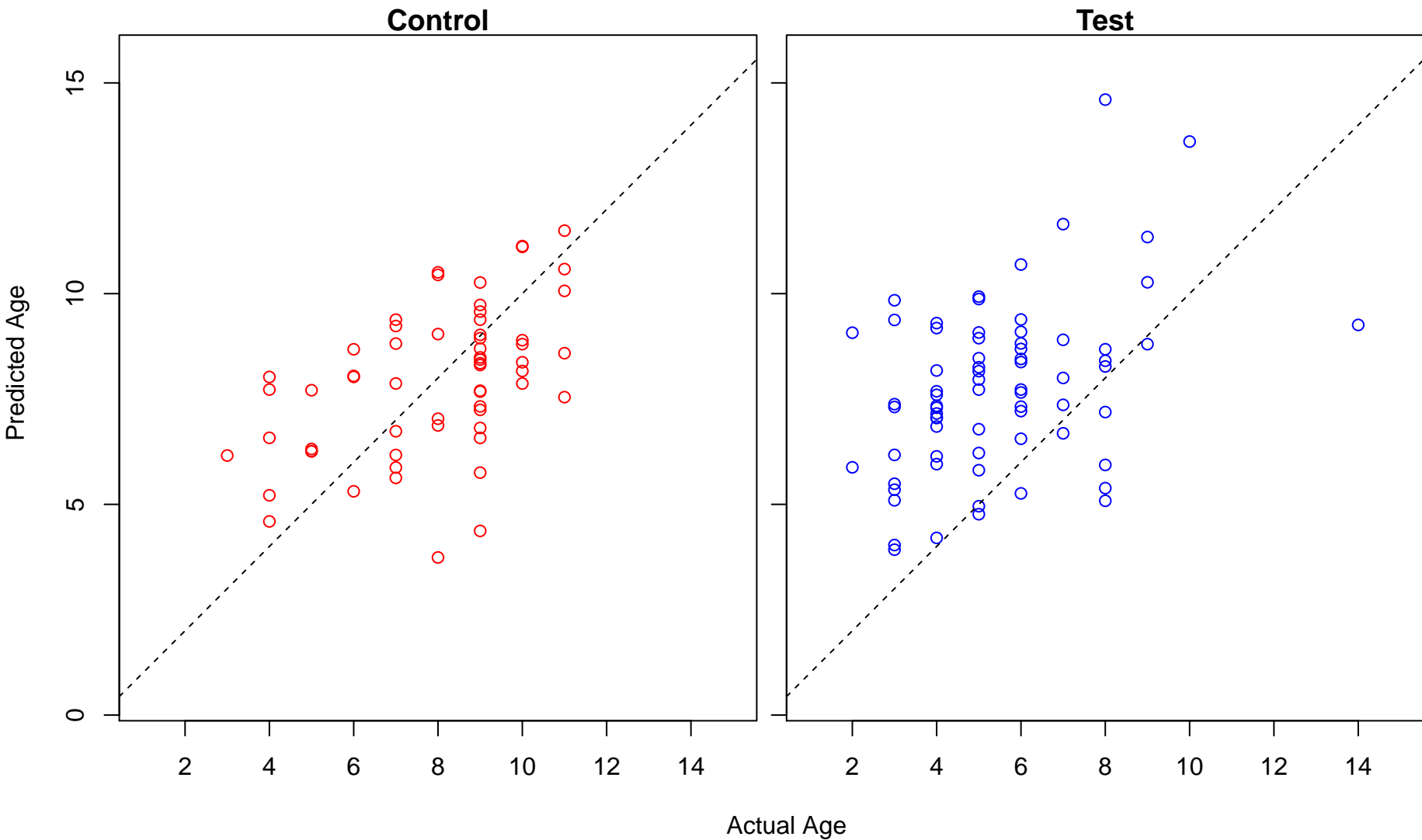
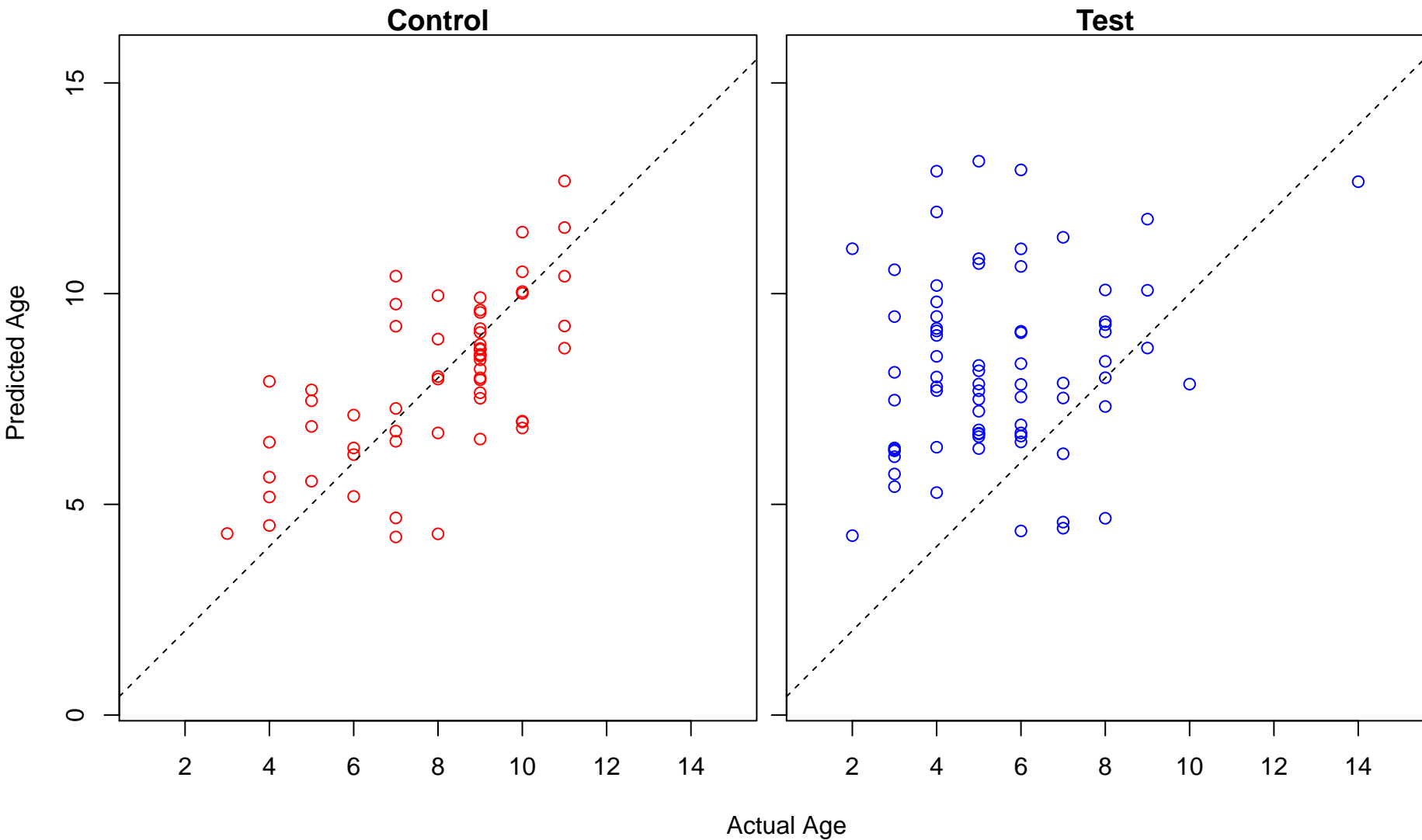


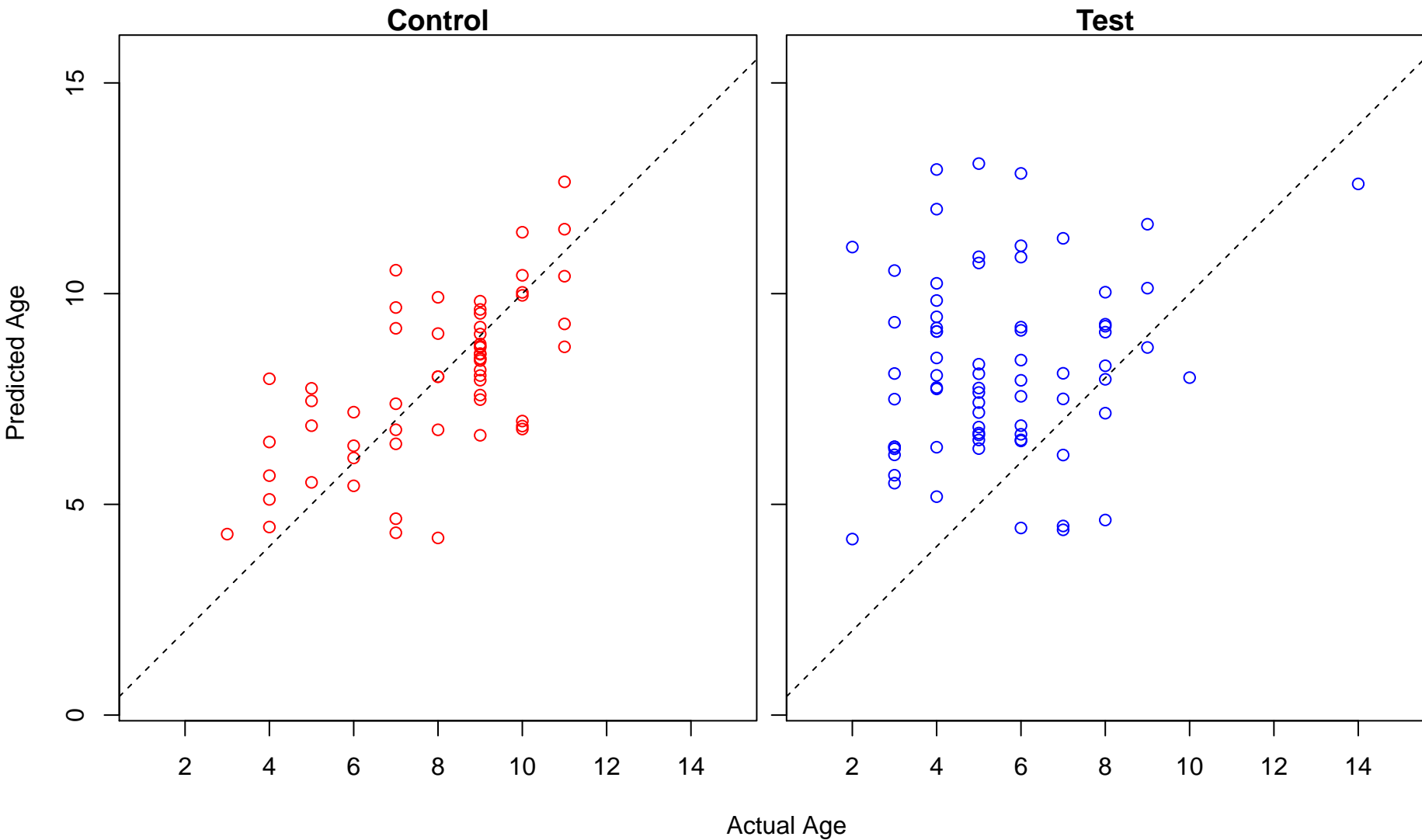
regulation of cell migration involved in sprouting angiogenesis (Score: 3.824242)



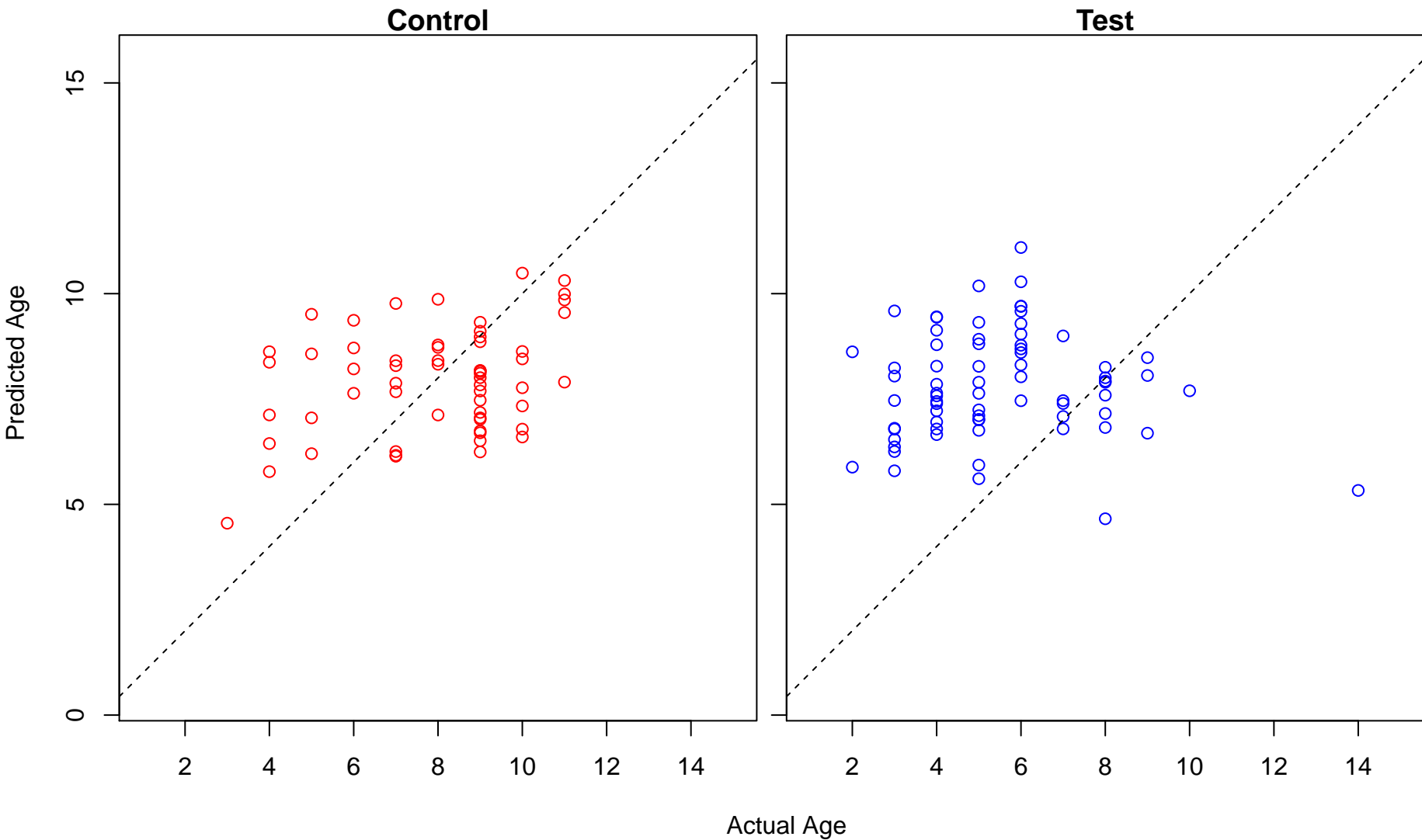
secretion by cell (Score: 2.274838)



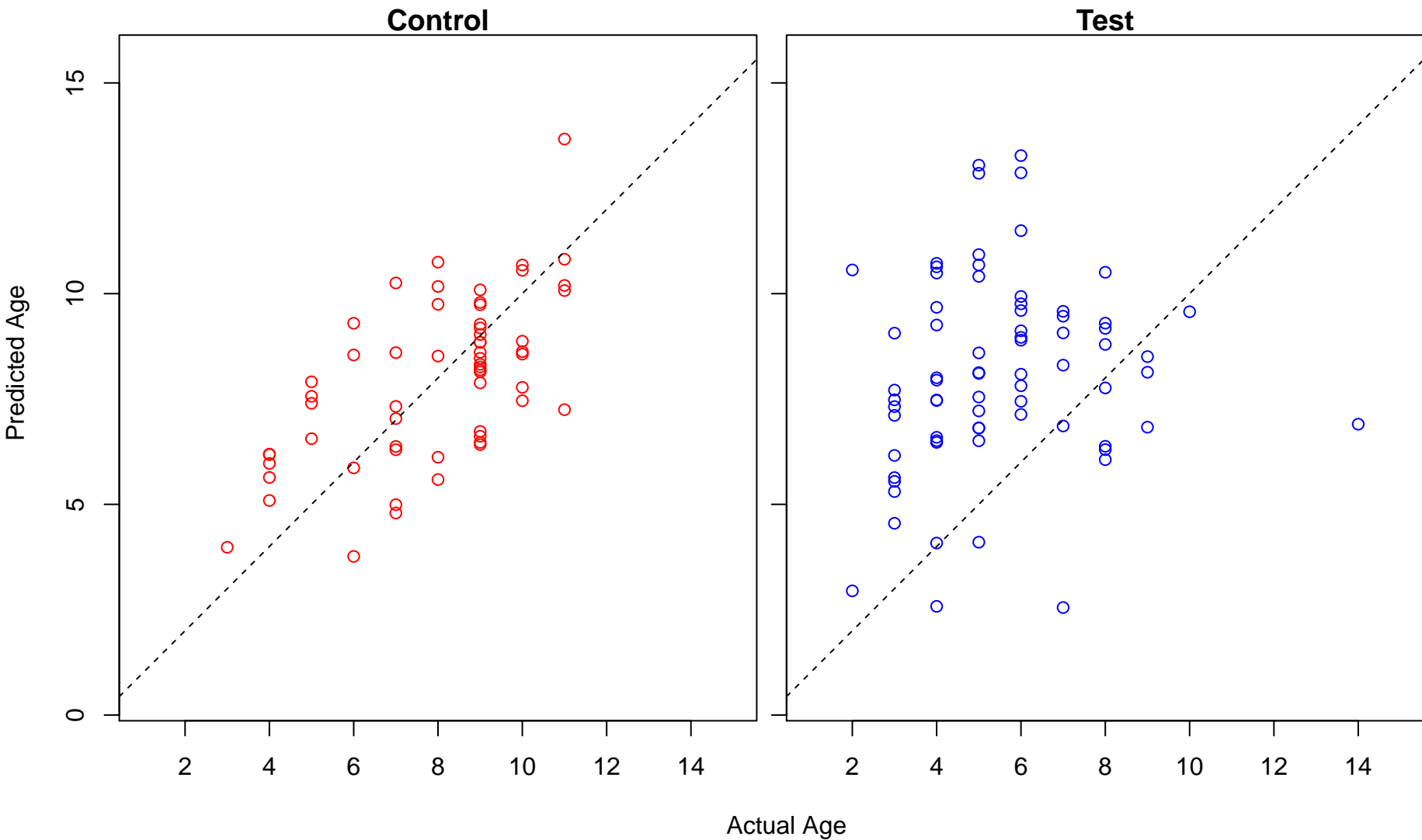
secretion (Score: 2.261927)



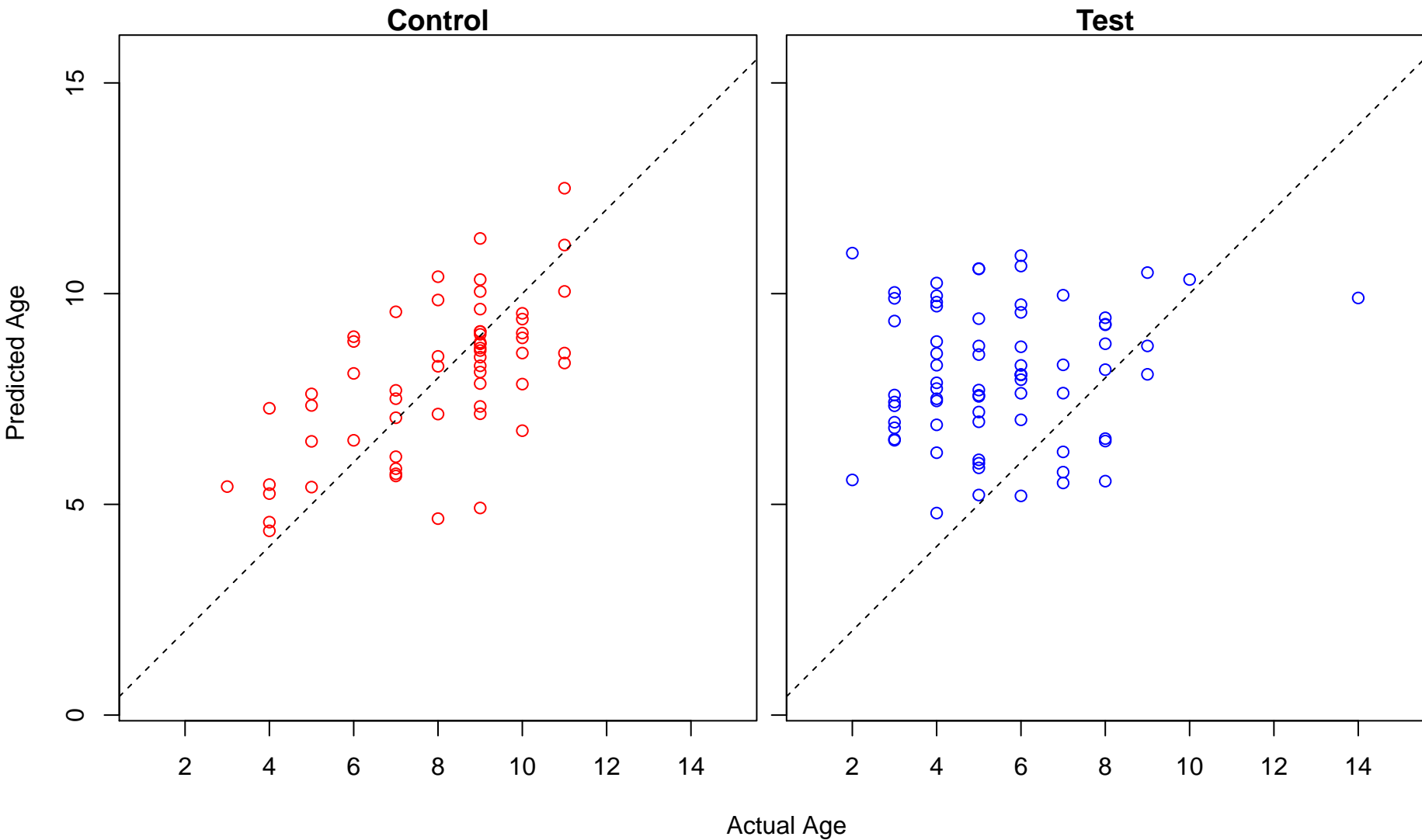
cell migration involved in sprouting angiogenesis (Score: 2.060228)



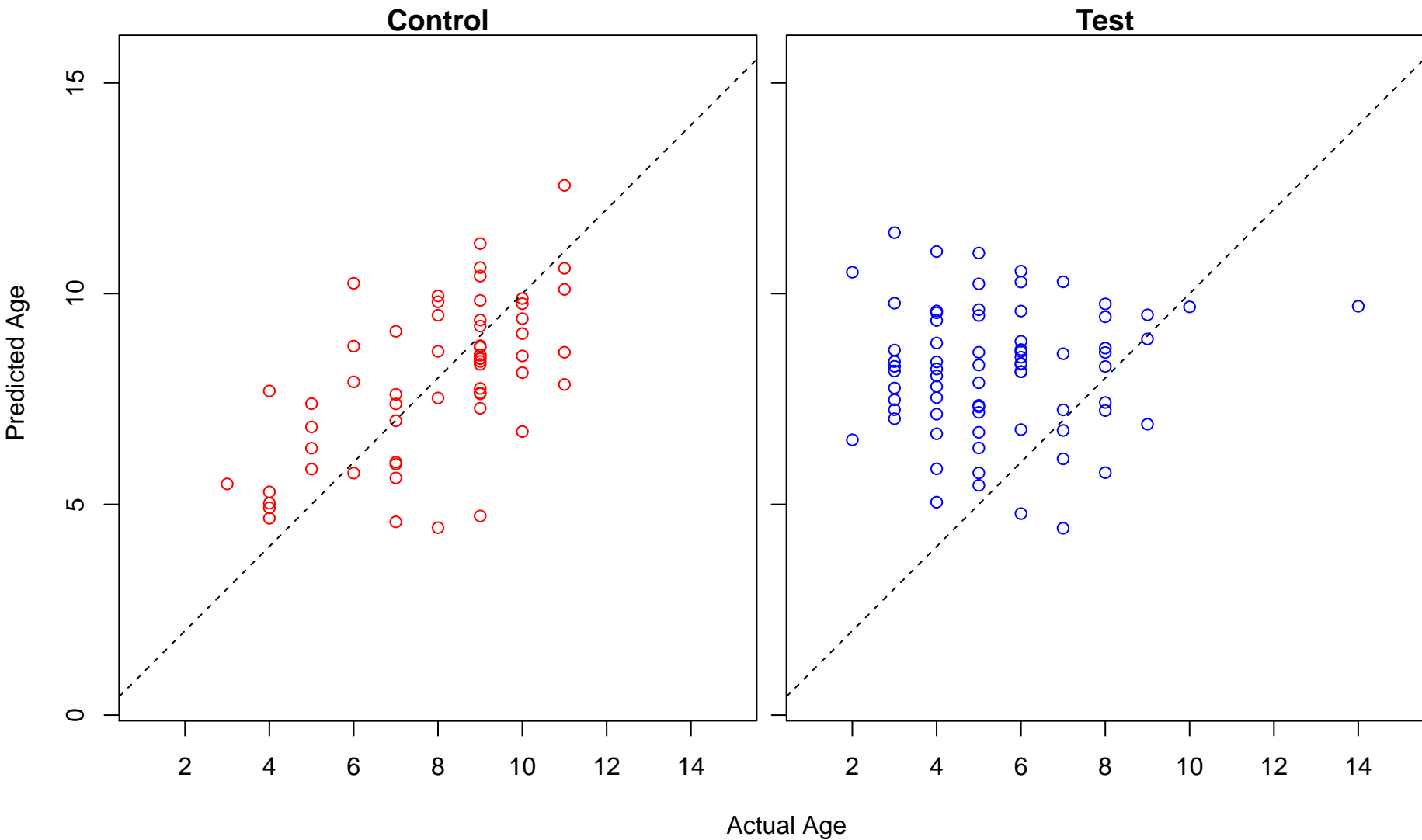
myeloid leukocyte activation (Score: 2.005137)



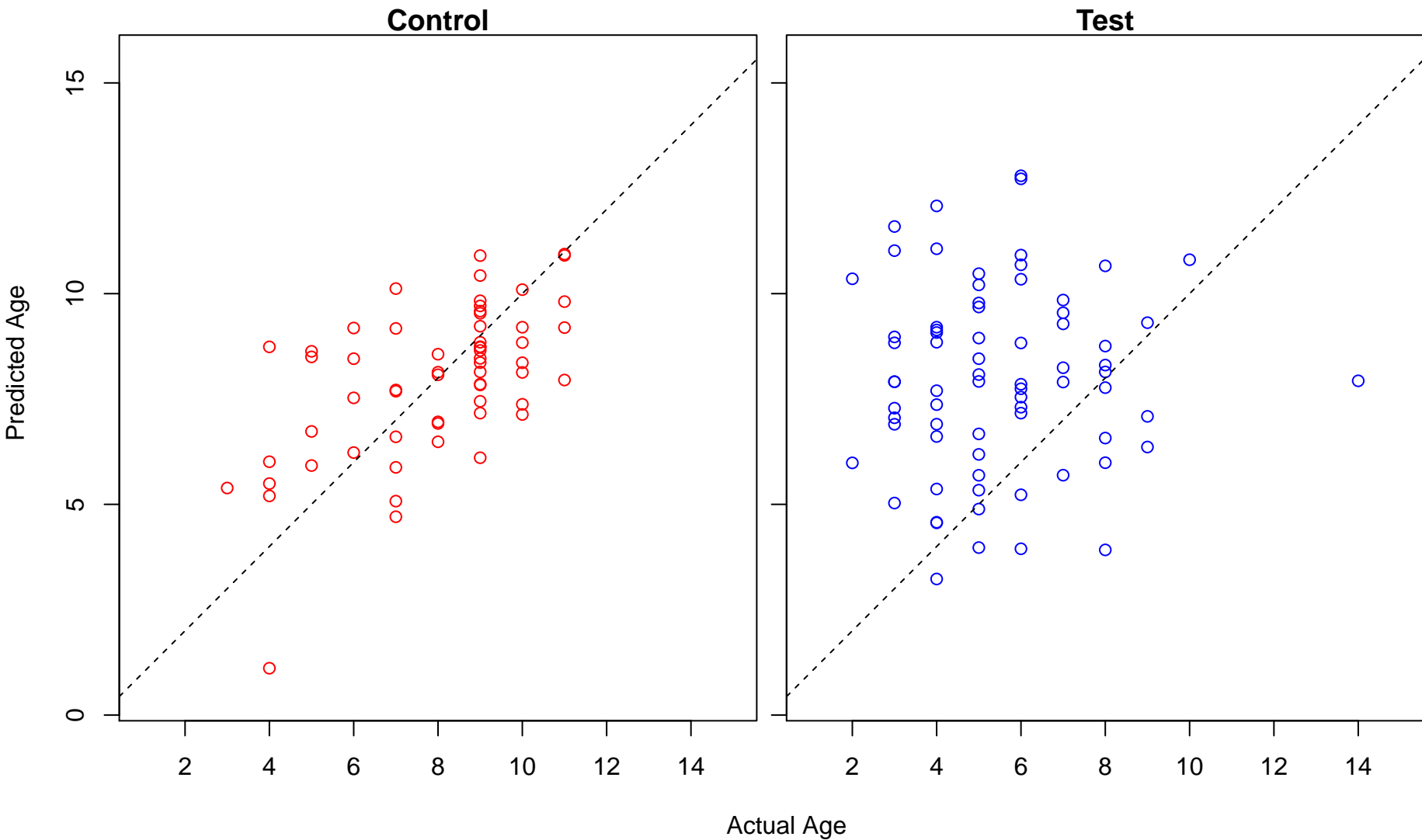
positive regulation of sequence-specific DNA binding transcription factor activity (Score: 1.927559)



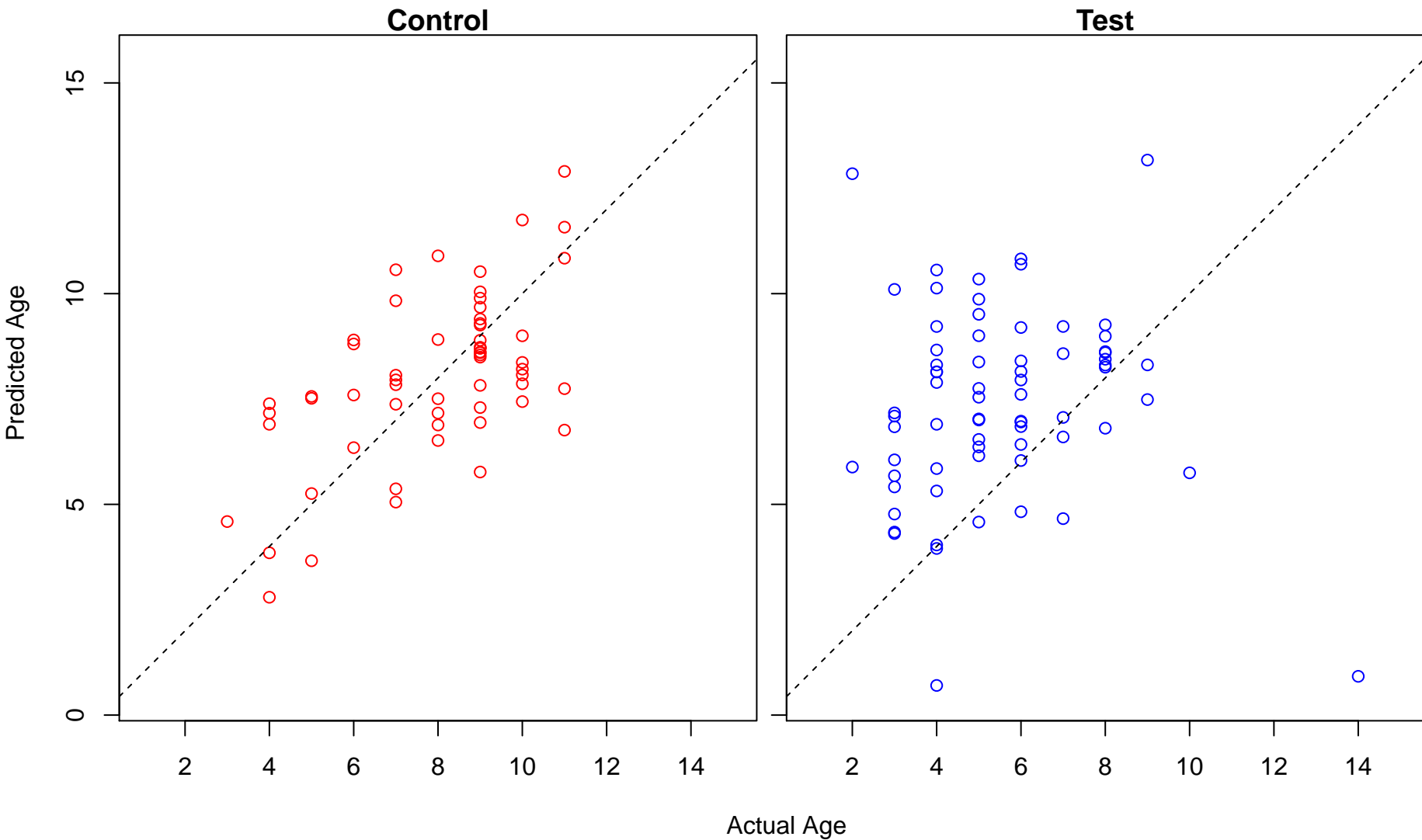
positive regulation of NF-kappaB transcription factor activity (Score: 1.893515)



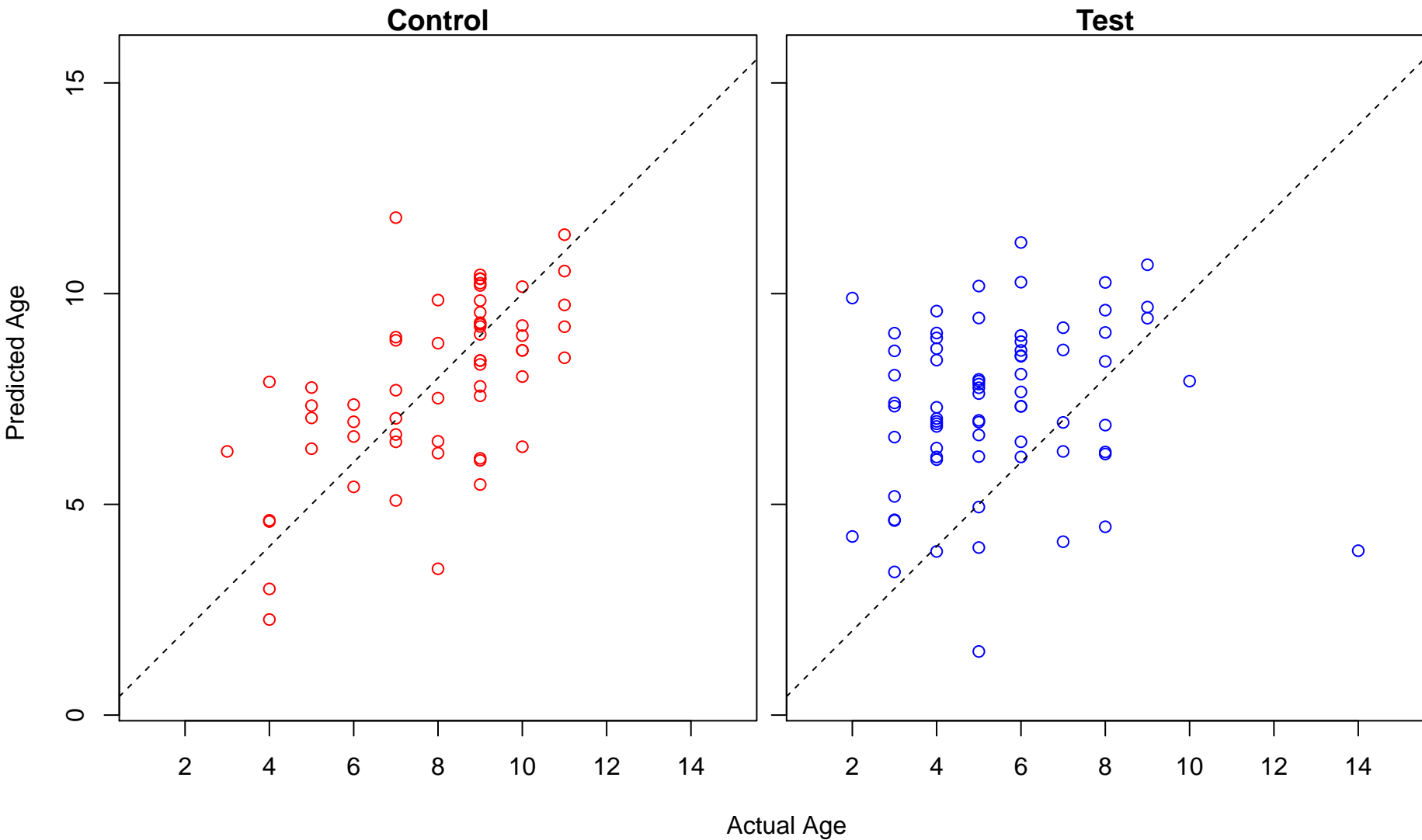
phospholipid metabolic process (Score: 1.869554)



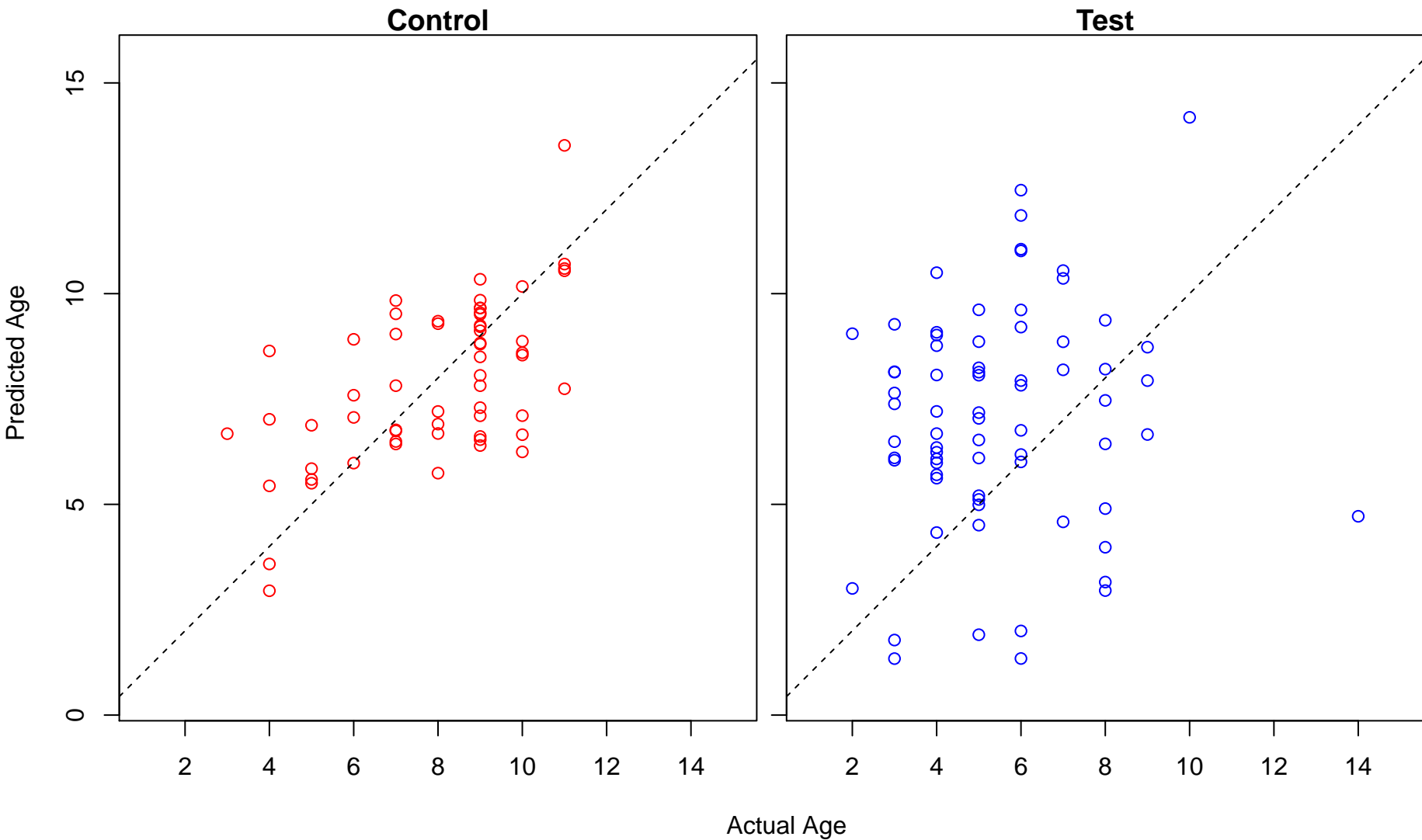
inflammatory response (Score: 1.865707)



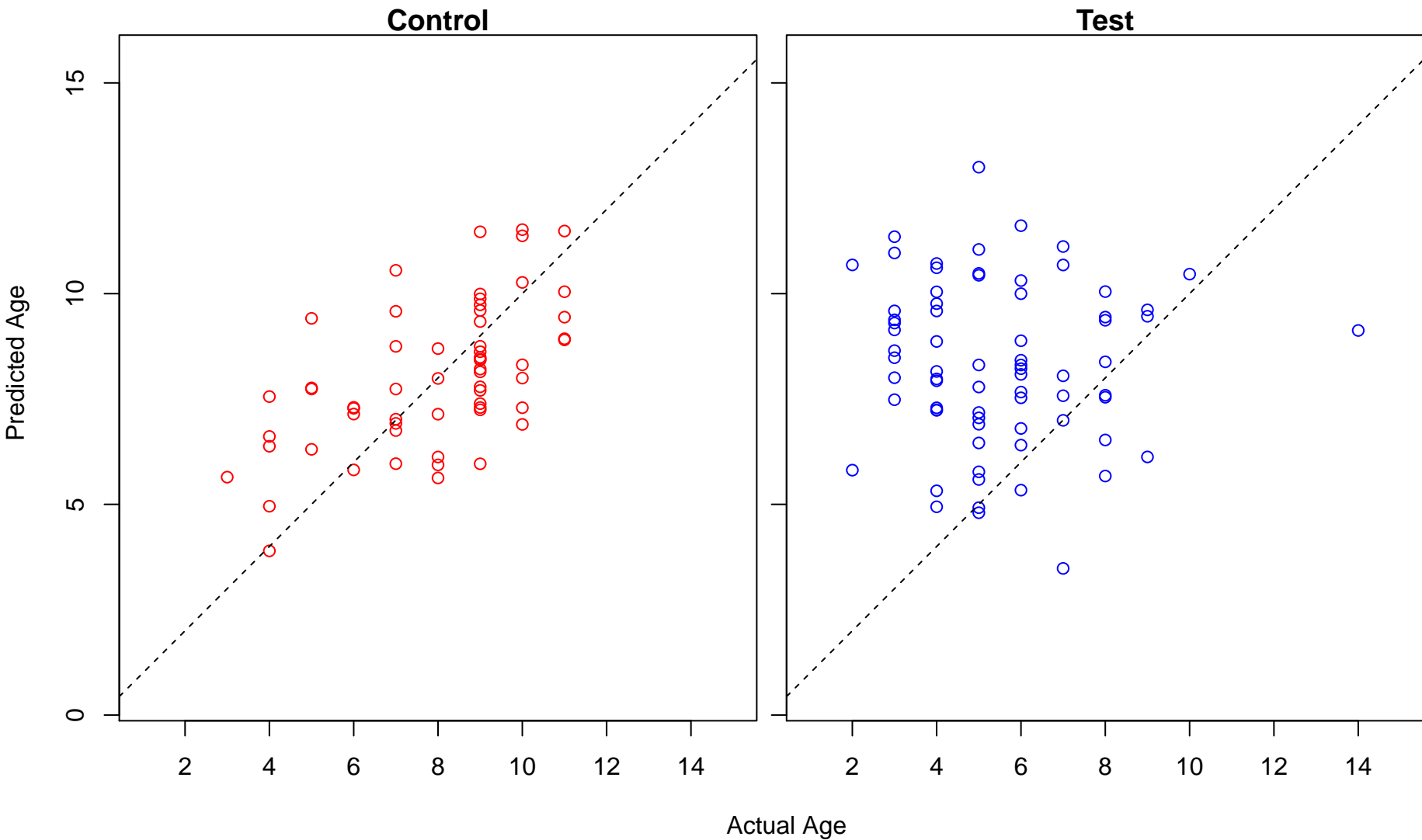
central nervous system neuron differentiation (Score: 1.861142)



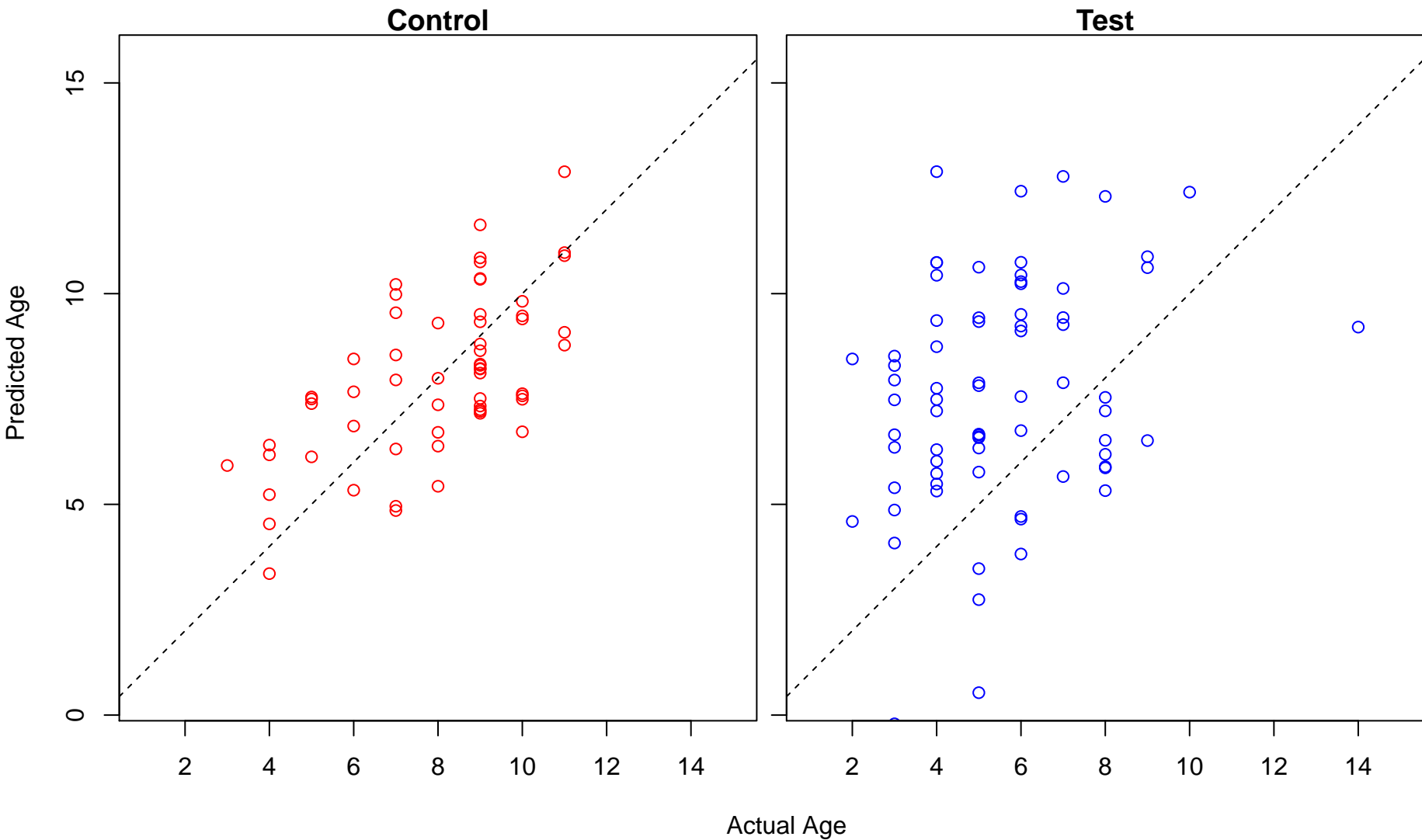
positive regulation of endothelial cell proliferation (Score: 1.855695)



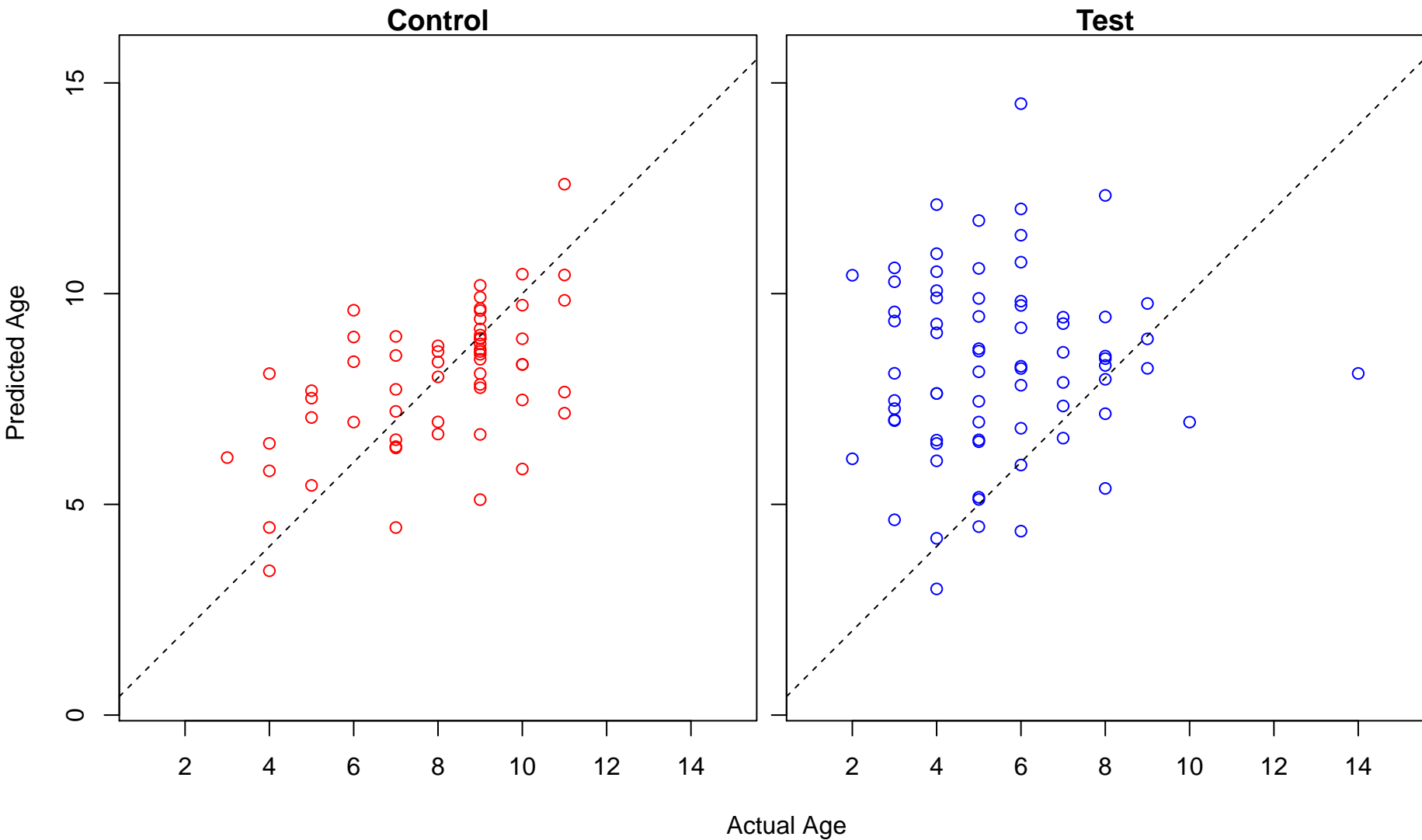
regulation of cell growth (Score: 1.824891)



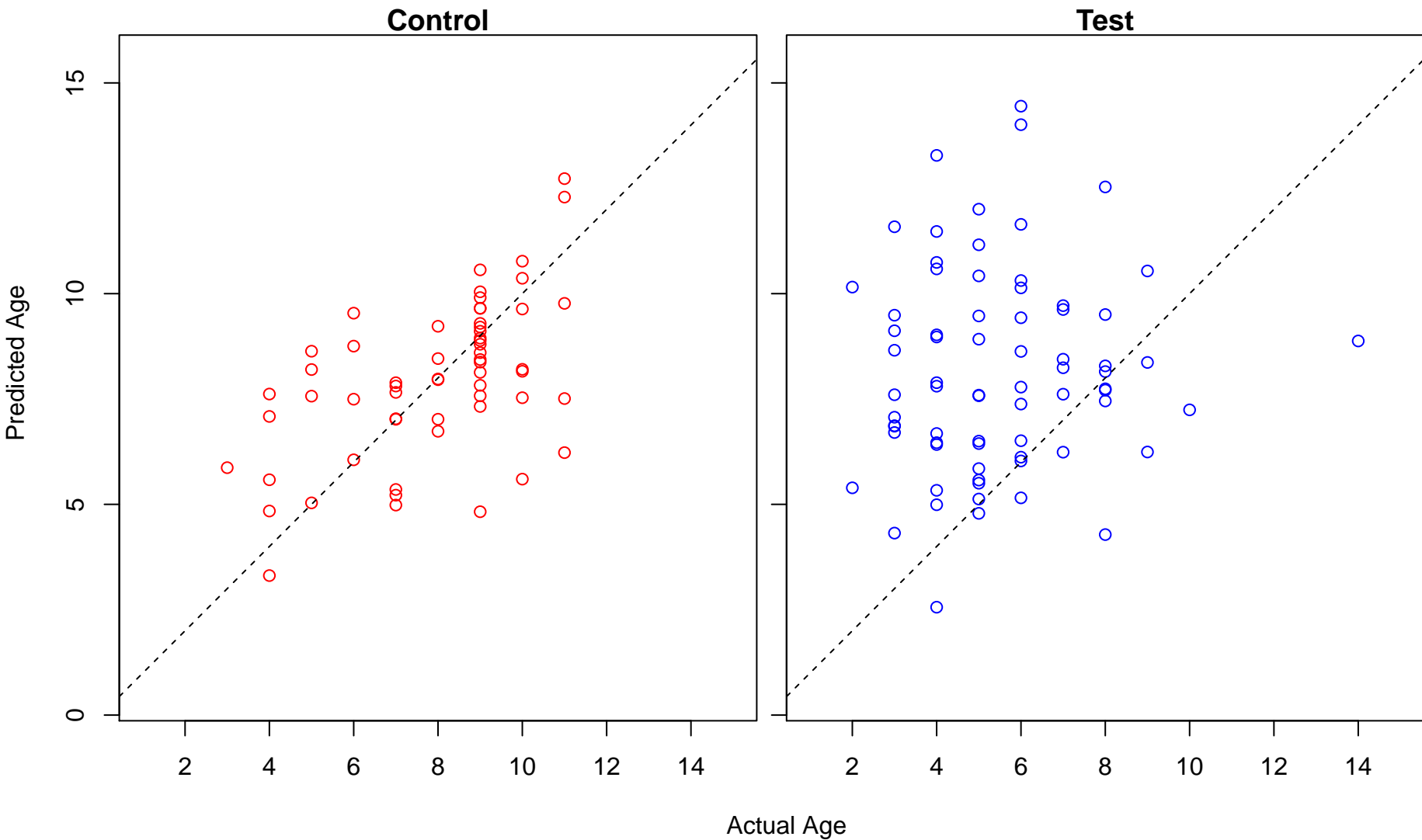
formation of primary germ layer (Score: 1.824752)



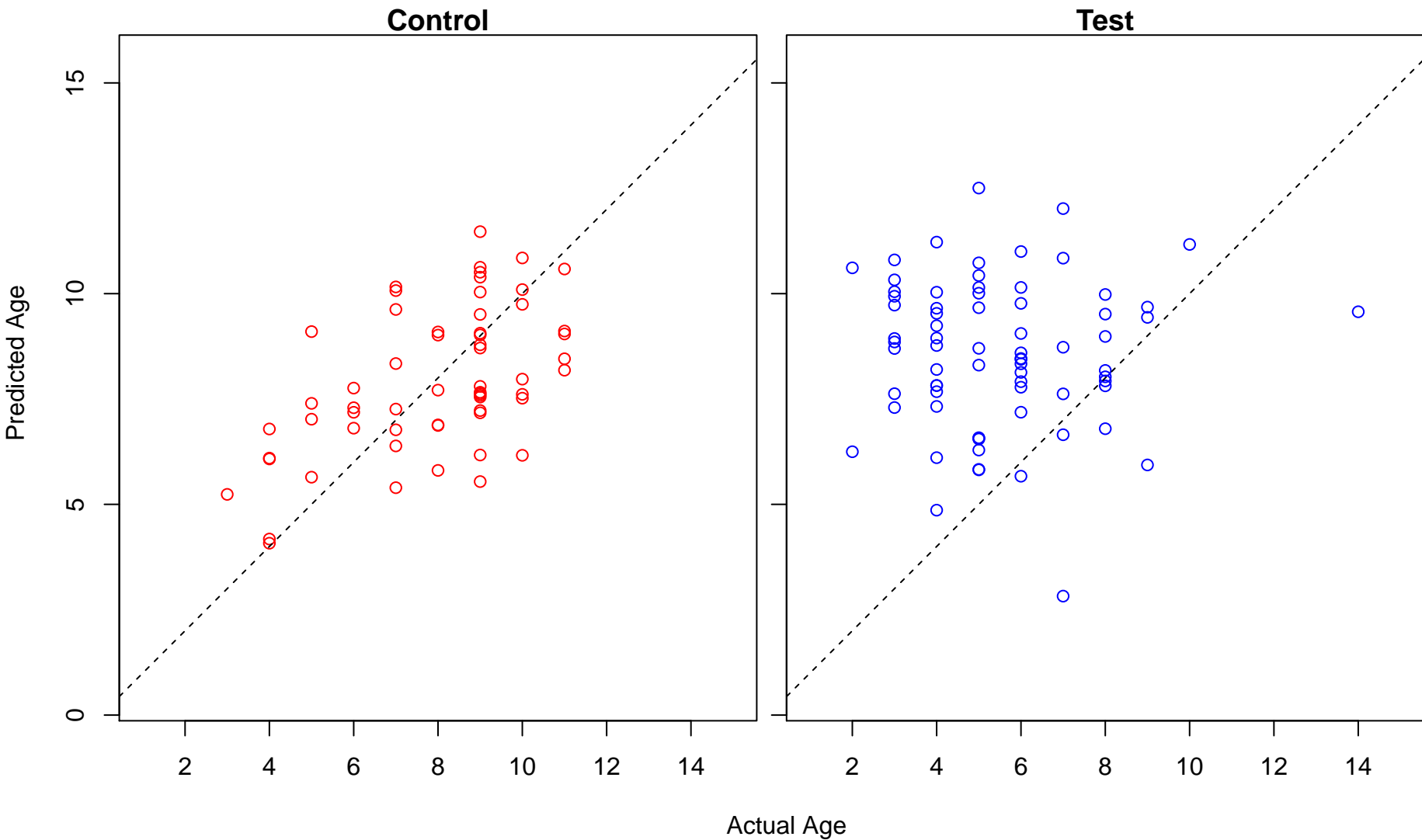
phosphatidylinositol biosynthetic process (Score: 1.821473)



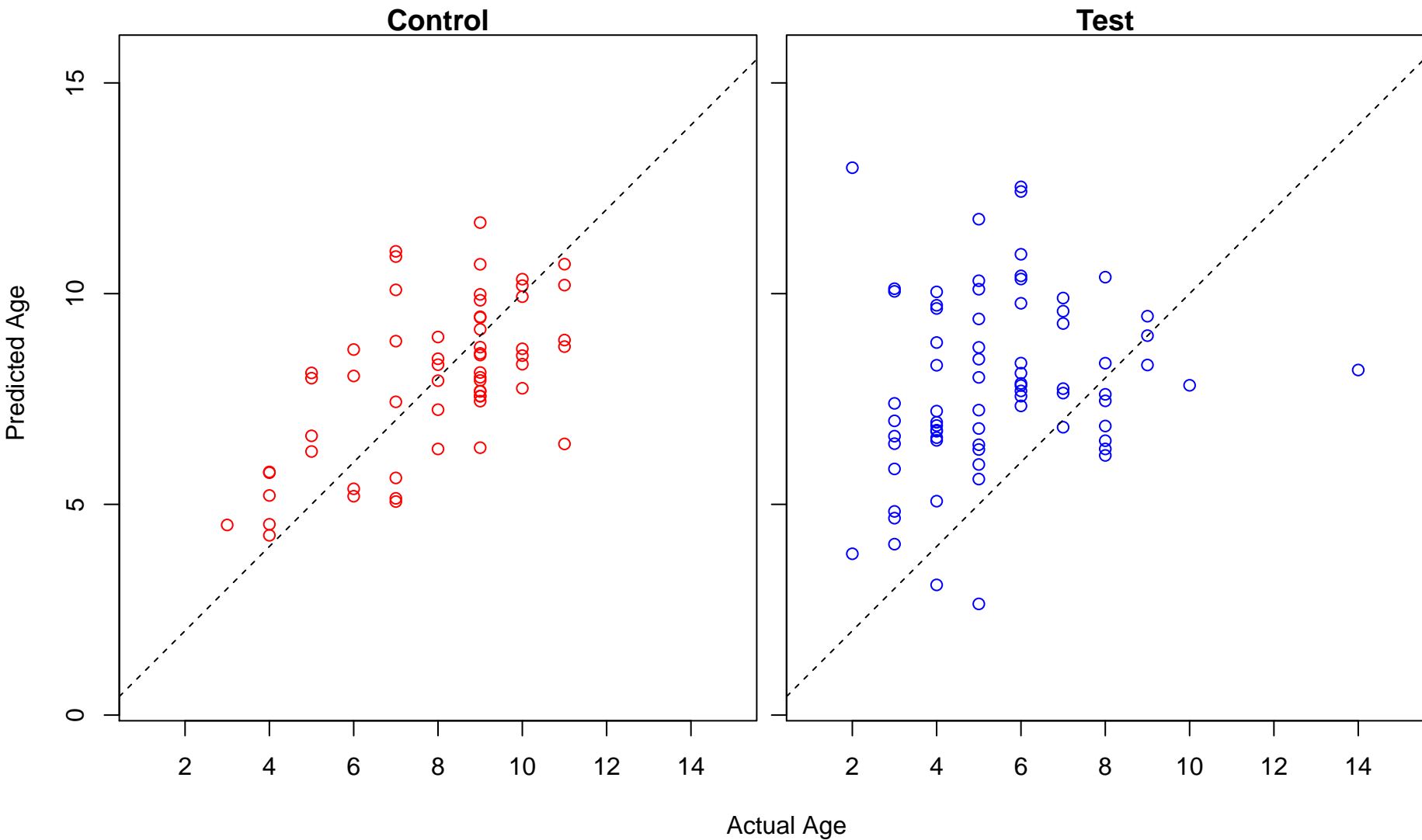
phosphatidylinositol metabolic process (Score: 1.800866)



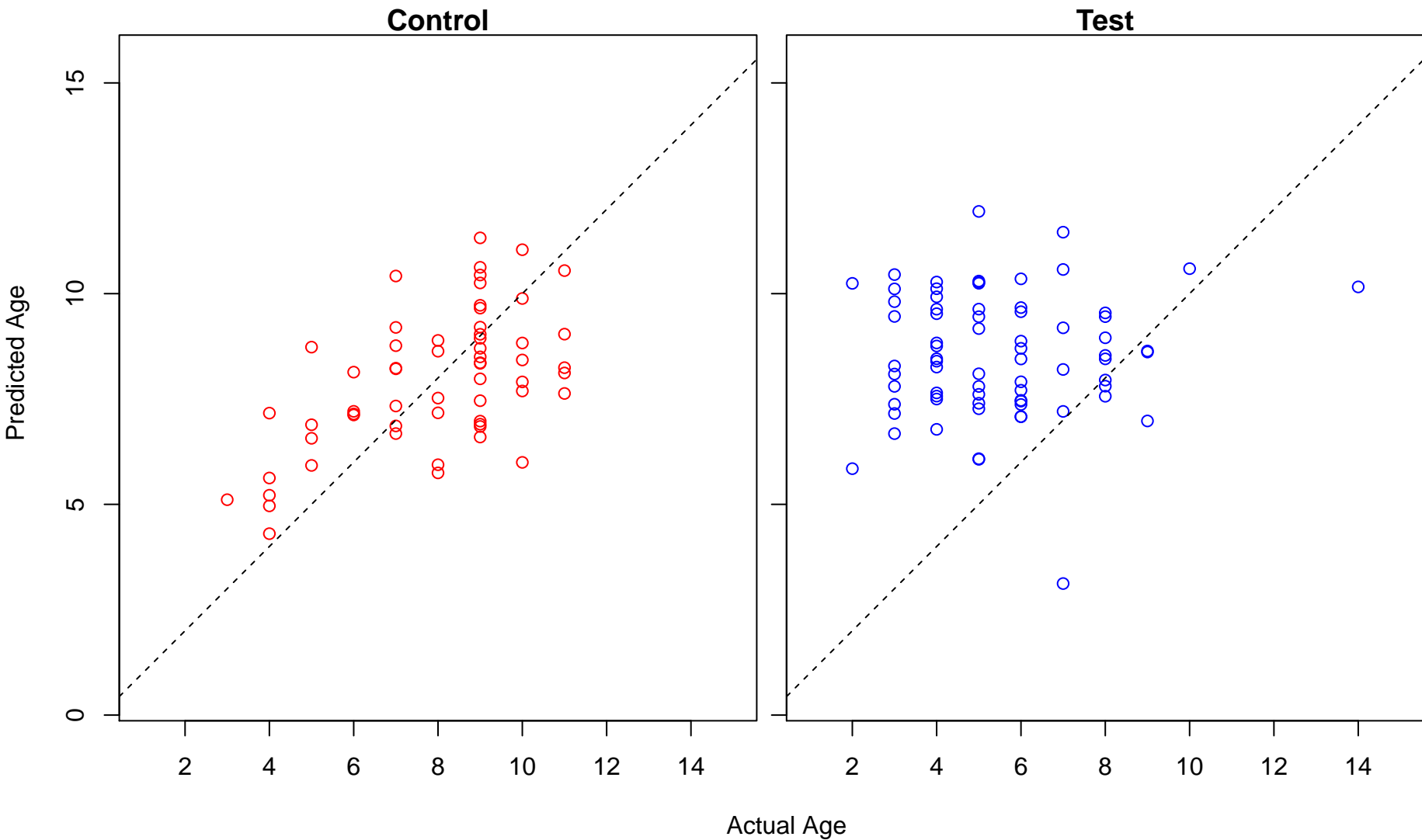
regulation of growth (Score: 1.774014)



myeloid dendritic cell activation (Score: 1.773905)

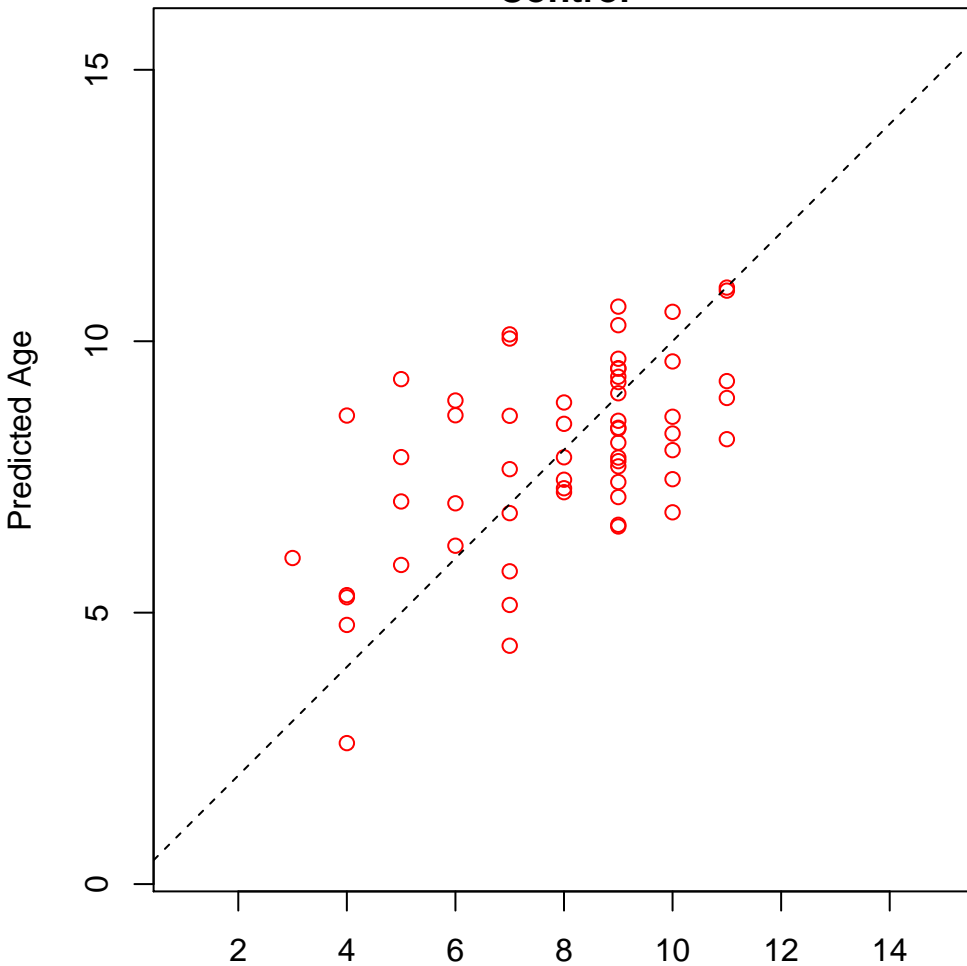


positive regulation of growth (Score: 1.763528)

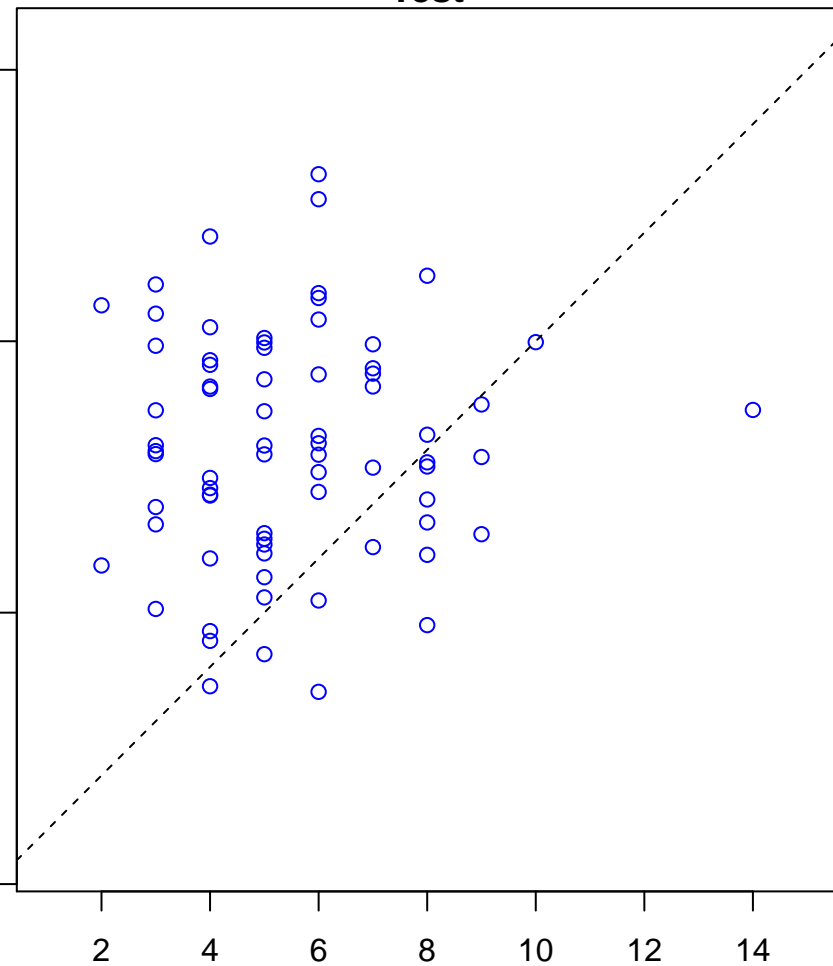


glycerophospholipid metabolic process (Score: 1.738131)

Control

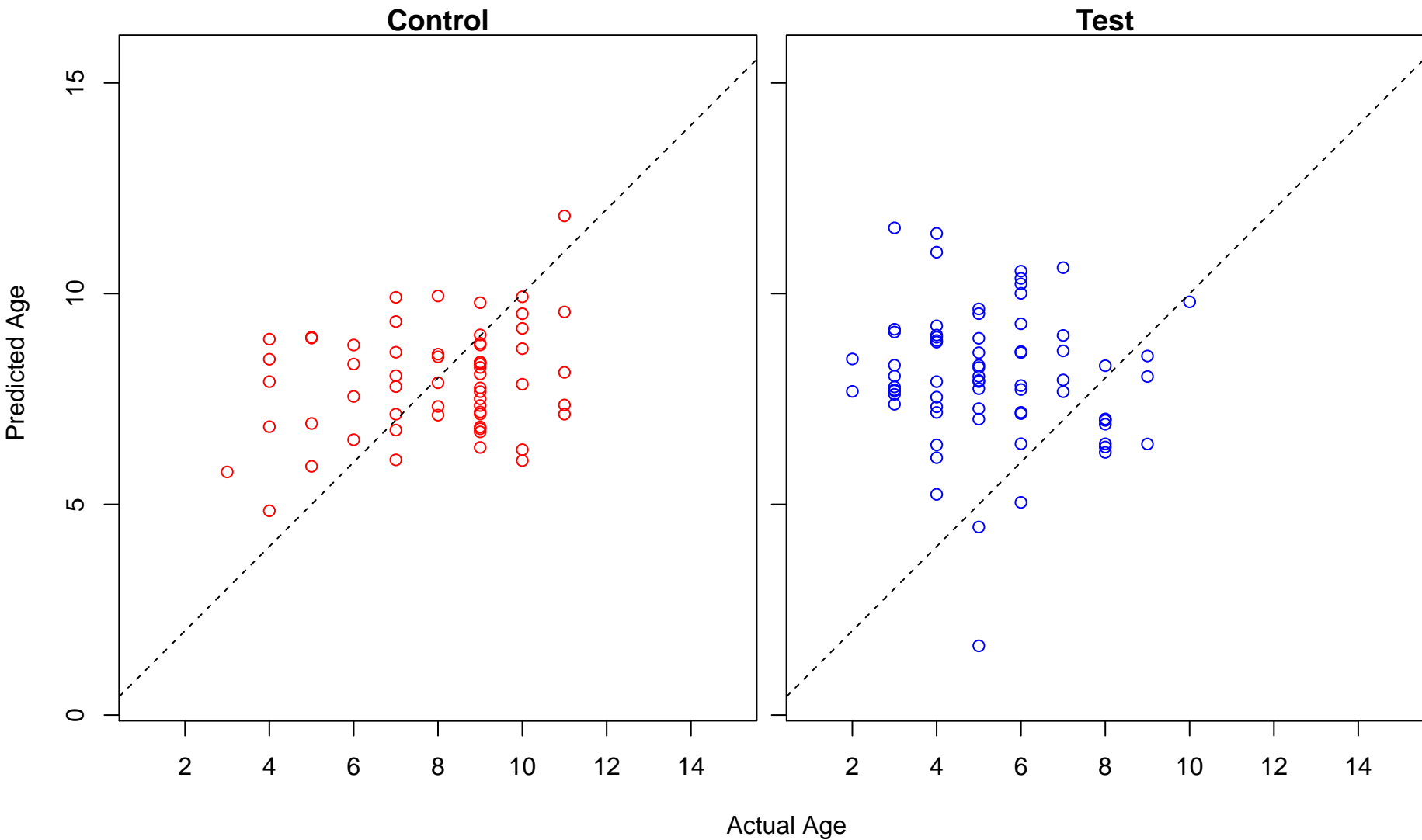


Test

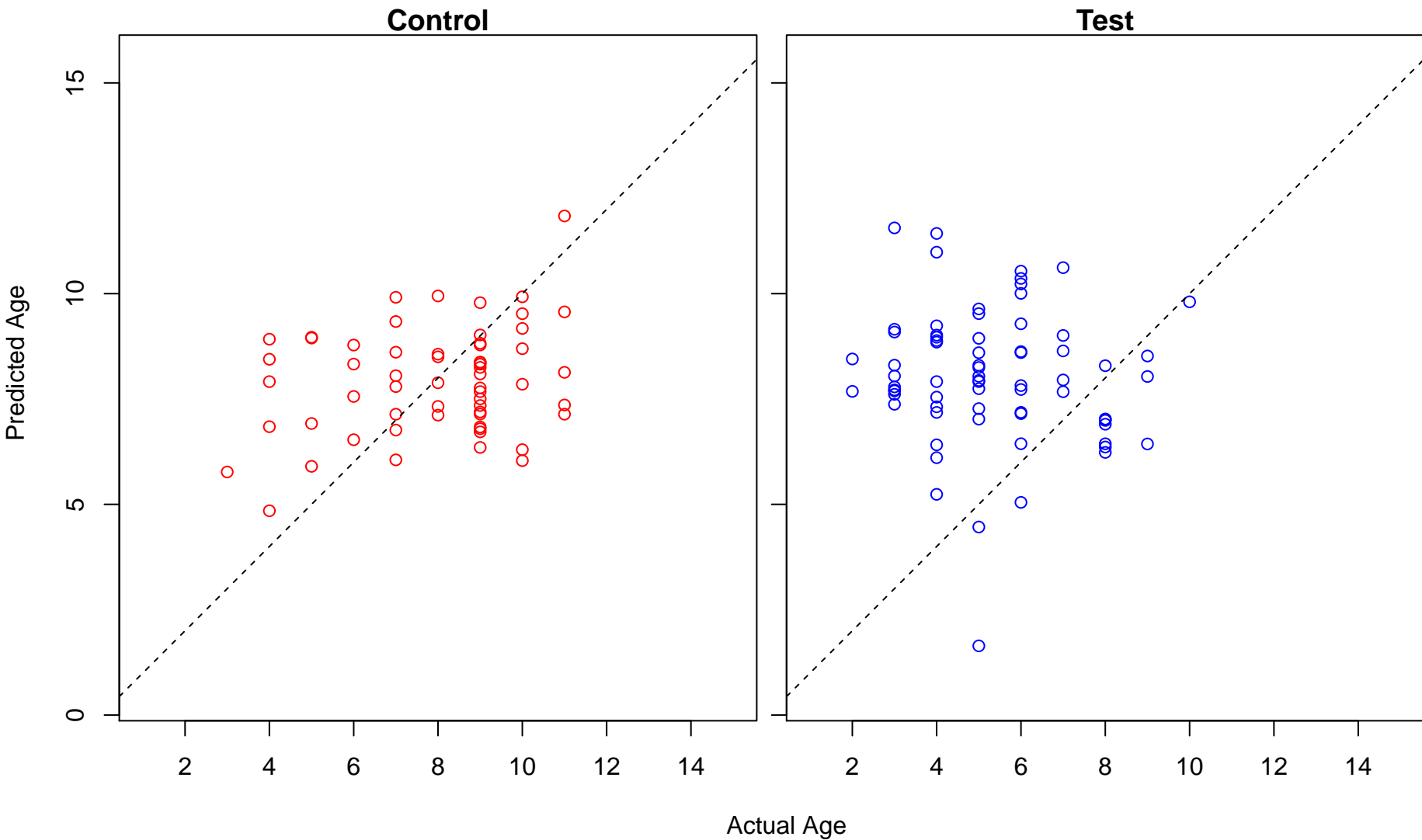


Actual Age

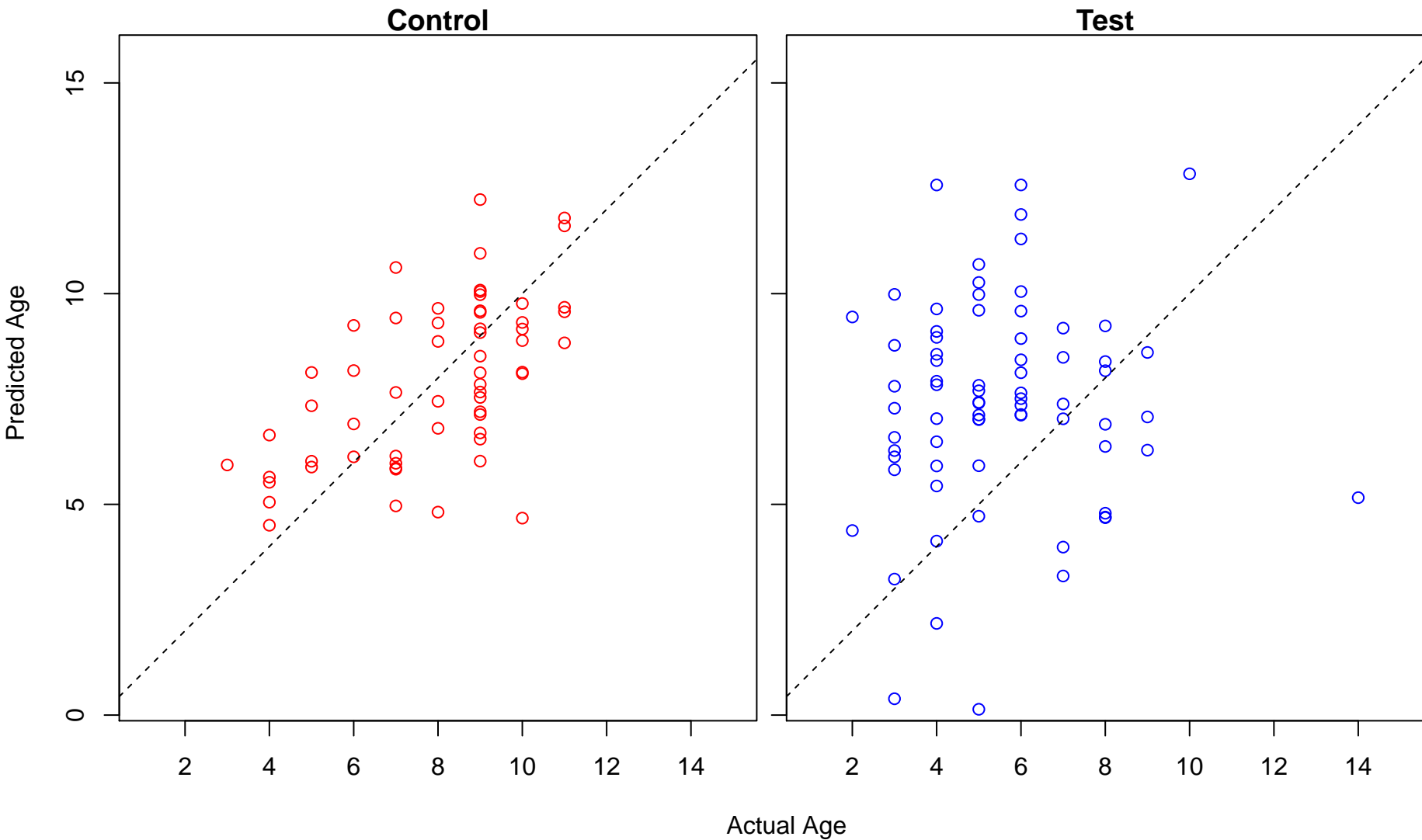
facial nerve development (Score: 1.720436)



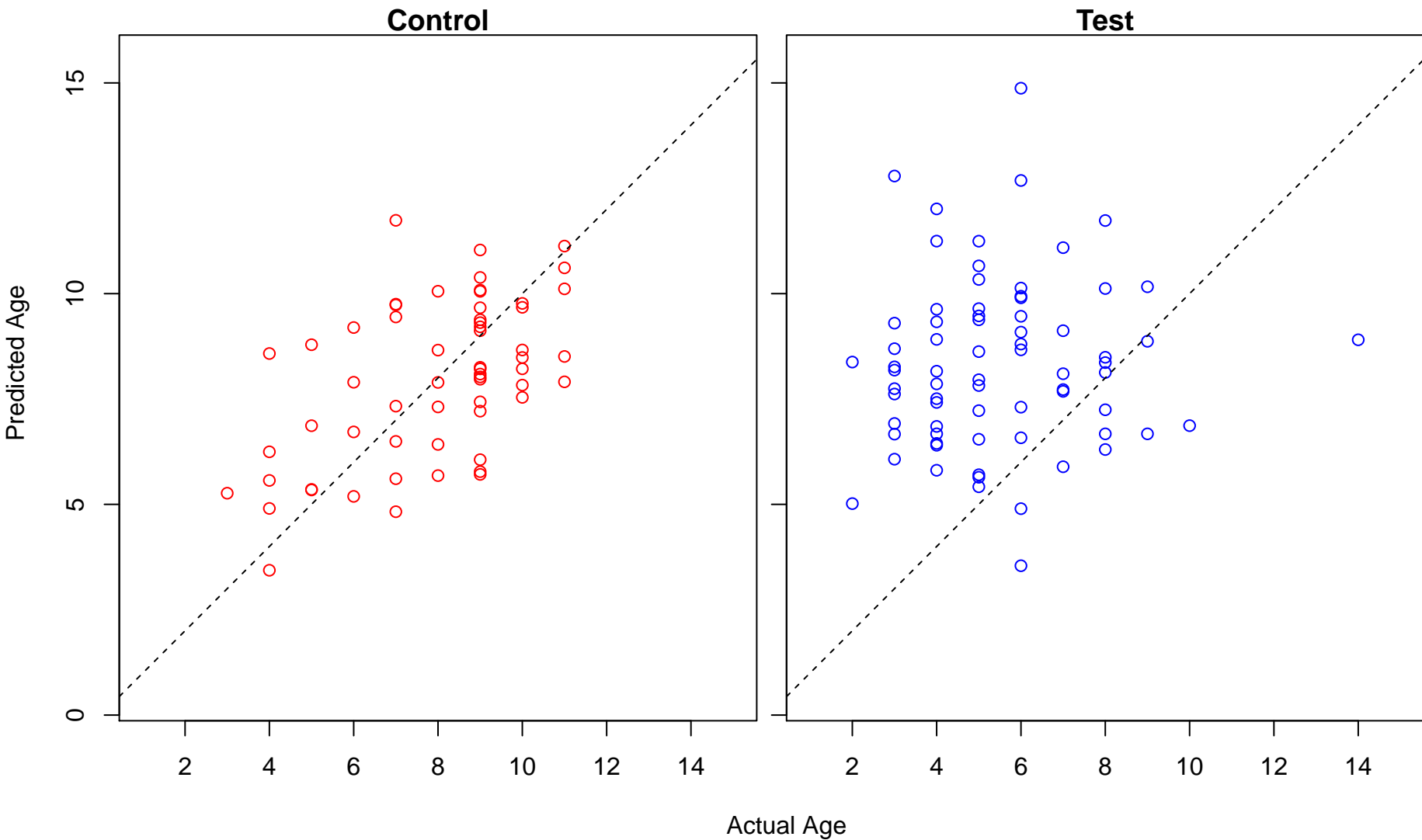
facial nerve morphogenesis (Score: 1.720436)



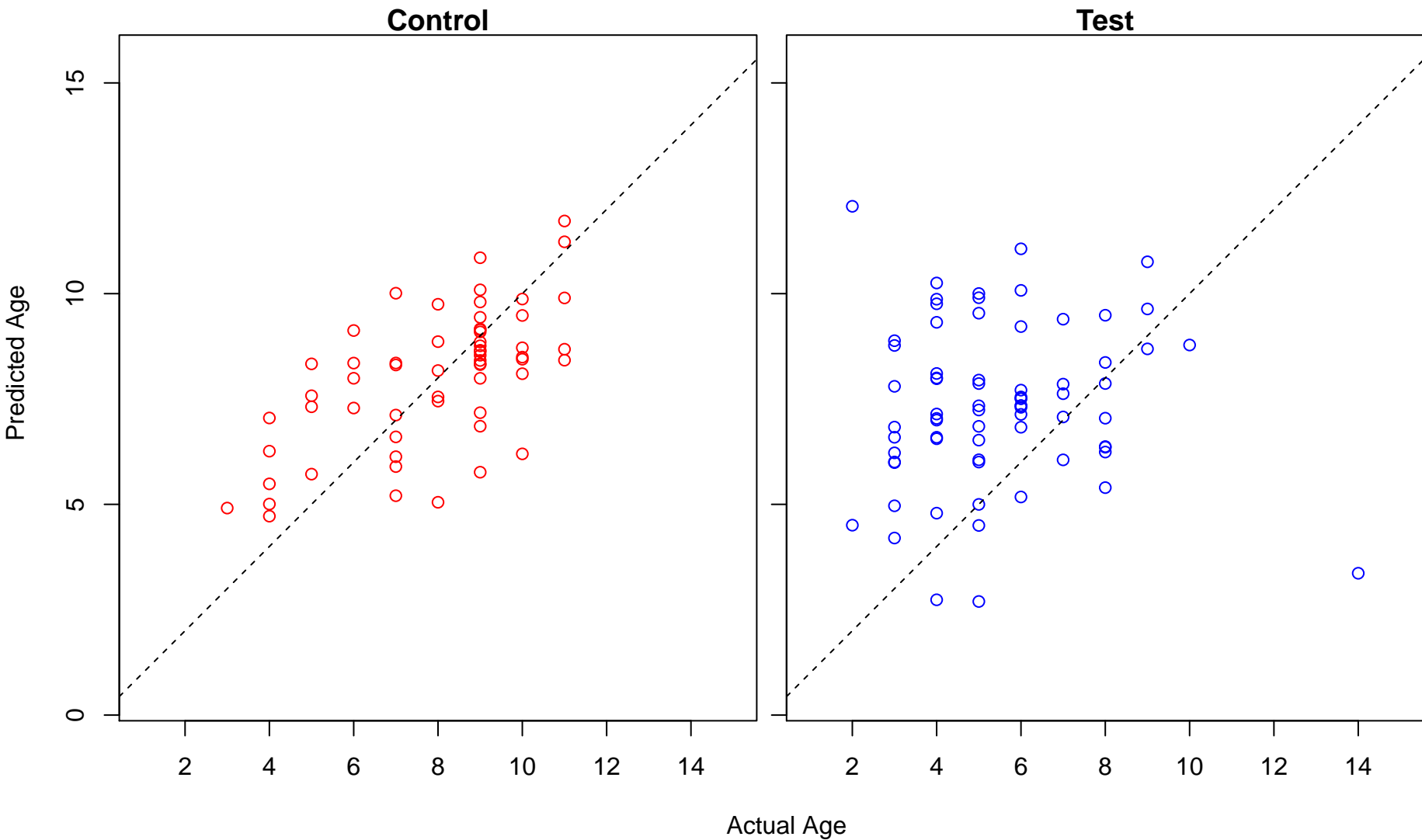
nuclear division (Score: 1.719429)



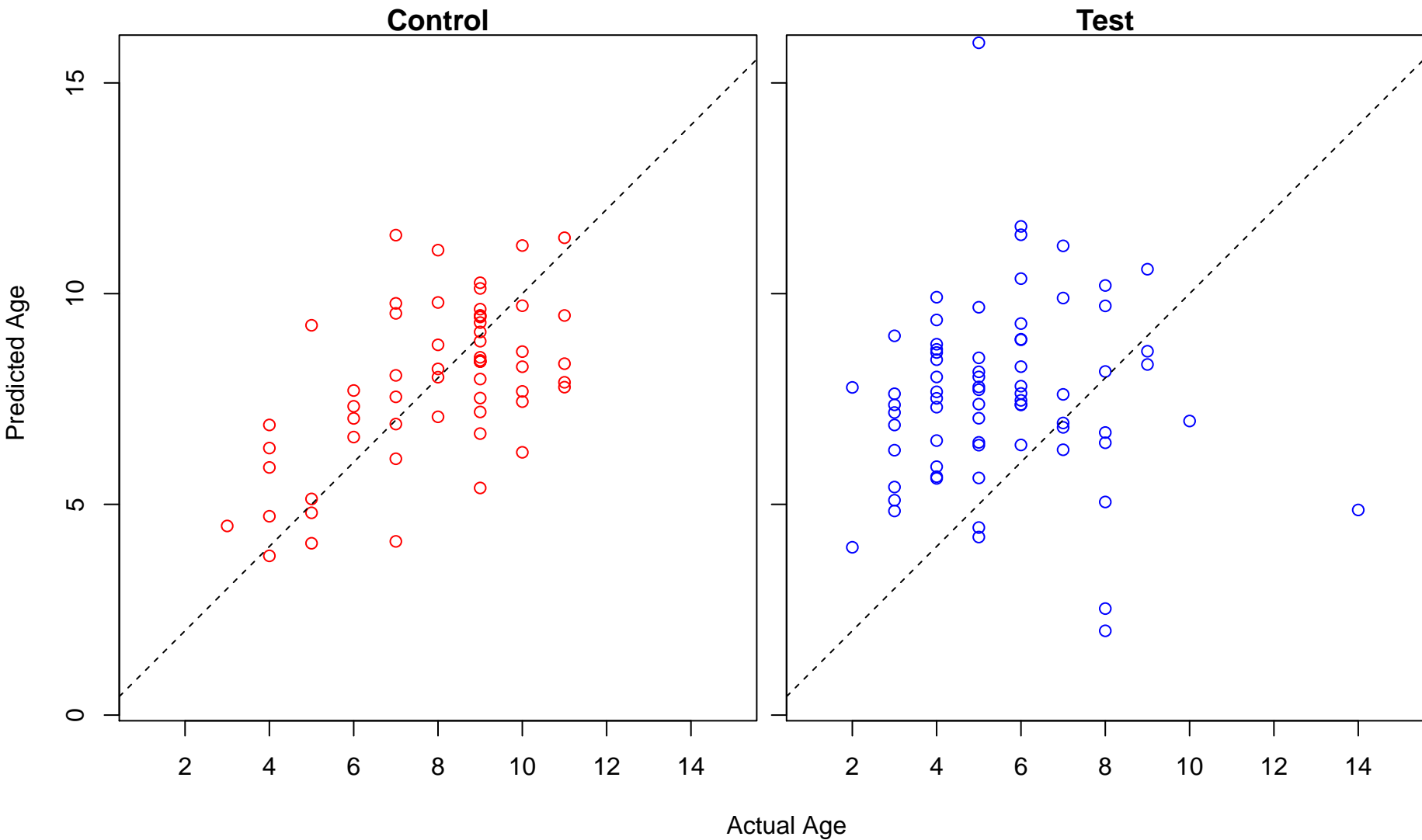
alcohol metabolic process (Score: 1.716233)



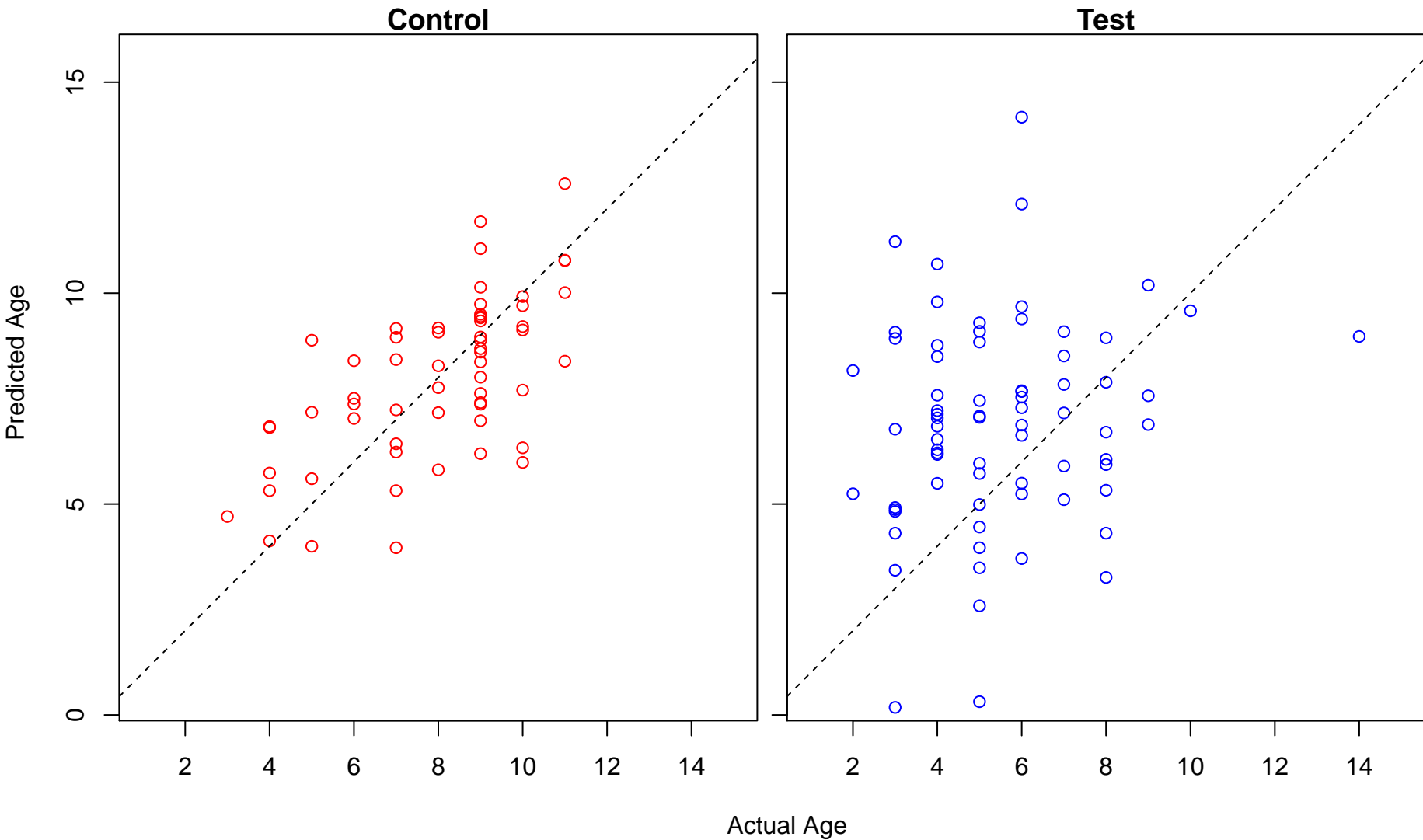
regulation of sequence-specific DNA binding transcription factor activity (Score: 1.715603)



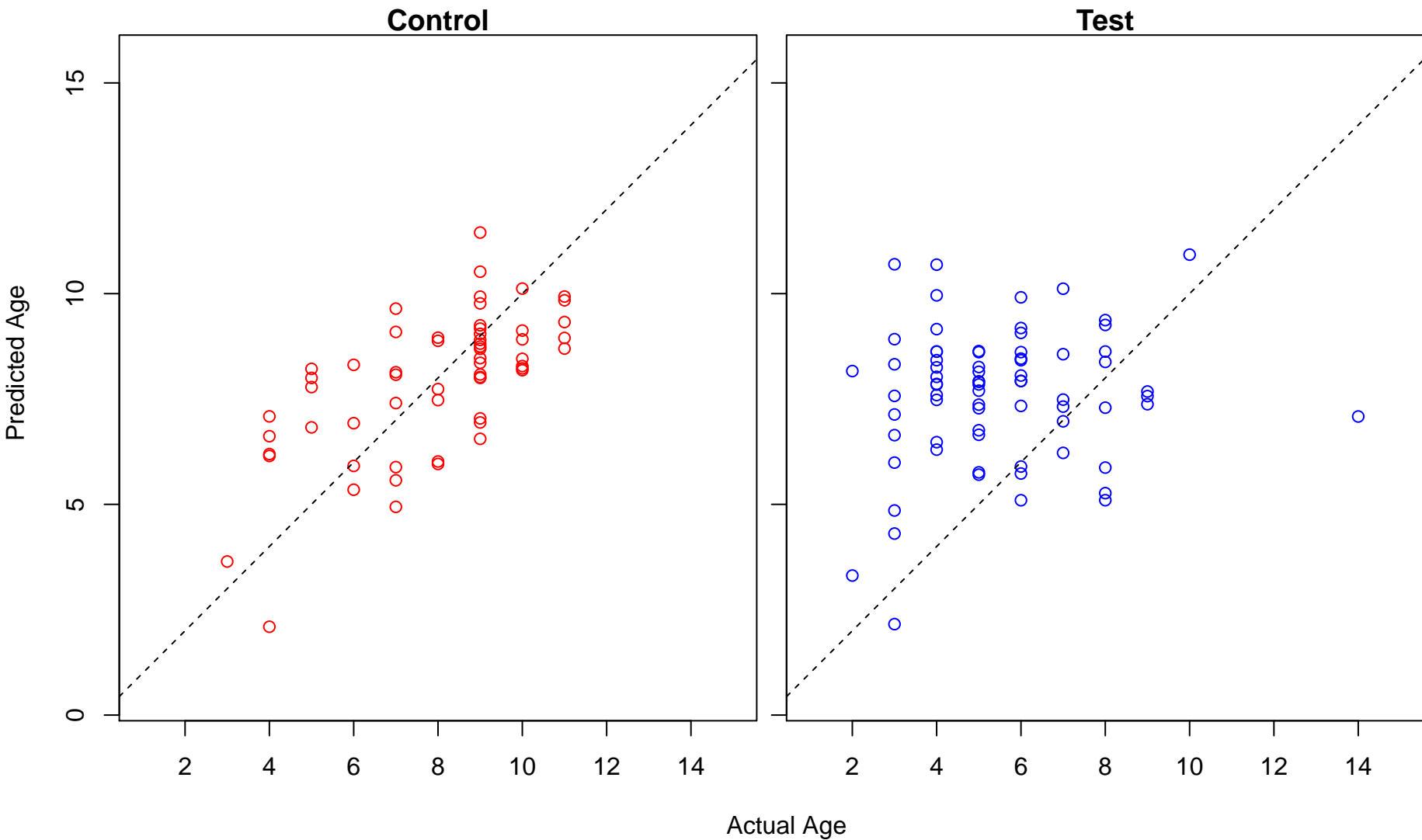
membrane fusion (Score: 1.713754)



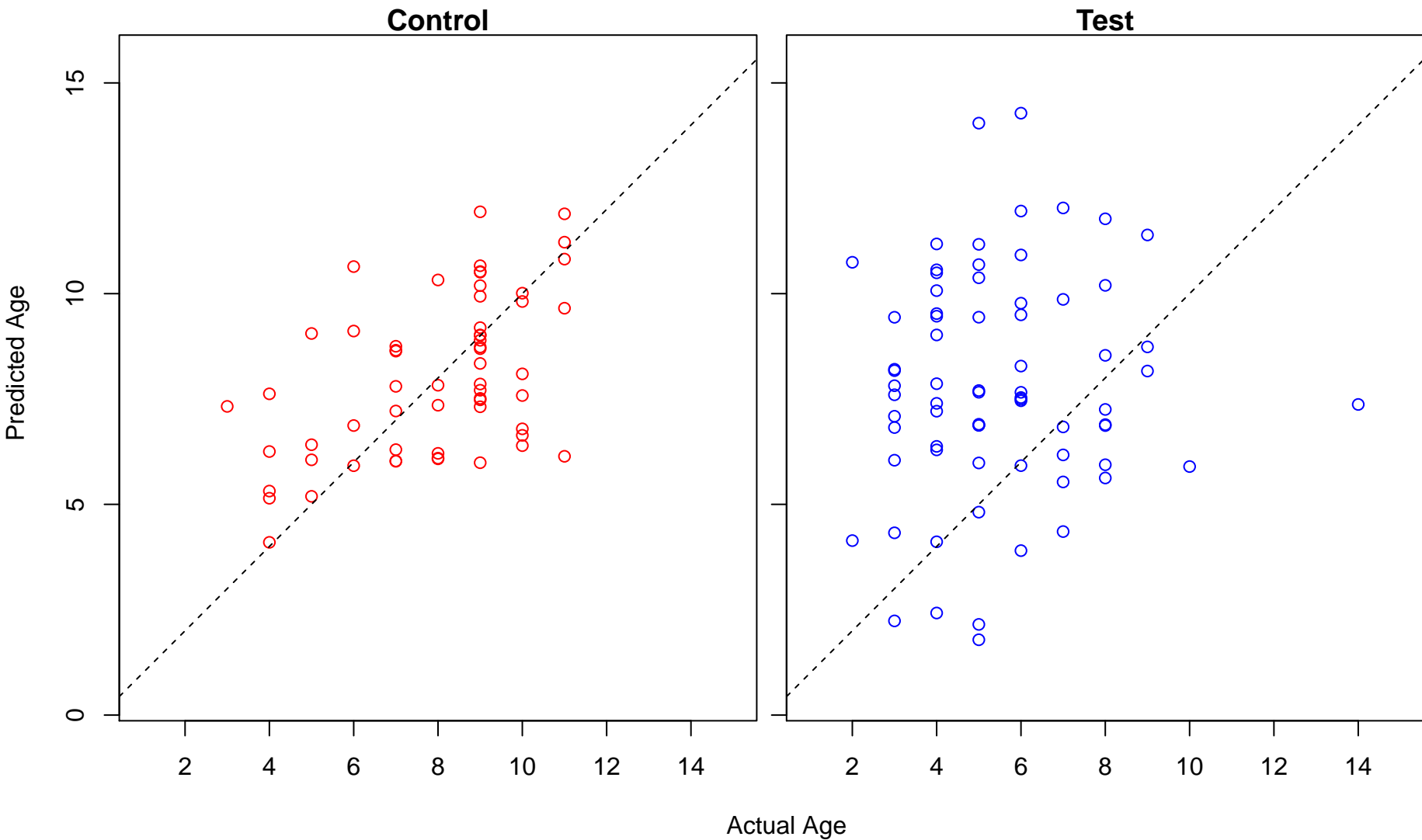
morphogenesis of an epithelial bud (Score: 1.702822)



middle ear morphogenesis (Score: 1.694770)

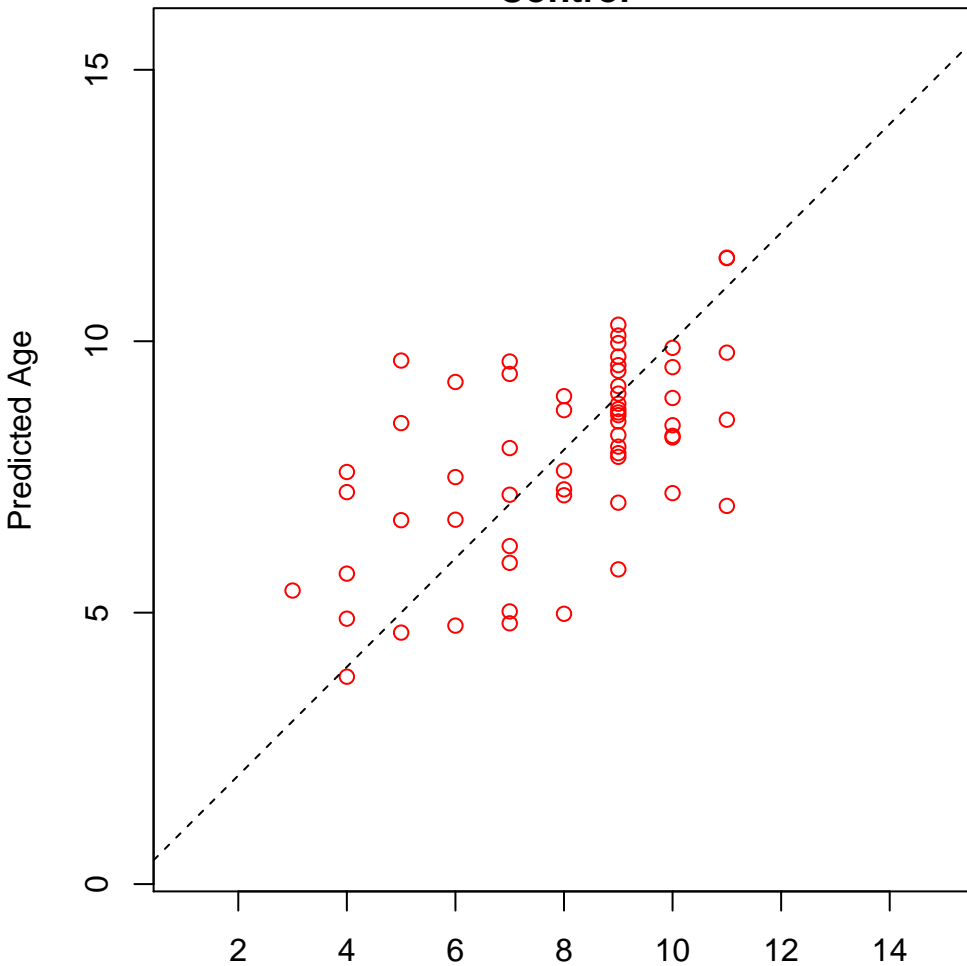


actomyosin structure organization (Score: 1.691341)

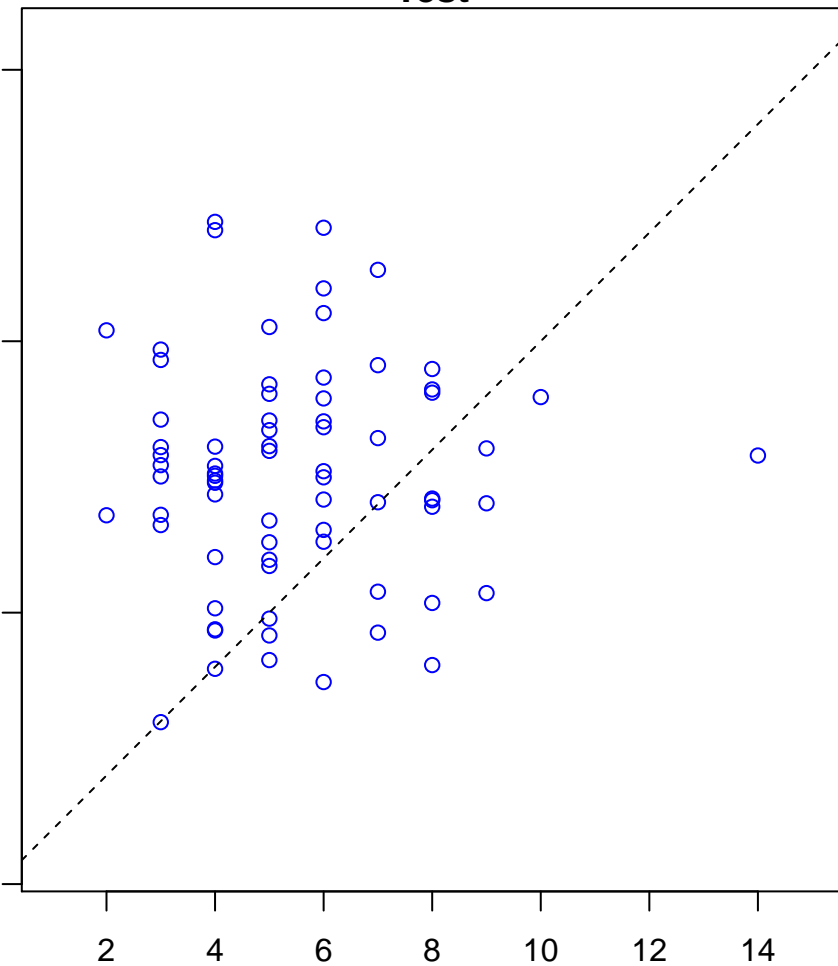


organophosphate biosynthetic process (Score: 1.672397)

Control

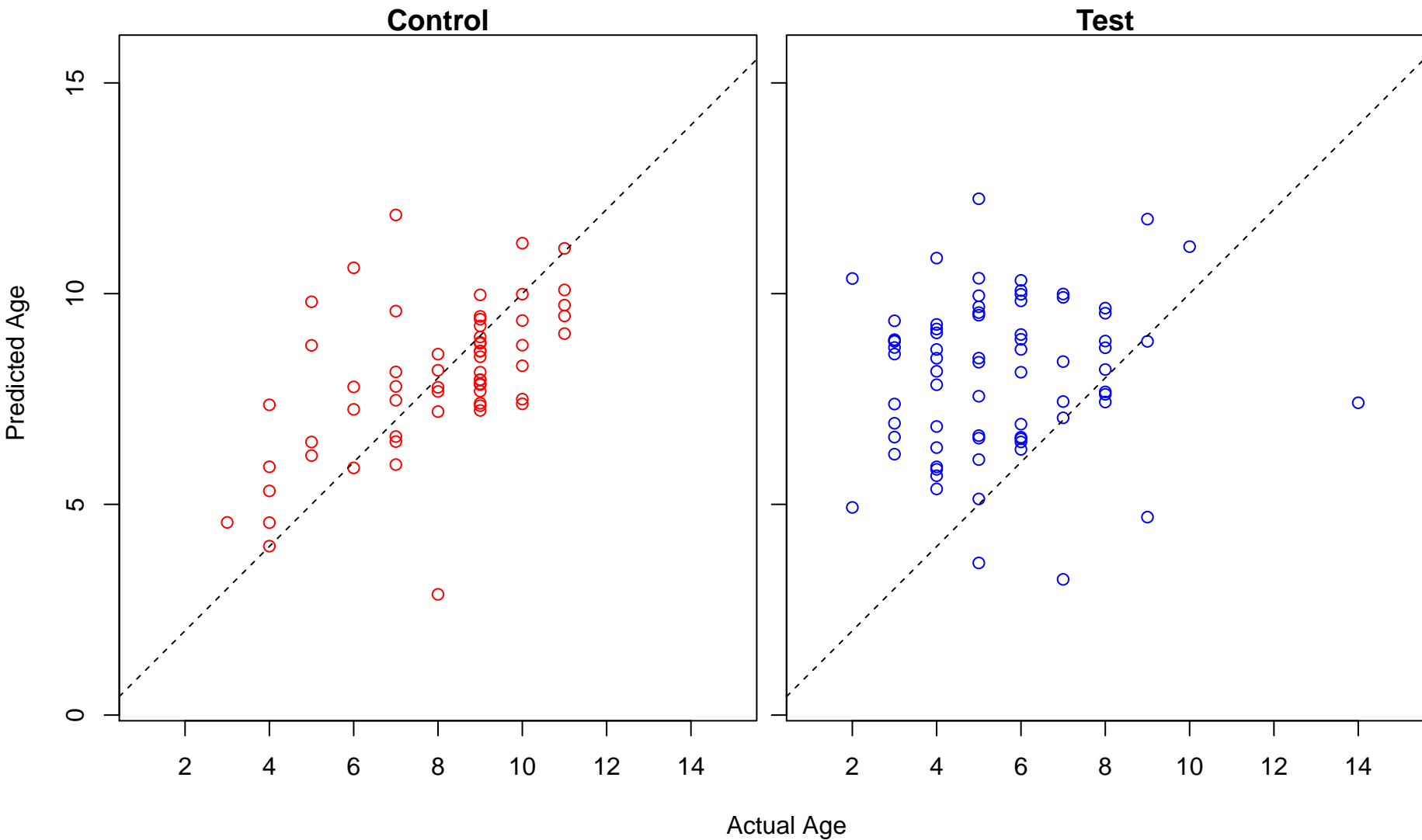


Test

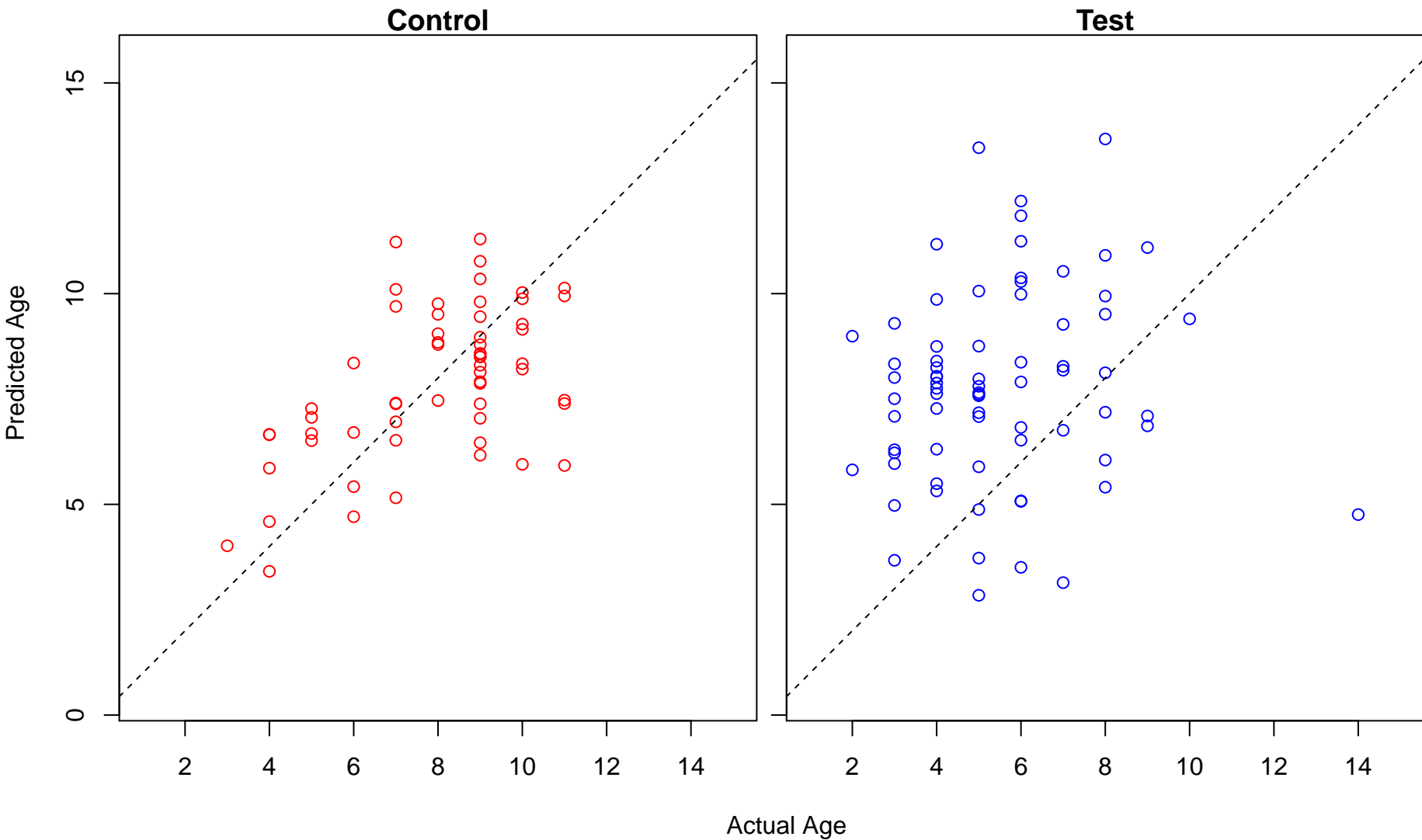


Actual Age

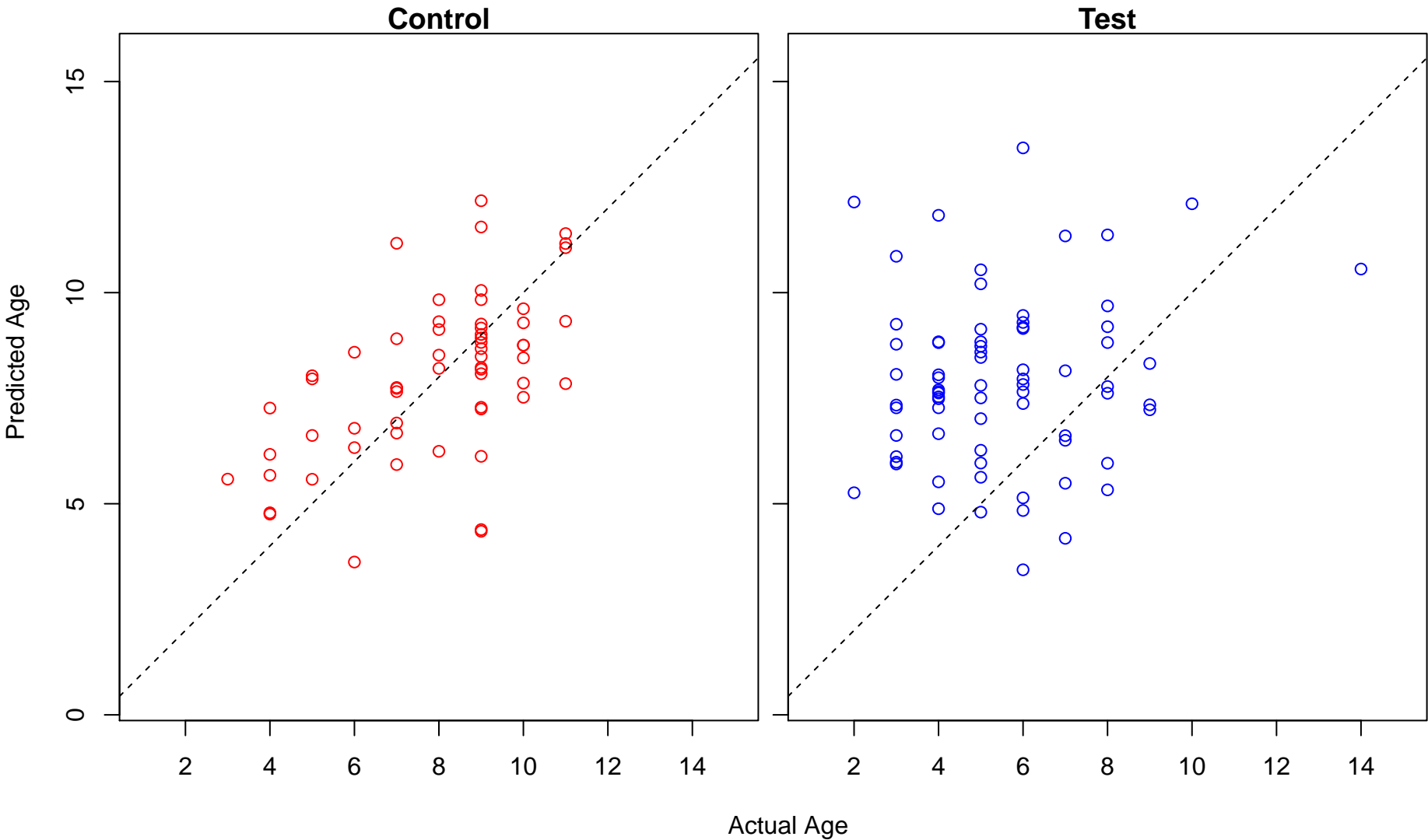
transition metal ion homeostasis (Score: 1.671200)



