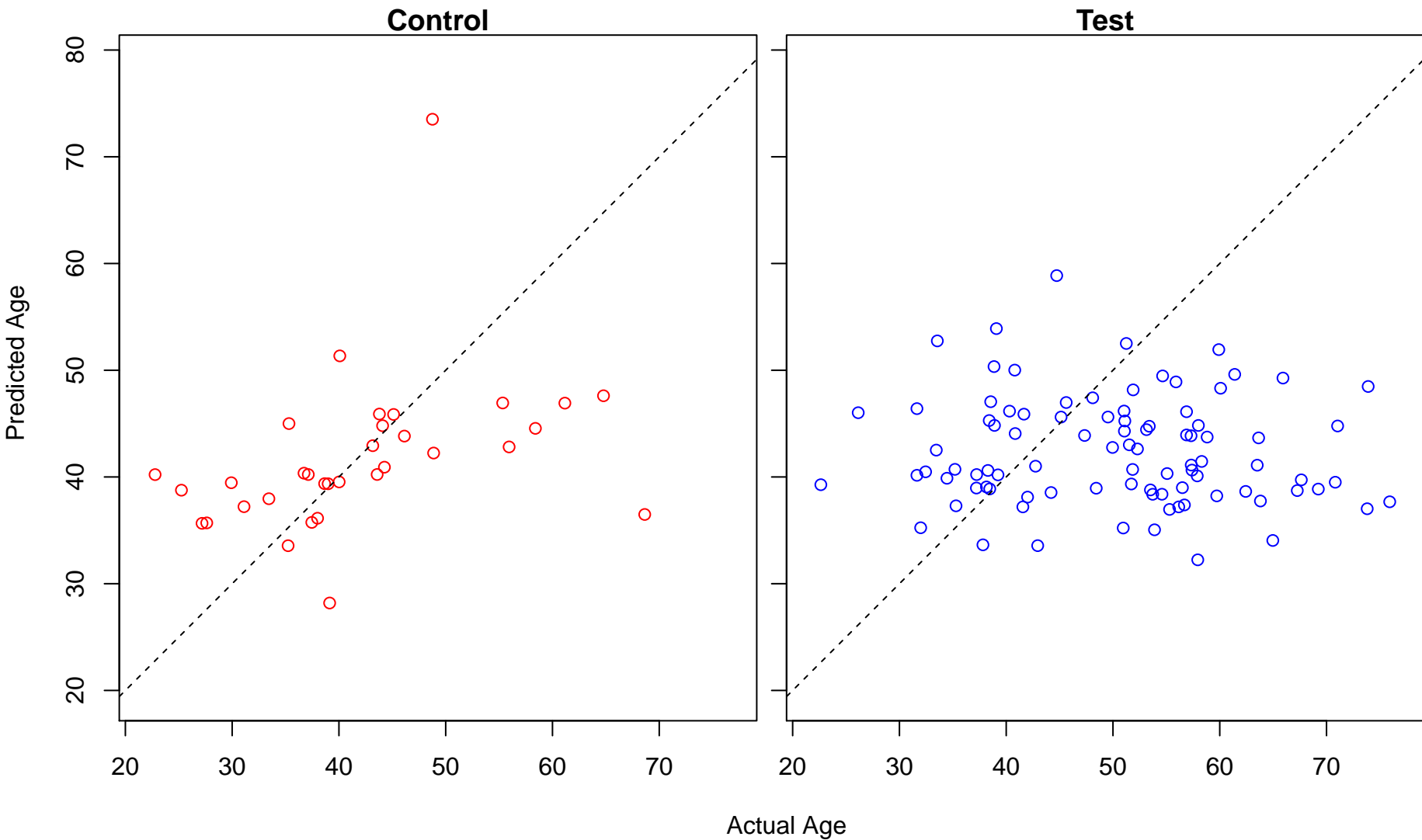
macromolecule glycosylation (Score: 0.634022)



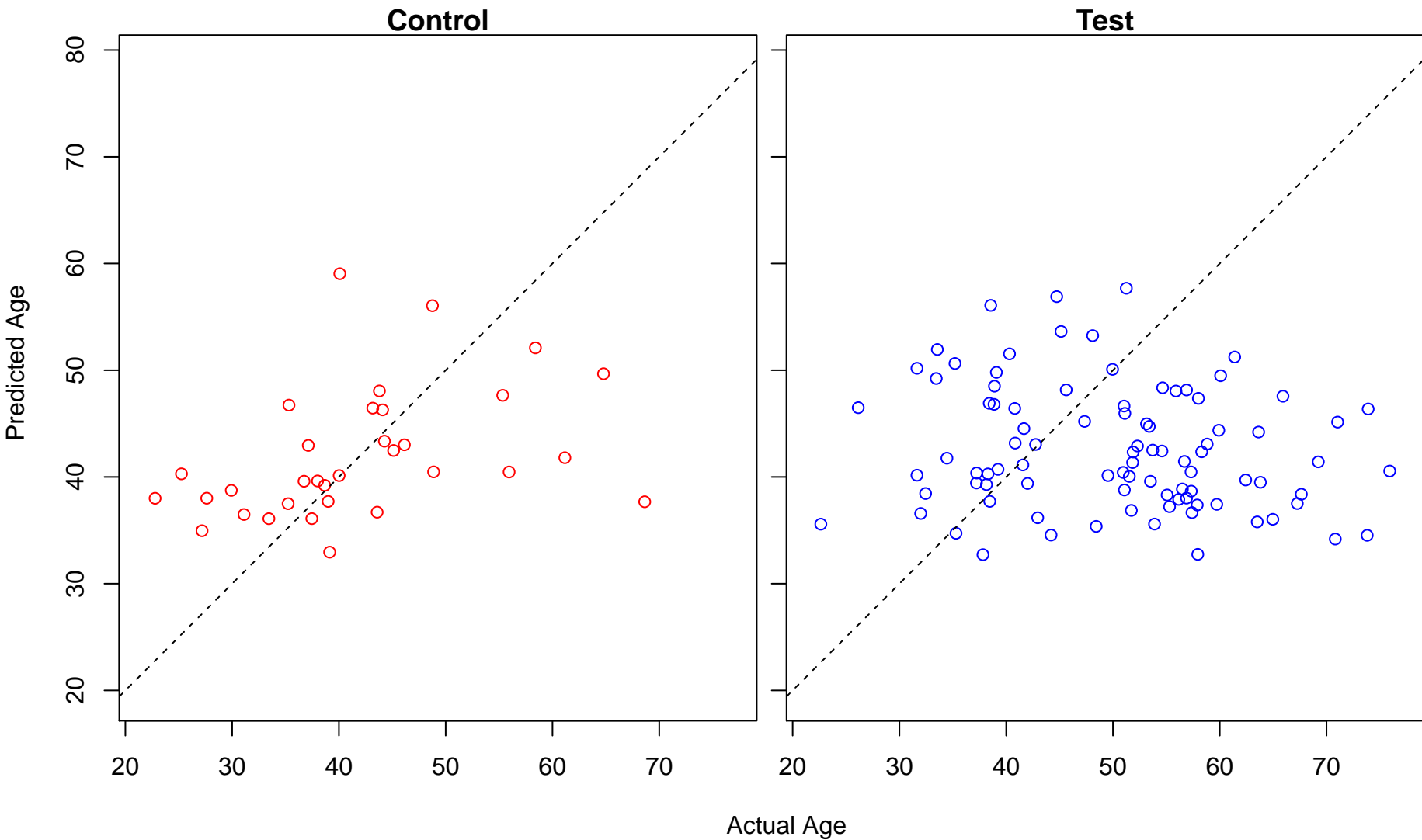
regulation of MHC class II biosynthetic process (Score: 0.633927)



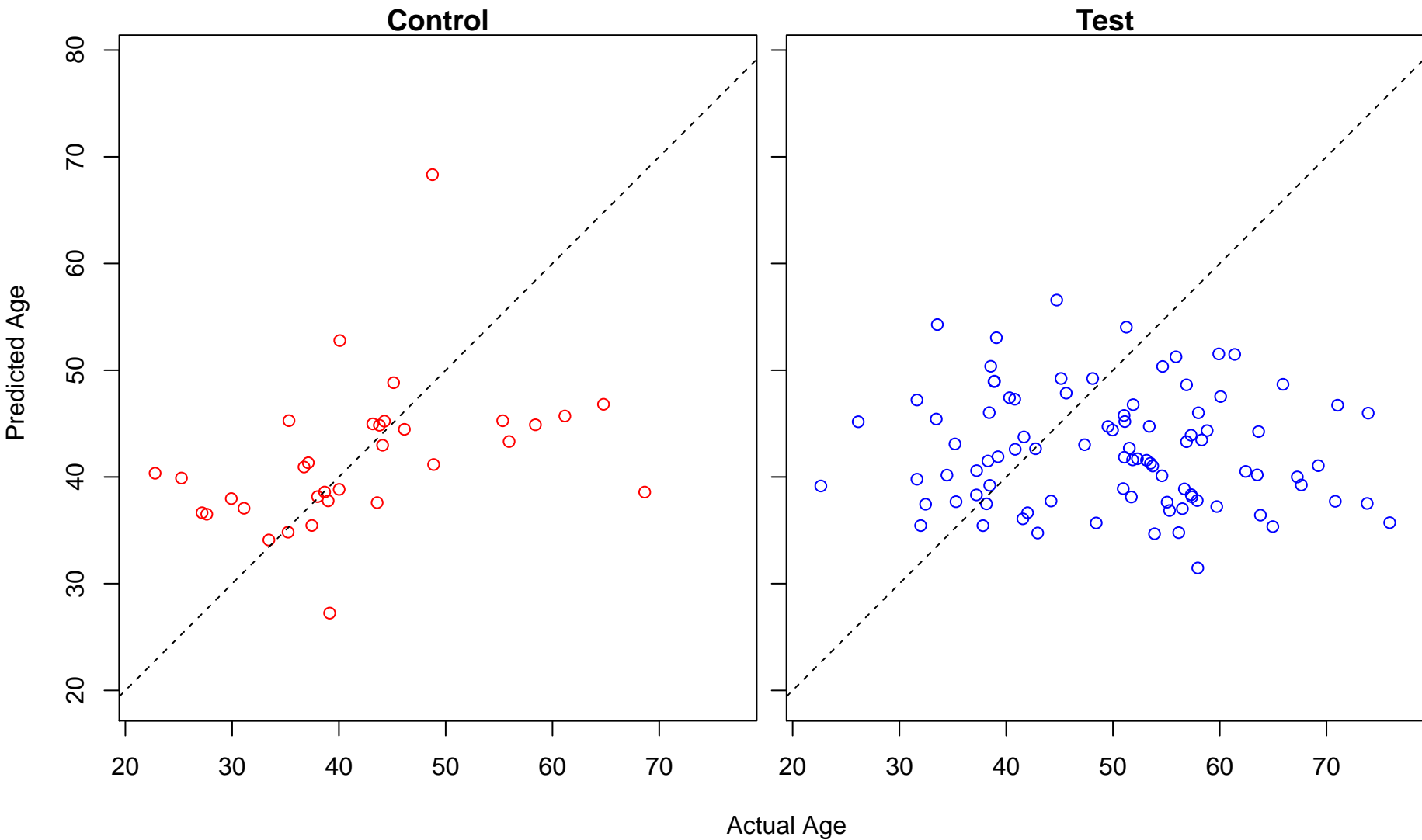
glycosylation (Score: 0.633680)



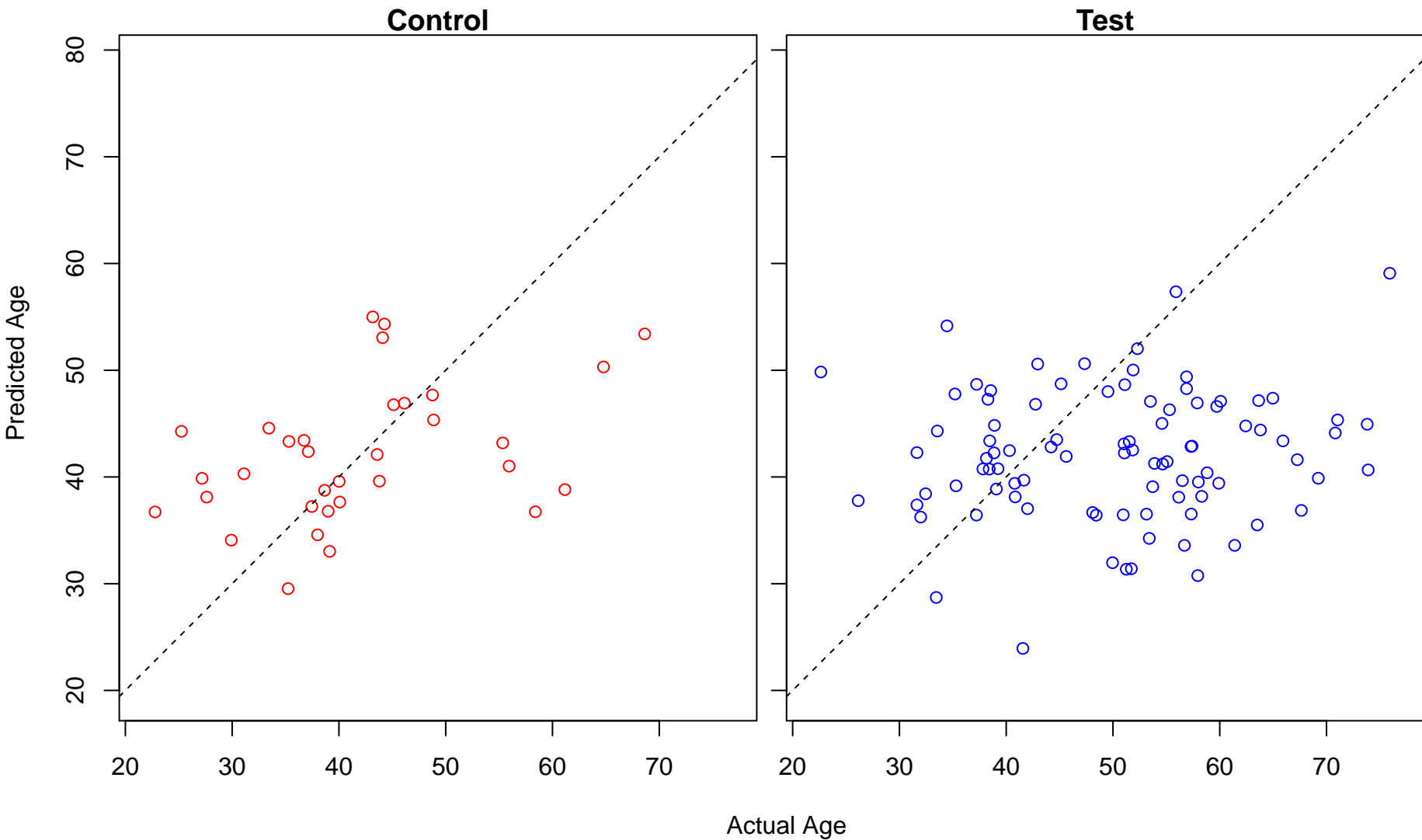
establishment or maintenance of apical/basal cell polarity (Score: 0.633285)



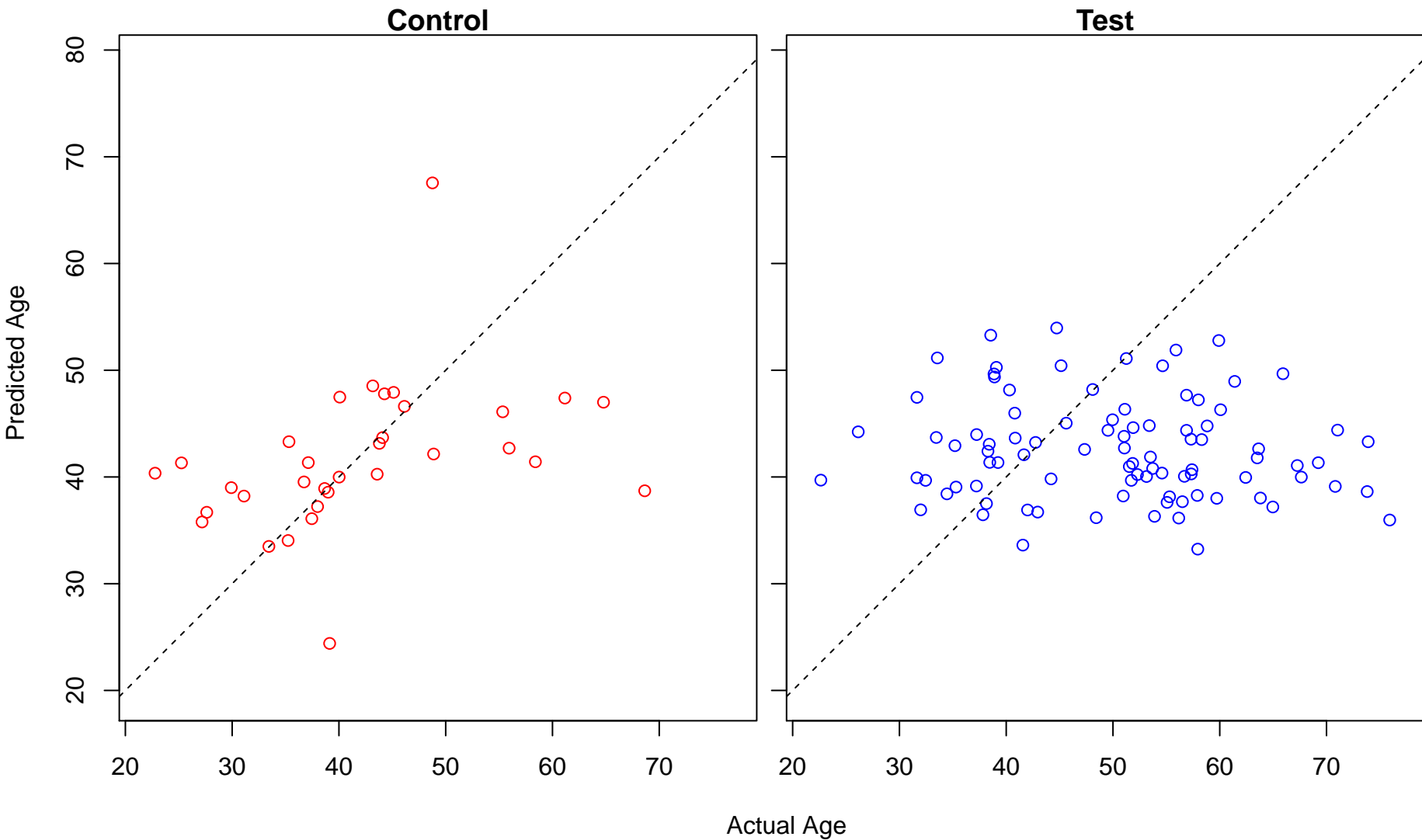
cellular metabolic process (Score: 0.633278)



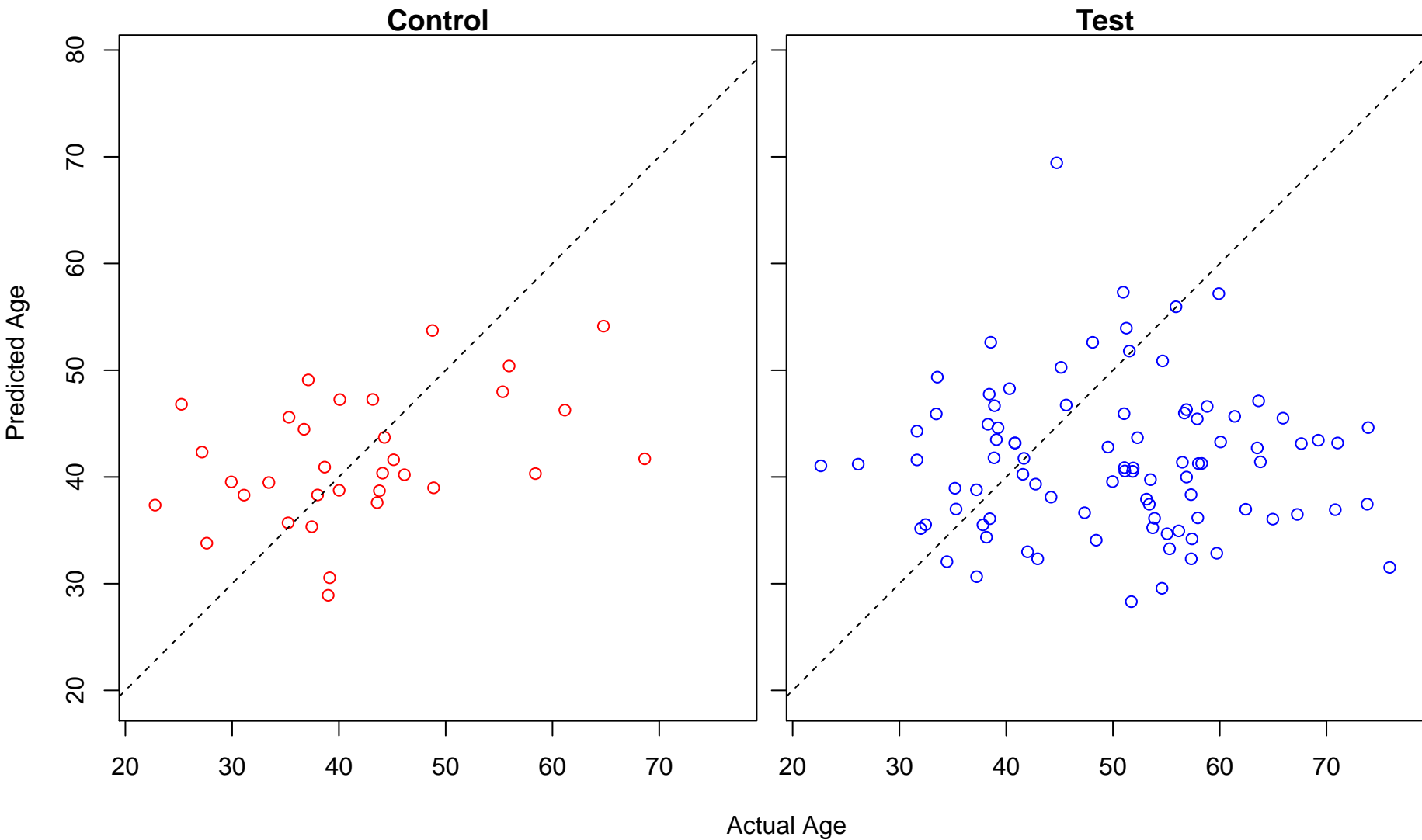
DNA integration (Score: 0.633270)



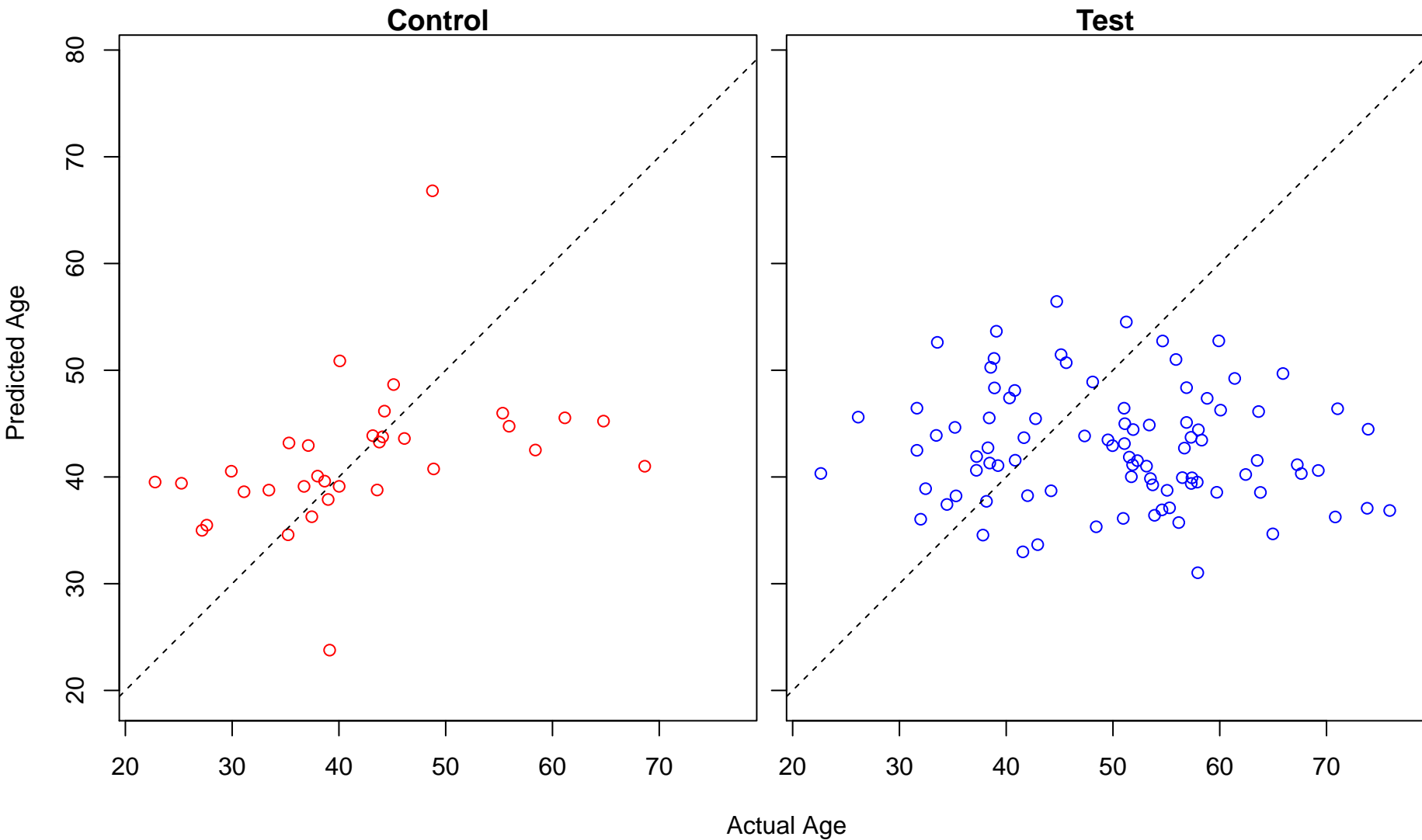
cell cycle process (Score: 0.633218)



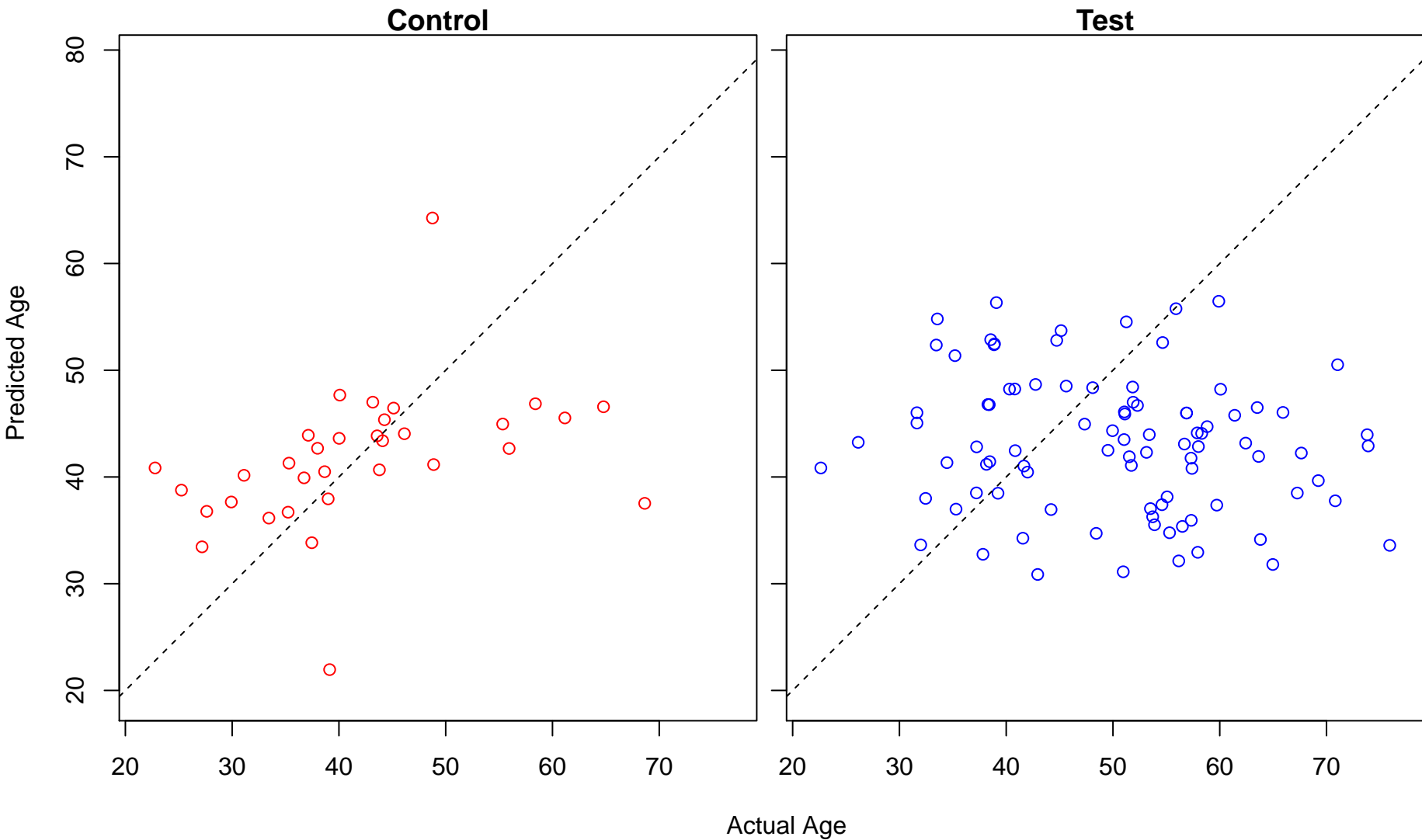
hepaticobiliary system development (Score: 0.633144)



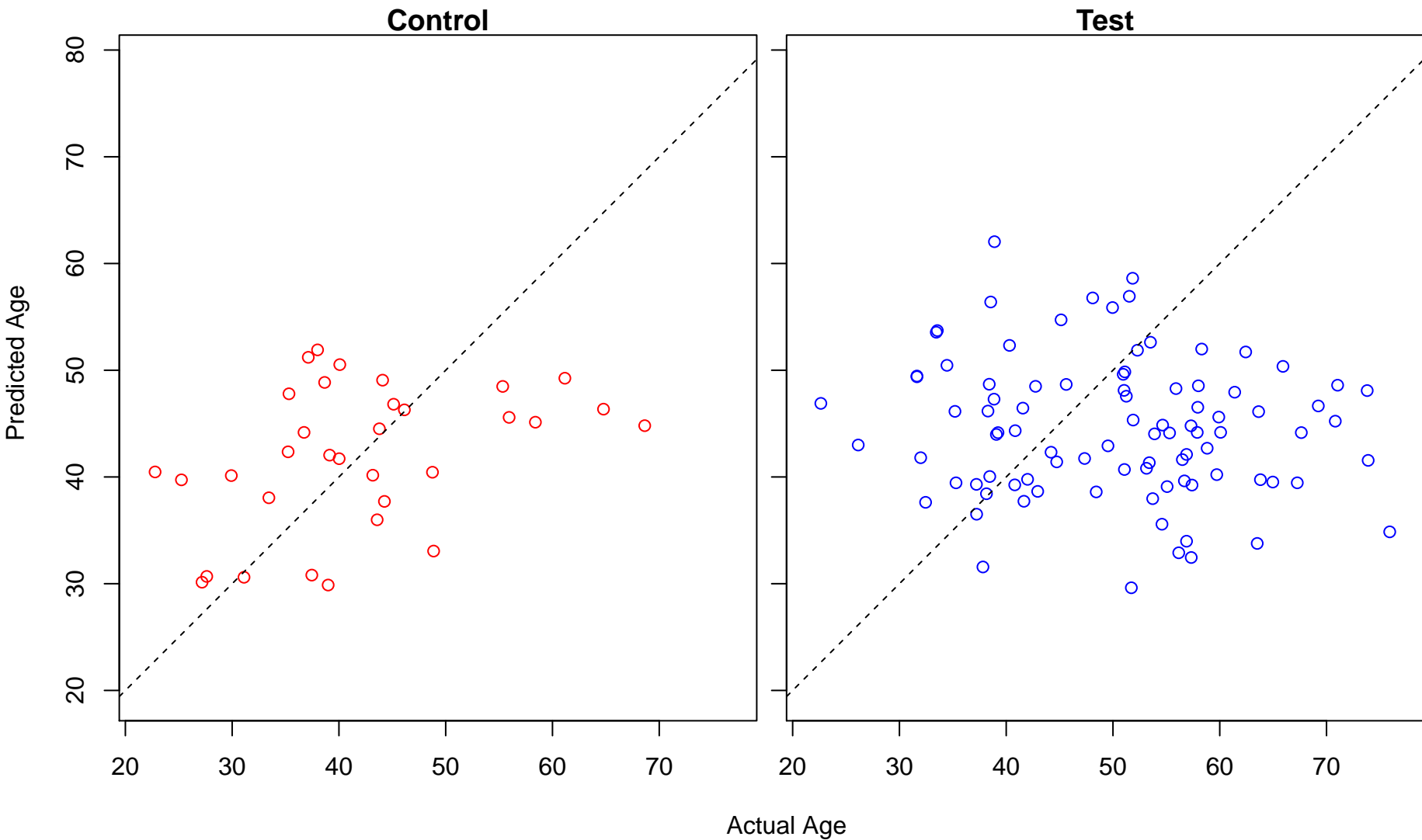
response to endogenous stimulus (Score: 0.633005)



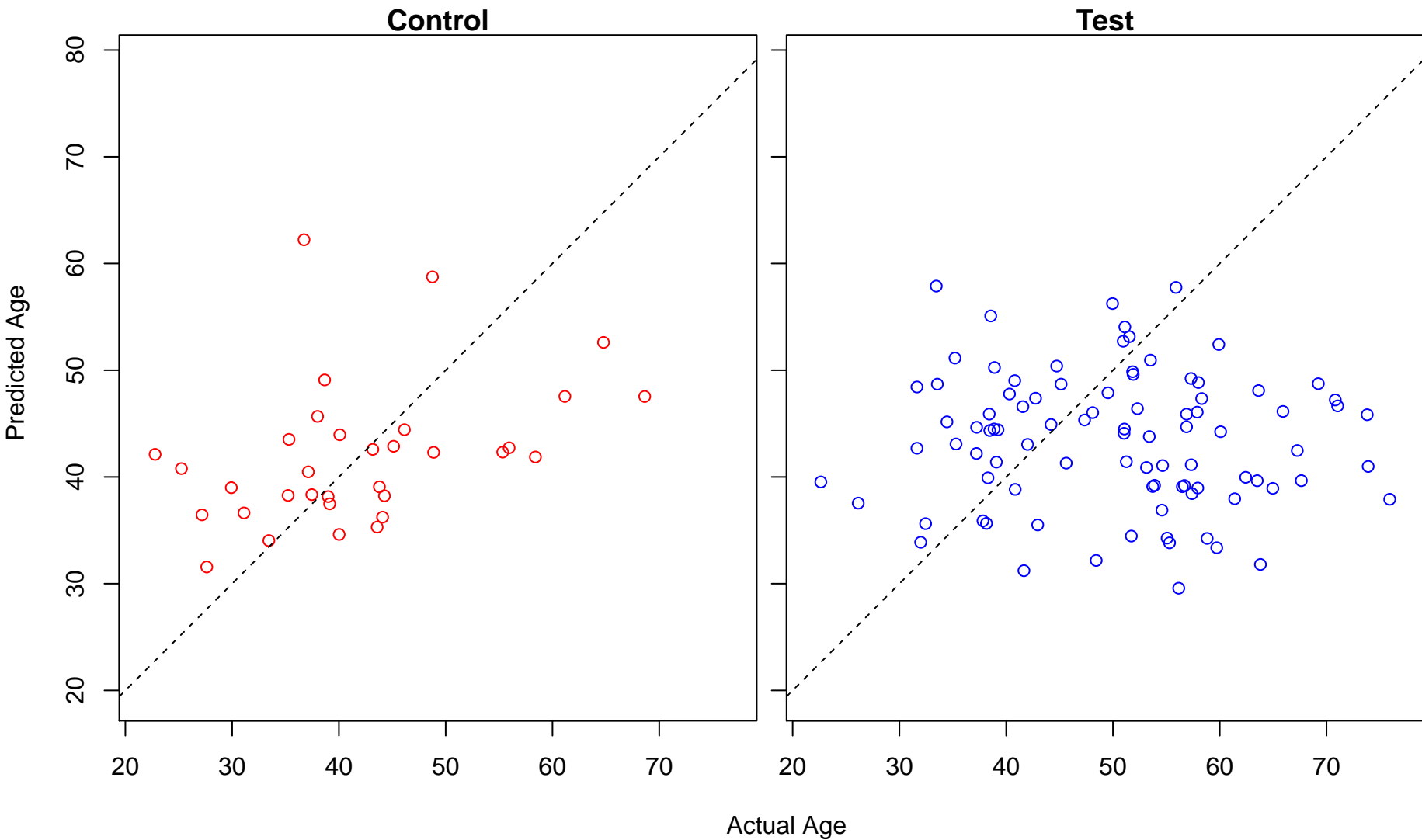
divalent metal ion transport (Score: 0.632894)



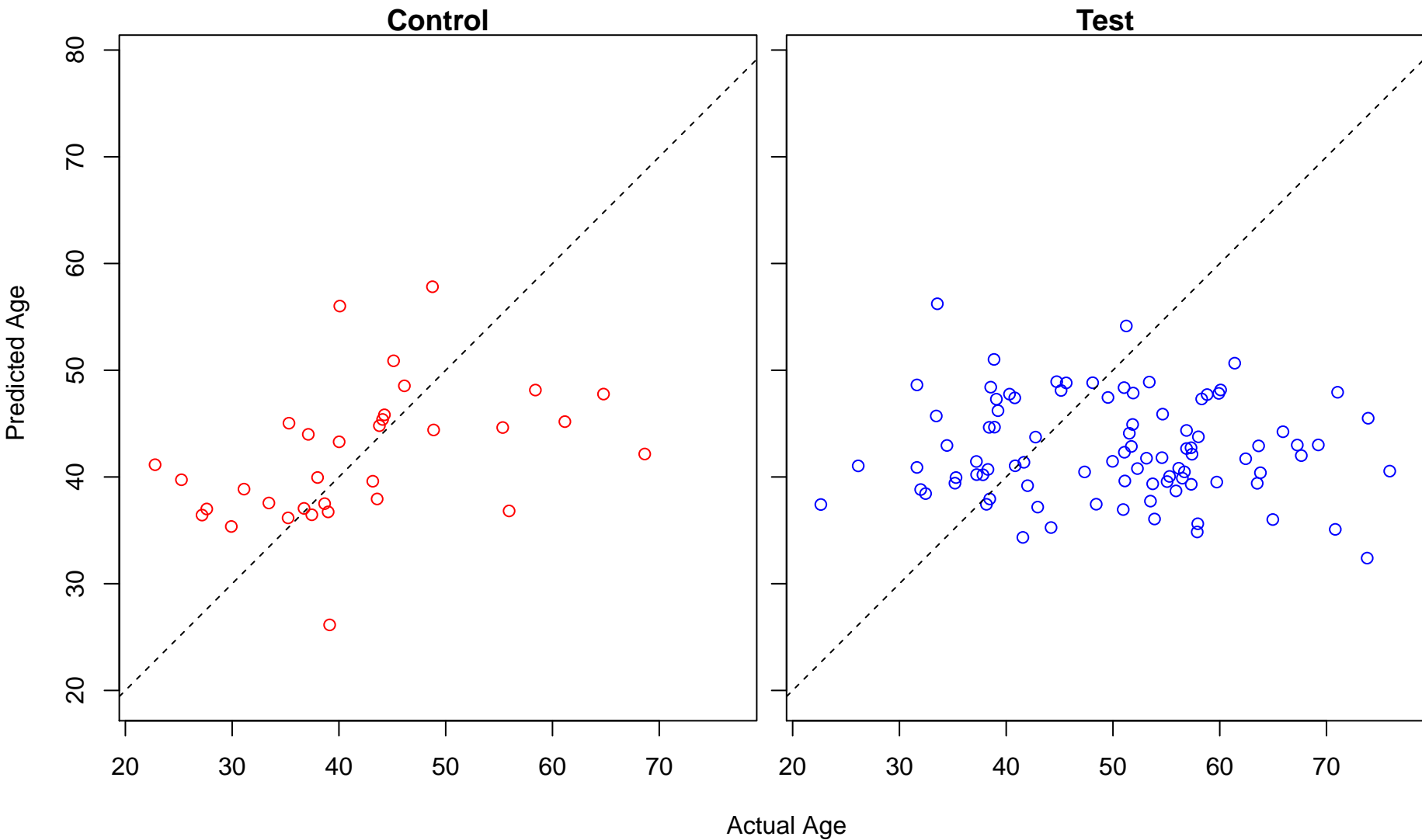
smooth muscle tissue development (Score: 0.631551)



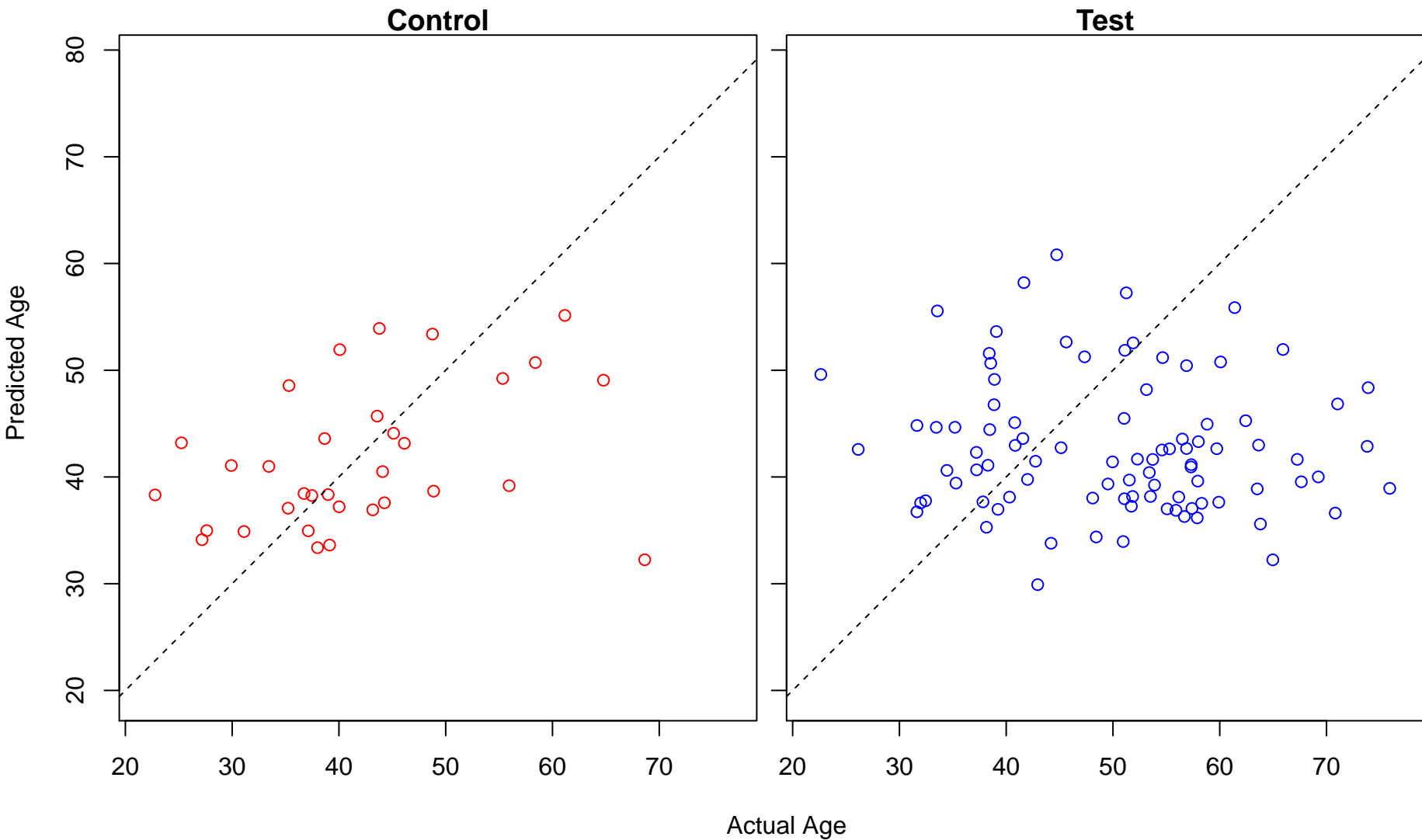
negative regulation of interleukin-1 production (Score: 0.630832)



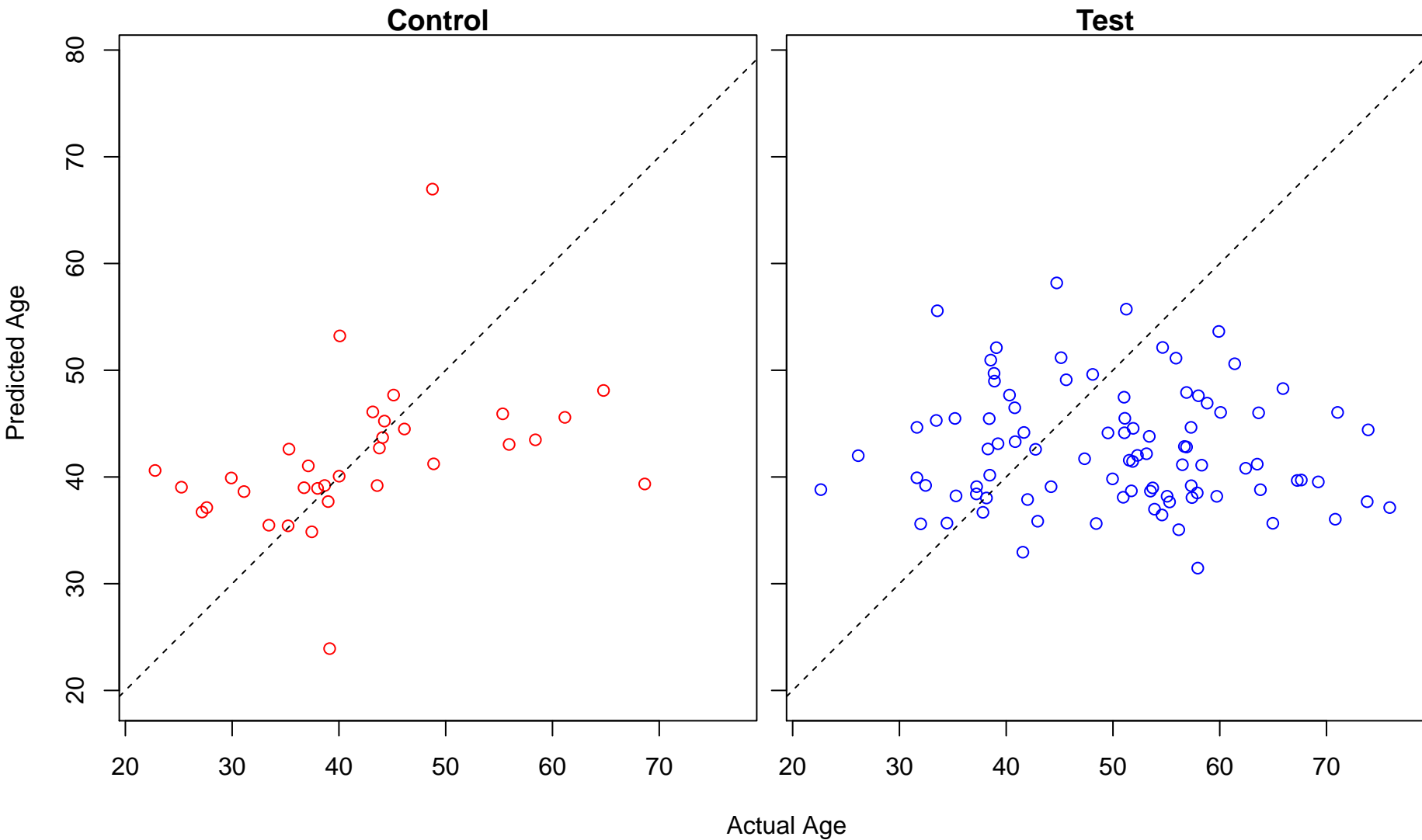
actin polymerization or depolymerization (Score: 0.630650)



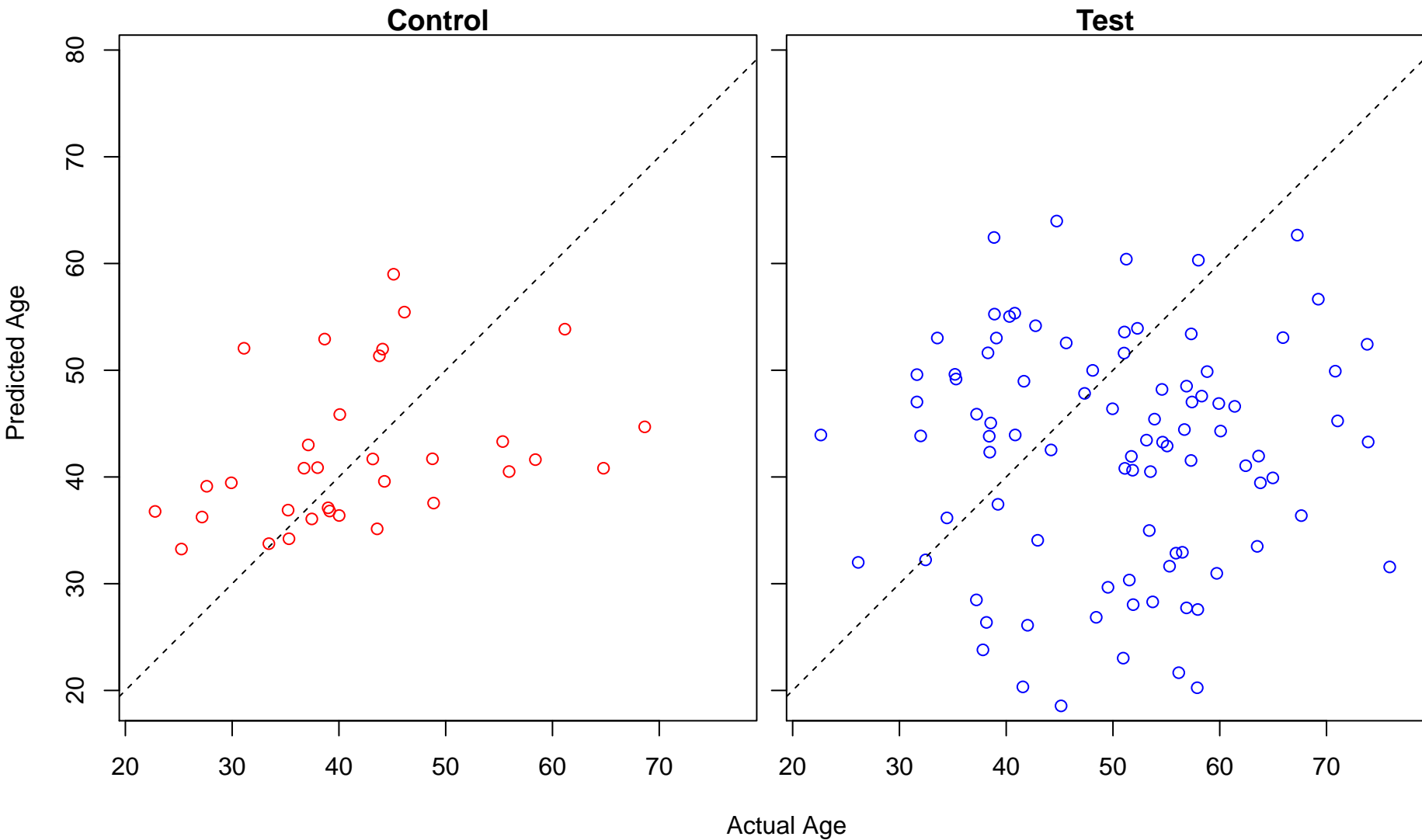
somatic recombination of immunoglobulin gene segments (Score: 0.630349)



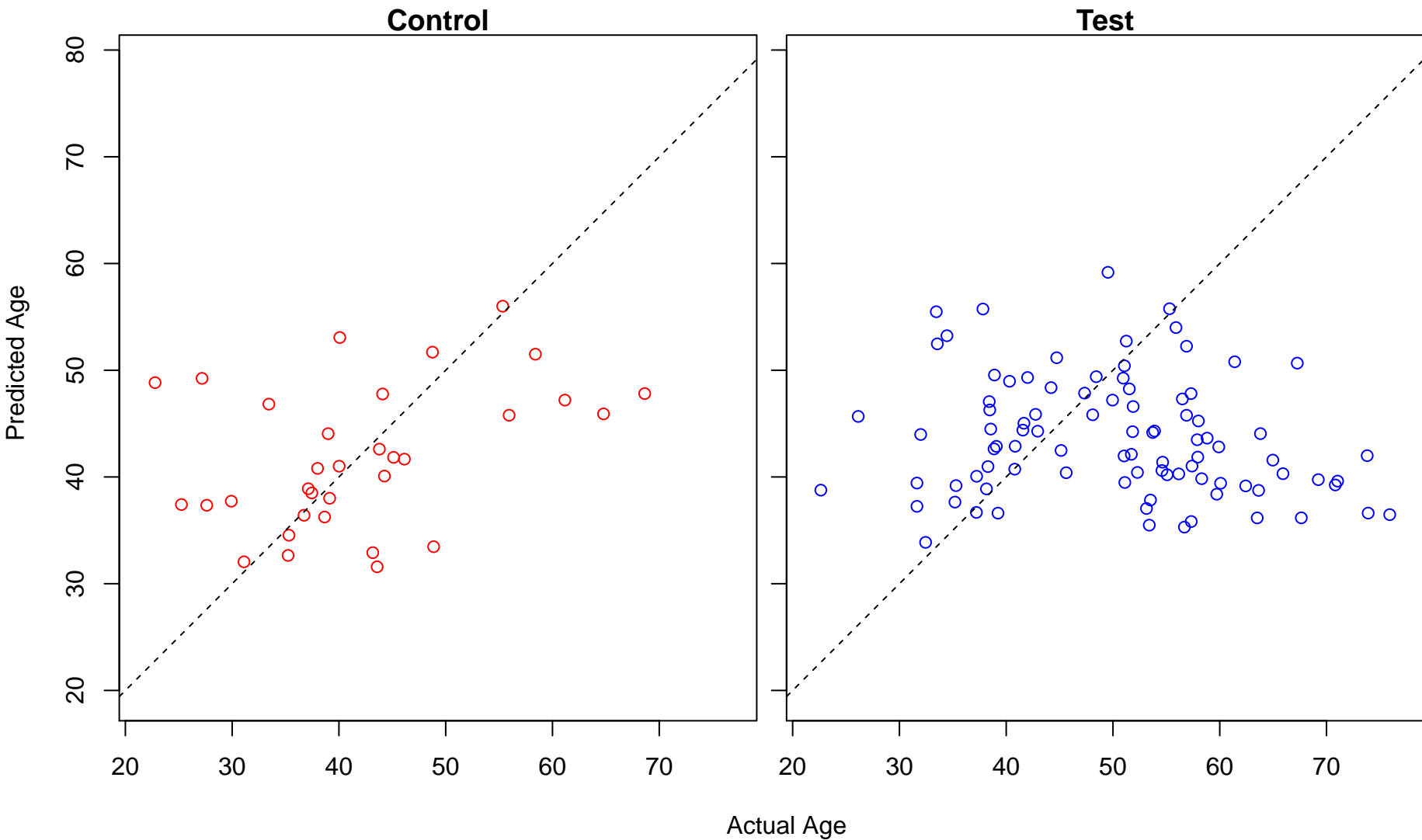
neurotrophin TRK receptor signaling pathway (Score: 0.628881)



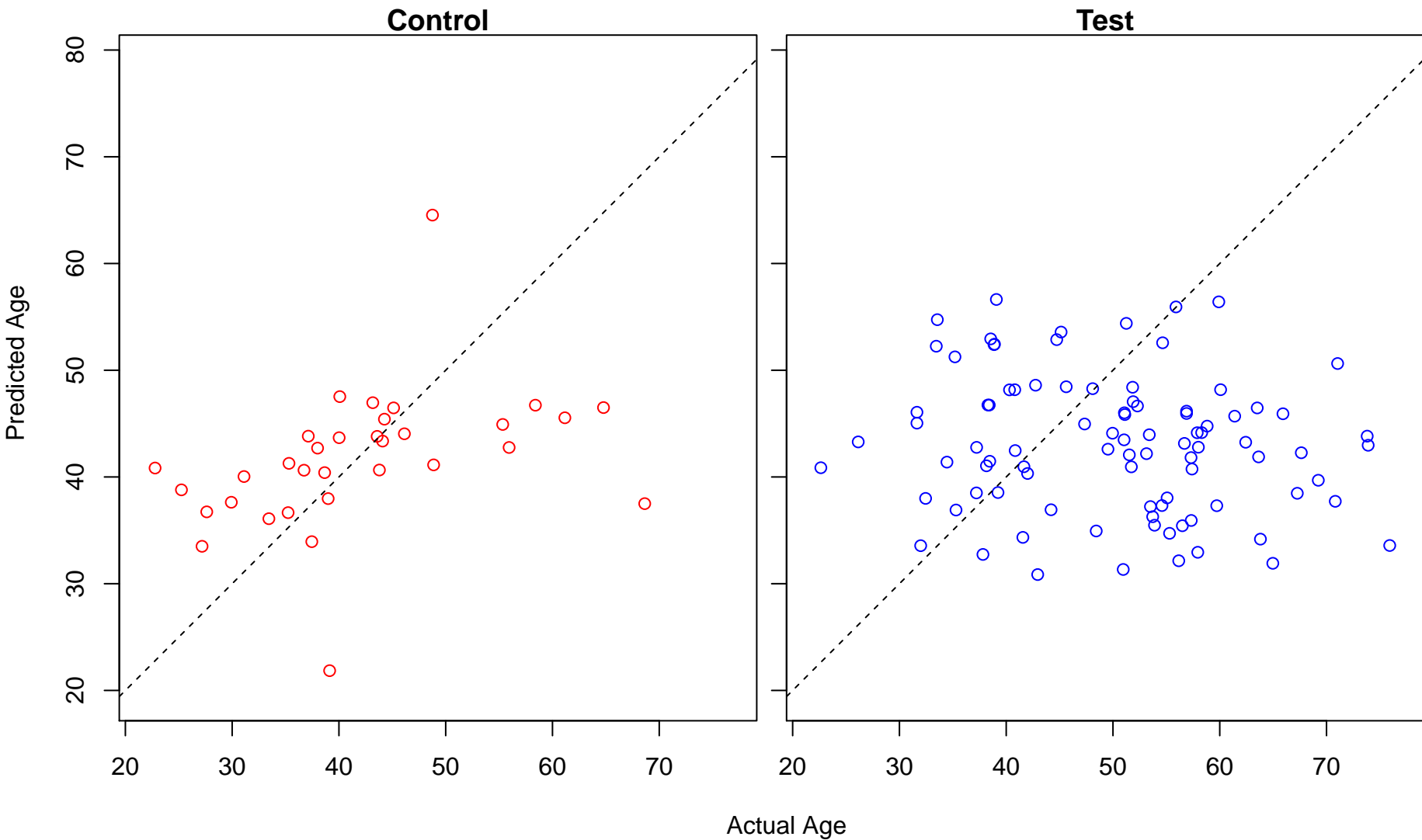
regulation of ventricular cardiac muscle cell action potential (Score: 0.628790)



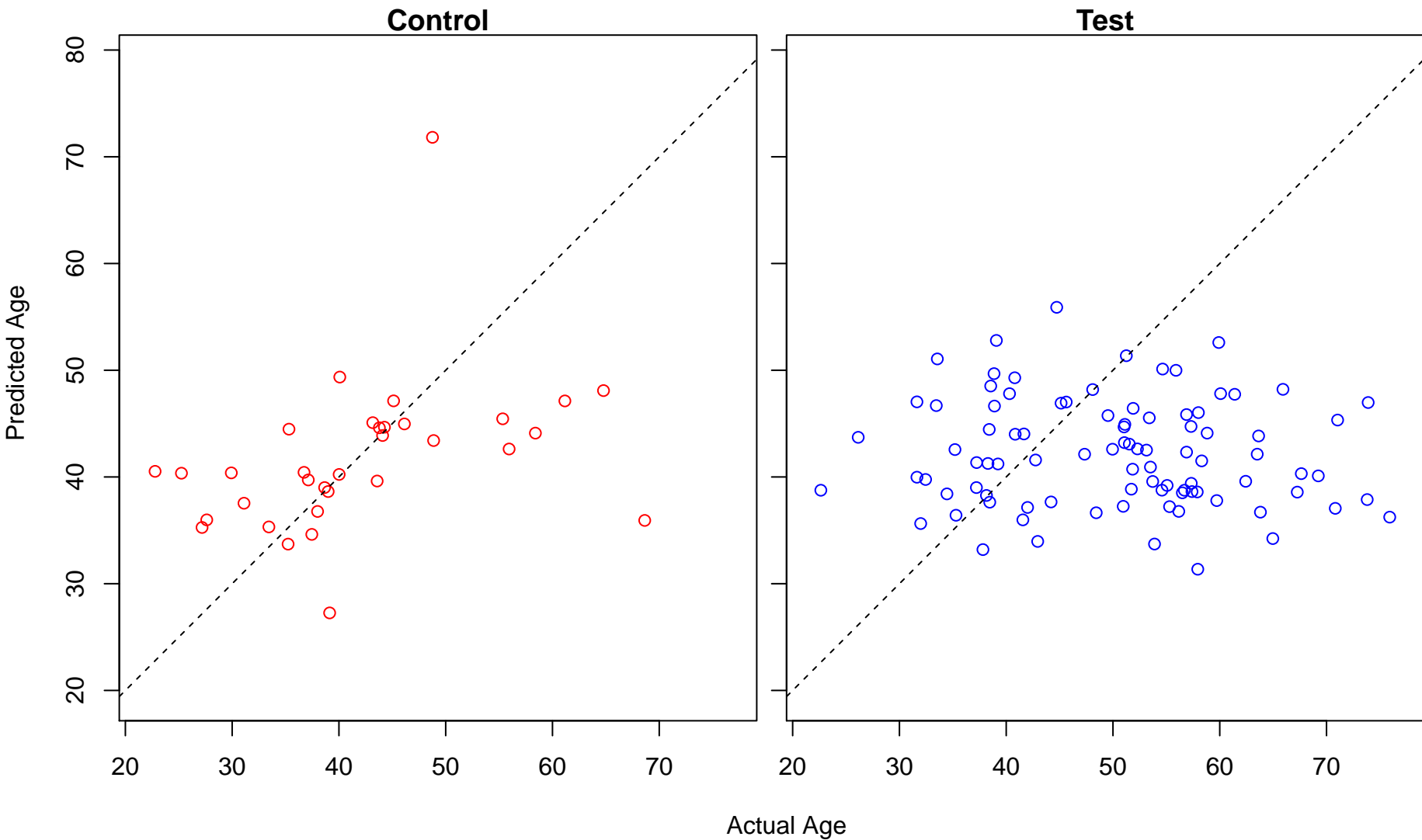
I-kappaB phosphorylation (Score: 0.628547)



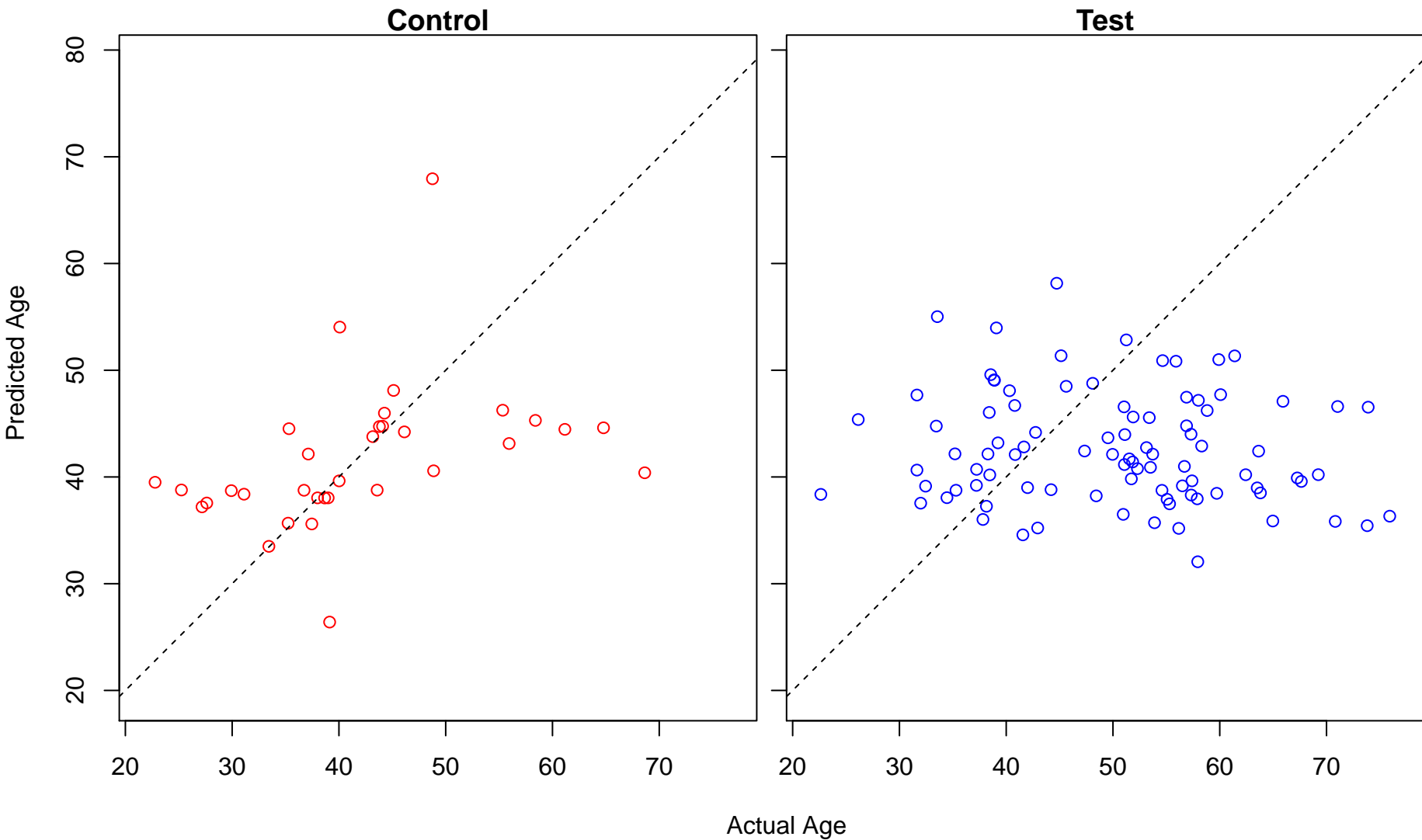
divalent inorganic cation transport (Score: 0.628471)



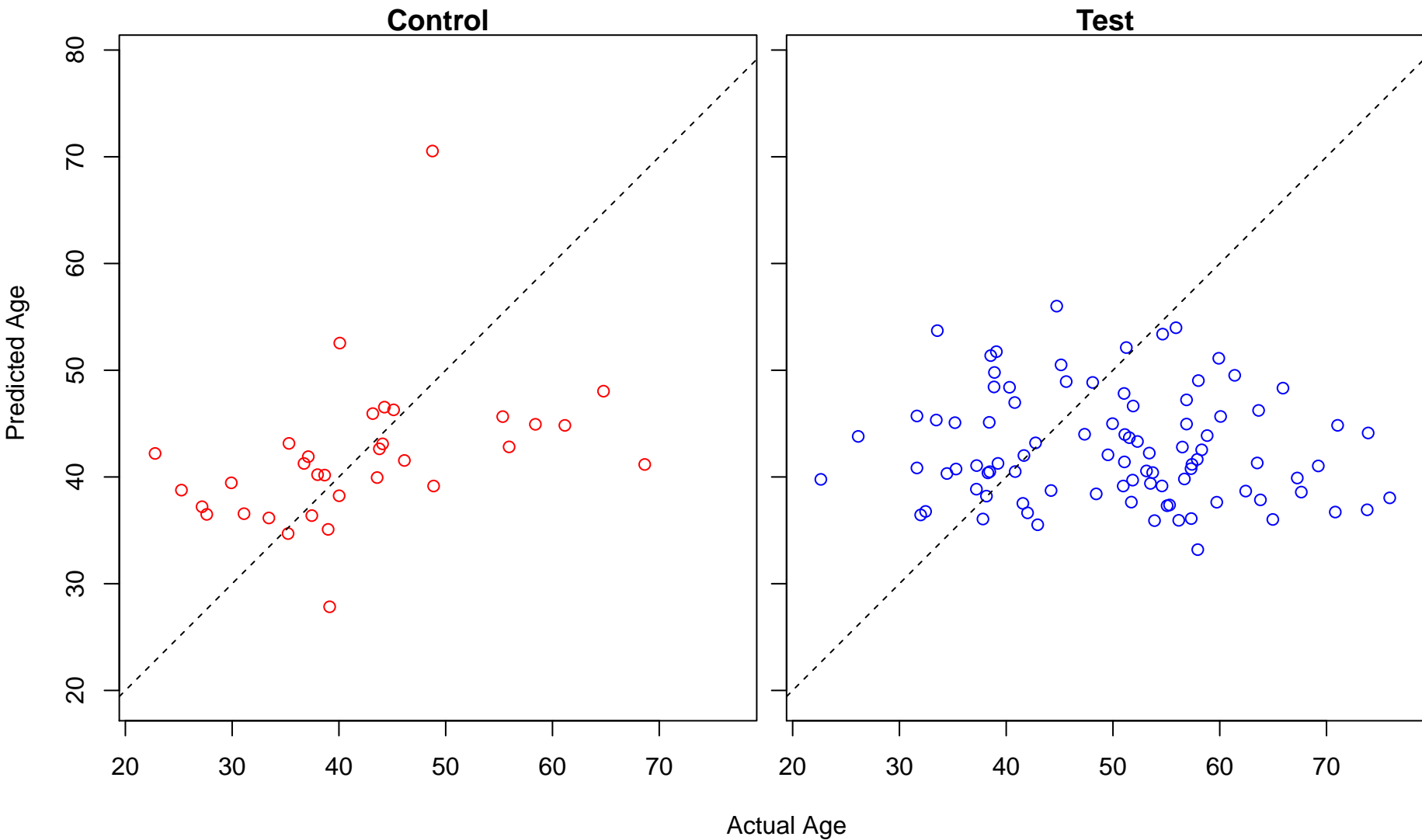
single-organism carbohydrate metabolic process (Score: 0.628022)



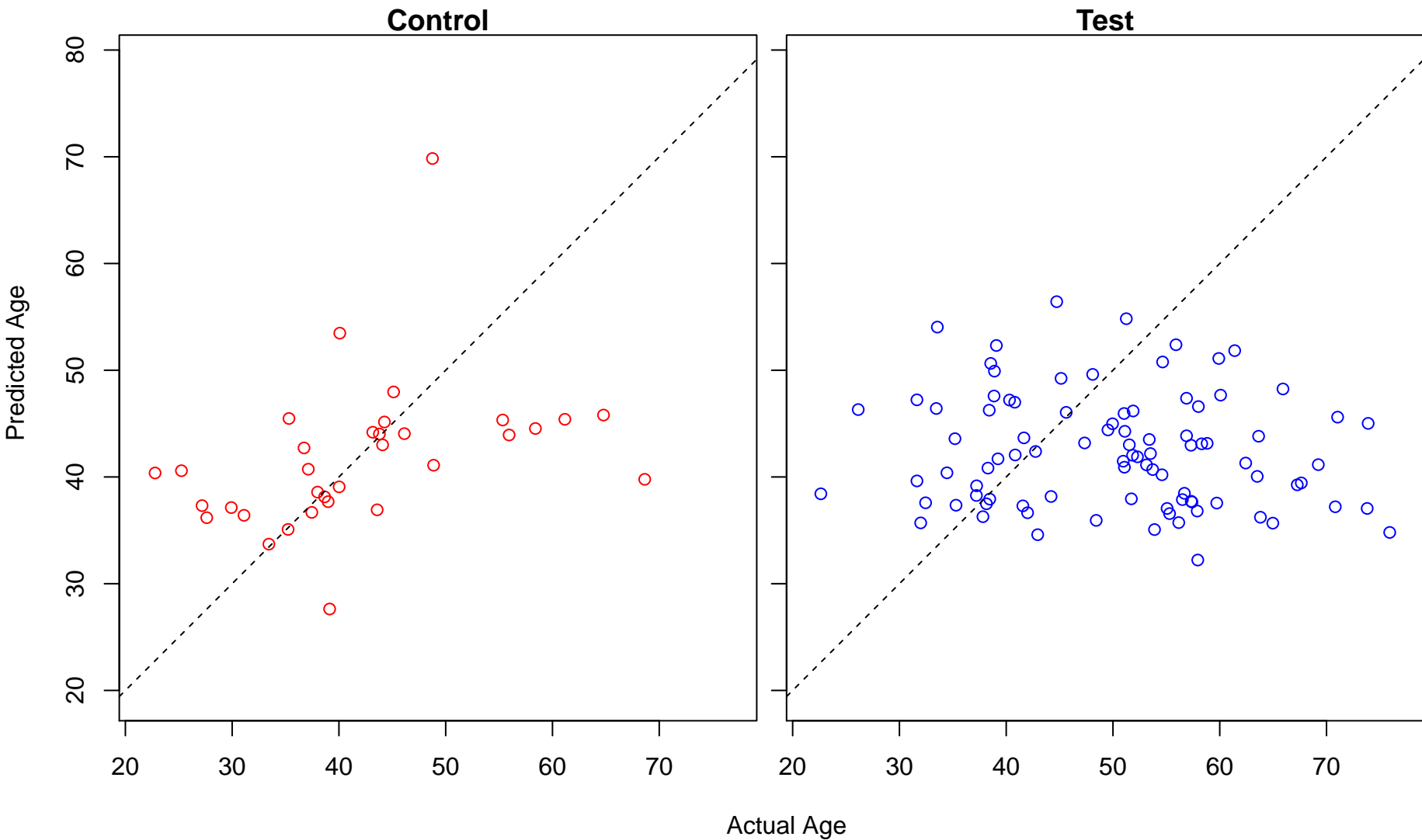
regulation of kinase activity (Score: 0.627993)



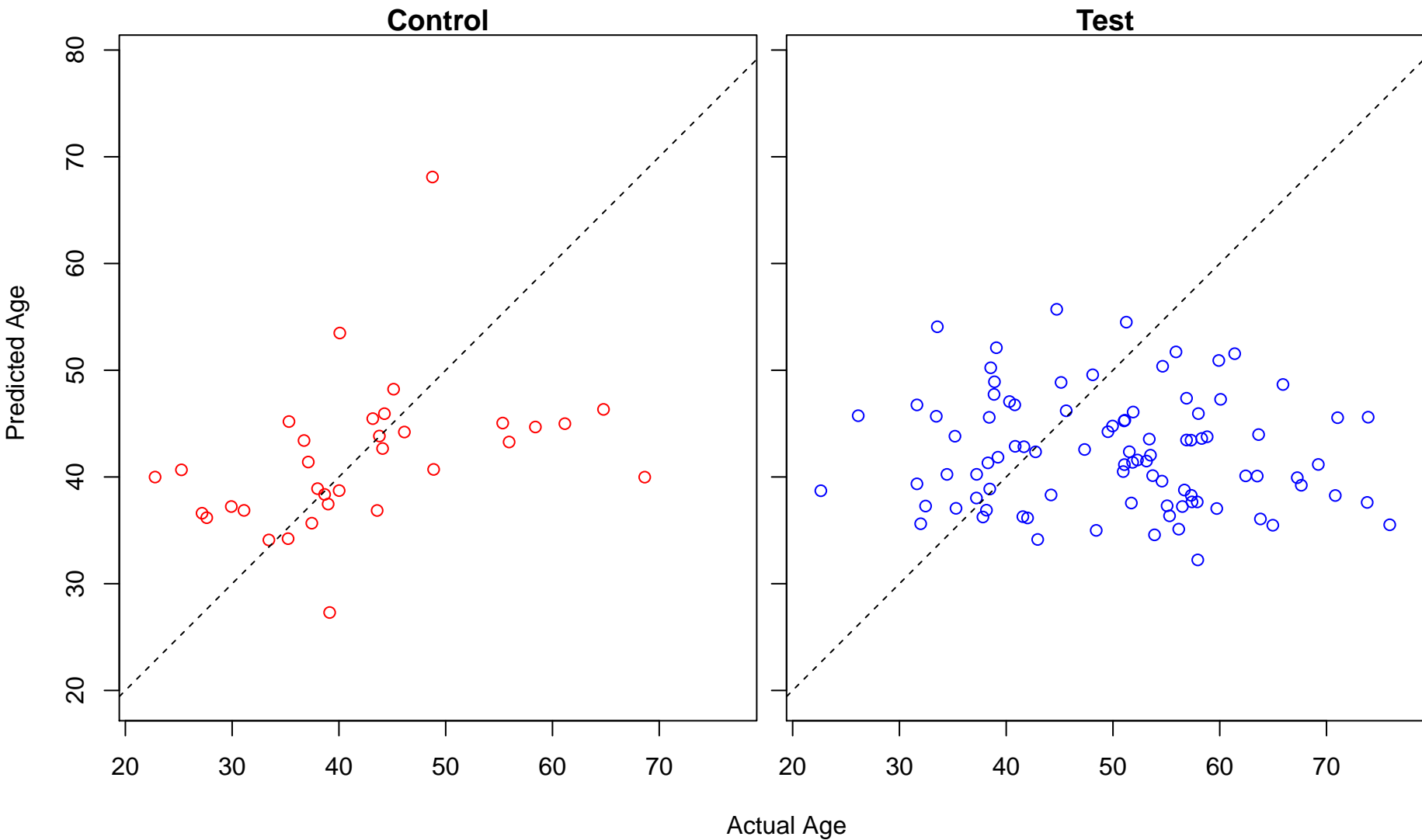
positive regulation of hydrolase activity (Score: 0.627689)



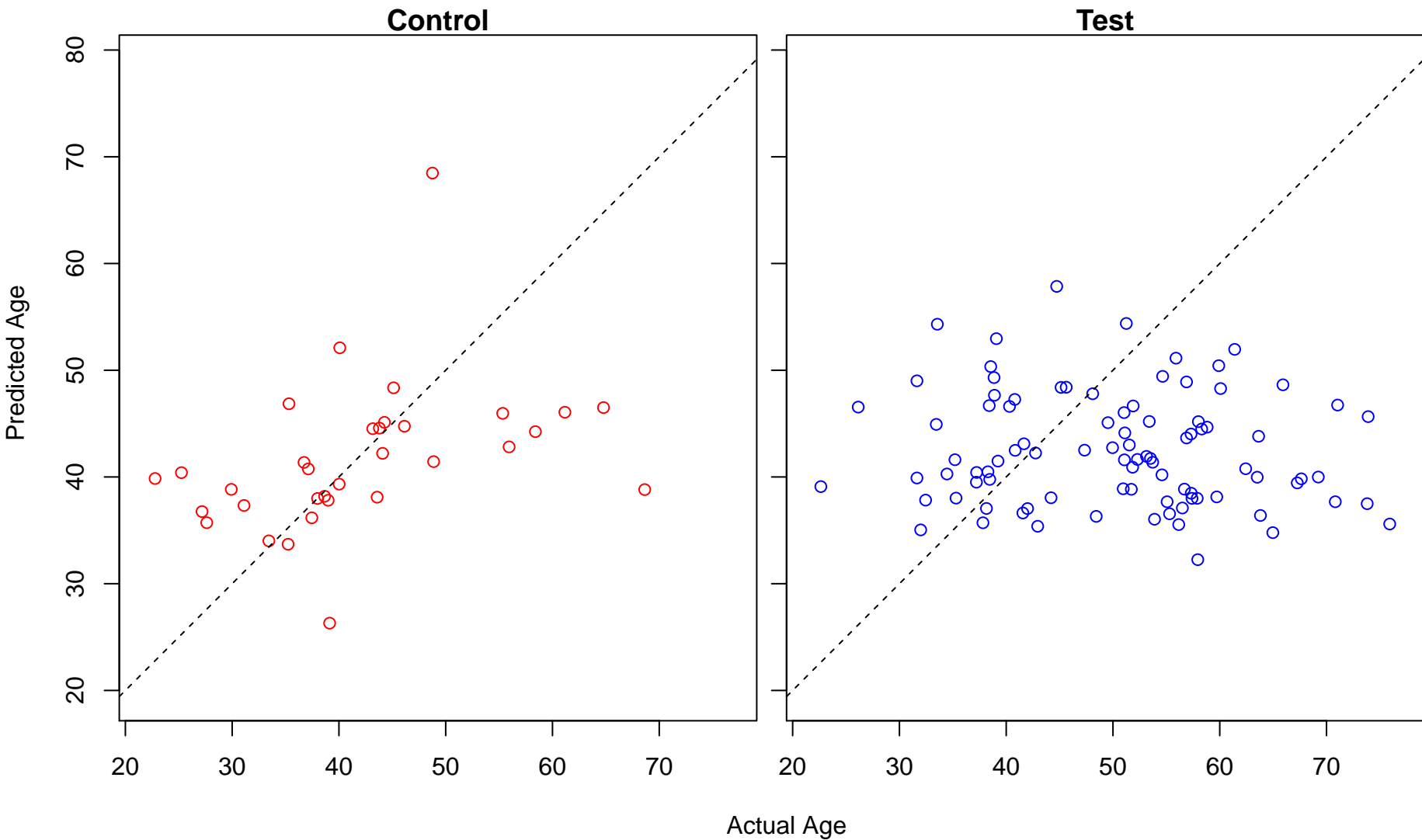
gene expression (Score: 0.626866)



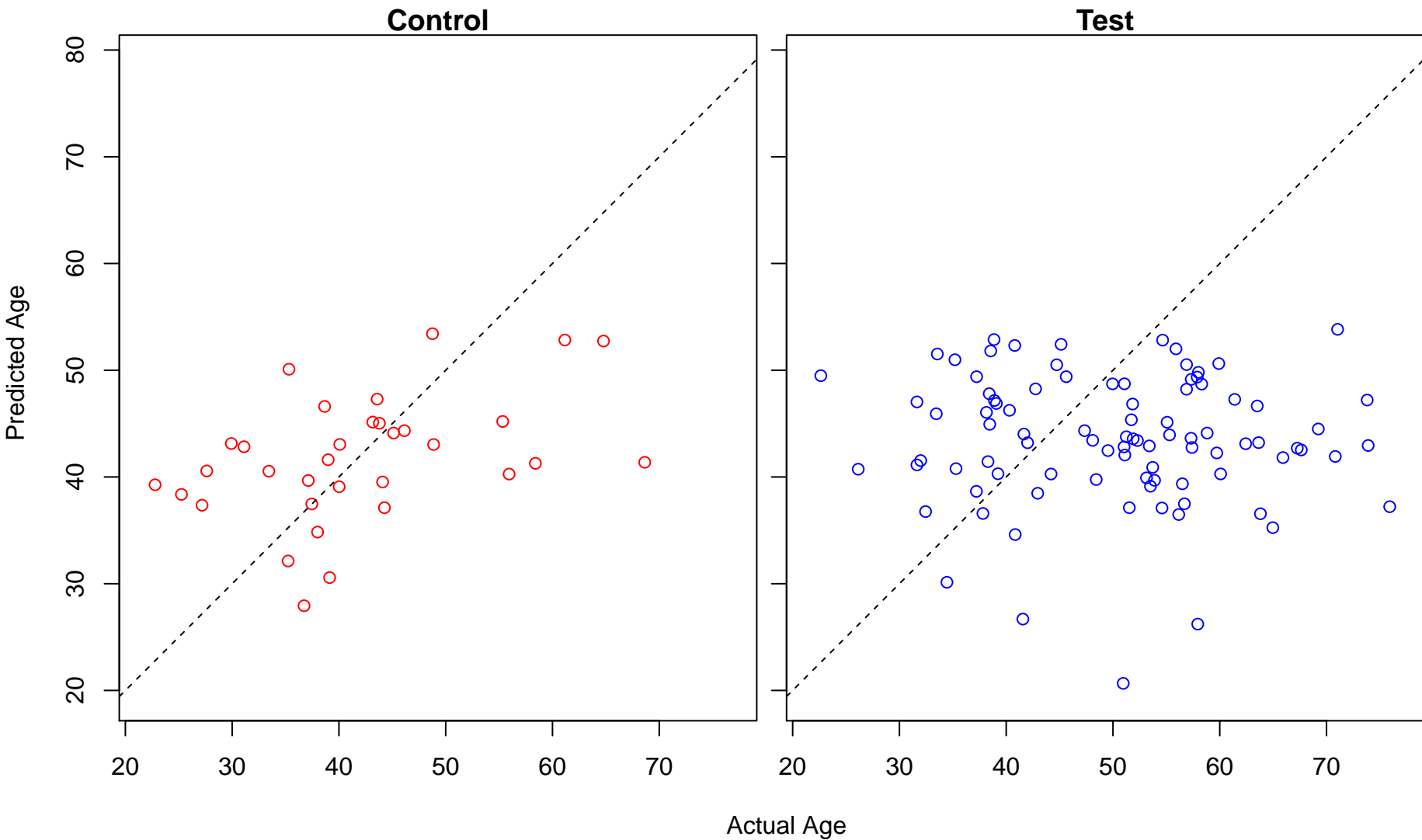
organic cyclic compound metabolic process (Score: 0.626184)



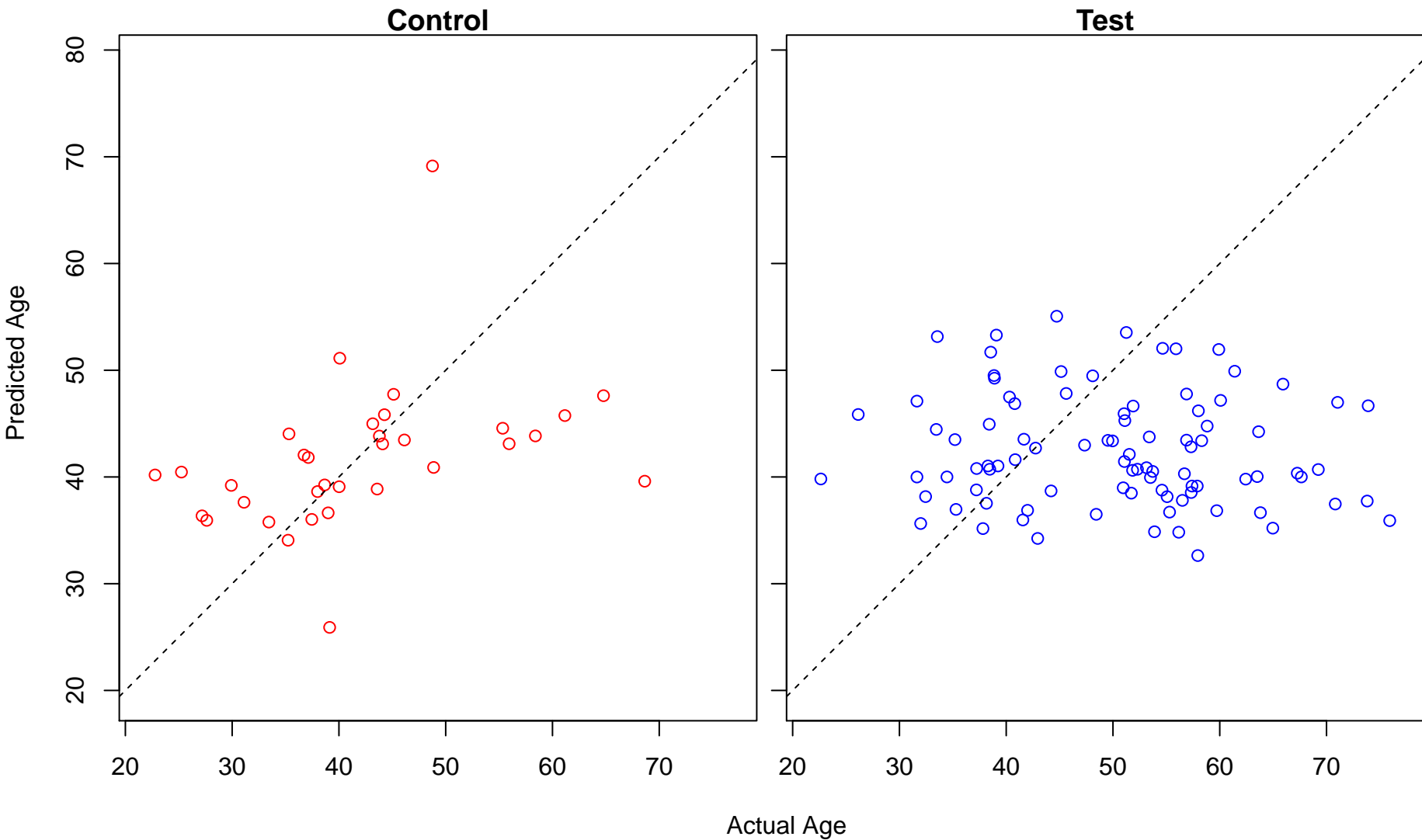
cellular response to stress (Score: 0.625070)



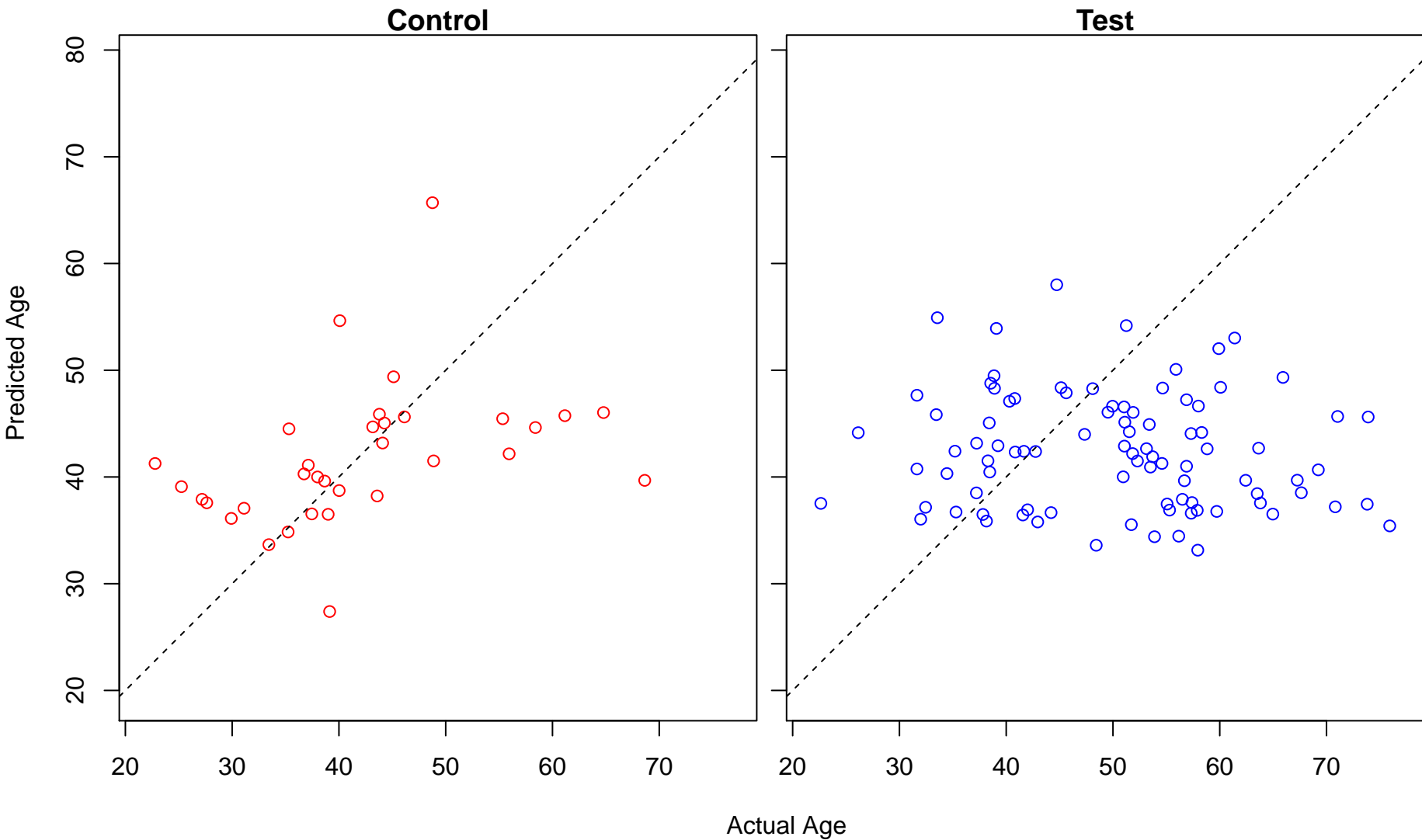
regulation of branching morphogenesis of a nerve (Score: 0.624918)



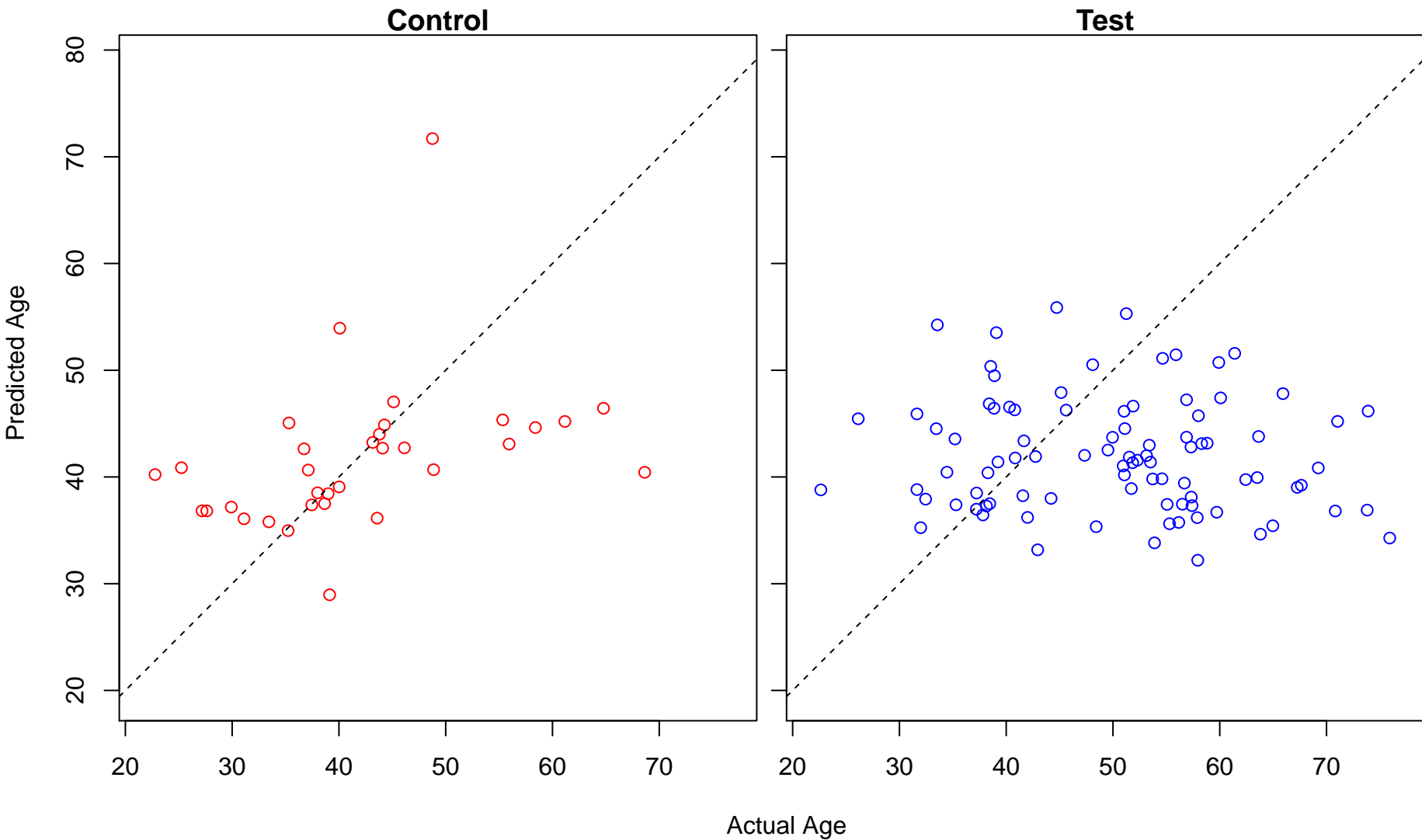
response to stimulus (Score: 0.624760)



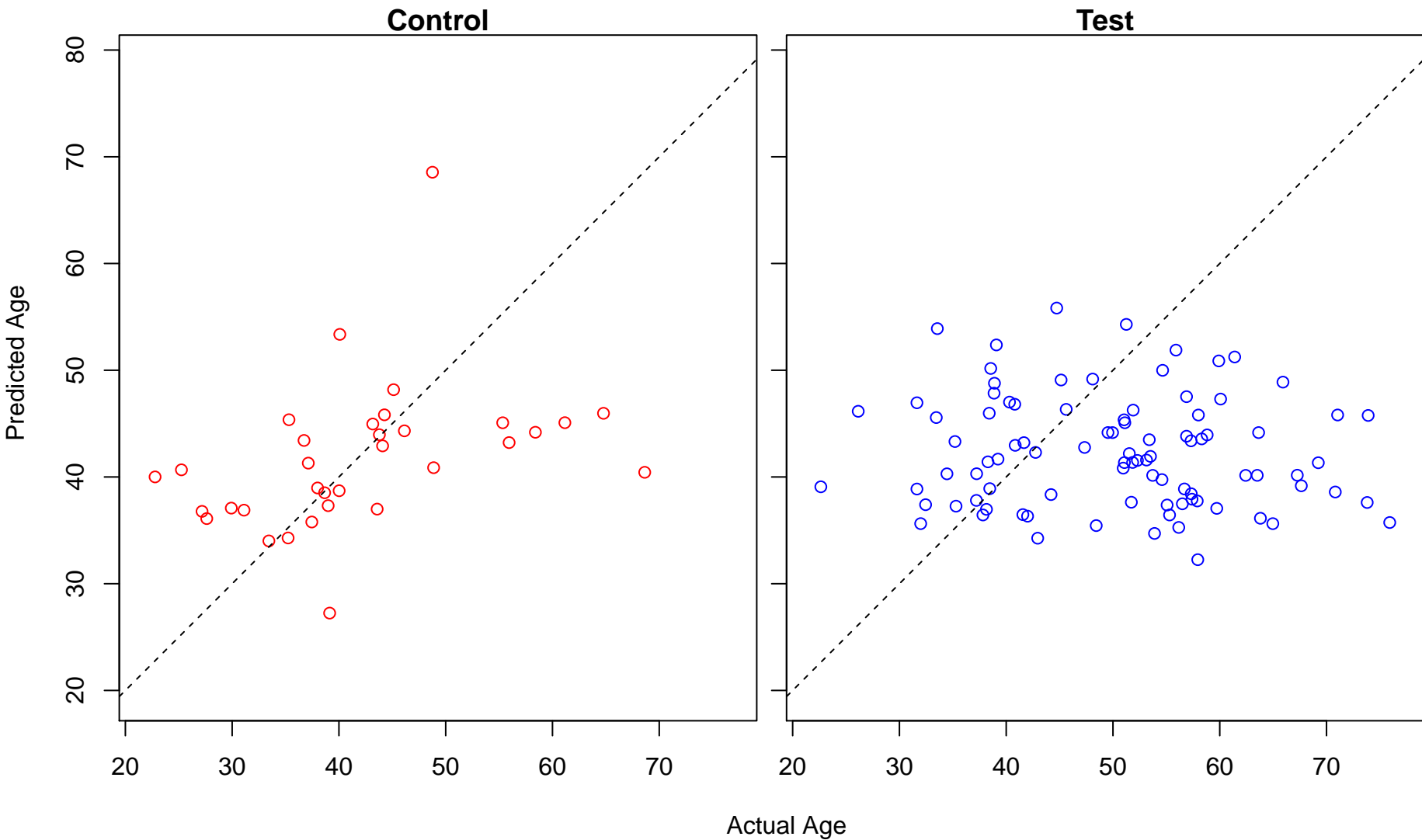
protein complex subunit organization (Score: 0.624028)



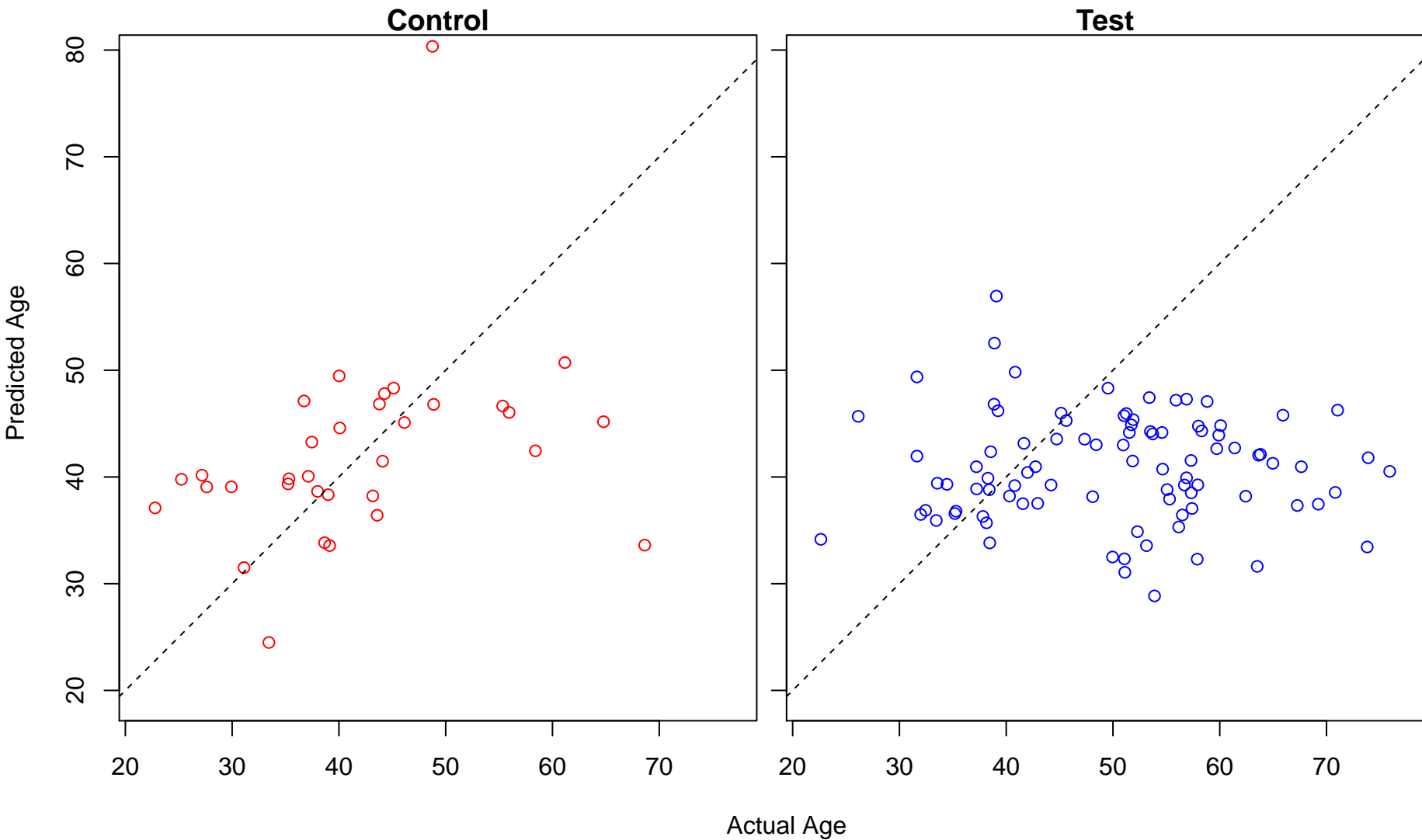
RNA biosynthetic process (Score: 0.623767)



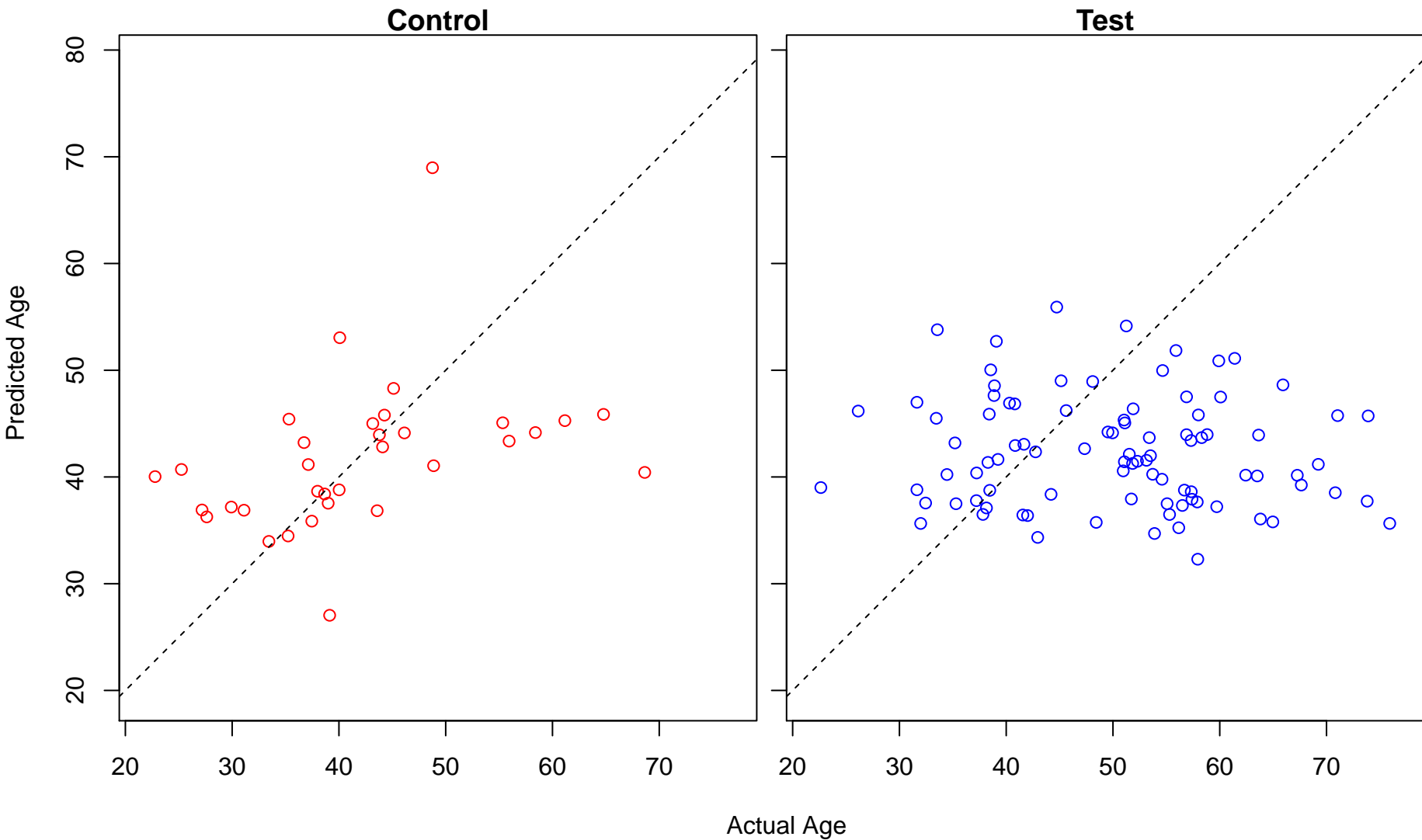
cellular aromatic compound metabolic process (Score: 0.623628)



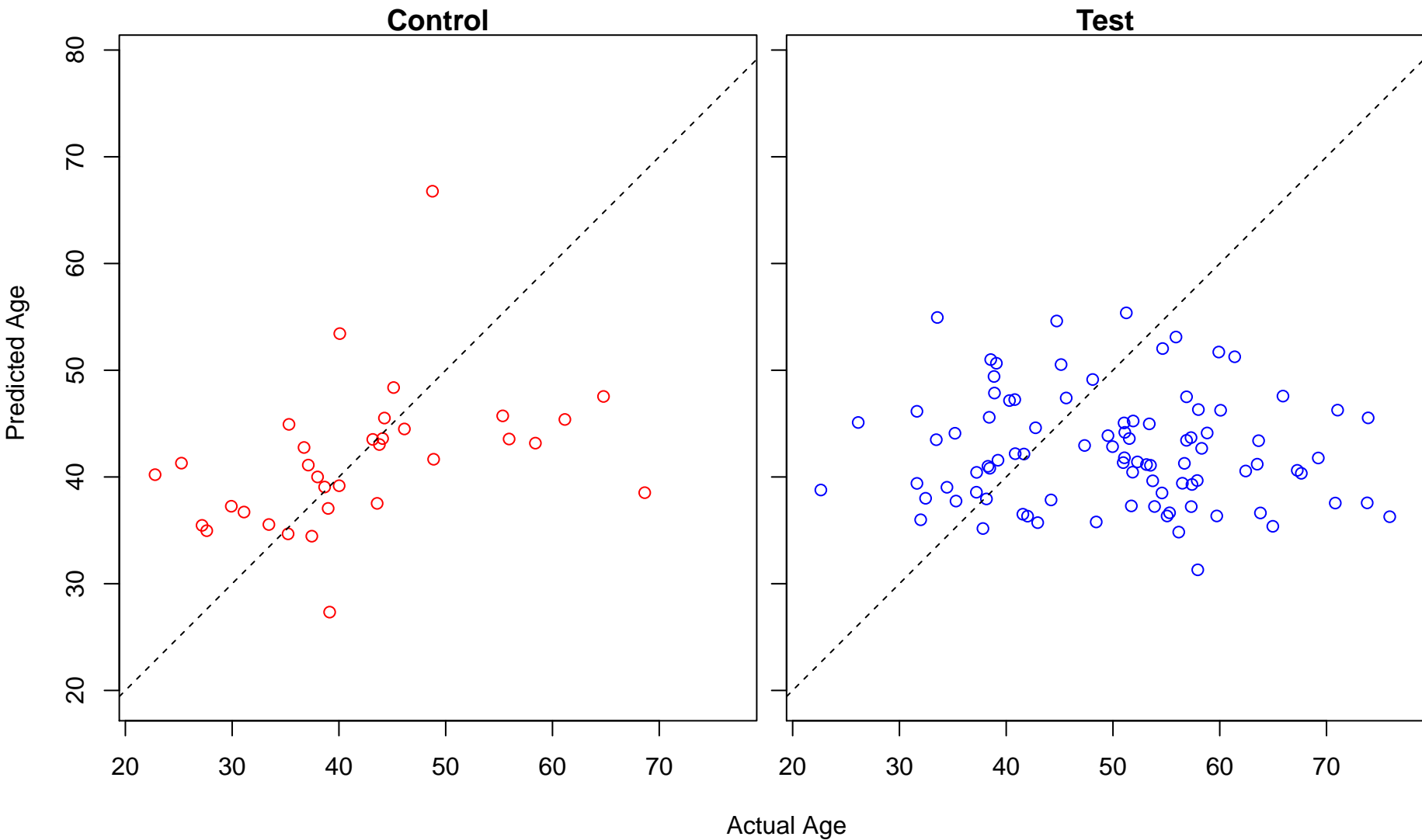
positive regulation of trophoblast cell migration (Score: 0.623215)



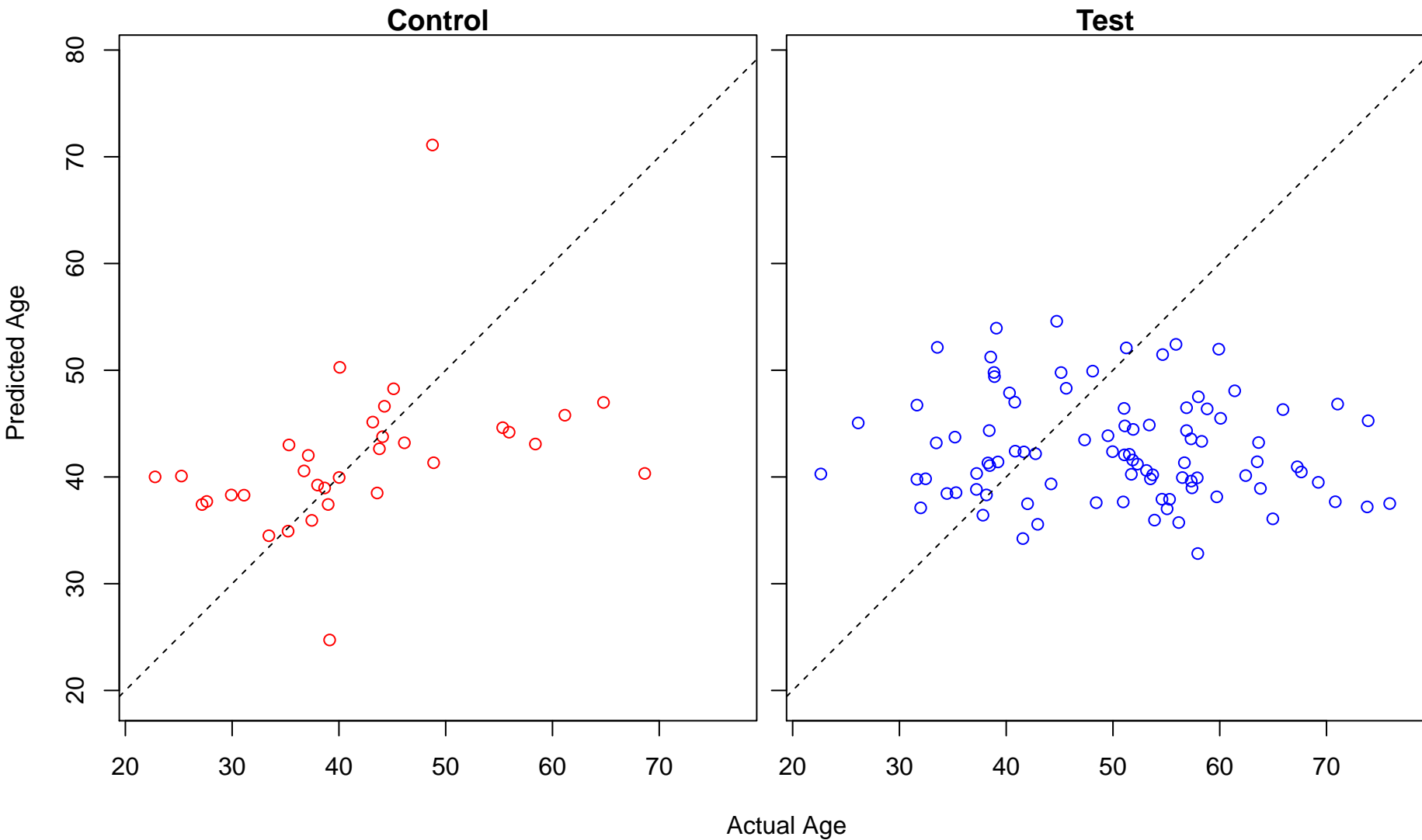
heterocycle metabolic process (Score: 0.623044)



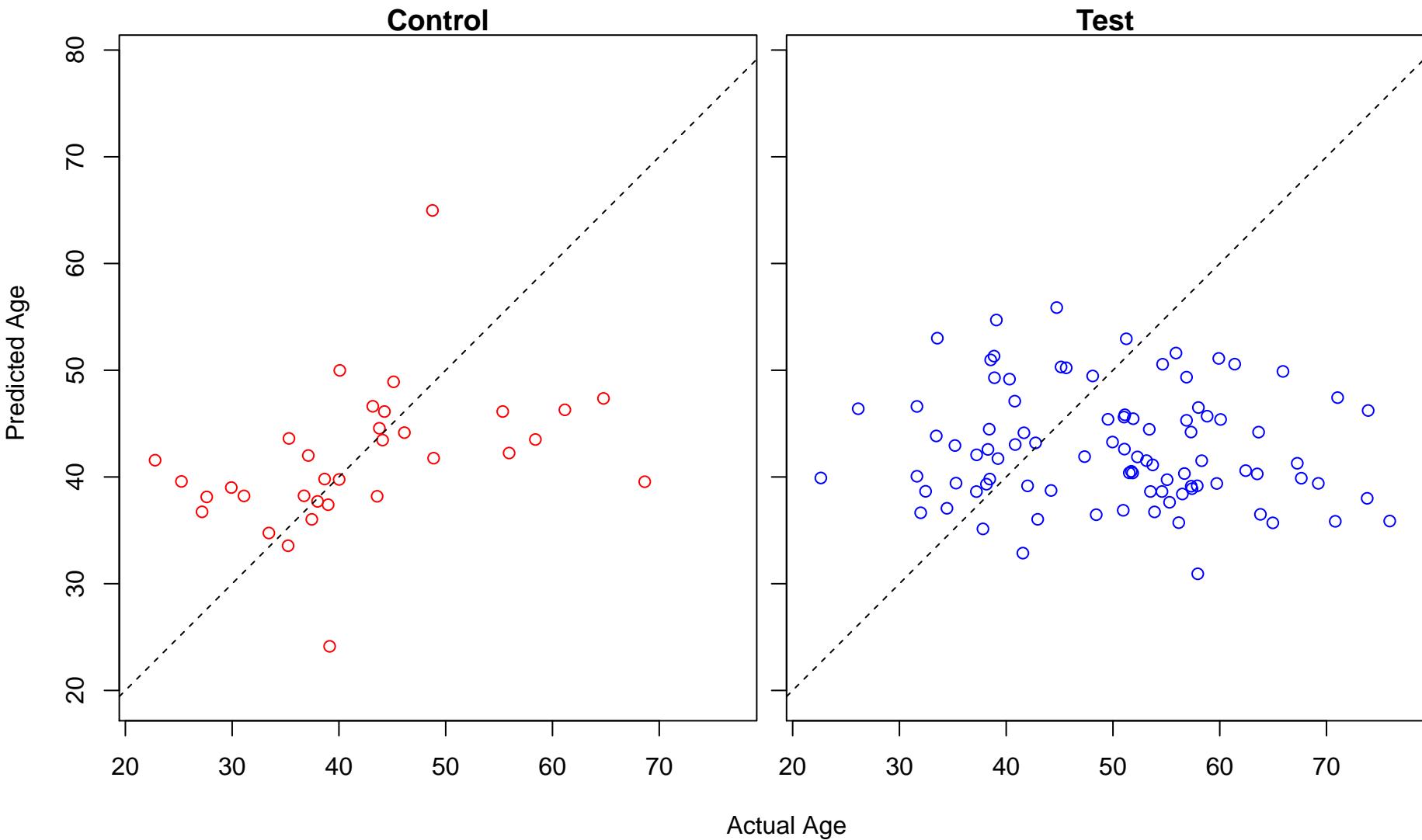
regulation of programmed cell death (Score: 0.622948)



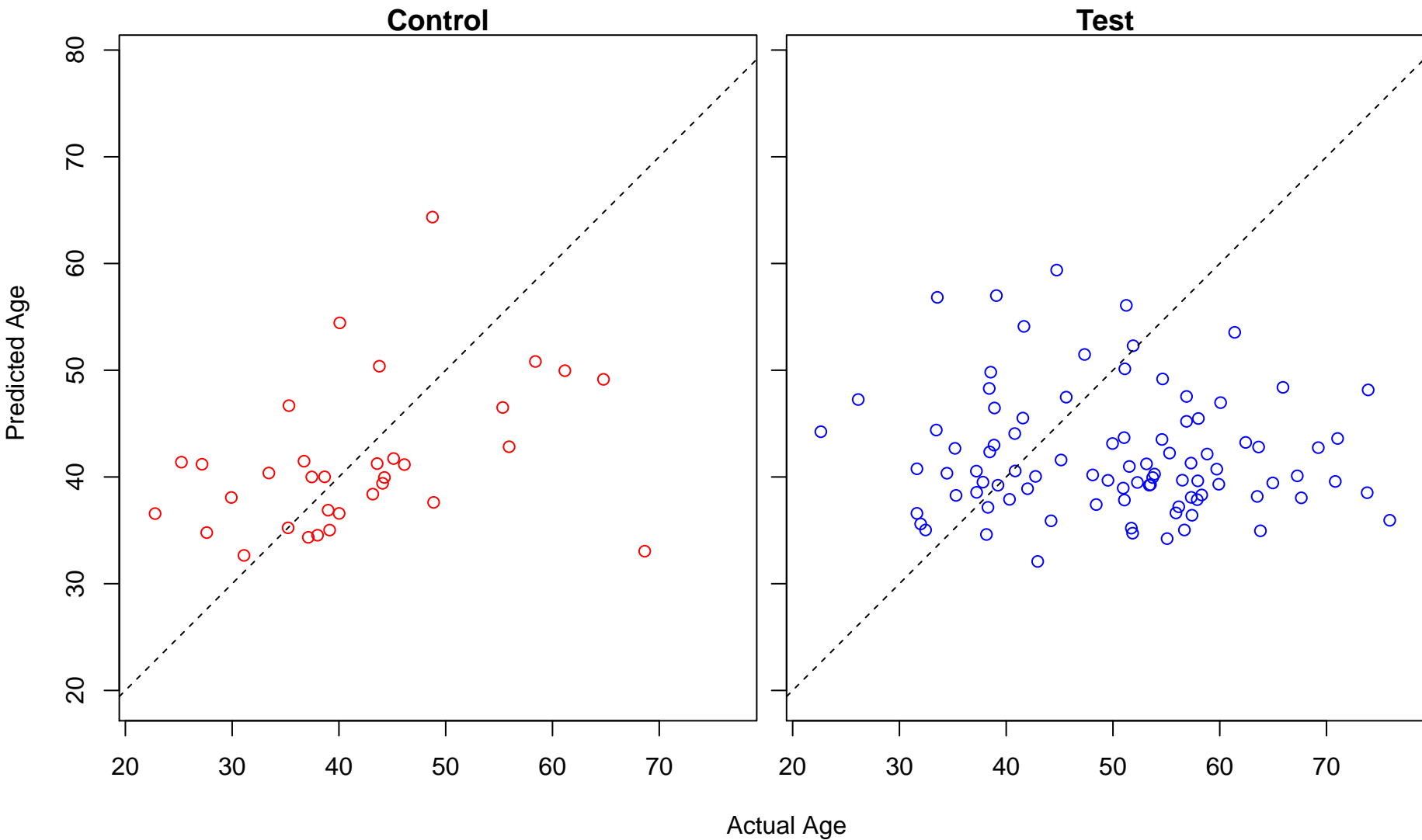
intracellular signal transduction (Score: 0.622877)



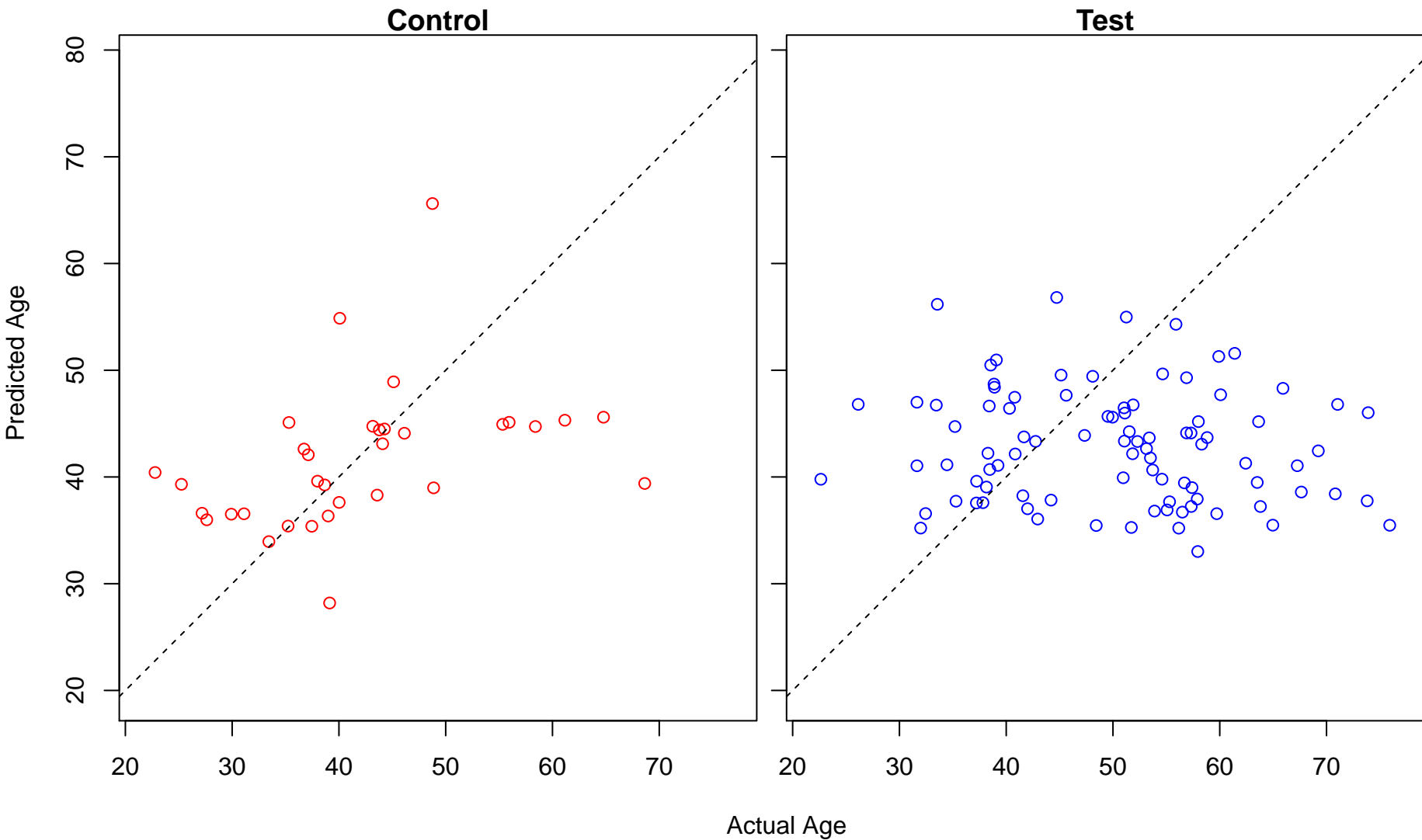
phosphorylation (Score: 0.622694)



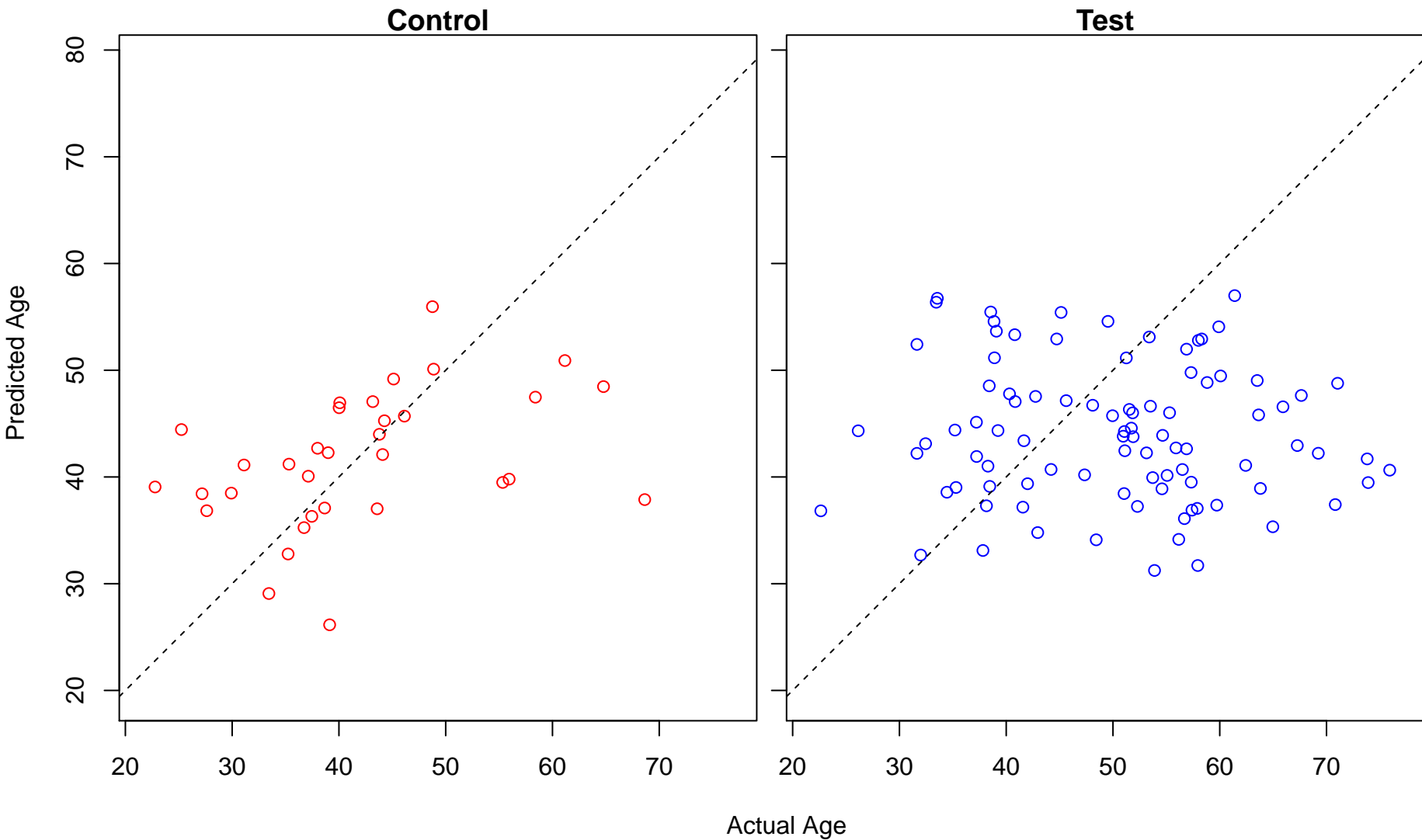
somatic cell DNA recombination (Score: 0.622250)



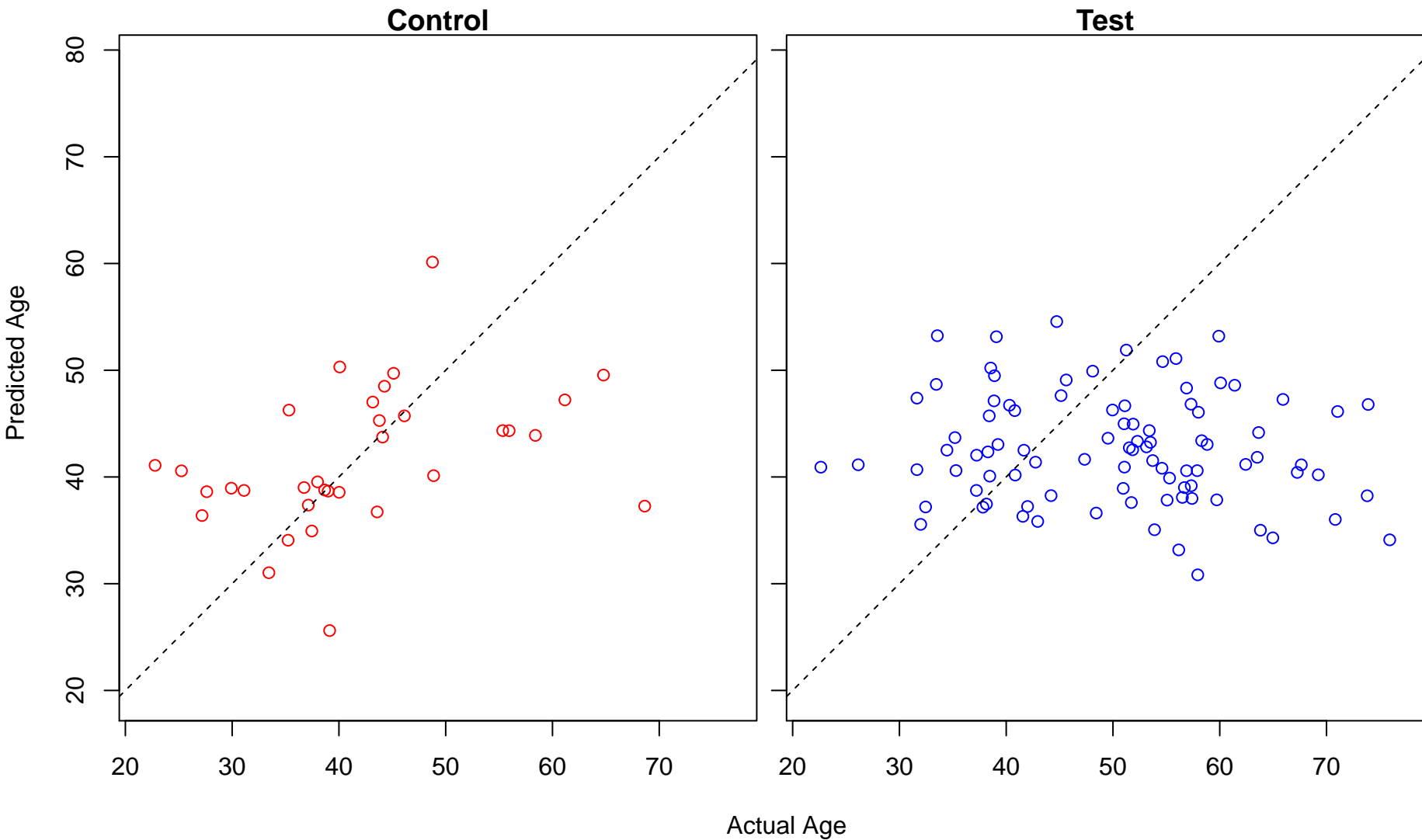
organonitrogen compound metabolic process (Score: 0.621886)



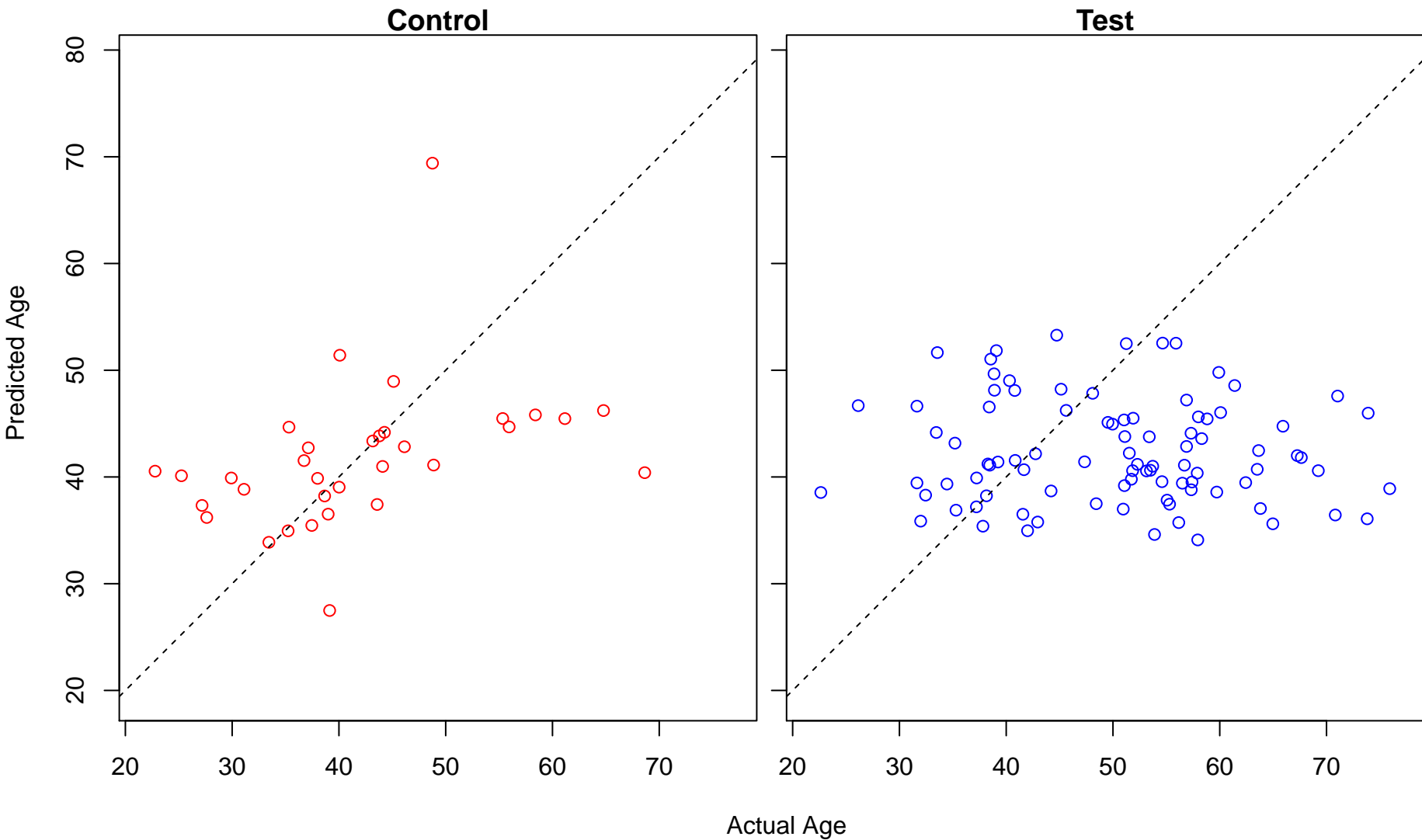
positive regulation of triglyceride biosynthetic process (Score: 0.621865)



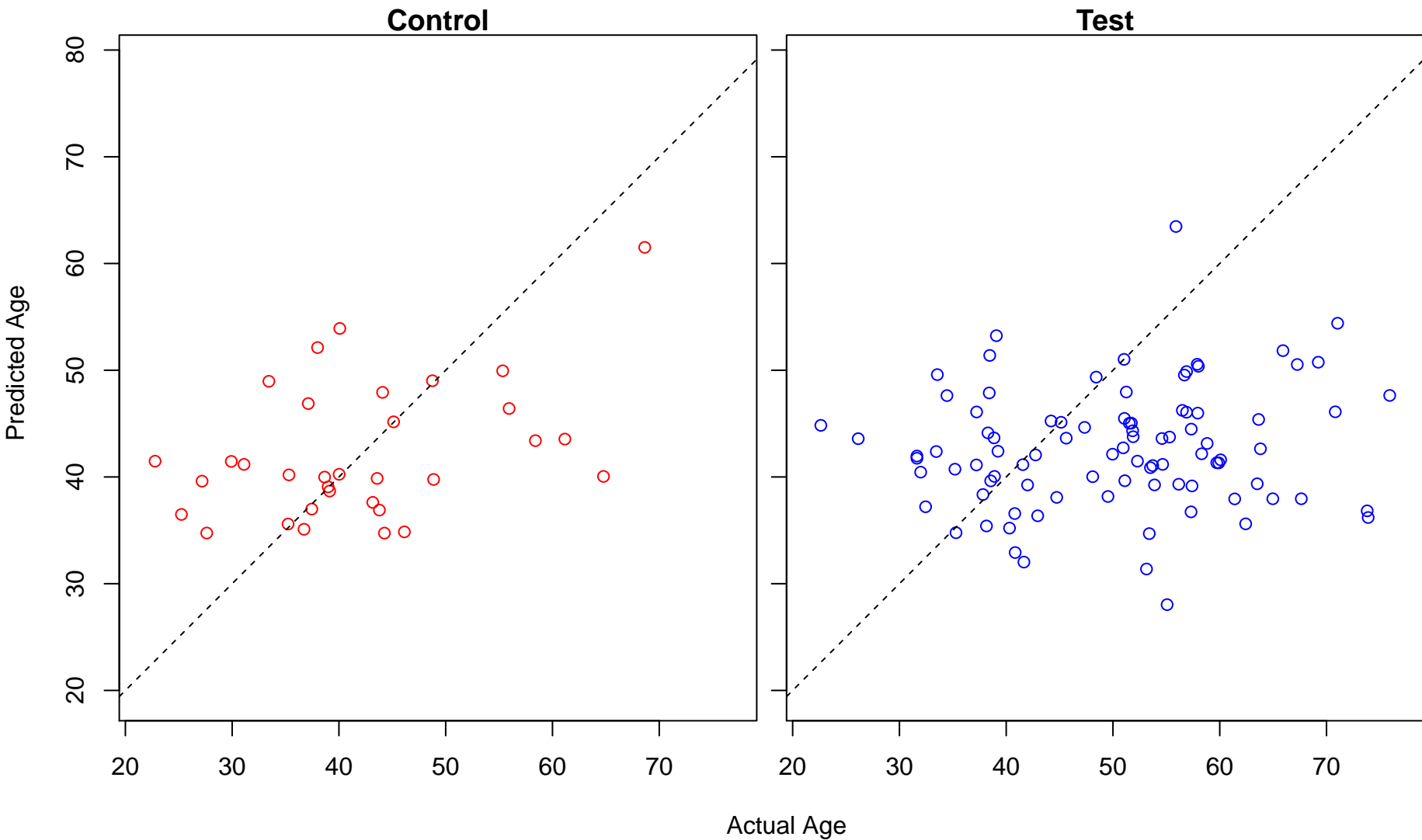
monocarboxylic acid metabolic process (Score: 0.621624)



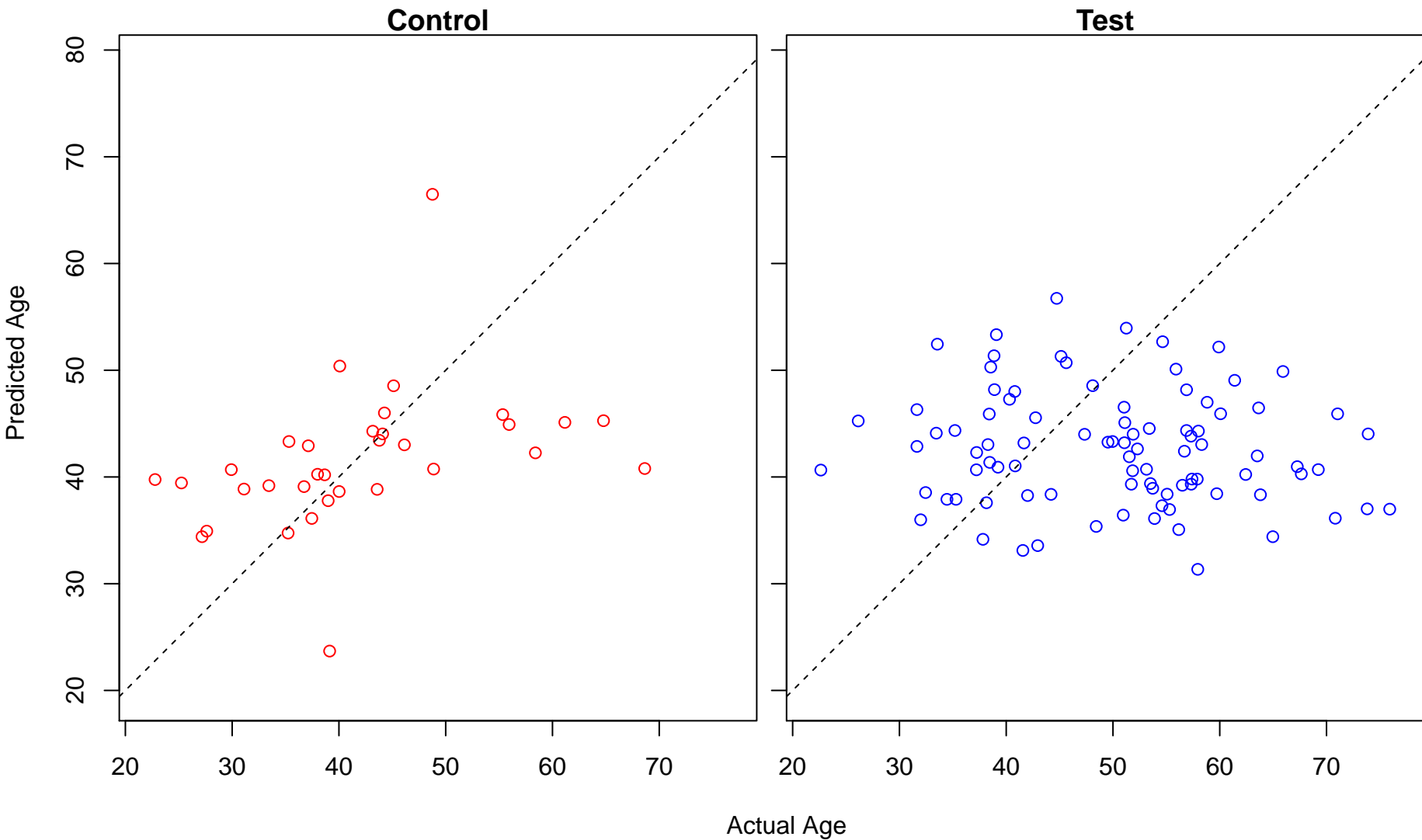
regulation of cell motility (Score: 0.621577)



platelet-derived growth factor receptor-beta signaling pathway (Score: 0.620048)

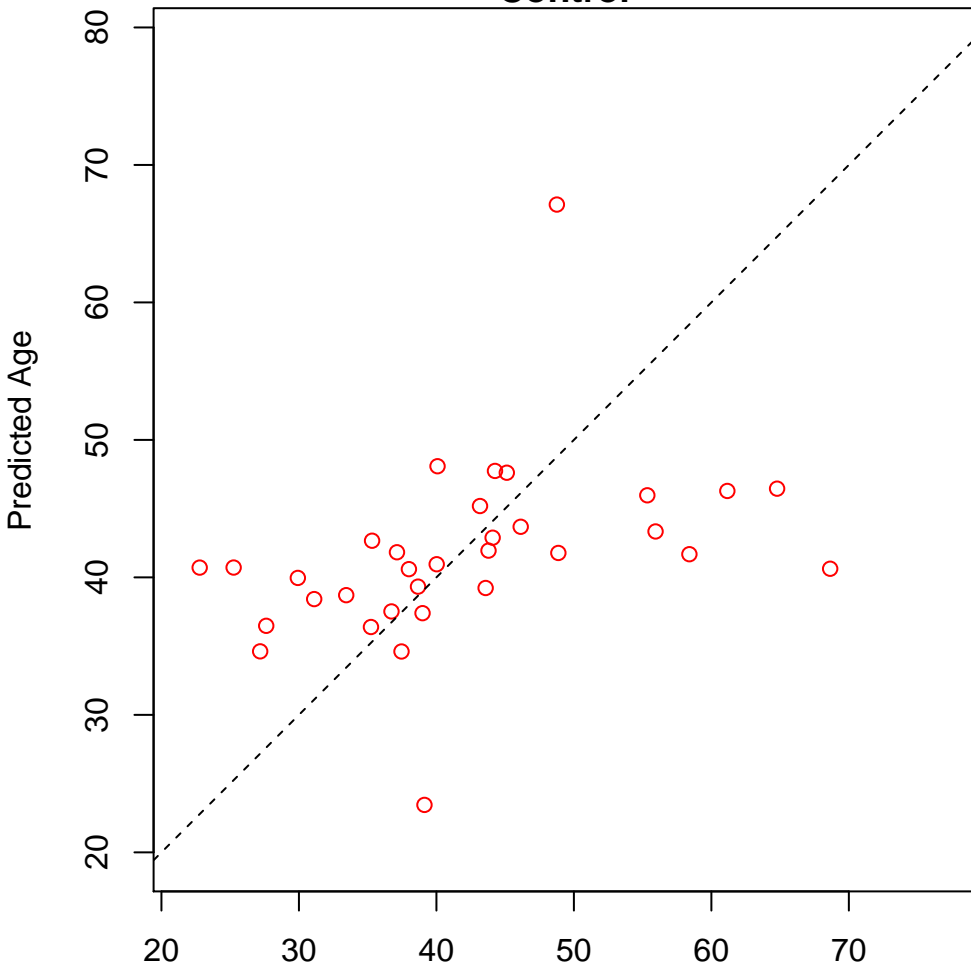


cellular response to endogenous stimulus (Score: 0.619416)

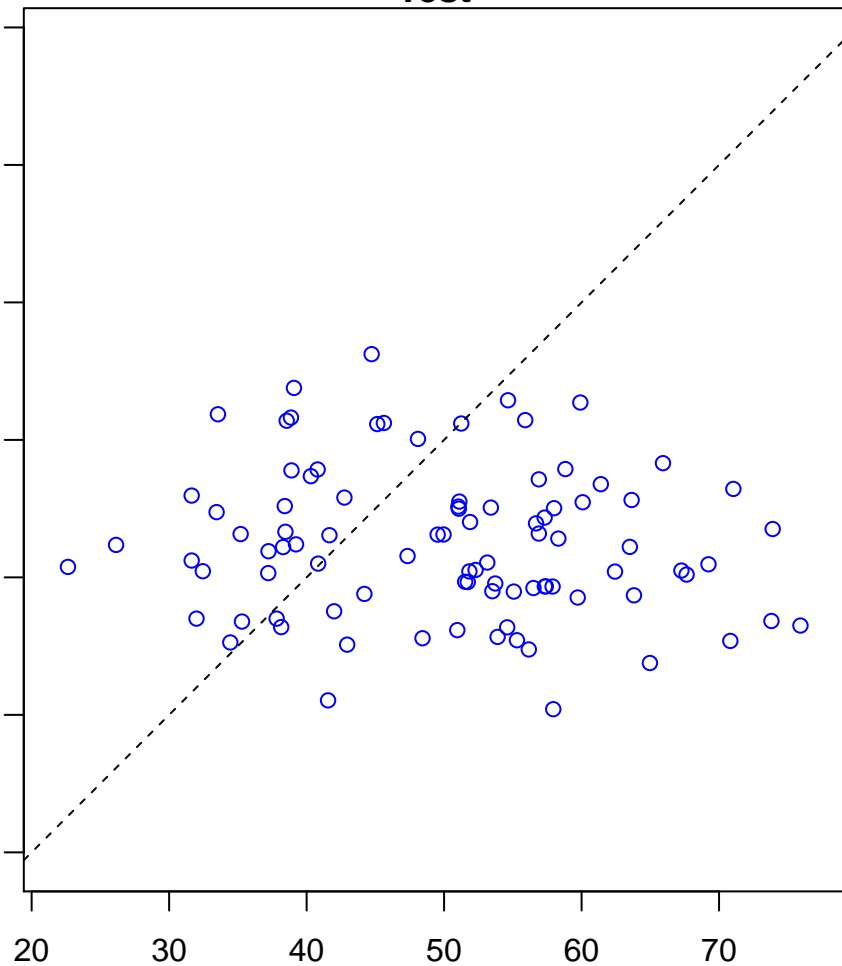


cellular response to nitrogen compound (Score: 0.619145)

Control

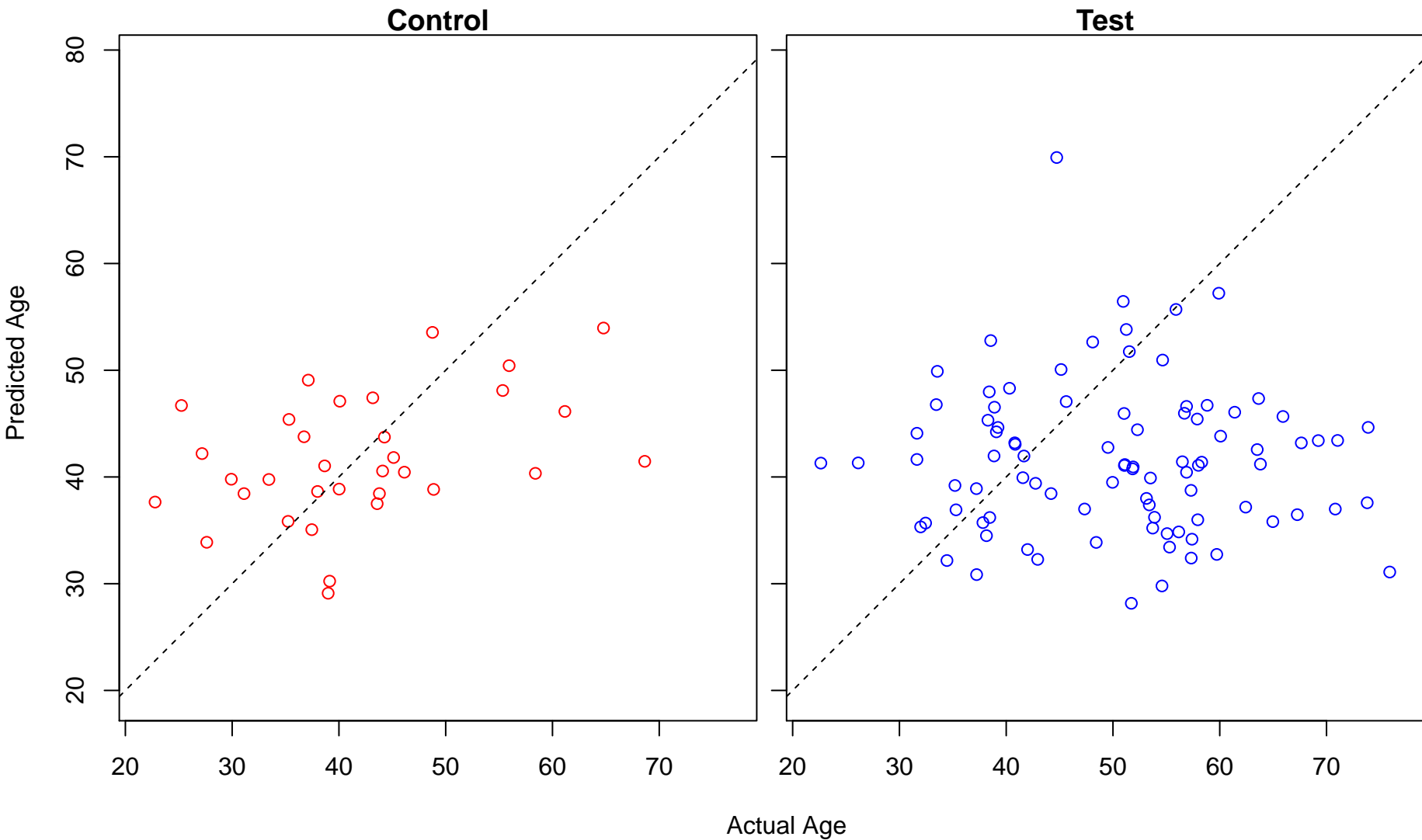


Test

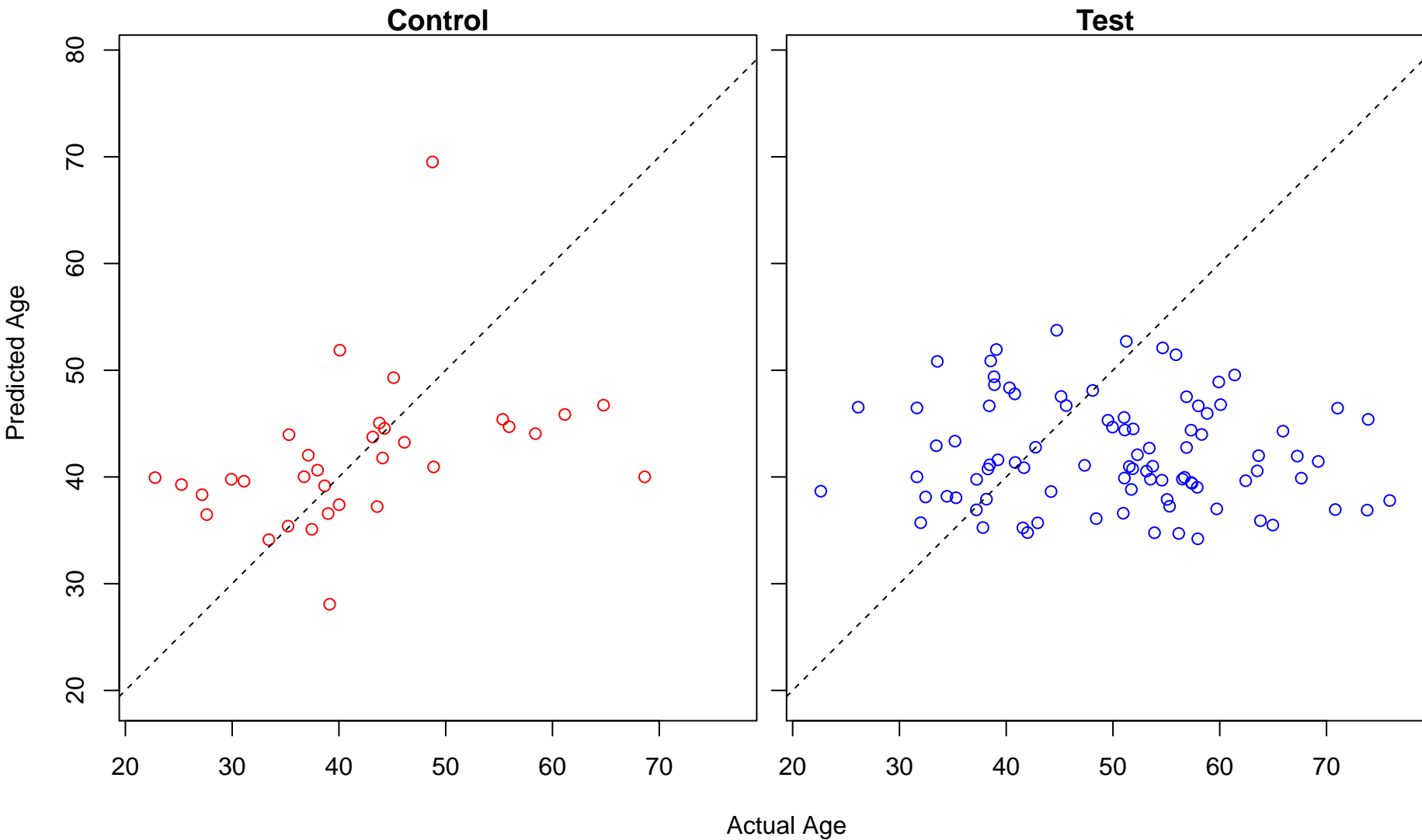


Actual Age

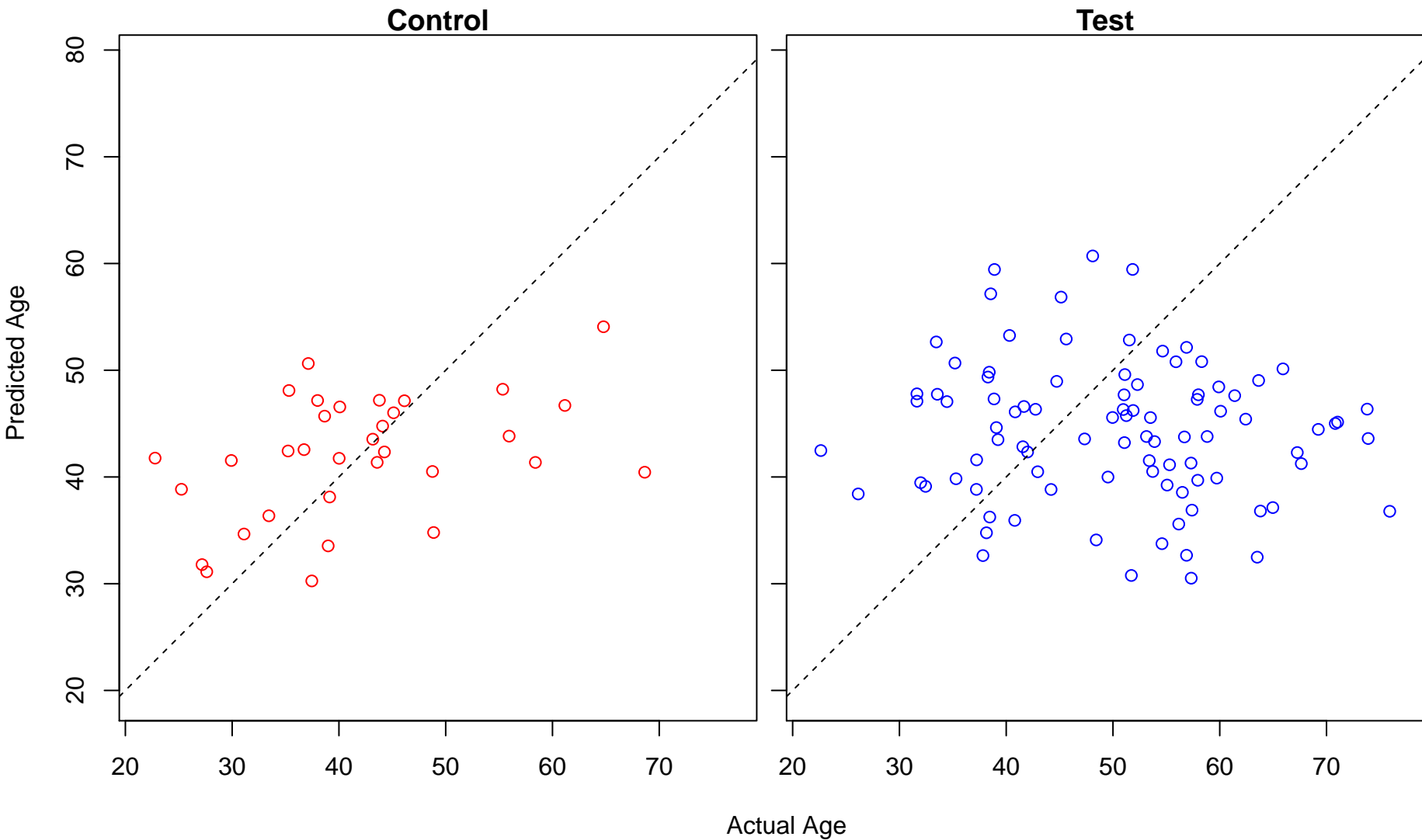
liver development (Score: 0.618958)



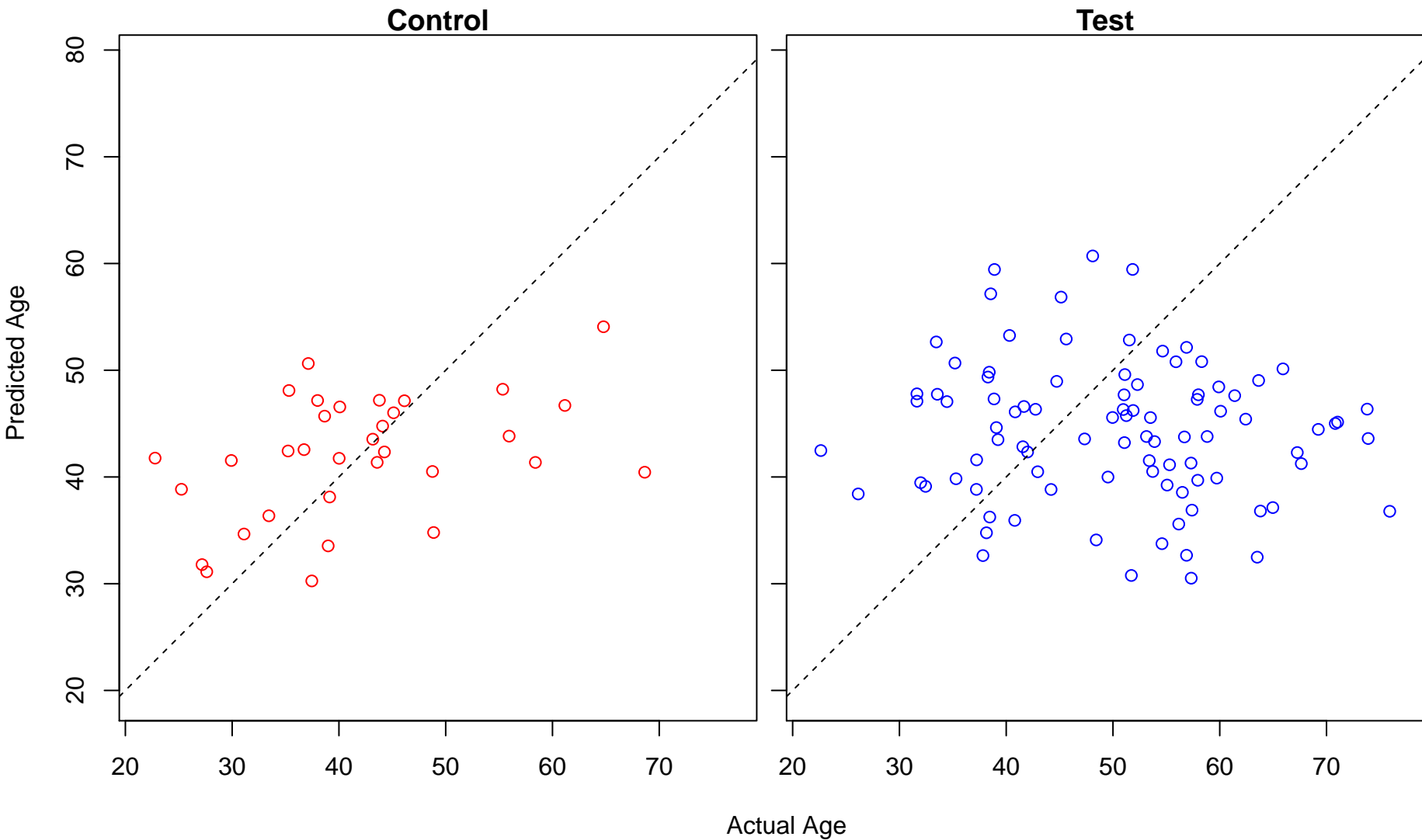
regulation of cellular component movement (Score: 0.618646)



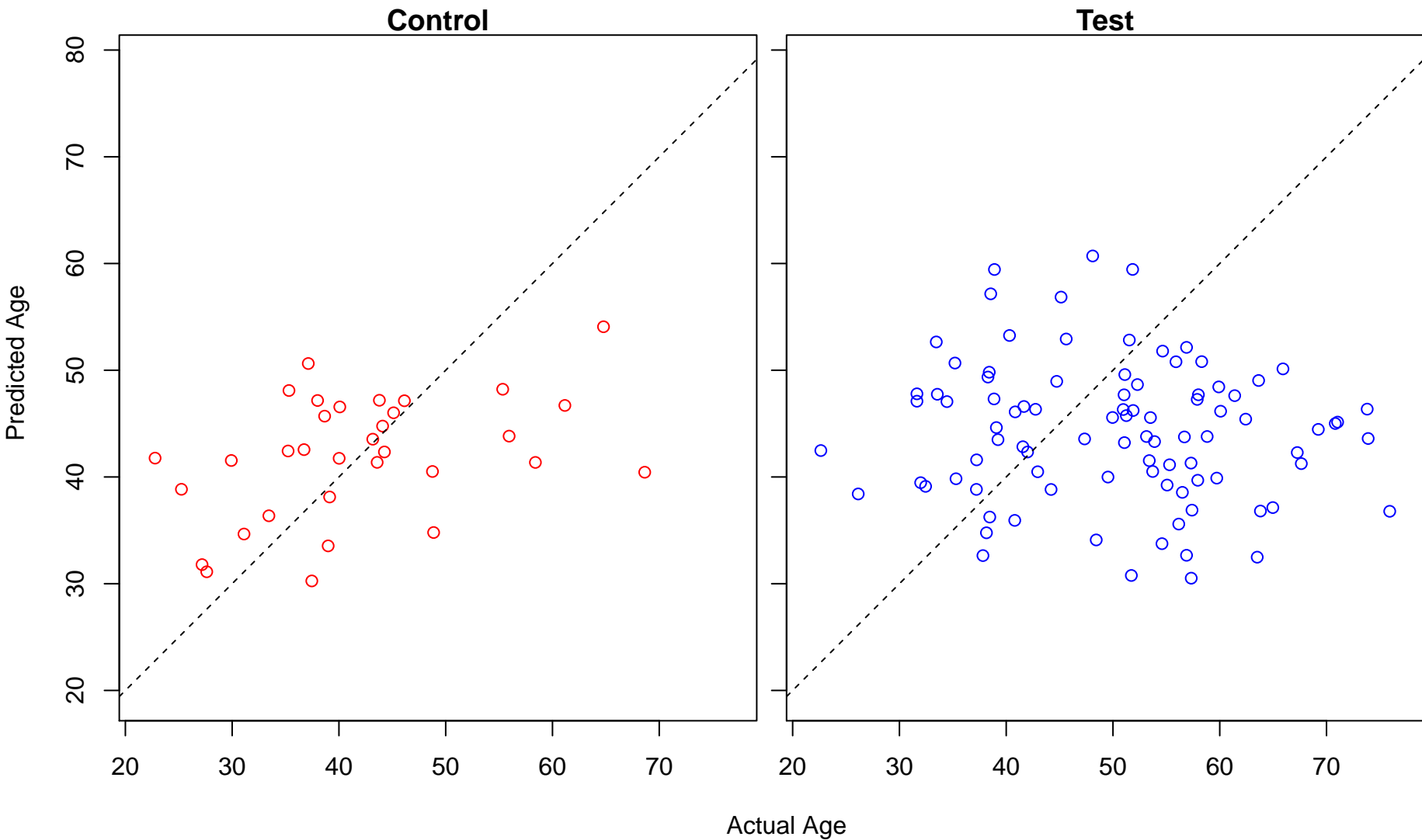
ascending thin limb development (Score: 0.618413)



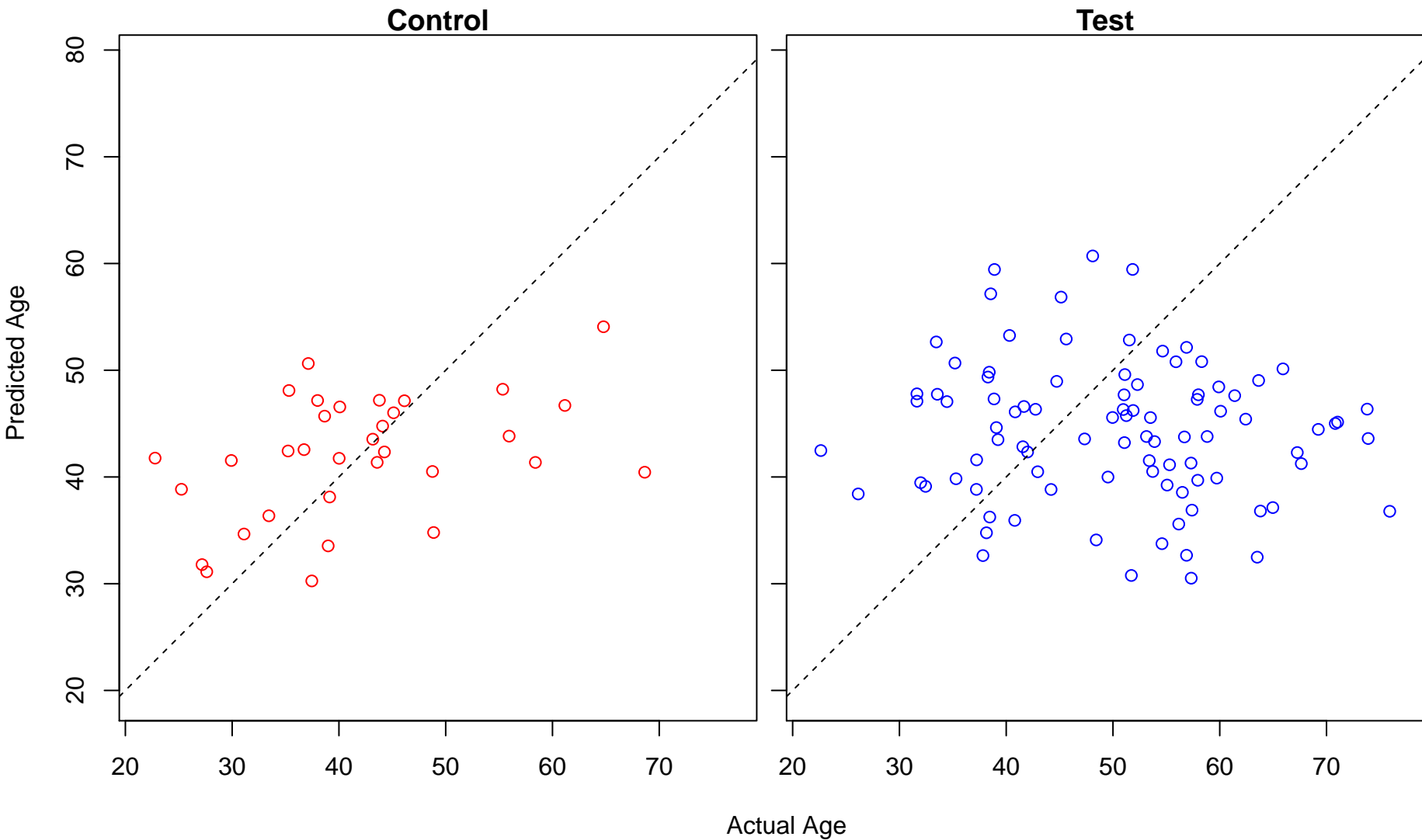
loop of Henle development (Score: 0.618413)



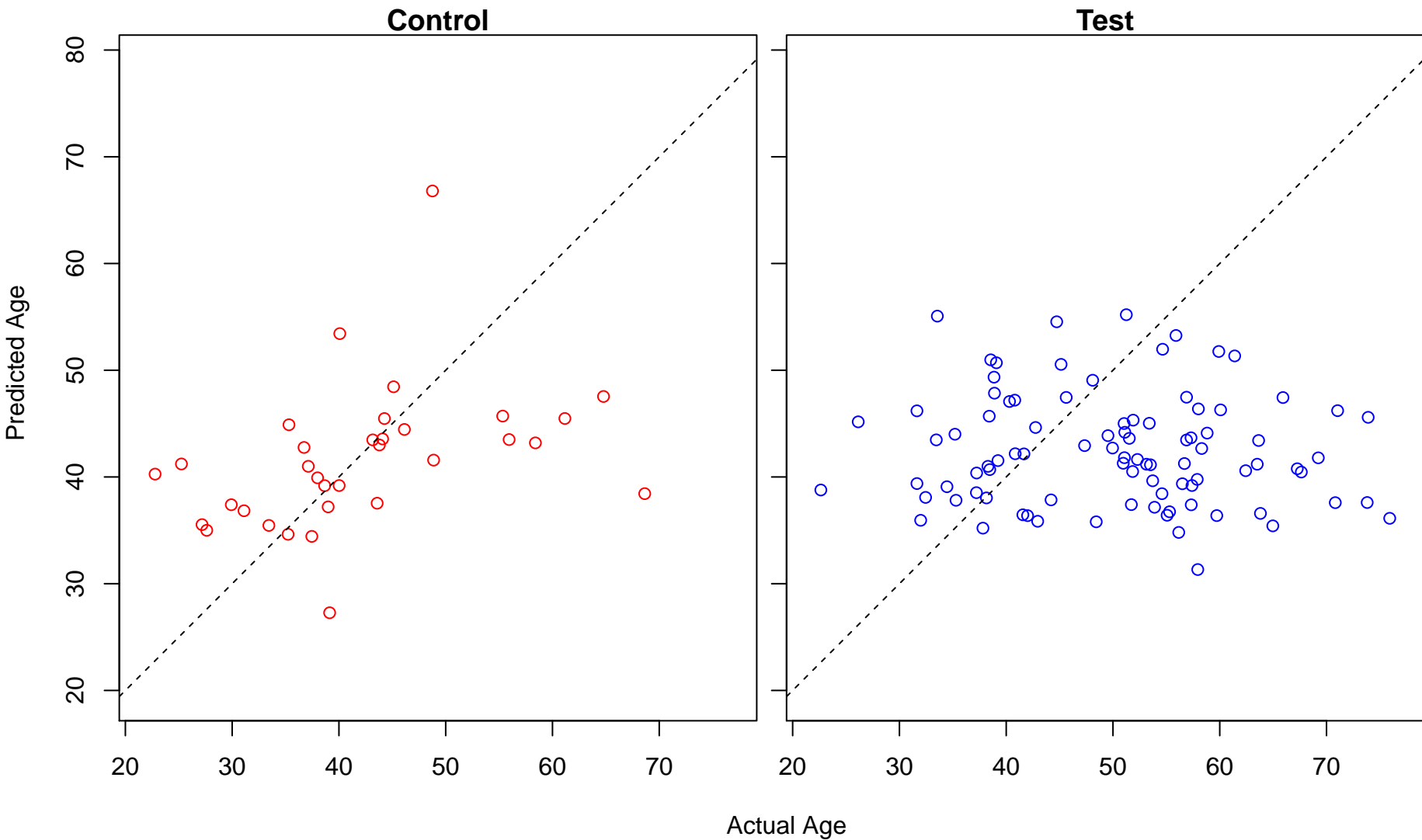
metanephric ascending thin limb development (Score: 0.618413)



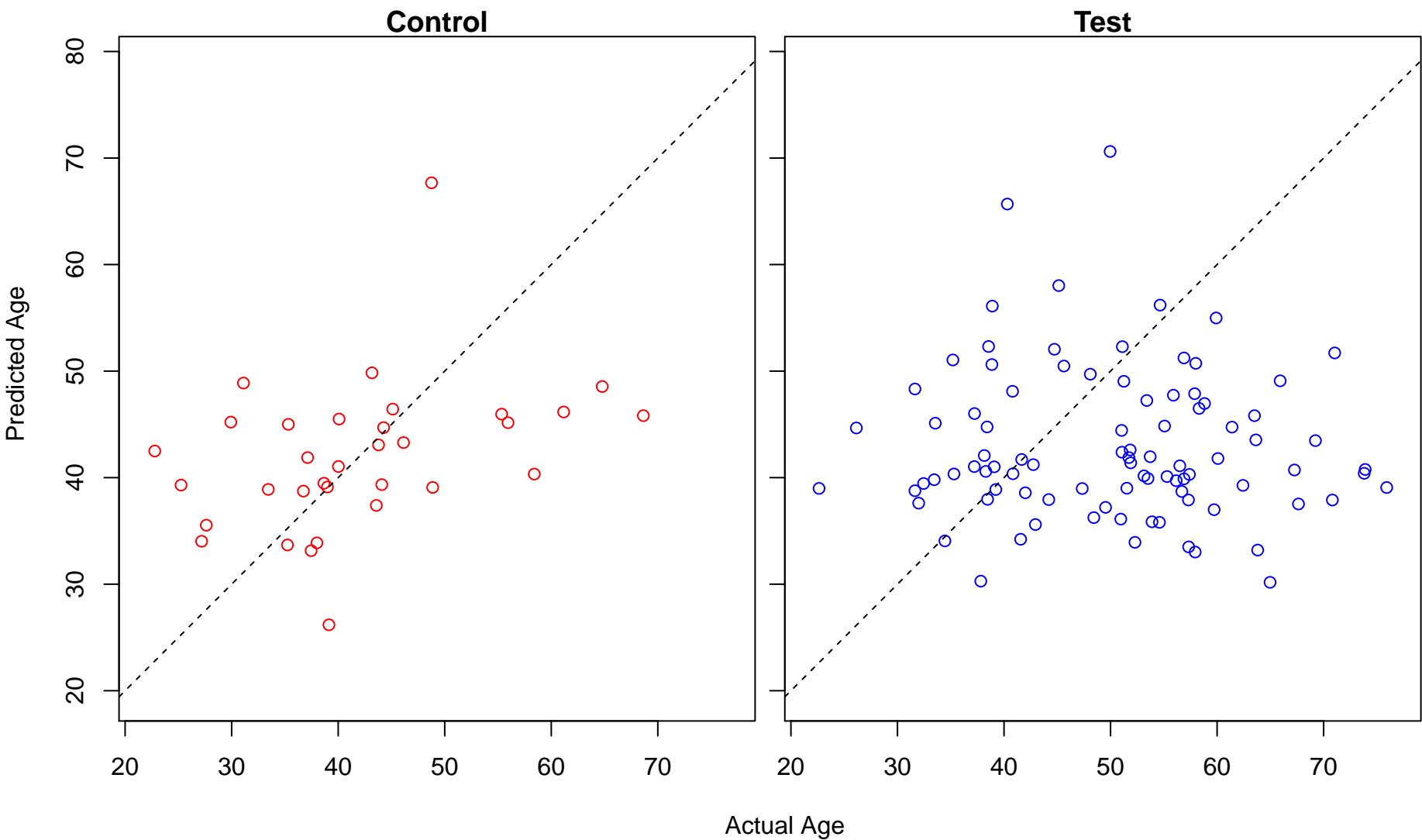
metanephric loop of Henle development (Score: 0.618413)



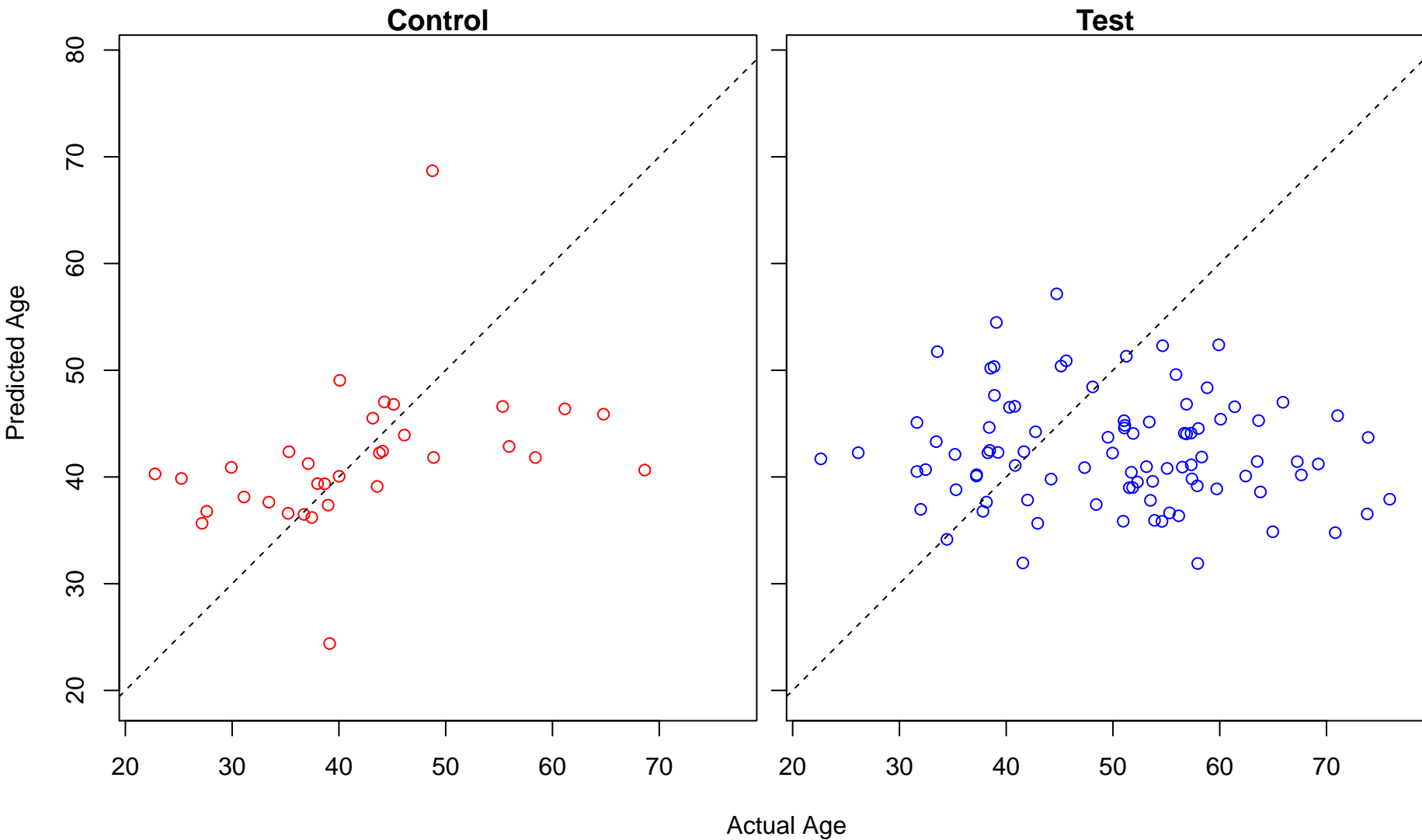
regulation of apoptotic process (Score: 0.618106)



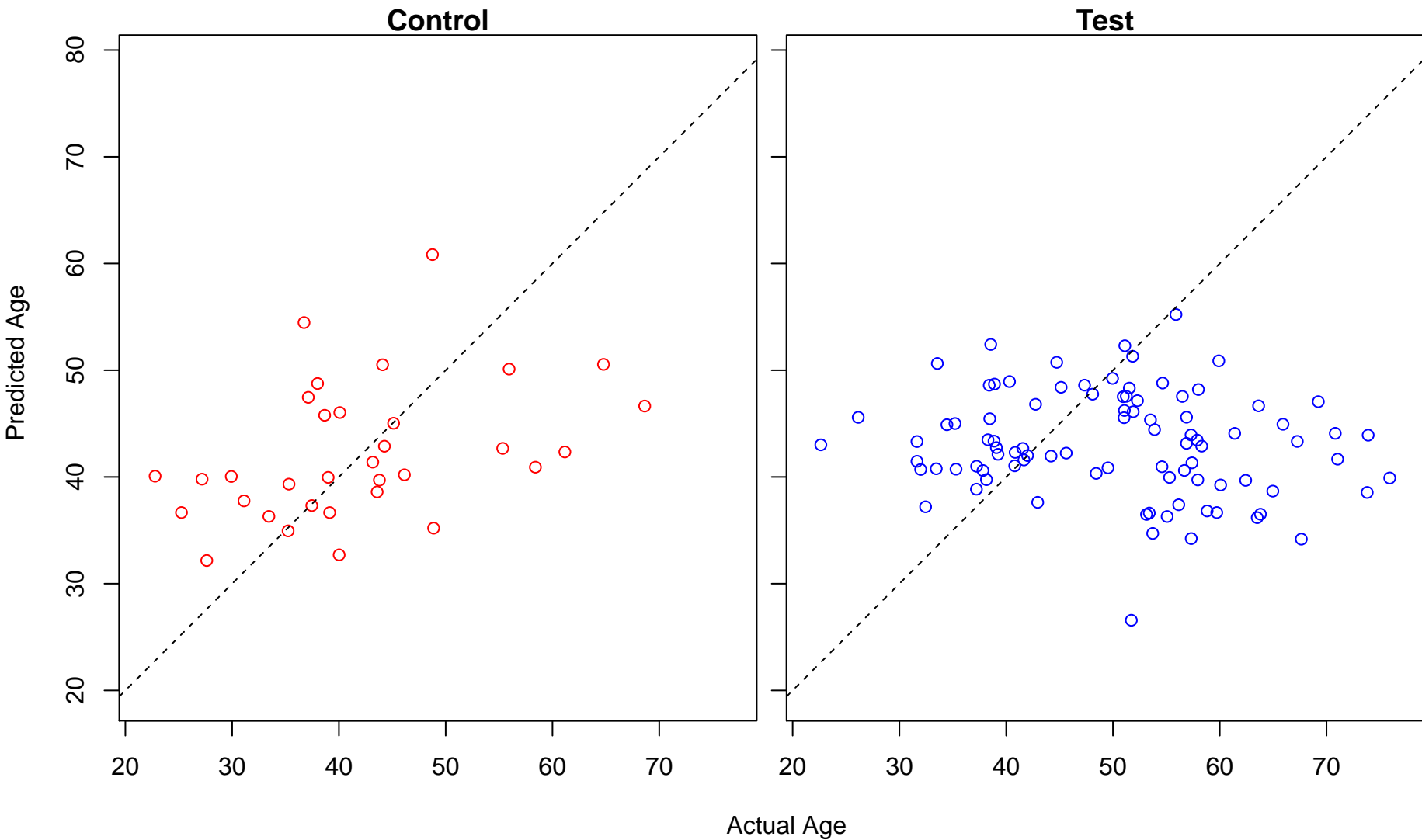
ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway (Score: 0.61)



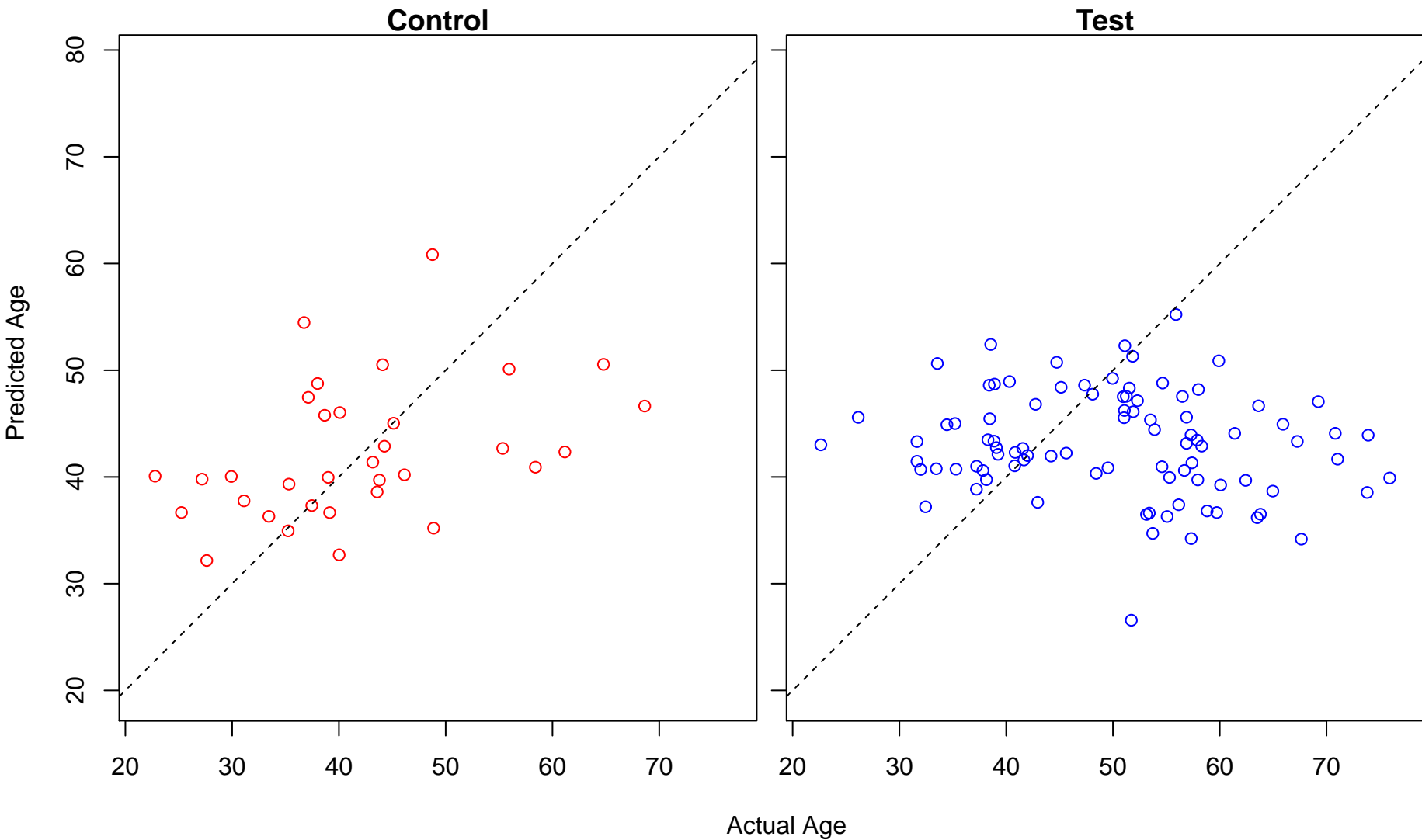
cellular response to peptide (Score: 0.617894)



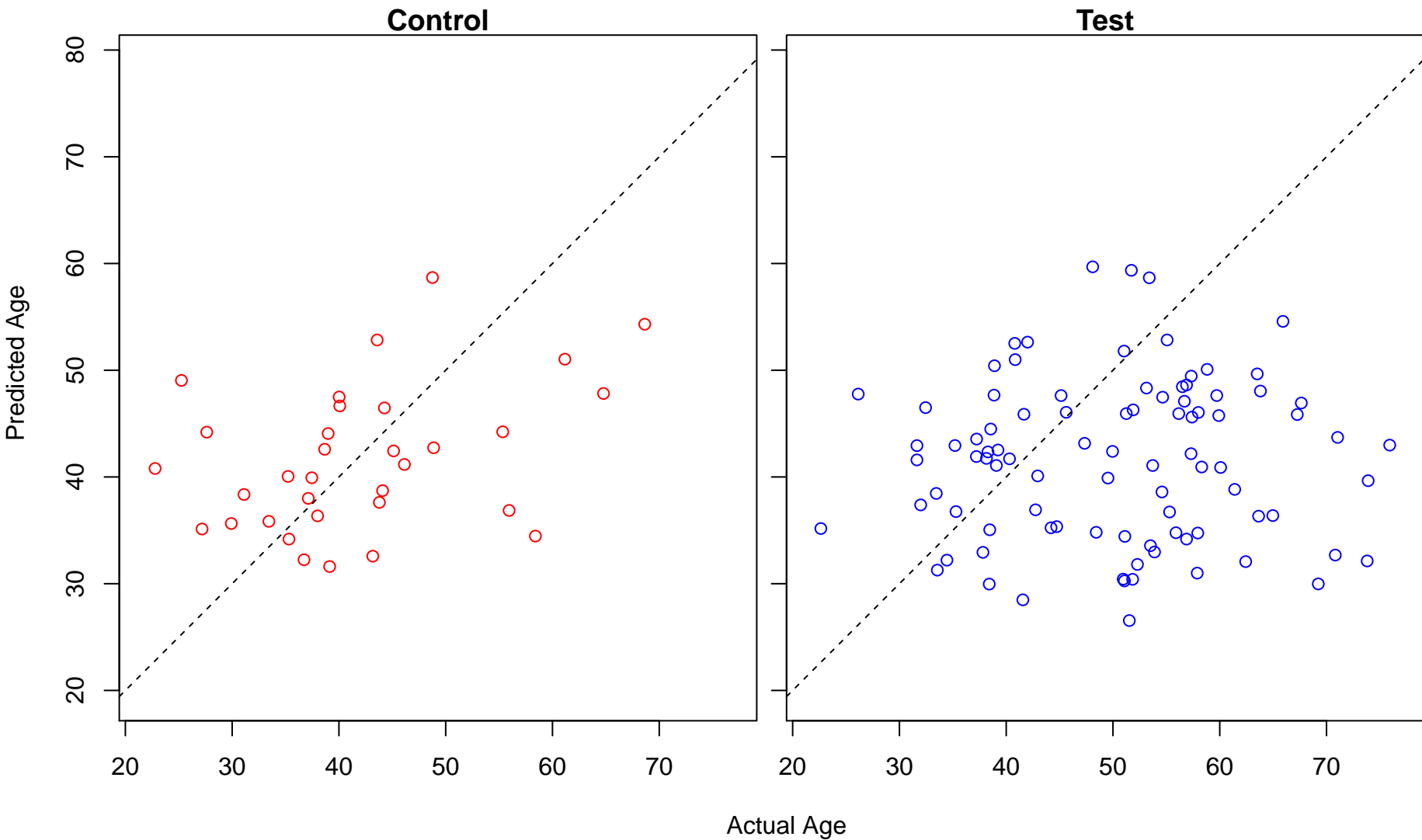
neurotrophin production (Score: 0.617880)



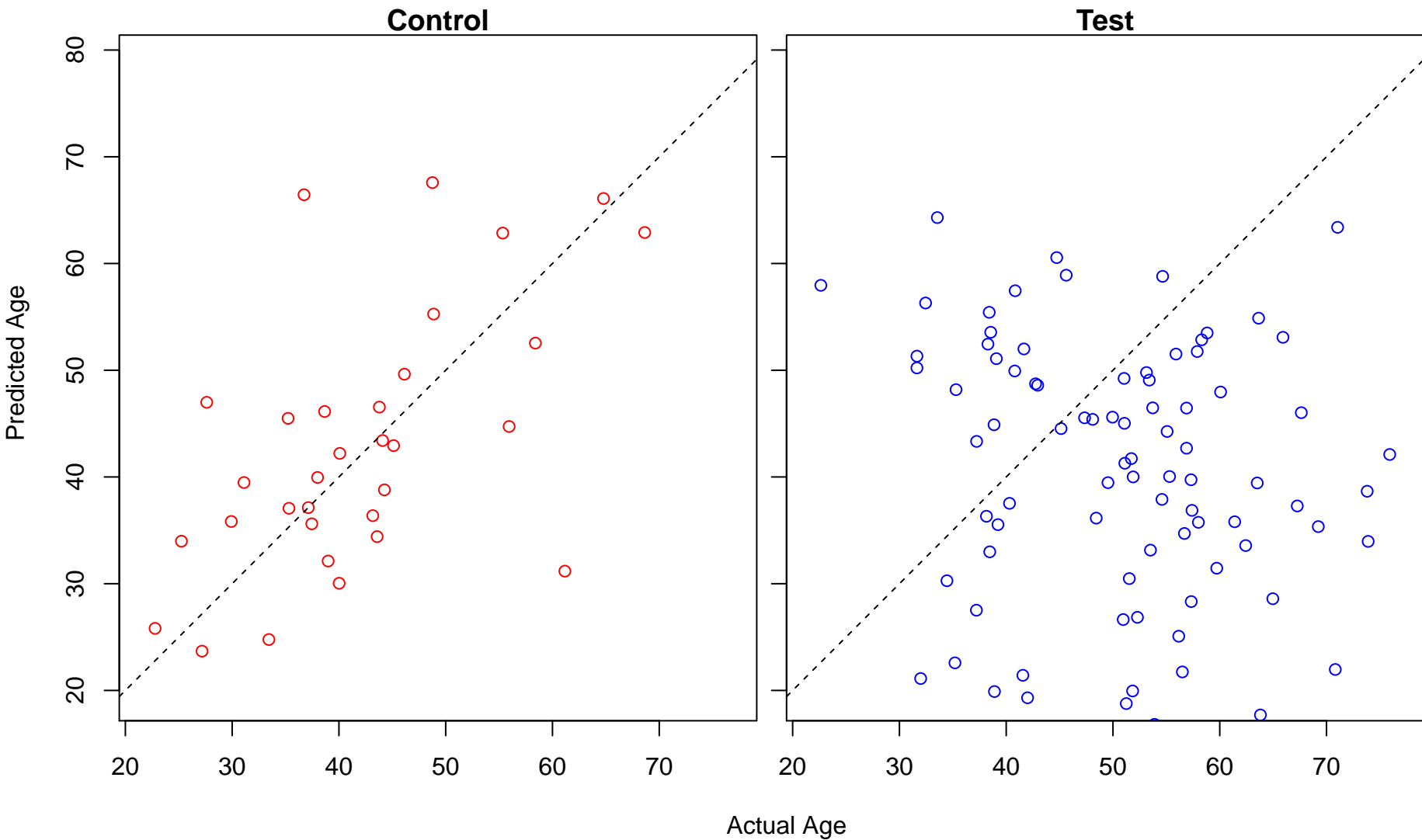
nerve growth factor production (Score: 0.617880)



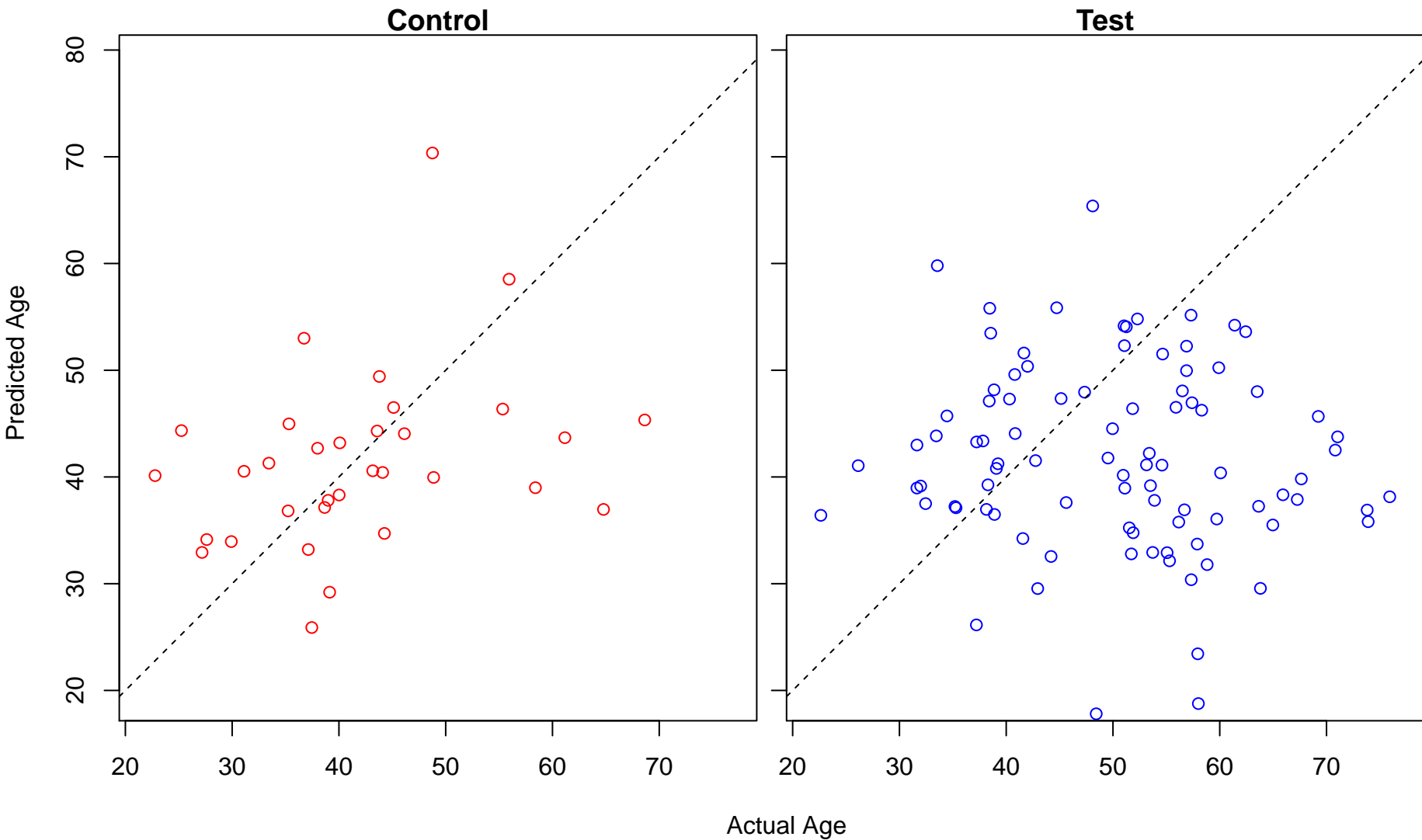
oocyte differentiation (Score: 0.617353)



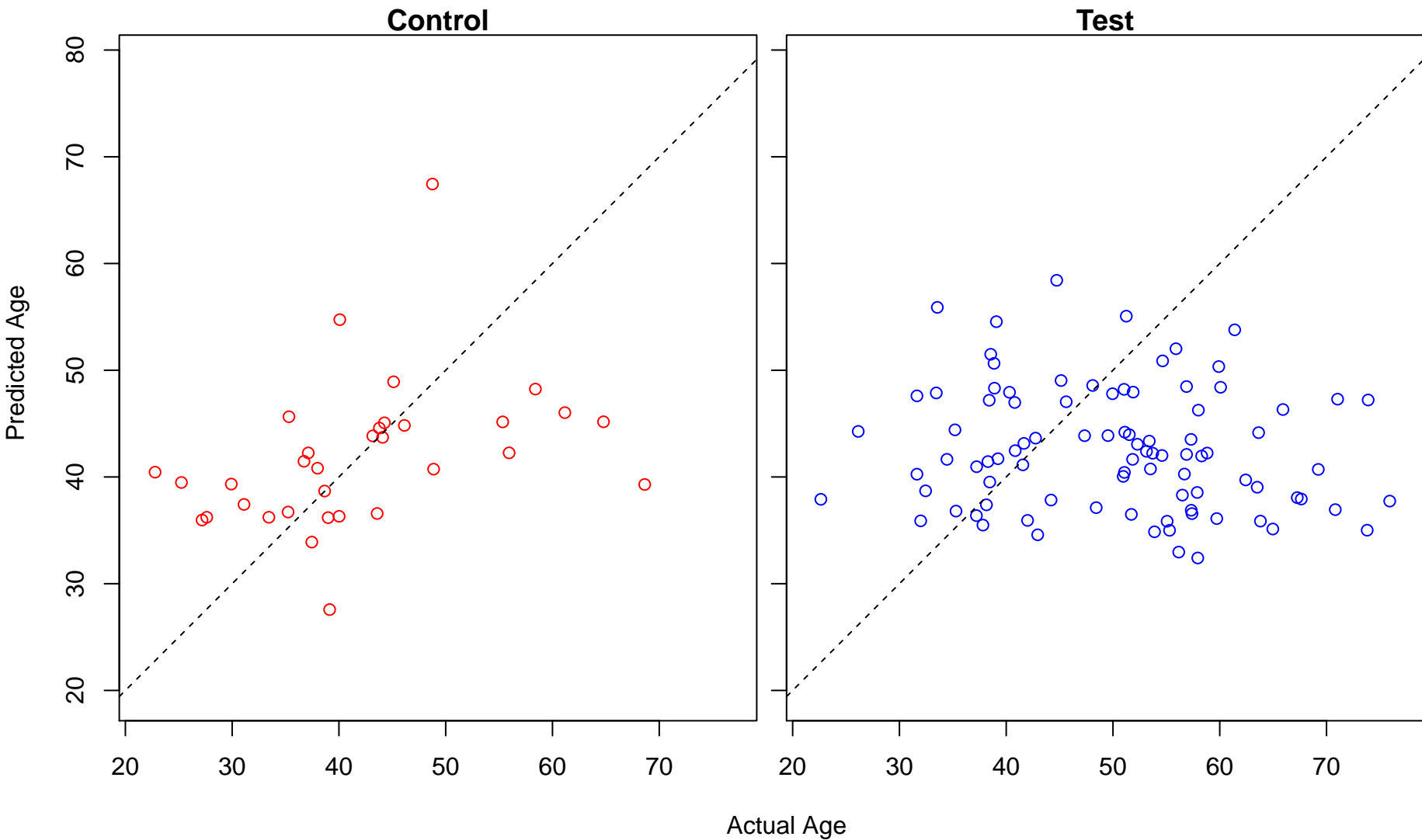
lipid phosphorylation (Score: 0.617347)



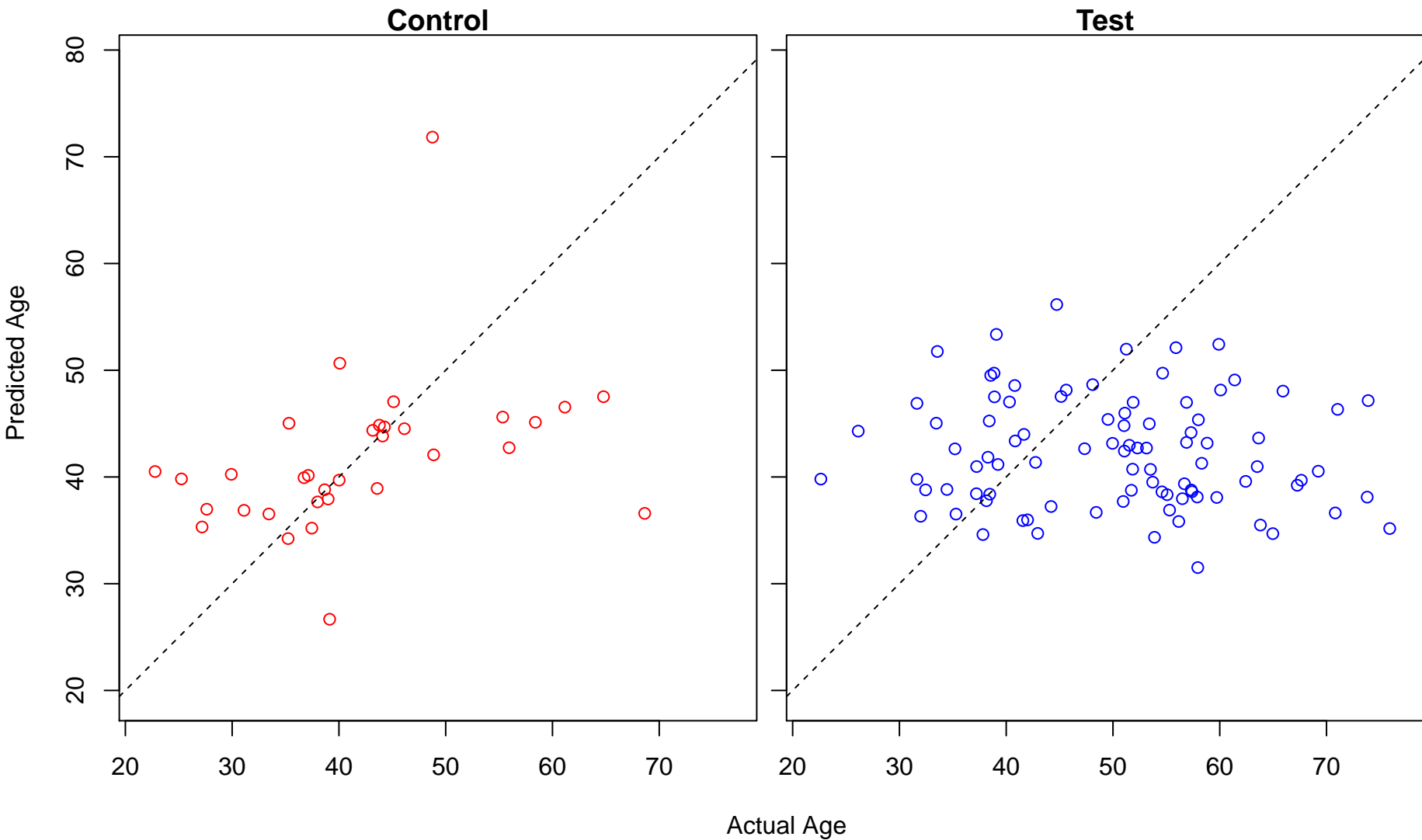
sexual reproduction (Score: 0.617254)



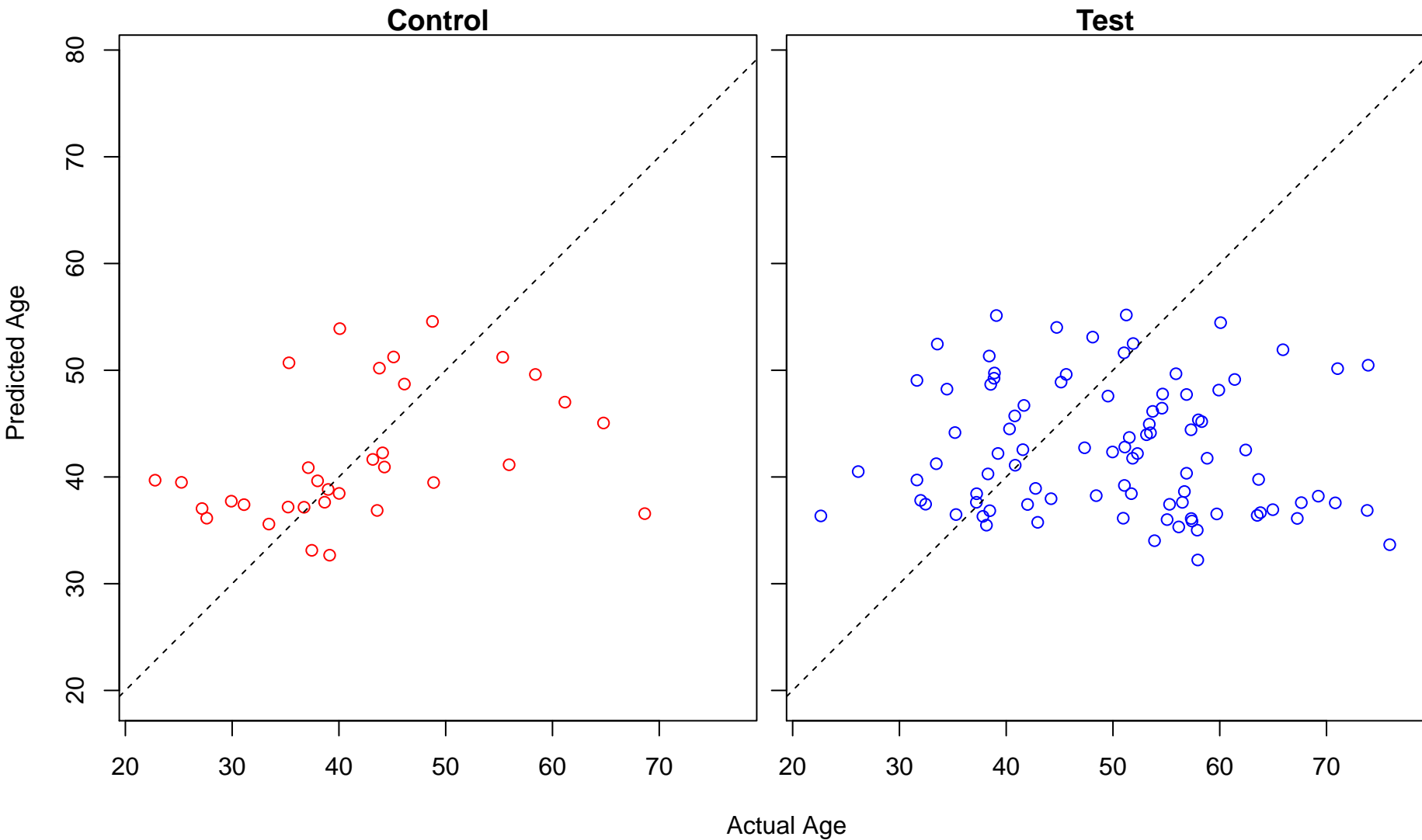
negative regulation of cellular component organization (Score: 0.616764)



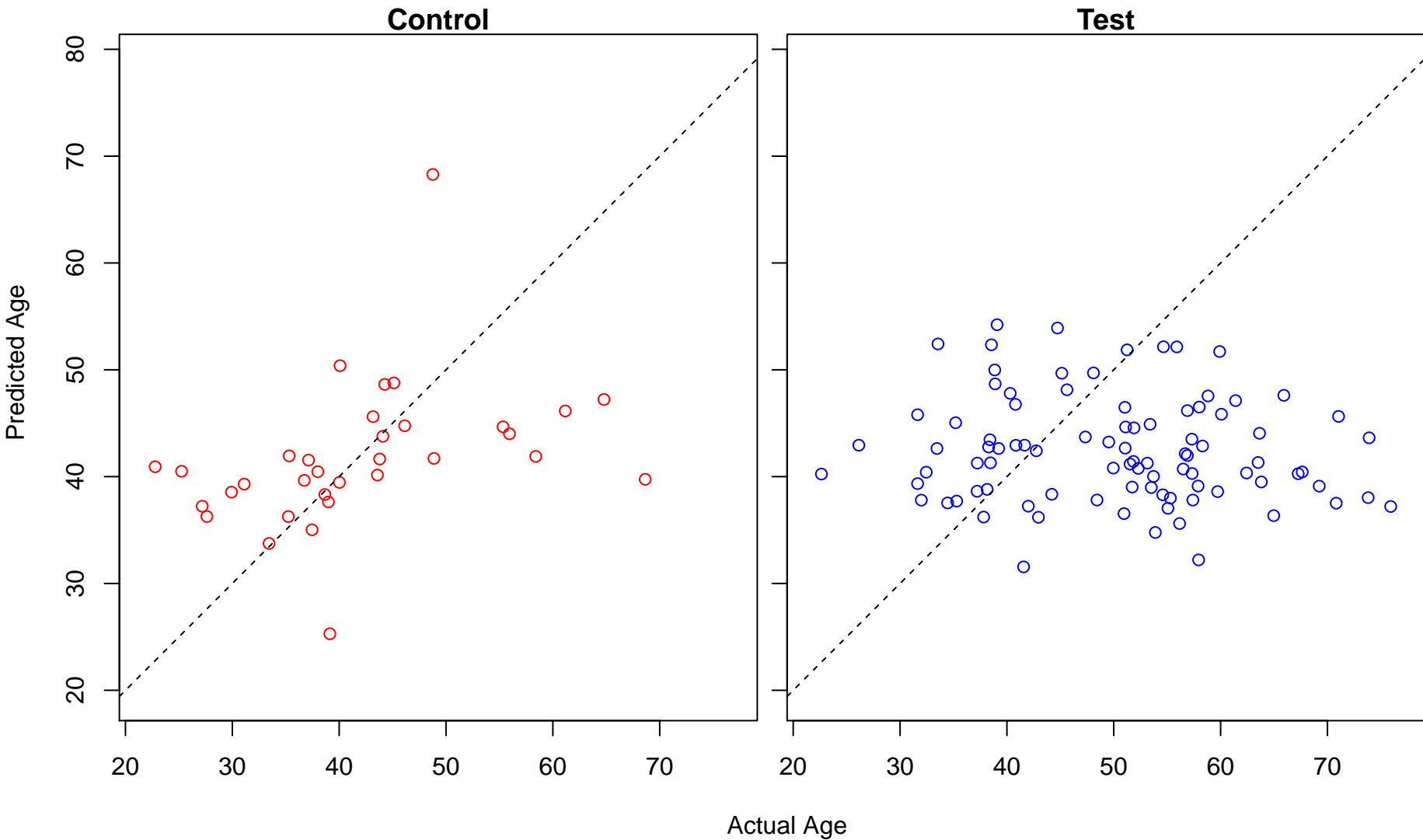
carbohydrate metabolic process (Score: 0.616716)



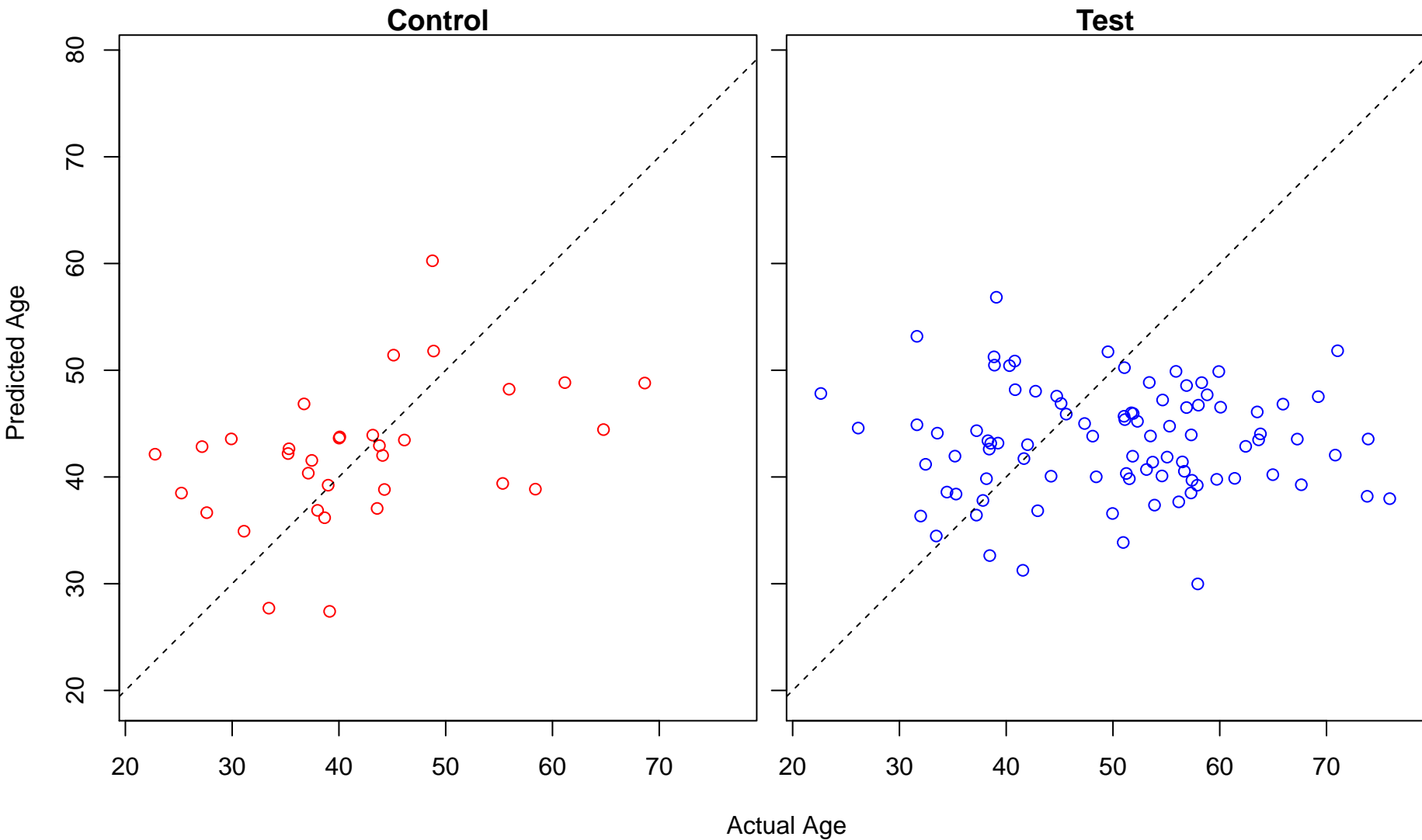
snRNA metabolic process (Score: 0.616404)



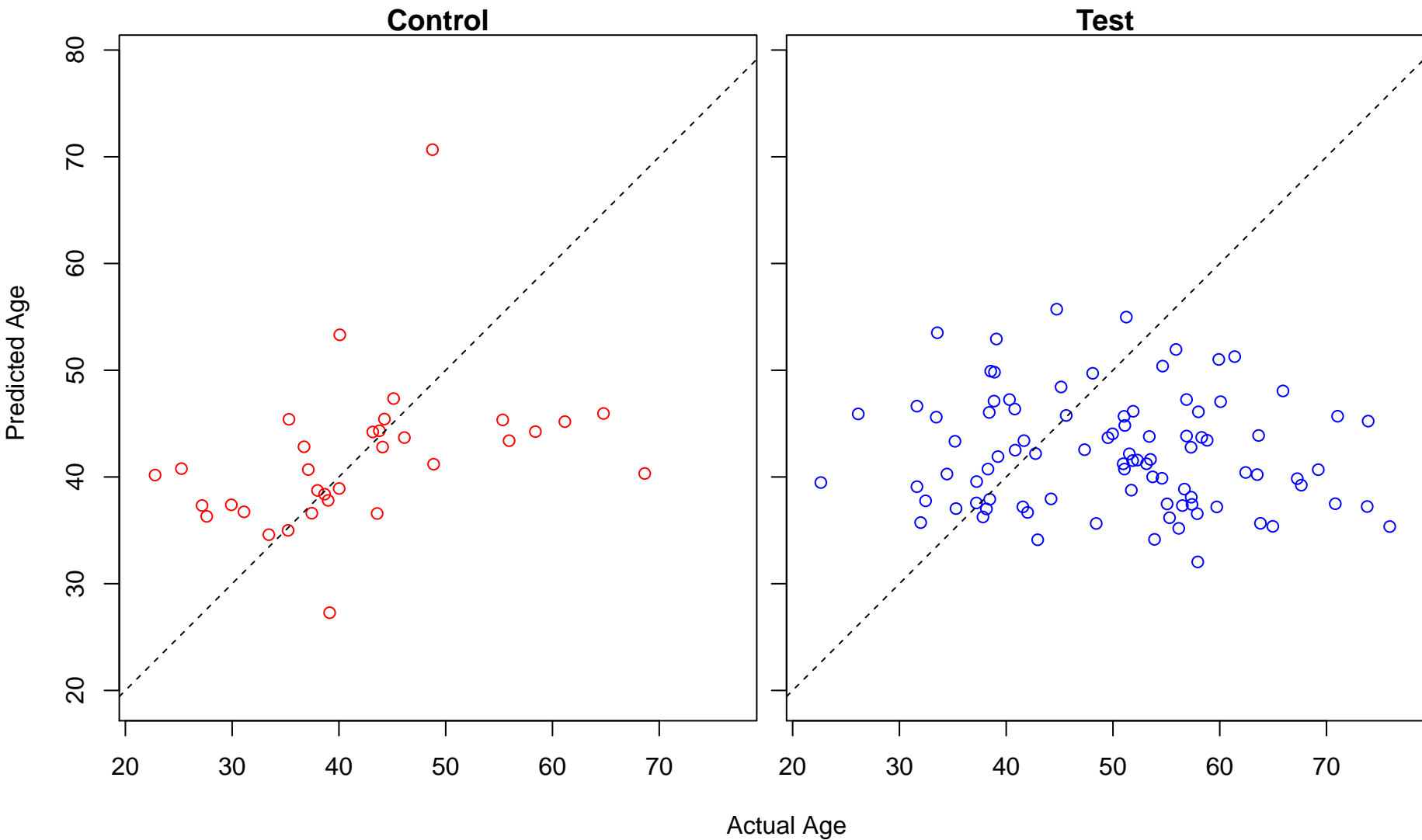
small GTPase mediated signal transduction (Score: 0.616338)



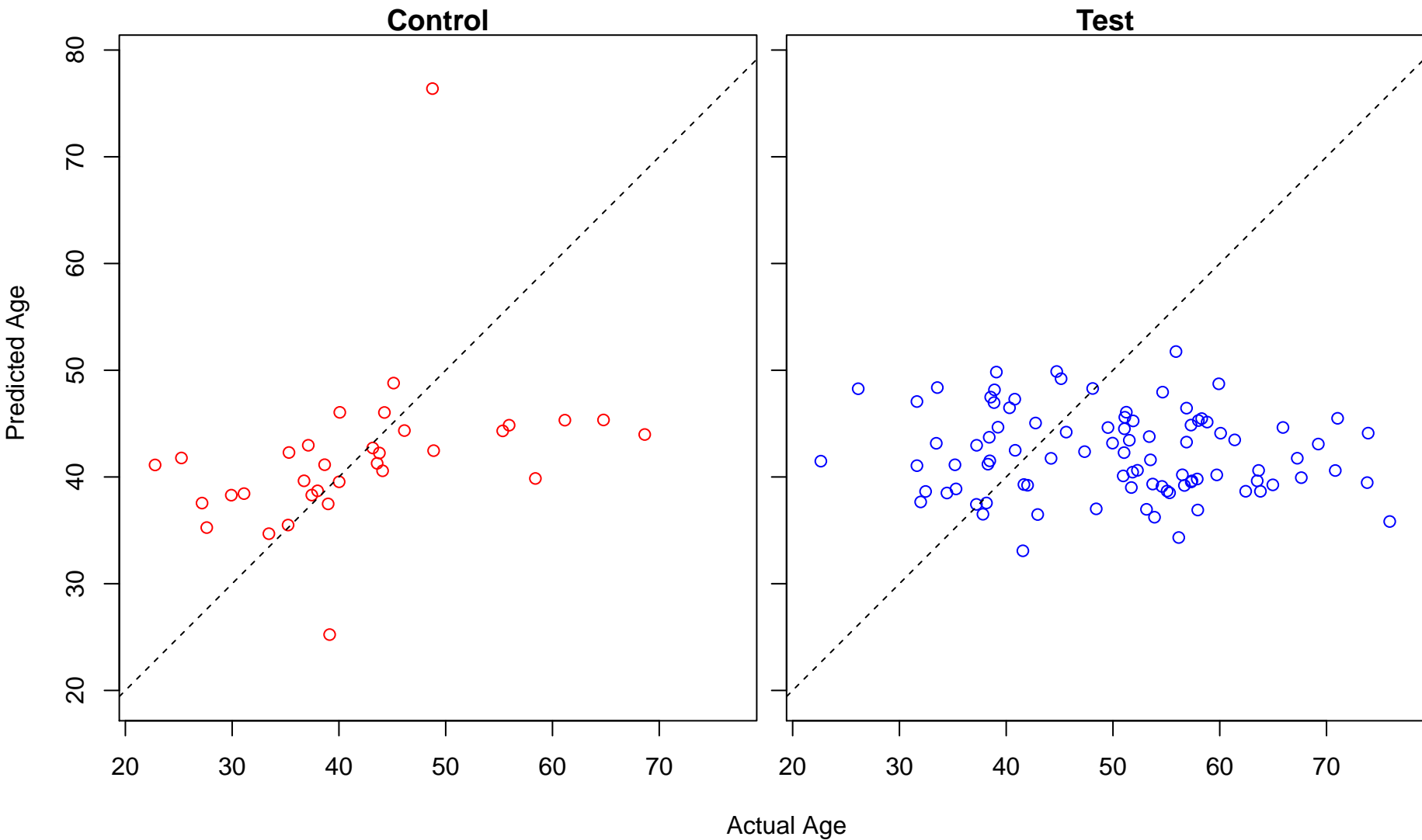
pigment granule aggregation in cell center (Score: 0.615885)



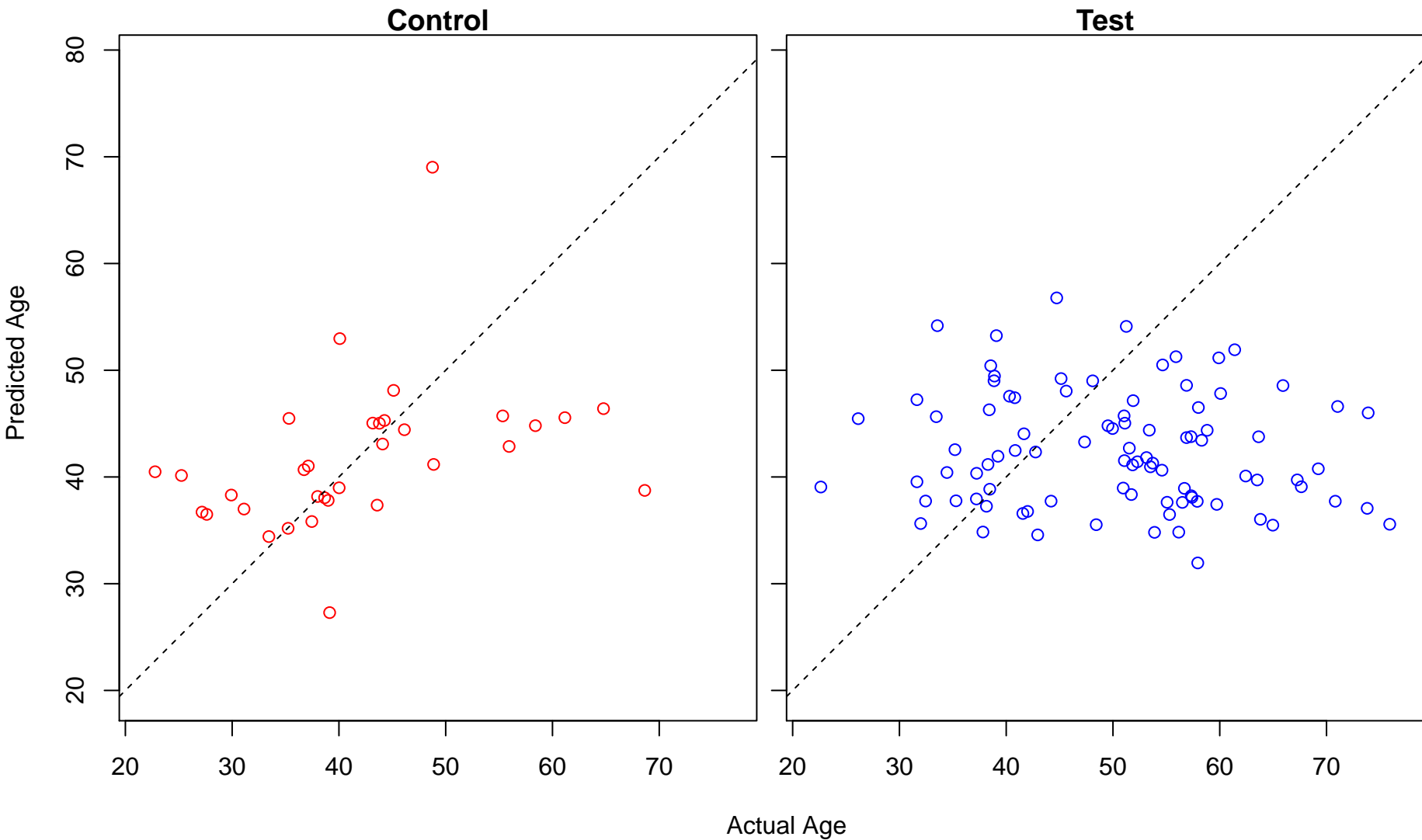
RNA metabolic process (Score: 0.615450)



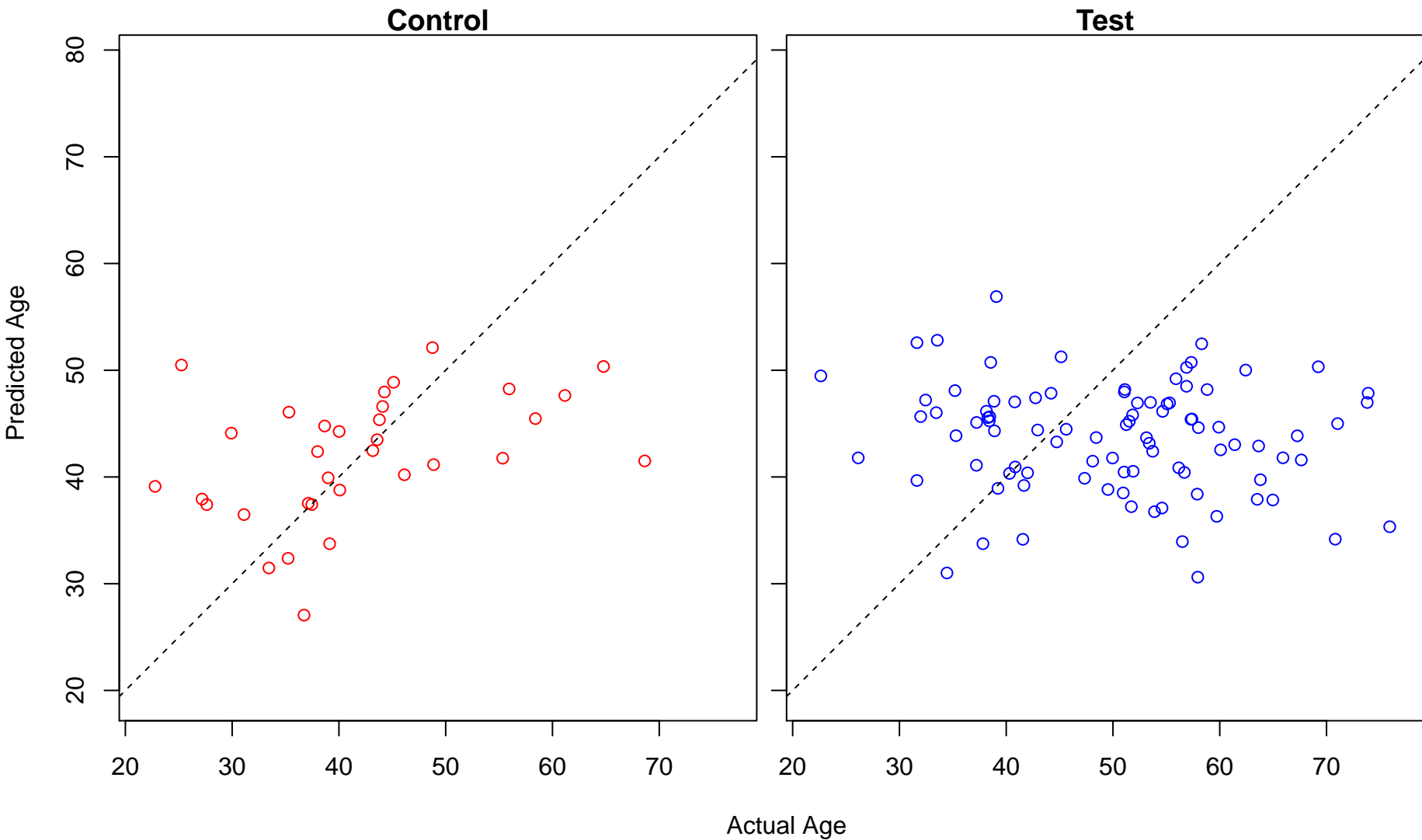
endocytosis (Score: 0.615070)



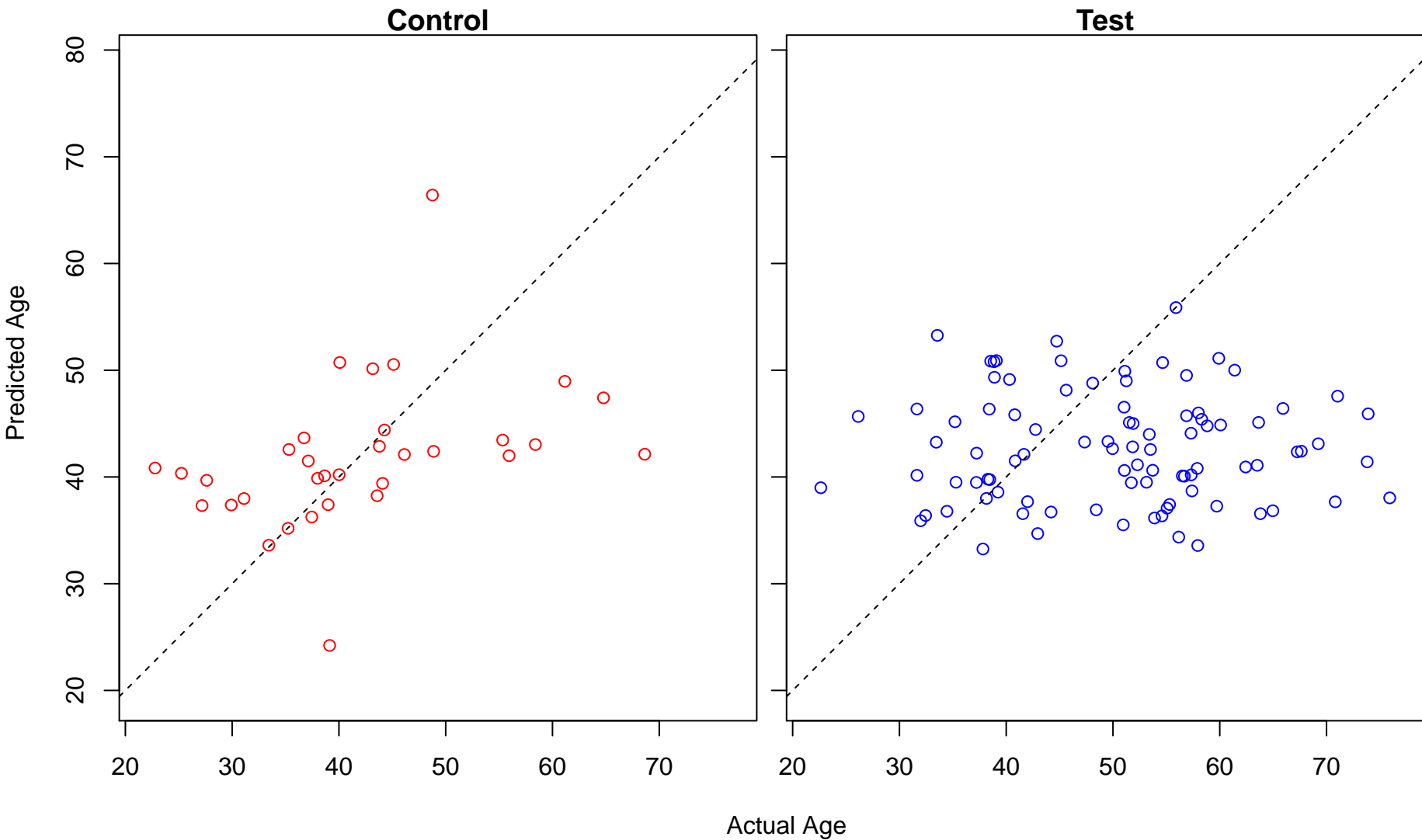
macromolecule metabolic process (Score: 0.613970)



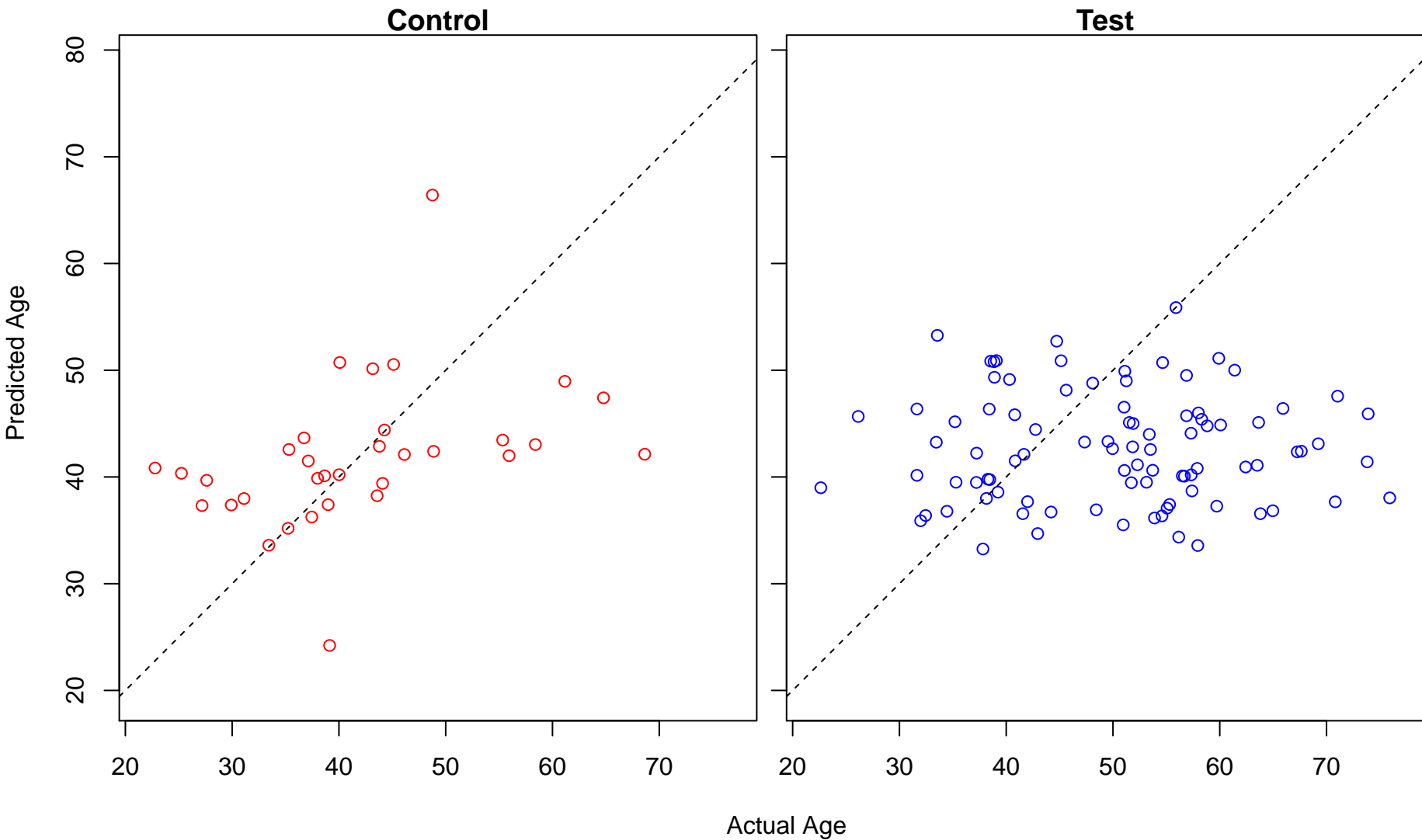
GTP metabolic process (Score: 0.613936)



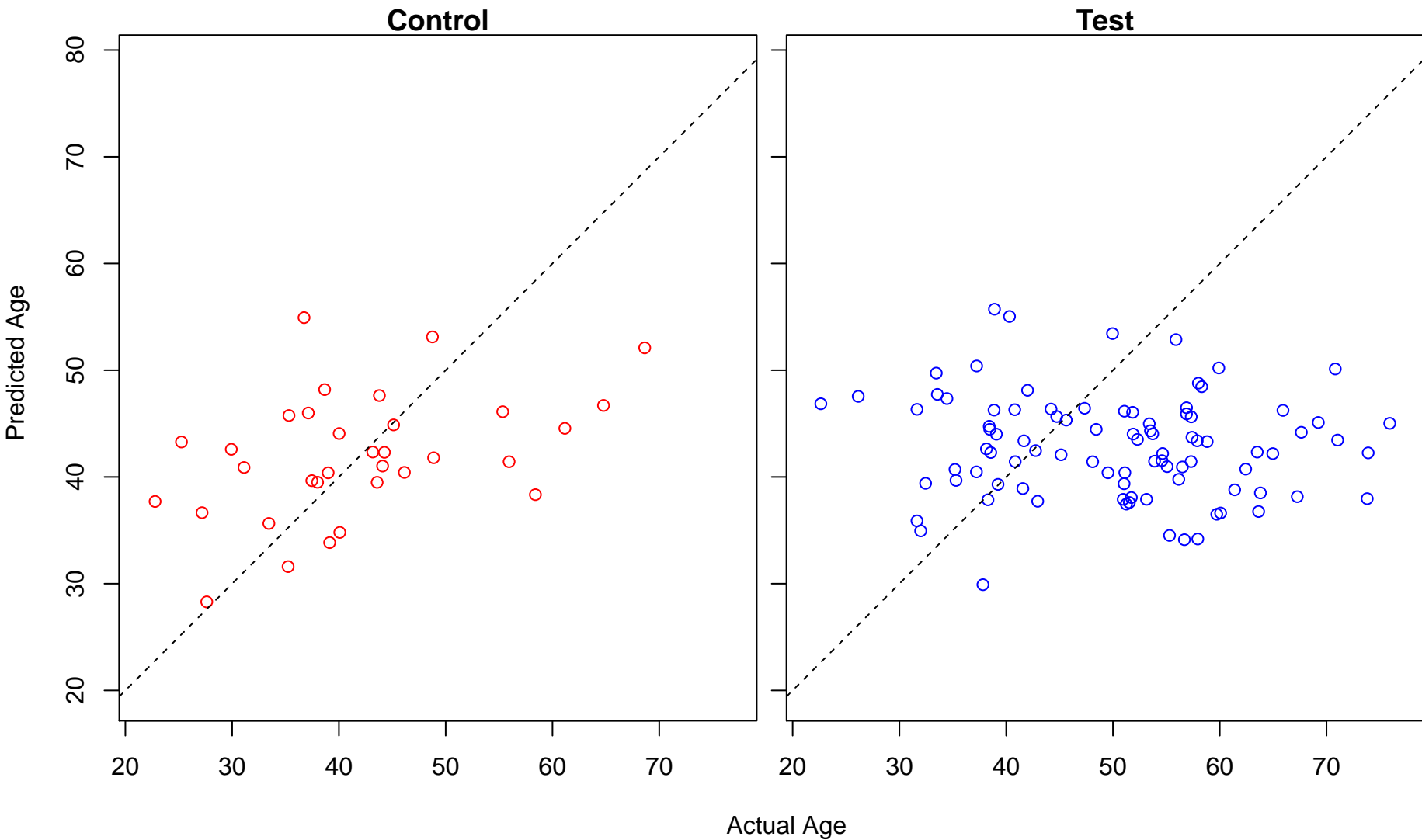
cell motility (Score: 0.613733)



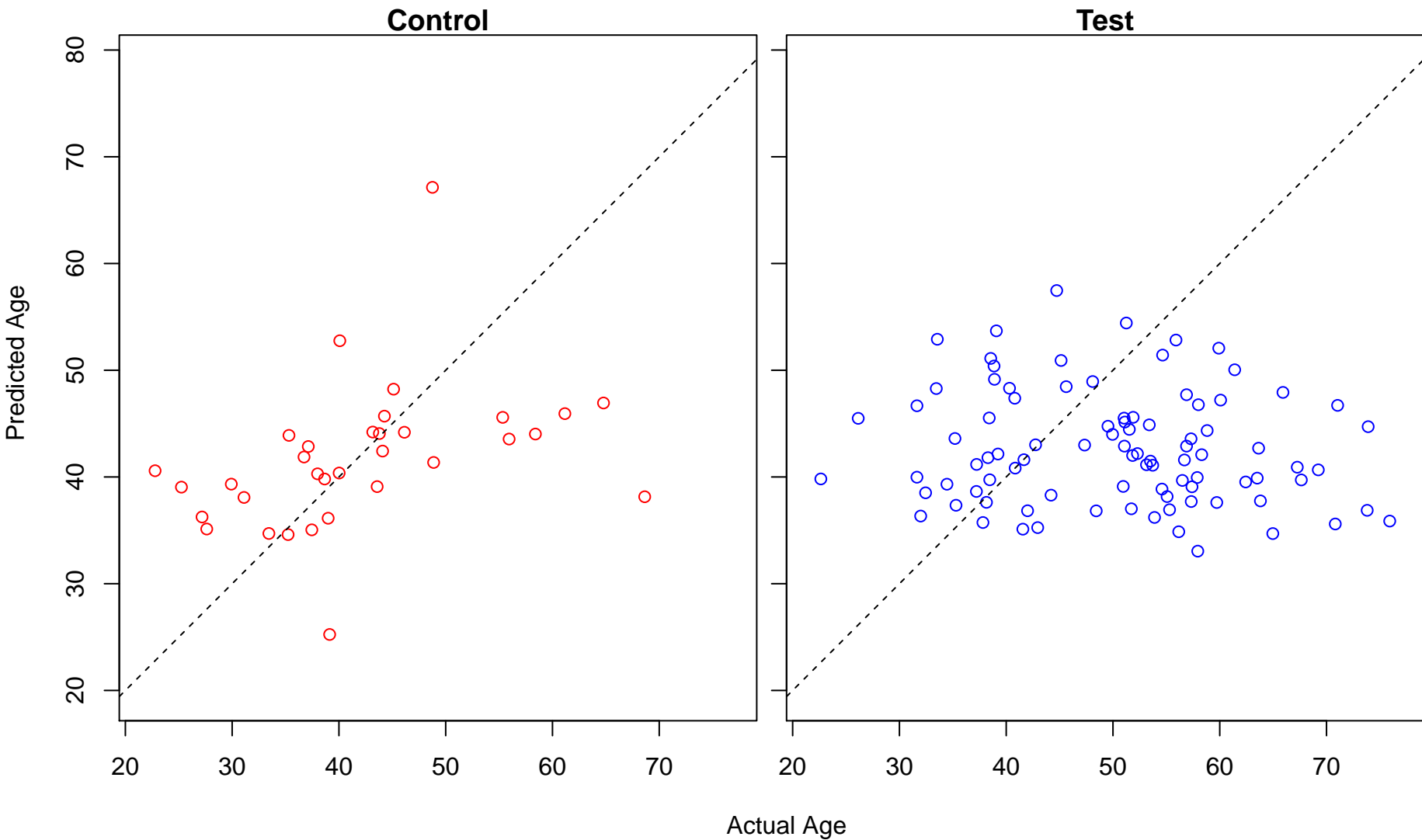
localization of cell (Score: 0.613733)



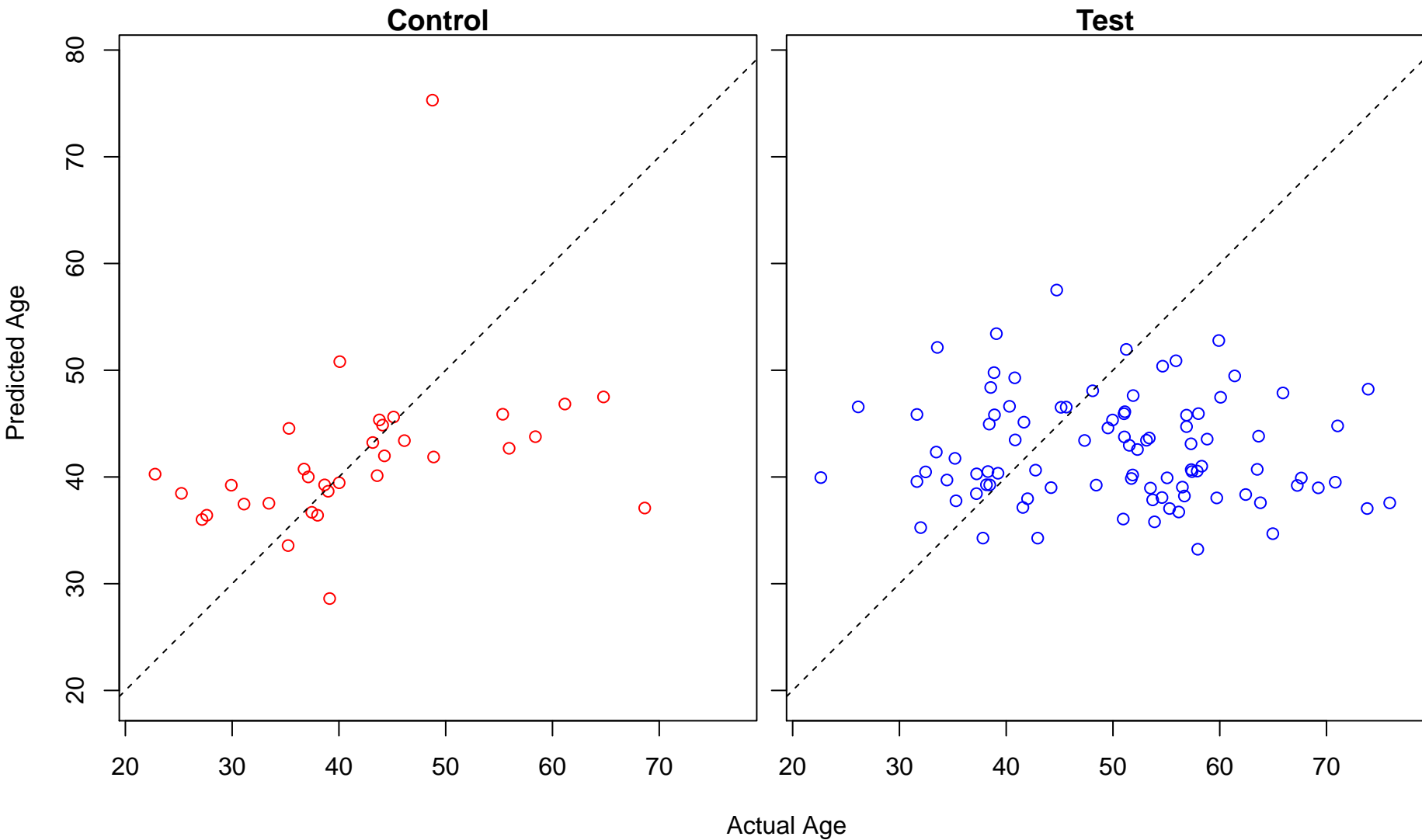
positive regulation of interleukin-10 secretion (Score: 0.613728)



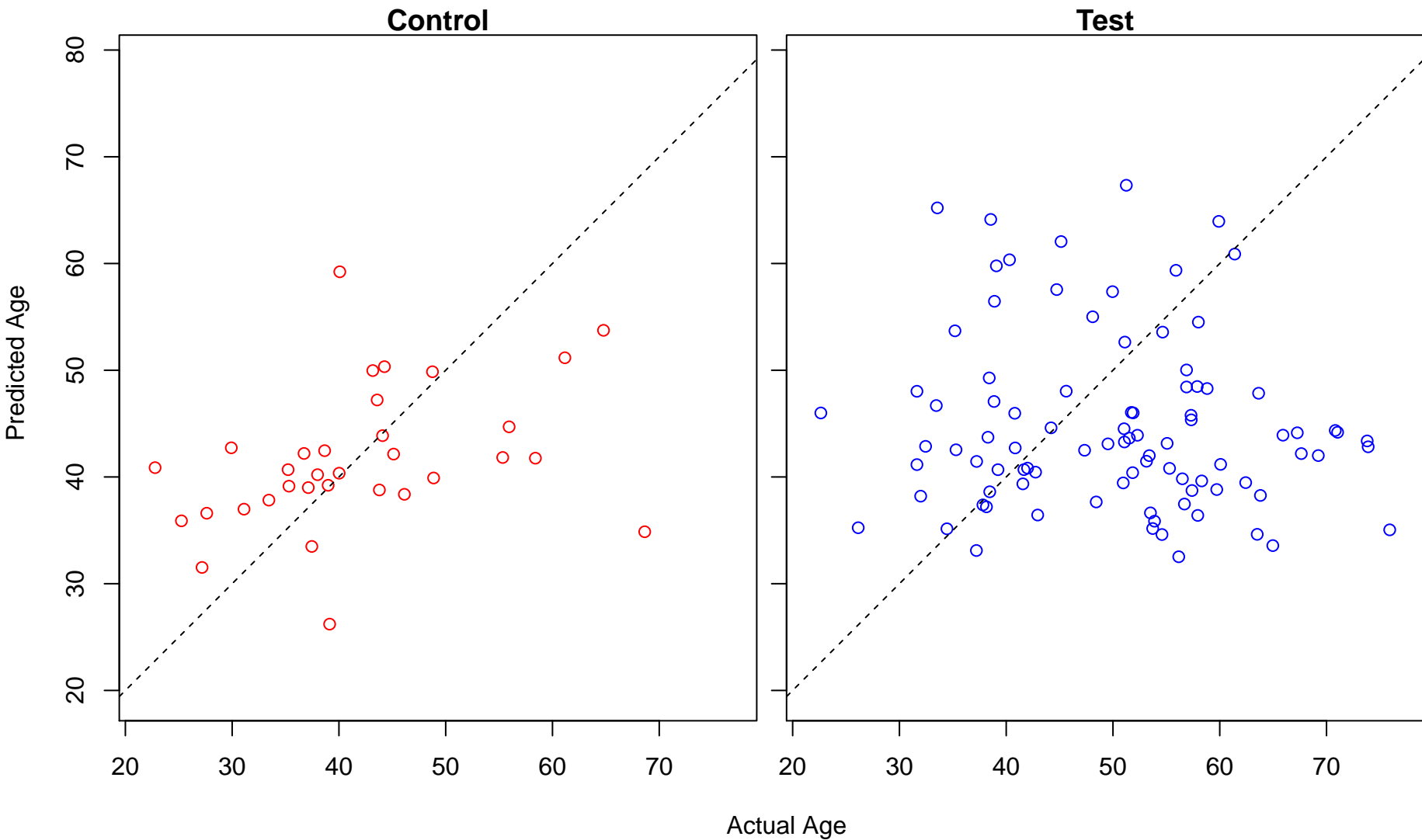
positive regulation of signaling (Score: 0.613644)



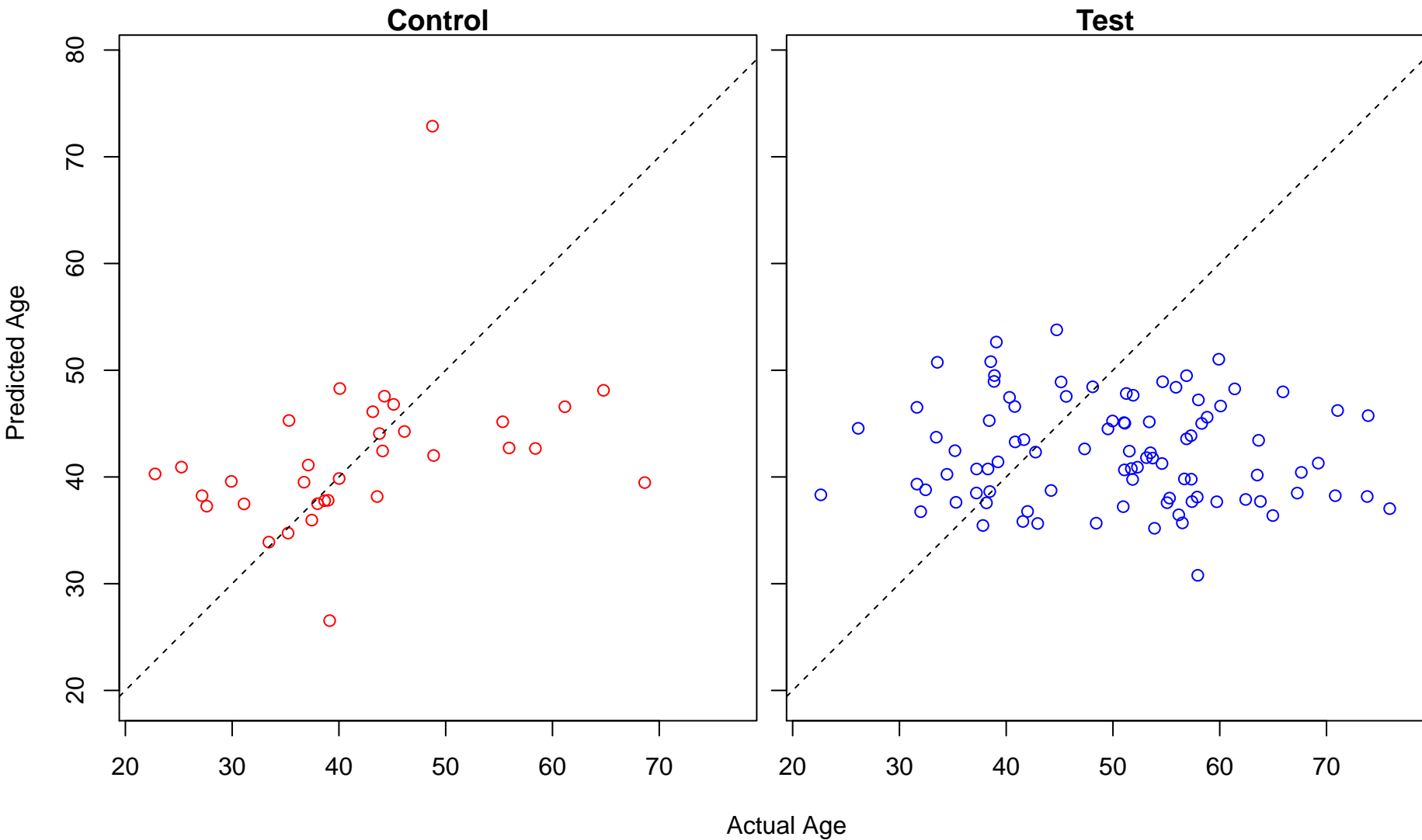
glycoprotein biosynthetic process (Score: 0.613586)



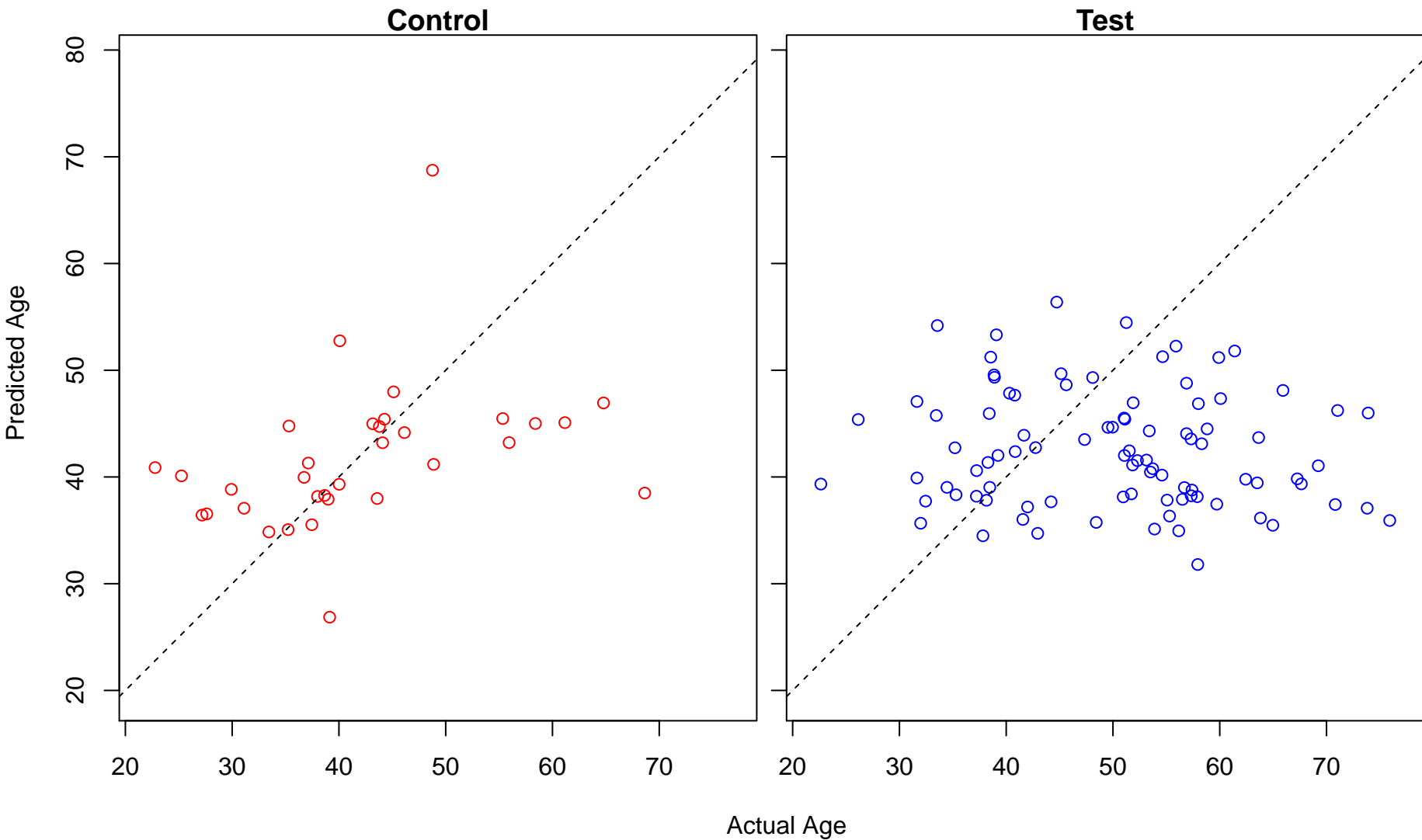
negative regulation of histone methylation (Score: 0.613461)



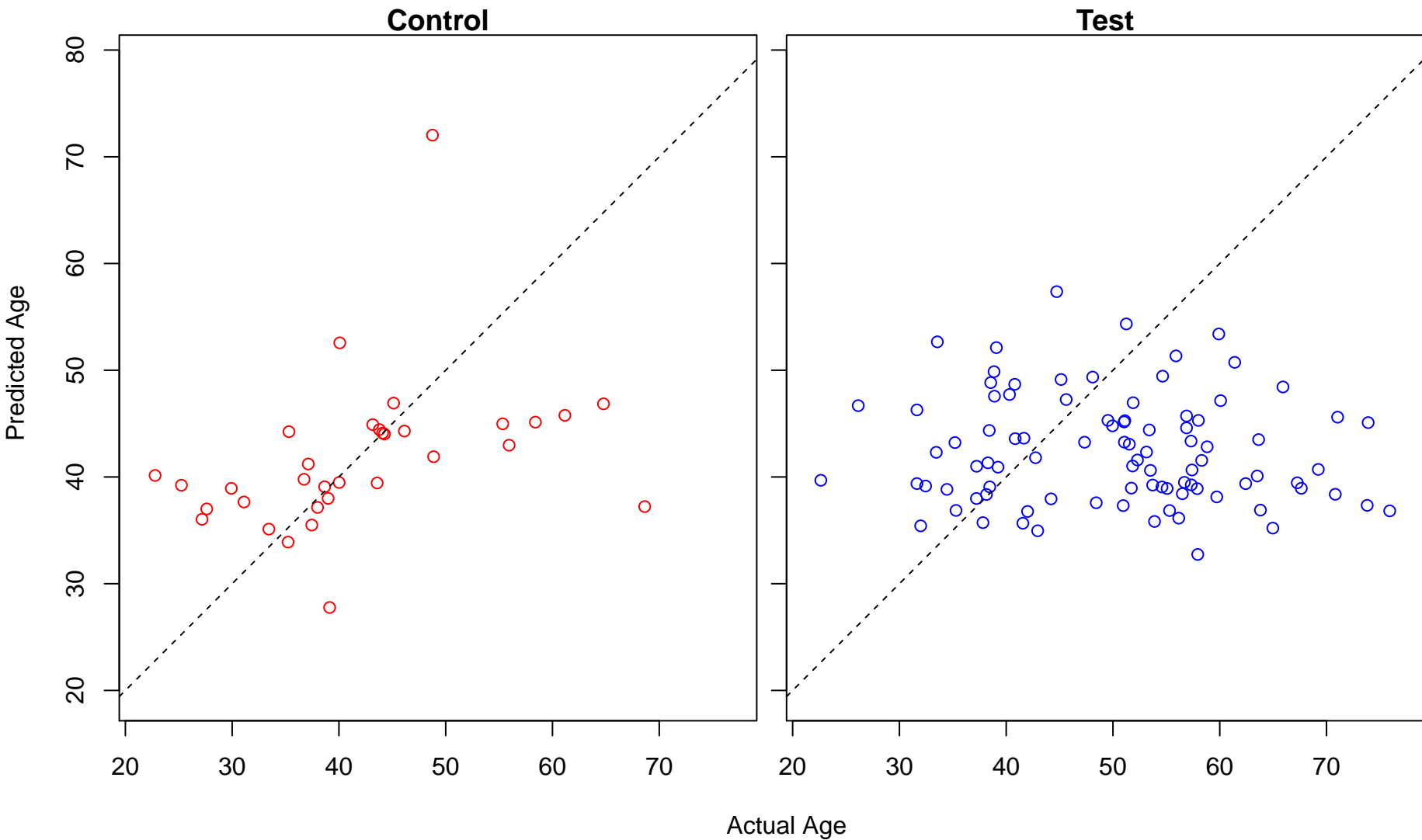
chromosome organization (Score: 0.613204)



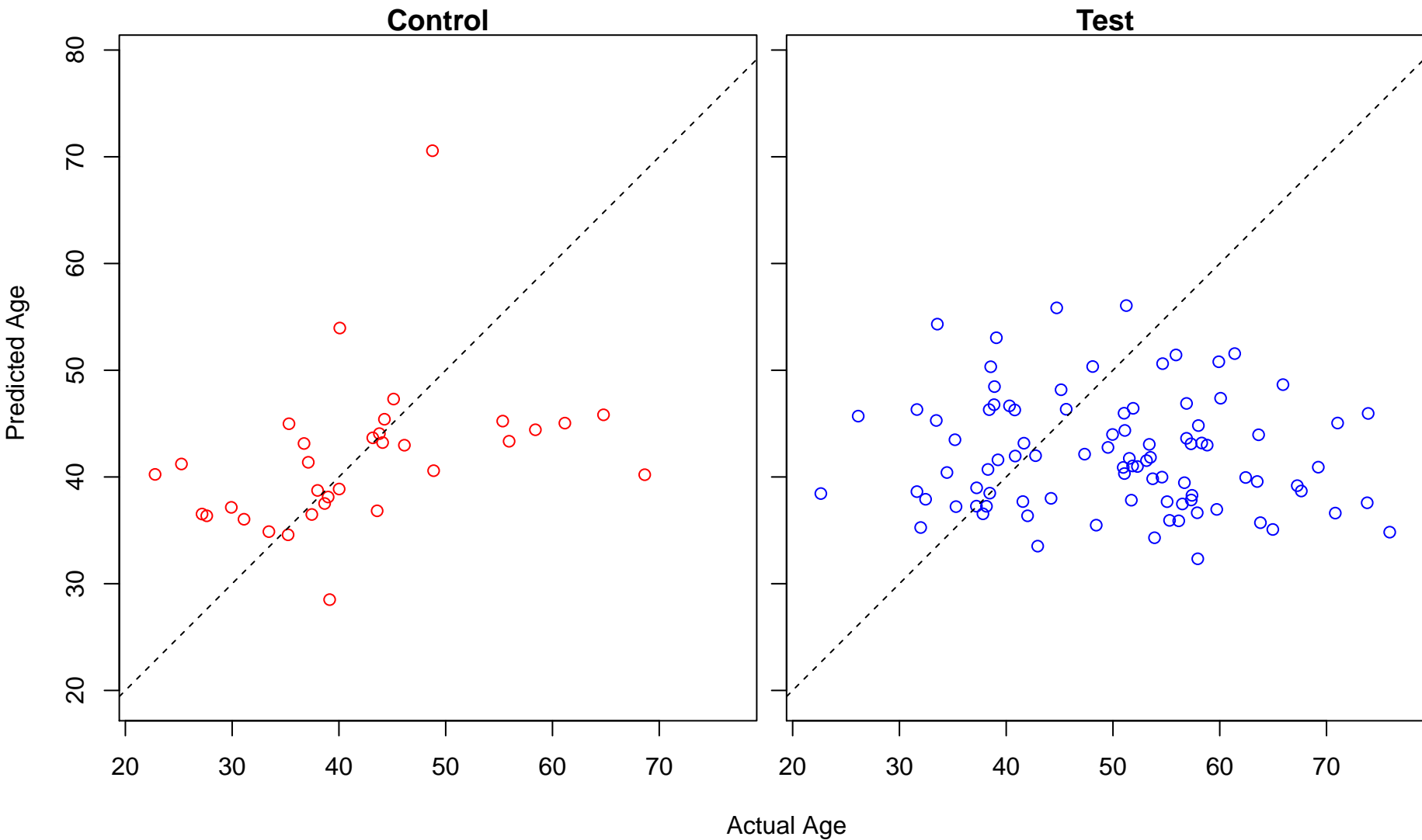
protein metabolic process (Score: 0.612877)



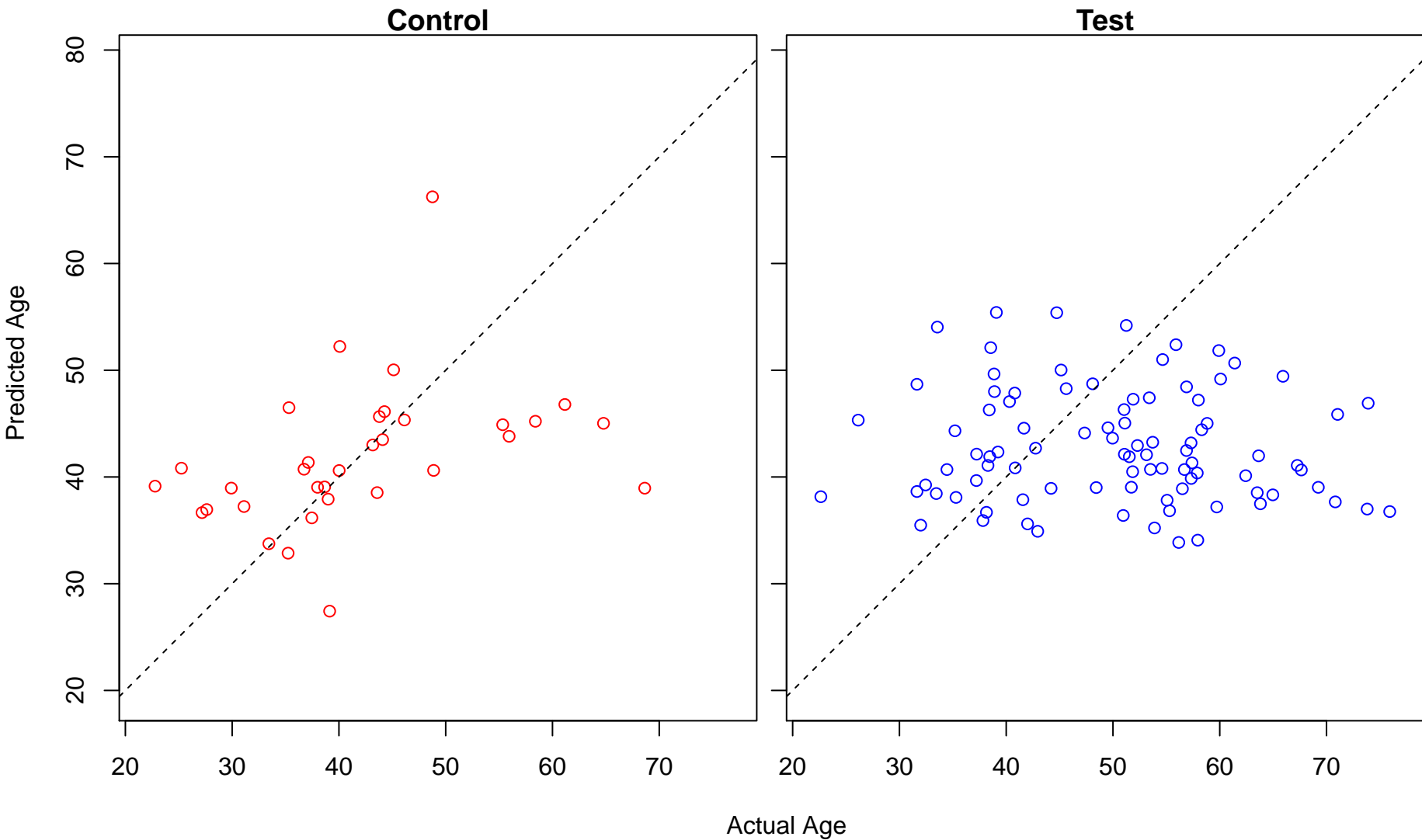
carbohydrate derivative biosynthetic process (Score: 0.612654)



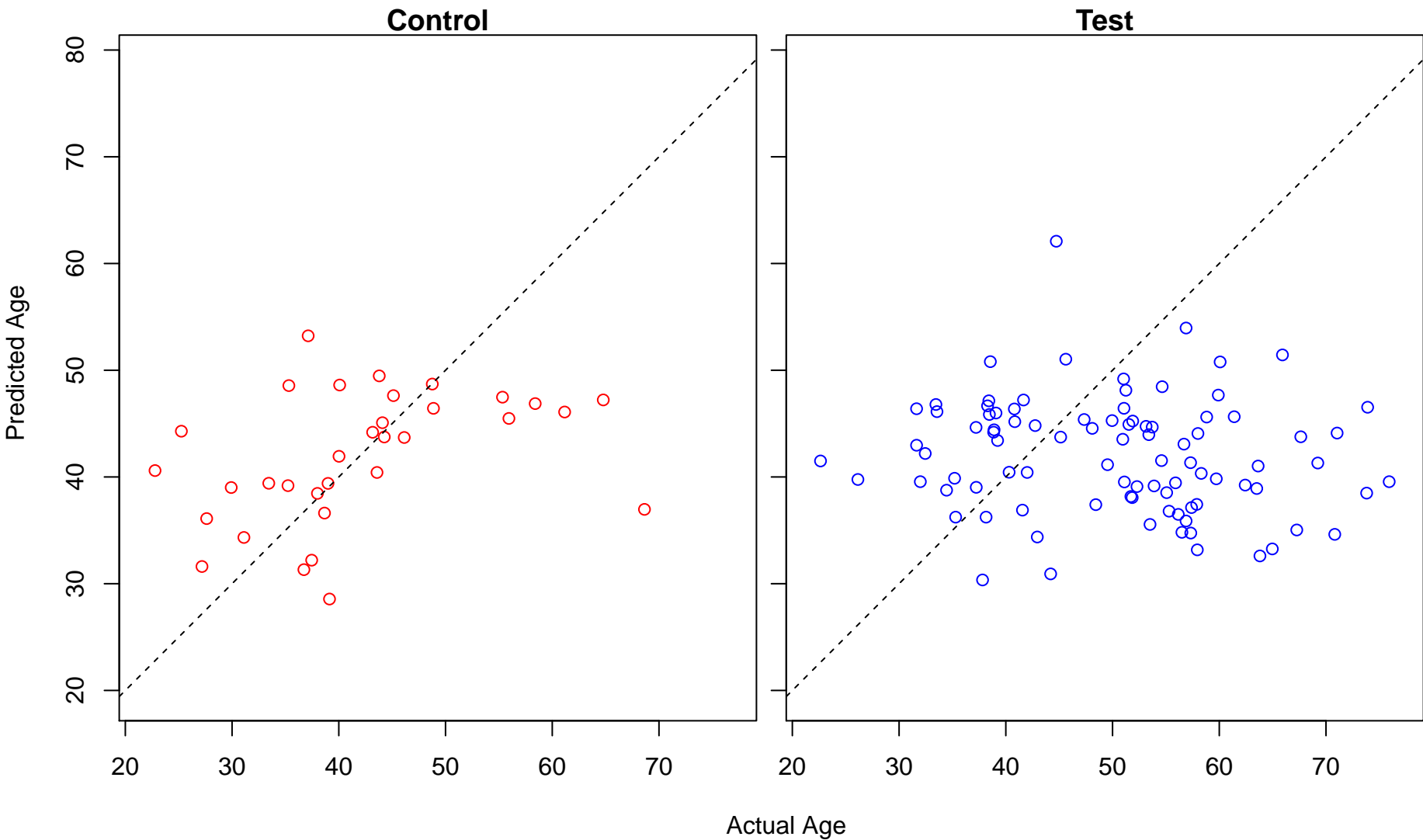
heterocycle biosynthetic process (Score: 0.612534)



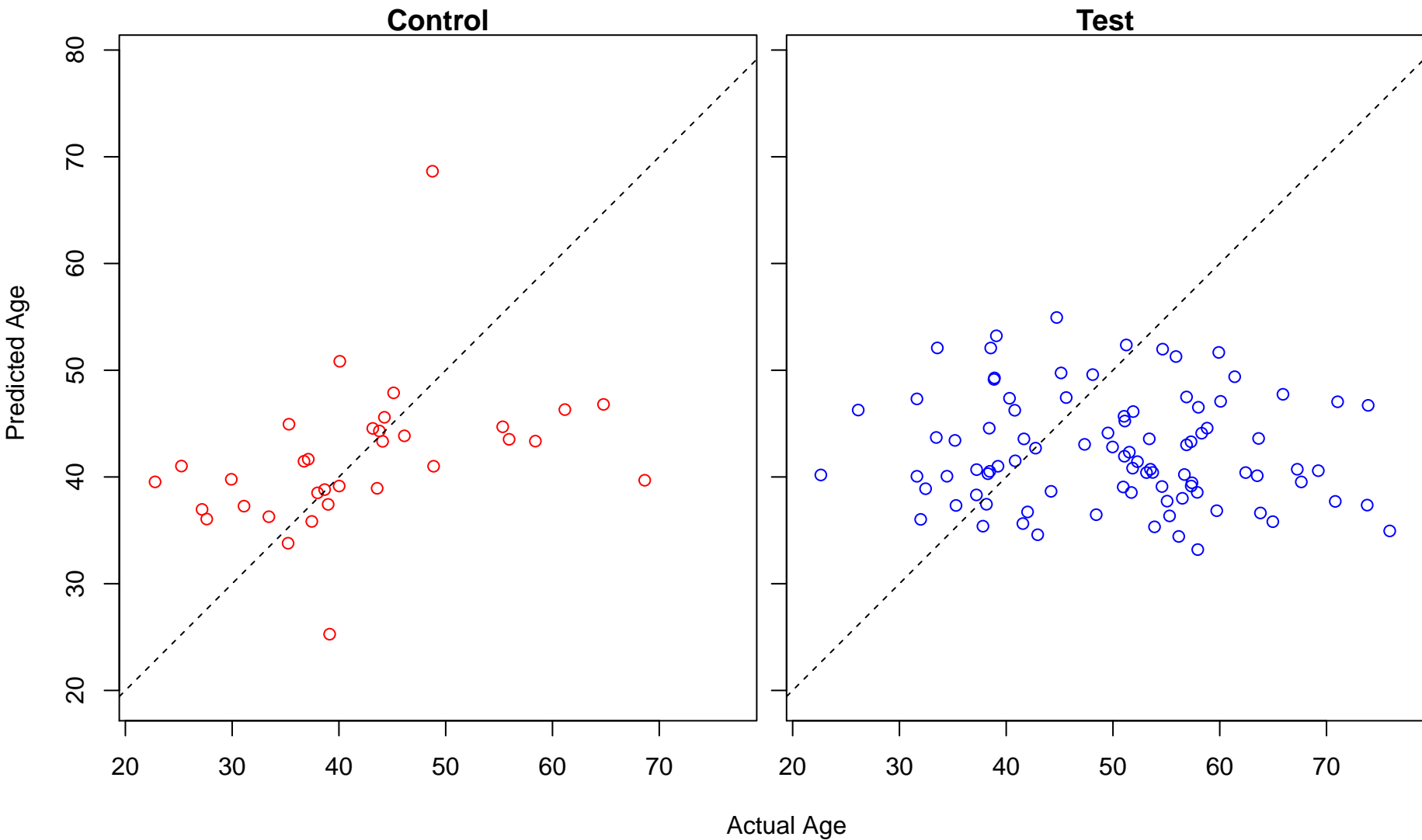
regulation of cell proliferation (Score: 0.611767)



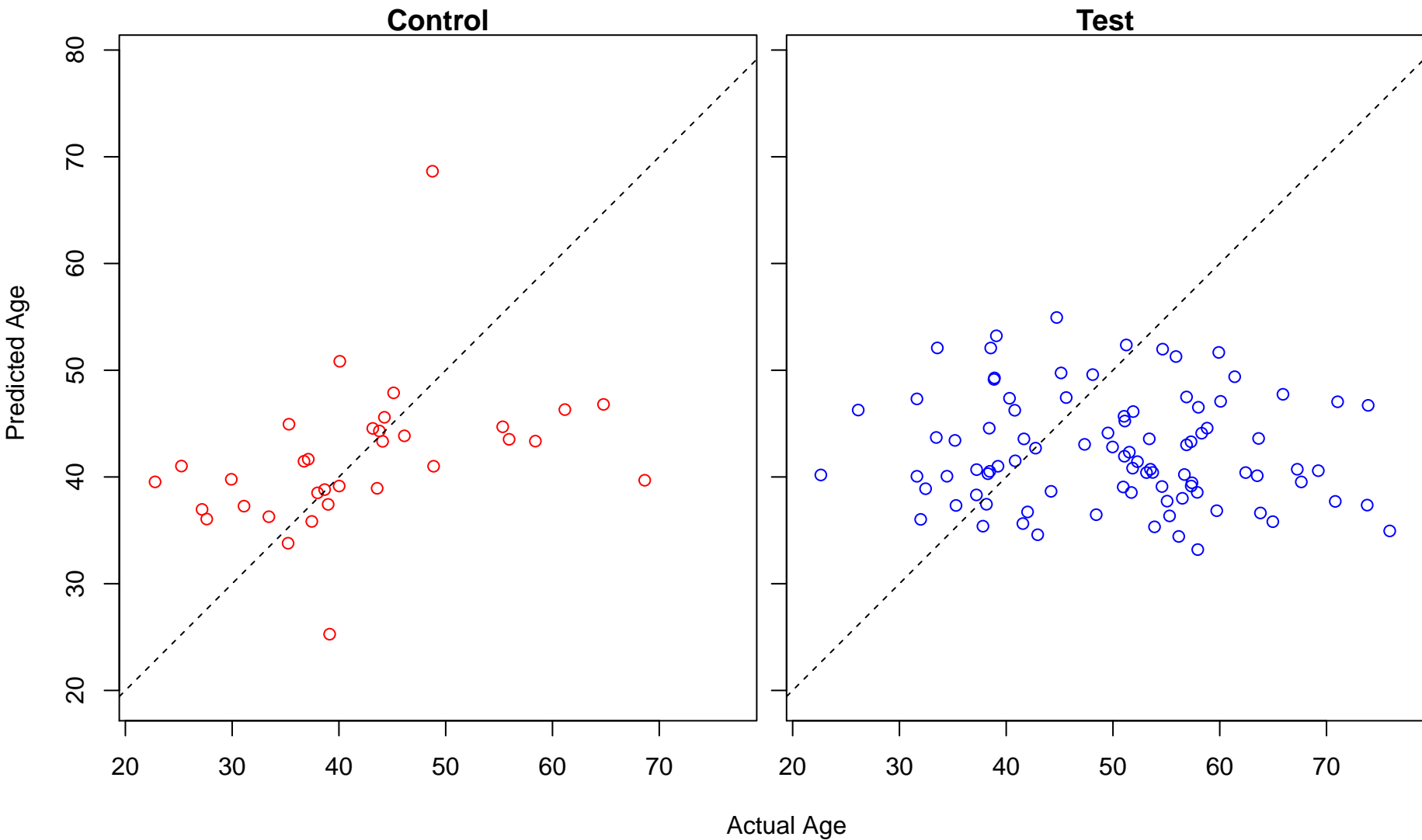
nucleotide-binding oligomerization domain containing 2 signaling pathway (Score: 0.611517)



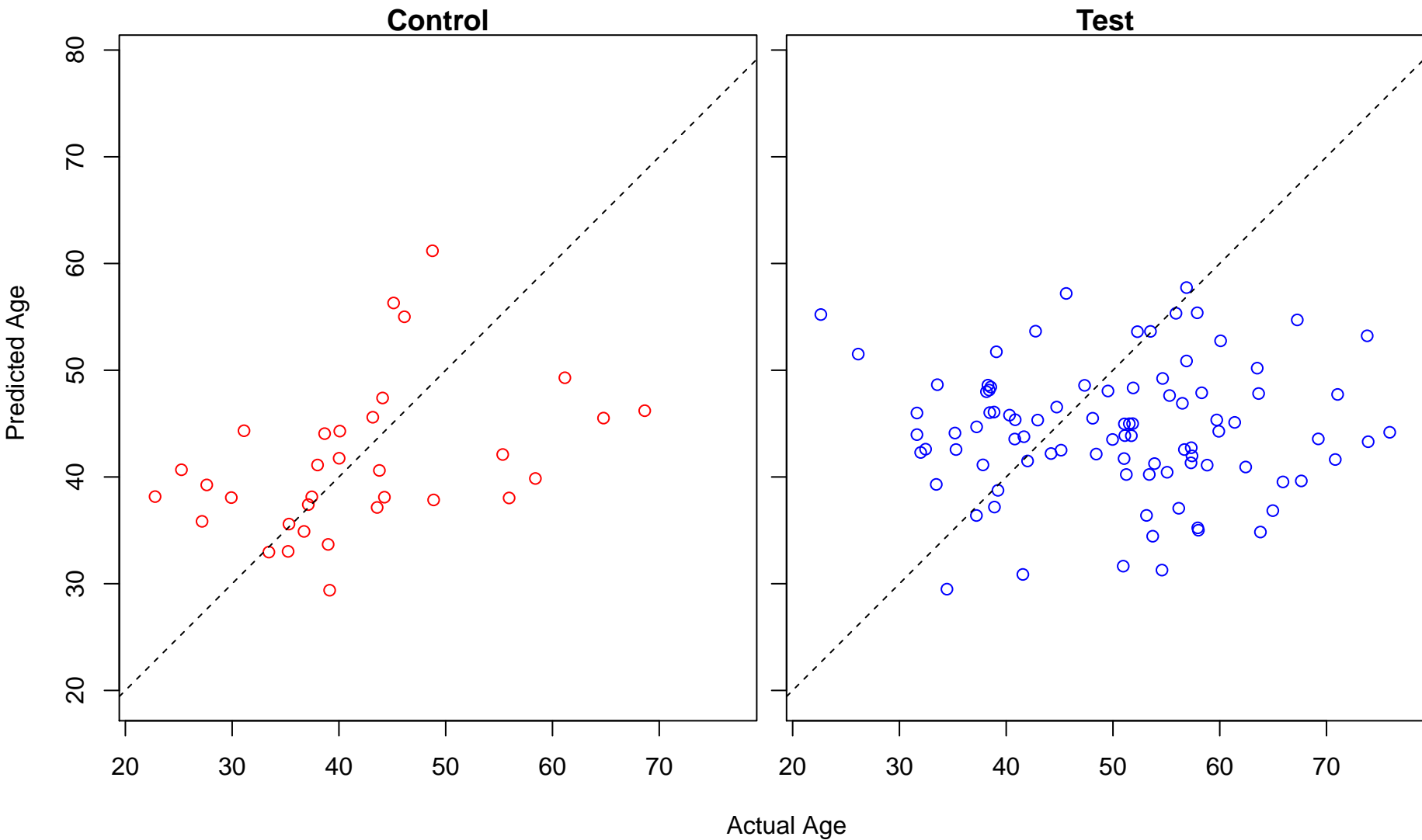
signaling (Score: 0.611372)



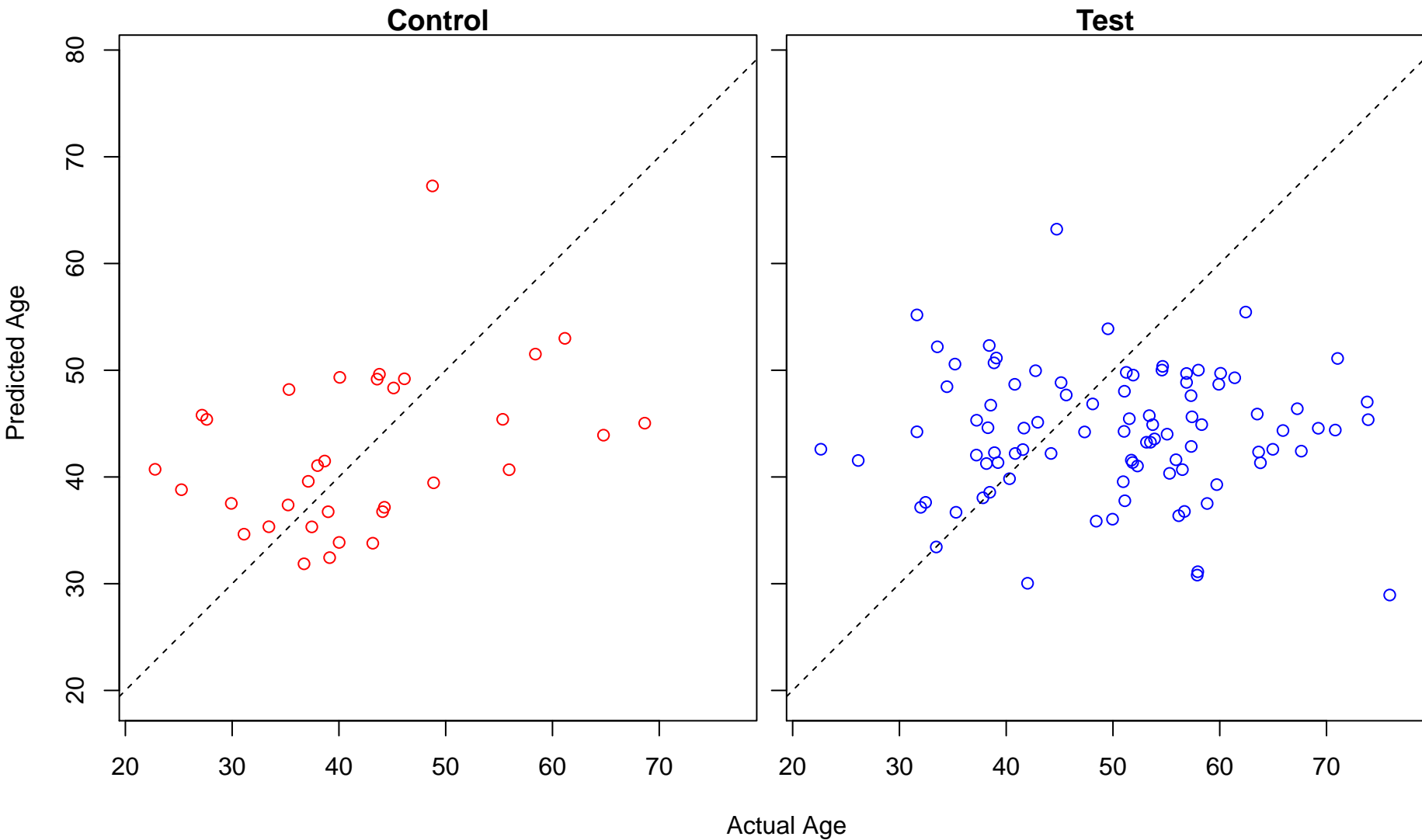
single organism signaling (Score: 0.611372)



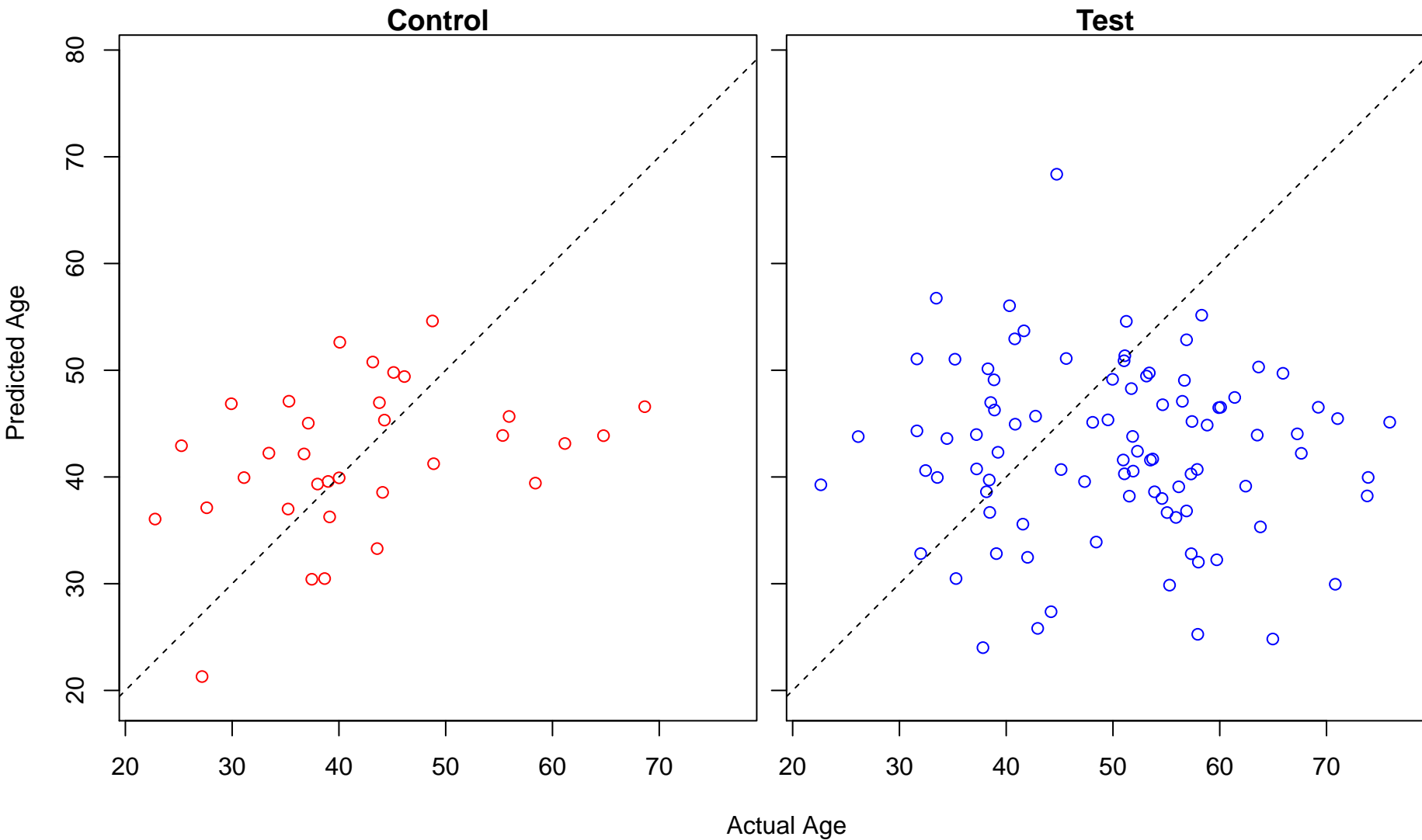
neutrophil activation involved in immune response (Score: 0.611061)



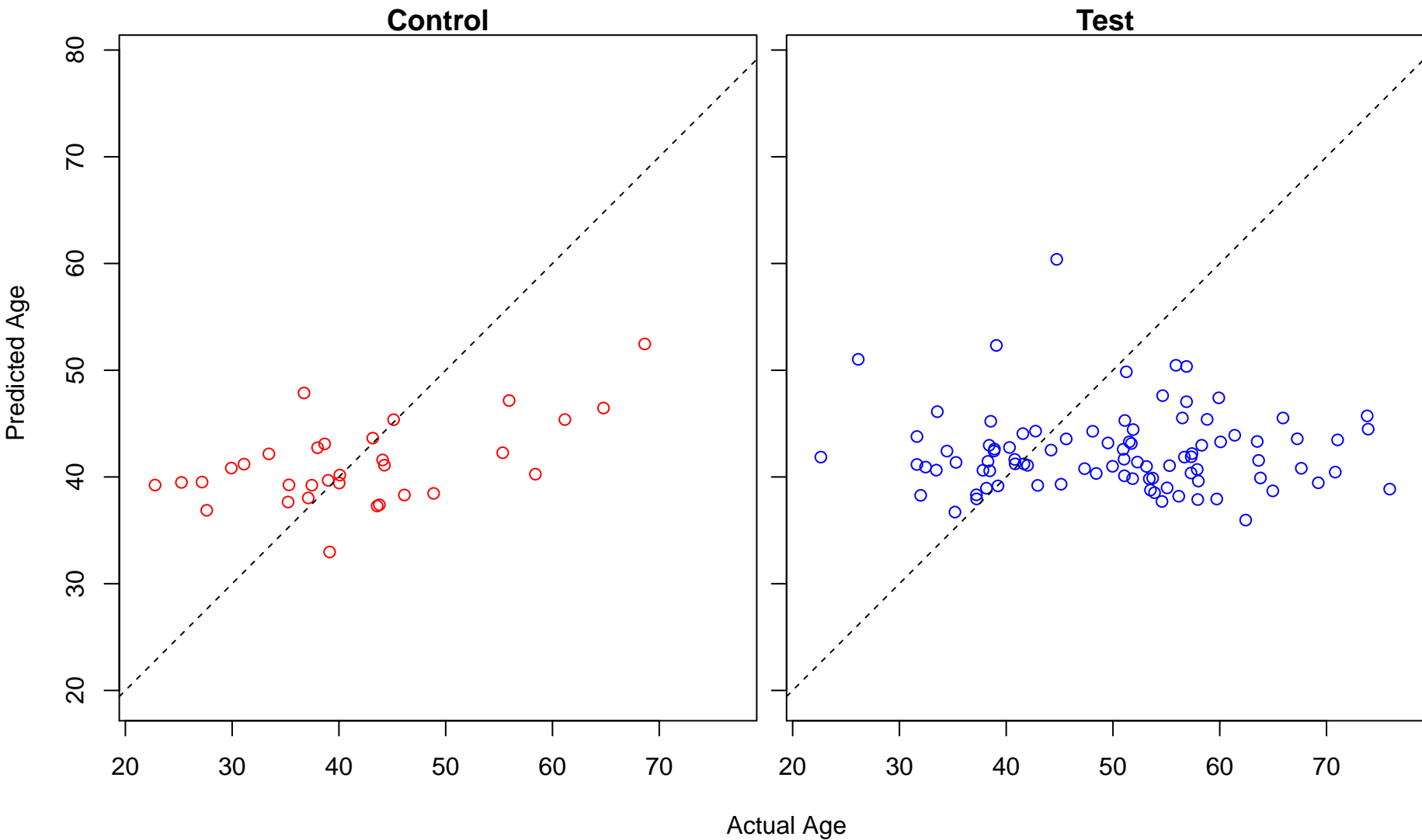
regulation of N-methyl-D-aspartate selective glutamate receptor activity (Score: 0.611059)



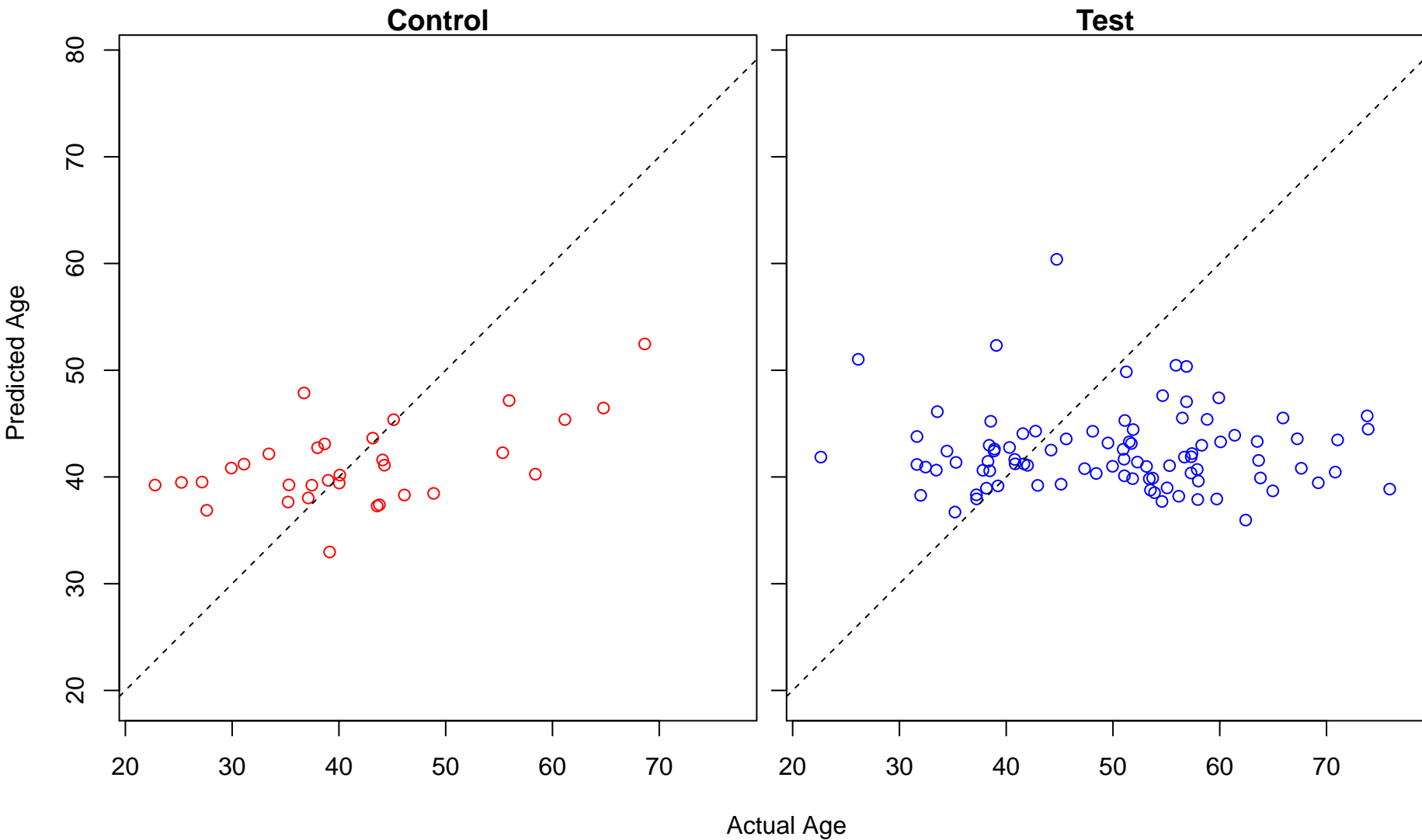
regulation of translational termination (Score: 0.610886)



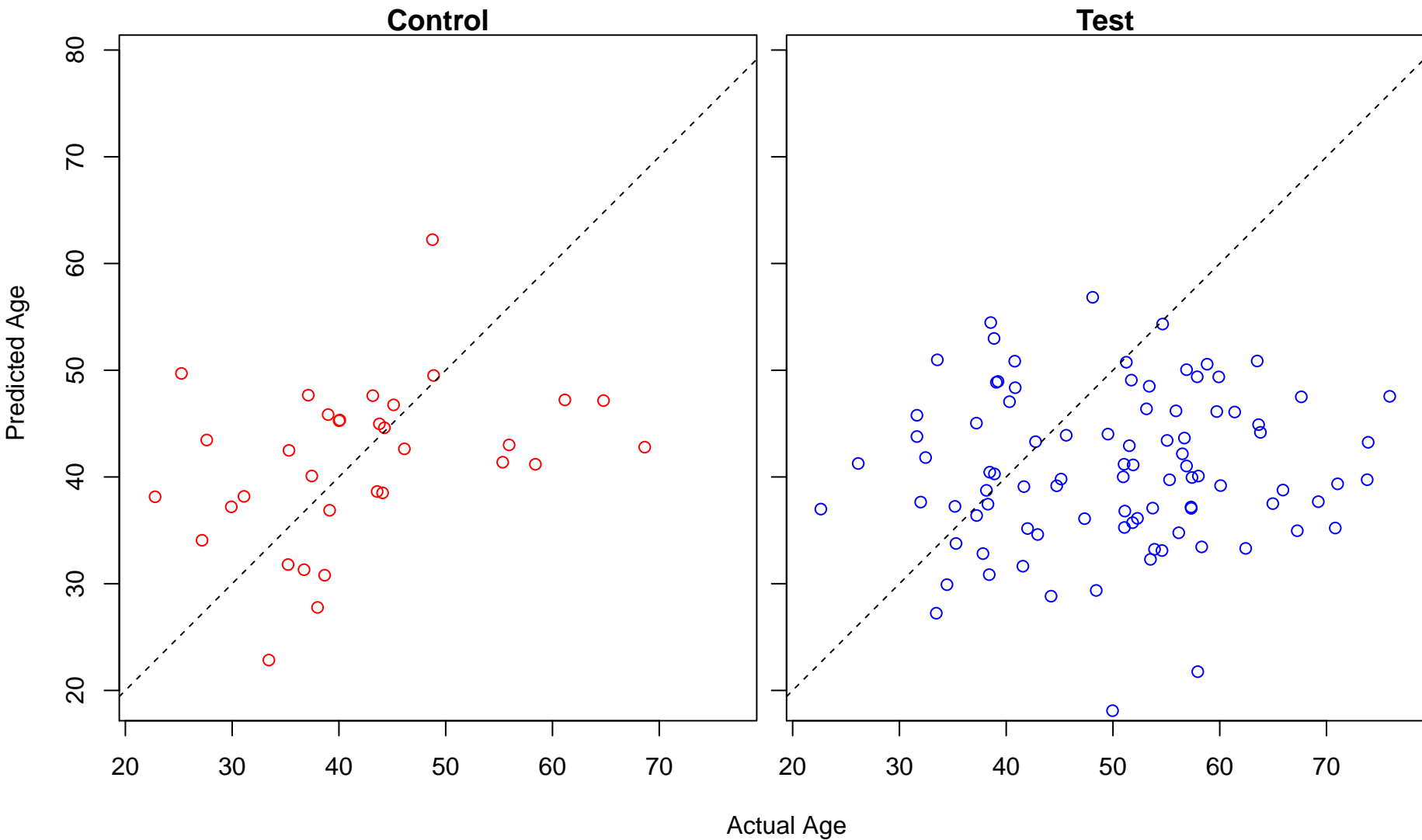
leucine metabolic process (Score: 0.610703)



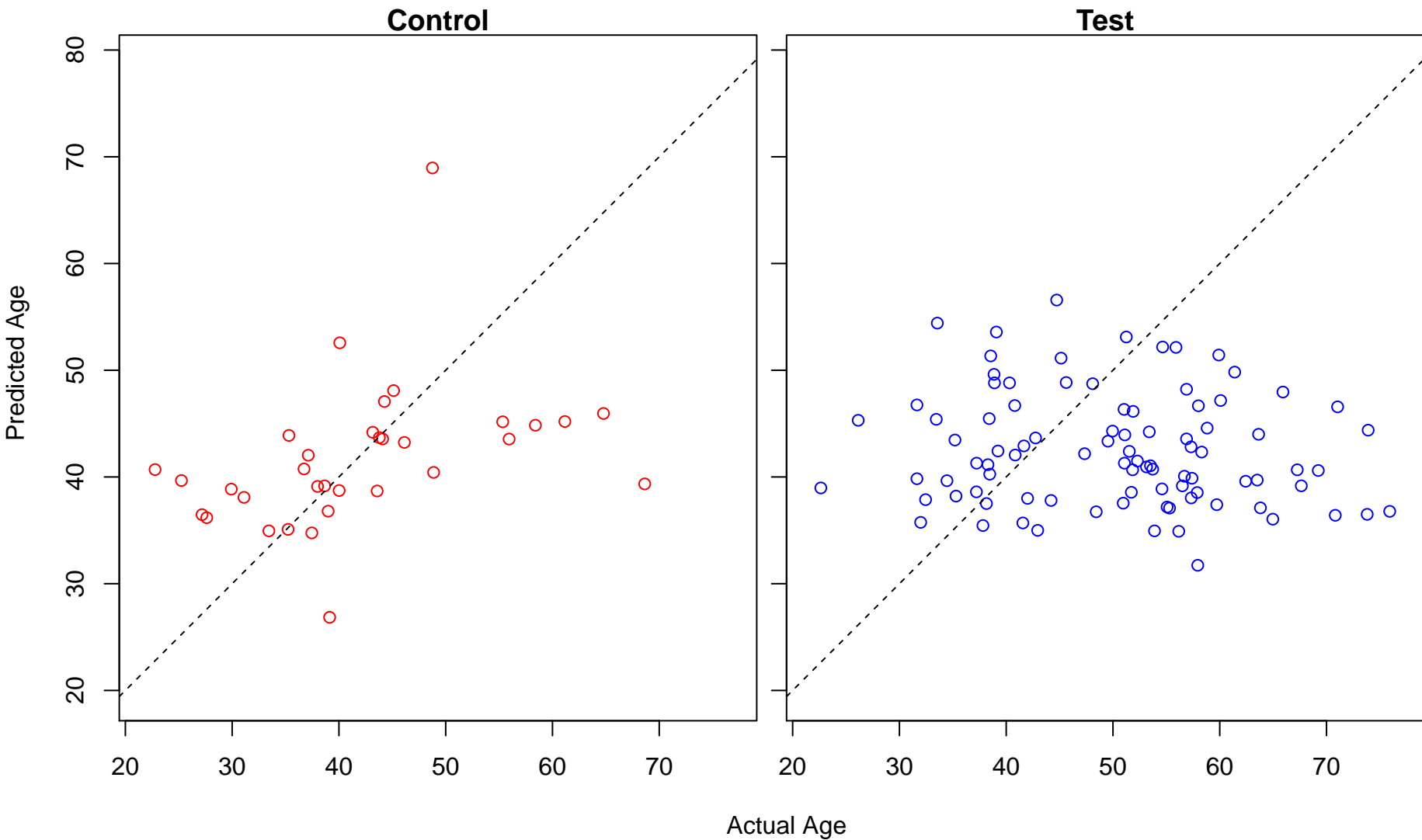
leucine catabolic process (Score: 0.610703)



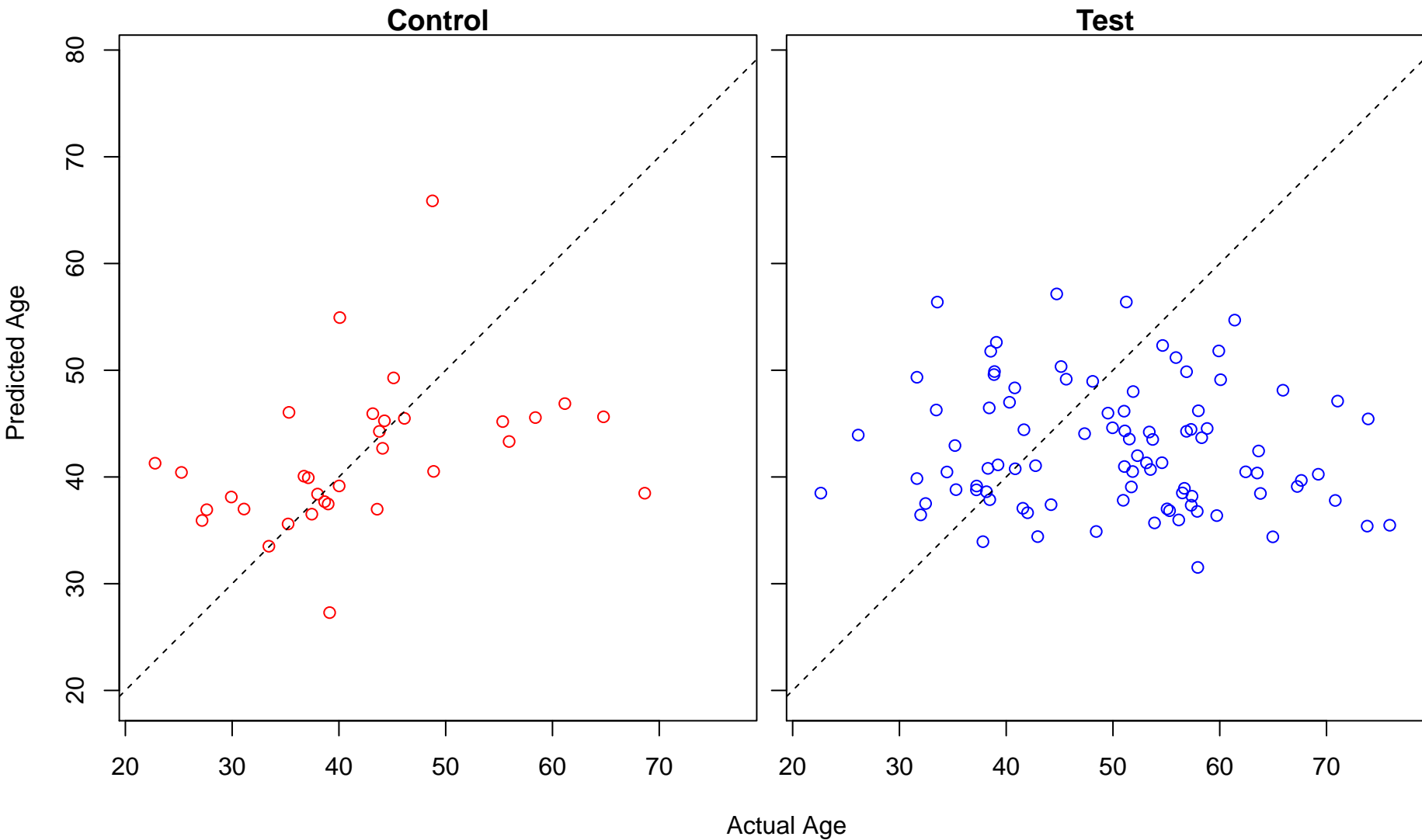
histone H3-K36 demethylation (Score: 0.610406)



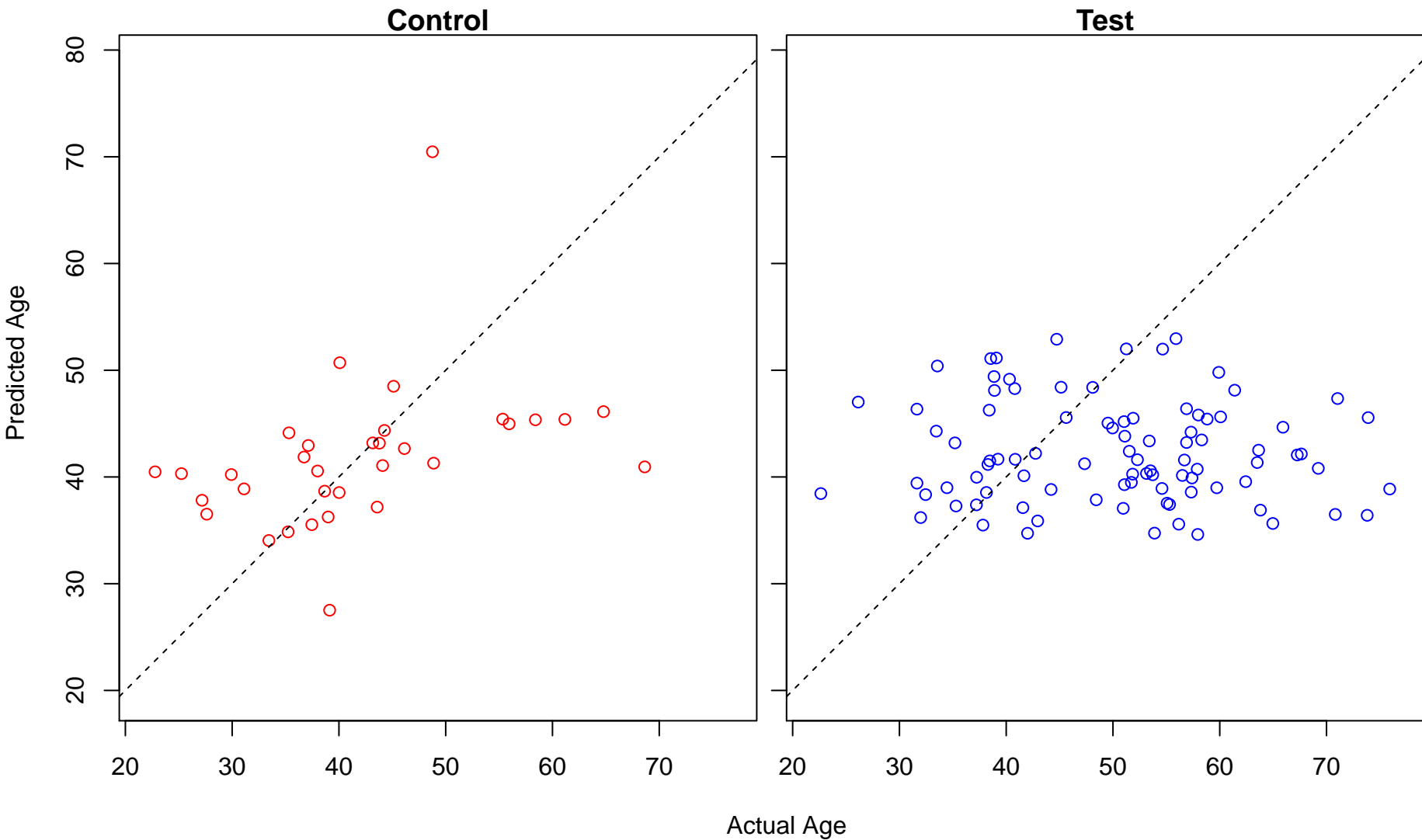
regulation of catalytic activity (Score: 0.610083)



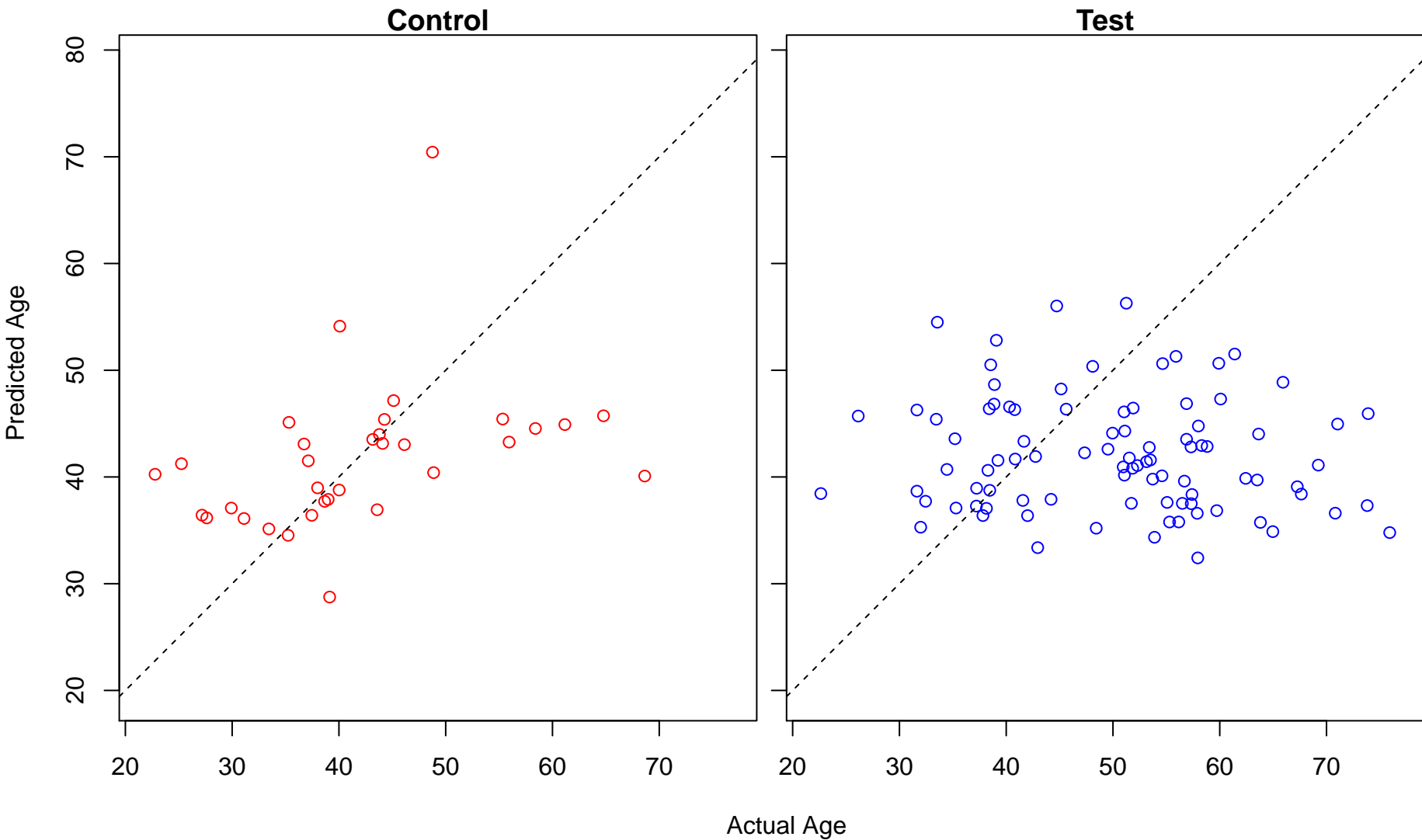
proteolysis (Score: 0.609989)



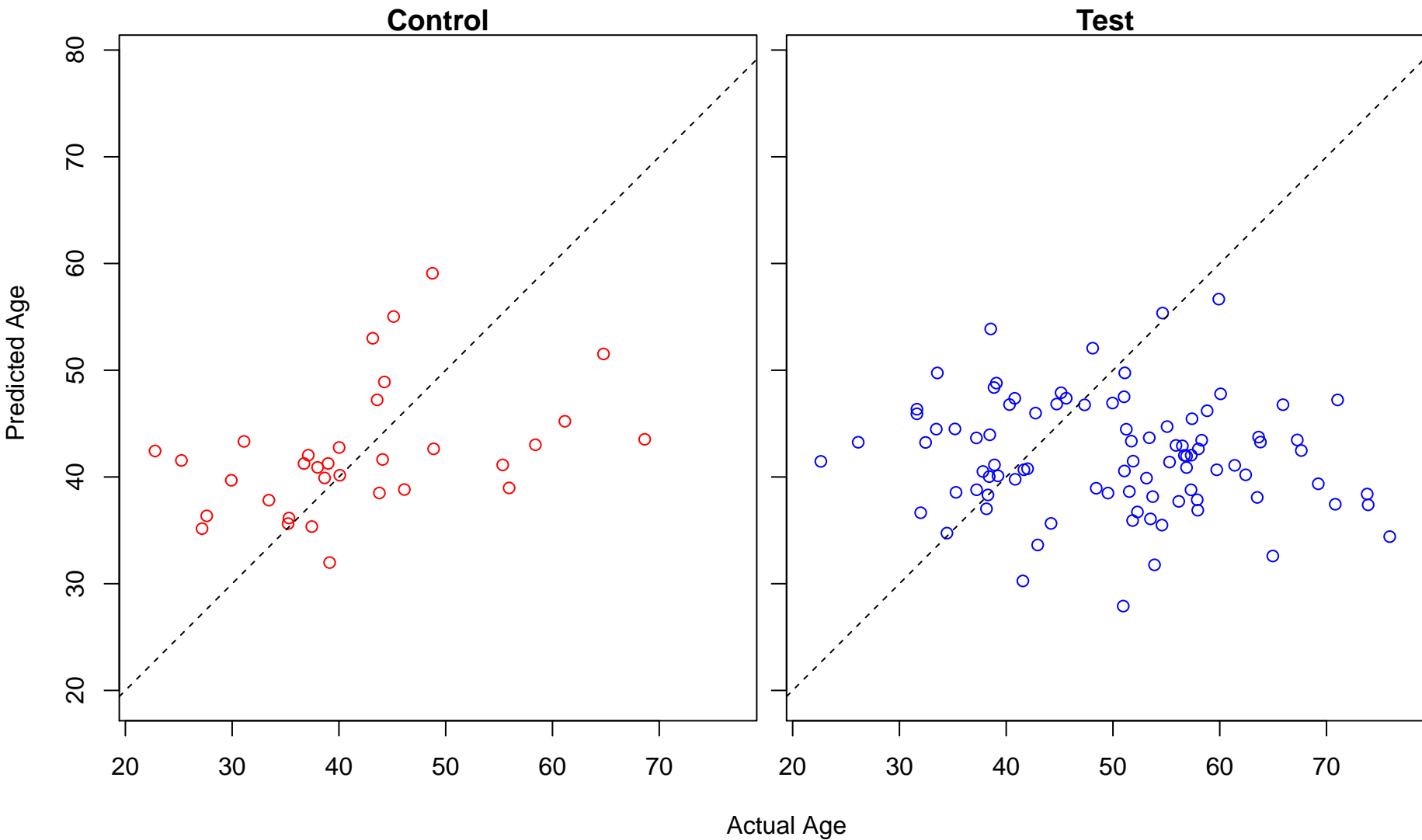
regulation of cell migration (Score: 0.609527)



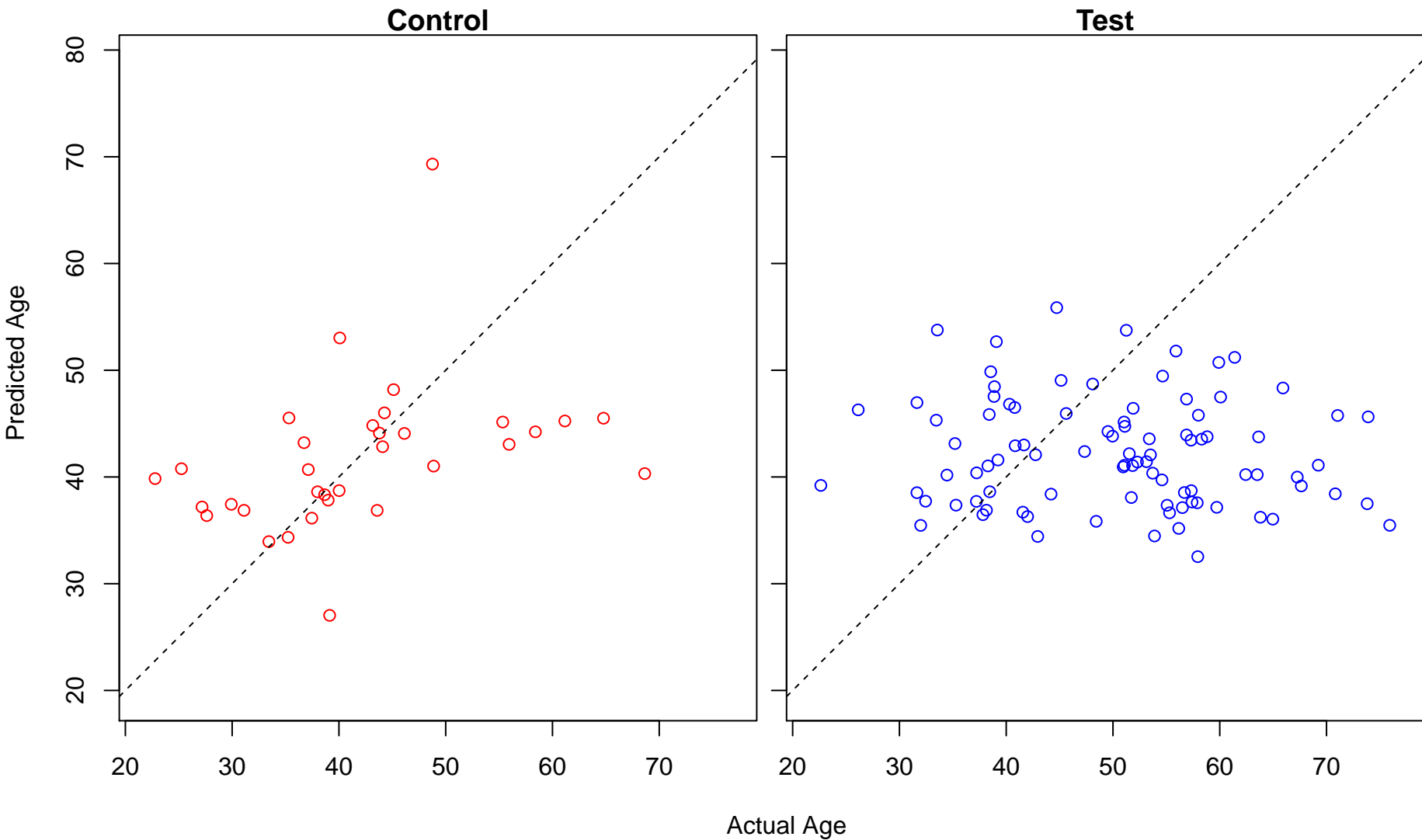
aromatic compound biosynthetic process (Score: 0.608831)



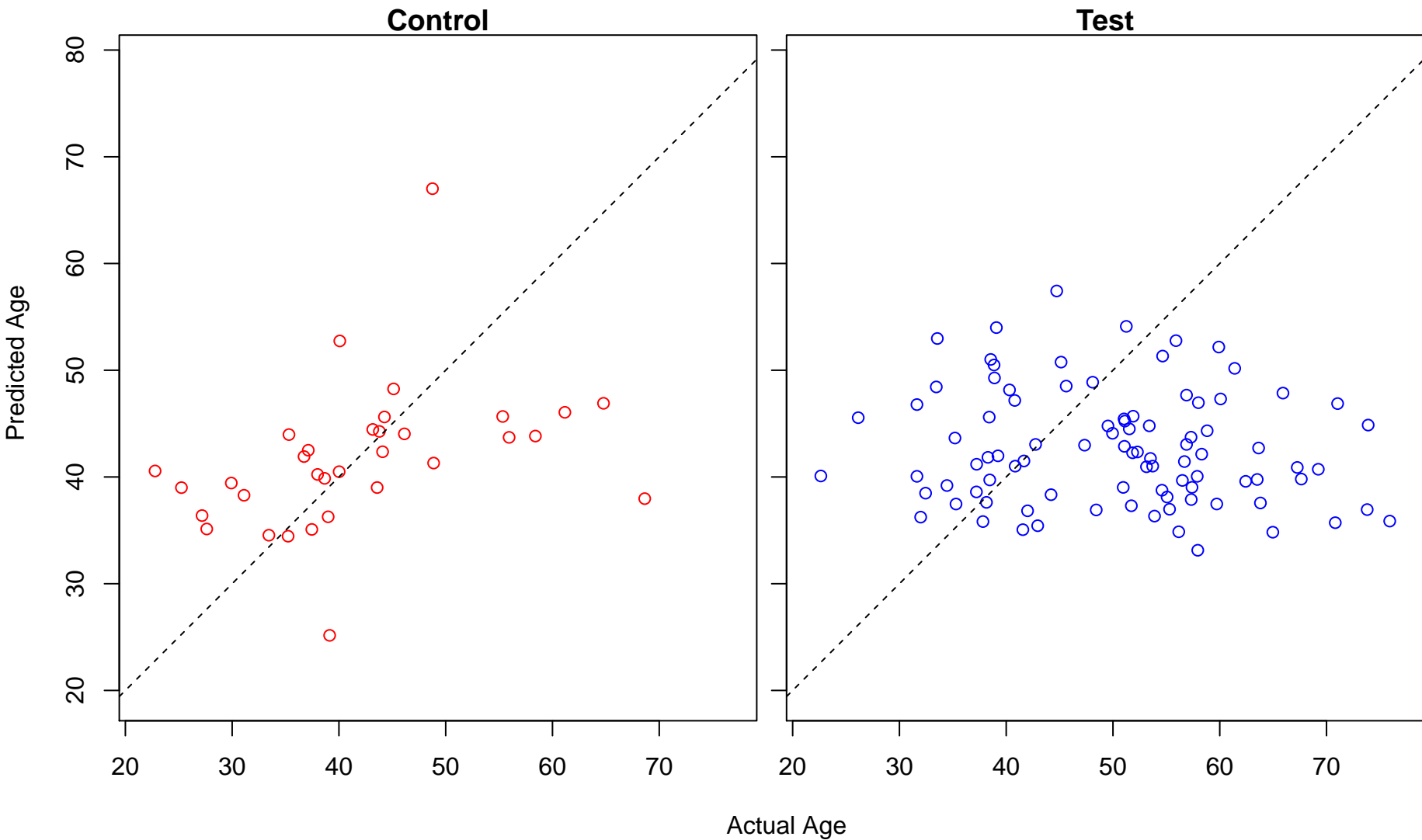
negative regulation of CD4-positive, alpha-beta T cell differentiation (Score: 0.608586)



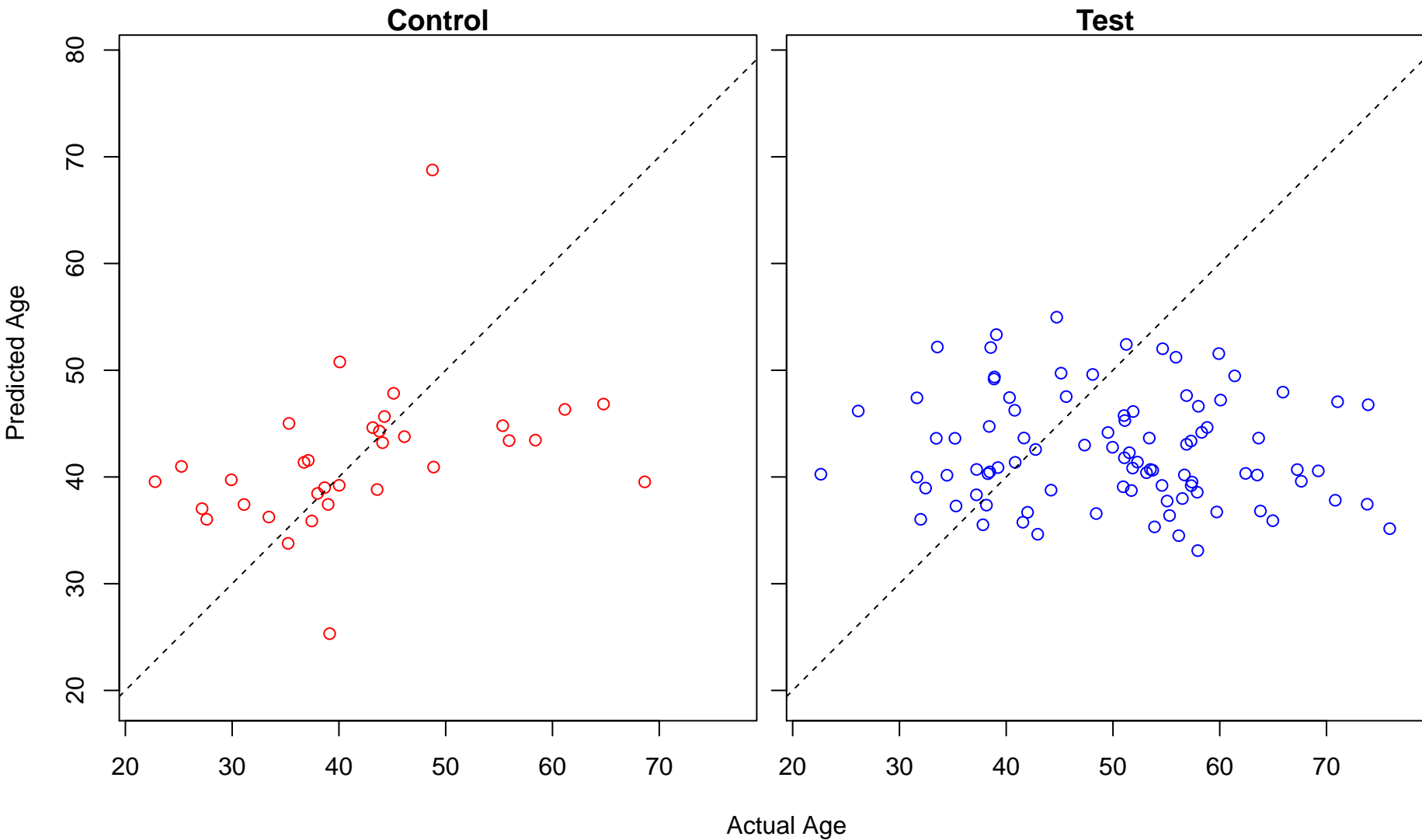
nucleobase-containing compound metabolic process (Score: 0.608112)



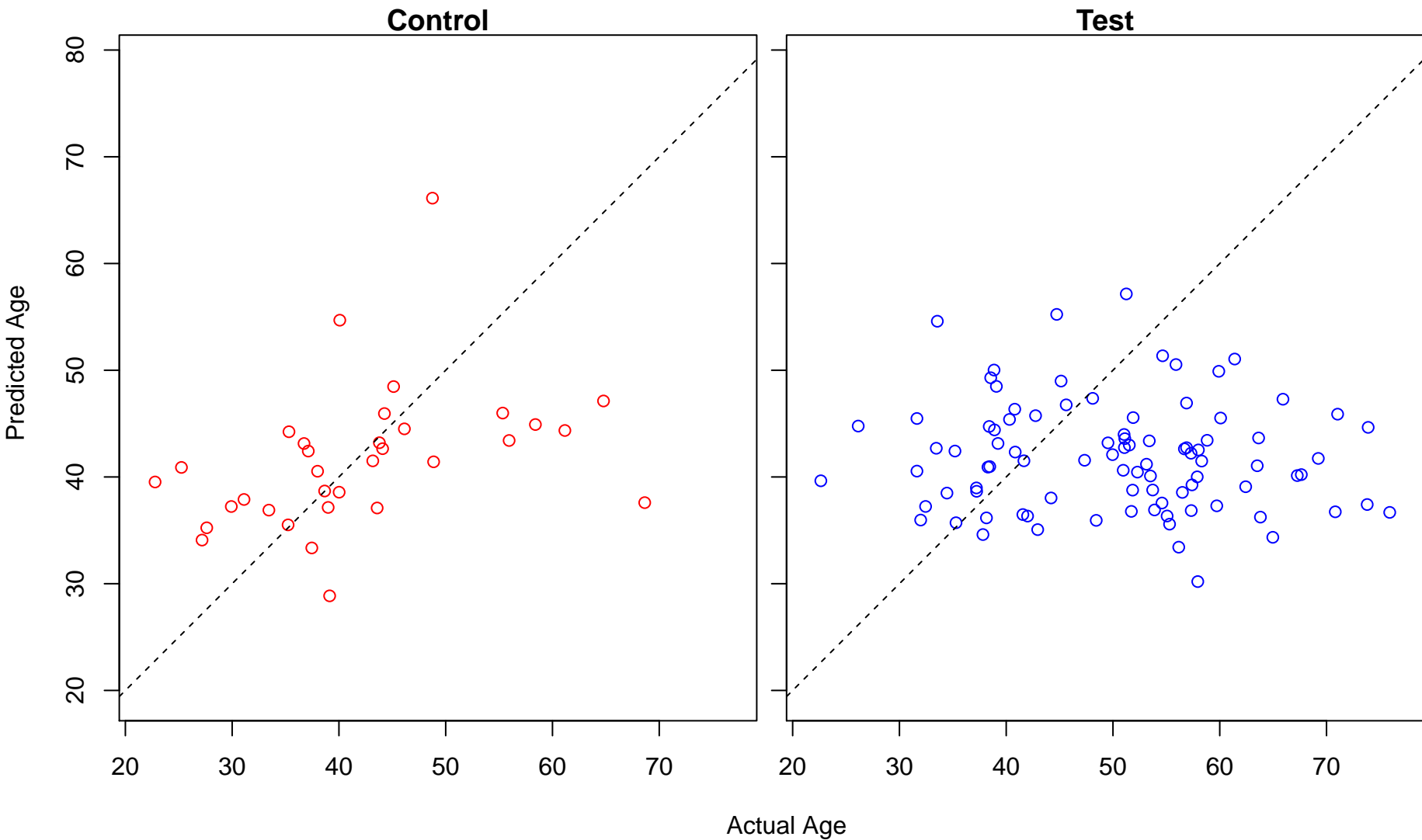
positive regulation of cell communication (Score: 0.607213)



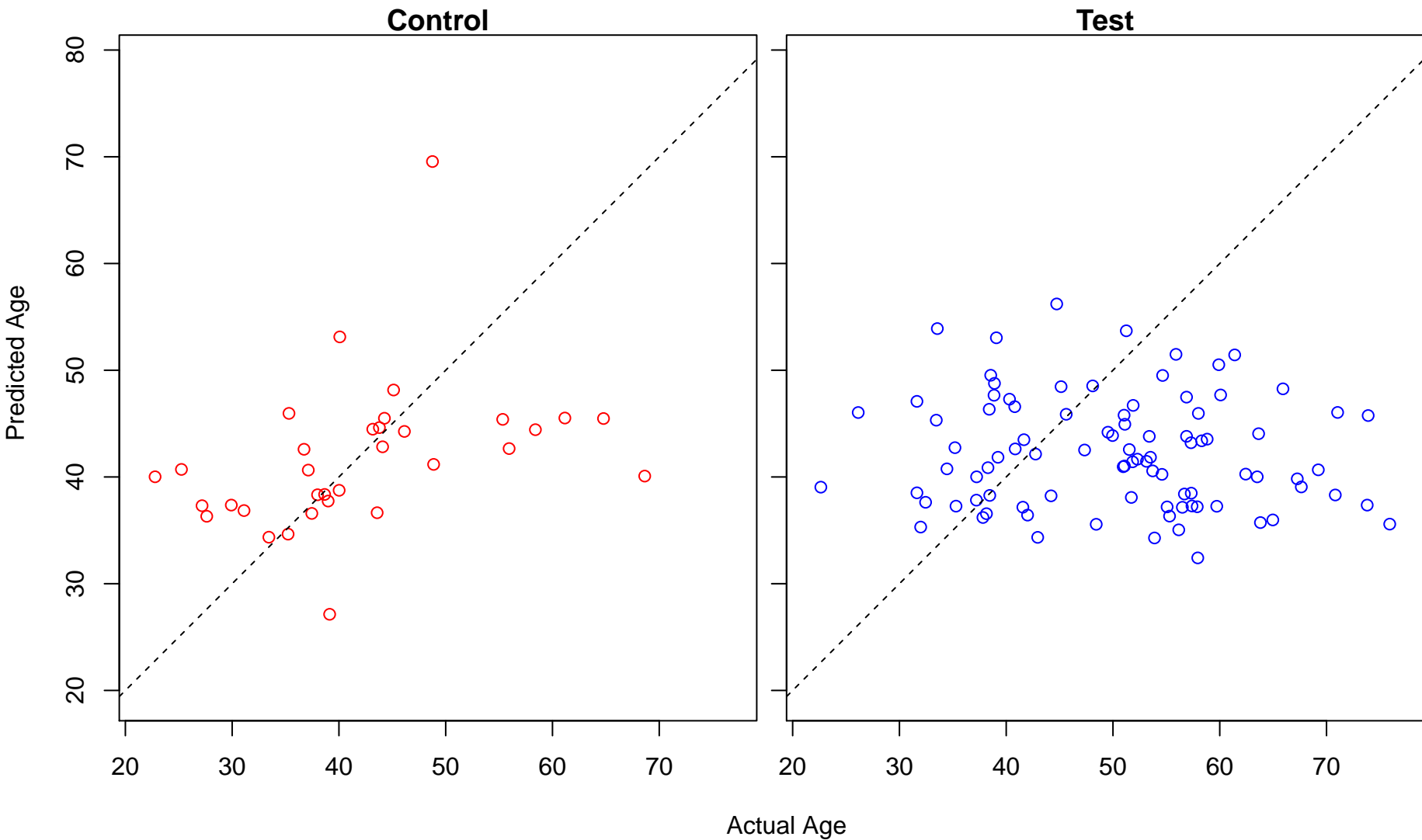
cell communication (Score: 0.606377)



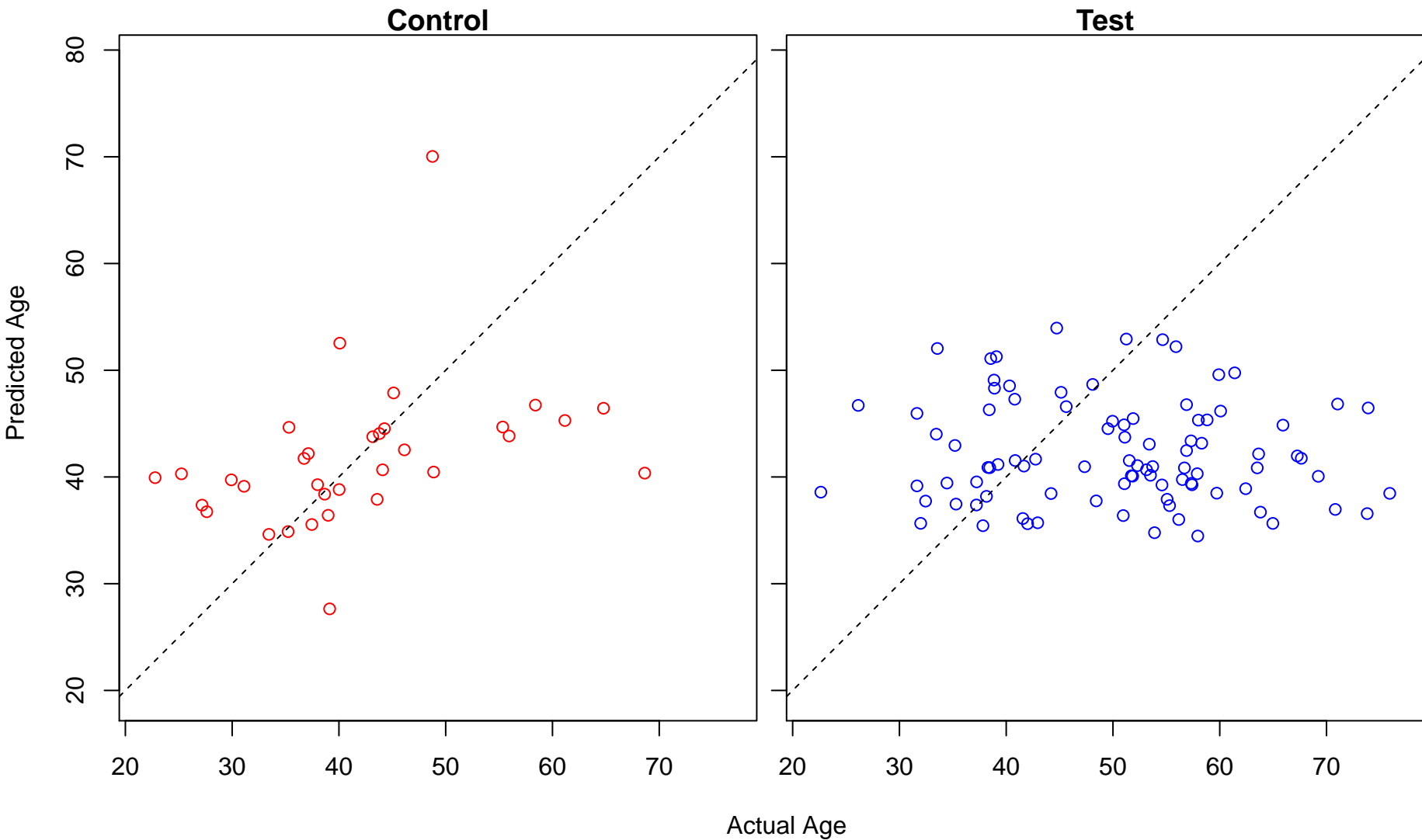
negative regulation of programmed cell death (Score: 0.605460)



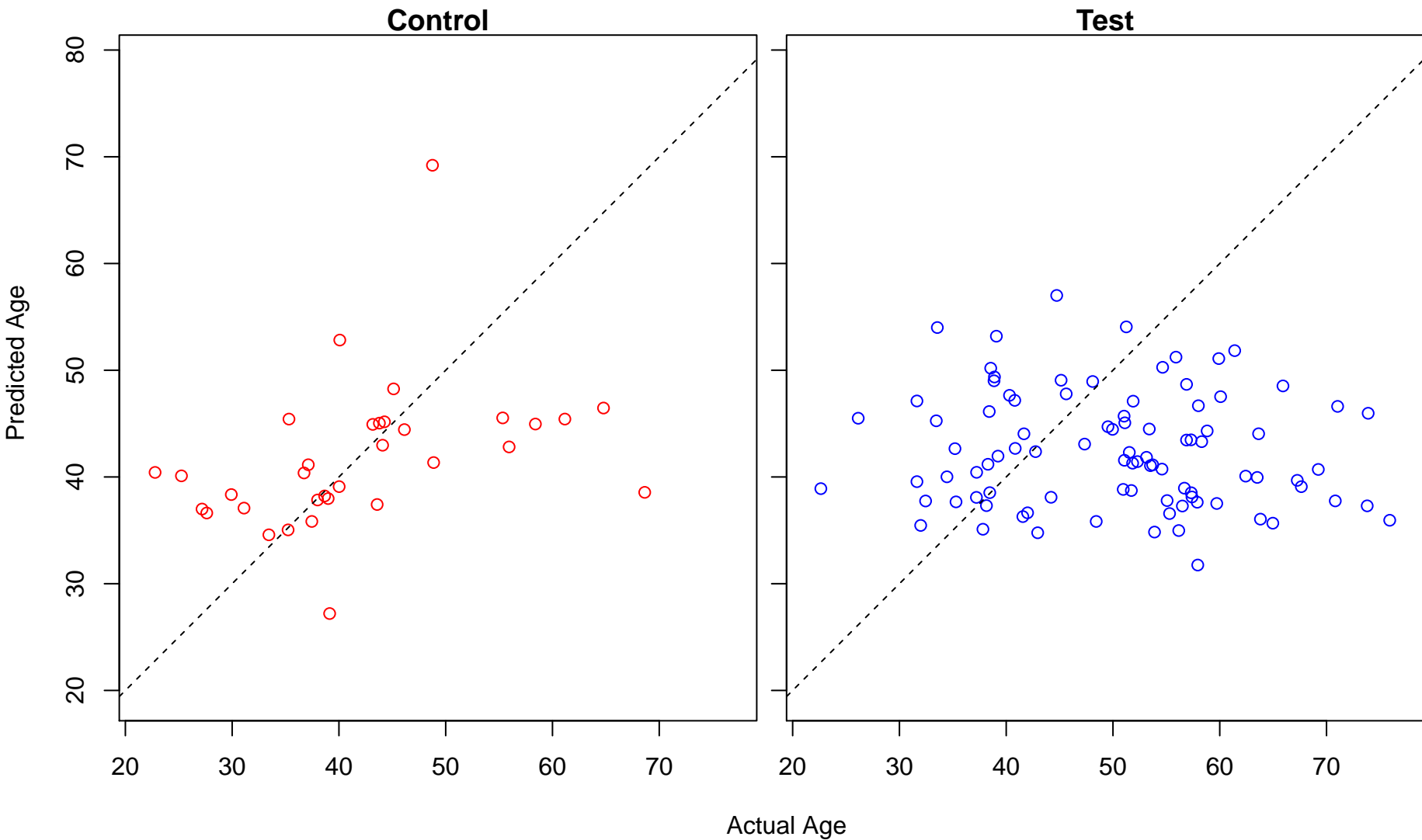
nucleic acid metabolic process (Score: 0.605141)



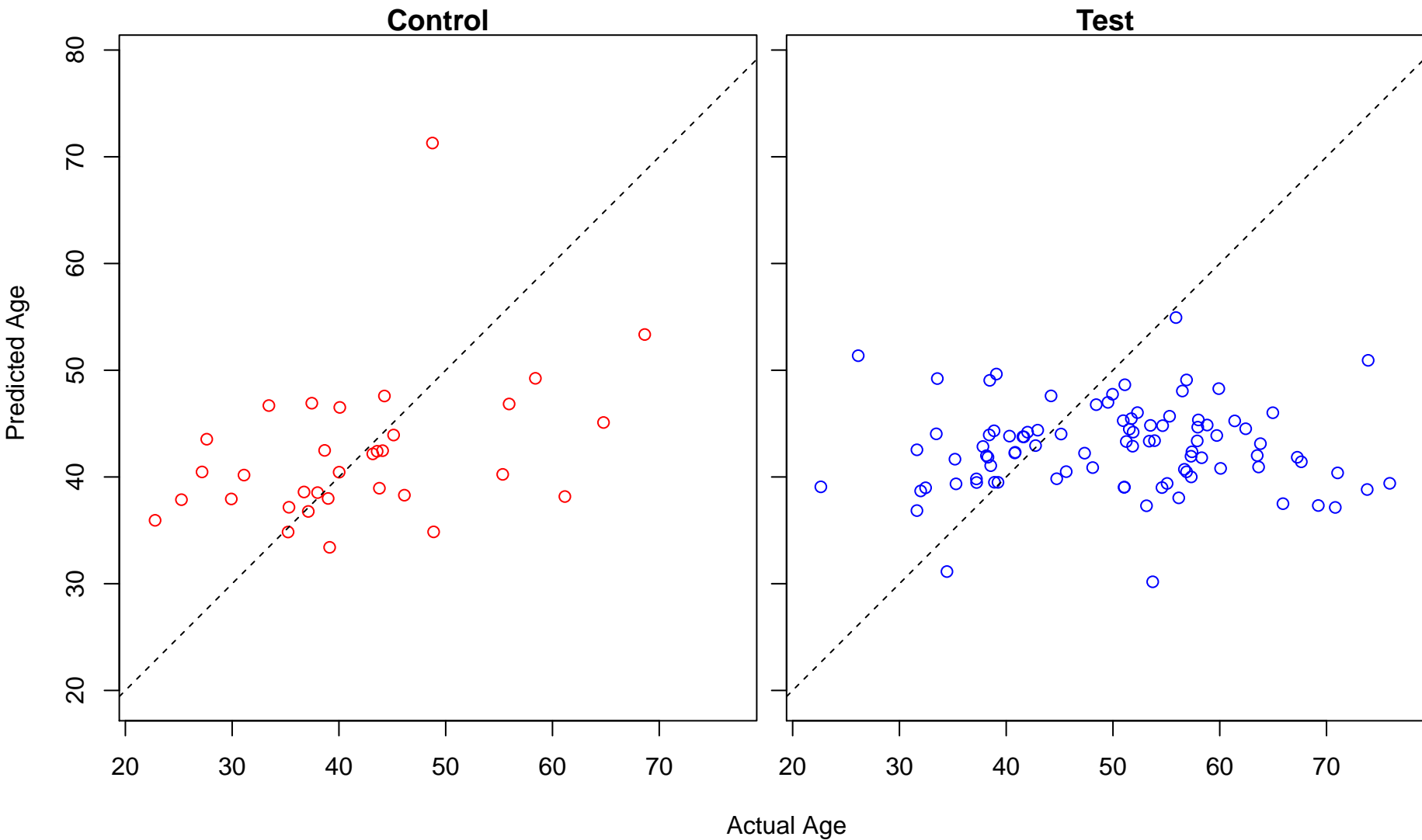
regulation of locomotion (Score: 0.605047)



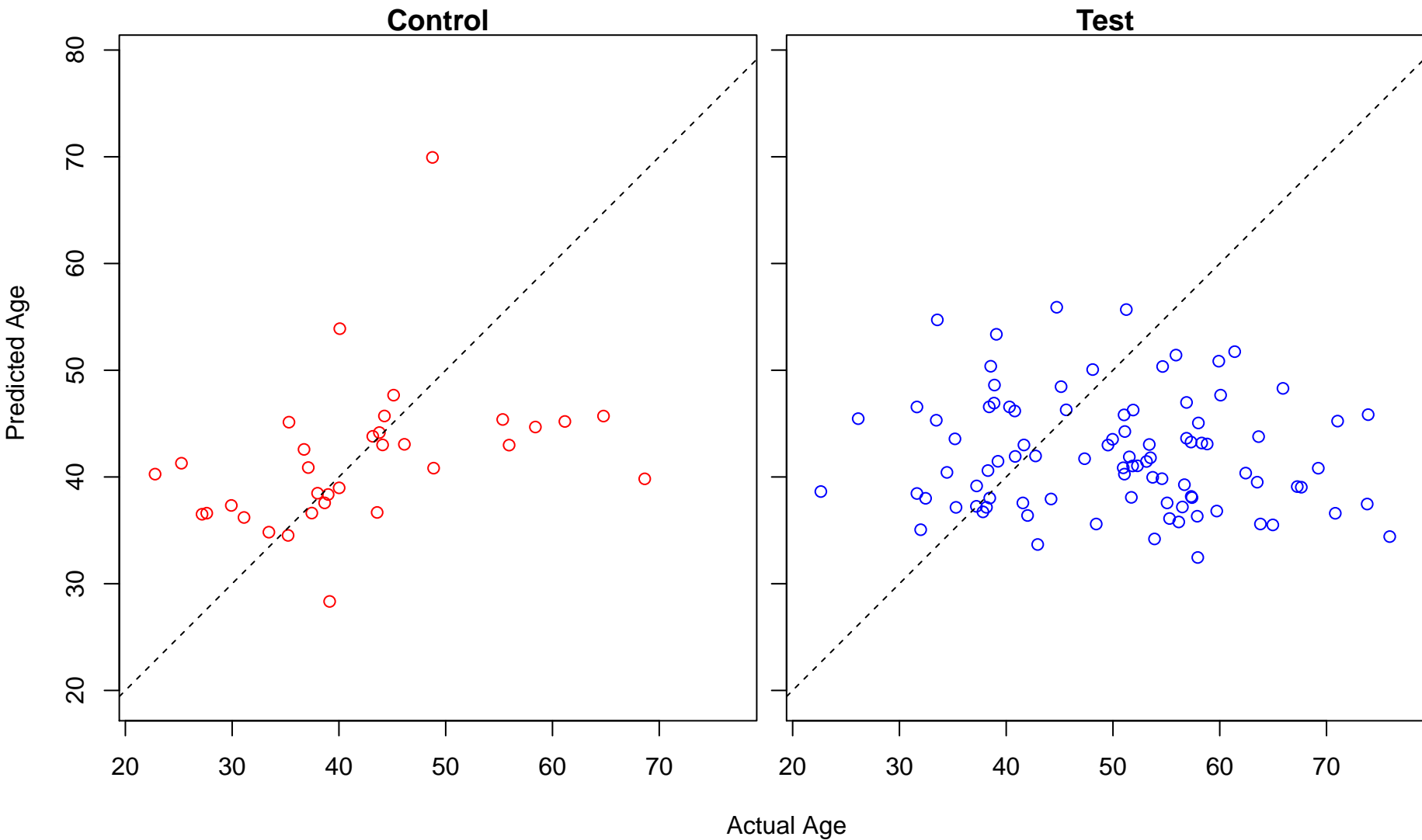
cellular macromolecule metabolic process (Score: 0.604974)



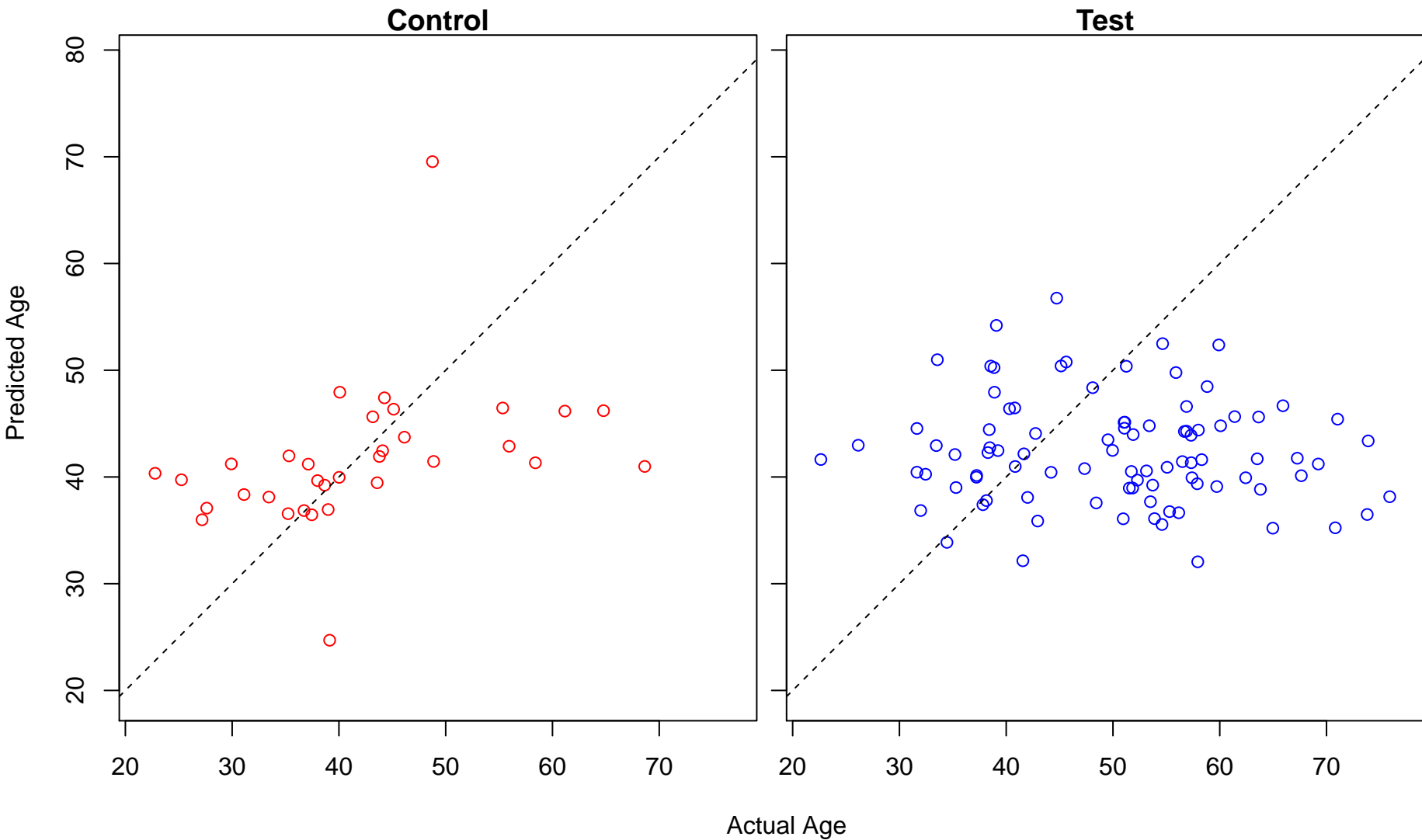
immature B cell differentiation (Score: 0.604940)



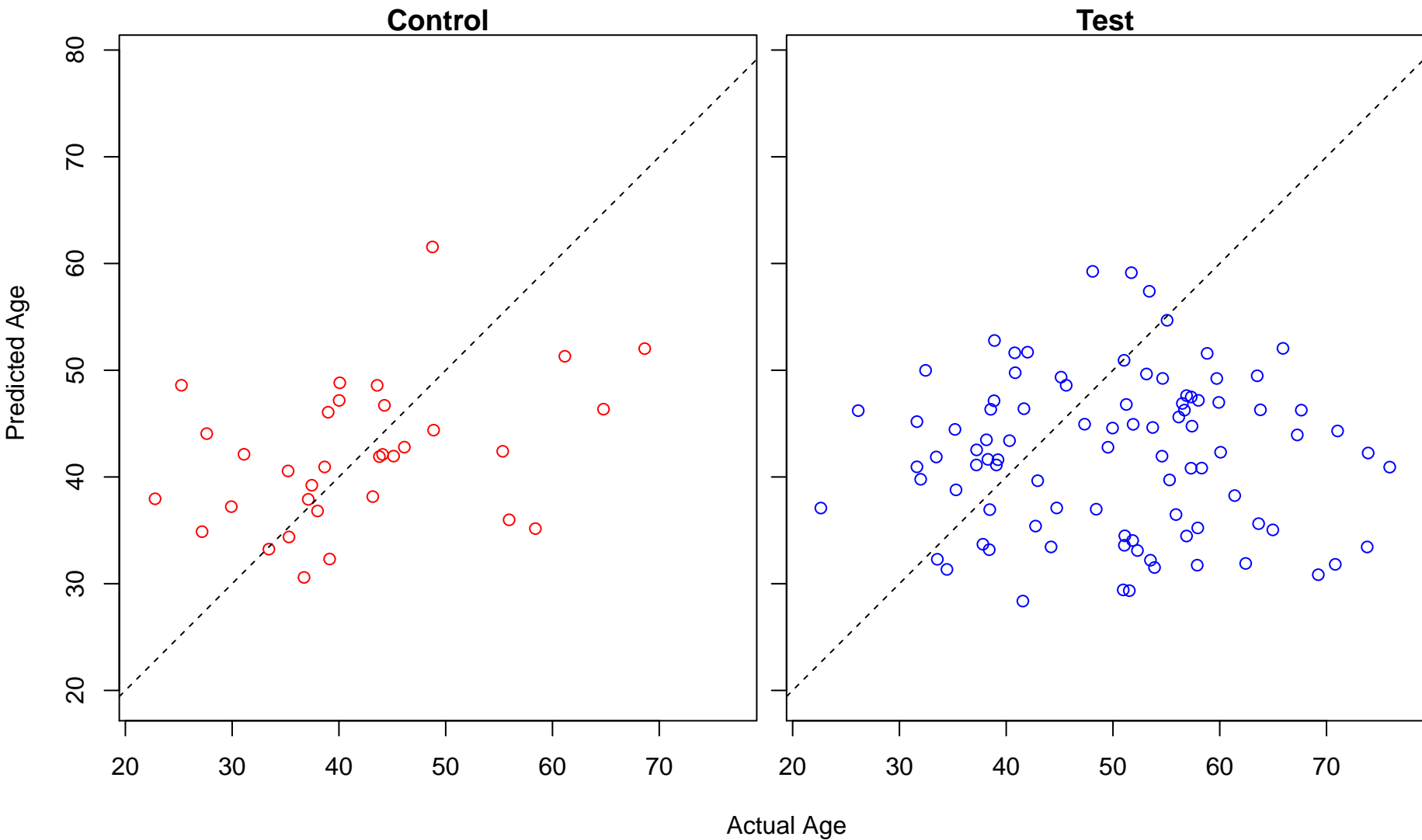
nucleobase-containing compound biosynthetic process (Score: 0.604701)



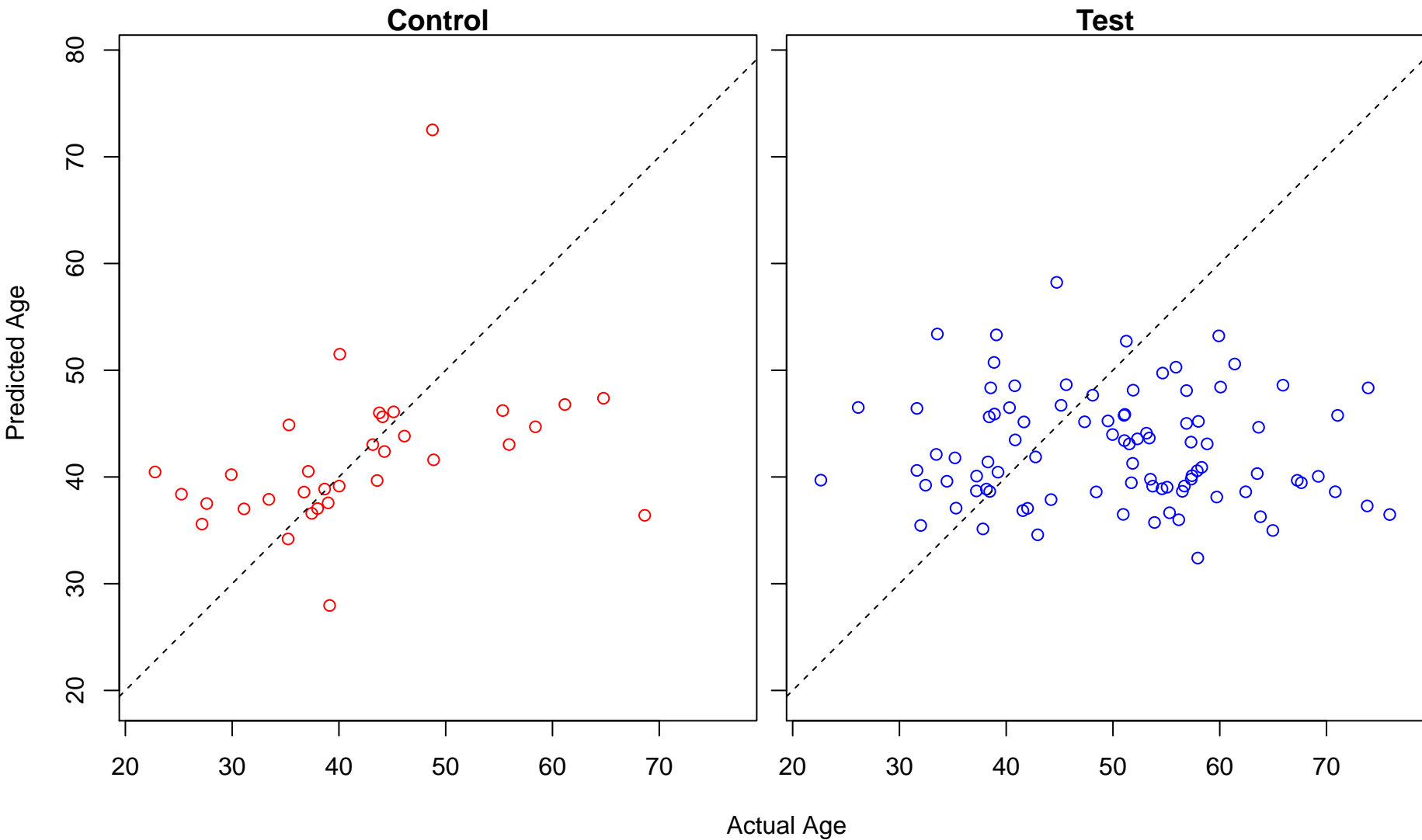
cellular response to peptide hormone stimulus (Score: 0.604479)



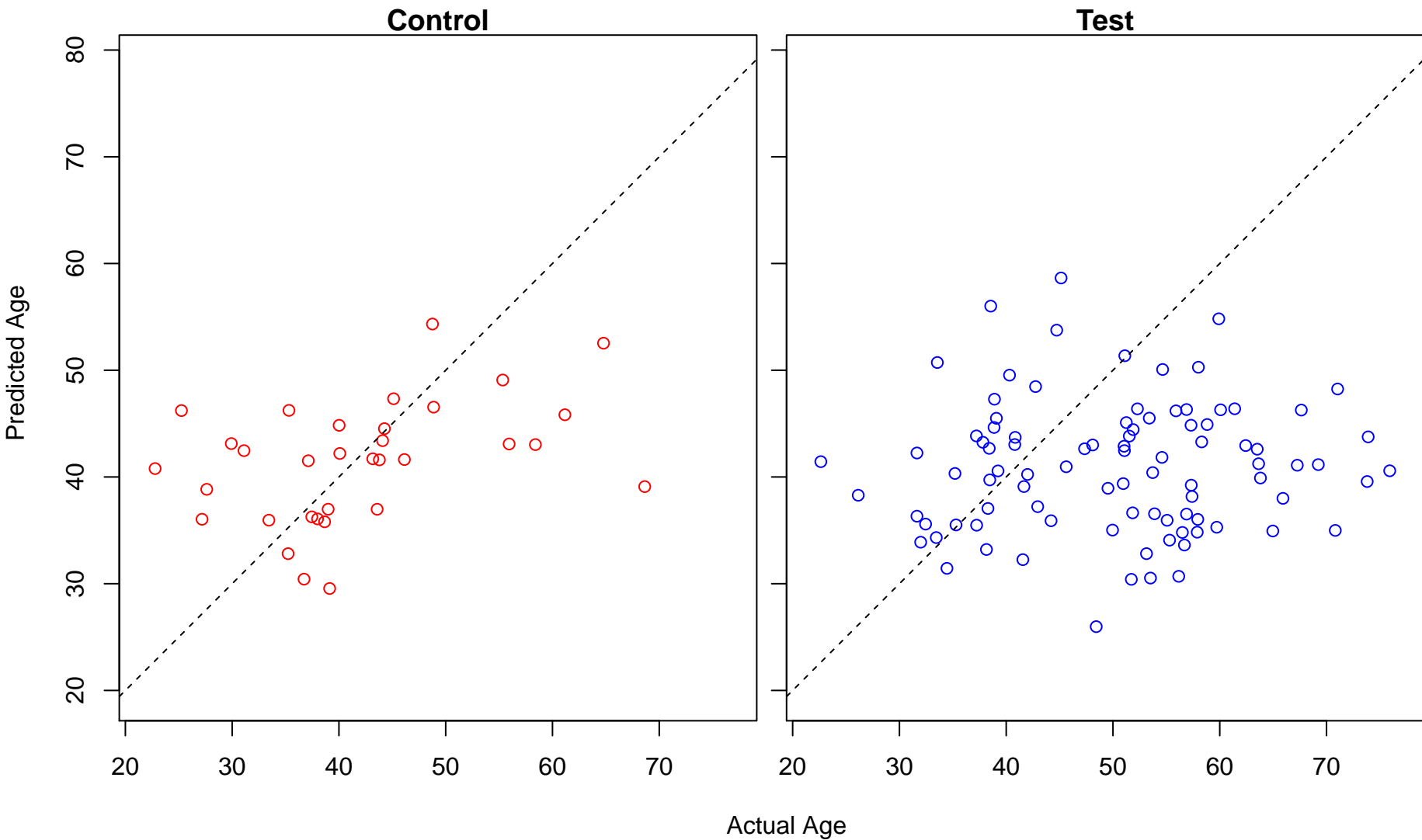
oocyte development (Score: 0.602389)



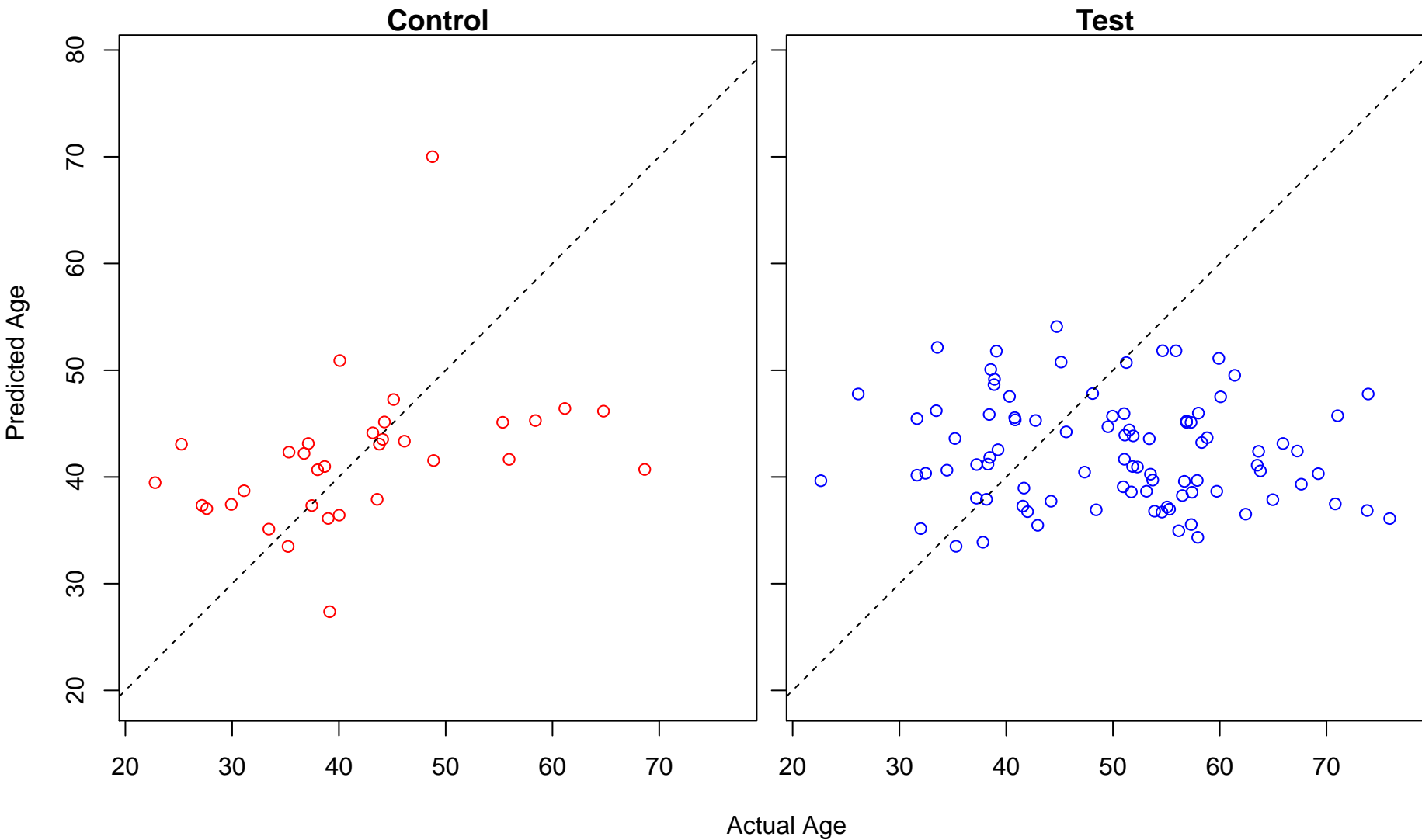
glycoprotein metabolic process (Score: 0.602307)



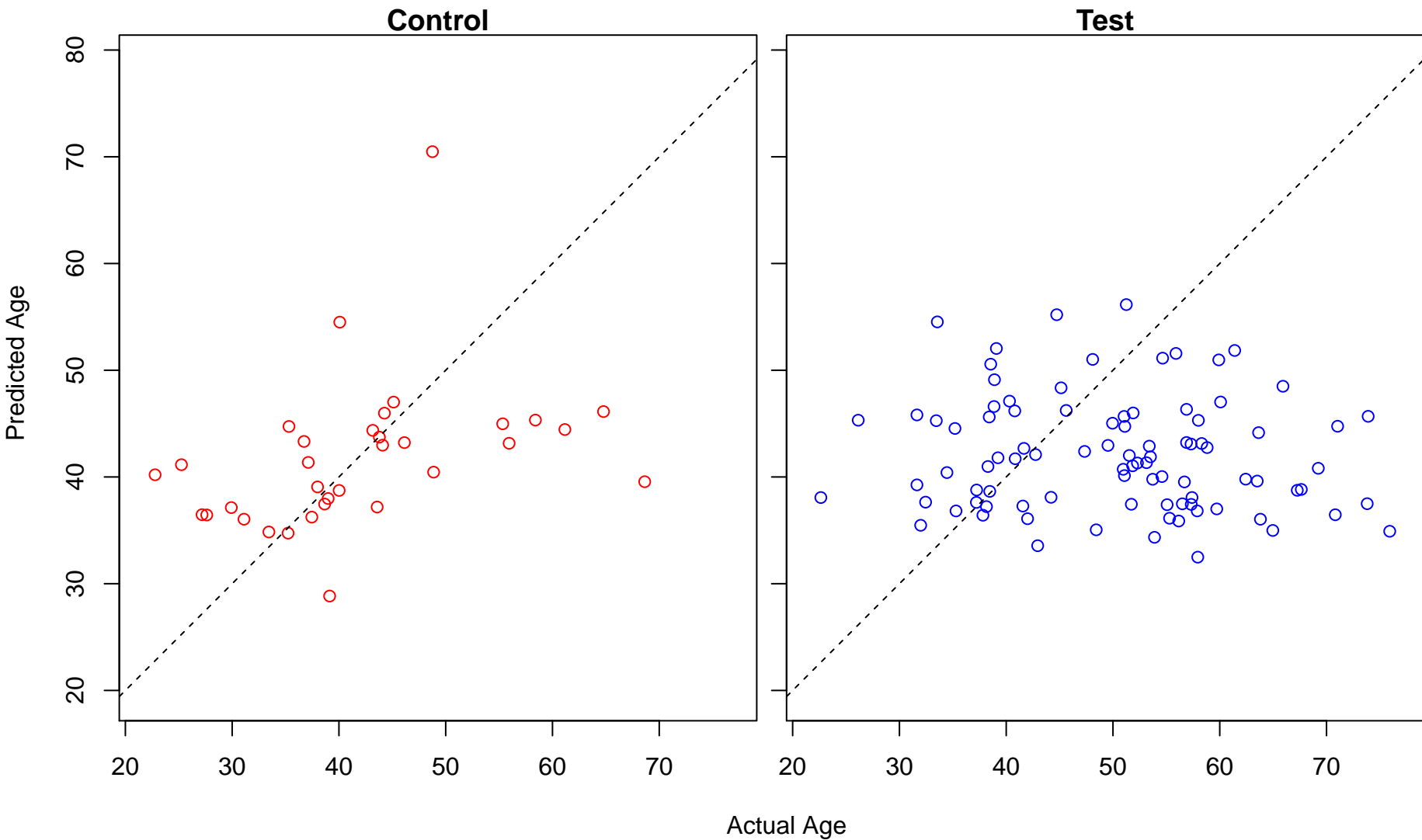
DNA strand renaturation (Score: 0.602170)



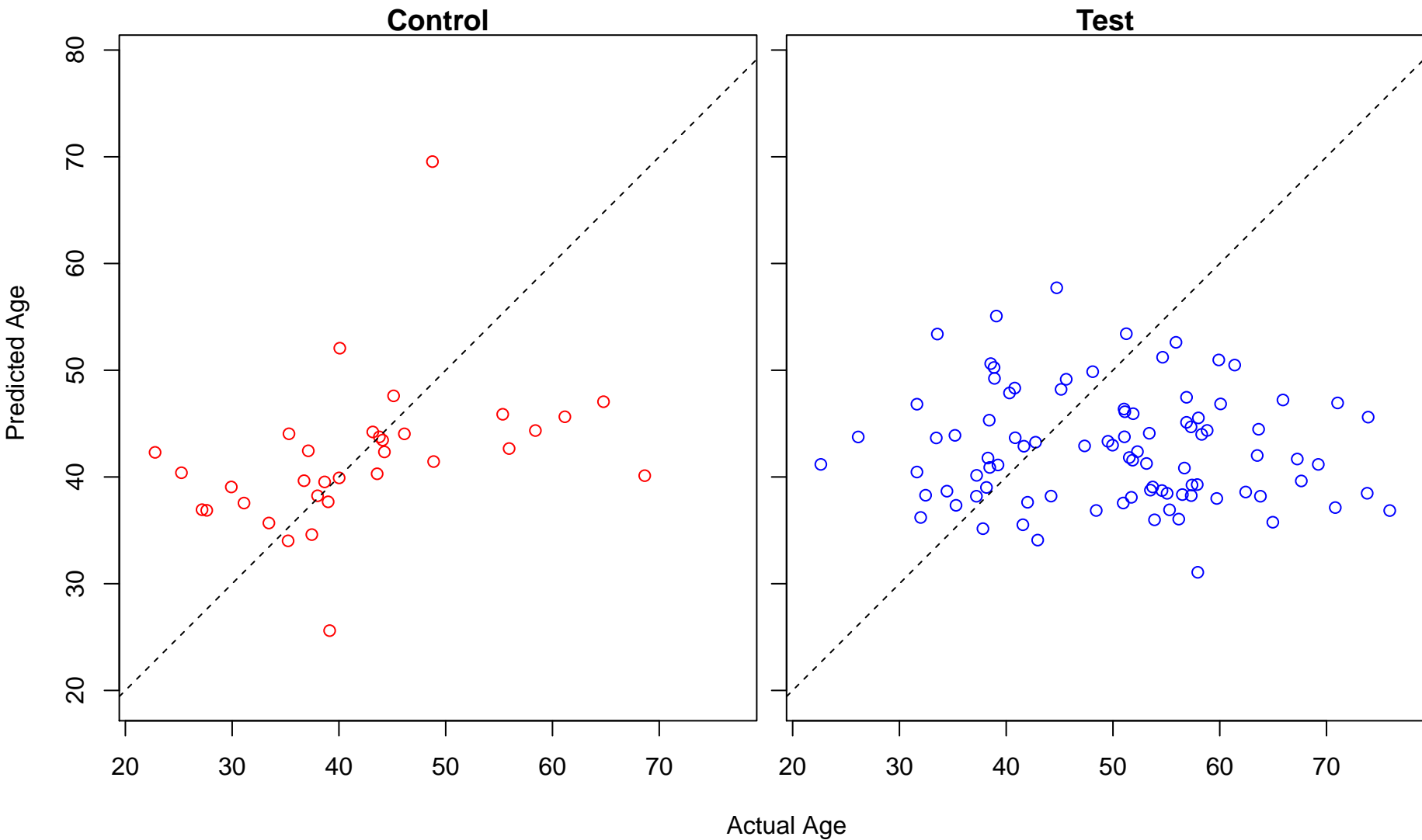
regulation of cell development (Score: 0.601774)



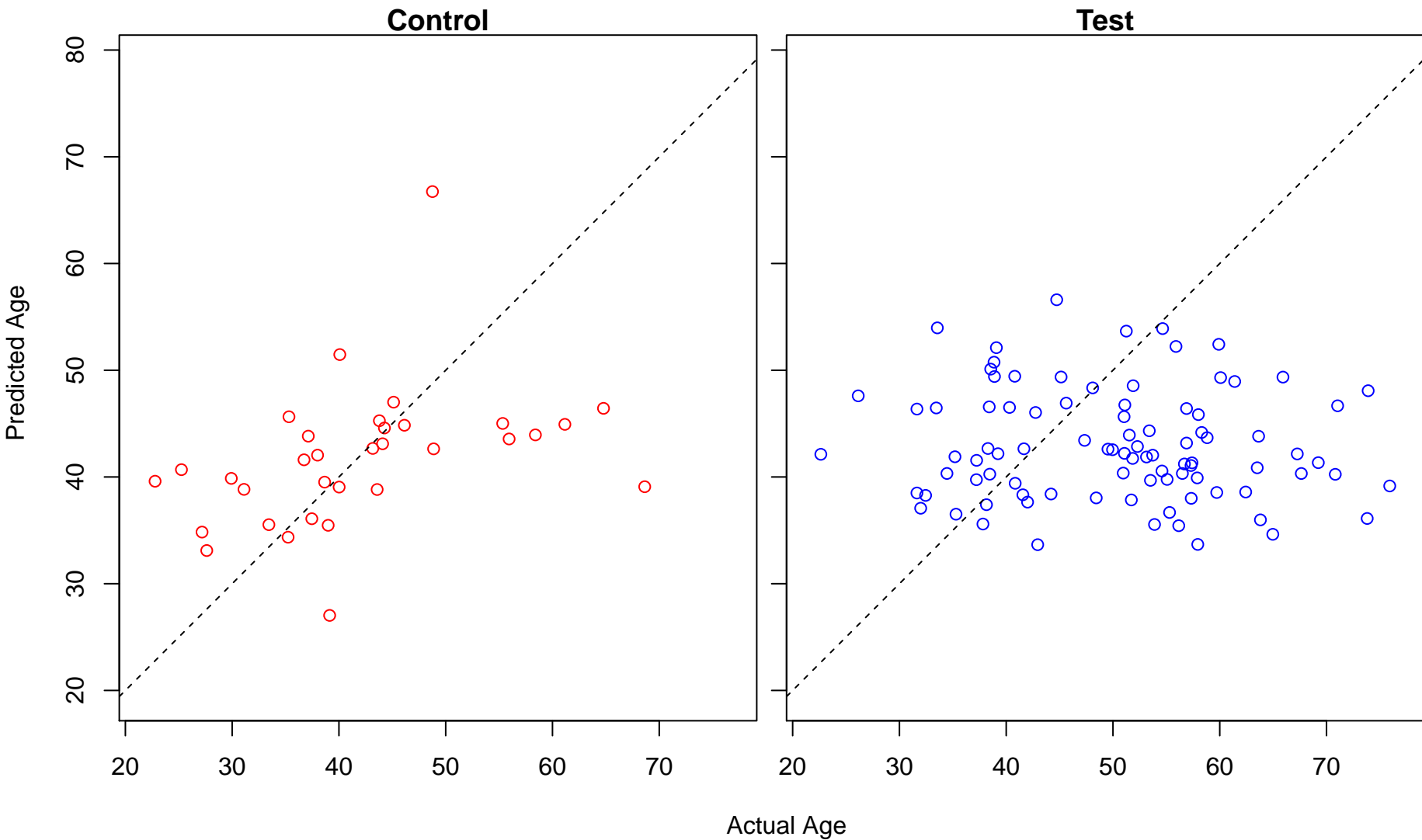
organic cyclic compound biosynthetic process (Score: 0.601134)



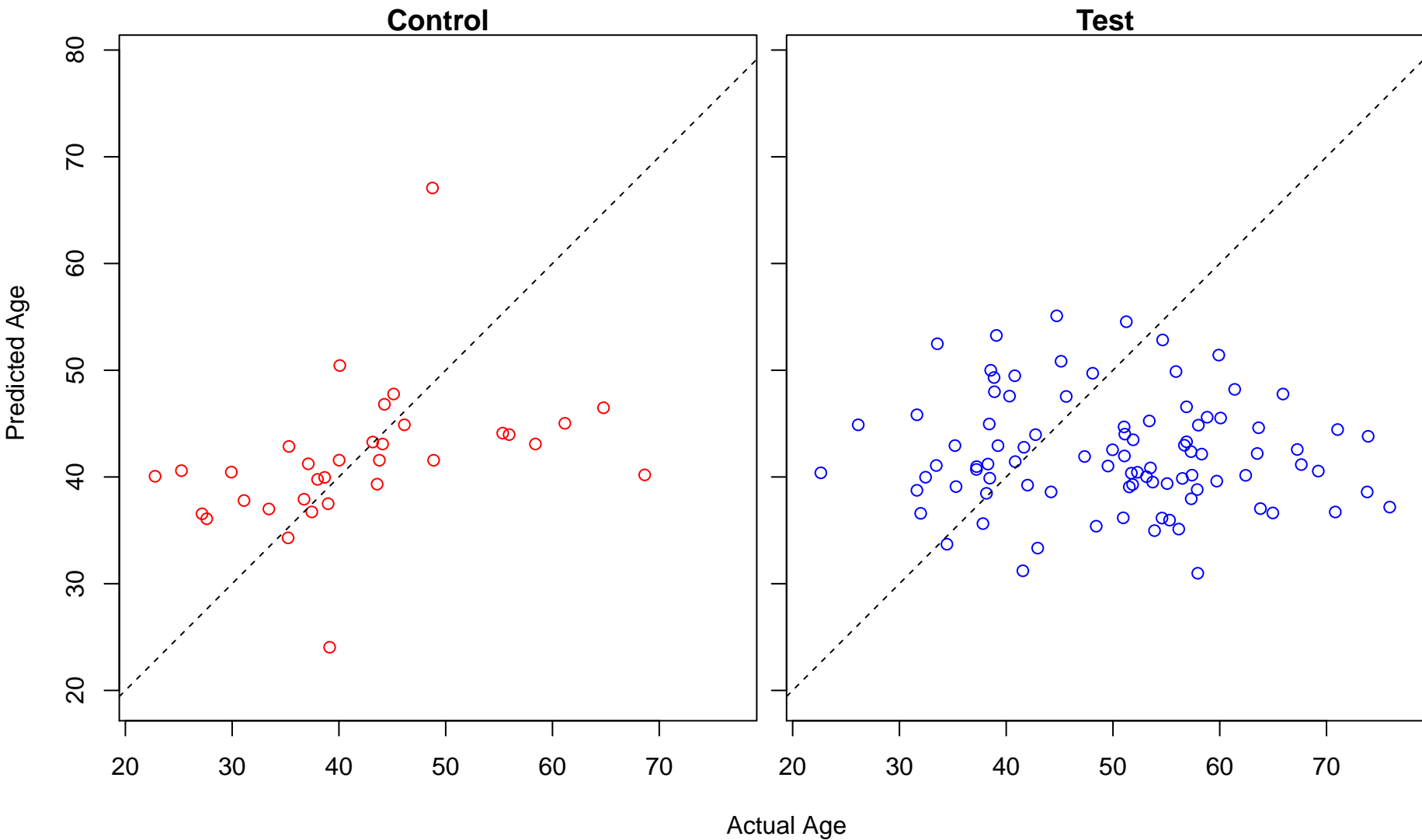
membrane organization (Score: 0.600971)



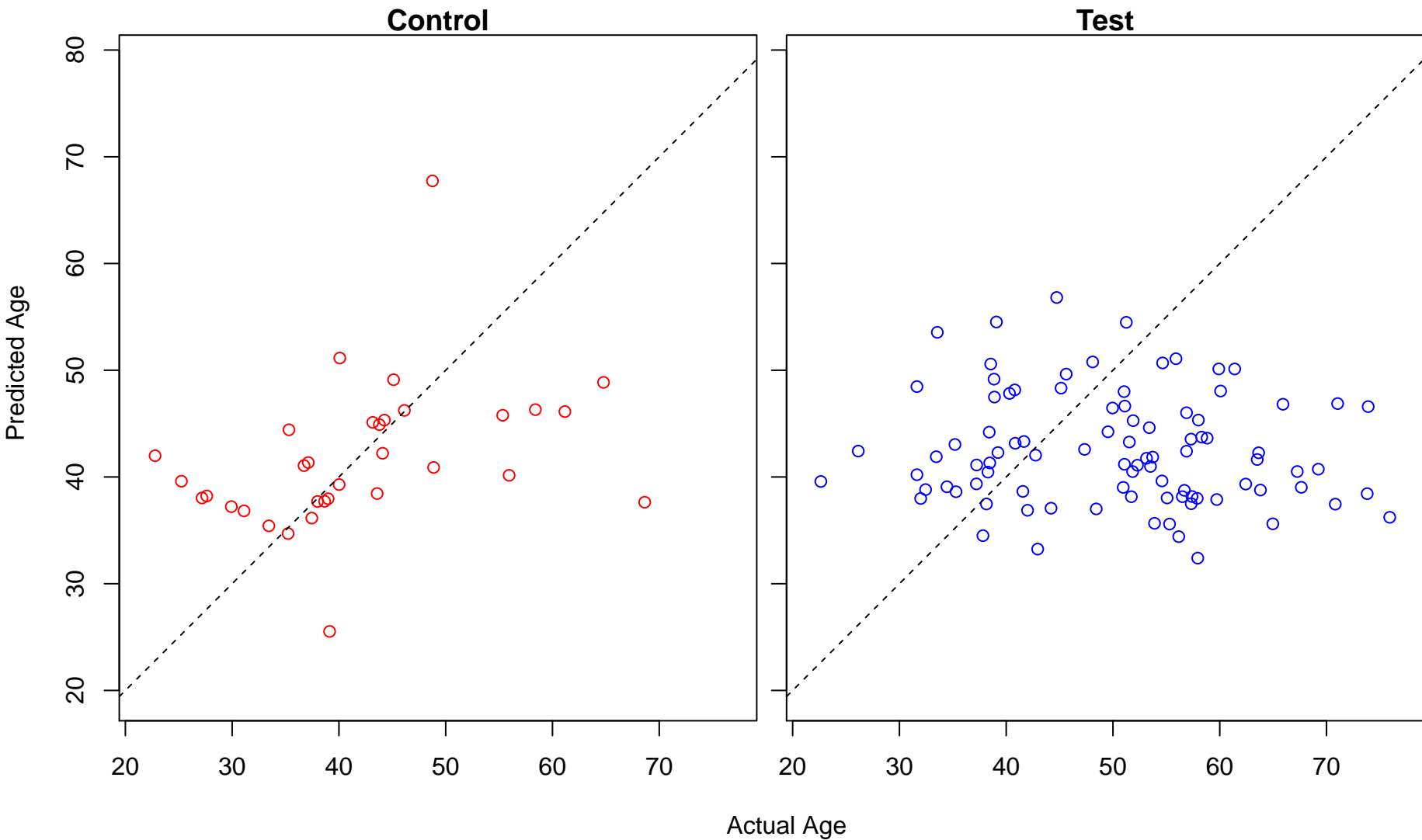
negative regulation of response to stimulus (Score: 0.599916)



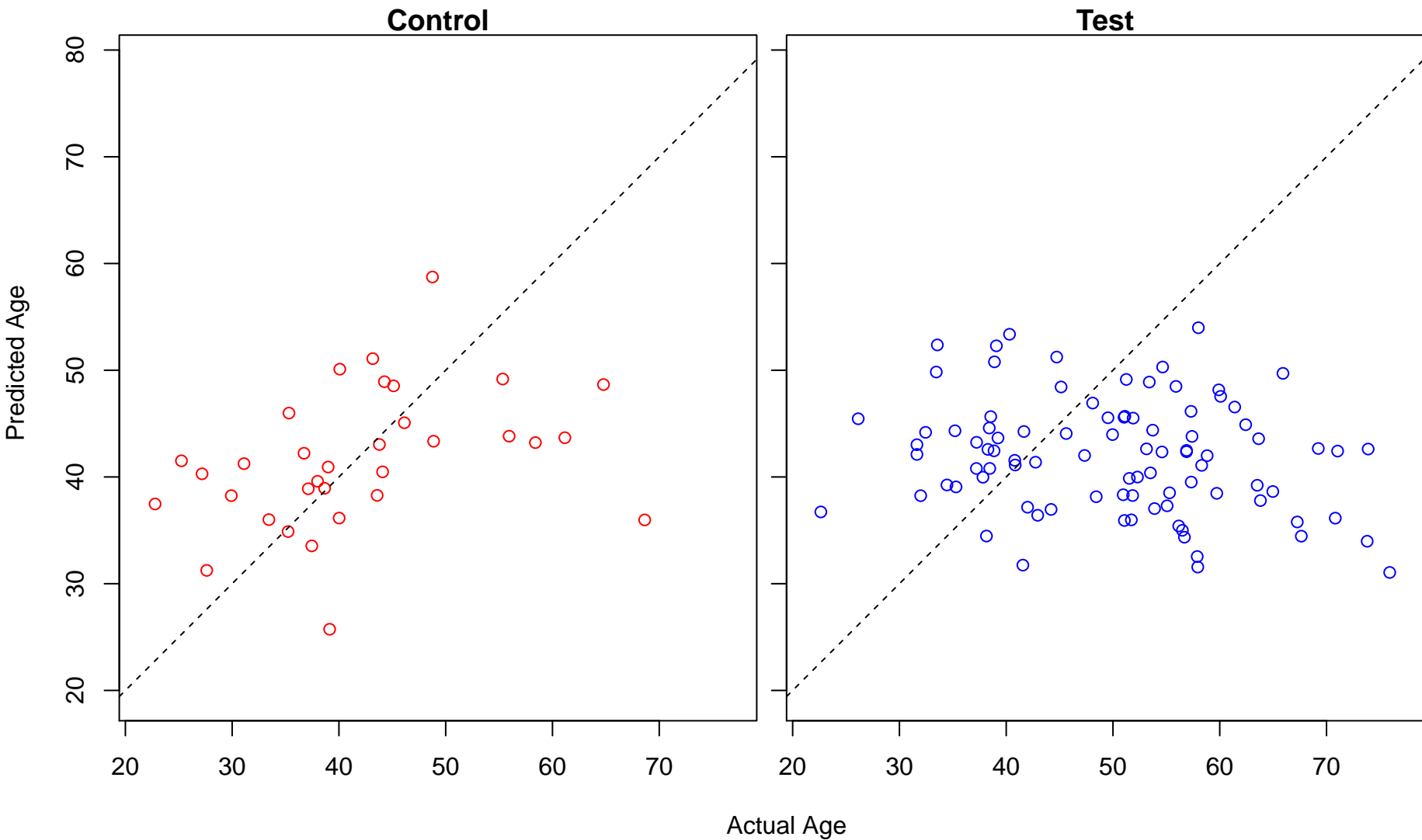
response to oxygen-containing compound (Score: 0.599756)



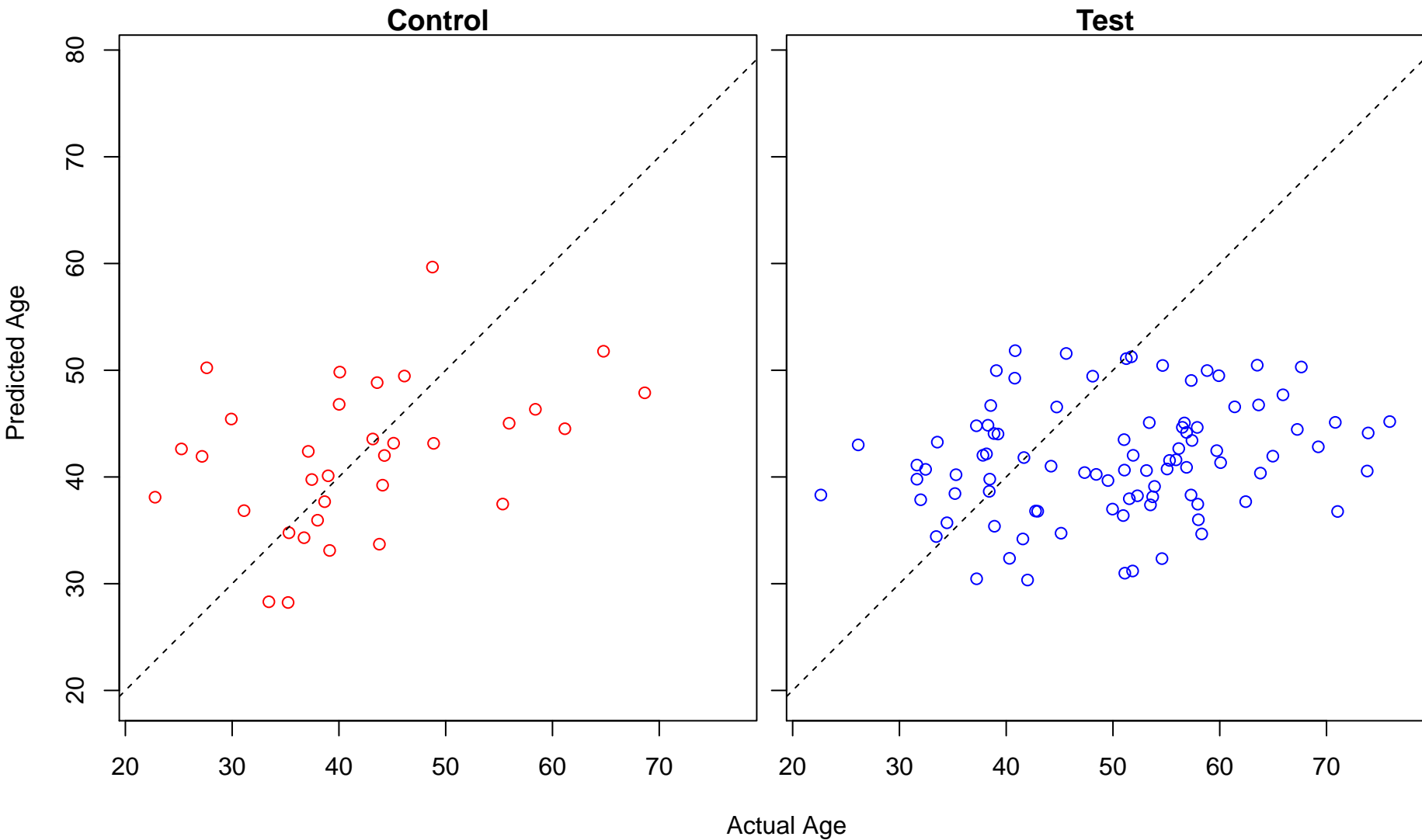
endomembrane system organization (Score: 0.599448)



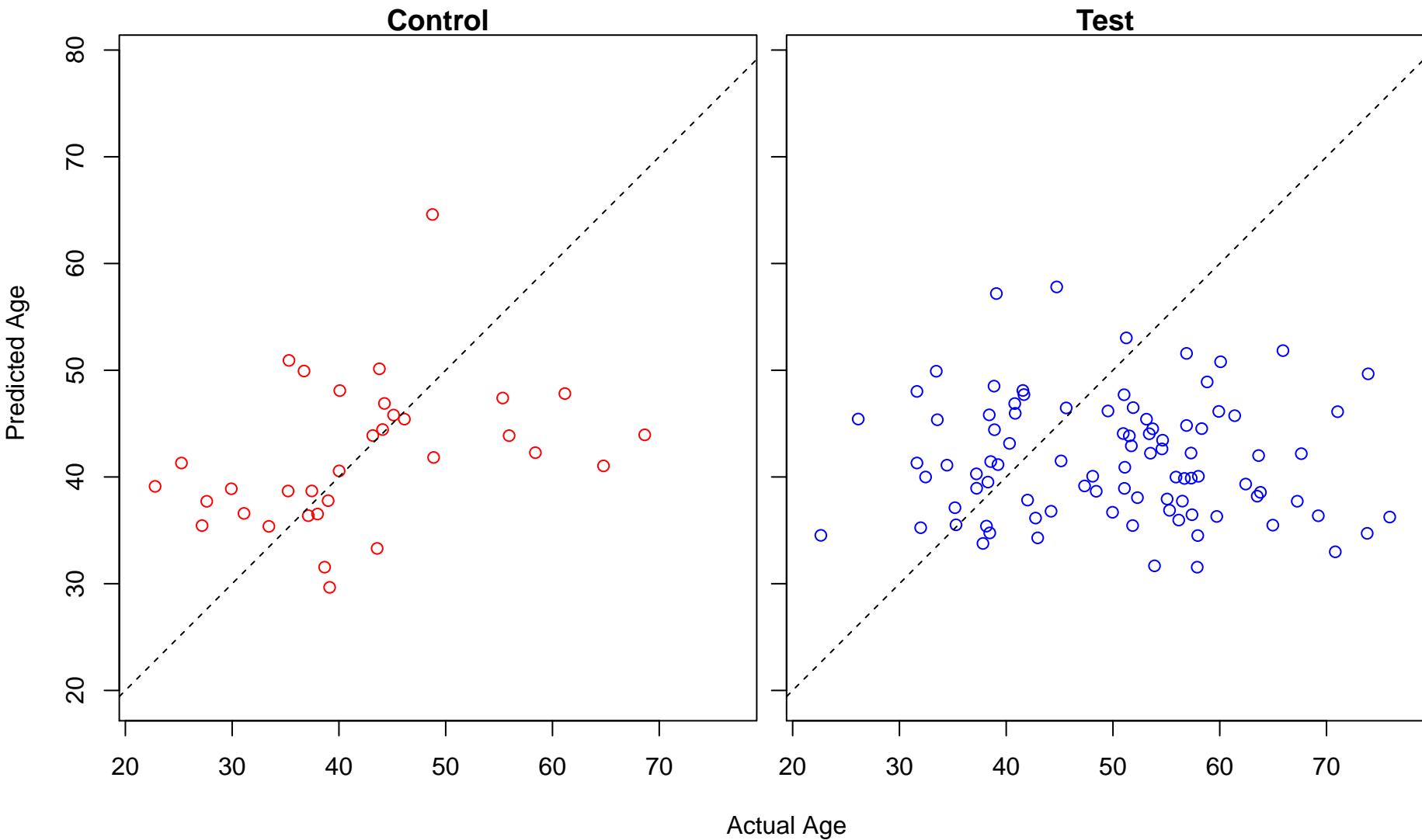
regulation of p38MAPK cascade (Score: 0.598561)



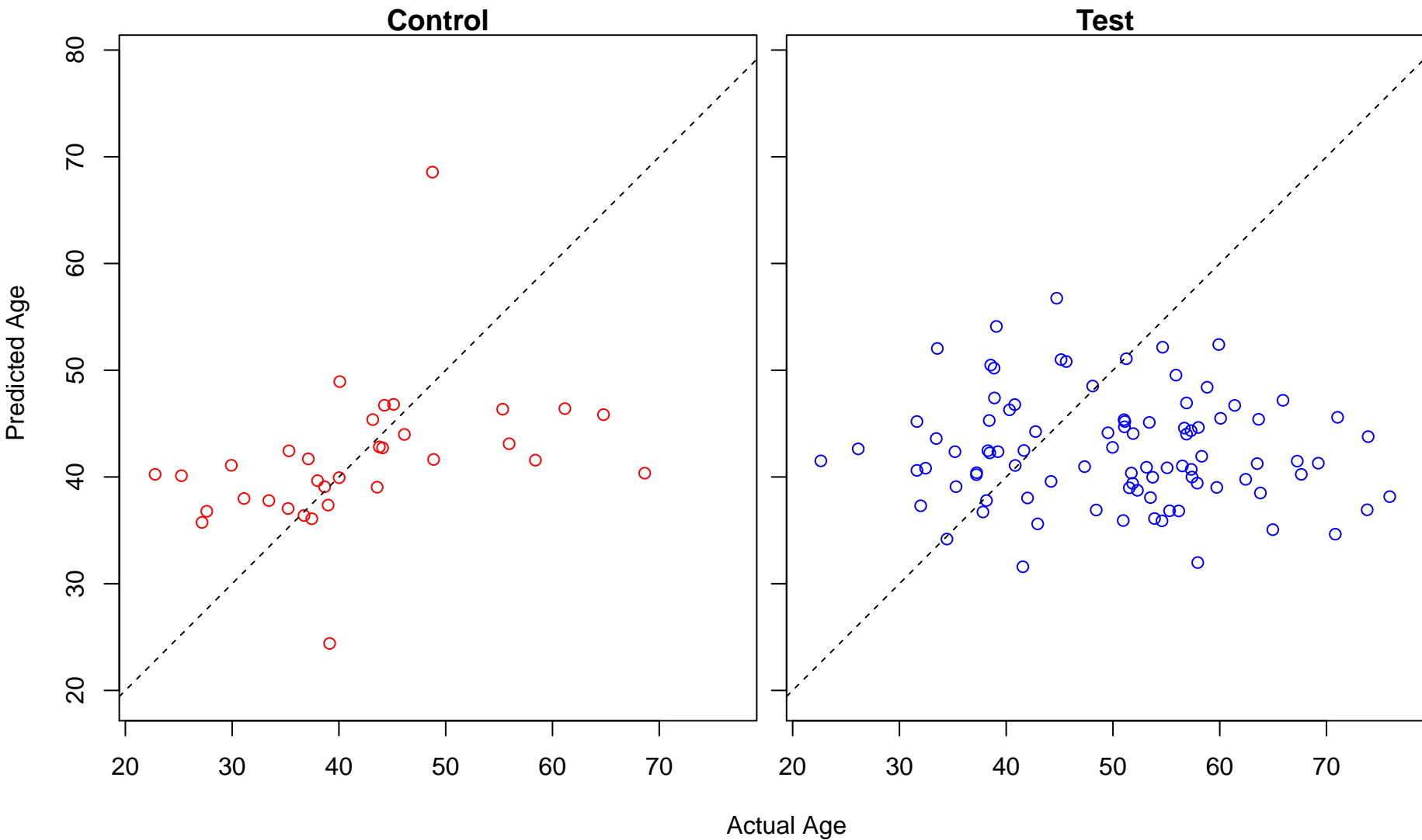
fucose metabolic process (Score: 0.597689)



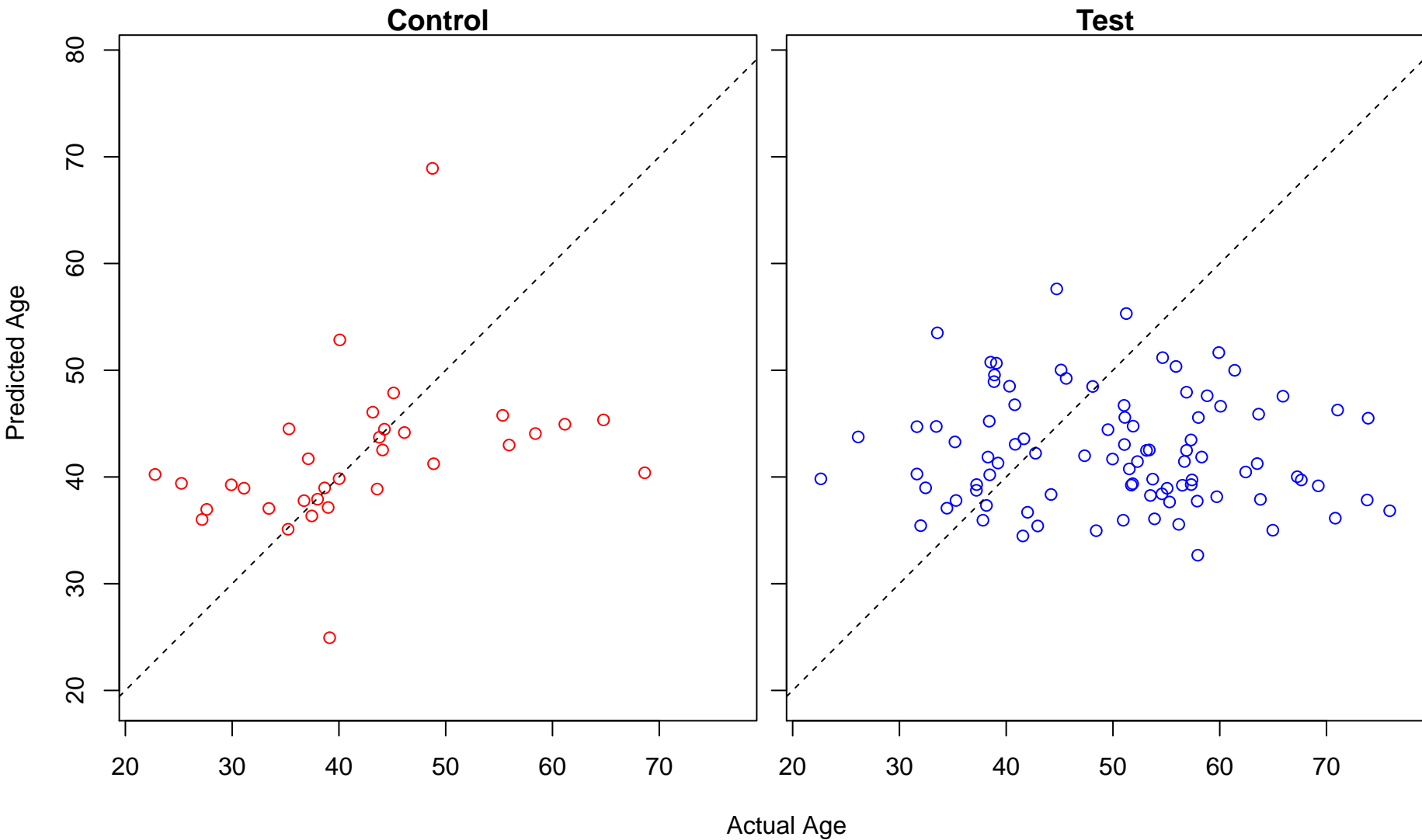
cellular response to laminar fluid shear stress (Score: 0.597347)



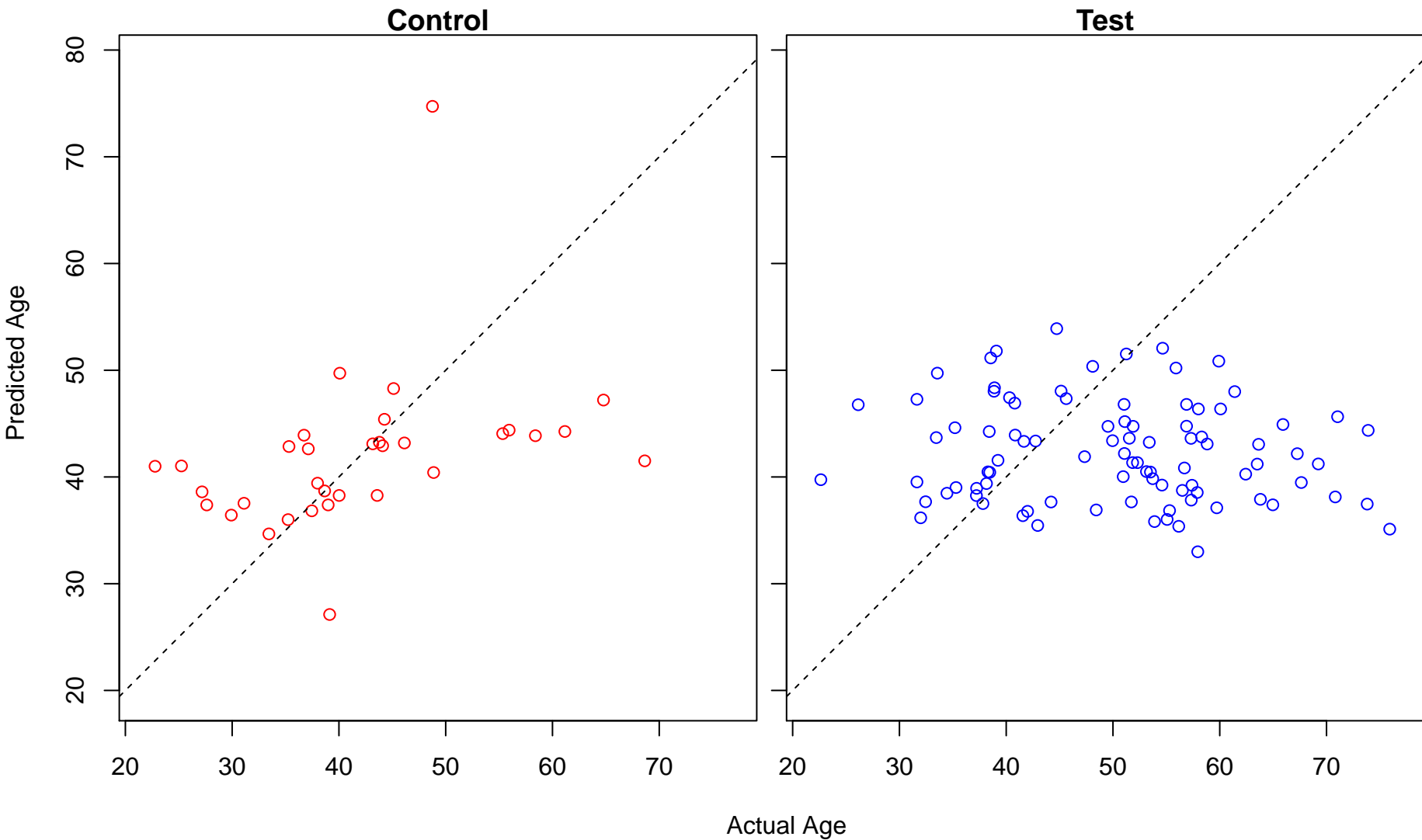
response to peptide (Score: 0.597298)



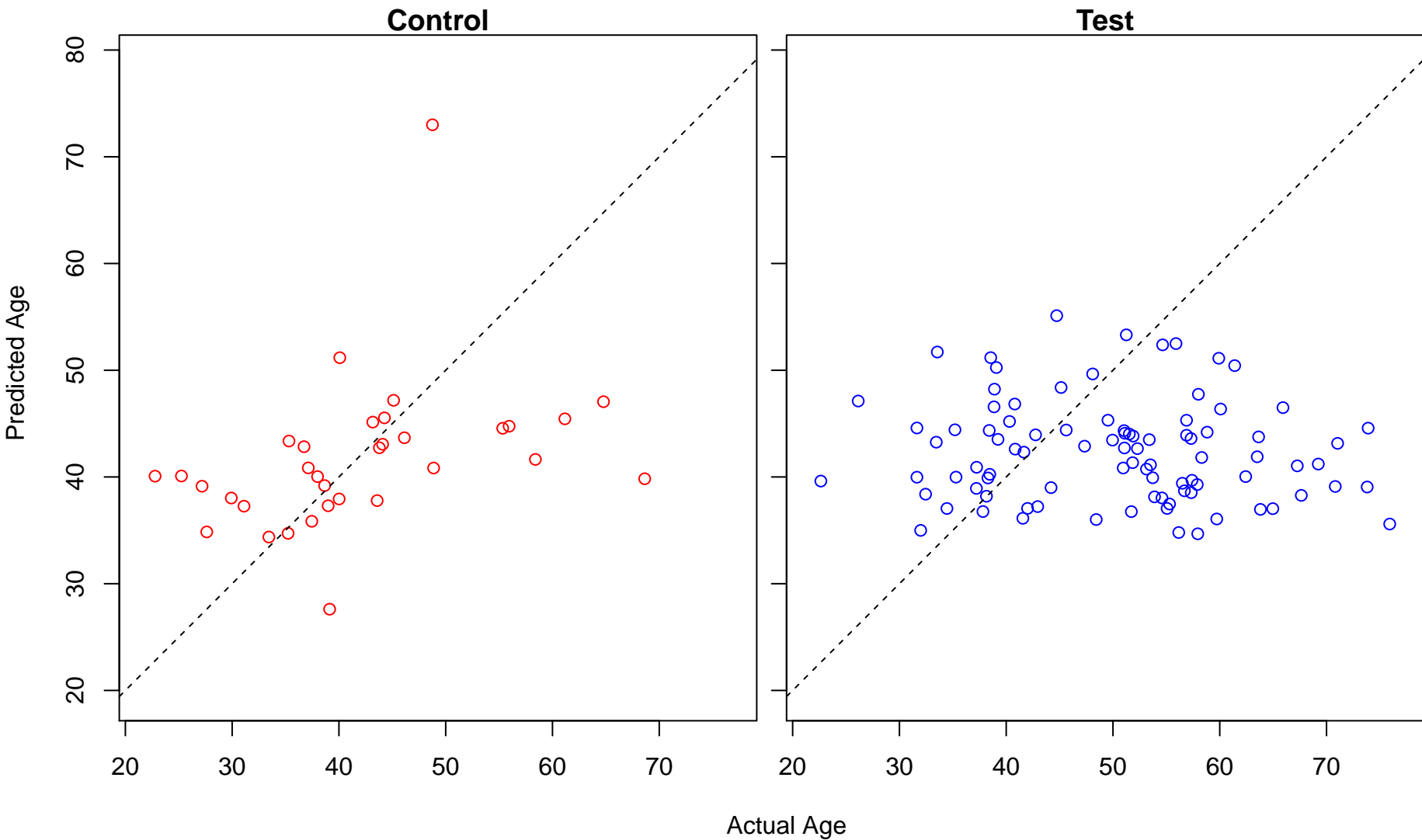
transmembrane receptor protein tyrosine kinase signaling pathway (Score: 0.596573)



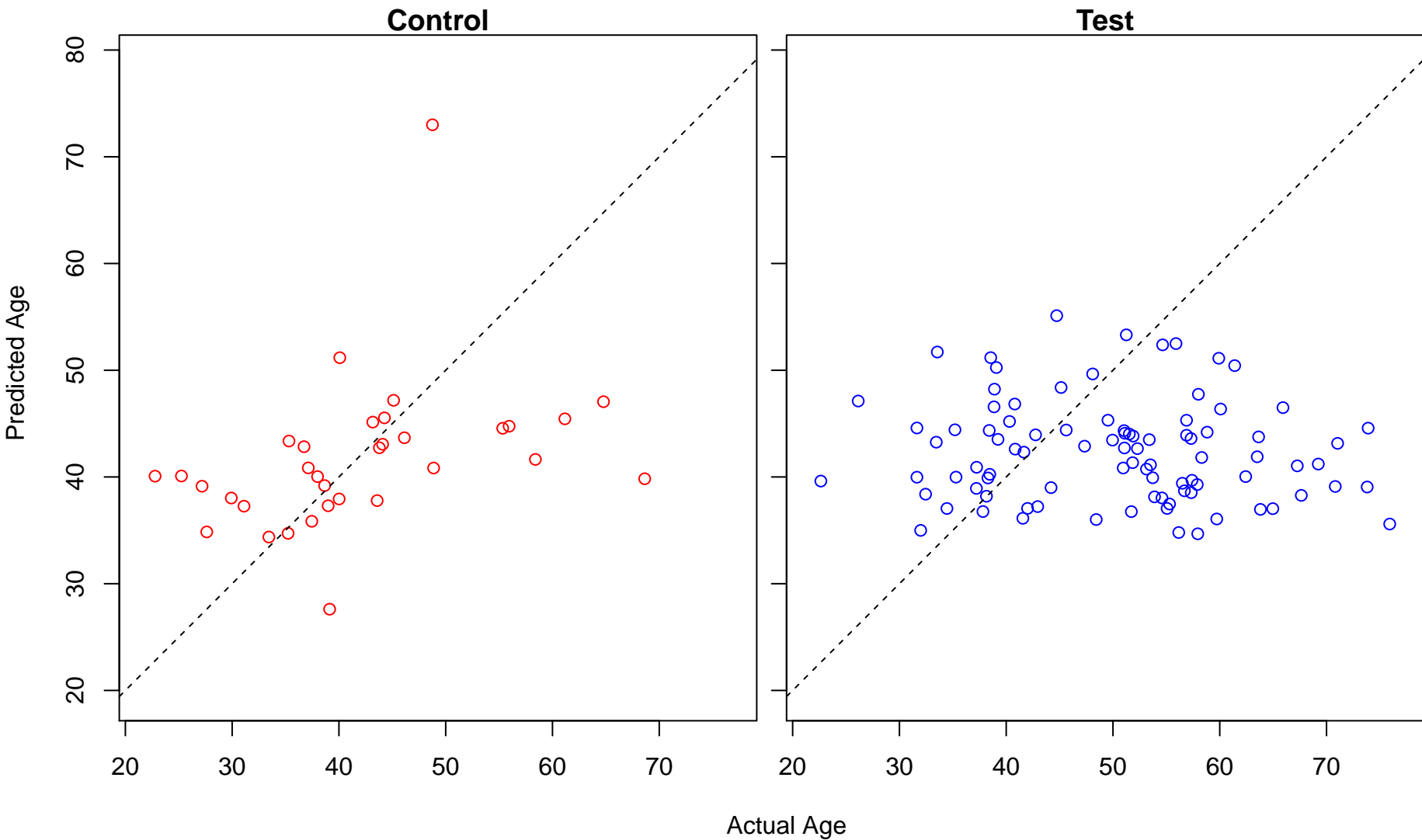
protein localization (Score: 0.596564)



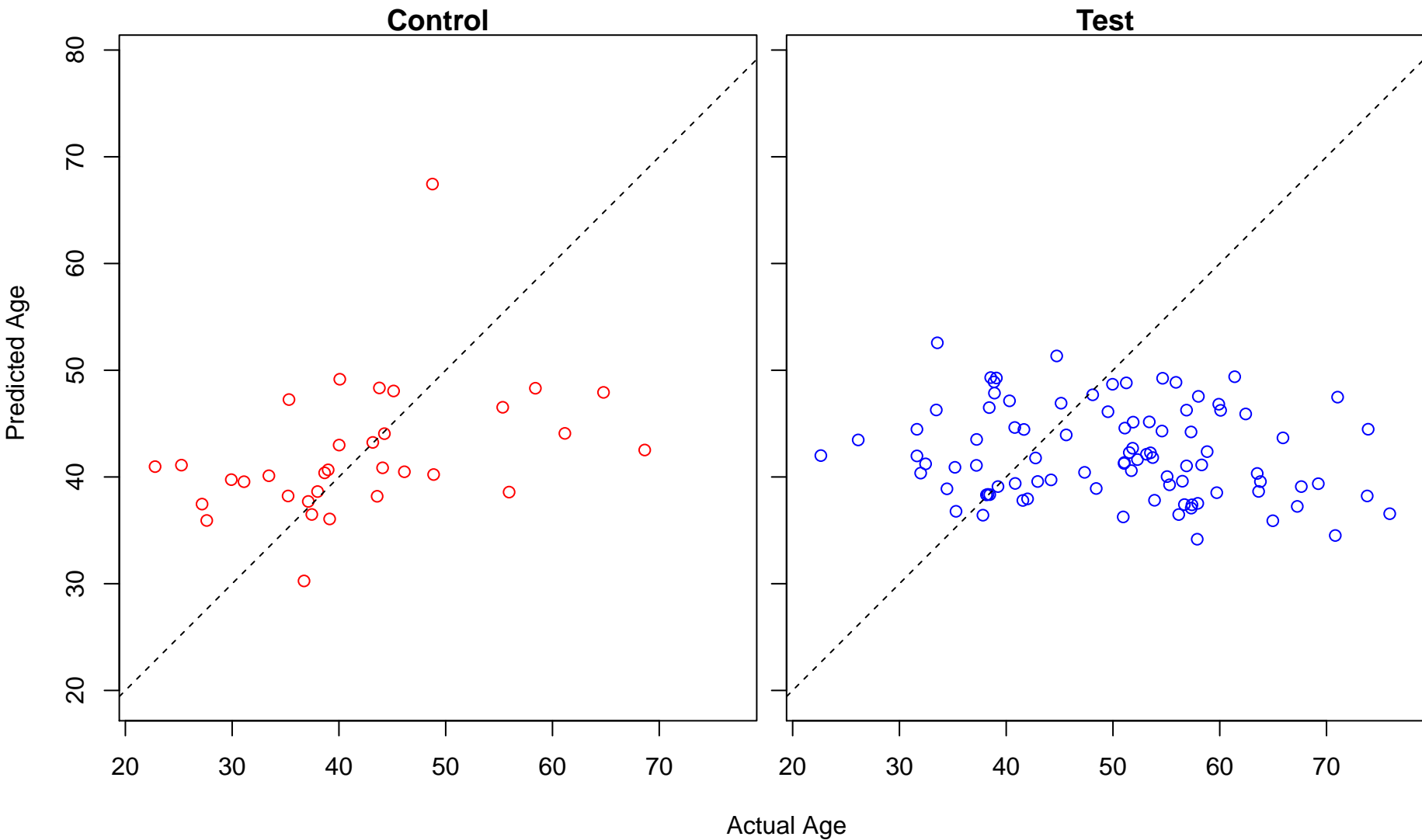
cell death (Score: 0.596423)



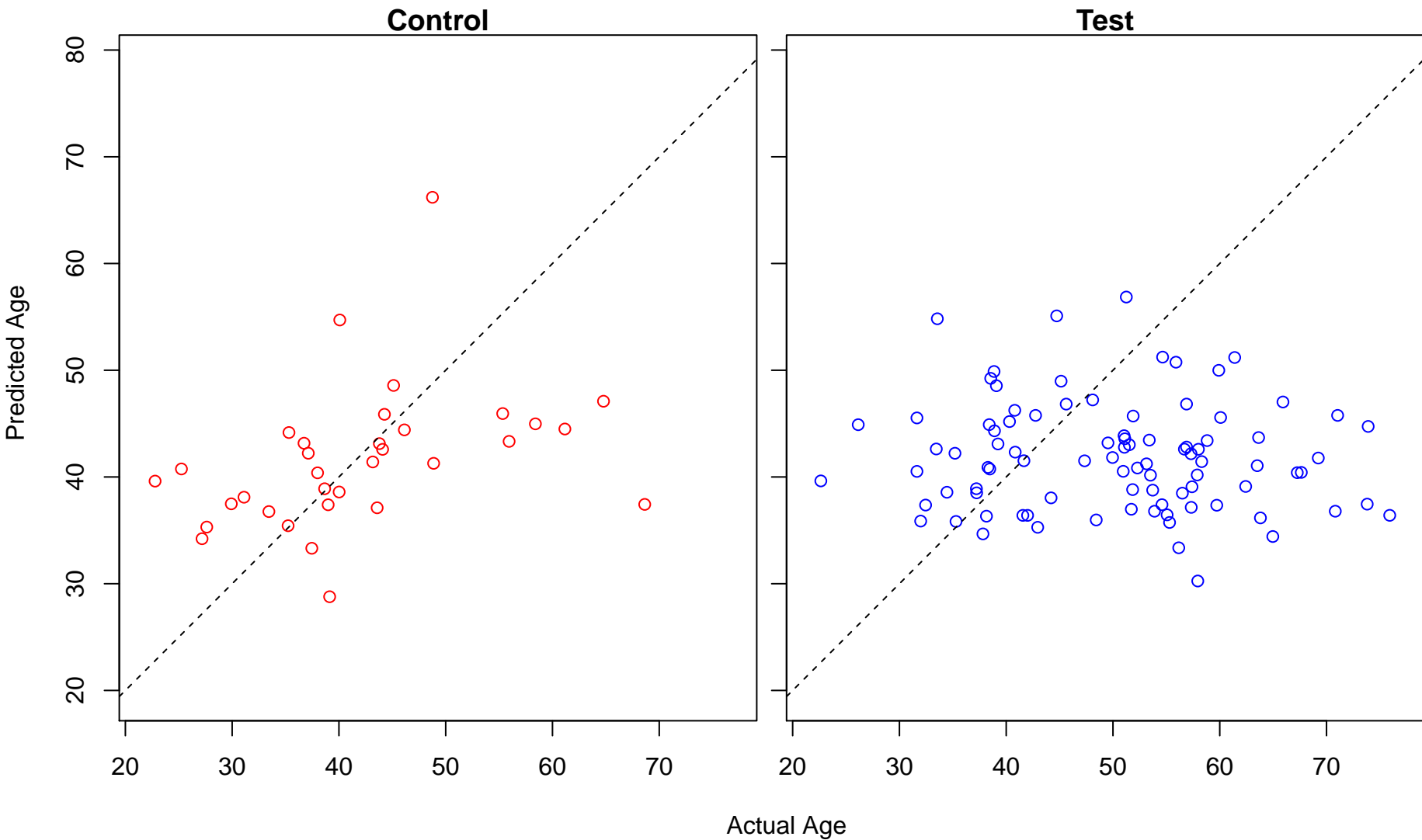
death (Score: 0.596423)



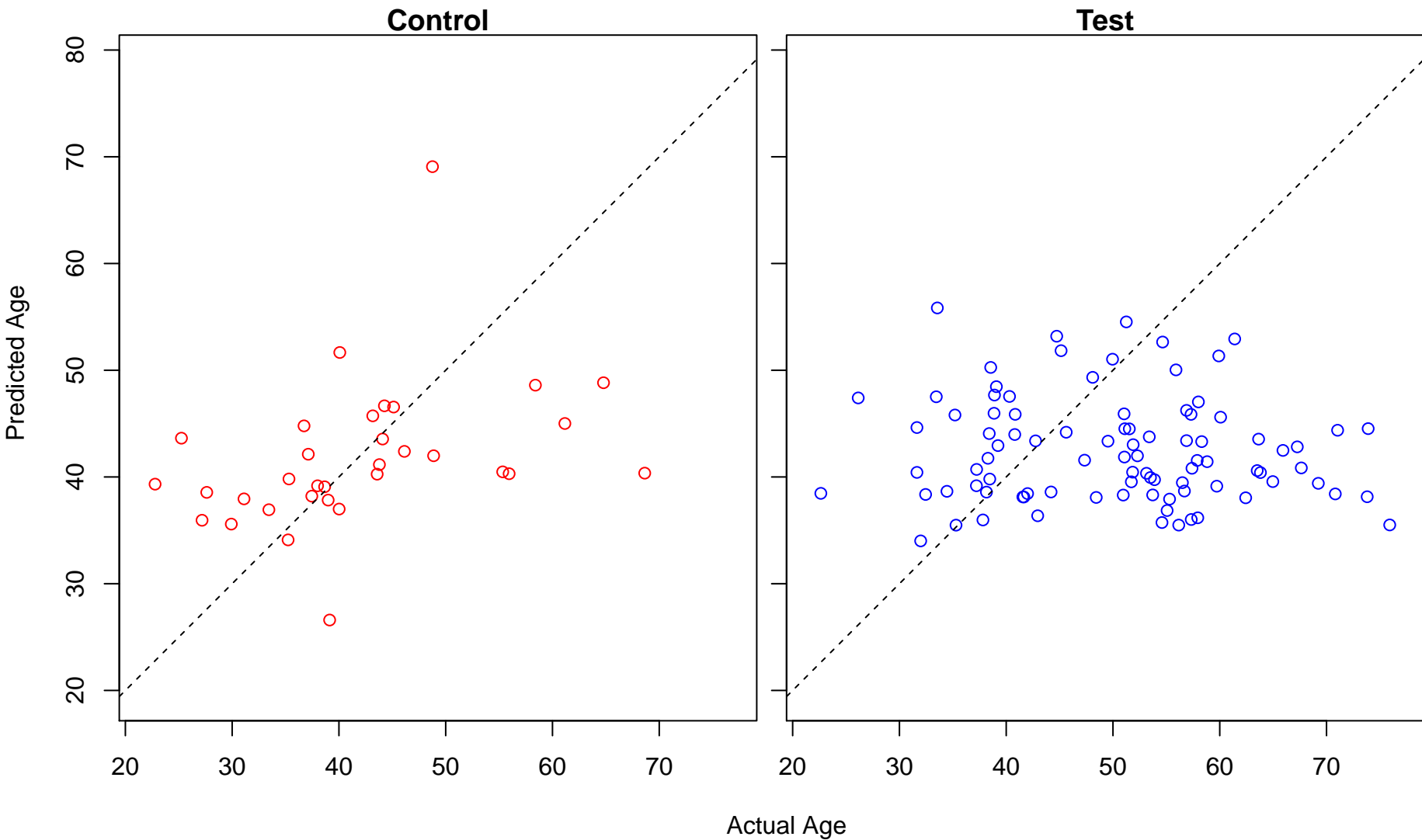
megakaryocyte development (Score: 0.596347)



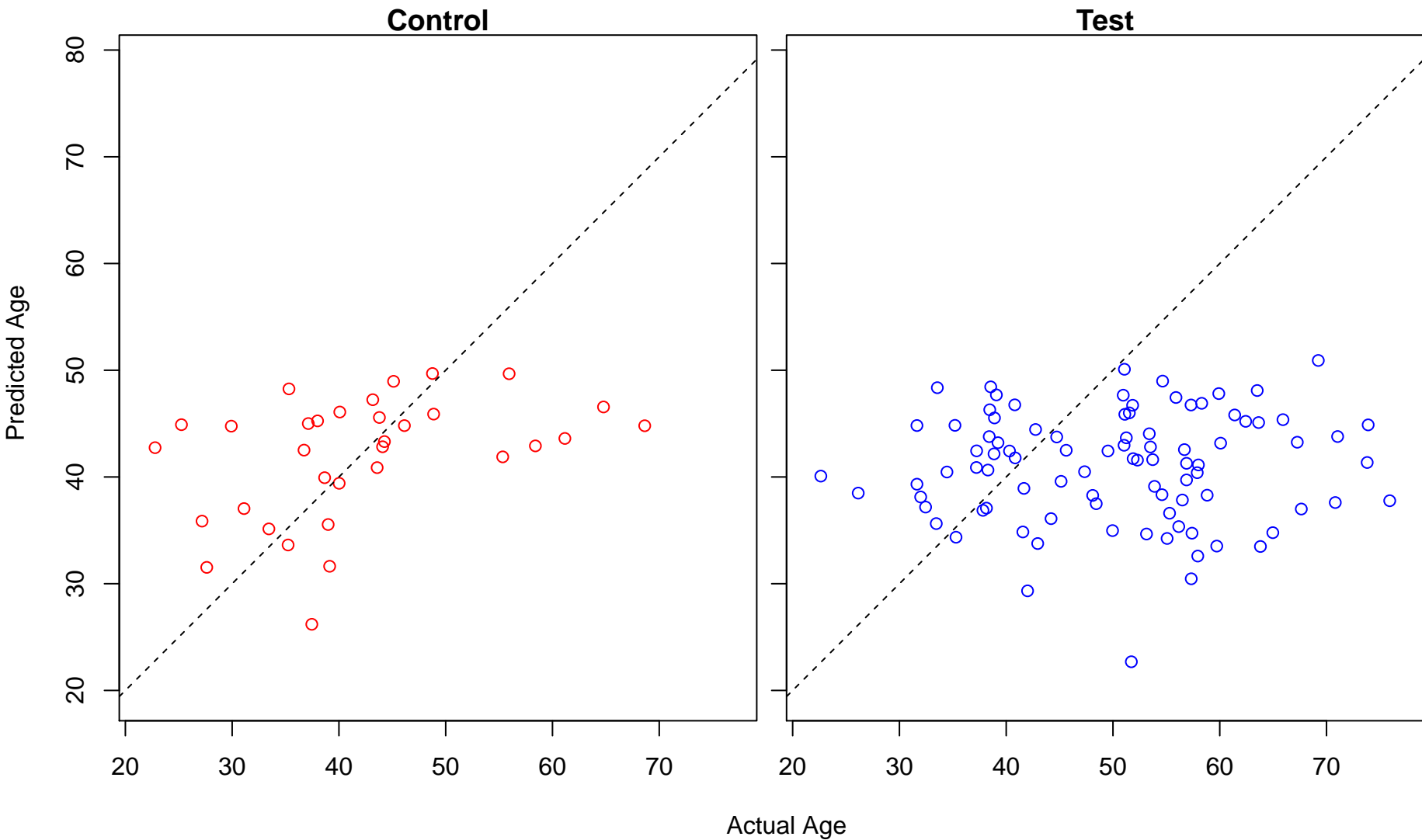
negative regulation of apoptotic process (Score: 0.596211)



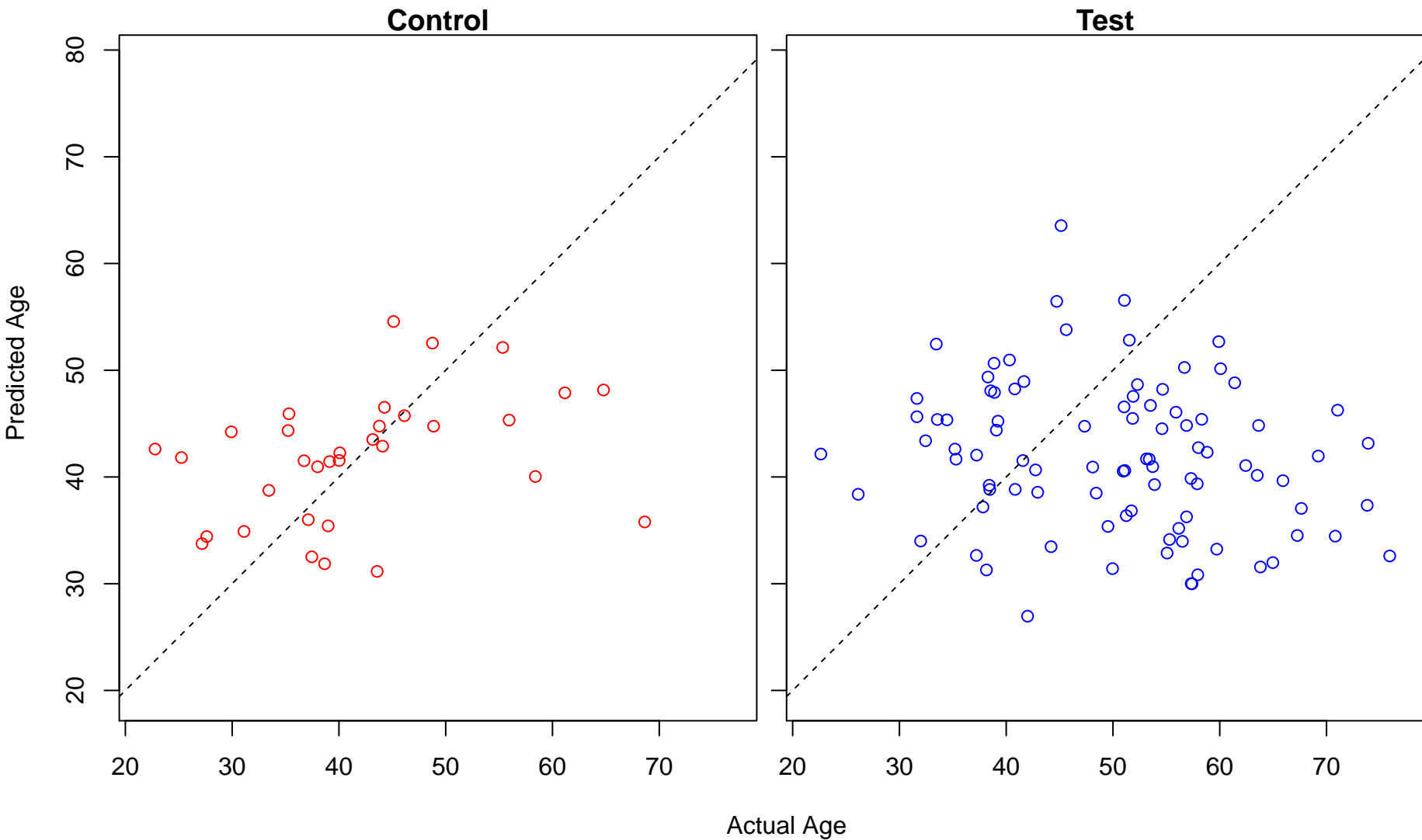
regulation of nervous system development (Score: 0.595777)



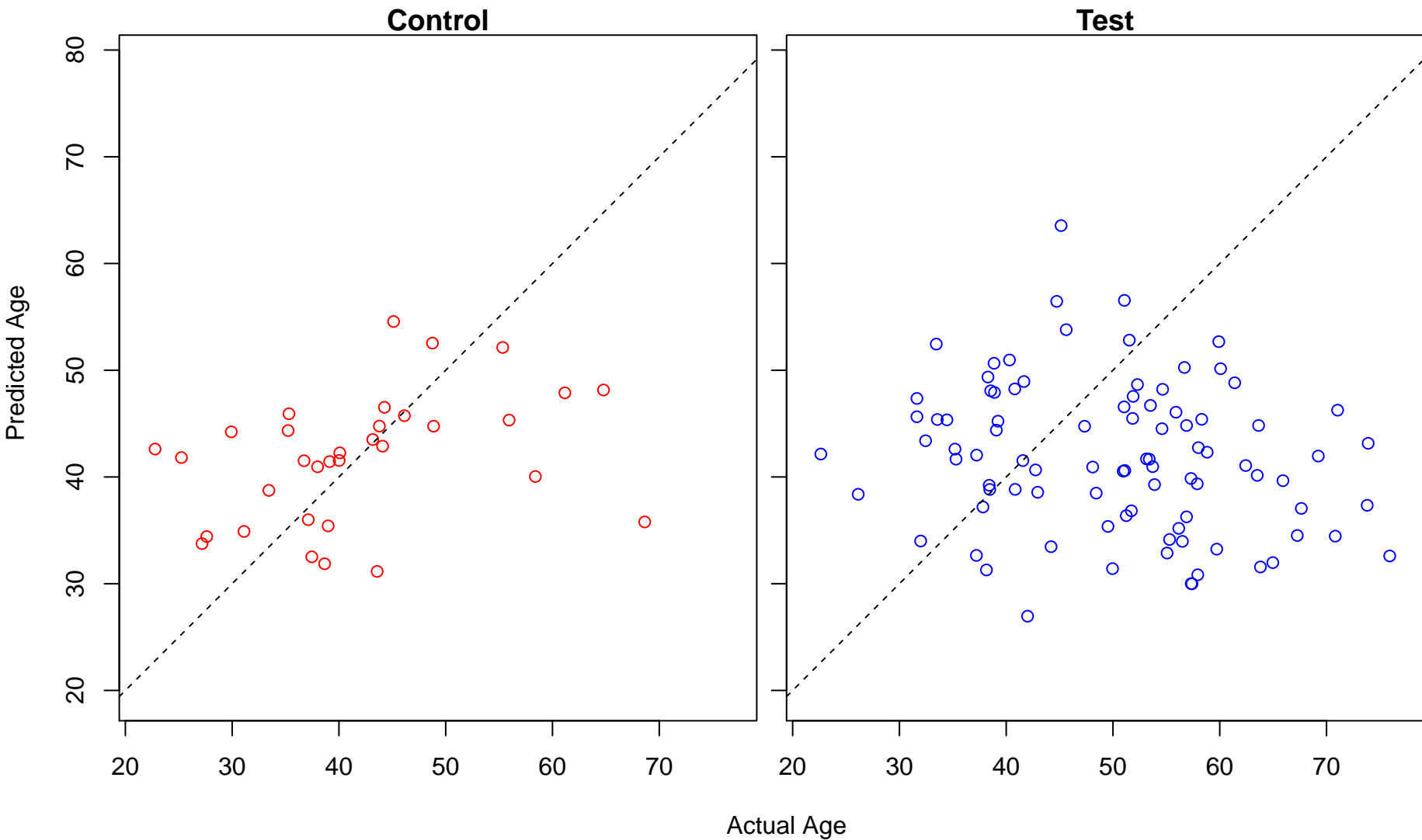
membrane to membrane docking (Score: 0.595143)



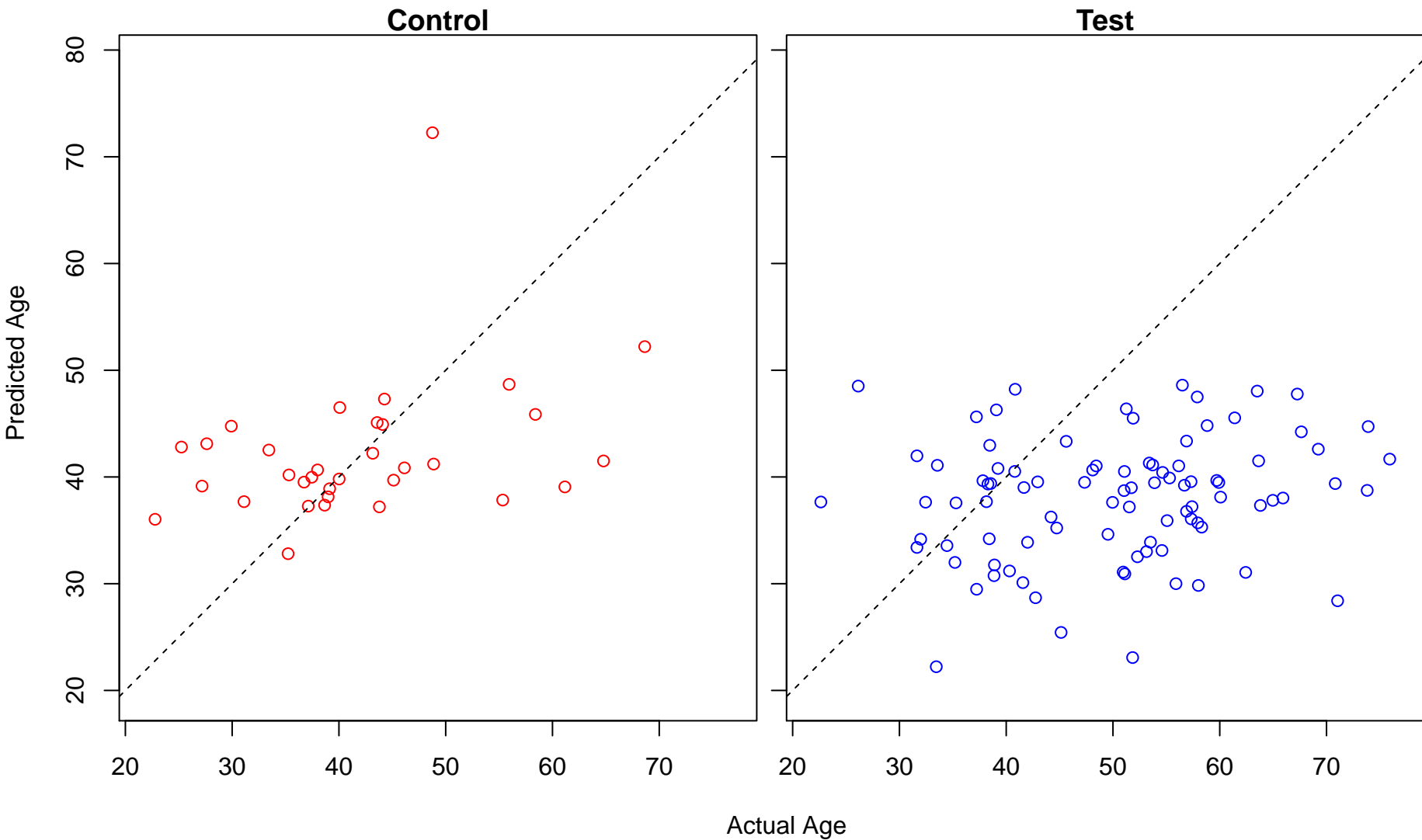
mechanoreceptor differentiation (Score: 0.594440)



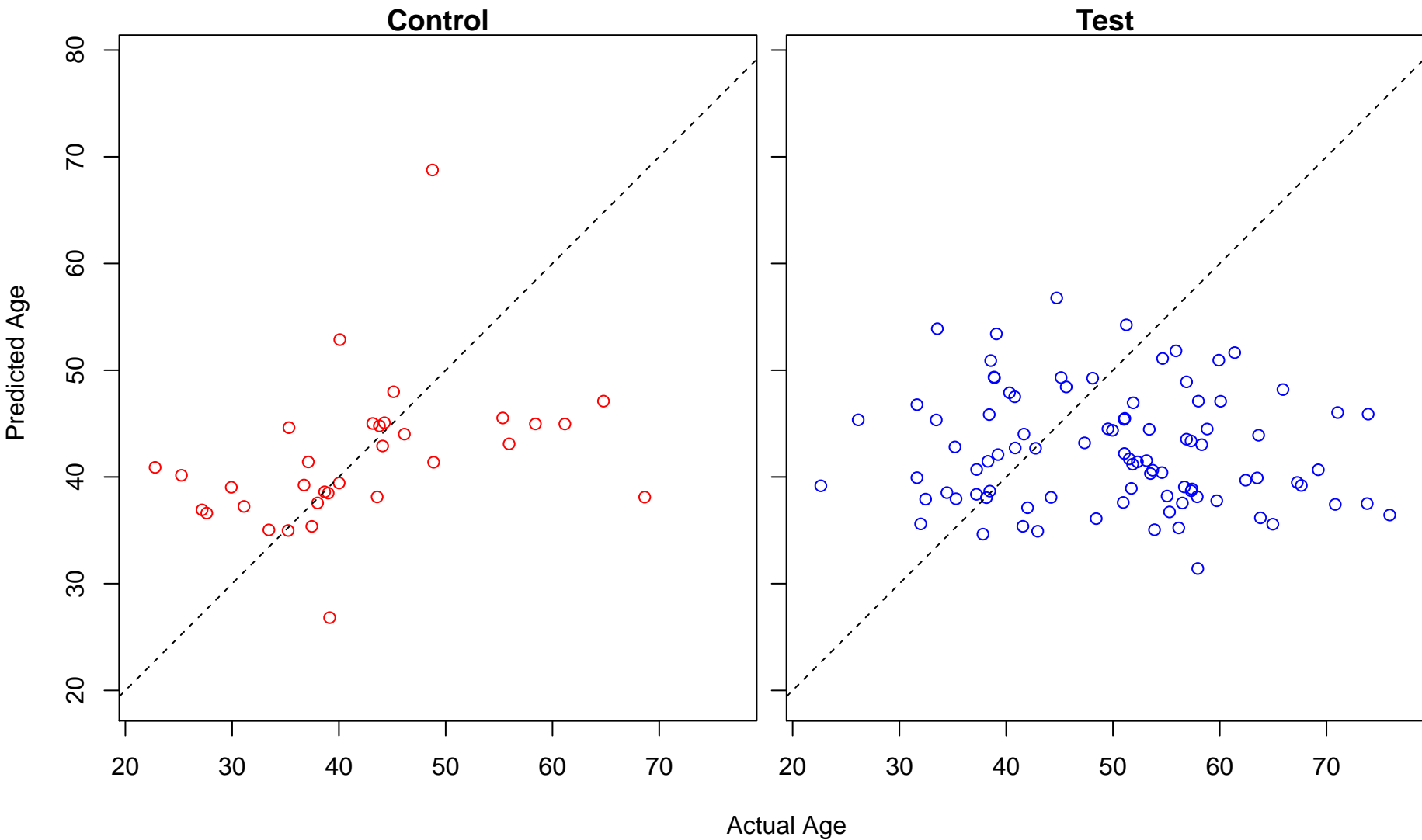
inner ear receptor cell differentiation (Score: 0.594440)



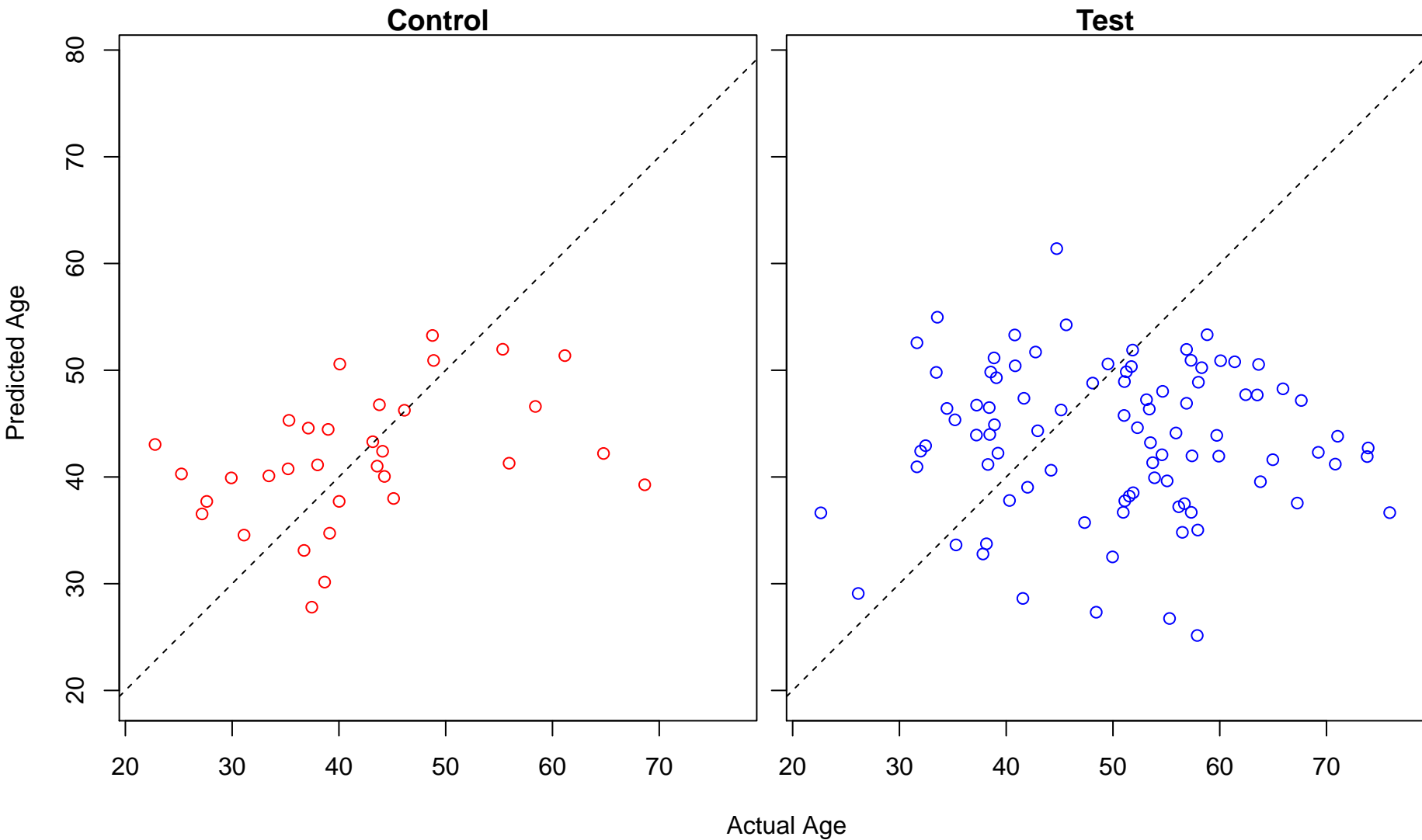
glutamate biosynthetic process (Score: 0.594304)



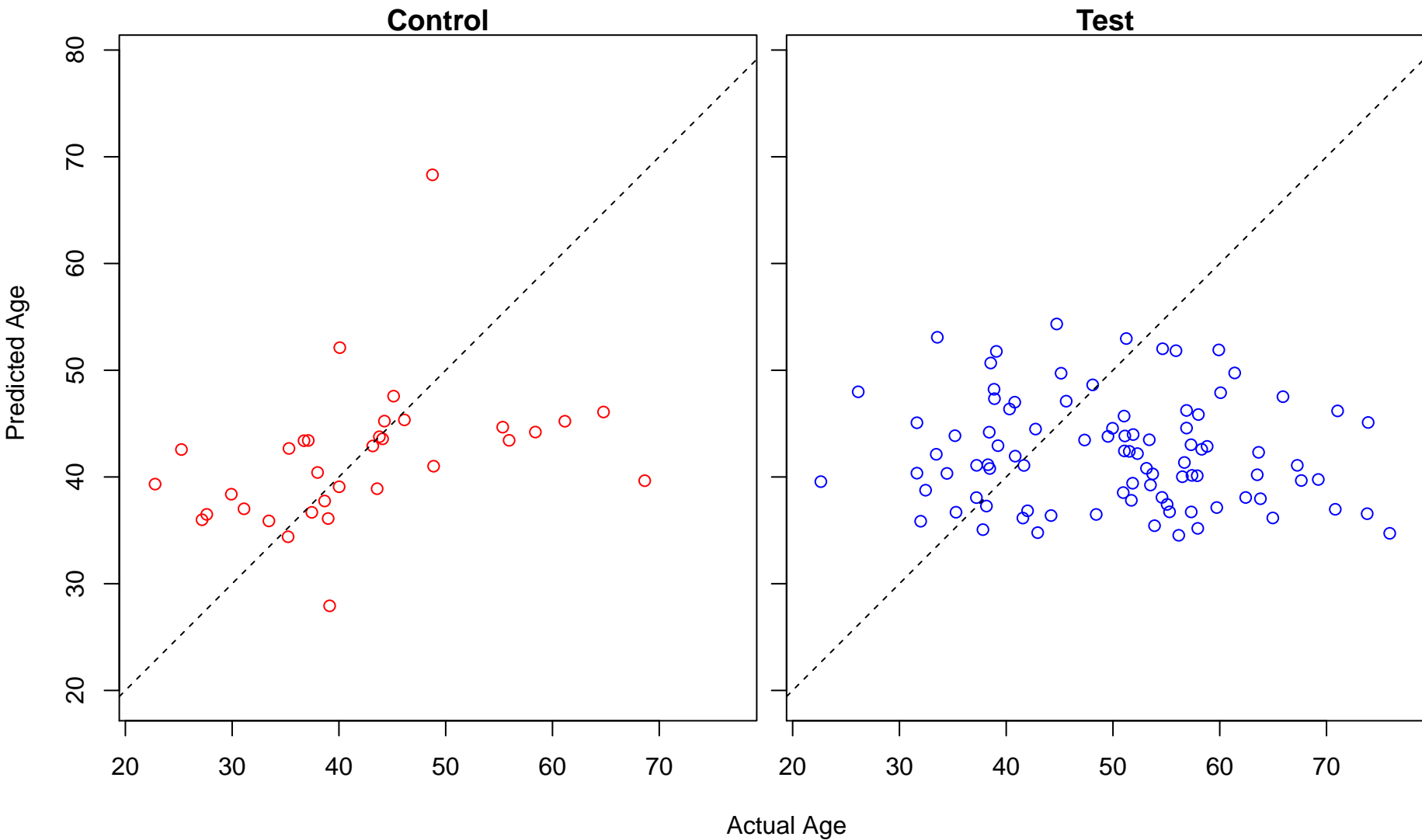
cellular protein metabolic process (Score: 0.594001)



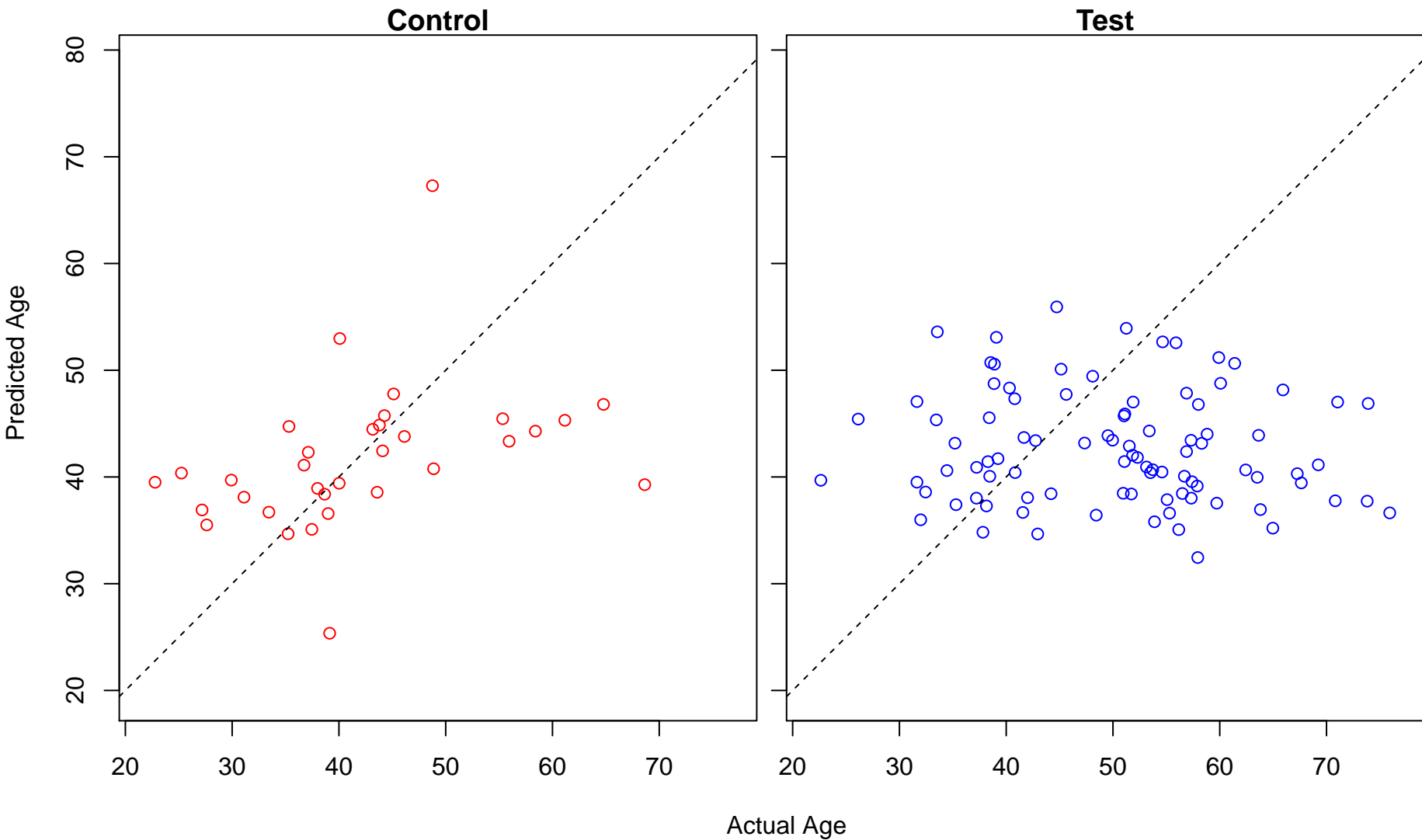
cellular response to alkaloid (Score: 0.593162)



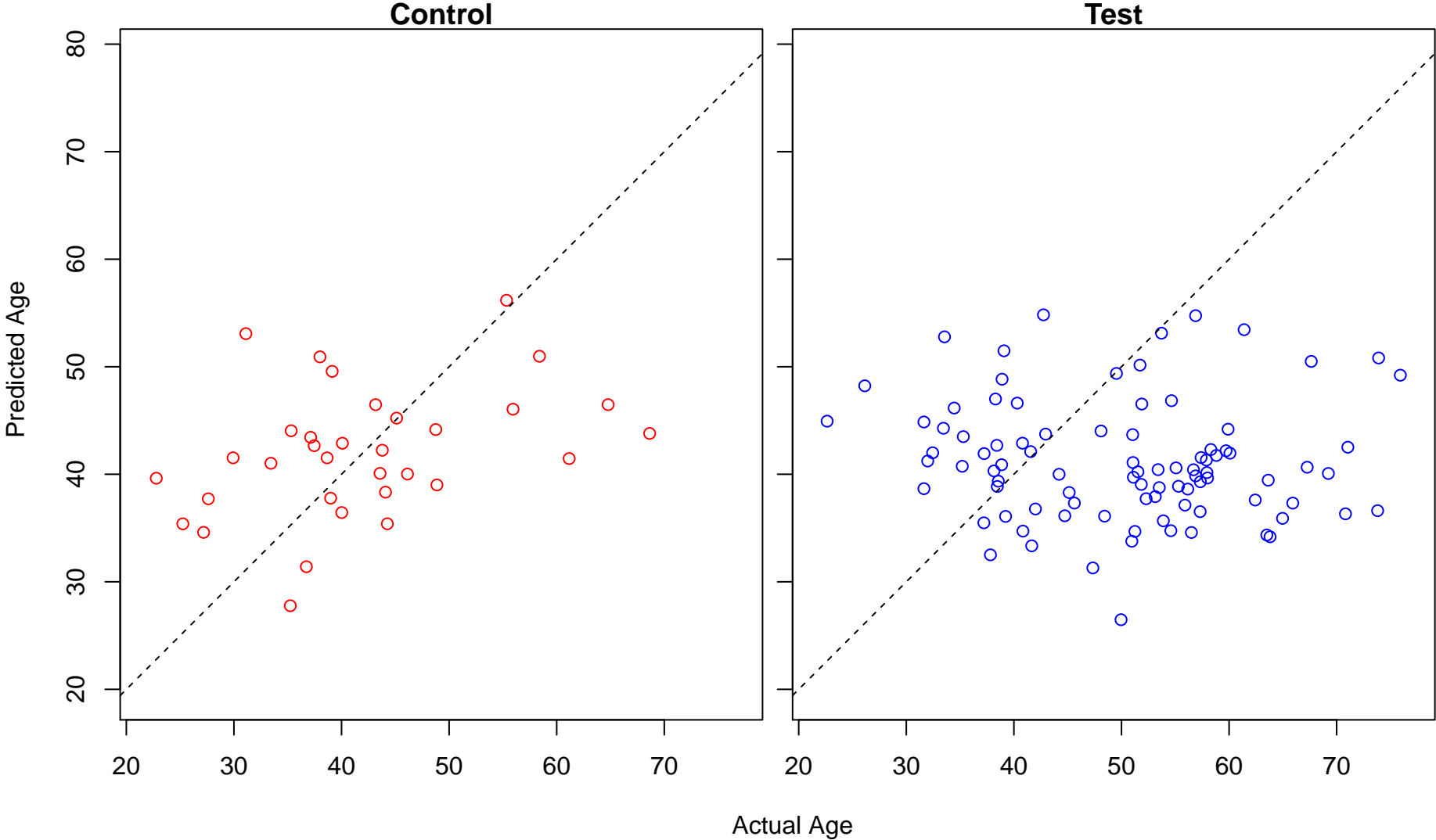
regulation of multicellular organismal process (Score: 0.593075)



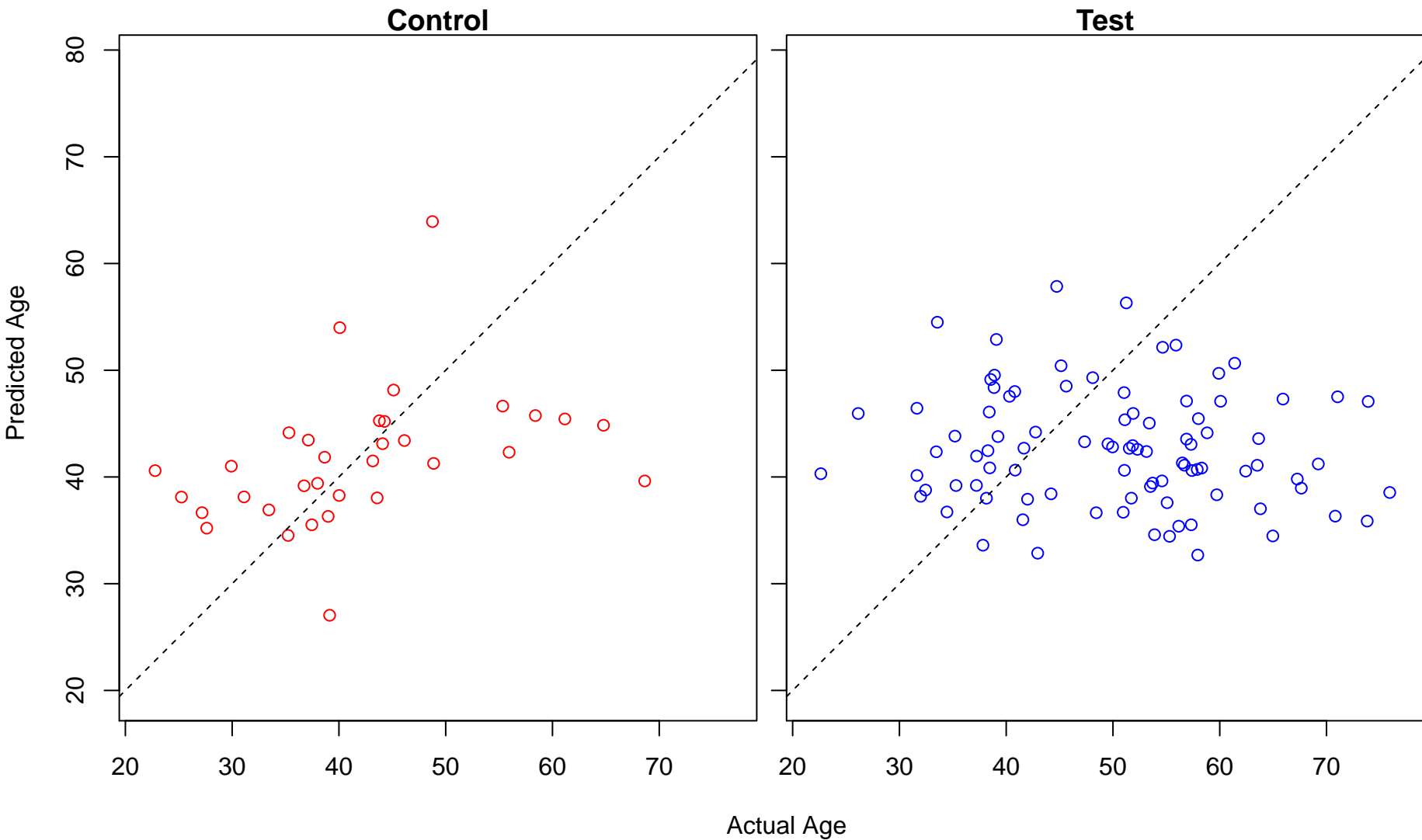
regulation of response to stimulus (Score: 0.593069)



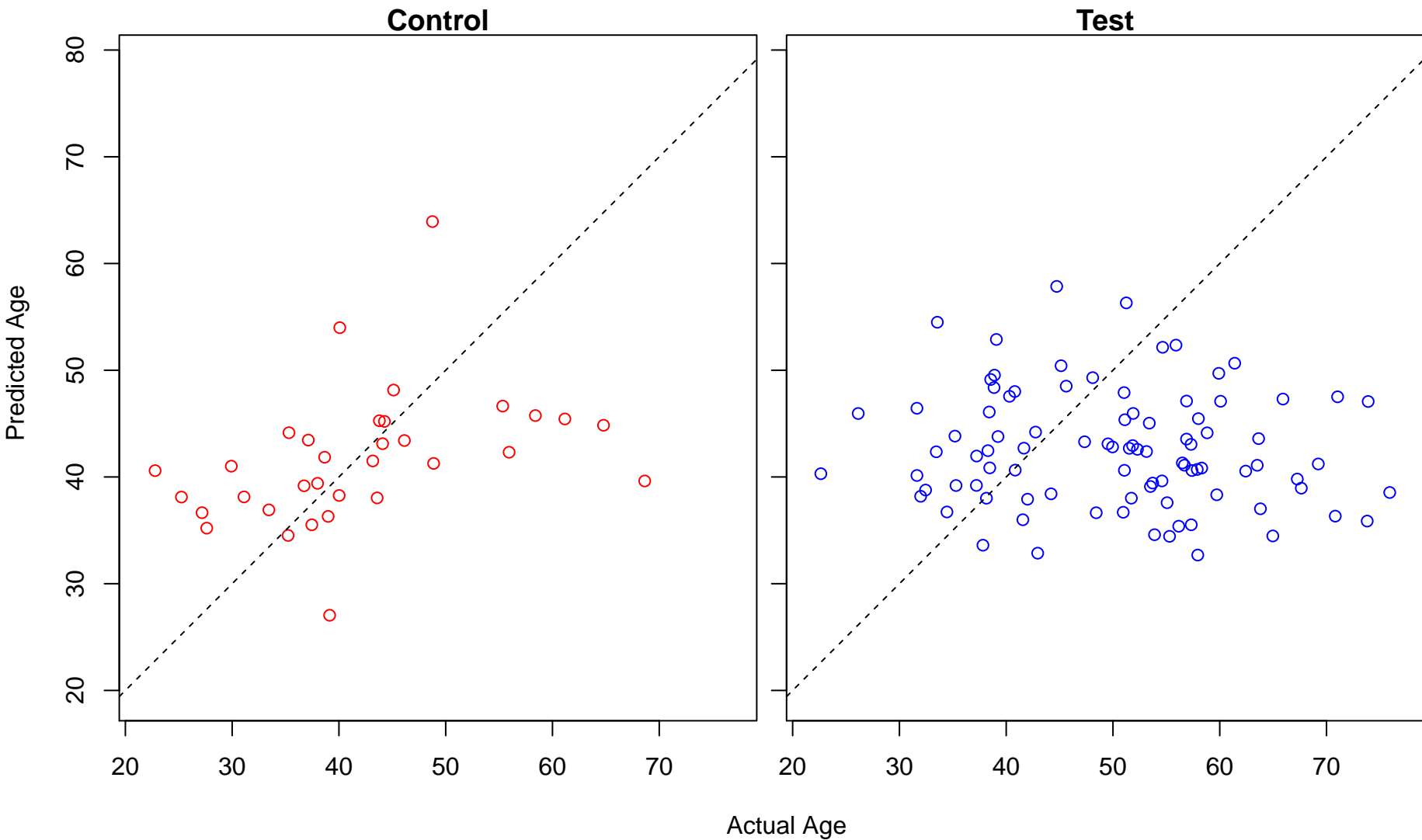
cell surface receptor signaling pathway involved in heart development (Score: 0.591858)



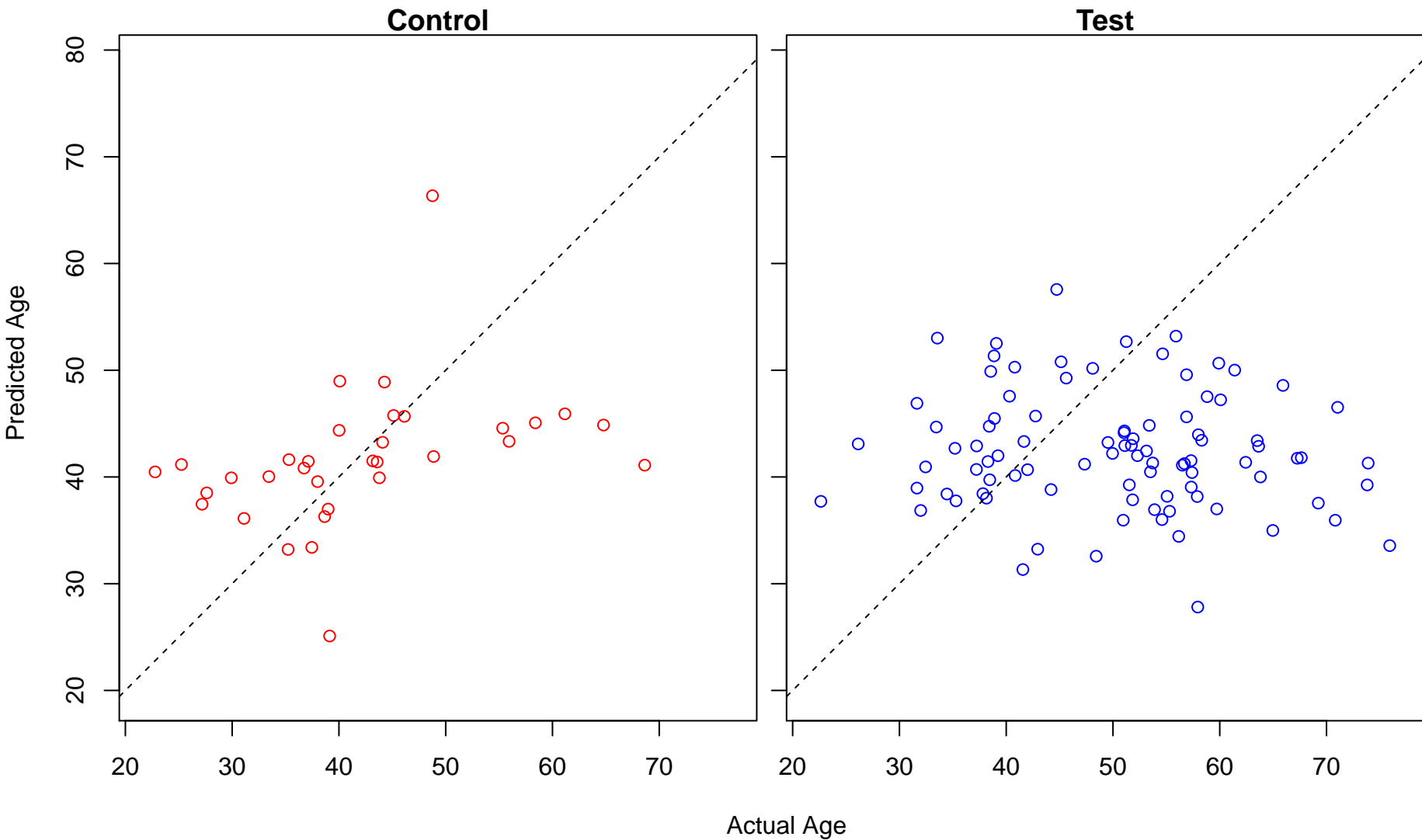
positive regulation of phosphorus metabolic process (Score: 0.591586)



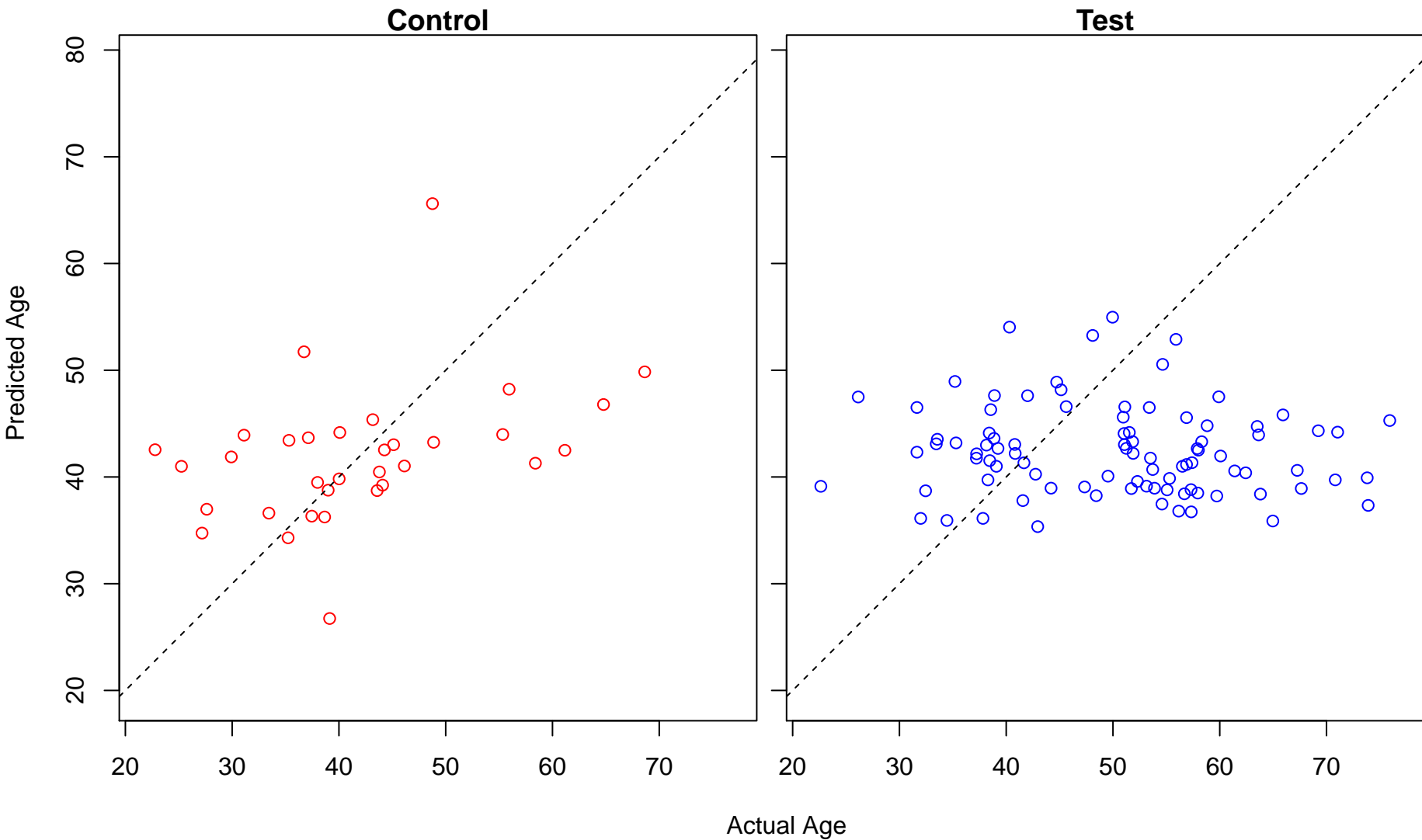
positive regulation of phosphate metabolic process (Score: 0.591586)



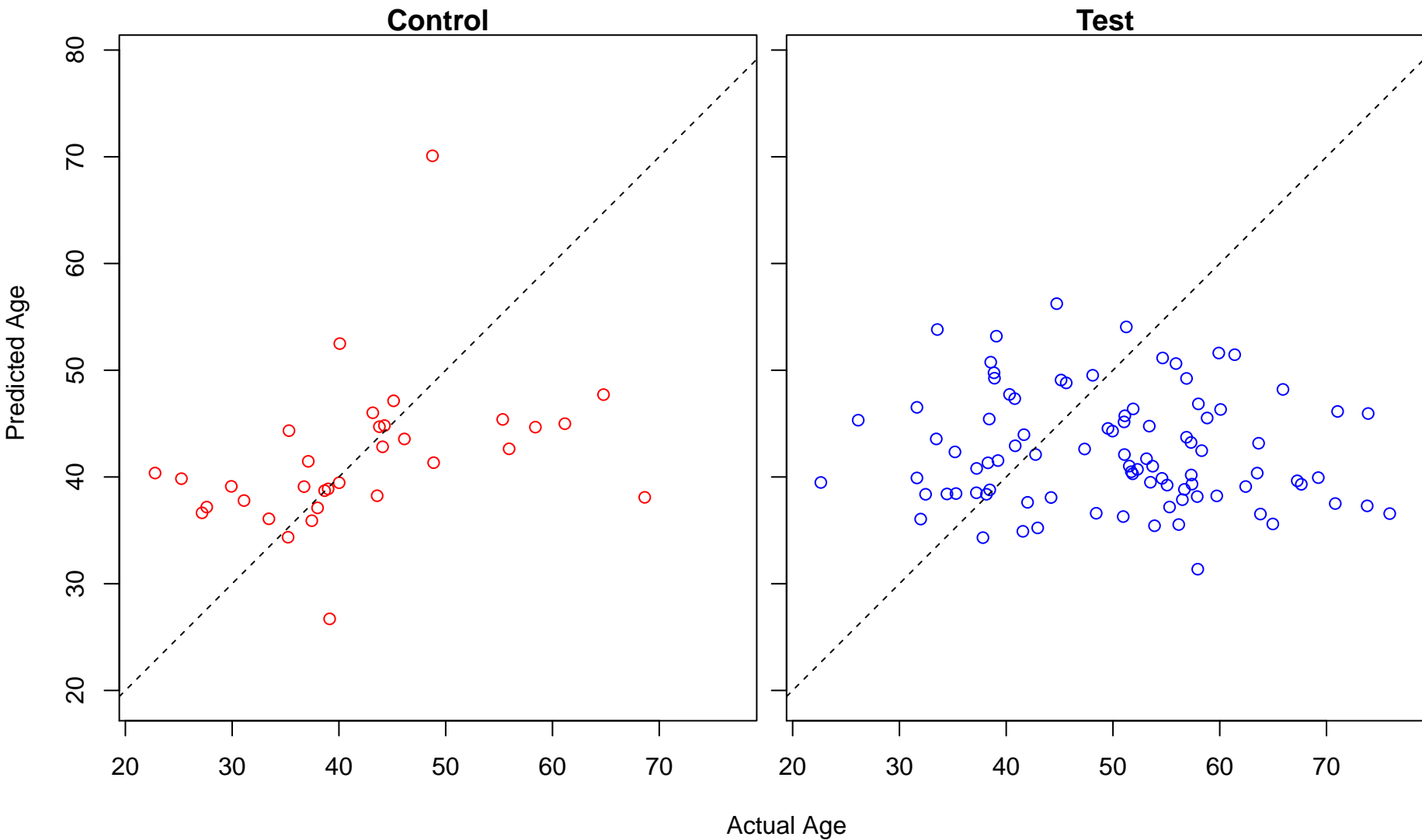
response to organic cyclic compound (Score: 0.591484)



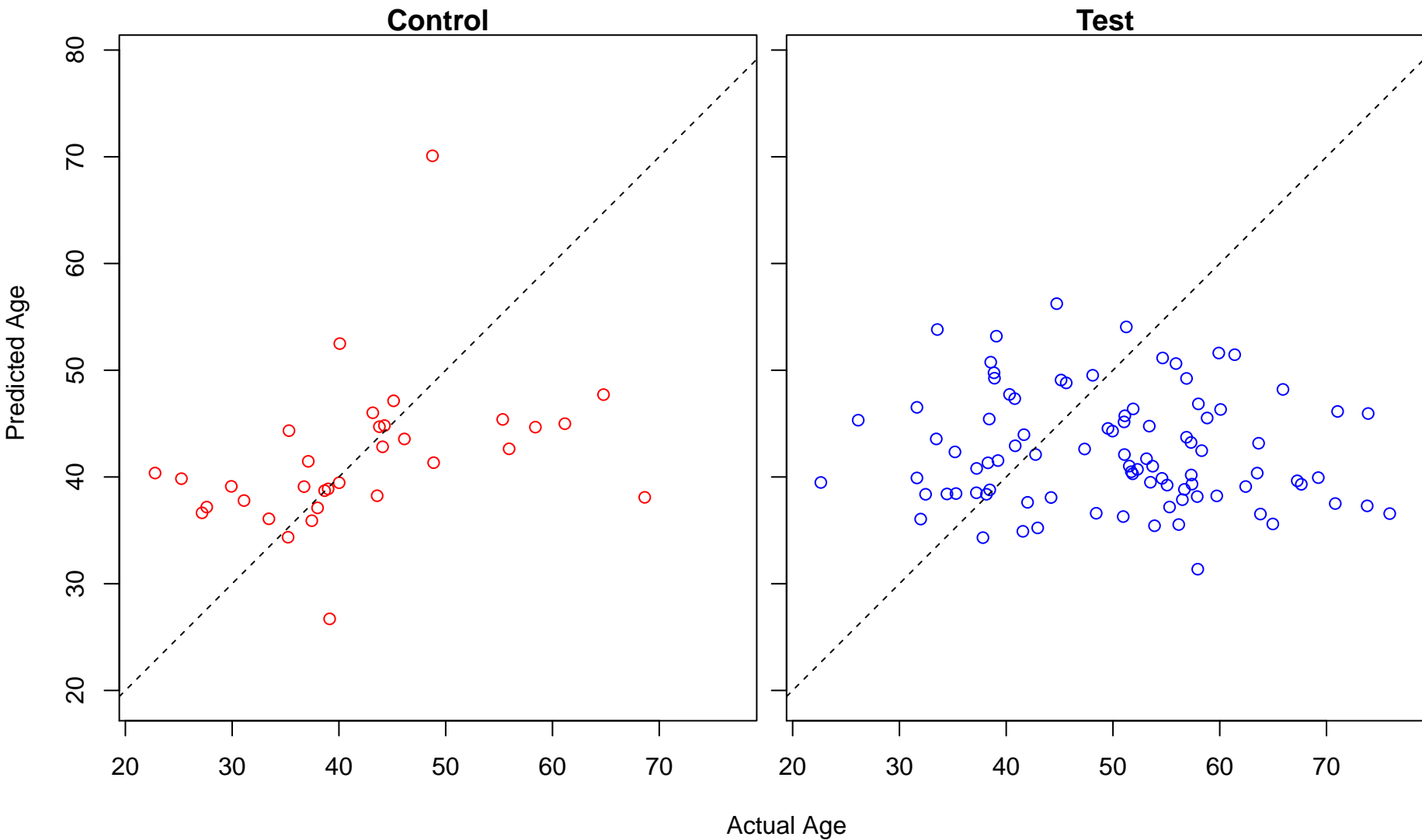
positive regulation of early endosome to late endosome transport (Score: 0.591292)



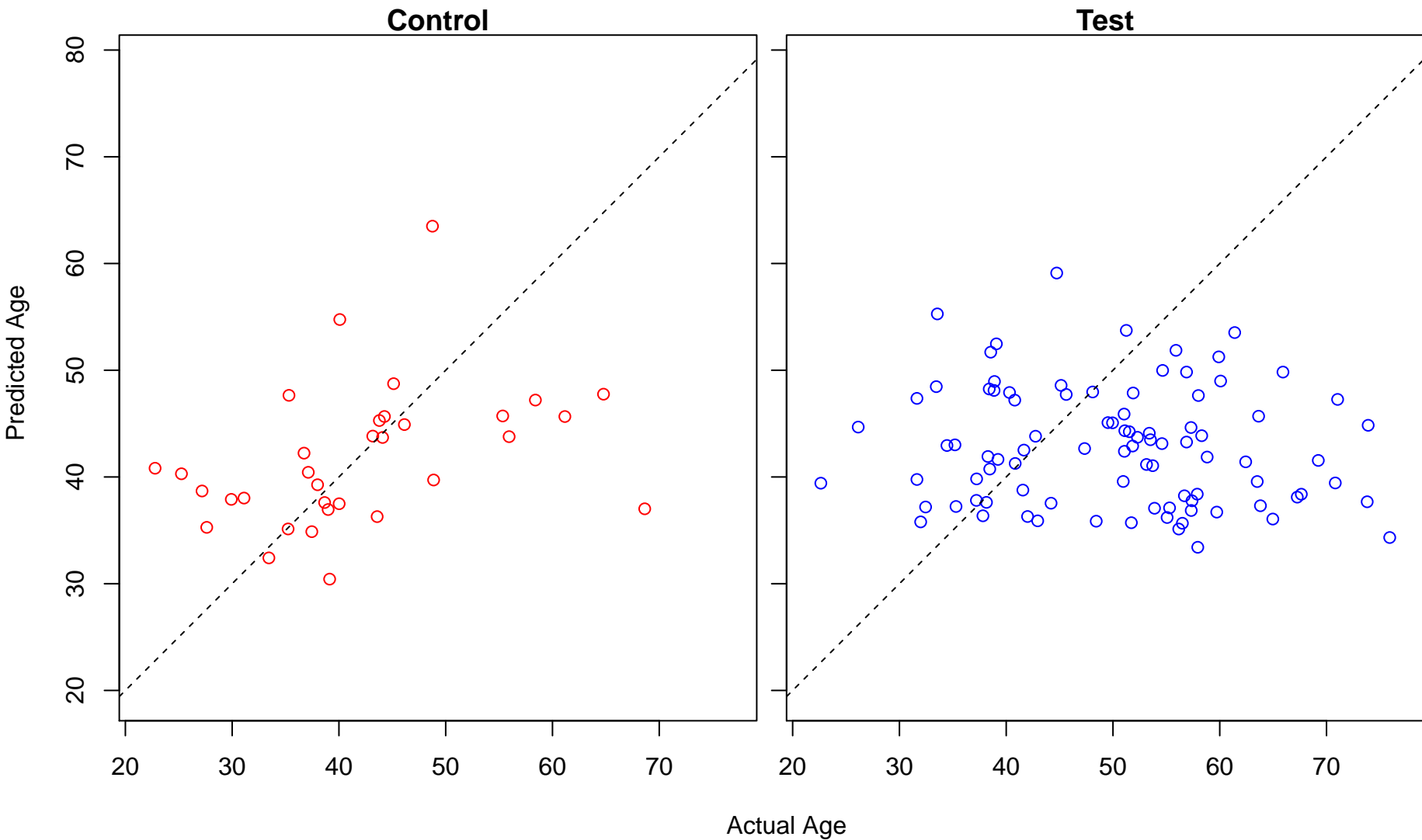
cellular protein modification process (Score: 0.591247)



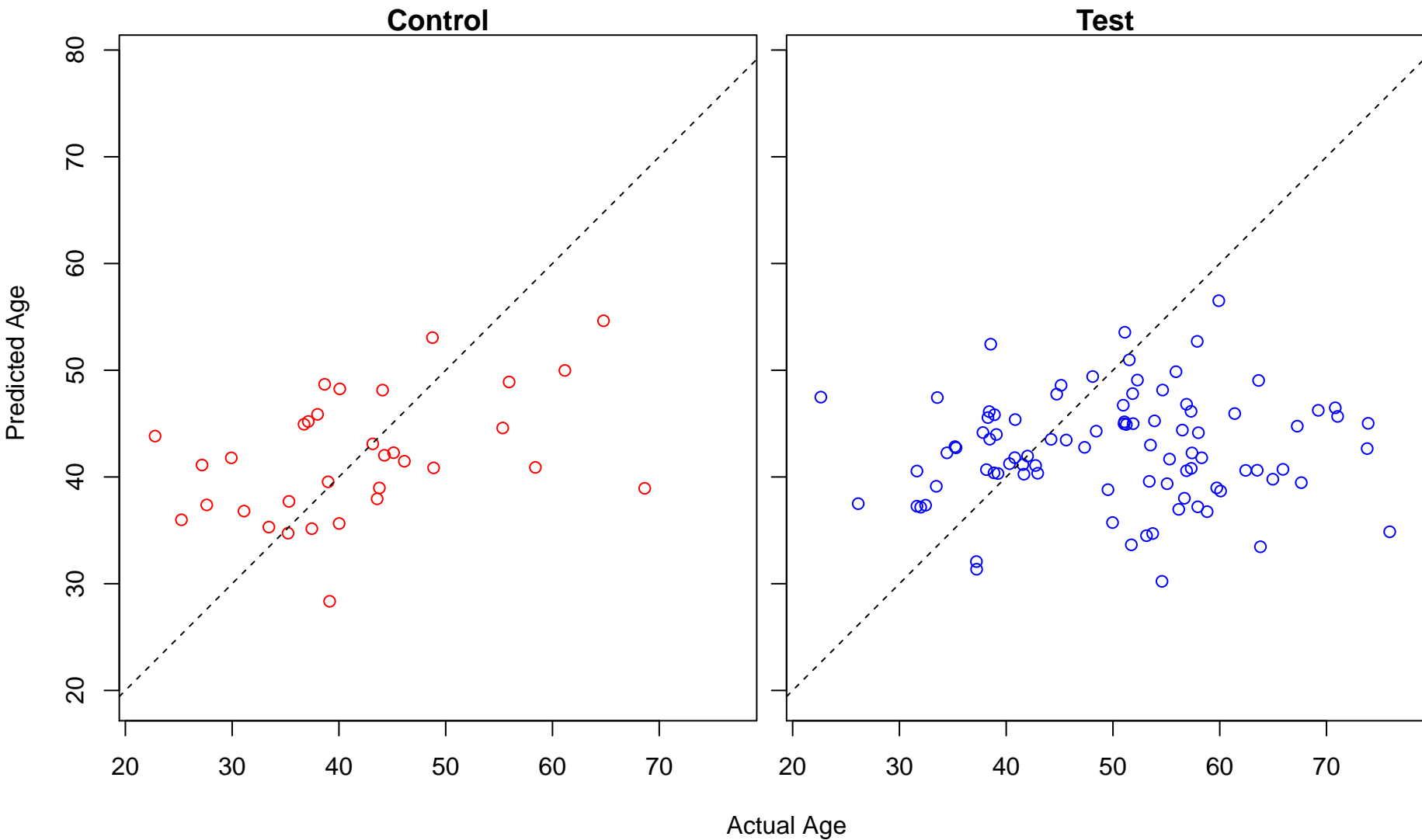
protein modification process (Score: 0.591247)



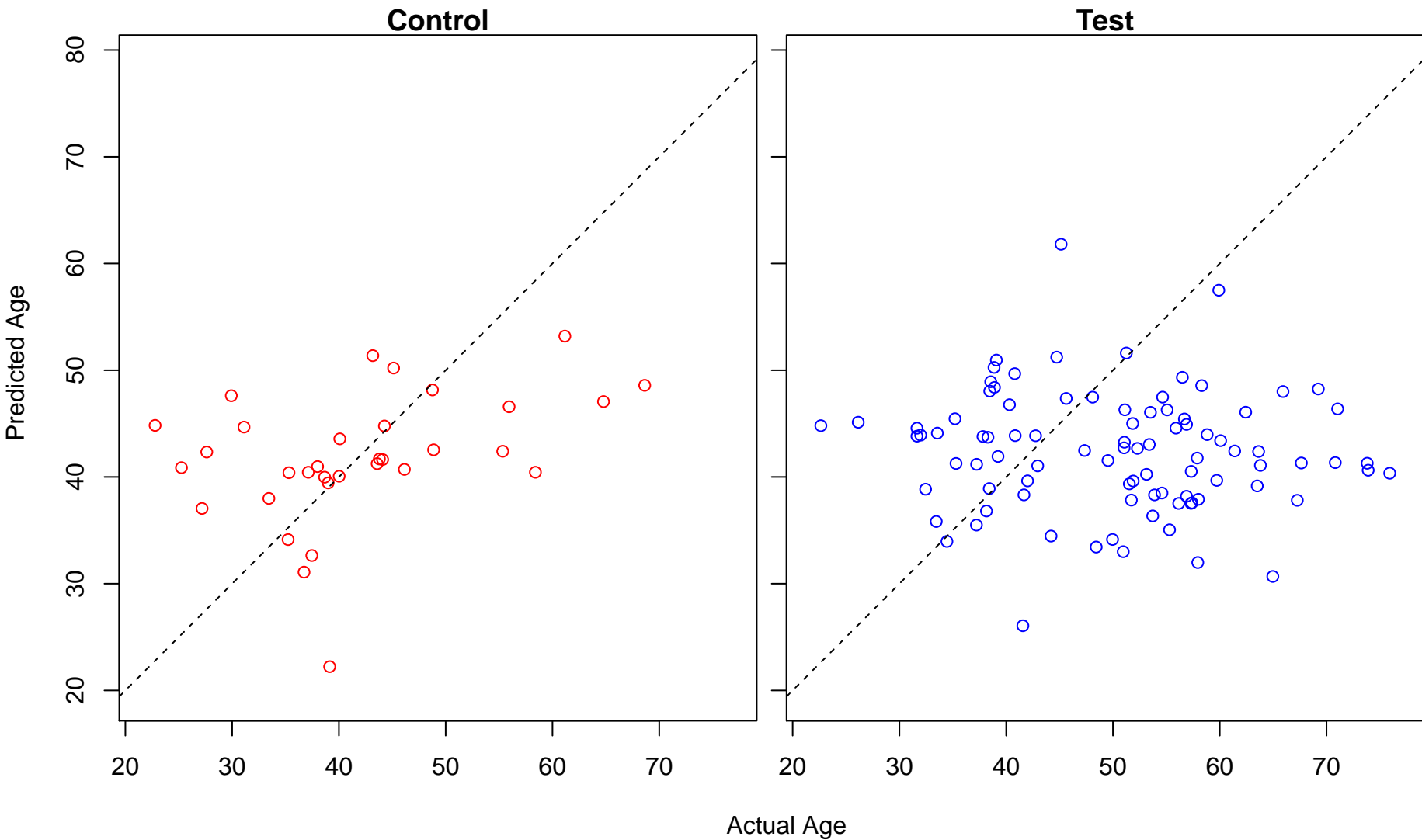
mitochondrion organization (Score: 0.591053)



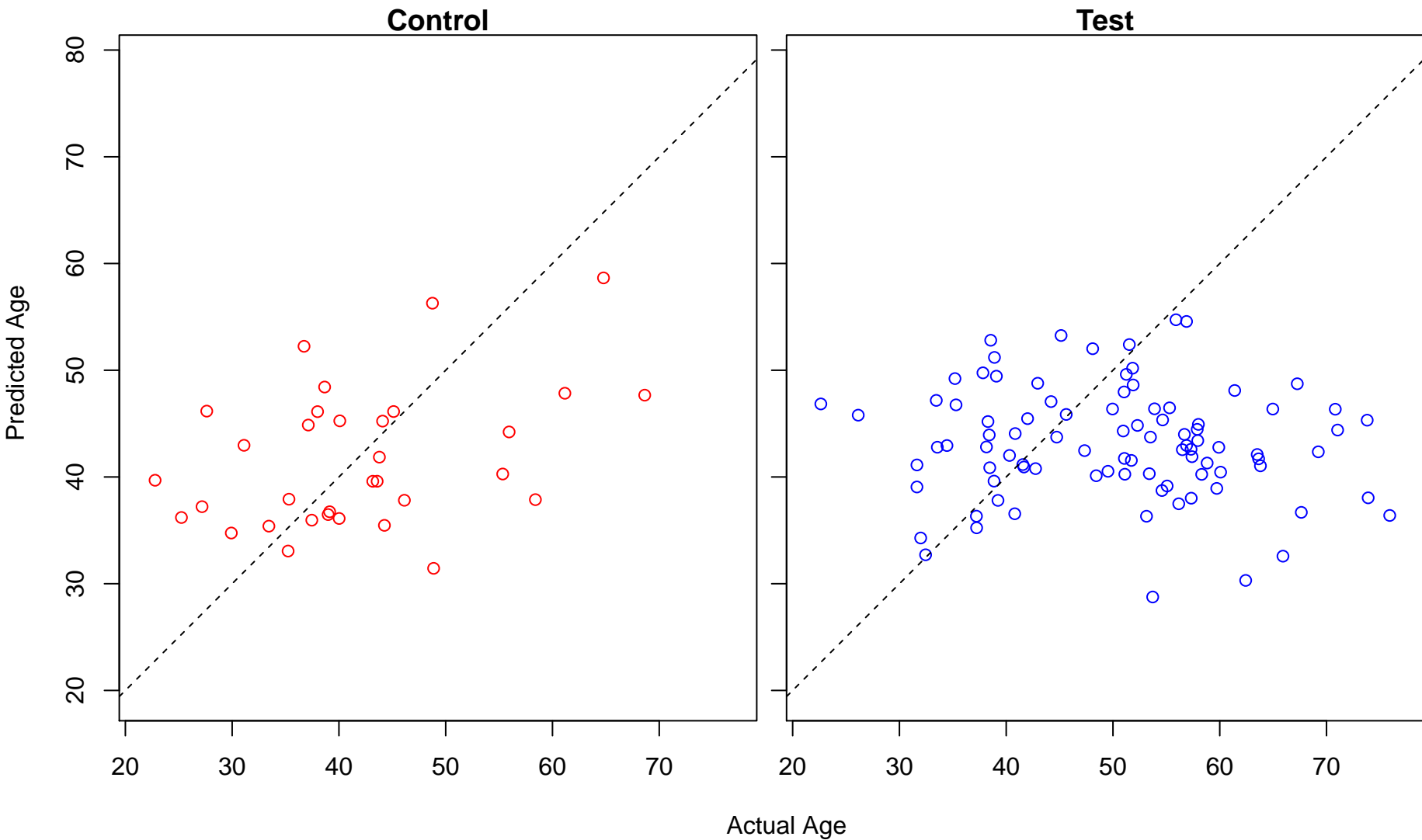
phagosome maturation (Score: 0.590850)



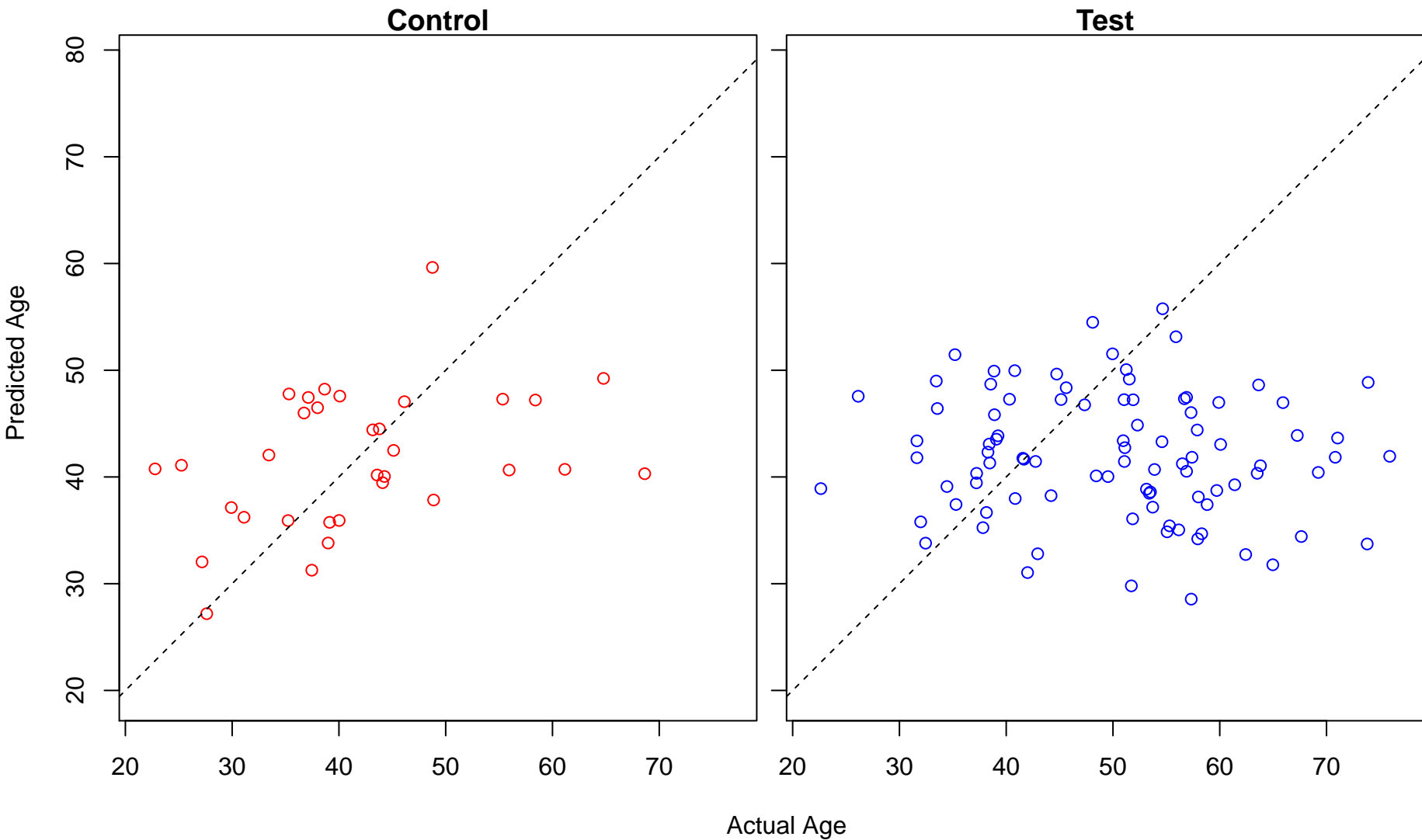
axonemal dynein complex assembly (Score: 0.590799)



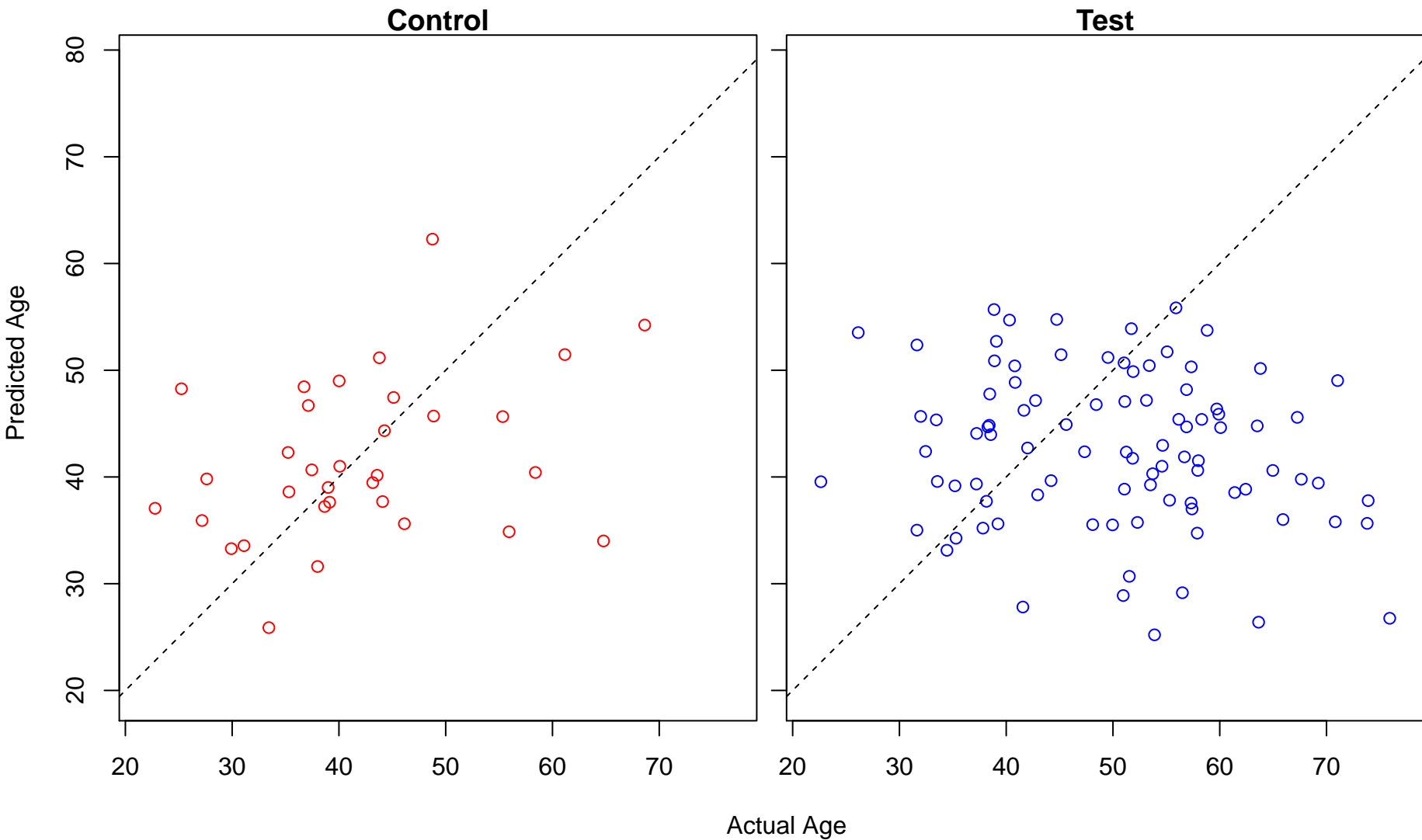
rRNA transport (Score: 0.590753)



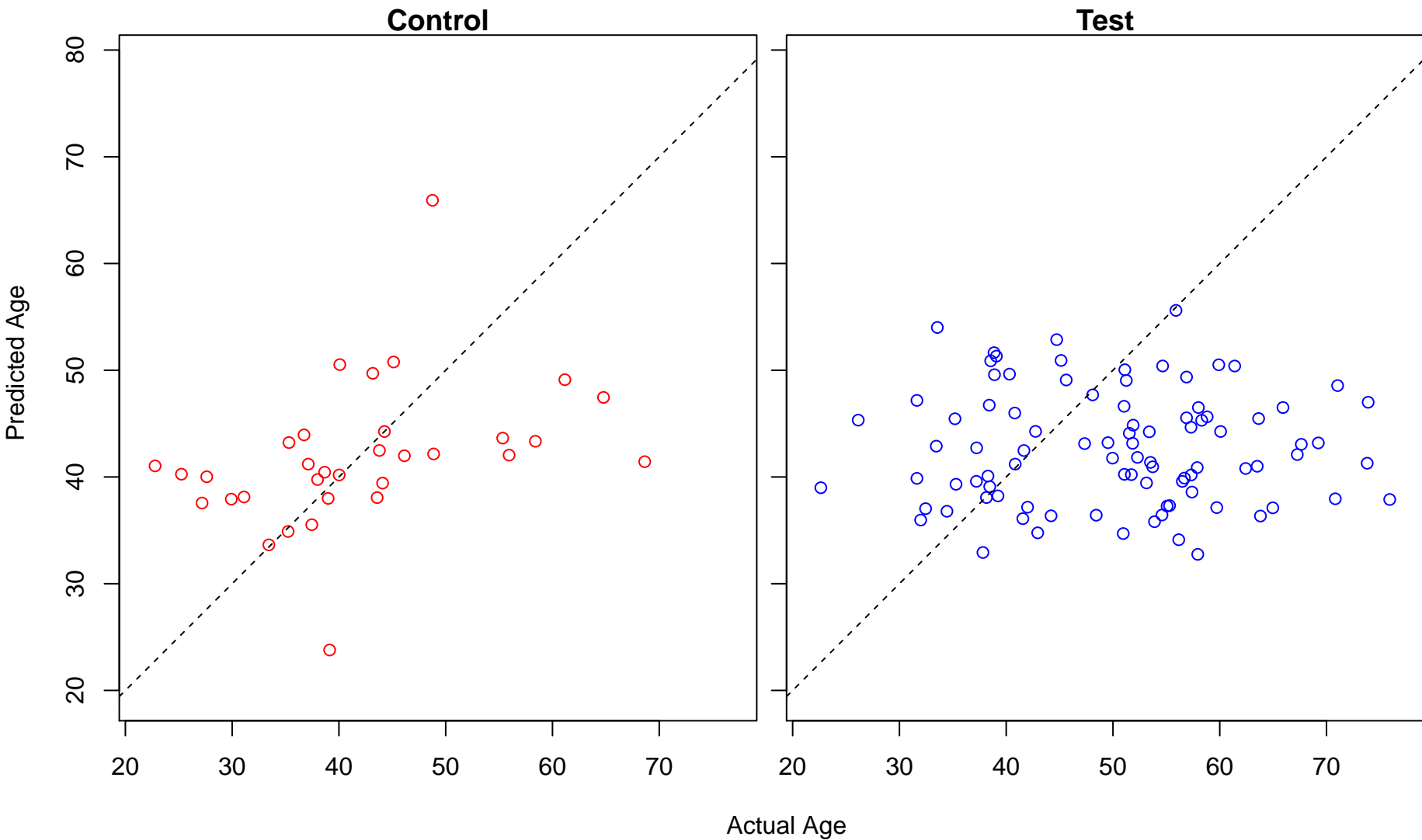
regulation of cell adhesion mediated by integrin (Score: 0.590164)



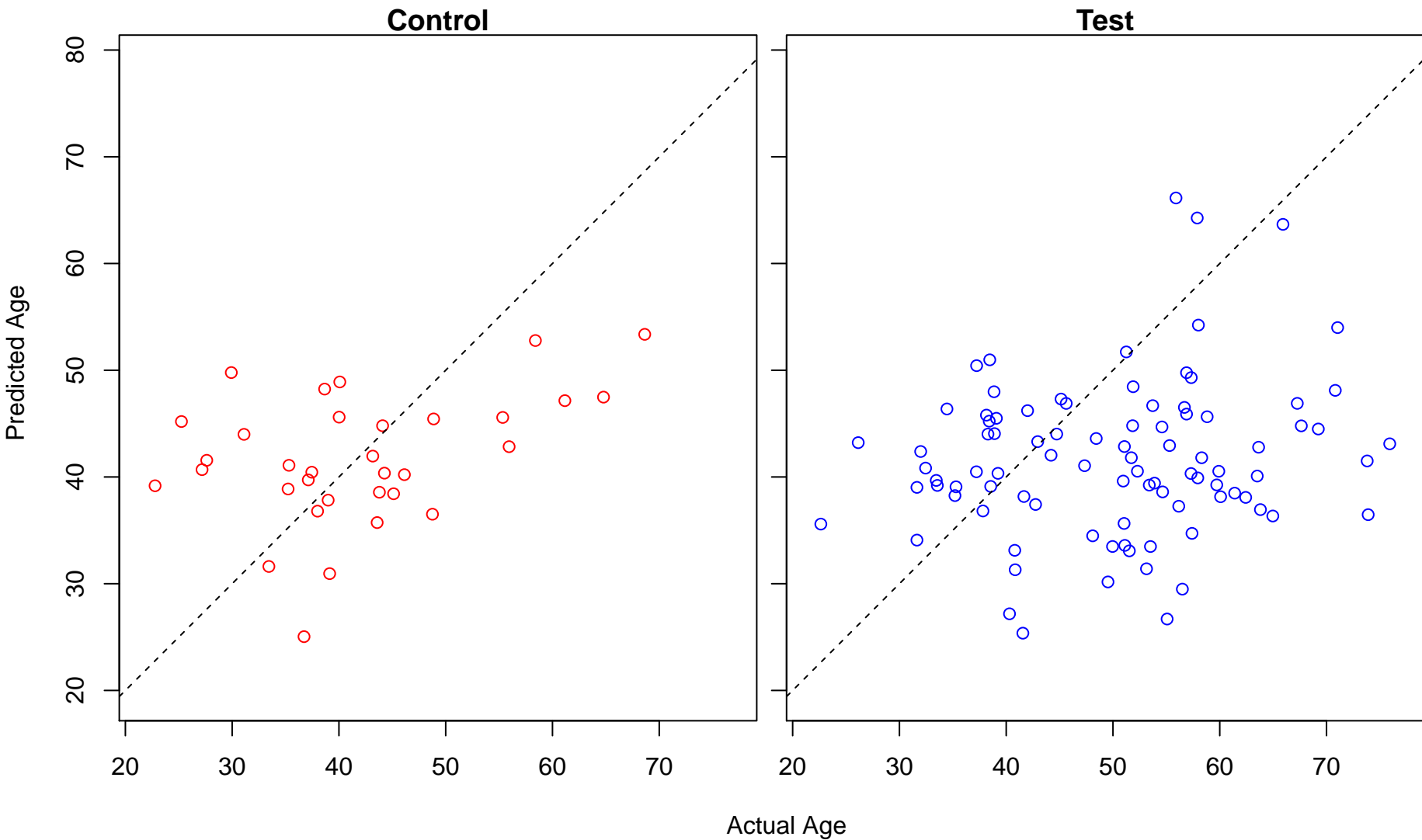
protein localization to kinetochore (Score: 0.589287)



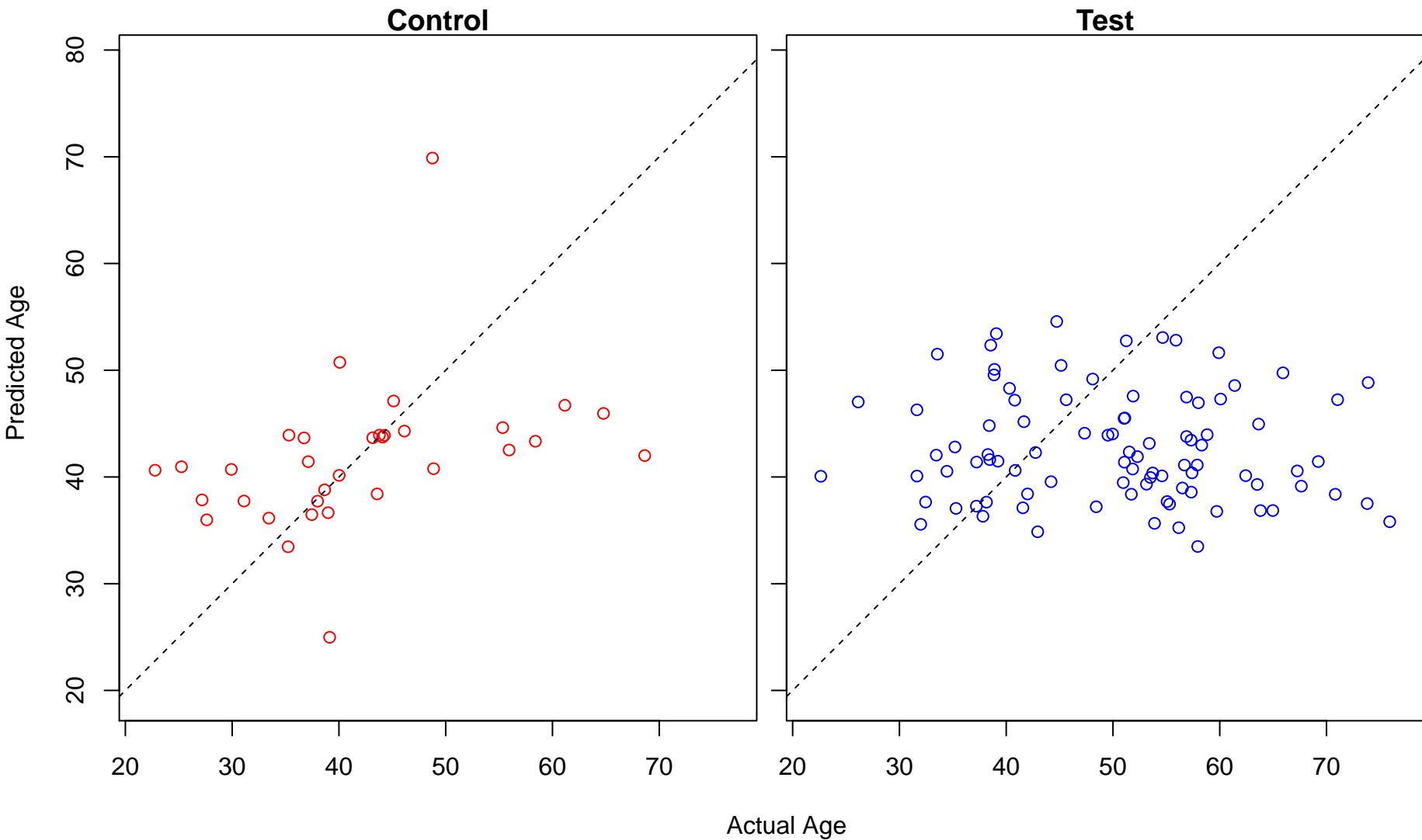
cell migration (Score: 0.588929)



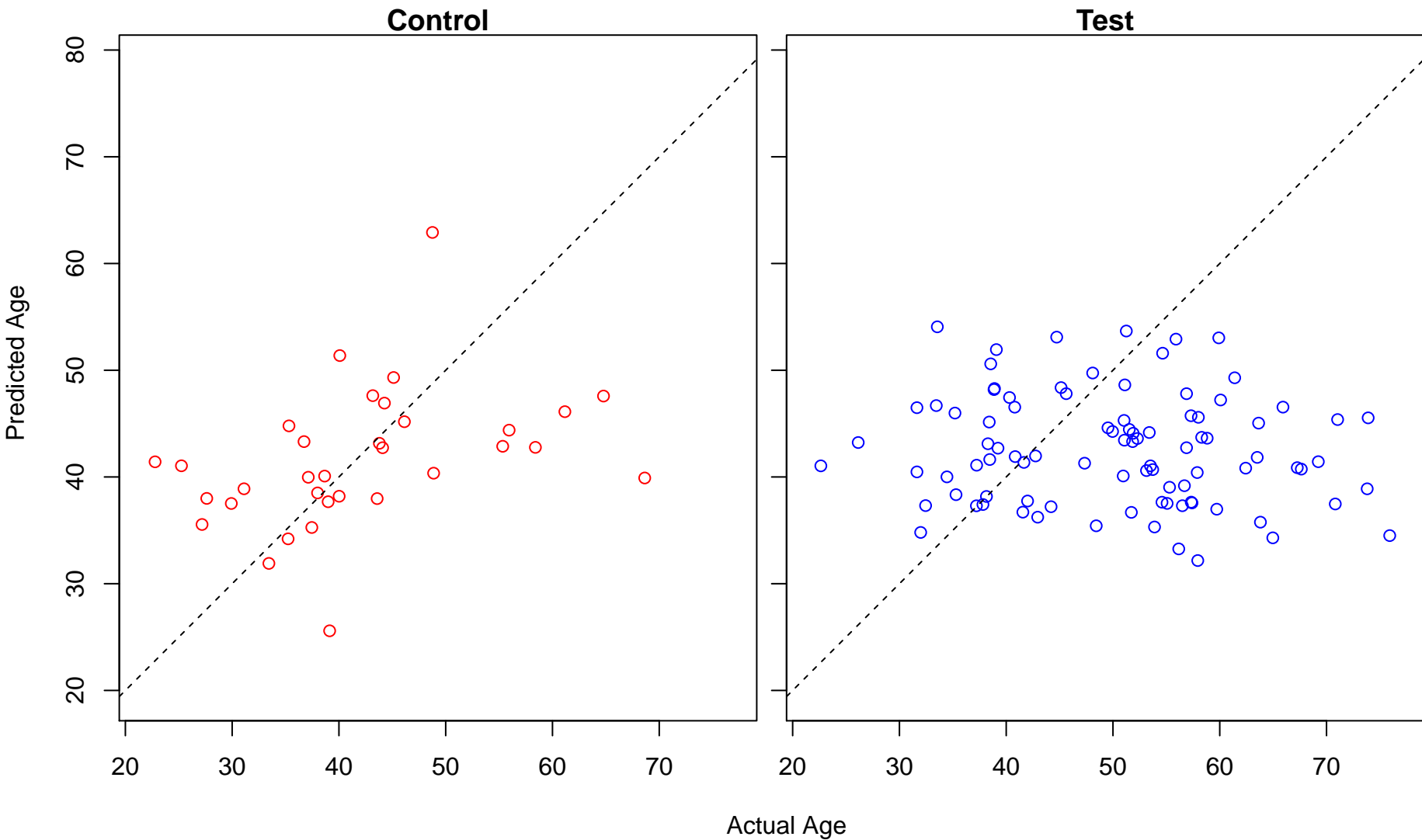
cell proliferation involved in metanephros development (Score: 0.588704)



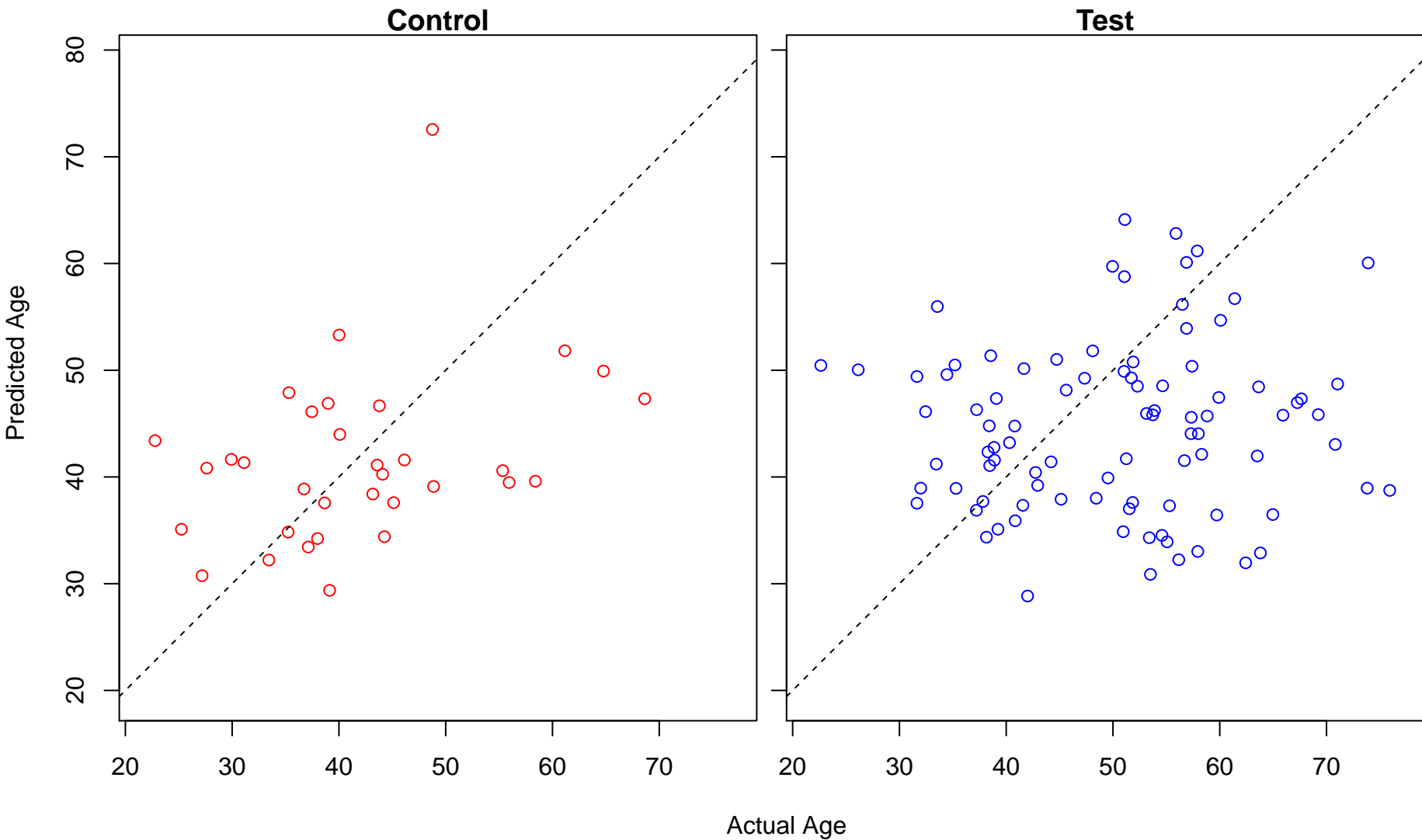
immune system process (Score: 0.588036)



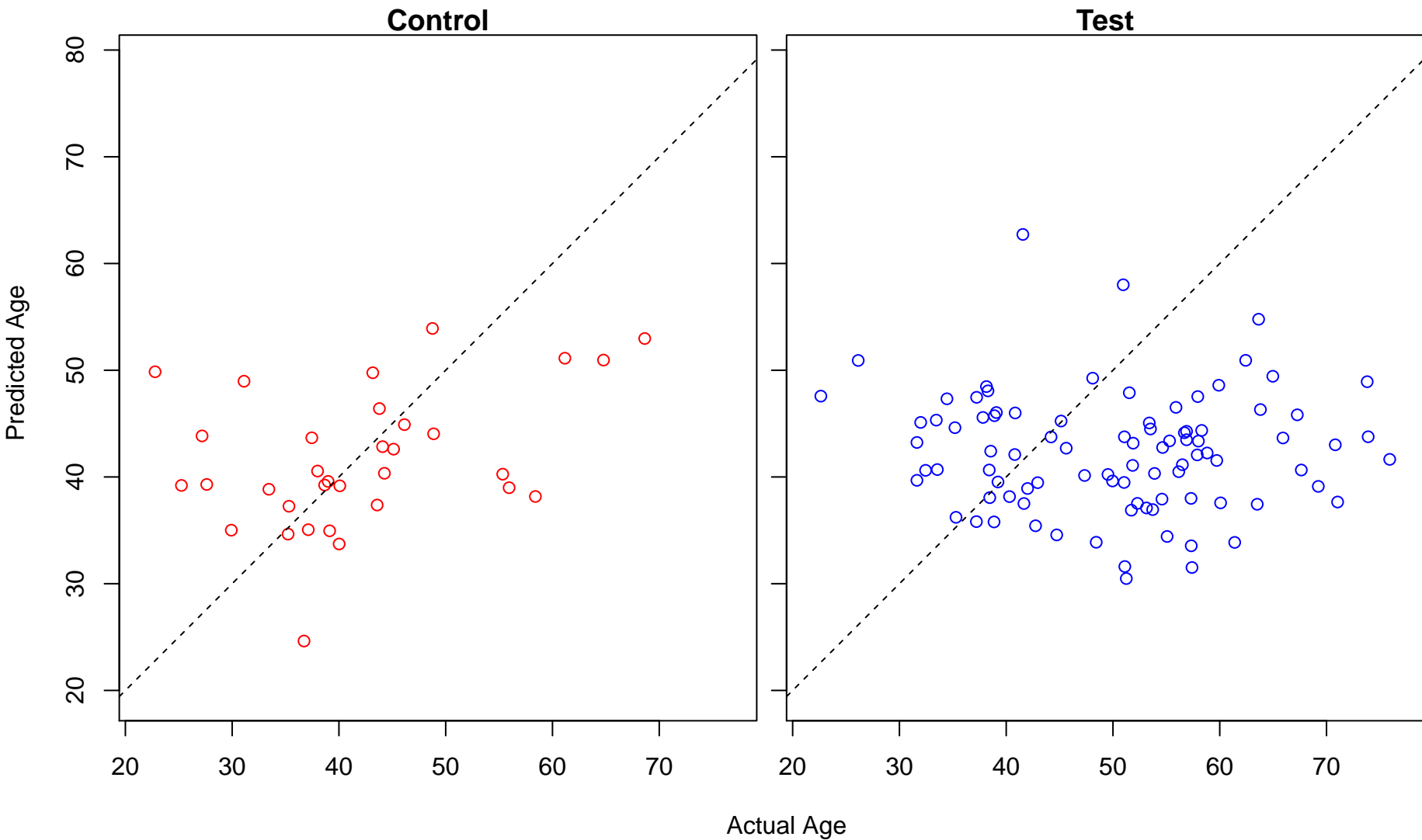
carboxylic acid metabolic process (Score: 0.587941)



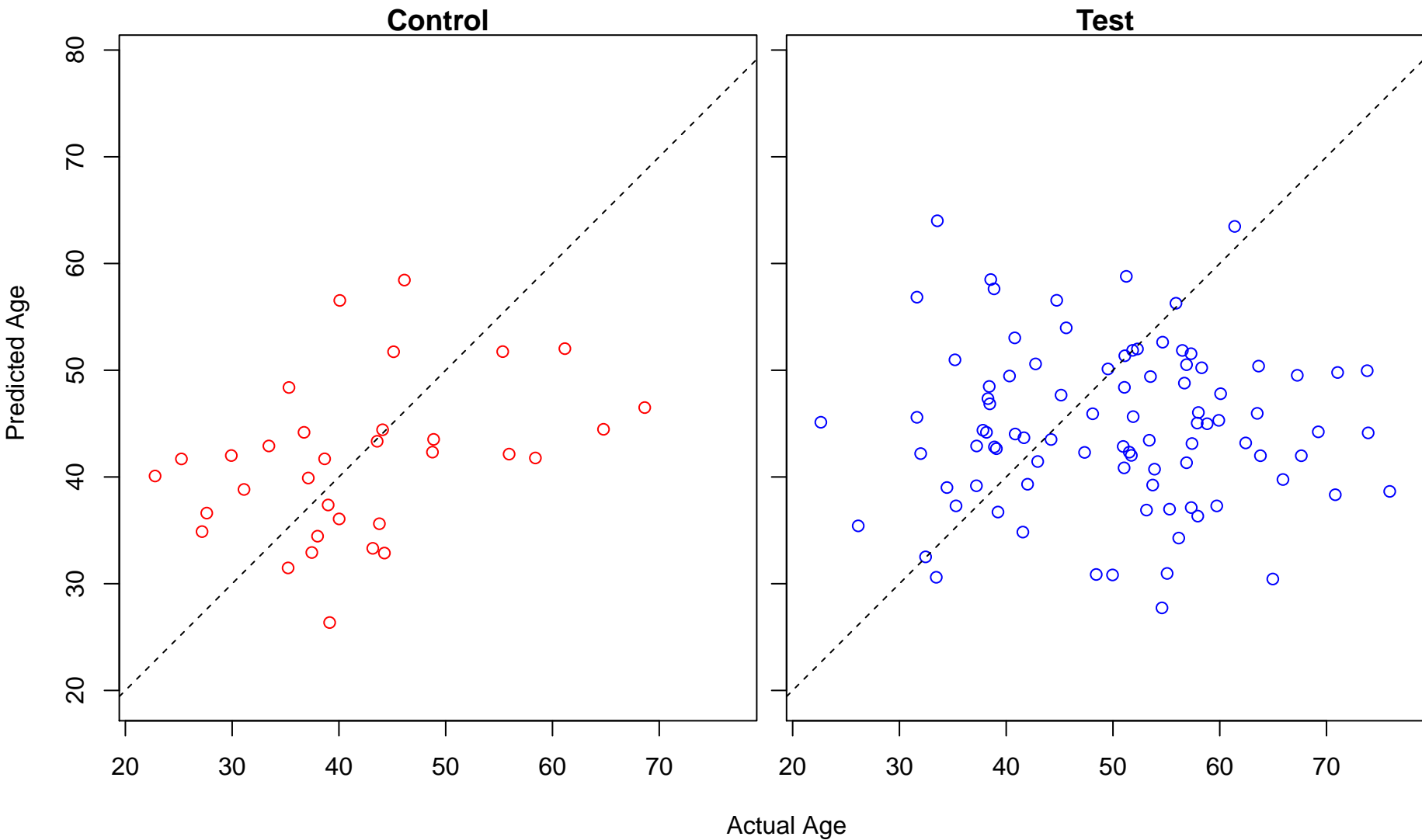
dermatan sulfate biosynthetic process (Score: 0.587934)



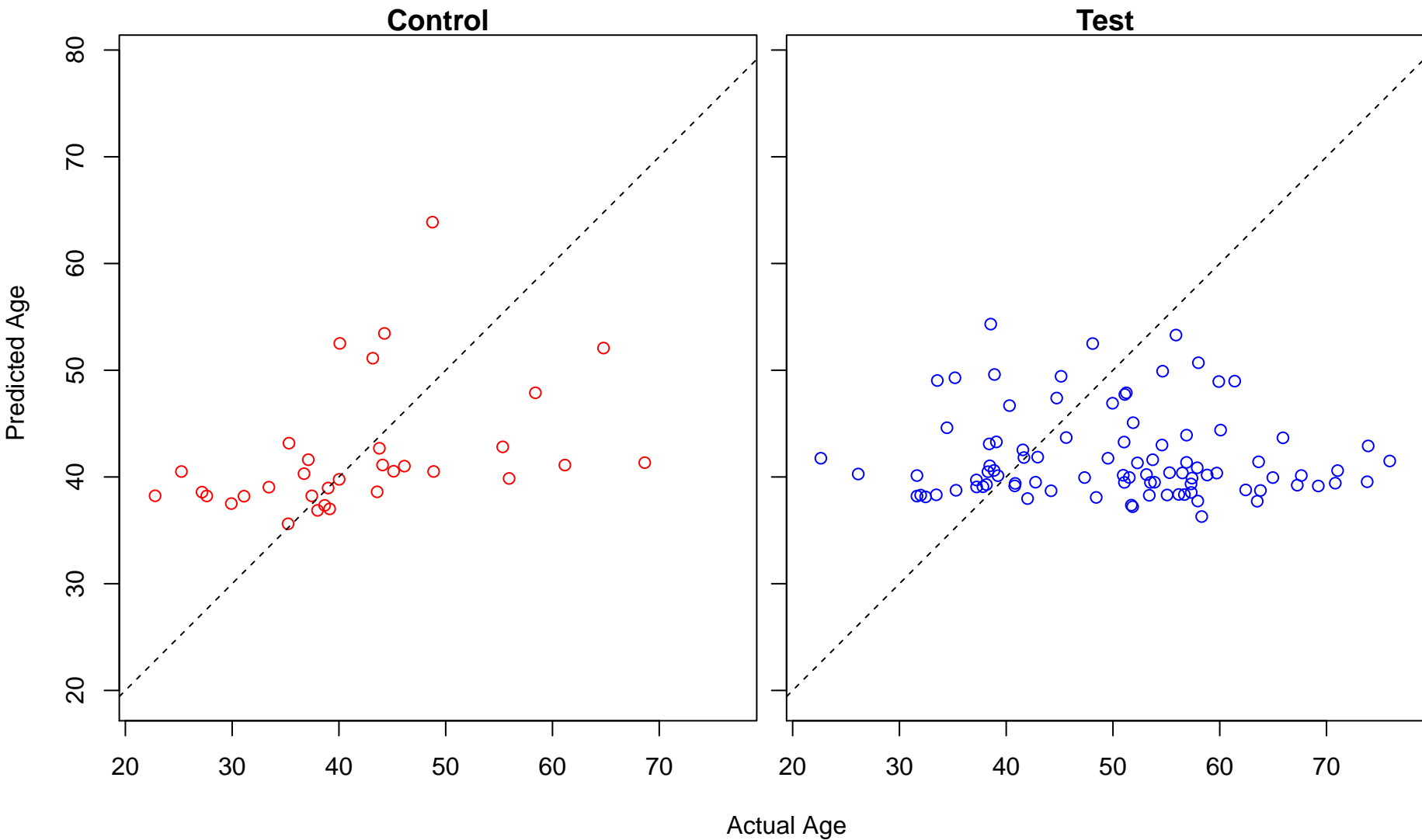
protein heterotrimerization (Score: 0.587510)



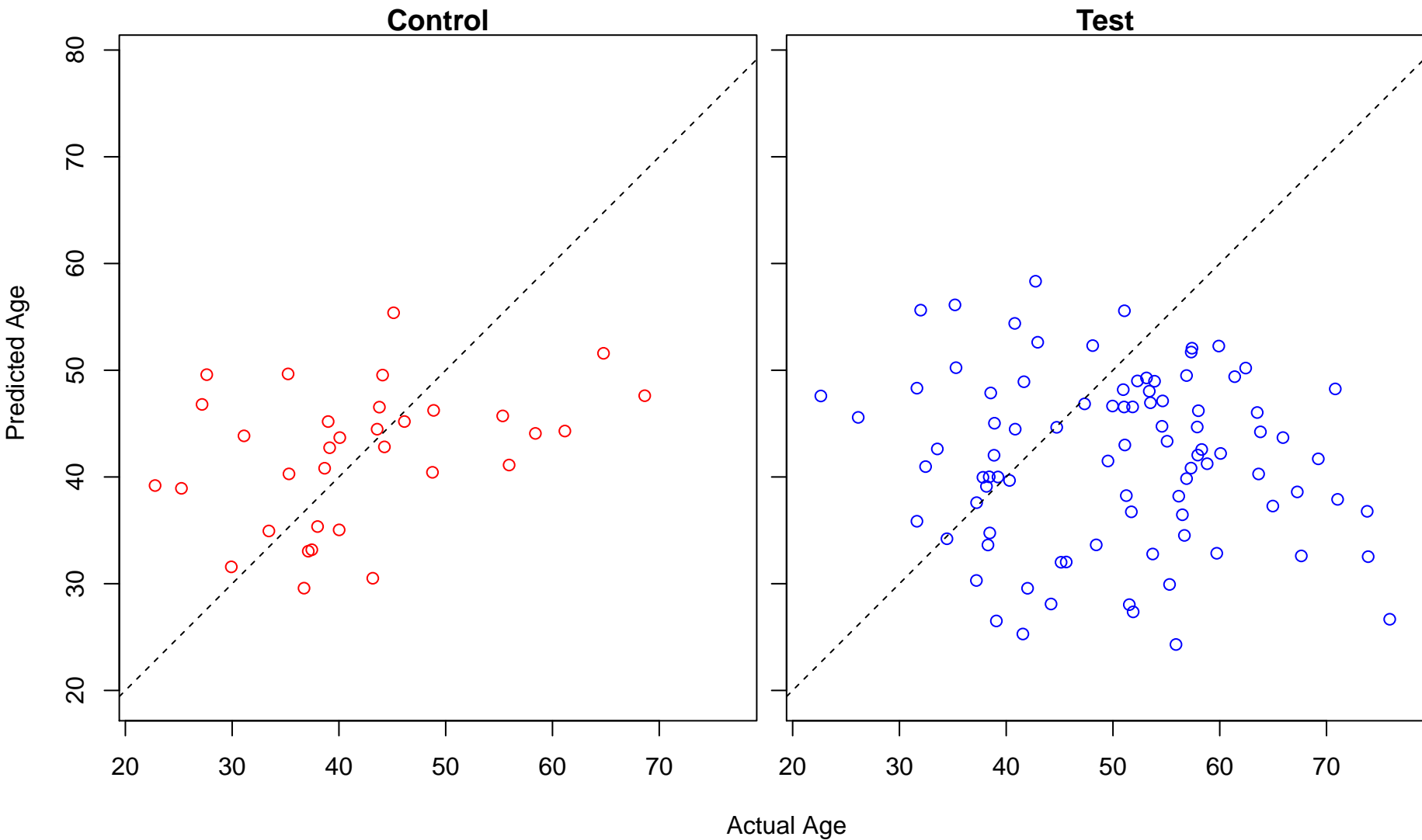
regulation of cholesterol homeostasis (Score: 0.587147)



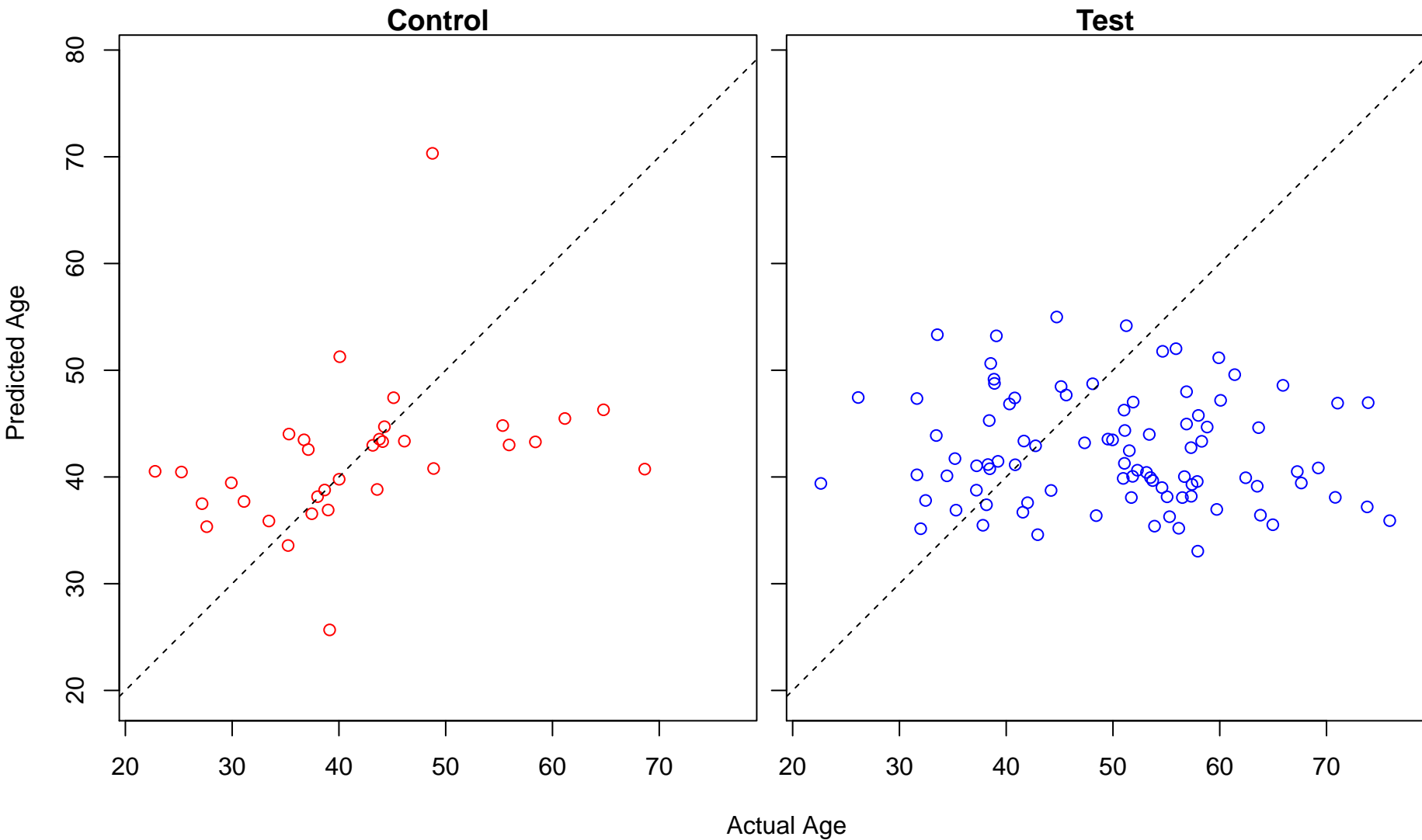
histone H3-K36 methylation (Score: 0.587014)



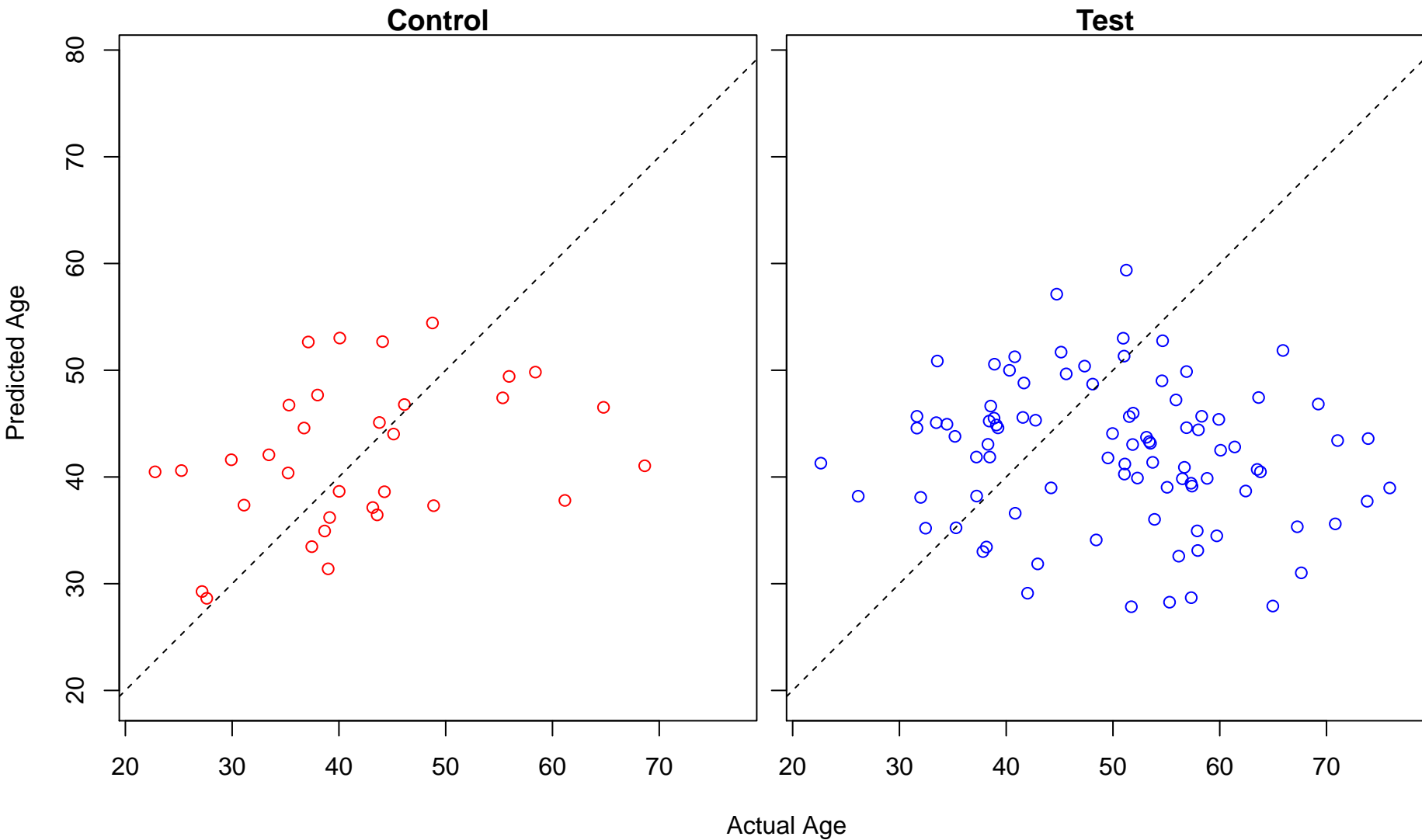
bundle of His cell to Purkinje myocyte communication (Score: 0.586446)



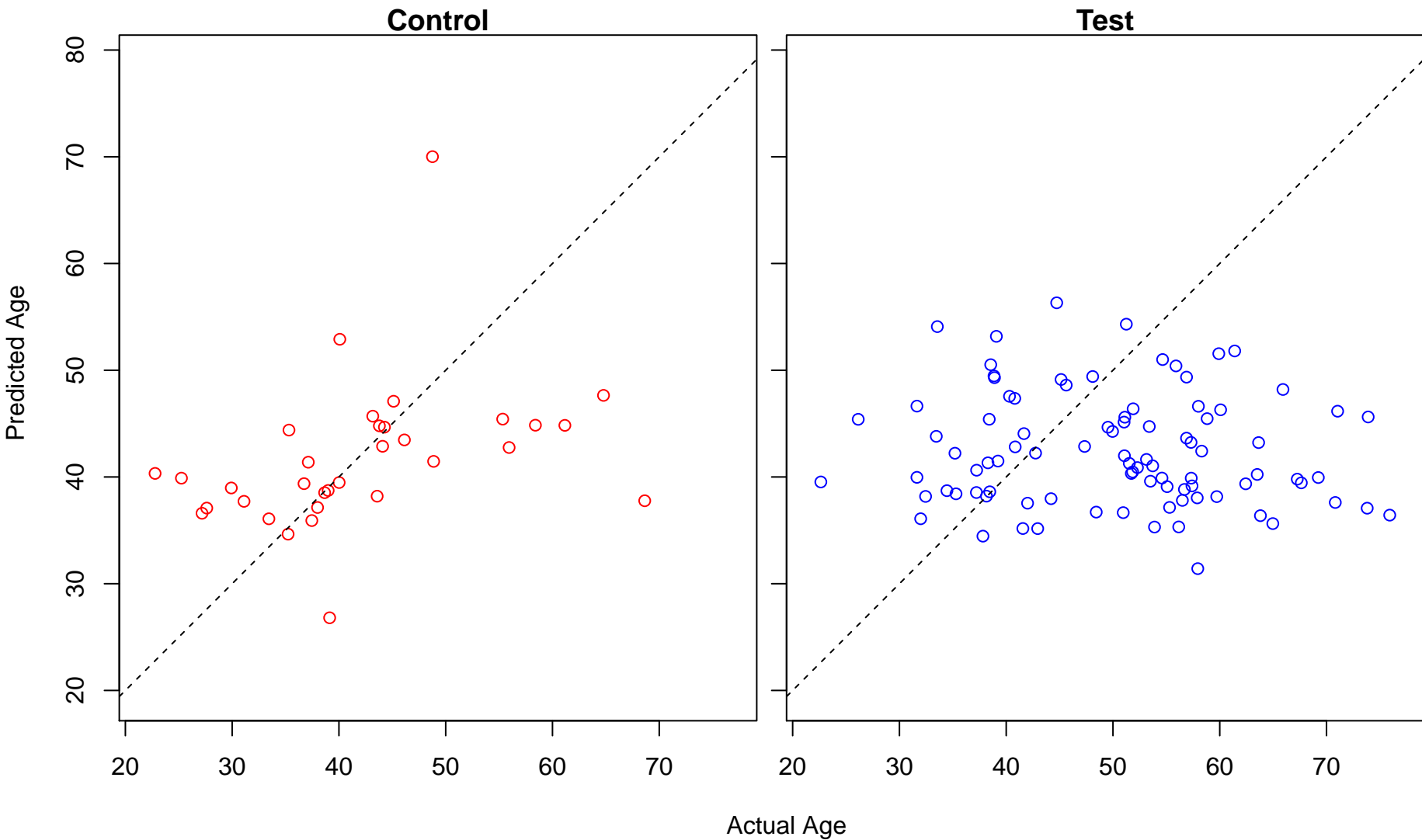
response to stress (Score: 0.586430)



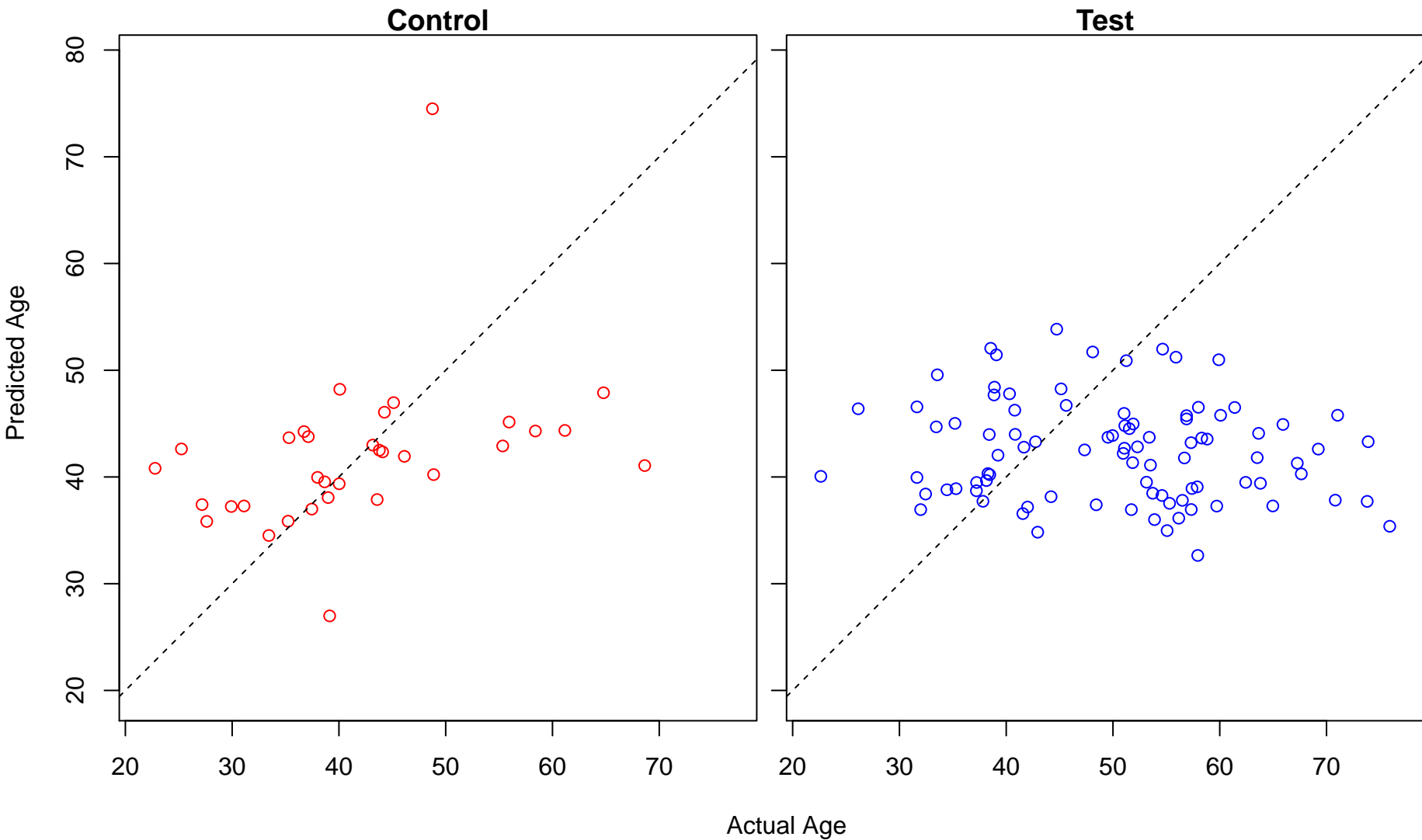
negative regulation of protein polymerization (Score: 0.586084)



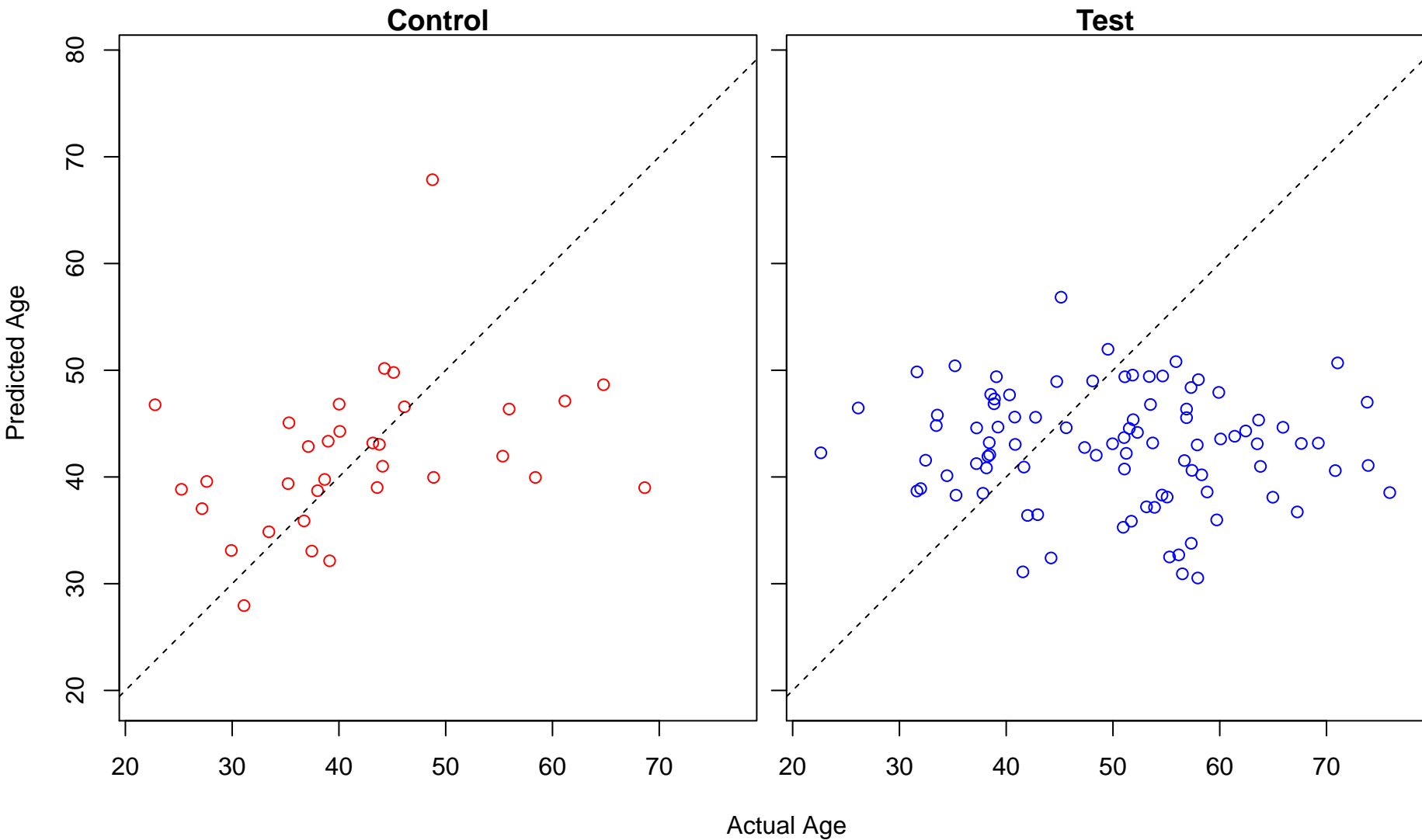
macromolecule modification (Score: 0.585513)



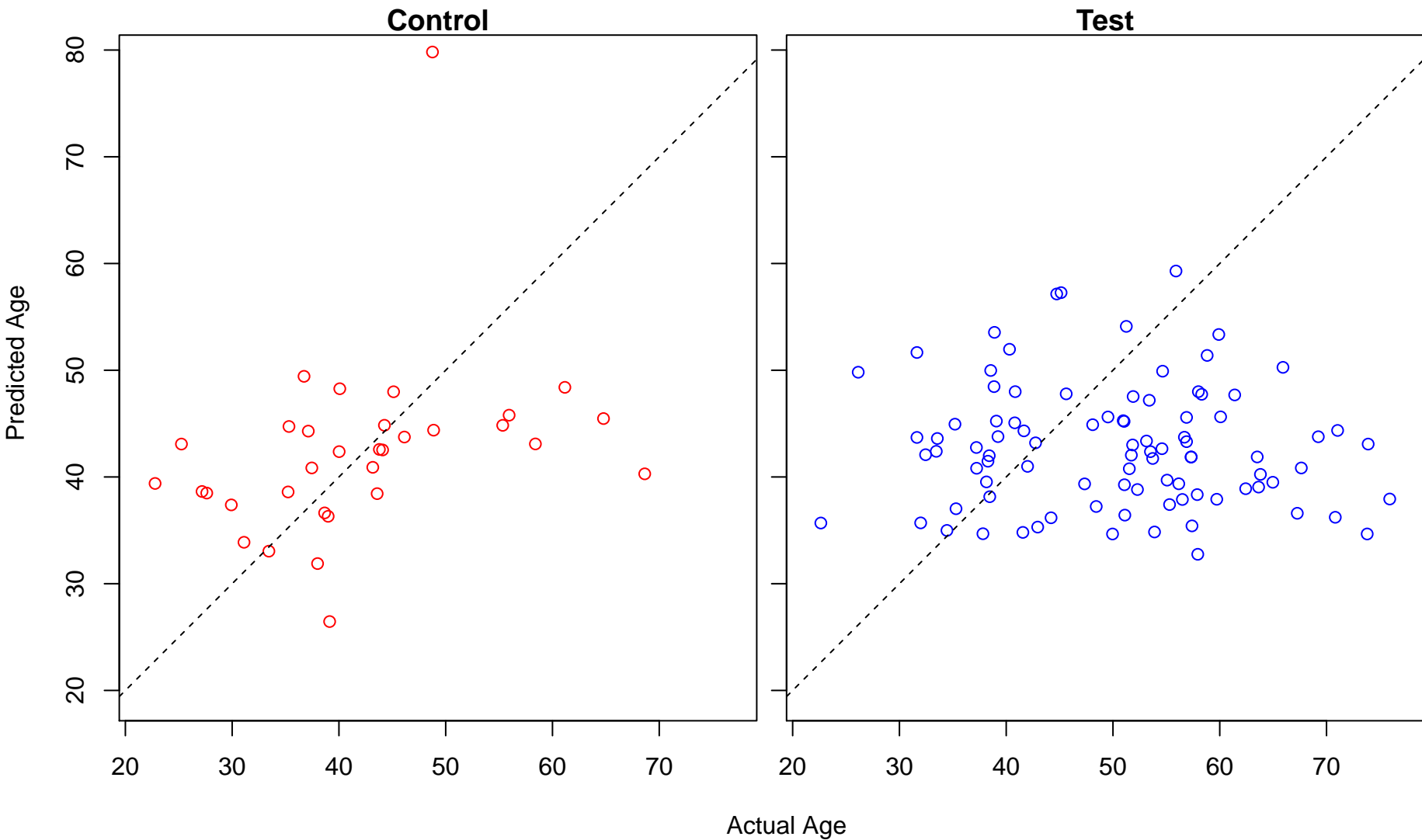
establishment of protein localization (Score: 0.585481)



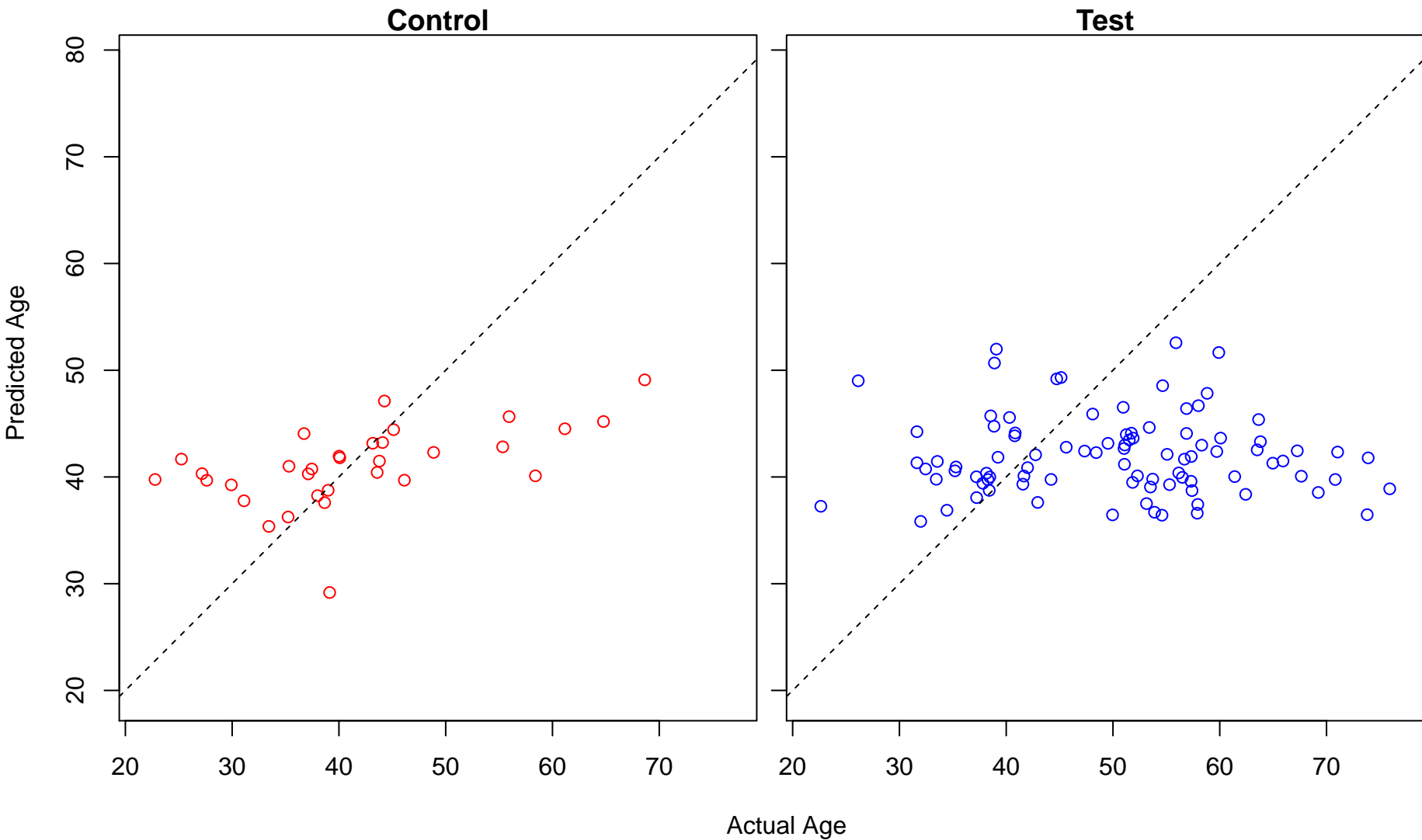
S-adenosylmethionine metabolic process (Score: 0.585316)



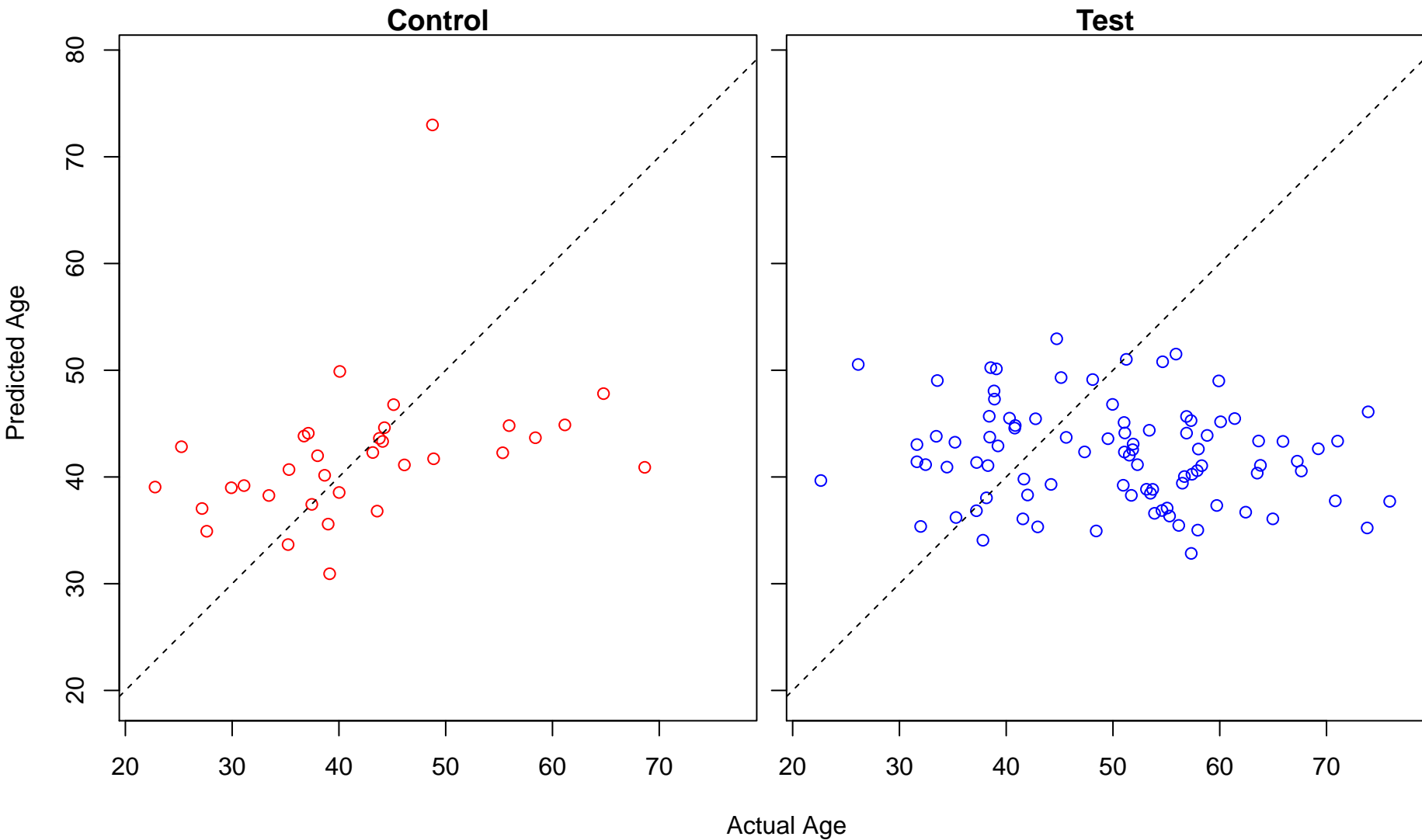
establishment of protein localization to vacuole (Score: 0.585121)



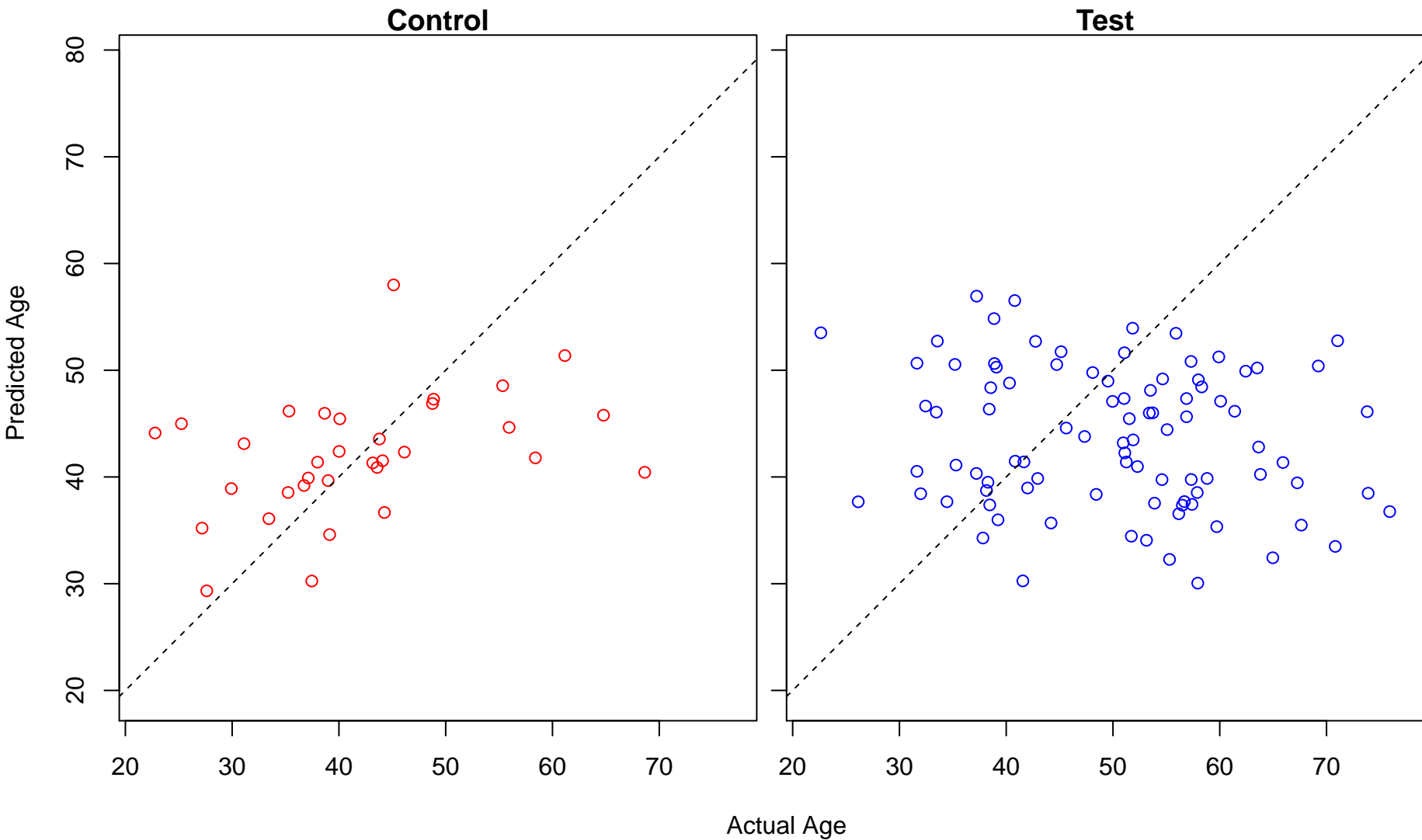
negative regulation of RNA splicing (Score: 0.584863)



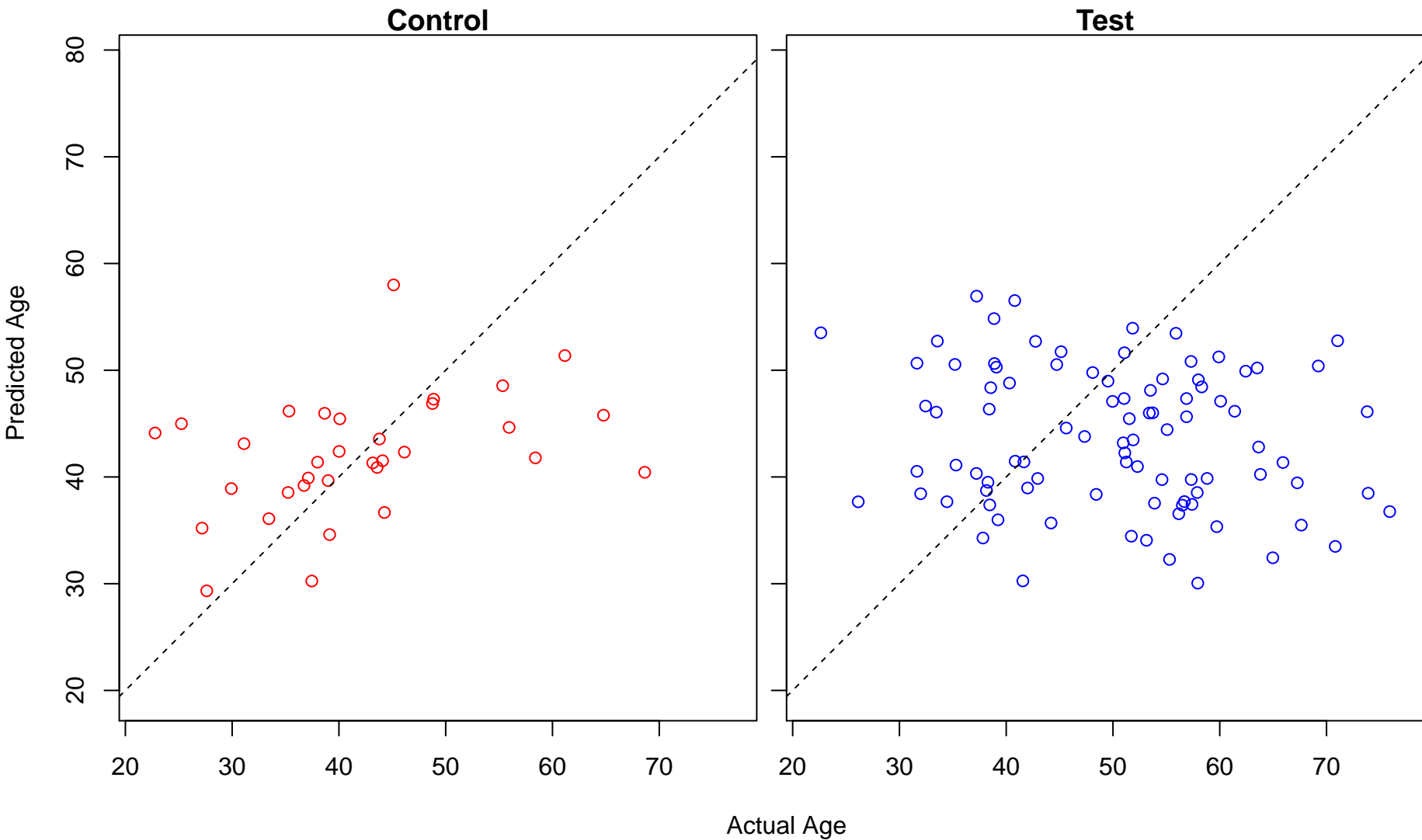
positive regulation of cell differentiation (Score: 0.584484)



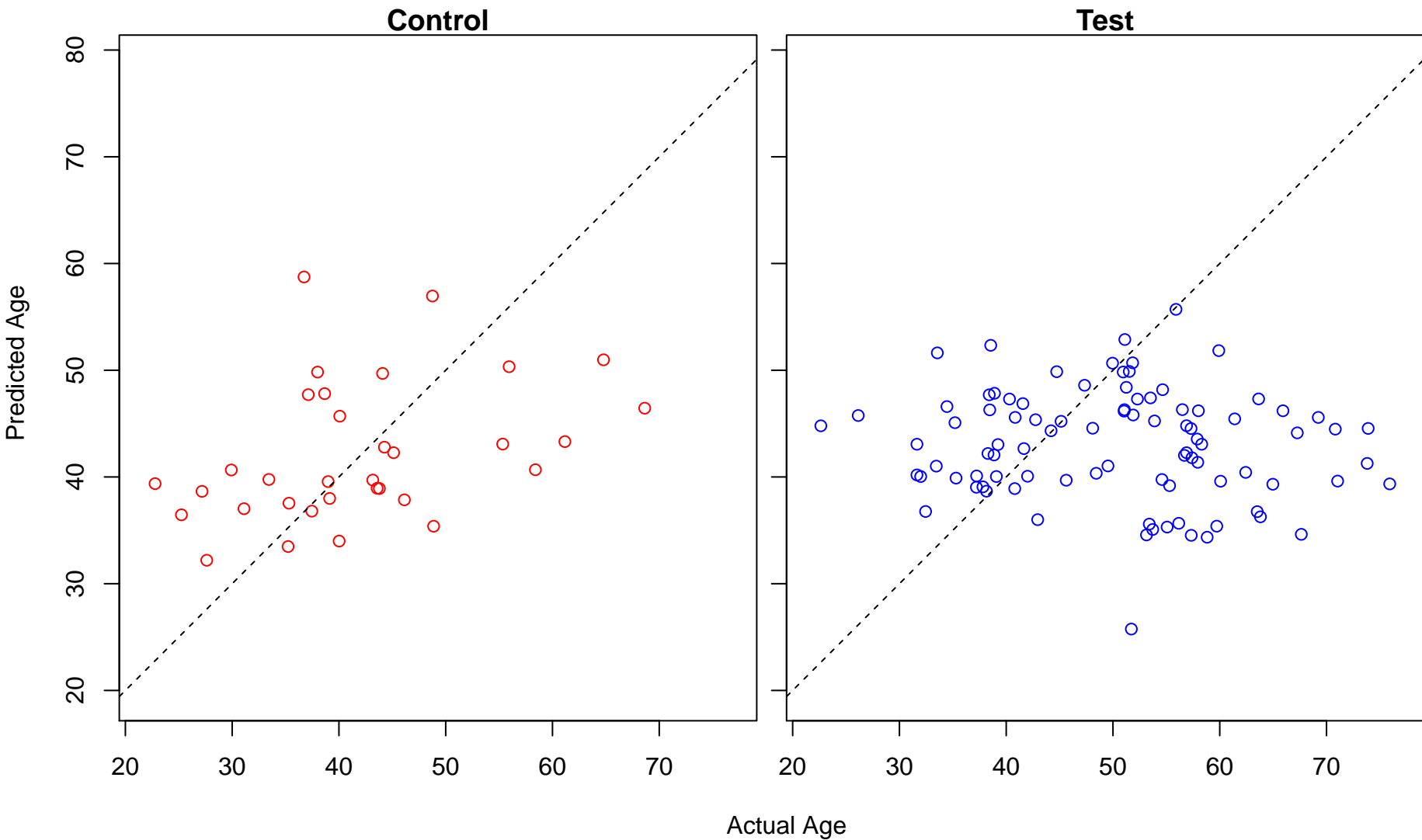
regulation of hematopoietic stem cell migration (Score: 0.584406)



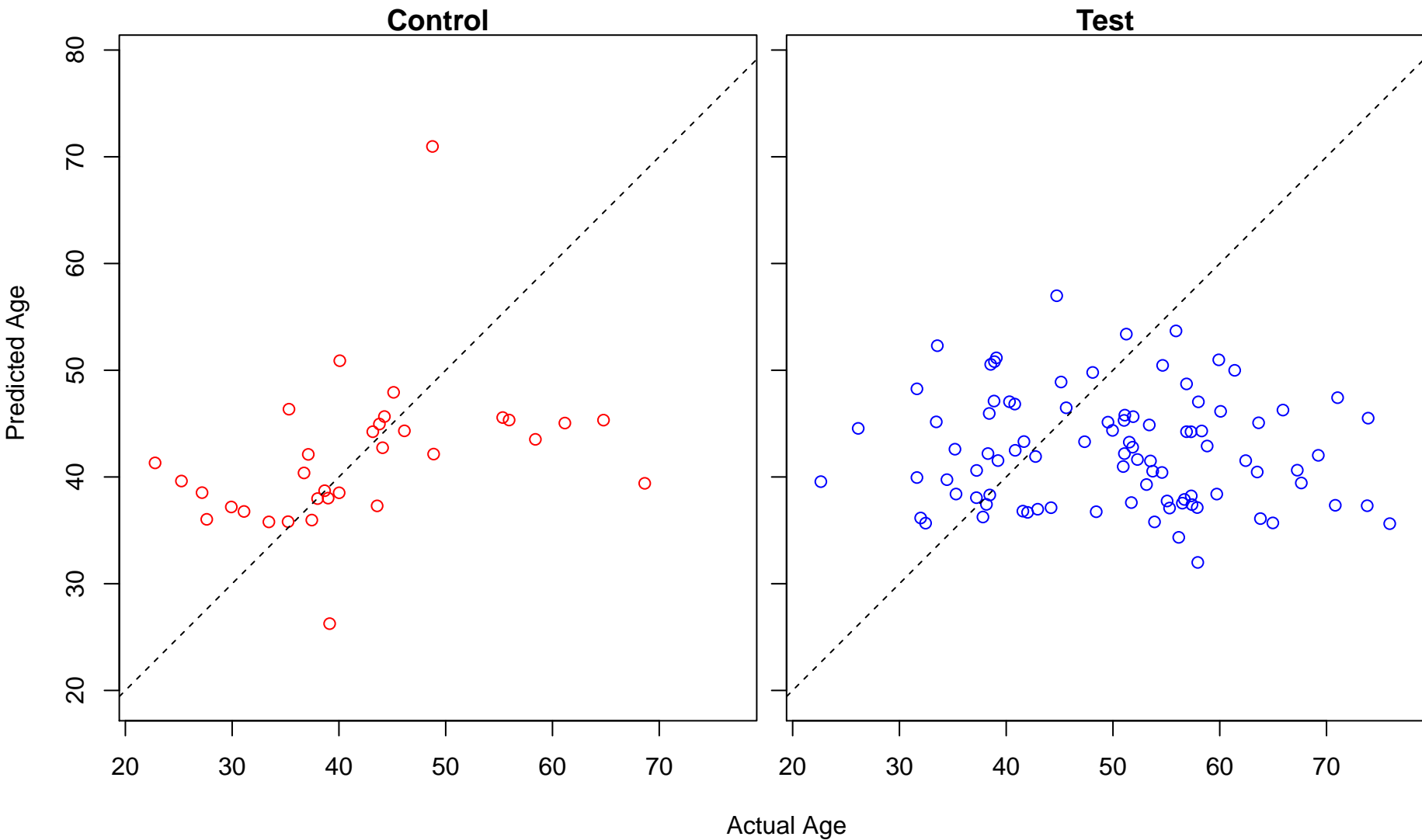
positive regulation of hematopoietic stem cell migration (Score: 0.584406)



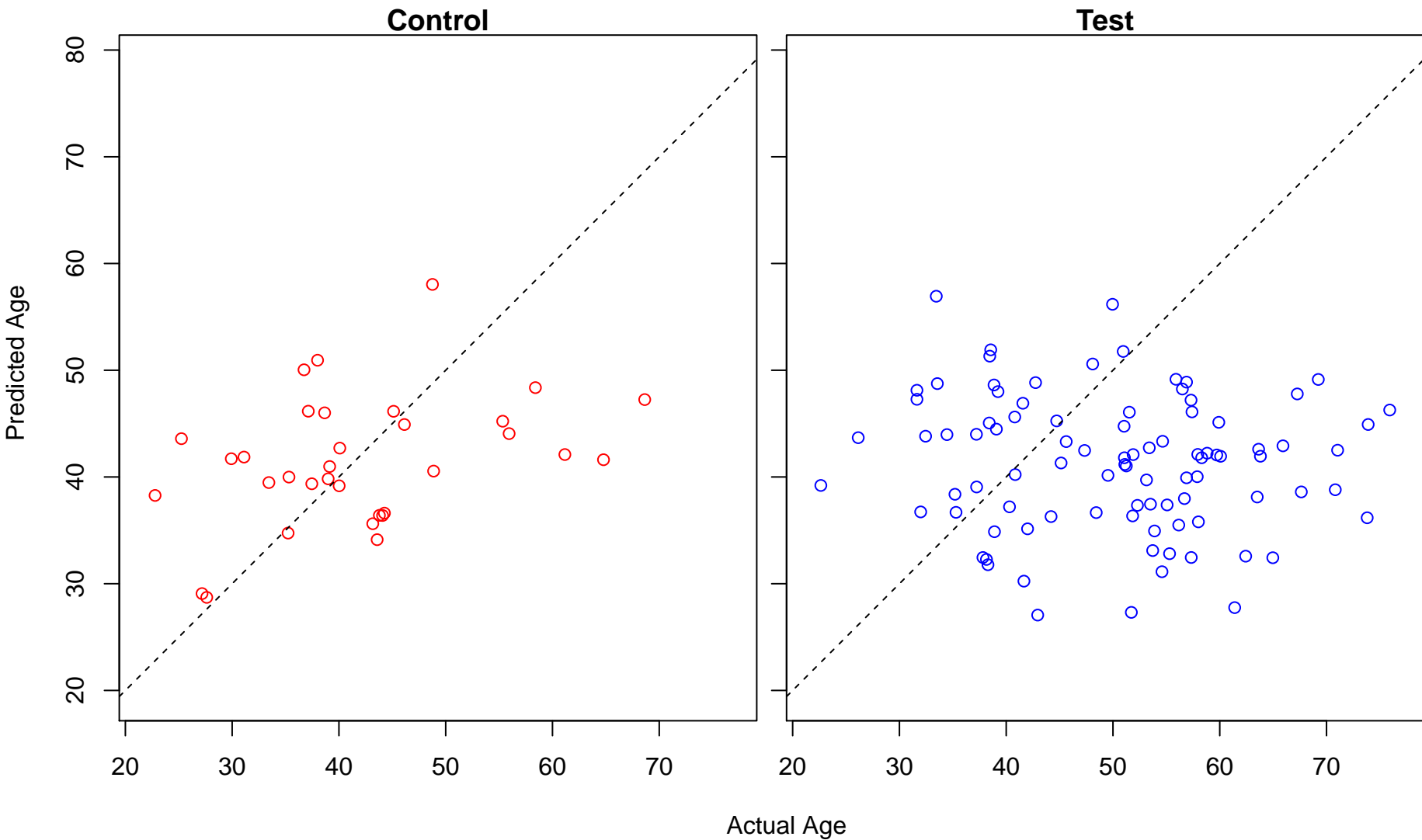
nerve growth factor processing (Score: 0.583774)



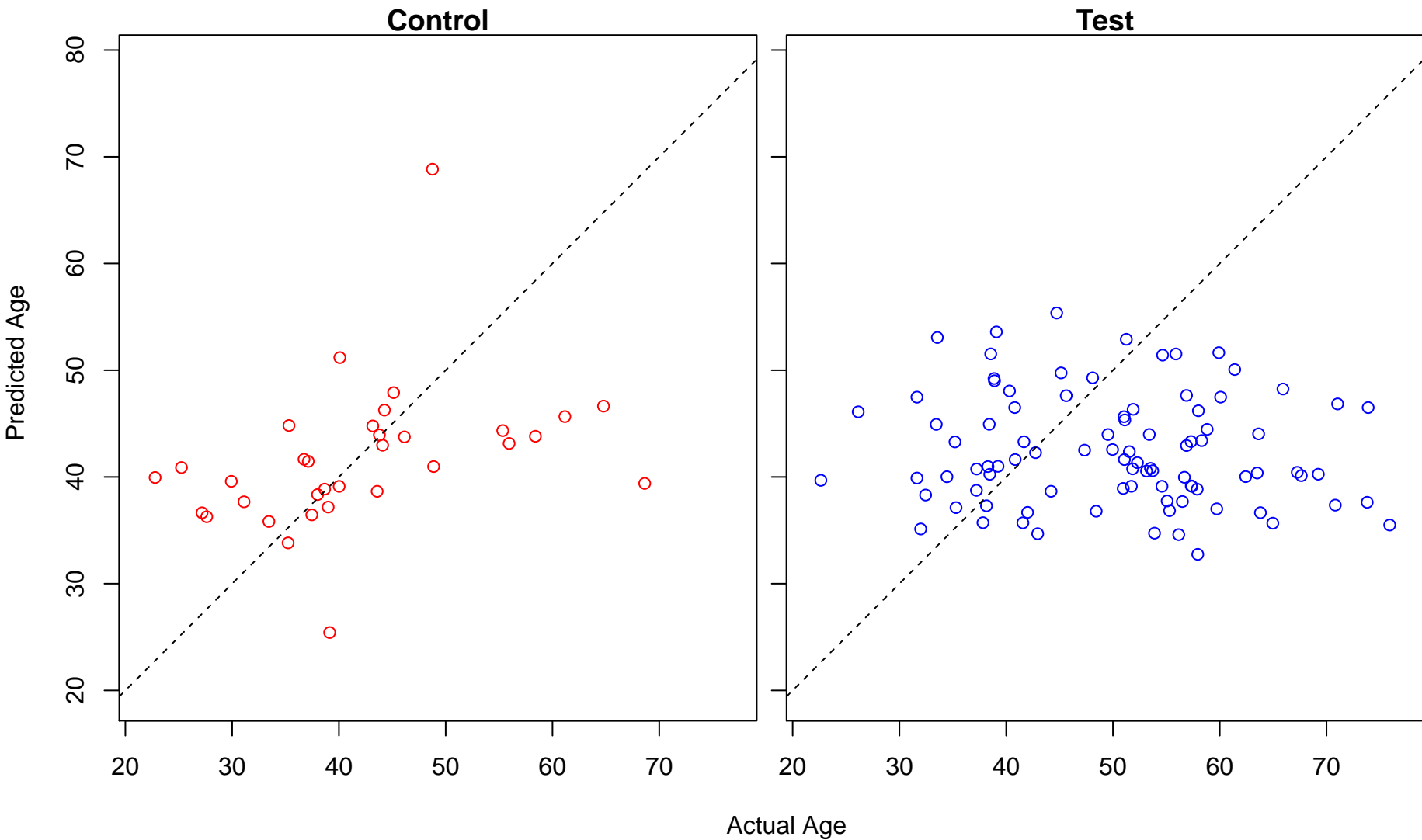
RNA processing (Score: 0.583761)



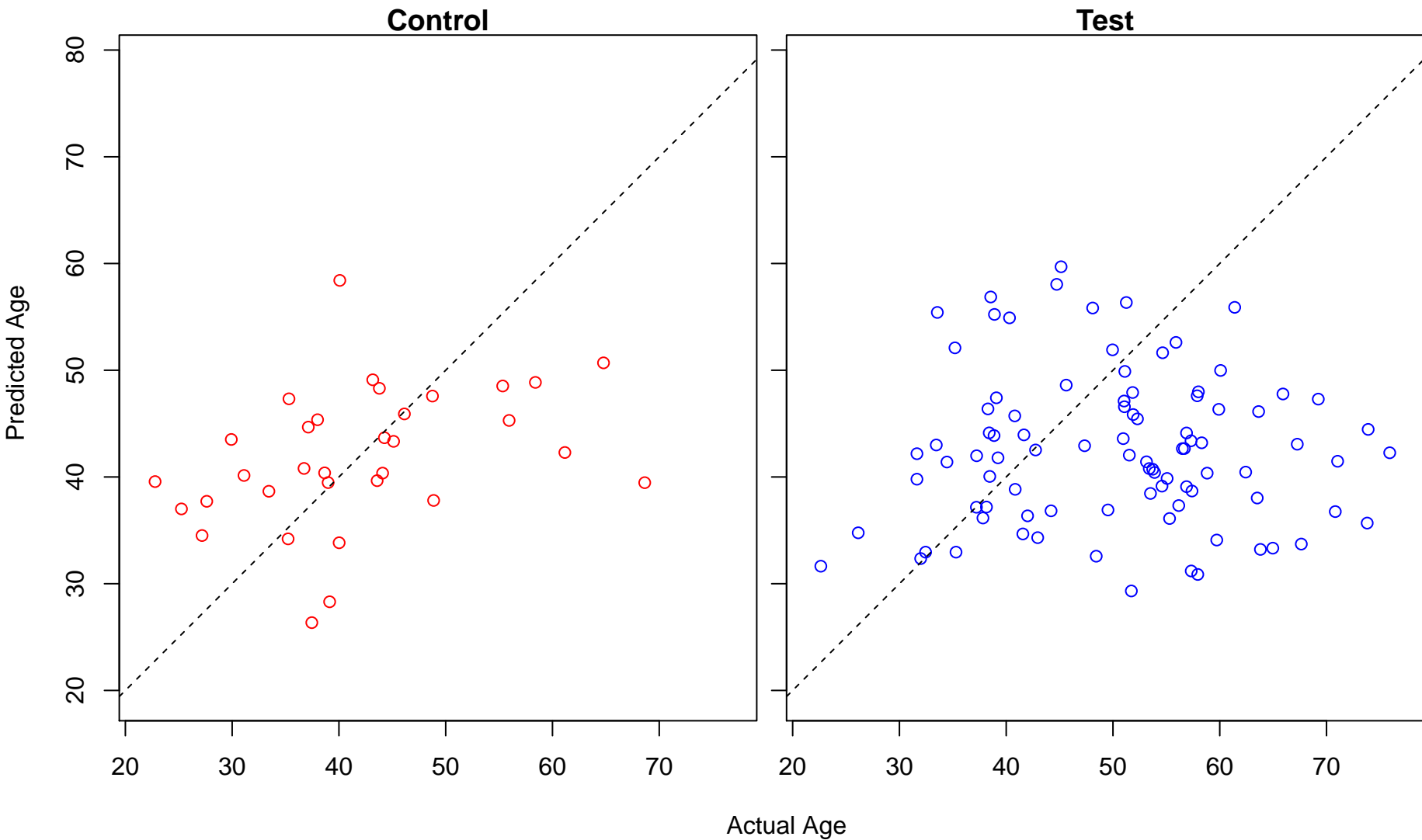
reverse cholesterol transport (Score: 0.583727)



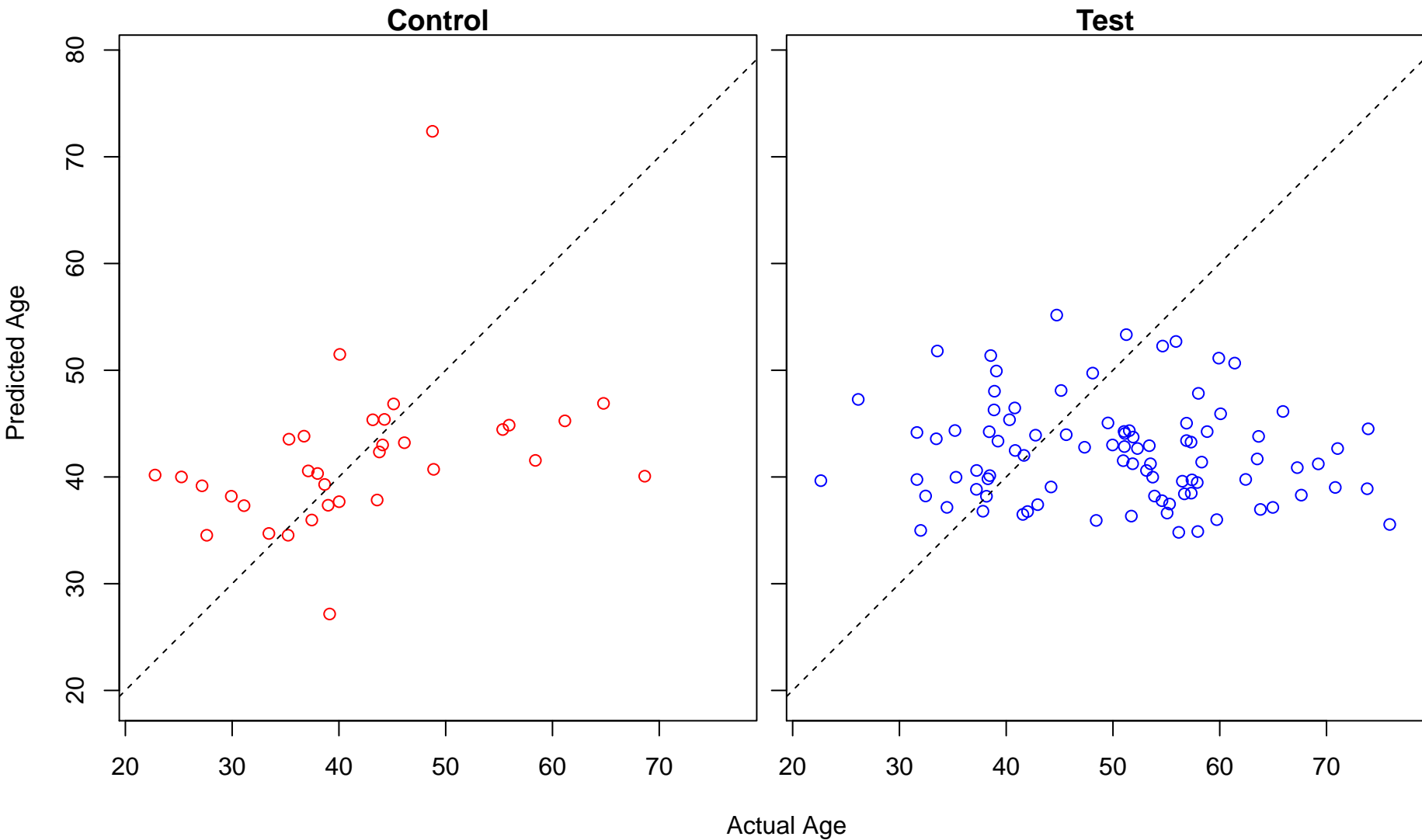
cellular response to stimulus (Score: 0.583082)



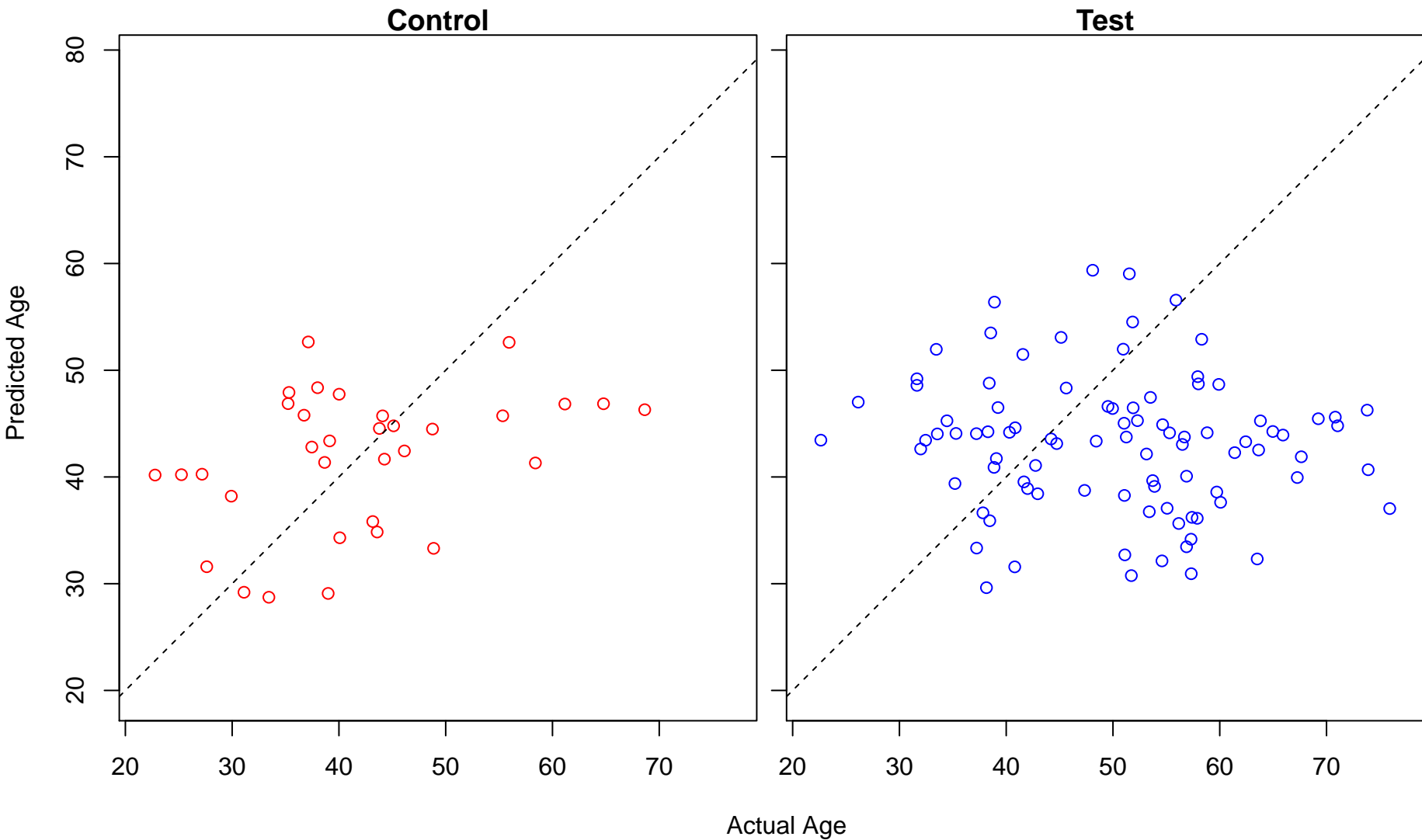
establishment of epithelial cell apical/basal polarity (Score: 0.582931)



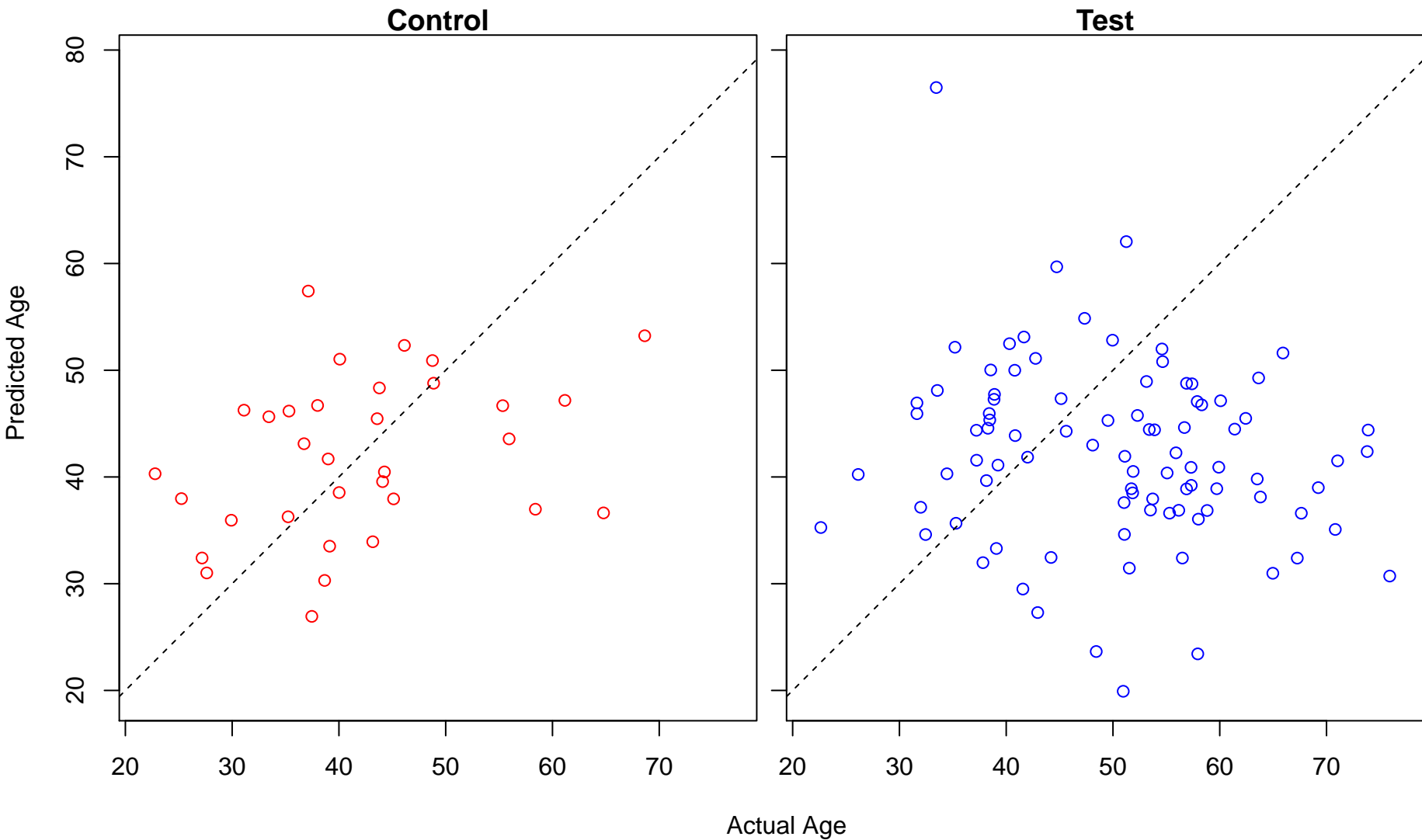
programmed cell death (Score: 0.582921)



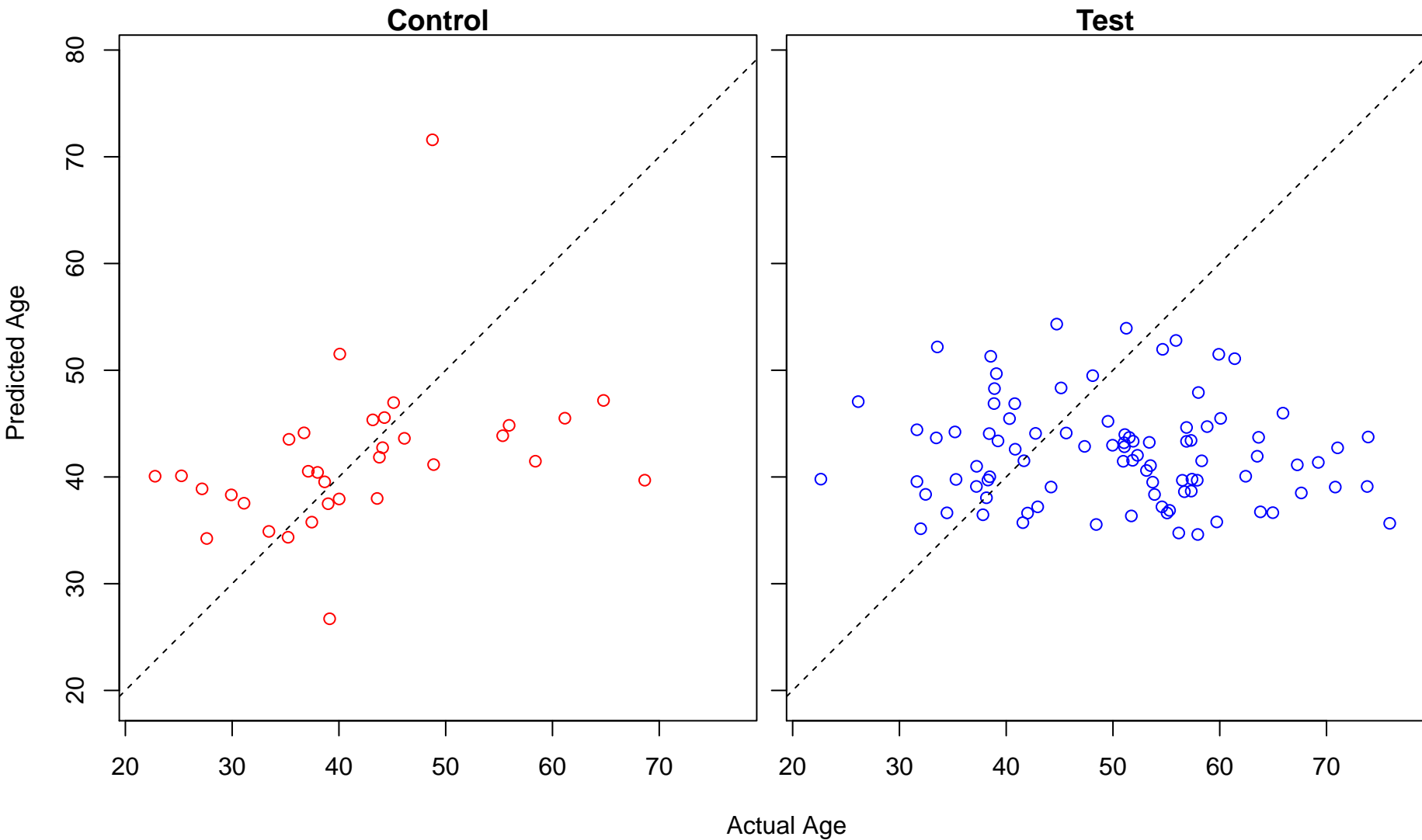
determination of liver left/right asymmetry (Score: 0.582335)



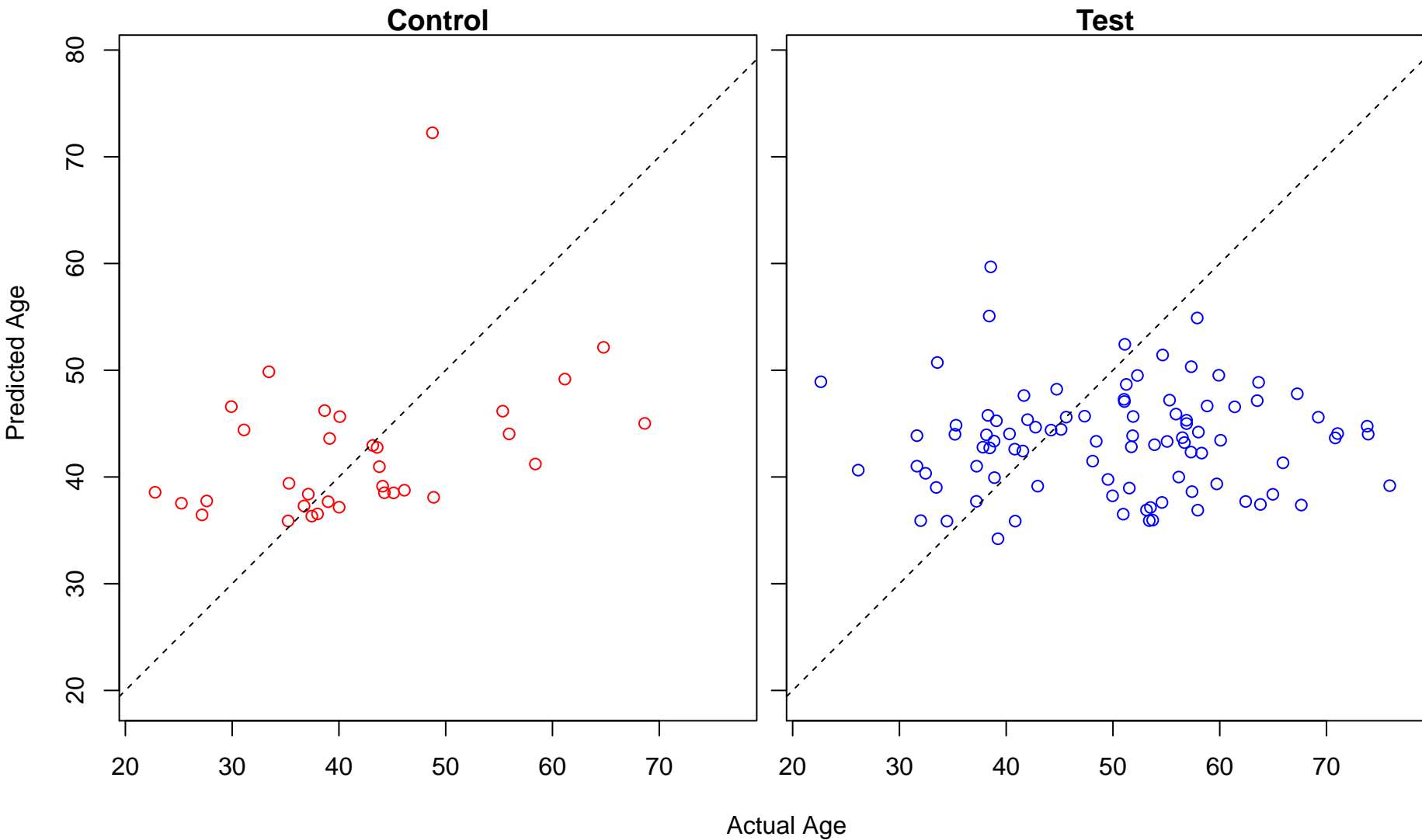
negative regulation of monooxygenase activity (Score: 0.582169)