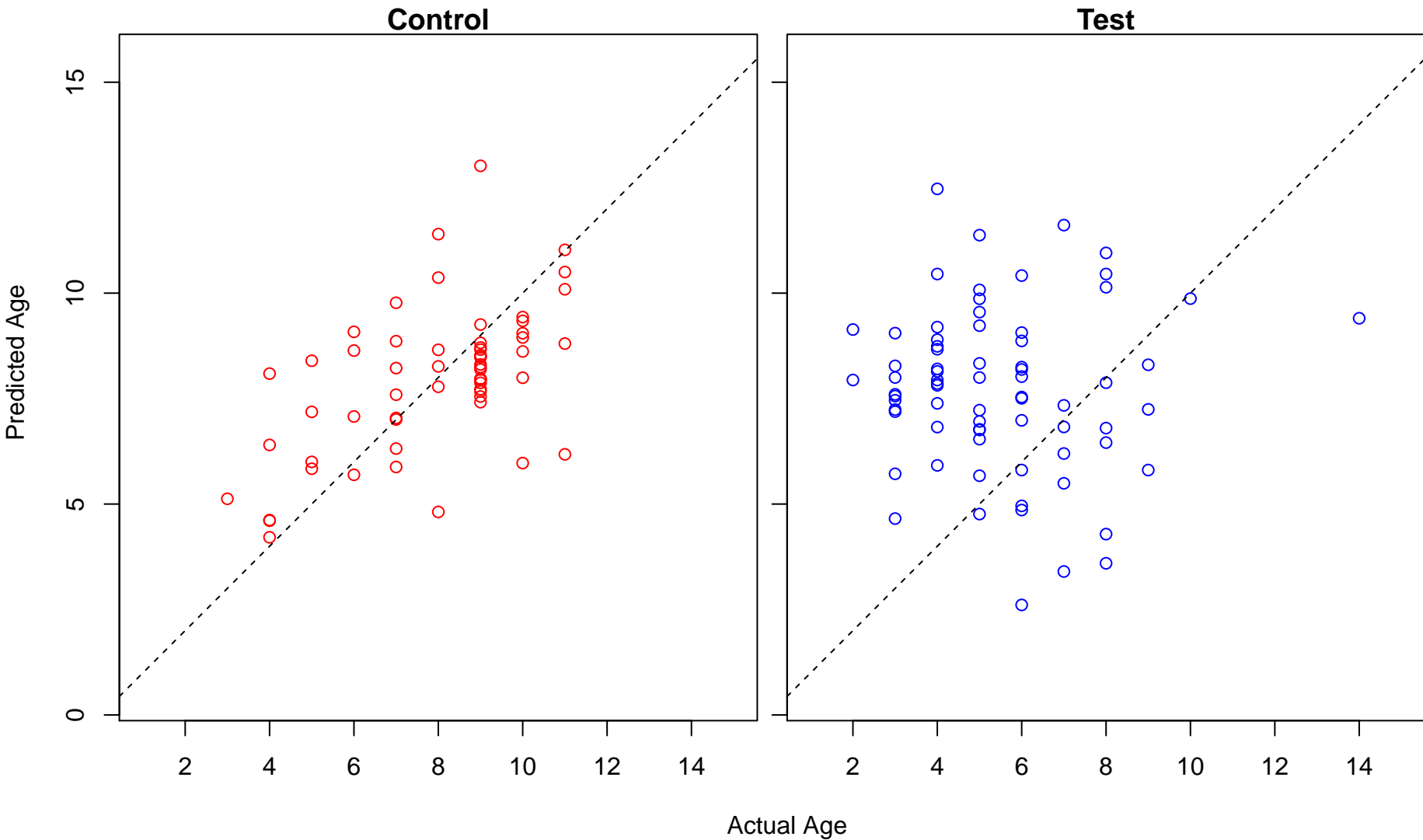
tissue homeostasis (Score: 1.647659)



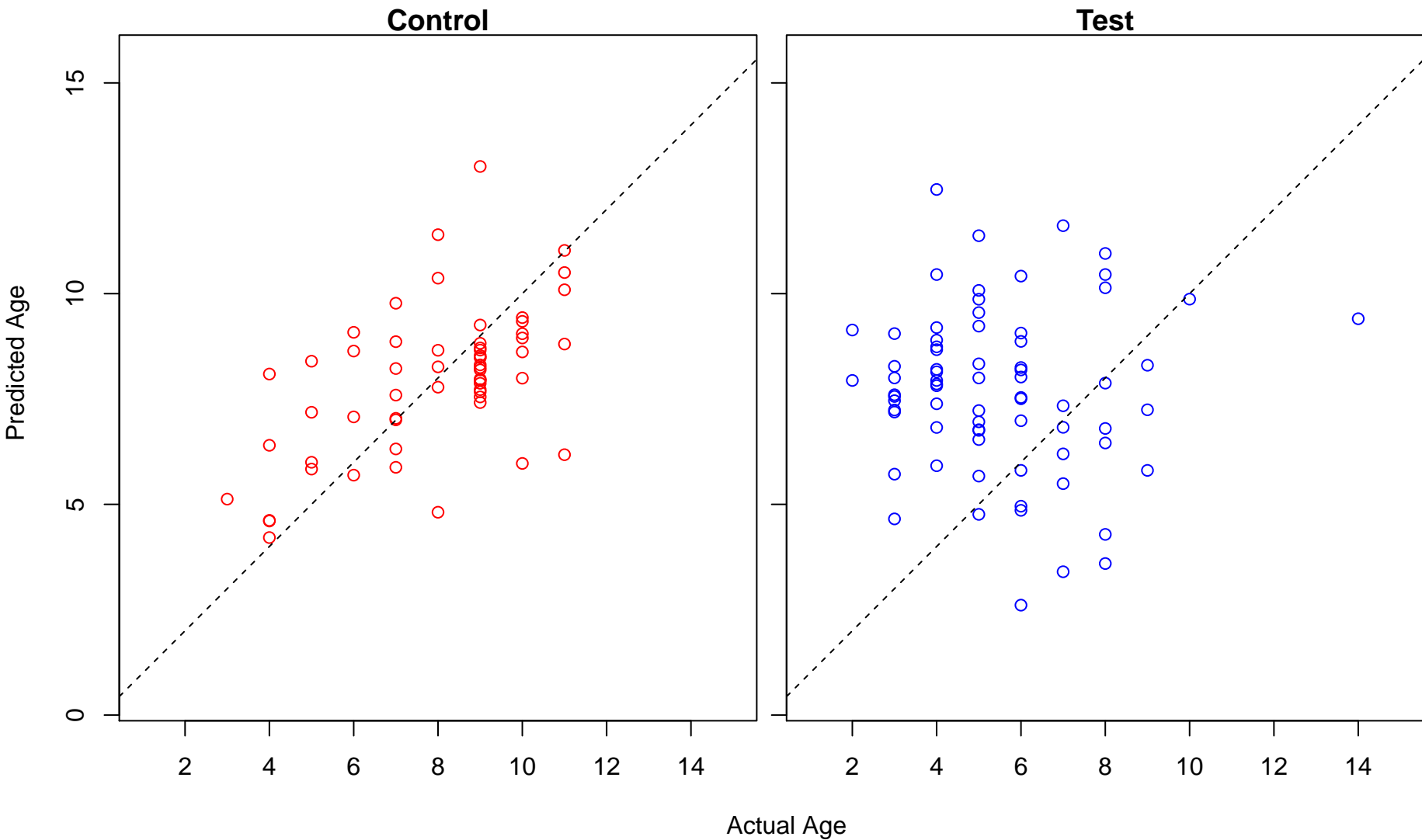
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 1.64)



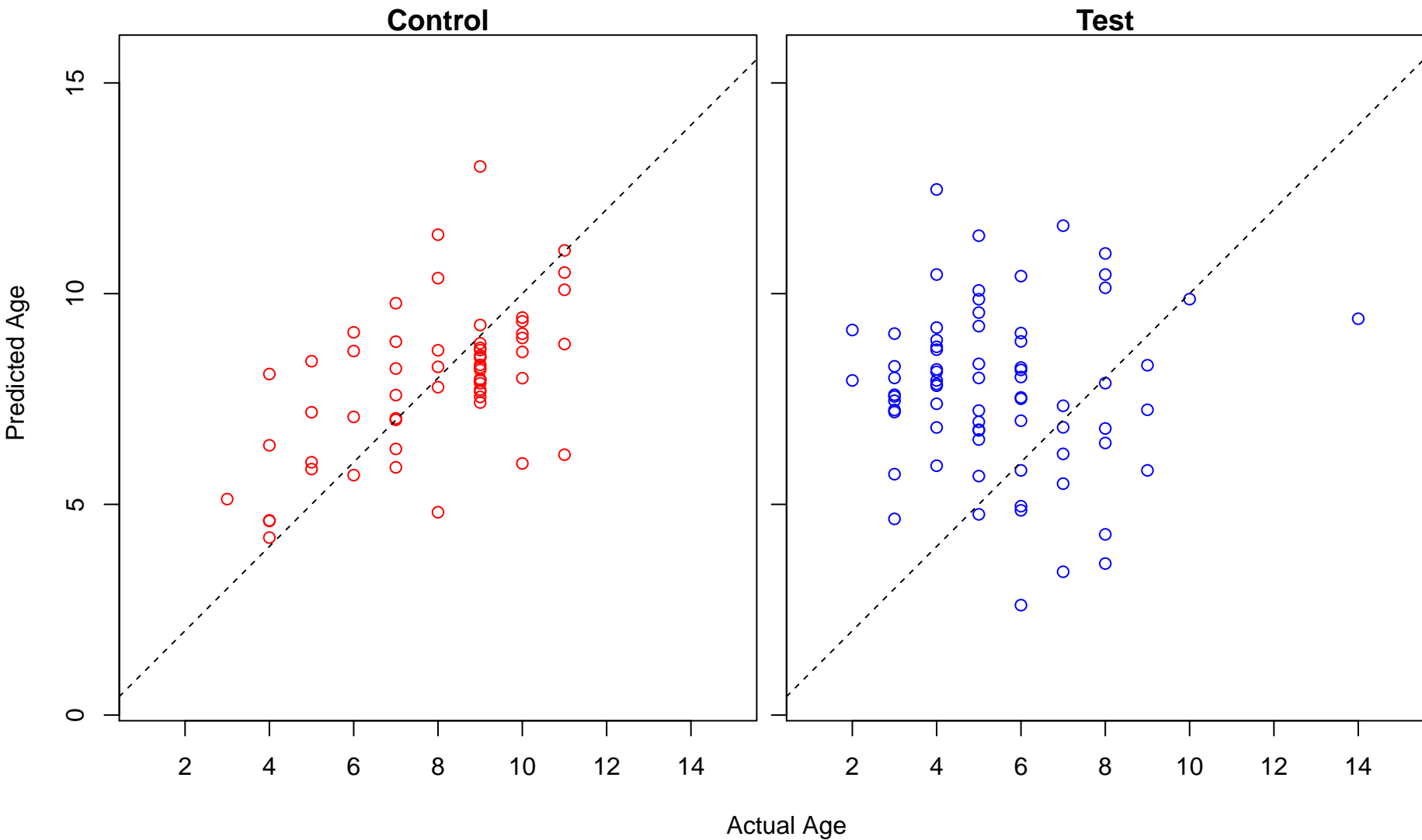
negative regulation of neurotransmitter uptake (Score: 1.645120)



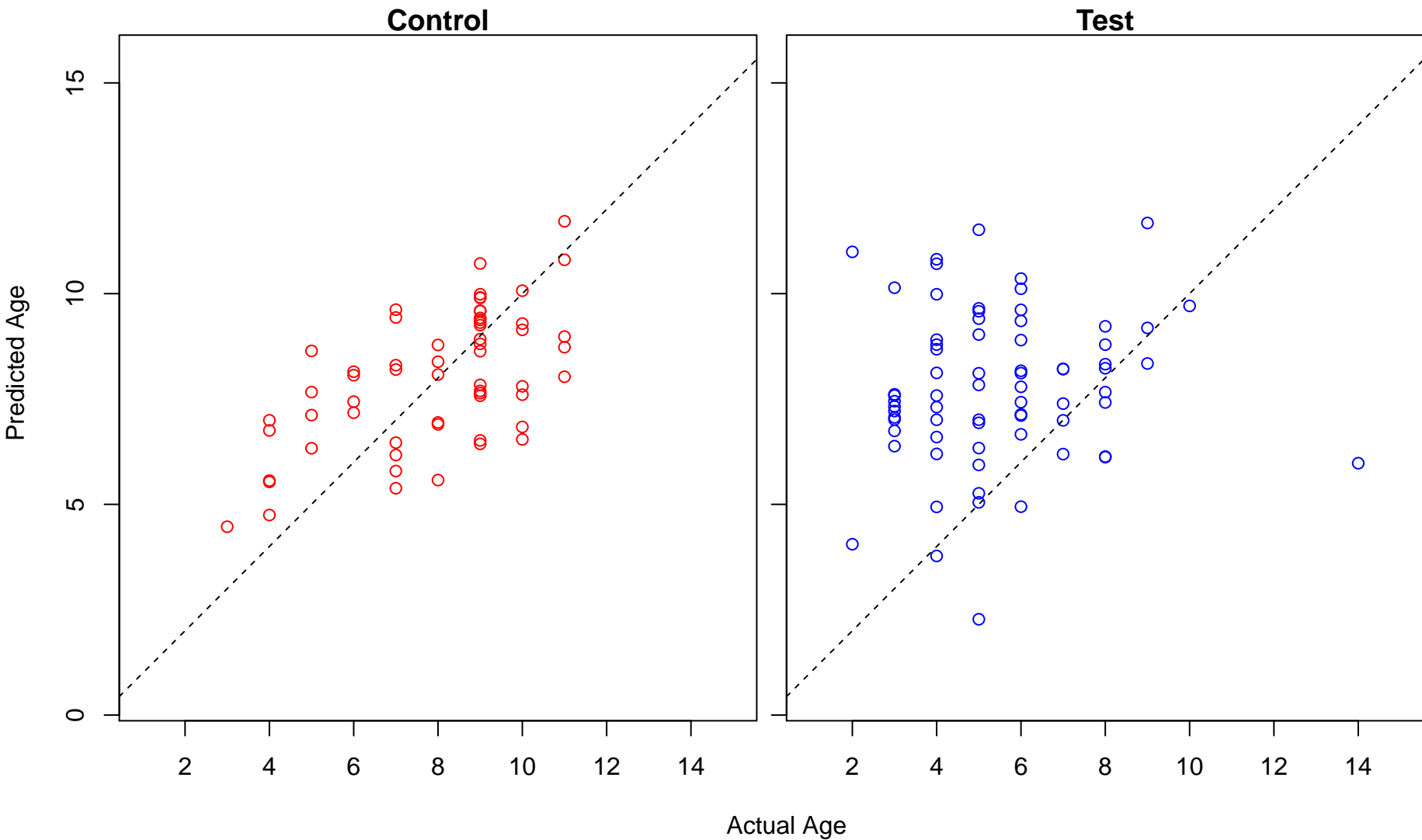
regulation of serotonin uptake (Score: 1.645120)



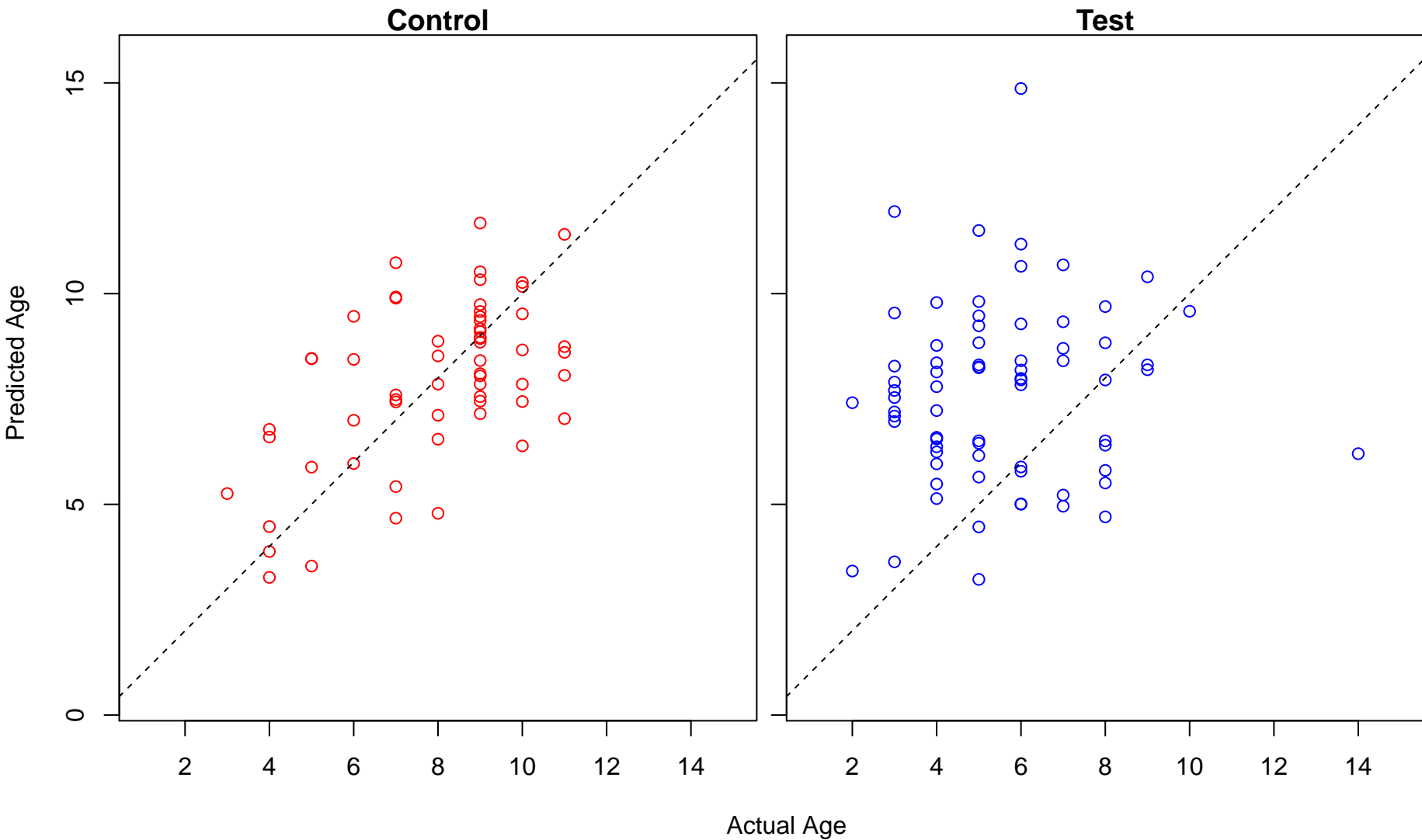
negative regulation of serotonin uptake (Score: 1.645120)



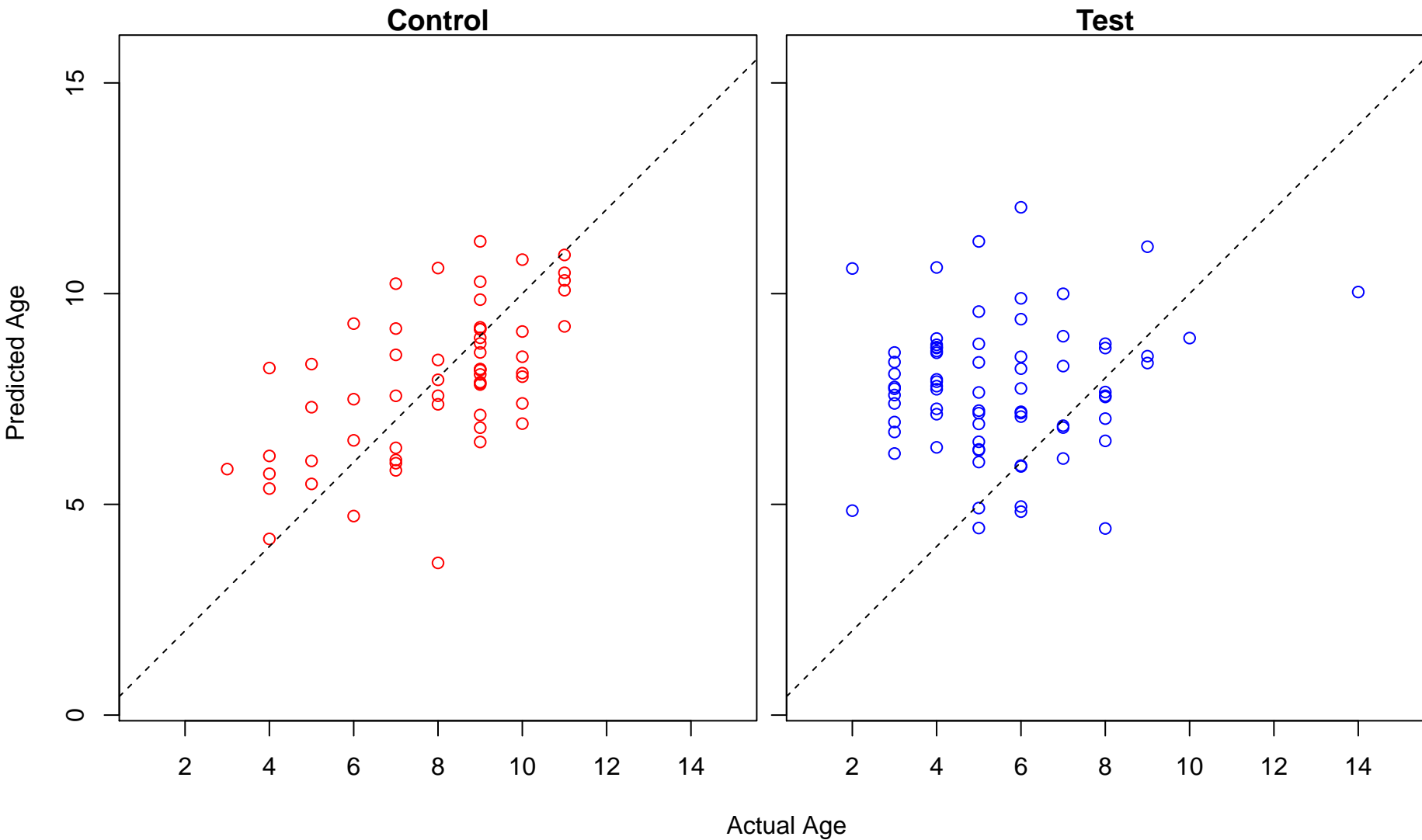
positive regulation of gene expression (Score: 1.624258)



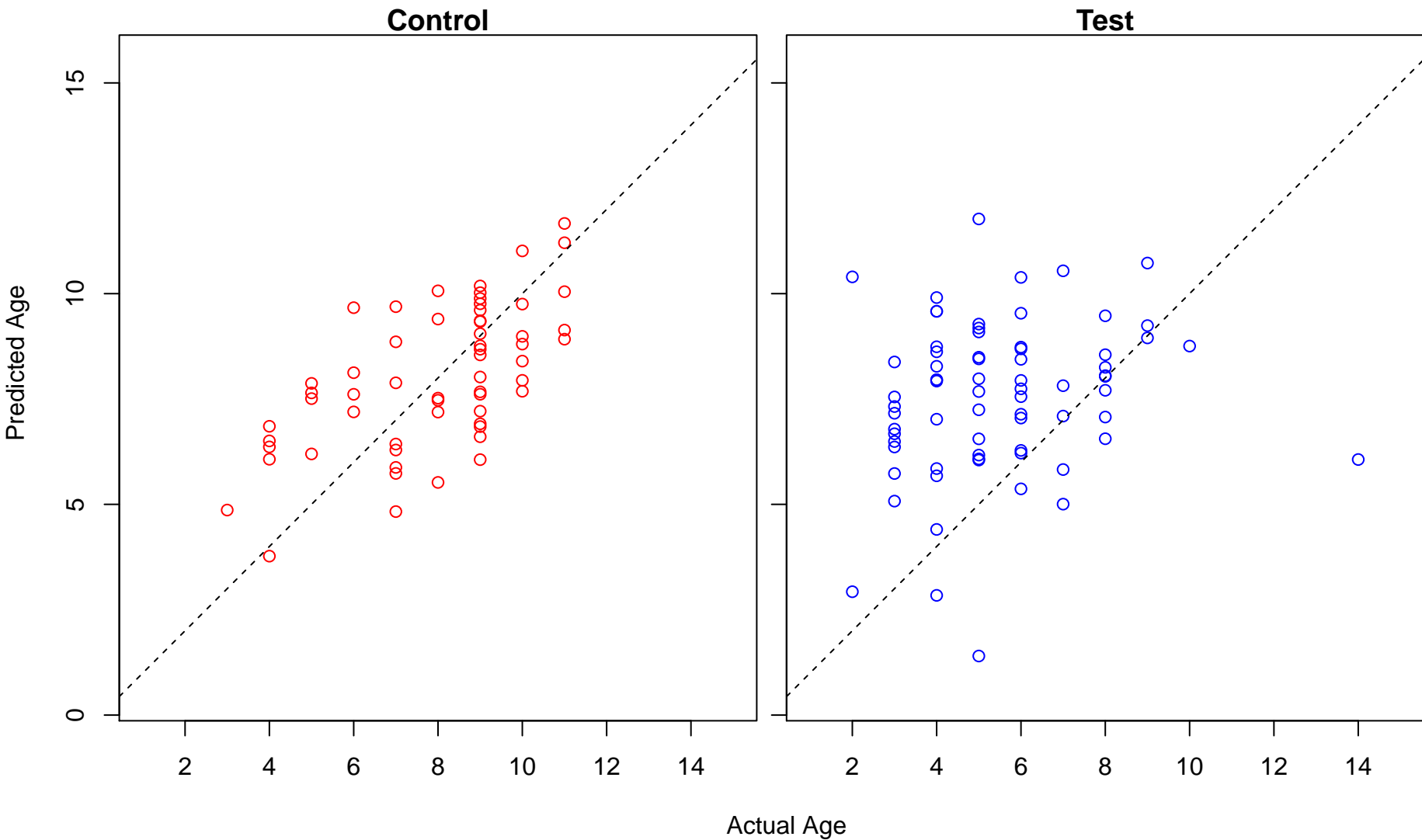
sulfur compound catabolic process (Score: 1.597678)



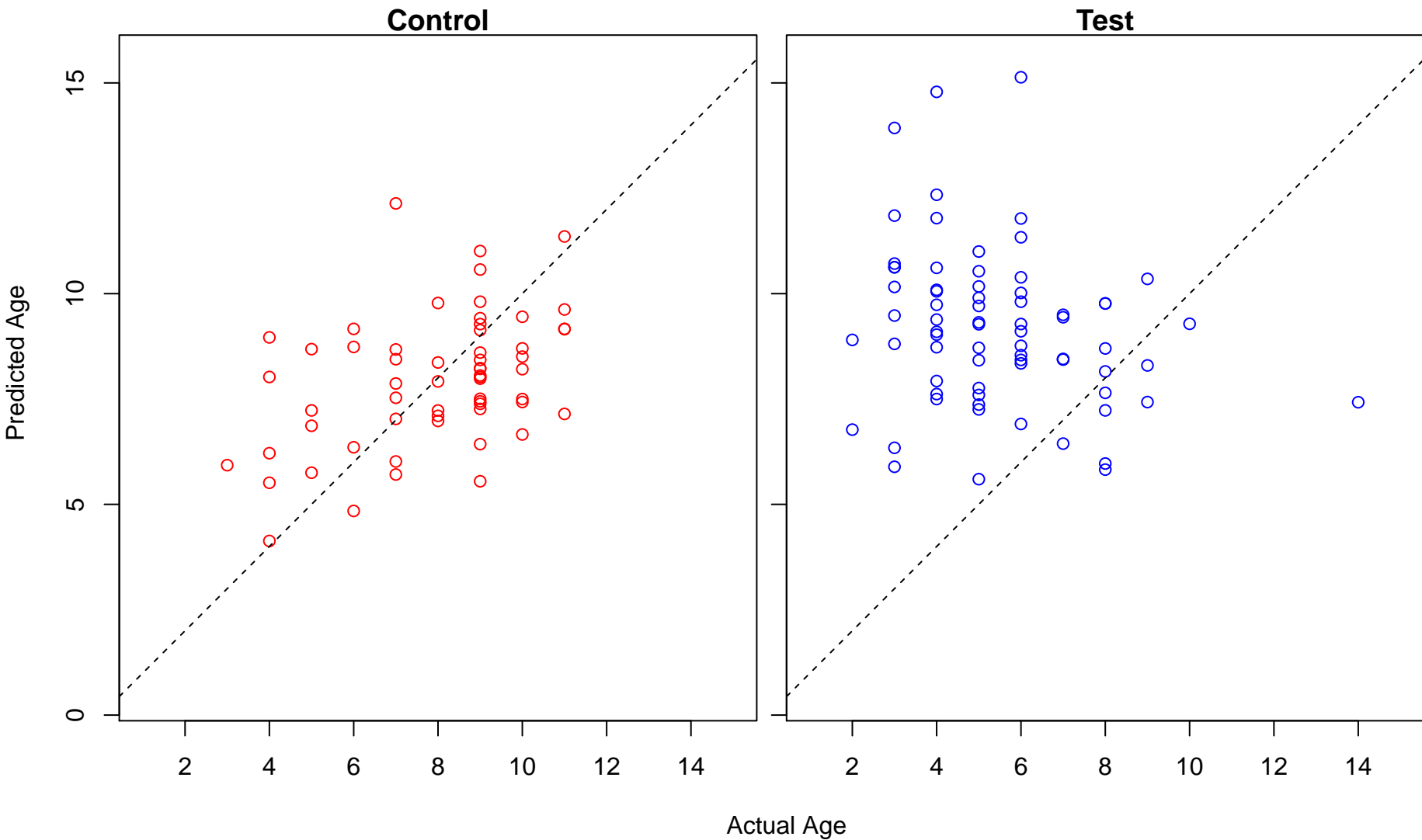
platelet degranulation (Score: 1.589720)



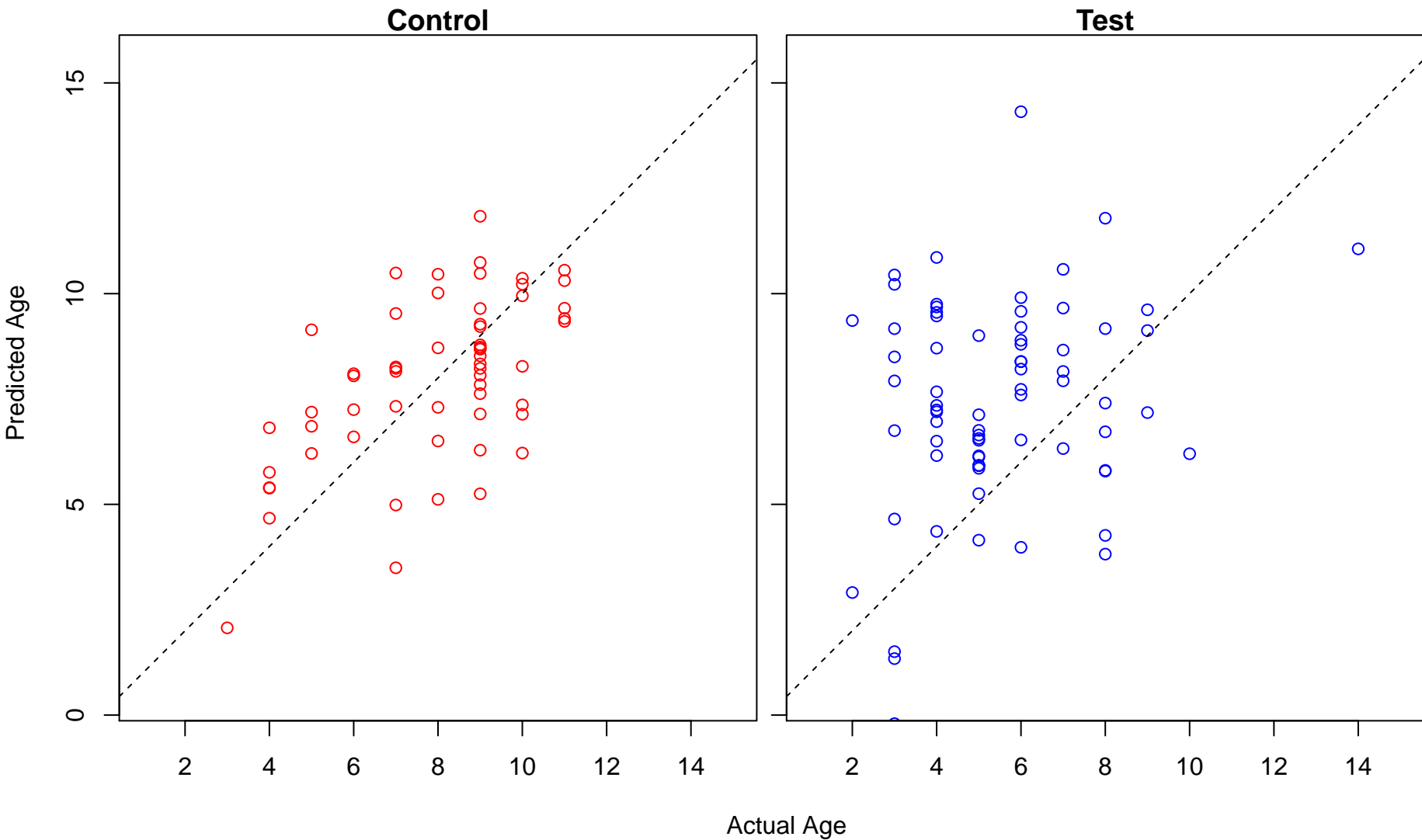
regulation of nucleobase-containing compound metabolic process (Score: 1.587298)



androgen metabolic process (Score: 1.573653)

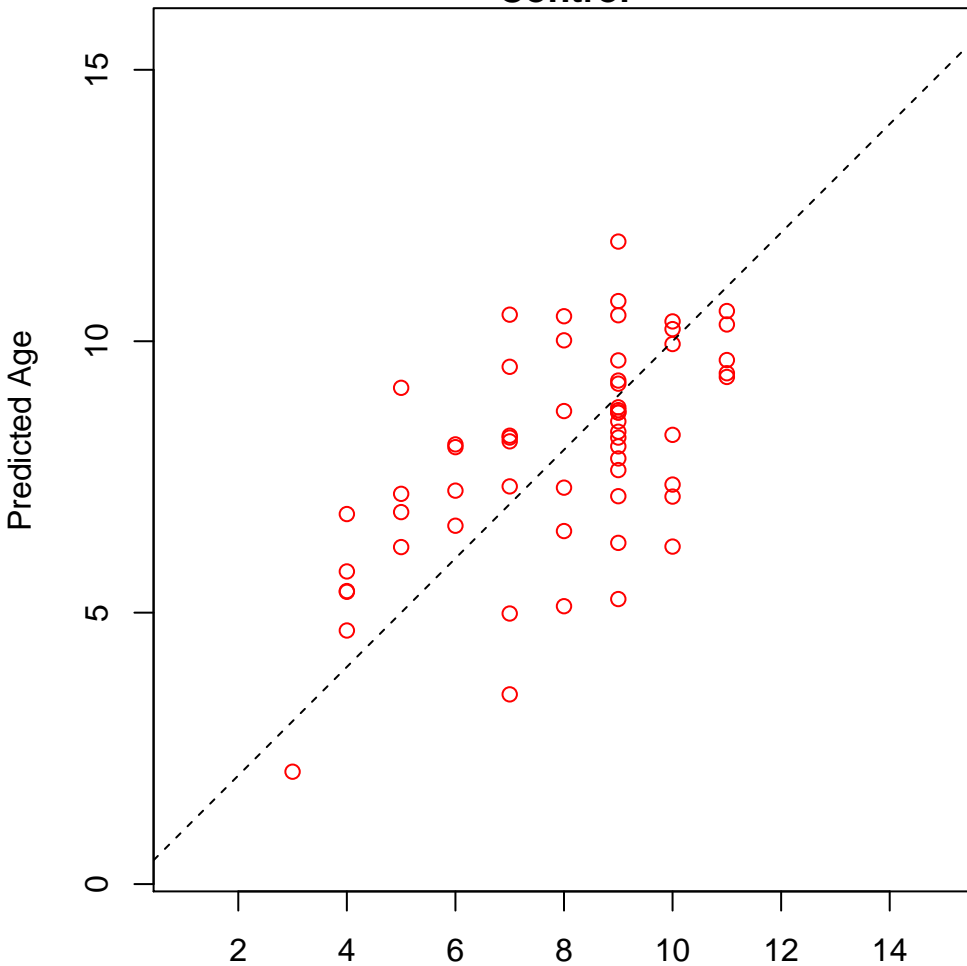


mesonephric epithelium development (Score: 1.570518)

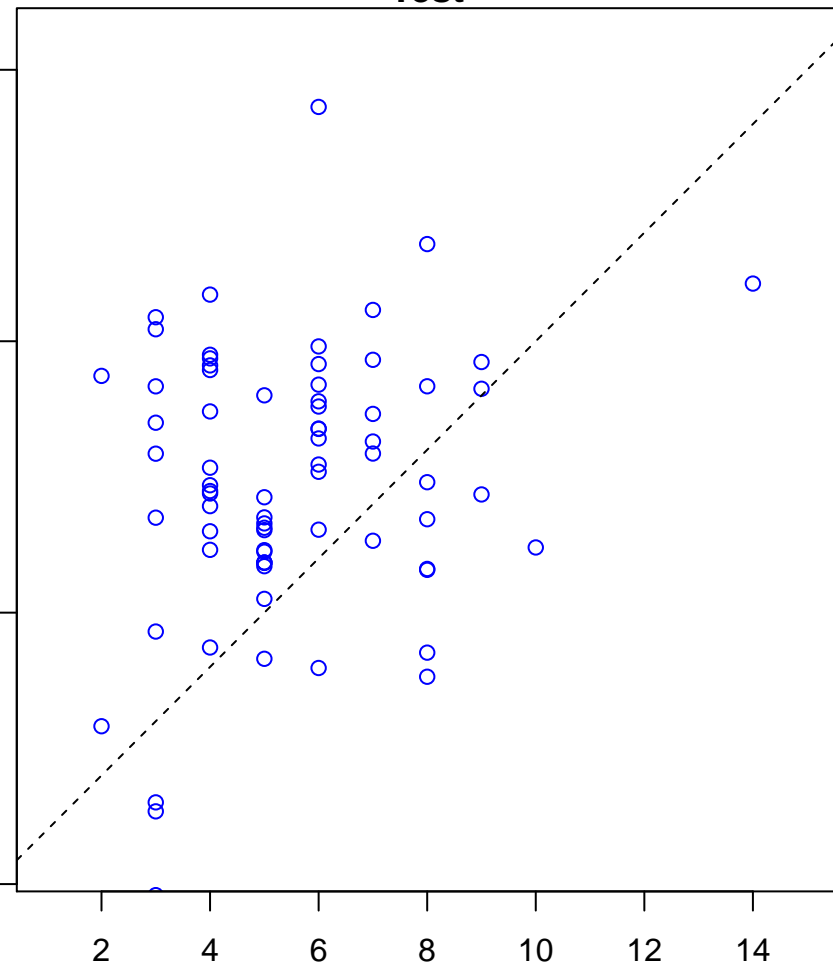


mesonephric tubule development (Score: 1.570518)

Control

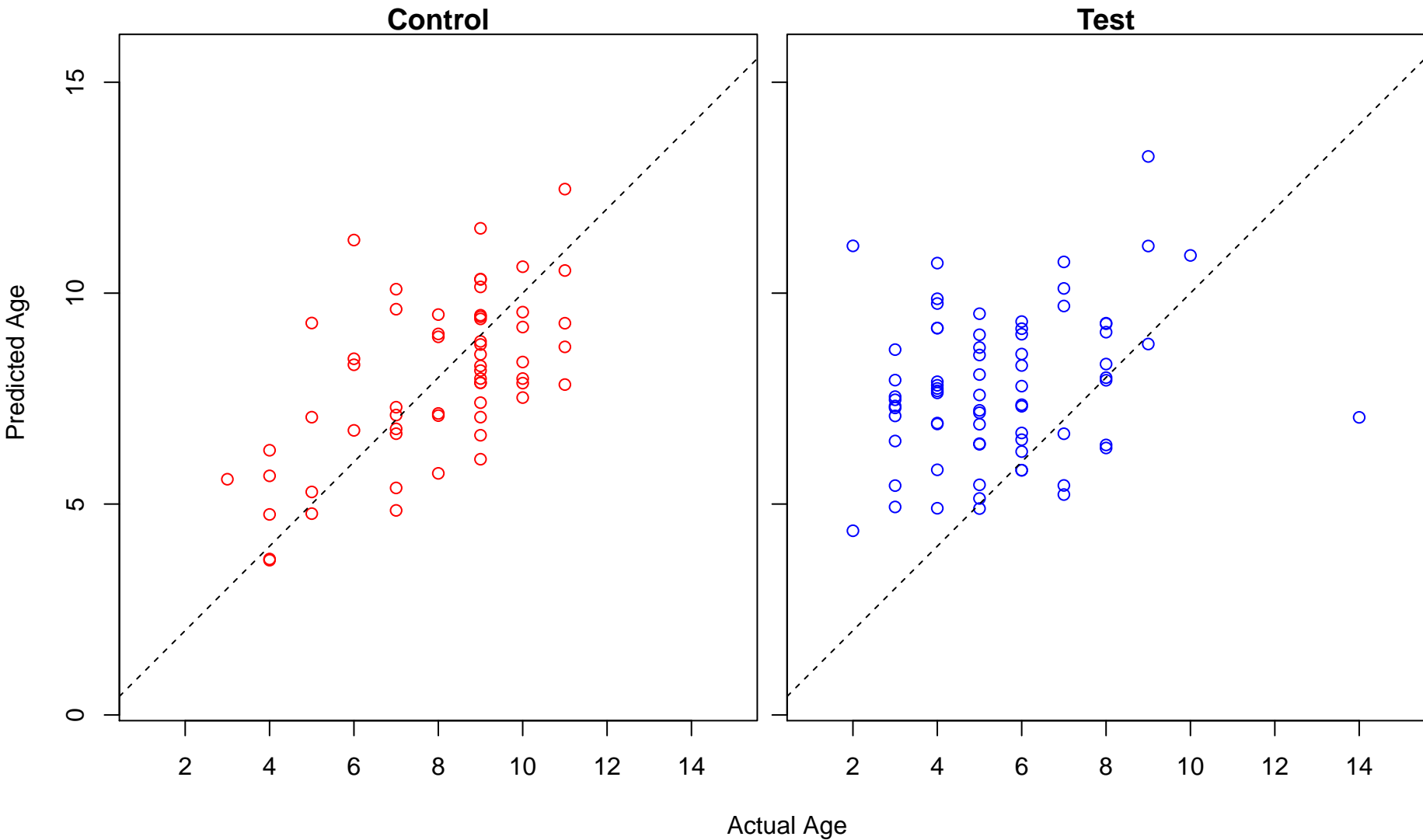


Test

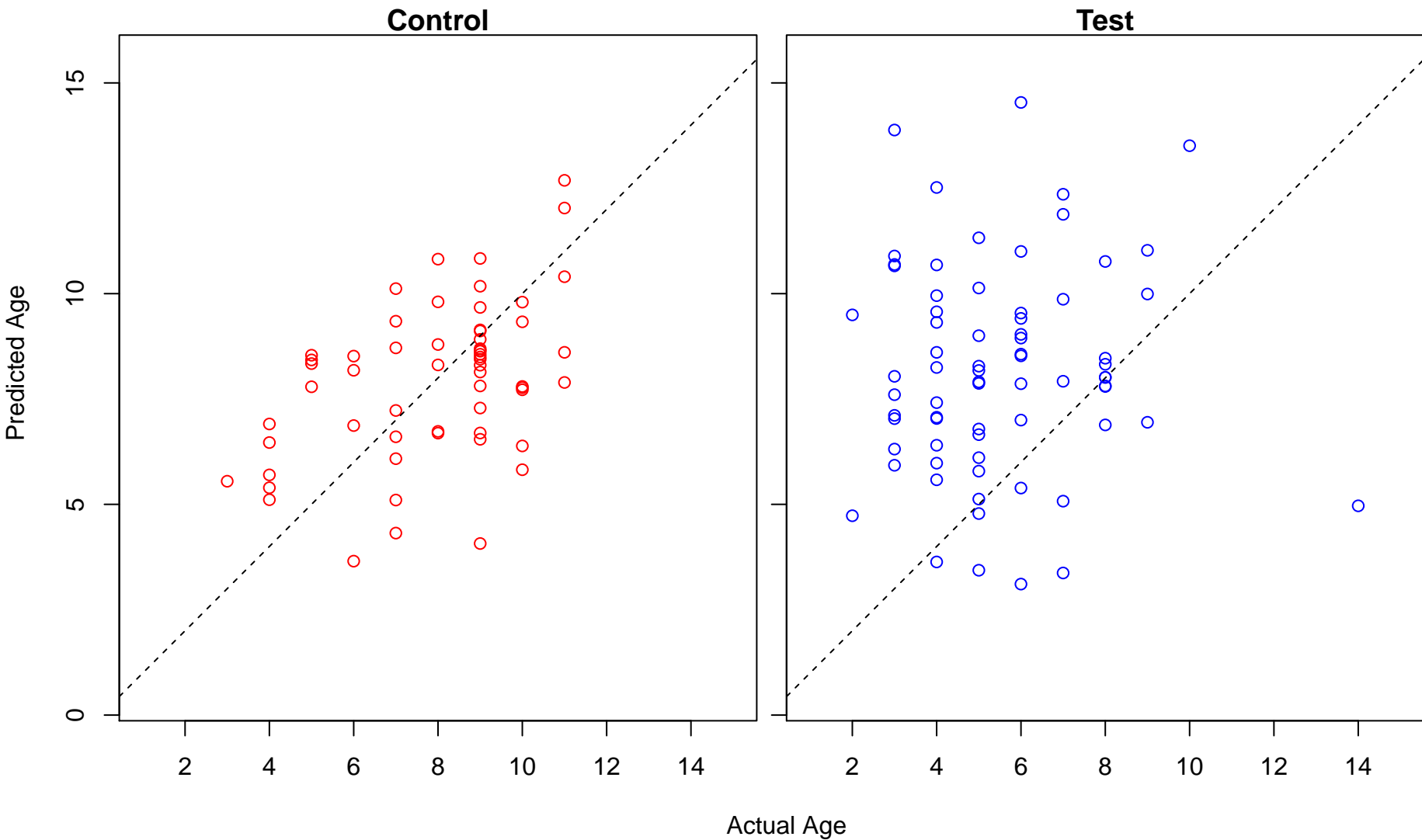


Actual Age

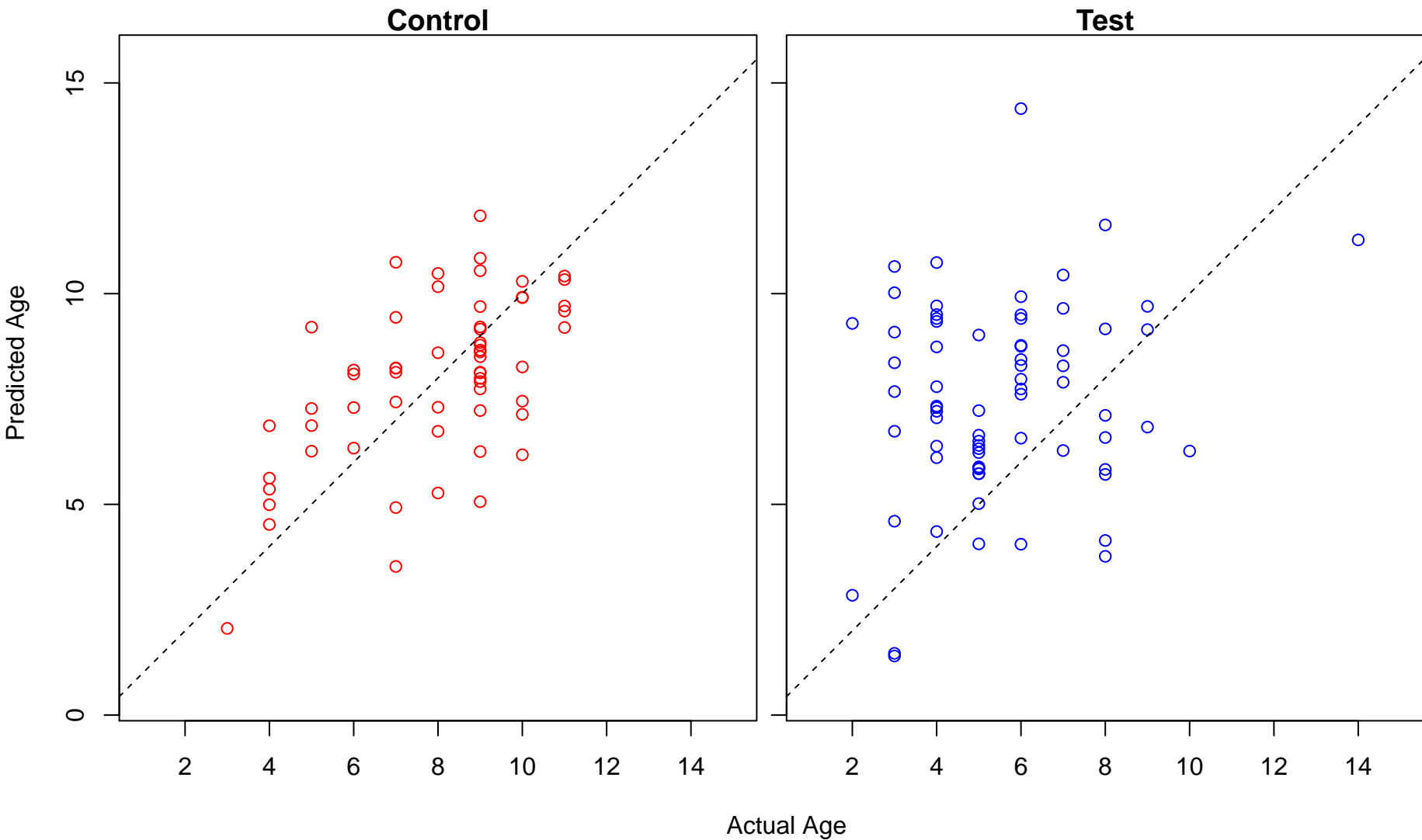
positive regulation of neuron differentiation (Score: 1.568309)



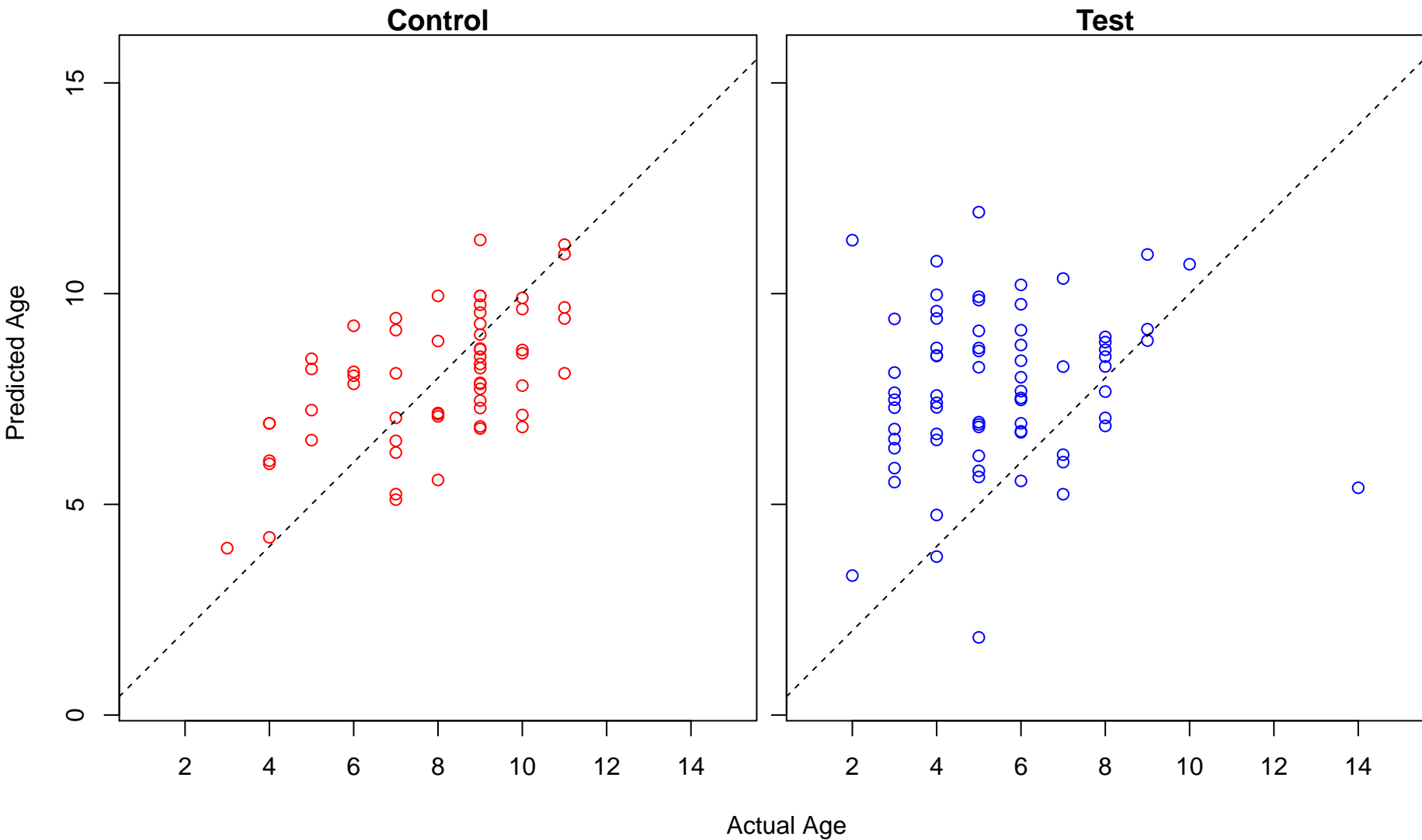
regulation of alpha-beta T cell activation (Score: 1.557835)



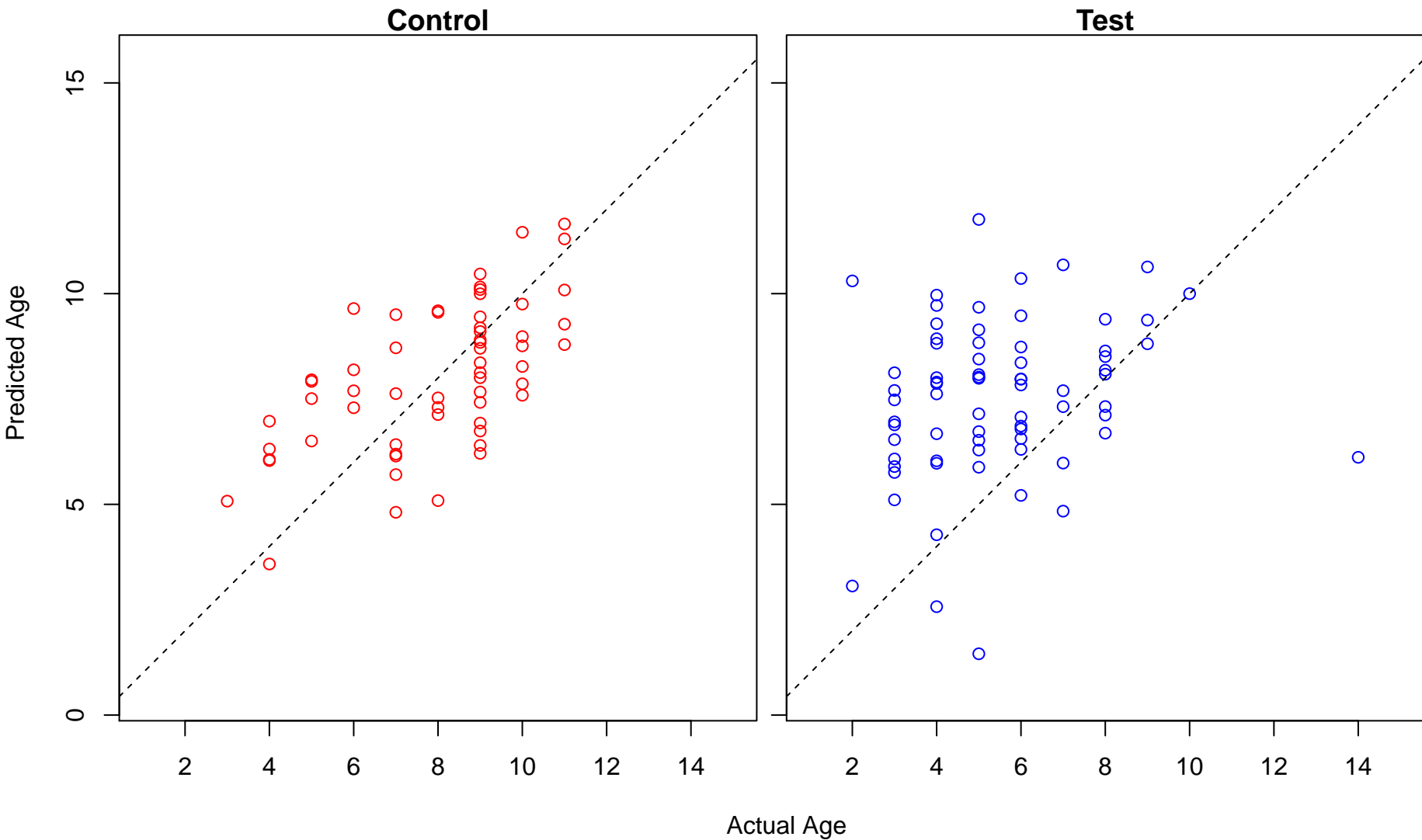
ureteric bud development (Score: 1.556653)



regulation of RNA biosynthetic process (Score: 1.551199)

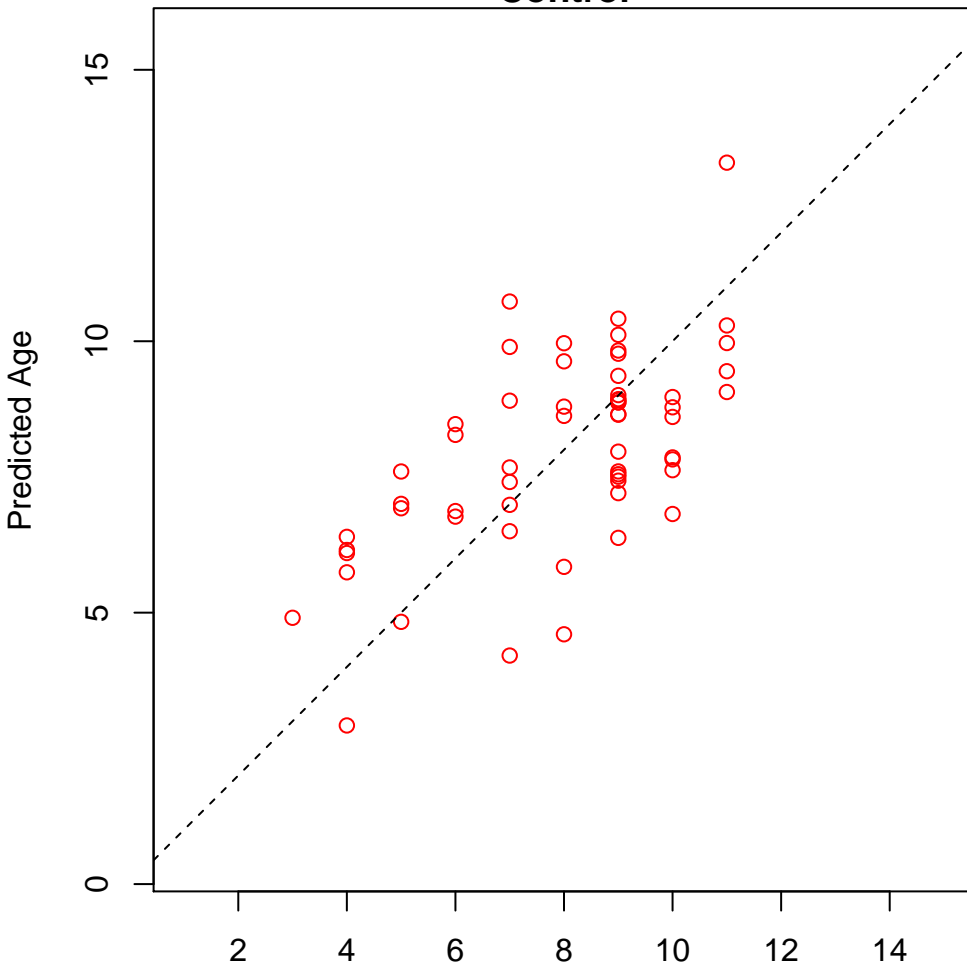


regulation of RNA metabolic process (Score: 1.551195)

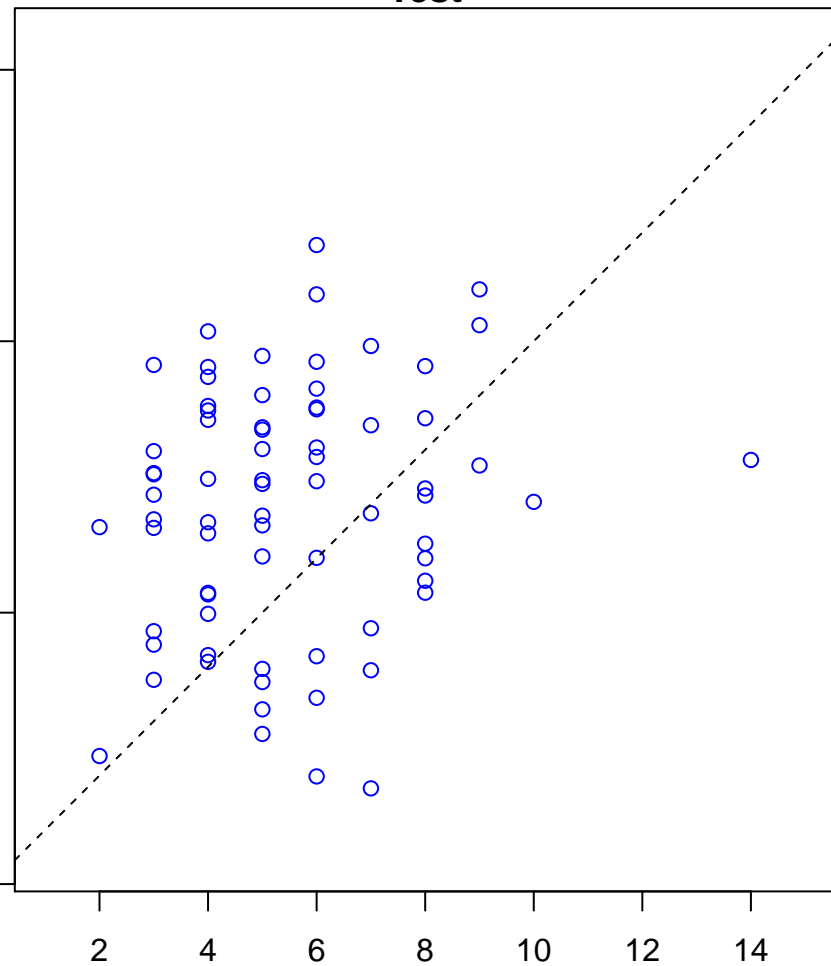


regulation of glucose metabolic process (Score: 1.544631)

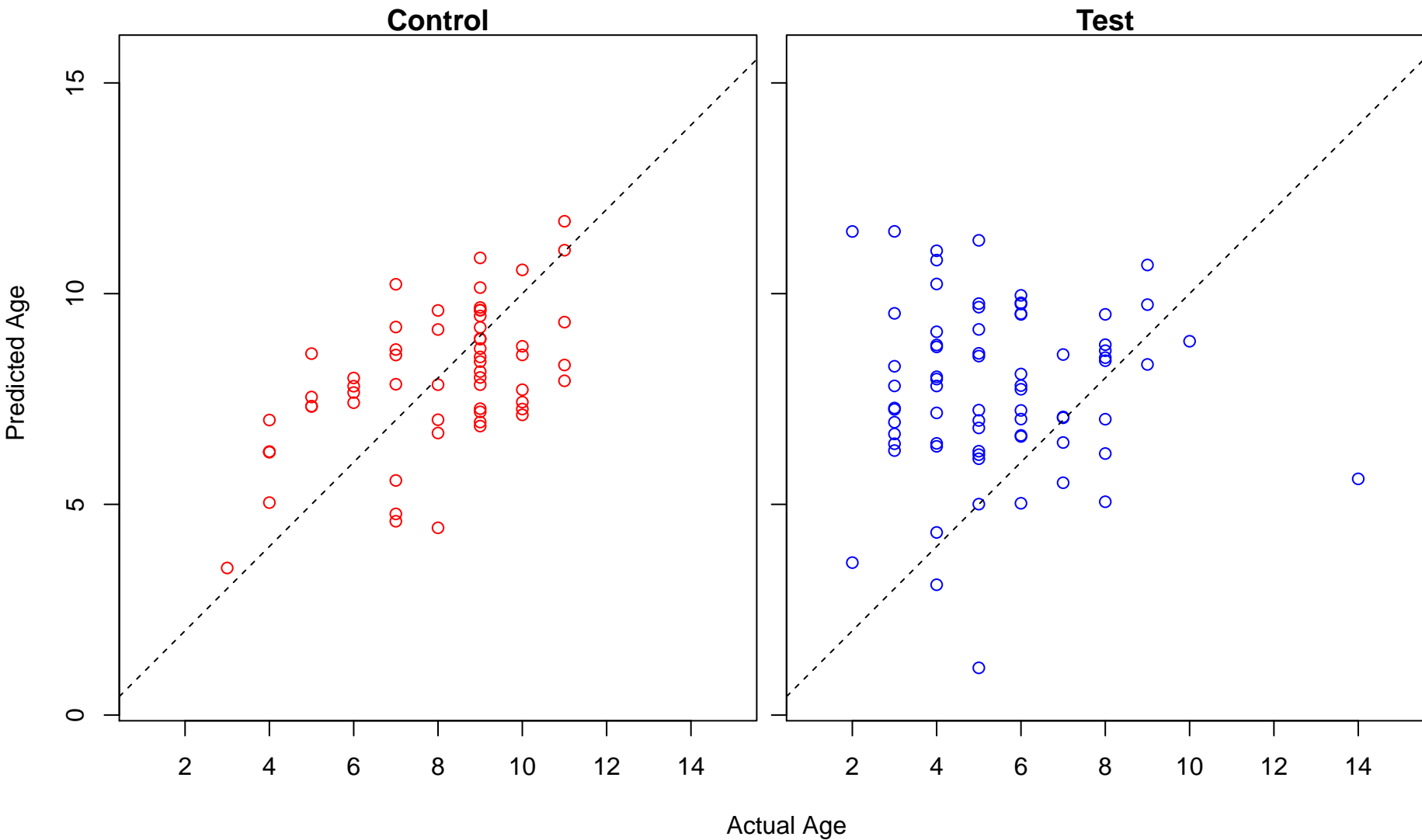
Control



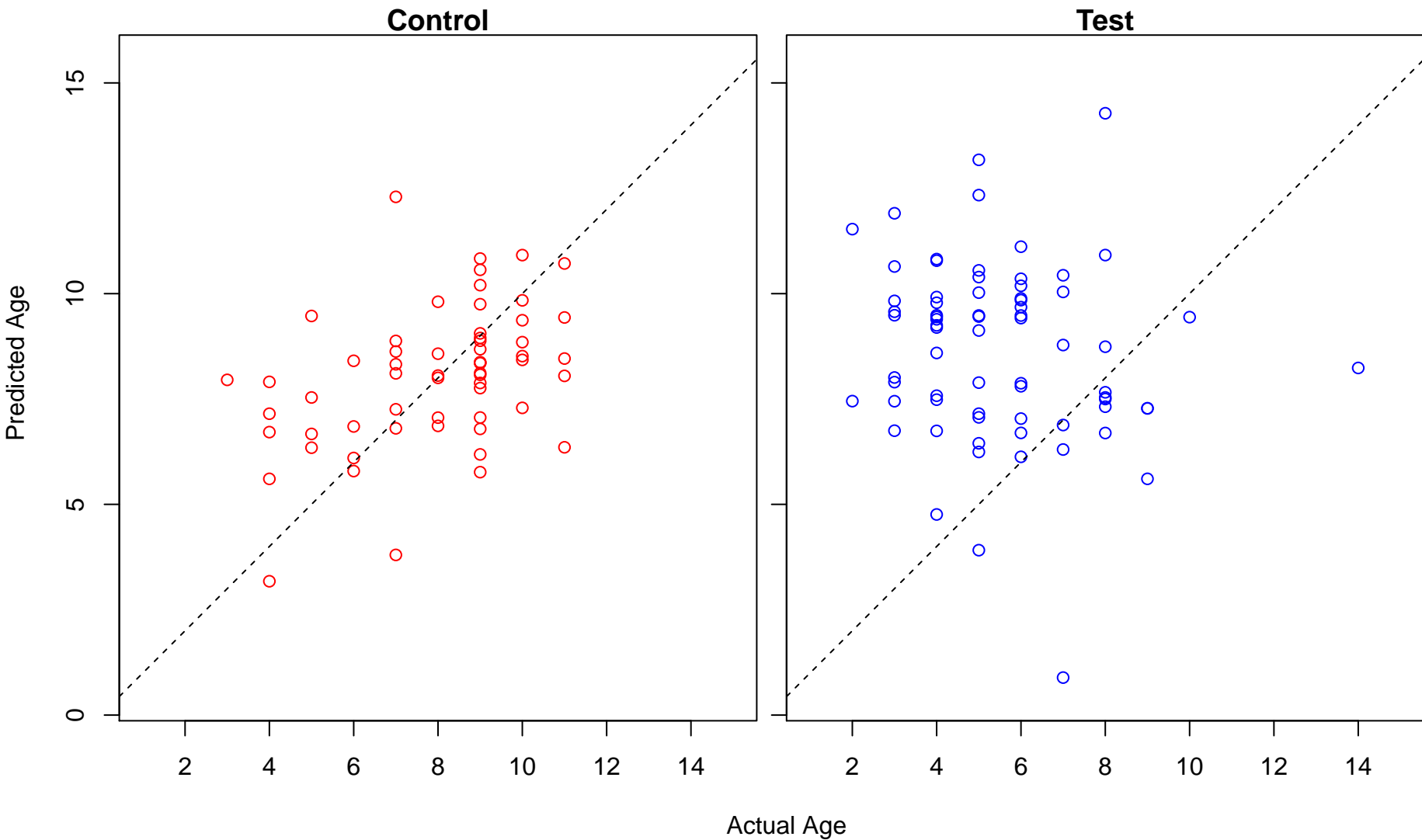
Test



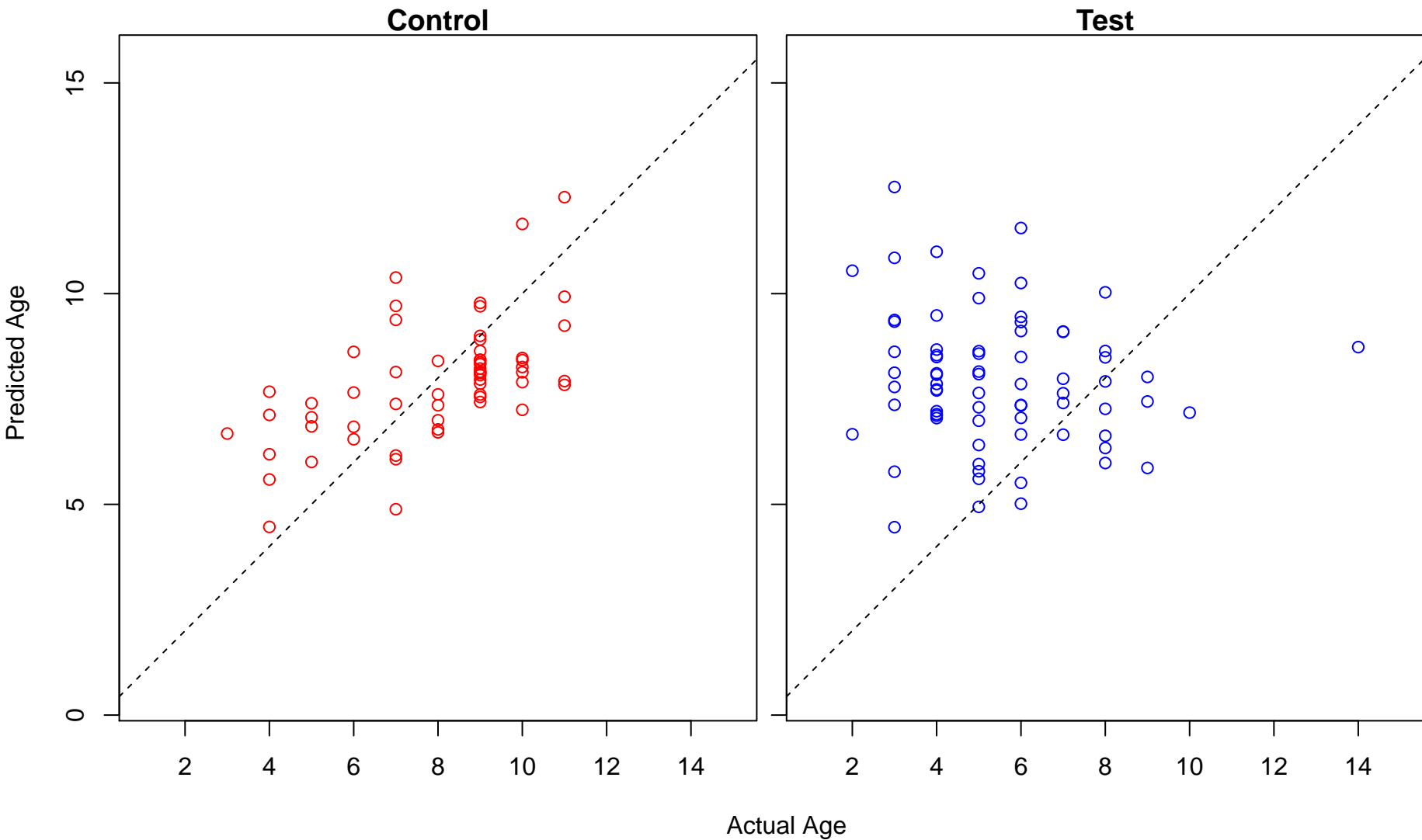
positive regulation of RNA metabolic process (Score: 1.543496)



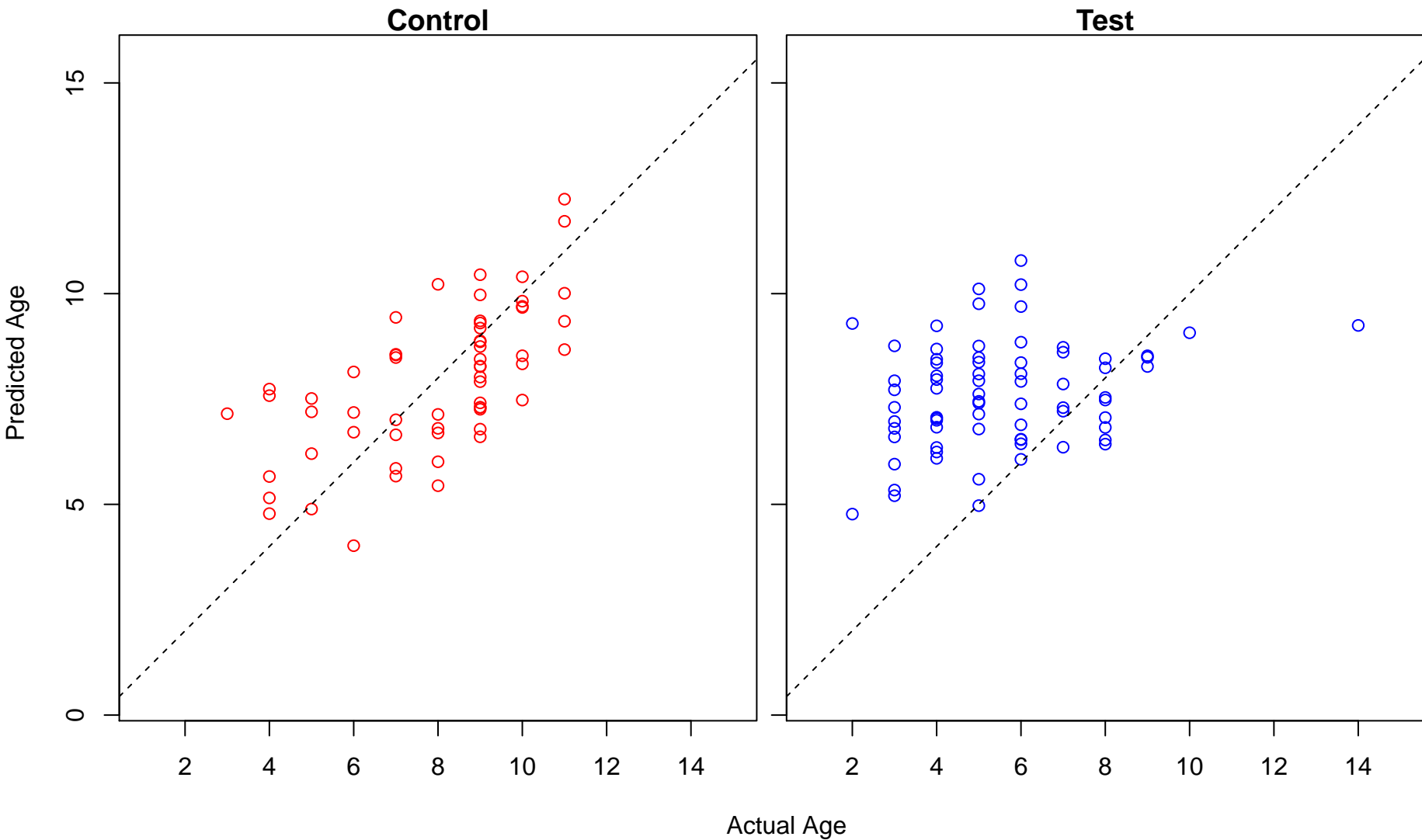
regulation of reproductive process (Score: 1.533780)



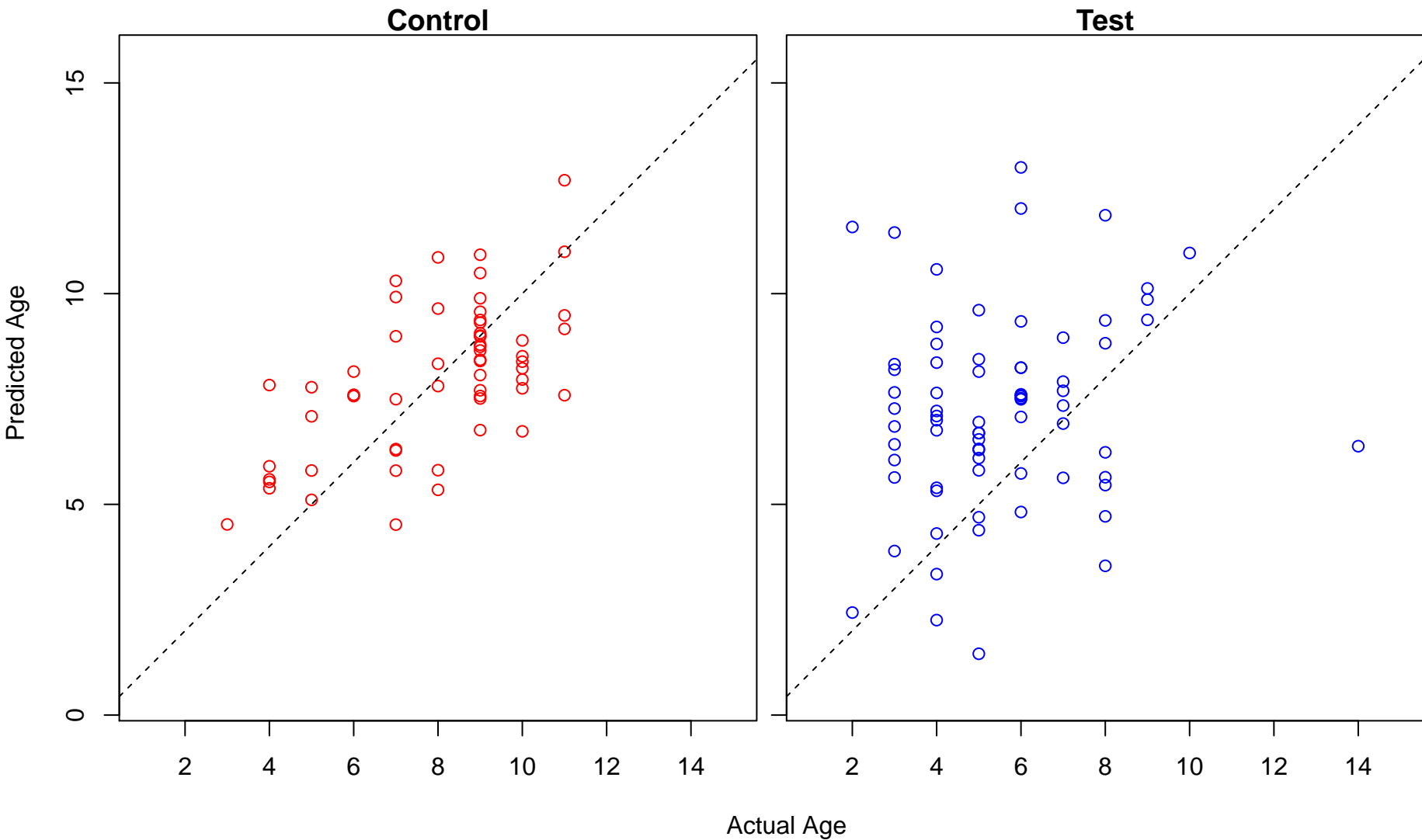
regulation of integrin-mediated signaling pathway (Score: 1.528758)



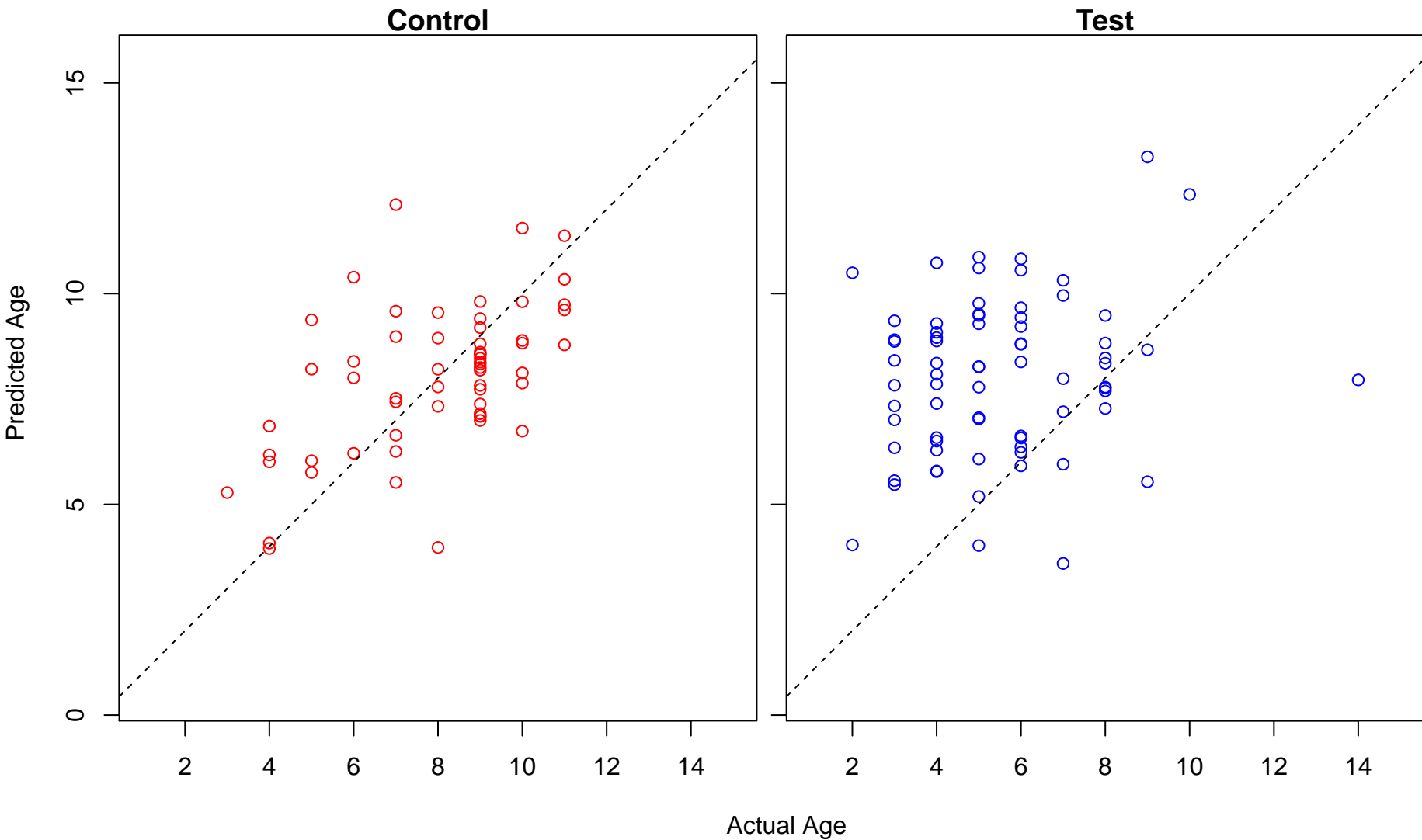
macromolecule localization (Score: 1.526266)



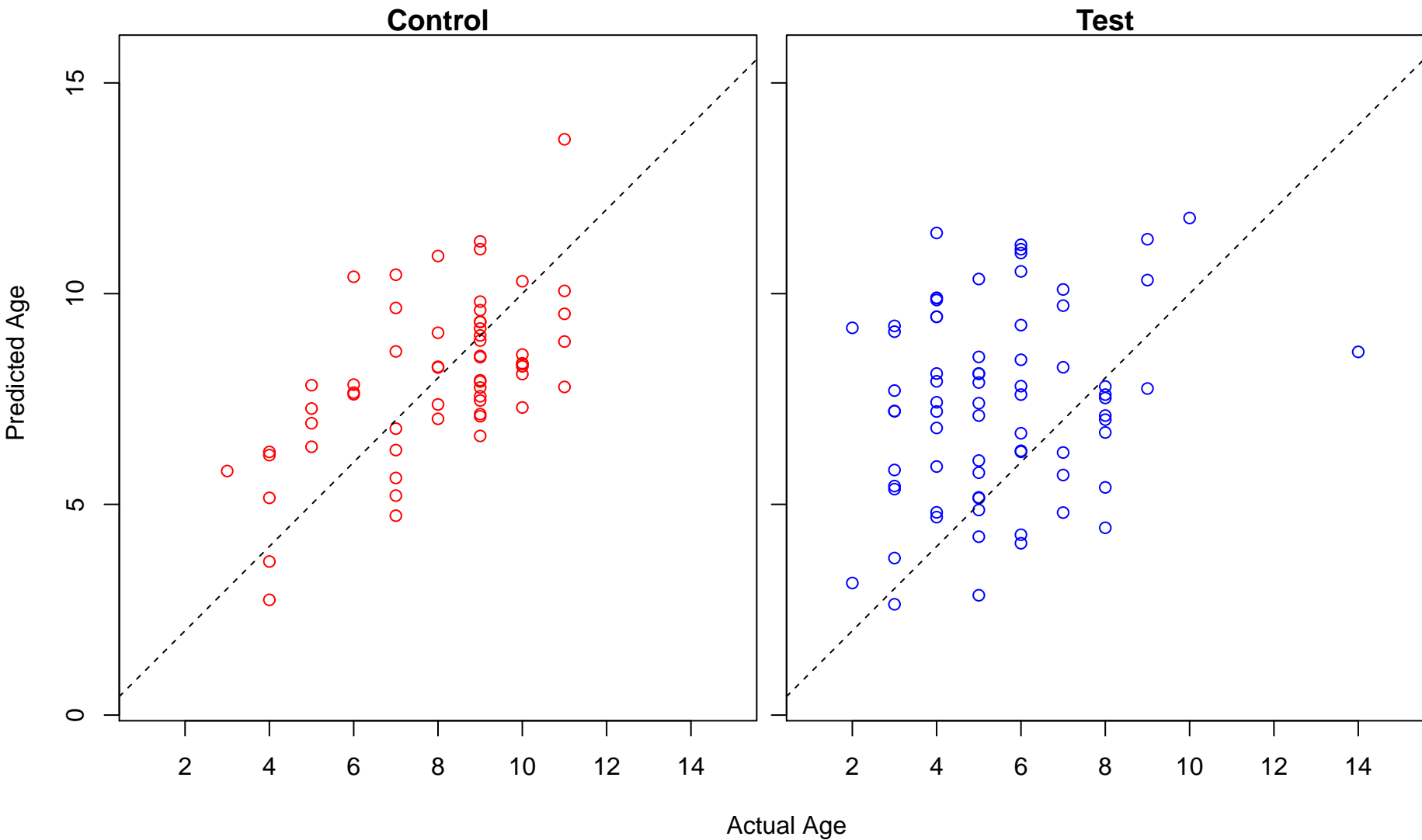
positive regulation of secretion (Score: 1.519002)



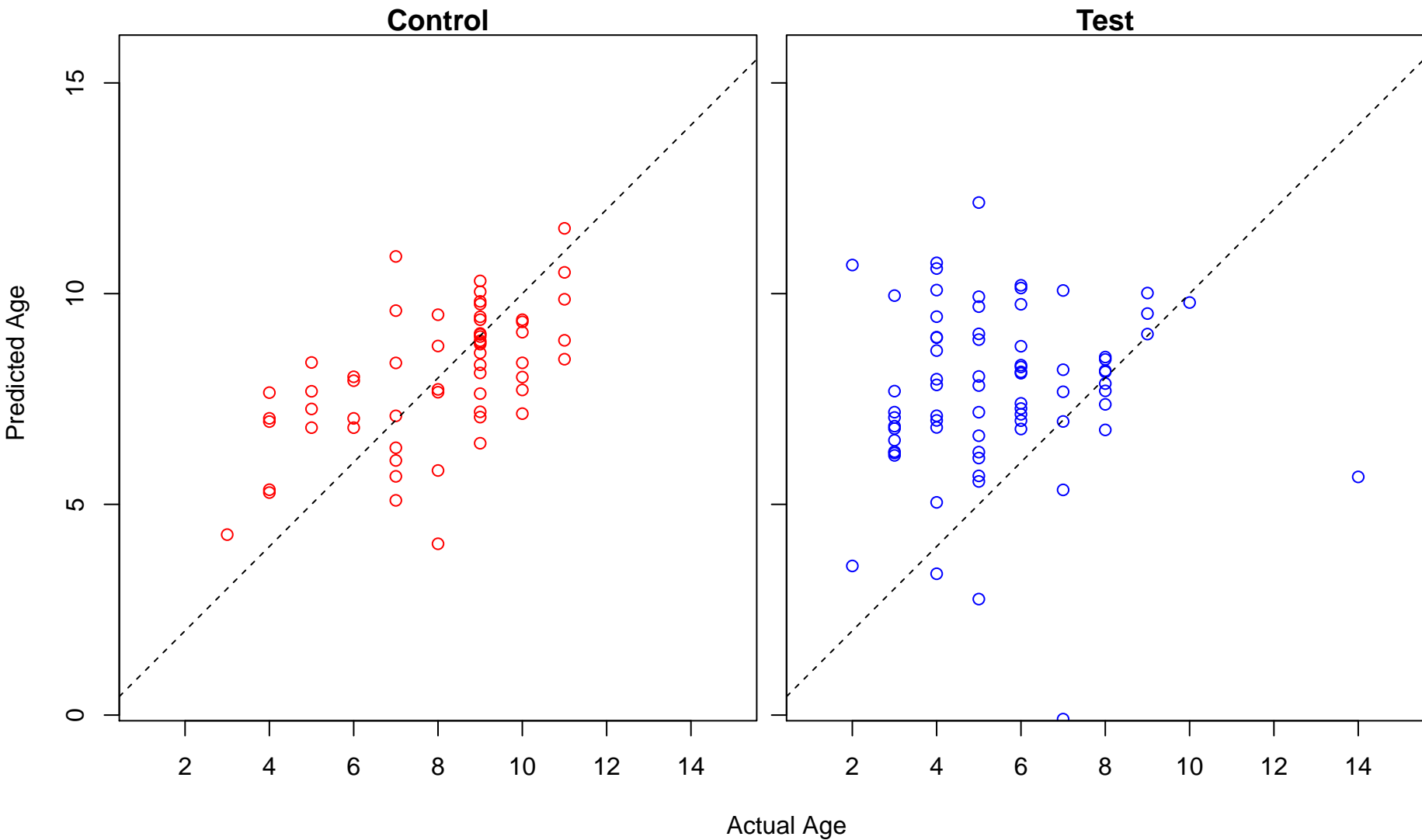
cellular transition metal ion homeostasis (Score: 1.515121)



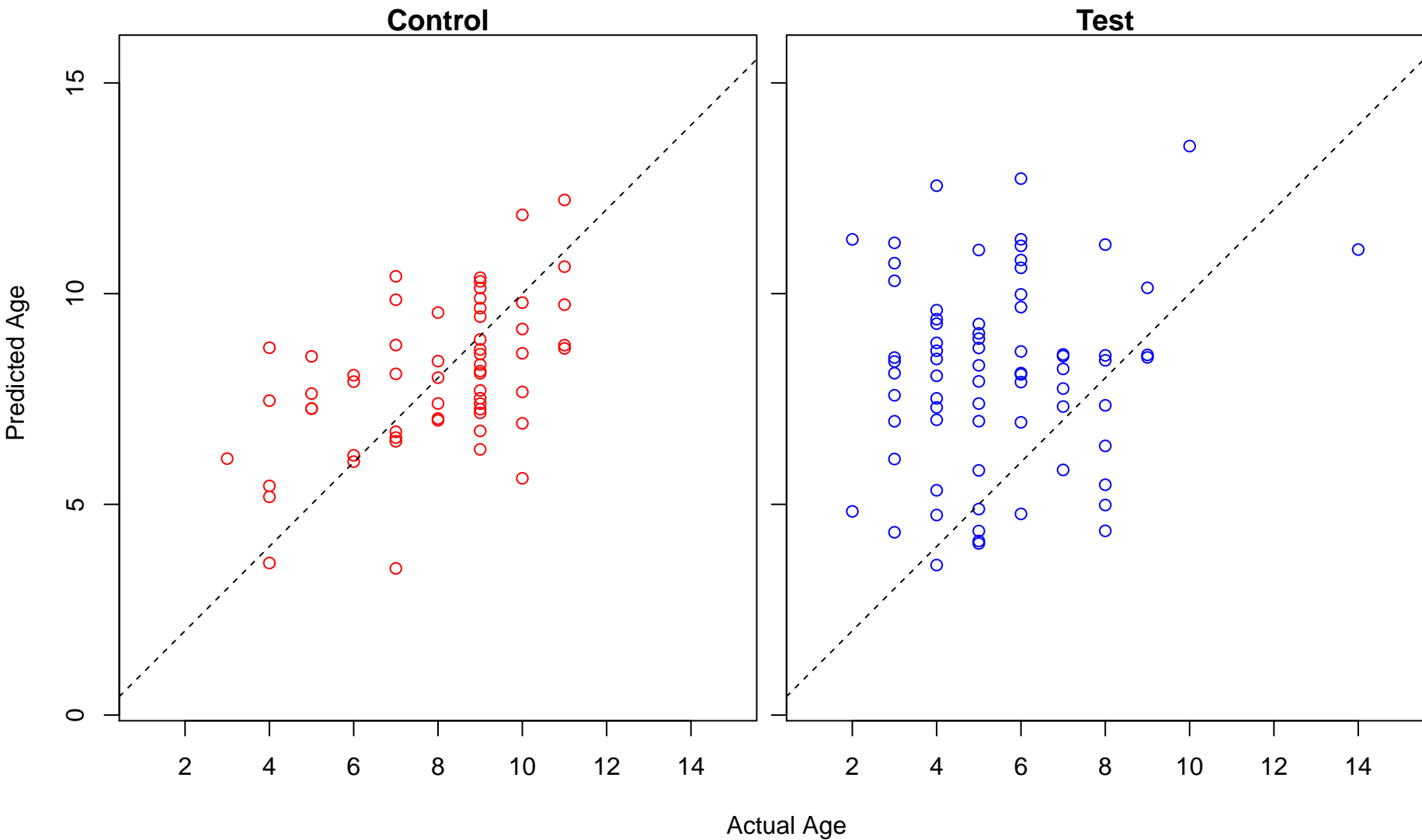
positive regulation of axonogenesis (Score: 1.511793)



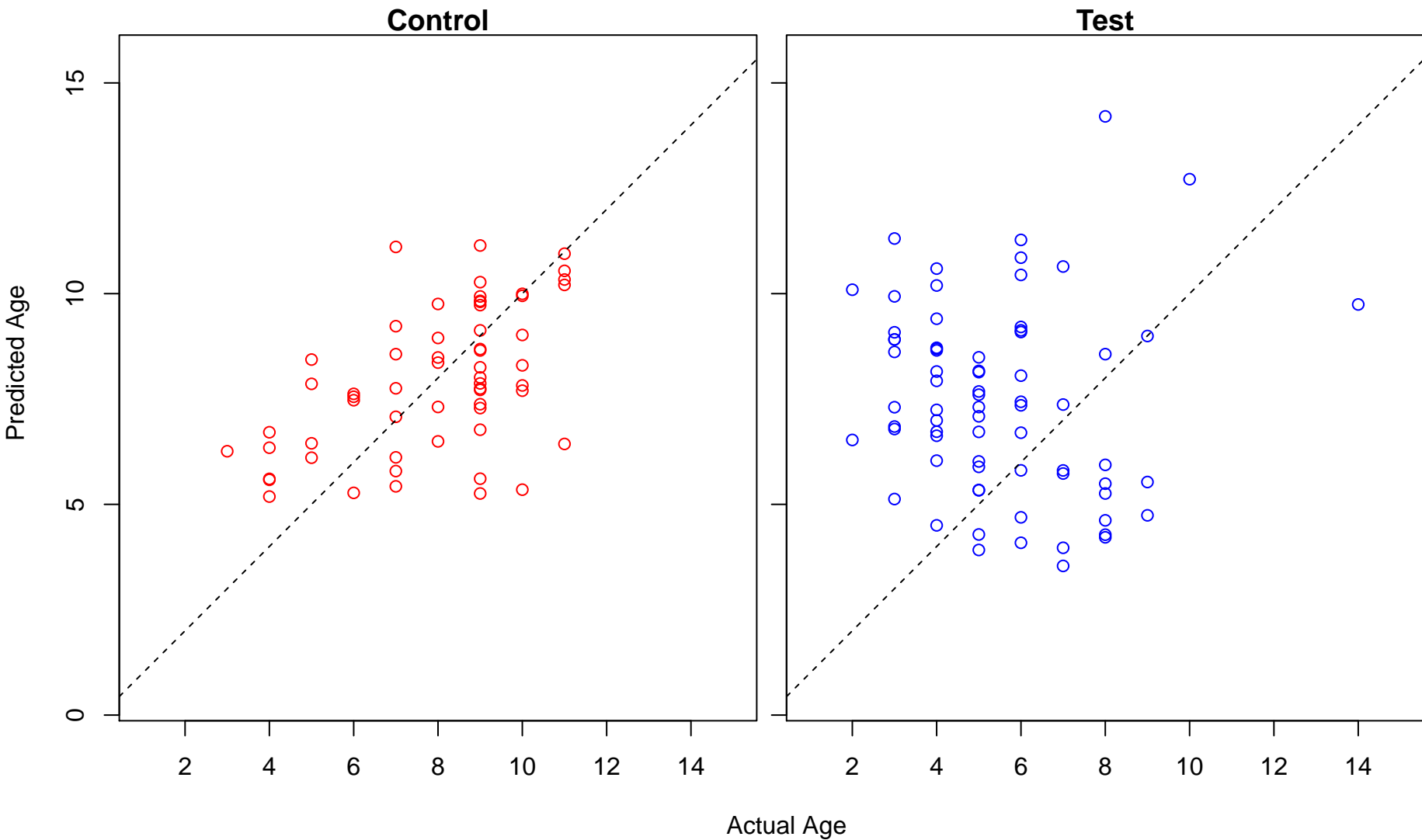
positive regulation of macromolecule metabolic process (Score: 1.509394)



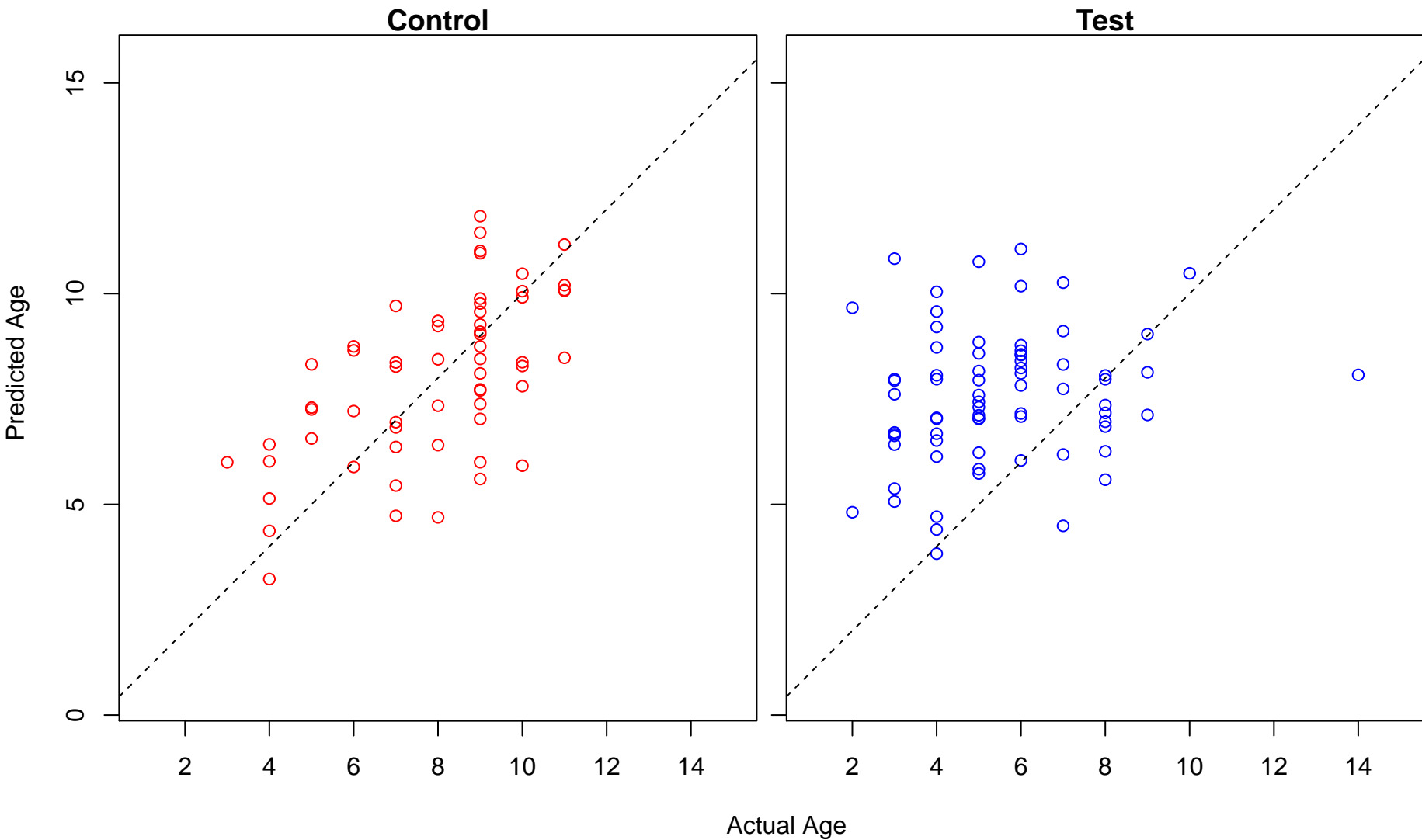
cell cycle arrest (Score: 1.502390)



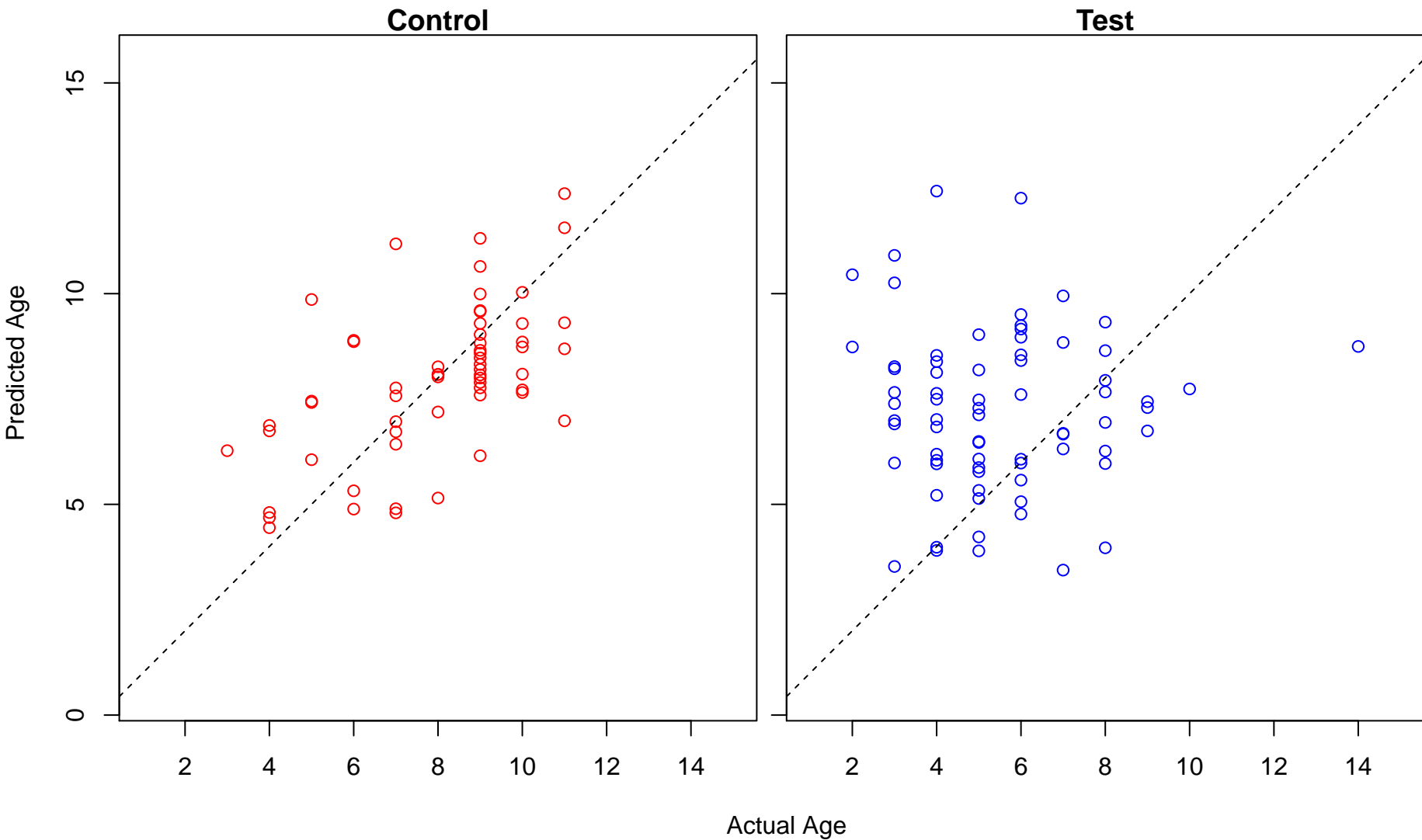
morphogenesis of a polarized epithelium (Score: 1.501375)



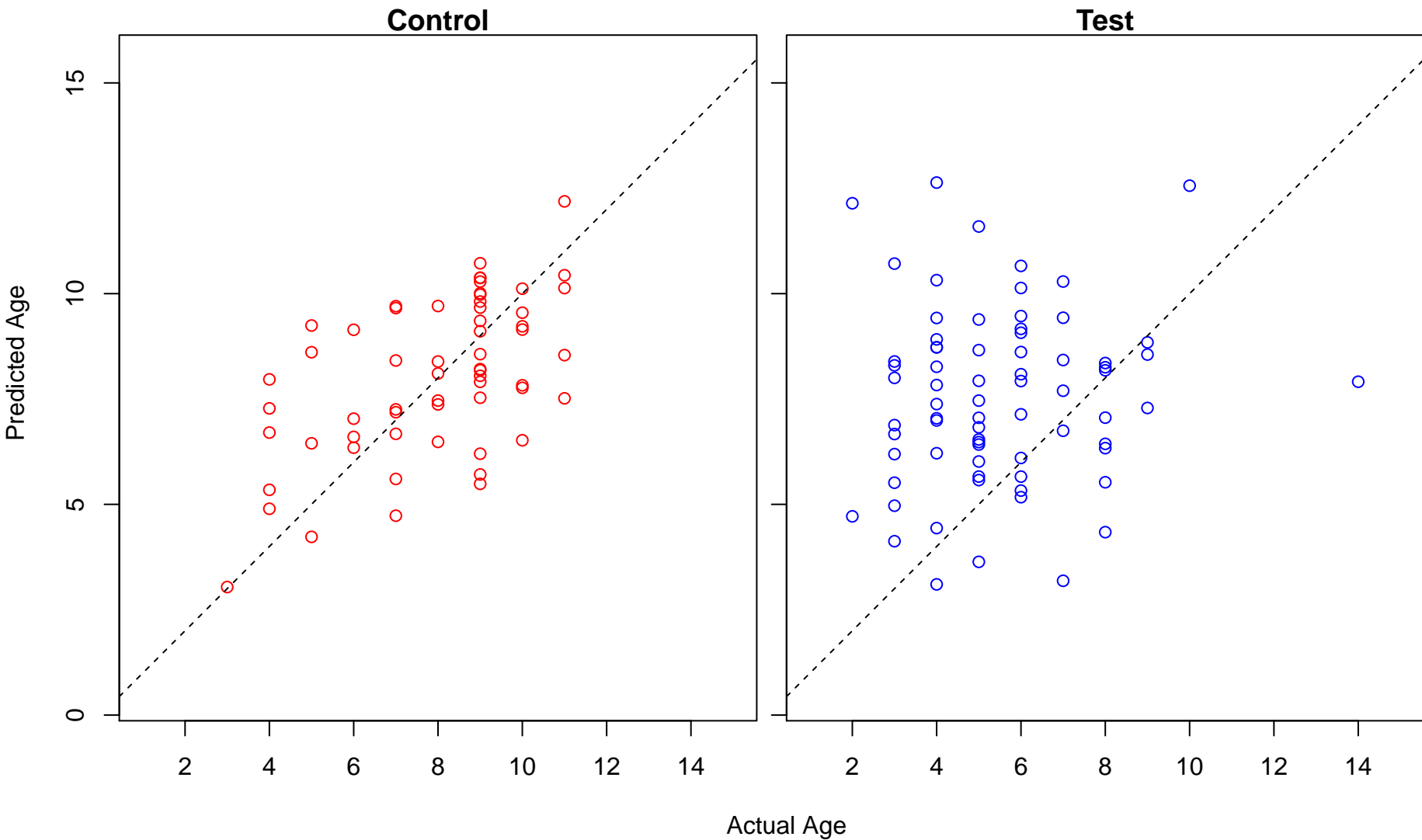
intrinsic apoptotic signaling pathway (Score: 1.501043)



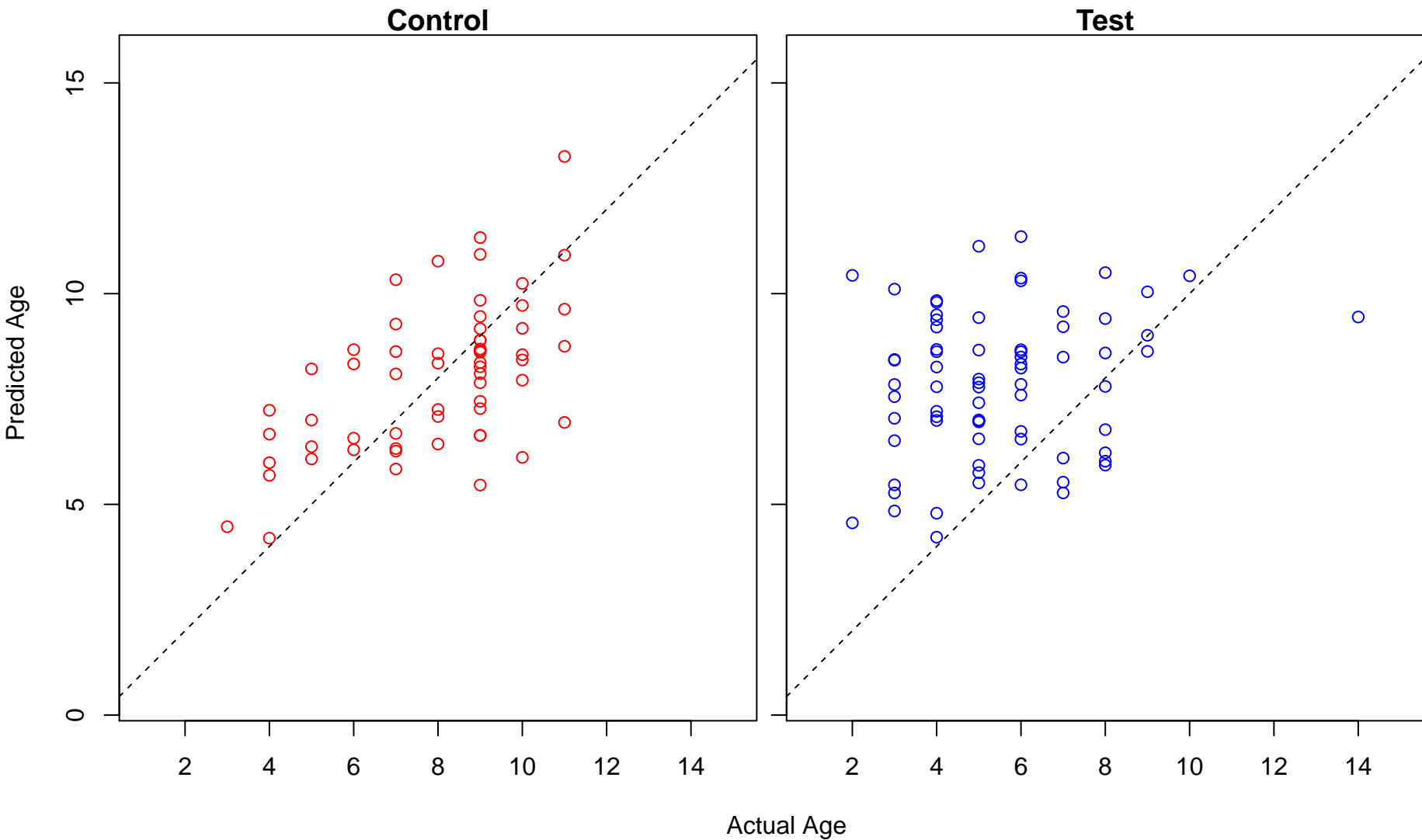
nucleotide biosynthetic process (Score: 1.501027)



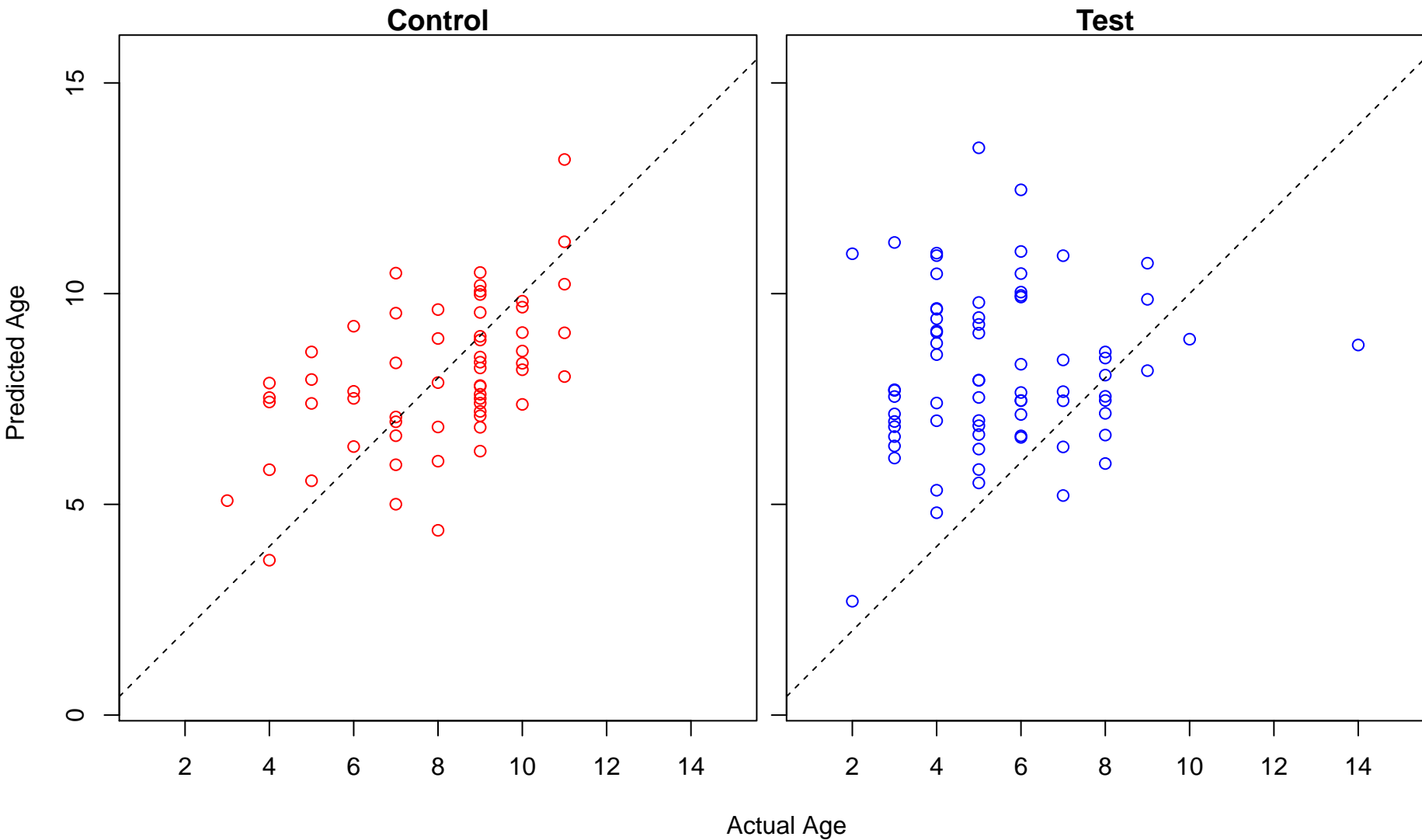
positive regulation of apoptotic signaling pathway (Score: 1.496082)



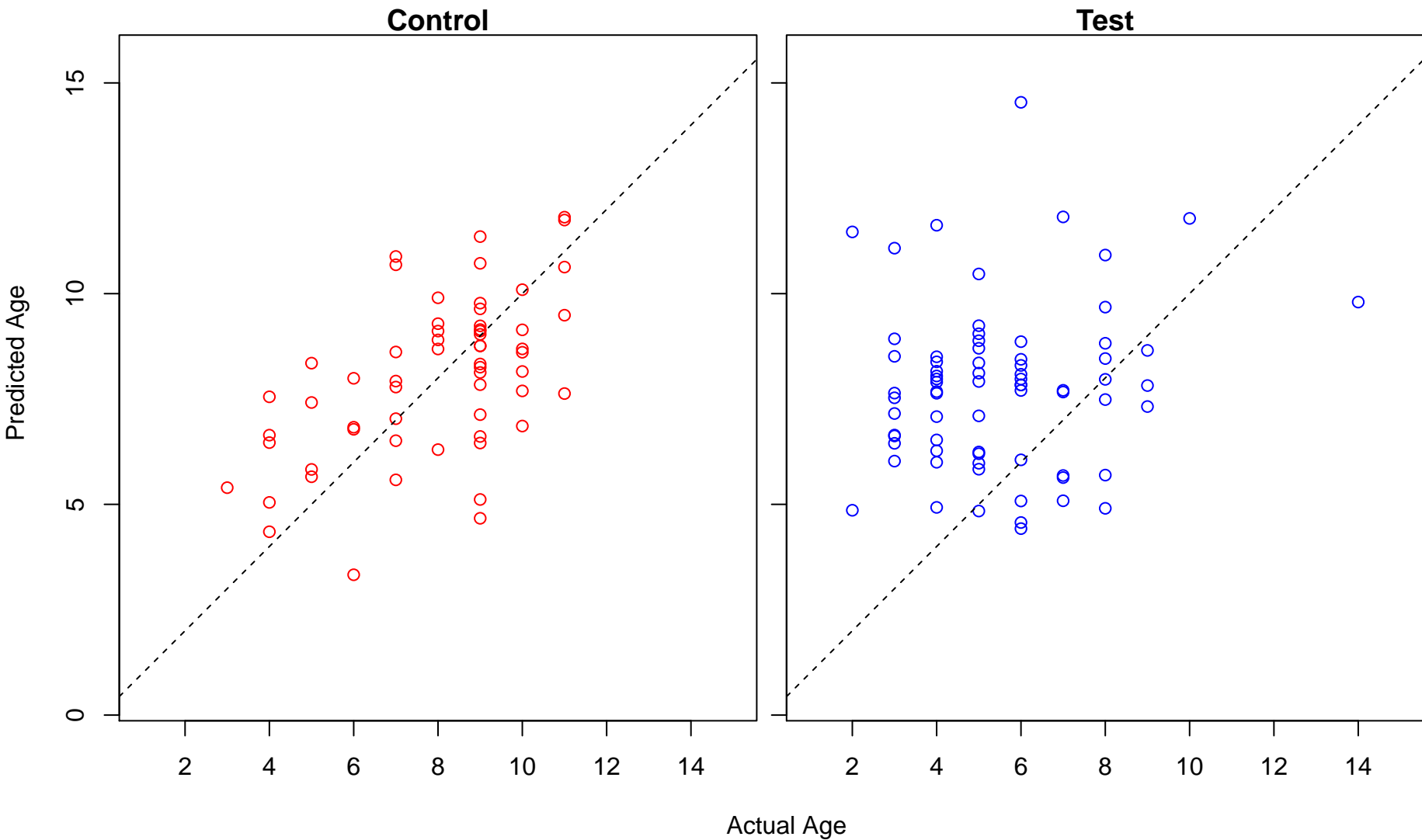
positive regulation of response to external stimulus (Score: 1.494261)