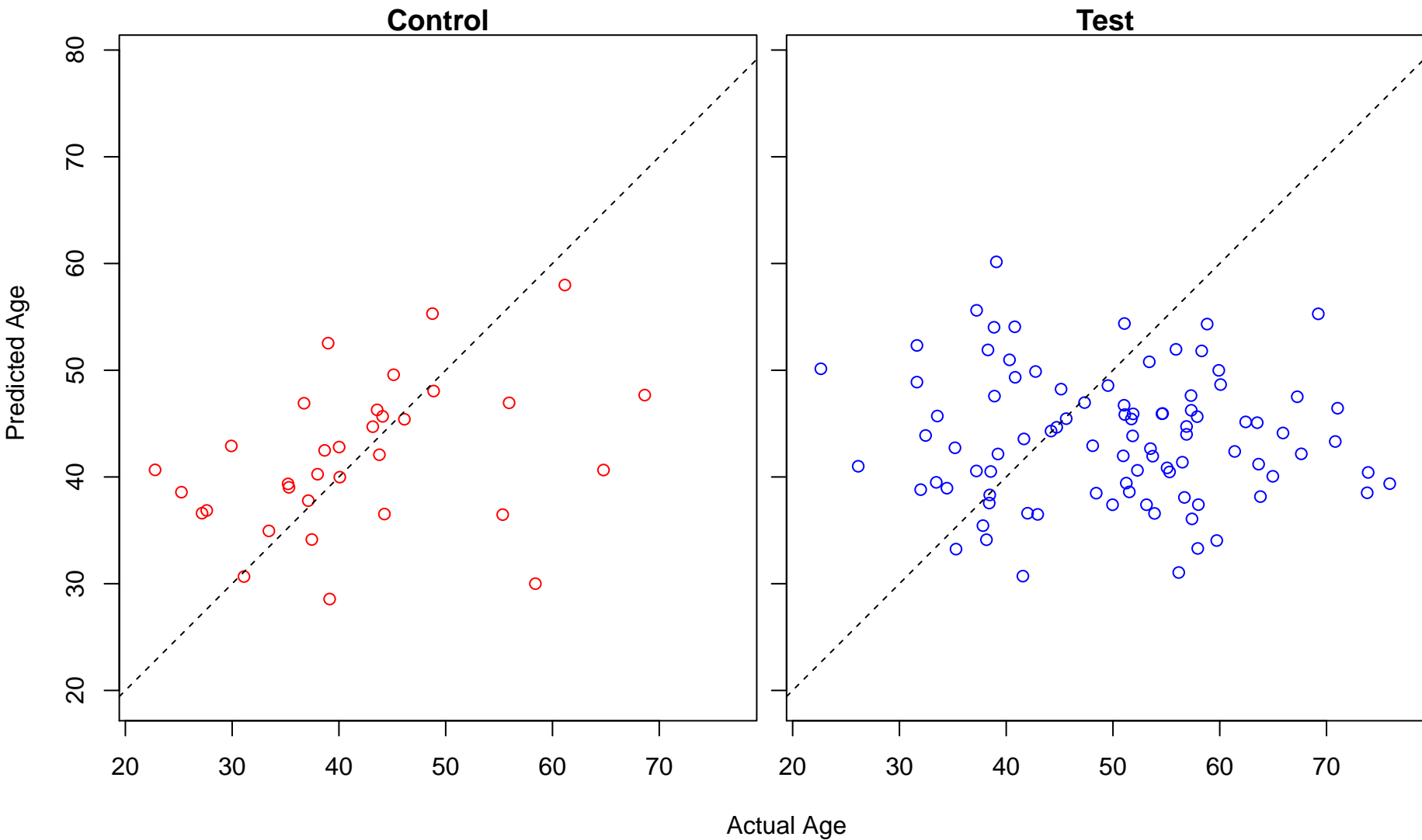
apoptotic process (Score: 0.581539)



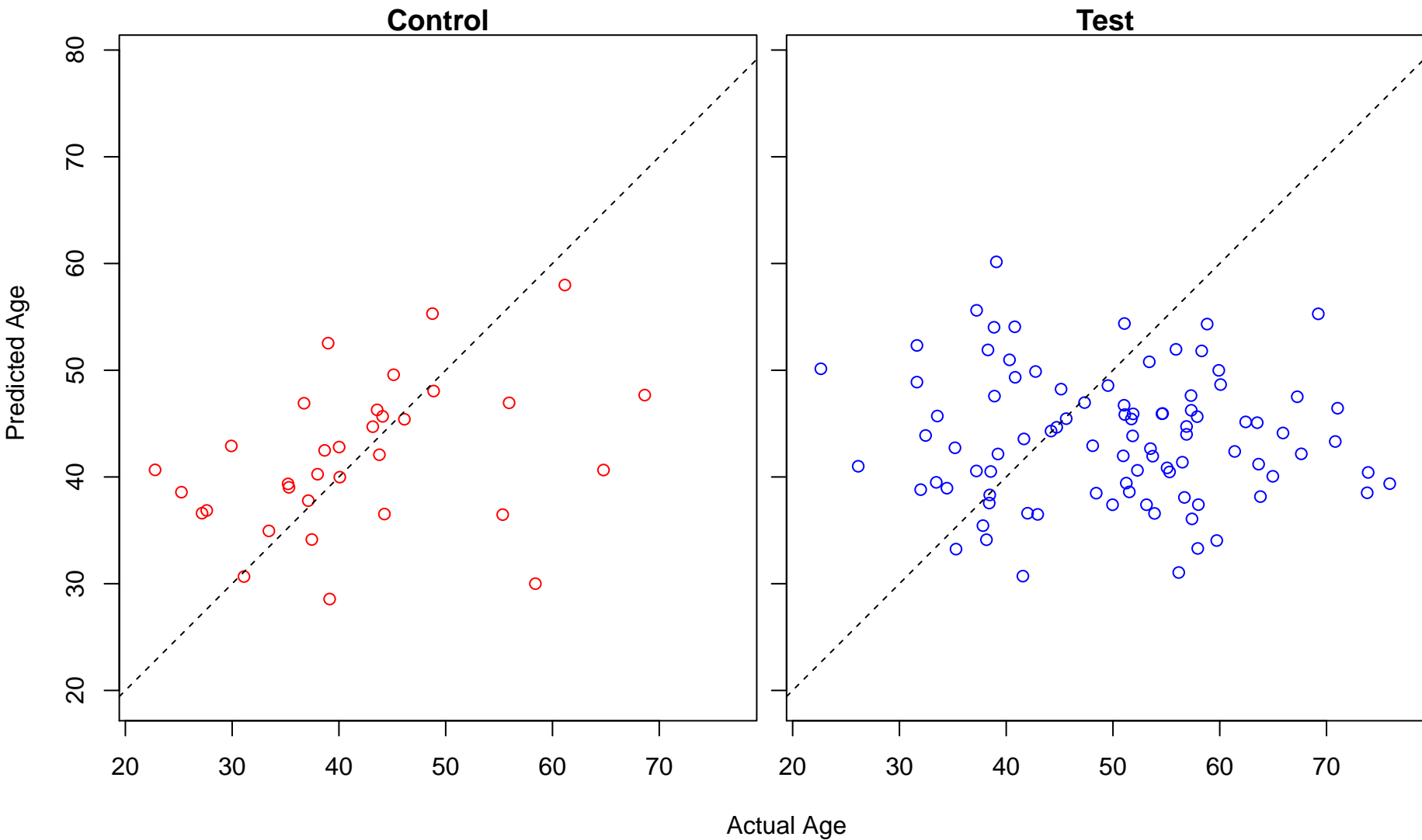
dentate gyrus development (Score: 0.580989)



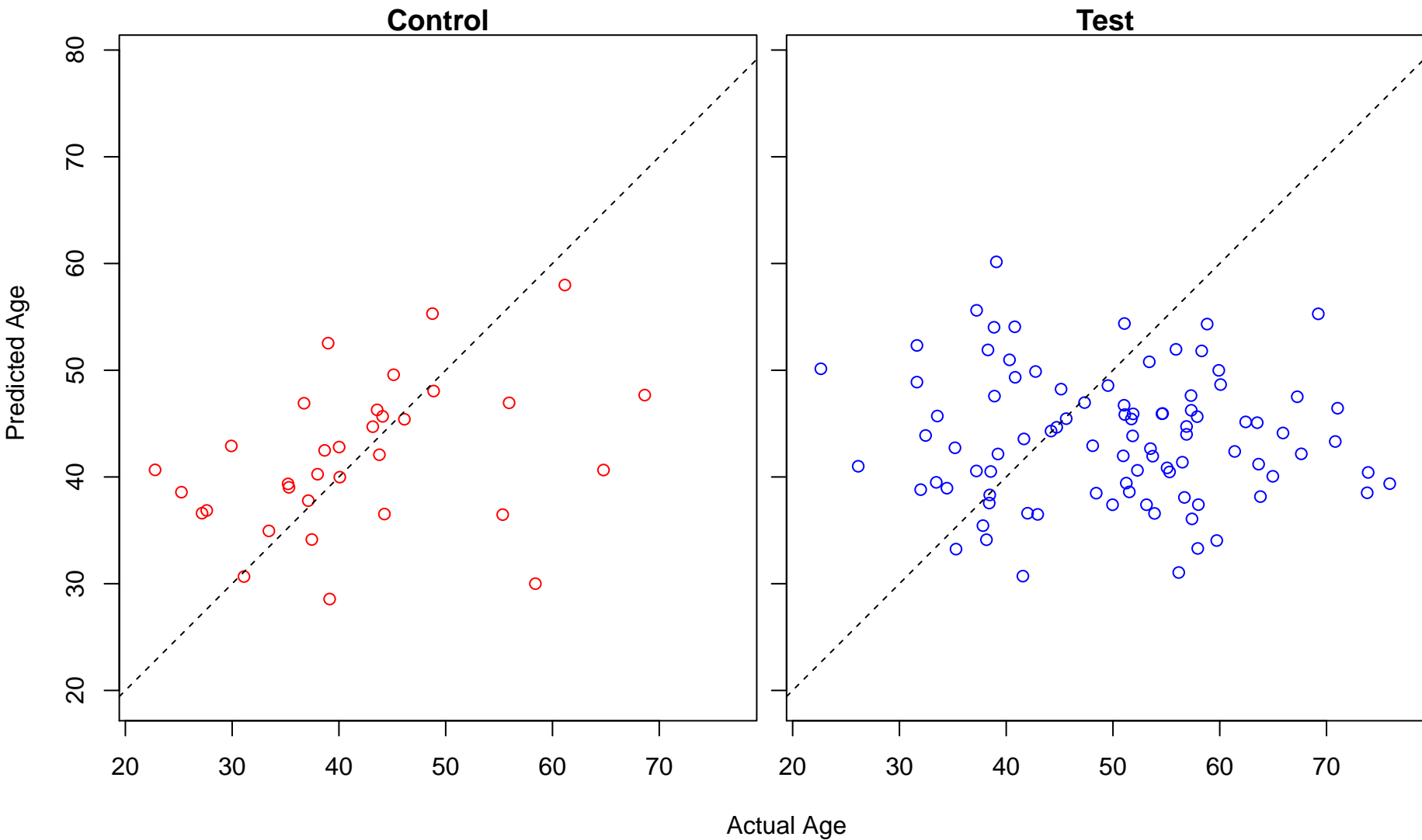
establishment of melanosome localization (Score: 0.580953)



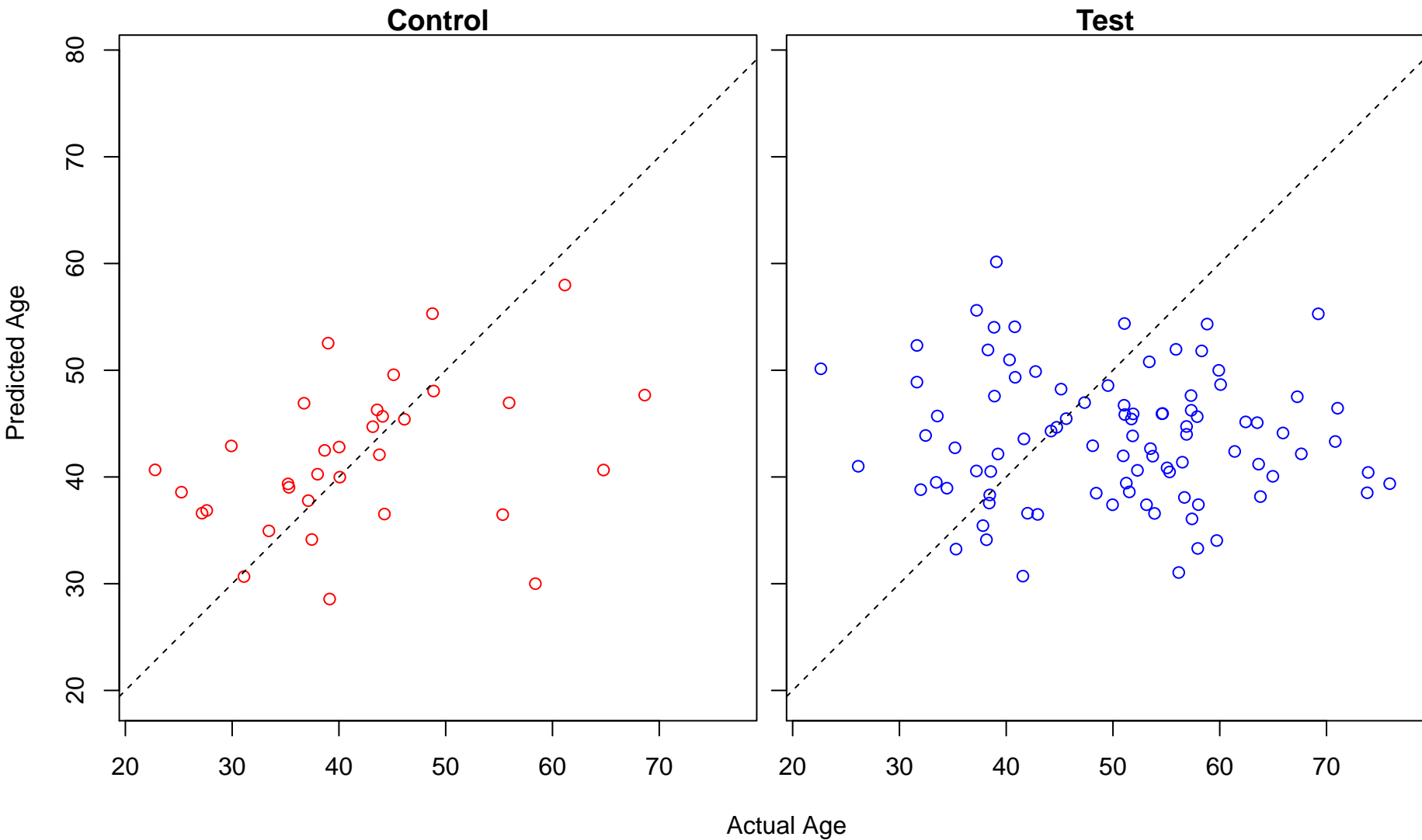
melanosome transport (Score: 0.580953)



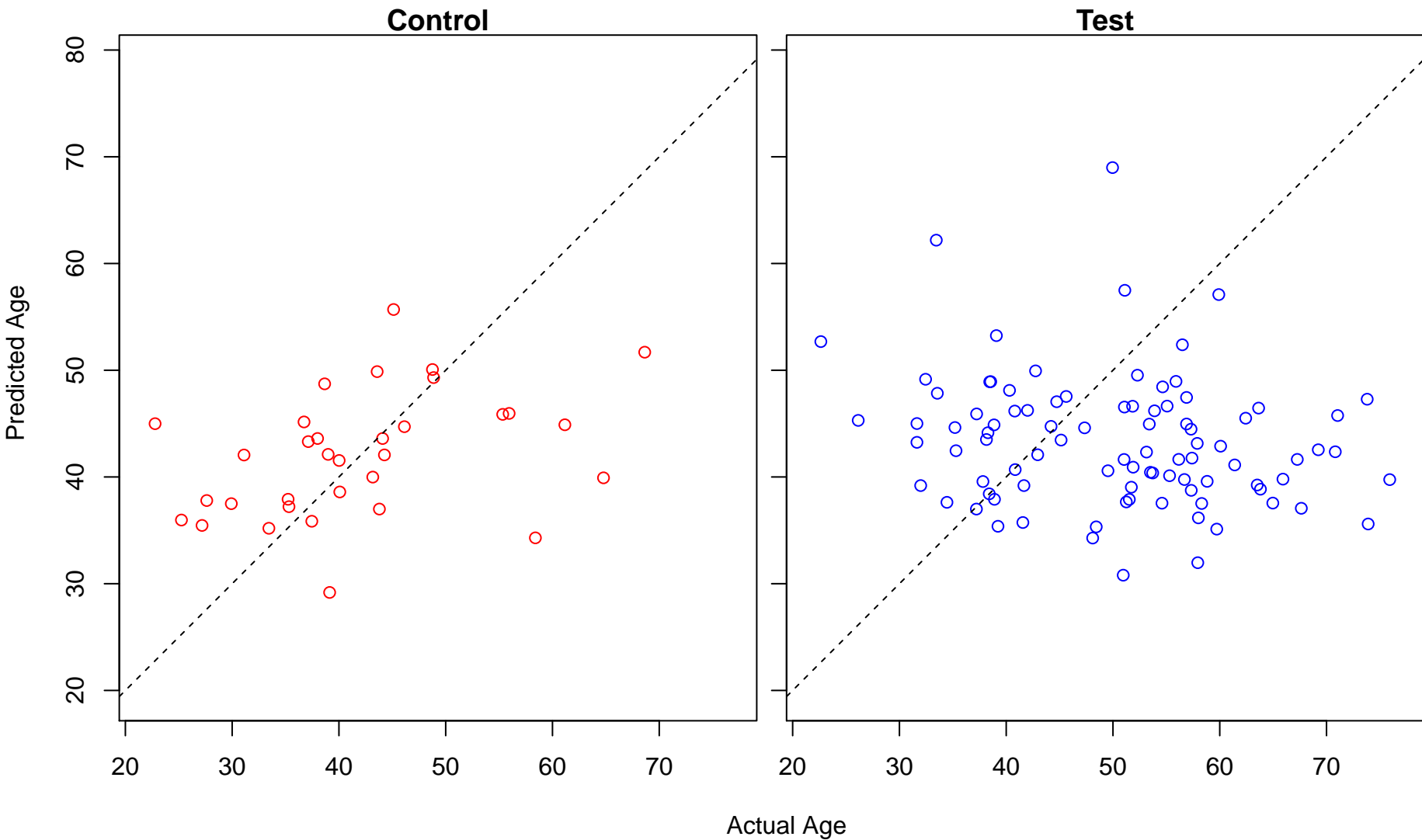
pigment granule transport (Score: 0.580953)



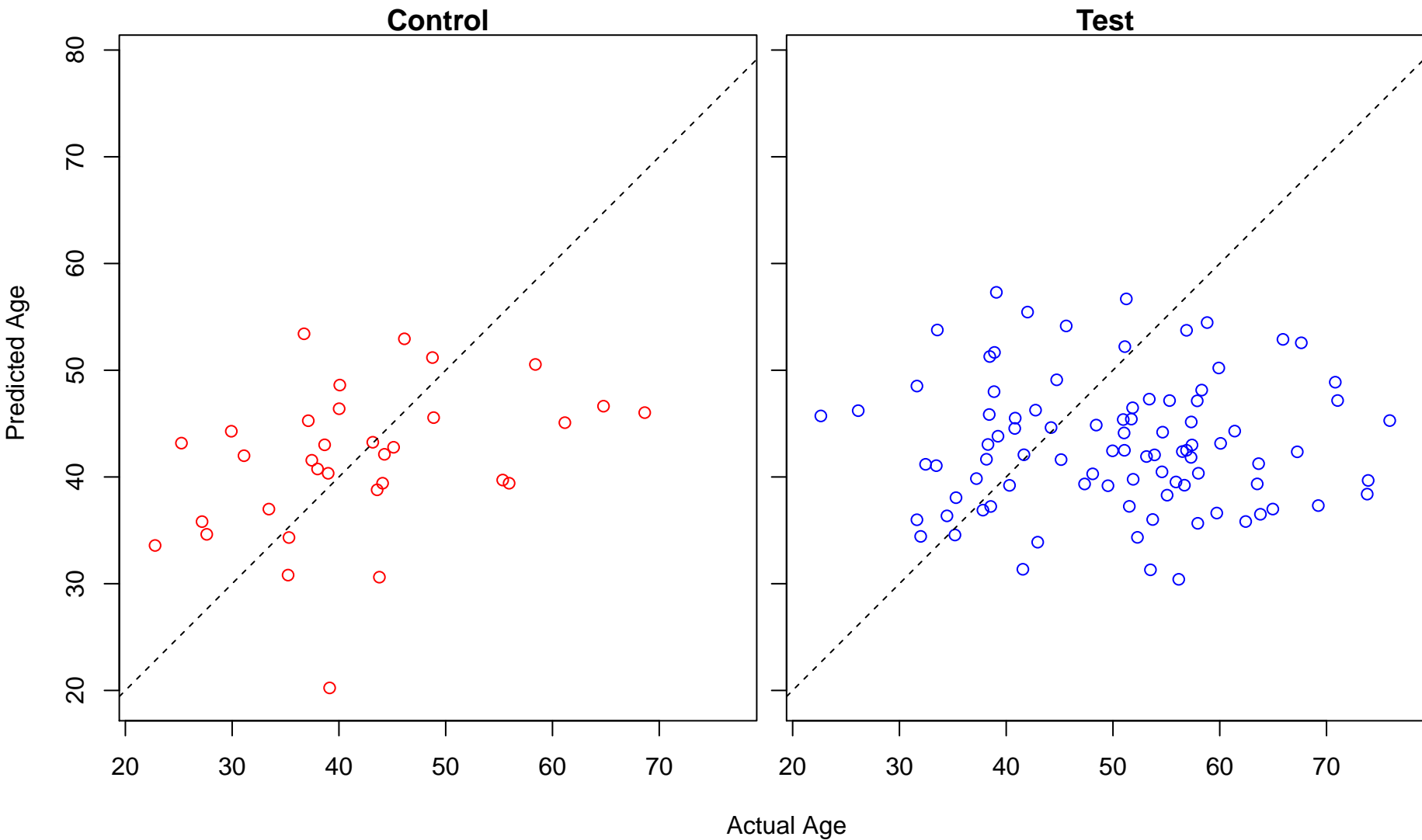
establishment of pigment granule localization (Score: 0.580953)



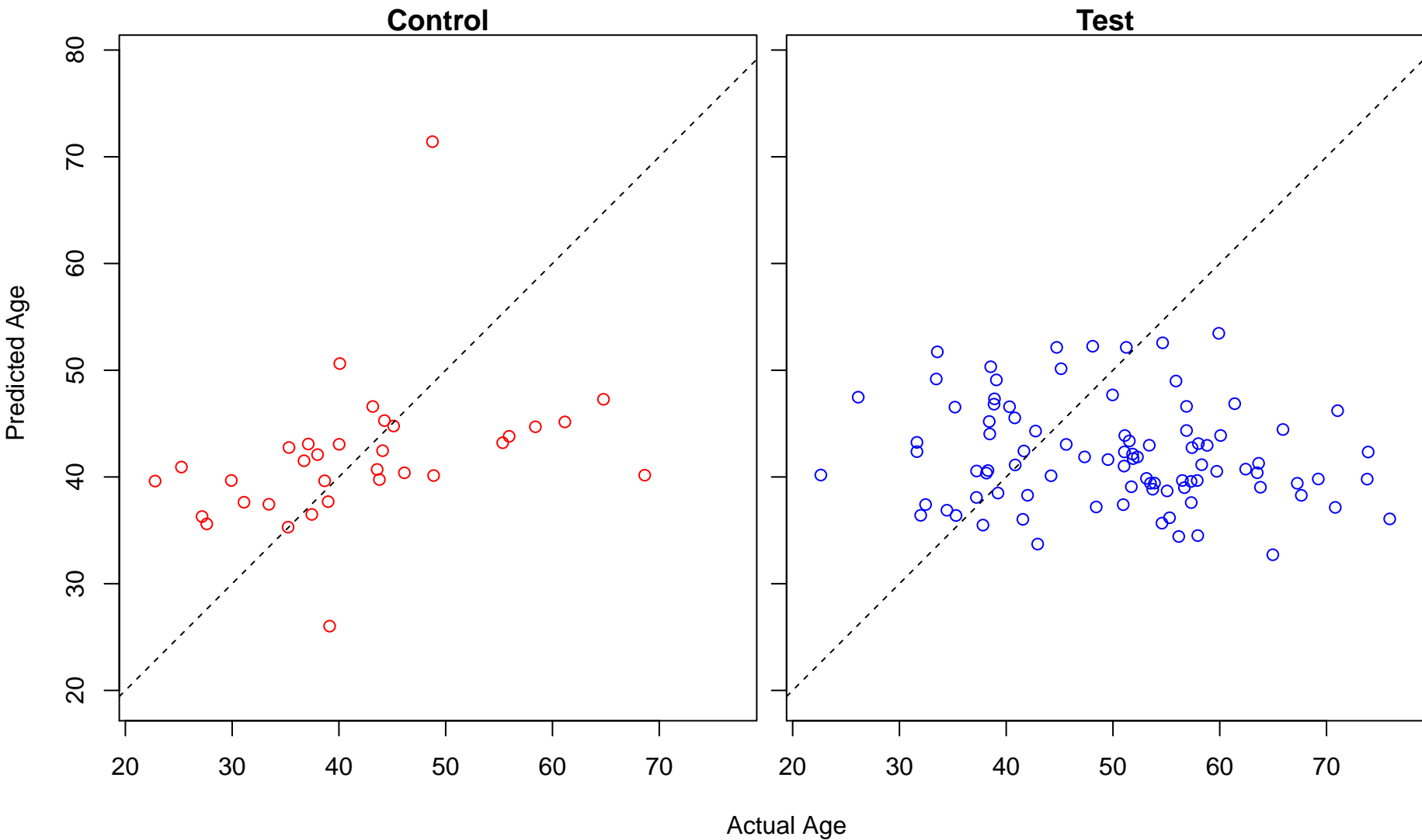
cobalt ion transport (Score: 0.580316)



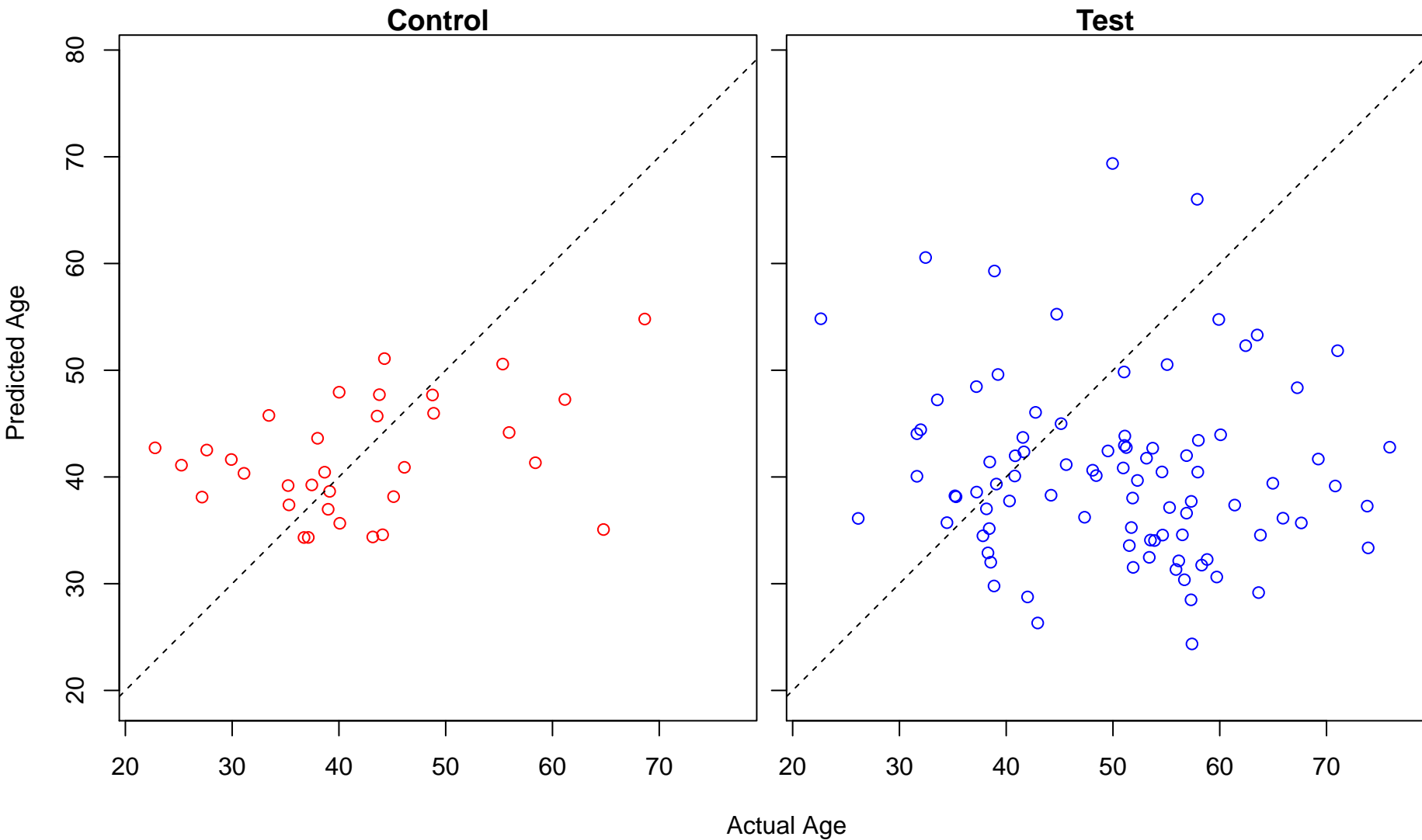
phagocytosis, engulfment (Score: 0.580114)



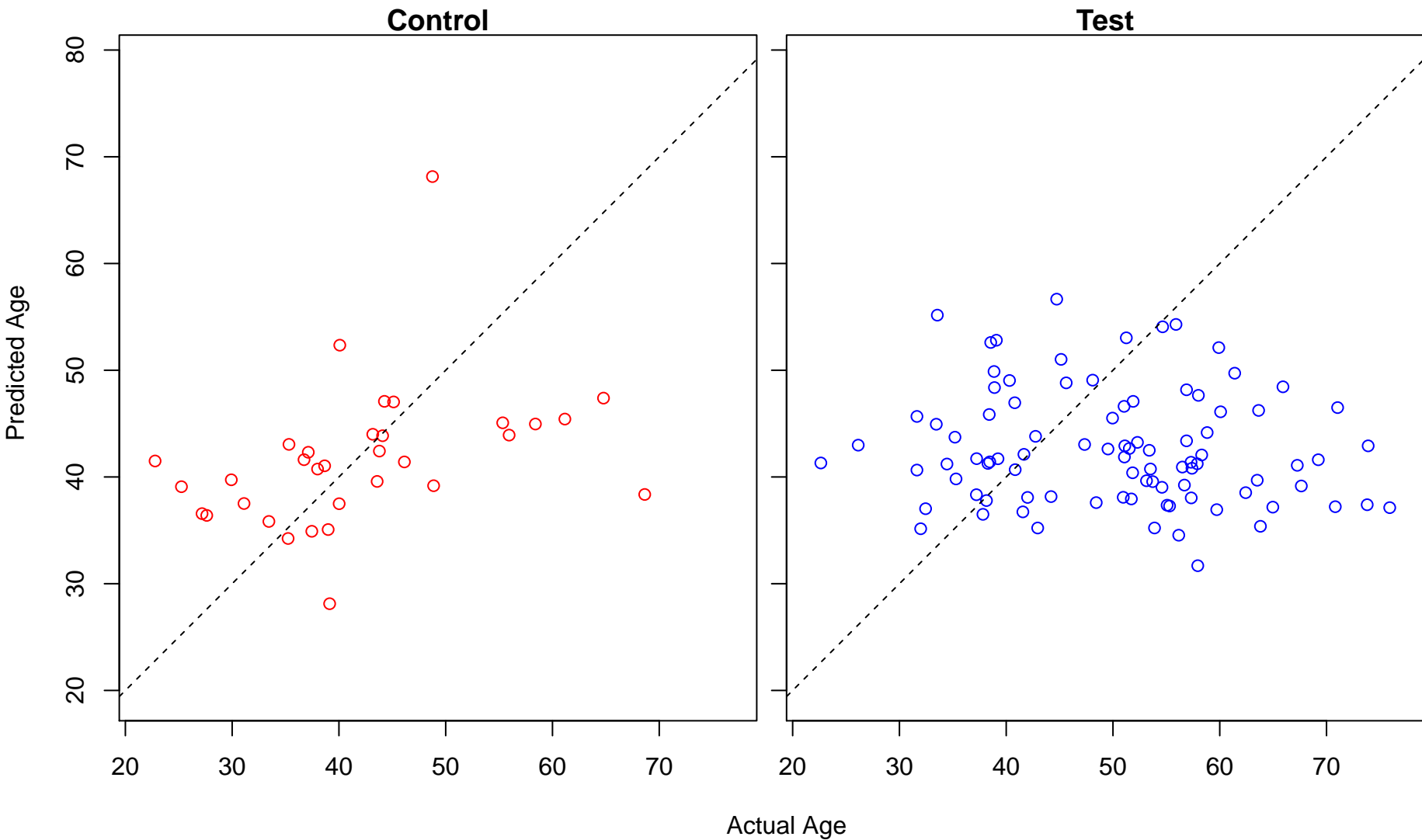
cation transport (Score: 0.579368)



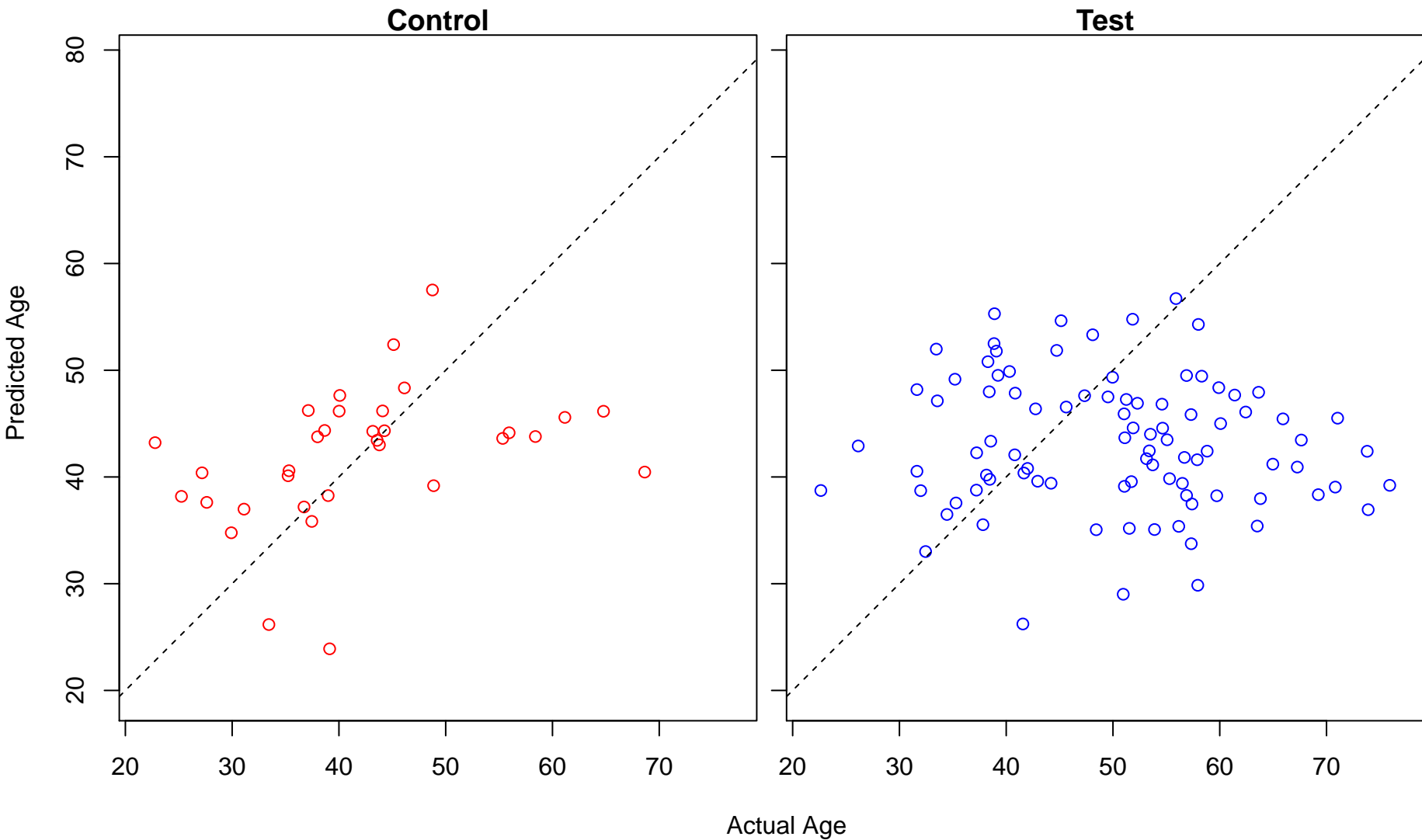
myoblast development (Score: 0.577301)



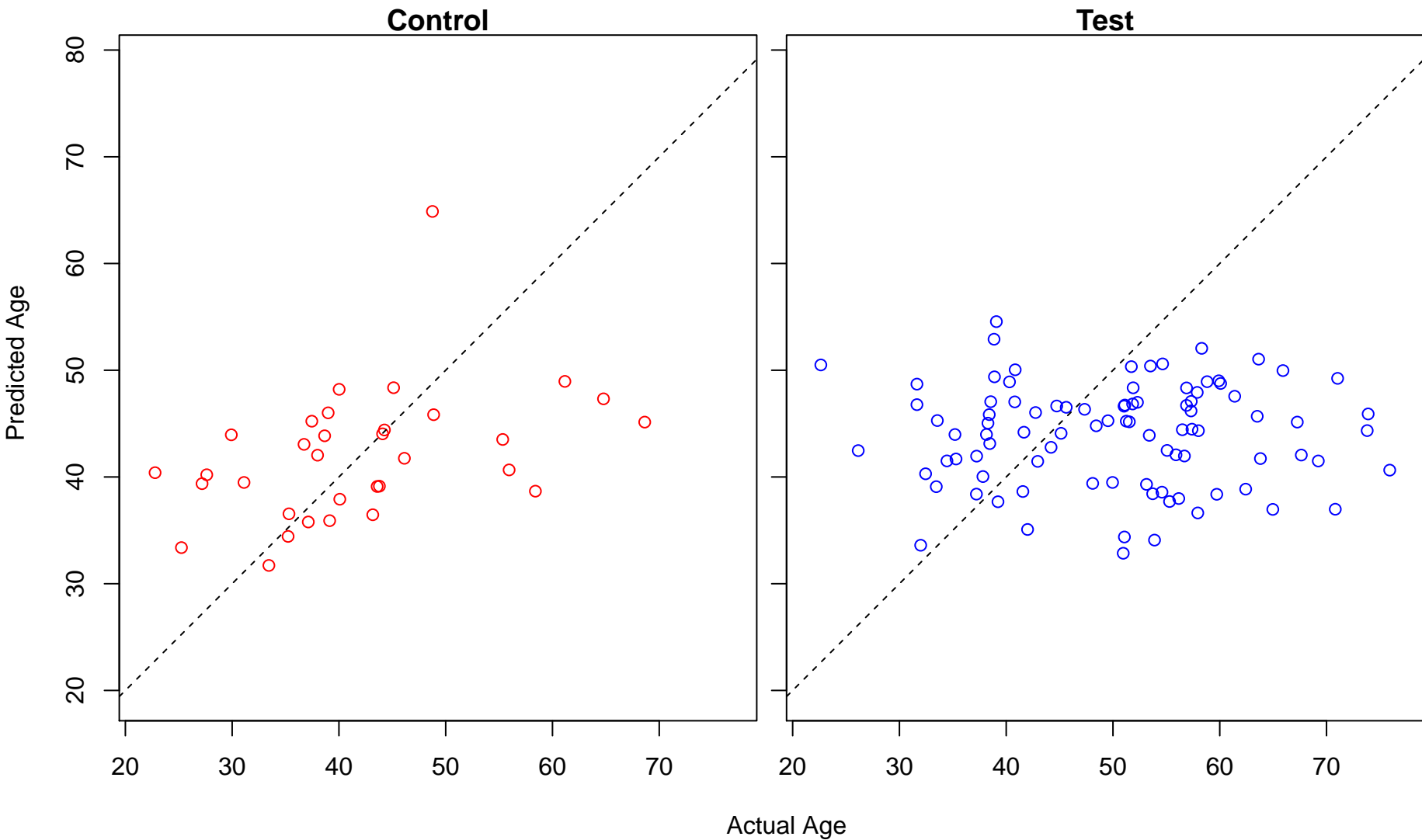
regulation of hydrolase activity (Score: 0.577038)



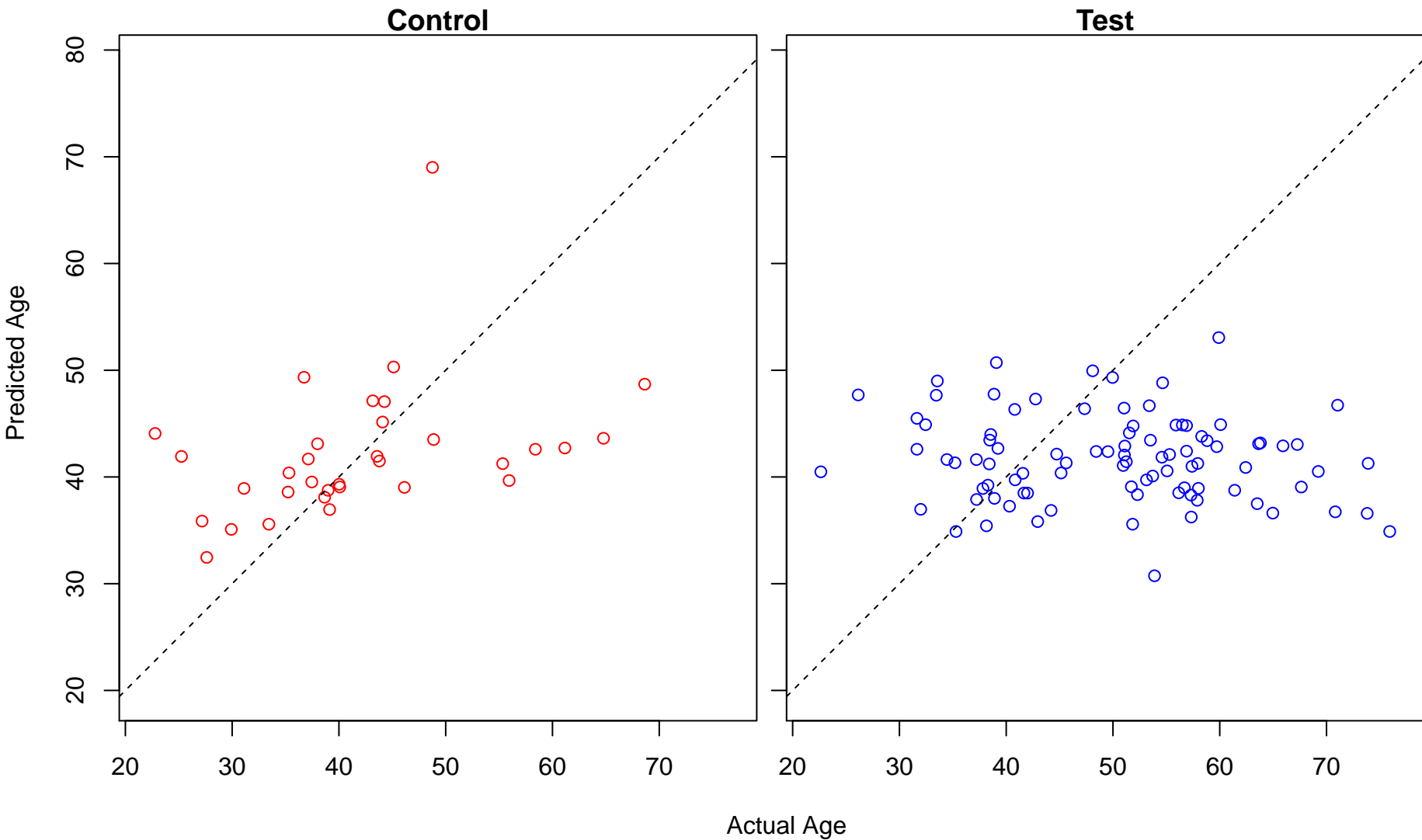
magnesium ion transport (Score: 0.576335)



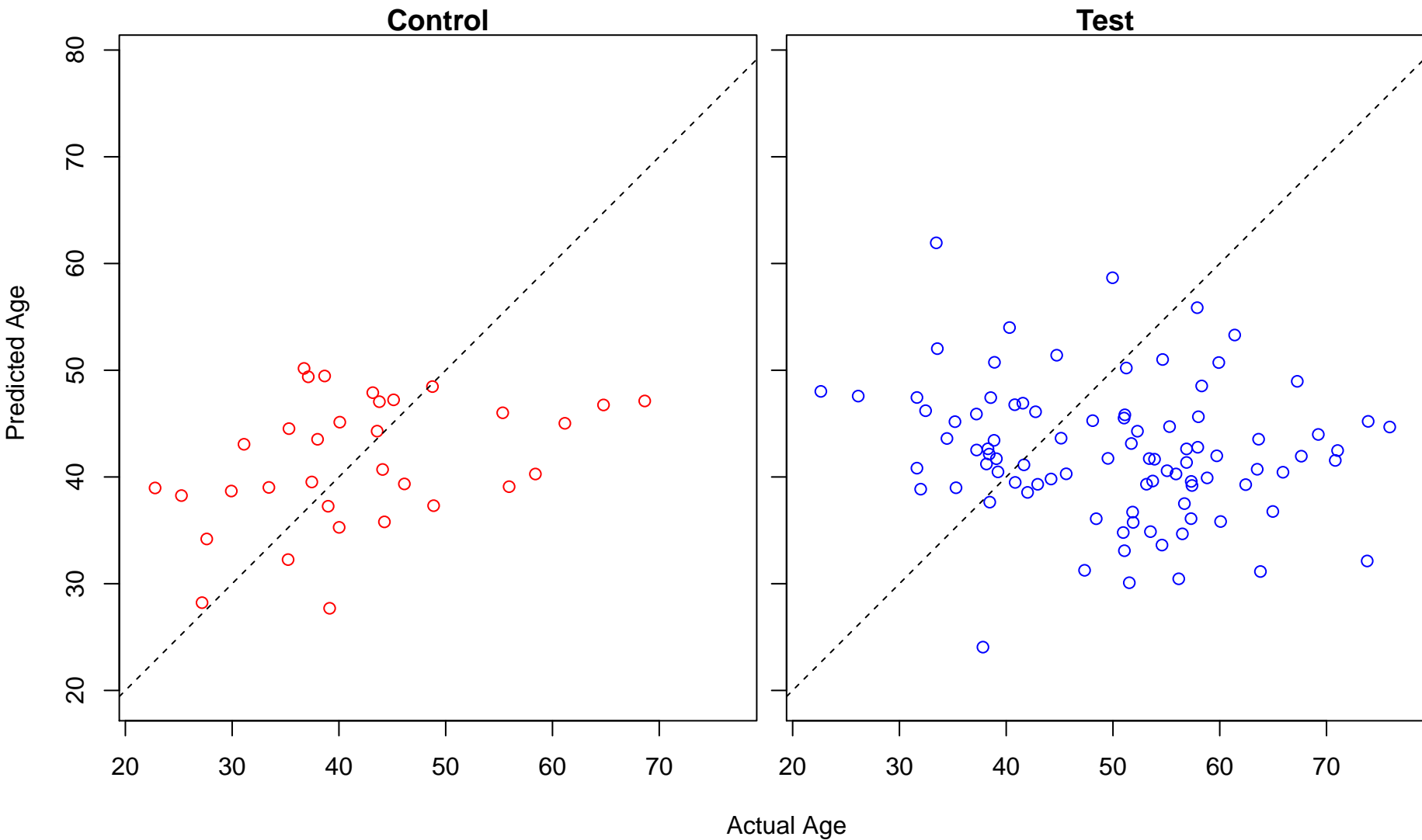
positive regulation of necrotic cell death (Score: 0.575836)



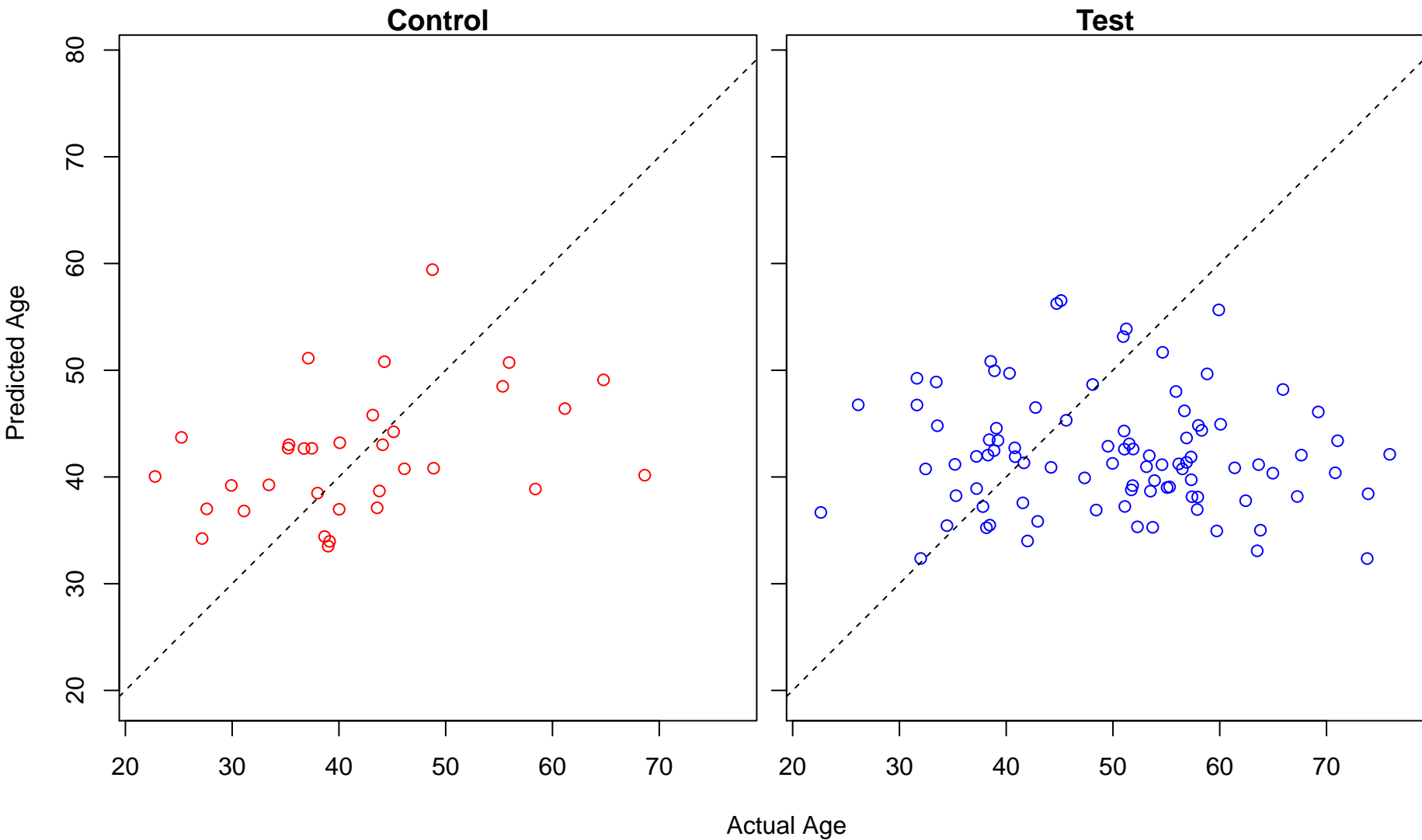
positive regulation of T-helper 2 cell differentiation (Score: 0.574481)



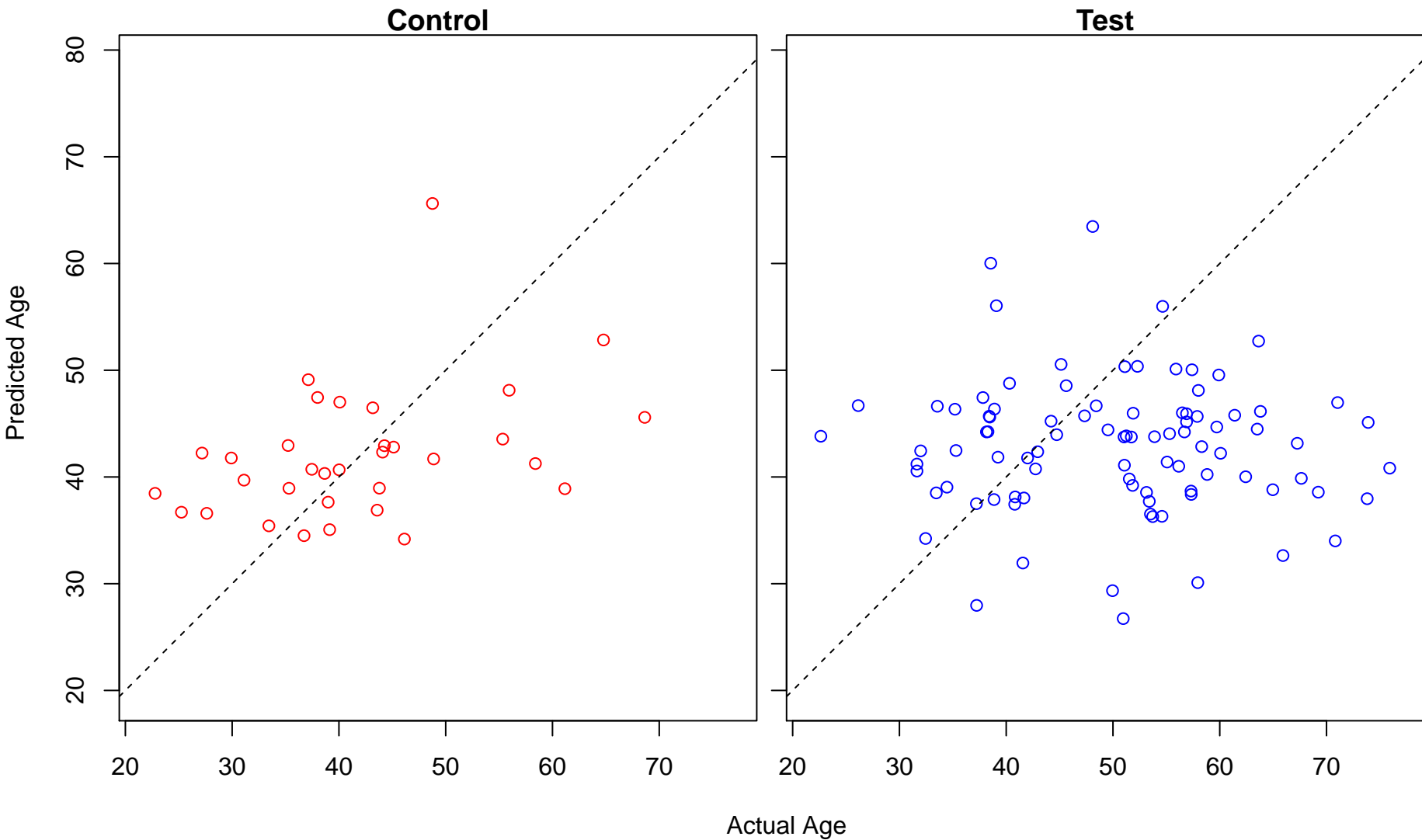
negative regulation of muscle organ development (Score: 0.573950)



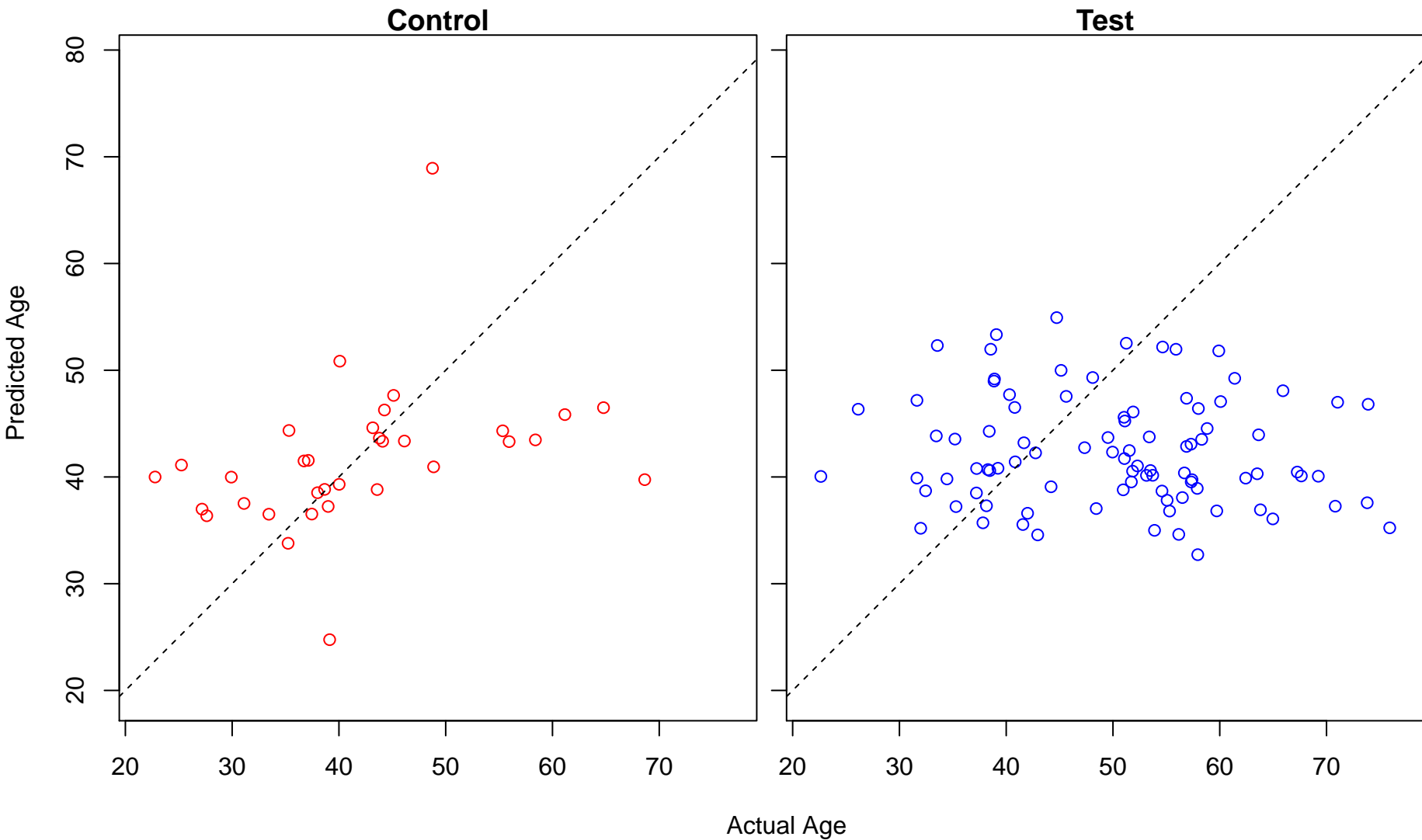
ubiquitin-dependent SMAD protein catabolic process (Score: 0.573504)



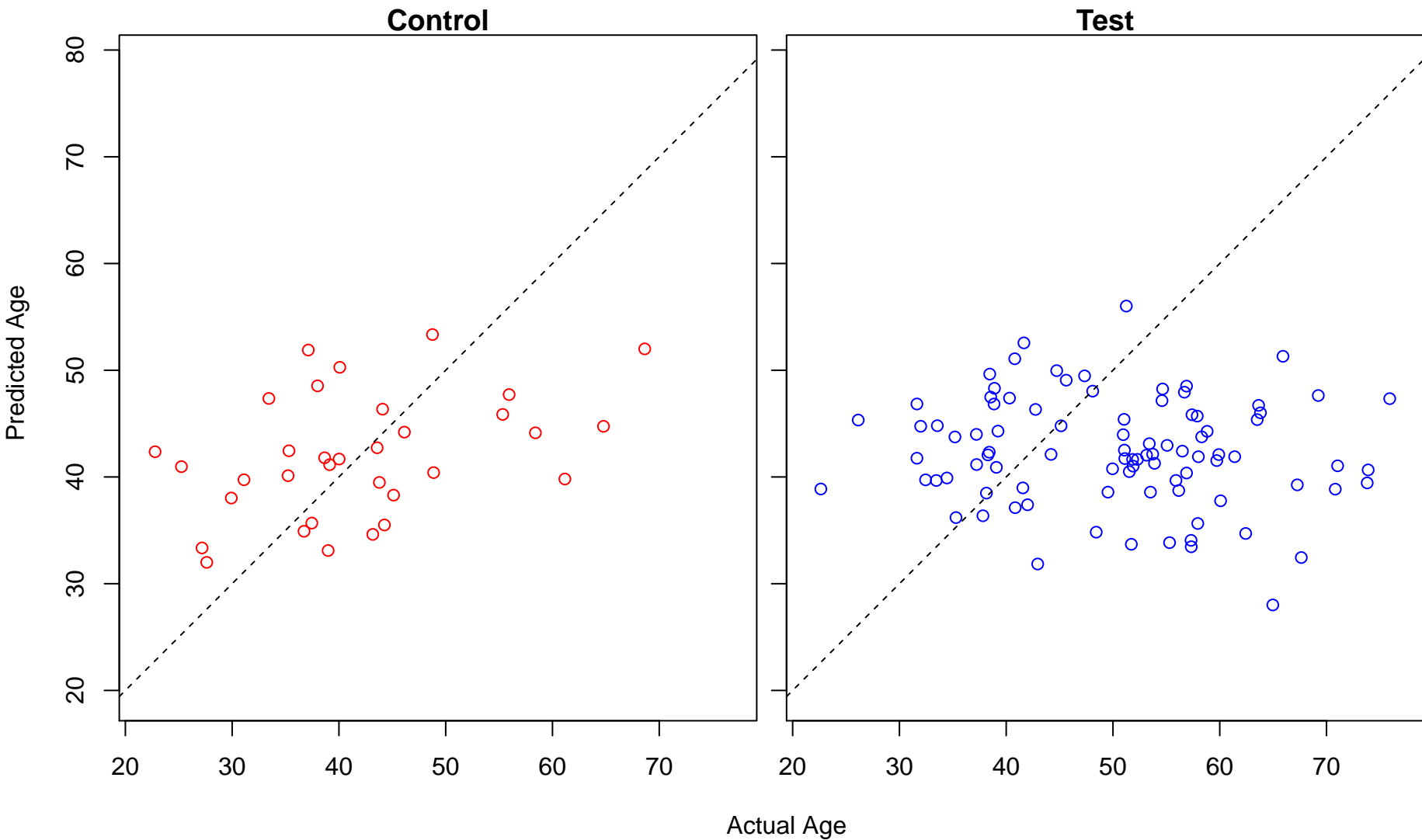
activation of anaphase-promoting complex activity (Score: 0.573407)



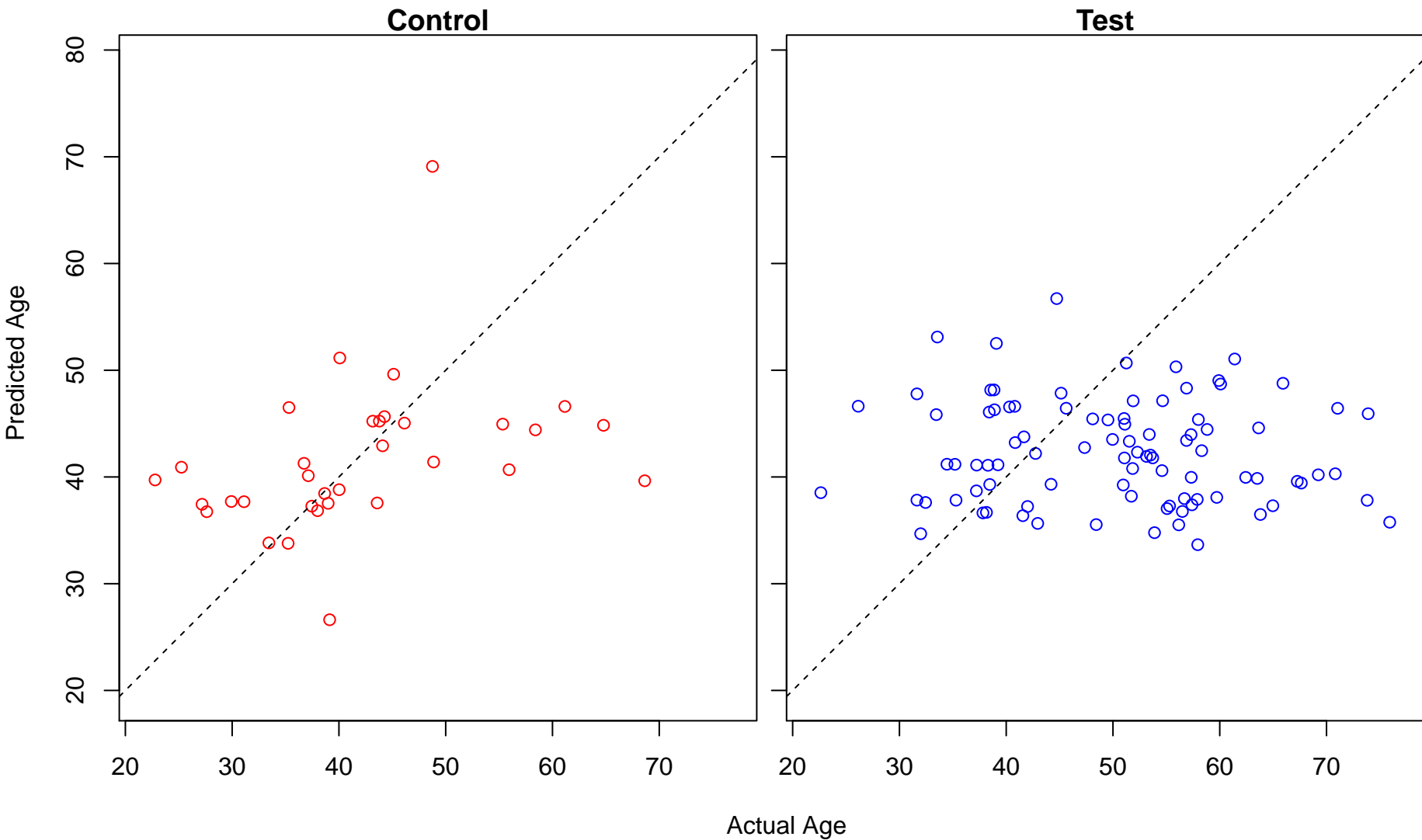
signal transduction (Score: 0.573335)



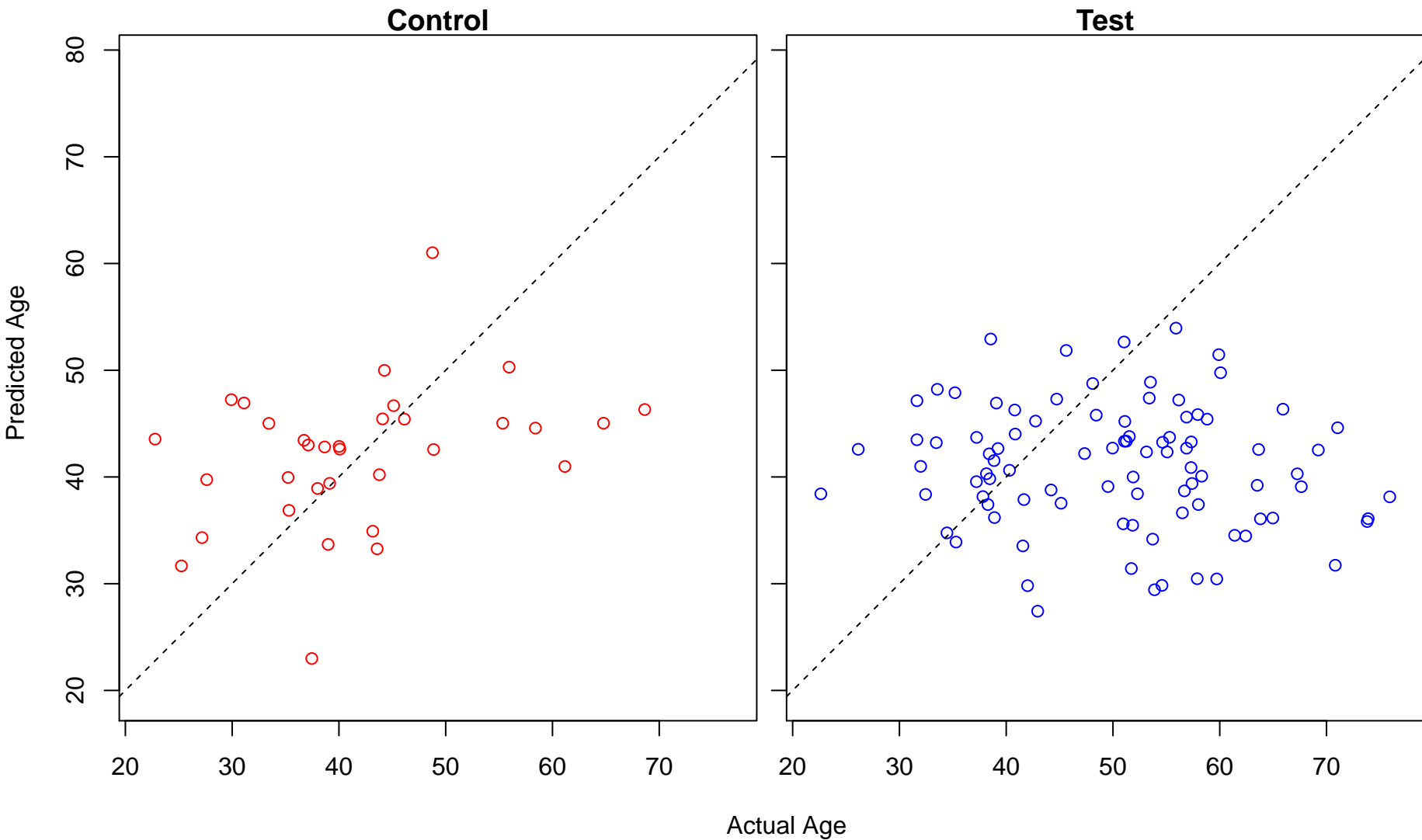
negative regulation of microtubule polymerization (Score: 0.573019)



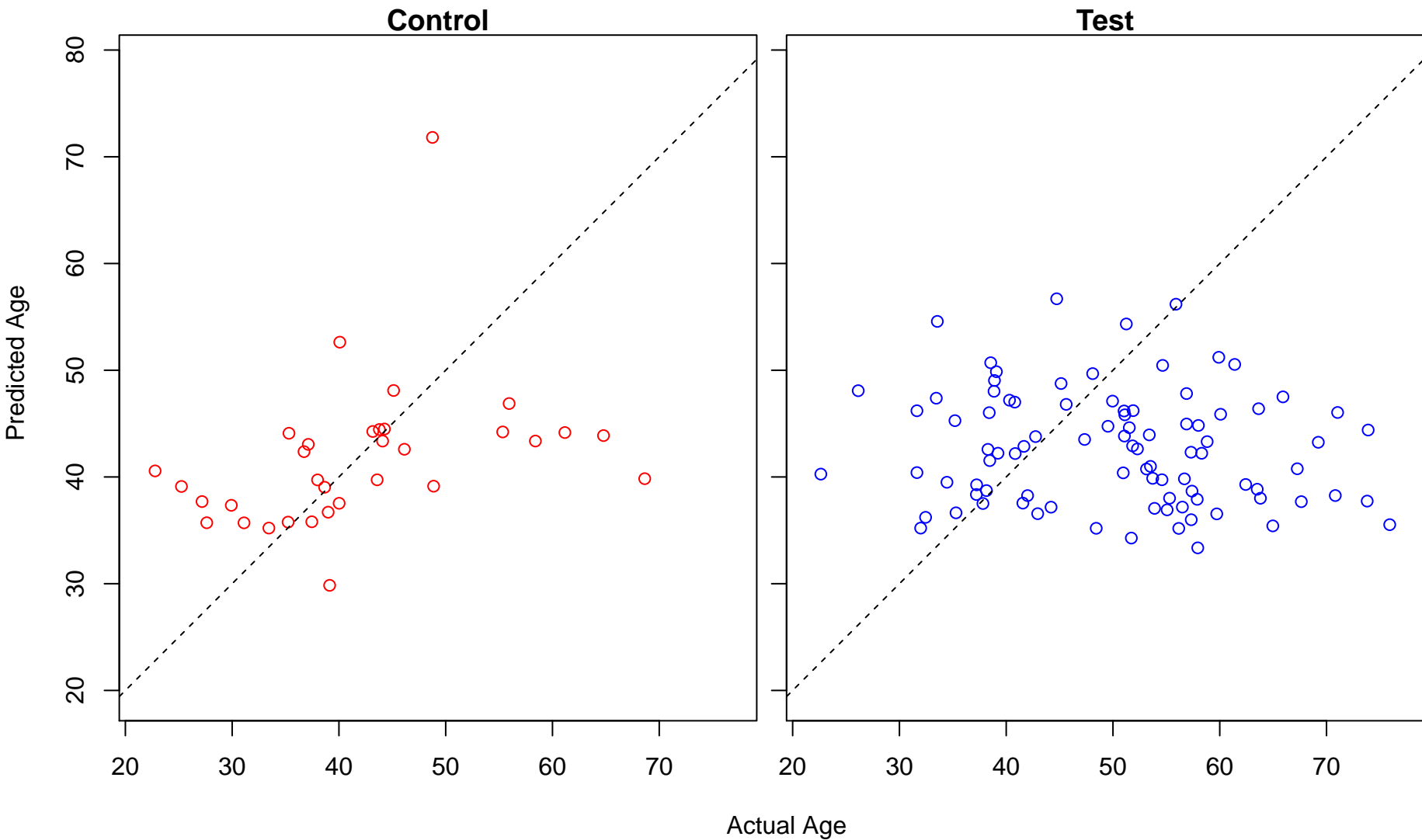
DNA metabolic process (Score: 0.572795)



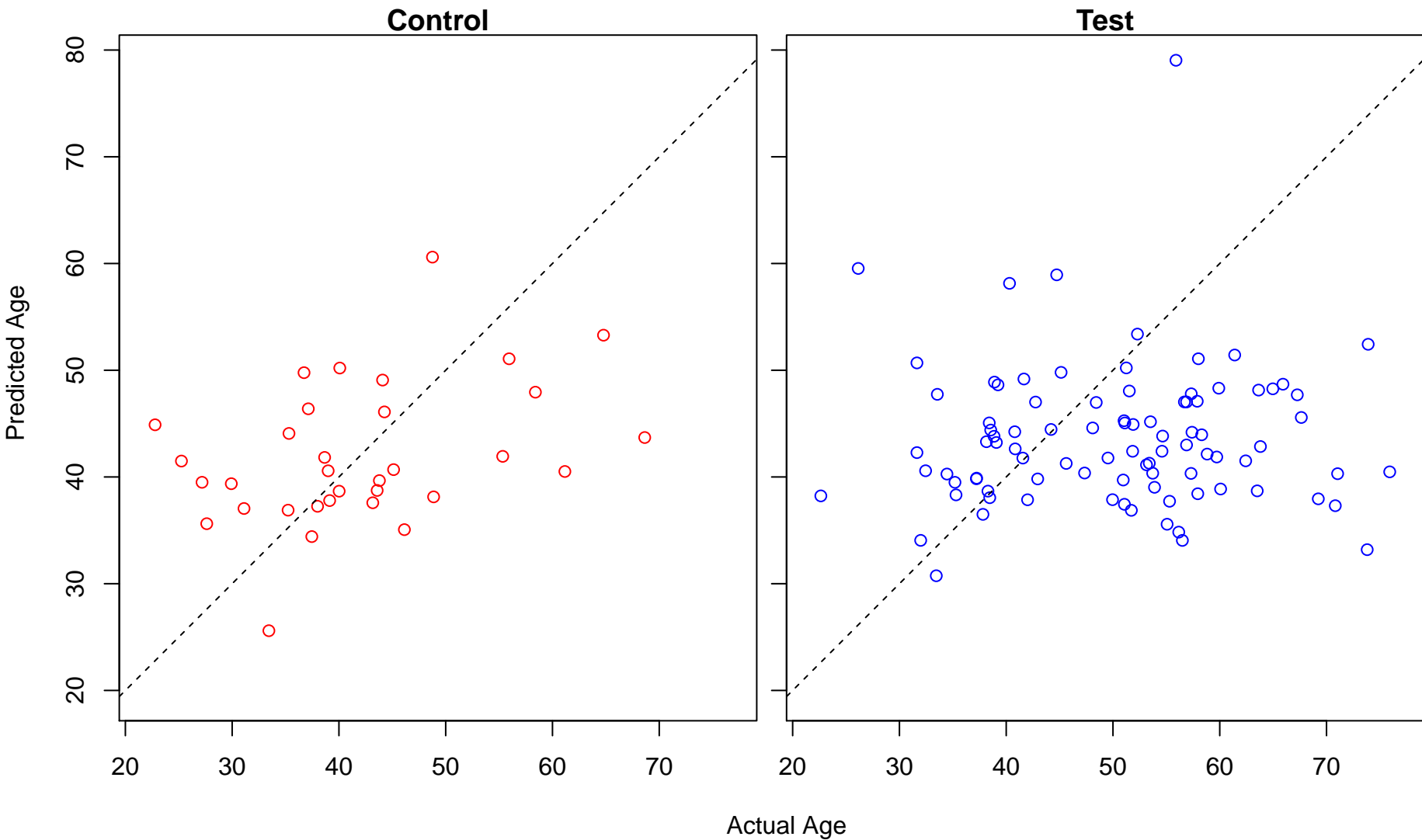
negative regulation of cyclase activity (Score: 0.572689)



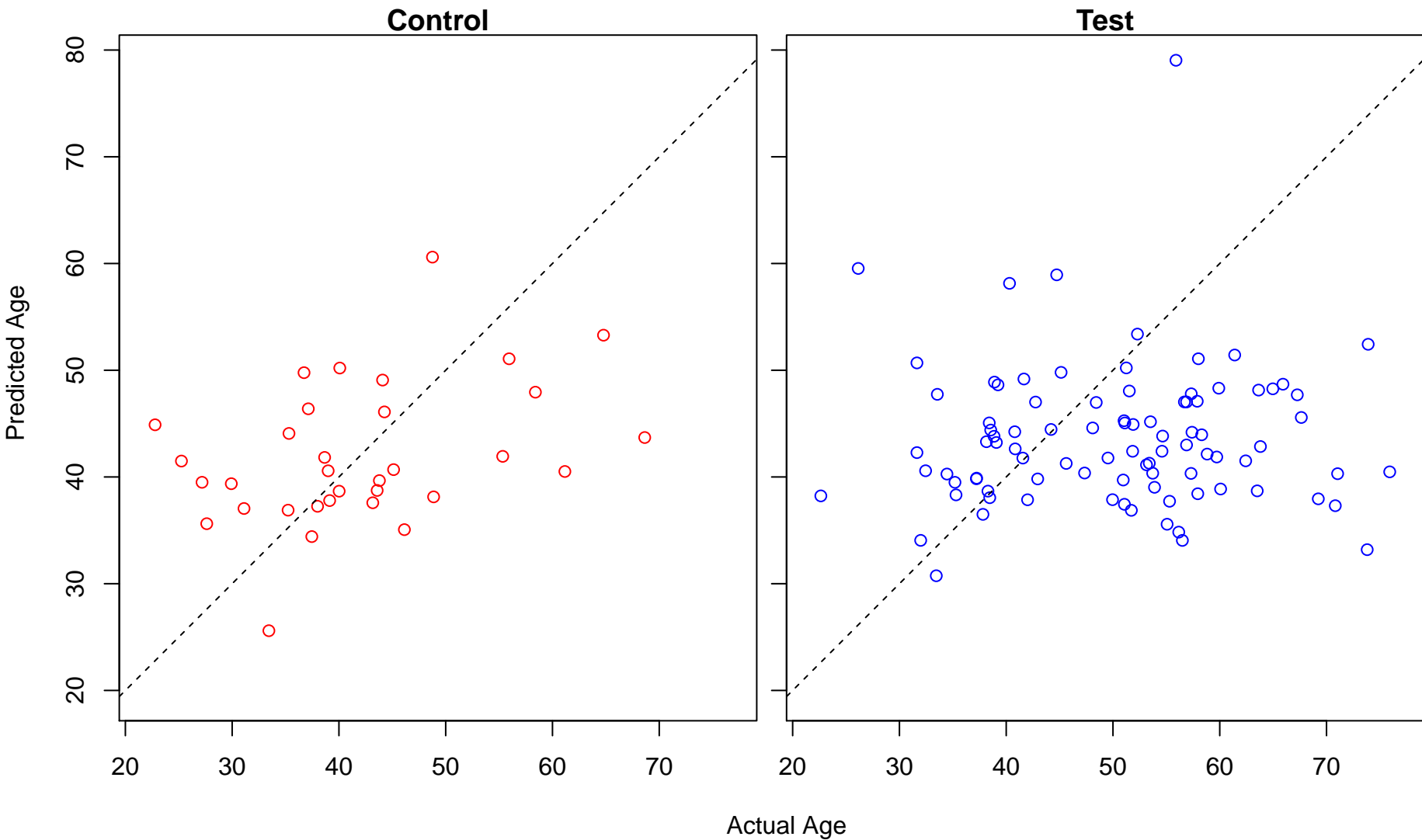
organonitrogen compound biosynthetic process (Score: 0.572633)



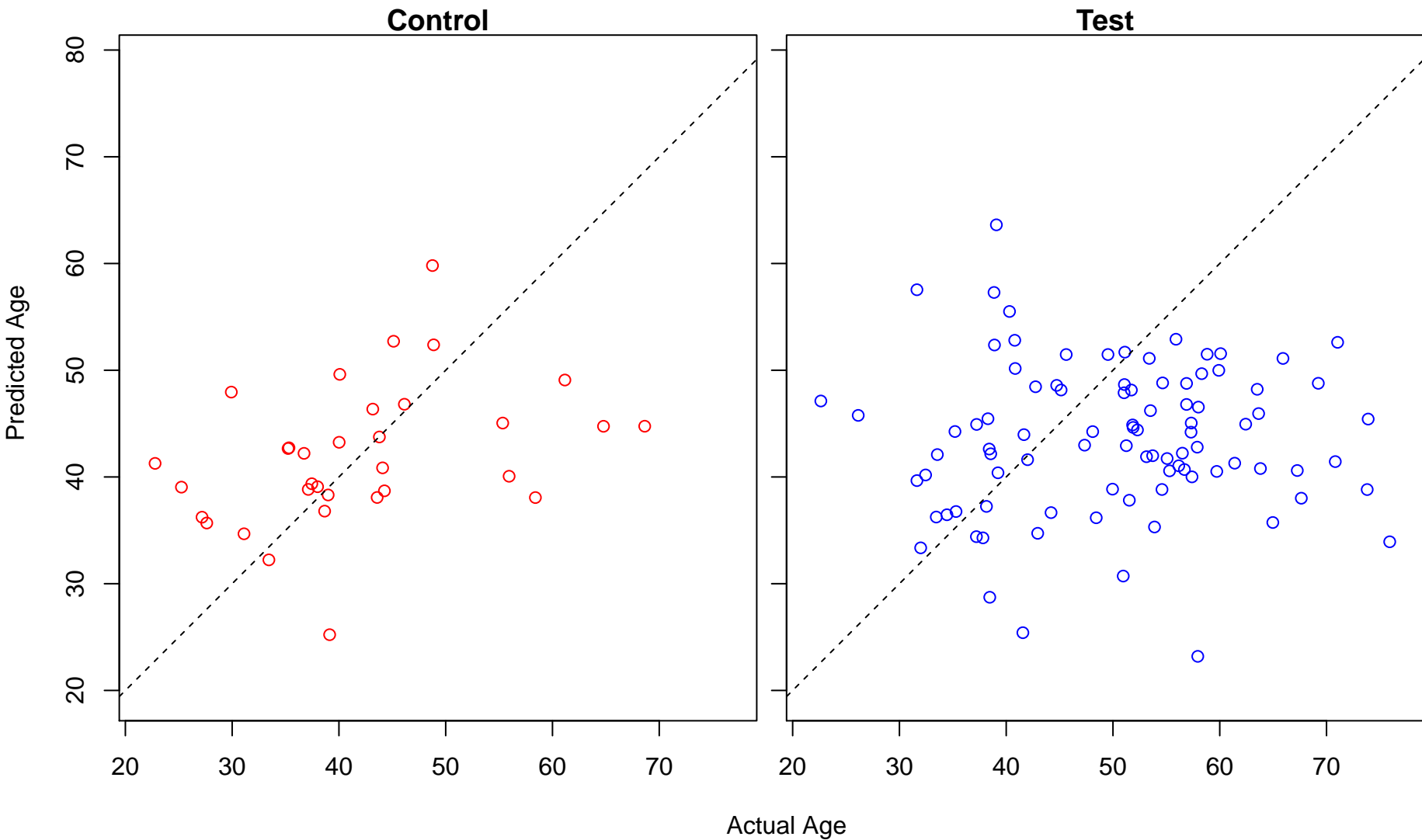
plus-end-directed vesicle transport along microtubule (Score: 0.572000)



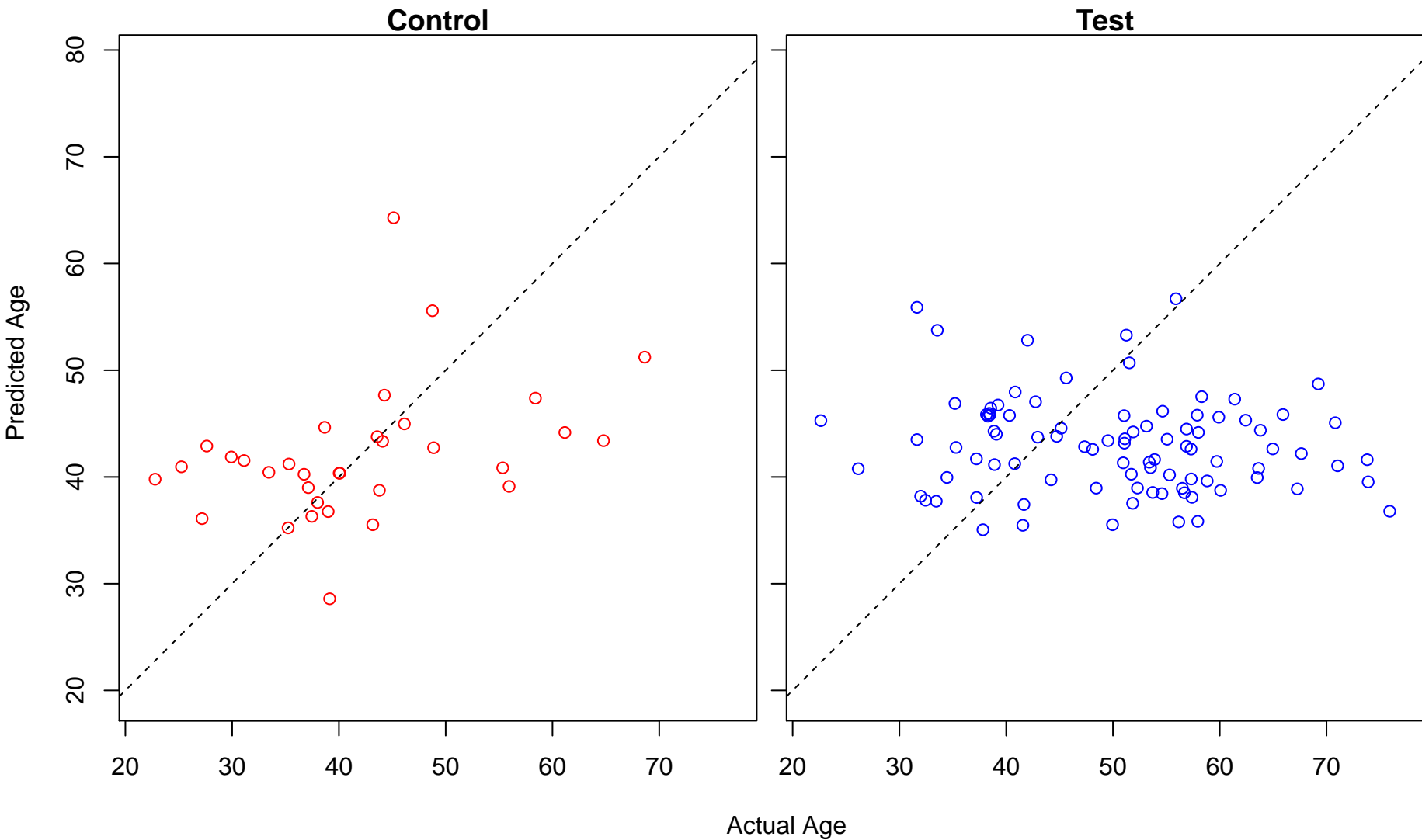
plus-end-directed organelle transport along microtubule (Score: 0.572000)



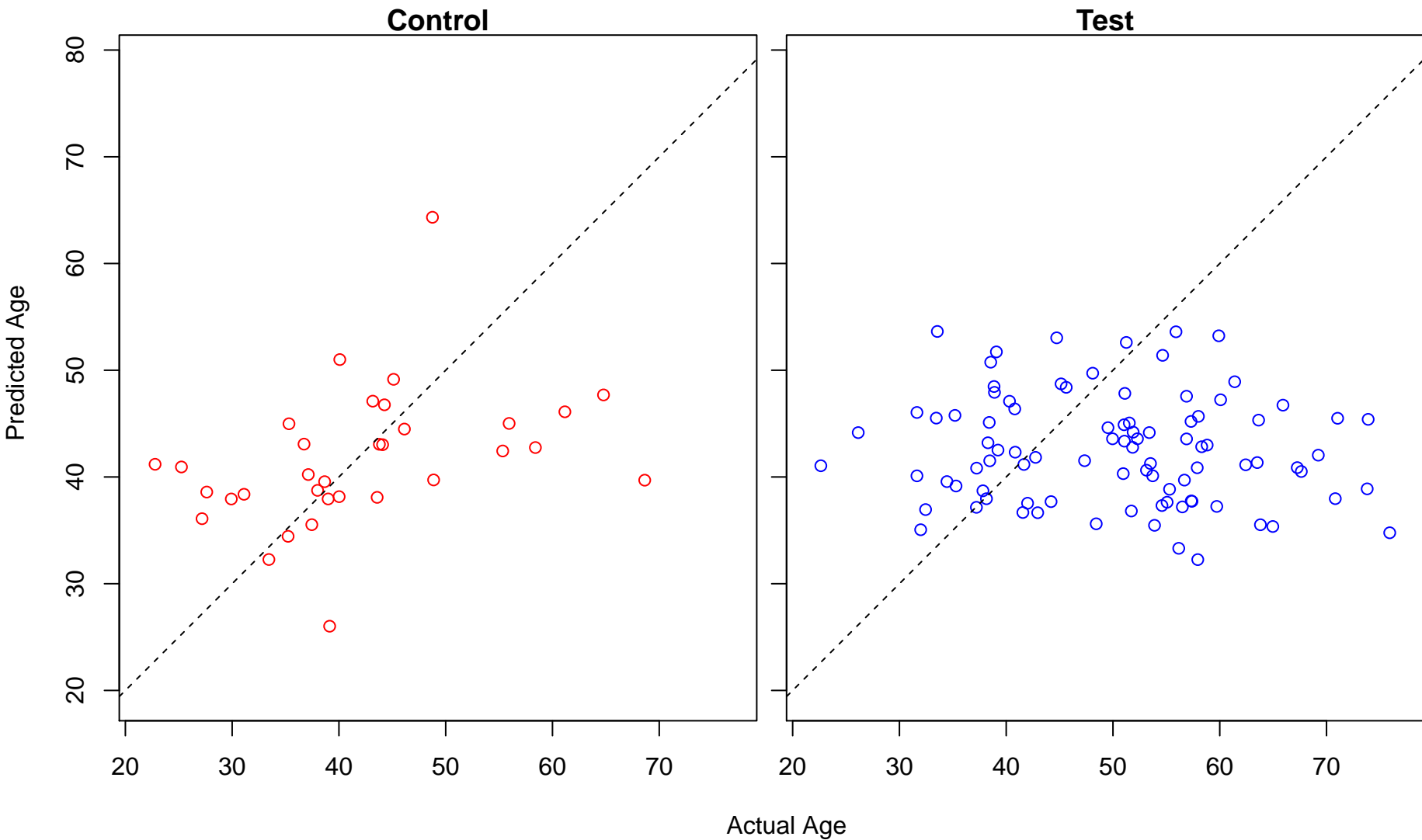
convergent extension (Score: 0.571900)



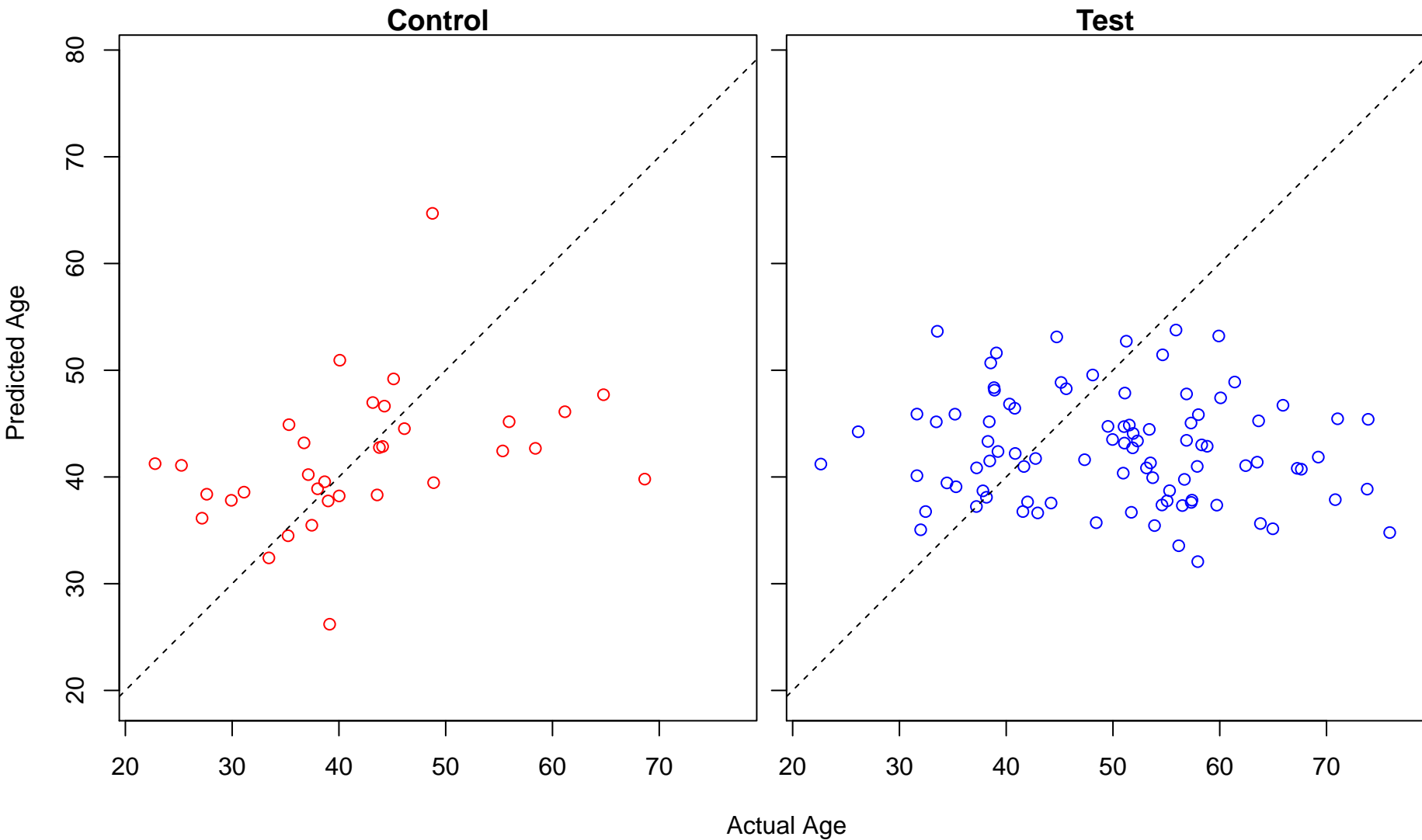
asparagine metabolic process (Score: 0.571696)



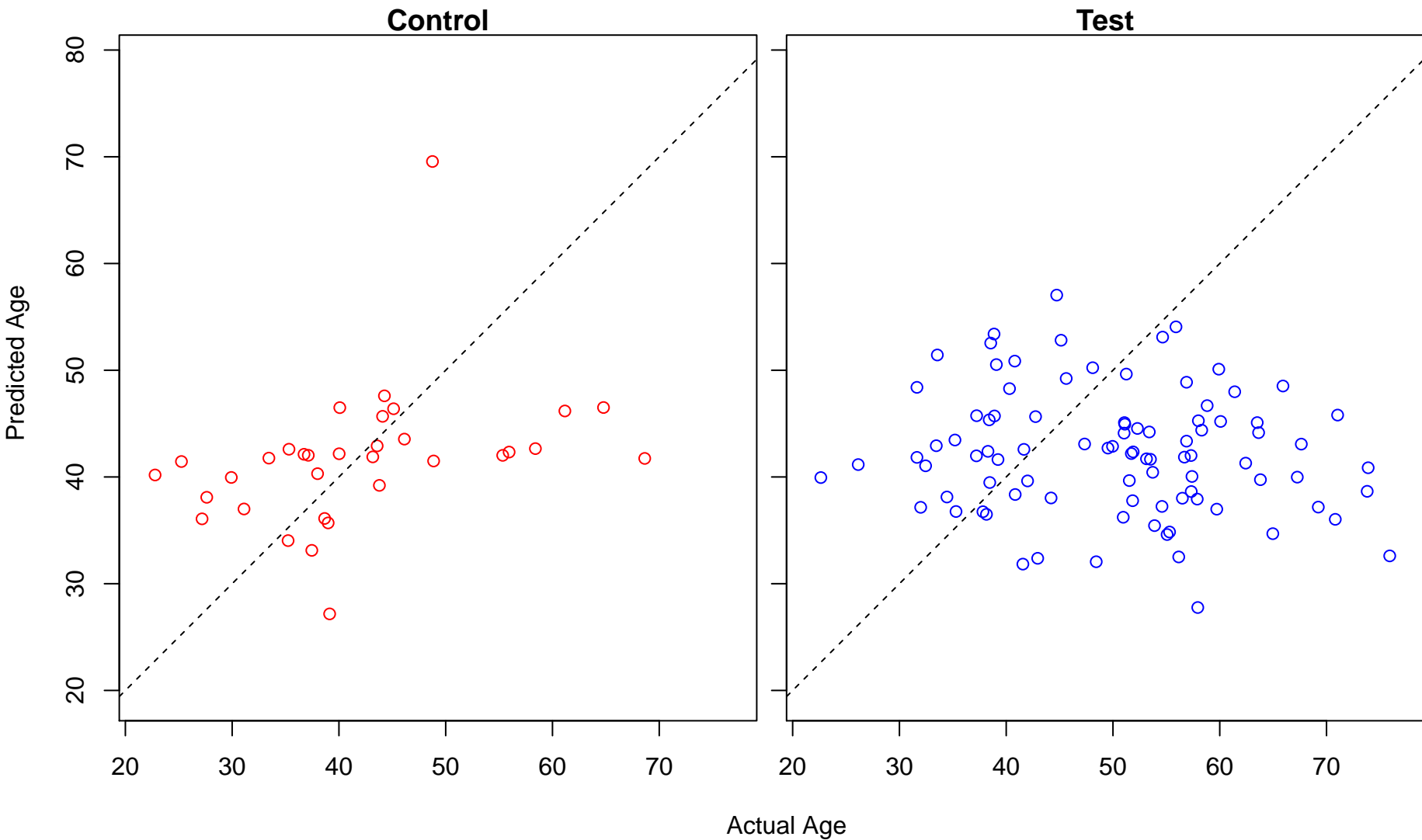
oxoacid metabolic process (Score: 0.571253)



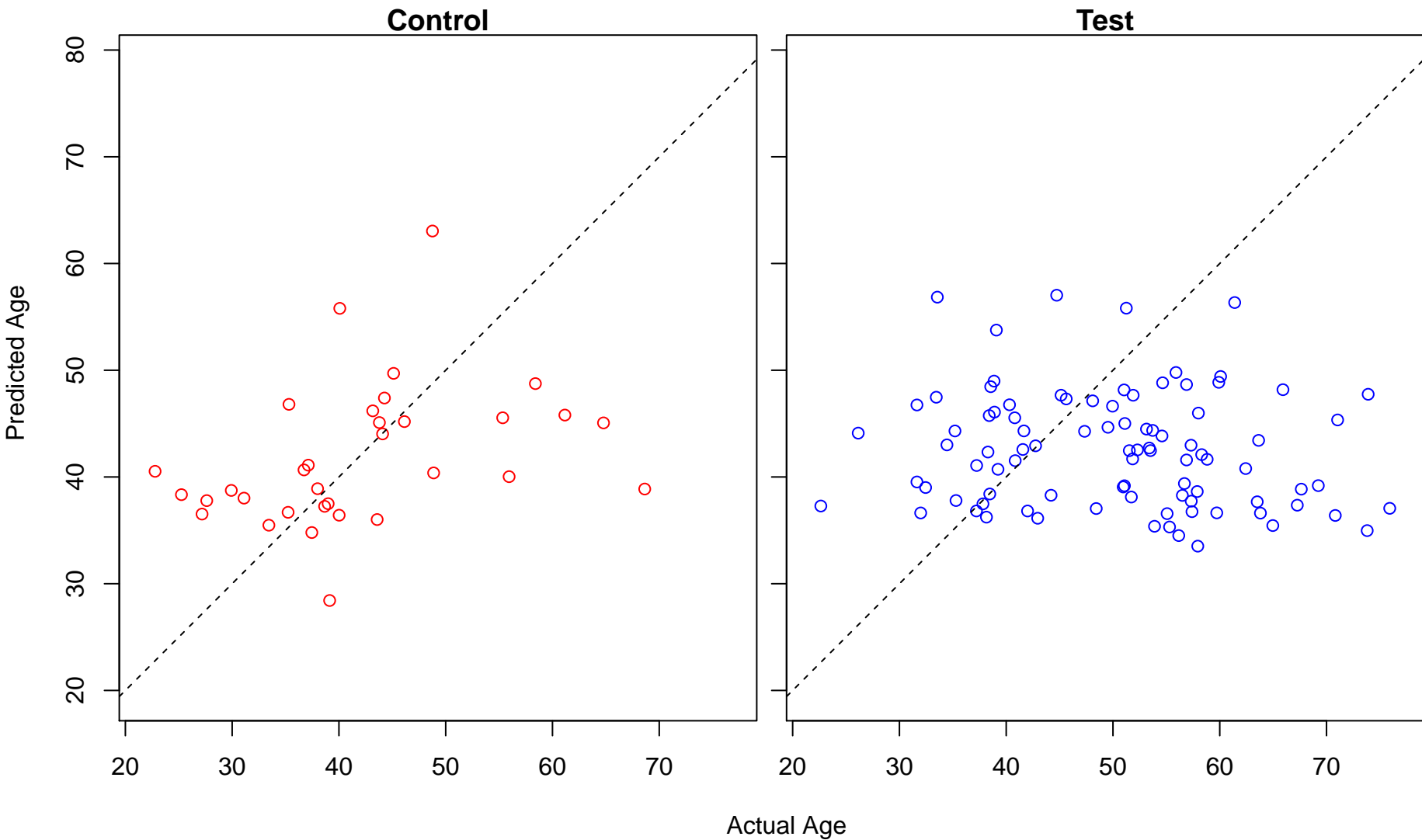
organic acid metabolic process (Score: 0.570771)



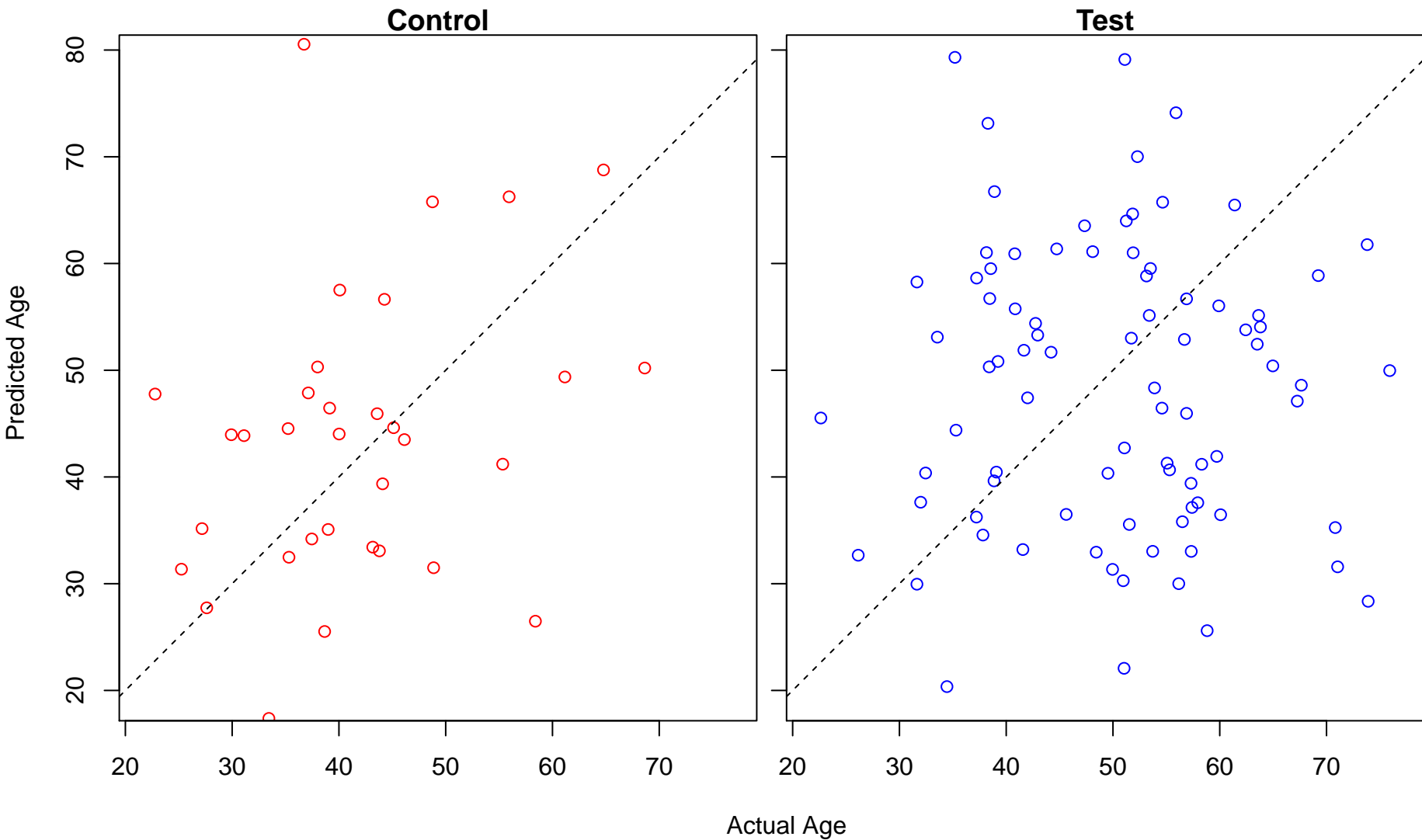
cellular response to organic cyclic compound (Score: 0.570691)



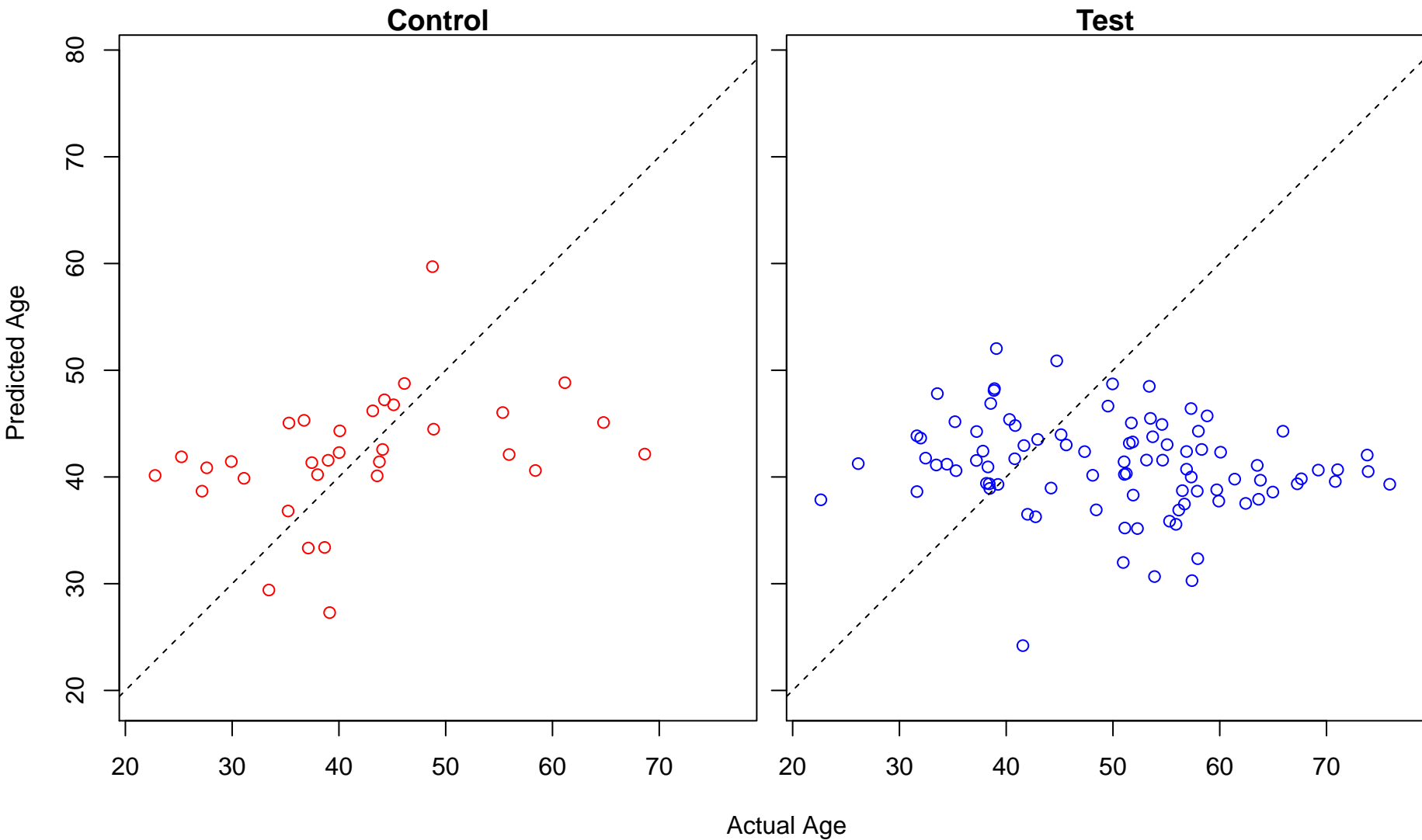
negative regulation of organelle organization (Score: 0.570469)



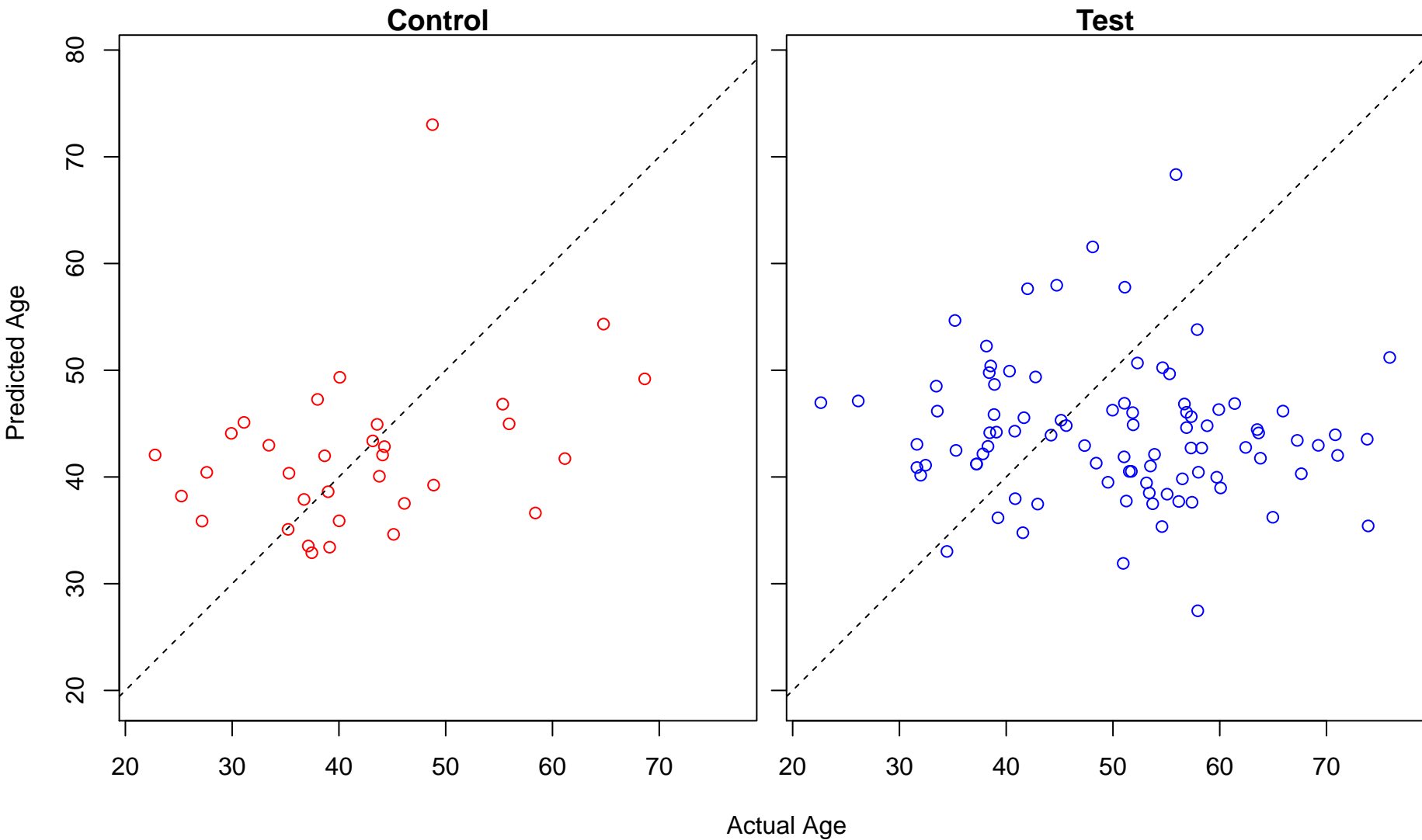
regulation of erythrocyte differentiation (Score: 0.569014)



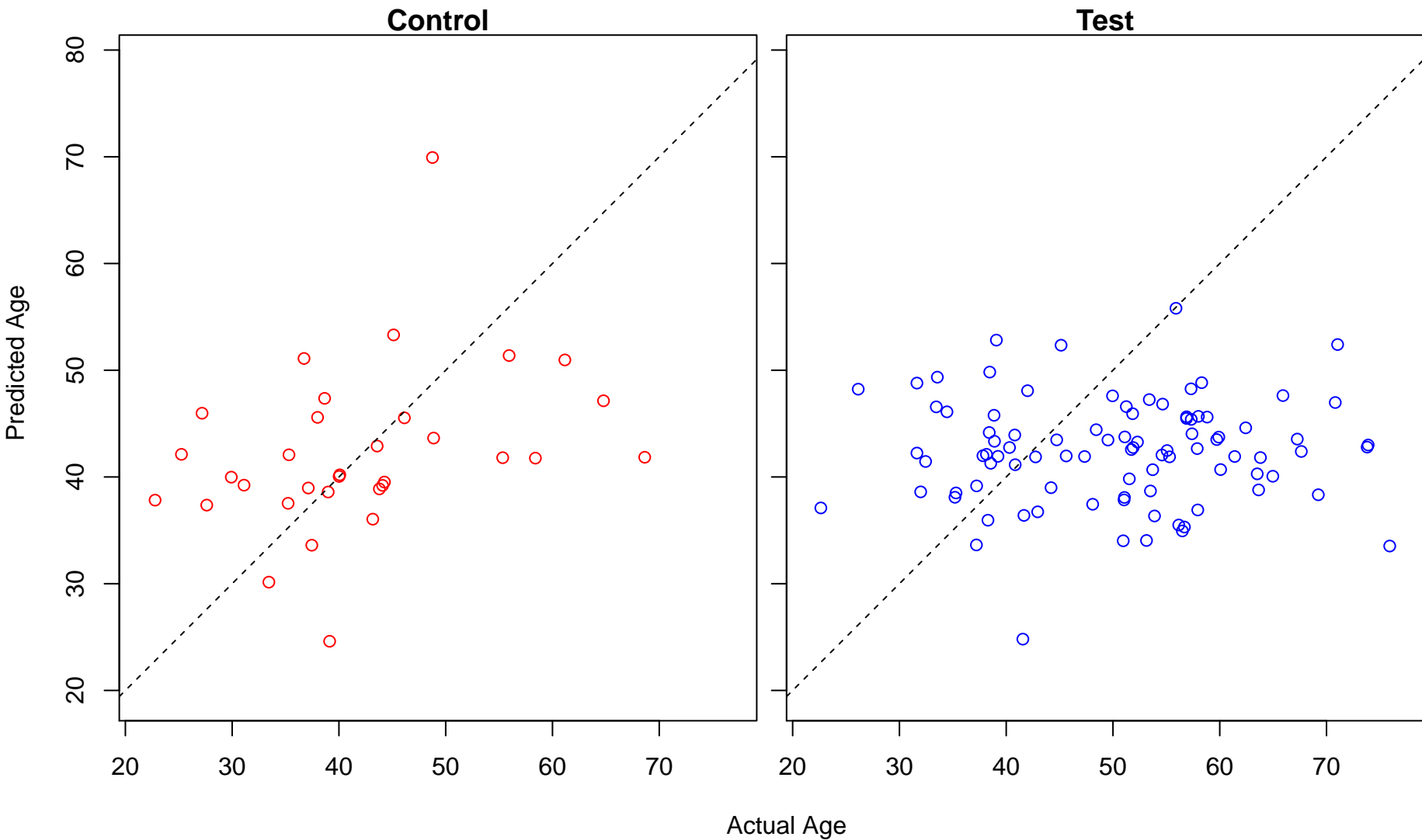
kinetochore organization (Score: 0.568776)



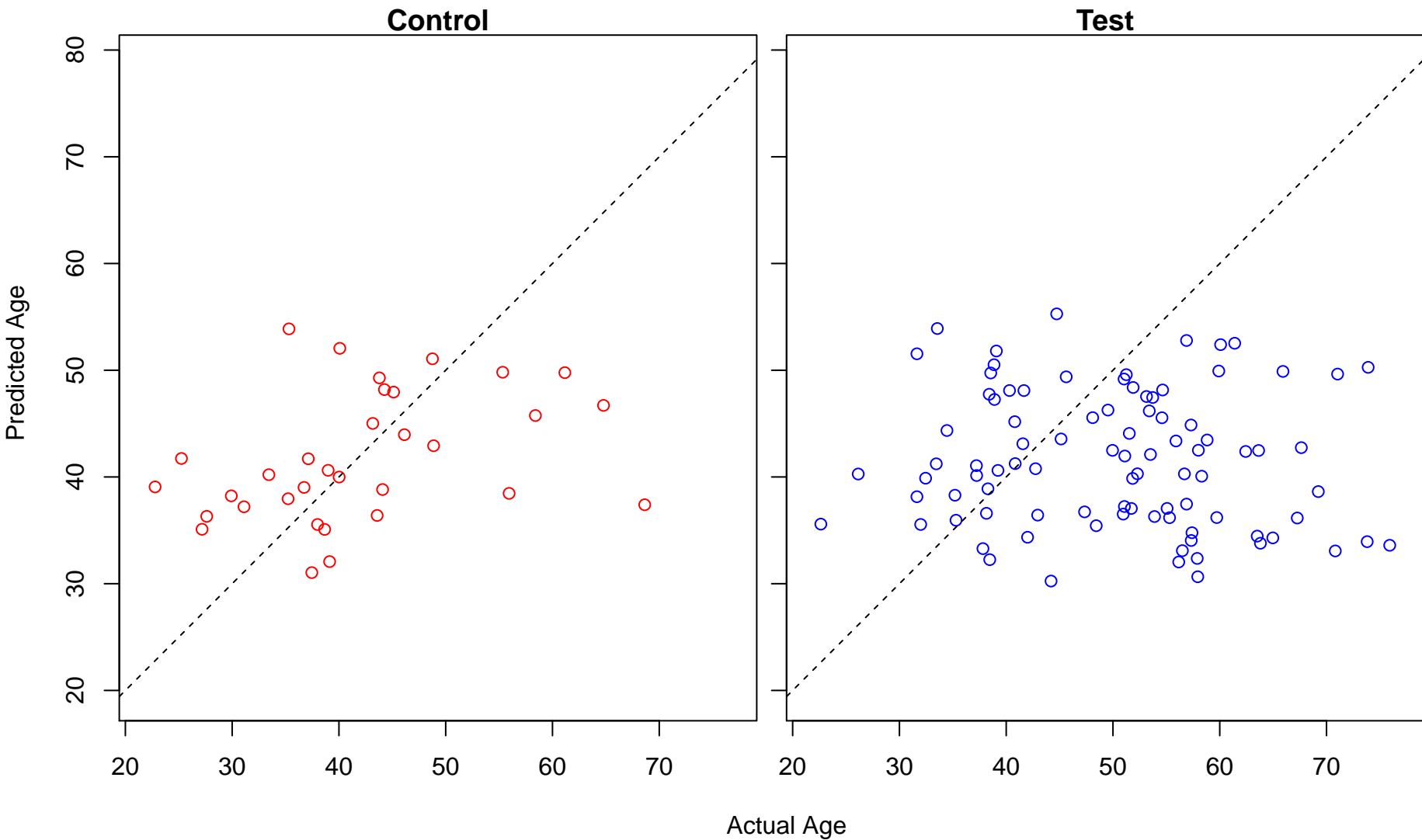
negative regulation of cell size (Score: 0.568631)



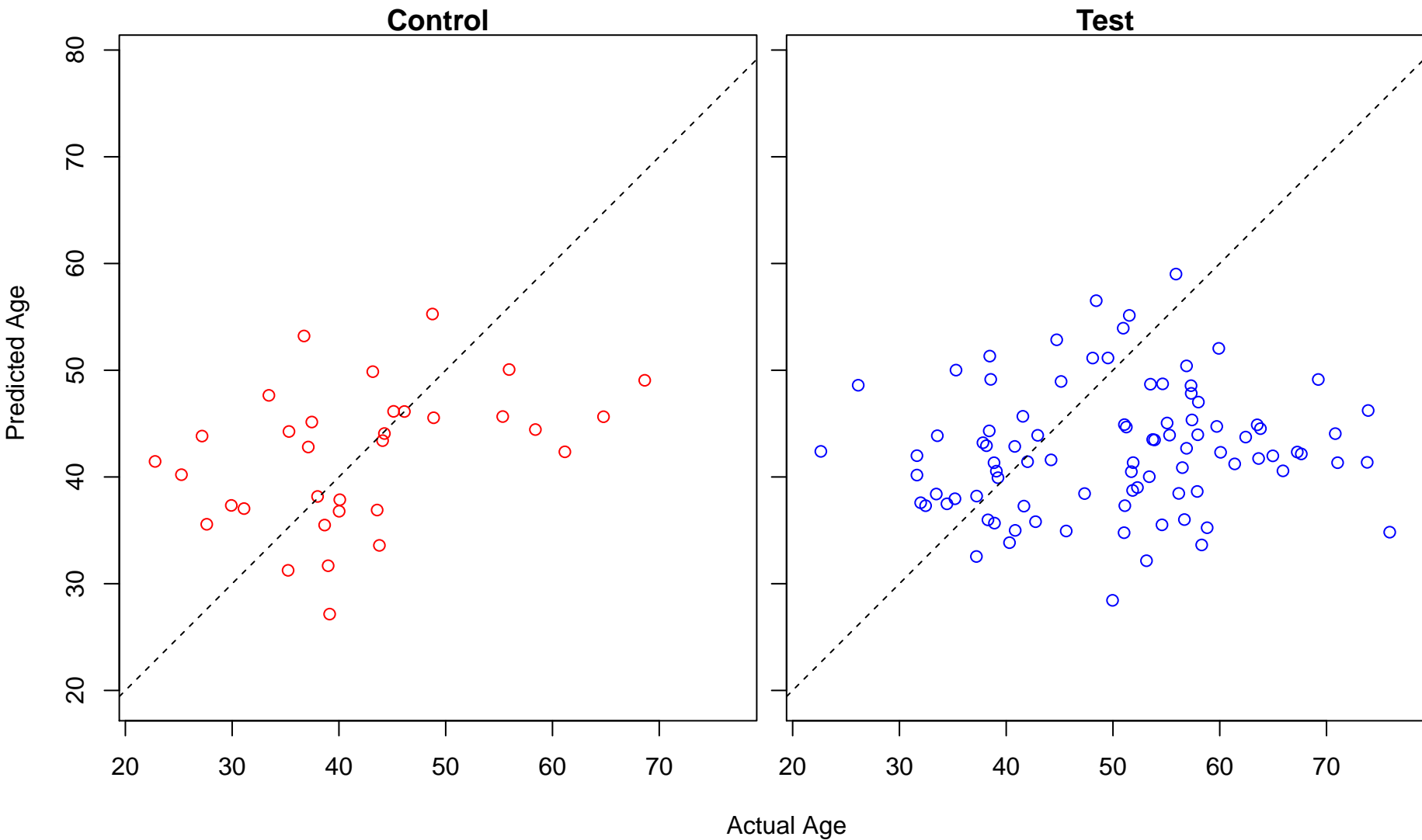
rRNA catabolic process (Score: 0.568269)



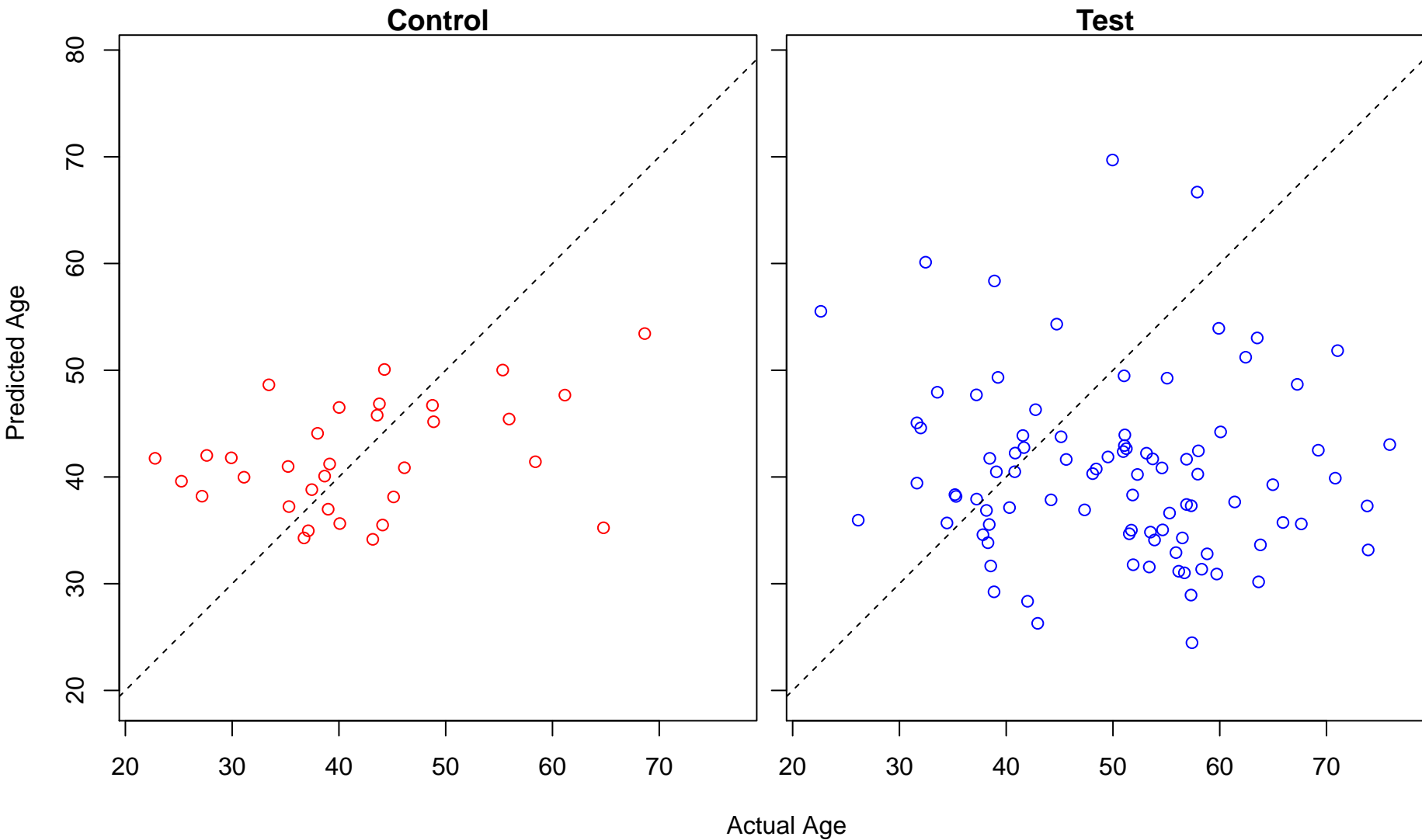
positive regulation of protein acetylation (Score: 0.568236)



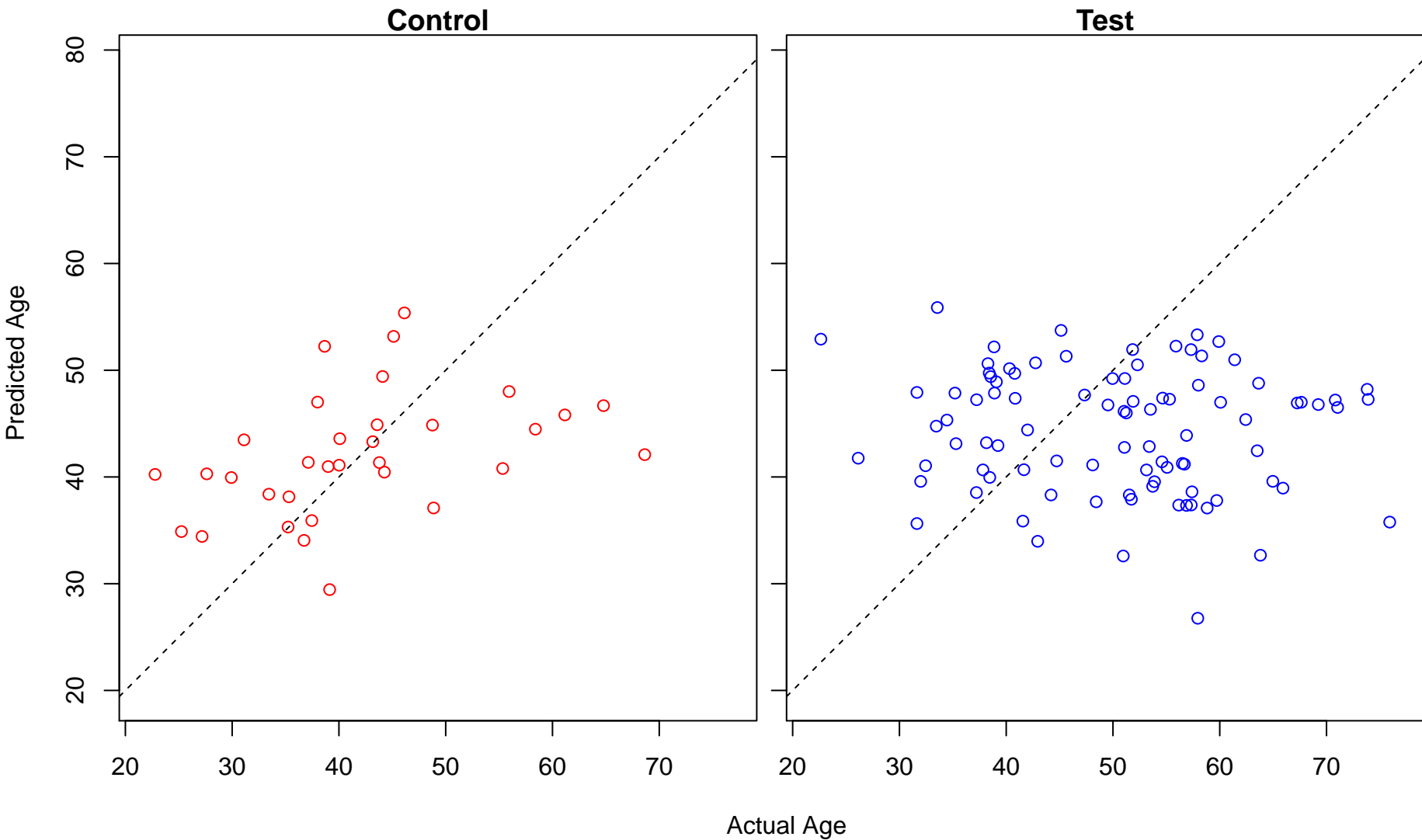
negative regulation of antigen processing and presentation (Score: 0.568235)



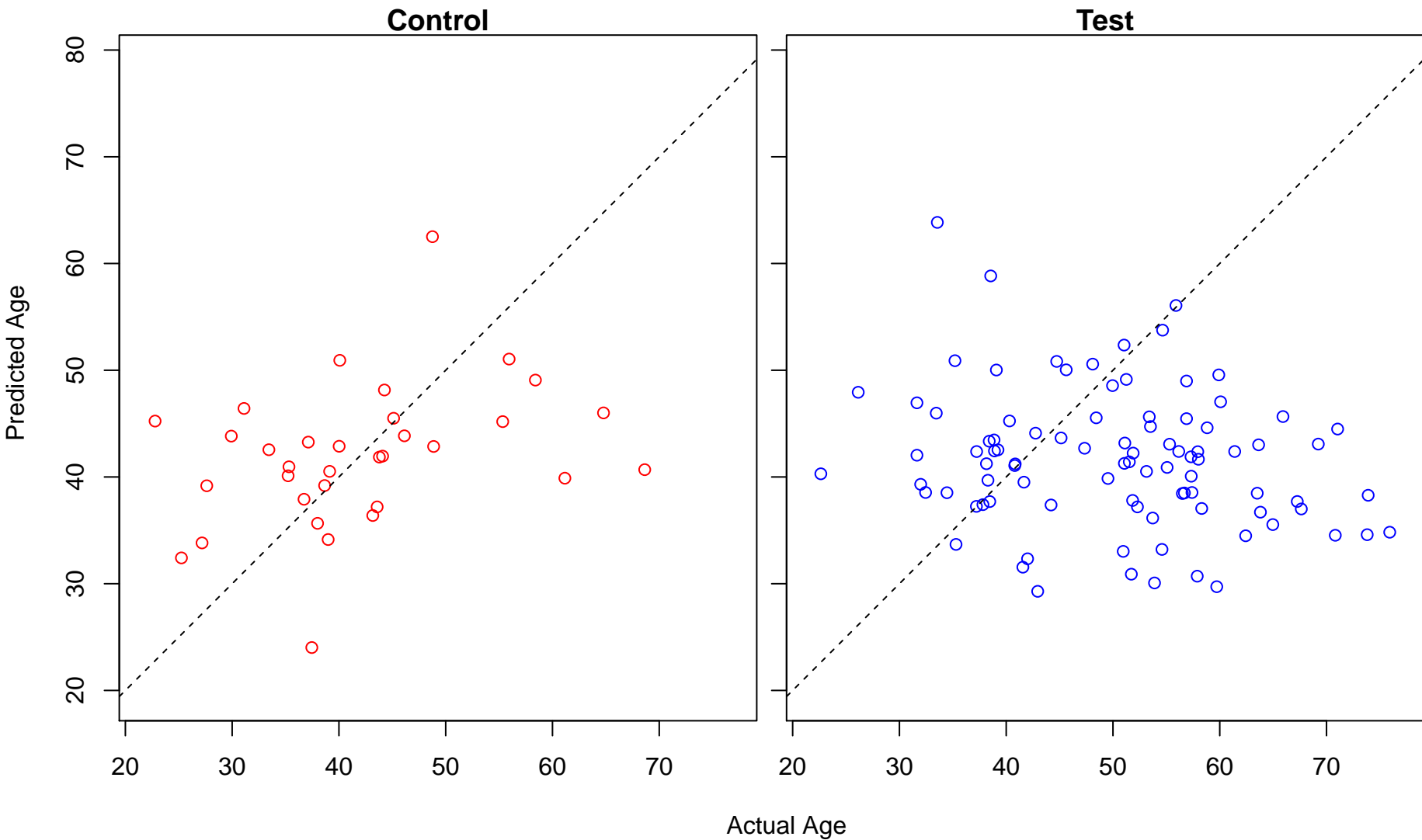
positive regulation of G0 to G1 transition (Score: 0.567203)



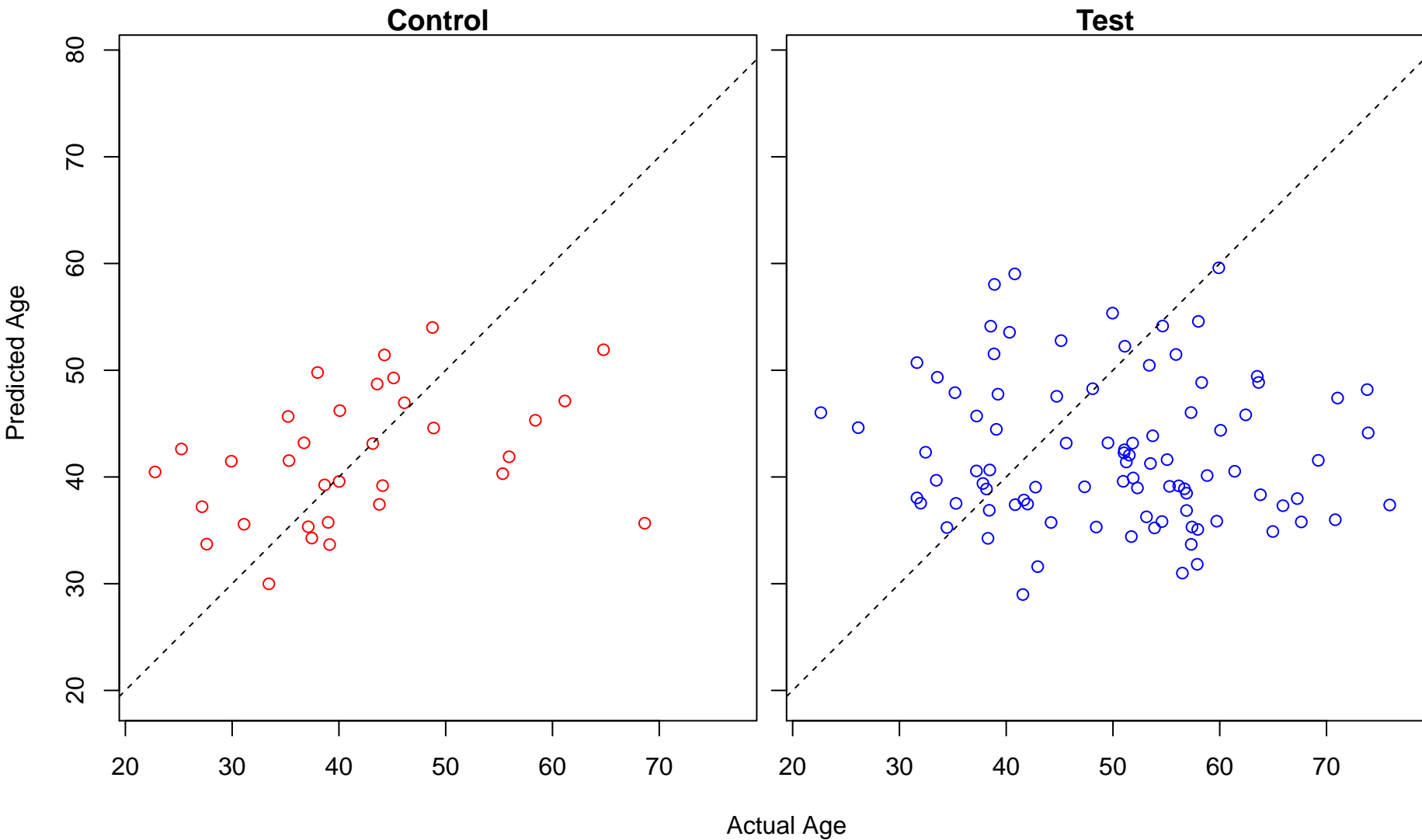
relaxation of smooth muscle (Score: 0.566737)



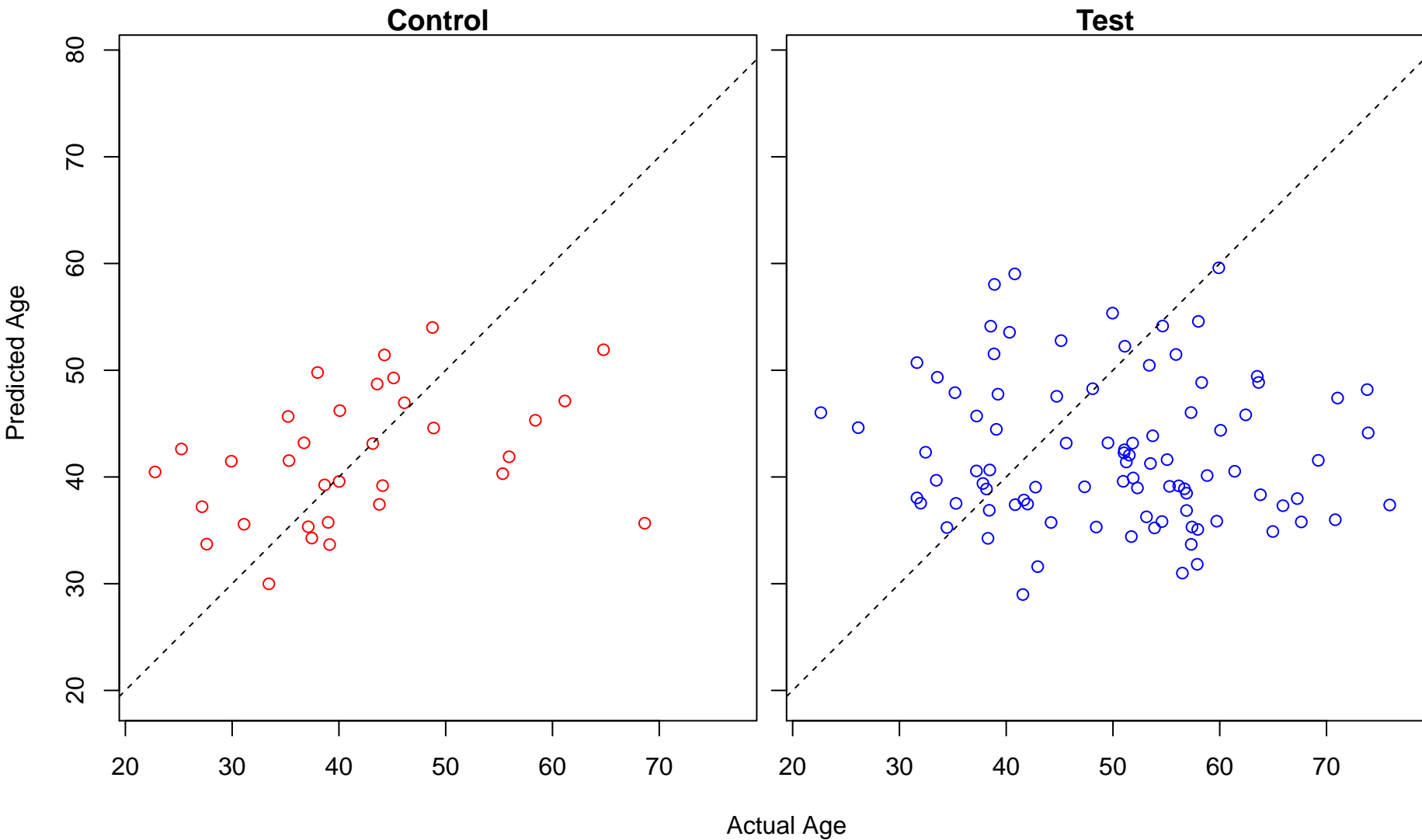
negative regulation of lyase activity (Score: 0.566388)



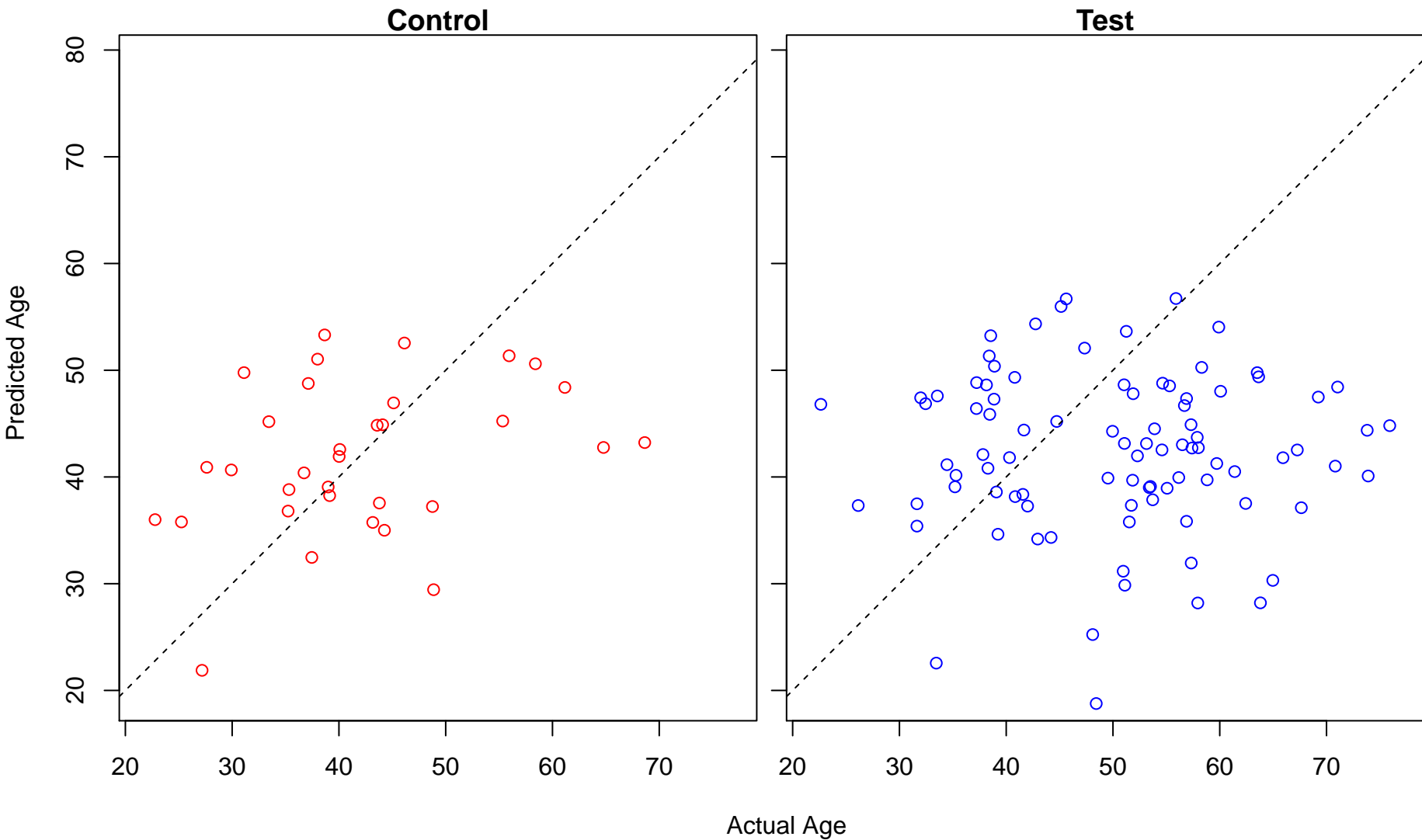
small nucleolar ribonucleoprotein complex assembly (Score: 0.566193)



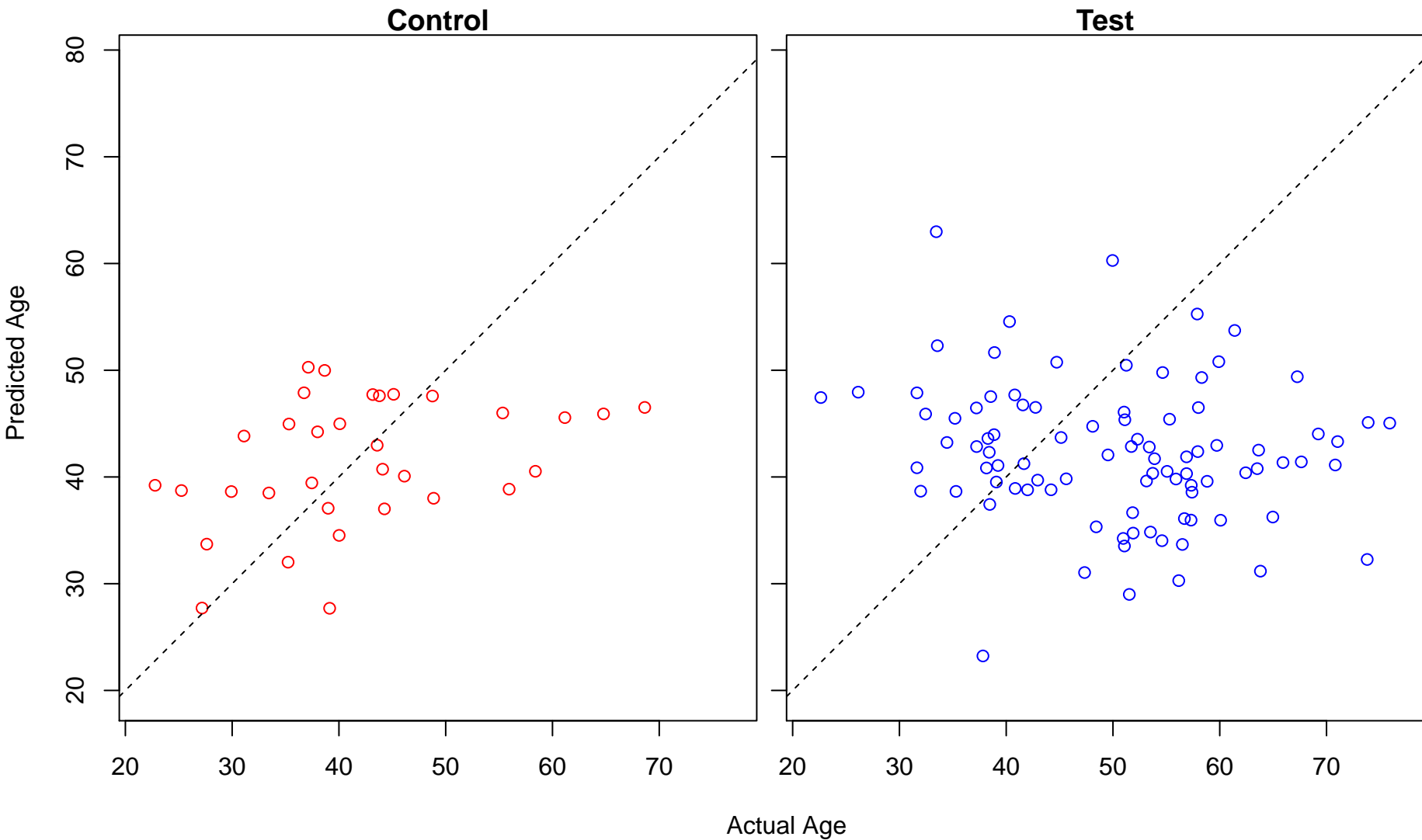
box C/D snoRNP assembly (Score: 0.566193)



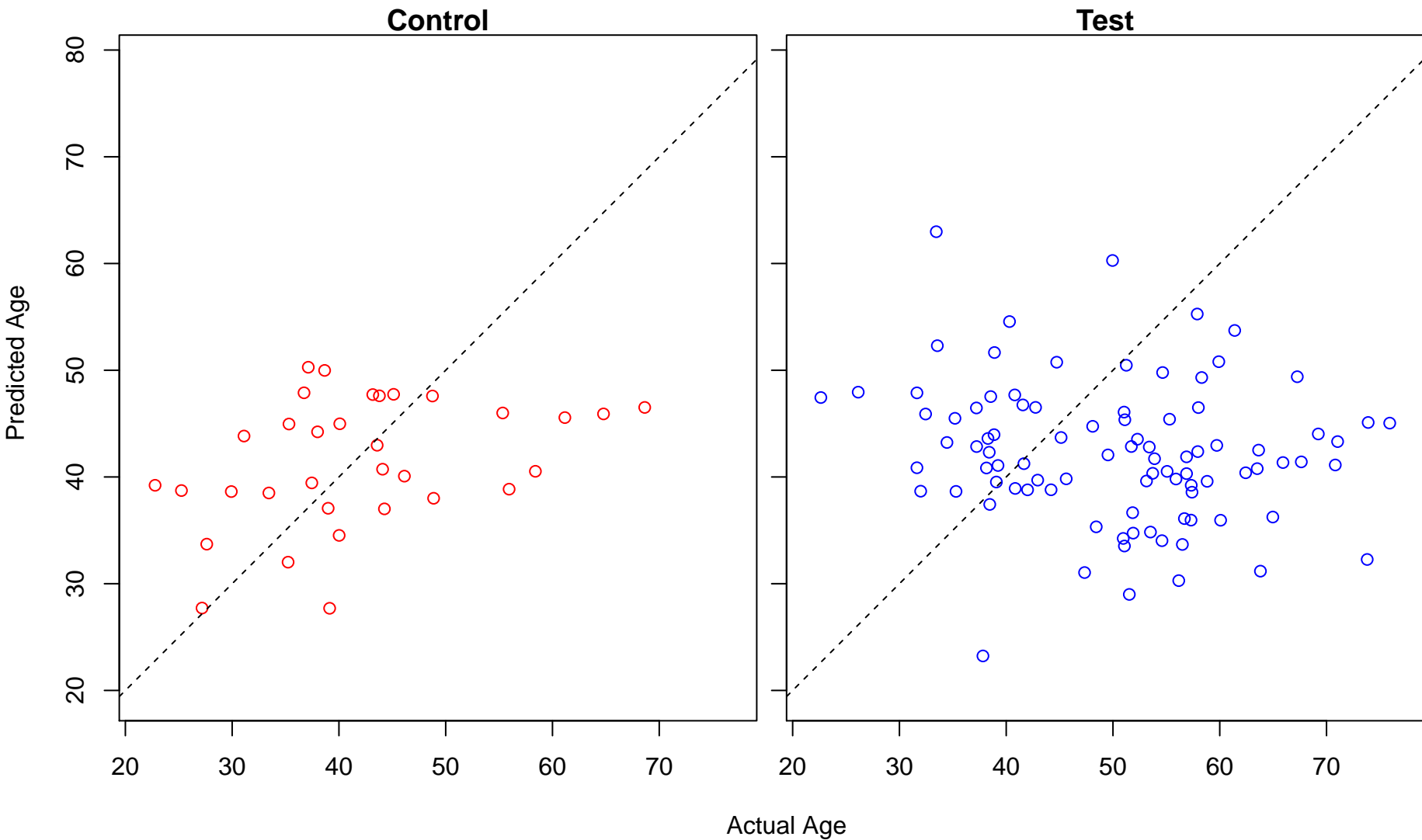
sodium ion homeostasis (Score: 0.564685)



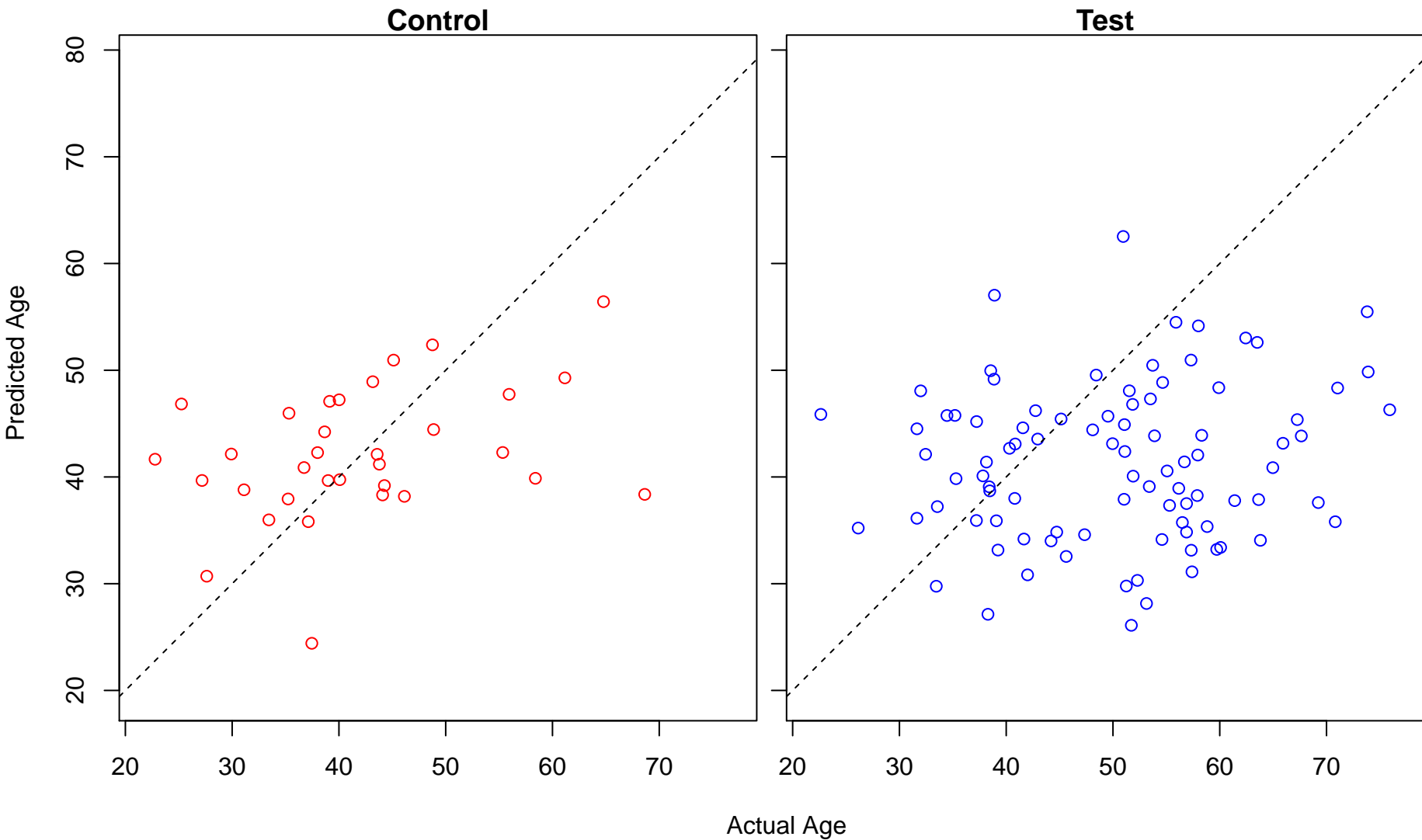
negative regulation of striated muscle tissue development (Score: 0.564673)



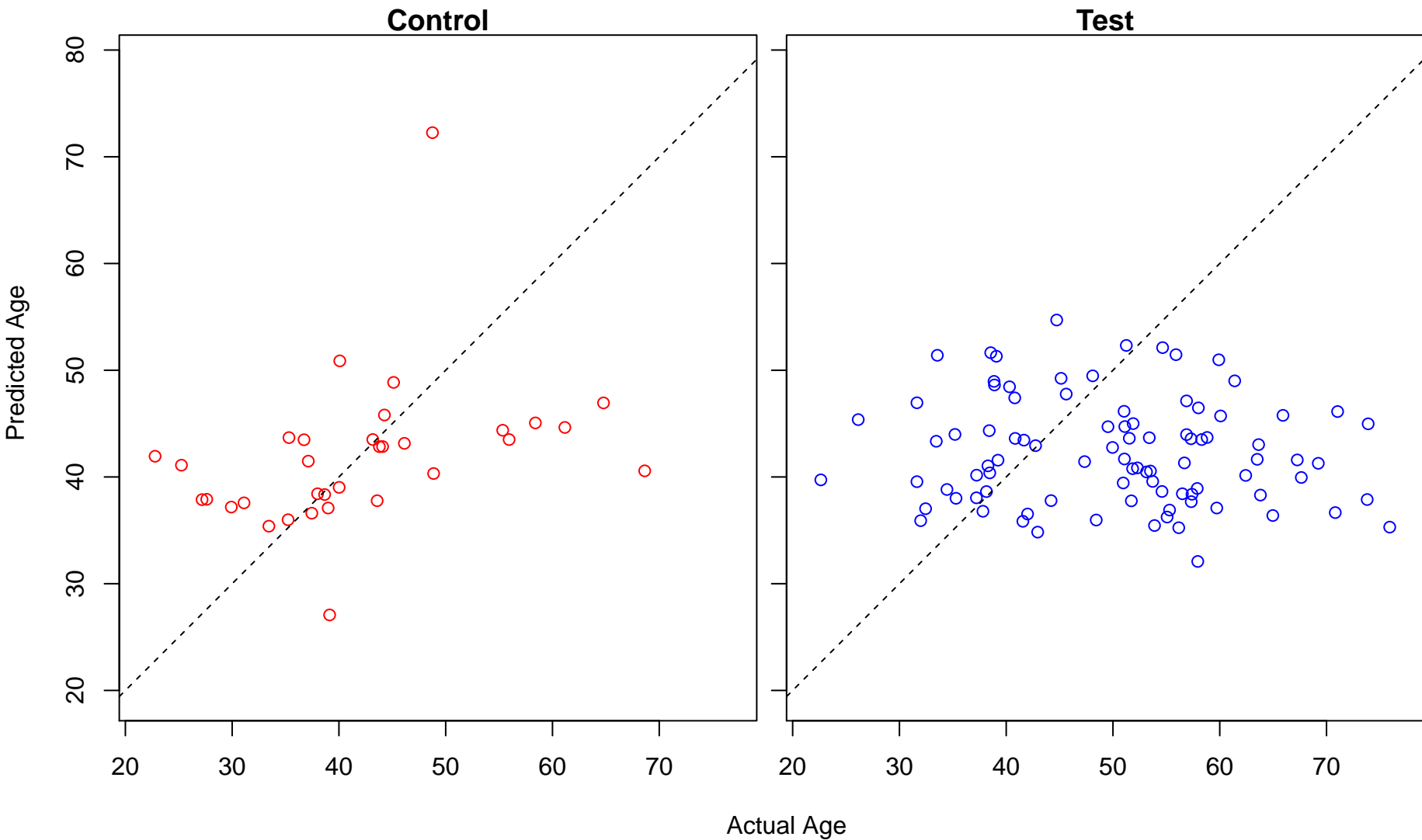
negative regulation of muscle tissue development (Score: 0.564673)



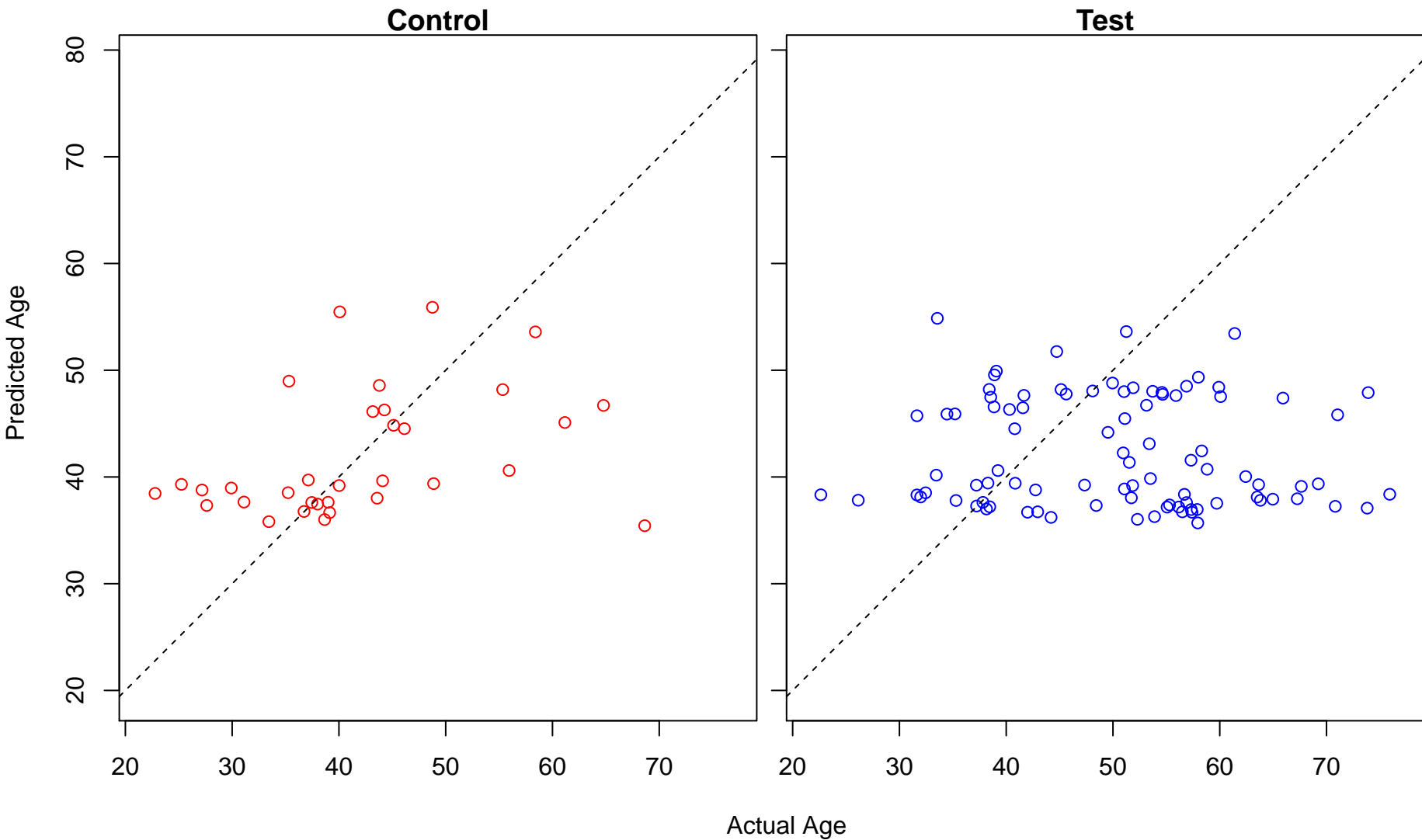
positive regulation of cellular extravasation (Score: 0.564642)



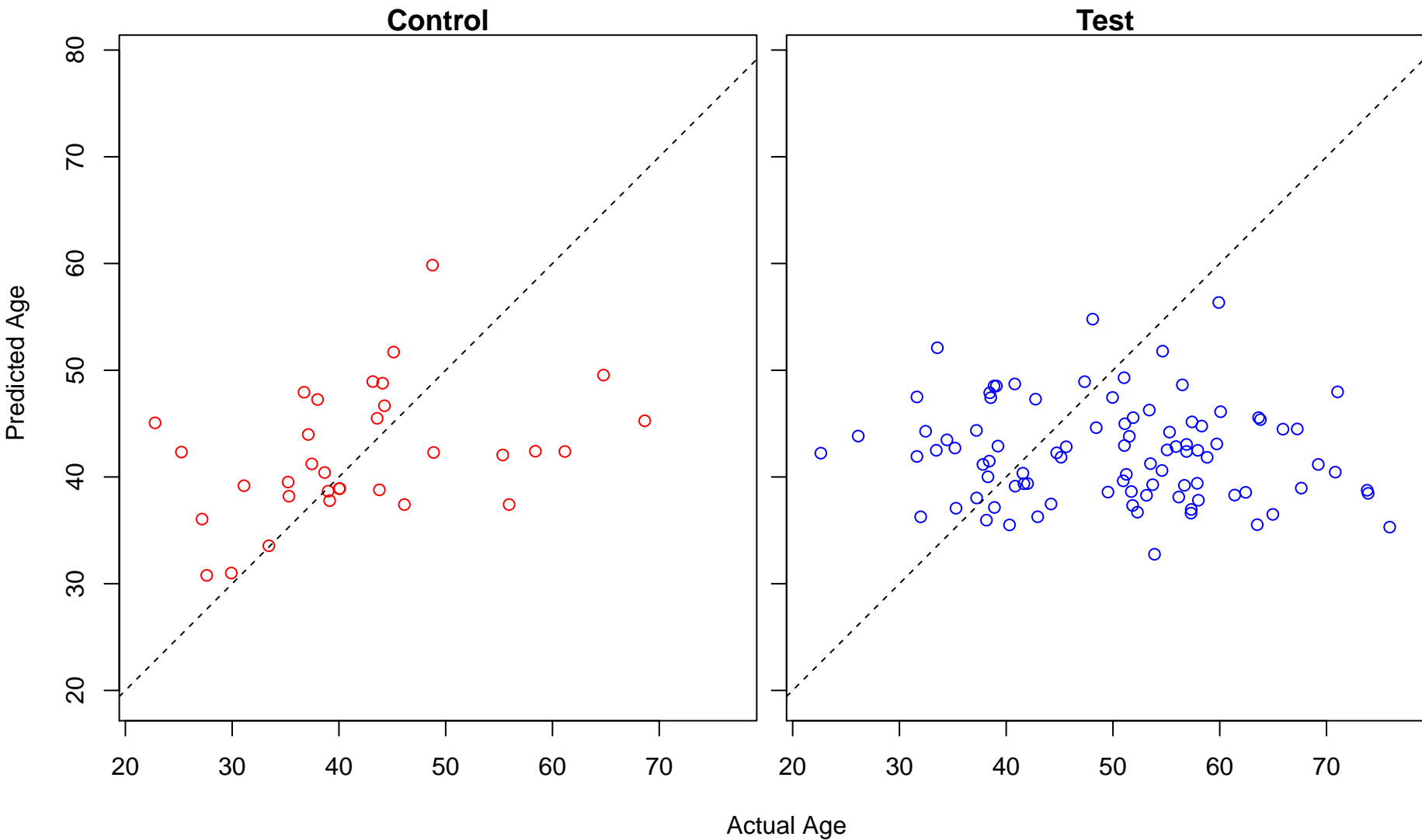
cellular macromolecule localization (Score: 0.564268)



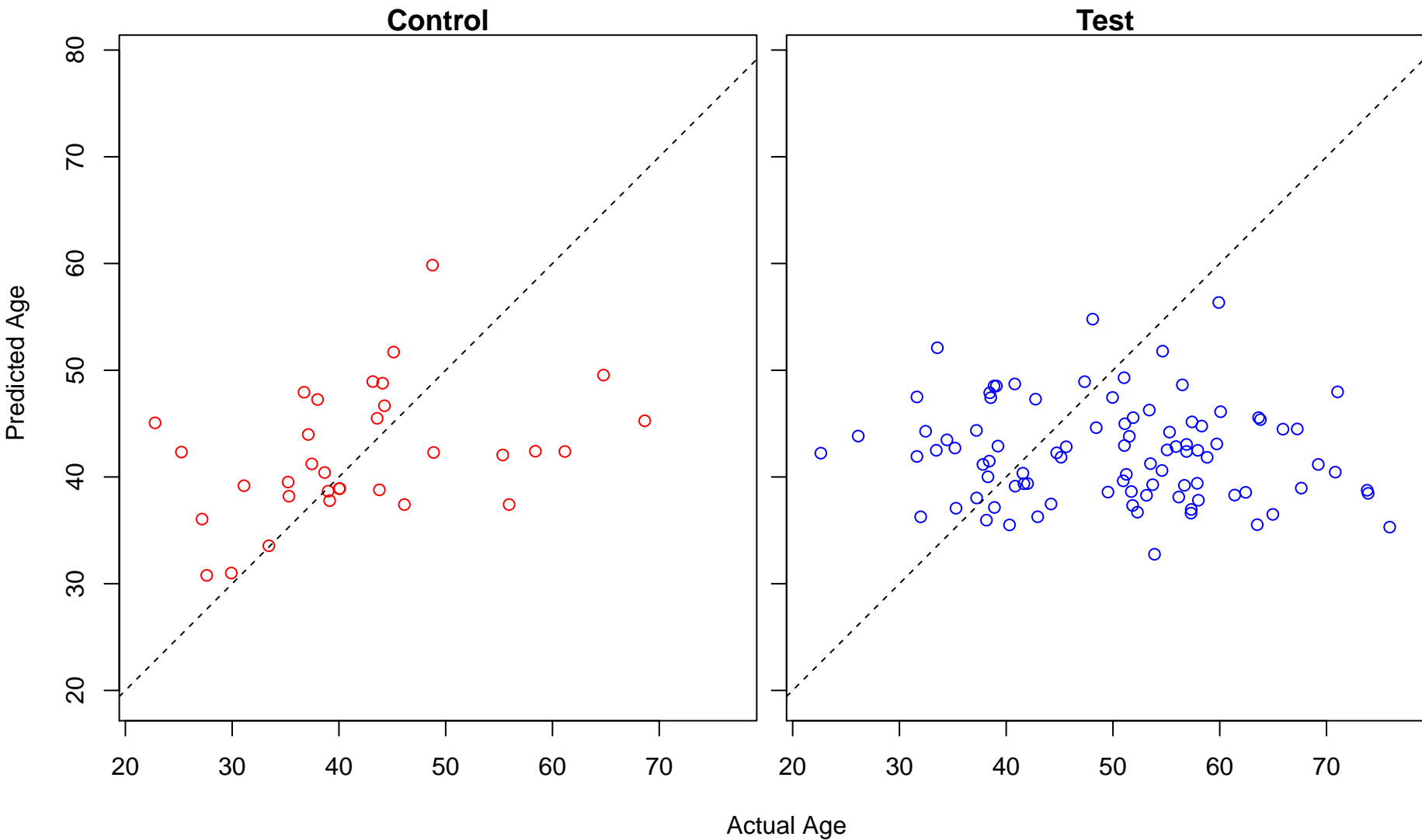
histone H2B ubiquitination (Score: 0.564134)



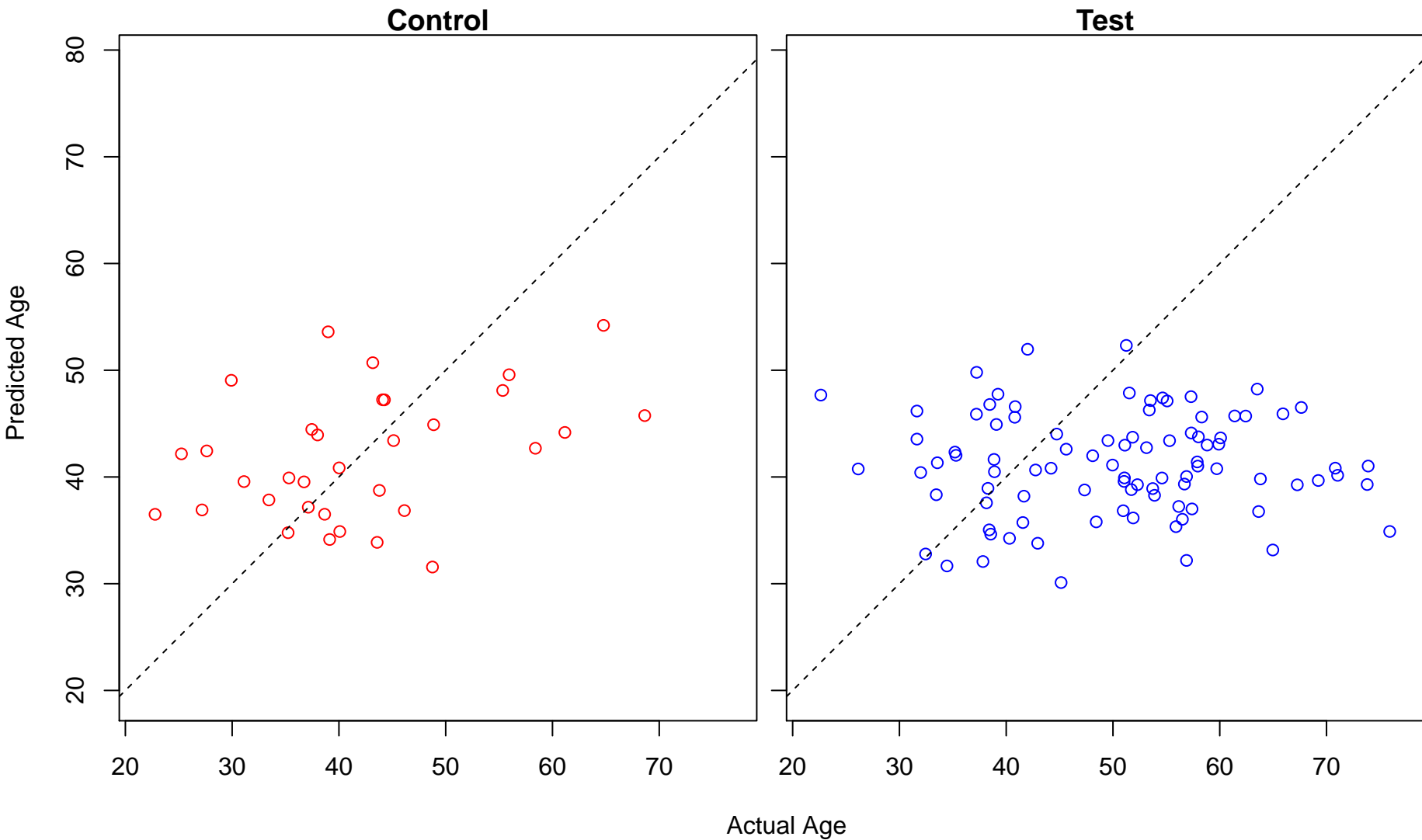
regulation of isotype switching to IgE isotypes (Score: 0.563311)



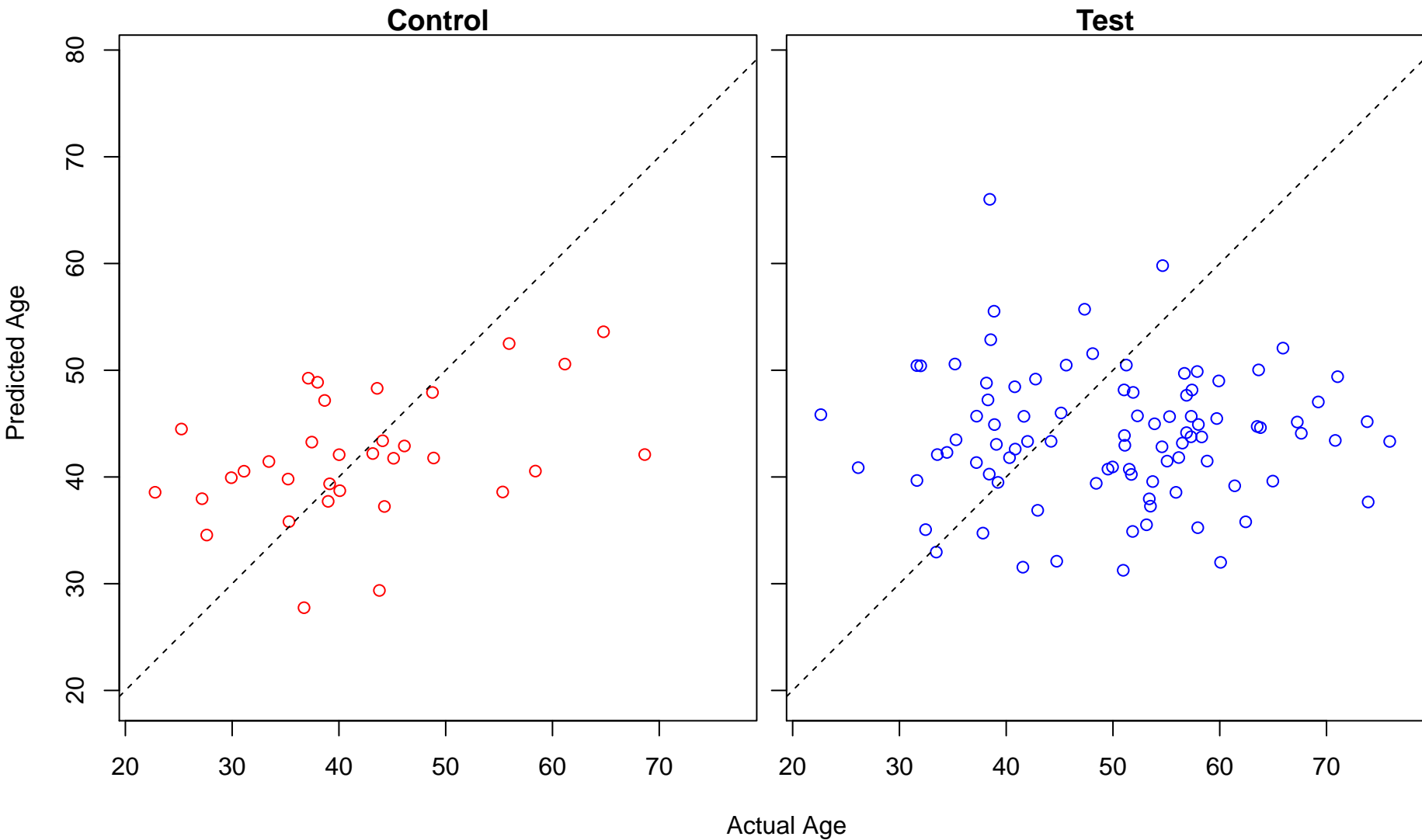
positive regulation of isotype switching to IgE isotypes (Score: 0.563311)



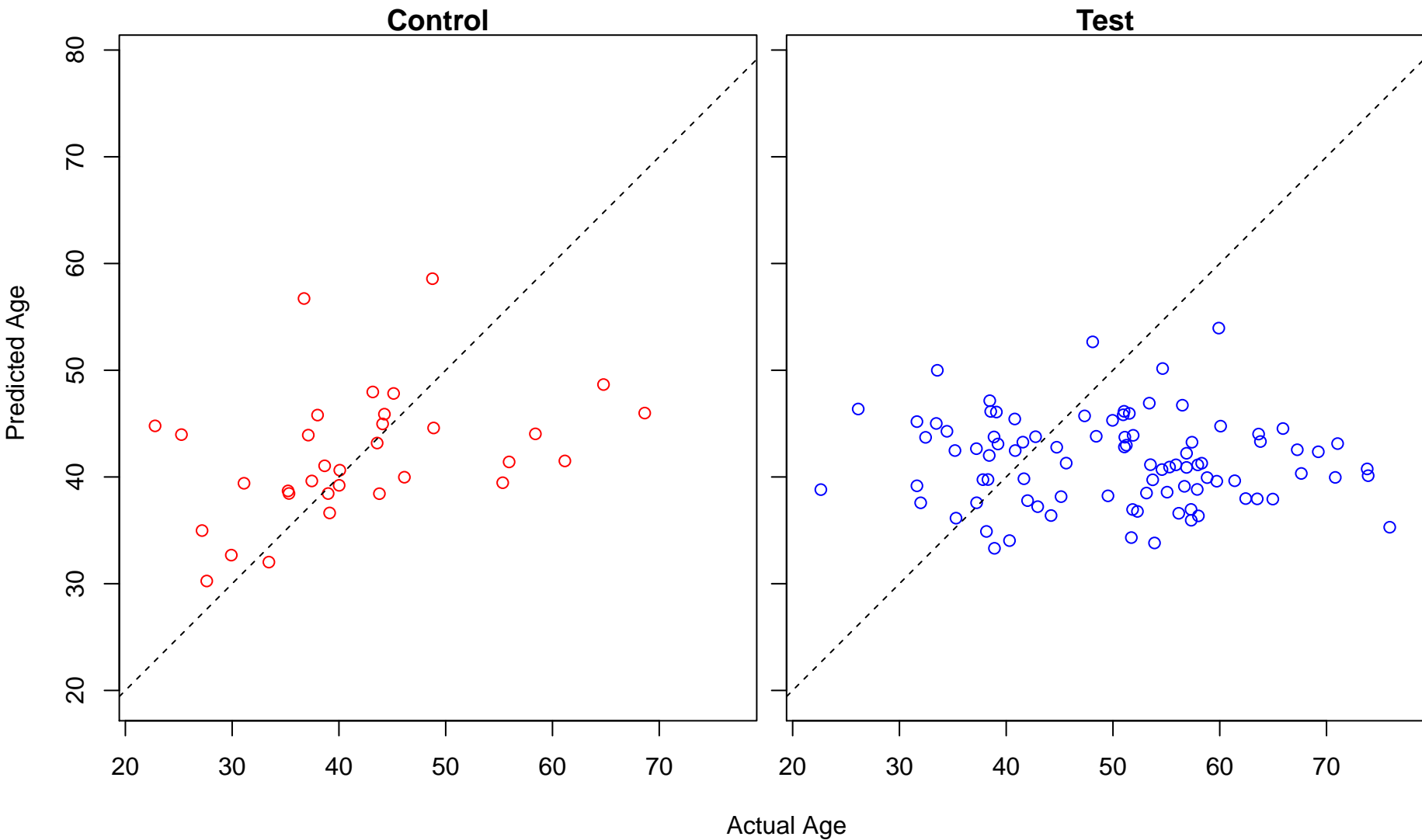
intestinal cholesterol absorption (Score: 0.562699)



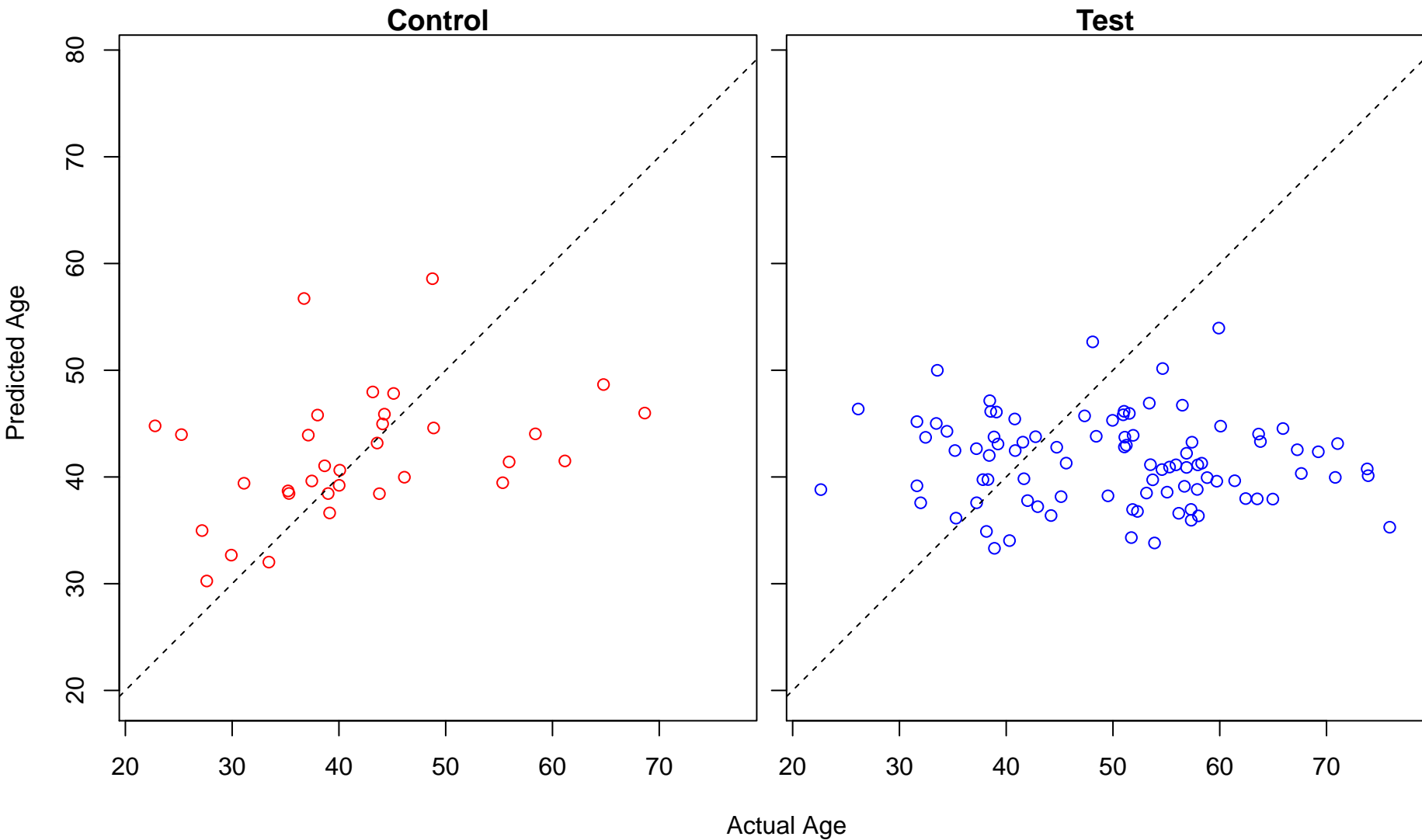
platelet activating factor biosynthetic process (Score: 0.562437)



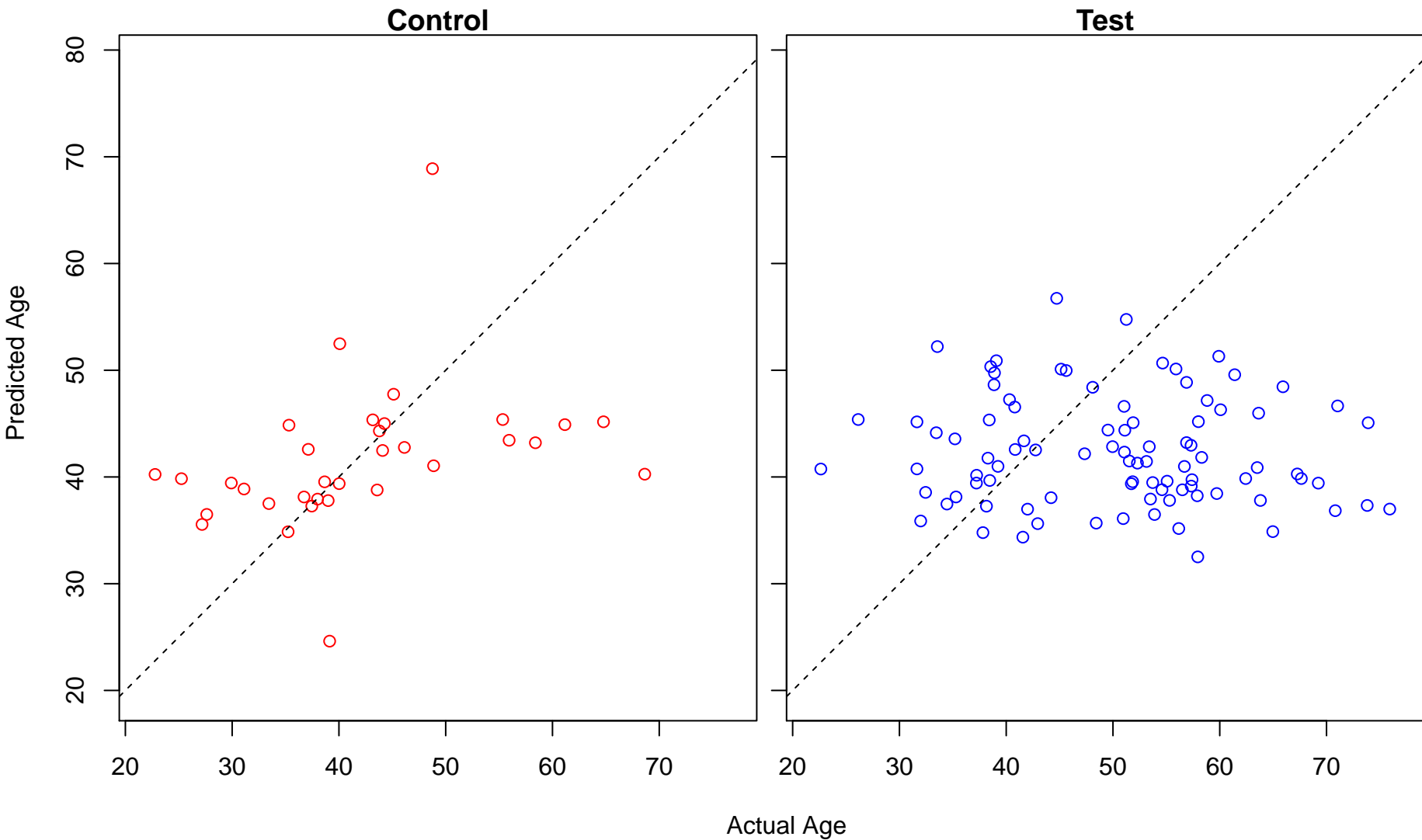
regulation of memory T cell differentiation (Score: 0.562024)



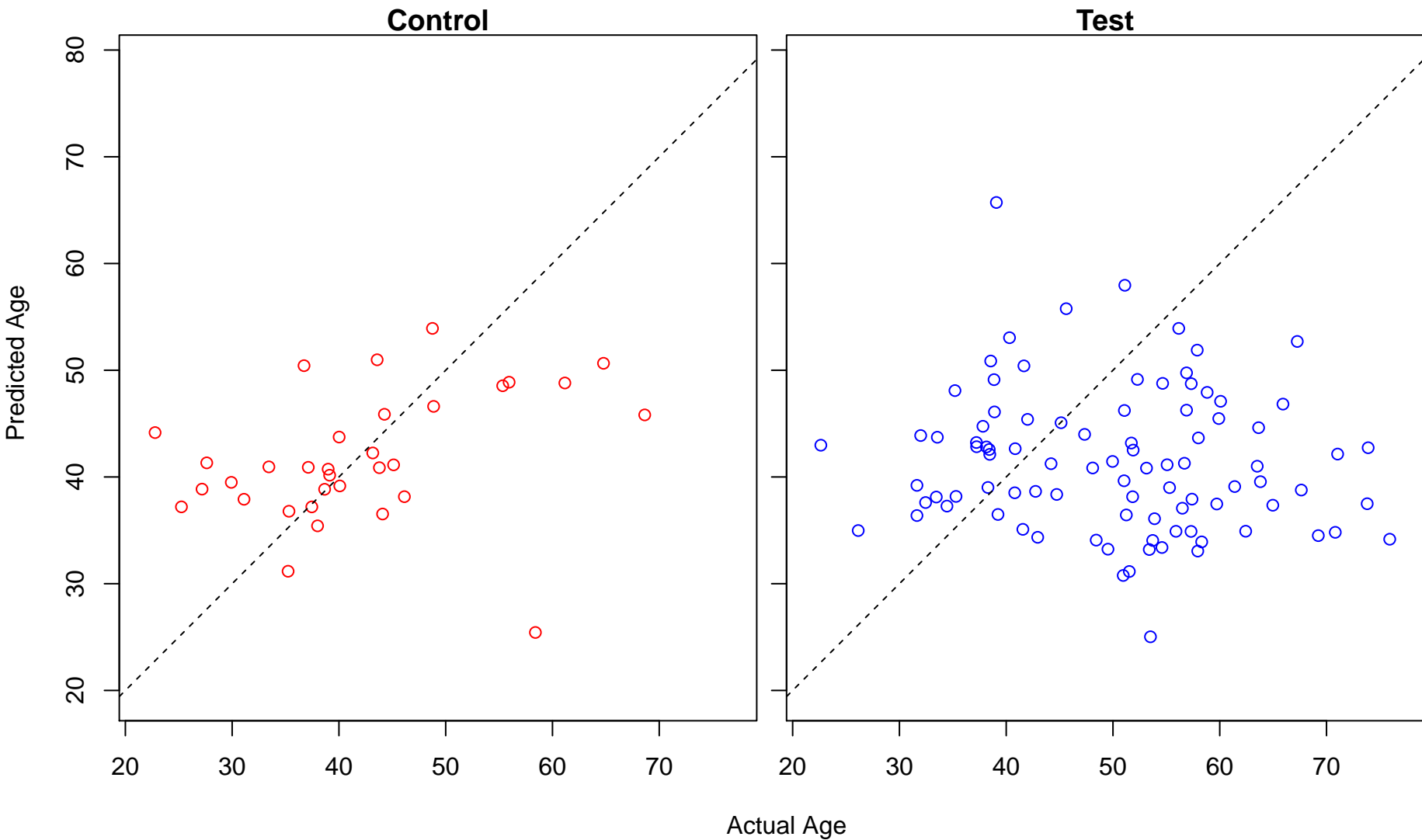
positive regulation of memory T cell differentiation (Score: 0.562024)



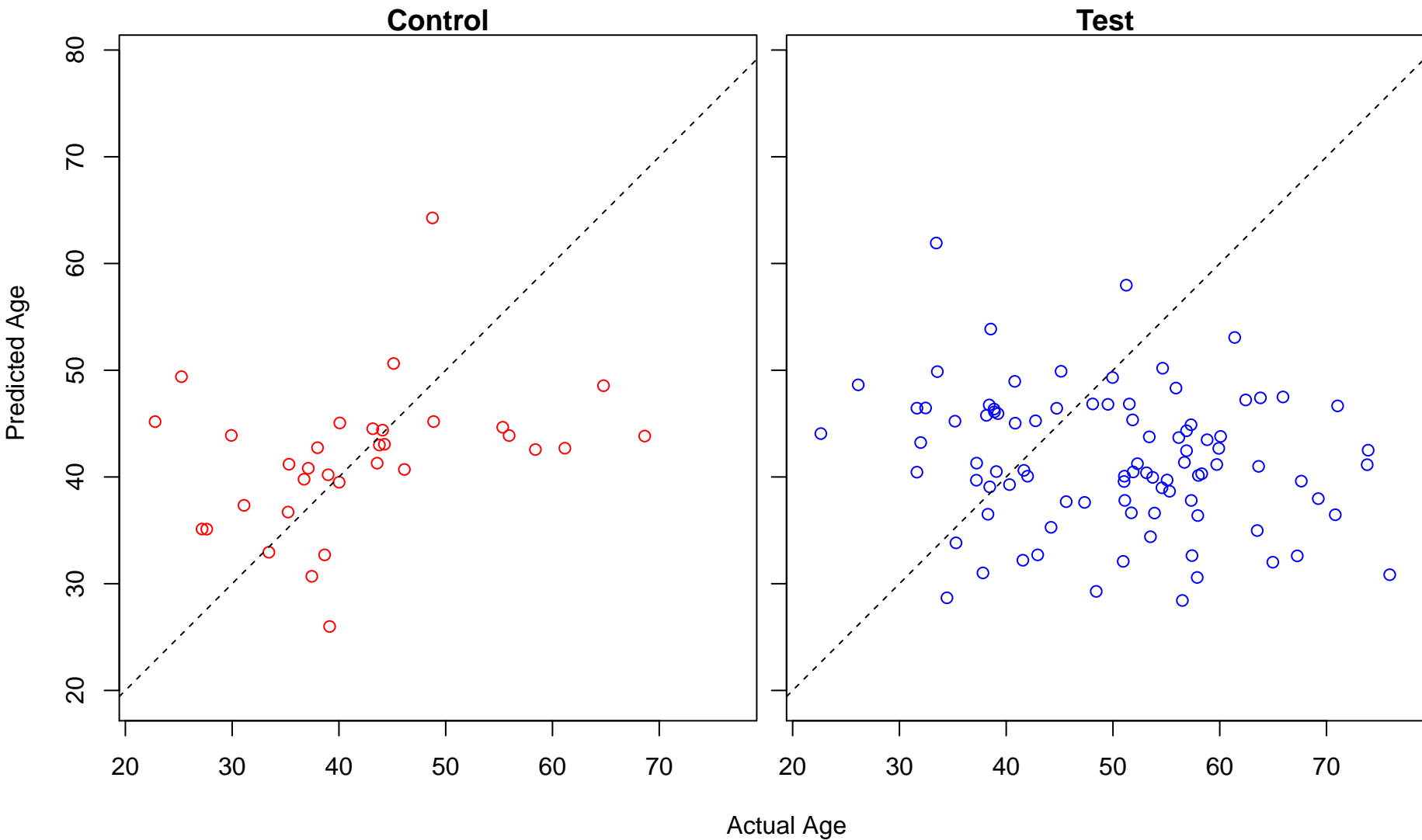
enzyme linked receptor protein signaling pathway (Score: 0.561922)



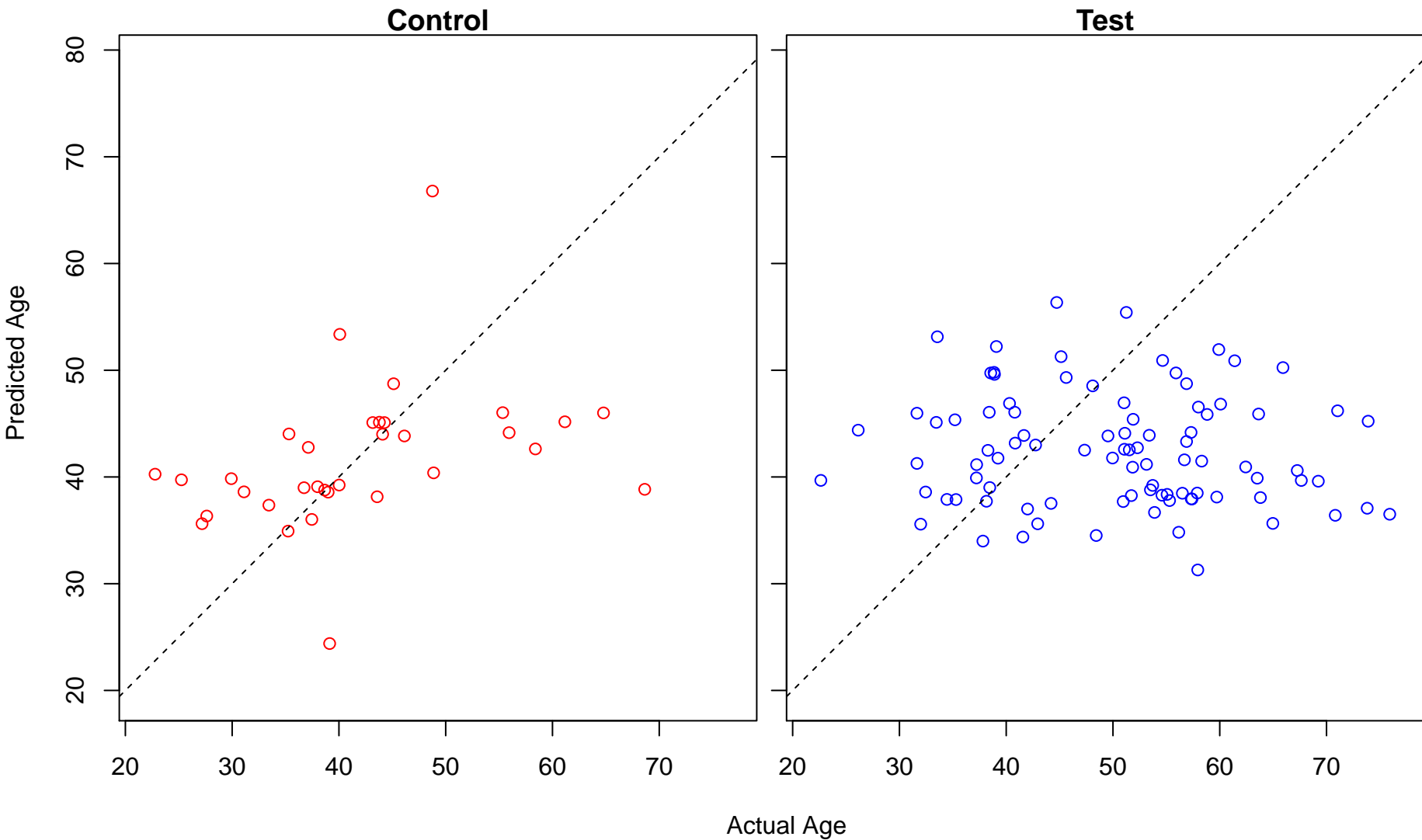
clathrin coat assembly (Score: 0.561740)



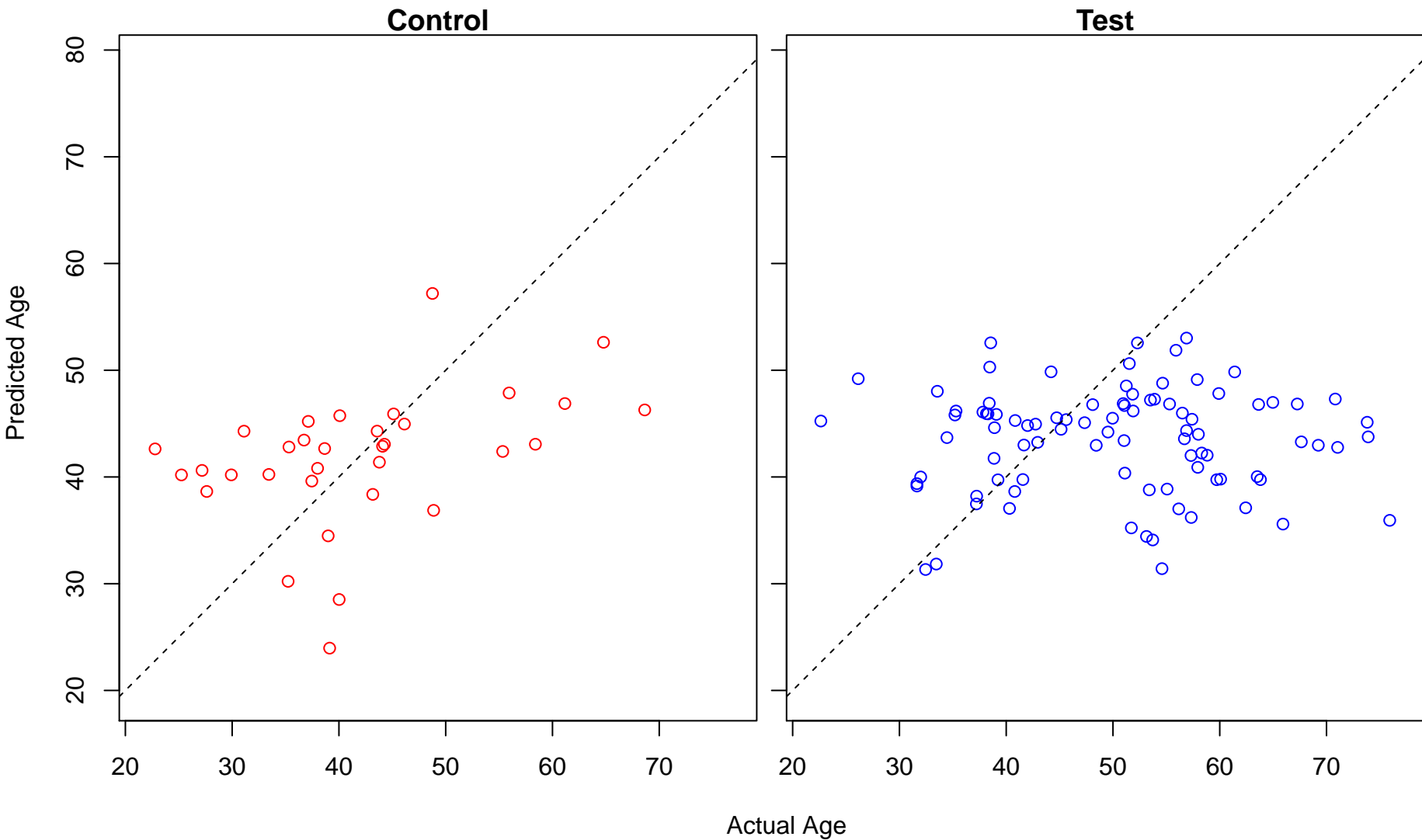
proteasomal ubiquitin-independent protein catabolic process (Score: 0.561260)



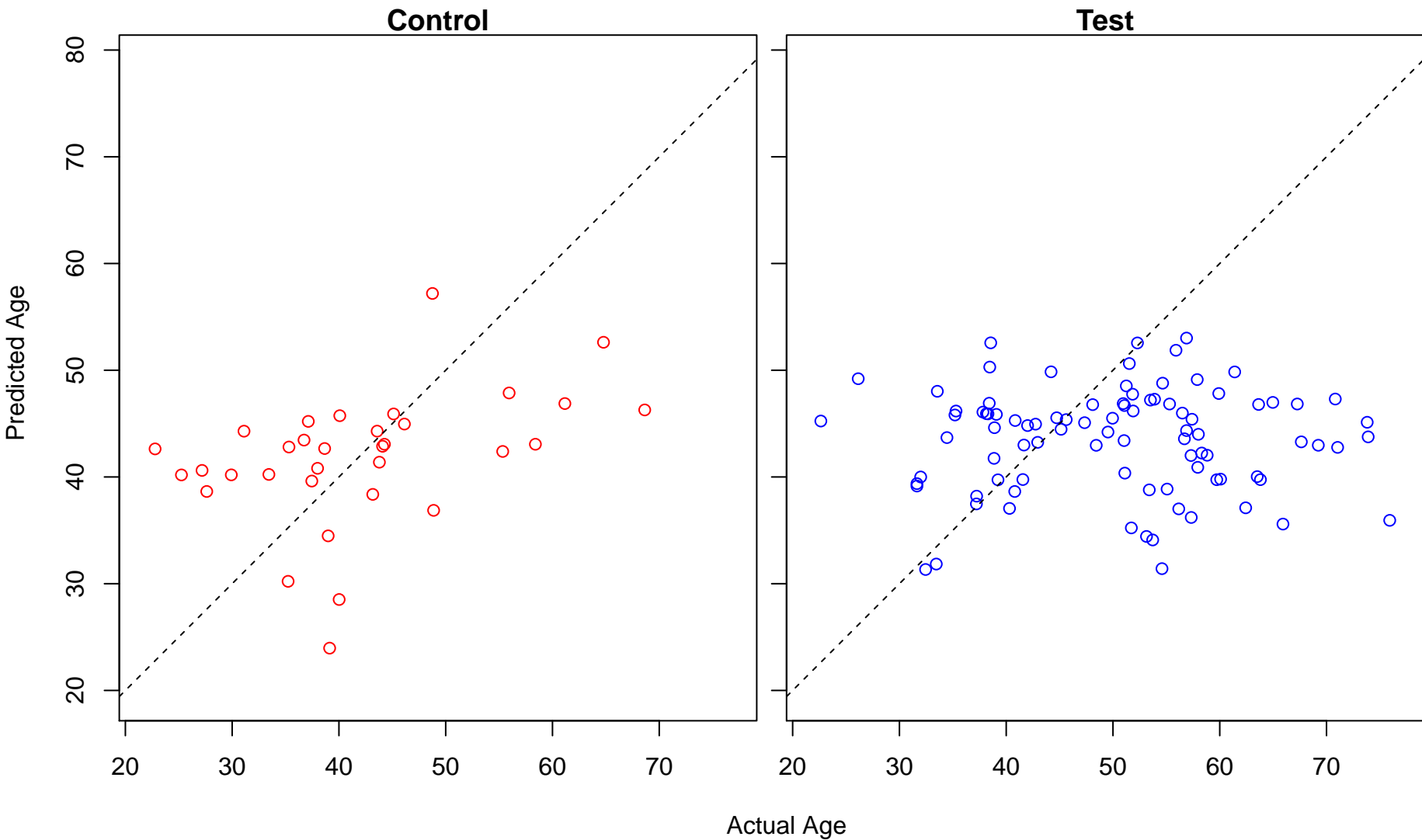
cellular response to growth factor stimulus (Score: 0.560107)



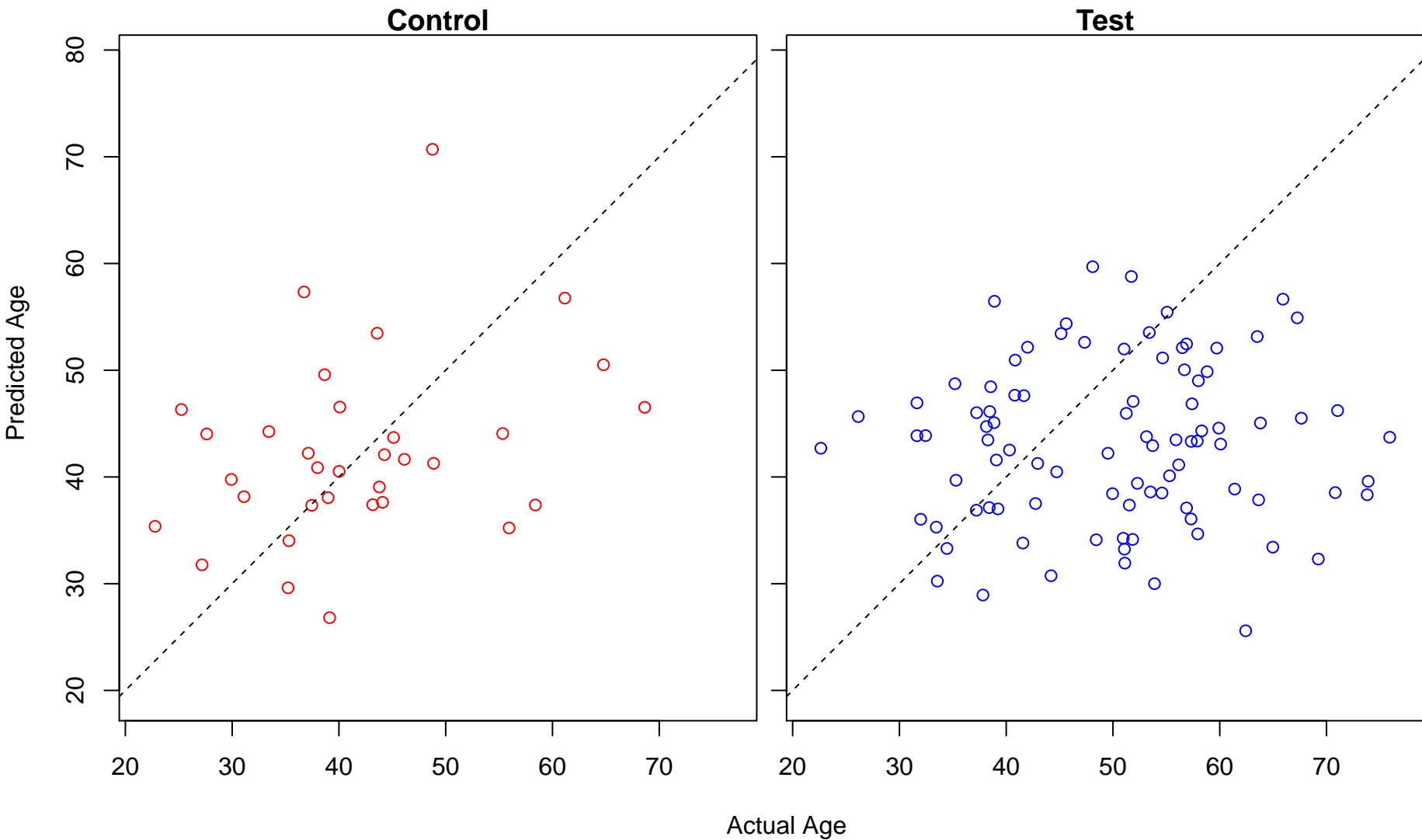
sulfide oxidation (Score: 0.559998)



sulfide oxidation, using sulfide:quinone oxidoreductase (Score: 0.559998)

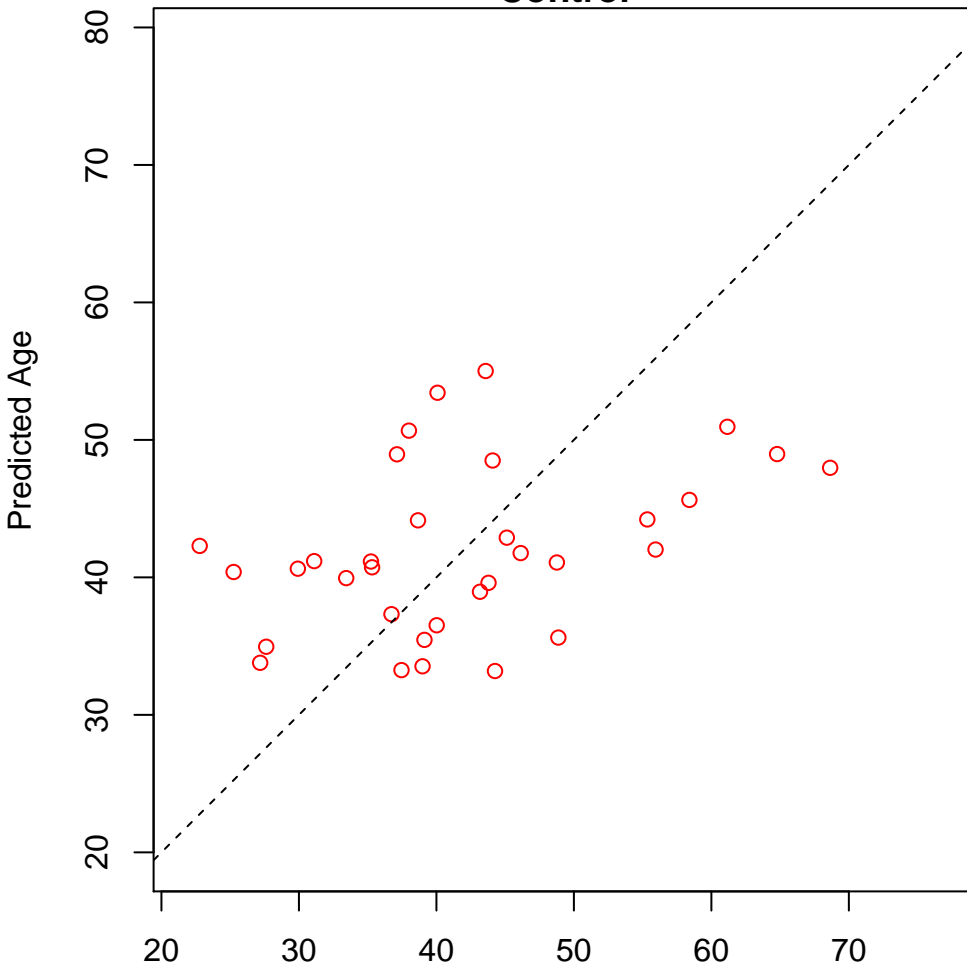


positive regulation of intracellular steroid hormone receptor signaling pathway (Score: 0.559713)

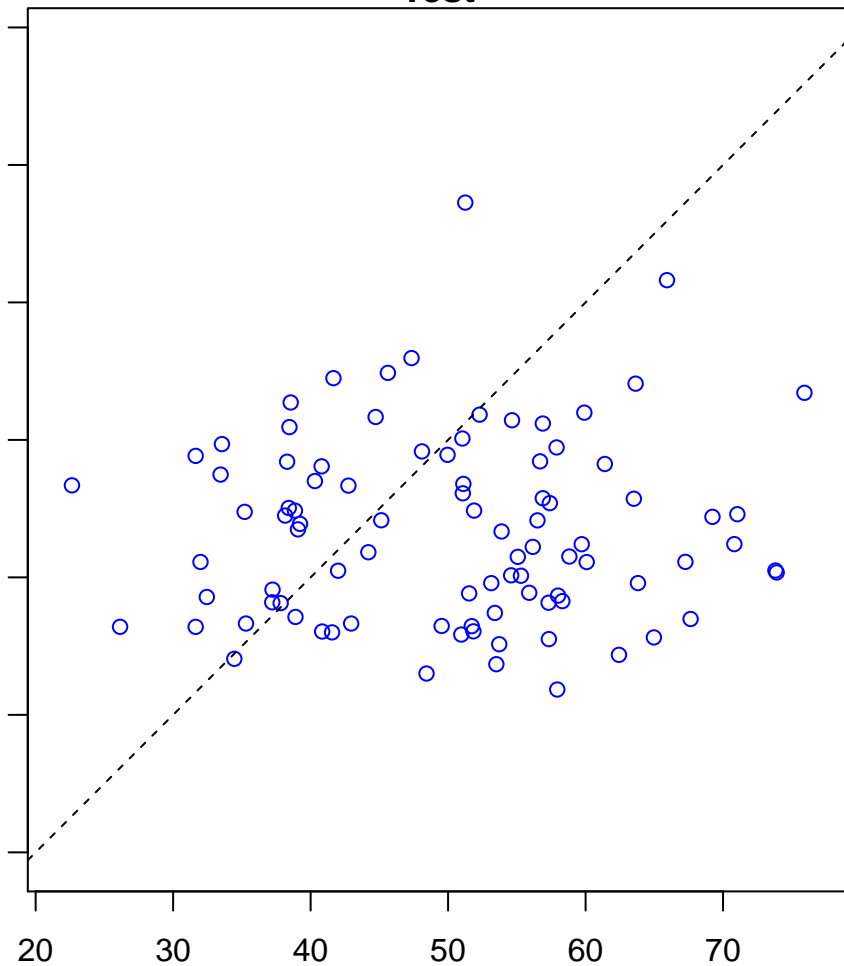


mitochondrial protein catabolic process (Score: 0.559688)

Control

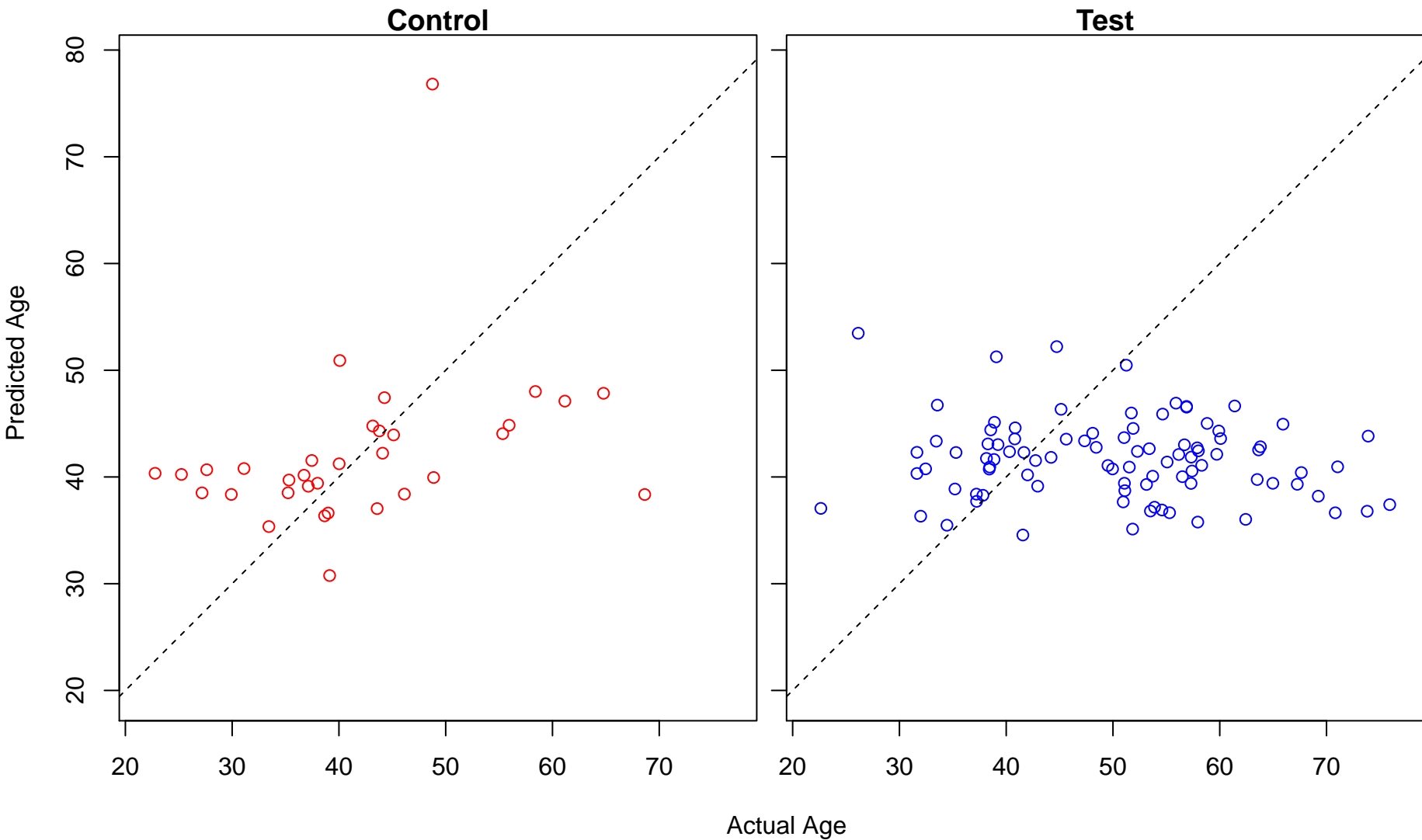


Test

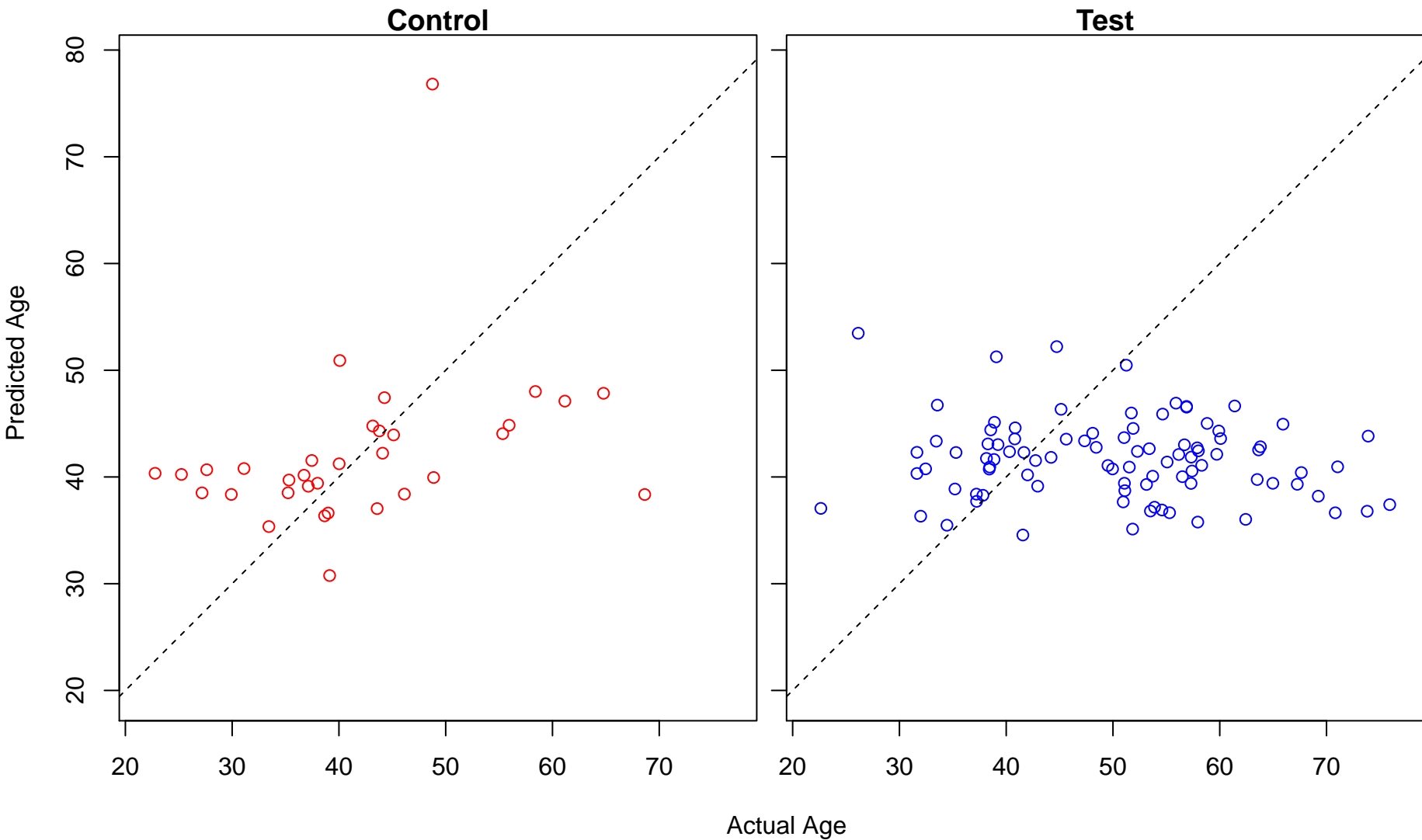


Actual Age

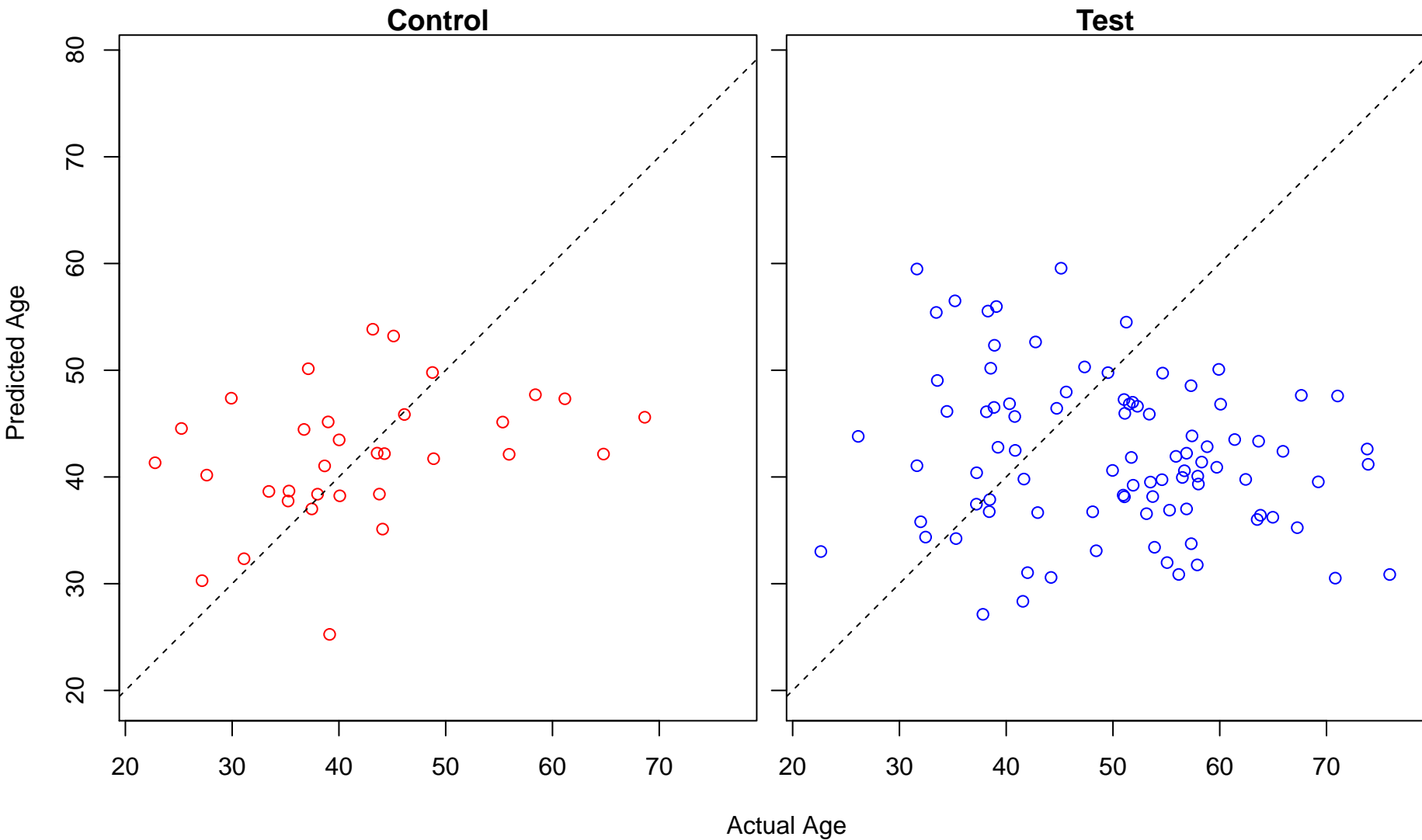
platelet formation (Score: 0.559421)



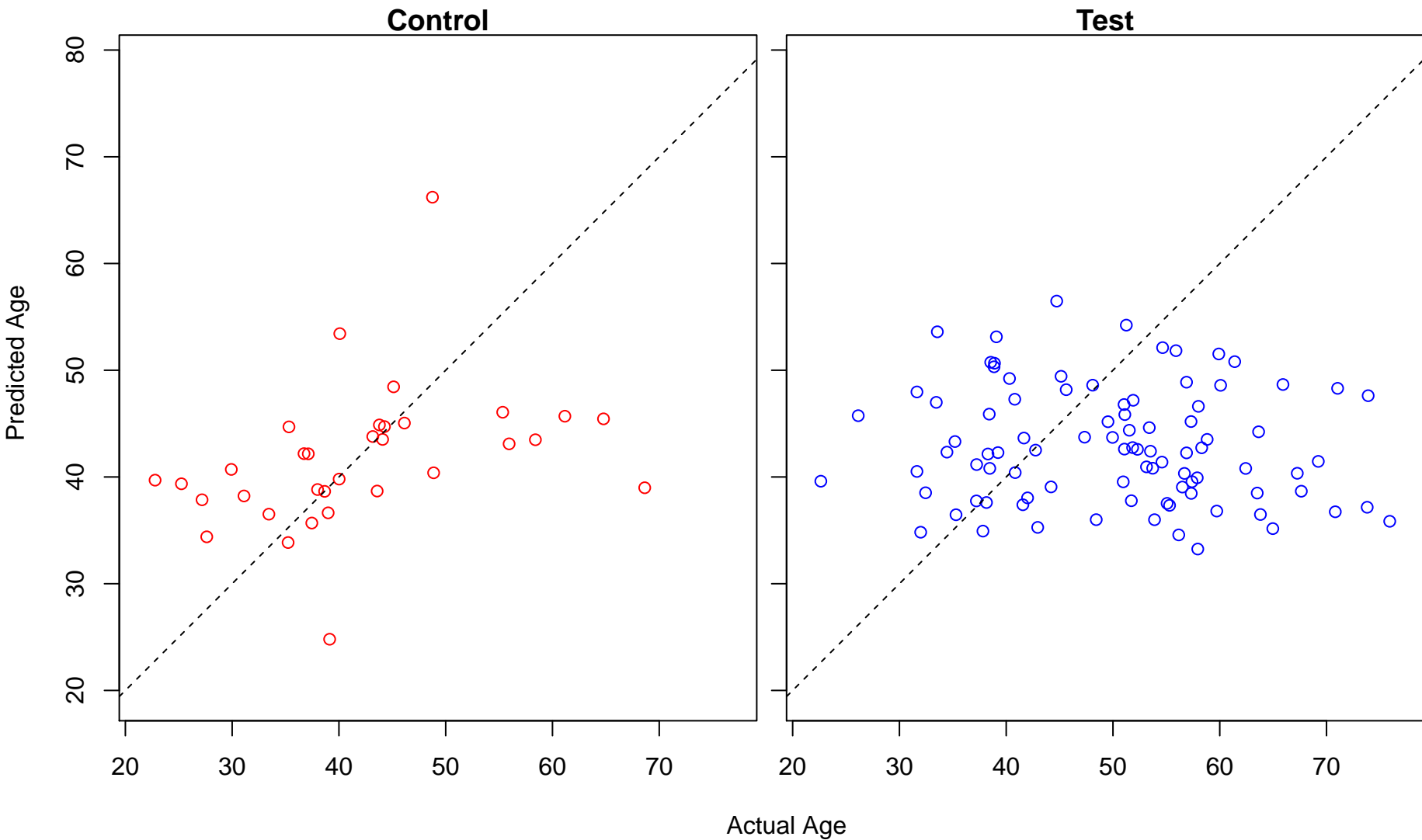
platelet morphogenesis (Score: 0.559421)



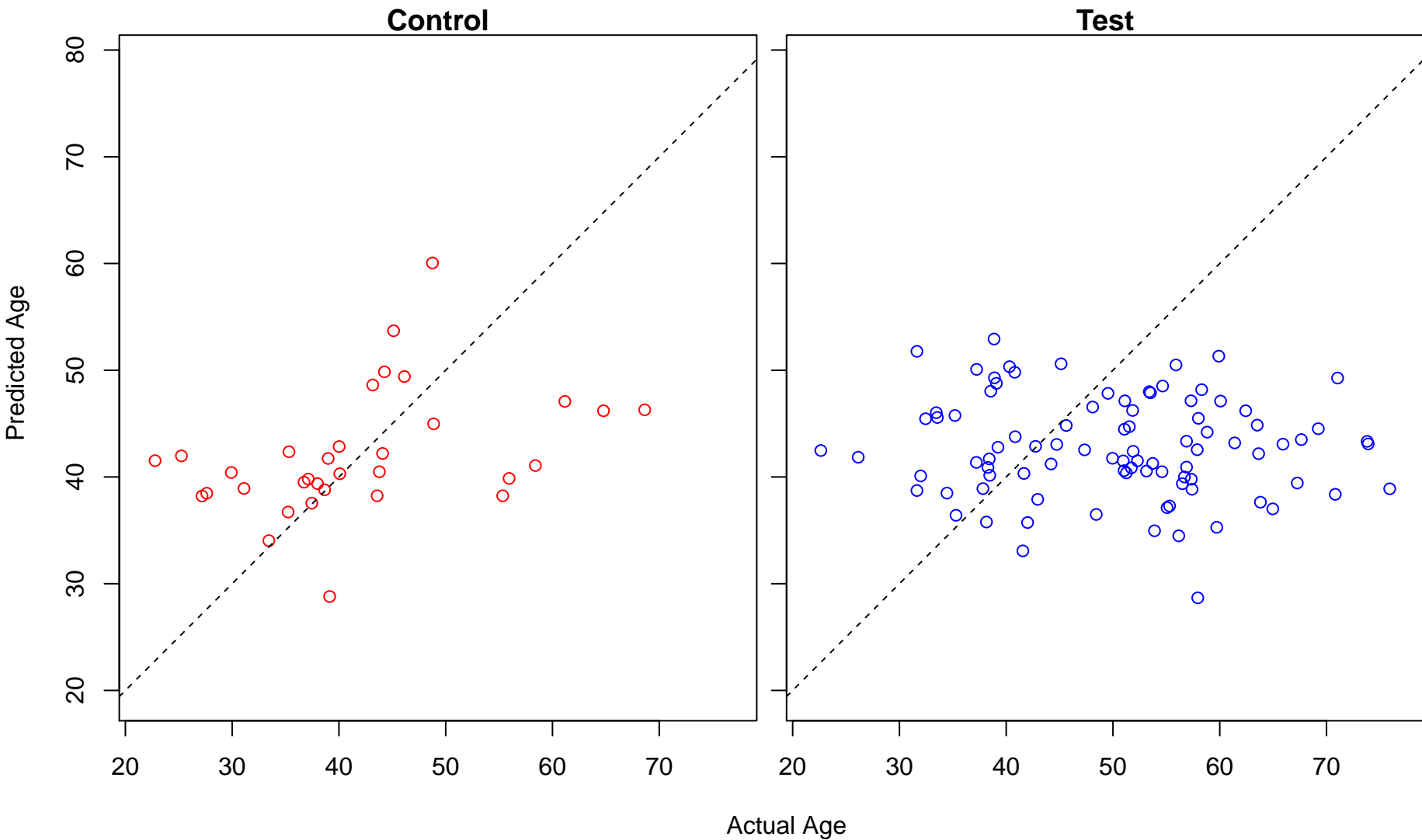
myoblast fusion (Score: 0.559051)



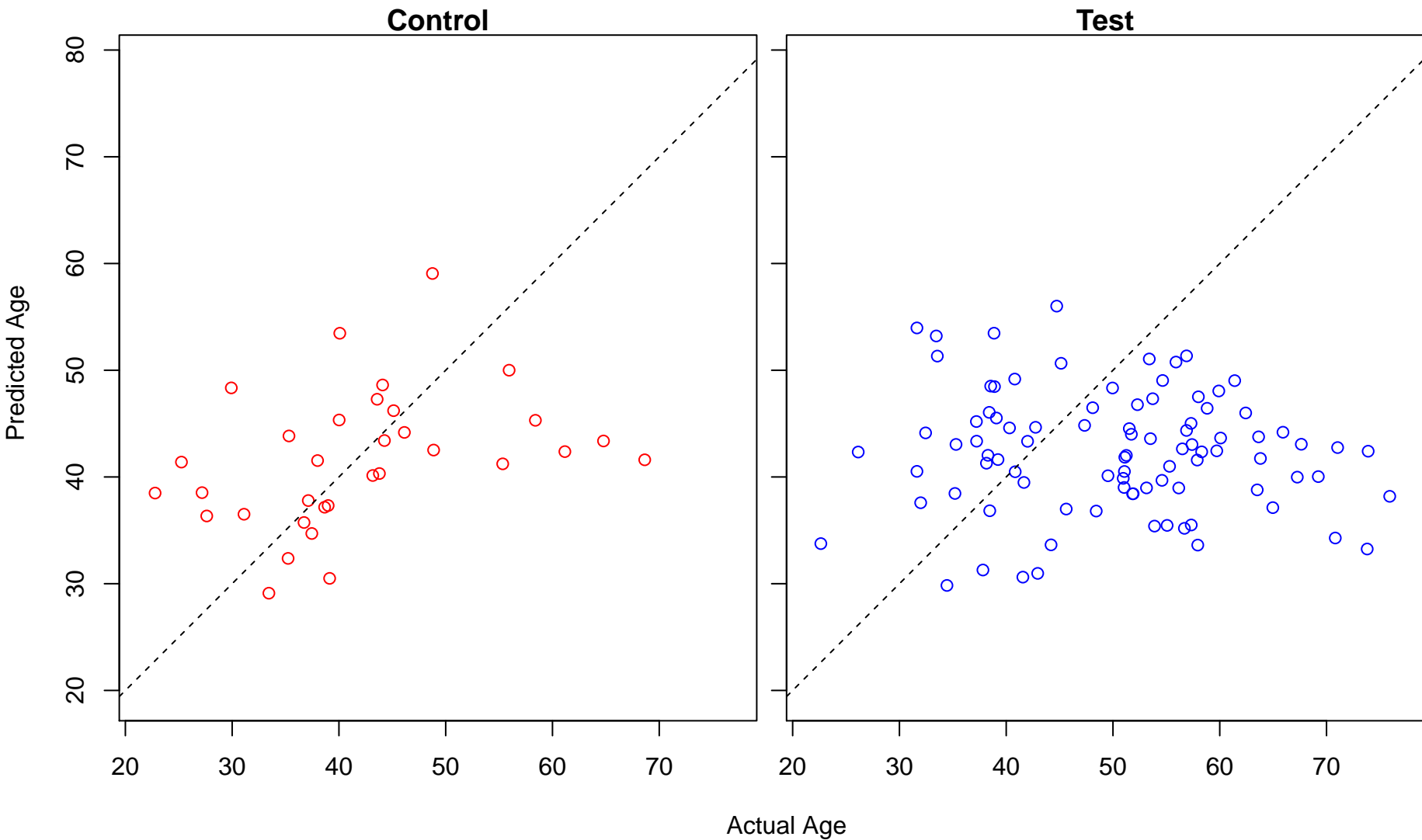
positive regulation of response to stimulus (Score: 0.558012)



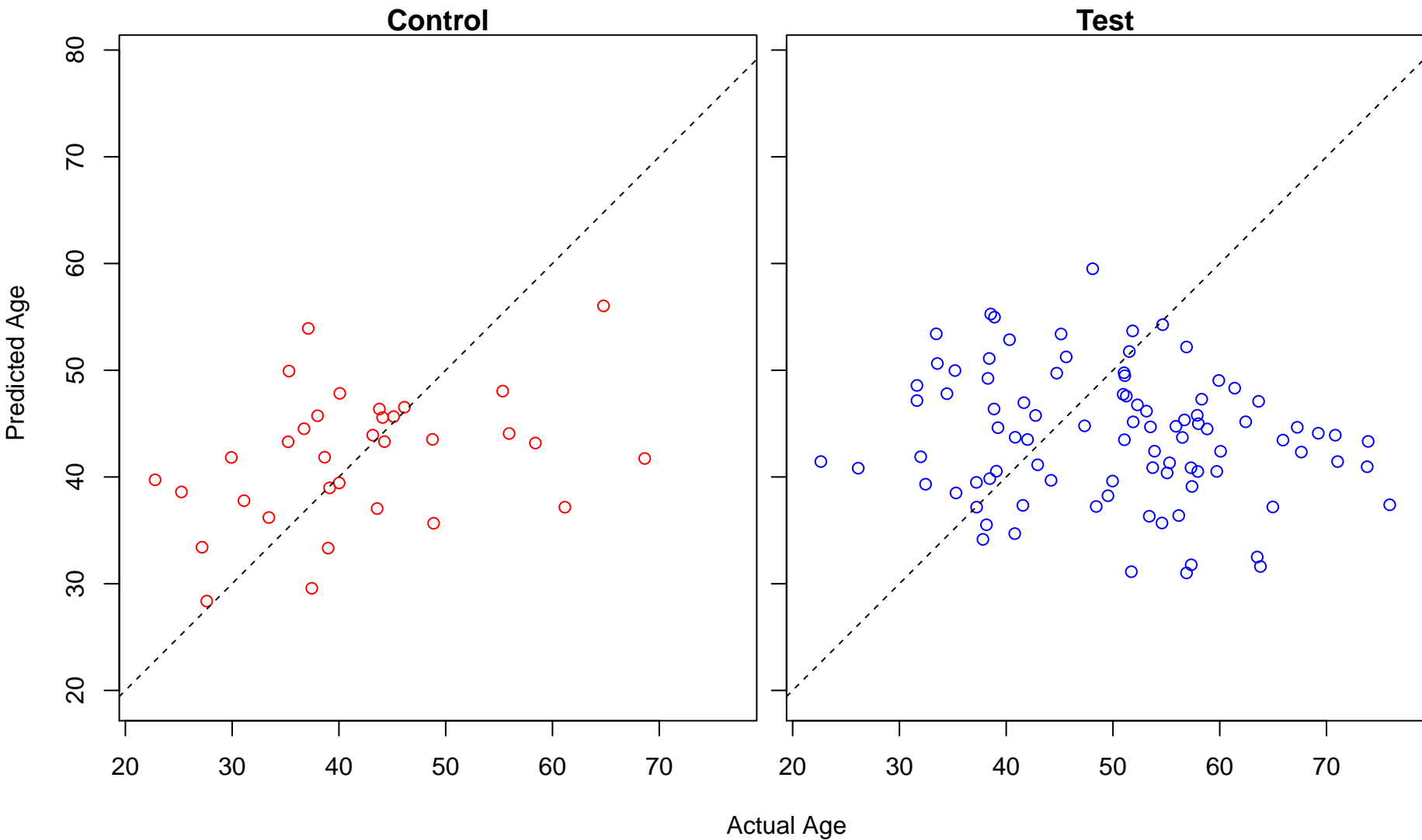
actin rod assembly (Score: 0.557726)



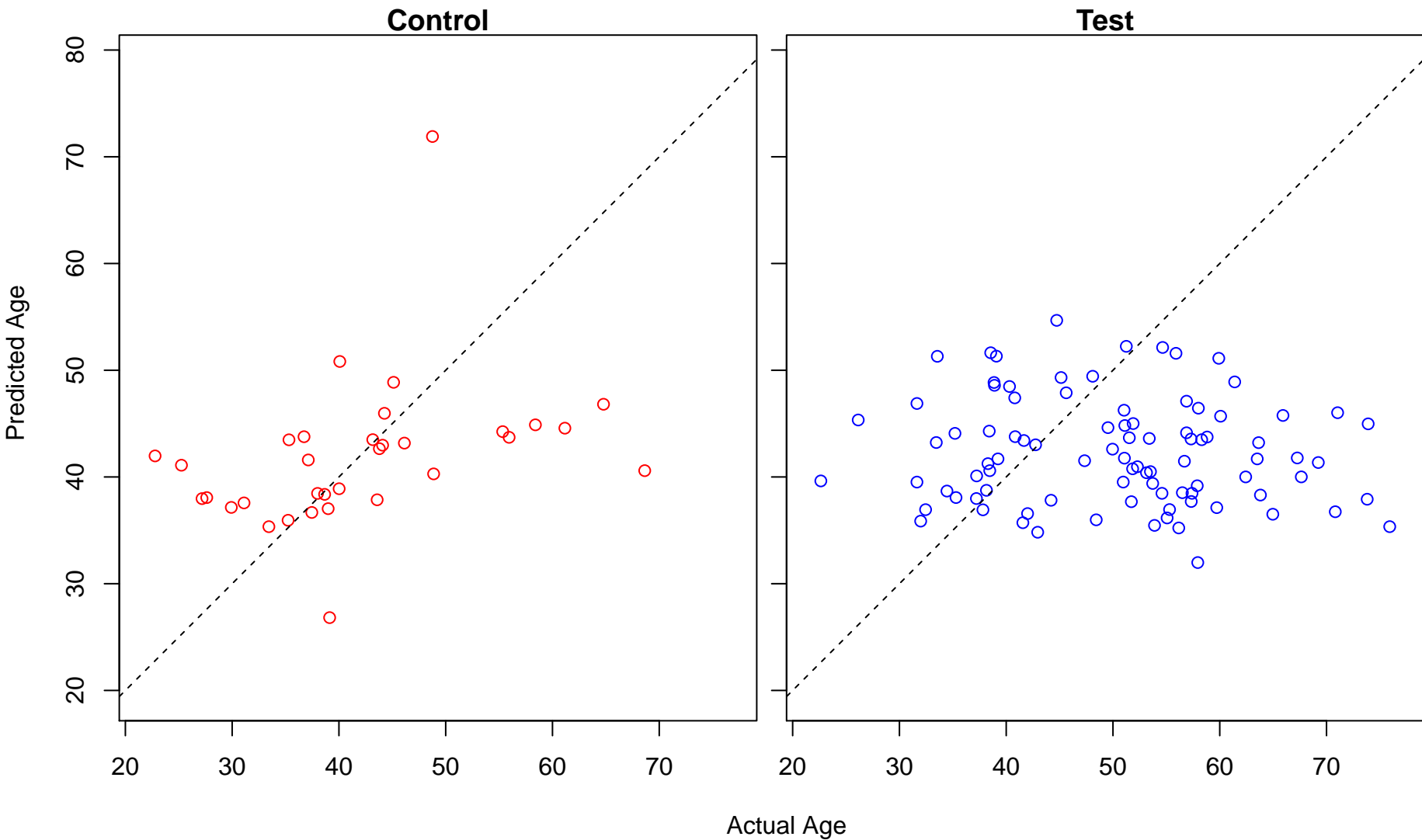
regulation of lipid transport (Score: 0.557326)



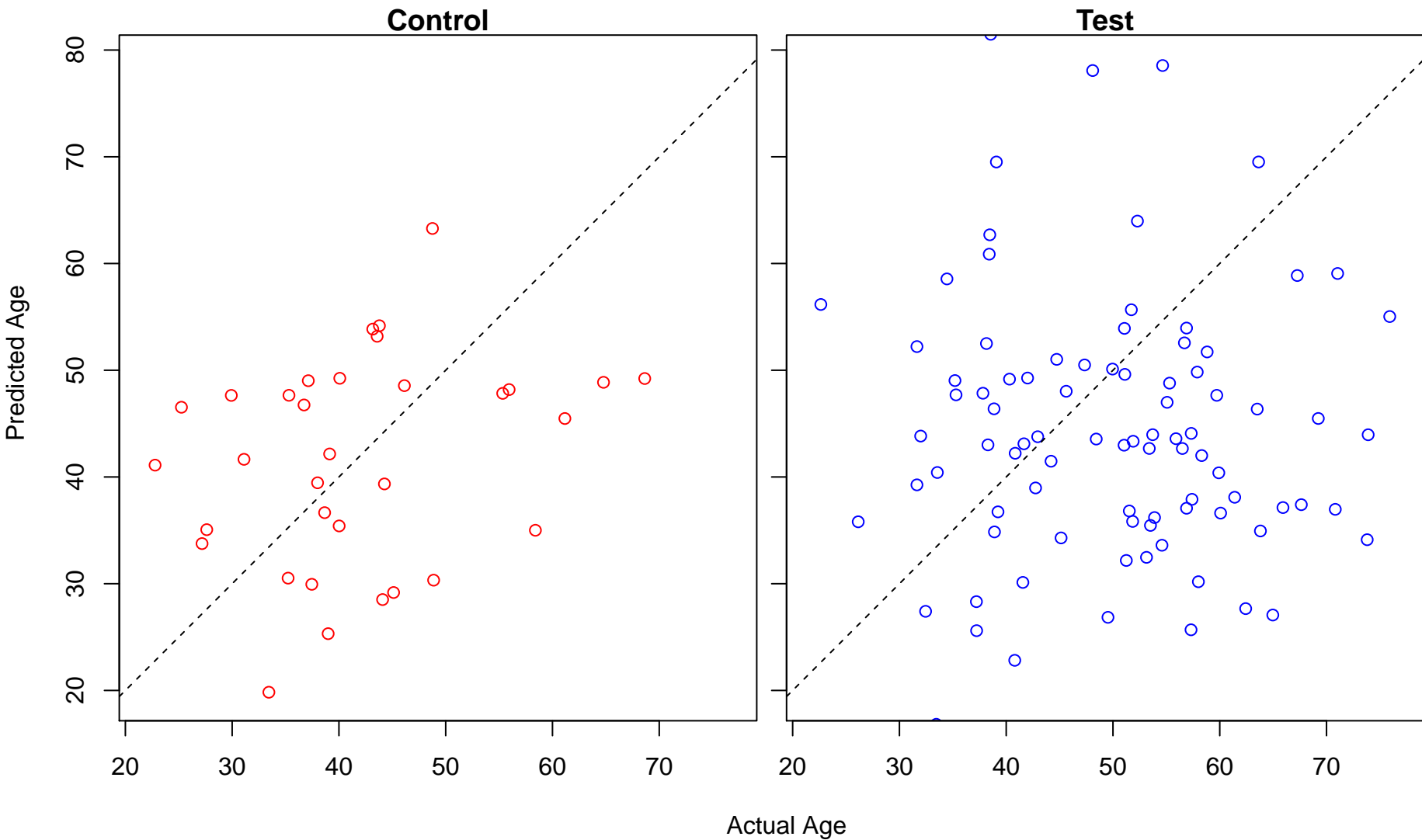
mesonephric duct development (Score: 0.556633)



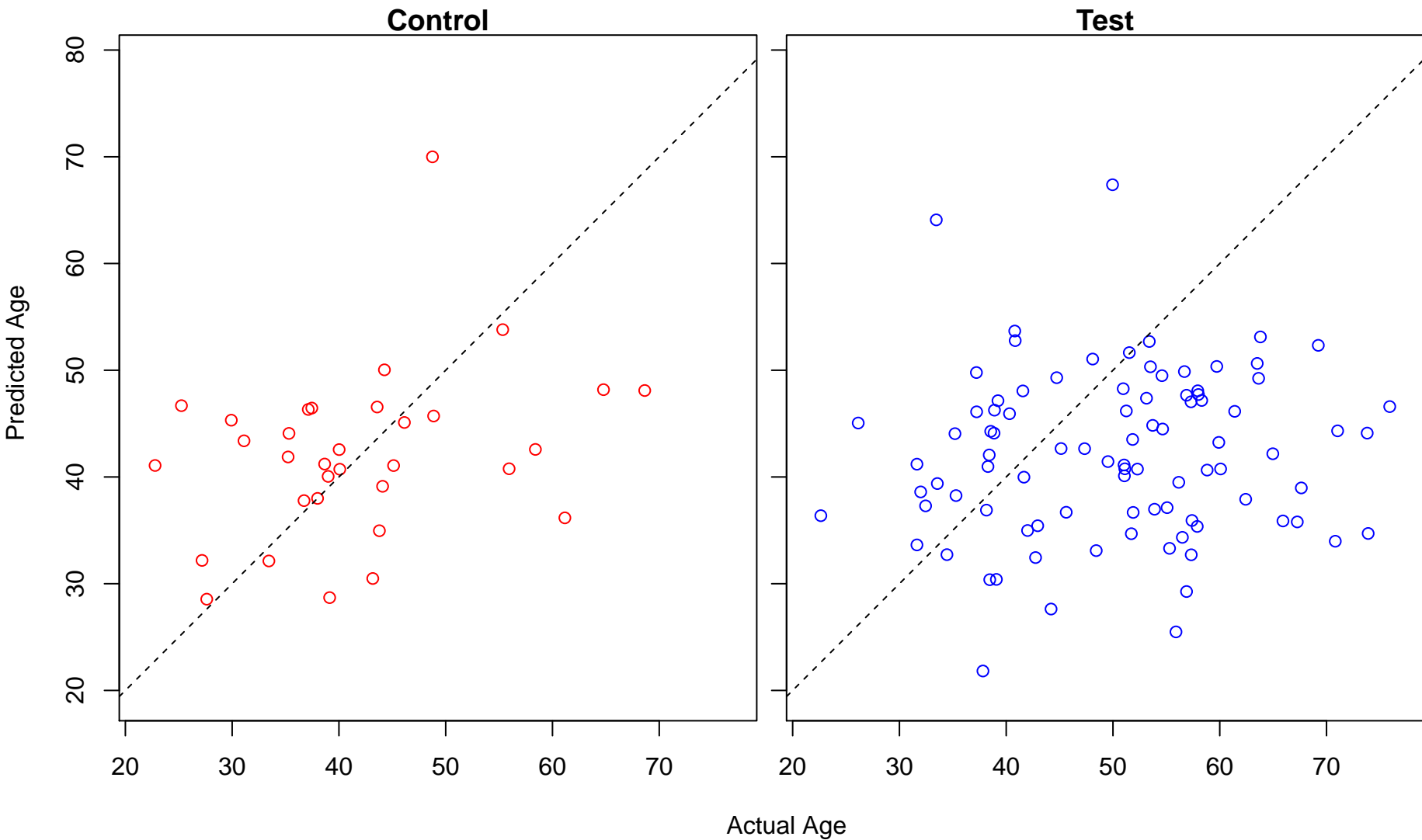
cellular protein localization (Score: 0.555340)



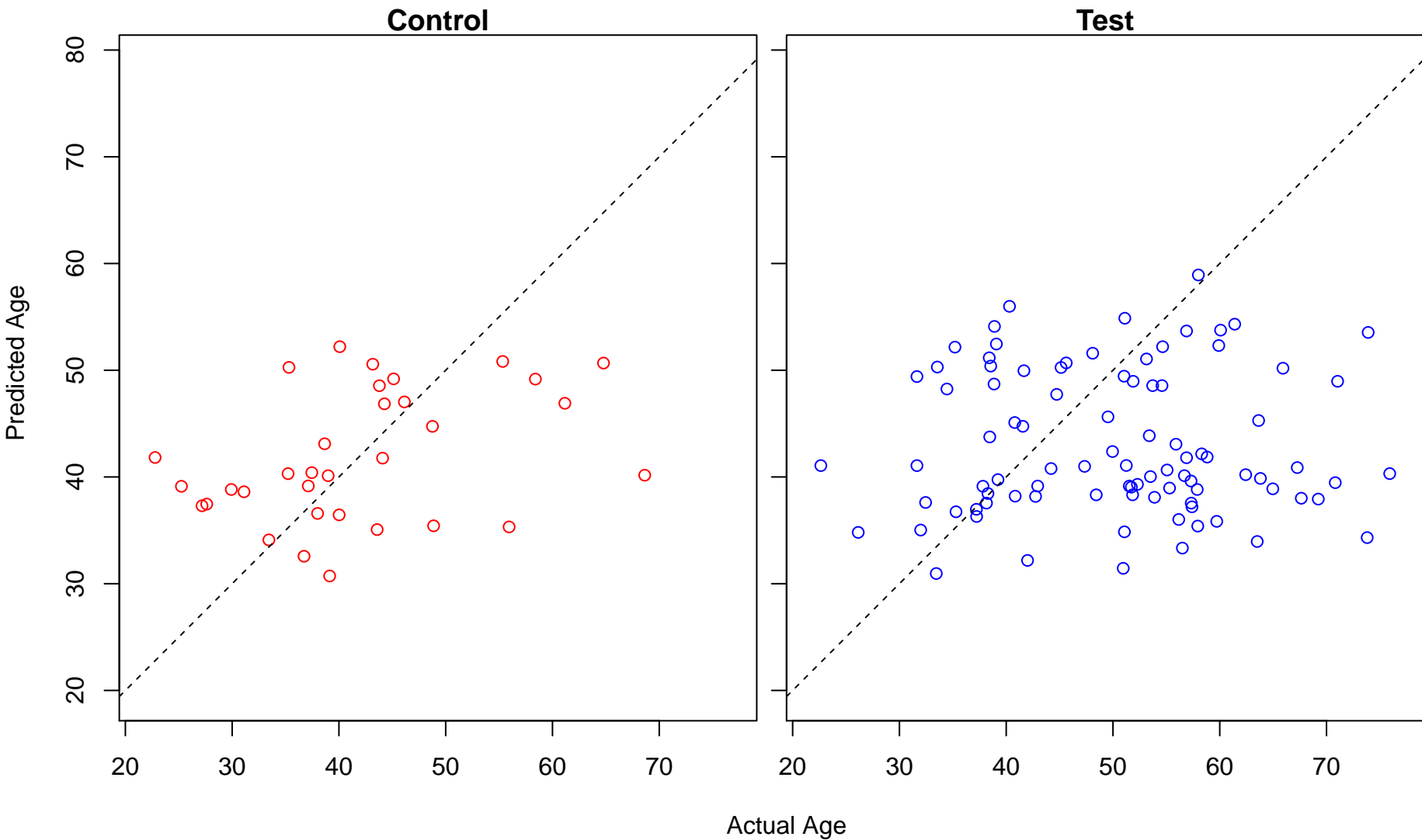
positive regulation of mitotic cell cycle phase transition (Score: 0.555066)



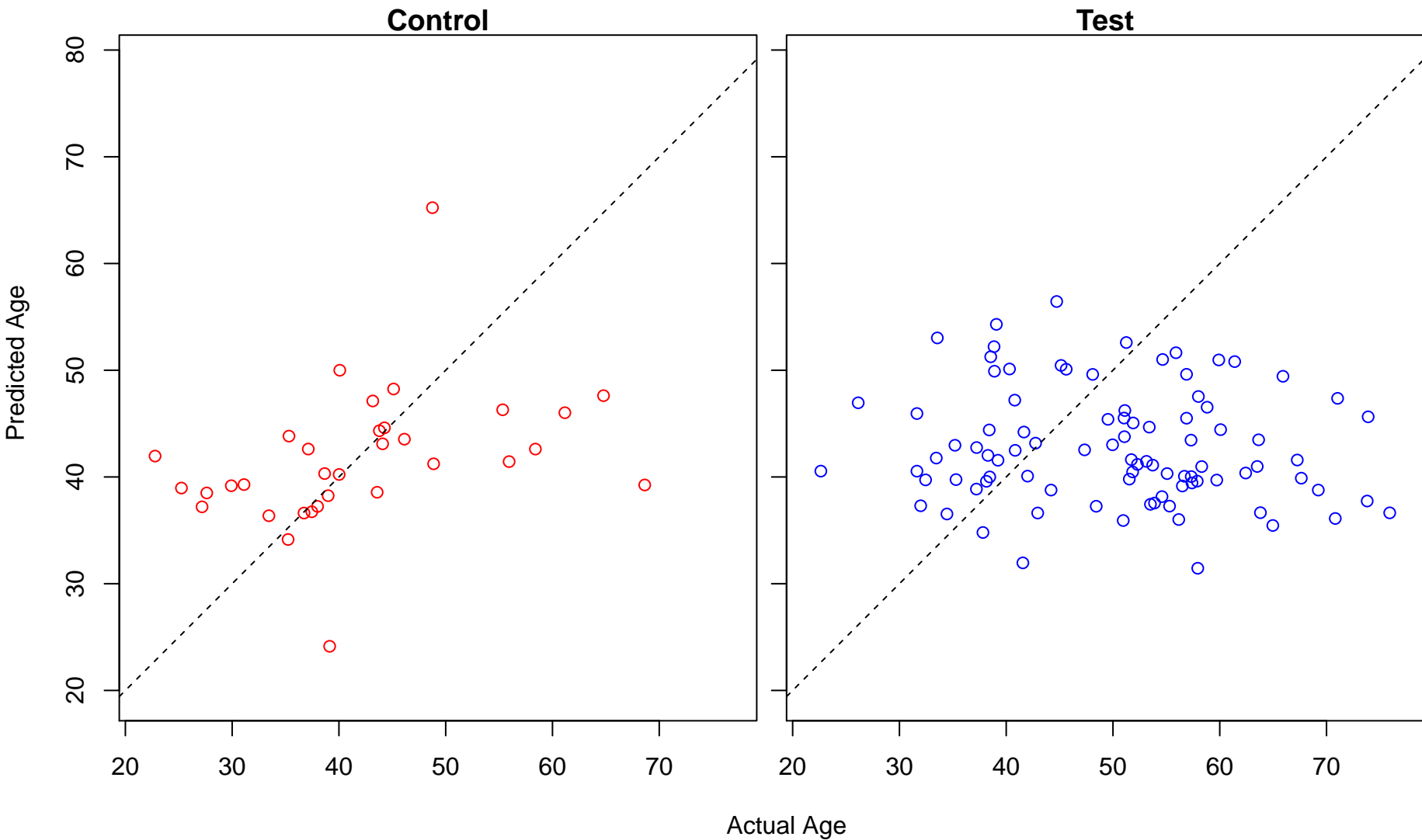
positive regulation of type I interferon-mediated signaling pathway (Score: 0.554864)



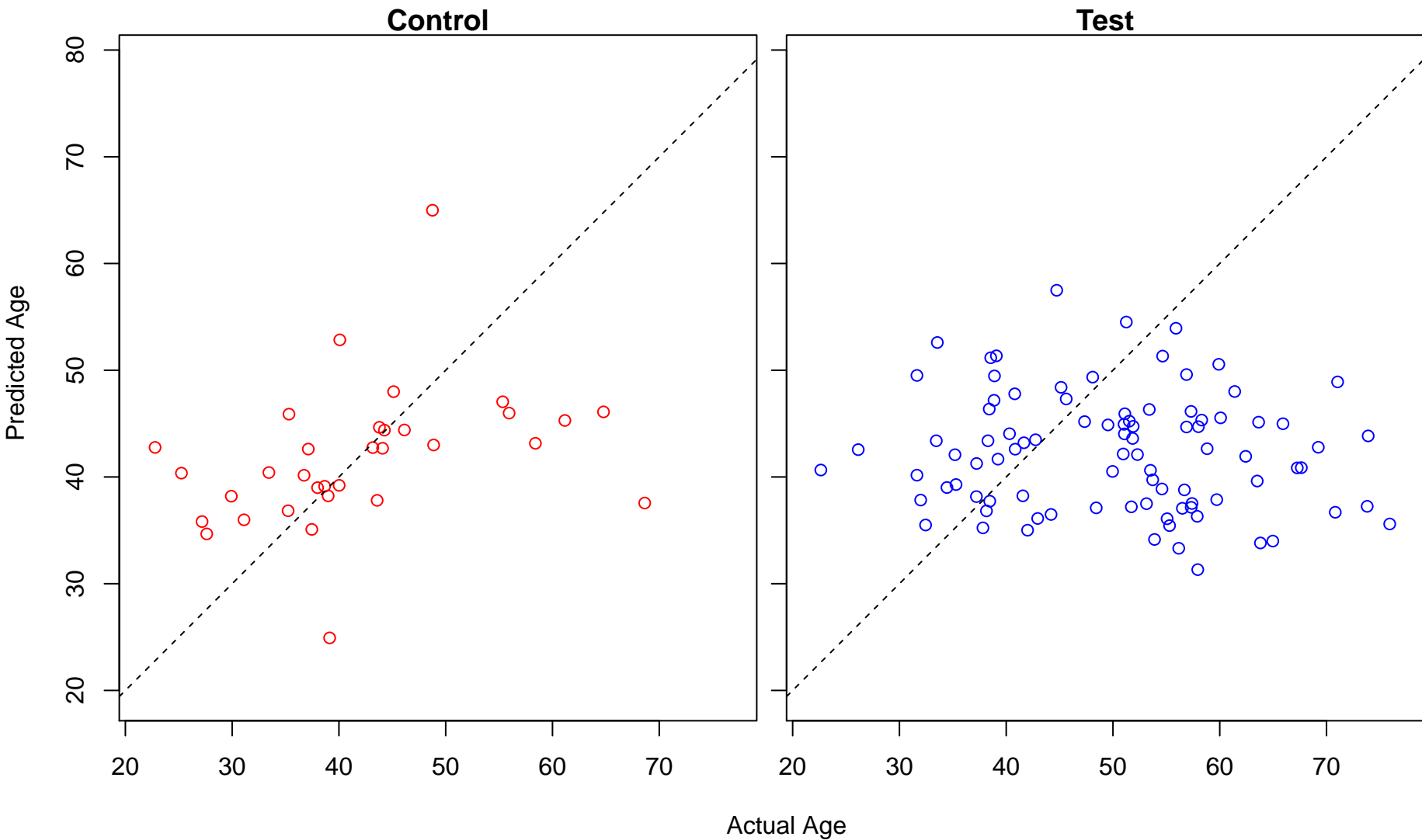
negative regulation of tyrosine phosphorylation of Stat3 protein (Score: 0.553271)



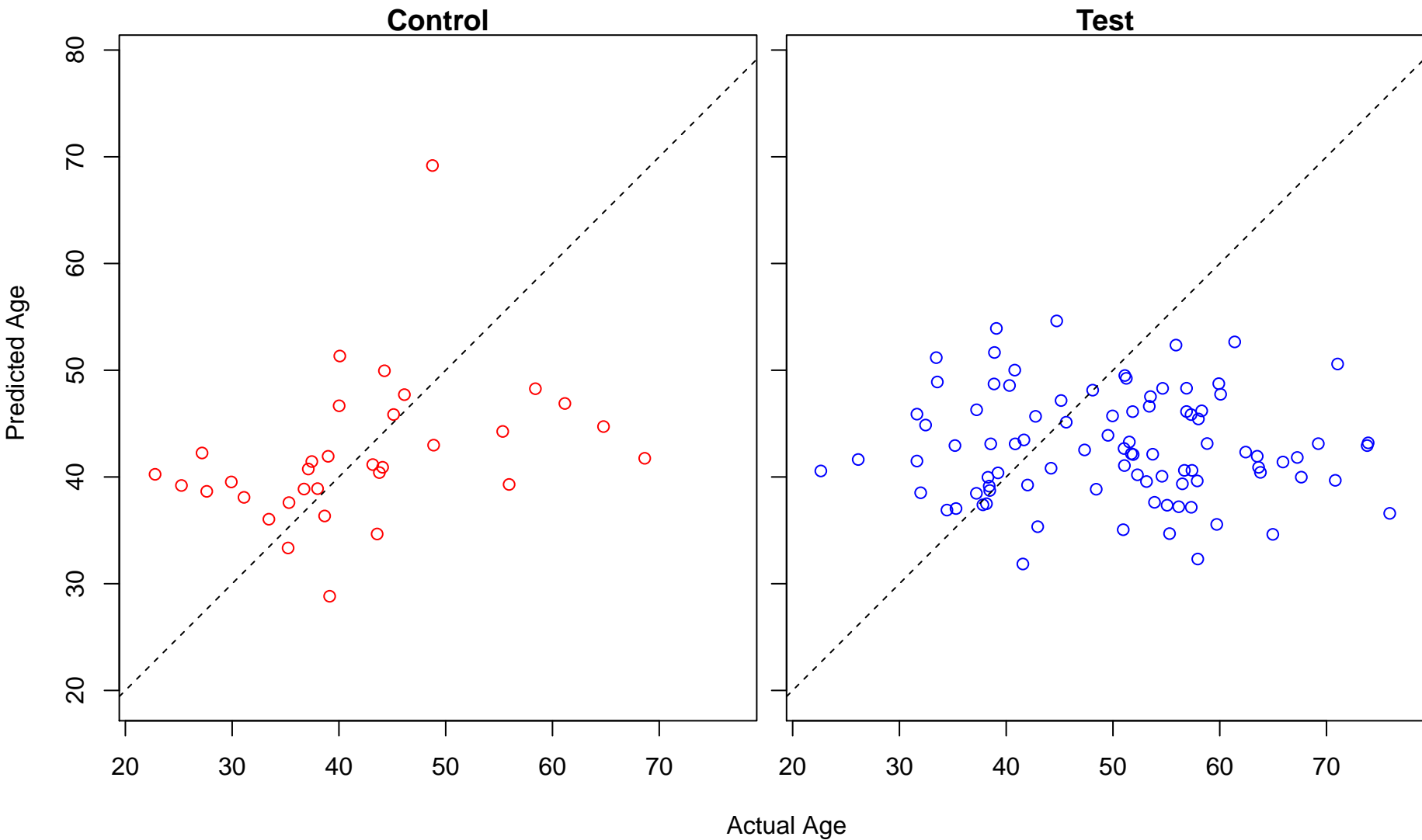
protein phosphorylation (Score: 0.553119)



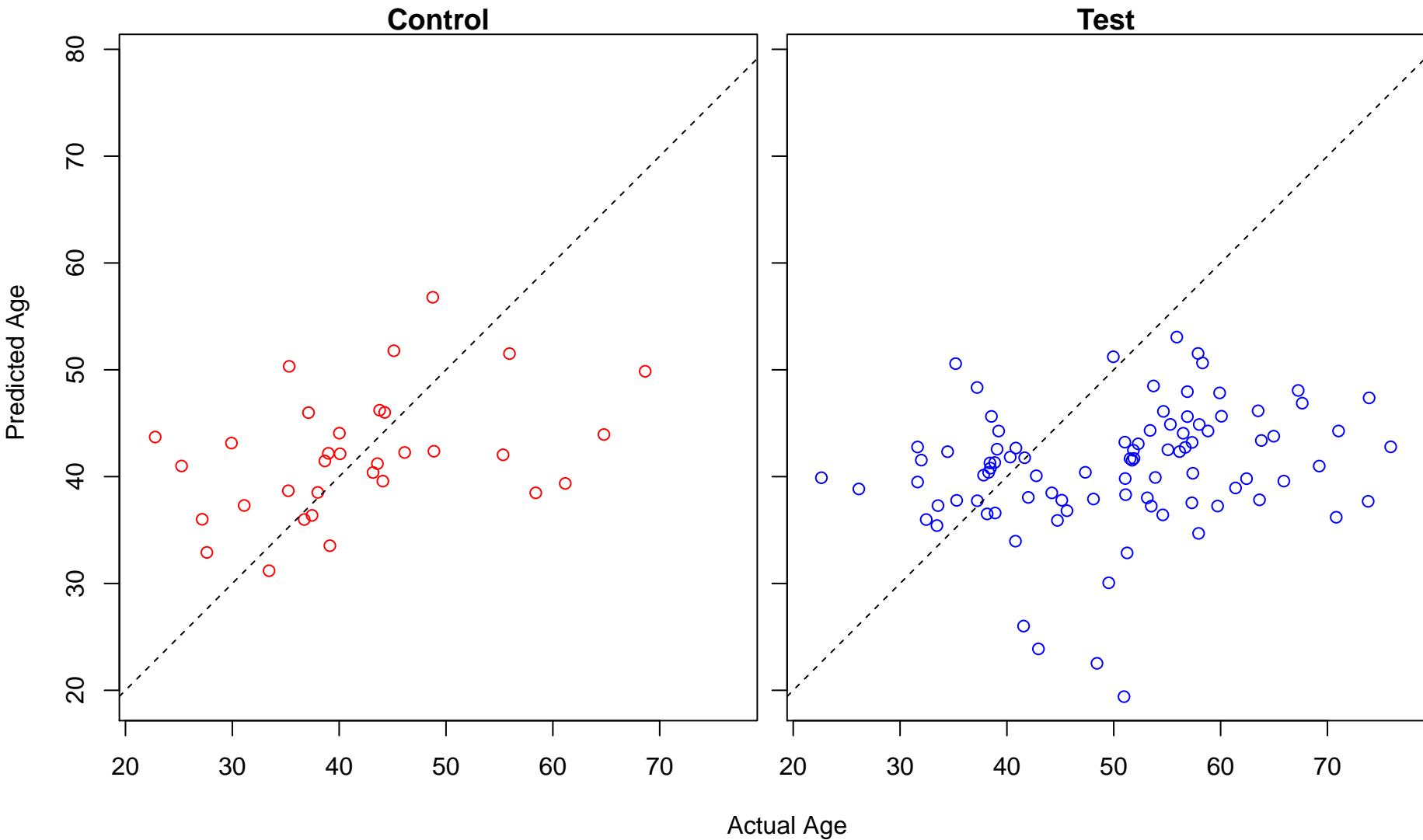
ncRNA processing (Score: 0.552509)



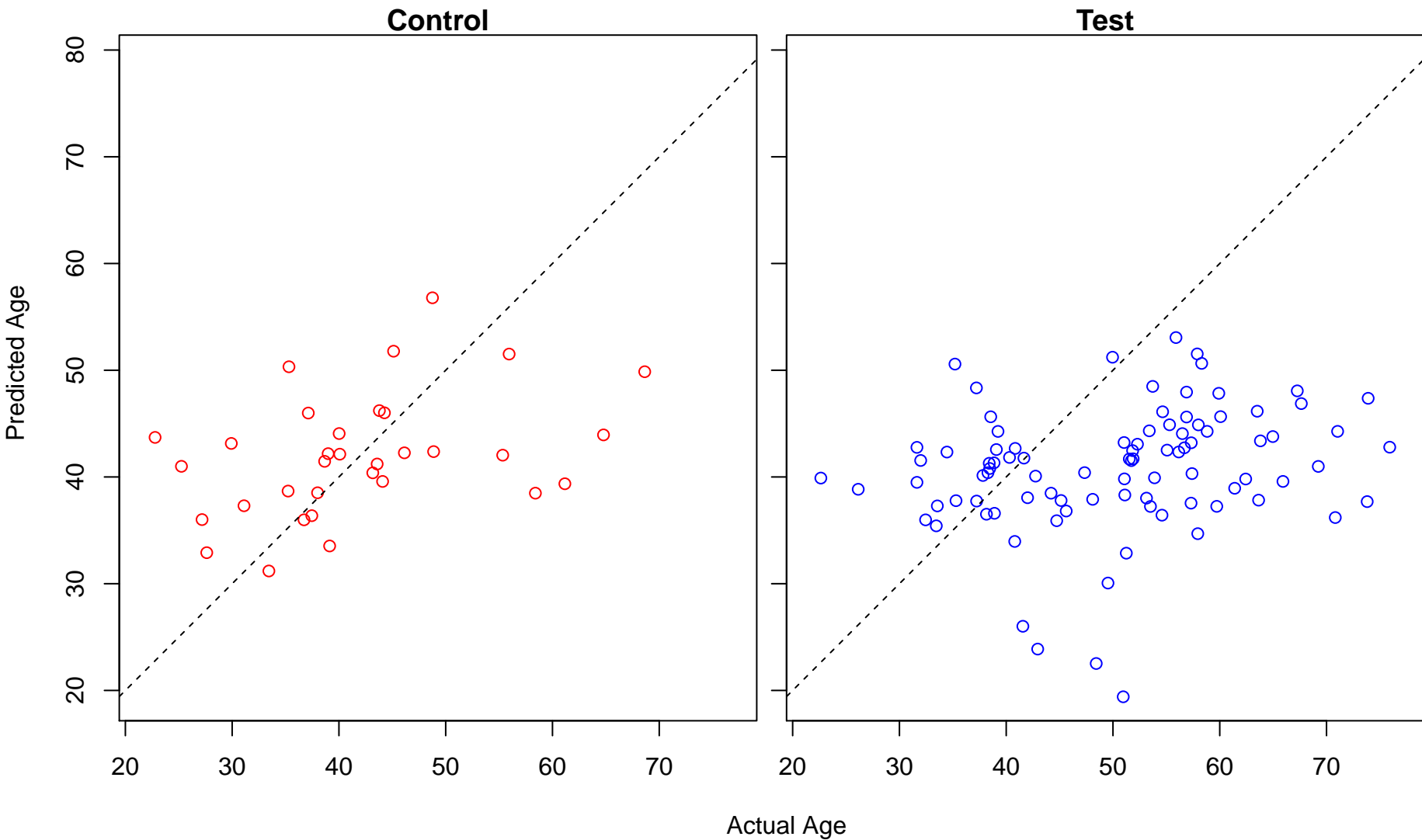
response to ATP (Score: 0.551743)



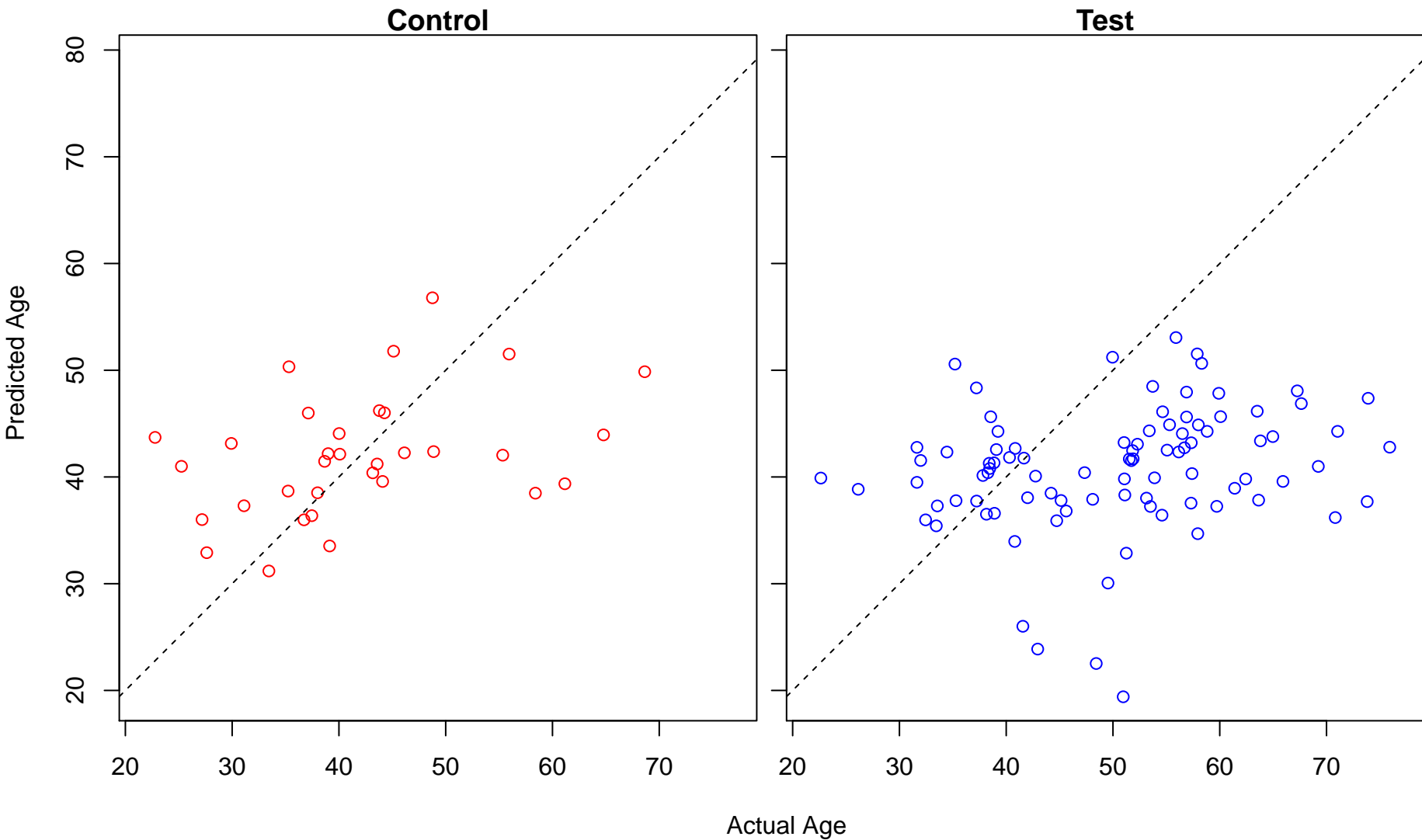
polar body extrusion after meiotic divisions (Score: 0.551586)



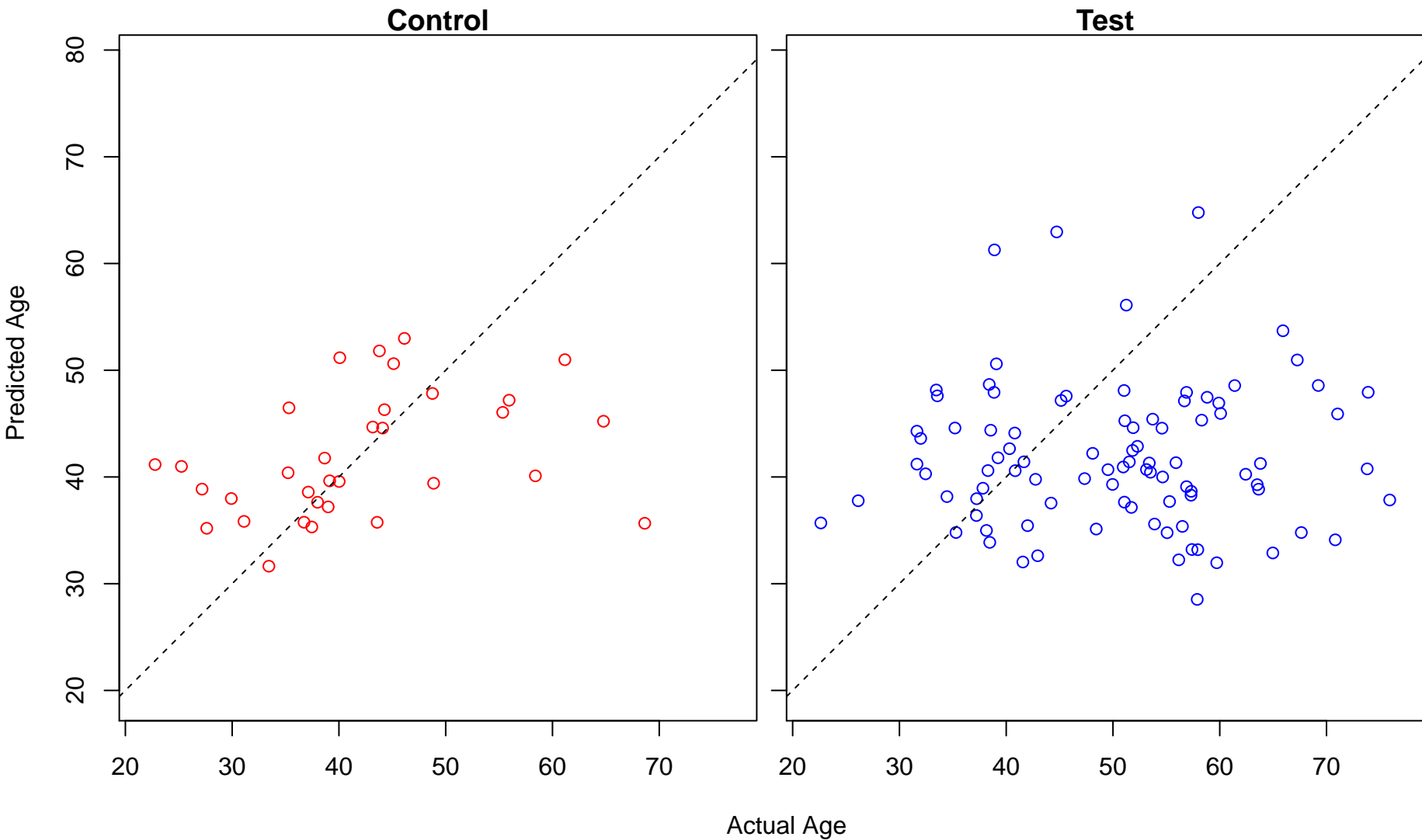
establishment of meiotic spindle localization (Score: 0.551586)



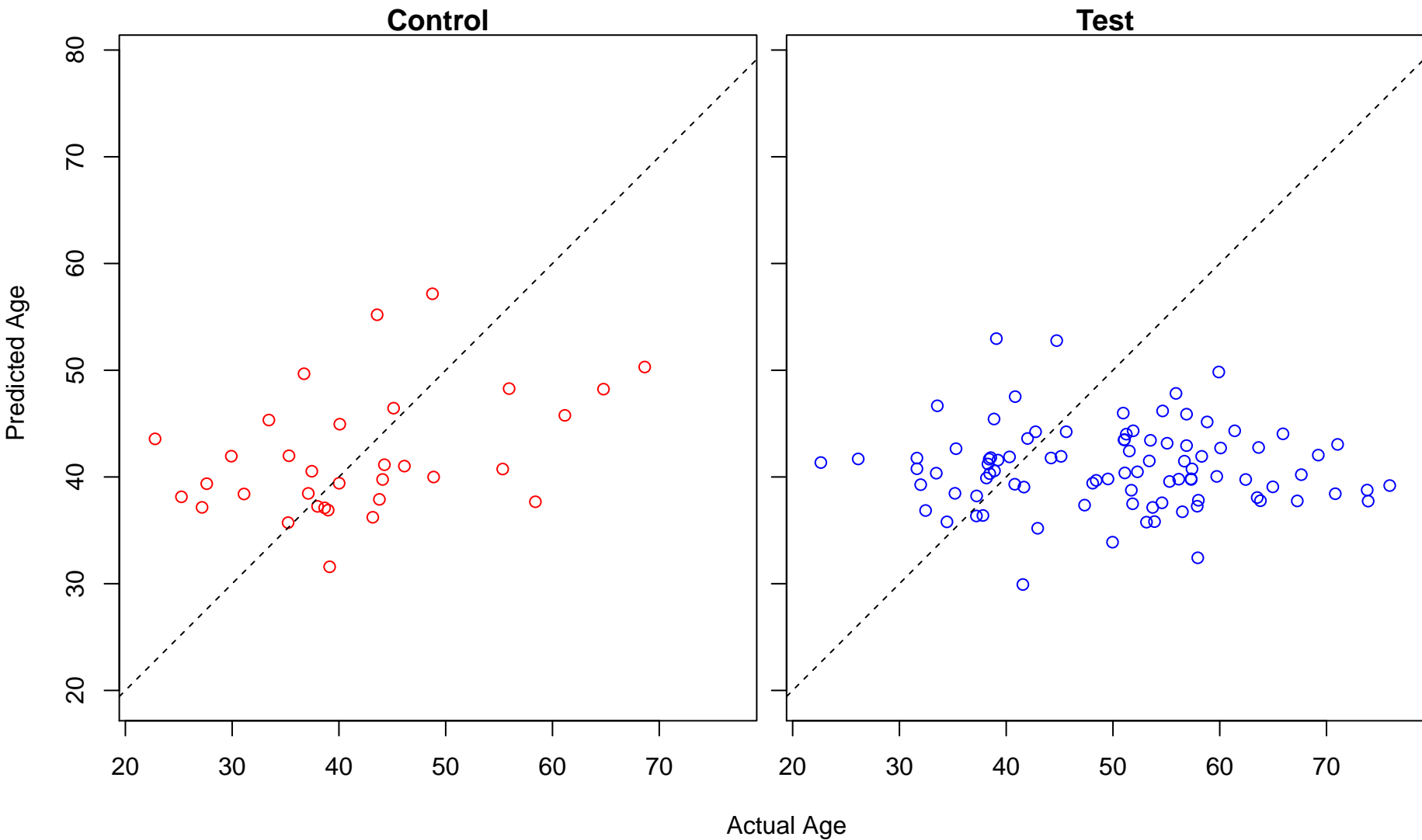
formin-nucleated actin cable assembly (Score: 0.551586)



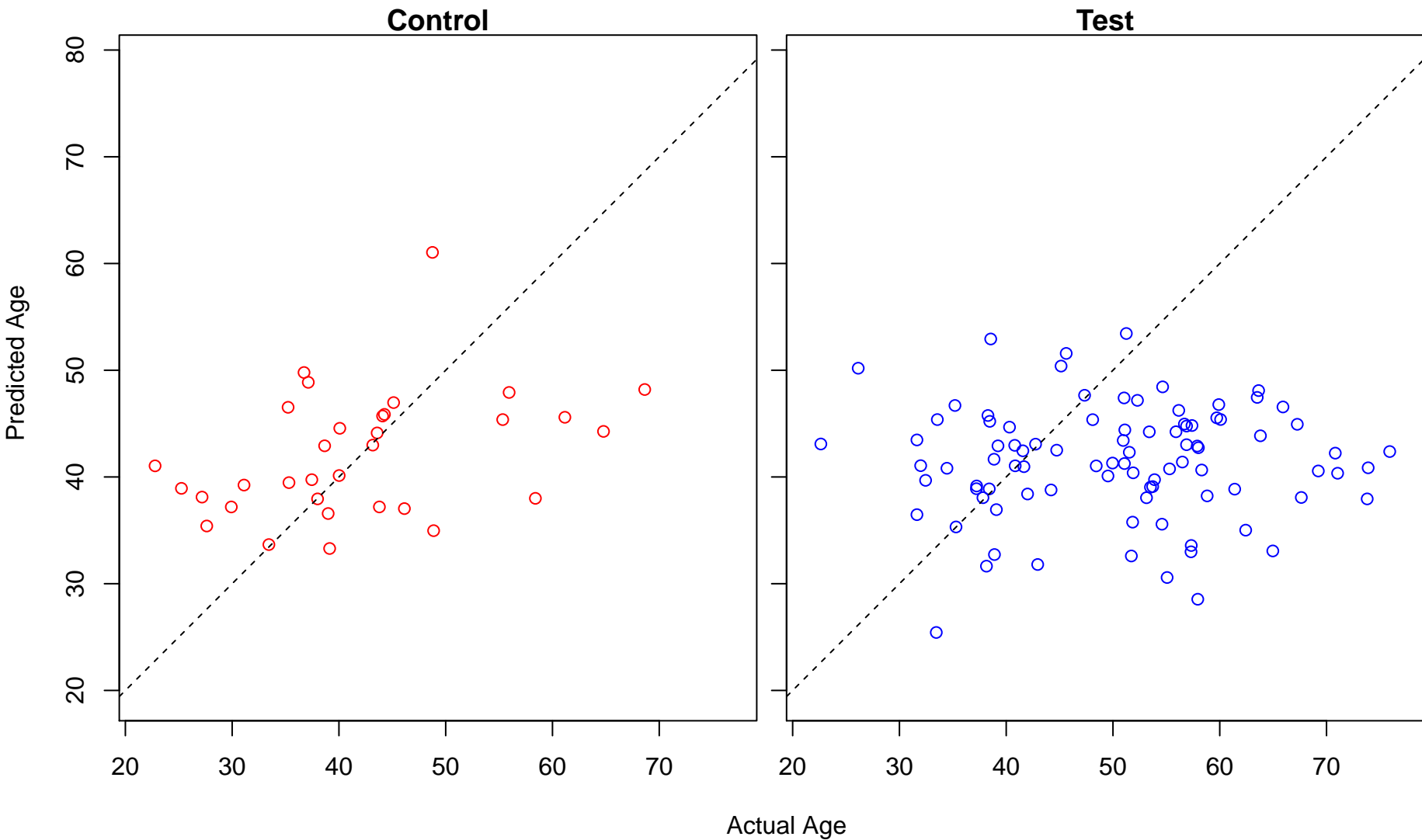
negative regulation of striated muscle contraction (Score: 0.551556)



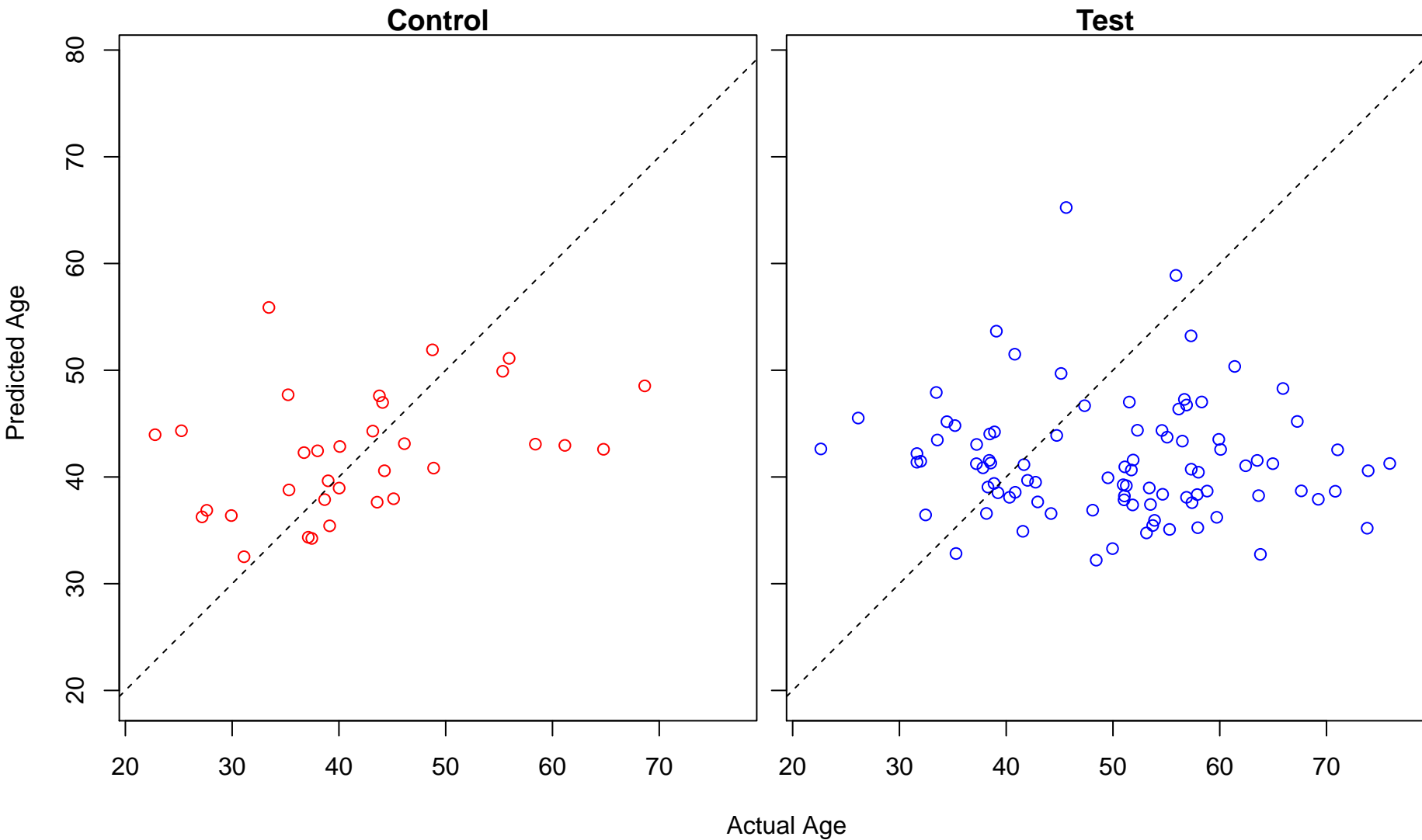
inositol metabolic process (Score: 0.551283)



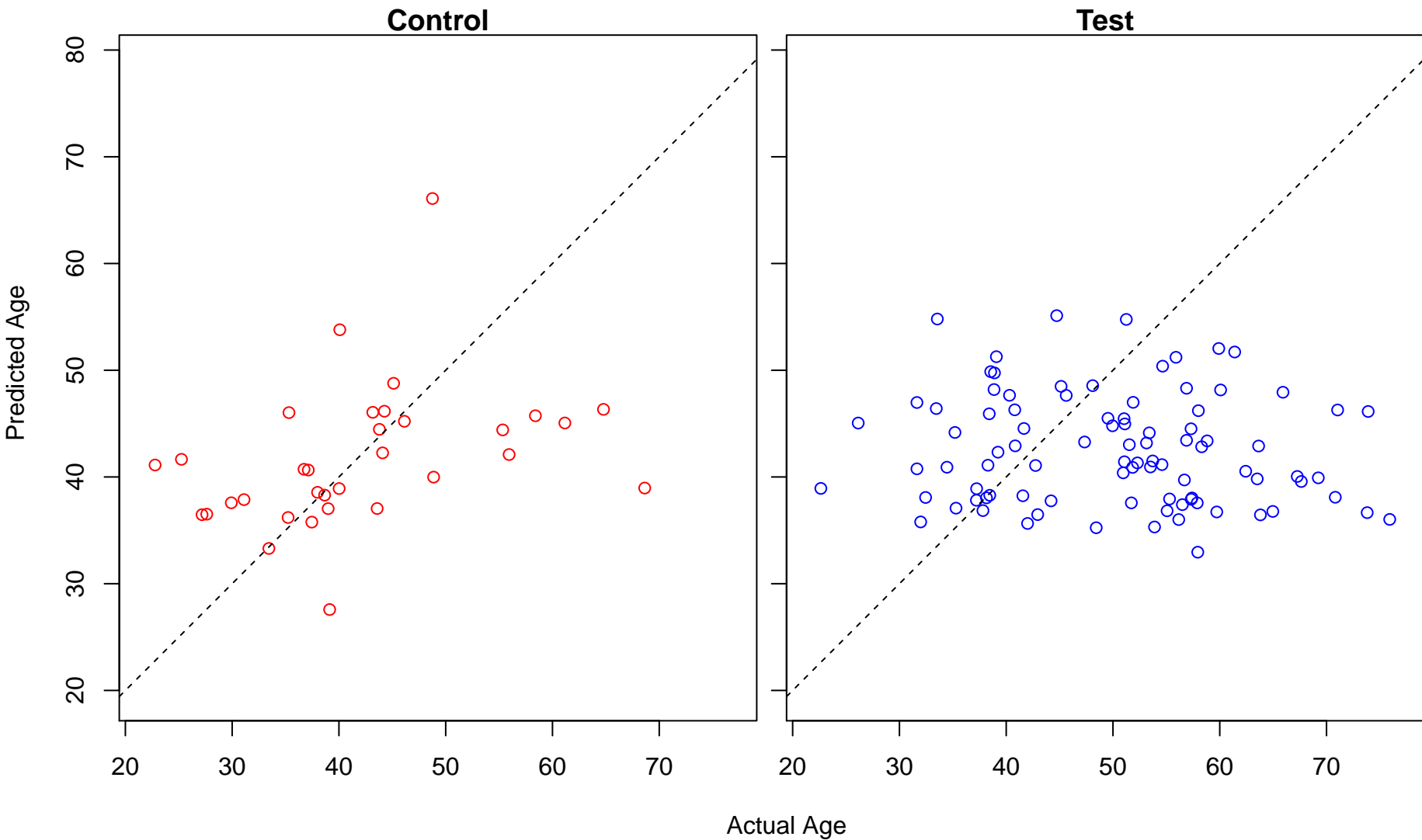
cardiolipin acyl-chain remodeling (Score: 0.550256)



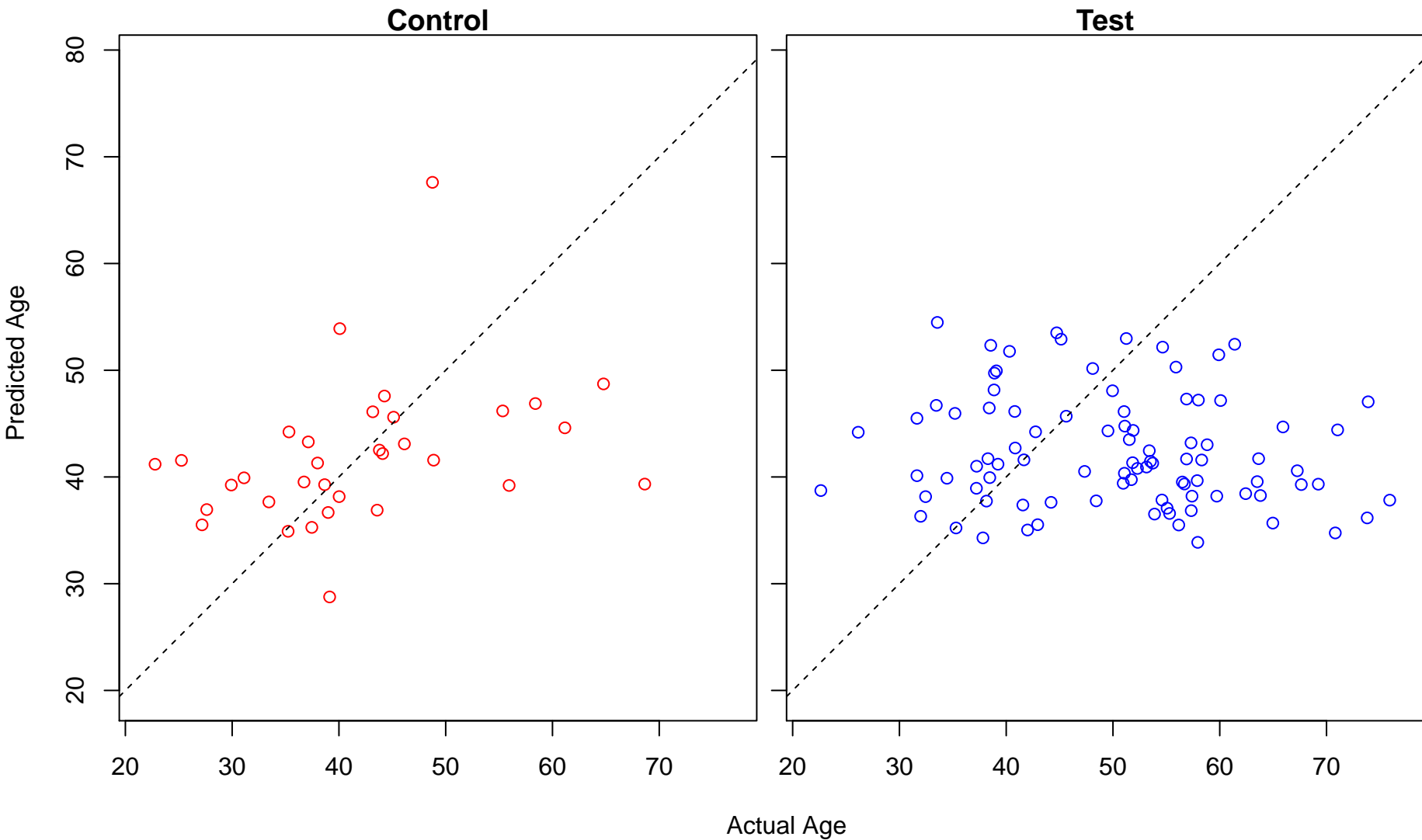
self proteolysis (Score: 0.550176)



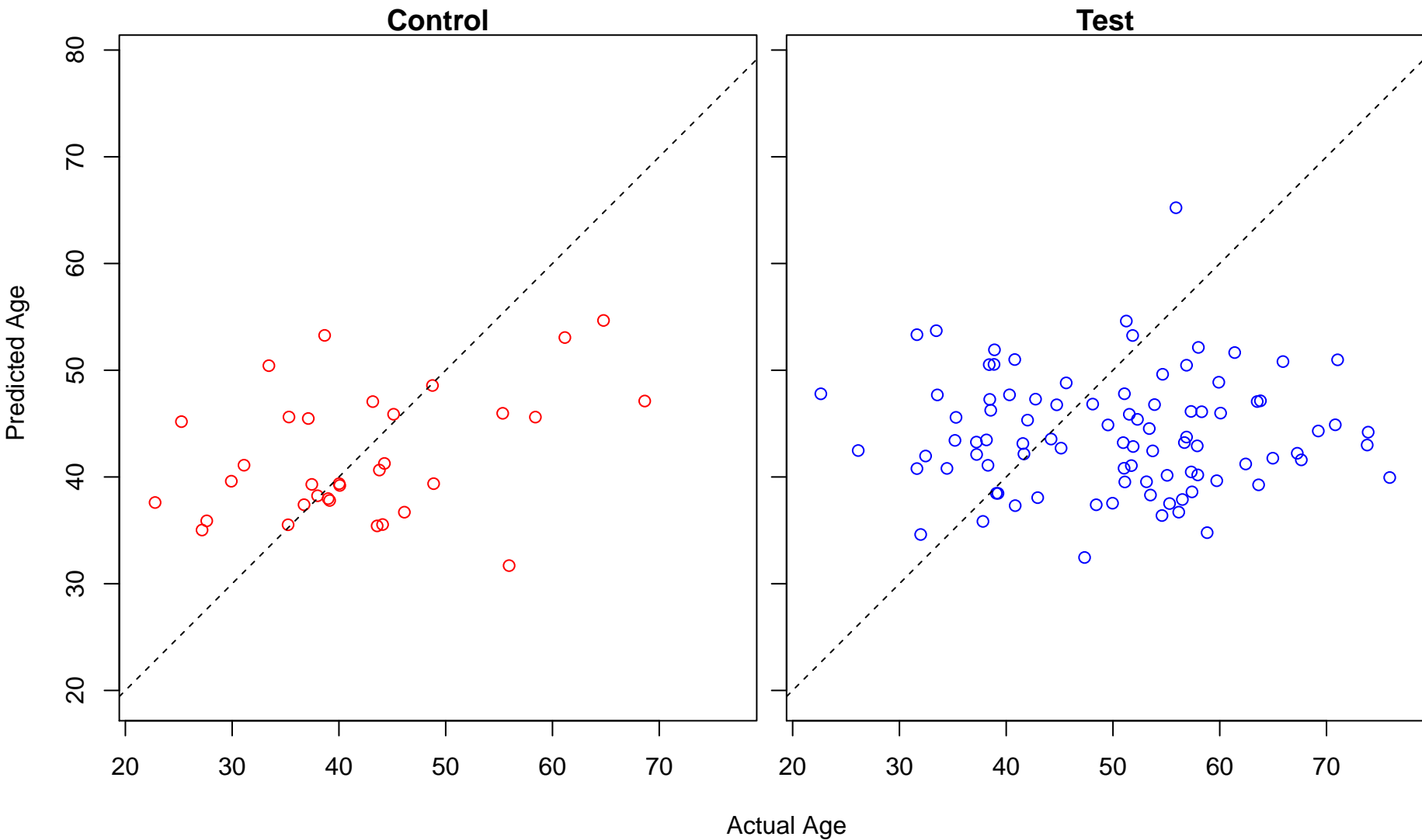
organic substance catabolic process (Score: 0.548540)



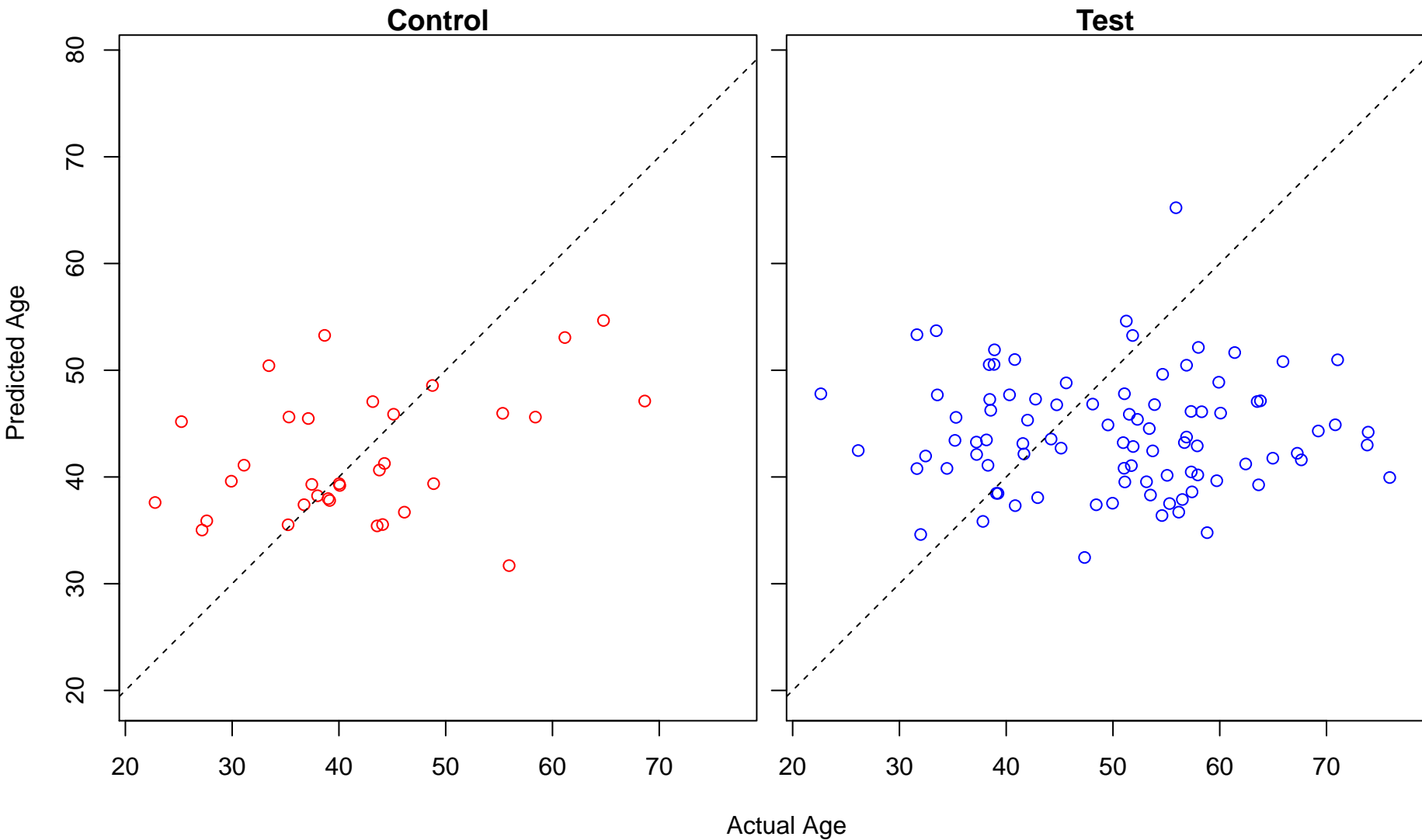
regulation of cell morphogenesis (Score: 0.548285)



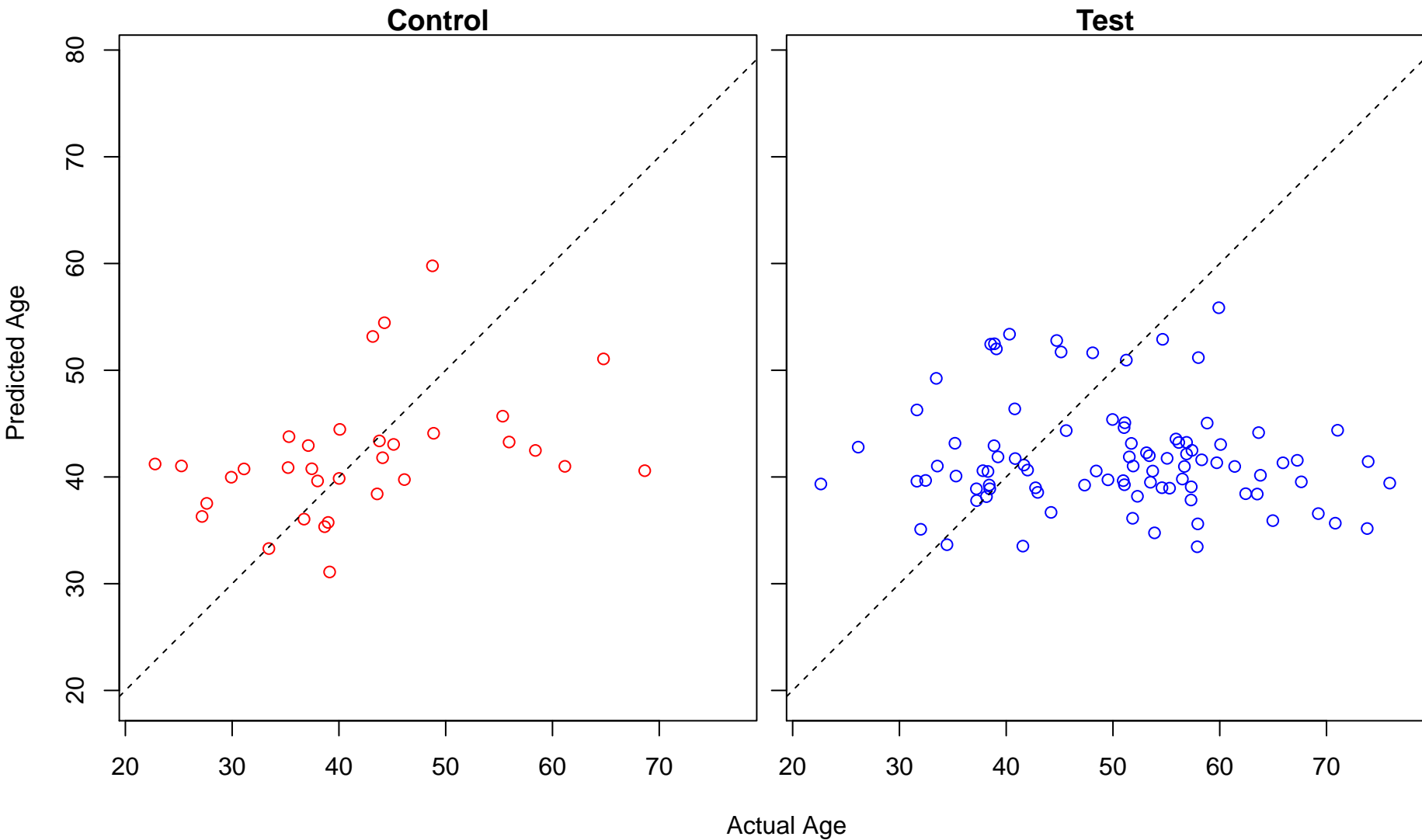
ventral spinal cord development (Score: 0.548252)



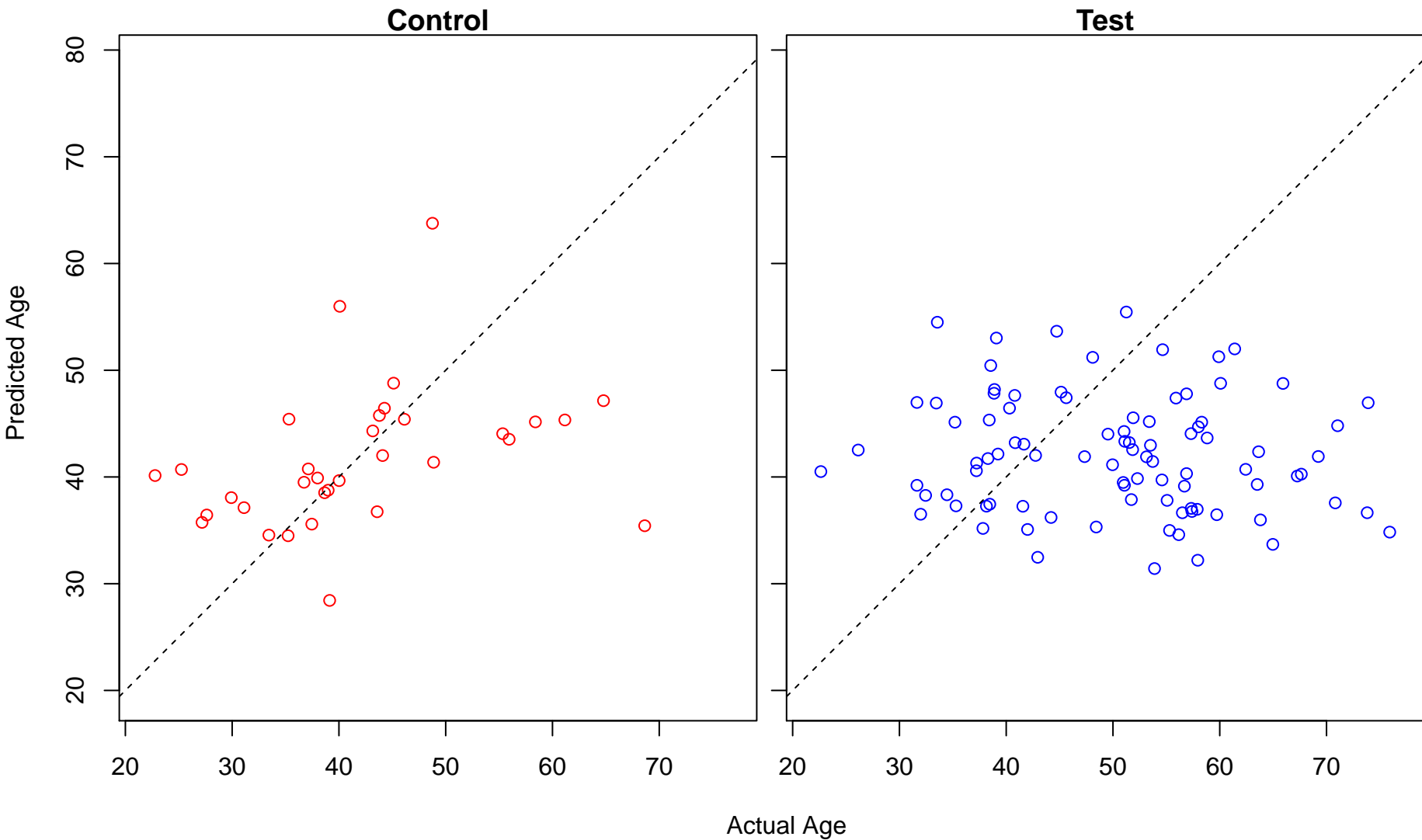
spinal cord motor neuron differentiation (Score: 0.548252)



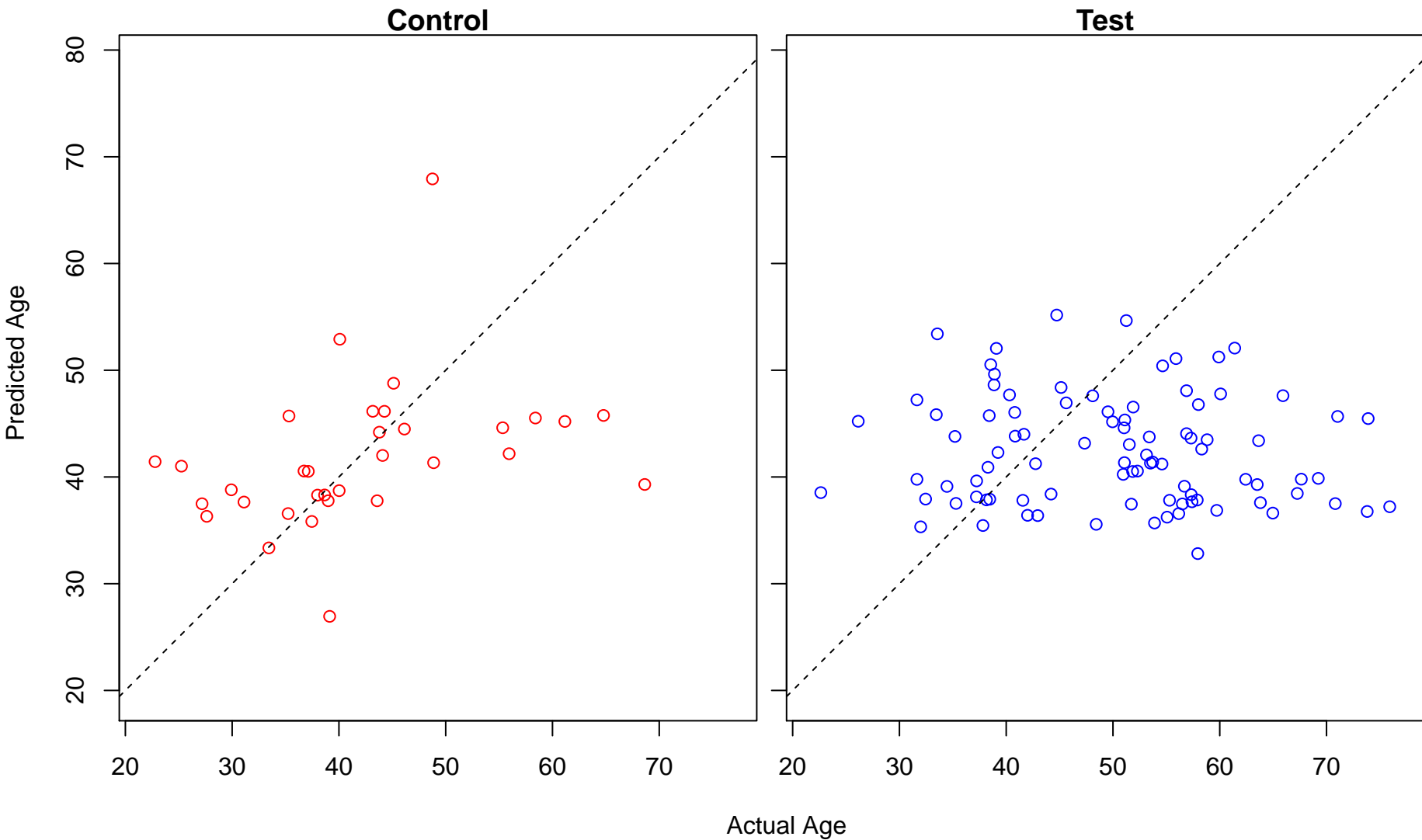
exit from mitosis (Score: 0.547684)



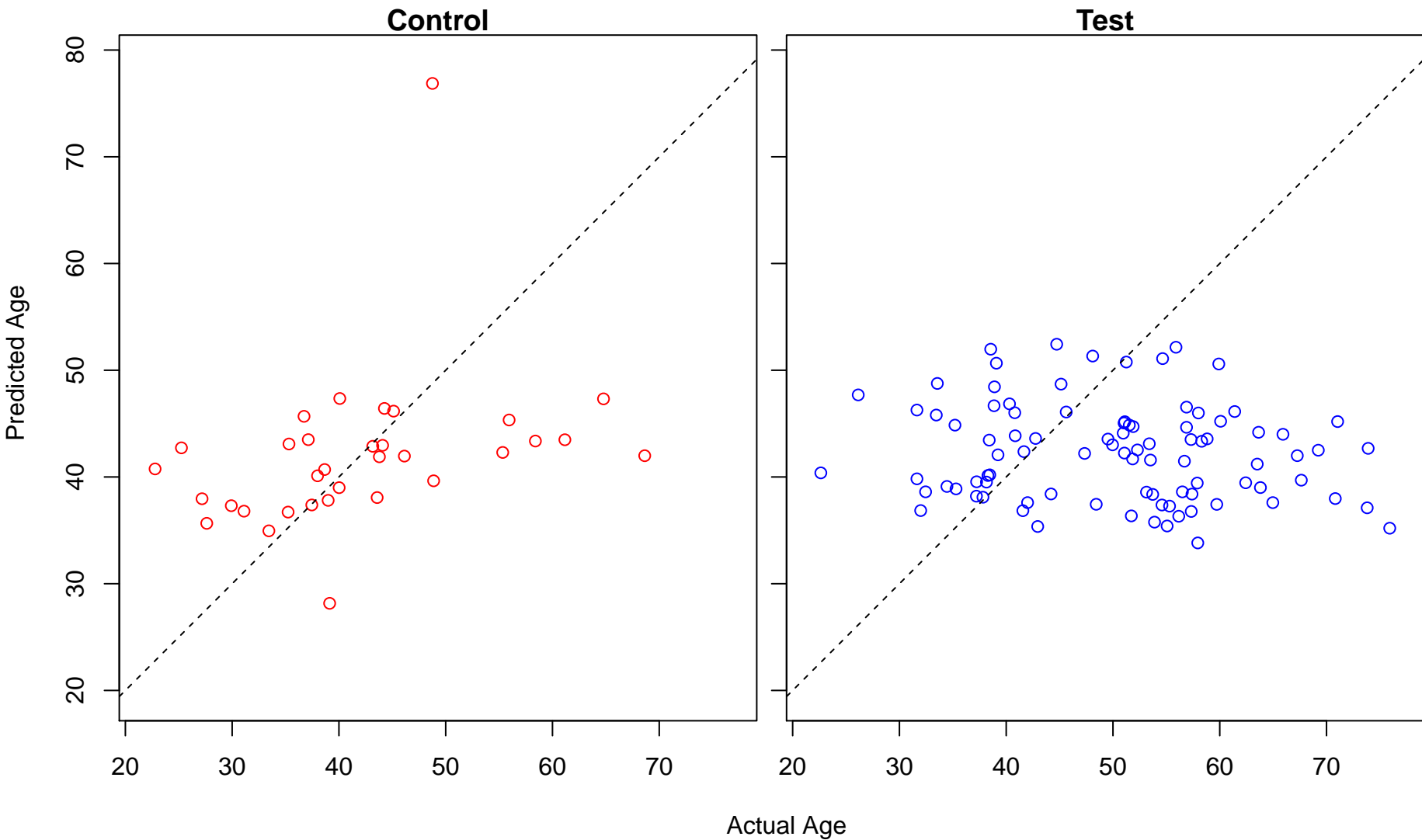
oxidation-reduction process (Score: 0.547402)



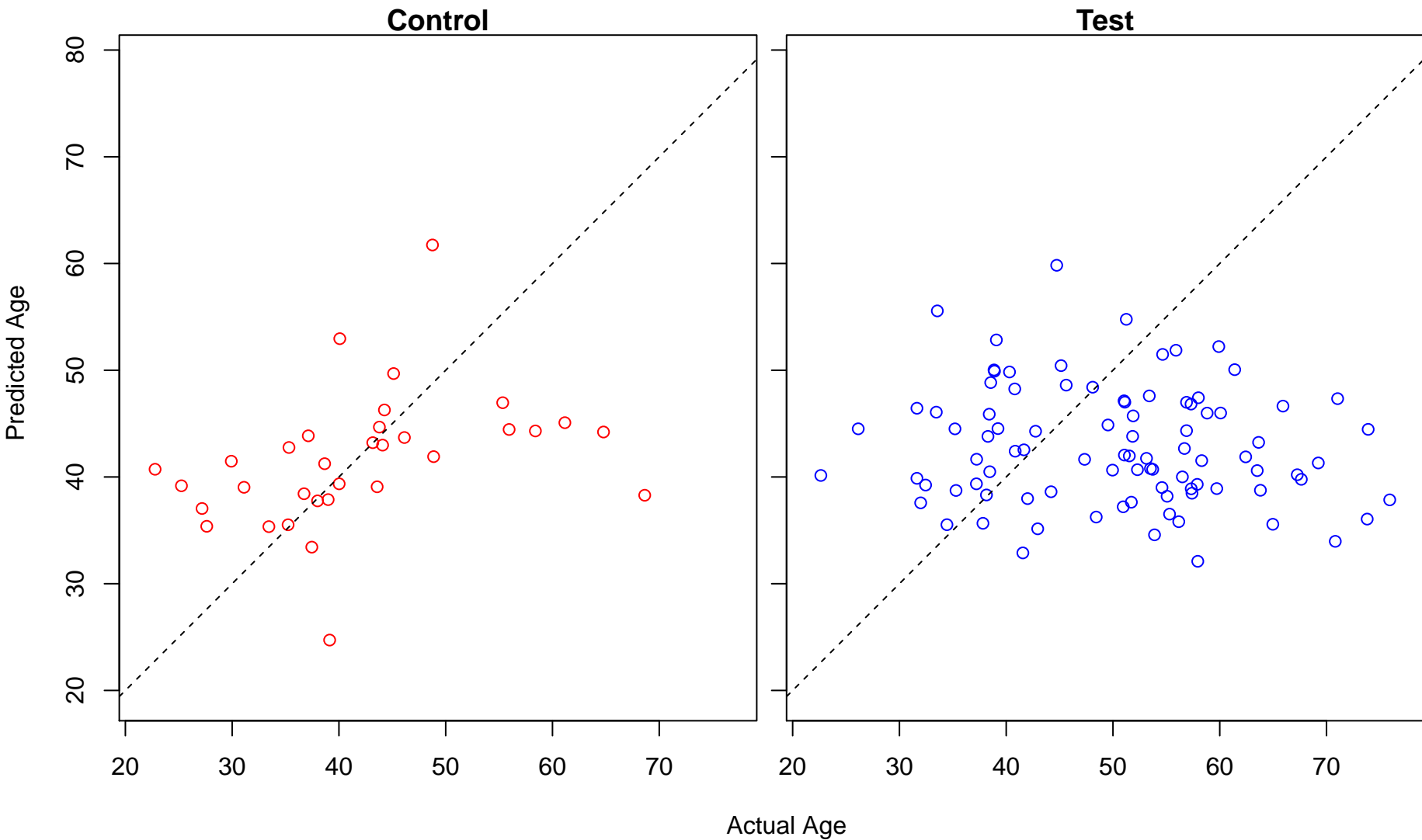
cellular macromolecule catabolic process (Score: 0.547271)



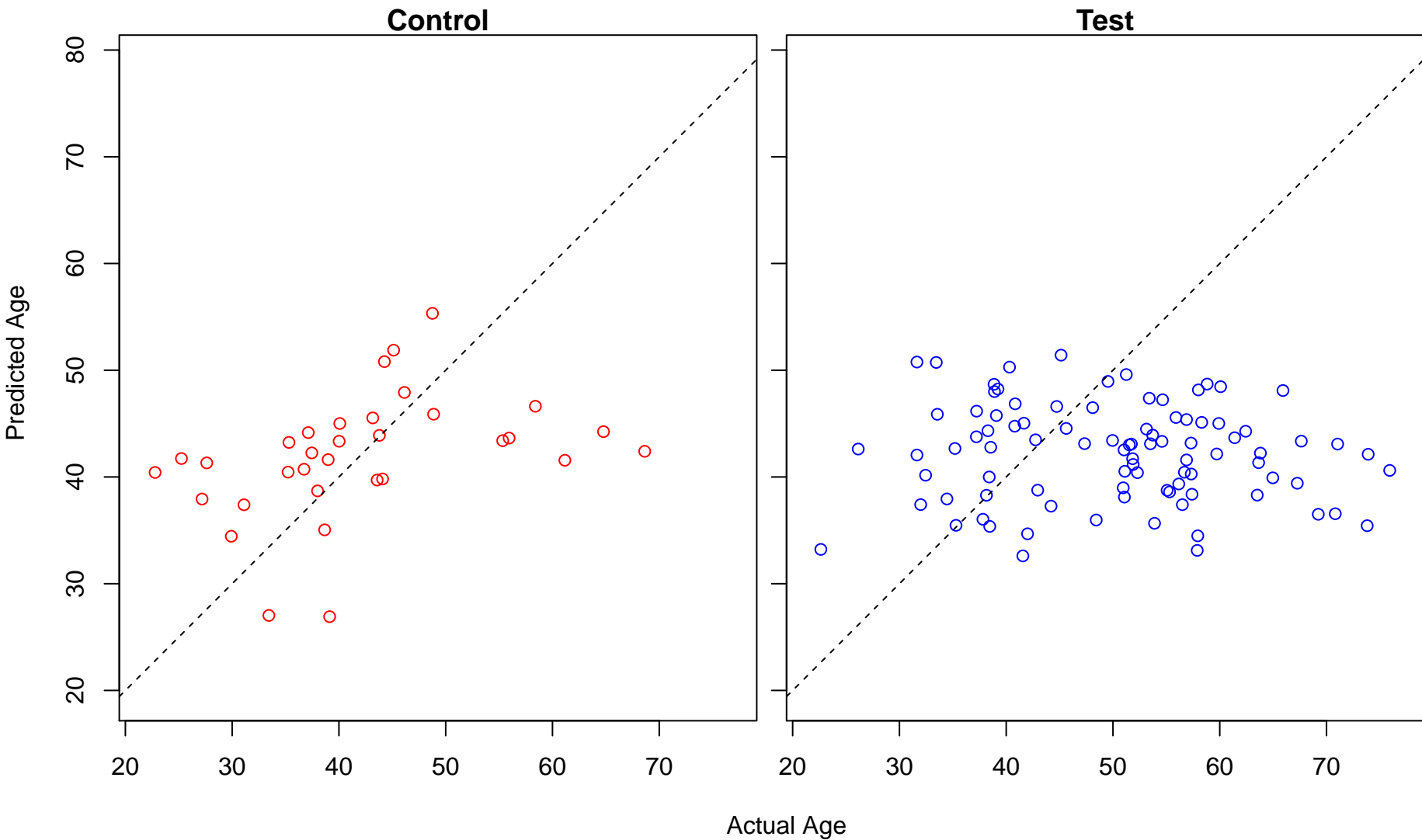
protein transport (Score: 0.547214)



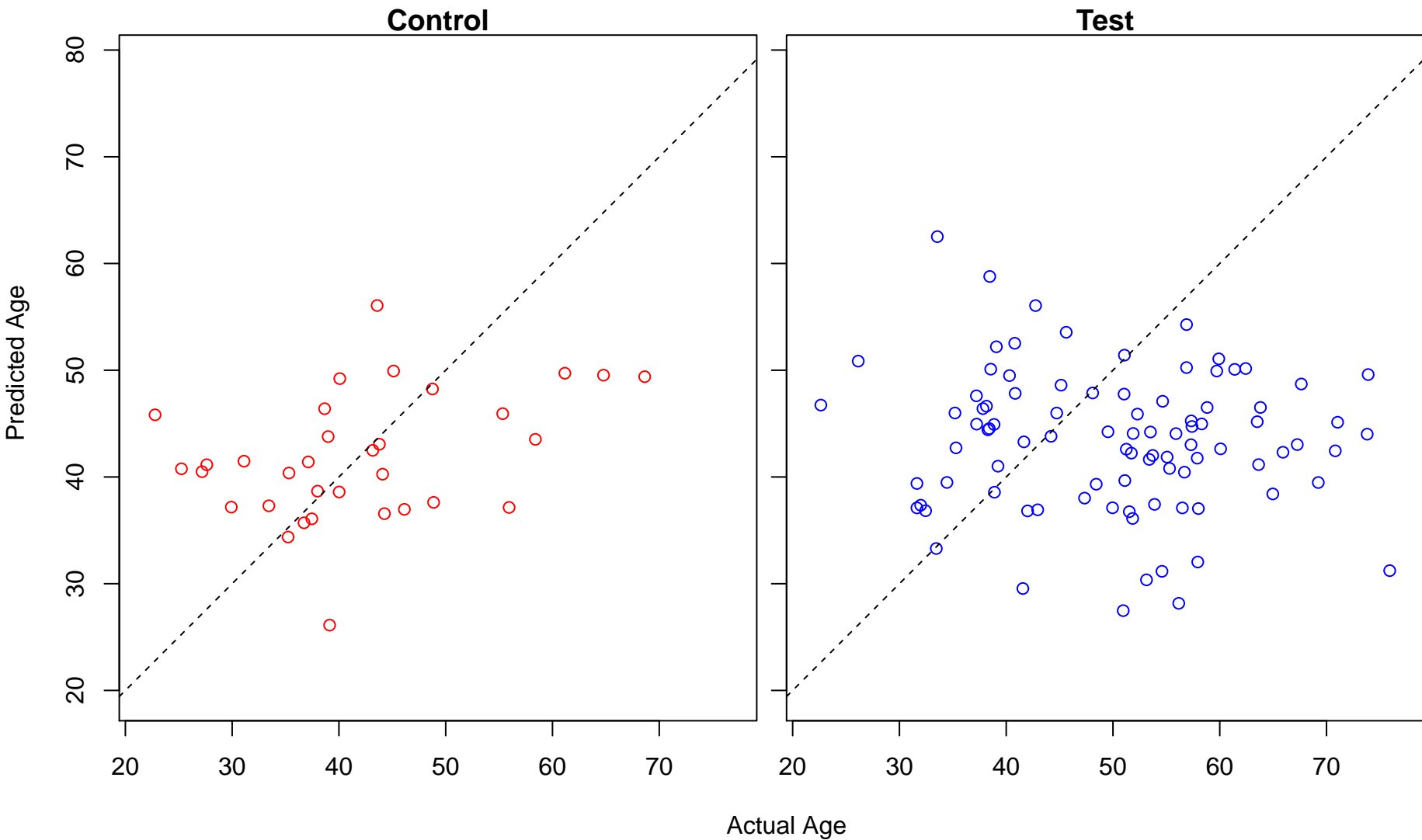
positive regulation of MAPK cascade (Score: 0.547181)



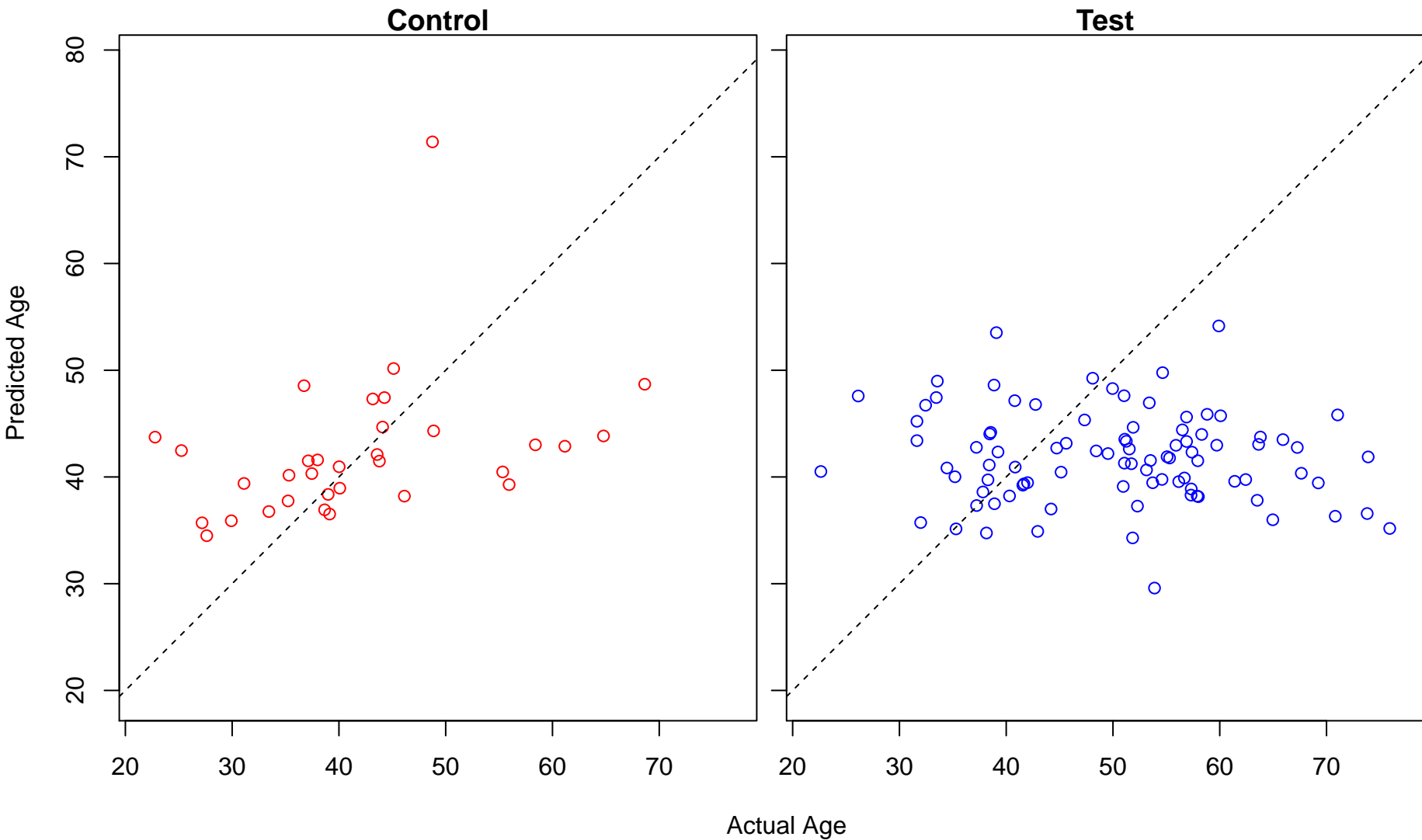
bradykinin catabolic process (Score: 0.546631)



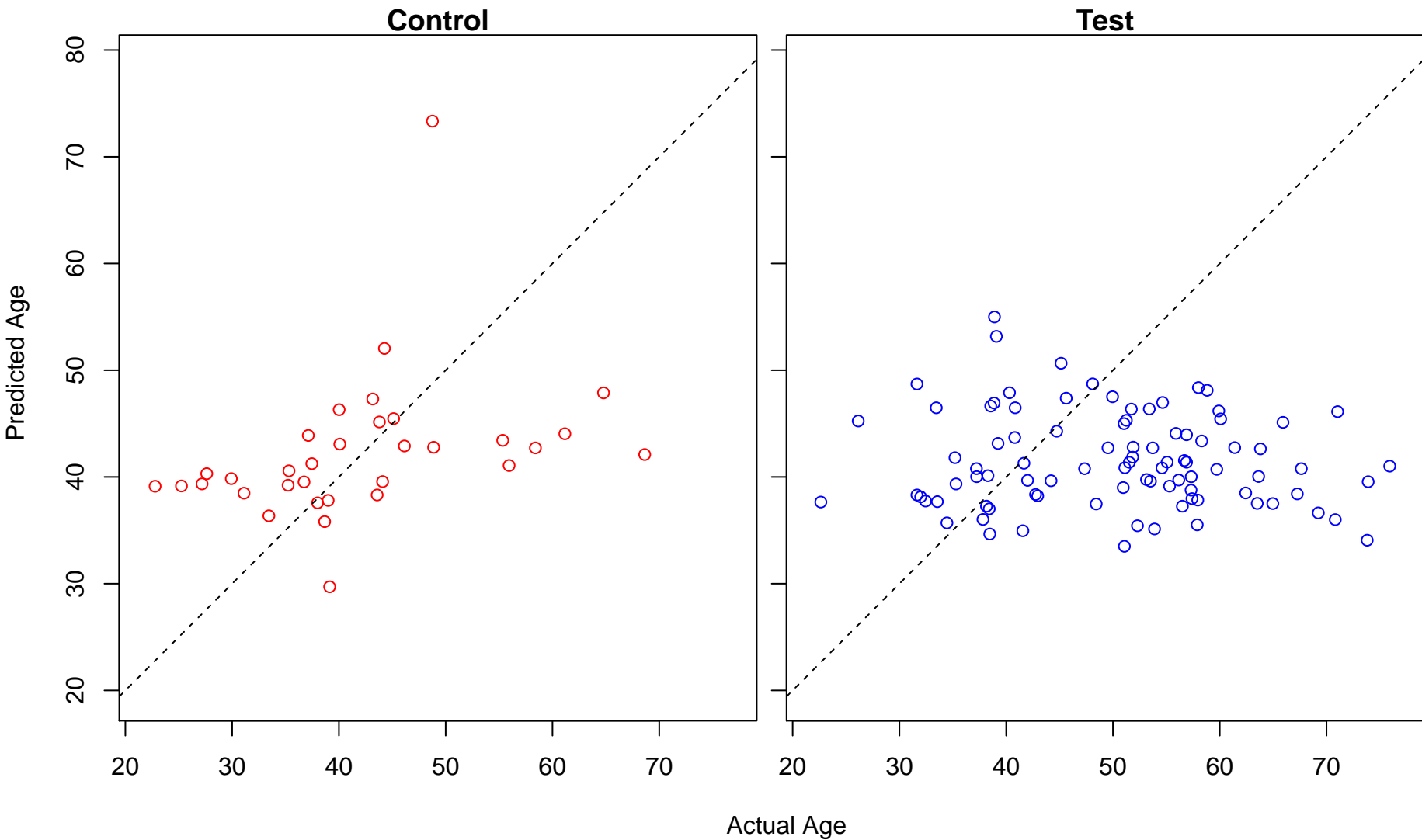
primary amino compound metabolic process (Score: 0.546158)



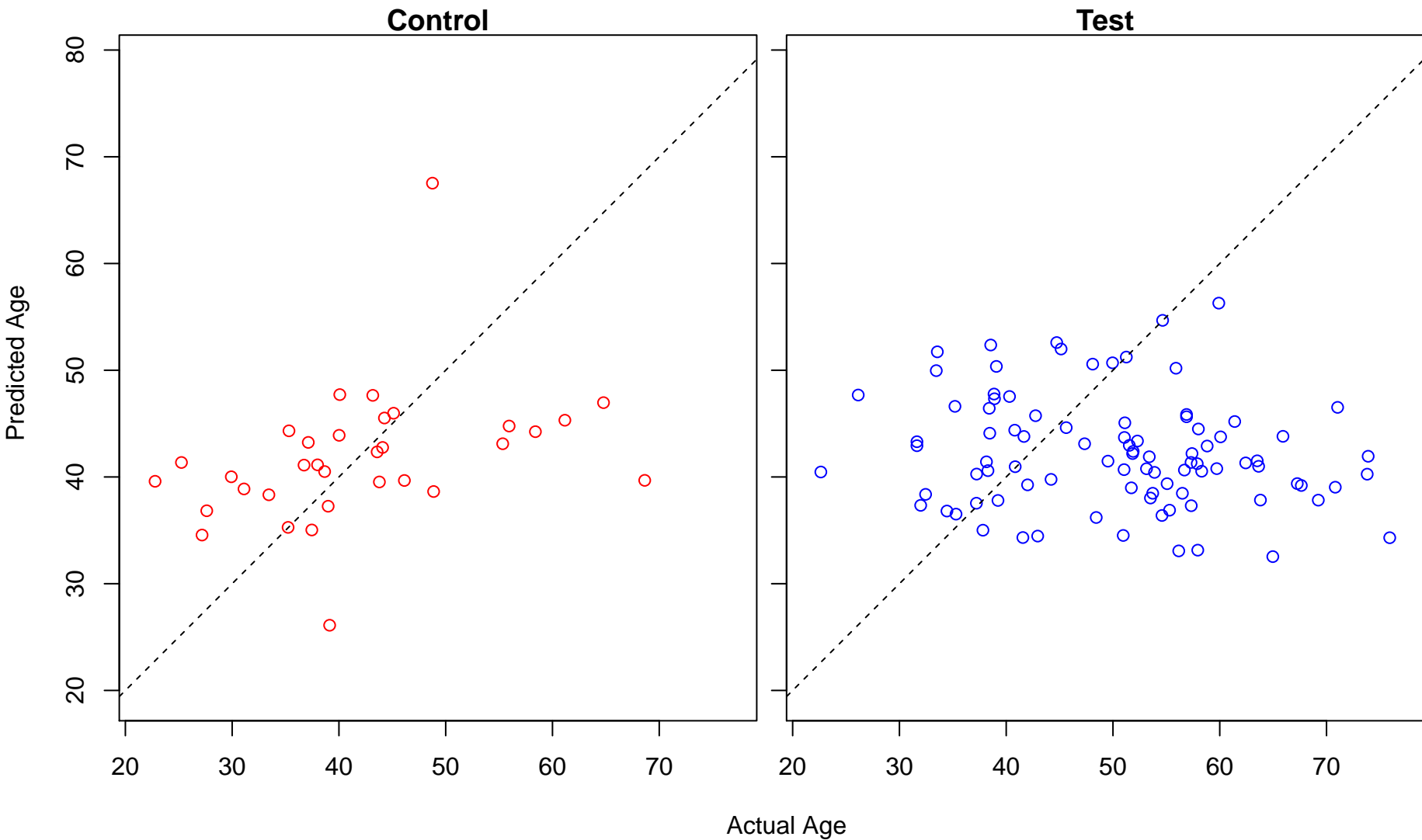
regulation of T-helper 2 cell differentiation (Score: 0.545275)



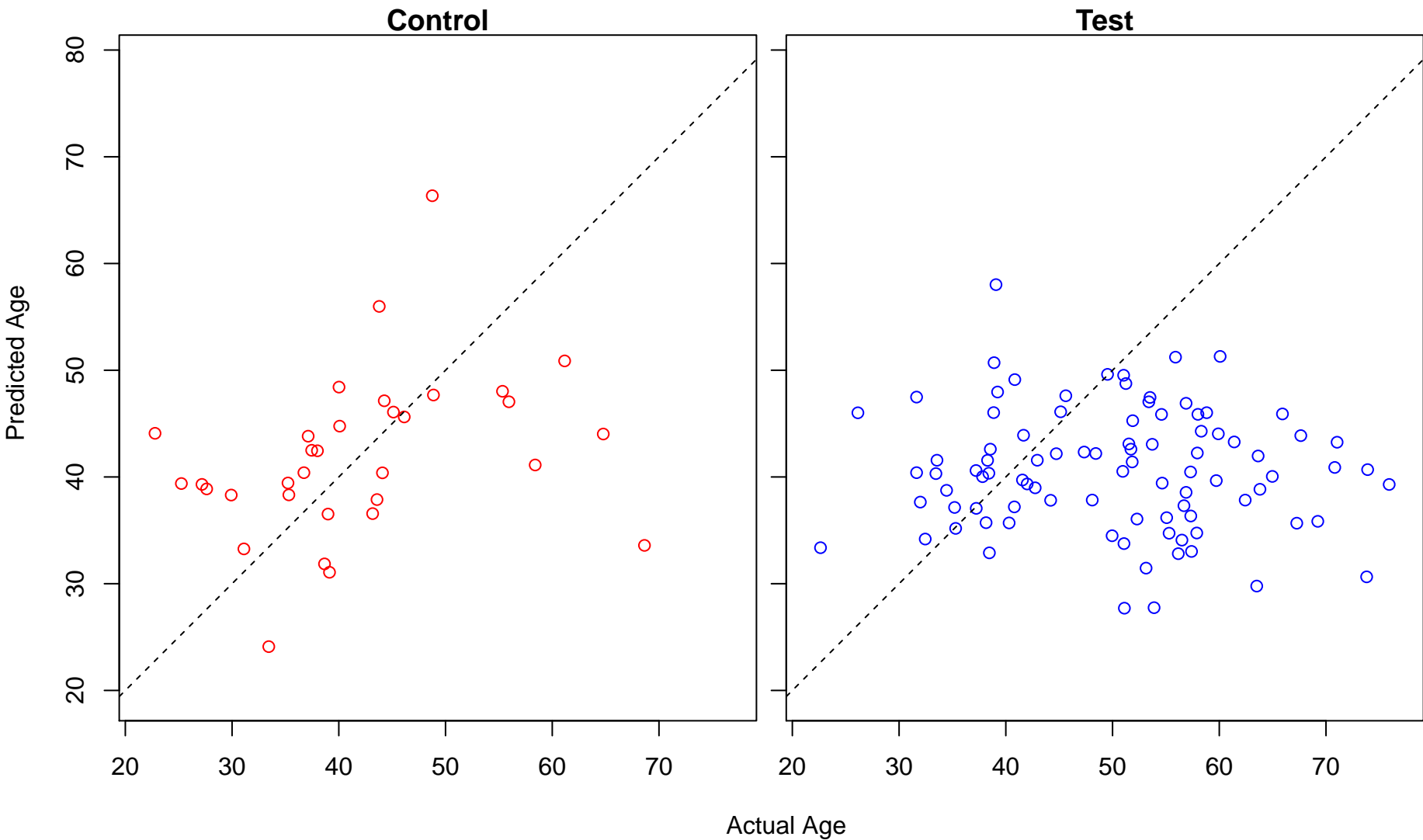
regulation of mitochondrial translation (Score: 0.545236)



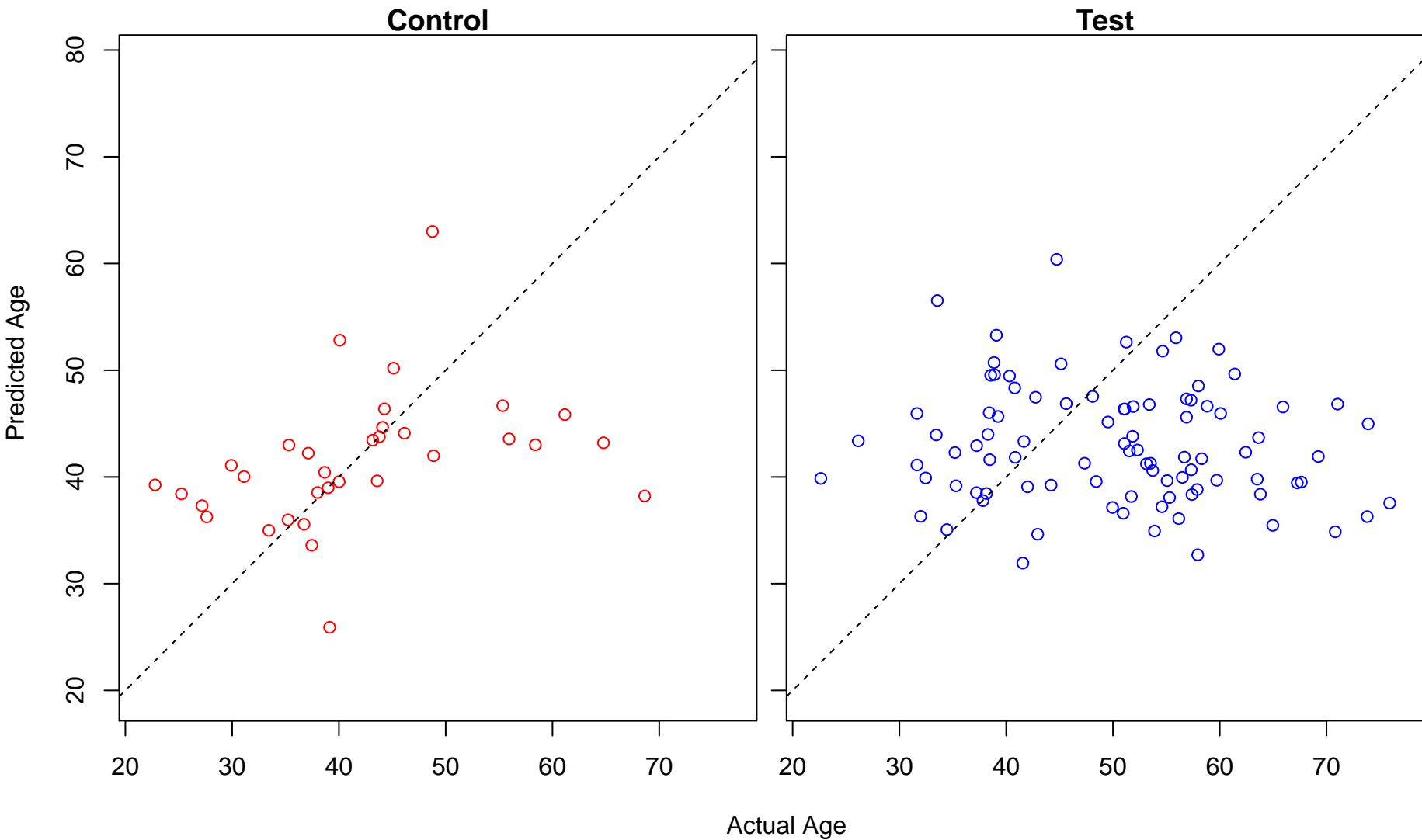
metal ion transport (Score: 0.544826)



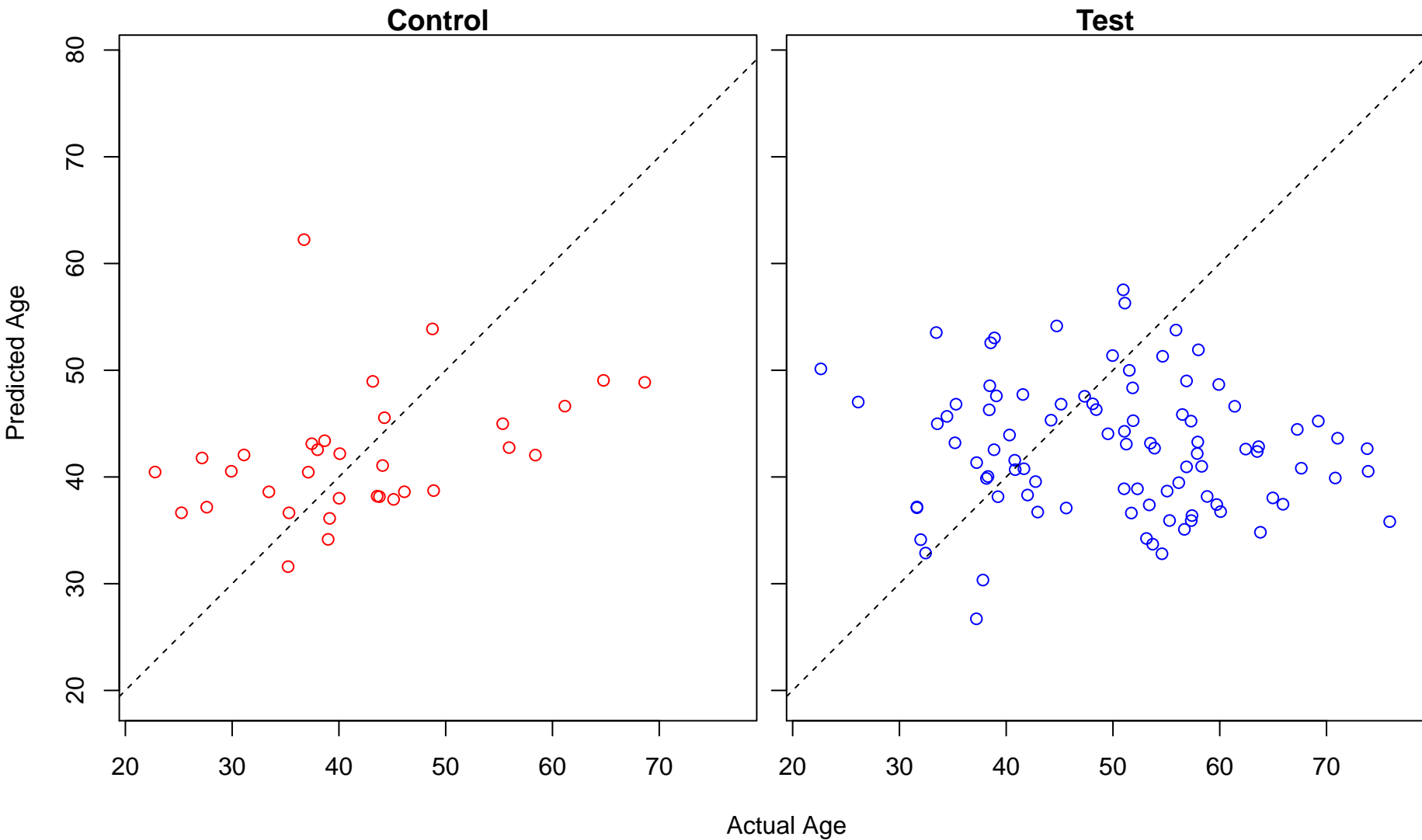
negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway (Score: 0



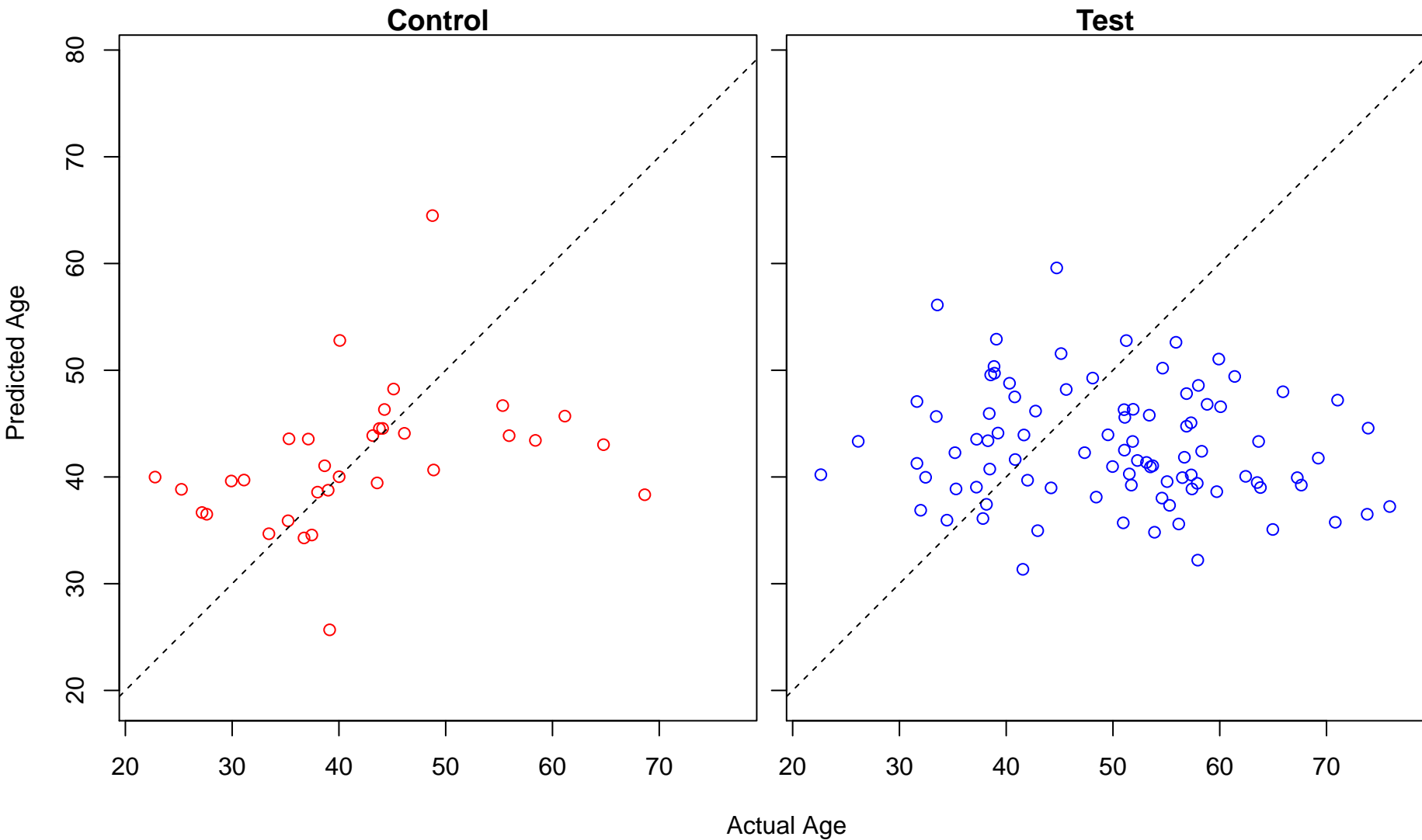
regulation of MAP kinase activity (Score: 0.541764)



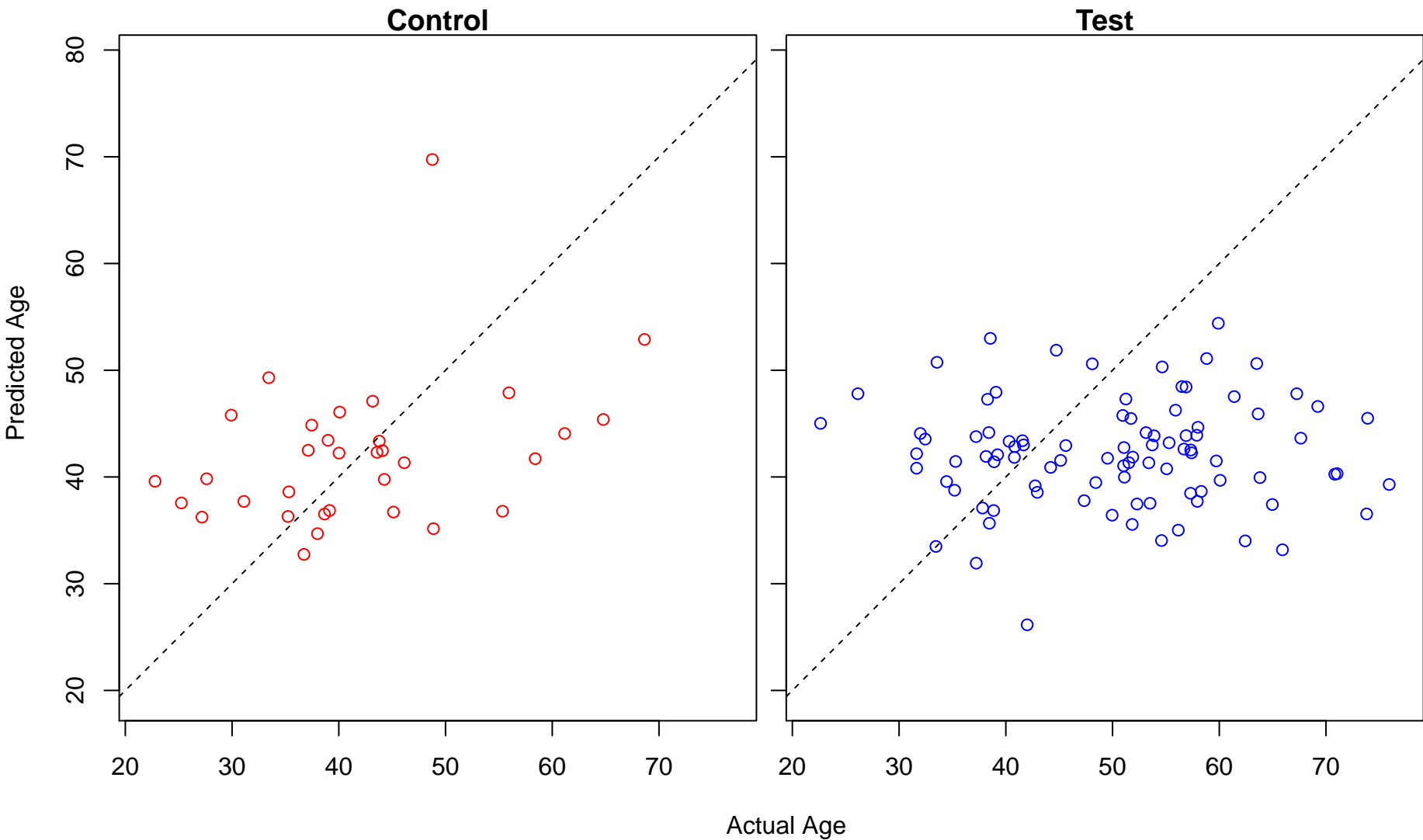
primitive hemopoiesis (Score: 0.540442)



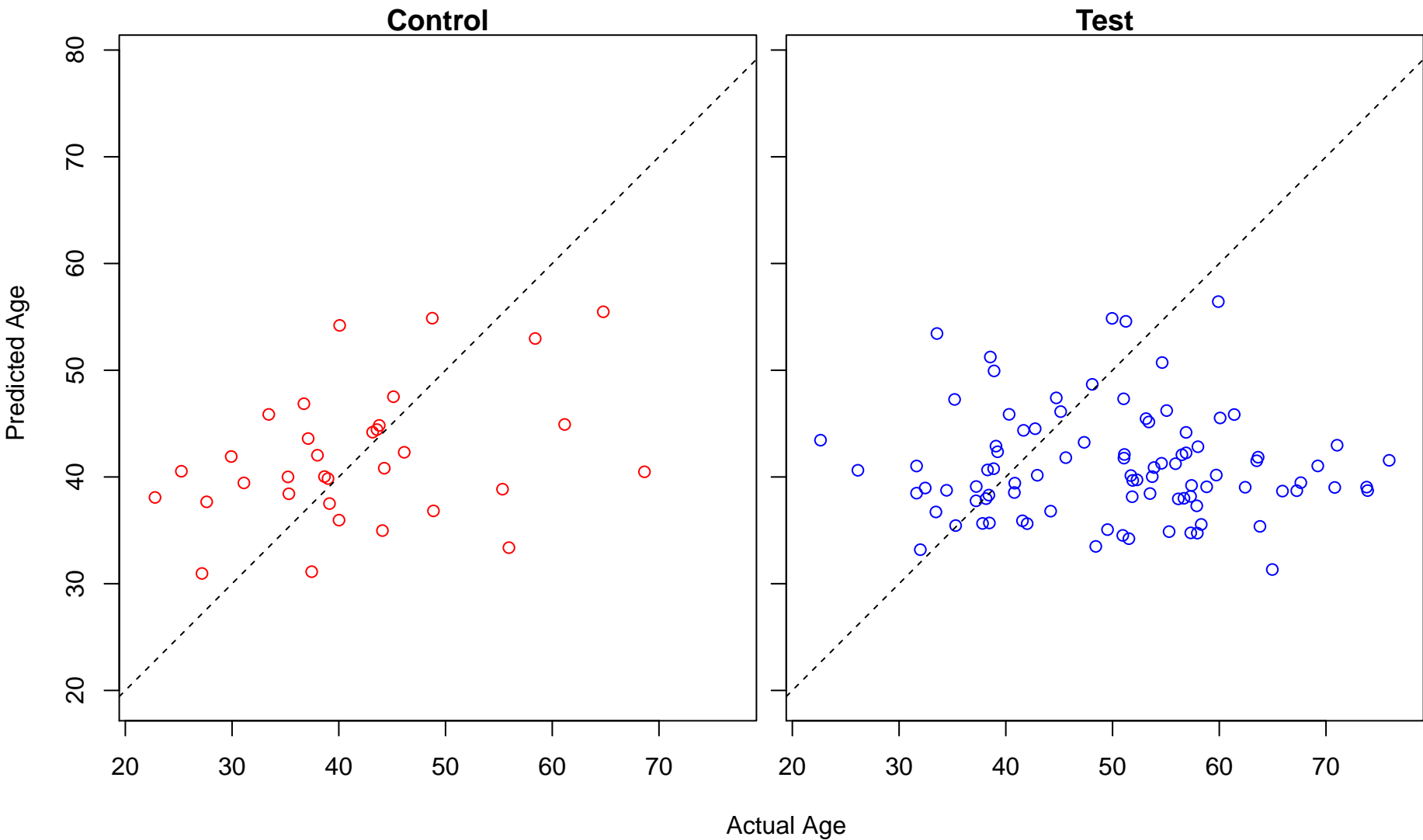
regulation of protein serine/threonine kinase activity (Score: 0.539554)



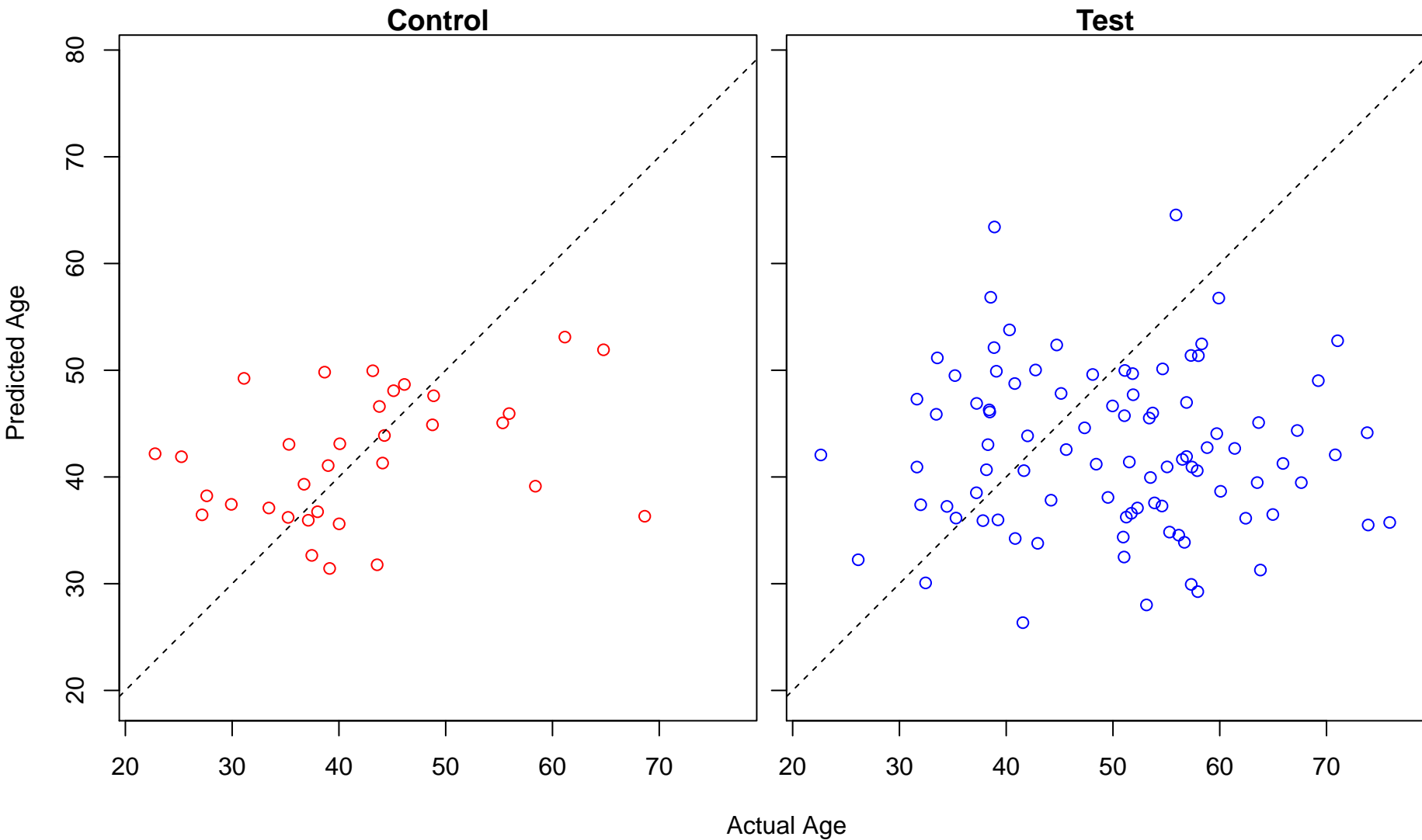
negative regulation of protein kinase activity by regulation of protein phosphorylation (Score: 0.5382)



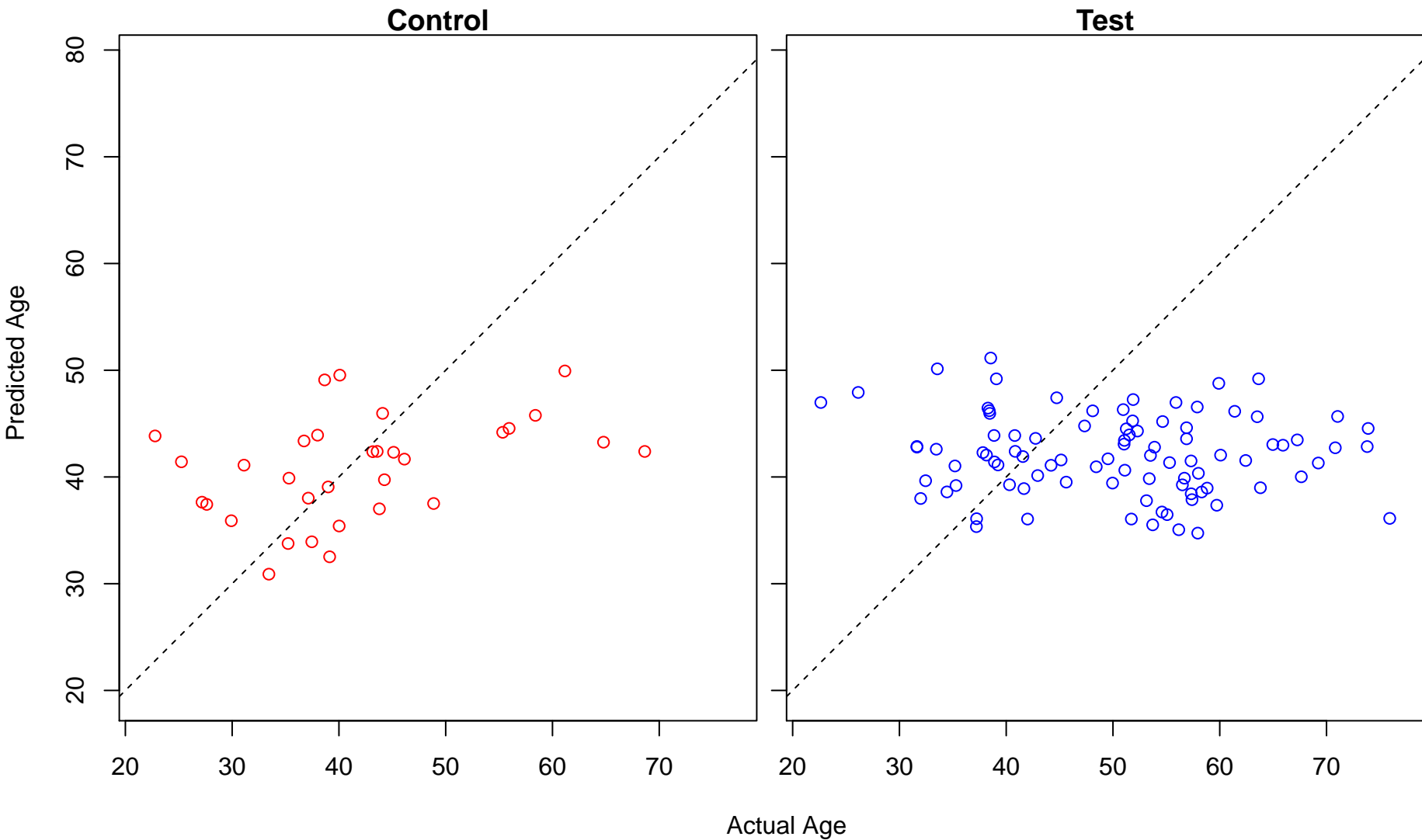
tion of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity (S



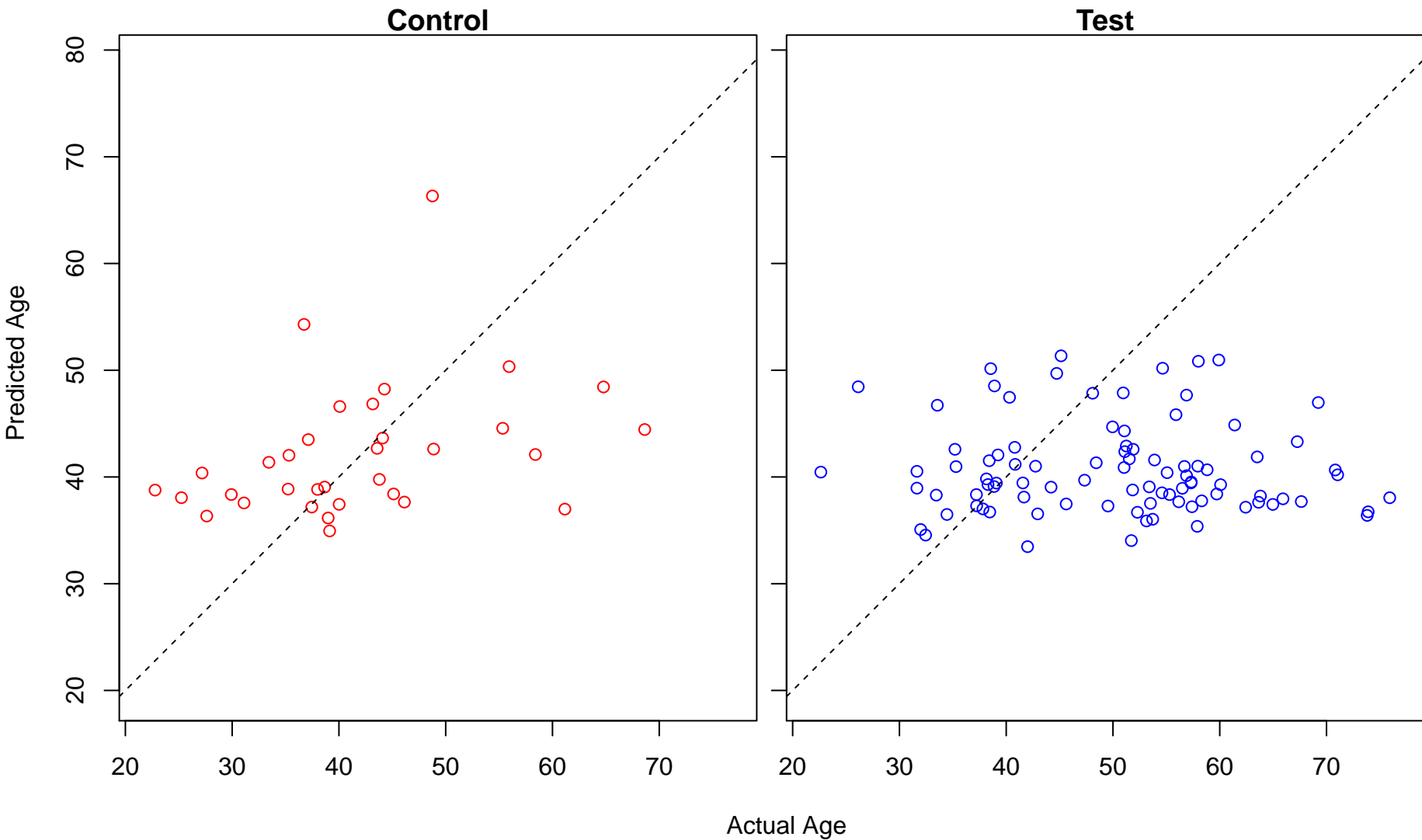
oxalate transport (Score: 0.537640)



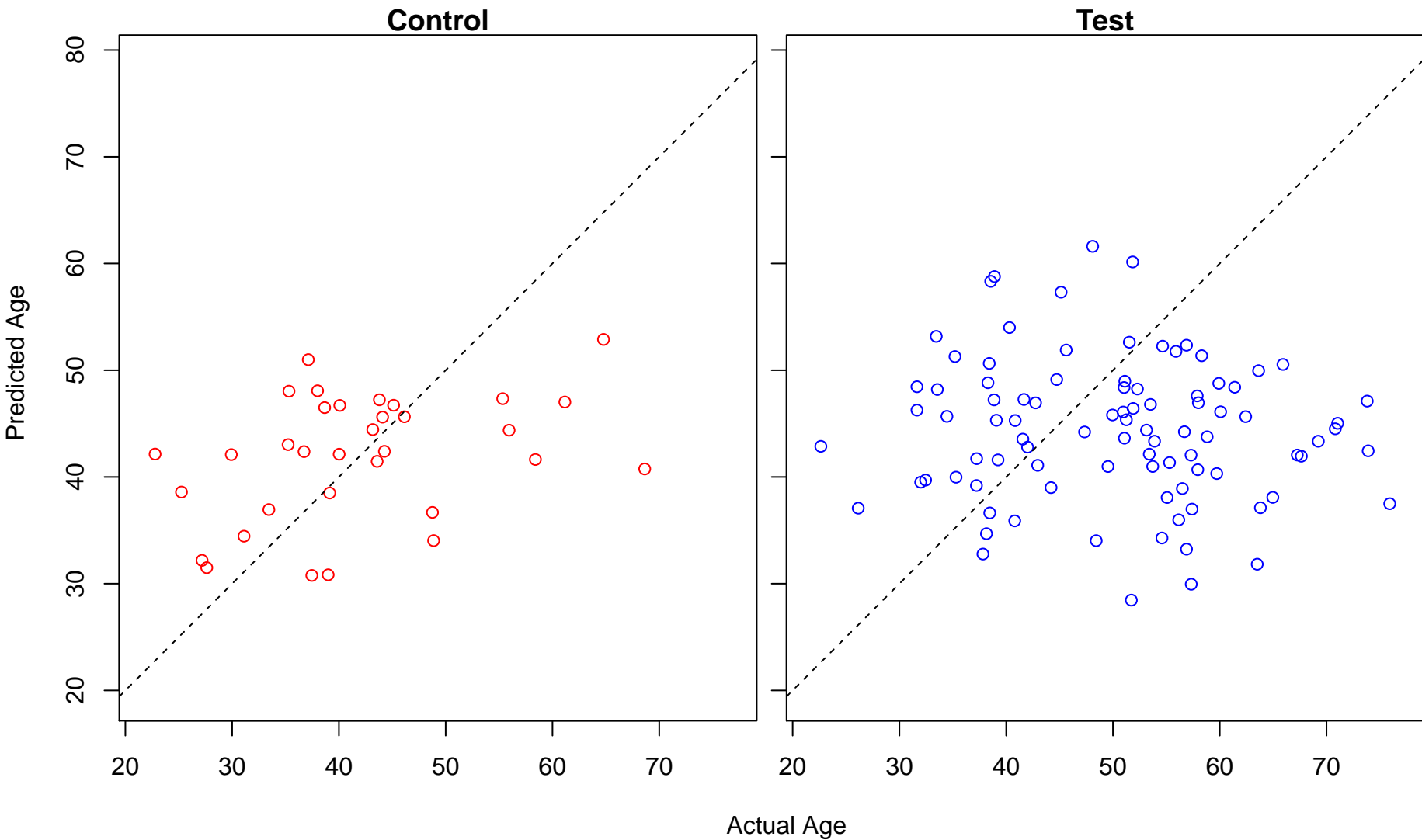
mRNA cis splicing, via spliceosome (Score: 0.537384)



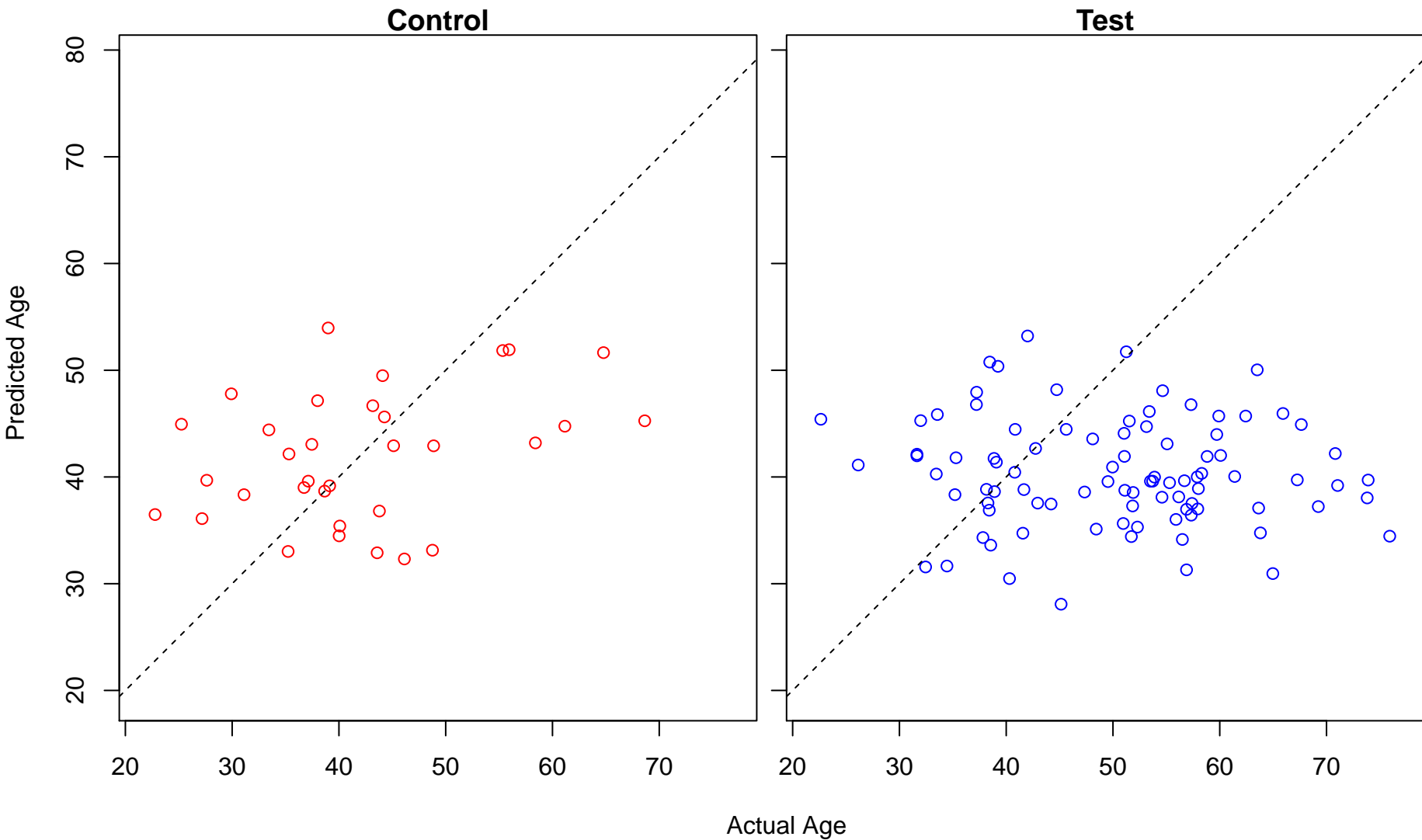
positive regulation of mRNA splicing, via spliceosome (Score: 0.537245)



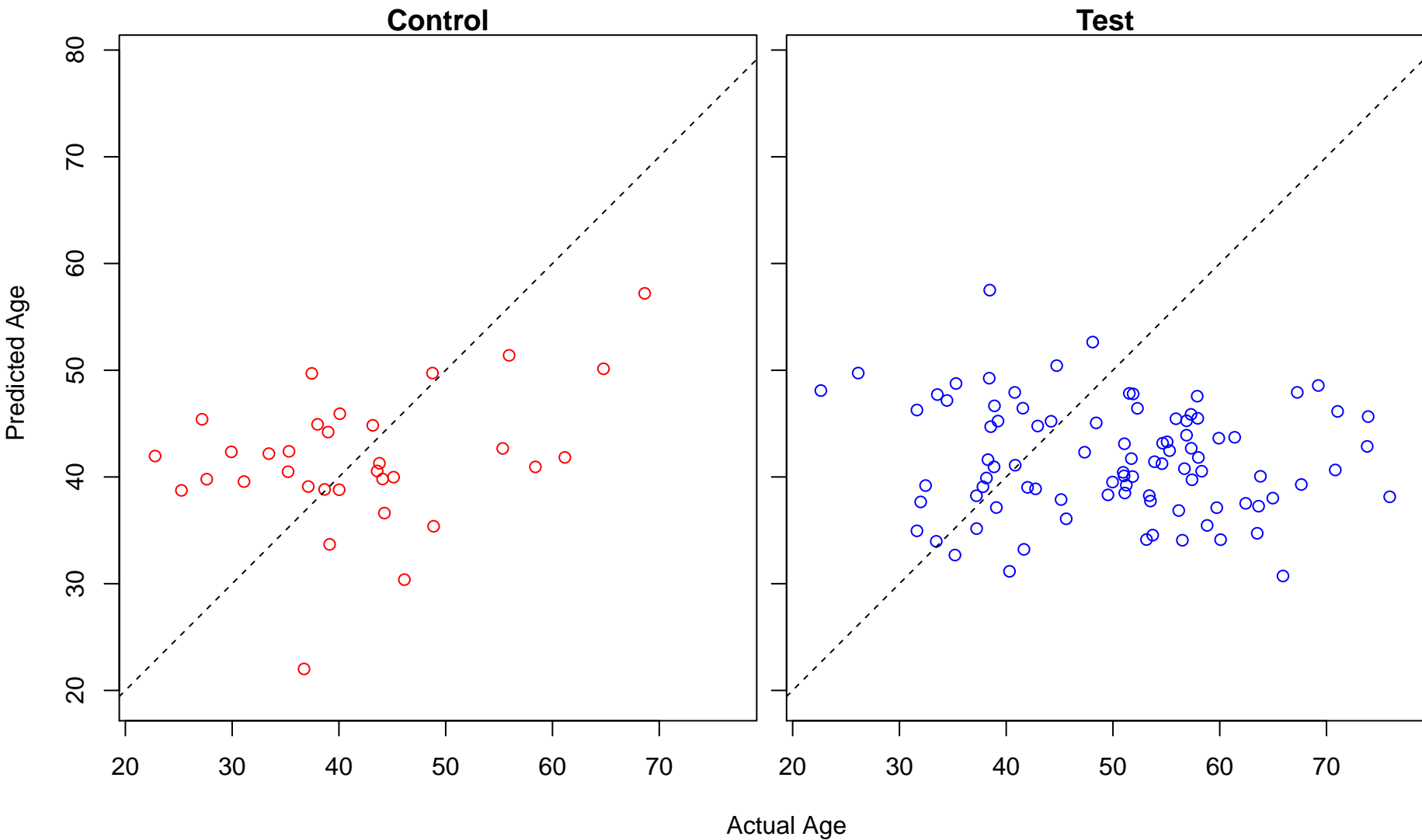
metanephric distal tubule development (Score: 0.536110)



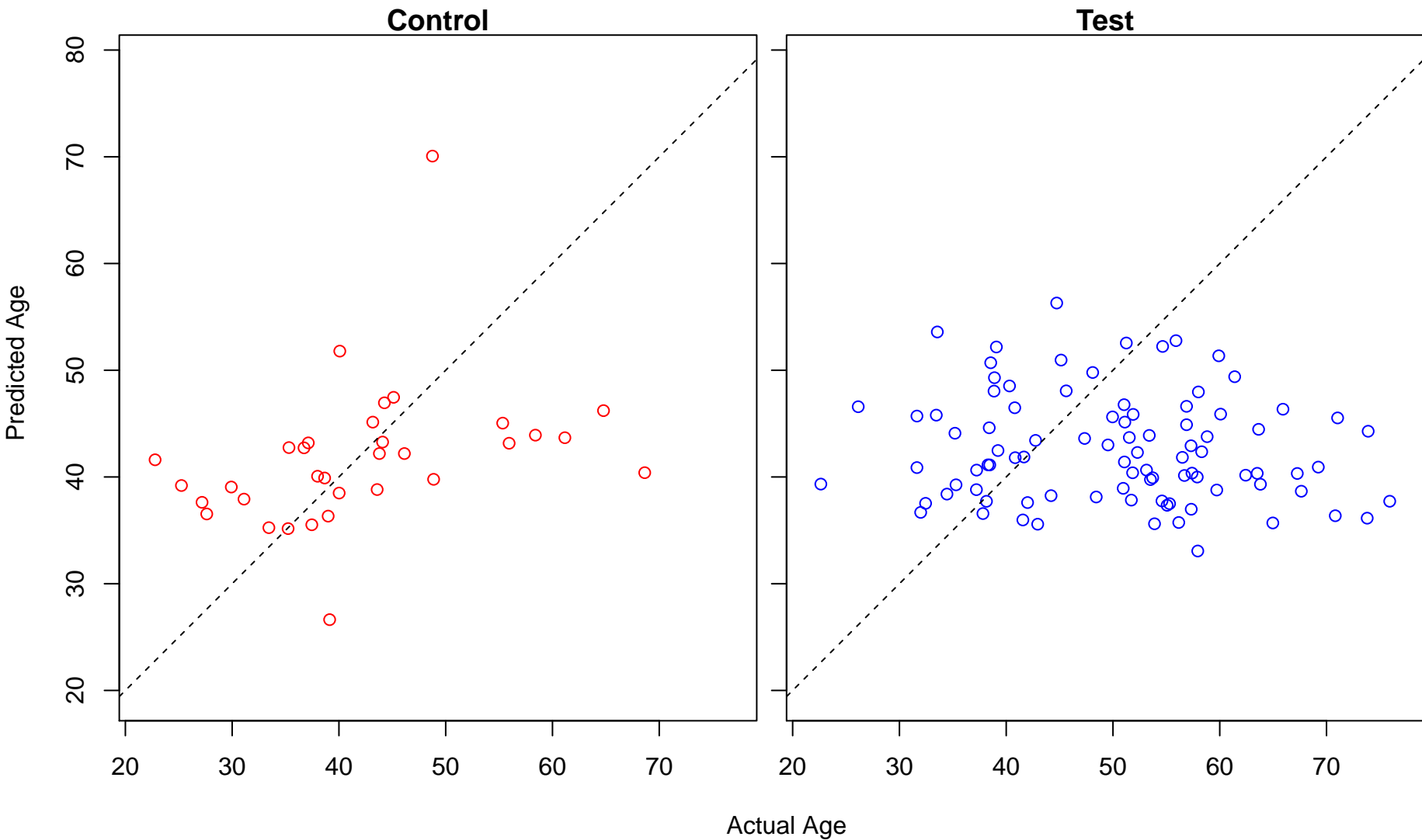
lipid digestion (Score: 0.534701)



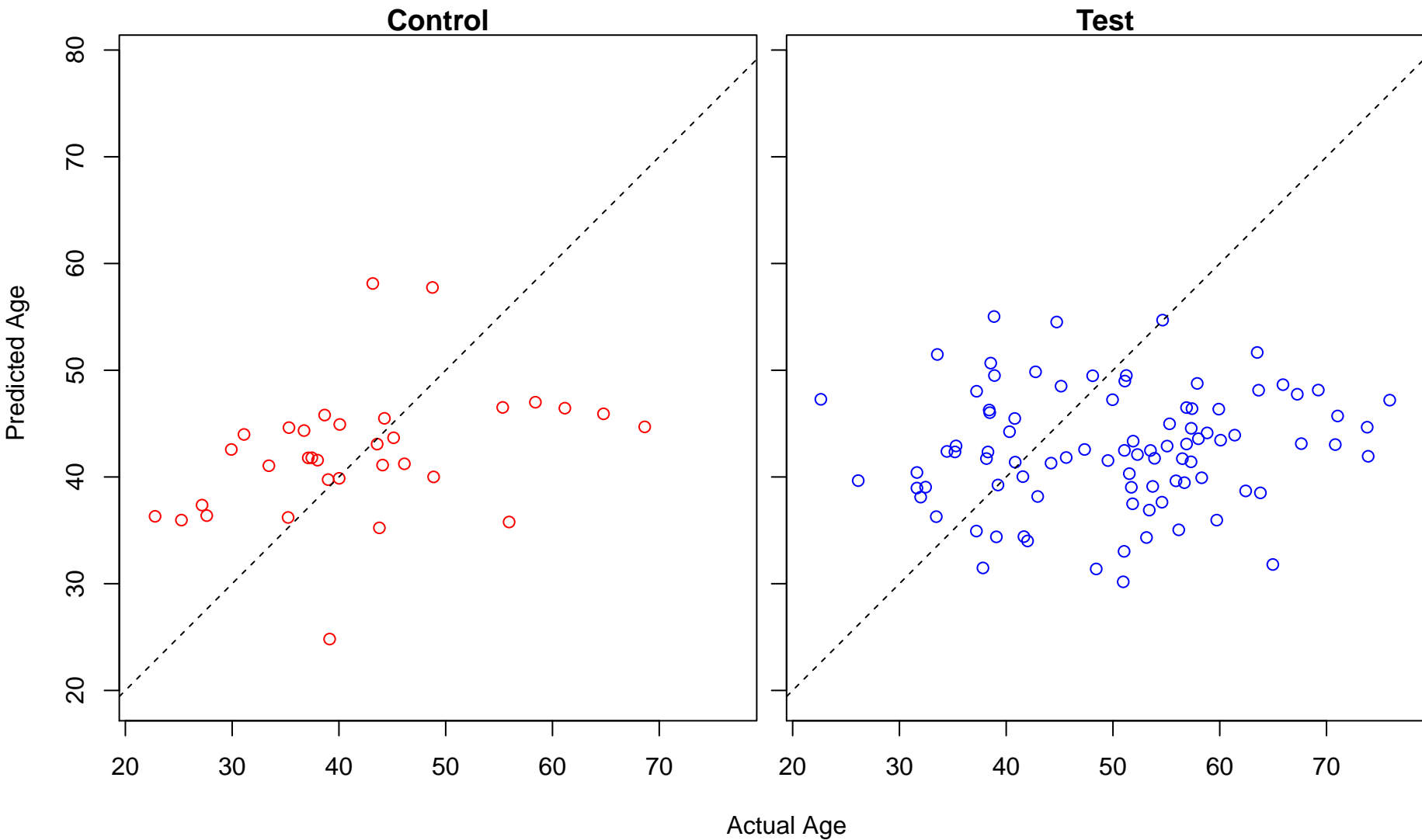
microtubule anchoring at microtubule organizing center (Score: 0.534102)



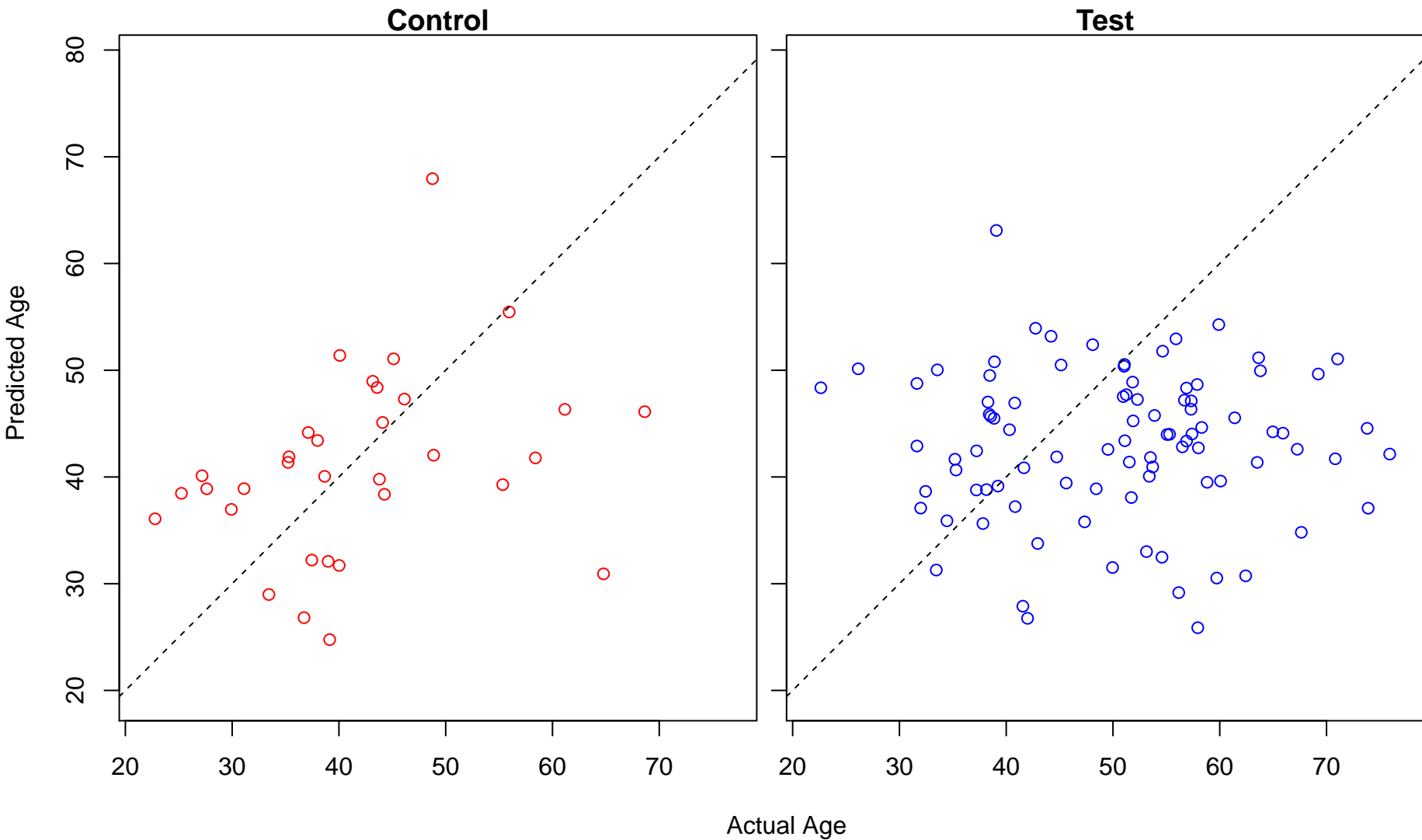
positive regulation of catalytic activity (Score: 0.533667)



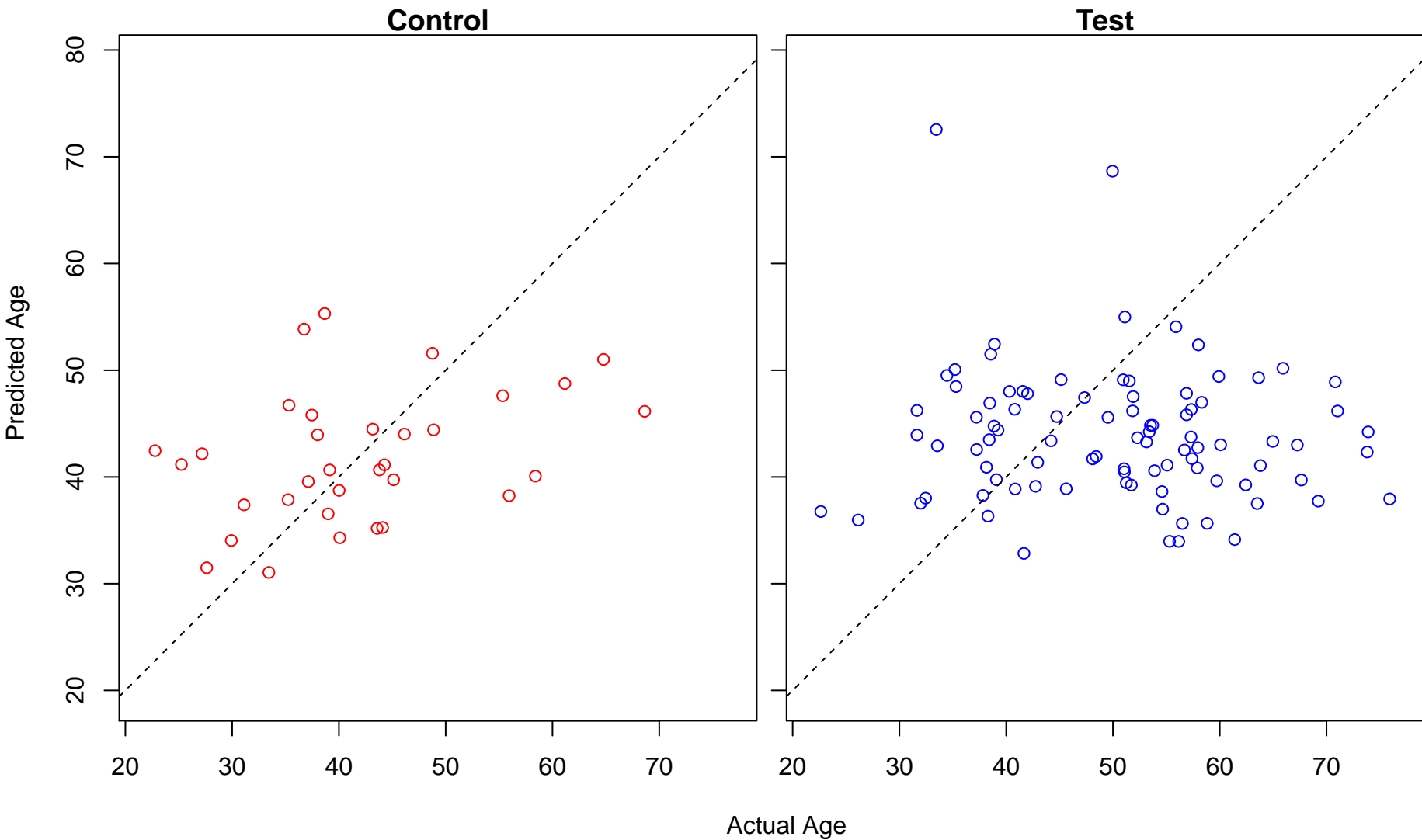
histone H3-K9 methylation (Score: 0.533155)



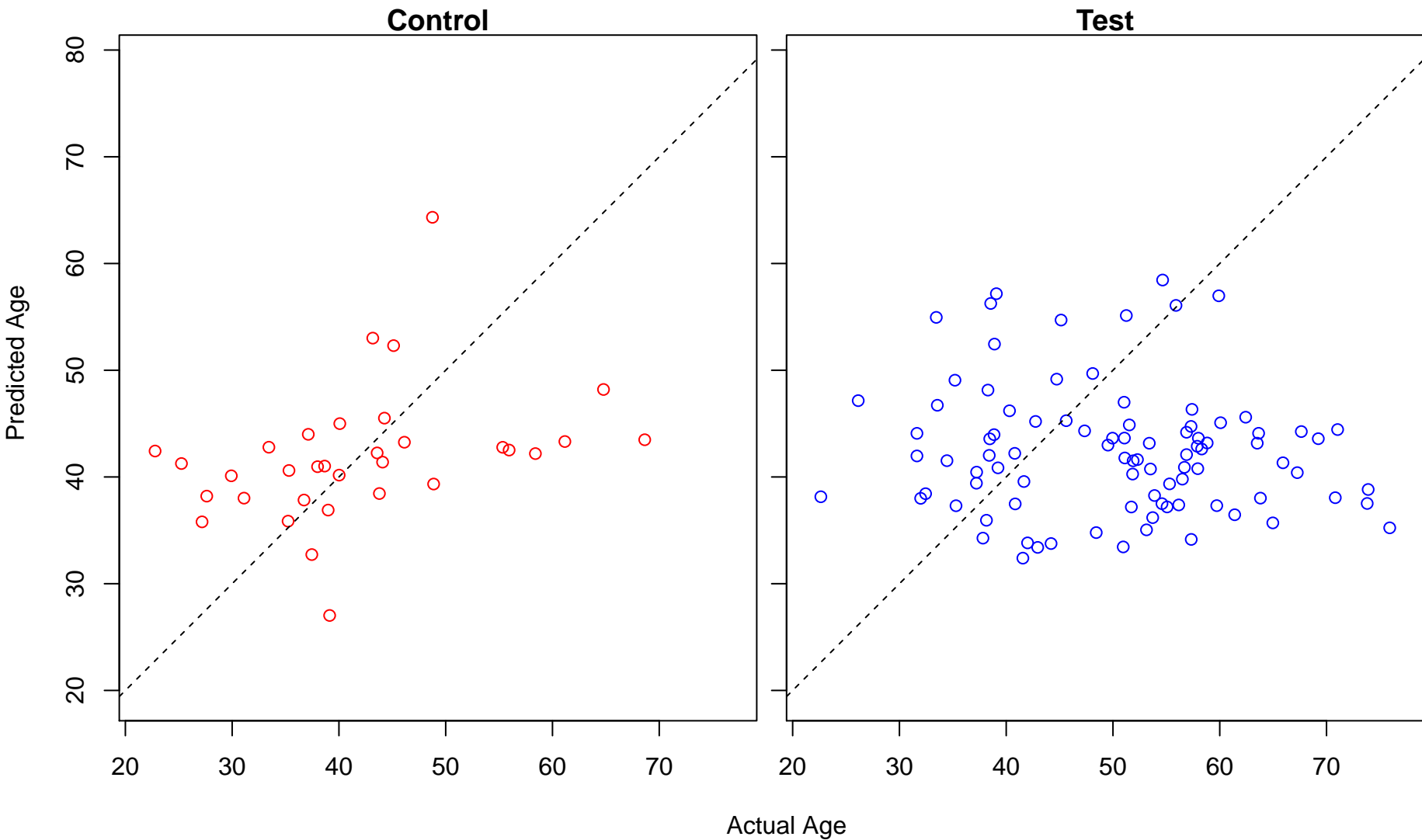
mRNA cleavage (Score: 0.532616)



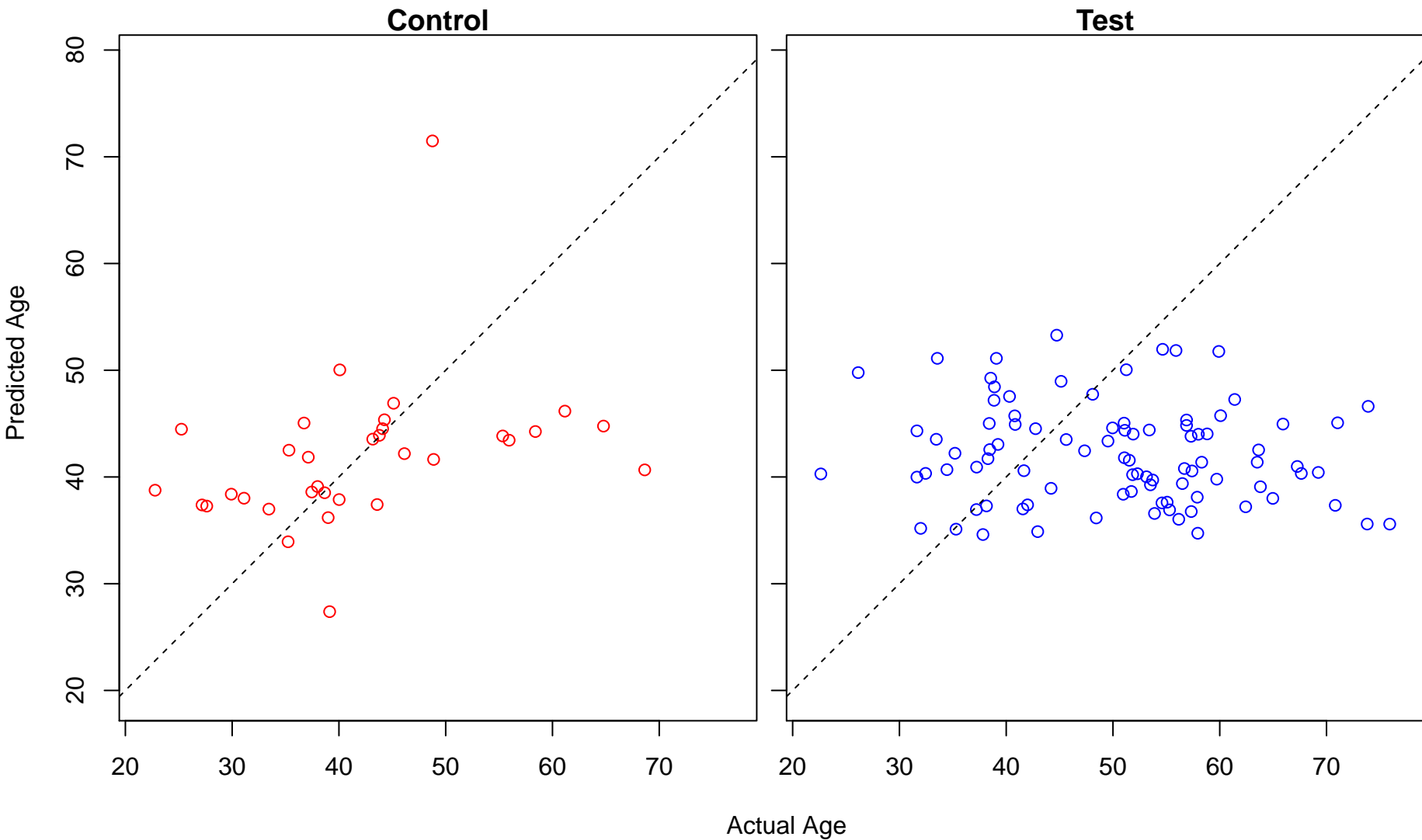
negative regulation of interleukin-1 beta secretion (Score: 0.530149)



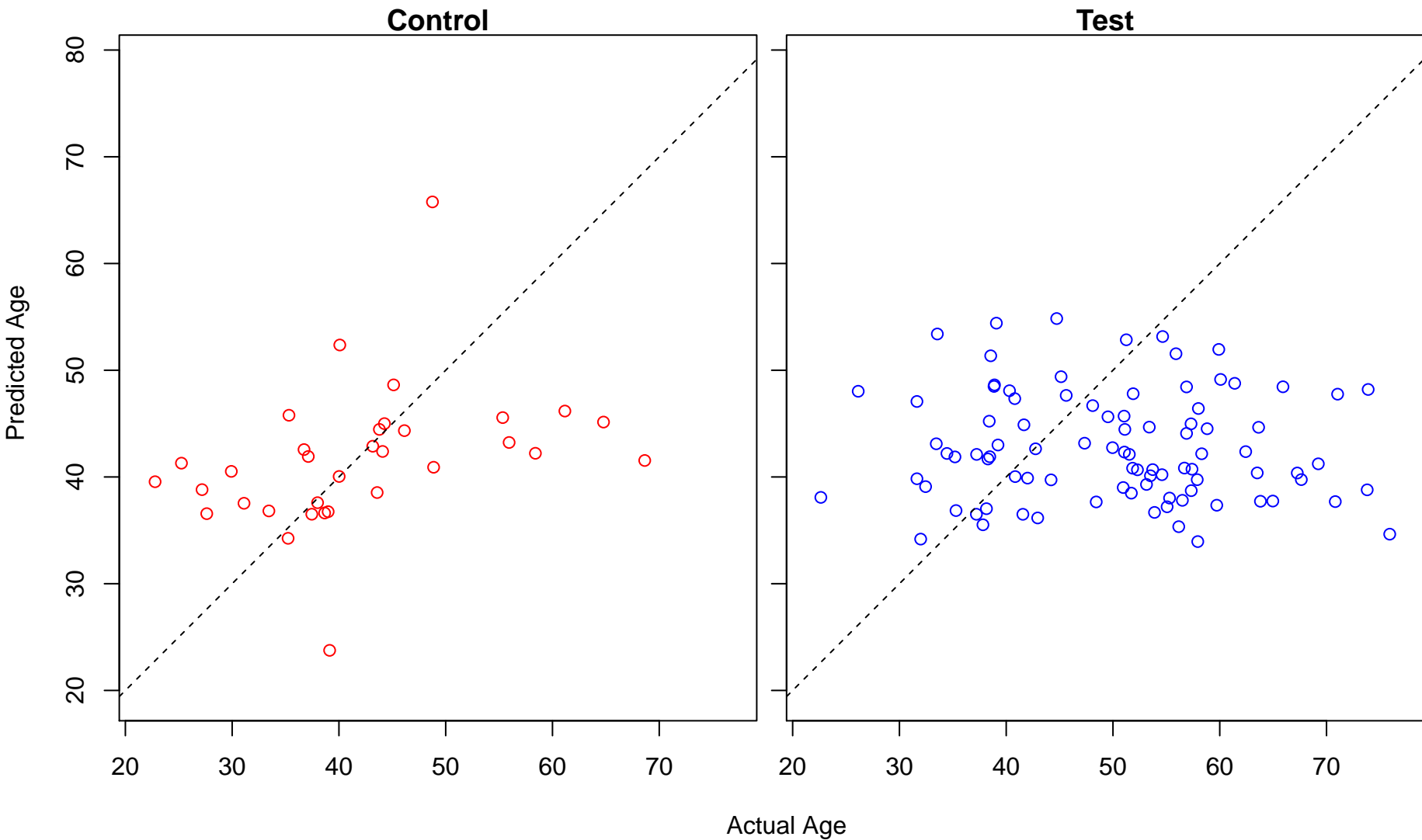
positive regulation of exocytosis (Score: 0.529992)



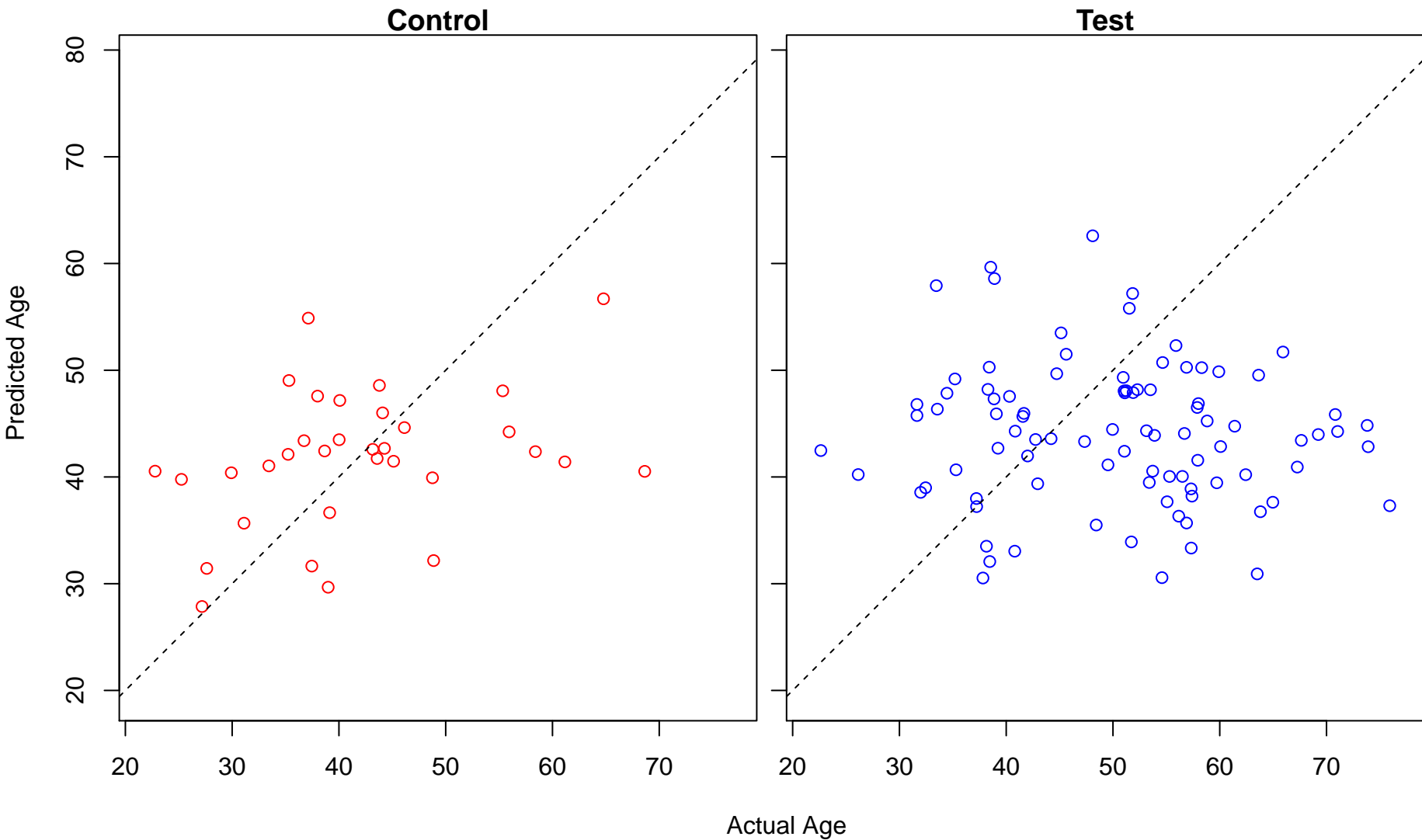
regulation of cell differentiation (Score: 0.529881)



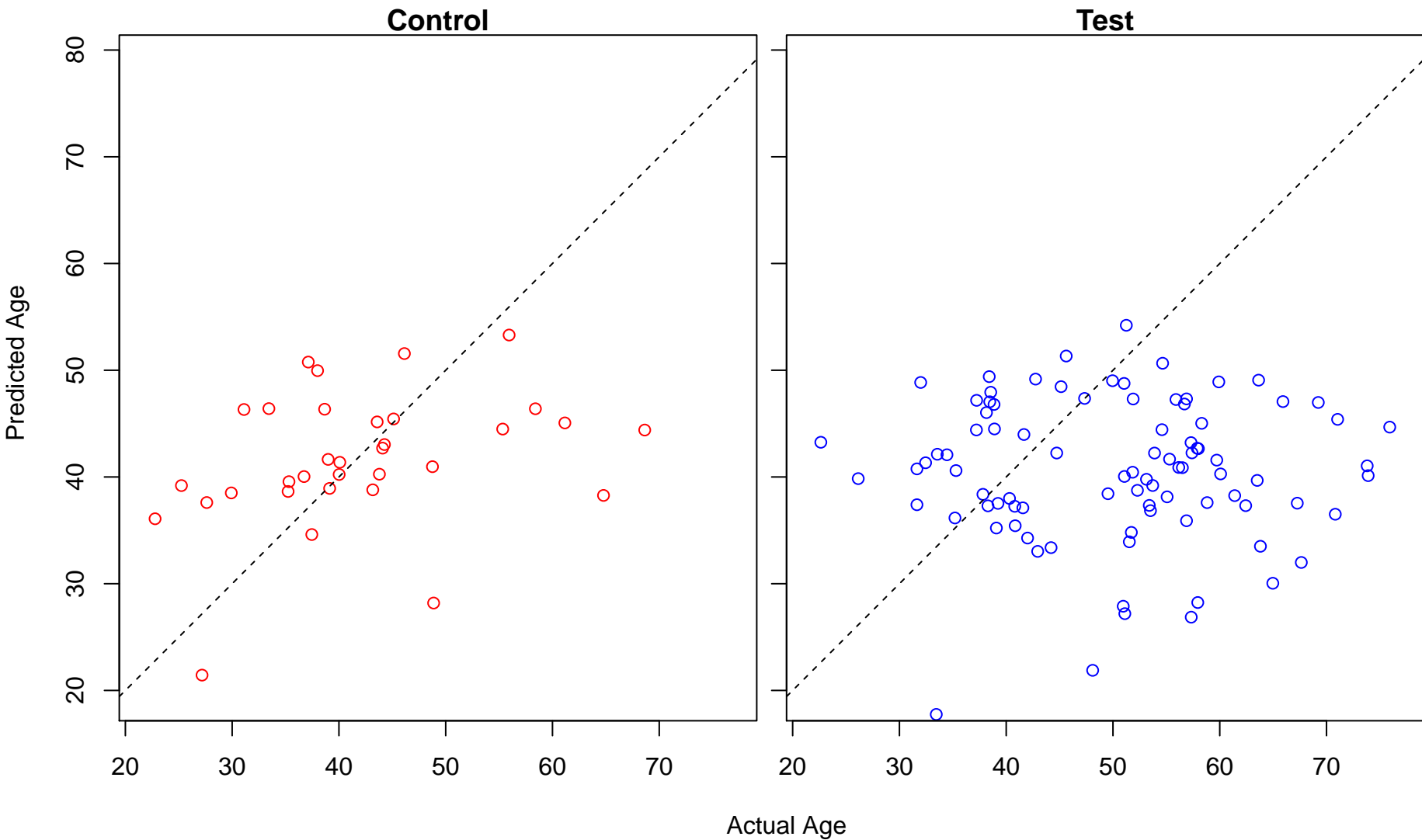
regulation of immune system process (Score: 0.529174)



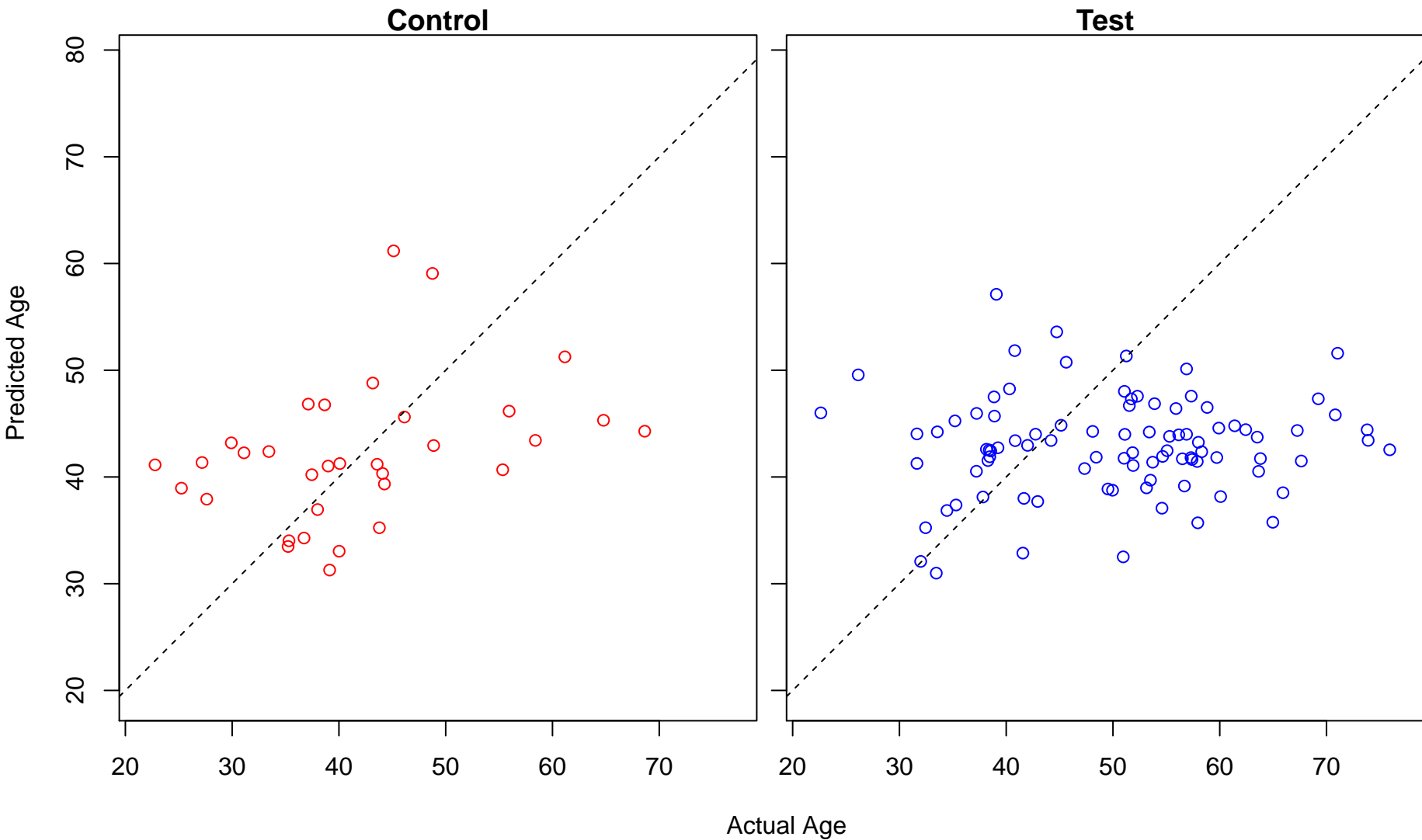
placenta blood vessel development (Score: 0.528795)



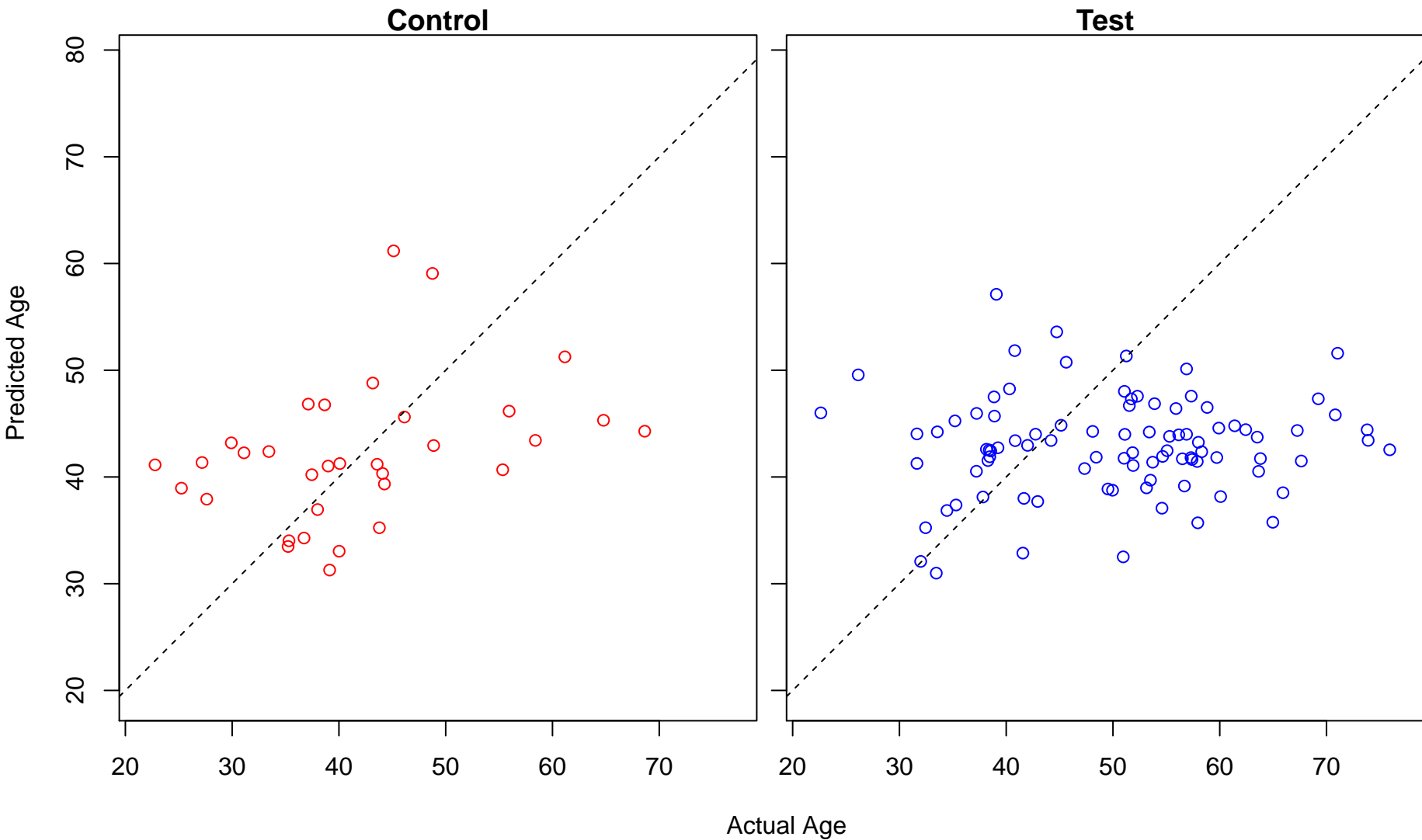
sodium ion export (Score: 0.528681)



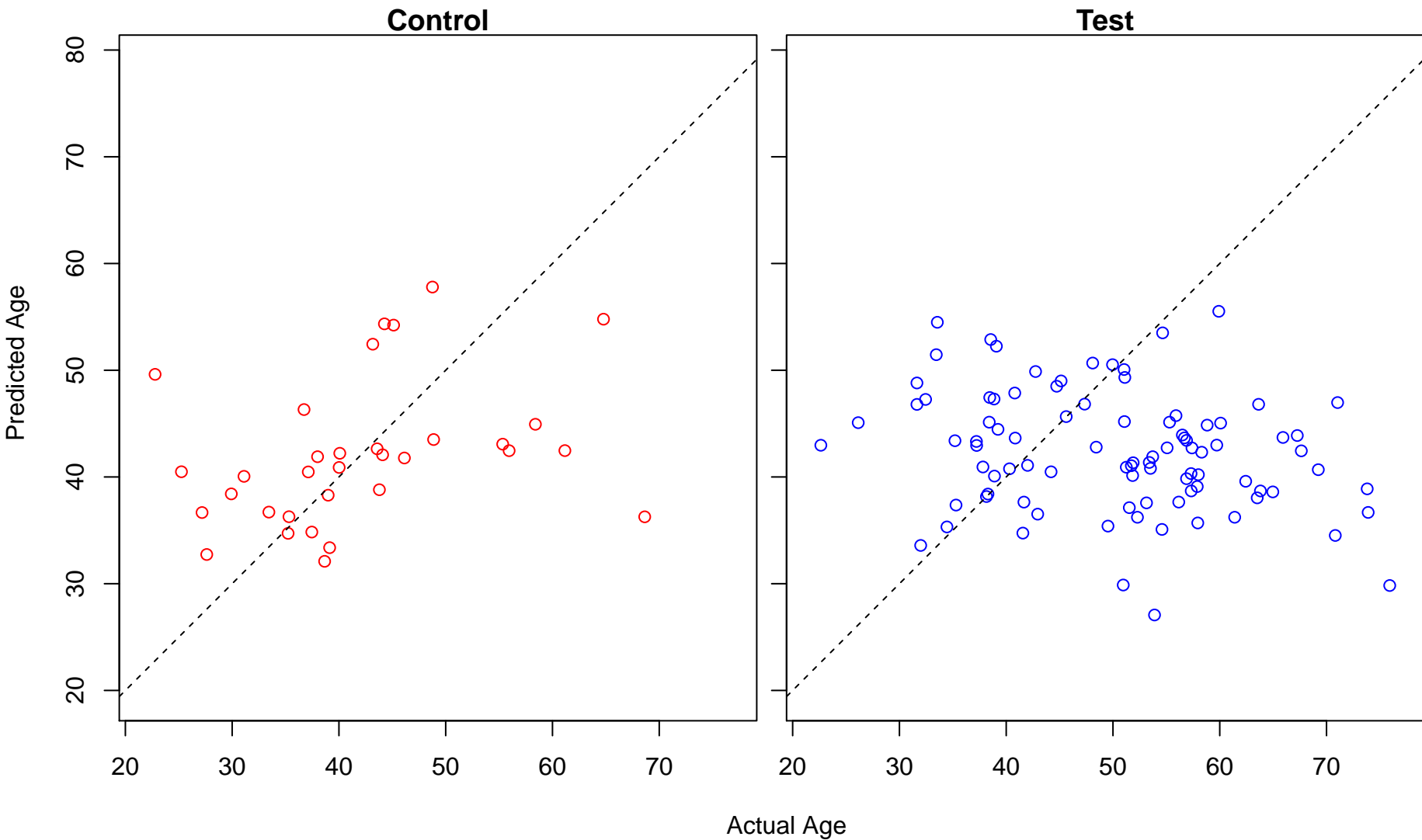
regulation of NK T cell proliferation (Score: 0.527250)



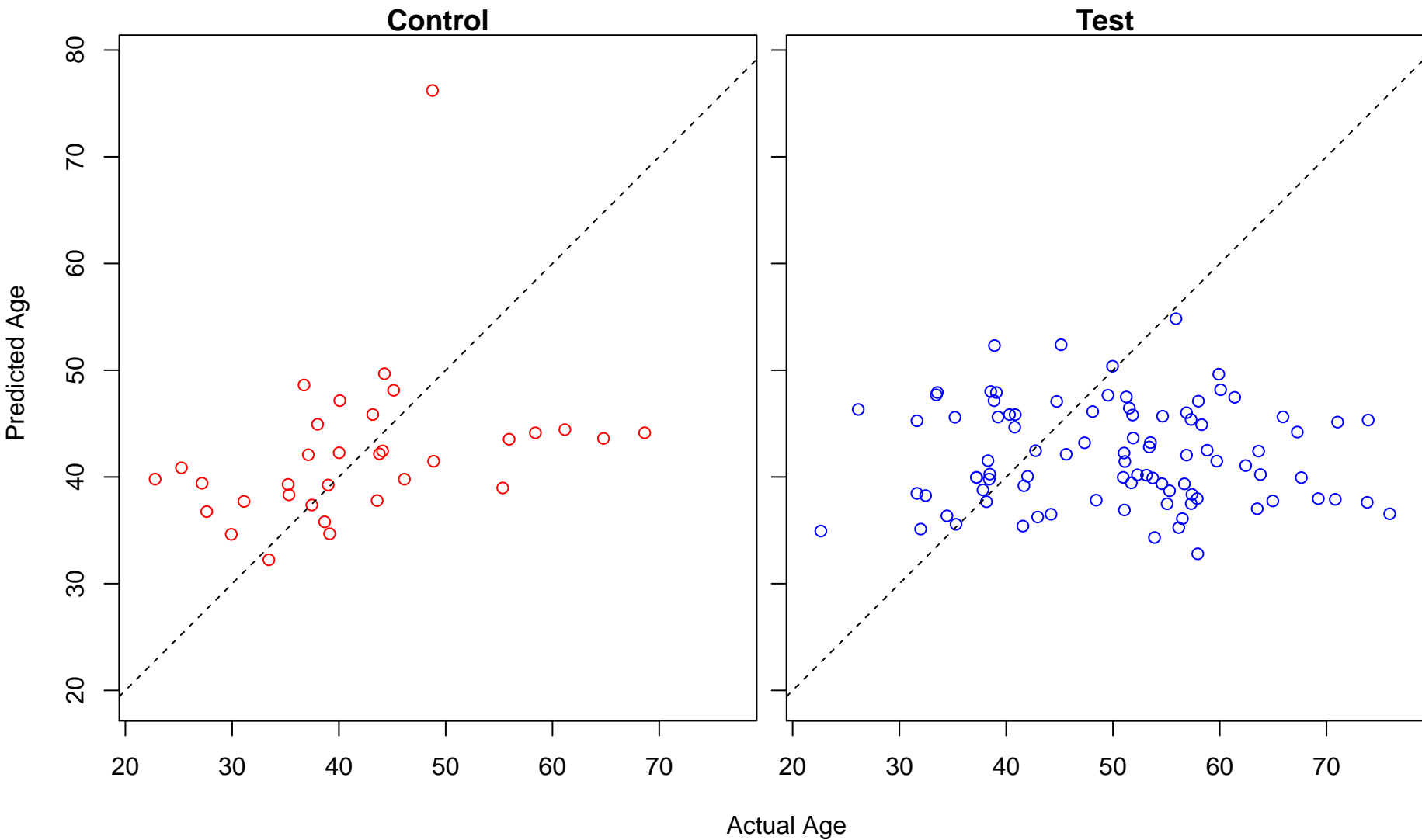
positive regulation of NK T cell proliferation (Score: 0.527250)



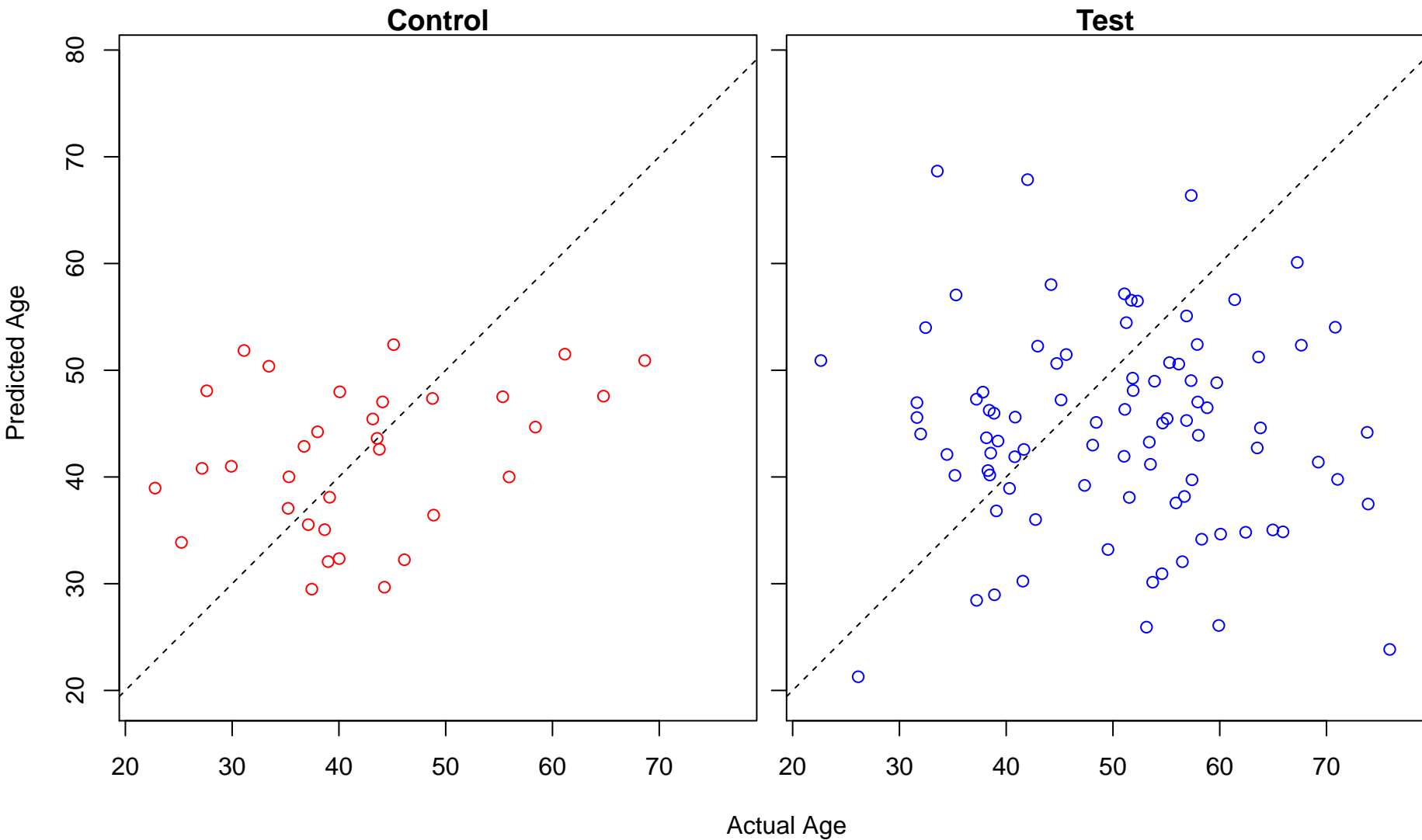
negative regulation of alpha-beta T cell differentiation (Score: 0.526619)



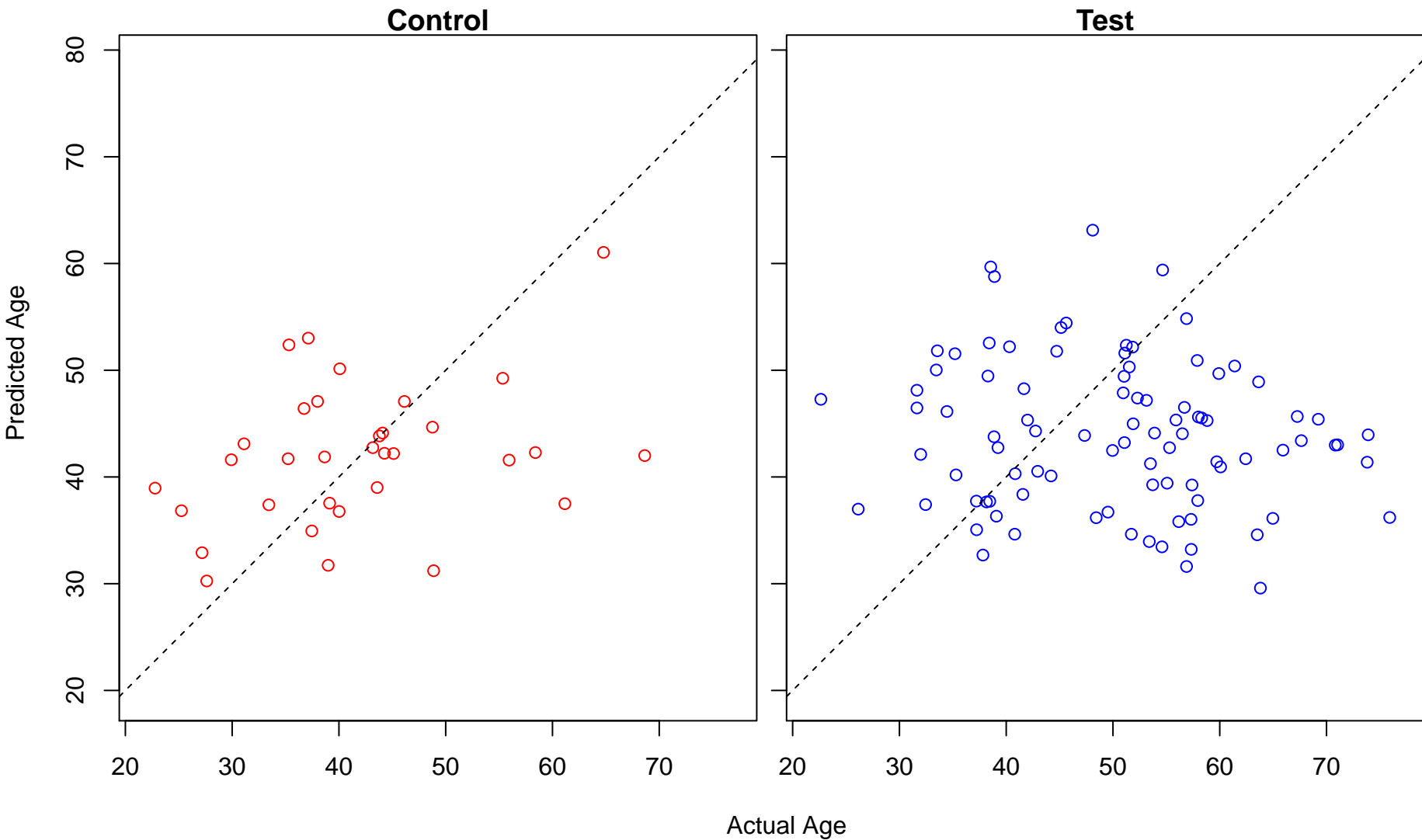
positive regulation of translational initiation (Score: 0.525630)



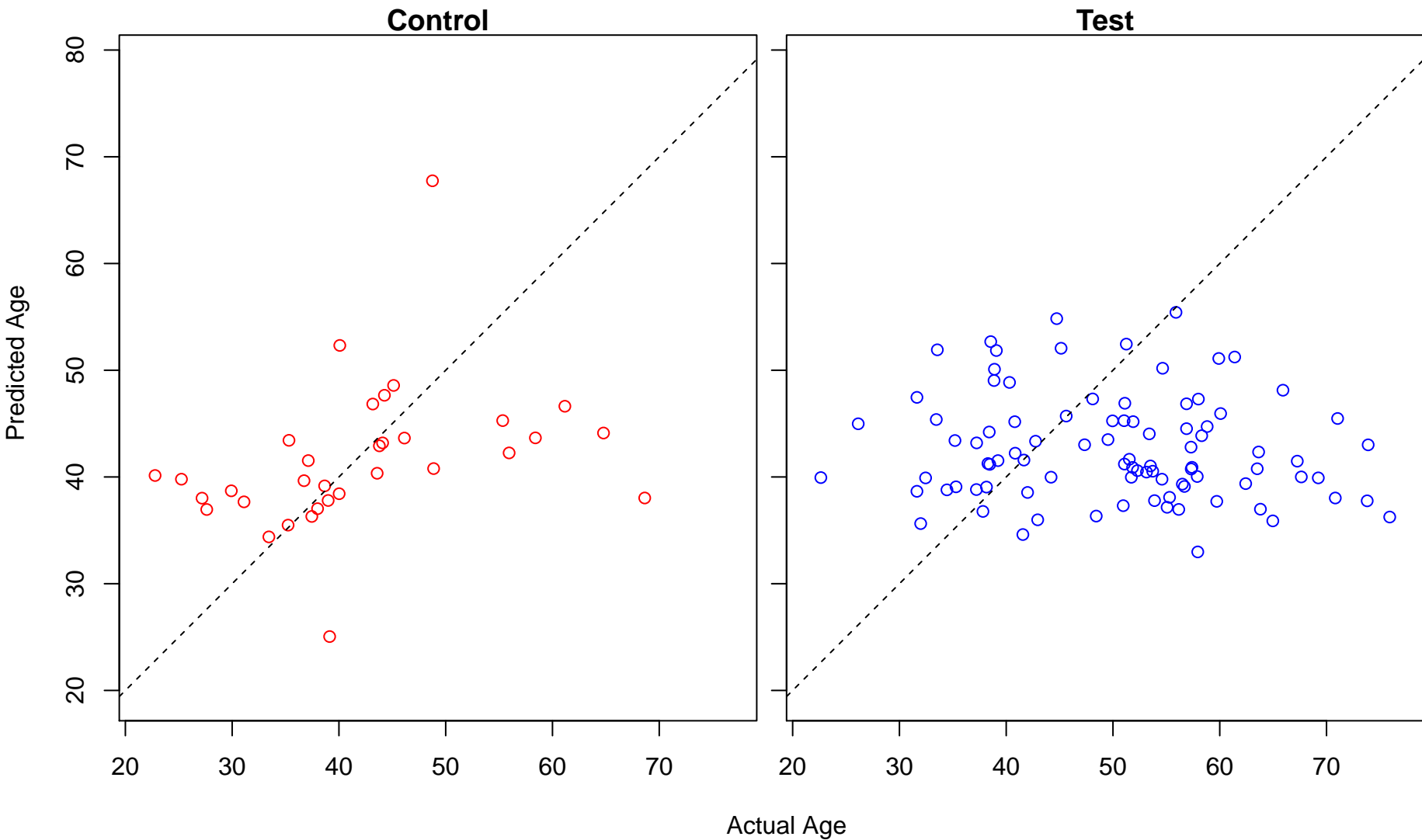
ER overload response (Score: 0.525590)



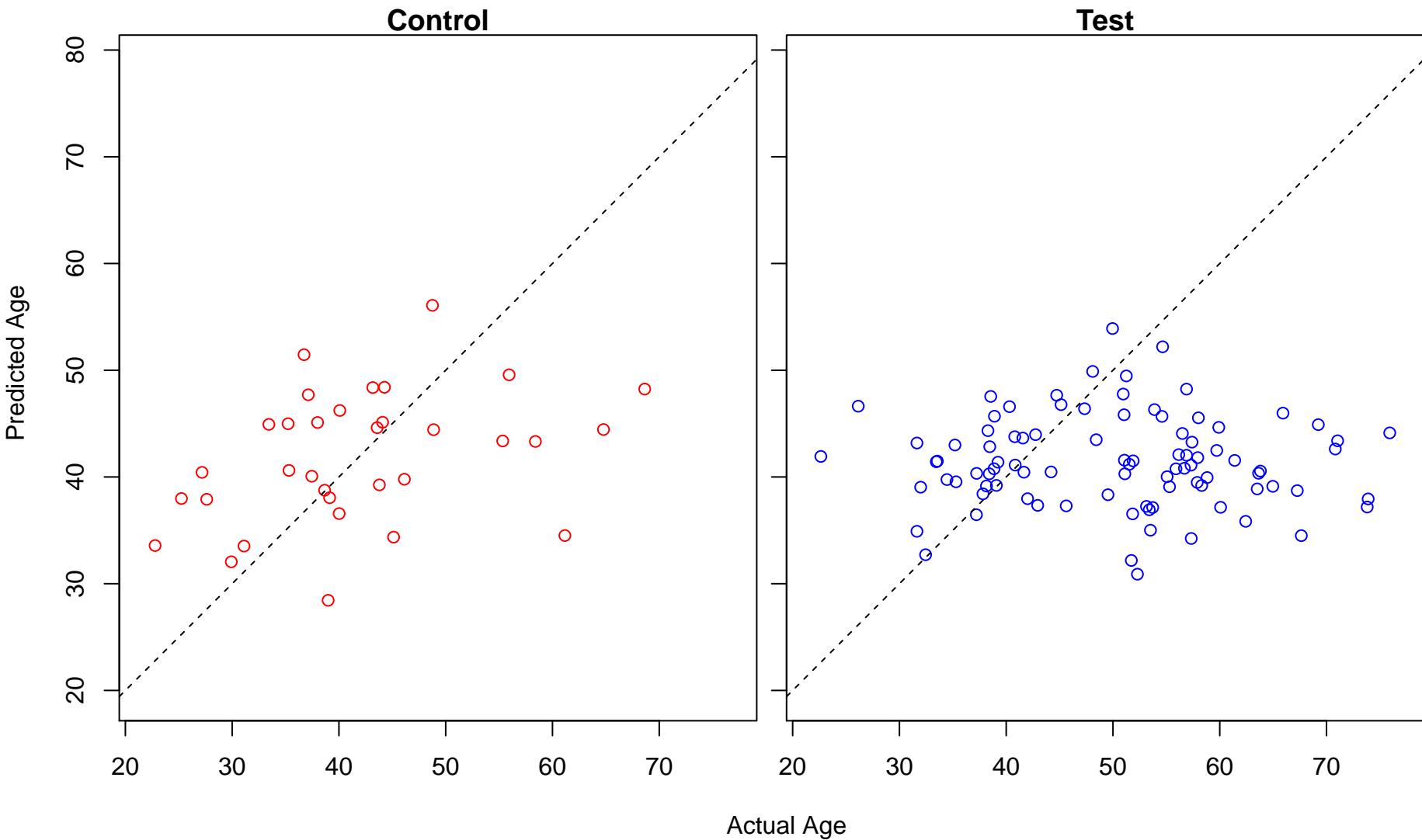
nephric duct development (Score: 0.525223)



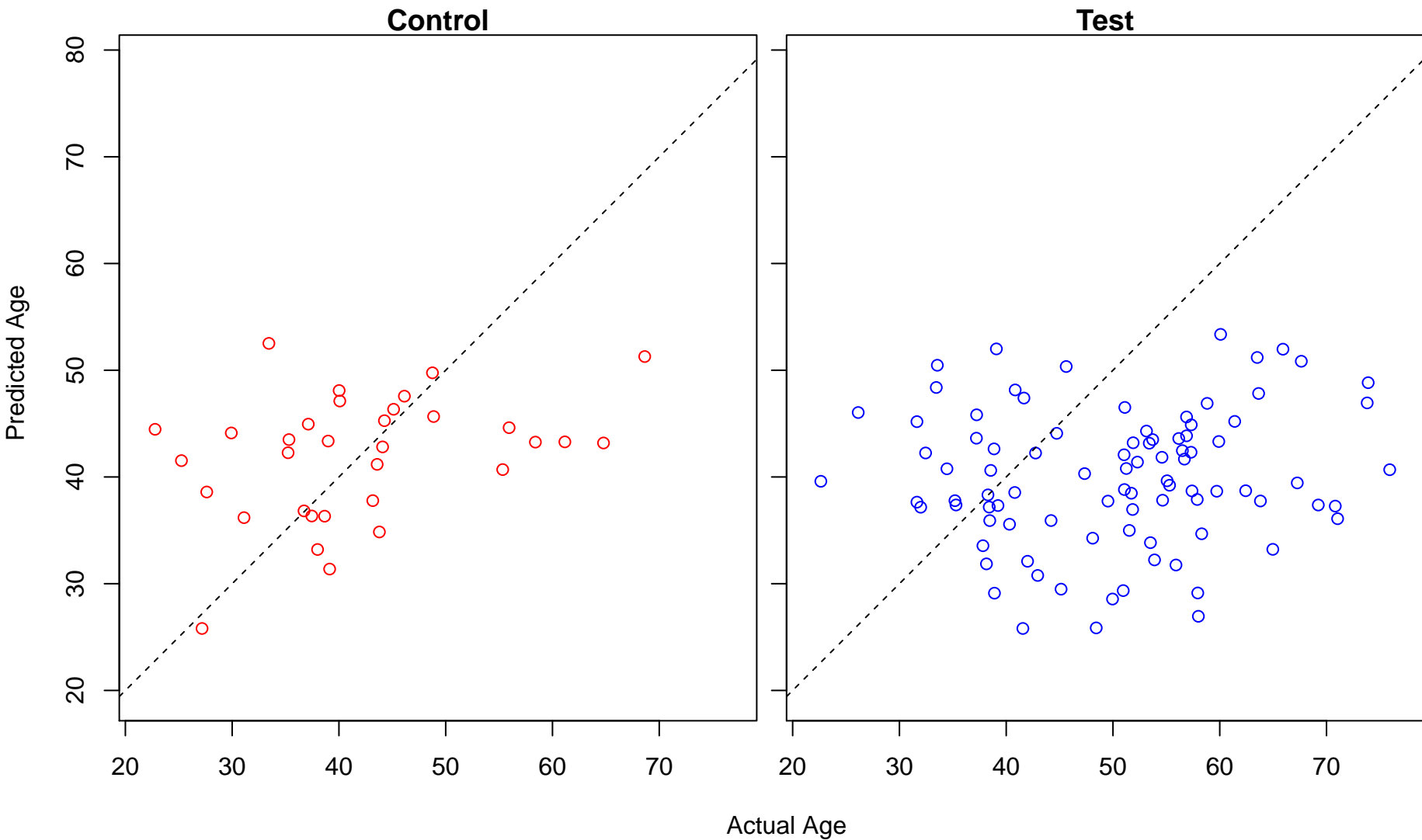
regulation of cell cycle (Score: 0.524808)



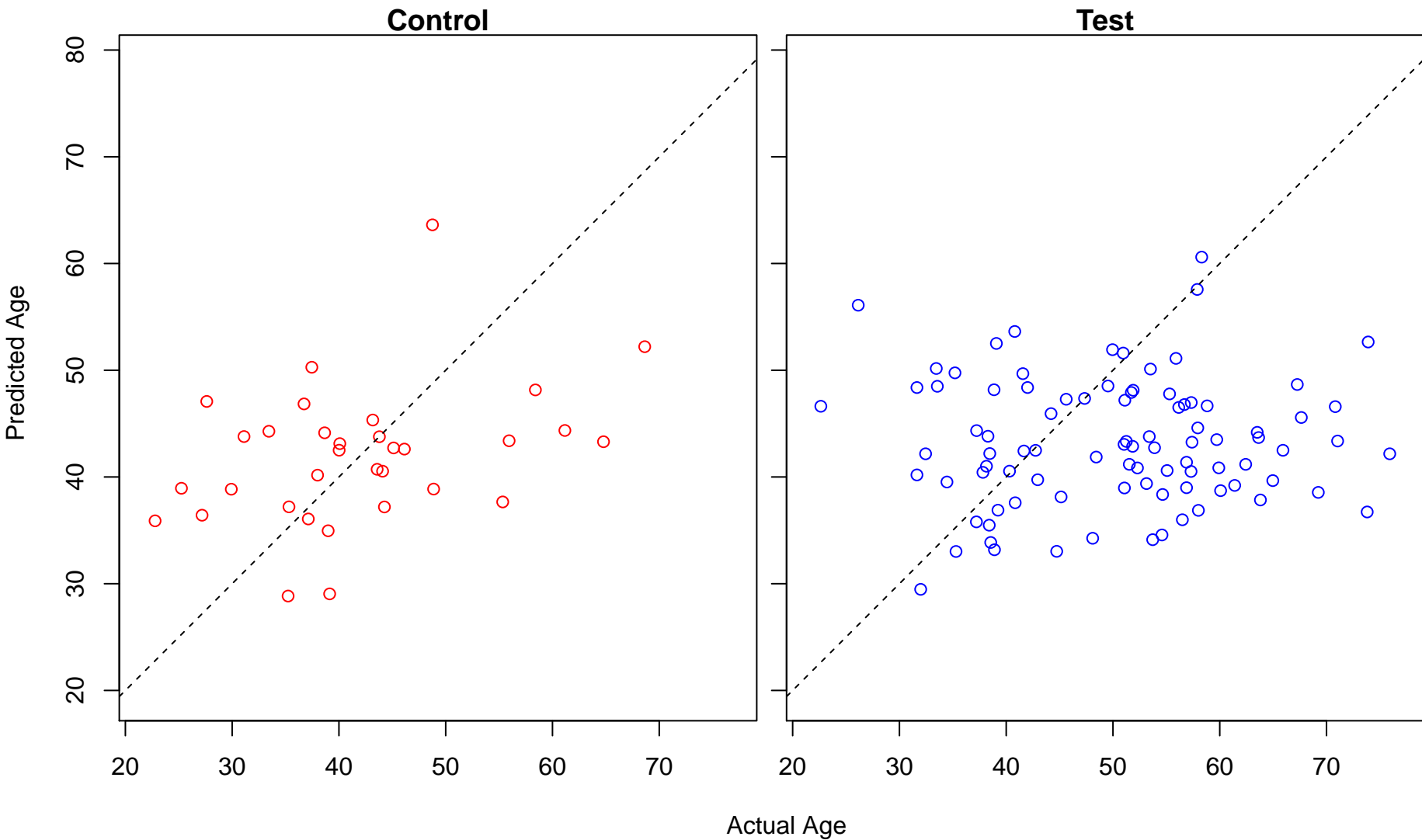
regulation of vitamin D receptor signaling pathway (Score: 0.523287)



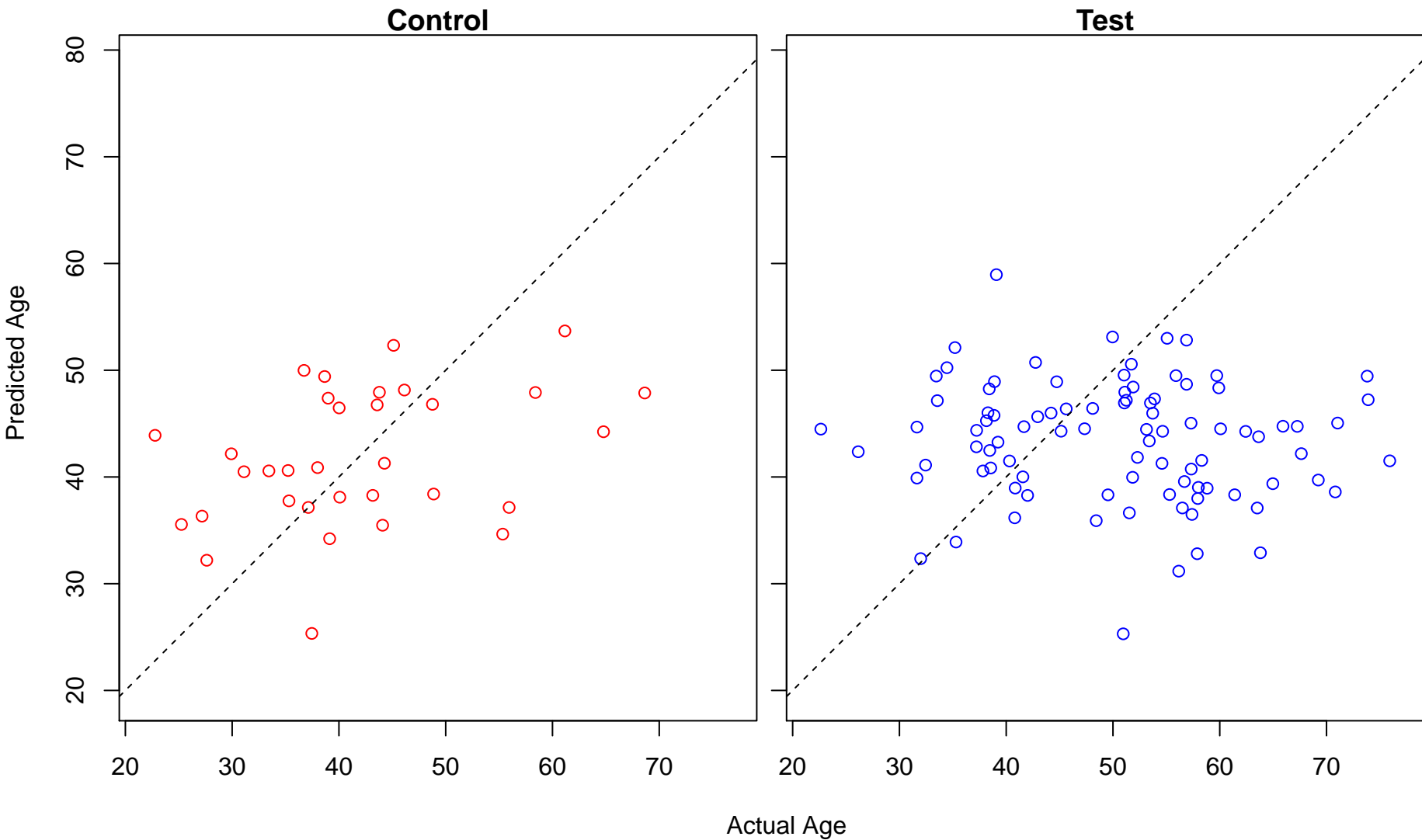
maintenance of DNA repeat elements (Score: 0.522753)



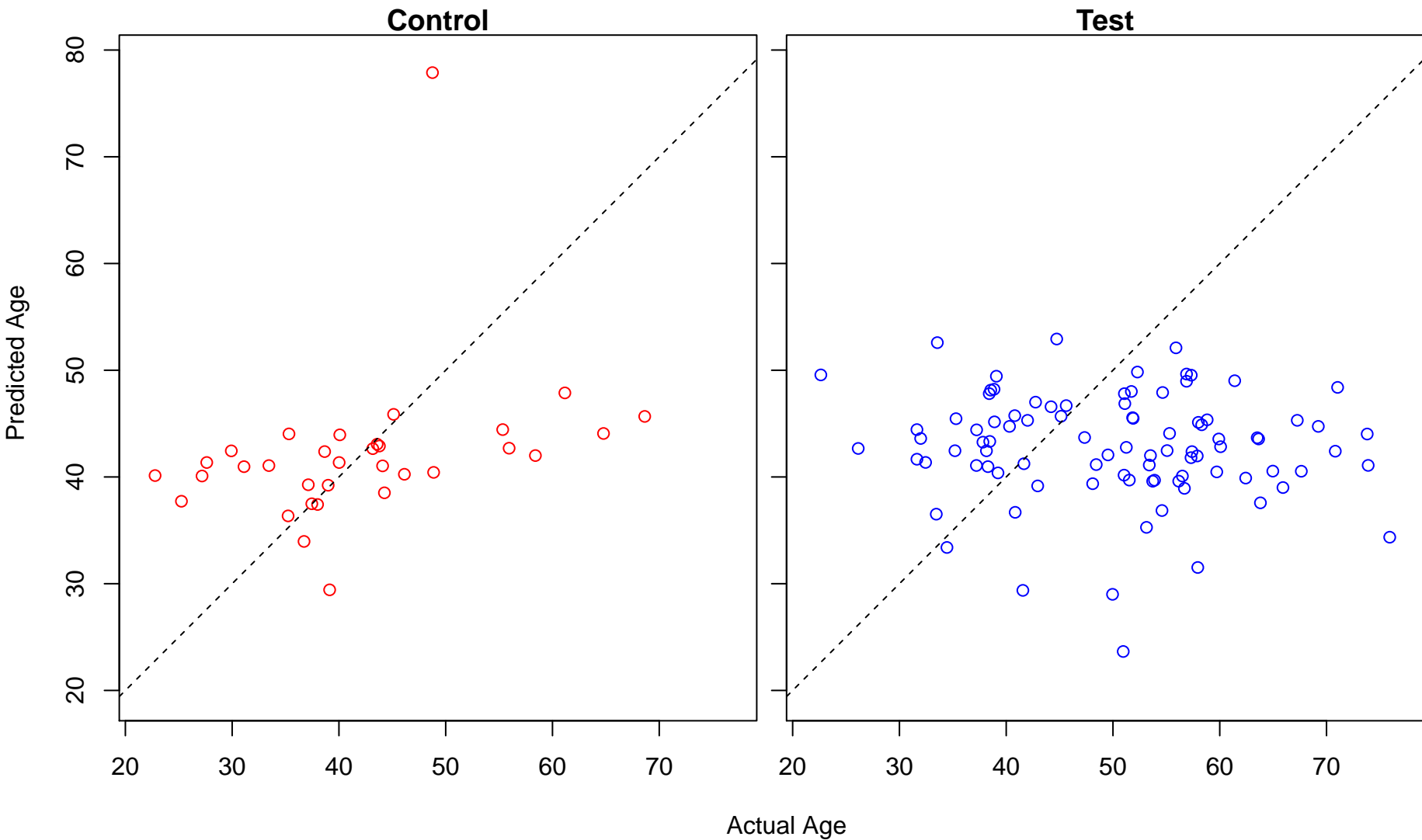
pre-B cell differentiation (Score: 0.52224)



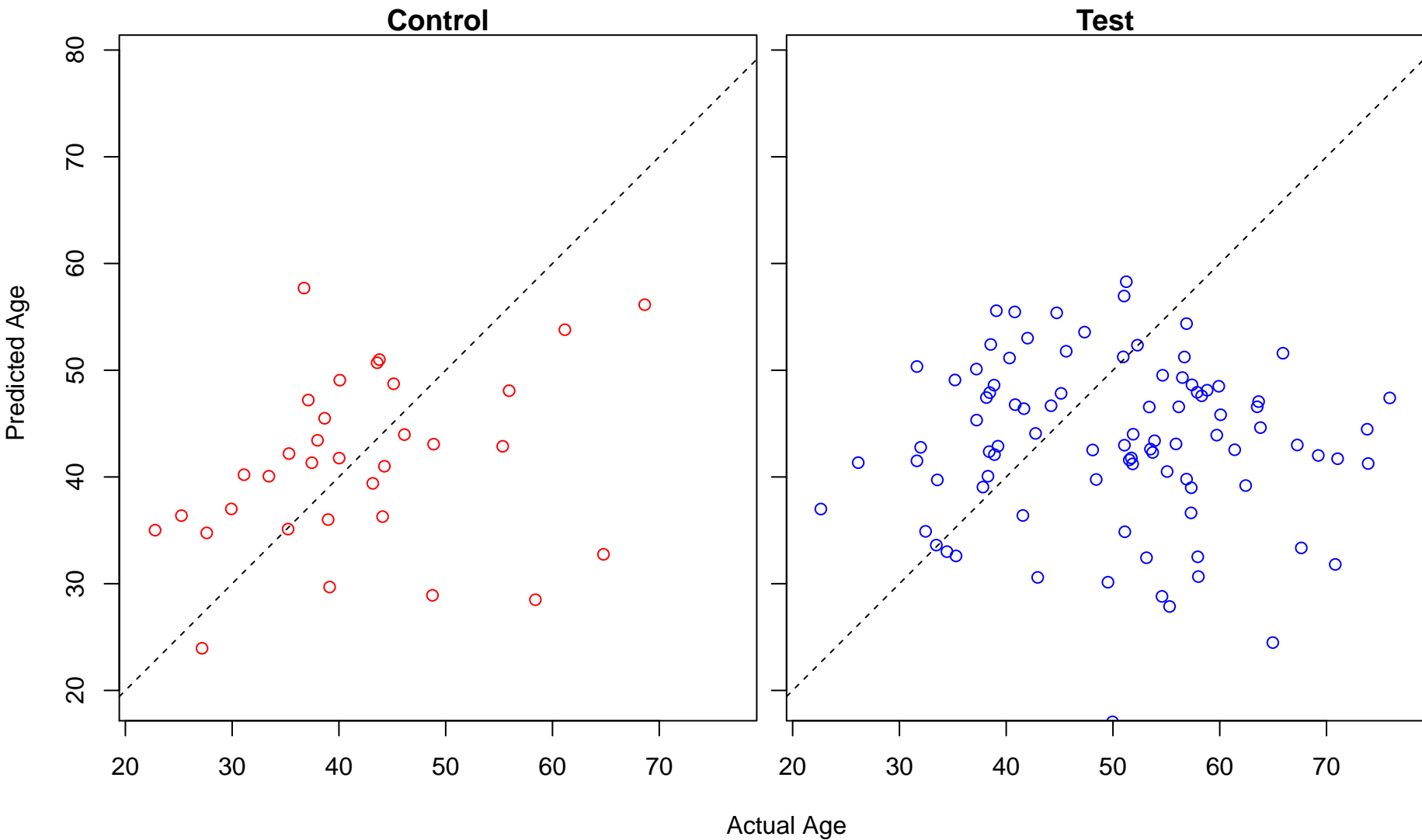
protein localization to synapse (Score: 0.521847)



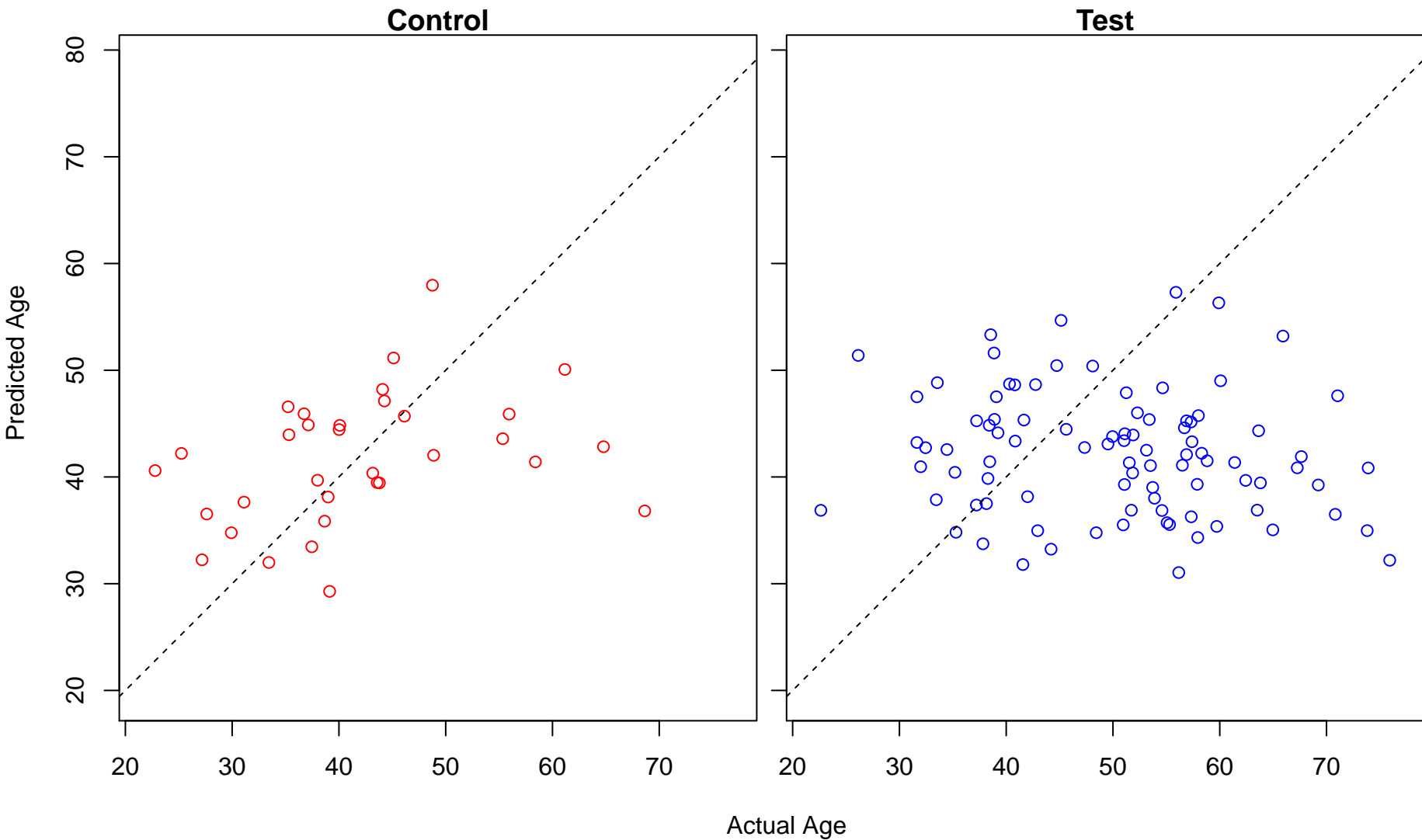
multicellular organismal aging (Score: 0.520926)



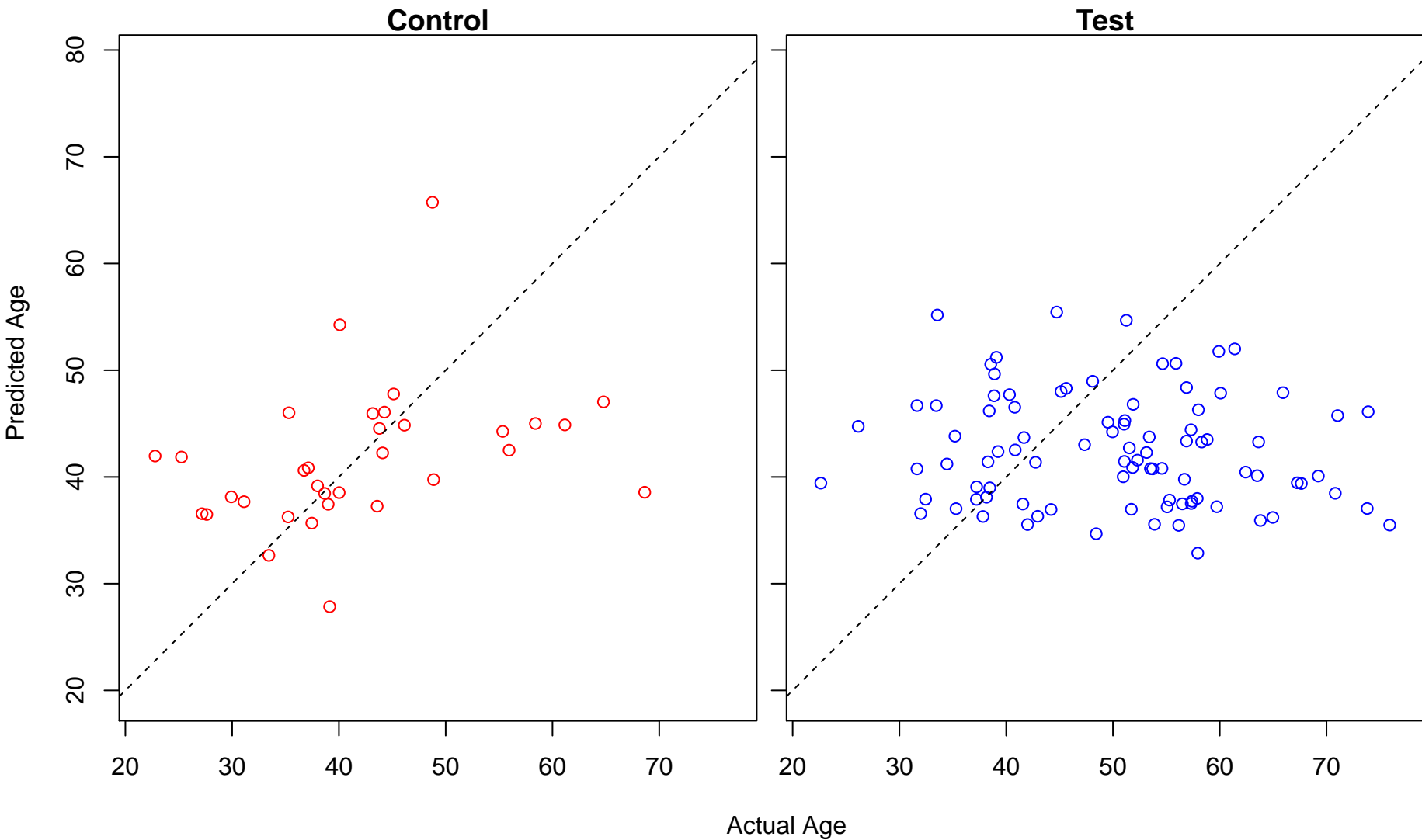
positive regulation of fibroblast migration (Score: 0.520660)



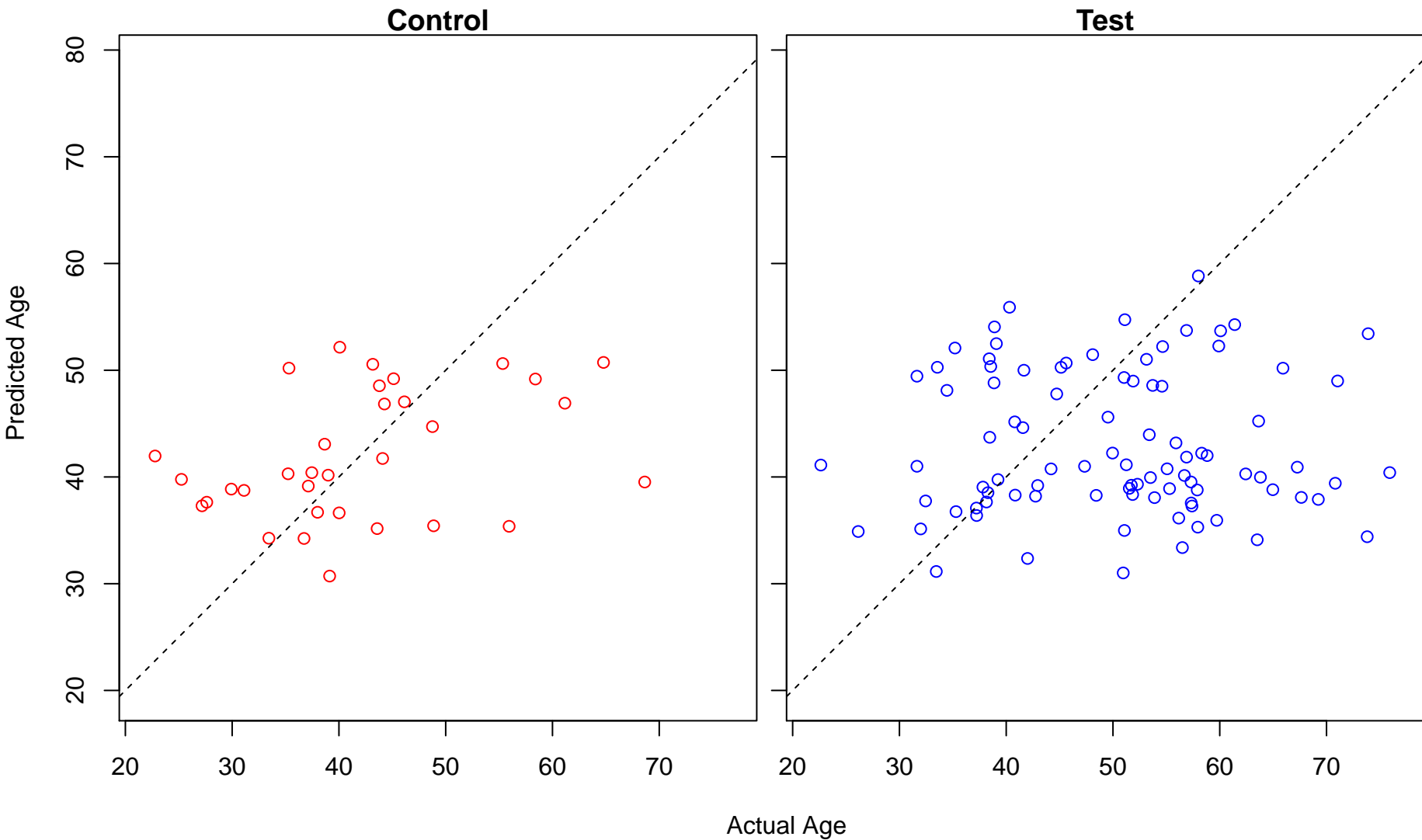
blood circulation (Score: 0.520650)



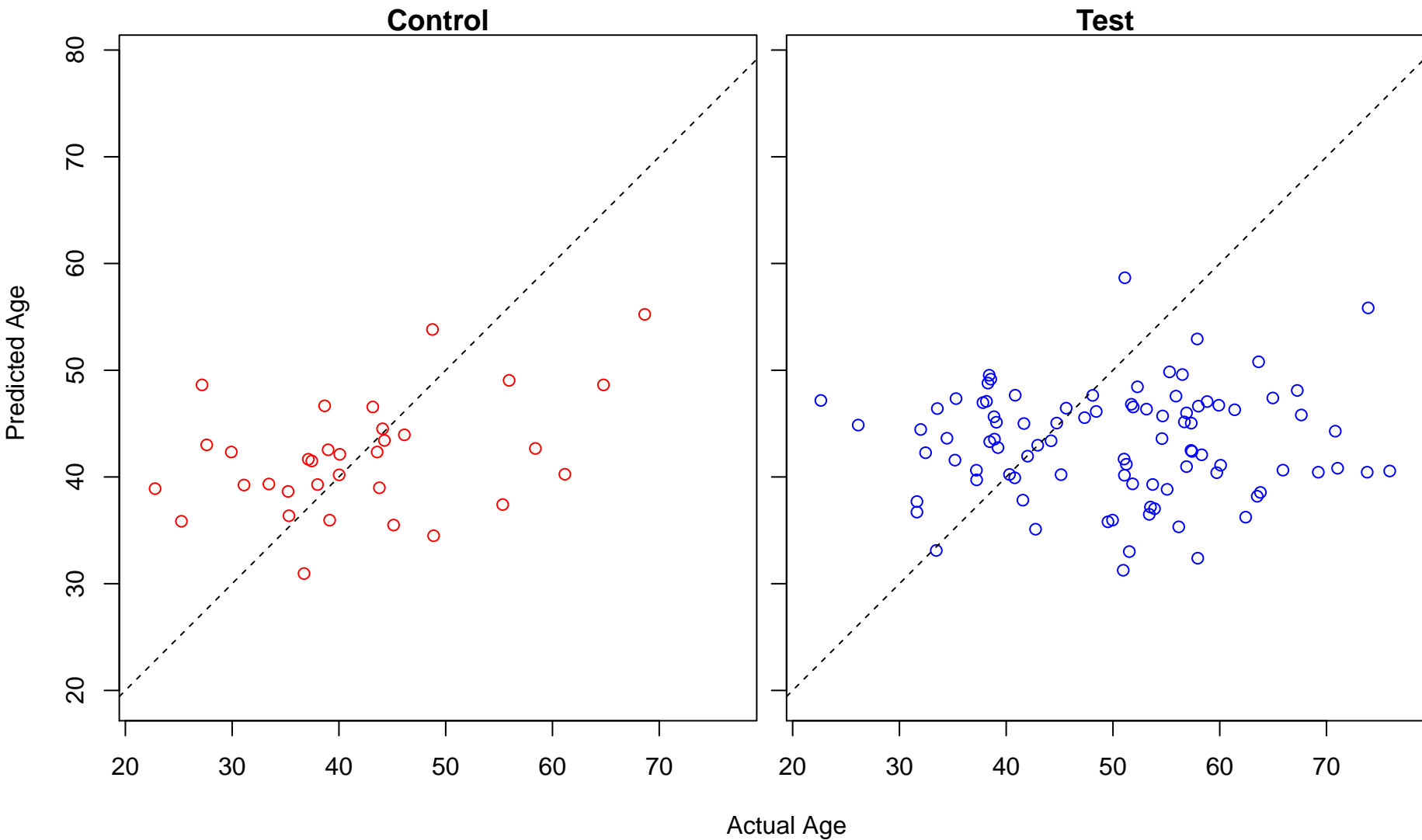
catabolic process (Score: 0.519725)



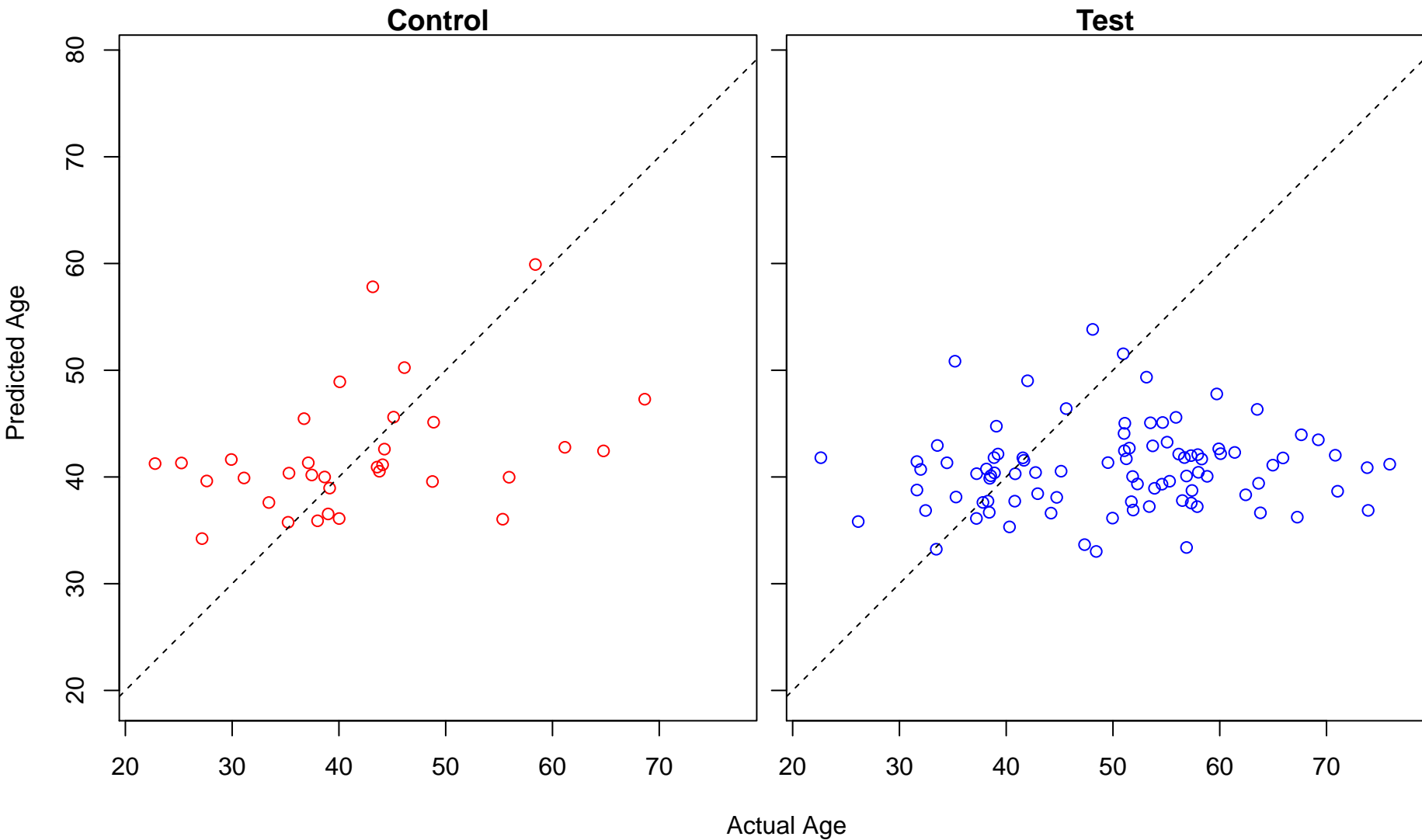
negative regulation of tyrosine phosphorylation of STAT protein (Score: 0.519676)



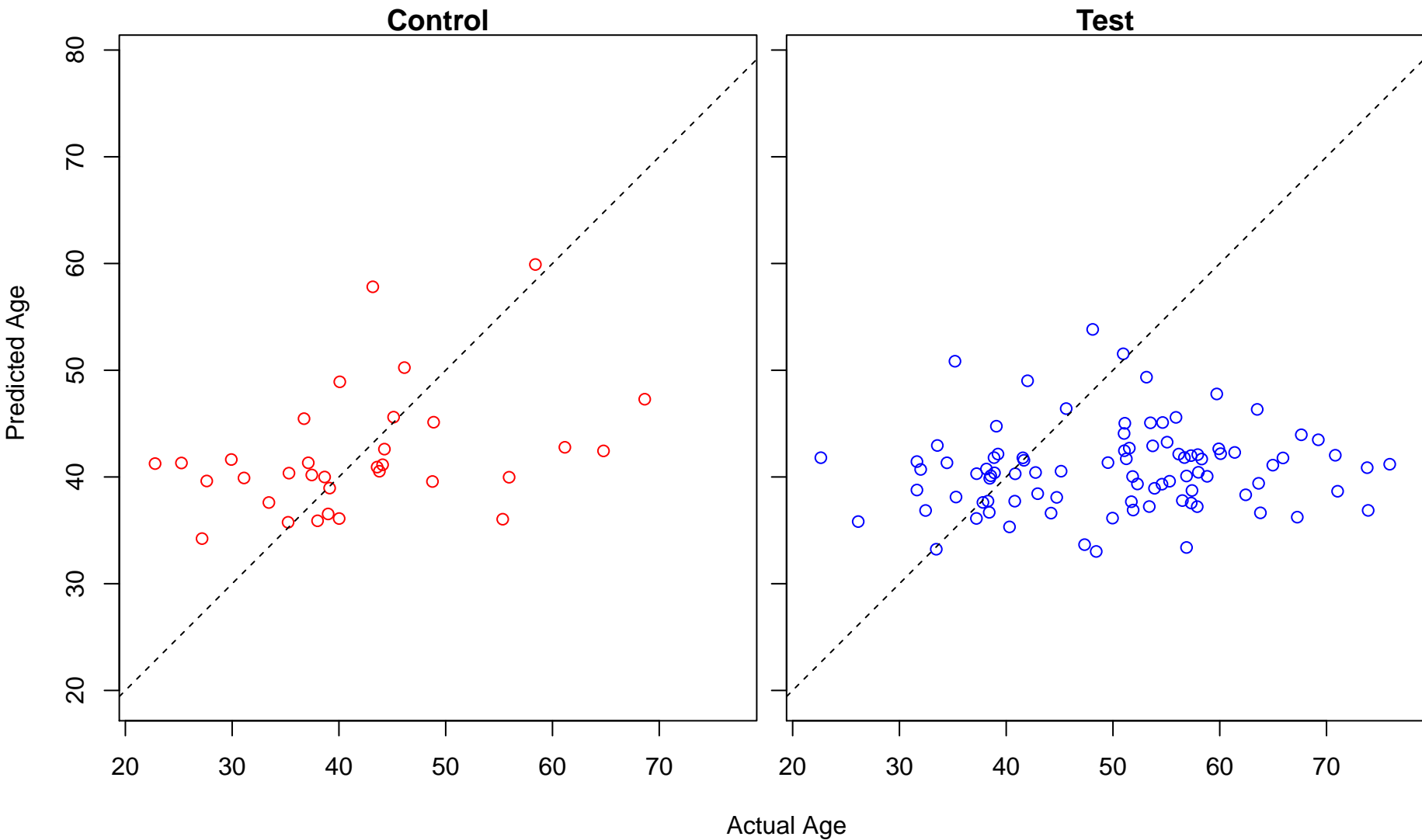
negative regulation of macrophage cytokine production (Score: 0.517740)



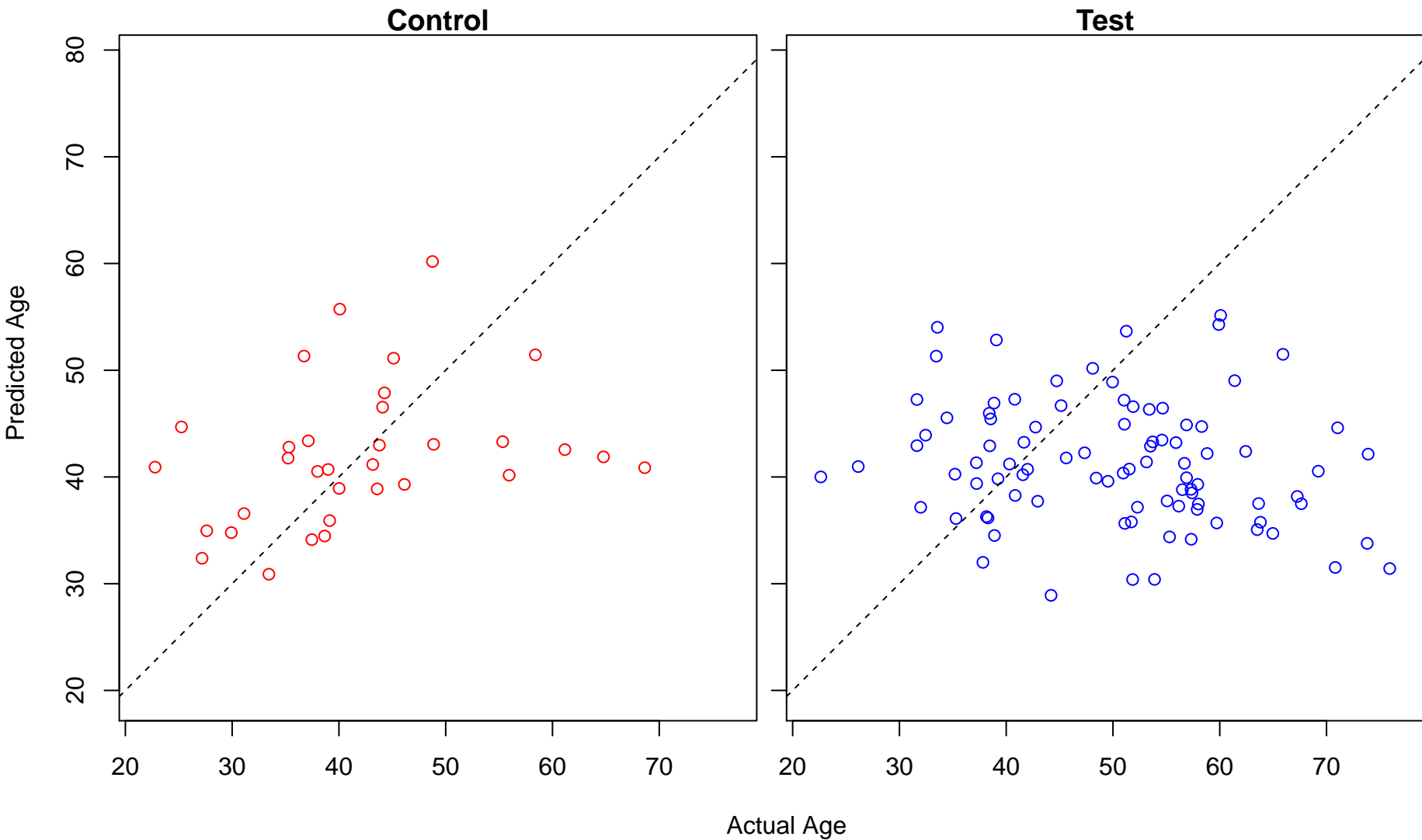
sulfur amino acid transport (Score: 0.517582)



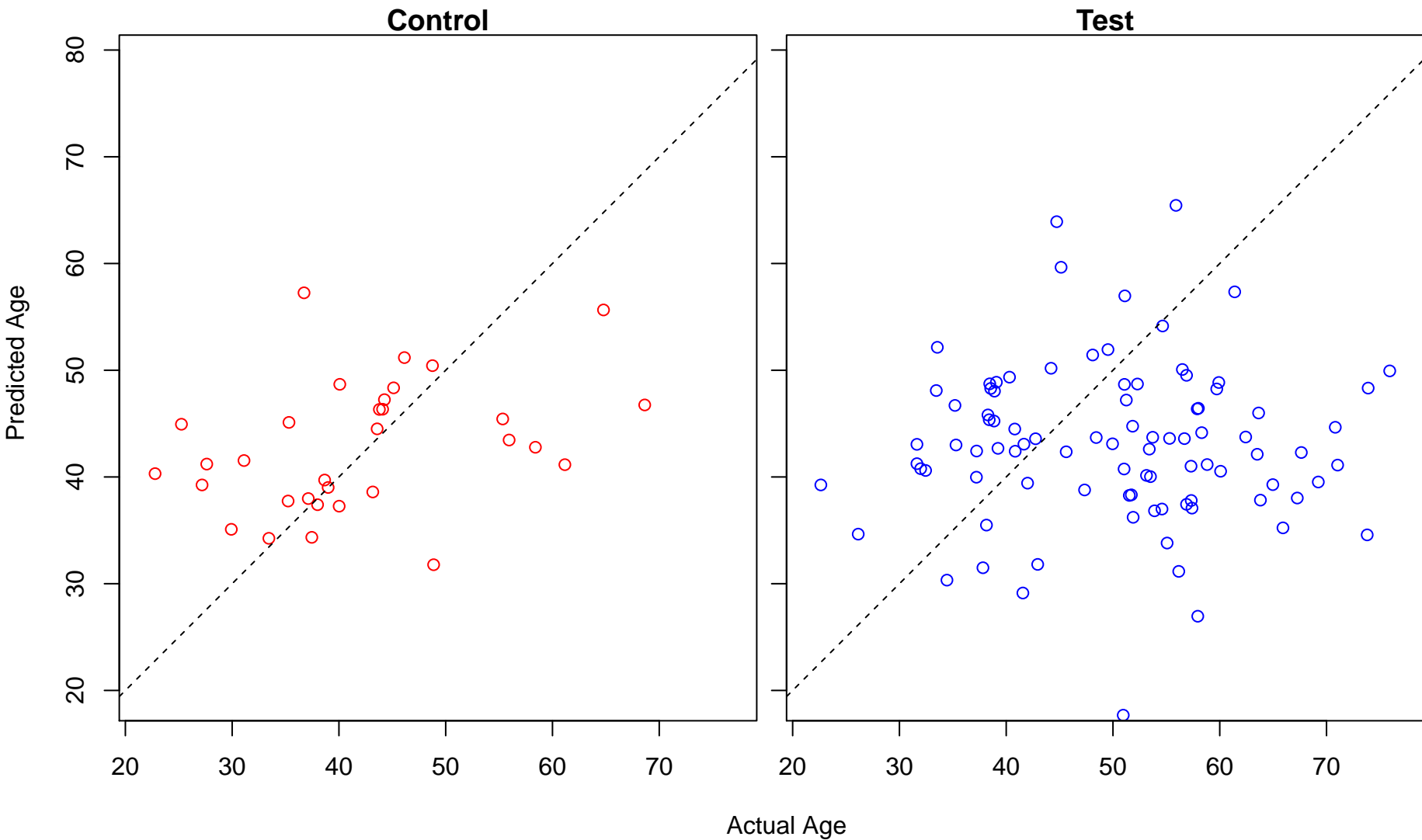
L-cystine transport (Score: 0.517582)



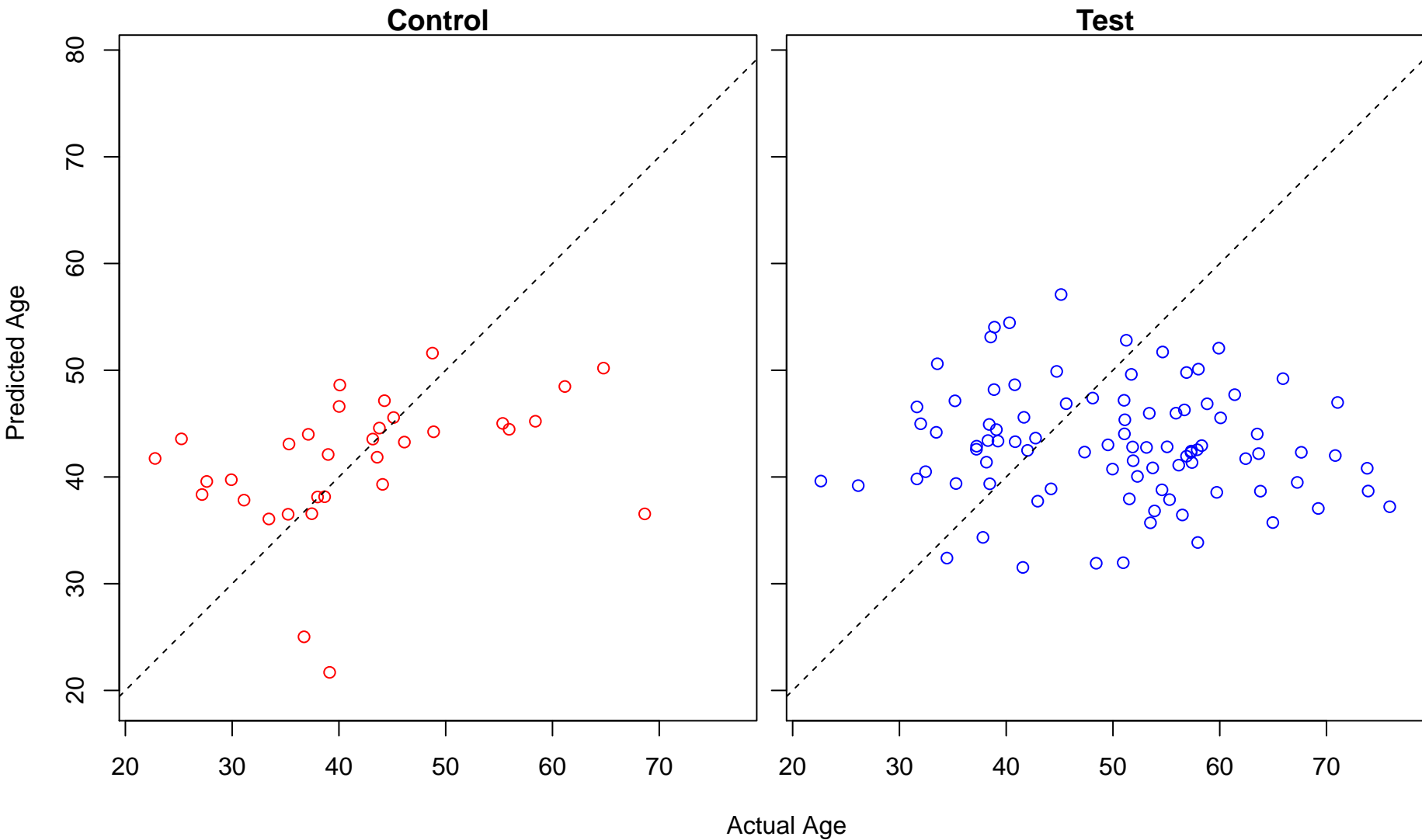
positive regulation of type 2 immune response (Score: 0.516502)



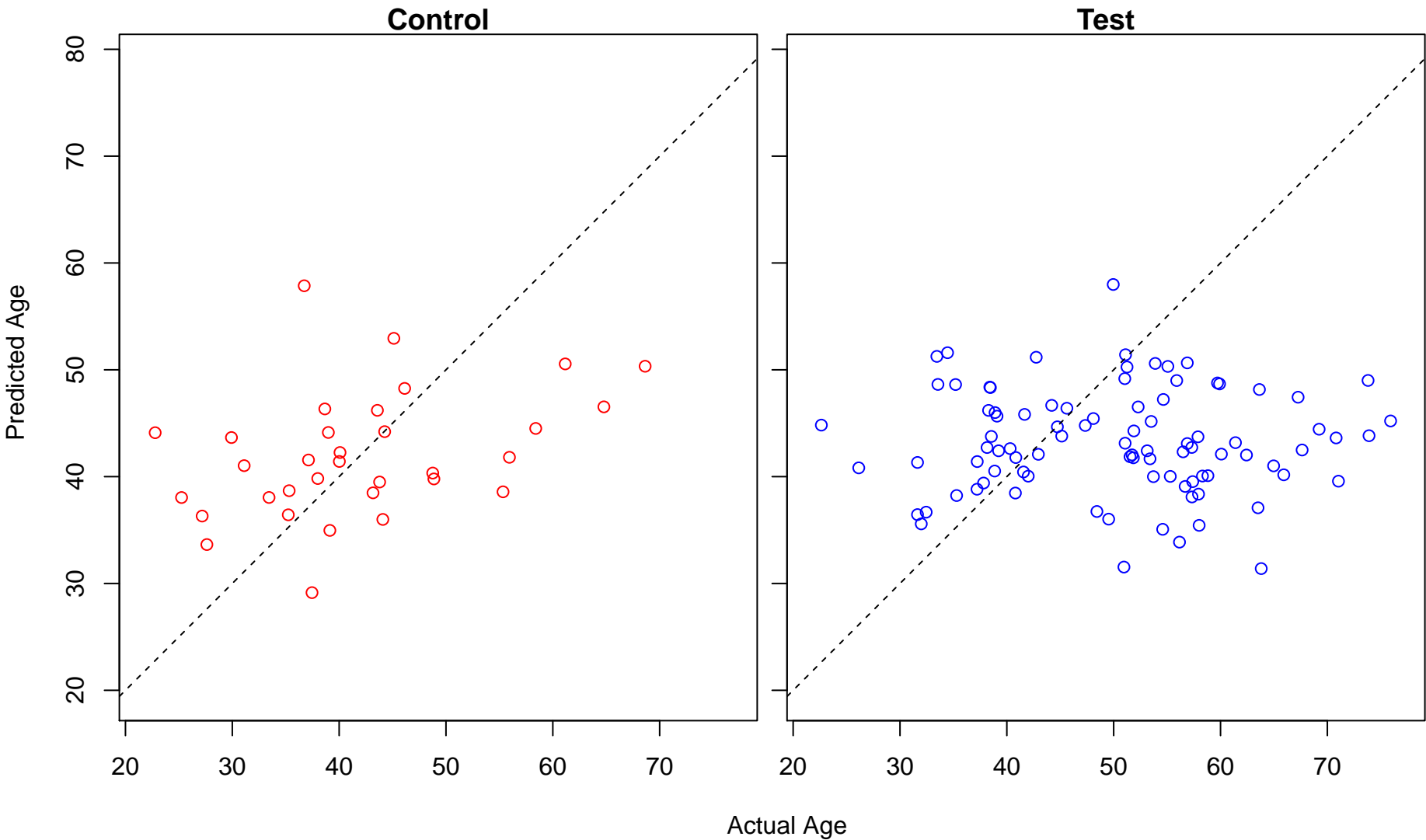
protein ADP-ribosylation (Score: 0.516463)



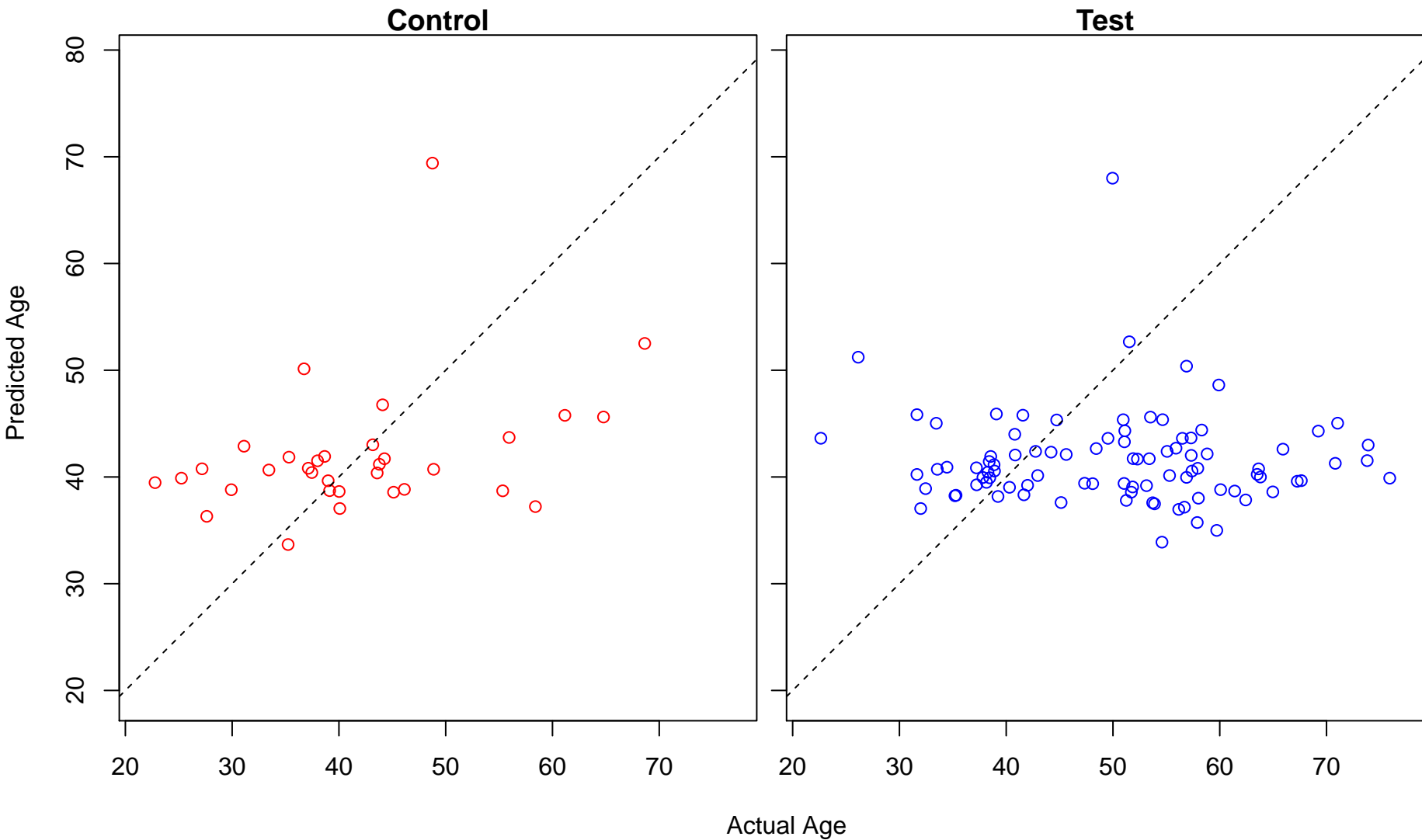
membrane protein ectodomain proteolysis (Score: 0.516377)



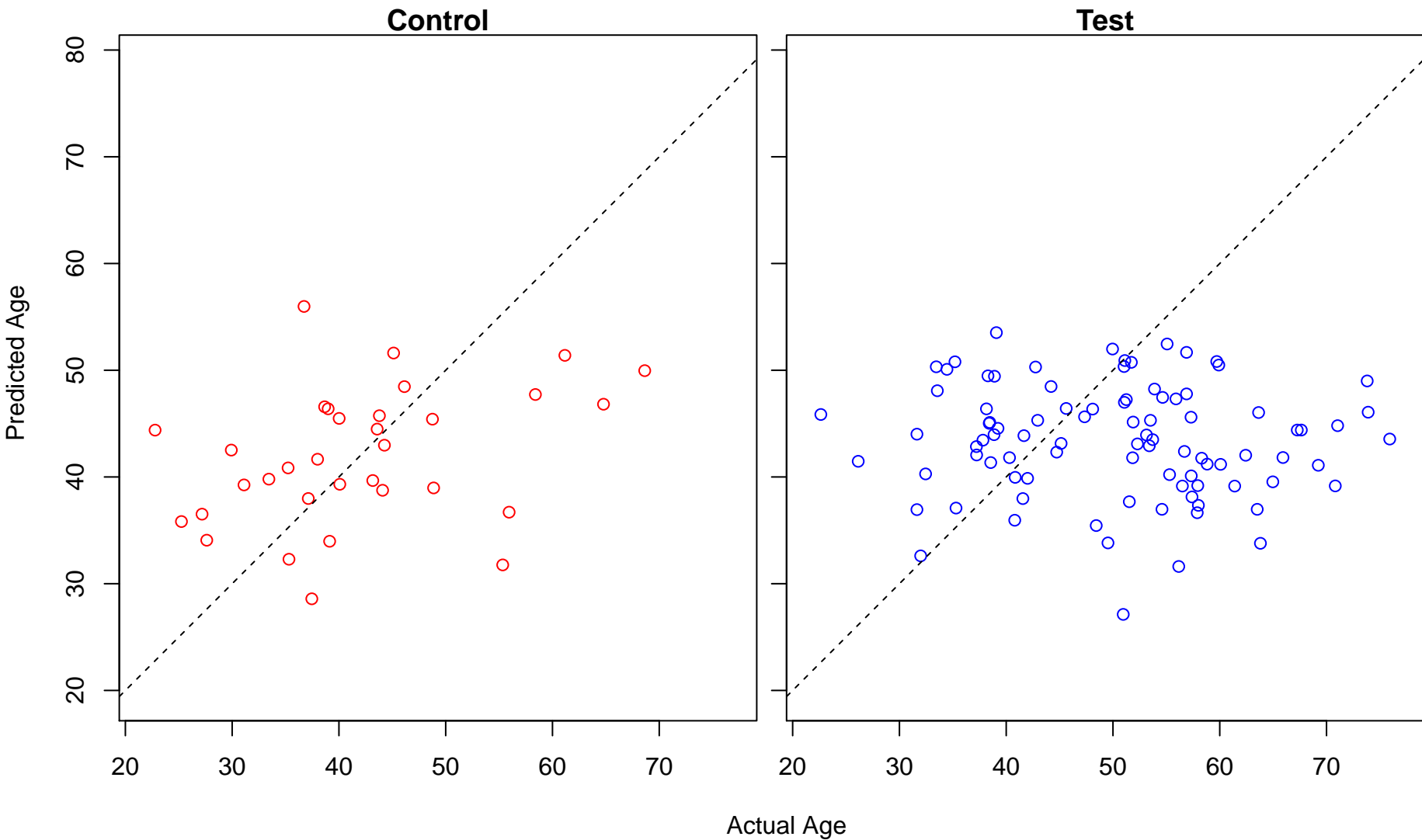
regulation of respiratory gaseous exchange by neurological system process (Score: 0.515257)



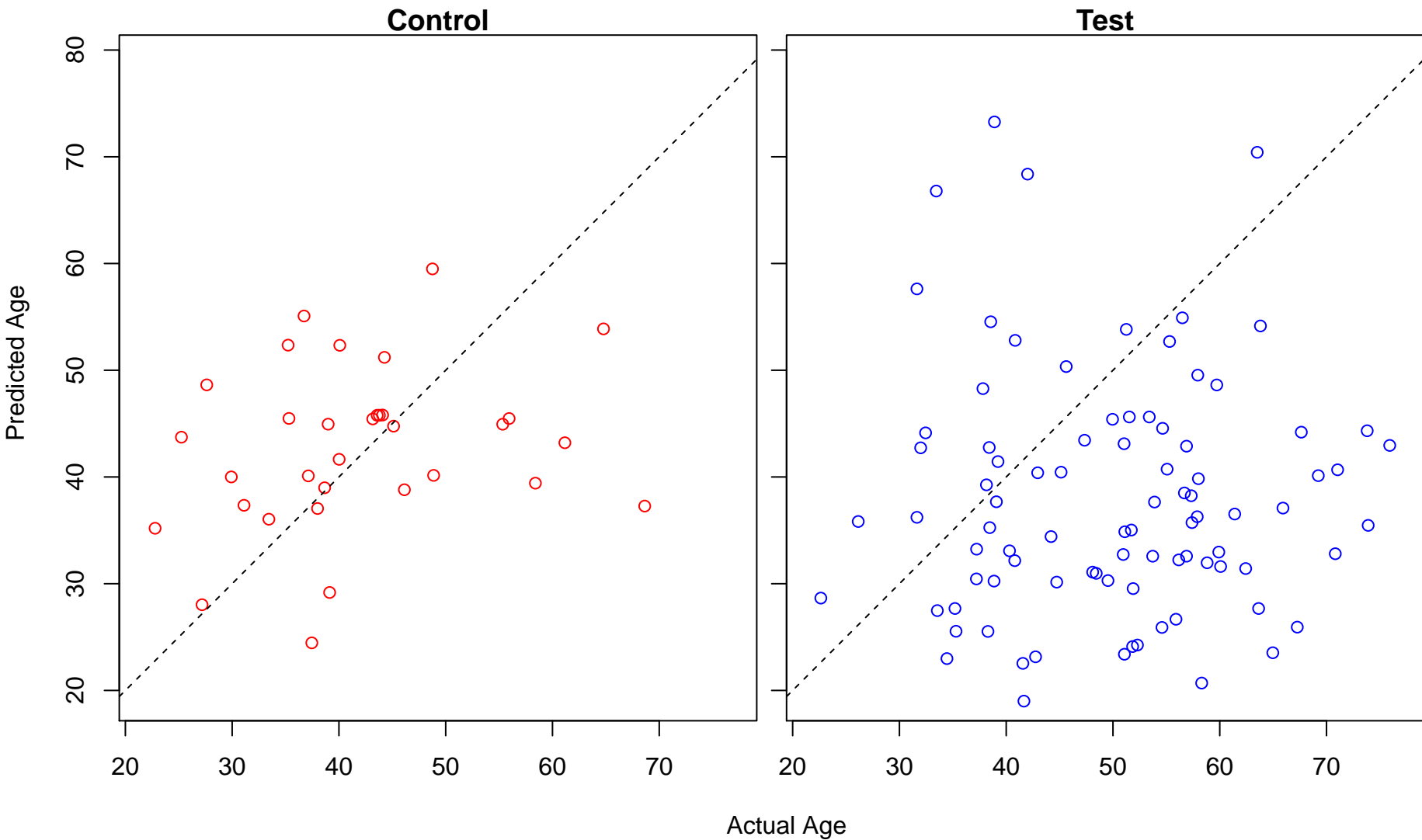
nucleotide-excision repair, DNA incision, 3'-to lesion (Score: 0.513627)



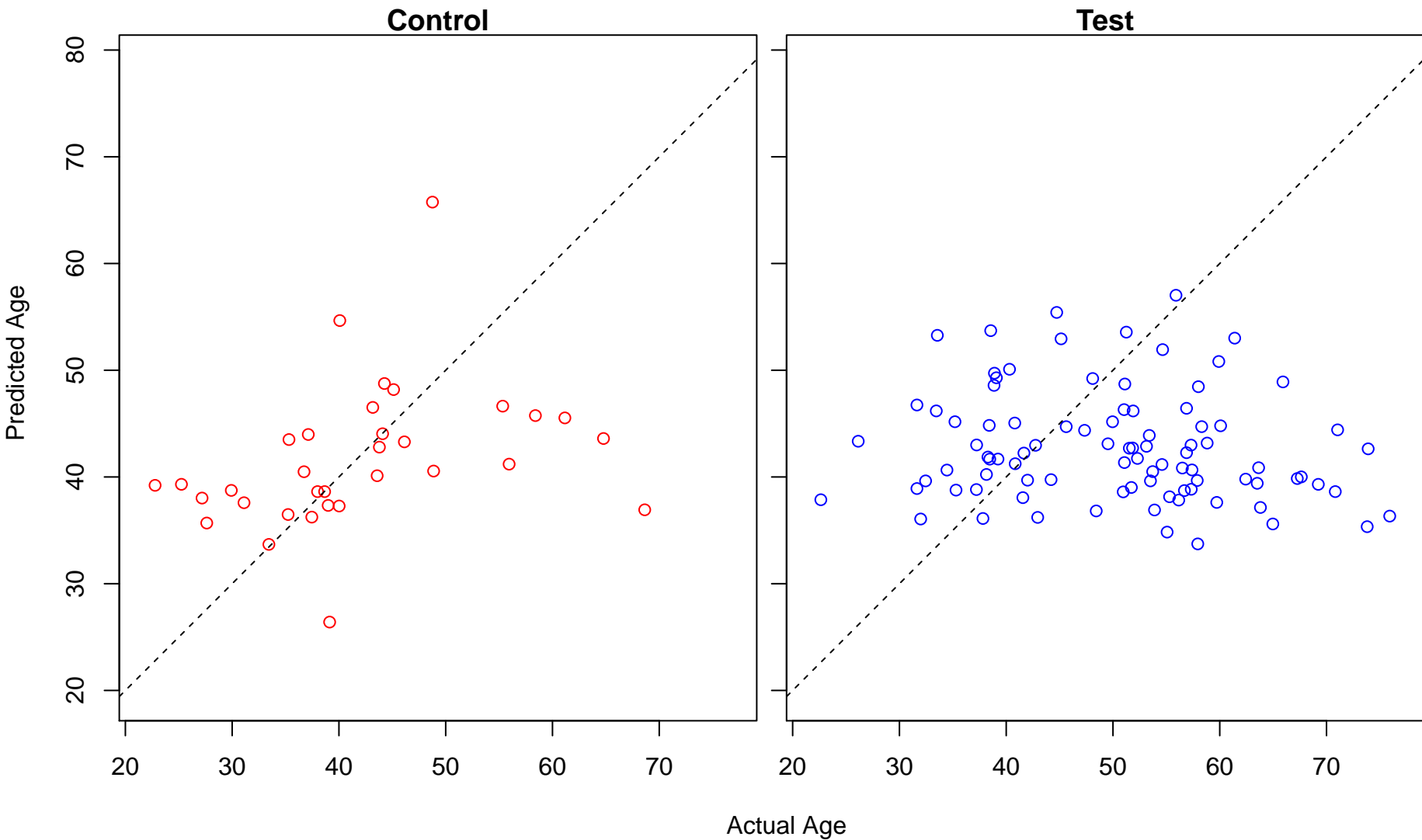
postsynaptic density protein 95 clustering (Score: 0.513134)



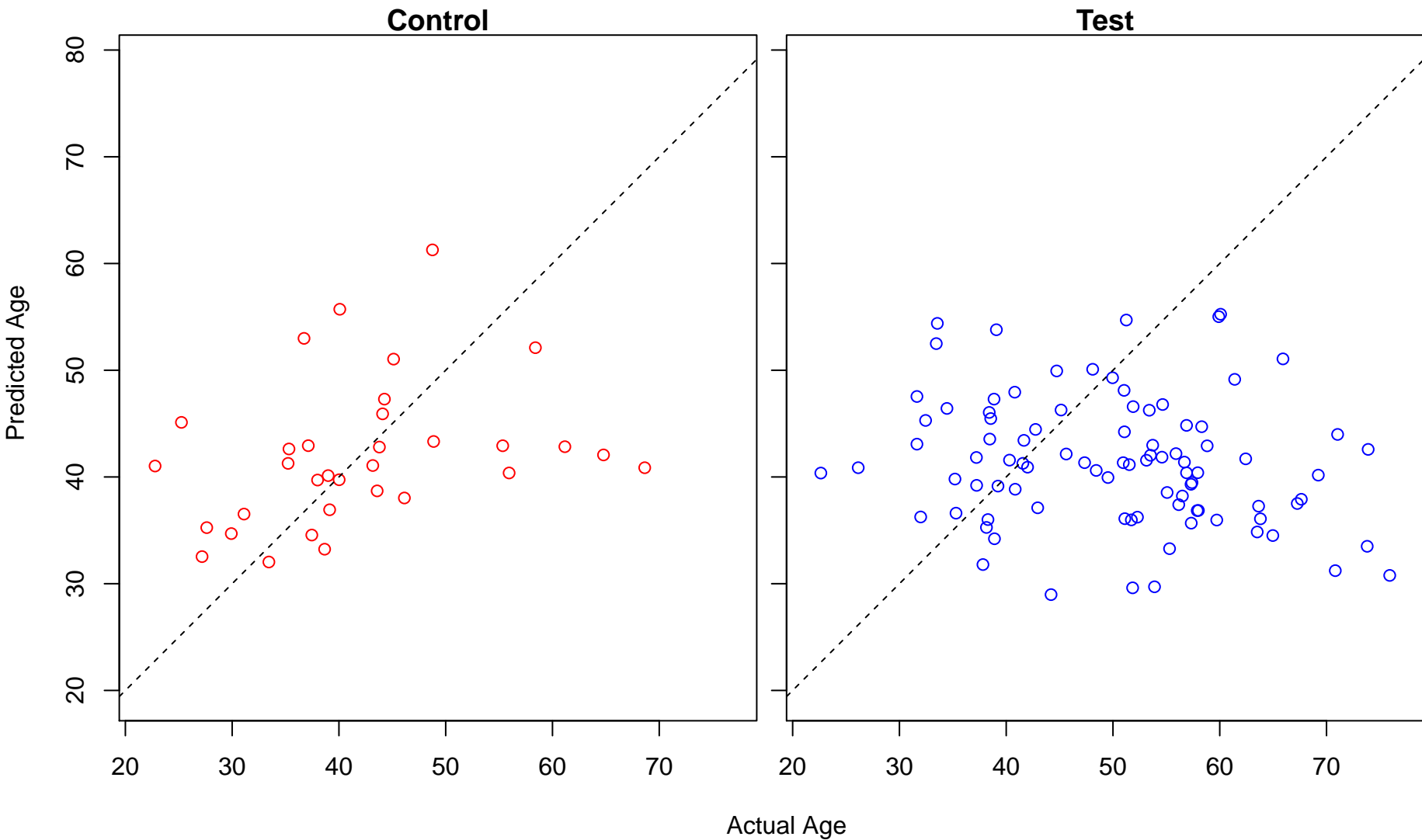
hemidesmosome assembly (Score: 0.512451)



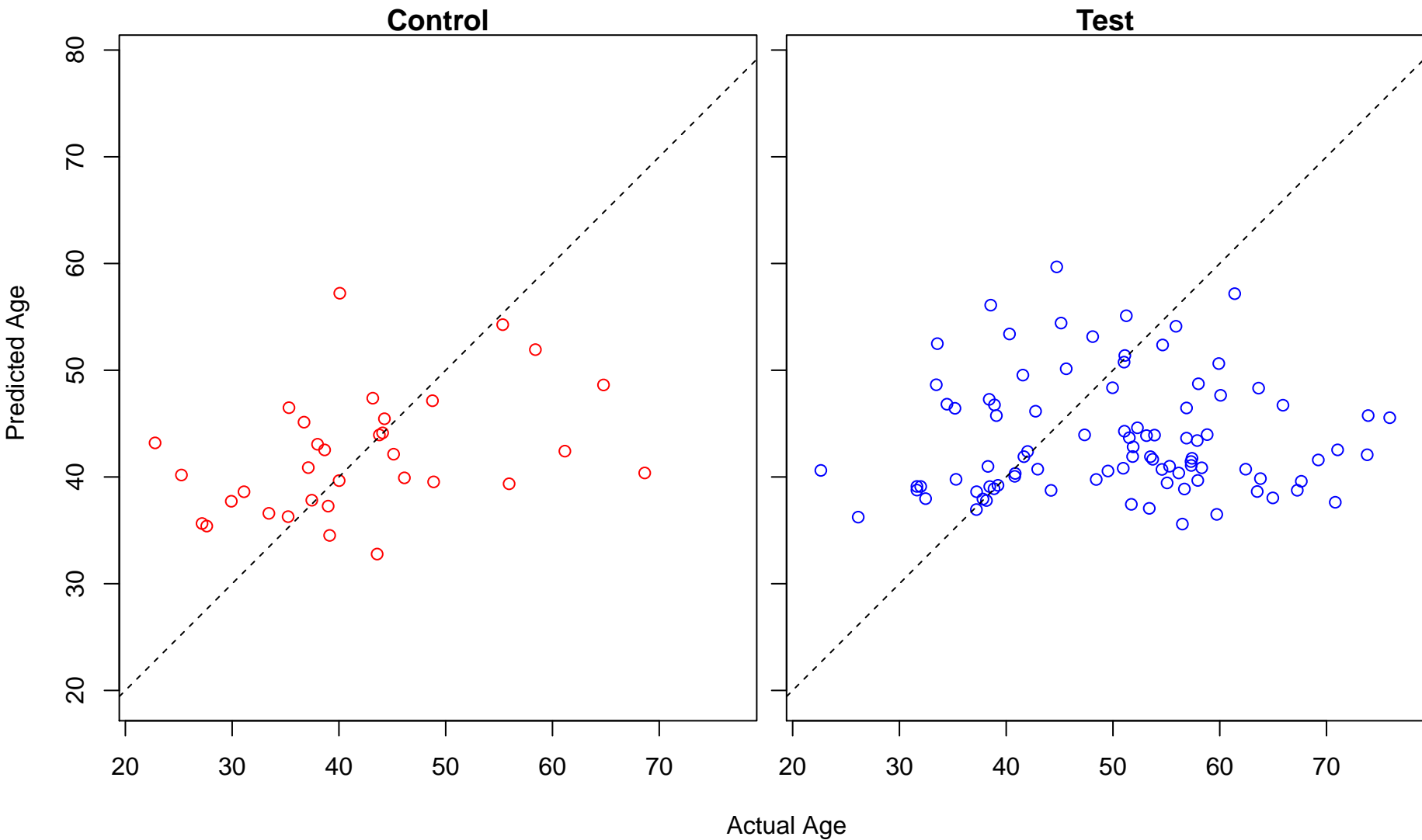
regulation of mitotic cell cycle (Score: 0.512213)



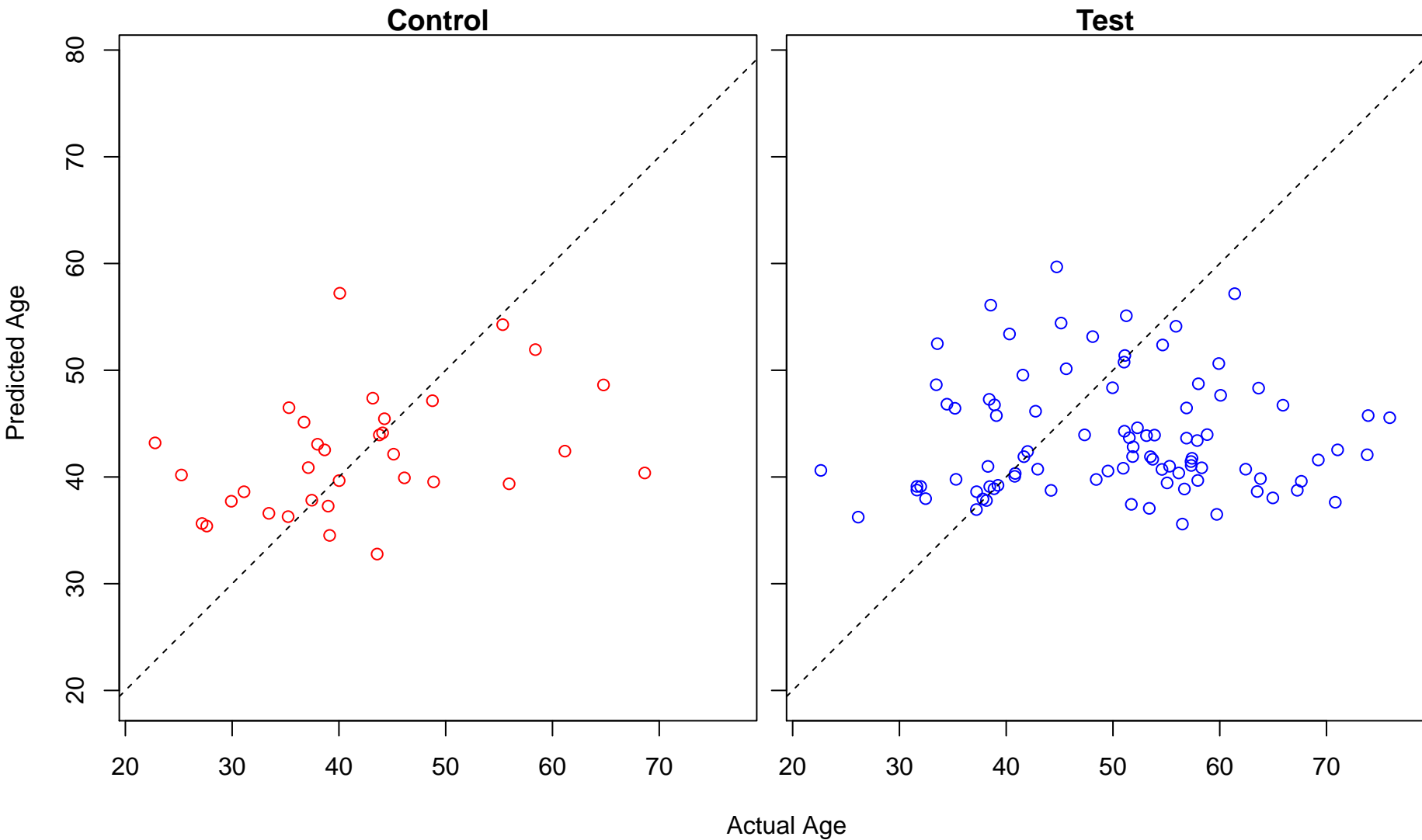
regulation of type 2 immune response (Score: 0.512138)



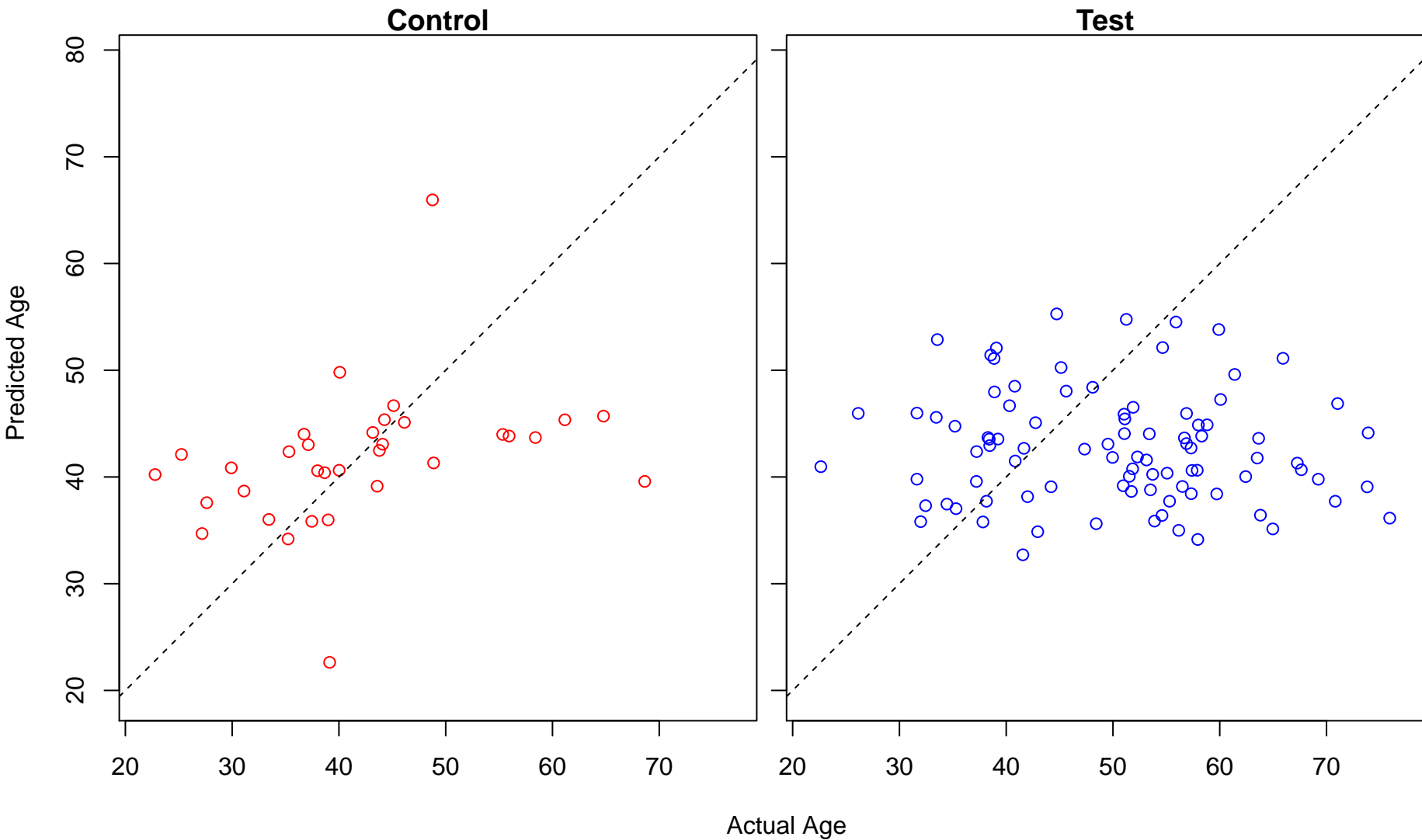
pyrimidine nucleoside triphosphate metabolic process (Score: 0.511037)



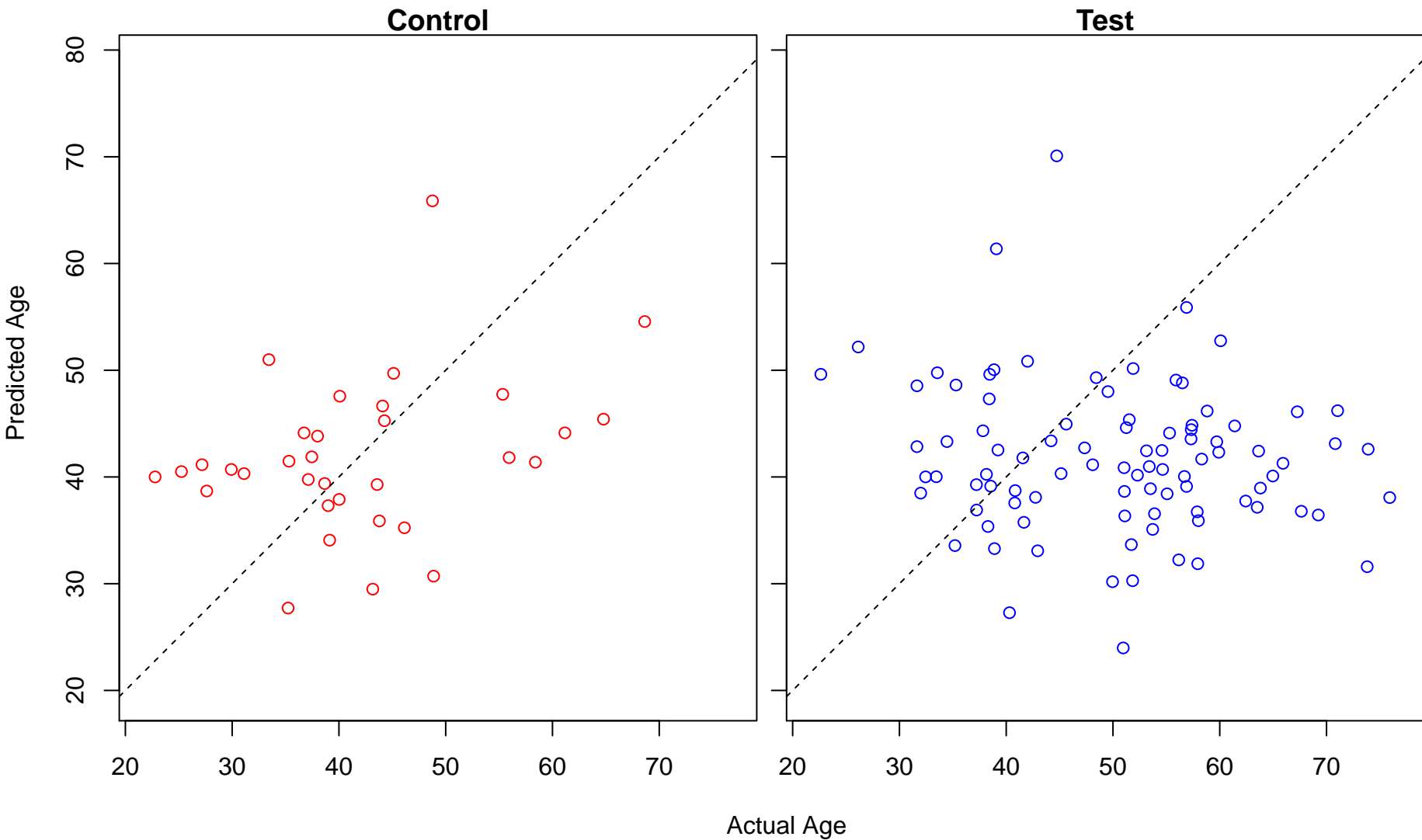
pyrimidine ribonucleoside triphosphate metabolic process (Score: 0.511037)



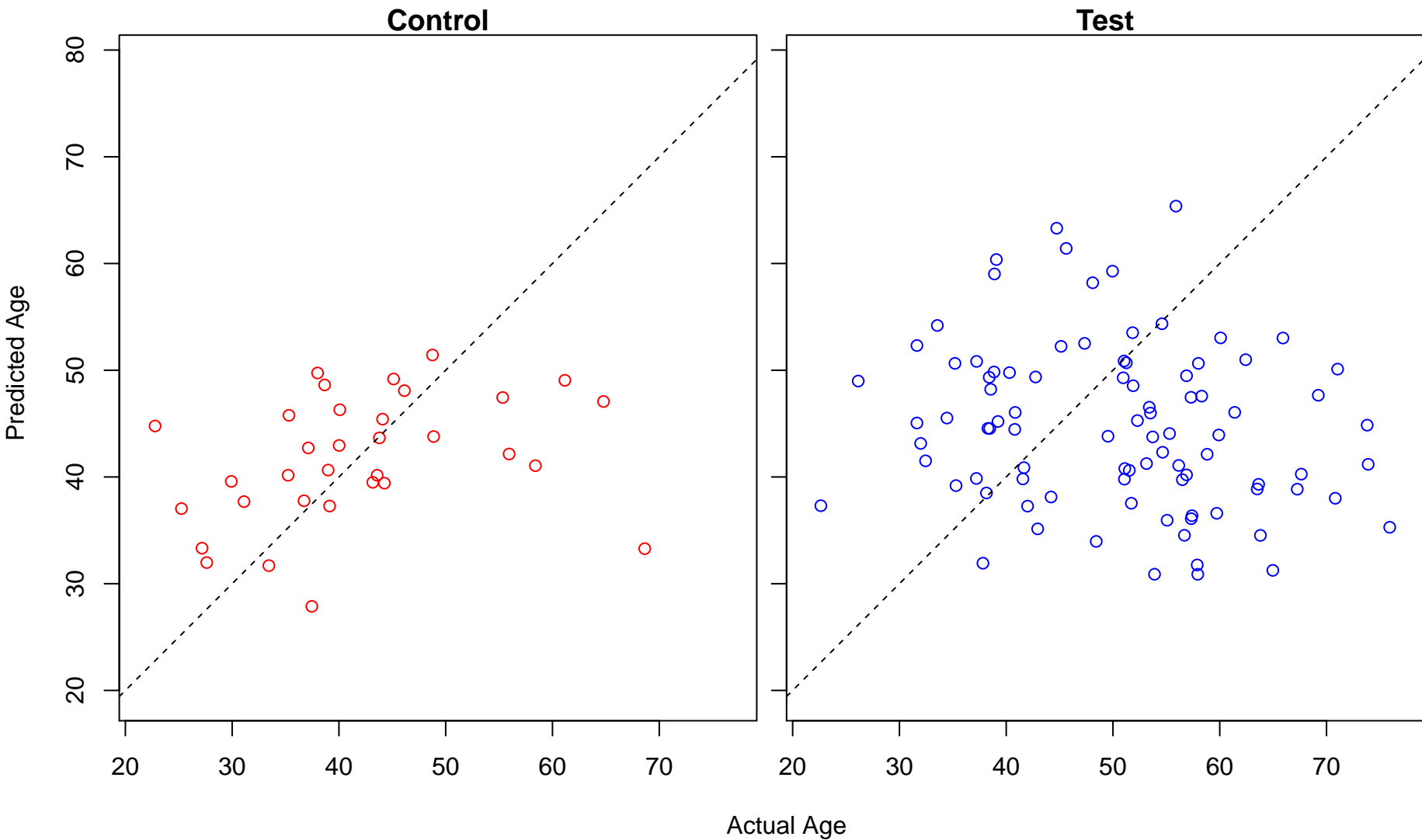
response to external stimulus (Score: 0.509998)



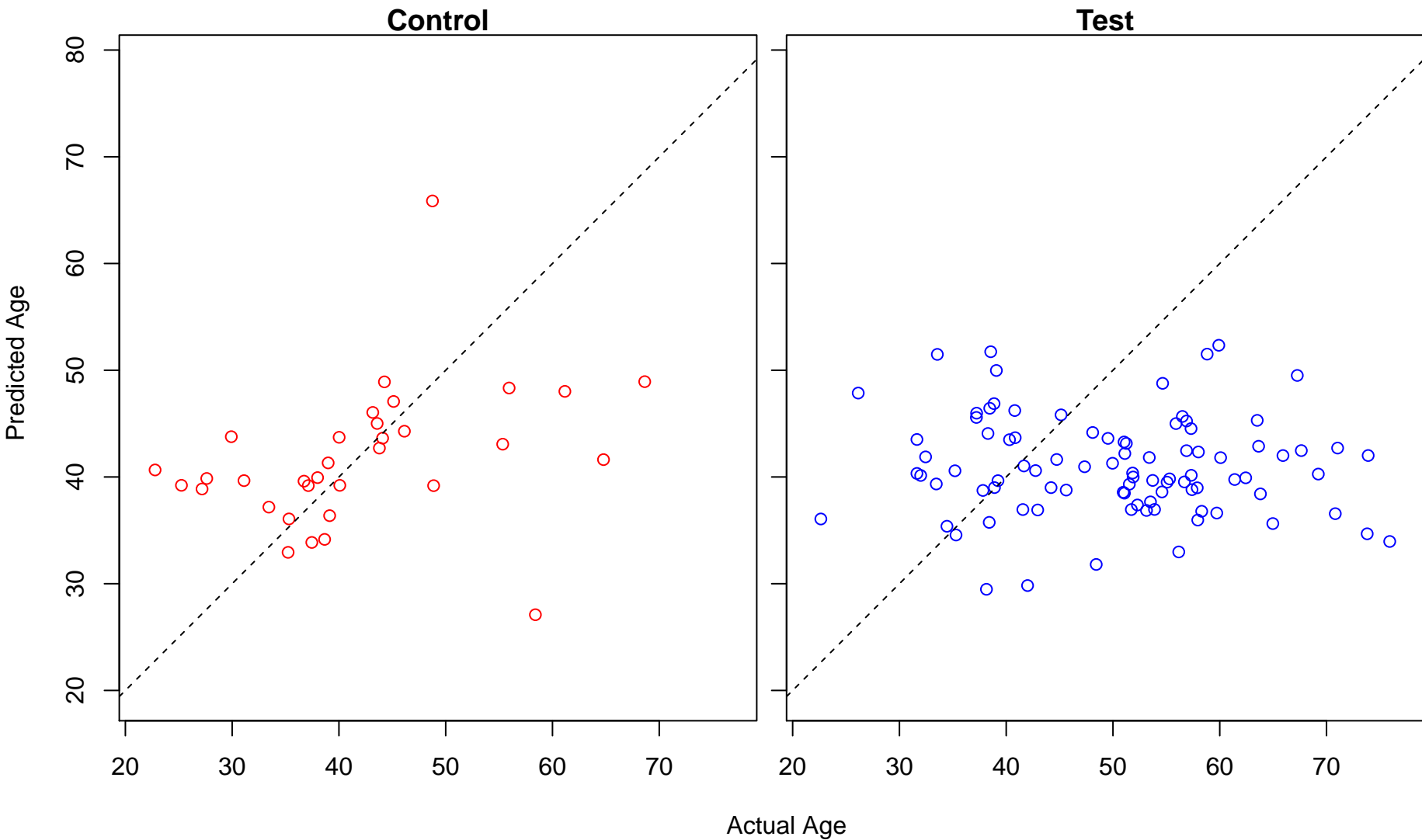
regulation of hyaluronan biosynthetic process (Score: 0.508573)



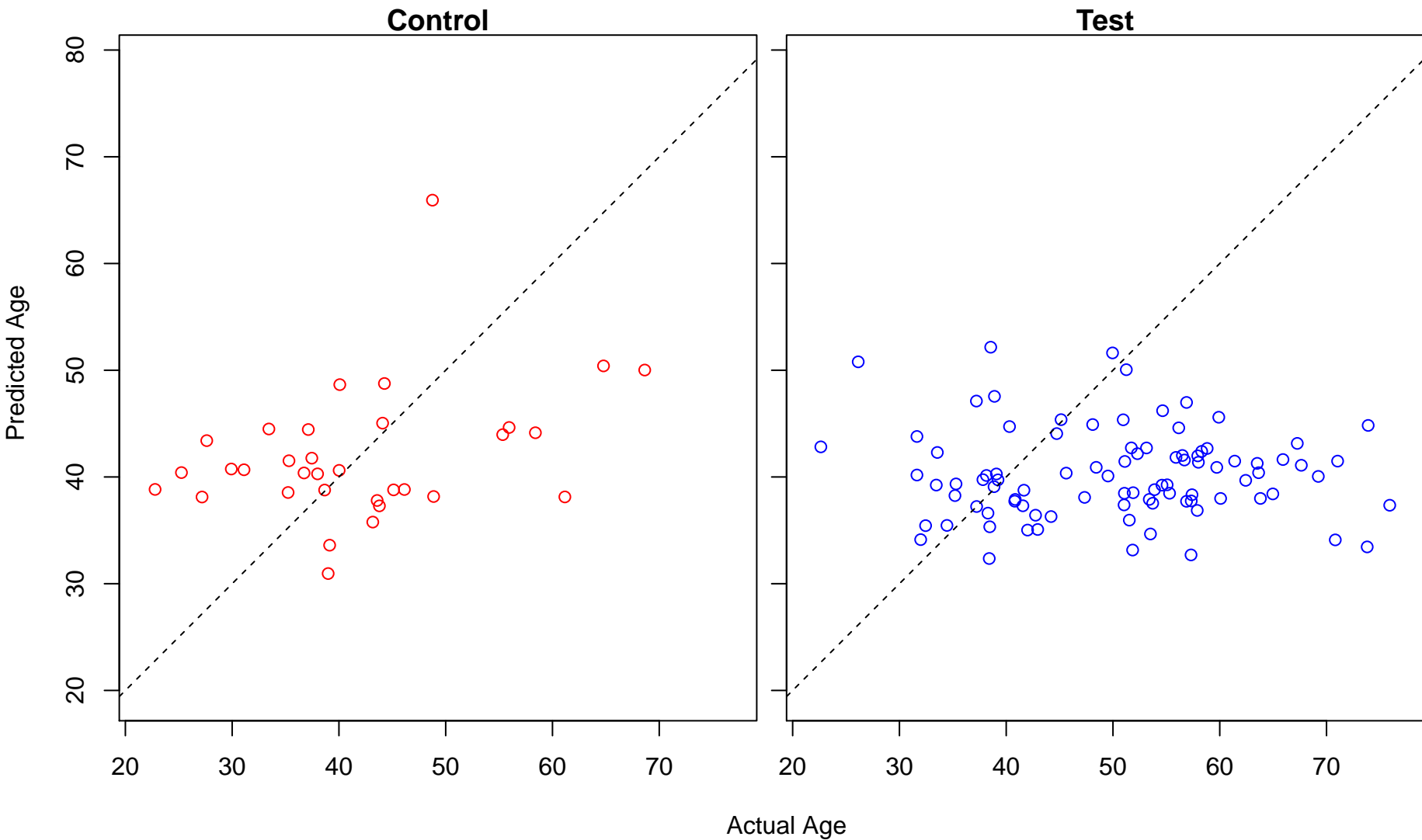
galactose metabolic process (Score: 0.507050)



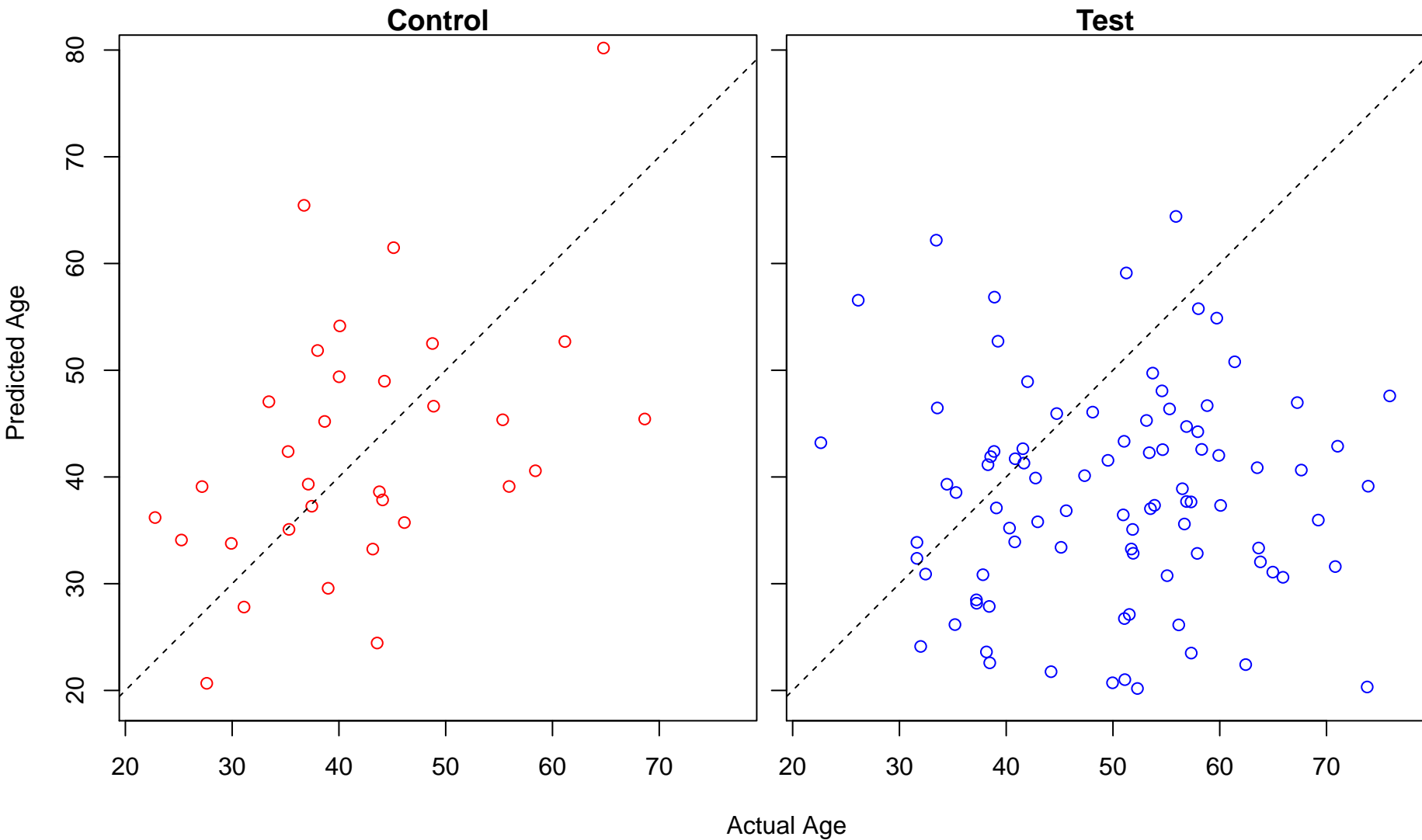
GDP-mannose biosynthetic process (Score: 0.505577)



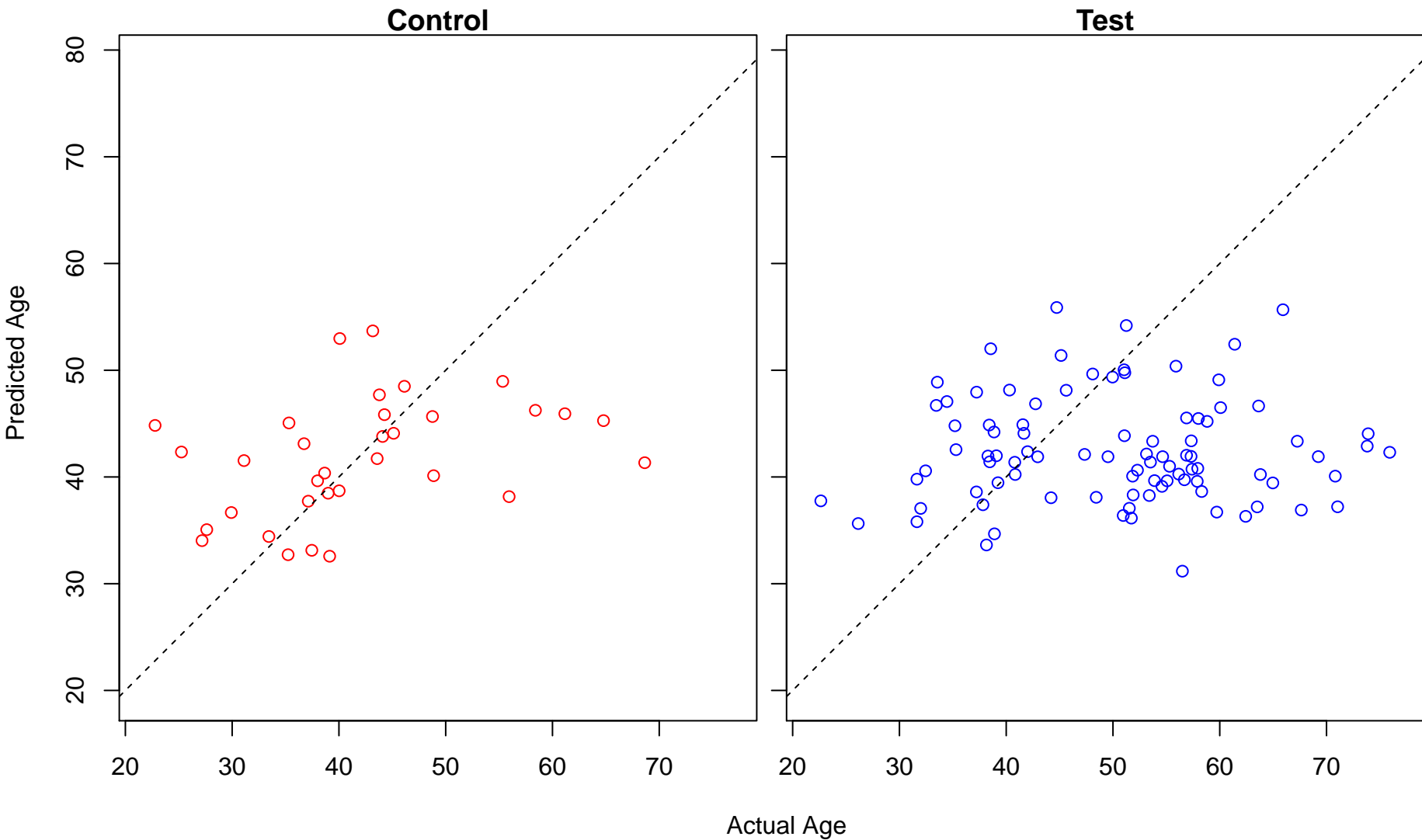
G-protein coupled acetylcholine receptor signaling pathway (Score: 0.505202)



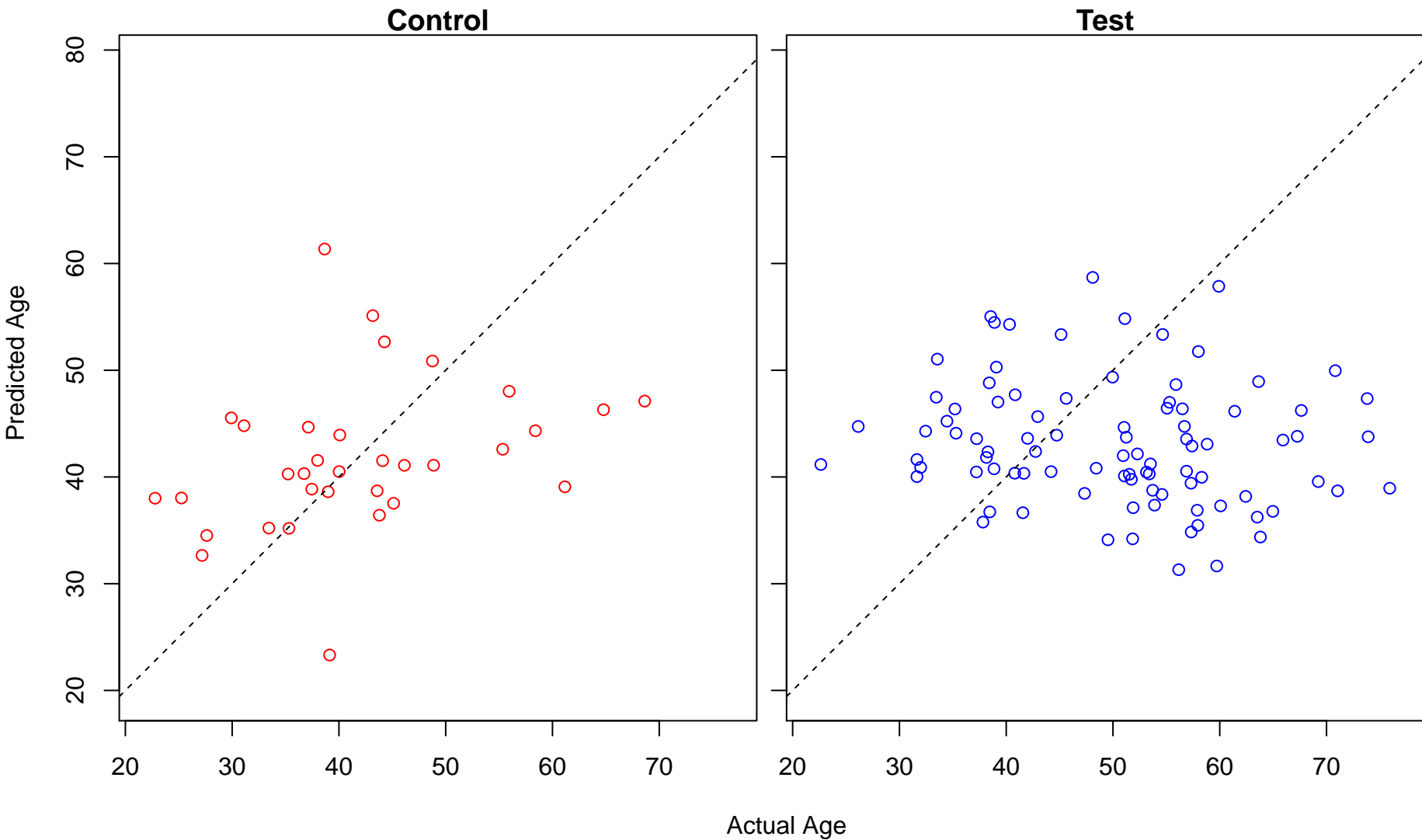
positive regulation of translation (Score: 0.505085)



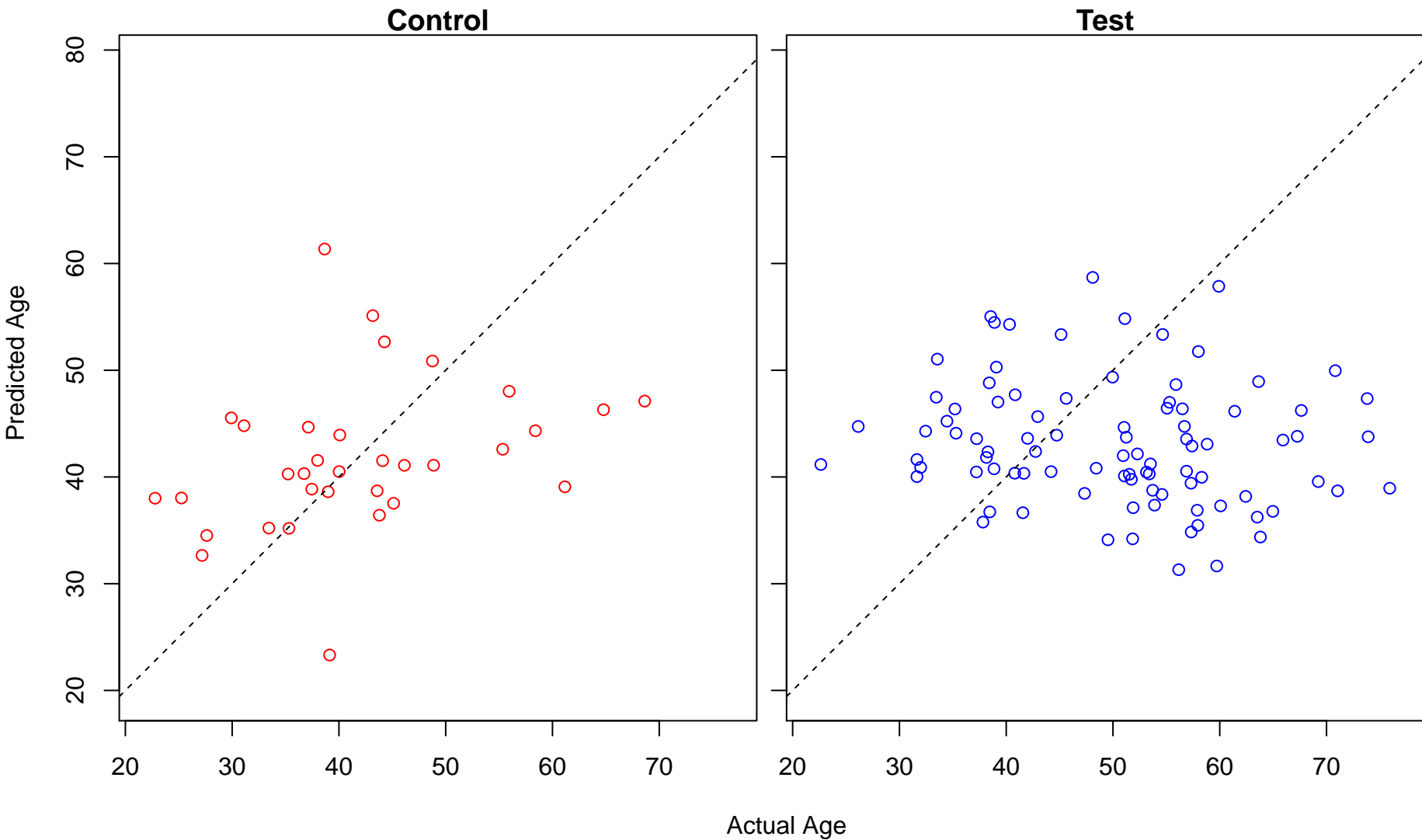
pyrimidine nucleotide biosynthetic process (Score: 0.503900)



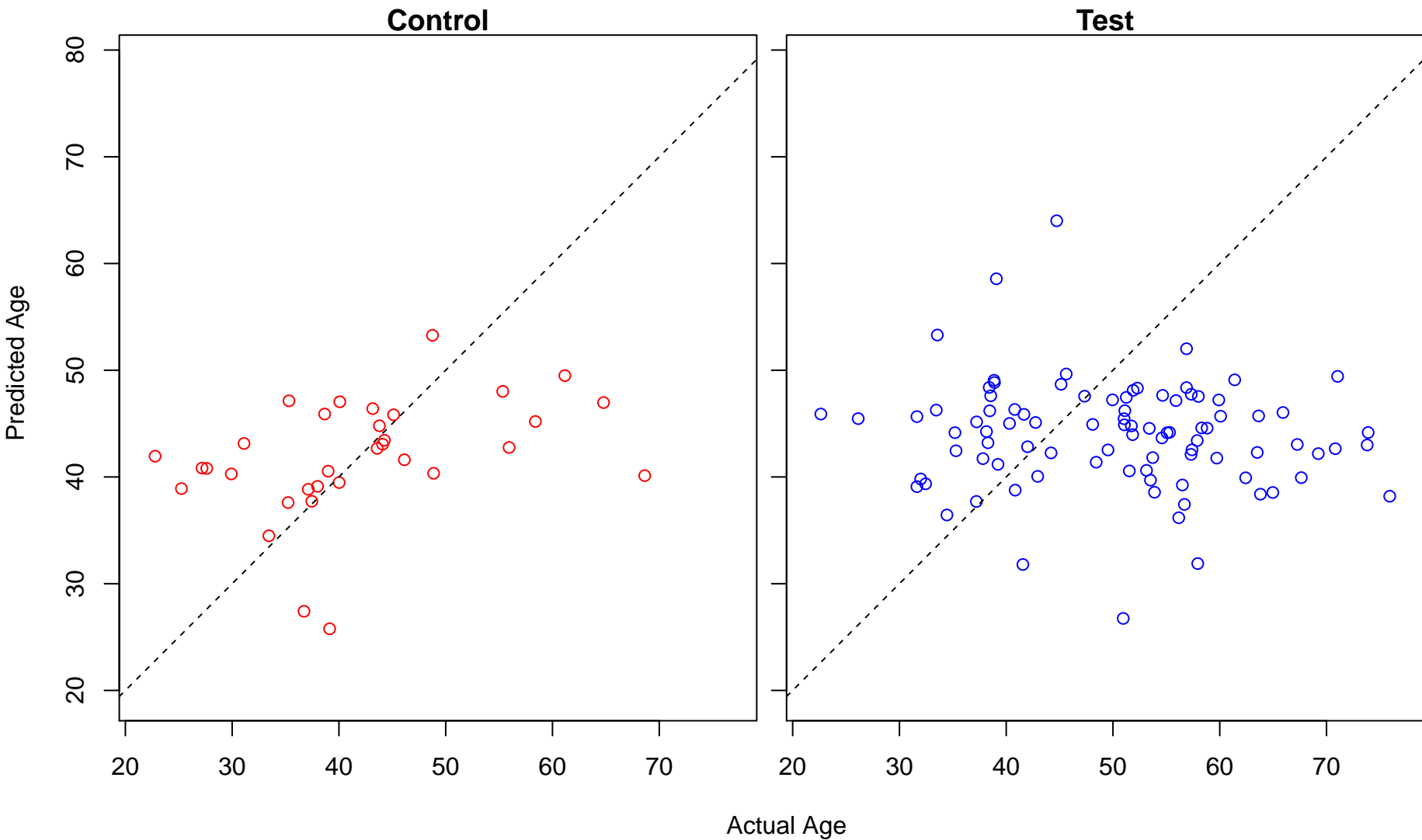
maternal placenta development (Score: 0.503845)



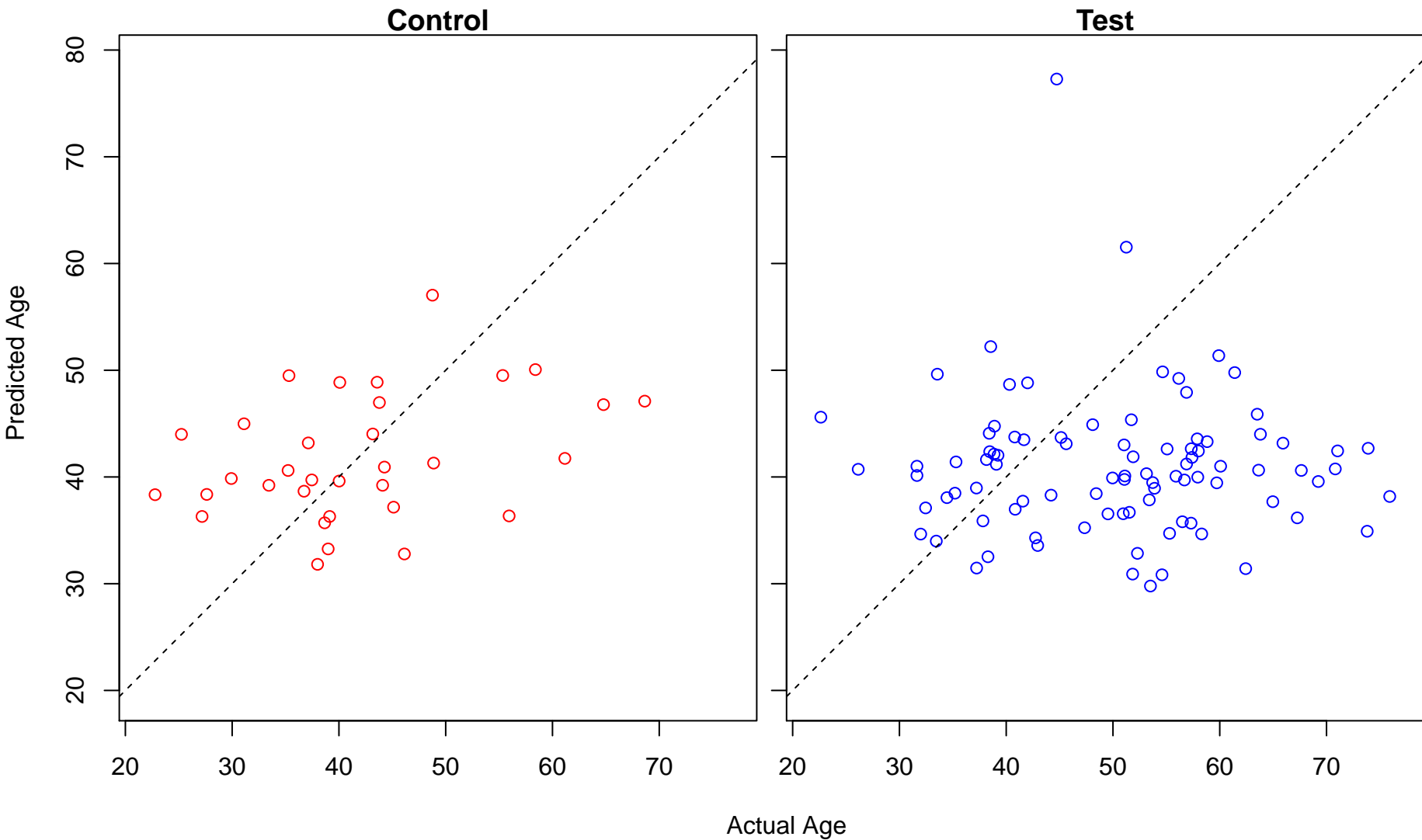
decidualization (Score: 0.503845)



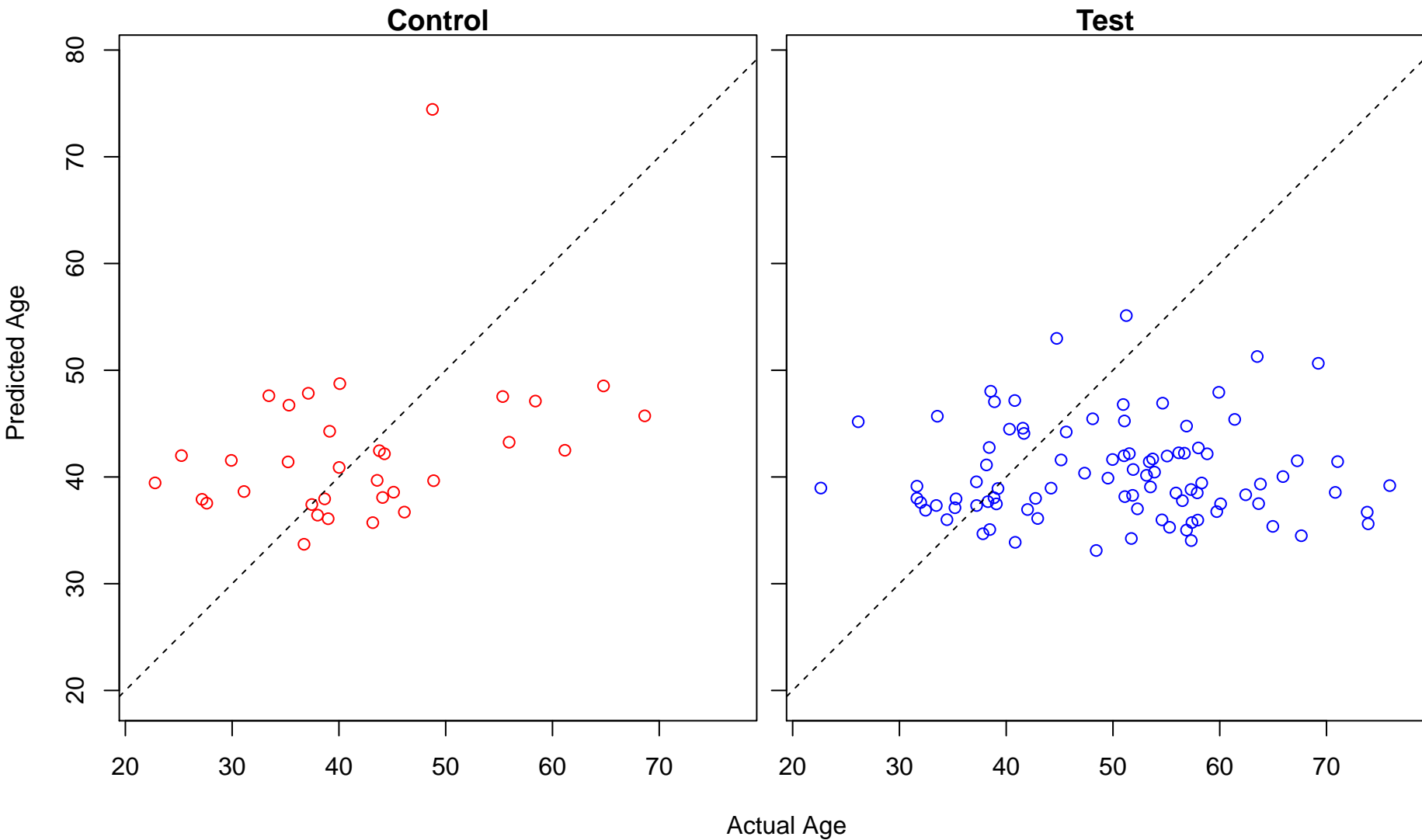
mitochondrion distribution (Score: 0.503447)



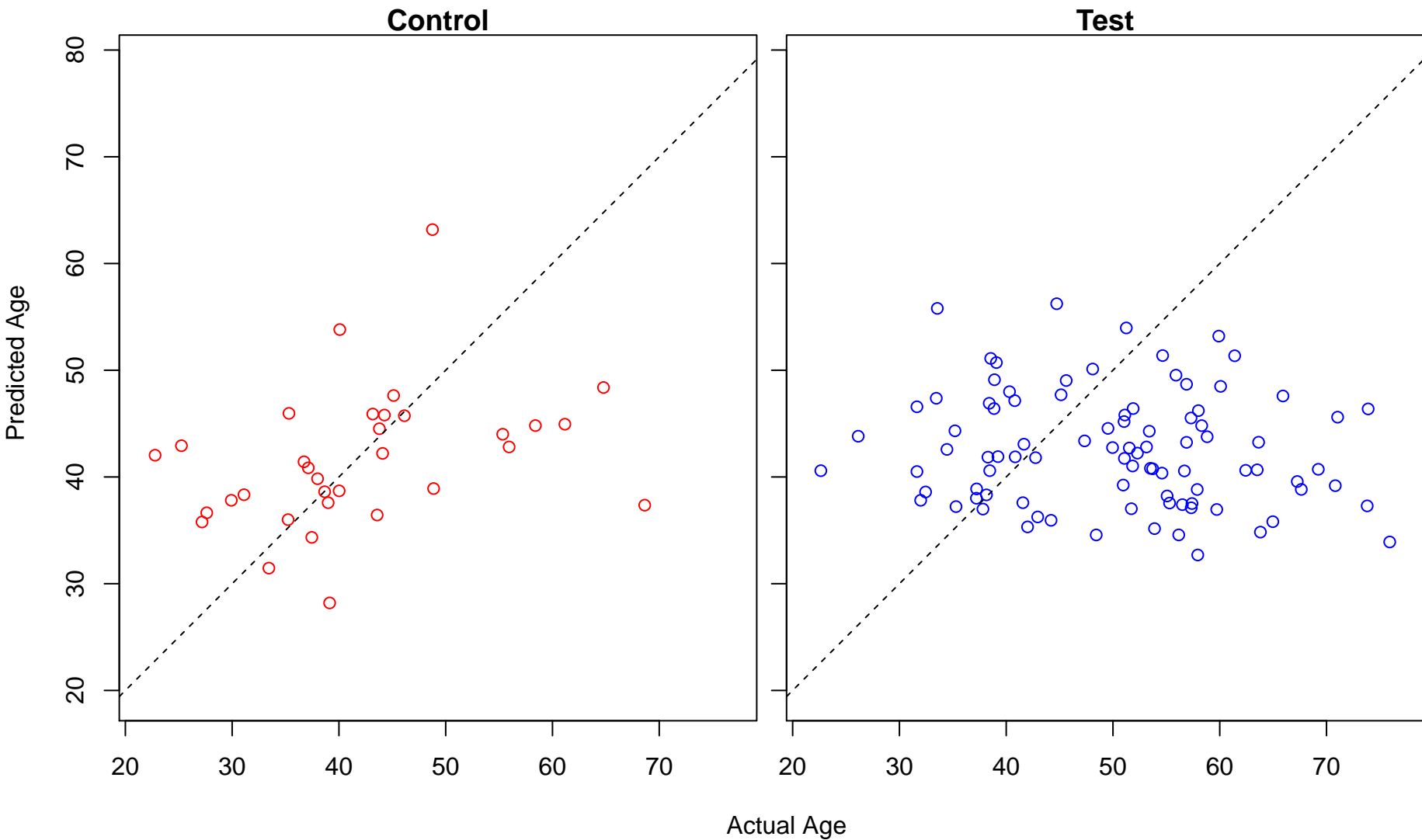
regulation of Golgi inheritance (Score: 0.502210)



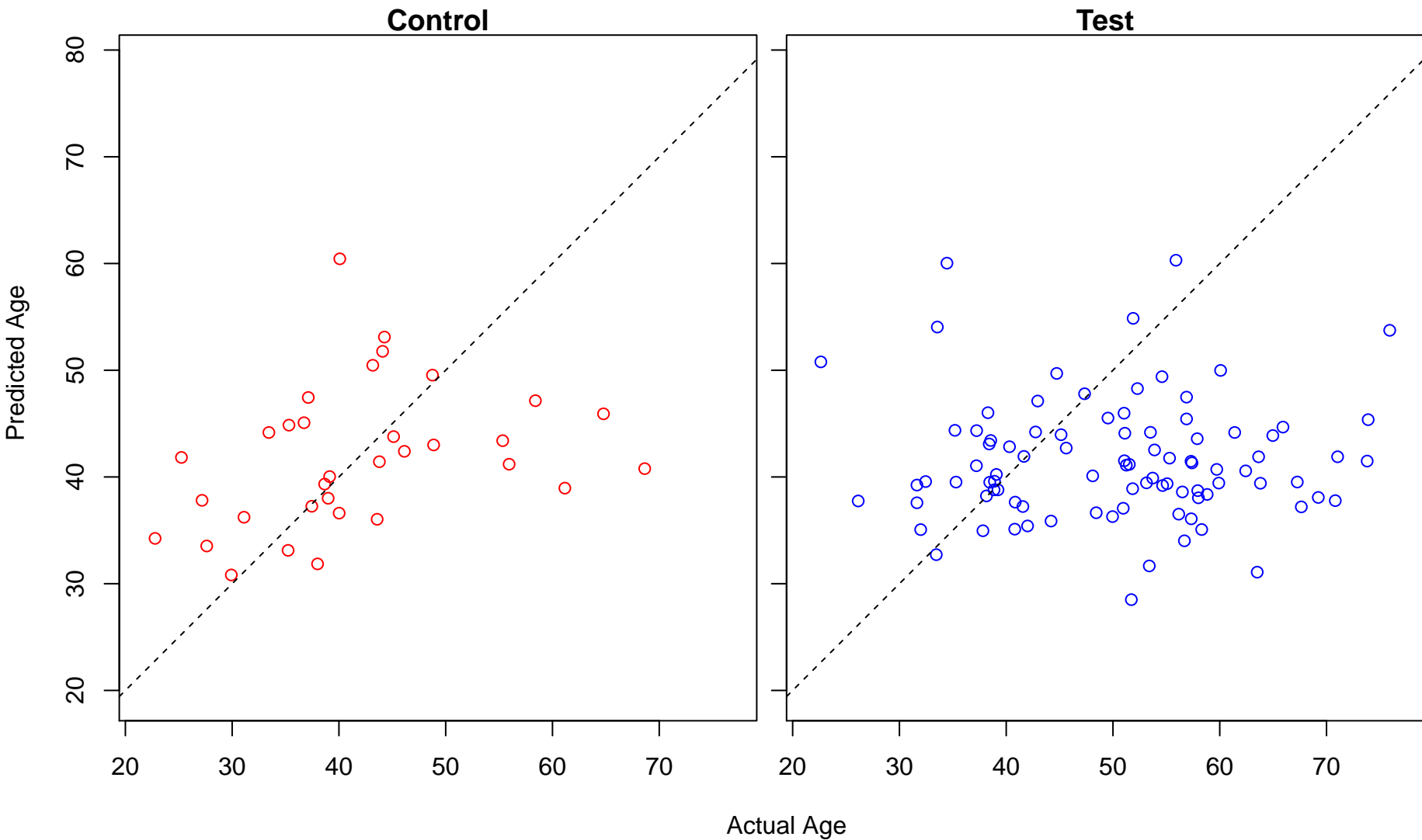
xylulose biosynthetic process (Score: 0.500163)



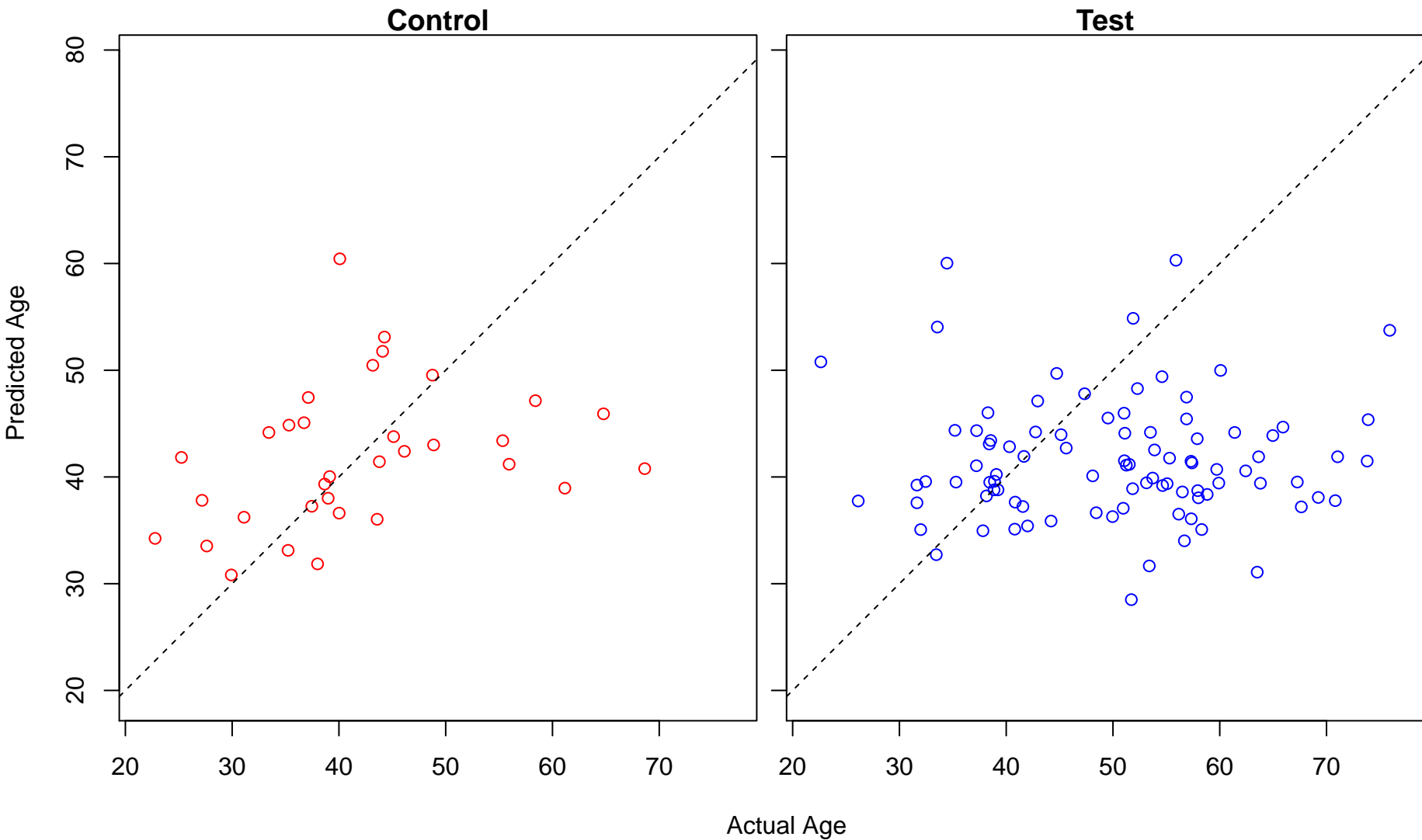
single-organism catabolic process (Score: 0.500077)



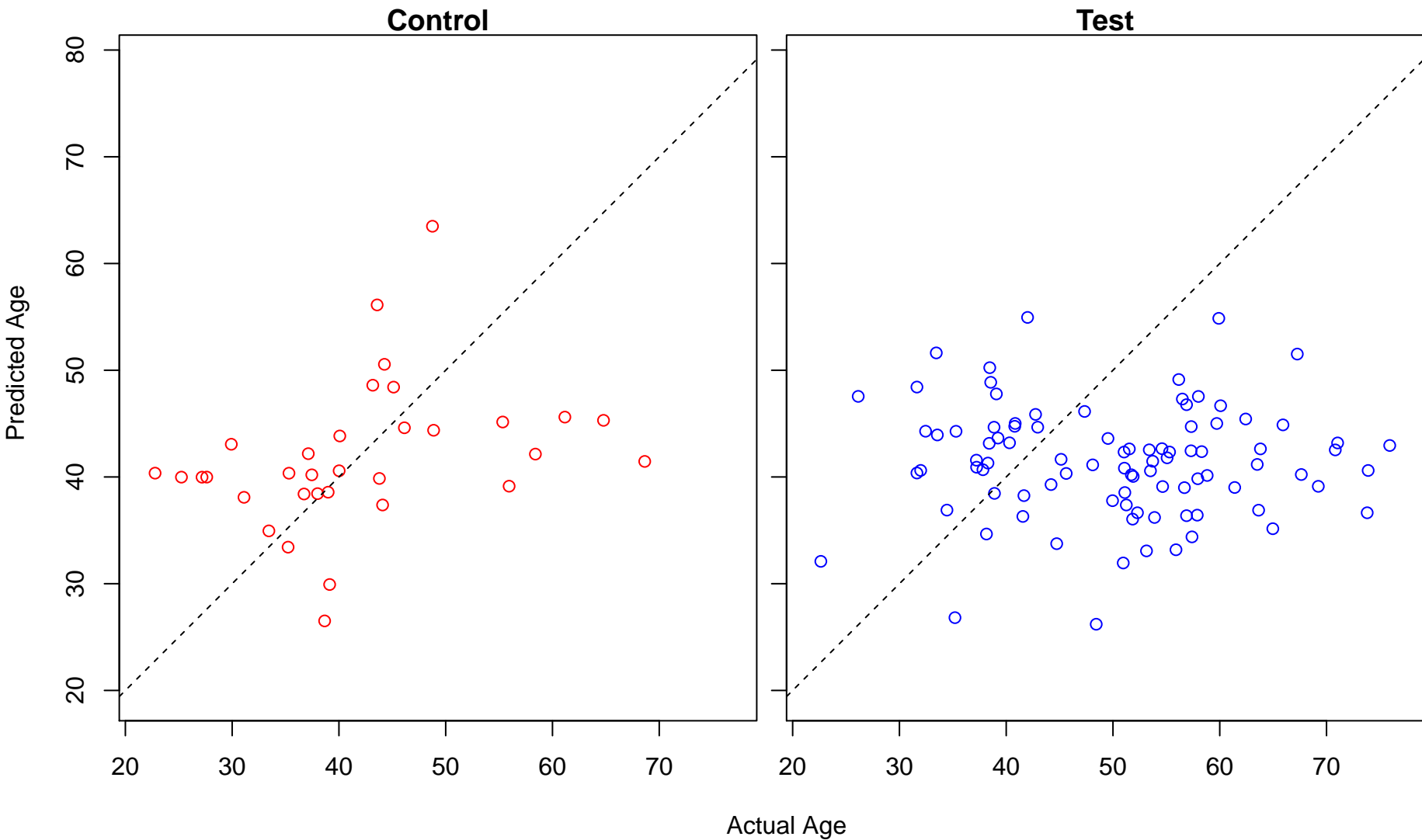
regulation of isomerase activity (Score: 0.498254)



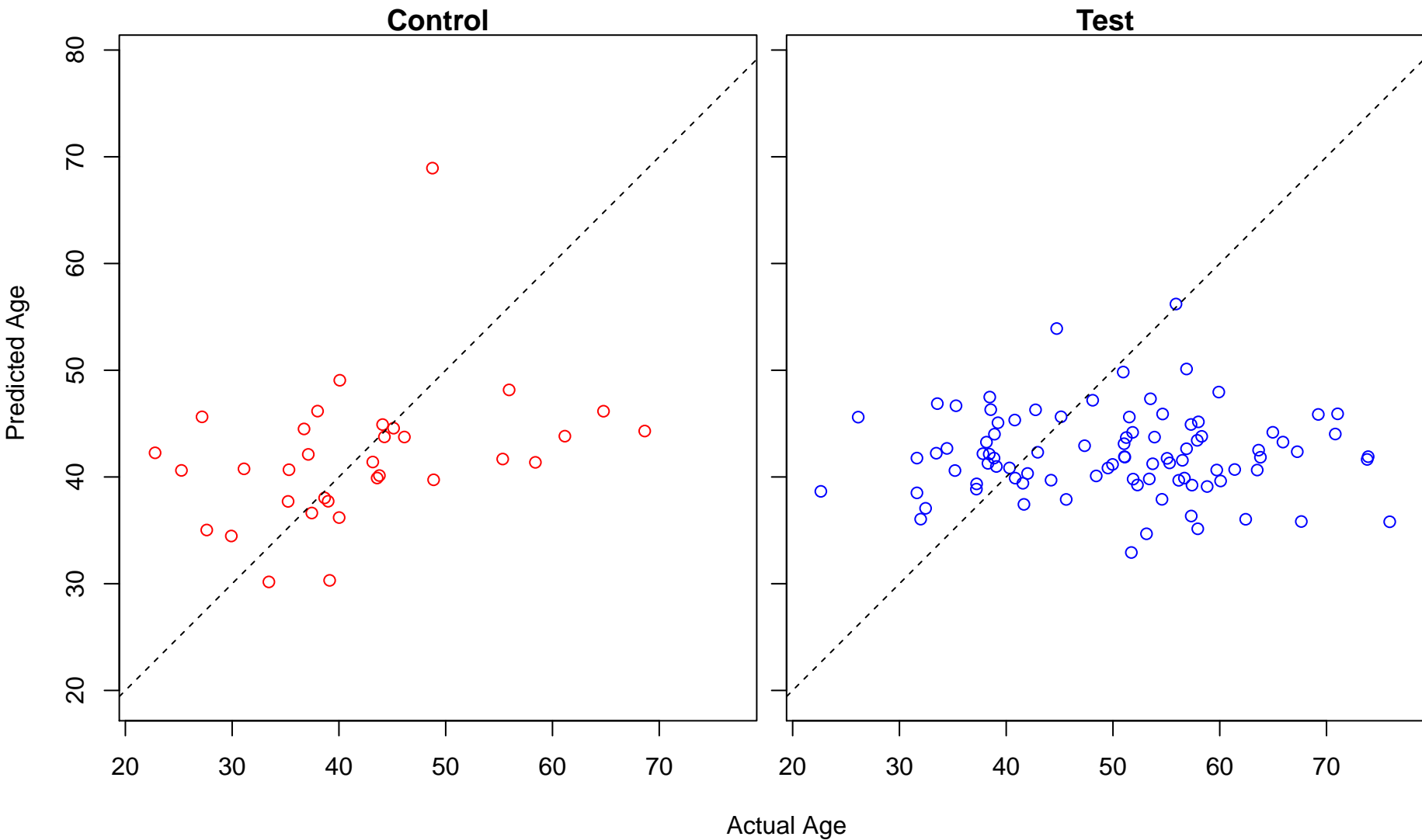
positive regulation of isomerase activity (Score: 0.498254)



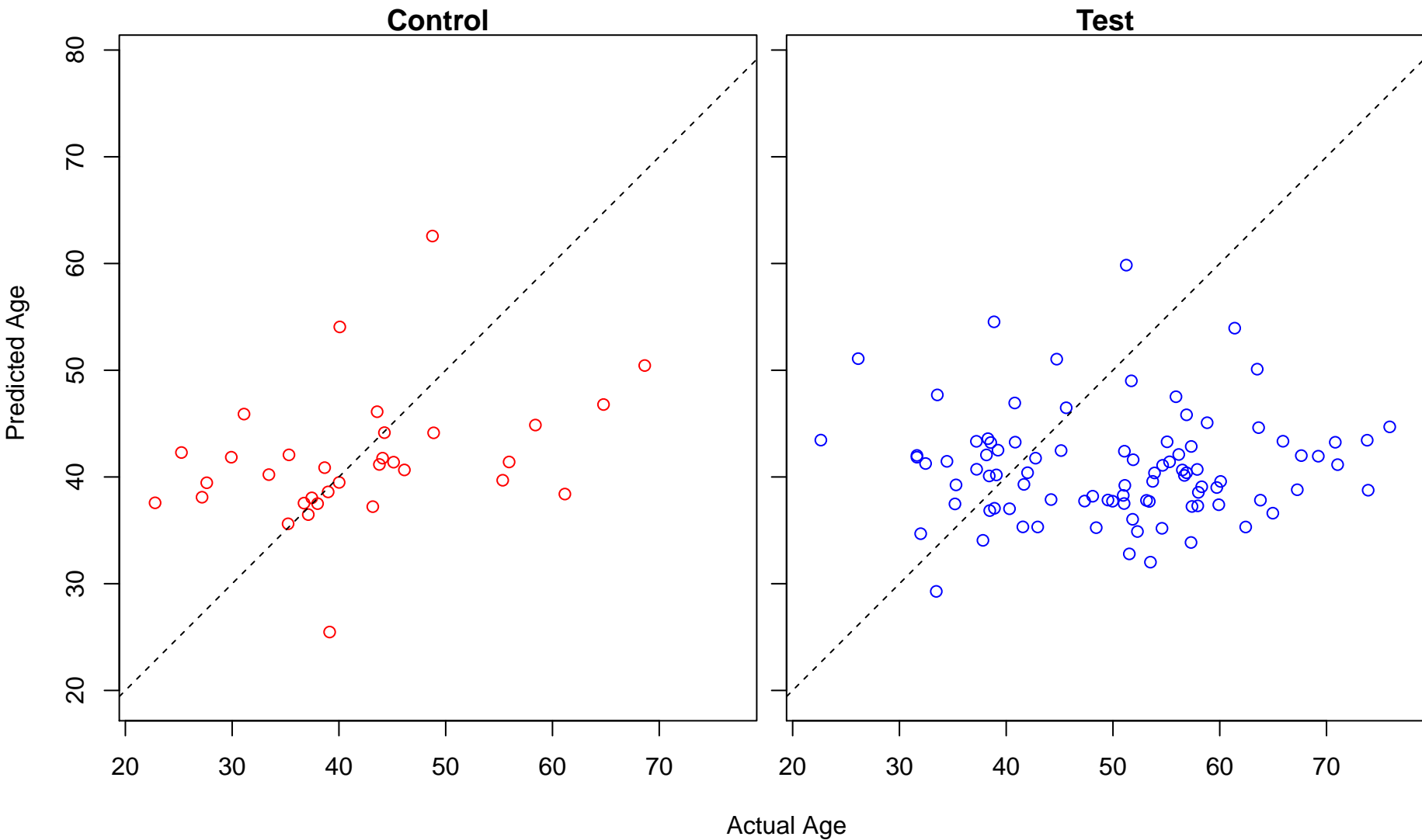
regulation of mitotic centrosome separation (Score: 0.497571)



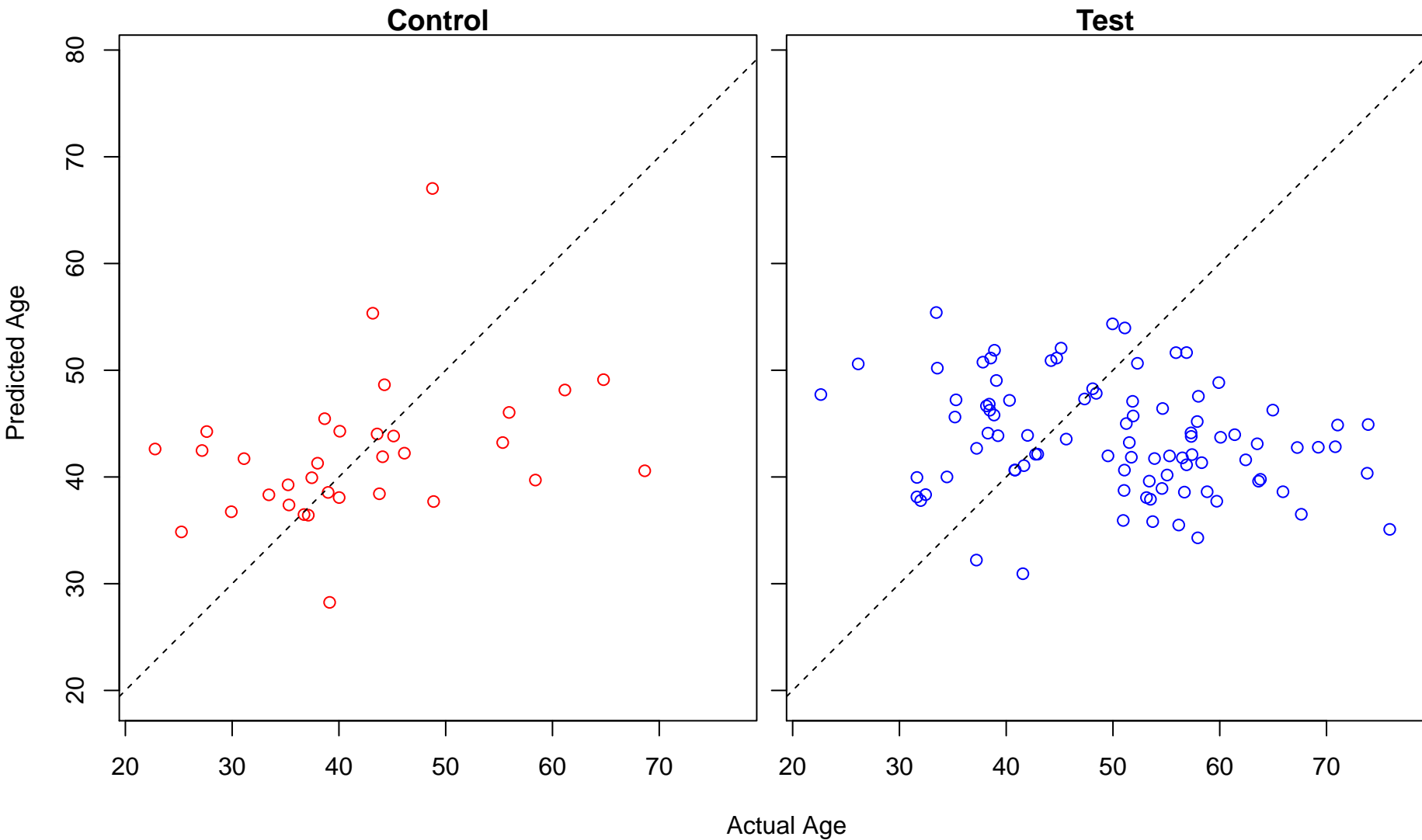
fatty acid beta-oxidation using acyl-CoA dehydrogenase (Score: 0.497397)



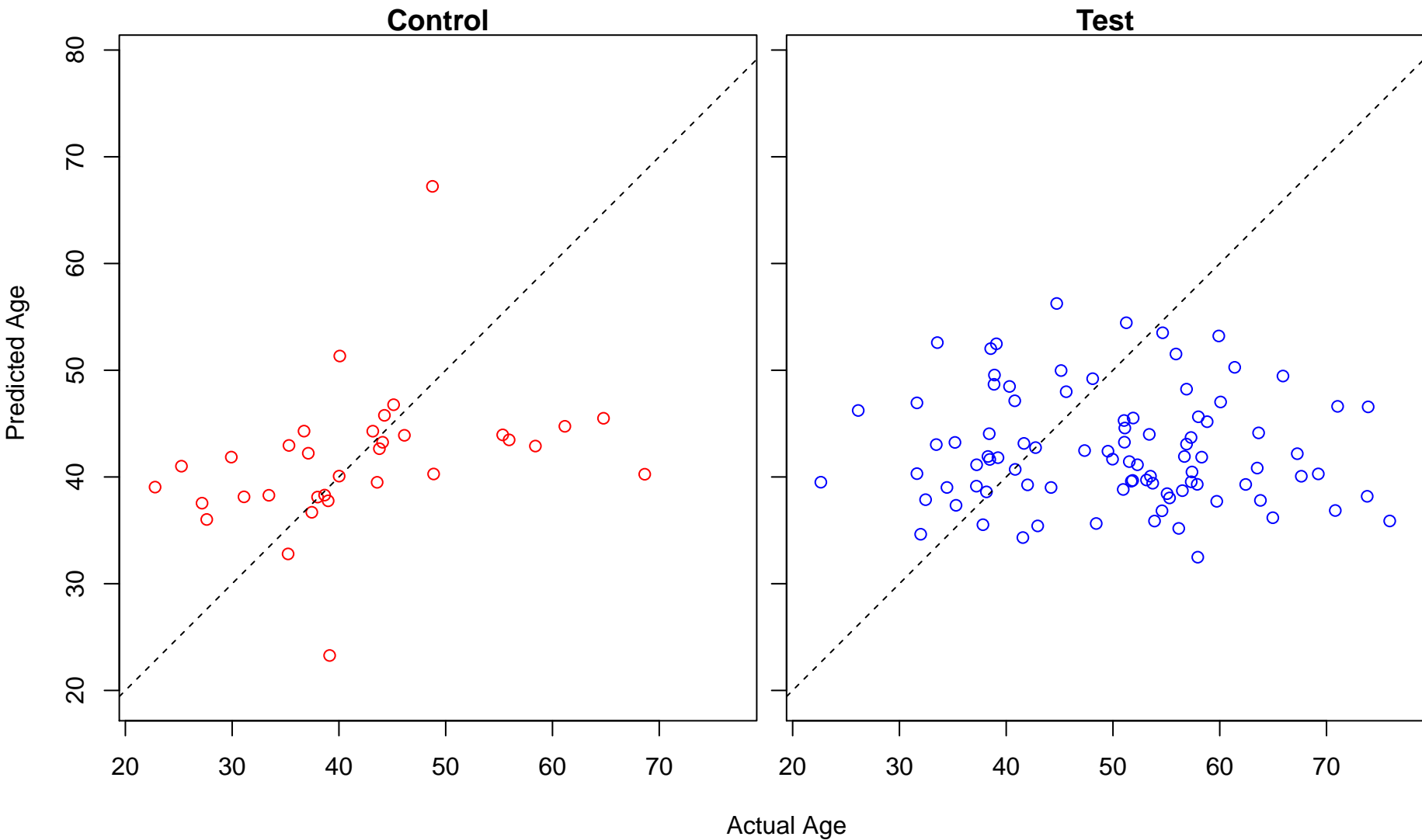
negative regulation of transcription from RNA polymerase III promoter (Score: 0.497374)



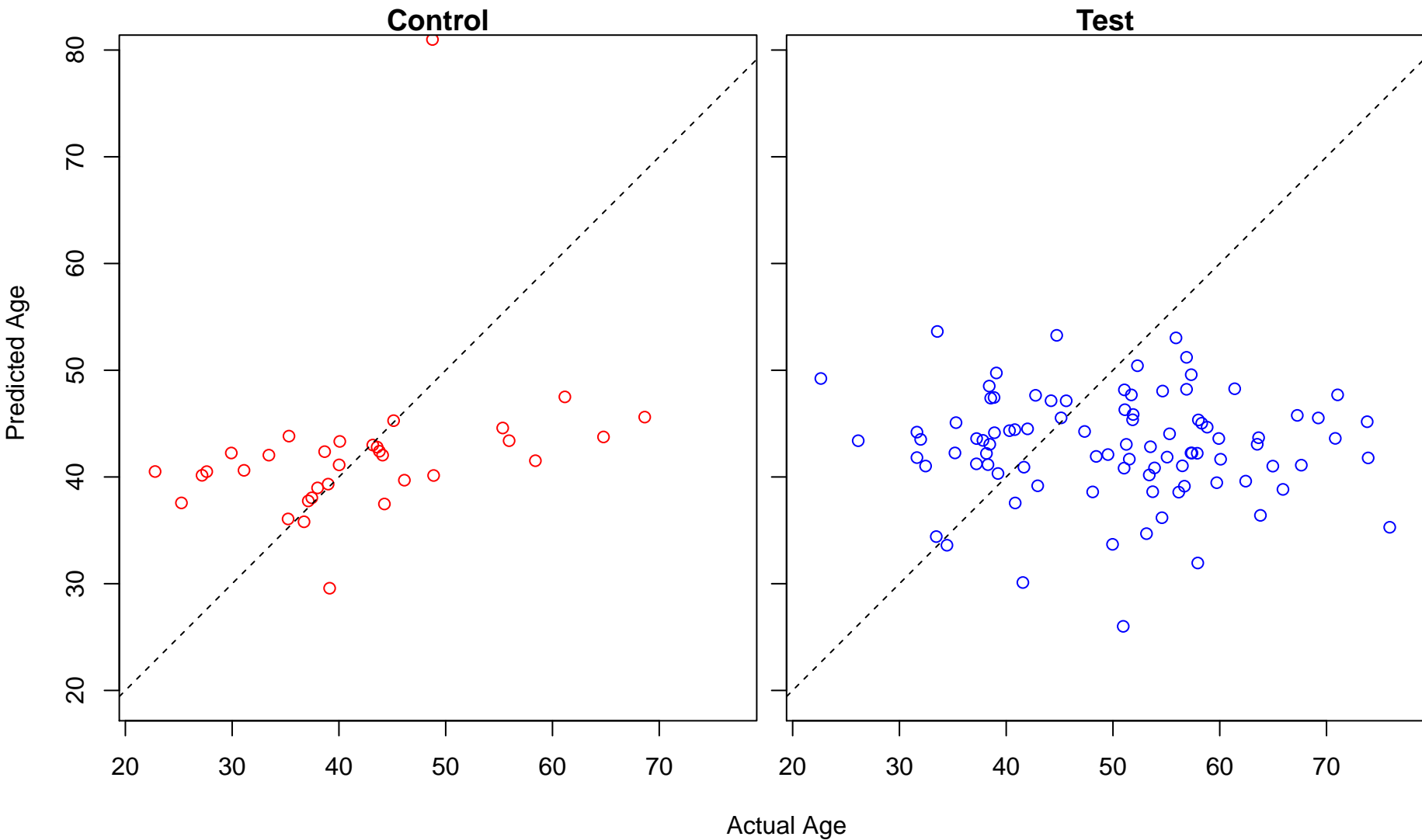
negative regulation of lipopolysaccharide-mediated signaling pathway (Score: 0.496366)



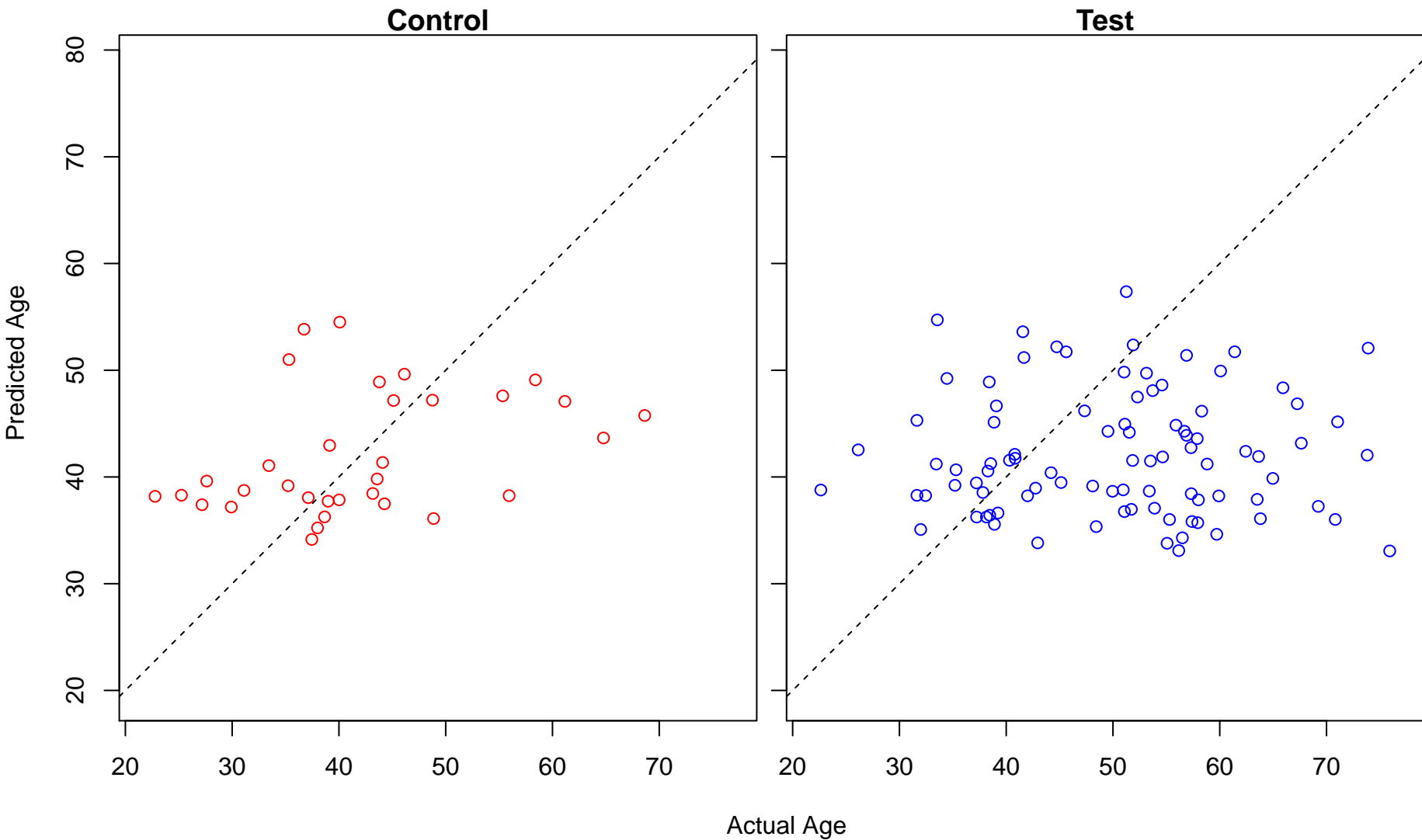
response to organic substance (Score: 0.496117)



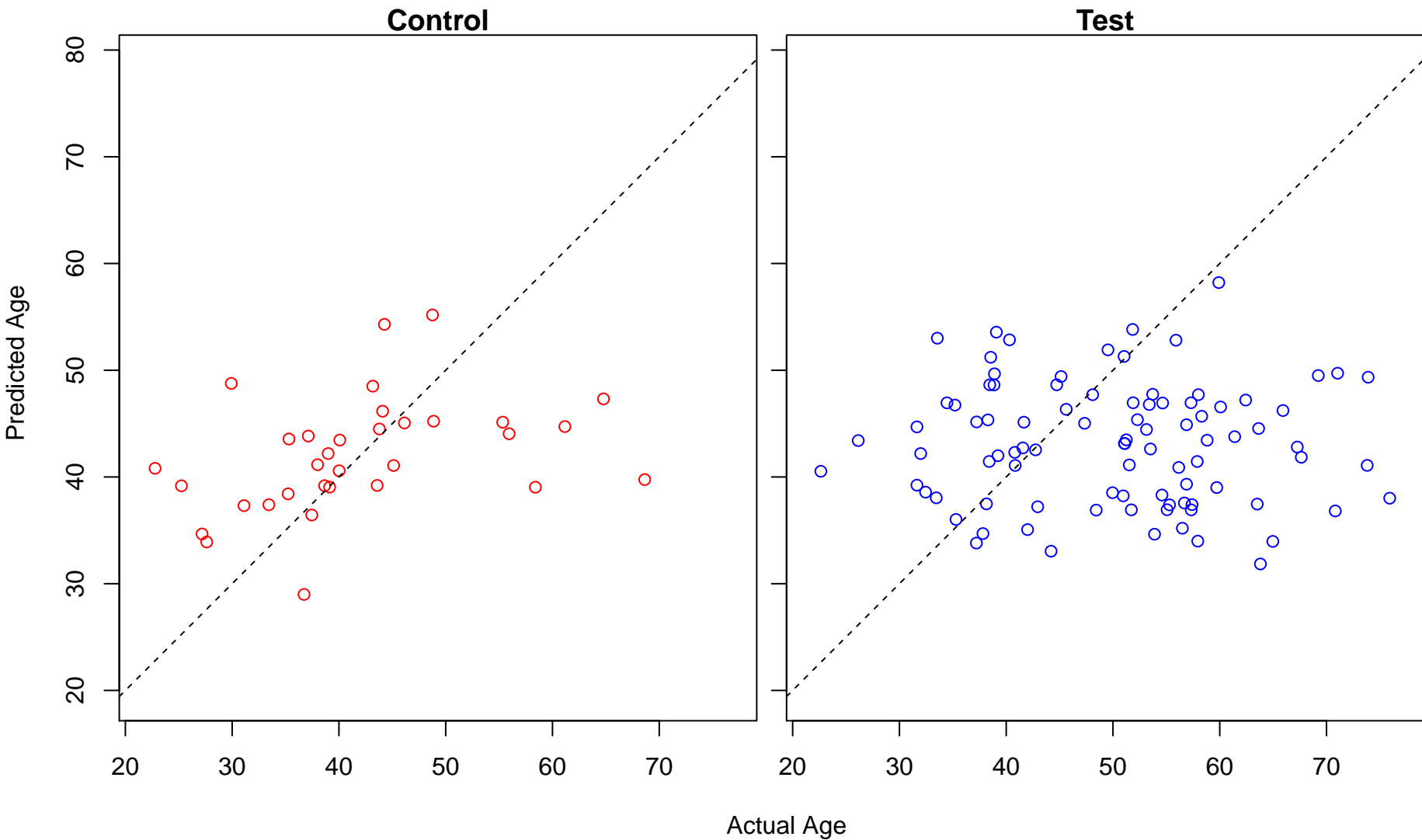
determination of adult lifespan (Score: 0.496109)



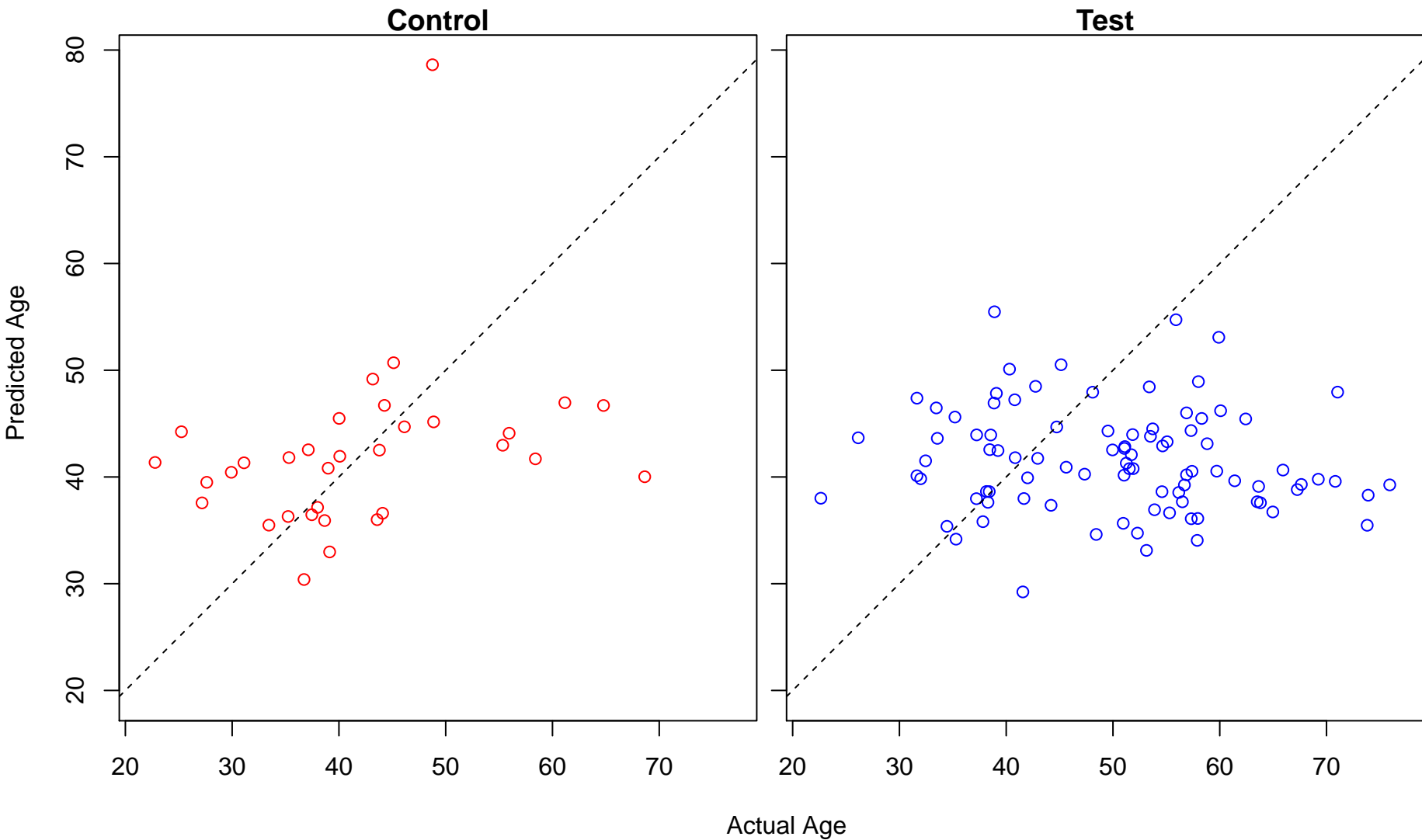
negative regulation of extracellular matrix disassembly (Score: 0.496008)