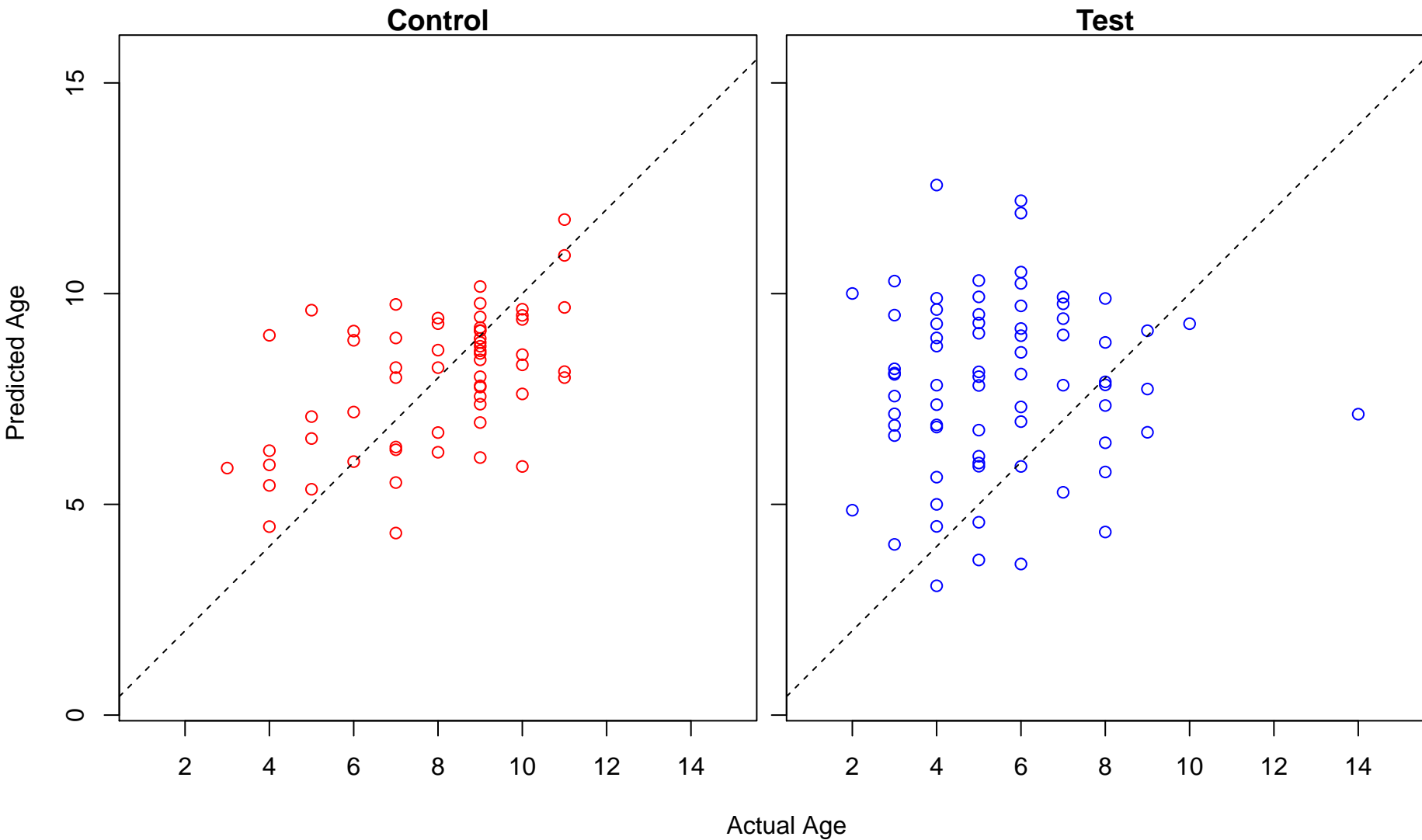
positive regulation of protein modification process (Score: 1.491620)



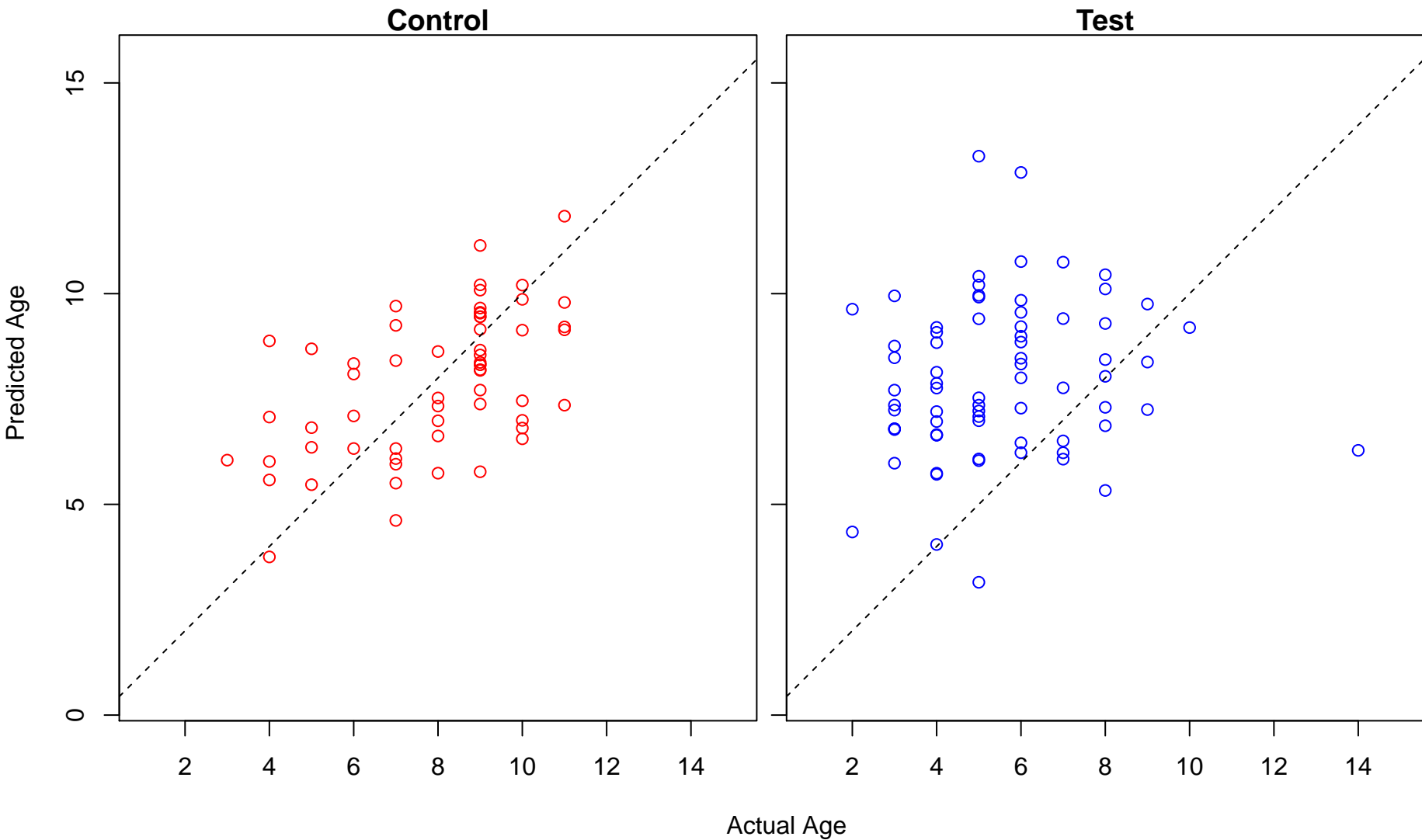
positive regulation of cysteine-type endopeptidase activity (Score: 1.486461)



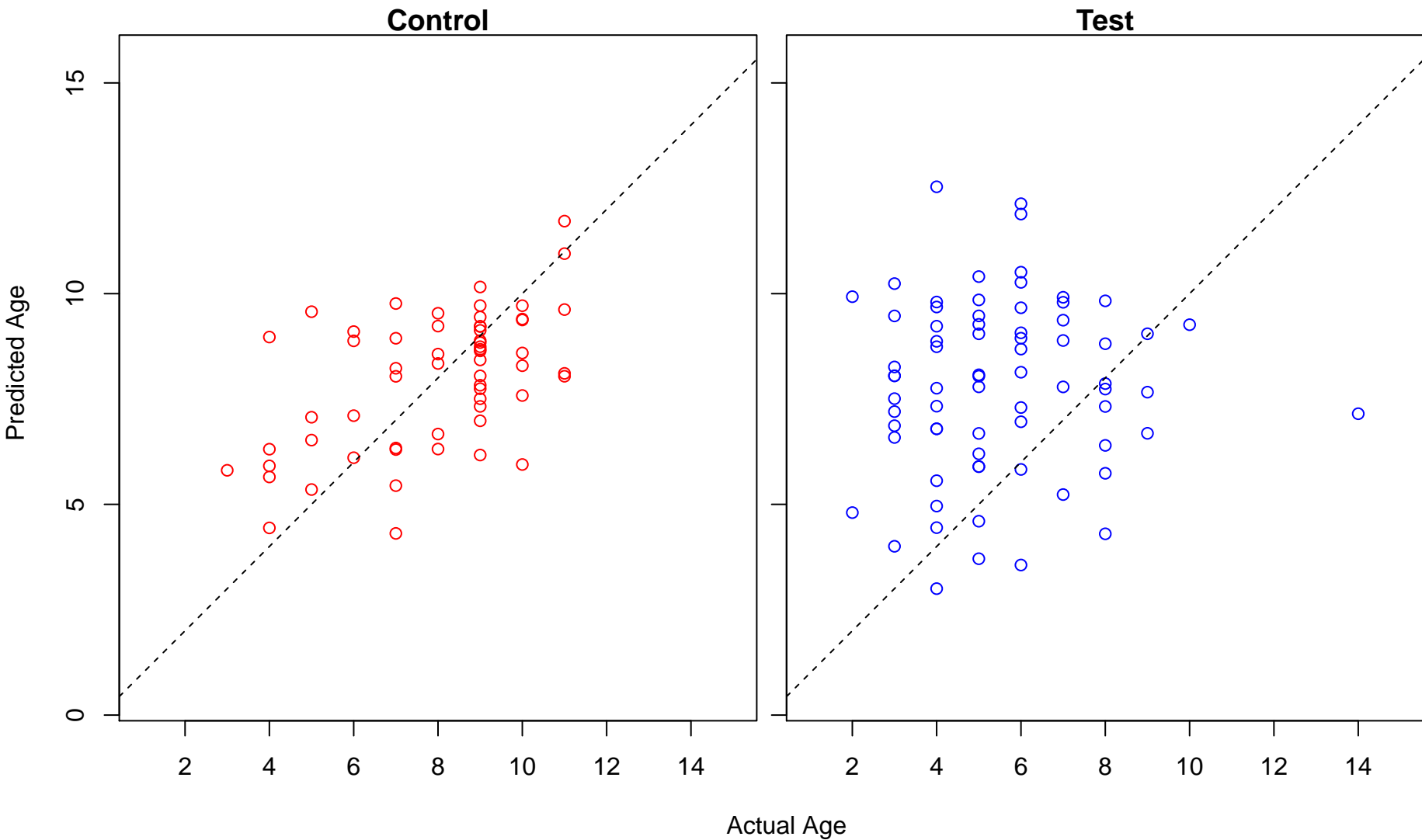
glycerophospholipid biosynthetic process (Score: 1.485979)



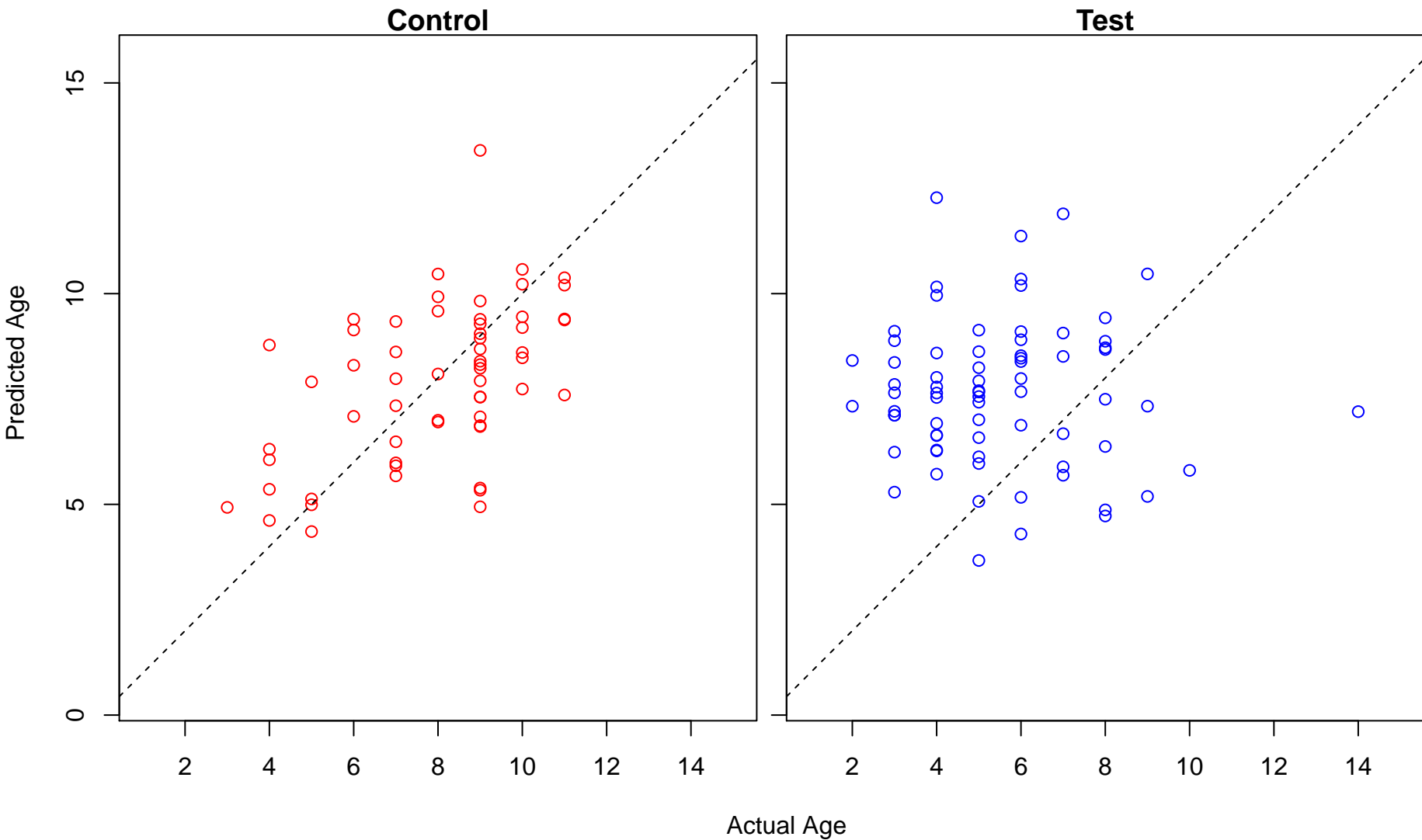
chondroitin sulfate catabolic process (Score: 1.483709)



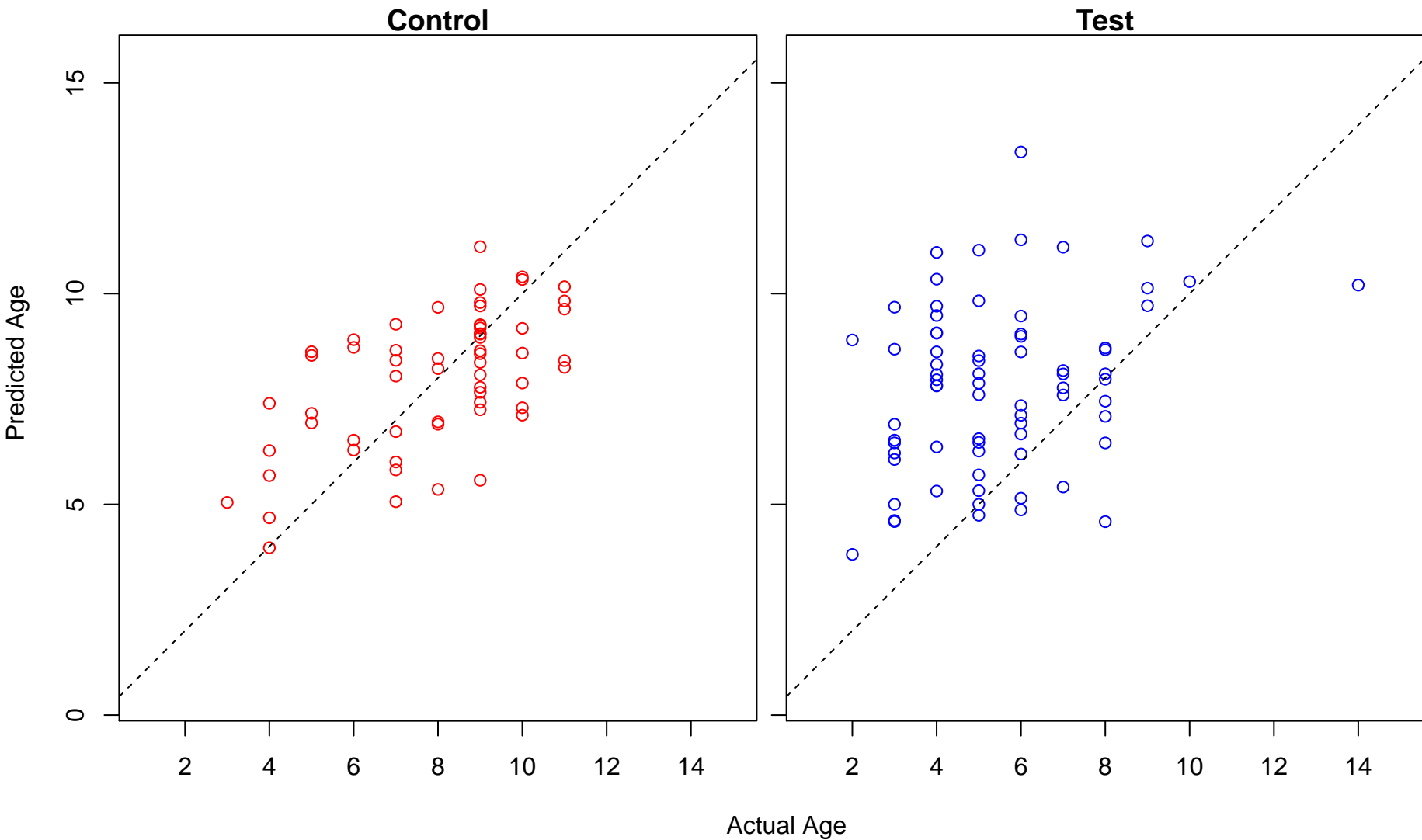
phospholipid biosynthetic process (Score: 1.478751)



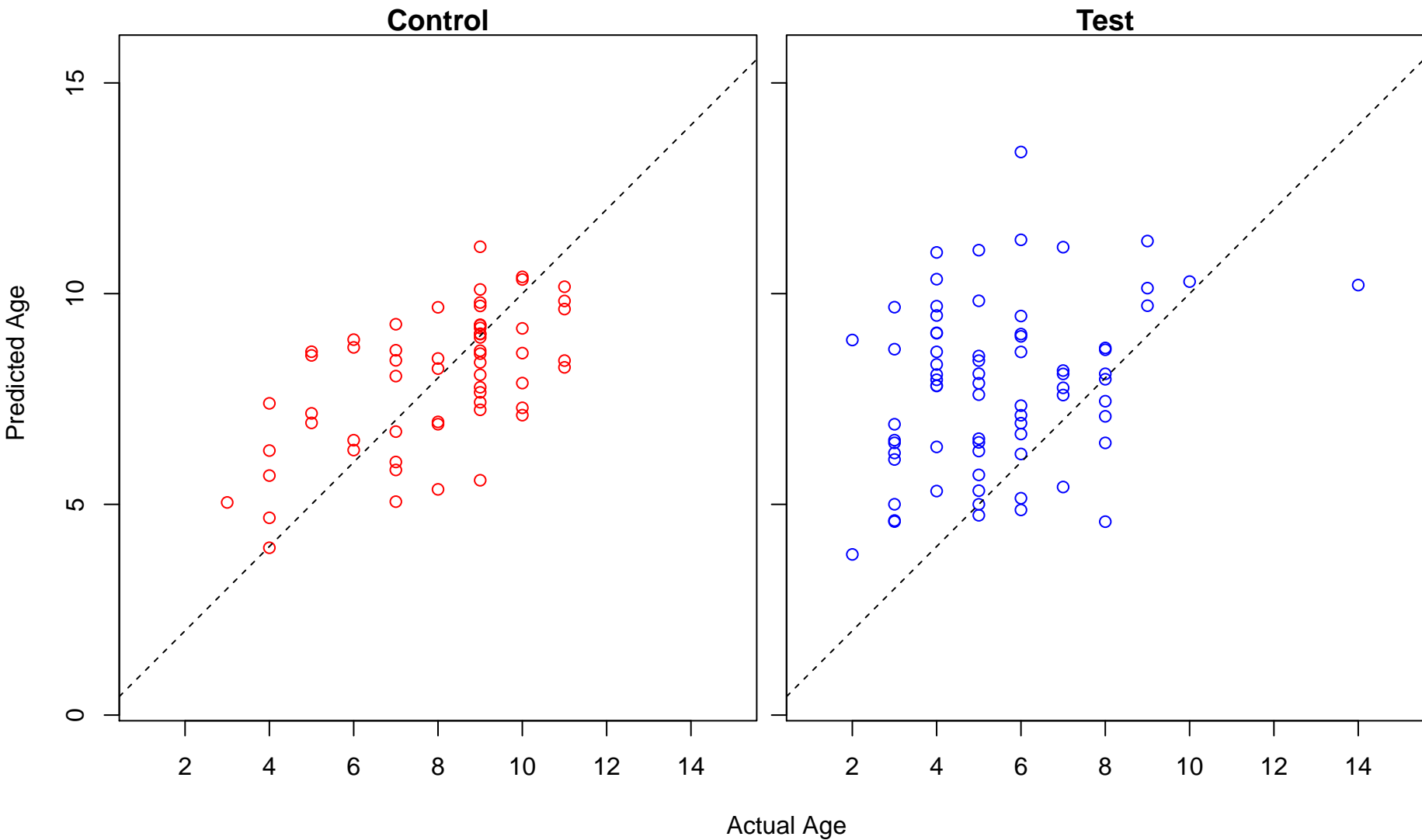
ovarian follicle development (Score: 1.478259)



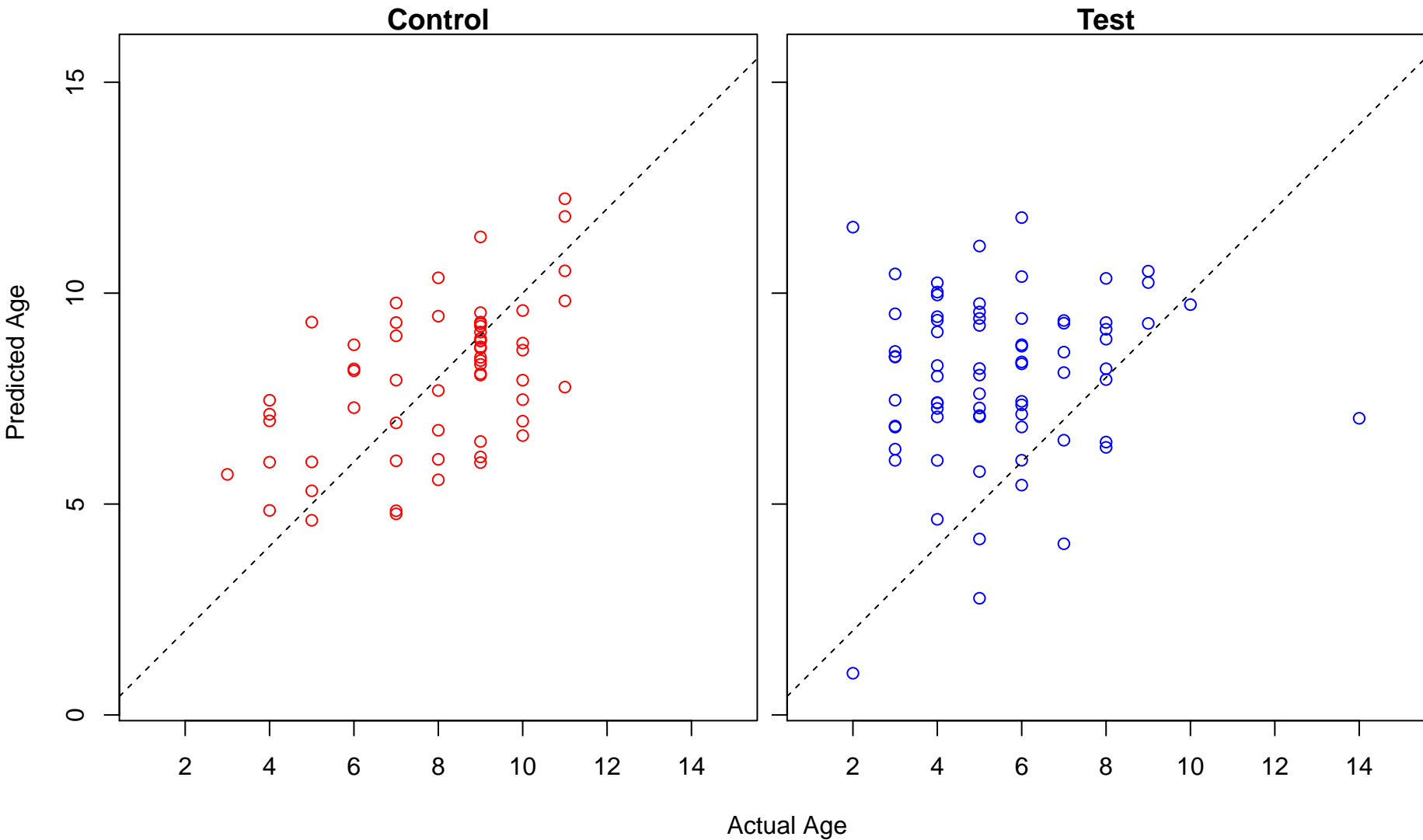
chemotaxis (Score: 1.475528)



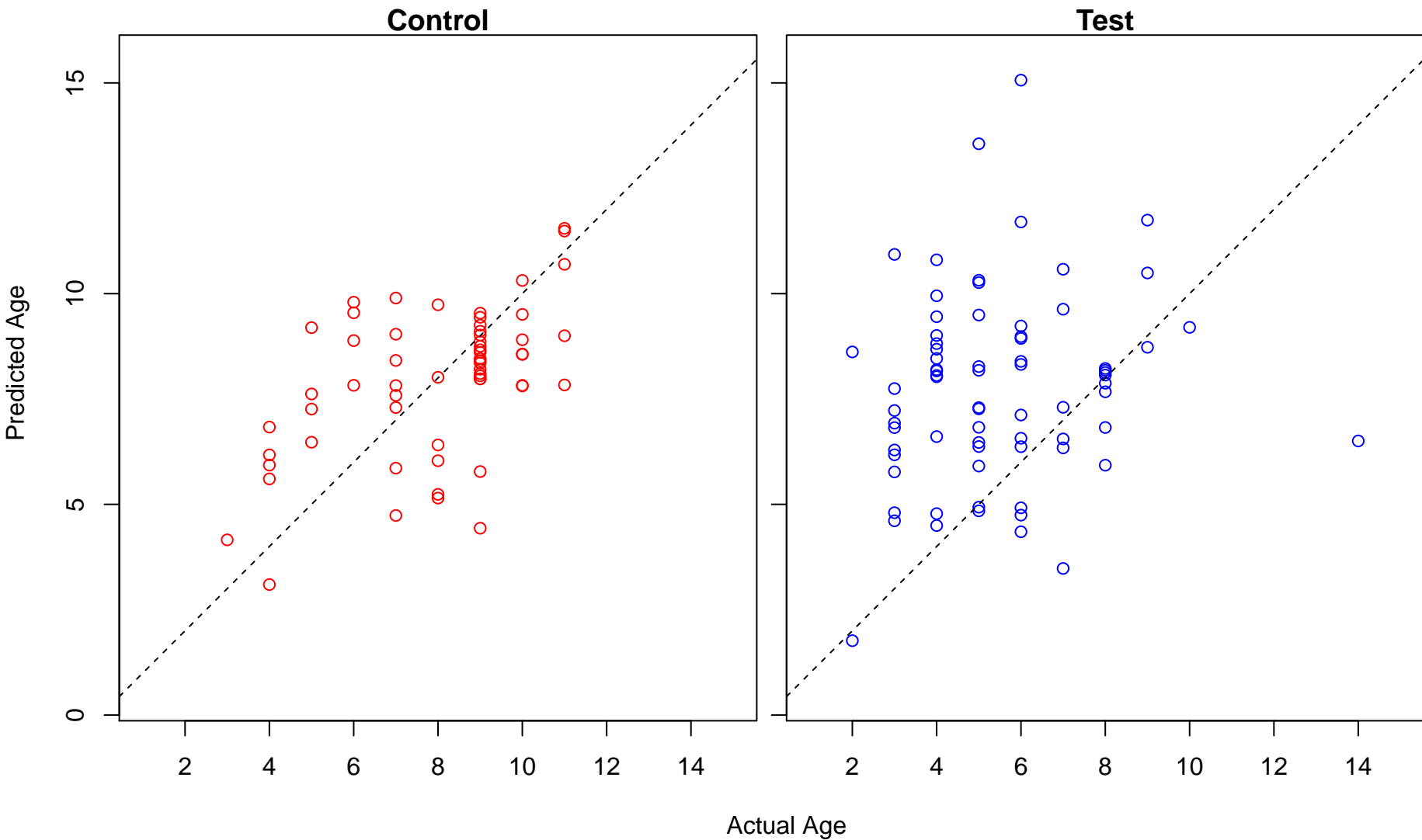
taxis (Score: 1.475528)



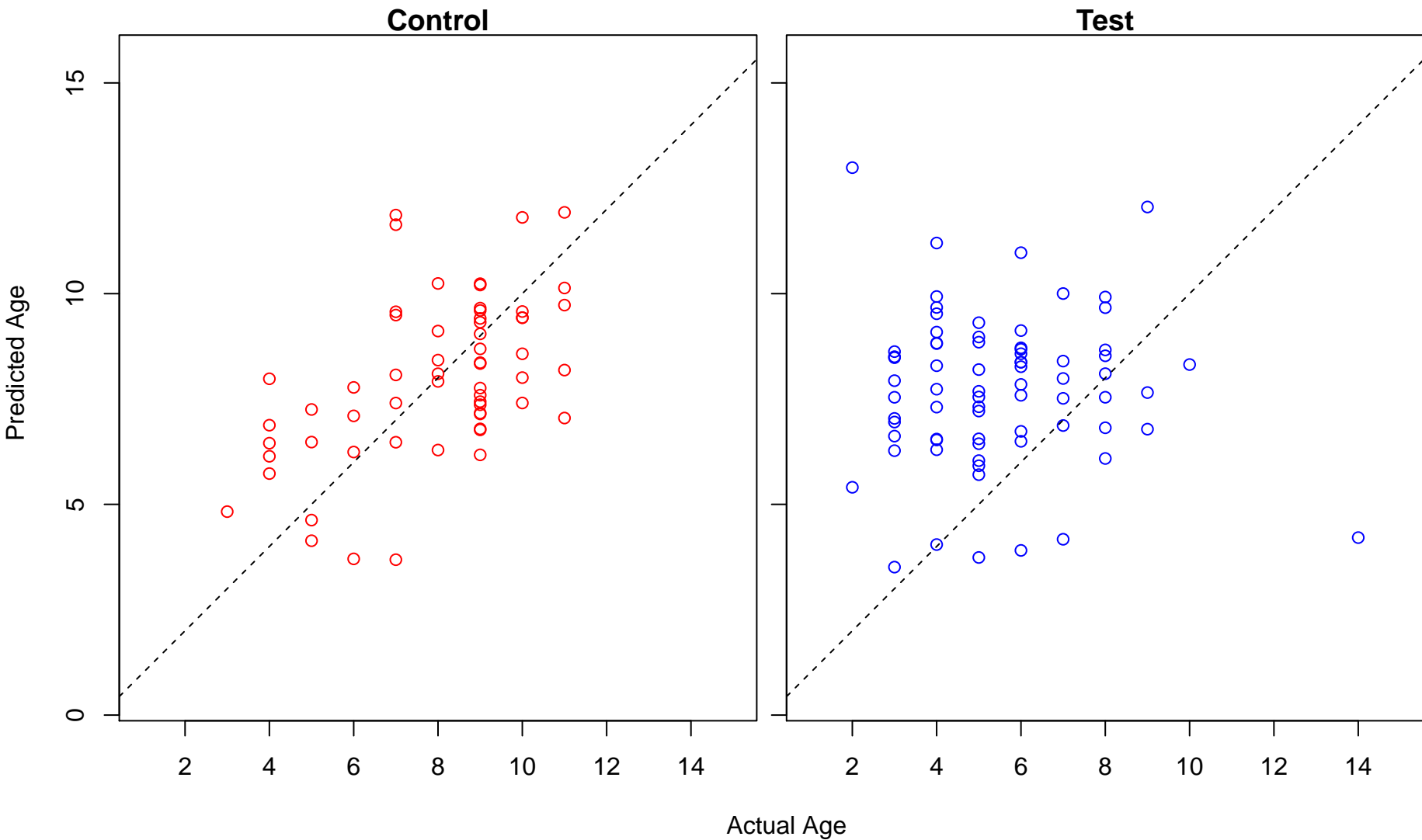
positive regulation of developmental process (Score: 1.475378)



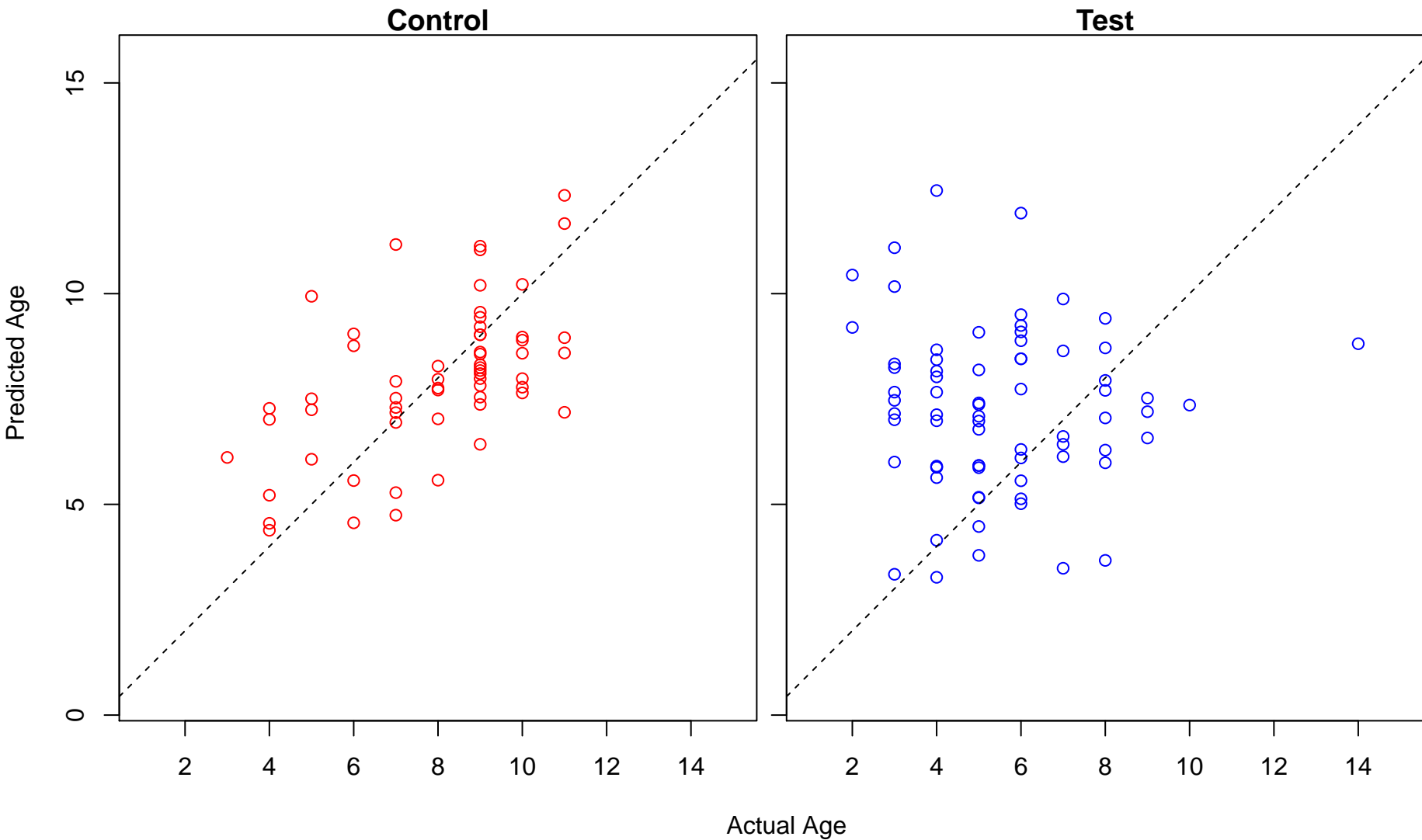
insulin receptor signaling pathway (Score: 1.474983)



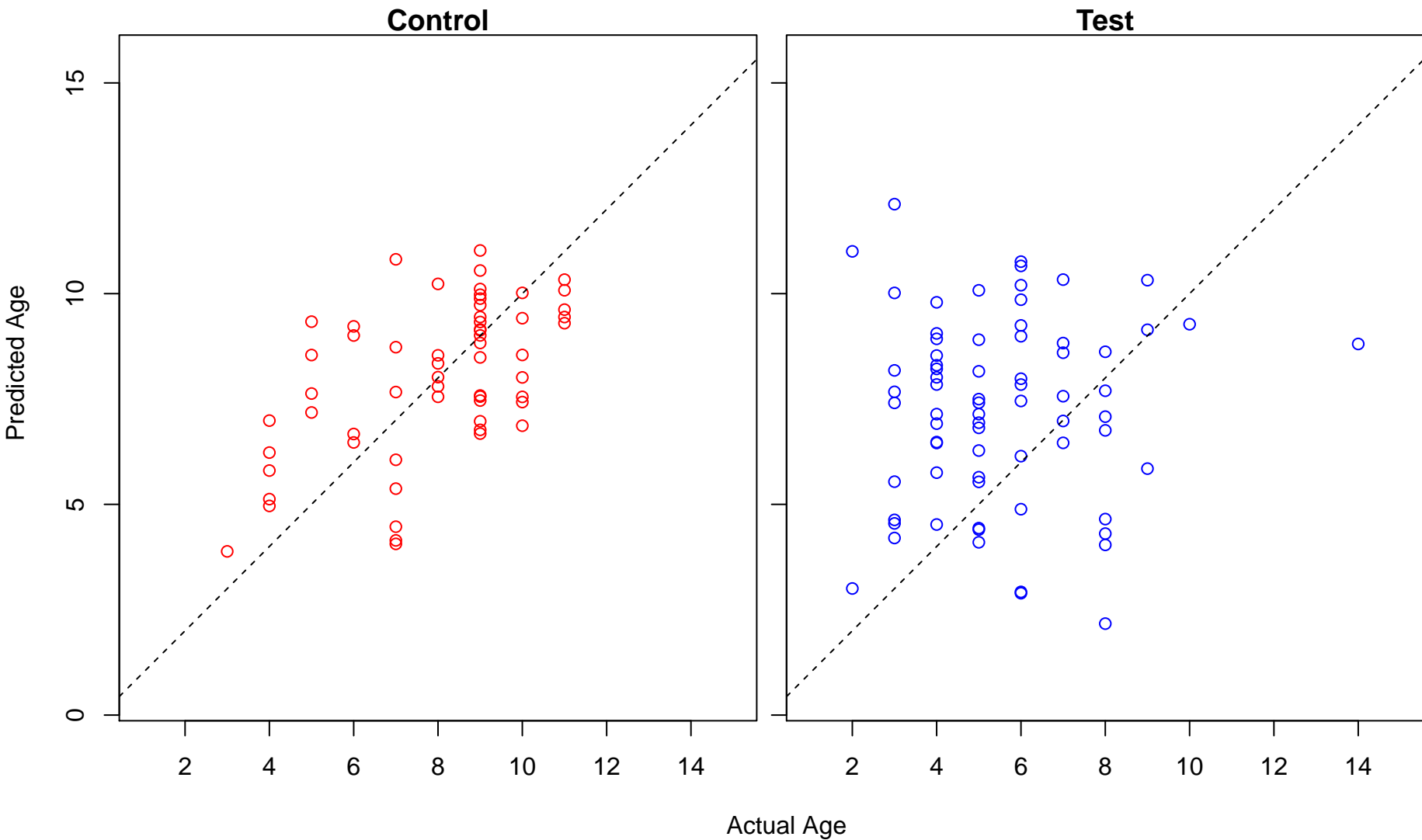
negative regulation of leukocyte proliferation (Score: 1.459236)



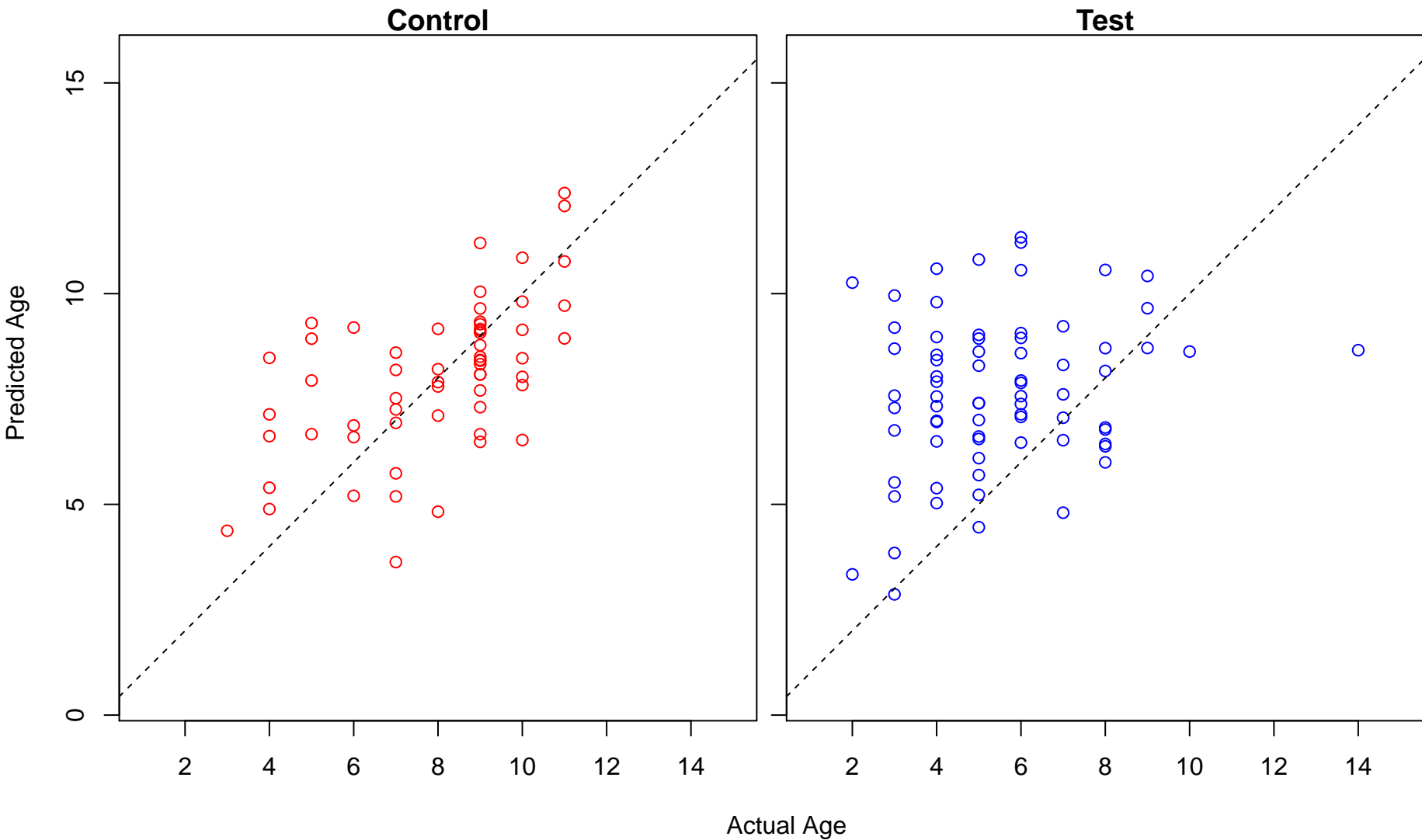
purine nucleotide biosynthetic process (Score: 1.454044)



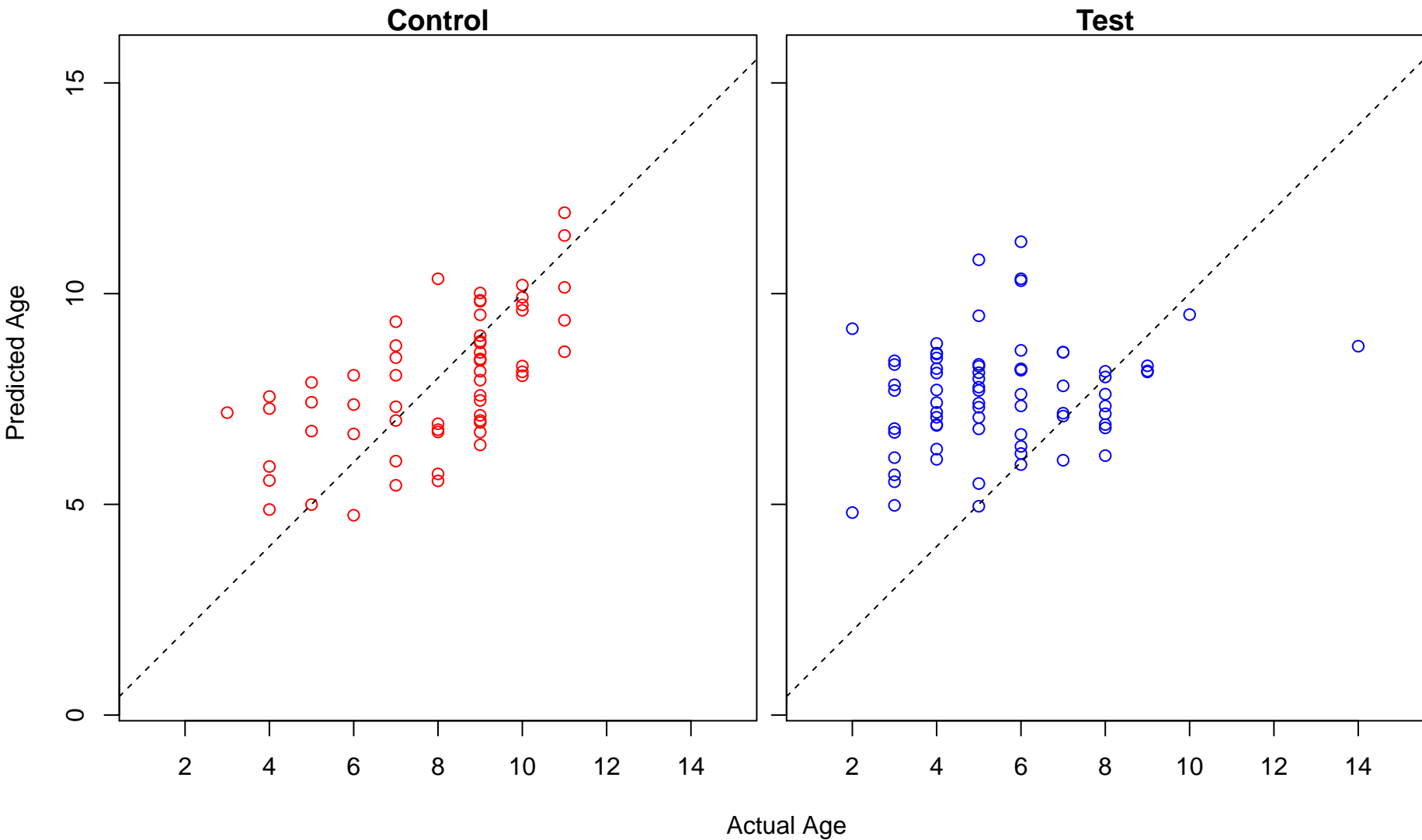
spinal cord development (Score: 1.451405)



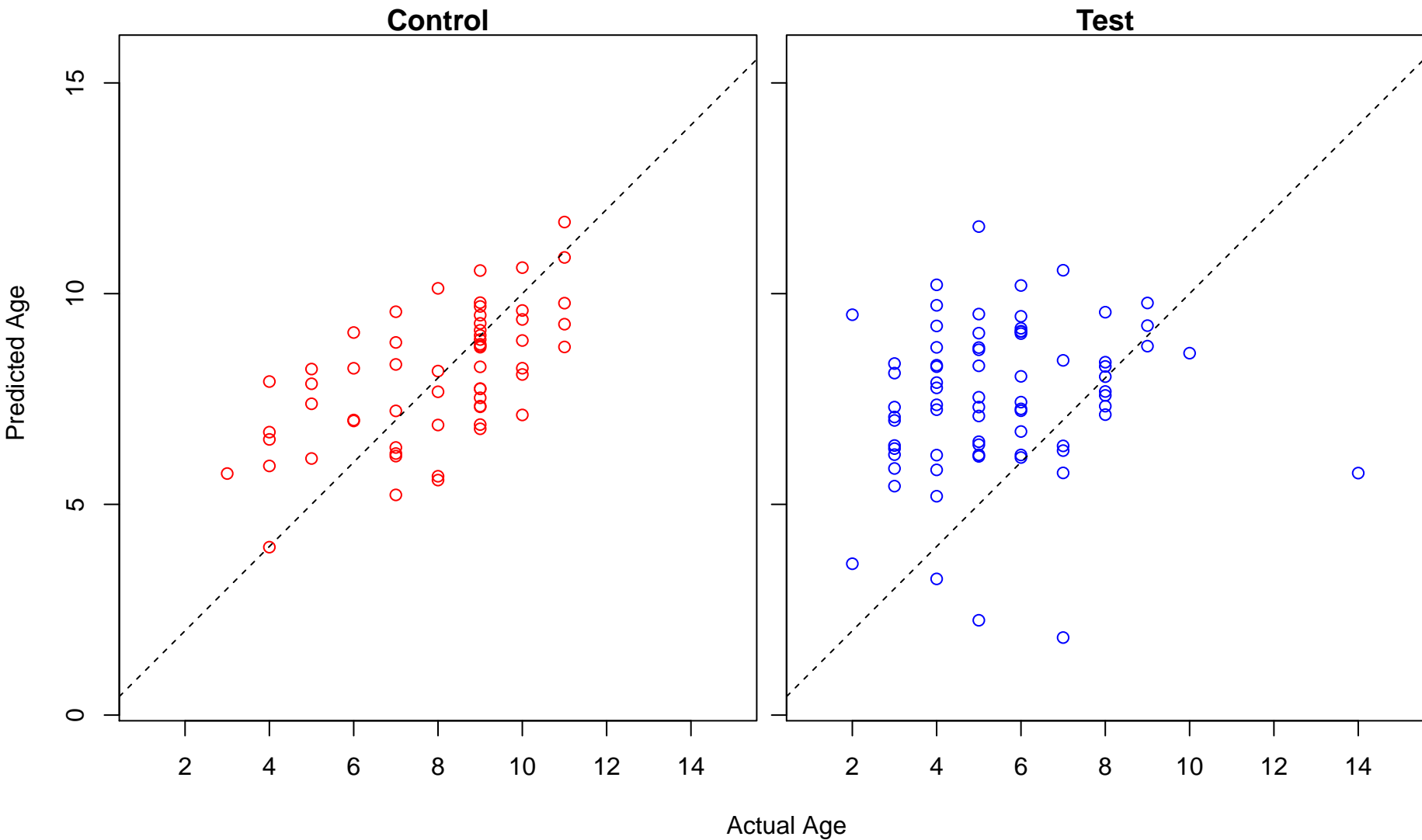
myeloid cell differentiation (Score: 1.450906)



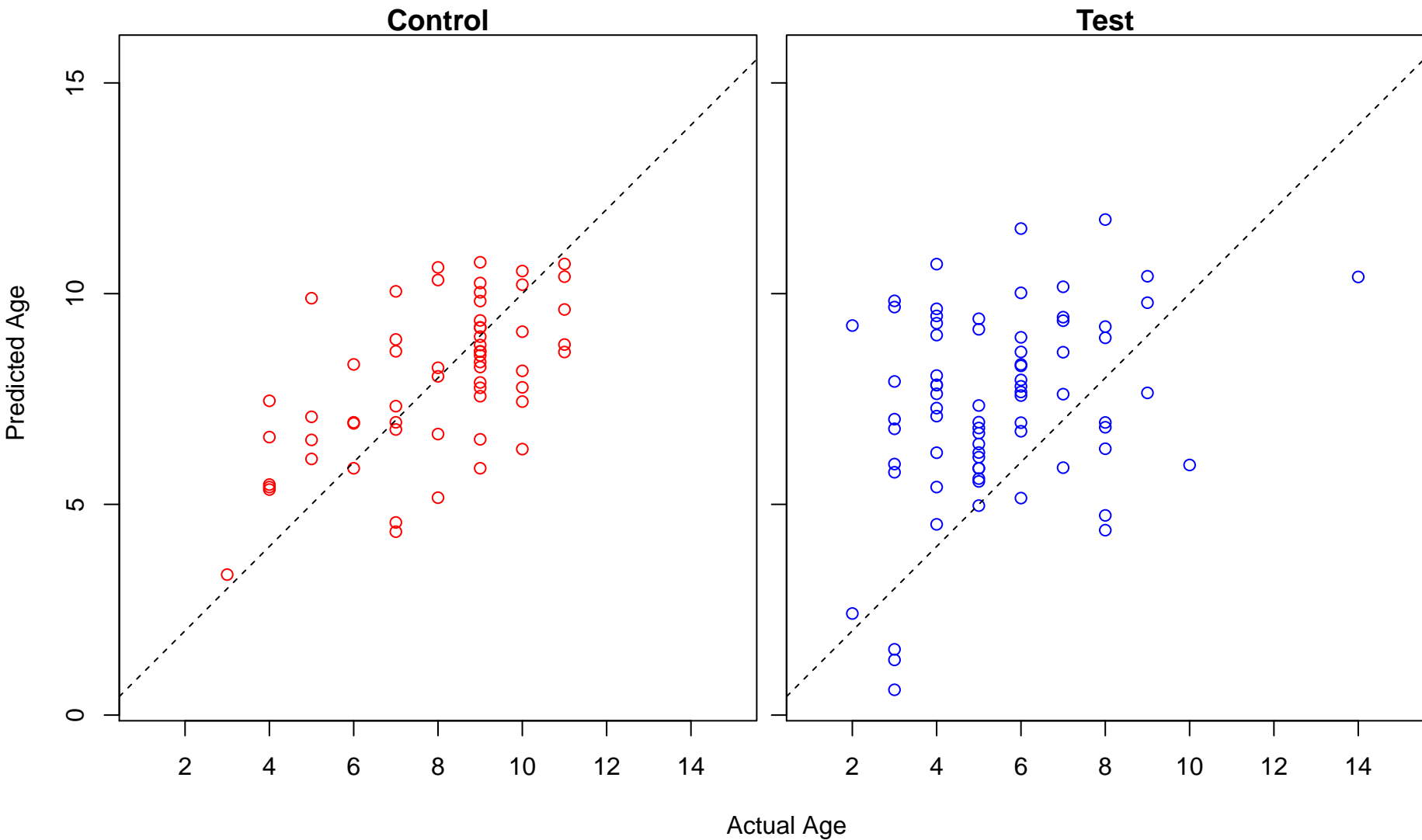
protein localization (Score: 1.449773)



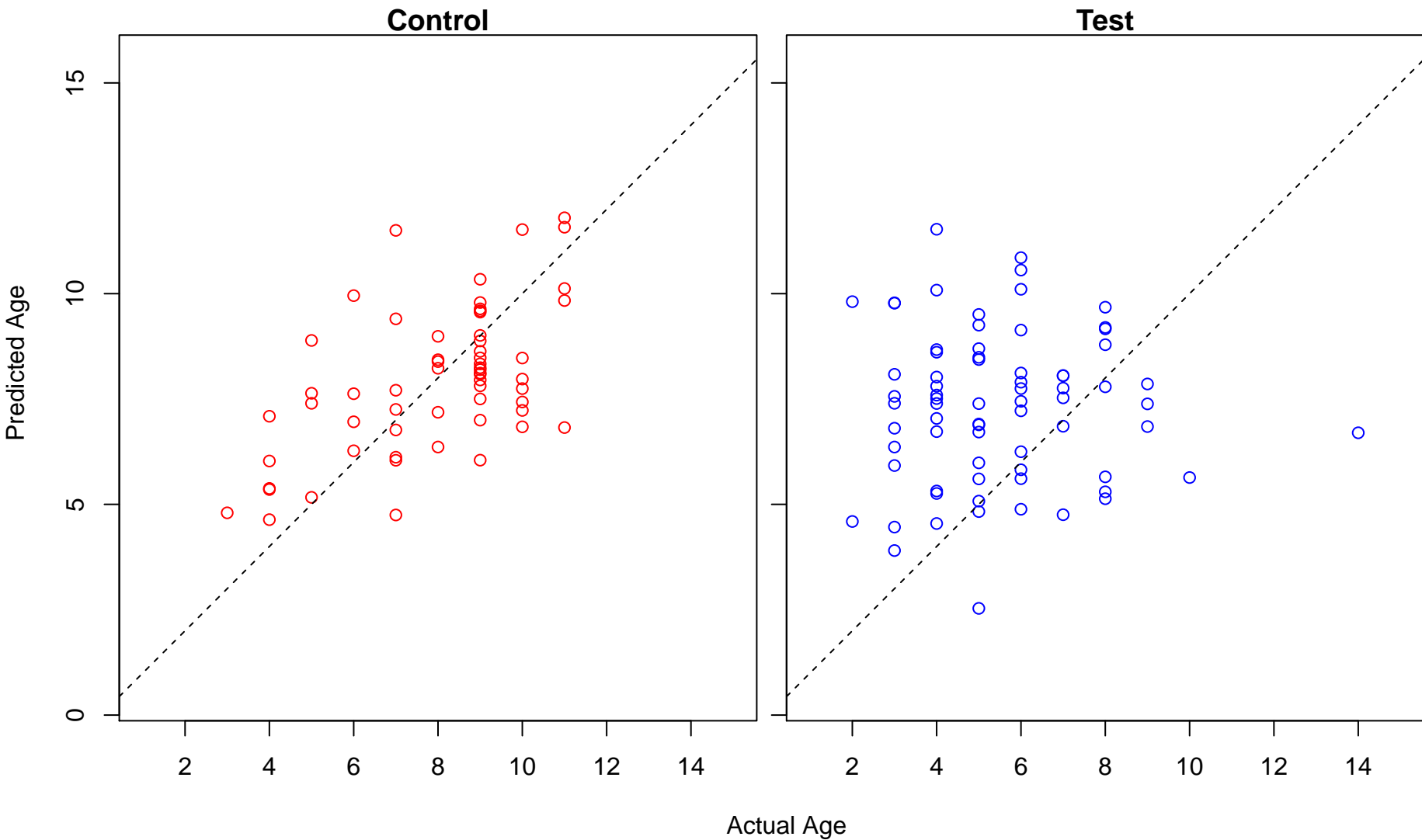
regulation of macromolecule metabolic process (Score: 1.449126)



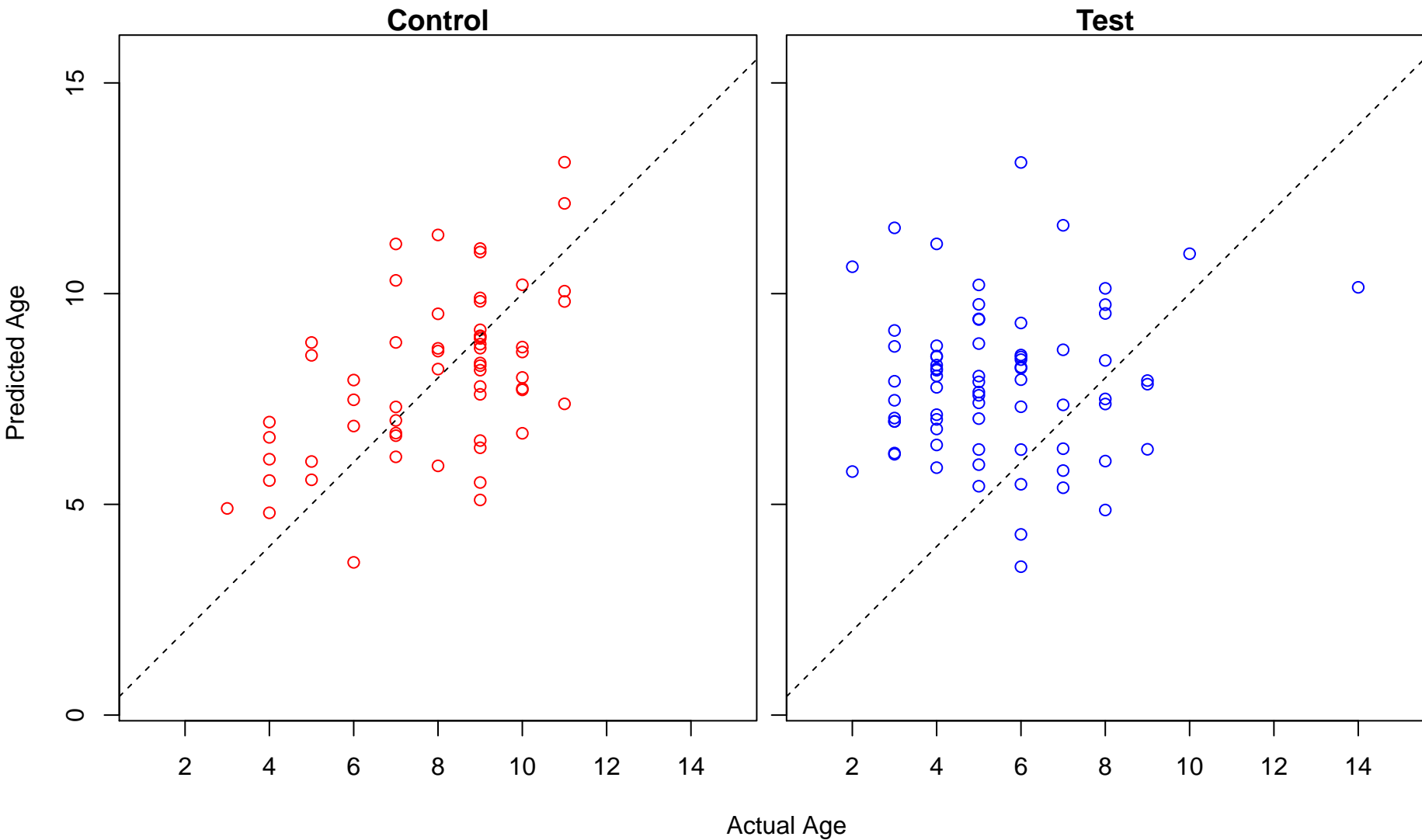
nephron tubule morphogenesis (Score: 1.446181)



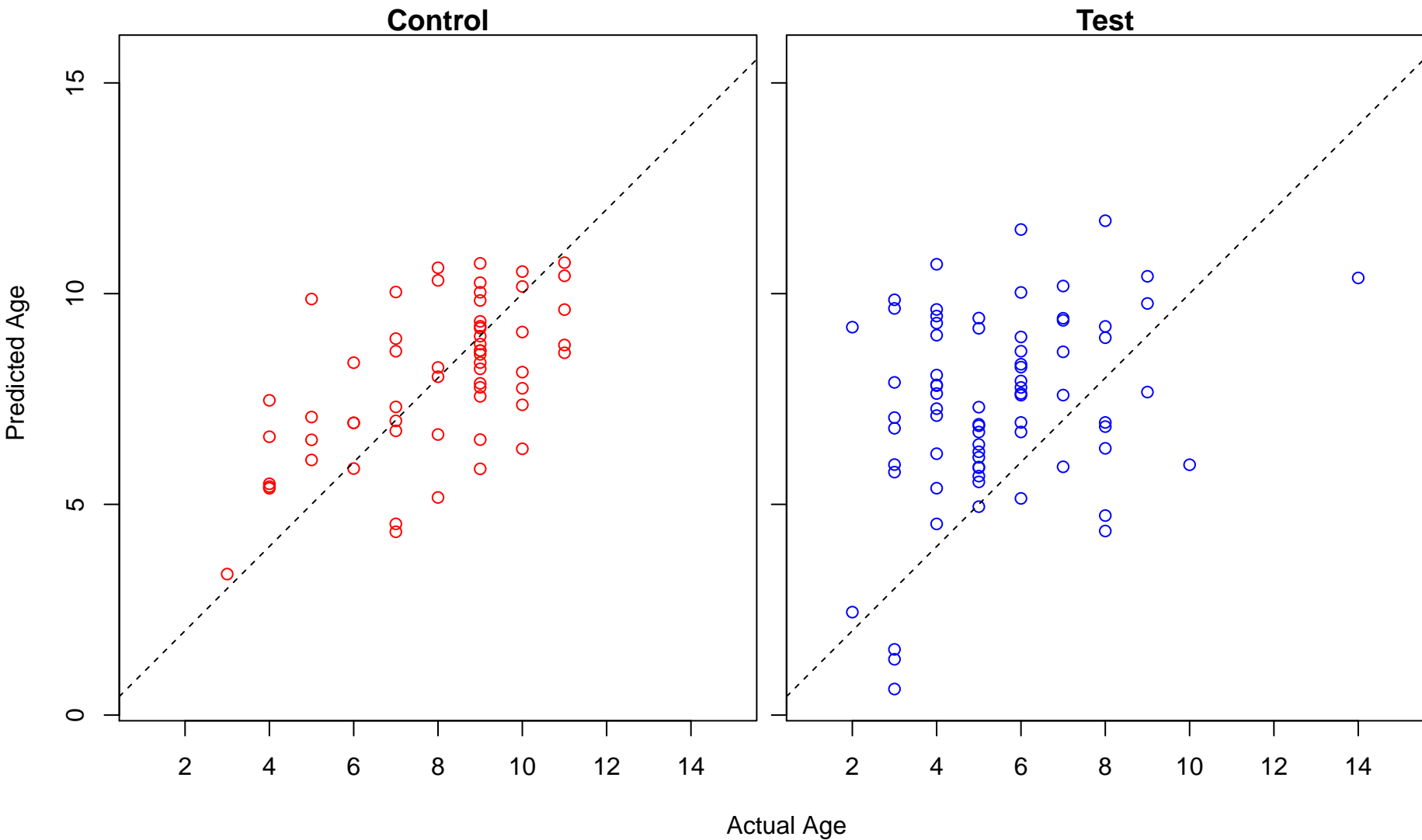
negative regulation of catabolic process (Score: 1.439588)



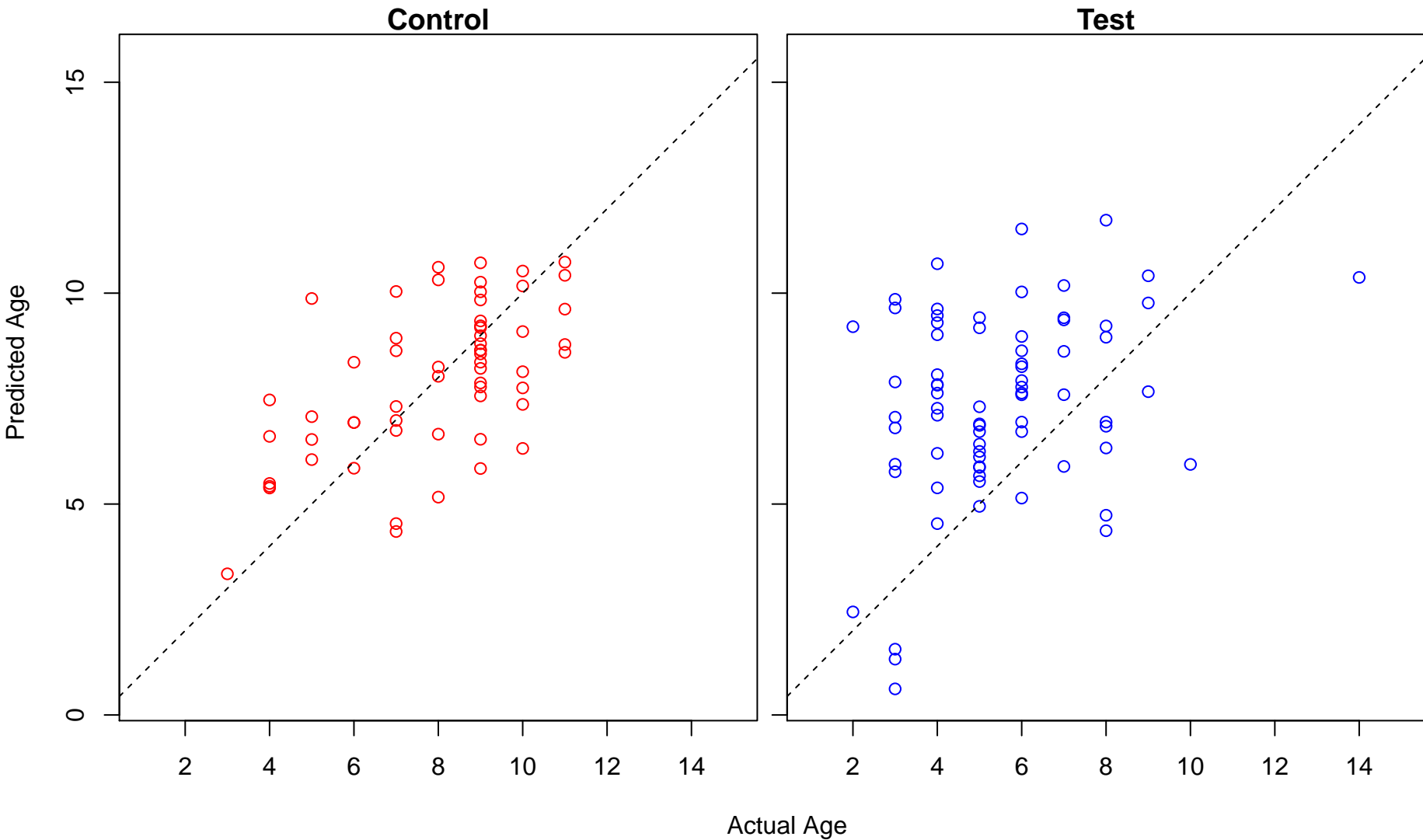
positive regulation of endopeptidase activity (Score: 1.437892)



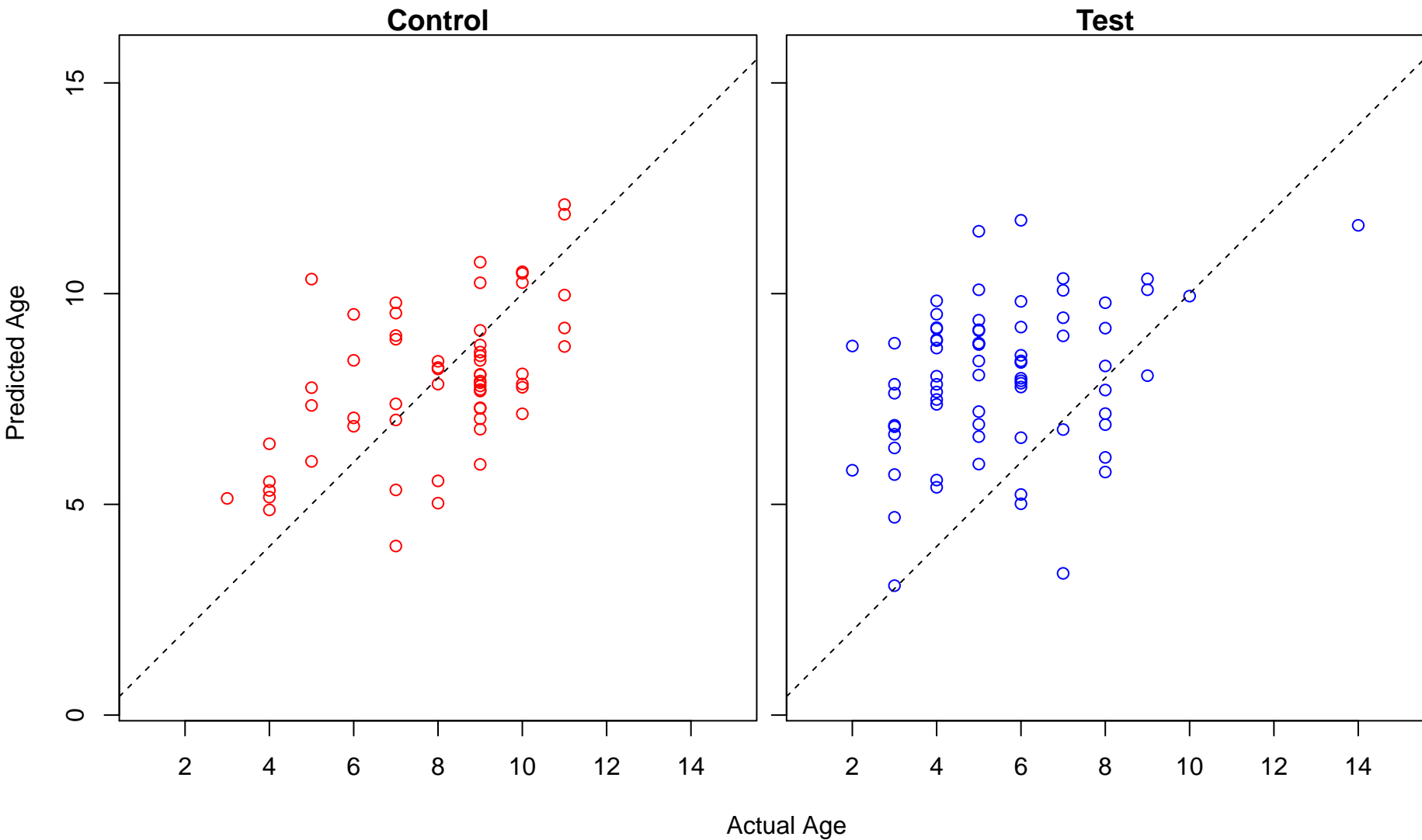
nephron morphogenesis (Score: 1.437429)



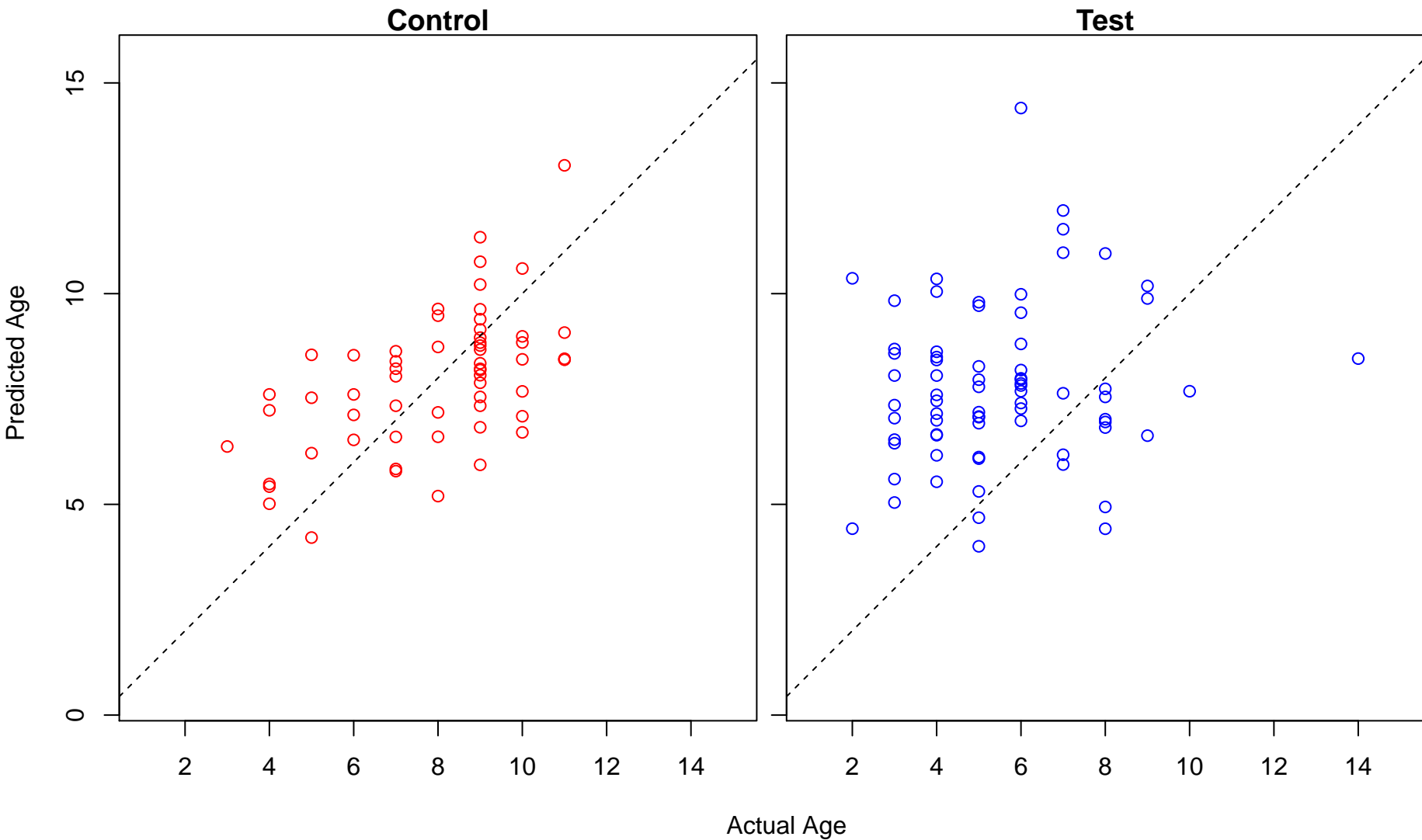
nephron epithelium morphogenesis (Score: 1.437429)



protein acylation (Score: 1.435680)

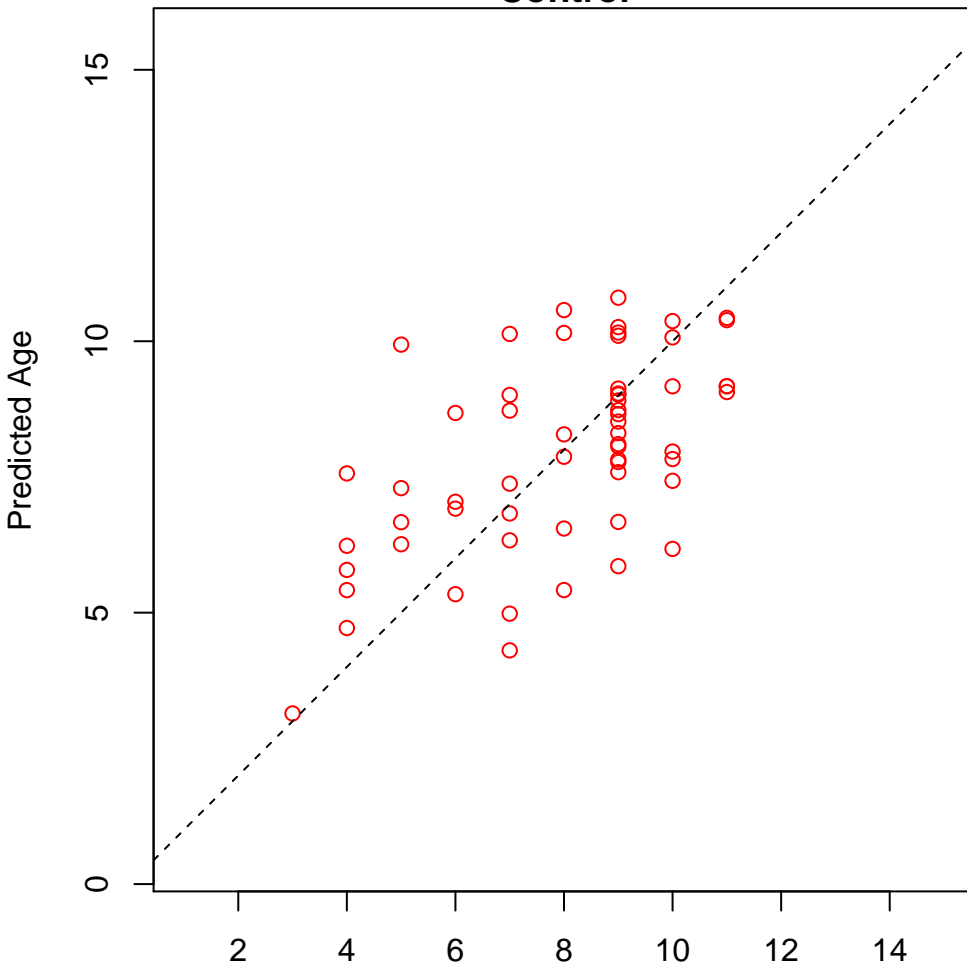


regulation of activated T cell proliferation (Score: 1.433110)

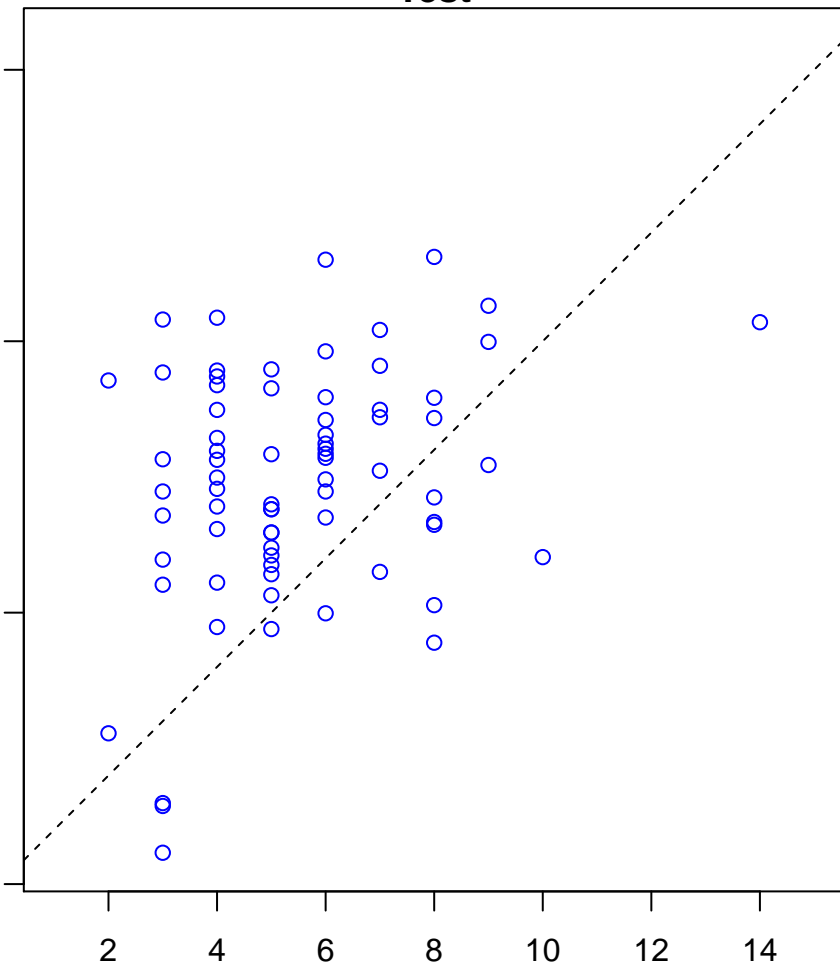


mesonephric tubule morphogenesis (Score: 1.432641)

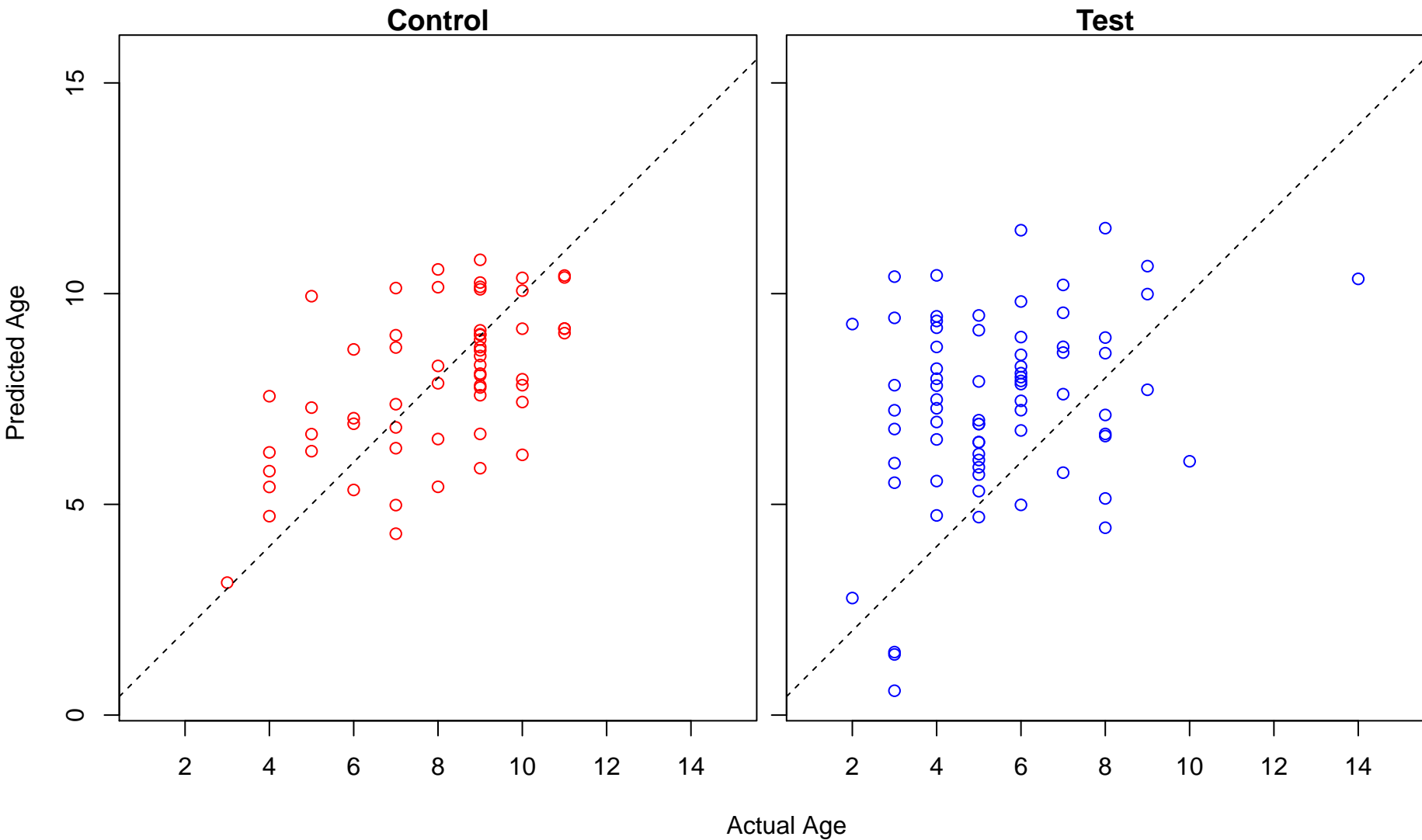
Control



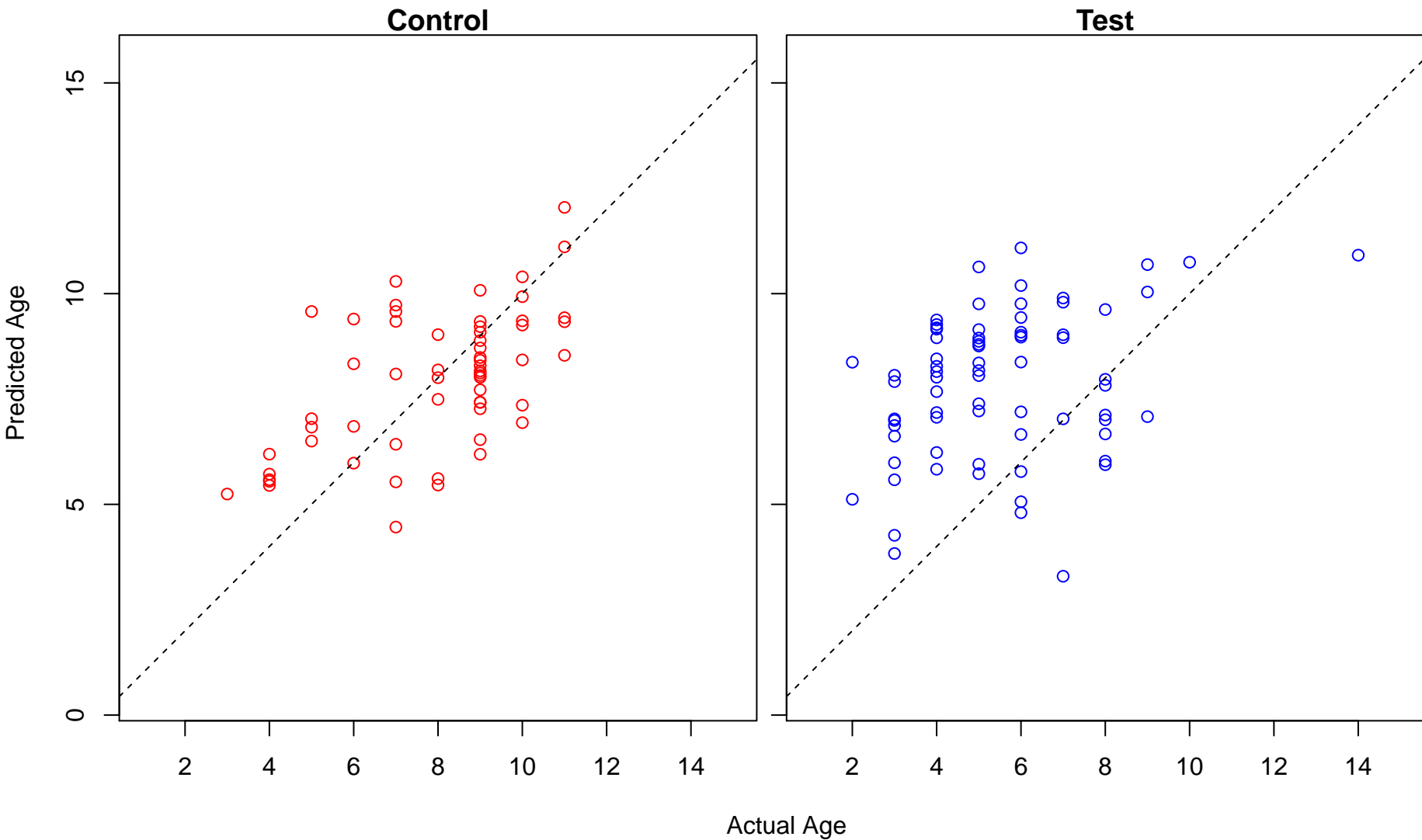
Test



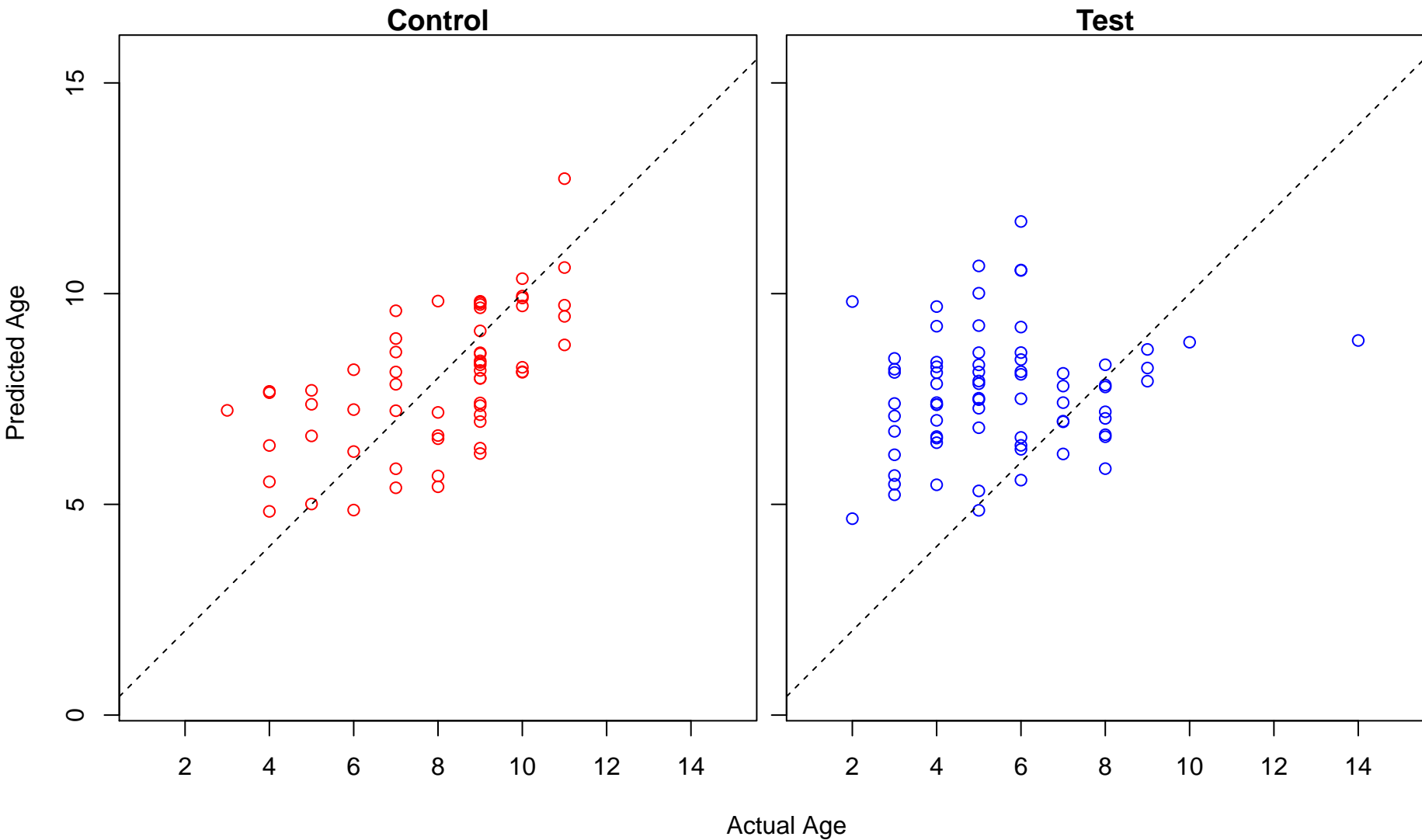
ureteric bud morphogenesis (Score: 1.432279)



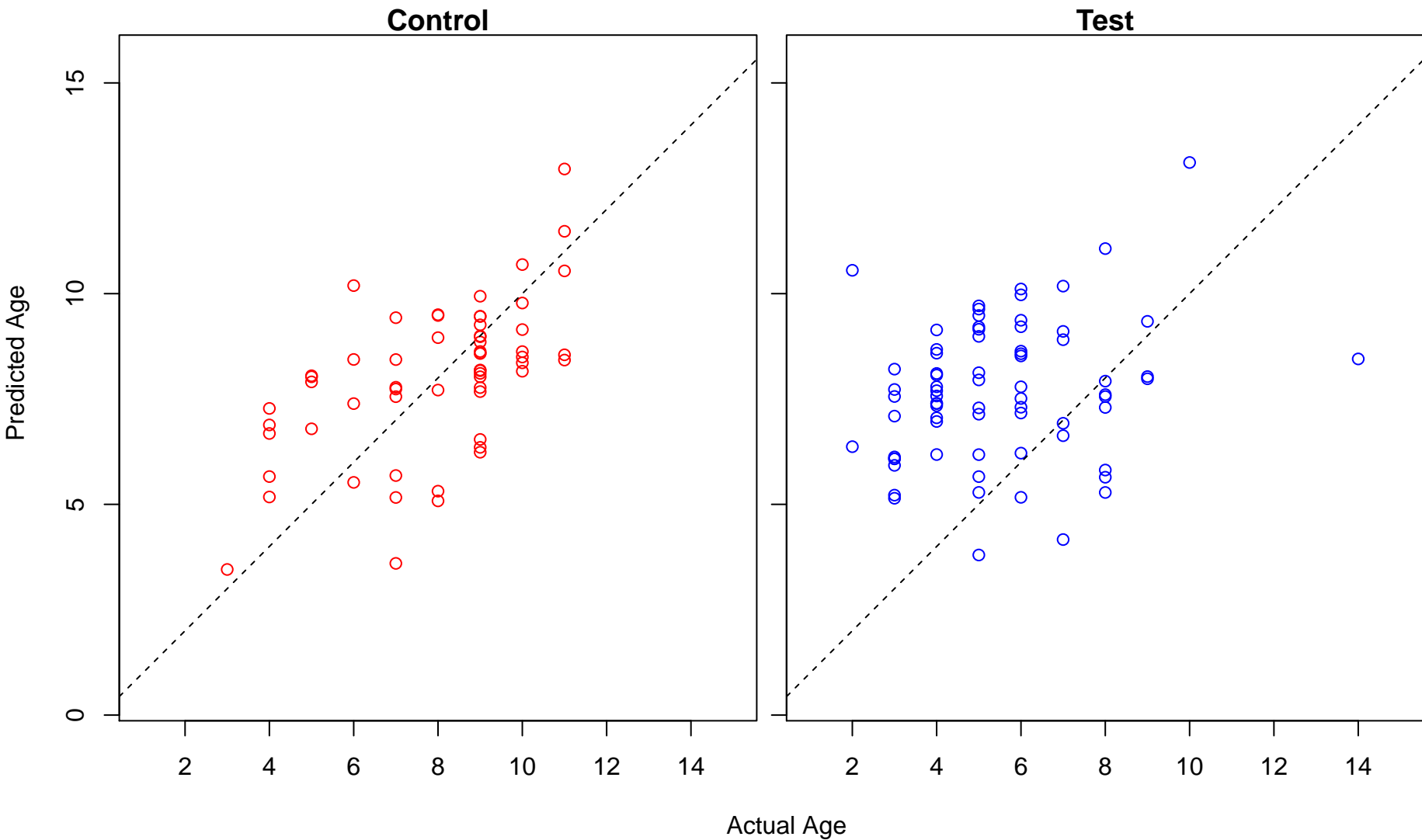
internal peptidyl-lysine acetylation (Score: 1.429152)



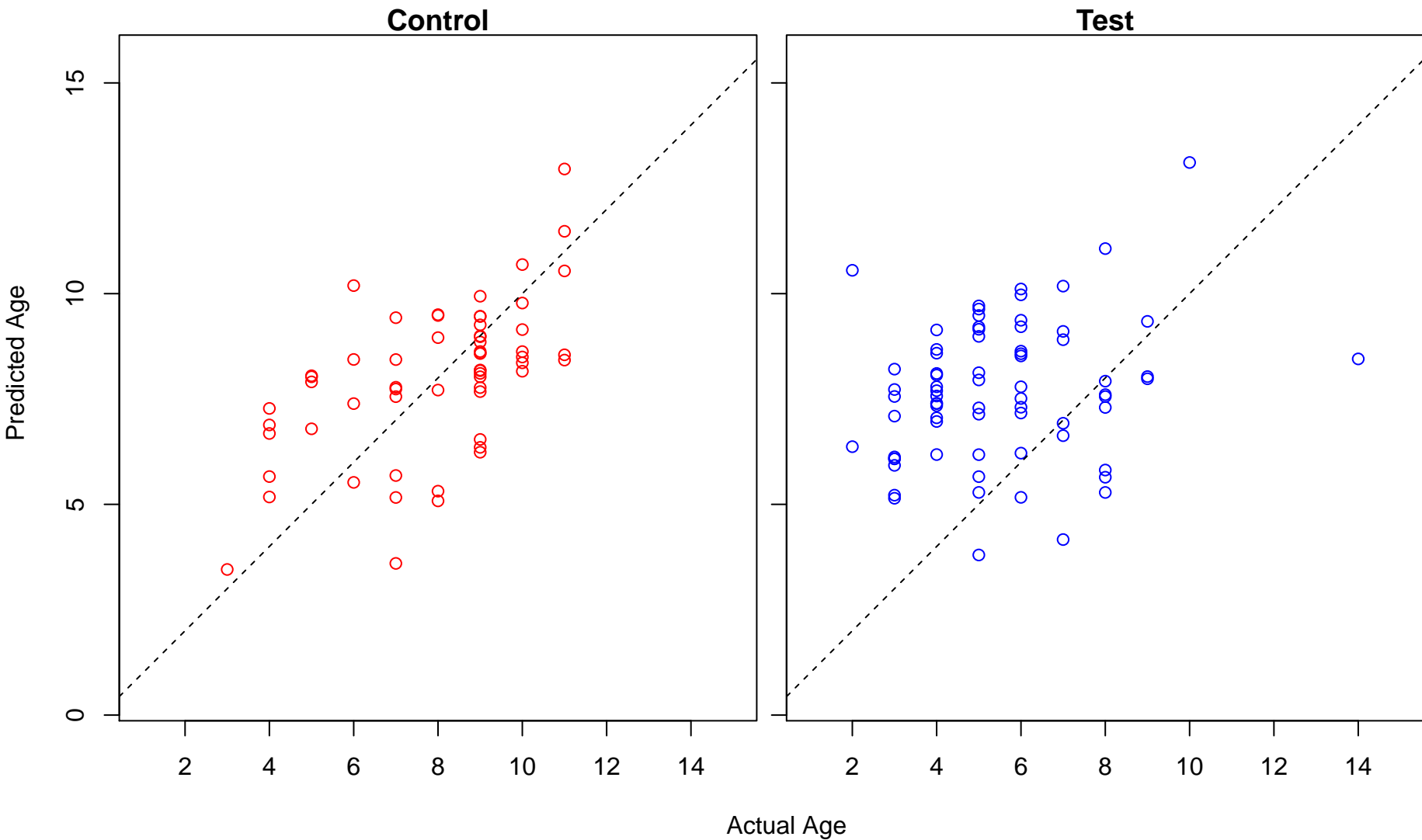
establishment of protein localization (Score: 1.427663)



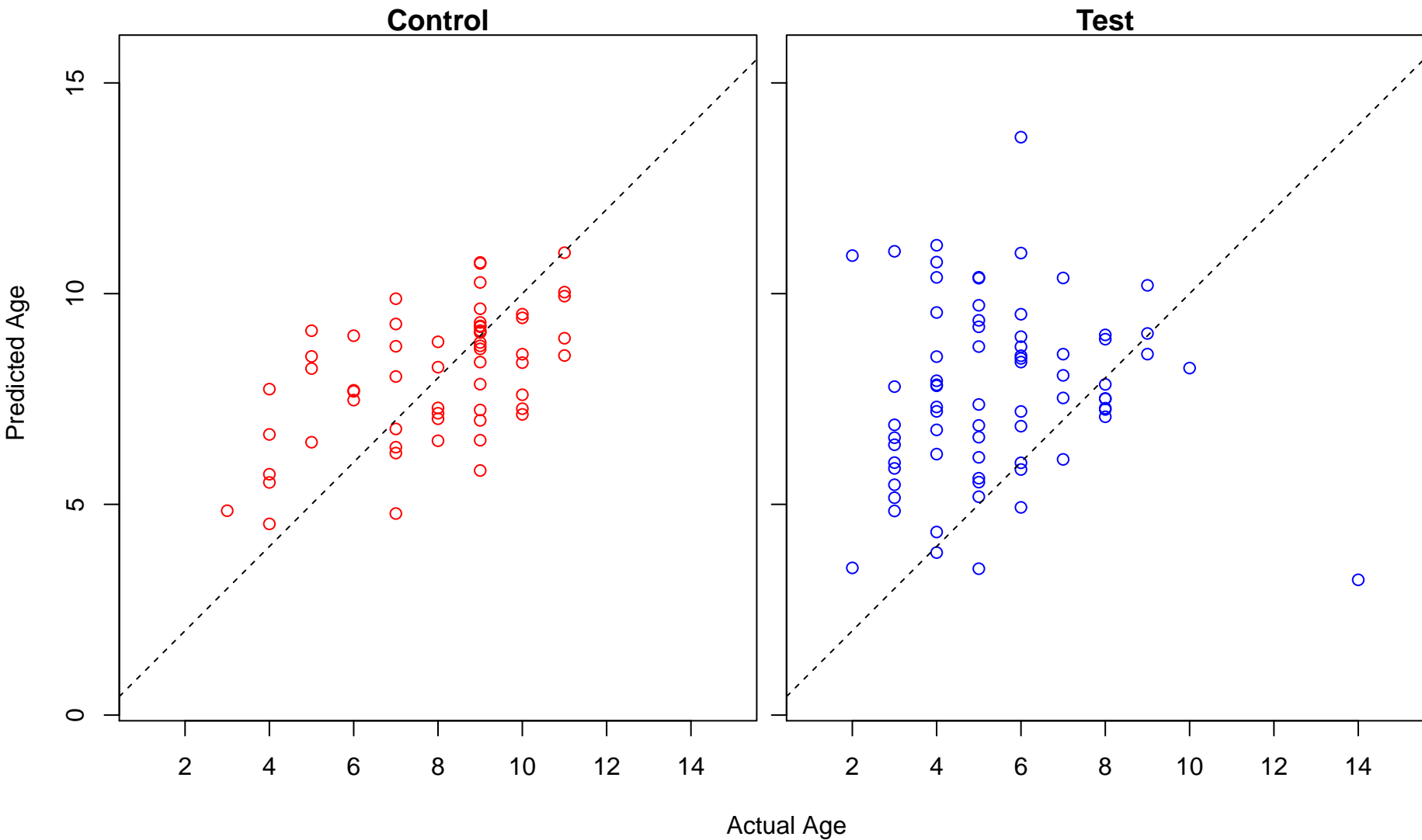
histone modification (Score: 1.426918)



covalent chromatin modification (Score: 1.426867)

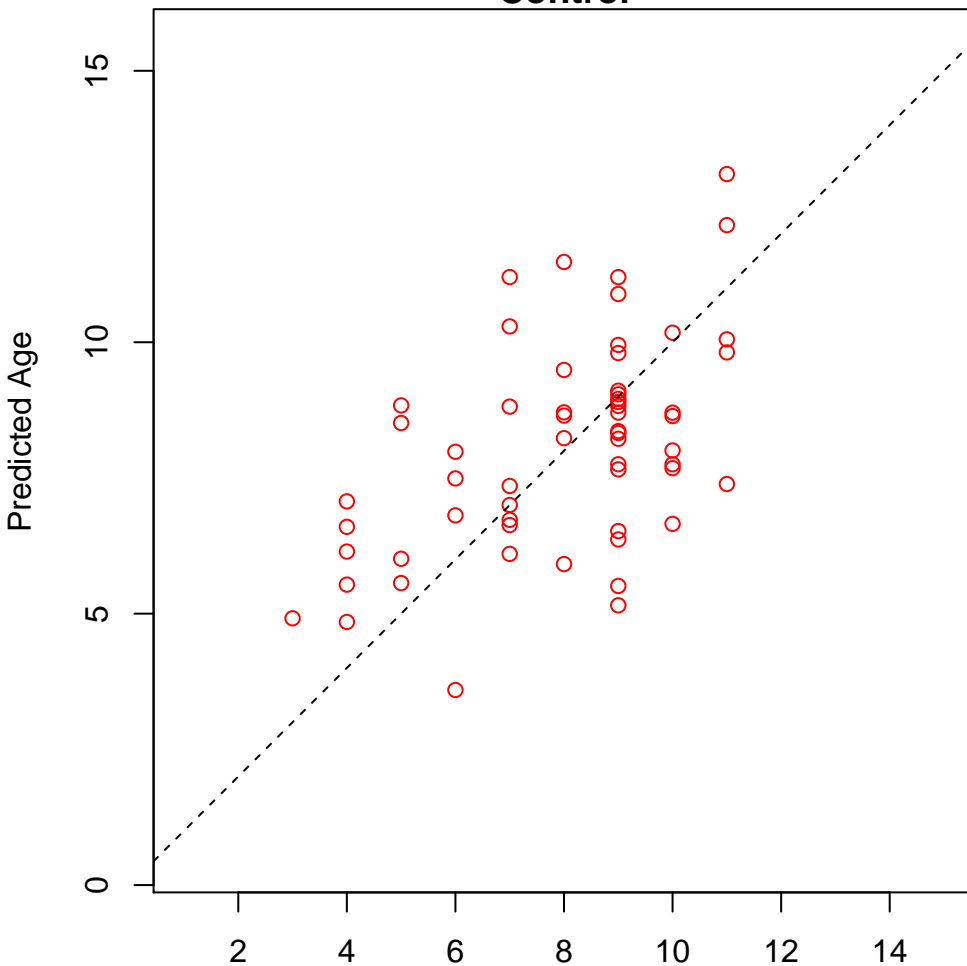


nervous system development (Score: 1.425870)

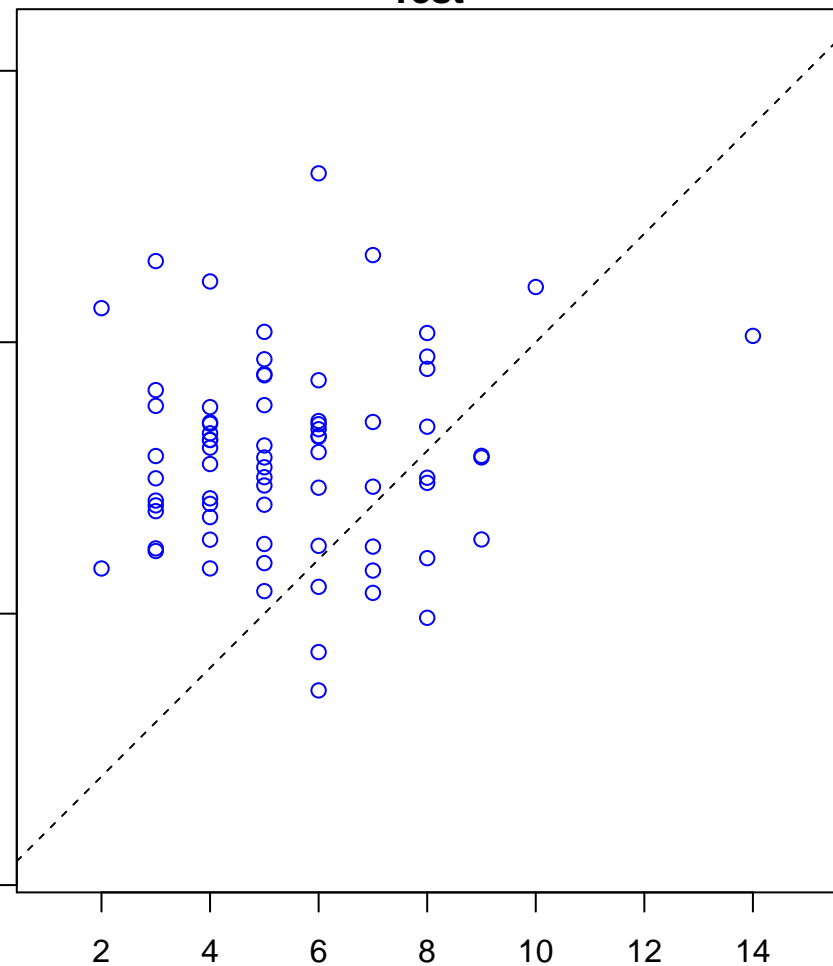


positive regulation of peptidase activity (Score: 1.422106)

Control

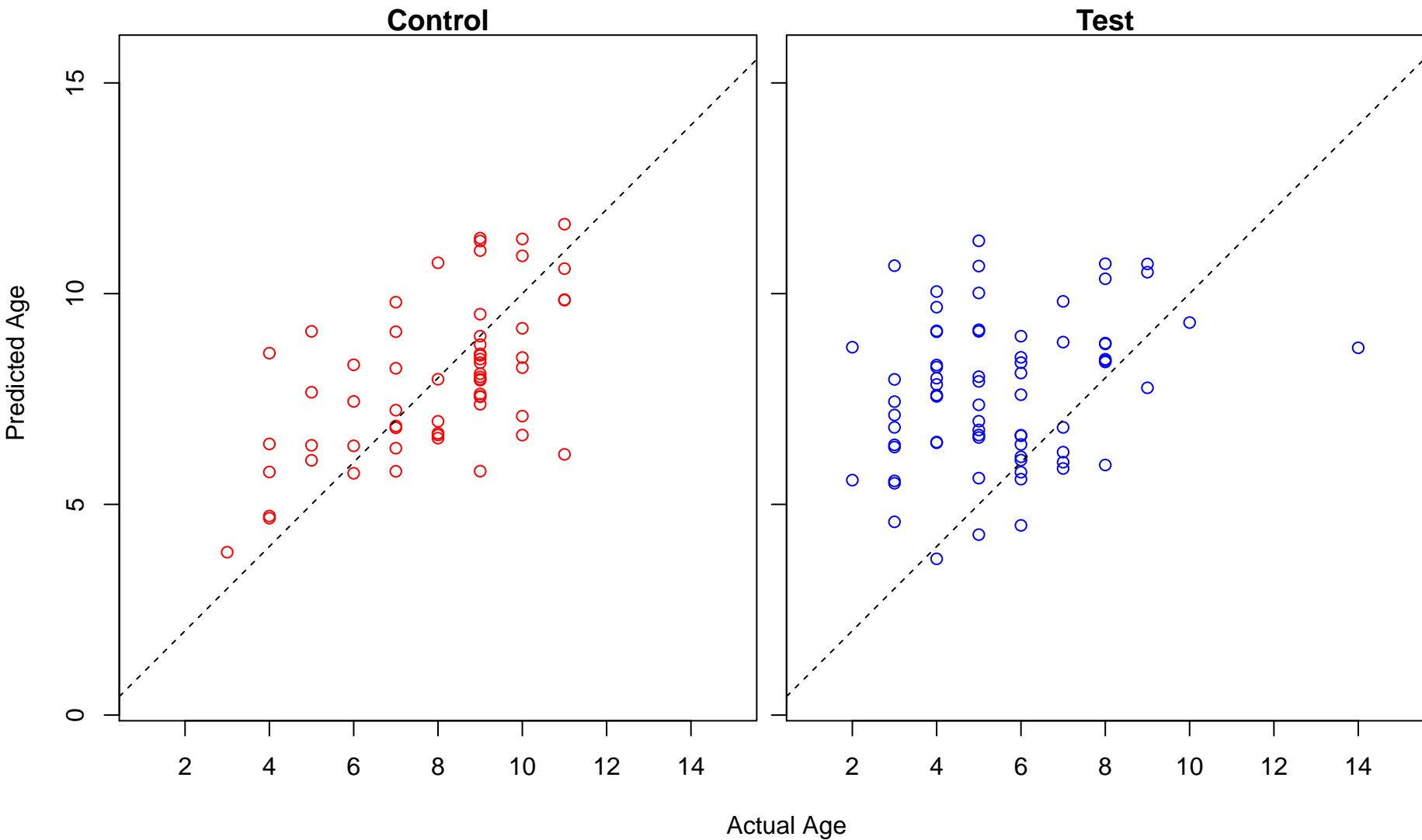


Test

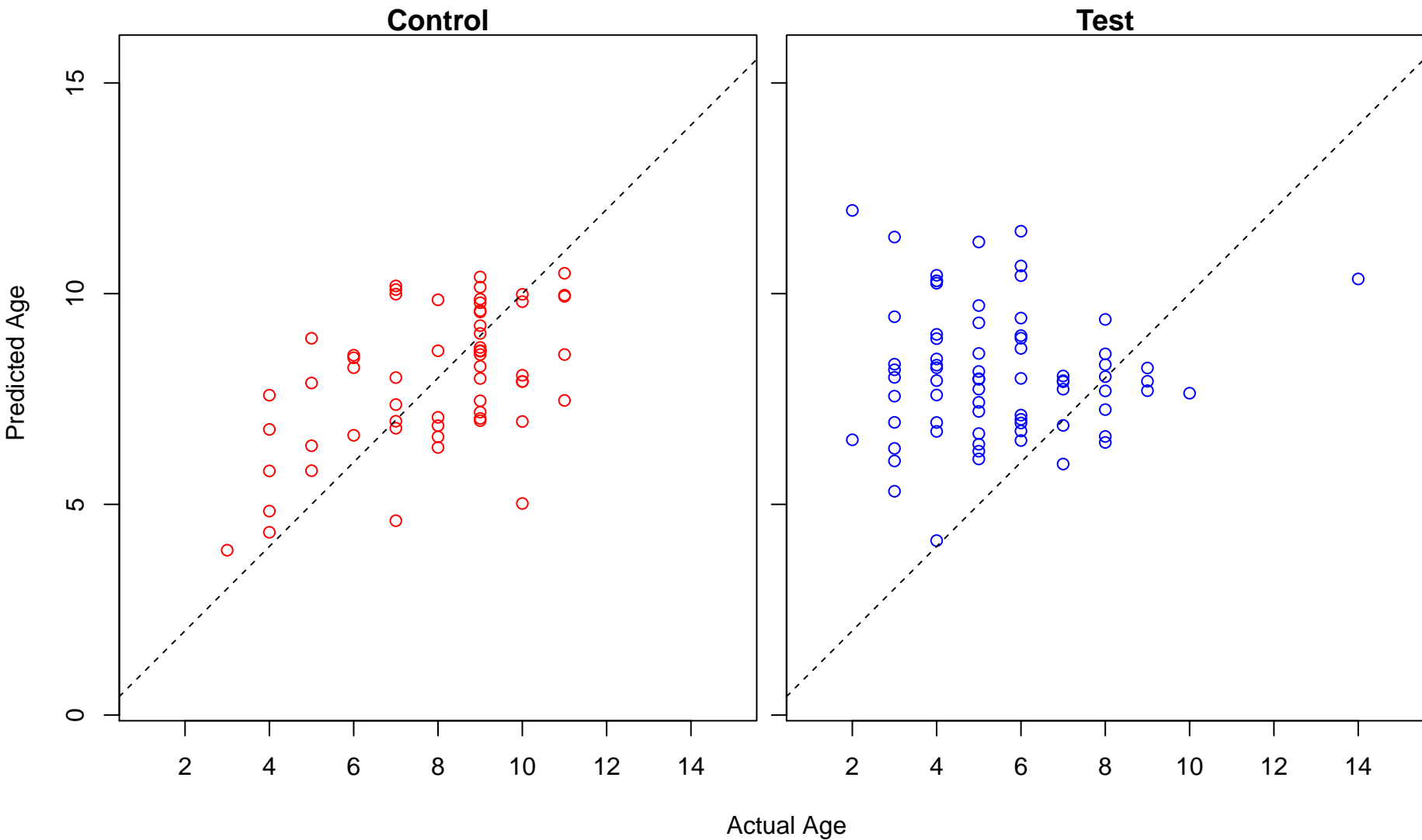


Actual Age

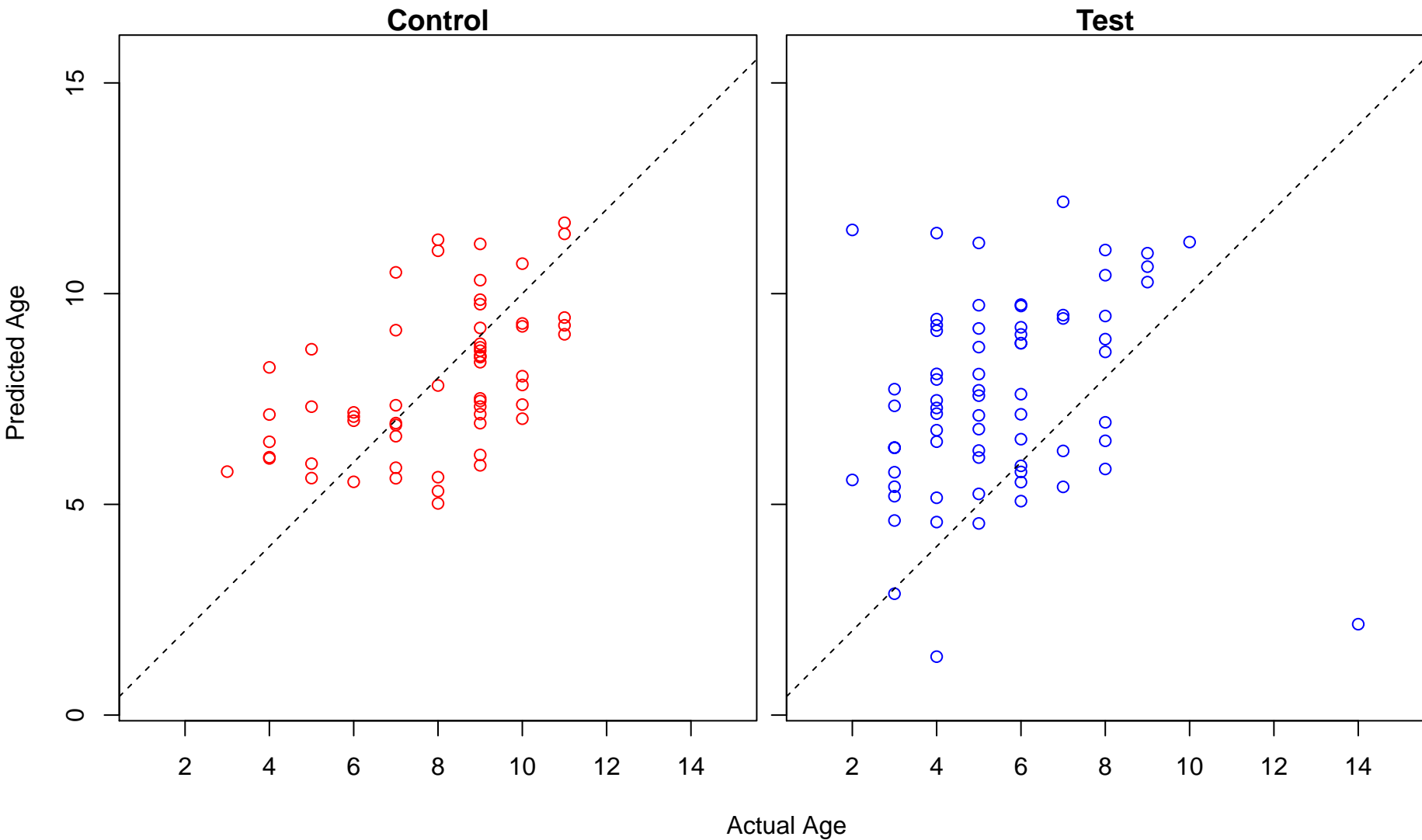
positive T cell selection (Score: 1.420389)