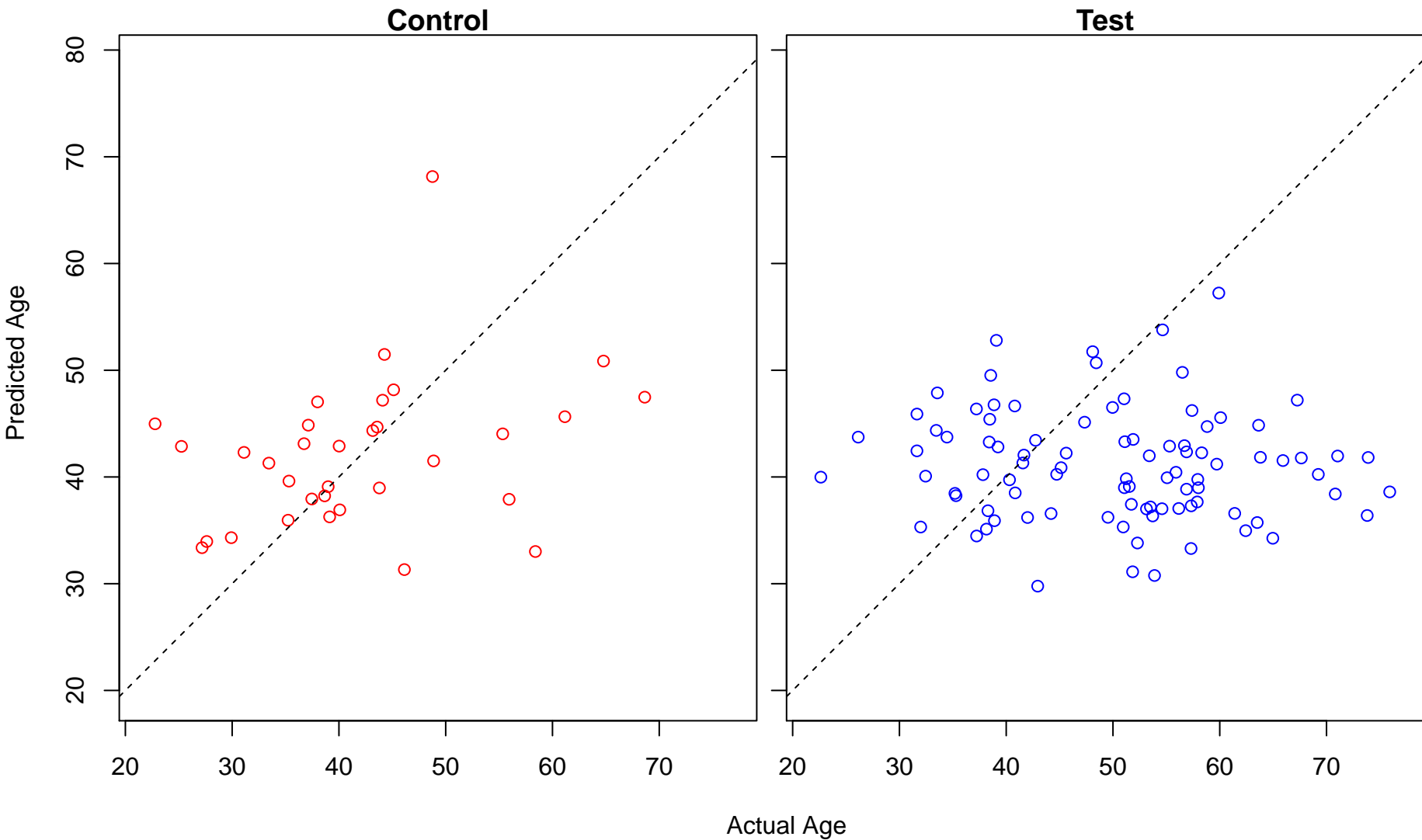
neuroblast division in subventricular zone (Score: 0.495769)



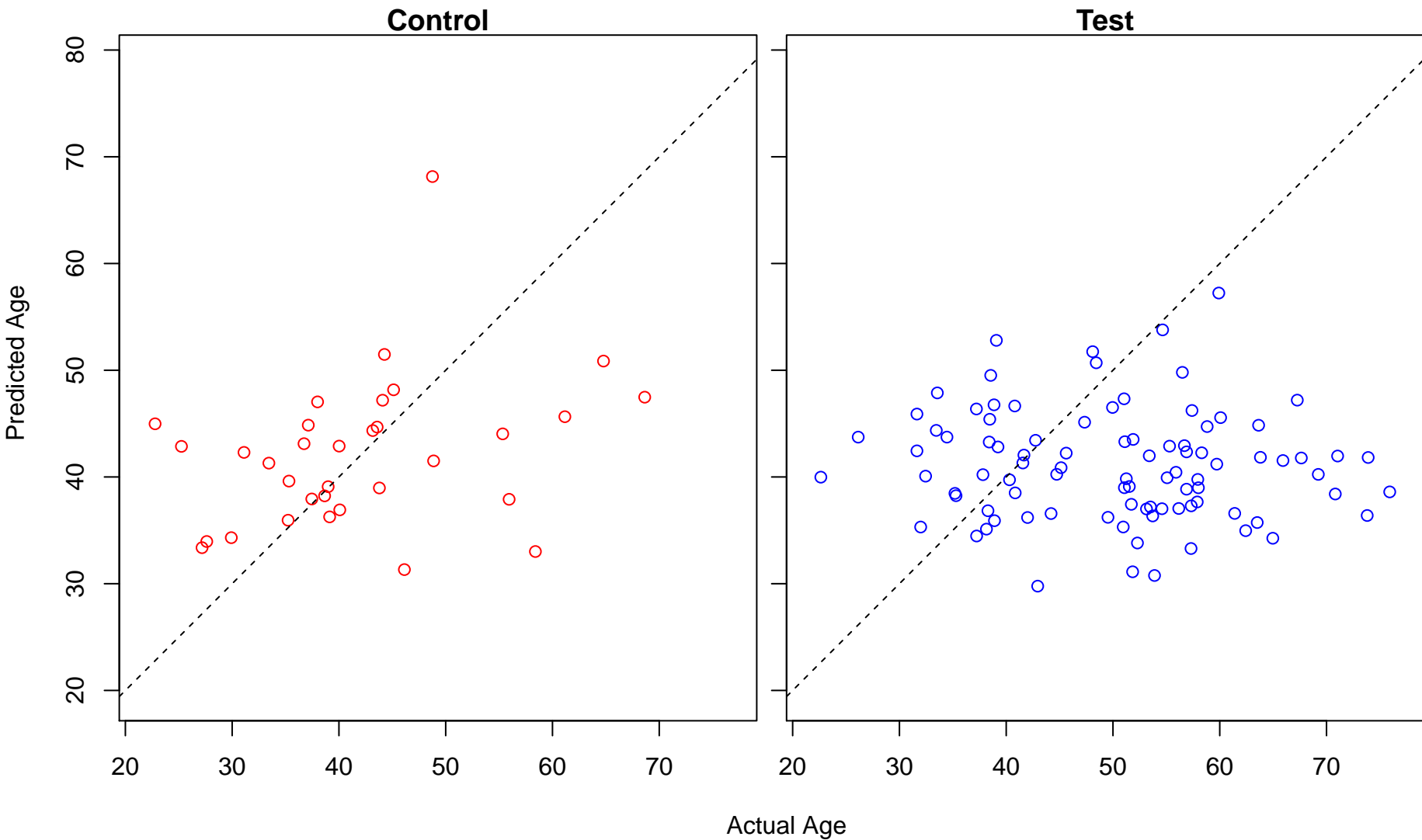
sperm capacitation (Score: 0.495075)



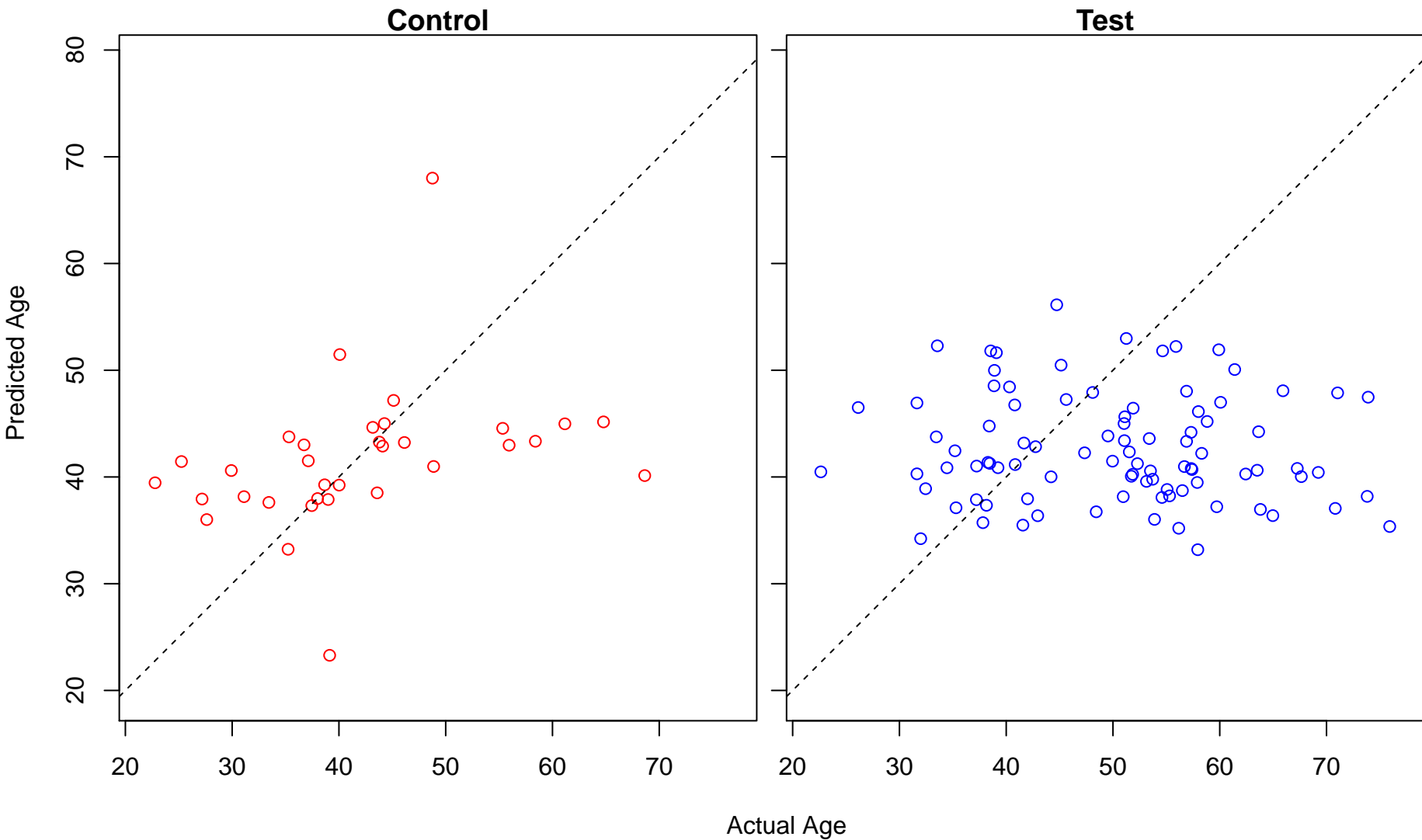
positive regulation of B cell mediated immunity (Score: 0.494735)



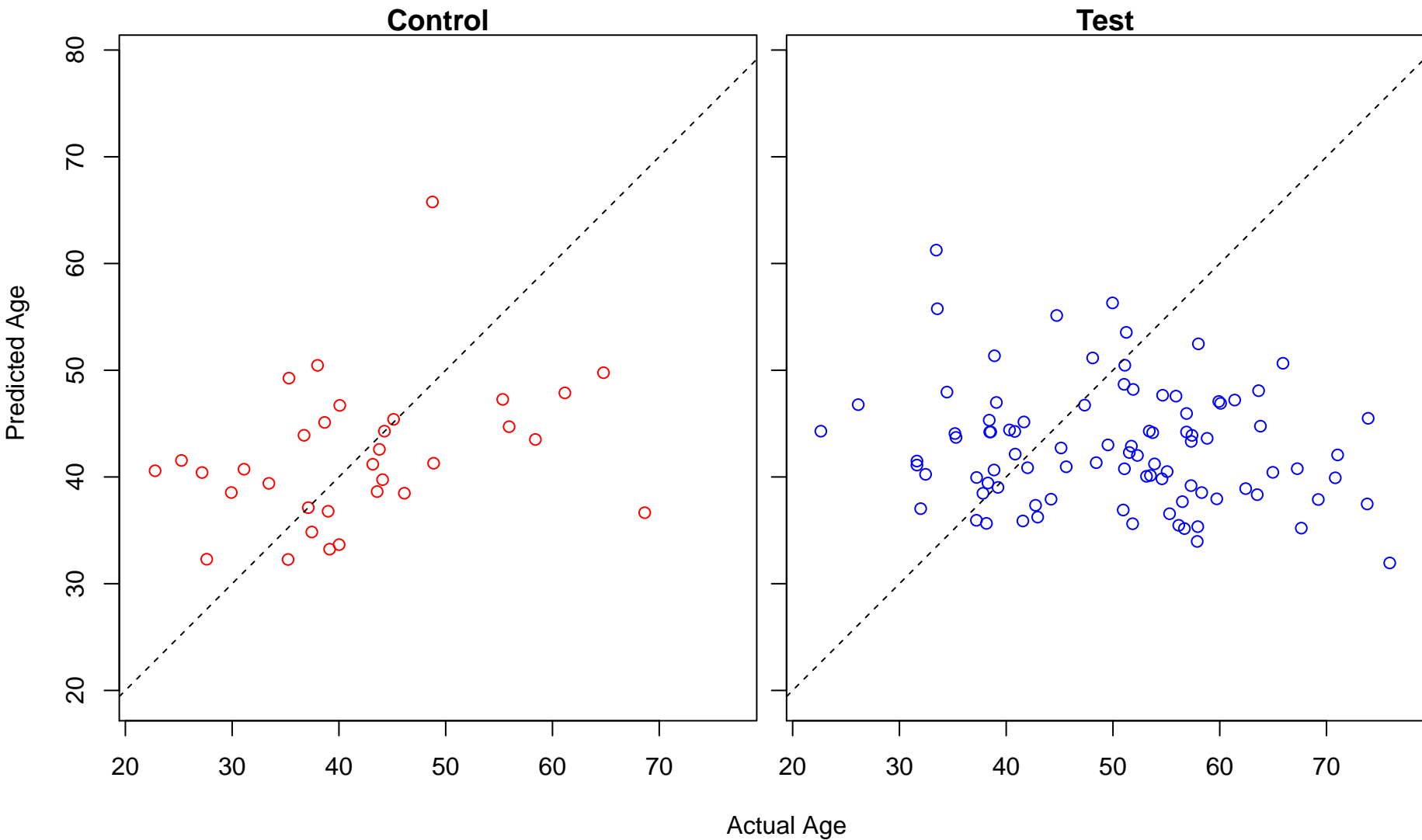
positive regulation of immunoglobulin mediated immune response (Score: 0.494735)



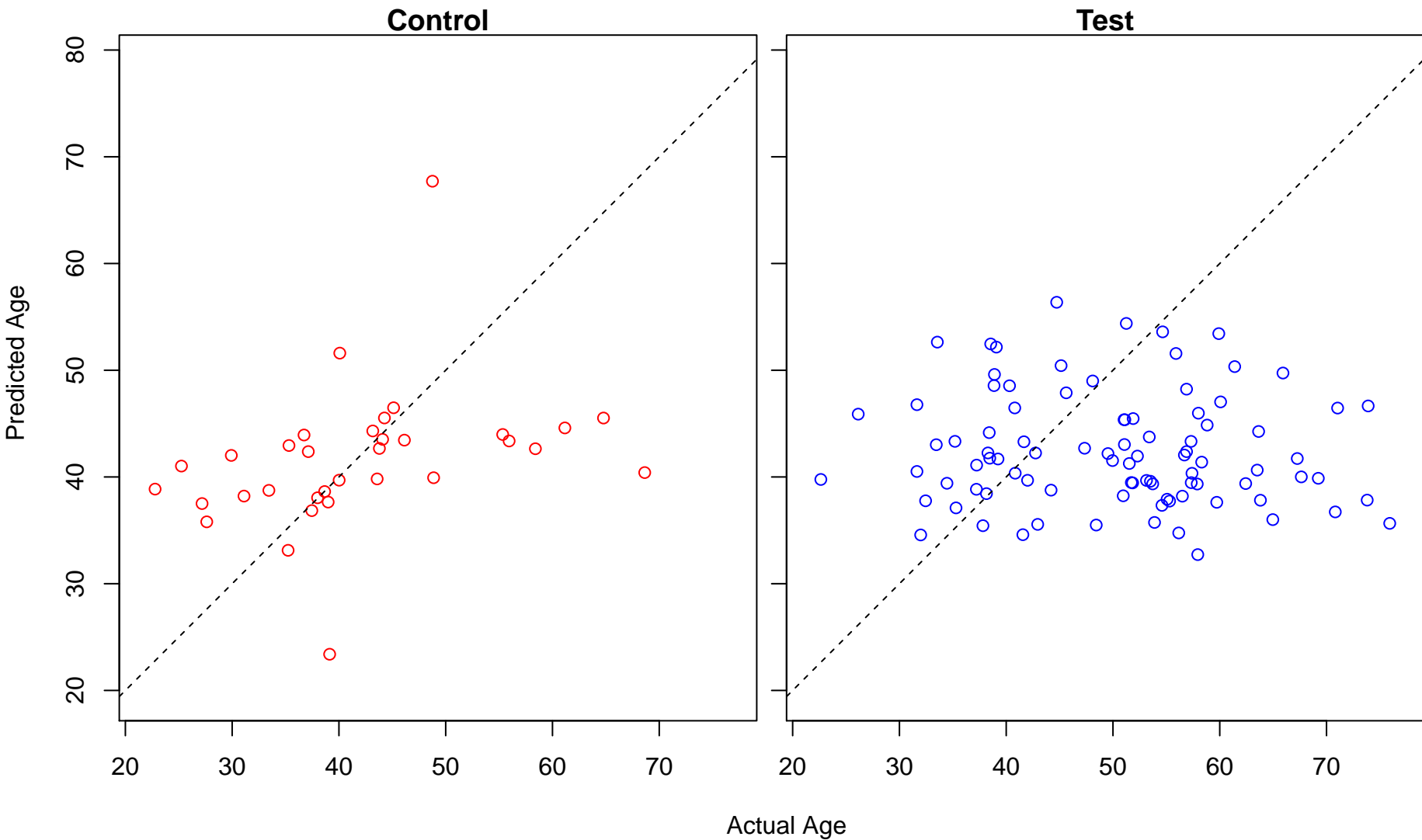
cell surface receptor signaling pathway (Score: 0.494608)



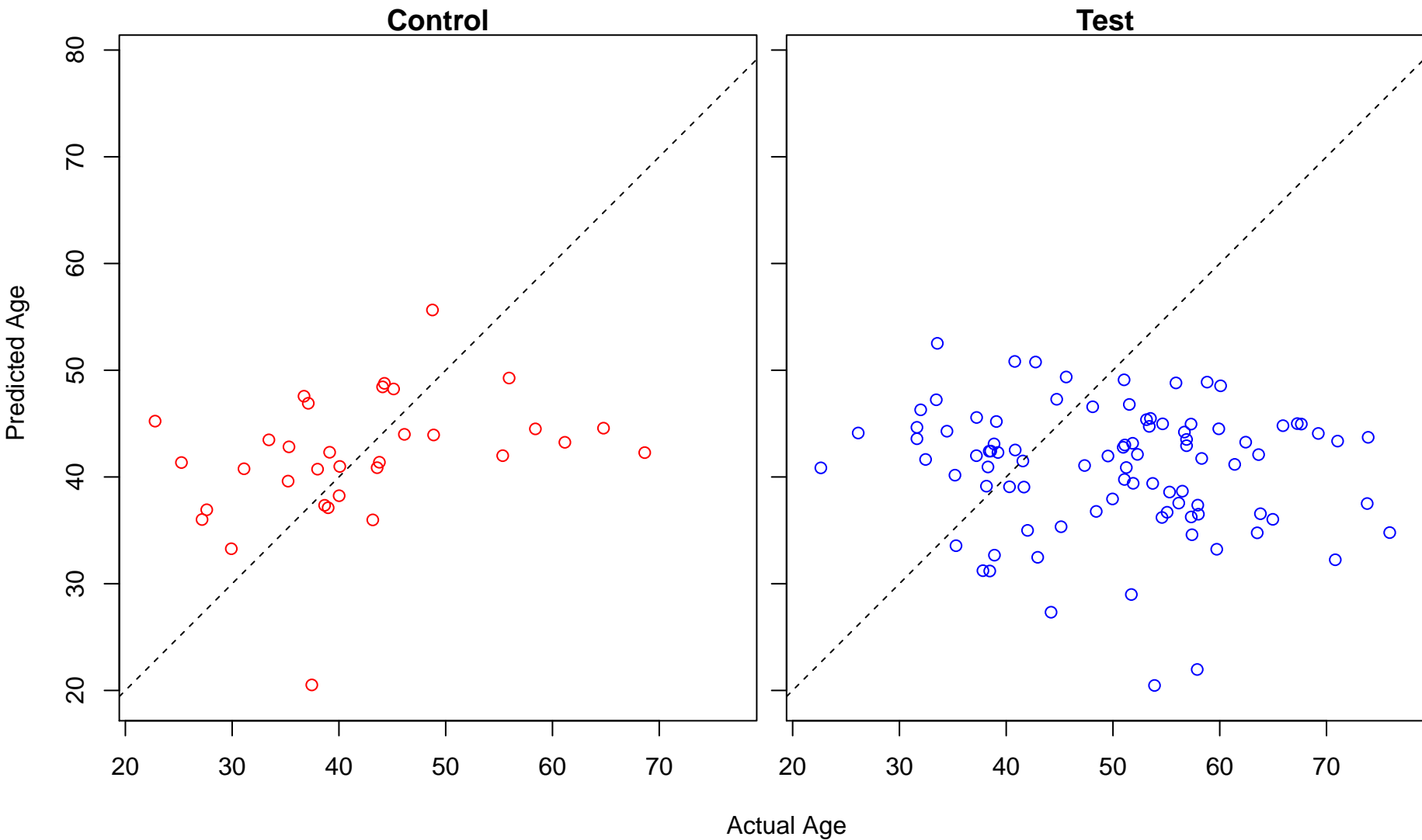
positive regulation of p38MAPK cascade (Score: 0.492389)



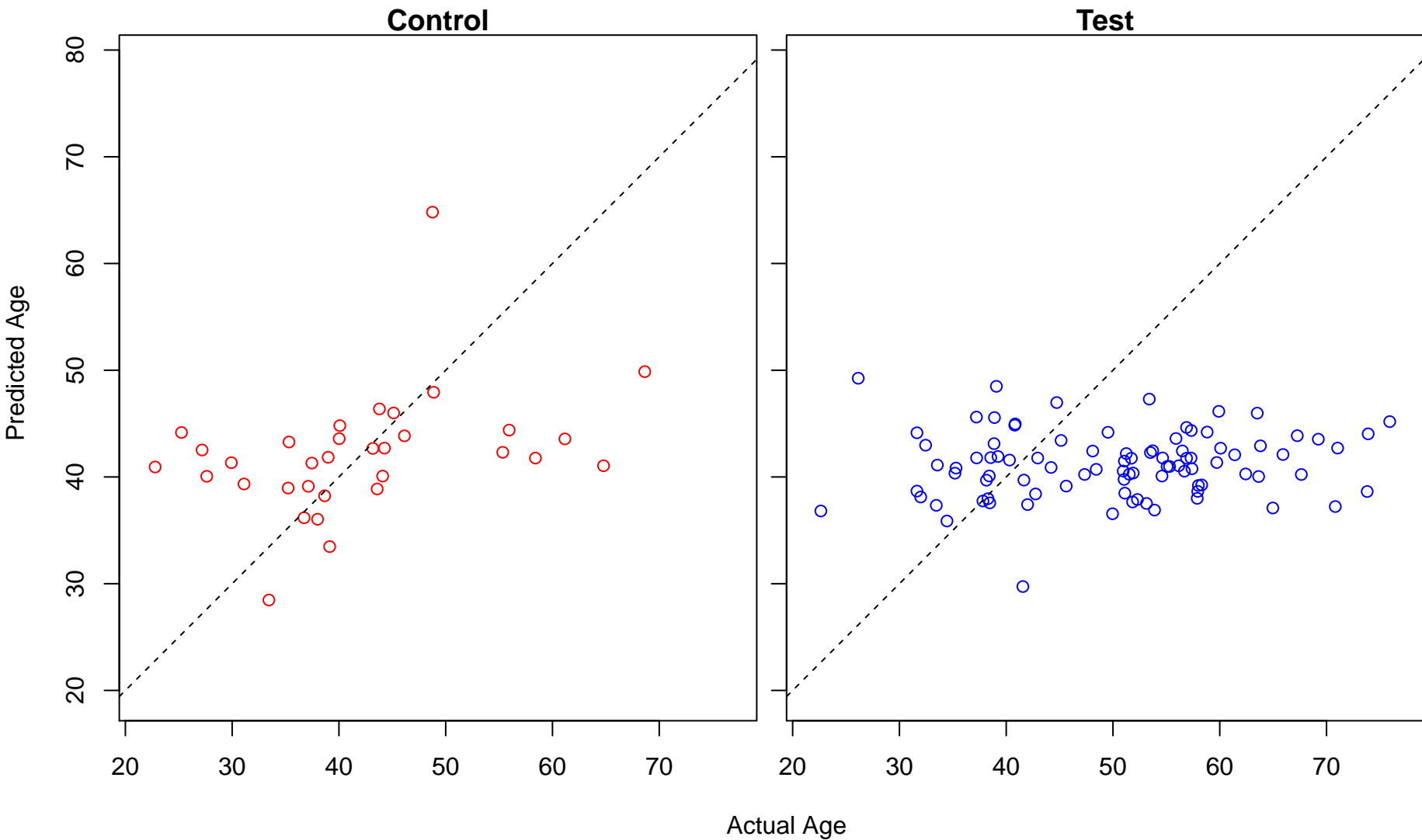
cellular response to organic substance (Score: 0.491882)



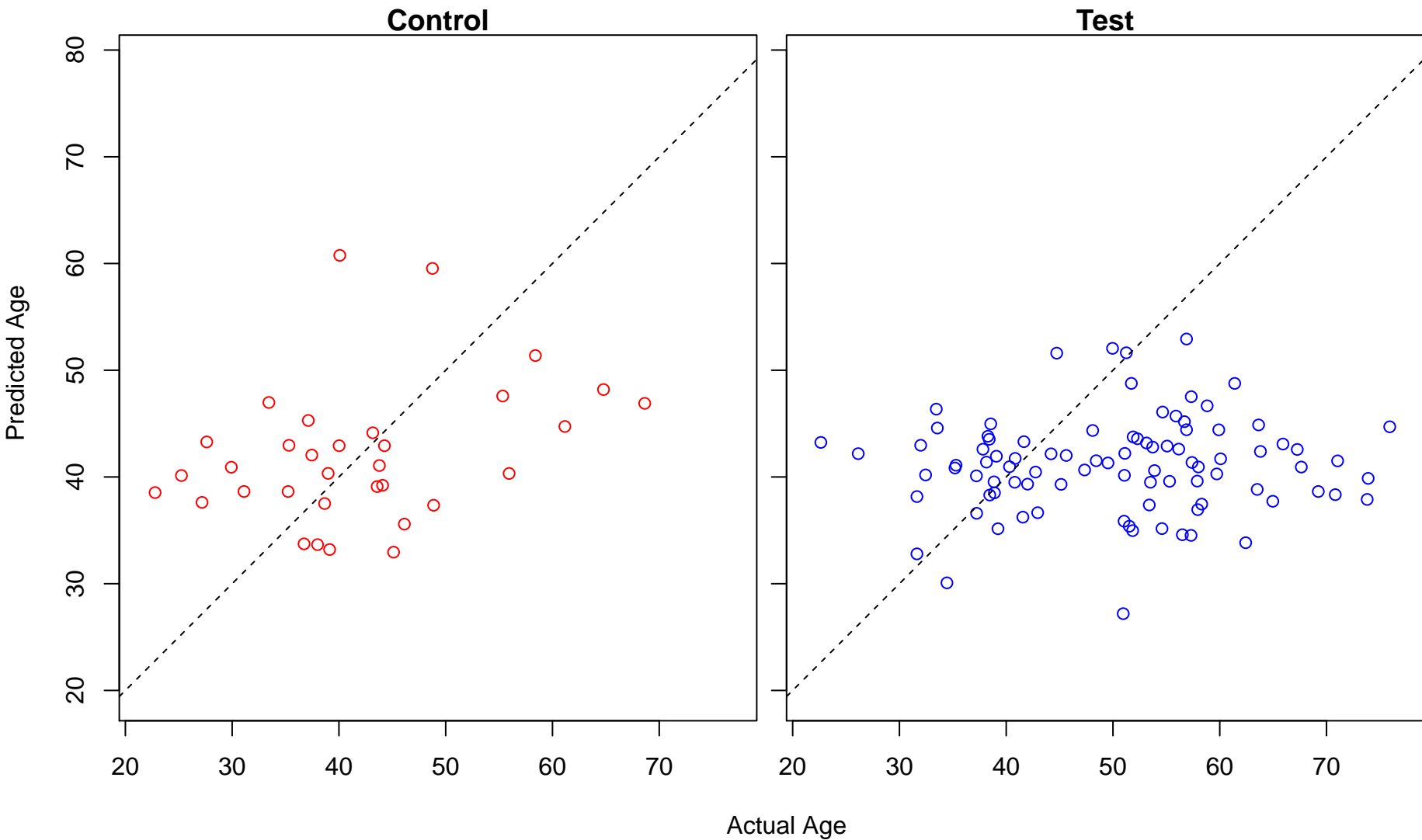
regulation of adrenergic receptor signaling pathway (Score: 0.491526)



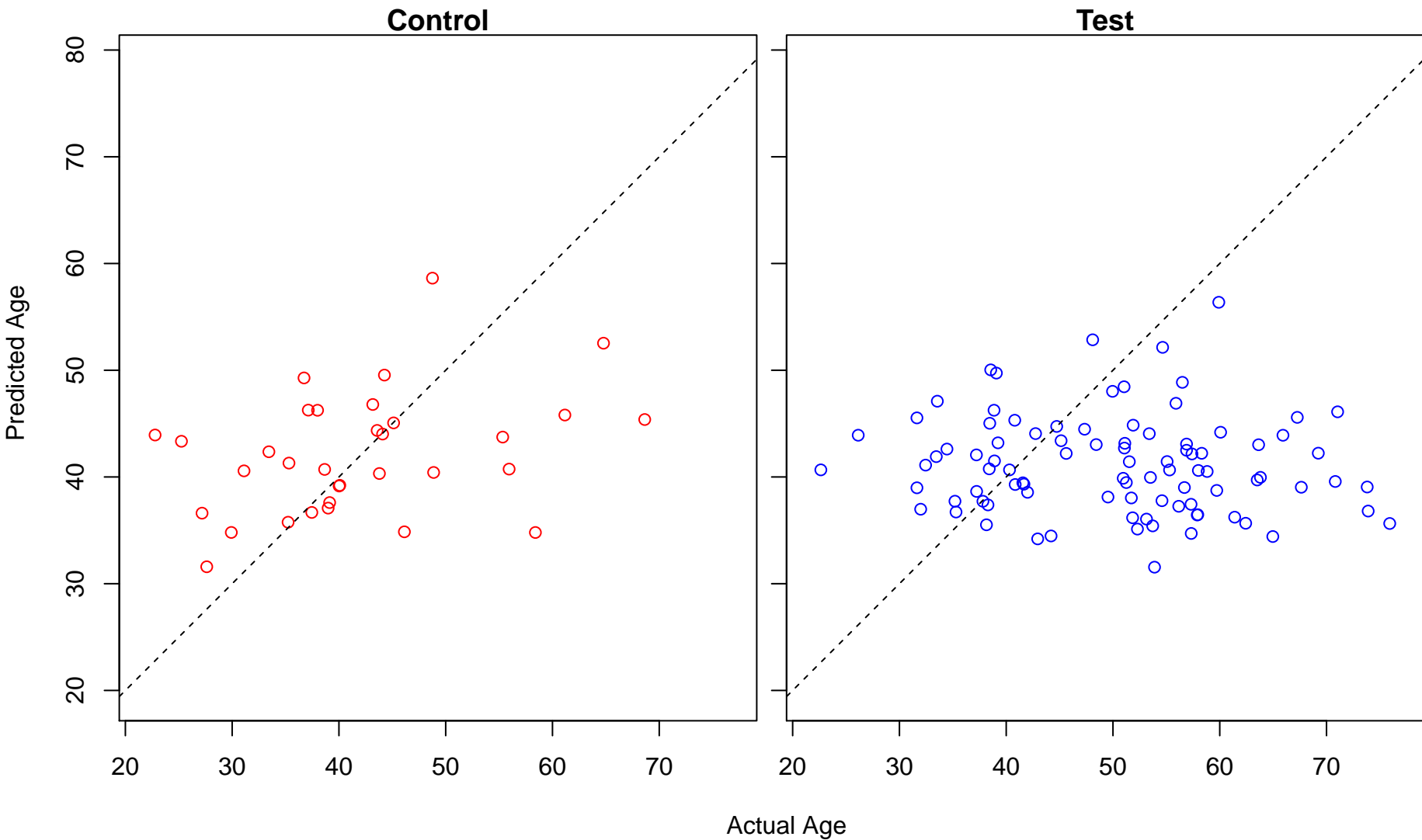
positive regulation of ligand-dependent nuclear receptor transcription coactivator activity (Score: 0.49)



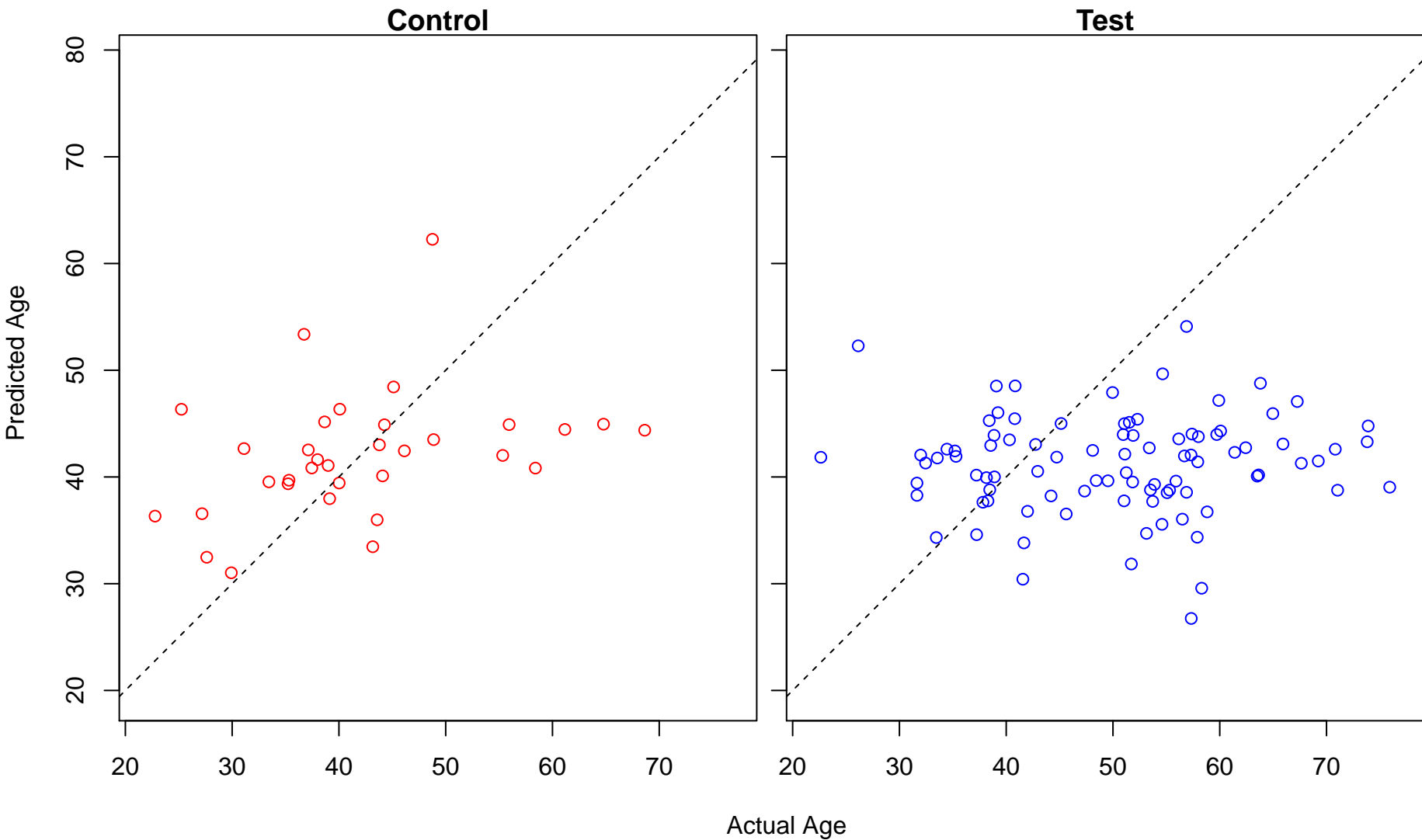
oxidative single-stranded DNA demethylation (Score: 0.490381)



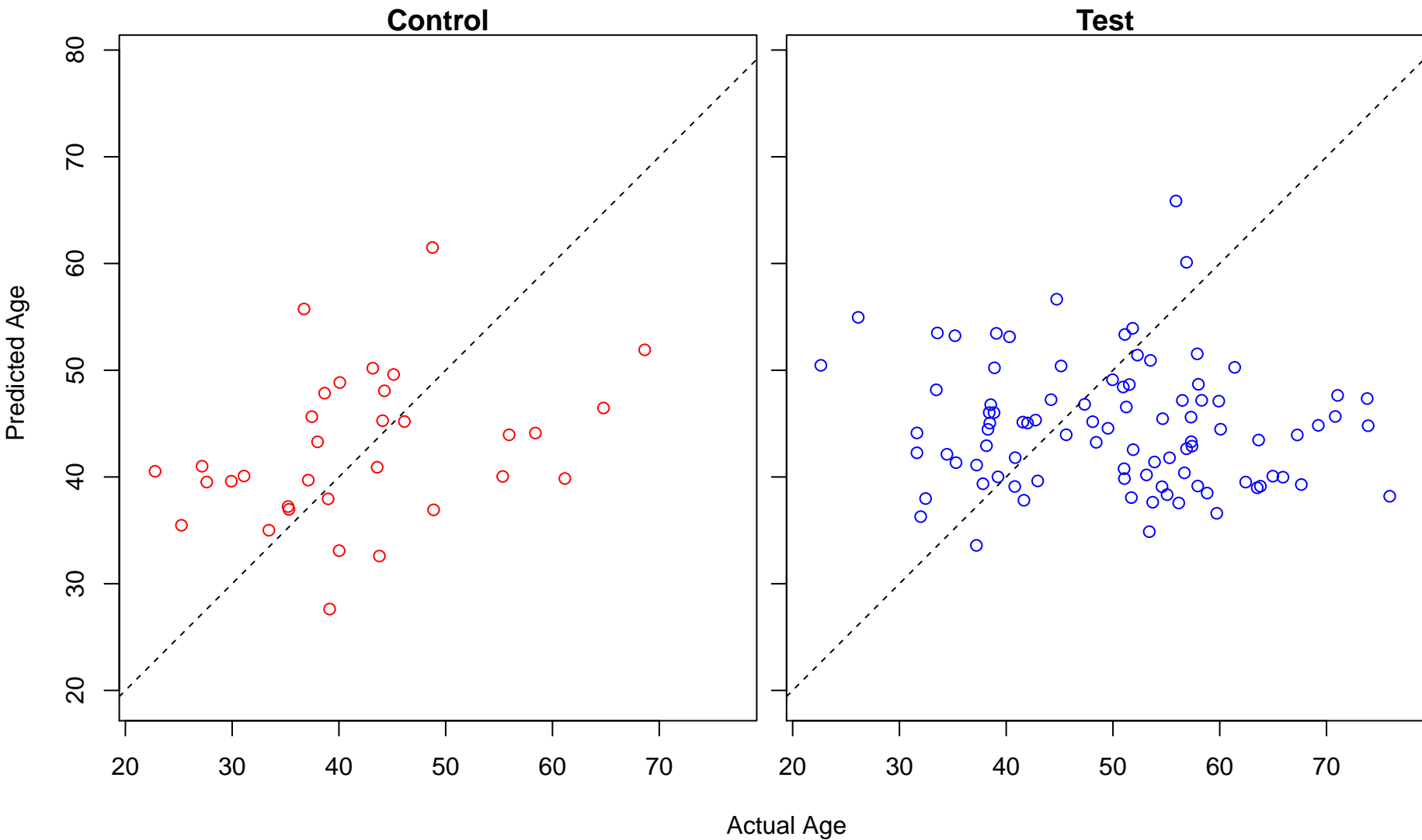
regulation of isotype switching (Score: 0.489959)



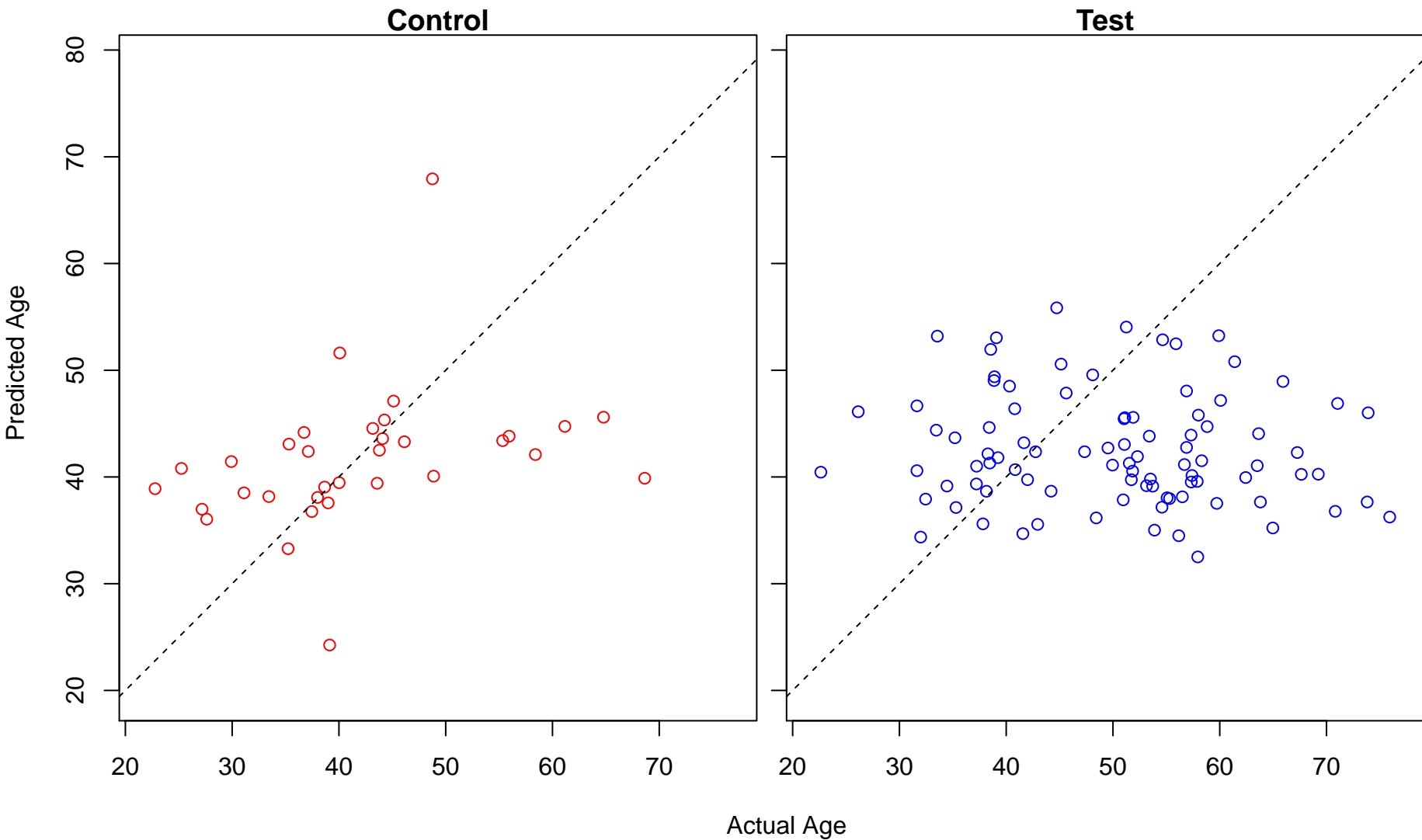
retinoic acid receptor signaling pathway (Score: 0.488936)



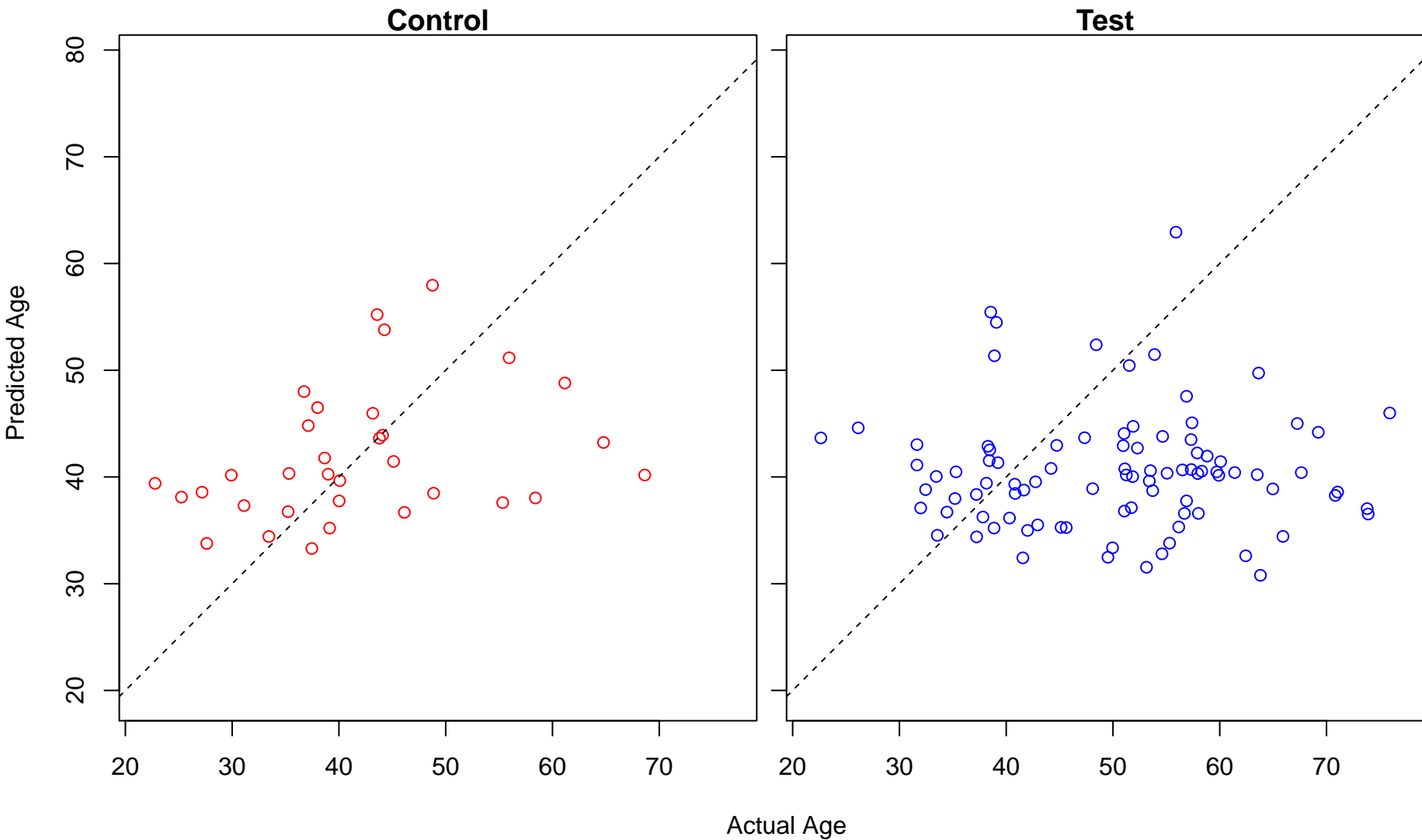
protein retention in ER lumen (Score: 0.487114)



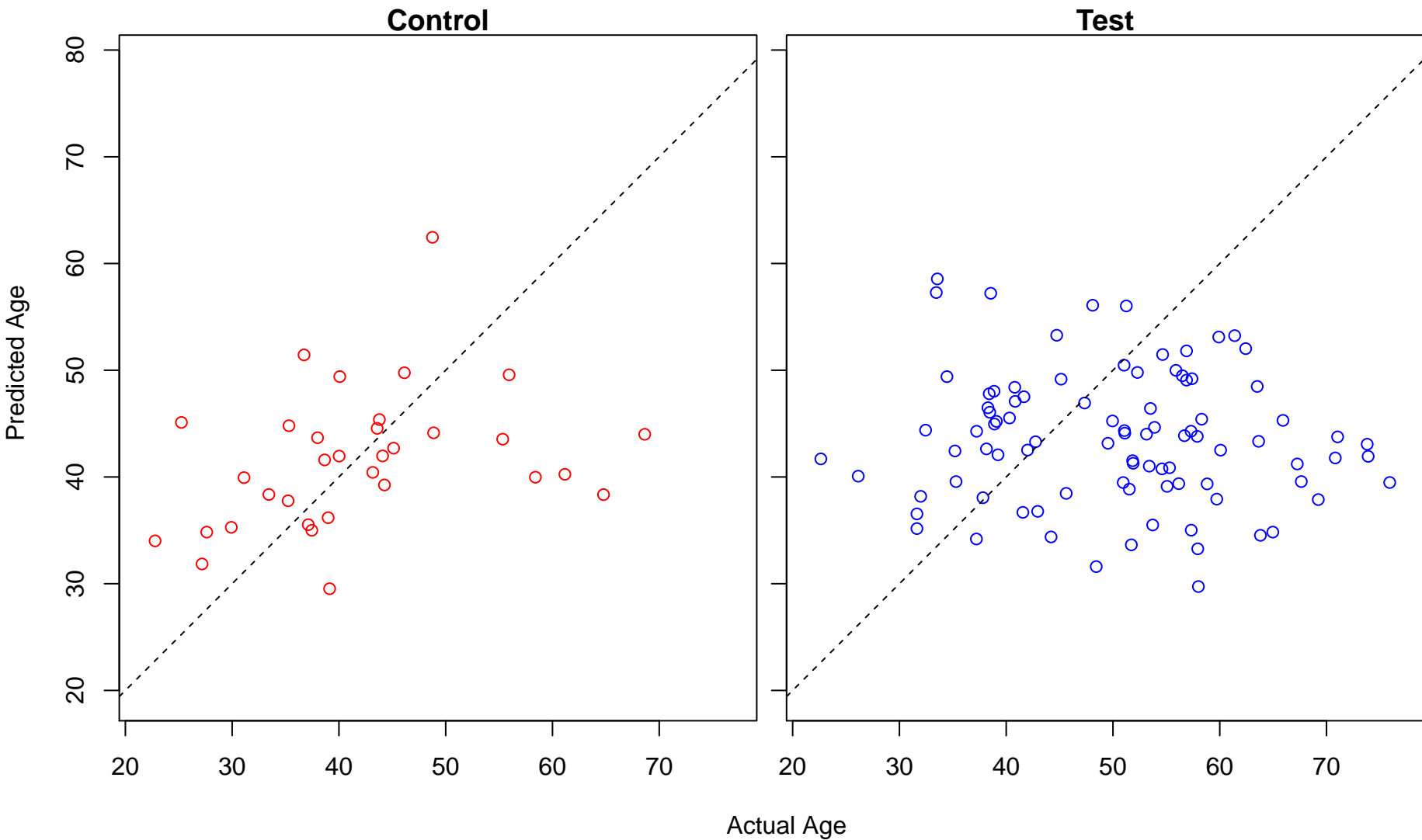
cellular response to chemical stimulus (Score: 0.485948)



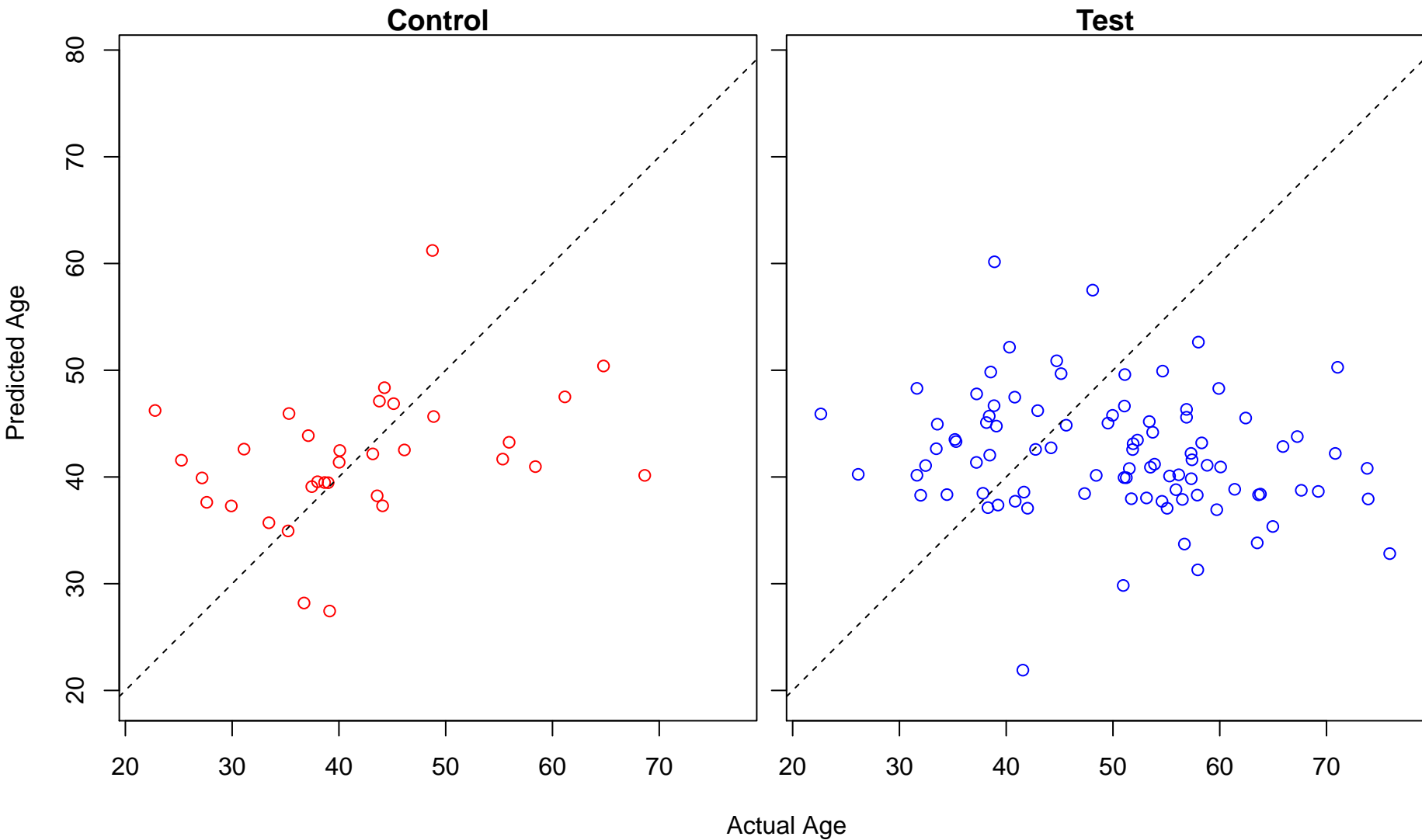
regulation of keratinocyte proliferation (Score: 0.484137)



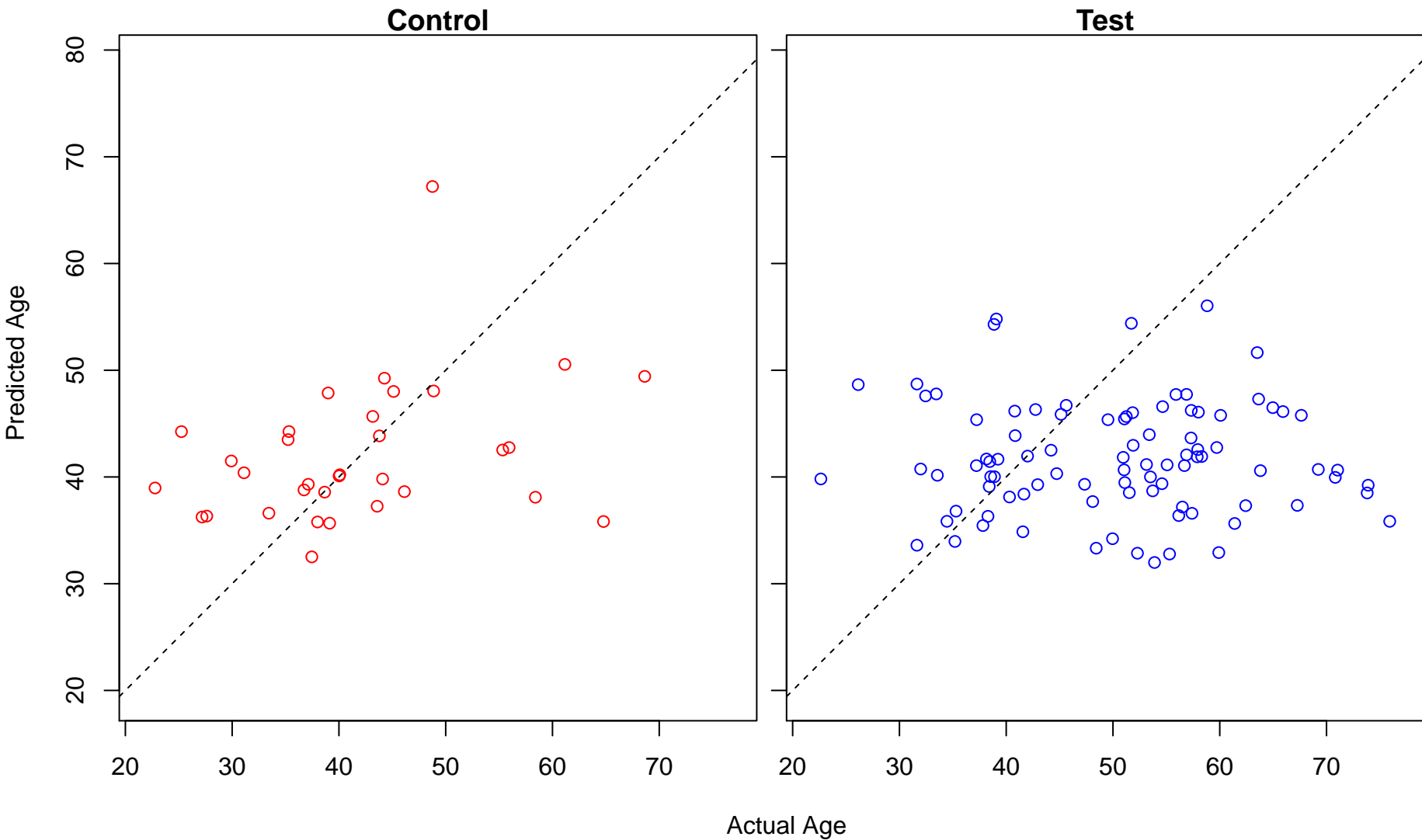
reproduction (Score: 0.48396)



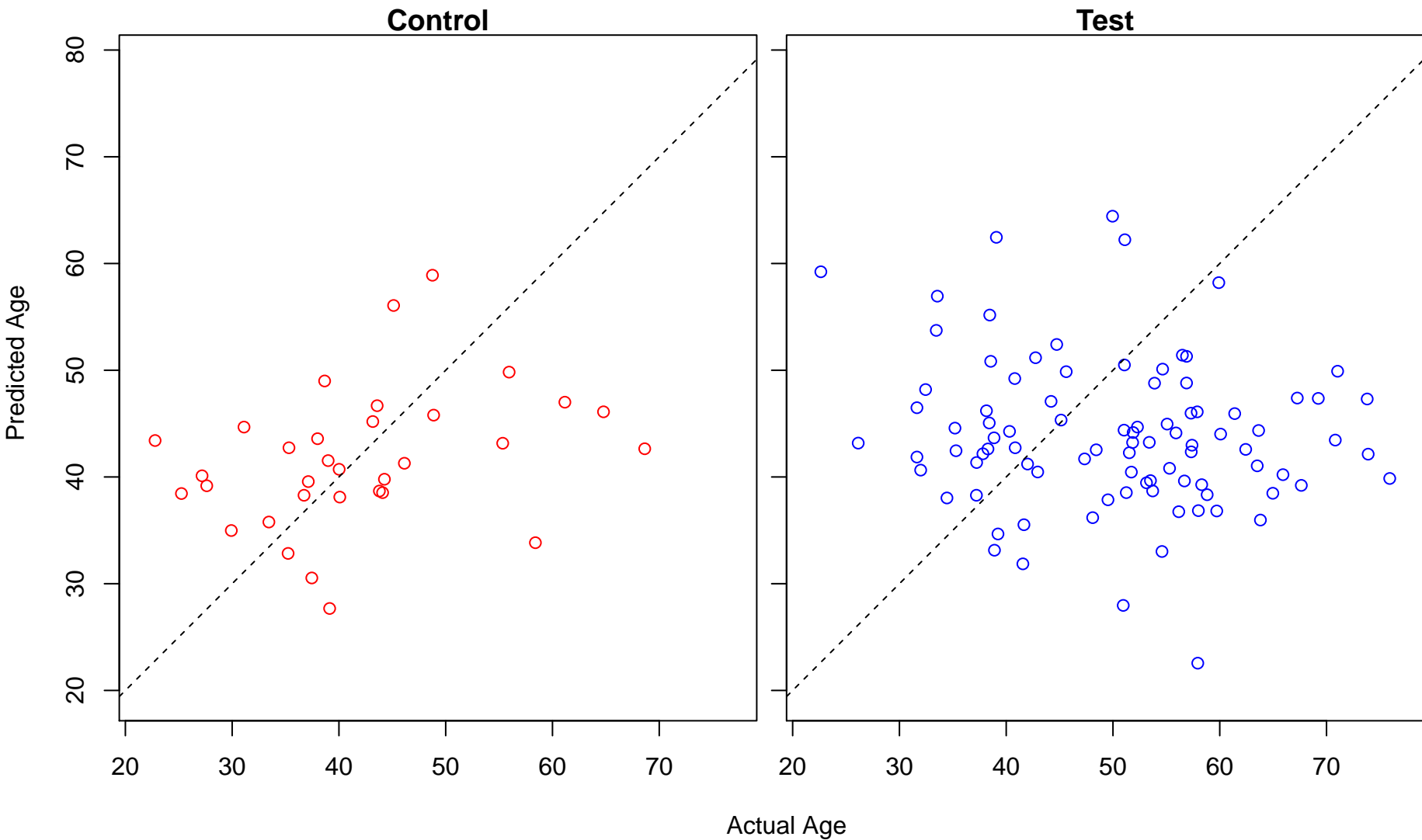
positive regulation of protein localization to cell surface (Score: 0.482659)



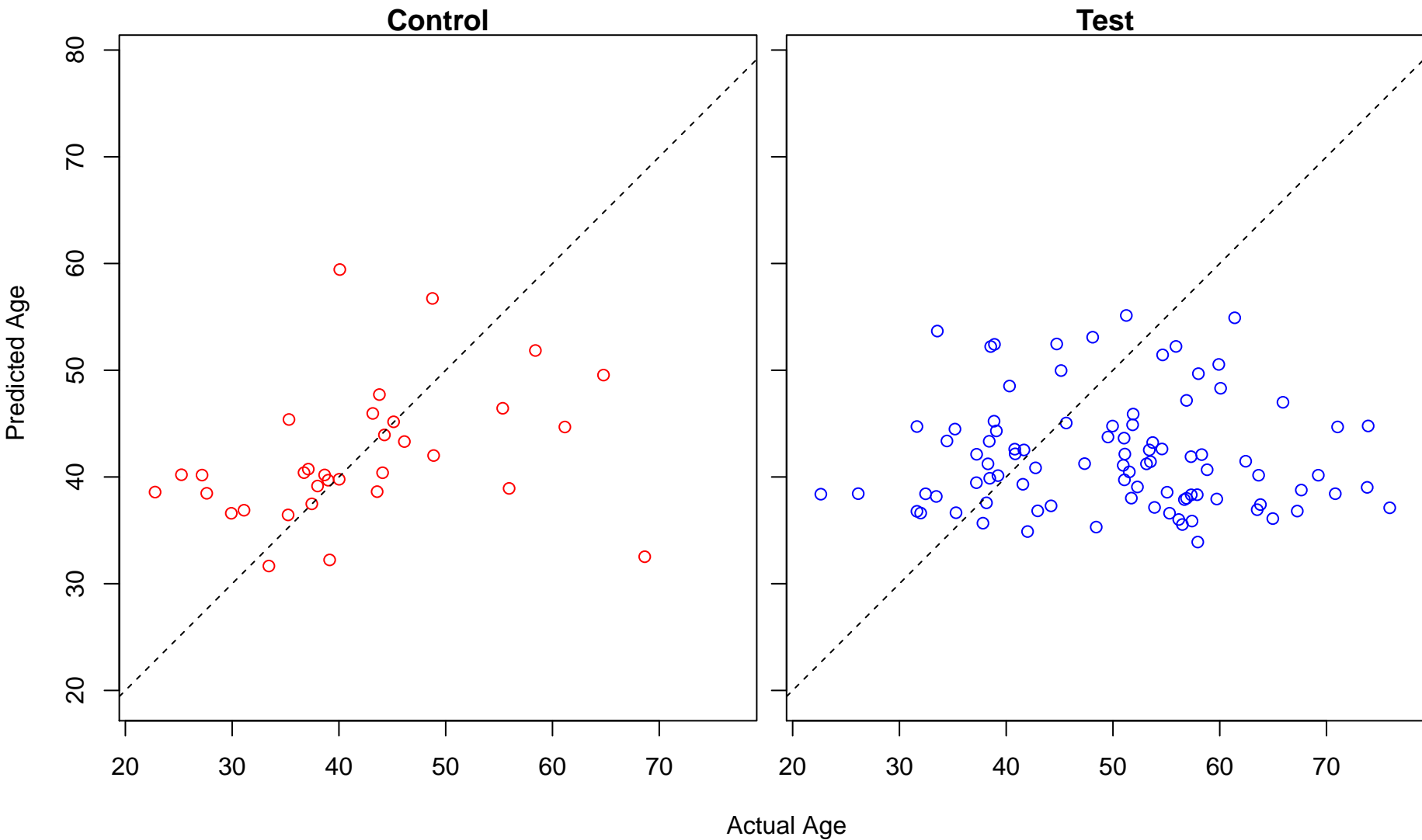
myotube cell development (Score: 0.481471)



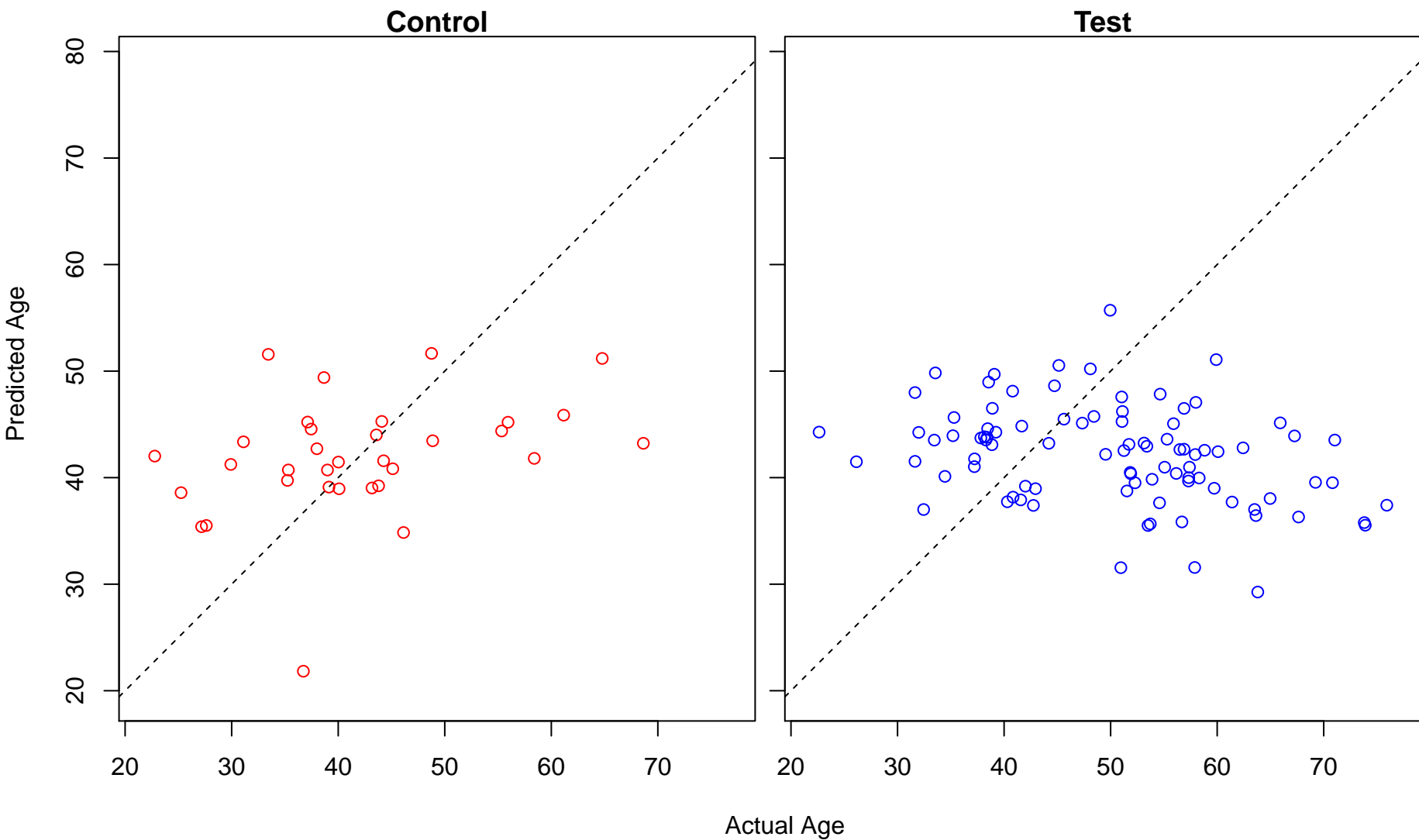
copper ion transmembrane transport (Score: 0.481410)



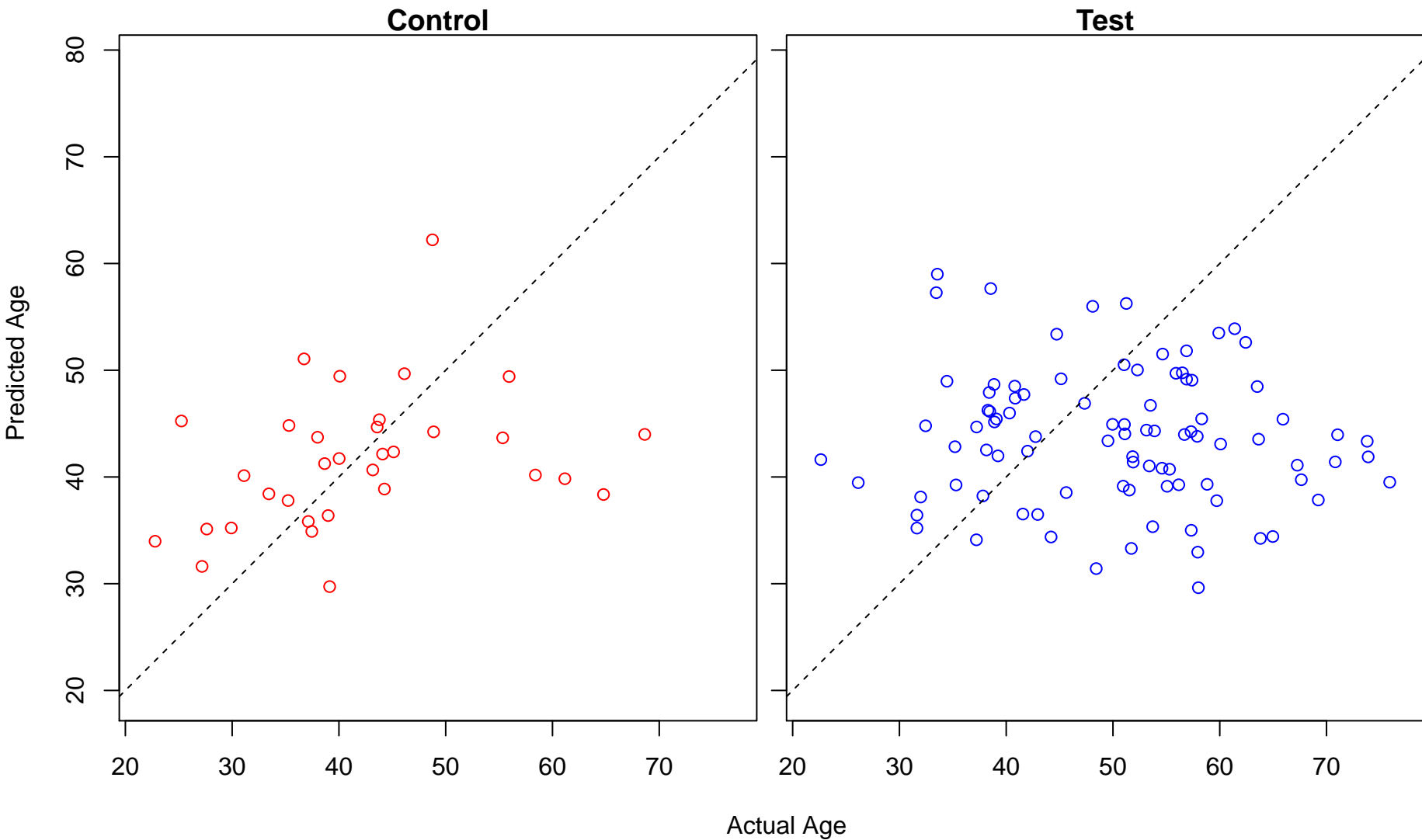
Golgi localization (Score: 0.479672)



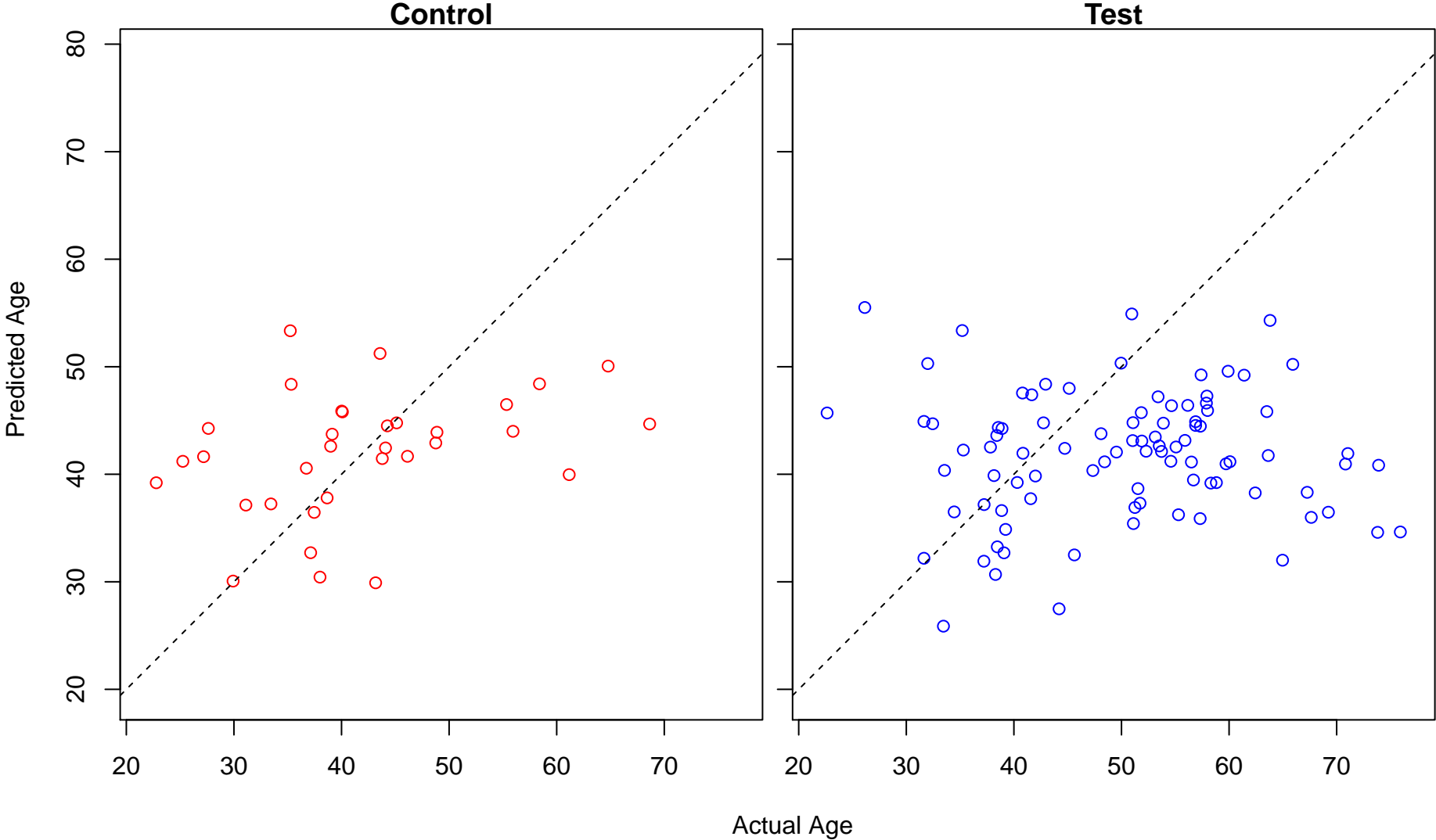
peptidyl-proline hydroxylation to 4-hydroxy-L-proline (Score: 0.478236)



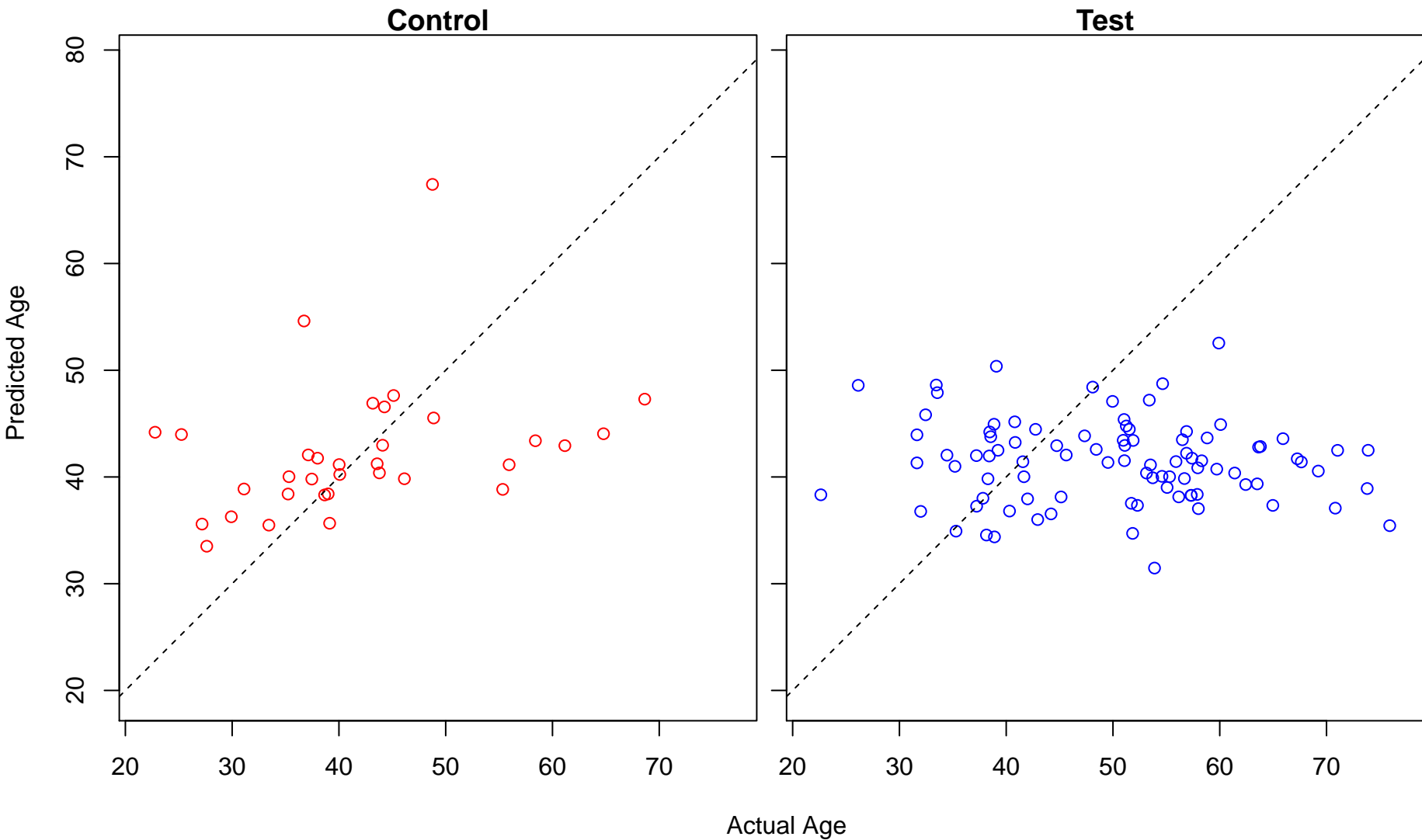
reproductive process (Score: 0.477609)



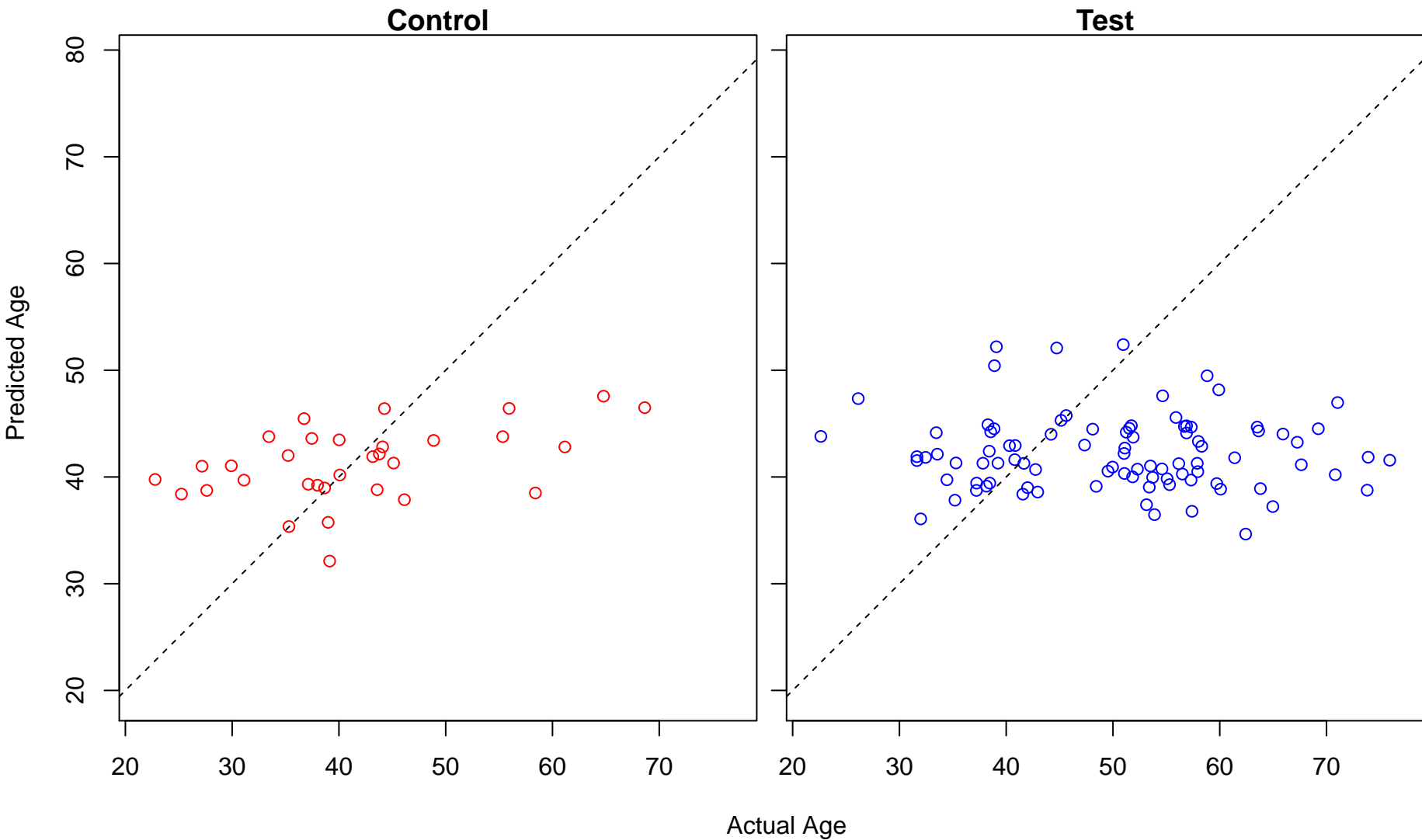
regulation of atrial cardiac muscle cell membrane repolarization (Score: 0.477371)



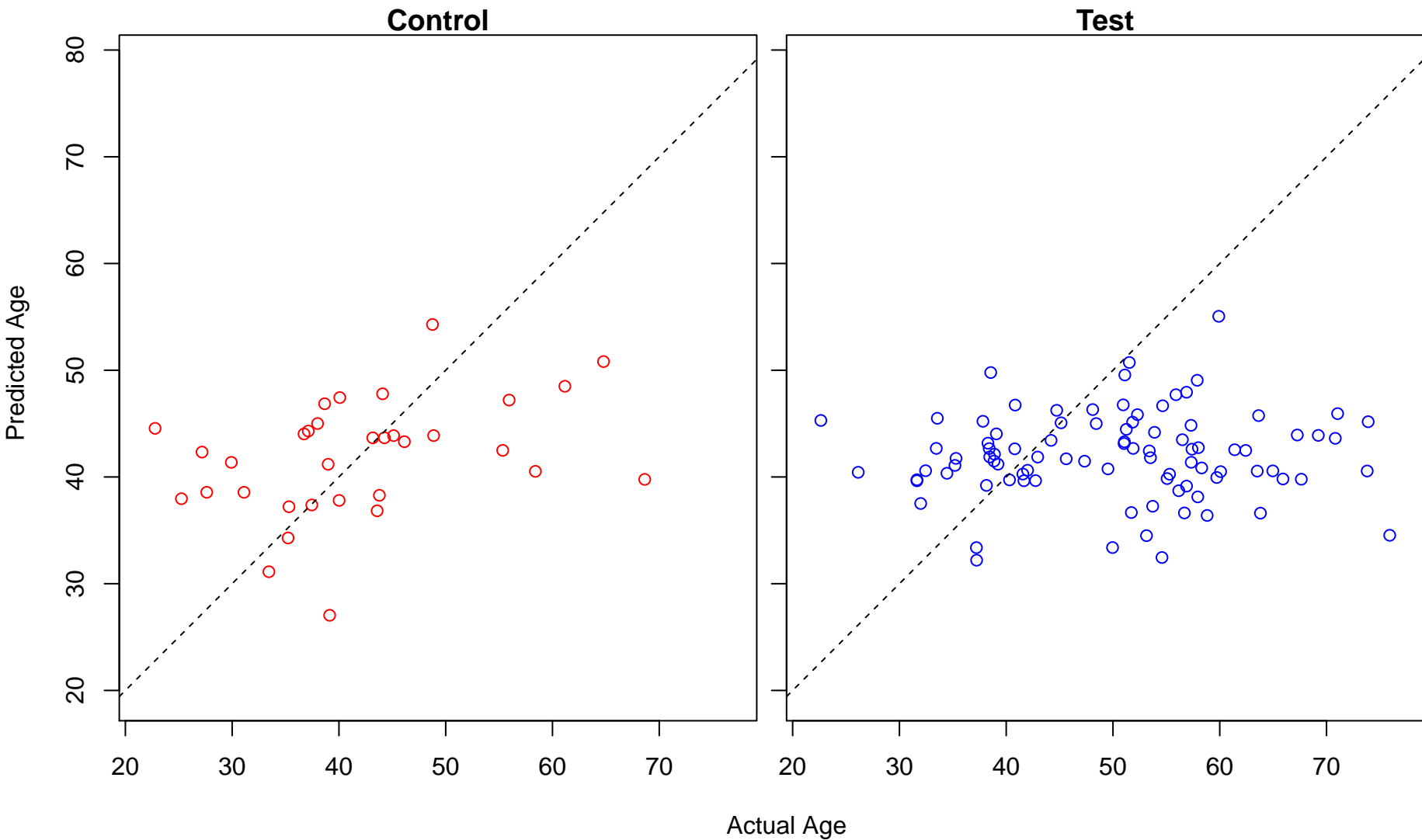
positive regulation of T-helper cell differentiation (Score: 0.476536)



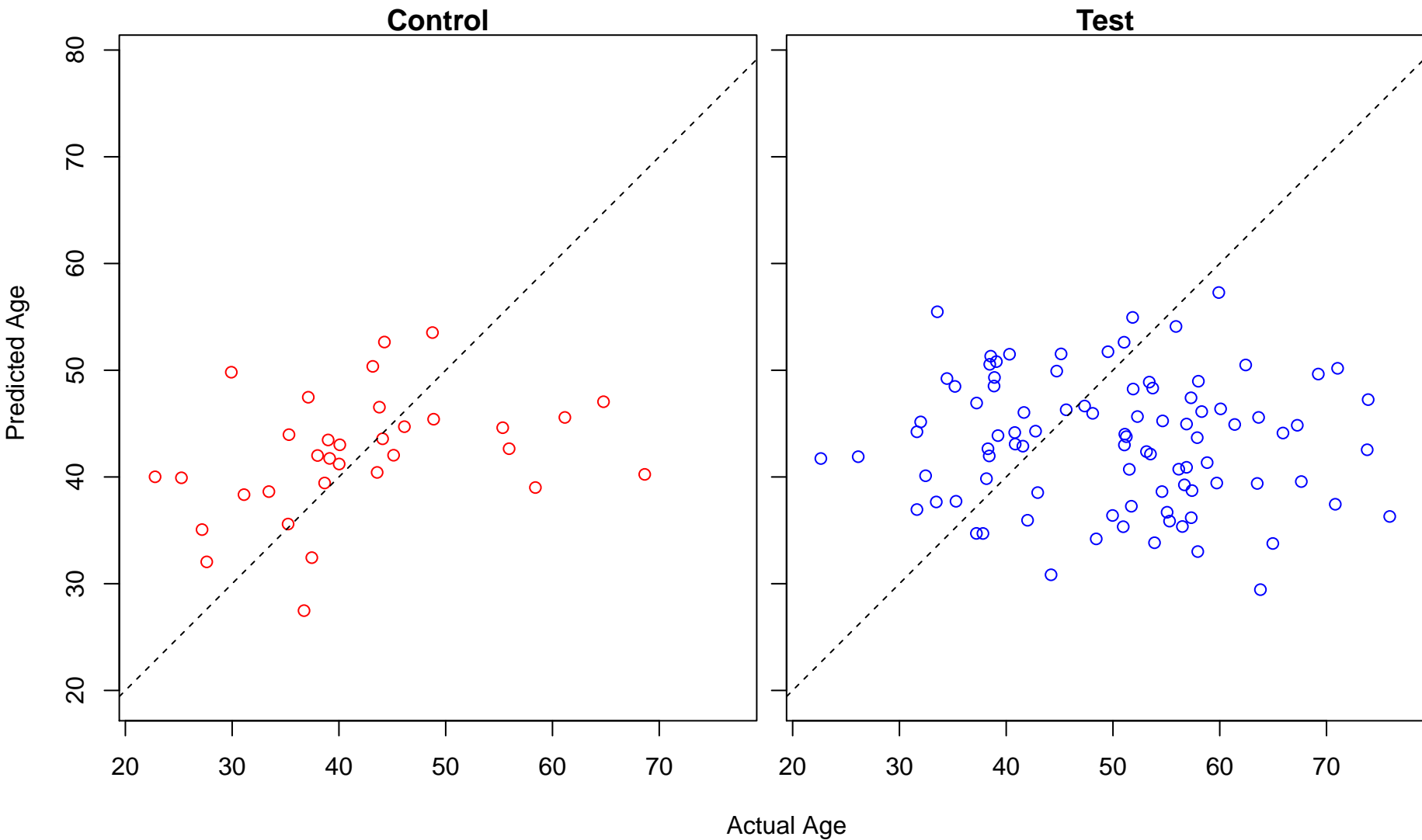
interleukin-2-mediated signaling pathway (Score: 0.475985)



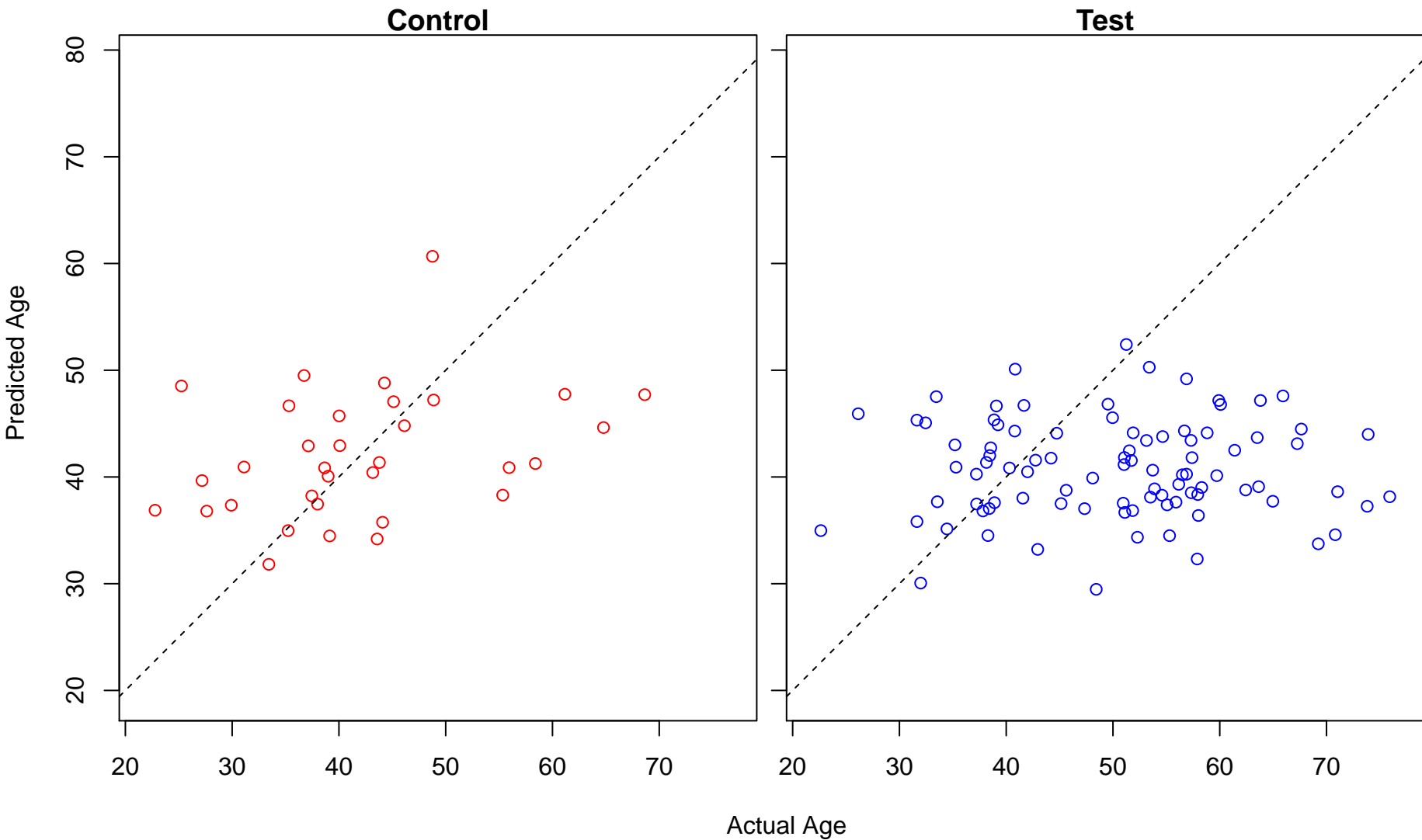
phagolysosome assembly (Score: 0.473592)



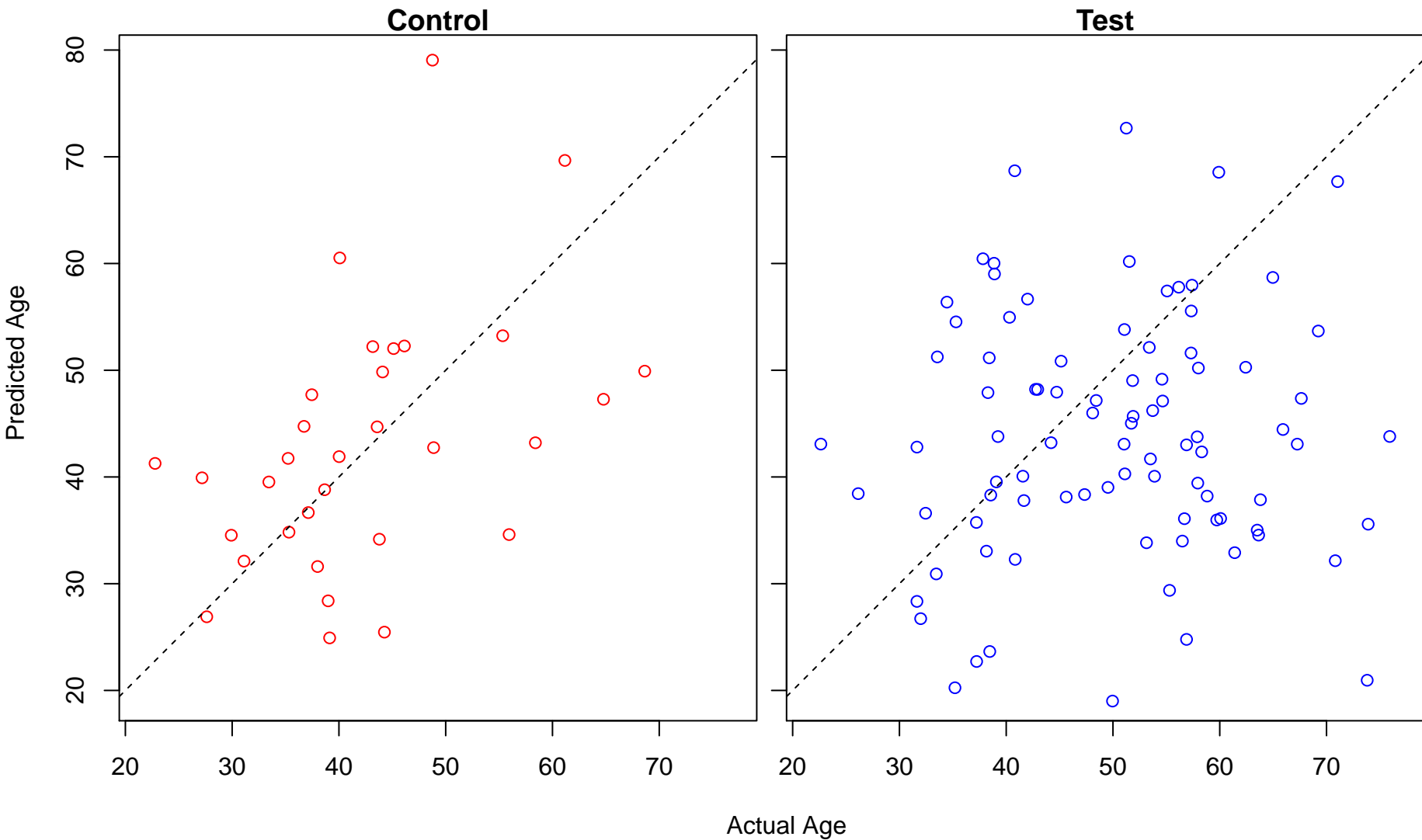
forebrain neuroblast division (Score: 0.472863)



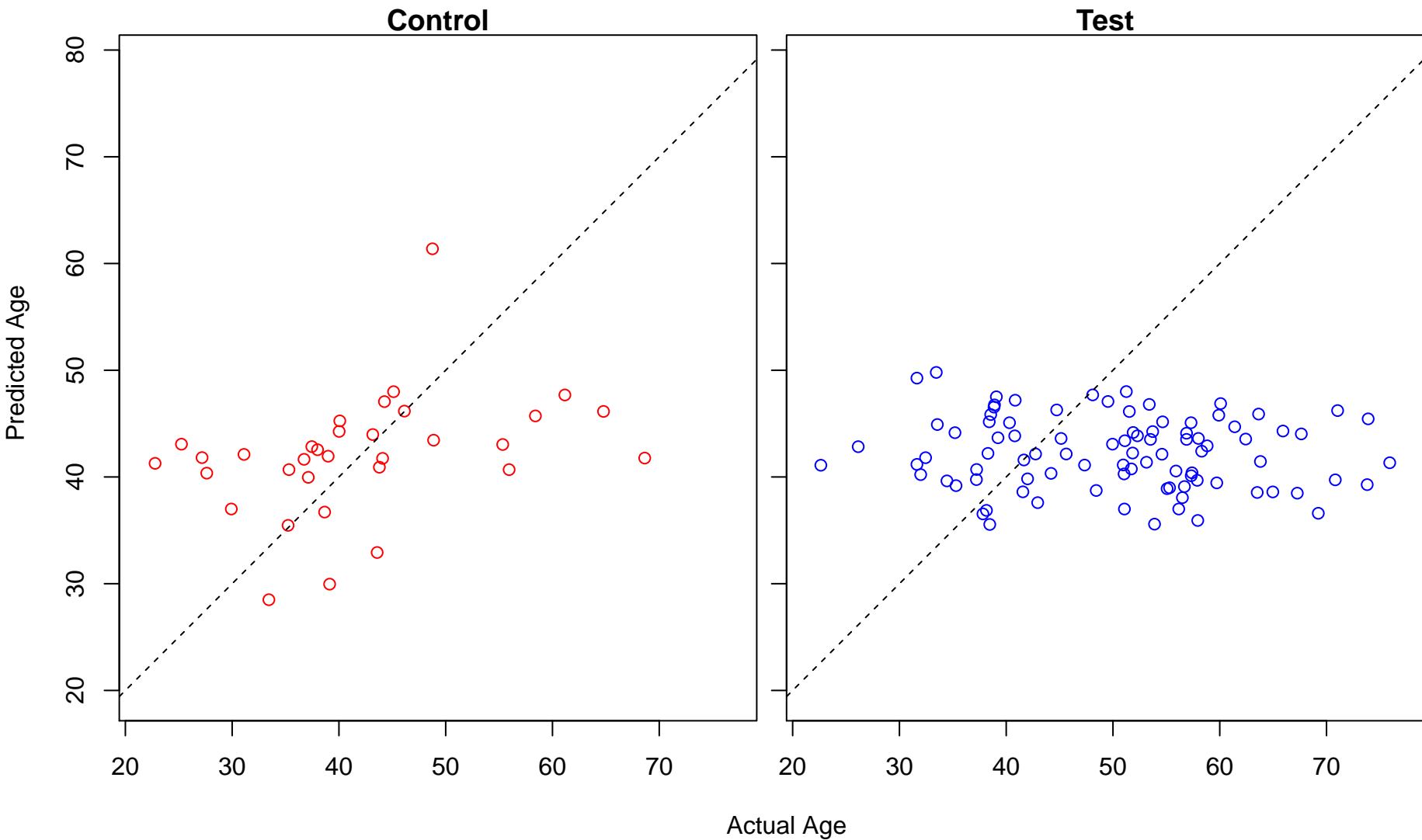
leukocyte apoptotic process (Score: 0.46958)



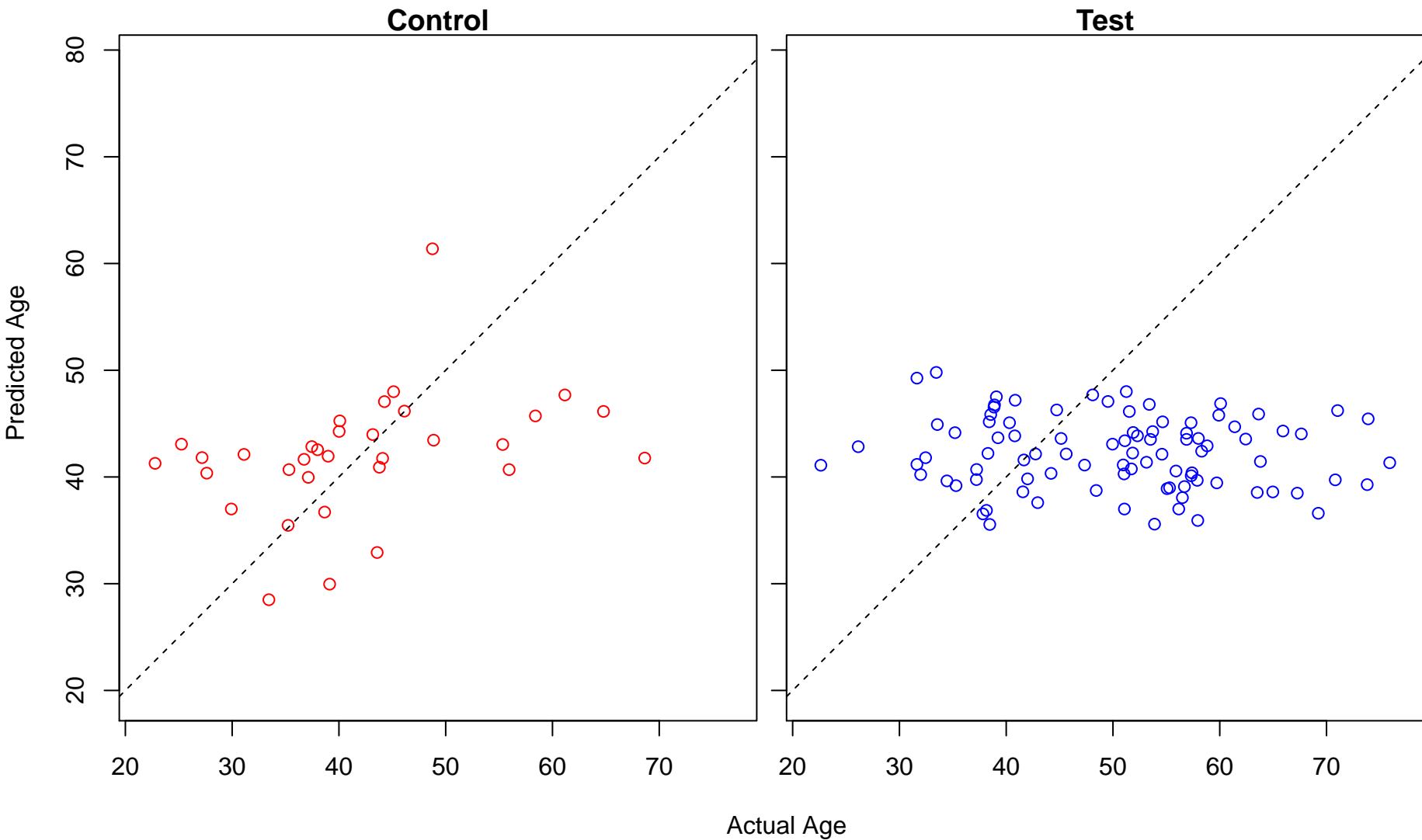
eye morphogenesis (Score: 0.469426)



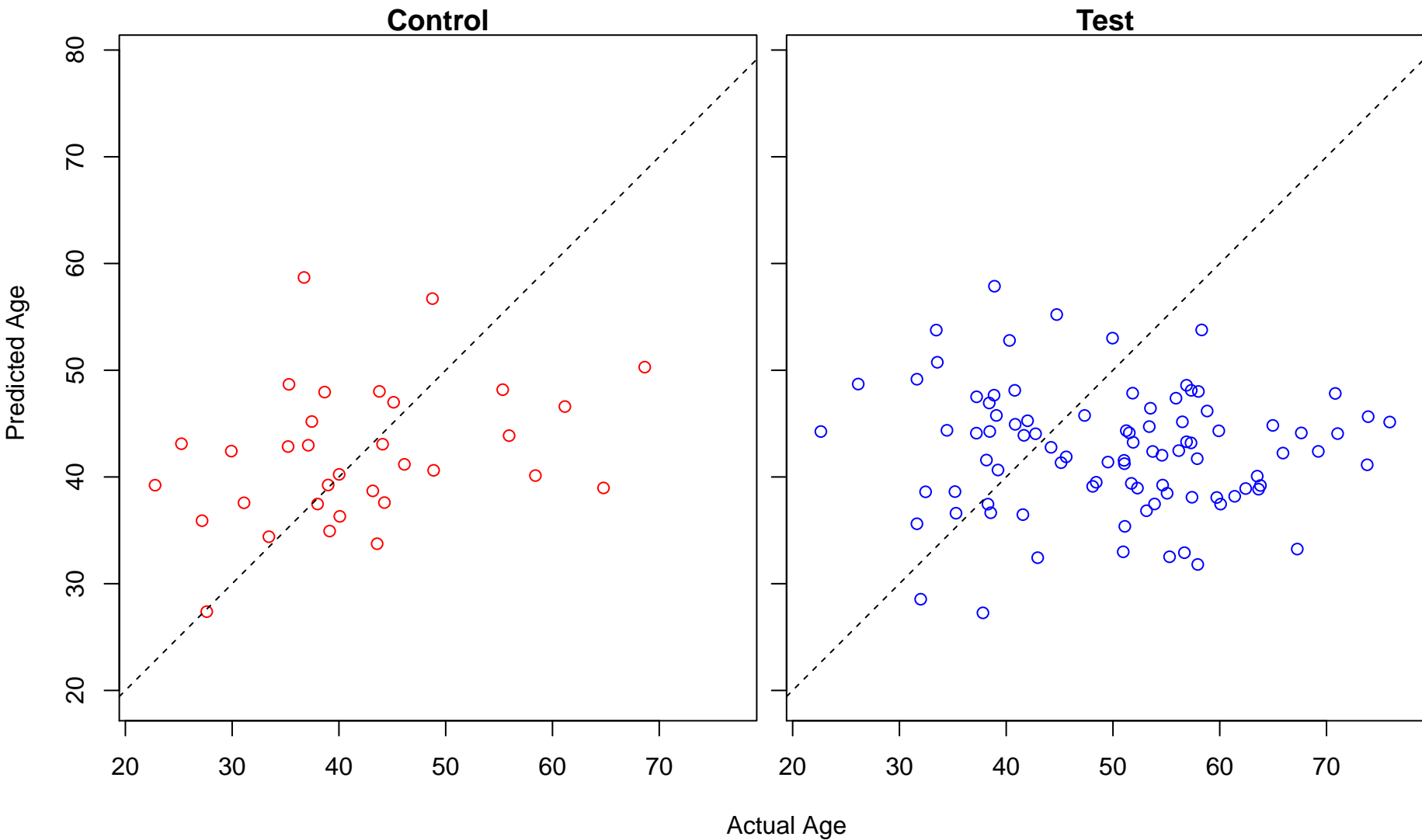
mitochondrial respiratory chain complex IV assembly (Score: 0.467924)



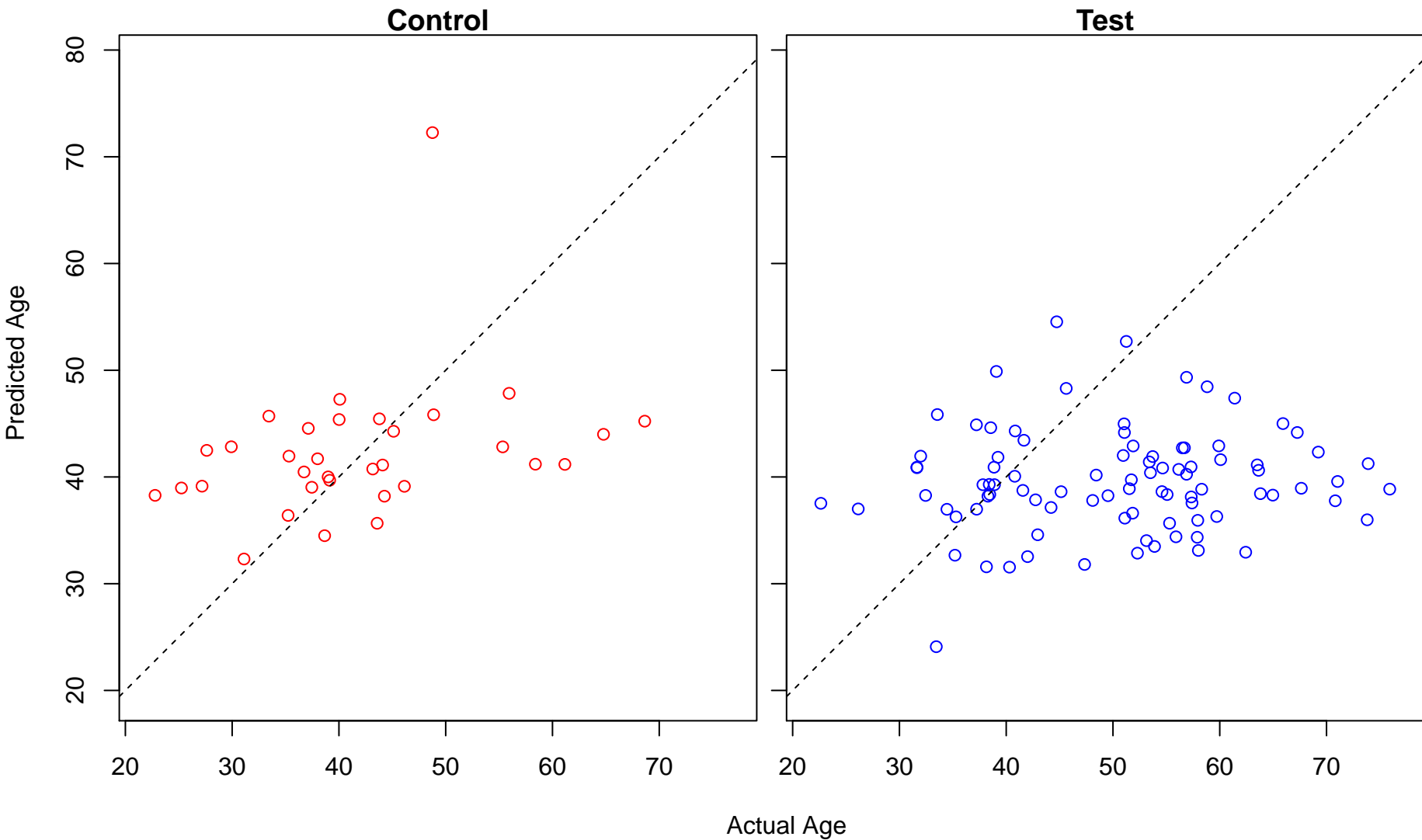
mitochondrial respiratory chain complex IV biogenesis (Score: 0.467924)



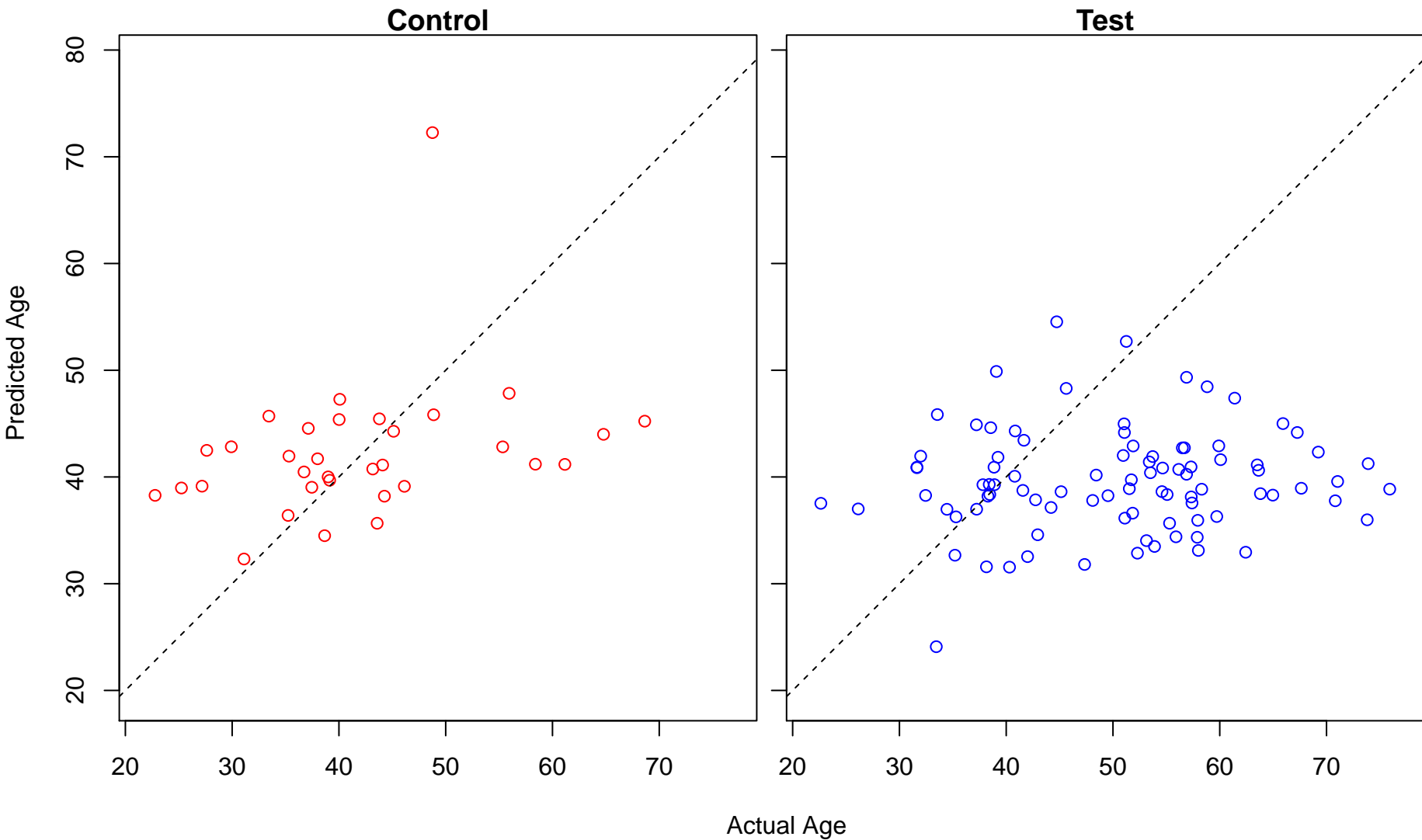
regulation of interleukin-10 secretion (Score: 0.467672)



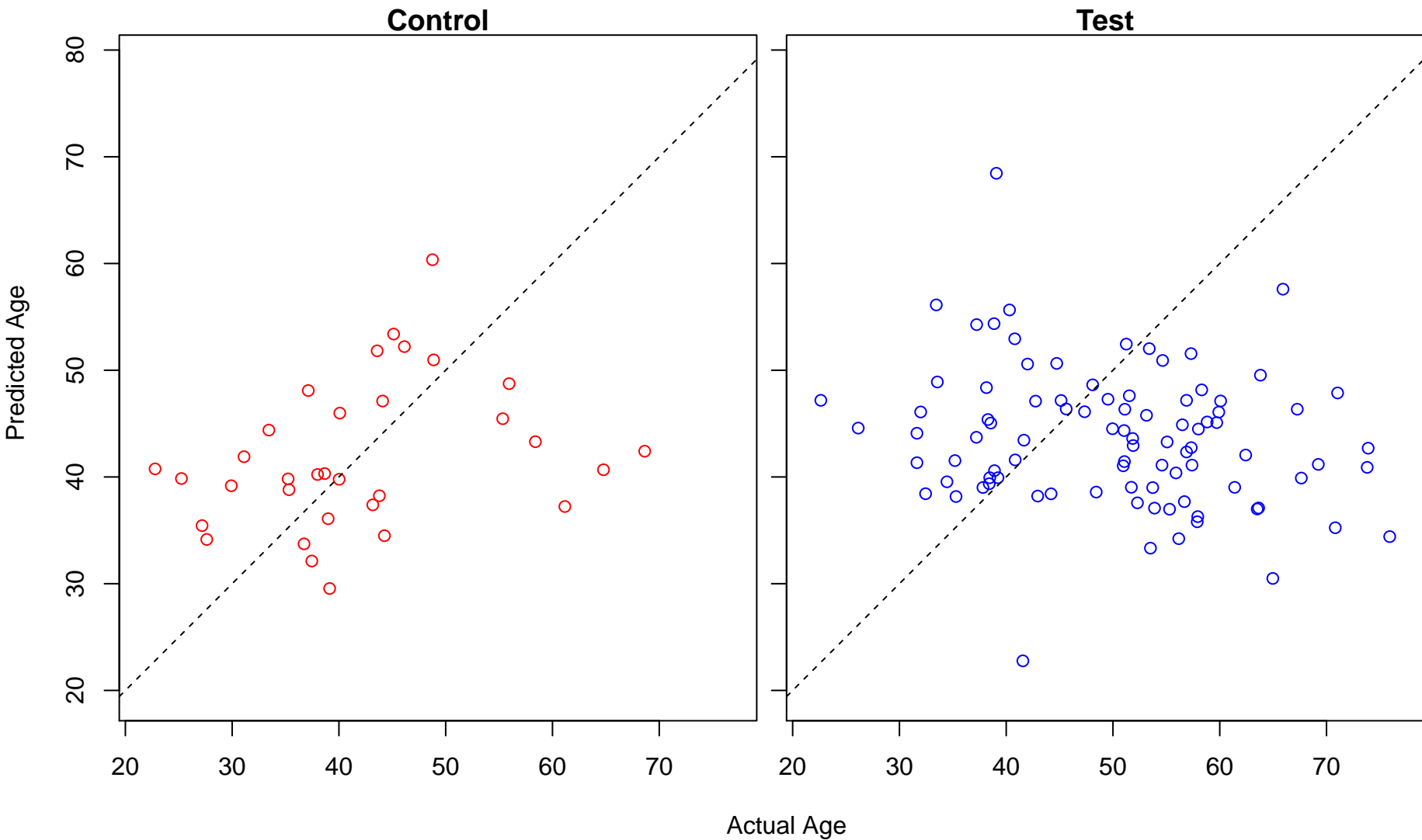
metal incorporation into metallo-sulfur cluster (Score: 0.467475)



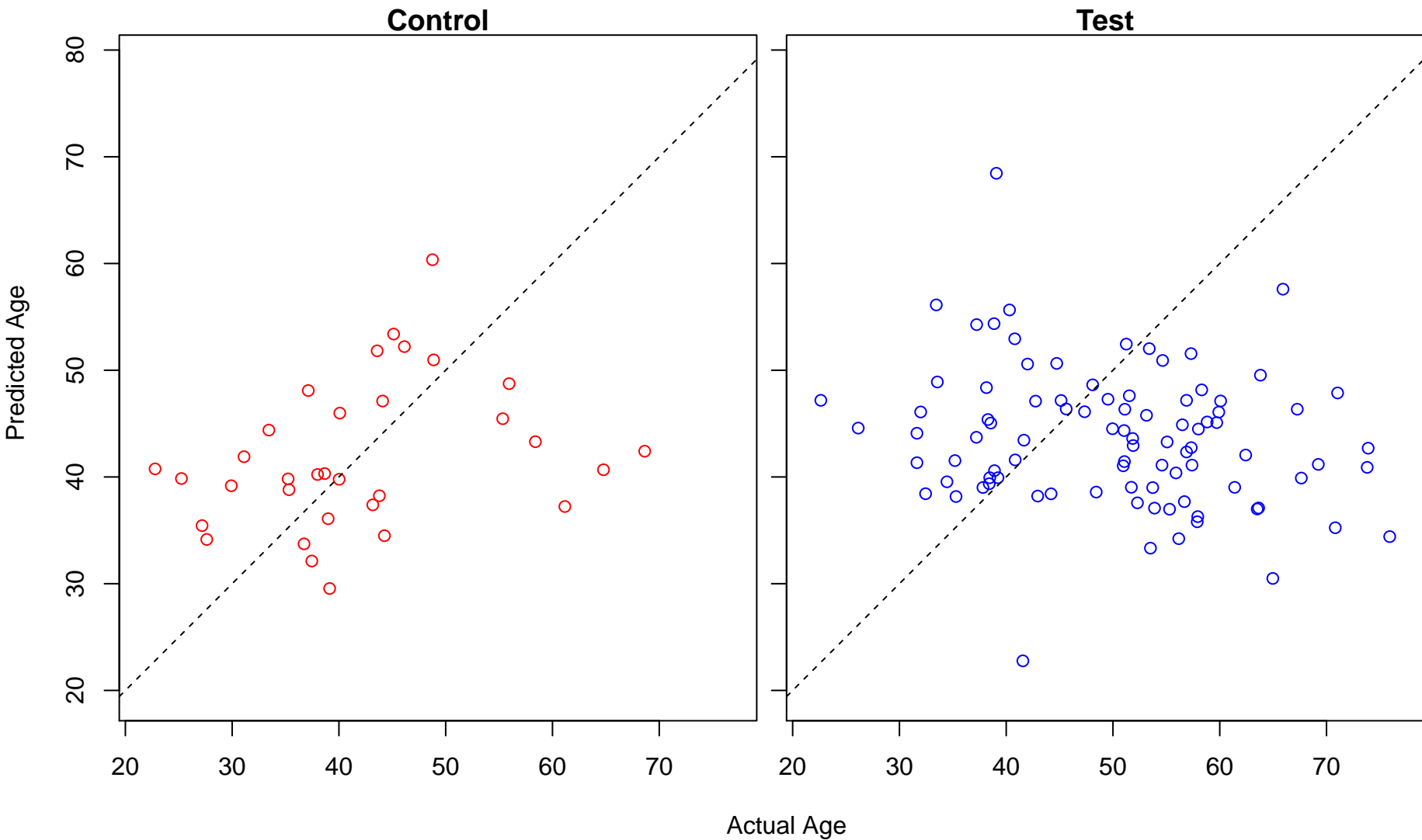
iron incorporation into metallo-sulfur cluster (Score: 0.467475)



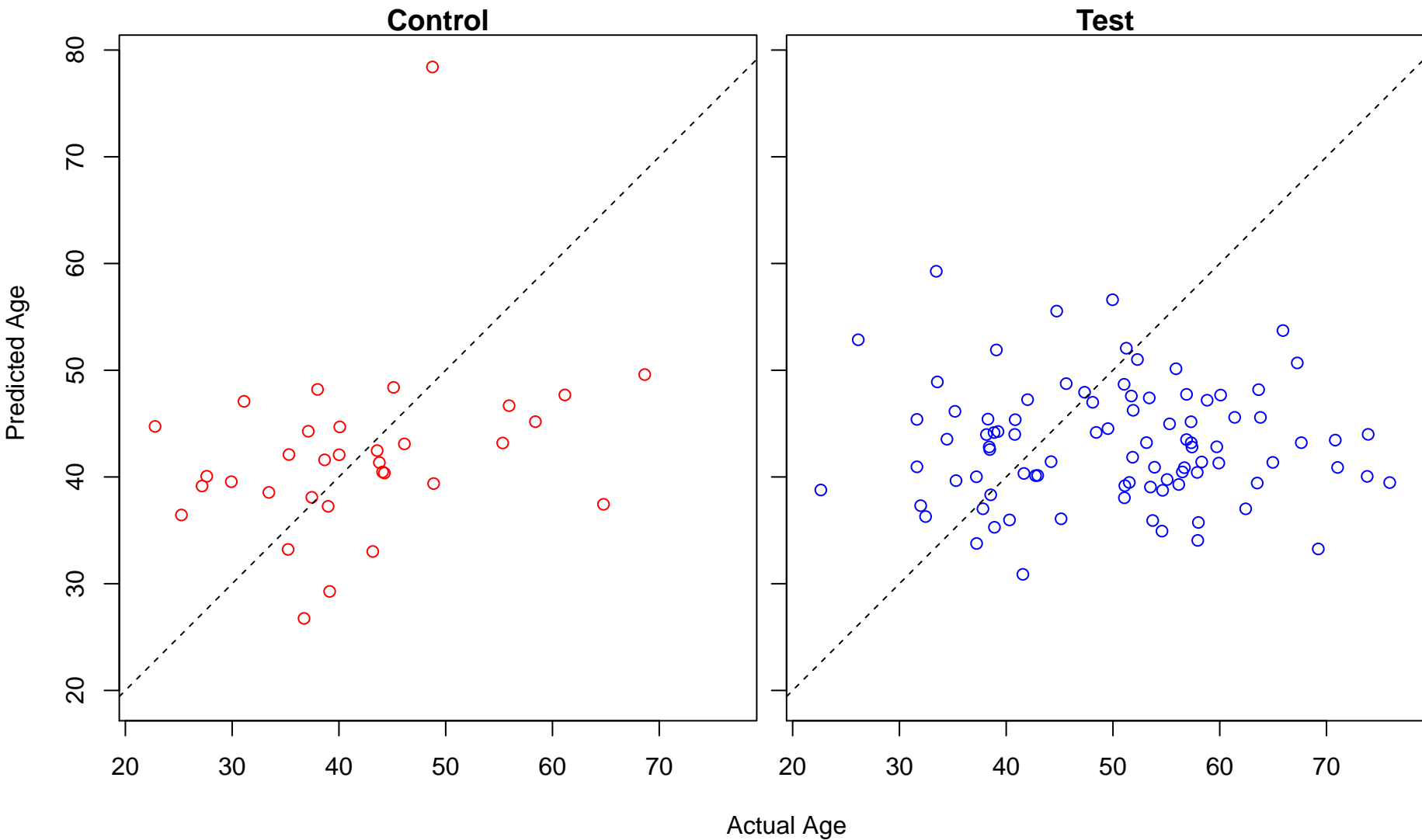
urea cycle (Score: 0.467390)



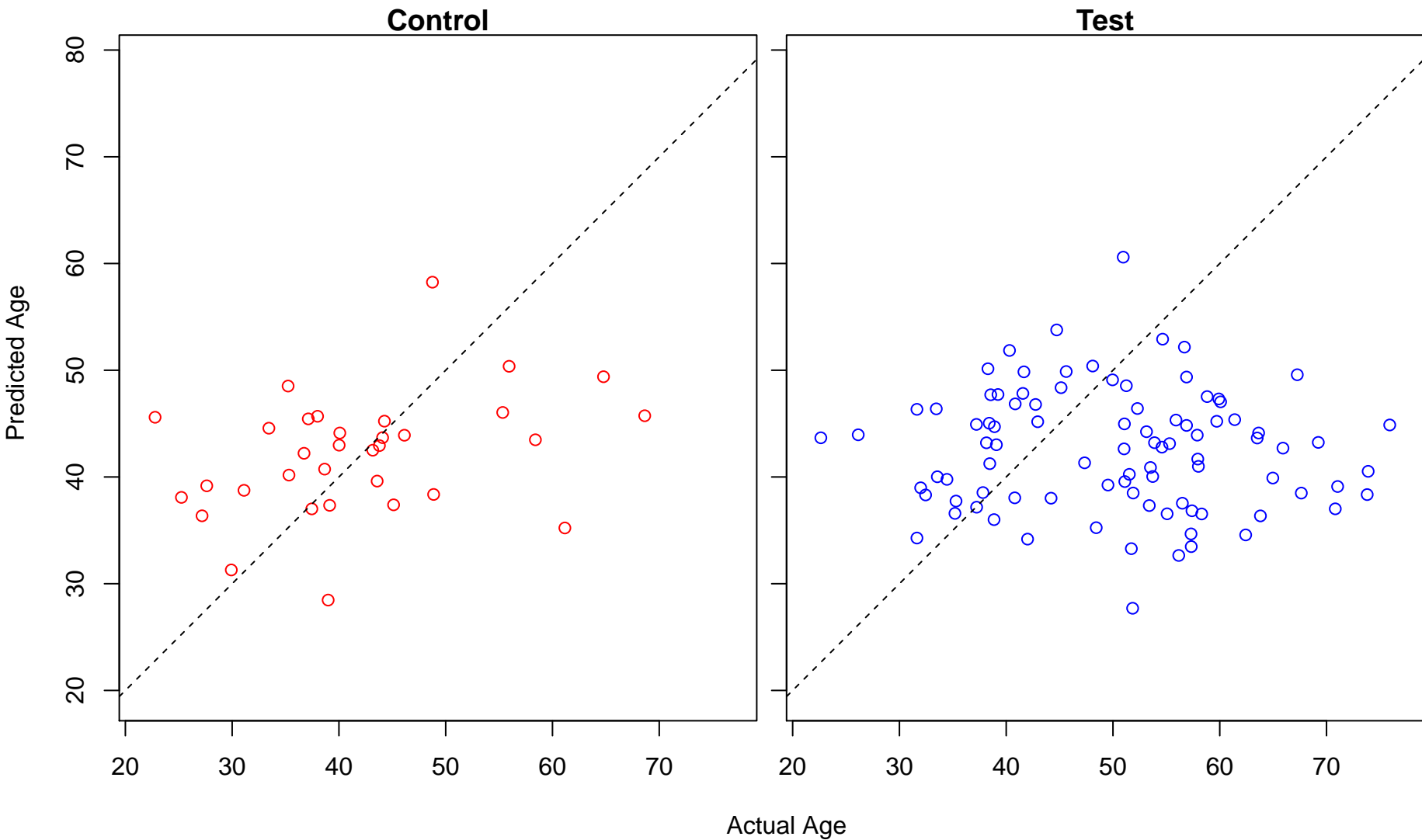
urea metabolic process (Score: 0.467390)



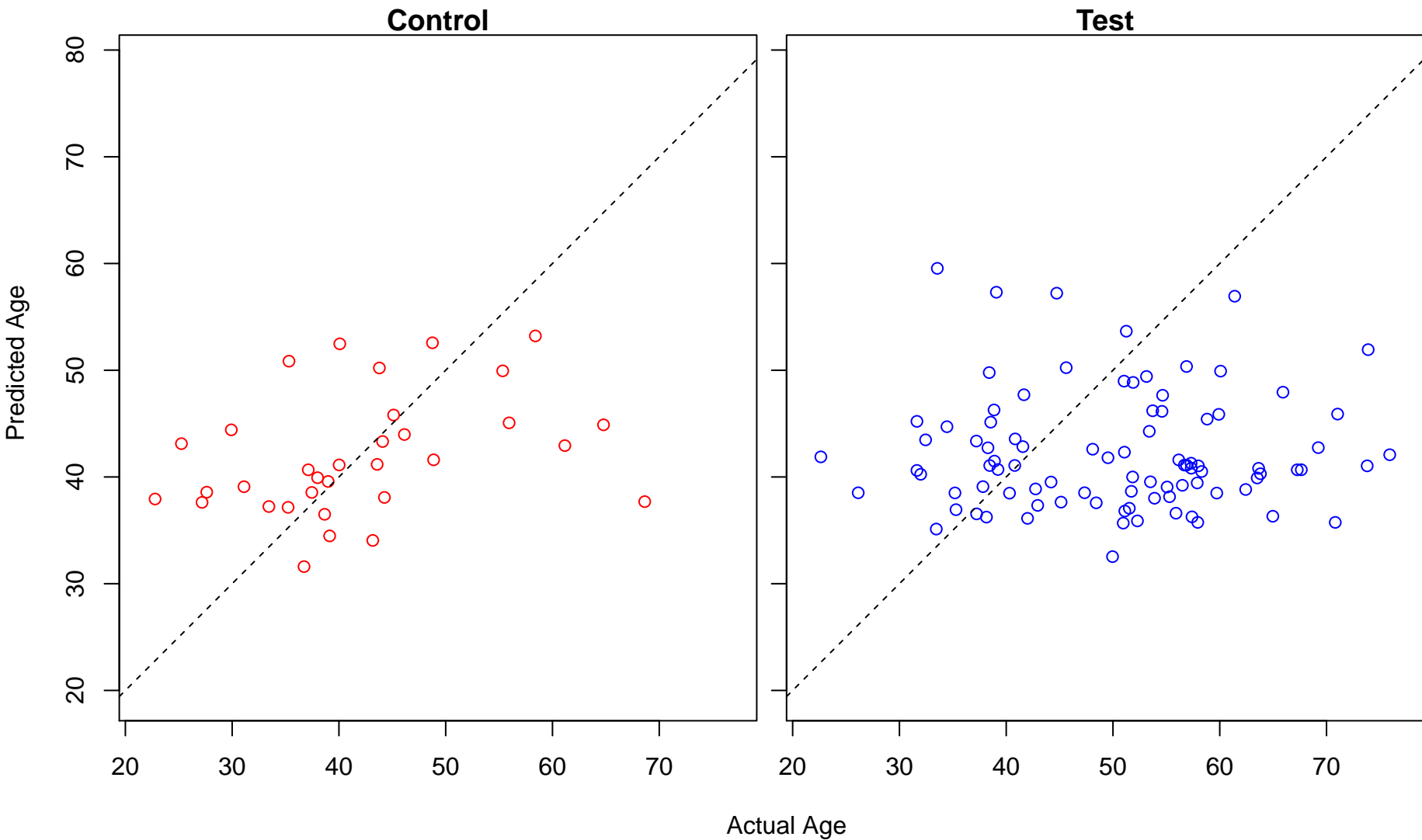
glucocorticoid receptor signaling pathway (Score: 0.467257)



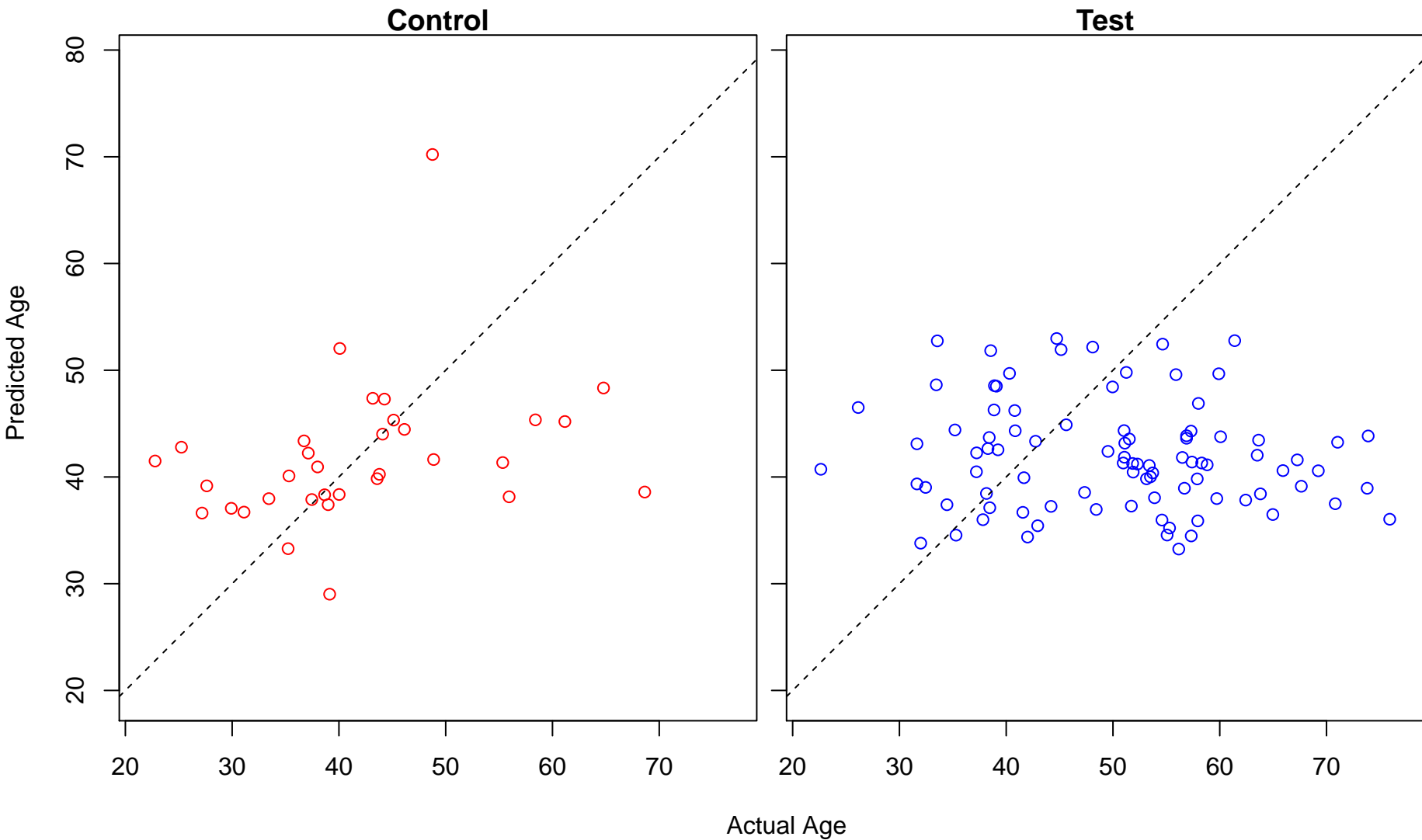
macrophage activation involved in immune response (Score: 0.466115)



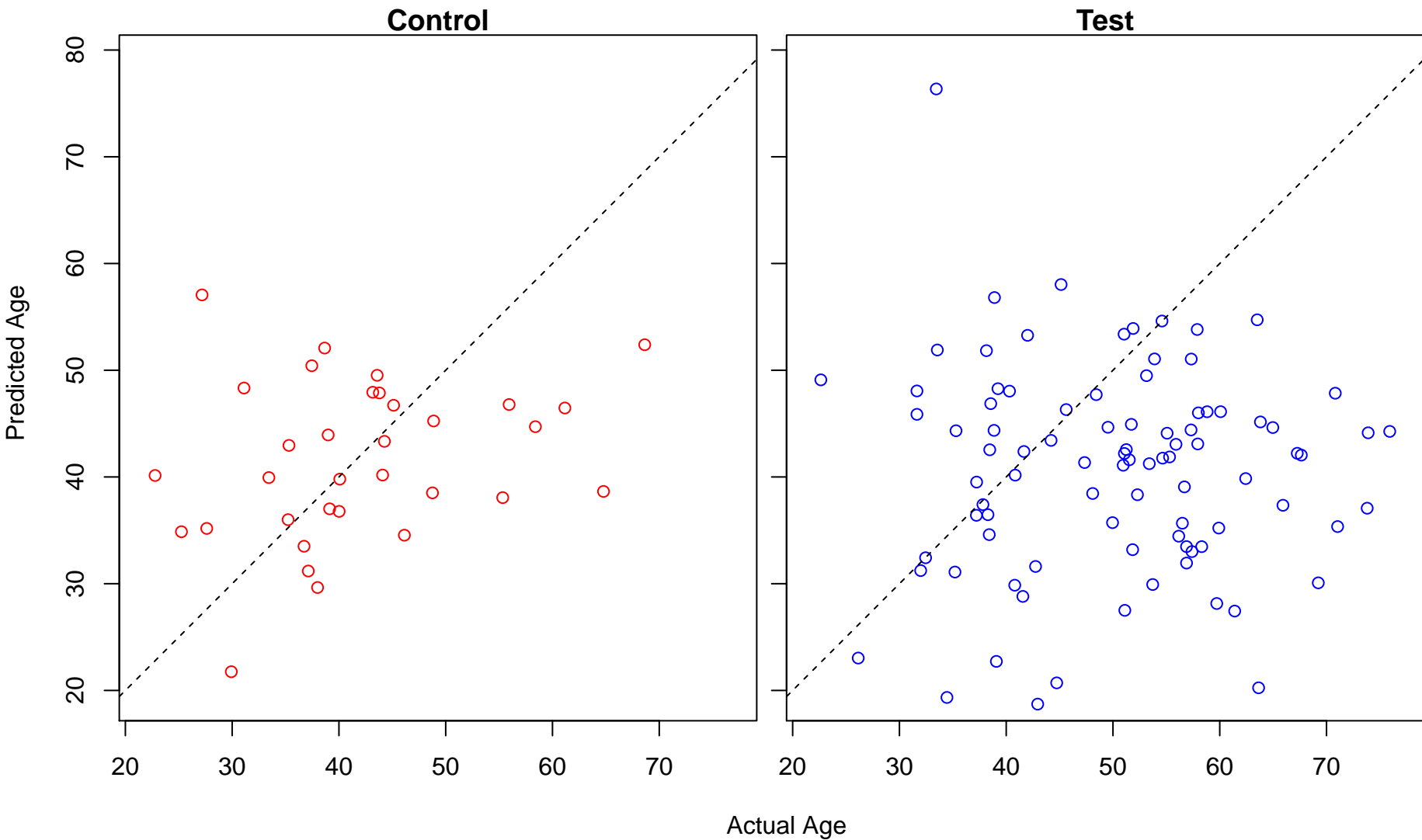
histone H2A K63-linked ubiquitination (Score: 0.463263)



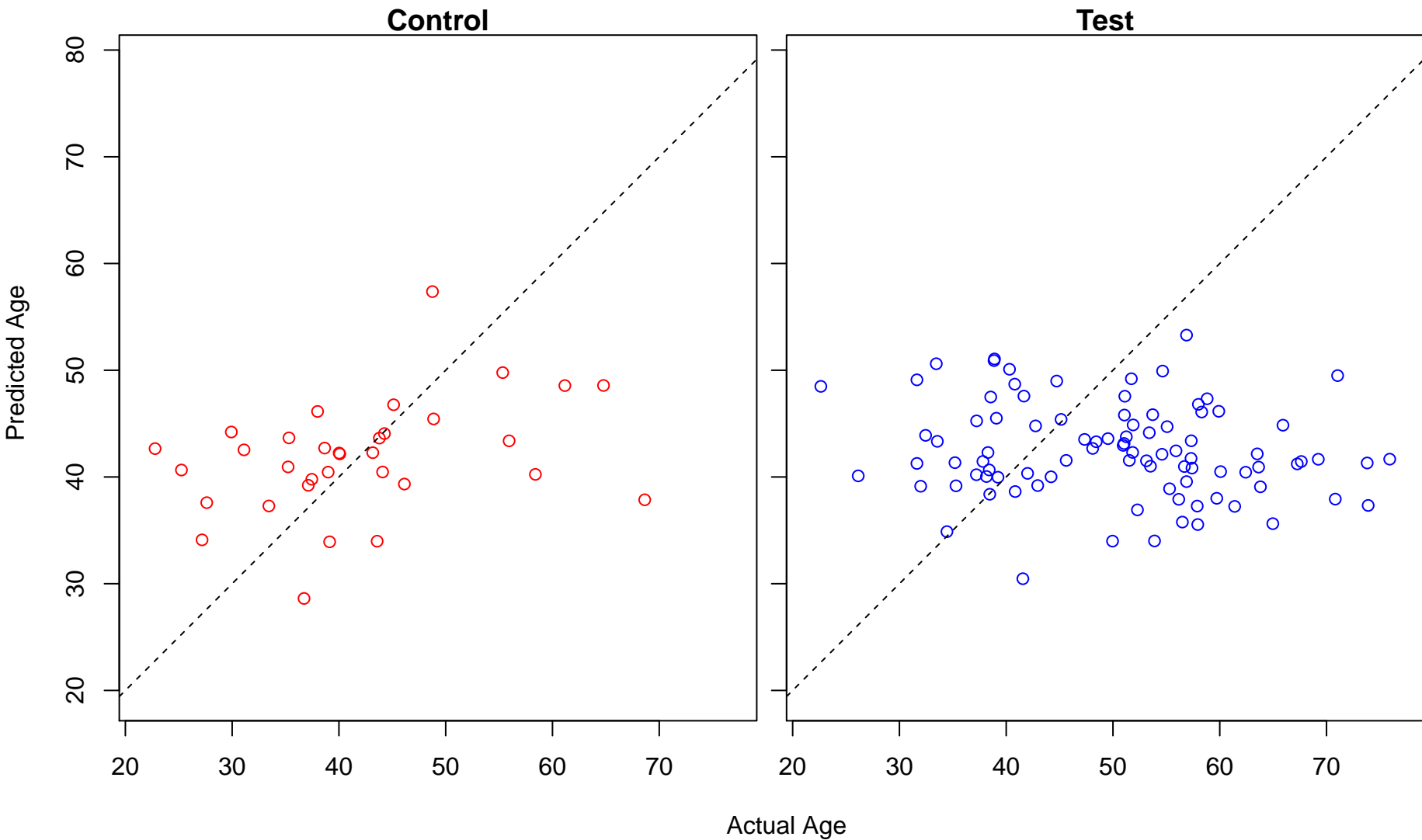
regulation of cell projection organization (Score: 0.461749)



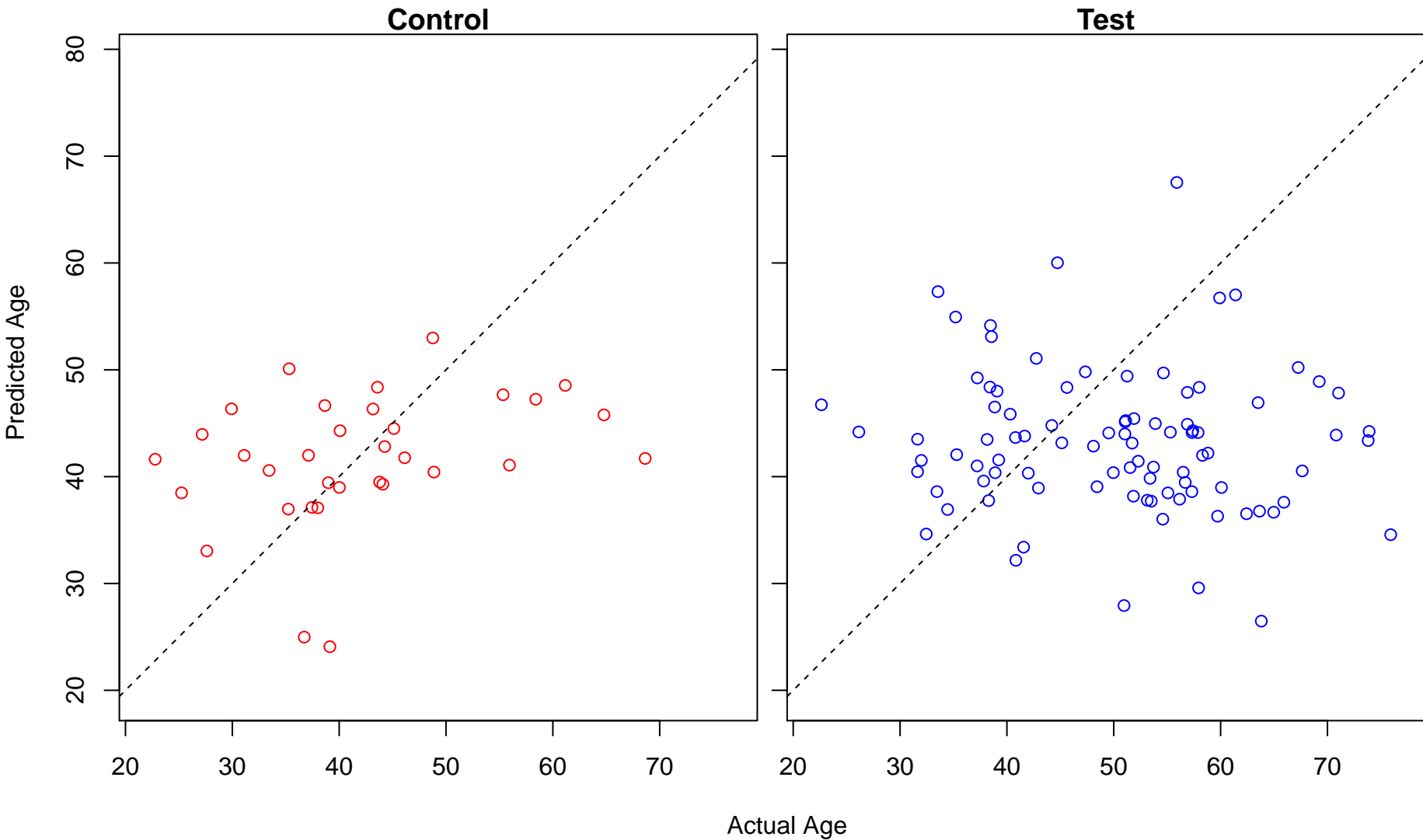
regulation of glucose import in response to insulin stimulus (Score: 0.461024)



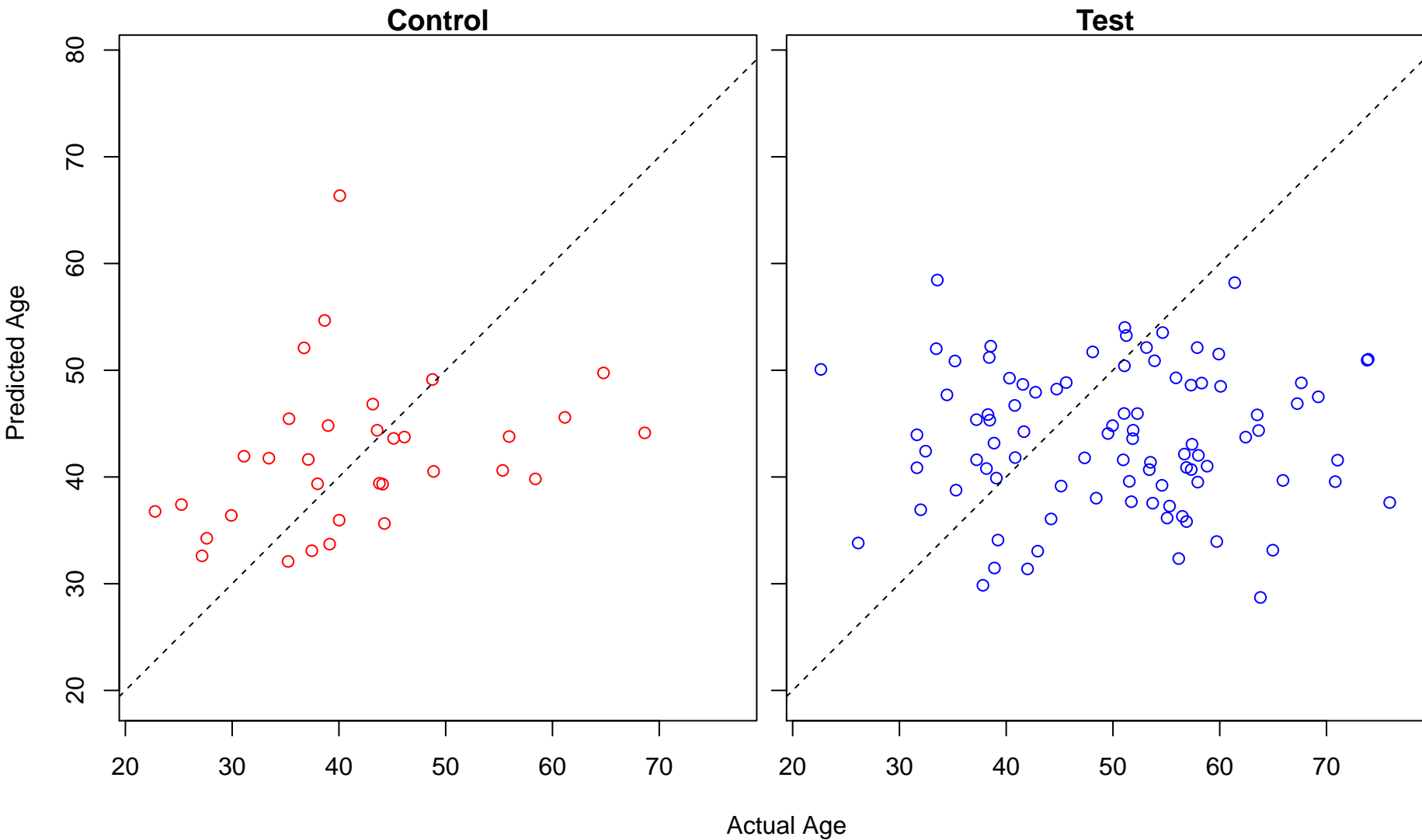
actin crosslink formation (Score: 0.459964)



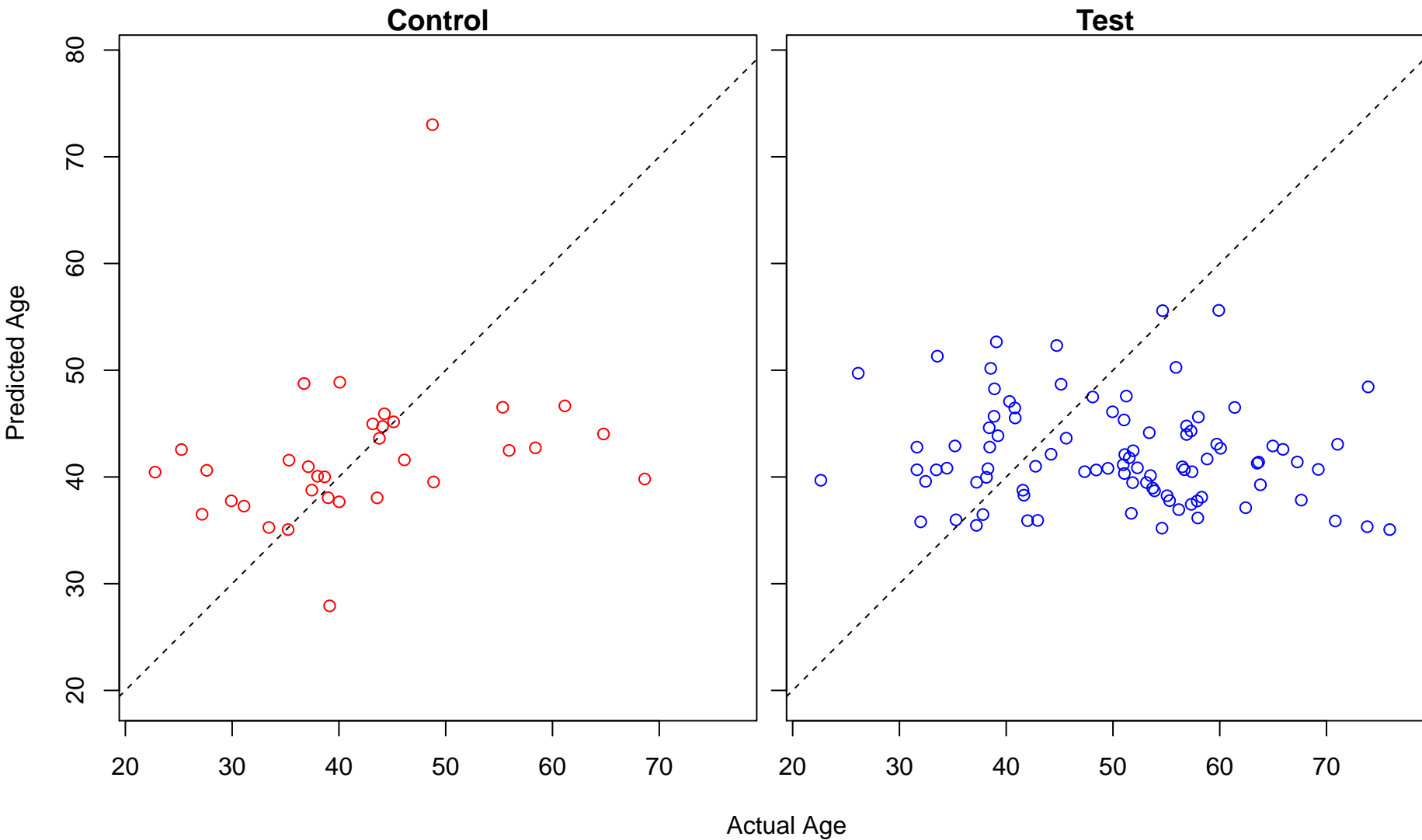
regulation of postsynaptic membrane potential (Score: 0.459466)



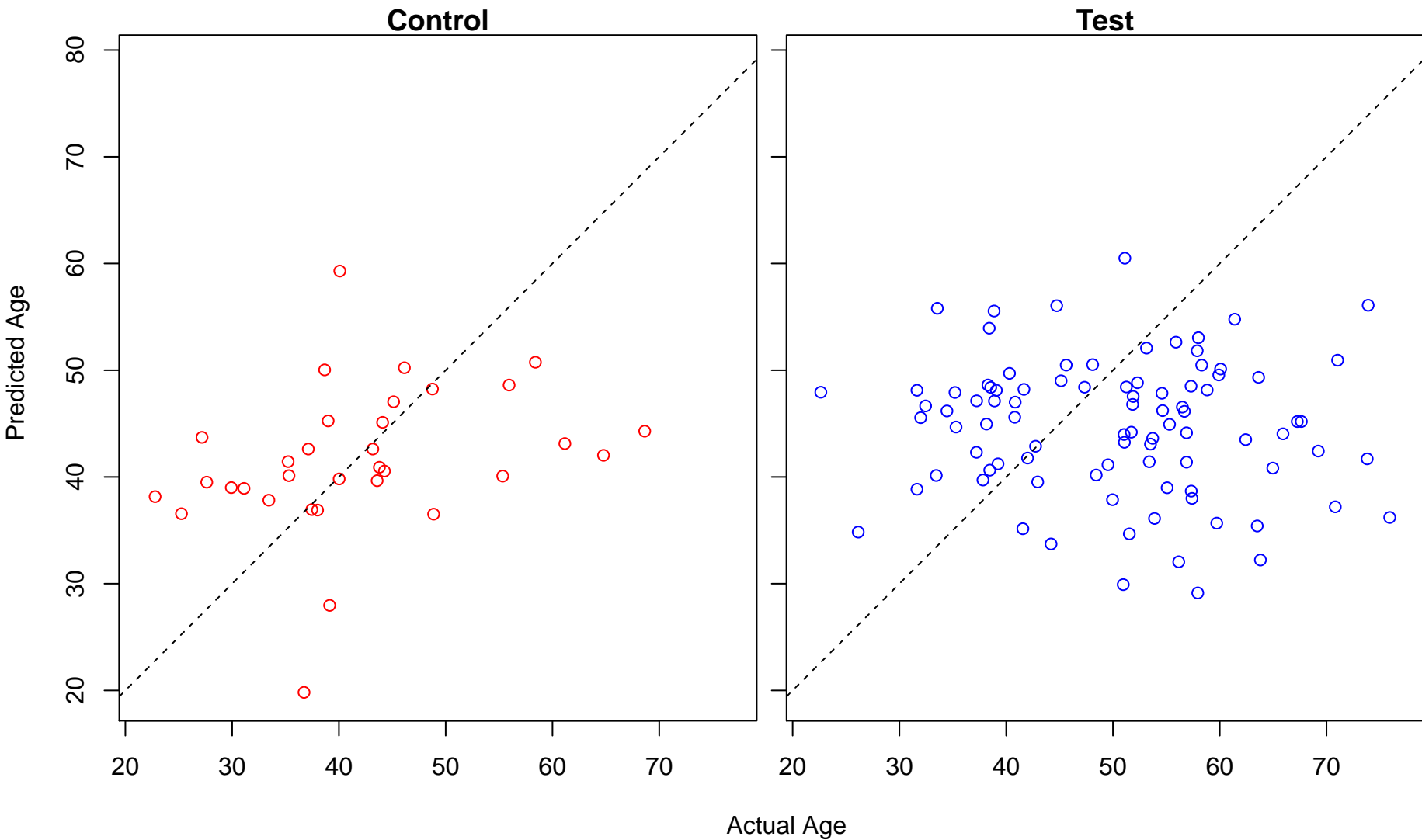
positive regulation of dendritic cell antigen processing and presentation (Score: 0.458642)



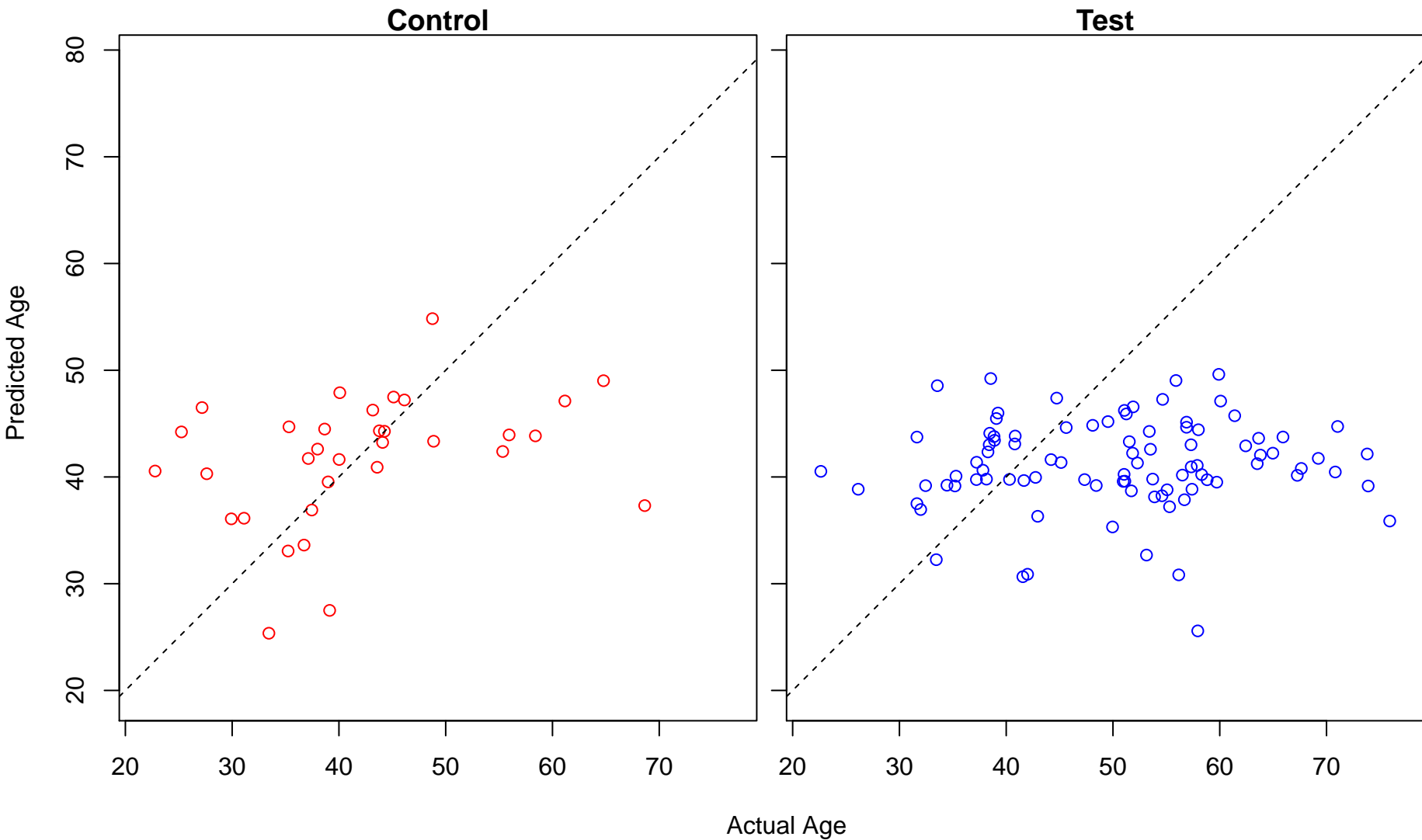
negative regulation of cell differentiation (Score: 0.457530)



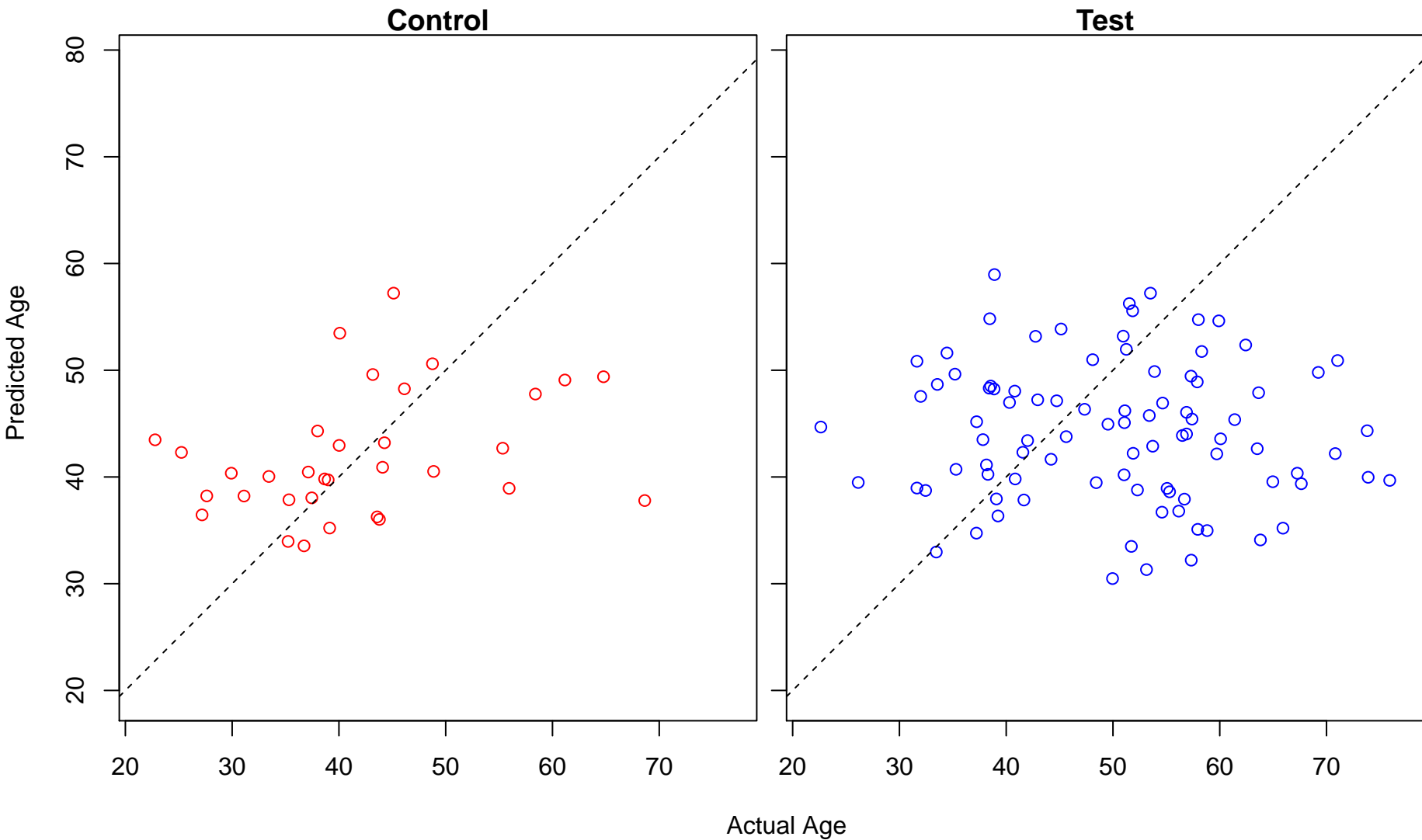
response to peptidoglycan (Score: 0.457305)



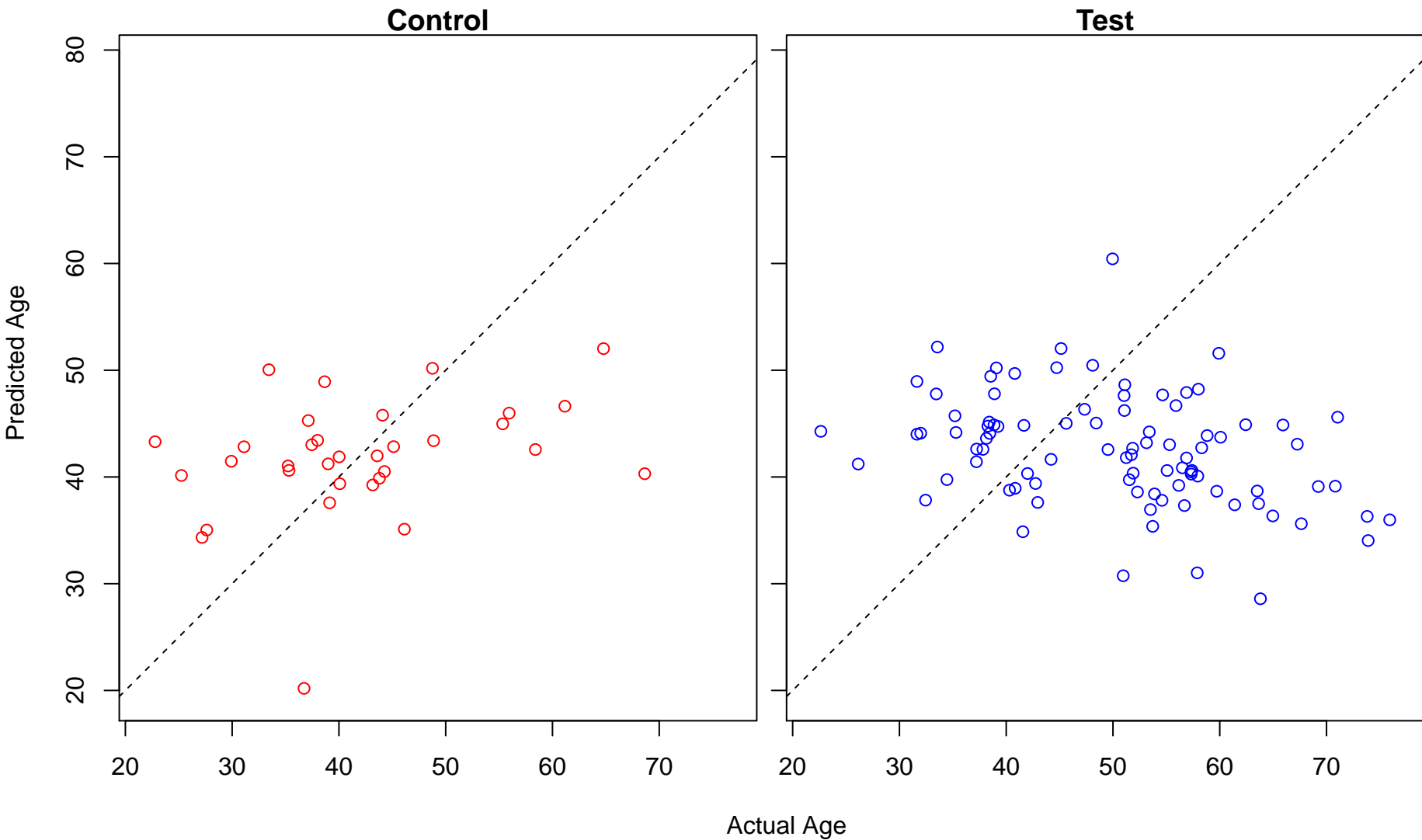
maintenance of Golgi location (Score: 0.456804)



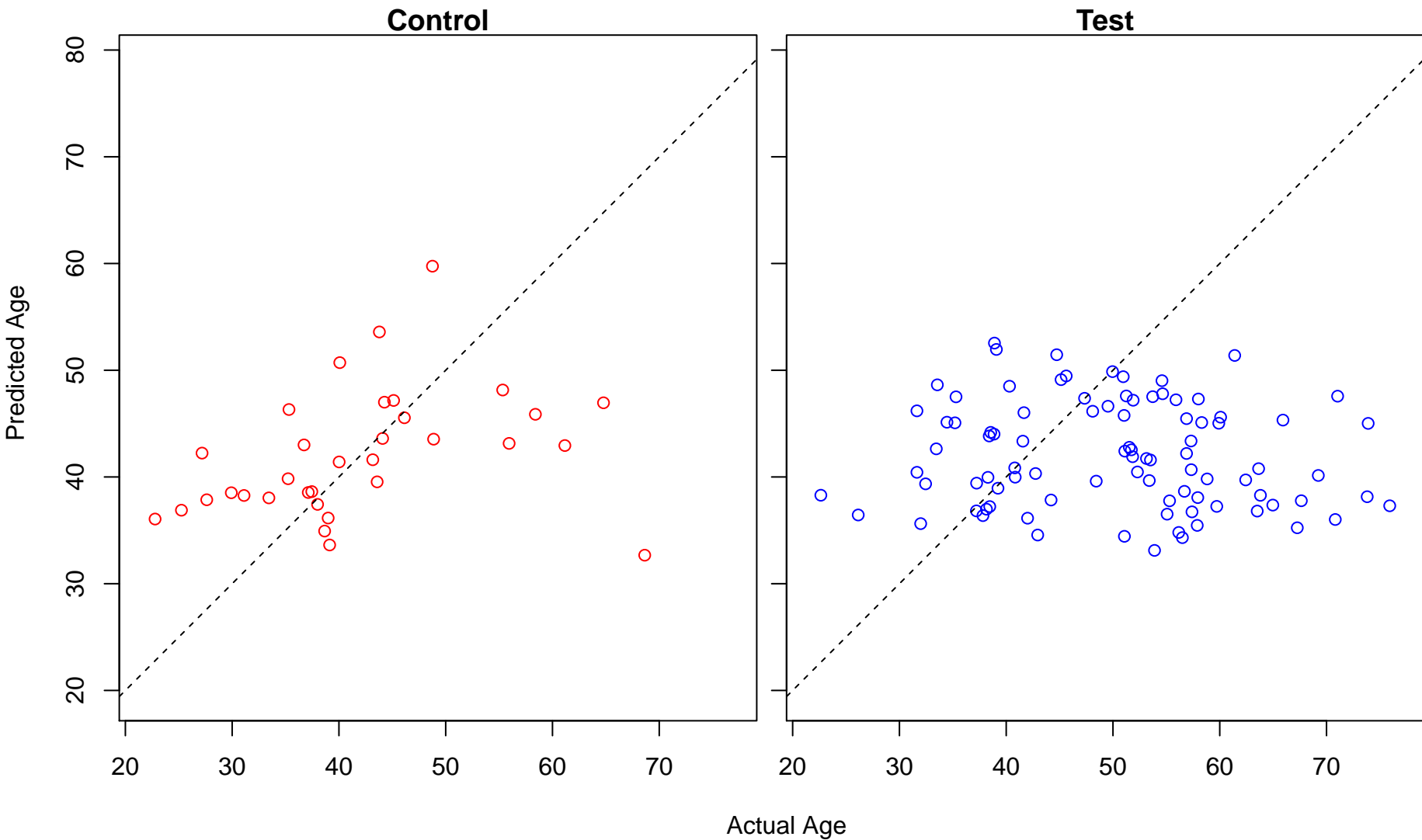
transepithelial chloride transport (Score: 0.456678)



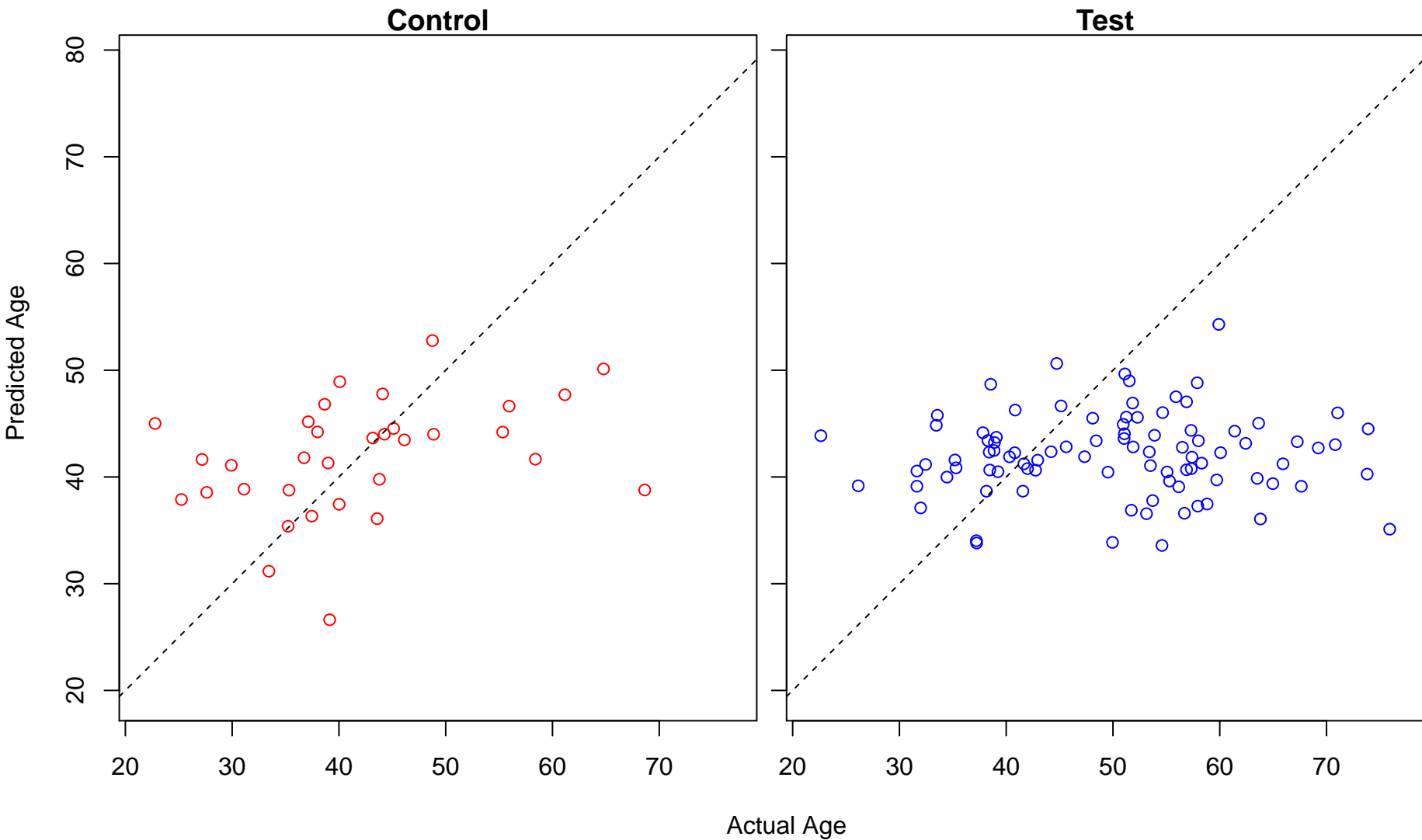
4-hydroxyproline metabolic process (Score: 0.455555)



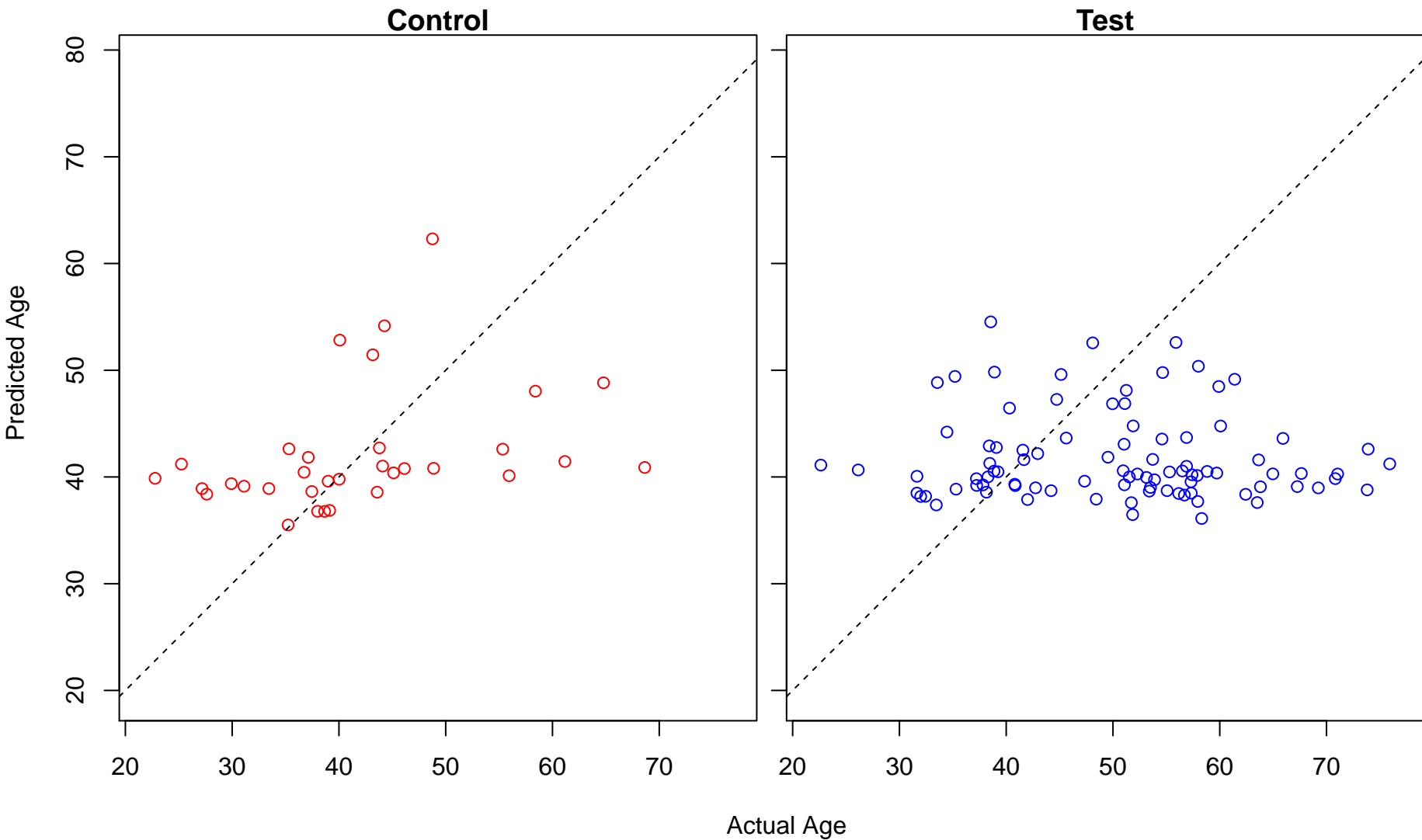
regulation of protein glycosylation (Score: 0.455139)



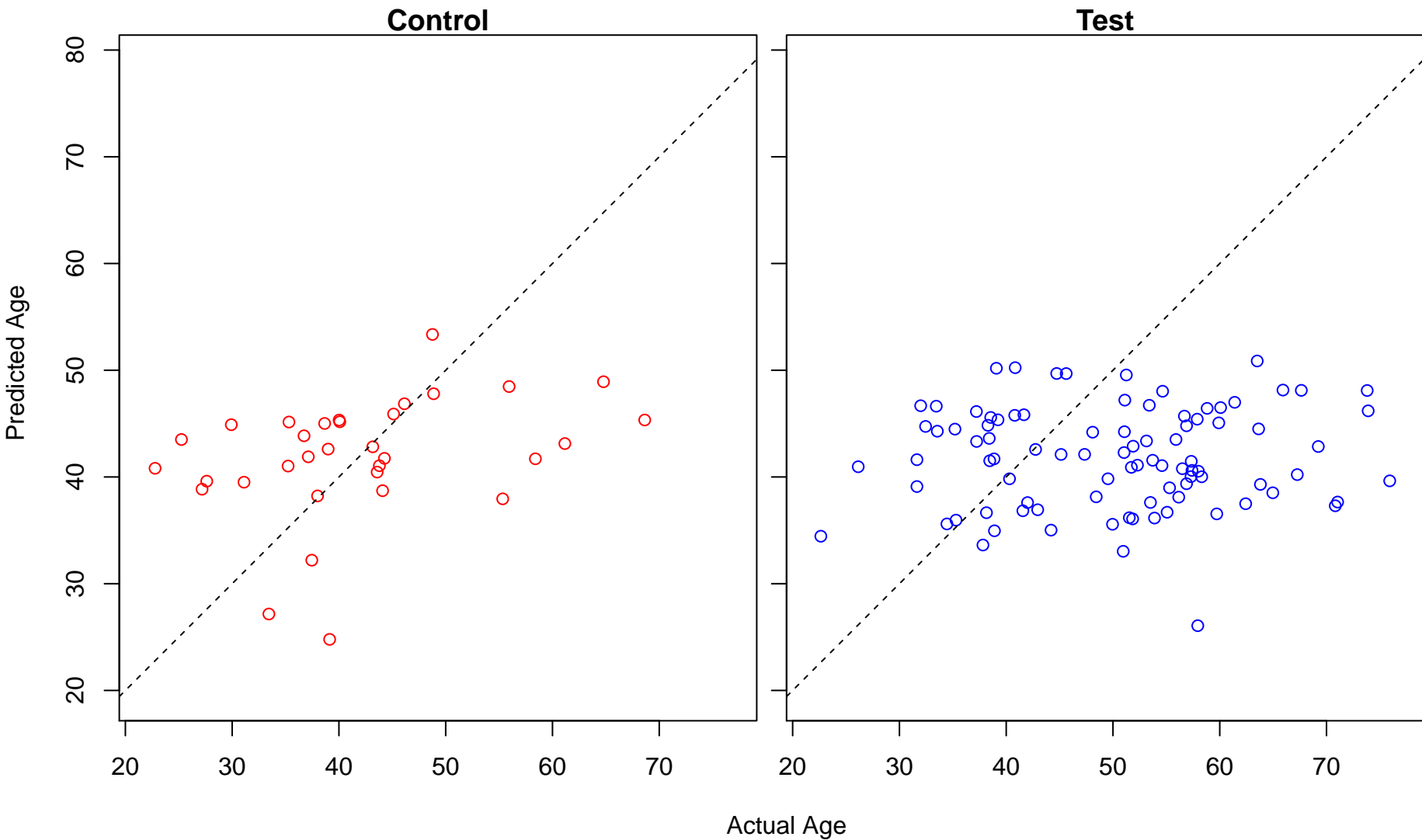
phagosome-lysosome fusion (Score: 0.453242)



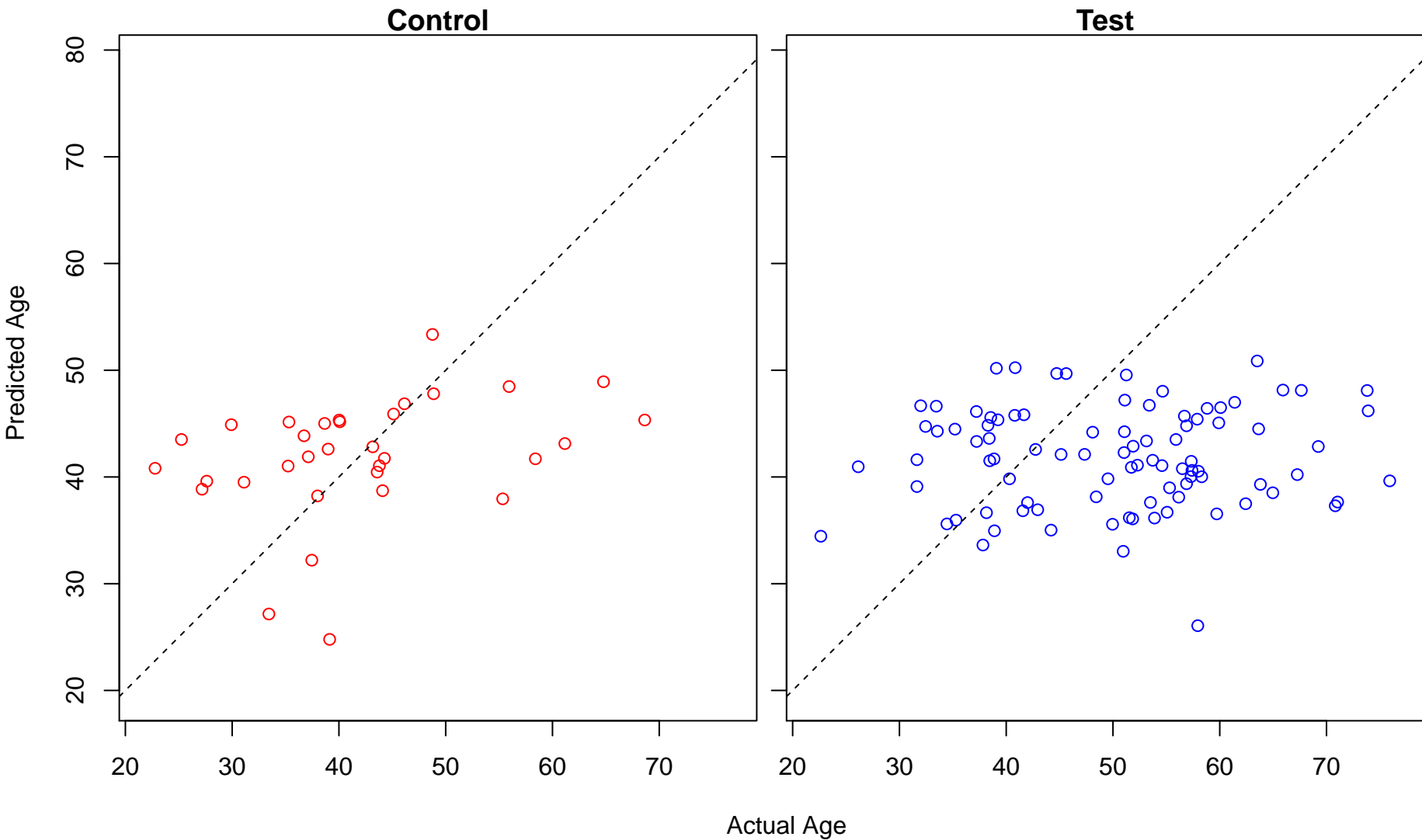
peptidyl-lysine dimethylation (Score: 0.452334)



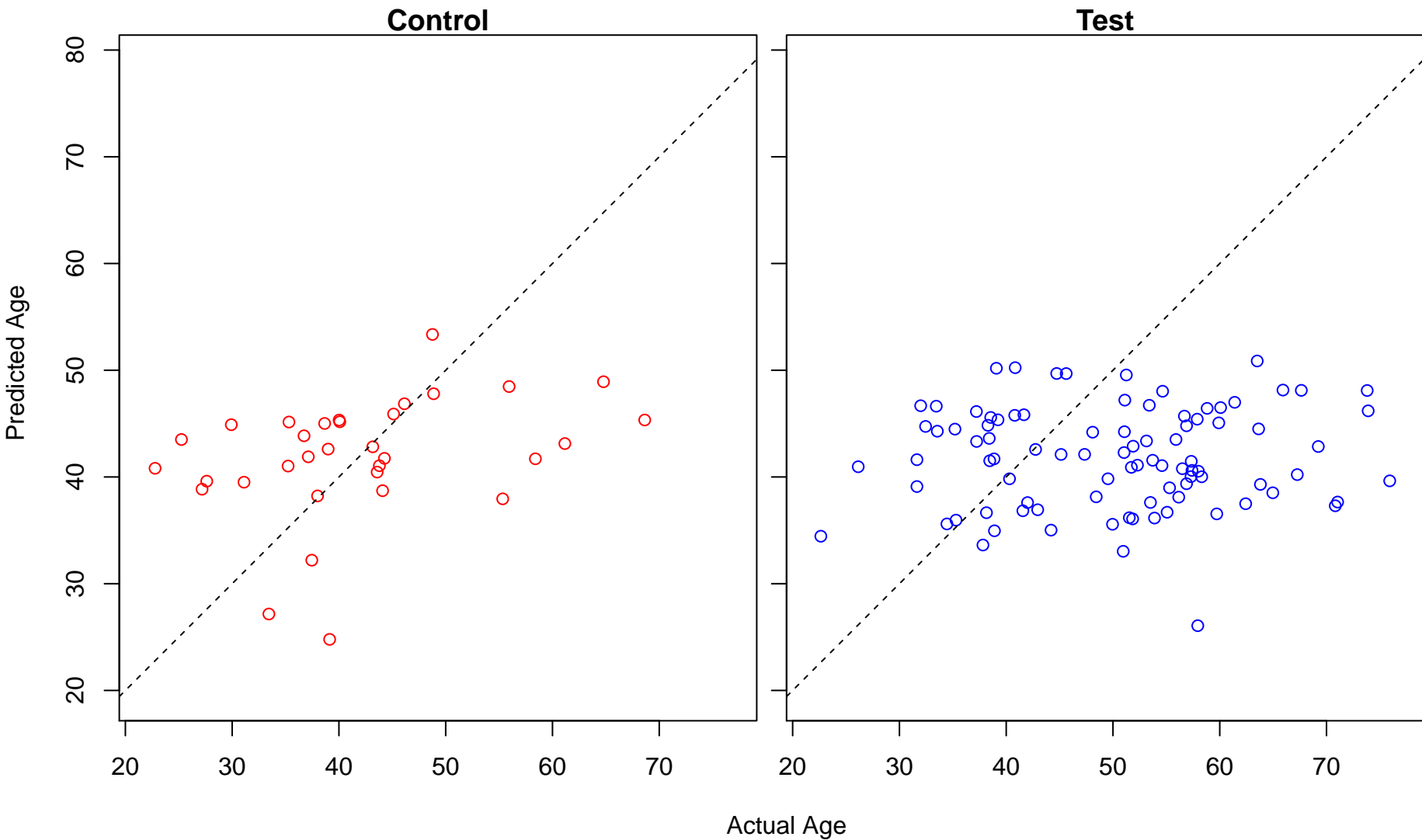
interleukin-12-mediated signaling pathway (Score: 0.450123)



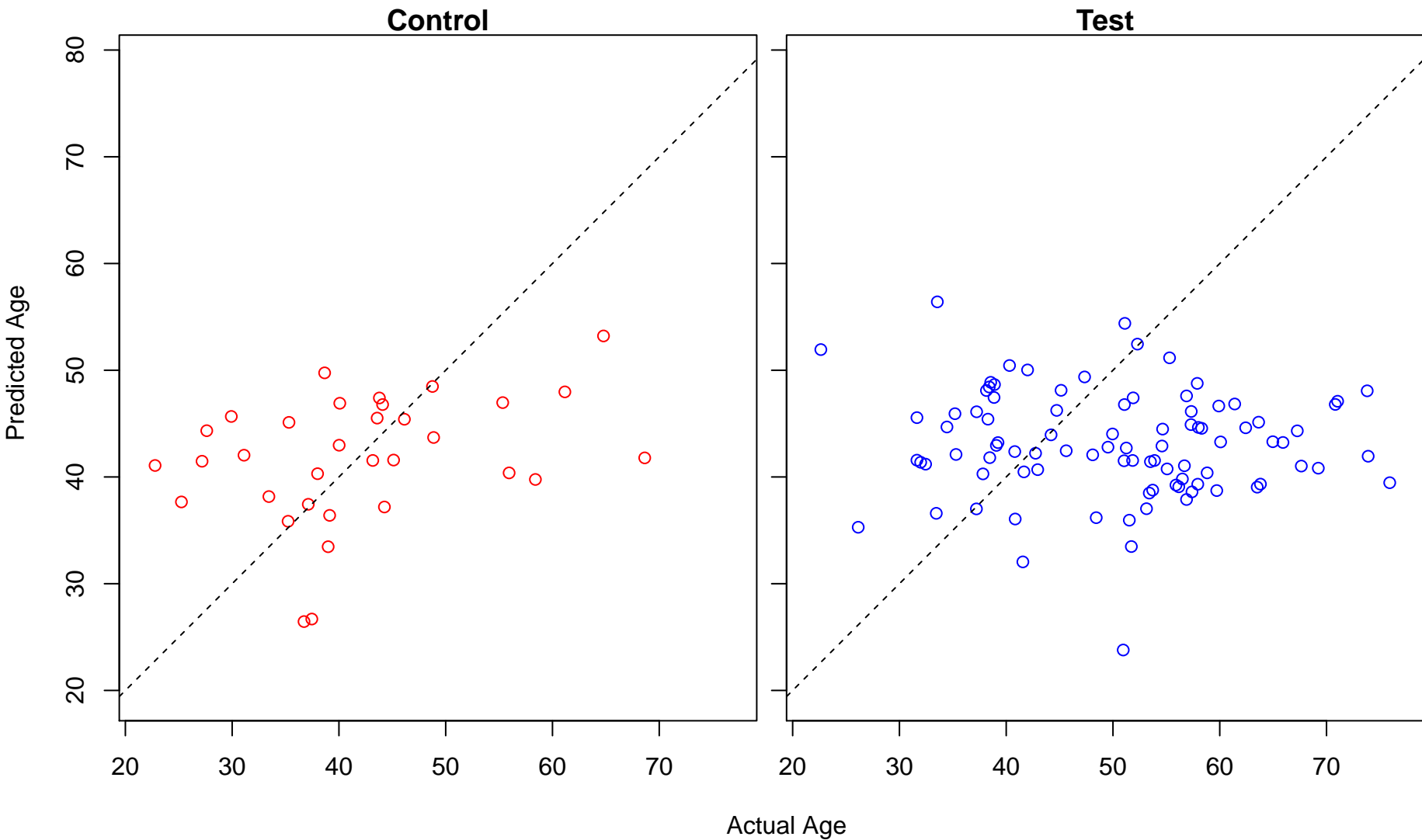
response to interleukin-12 (Score: 0.450123)



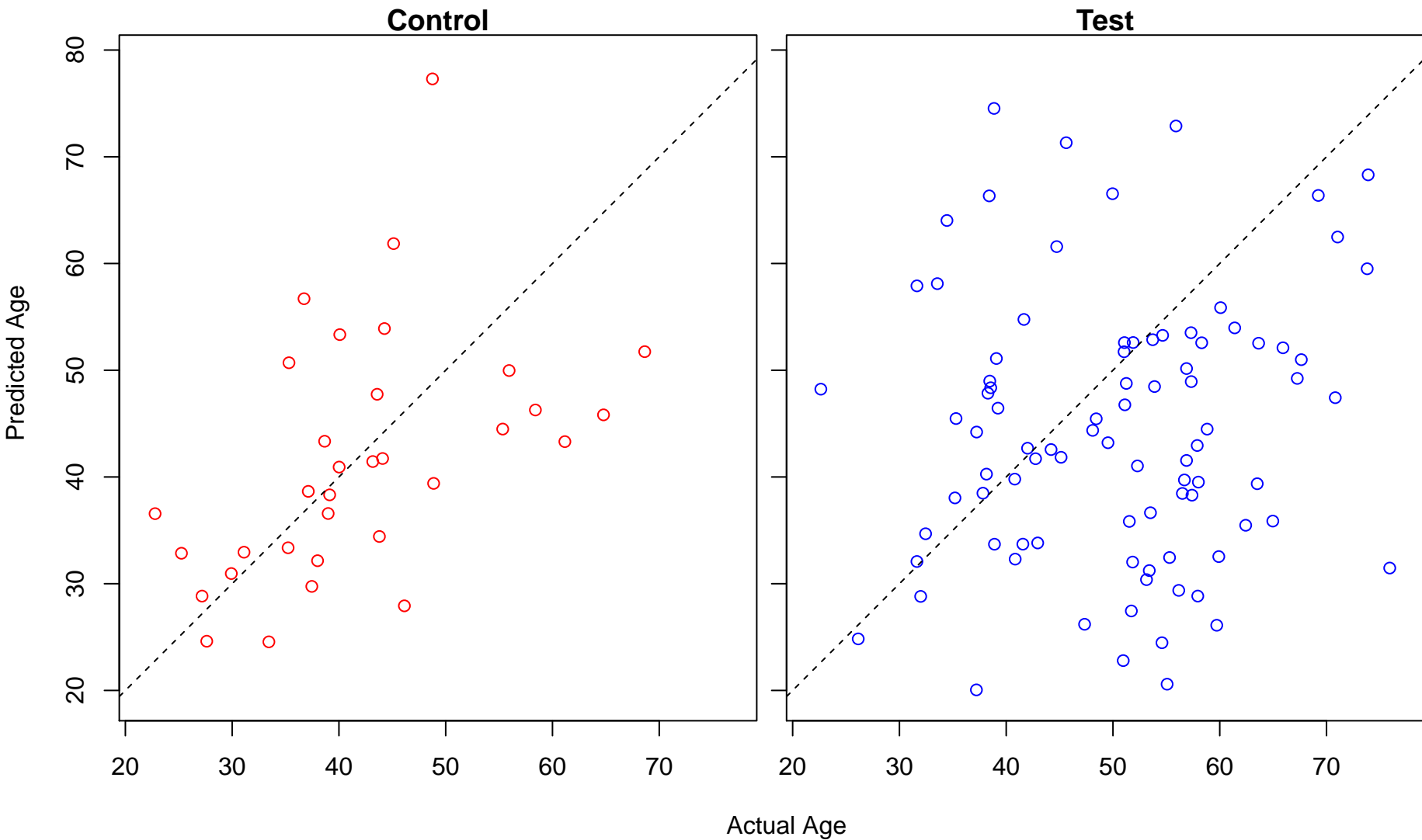
cellular response to interleukin-12 (Score: 0.450123)



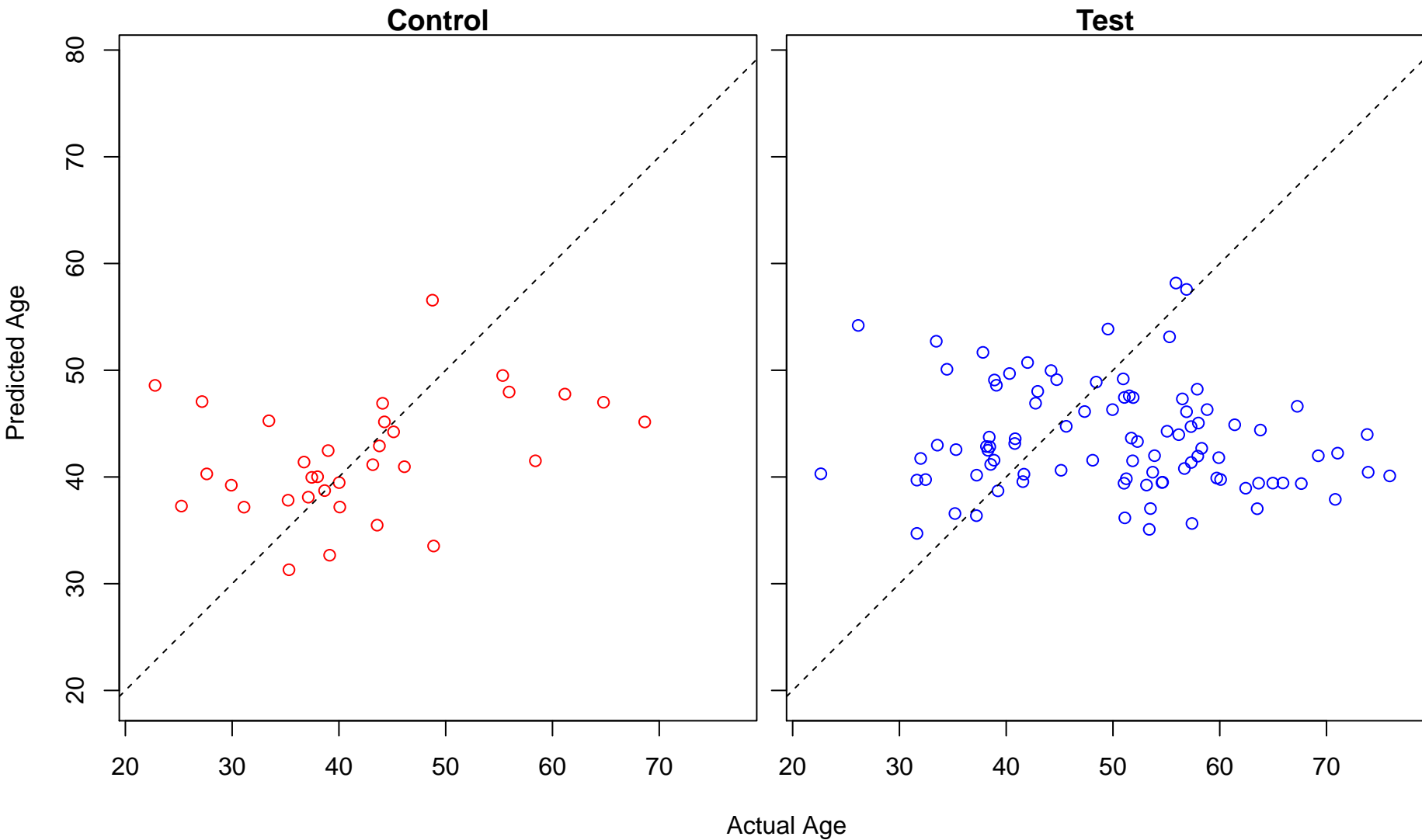
forebrain morphogenesis (Score: 0.449564)



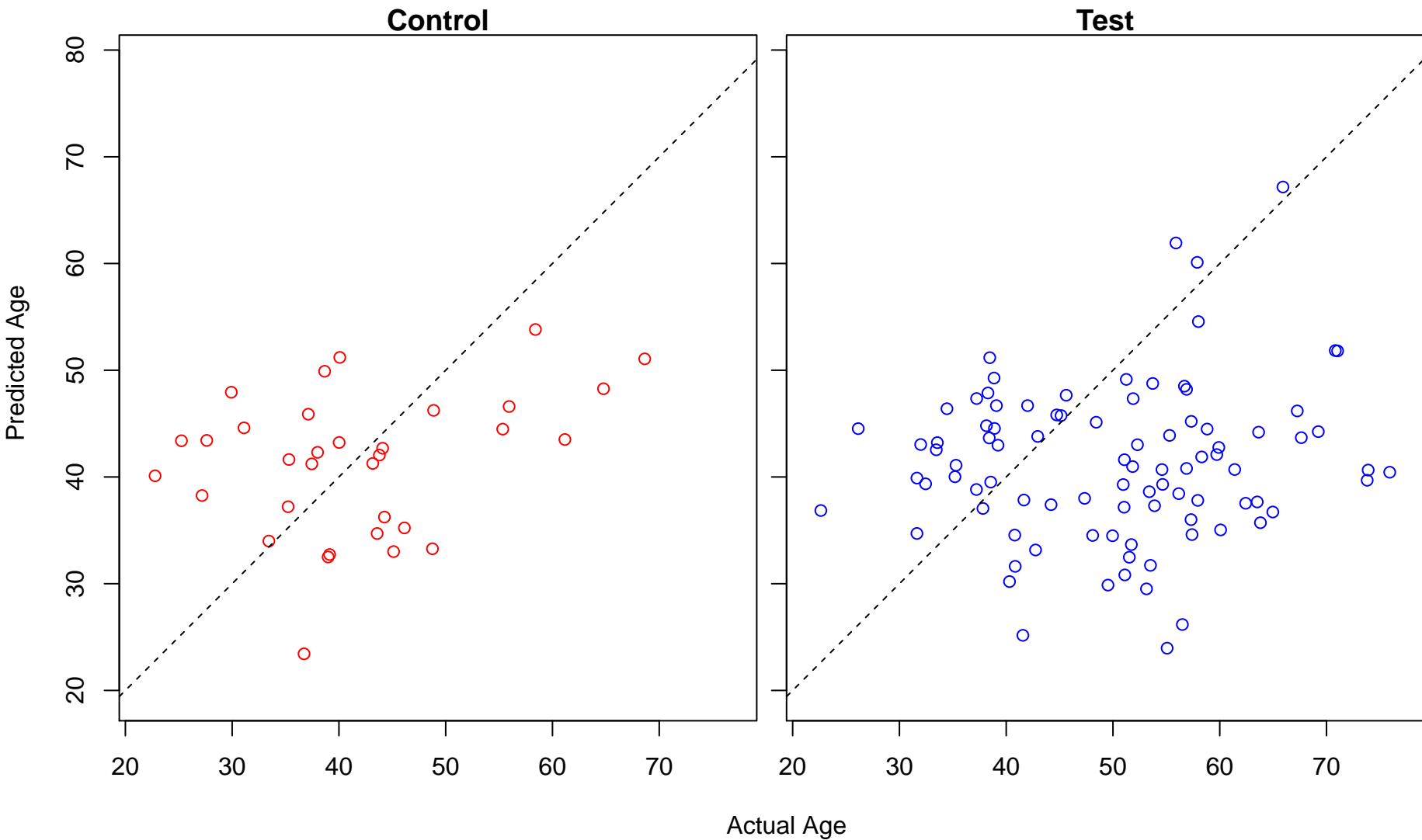
cellular response to starvation (Score: 0.449541)



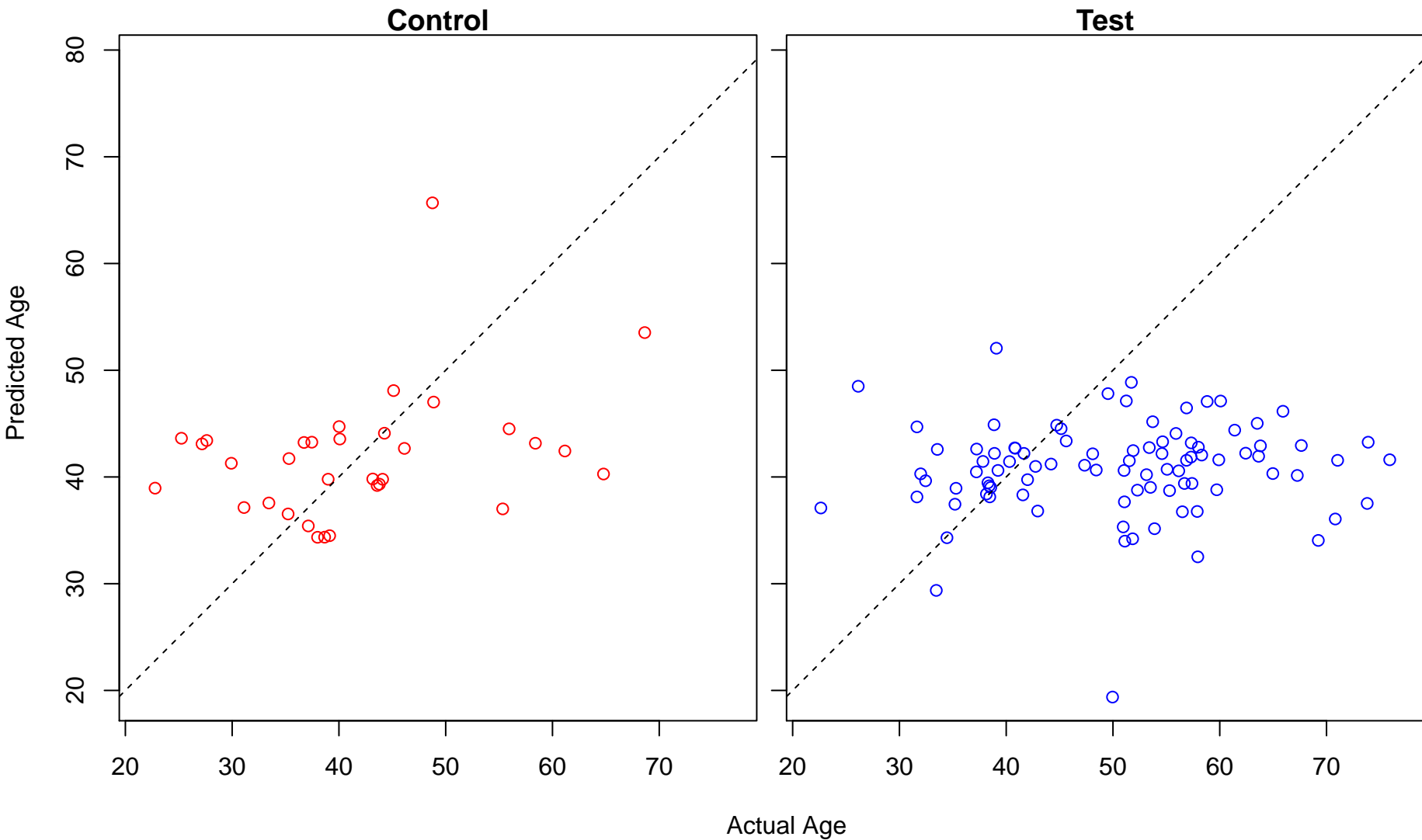
positive regulation of interferon-gamma biosynthetic process (Score: 0.448406)



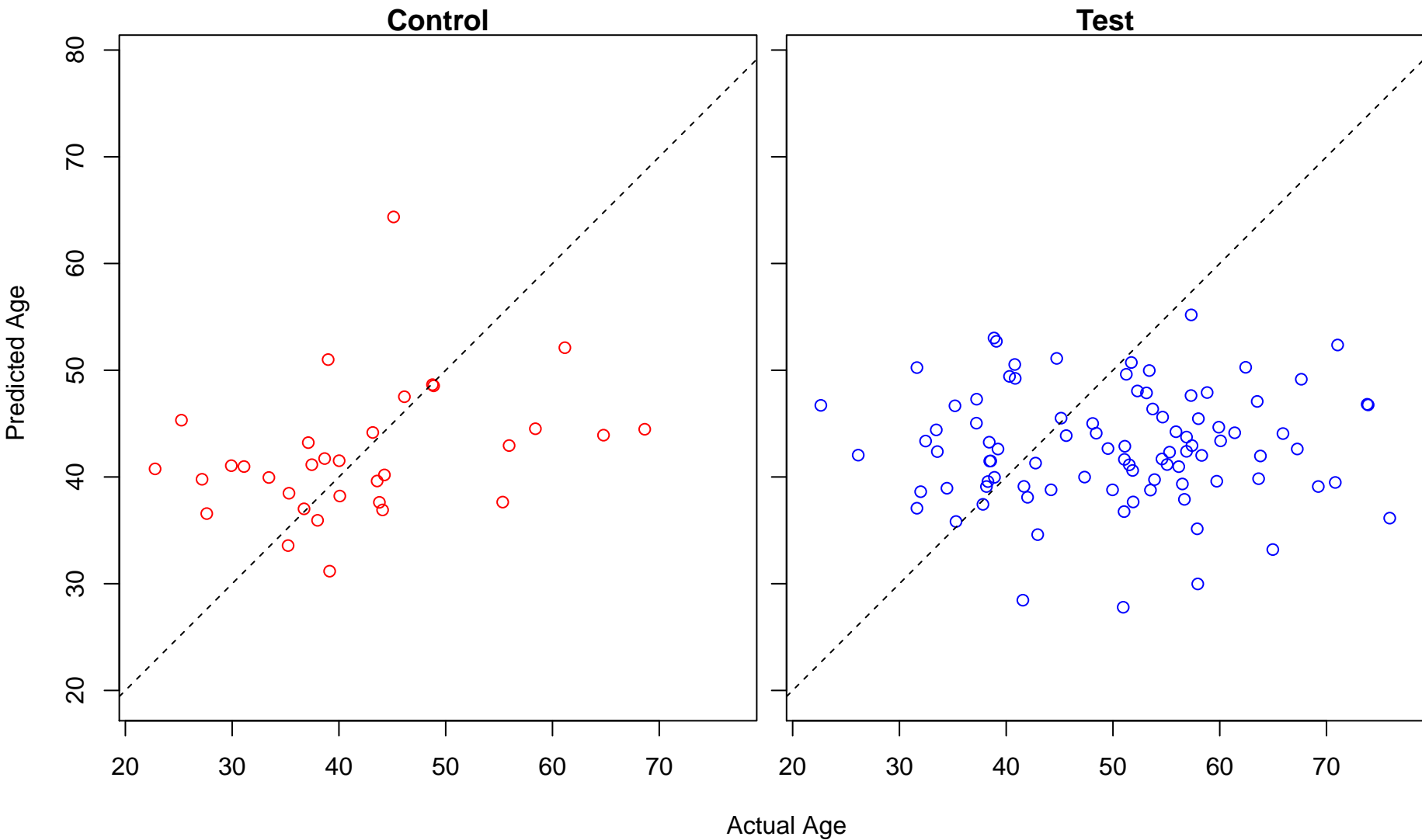
cell proliferation involved in kidney development (Score: 0.447869)



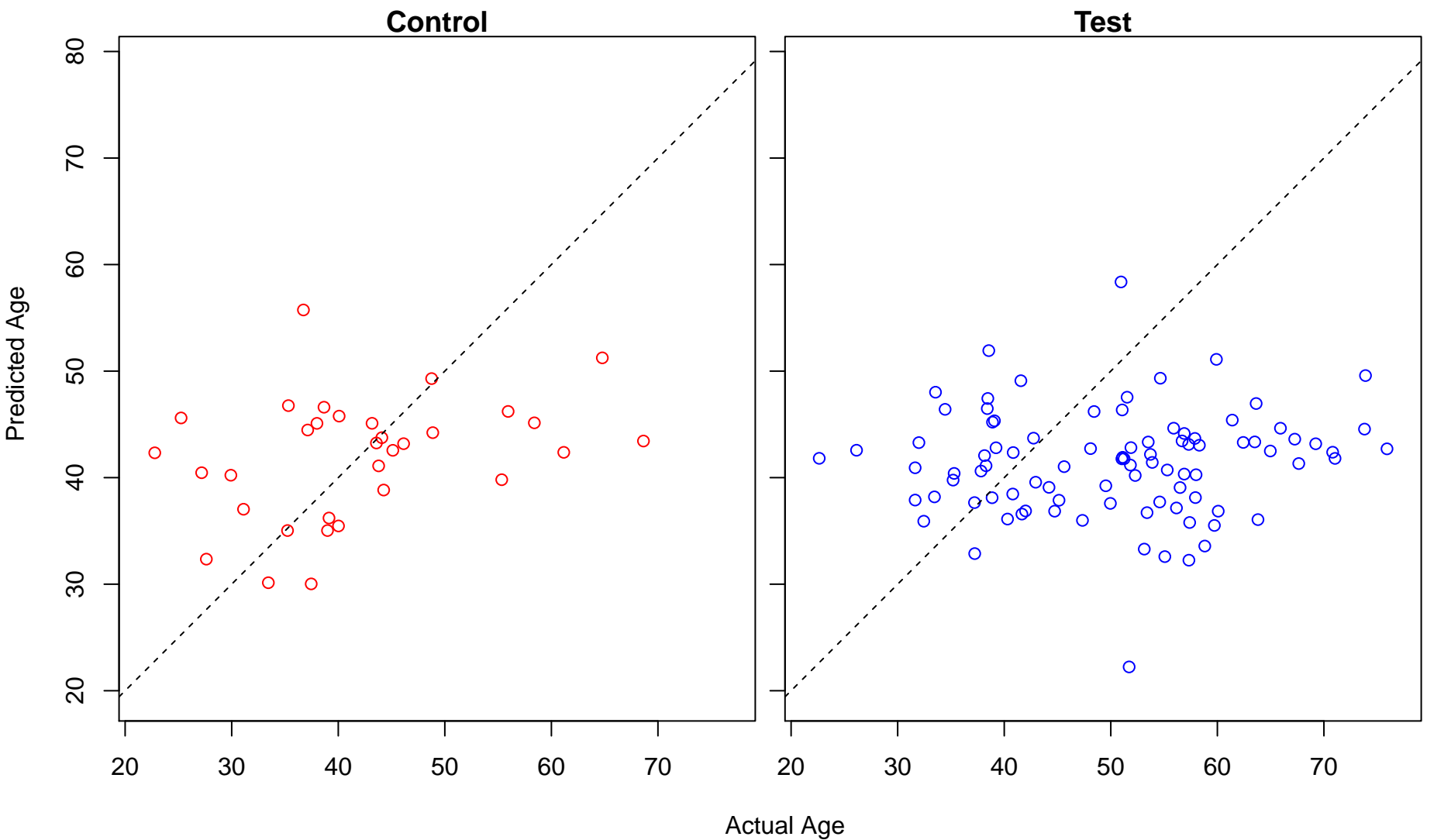
protein desumoylation (Score: 0.447686)



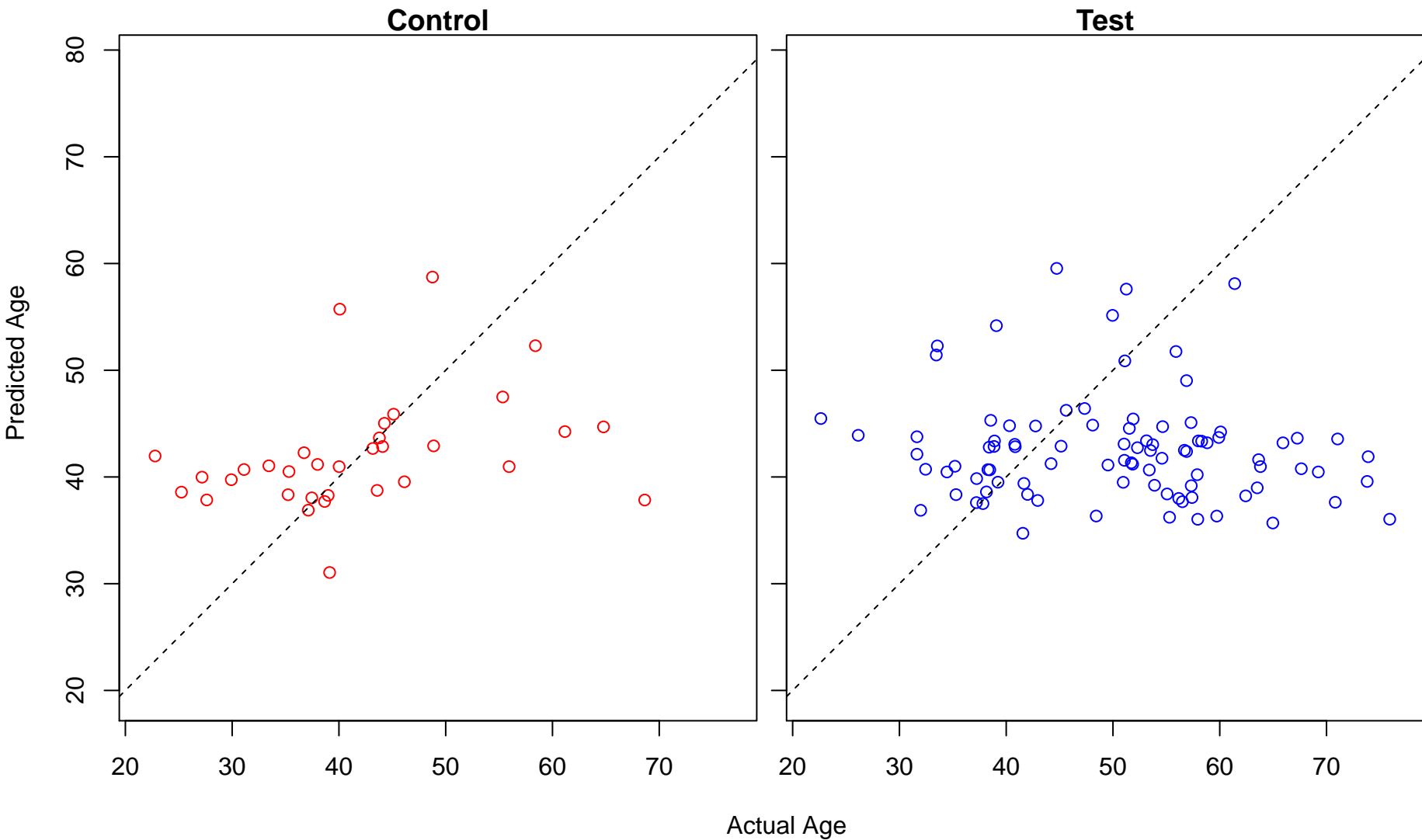
regulation of natural killer cell proliferation (Score: 0.446878)



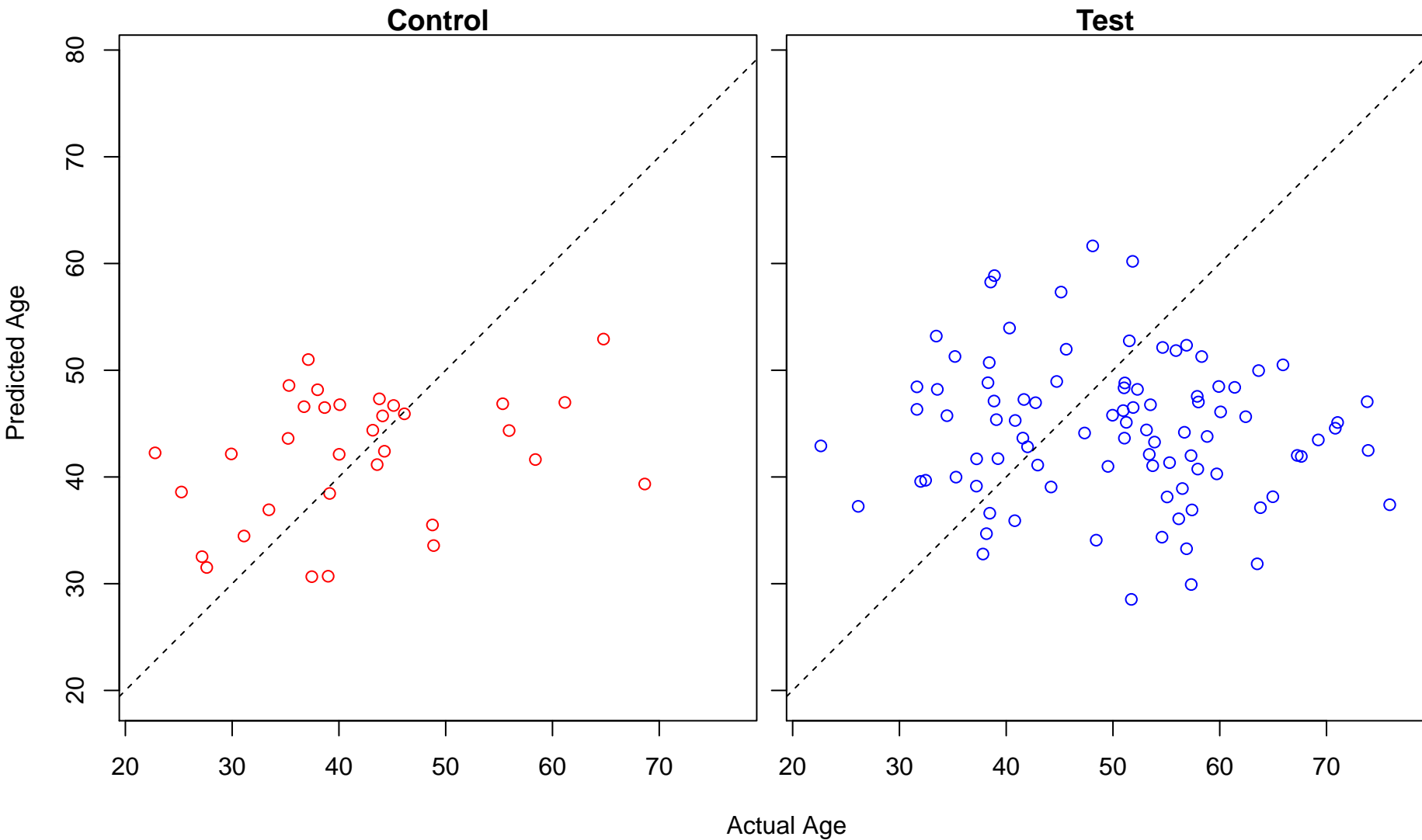
activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell (Sc



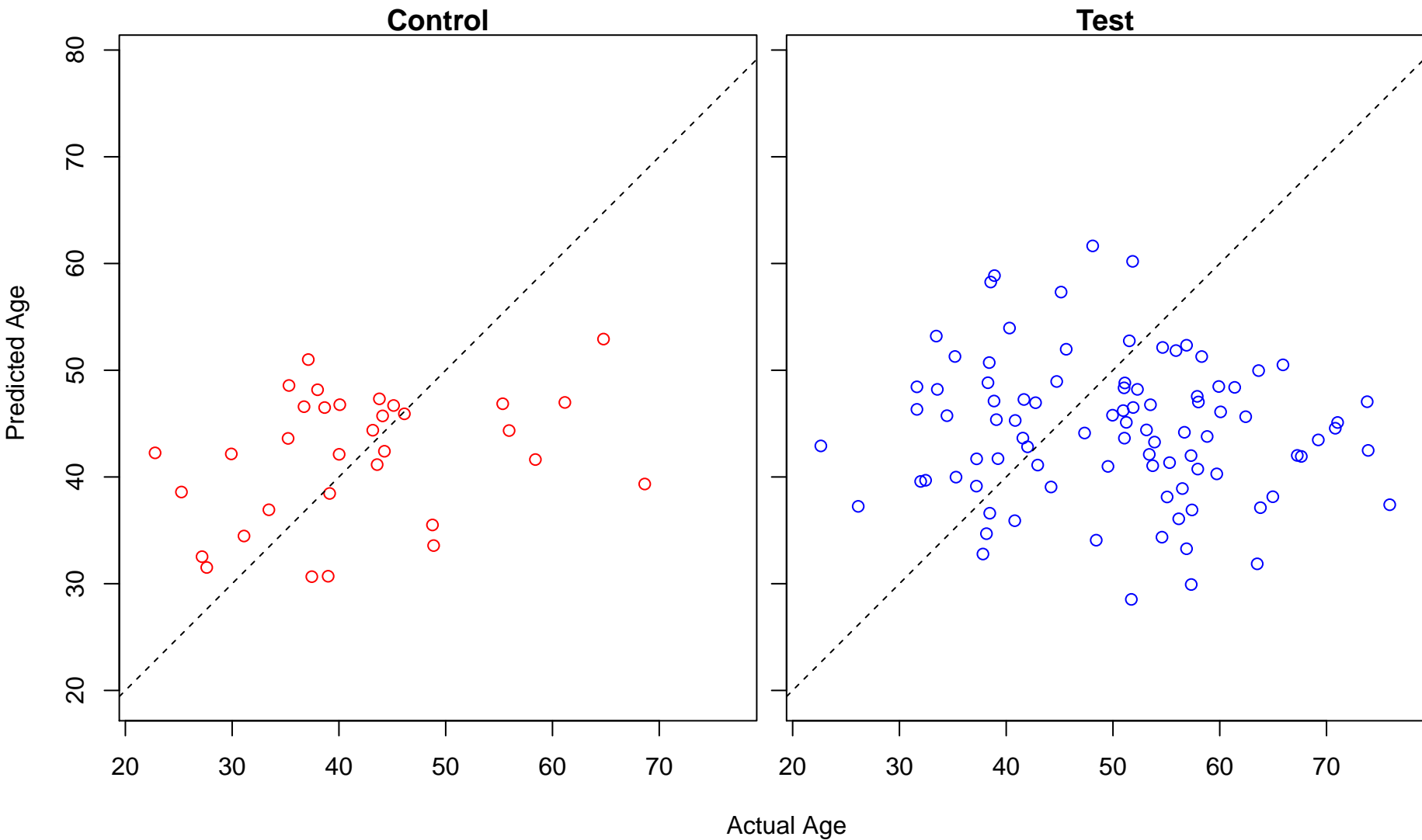
adenosine receptor signaling pathway (Score: 0.446221)



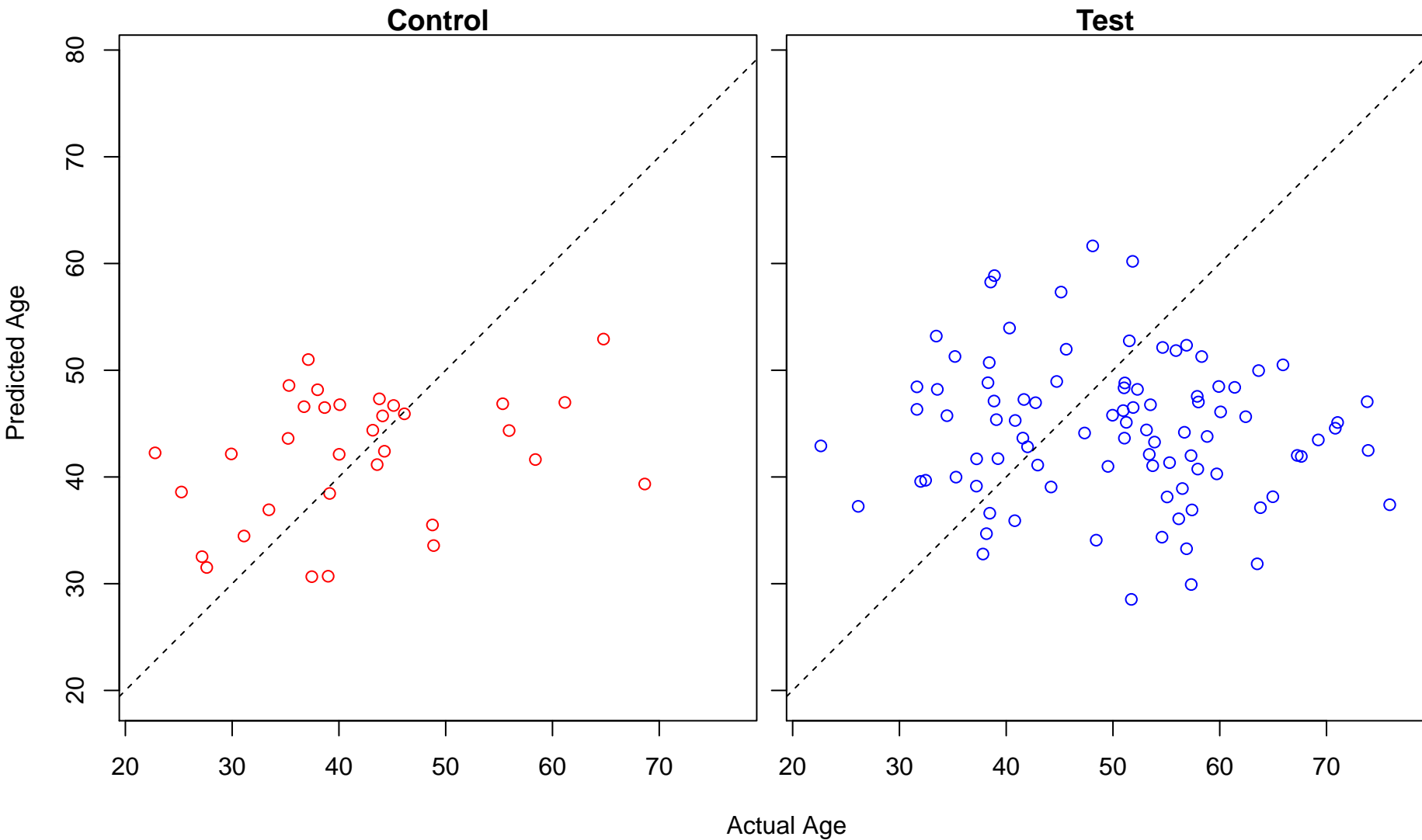
metanephric tubule development (Score: 0.446088)



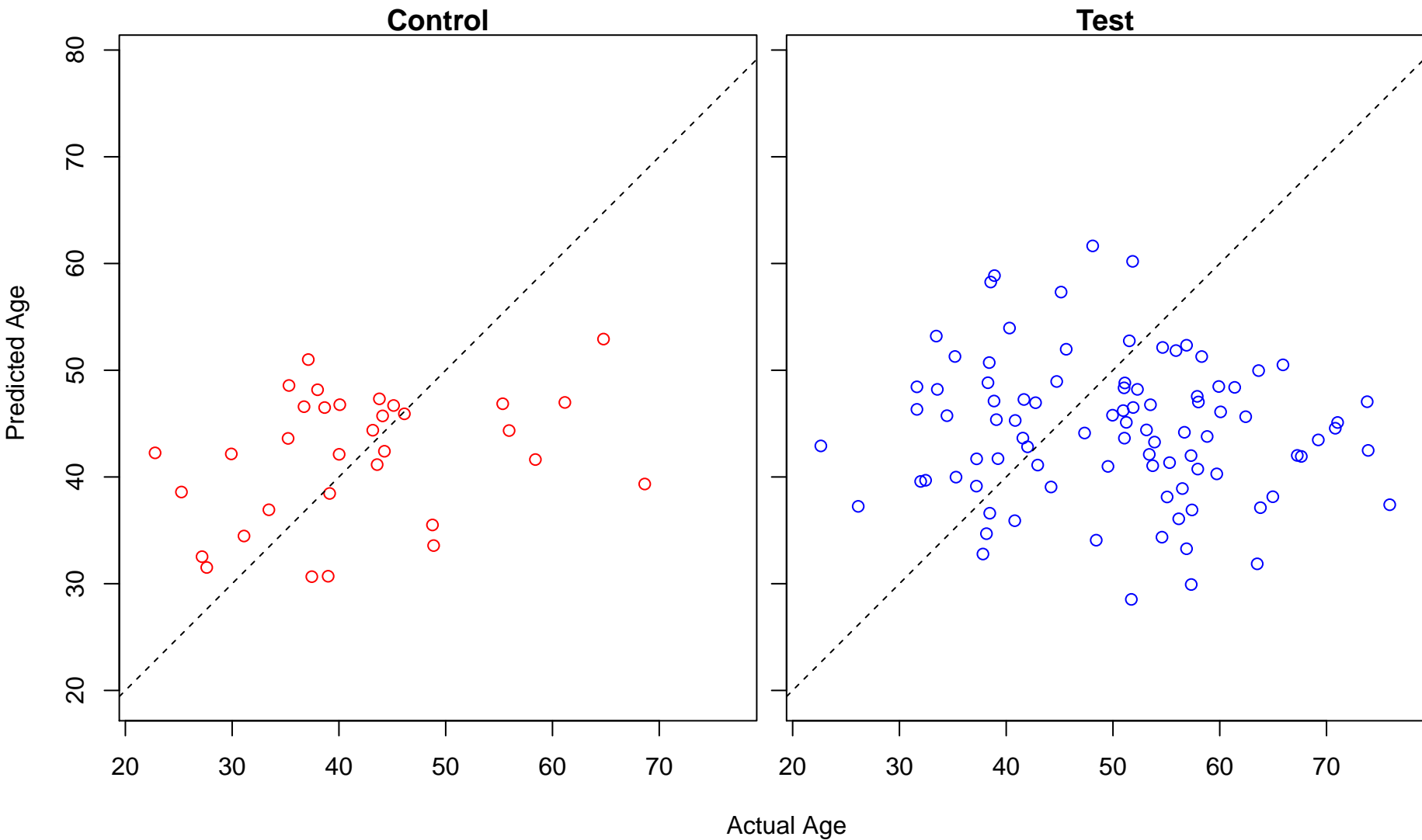
metanephric epithelium development (Score: 0.446088)



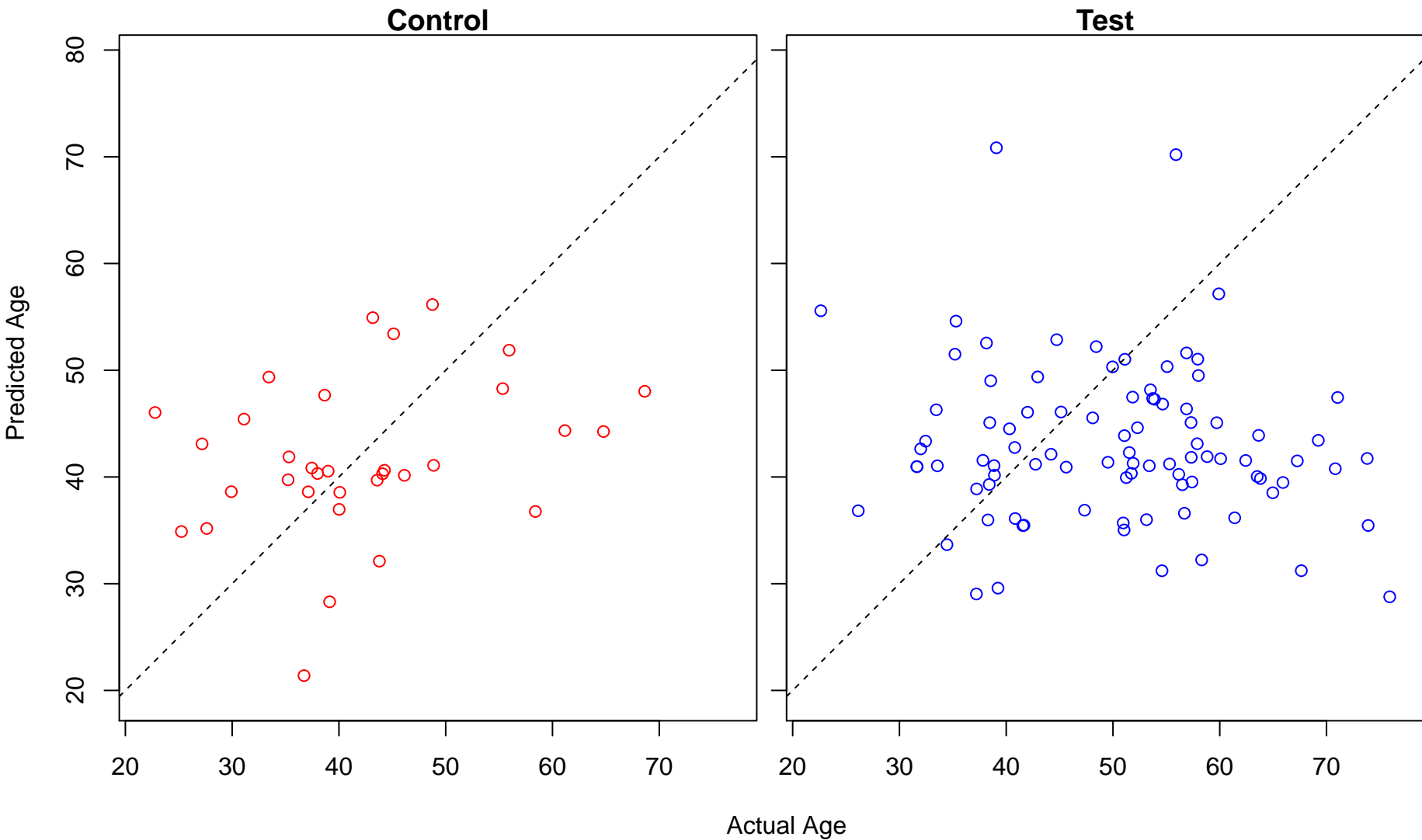
metanephric nephron tubule development (Score: 0.446088)



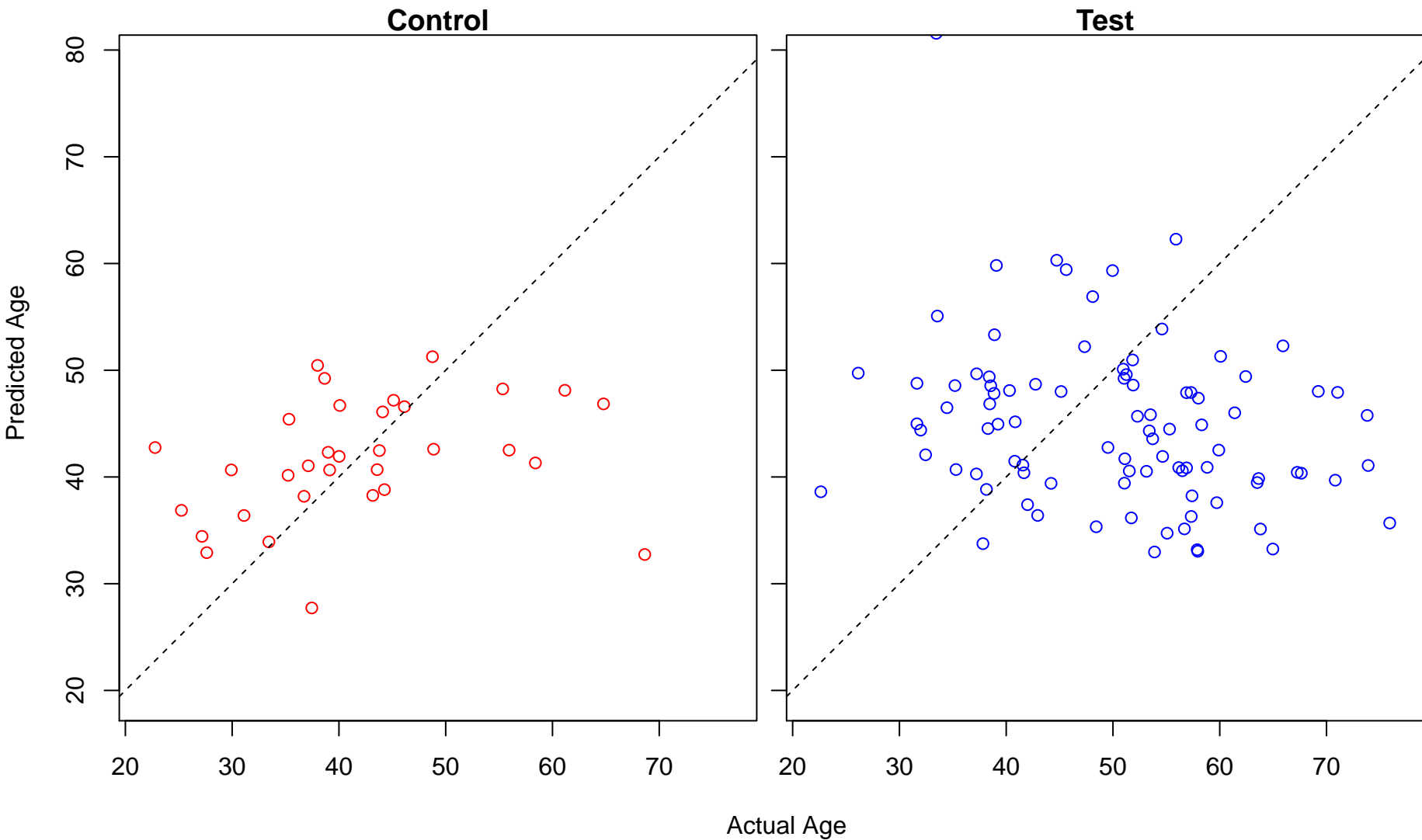
metanephric nephron epithelium development (Score: 0.446088)



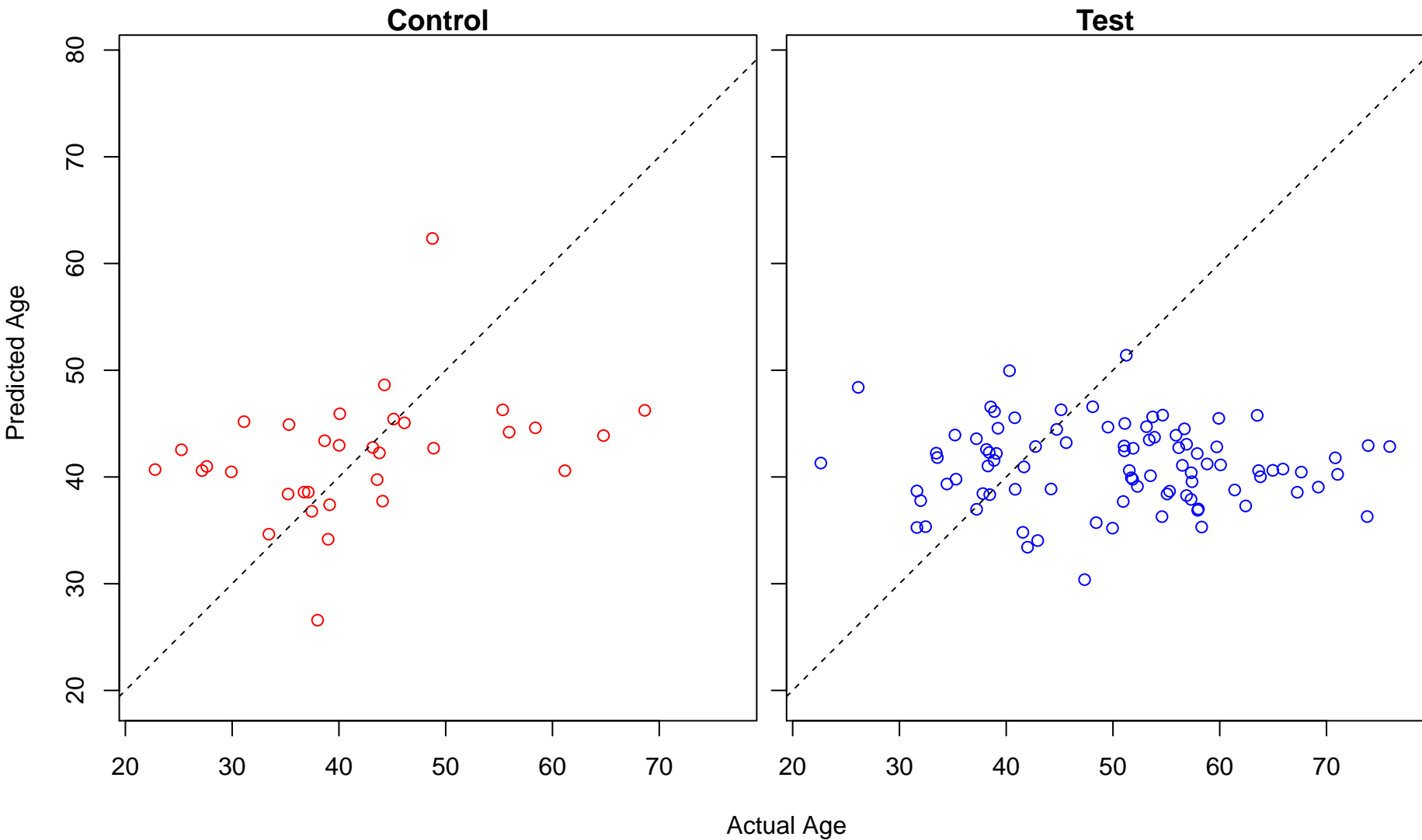
iron ion import (Score: 0.445775)



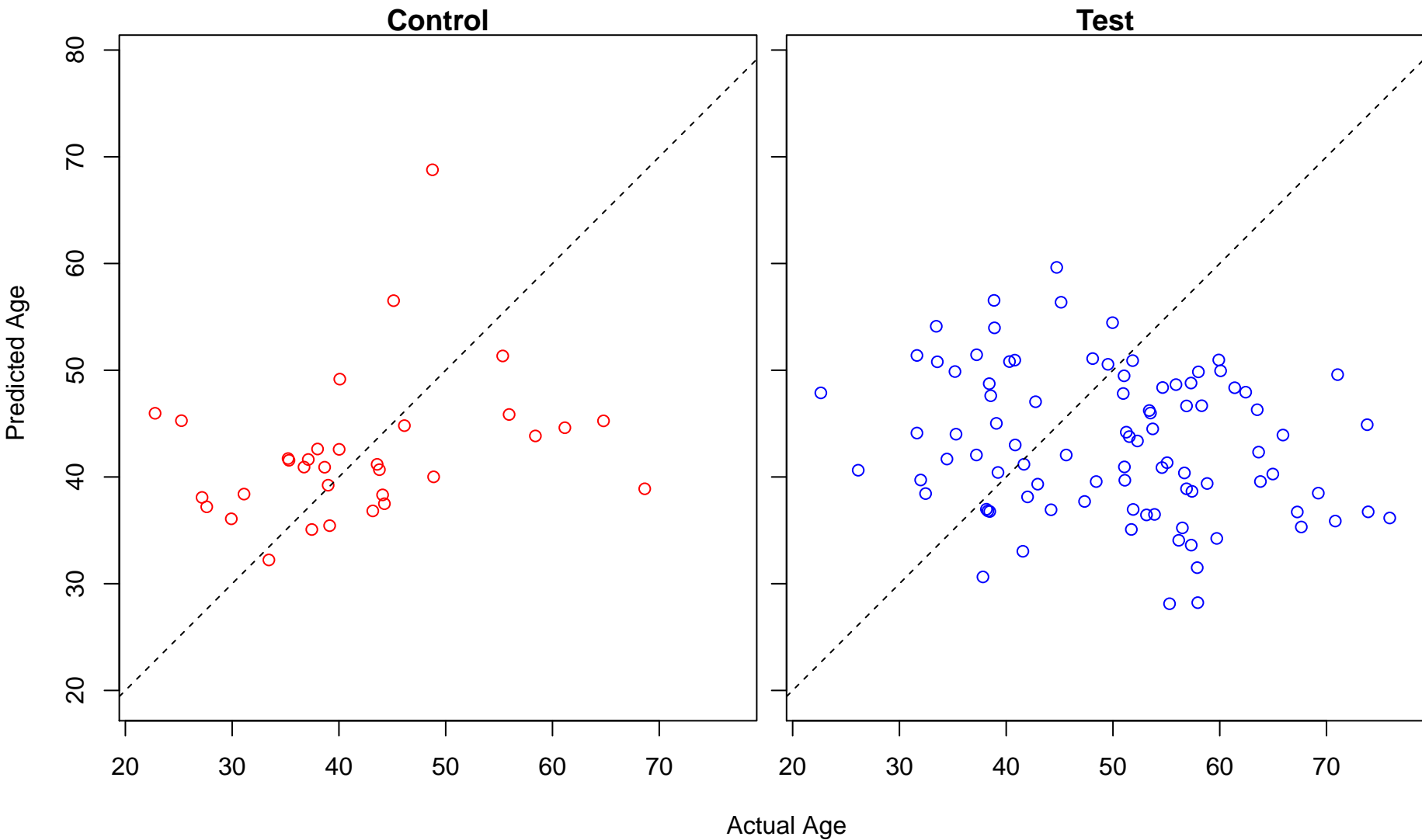
galactose catabolic process (Score: 0.444911)



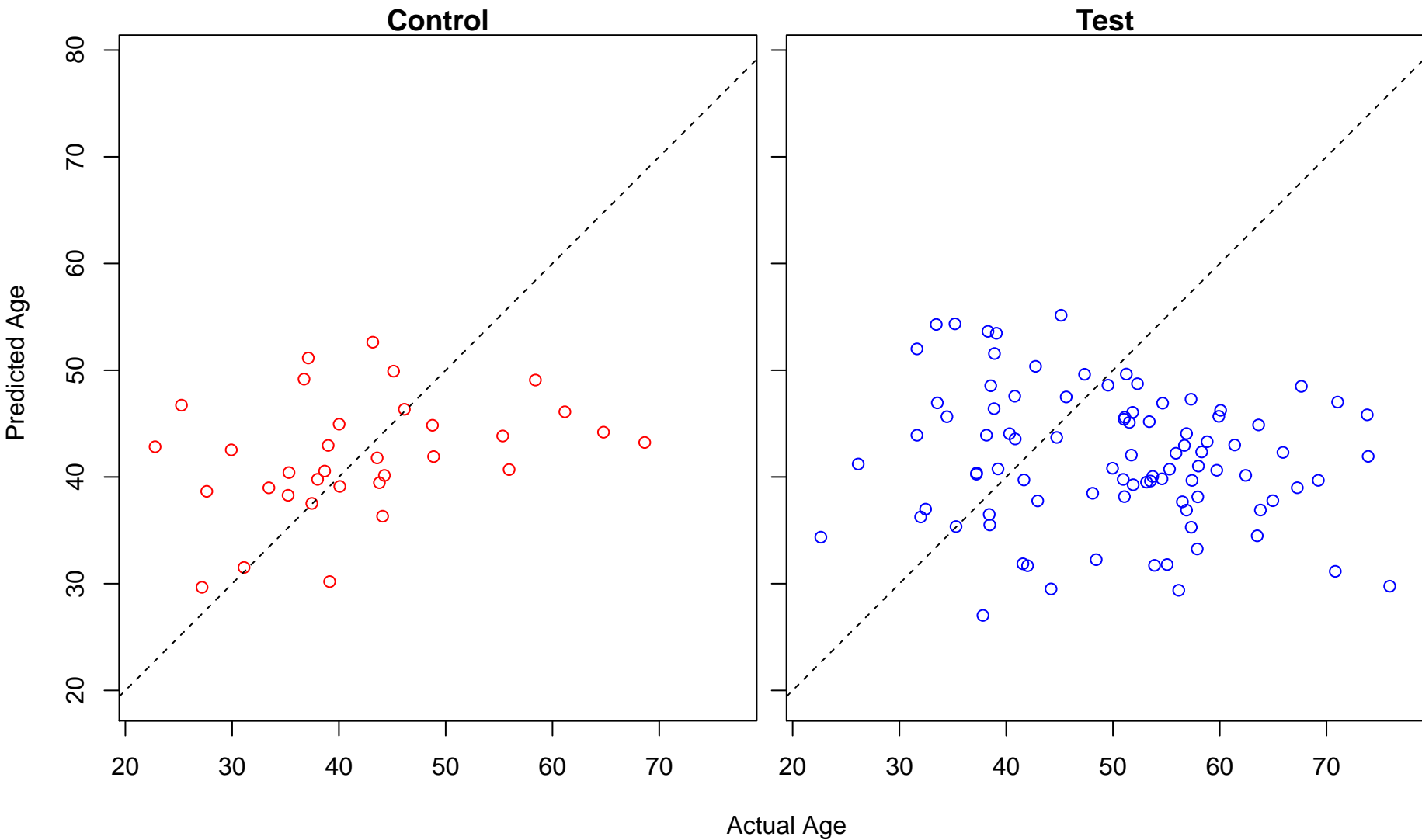
xylulose metabolic process (Score: 0.444828)



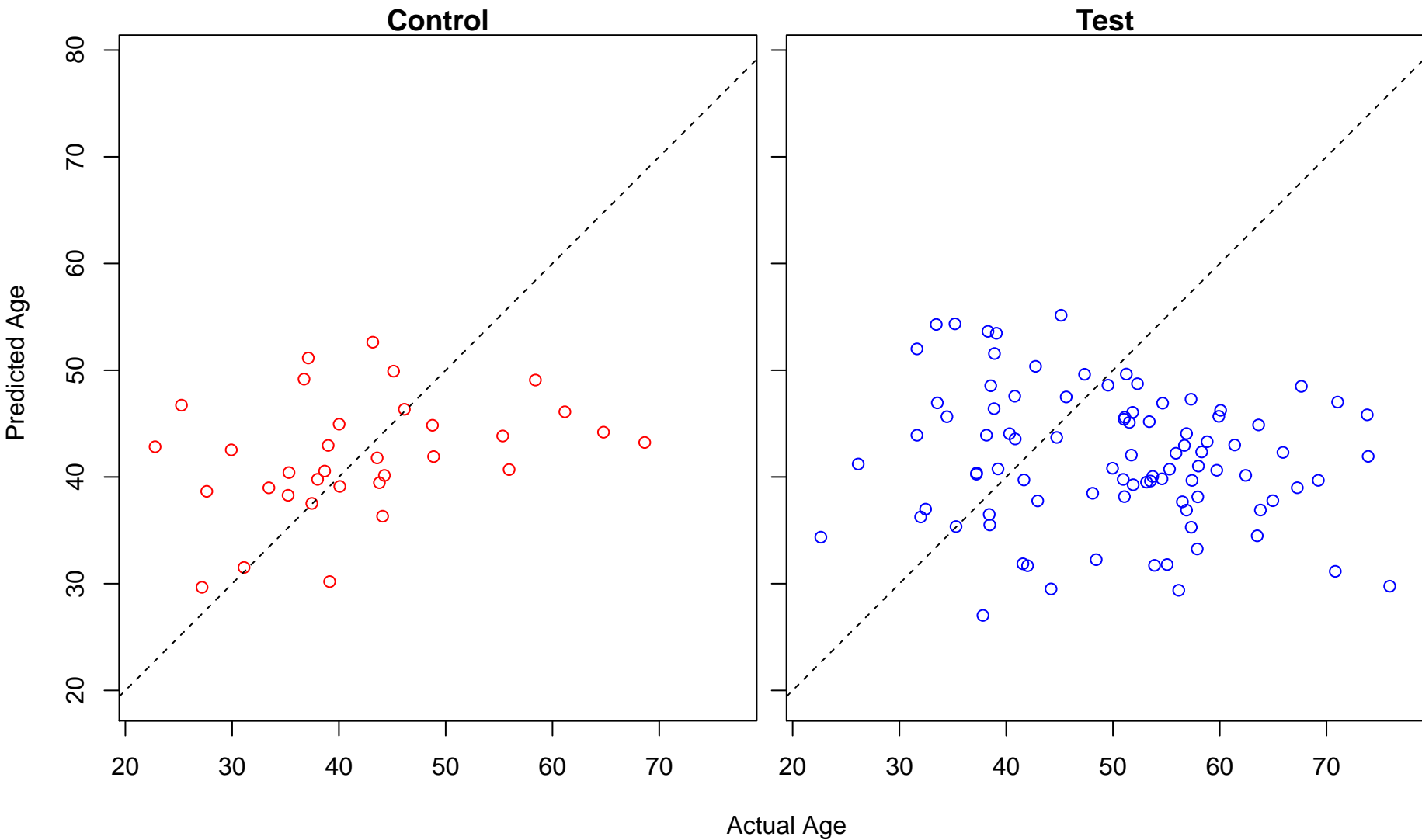
positive regulation of T cell chemotaxis (Score: 0.444472)



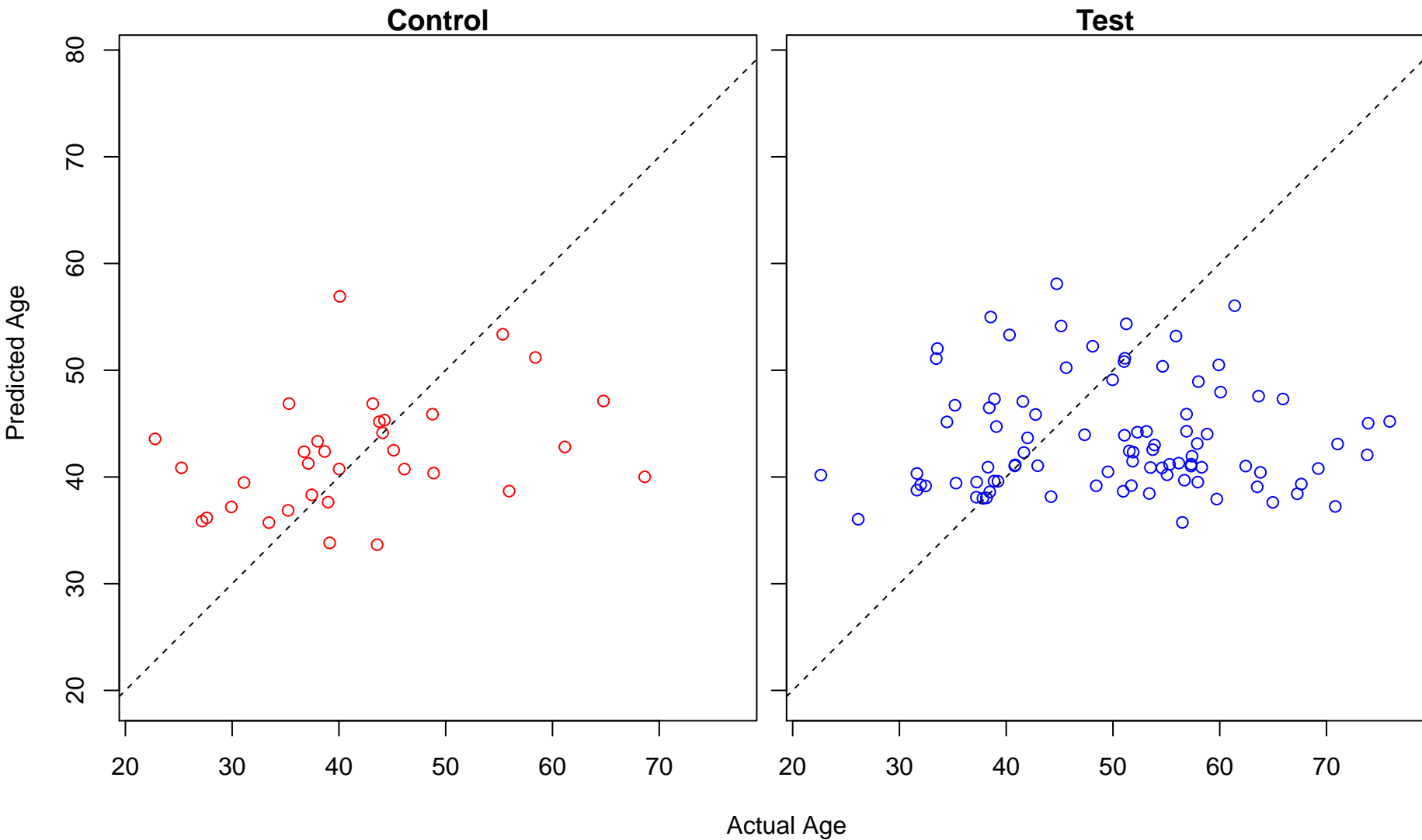
syncytium formation by plasma membrane fusion (Score: 0.441910)



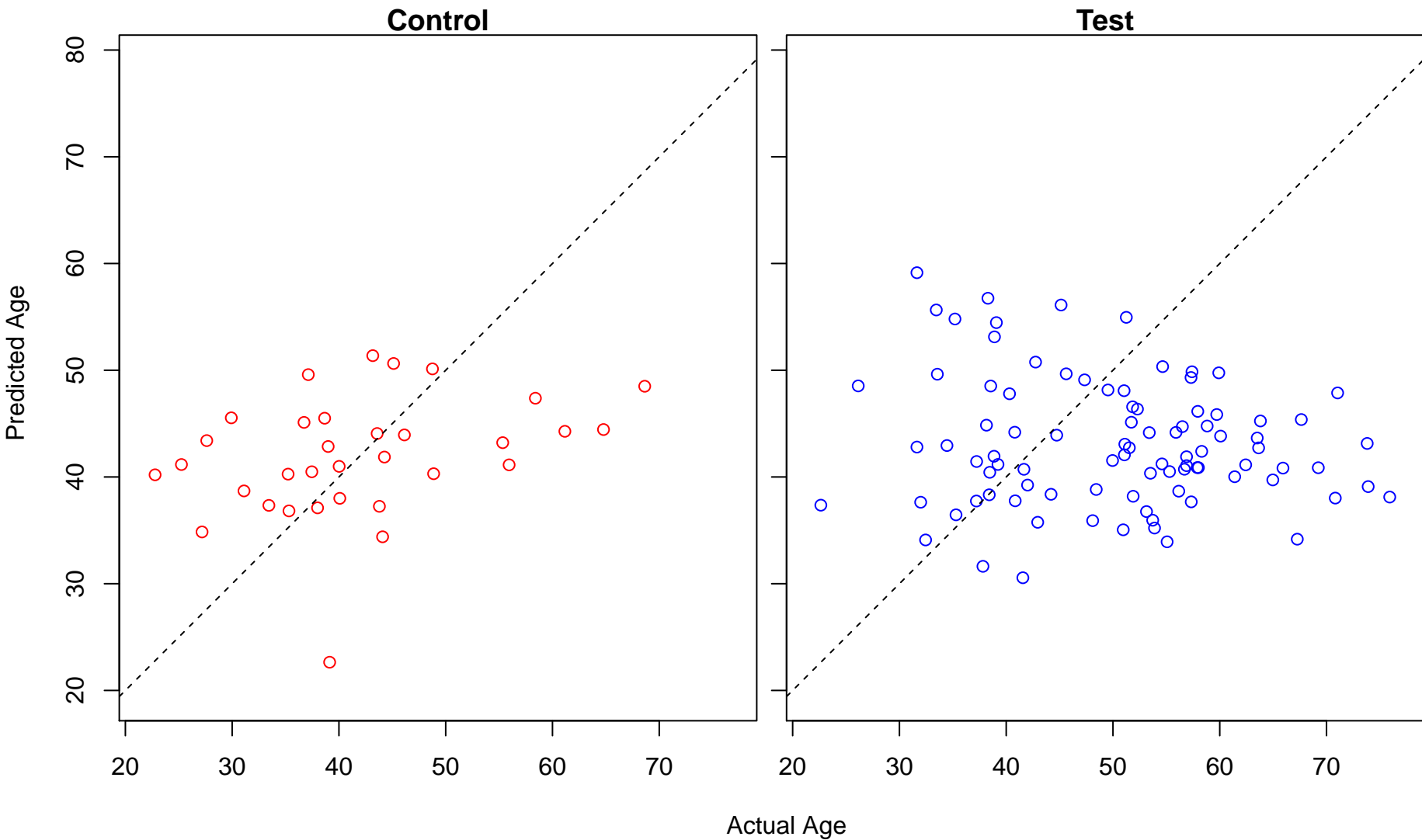
syncytium formation (Score: 0.441910)



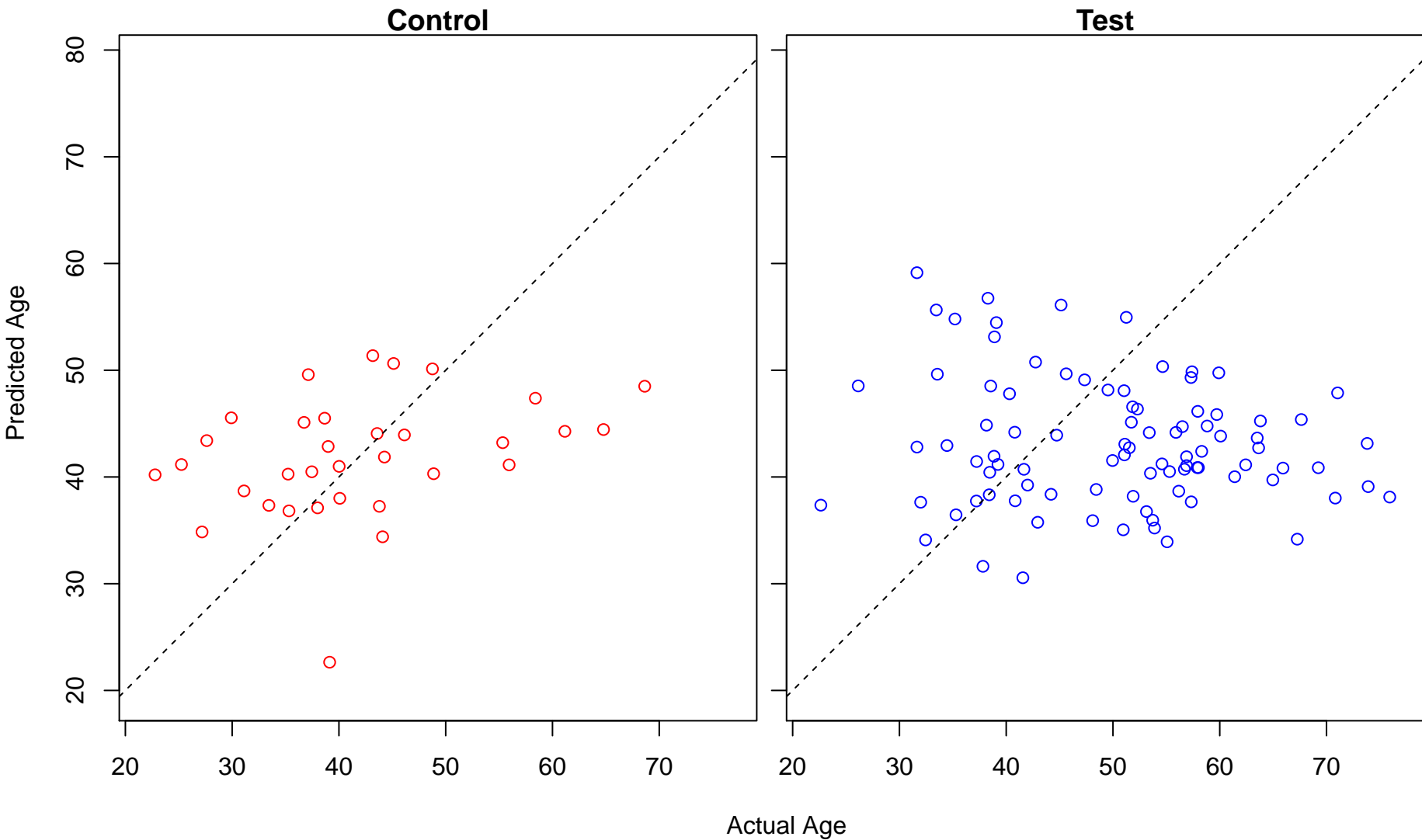
pyrimidine ribonucleoside biosynthetic process (Score: 0.441359)



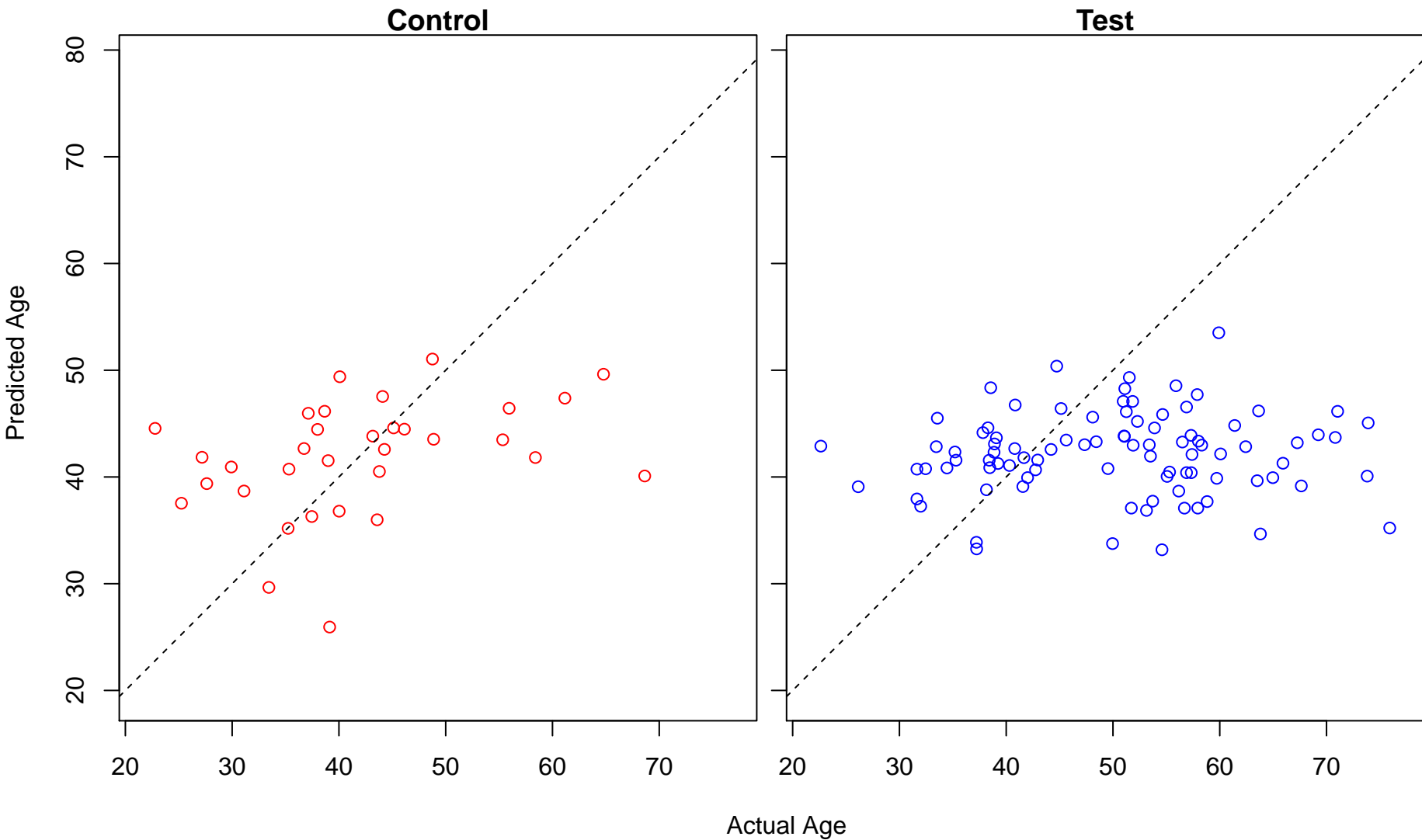
regulation of acrosome reaction (Score: 0.440796)



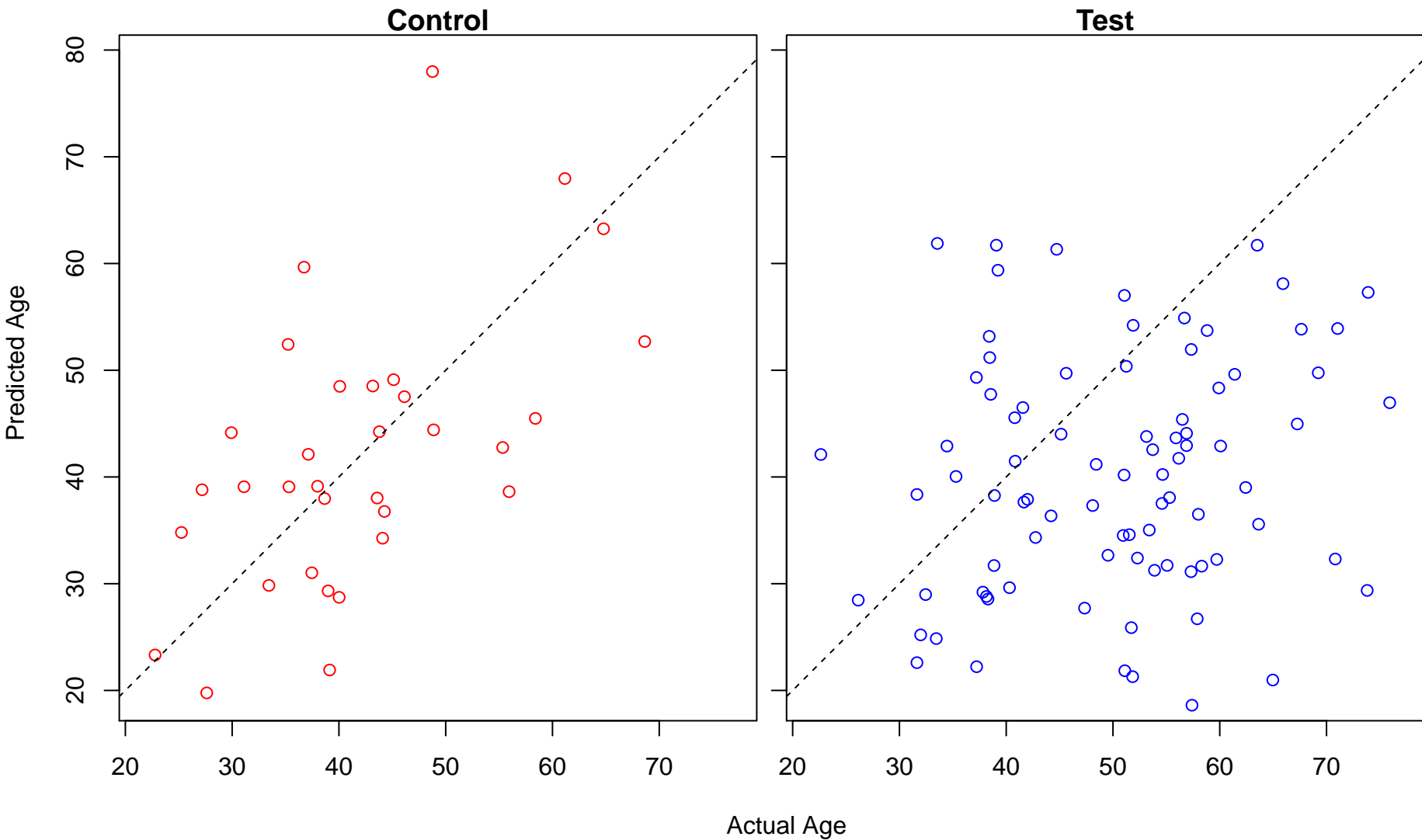
positive regulation of acrosome reaction (Score: 0.440796)



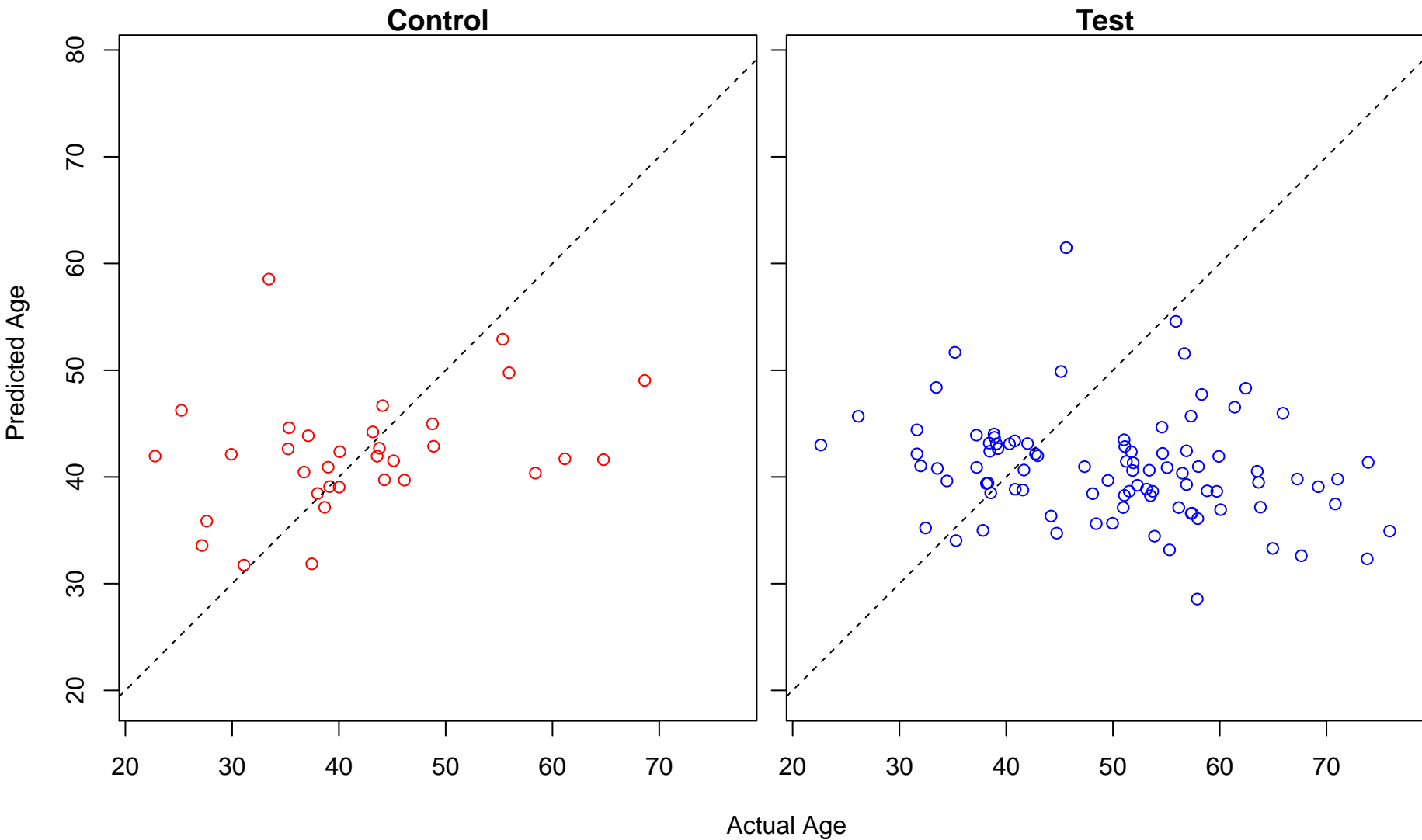
phagosome acidification (Score: 0.440740)



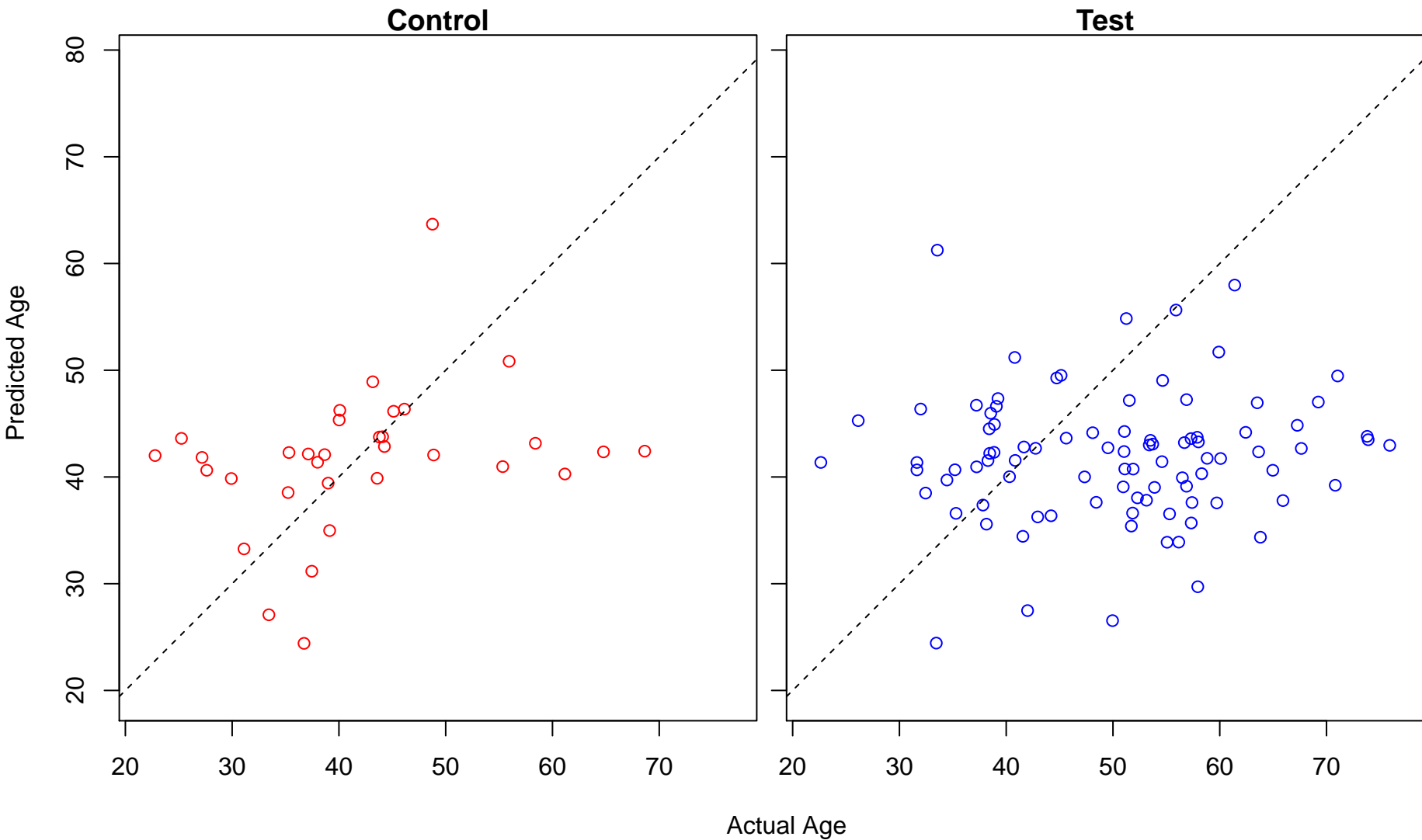
cellular response to lipopolysaccharide (Score: 0.439316)



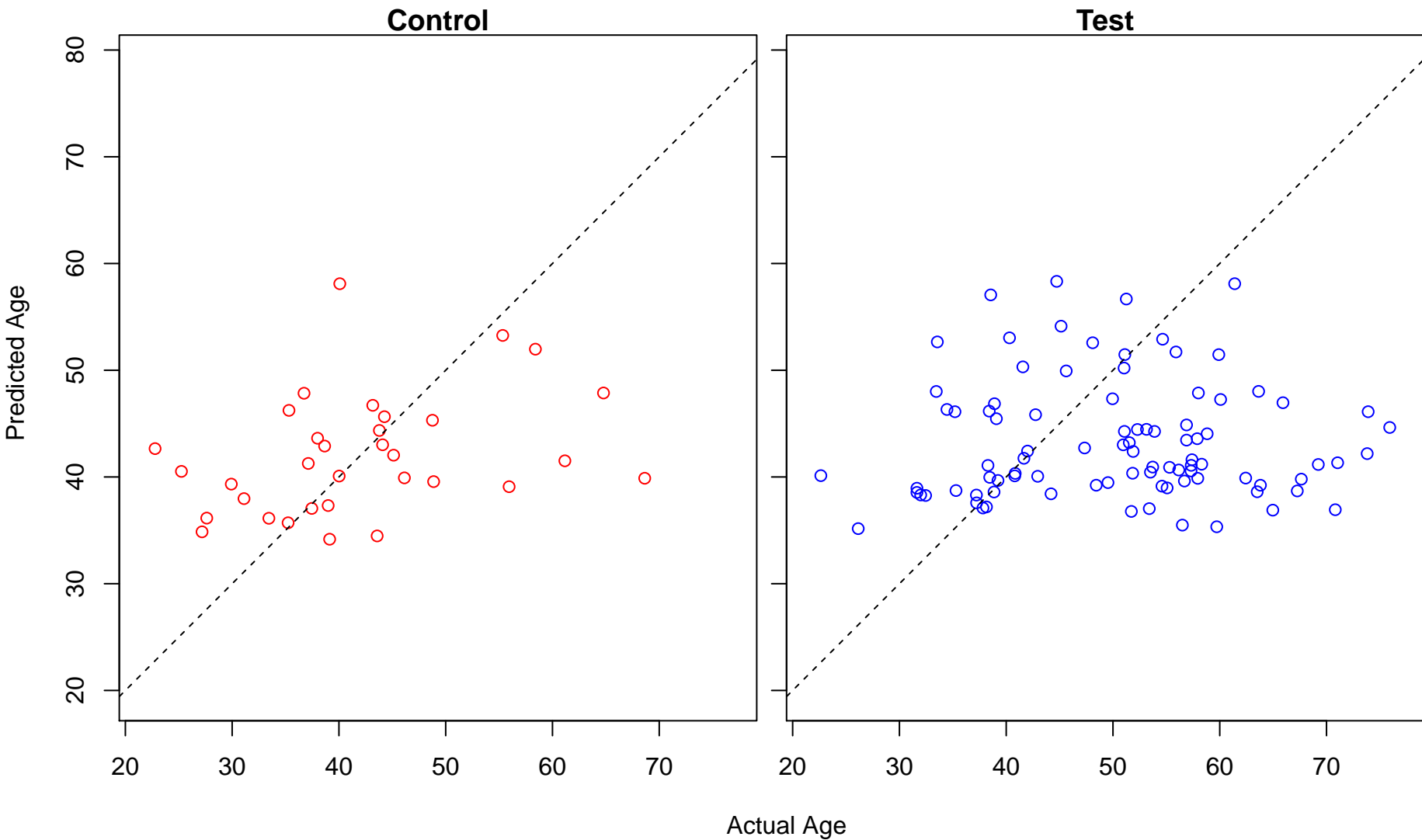
response to salt stress (Score: 0.437432)



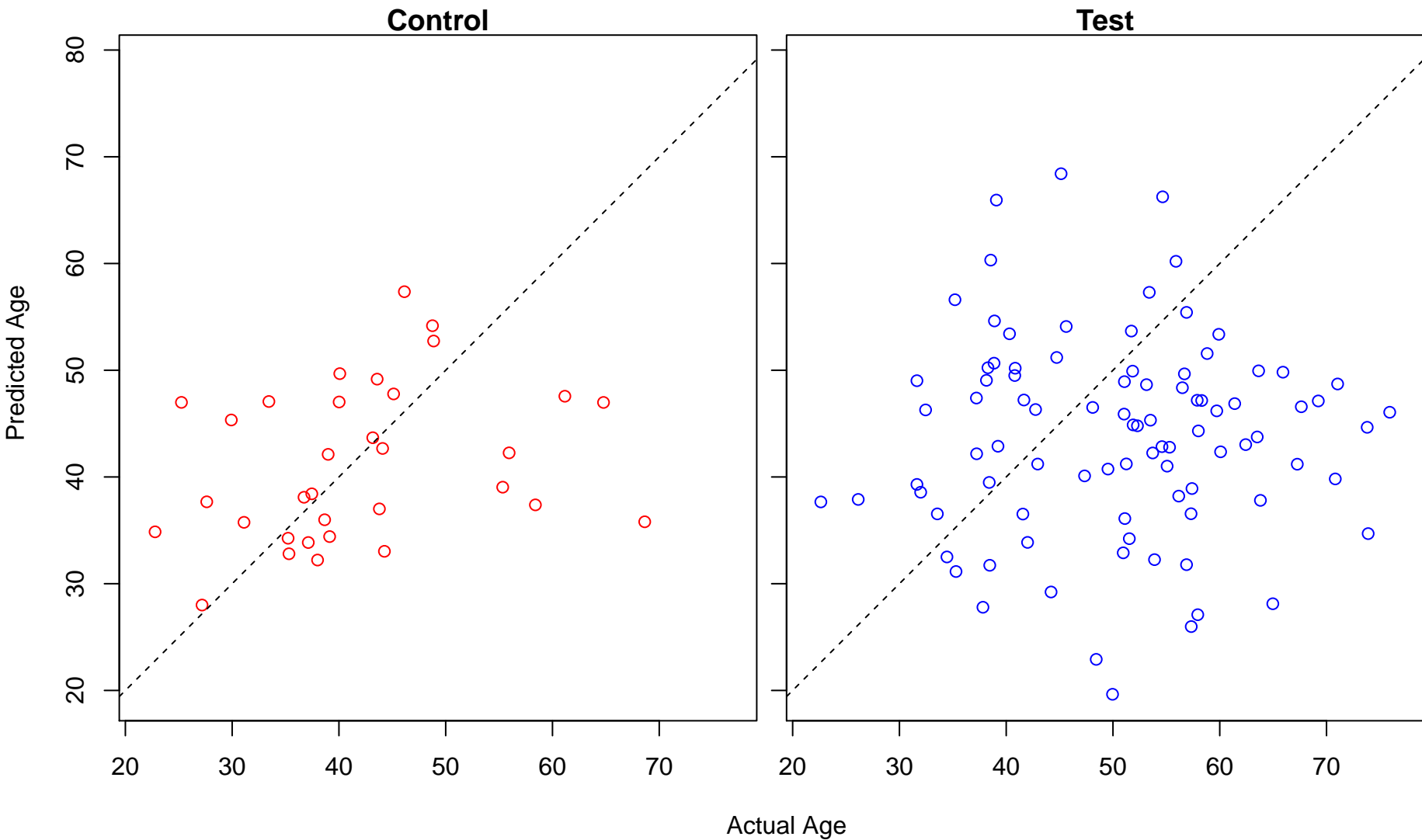
secretory granule organization (Score: 0.437422)



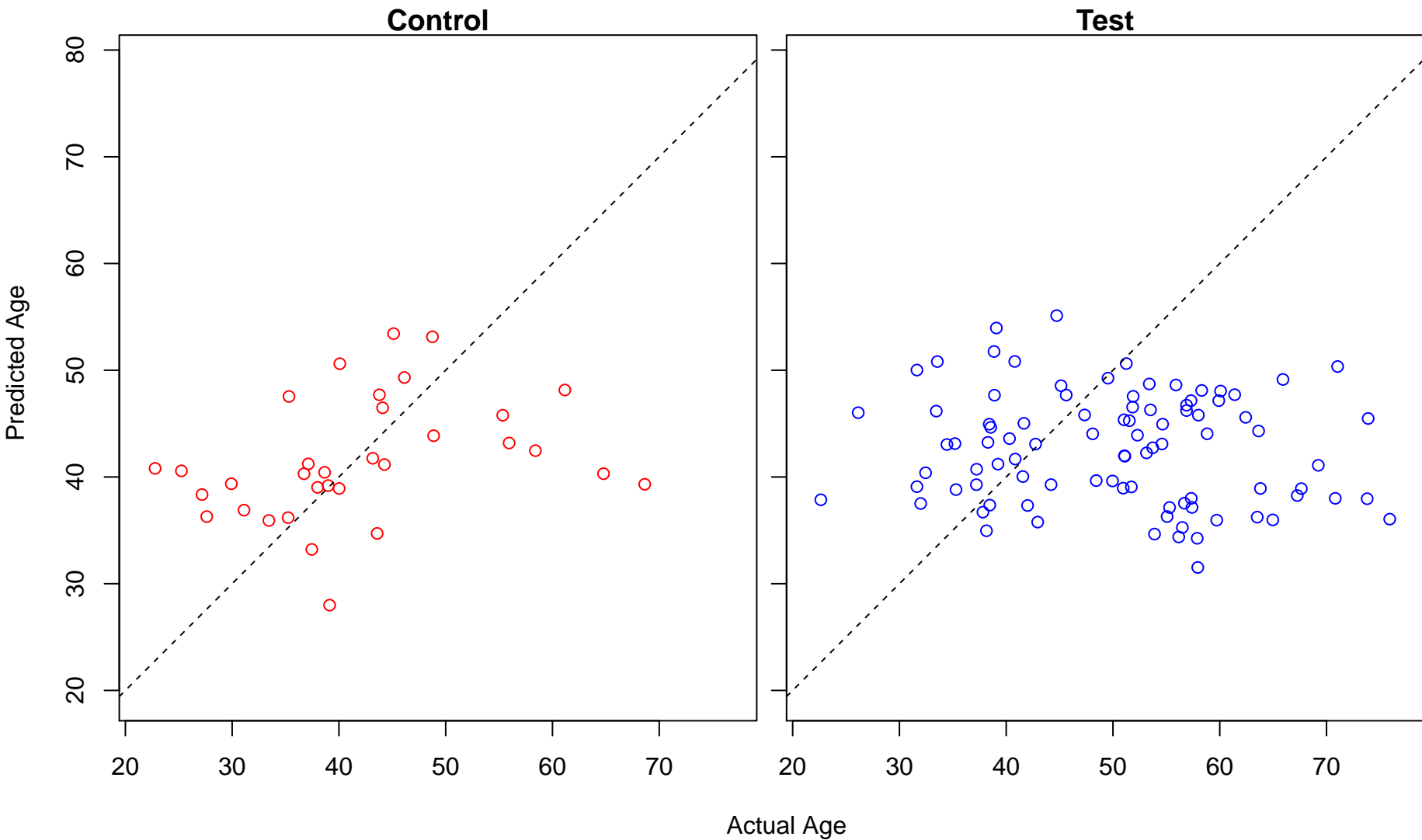
pyrimidine ribonucleotide metabolic process (Score: 0.435807)



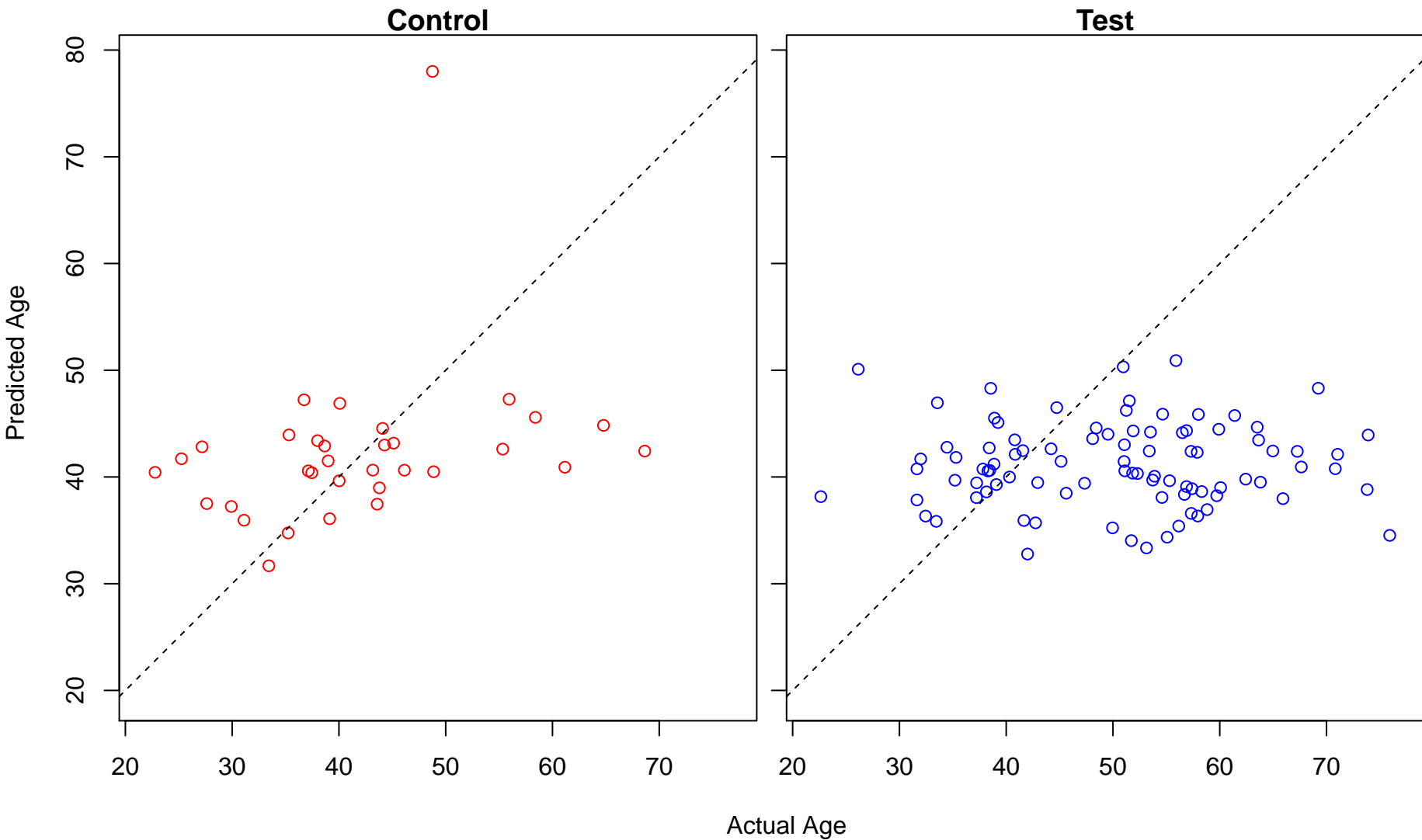
regulation of adiponectin secretion (Score: 0.435143)



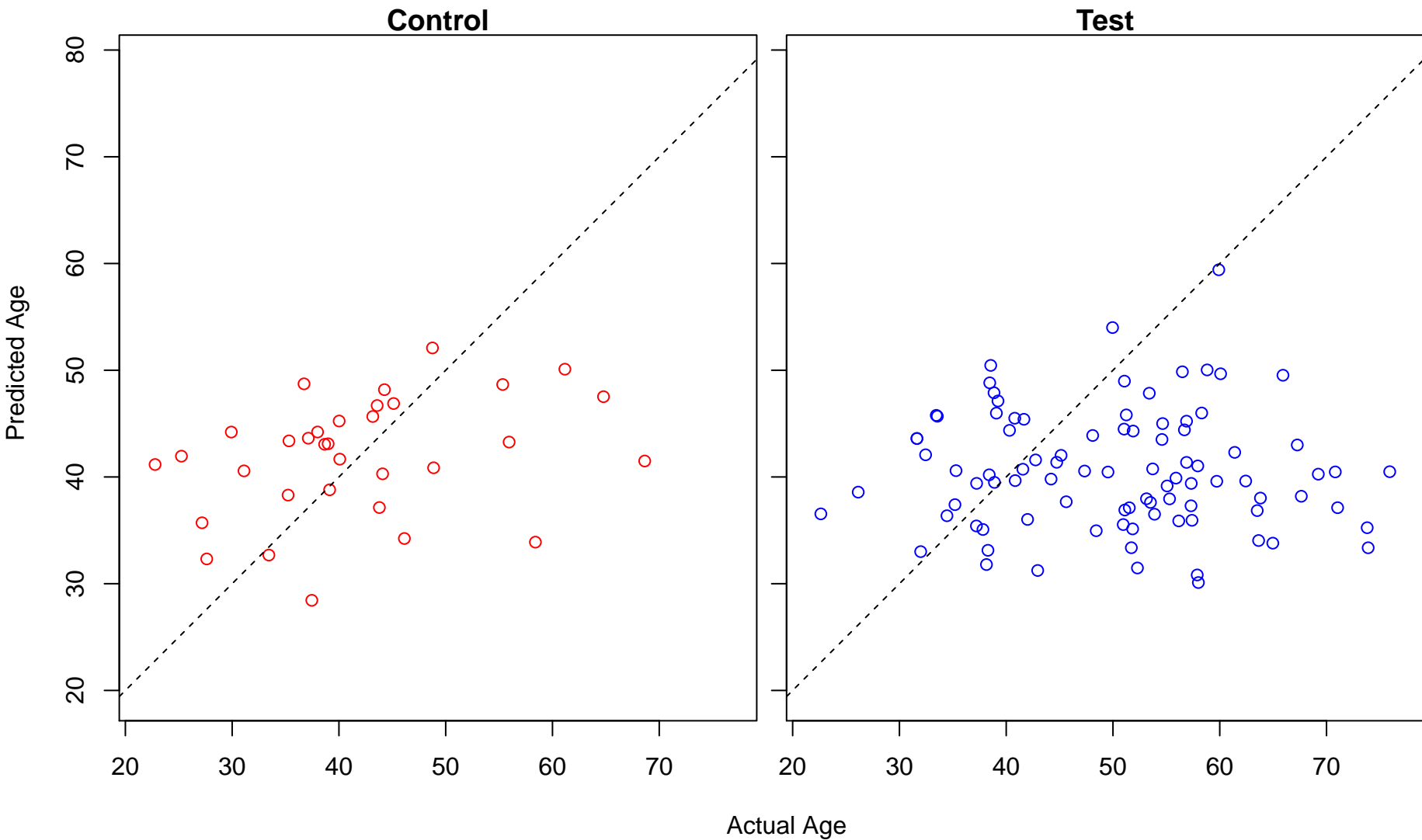
snRNA processing (Score: 0.434921)



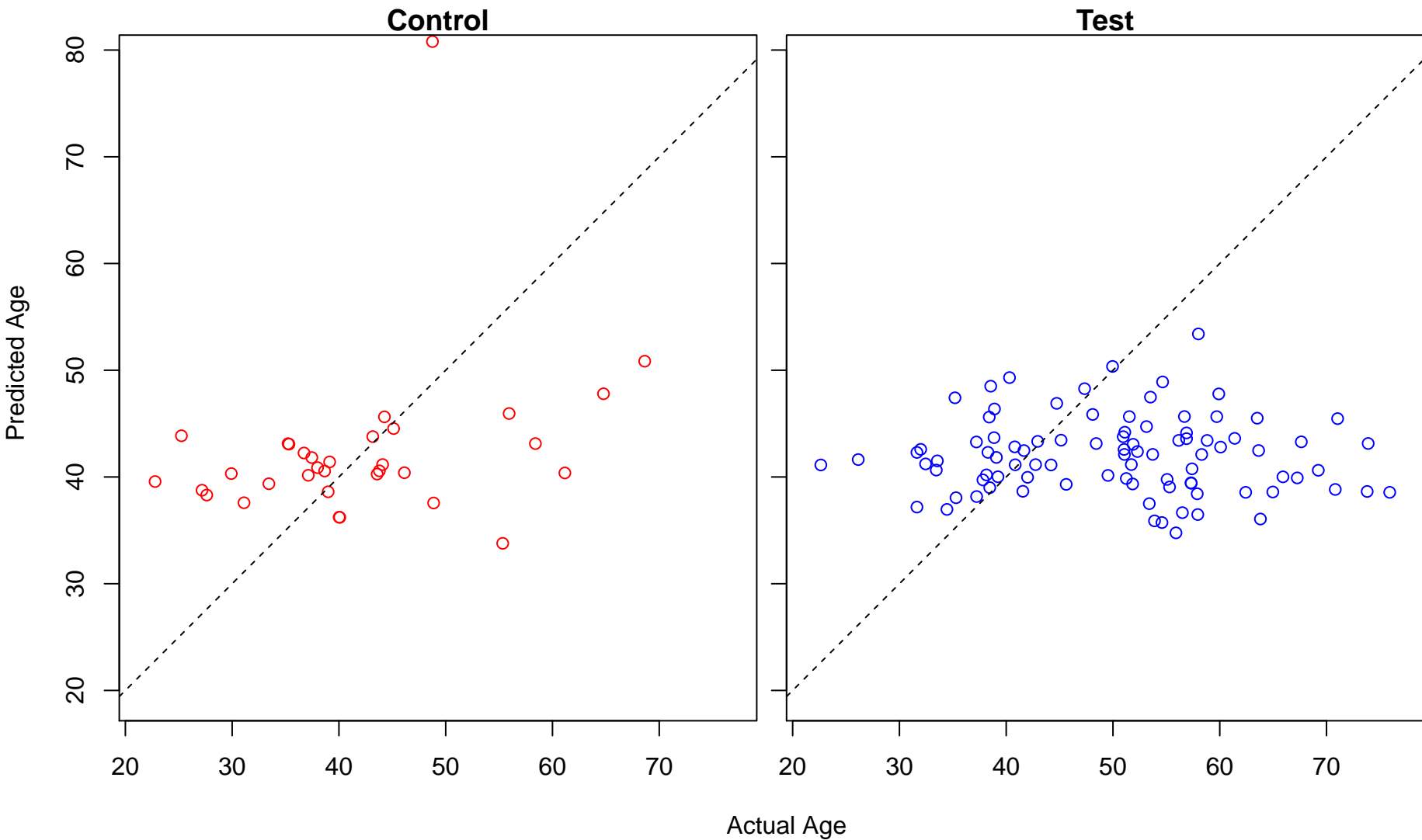
lamellipodium morphogenesis (Score: 0.434865)



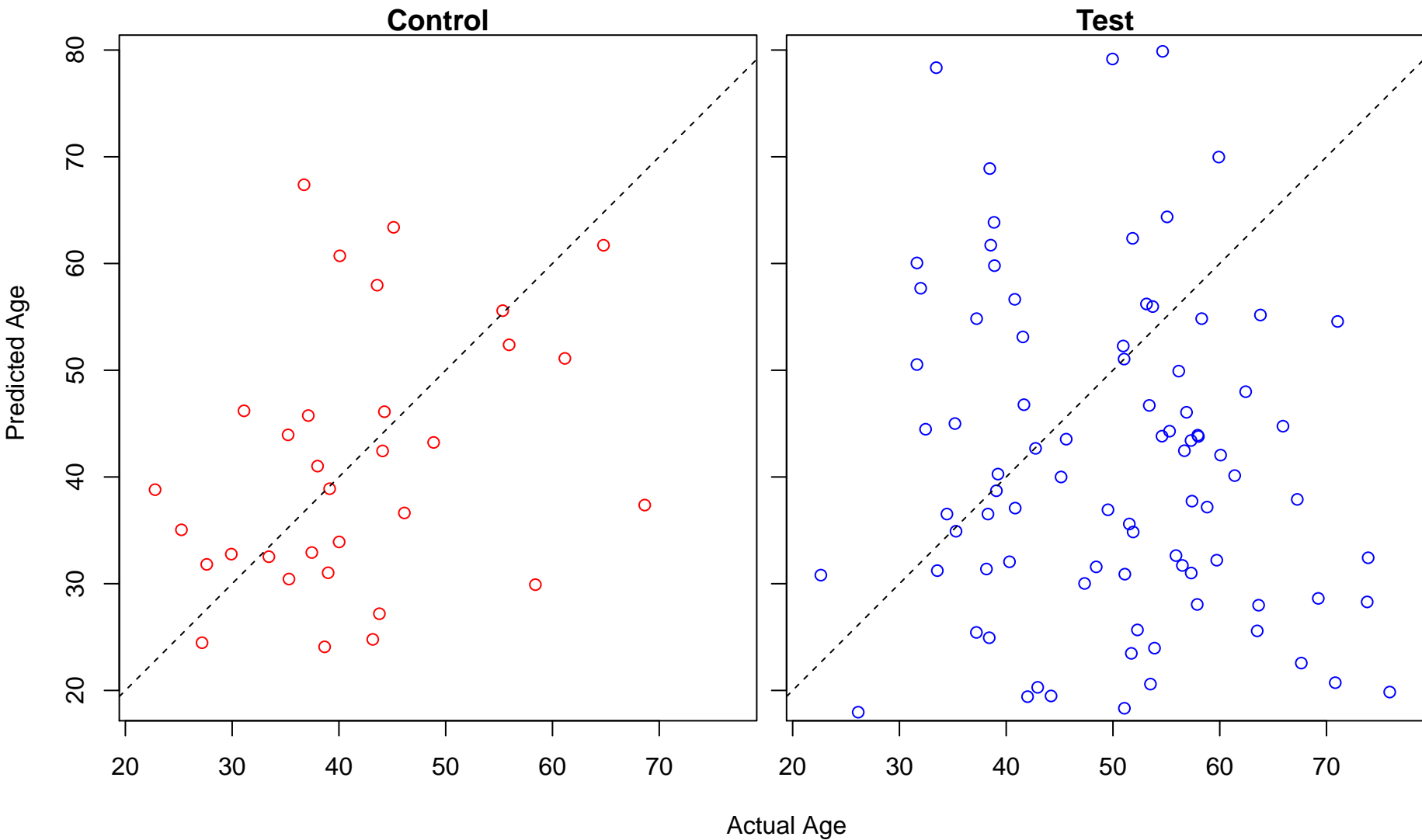
regulation of immunoglobulin production (Score: 0.434391)



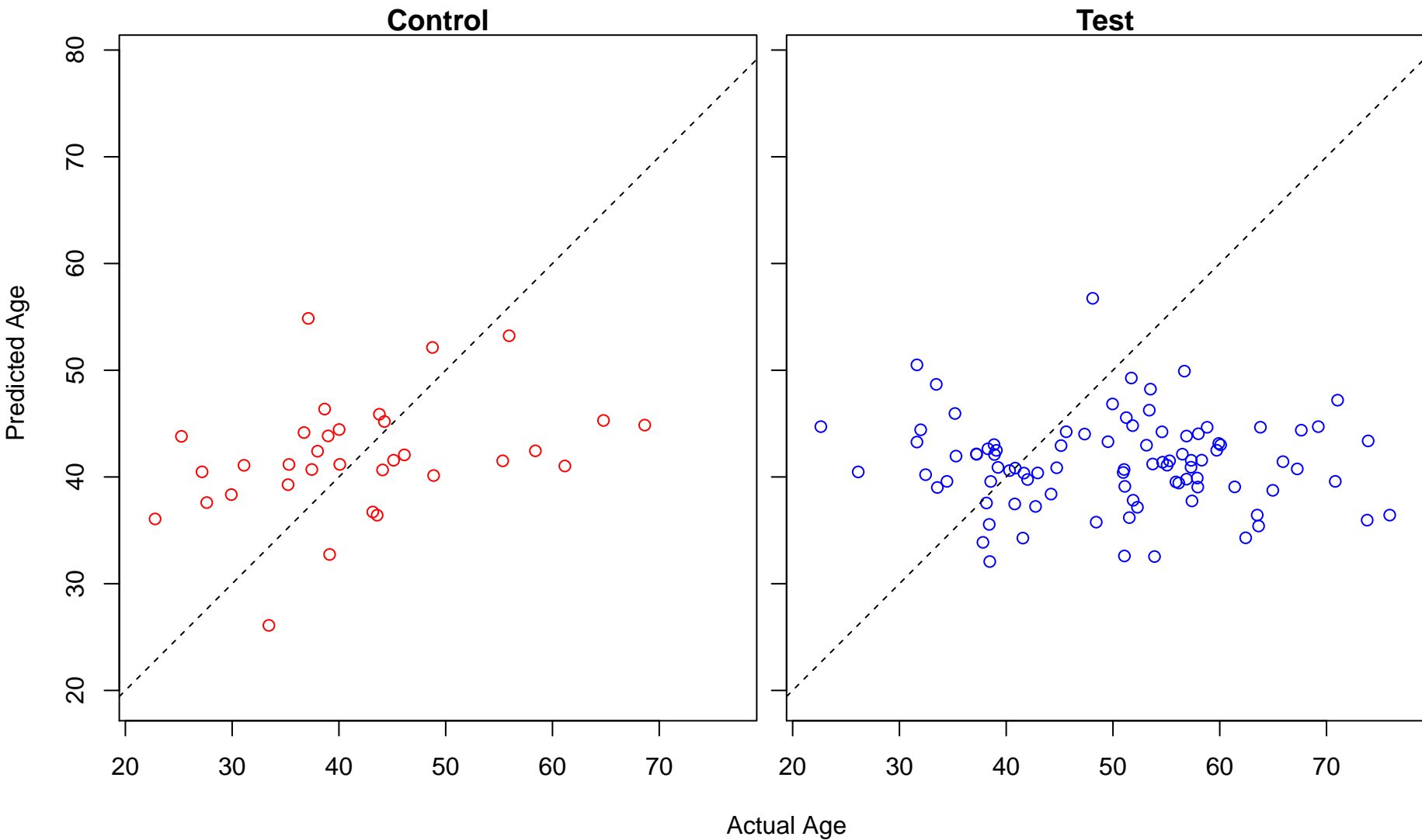
histone H4-K12 acetylation (Score: 0.434169)



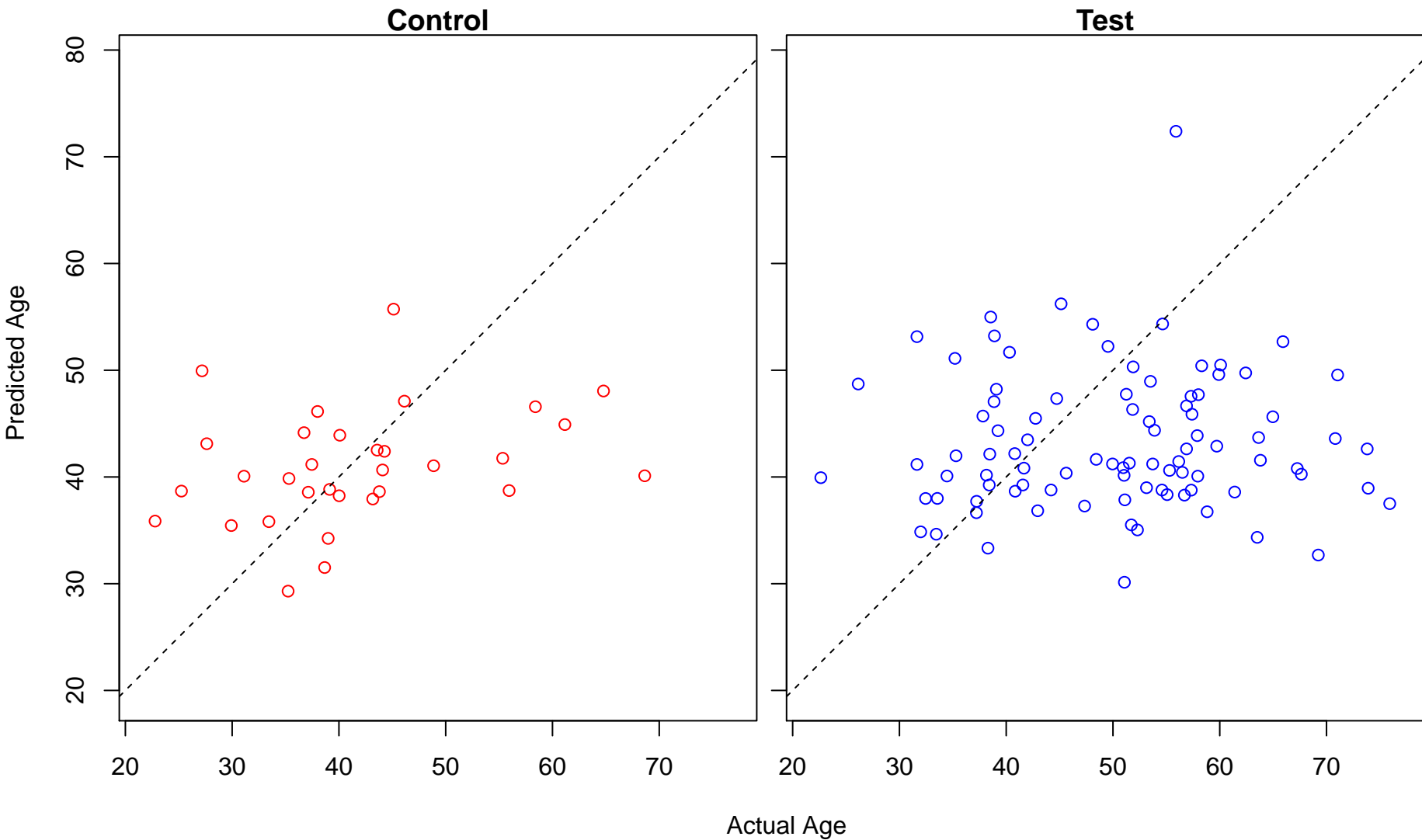
endosome to lysosome transport (Score: 0.432712)



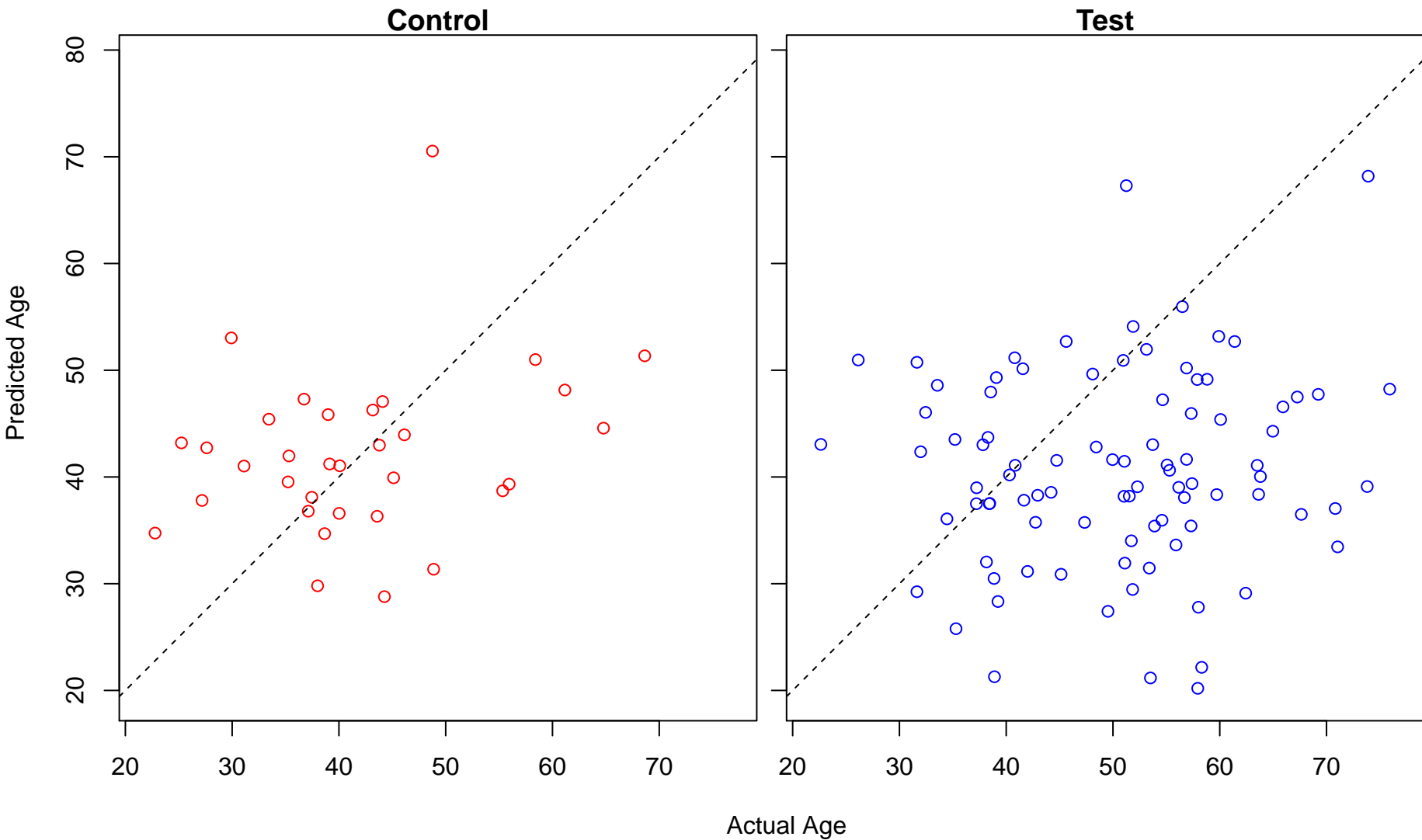
interleukin-8 production (Score: 0.430683)



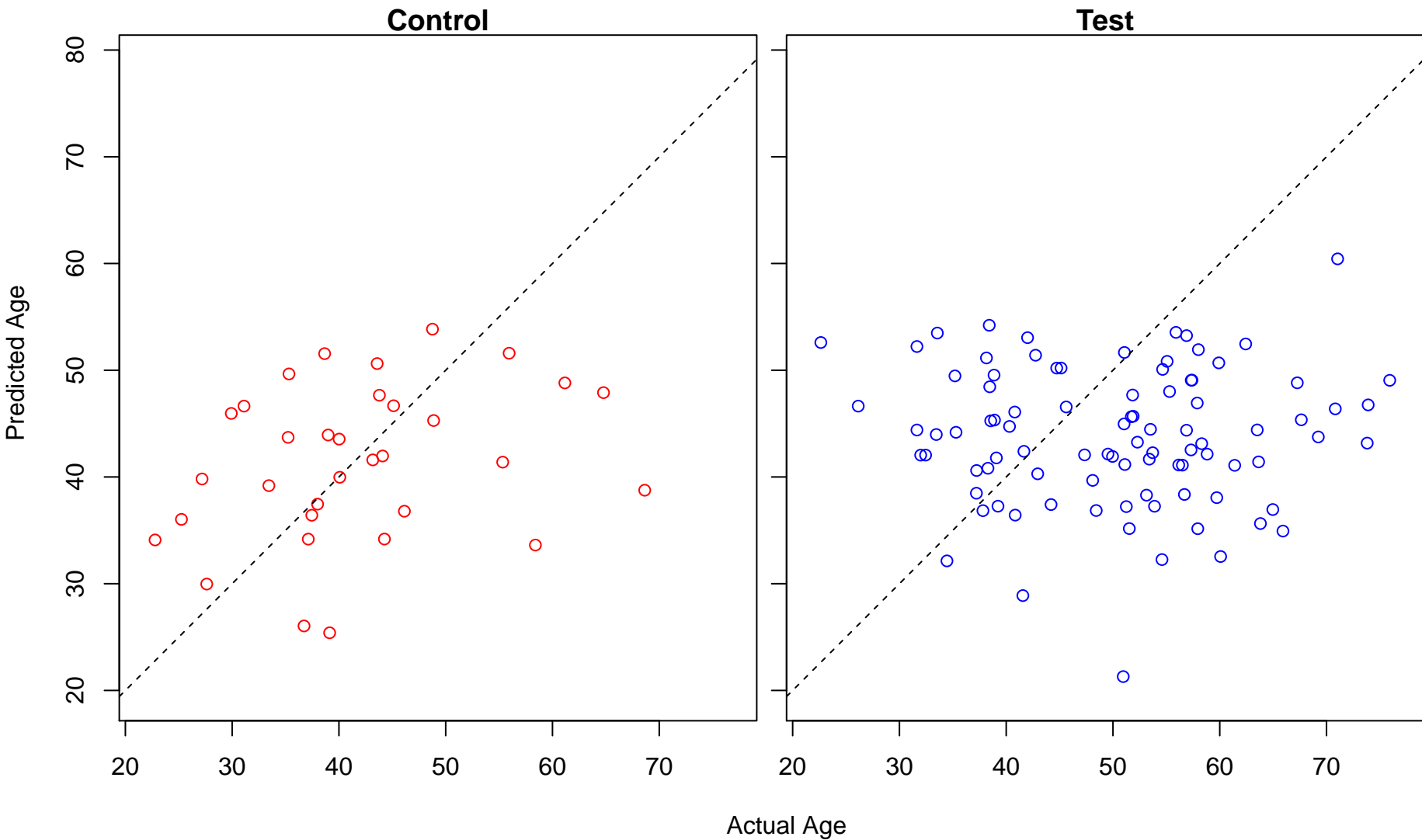
positive regulation of mast cell activation involved in immune response (Score: 0.429639)



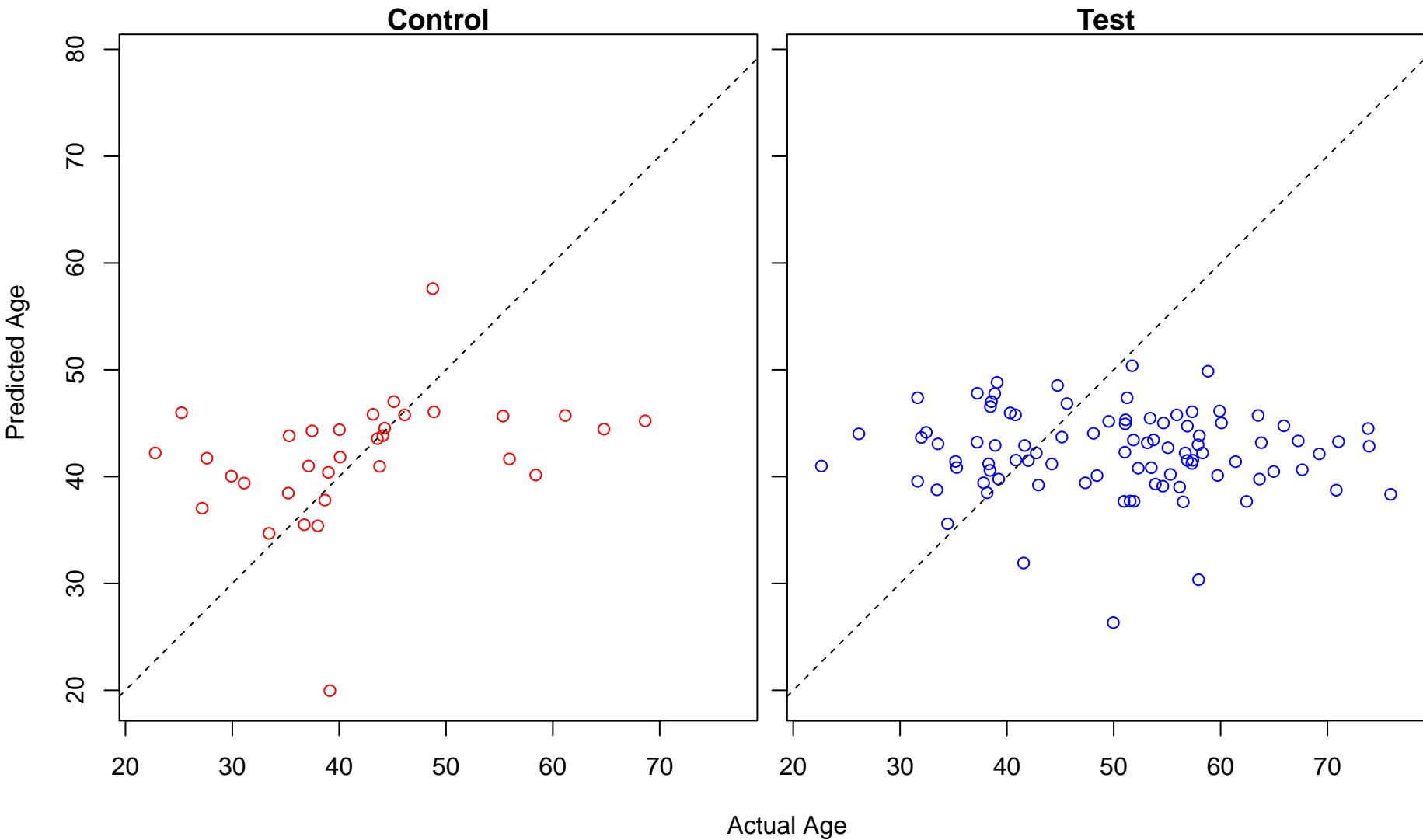
positive regulation of osteoclast differentiation (Score: 0.427111)



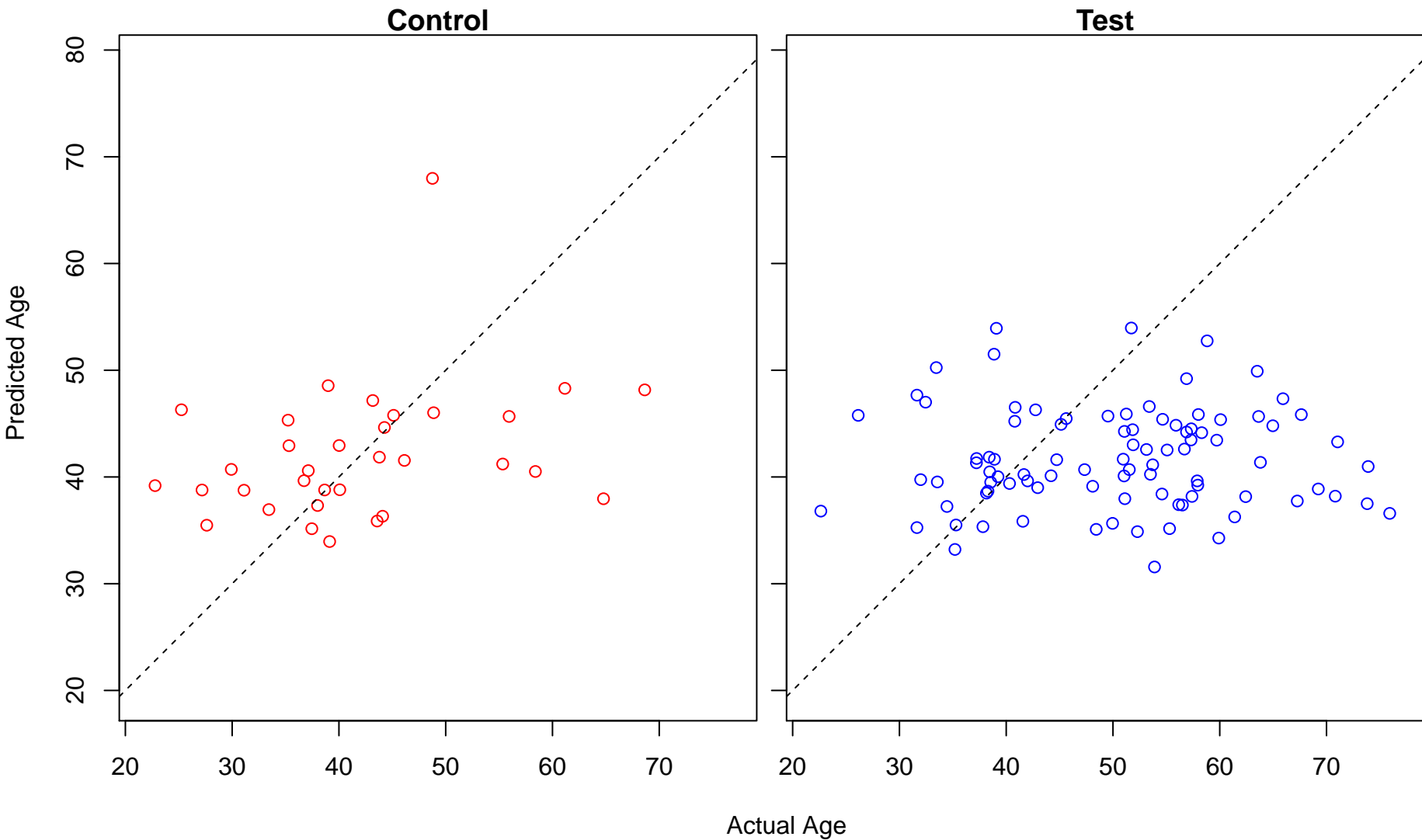
response to manganese ion (Score: 0.425589)



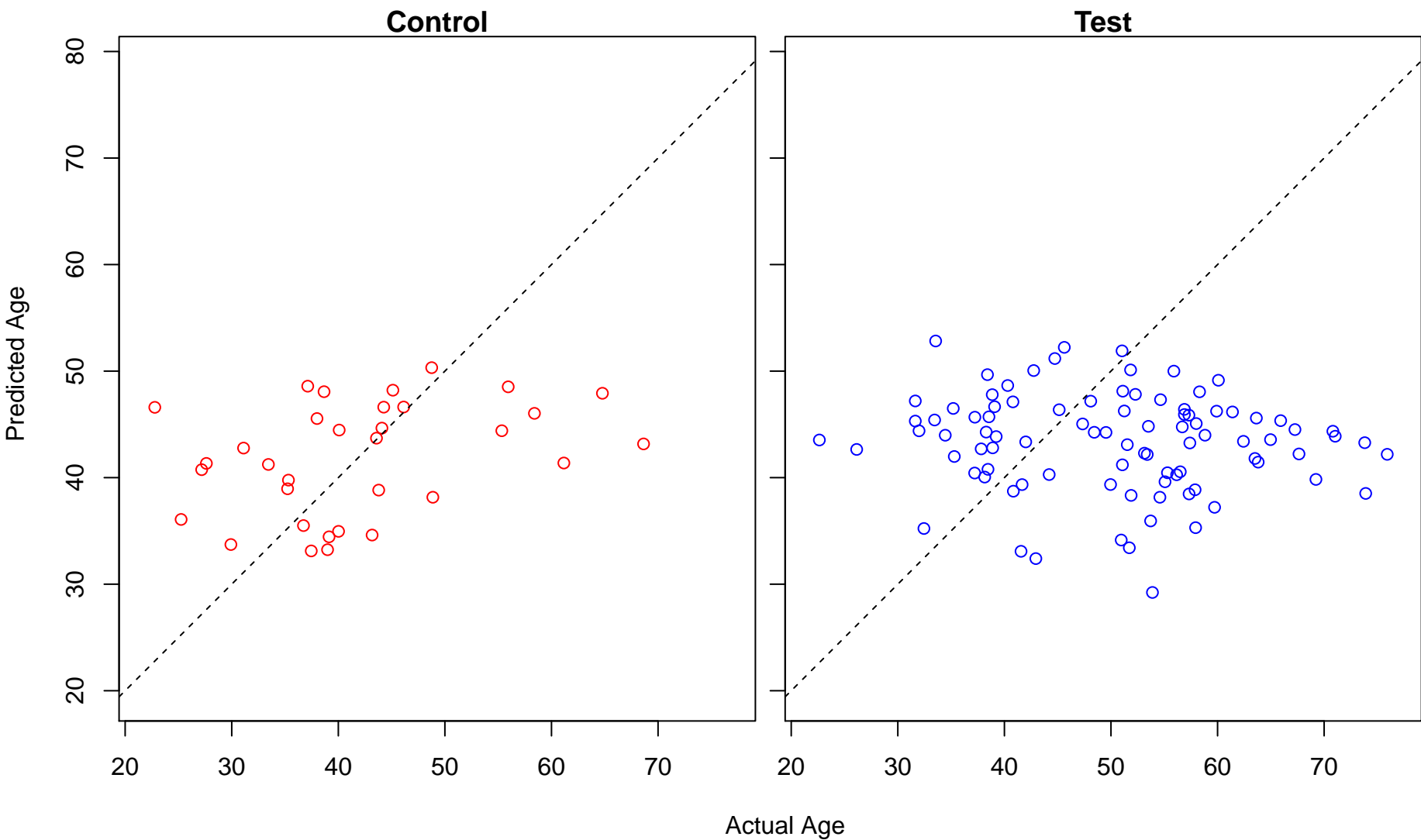
establishment of mitotic spindle orientation (Score: 0.424373)



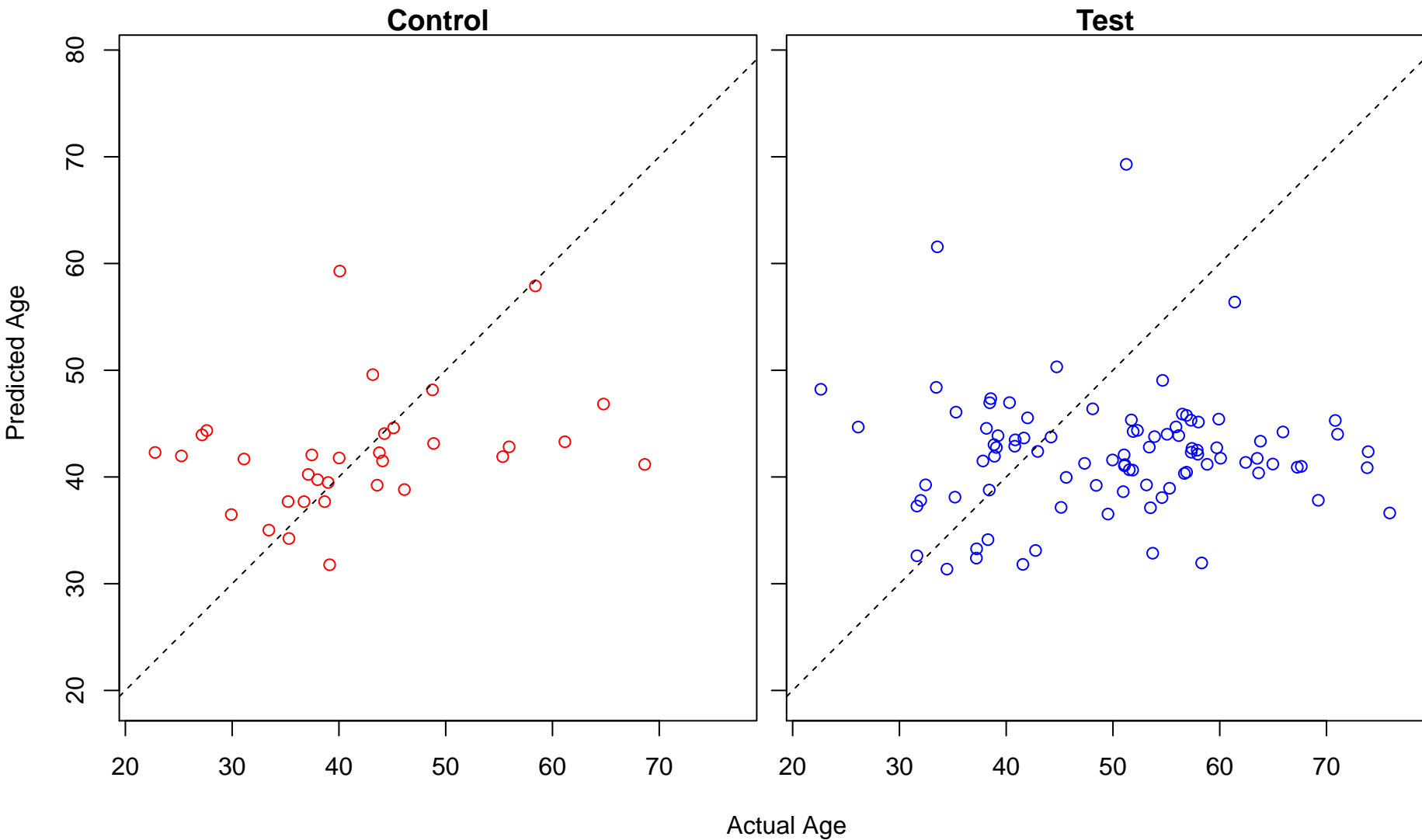
skeletal muscle fiber development (Score: 0.423735)



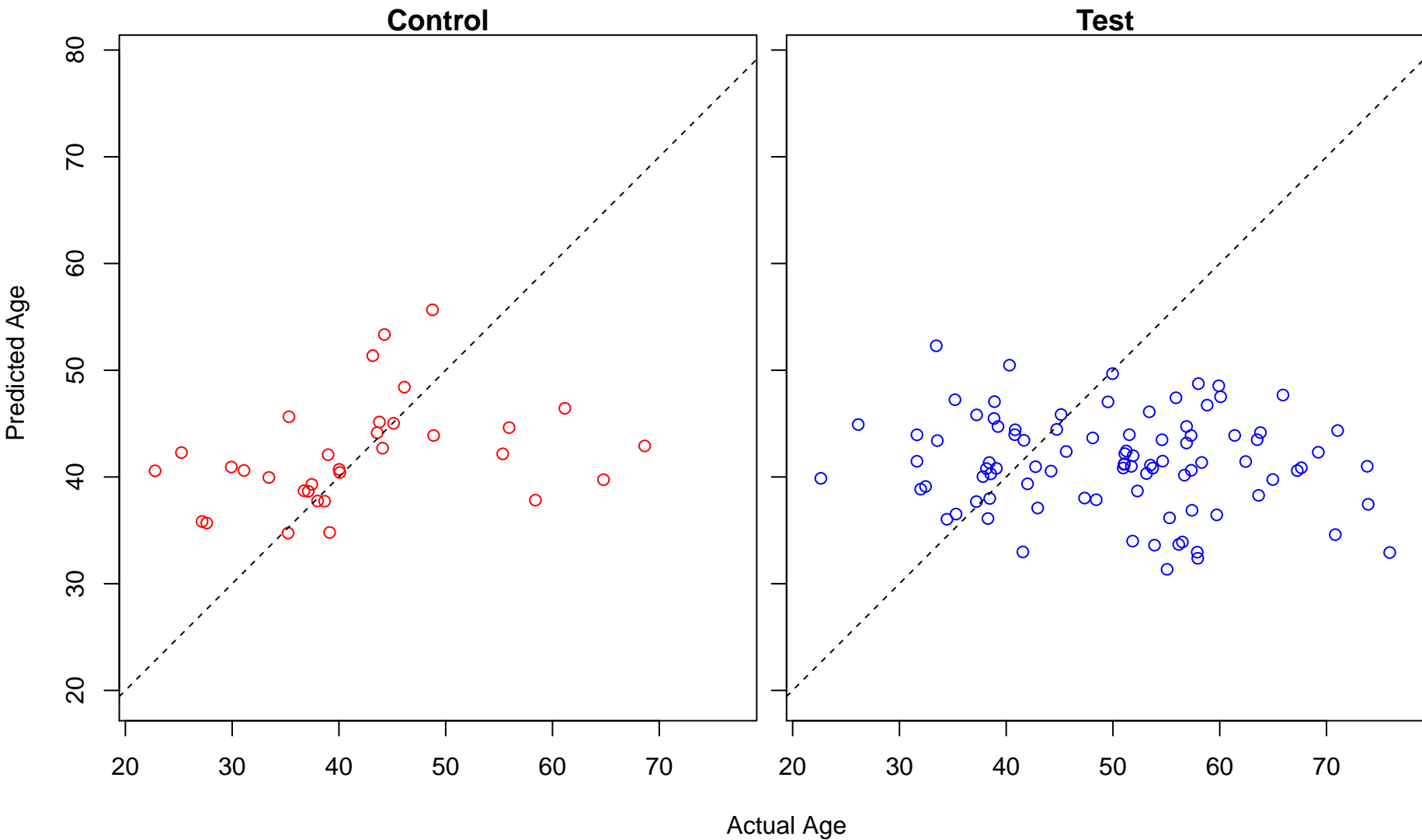
mal growth factor-activated receptor transactivation by G-protein coupled receptor signaling pathway (S



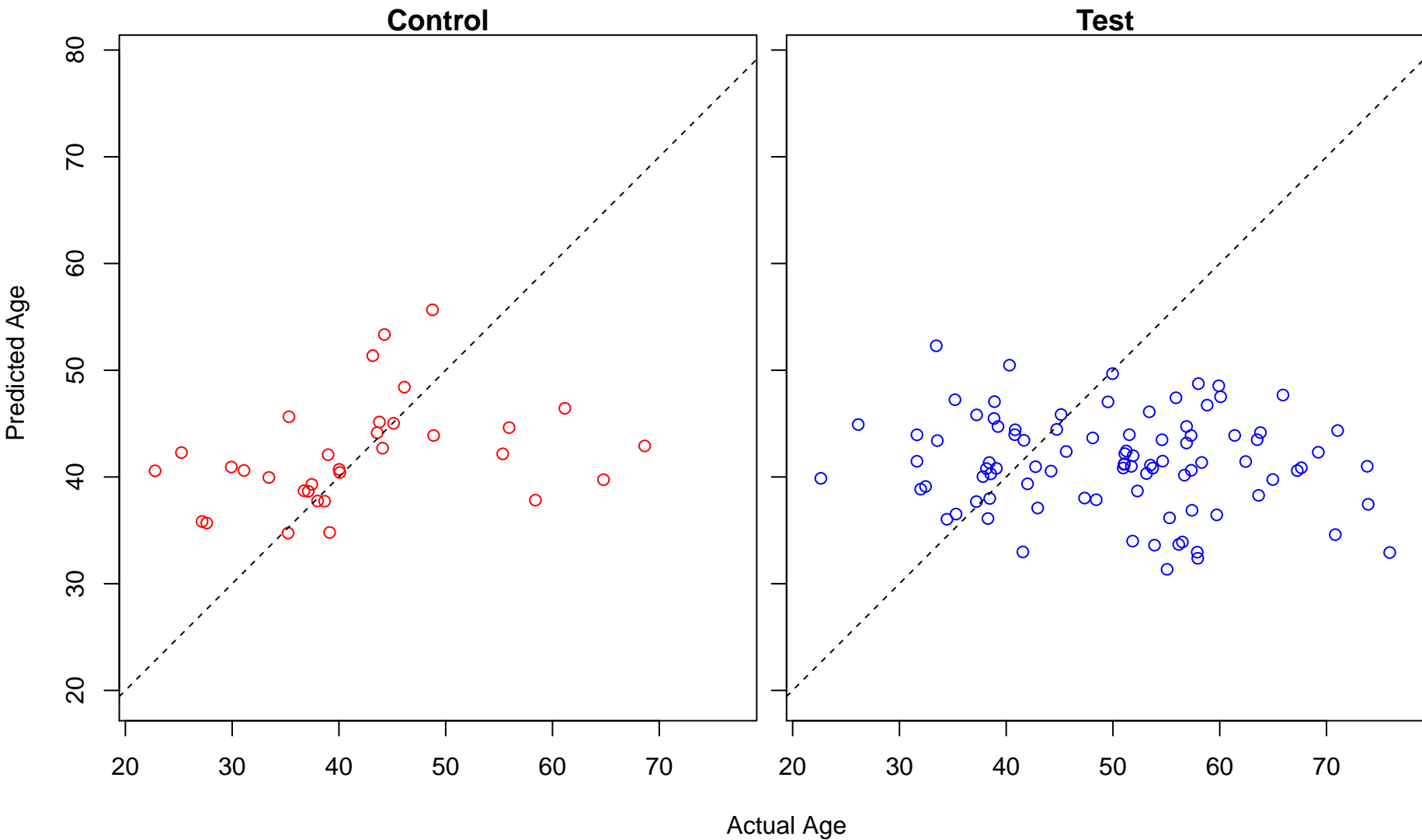
positive regulation of synaptic plasticity (Score: 0.421519)



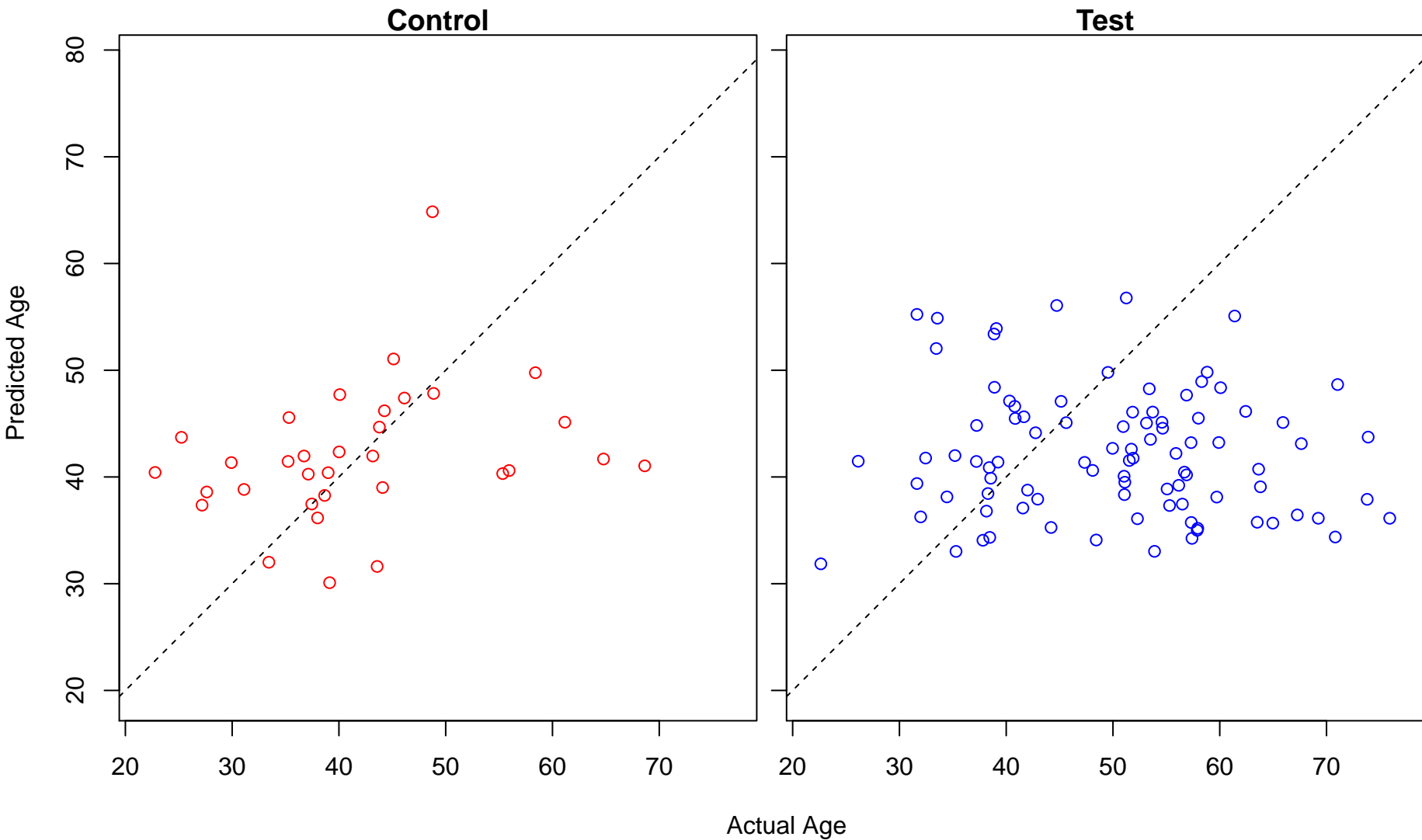
DNA replication, Okazaki fragment processing (Score: 0.421462)



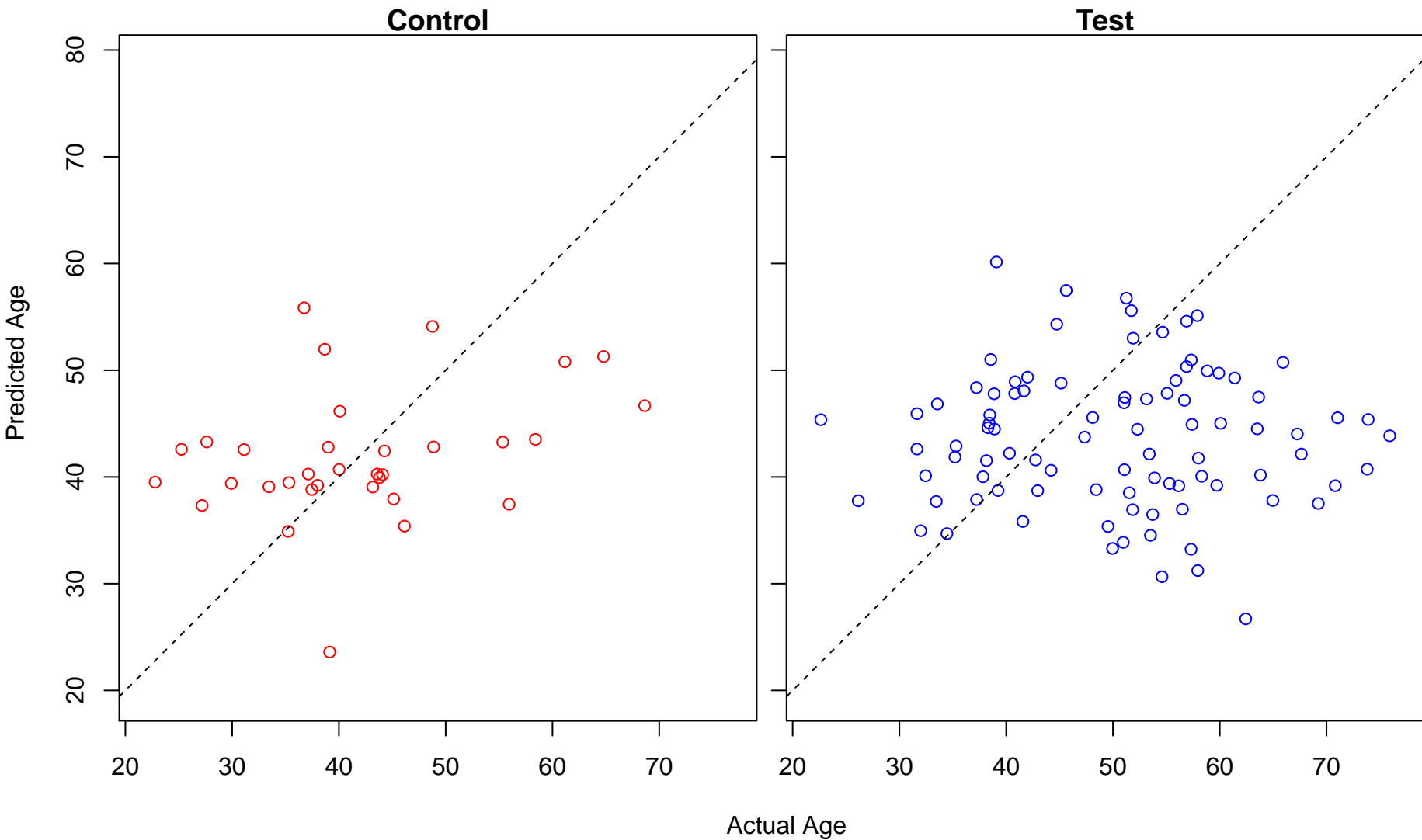
DNA replication, removal of RNA primer (Score: 0.421462)



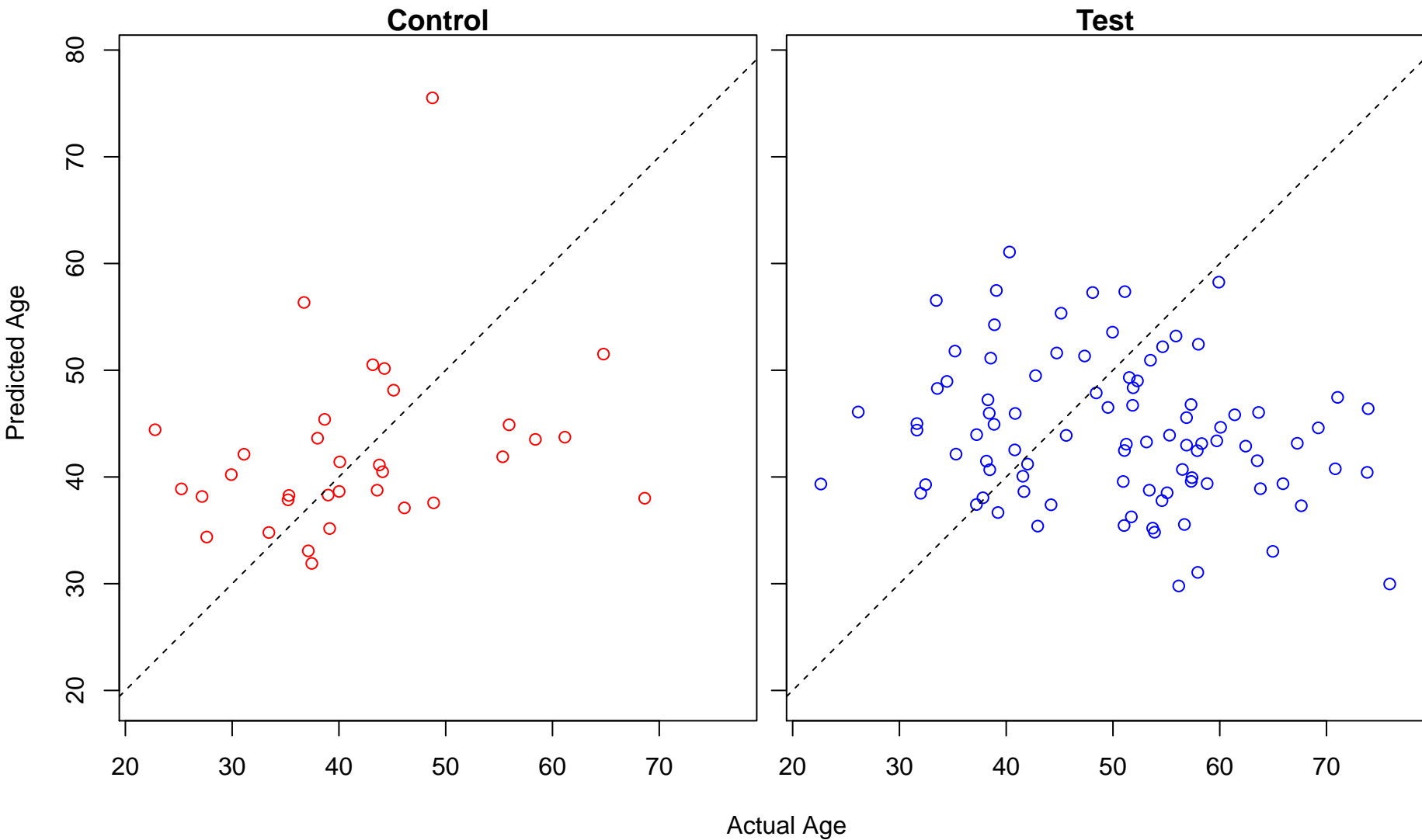
positive regulation of fatty acid biosynthetic process (Score: 0.421161)



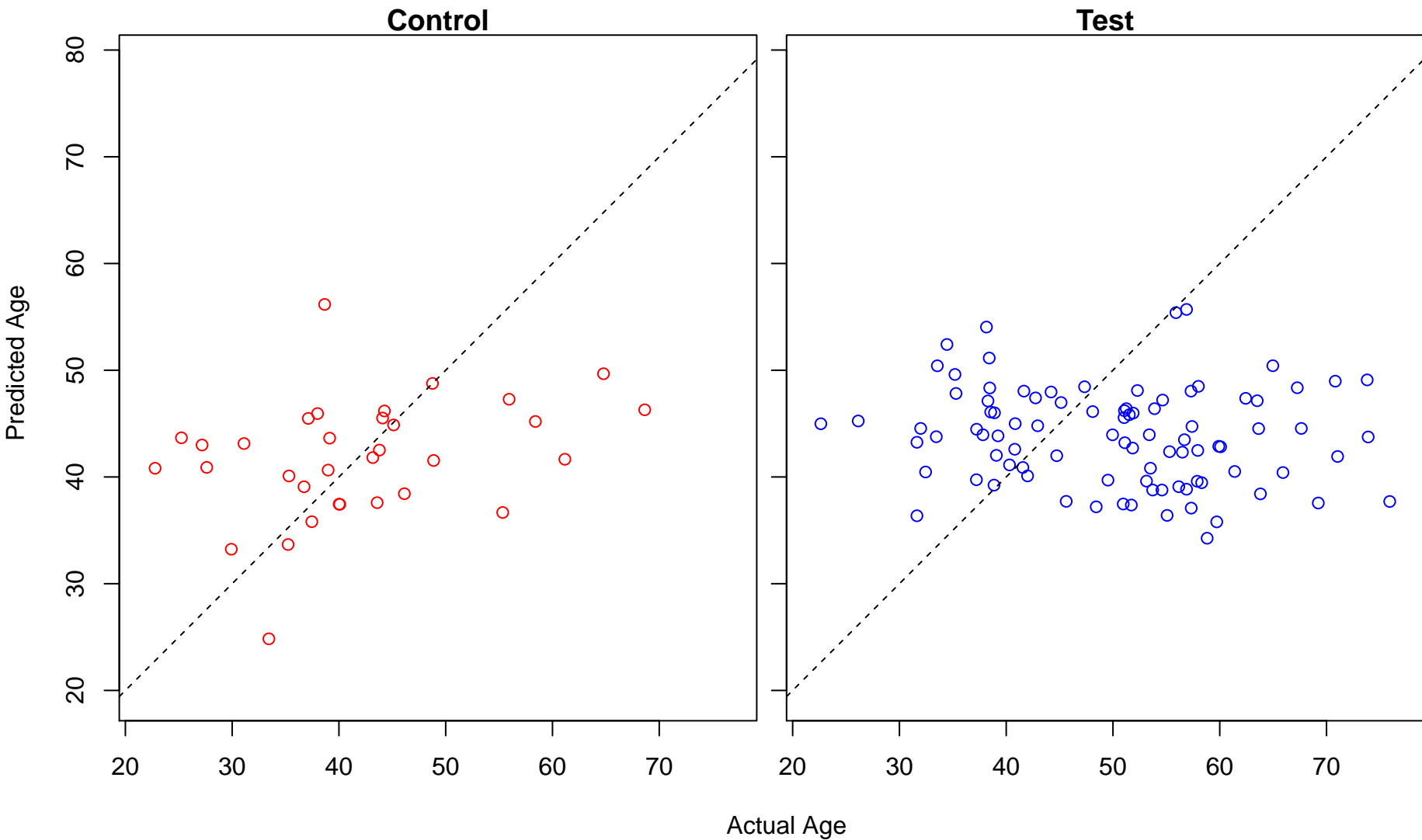
macrophage chemotaxis (Score: 0.420450)



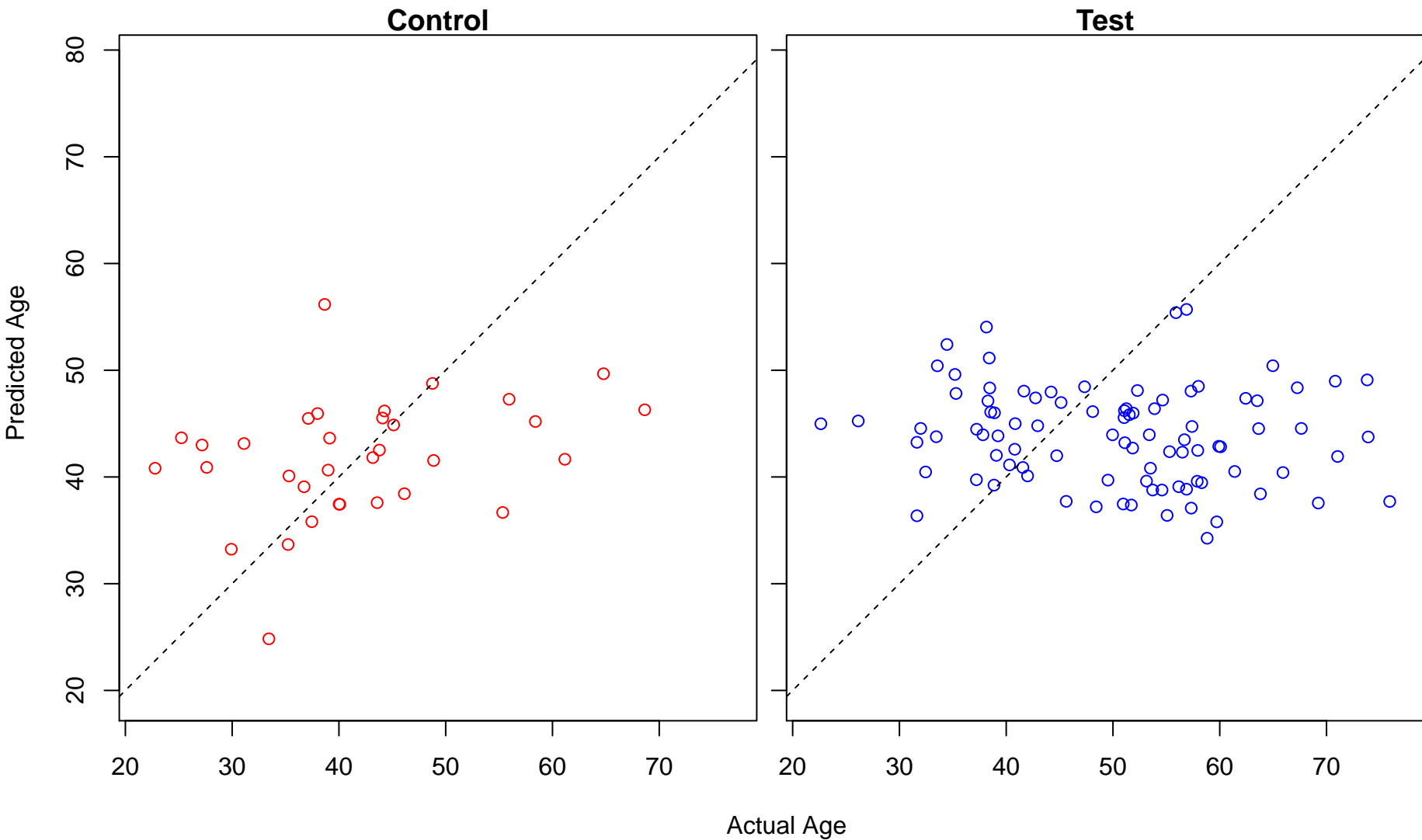
release of cytoplasmic sequestered NF-kappaB (Score: 0.419522)



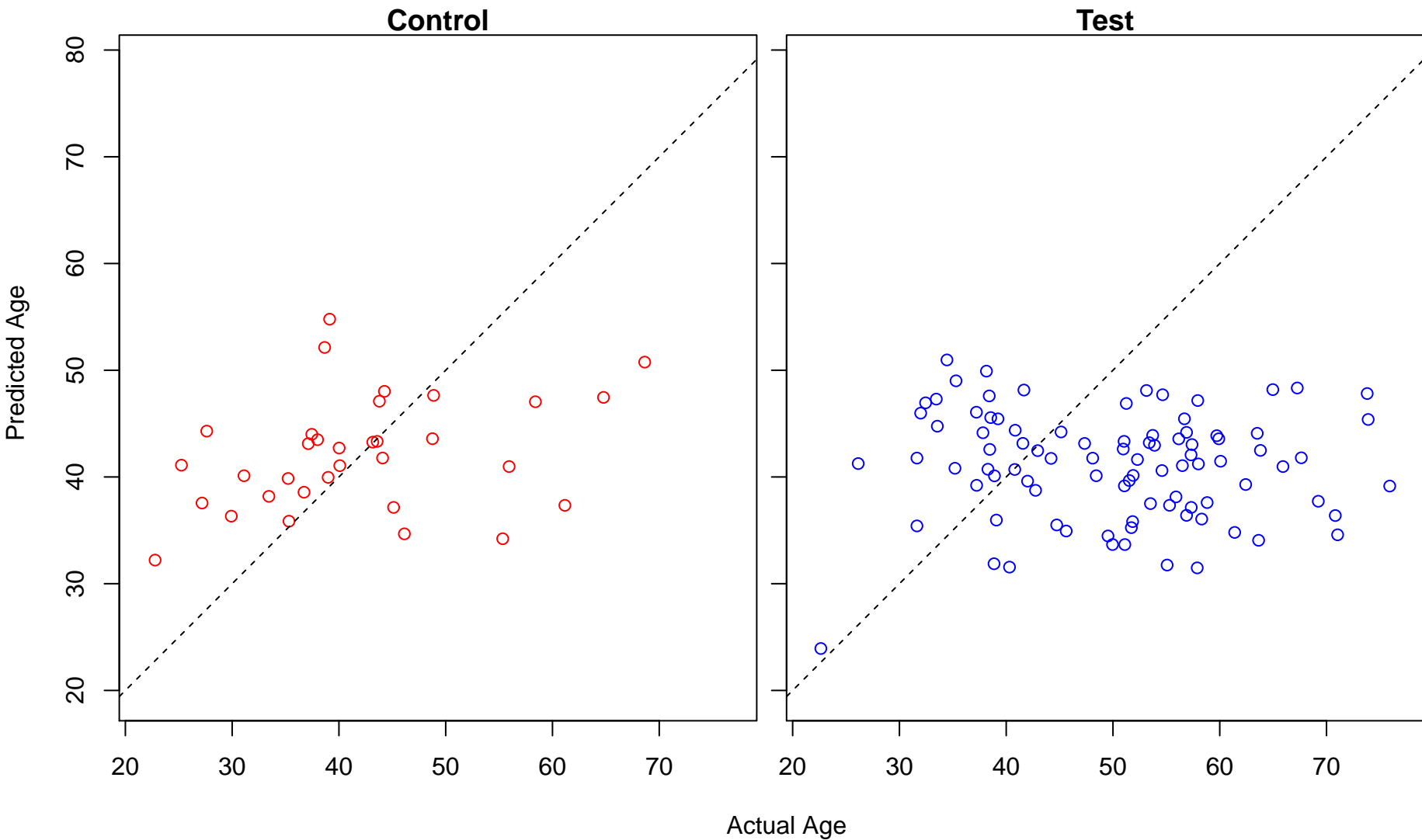
regulation of sphingolipid biosynthetic process (Score: 0.419120)



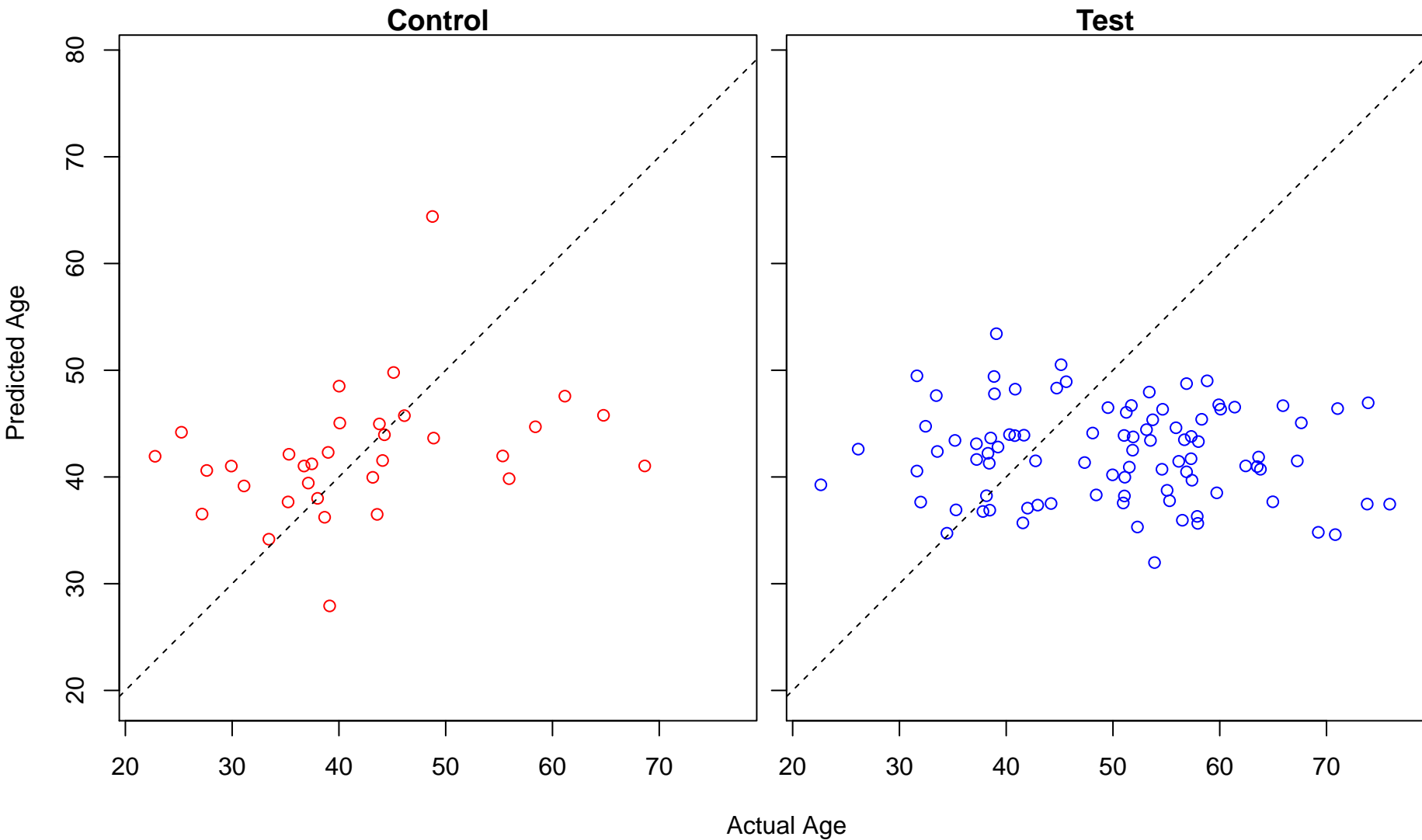
regulation of ceramide biosynthetic process (Score: 0.419120)



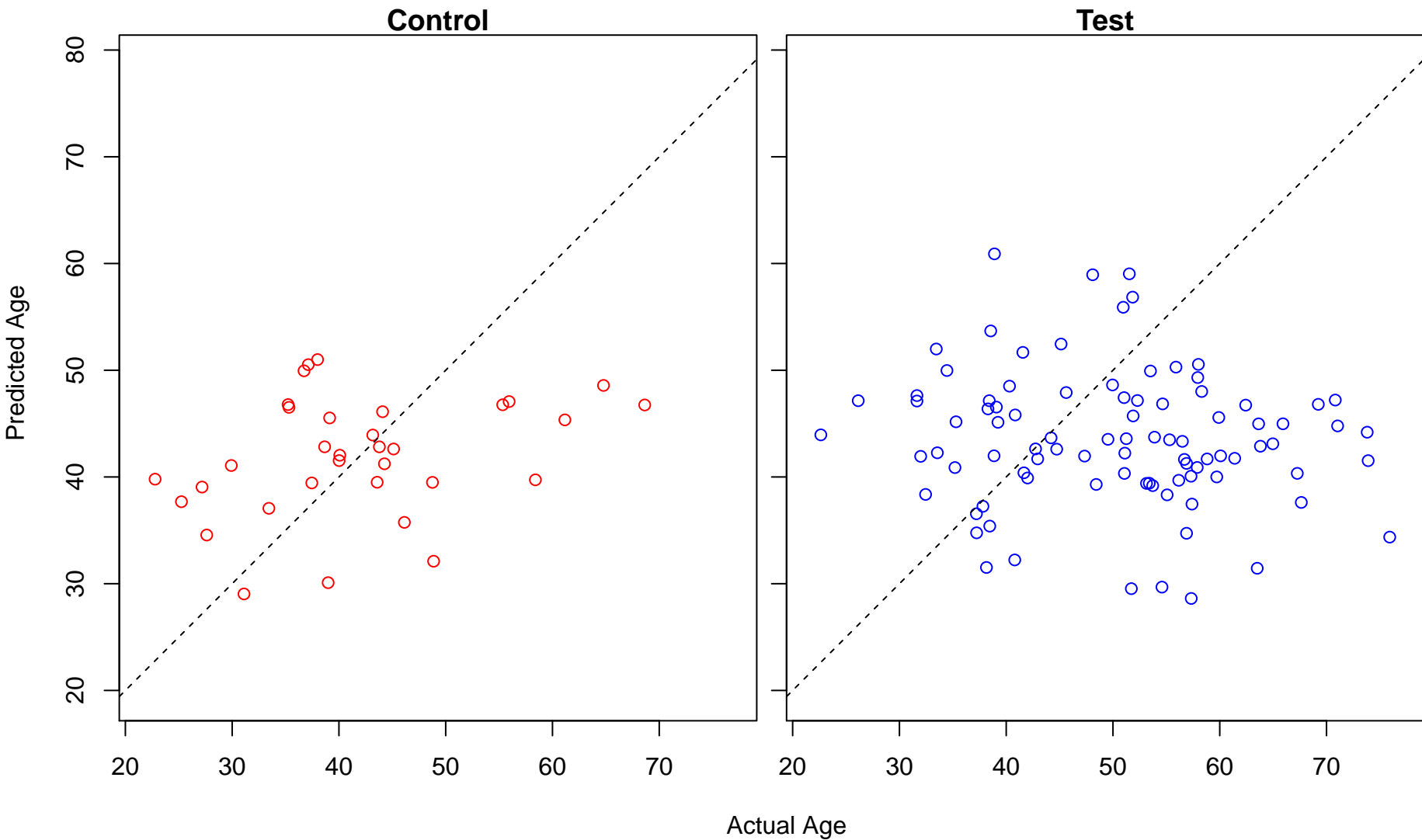
sphingomyelin catabolic process (Score: 0.418927)



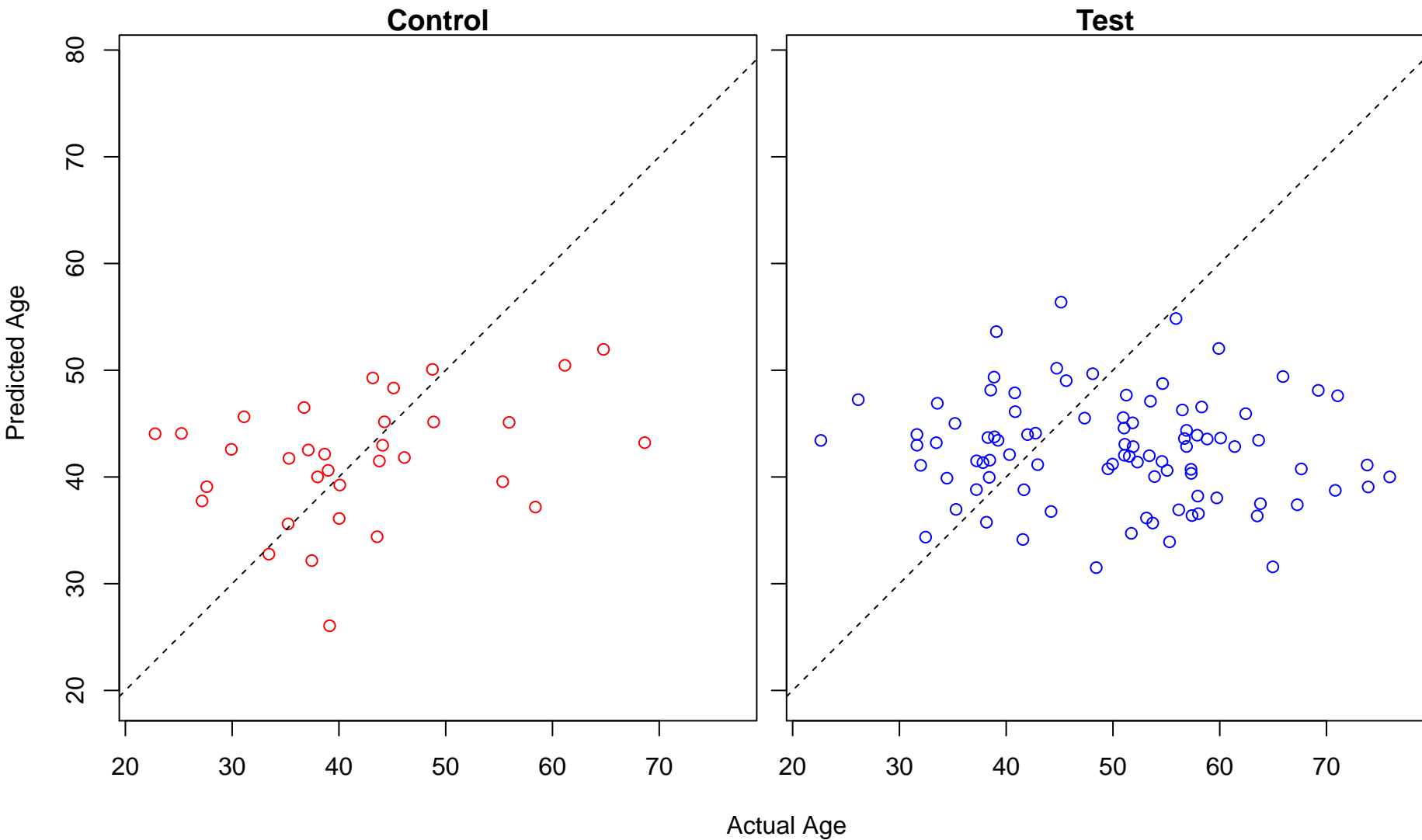
proteasome assembly (Score: 0.417543)



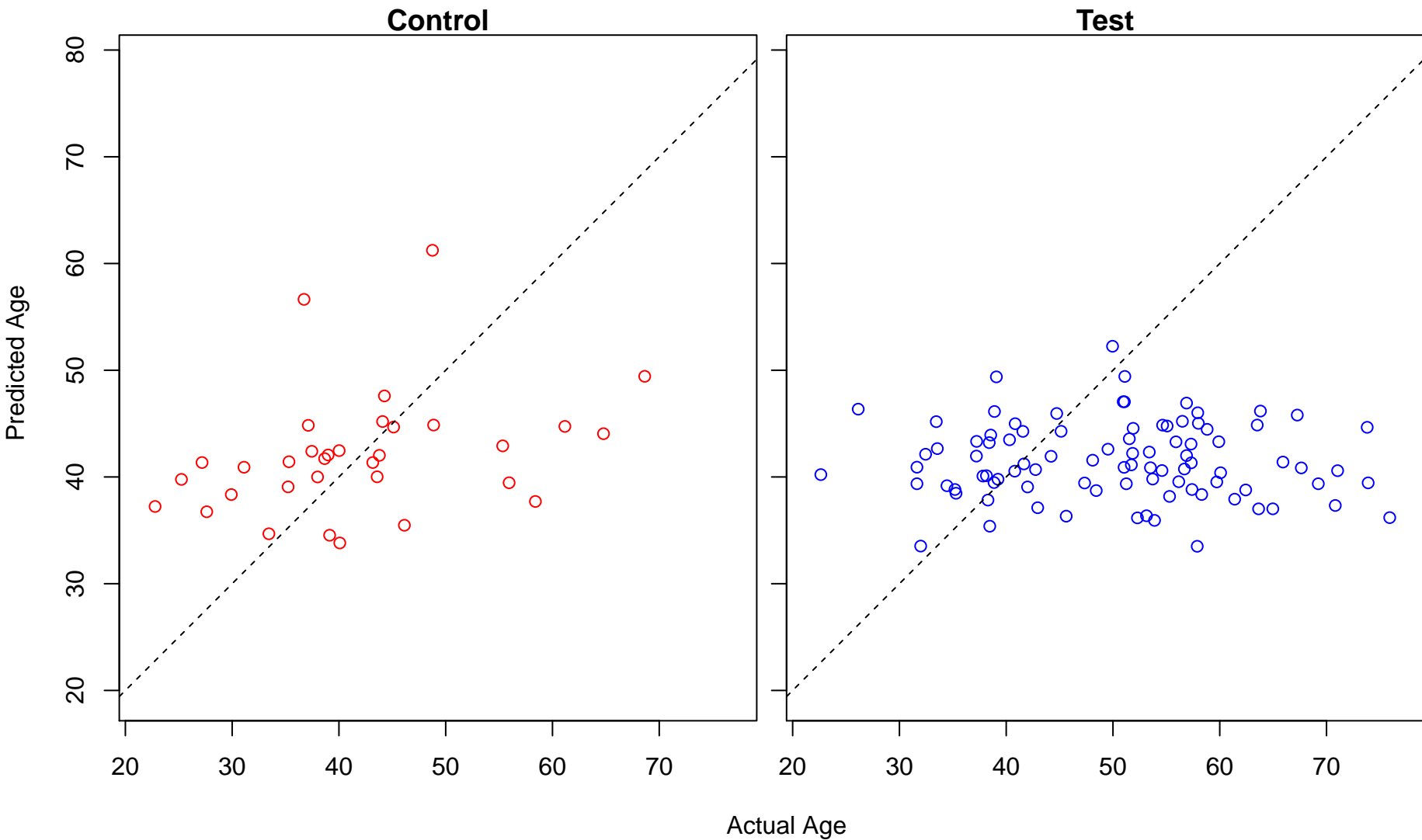
metanephric part of ureteric bud development (Score: 0.417393)



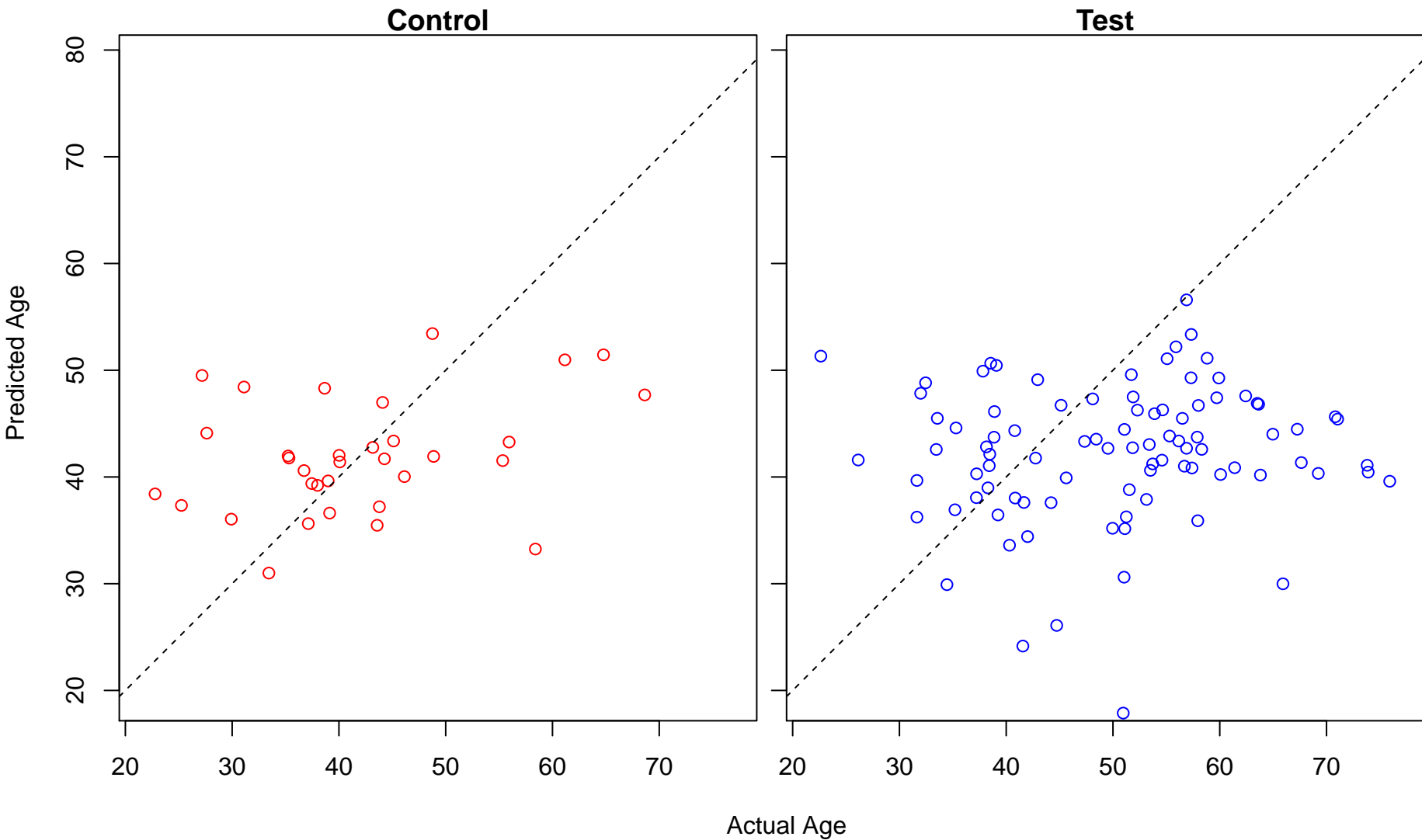
cilium movement (Score: 0.417028)



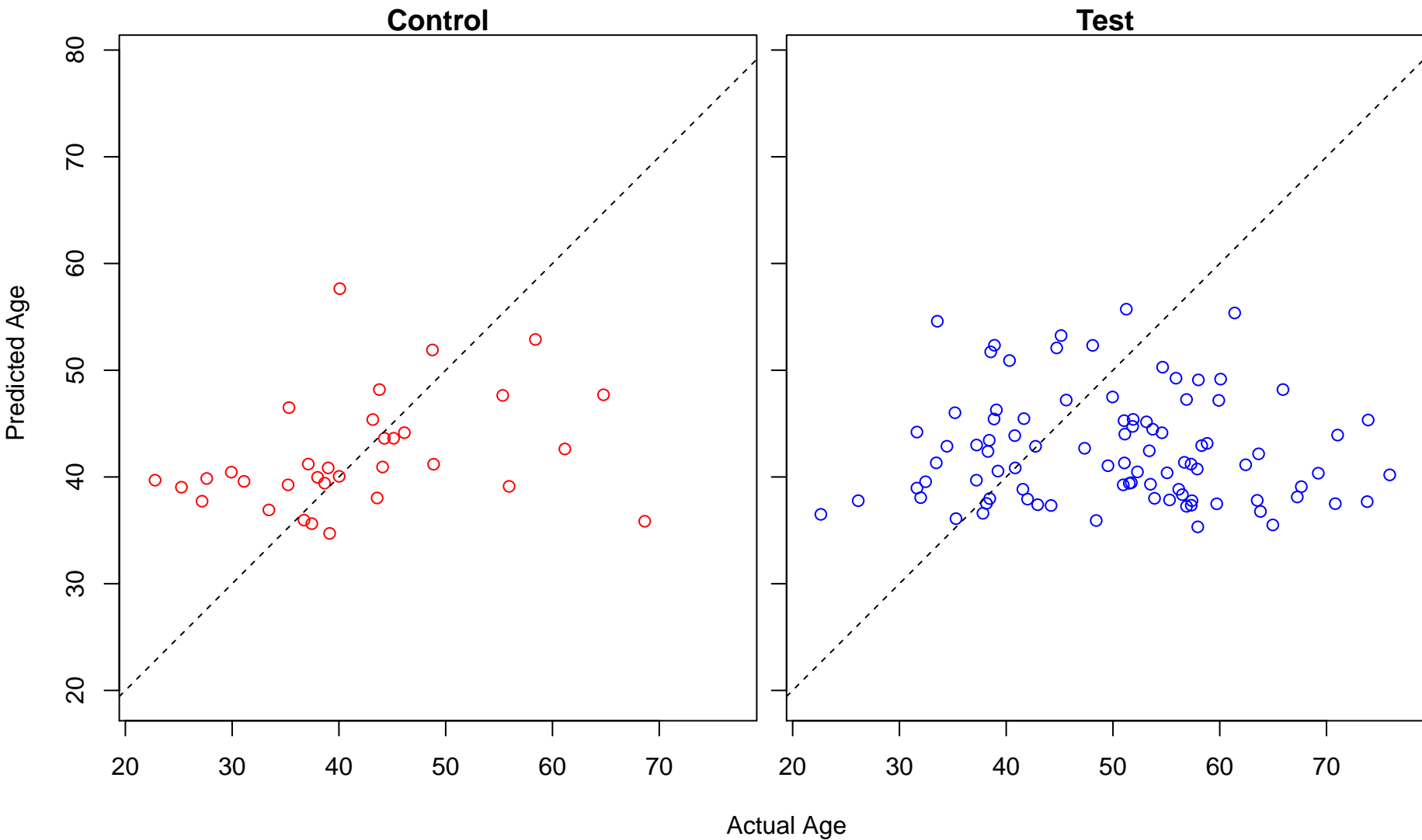
autocrine signaling (Score: 0.415131)



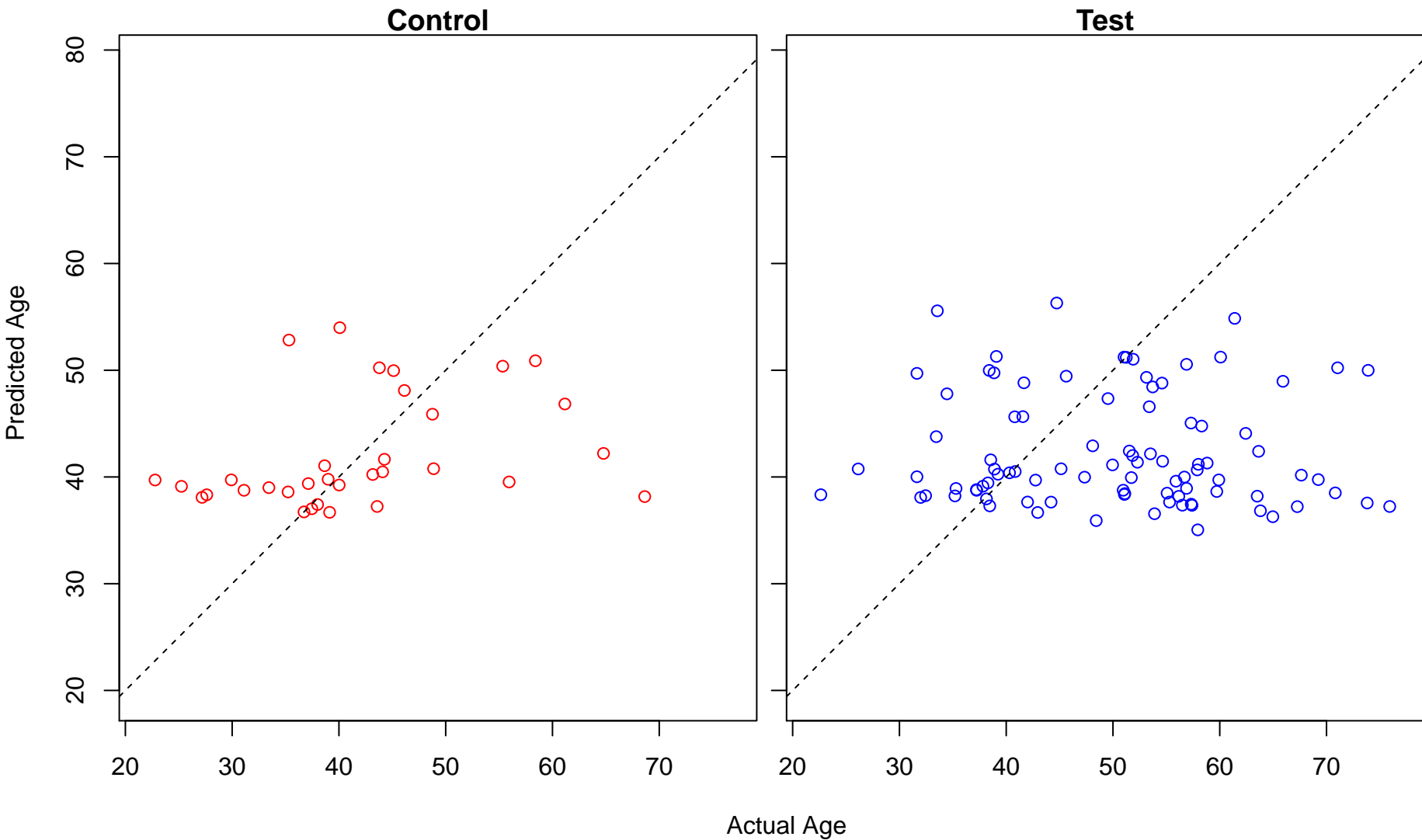
JUN phosphorylation (Score: 0.412951)



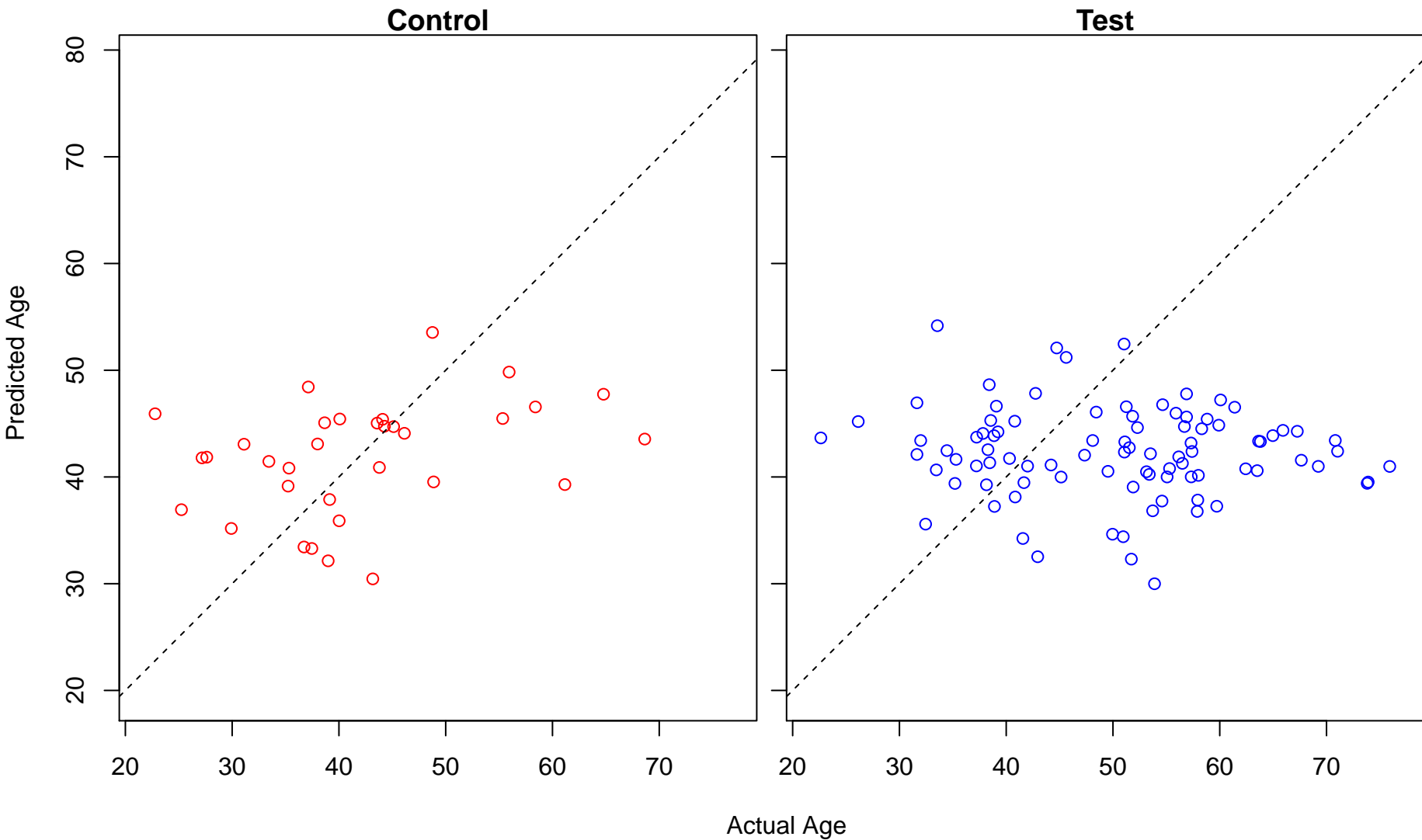
polarized epithelial cell differentiation (Score: 0.412319)



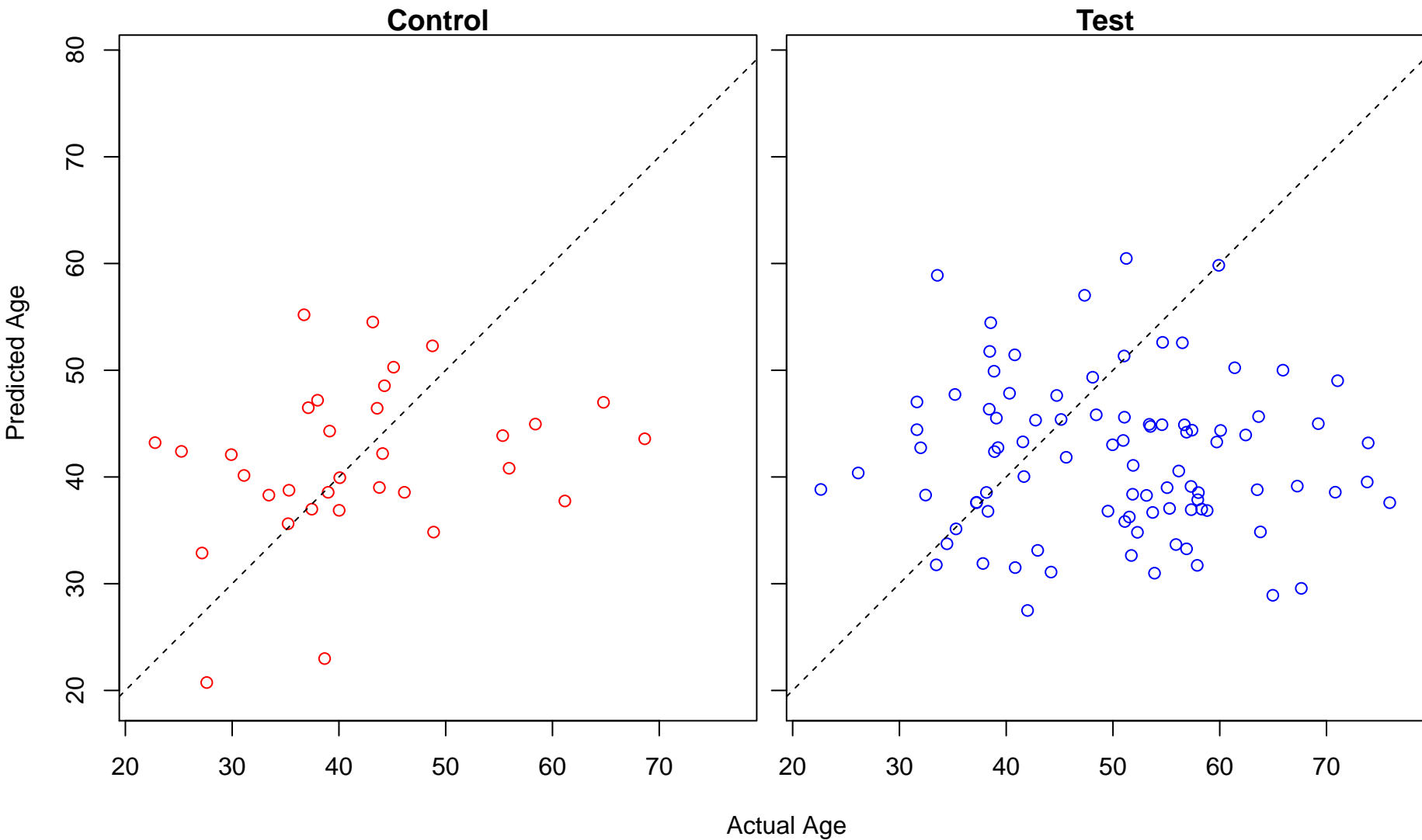
telomere maintenance in response to DNA damage (Score: 0.411889)



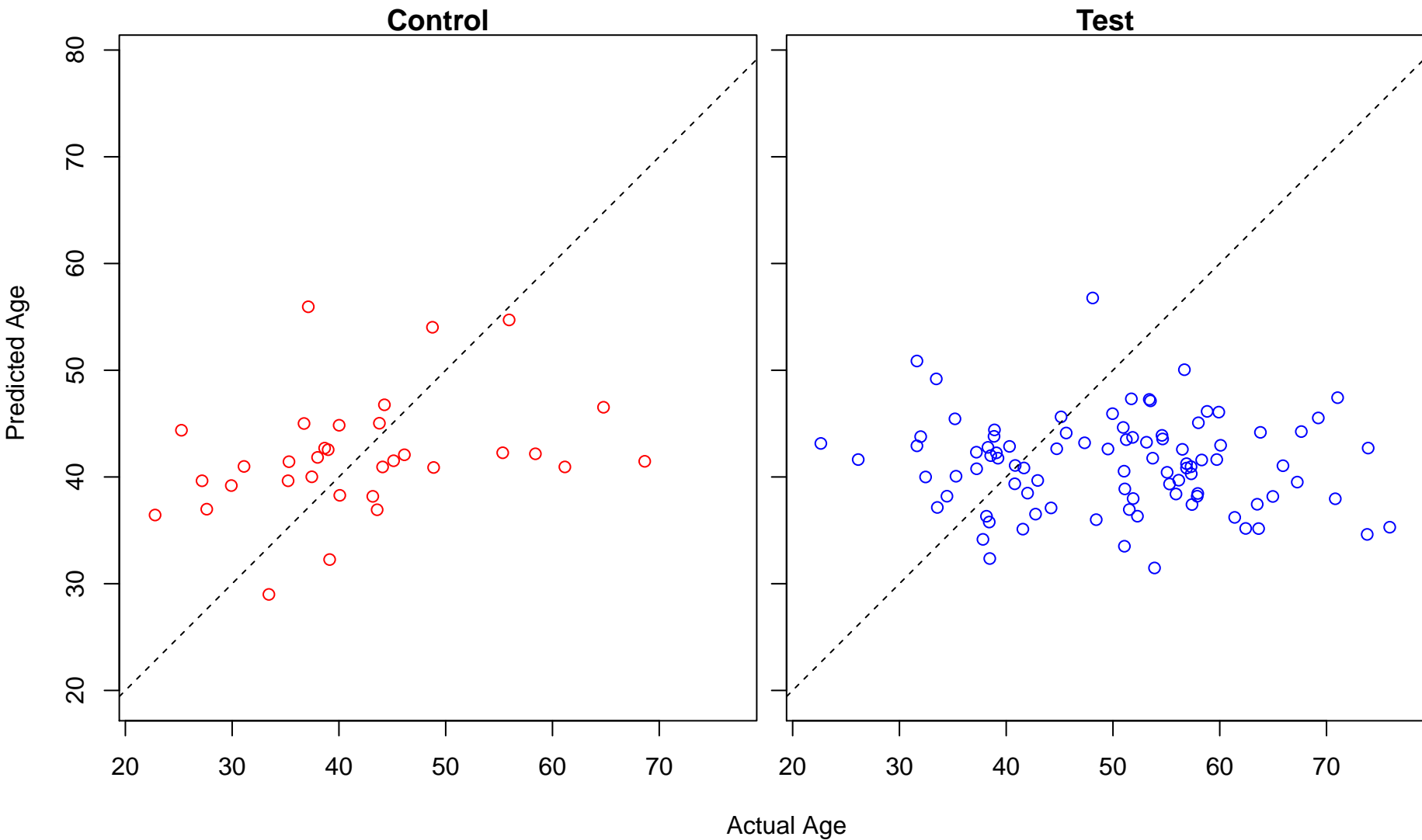
receptor transactivation (Score: 0.411269)



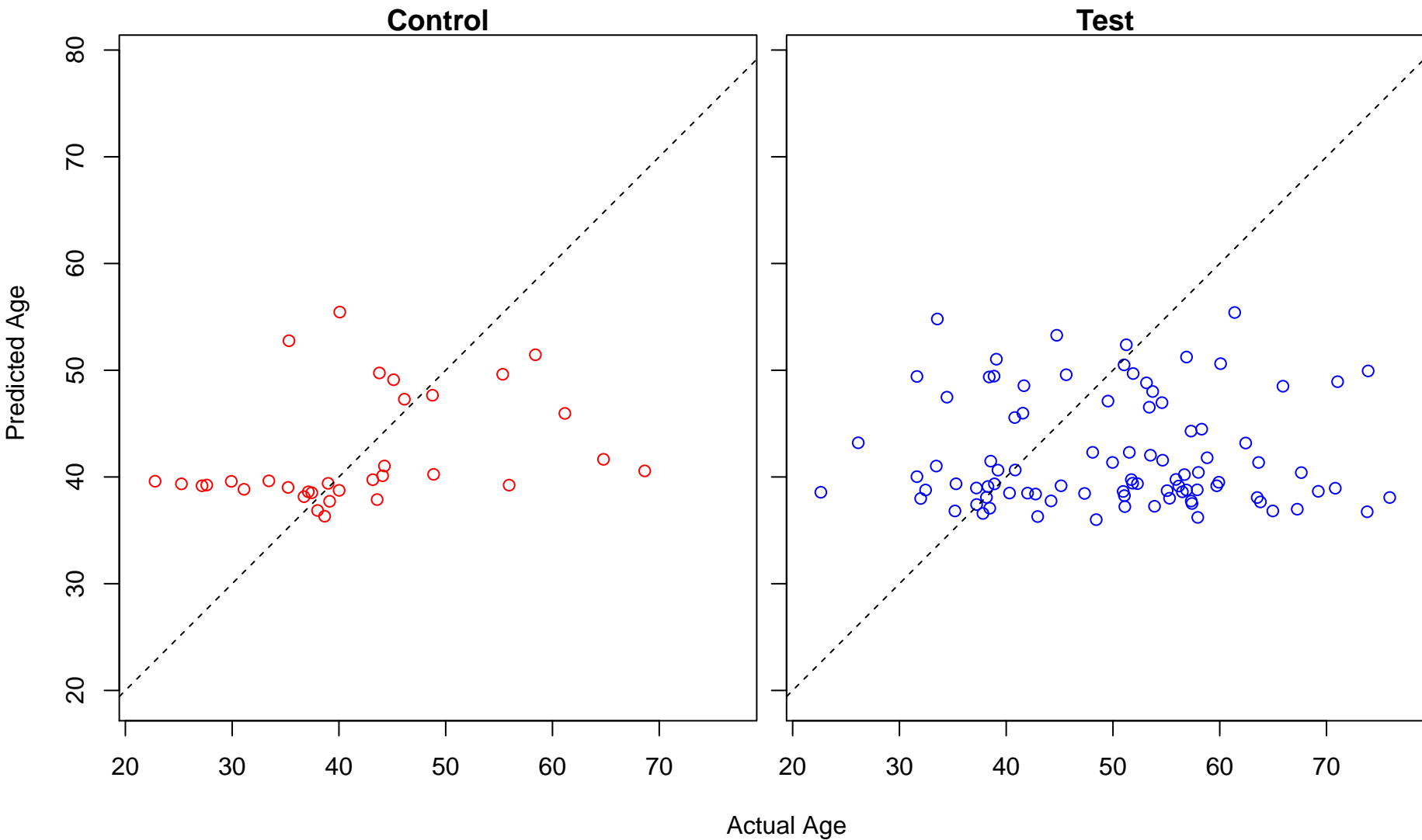
positive regulation of T cell cytokine production (Score: 0.410791)



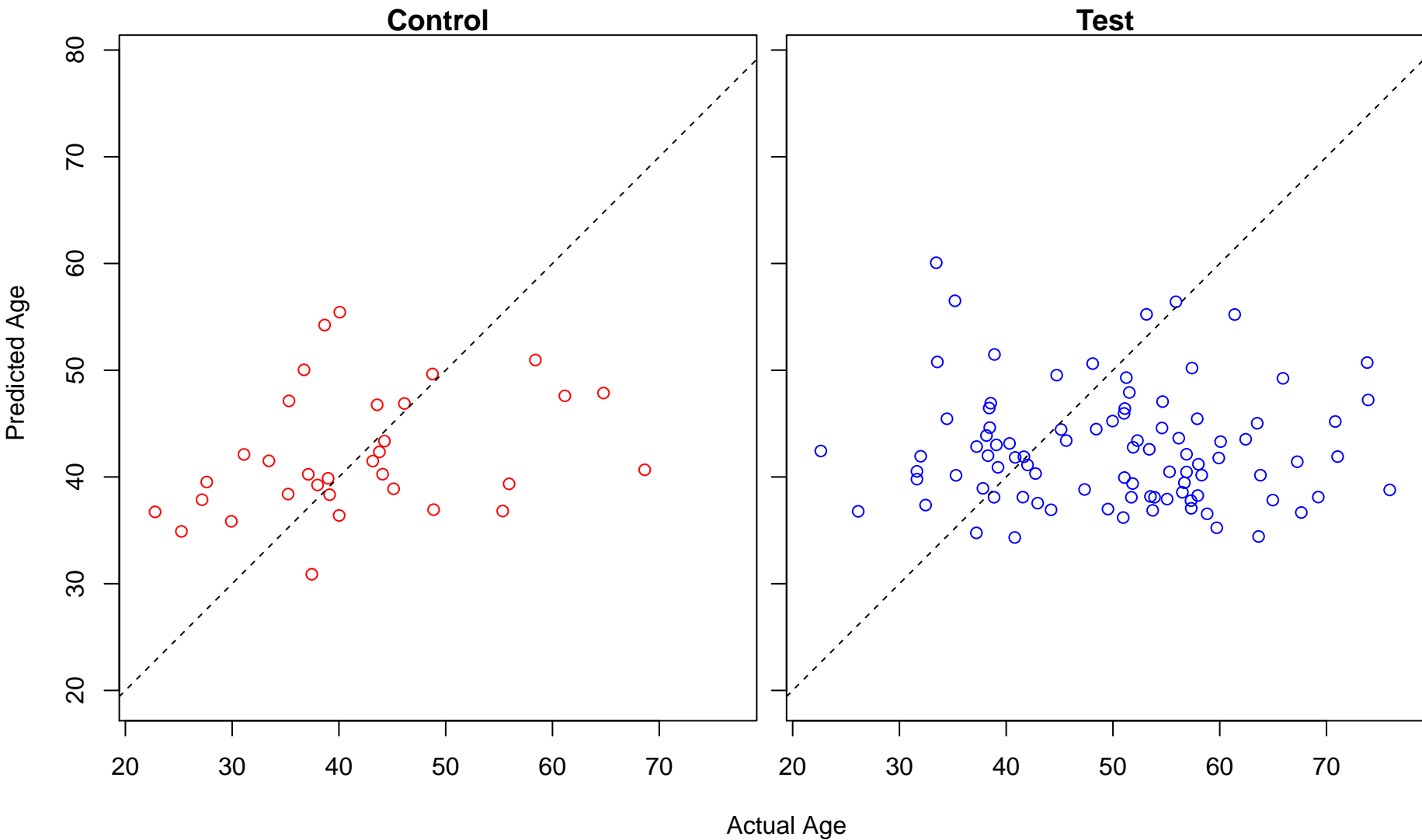
activation of NF-kappaB-inducing kinase activity (Score: 0.410301)



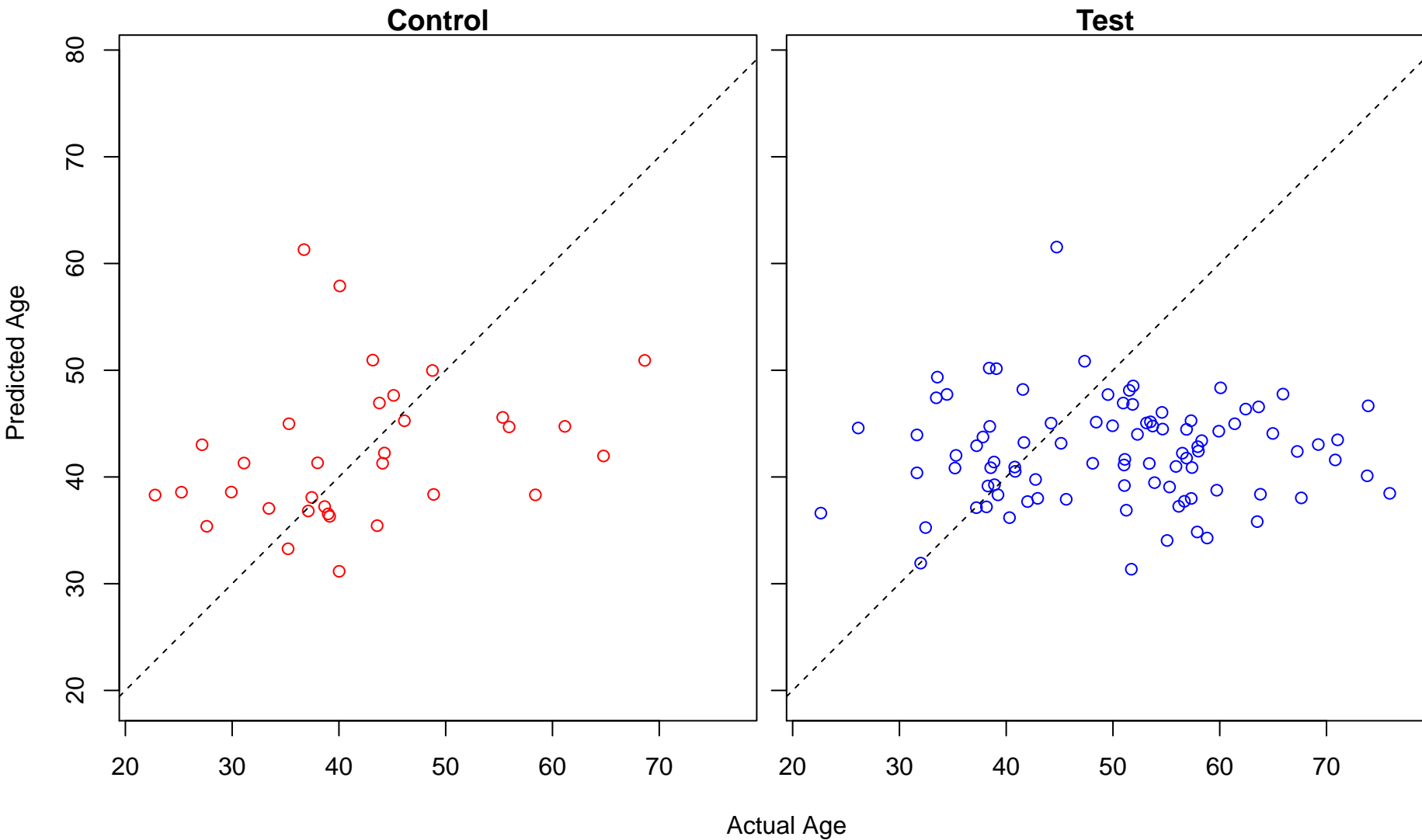
protection from non-homologous end joining at telomere (Score: 0.409442)



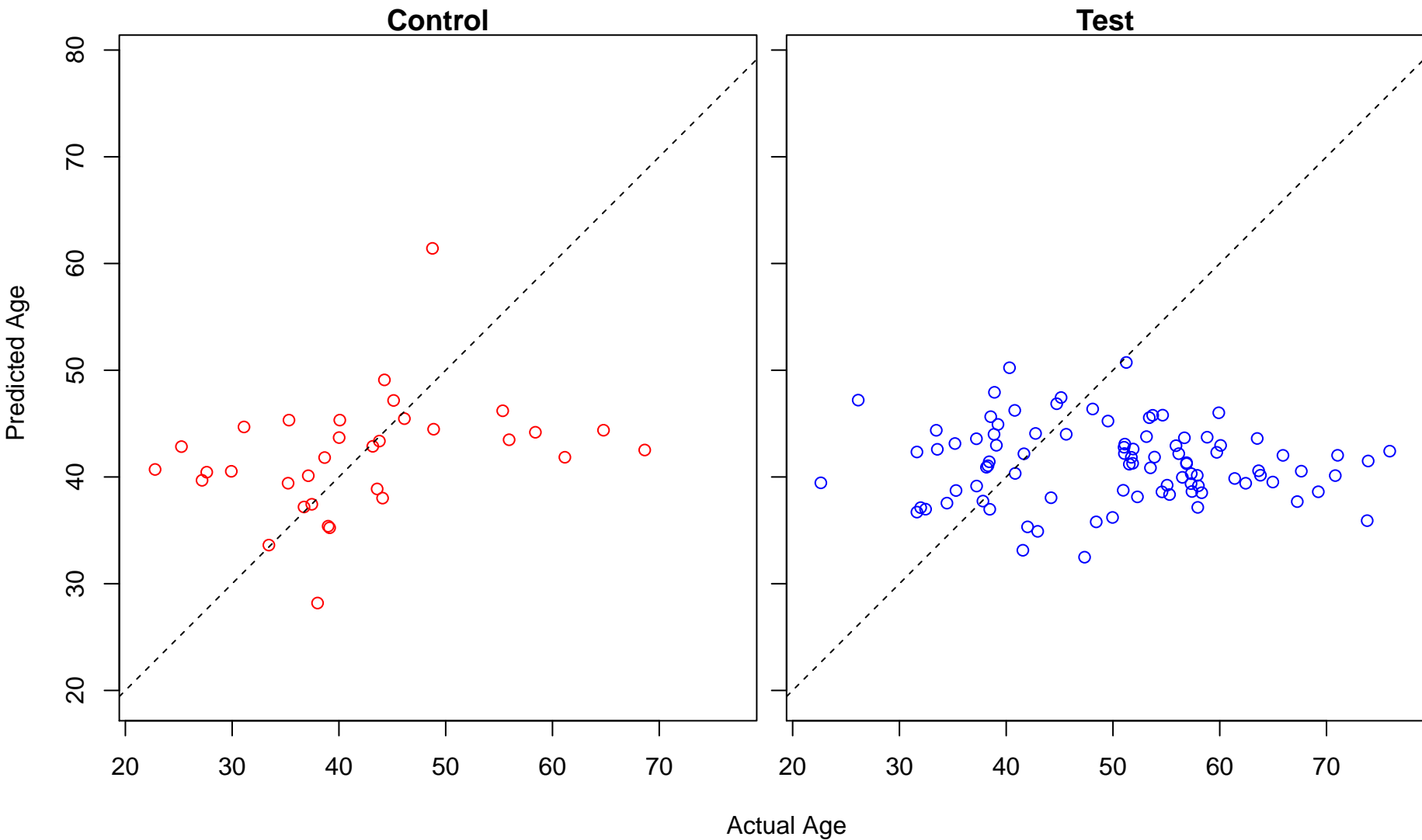
craniofacial suture morphogenesis (Score: 0.409391)



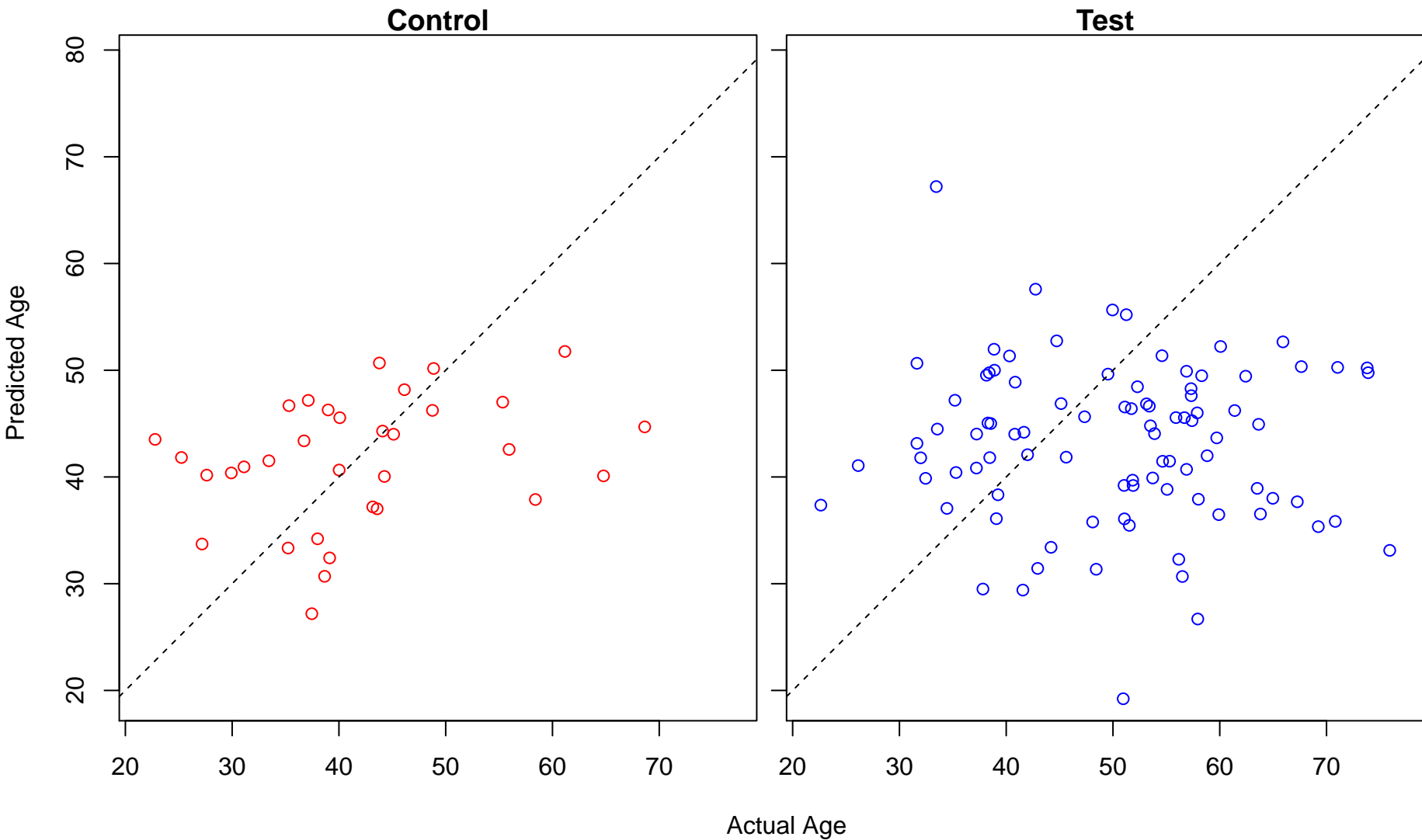
lysosomal lumen acidification (Score: 0.409234)



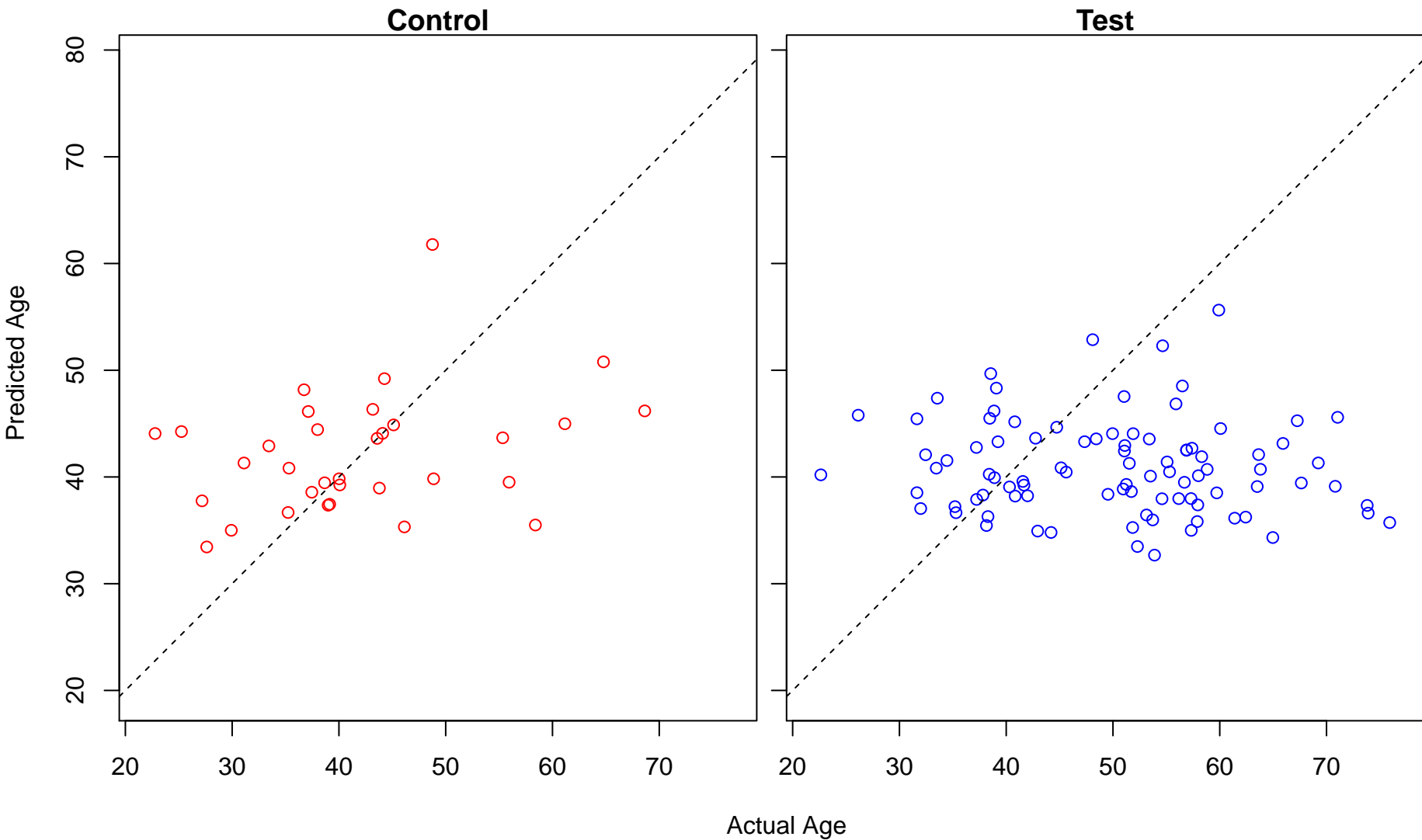
pentose metabolic process (Score: 0.405785)



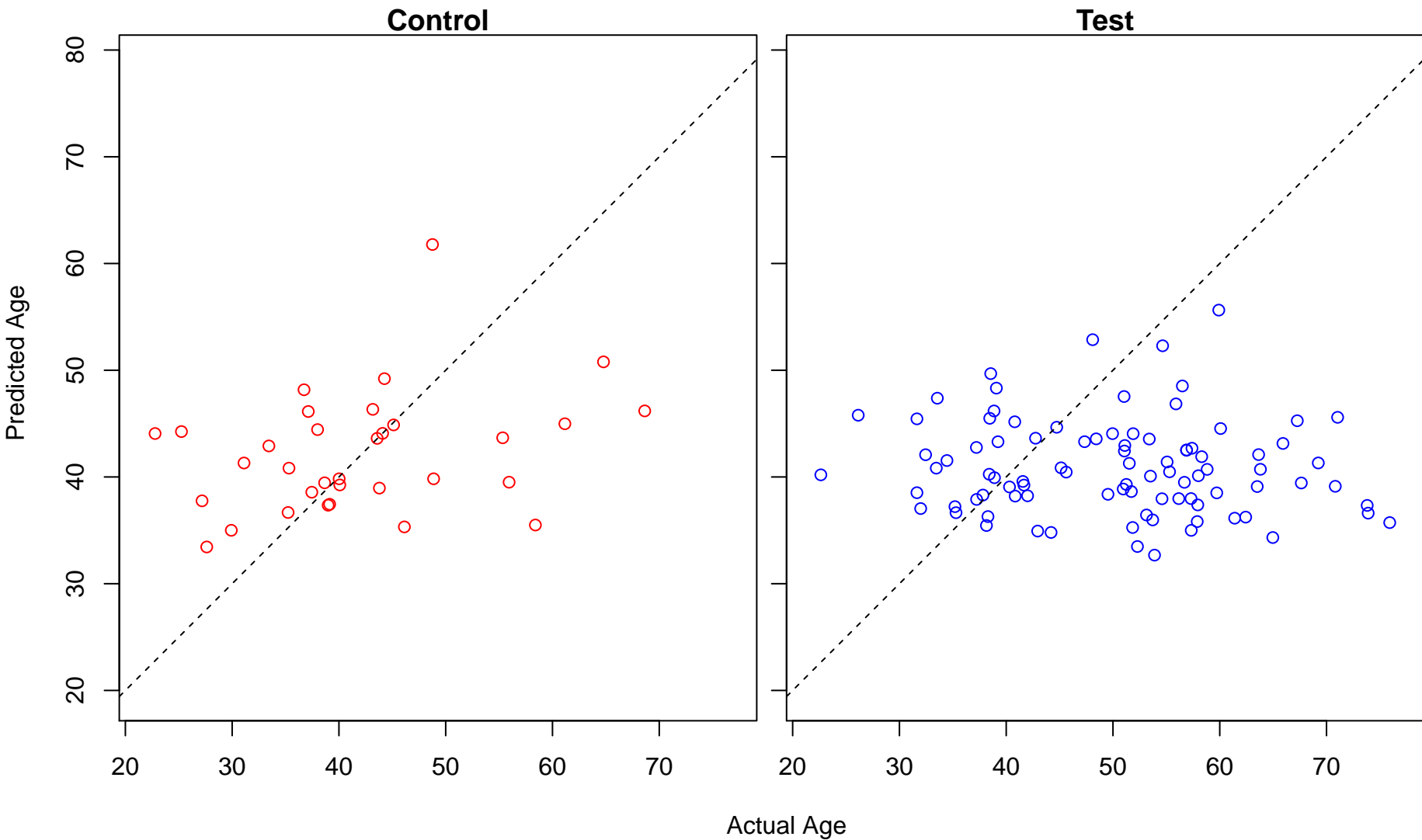
negative regulation of nitric-oxide synthase activity (Score: 0.404284)



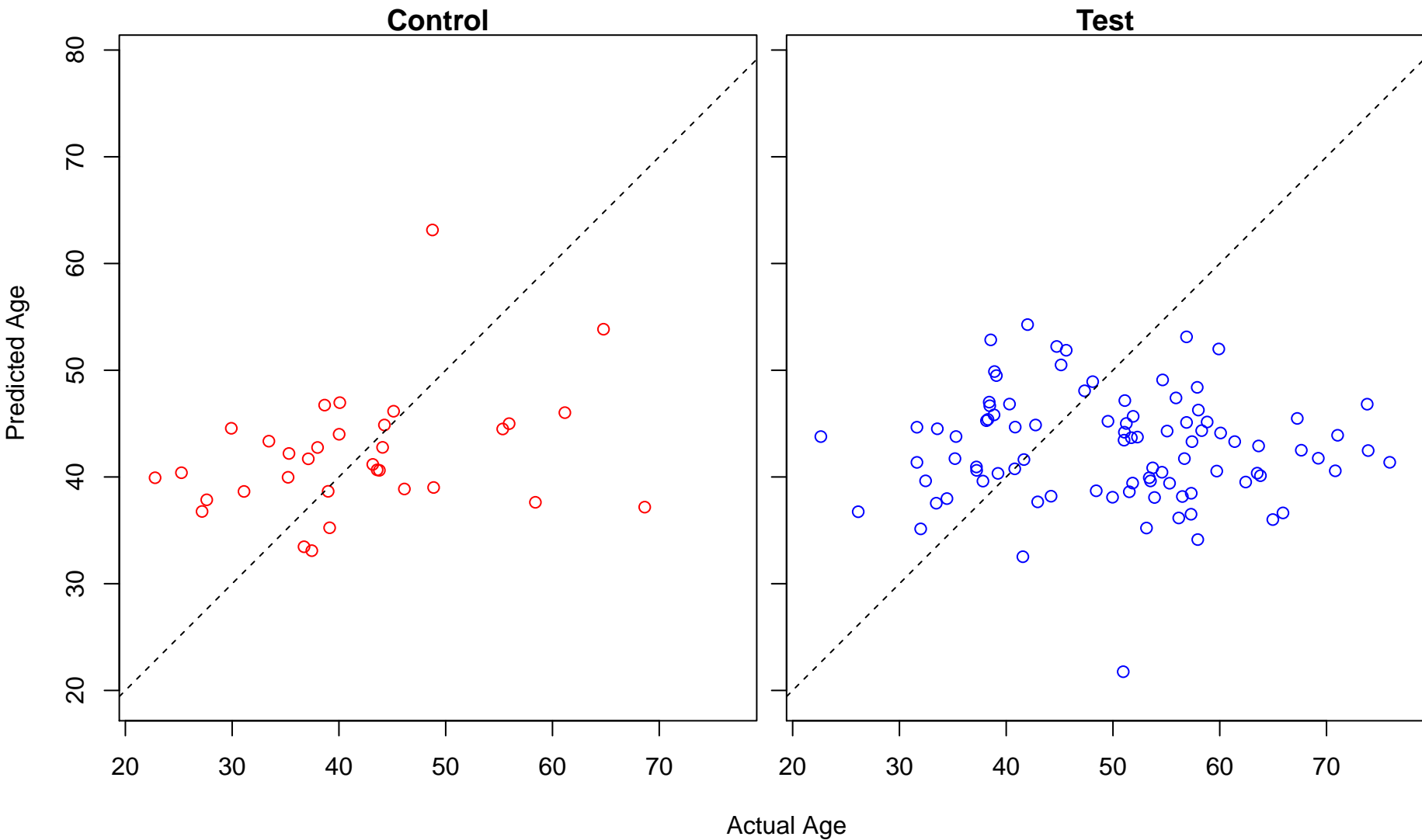
positive regulation of isotype switching (Score: 0.402668)



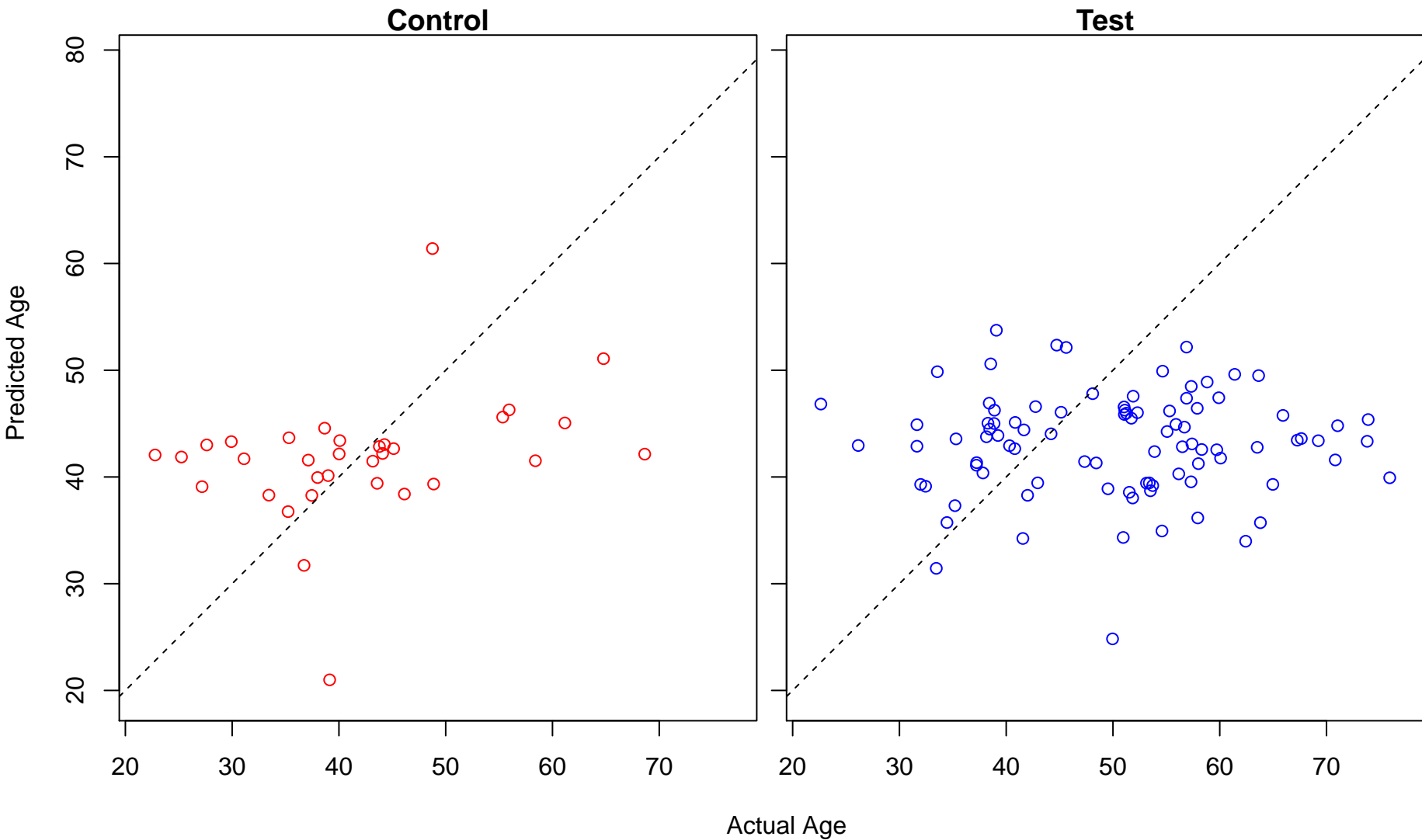
positive regulation of DNA recombination (Score: 0.402668)



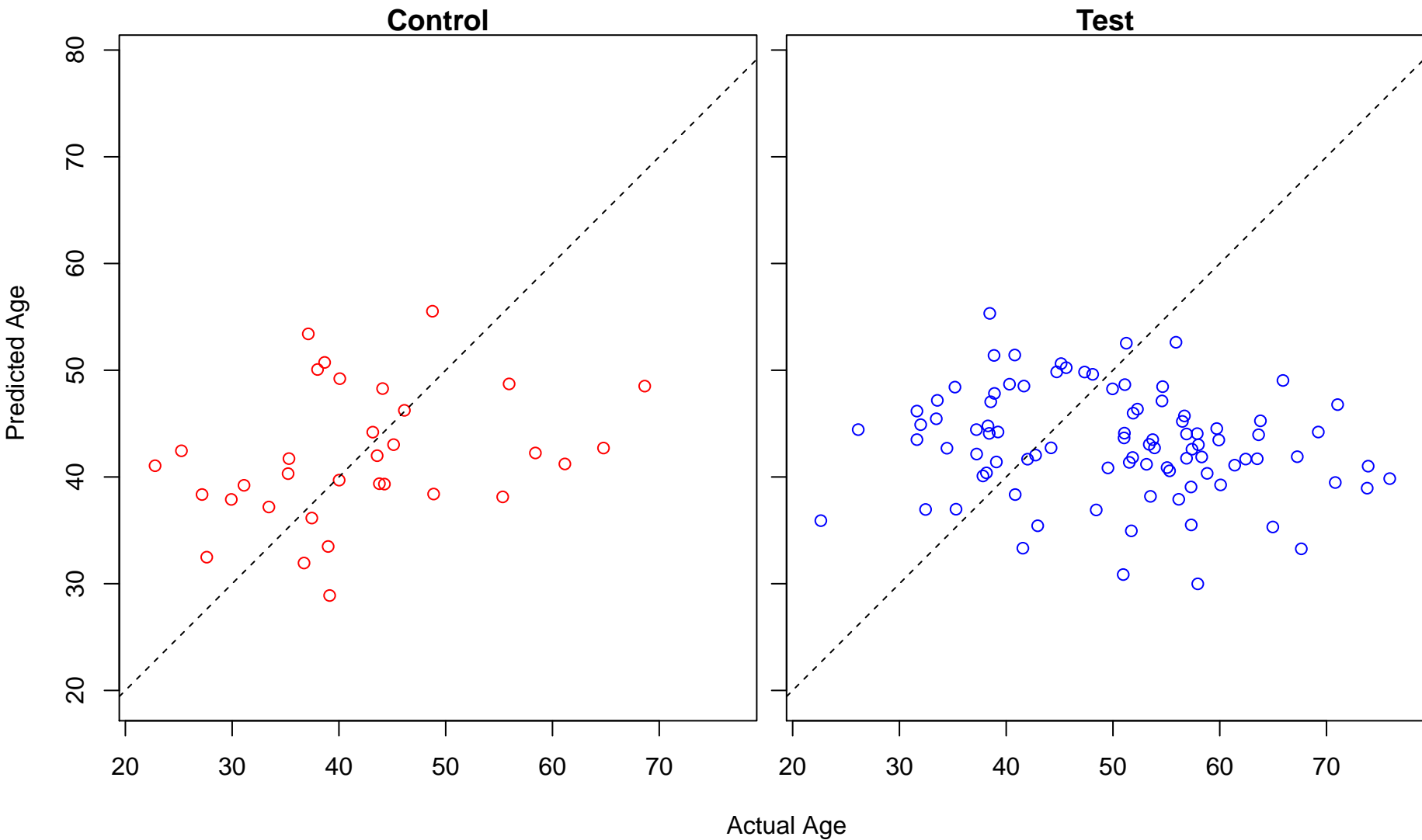
base-excision repair, gap-filling (Score: 0.401984)



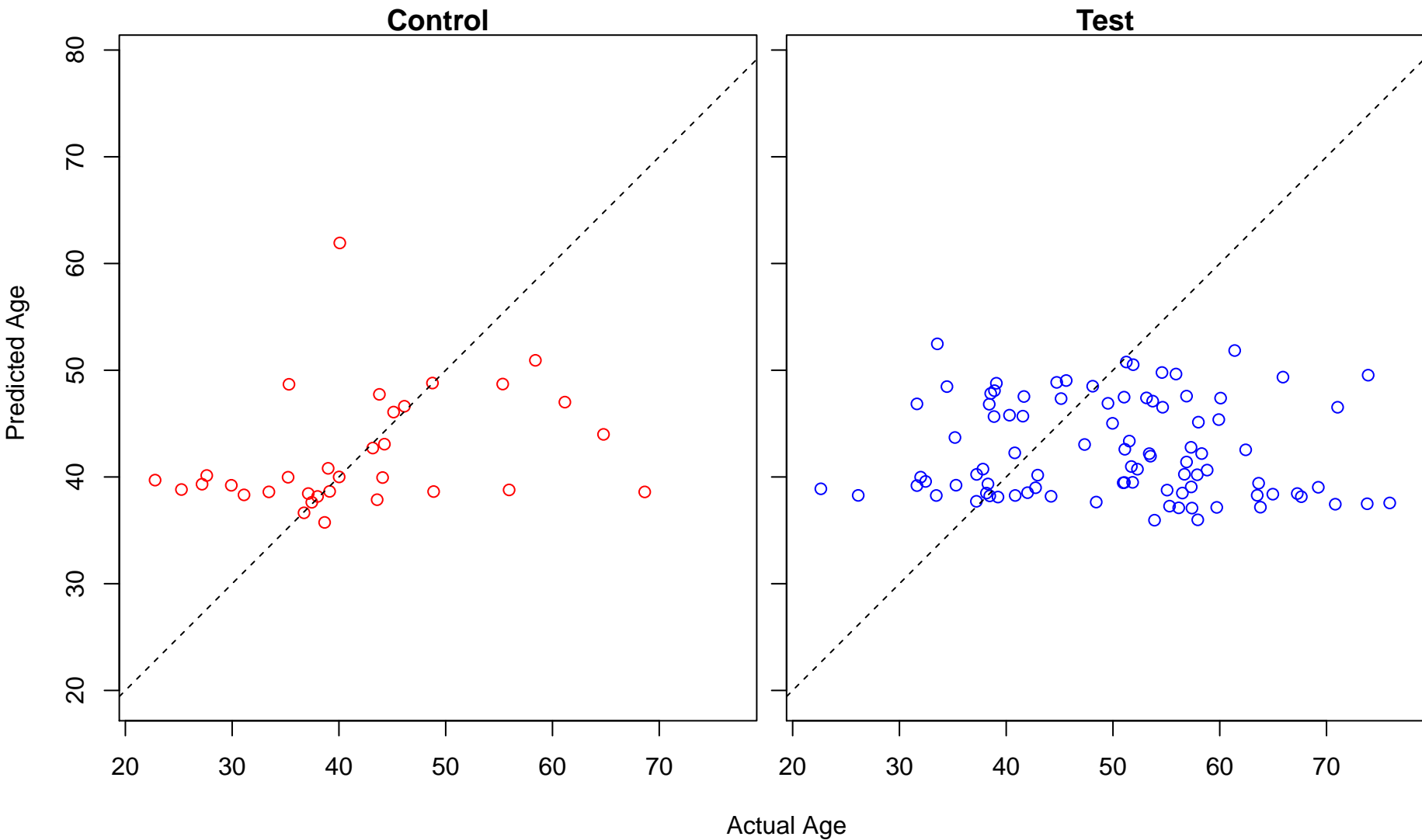
melanosome organization (Score: 0.401688)



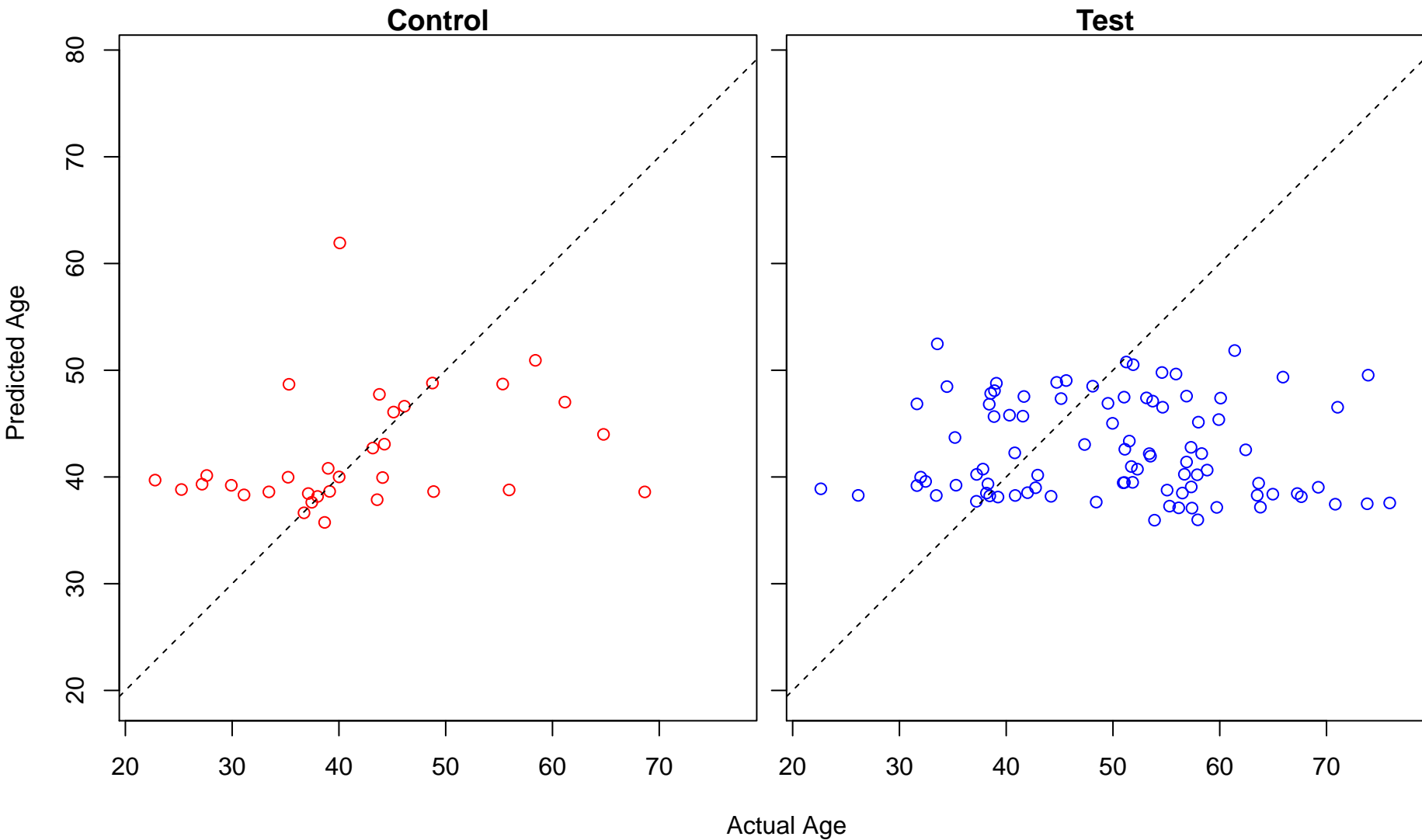
response to copper ion (Score: 0.401325)



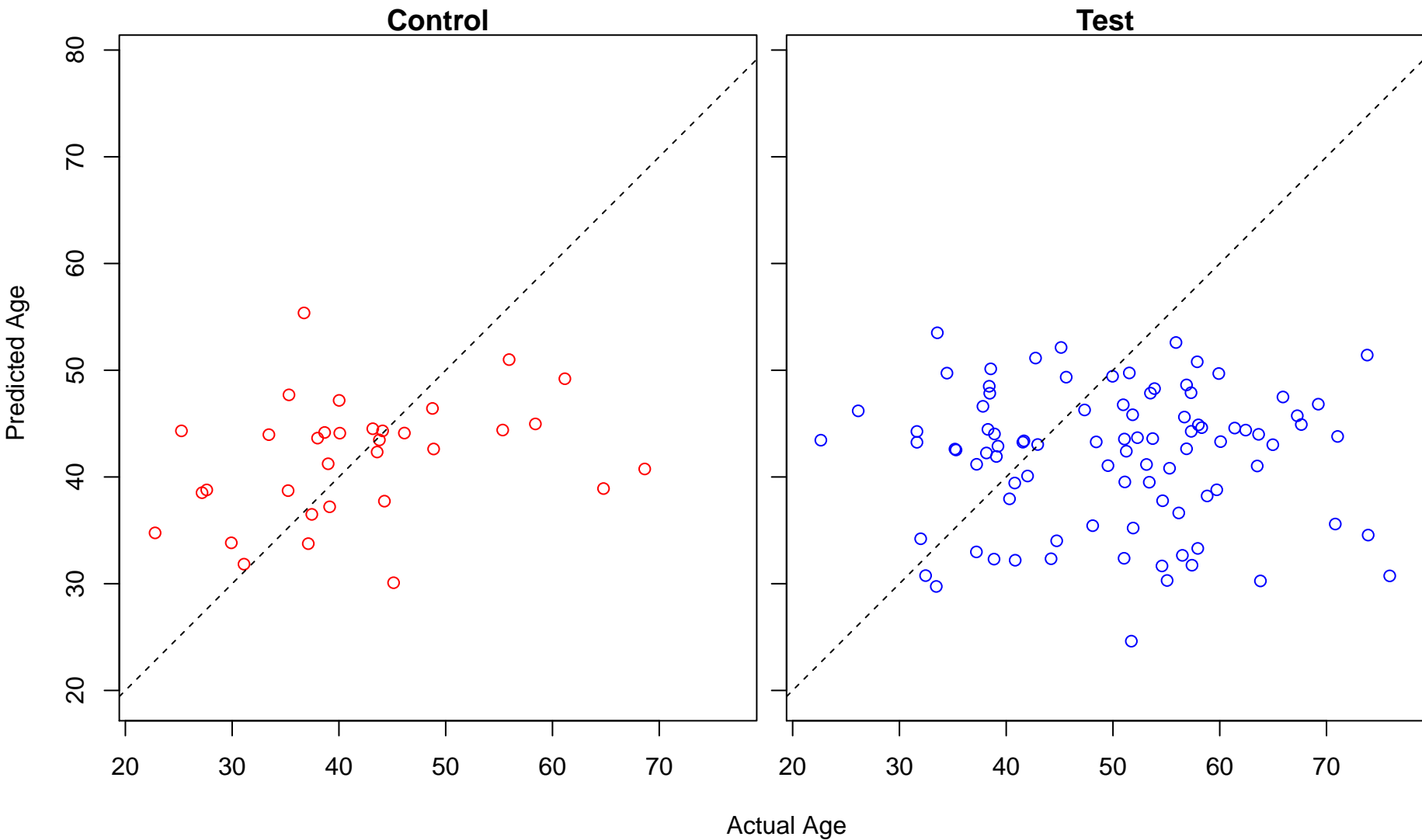
nuclear migration (Score: 0.398282)



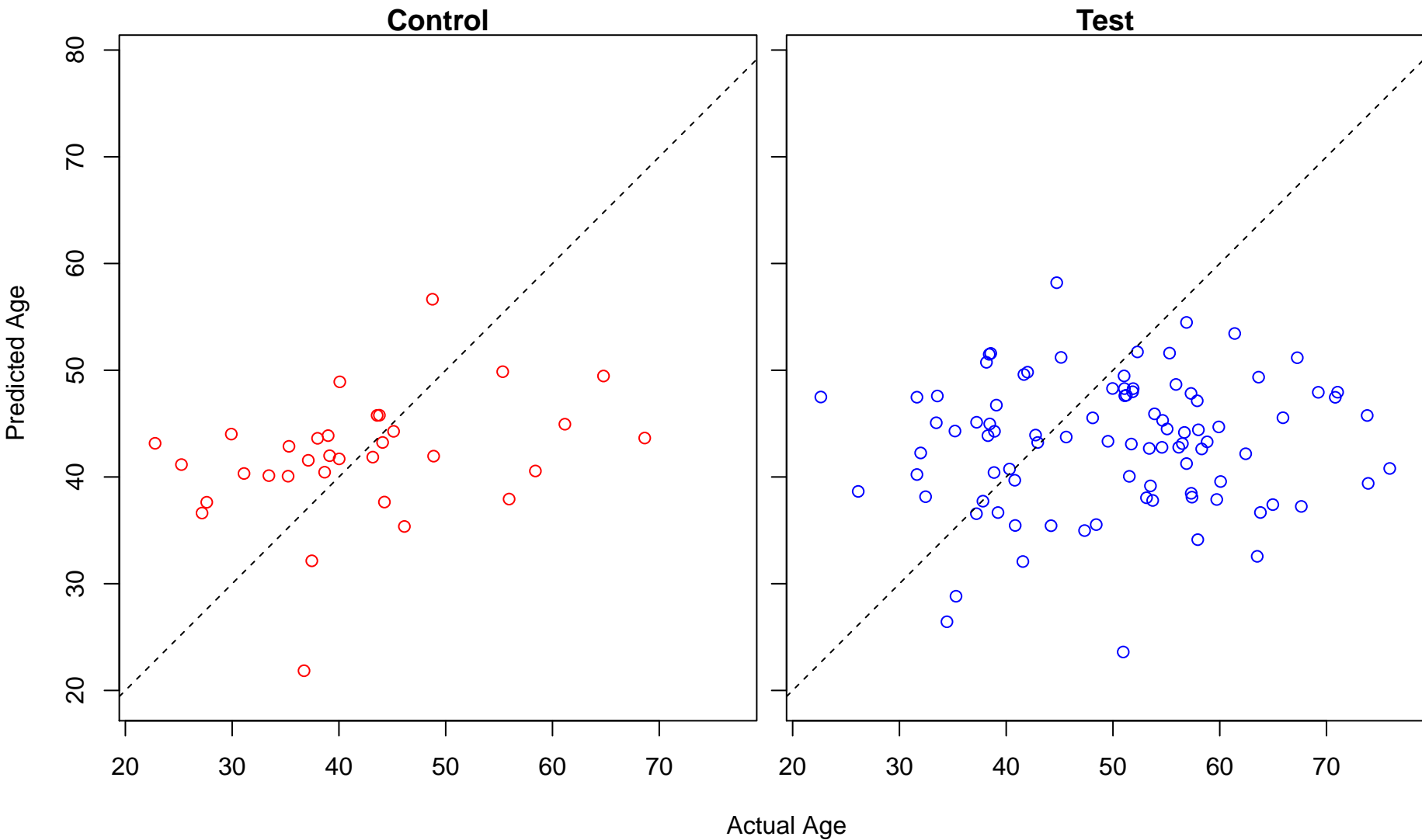
nuclear migration along microfilament (Score: 0.398282)



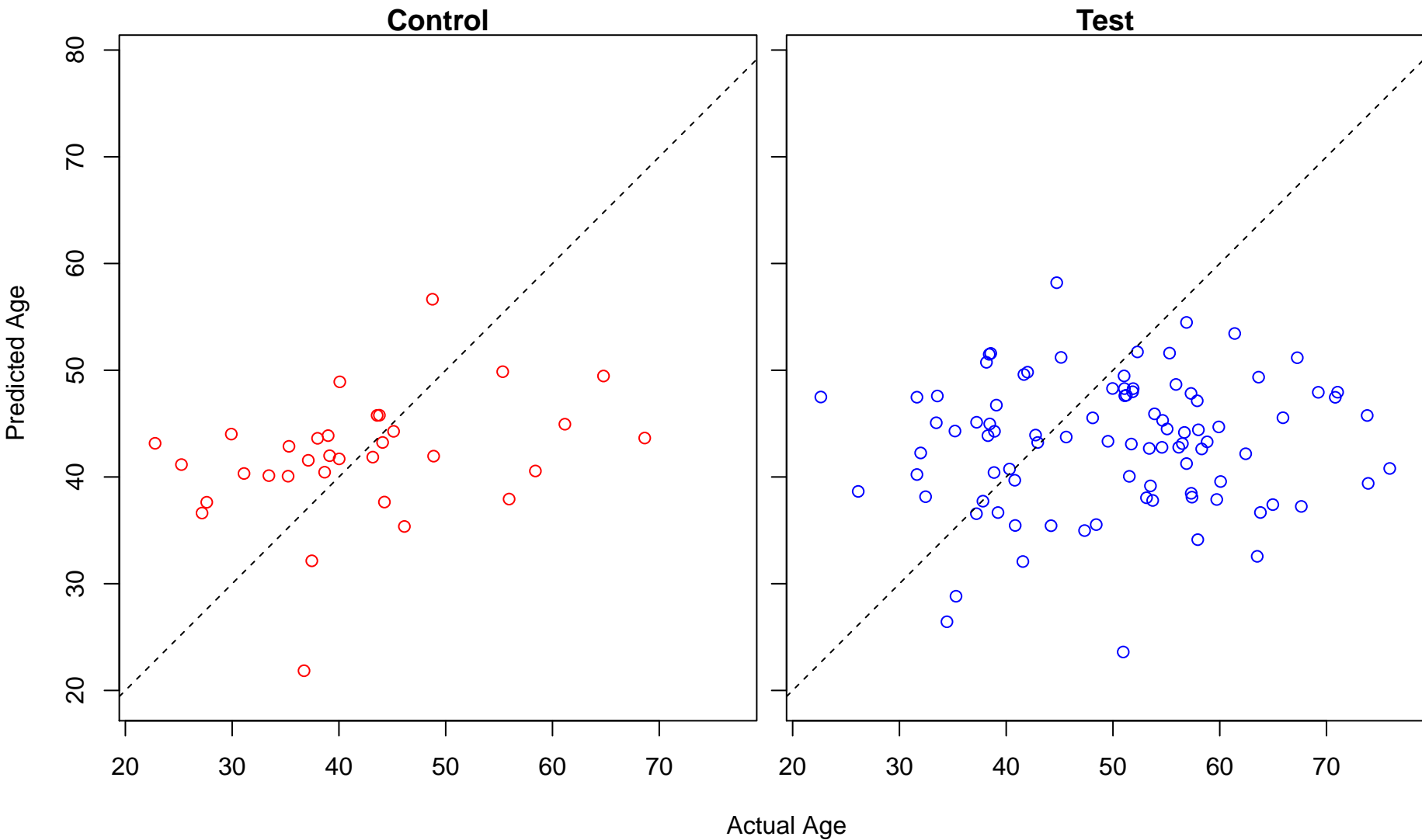
regulation of MyD88-dependent toll-like receptor signaling pathway (Score: 0.398030)



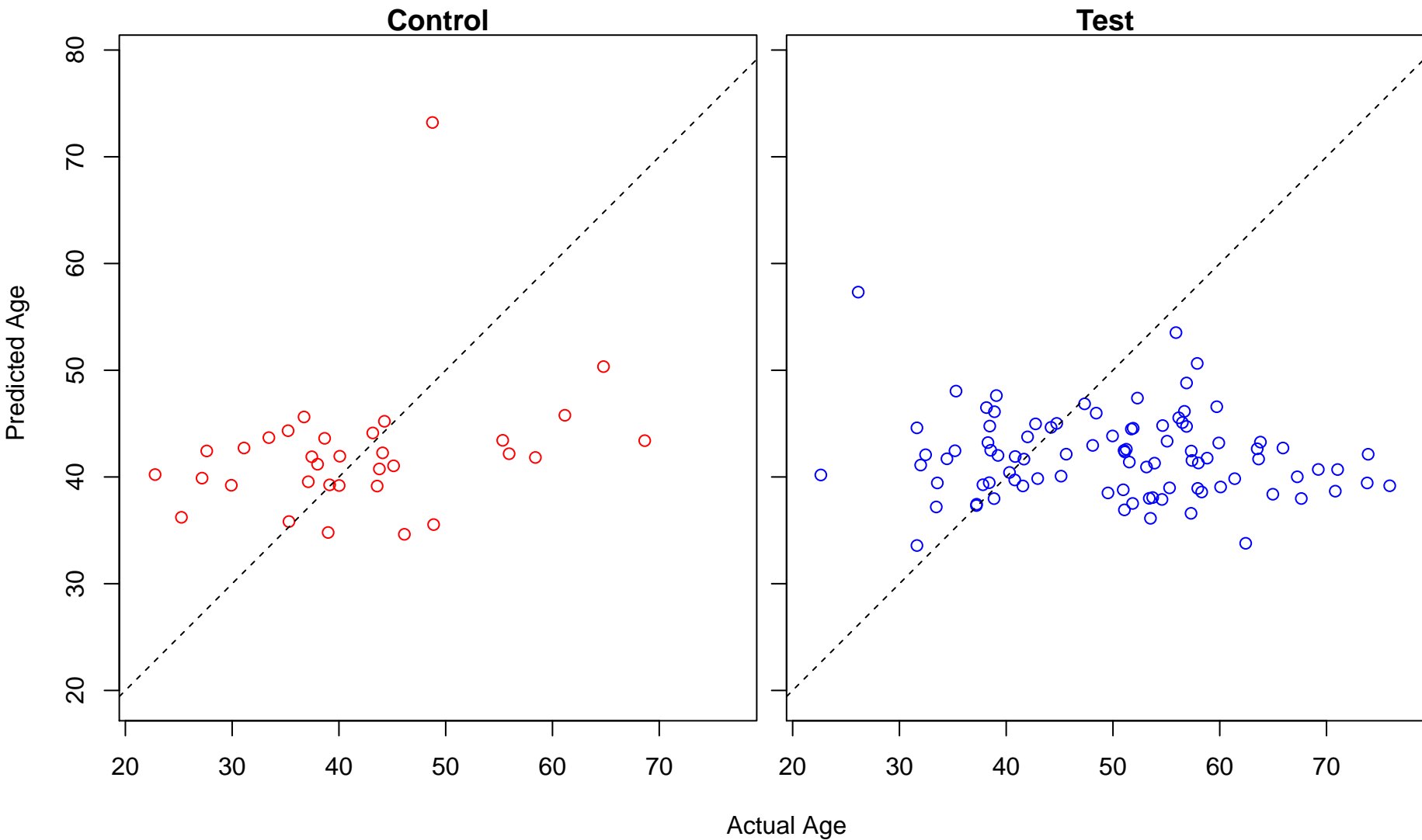
startle response (Score: 0.396400)



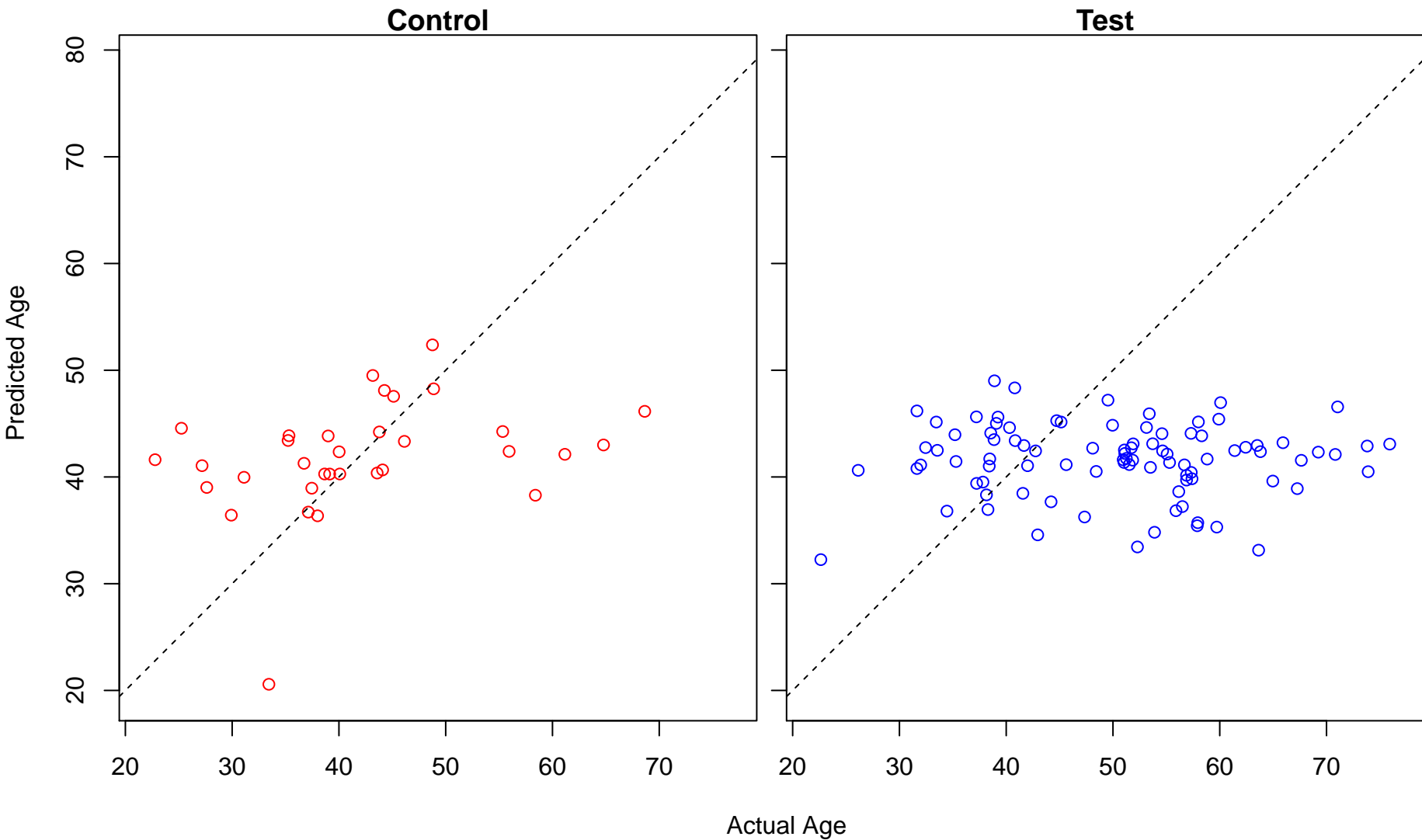
prepulse inhibition (Score: 0.396400)



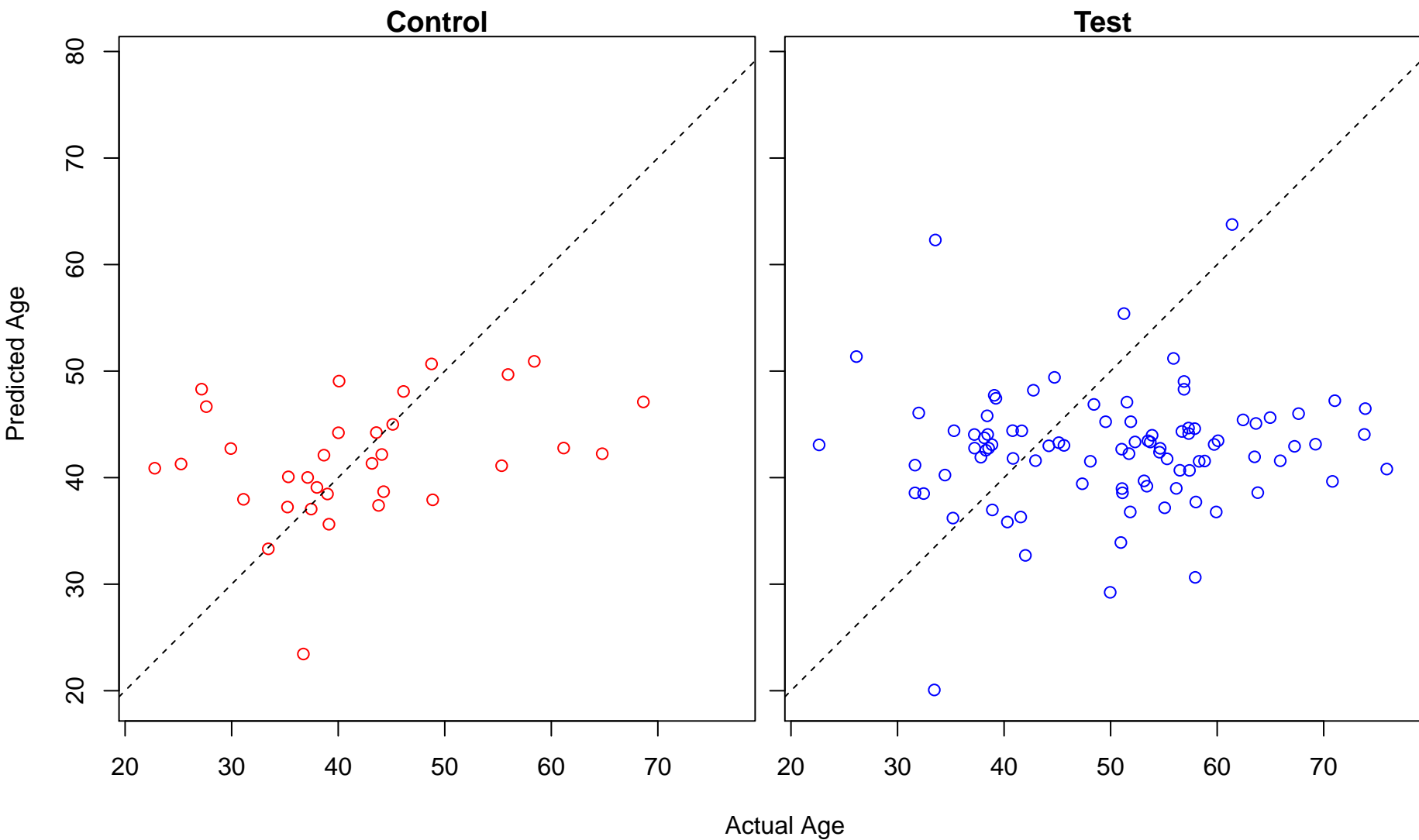
regulation of definitive erythrocyte differentiation (Score: 0.396264)



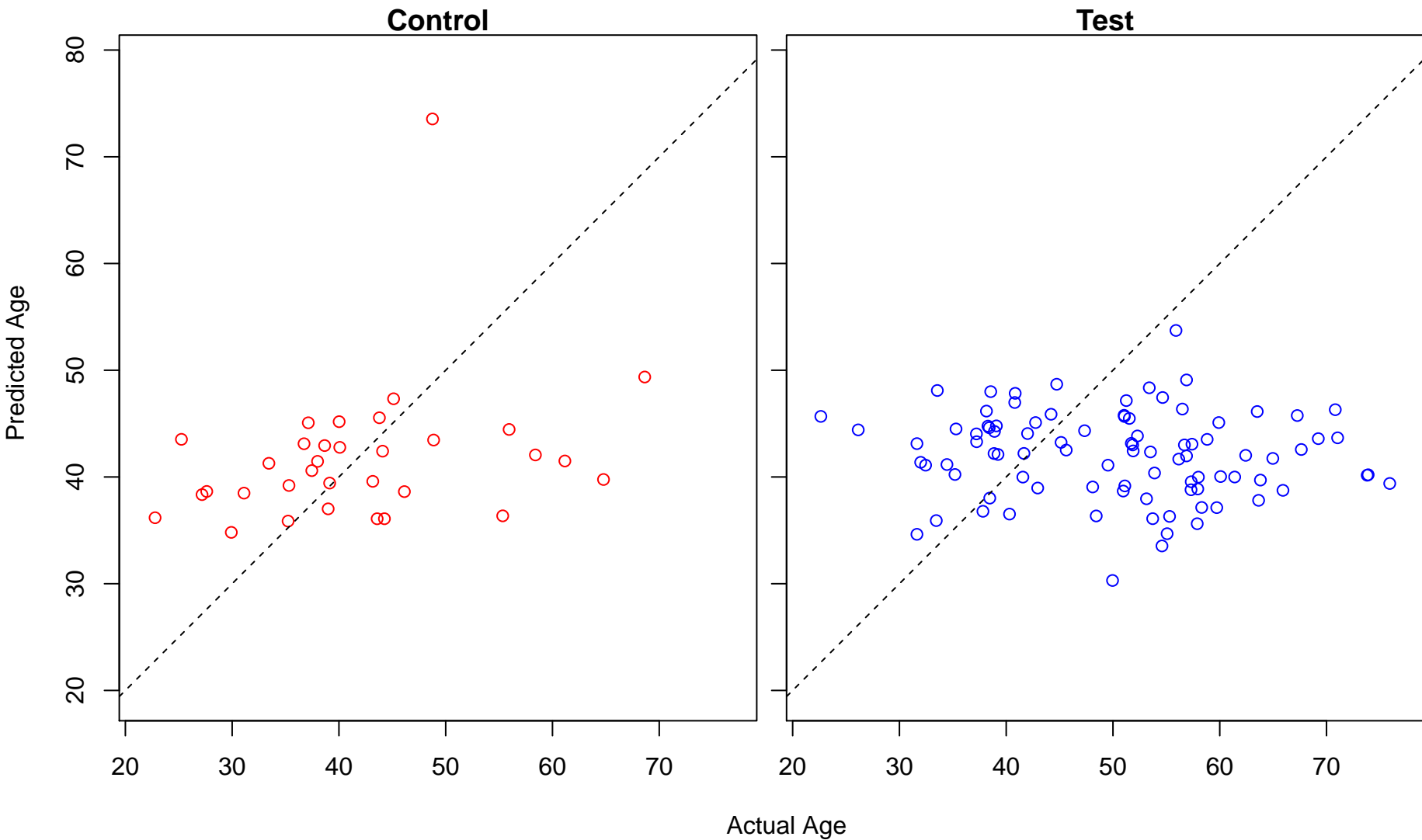
regulation of sequestering of zinc ion (Score: 0.394683)



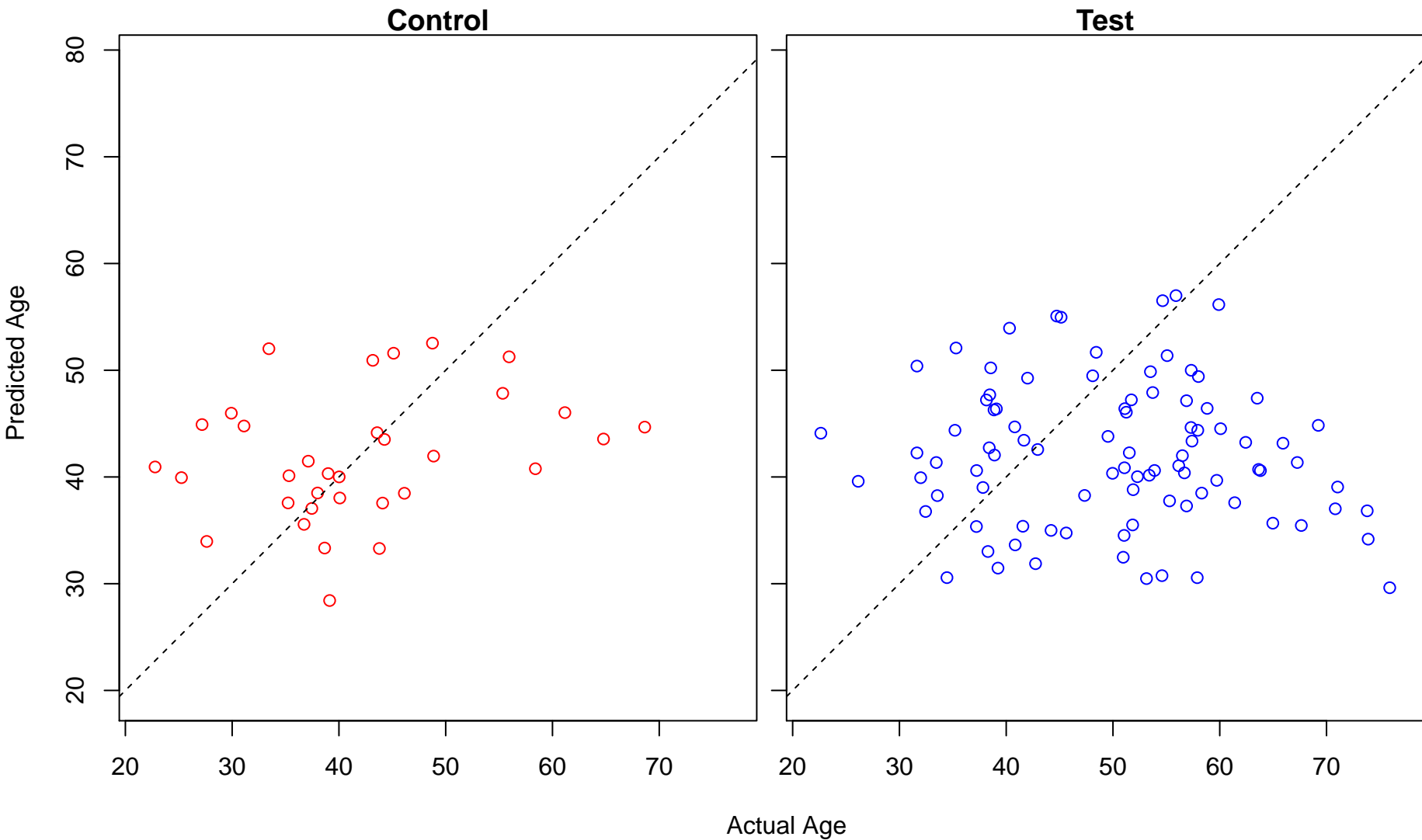
mast cell secretory granule organization (Score: 0.393705)



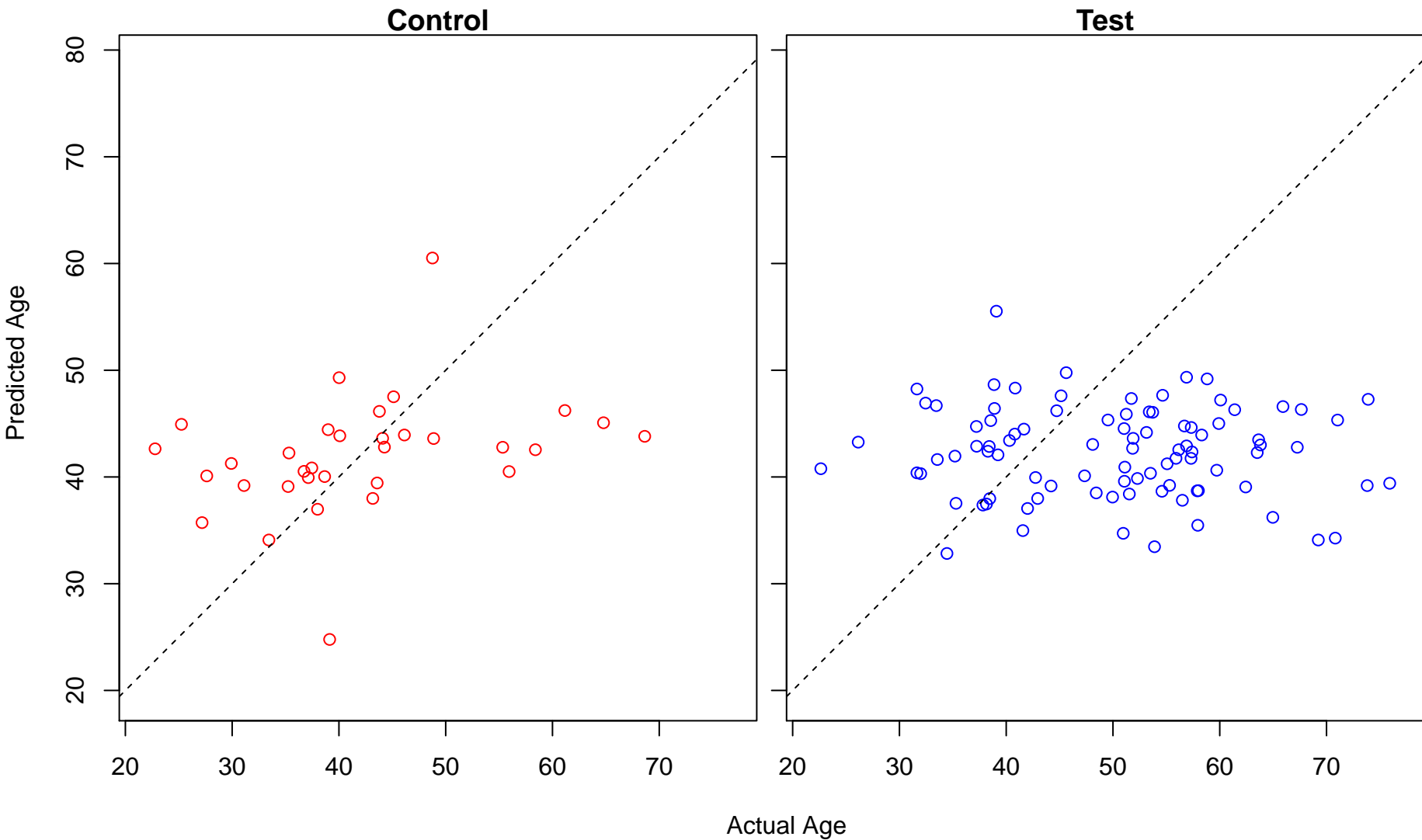
positive regulation of T cell apoptotic process (Score: 0.393468)



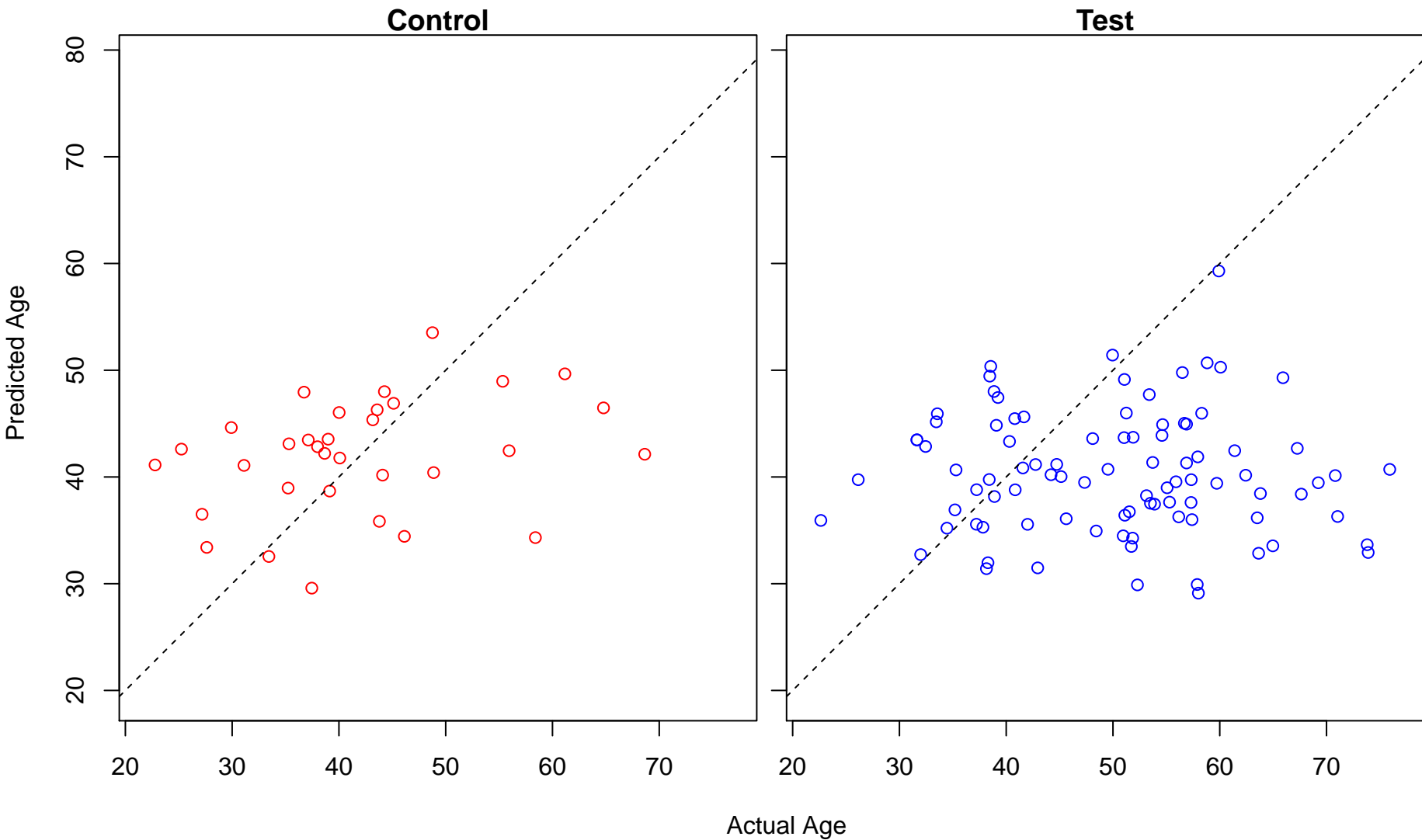
negative regulation of T cell cytokine production (Score: 0.392366)



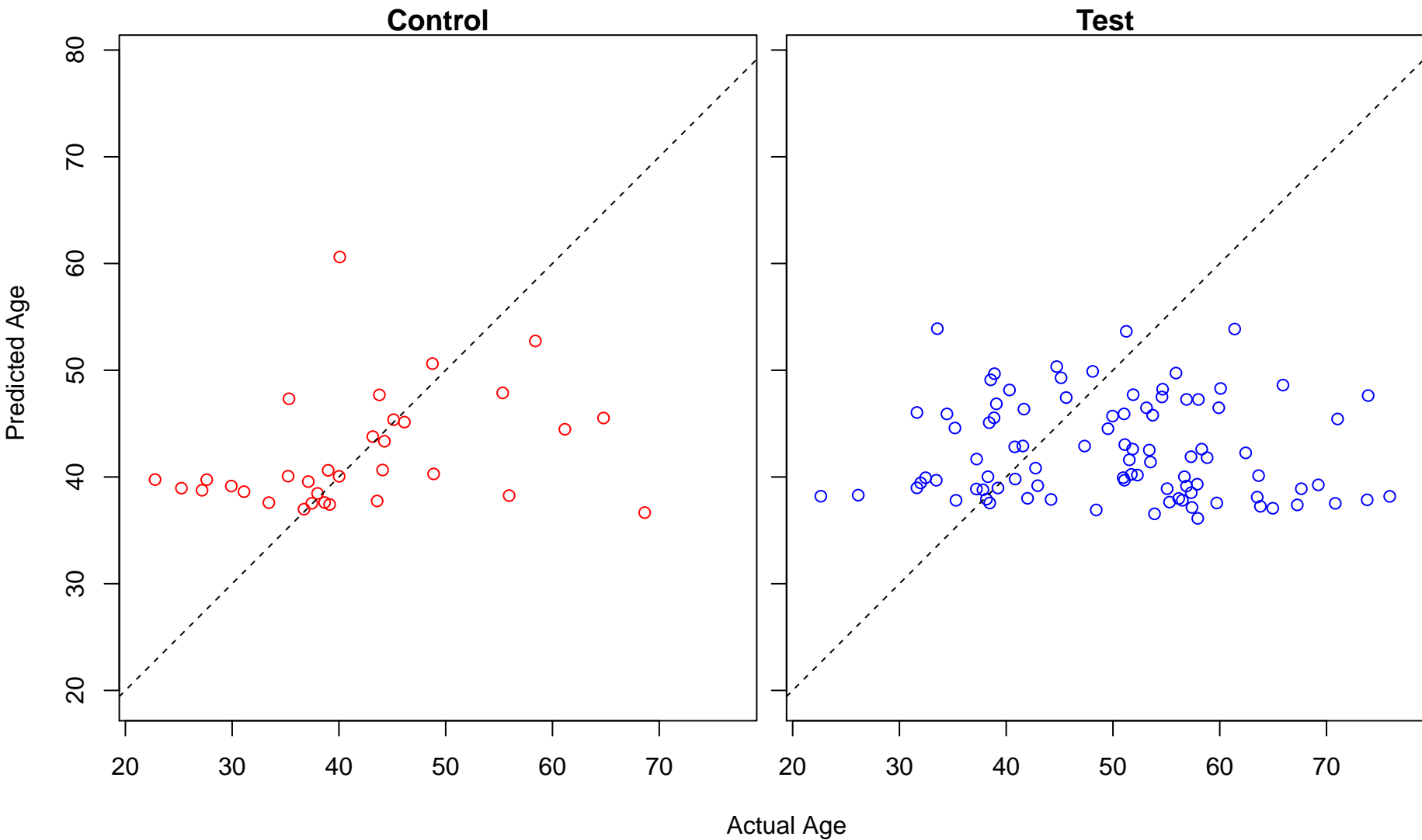
proteasome regulatory particle assembly (Score: 0.389590)



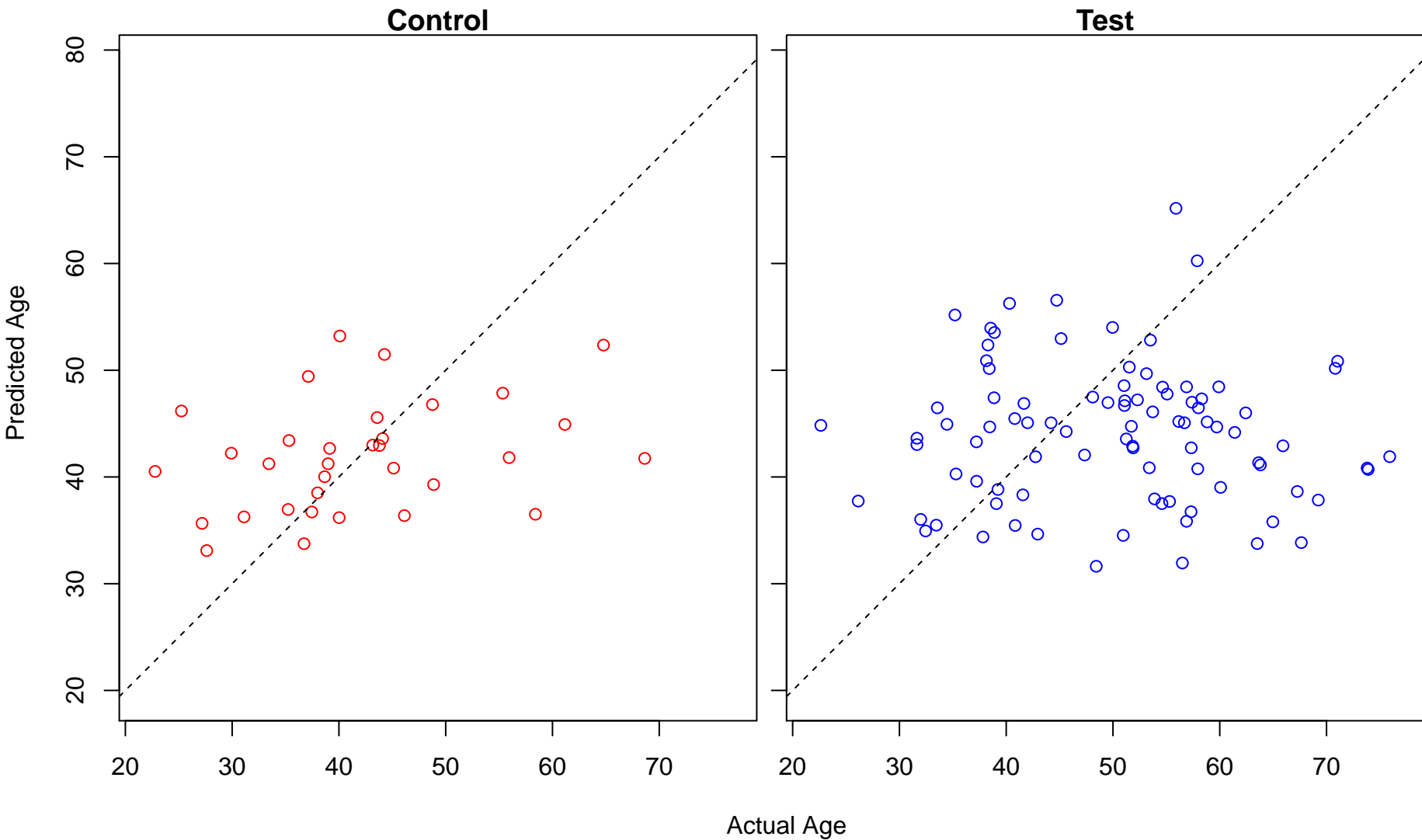
positive regulation of immunoglobulin production (Score: 0.389308)



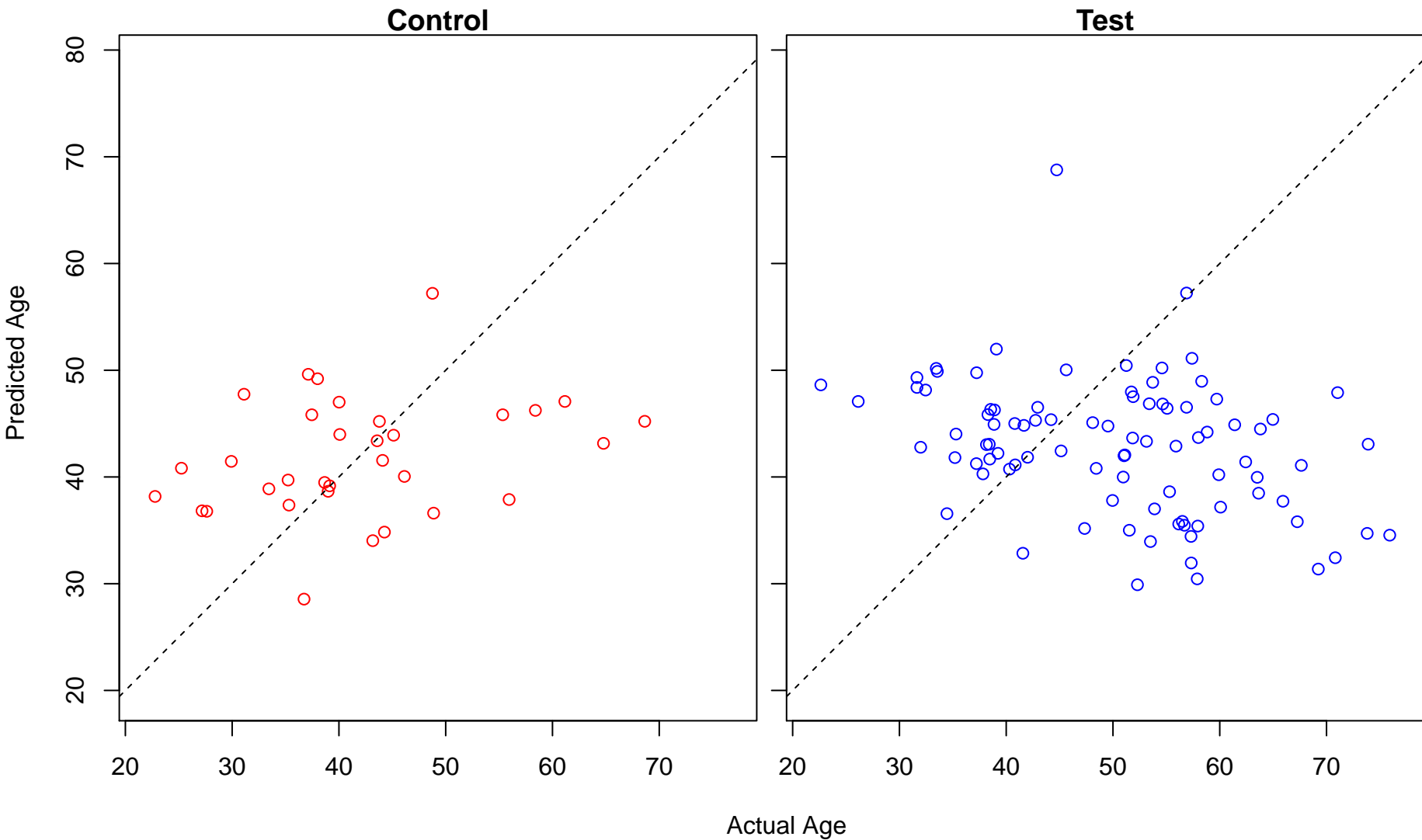
establishment of nucleus localization (Score: 0.388494)



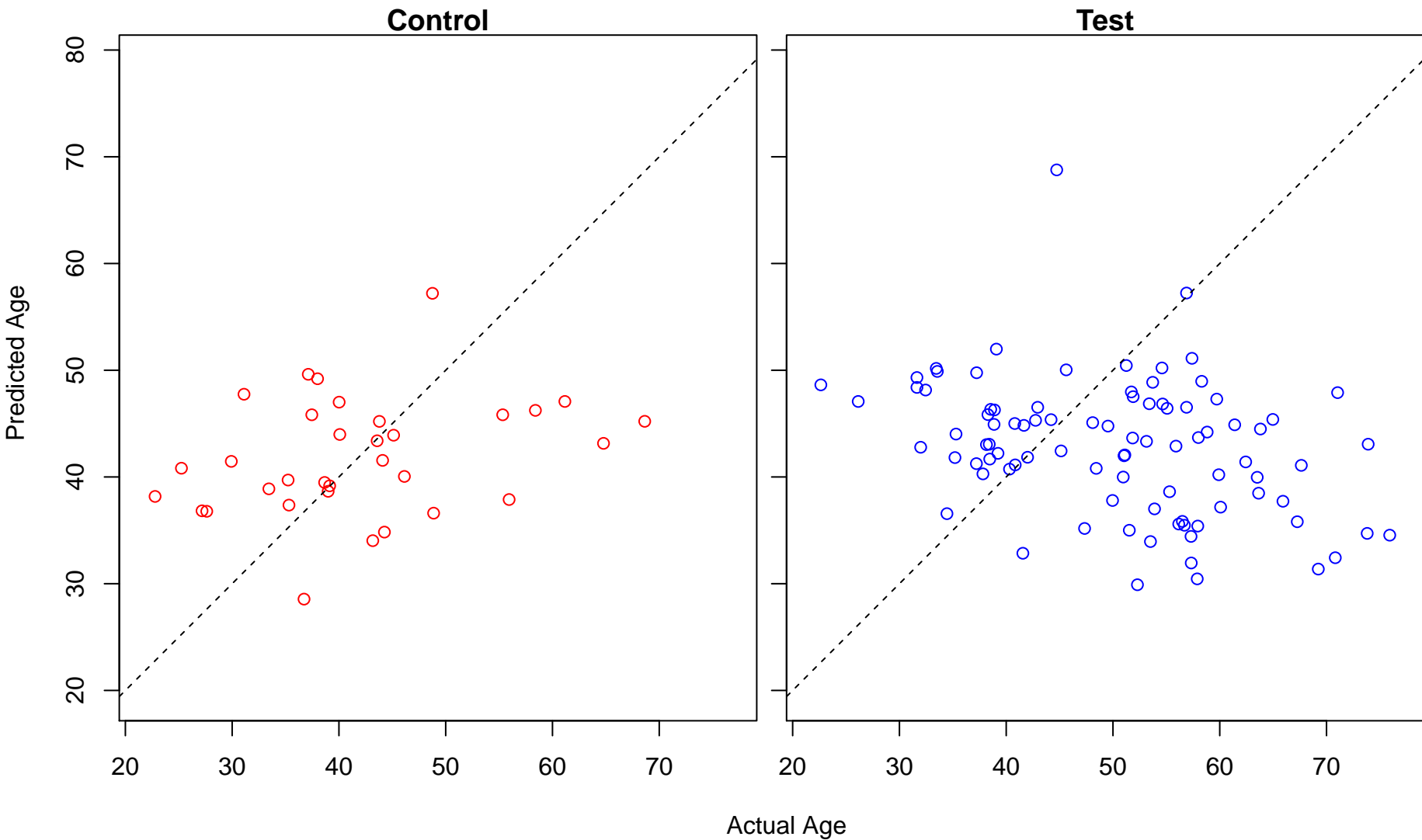
regulation of embryonic cell shape (Score: 0.386472)



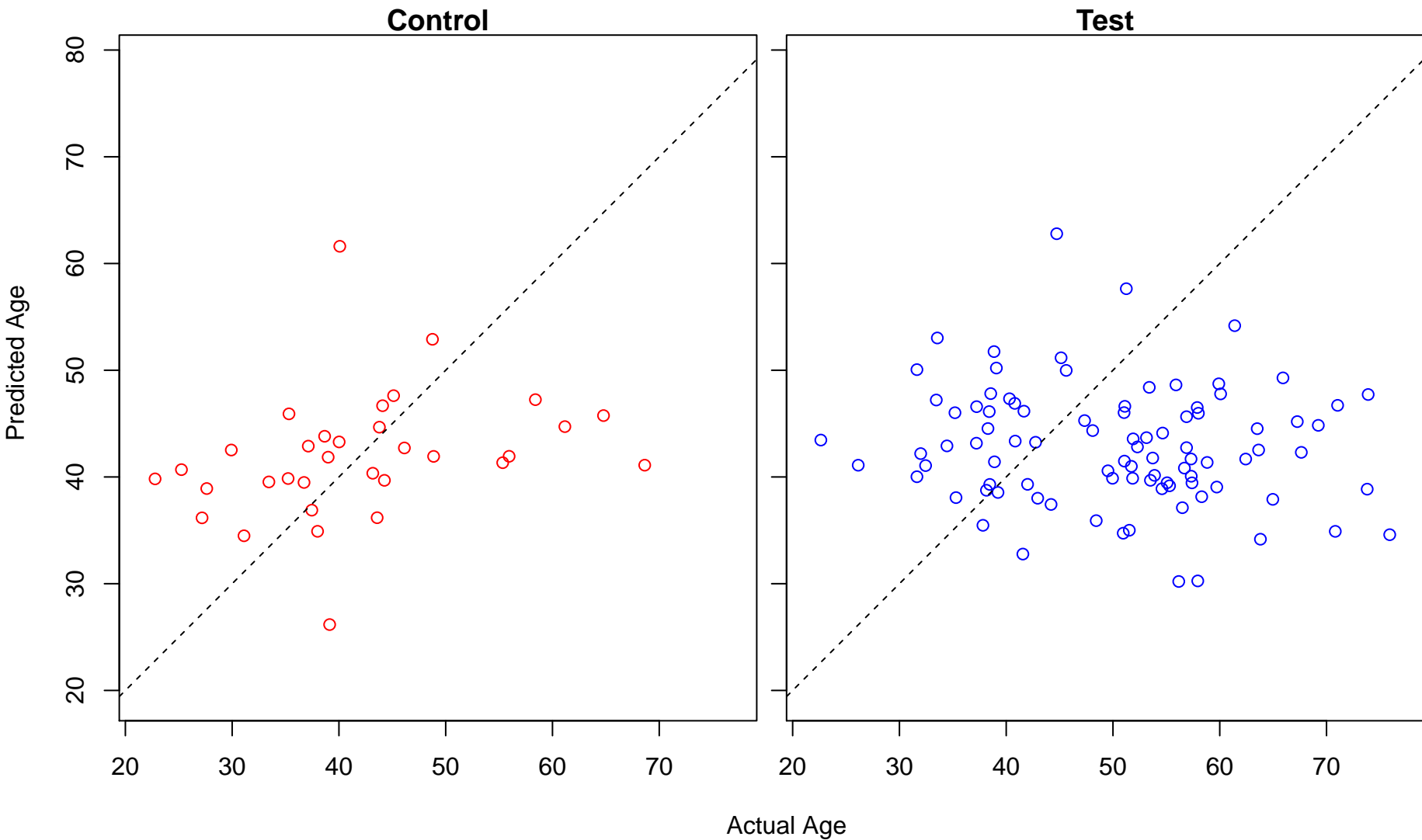
endochondral ossification (Score: 0.386265)



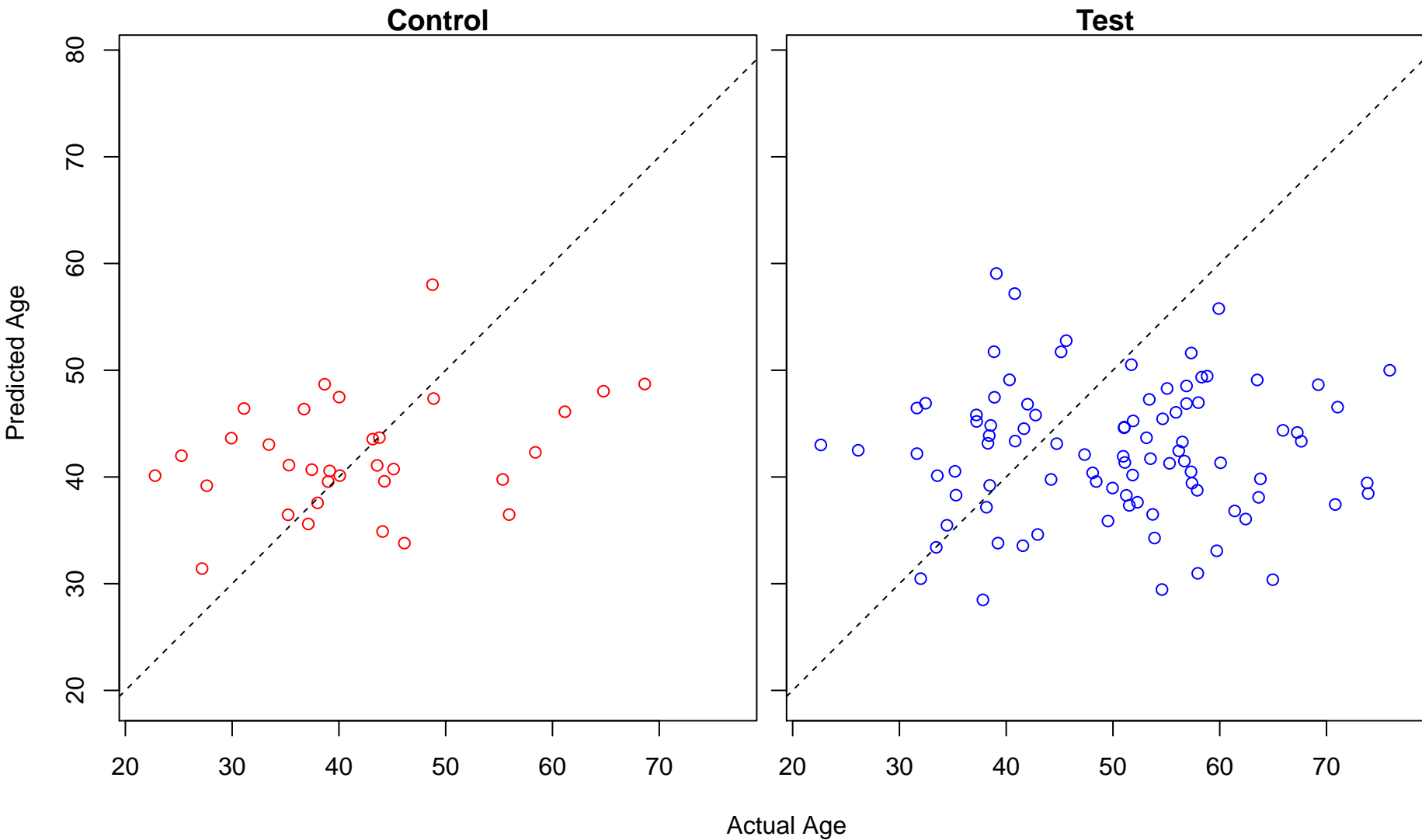
replacement ossification (Score: 0.386265)



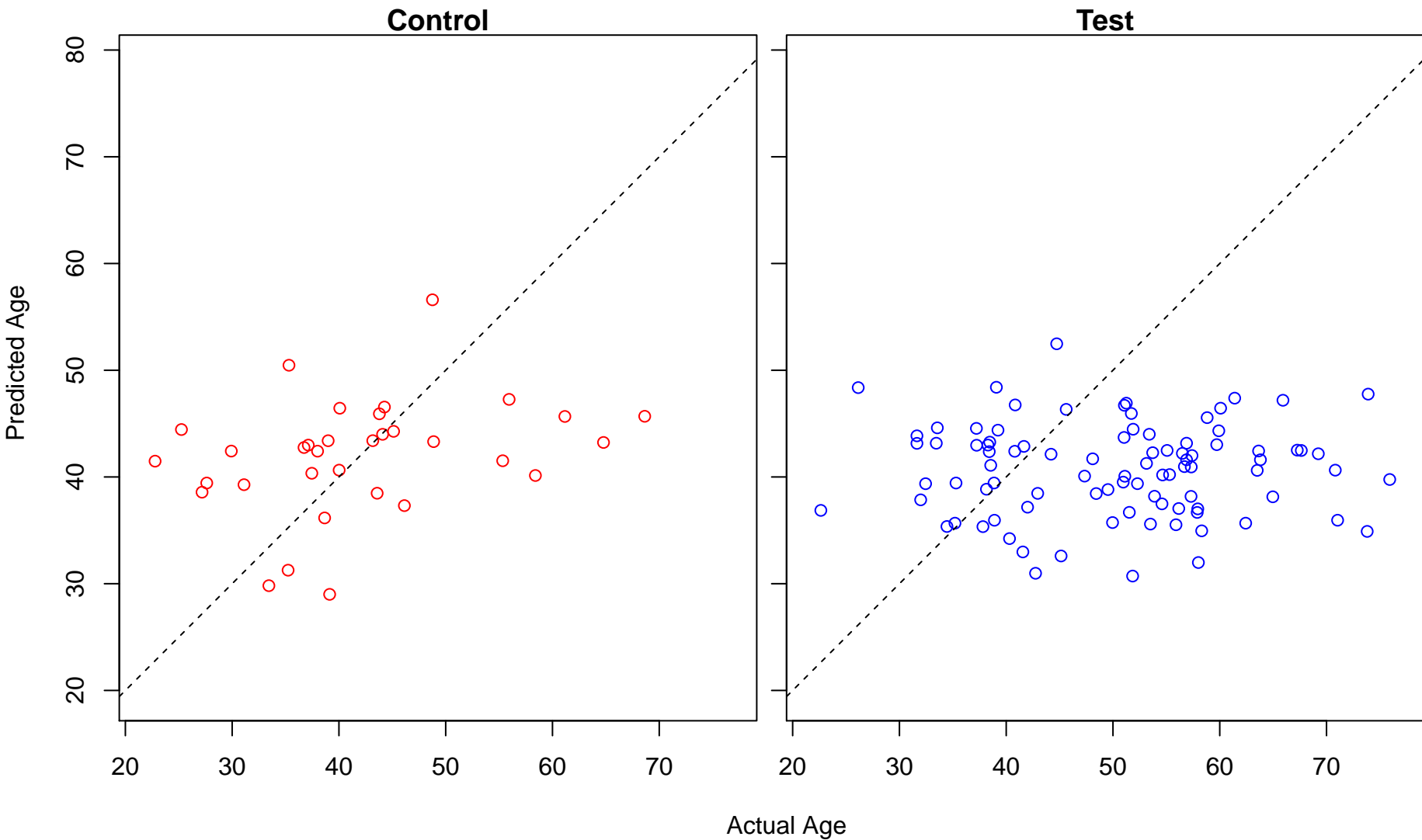
positive regulation of nitric-oxide synthase biosynthetic process (Score: 0.385409)



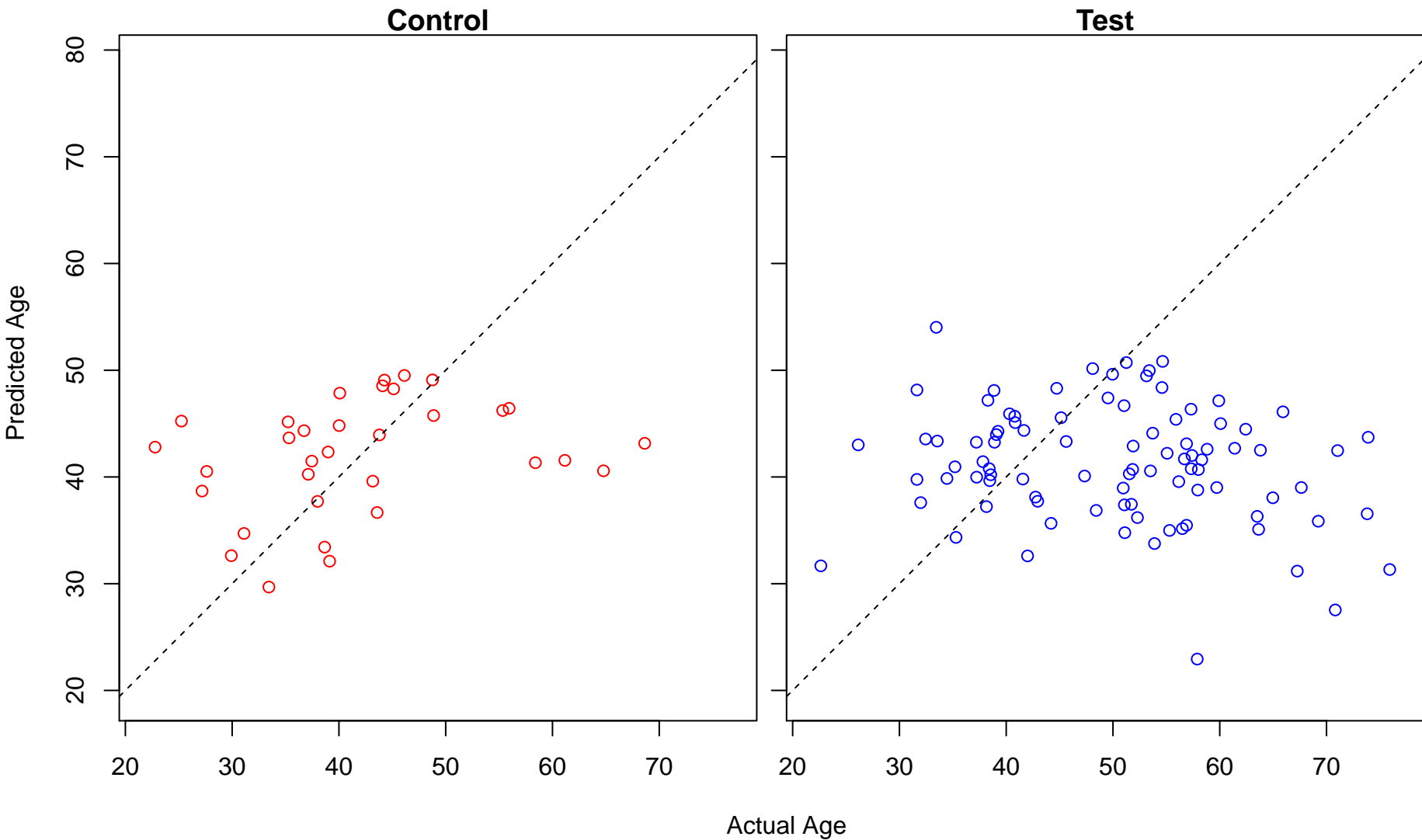
detection of lipopolysaccharide (Score: 0.385282)



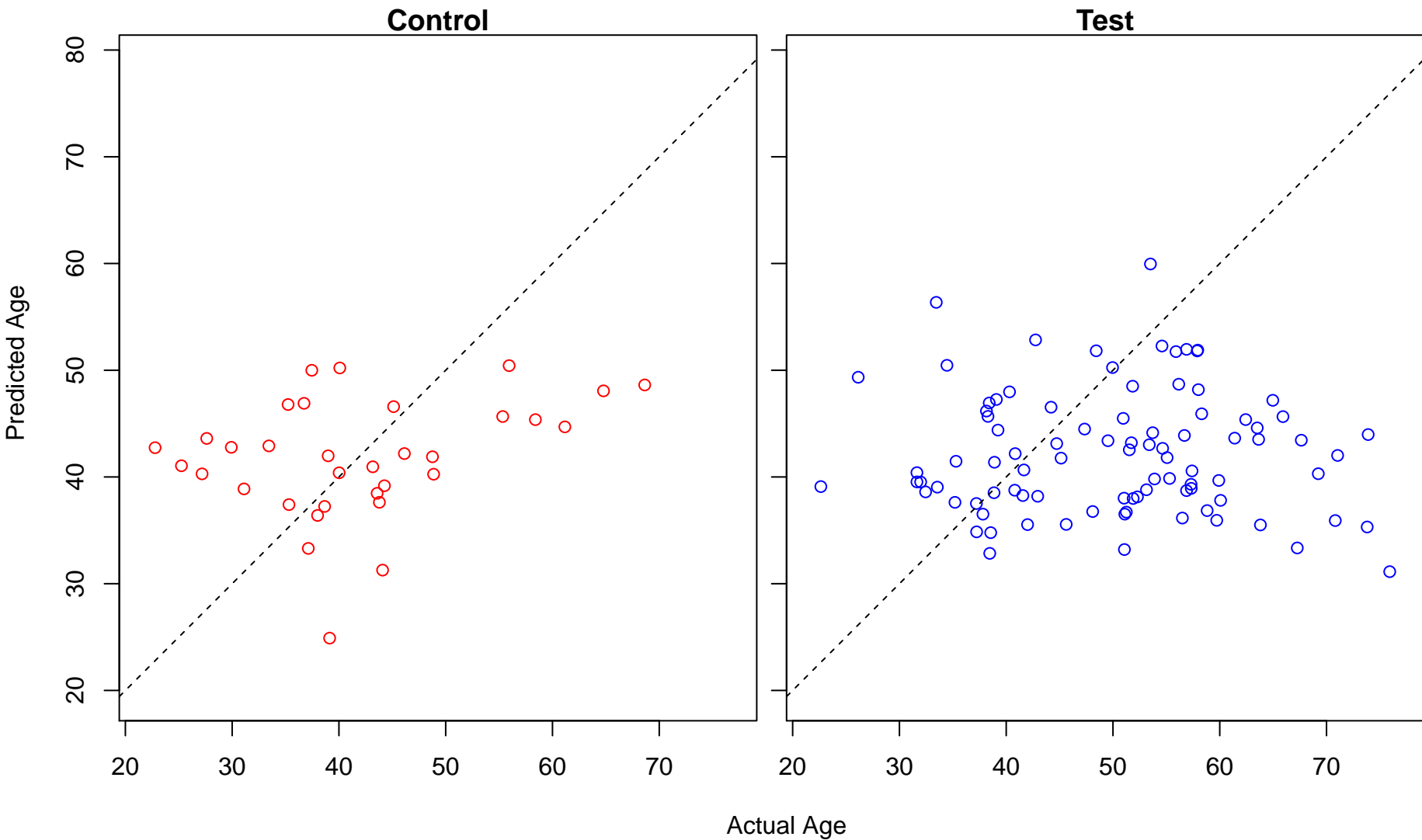
positive regulation of phospholipid biosynthetic process (Score: 0.383390)



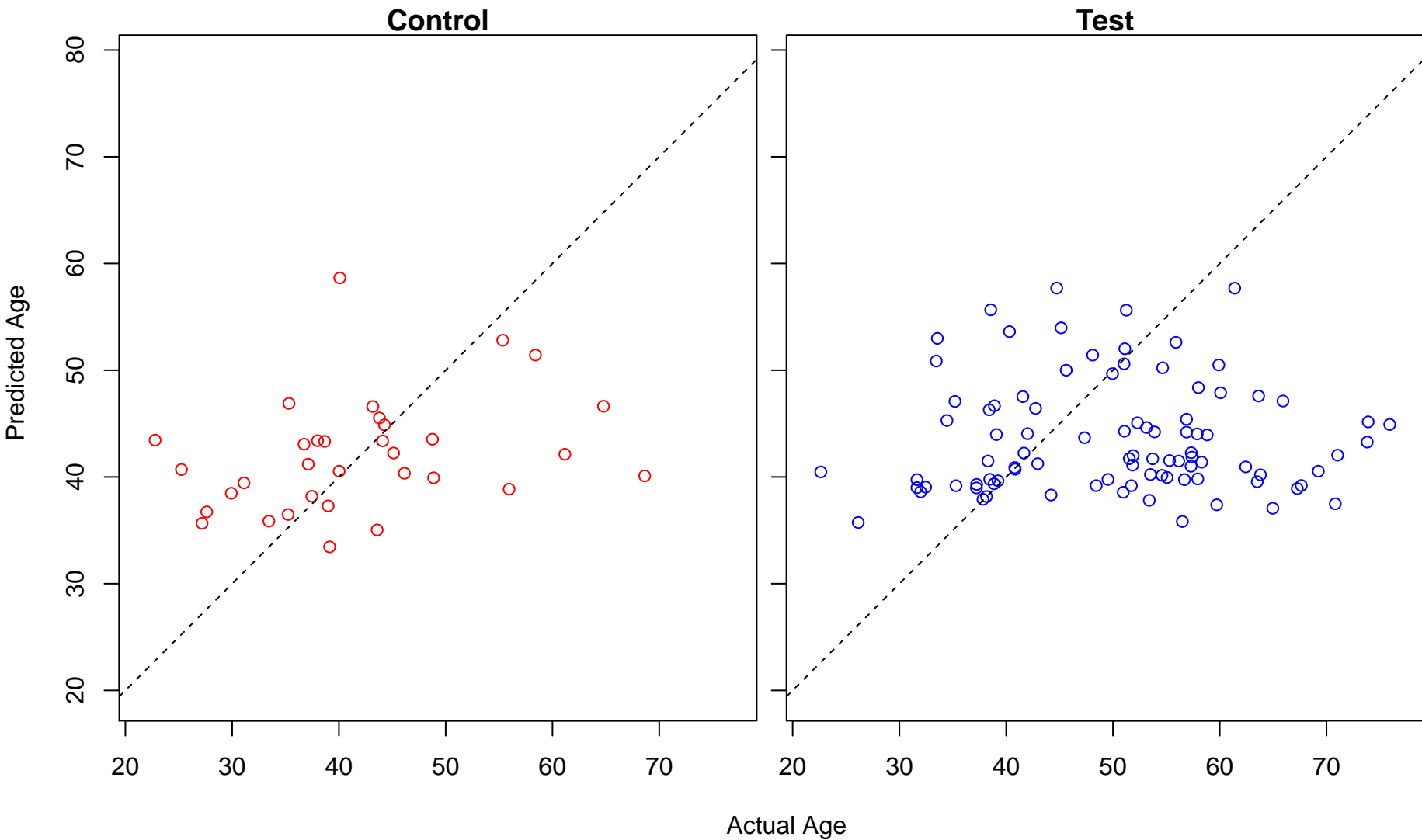
positive regulation of interleukin-6 biosynthetic process (Score: 0.382472)



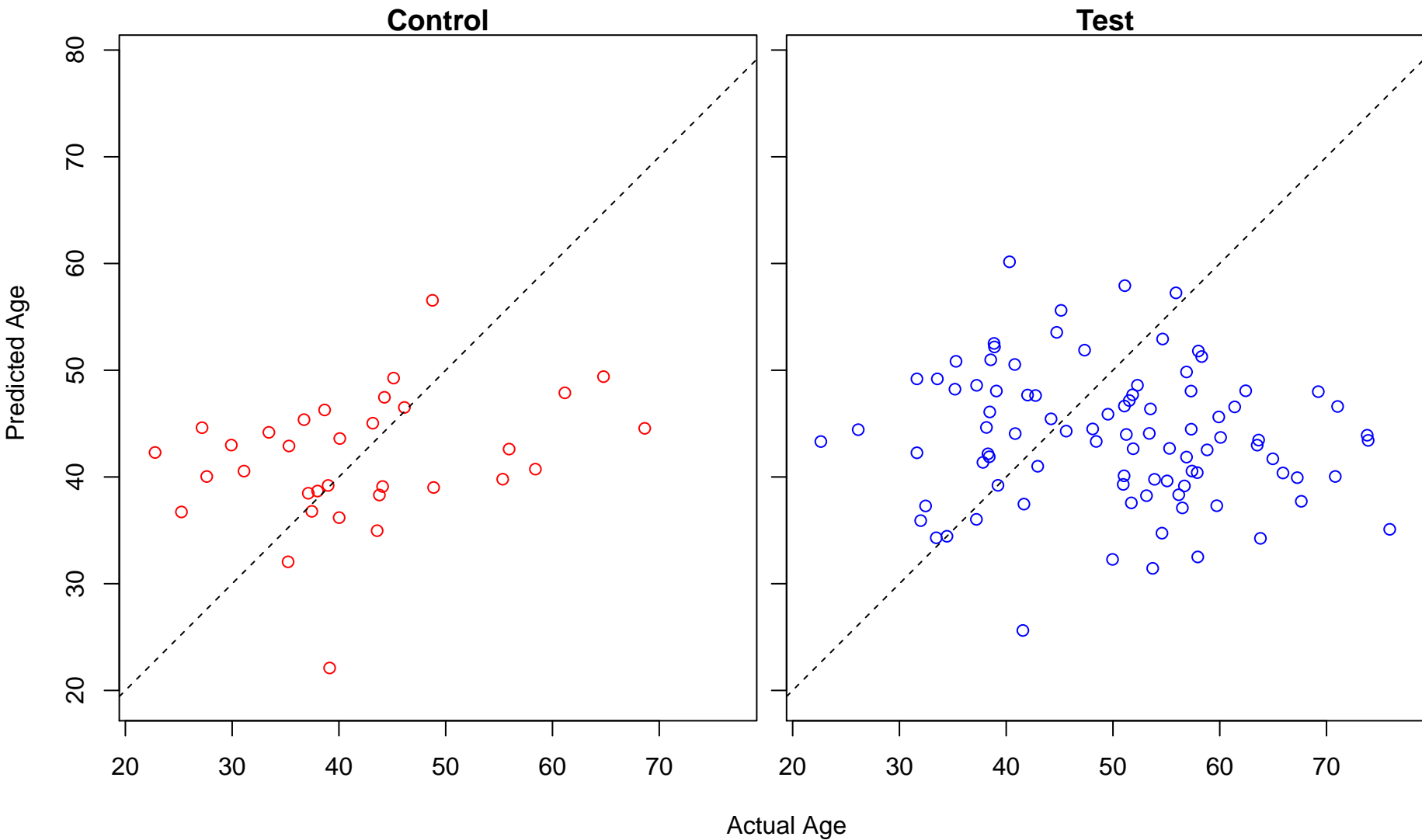
G-protein coupled glutamate receptor signaling pathway (Score: 0.382108)



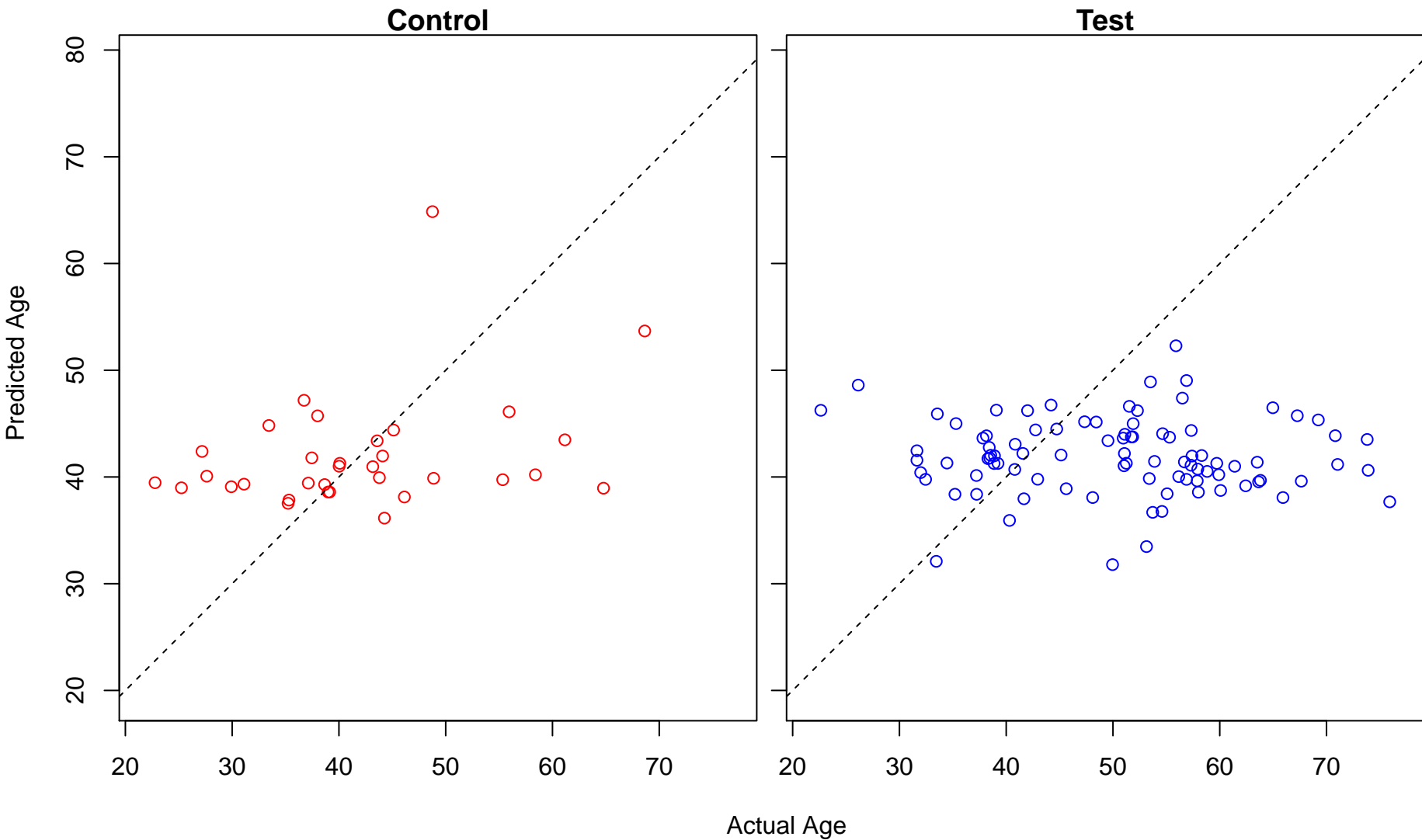
pyrimidine ribonucleotide biosynthetic process (Score: 0.381119)



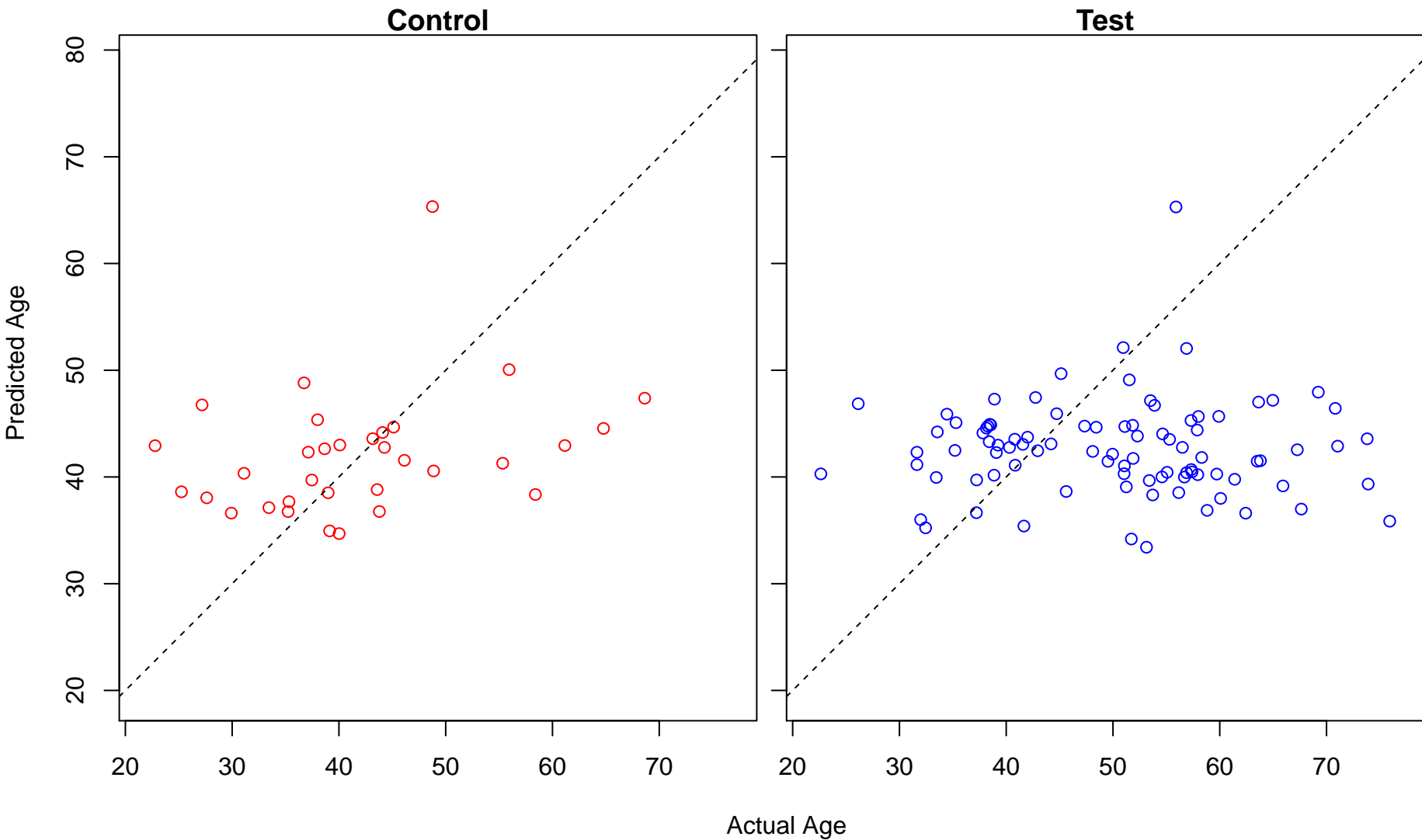
viral release from host cell (Score: 0.378768)



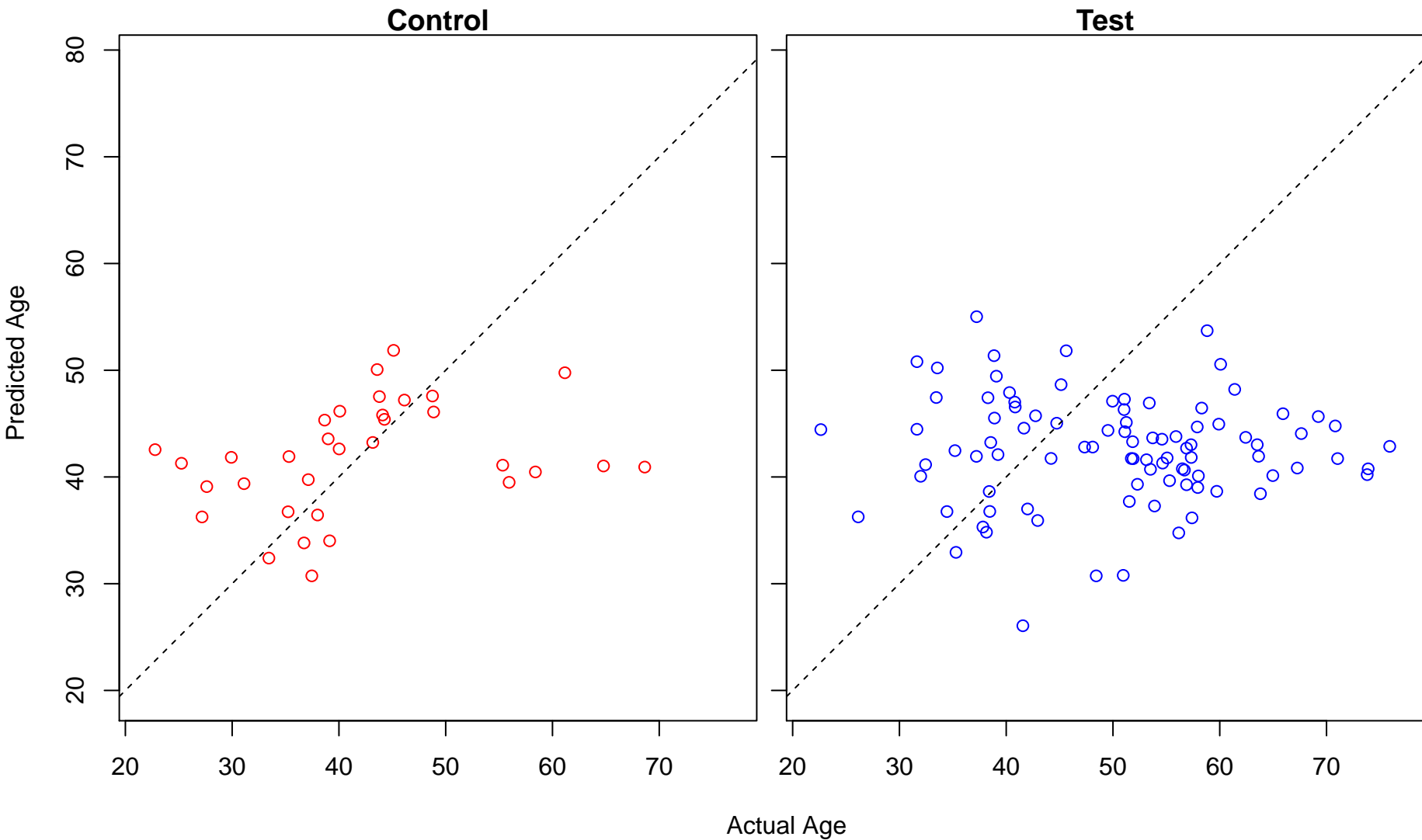
positive regulation of thymocyte apoptotic process (Score: 0.378605)



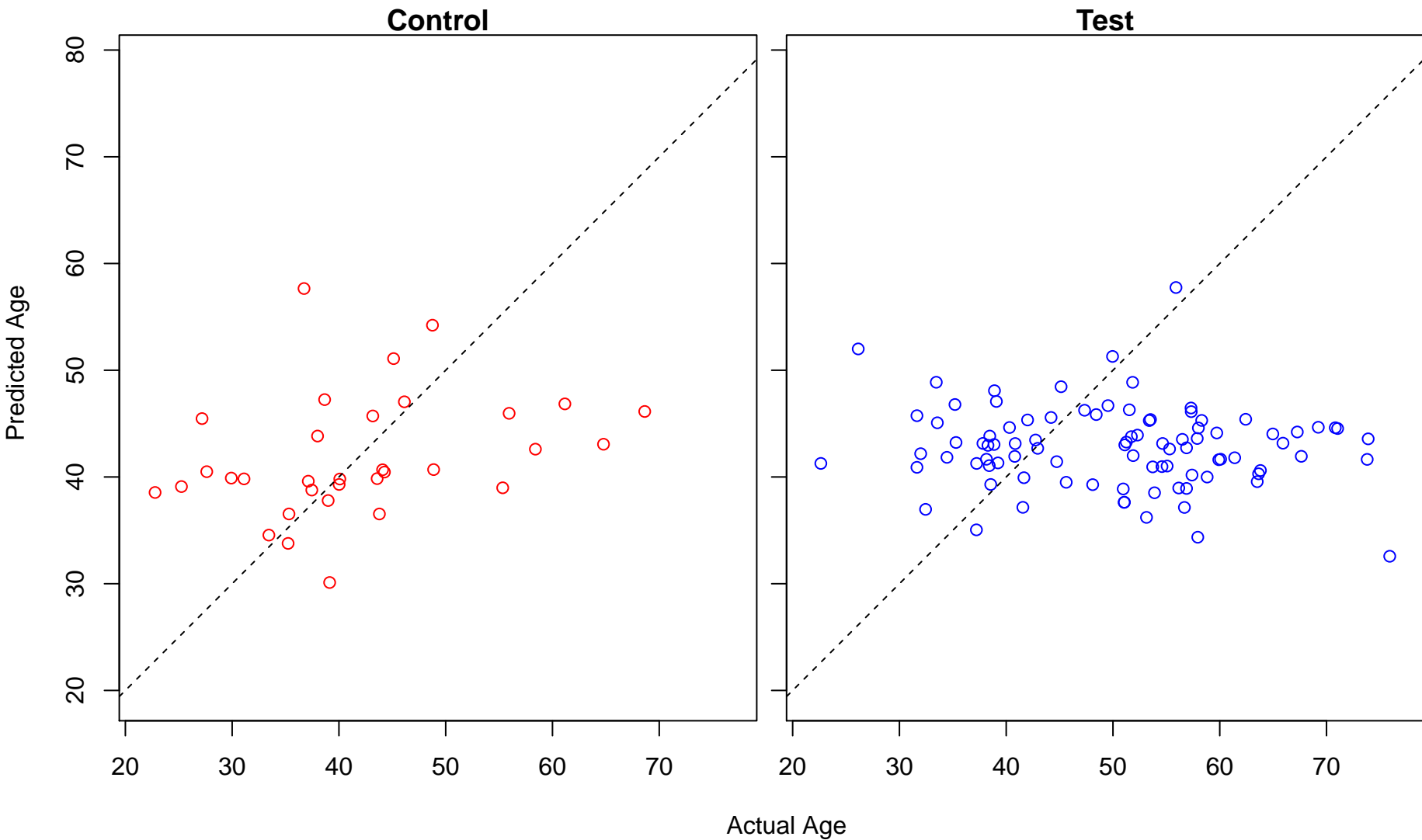
medium-chain fatty acid metabolic process (Score: 0.378440)



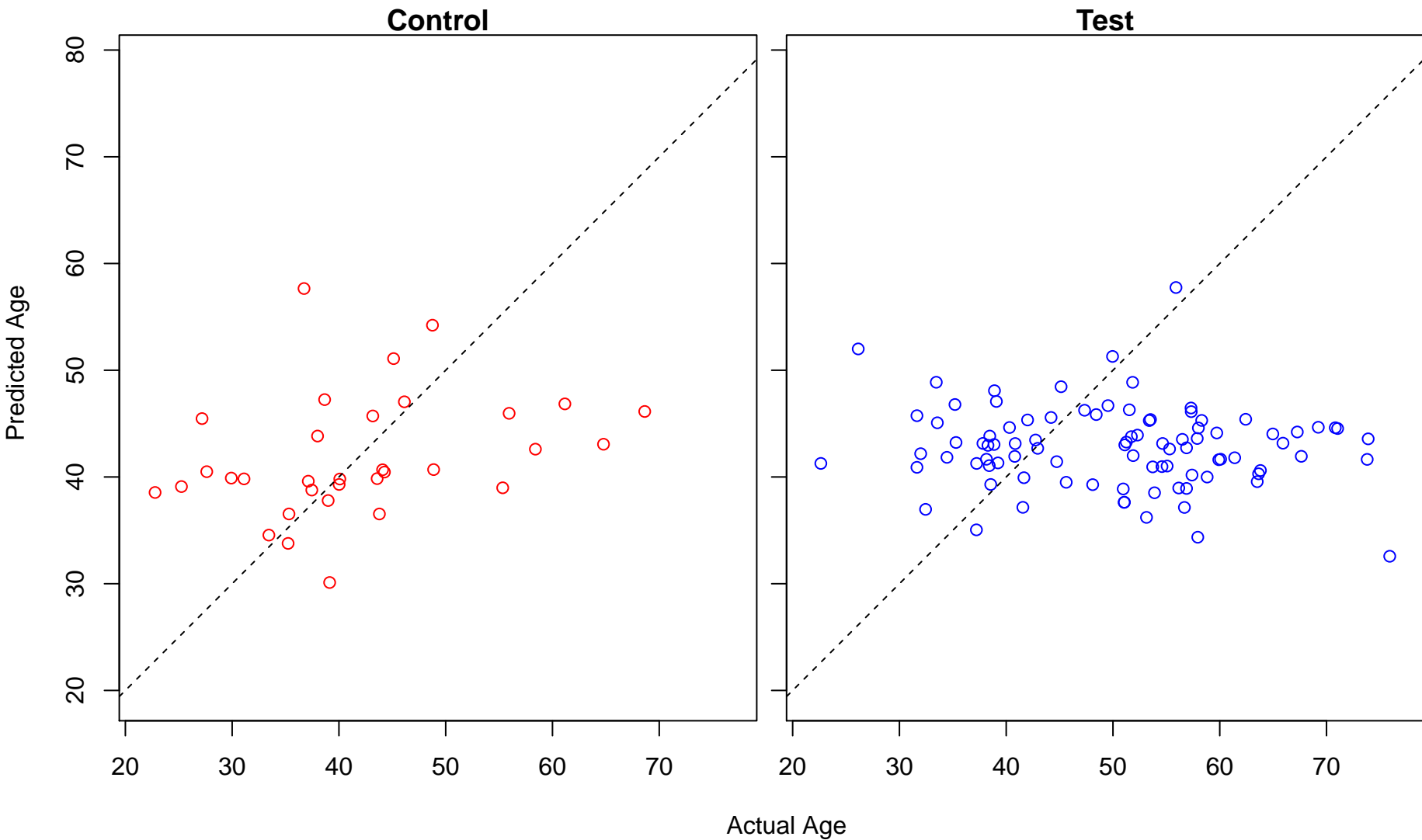
positive regulation of developmental pigmentation (Score: 0.377773)



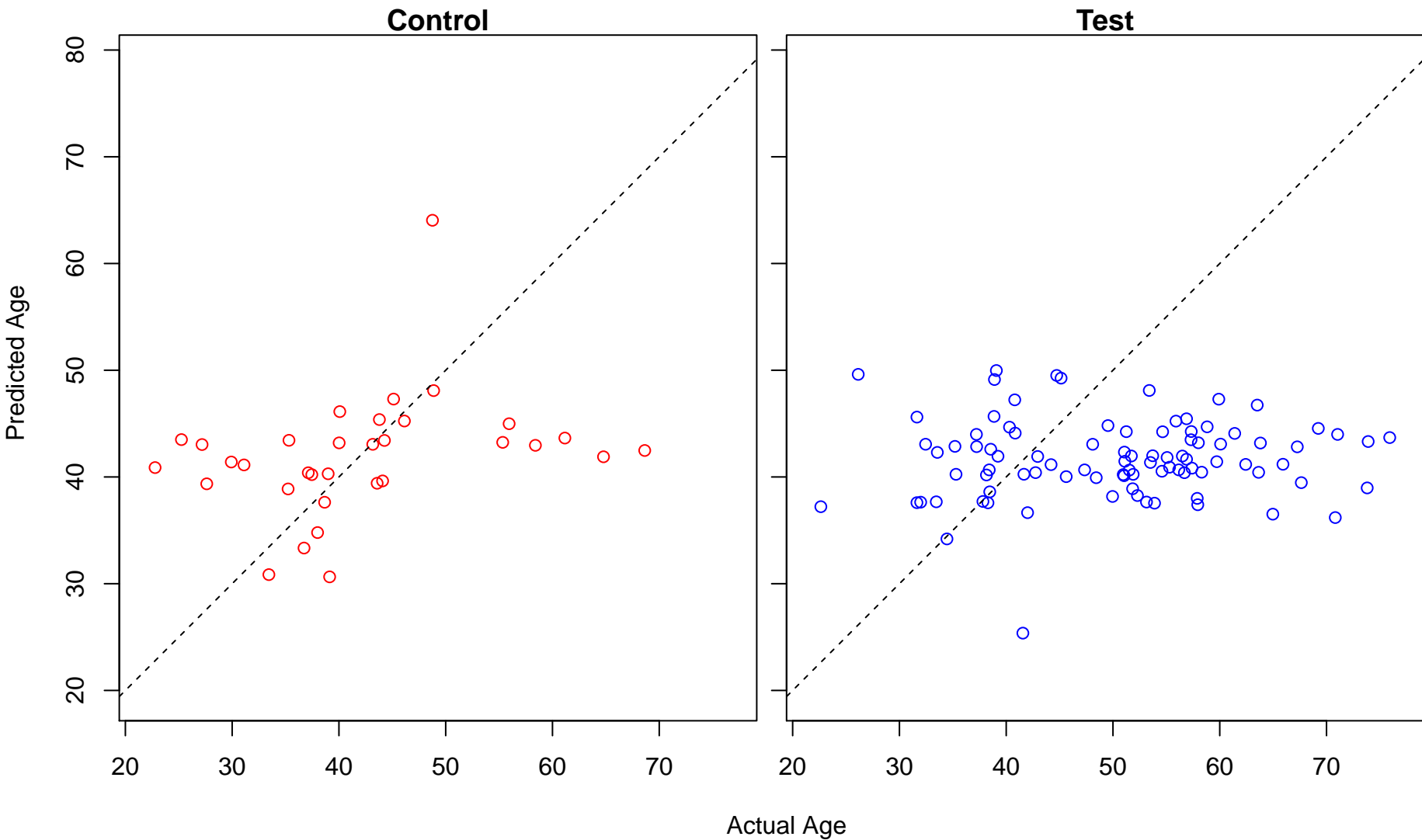
nuclear RNA surveillance (Score: 0.377212)



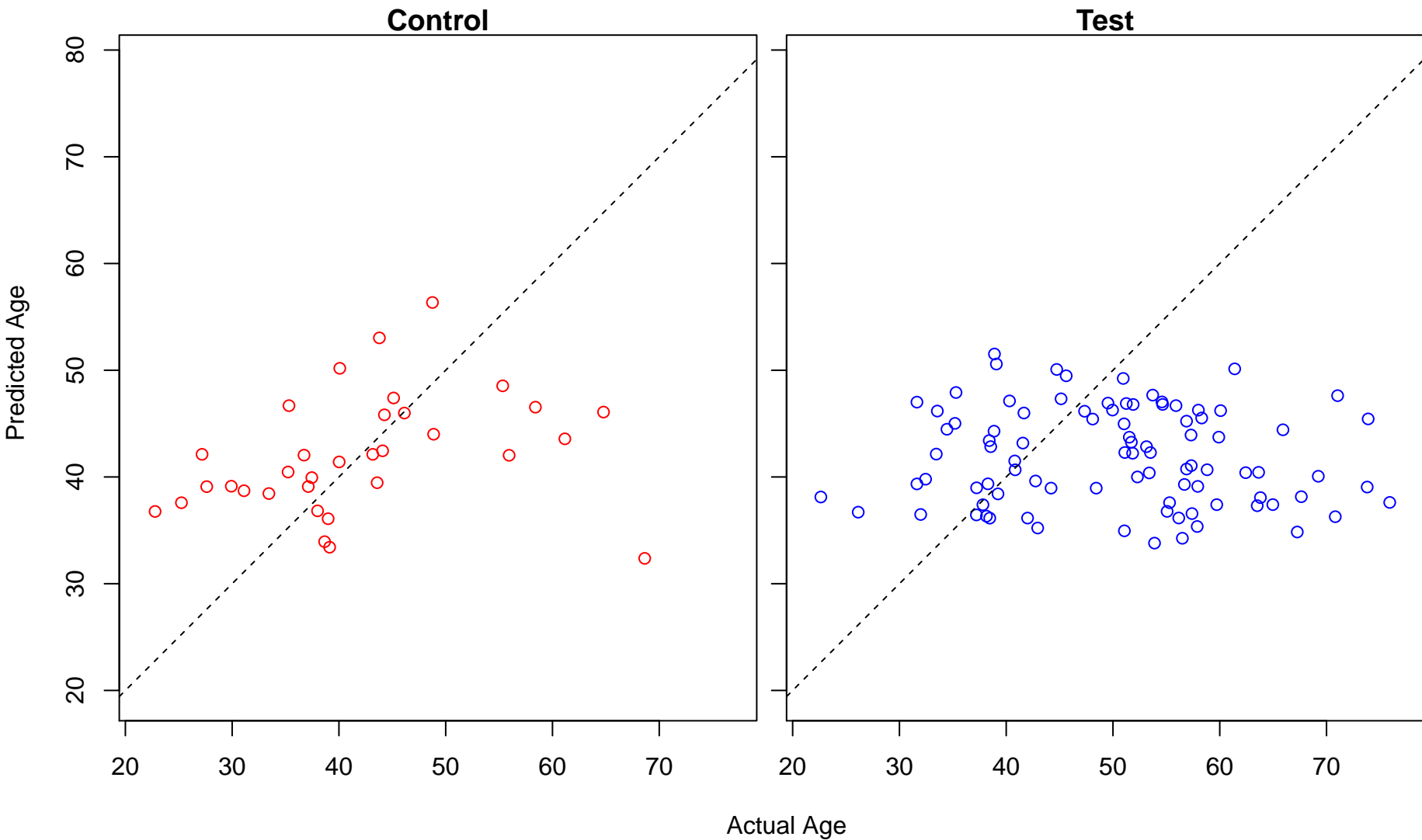
nuclear mRNA surveillance (Score: 0.377212)



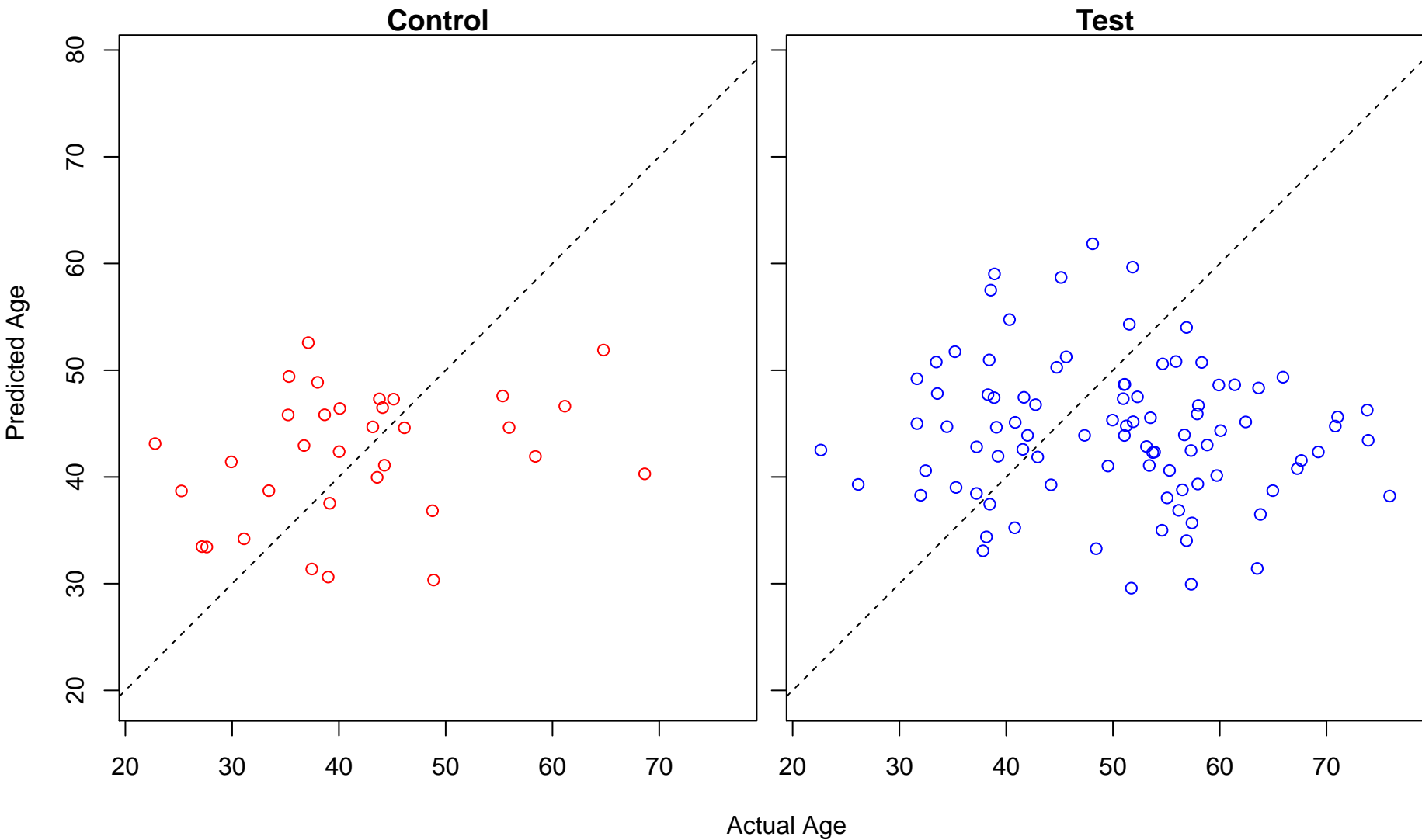
regulation of ligand-dependent nuclear receptor transcription coactivator activity (Score: 0.375396)



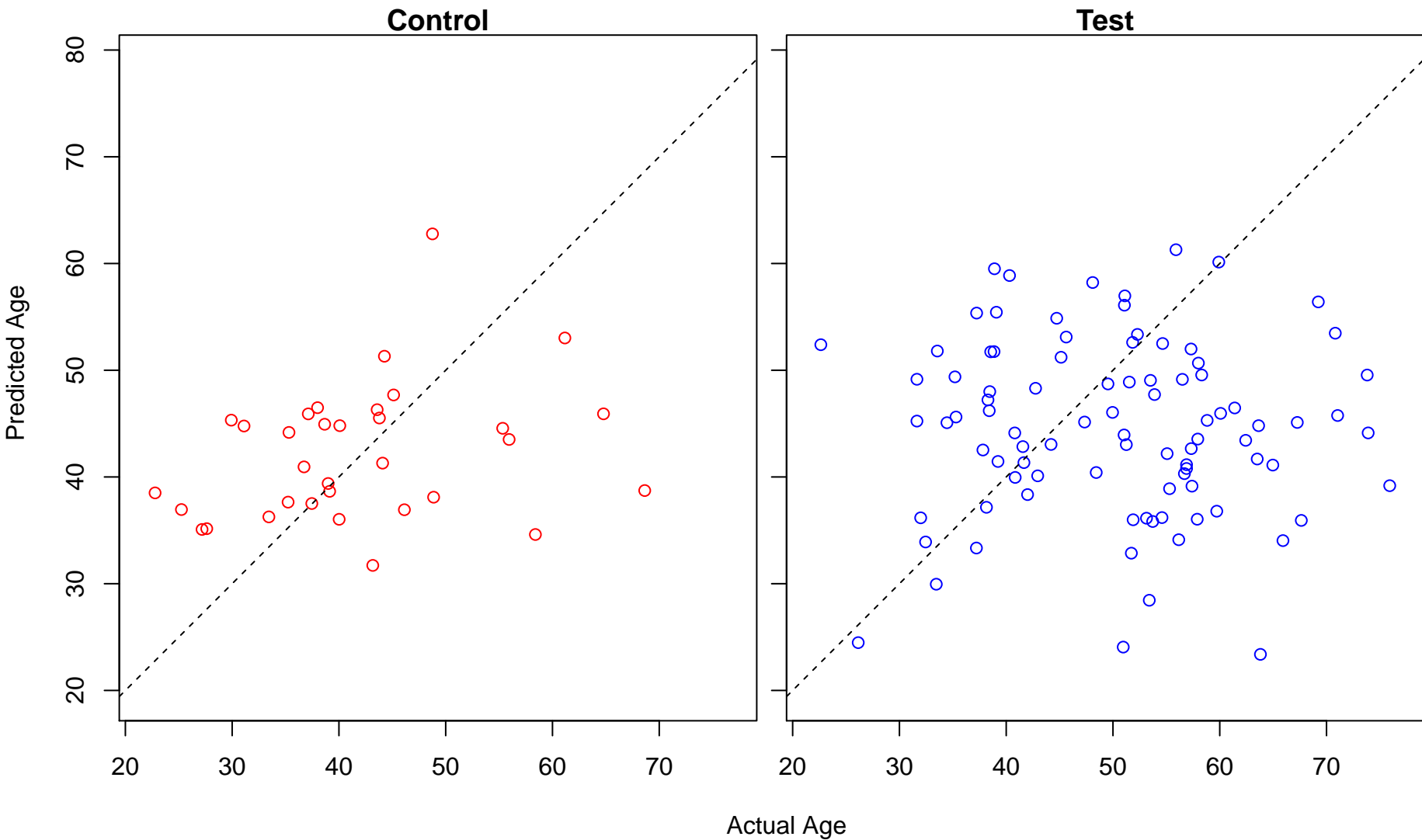
positive regulation of protein glycosylation (Score: 0.375362)



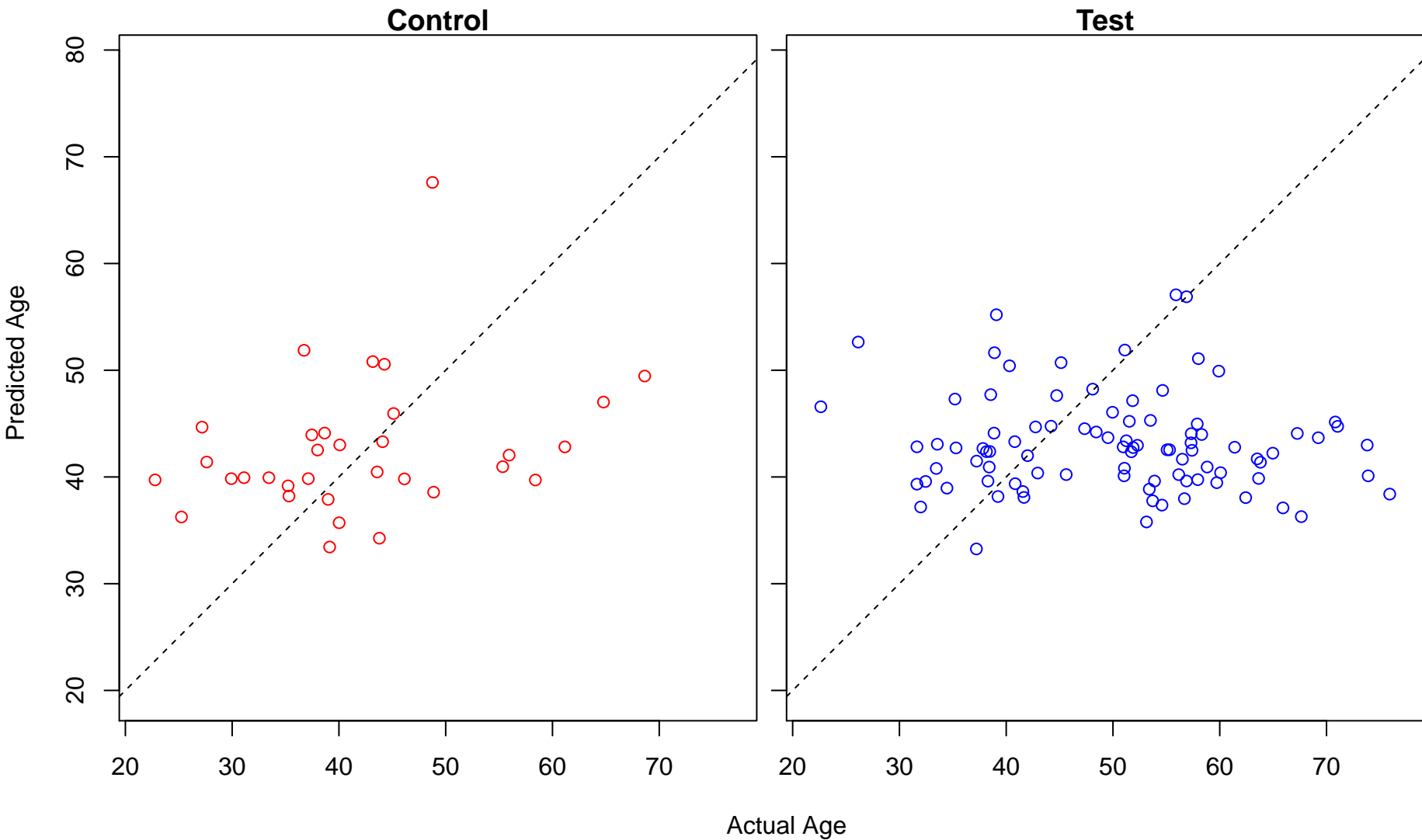
distal tubule development (Score: 0.374922)



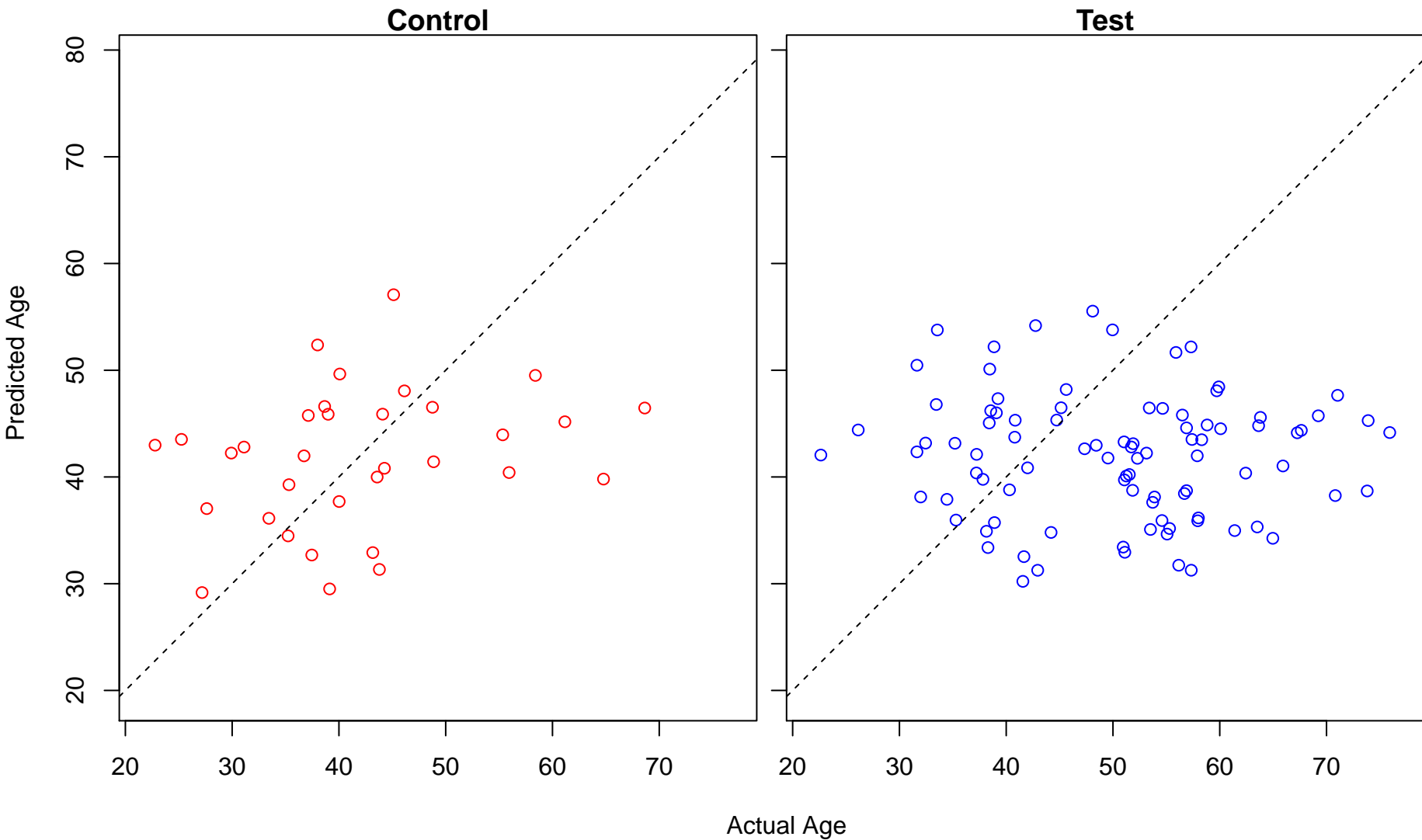
caveolin-mediated endocytosis (Score: 0.373718)



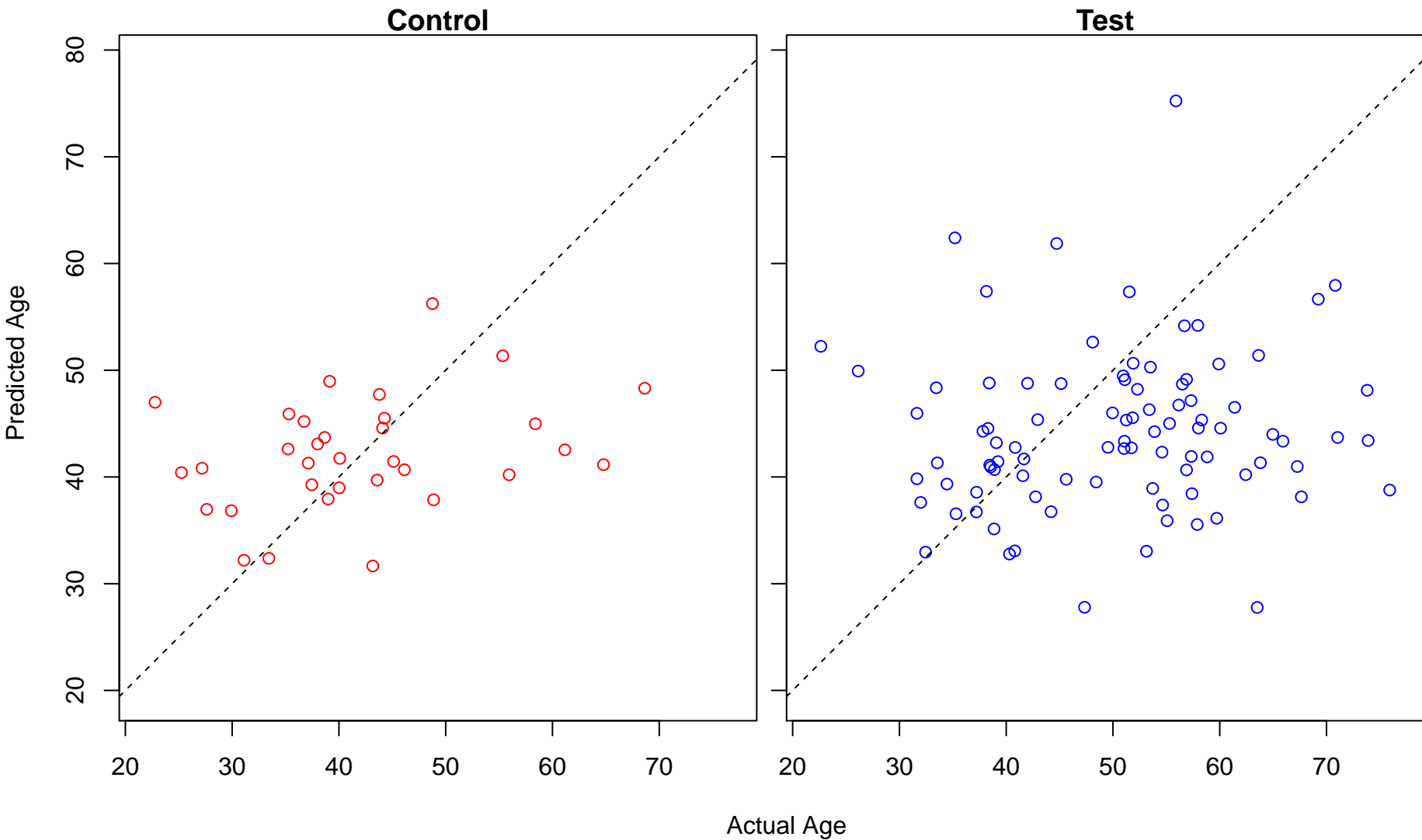
maintenance of protein localization in endoplasmic reticulum (Score: 0.373370)



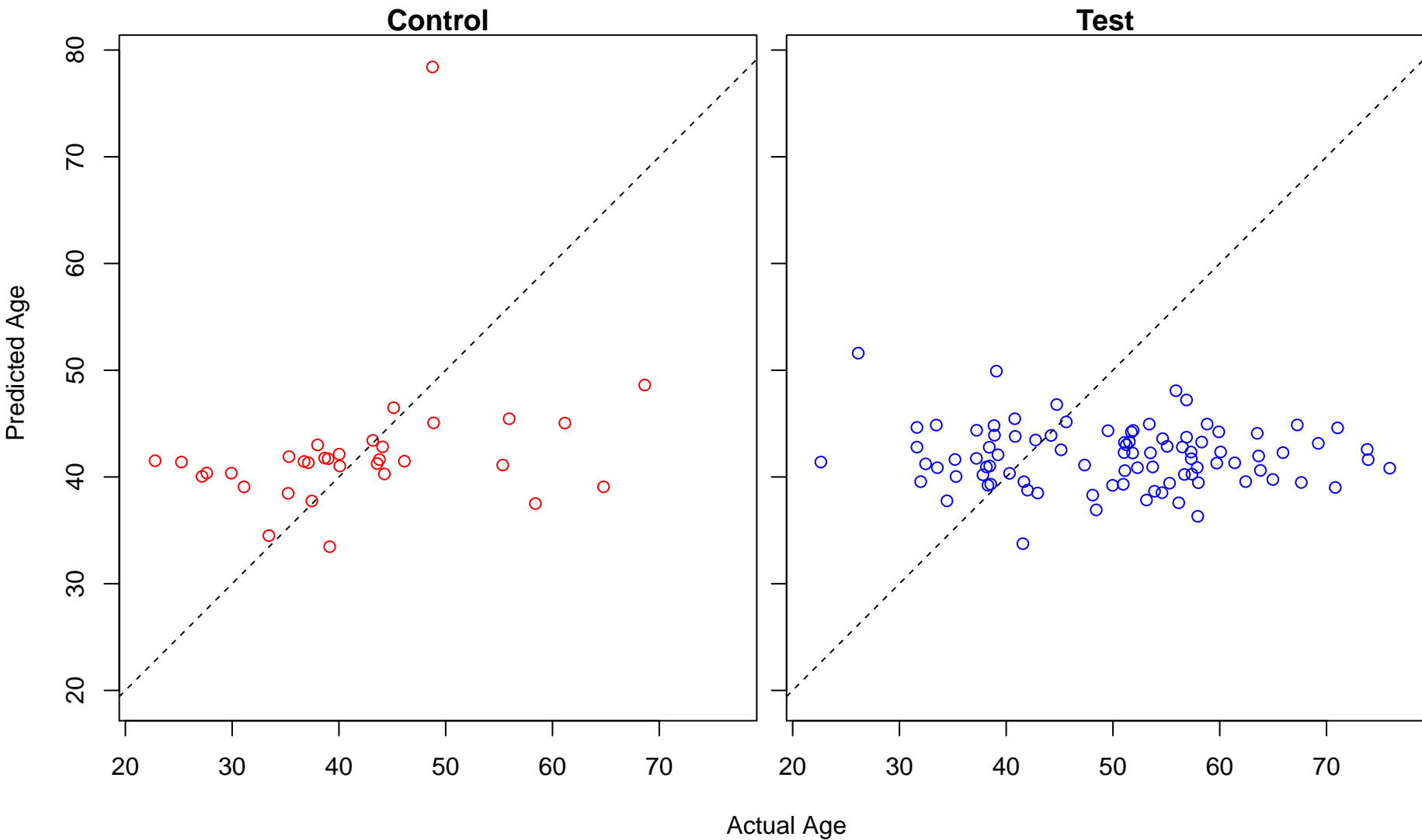
nitric oxide mediated signal transduction (Score: 0.37349)



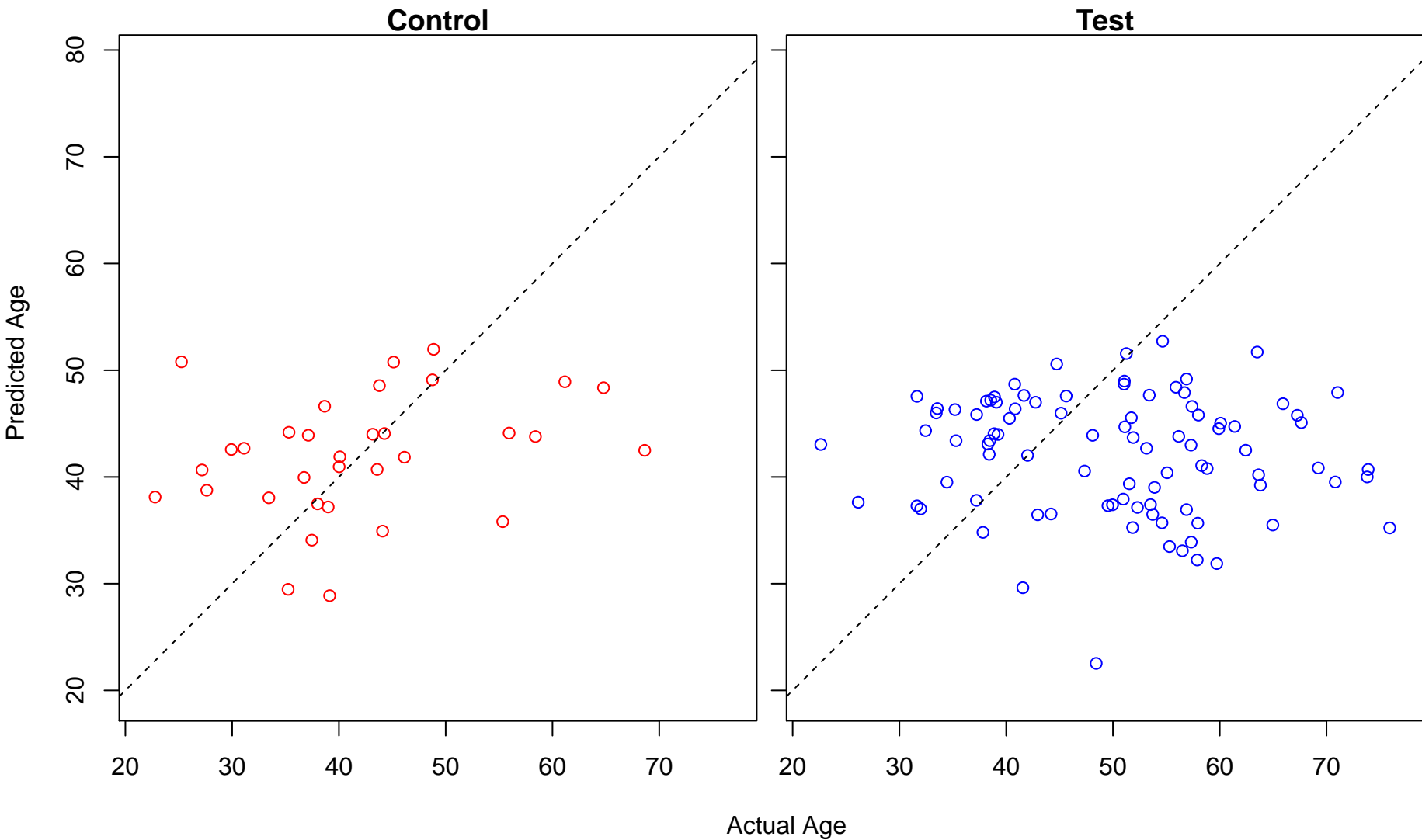
cell migration in hindbrain (Score: 0.373016)



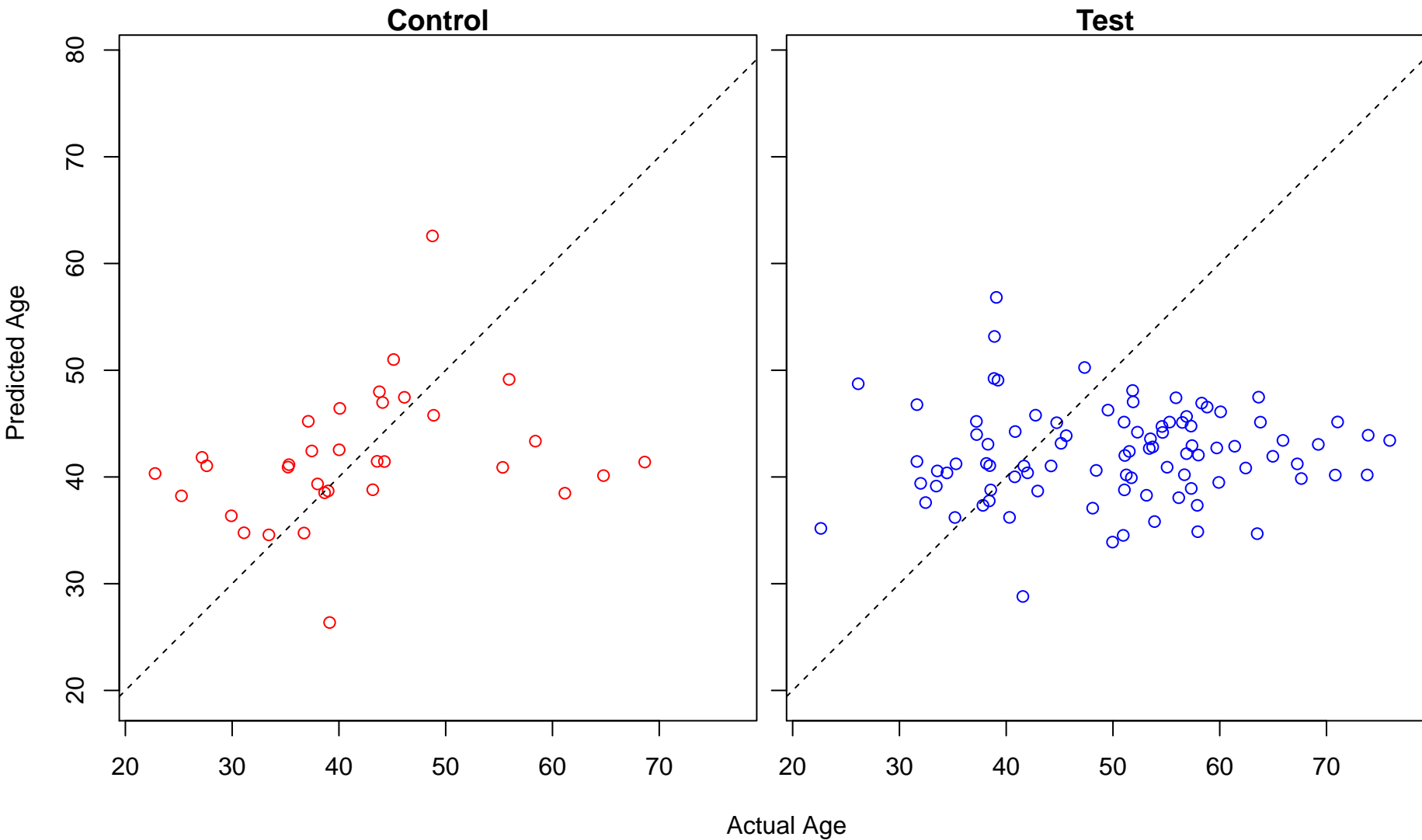
corpus callosum morphogenesis (Score: 0.372118)



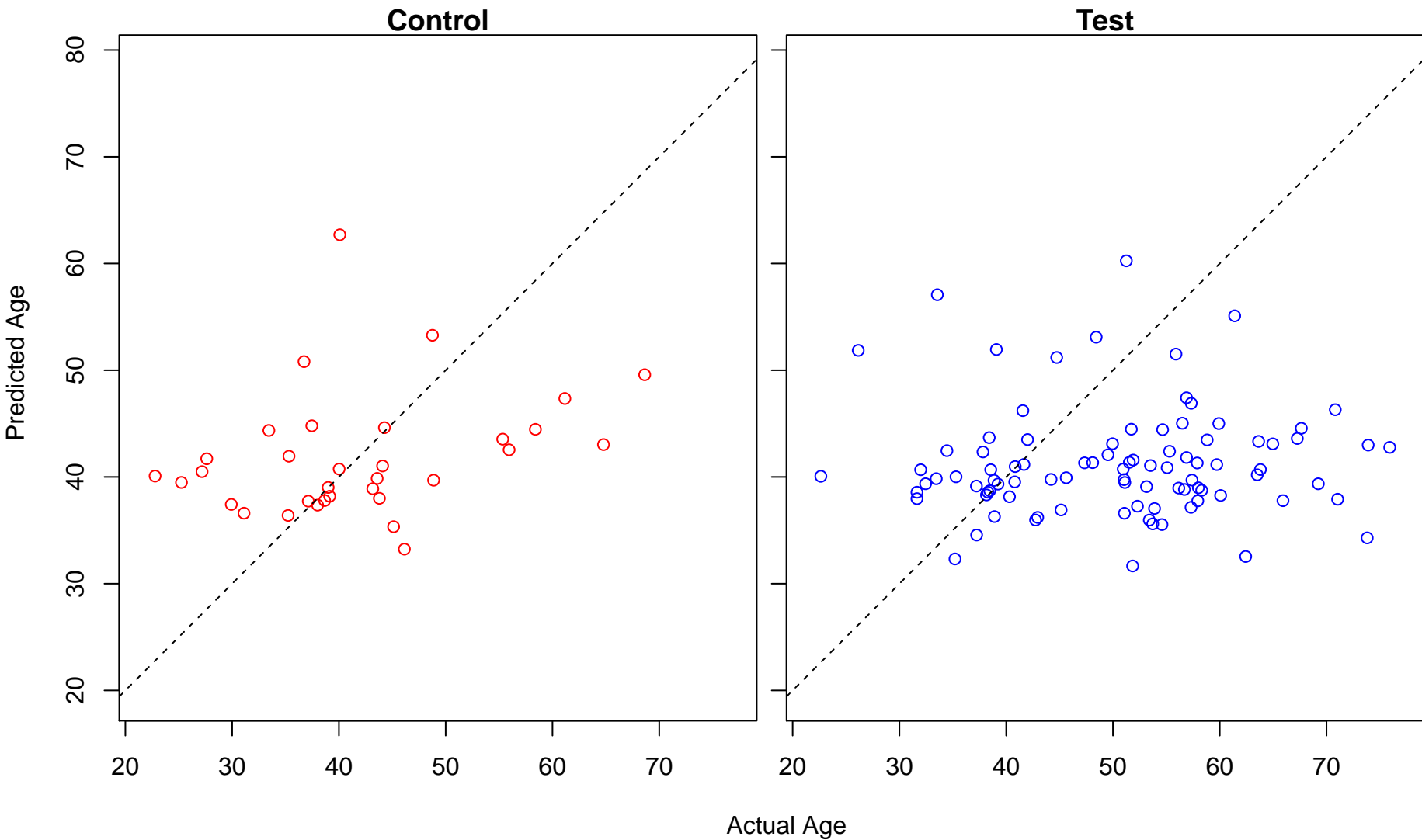
regulation of T cell tolerance induction (Score: 0.372003)



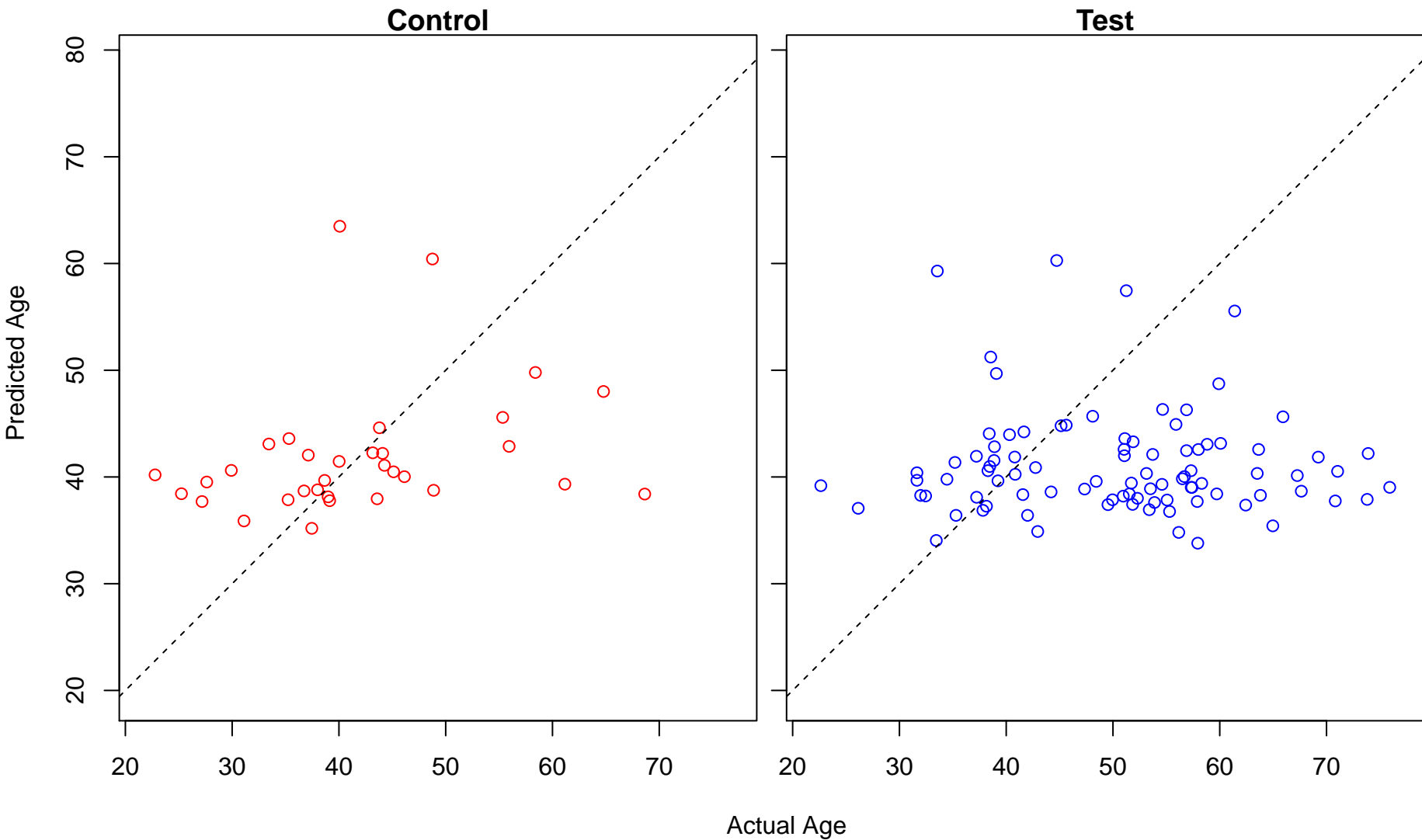
monocyte aggregation (Score: 0.371535)



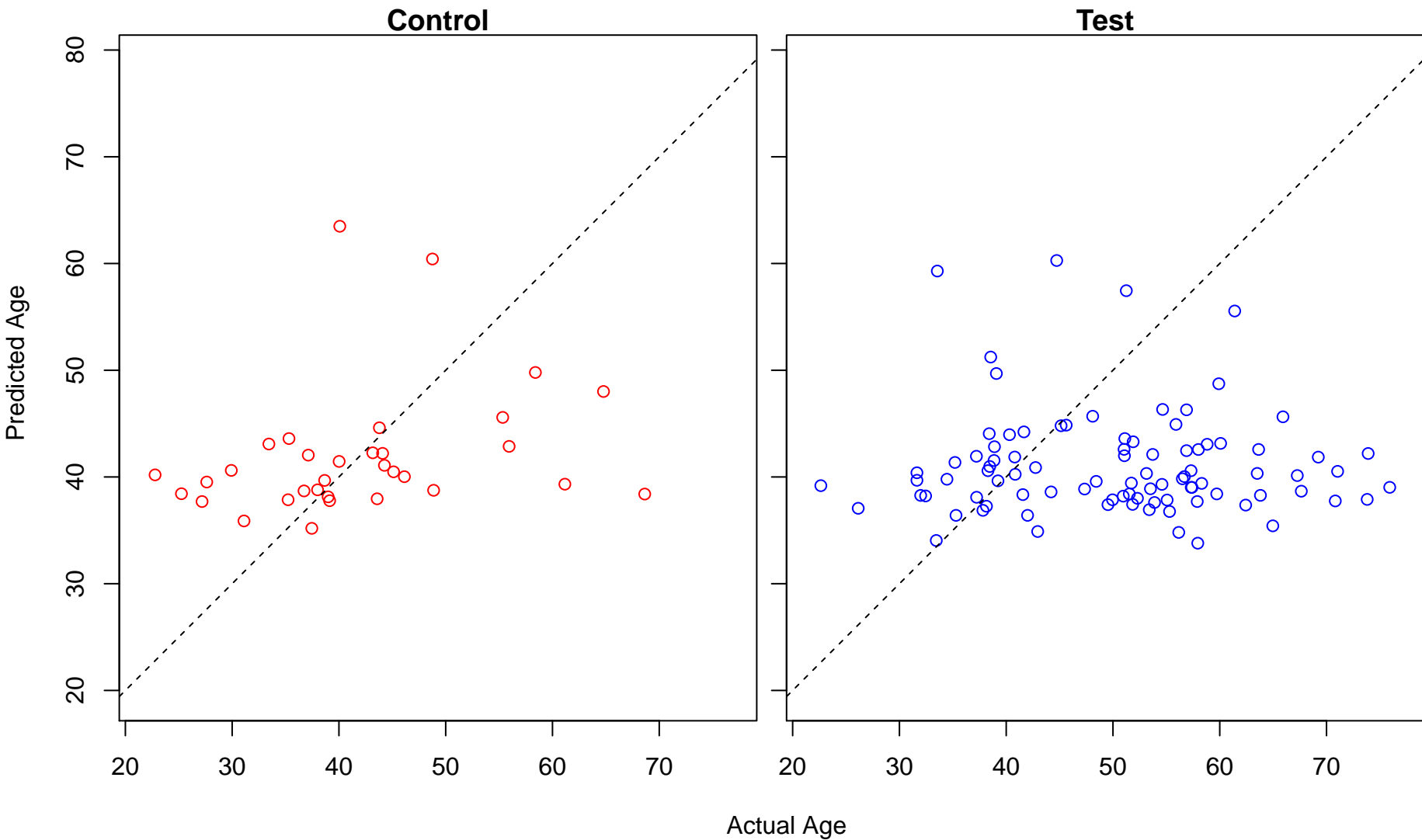
regulation of histone H3-K36 methylation (Score: 0.371091)



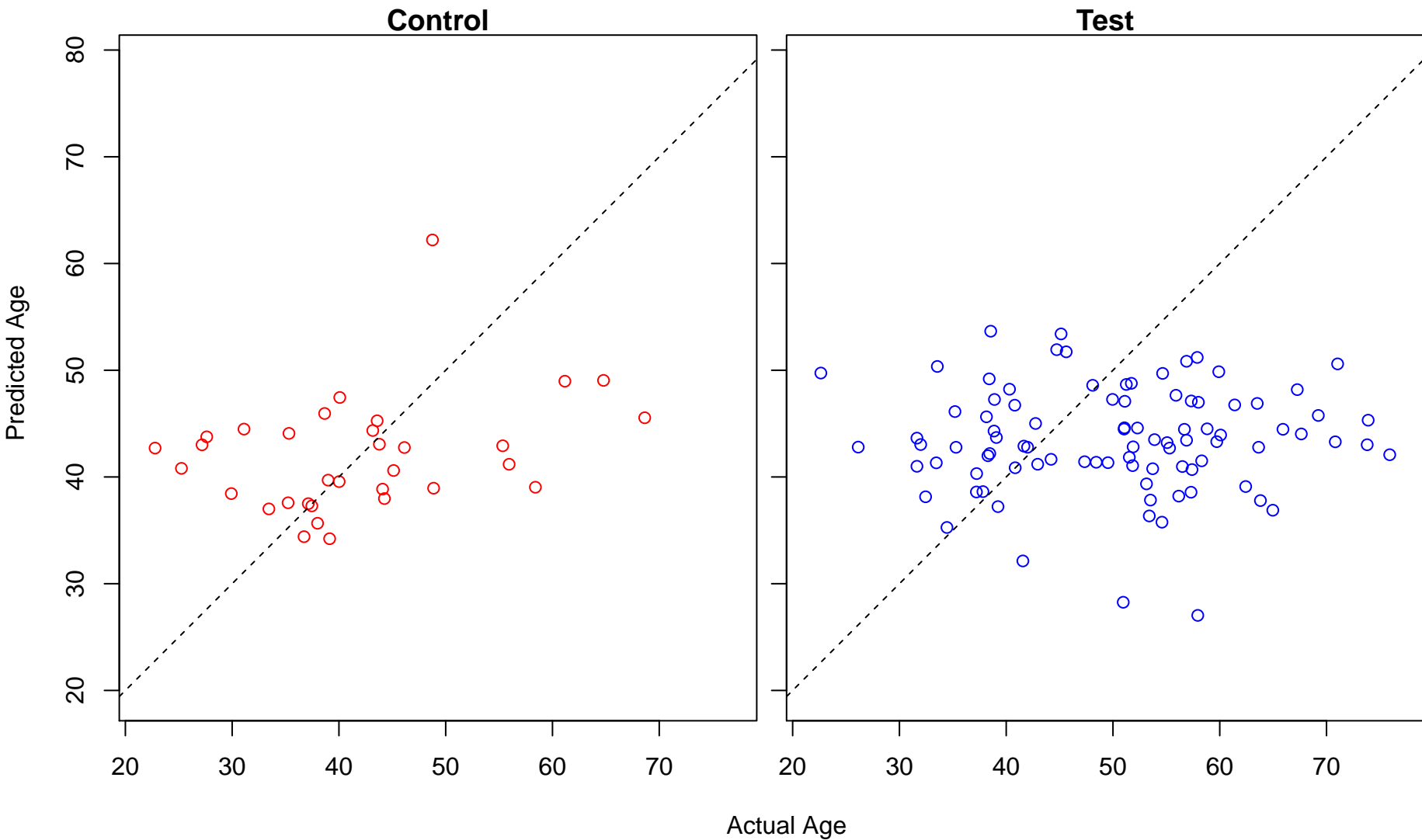
iron-sulfur cluster assembly (Score: 0.370402)



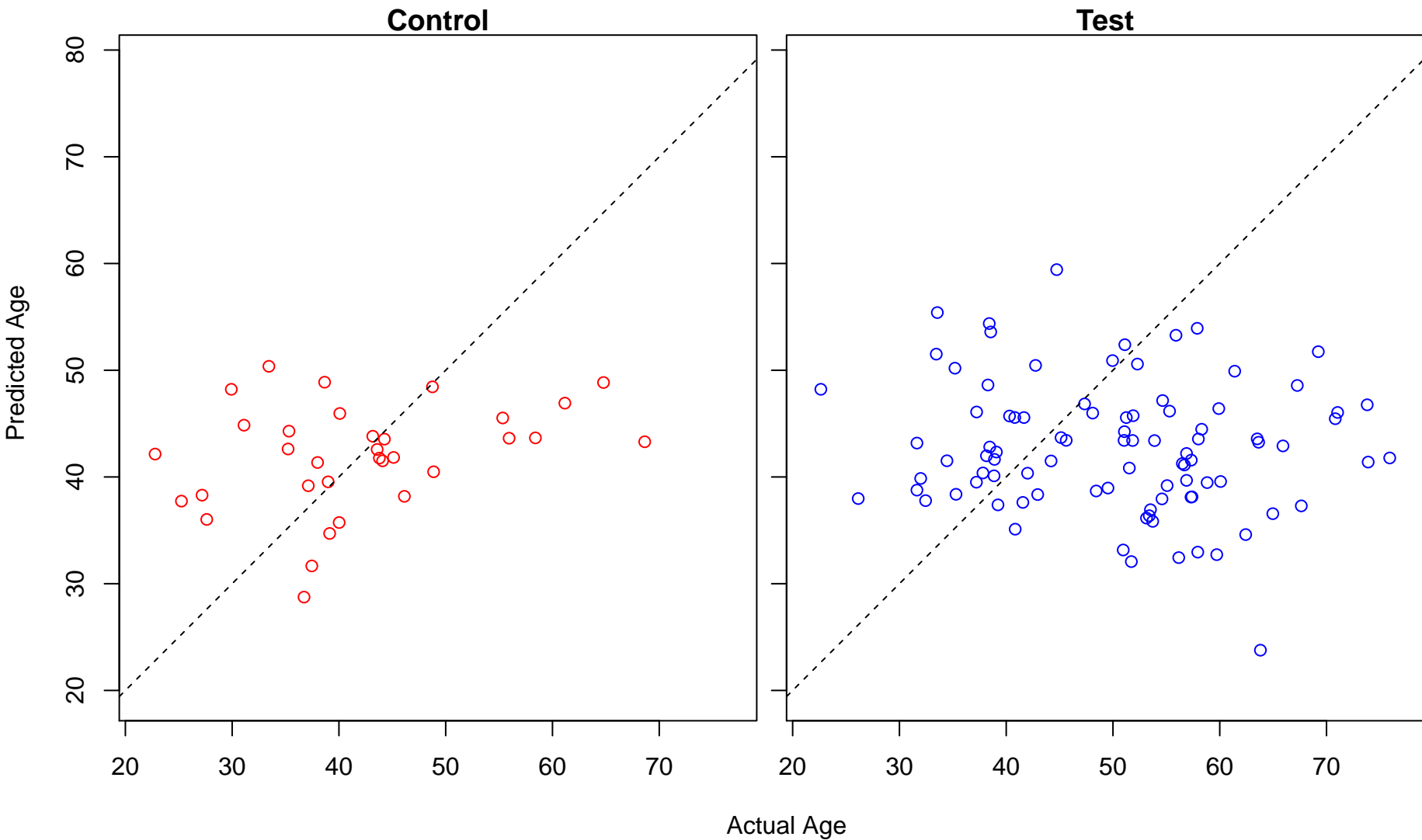
metallo-sulfur cluster assembly (Score: 0.370402)



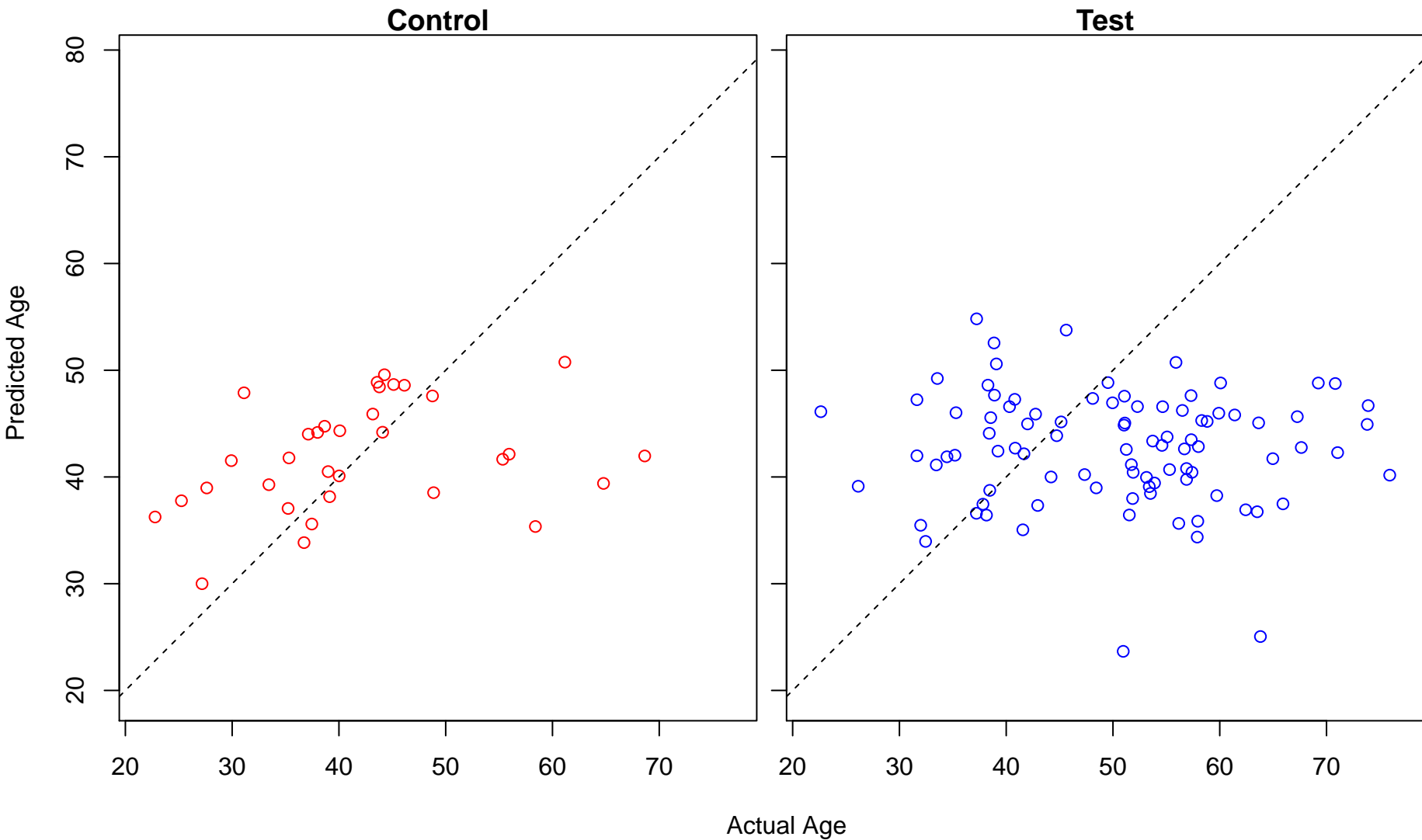
norepinephrine metabolic process (Score: 0.369811)



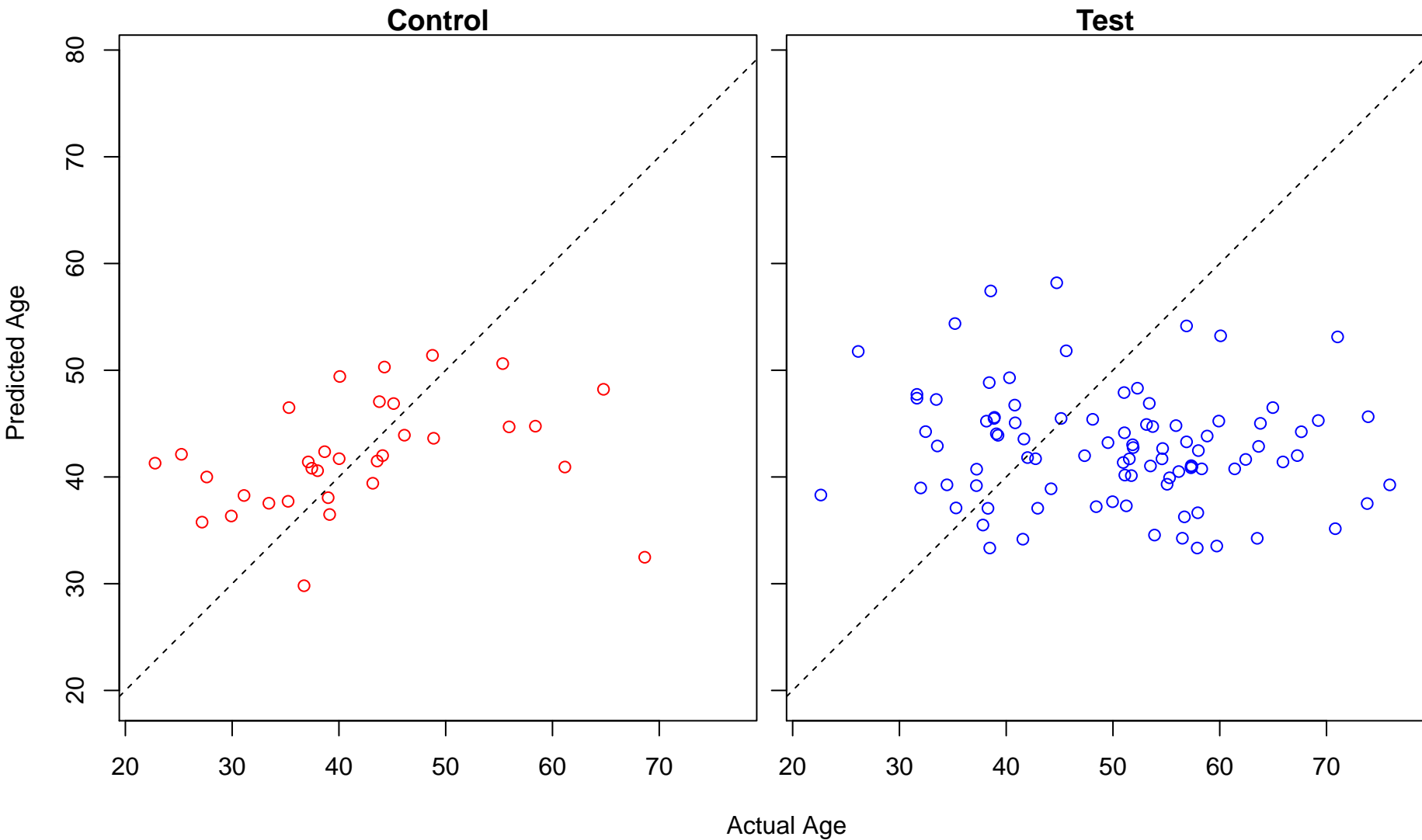
rhythmic synaptic transmission (Score: 0.369106)



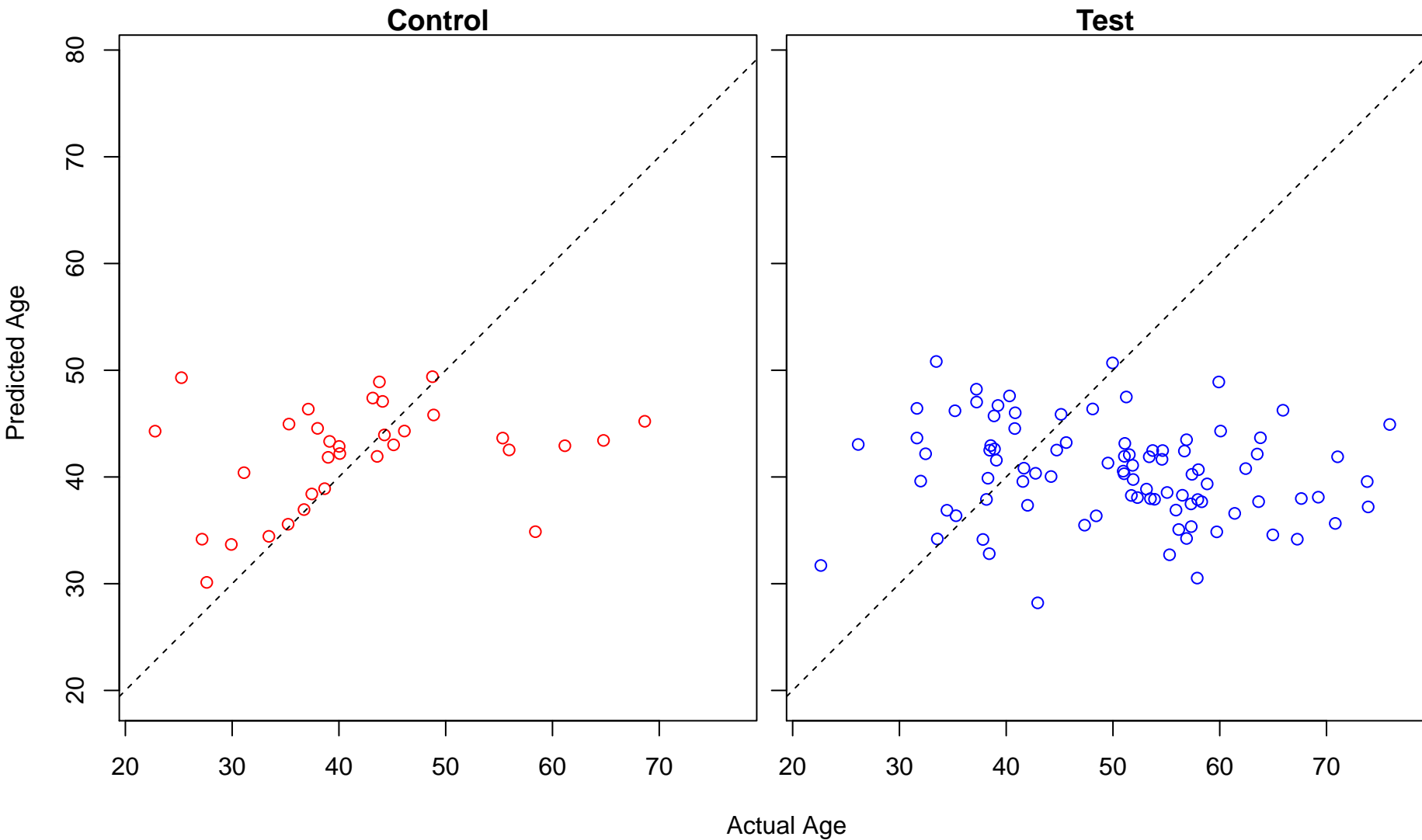
regulation of cell communication by electrical coupling (Score: 0.368243)



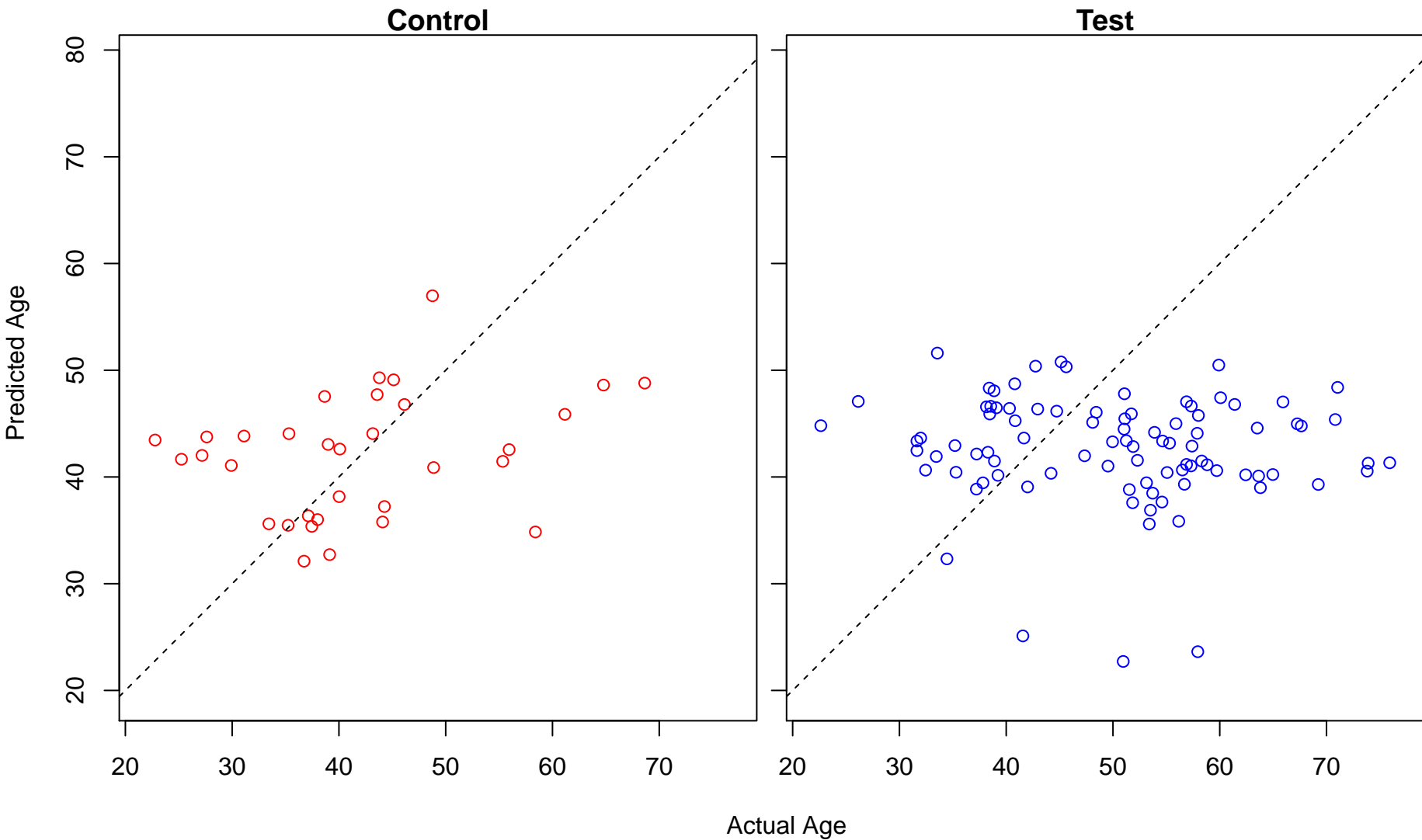
somitogenesis (Score: 0.367743)