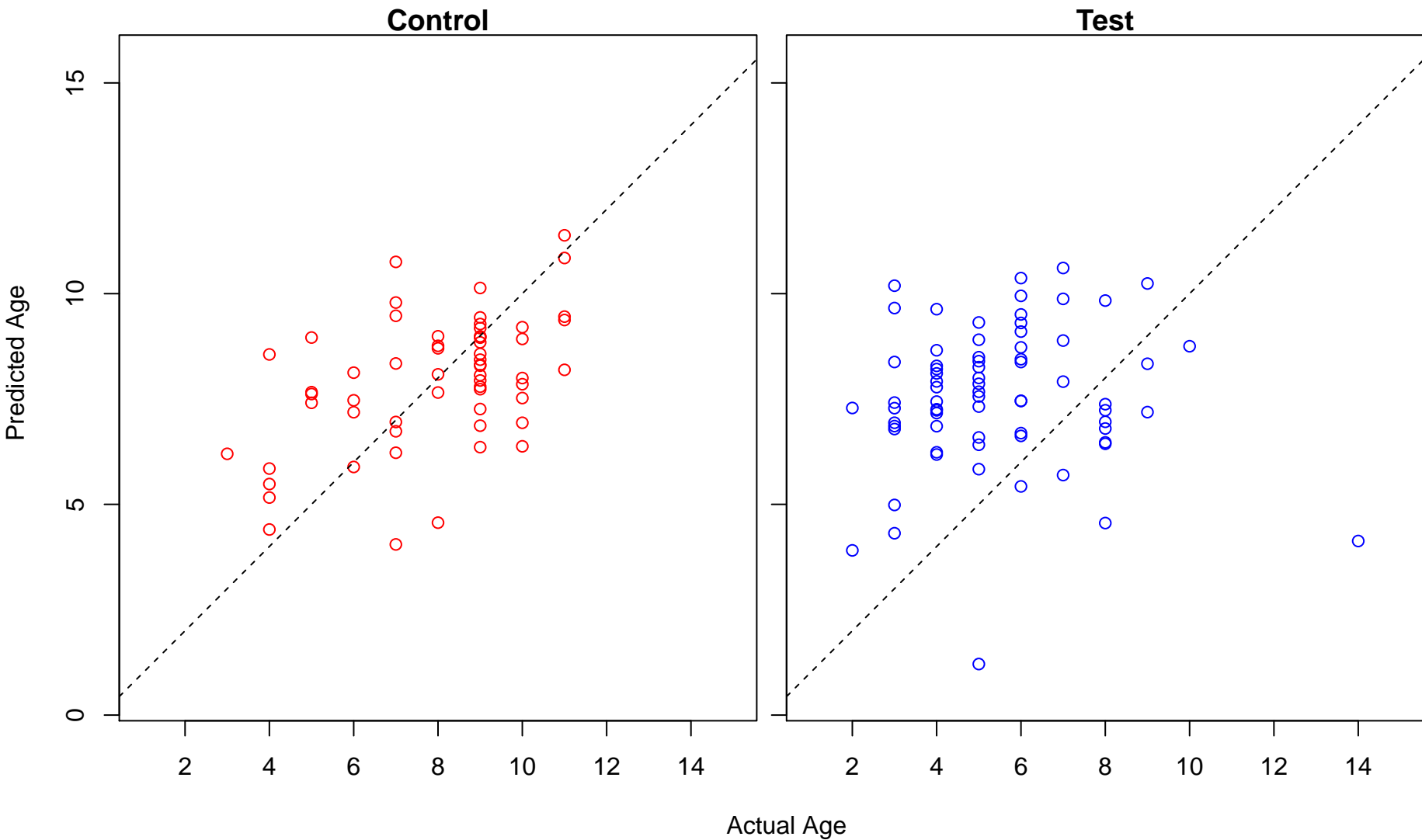
cytokine production (Score: 1.417122)



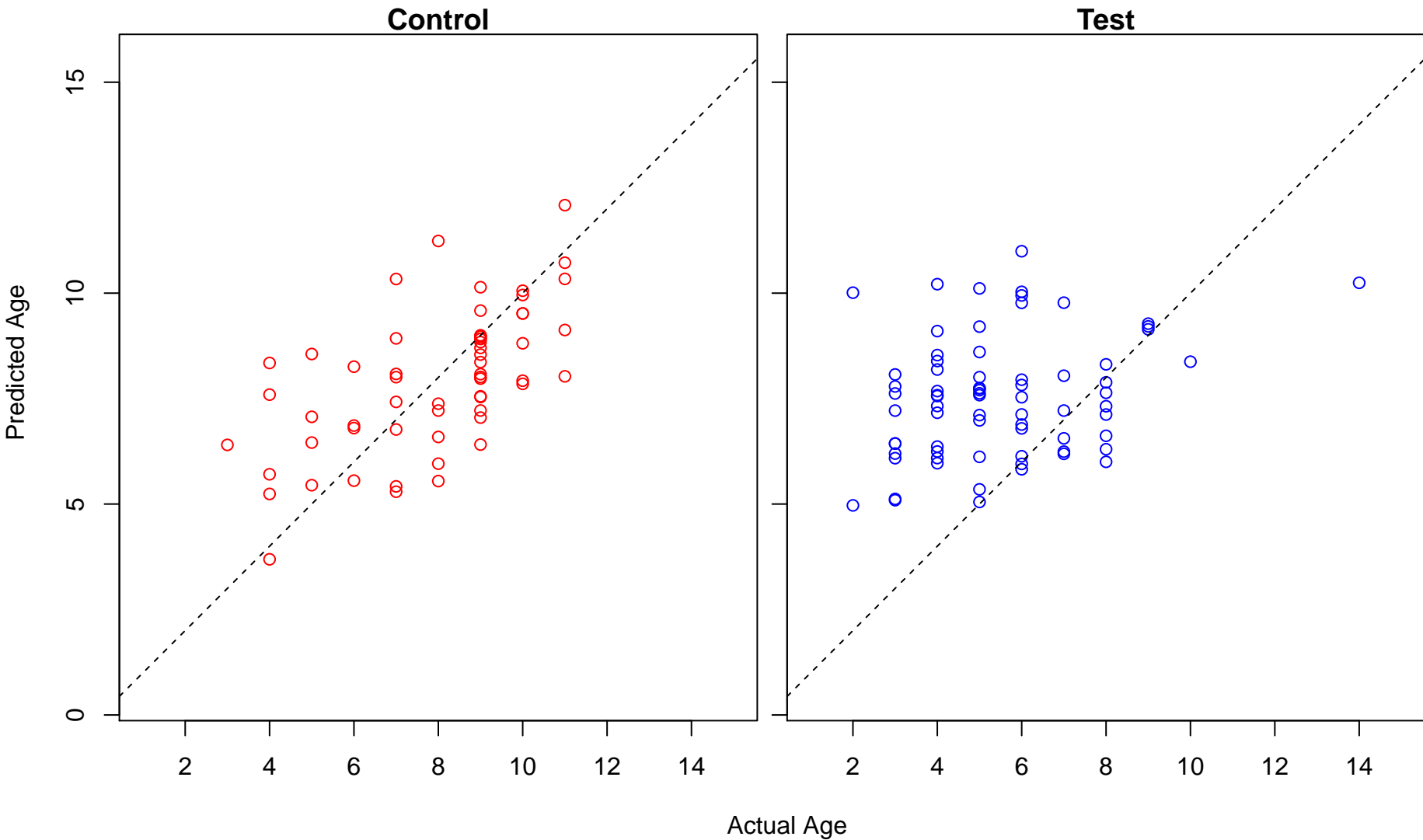
Fc receptor signaling pathway (Score: 1.413357)



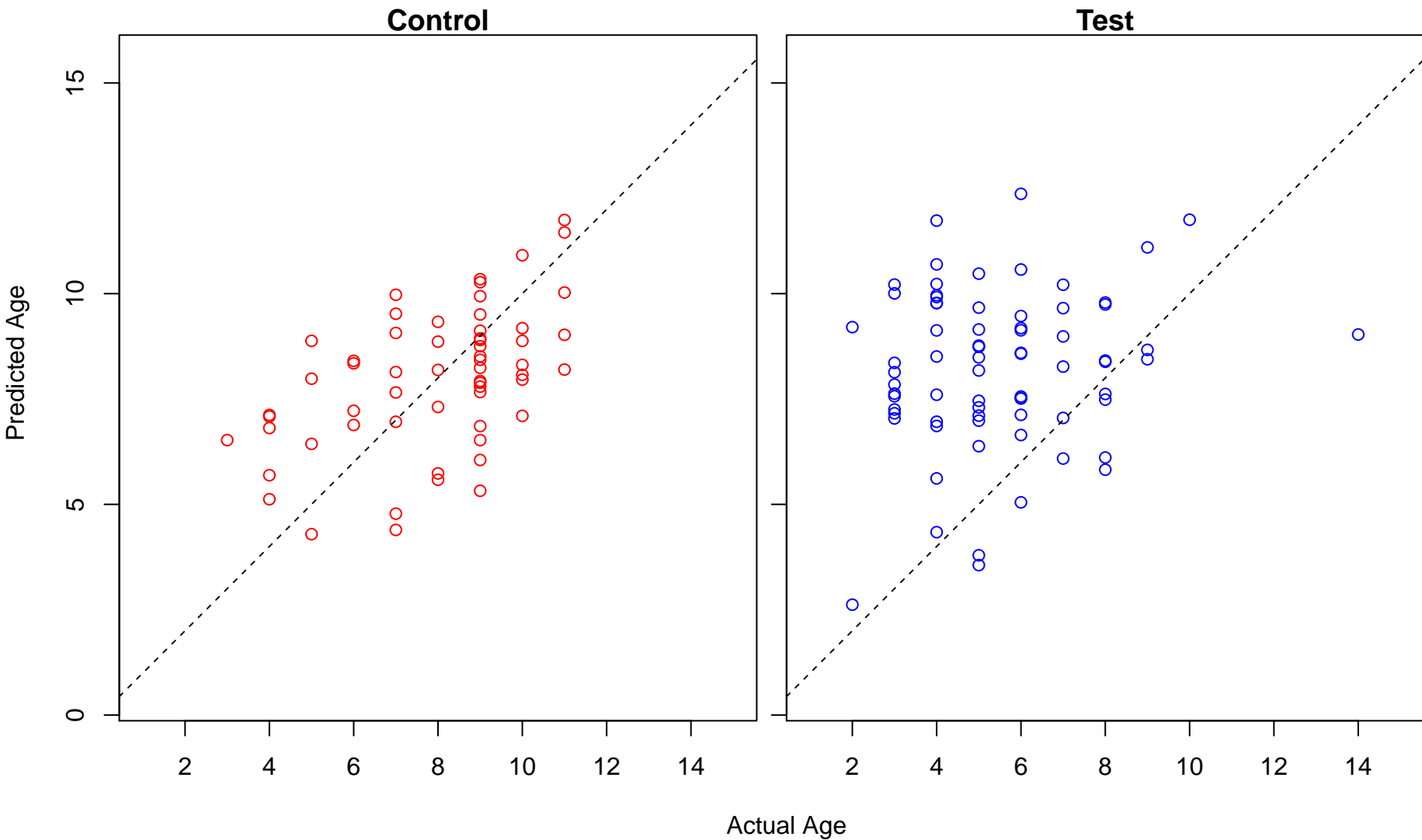
positive regulation of tyrosine phosphorylation of Stat3 protein (Score: 1.413330)



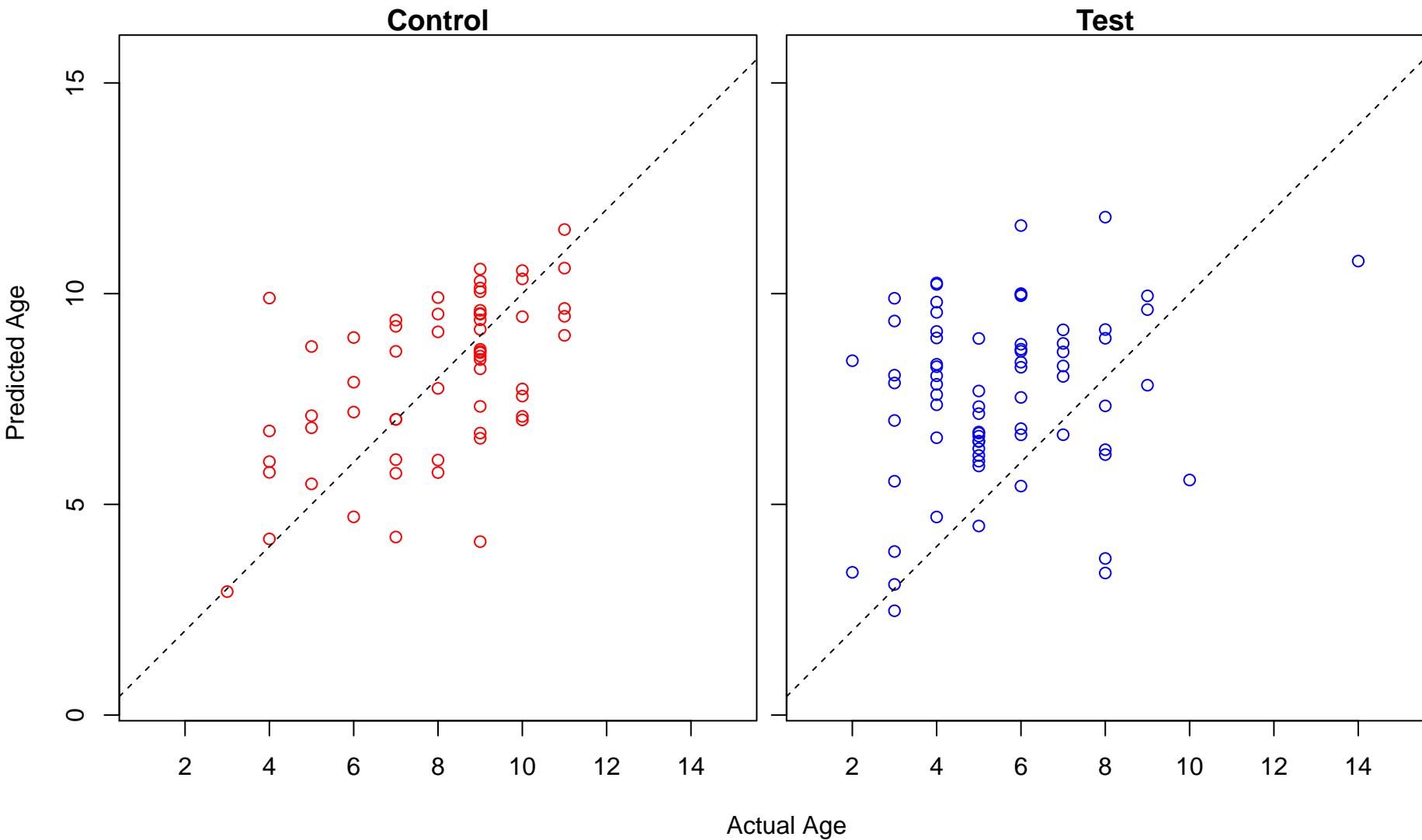
establishment of localization in cell (Score: 1.413046)



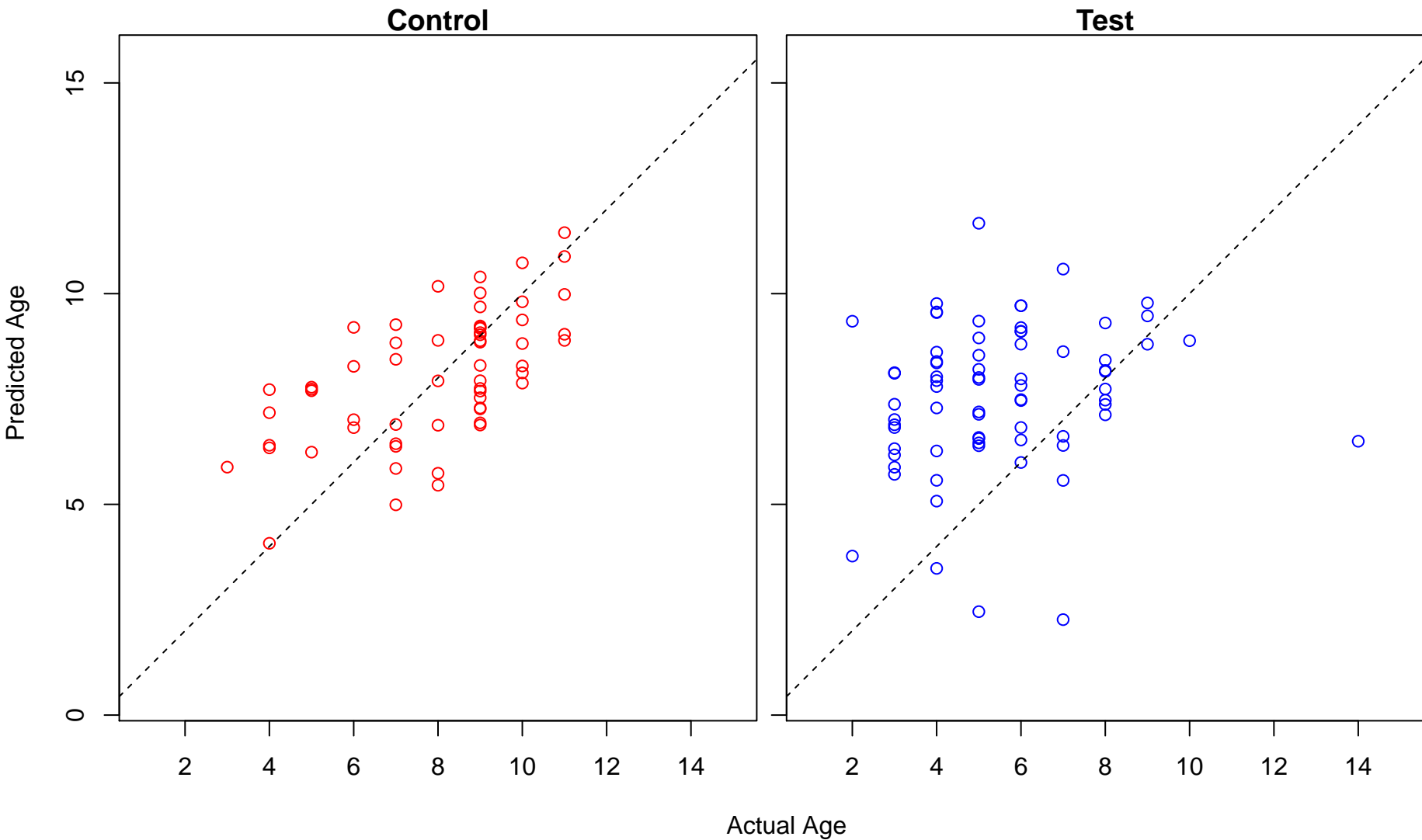
regulation of multicellular organismal development (Score: 1.412897)



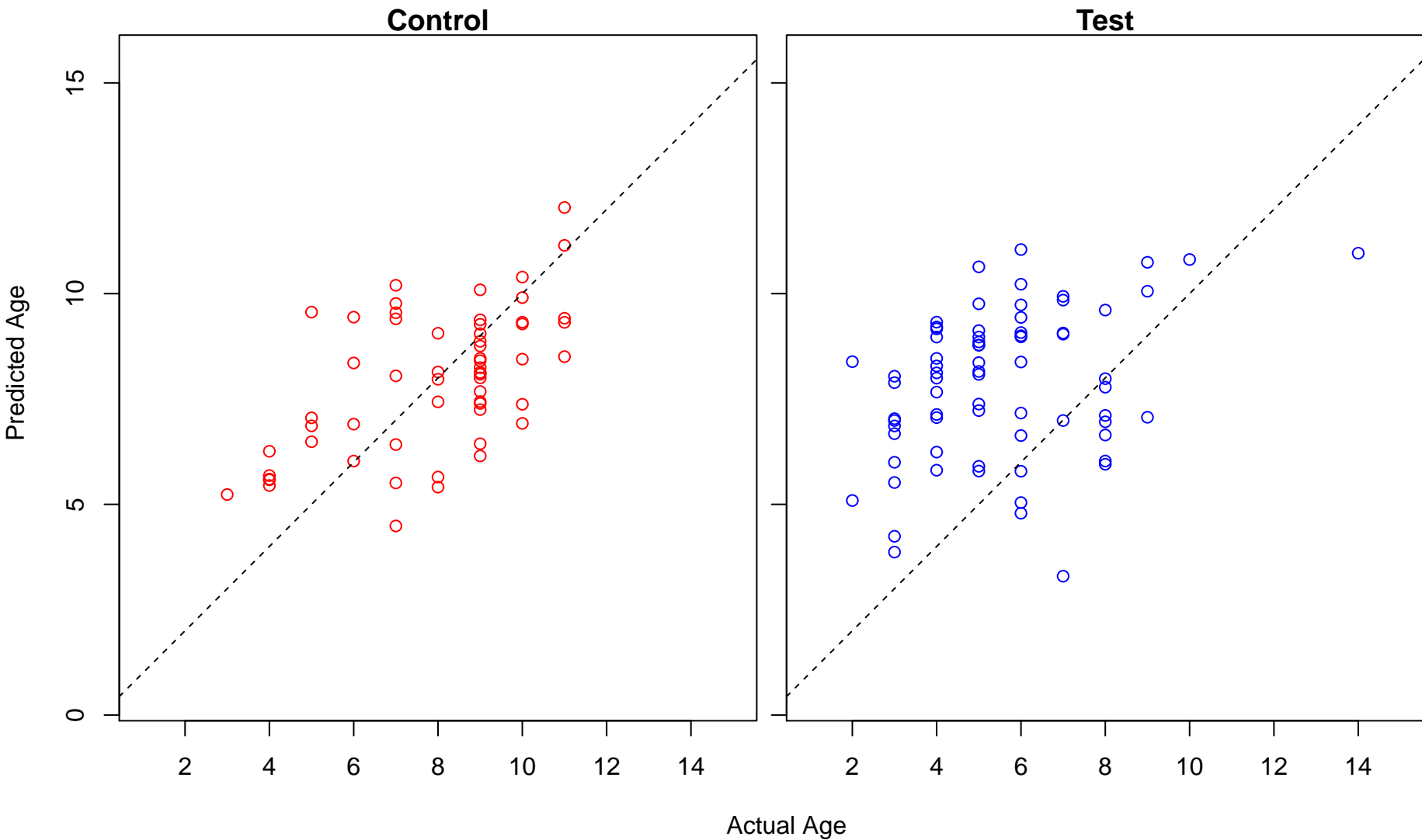
kidney morphogenesis (Score: 1.412734)



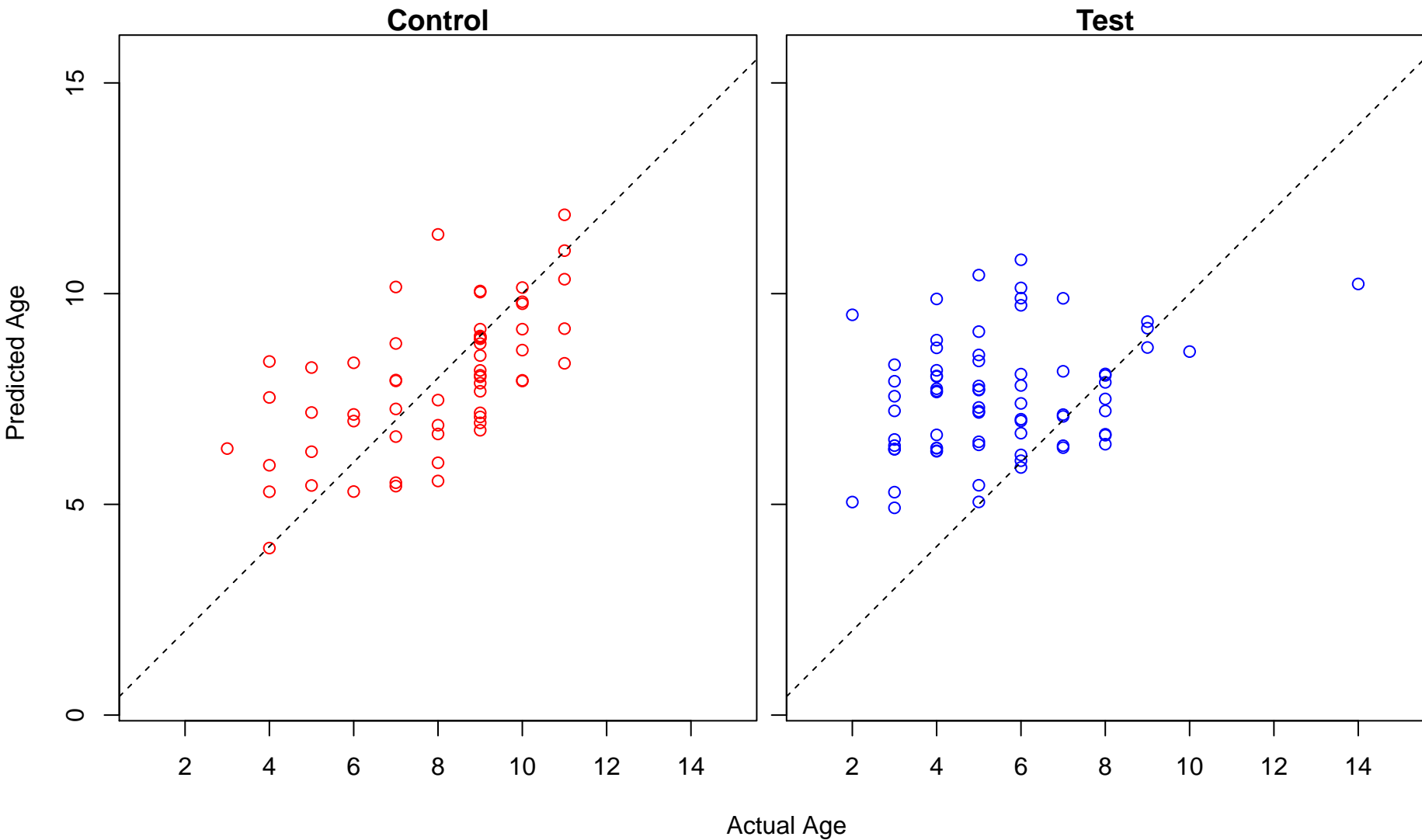
regulation of cellular metabolic process (Score: 1.412614)



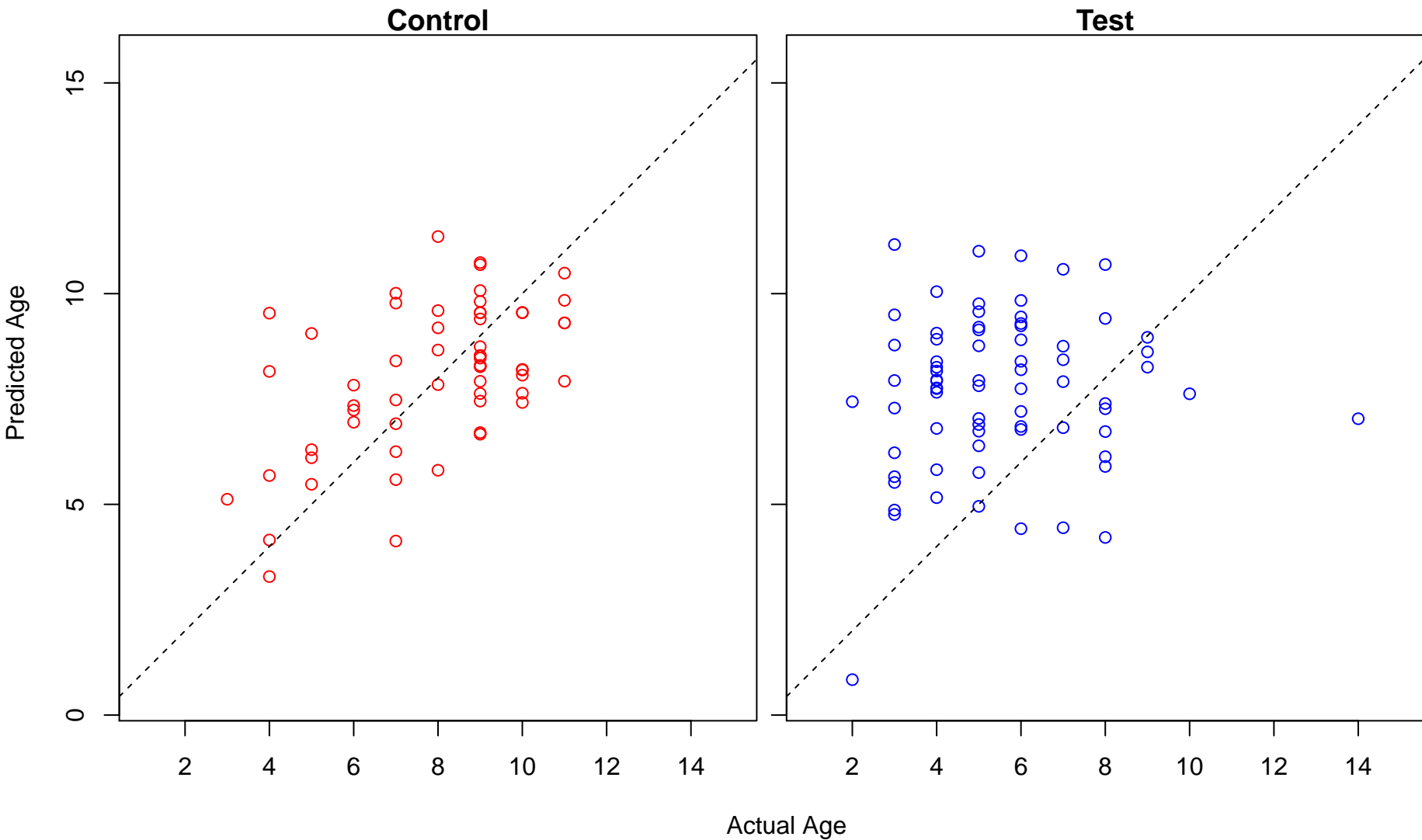
internal protein amino acid acetylation (Score: 1.412272)



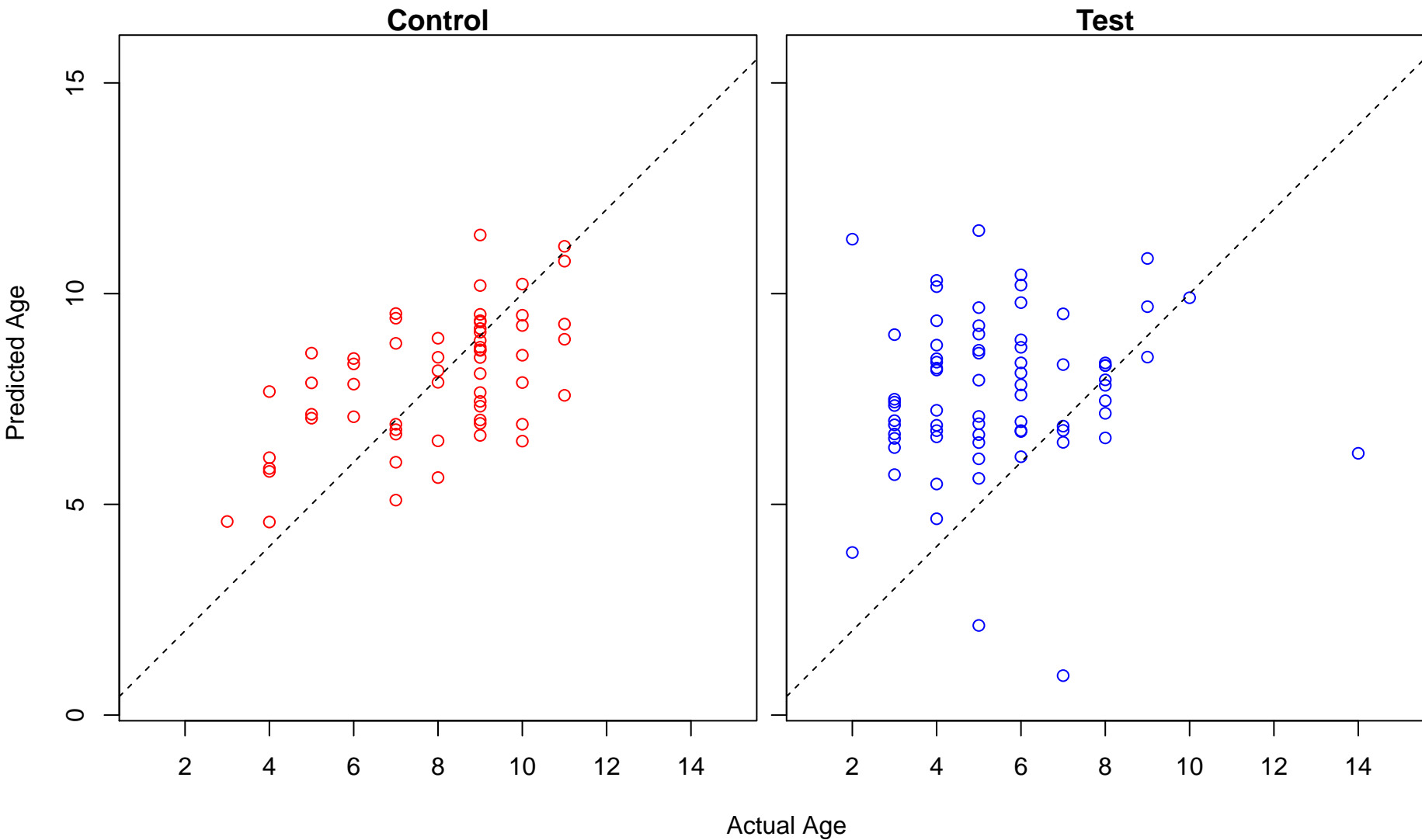
cellular localization (Score: 1.411501)



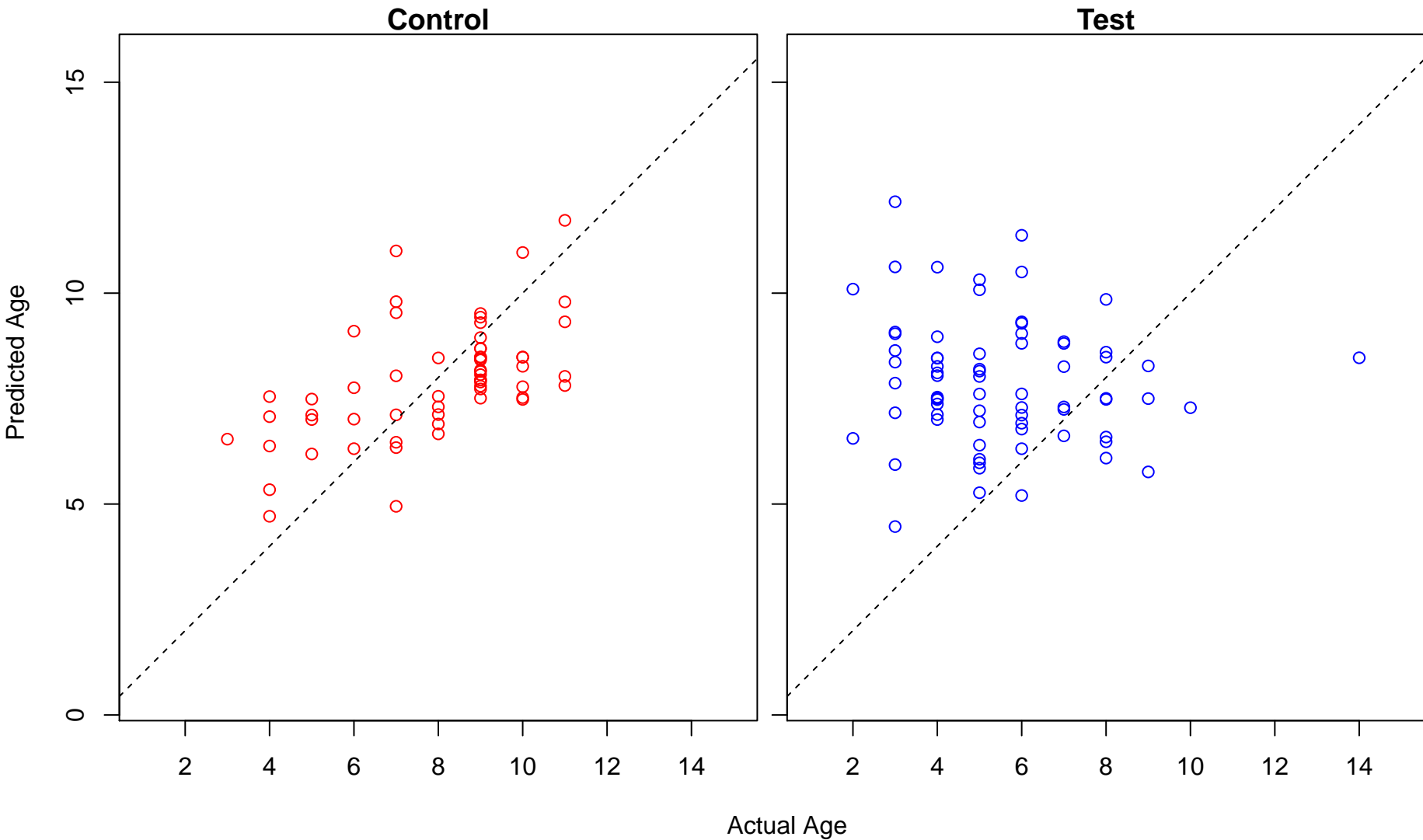
regulation of tyrosine phosphorylation of STAT protein (Score: 1.411000)



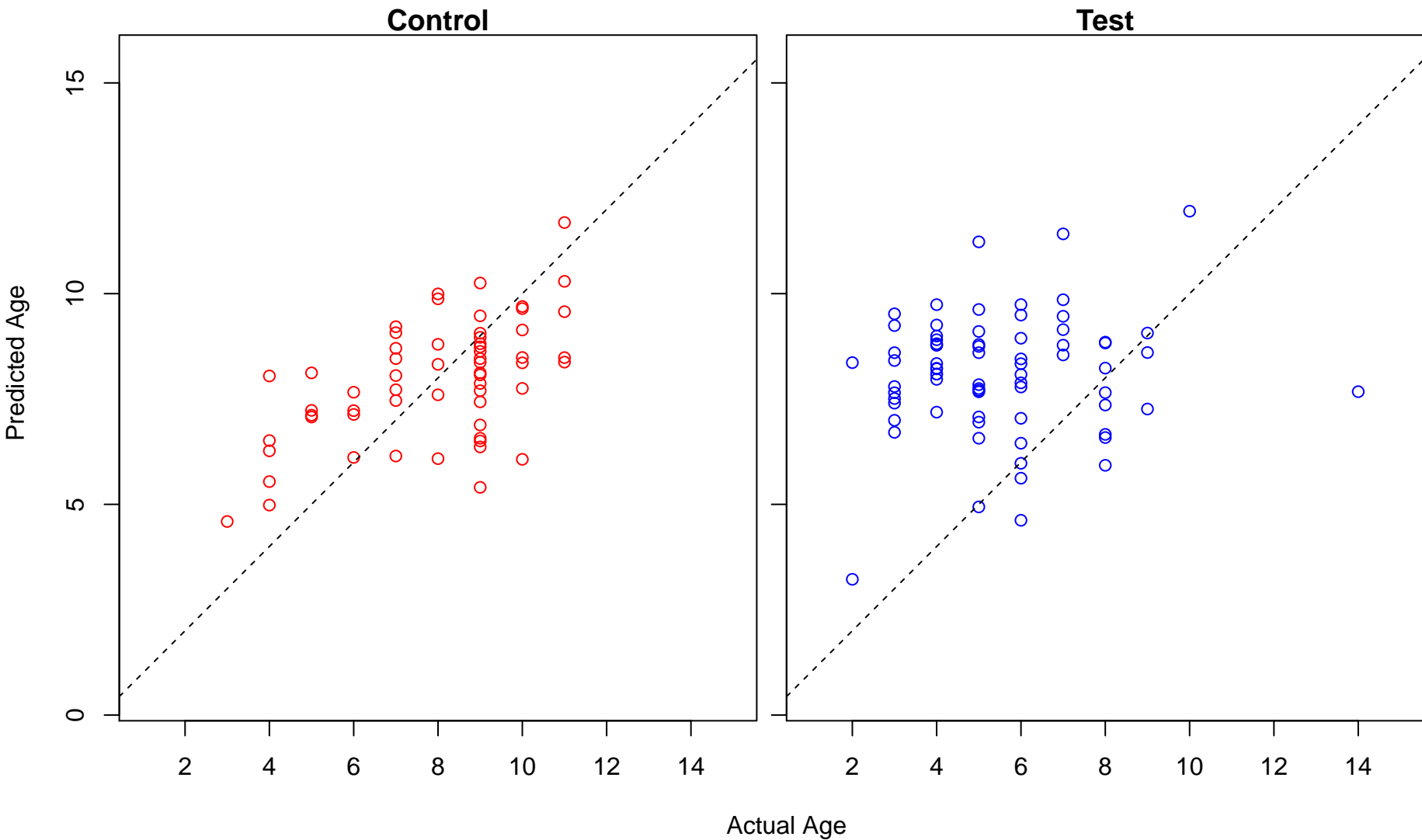
regulation of cellular macromolecule biosynthetic process (Score: 1.405697)



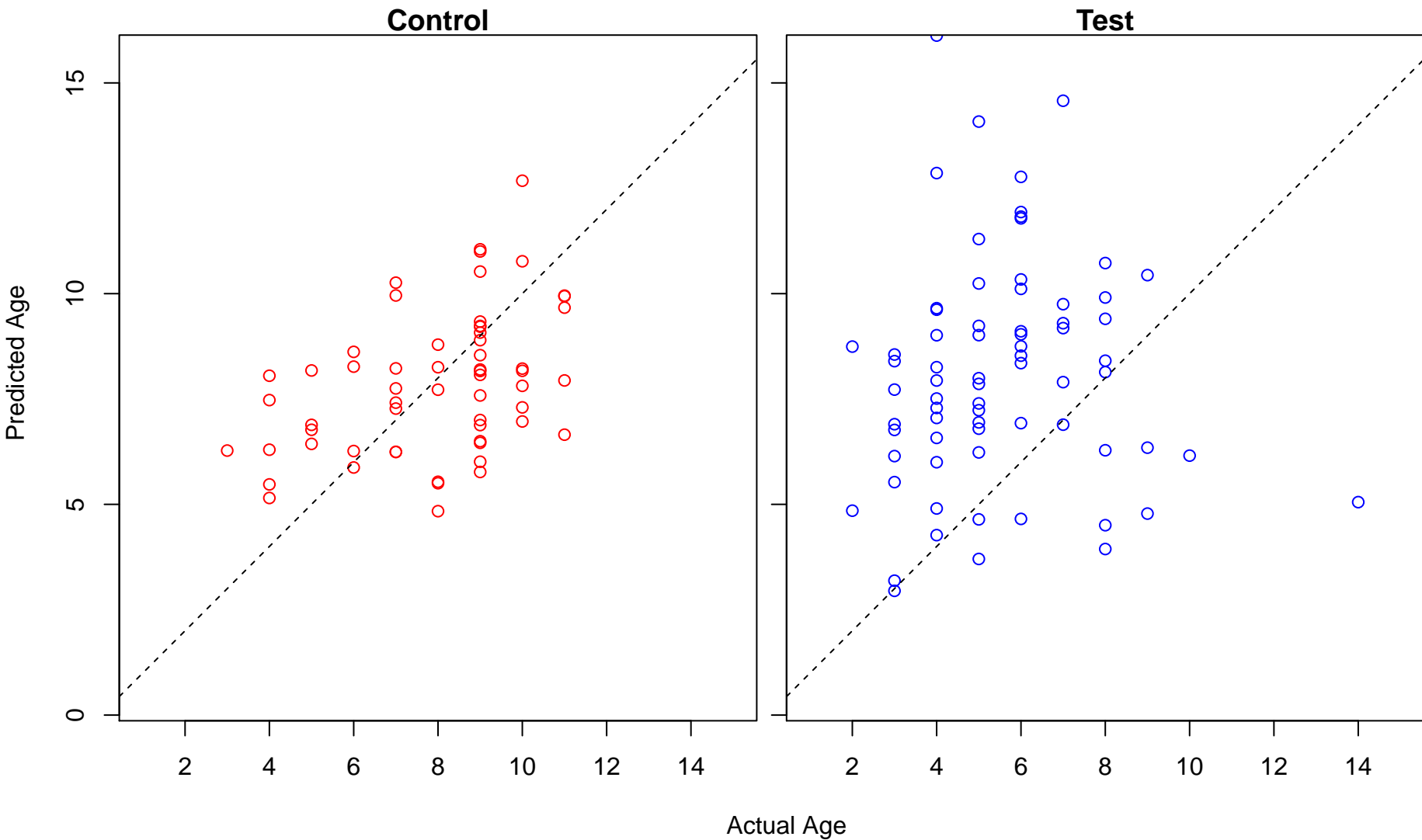
positive regulation of integrin-mediated signaling pathway (Score: 1.403348)



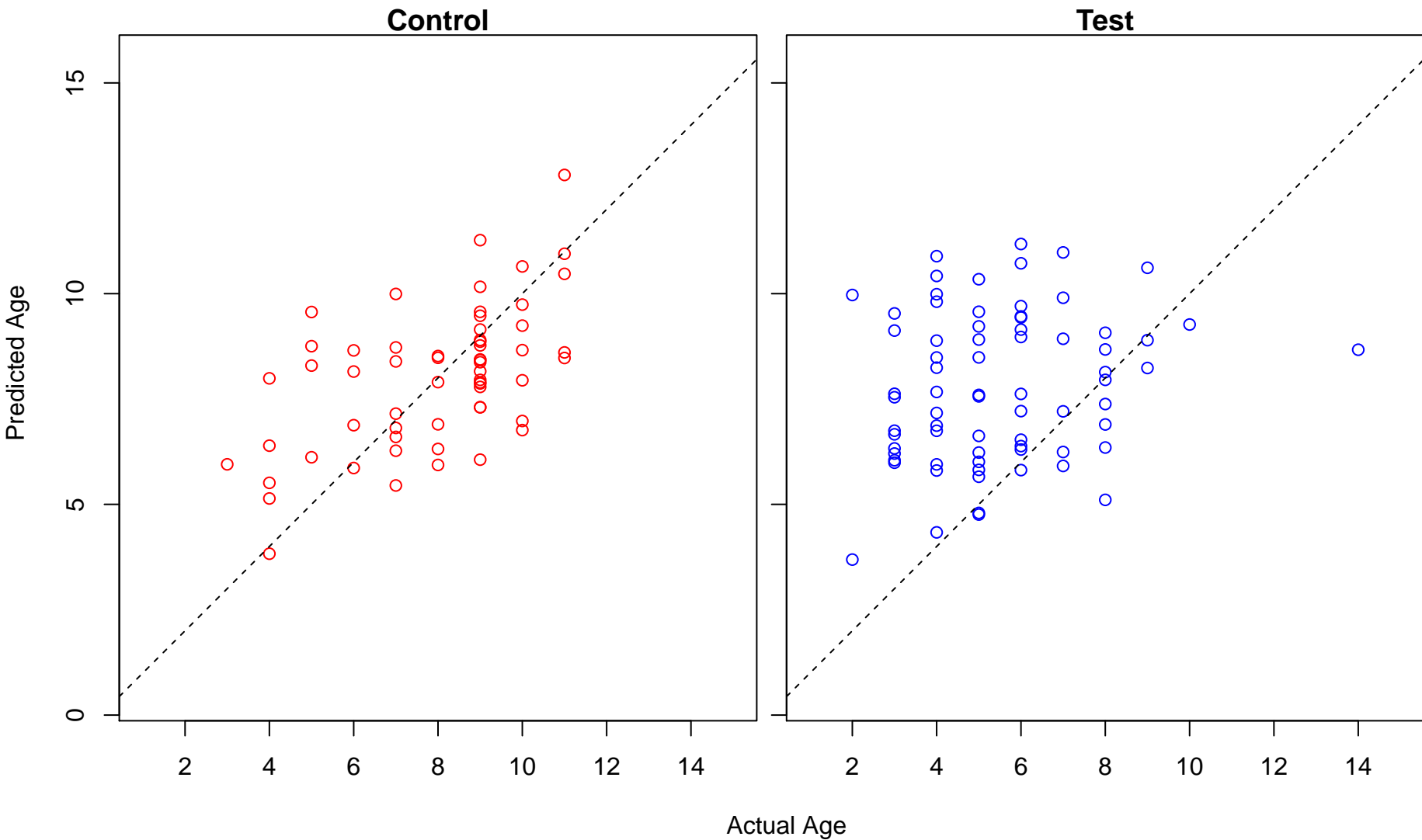
protein polyglutamylation (Score: 1.399547)



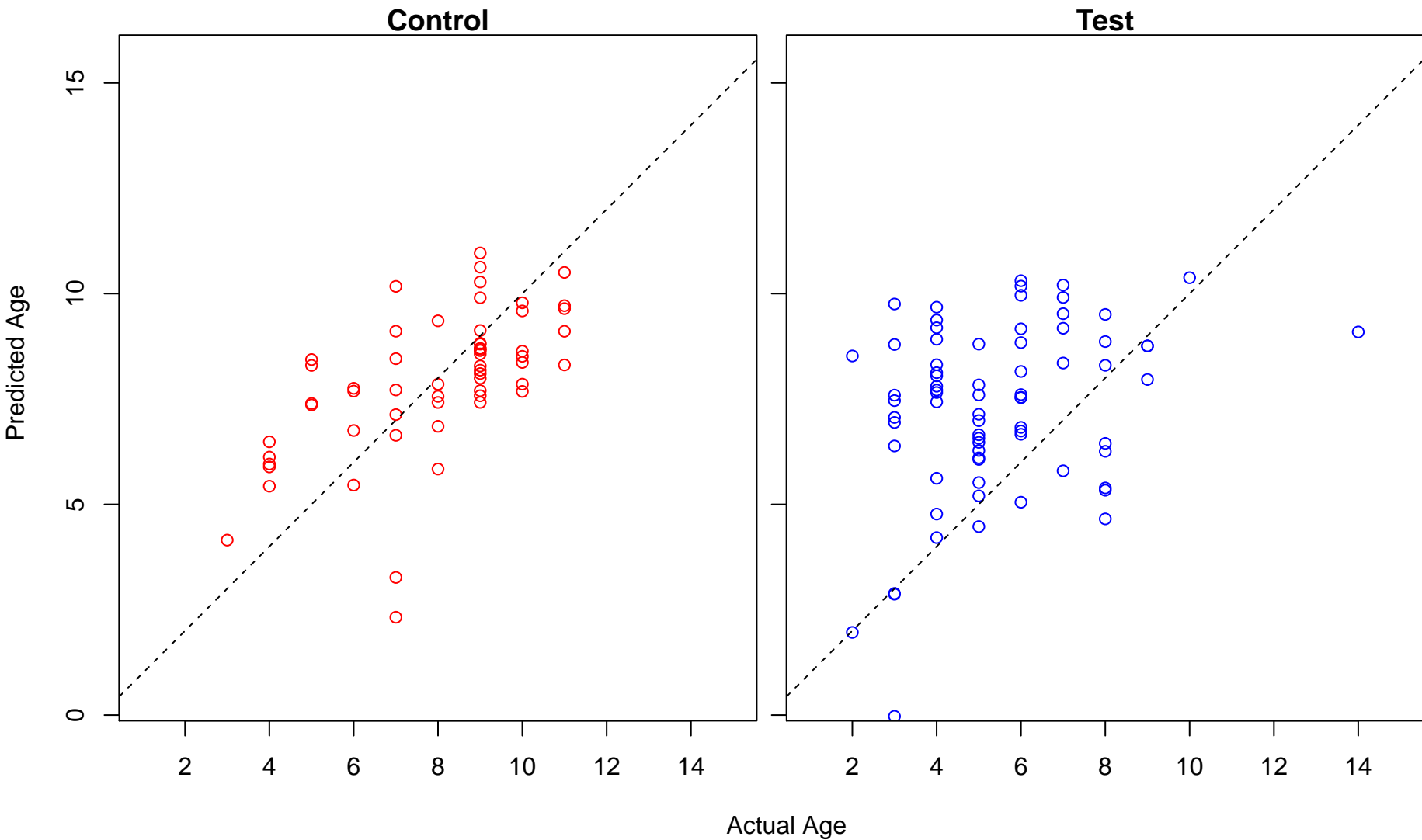
endochondral bone growth (Score: 1.398480)



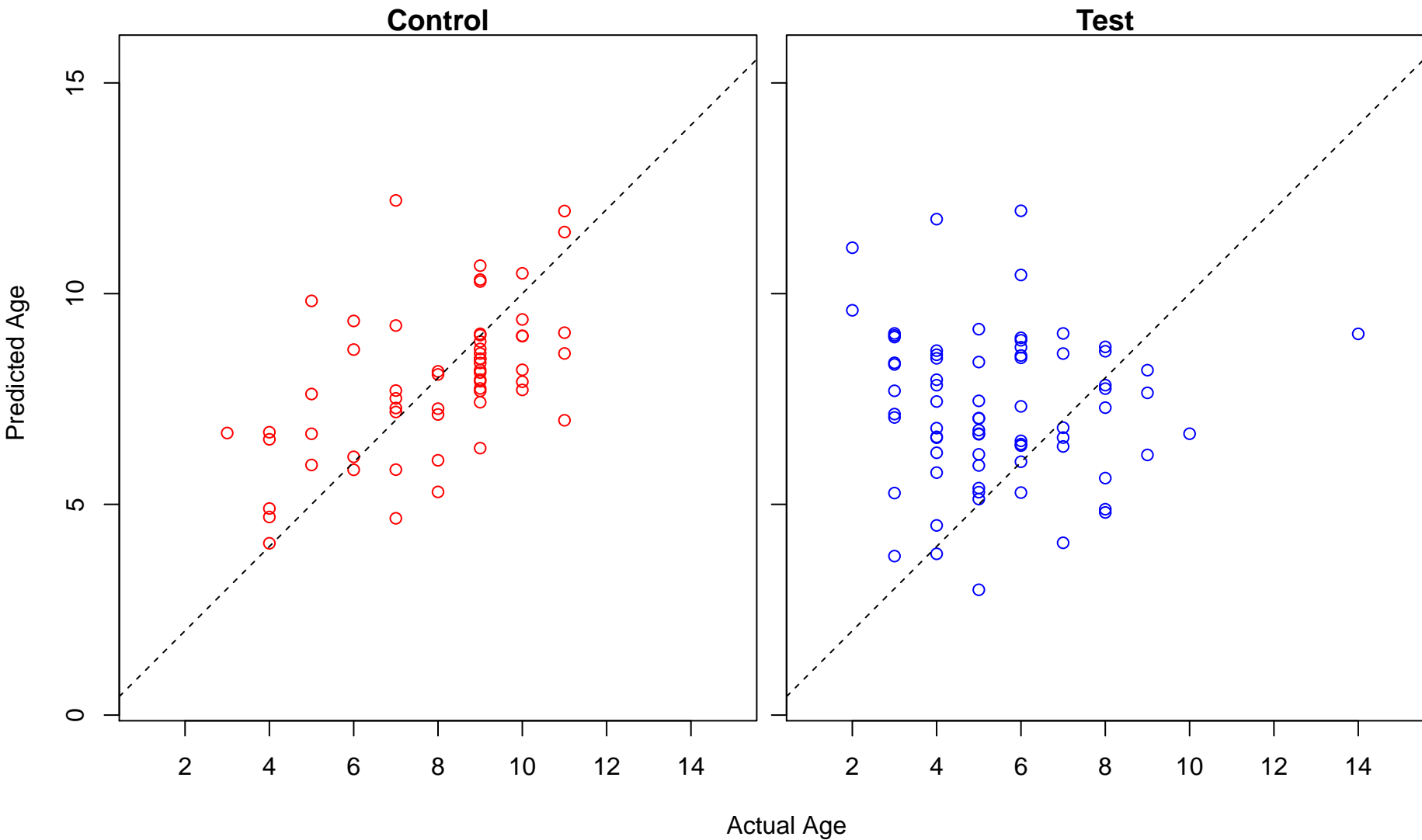
programmed cell death (Score: 1.397244)



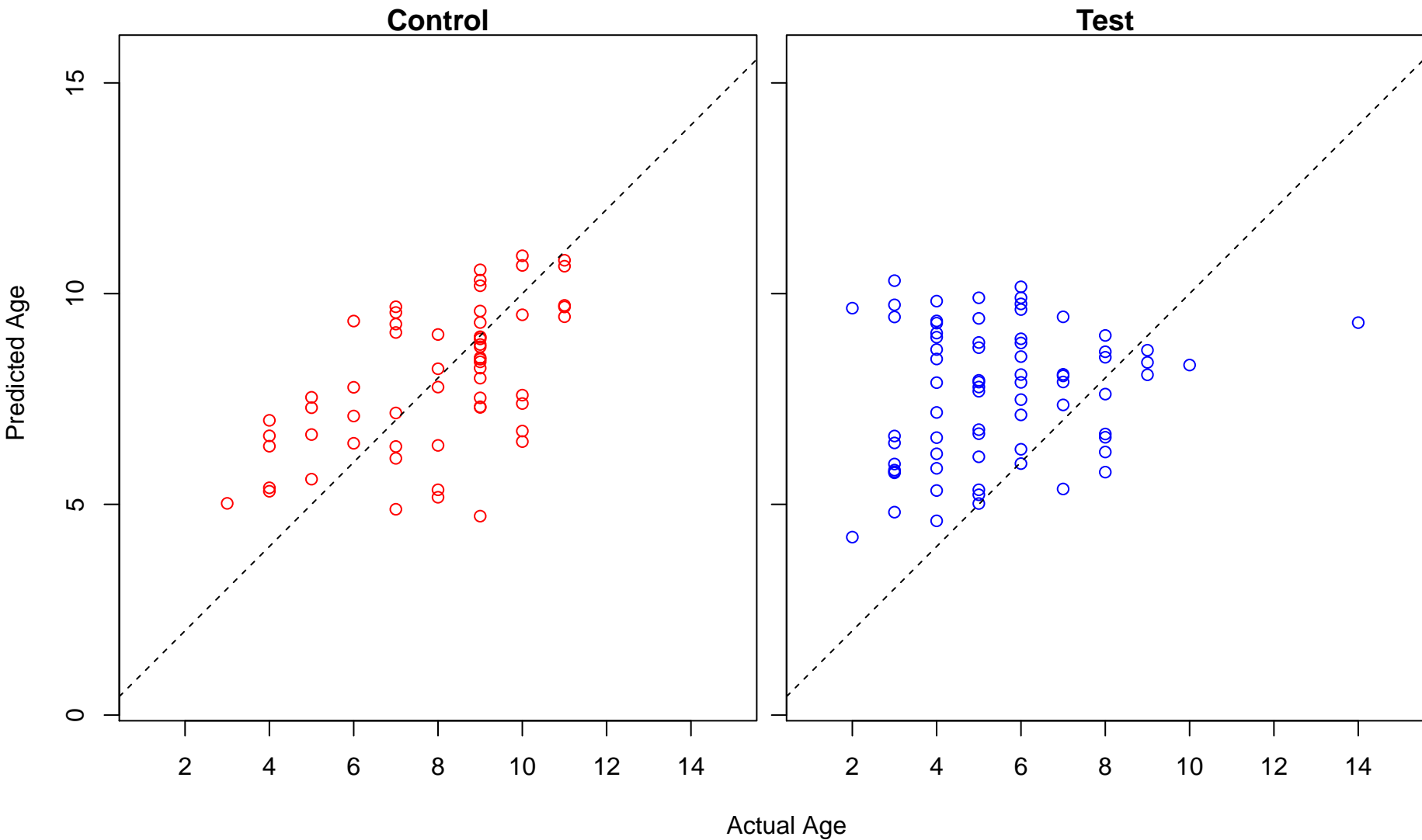
negative regulation of osteoblast differentiation (Score: 1.393283)



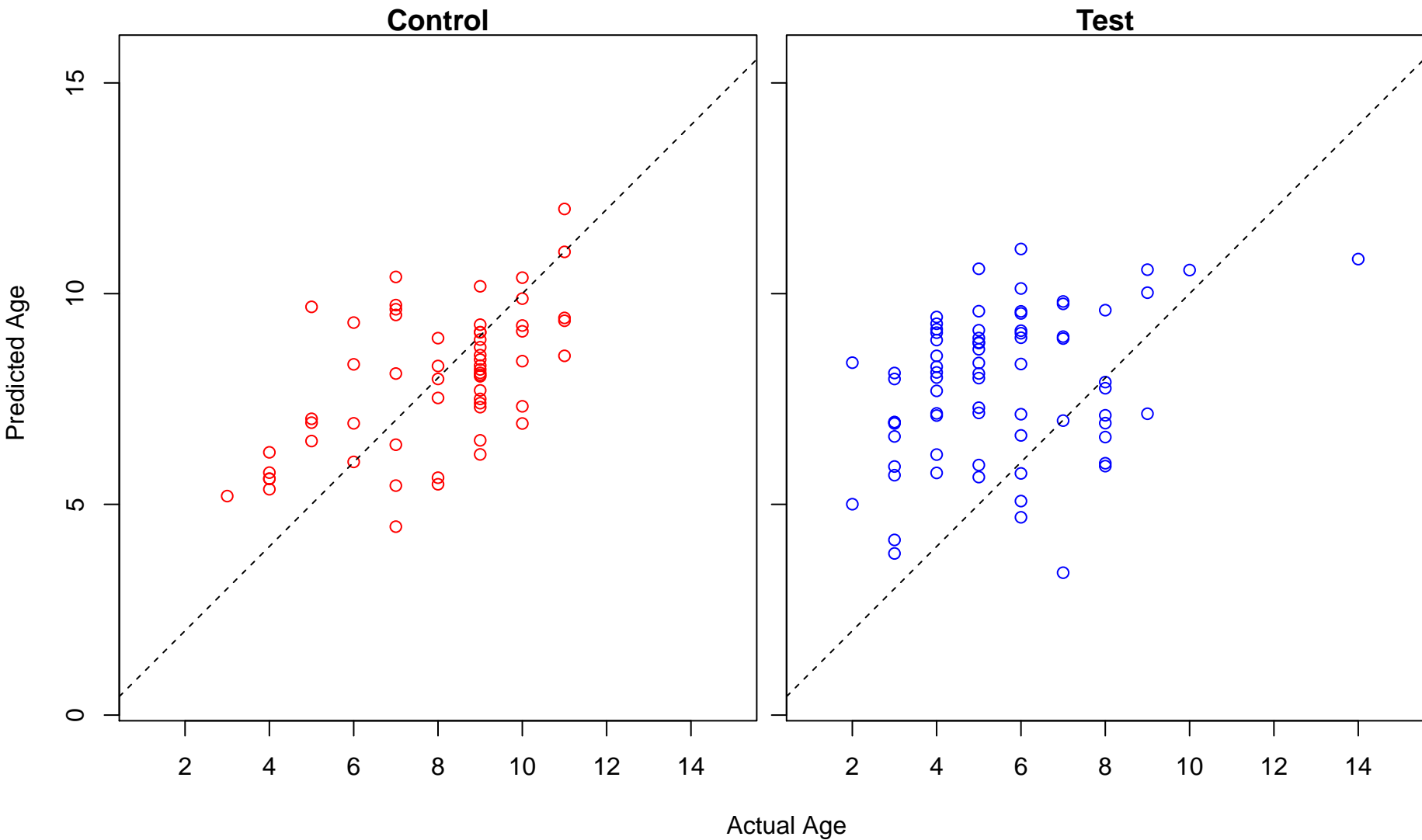
ribose phosphate biosynthetic process (Score: 1.391291)



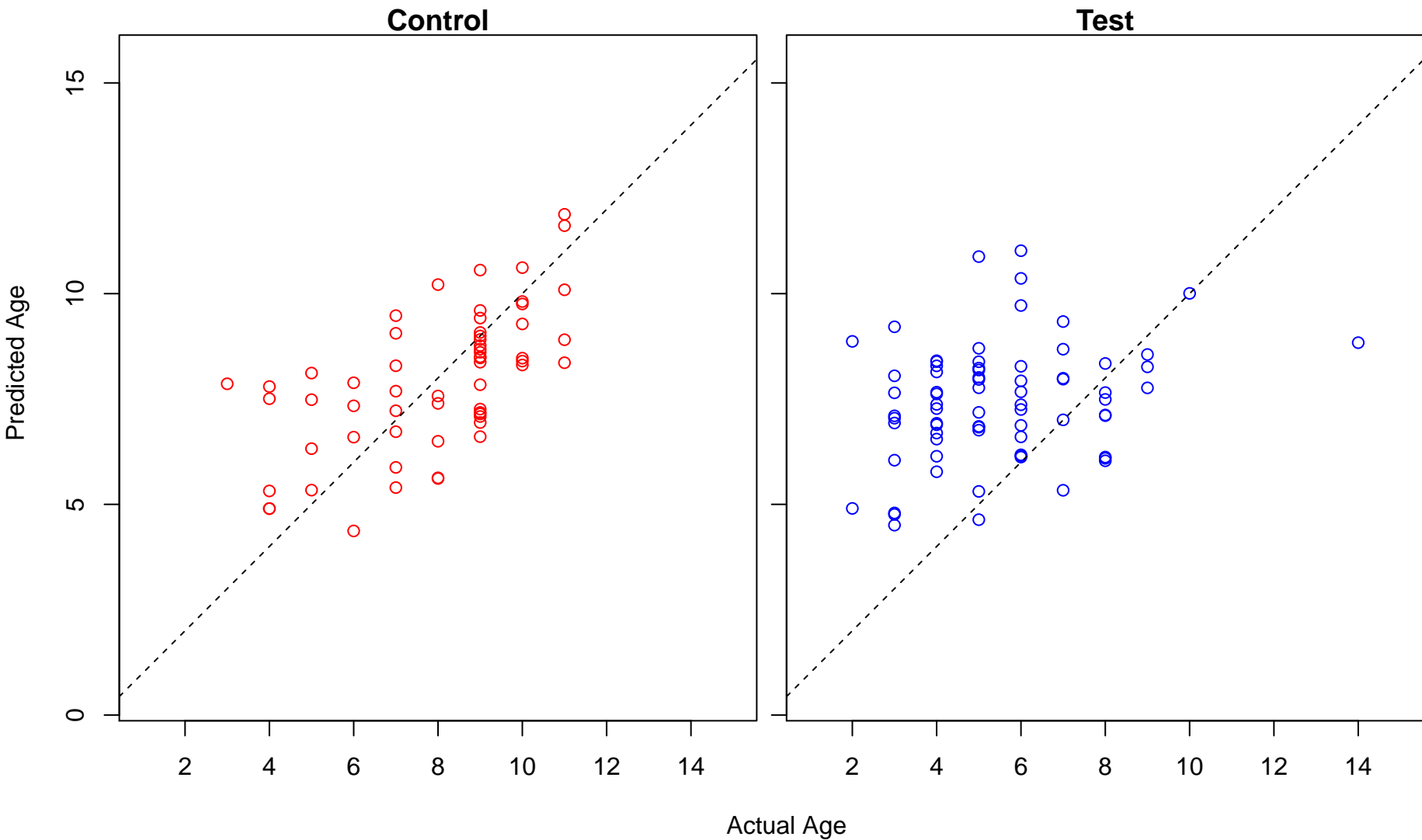
mesenchymal cell development (Score: 1.391226)



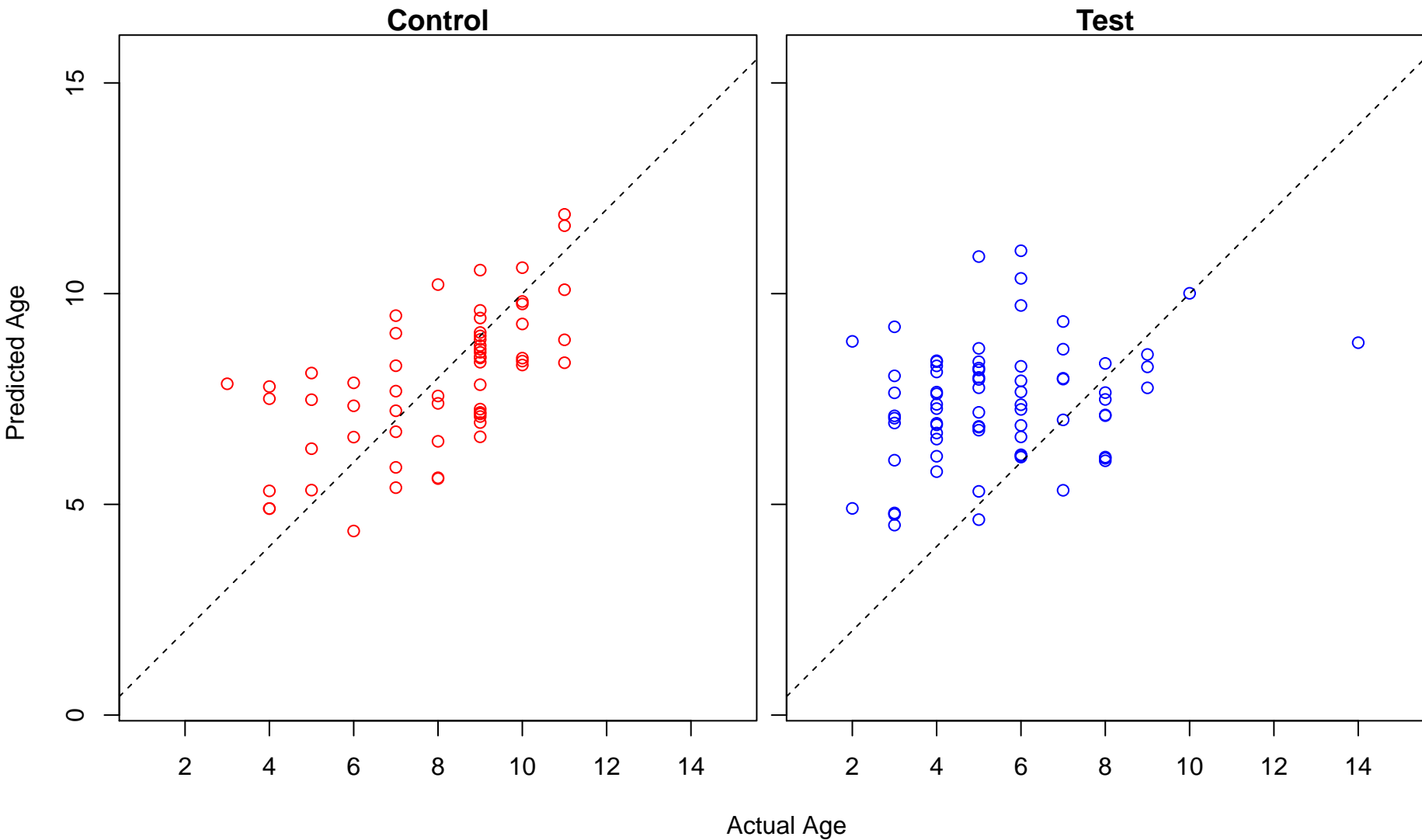
peptidyl-lysine acetylation (Score: 1.389611)



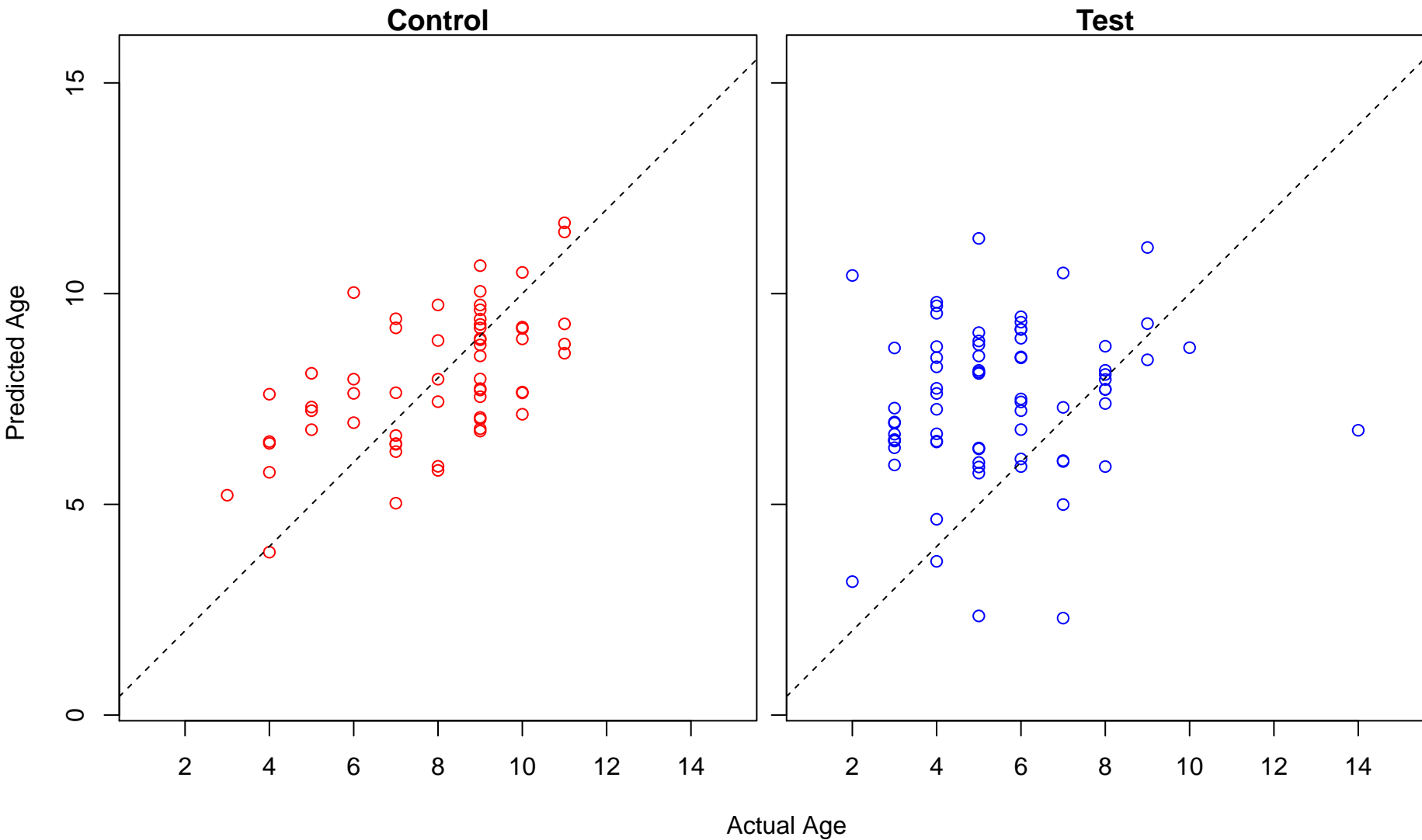
cellular protein localization (Score: 1.388081)



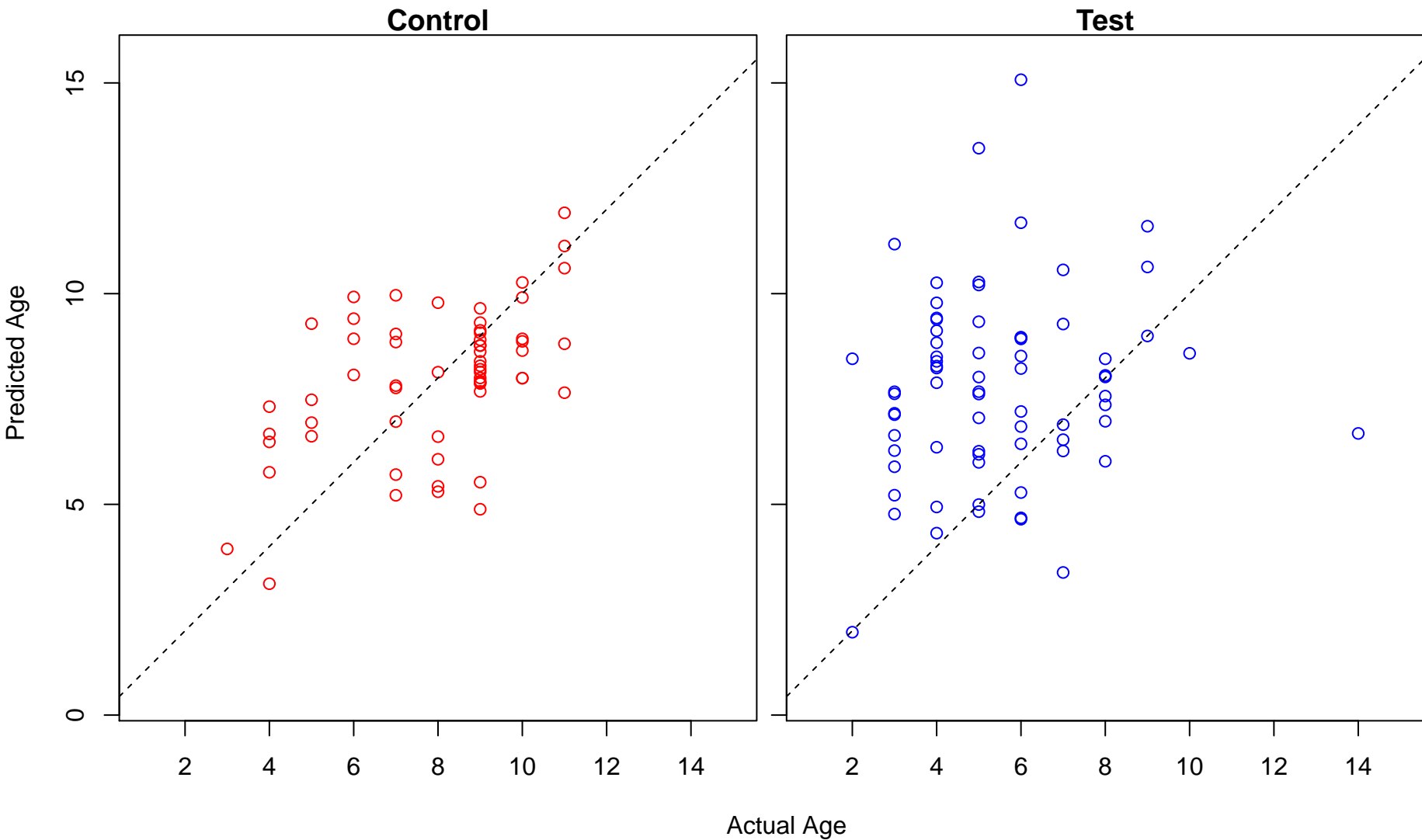
cellular macromolecule localization (Score: 1.387761)



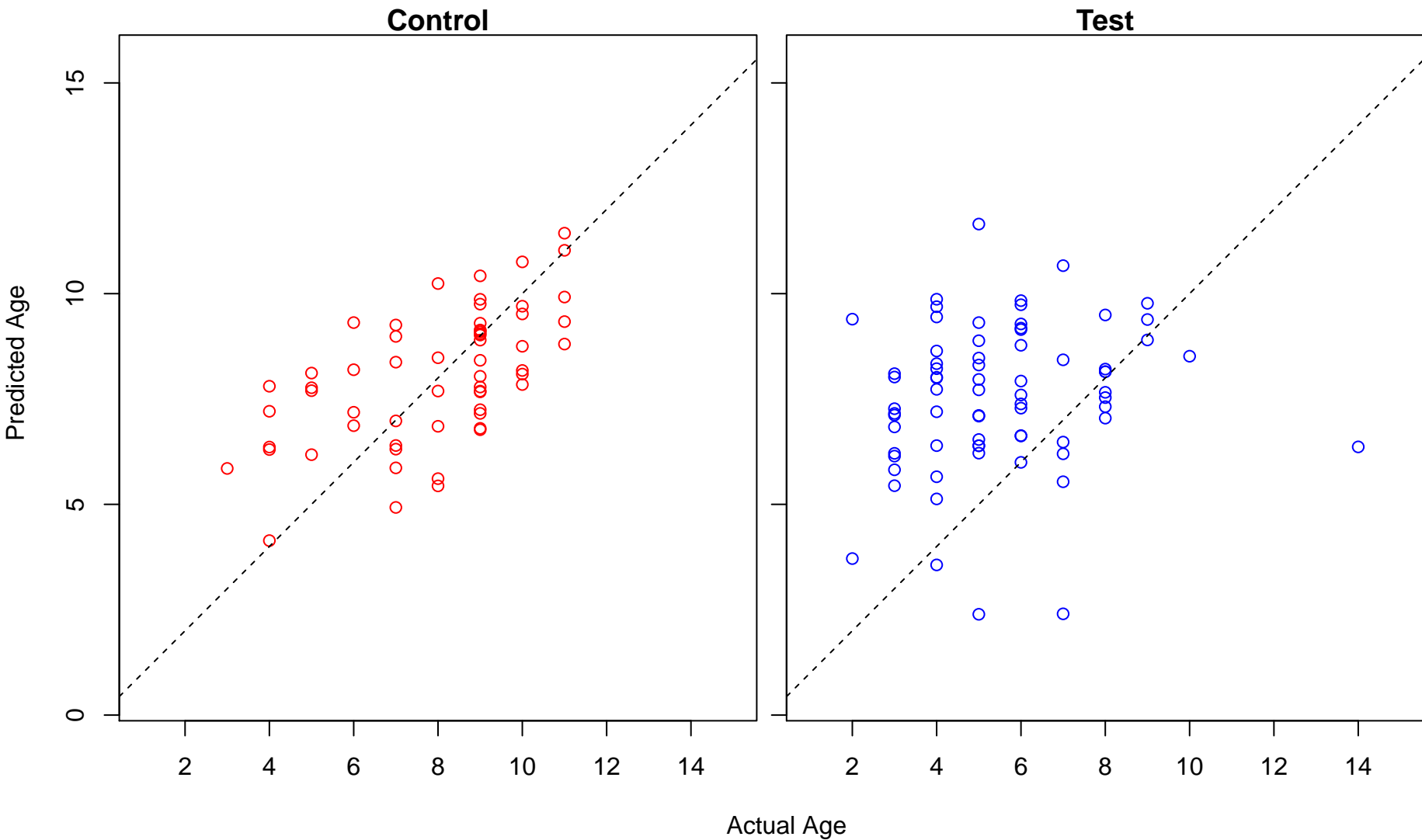
regulation of gene expression (Score: 1.387635)



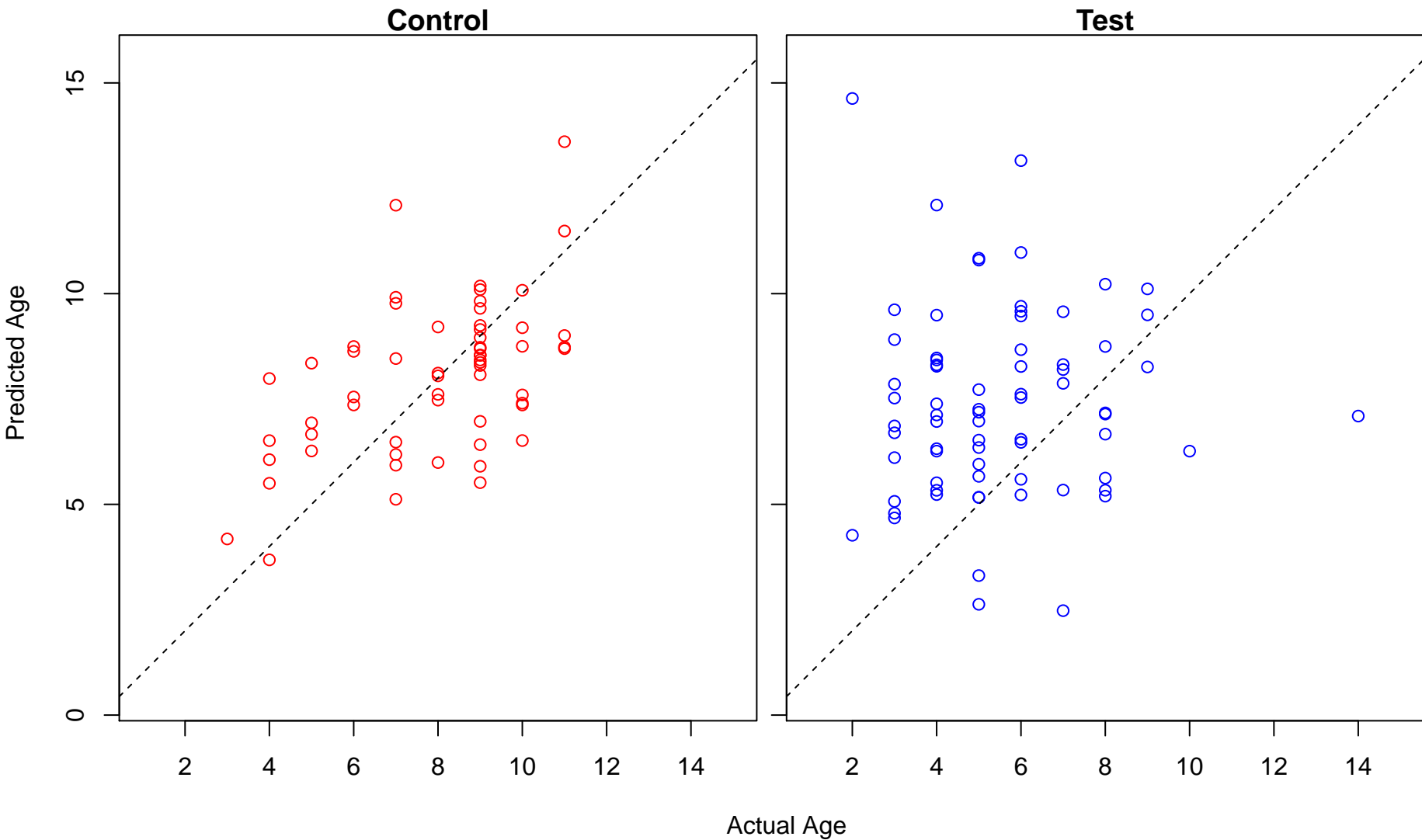
cellular response to insulin stimulus (Score: 1.383385)



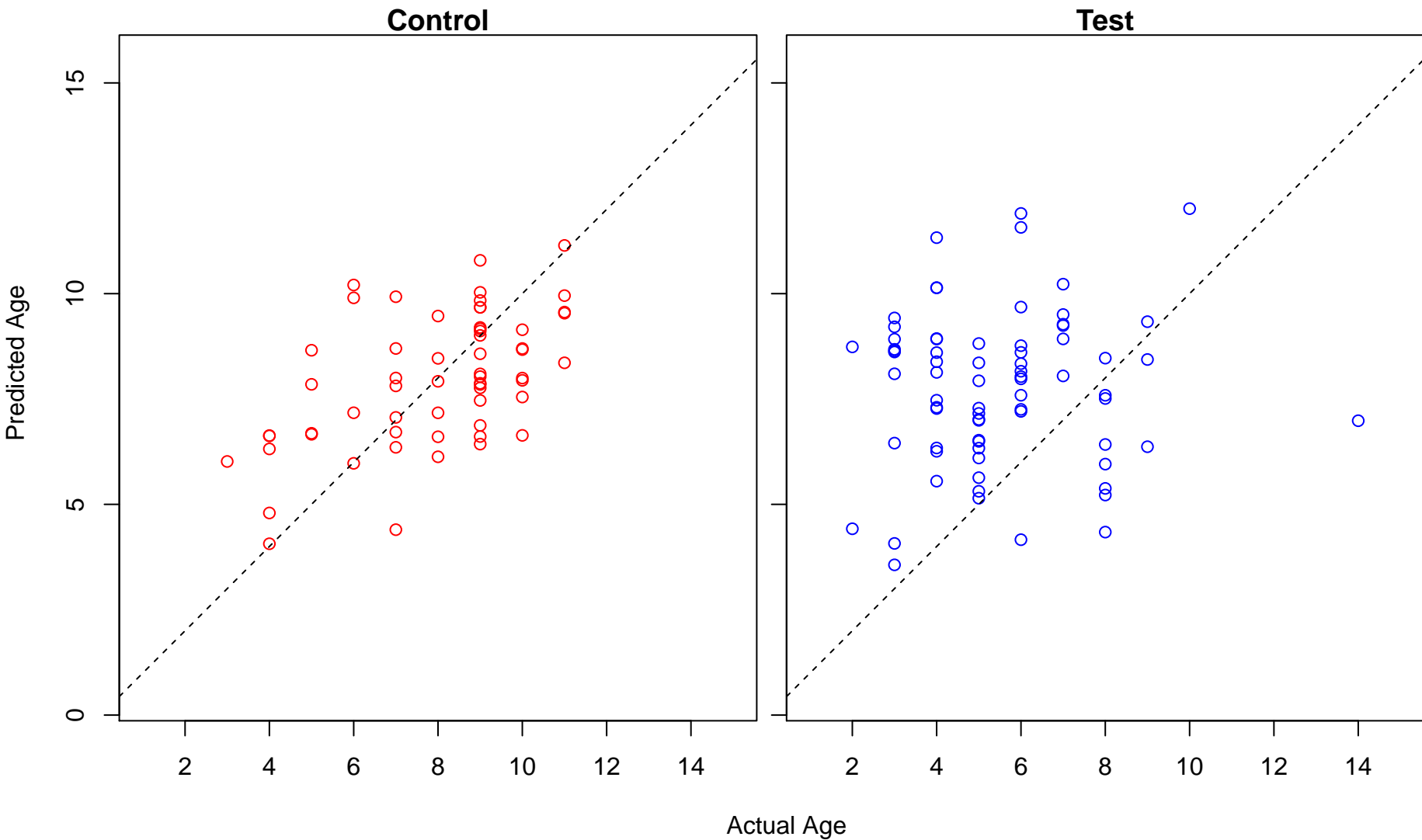
regulation of primary metabolic process (Score: 1.379575)



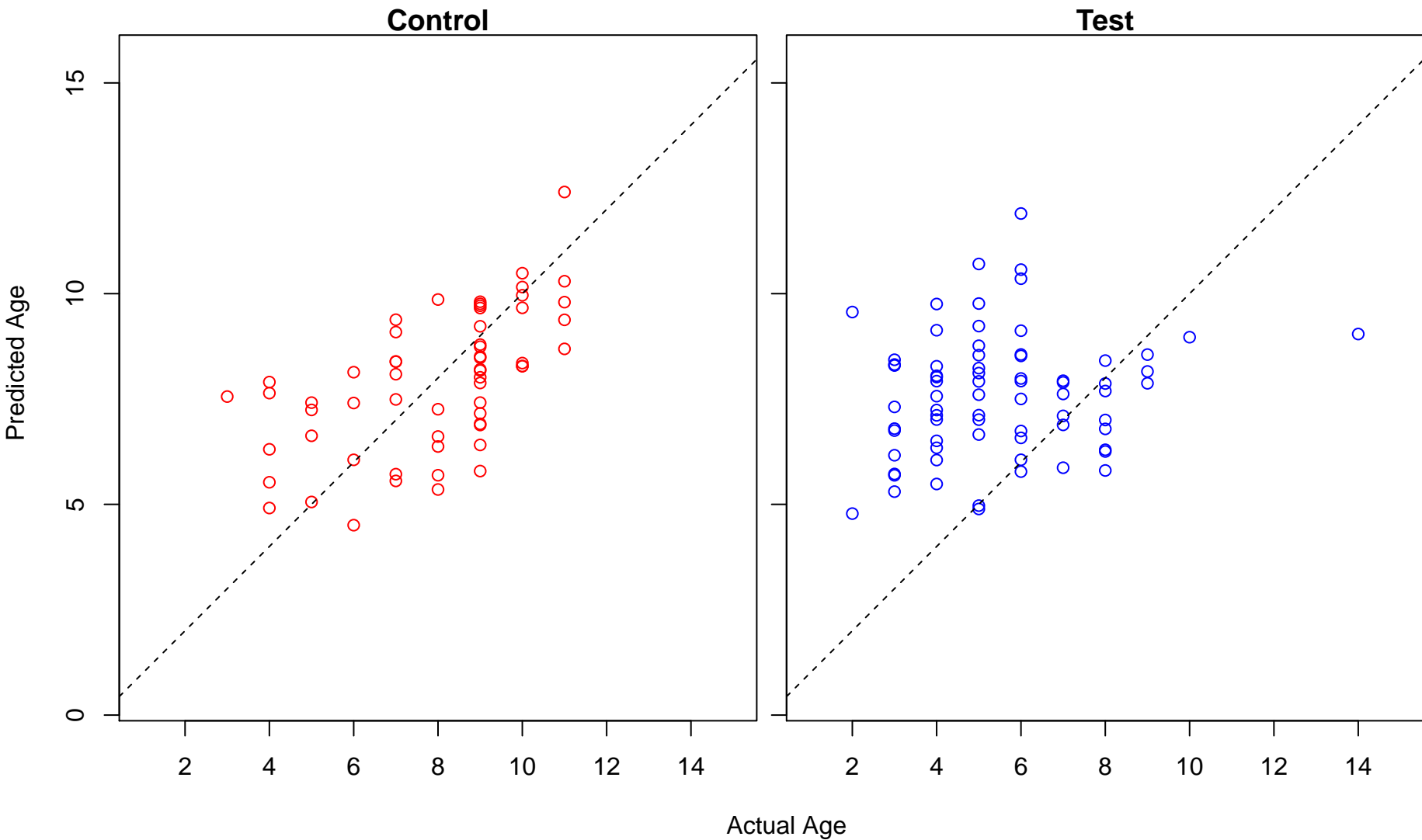
negative regulation of cell proliferation (Score: 1.378171)



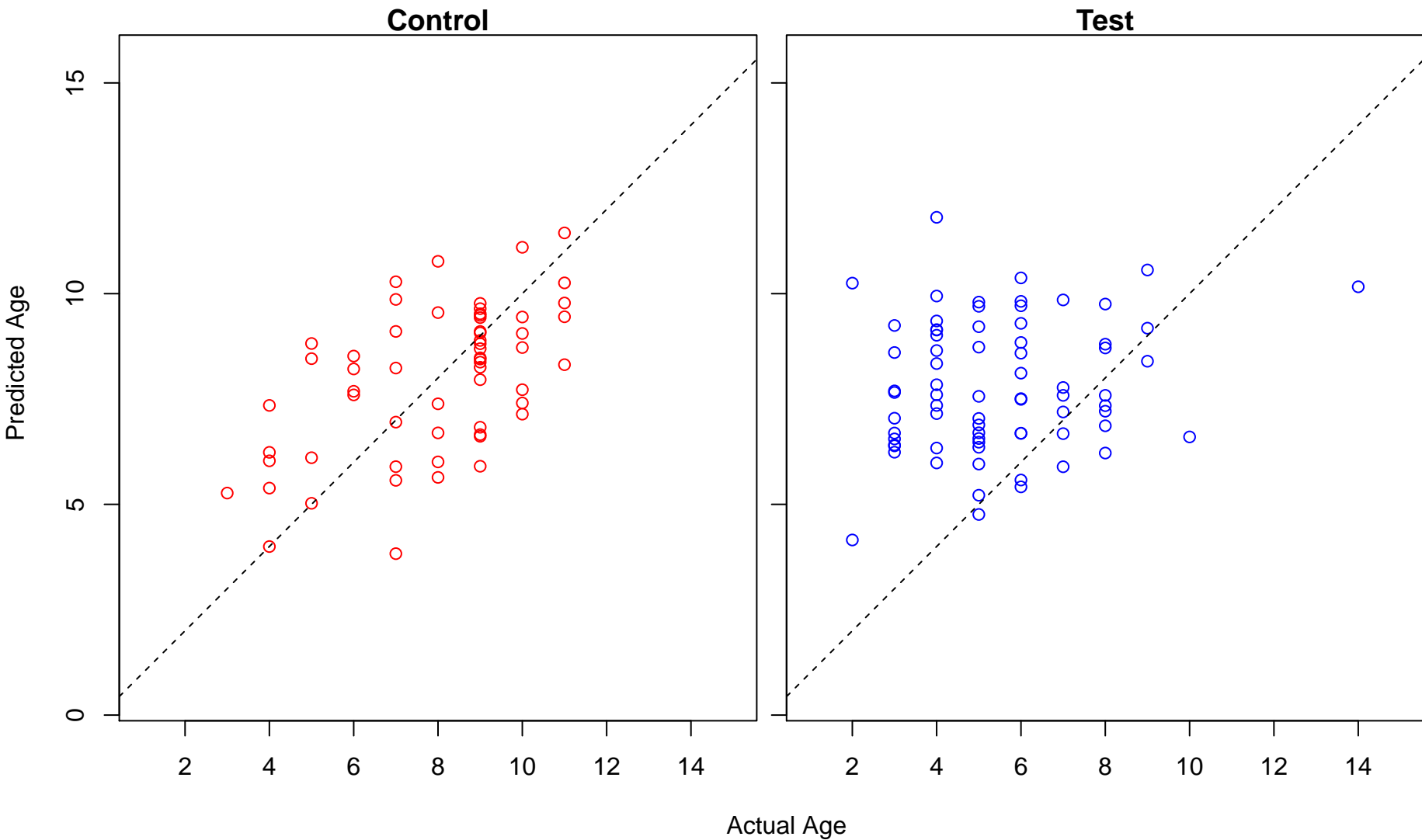
nucleus localization (Score: 1.376797)



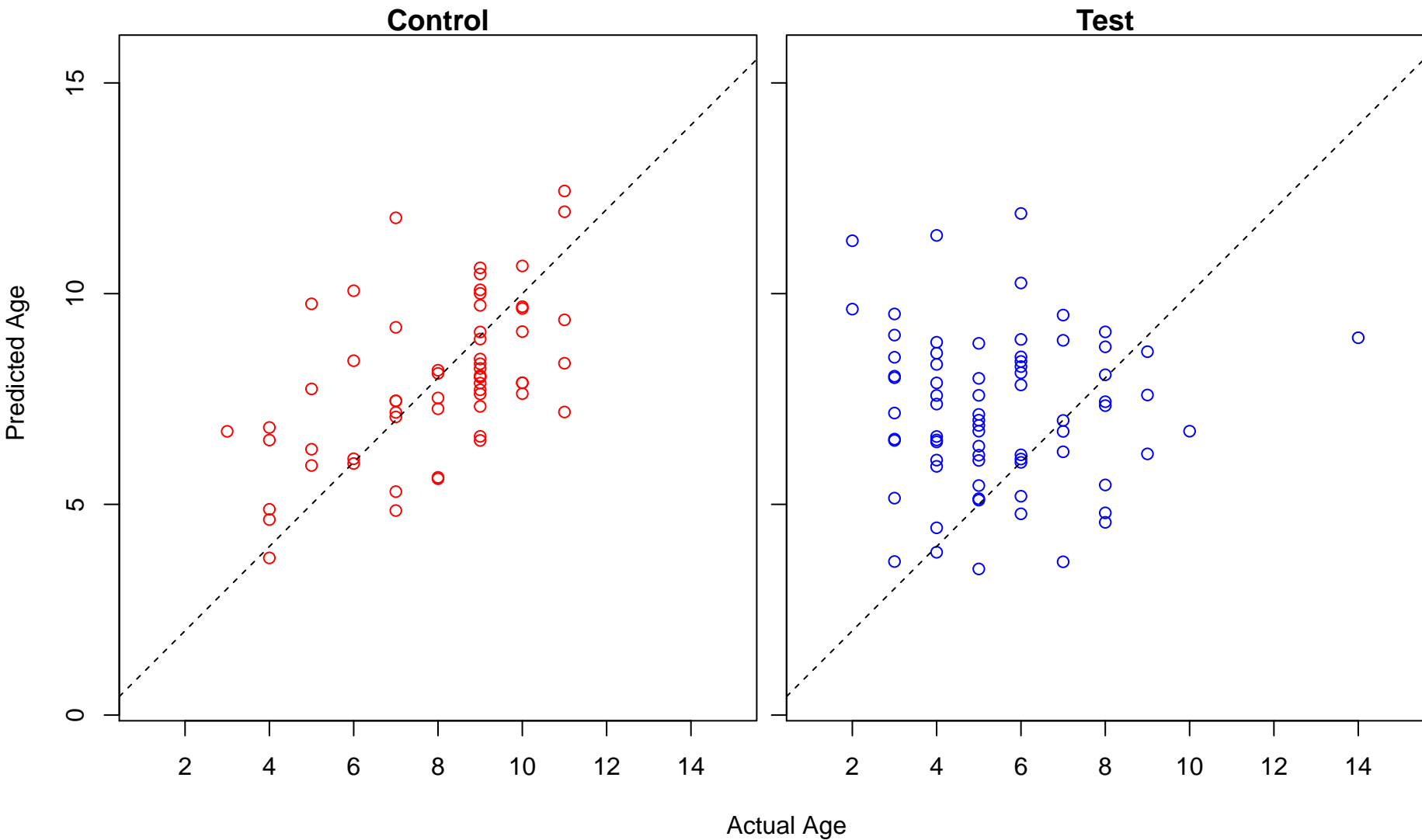
protein transport (Score: 1.374852)



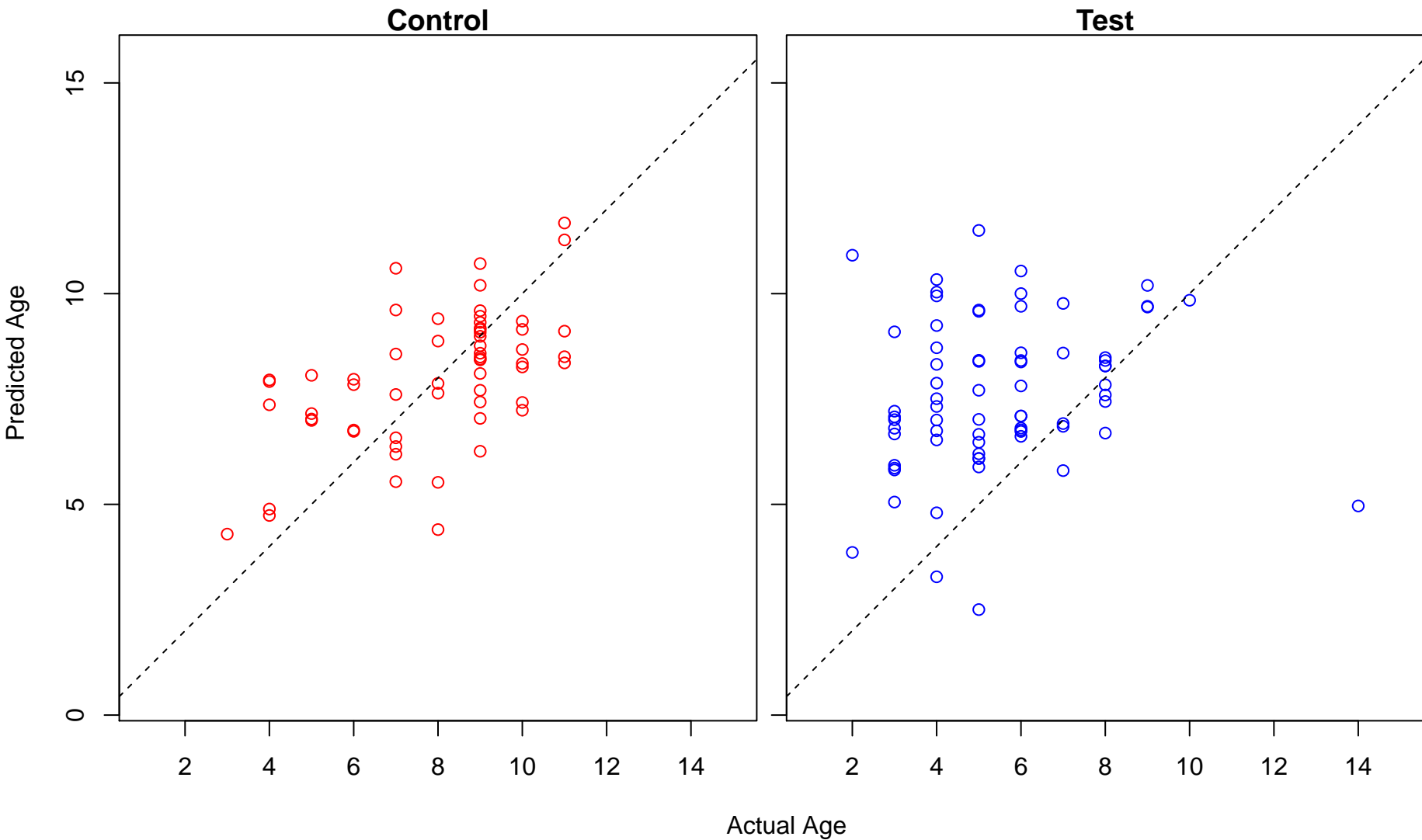
leukocyte migration (Score: 1.373133)



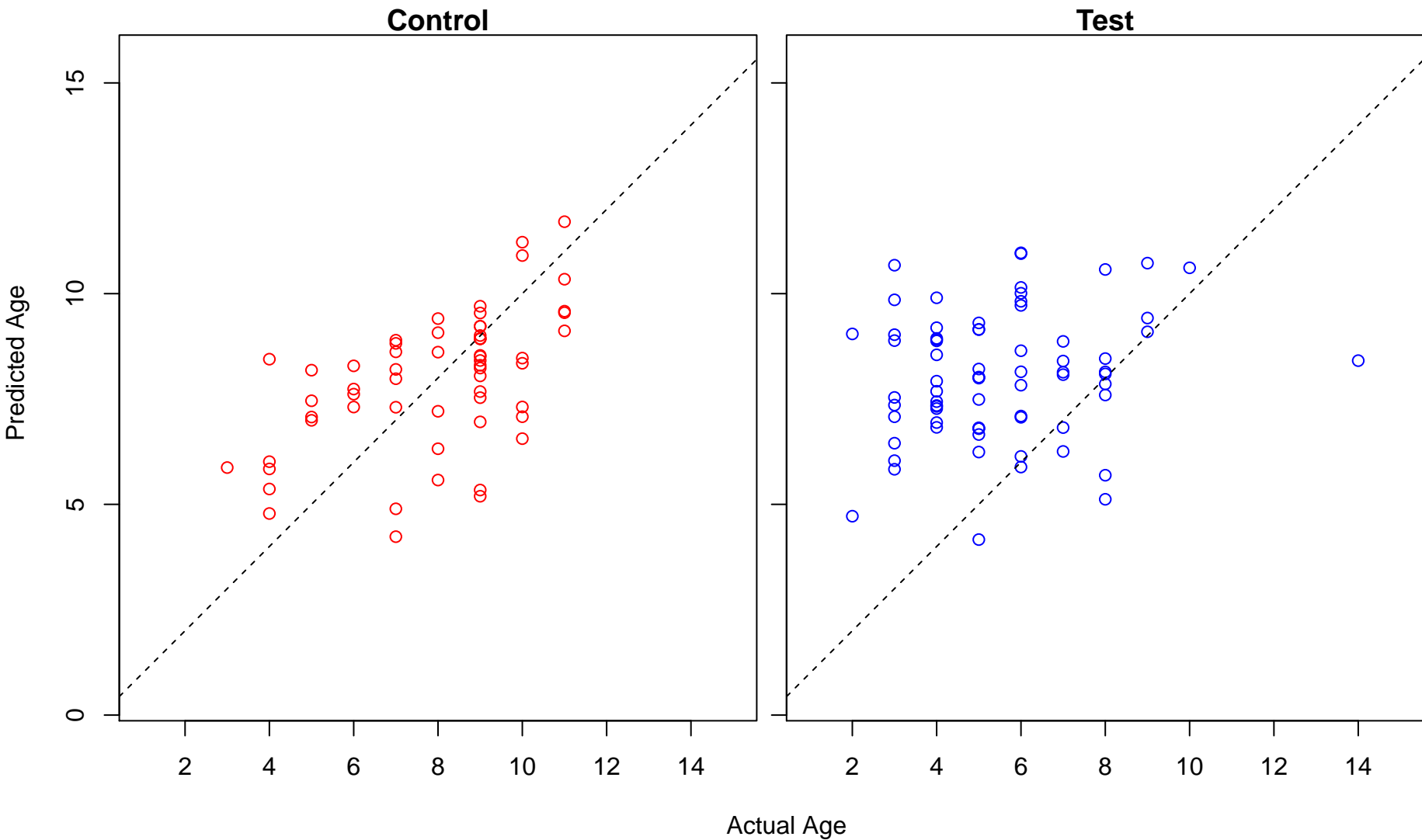
ribonucleotide biosynthetic process (Score: 1.371668)



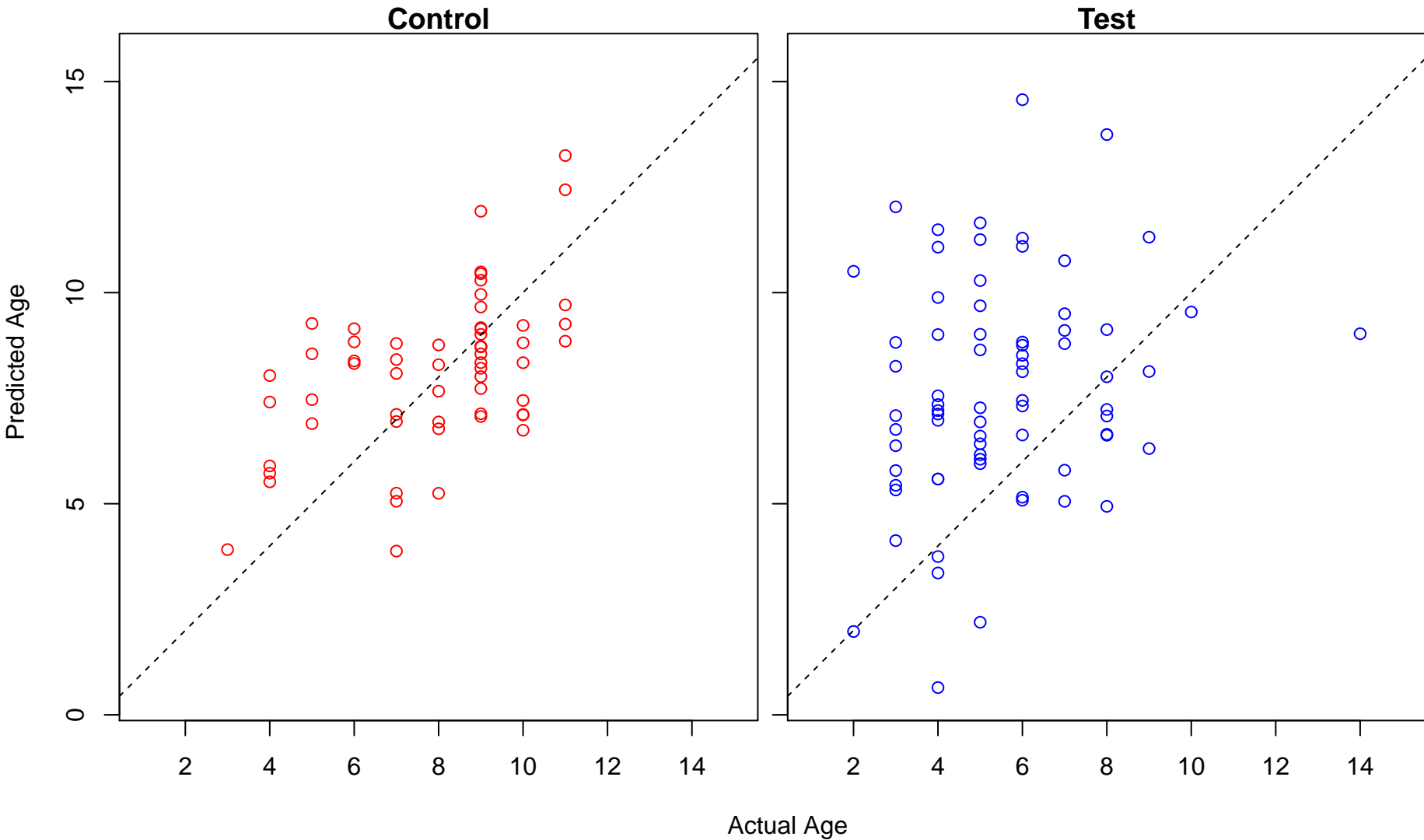
positive regulation of metabolic process (Score: 1.367696)



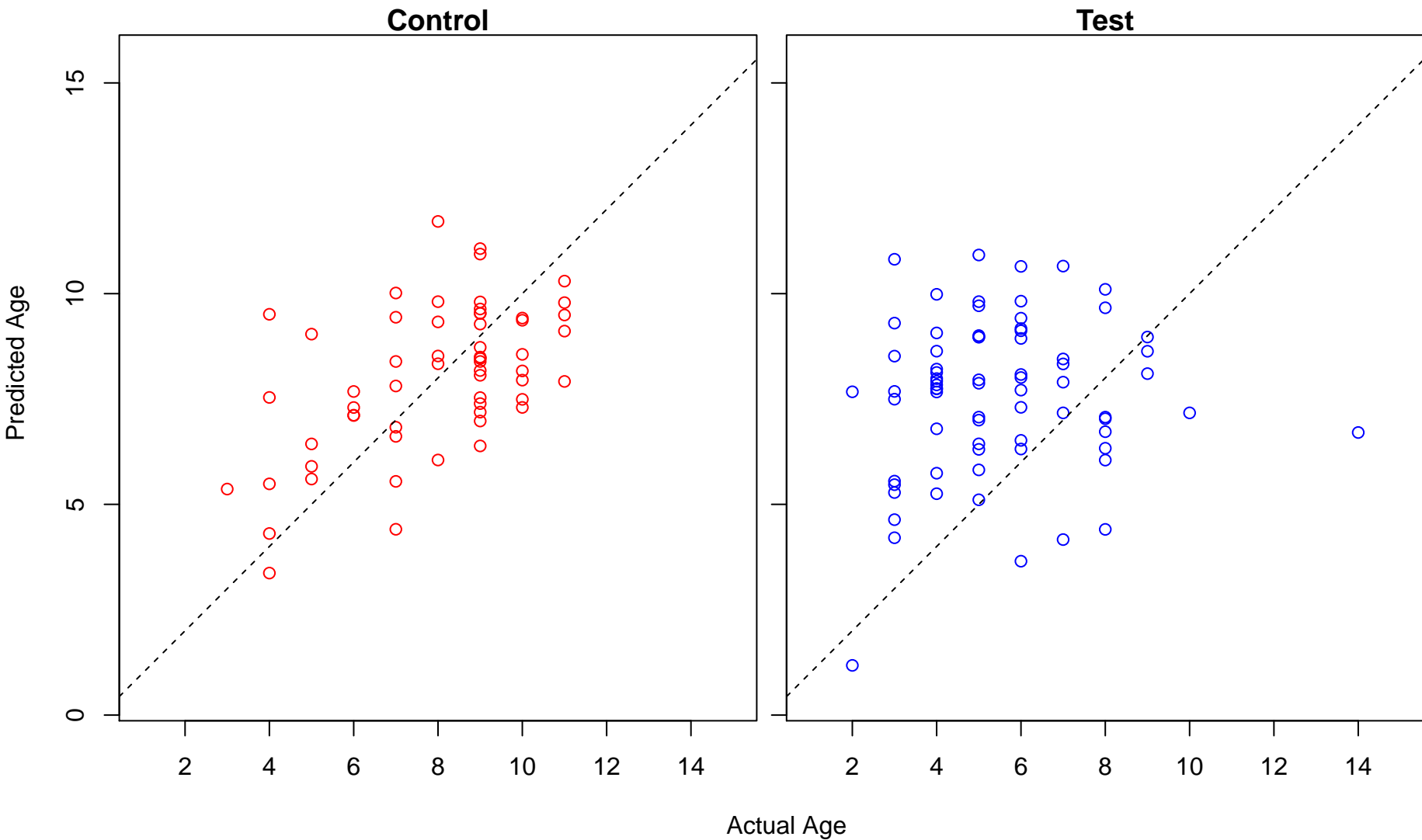
thymus development (Score: 1.366865)



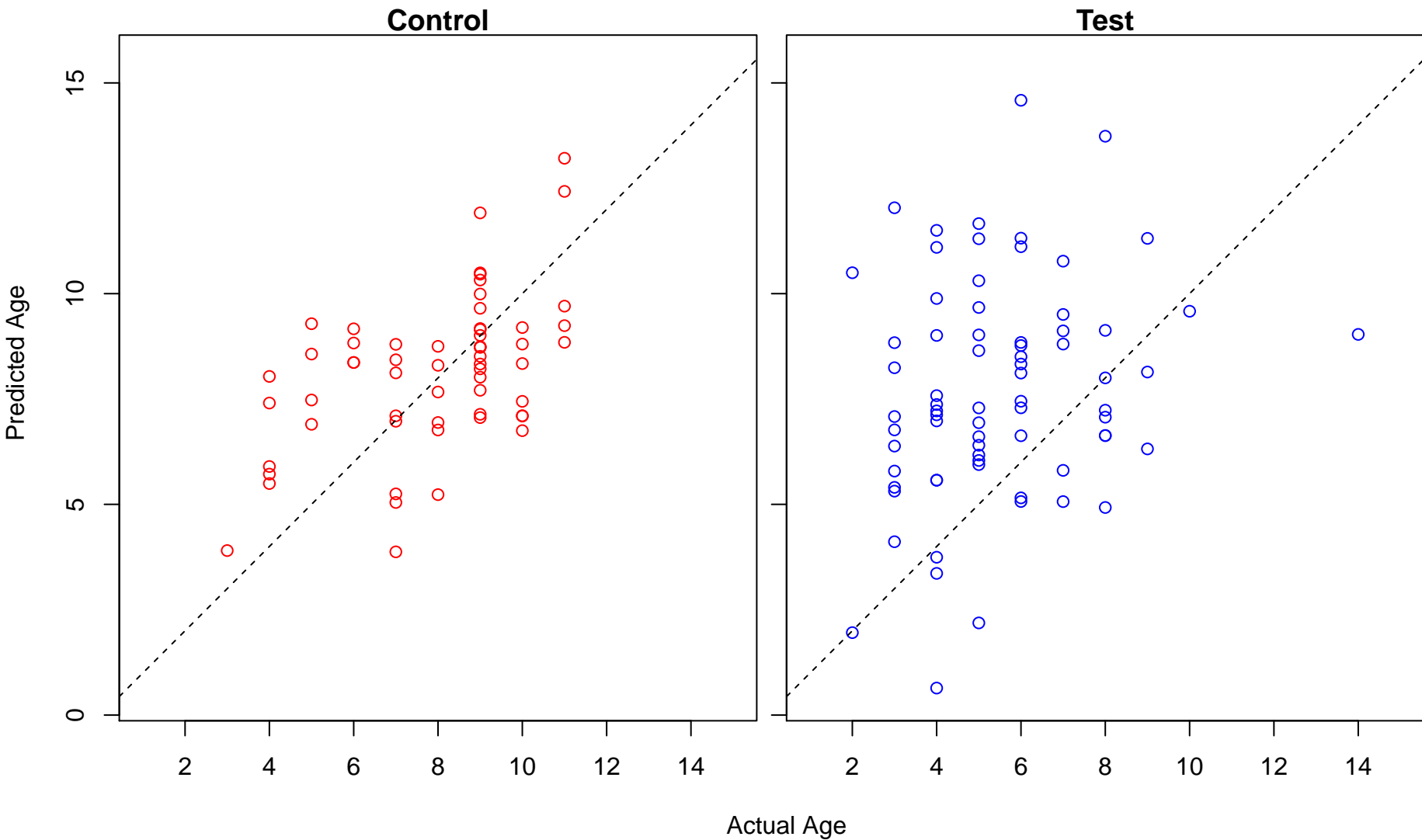
cell activation involved in immune response (Score: 1.365638)



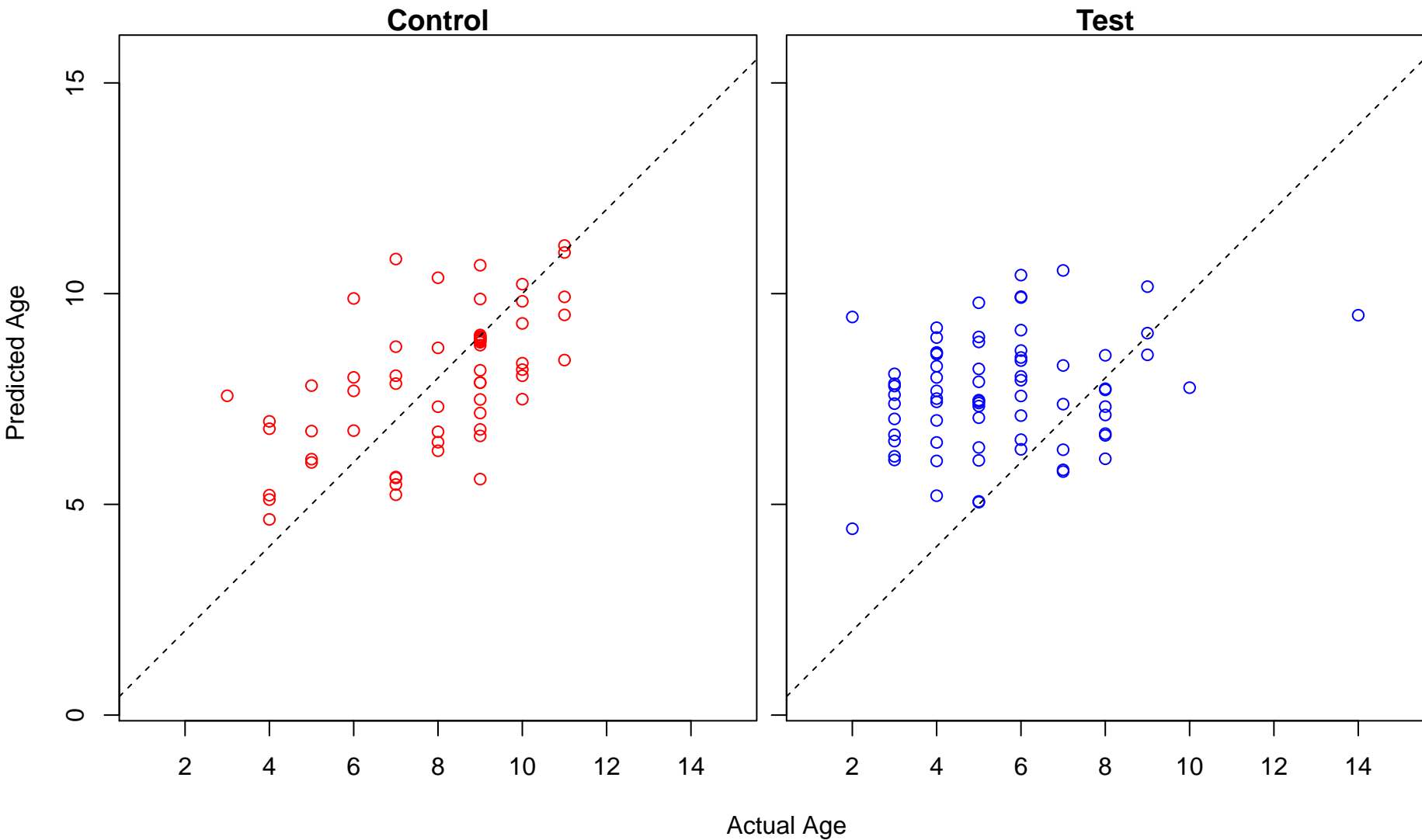
positive regulation of tyrosine phosphorylation of STAT protein (Score: 1.362190)



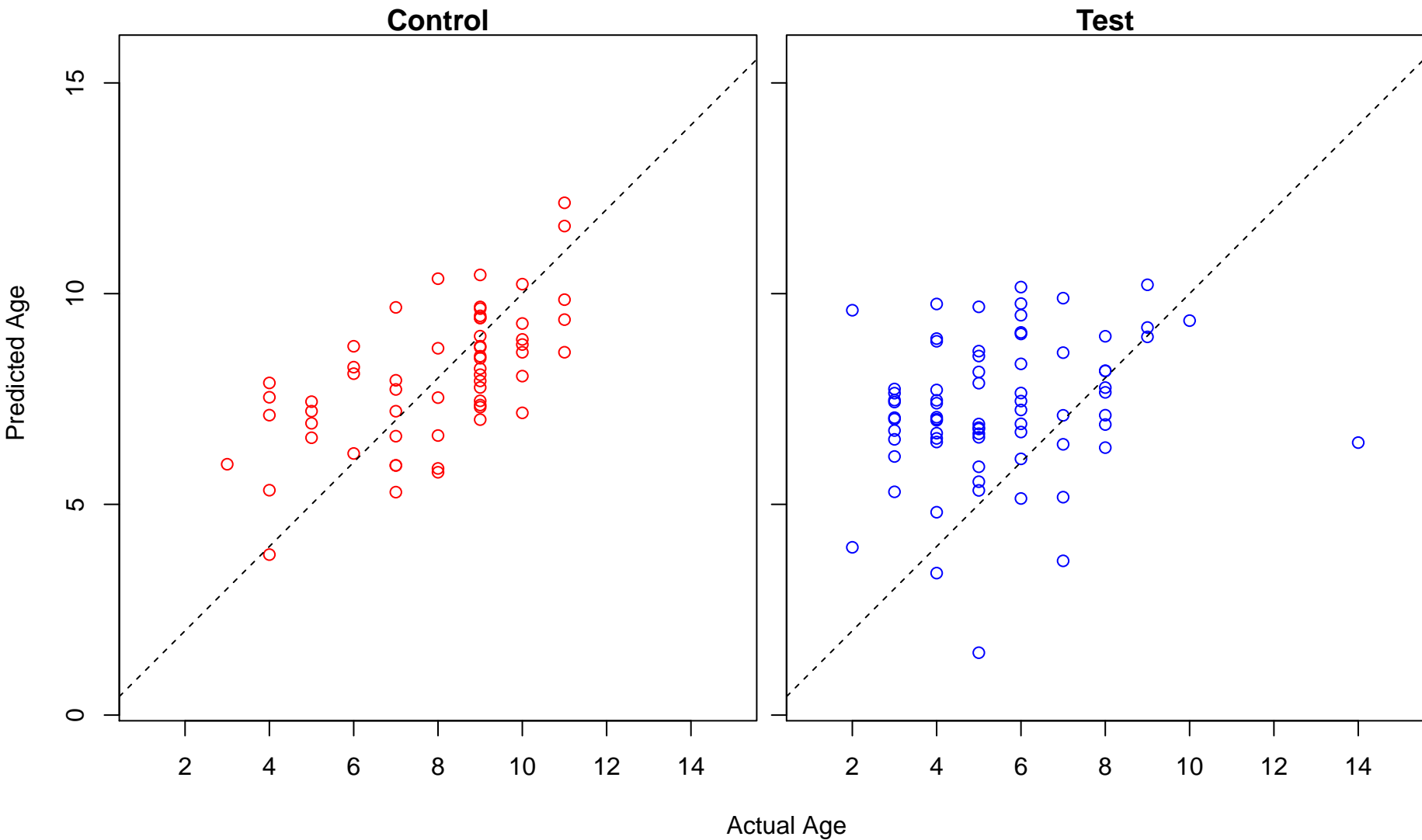
leukocyte activation involved in immune response (Score: 1.361019)



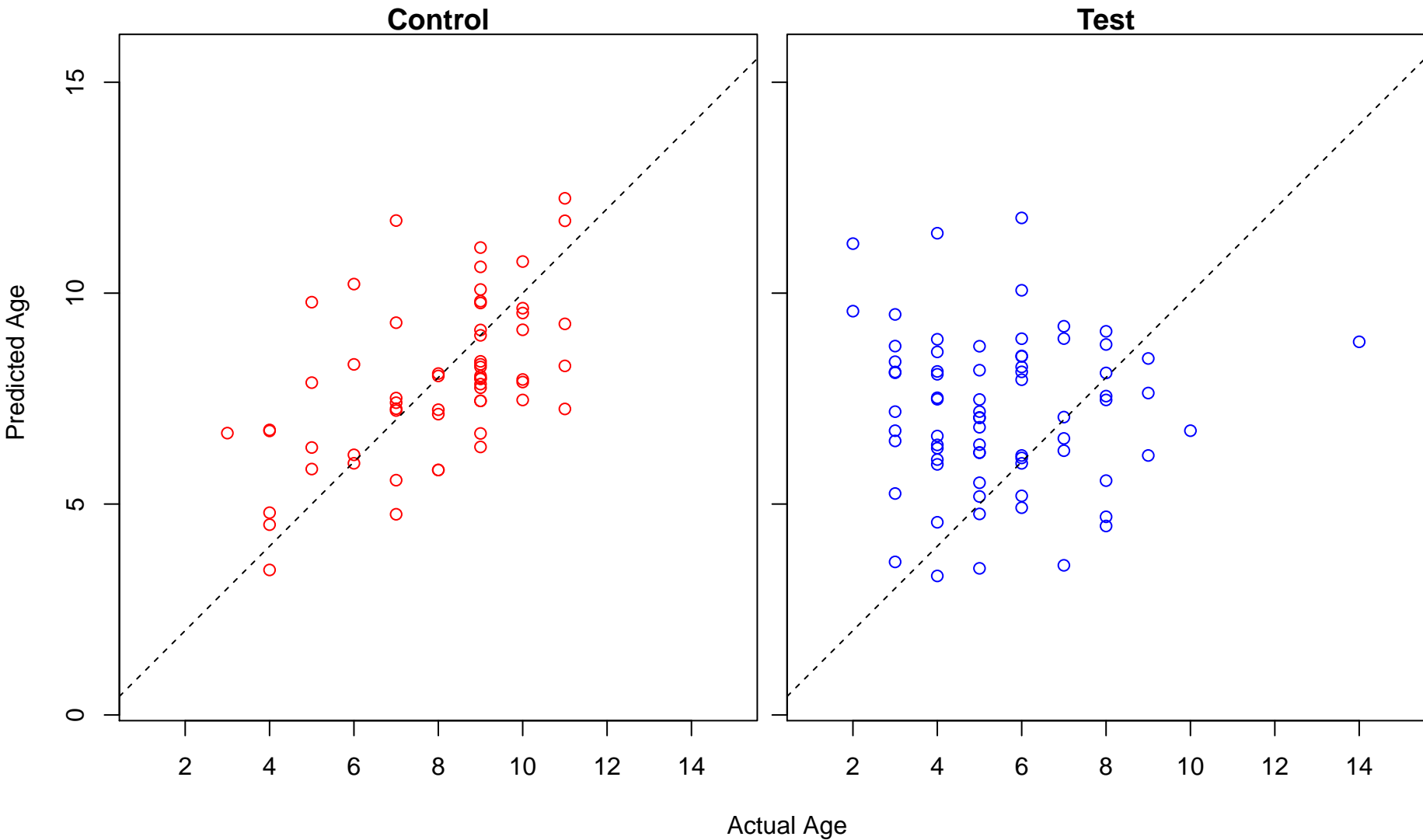
regulation of nitrogen compound metabolic process (Score: 1.357540)



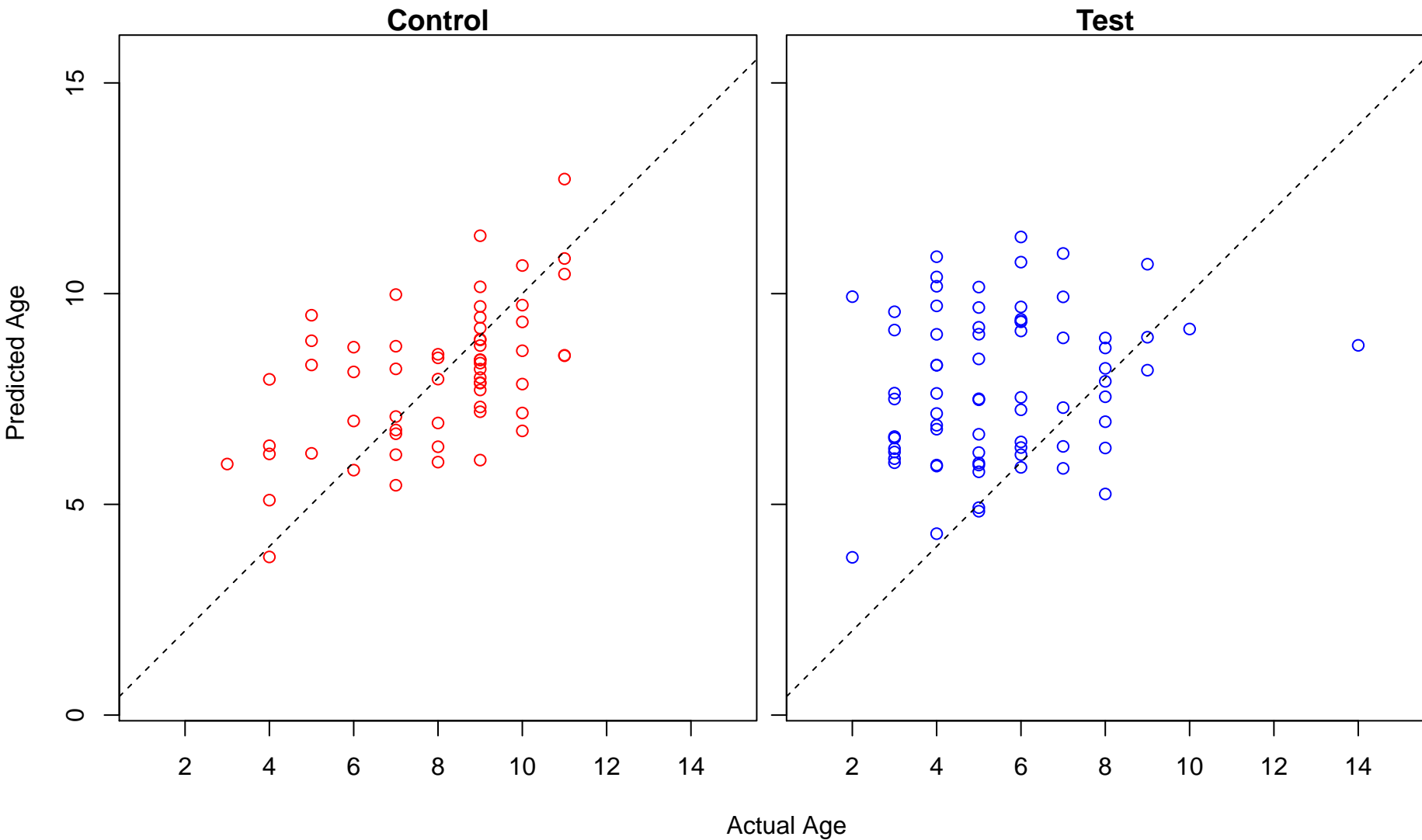
regulation of metabolic process (Score: 1.355744)



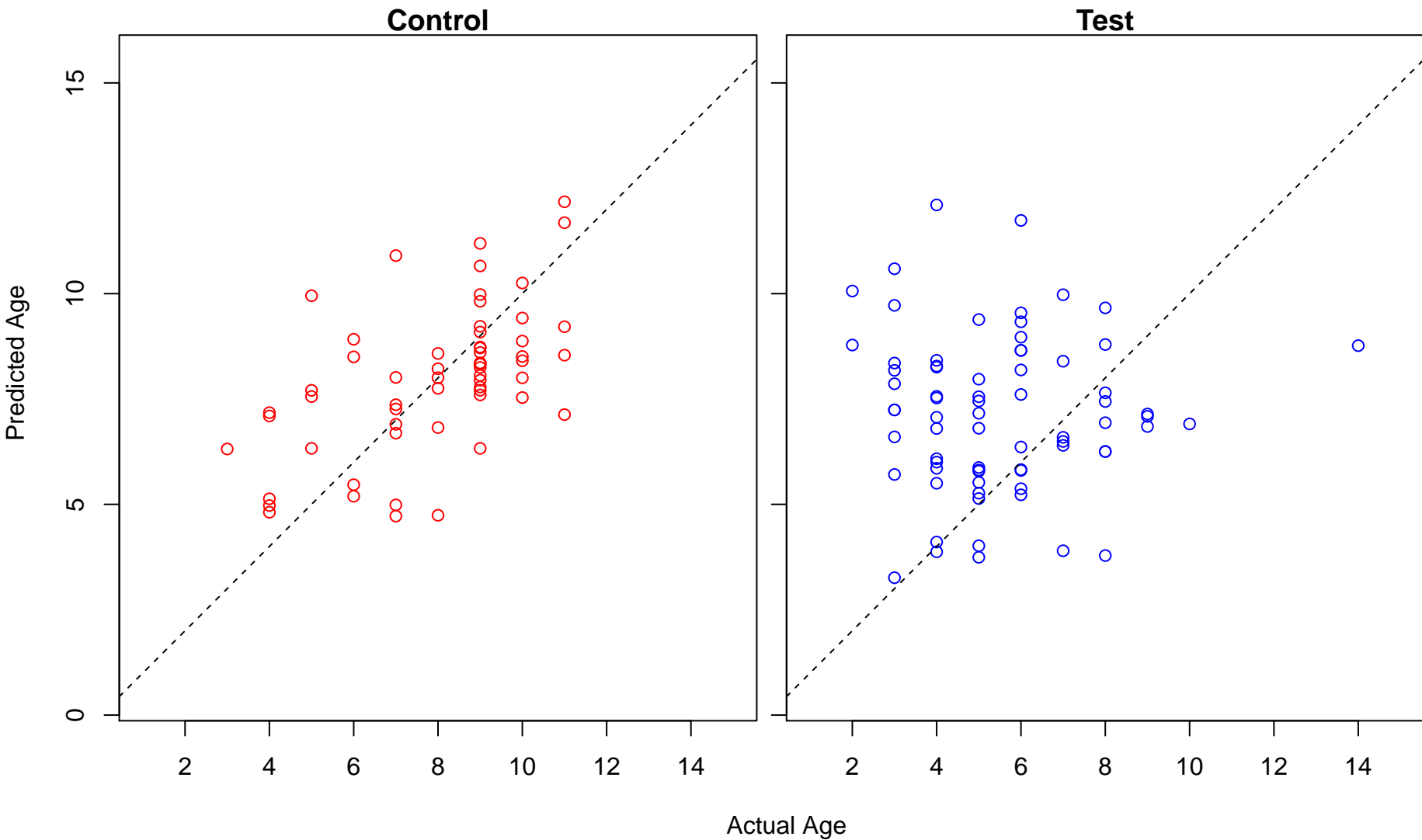
purine ribonucleotide biosynthetic process (Score: 1.354926)



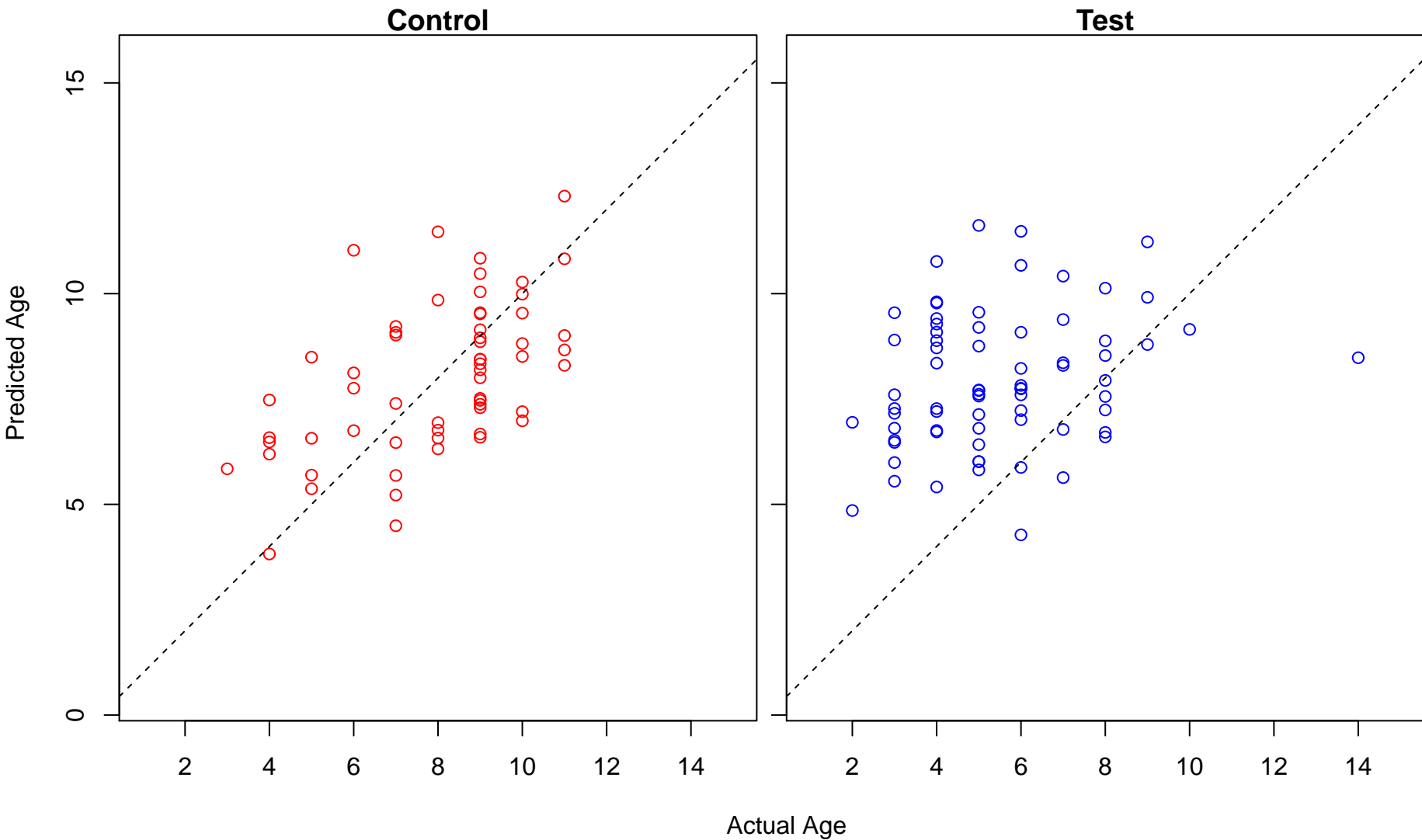
apoptotic process (Score: 1.353360)



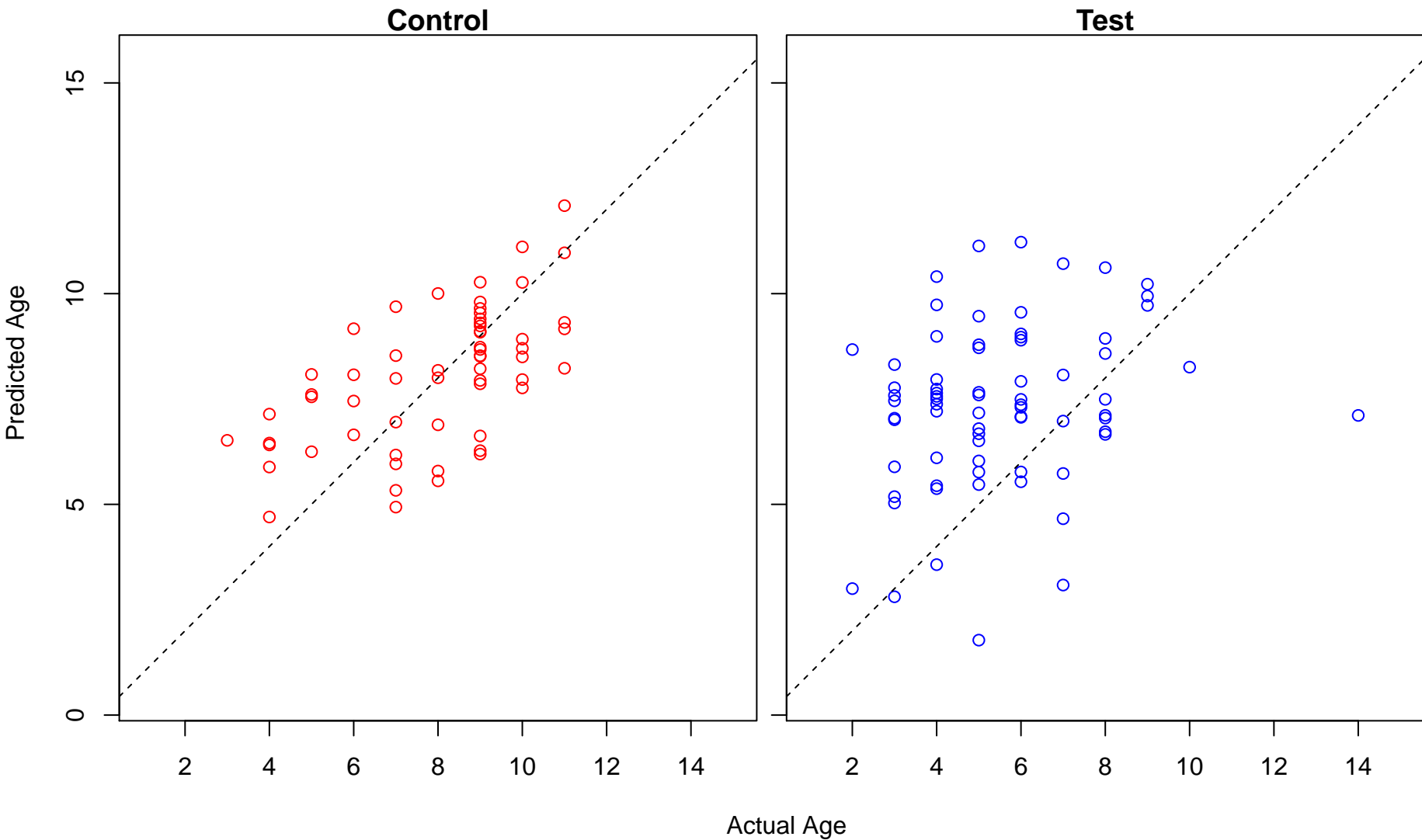
nucleoside phosphate biosynthetic process (Score: 1.351957)



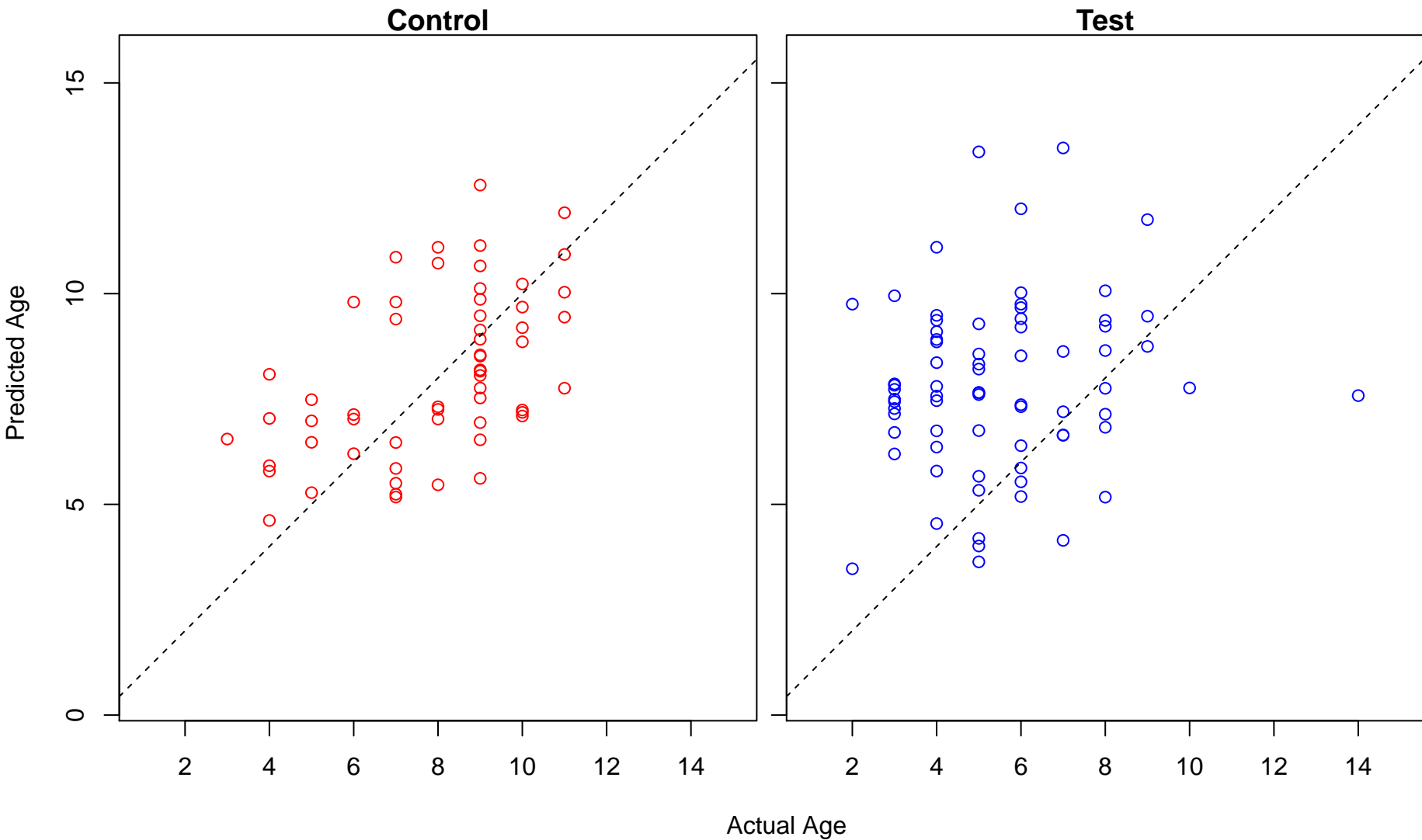
regulation of neuron differentiation (Score: 1.351842)



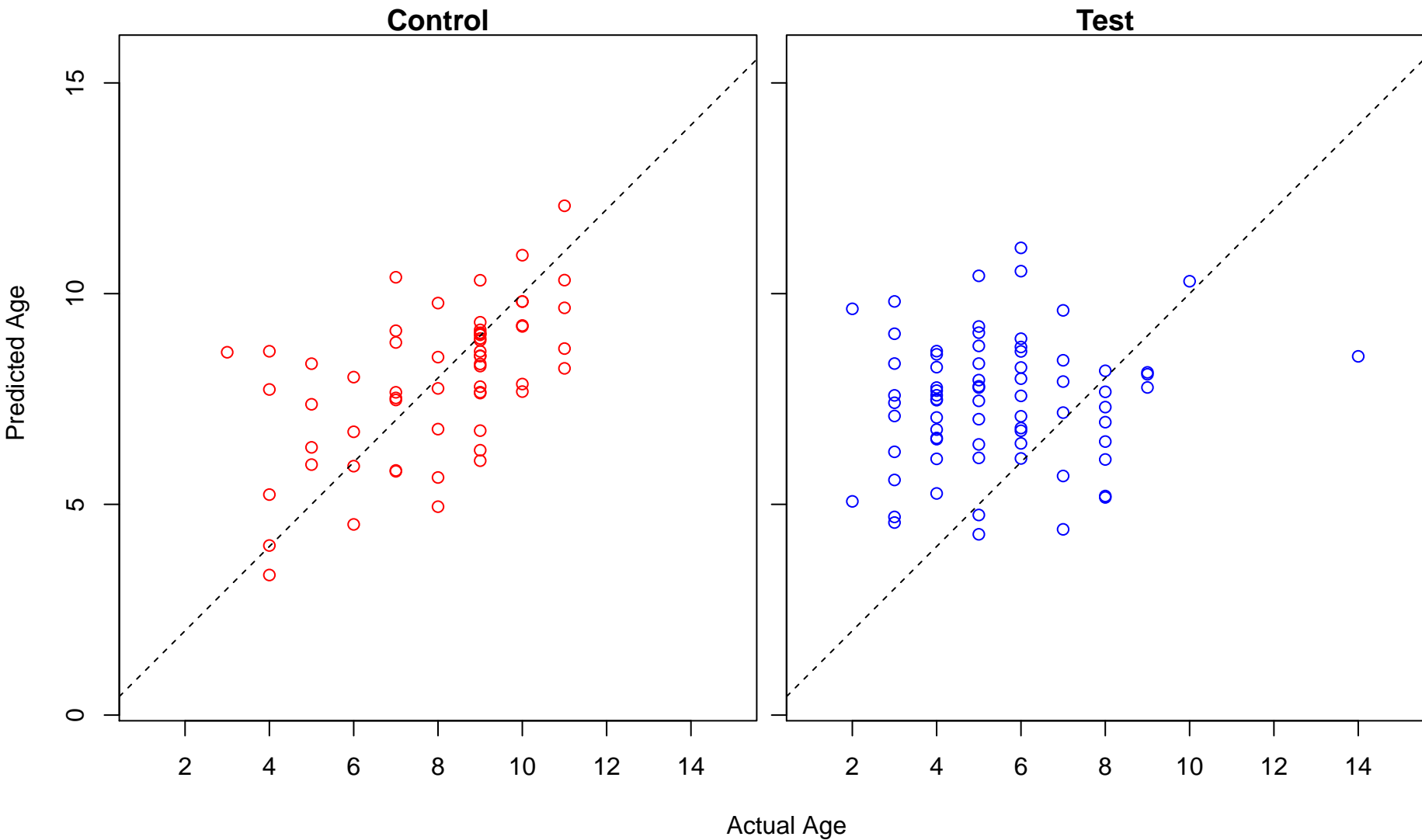
negative regulation of metabolic process (Score: 1.348953)



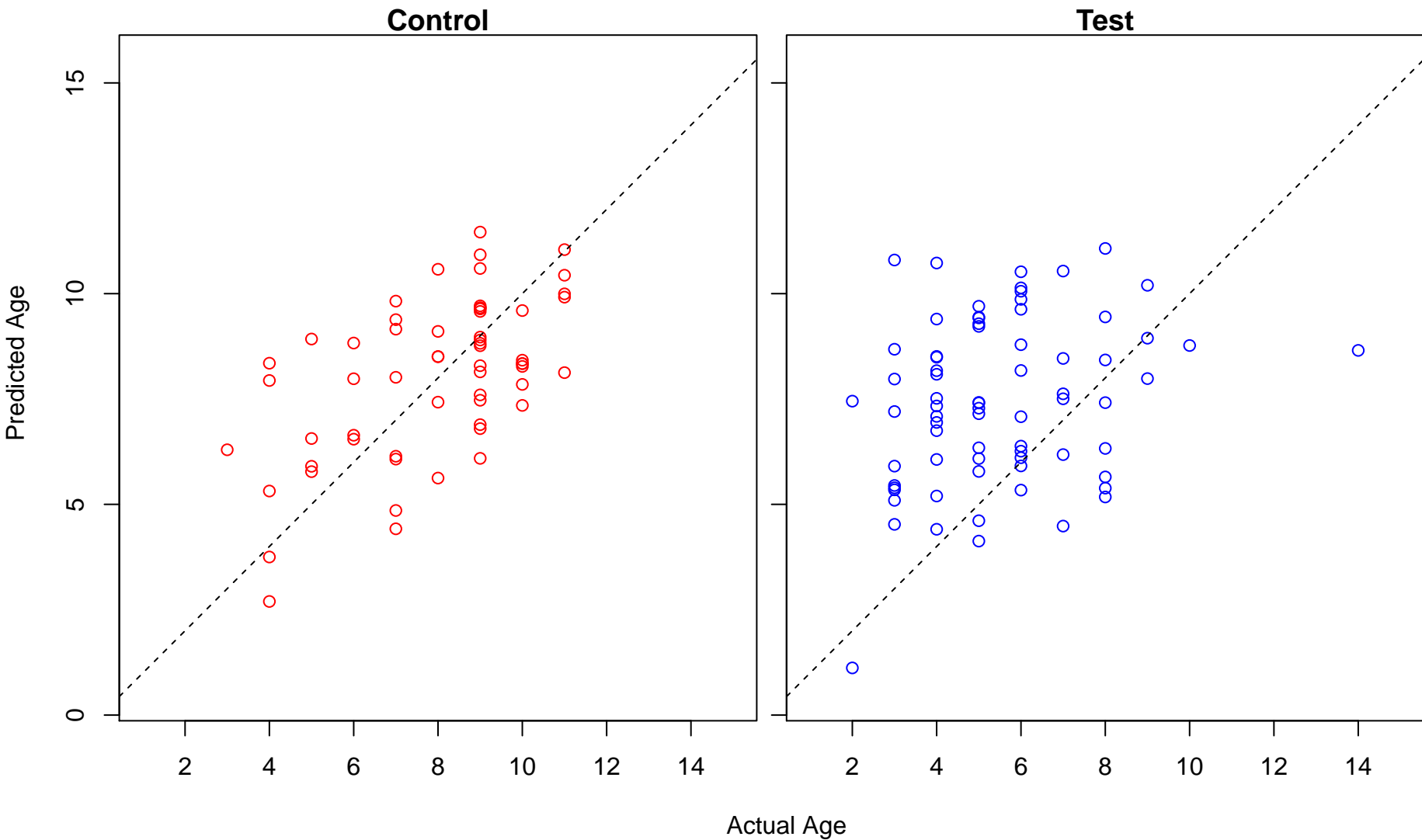
positive regulation of cell projection organization (Score: 1.348252)



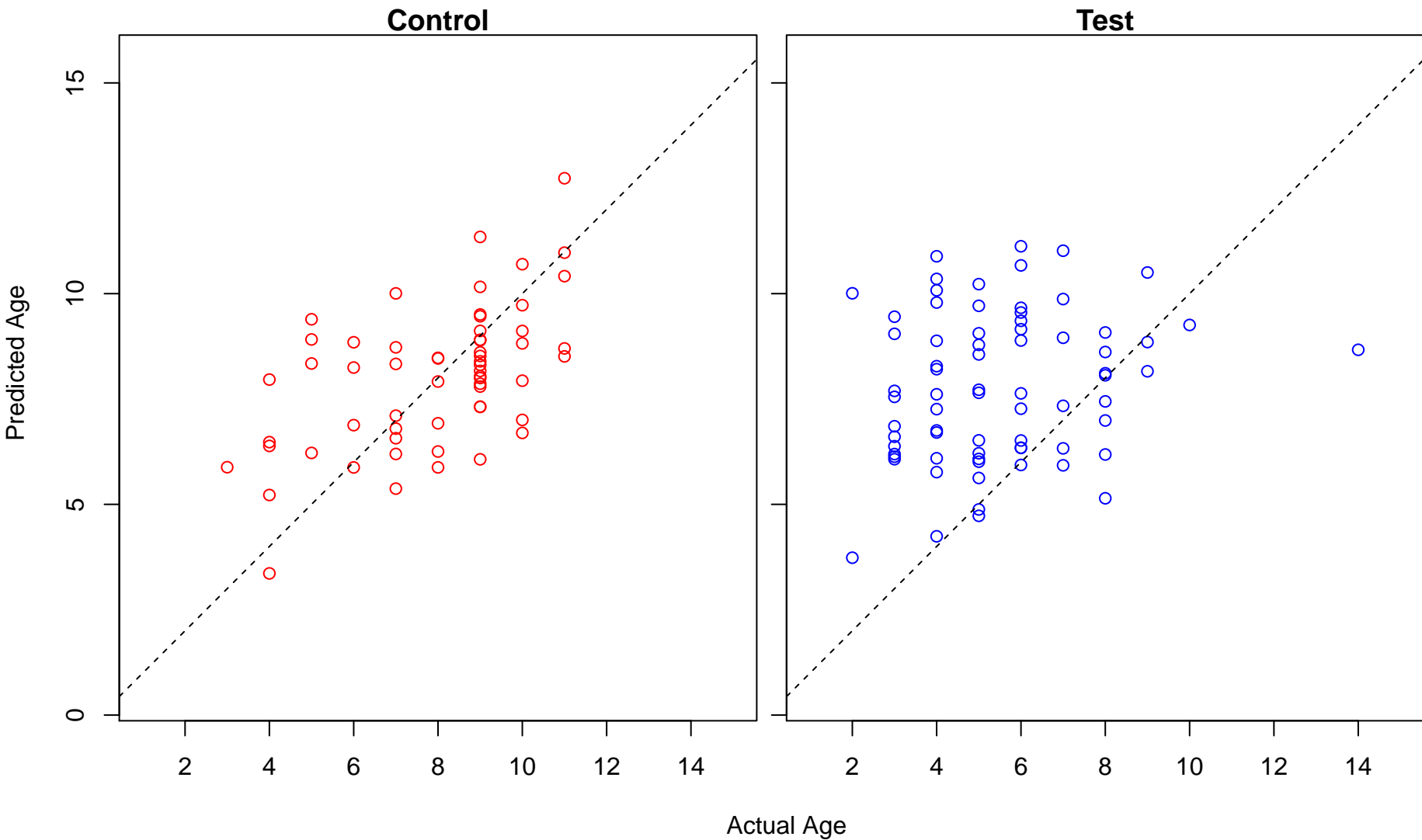
protein localization to organelle (Score: 1.346755)



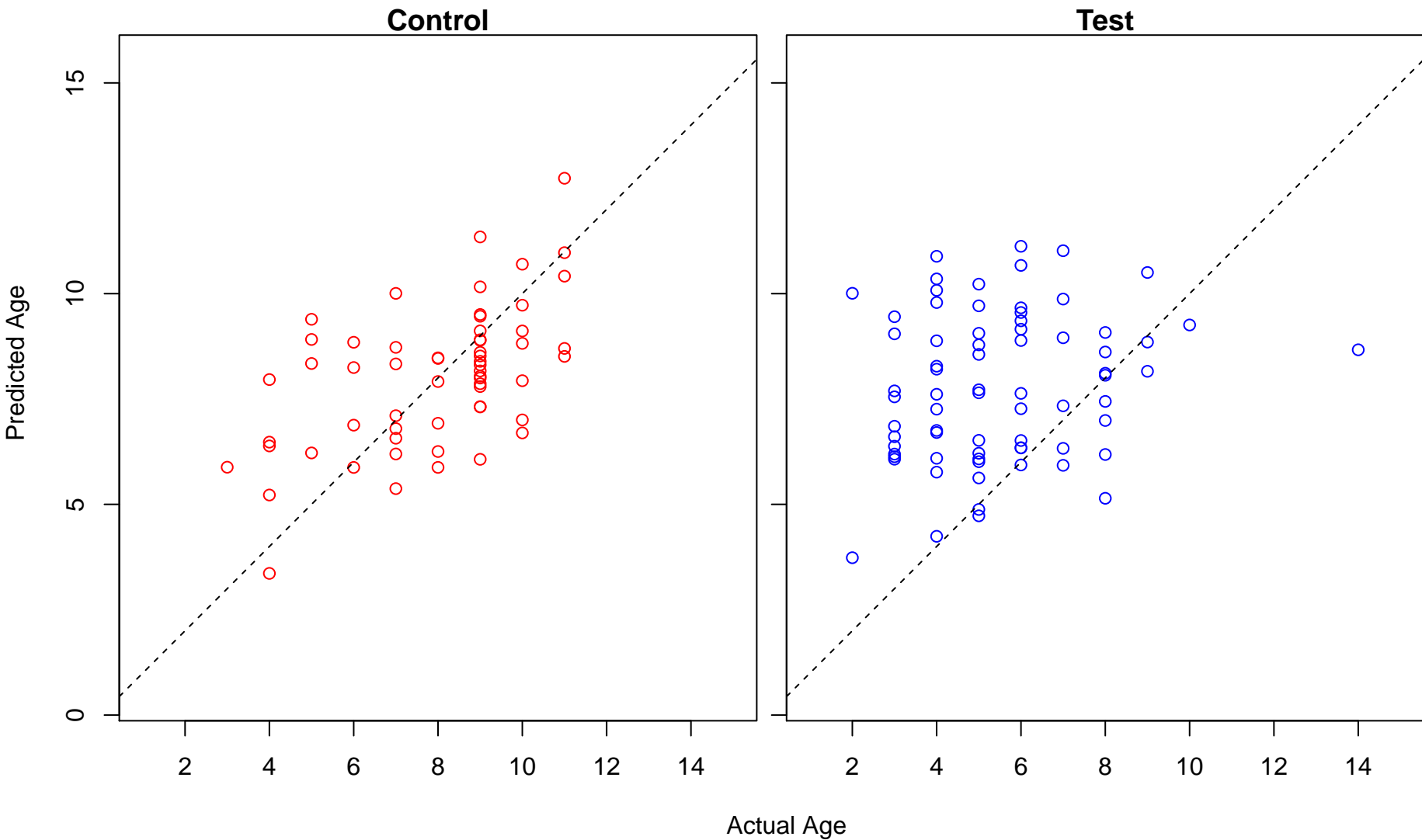
regulation of JAK-STAT cascade (Score: 1.345050)



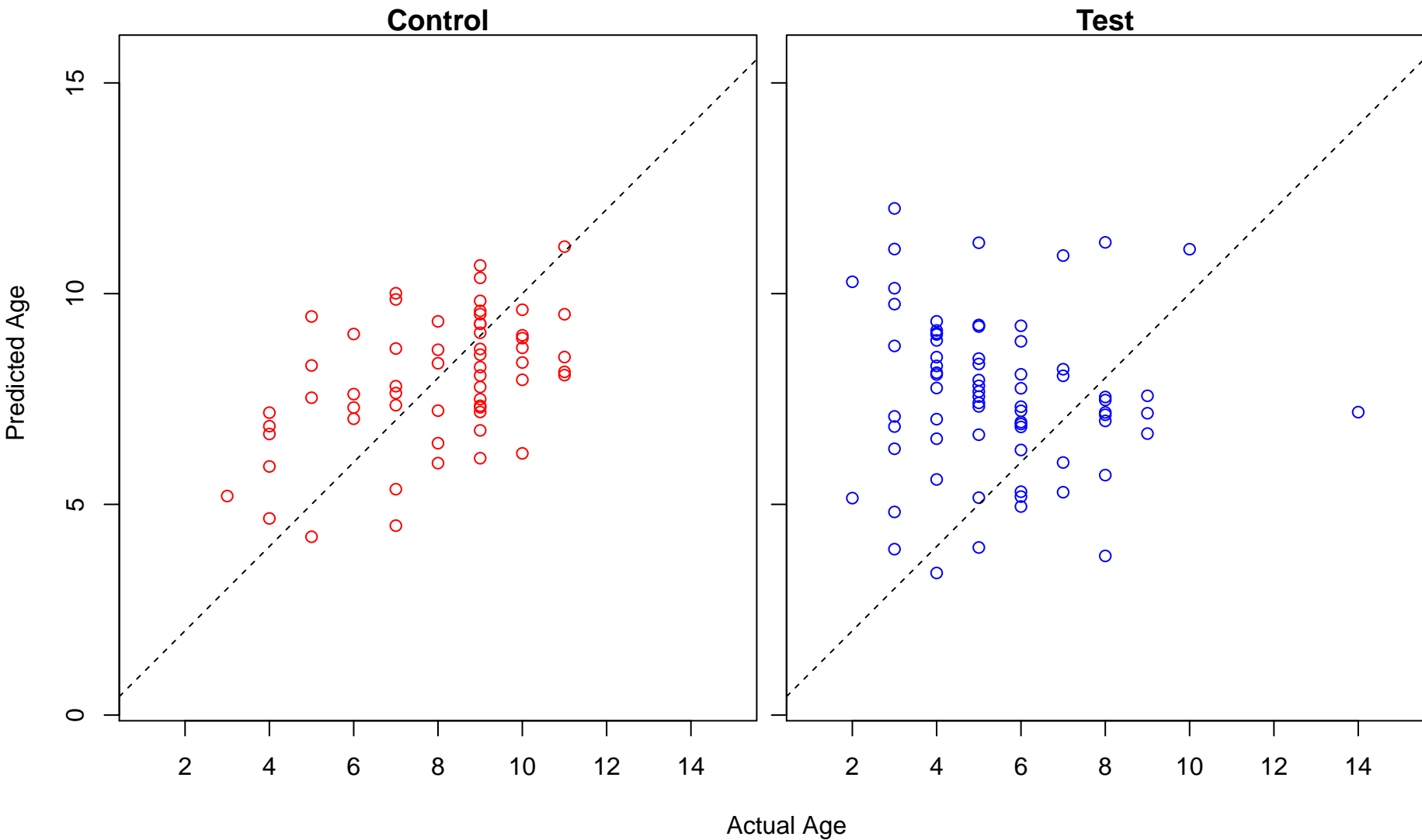
cell death (Score: 1.344192)



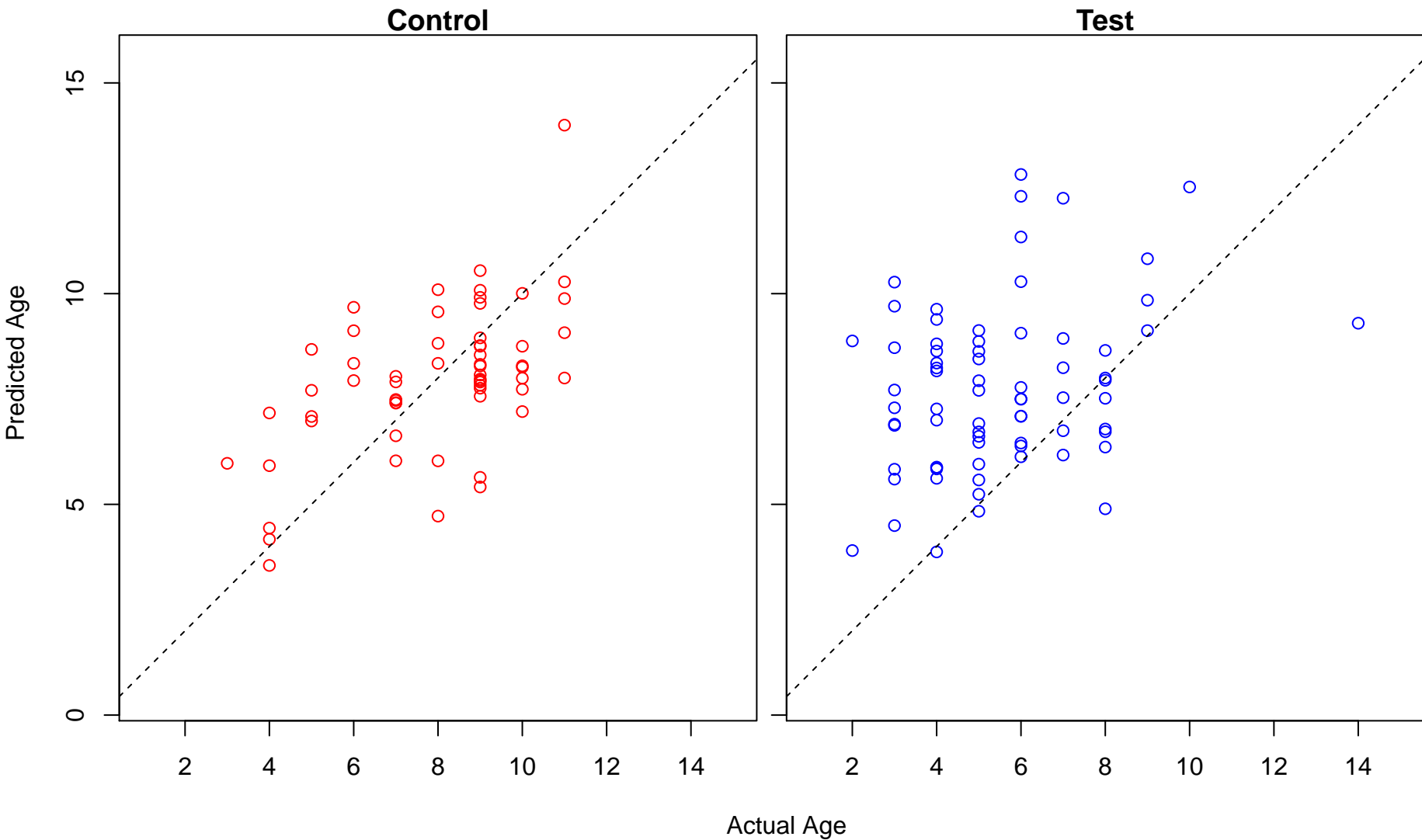
death (Score: 1.344192)



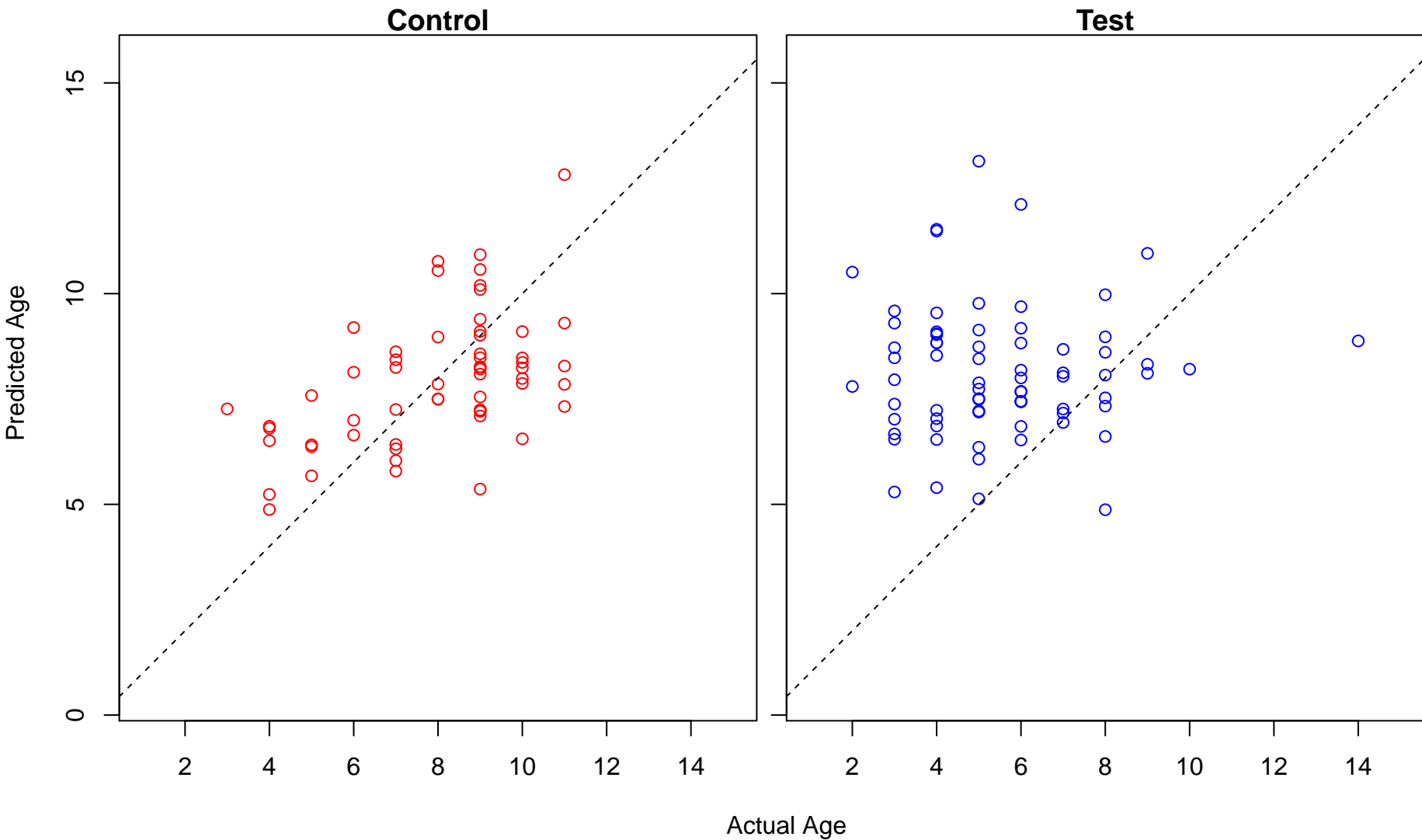
regulation of meiotic cell cycle (Score: 1.342956)



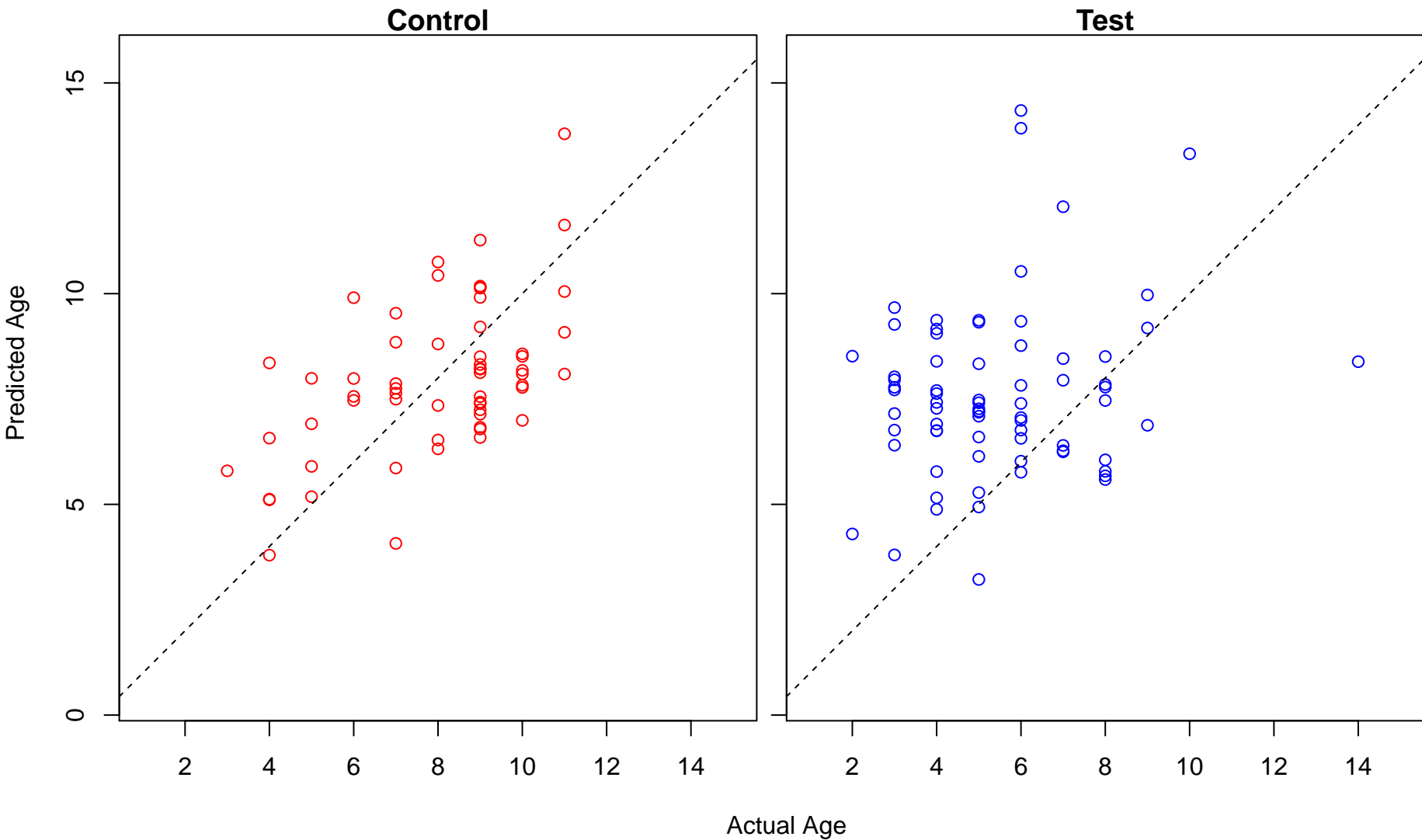
regulation of phagocytosis (Score: 1.342107)



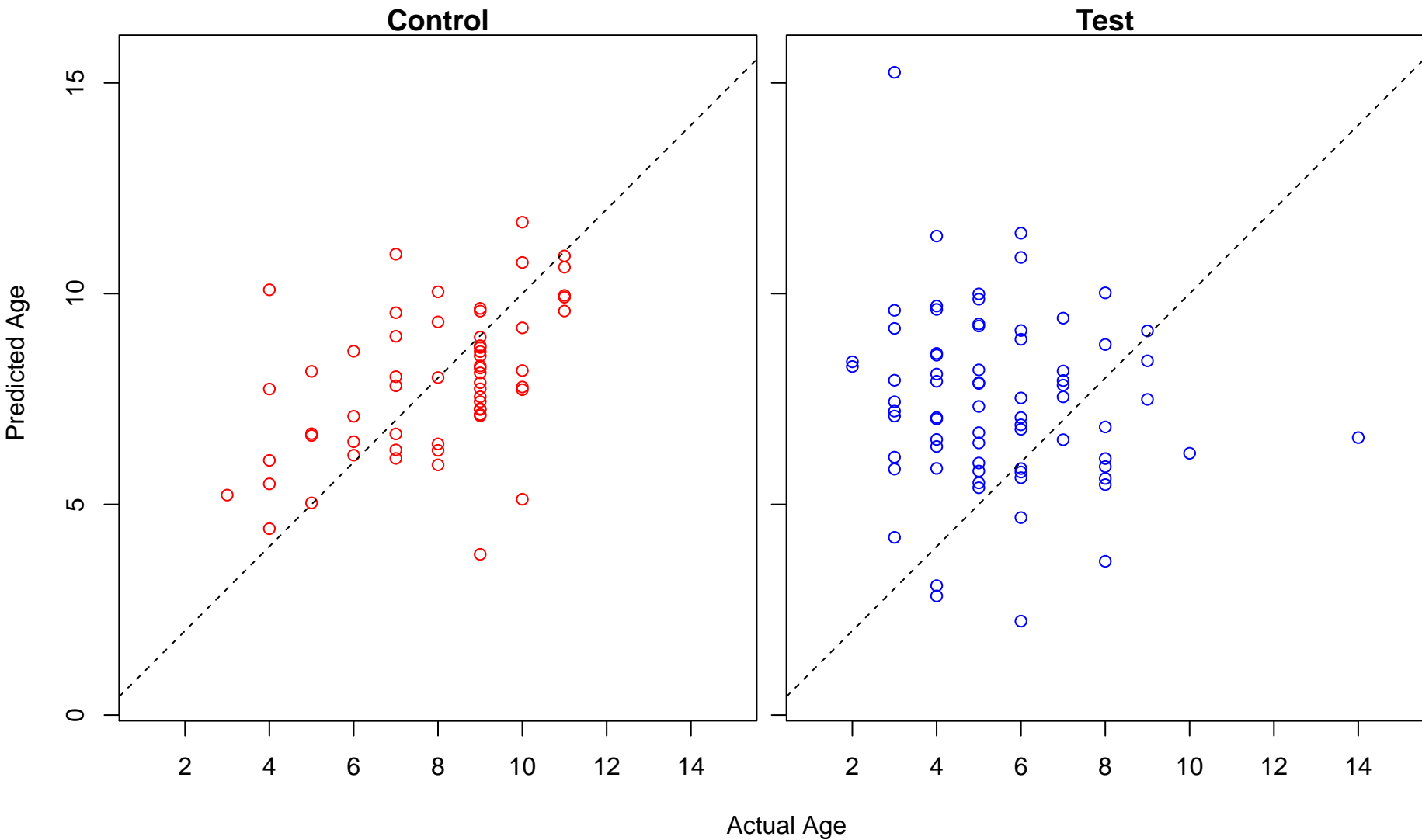
positive regulation of extrinsic apoptotic signaling pathway in absence of ligand (Score: 1.341157)



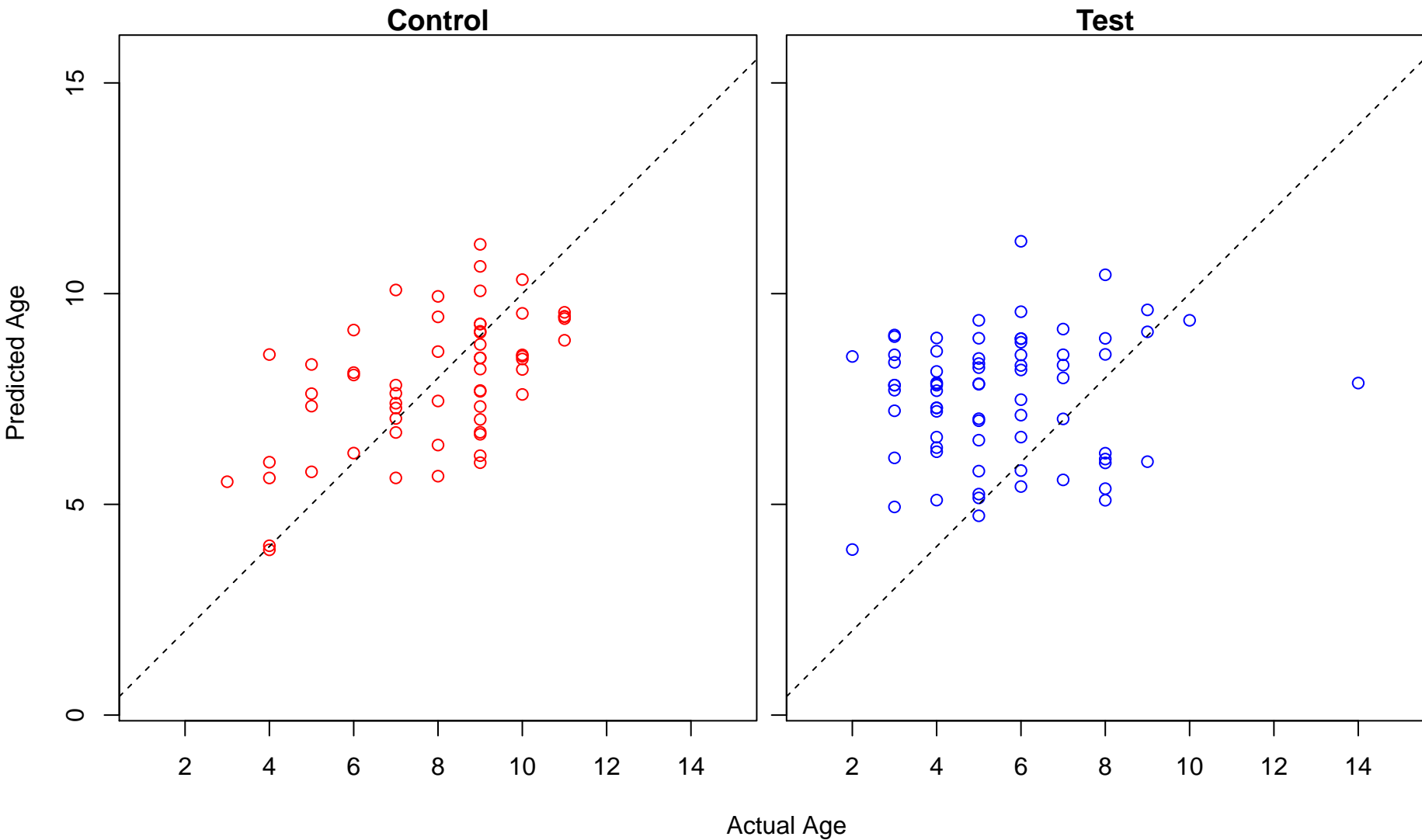
positive regulation of endocytosis (Score: 1.340326)



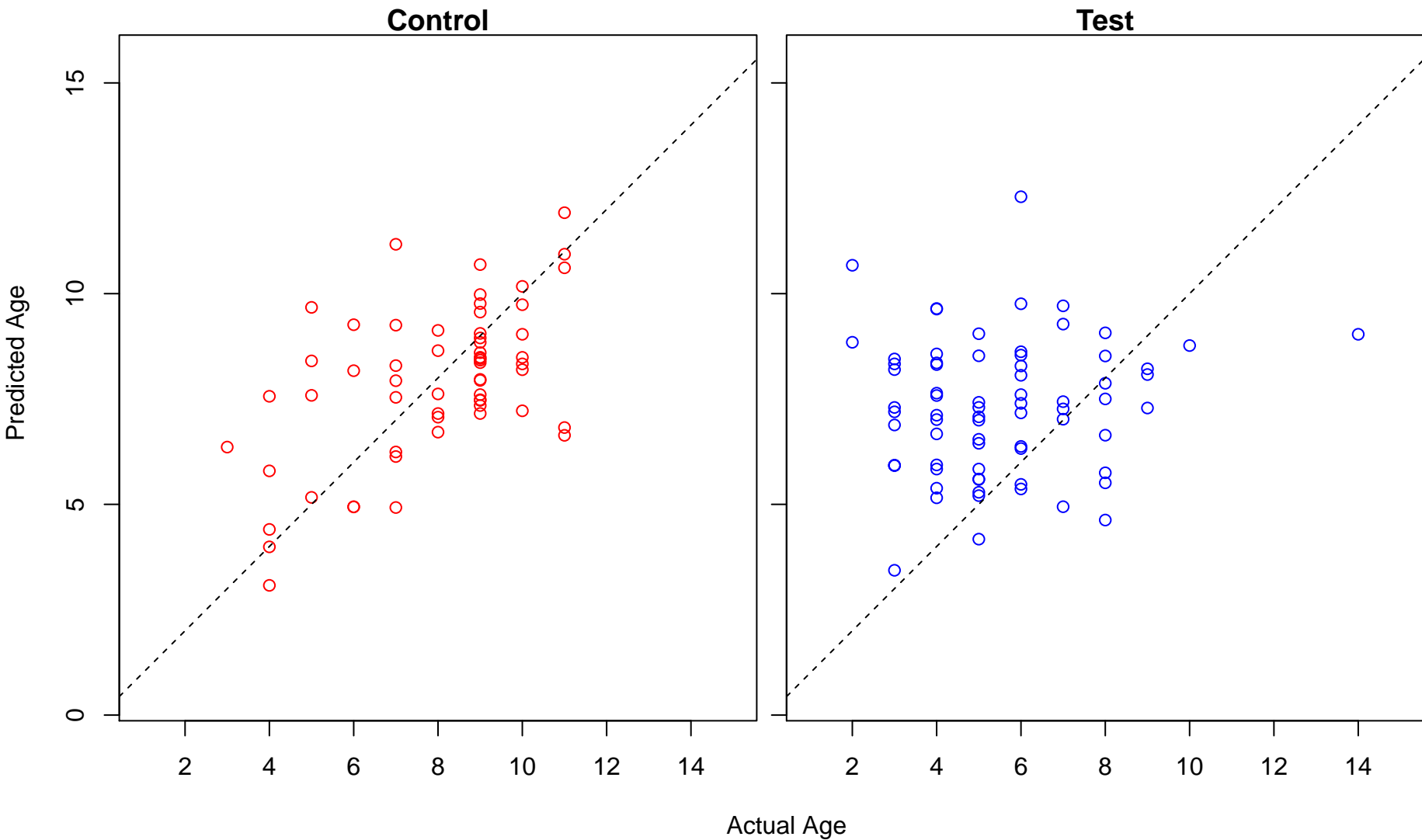
axon extension involved in axon guidance (Score: 1.338078)



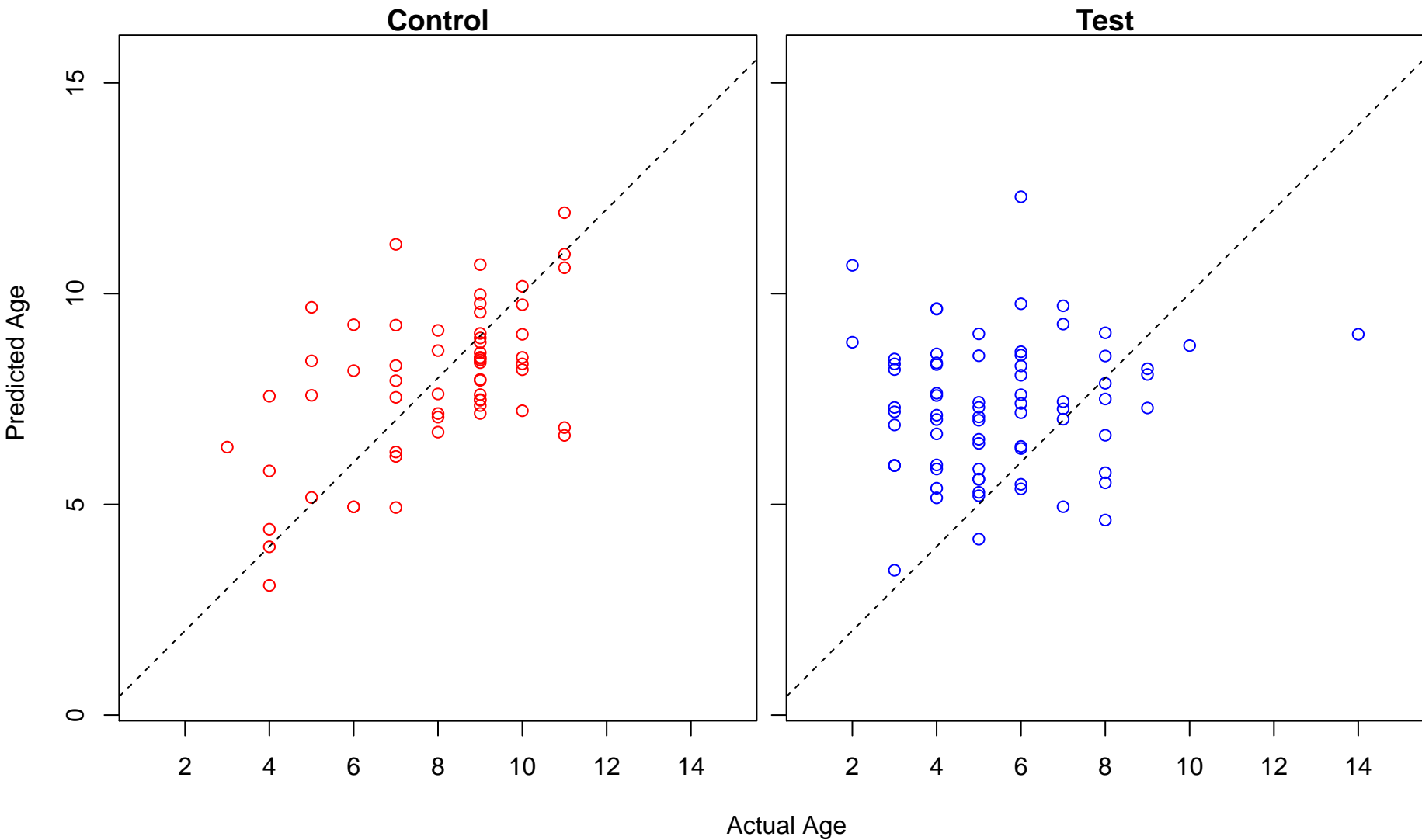
pigment cell differentiation (Score: 1.337884)



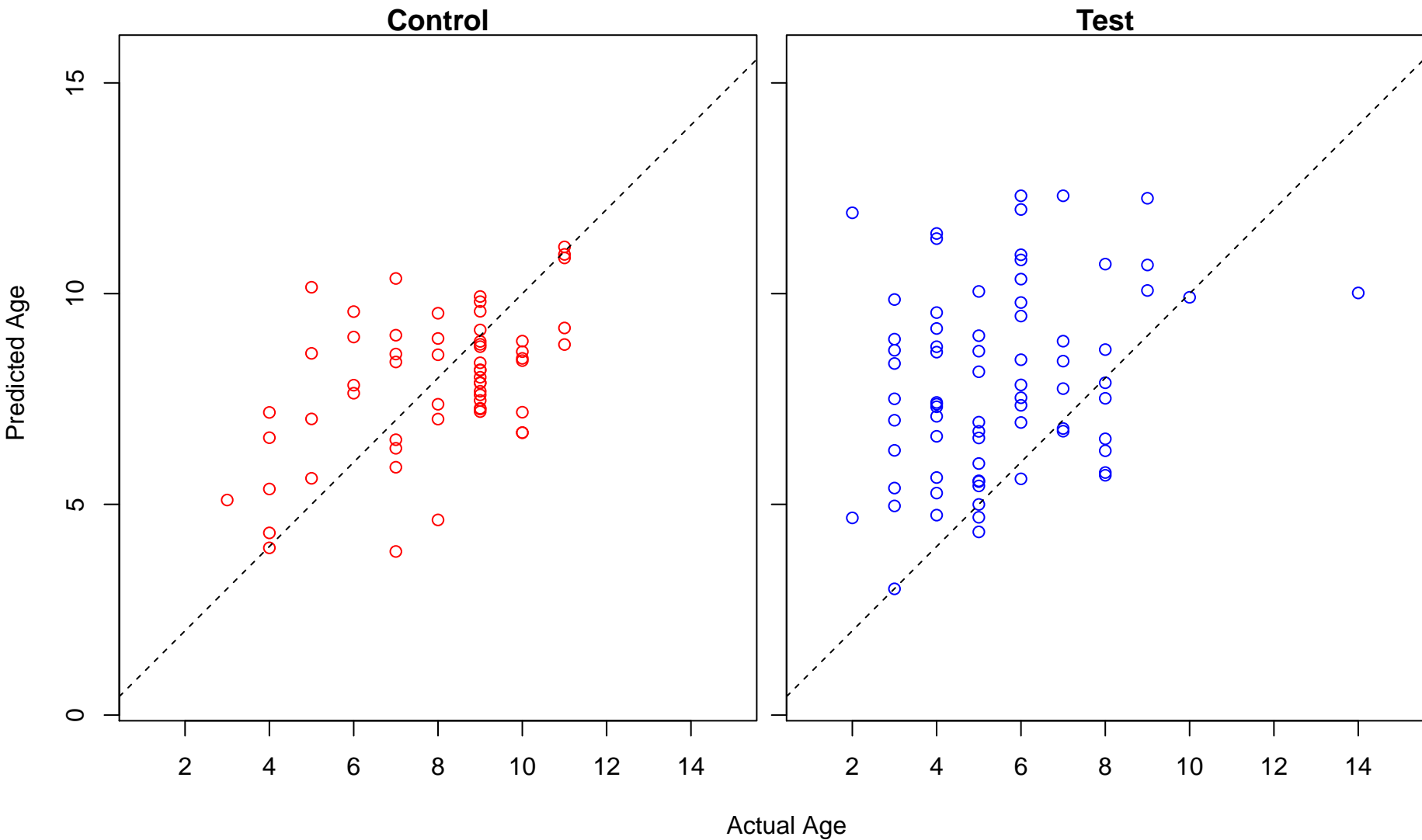
glycosyl compound biosynthetic process (Score: 1.337373)



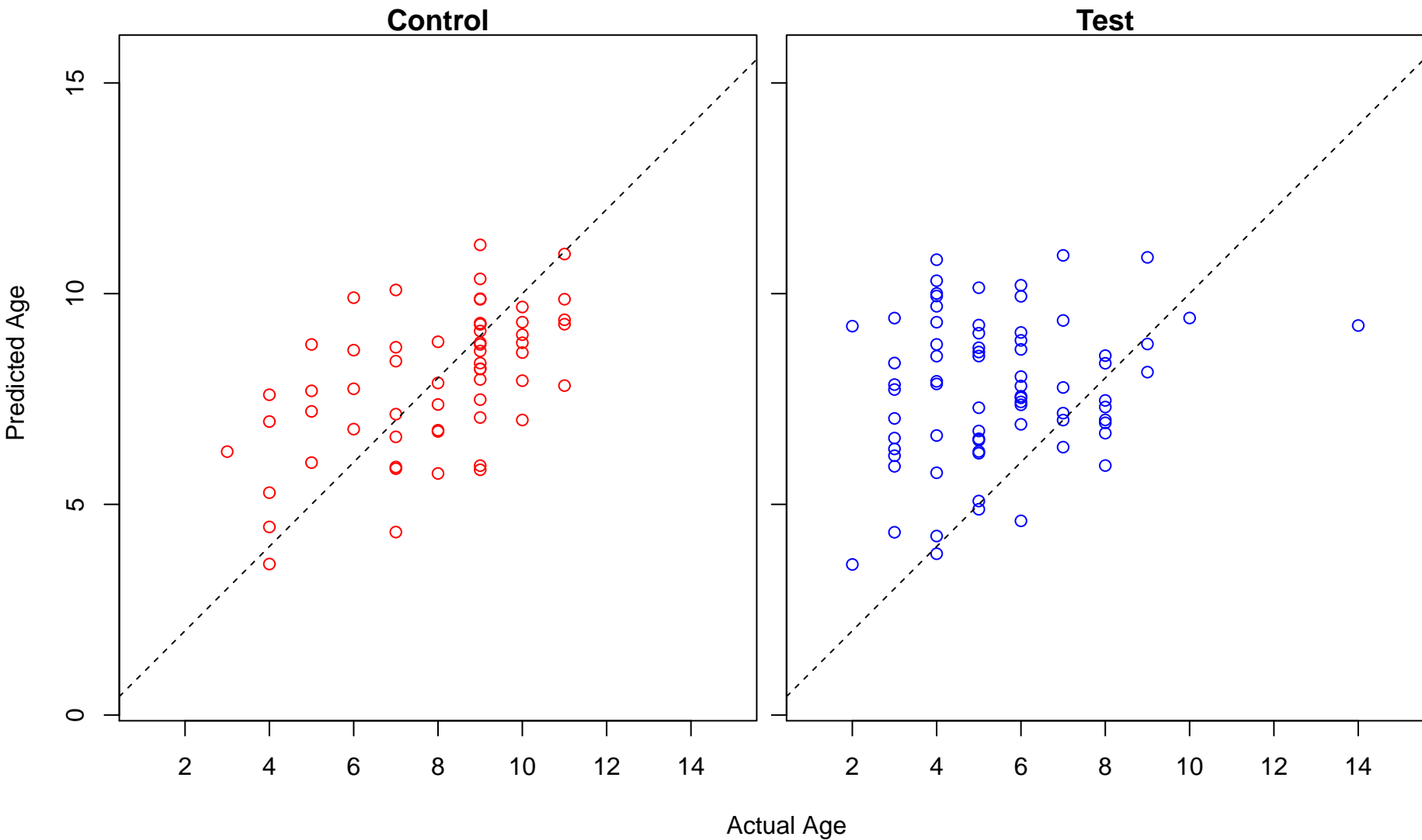
nucleoside biosynthetic process (Score: 1.337130)



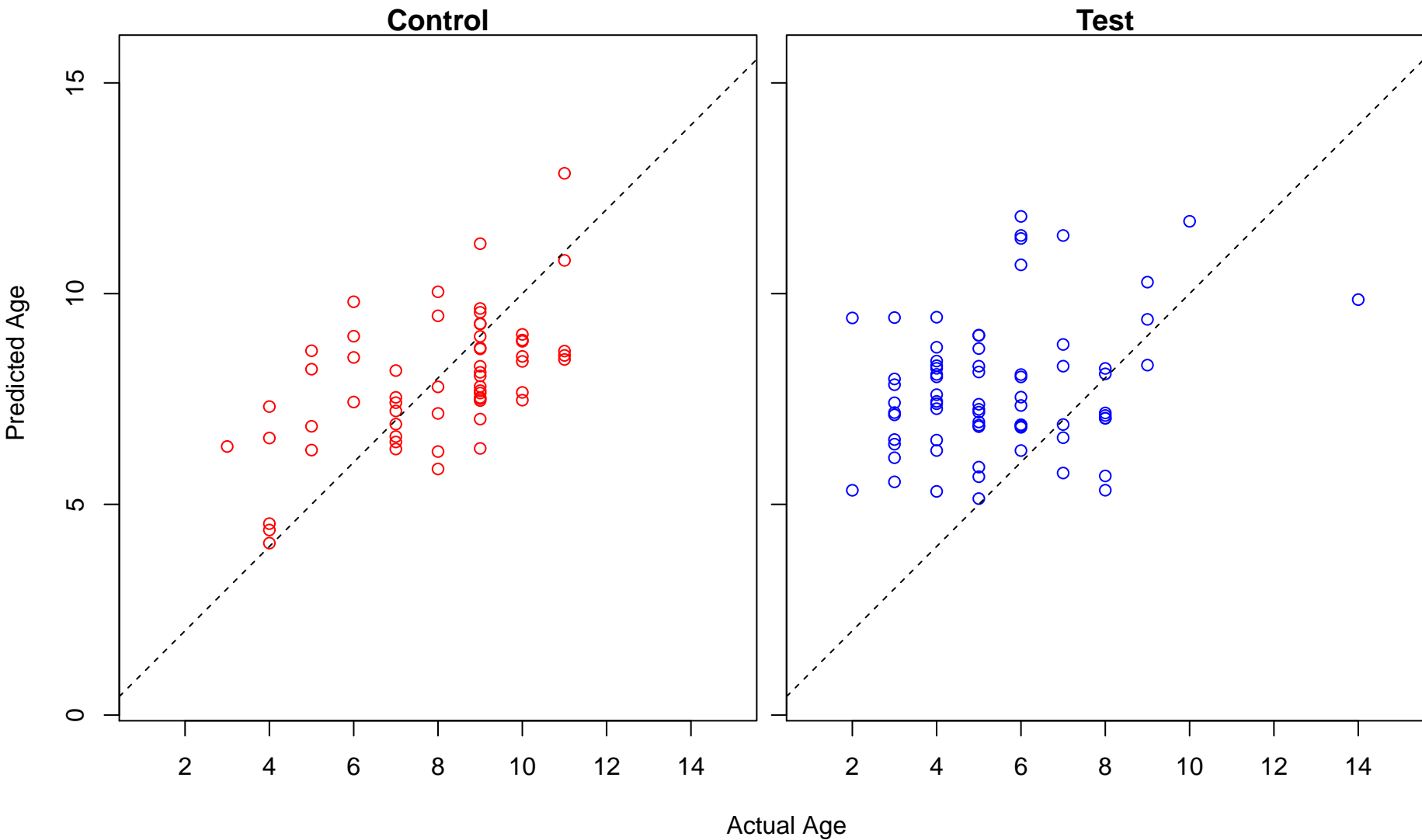
blastocyst development (Score: 1.336436)



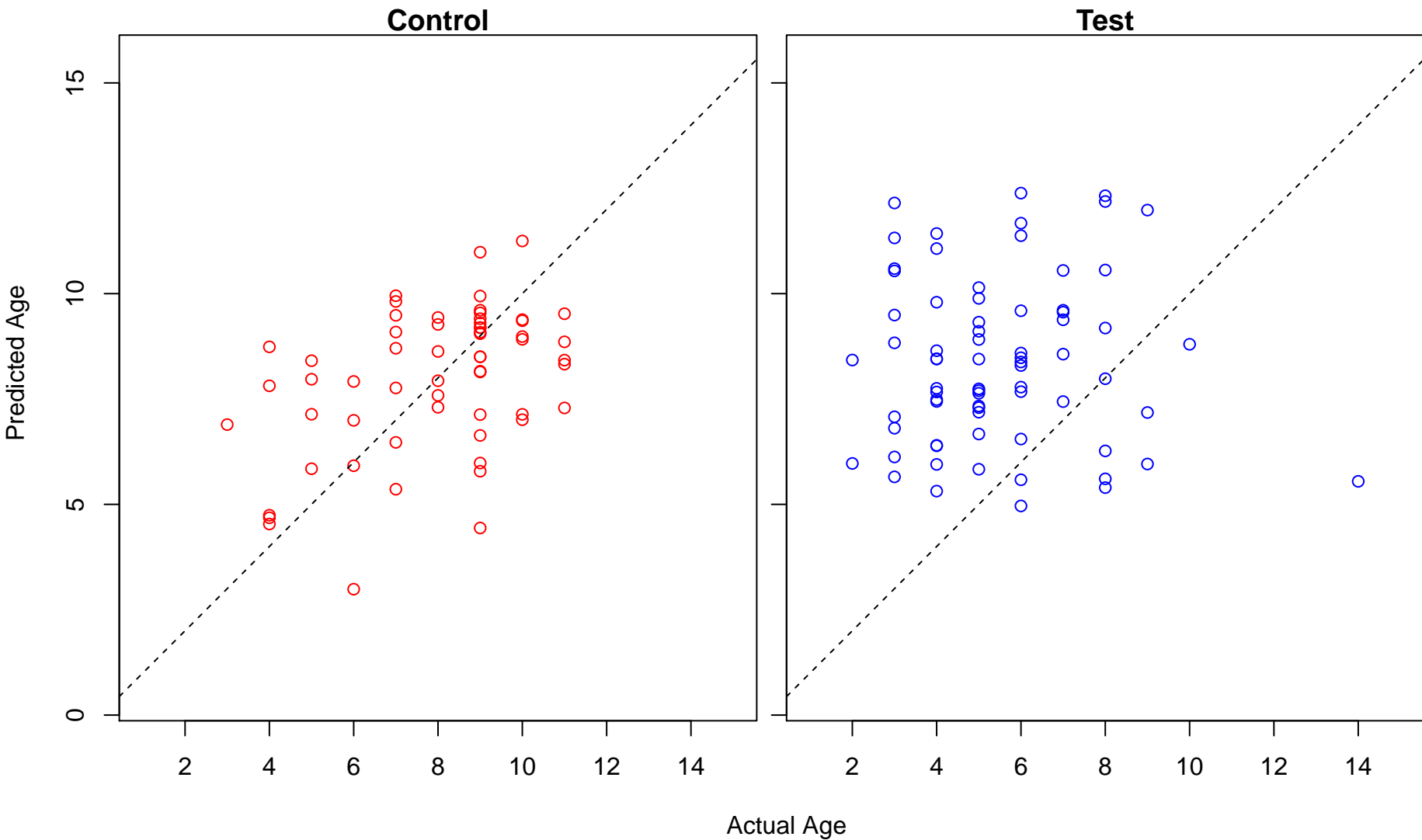
regulation of cell development (Score: 1.336406)



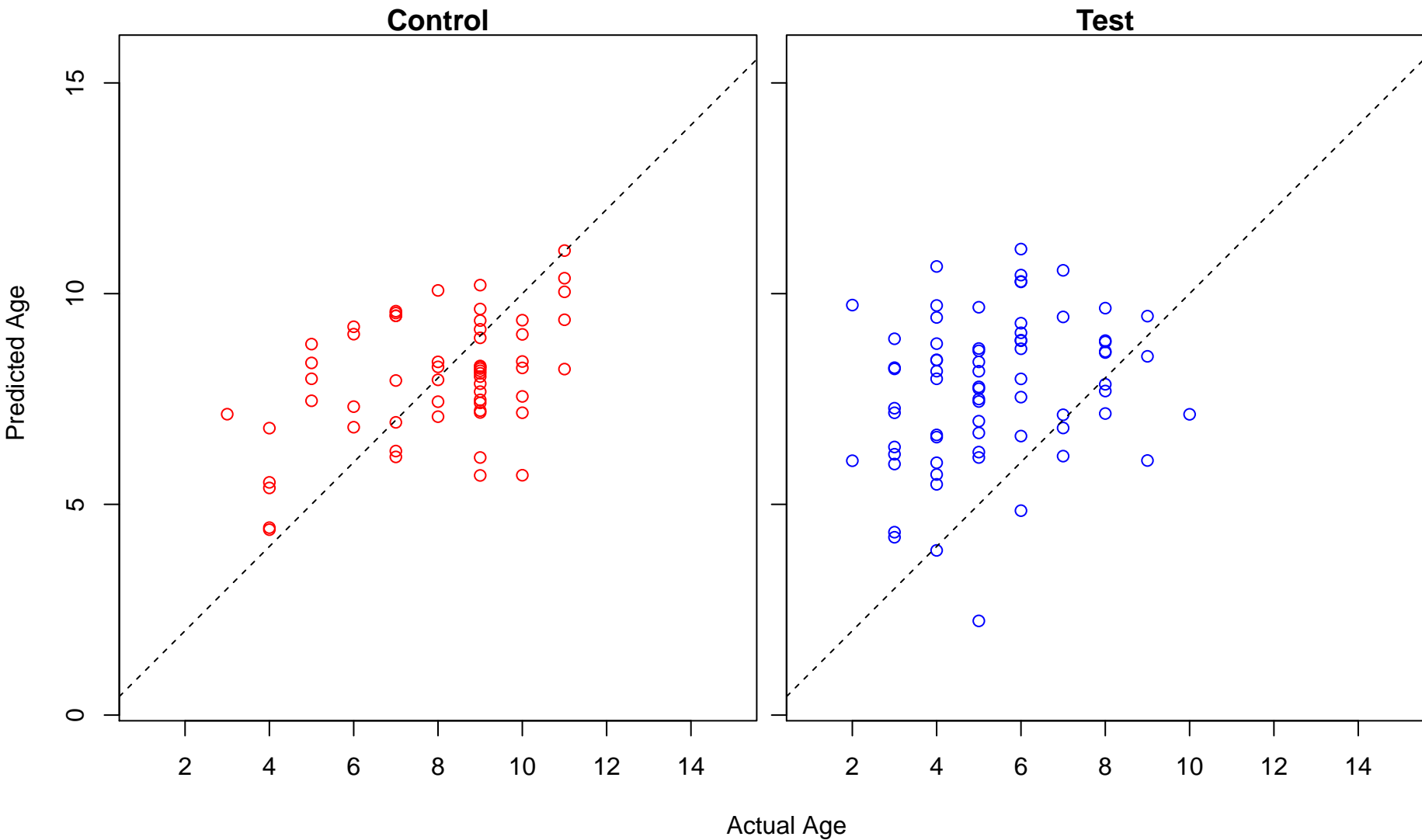
positive regulation of phagocytosis (Score: 1.334572)



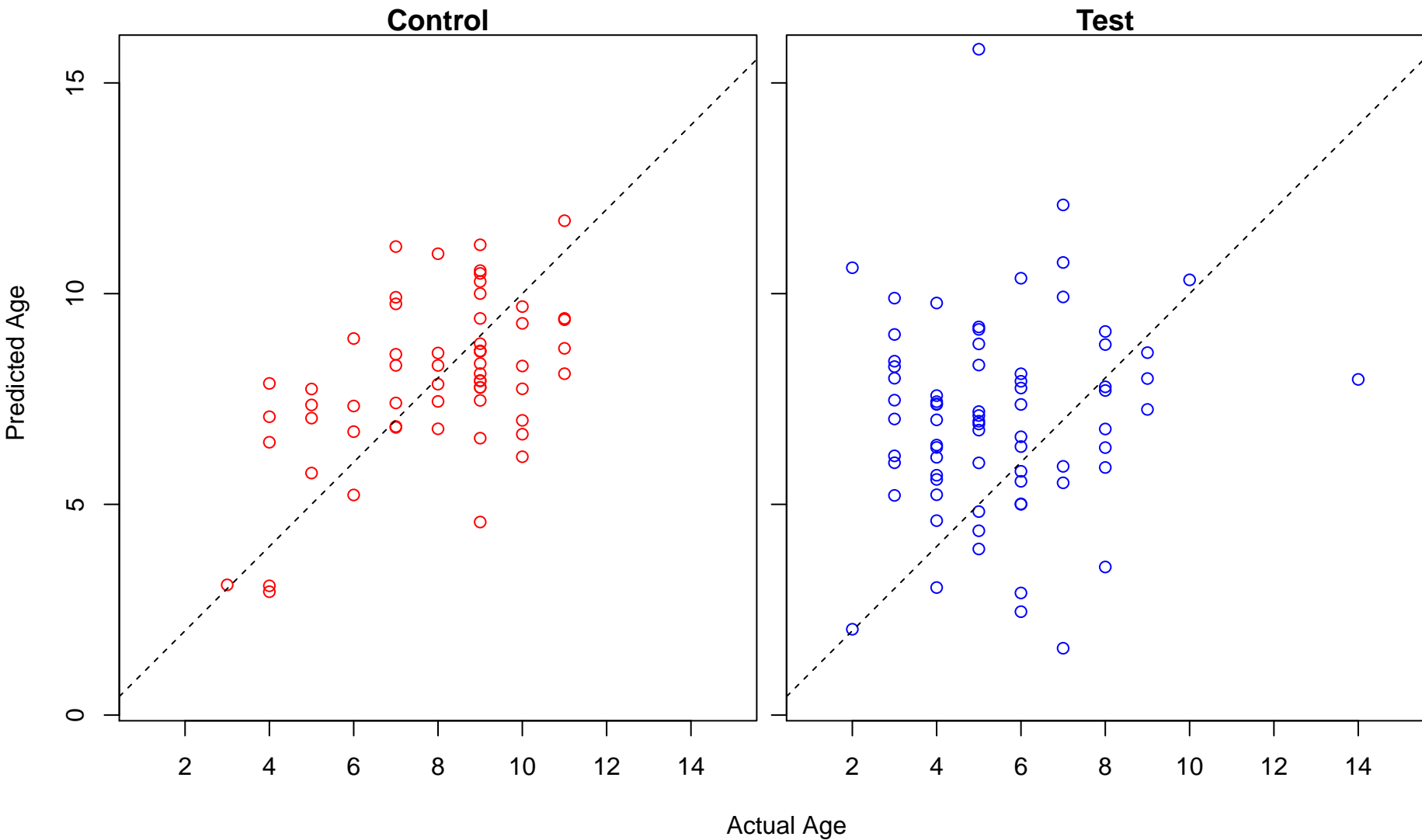
pons development (Score: 1.333976)



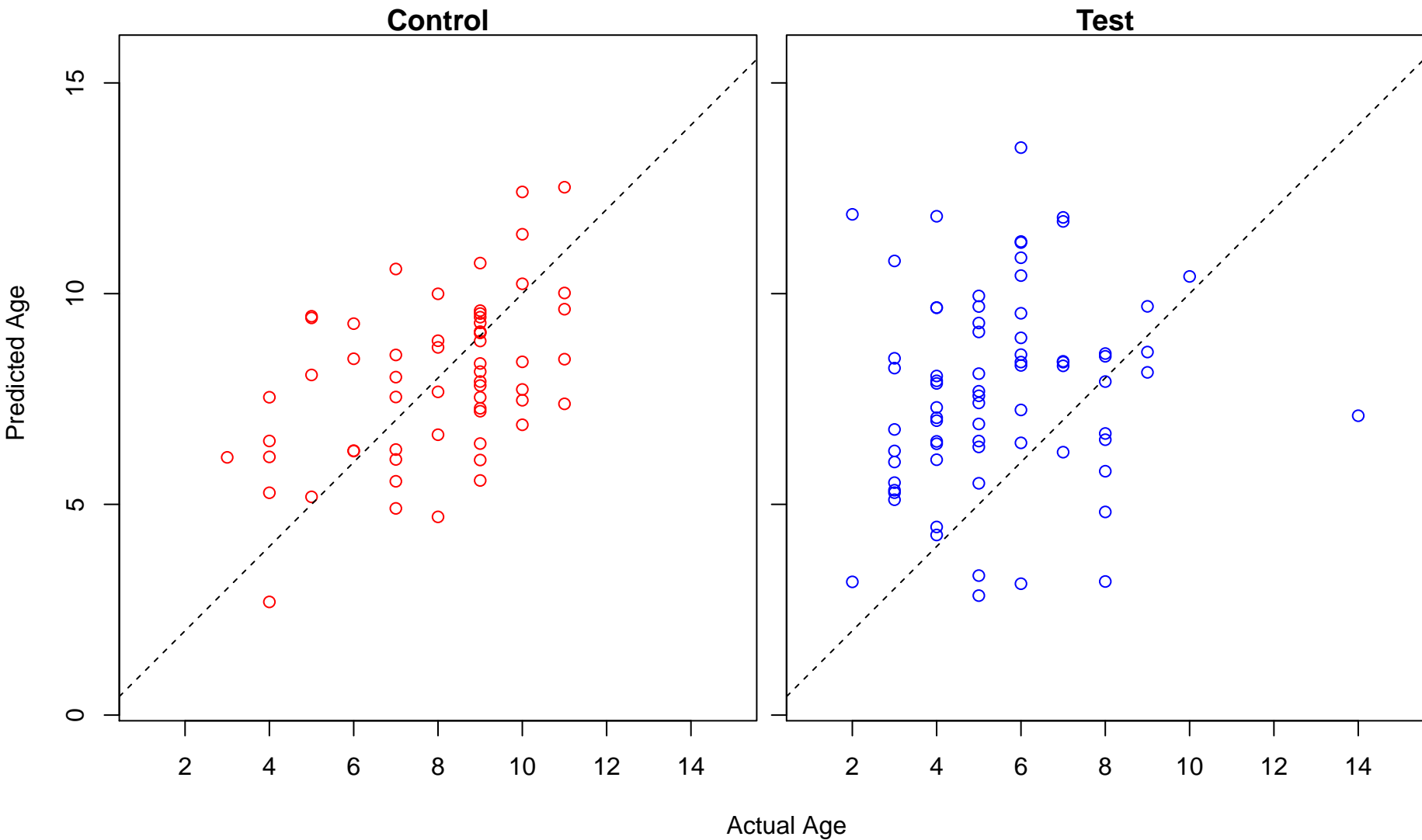
skeletal muscle cell differentiation (Score: 1.330431)



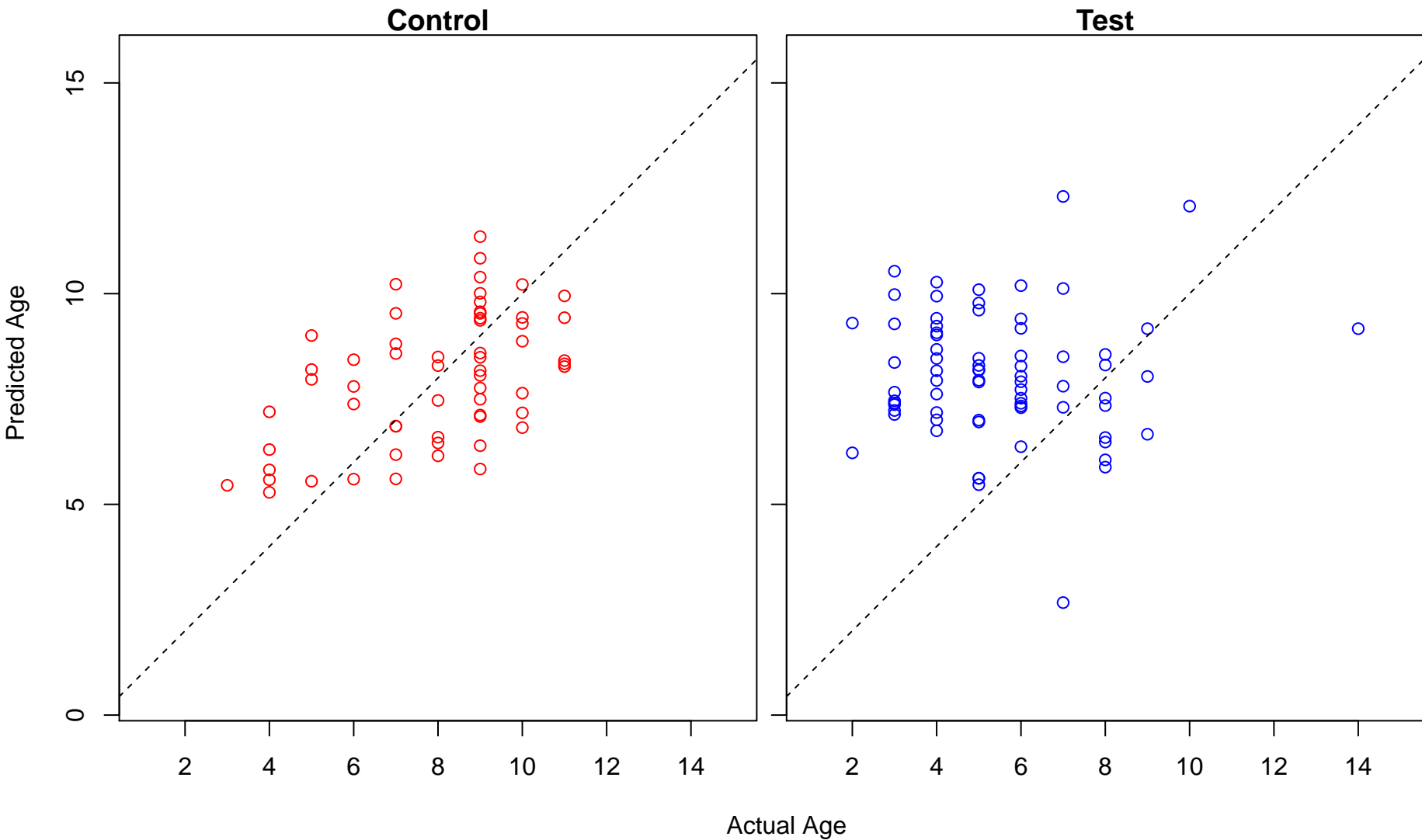
sphingolipid biosynthetic process (Score: 1.329150)



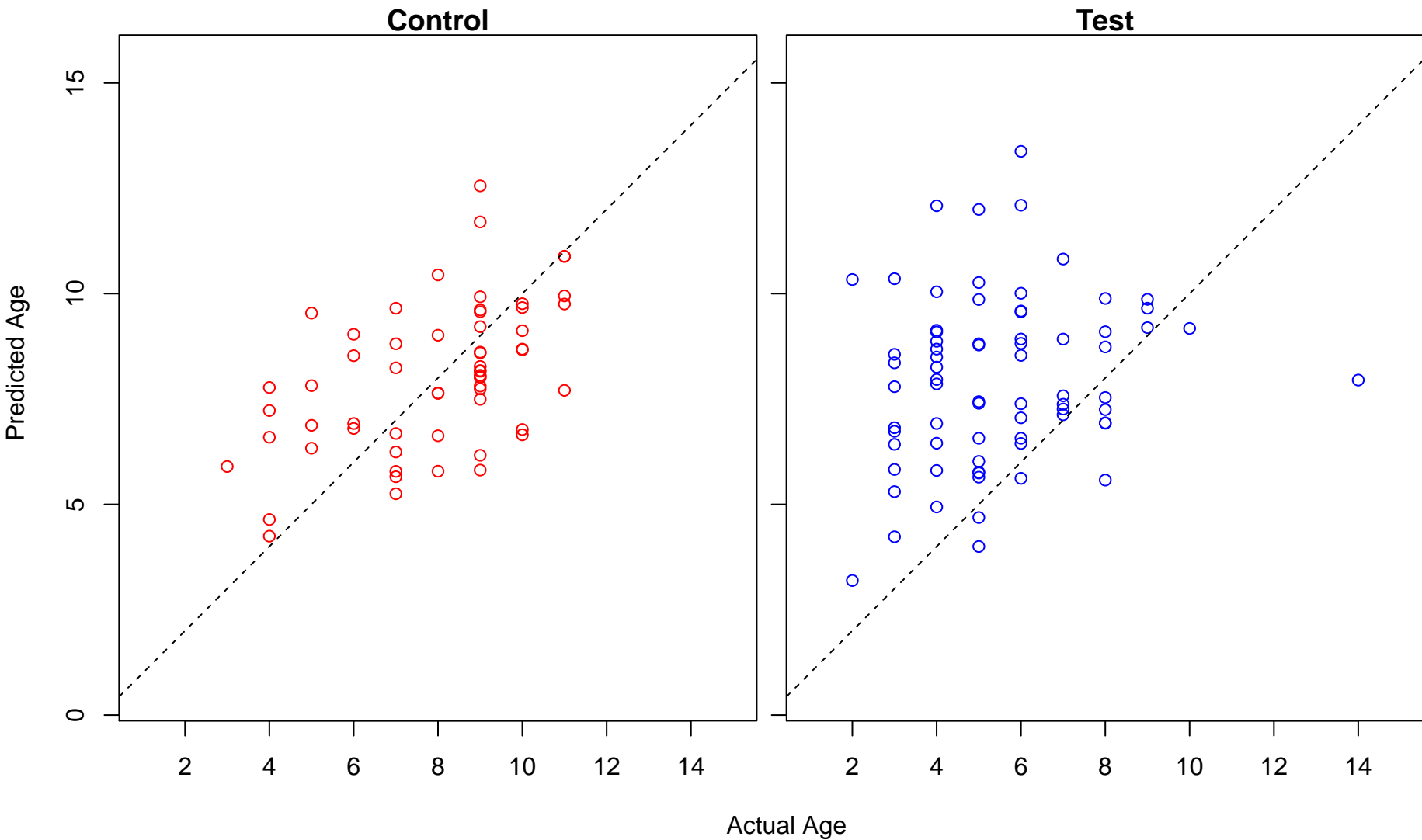
negative regulation of transforming growth factor beta receptor signaling pathway (Score: 1.325007)



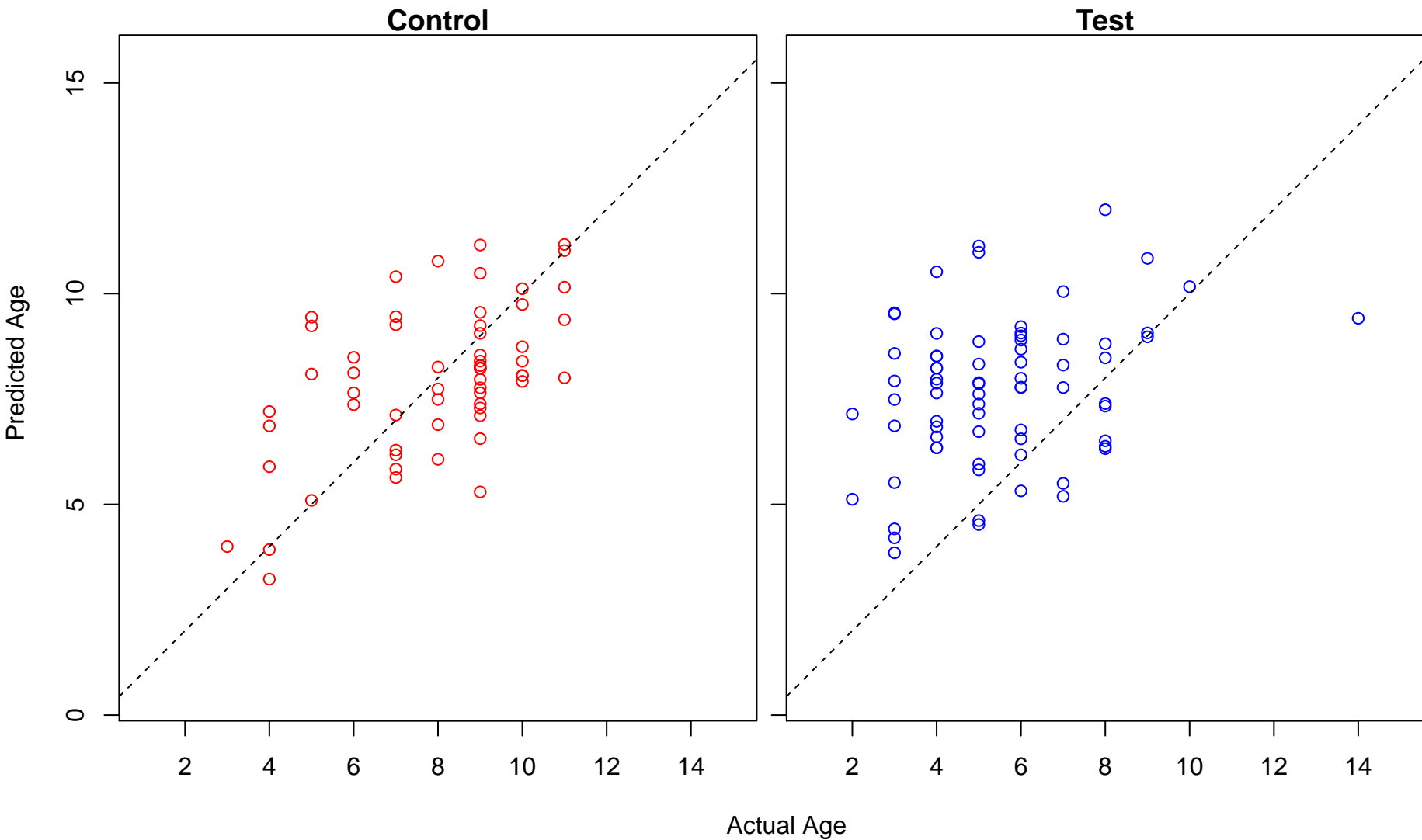
positive regulation of cell growth (Score: 1.324193)



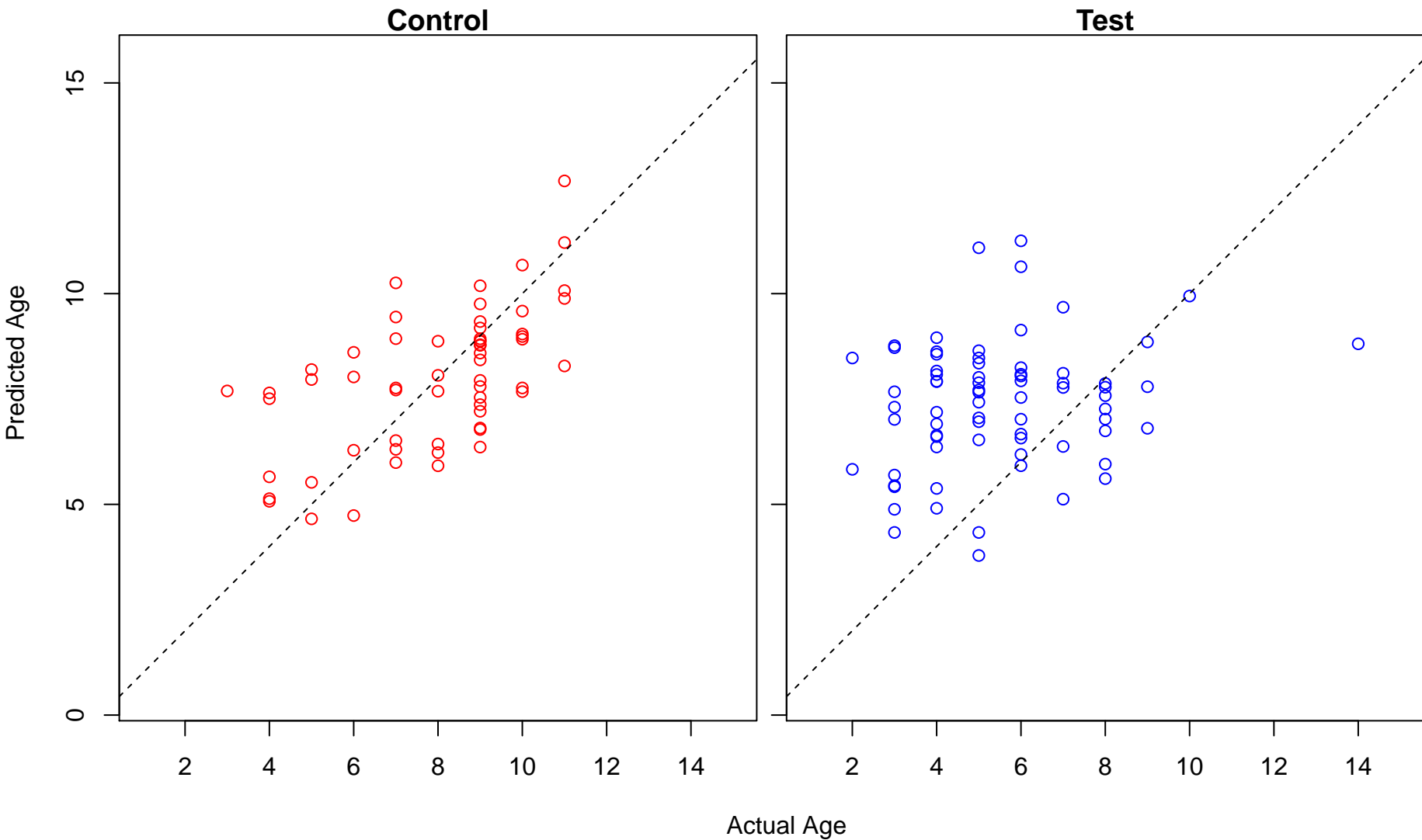
cell part morphogenesis (Score: 1.324178)



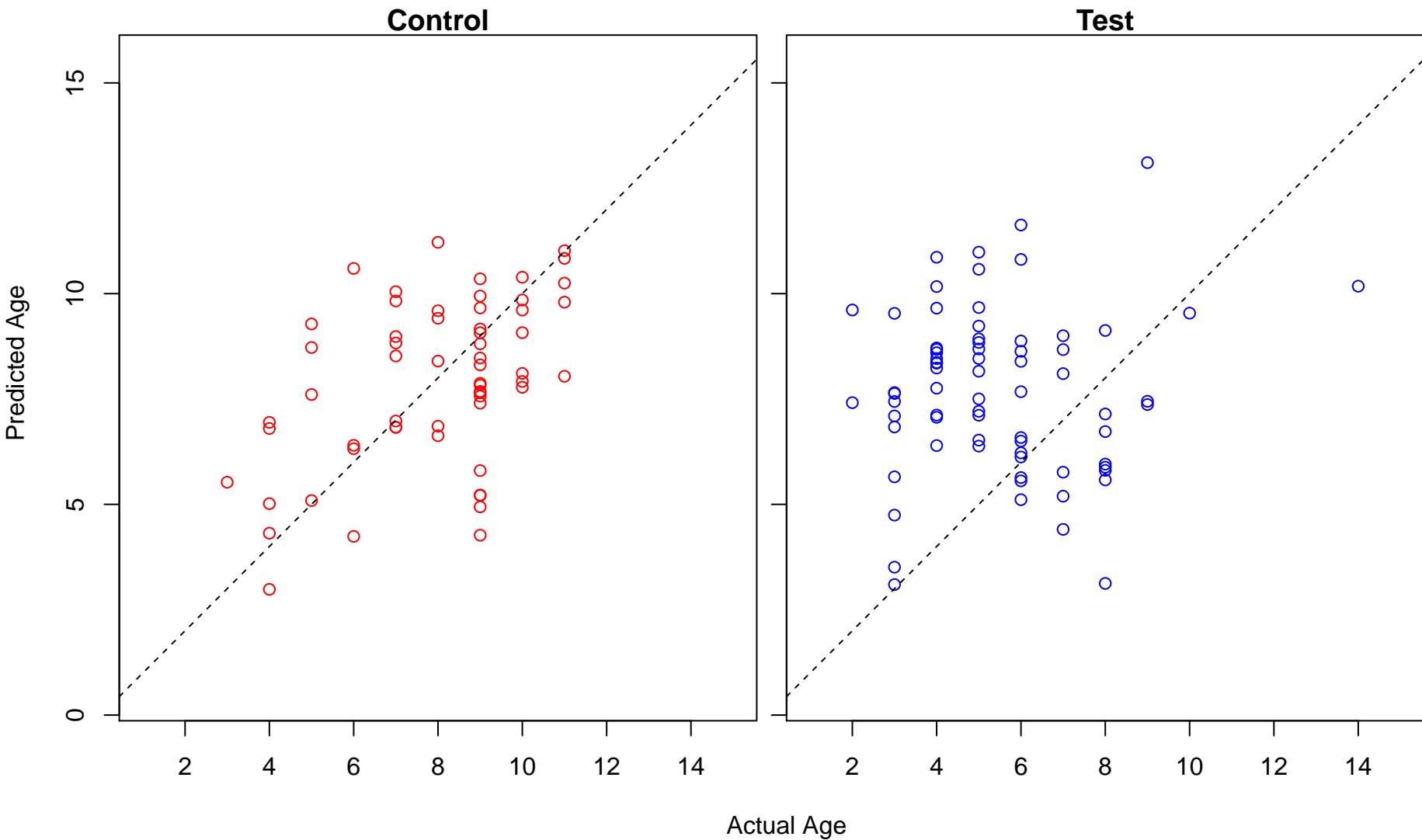
T cell selection (Score: 1.324077)



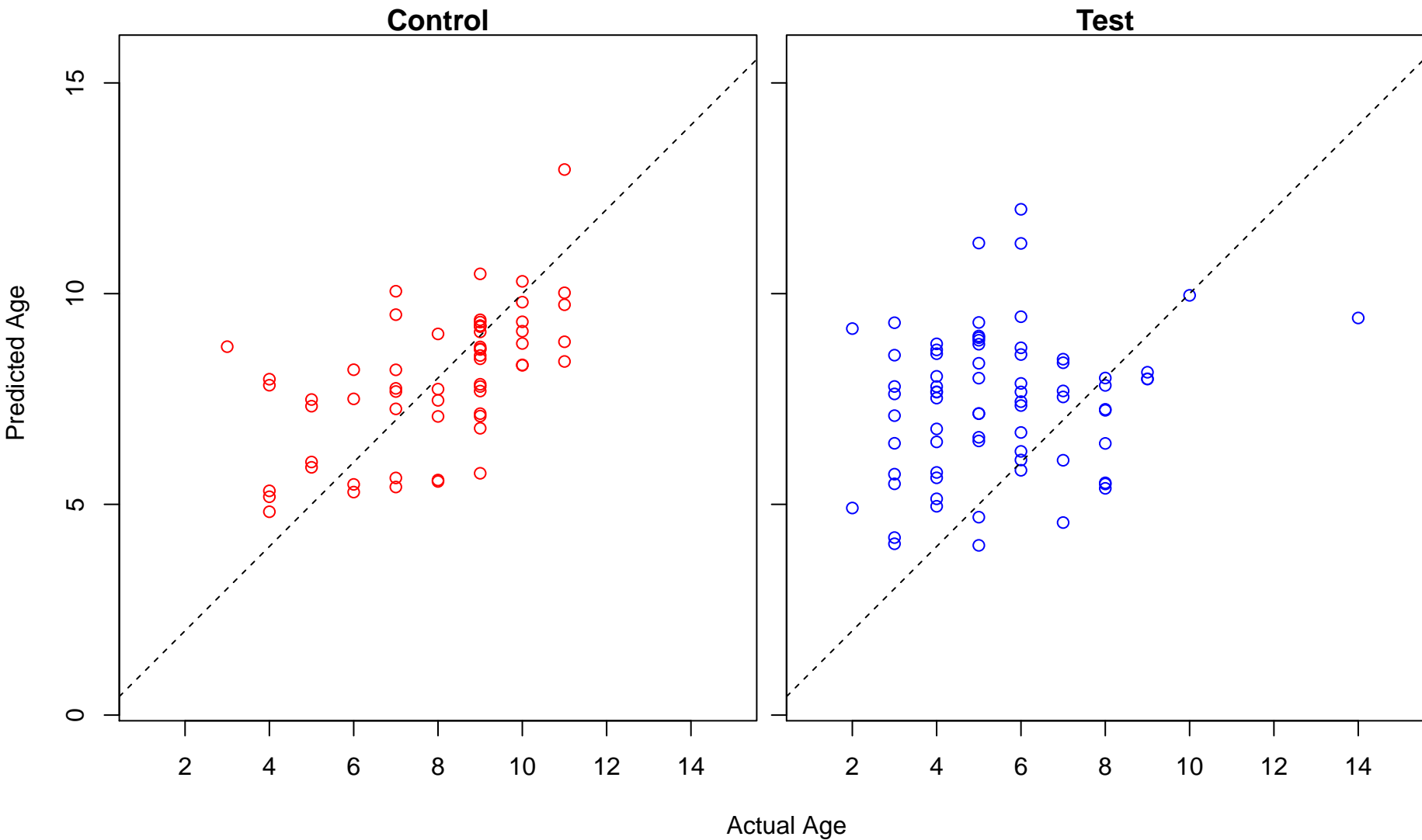
protein localization to membrane (Score: 1.323531)



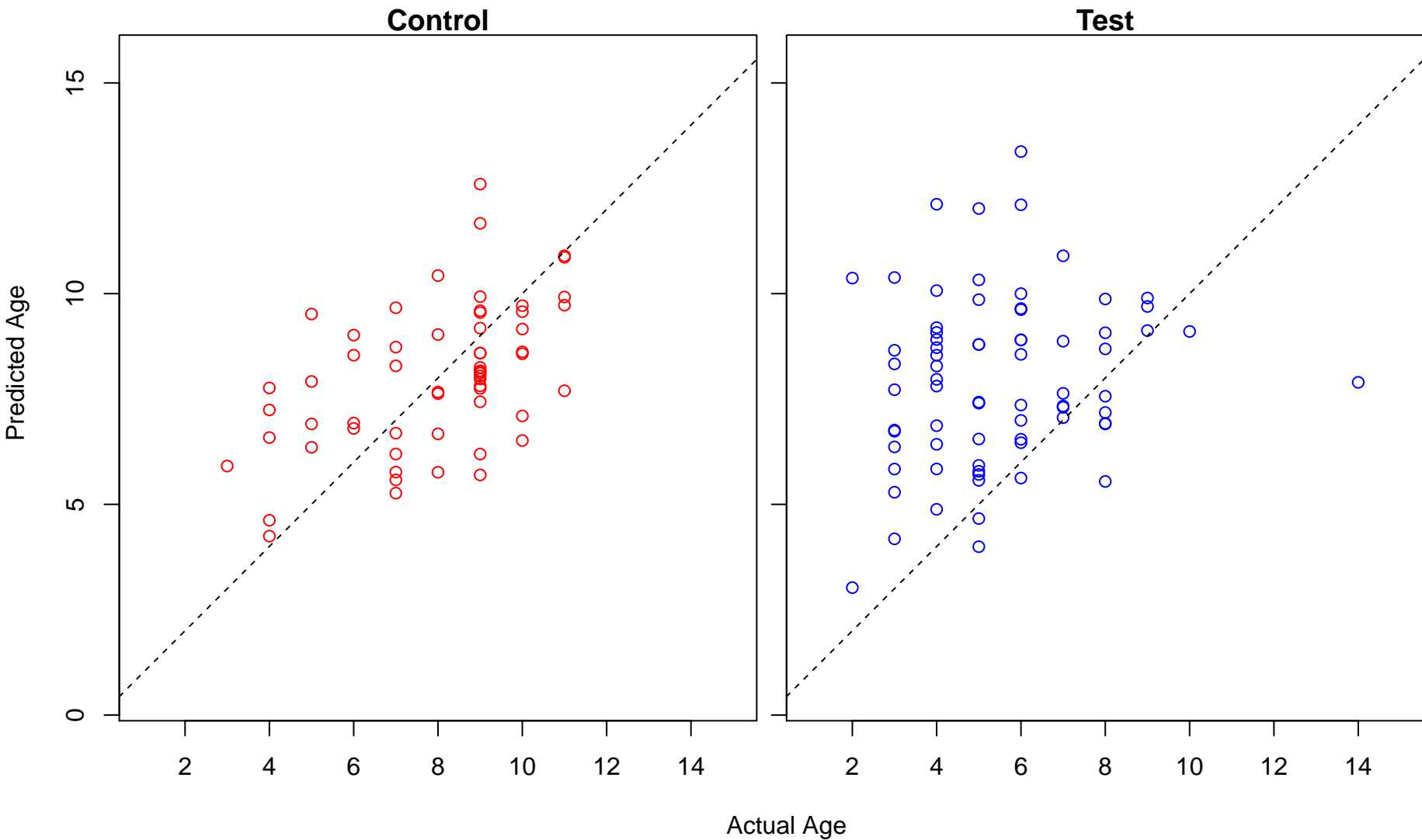
protein deacetylation (Score: 1.322418)