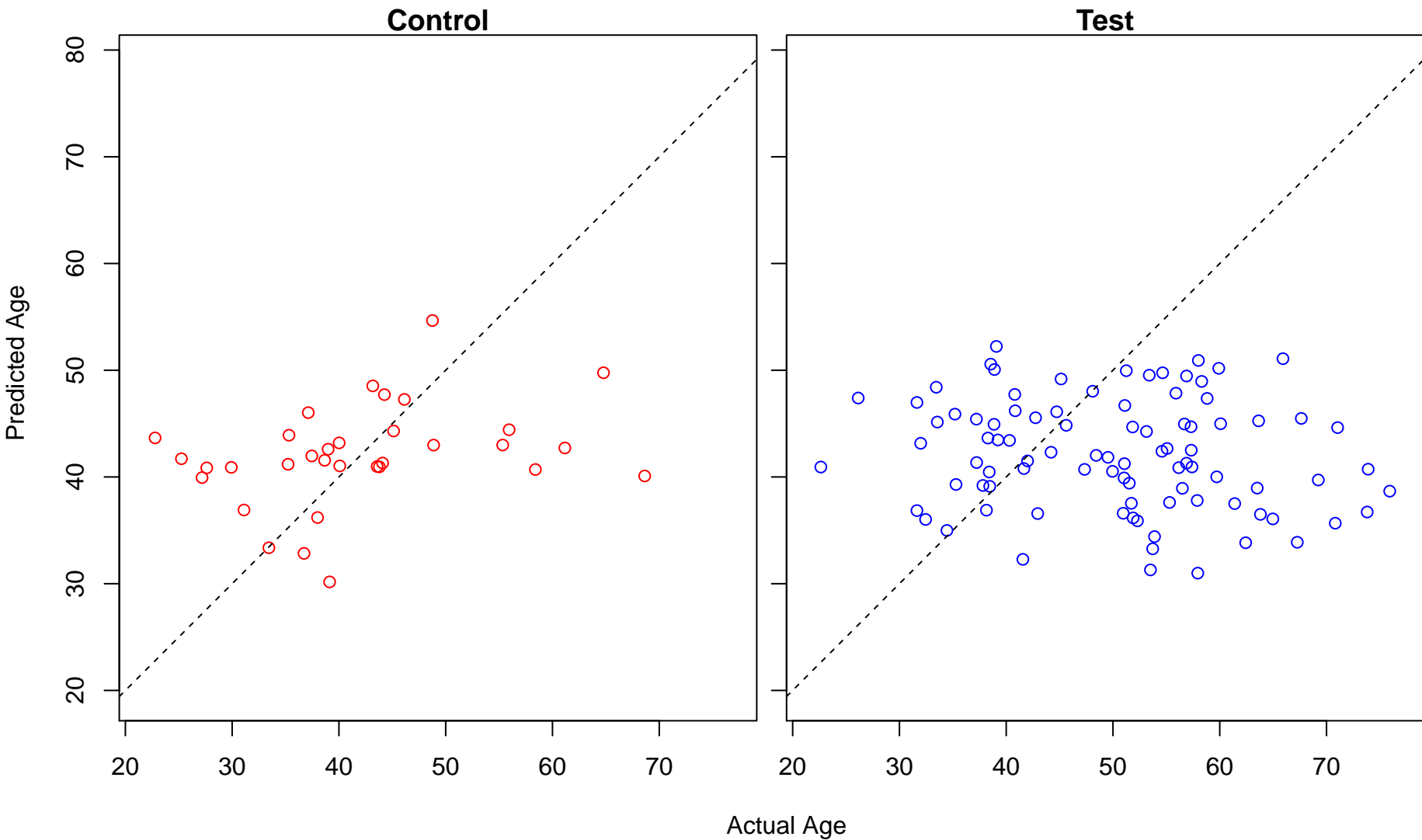
negative regulation of necrotic cell death (Score: 0.367361)



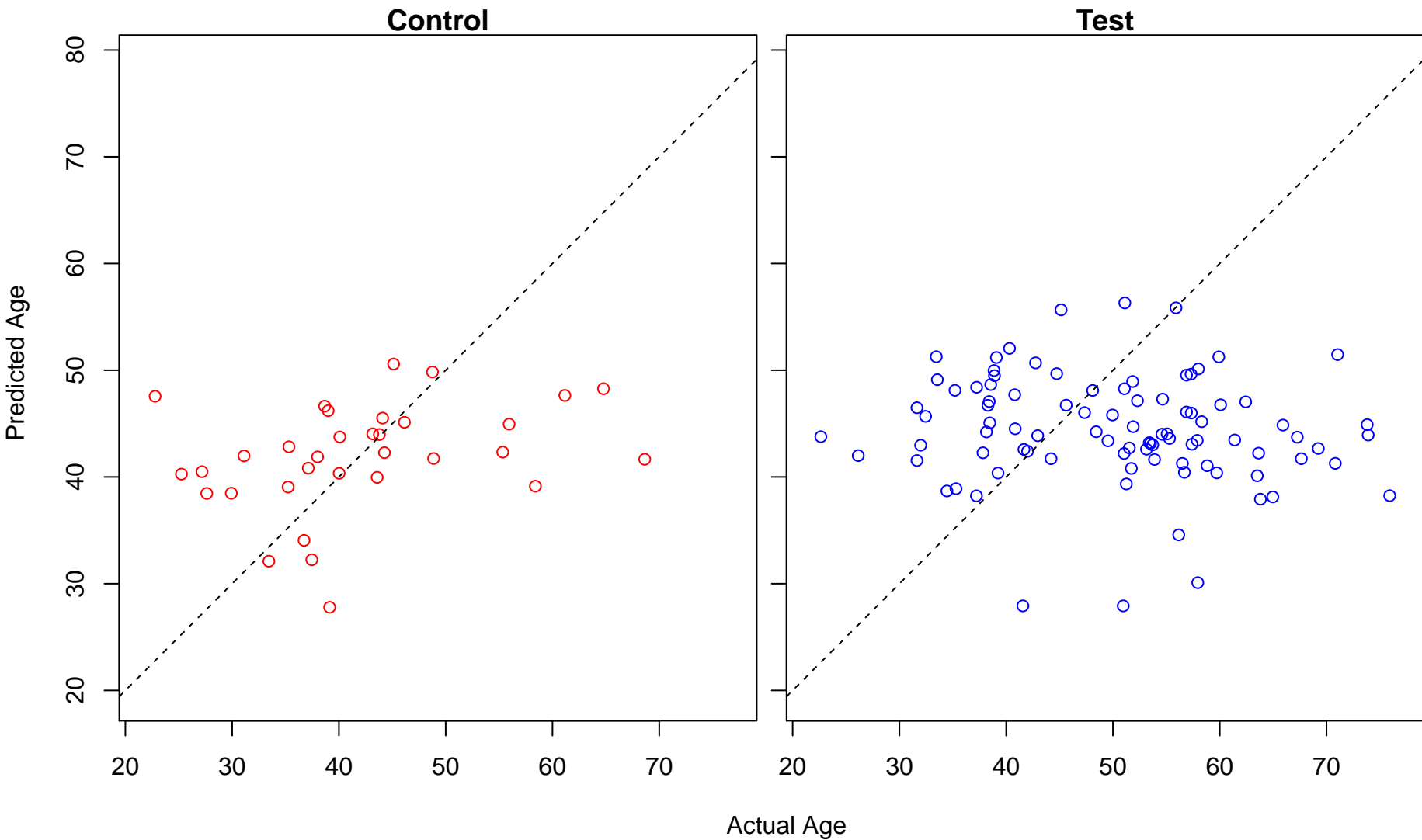
elastic fiber assembly (Score: 0.36945)



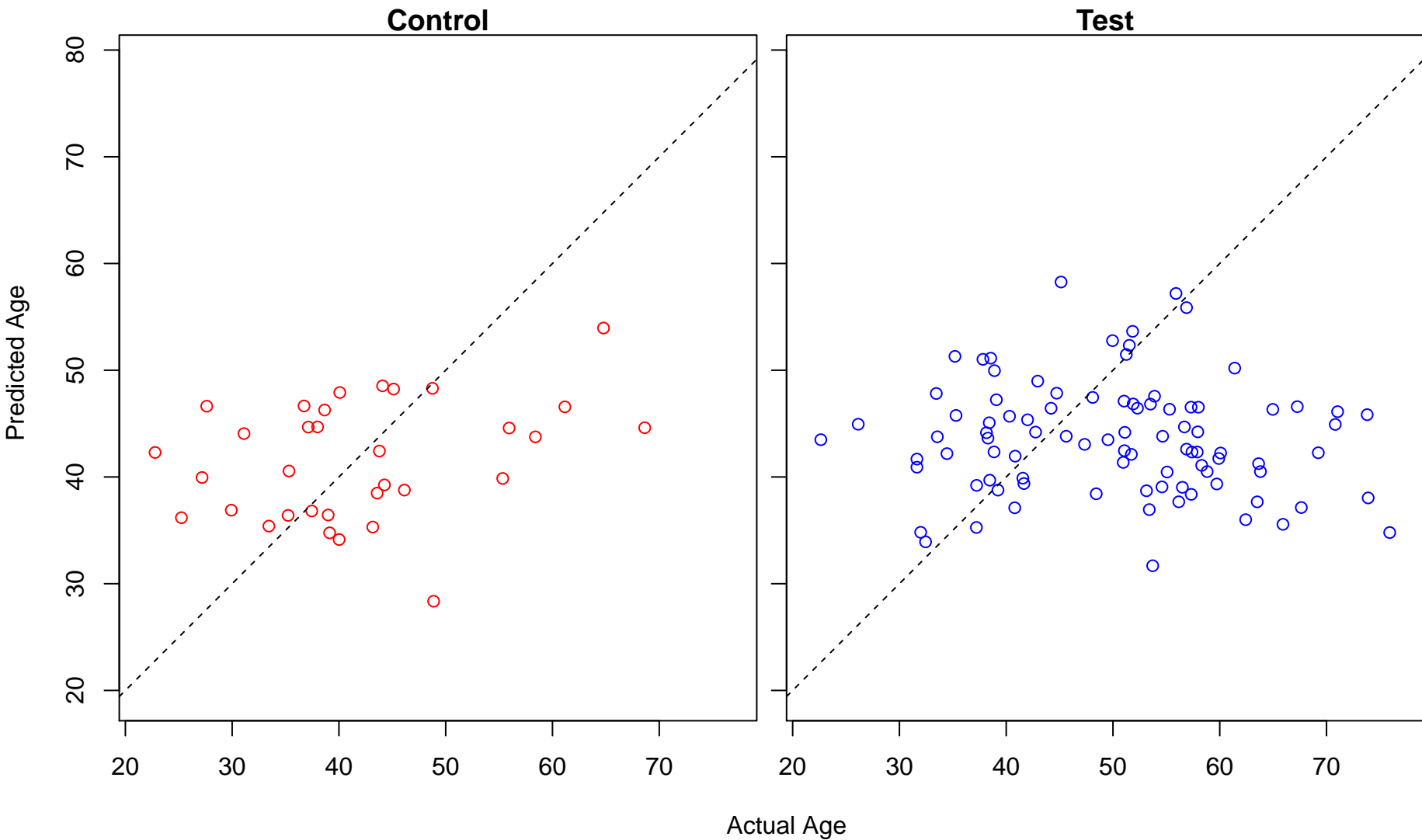
heme transport (Score: 0.366166)



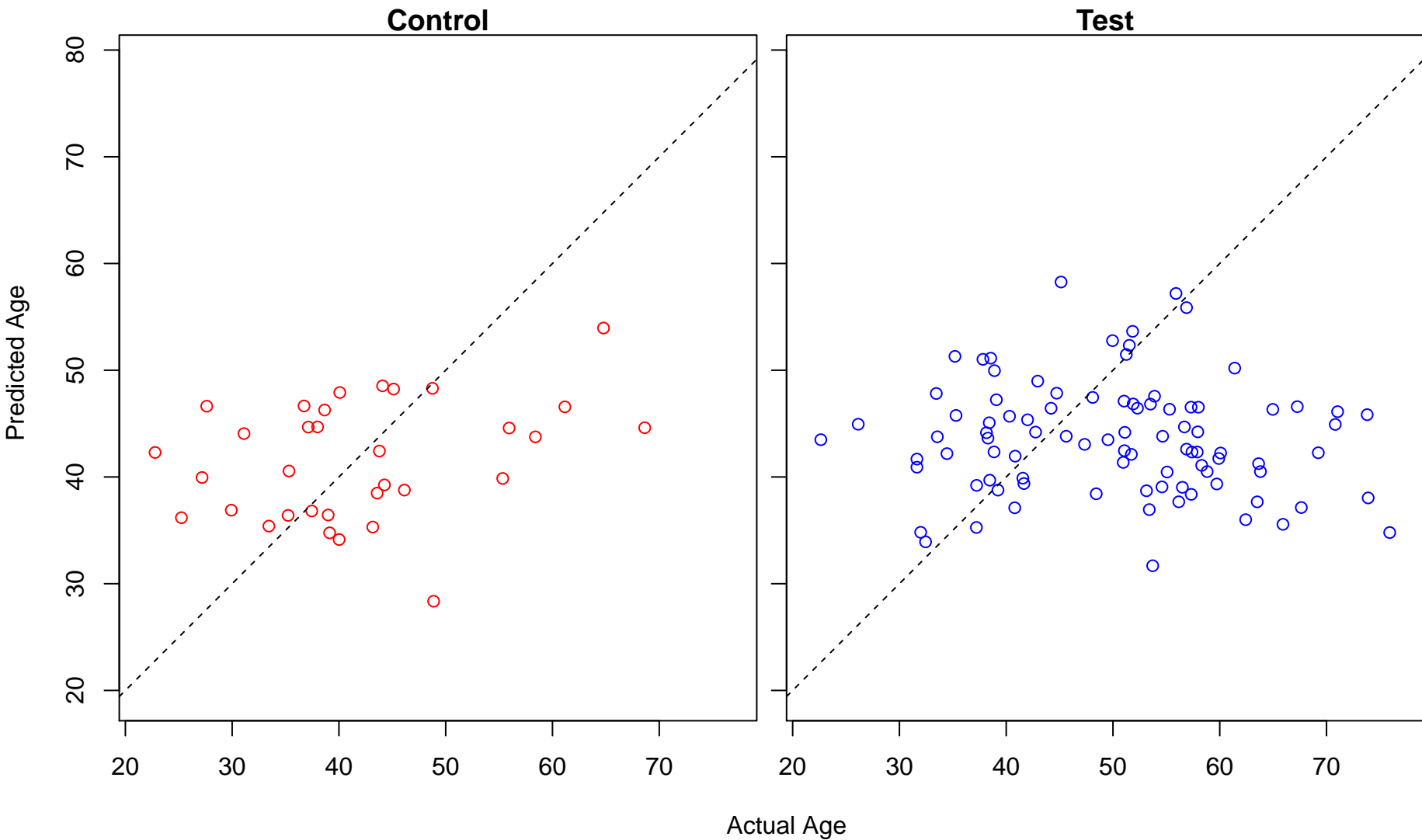
elastin metabolic process (Score: 0.365482)



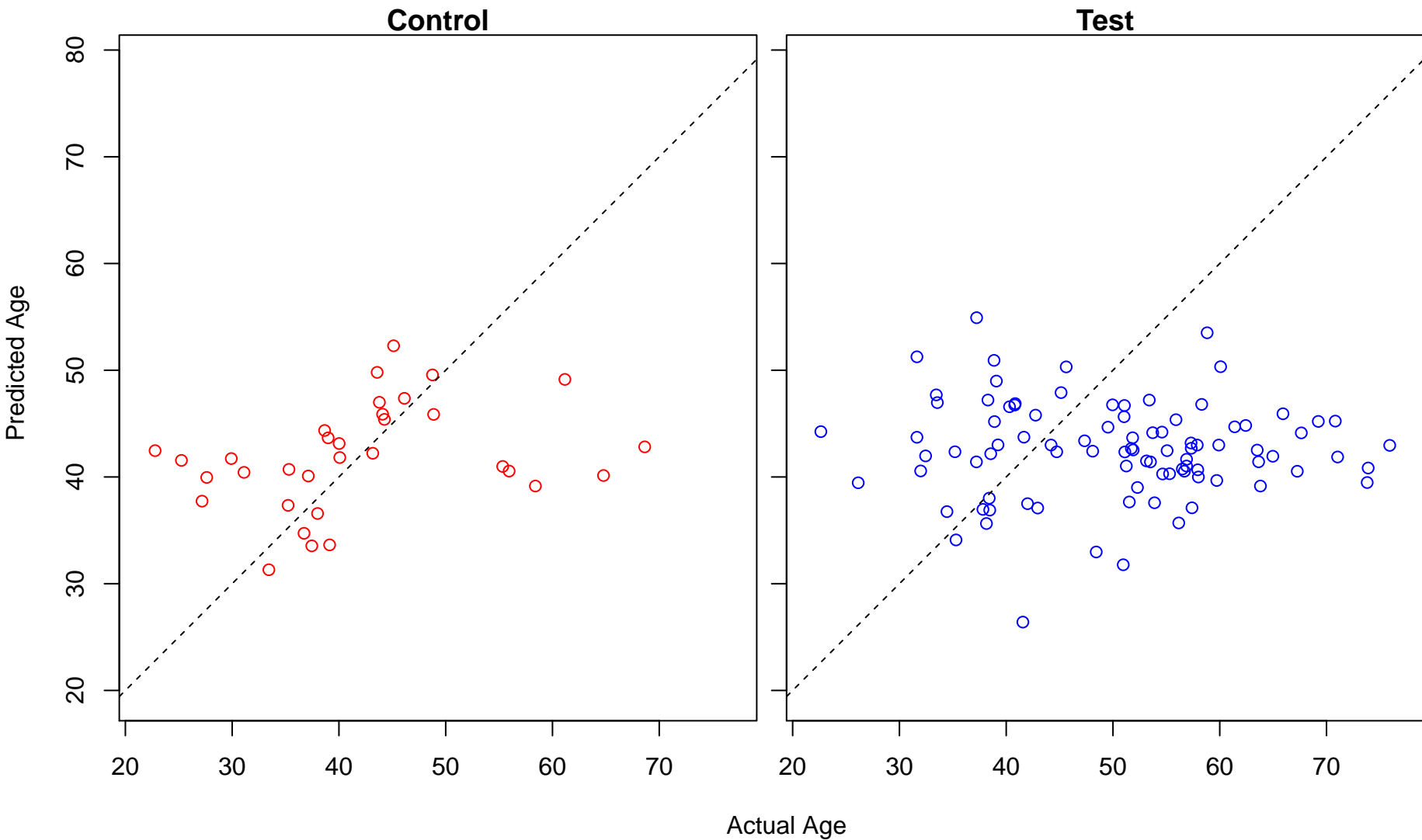
RNA import into mitochondrion (Score: 0.365385)



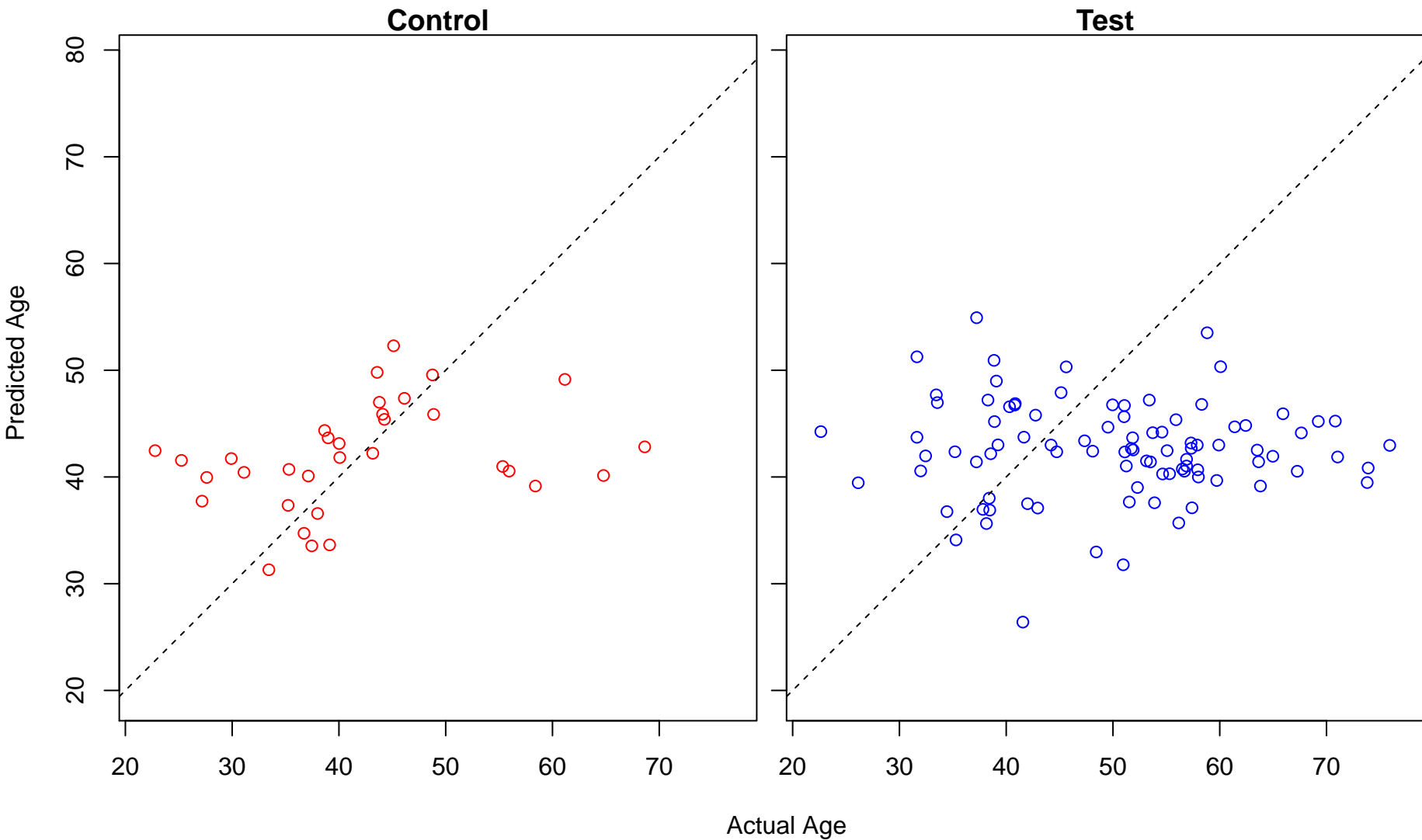
rRNA import into mitochondrion (Score: 0.365385)



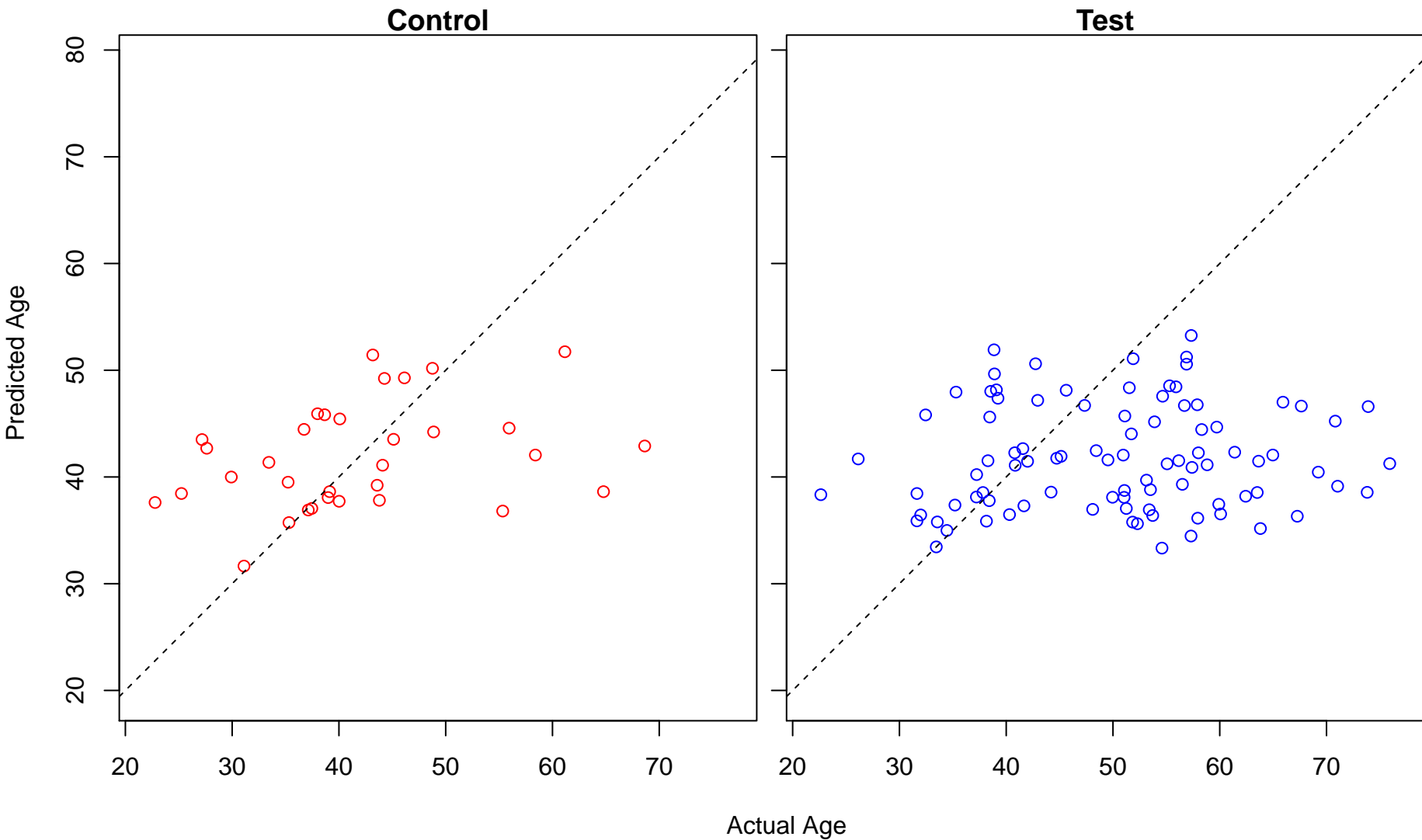
regulation of pigment cell differentiation (Score: 0.365347)



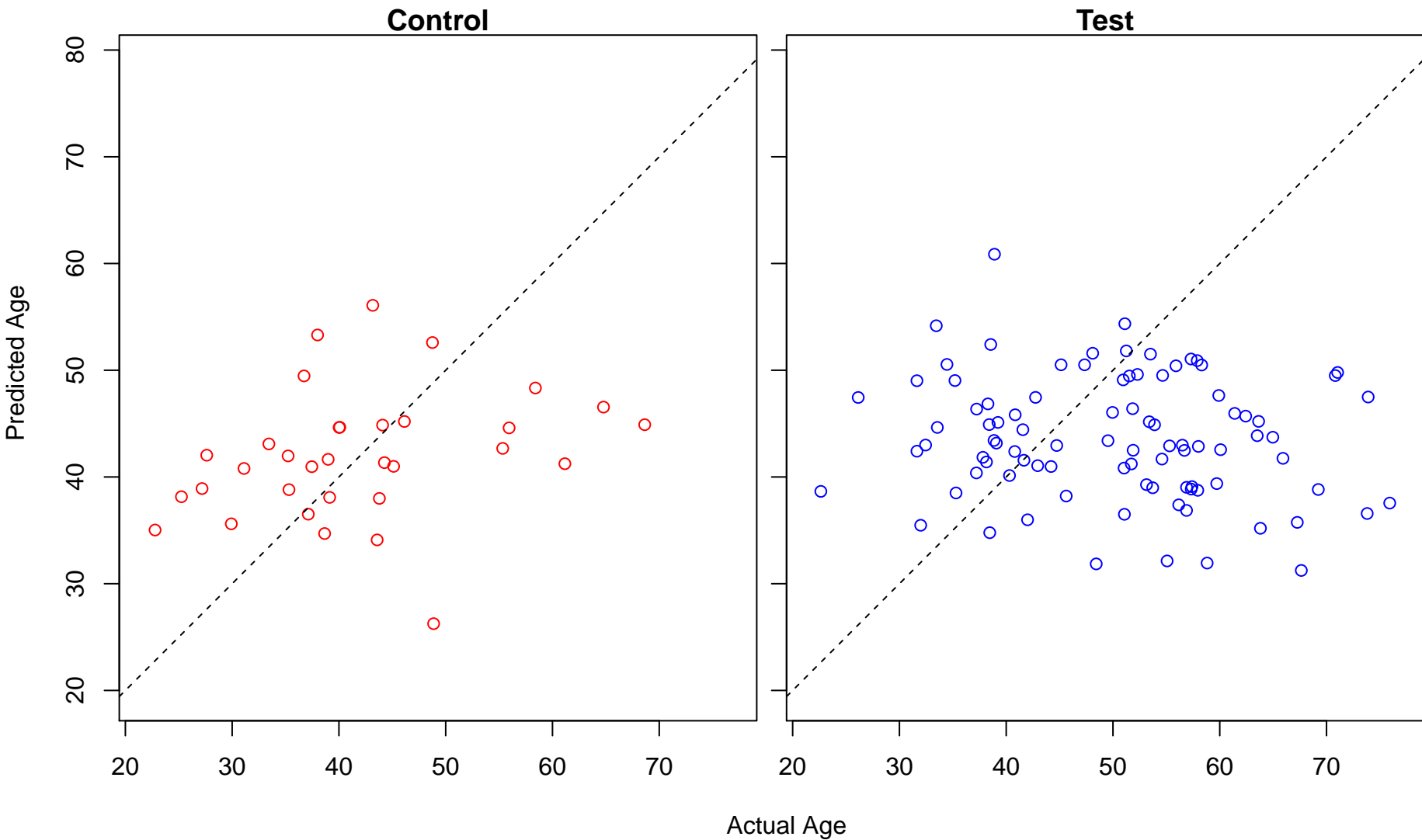
positive regulation of pigment cell differentiation (Score: 0.365347)



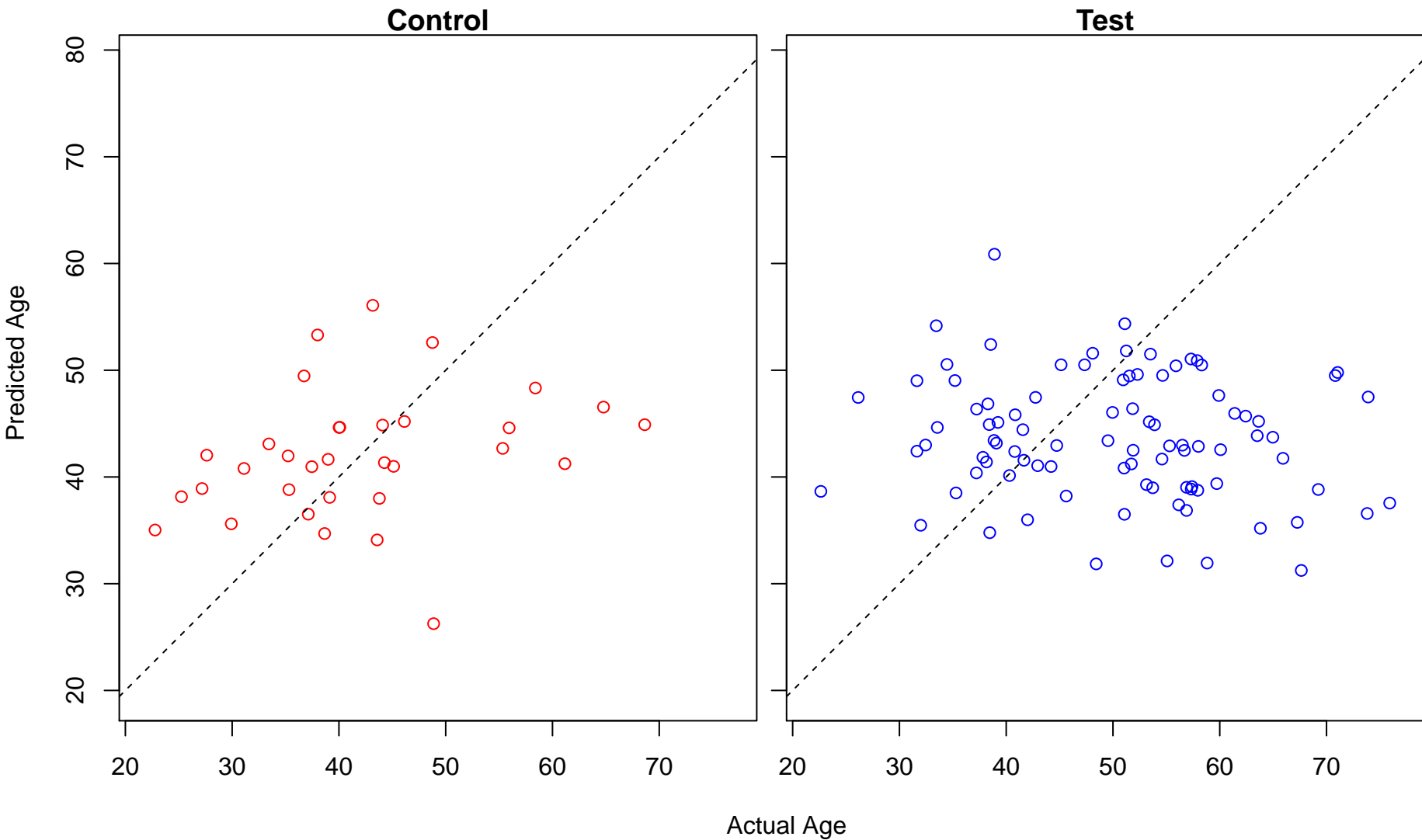
mitotic sister chromatid separation (Score: 0.360263)



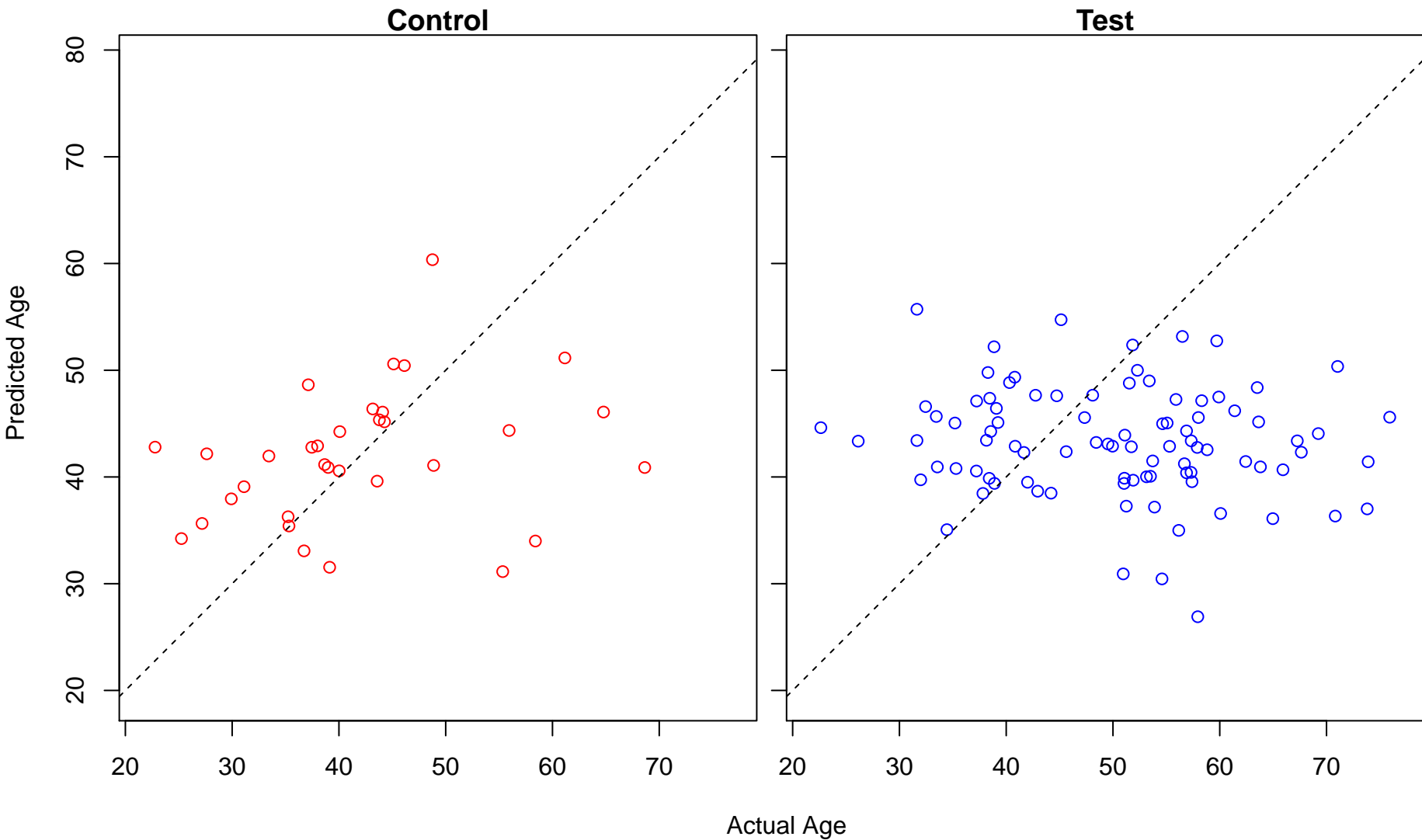
response to cGMP (Score: 0.358098)



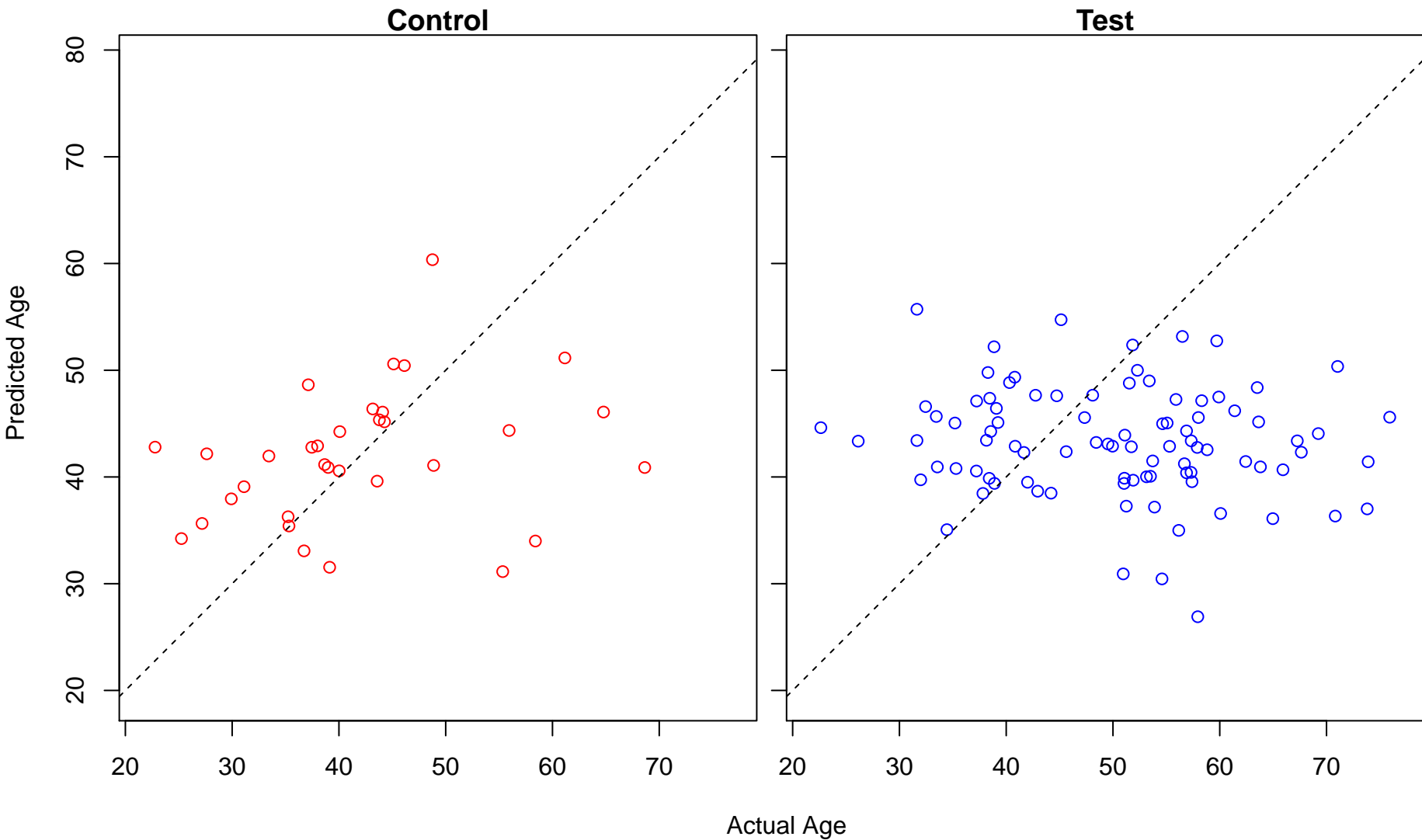
cellular response to cGMP (Score: 0.358098)



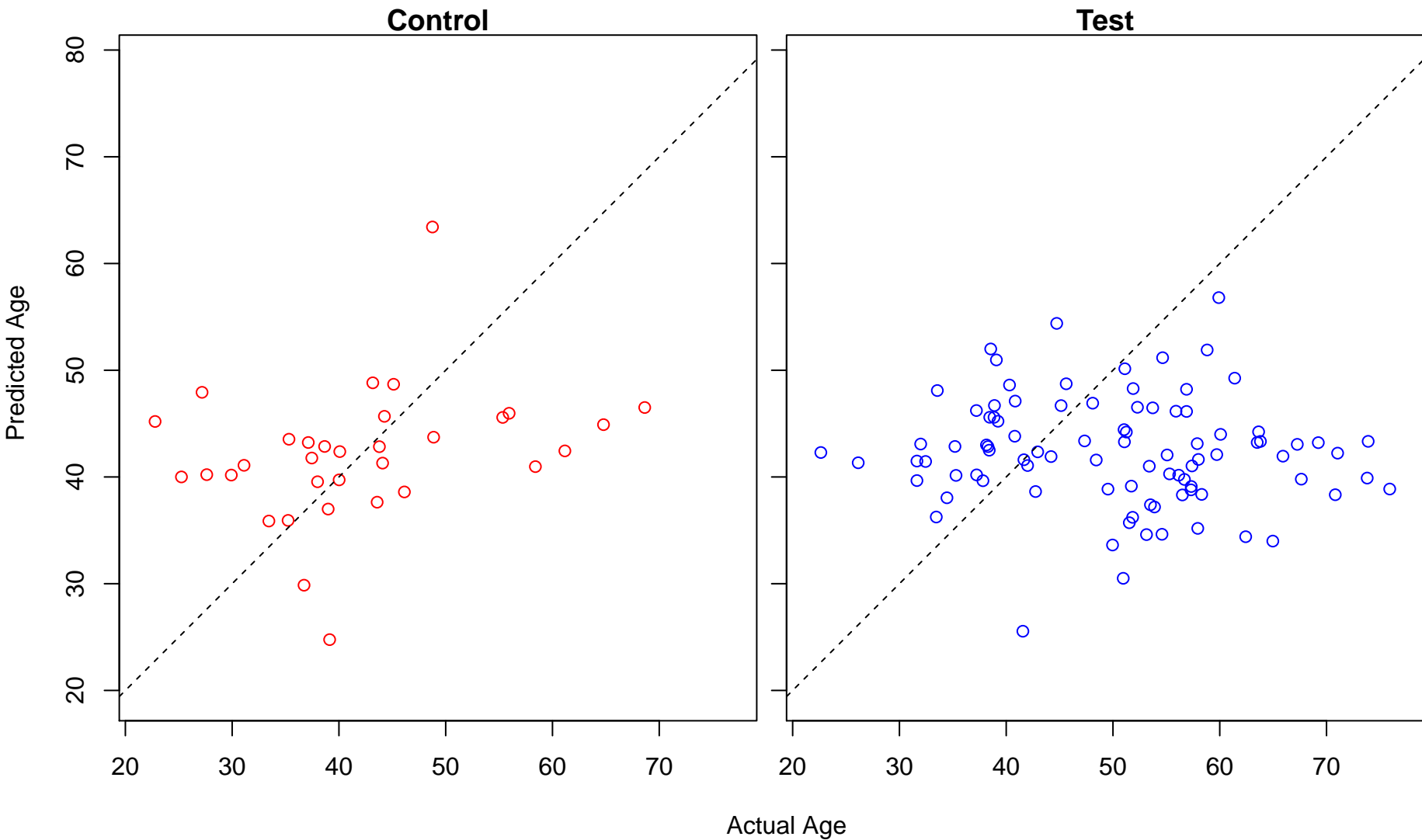
regulation of SMAD protein complex assembly (Score: 0.357618)



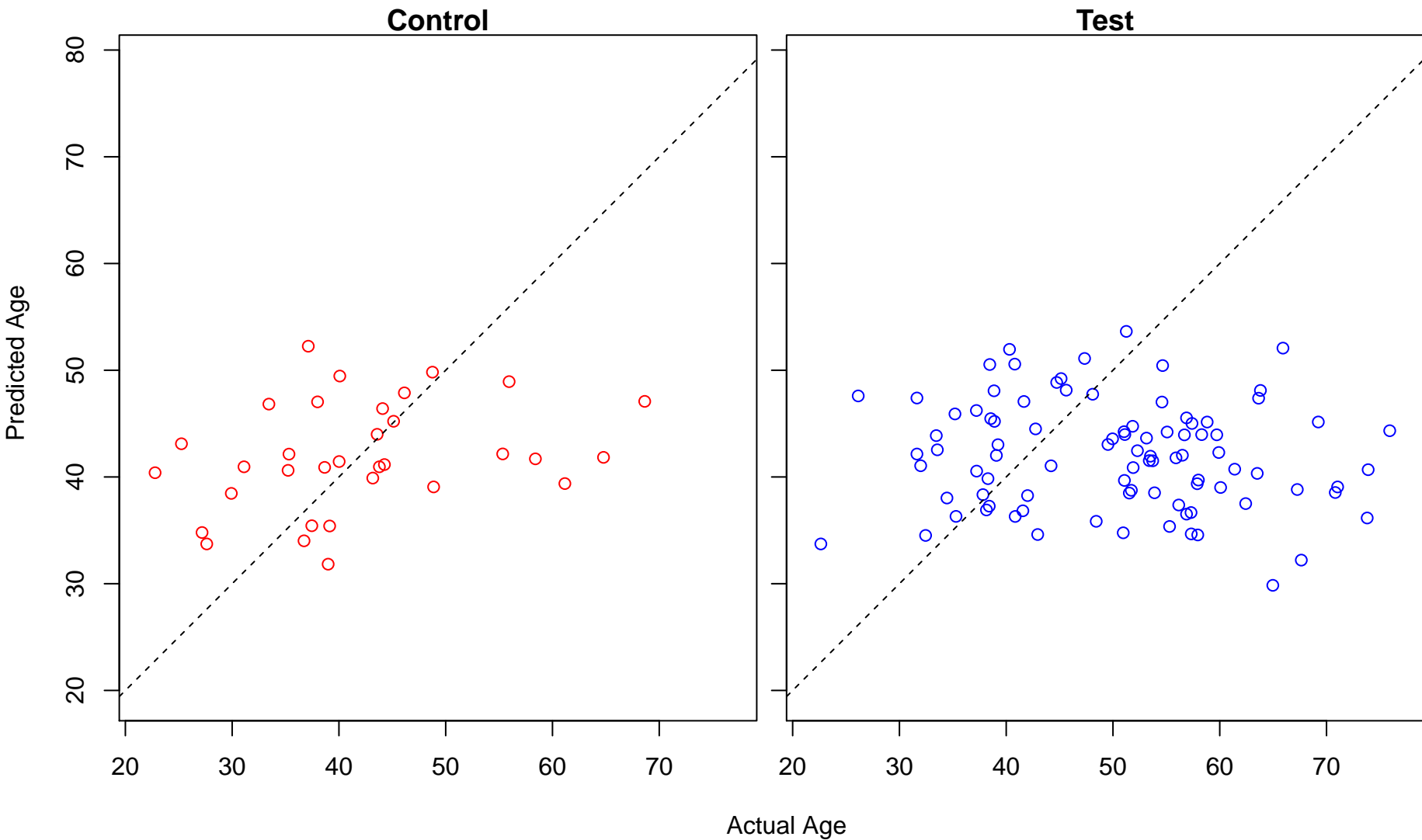
negative regulation of SMAD protein complex assembly (Score: 0.357618)



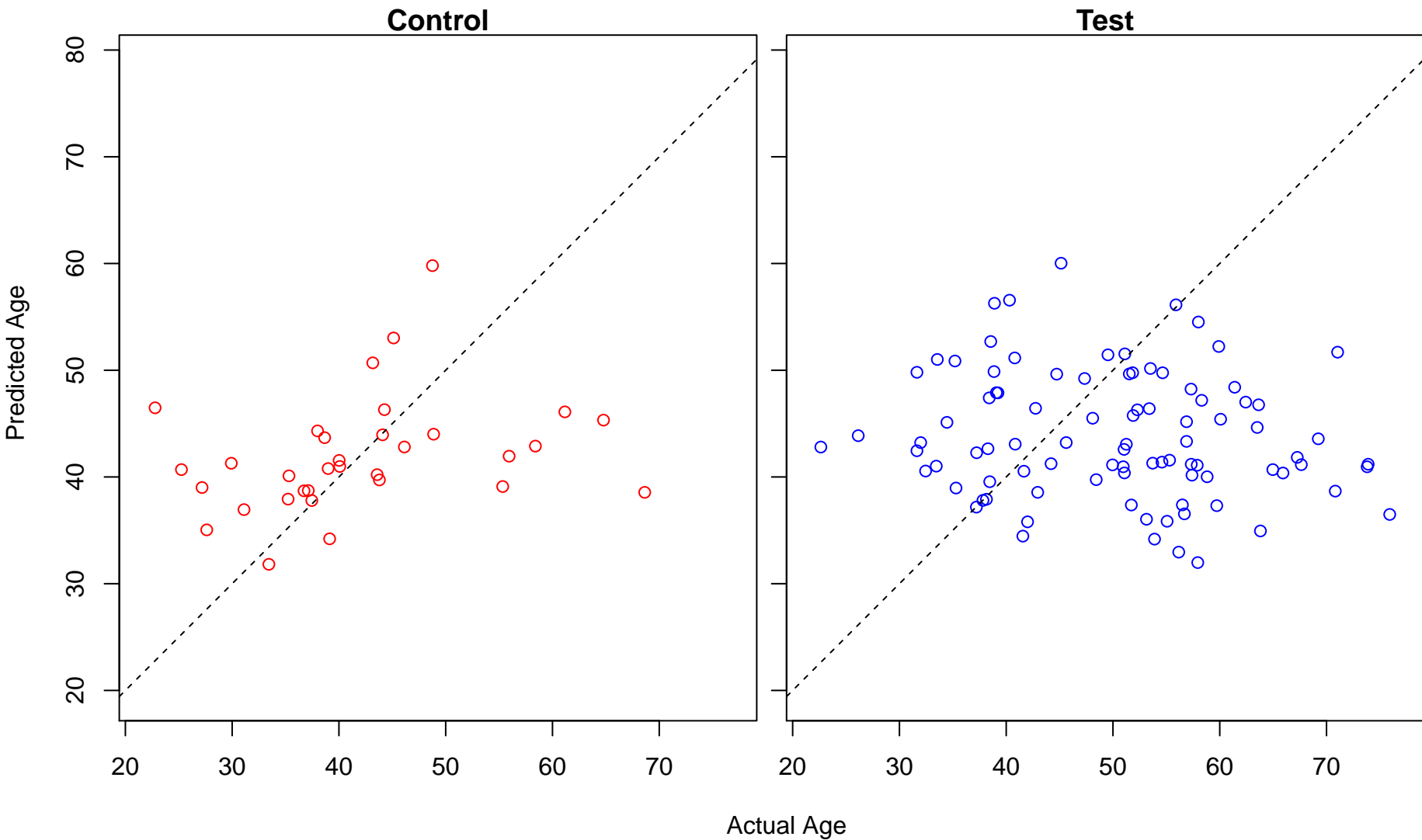
Arp2/3 complex-mediated actin nucleation (Score: 0.357472)



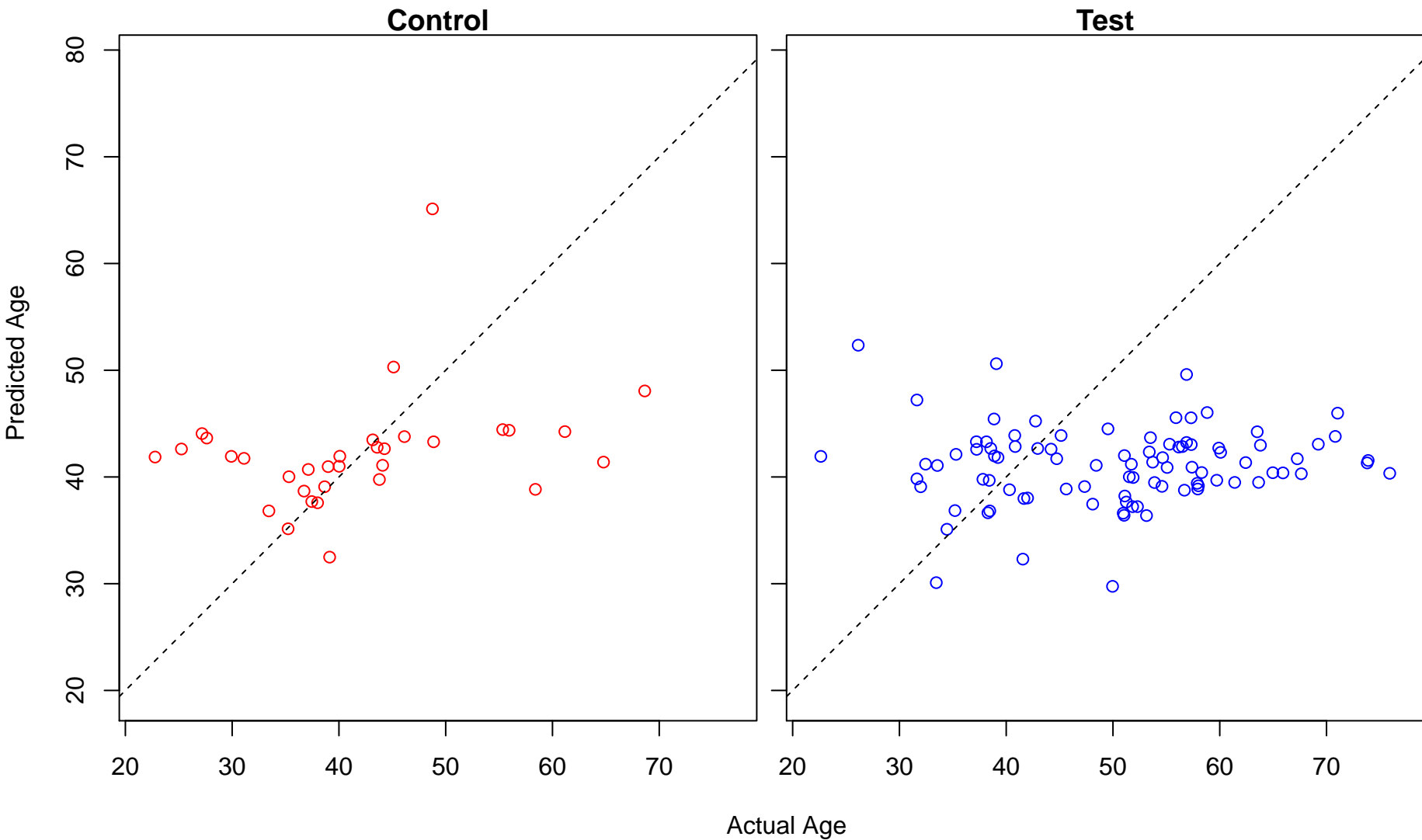
cellular response to copper ion (Score: 0.355224)



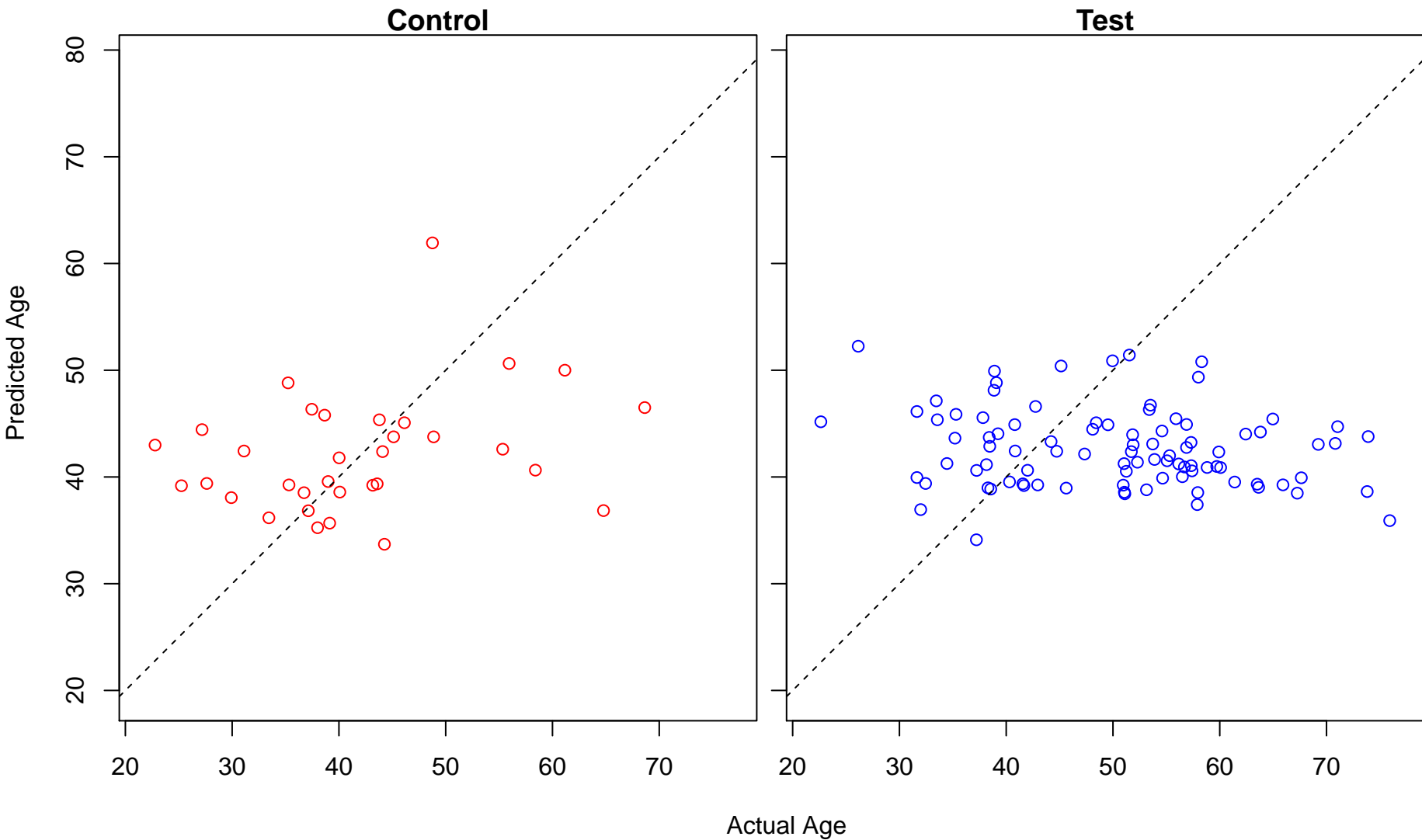
lipoprotein transport (Score: 0.353180)



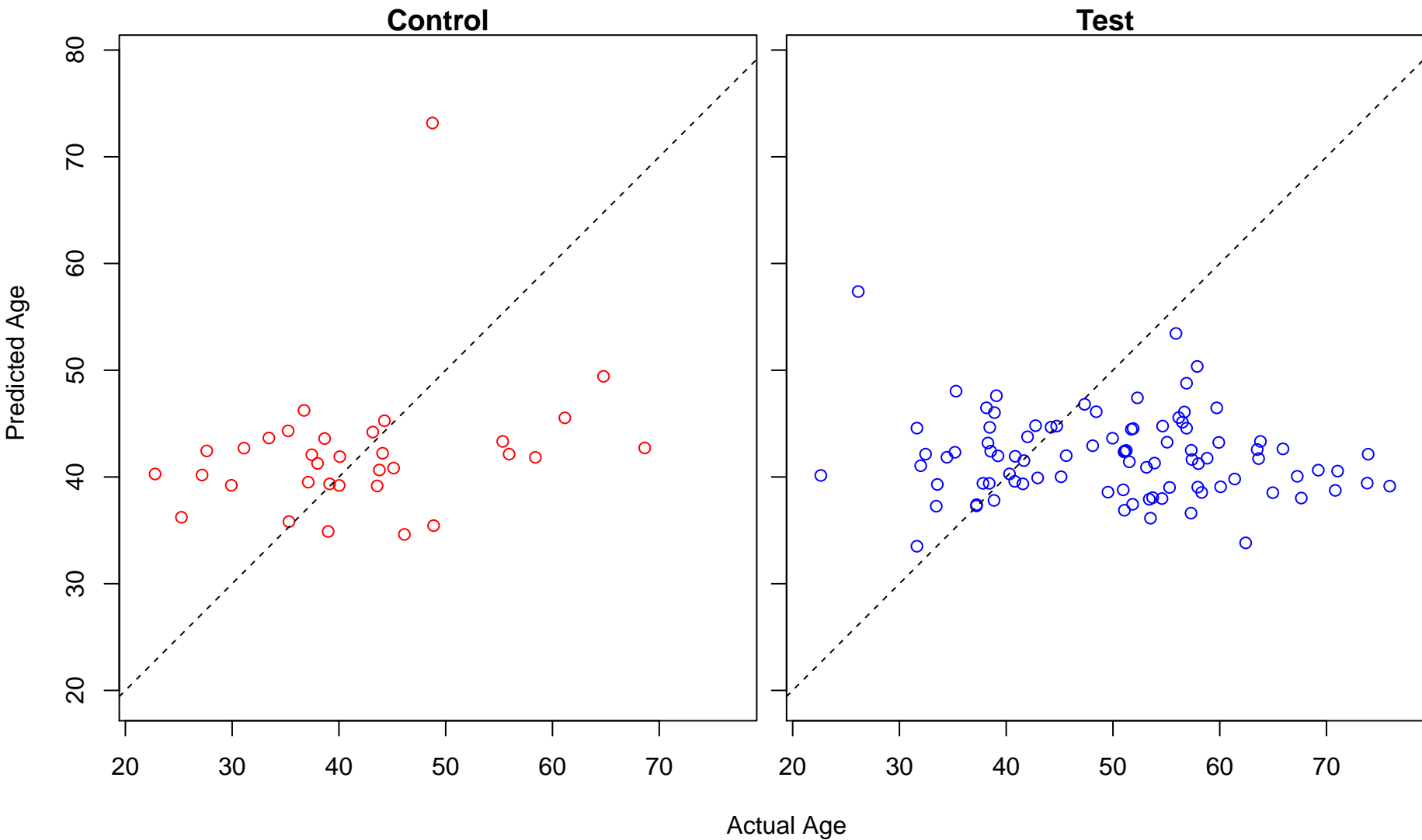
nuclear-transcribed mRNA catabolic process, no-go decay (Score: 0.347636)



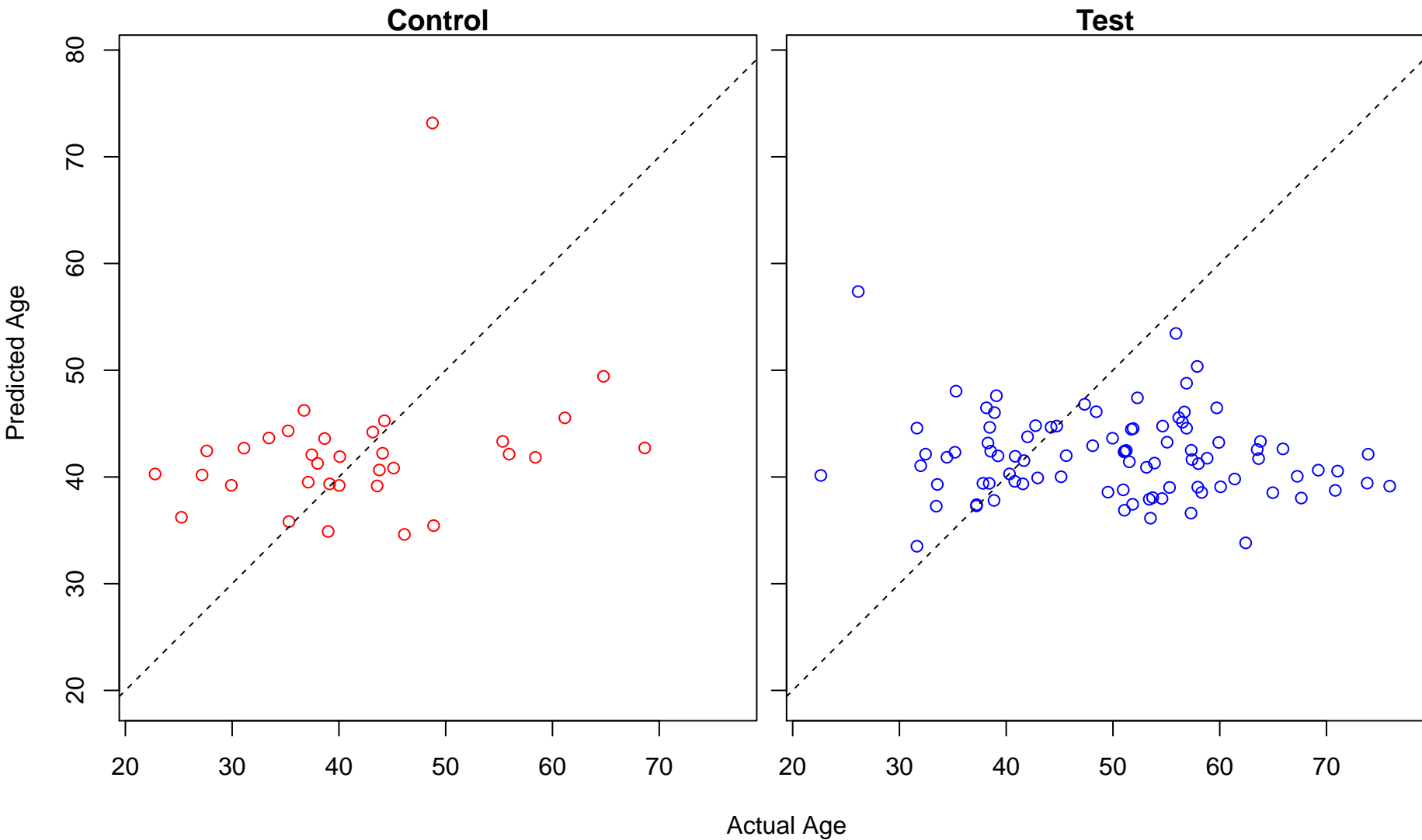
negative regulation of interferon-beta production (Score: 0.347550)



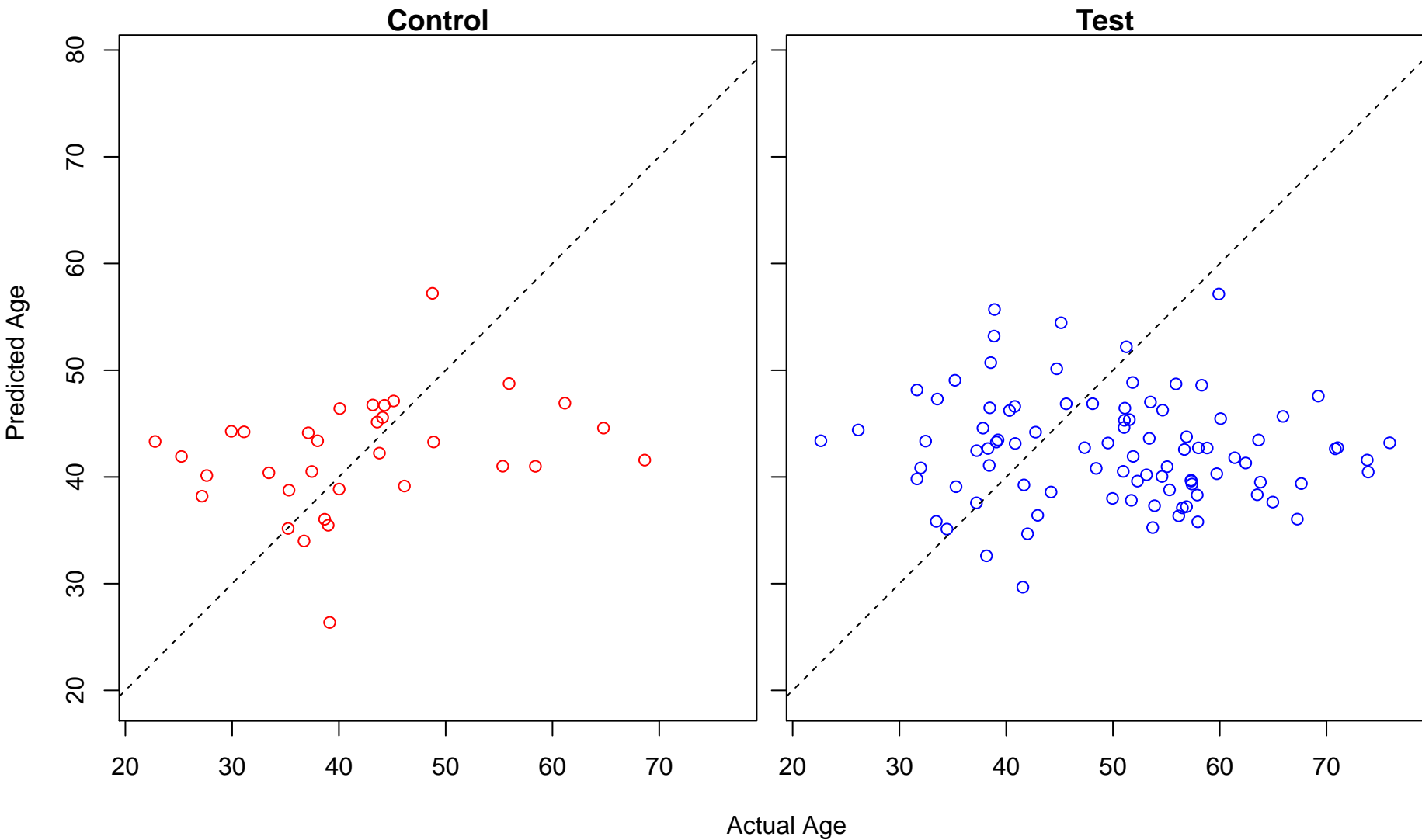
transcriptional activation by promoter-enhancer looping (Score: 0.347386)



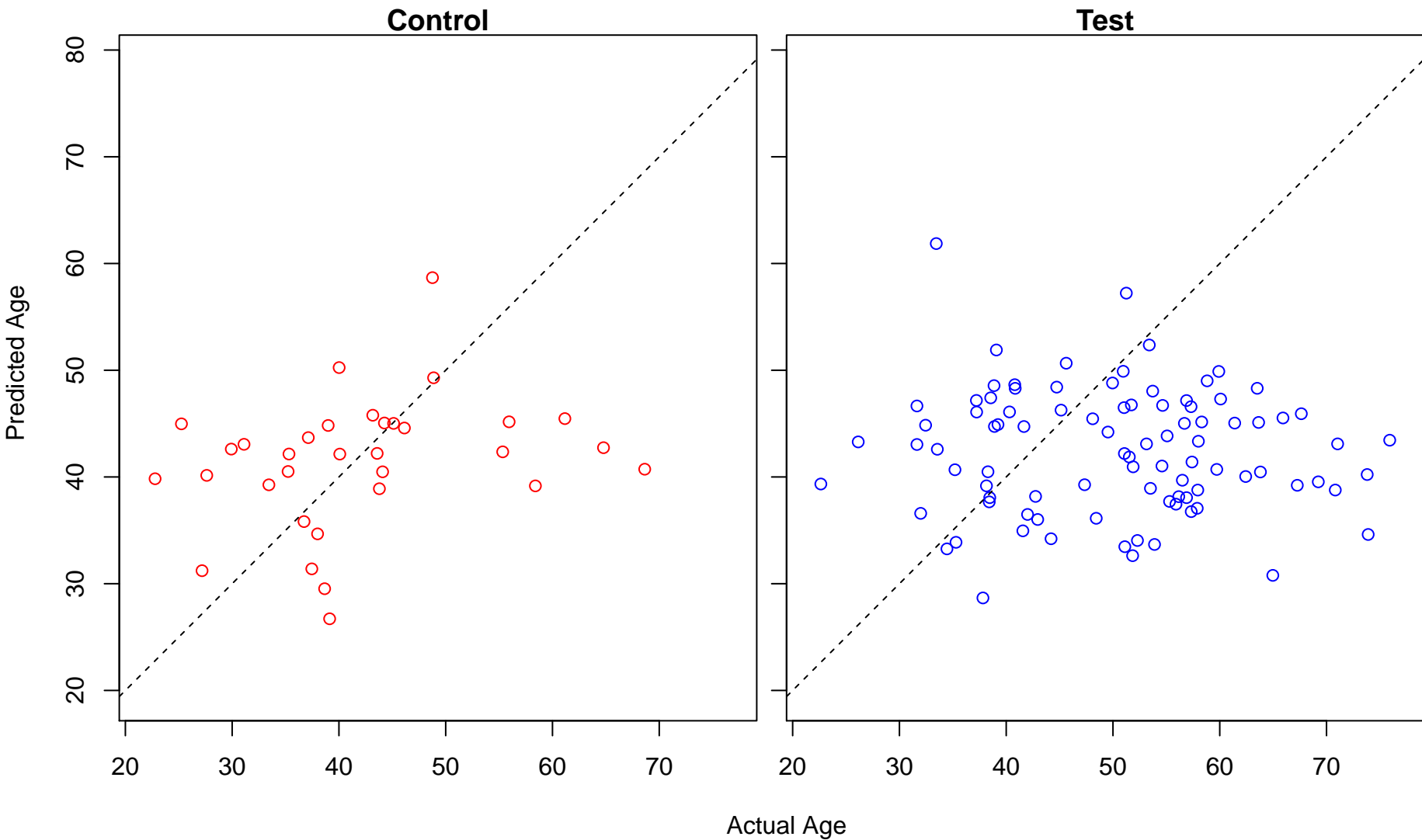
gene looping (Score: 0.347386)



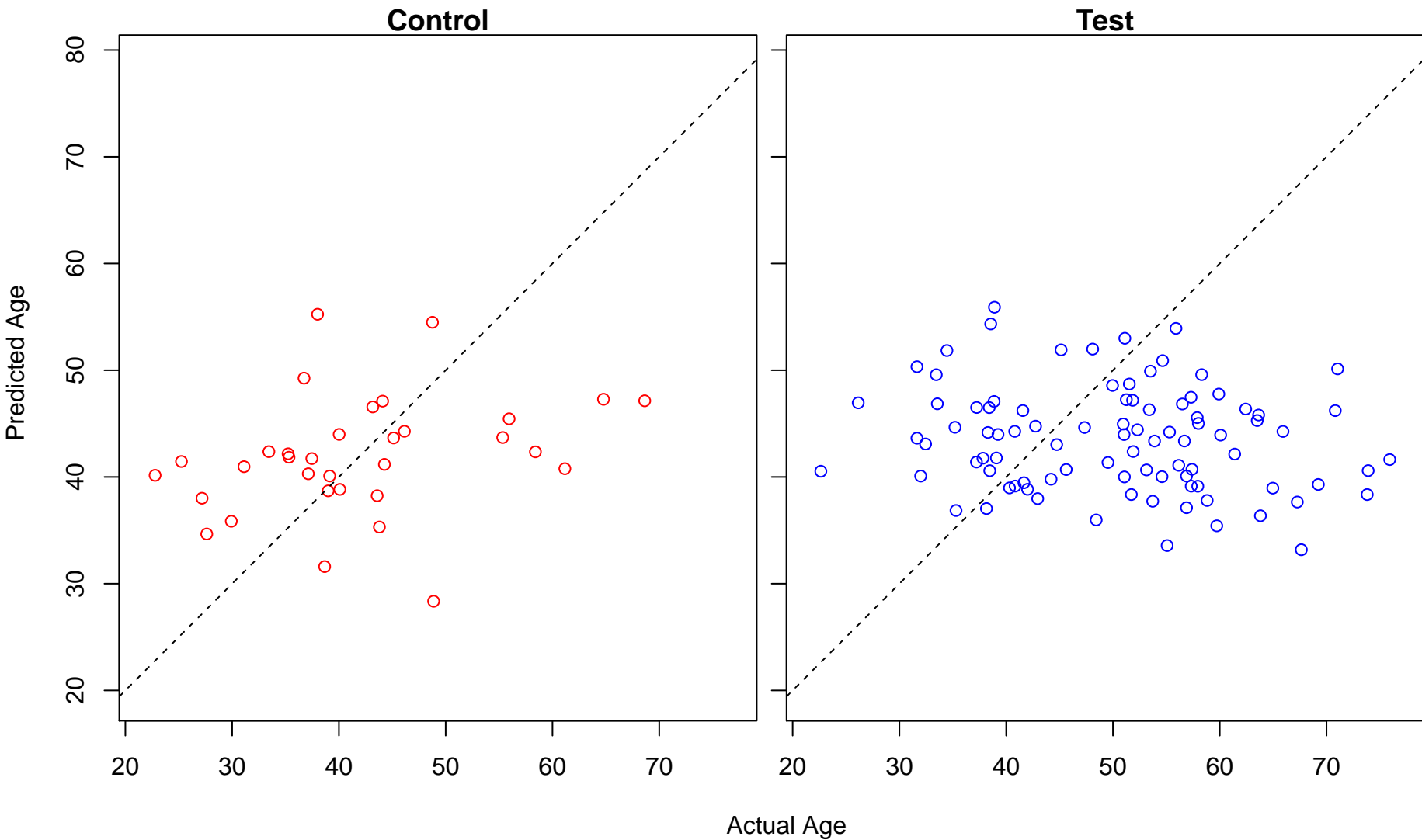
inner dynein arm assembly (Score: 0.344026)



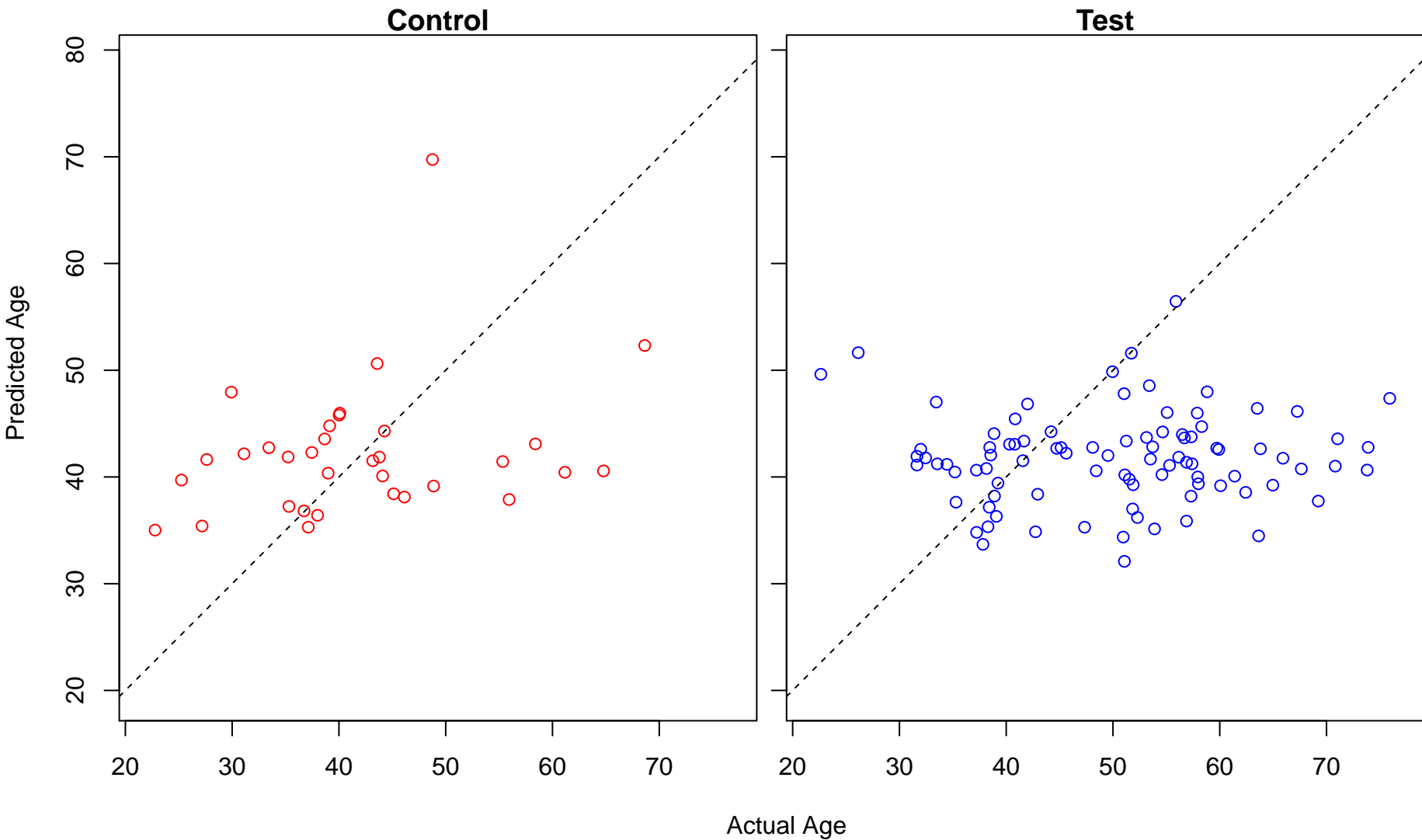
poly(A)+ mRNA export from nucleus (Score: 0.340034)



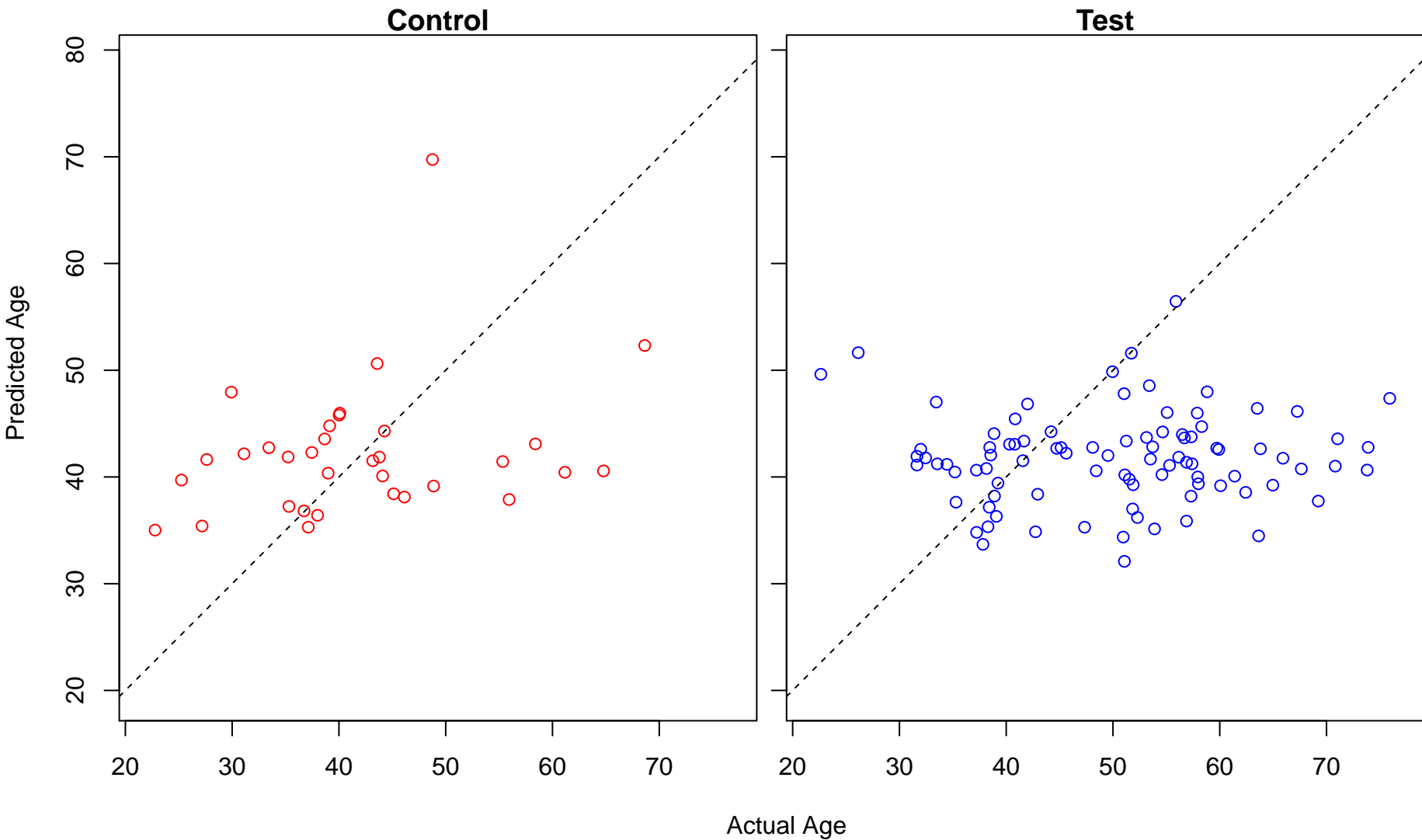
cellular response to macrophage colony-stimulating factor stimulus (Score: 0.336751)



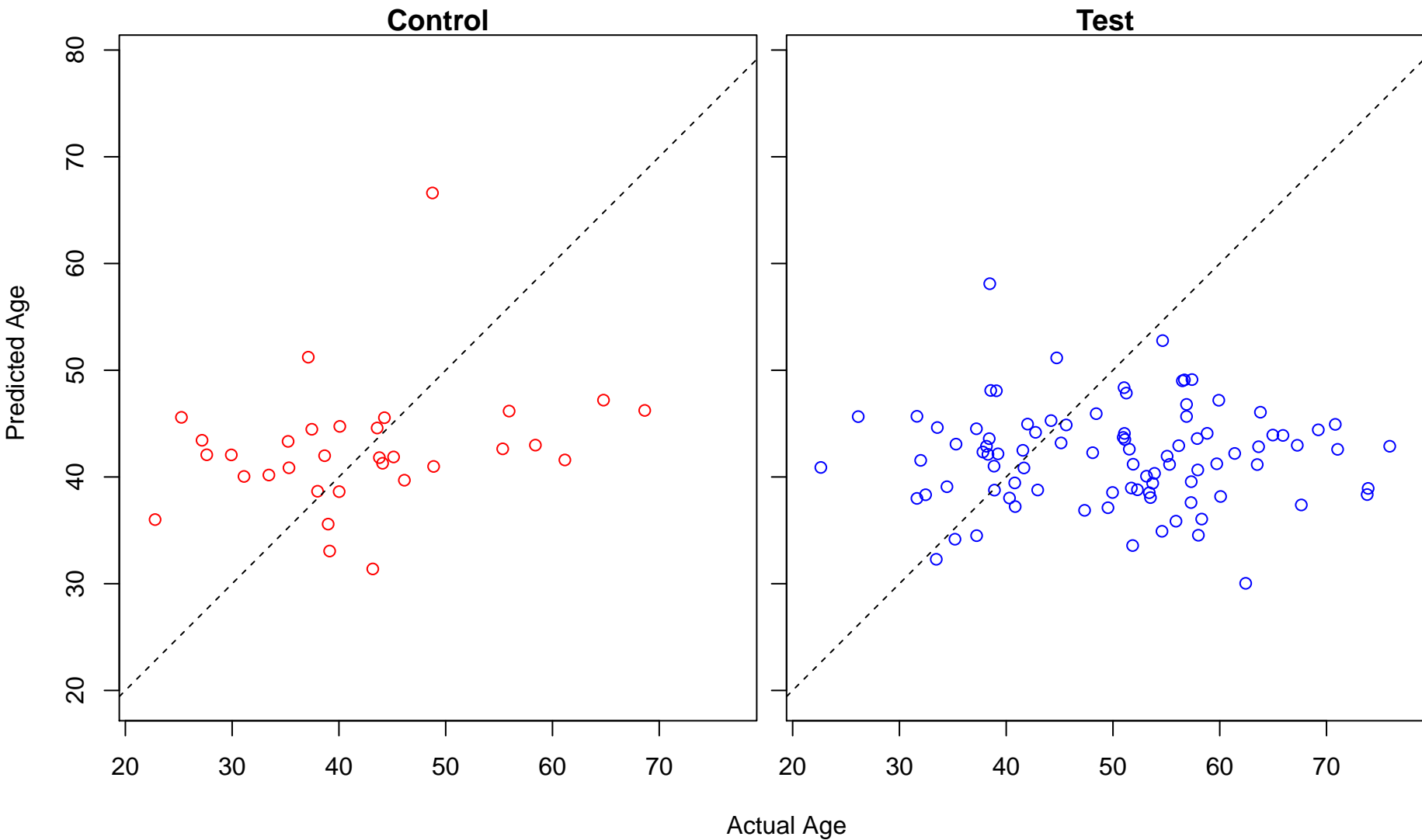
optic cup morphogenesis involved in camera-type eye development (Score: 0.336234)



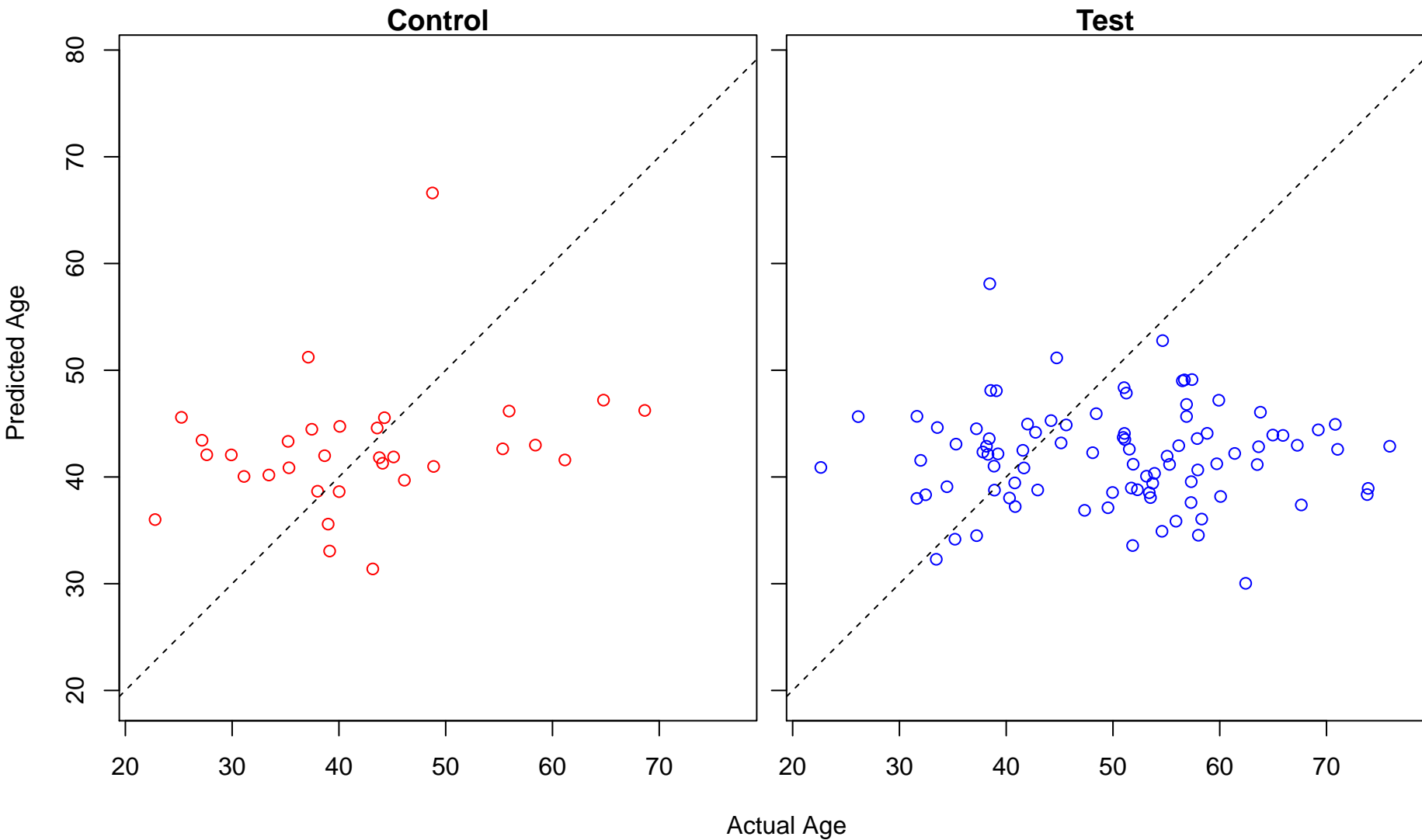
embryonic camera-type eye formation (Score: 0.336234)



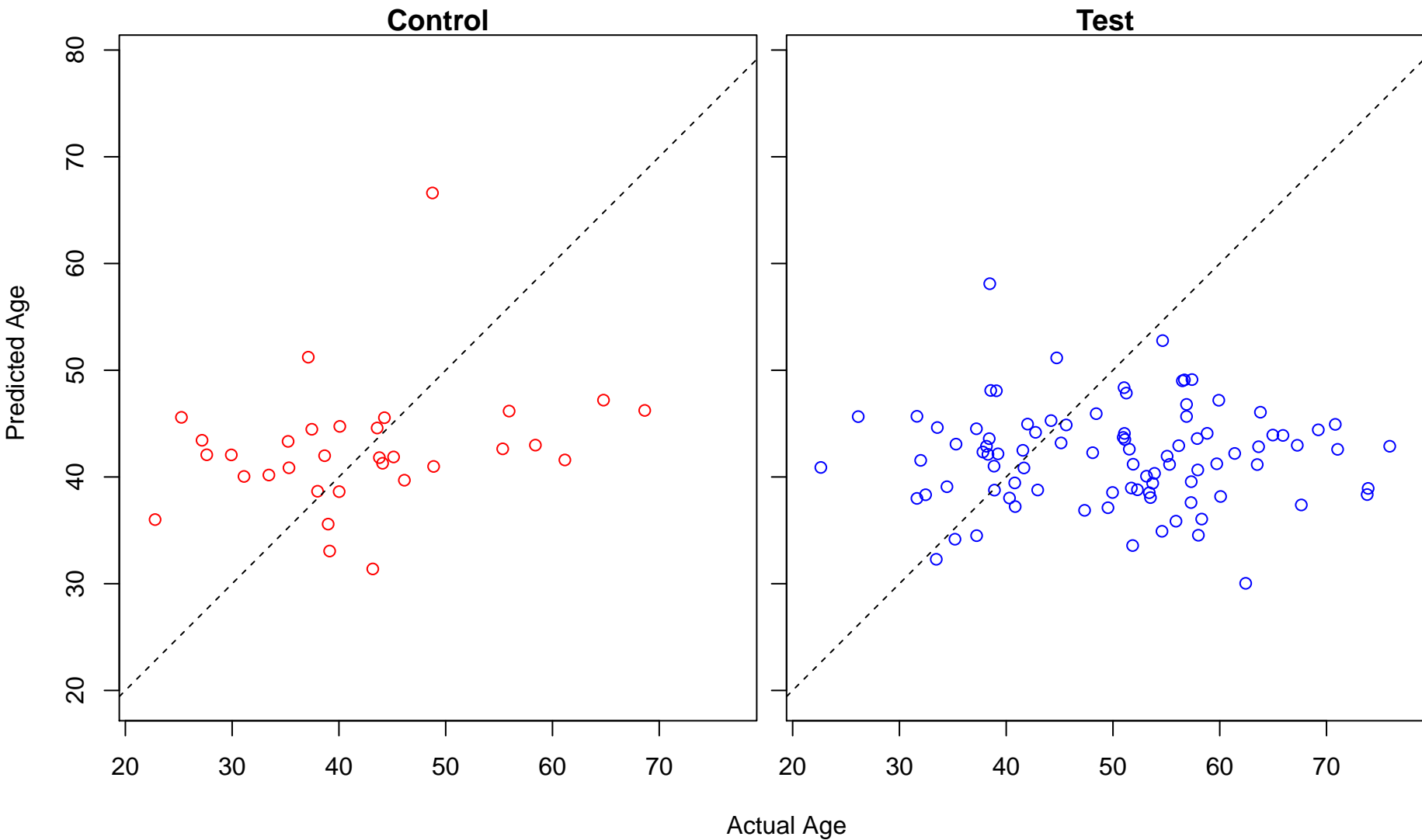
ectodermal placode formation (Score: 0.332472)



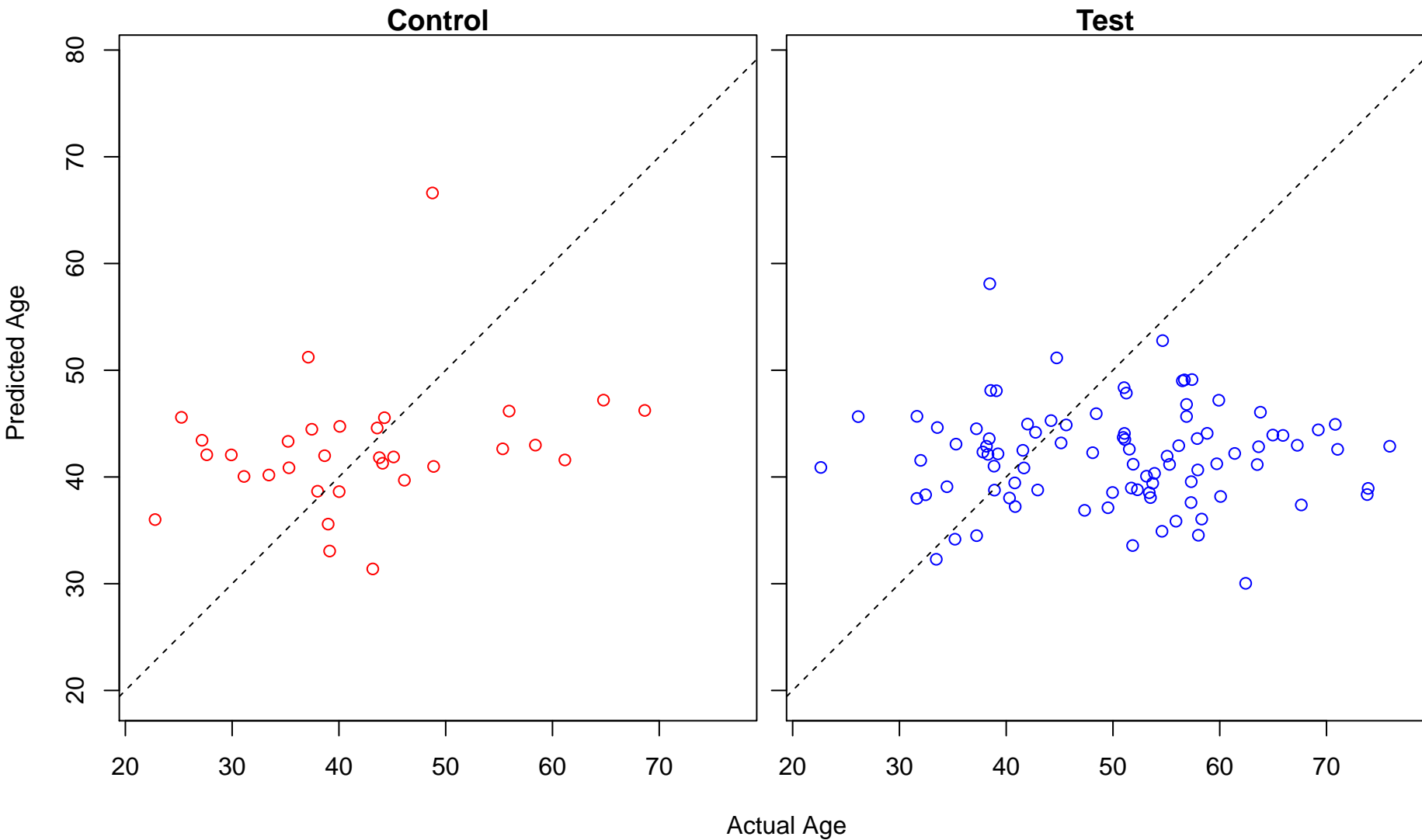
hair follicle placode formation (Score: 0.332472)



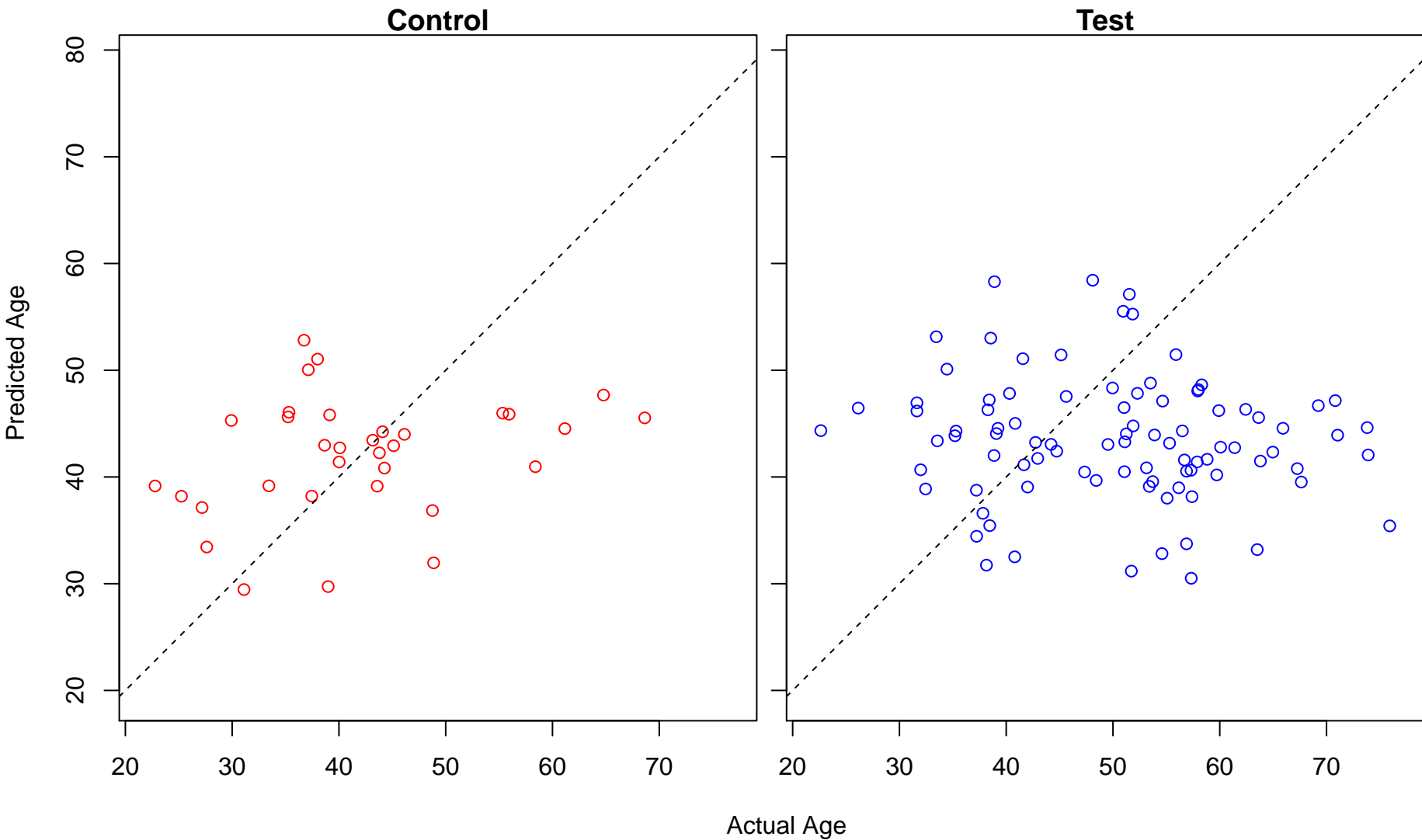
ectodermal placode development (Score: 0.332472)



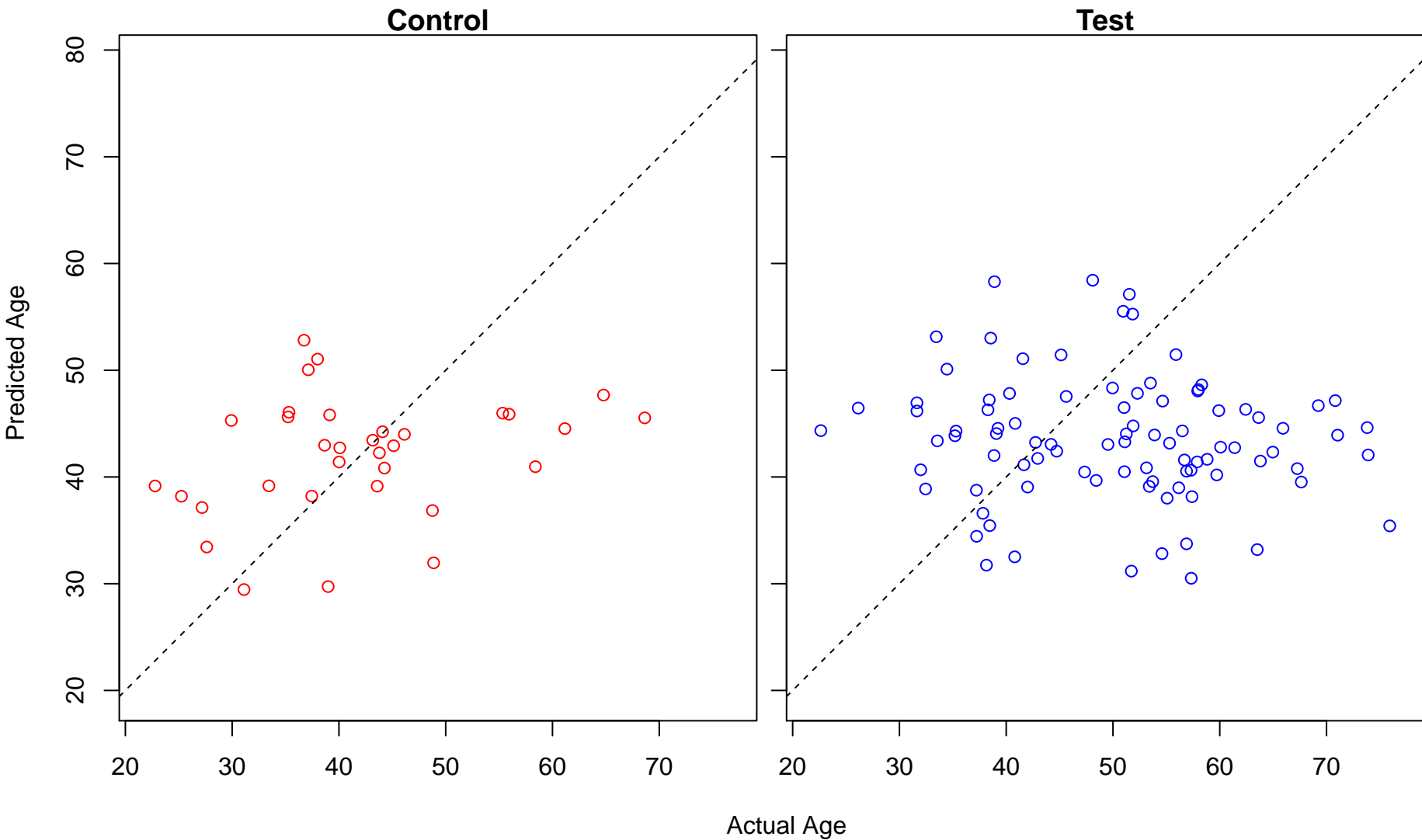
ectodermal placode morphogenesis (Score: 0.332472)



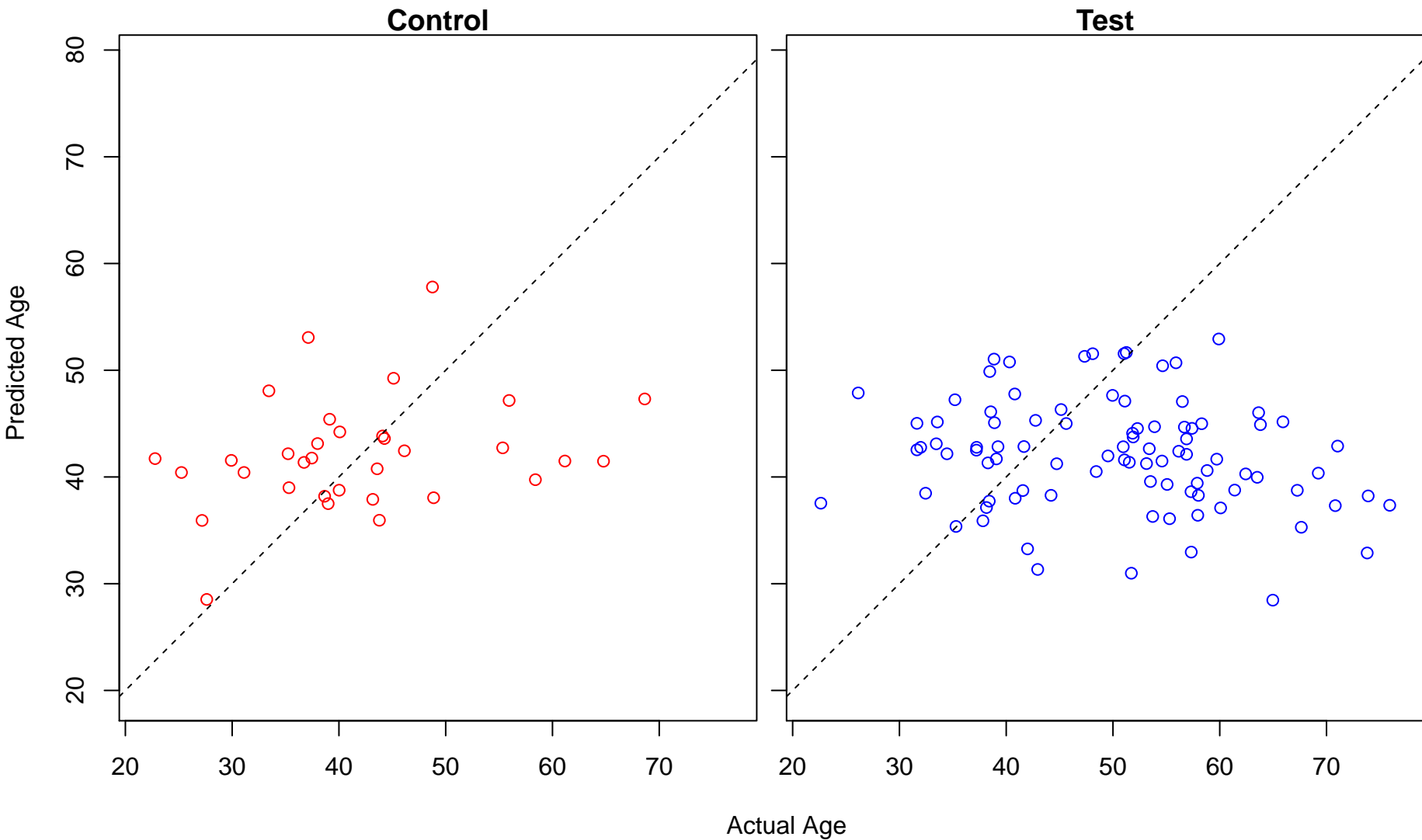
S-shaped body morphogenesis (Score: 0.331908)



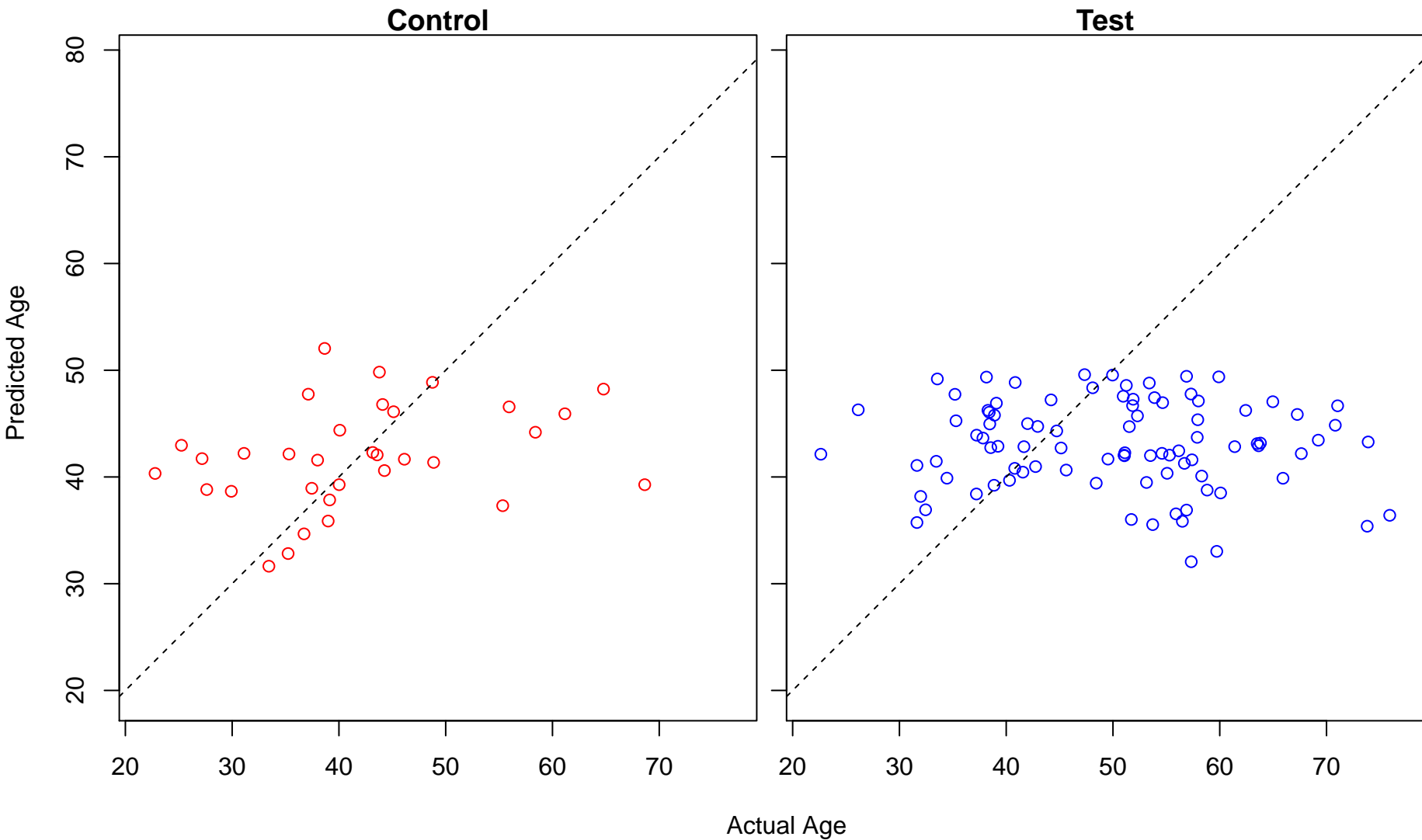
metanephric S-shaped body morphogenesis (Score: 0.331908)



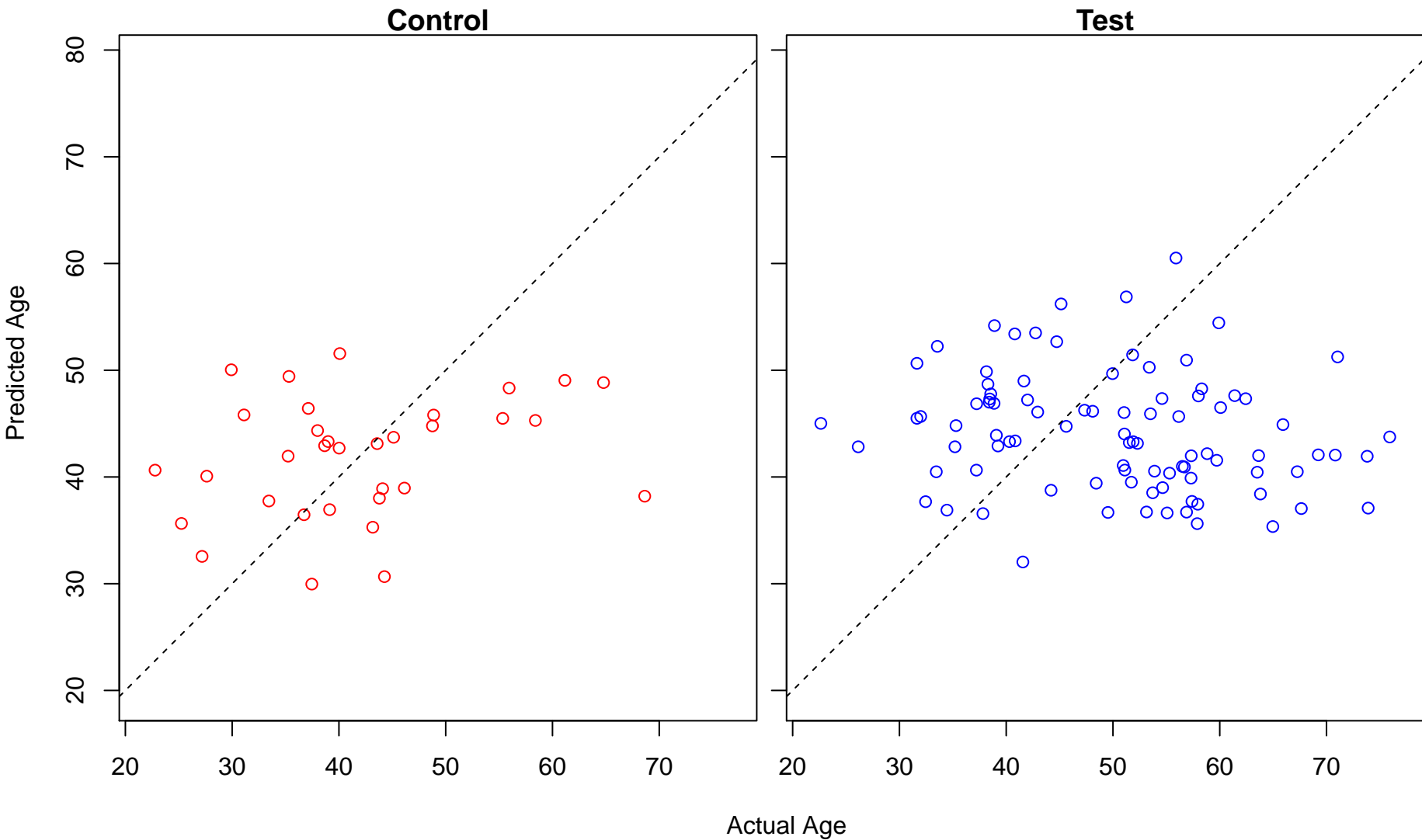
regulation of chromatin assembly or disassembly (Score: 0.331728)



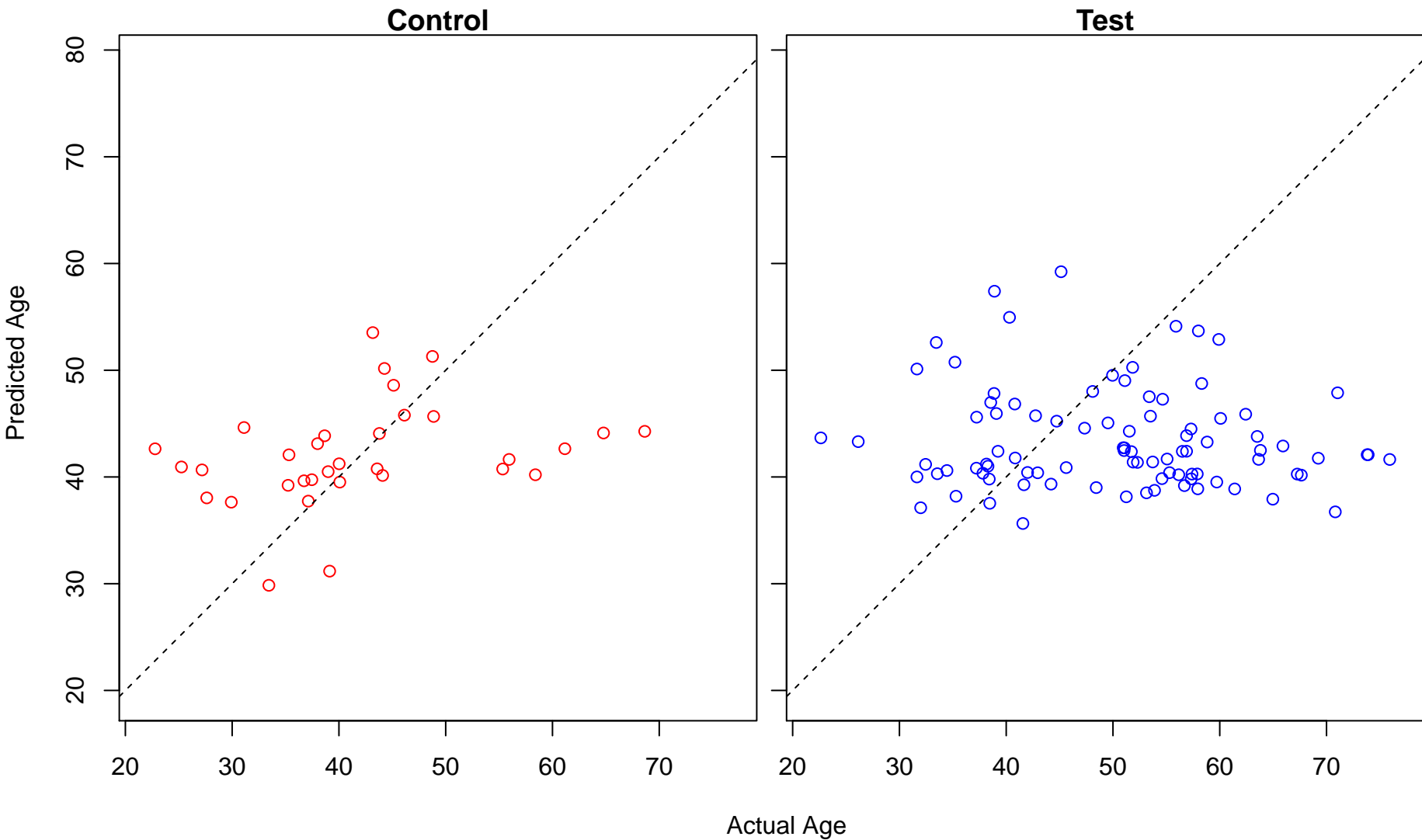
negative regulation of oligodendrocyte differentiation (Score: 0.331033)



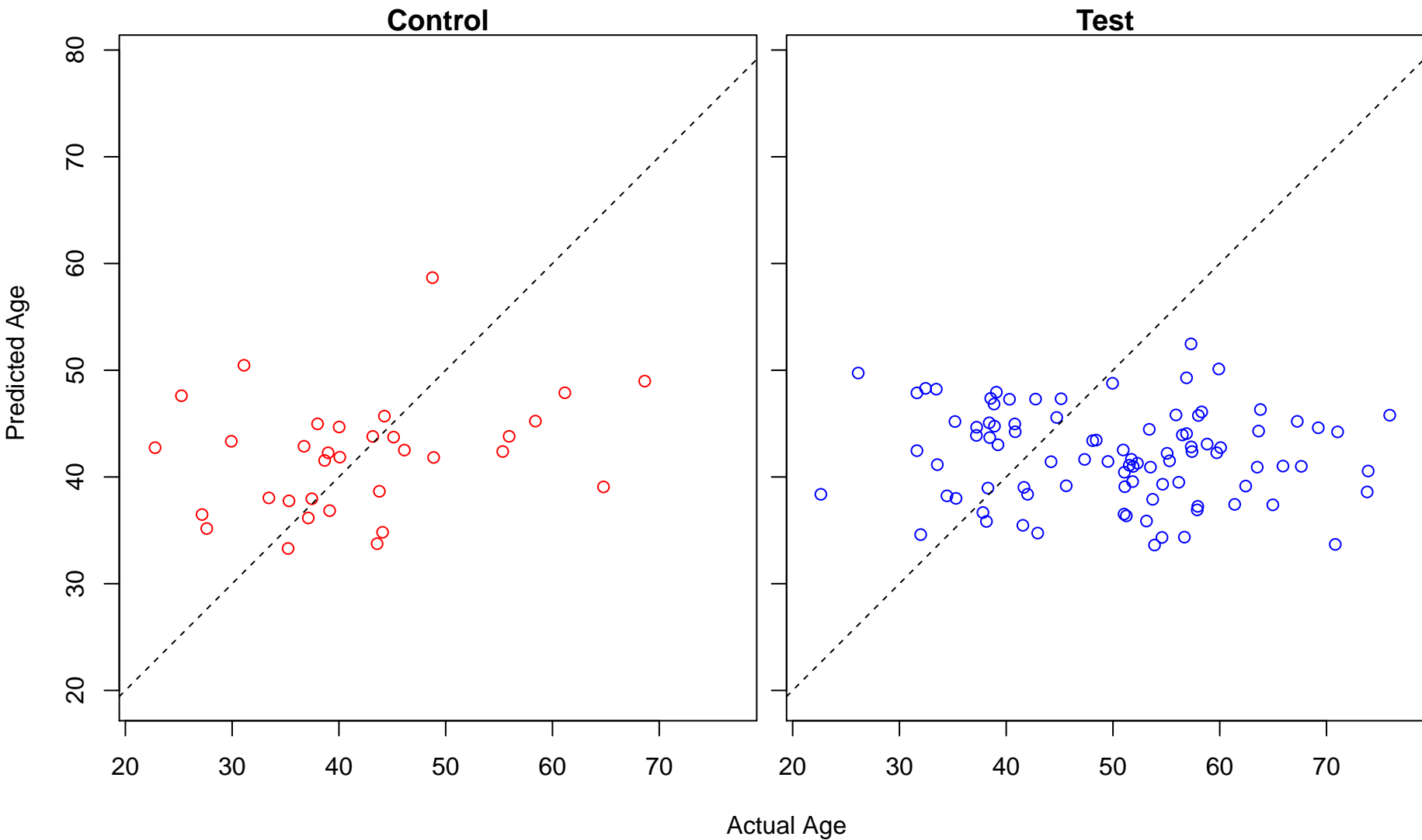
centrosome separation (Score: 0.329788)



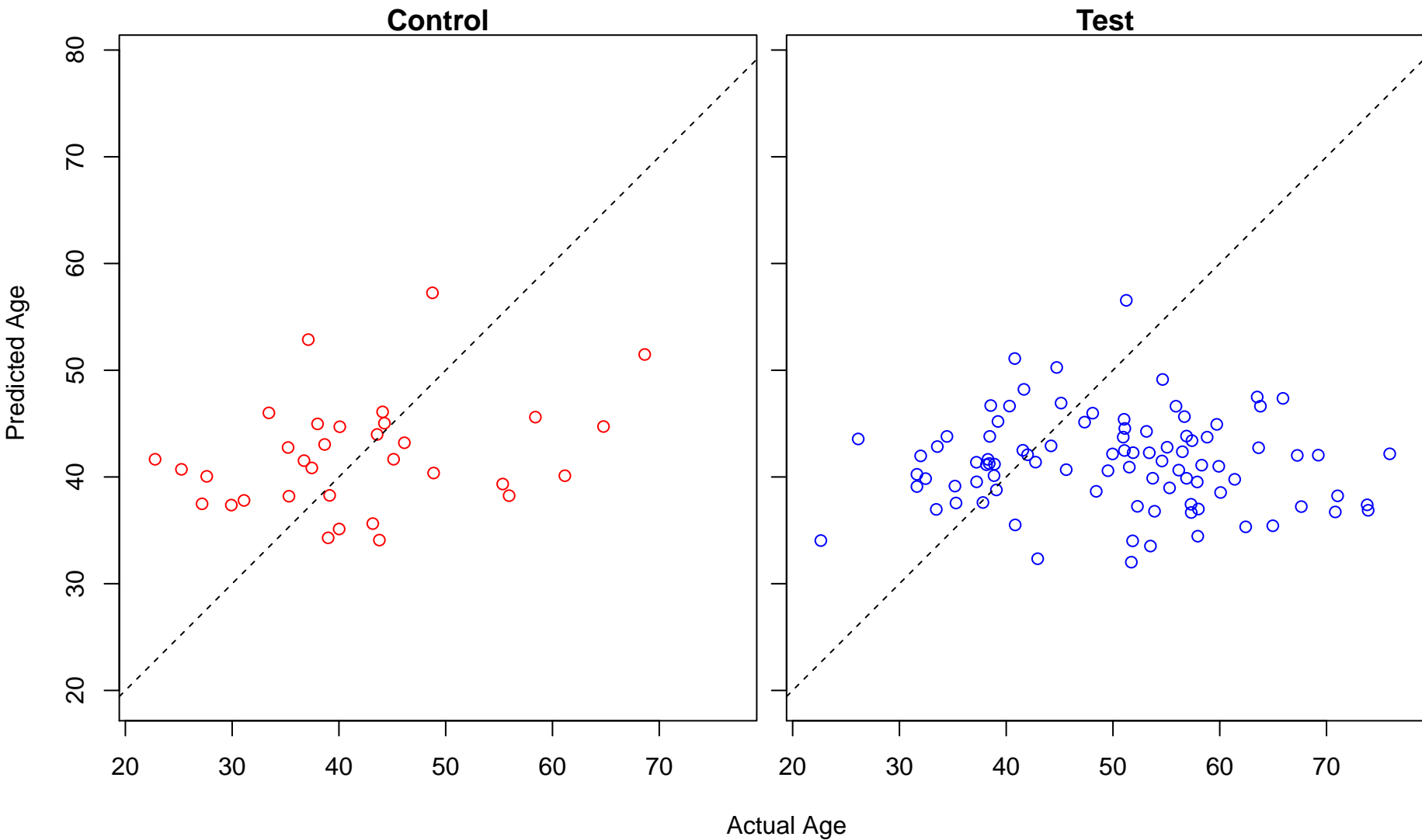
UDP-galactose transport (Score: 0.328107)



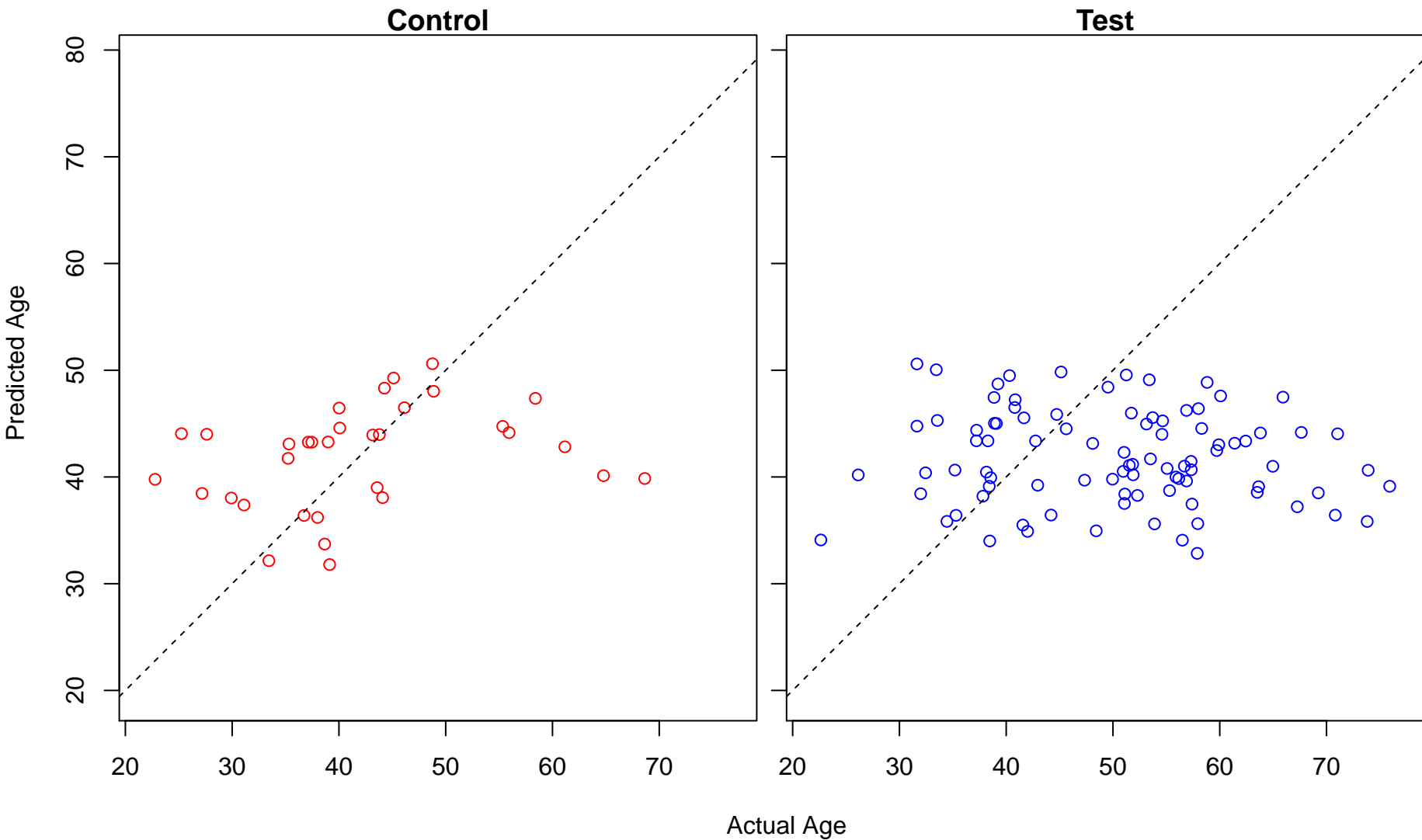
high-density lipoprotein particle clearance (Score: 0.327523)



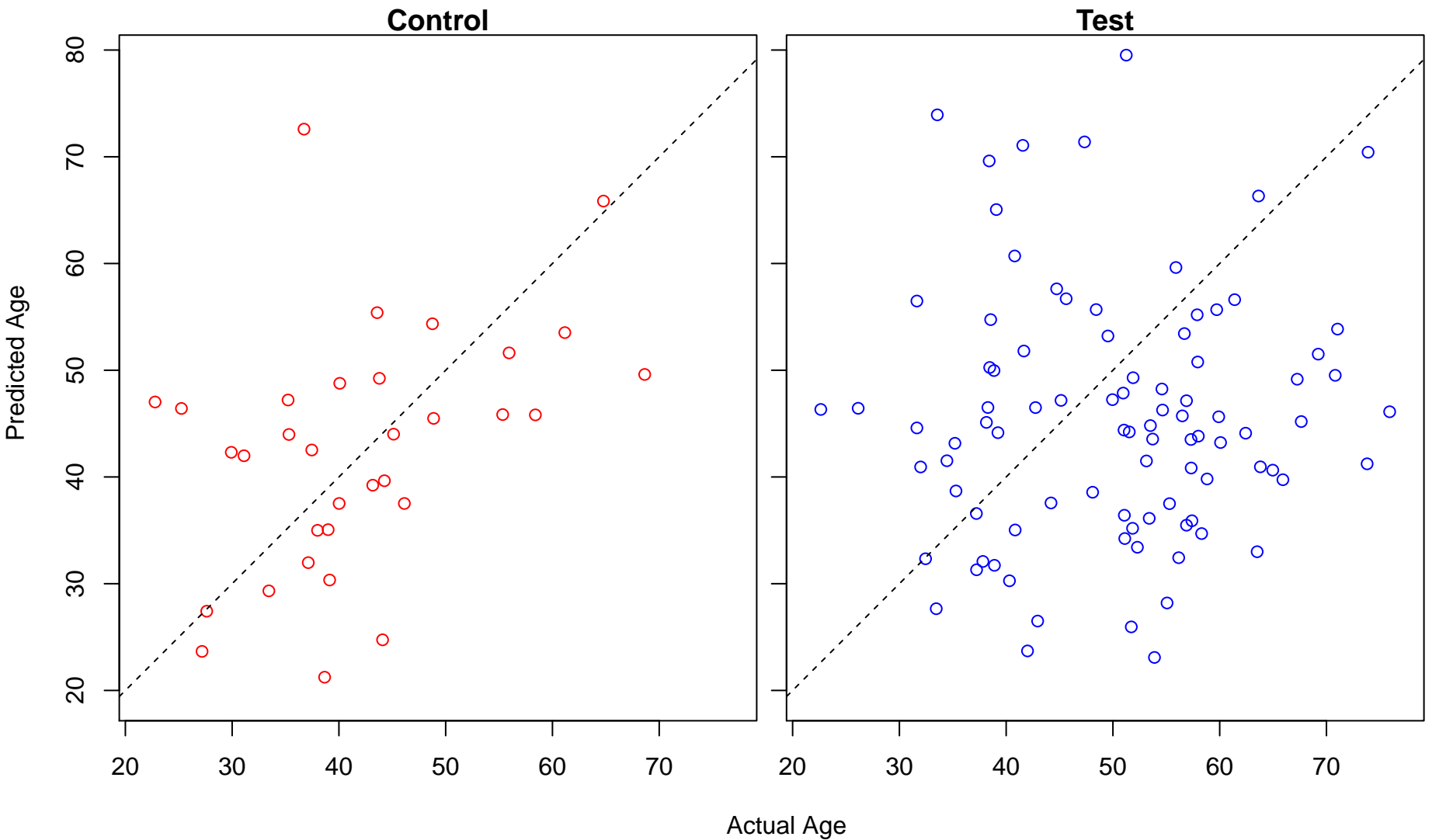
positive regulation of receptor recycling (Score: 0.327447)



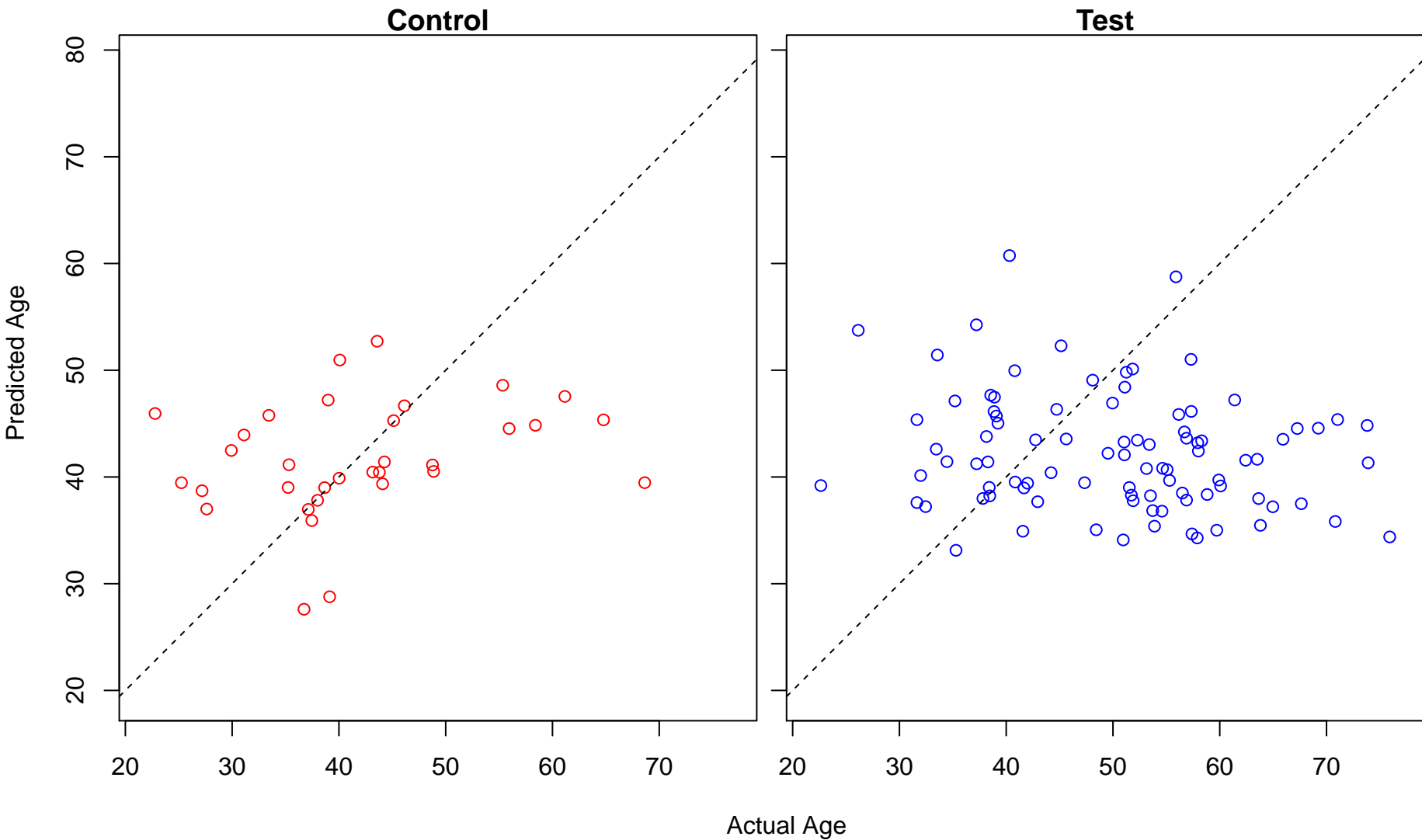
neuropeptide catabolic process (Score: 0.327221)



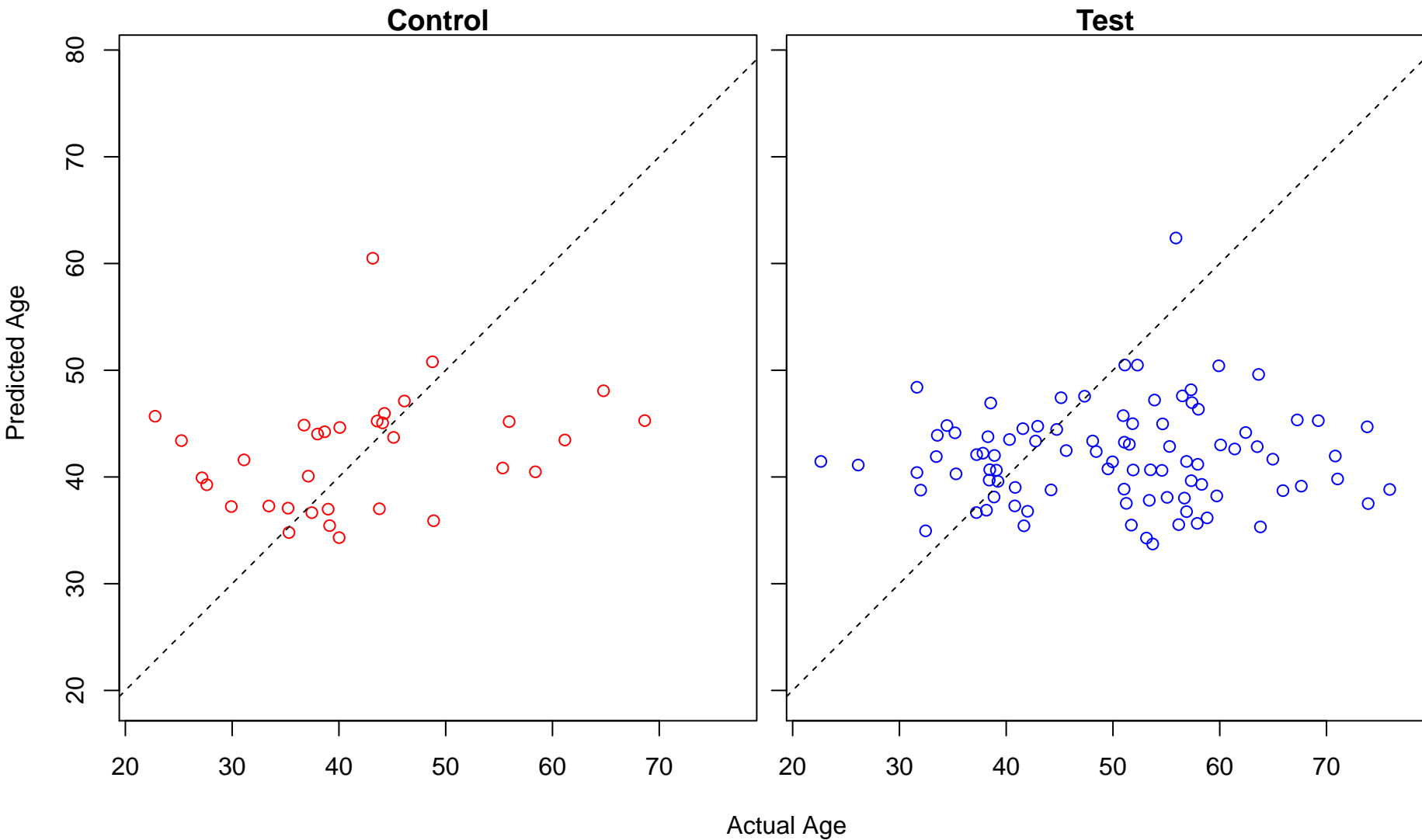
Immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily



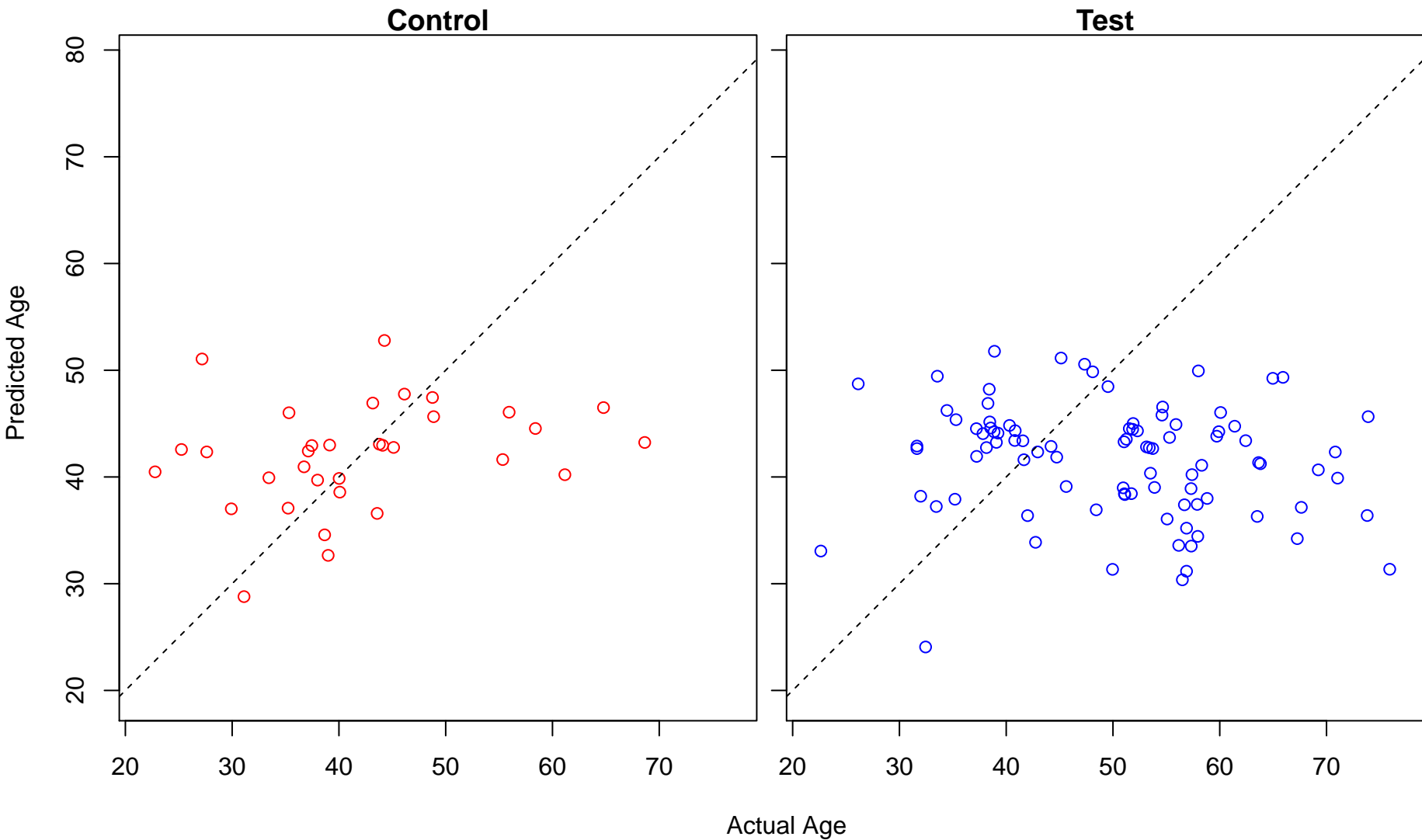
cellular ketone body metabolic process (Score: 0.322204)



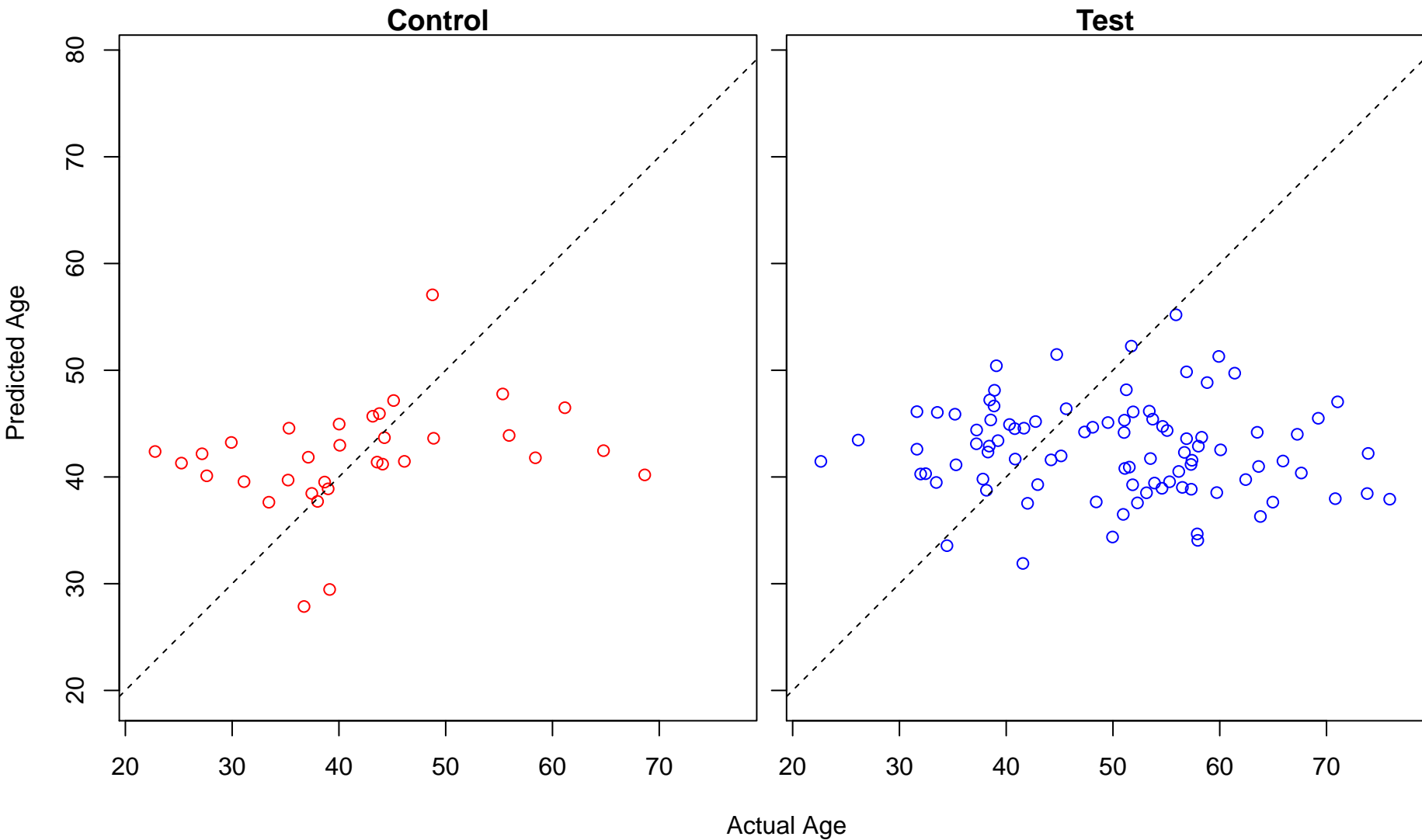
short-chain fatty acid biosynthetic process (Score: 0.320737)



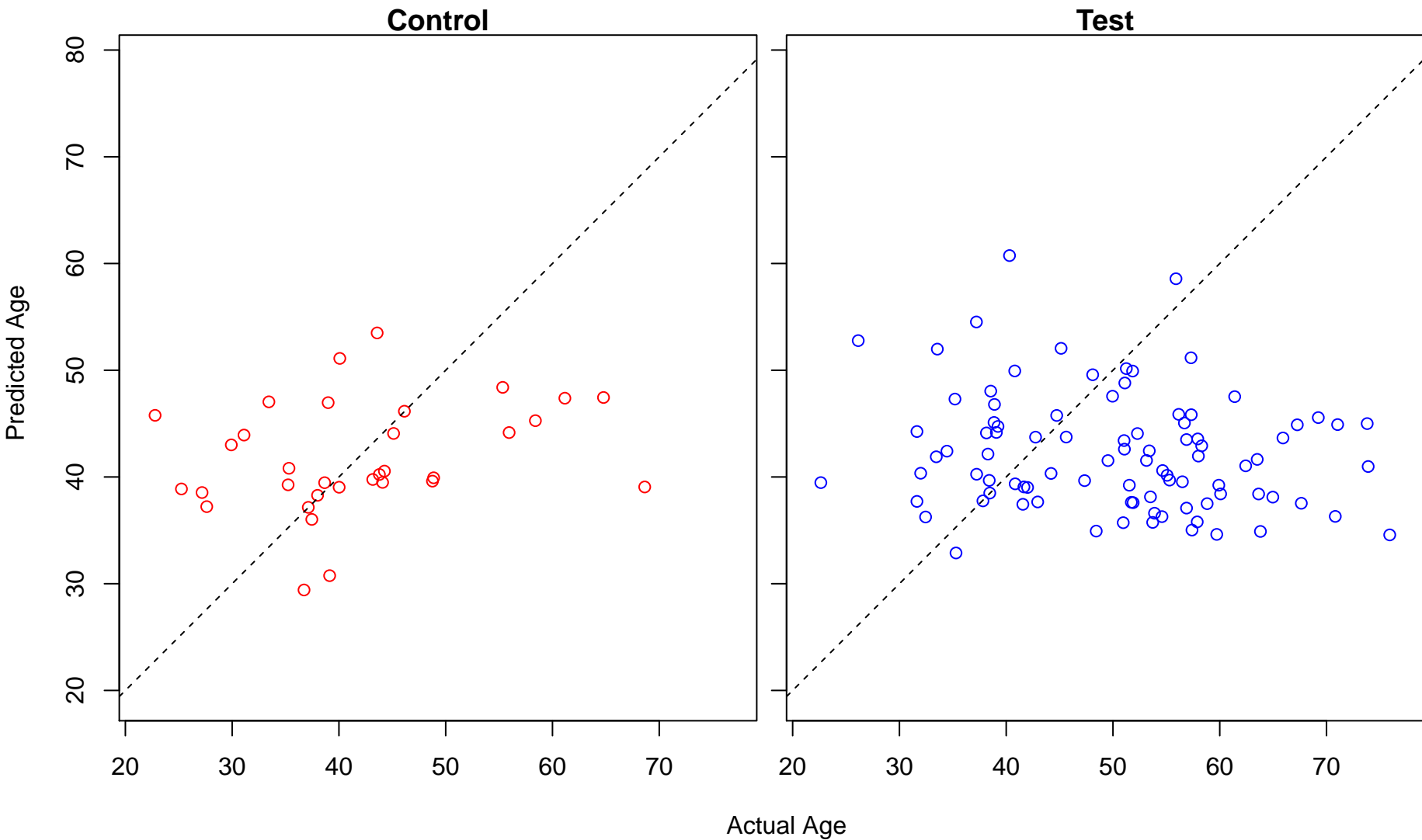
detection of diacyl bacterial lipopeptide (Score: 0.31644)



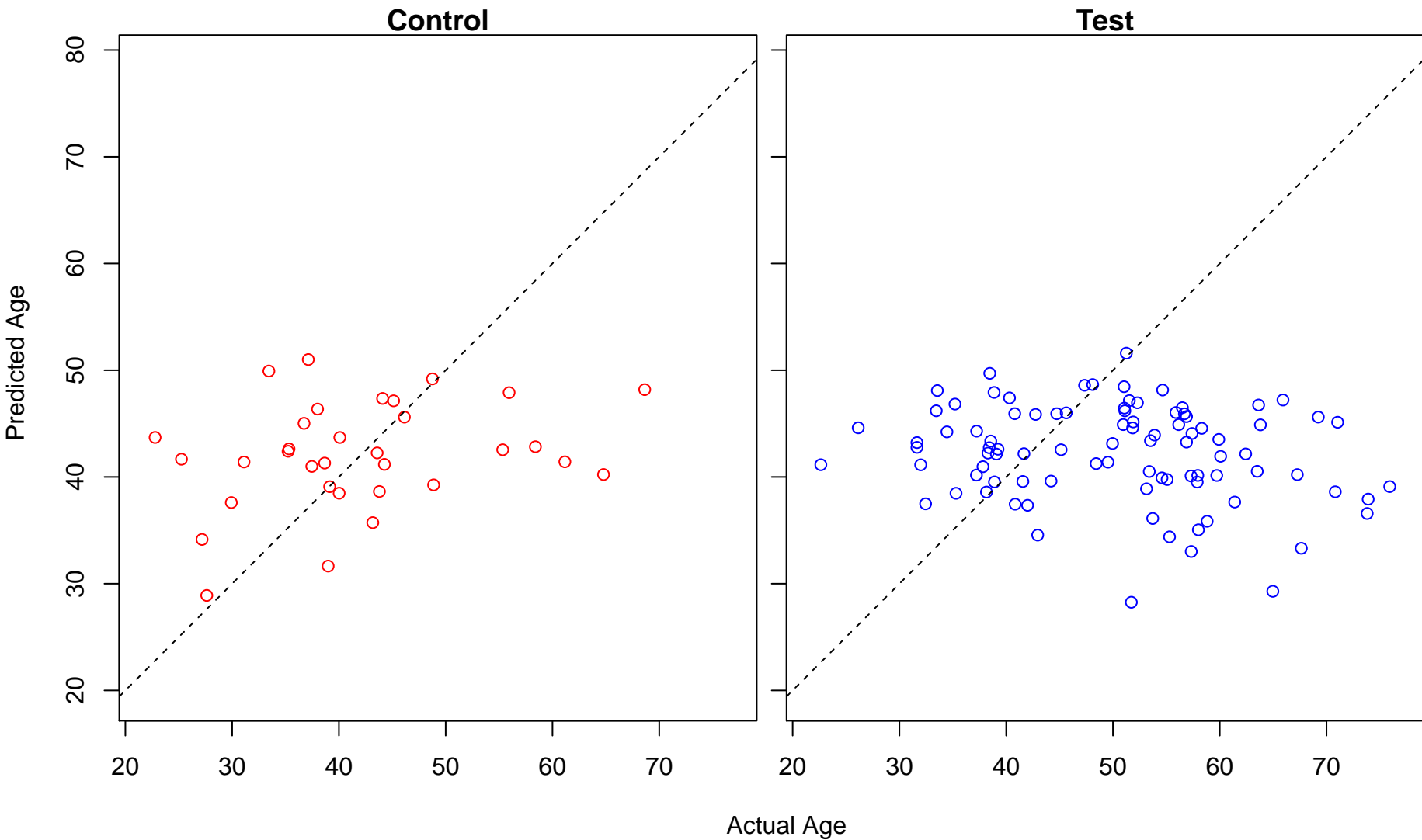
adenylate cyclase-inhibiting dopamine receptor signaling pathway (Score: 0.316567)



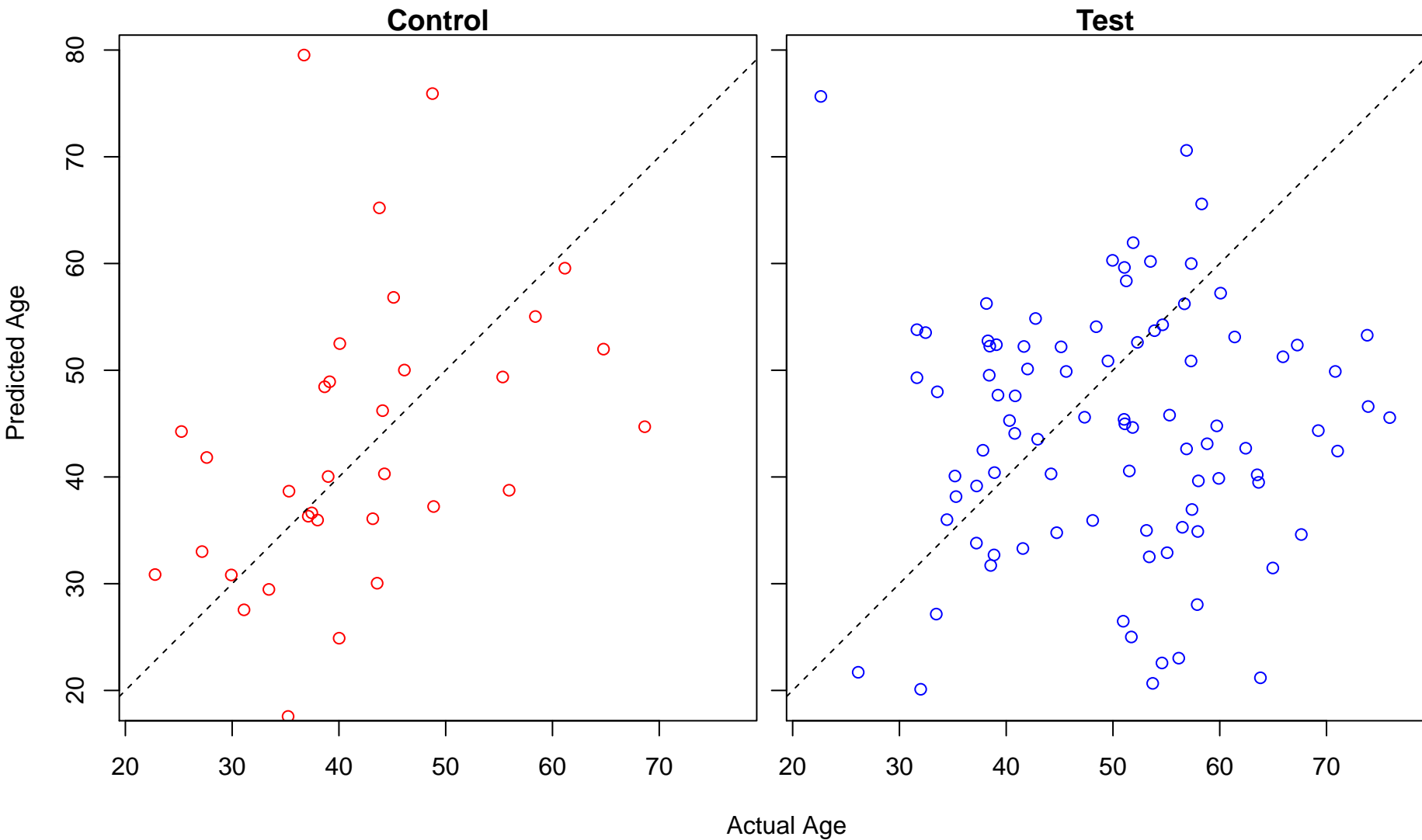
ketone body biosynthetic process (Score: 0.315721)



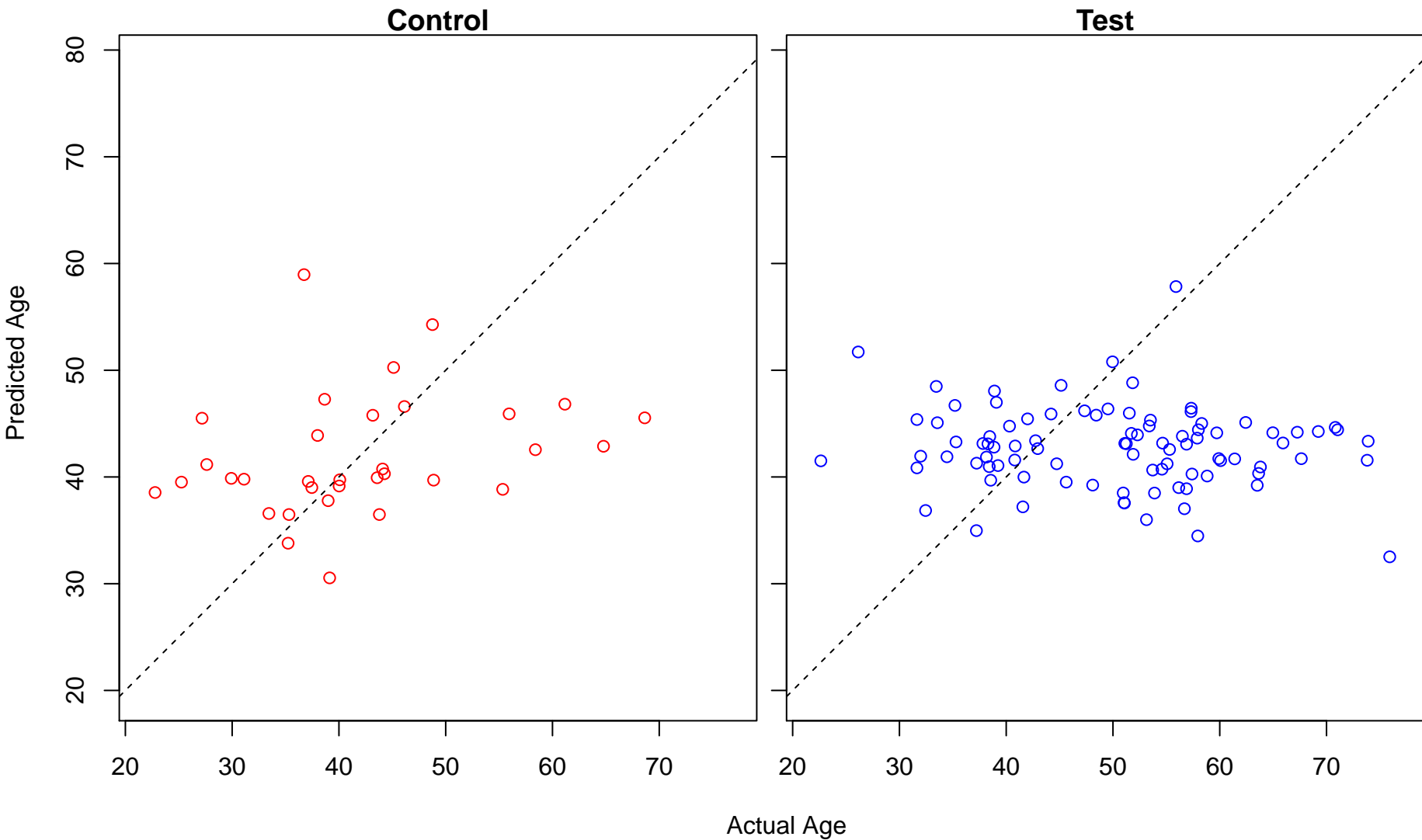
positive regulation of chromatin assembly or disassembly (Score: 0.314854)



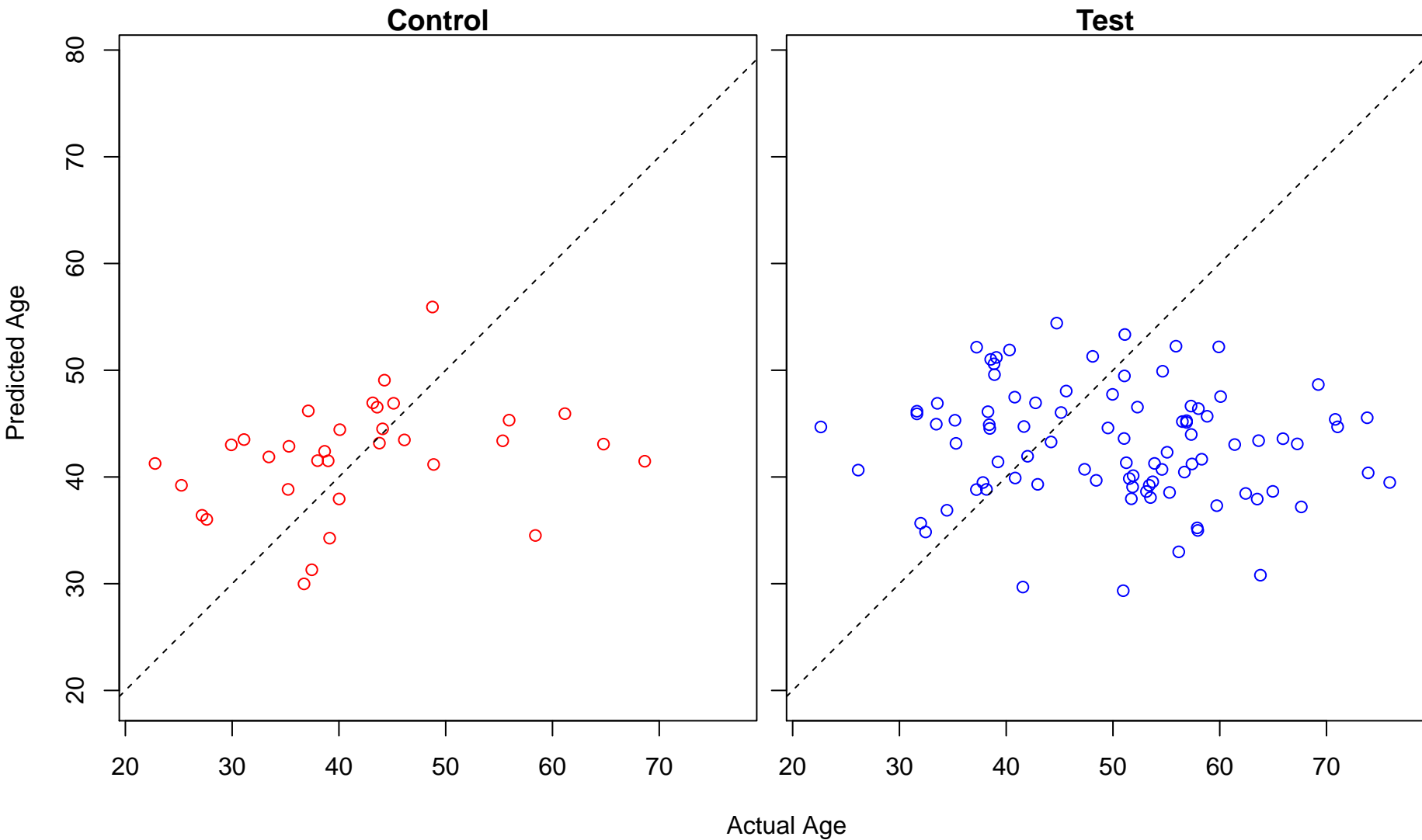
regulation of myeloid leukocyte mediated immunity (Score: 0.313098)



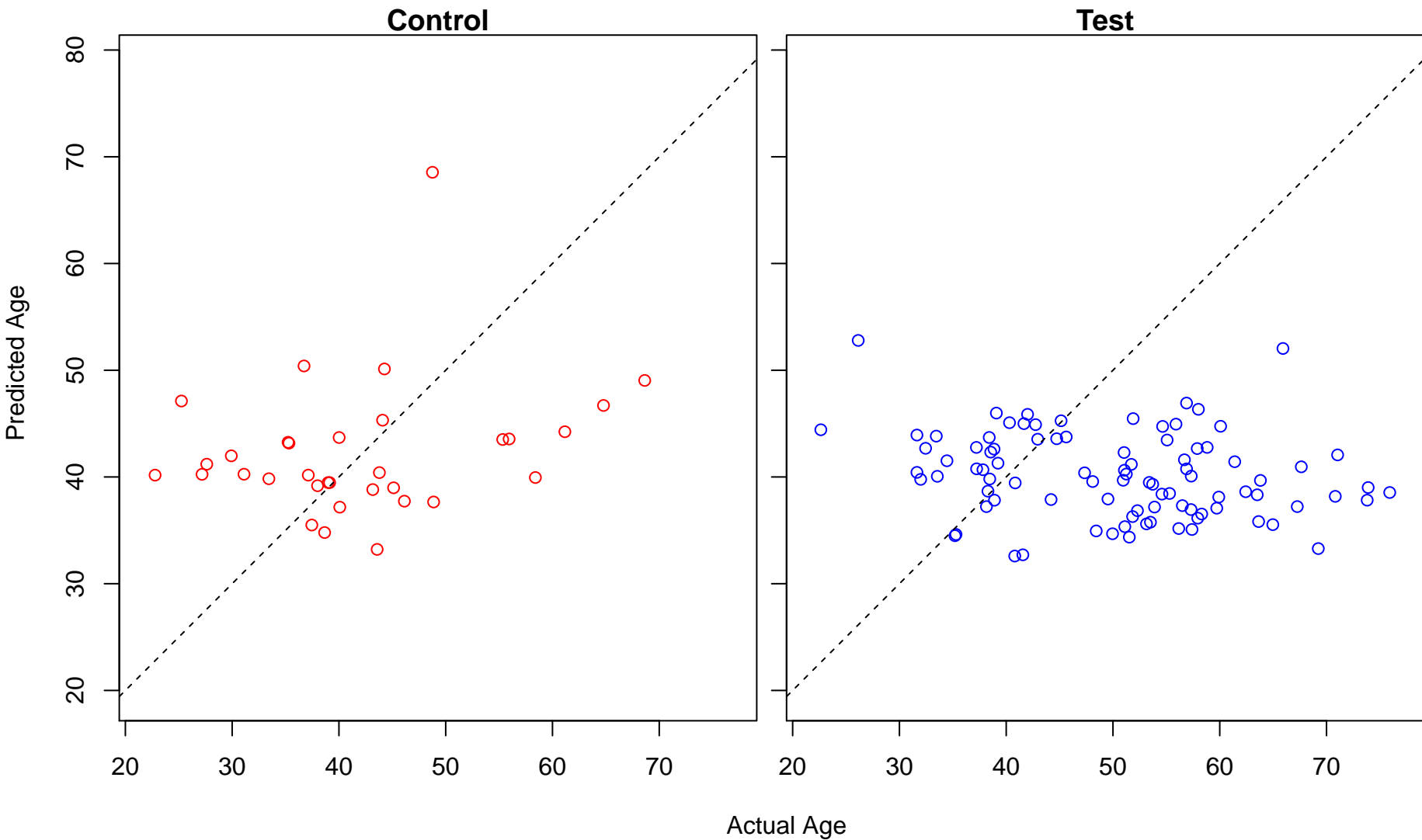
RNA surveillance (Score: 0.310842)



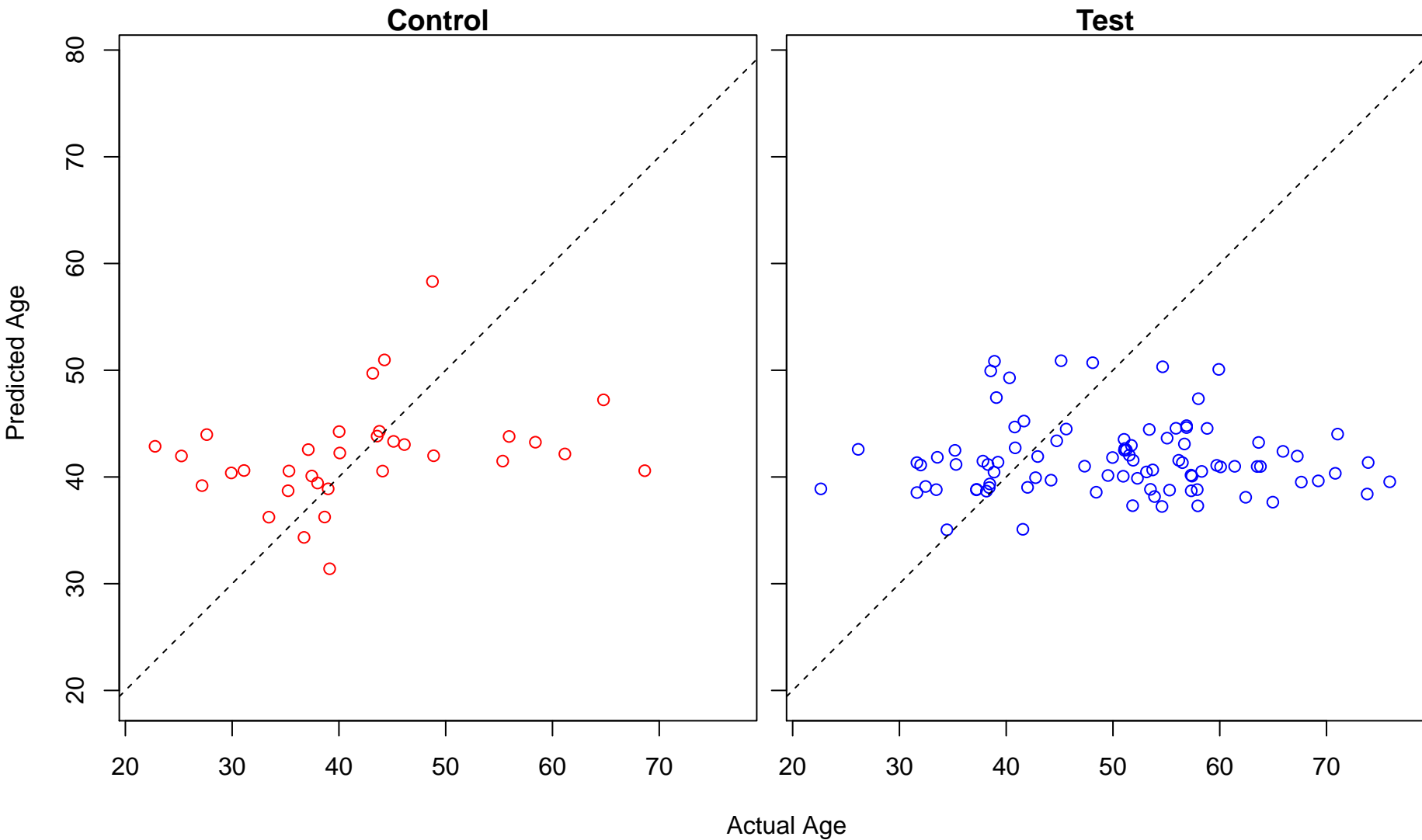
gas homeostasis (Score: 0.308031)



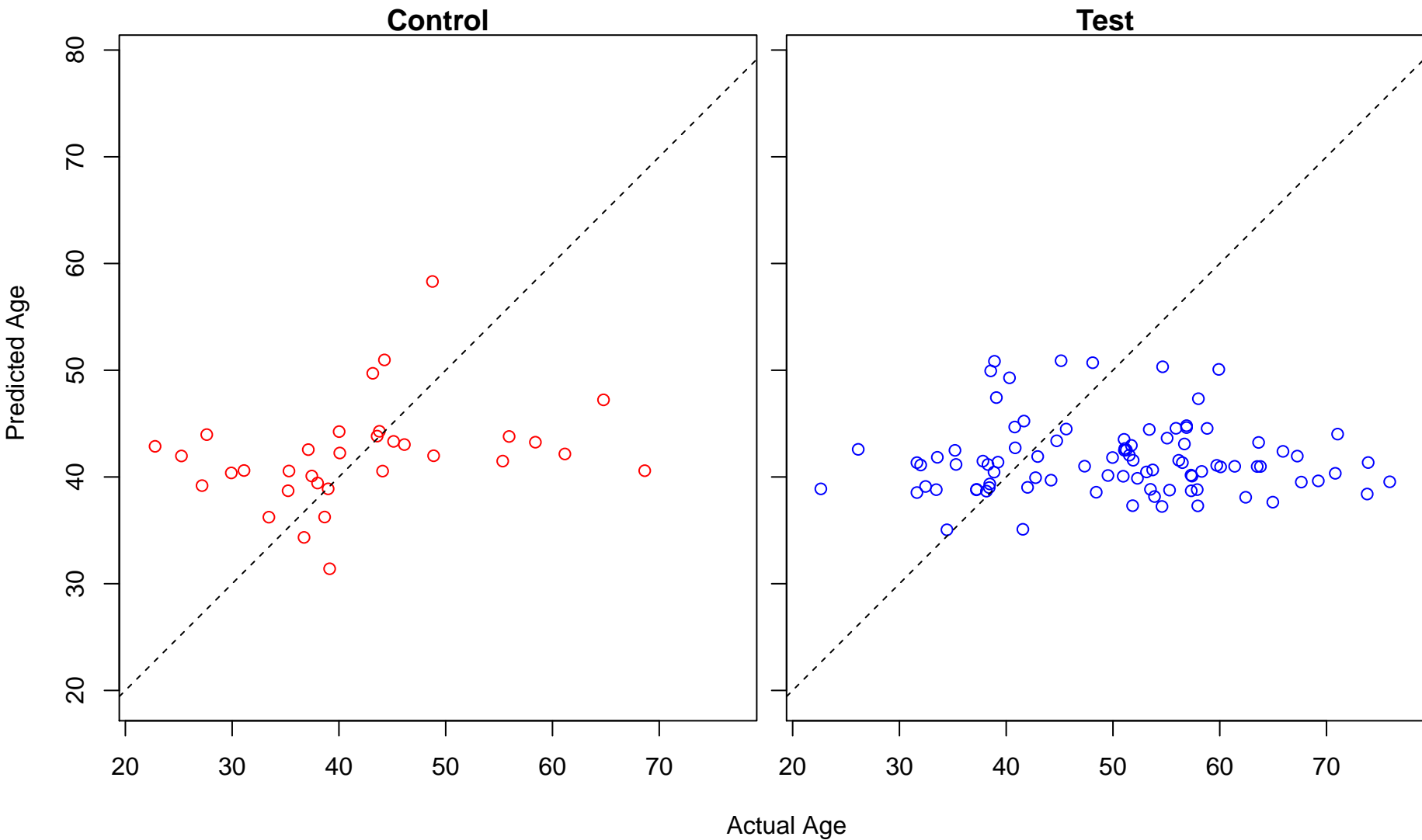
negative regulation of mitochondrial depolarization (Score: 0.307256)



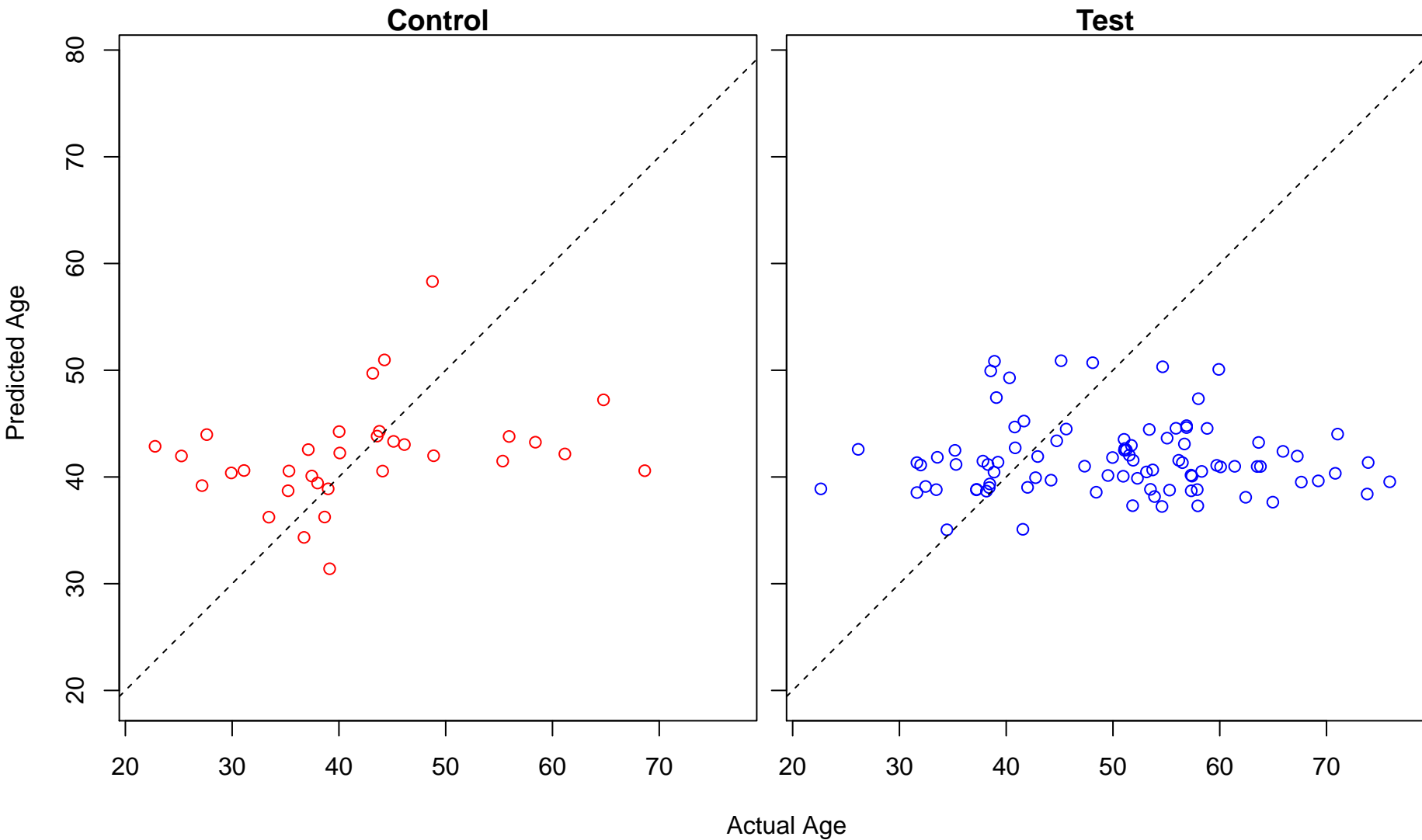
regulation of intracellular lipid transport (Score: 0.306714)



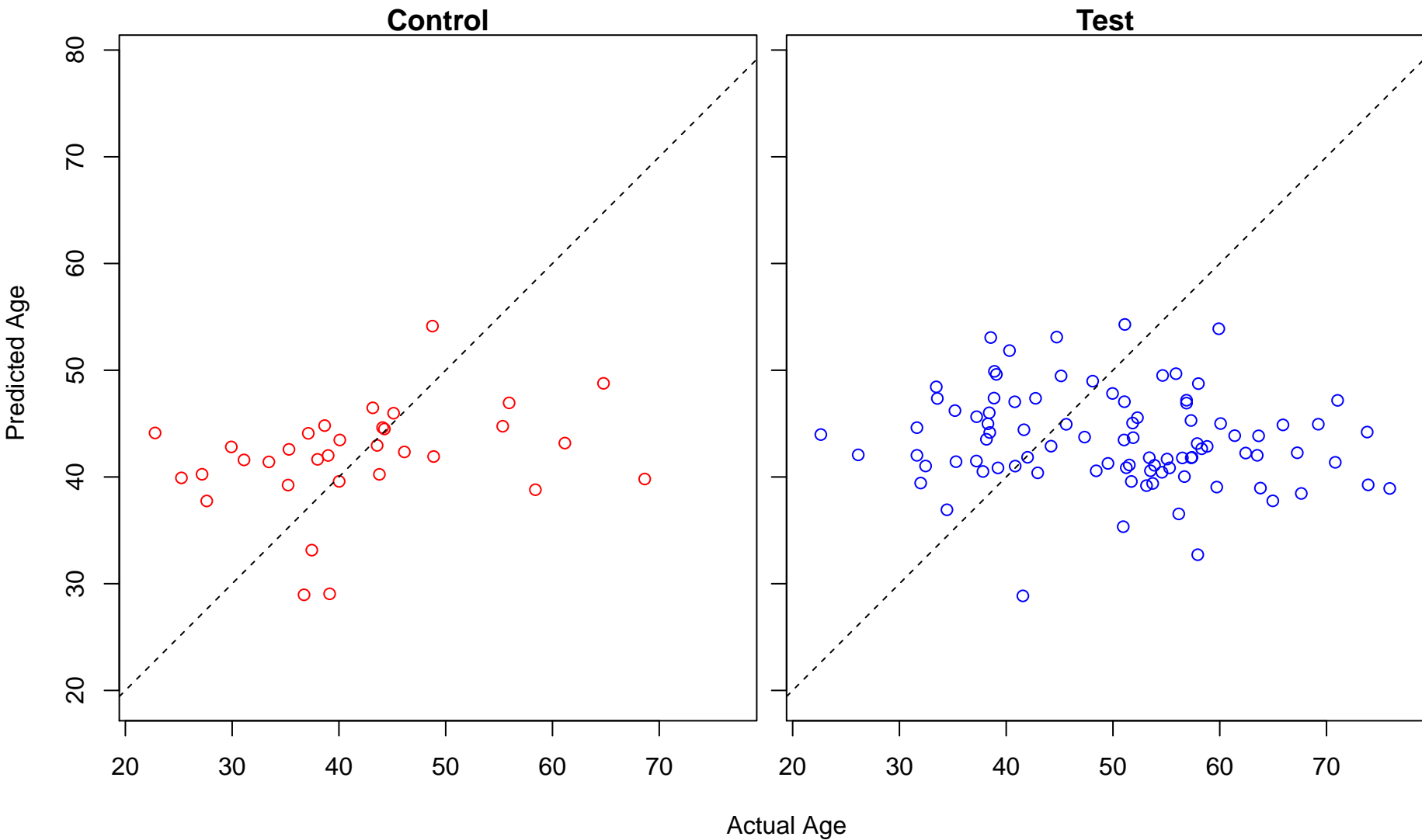
regulation of intracellular sterol transport (Score: 0.306714)



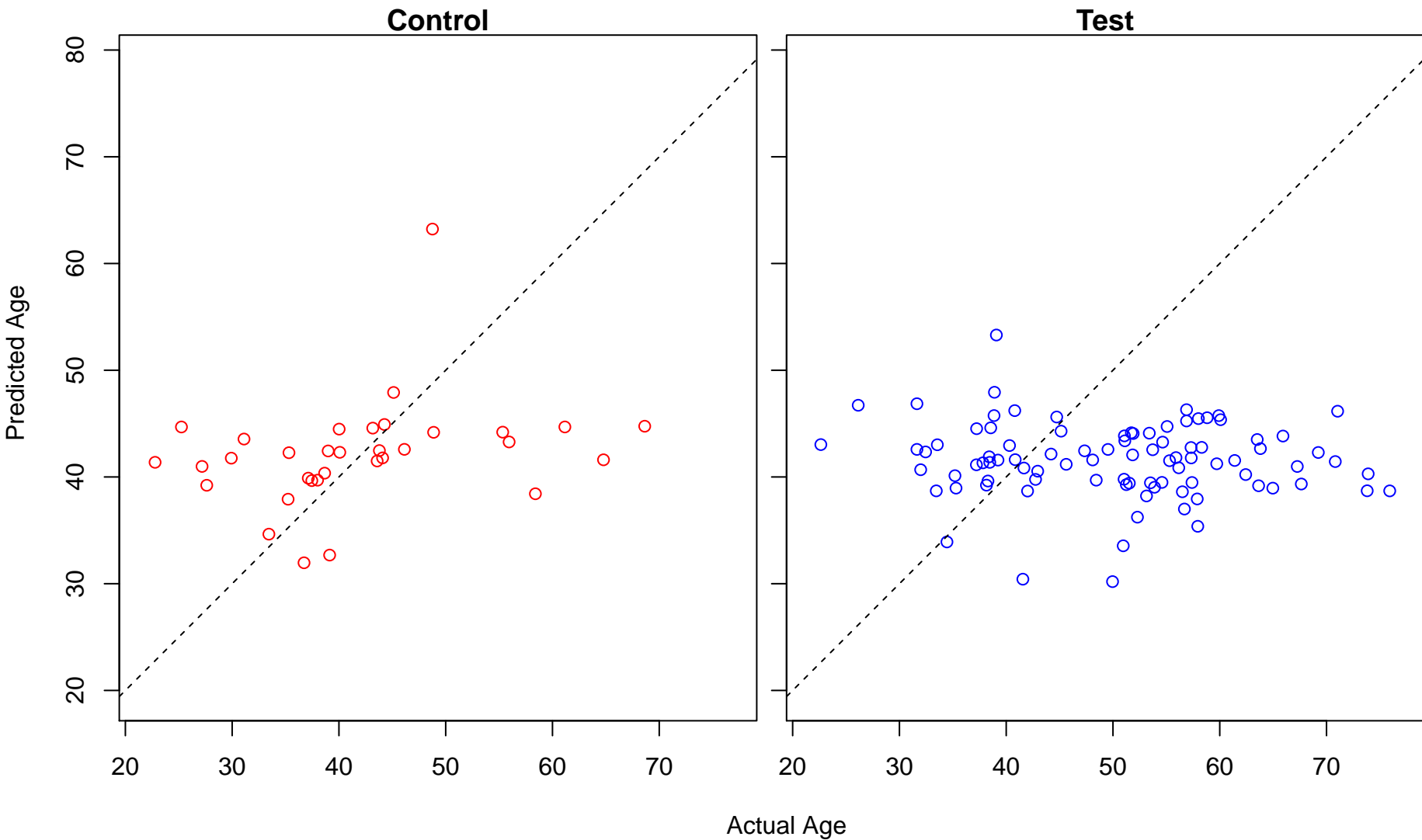
regulation of intracellular cholesterol transport (Score: 0.306714)



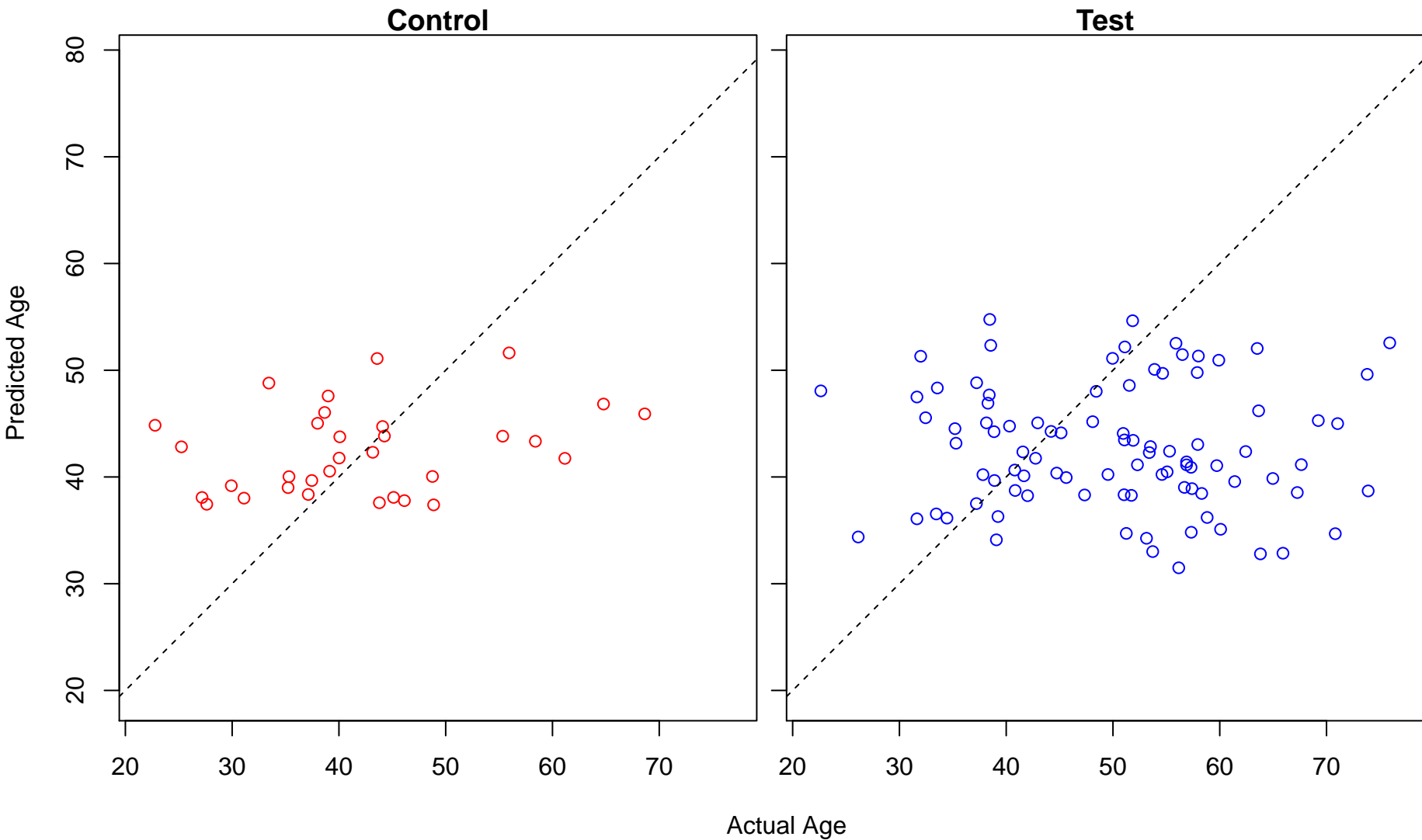
oxygen homeostasis (Score: 0.305603)



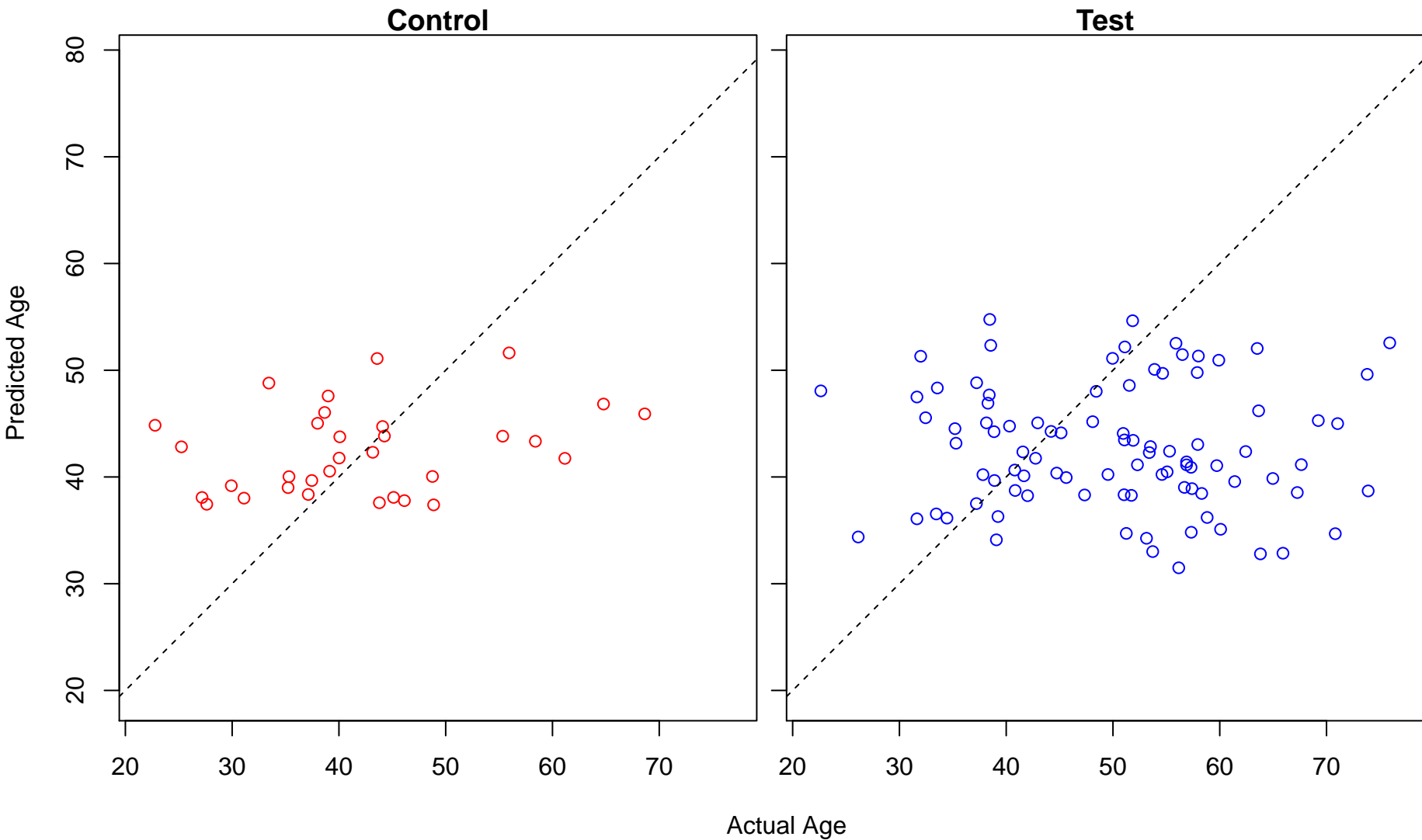
N-glycan processing (Score: 0.305163)



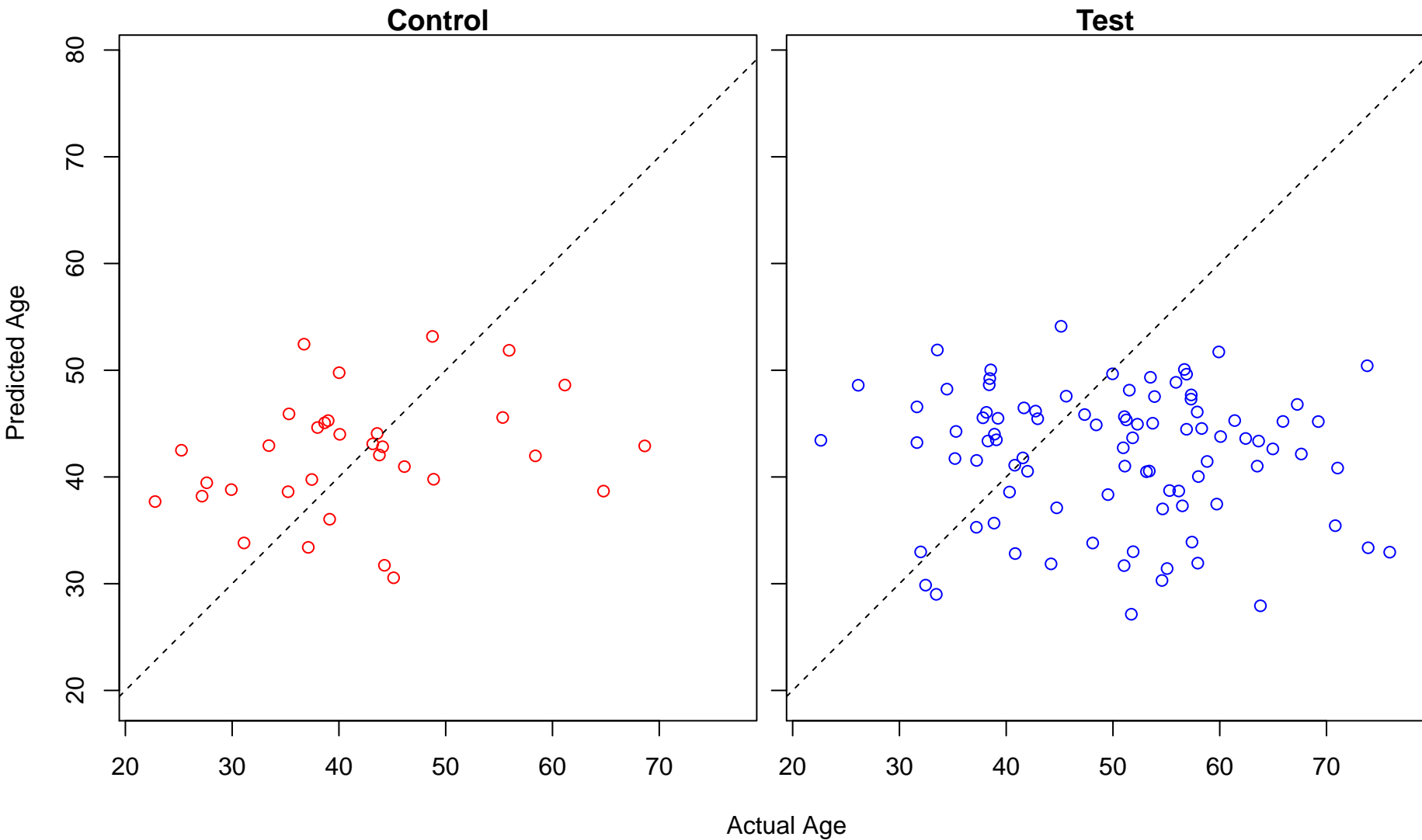
cellular response to stem cell factor stimulus (Score: 0.304475)



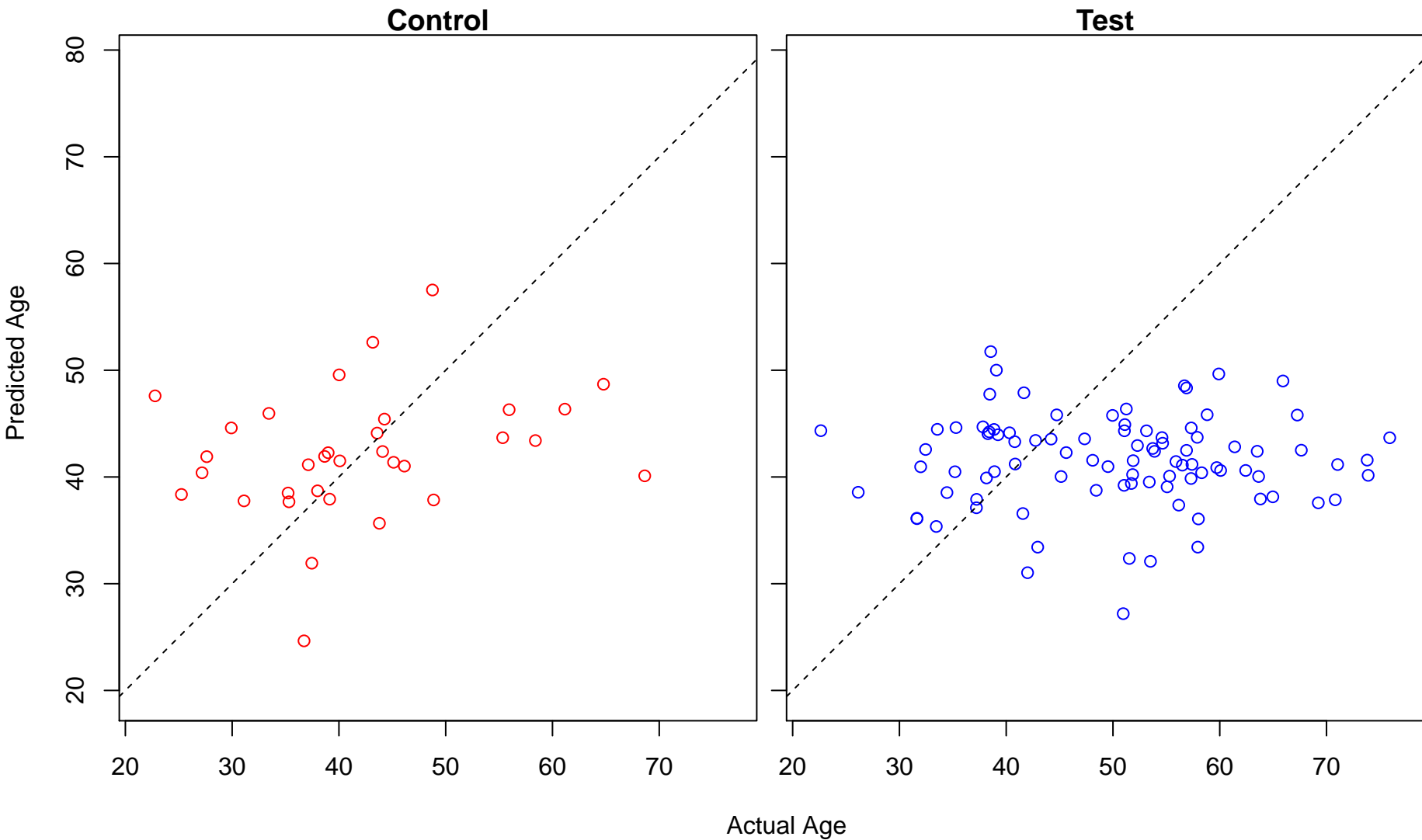
Kit signaling pathway (Score: 0.304475)



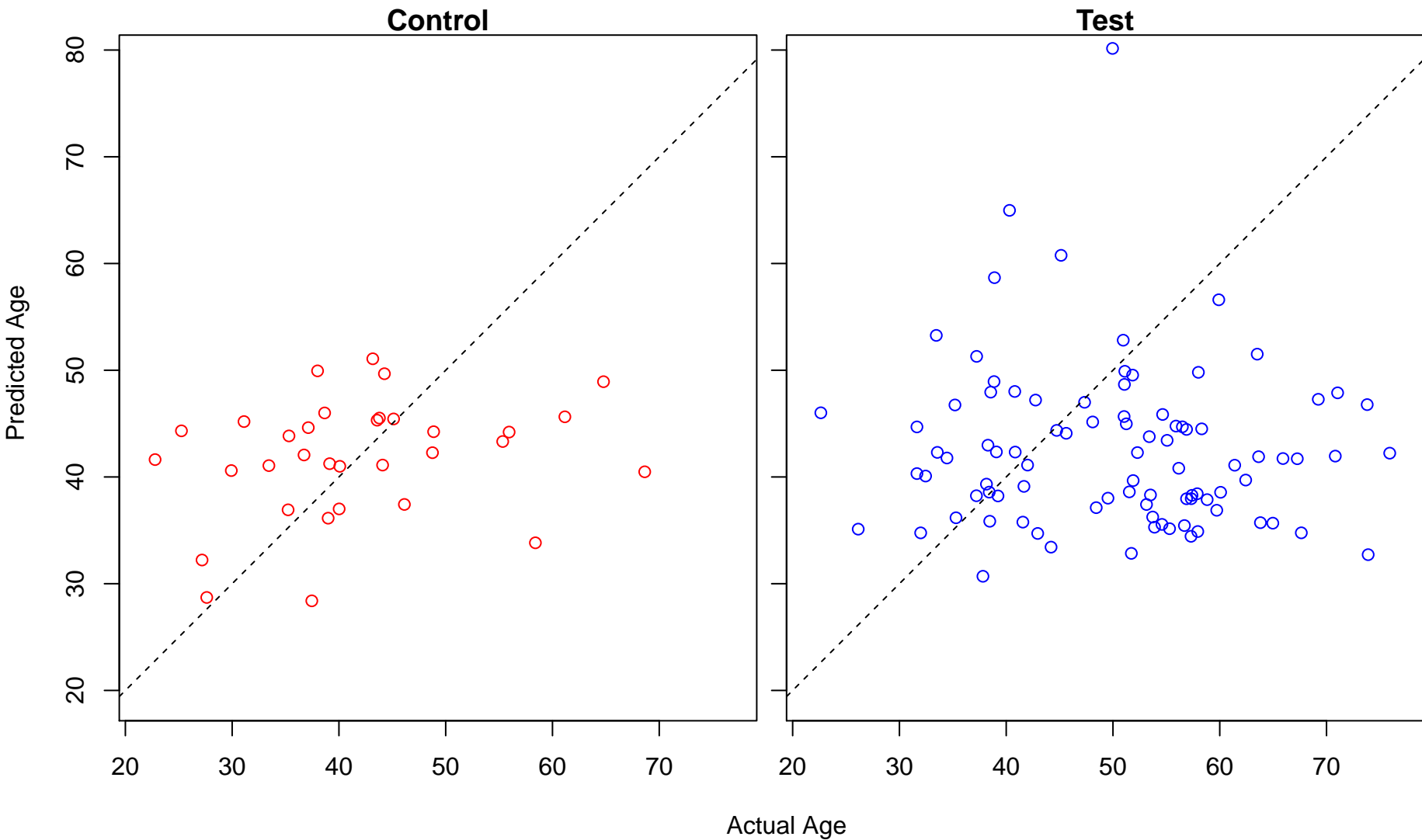
regulation of CD8-positive, alpha-beta T cell proliferation (Score: 0.302860)



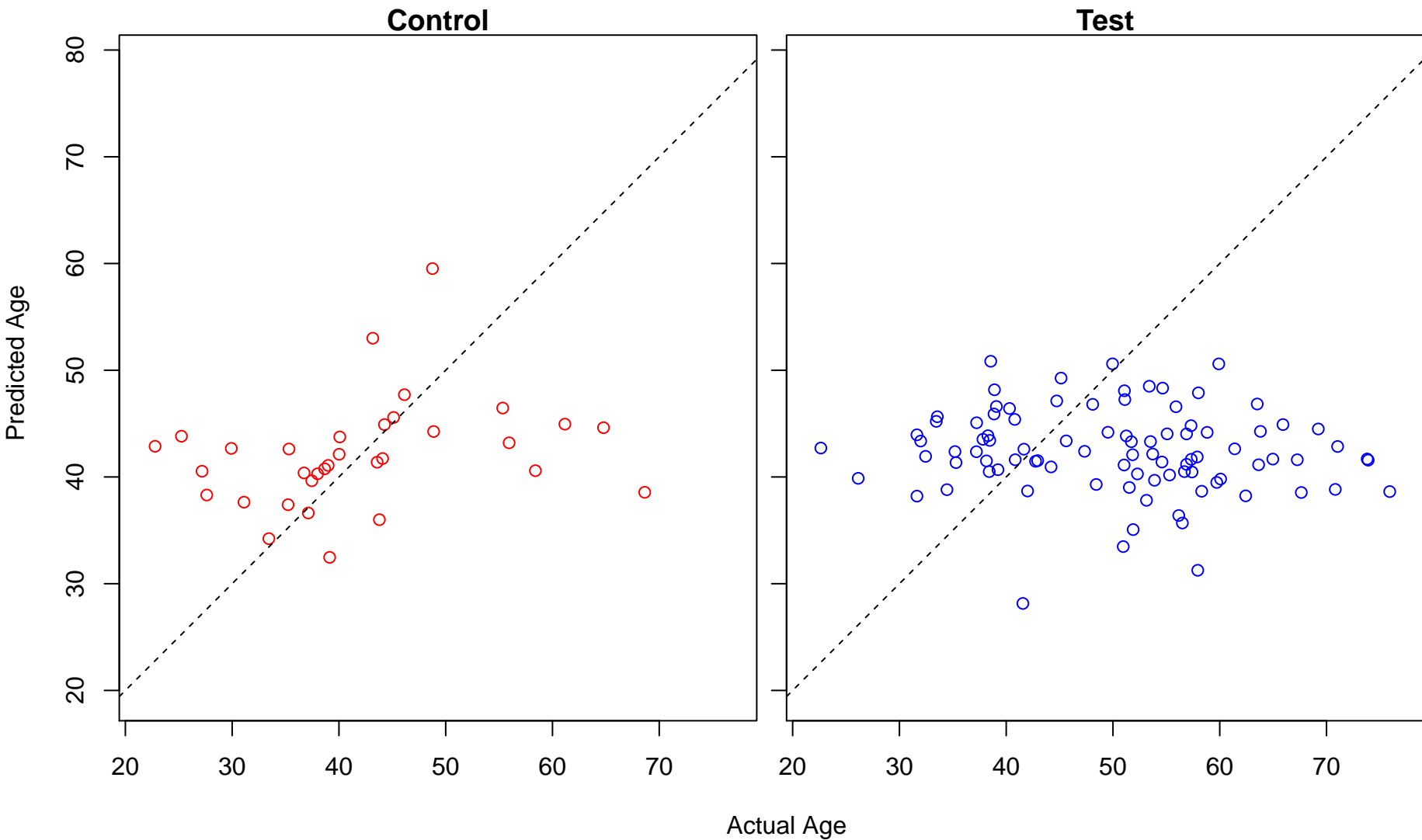
negative regulation of chemokine biosynthetic process (Score: 0.302275)



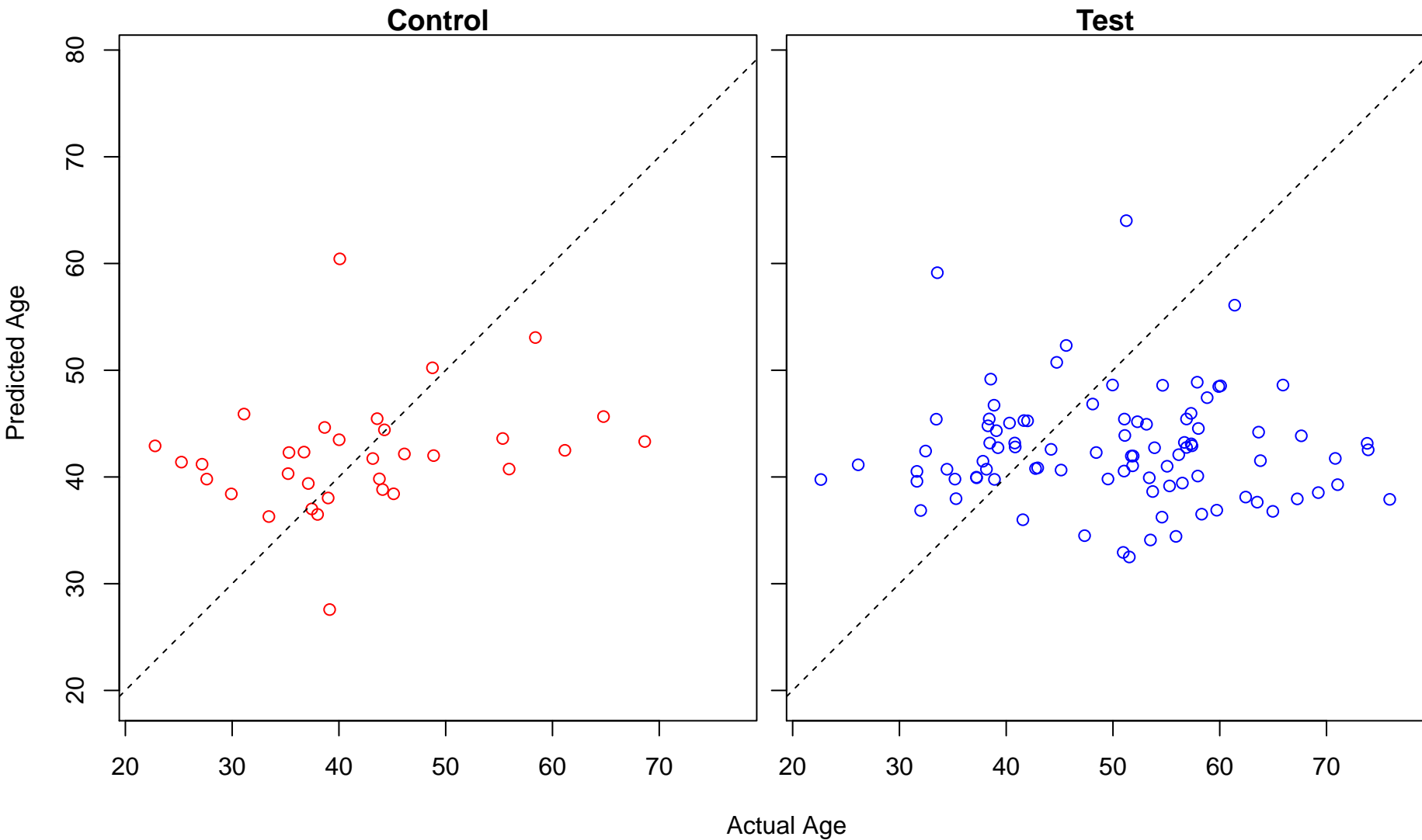
regulation of isotype switching to IgA isotypes (Score: 0.301632)



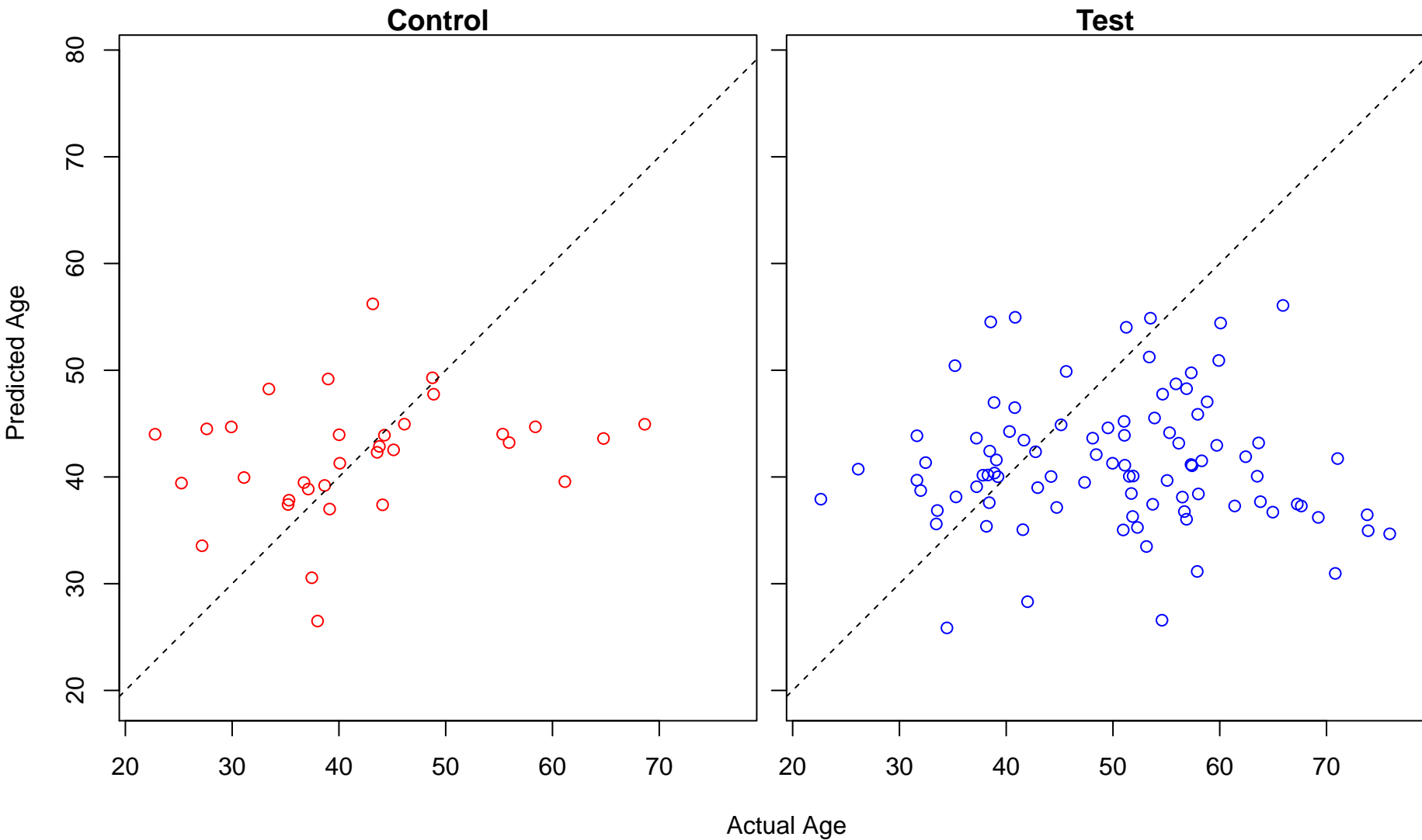
kinetochore assembly (Score: 0.300323)



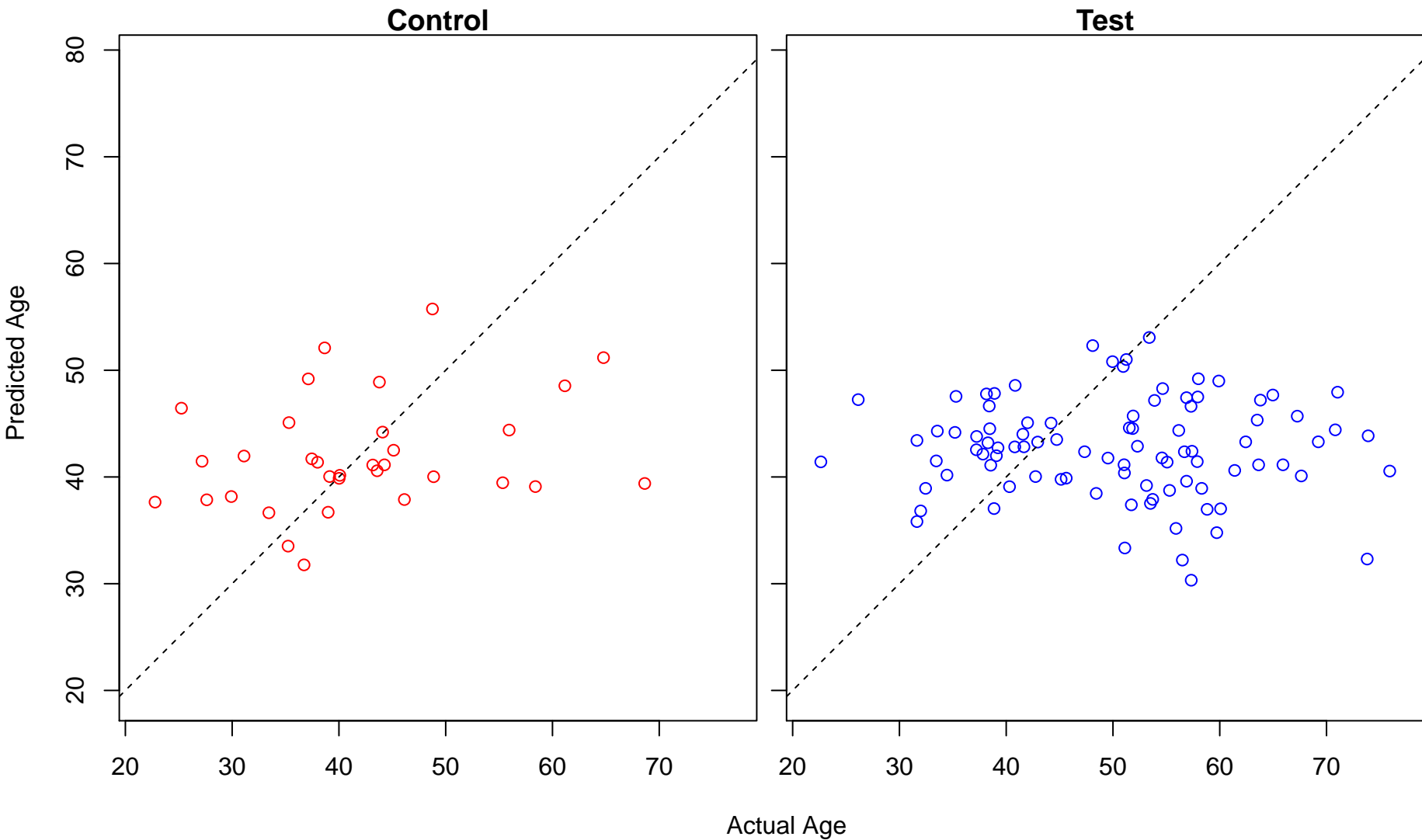
regulation of RNA polymerase II transcriptional preinitiation complex assembly (Score: 0.299891)



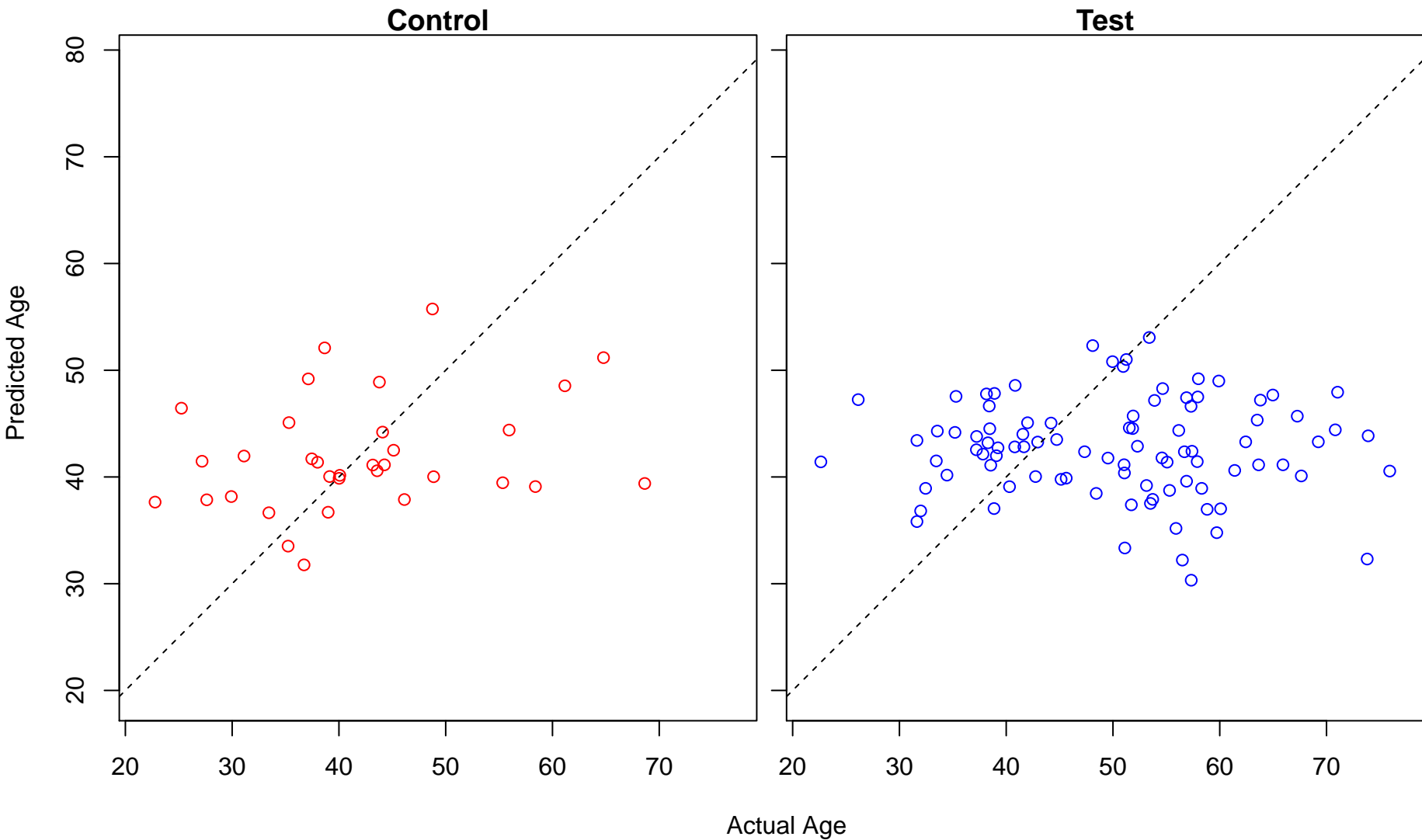
regulation of guanylate cyclase activity (Score: 0.299484)



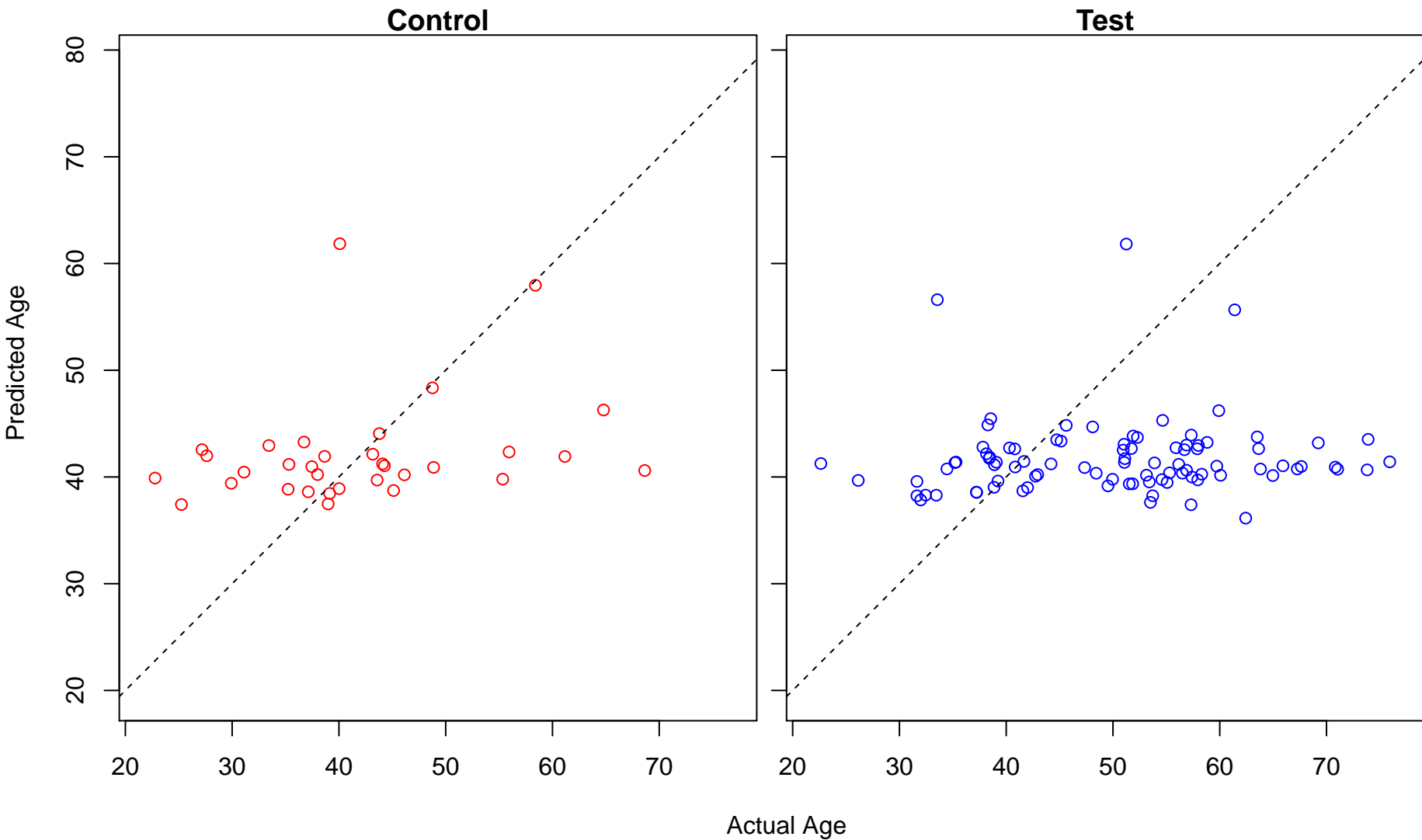
ascending aorta development (Score: 0.298829)



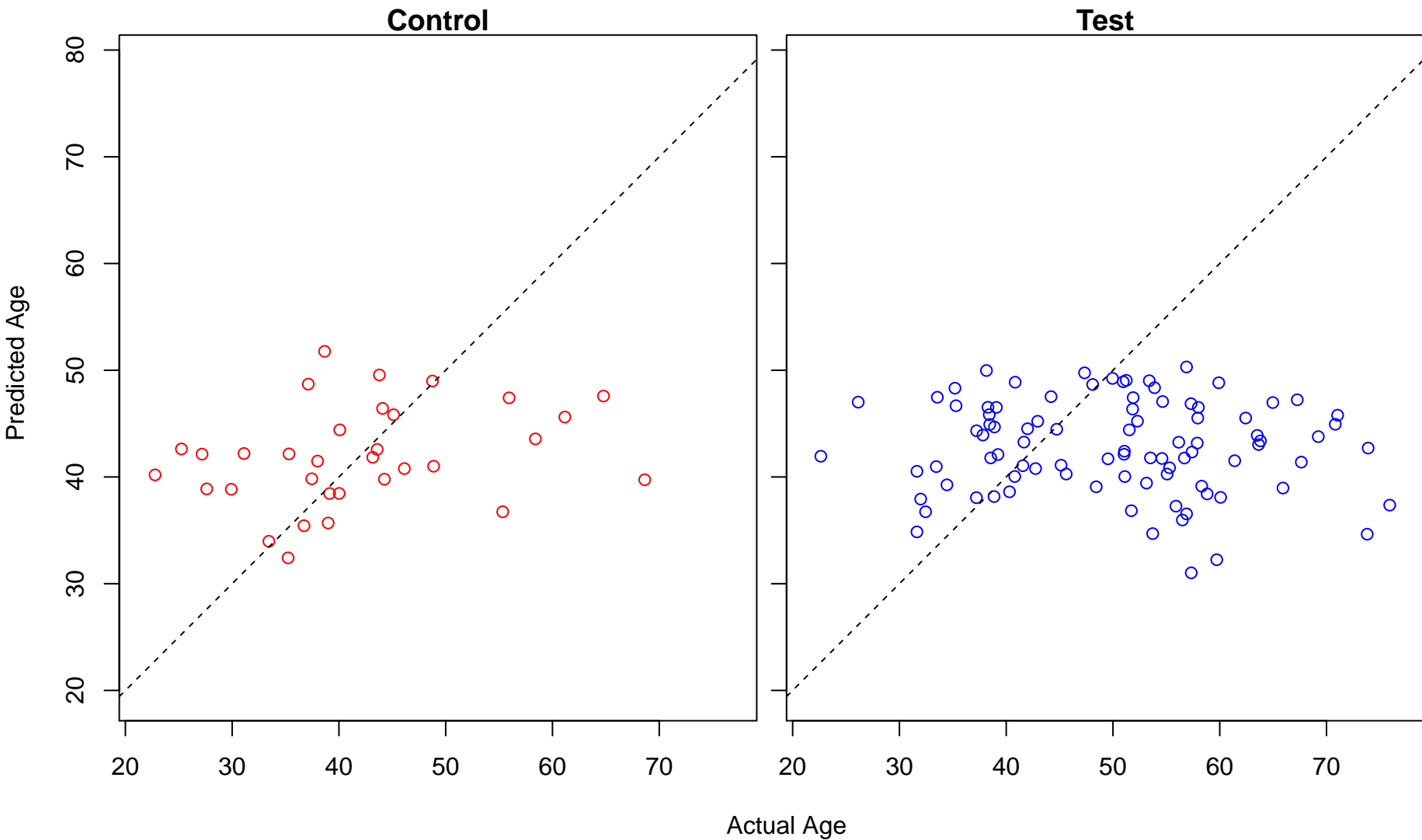
ascending aorta morphogenesis (Score: 0.298829)



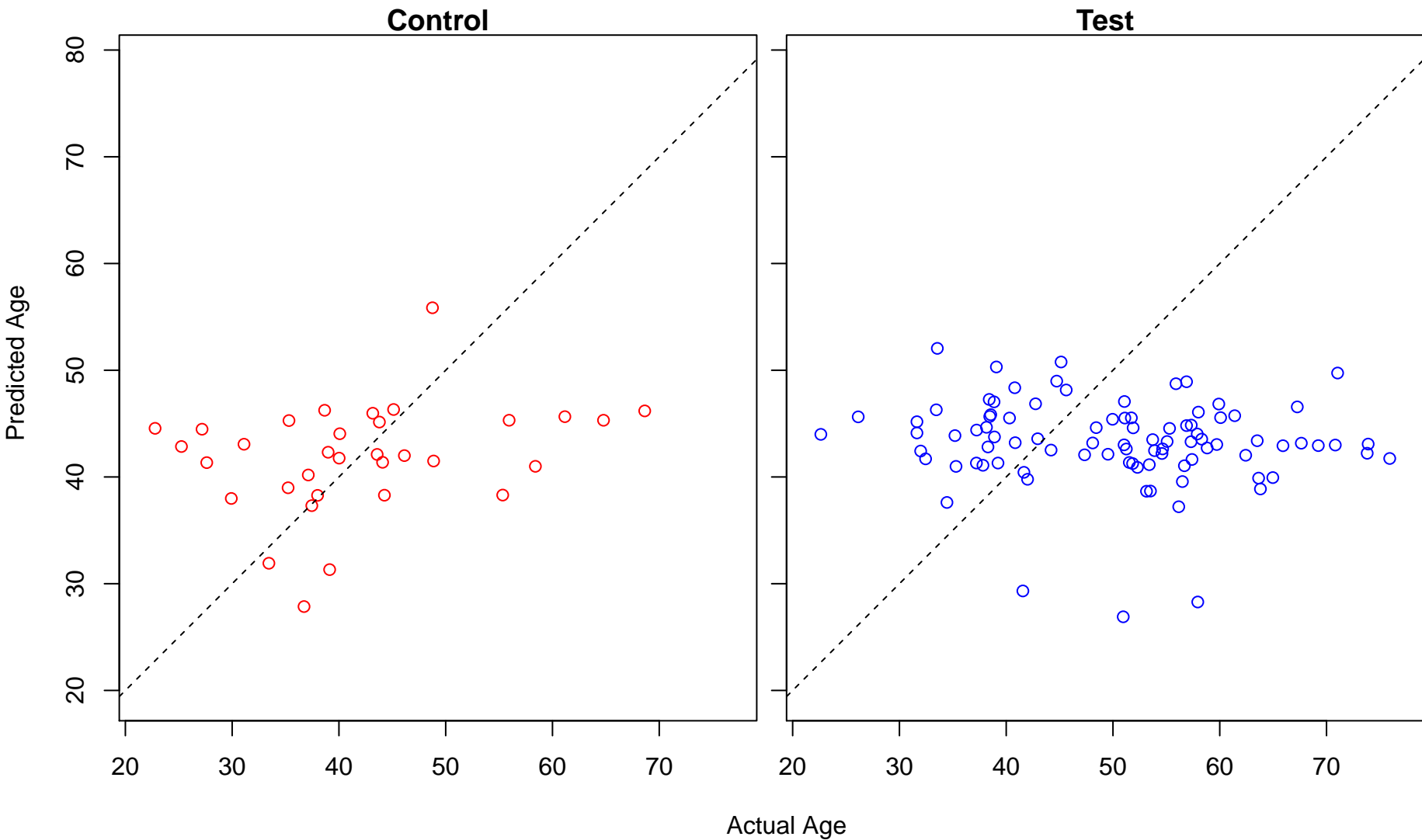
positive regulation of glial cell proliferation (Score: 0.294150)



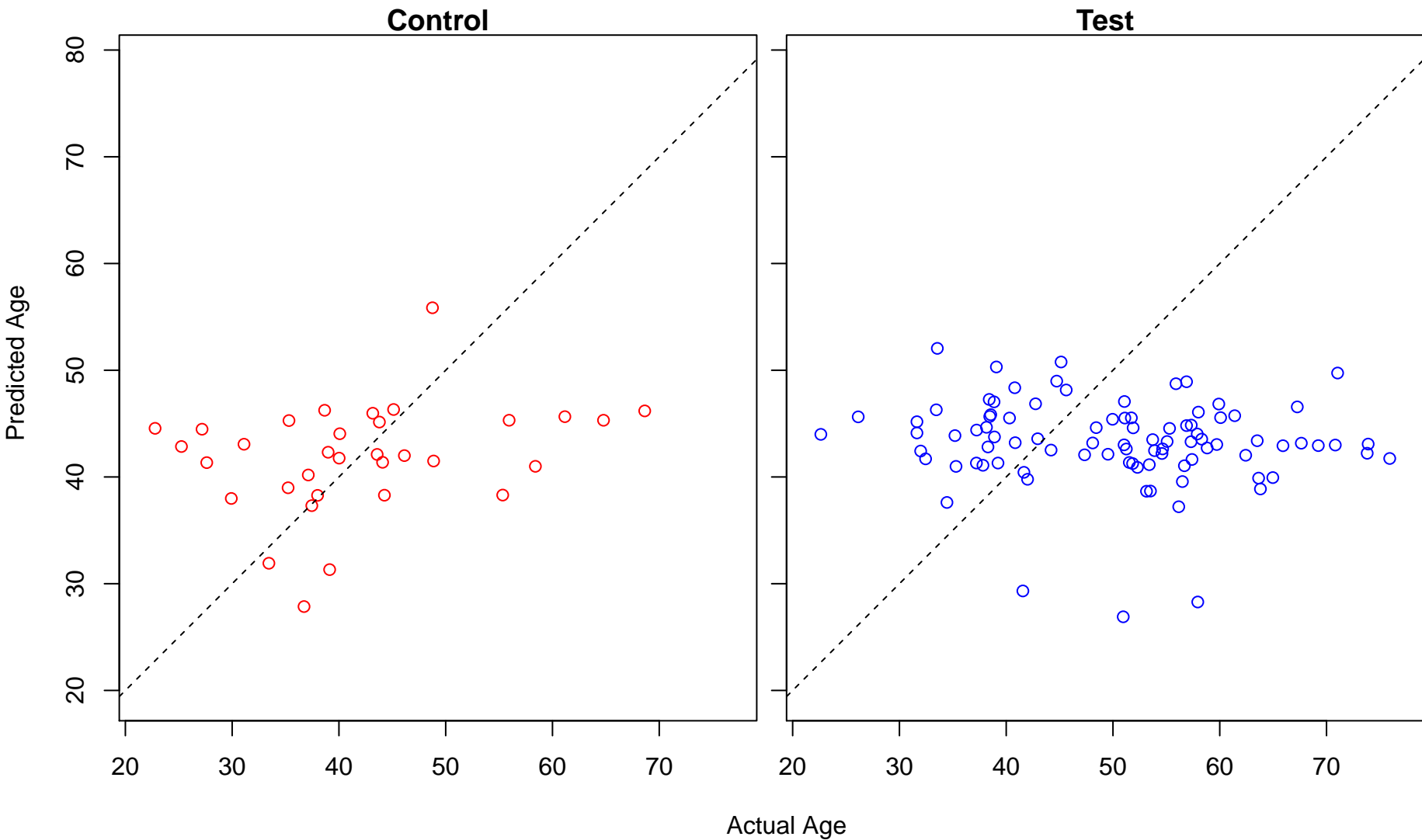
negative regulation of pro-B cell differentiation (Score: 0.291595)



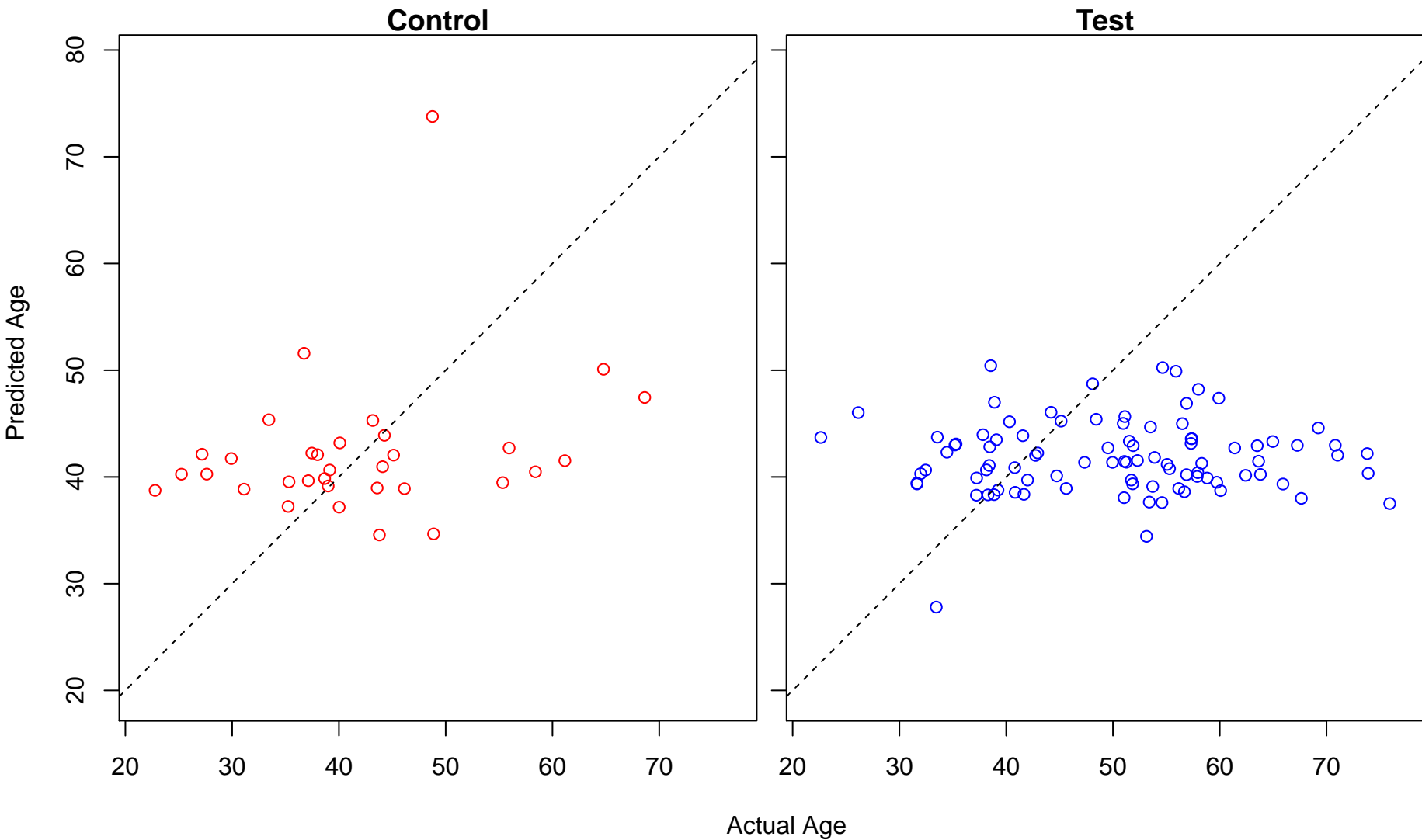
copper ion import (Score: 0.291236)



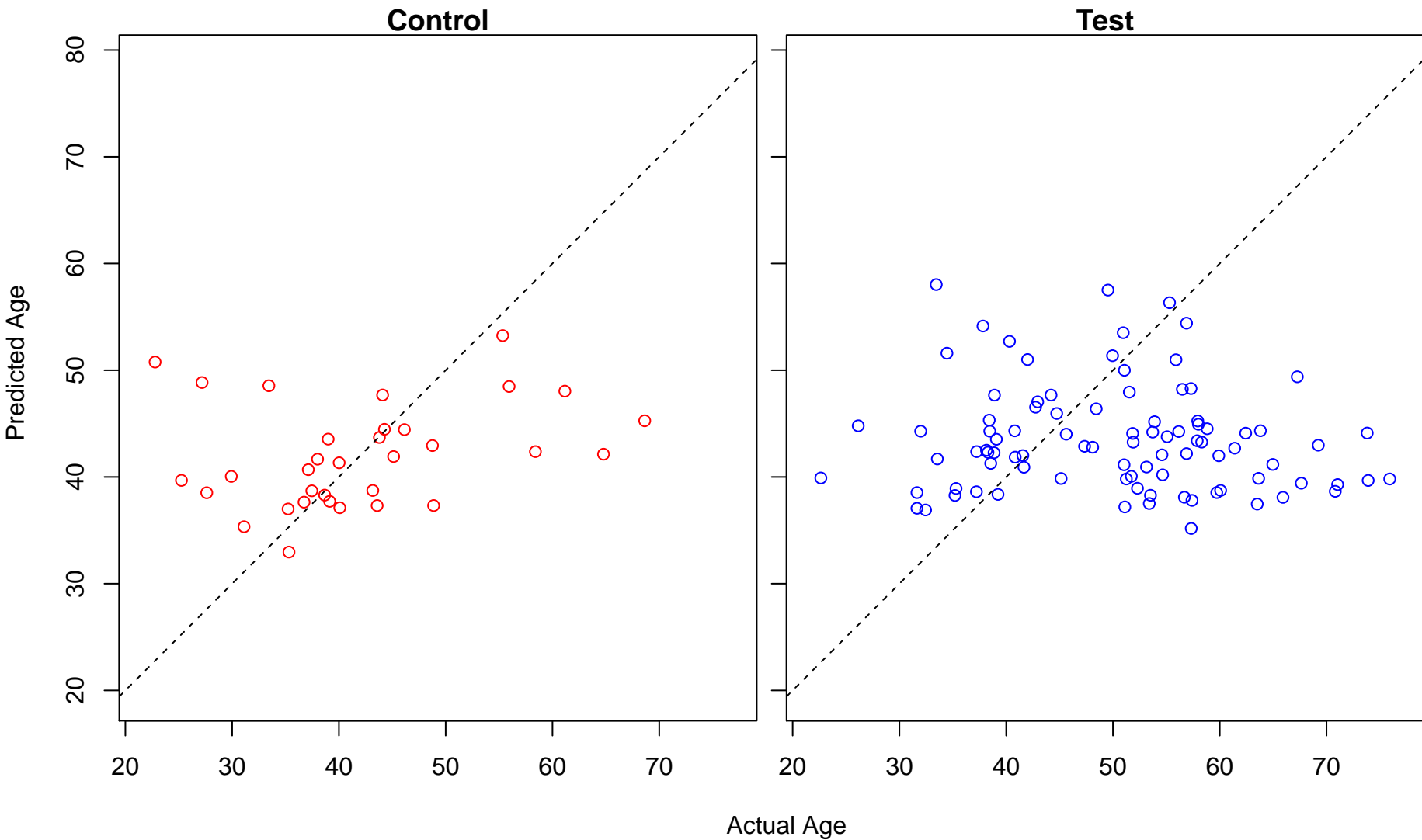
copper ion export (Score: 0.291236)



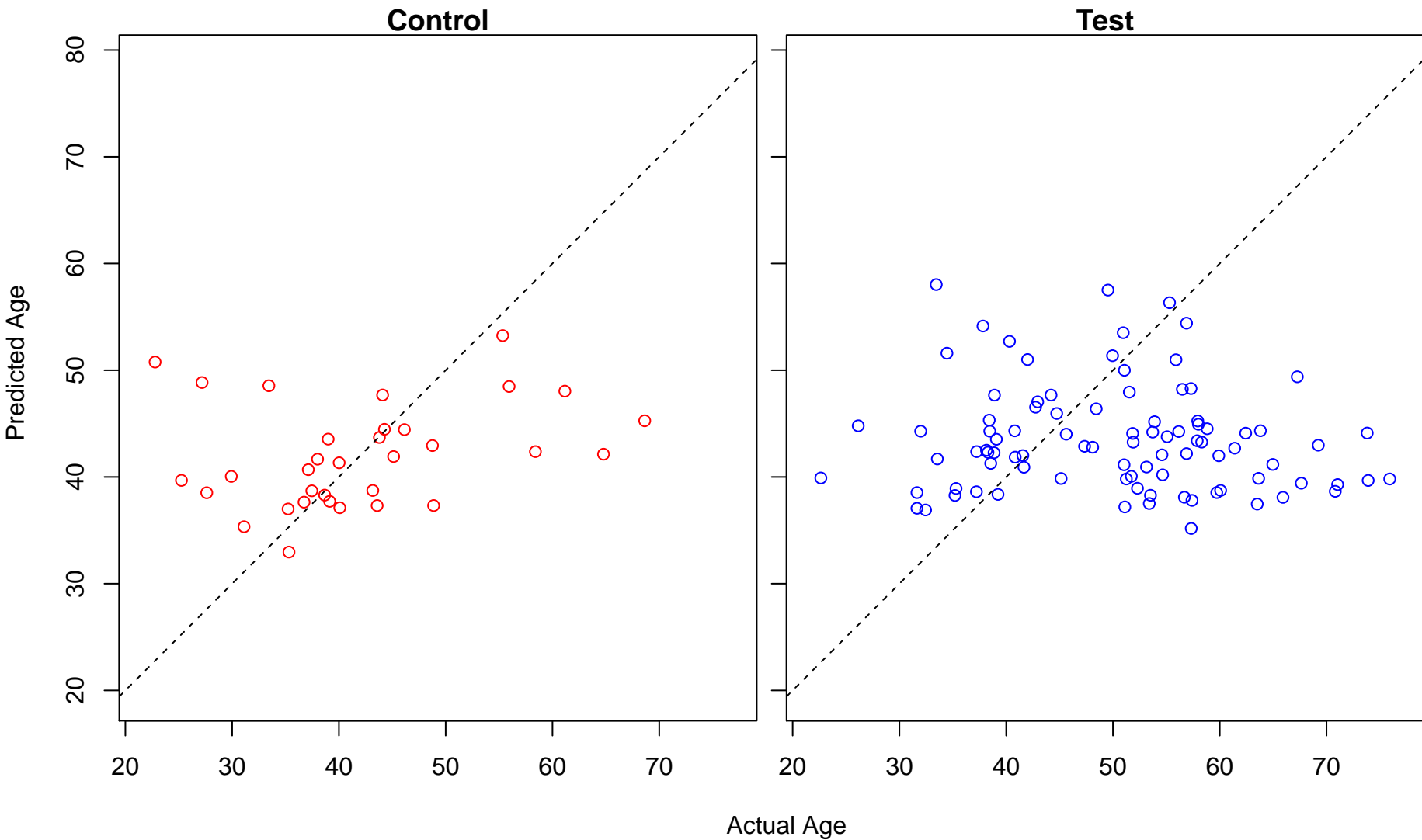
interleukin-8-mediated signaling pathway (Score: 0.288307)



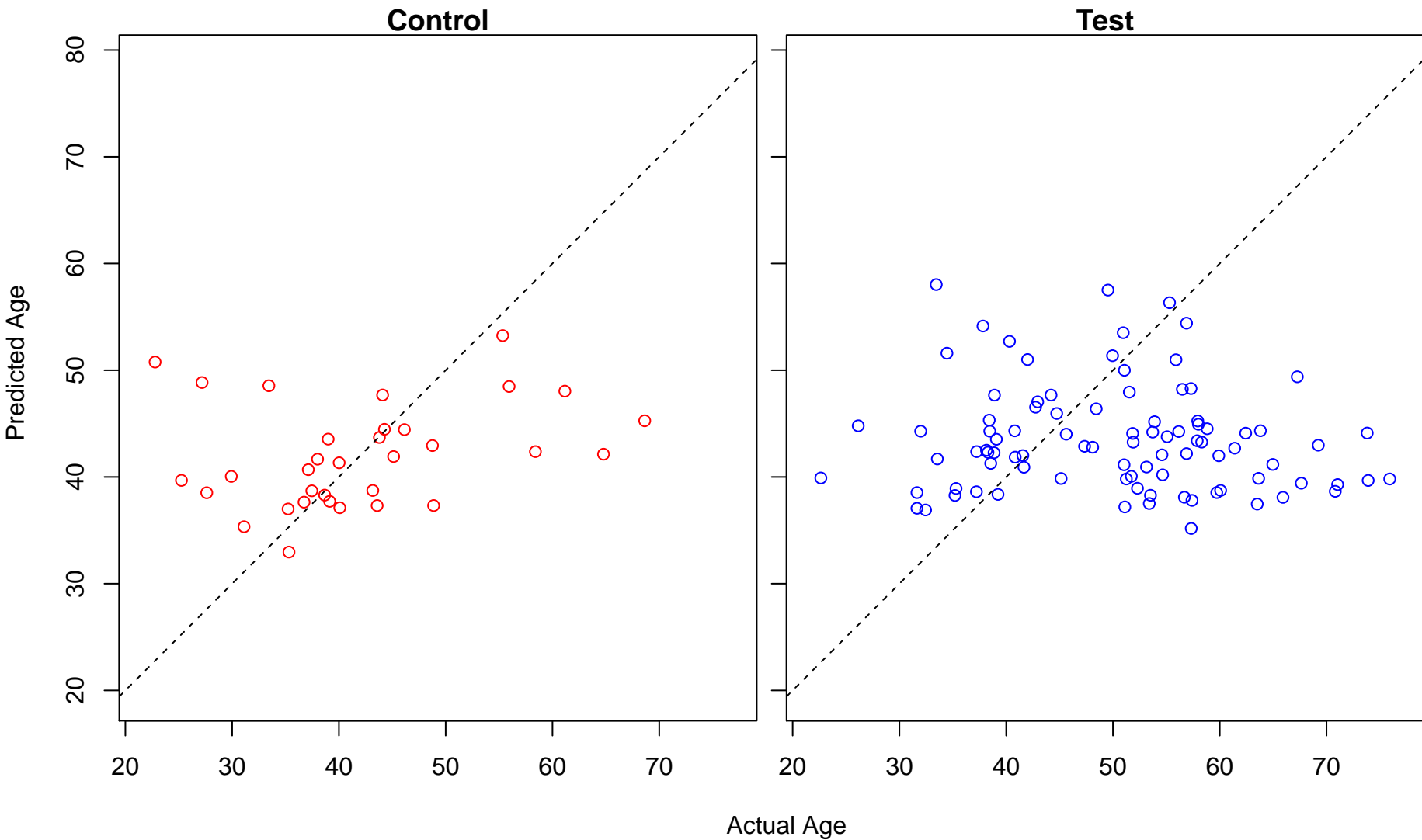
regulation of interferon- α biosynthetic process (Score: 0.287337)



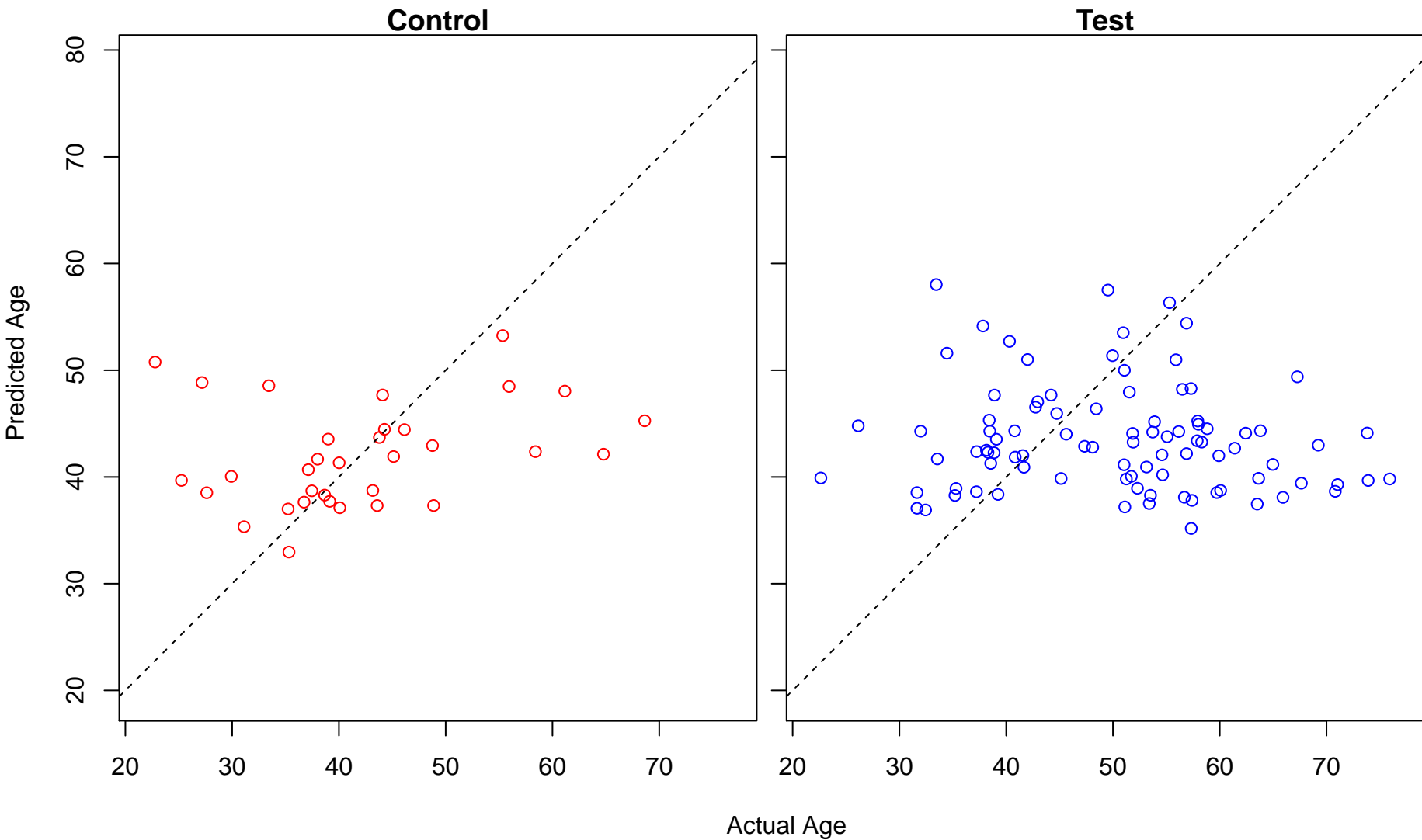
positive regulation of interferon- α biosynthetic process (Score: 0.287337)



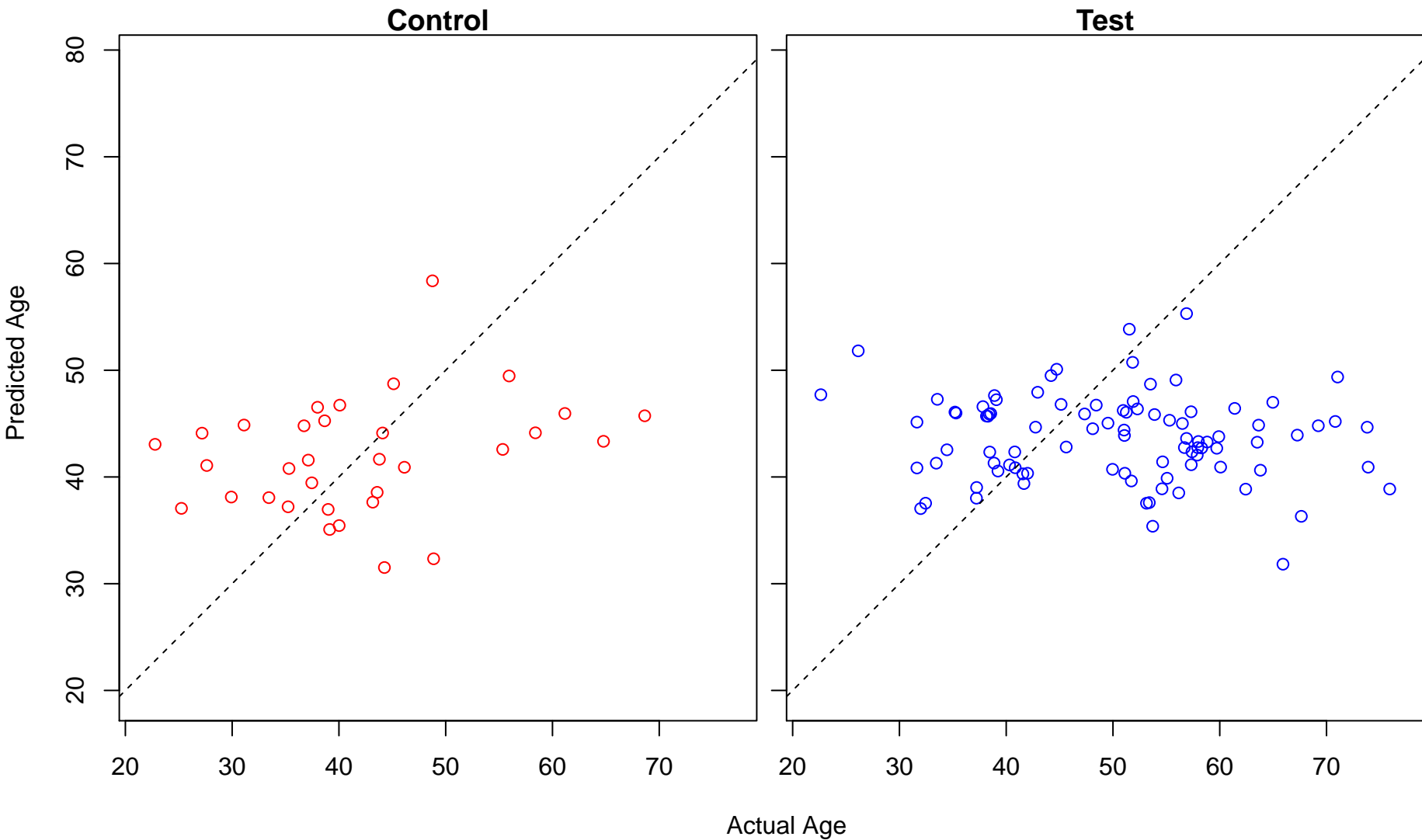
regulation of interferon-beta biosynthetic process (Score: 0.287337)



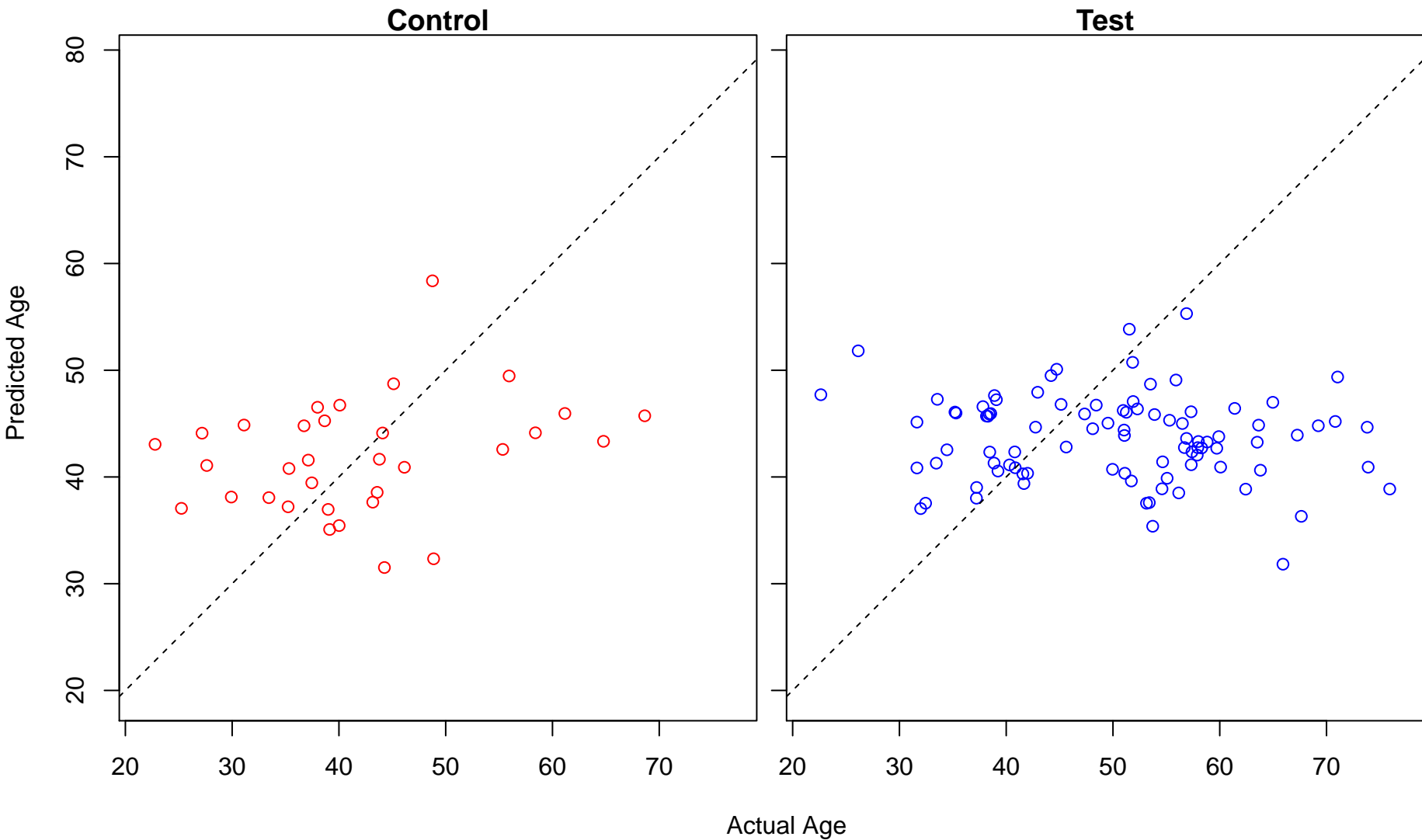
positive regulation of interferon-beta biosynthetic process (Score: 0.287337)



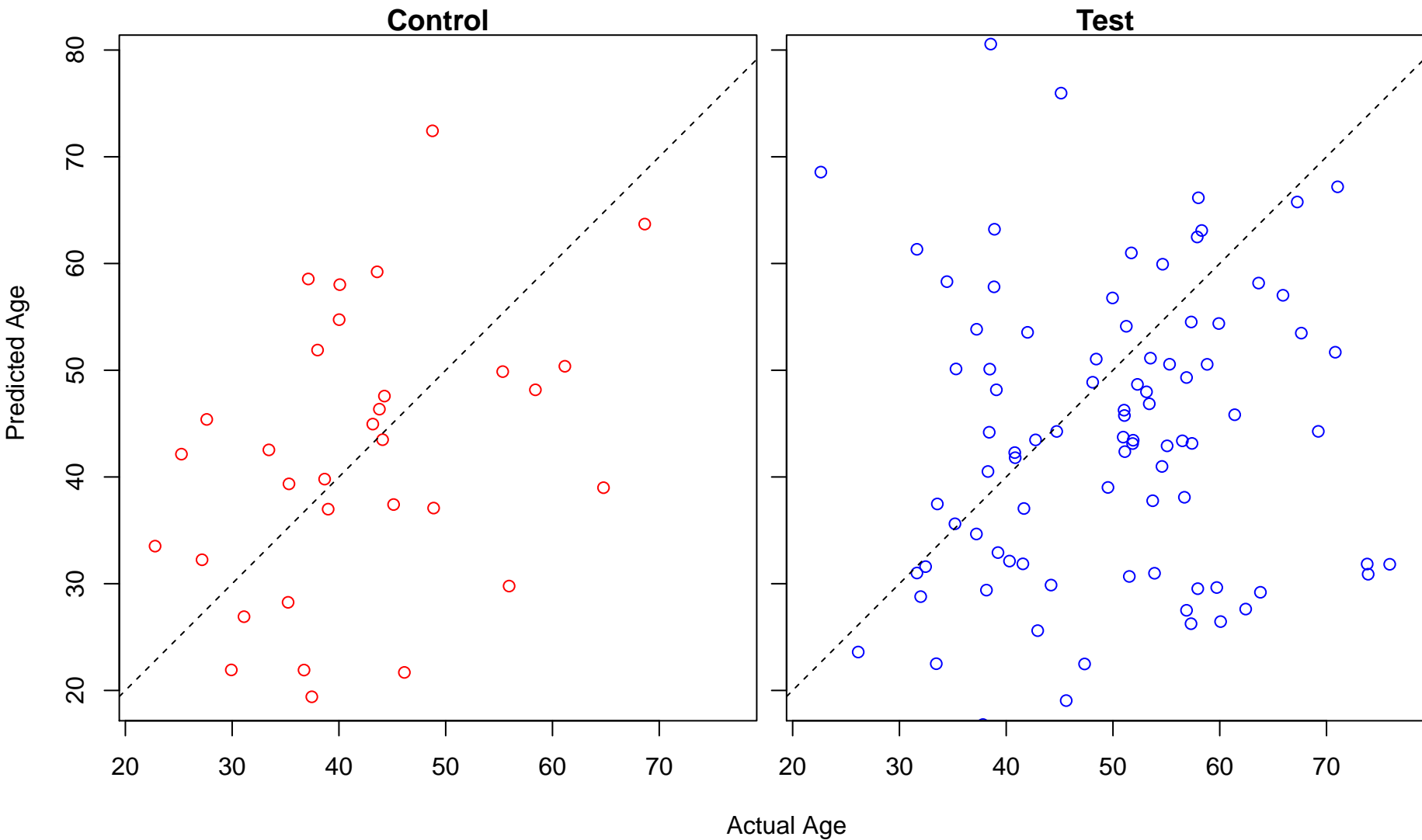
cyanate metabolic process (Score: 0.286871)



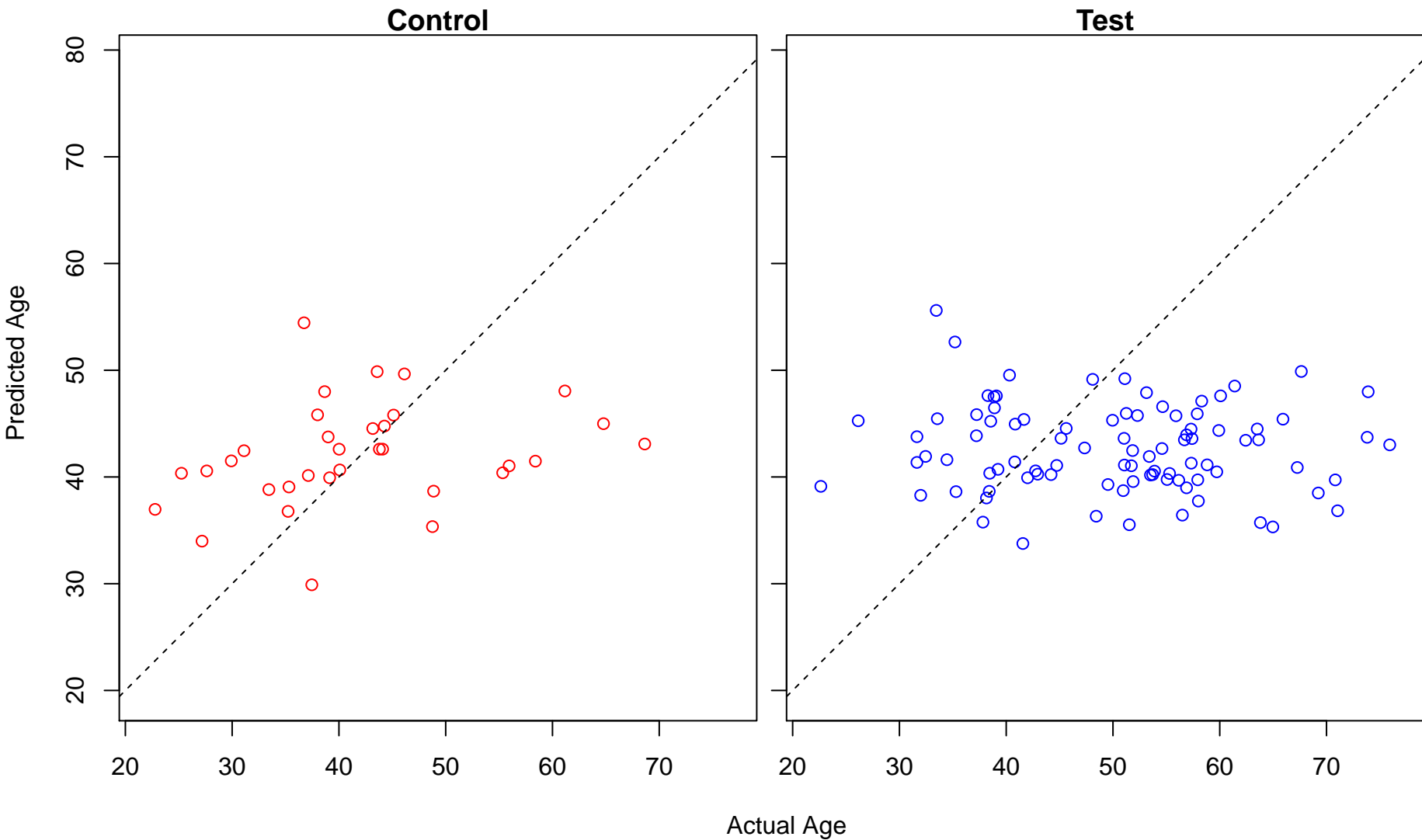
cyanate catabolic process (Score: 0.286871)



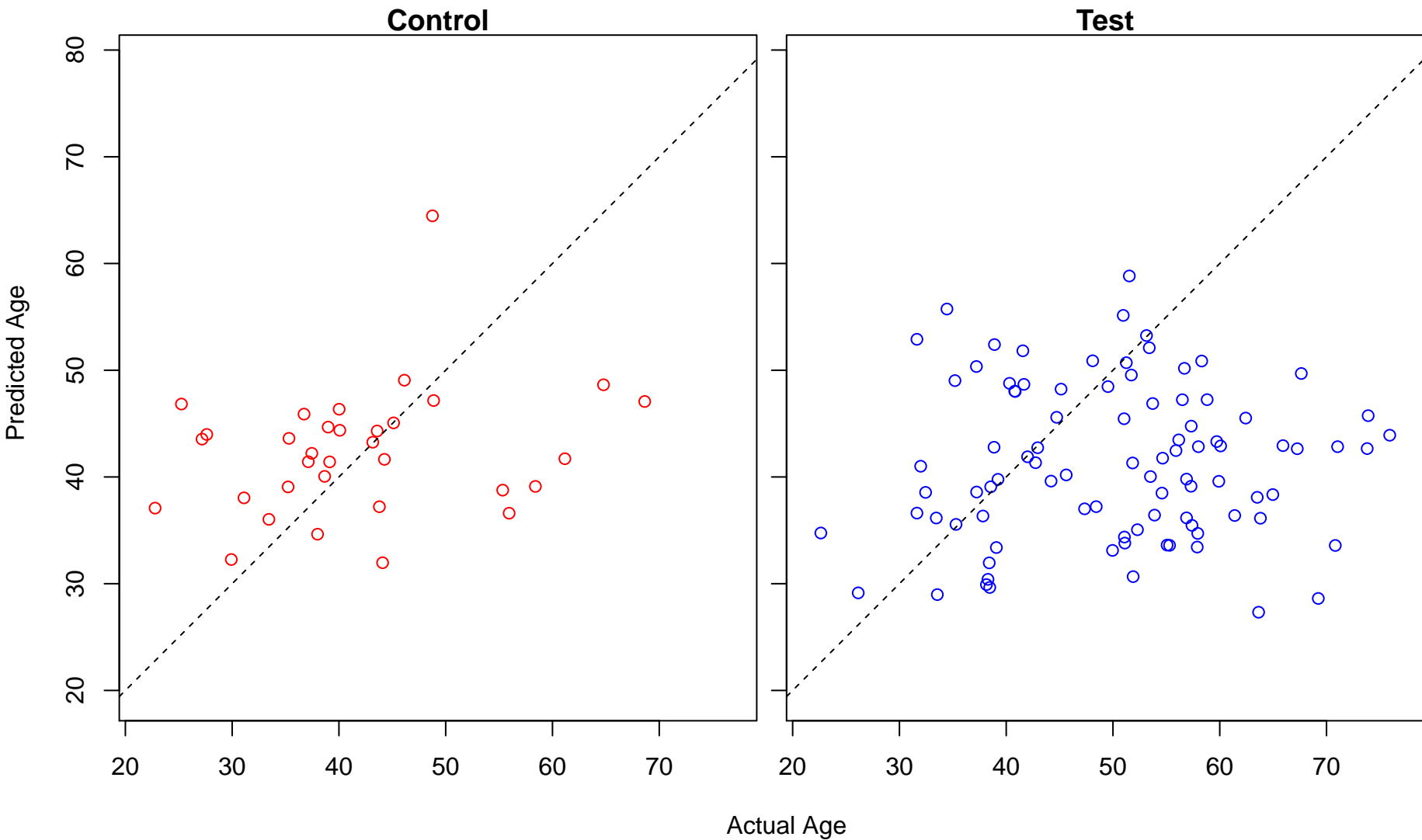
positive regulation of nuclear division (Score: 0.286798)



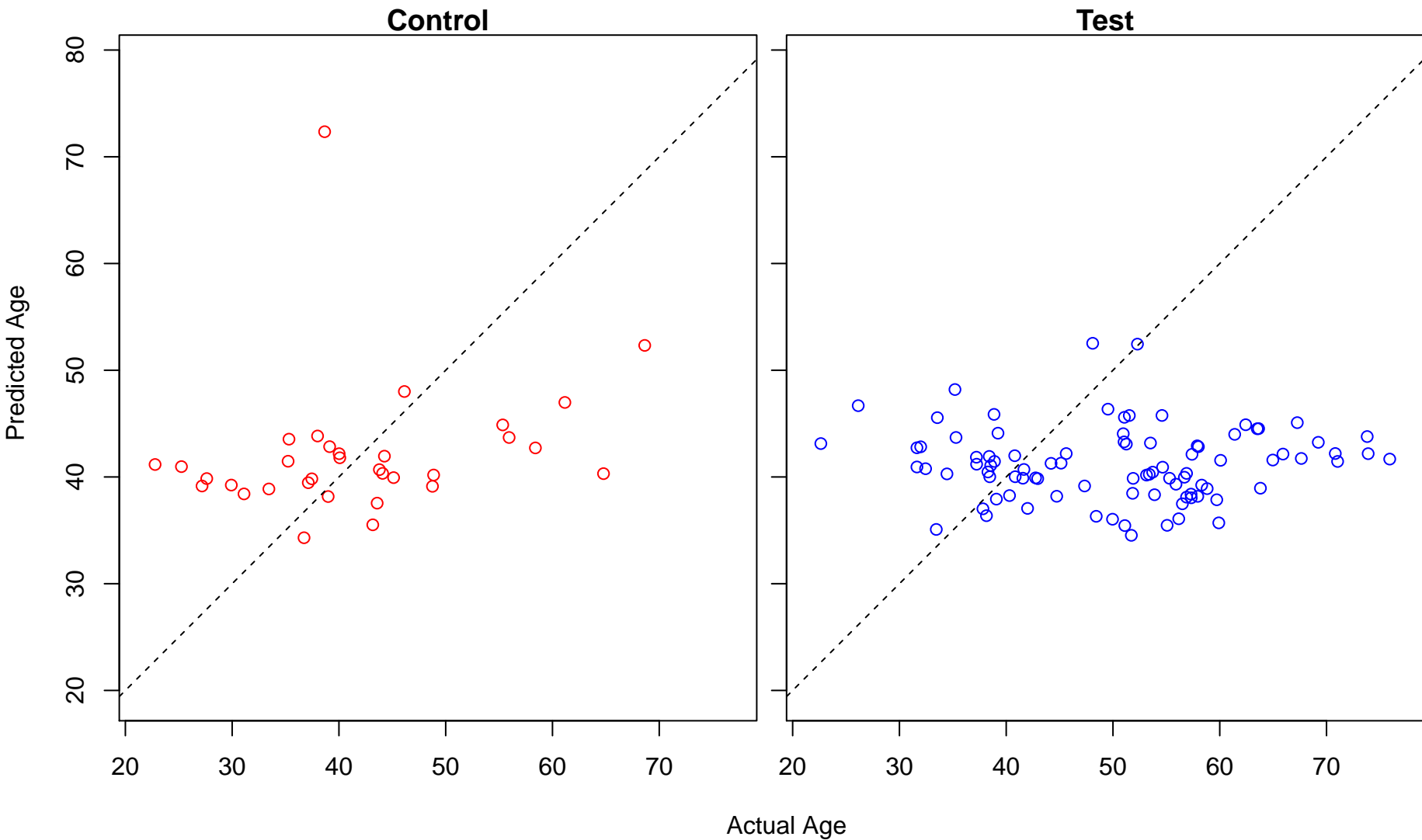
phenylpropanoid metabolic process (Score: 0.284317)



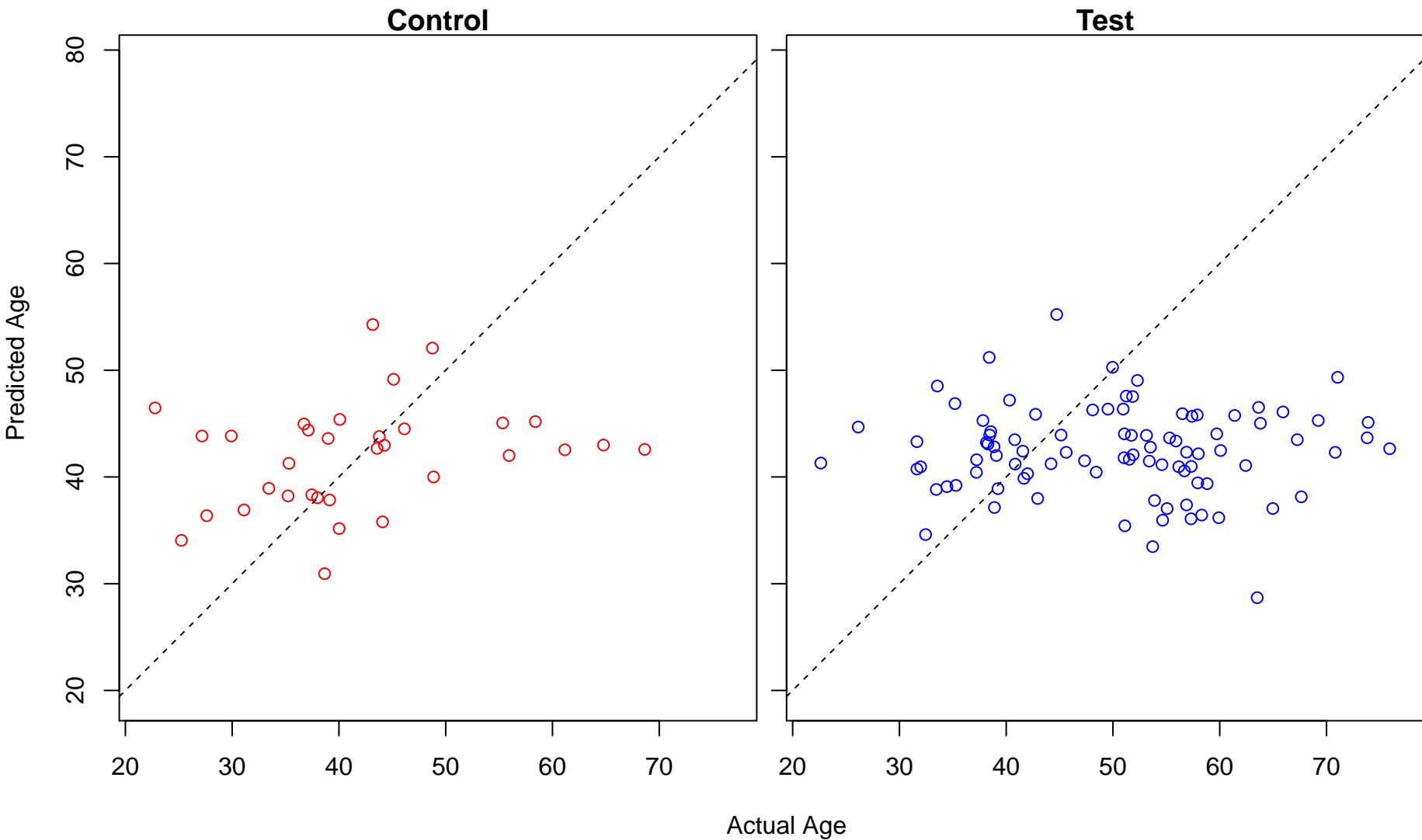
embryonic body morphogenesis (Score: 0.282109)



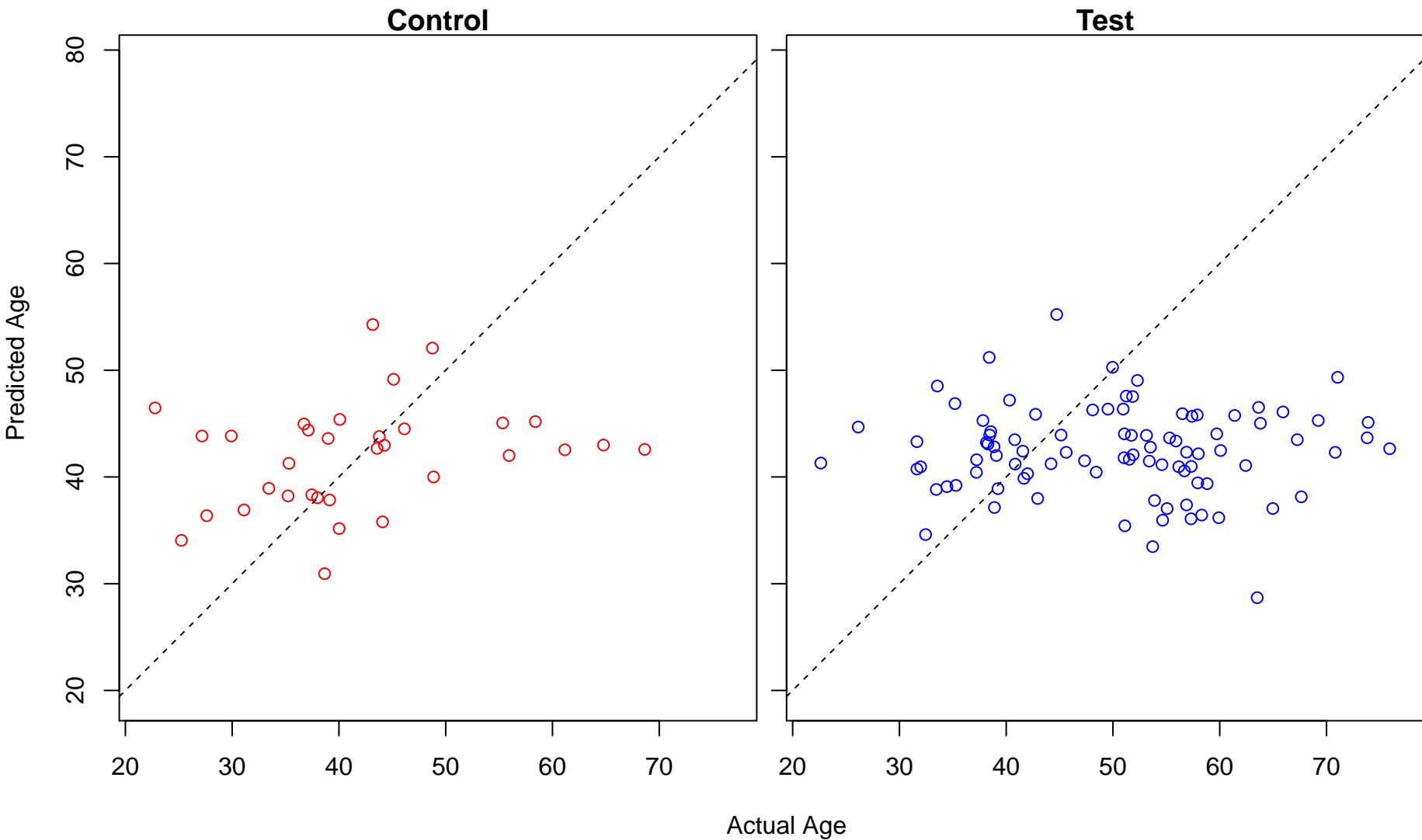
diphosphate metabolic process (Score: 0.281600)



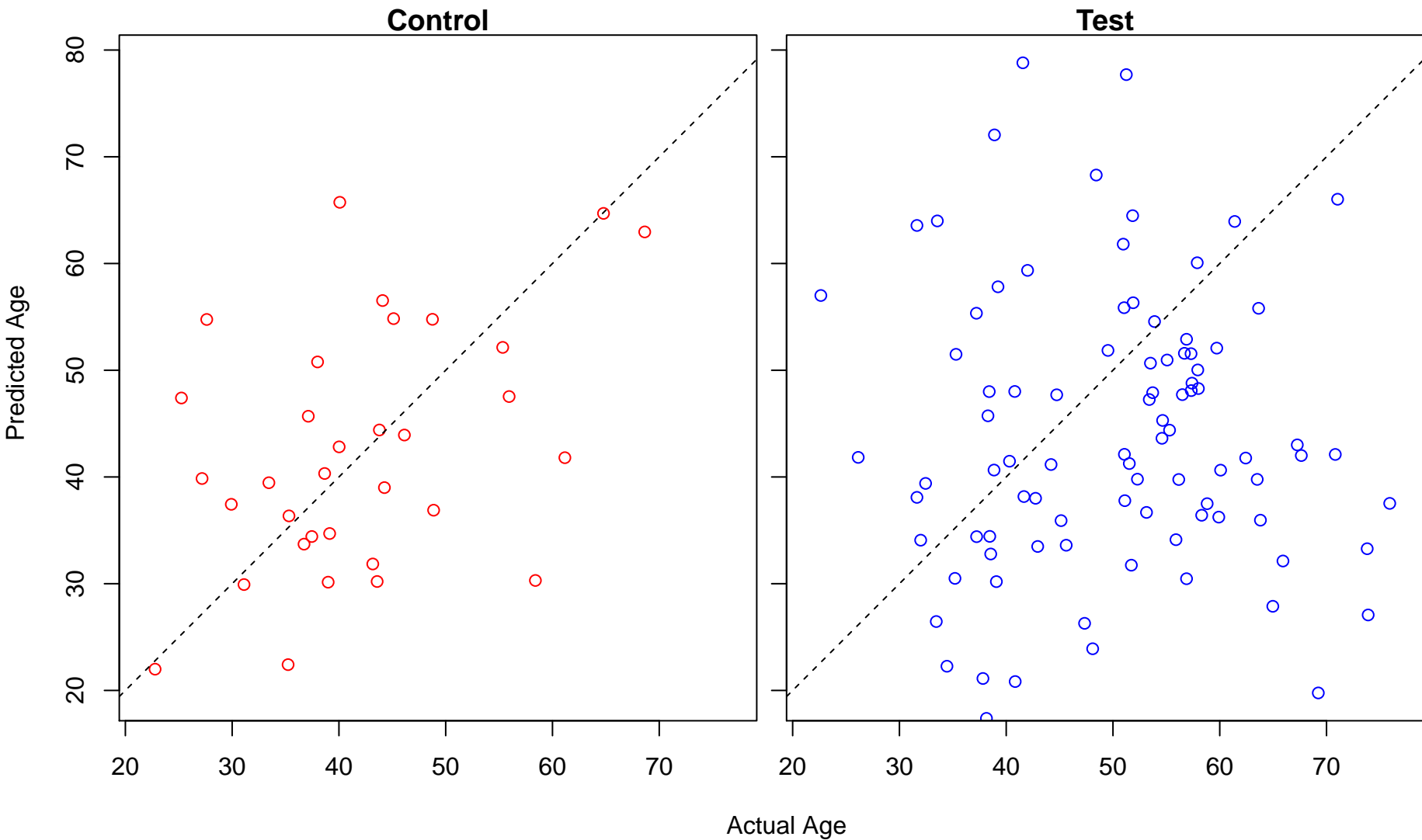
L-serine transport (Score: 0.280444)



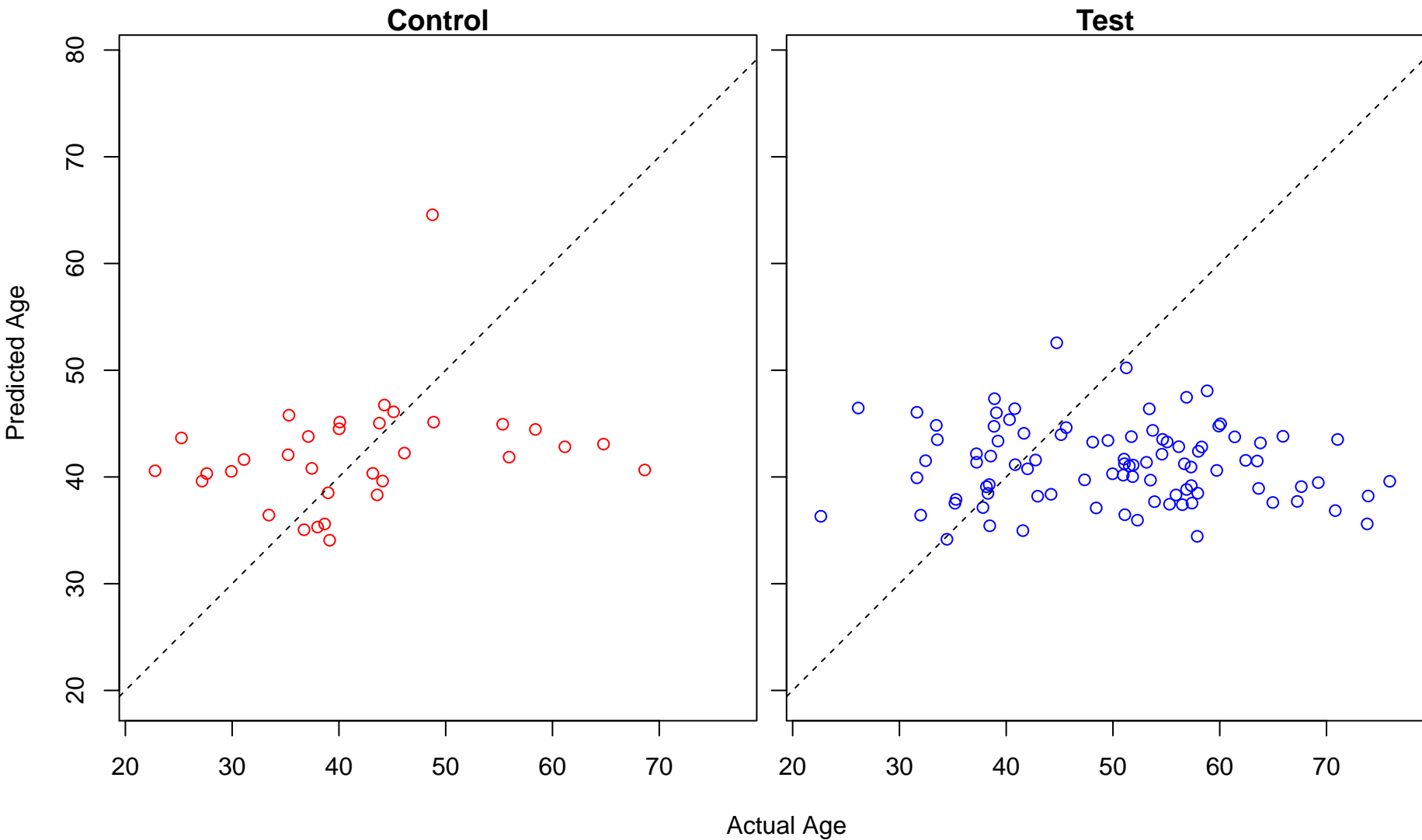
serine transport (Score: 0.280444)



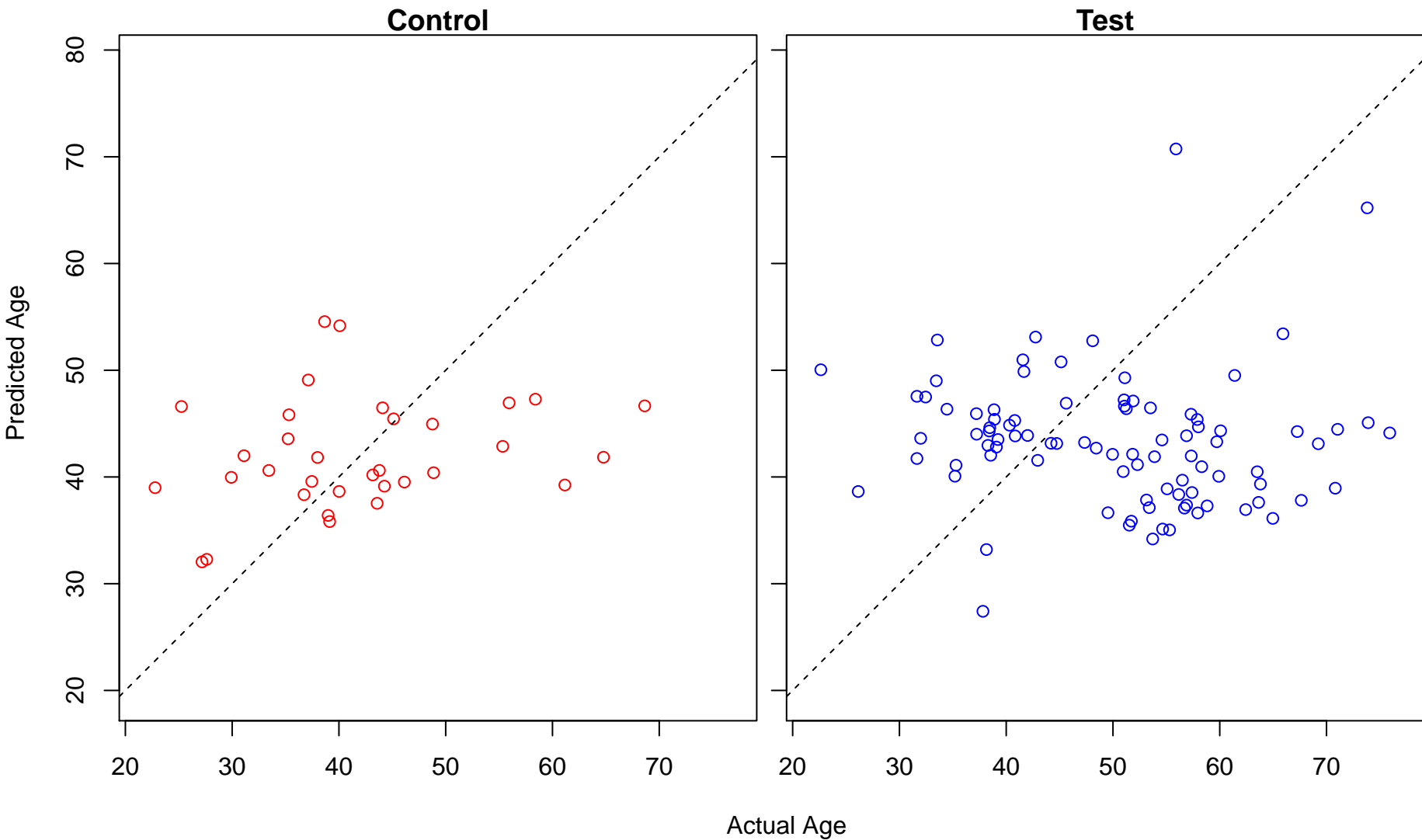
regionalization (Score: 0.279370)



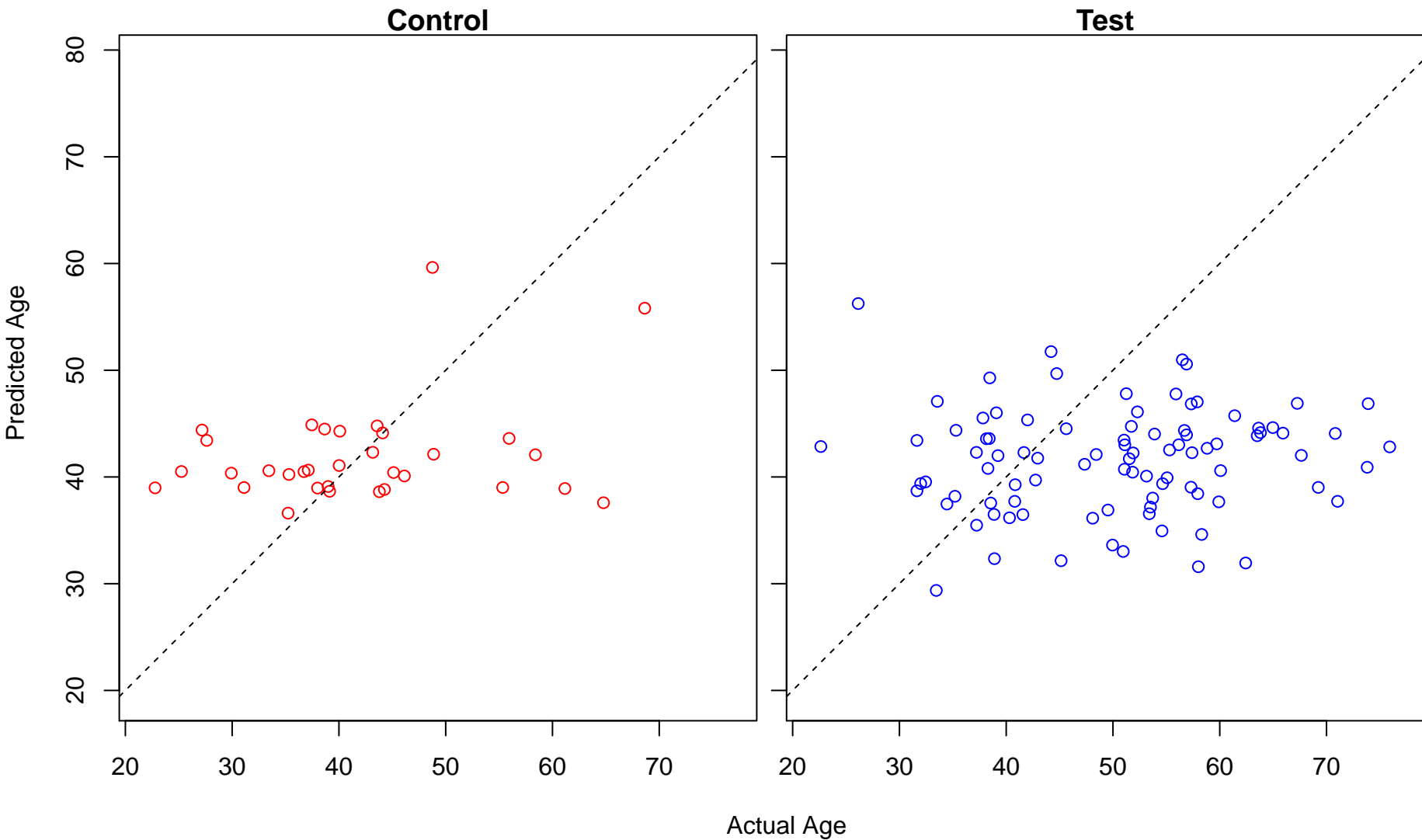
pentose biosynthetic process (Score: 0.278723)



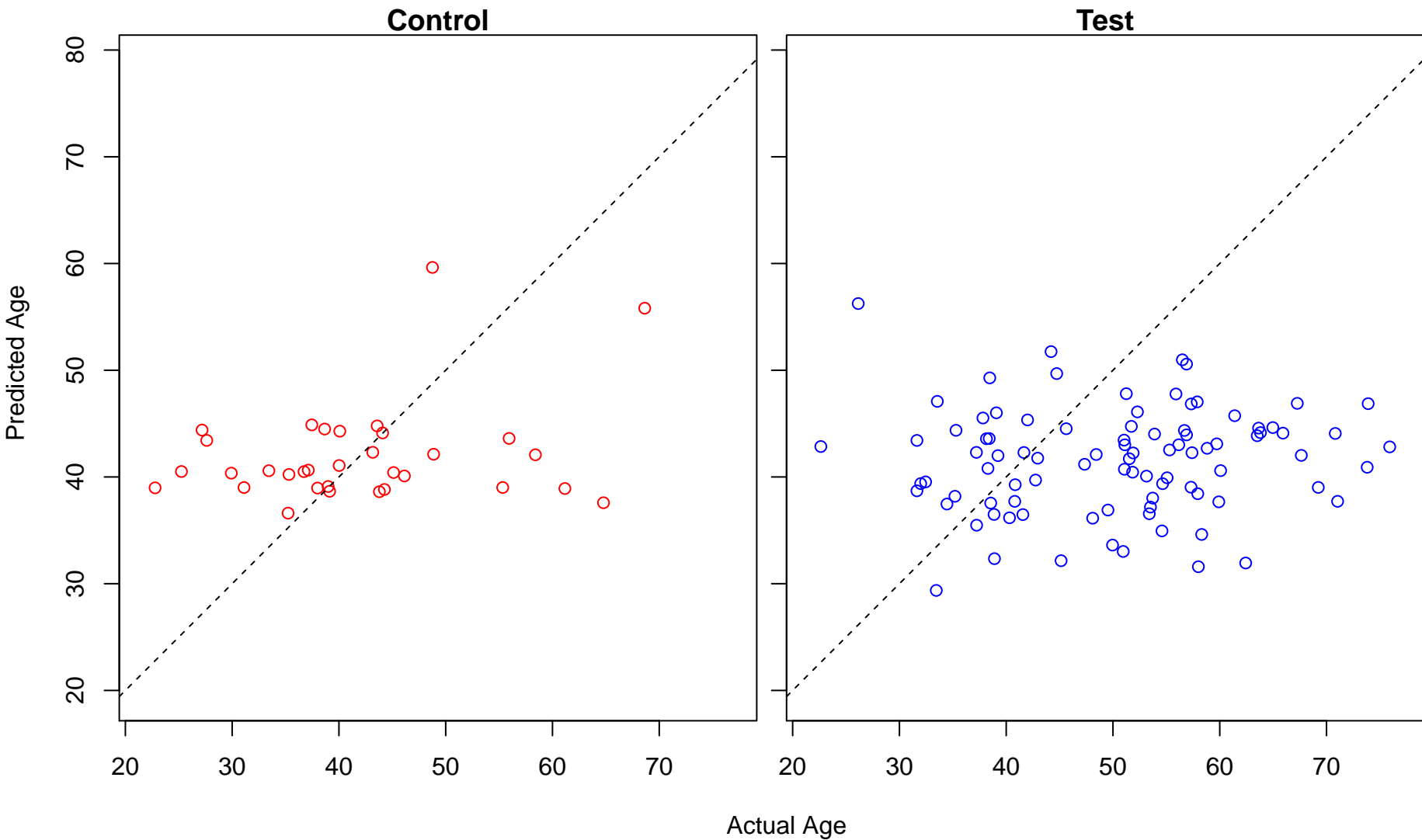
spermine metabolic process (Score: 0.277463)



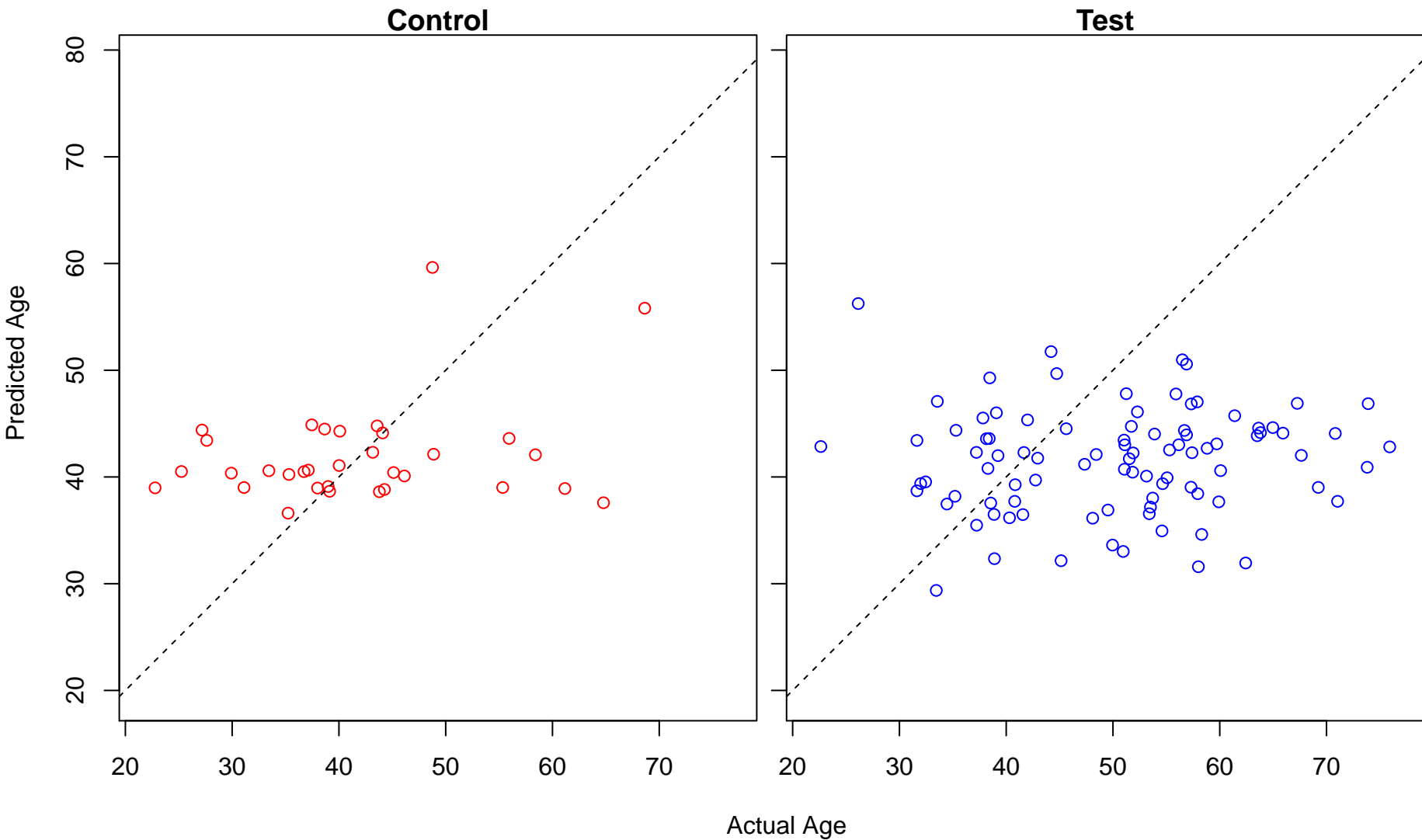
negative regulation of histone ubiquitination (Score: 0.276960)