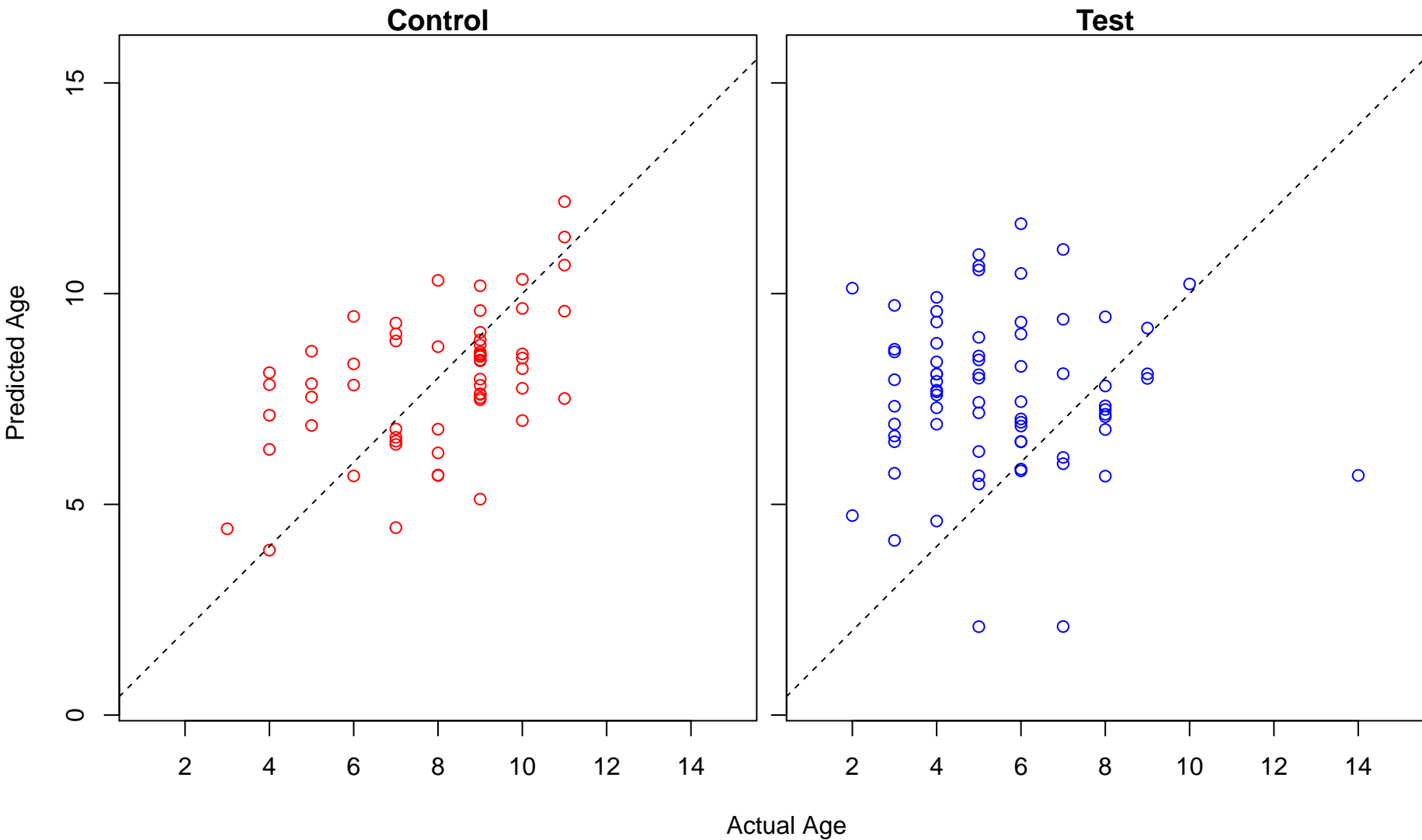
protein targeting (Score: 1.321933)



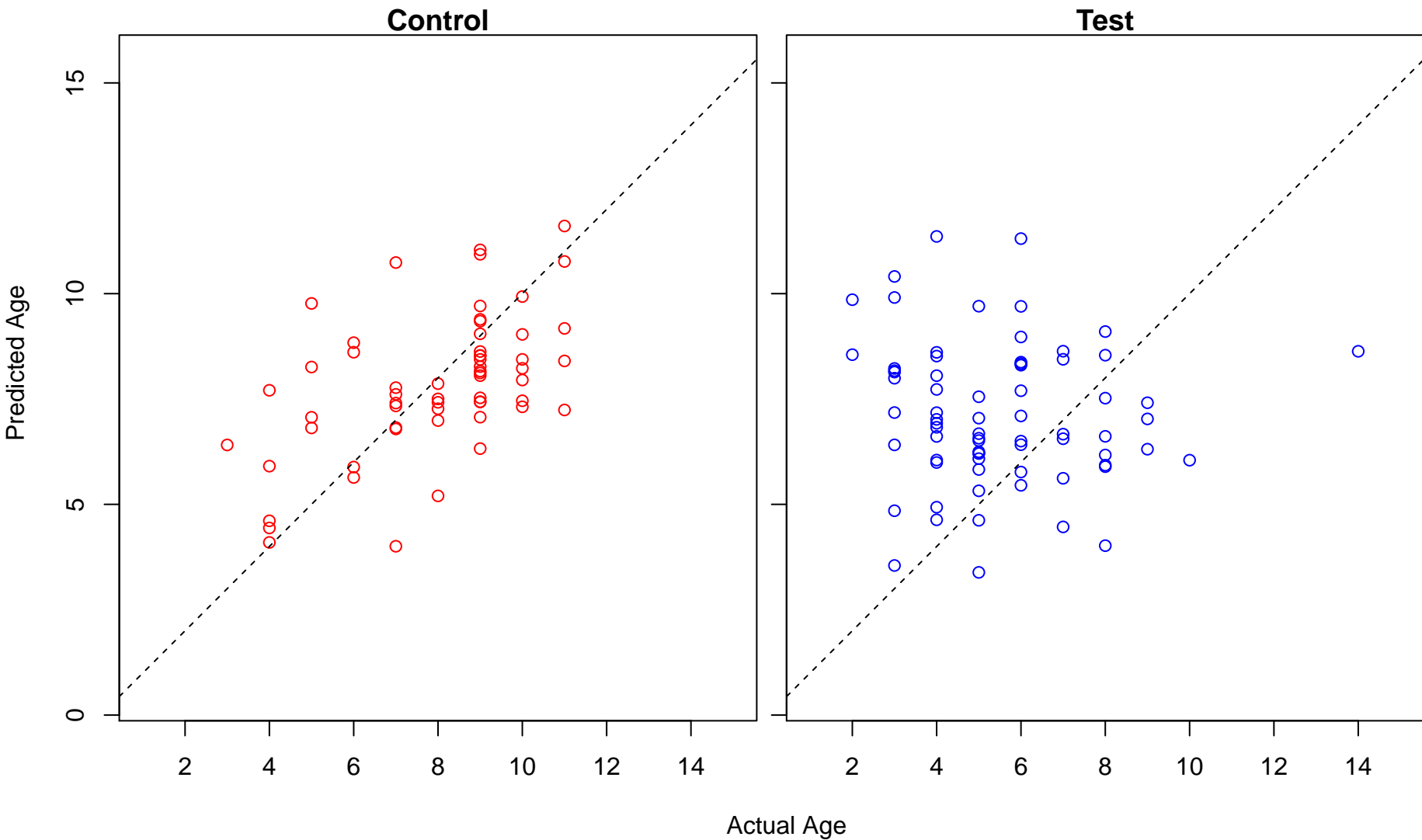
cell projection morphogenesis (Score: 1.317622)



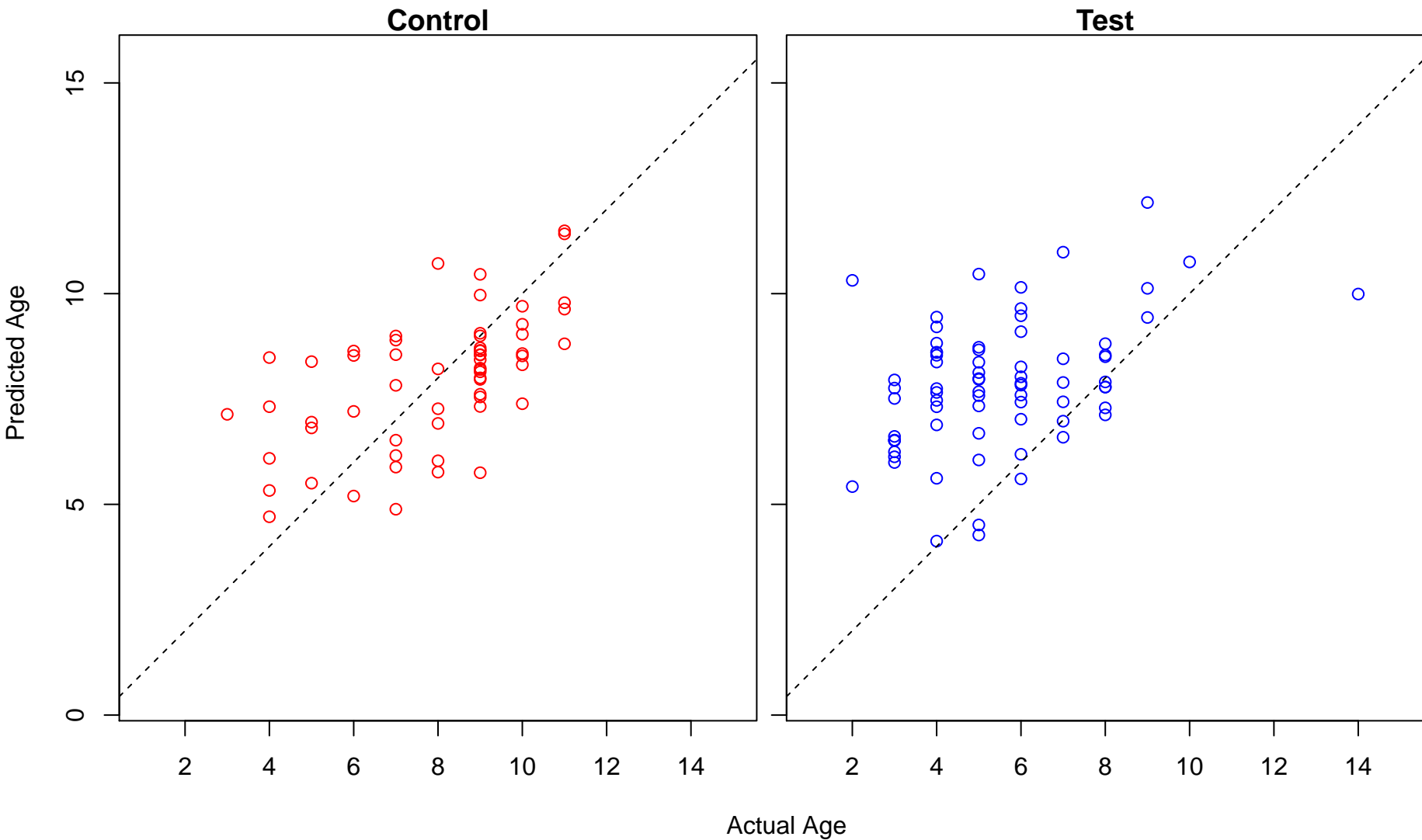
regulation of cell cycle (Score: 1.317616)



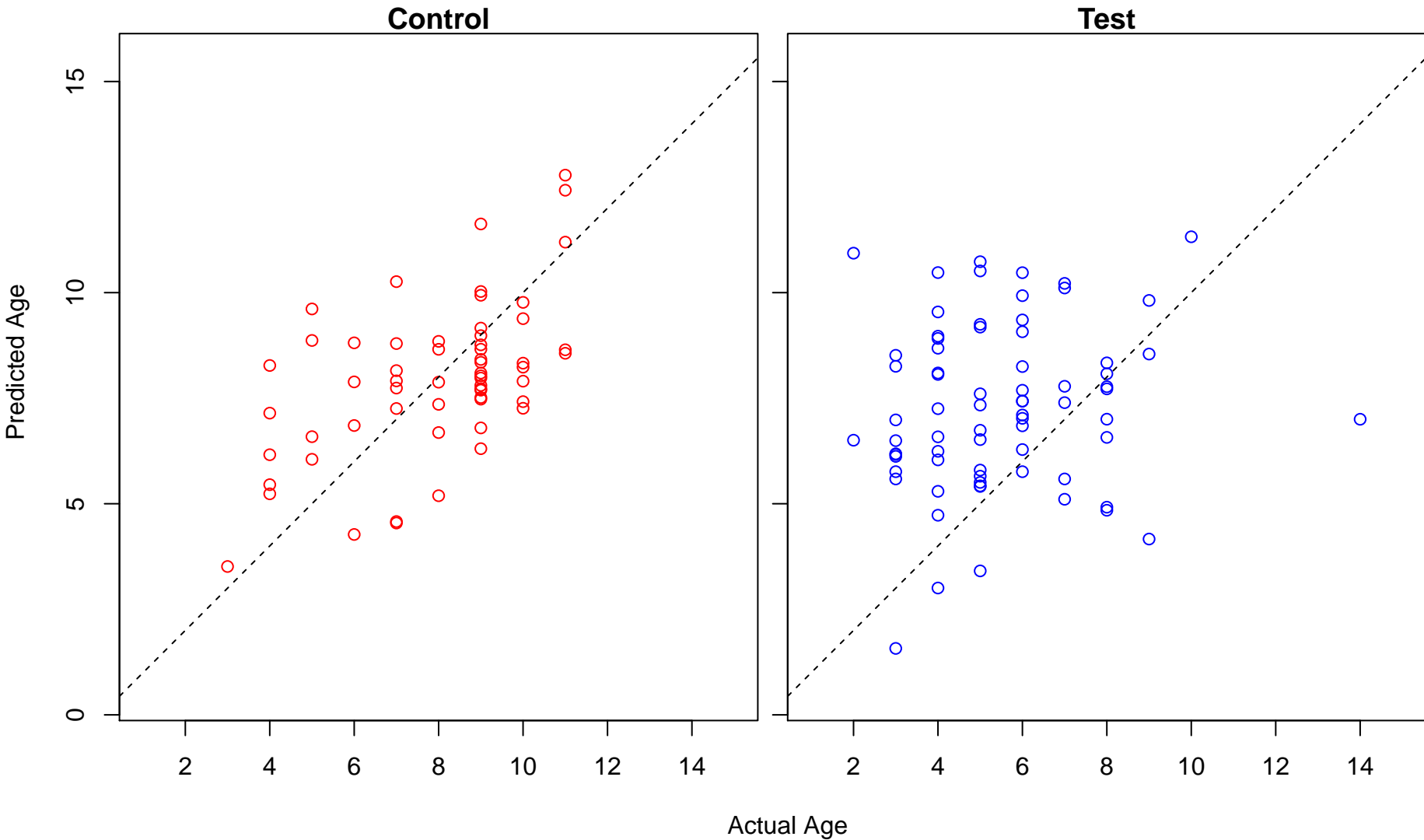
purine-containing compound biosynthetic process (Score: 1.315584)



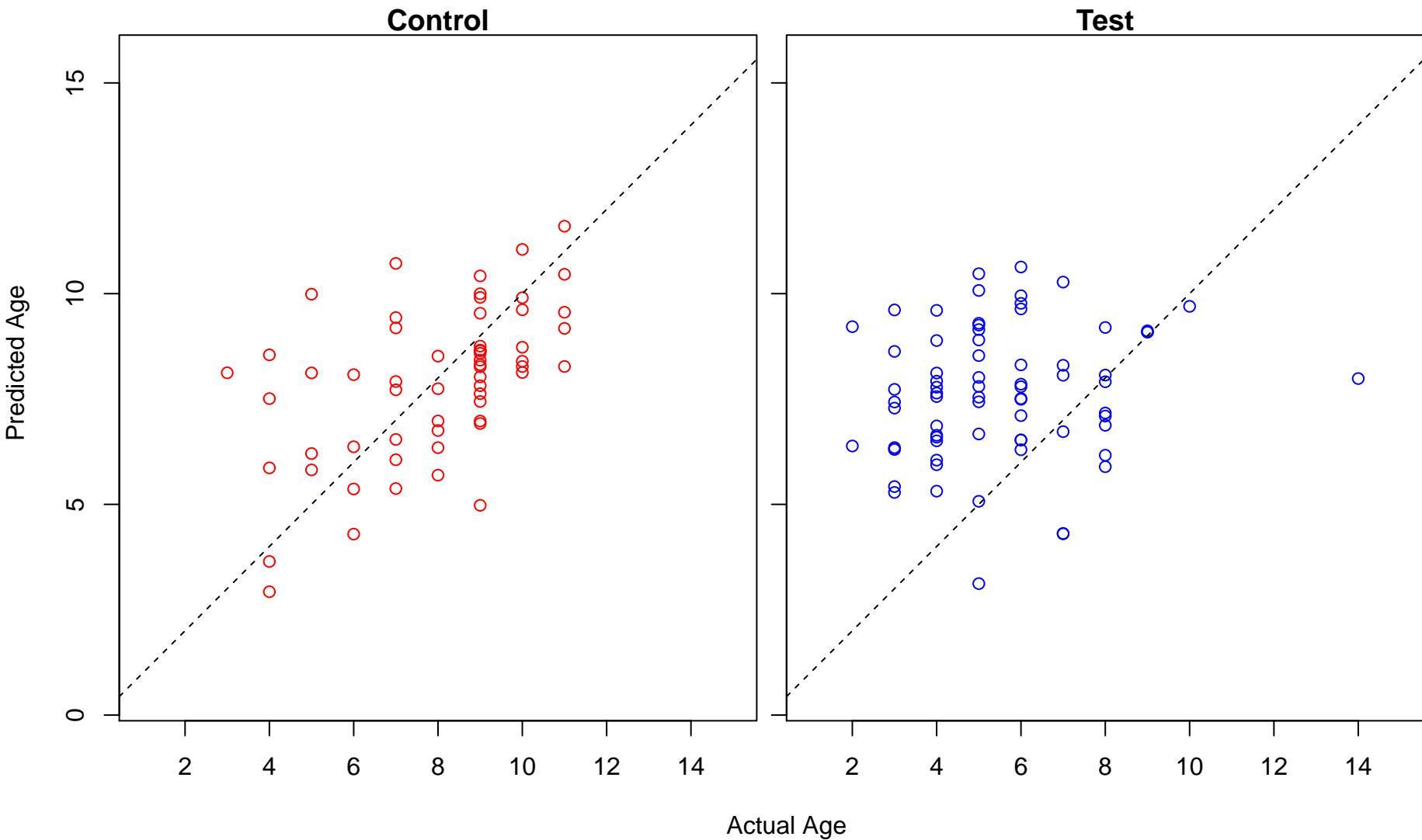
multi-organism process (Score: 1.313435)



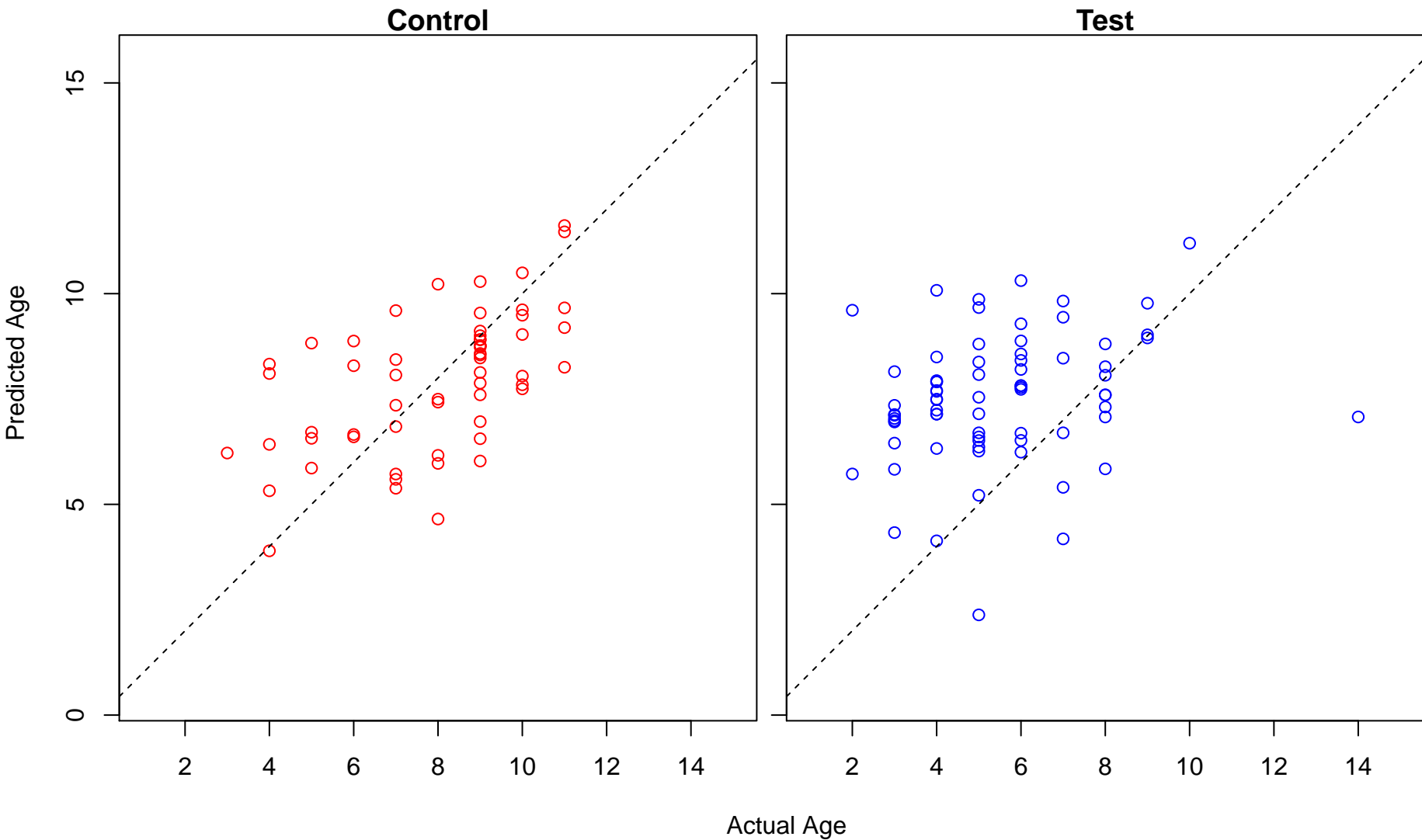
regulation of intrinsic apoptotic signaling pathway (Score: 1.312708)



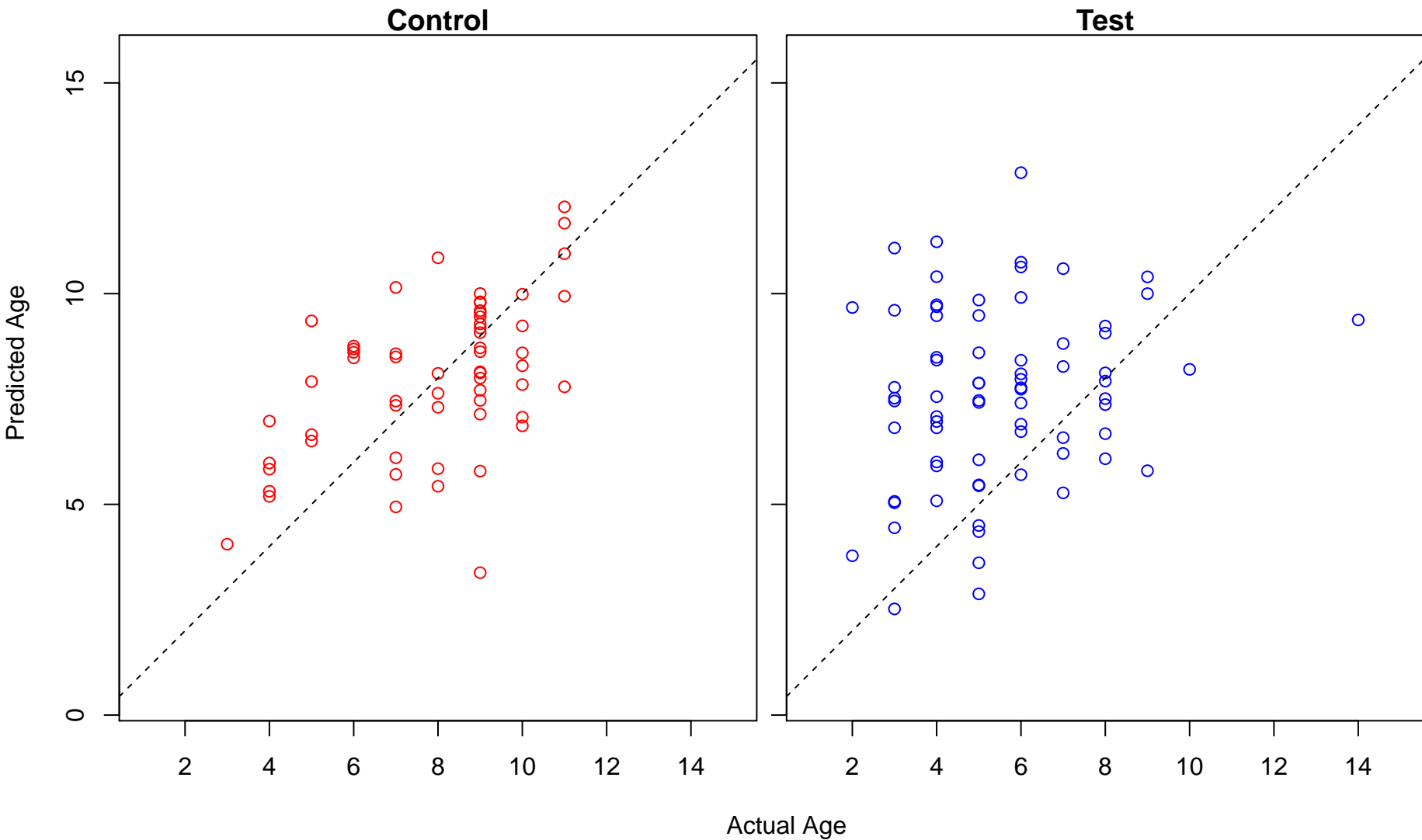
cellular macromolecule catabolic process (Score: 1.312314)



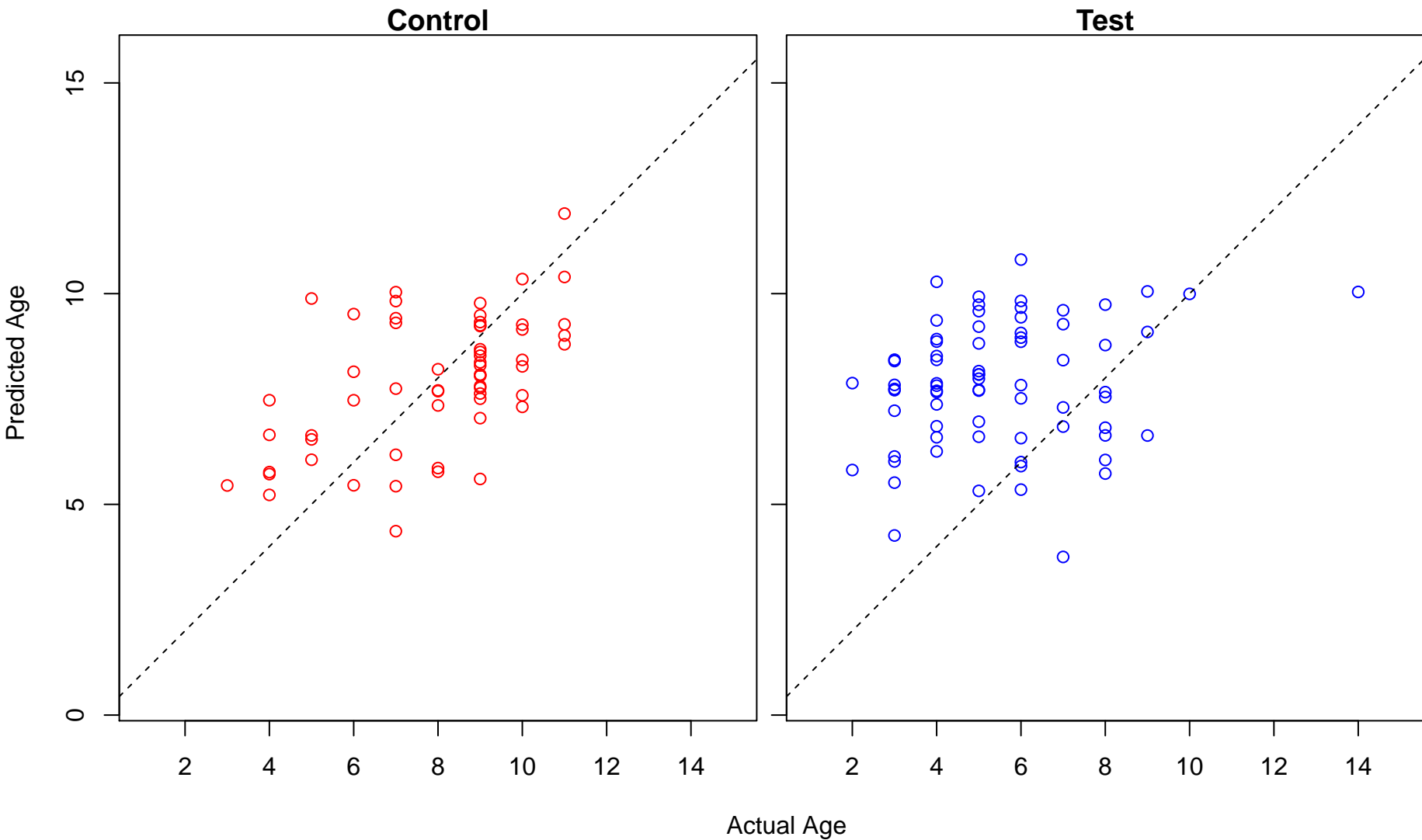
organic substance metabolic process (Score: 1.307553)



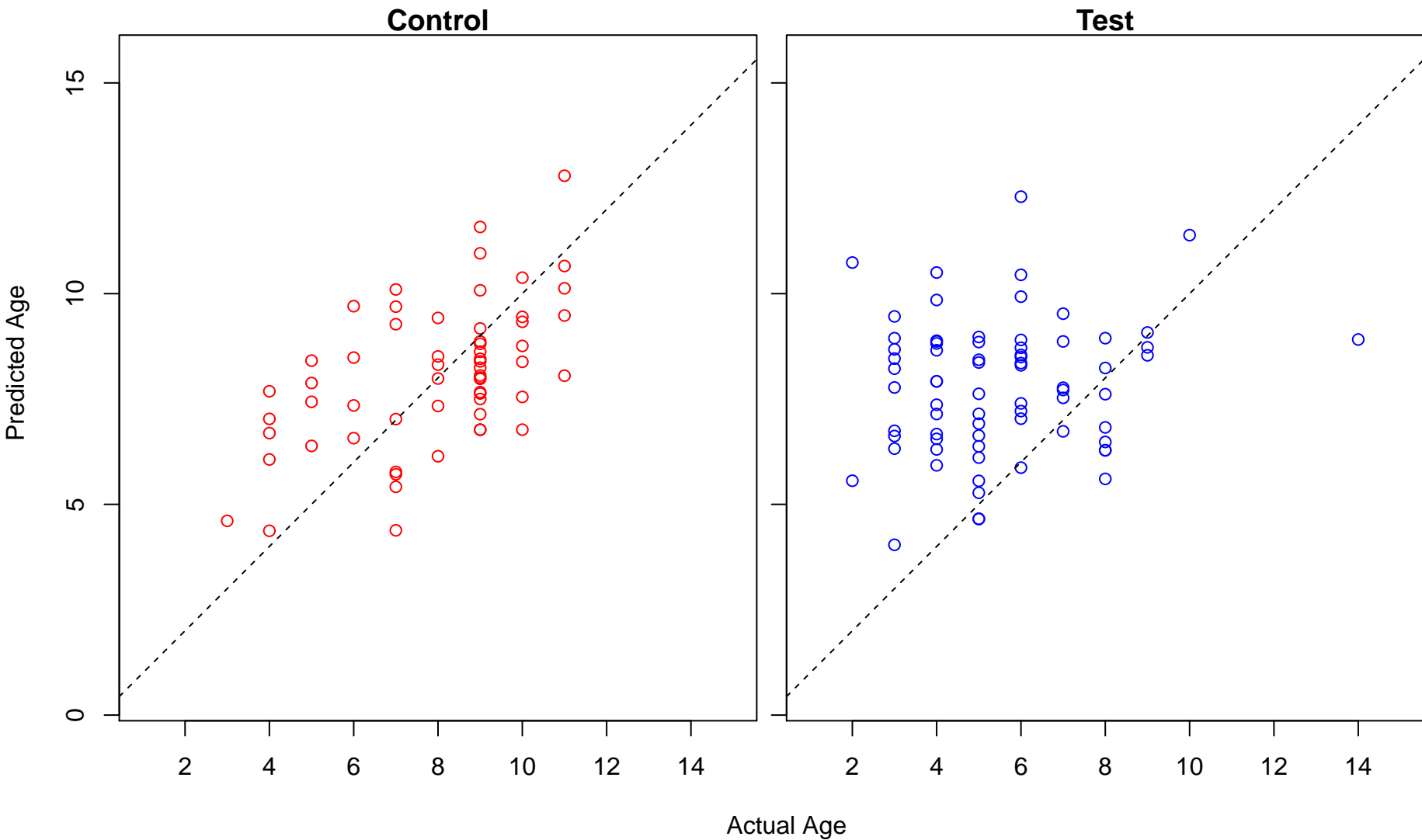
anatomical structure formation involved in morphogenesis (Score: 1.304840)



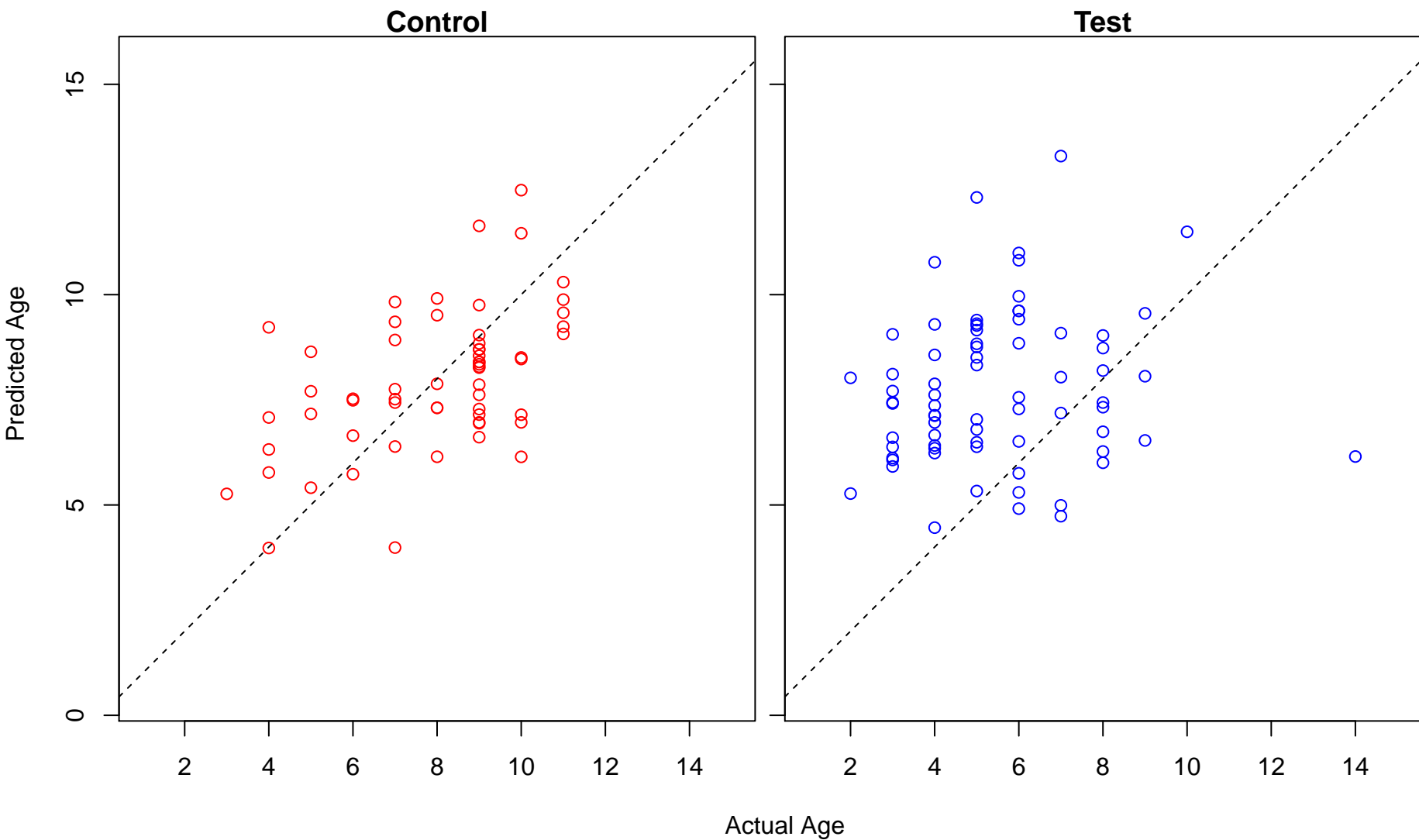
protein acetylation (Score: 1.304139)



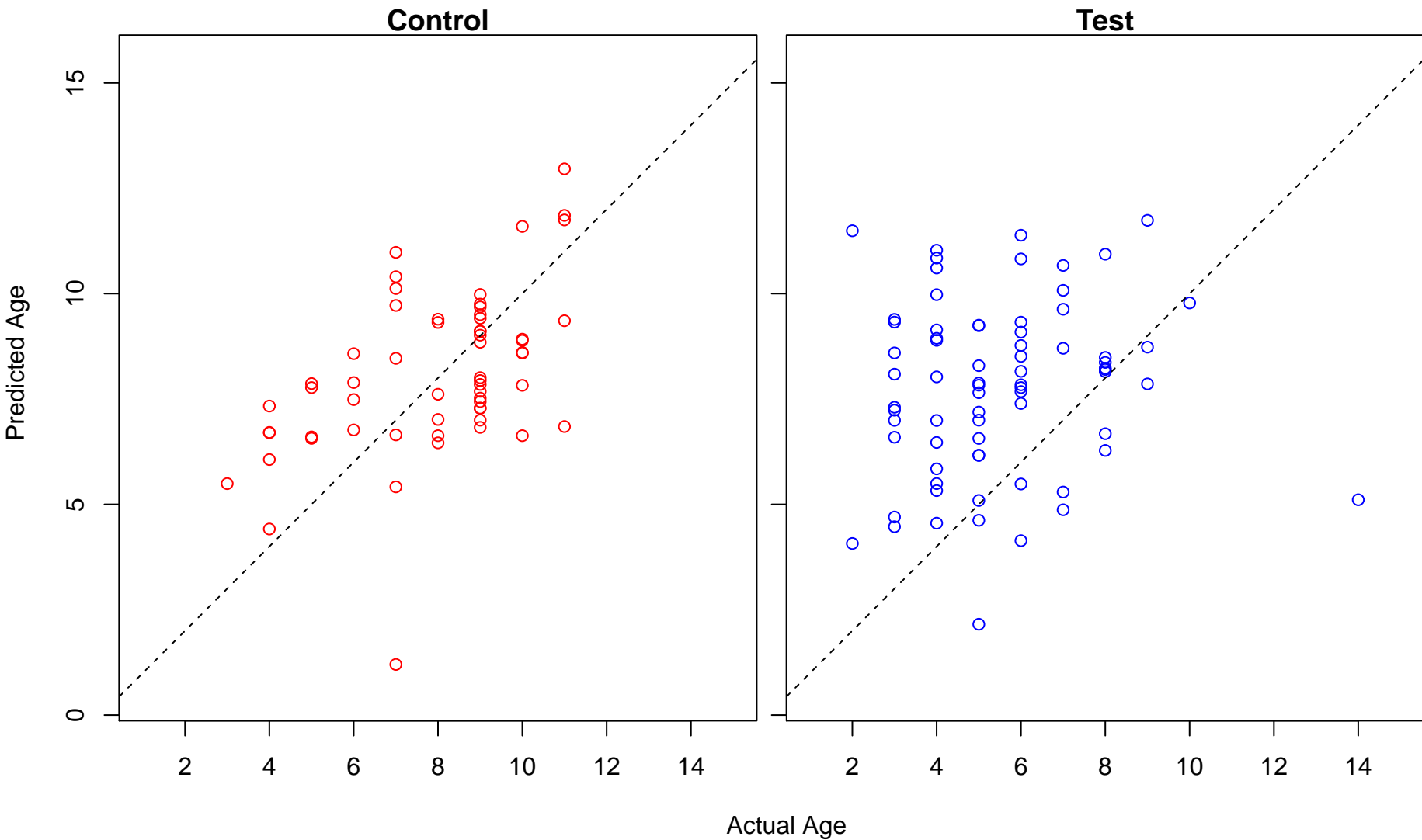
positive regulation of organelle organization (Score: 1.300531)



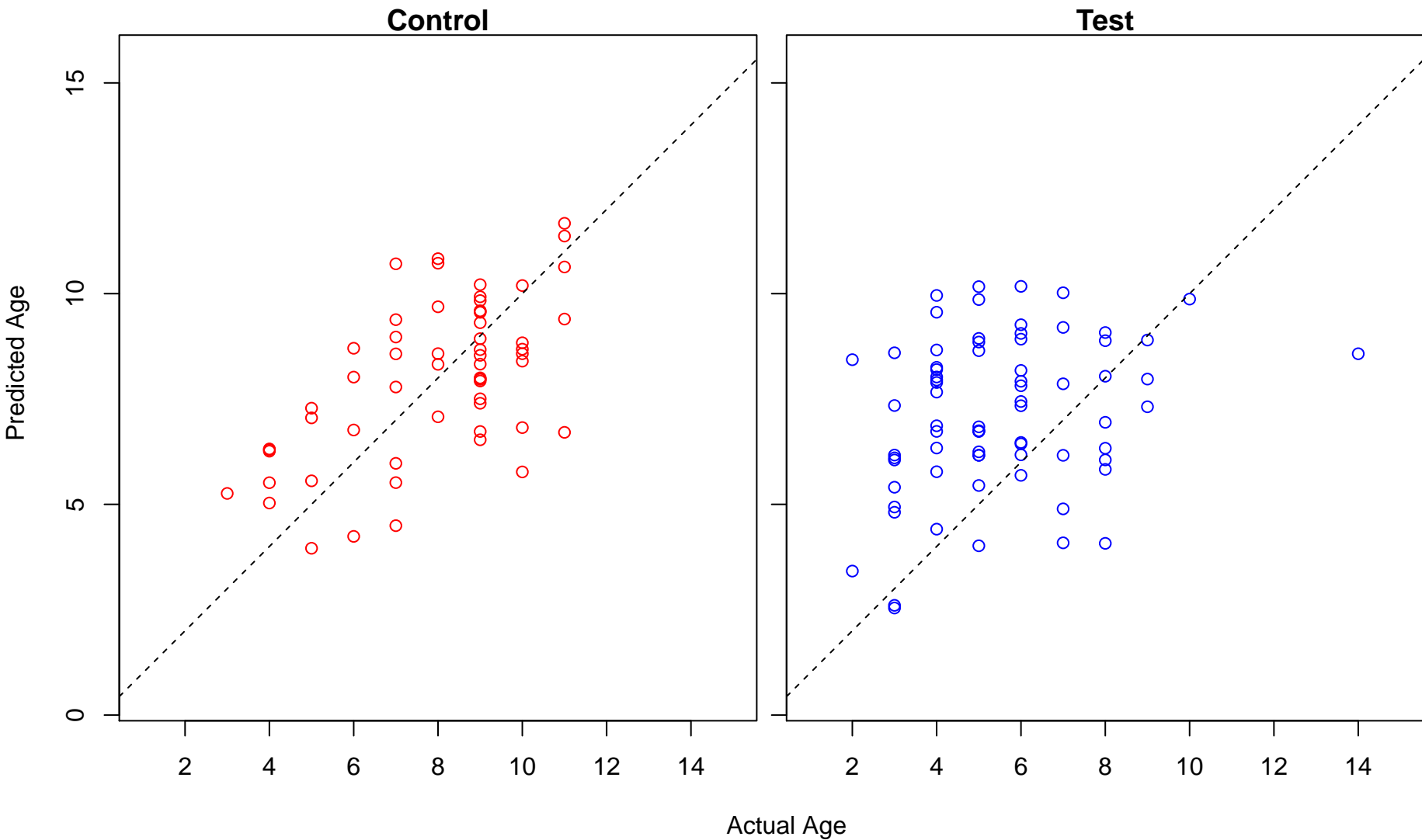
intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress (Score: 1.29883)



negative regulation of cell adhesion (Score: 1.298150)

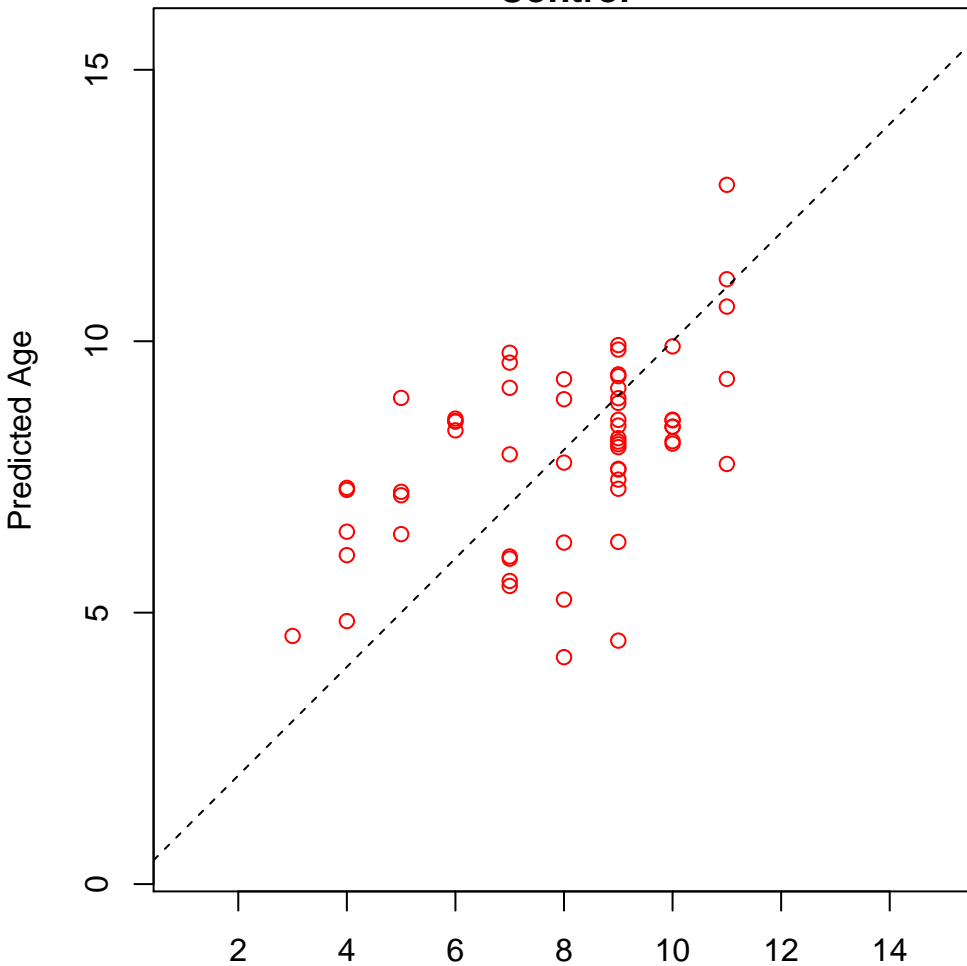


negative regulation of nucleocytoplasmic transport (Score: 1.297339)

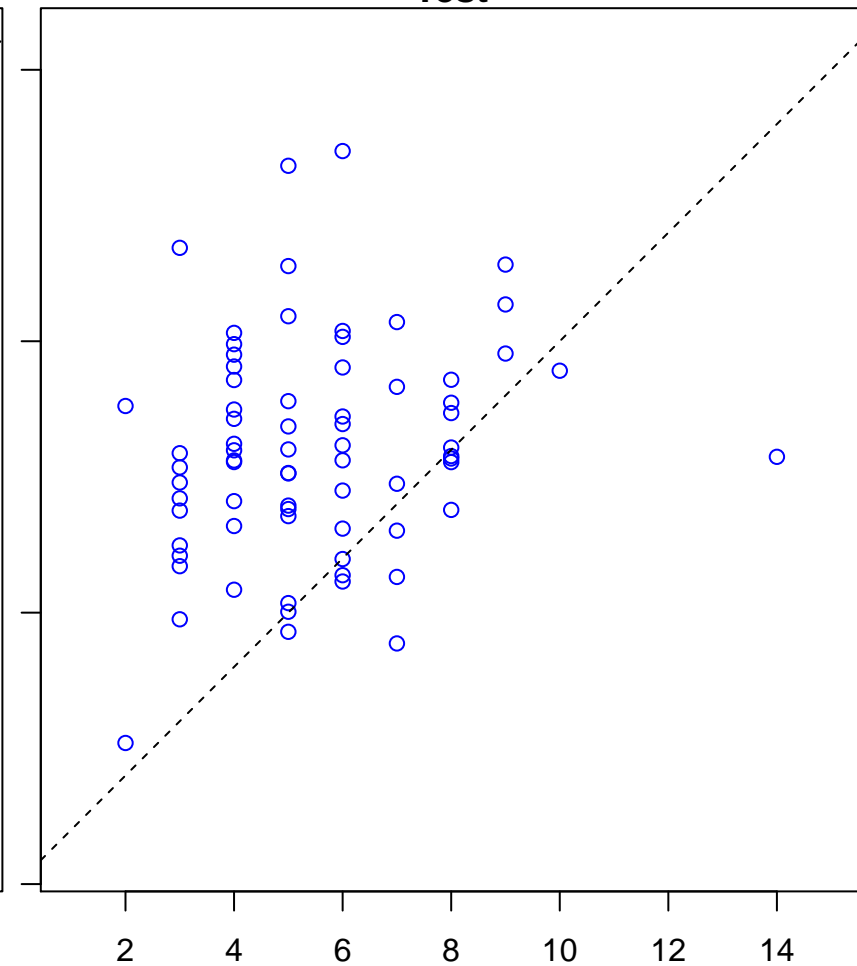


cellular response to hormone stimulus (Score: 1.297072)

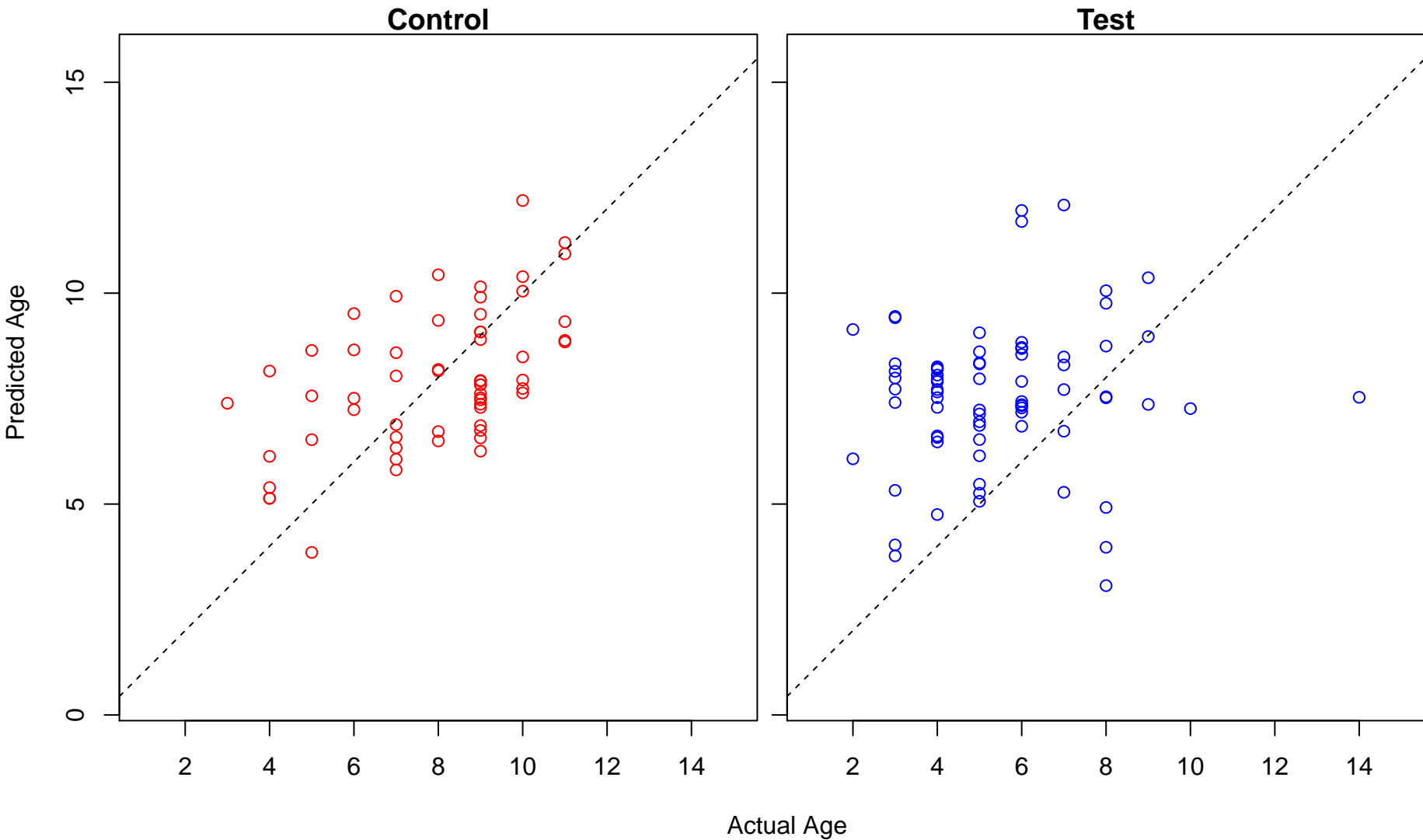
Control



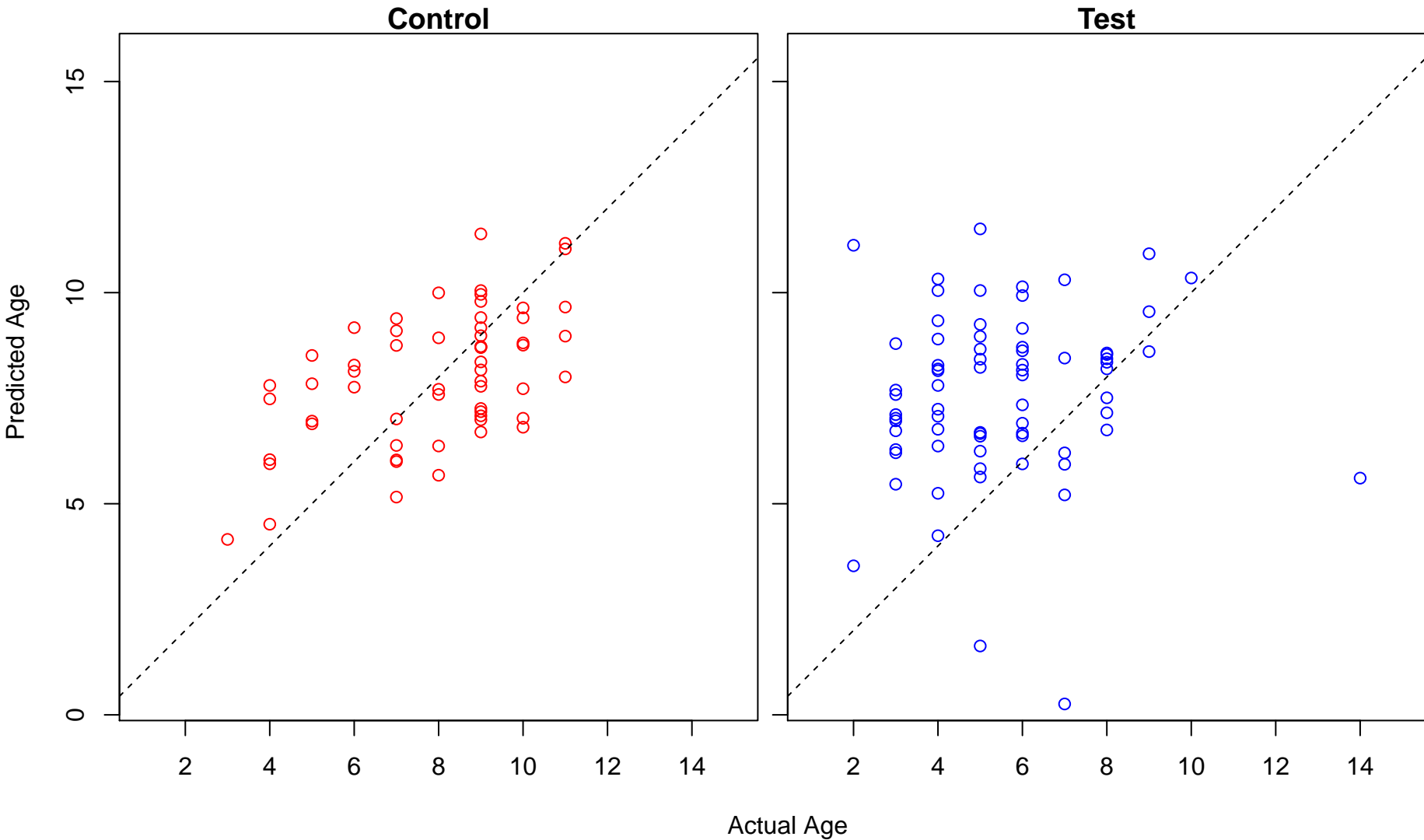
Test



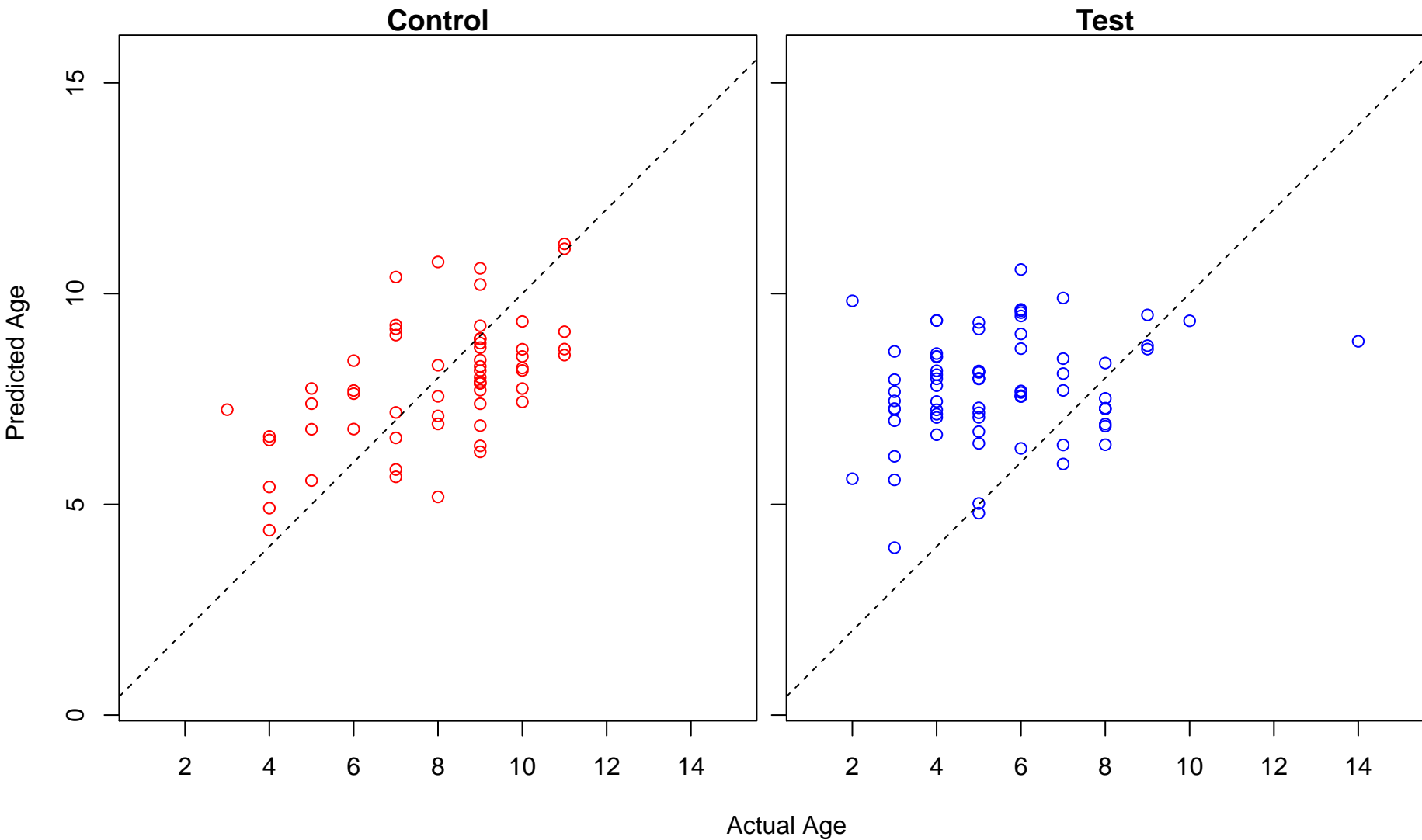
positive regulation of blood vessel endothelial cell migration (Score: 1.295996)



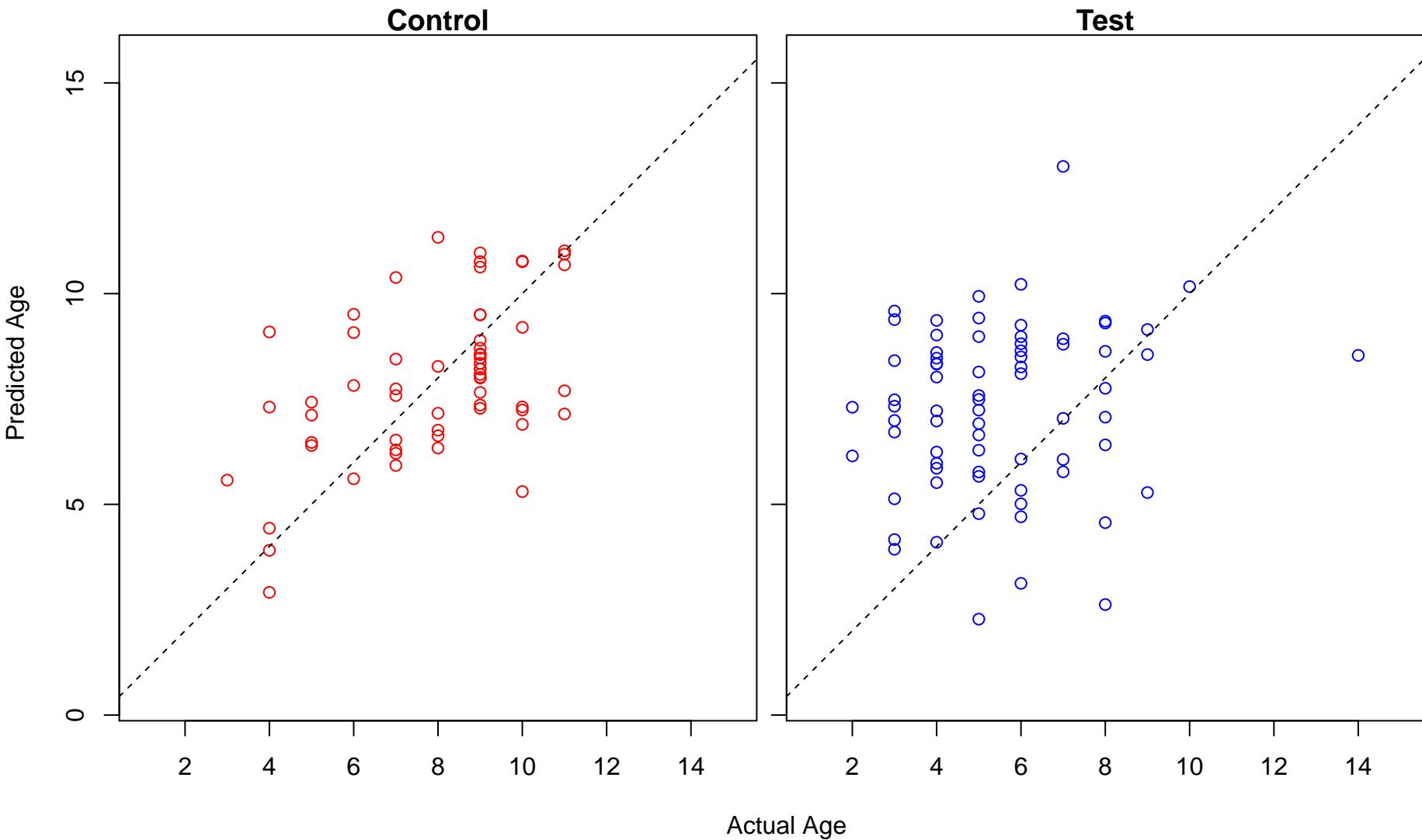
regulation of macromolecule biosynthetic process (Score: 1.294488)



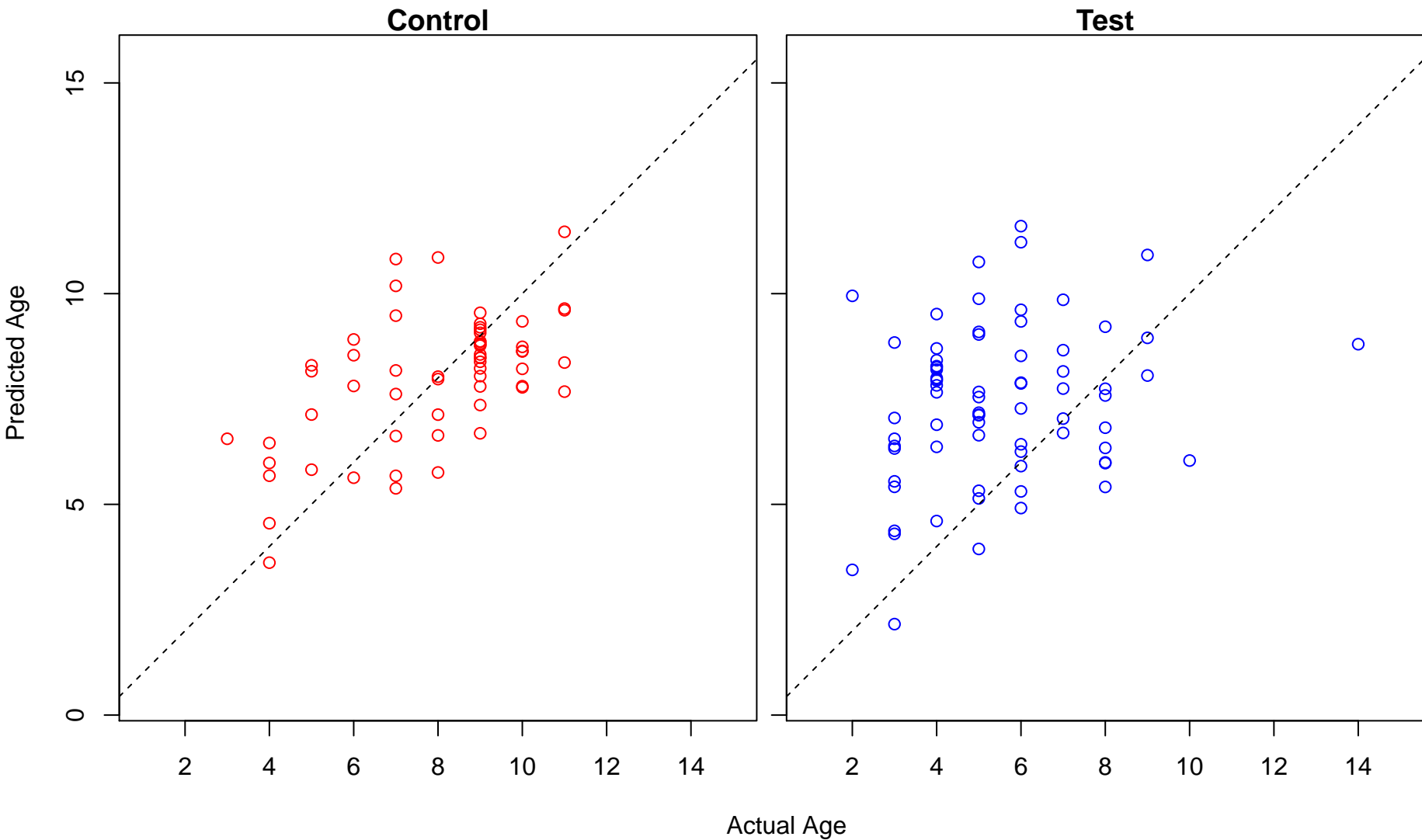
cellular metabolic process (Score: 1.289885)



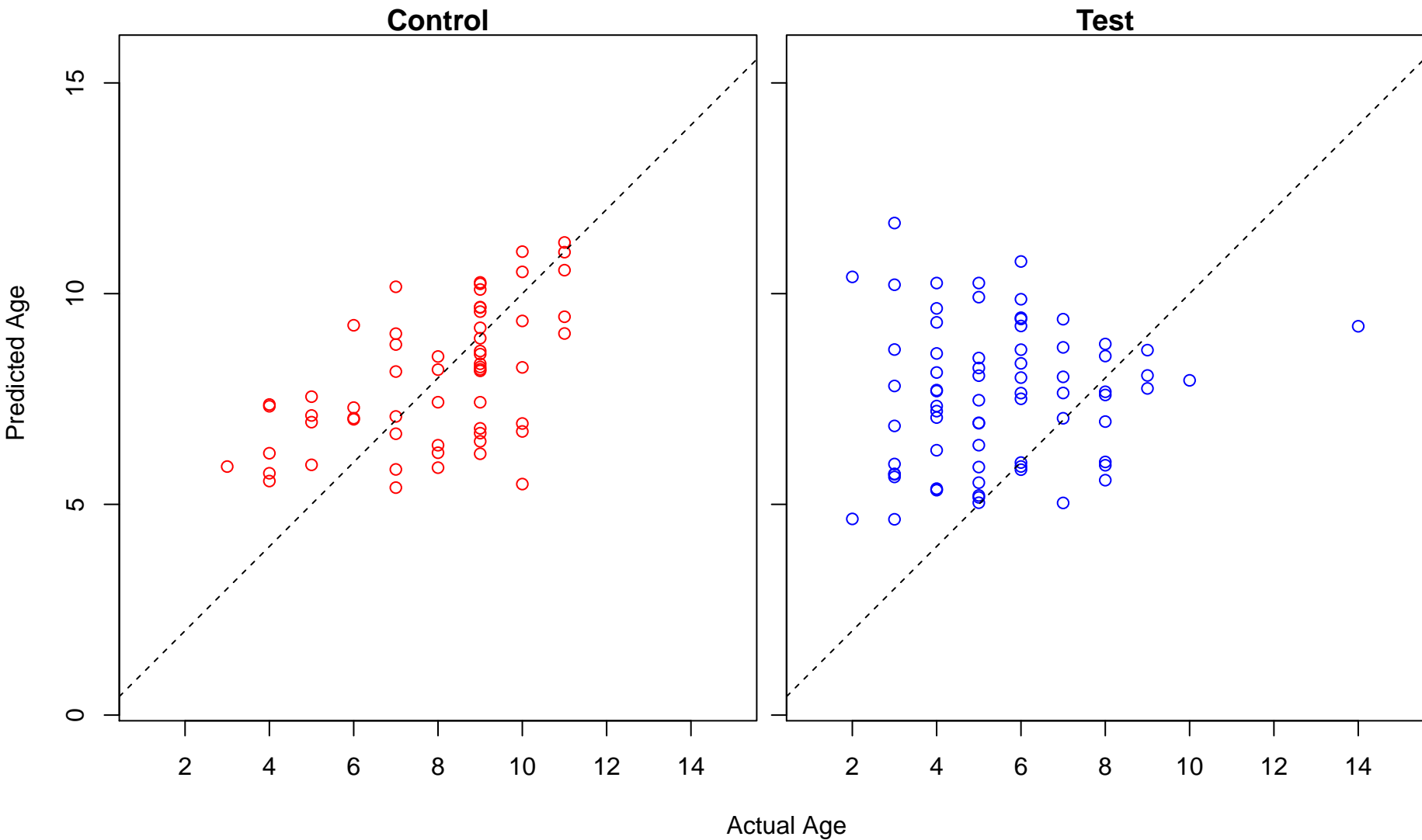
cellular response to topologically incorrect protein (Score: 1.288970)



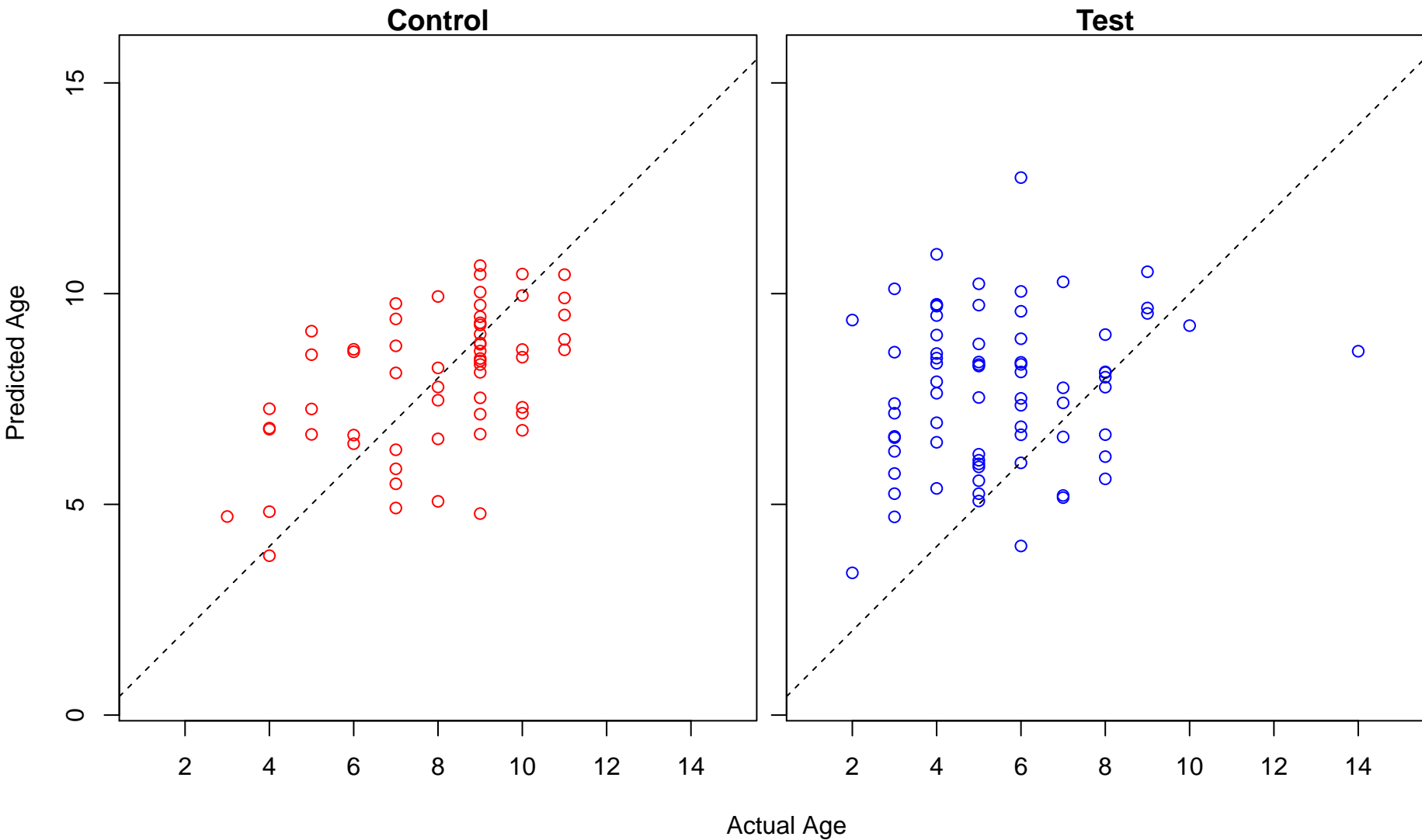
lymphocyte migration (Score: 1.287291)



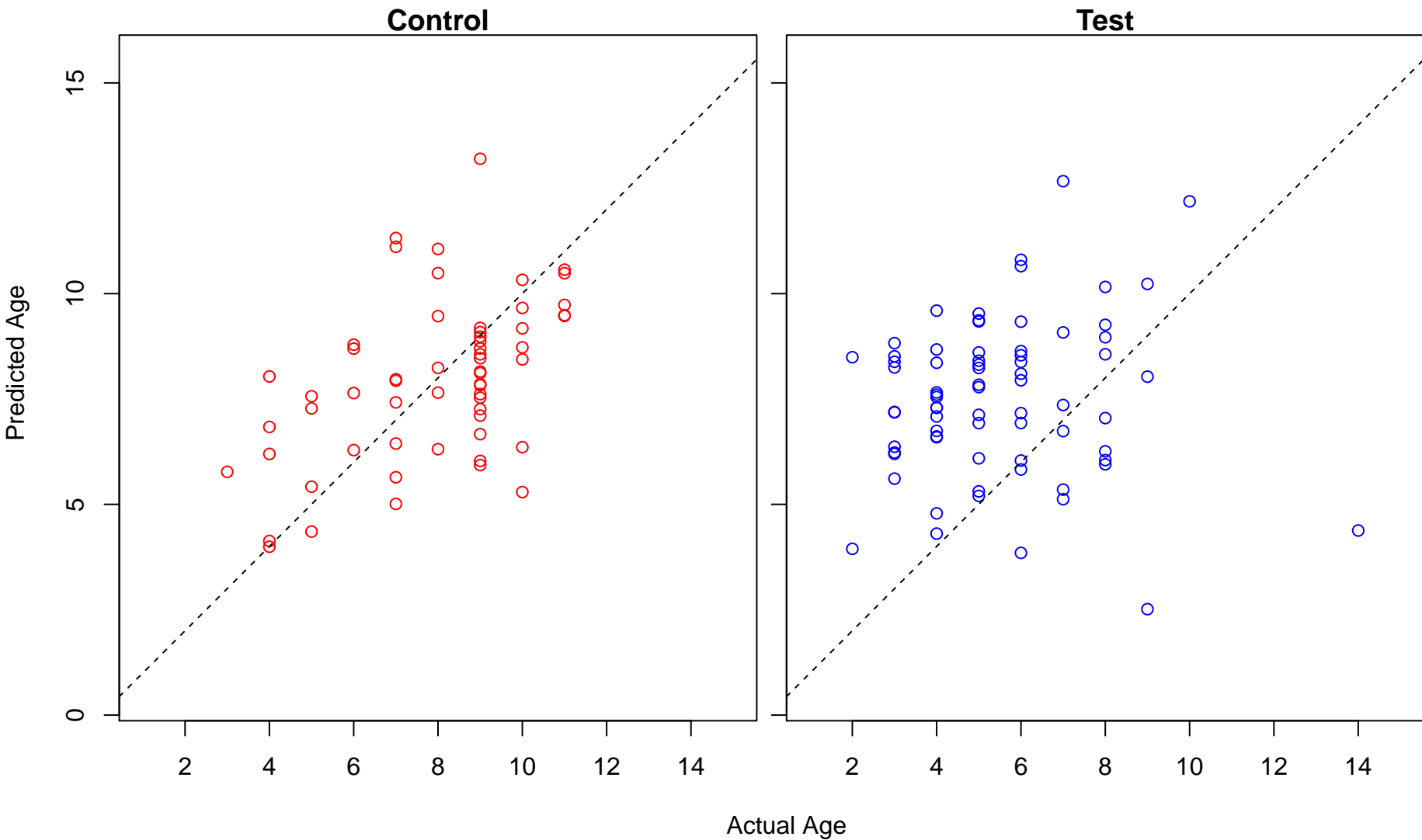
mesenchymal cell differentiation (Score: 1.284138)



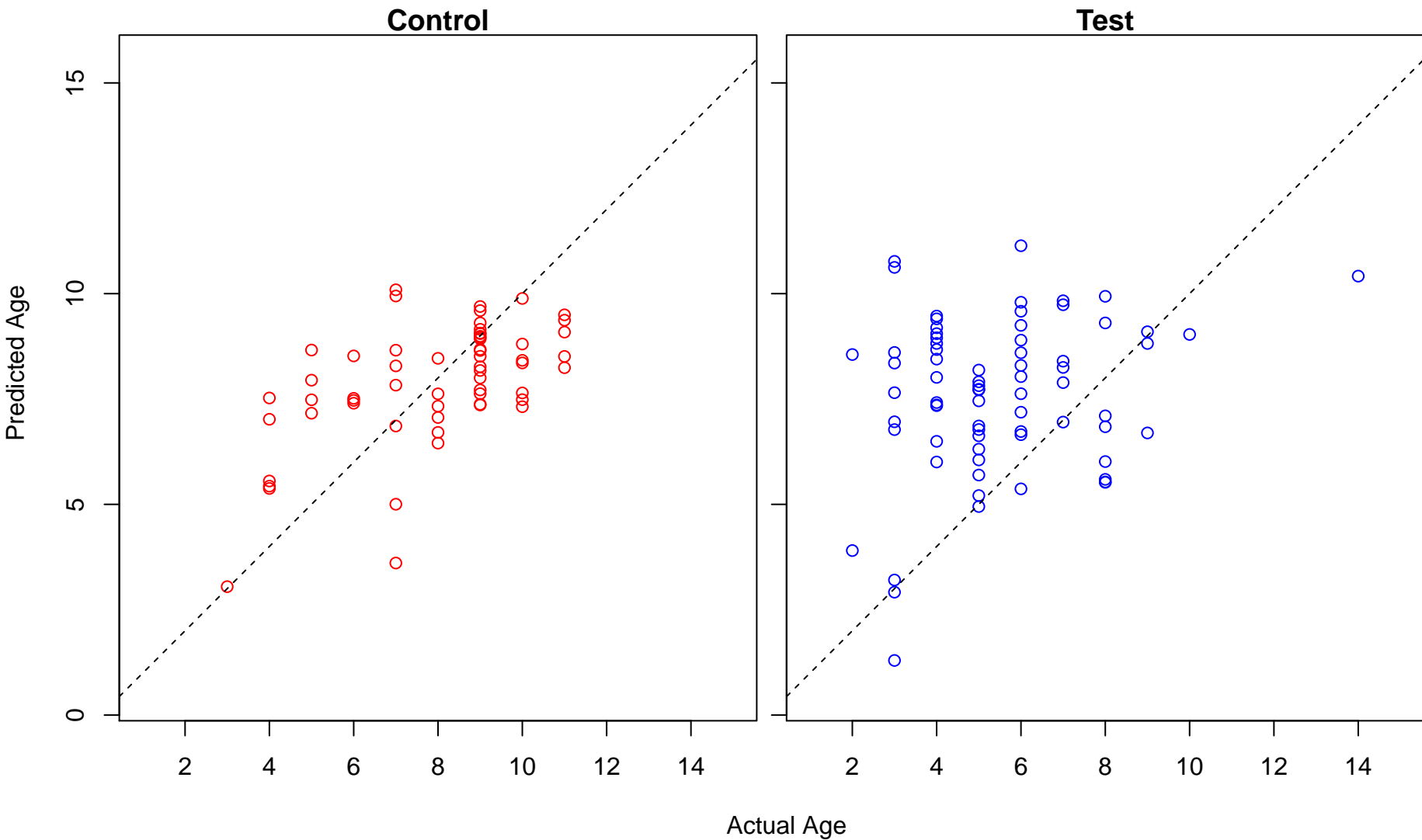
locomotion (Score: 1.284092)



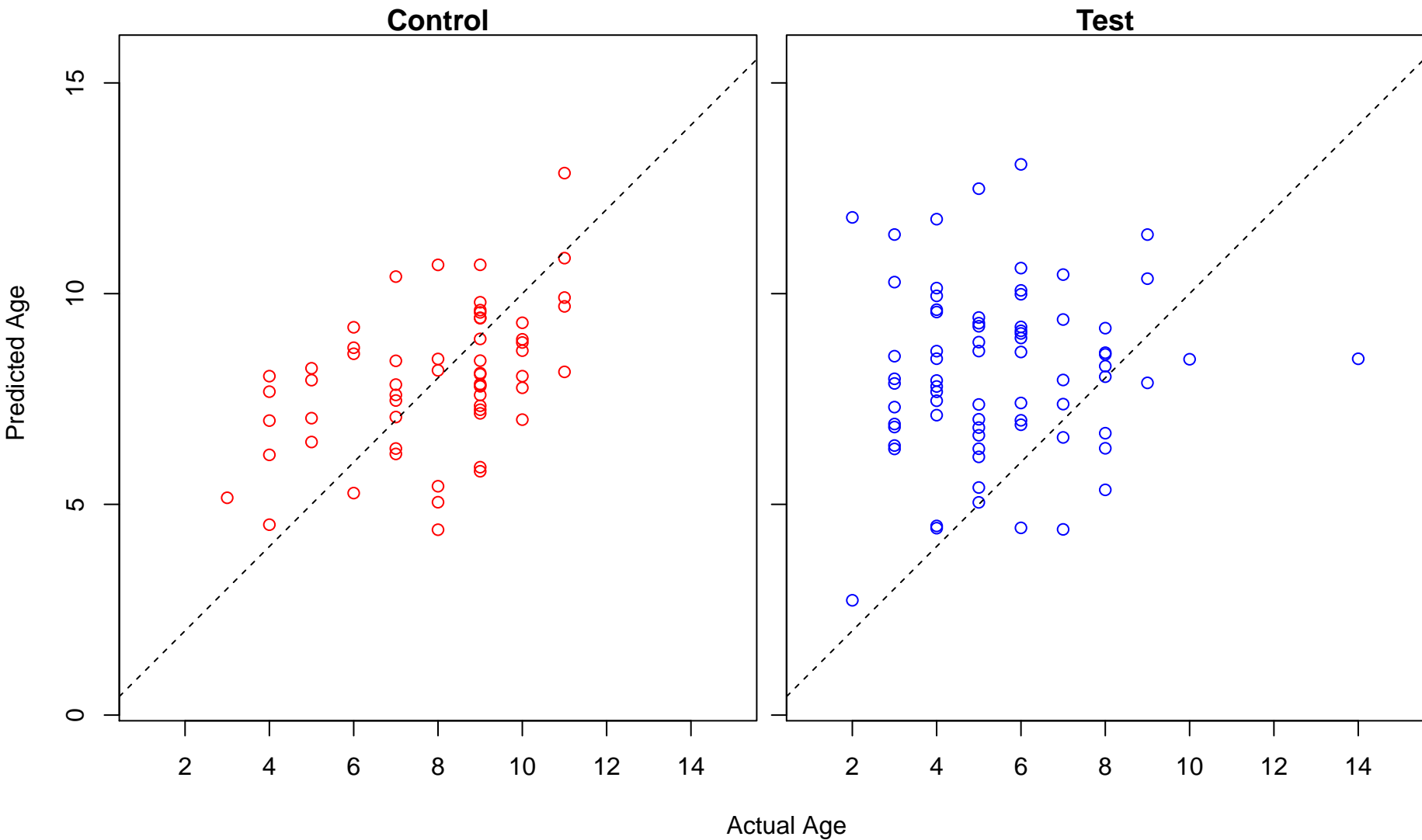
negative regulation of neuron death (Score: 1.284014)



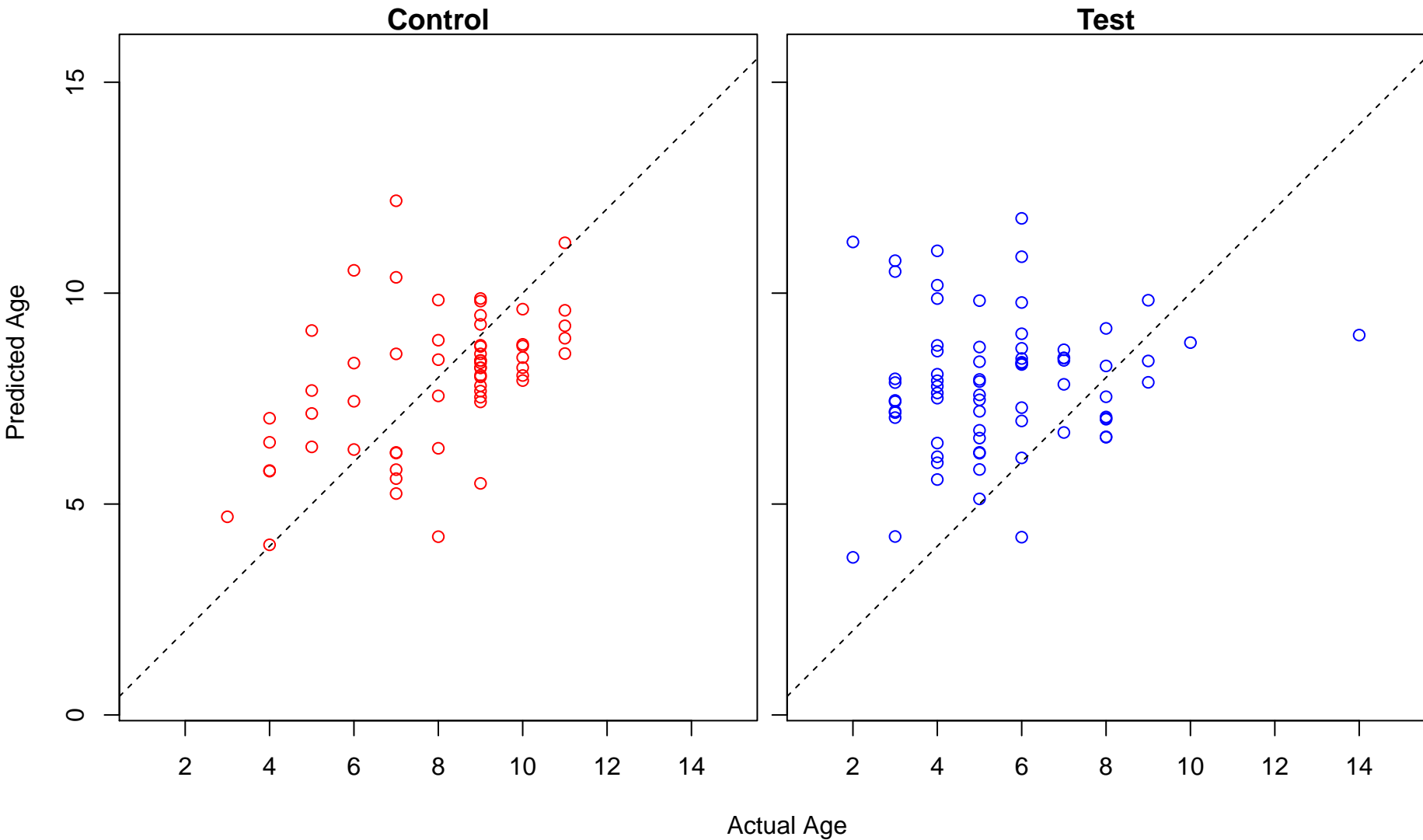
neural plate pattern specification (Score: 1.283170)



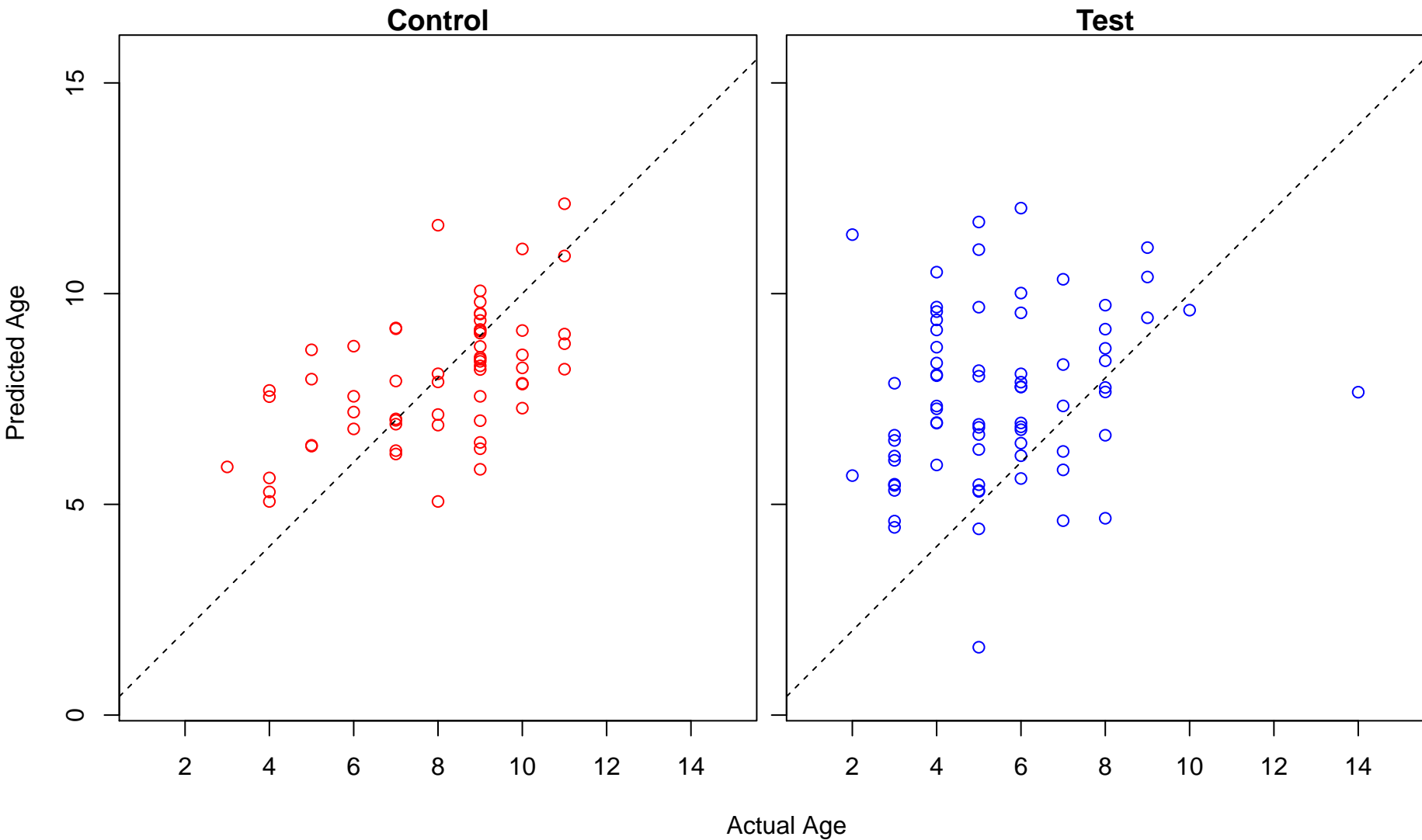
positive regulation of MAPK cascade (Score: 1.279656)



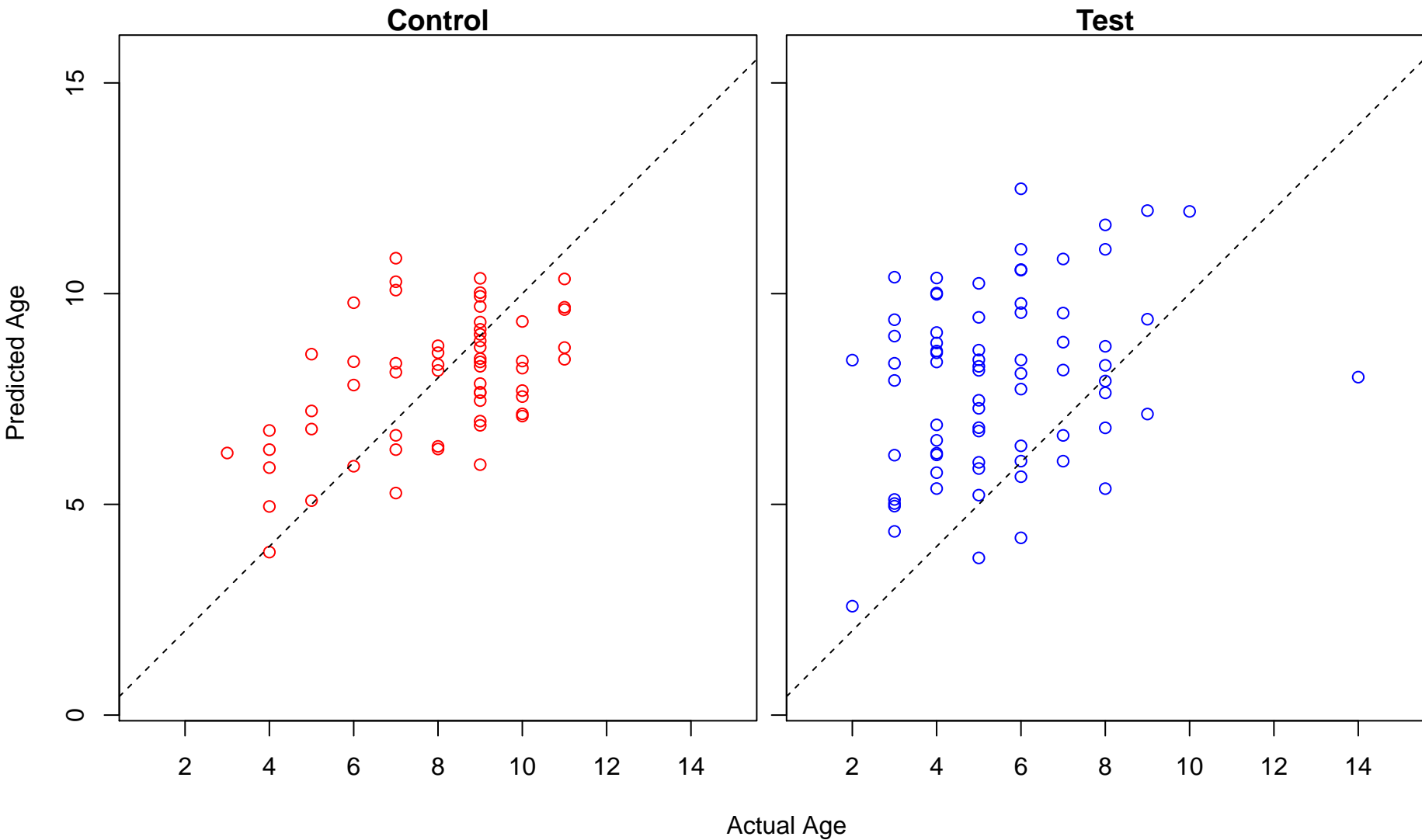
positive regulation of intracellular transport (Score: 1.278122)



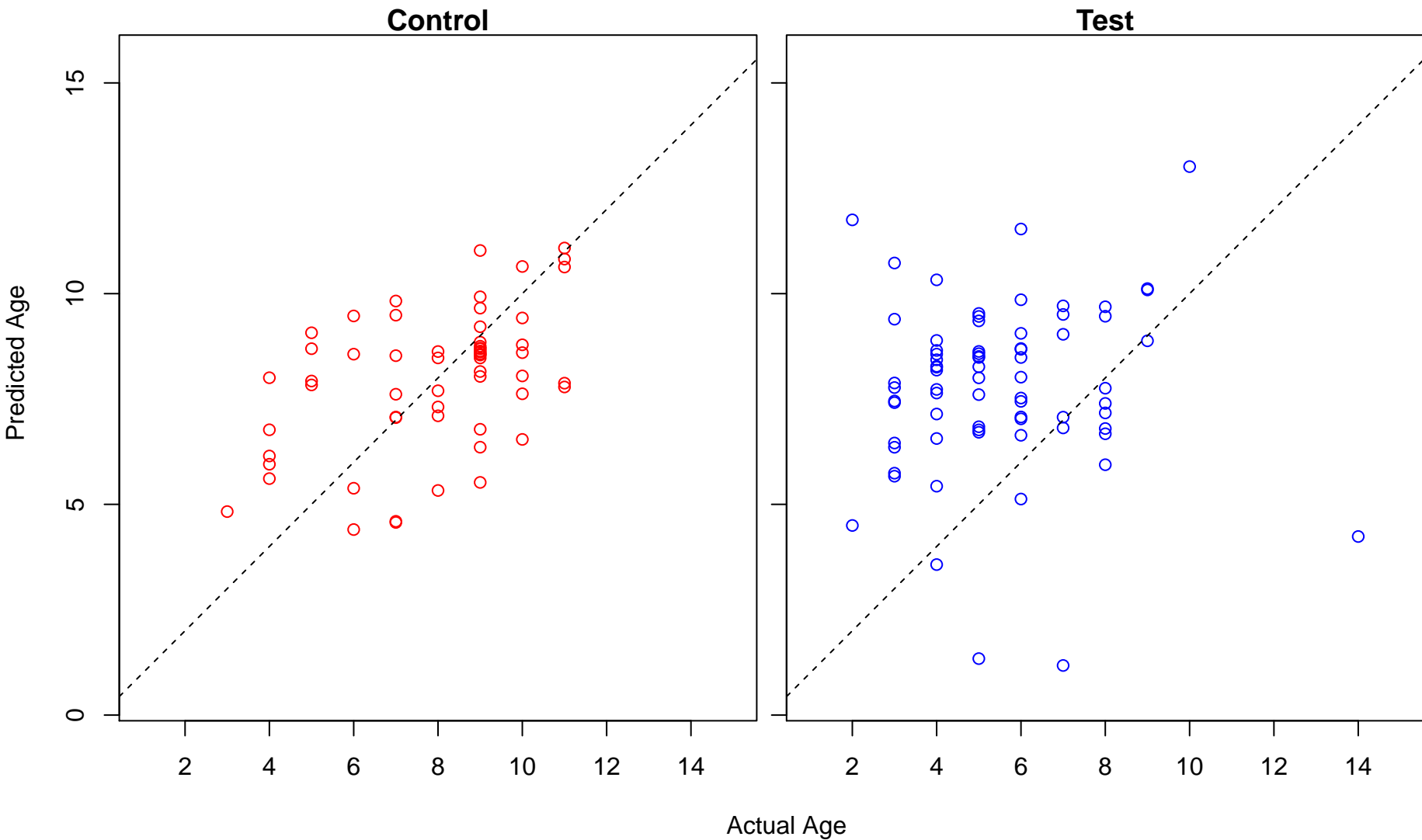
defense response (Score: 1.275665)



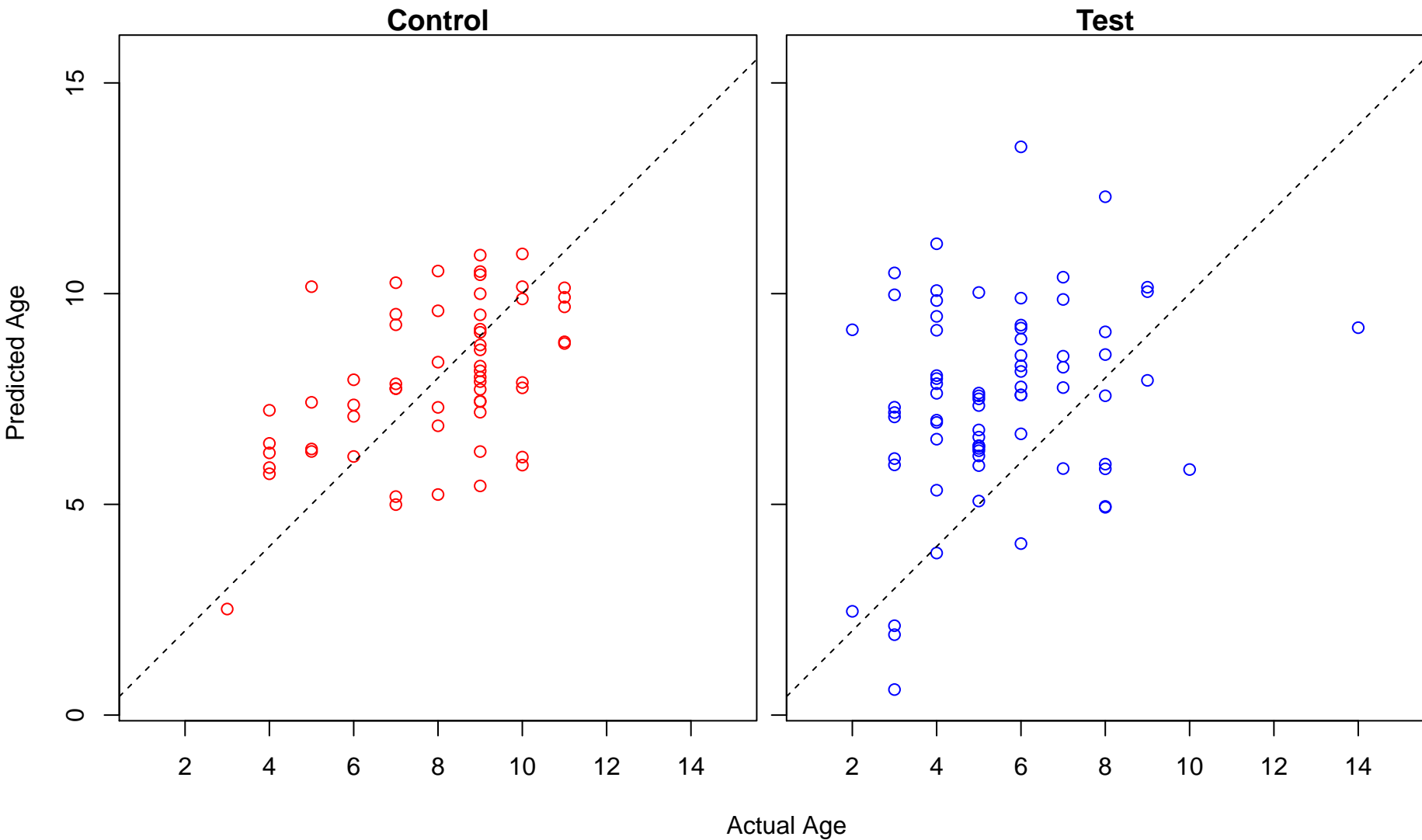
cerebral cortex neuron differentiation (Score: 1.274190)



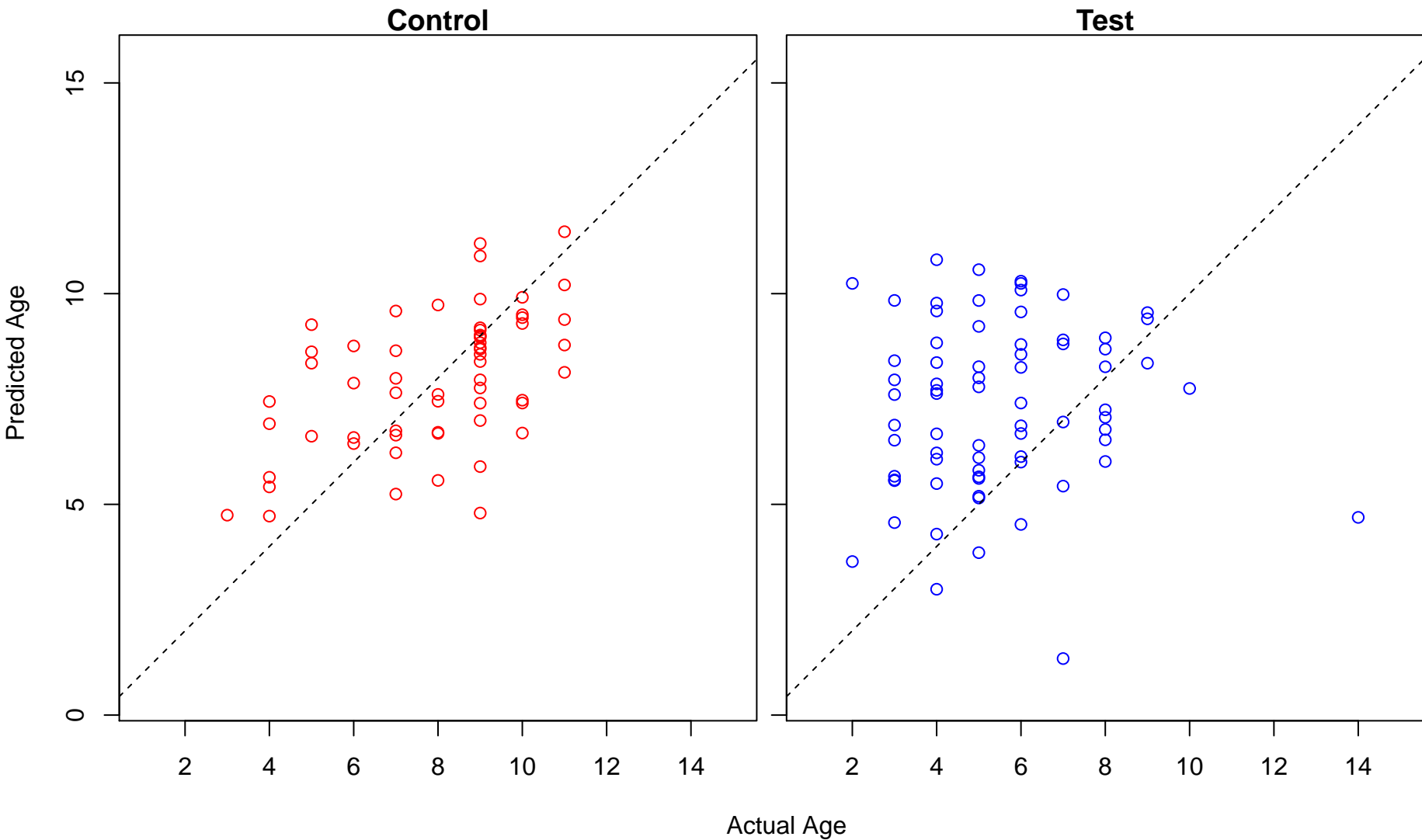
negative regulation of transcription from RNA polymerase II promoter (Score: 1.272744)



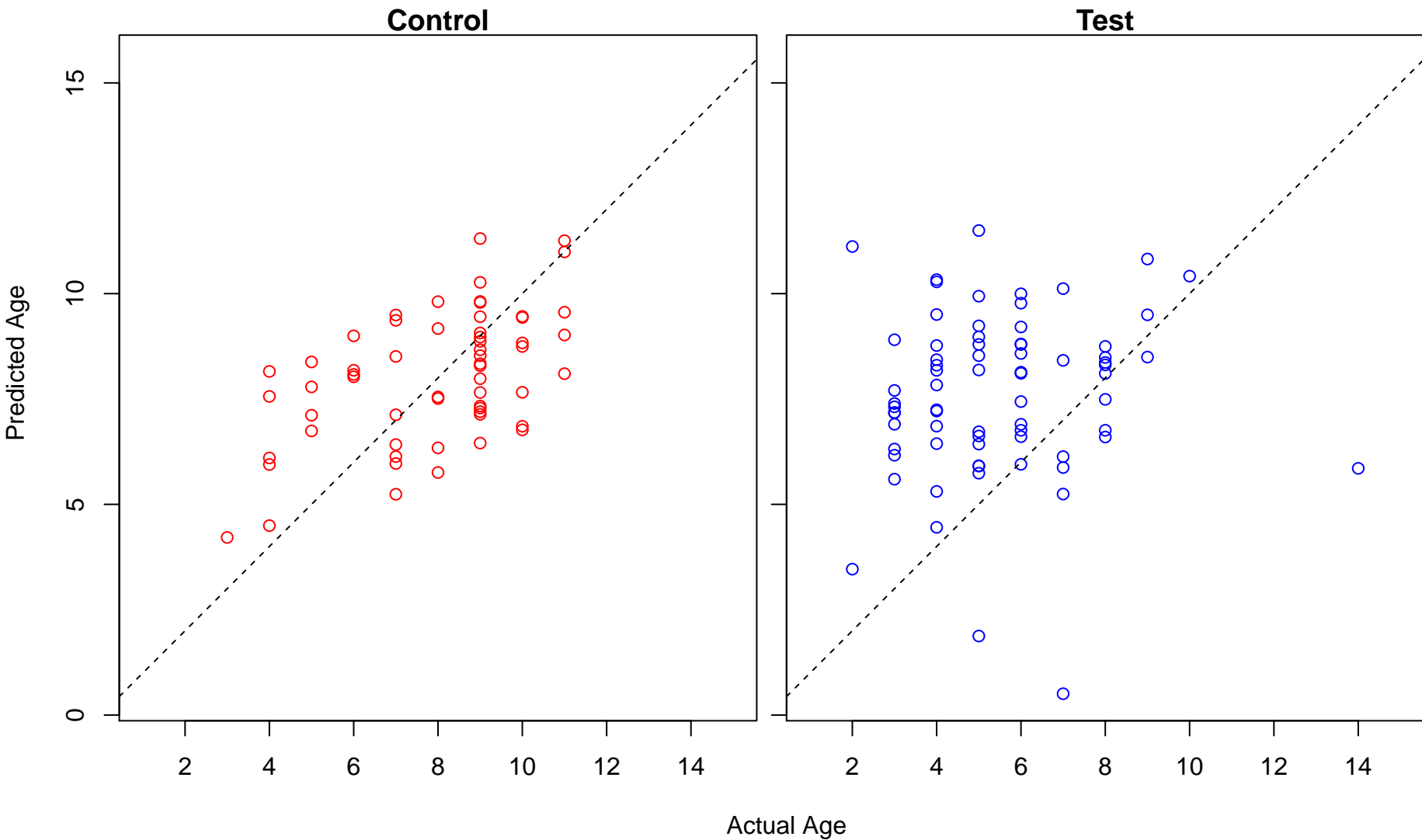
mesonephros development (Score: 1.267263)



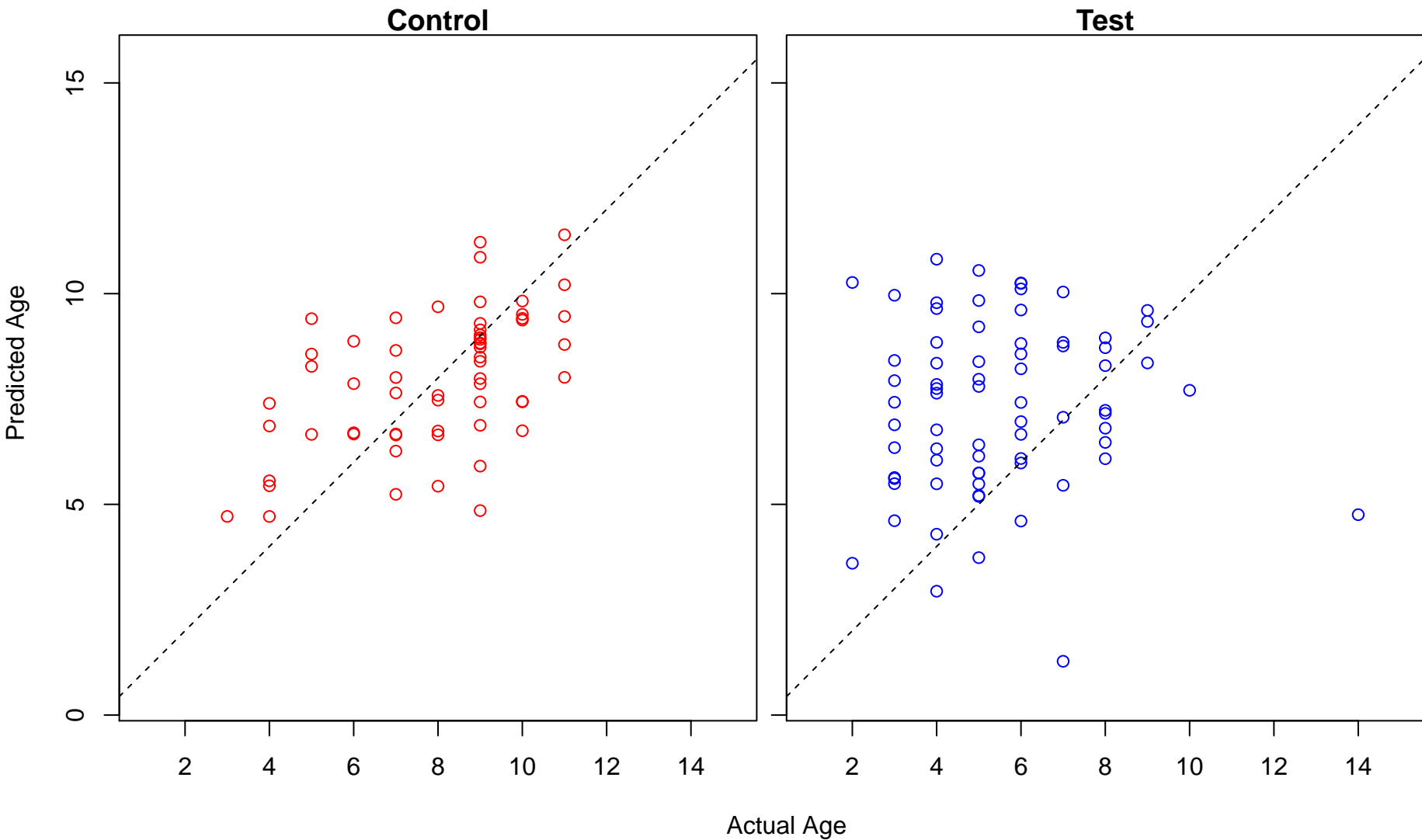
cell differentiation (Score: 1.266052)



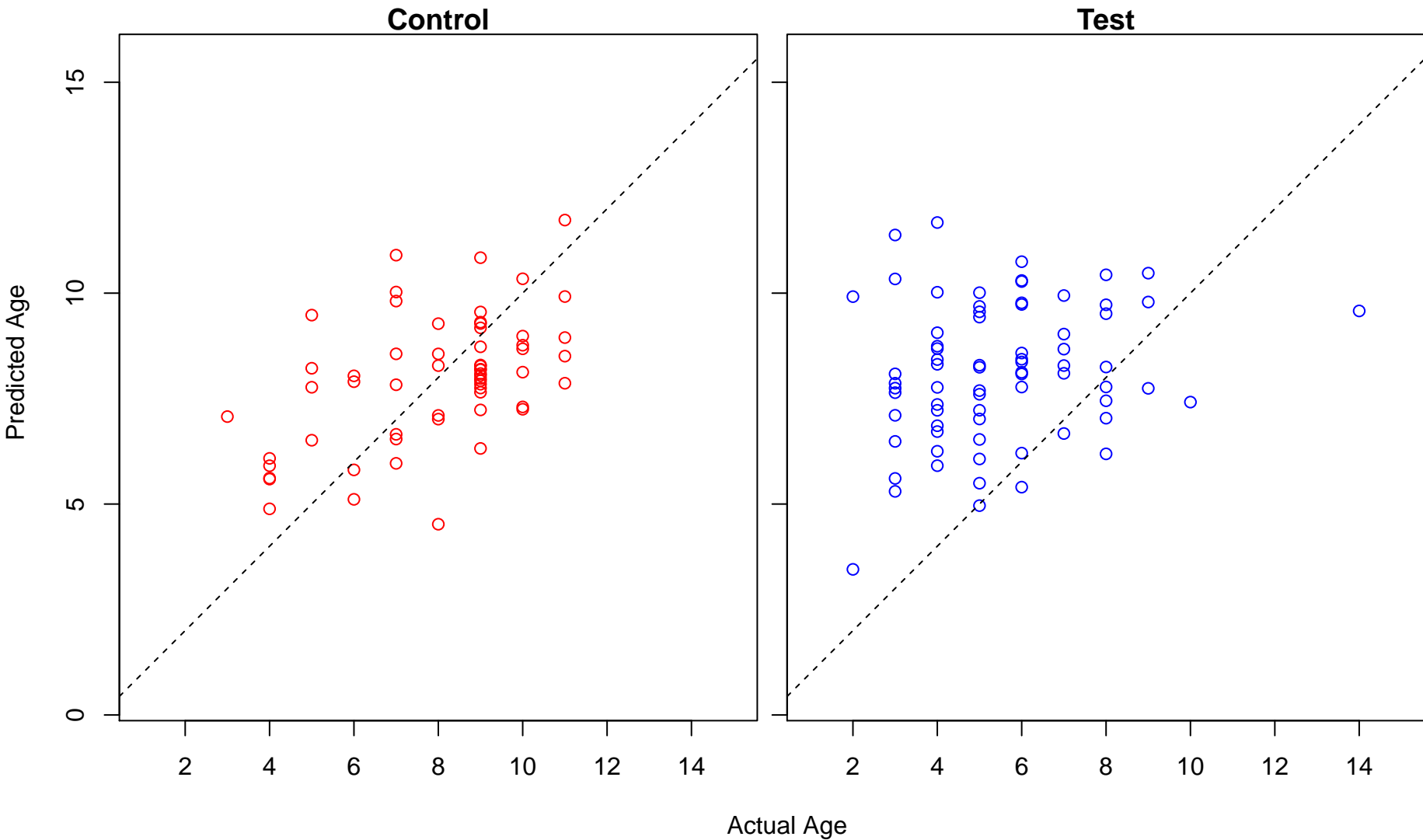
regulation of cellular biosynthetic process (Score: 1.265722)