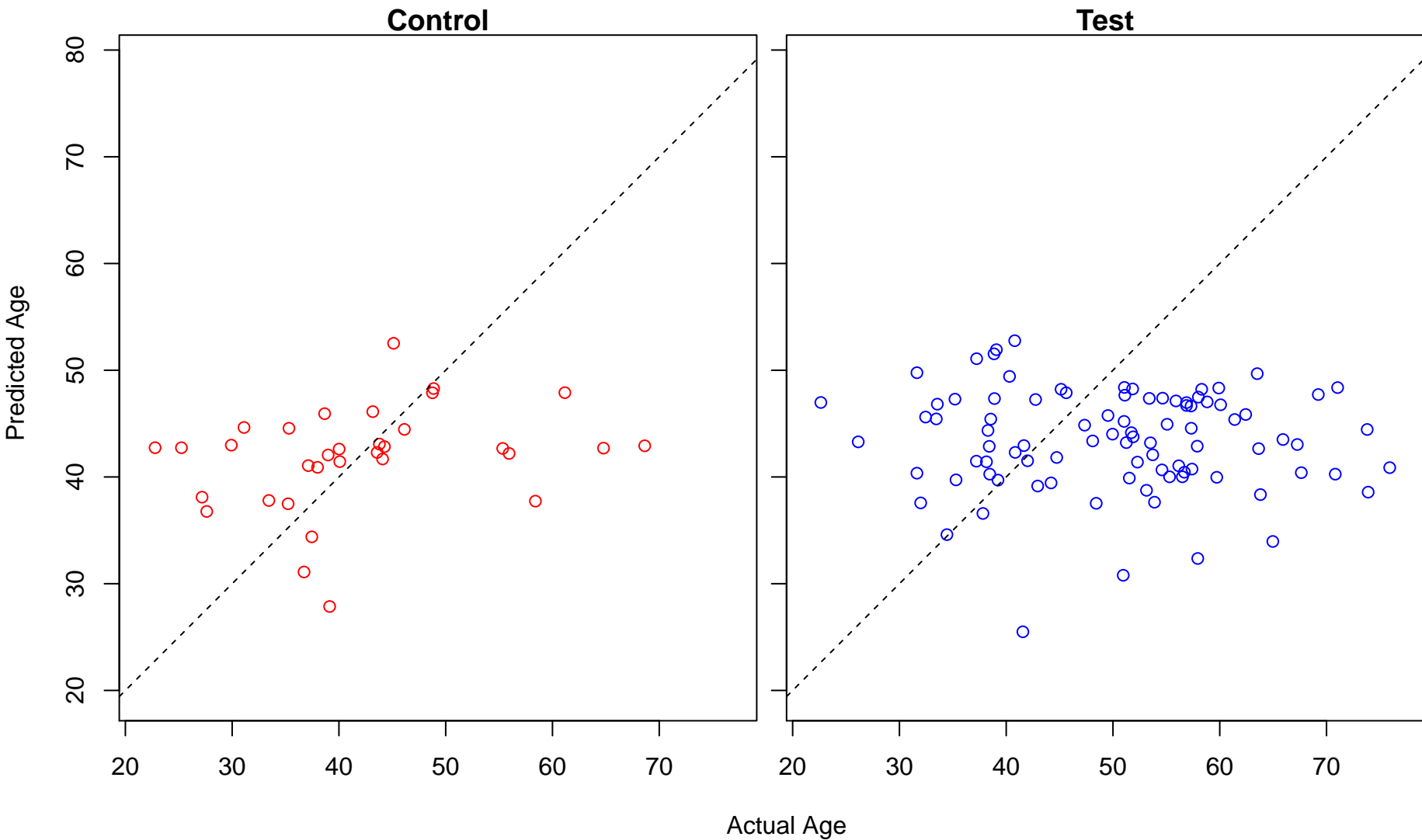
regulation of histone H2A K63-linked ubiquitination (Score: 0.276960)



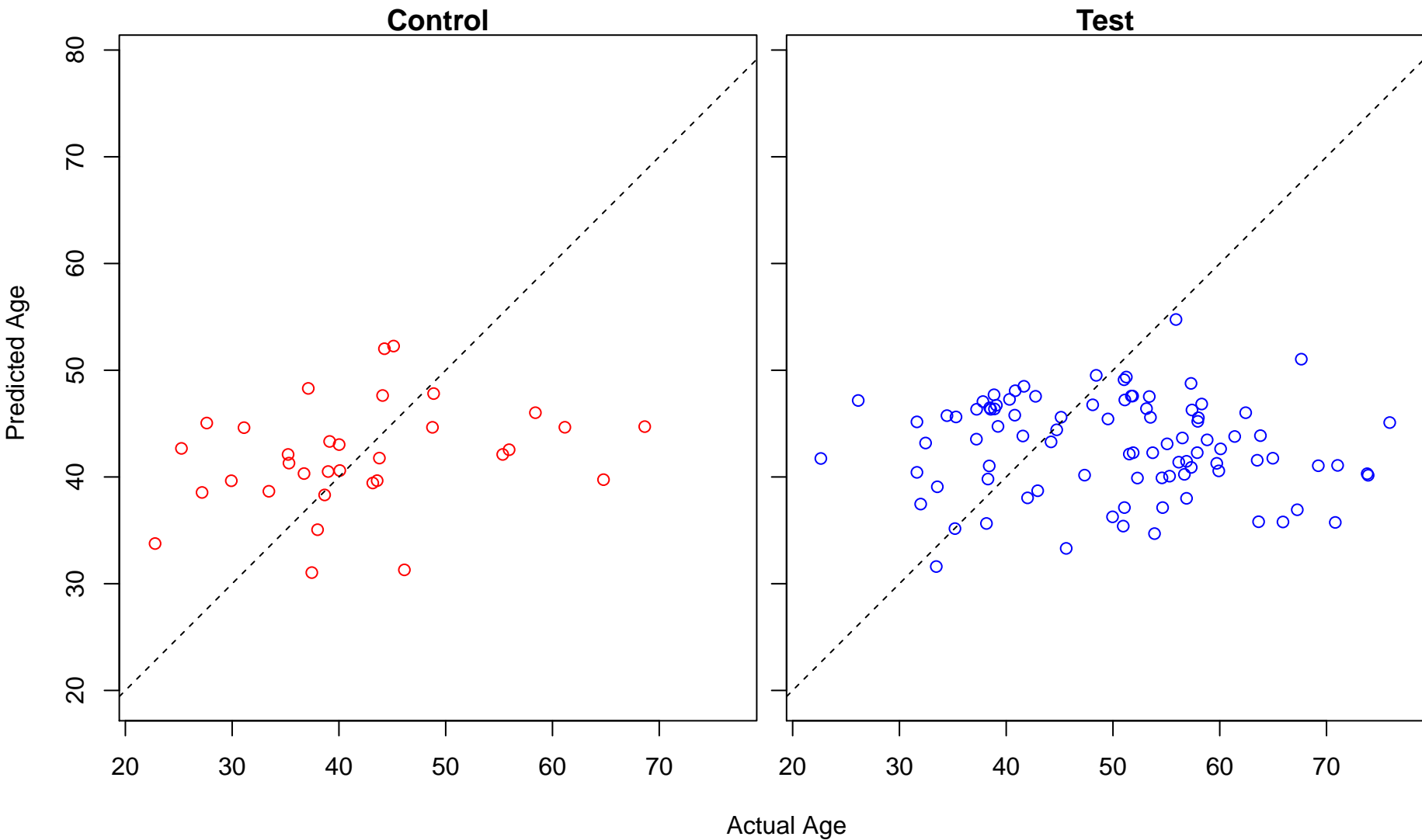
negative regulation of histone H2A K63-linked ubiquitination (Score: 0.276960)



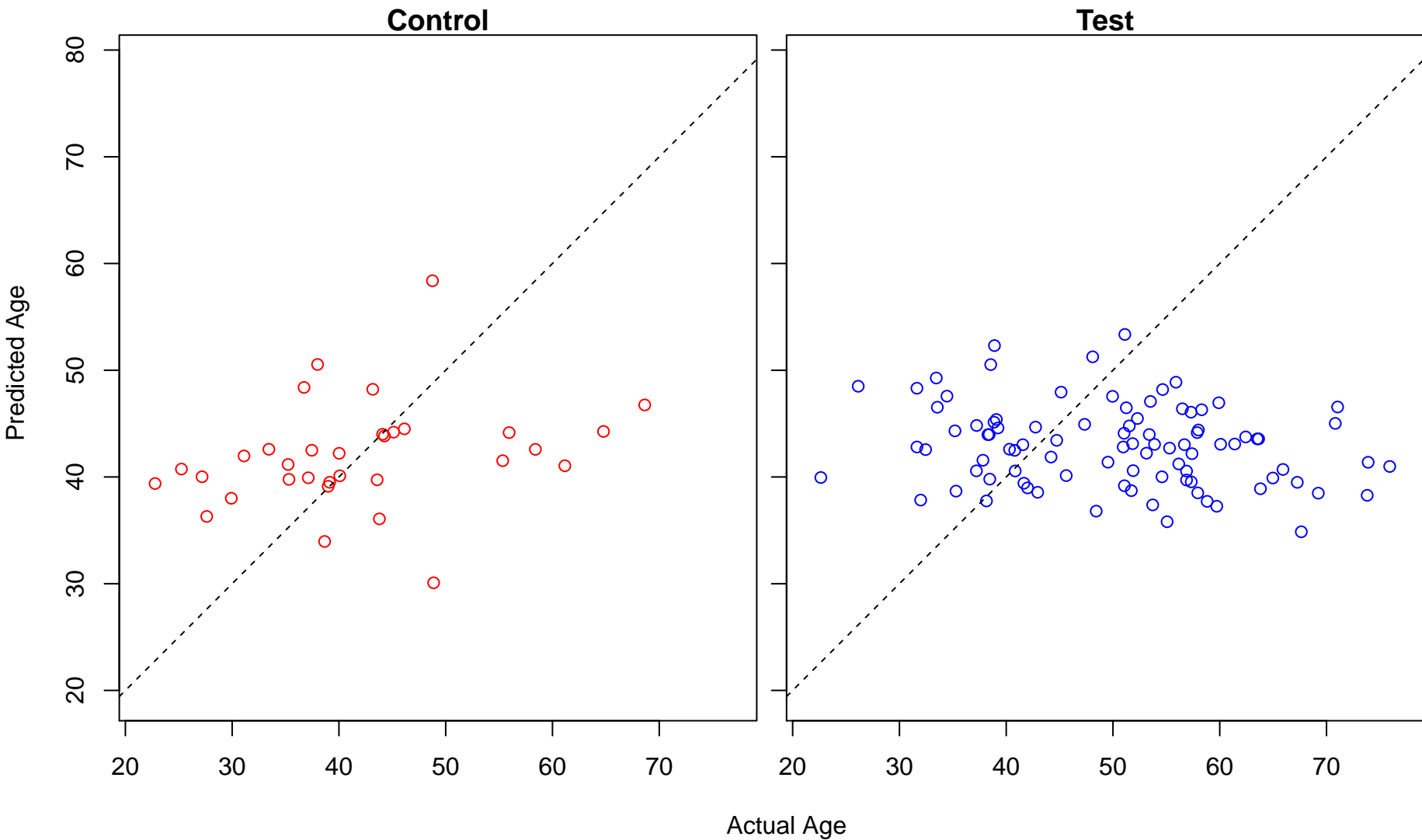
immunoglobulin biosynthetic process (Score: 0.274683)



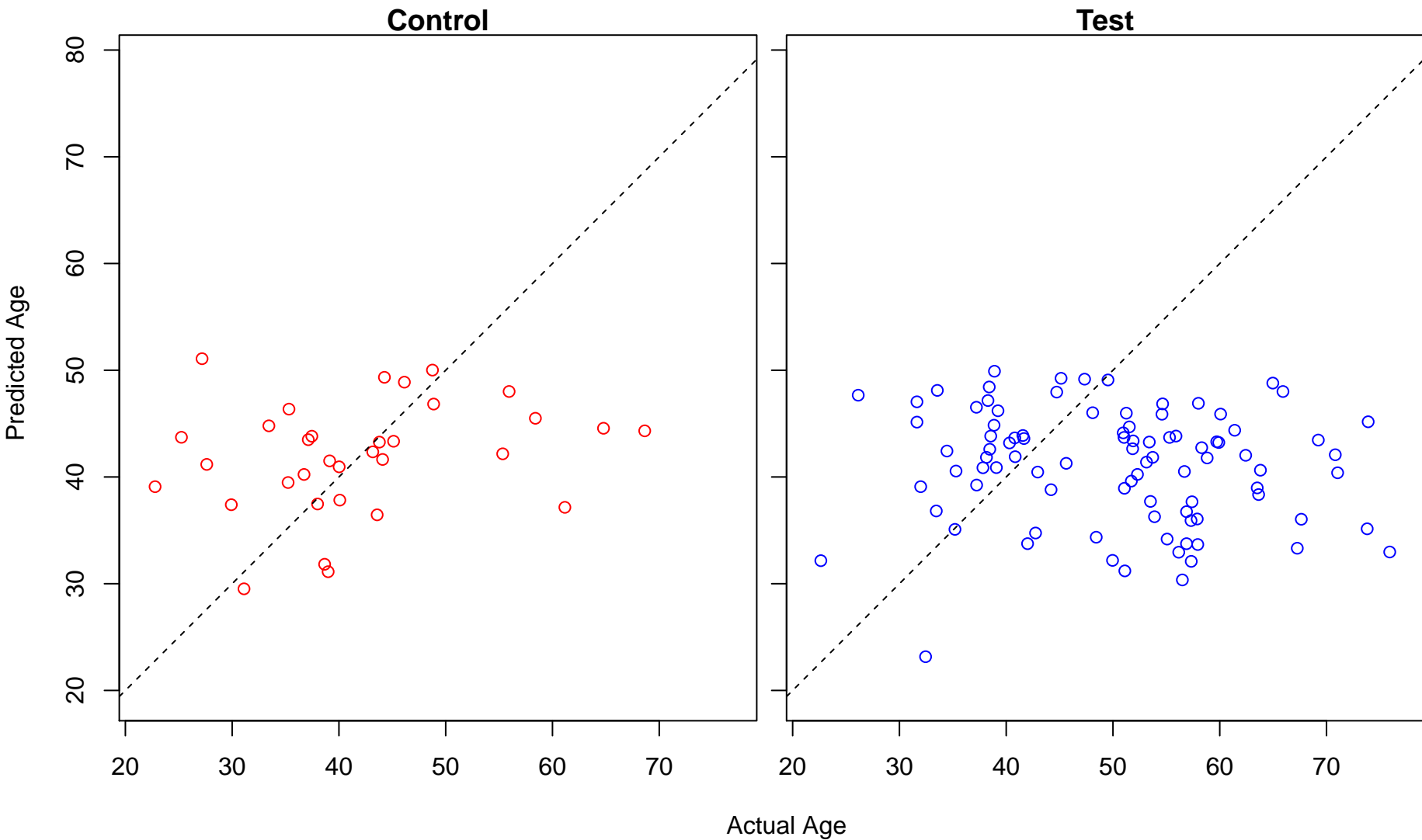
positive regulation of heart rate (Score: 0.272135)



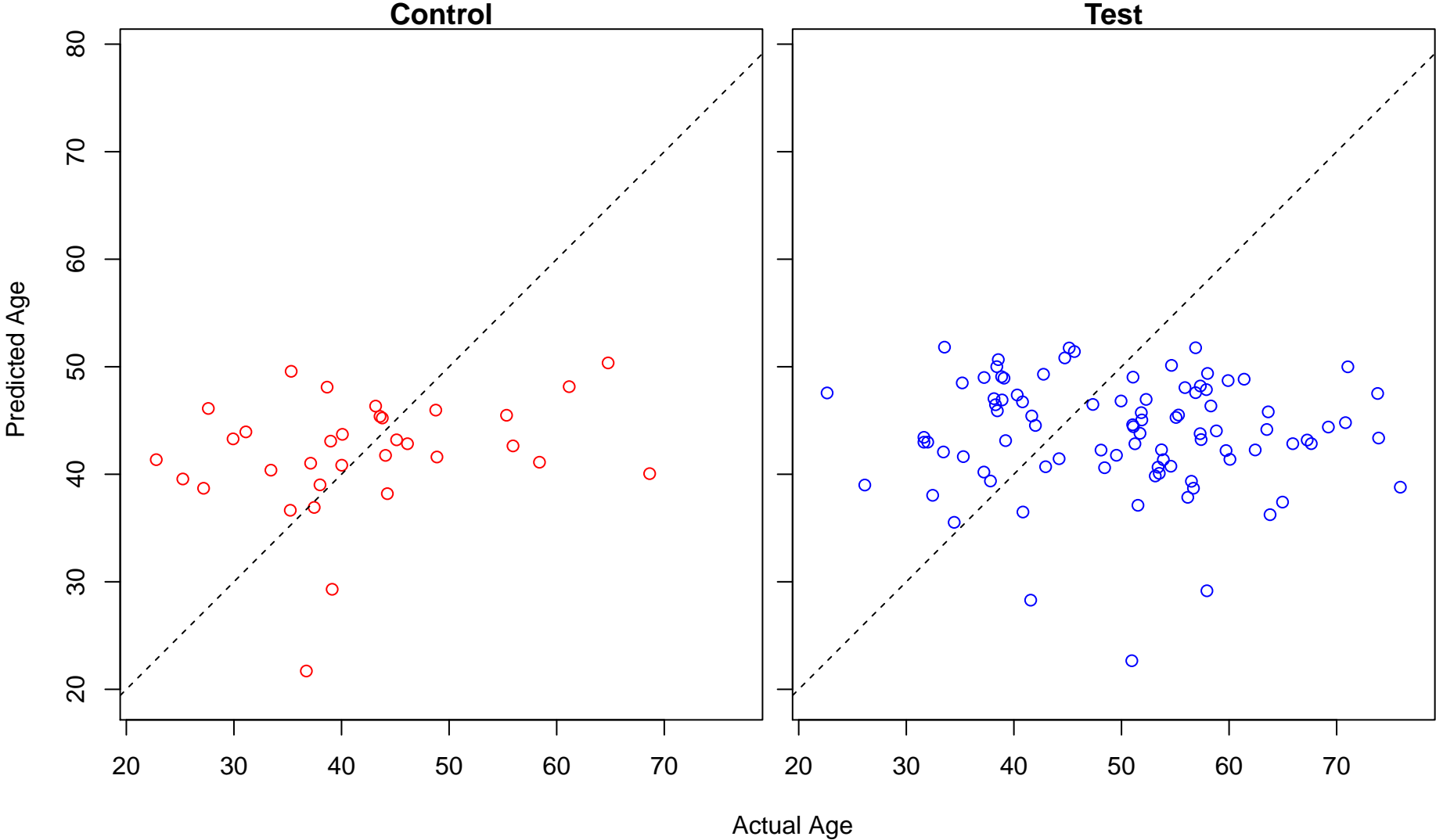
negative regulation of protein import into nucleus, translocation (Score: 0.271944)



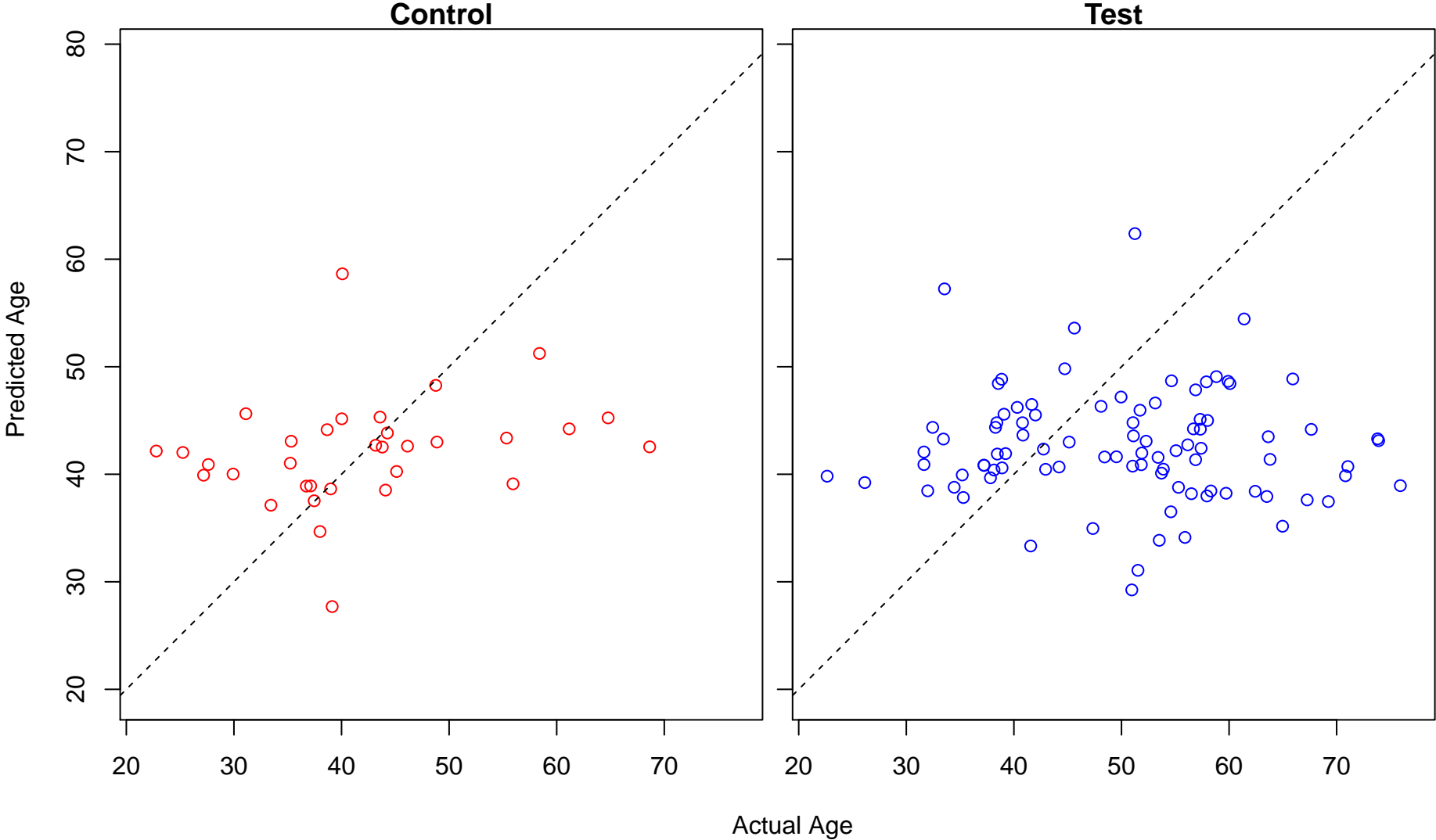
detection of bacterial lipopeptide (Score: 0.271510)



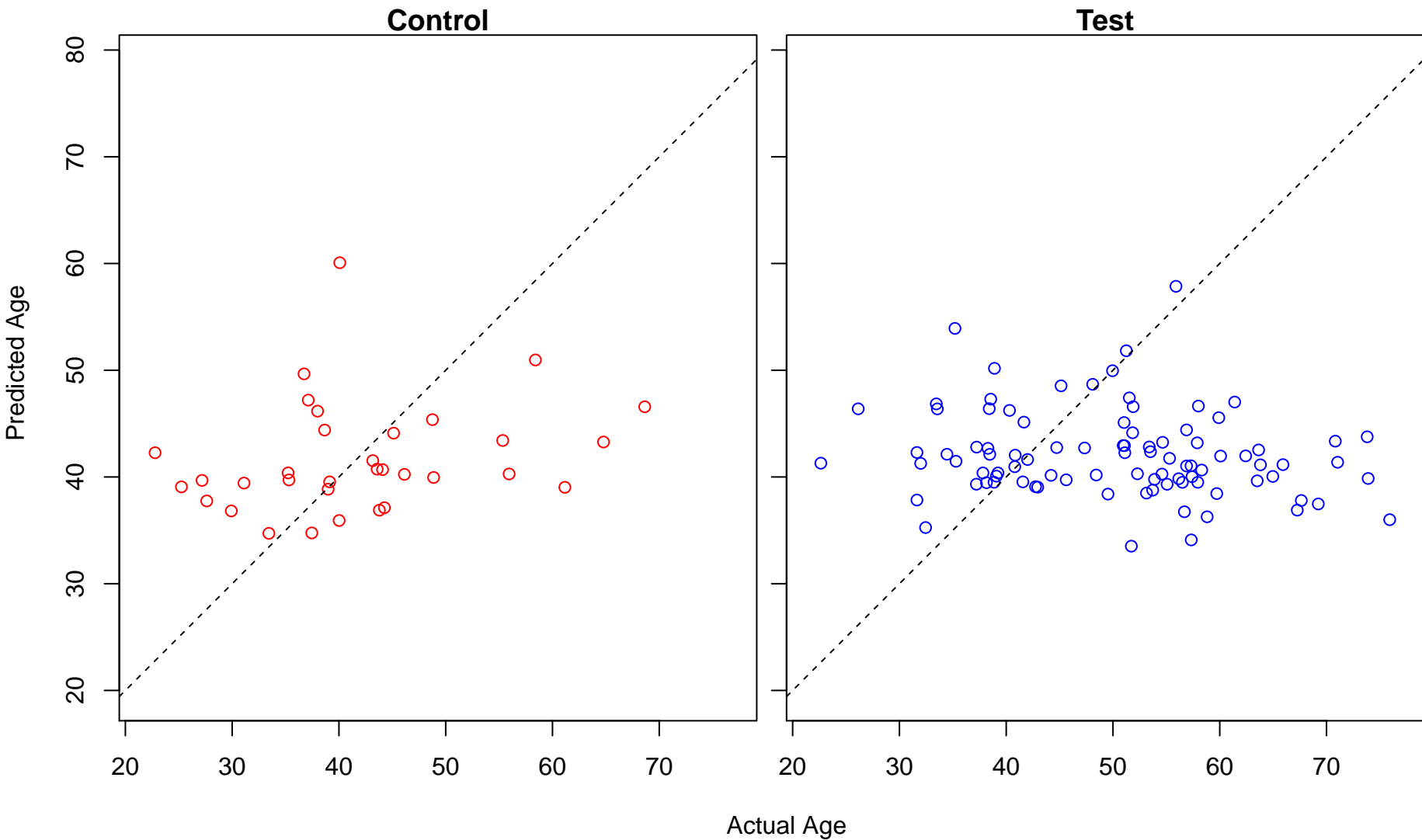
positive regulation of dopamine receptor signaling pathway (Score: 0.270742)



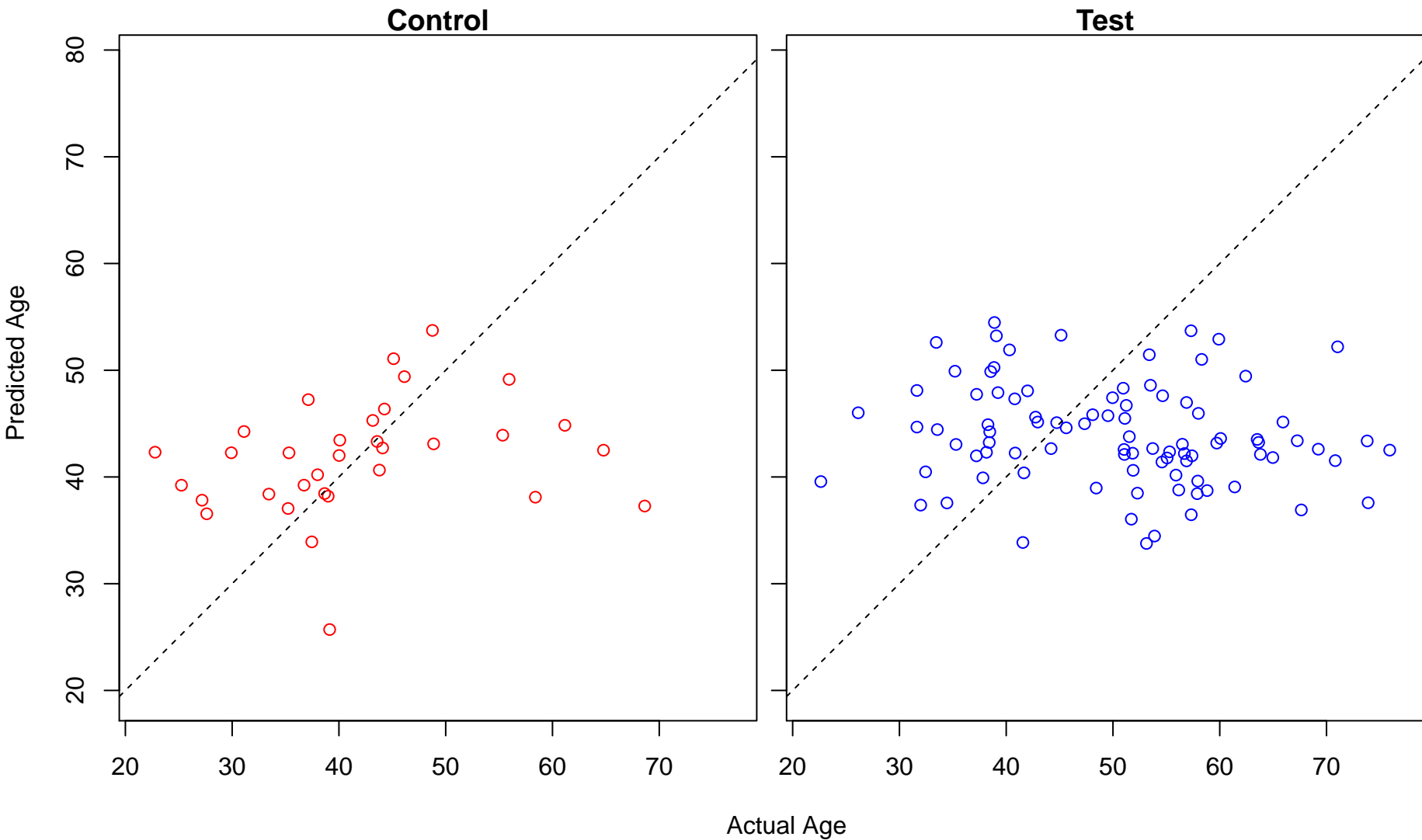
negative regulation of RNA polymerase II transcriptional preinitiation complex assembly (Score: 0.270)



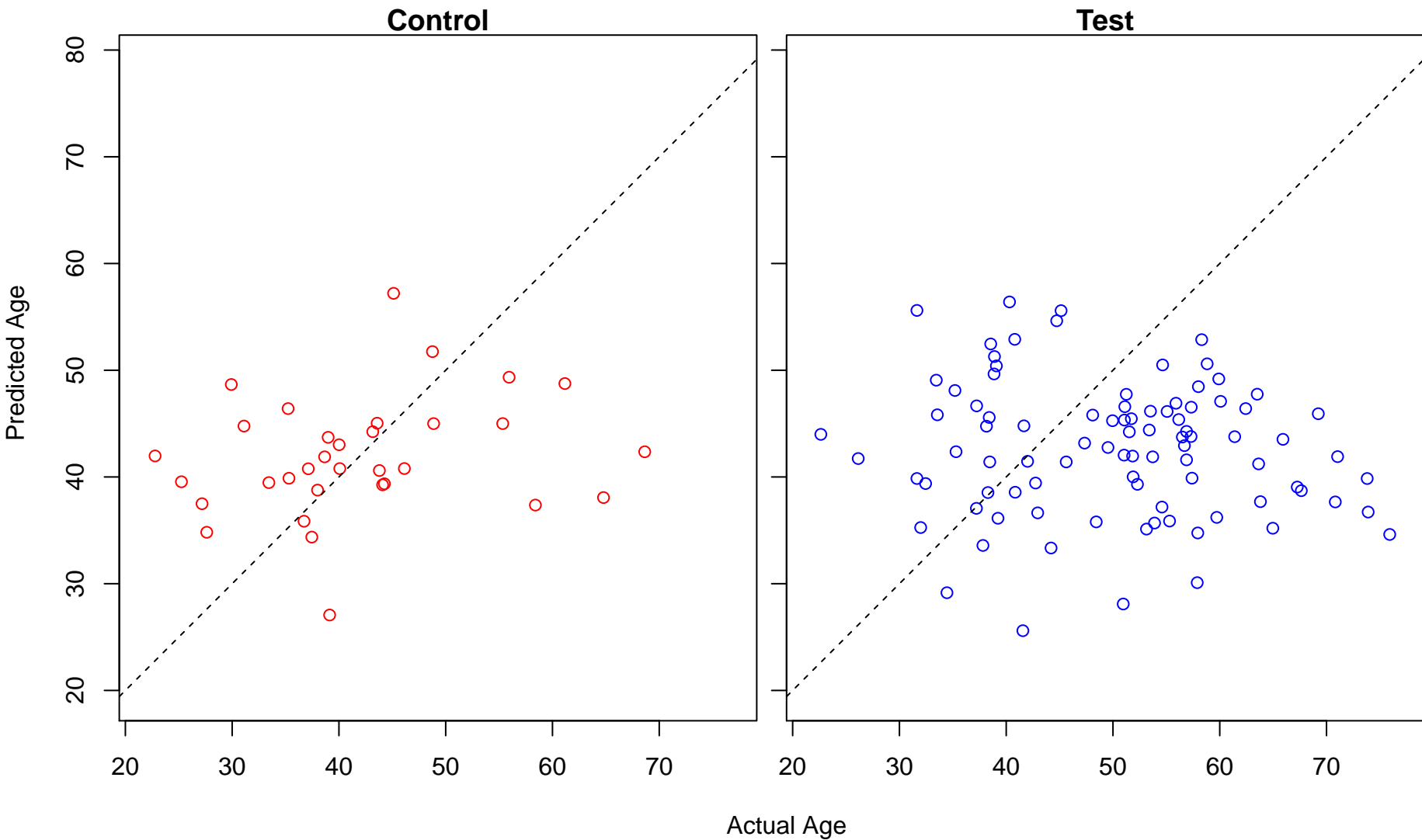
dephosphorylation of RNA polymerase II C-terminal domain (Score: 0.270151)



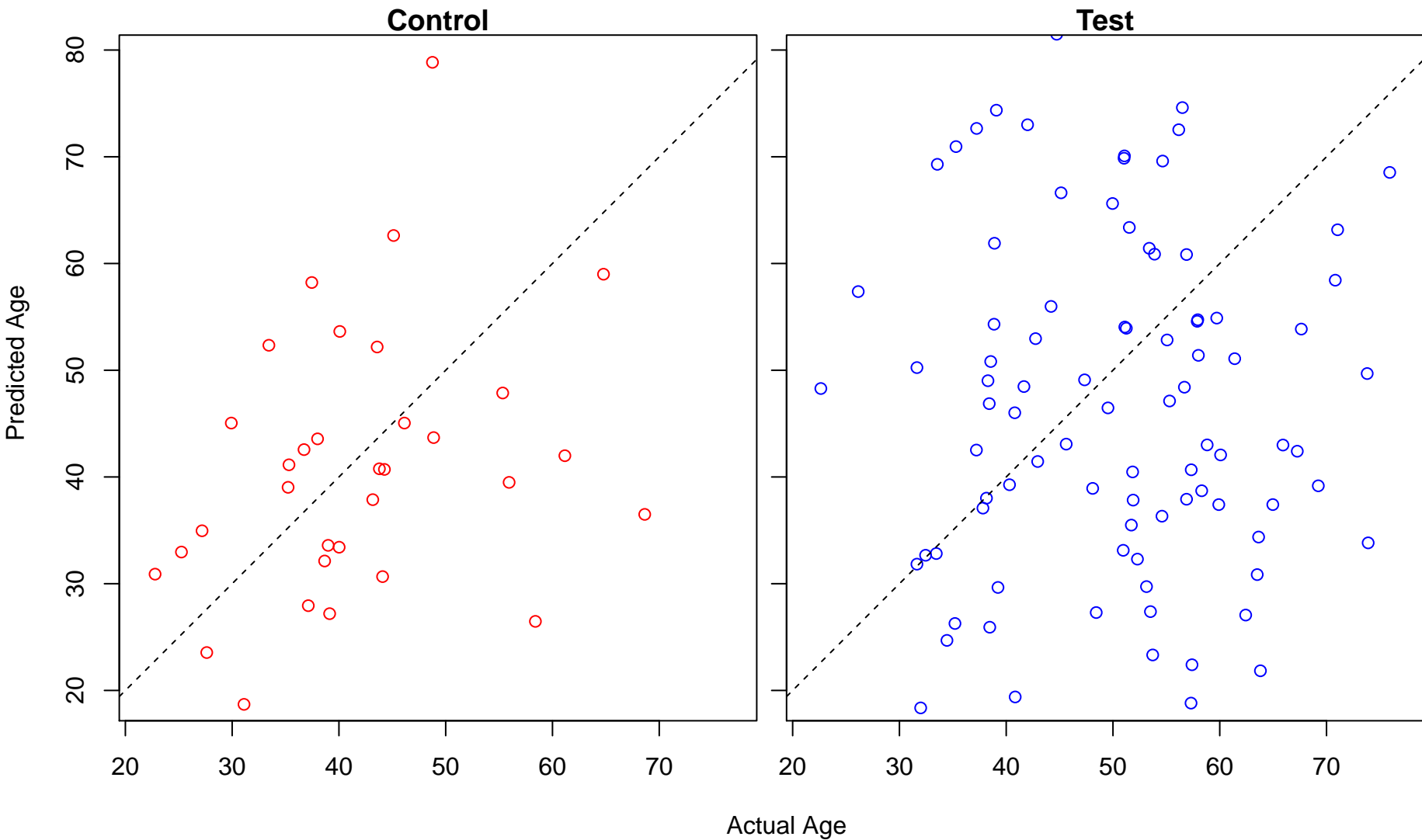
G0 to G1 transition (Score: 0.266739)



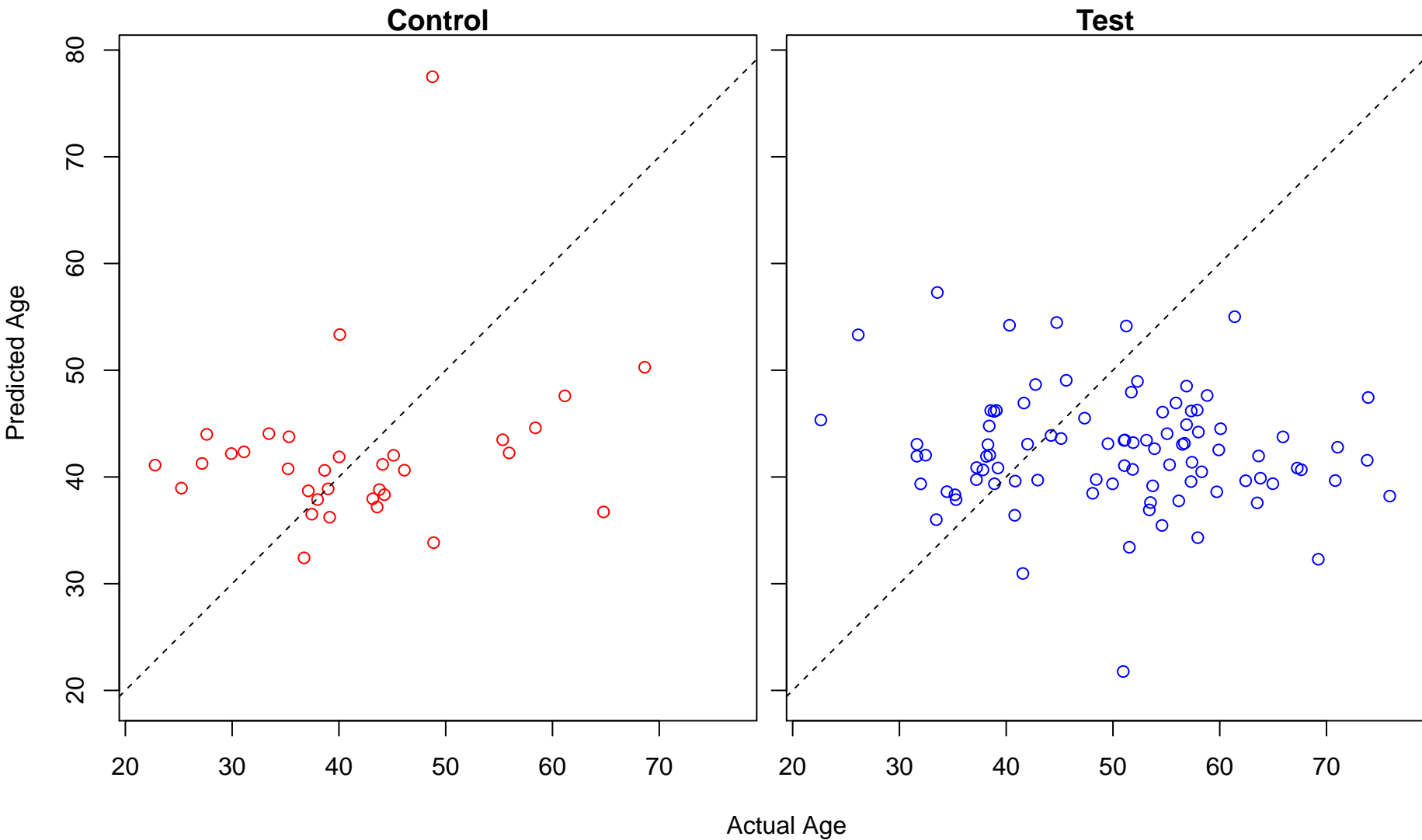
negative regulation of T cell mediated immunity (Score: 0.266337)



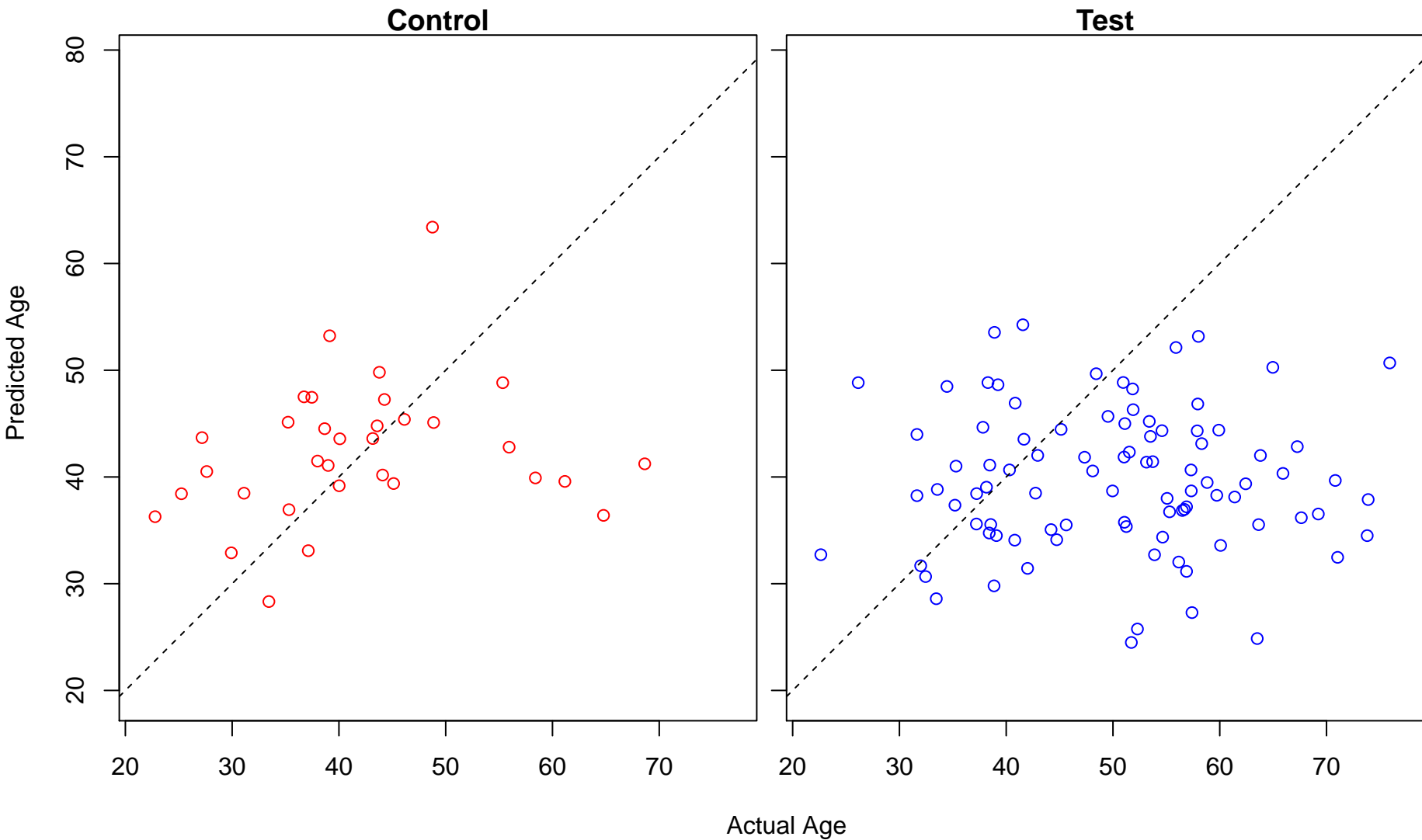
response to ketone (Score: 0.264767)



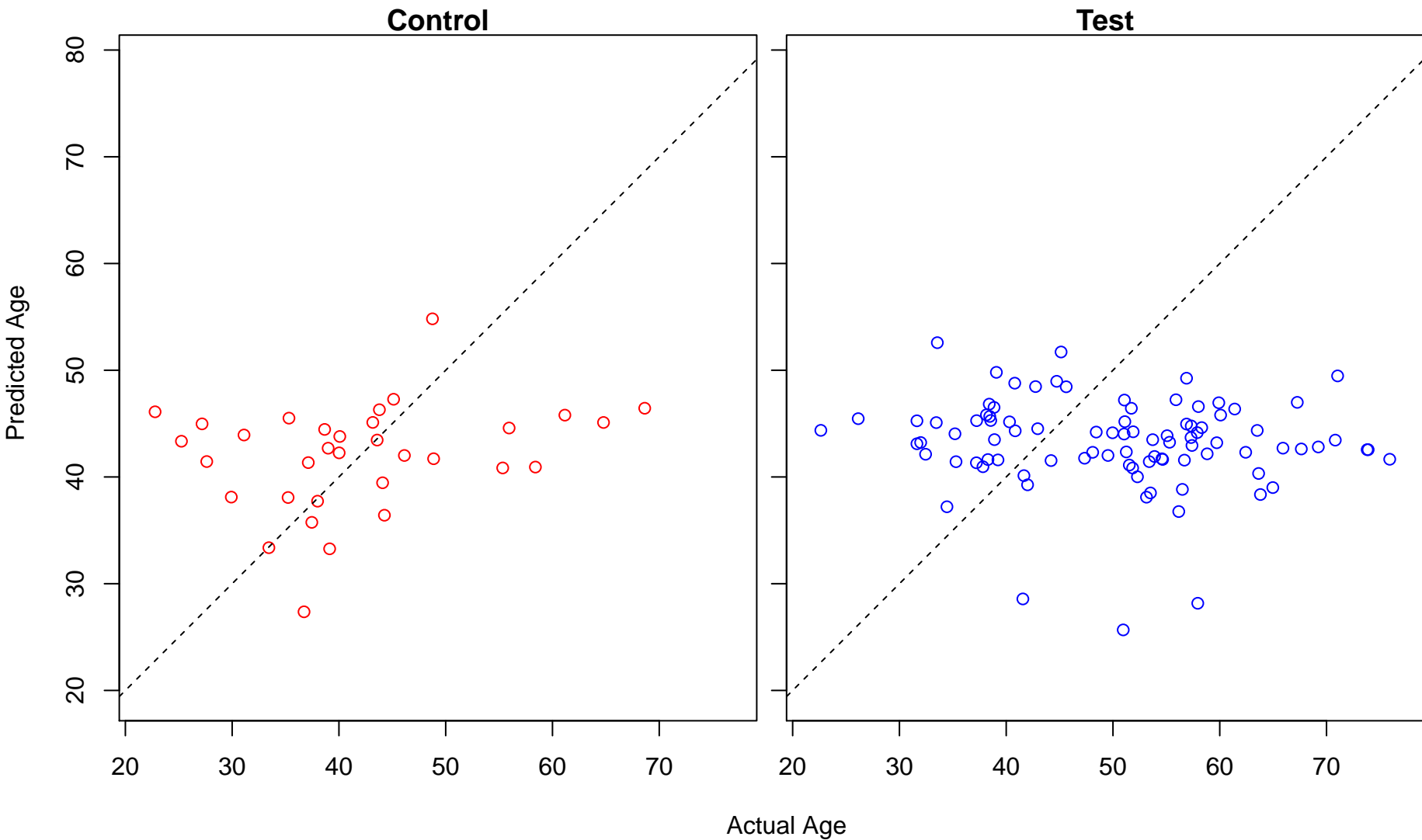
signal complex assembly (Score: 0.263049)



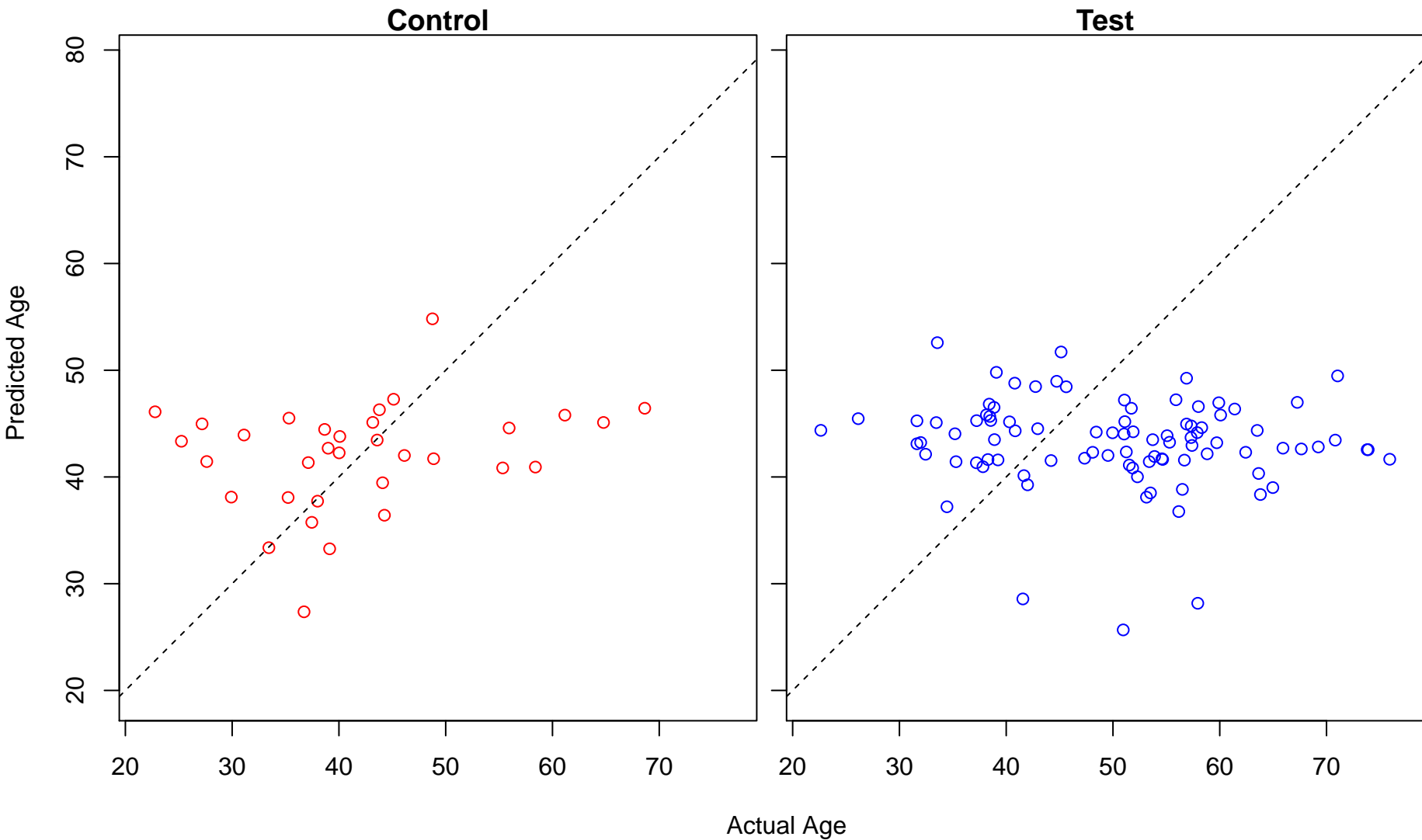
glycine metabolic process (Score: 0.262753)



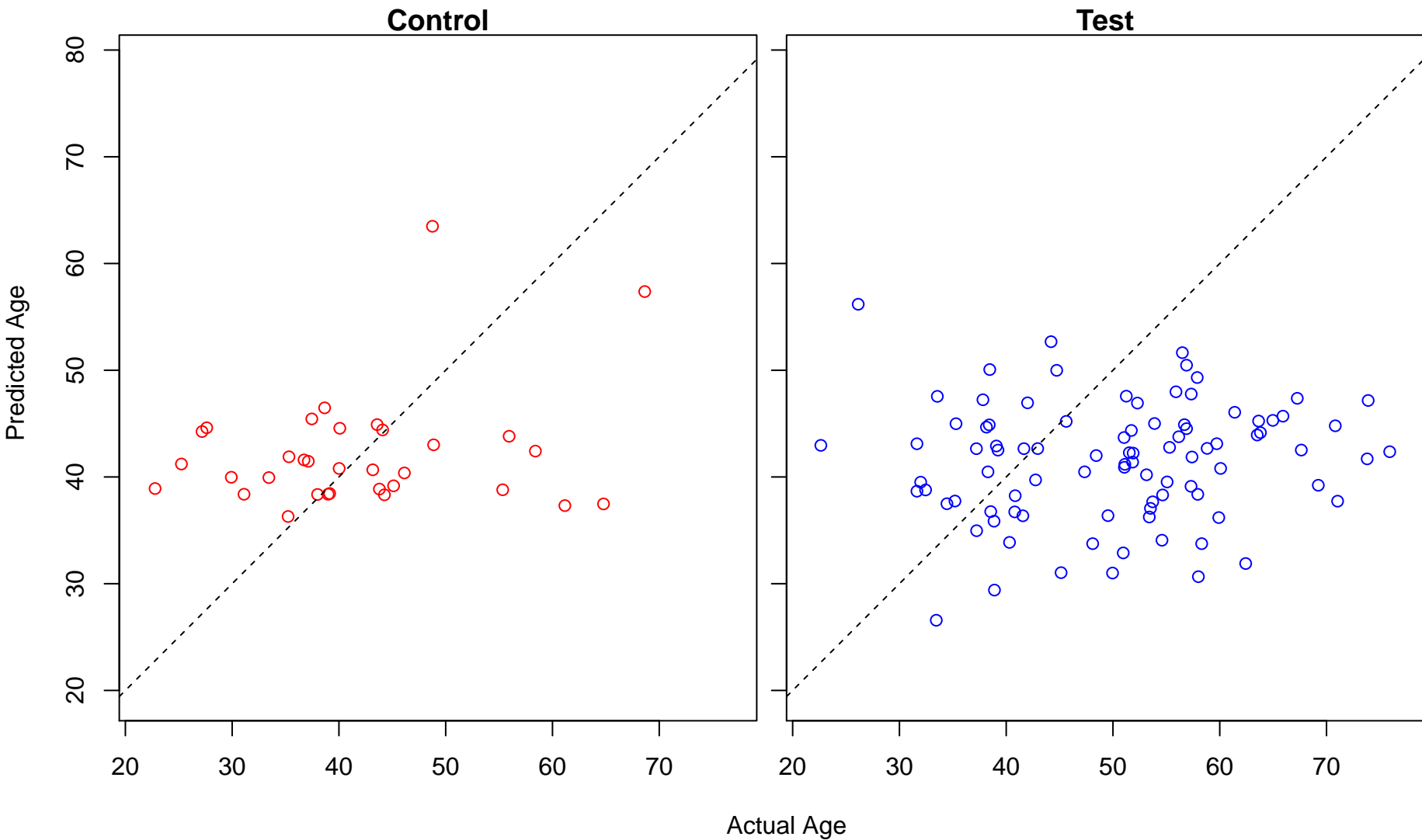
pyramidal neuron differentiation (Score: 0.260733)



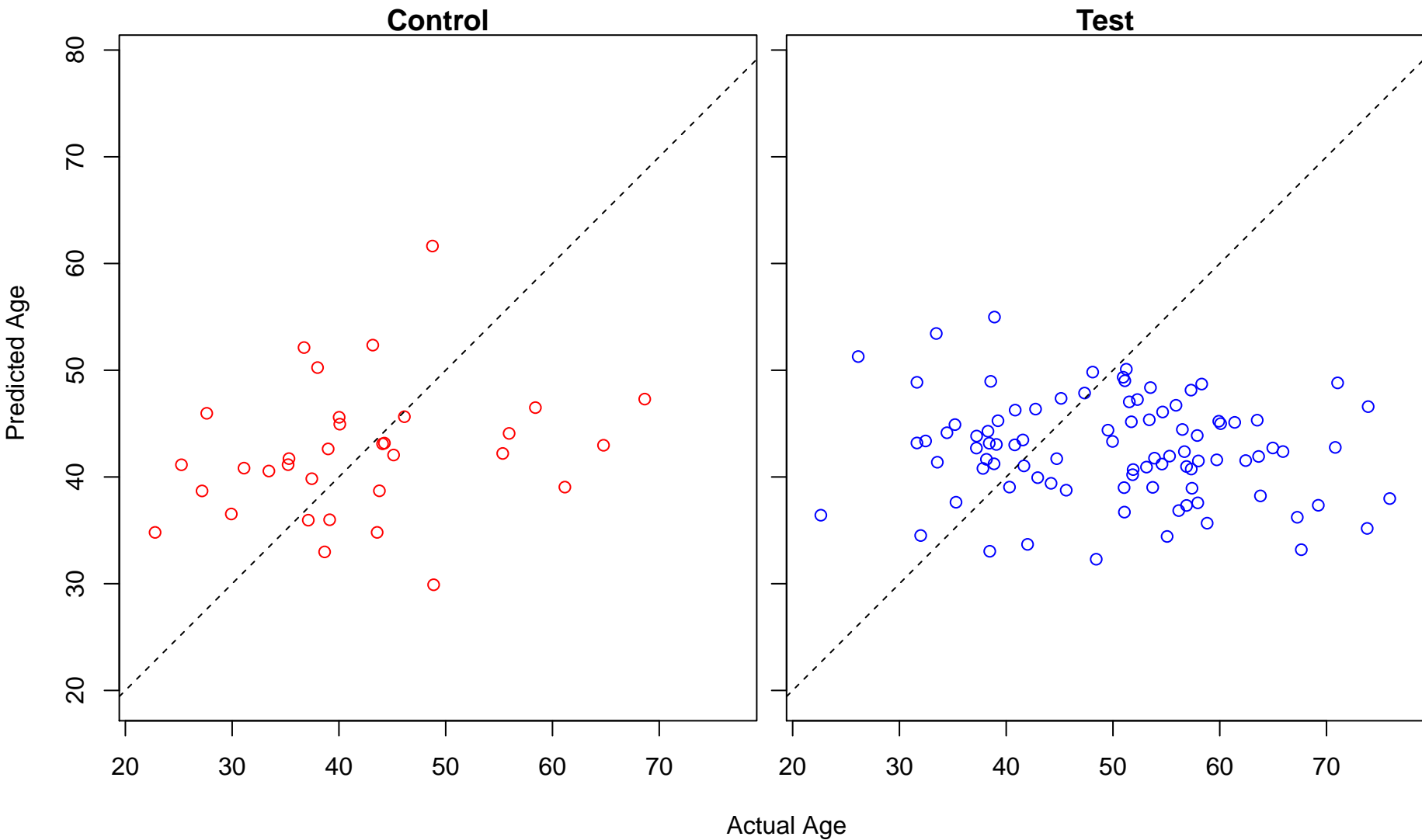
pyramidal neuron development (Score: 0.260733)



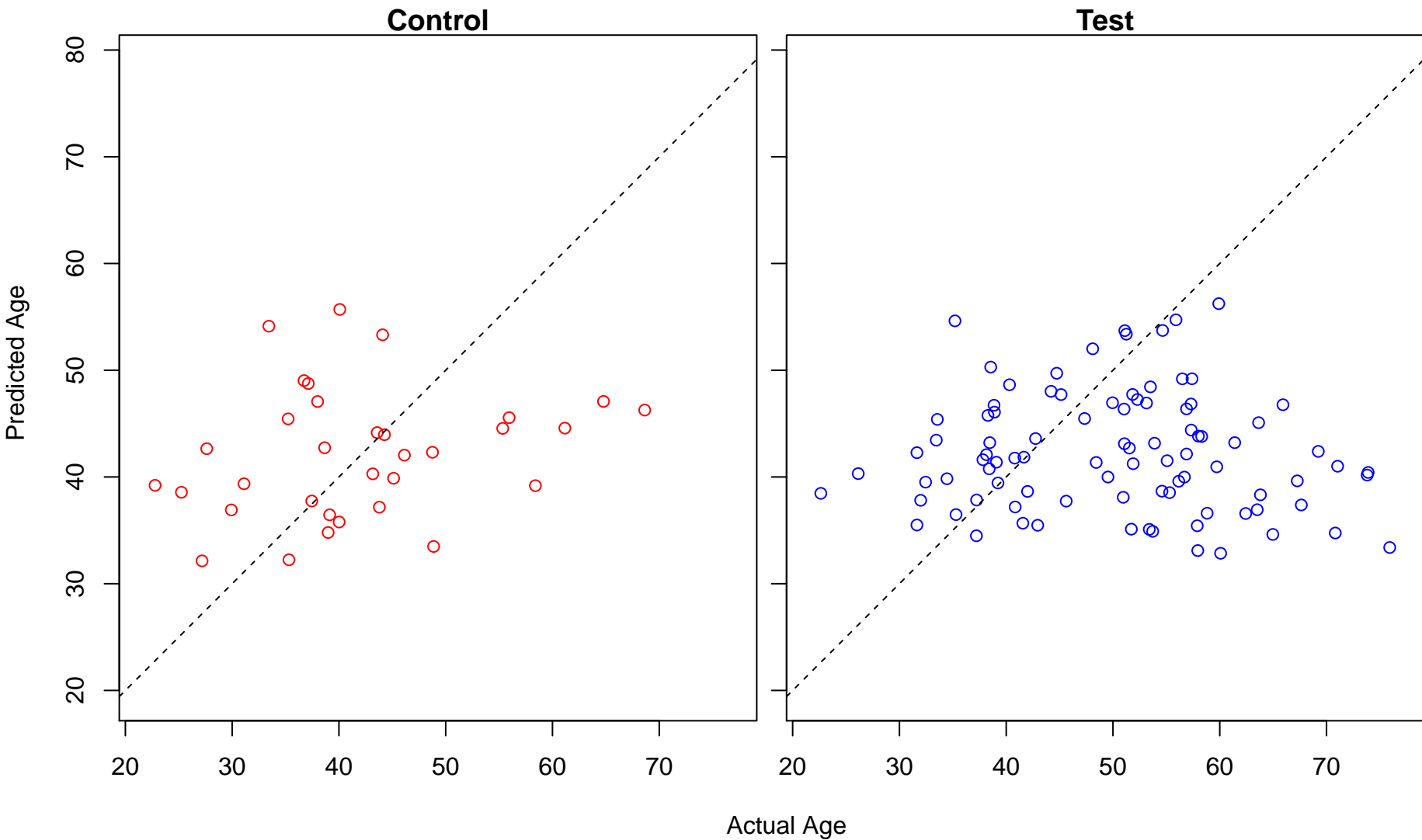
negative regulation of protein K63-linked ubiquitination (Score: 0.260121)



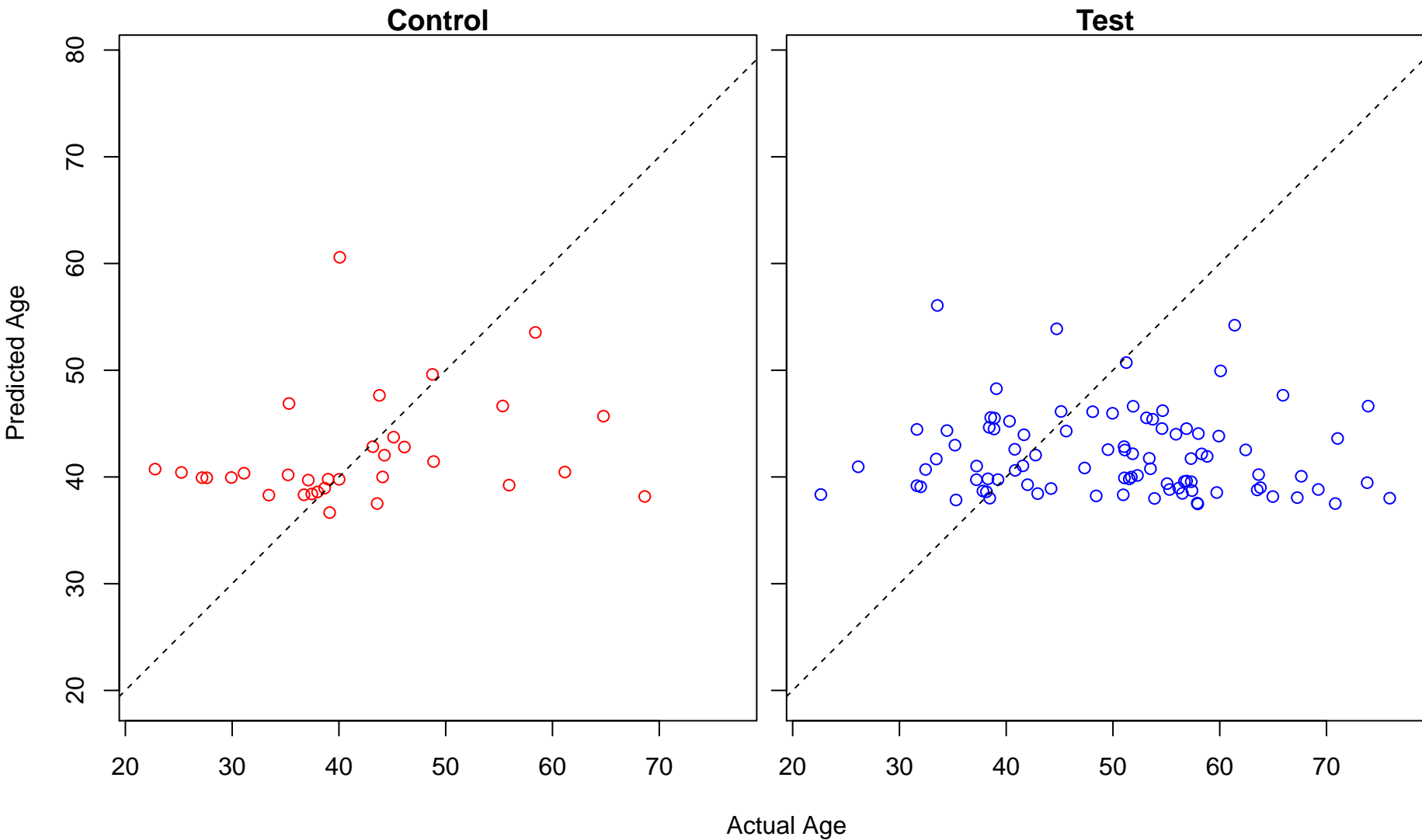
negative regulation of vascular permeability (Score: 0.259743)



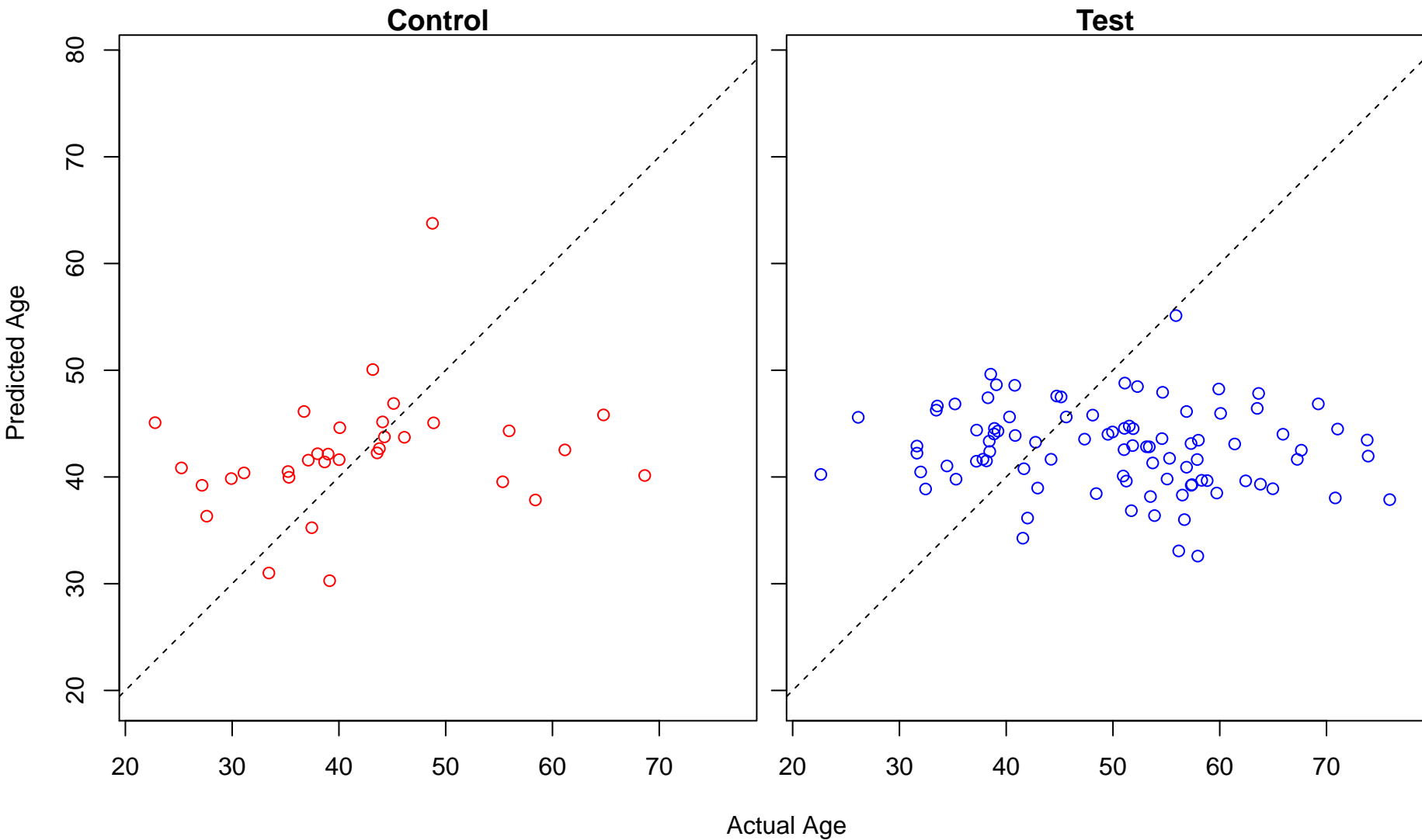
negative regulation of smooth muscle cell differentiation (Score: 0.259722)



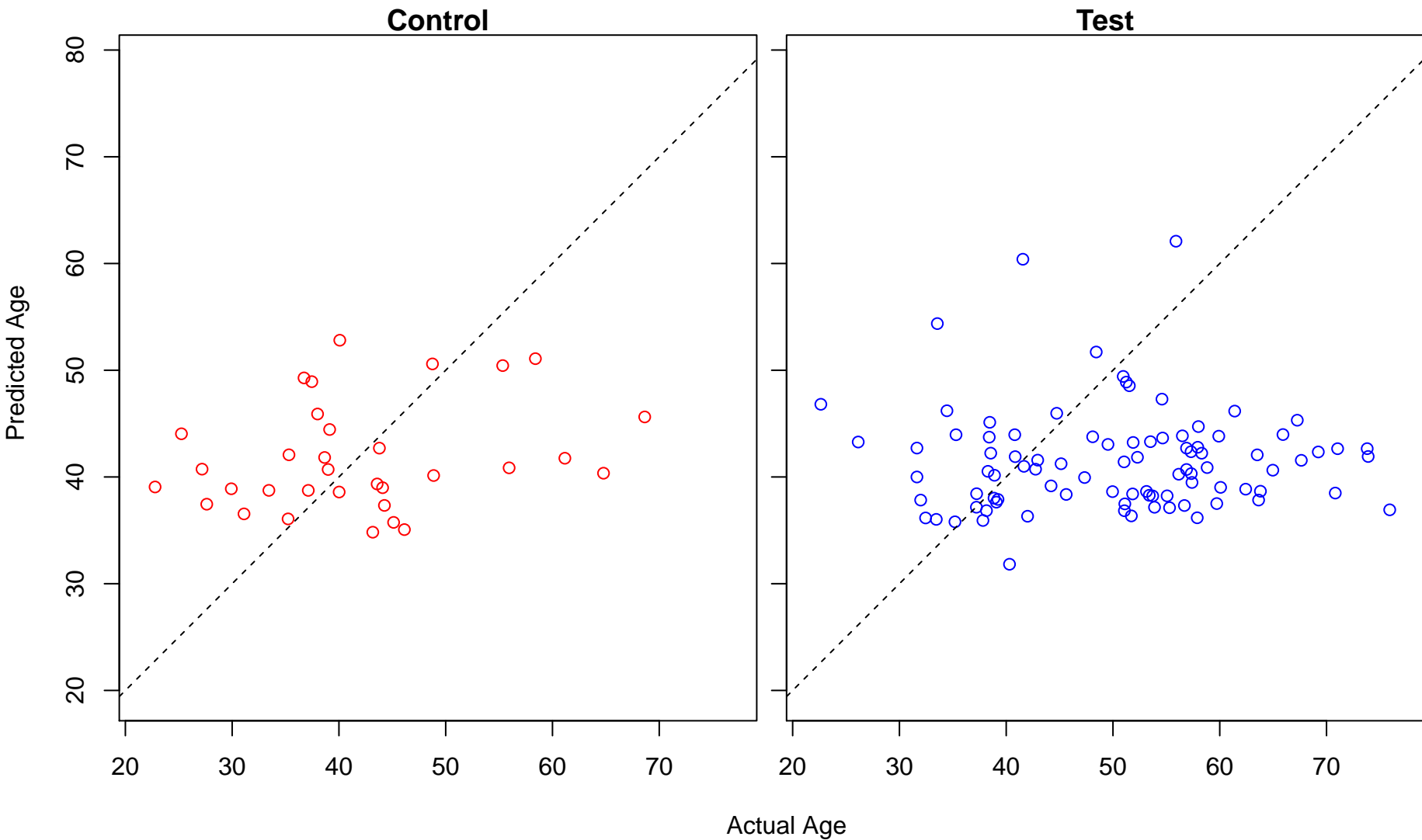
visual behavior (Score: 0.258993)



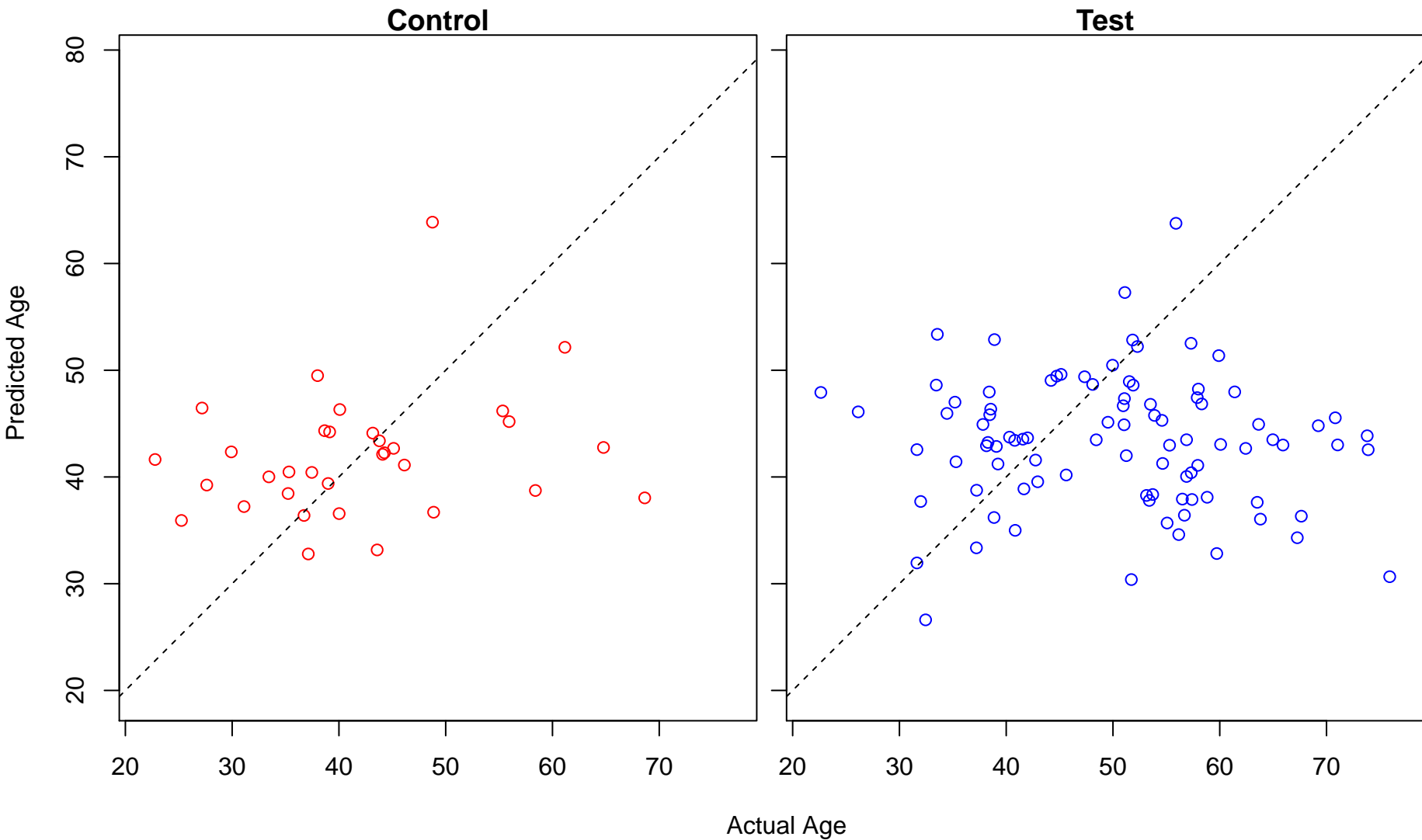
vesicle transport along actin filament (Score: 0.257223)



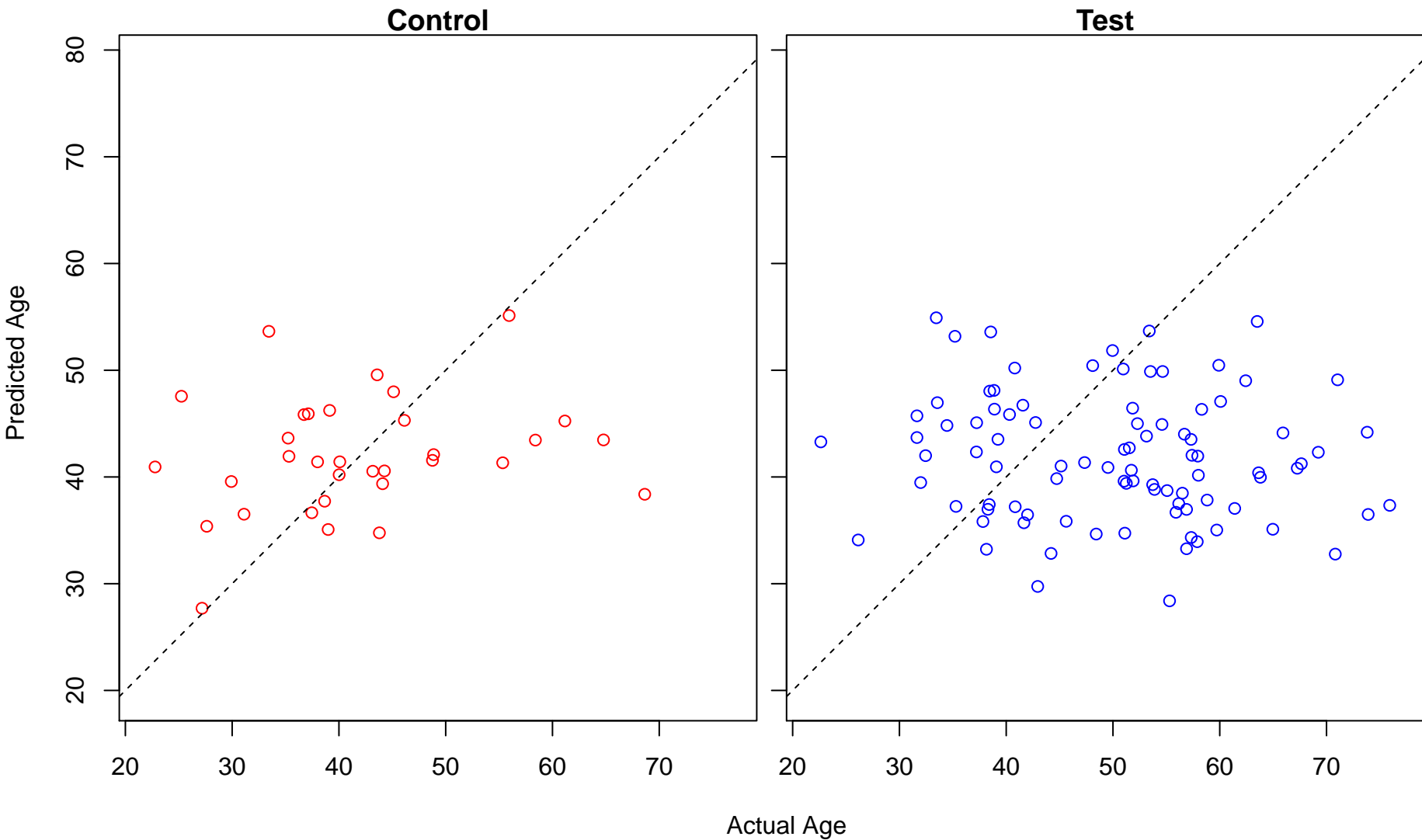
interkinetic nuclear migration (Score: 0.255321)



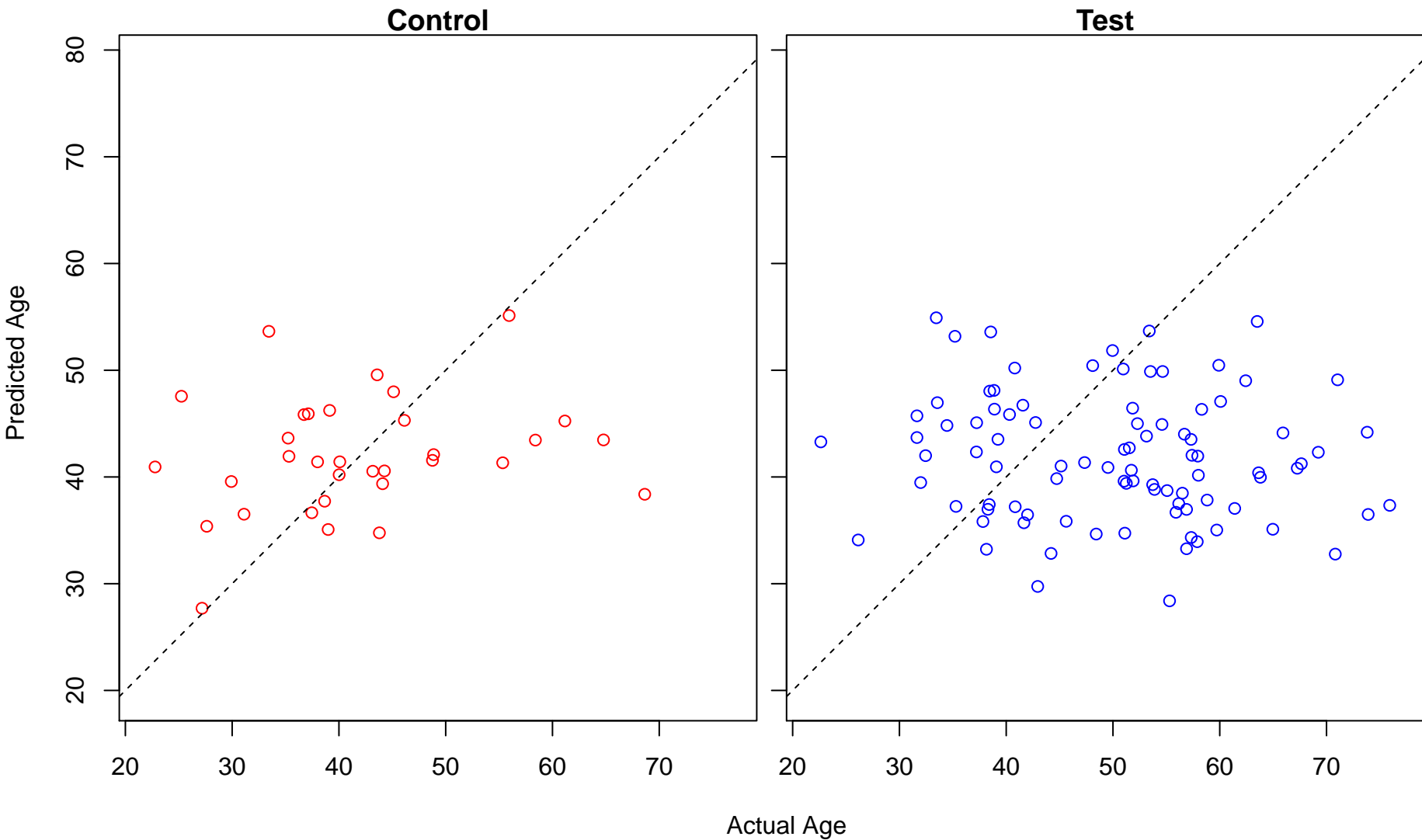
retrograde transport, plasma membrane to Golgi (Score: 0.255287)



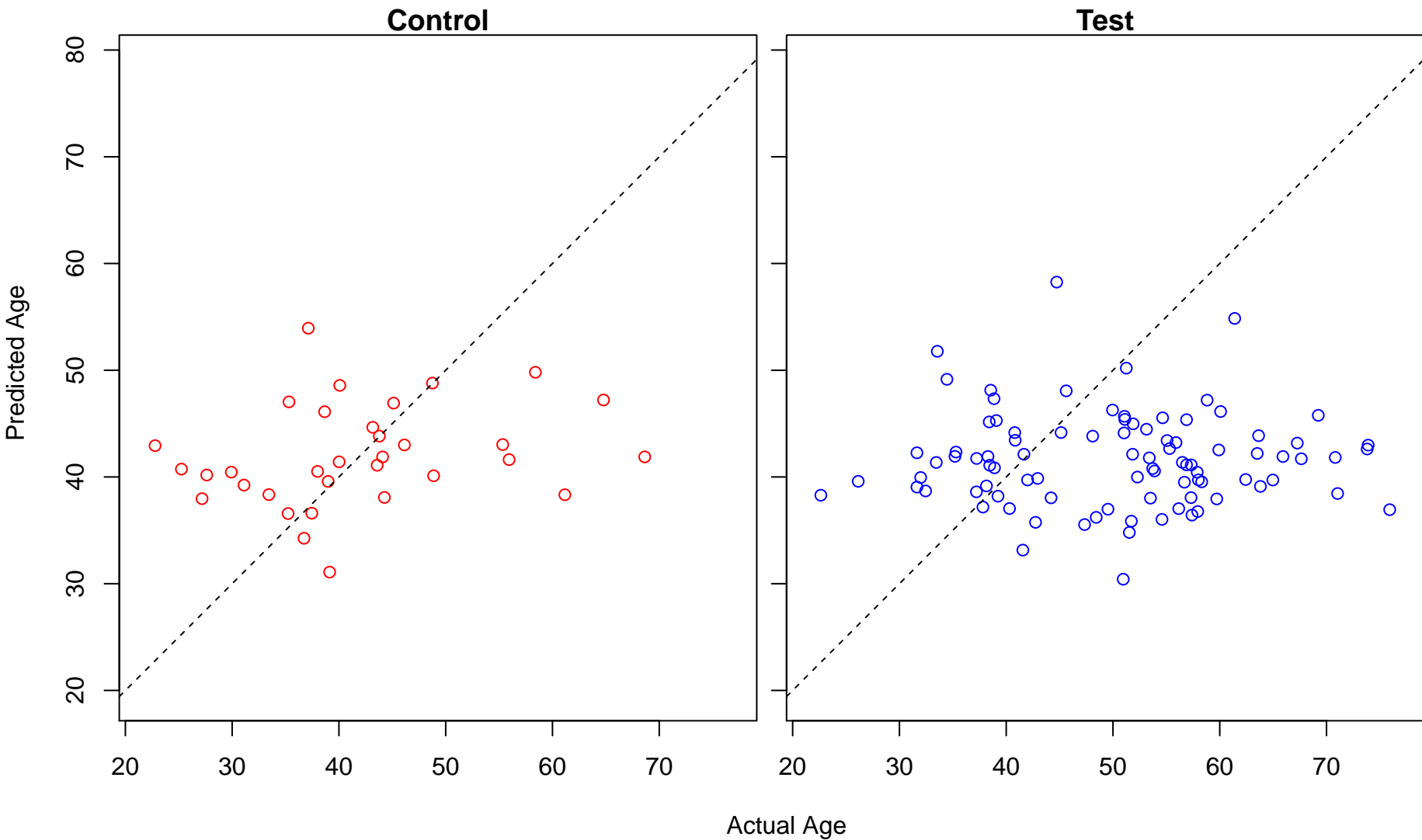
hypotonic response (Score: 0.251688)



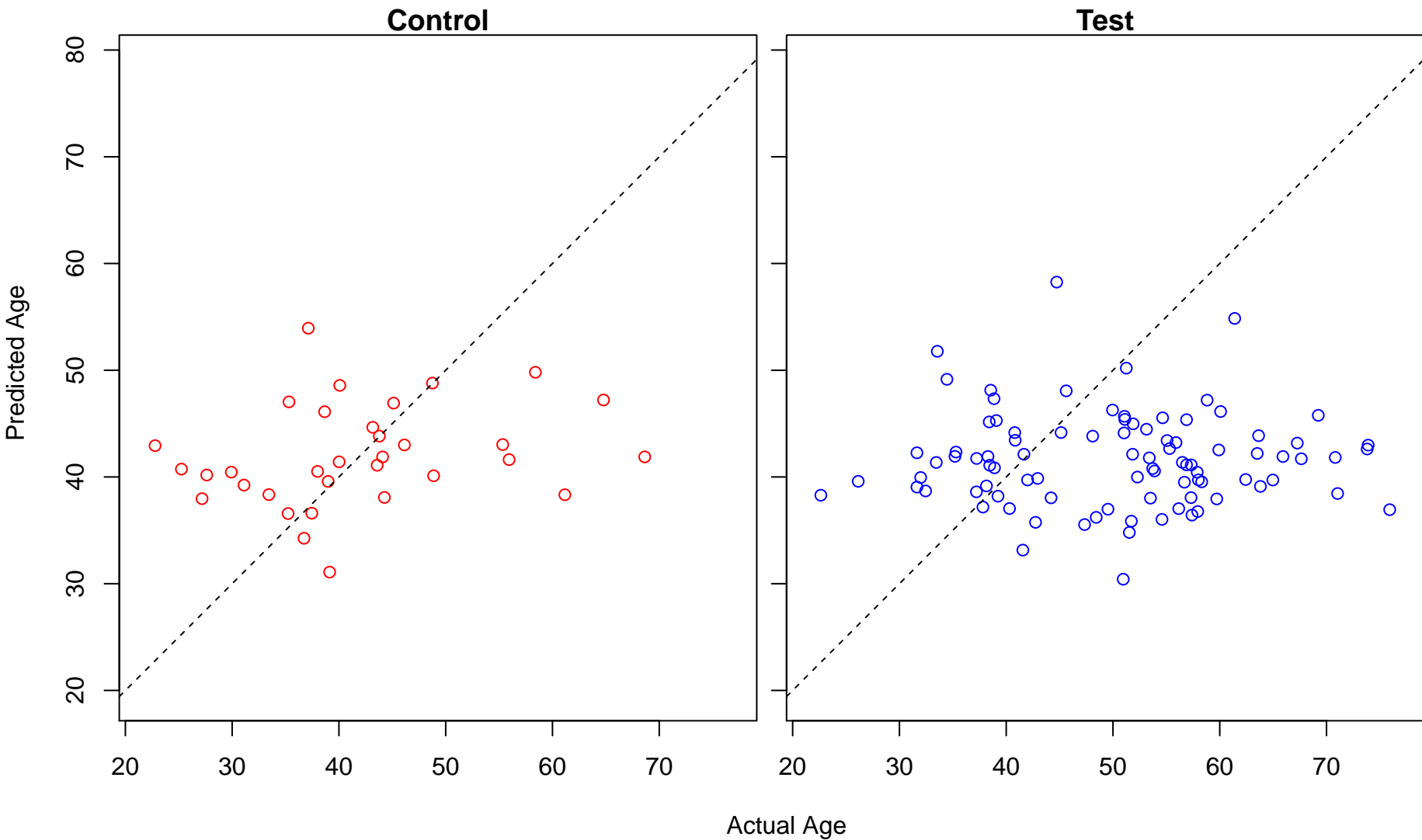
cellular hypotonic response (Score: 0.251688)



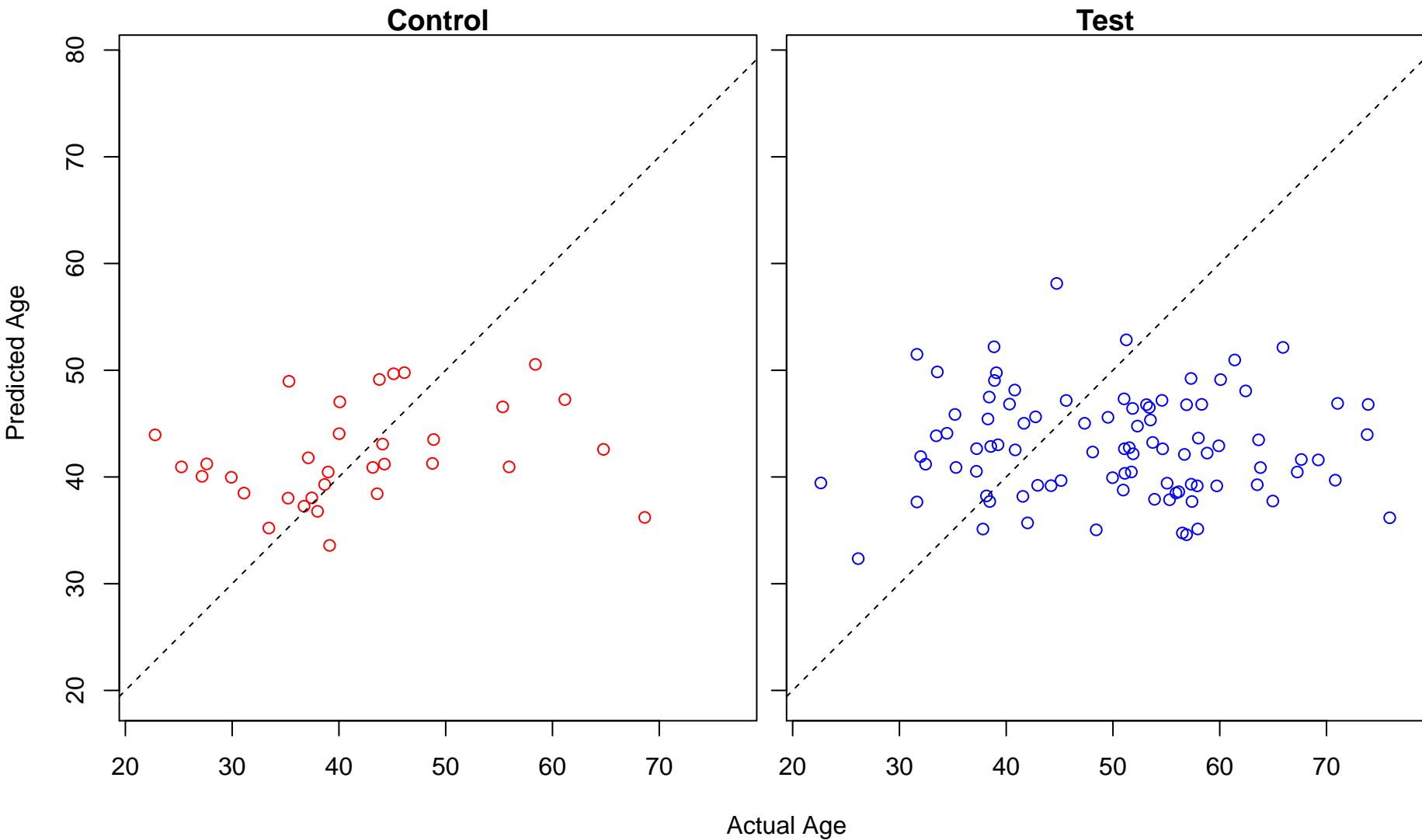
macrophage derived foam cell differentiation (Score: 0.250917)



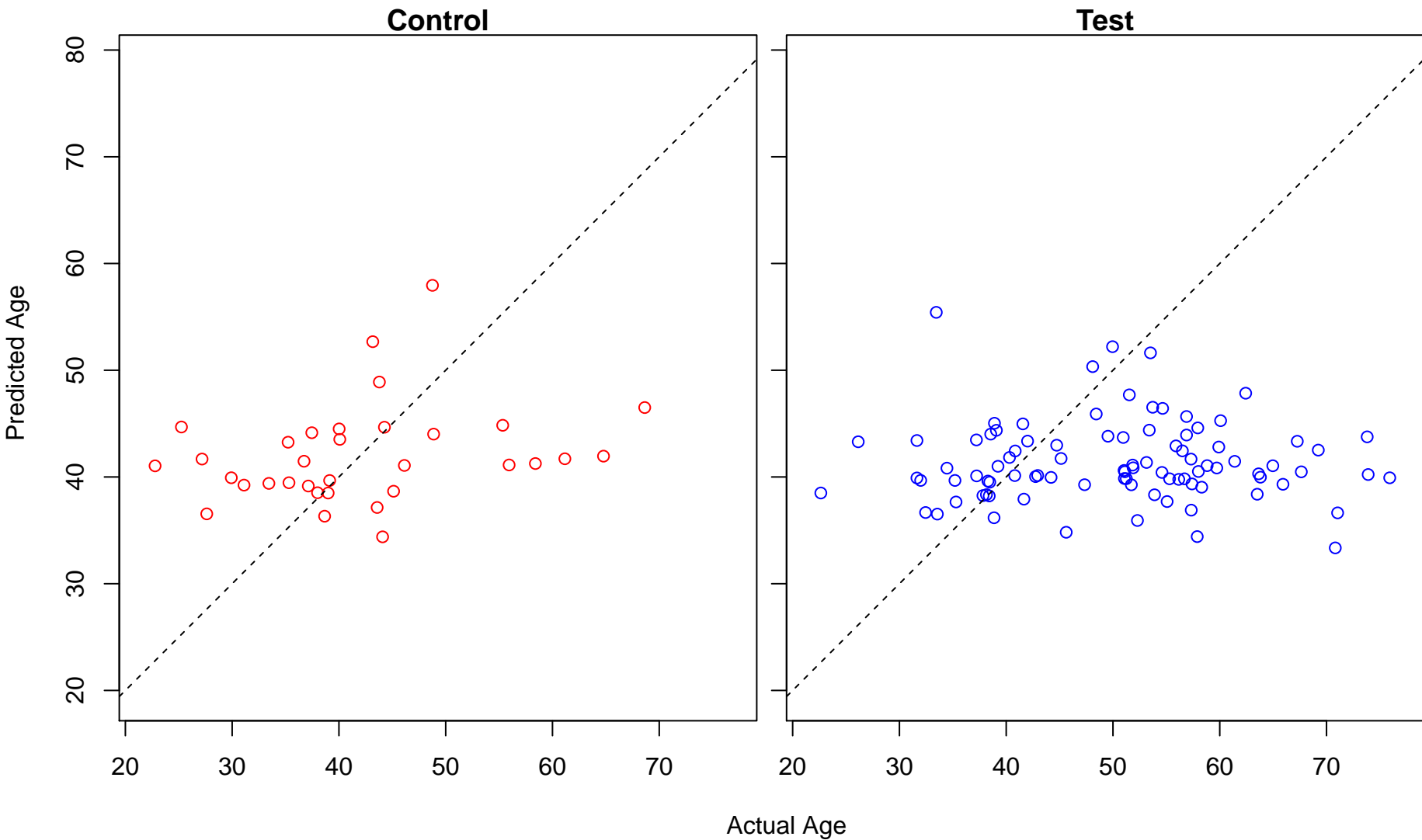
foam cell differentiation (Score: 0.250917)



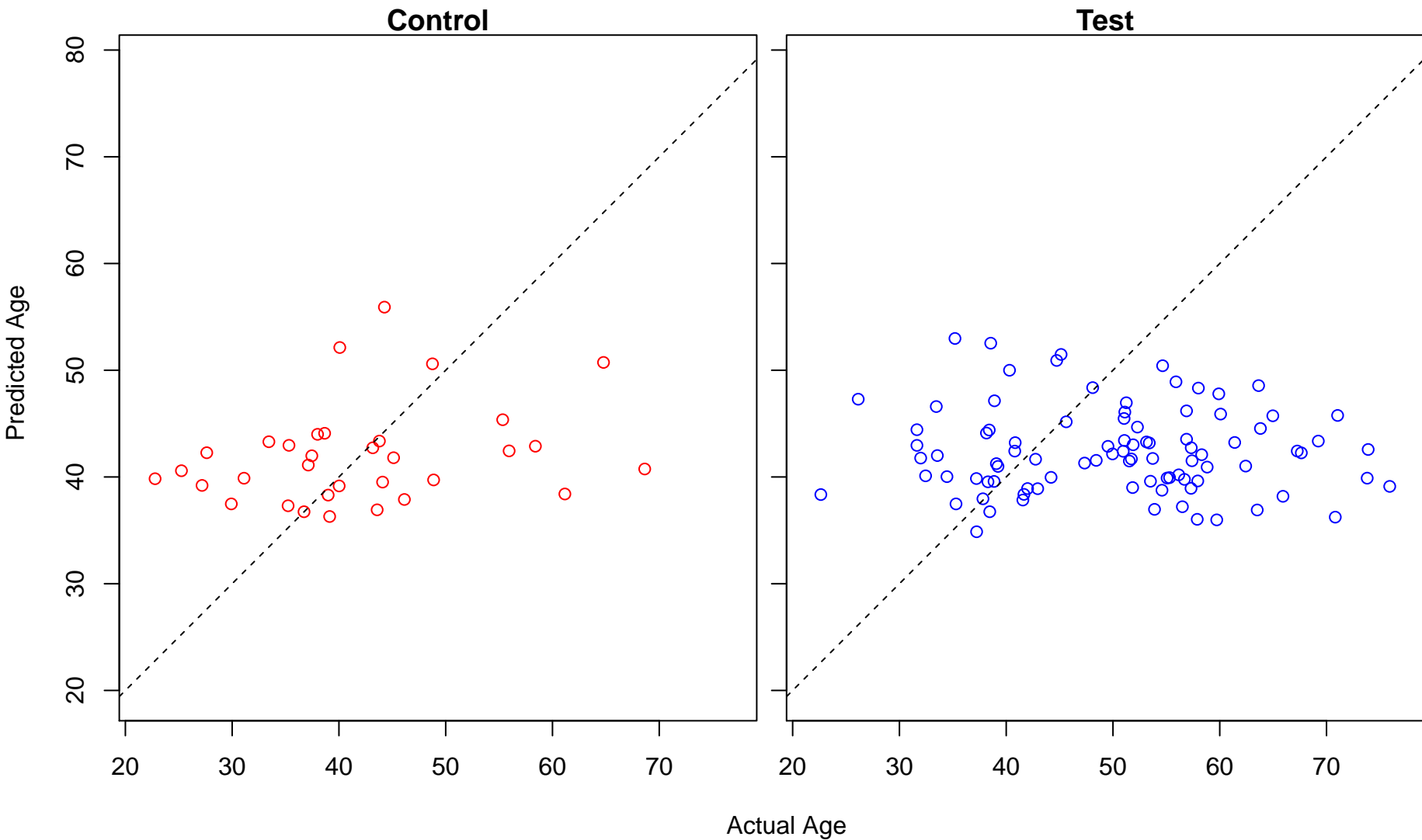
cell junction maintenance (Score: 0.249311)



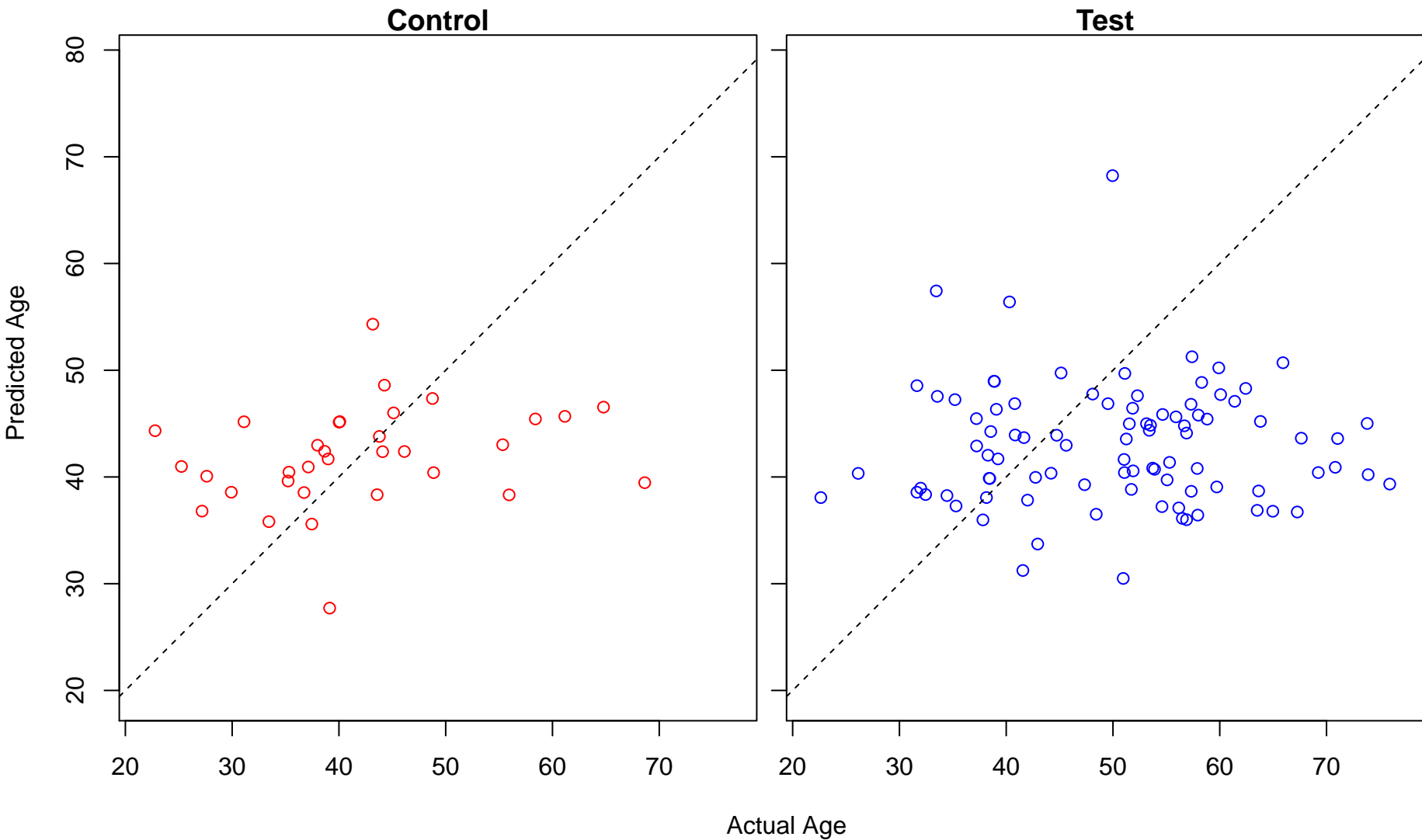
amine transport (Score: 0.249252)



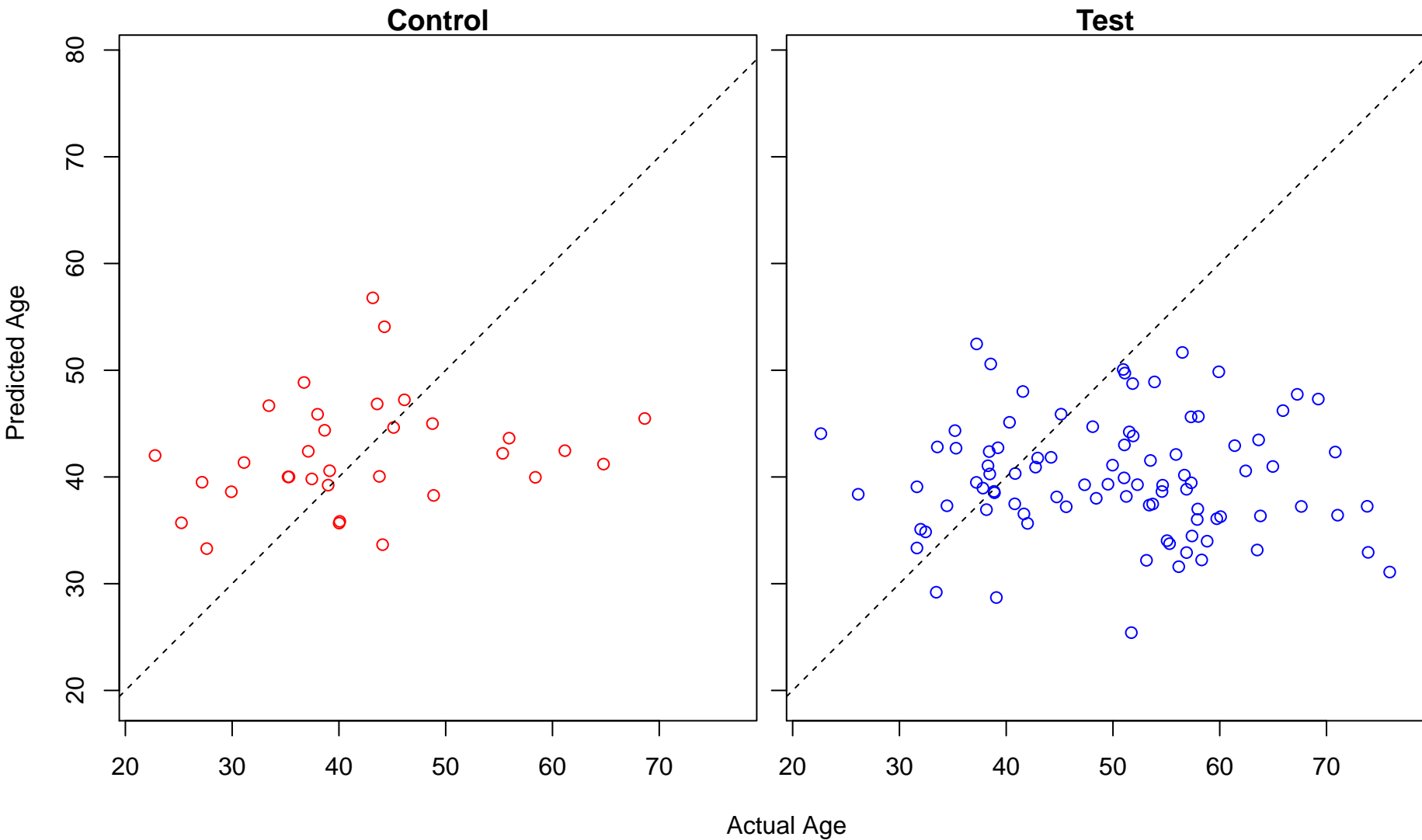
notochord development (Score: 0.248319)



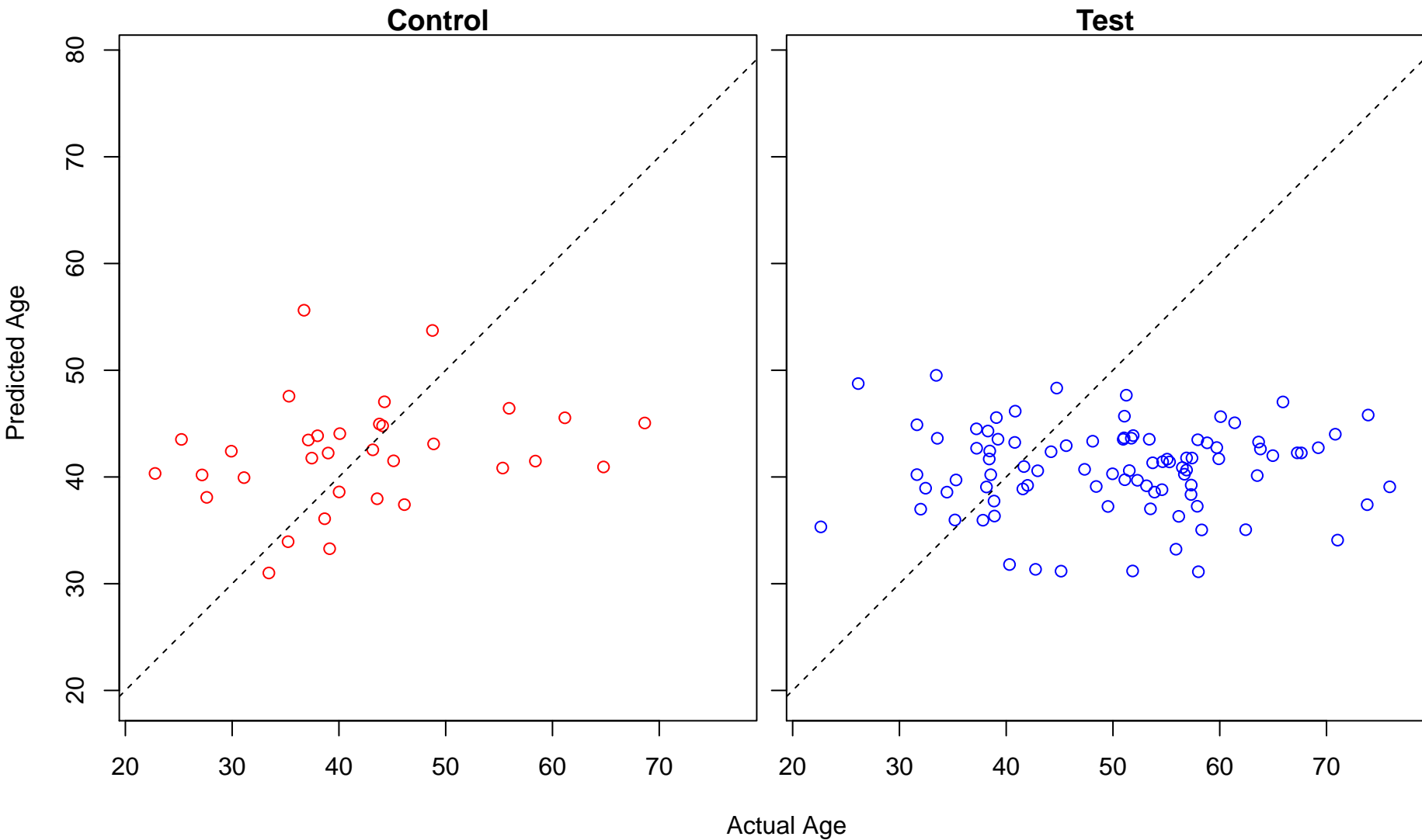
AMP biosynthetic process (Score: 0.247671)



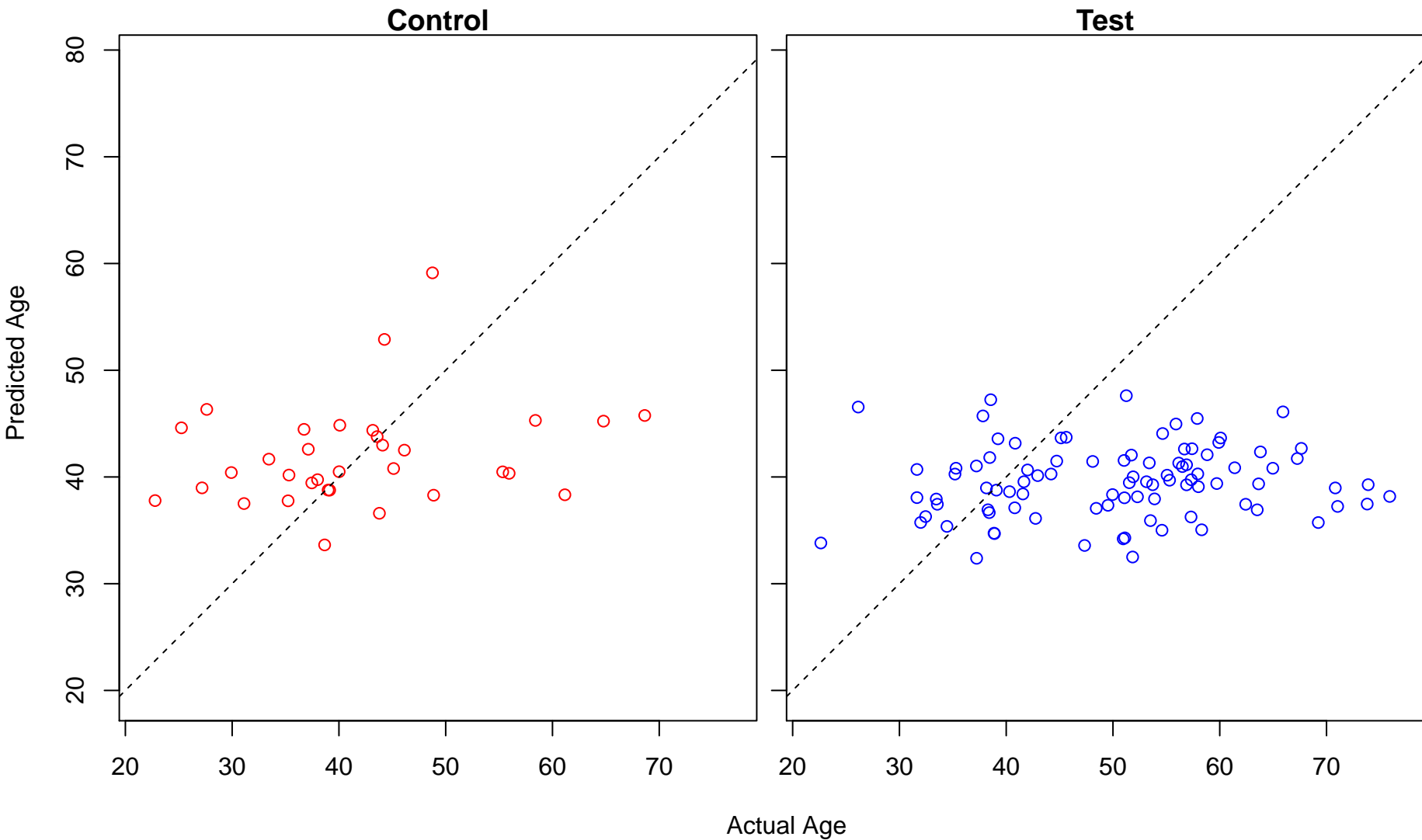
mitotic spindle stabilization (Score: 0.241362)



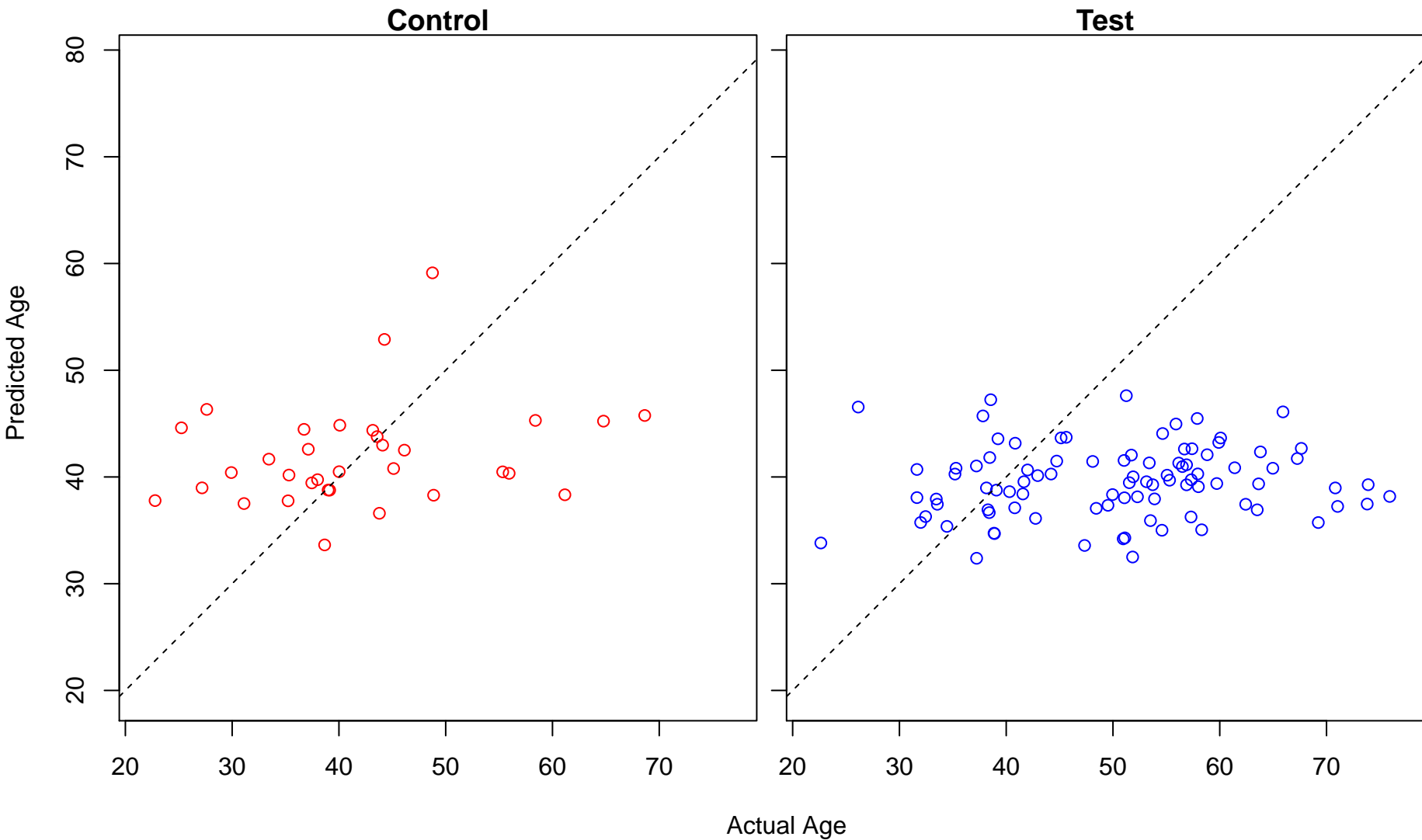
regulation of hepatocyte proliferation (Score: 0.240764)



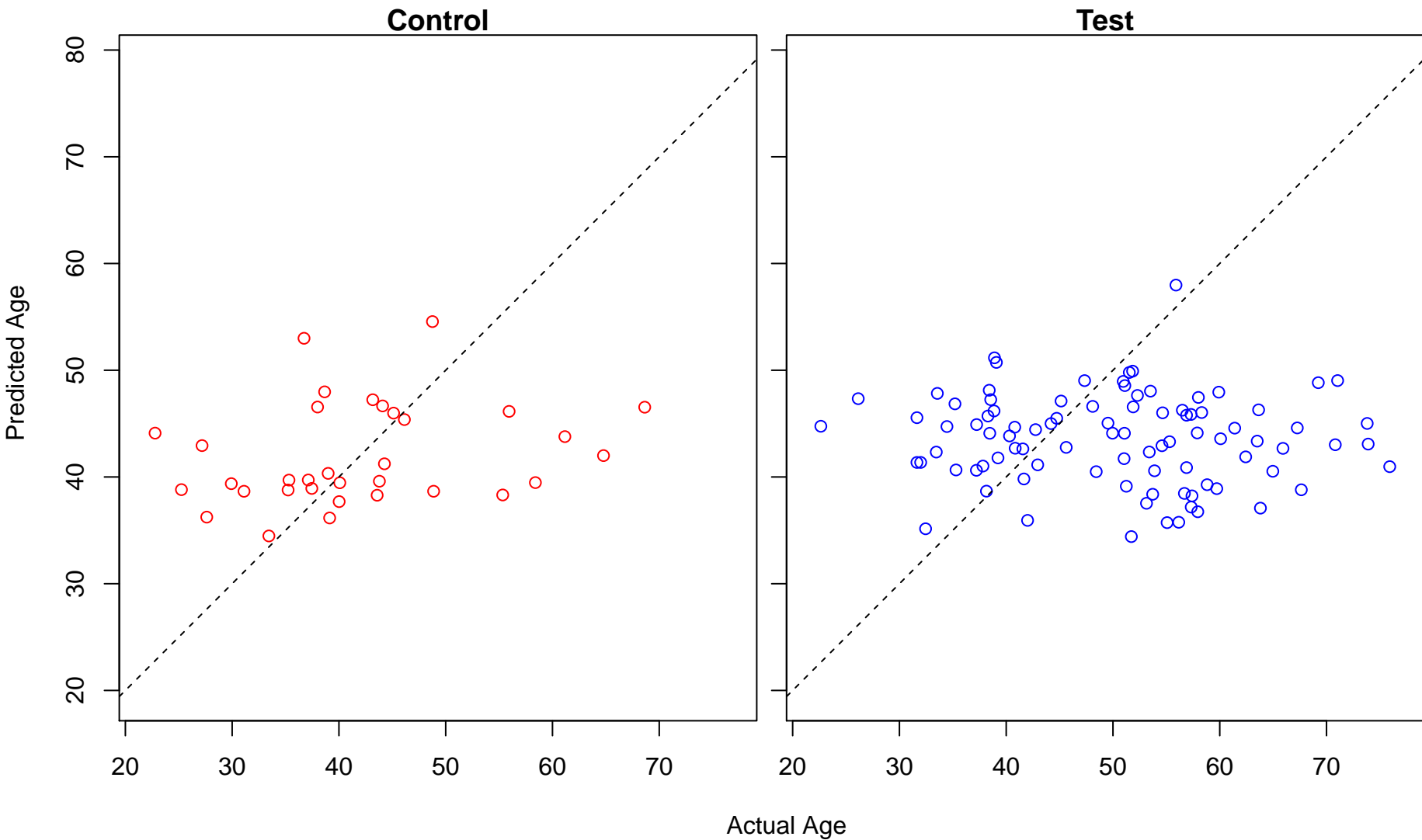
regulation of dendritic cell cytokine production (Score: 0.235573)



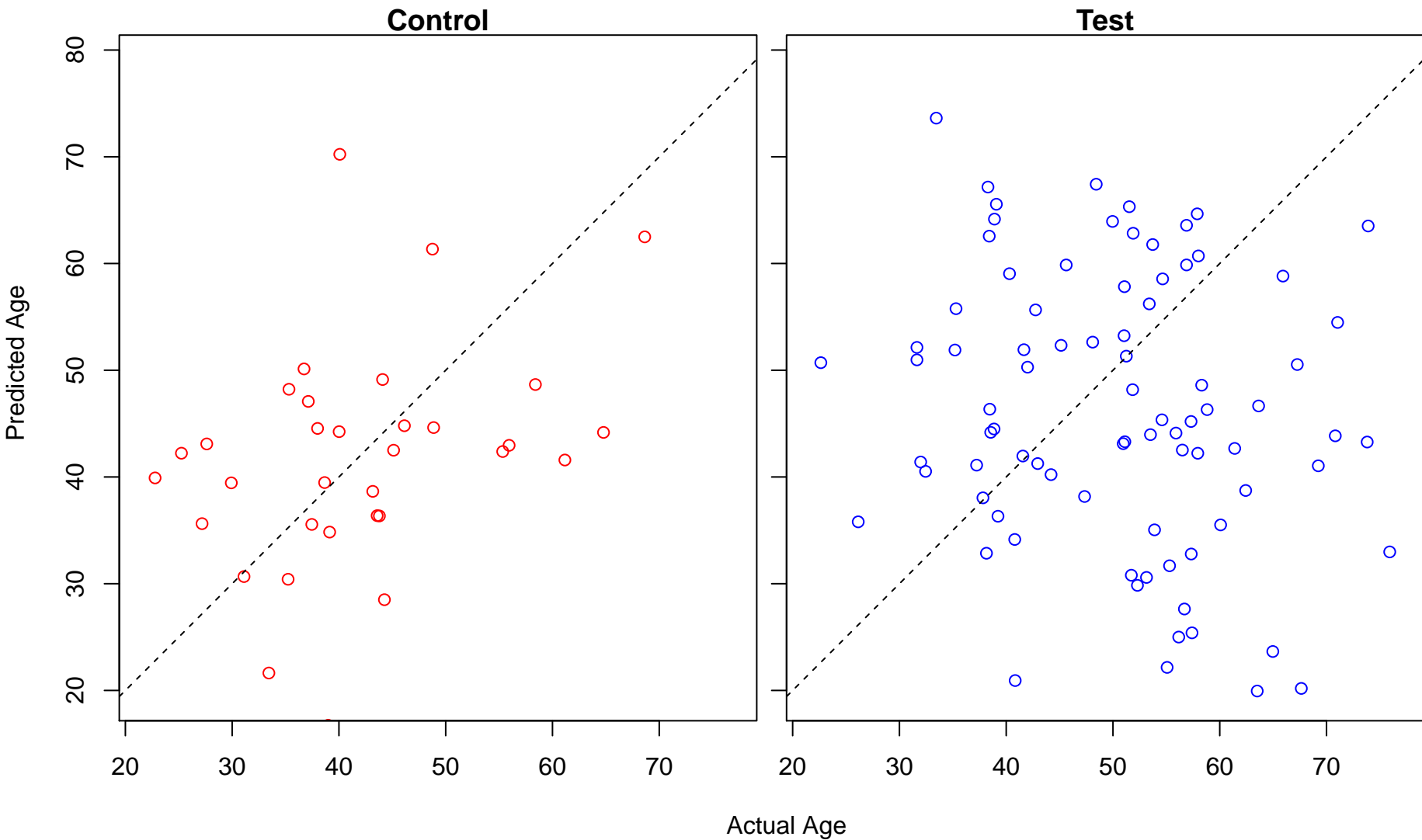
negative regulation of dendritic cell cytokine production (Score: 0.235573)



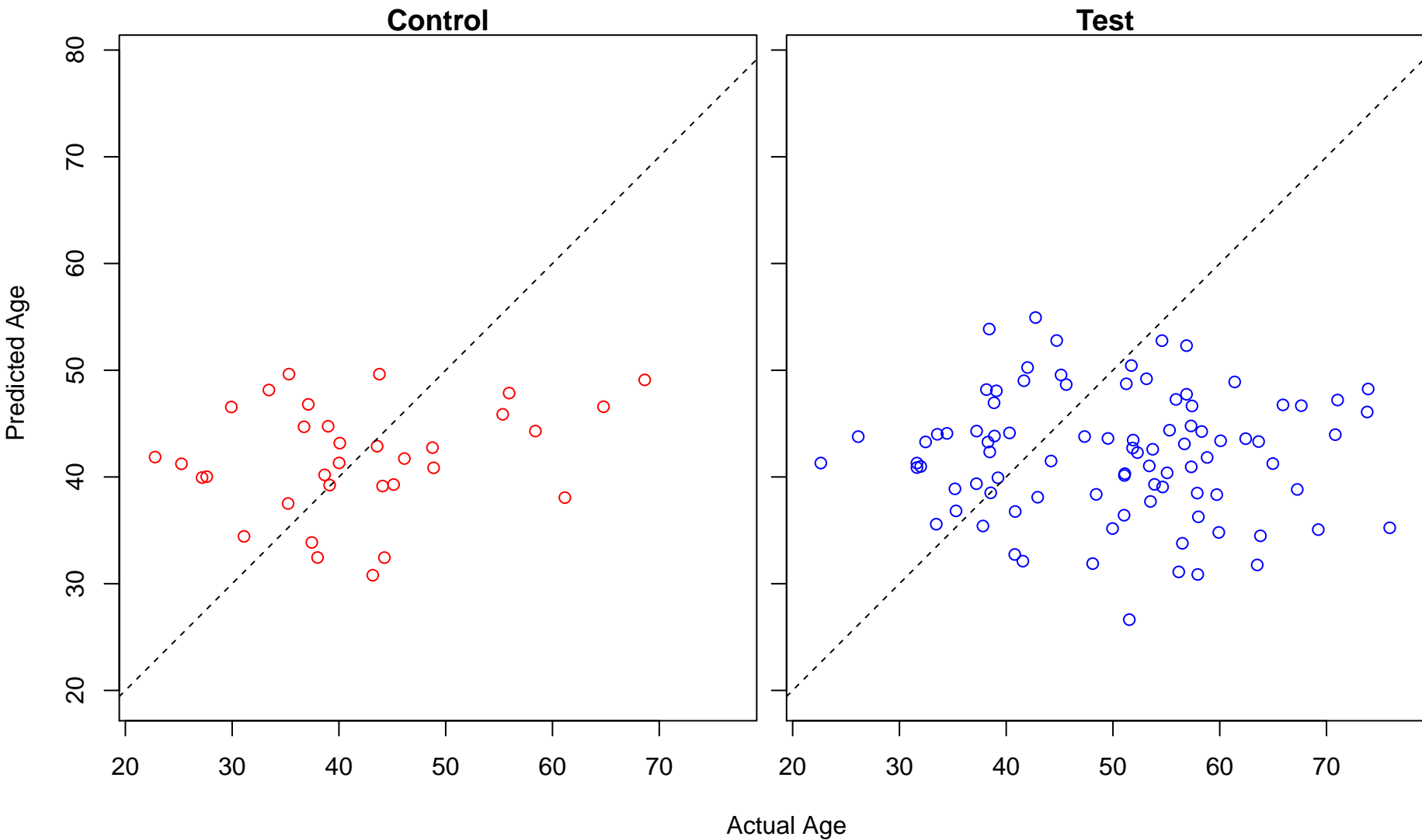
fibroblast activation (Score: 0.235218)



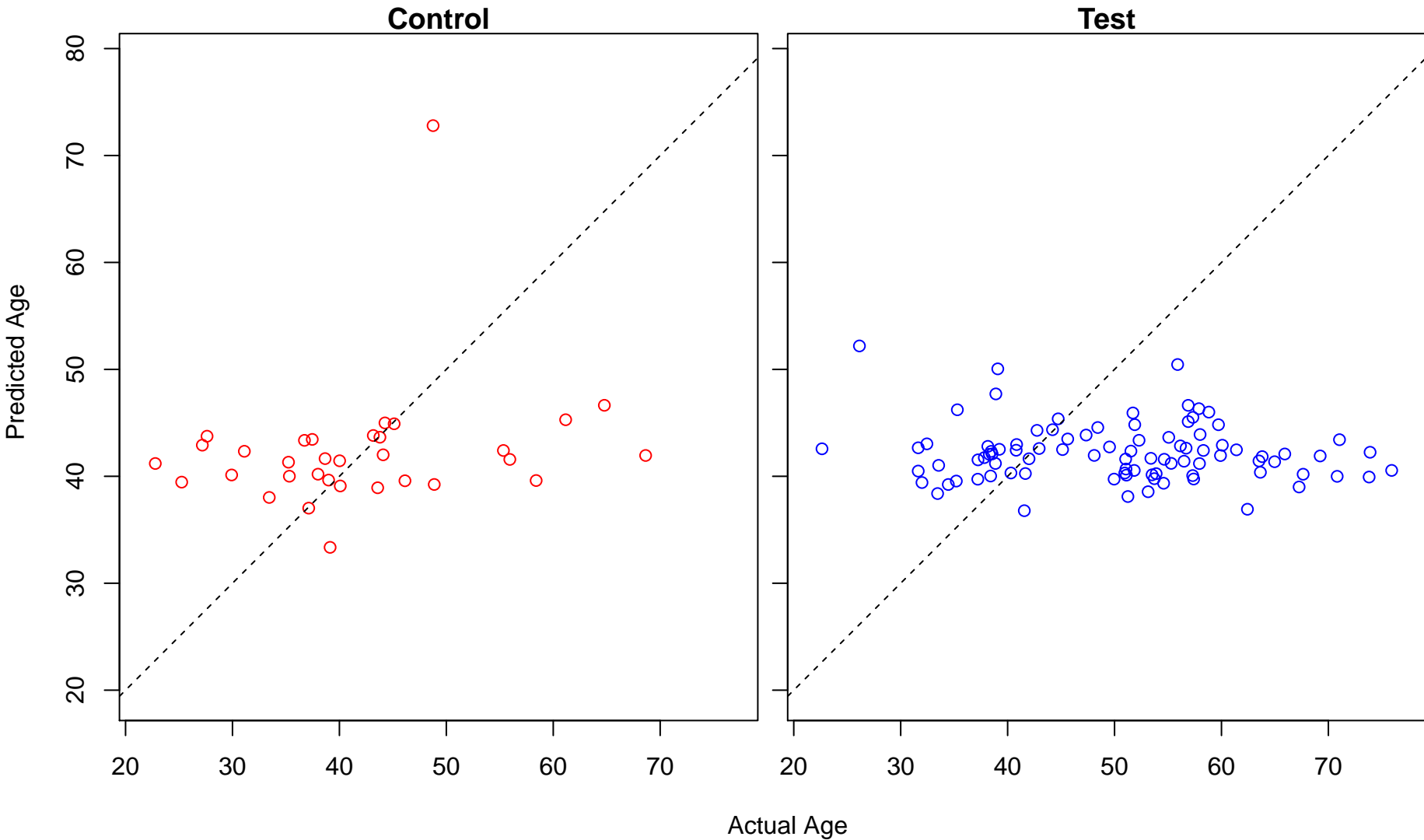
chondroitin sulfate metabolic process (Score: 0.233833)



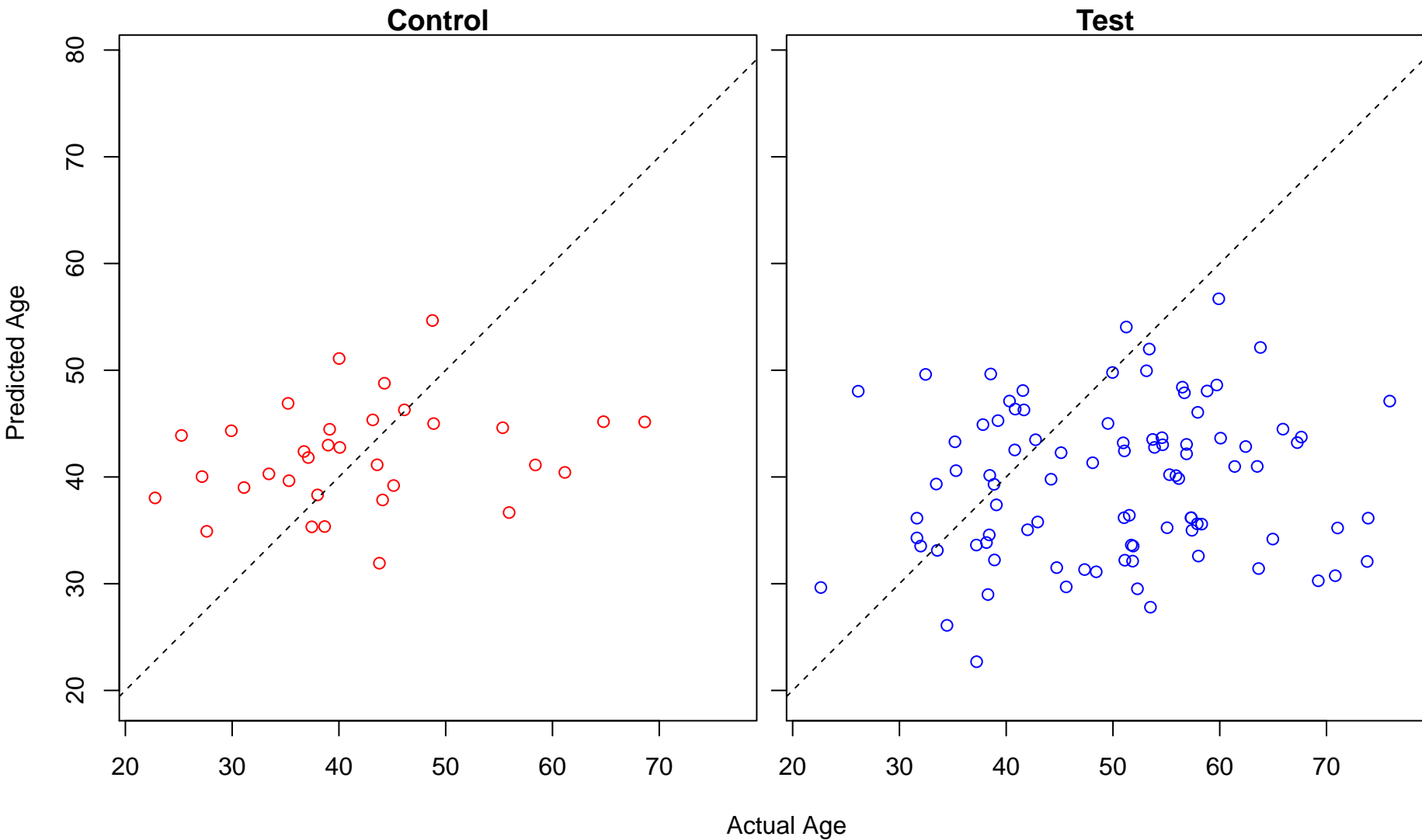
glycosylceramide catabolic process (Score: 0.233099)



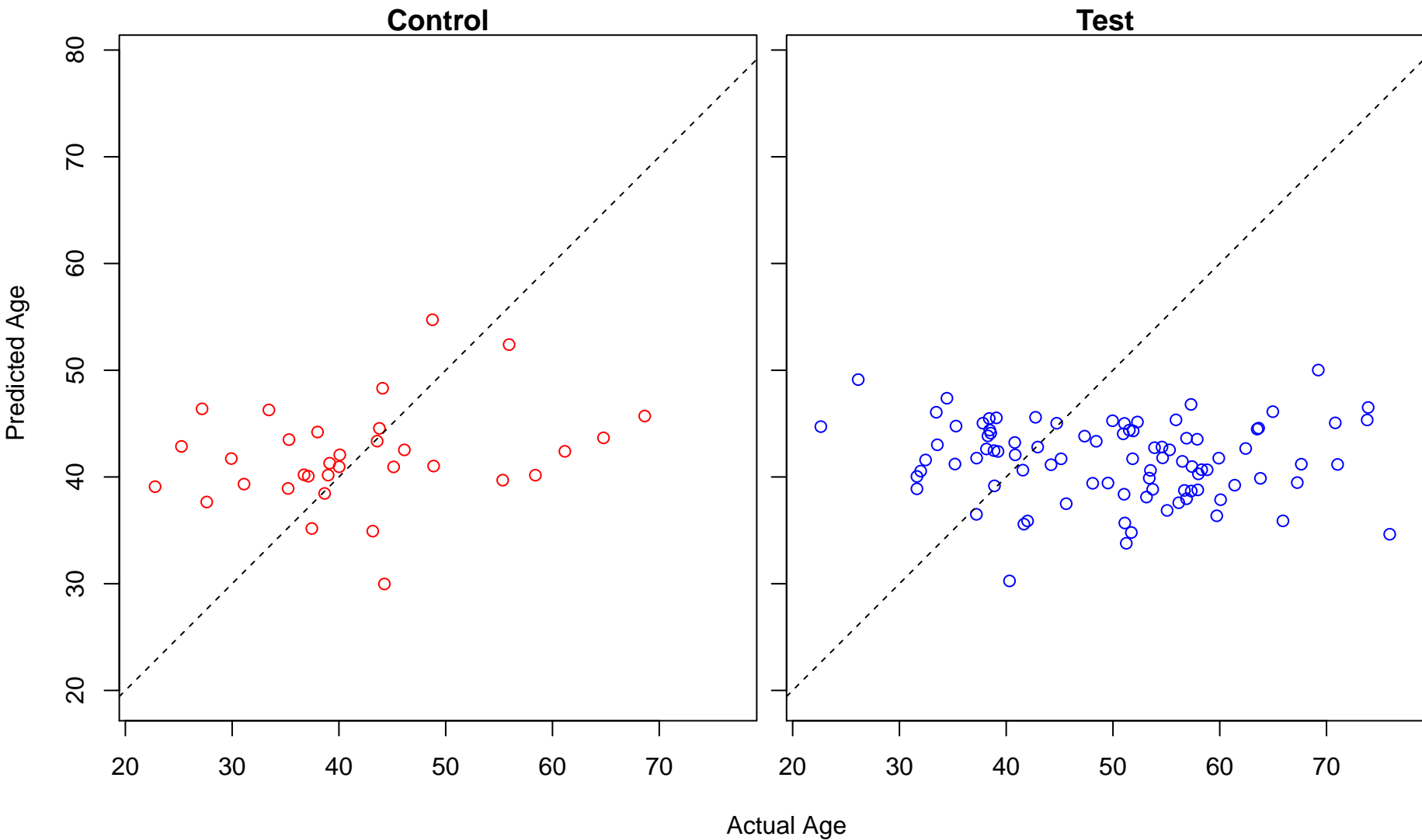
regulation of interleukin-4 biosynthetic process (Score: 0.232993)



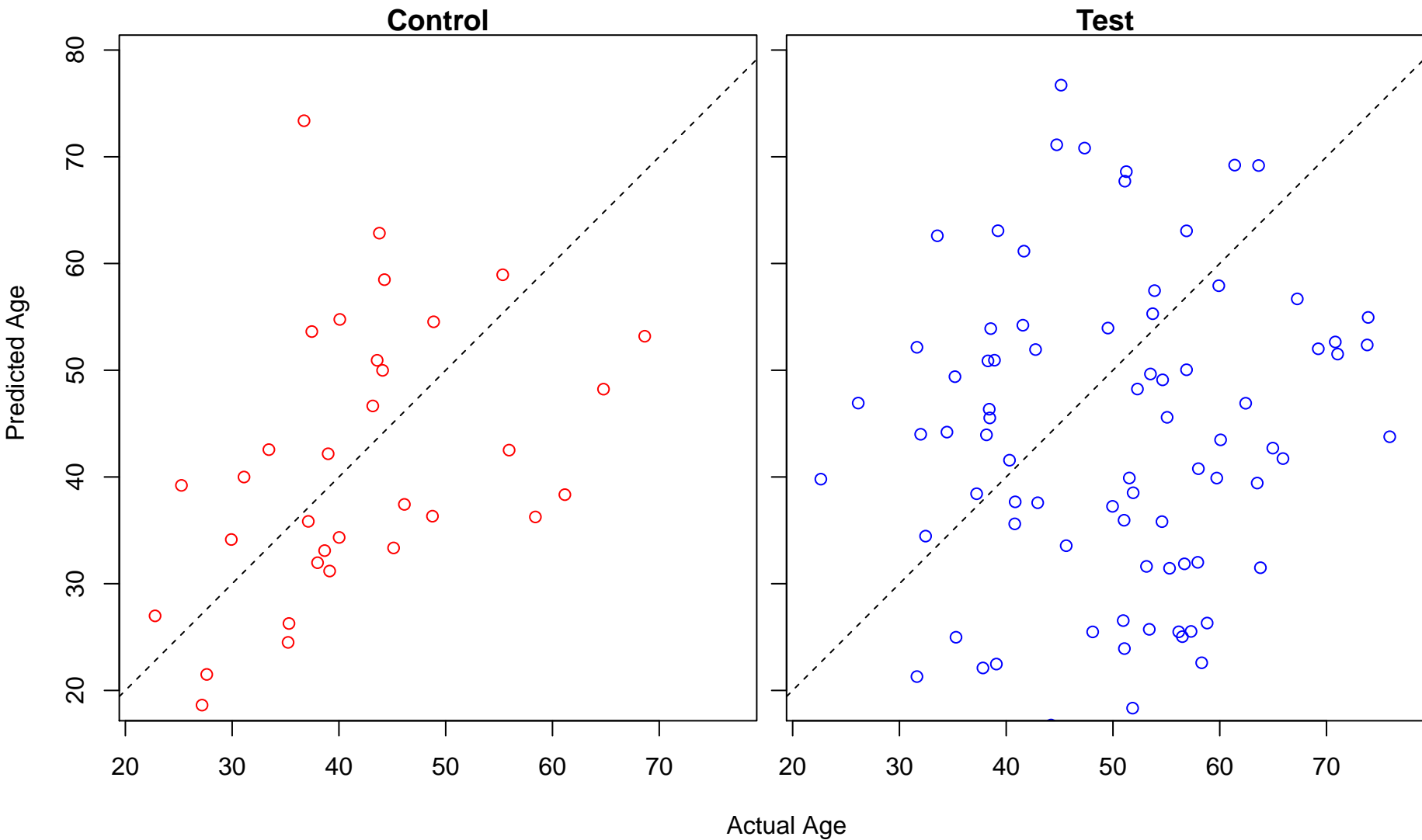
neutrophil apoptotic process (Score: 0.231624)



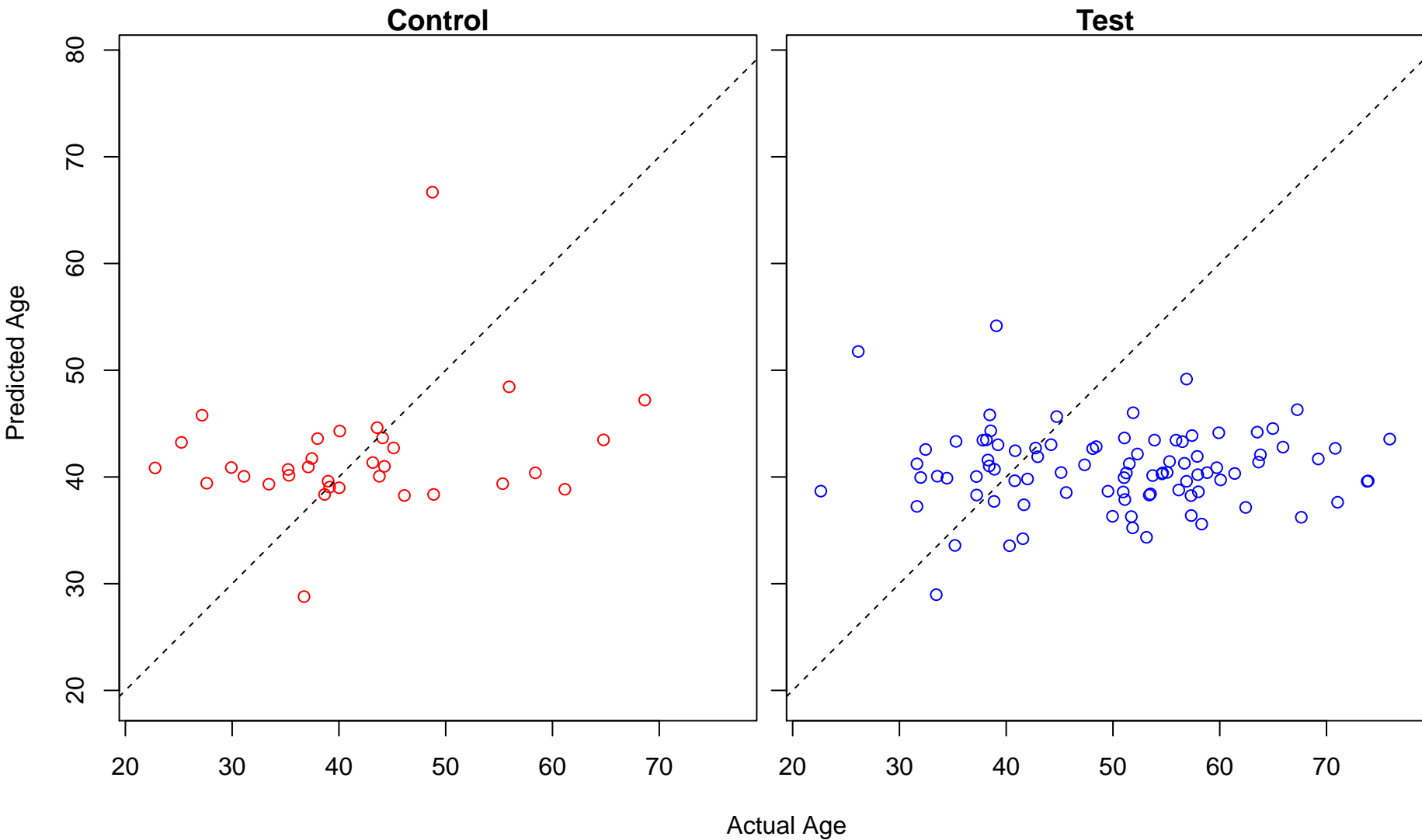
urate biosynthetic process (Score: 0.225181)



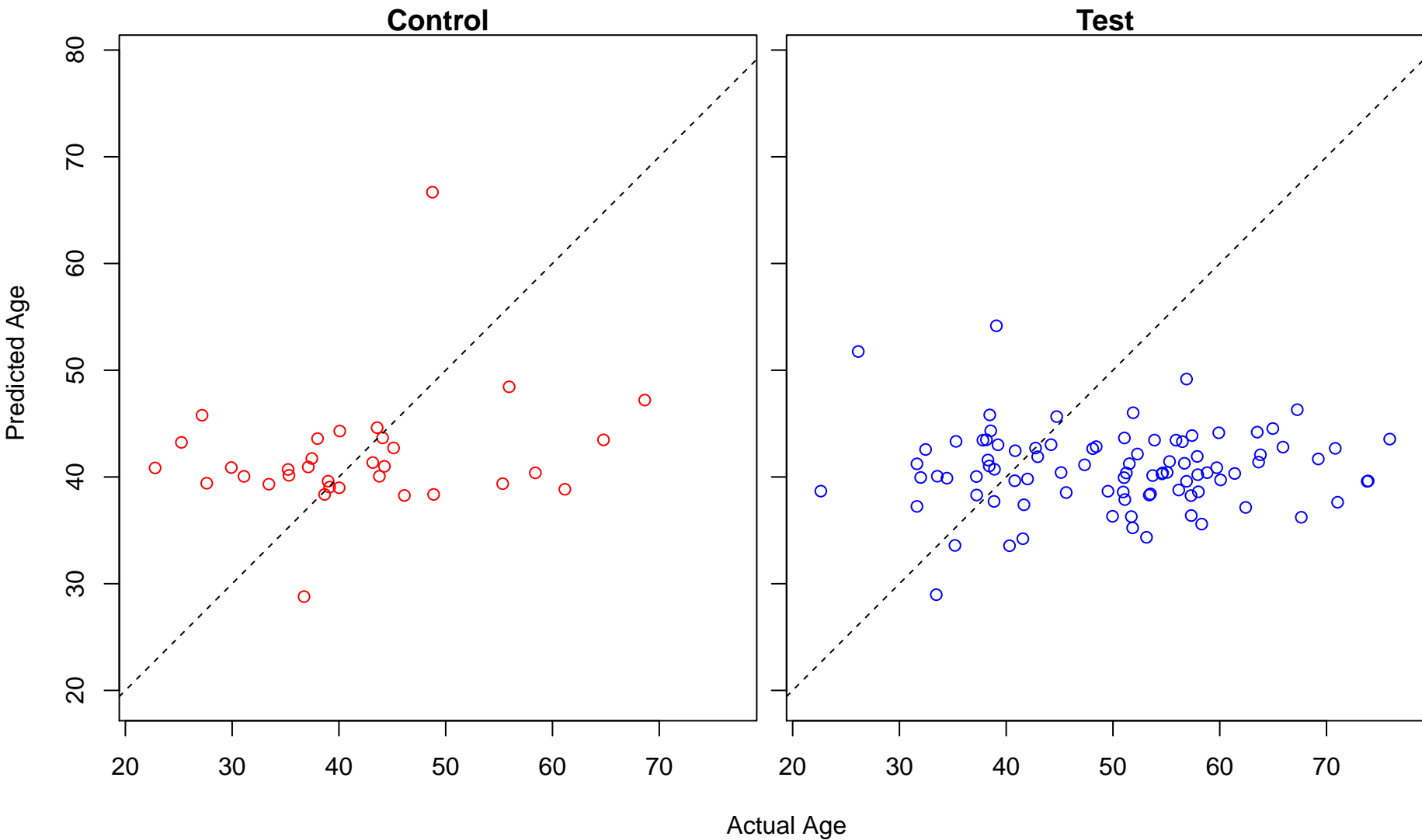
sex differentiation (Score: 0.223544)



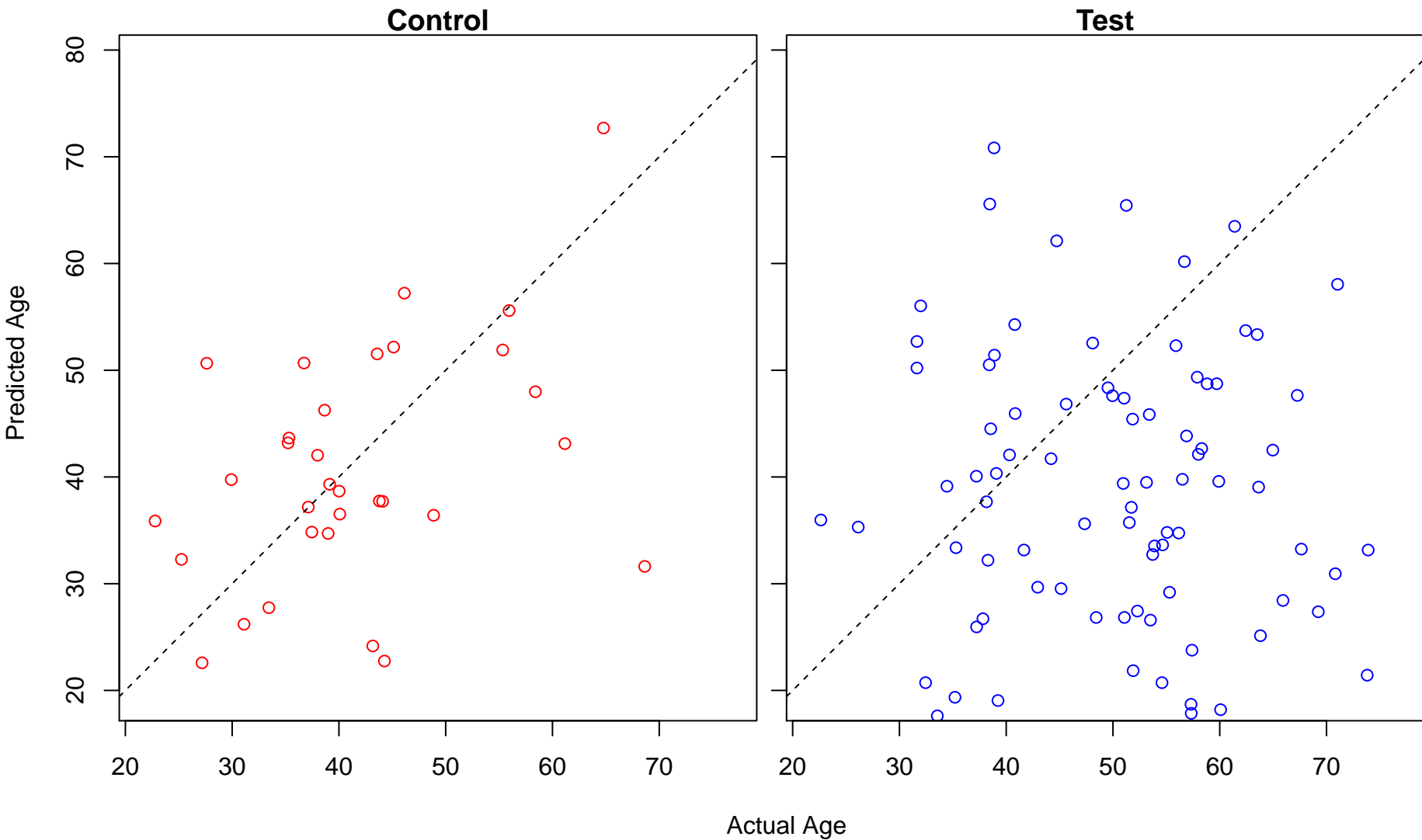
positive regulation of nucleobase-containing compound transport (Score: 0.223108)



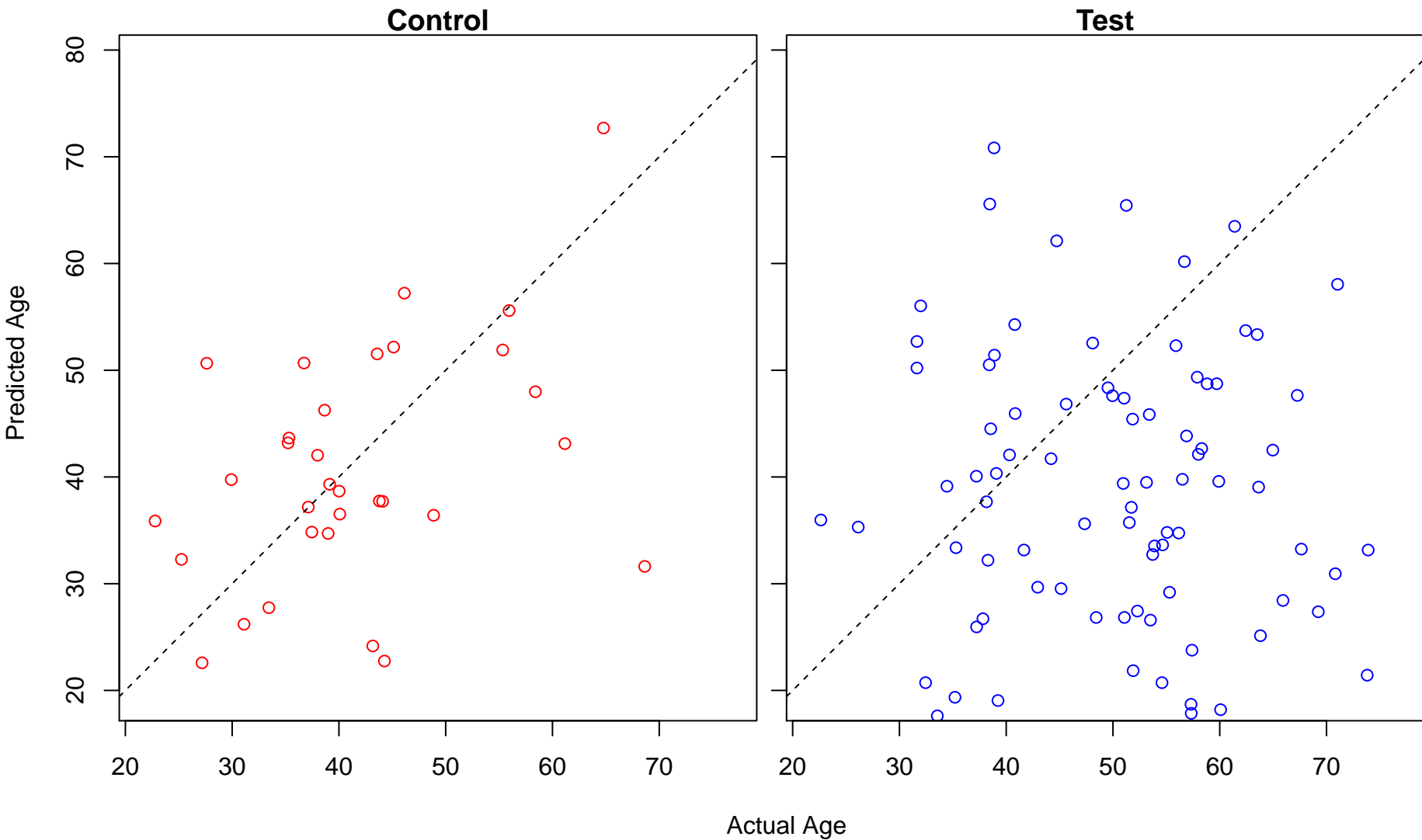
positive regulation of RNA export from nucleus (Score: 0.223108)



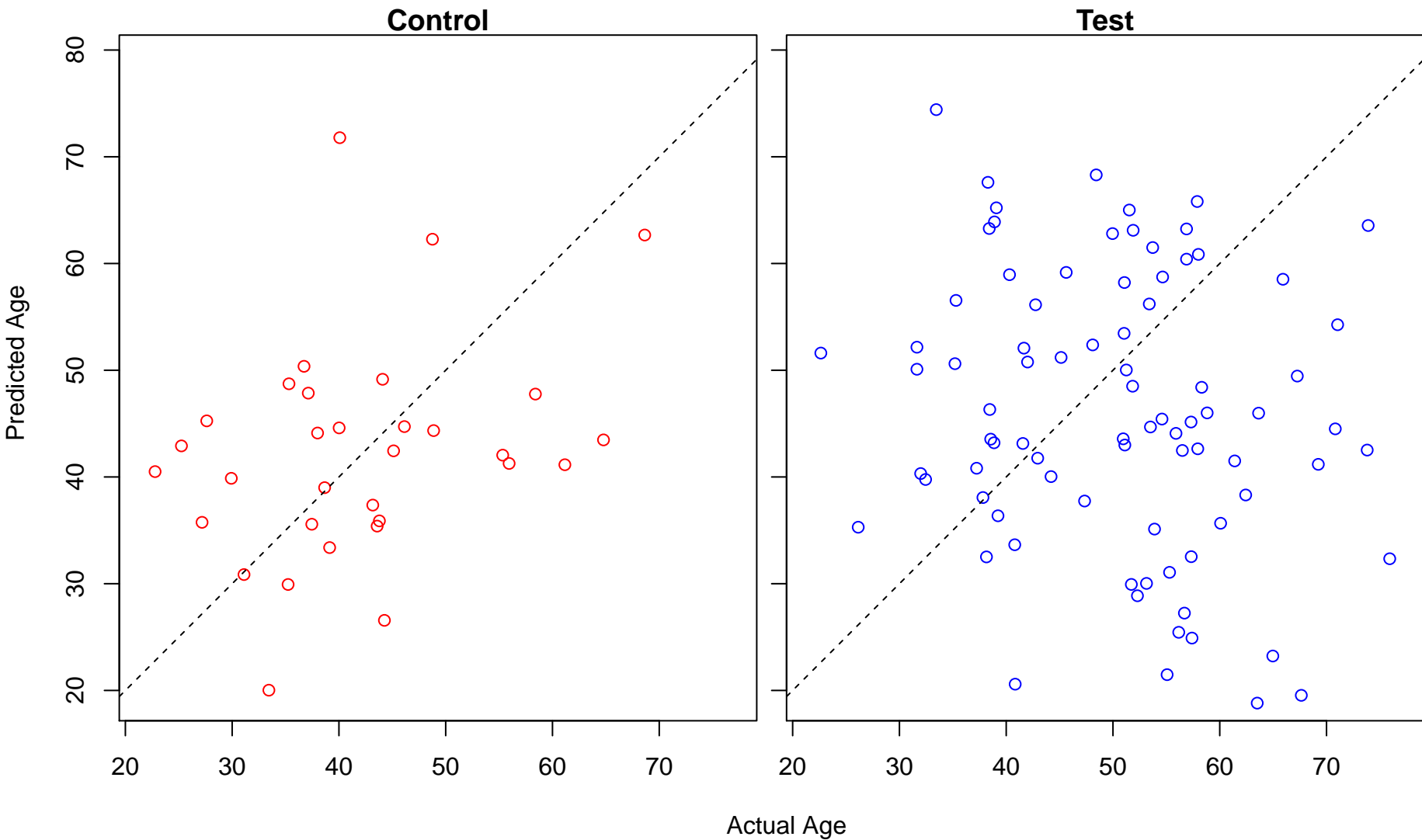
regulation of focal adhesion assembly (Score: 0.221431)



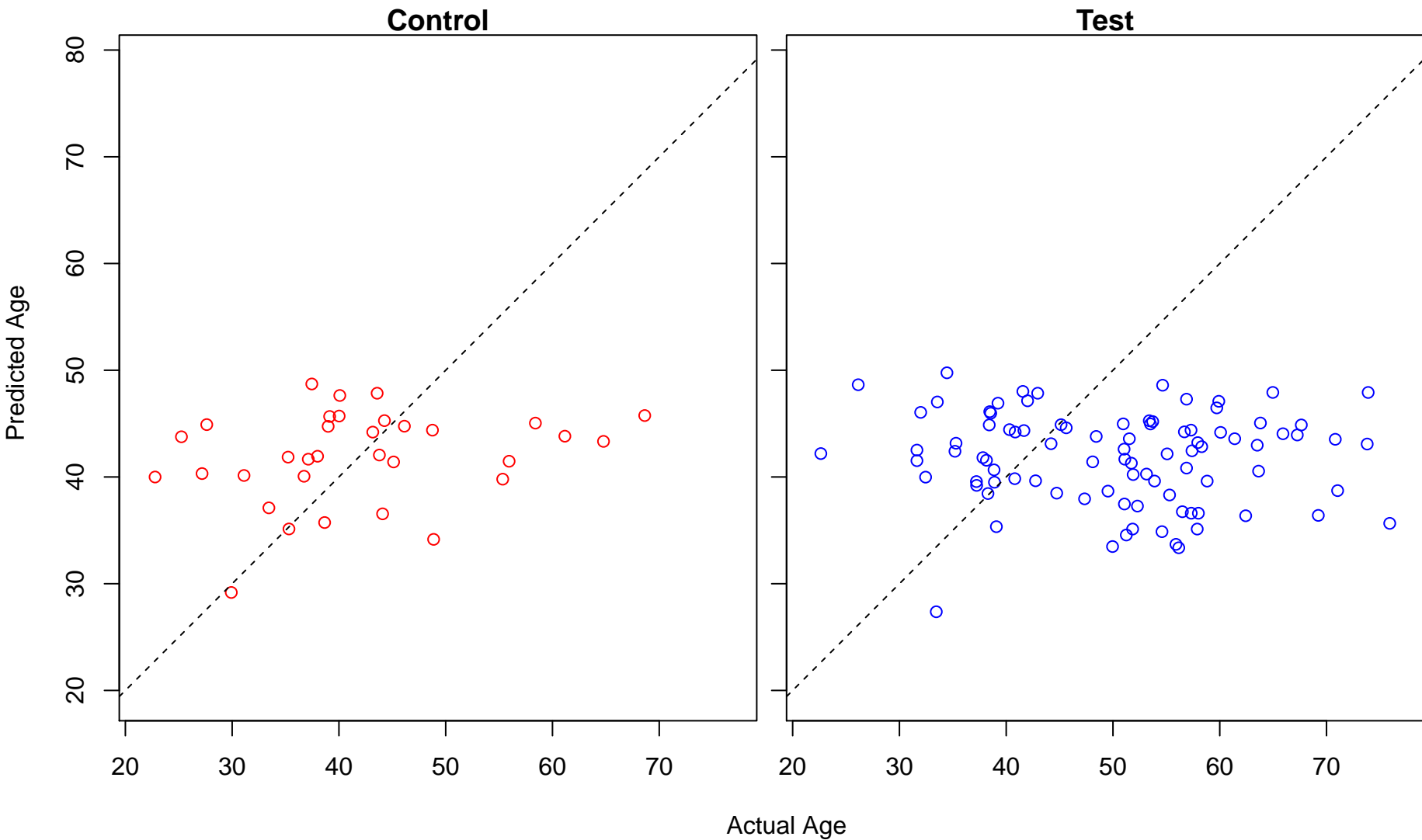
regulation of cell-substrate junction assembly (Score: 0.221431)



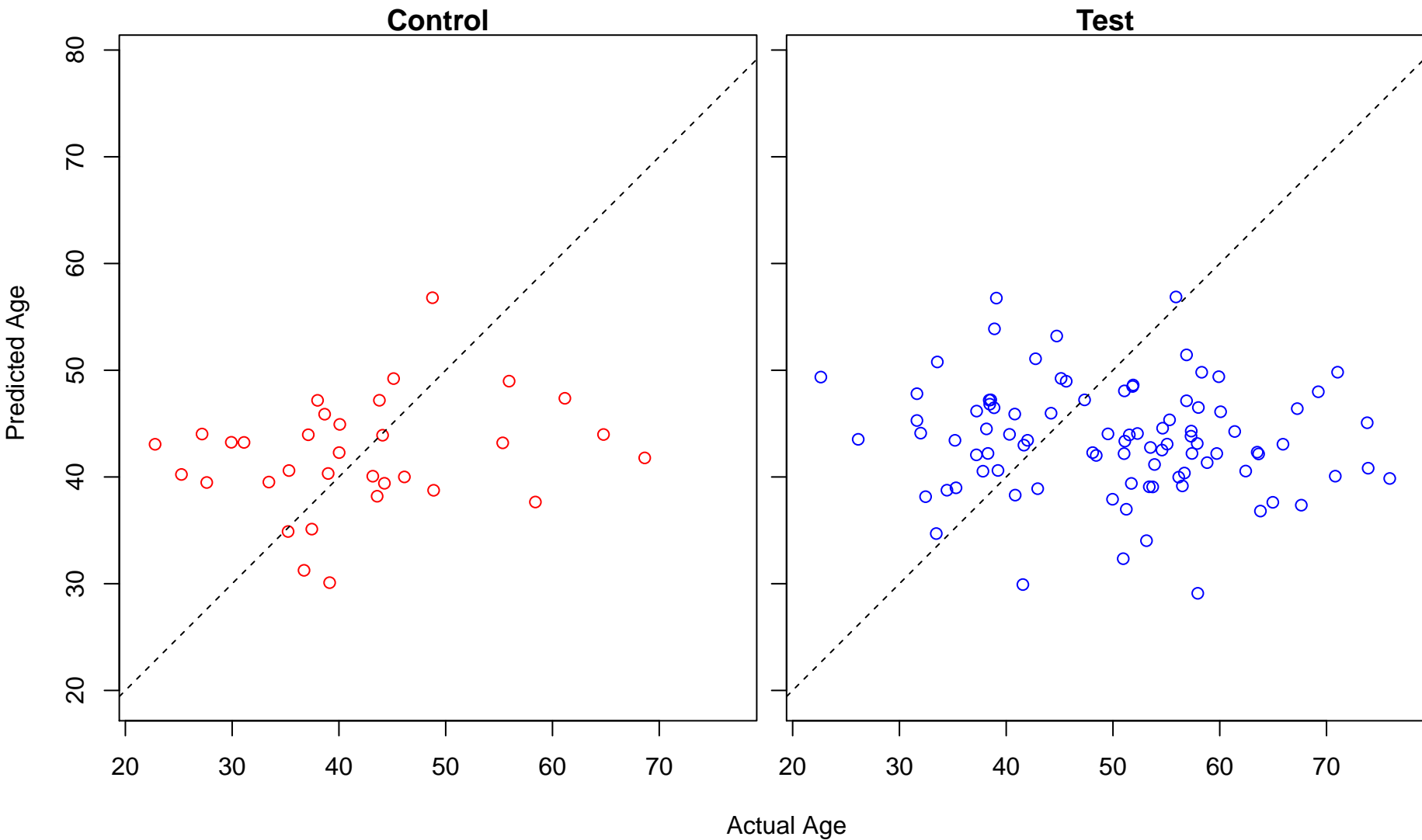
chondroitin sulfate proteoglycan metabolic process (Score: 0.221210)



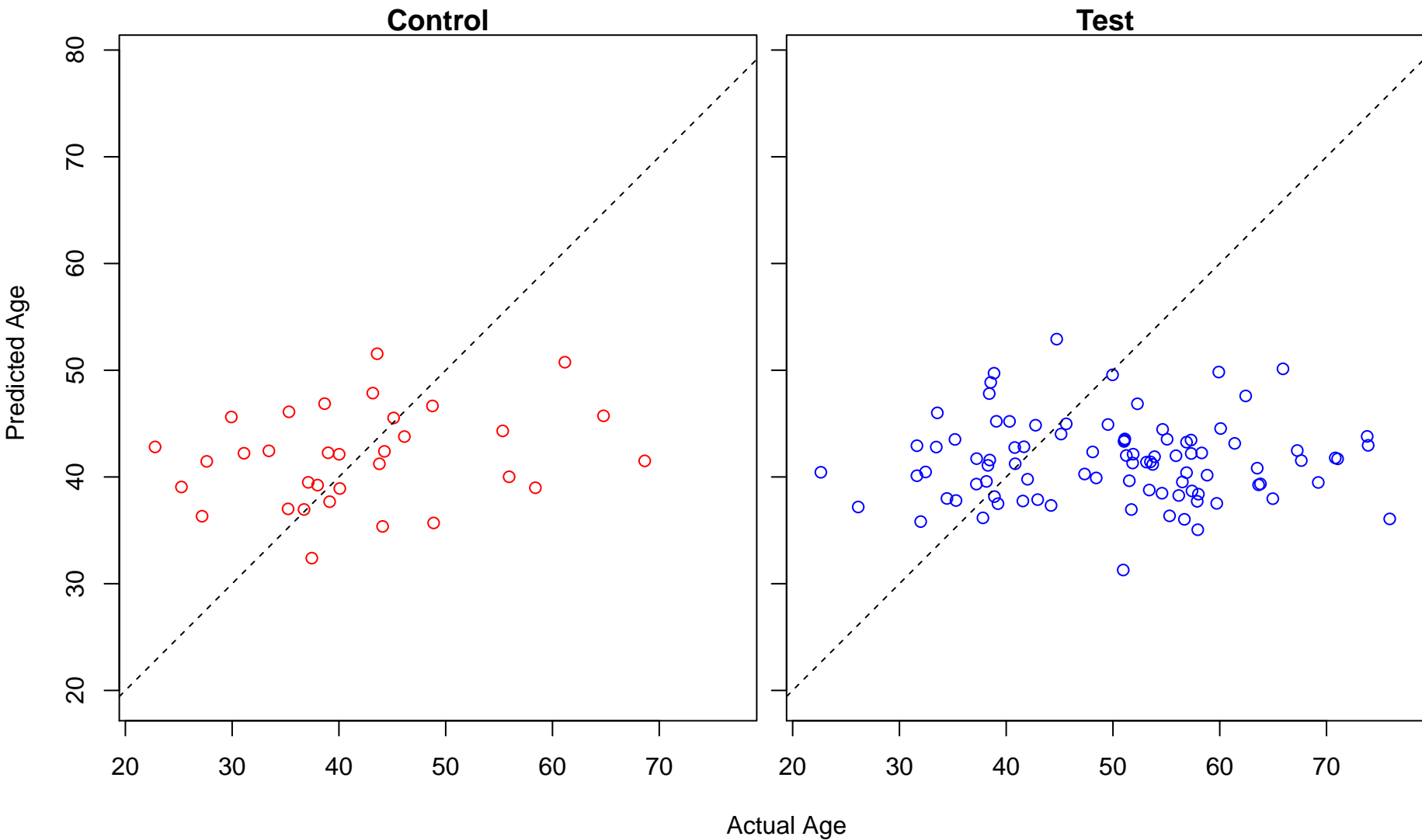
tyrosine phosphorylation of Stat3 protein (Score: 0.219177)



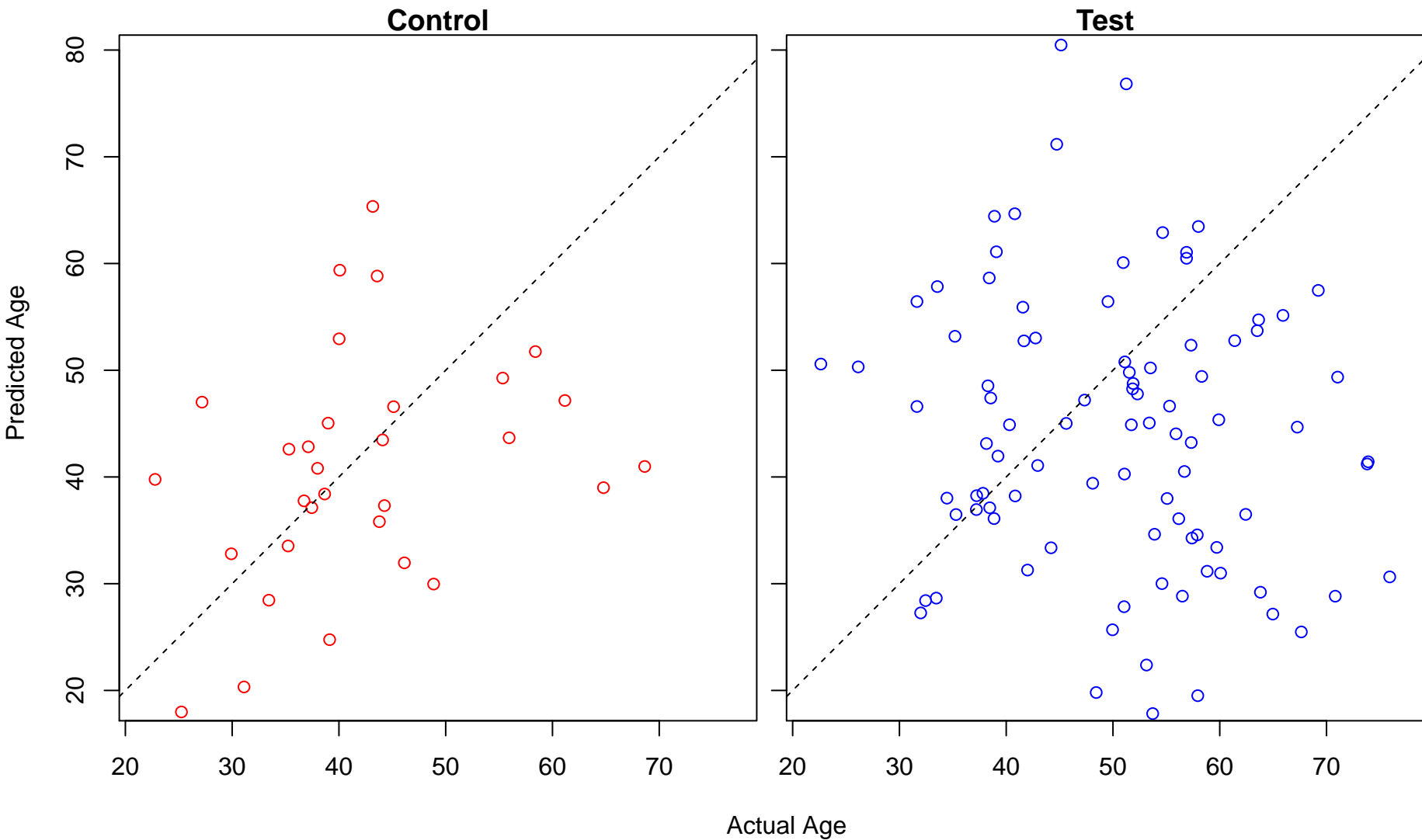
ganglioside biosynthetic process (Score: 0.214354)

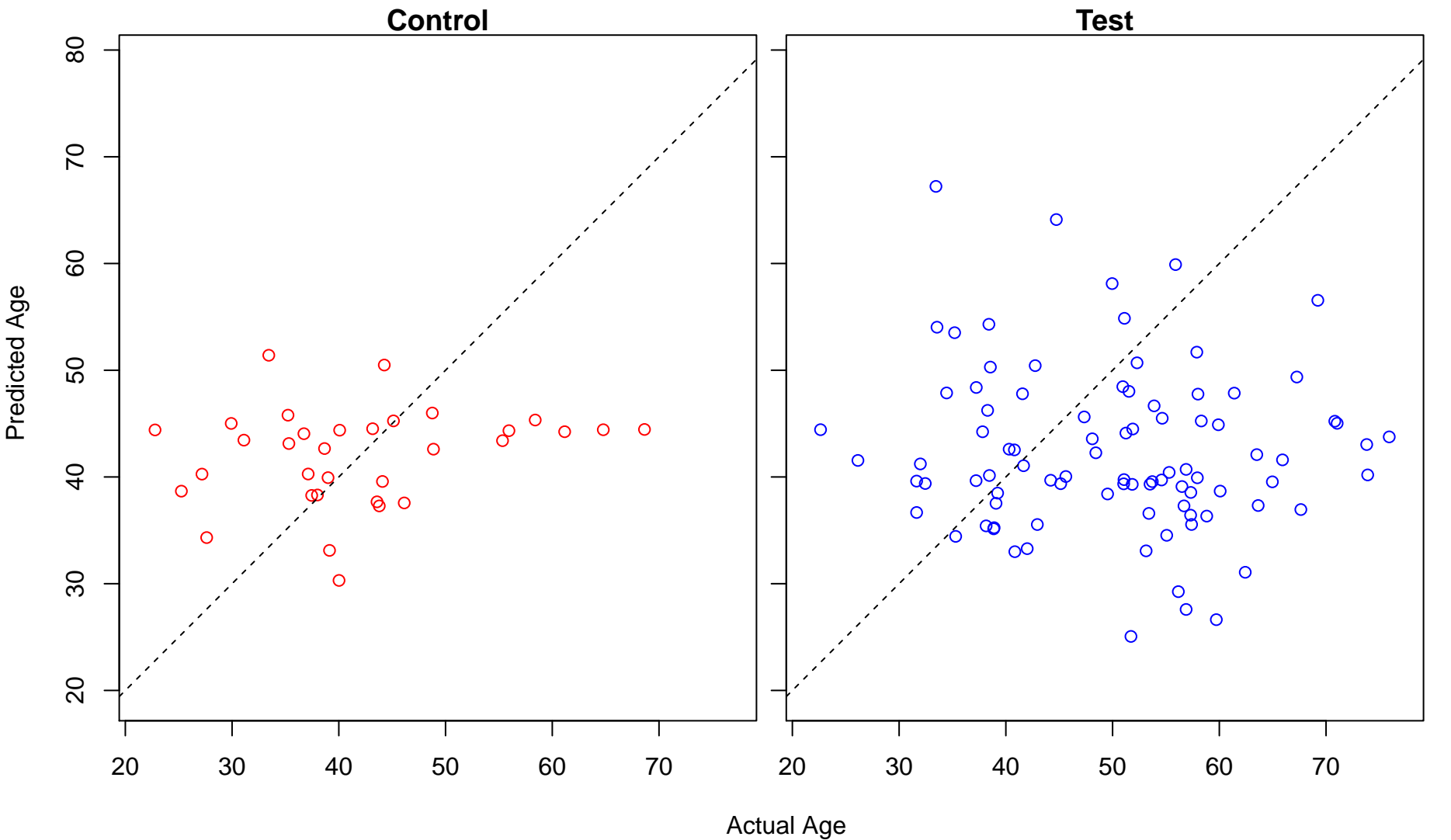


synaptic vesicle maturation (Score: 0.213882)

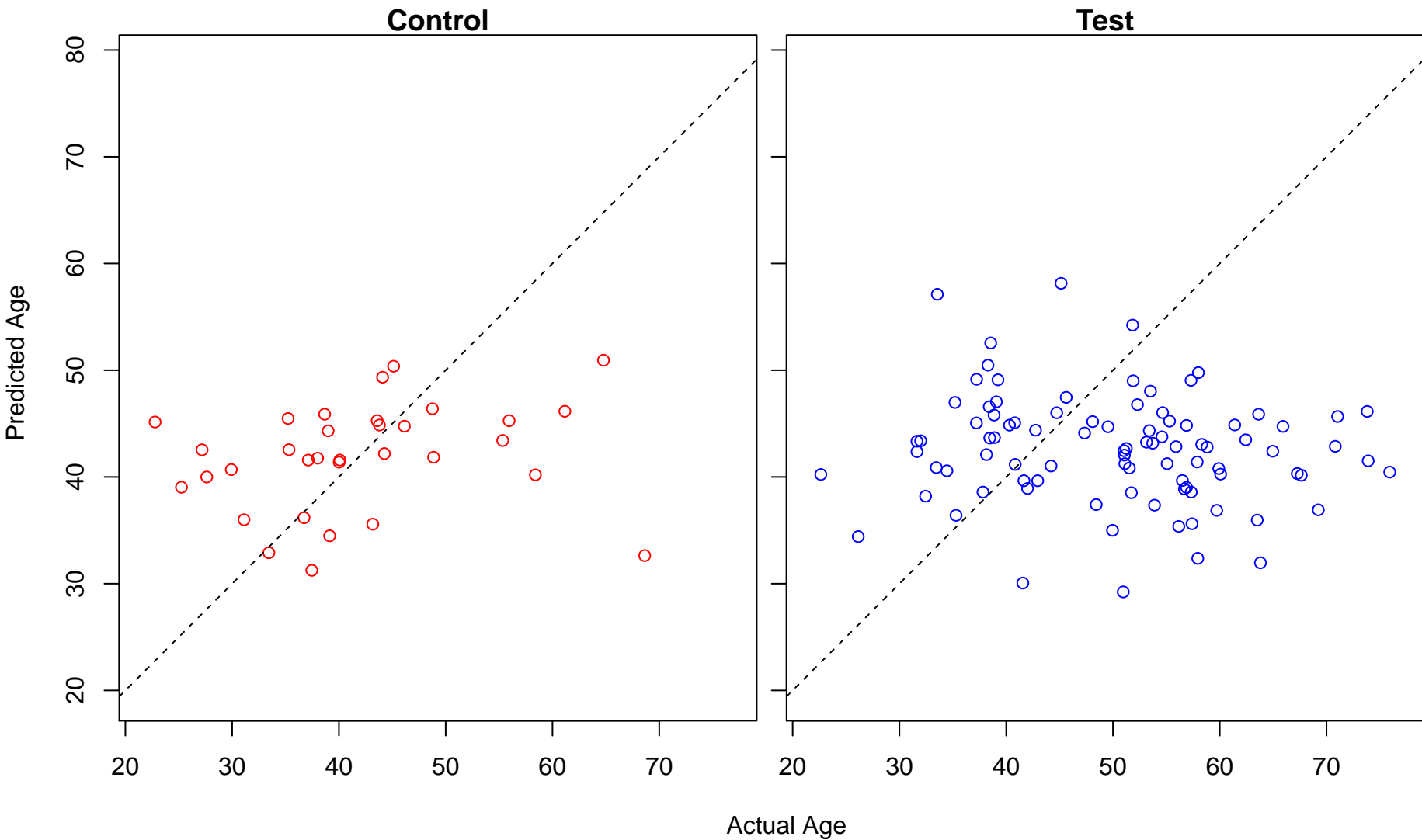


positive regulation of response to nutrient levels (Score: 0.210859)

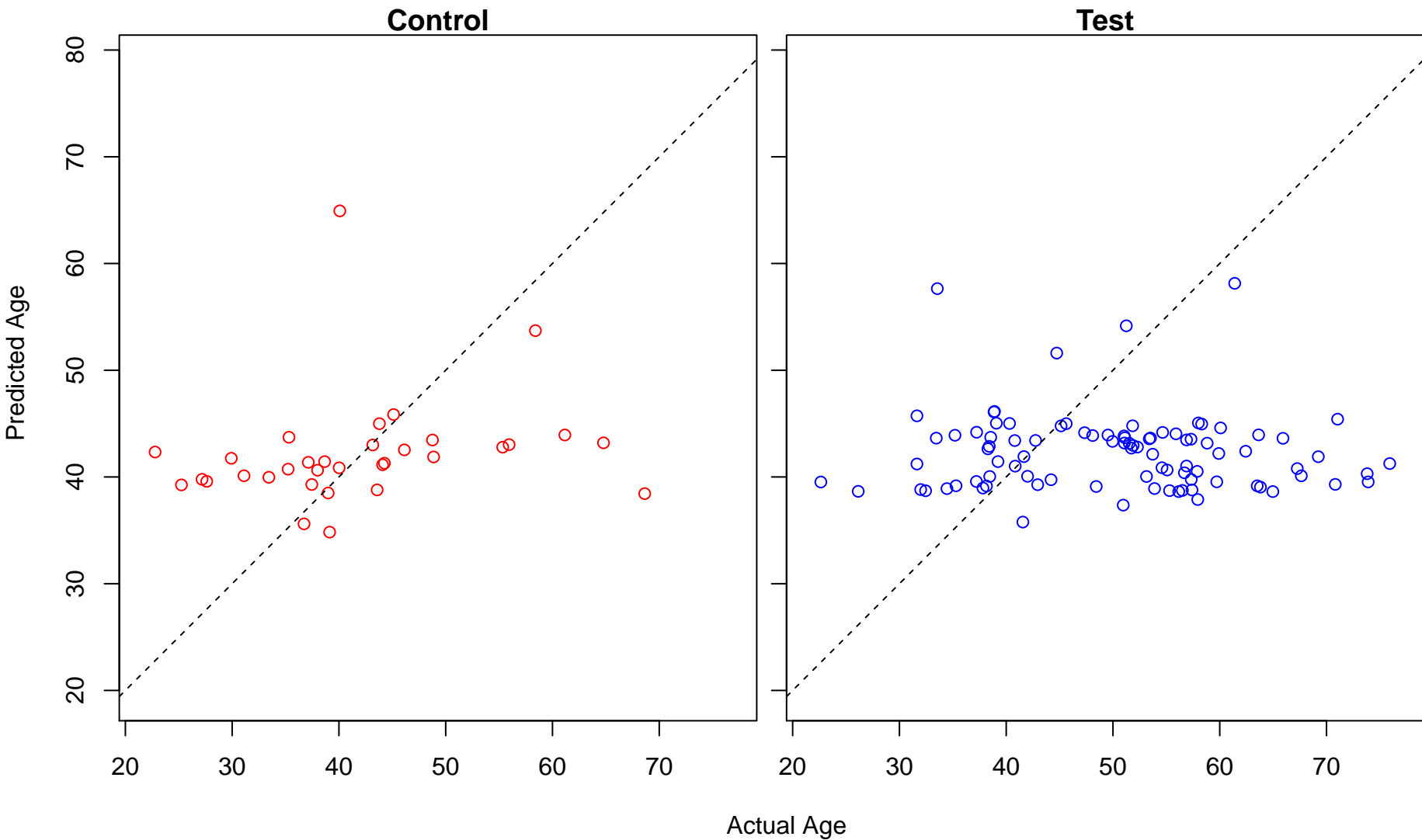




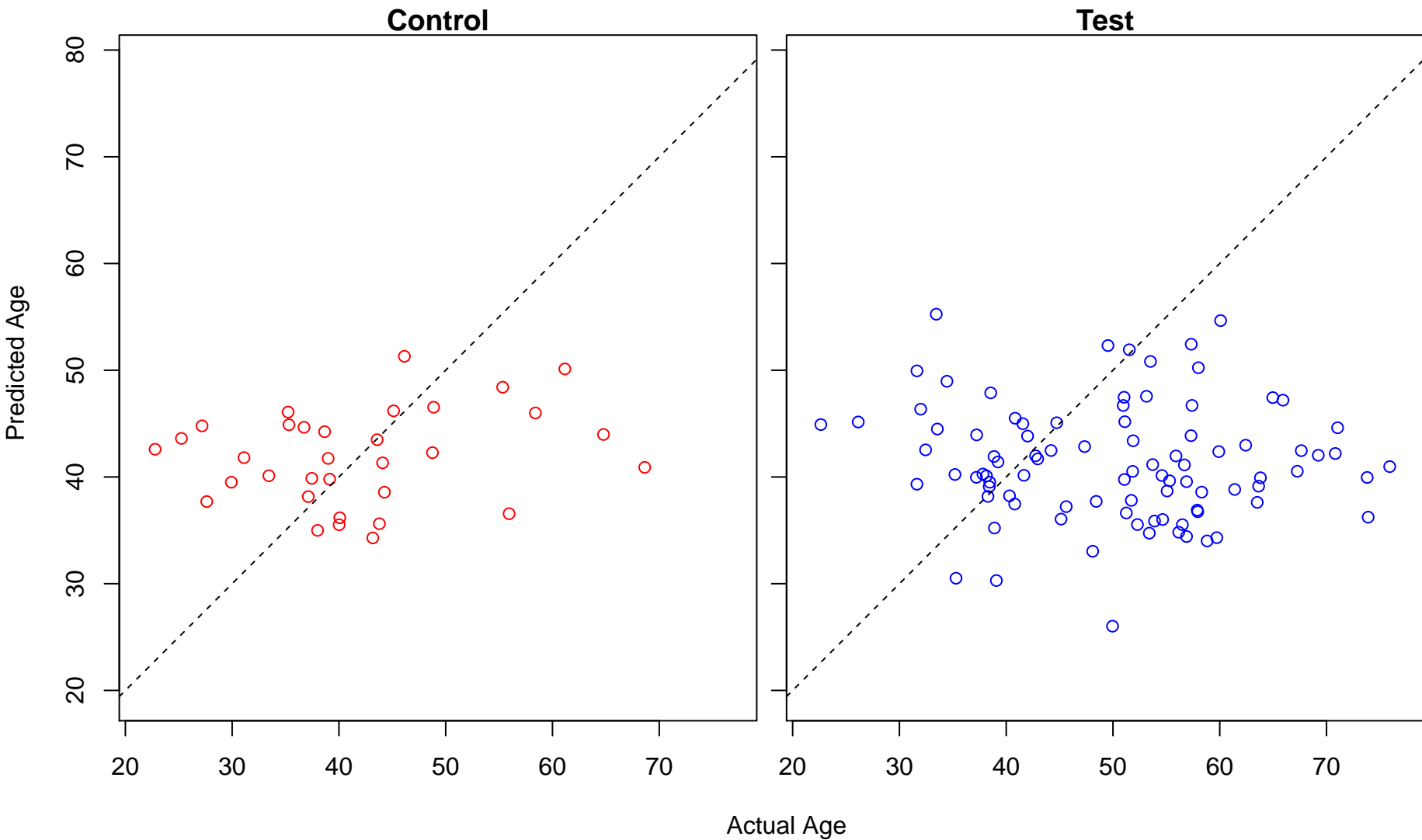
coenzyme transport (Score: 0.202808)



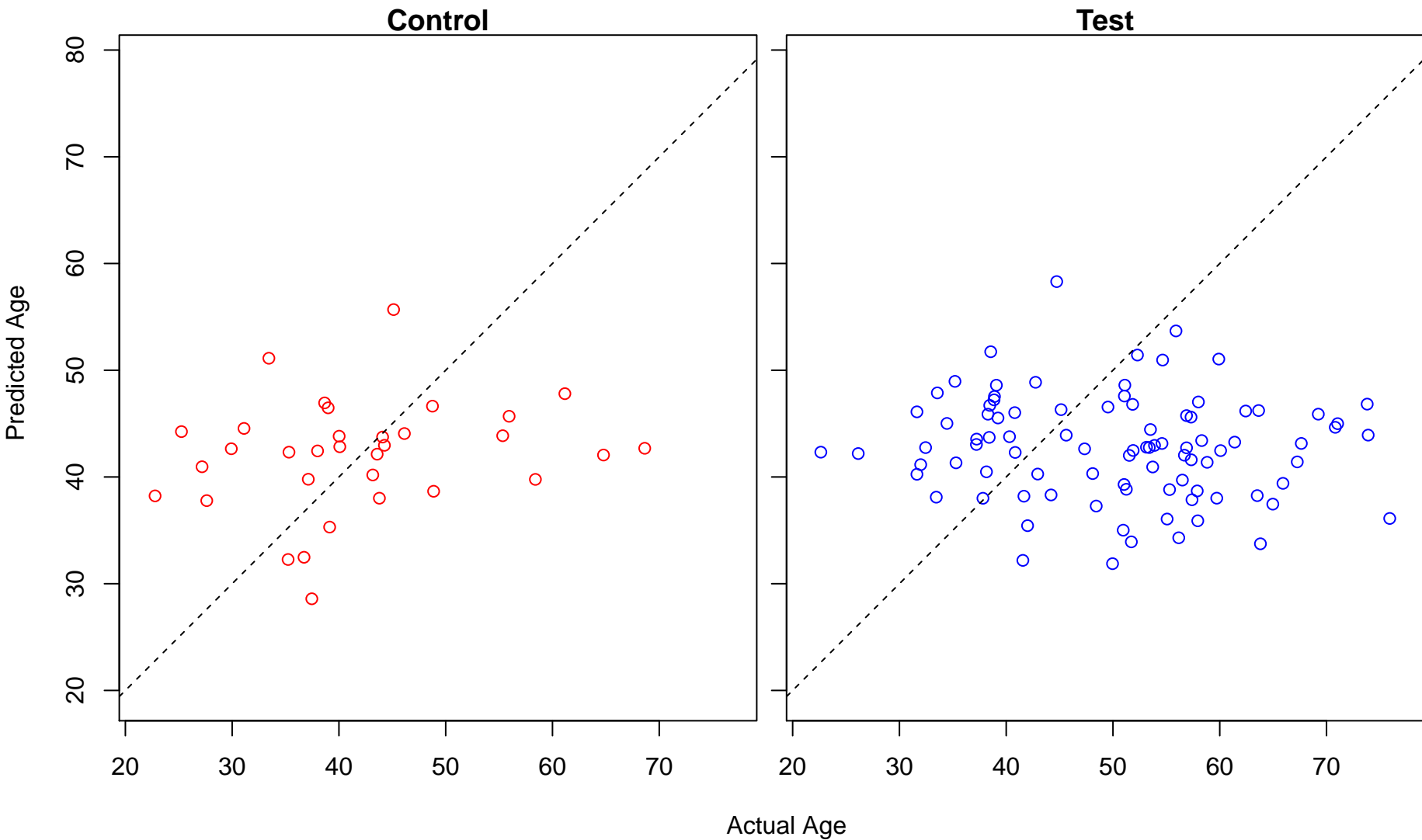
tRNA transcription (Score: 0.202616)



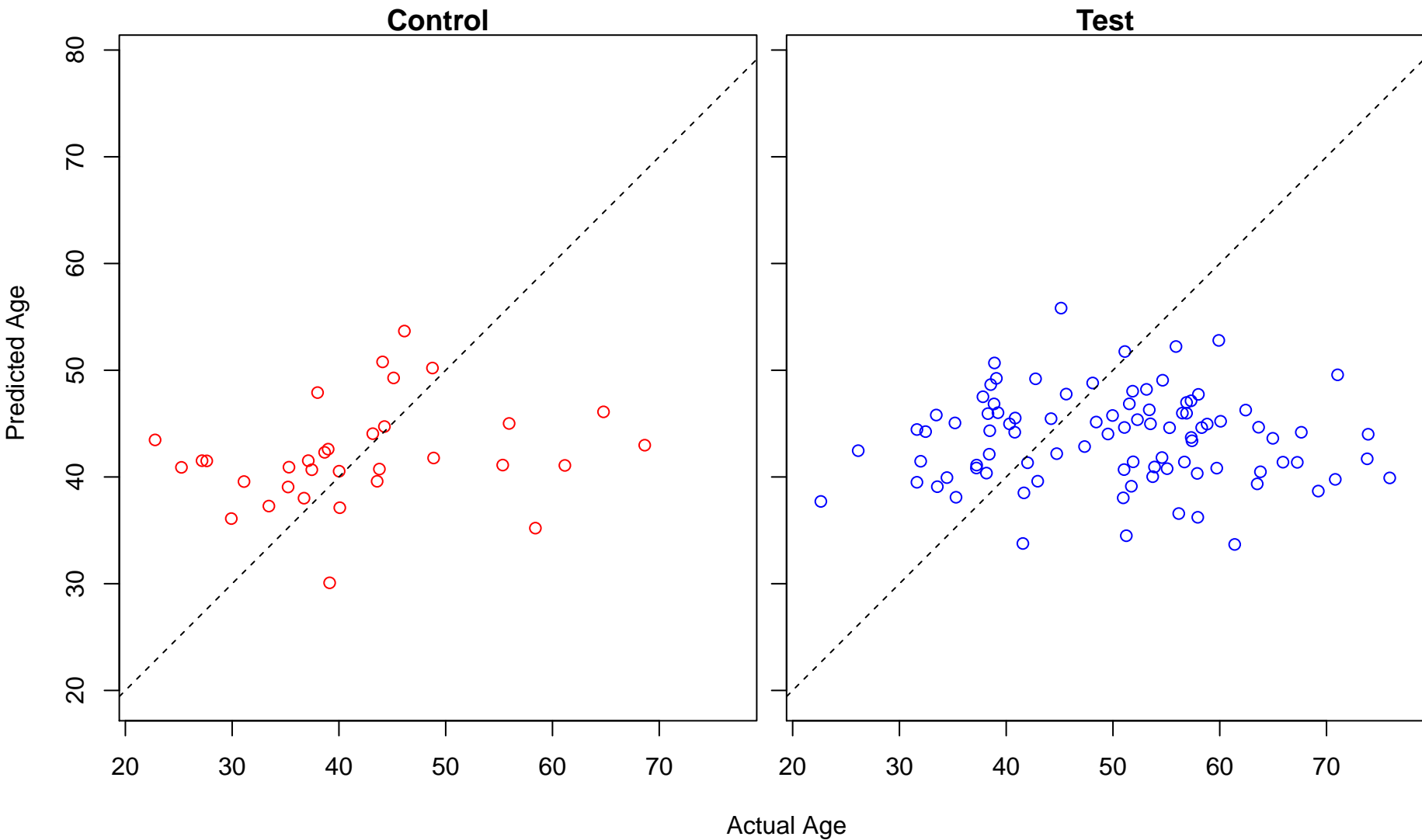
serotonin receptor signaling pathway (Score: 0.198381)



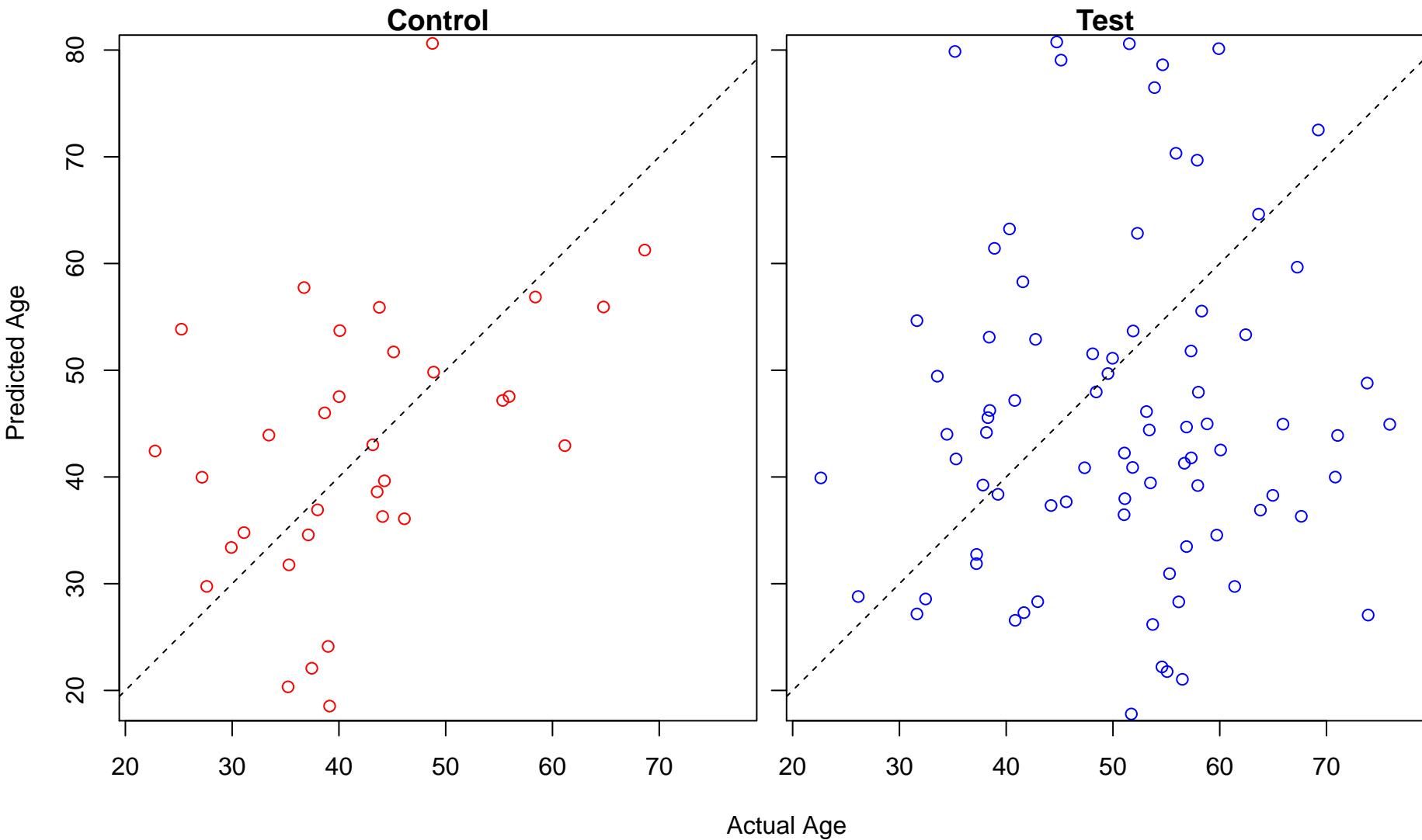
ketone body catabolic process (Score: 0.194403)



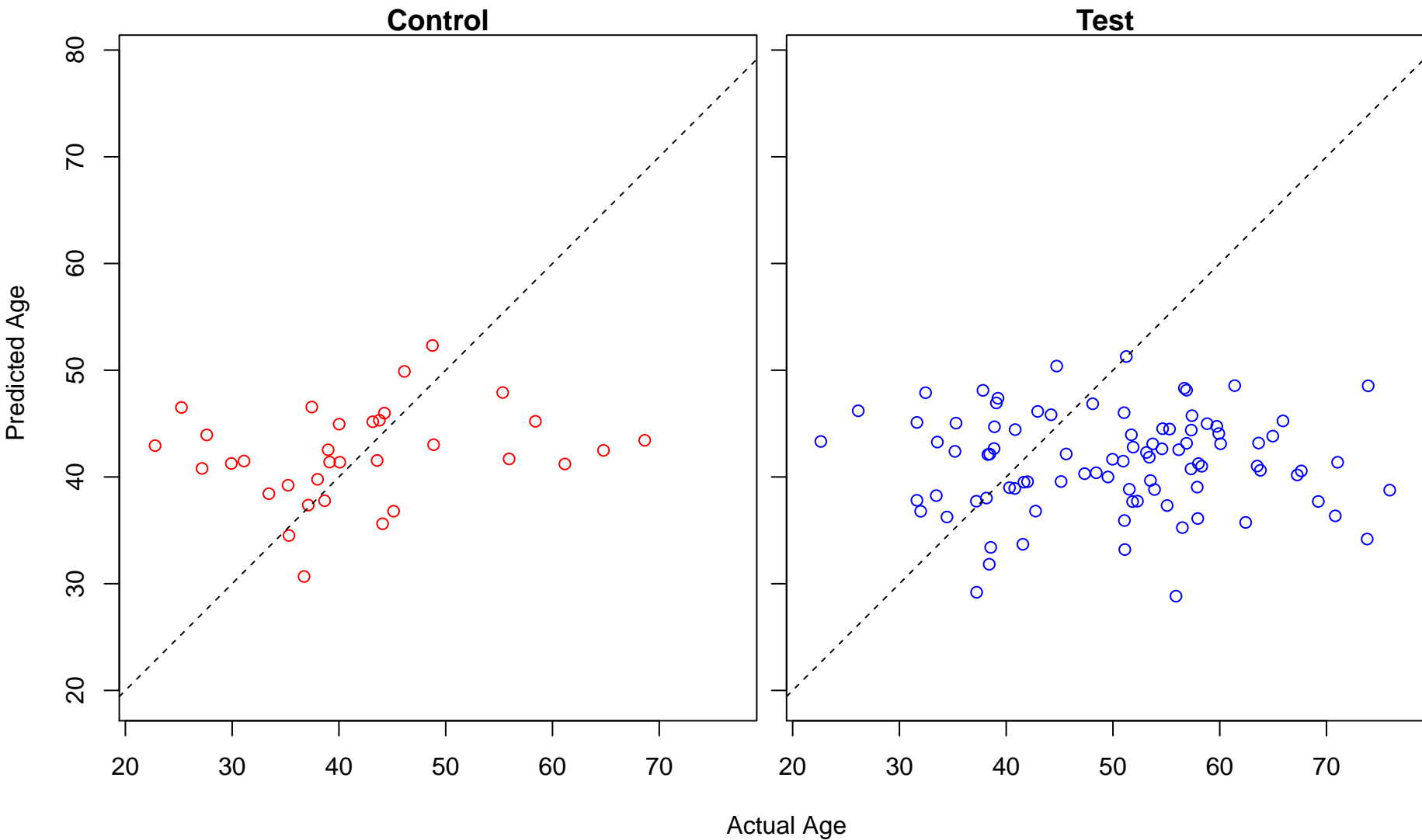
positive regulation of transforming growth factor beta1 production (Score: 0.194196)



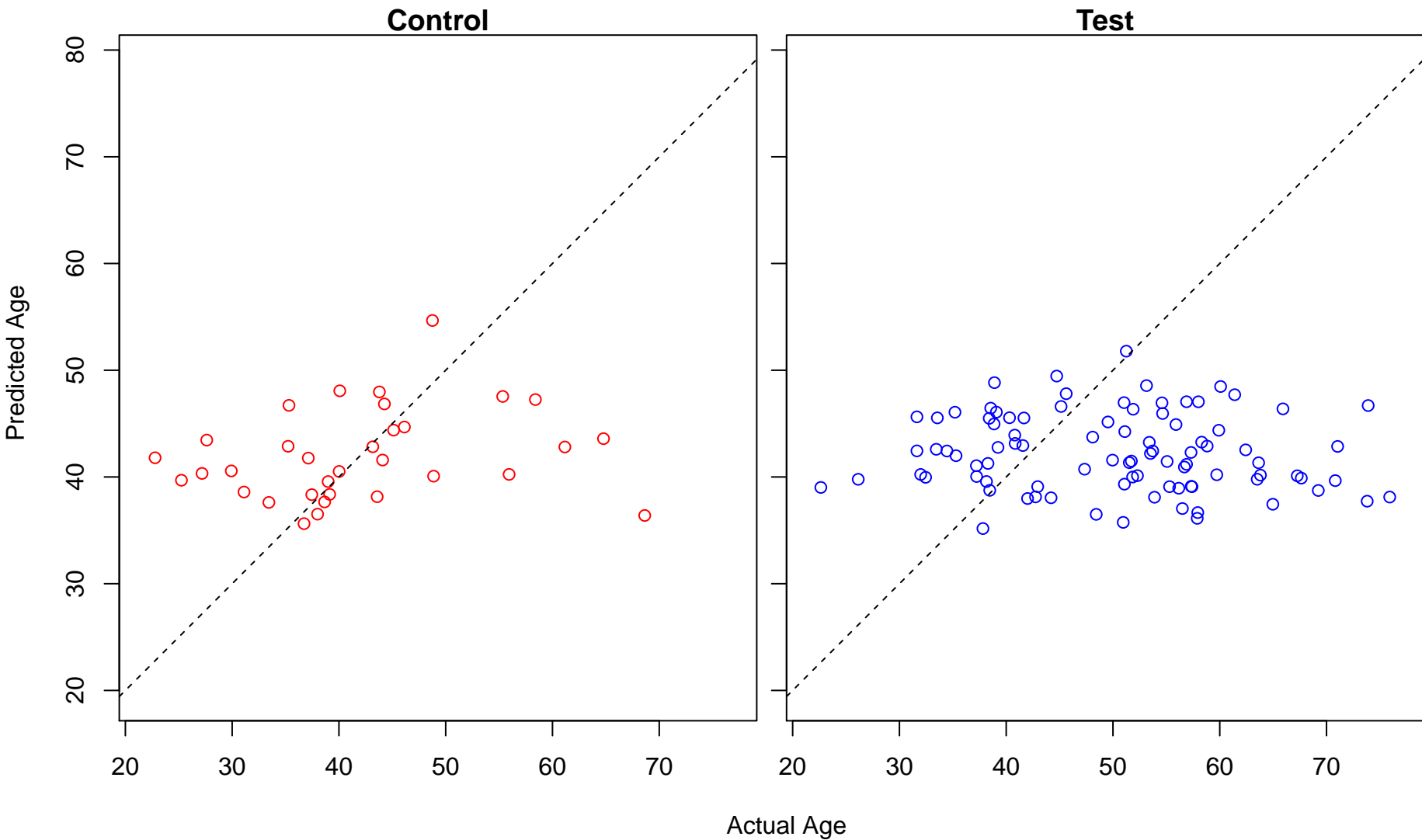
regulation of interferon-gamma-mediated signaling pathway (Score: 0.192463)



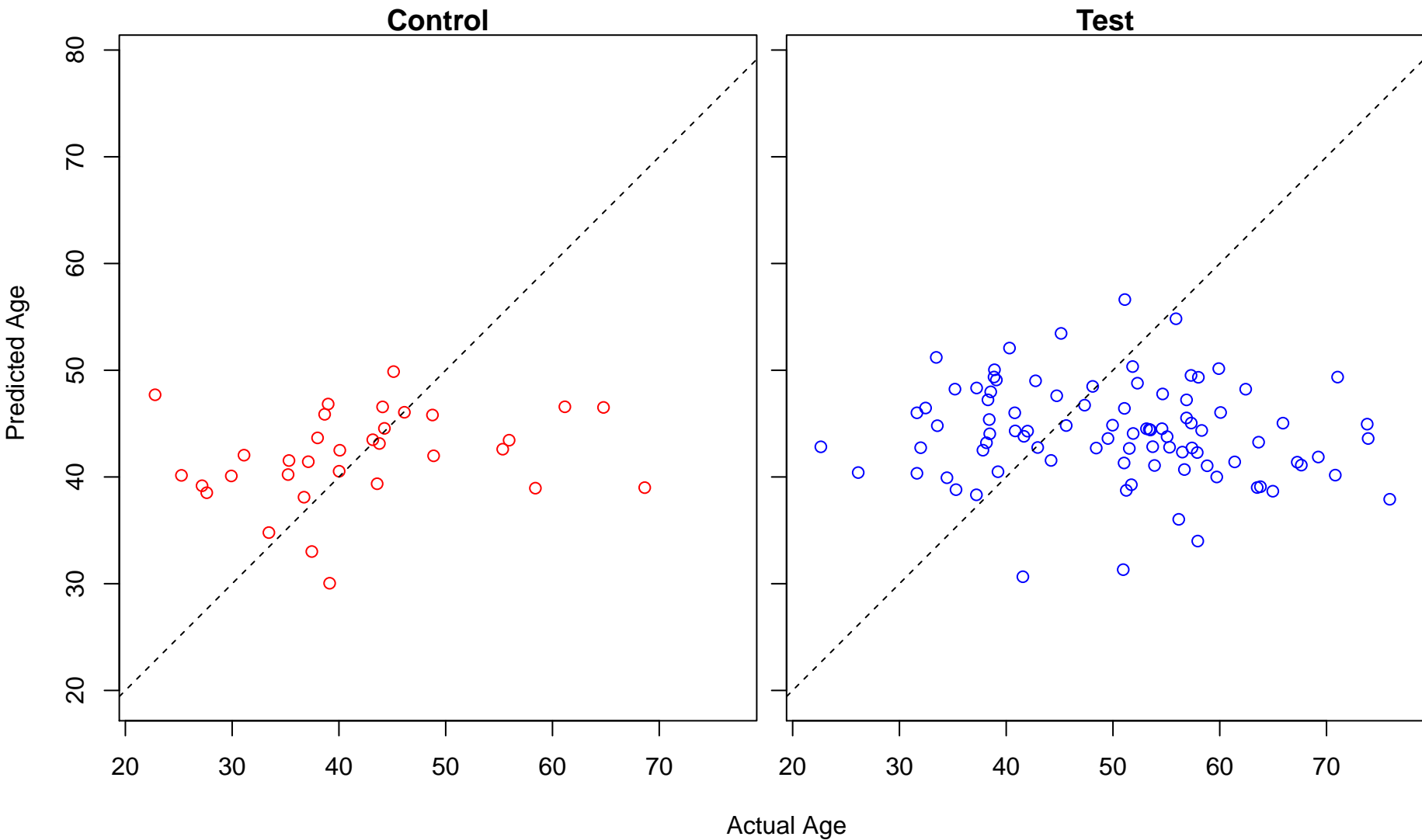
methyl-branched fatty acid metabolic process (Score: 0.191739)



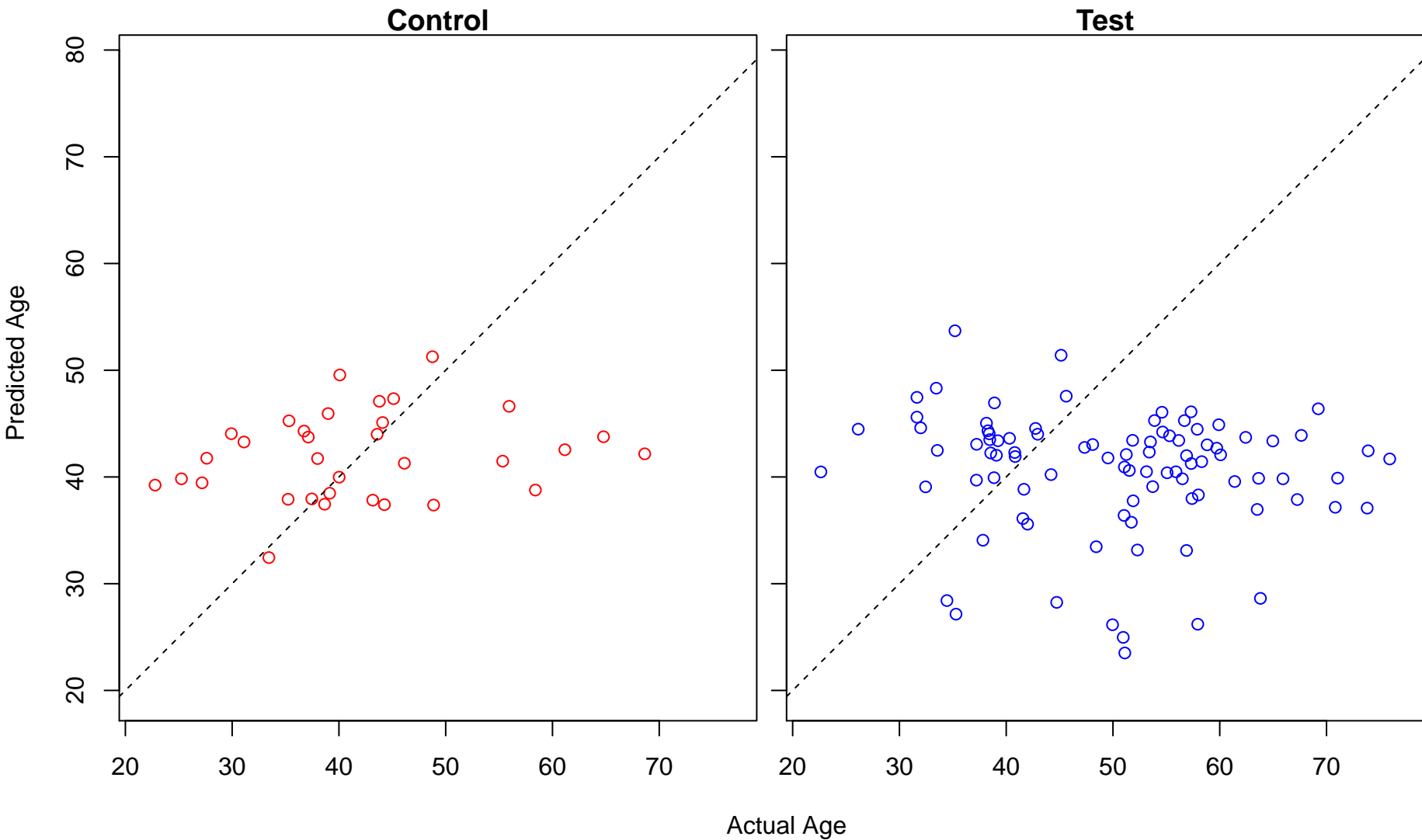
positive regulation of fibroblast growth factor receptor signaling pathway (Score: 0.186553)



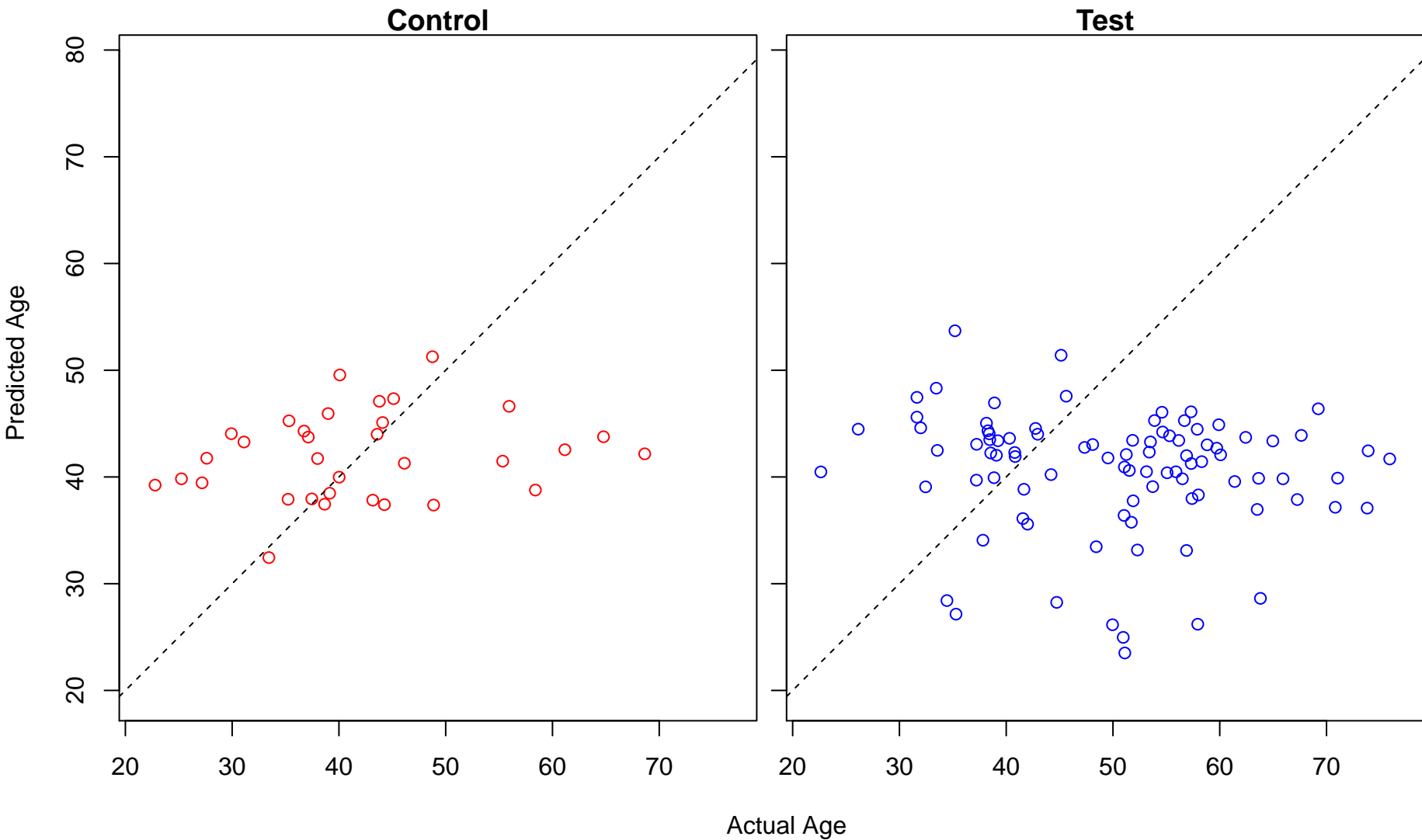
axon transport of mitochondrion (Score: 0.183633)



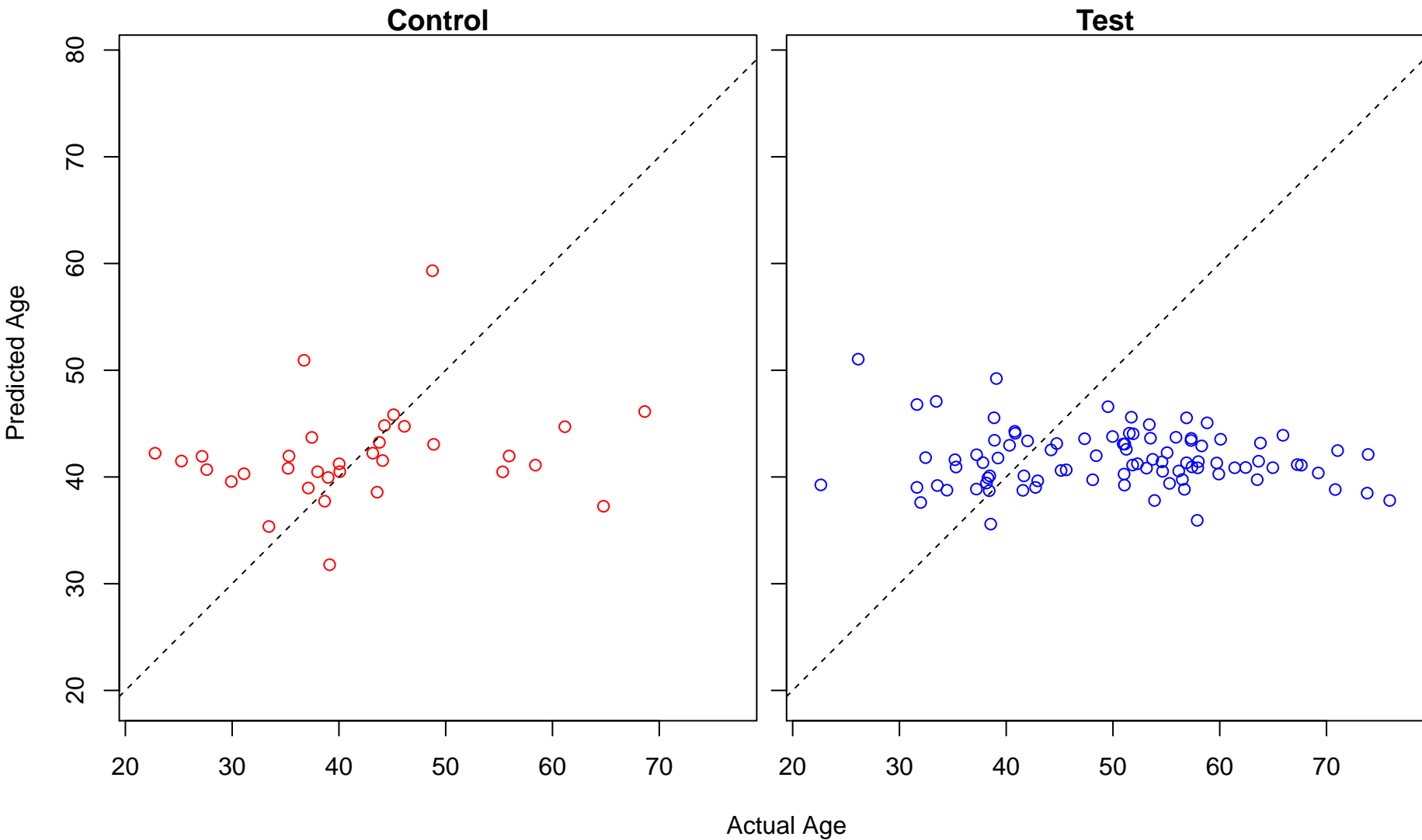
nicotinamide nucleotide biosynthetic process (Score: 0.161375)



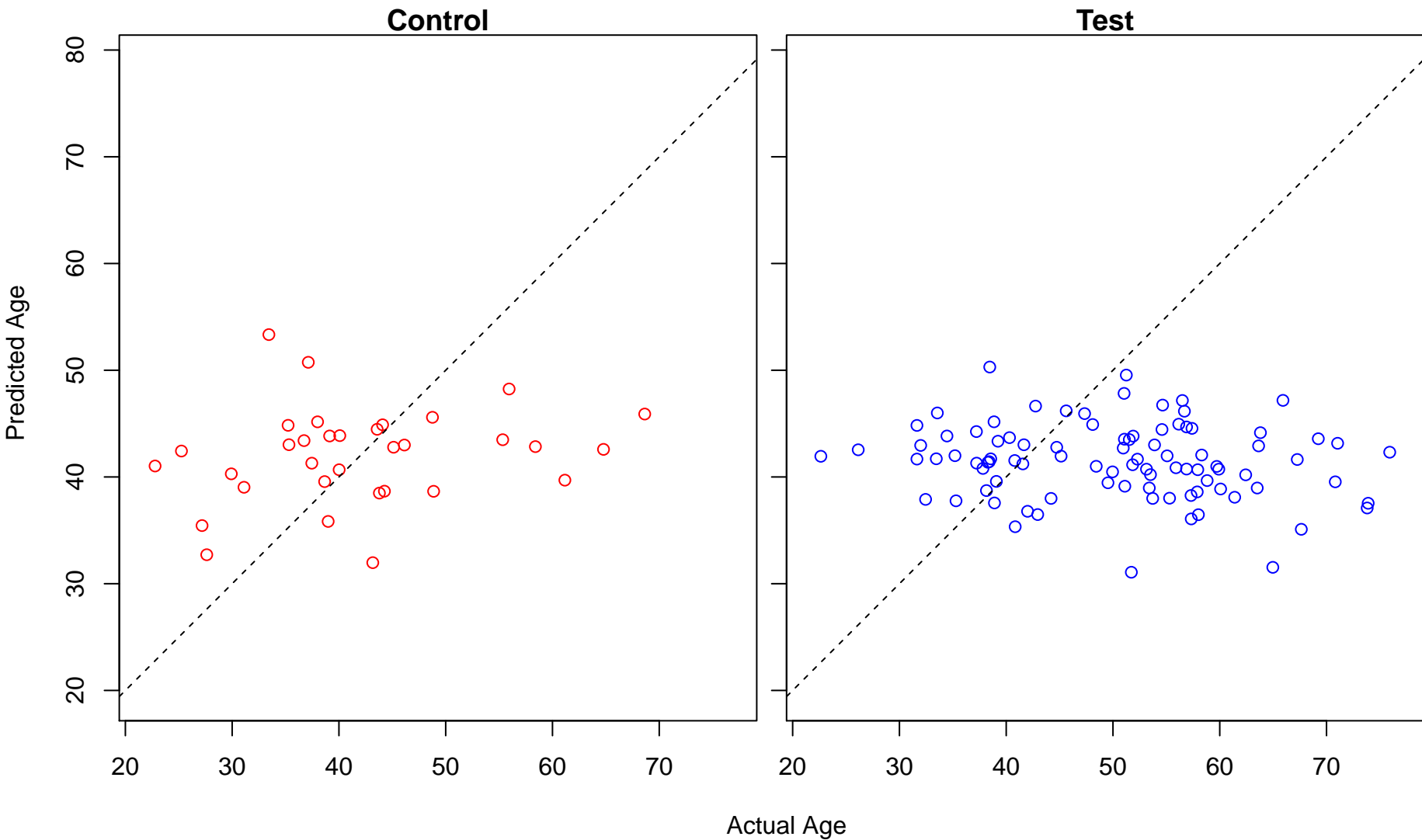
pyridine nucleotide biosynthetic process (Score: 0.161375)



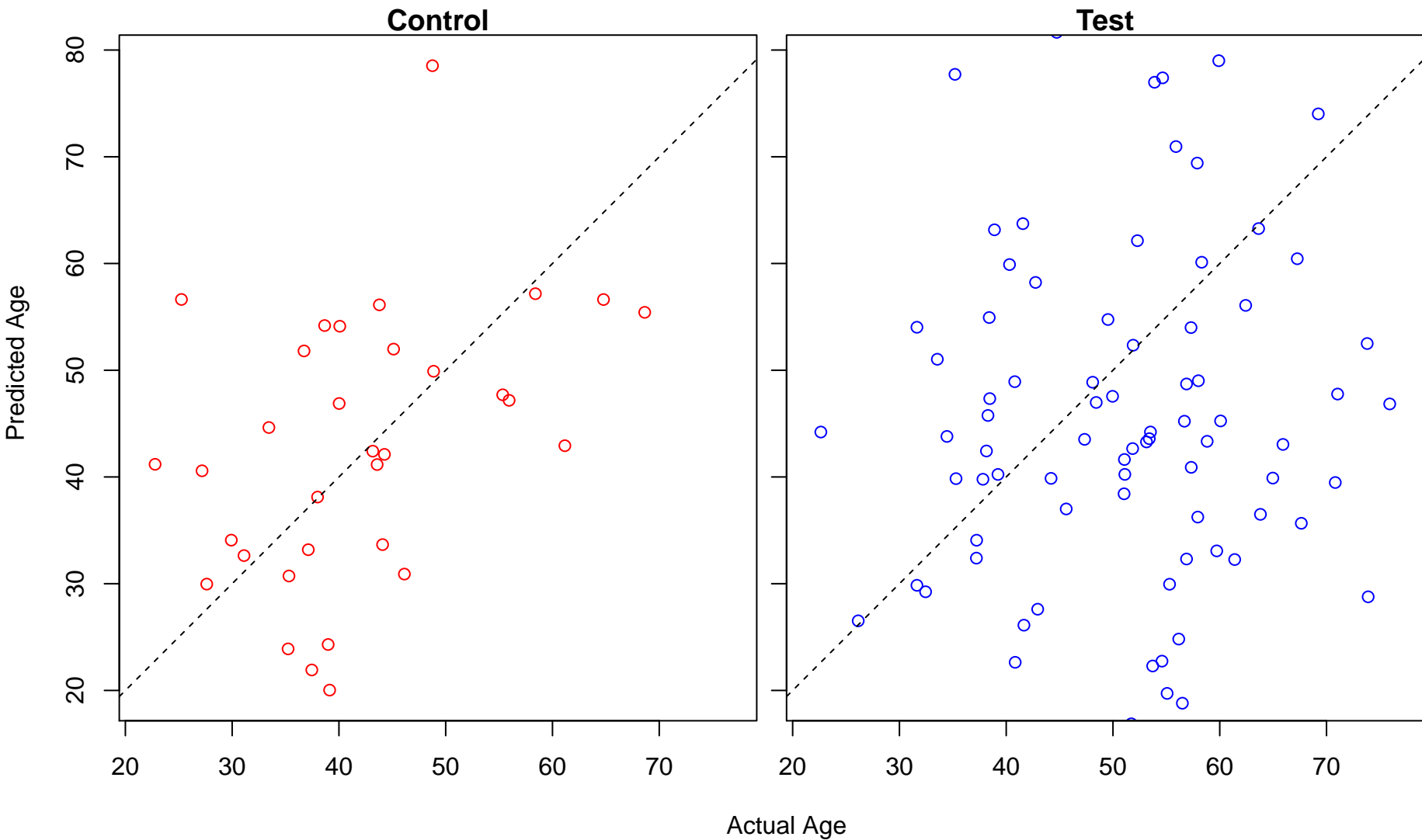
activation-induced cell death of T cells (Score: 0.159618)



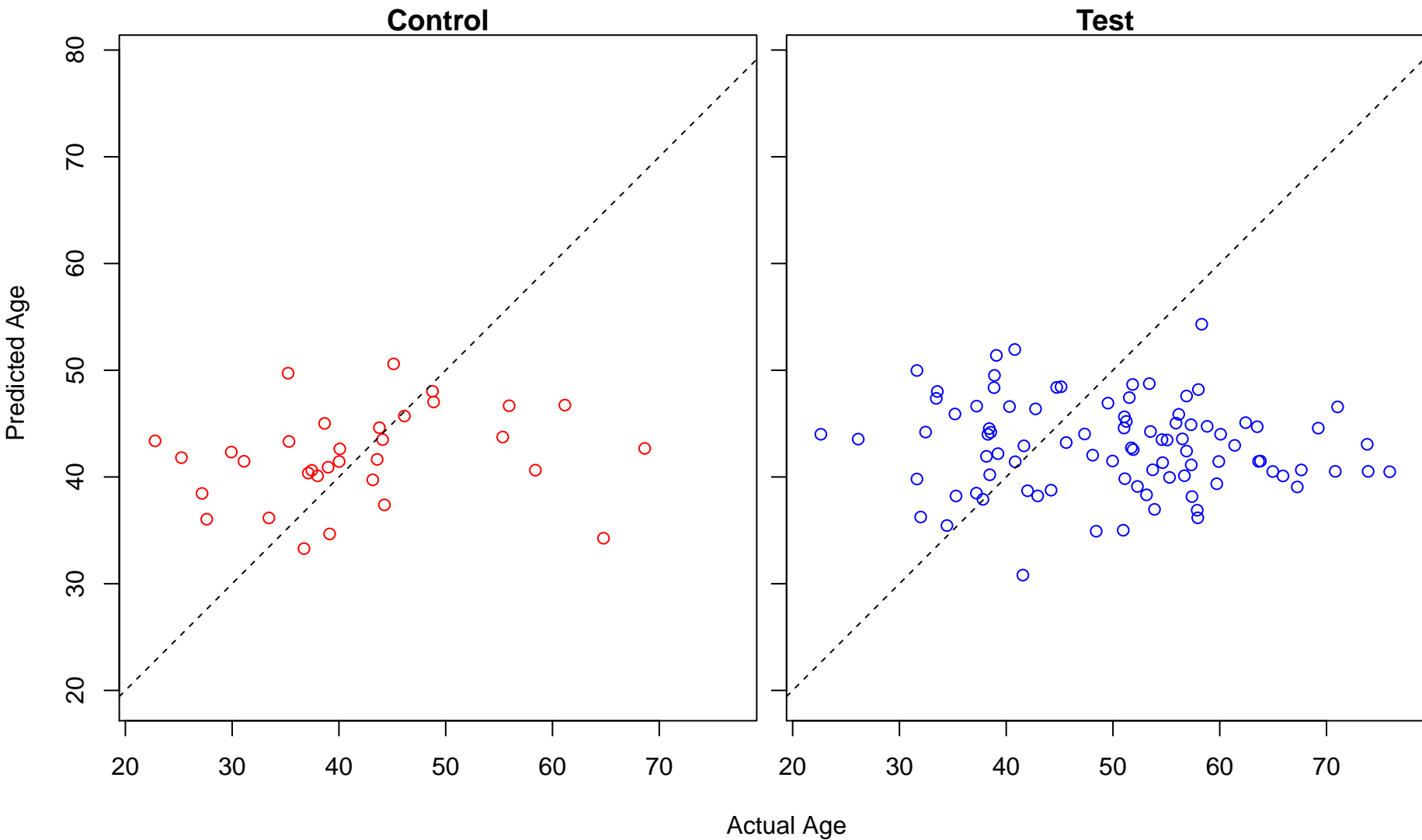
basophil differentiation (Score: 0.158045)



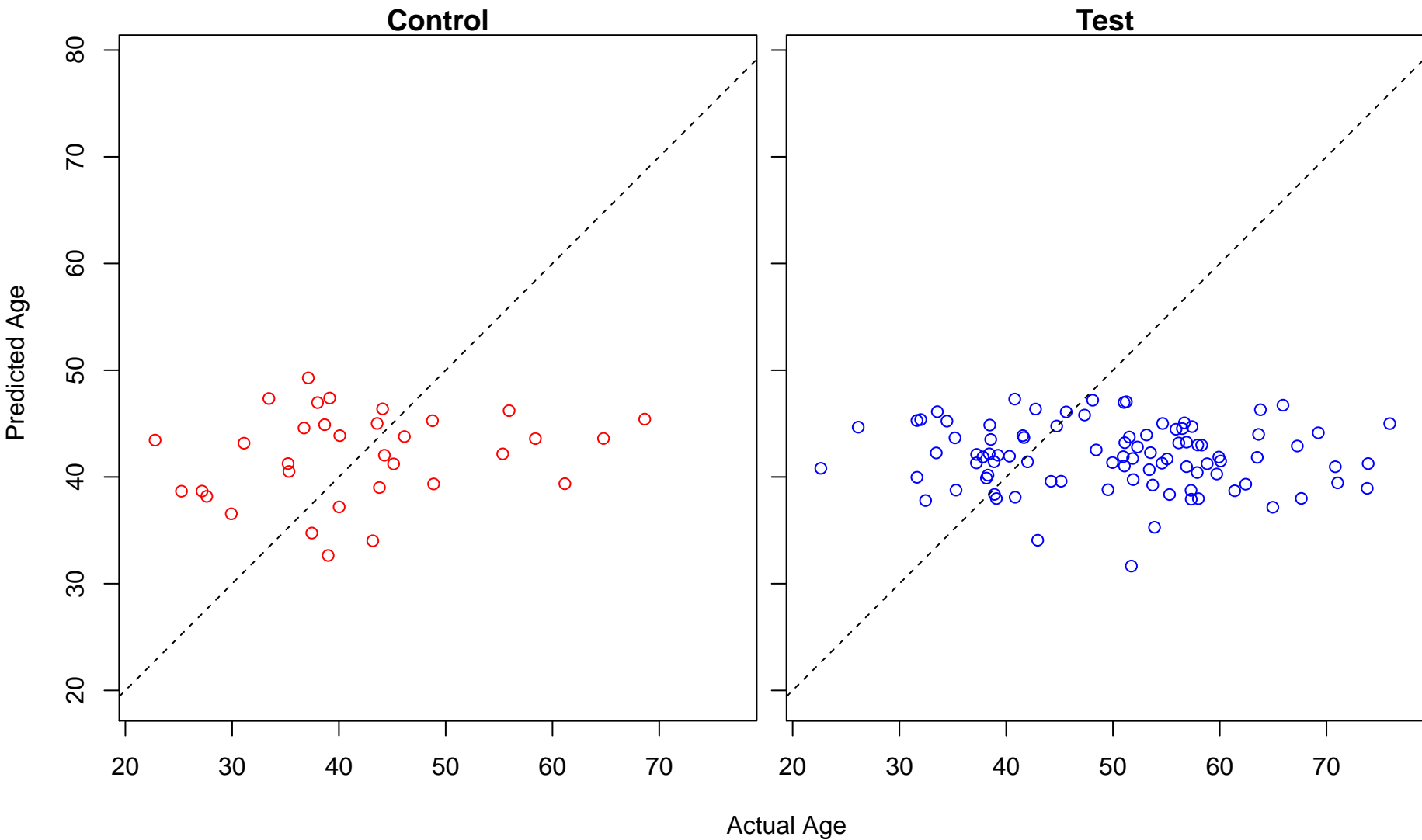
regulation of response to interferon- γ (Score: 0.153651)



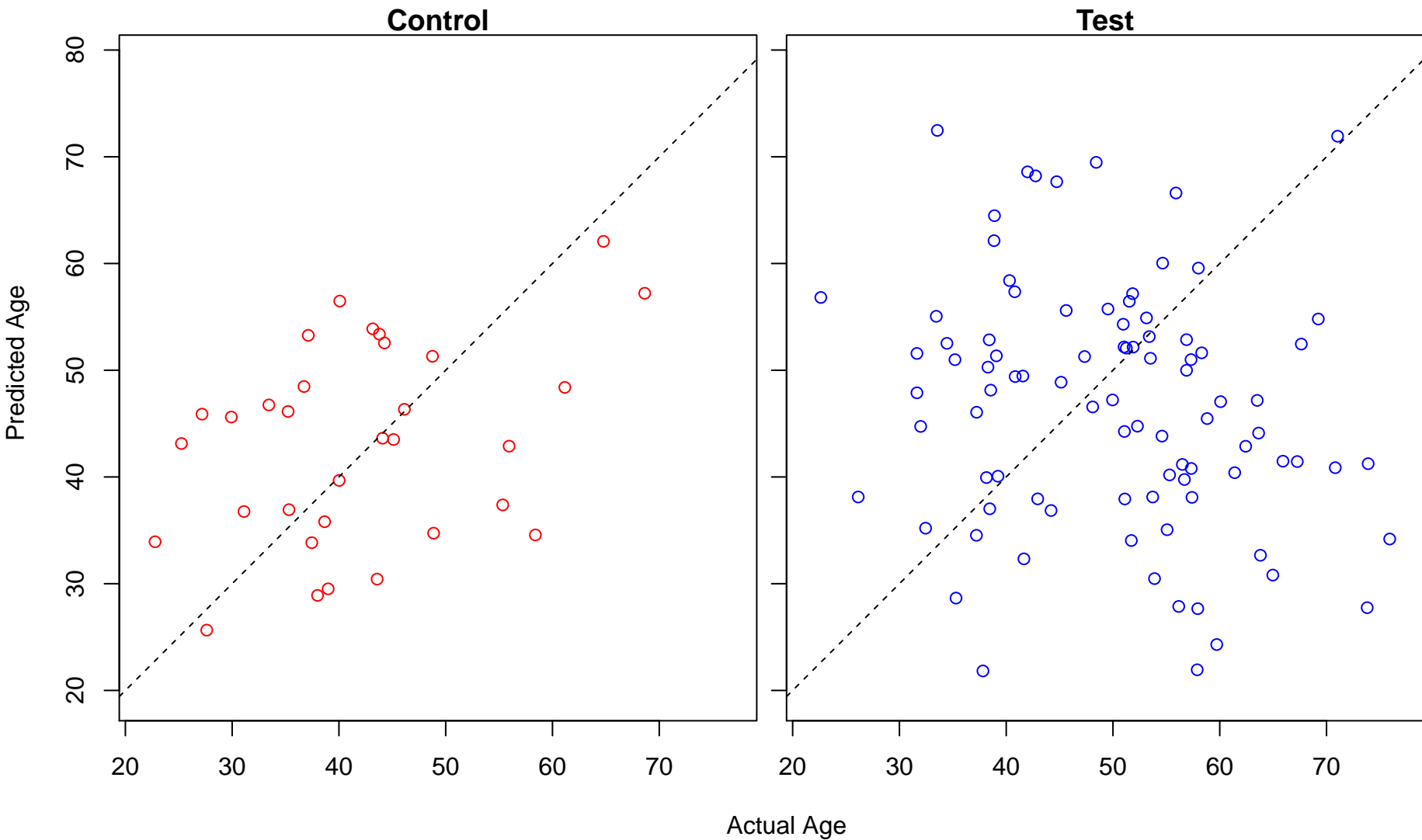
negative regulation of T cell mediated cytotoxicity (Score: 0.144085)



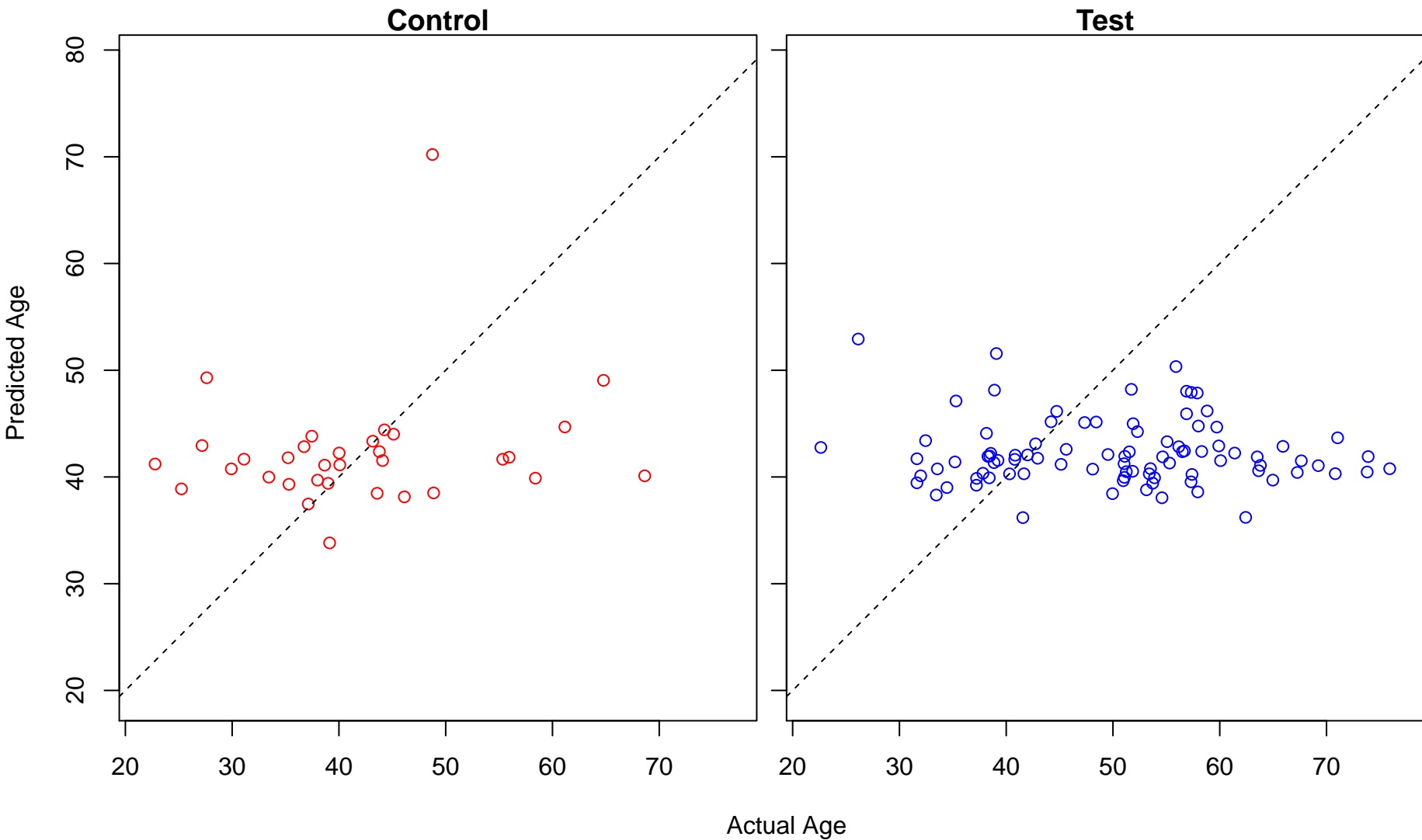
negative regulation of amine transport (Score: 0.143575)



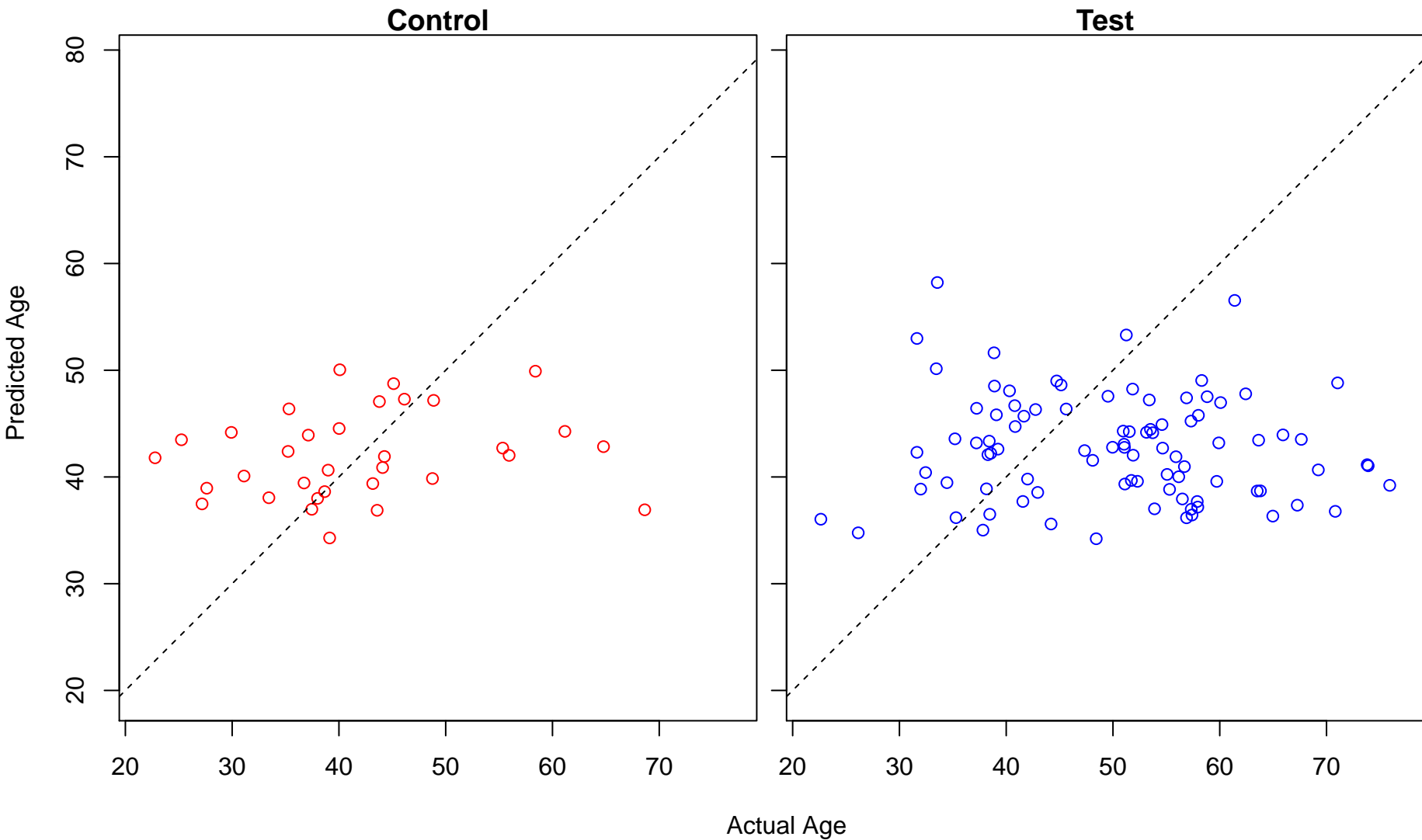
cellular response to light stimulus (Score: 0.133509)



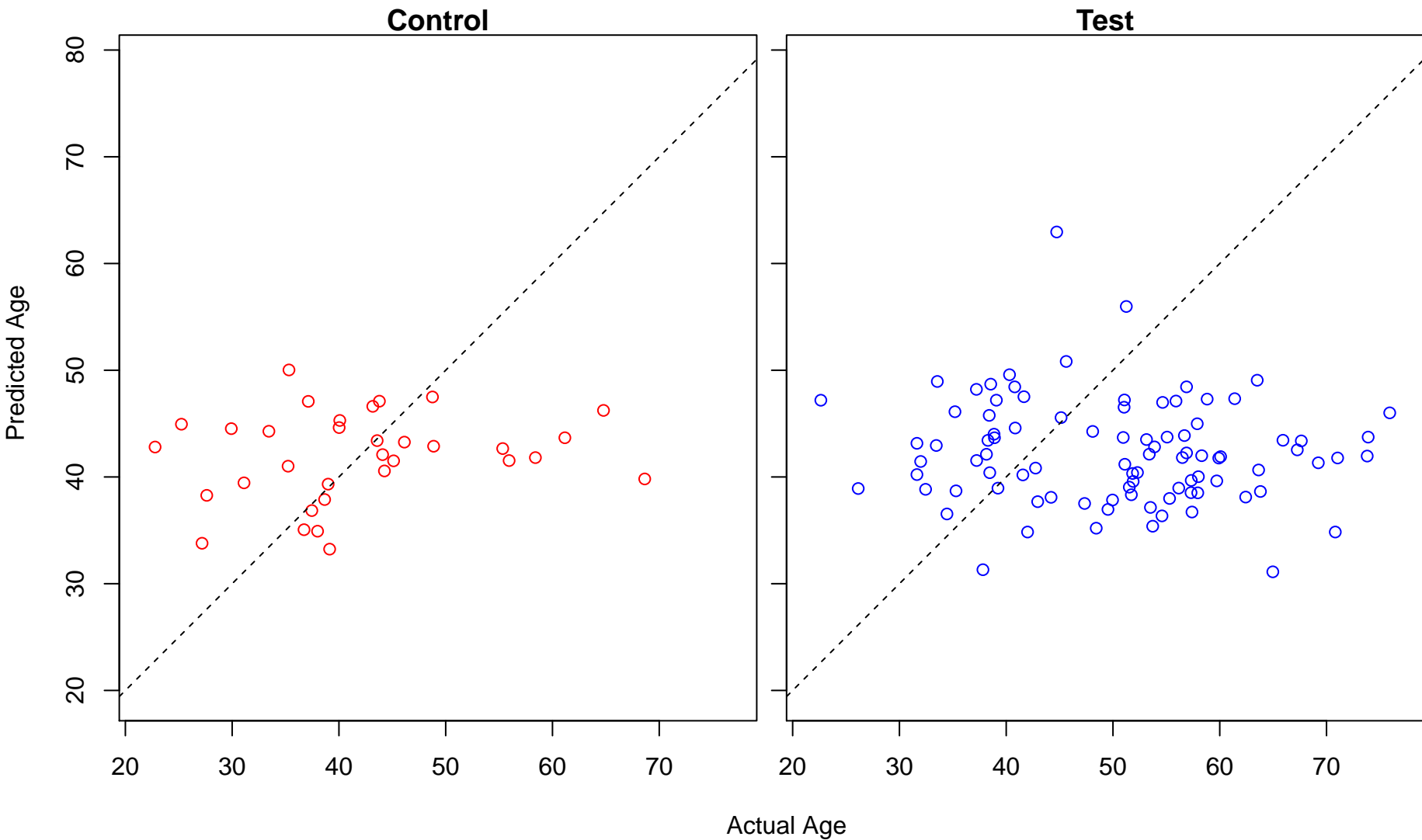
tricuspid valve morphogenesis (Score: 0.133106)



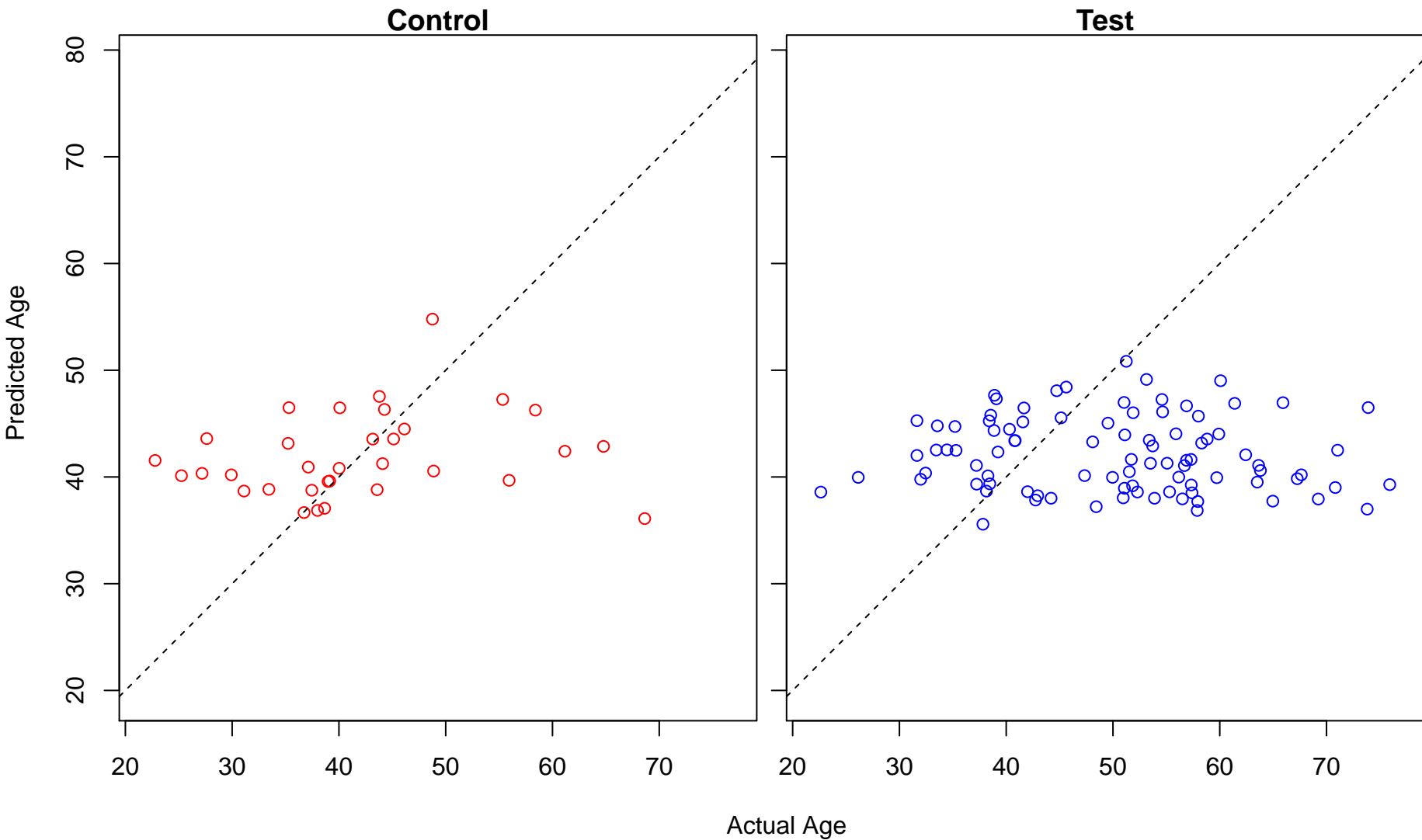
positive regulation of lipoprotein lipase activity (Score: 0.129854)



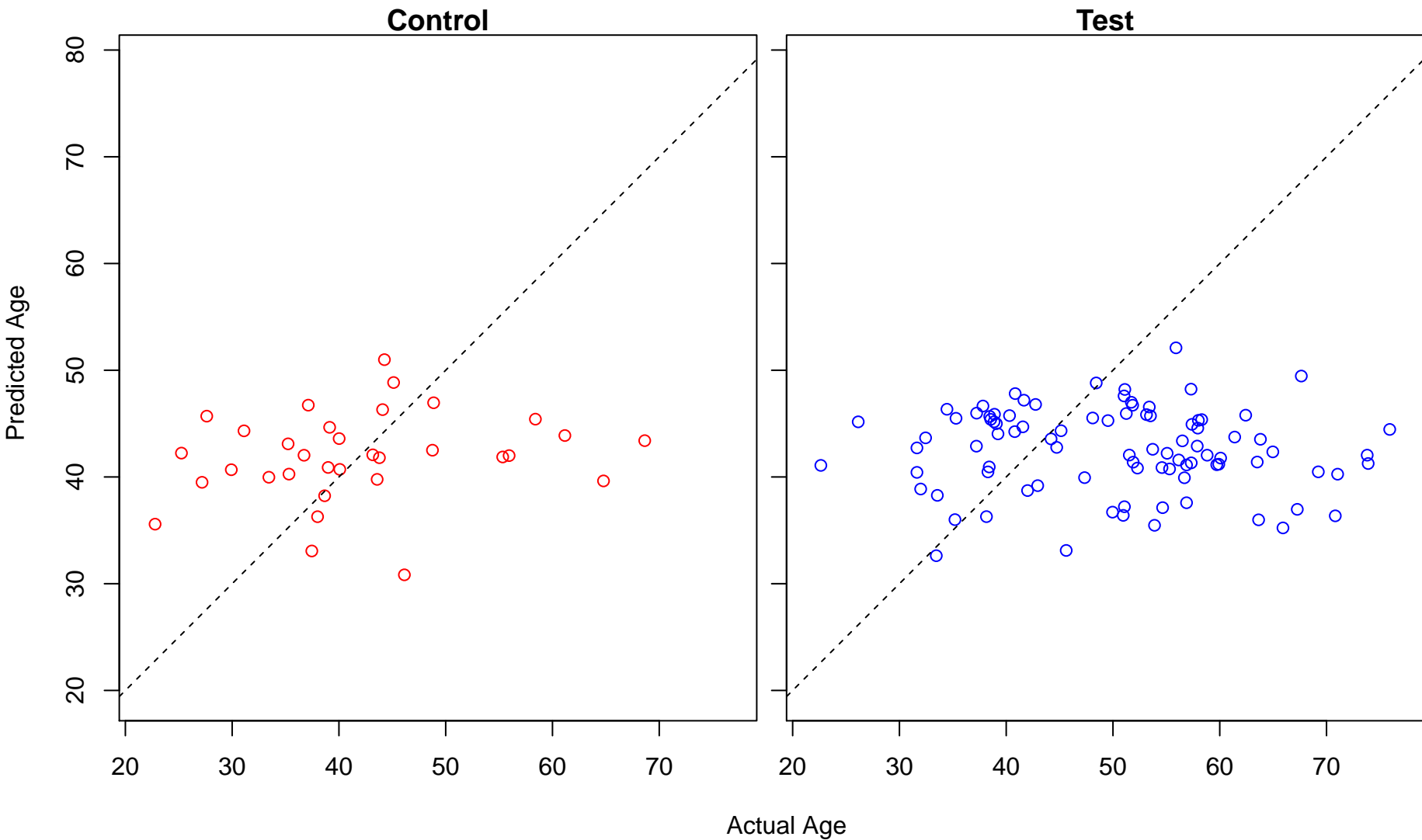
ribosomal small subunit assembly (Score: 0.129549)



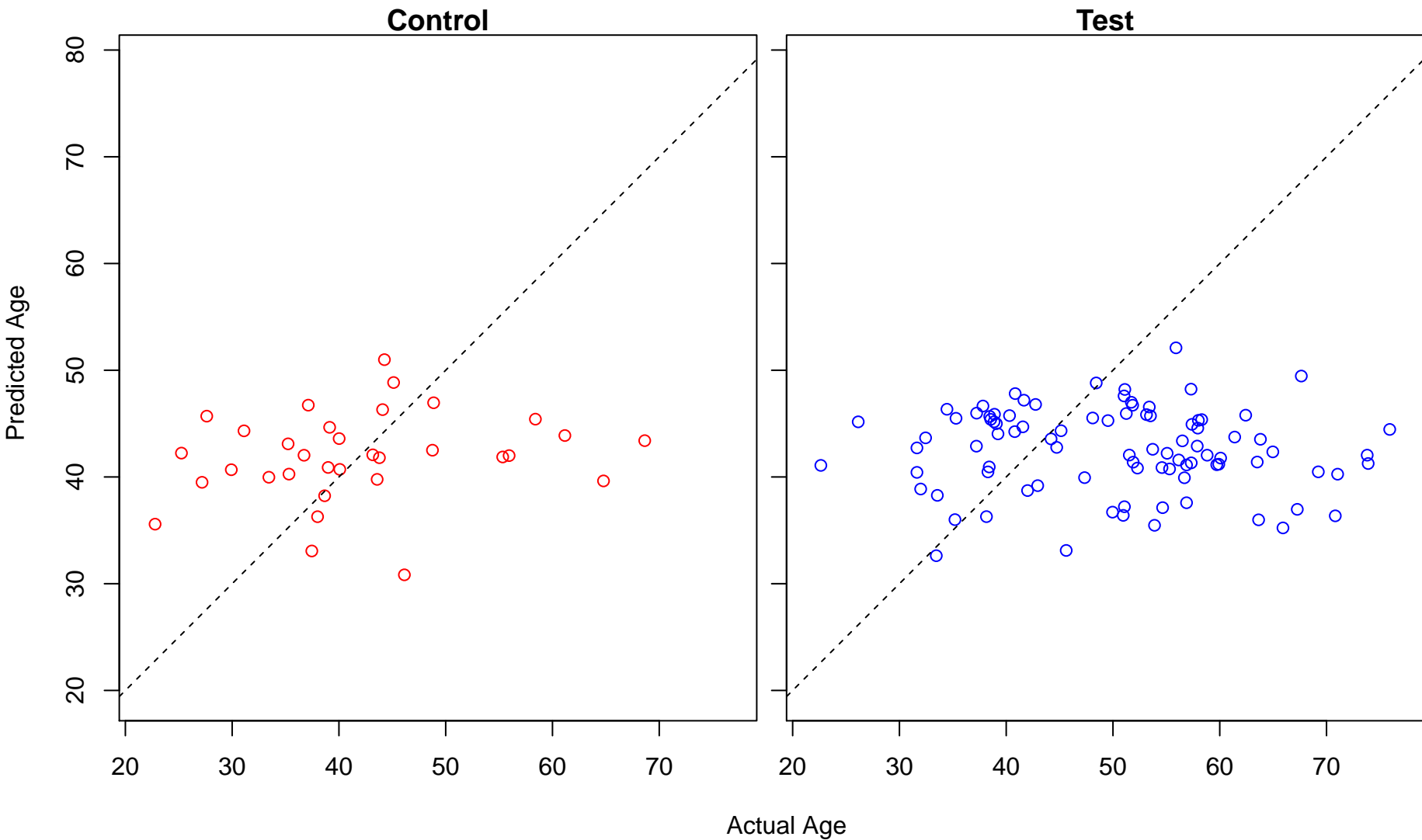
positive regulation of histone deacetylase activity (Score: 0.128285)



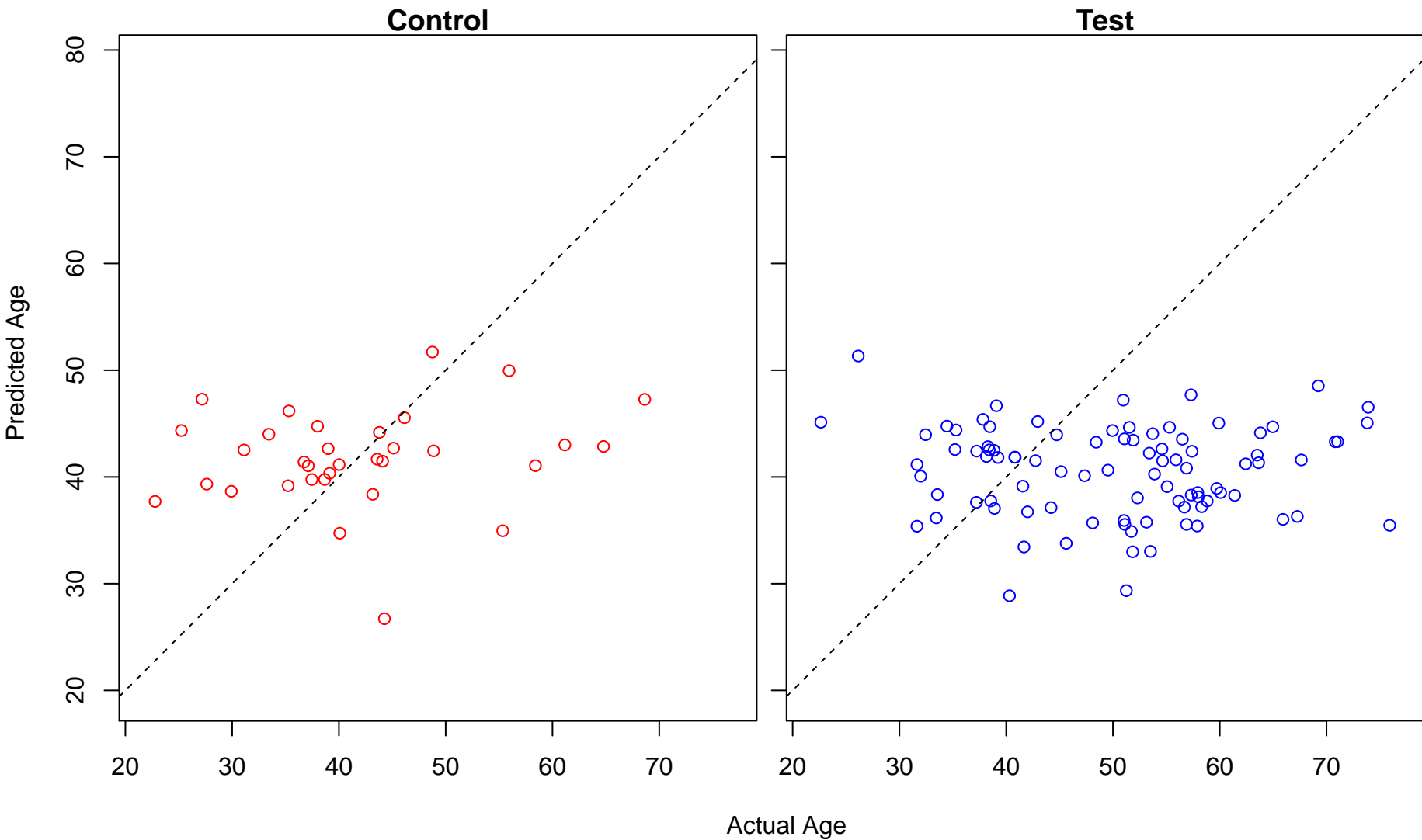
phasic smooth muscle contraction (Score: 0.124010)



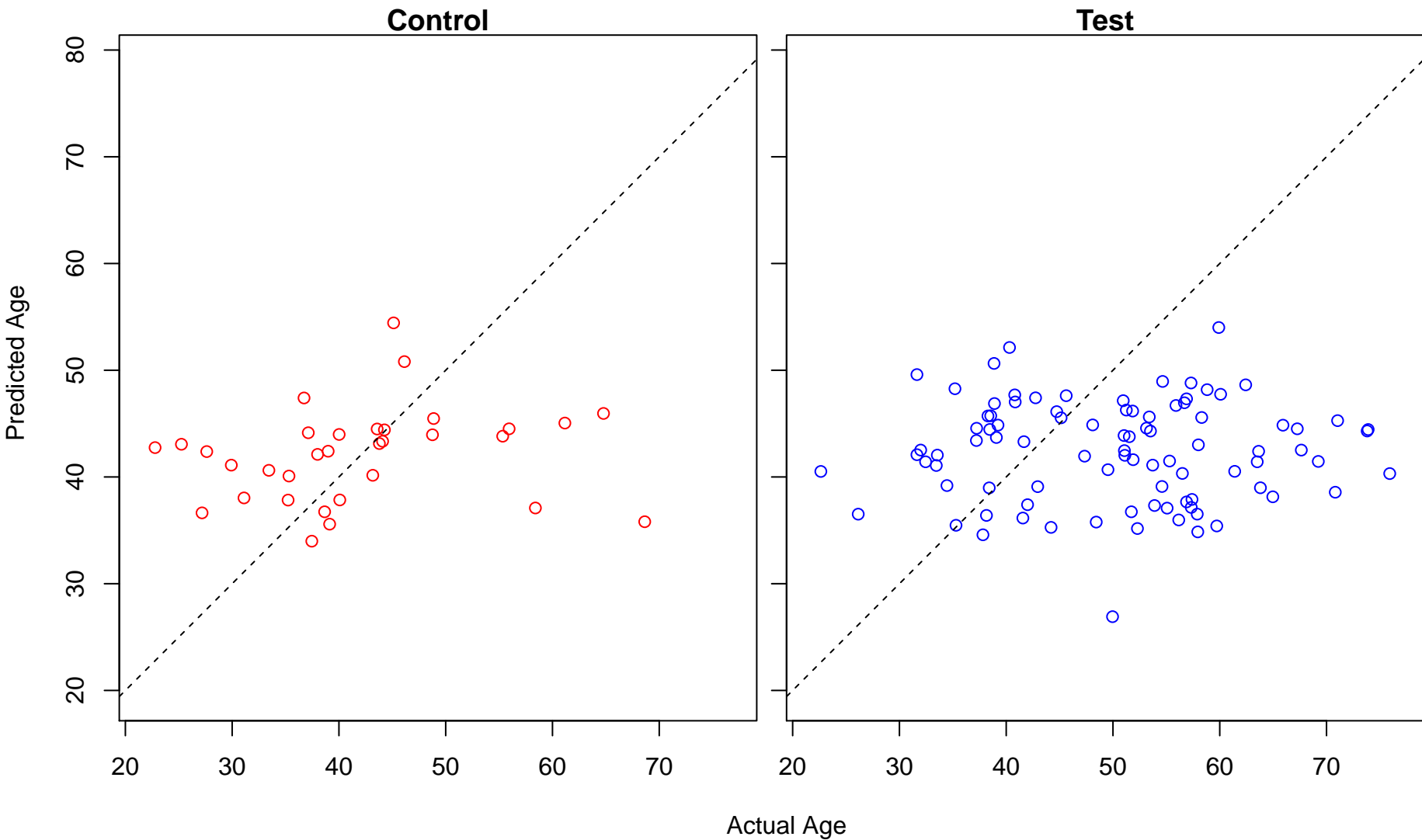
vein smooth muscle contraction (Score: 0.124010)



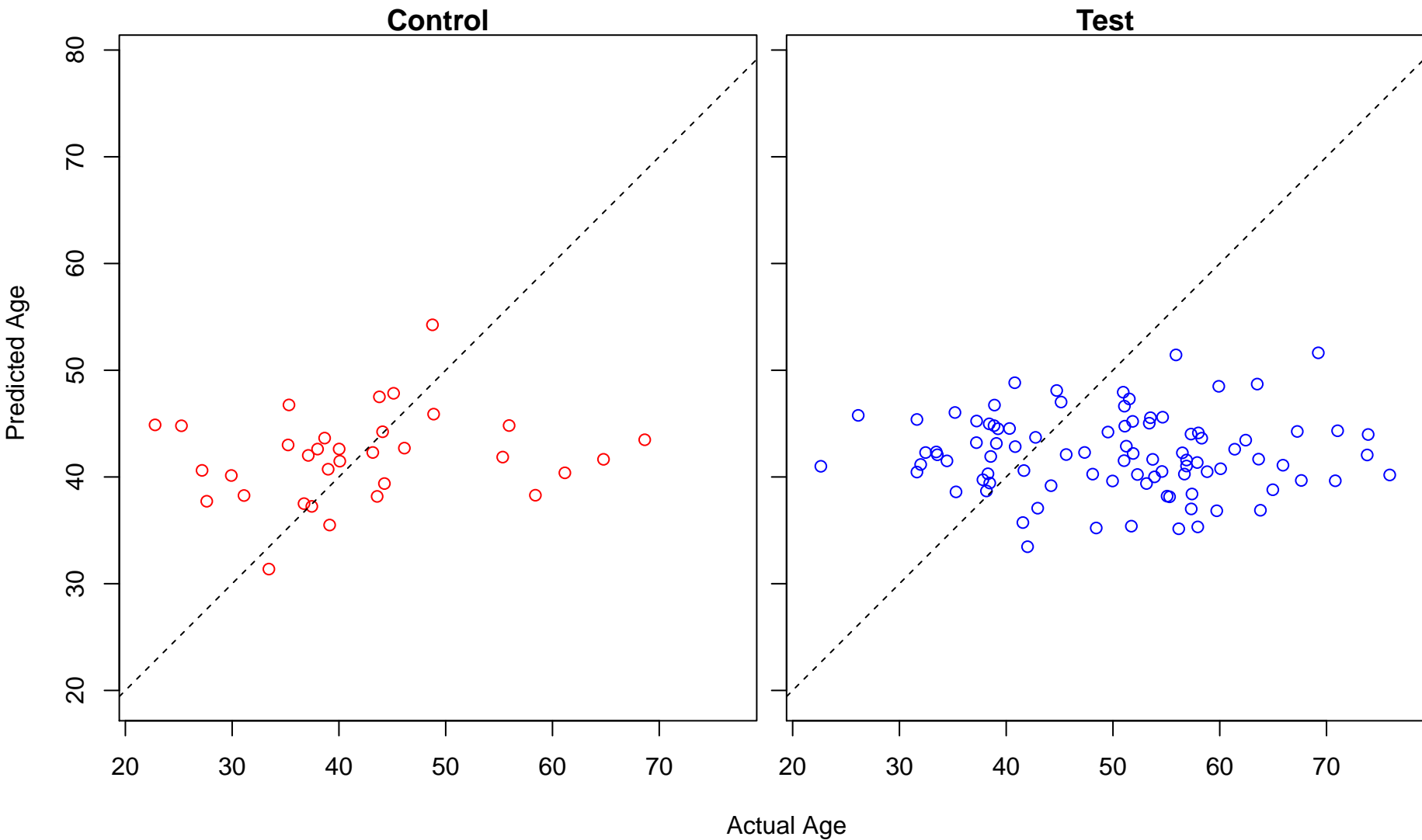
inosine metabolic process (Score: 0.123978)



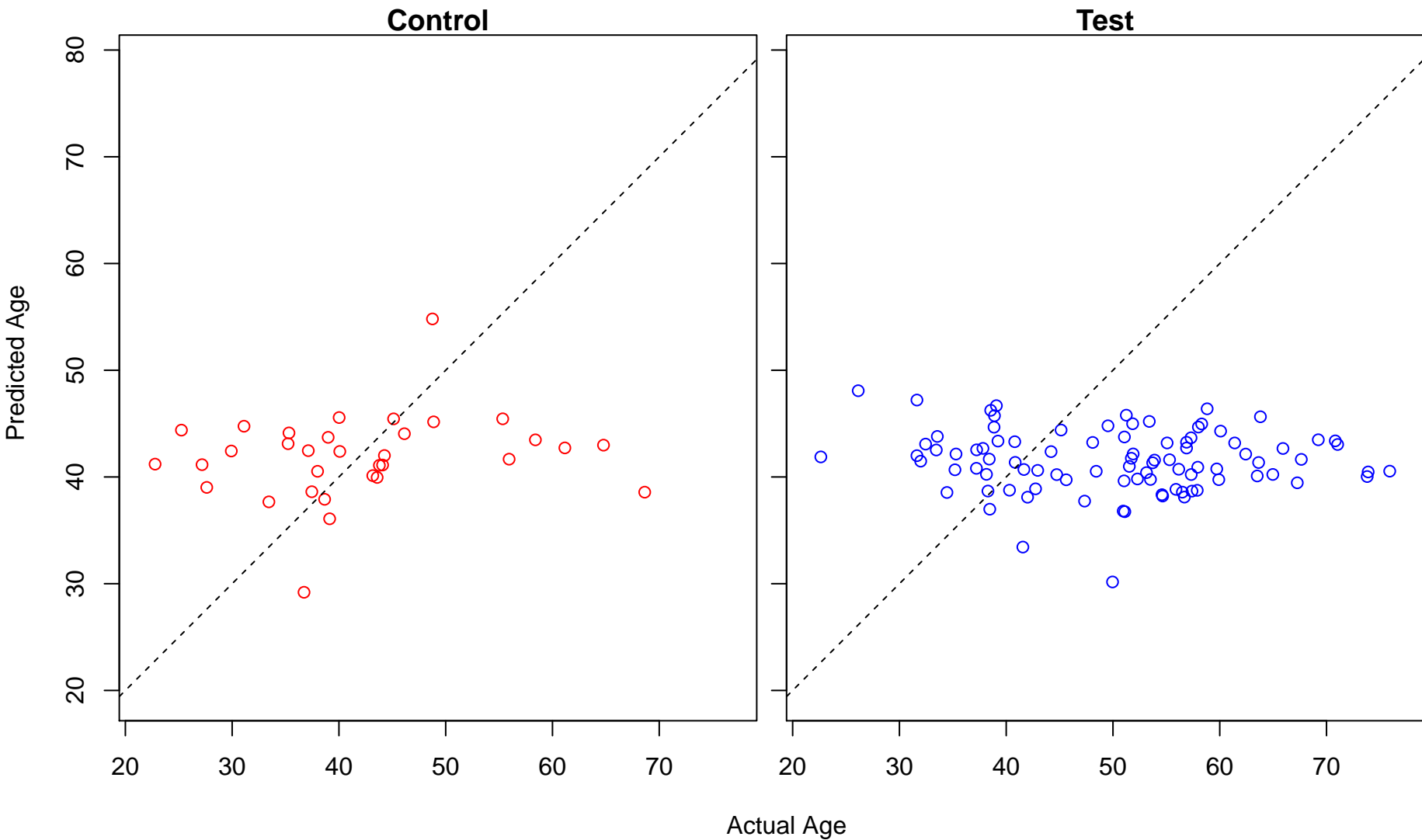
L-kynurenine metabolic process (Score: 0.120134)



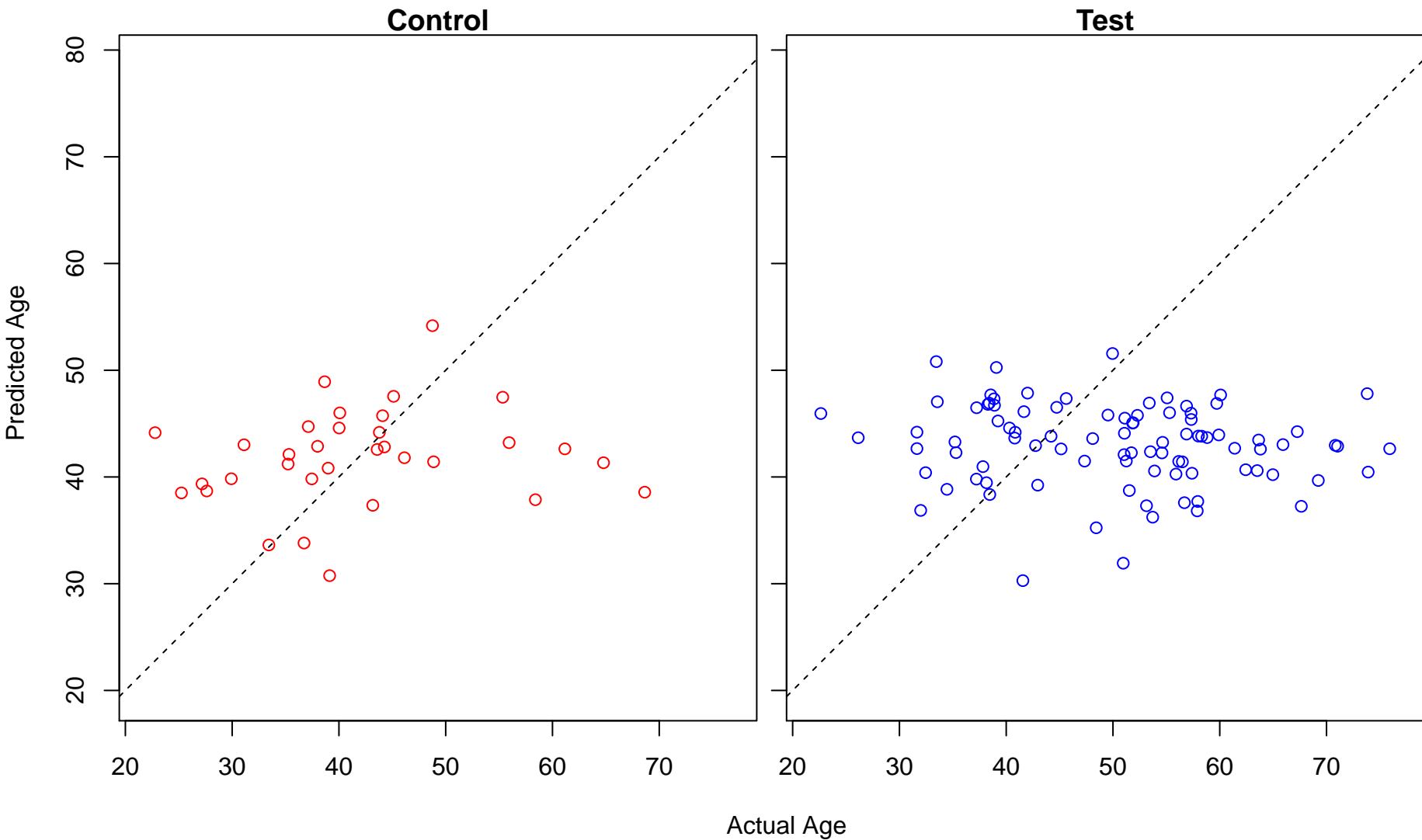
layer formation in cerebral cortex (Score: 0.119859)



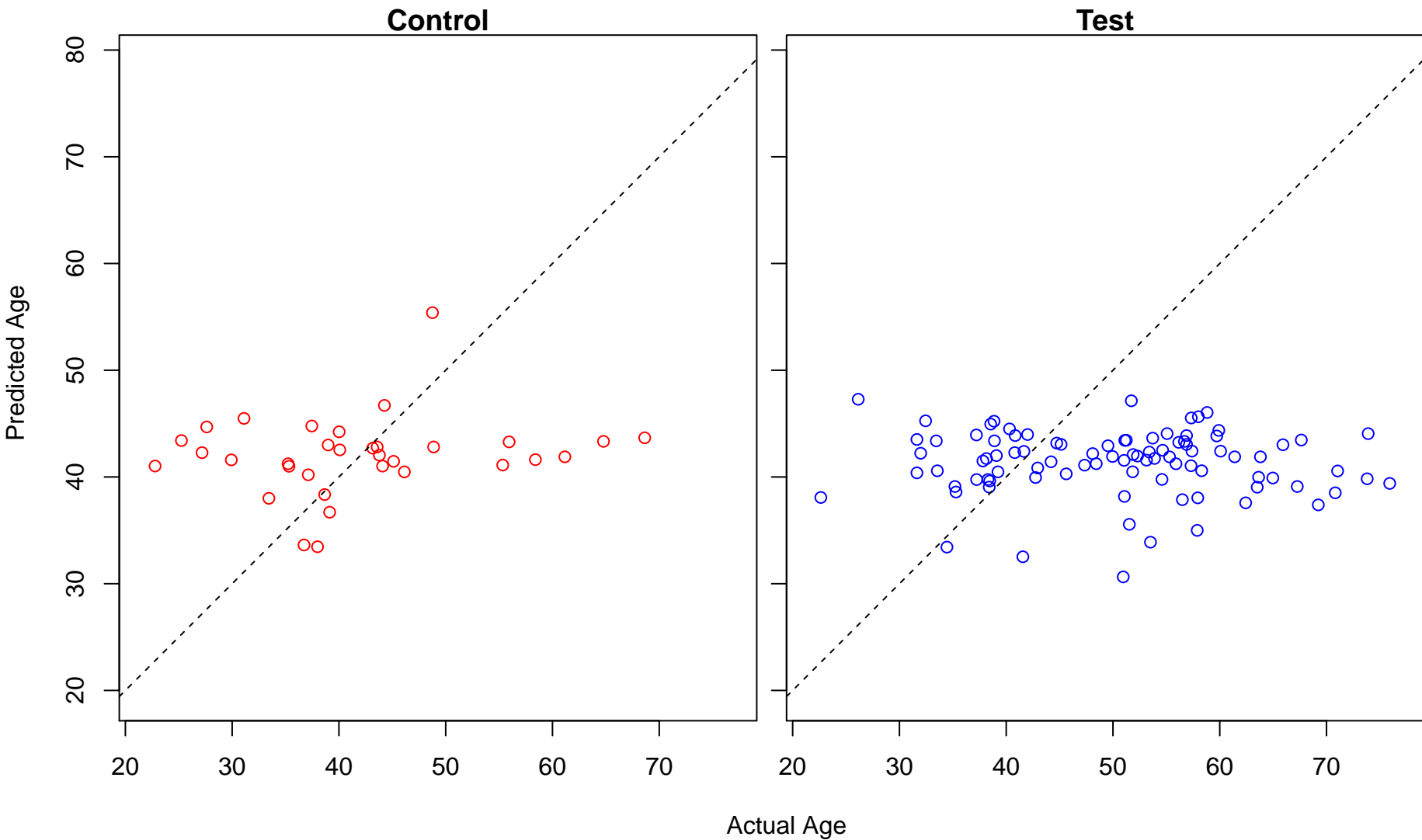
GDP-L-fucose metabolic process (Score: 0.108023)



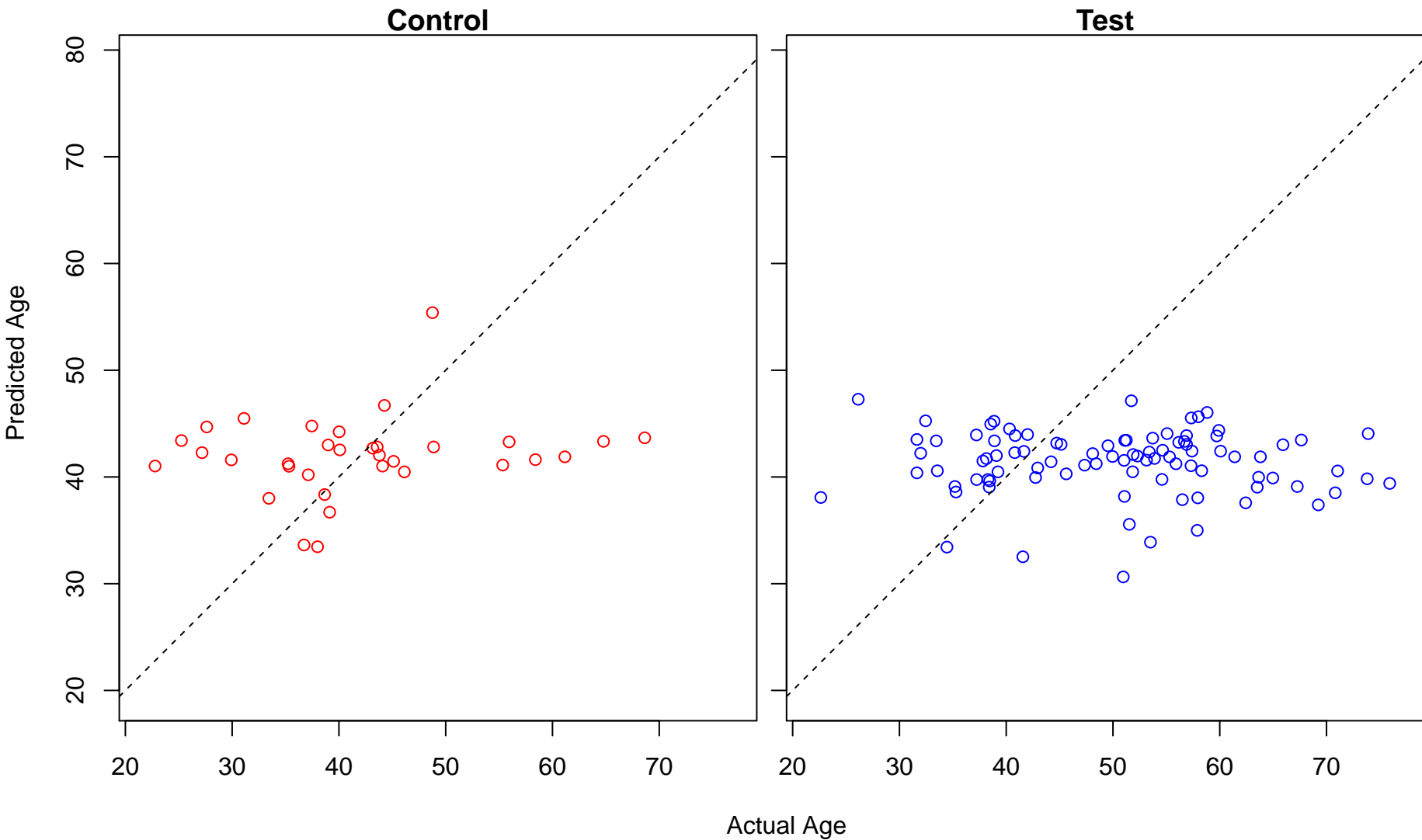
histone H3-T11 phosphorylation (Score: 0.107007)



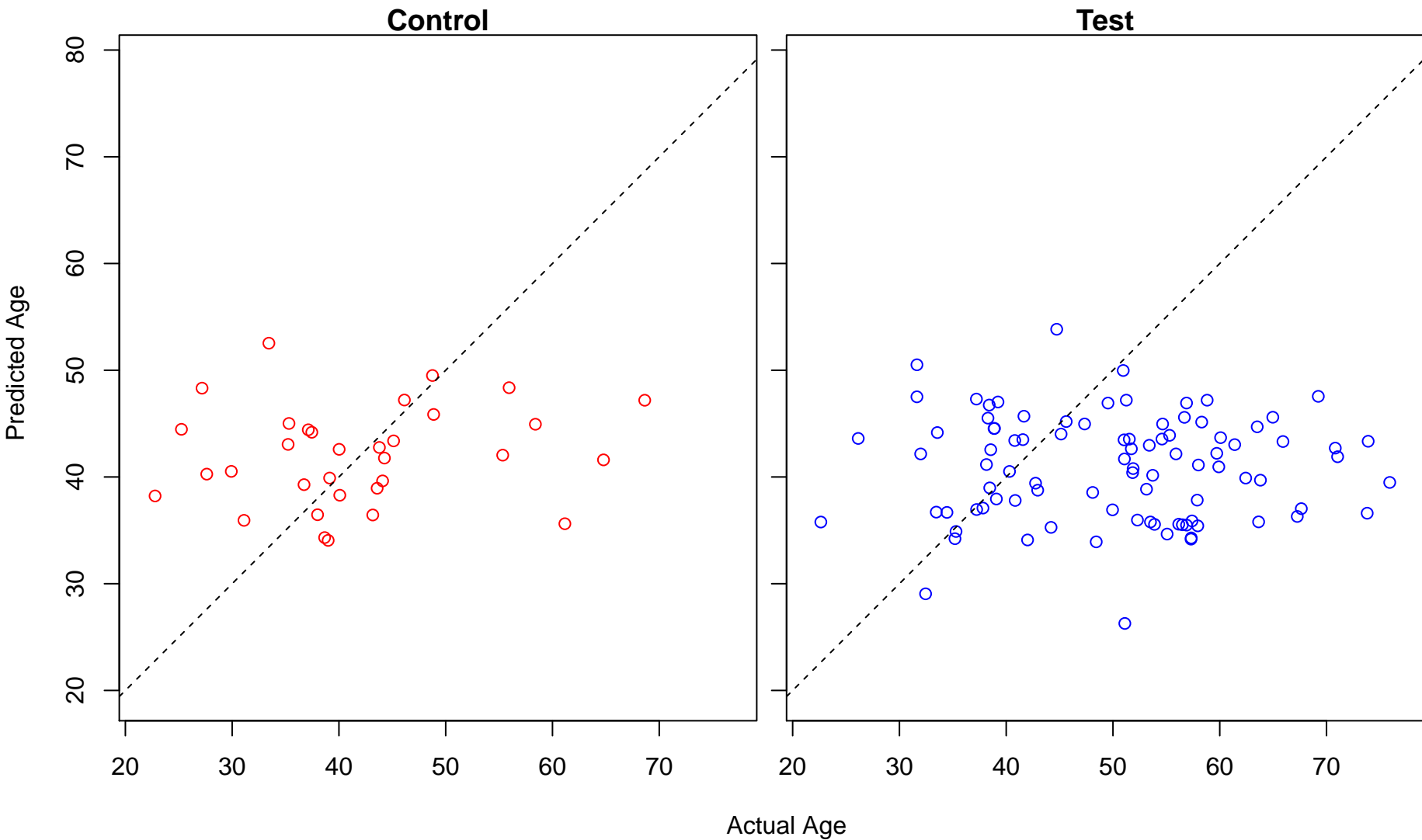
selenocysteine incorporation (Score: 0.102349)



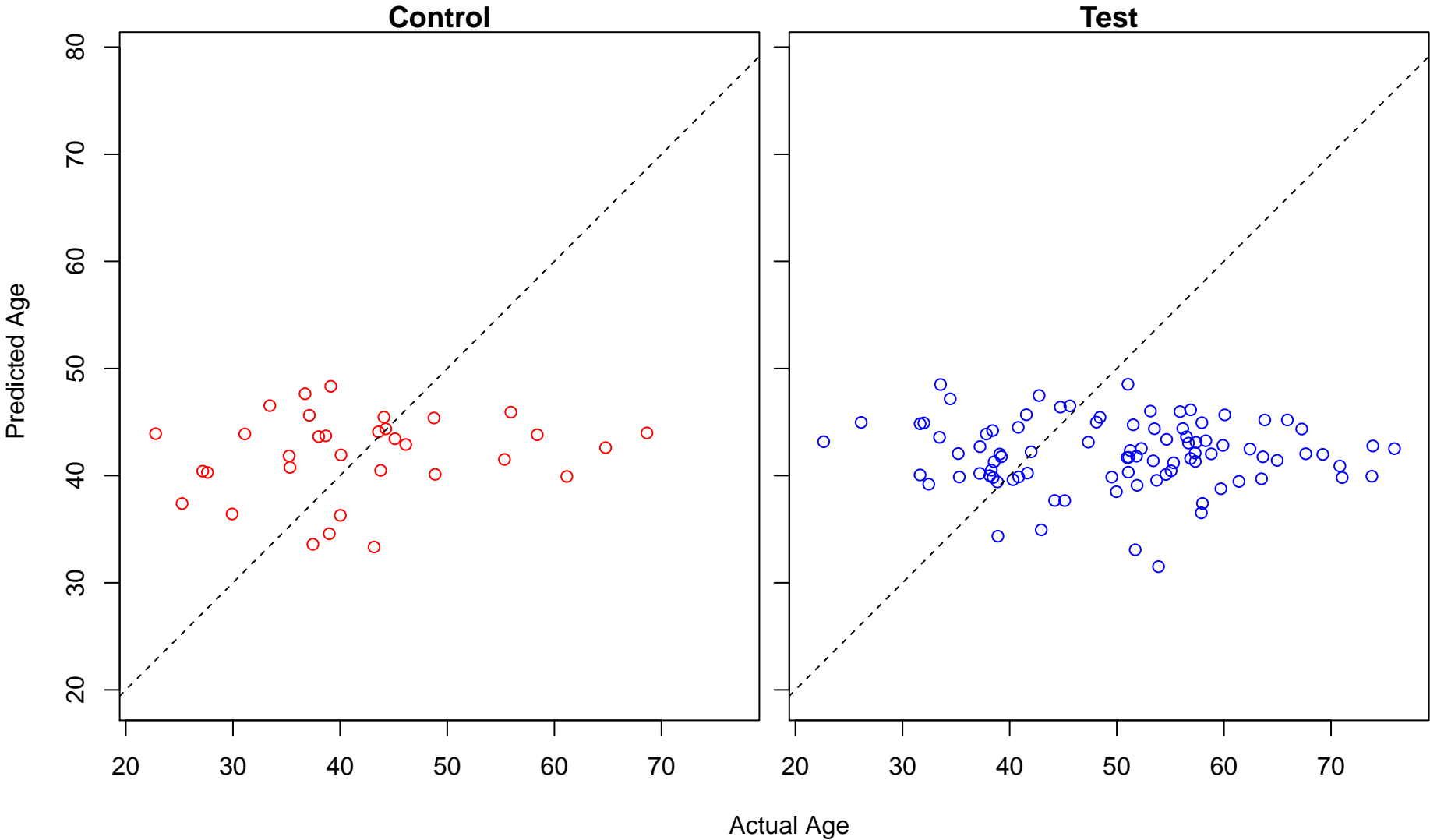
translational readthrough (Score: 0.102349)



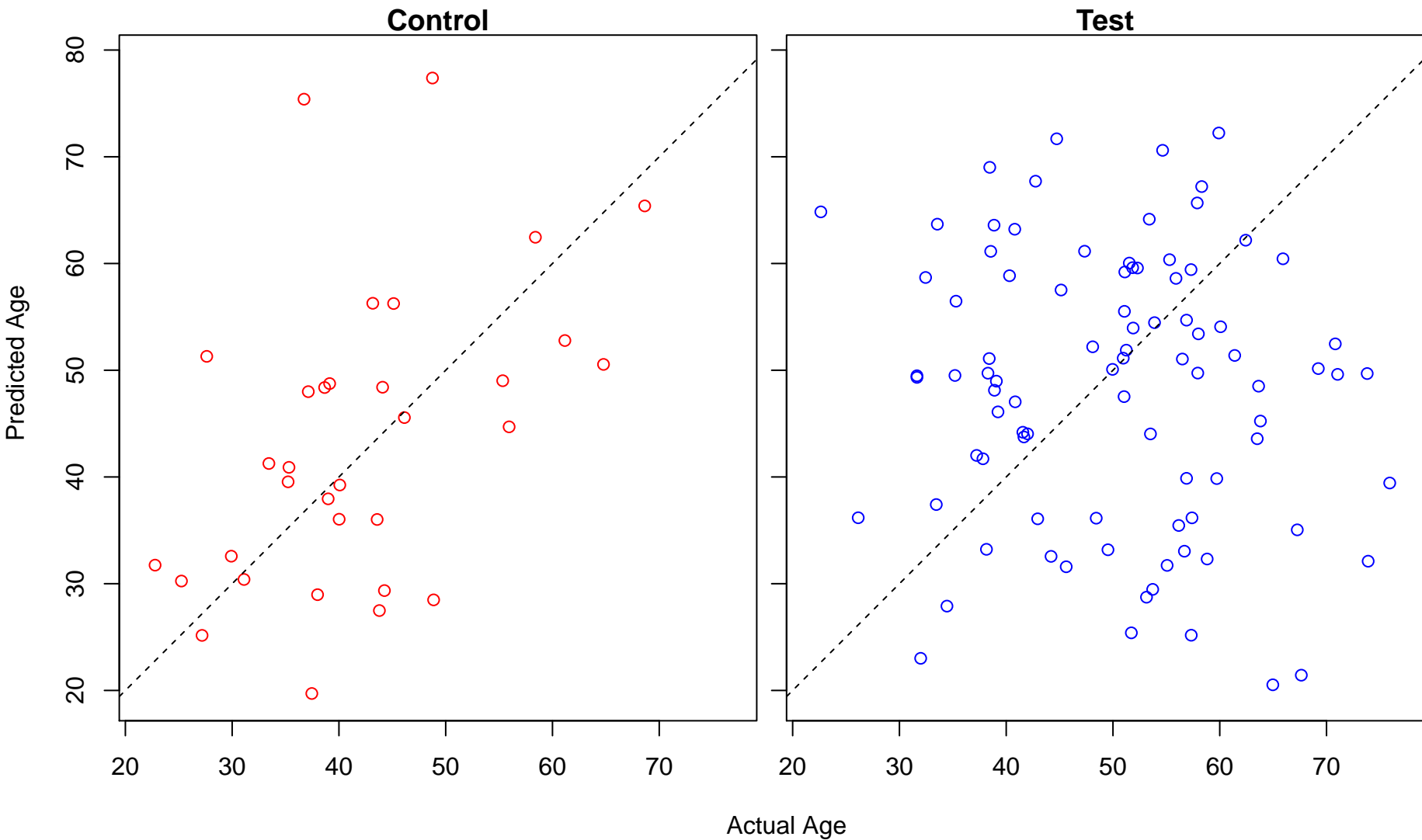
detection of triacyl bacterial lipopeptide (Score: 0.095232)



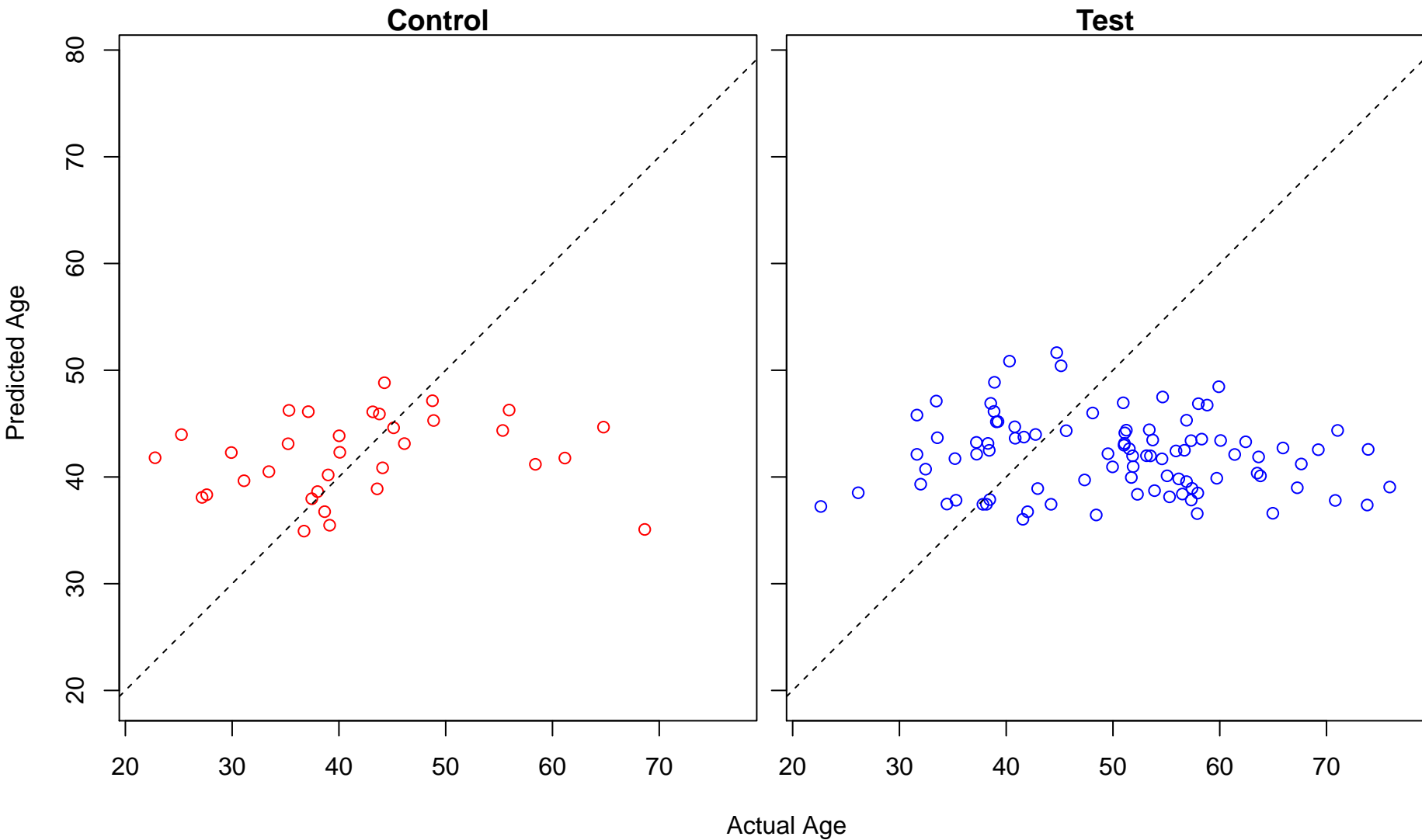
negative regulation of insulin secretion involved in cellular response to glucose stimulus (Score: 0.093)



positive regulation of inflammatory response (Score: 0.087405)



tachykinin receptor signaling pathway (Score: 0.086315)



regulation of Notch signaling pathway (Score: 0.052299)