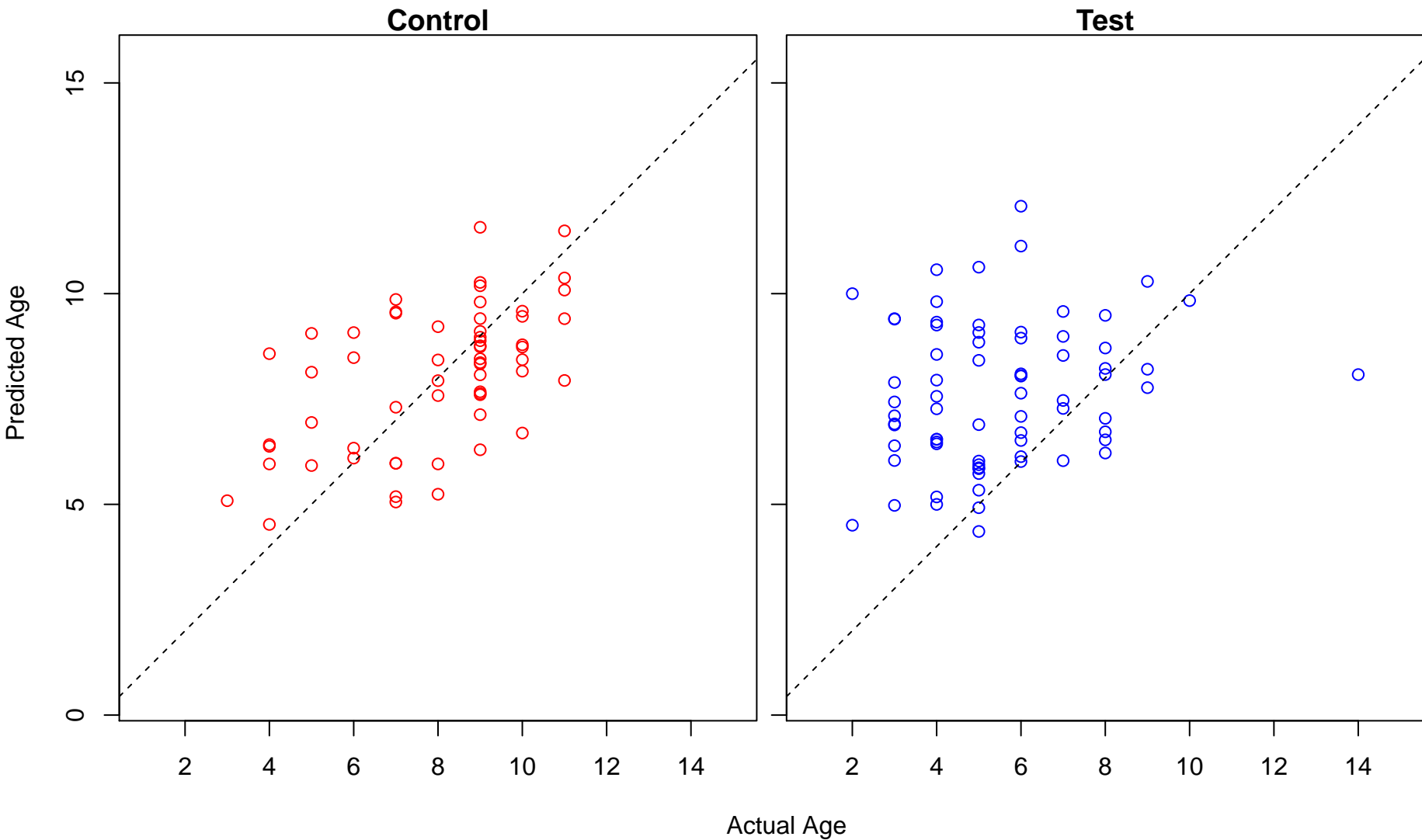
cellular developmental process (Score: 1.265516)



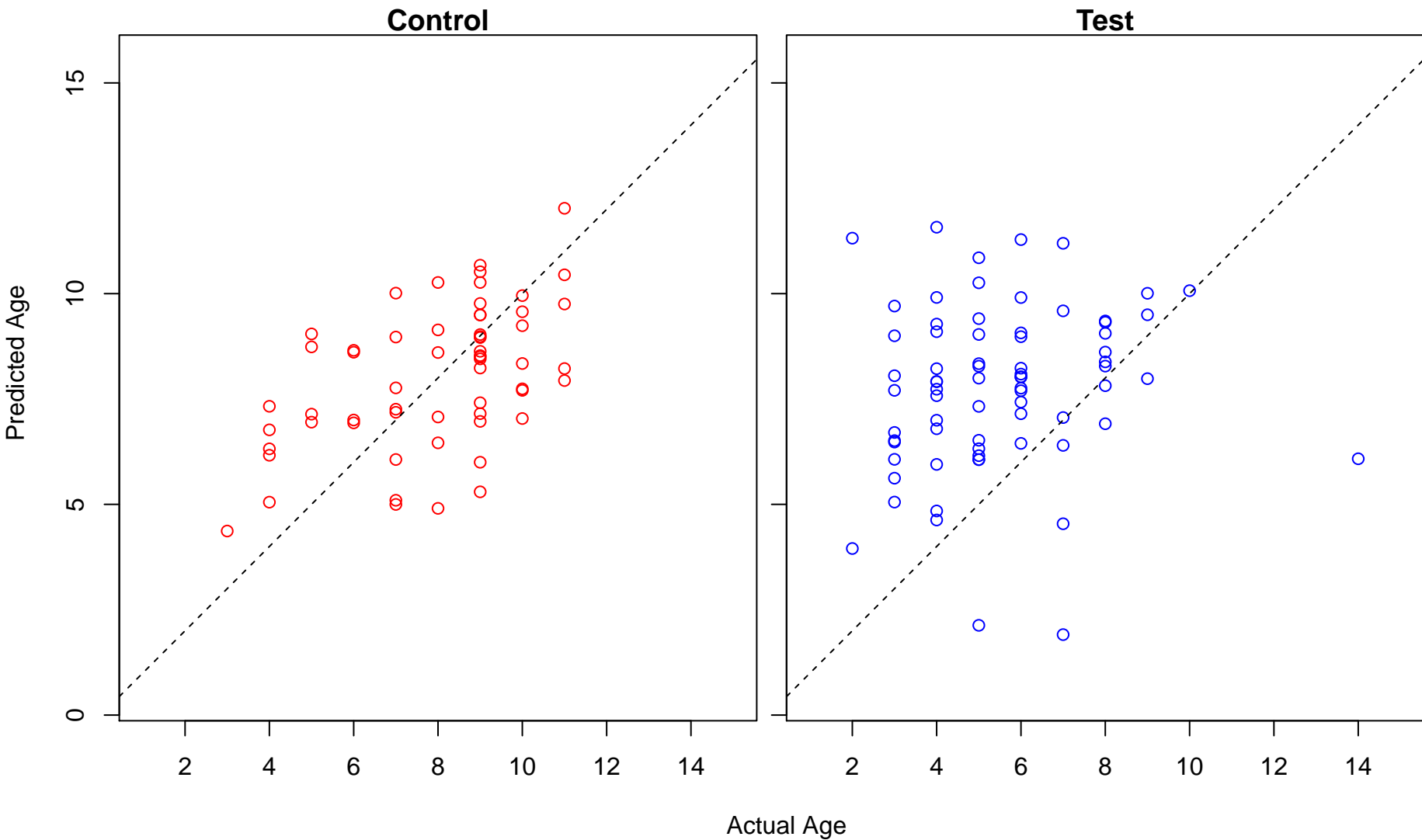
morphogenesis of an epithelial sheet (Score: 1.264913)



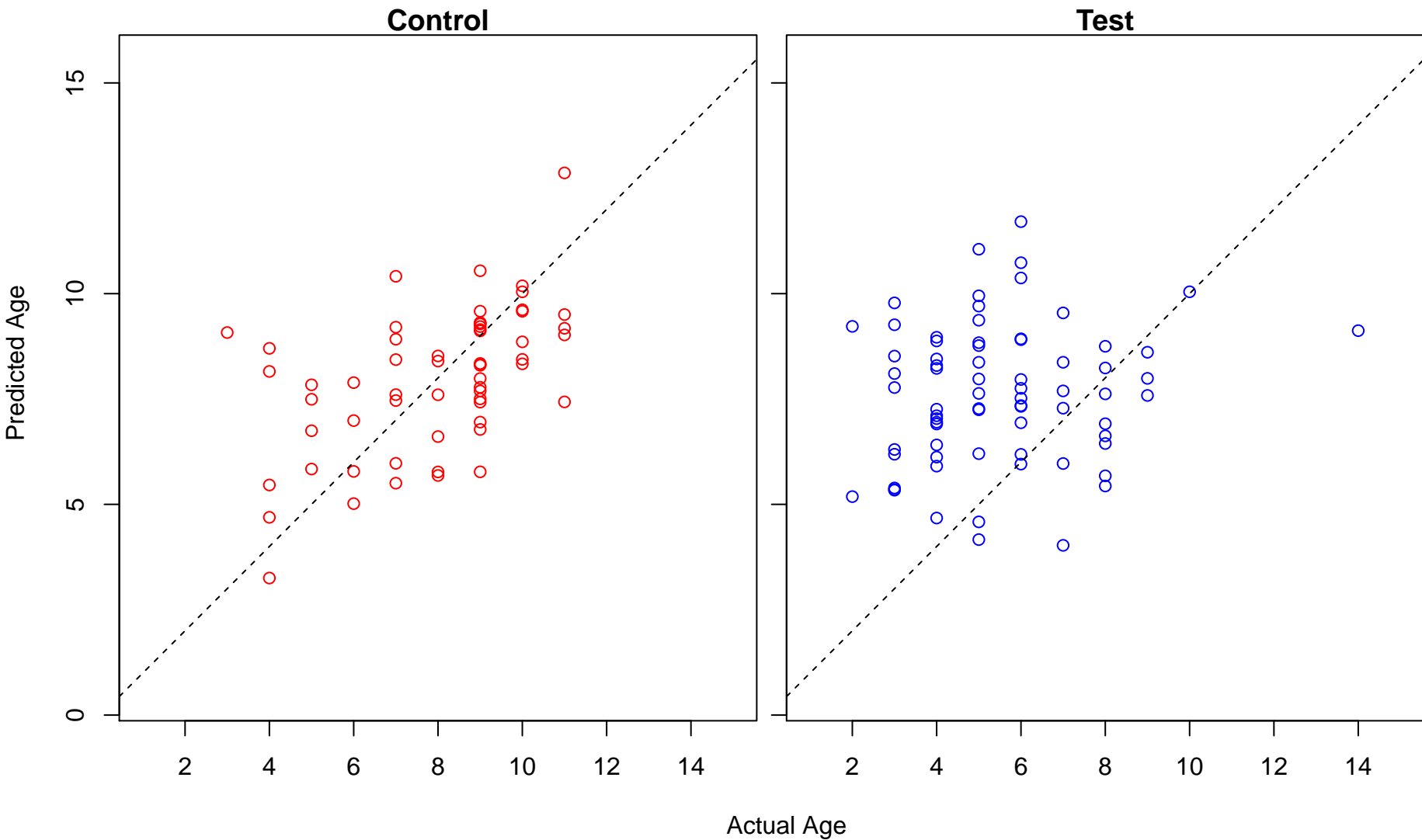
regulation of cellular component organization (Score: 1.262601)



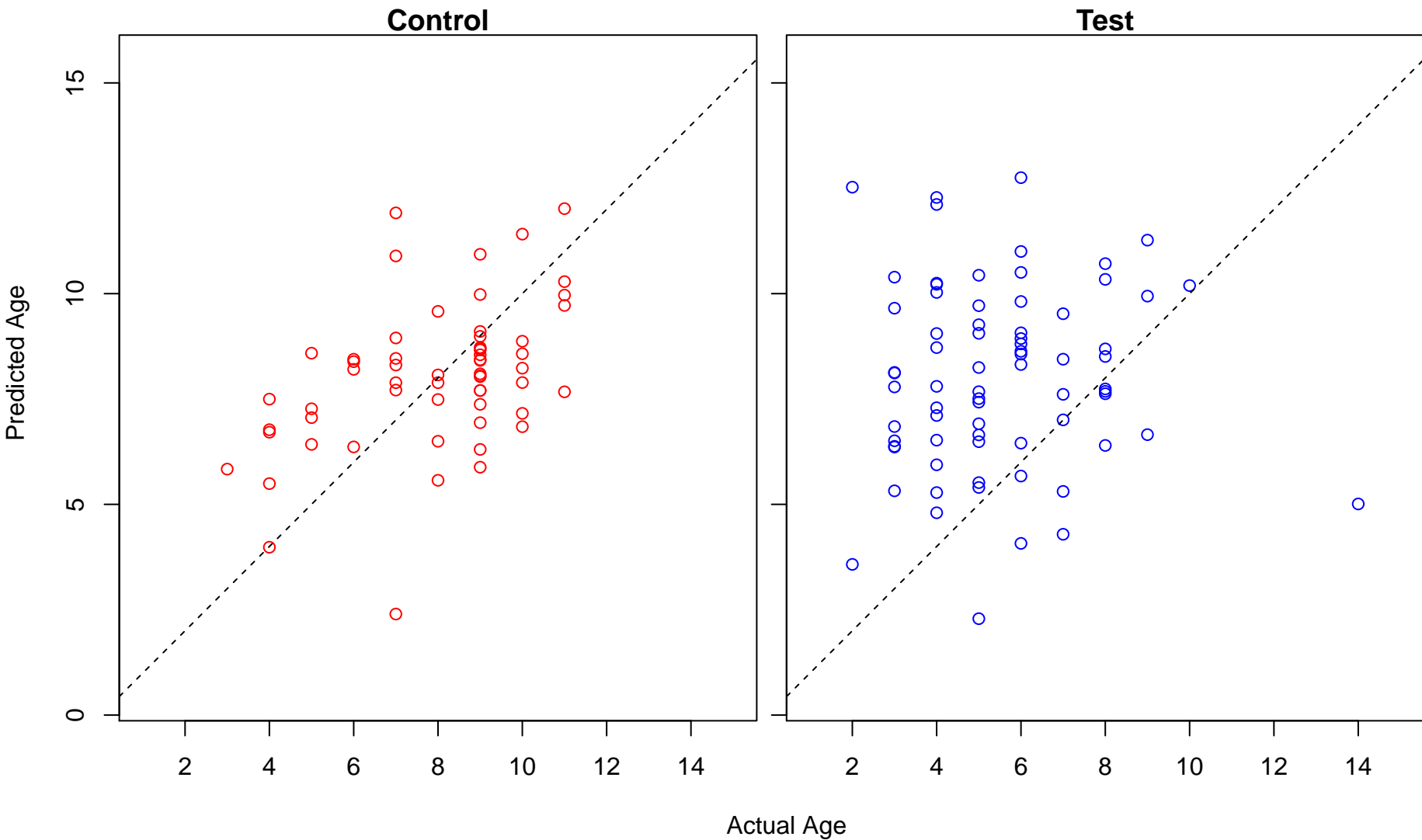
negative regulation of cellular biosynthetic process (Score: 1.261666)



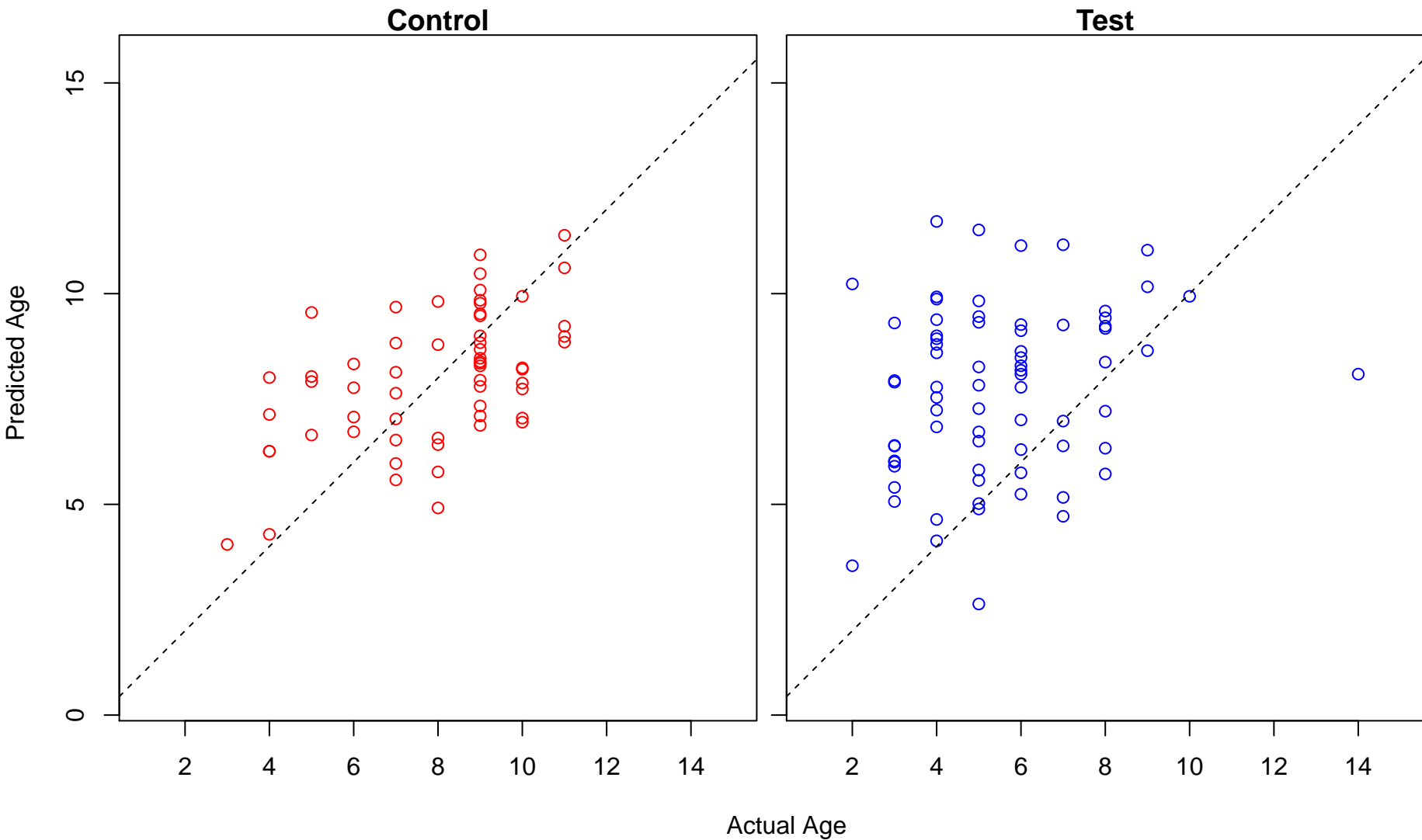
establishment of protein localization to organelle (Score: 1.261386)



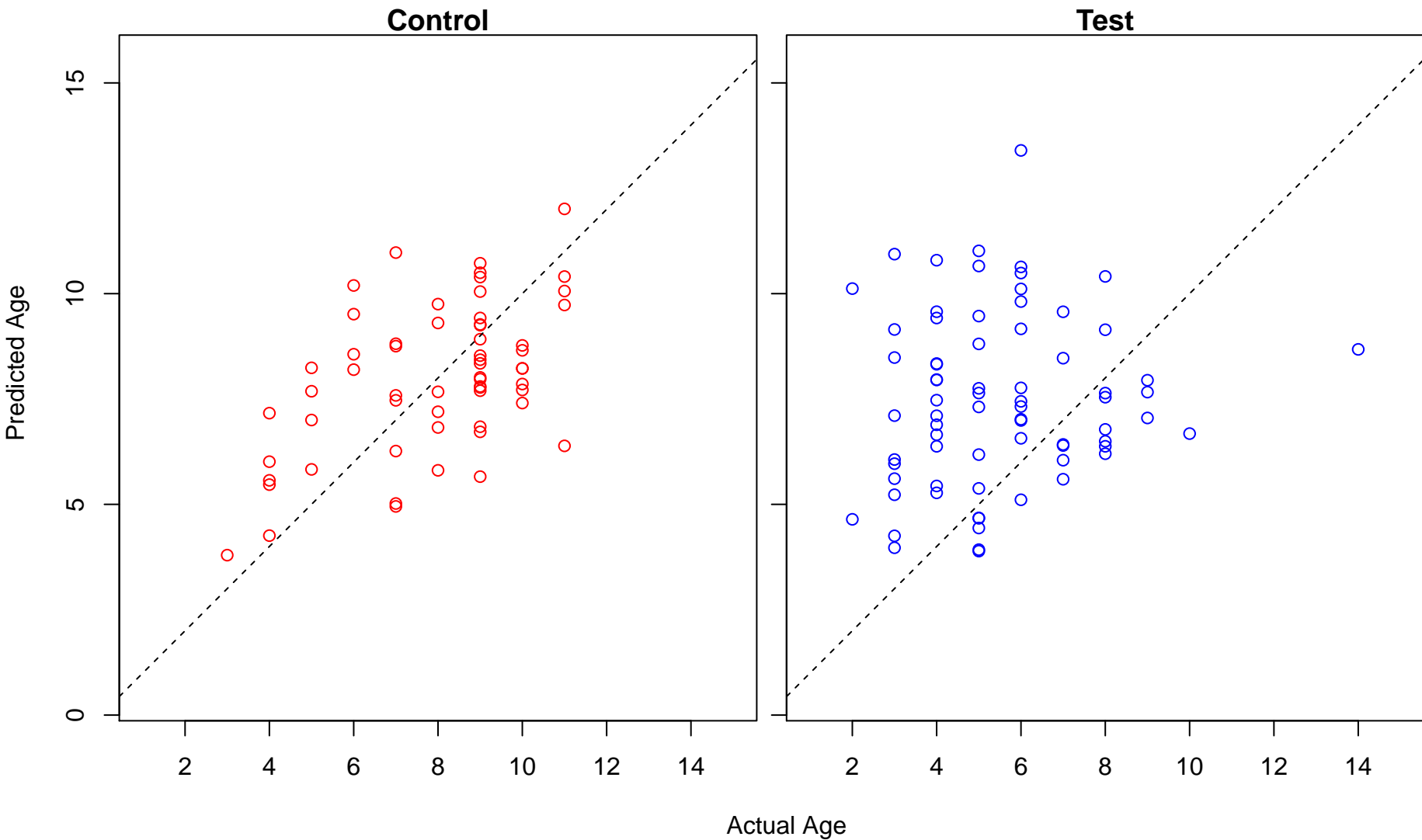
negative regulation of cell-cell adhesion (Score: 1.260348)



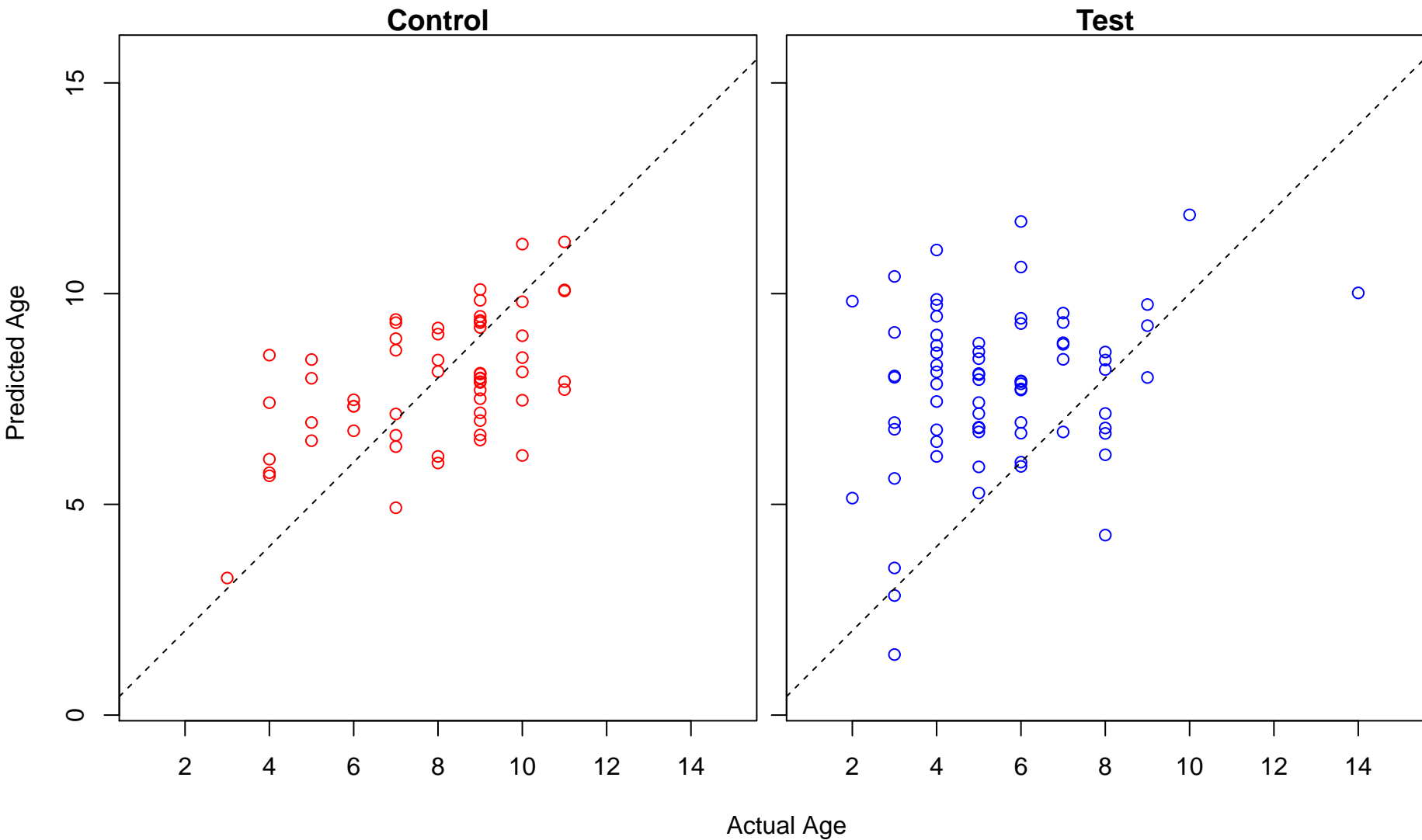
response to external stimulus (Score: 1.258516)



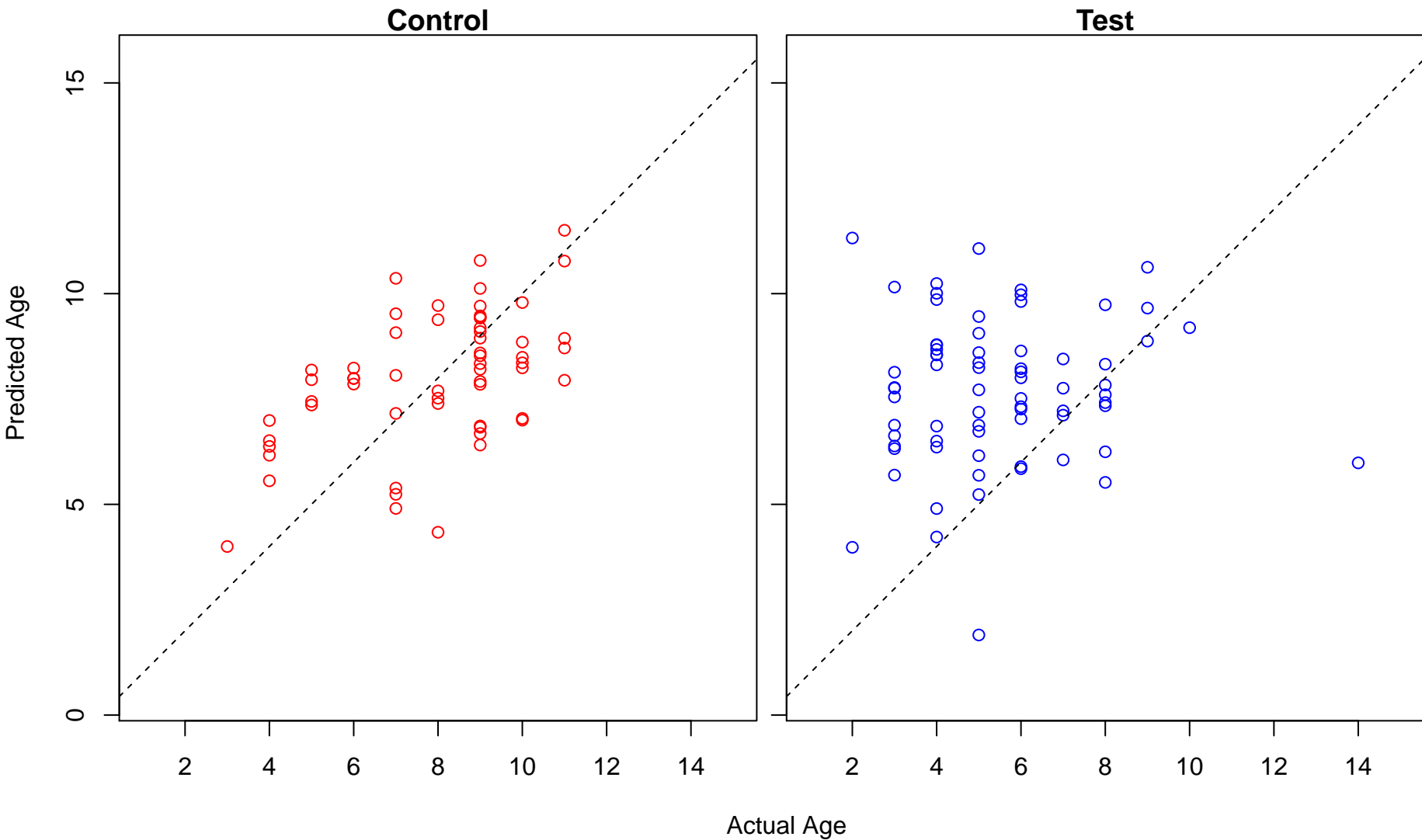
cellular component assembly involved in morphogenesis (Score: 1.257701)



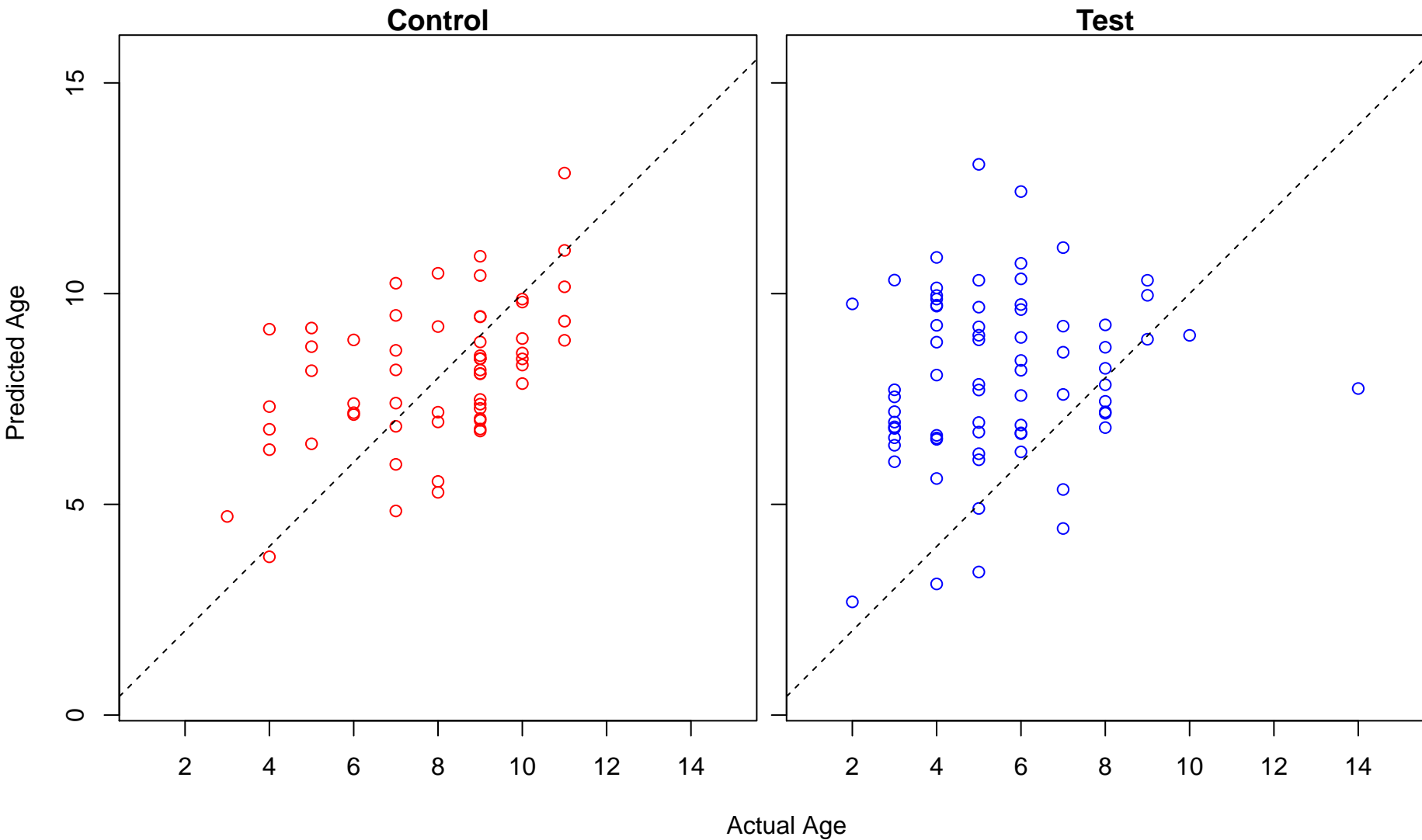
regulation of mesonephros development (Score: 1.256978)



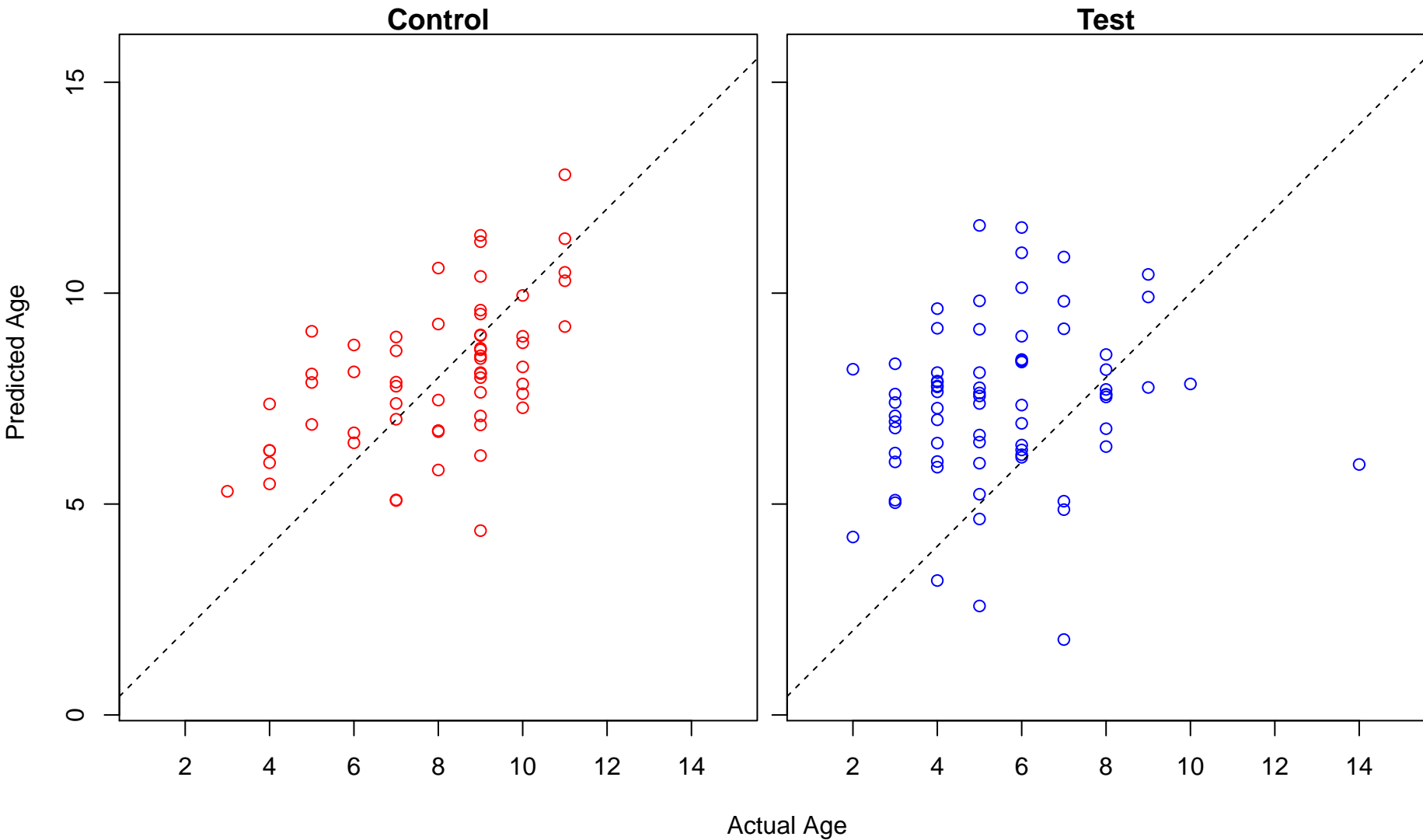
positive regulation of nucleobase-containing compound metabolic process (Score: 1.256701)



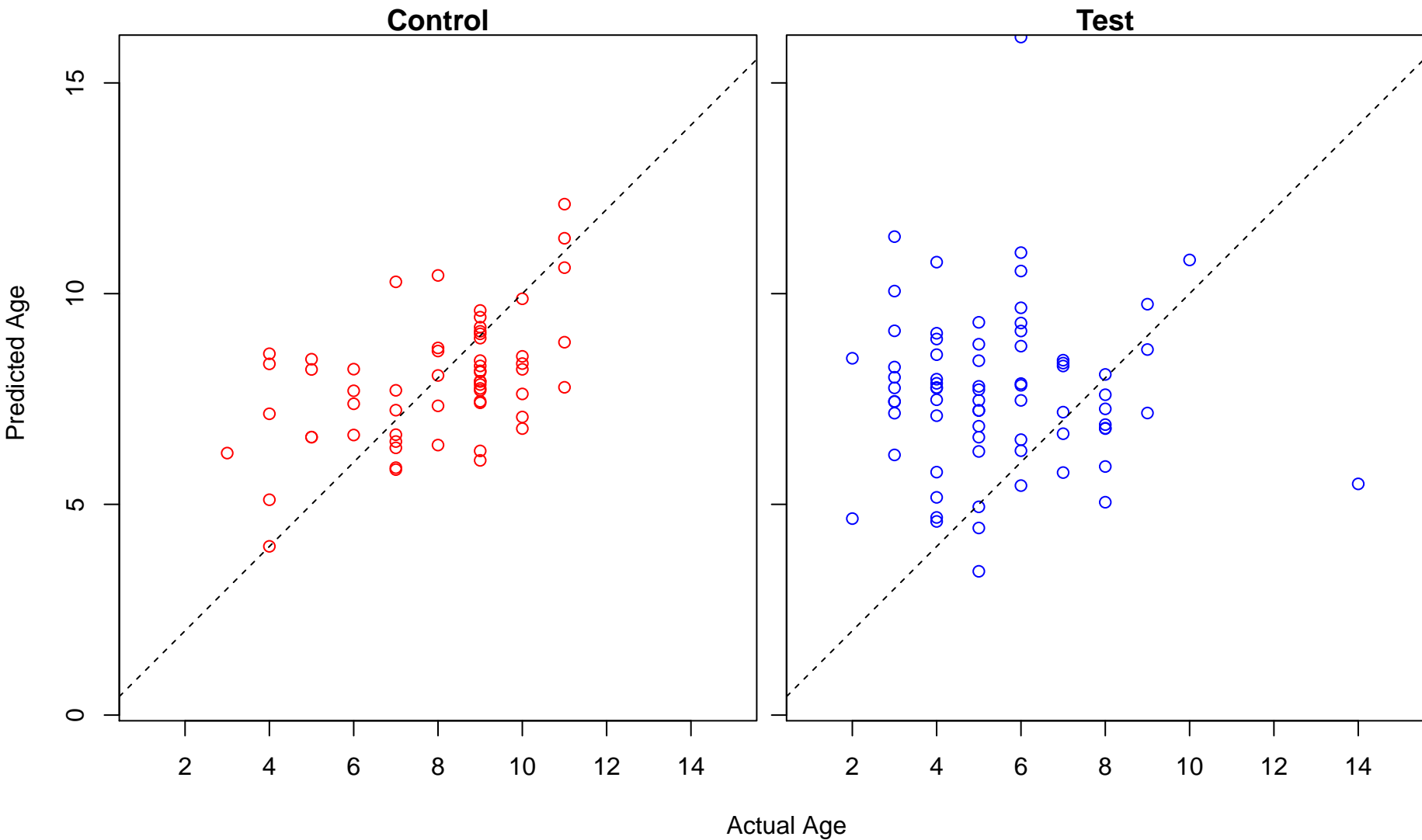
regulation of protein modification process (Score: 1.255636)



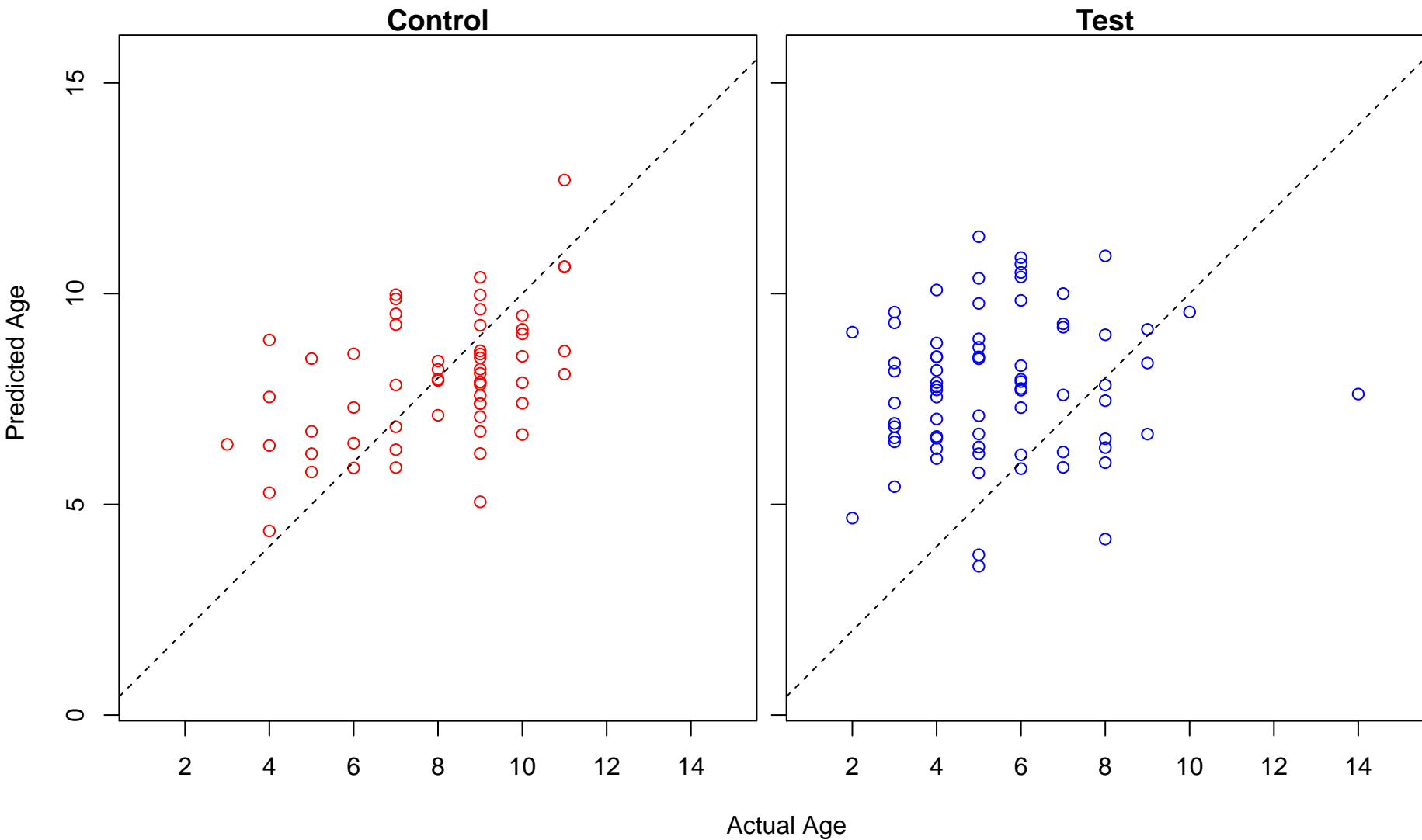
positive regulation of innate immune response (Score: 1.253292)



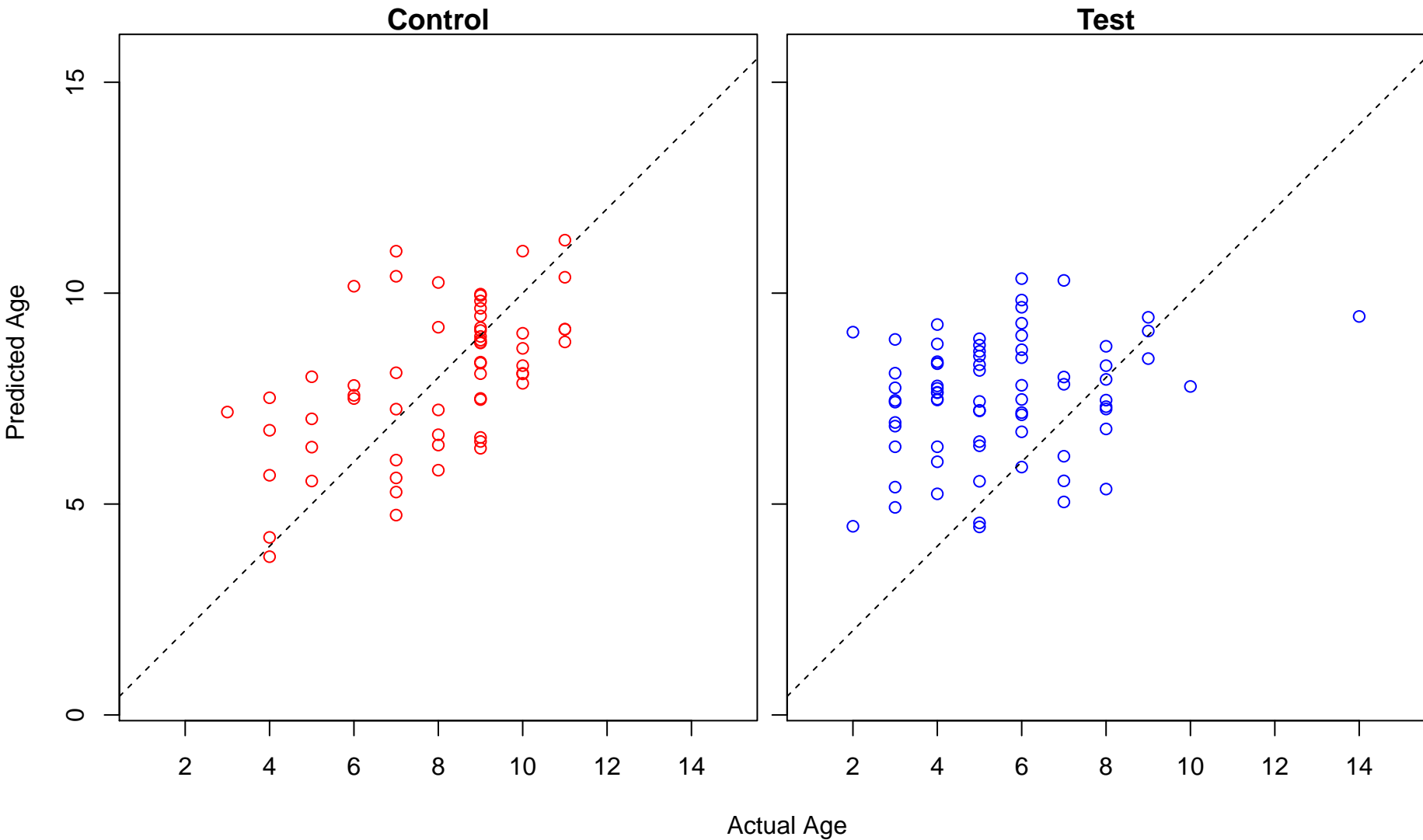
positive regulation of alpha-beta T cell differentiation (Score: 1.252046)



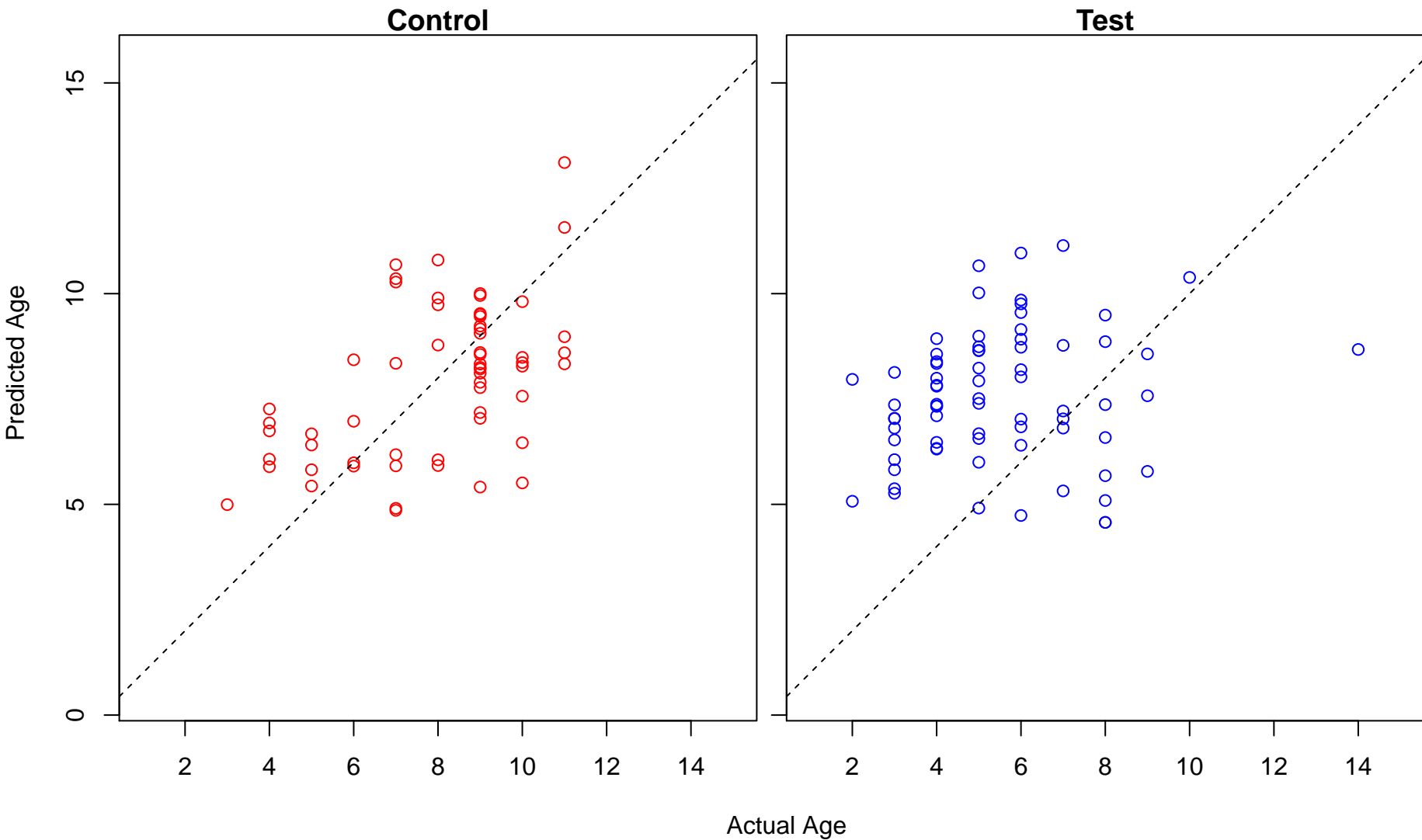
ribonucleoprotein complex disassembly (Score: 1.251584)



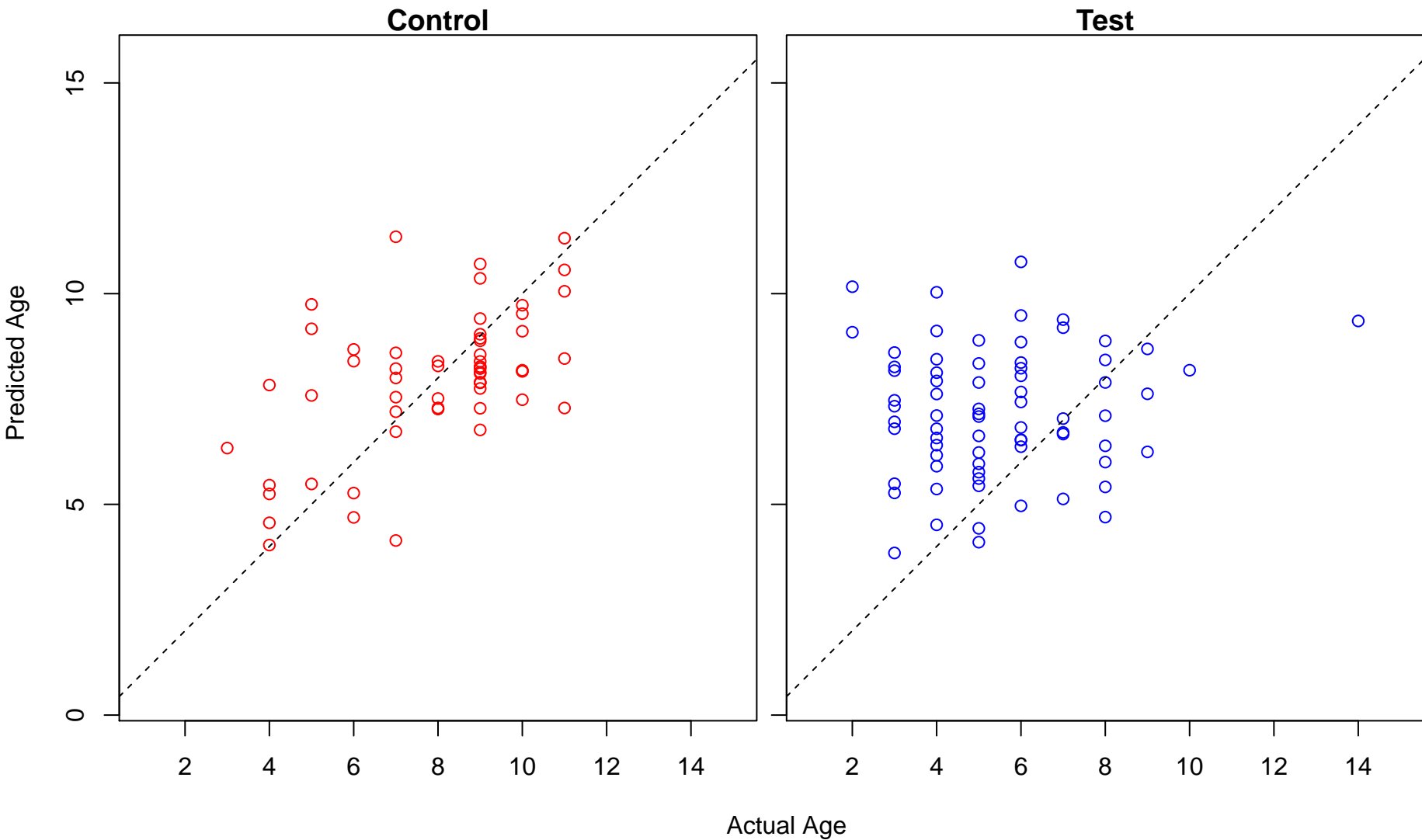
negative regulation of nucleobase-containing compound metabolic process (Score: 1.250027)



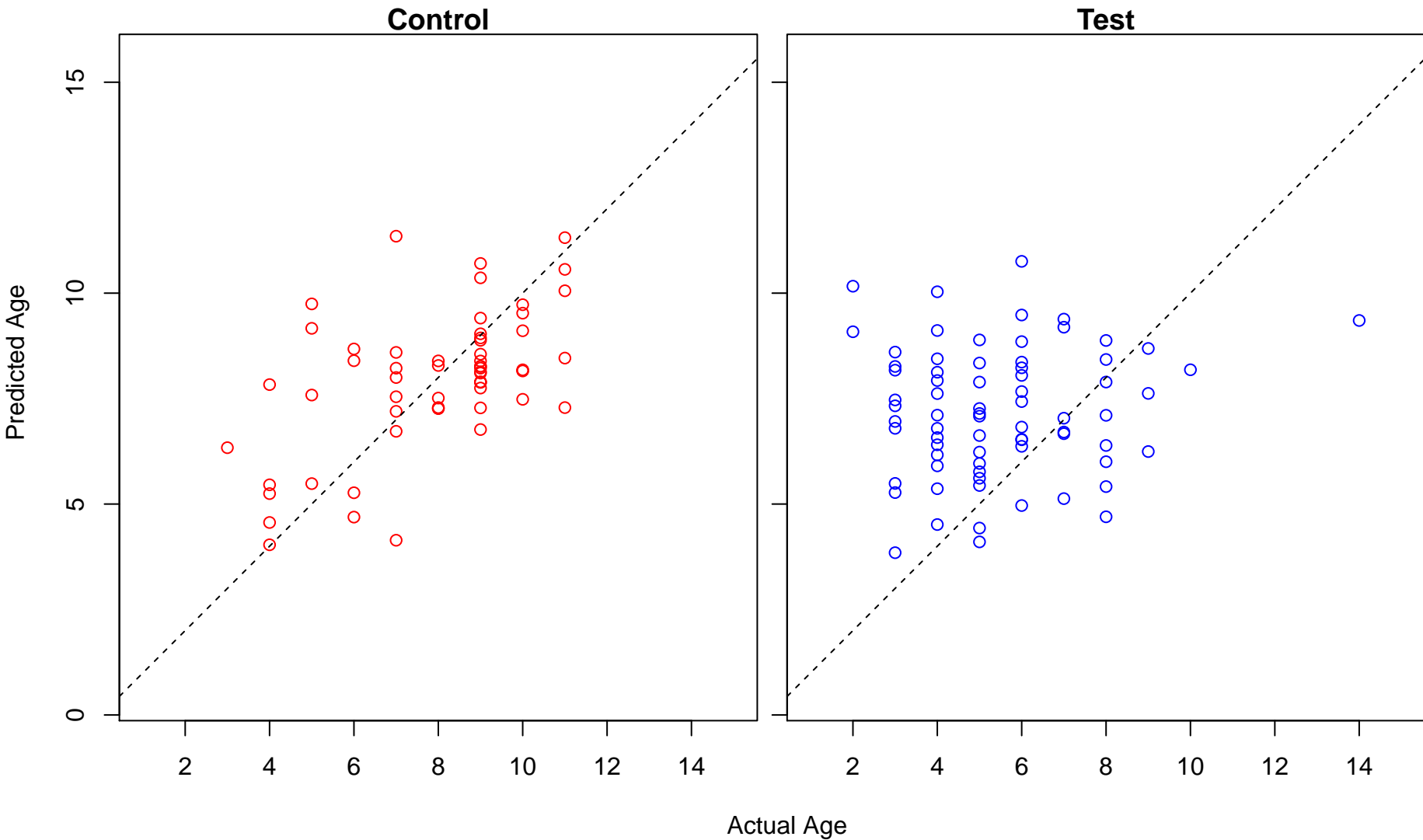
peptidyl–threonine phosphorylation (Score: 1.249231)



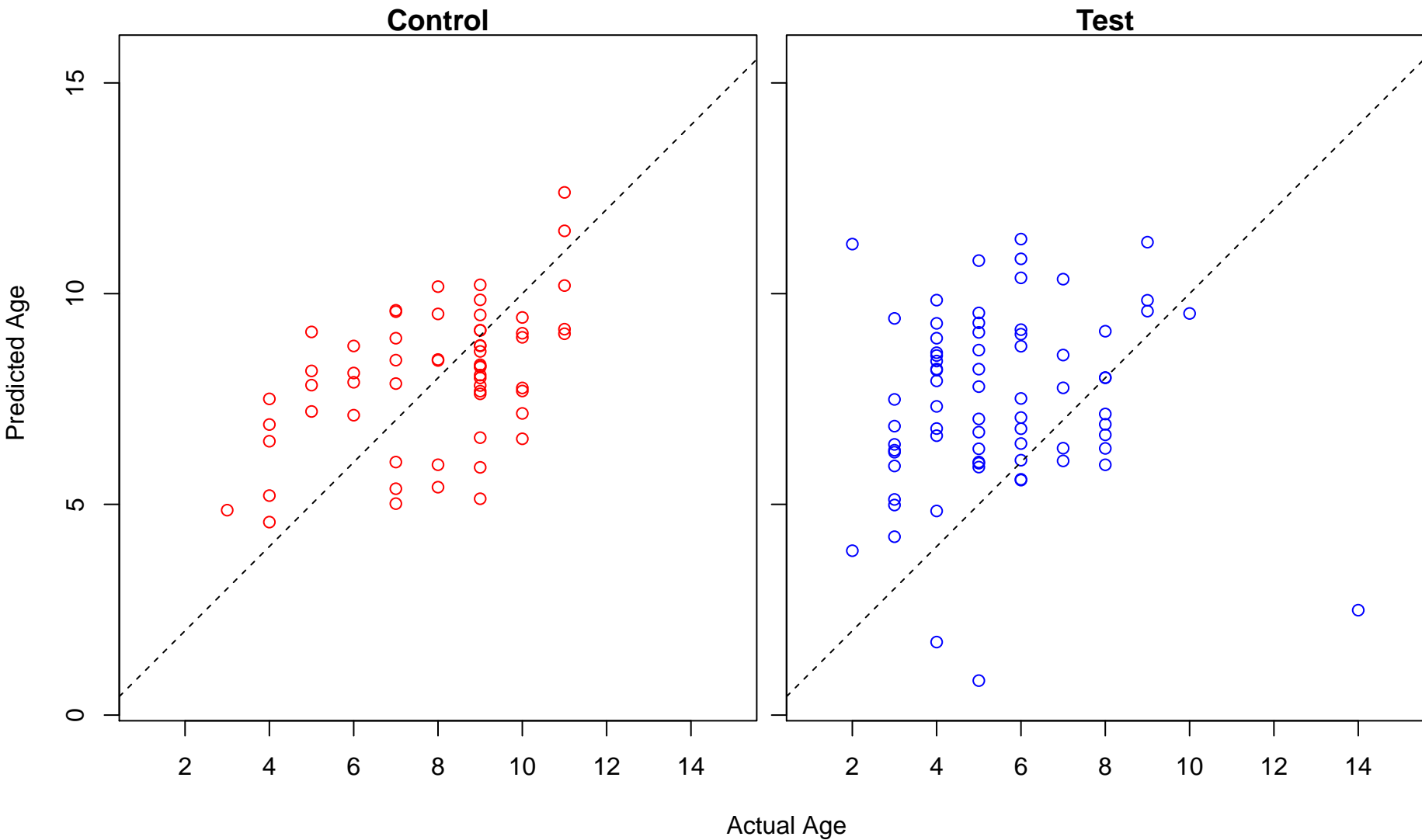
purine nucleoside biosynthetic process (Score: 1.248049)



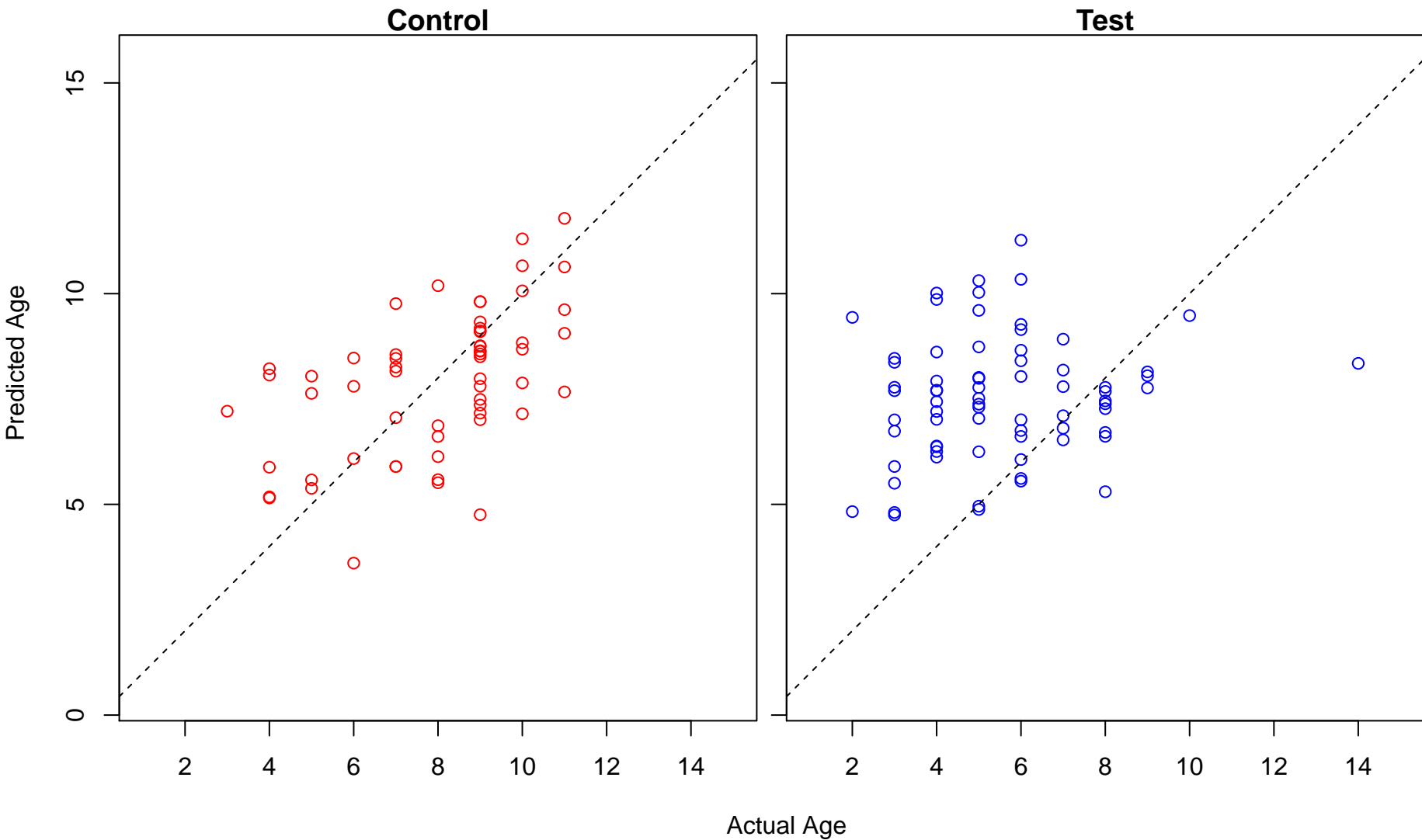
purine ribonucleoside biosynthetic process (Score: 1.248049)



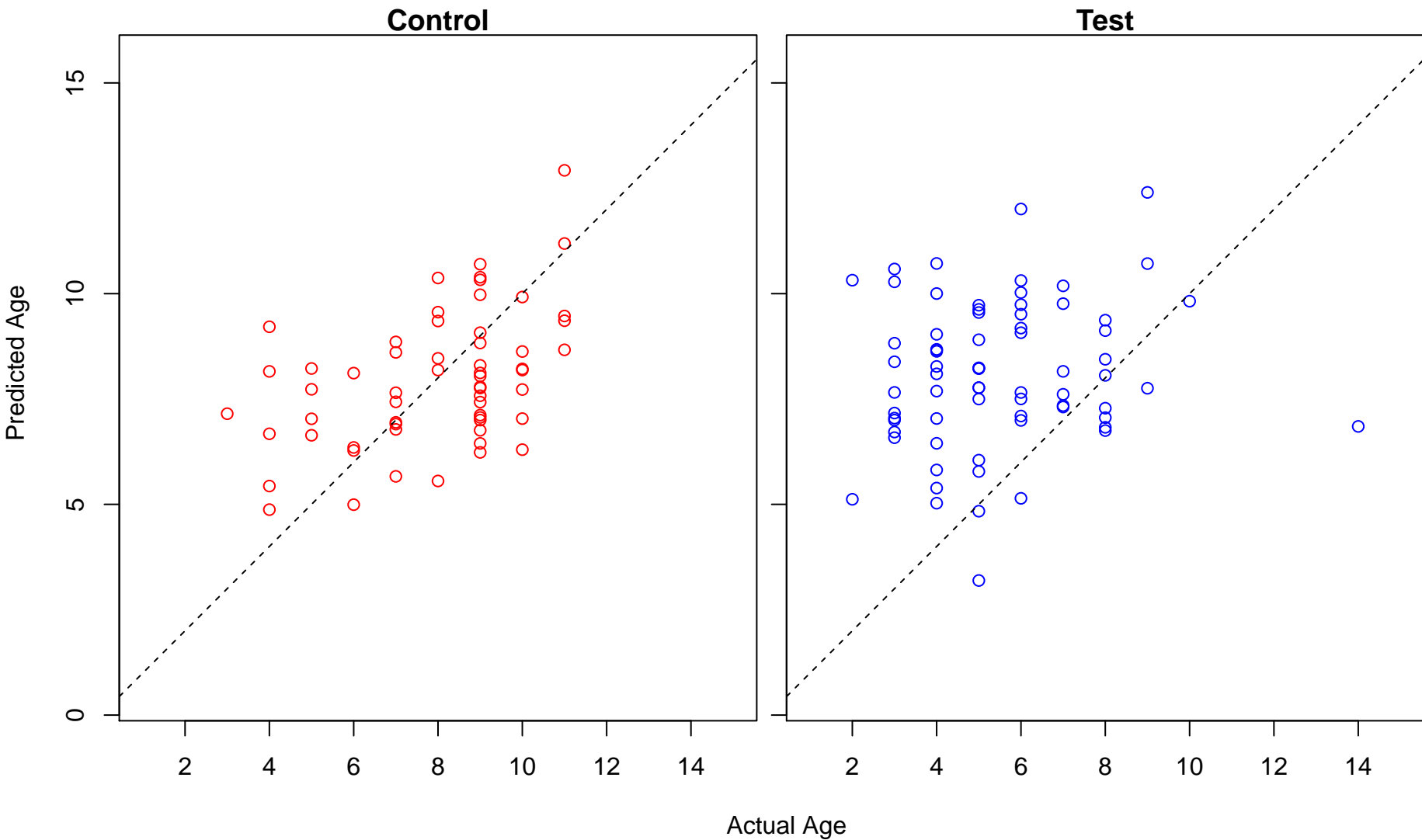
phosphorylation (Score: 1.247718)



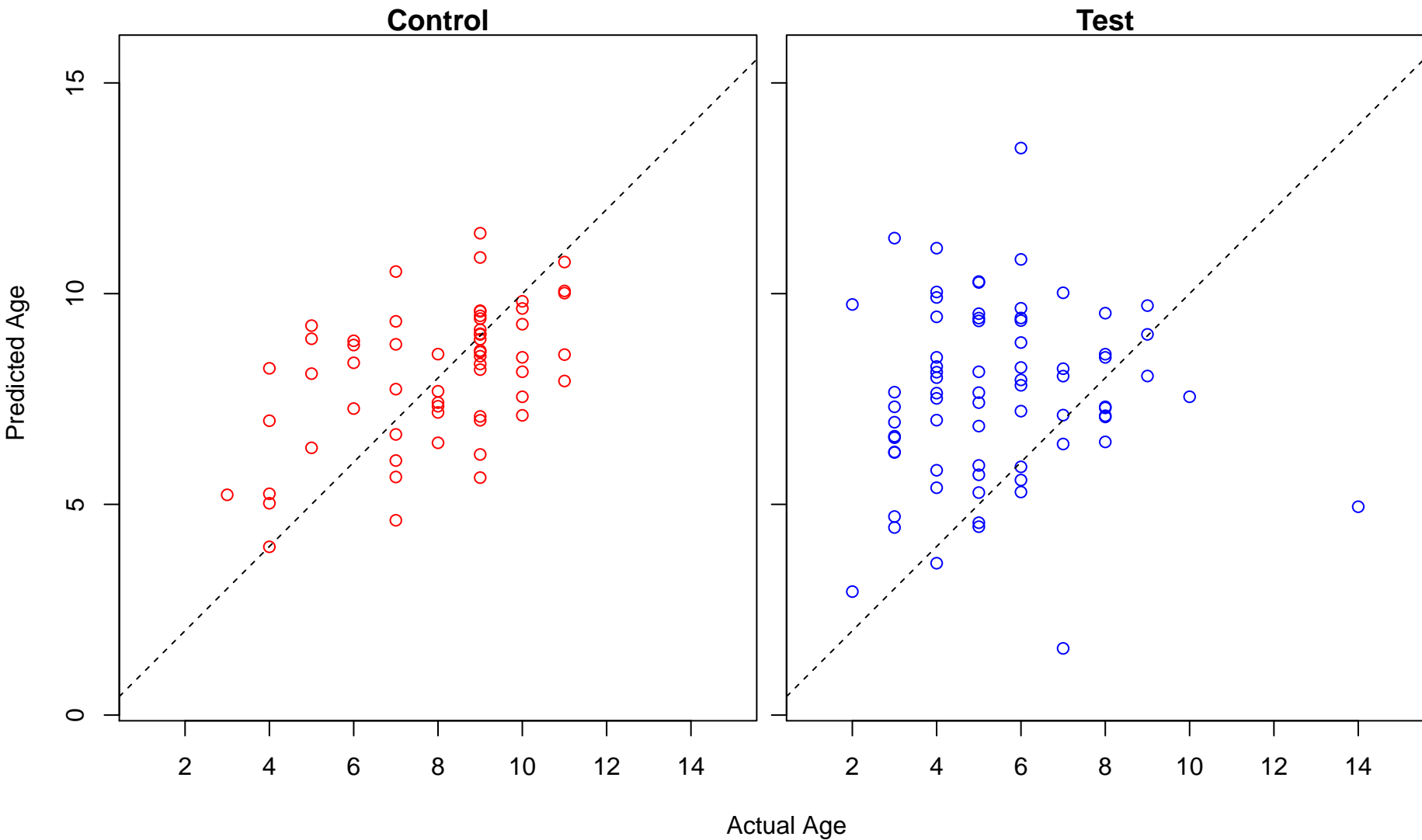
organic substance transport (Score: 1.247177)



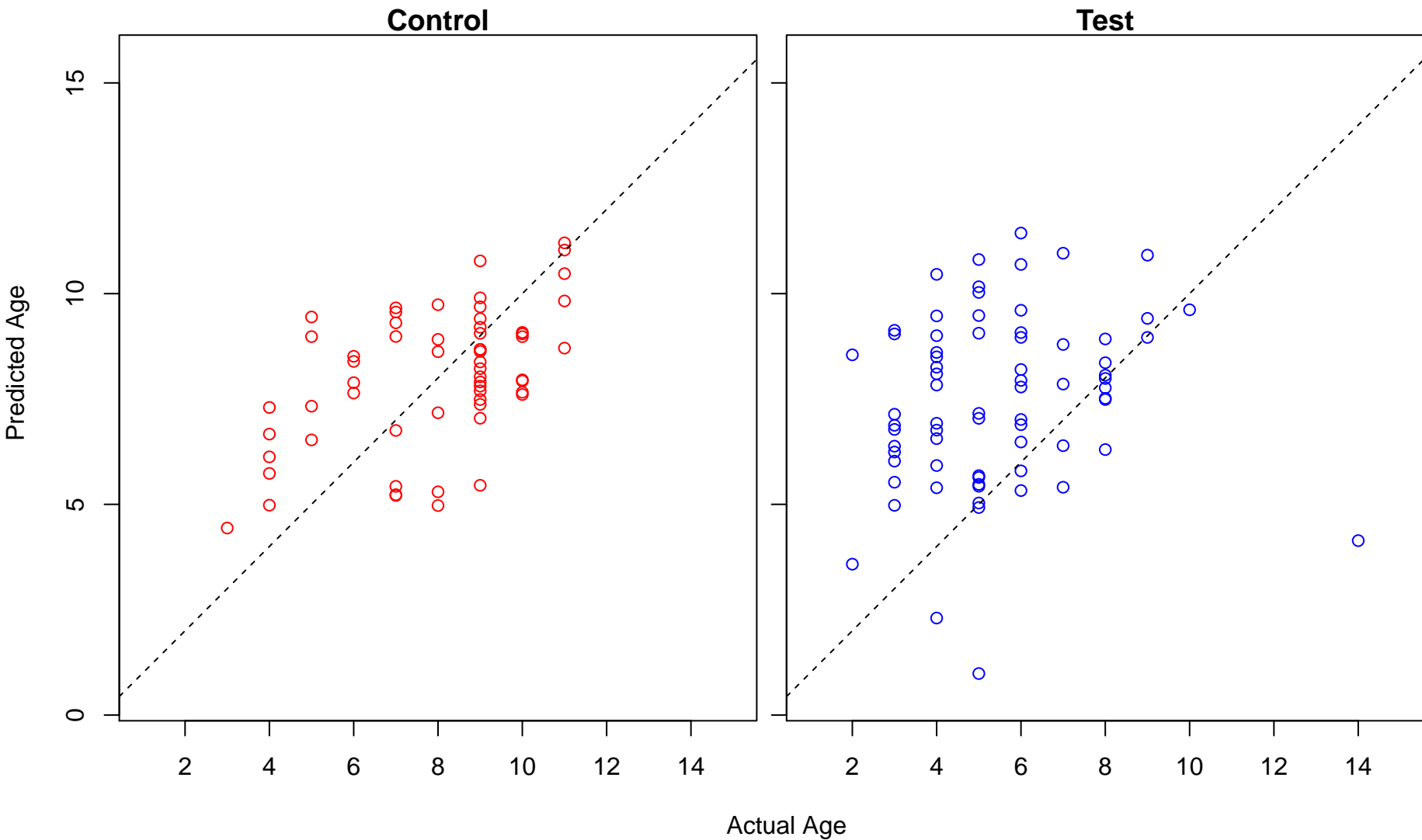
regulation of alpha-beta T cell differentiation (Score: 1.246333)



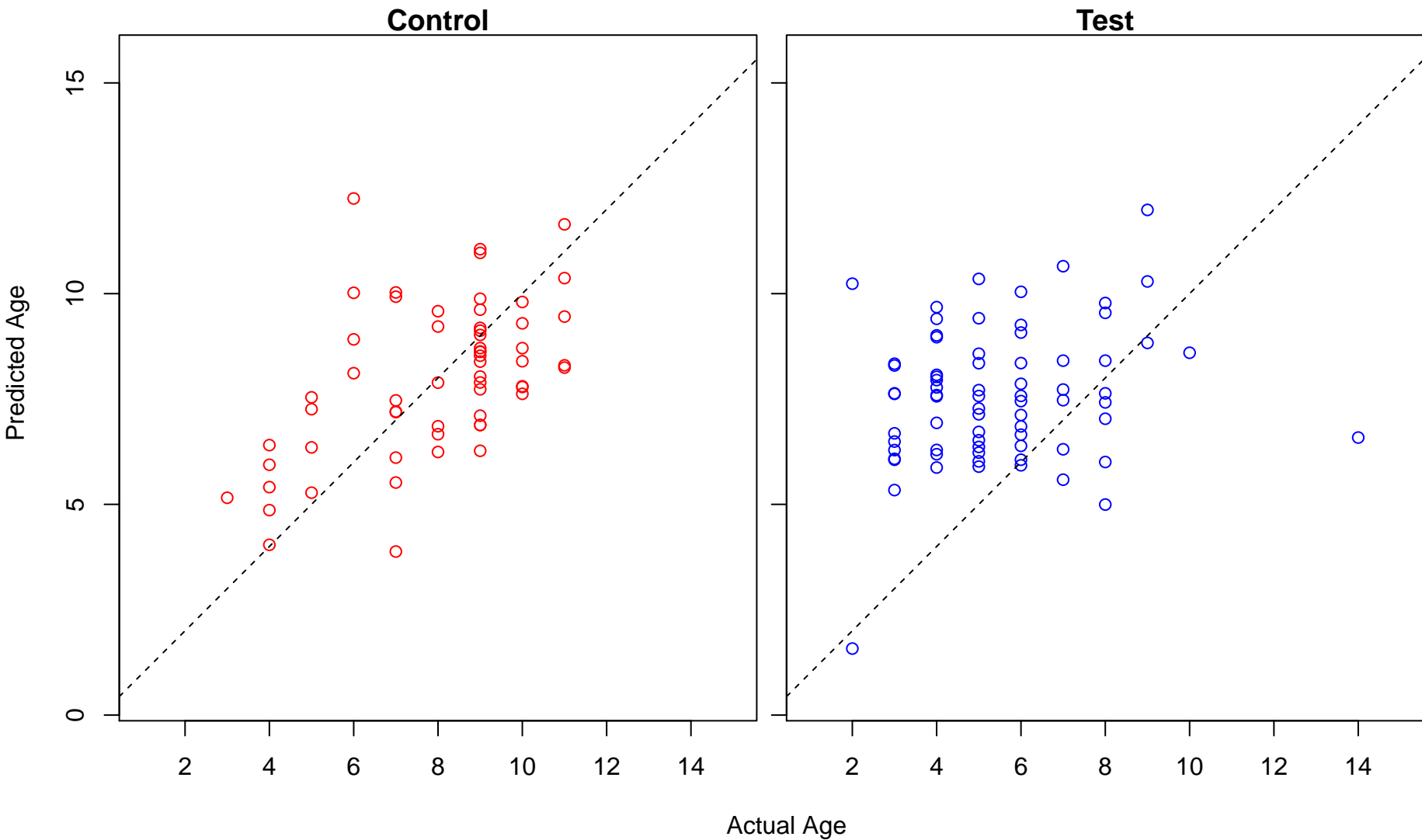
neurogenesis (Score: 1.246010)



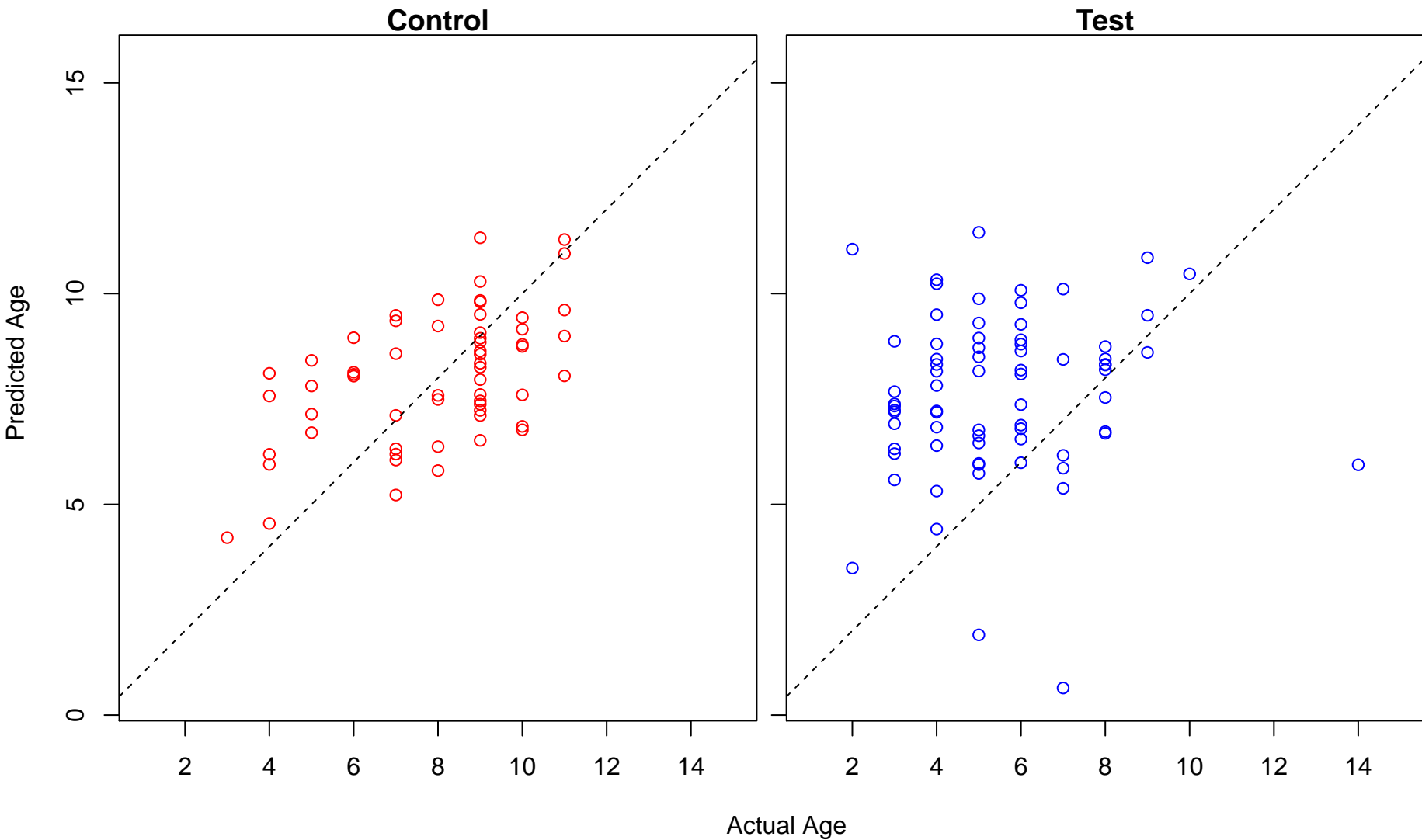
response to endogenous stimulus (Score: 1.245978)



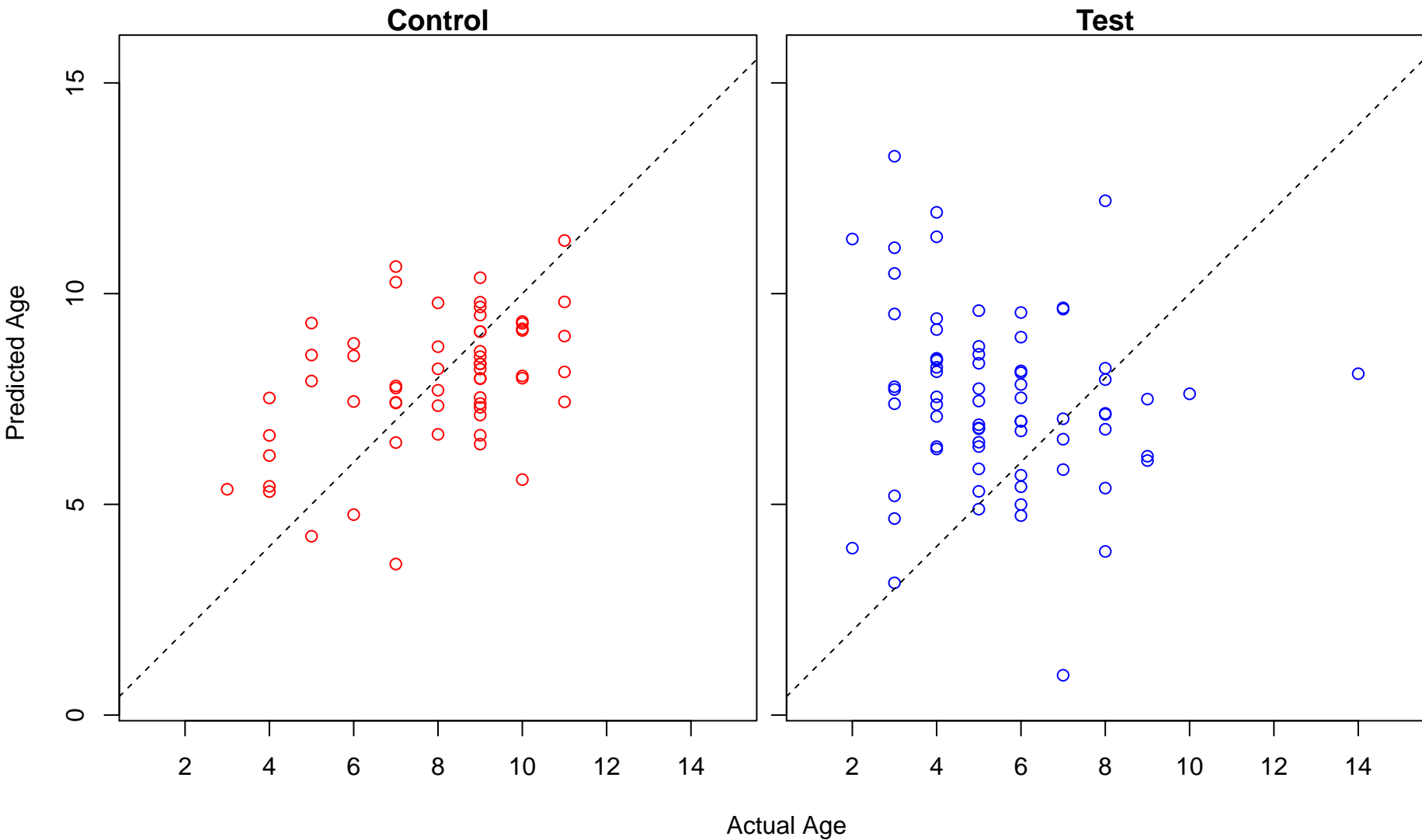
positive regulation of neurogenesis (Score: 1.245595)



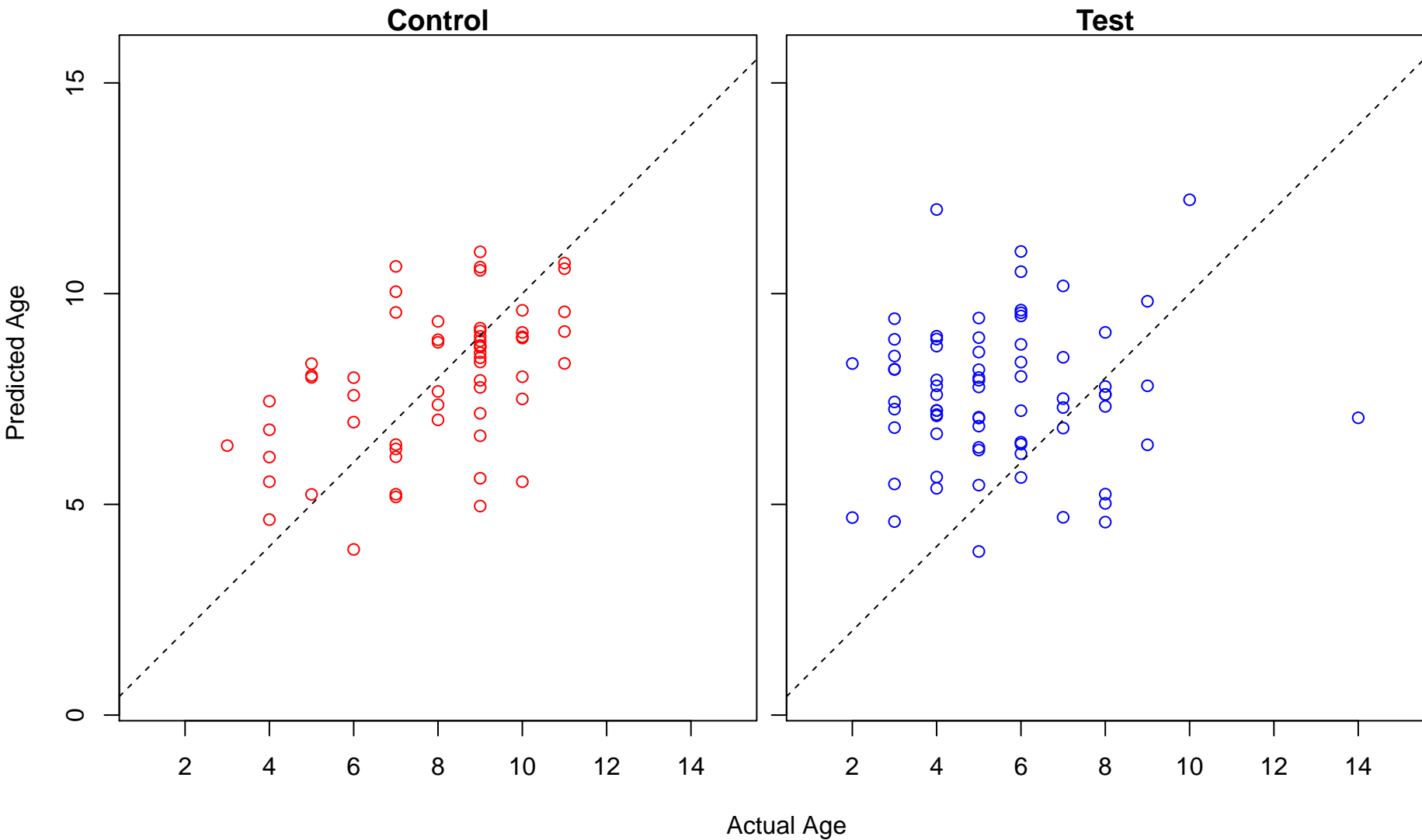
regulation of biosynthetic process (Score: 1.245434)



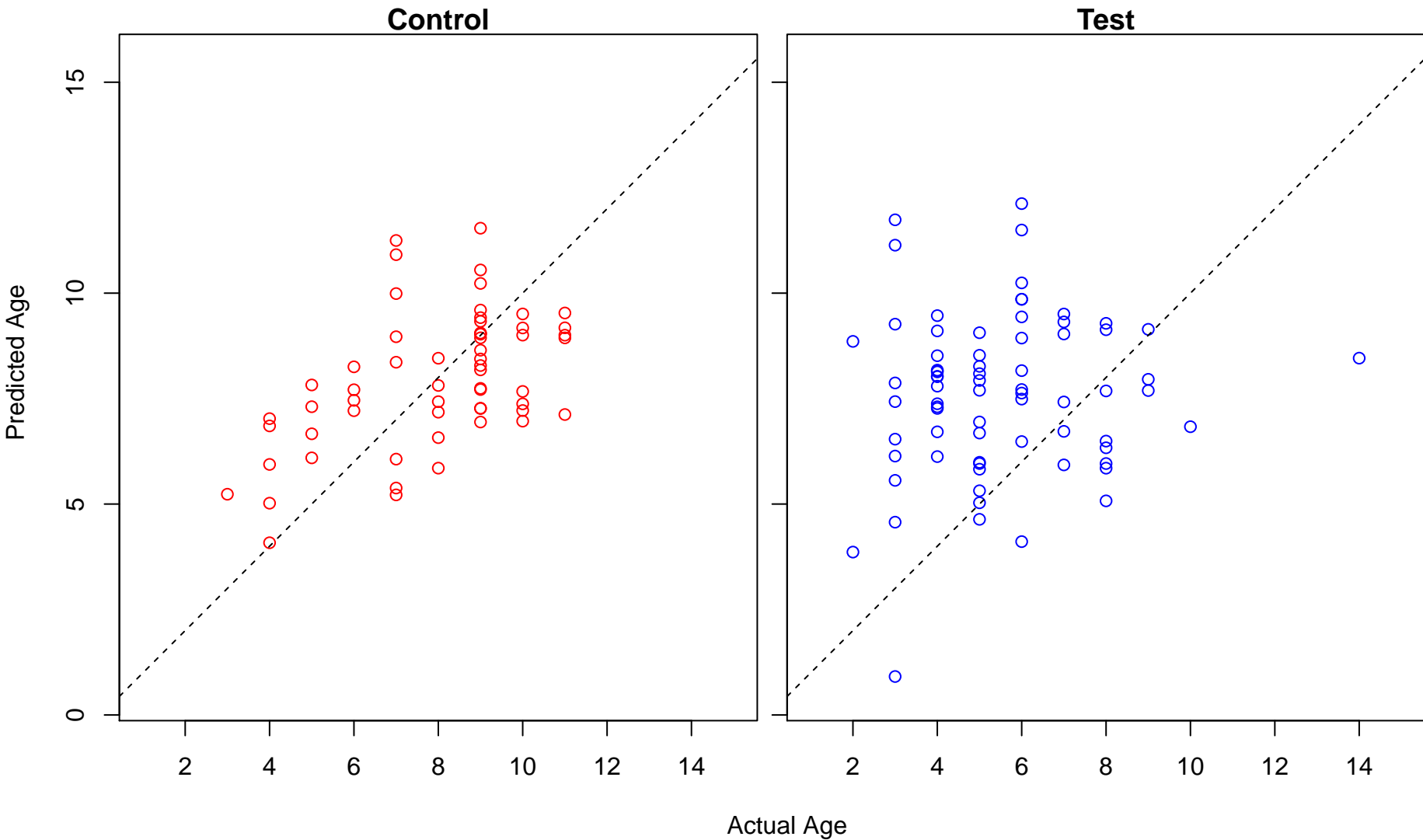
negative regulation of reproductive process (Score: 1.245324)



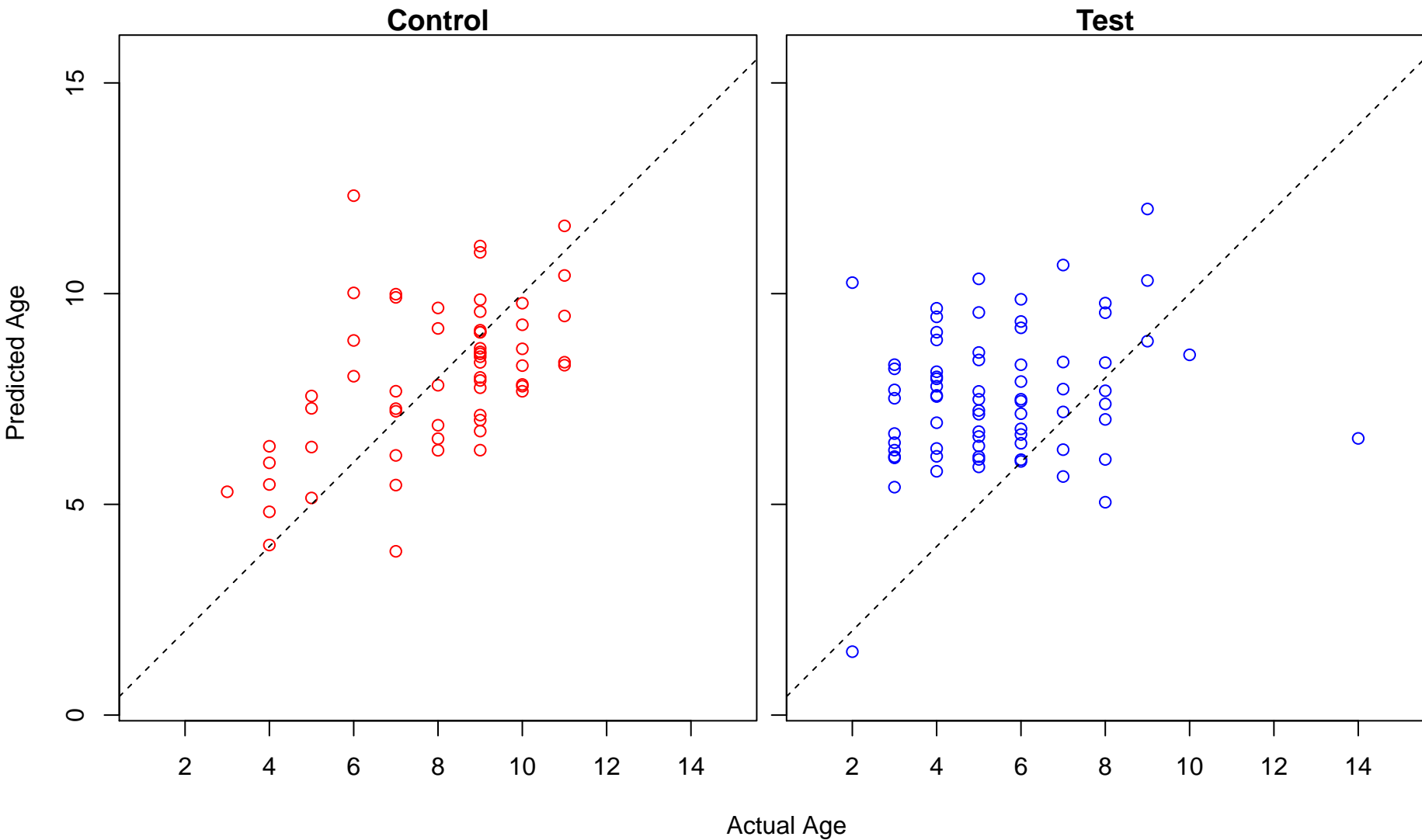
chromosome segregation (Score: 1.244259)



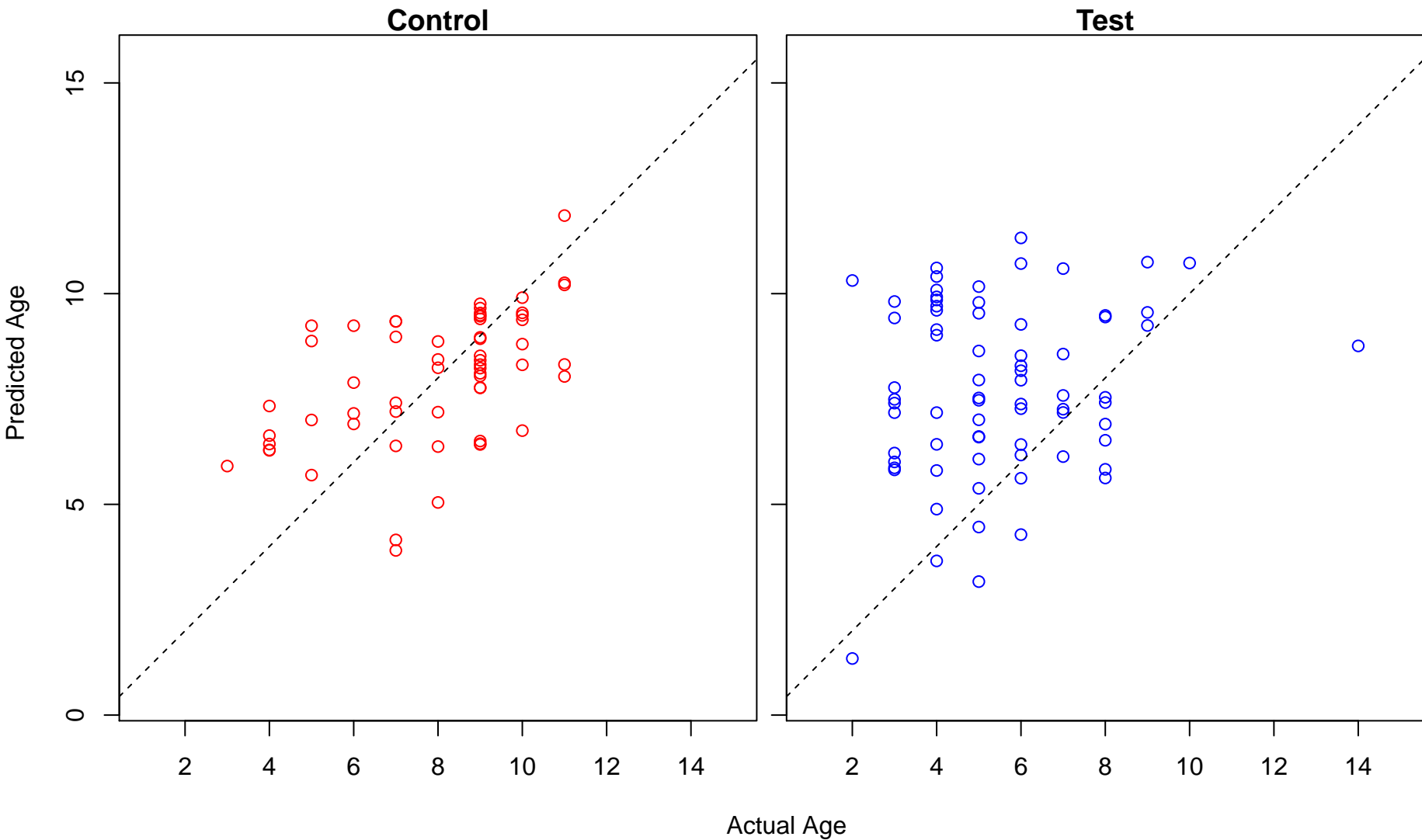
regulation of pathway-restricted SMAD protein phosphorylation (Score: 1.242165)



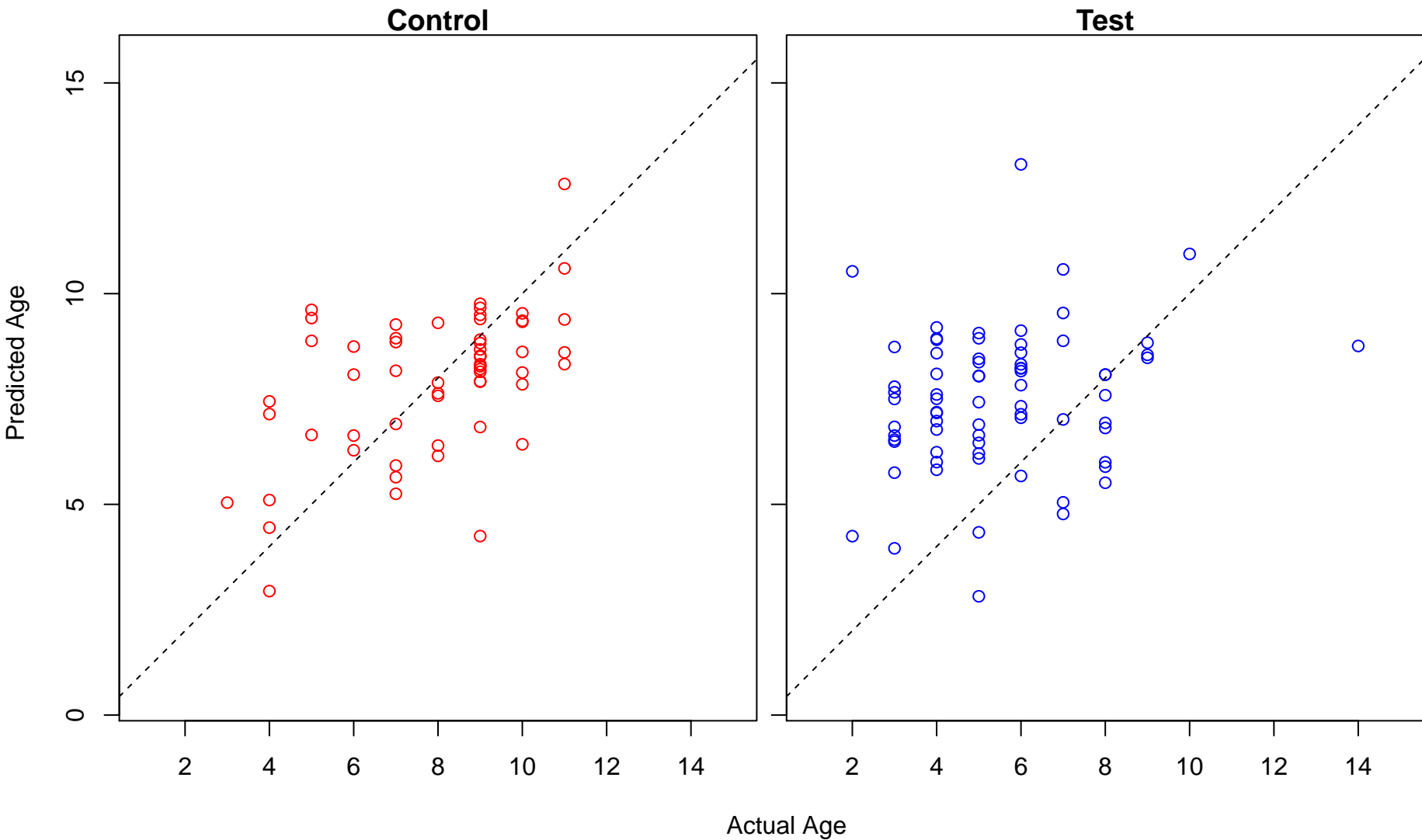
positive regulation of nervous system development (Score: 1.238316)



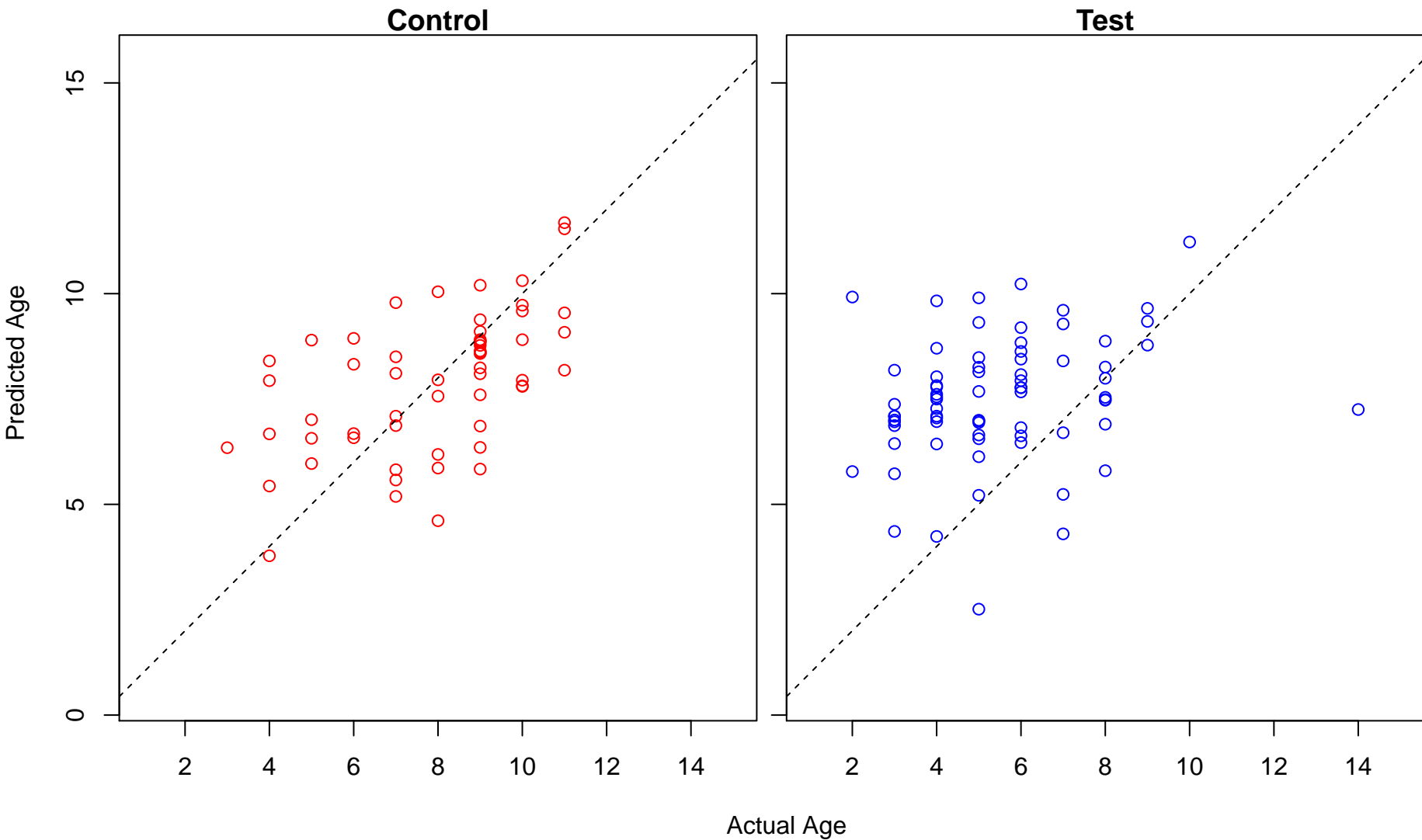
regulation of cell differentiation (Score: 1.237862)



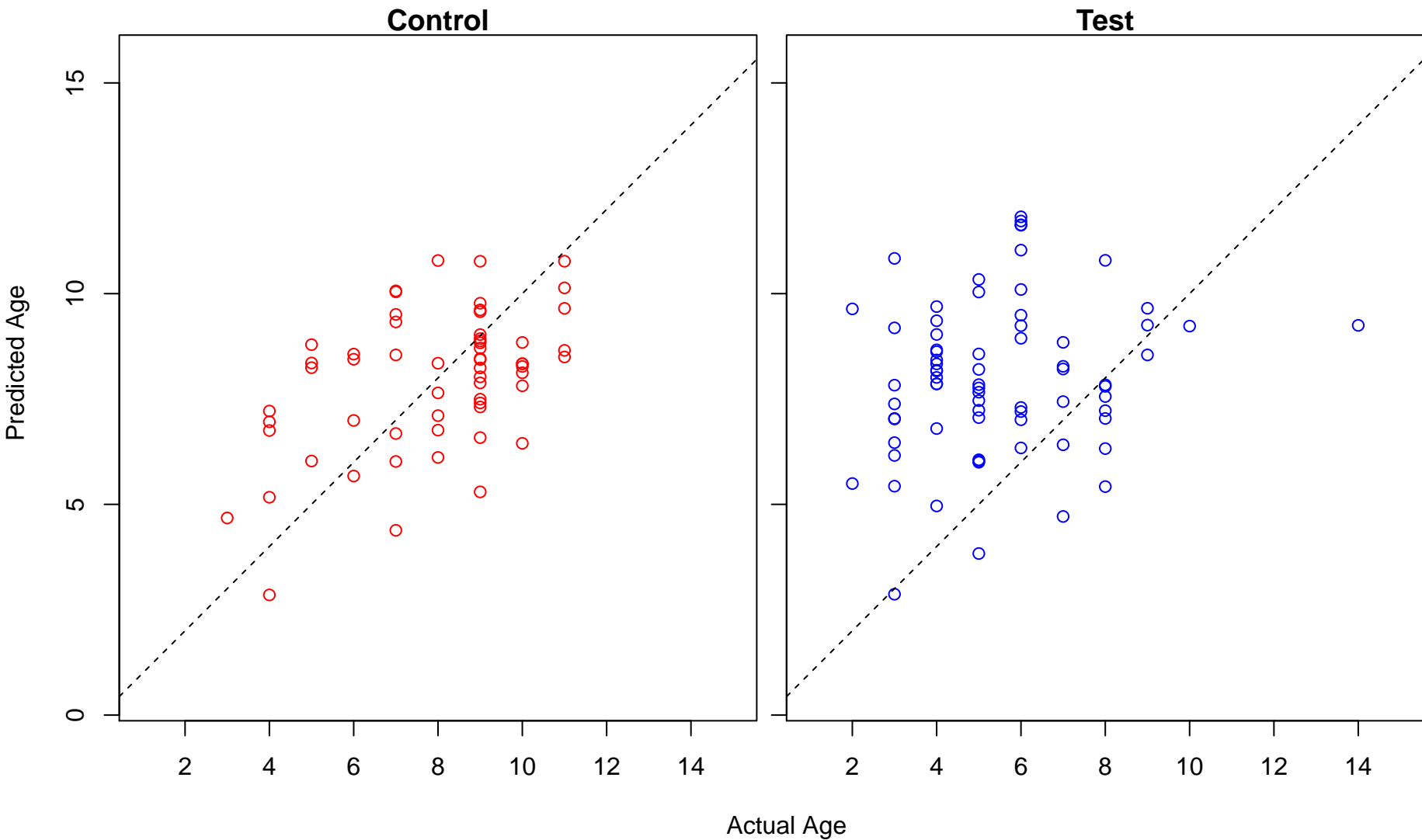
organelle organization (Score: 1.236842)



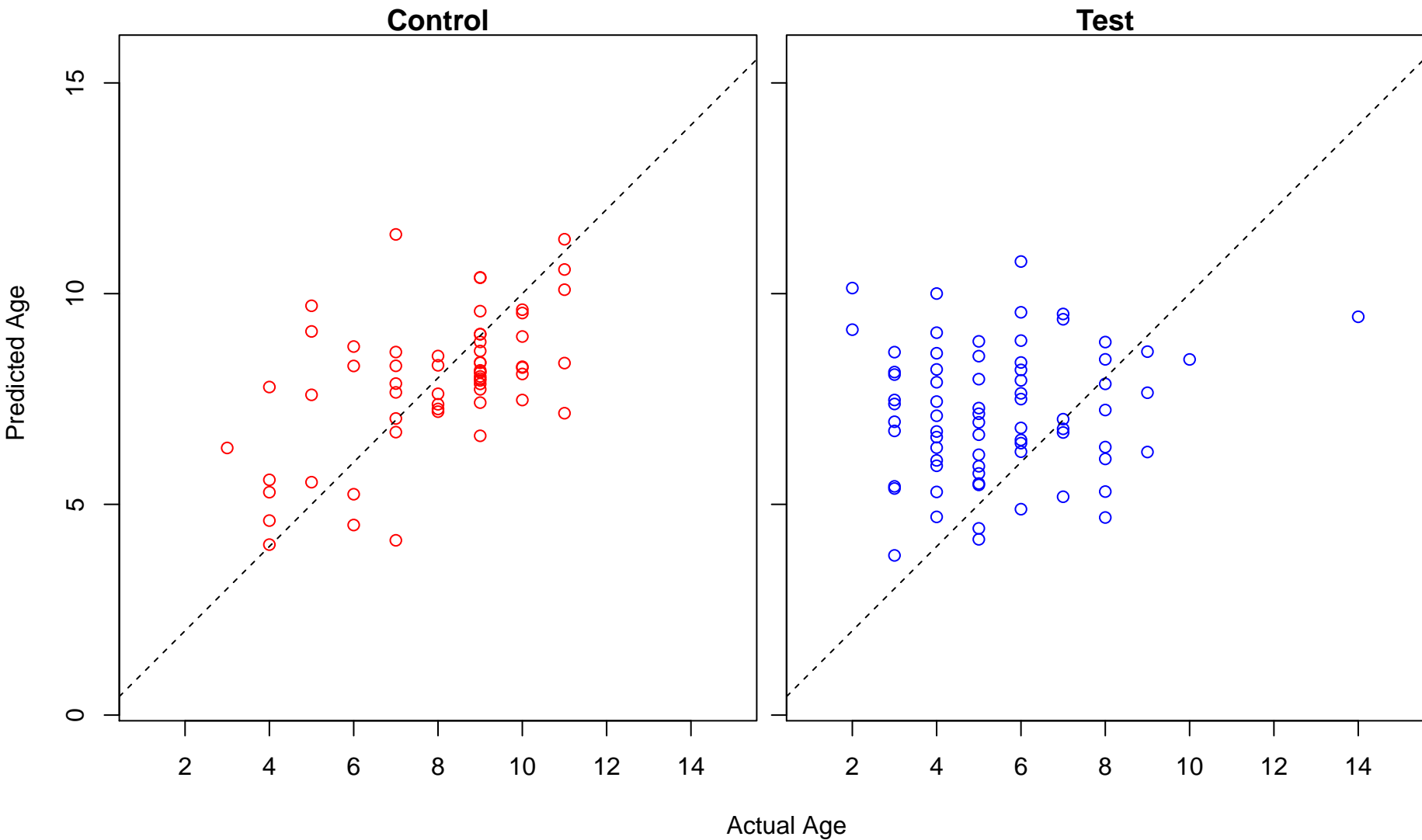
primary metabolic process (Score: 1.236107)



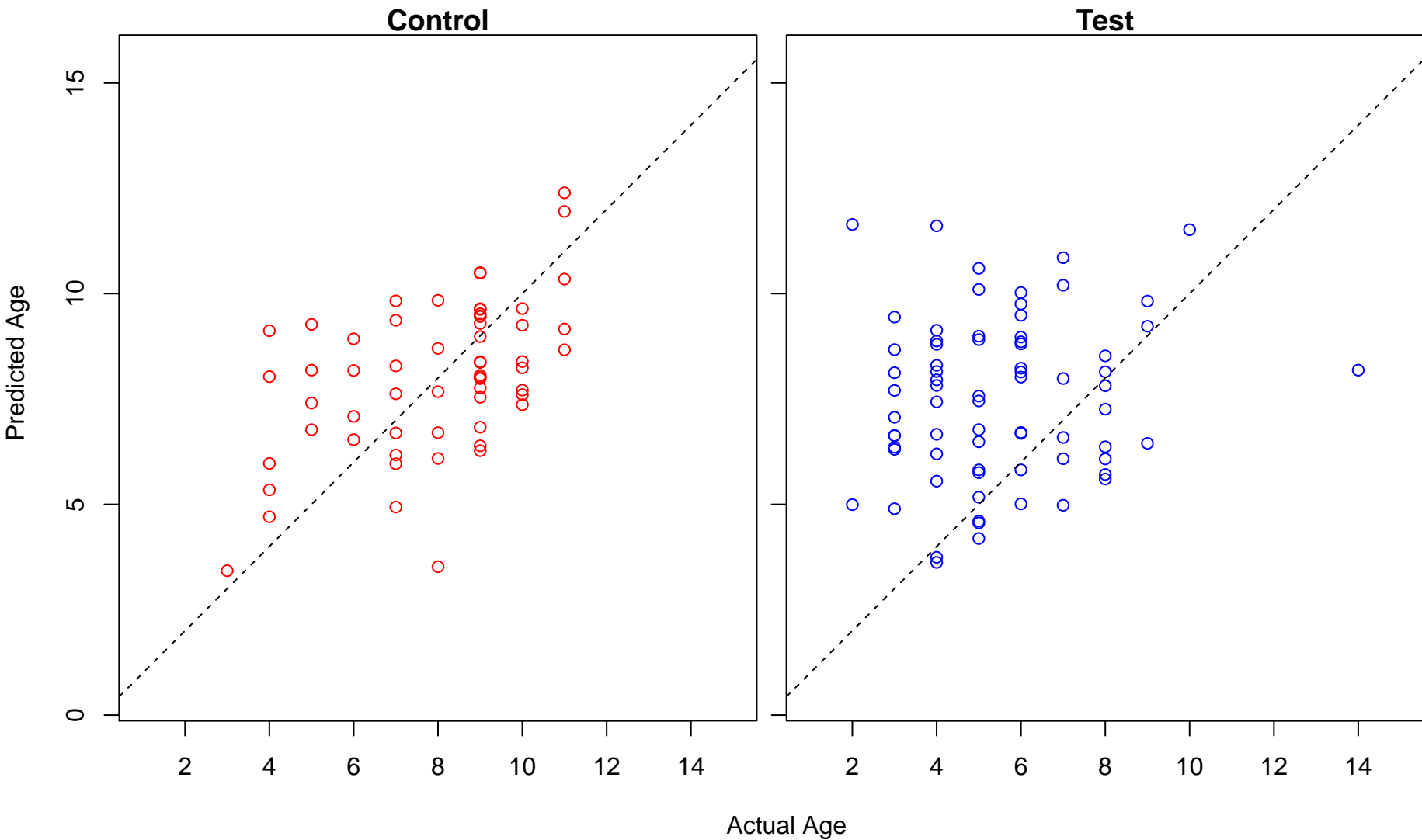
dendritic cell differentiation (Score: 1.232947)



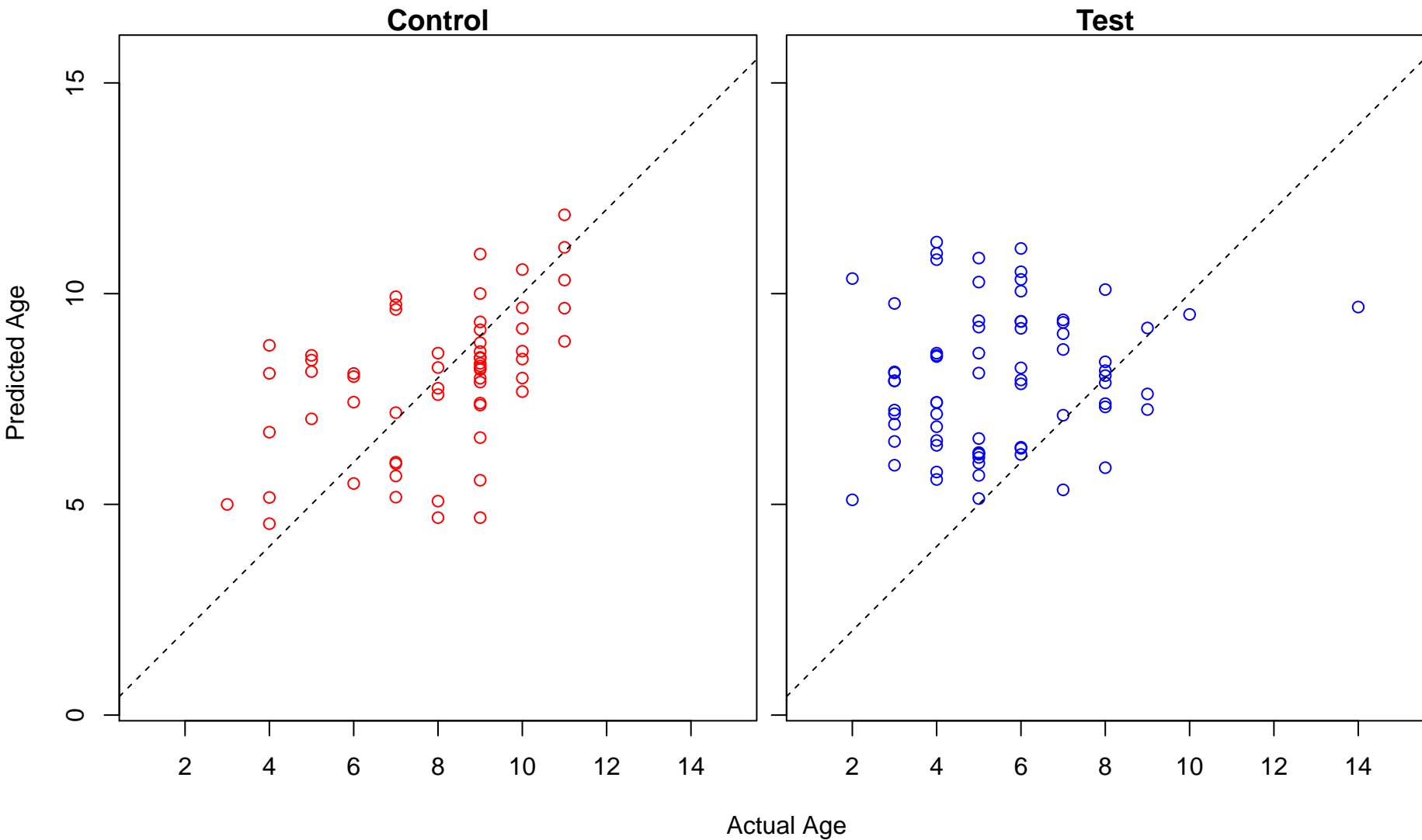
ribonucleoside biosynthetic process (Score: 1.232663)



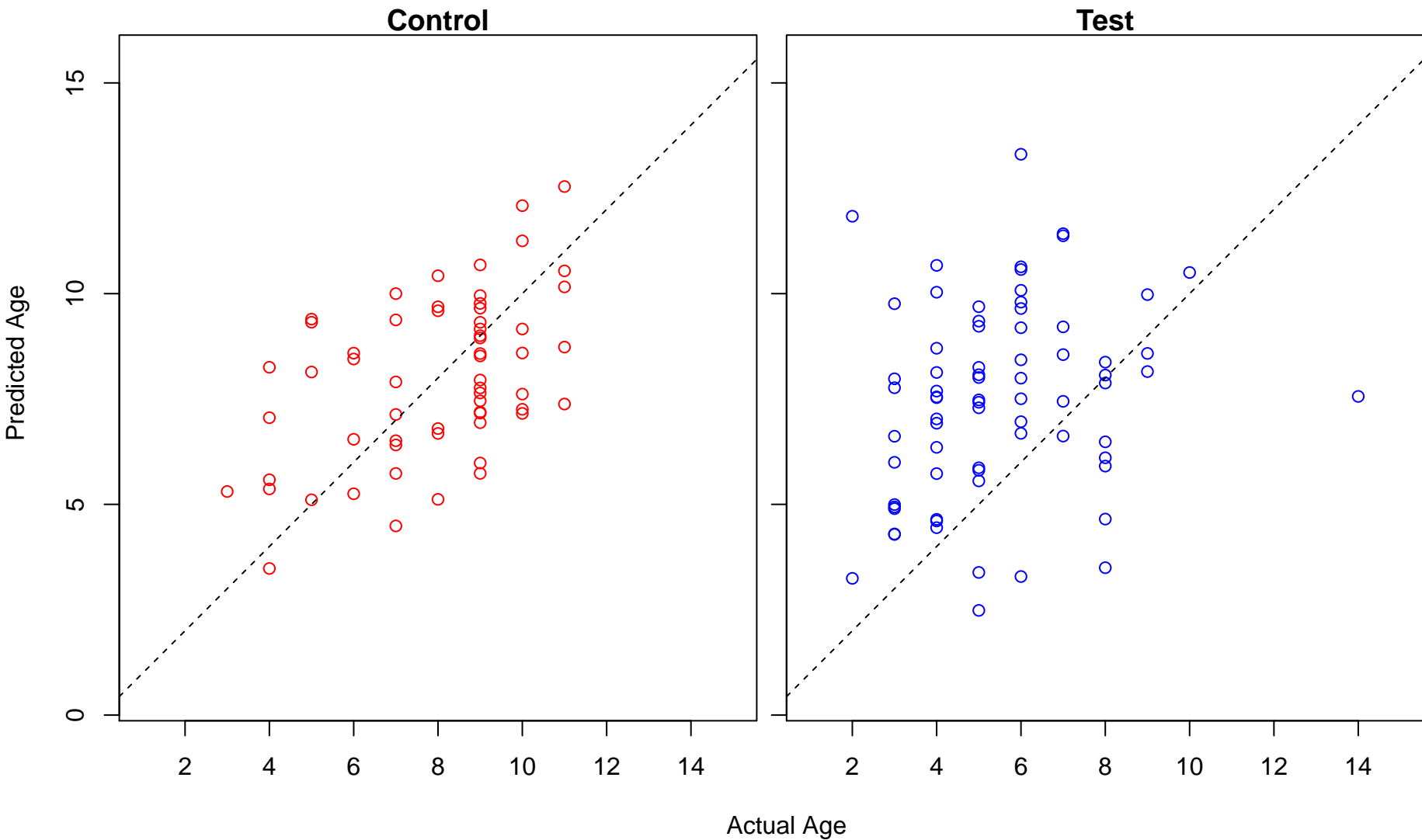
regulation of apoptotic signaling pathway (Score: 1.230921)



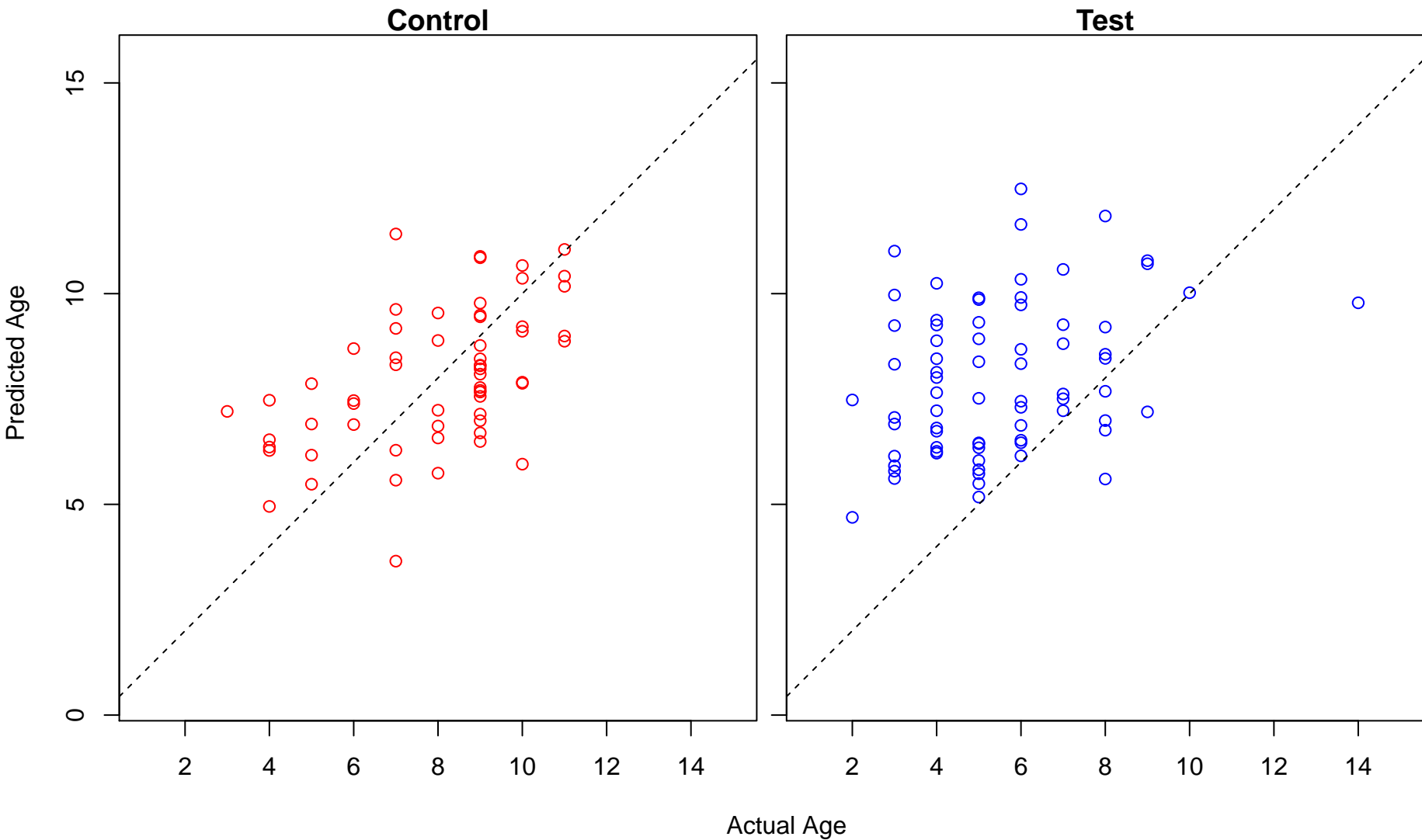
organ morphogenesis (Score: 1.230373)



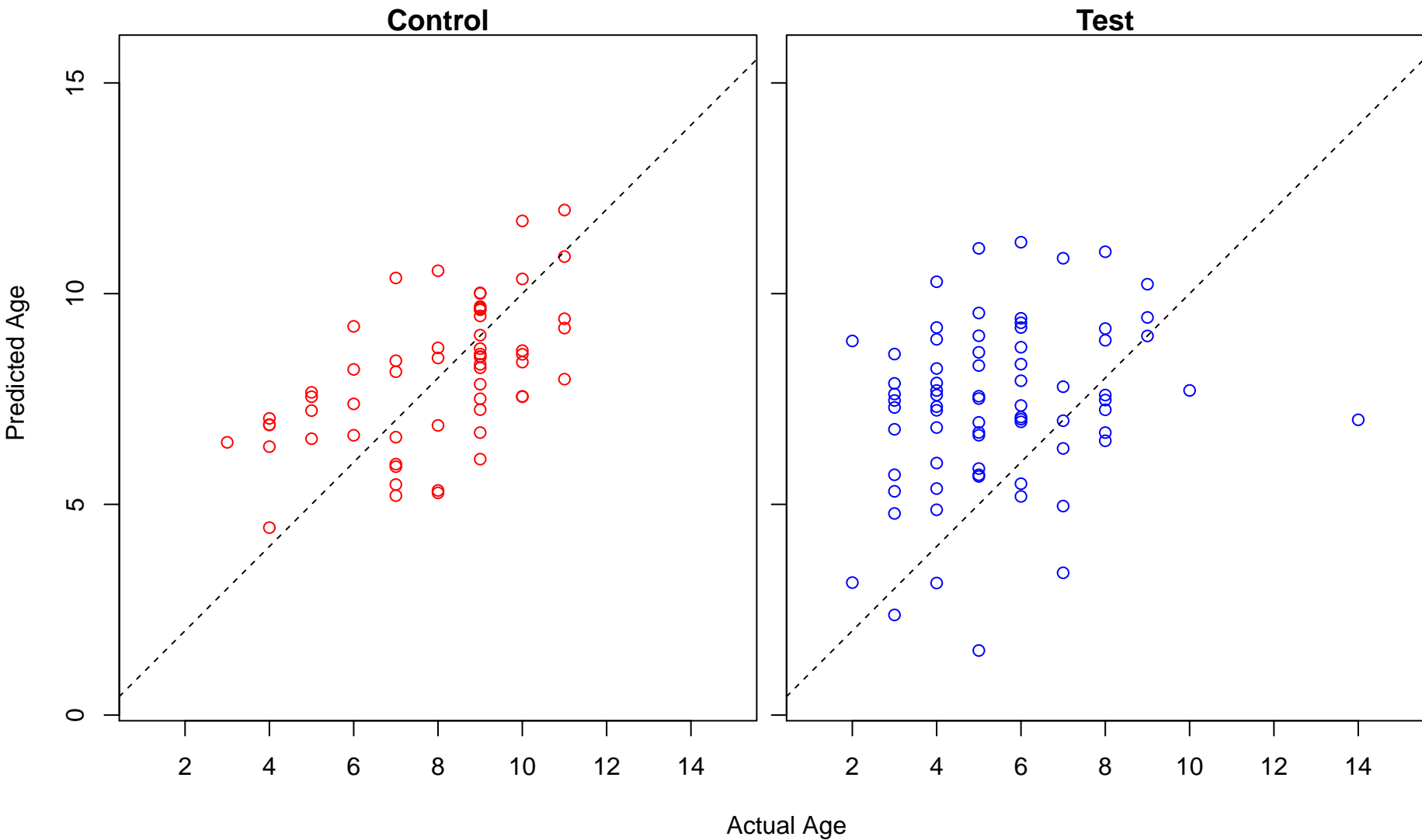
Negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 1)



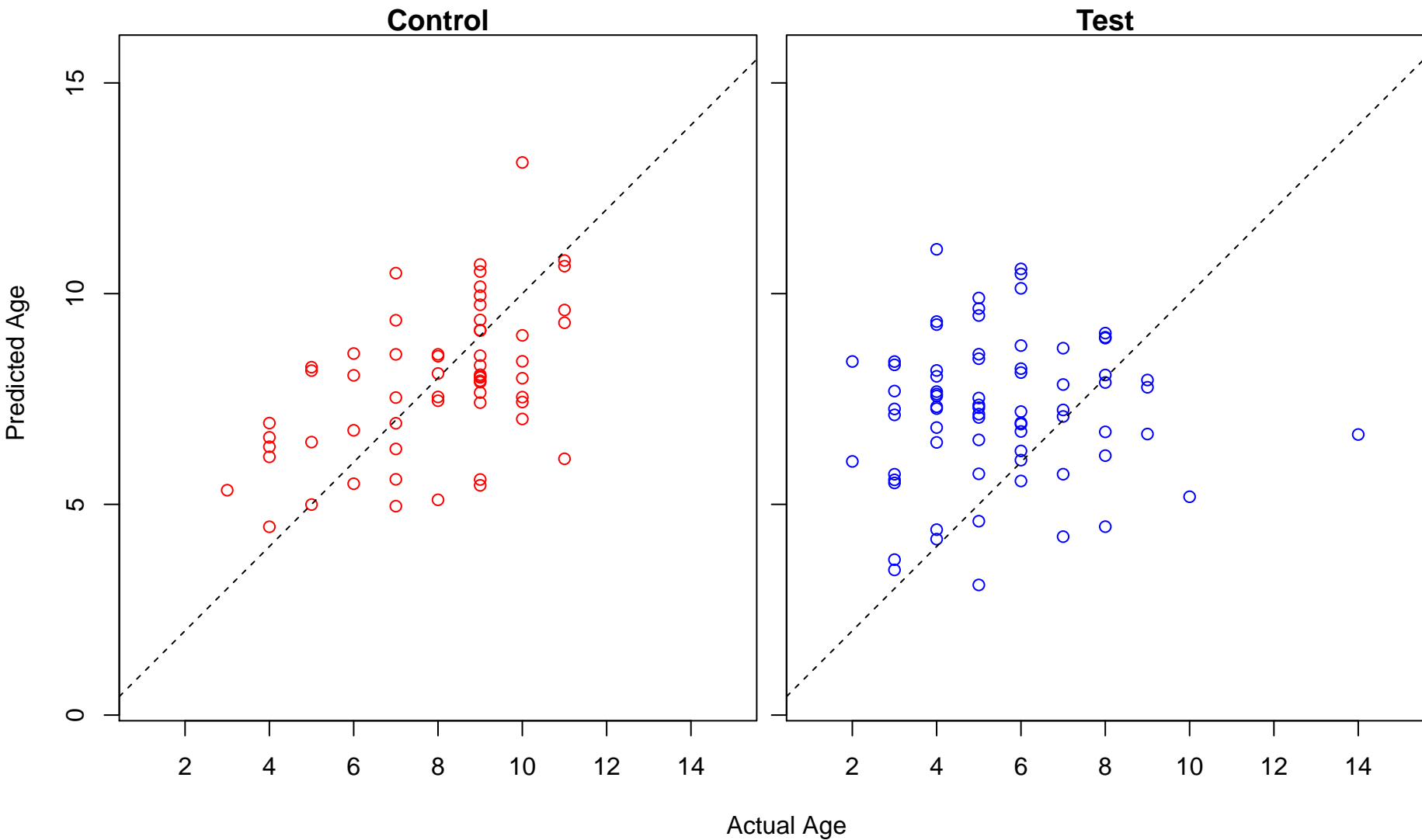
cell-substrate adhesion (Score: 1.229591)



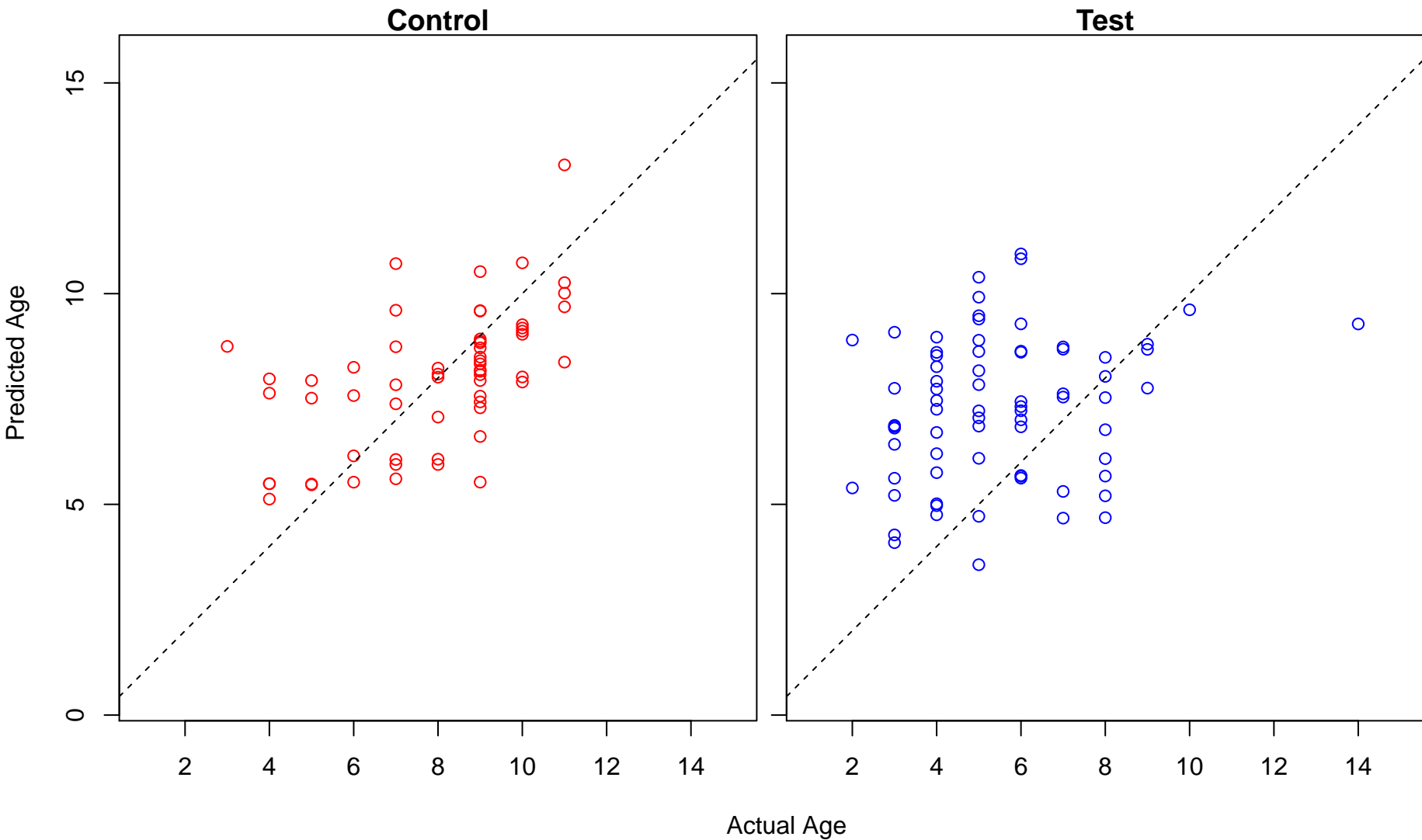
negative regulation of macromolecule metabolic process (Score: 1.227731)



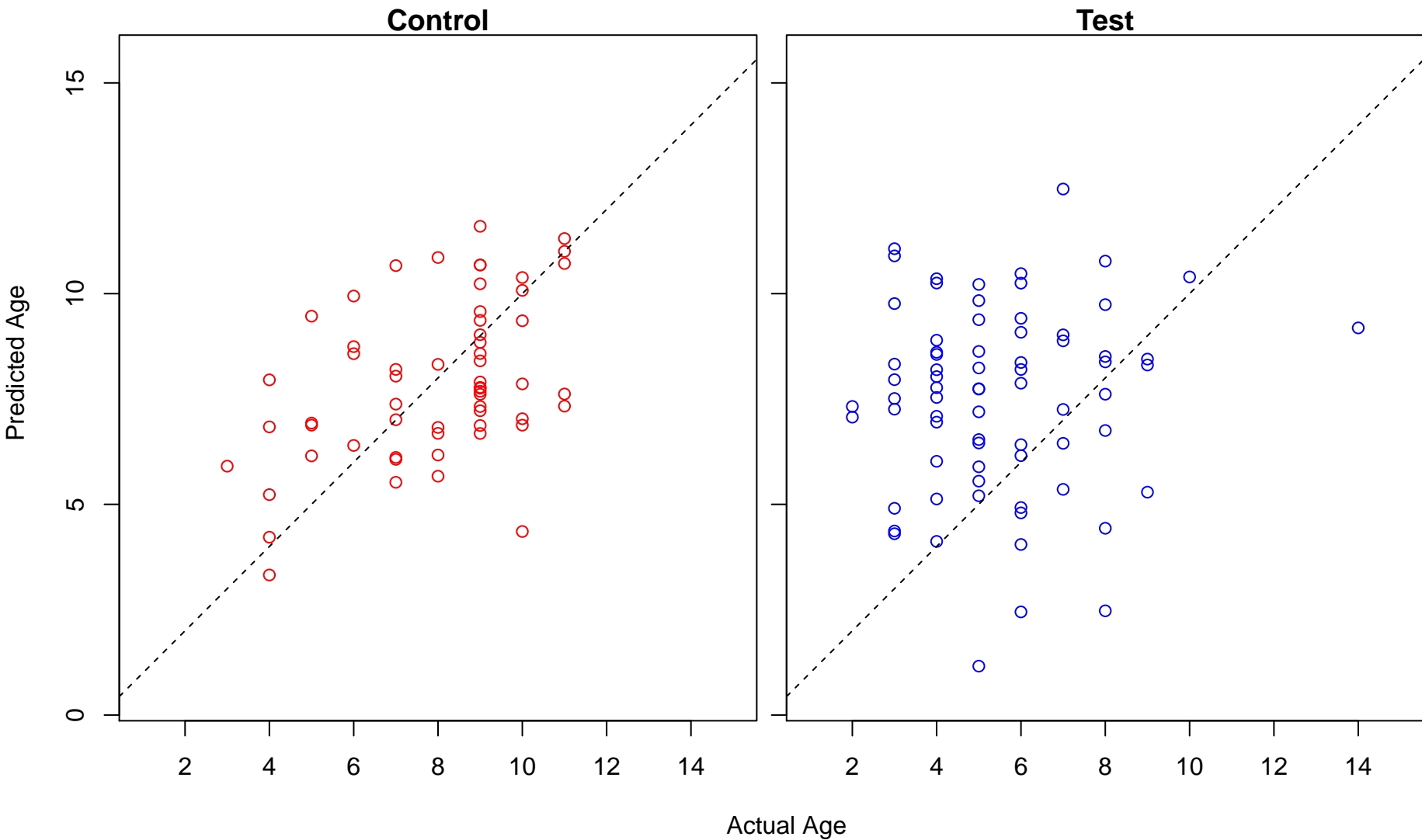
negative regulation of cellular catabolic process (Score: 1.226677)



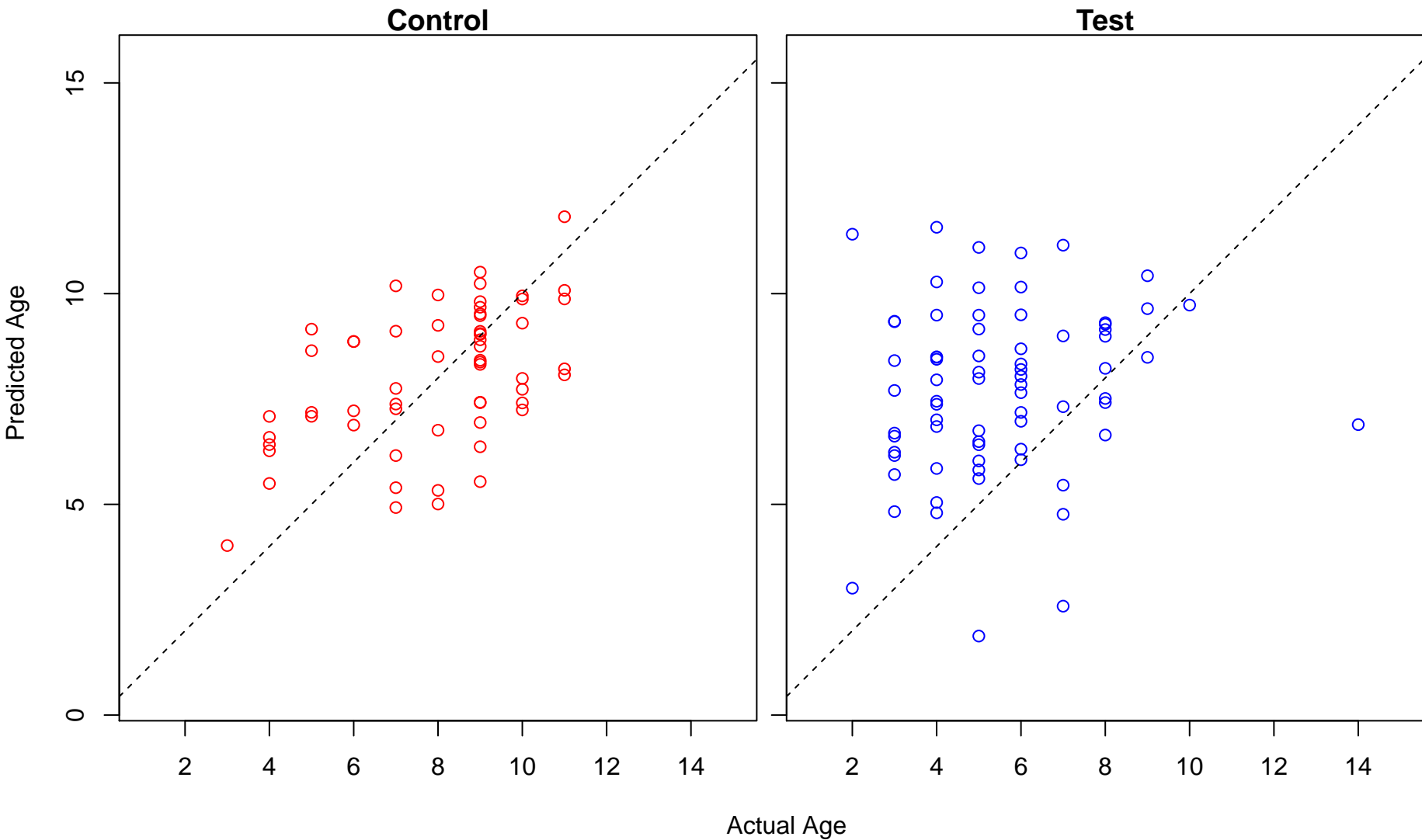
establishment of protein localization to membrane (Score: 1.226604)



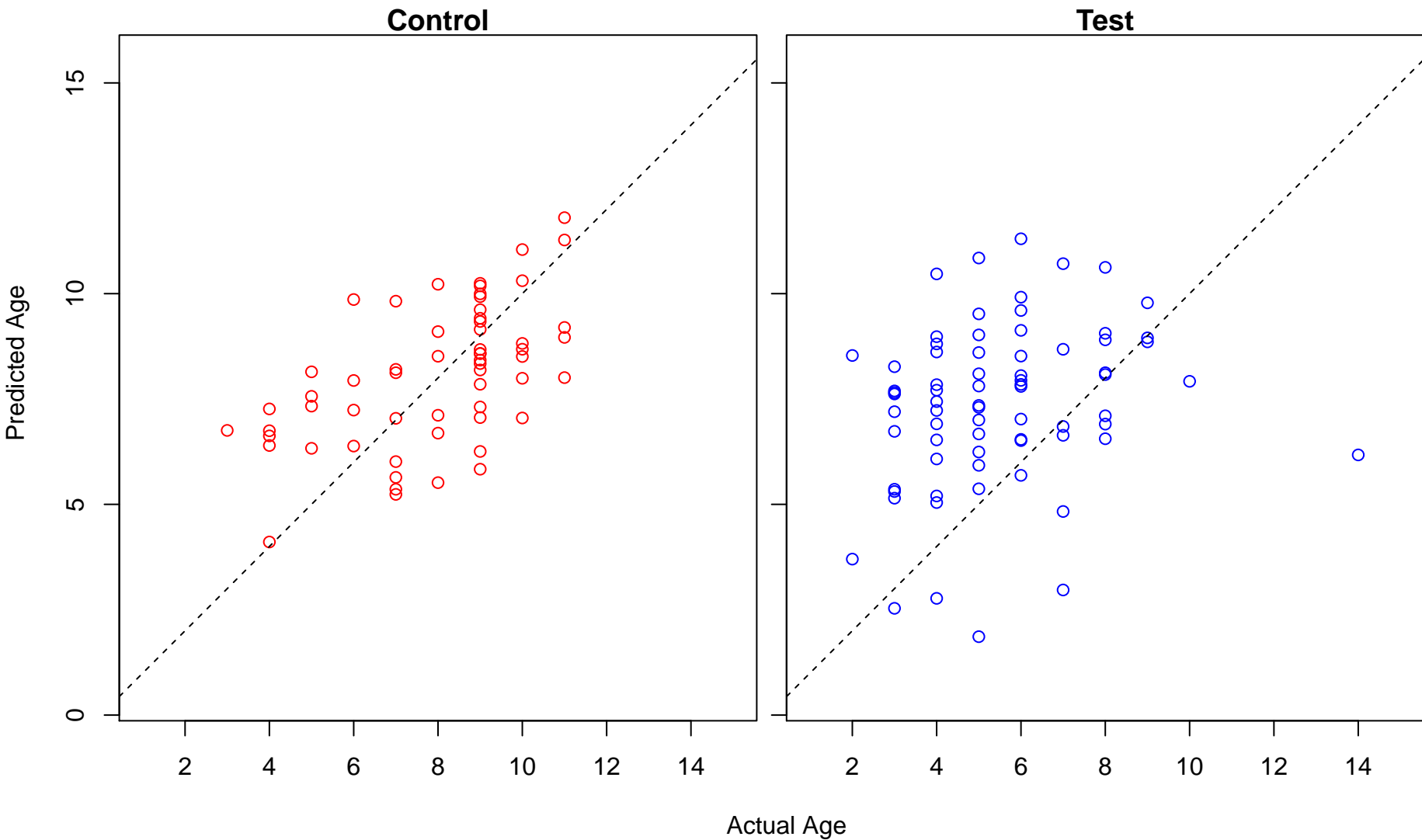
response to unfolded protein (Score: 1.226475)



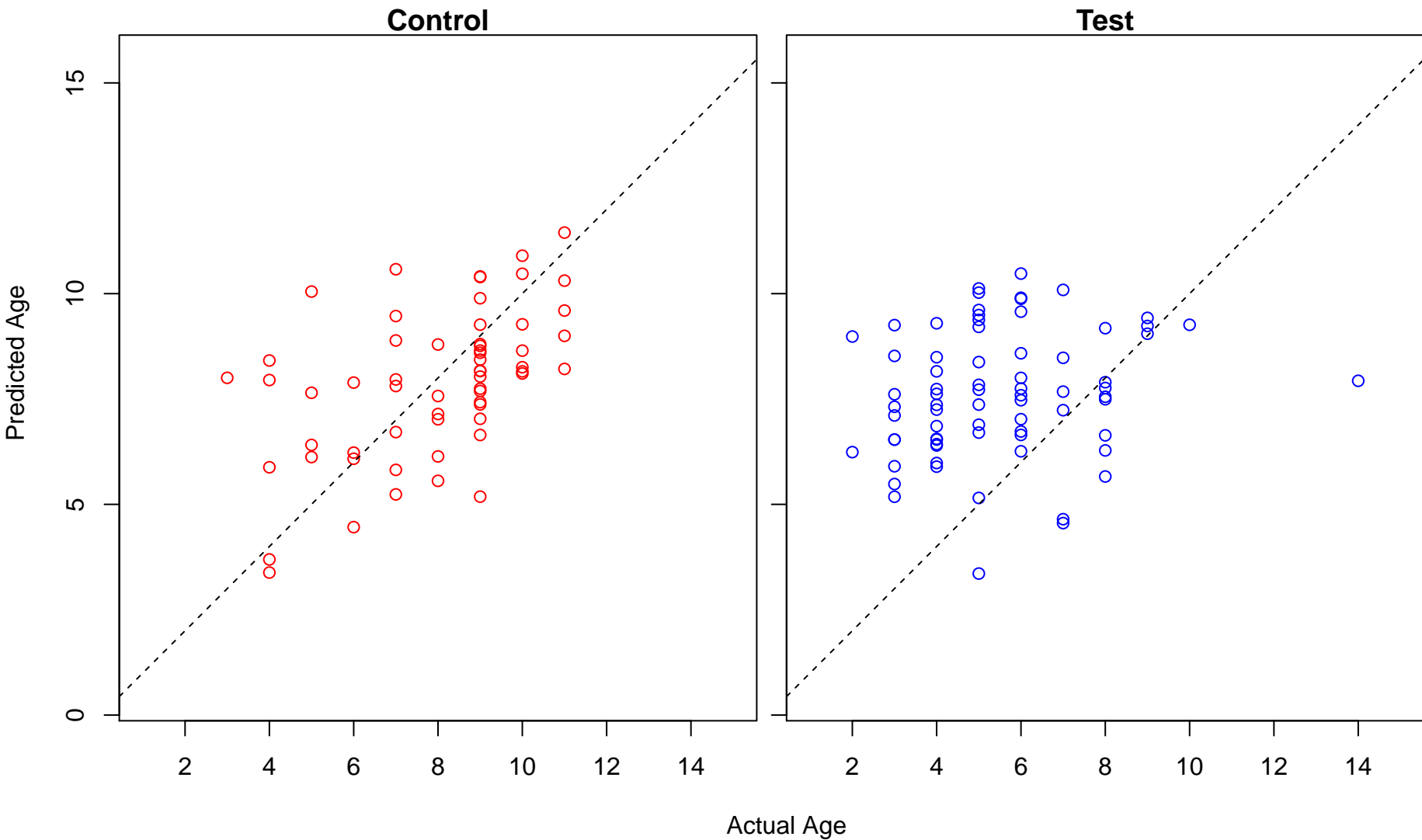
negative regulation of biosynthetic process (Score: 1.226418)



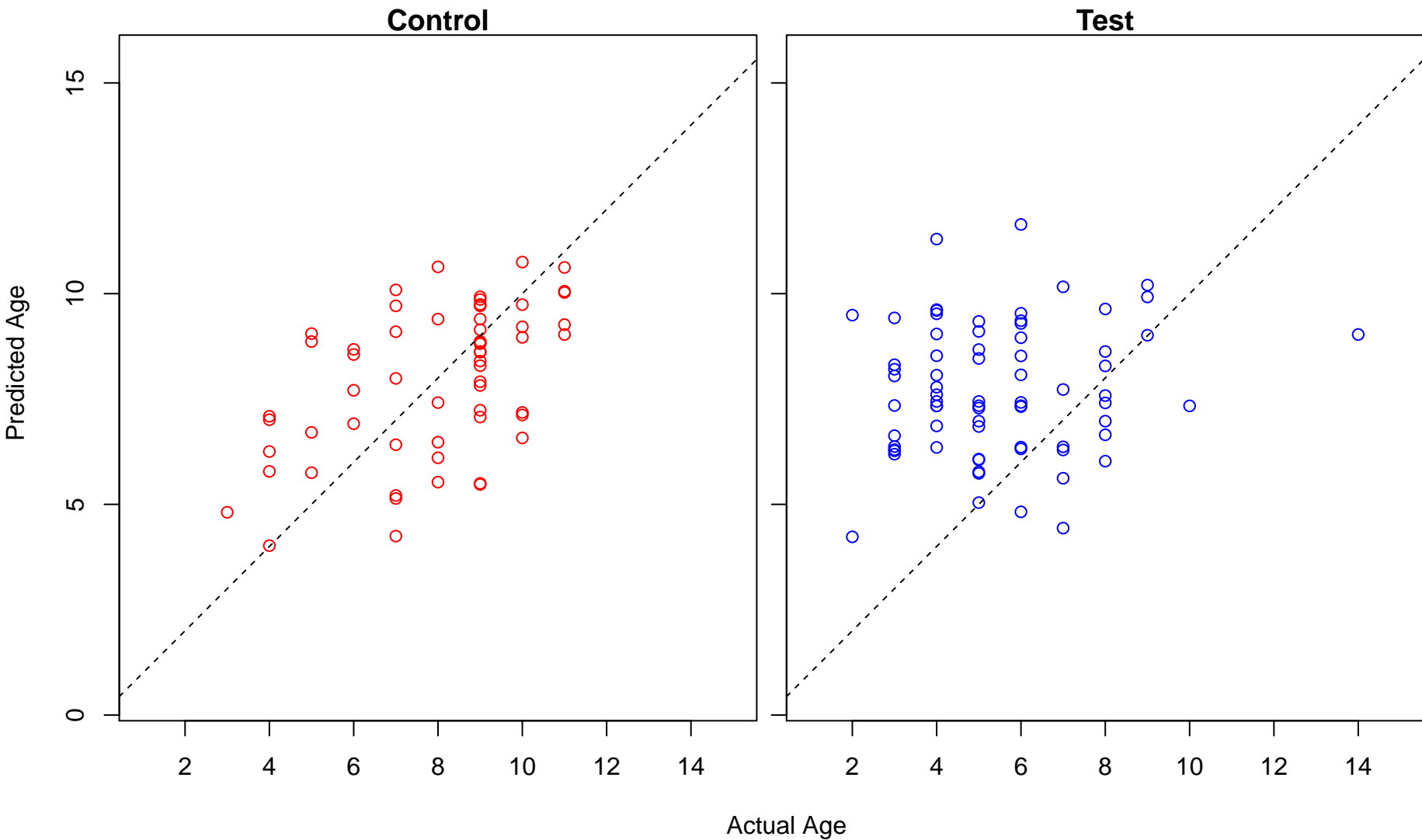
negative regulation of cellular metabolic process (Score: 1.225491)



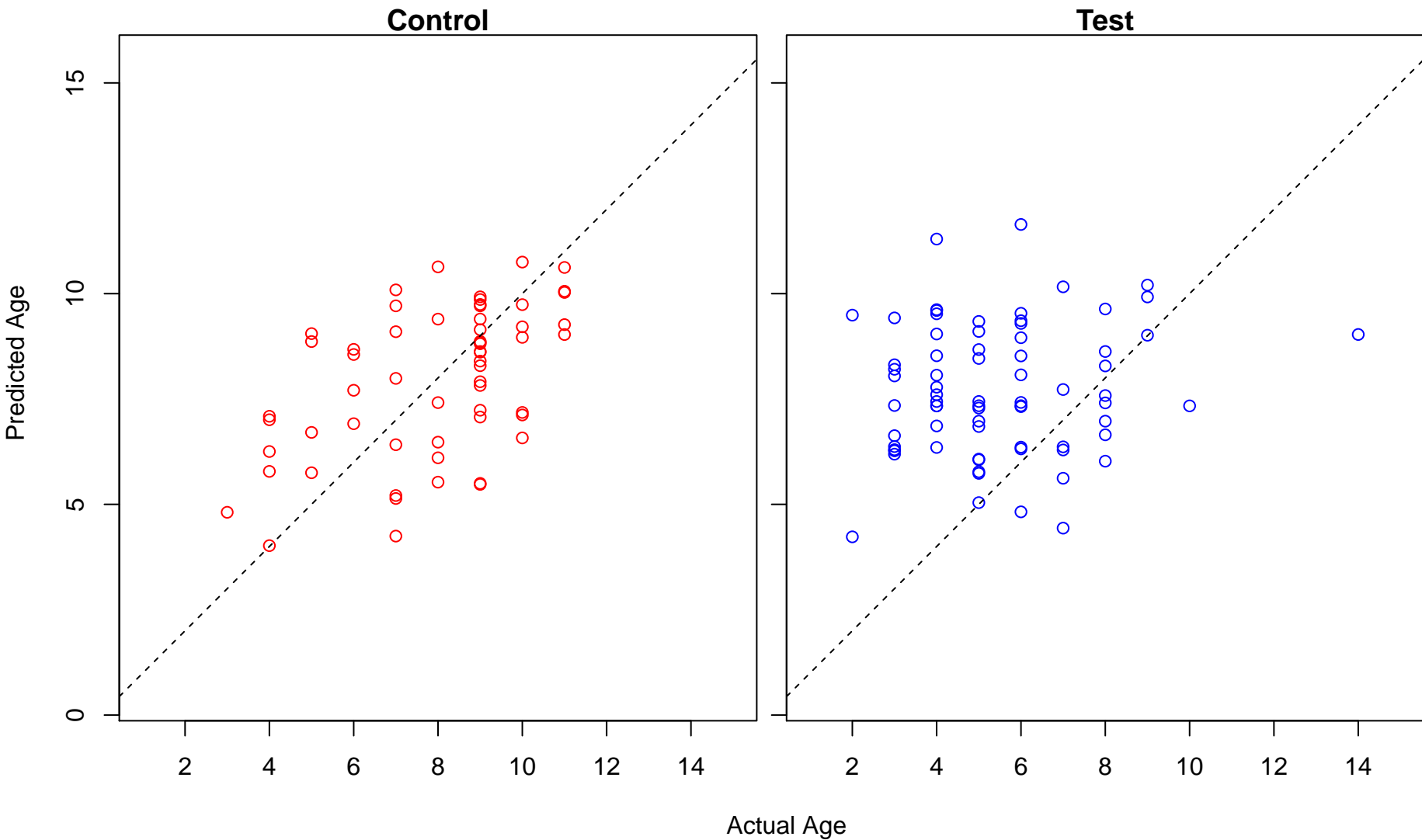
macromolecule catabolic process (Score: 1.225103)



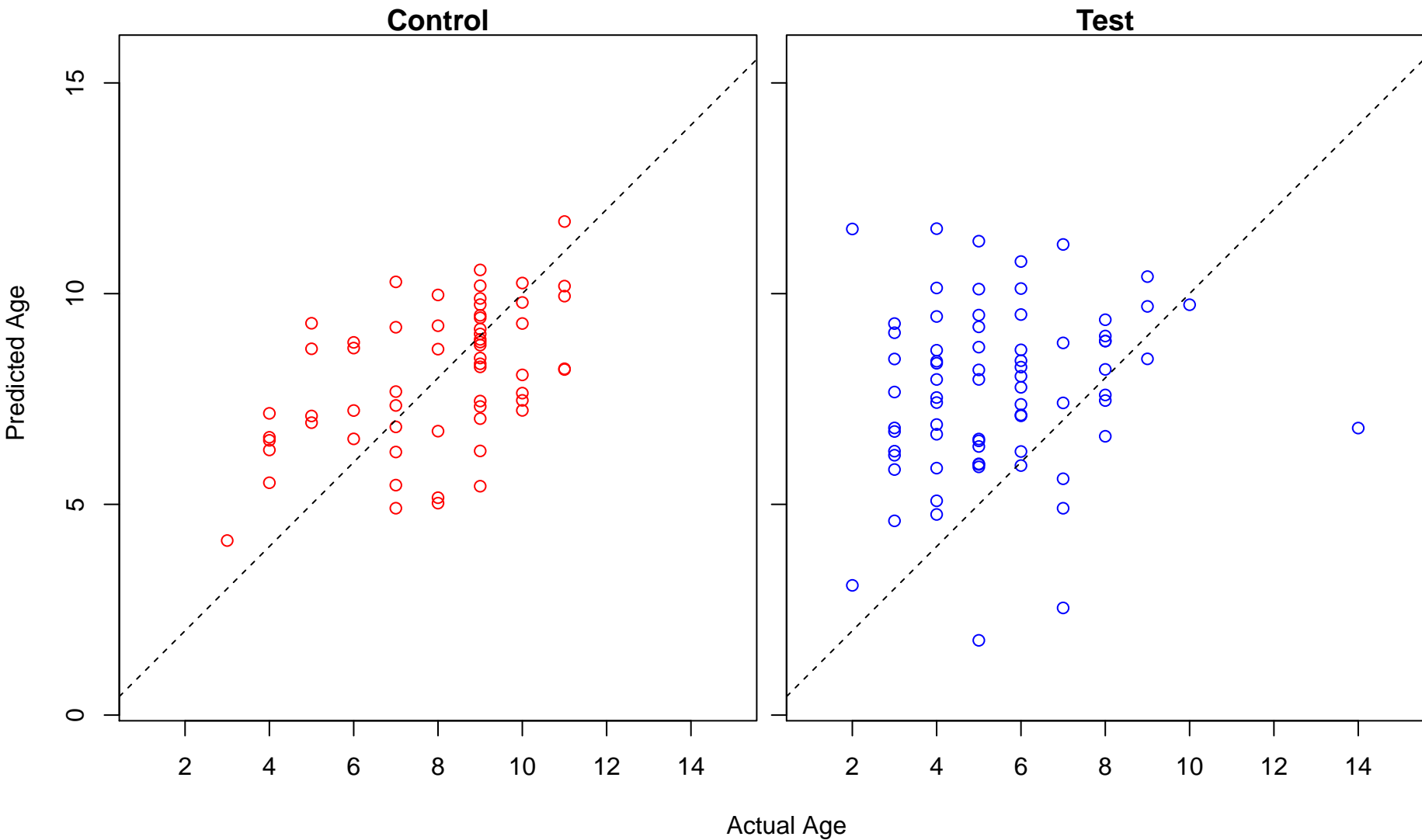
cell motility (Score: 1.224889)



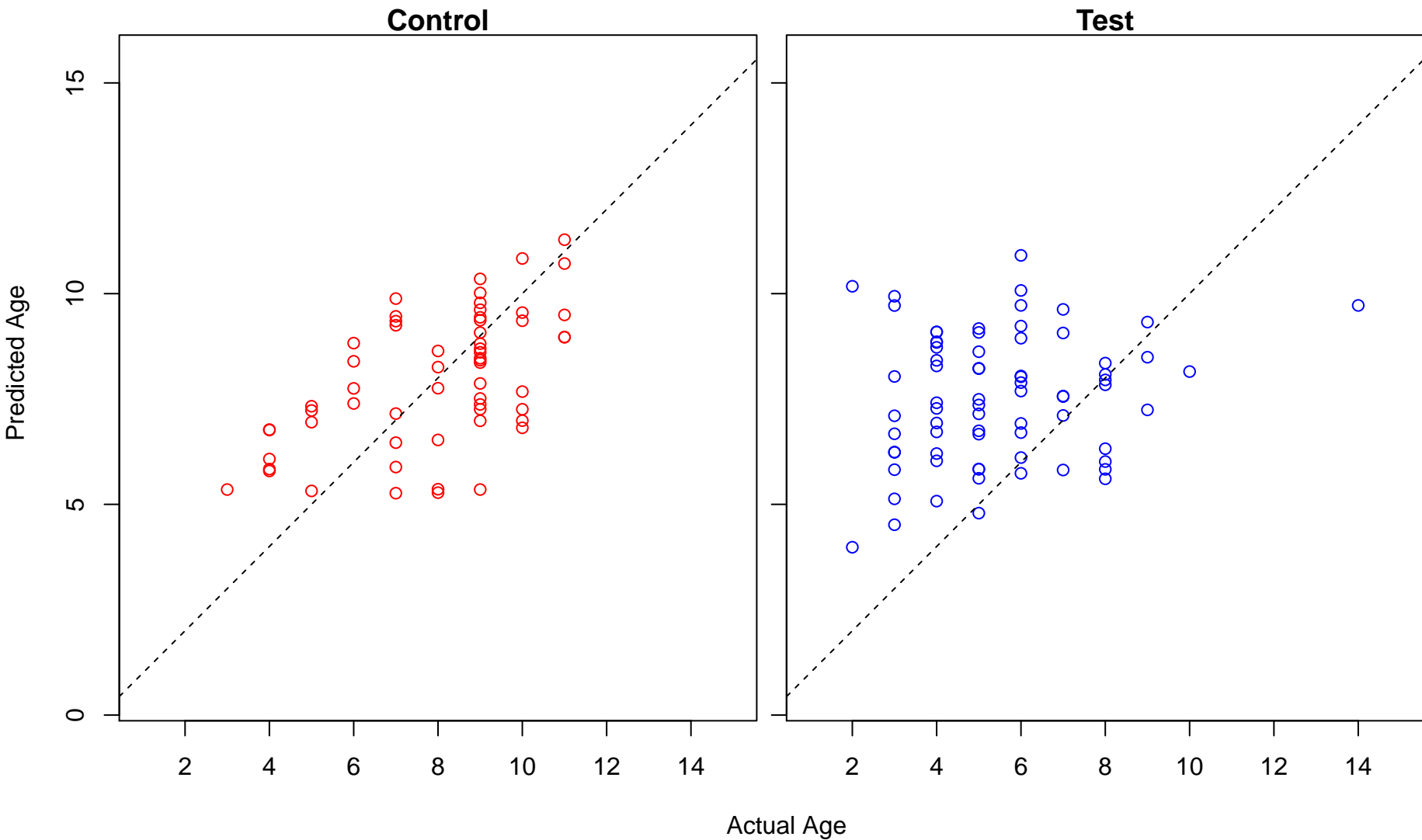
localization of cell (Score: 1.224889)



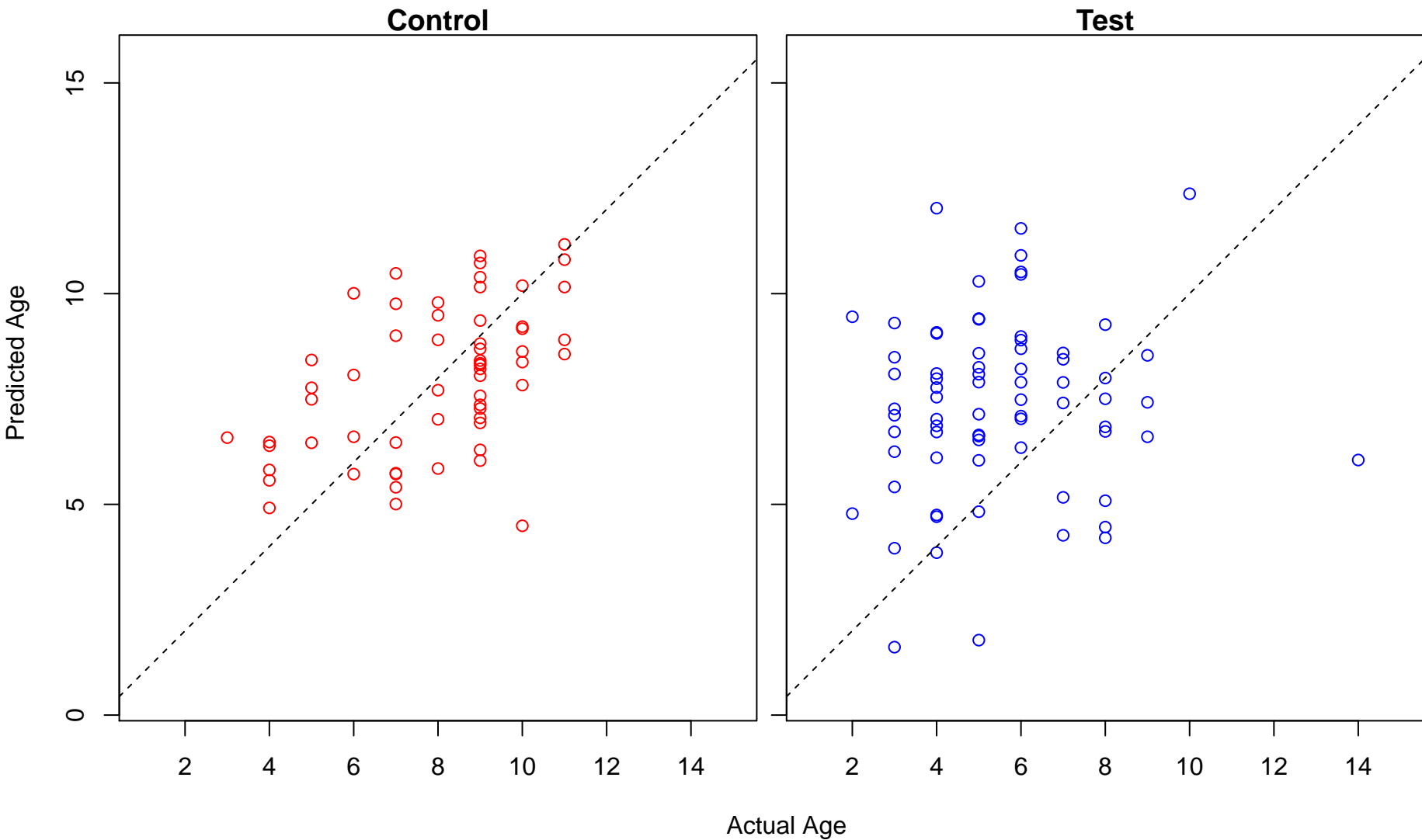
negative regulation of macromolecule biosynthetic process (Score: 1.223509)



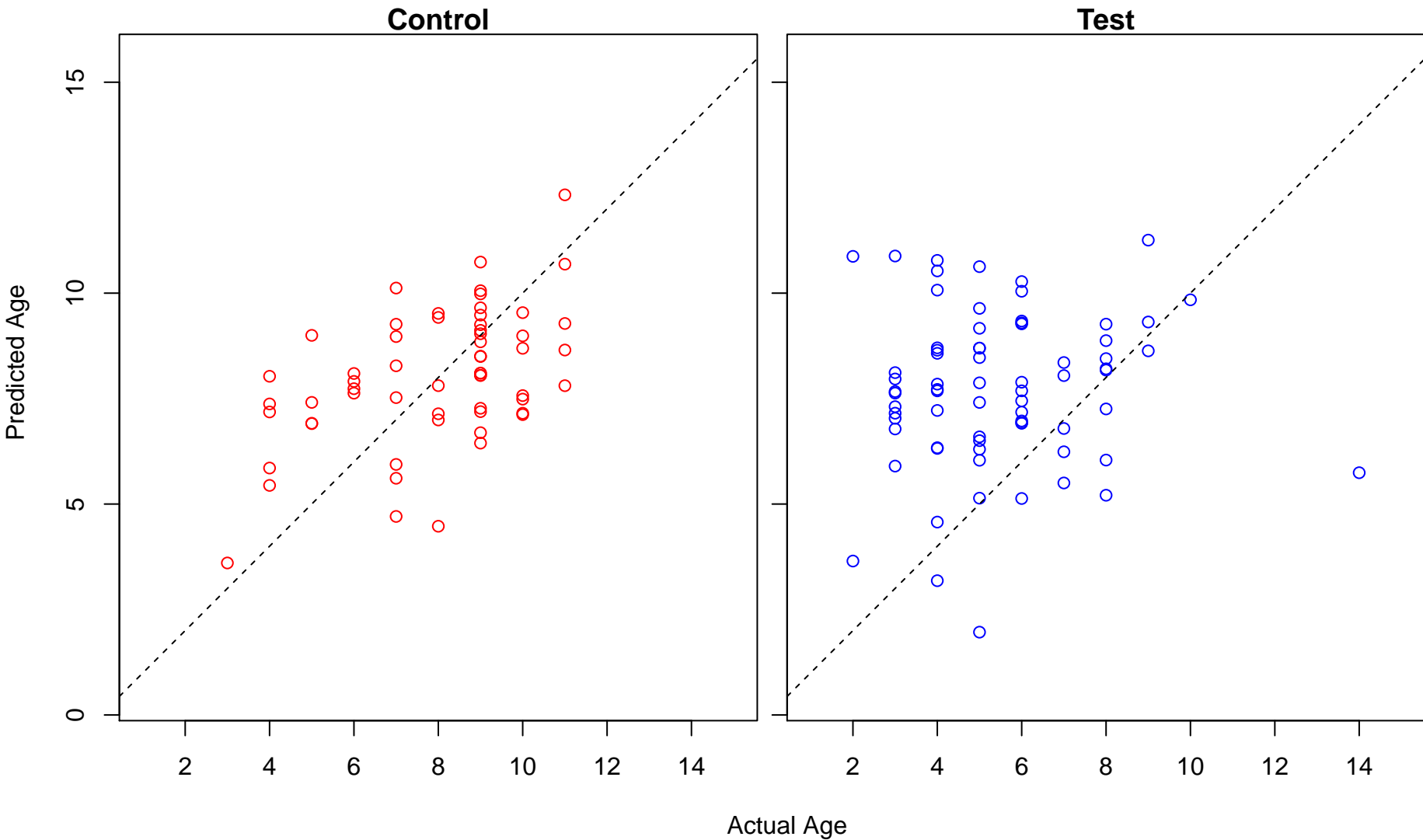
epithelial to mesenchymal transition (Score: 1.222304)



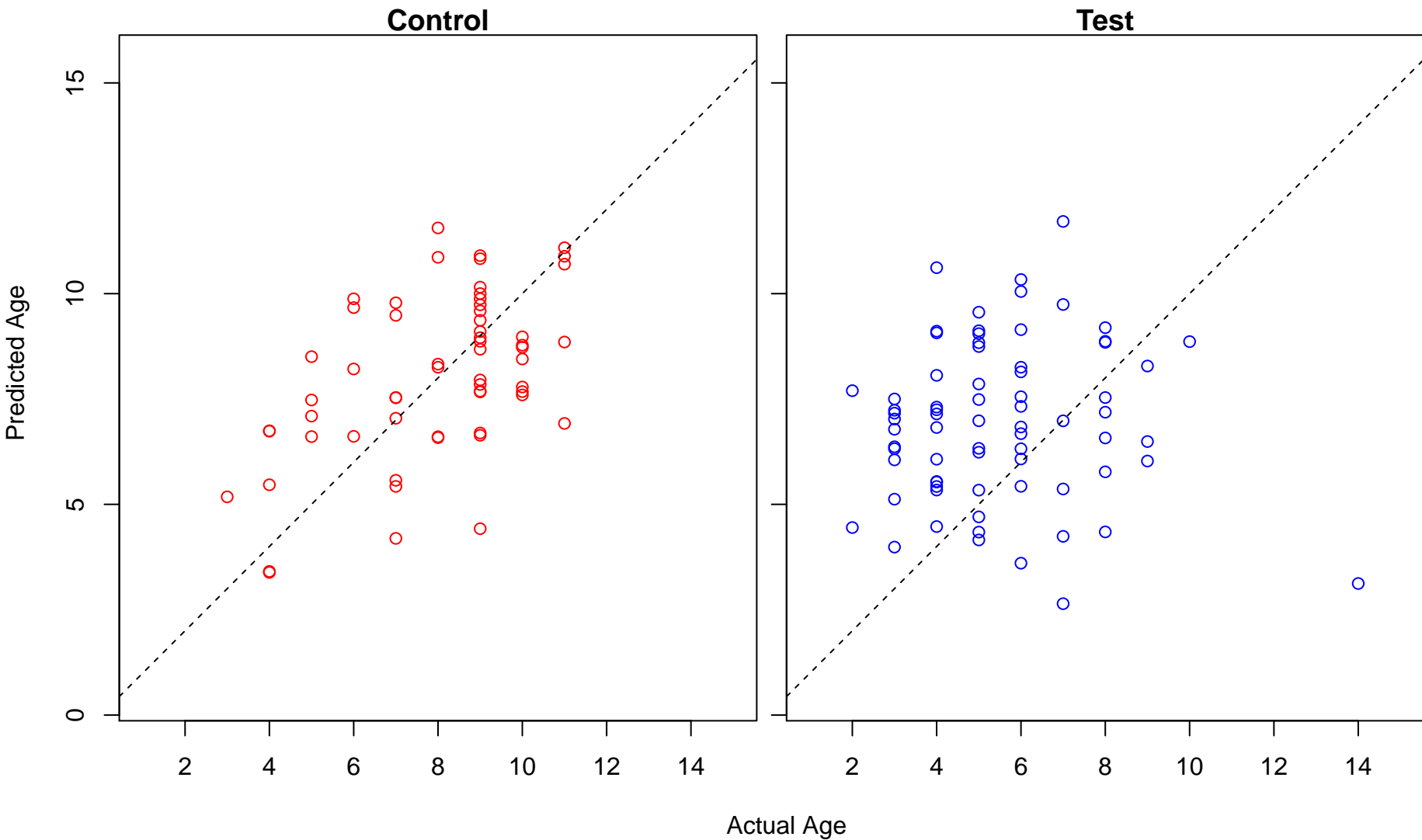
organelle fission (Score: 1.221268)



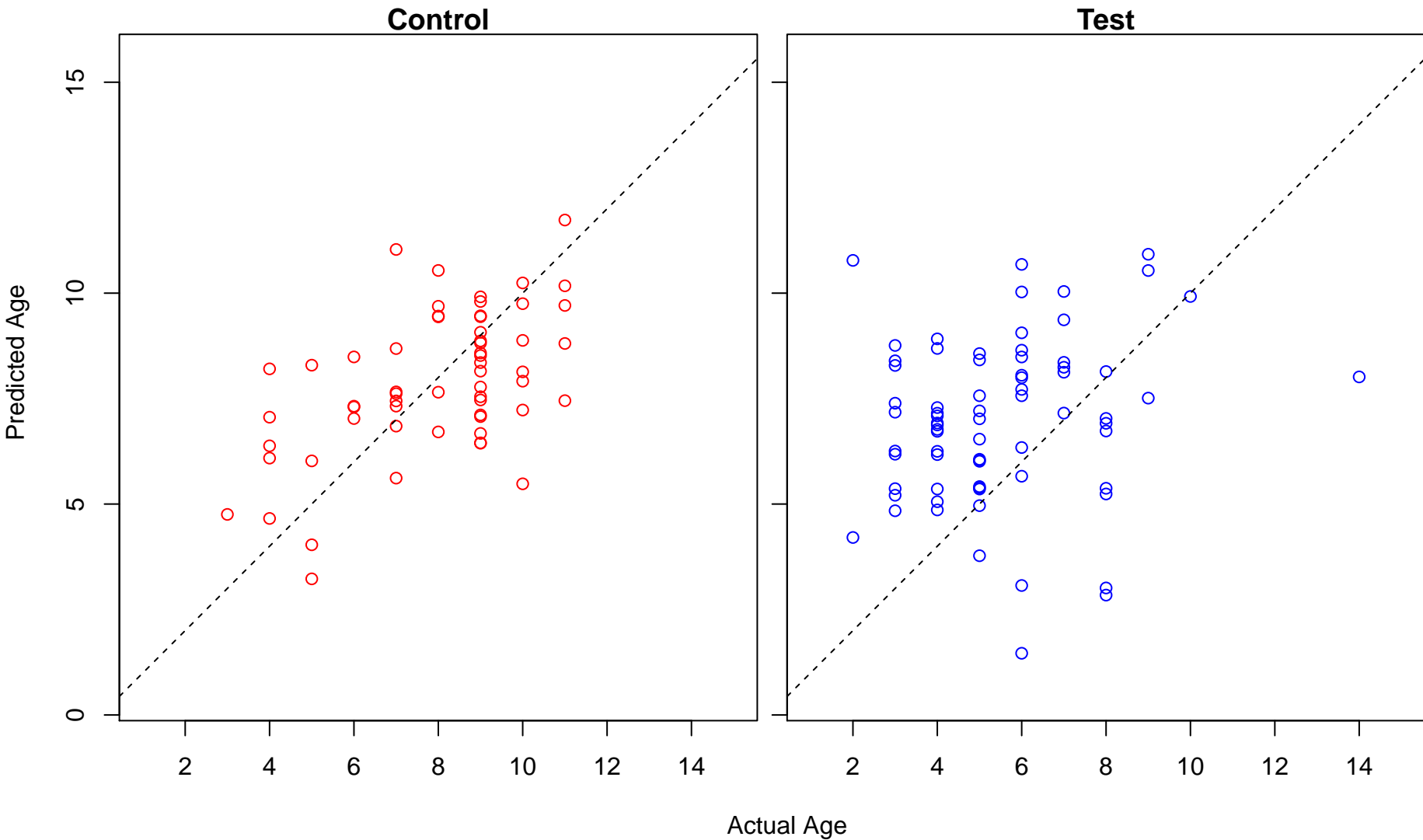
positive regulation of macromolecule biosynthetic process (Score: 1.219960)



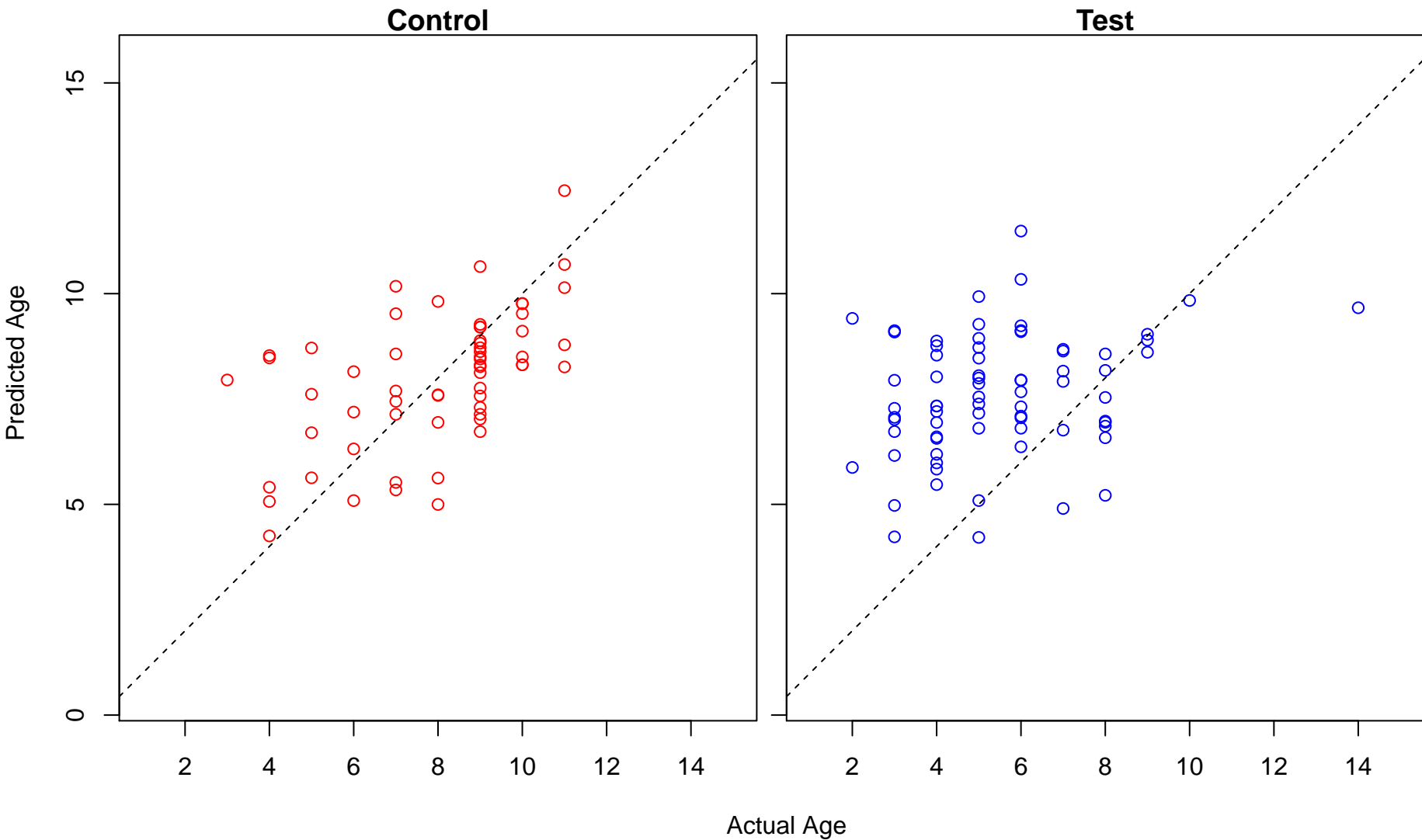
regulation of protein dephosphorylation (Score: 1.219878)



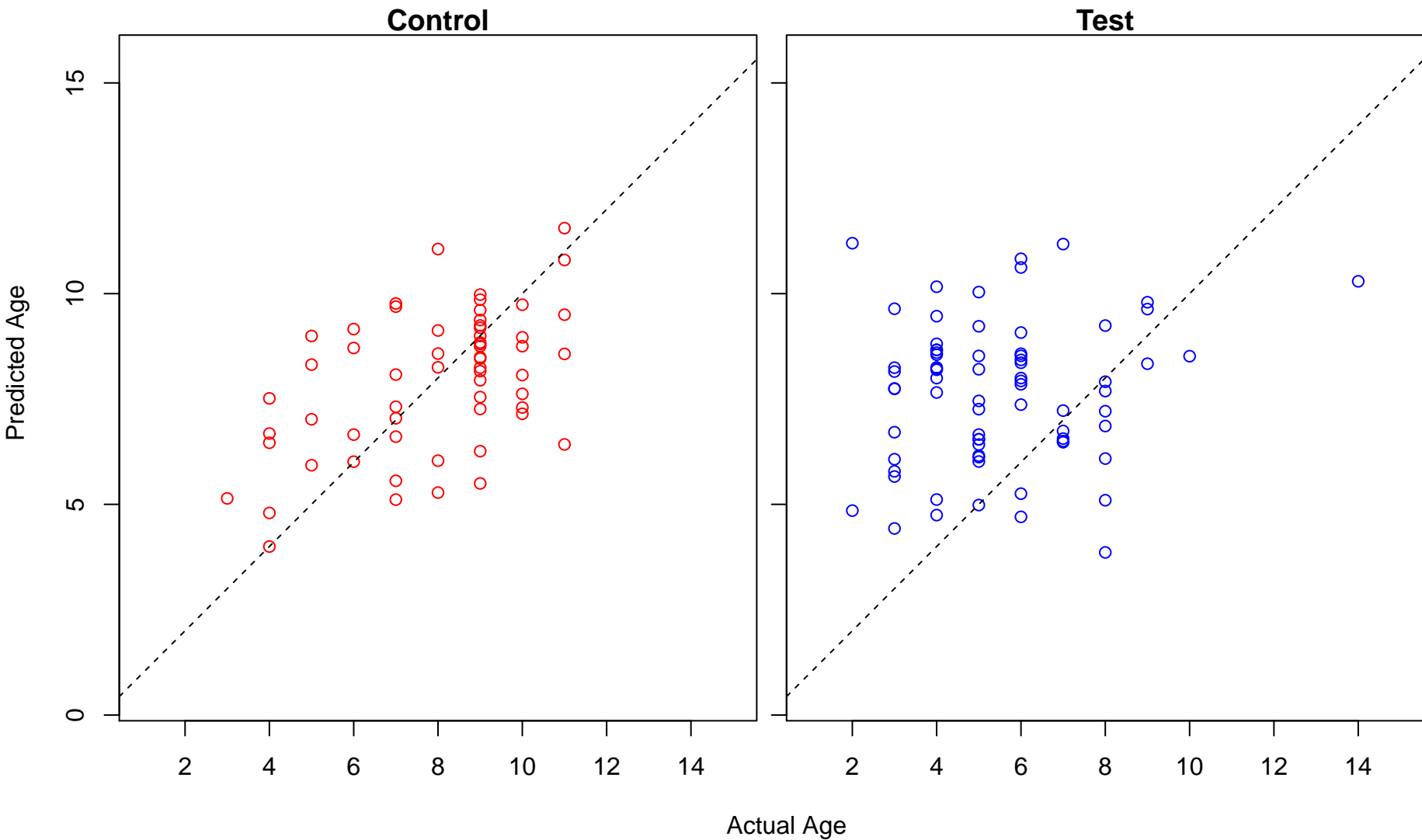
phosphatidylglycerol acyl-chain remodeling (Score: 1.219583)



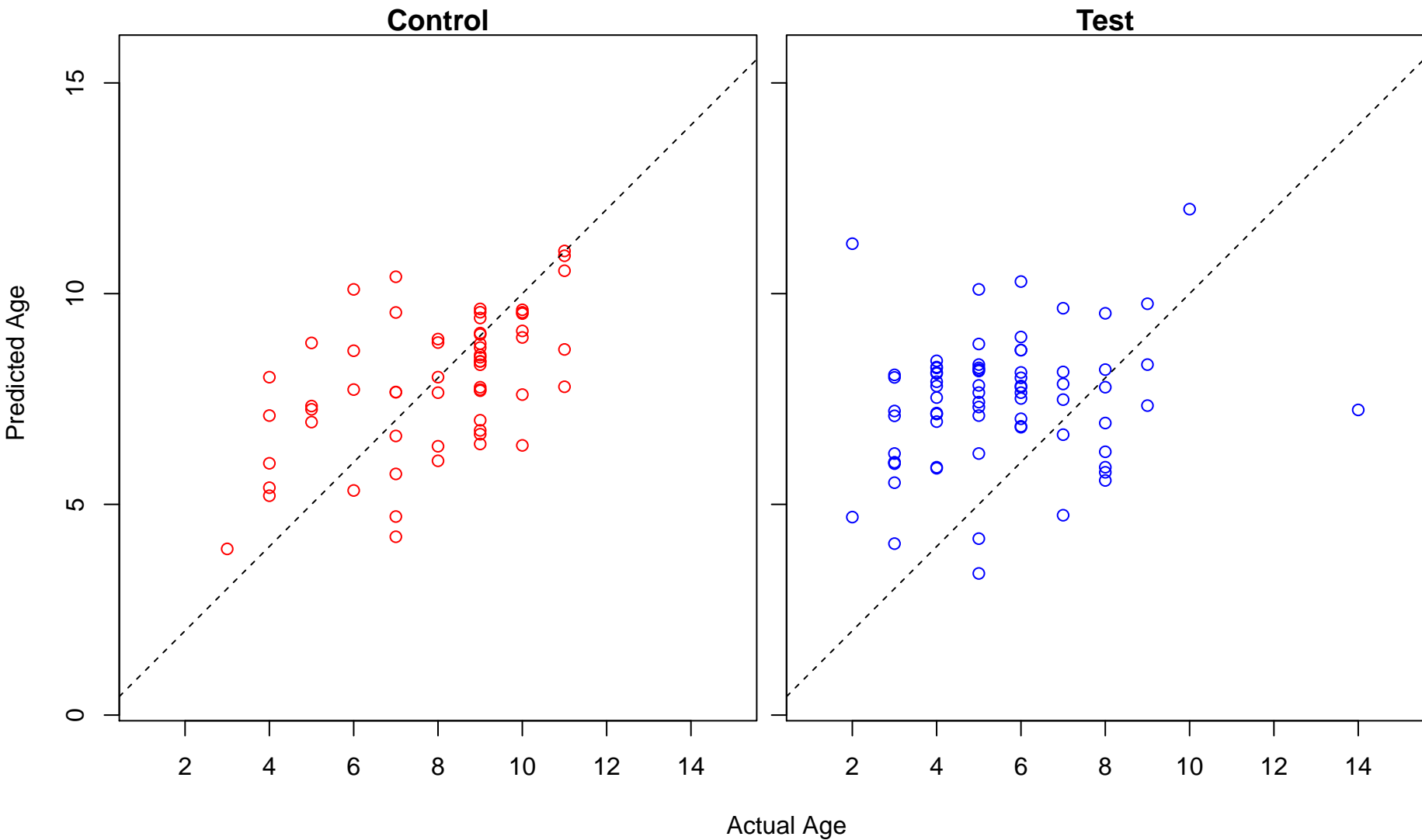
intracellular transport (Score: 1.219045)



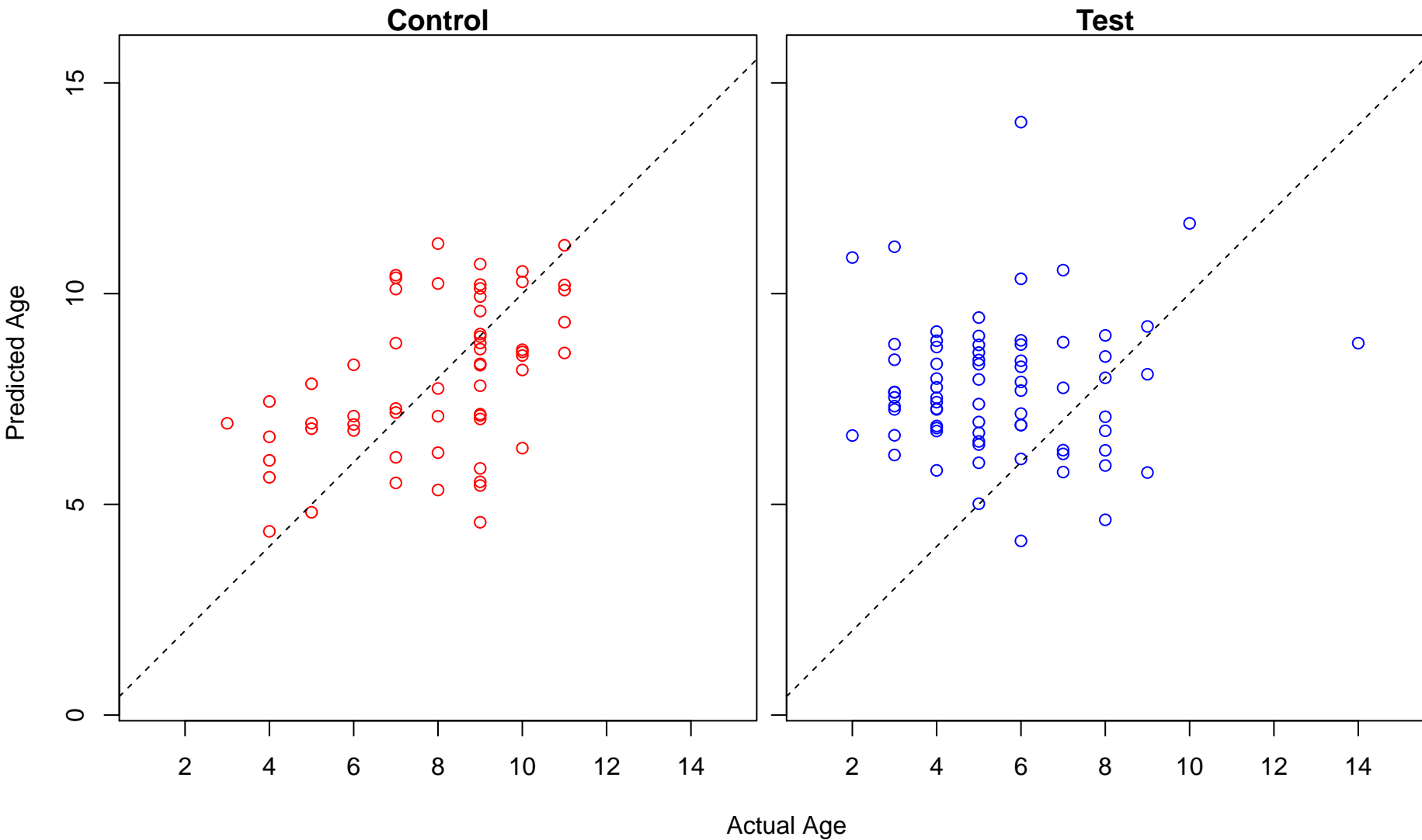
cell activation (Score: 1.217155)



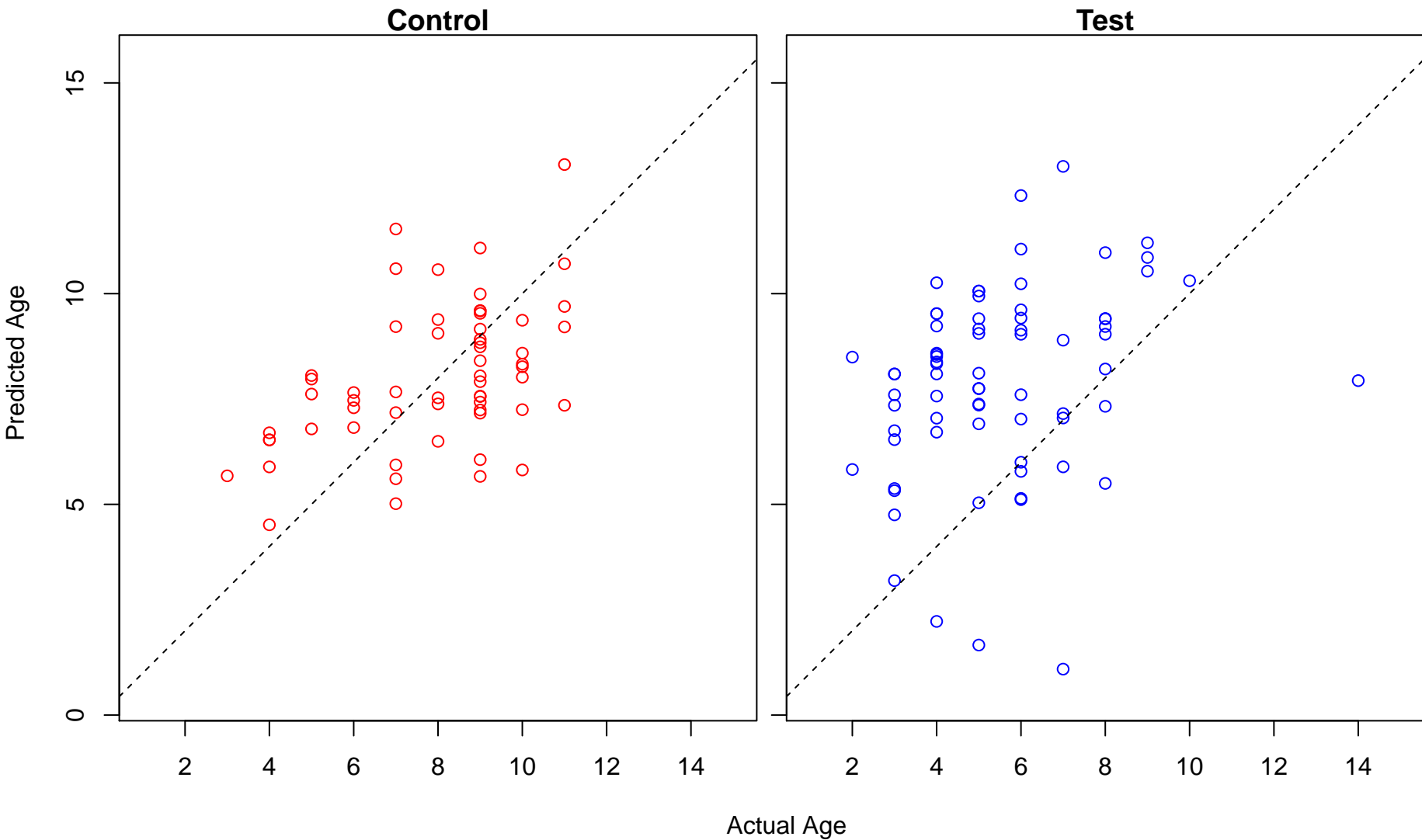
chromatin modification (Score: 1.216098)



activation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 1.215382)

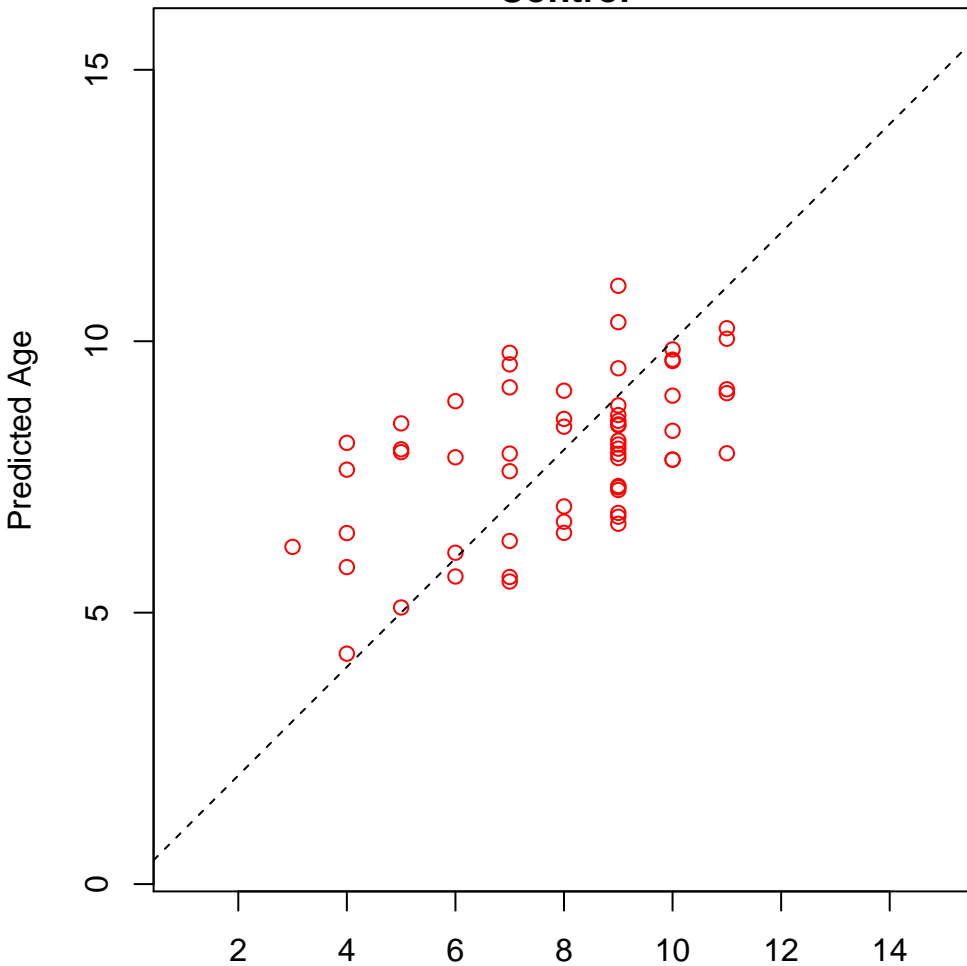


positive regulation of cell proliferation (Score: 1.213355)

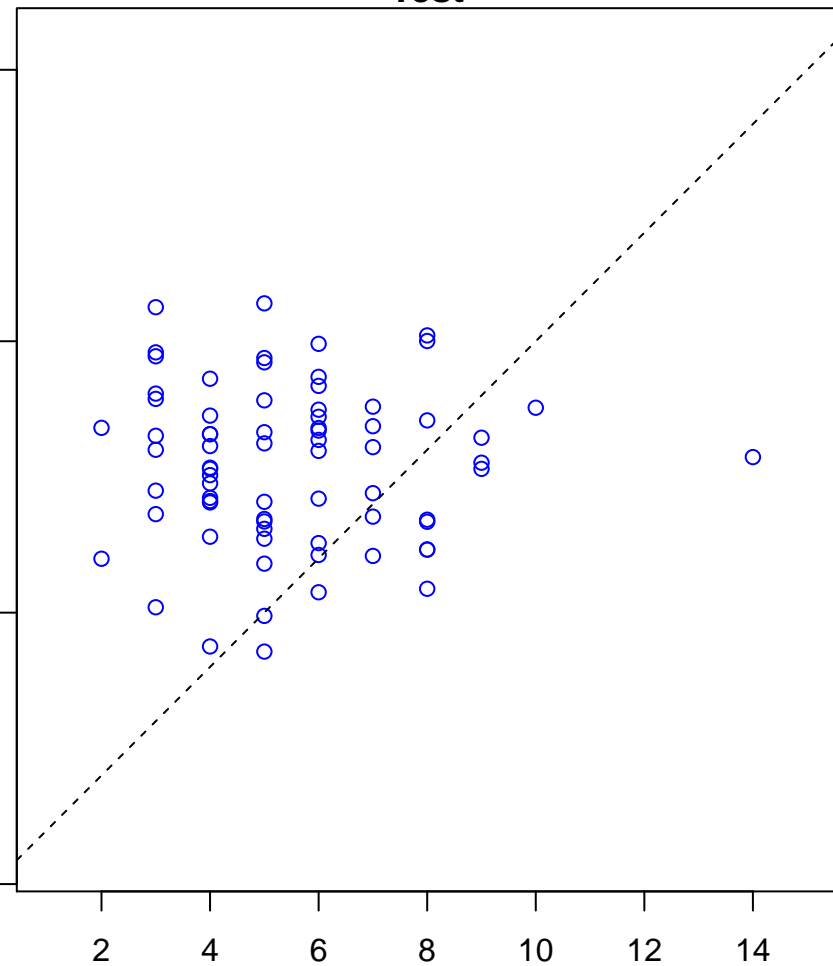


endosome to melanosome transport (Score: 1.211551)

Control



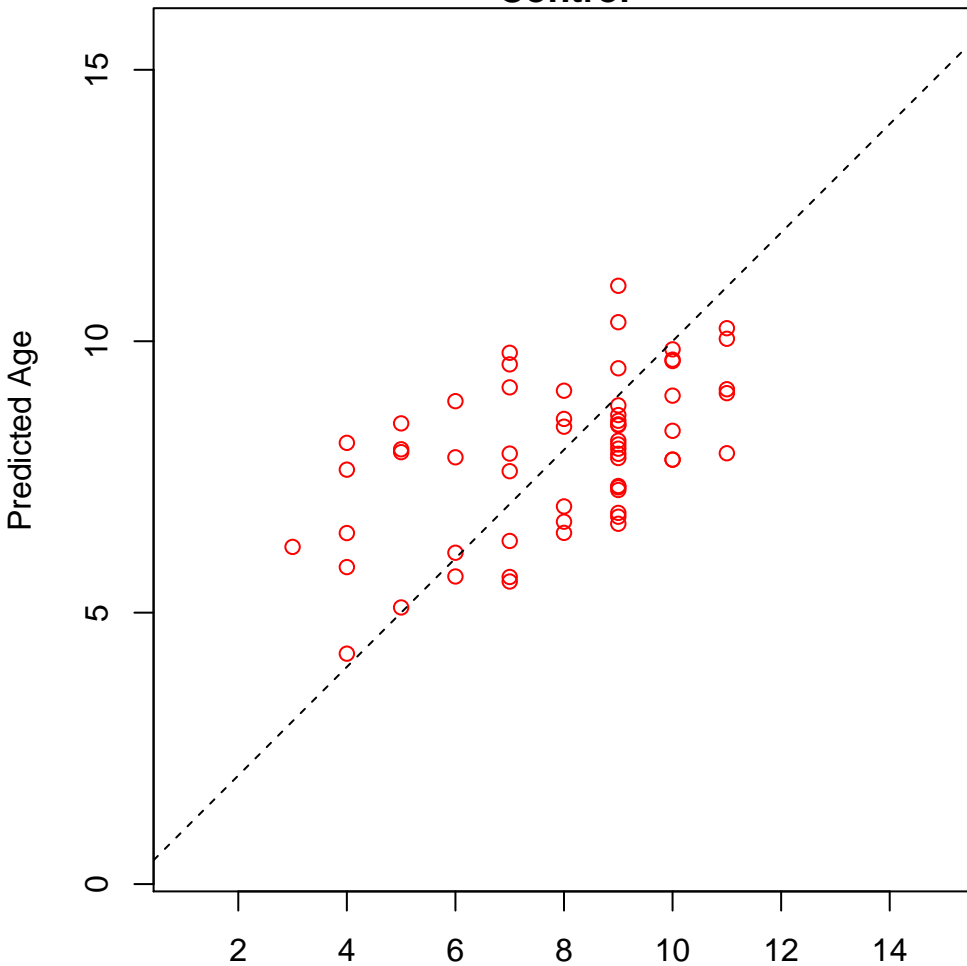
Test



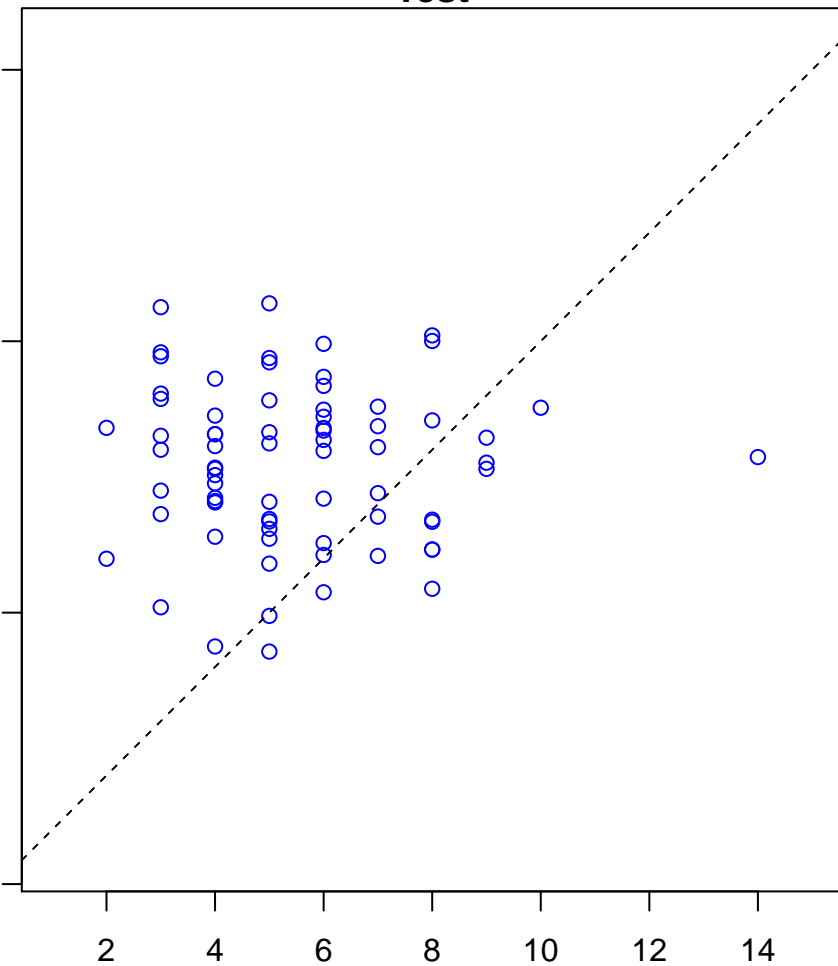
Actual Age

endosome to pigment granule transport (Score: 1.211551)

Control

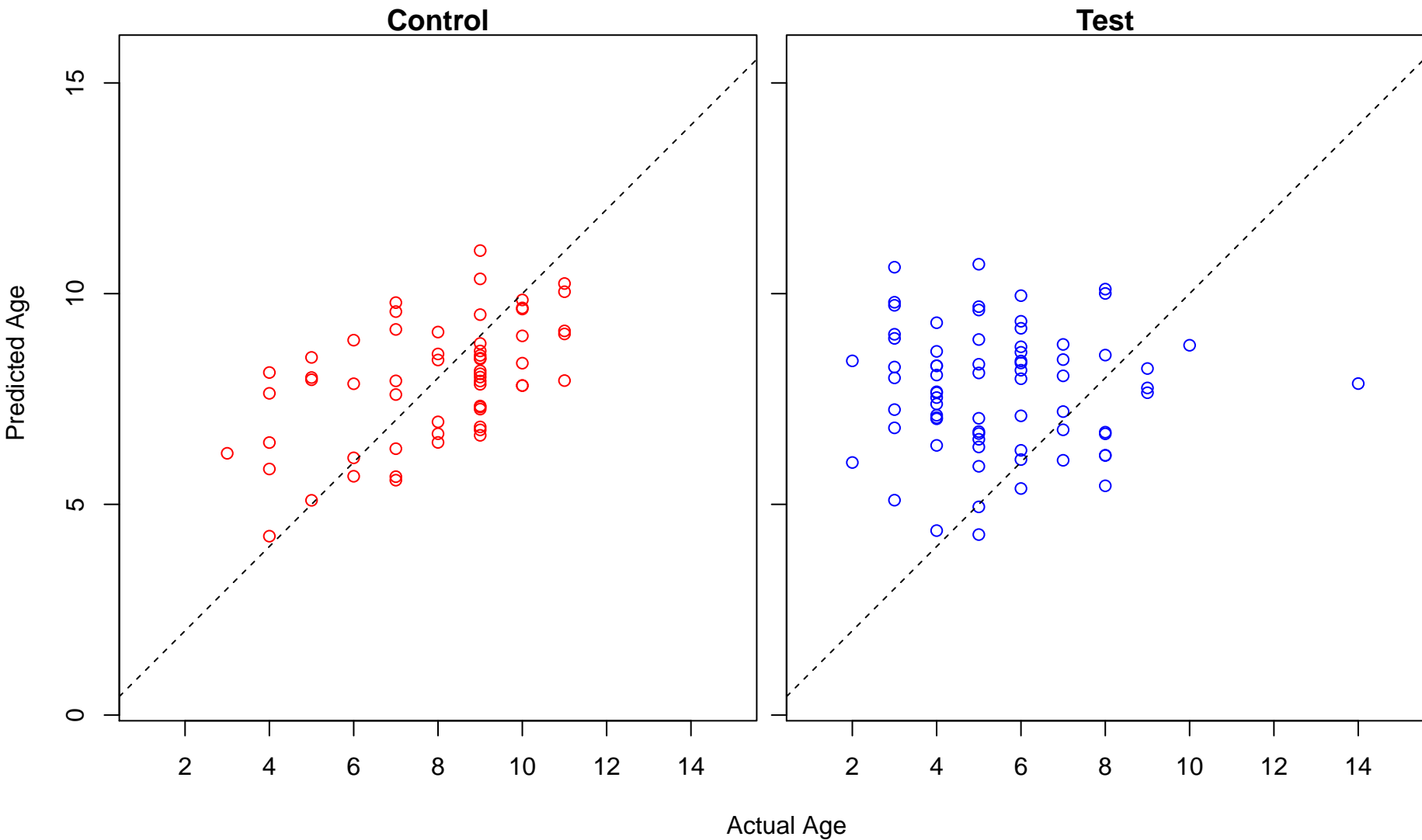


Test

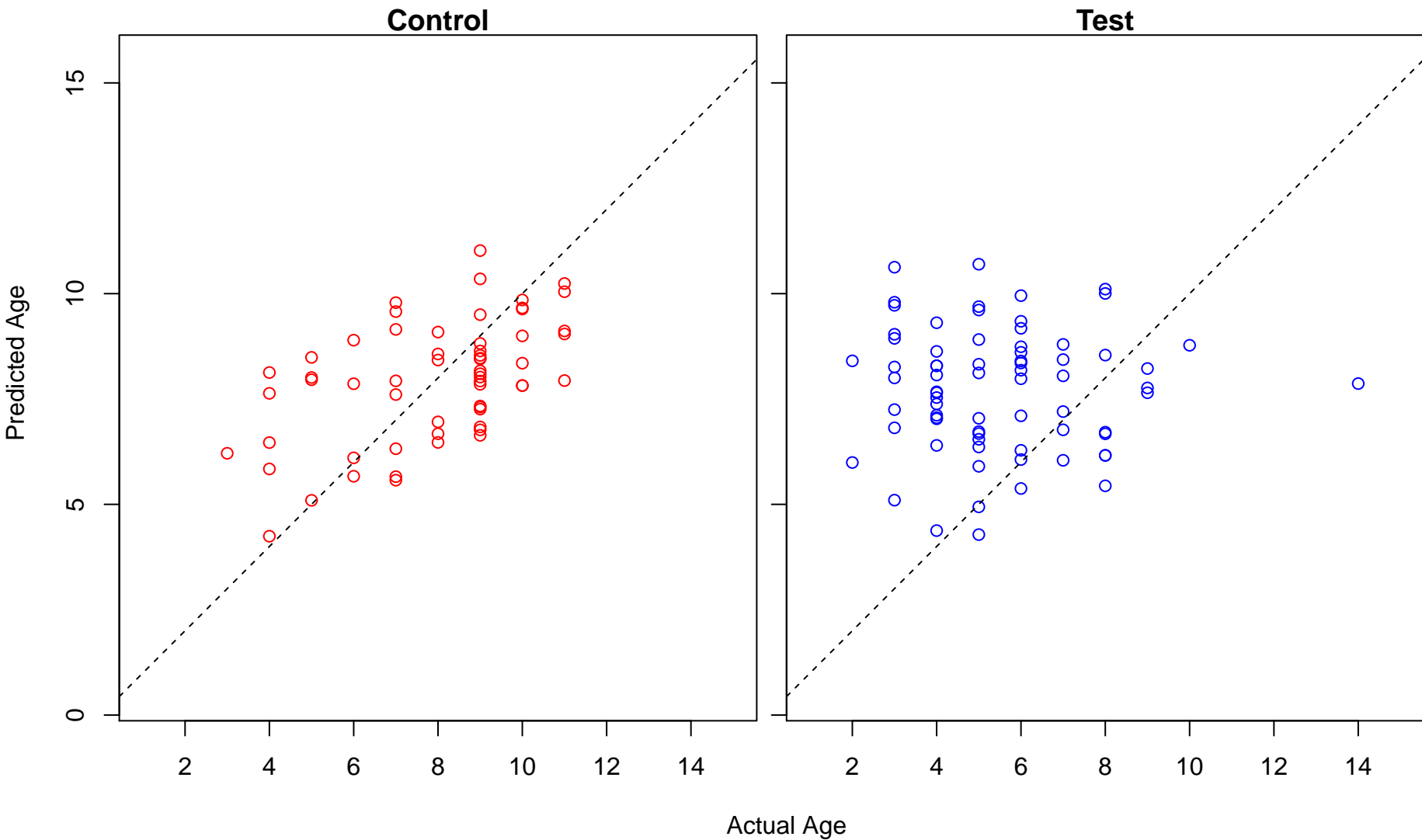


Actual Age

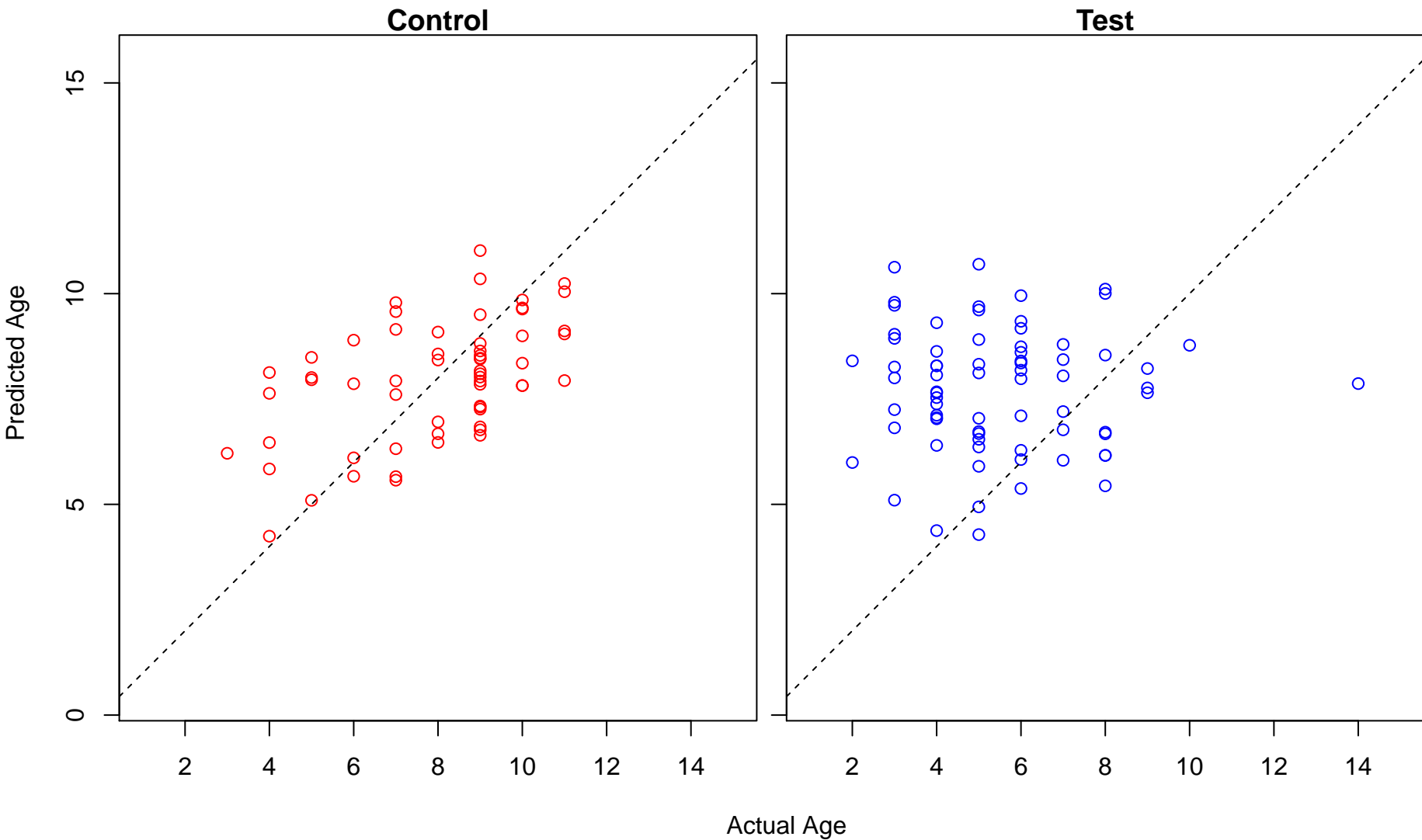
pigment granule maturation (Score: 1.211551)



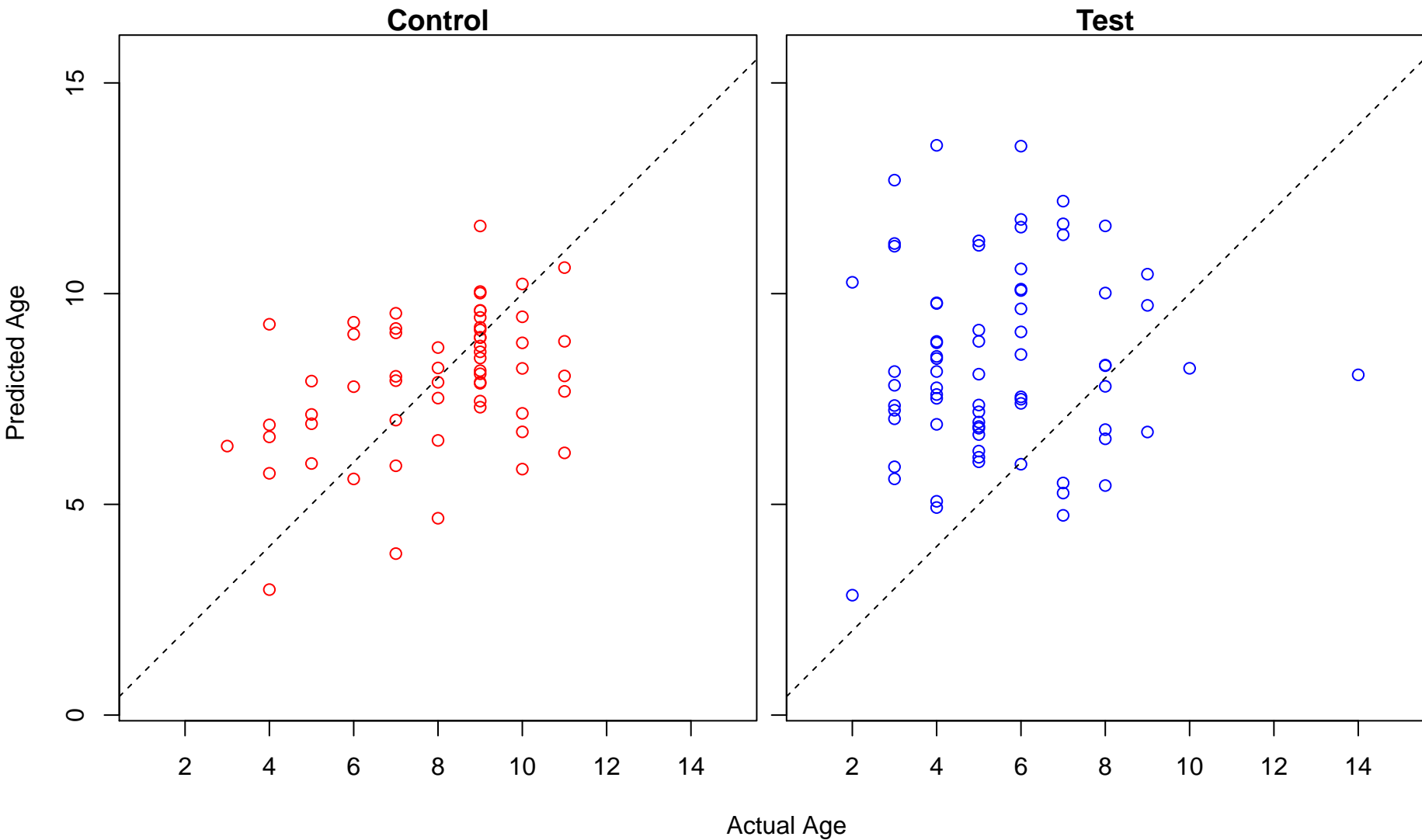
pigment accumulation (Score: 1.211495)



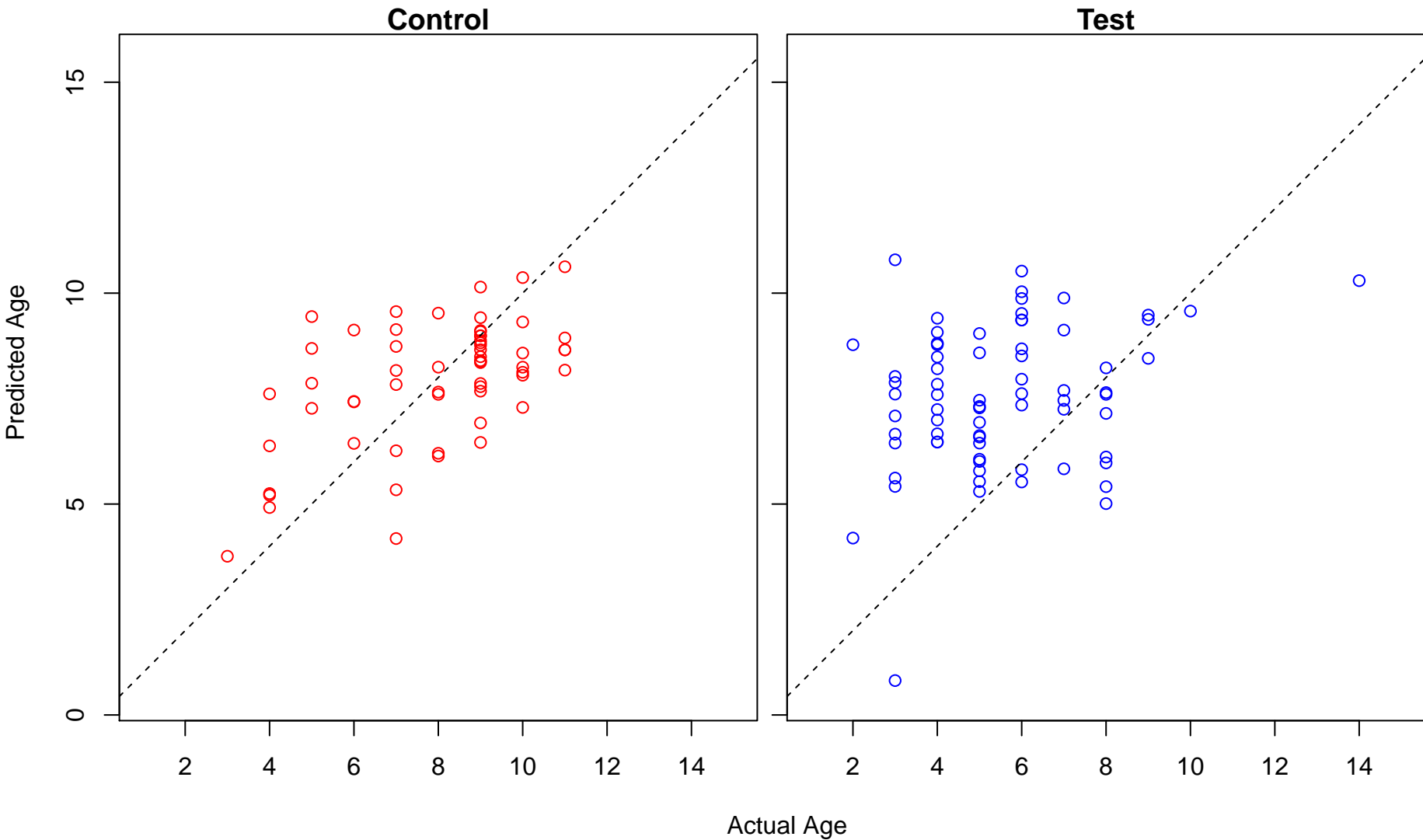
cellular pigment accumulation (Score: 1.211495)



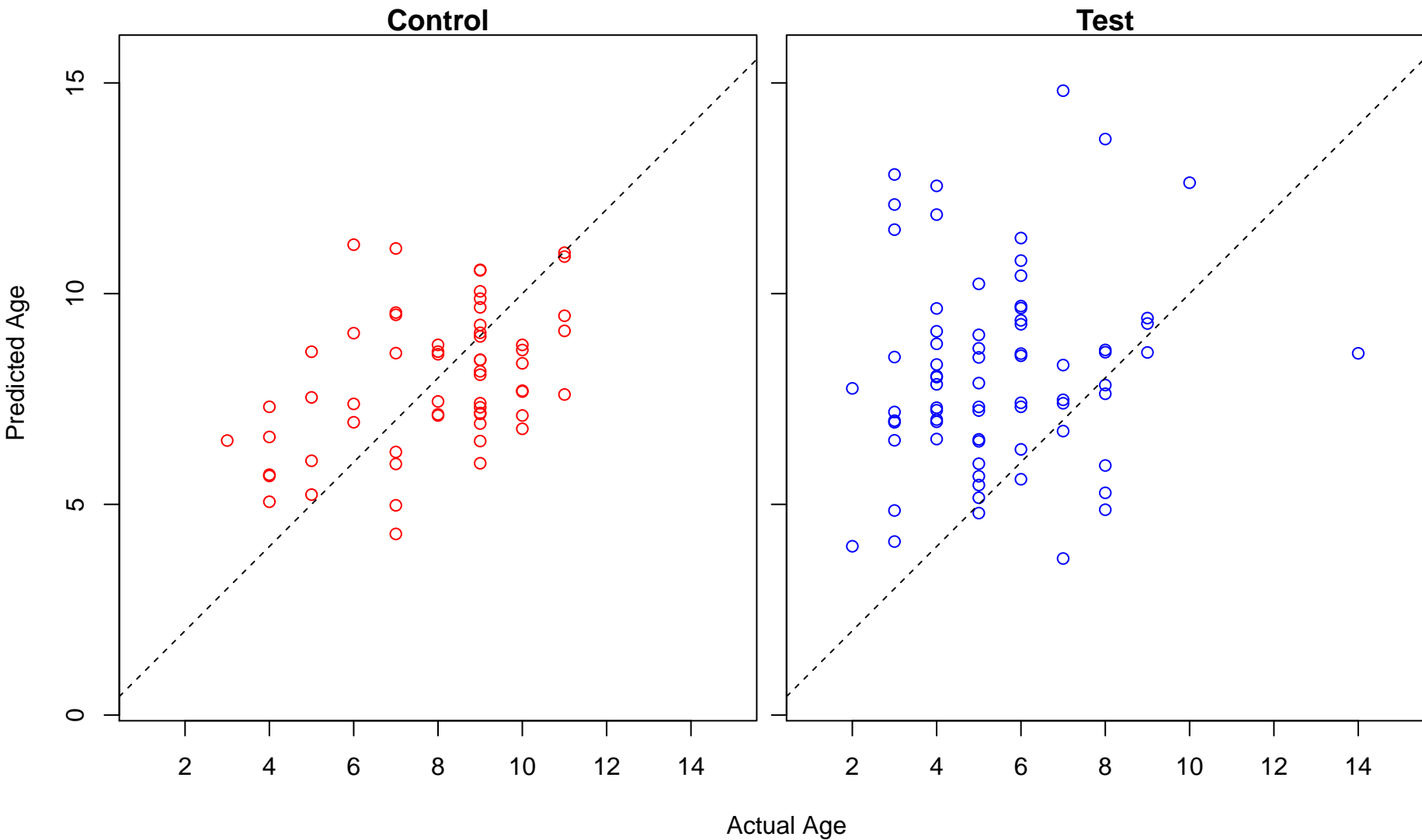
ER-nucleus signaling pathway (Score: 1.209465)



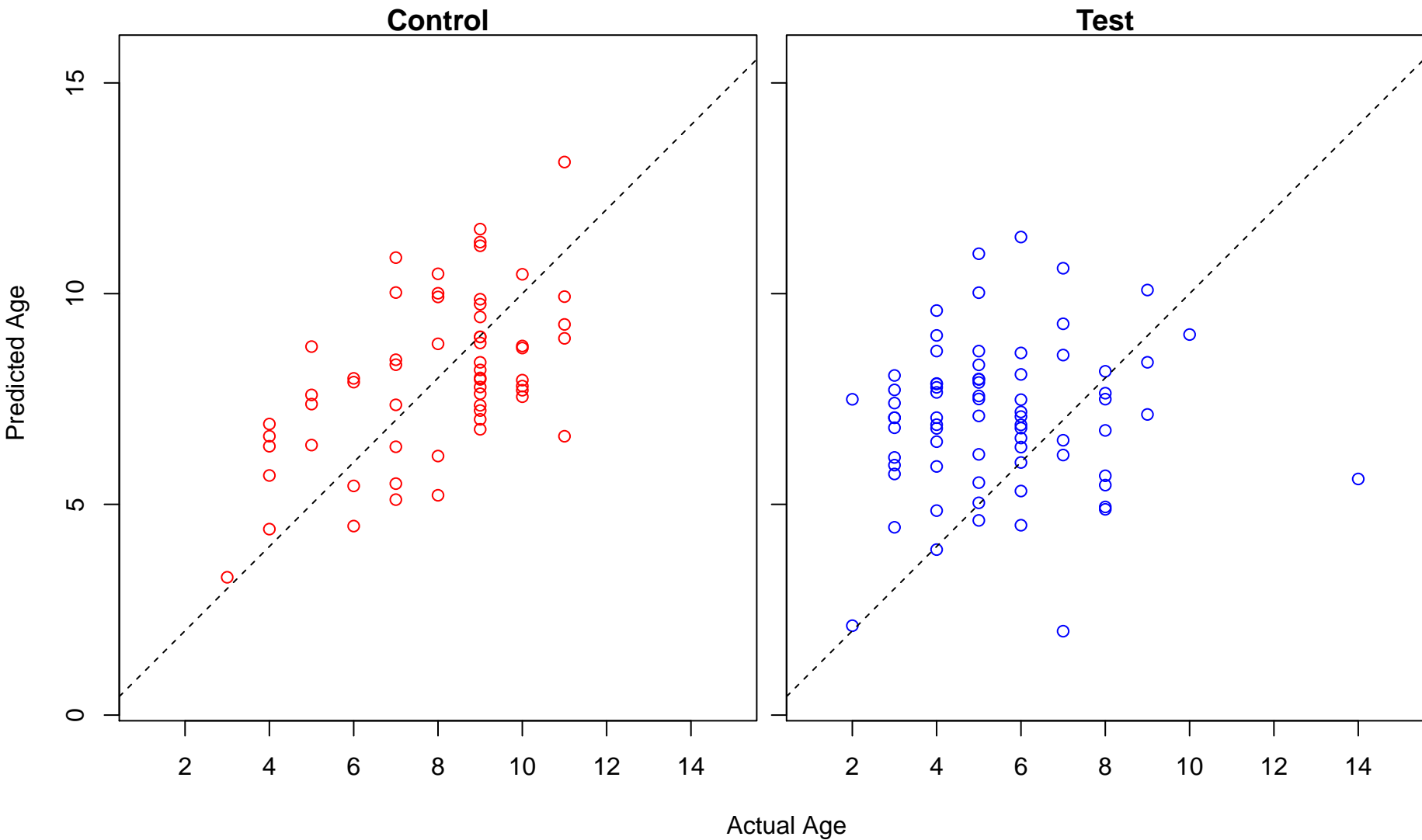
negative regulation of pathway-restricted SMAD protein phosphorylation (Score: 1.207423)



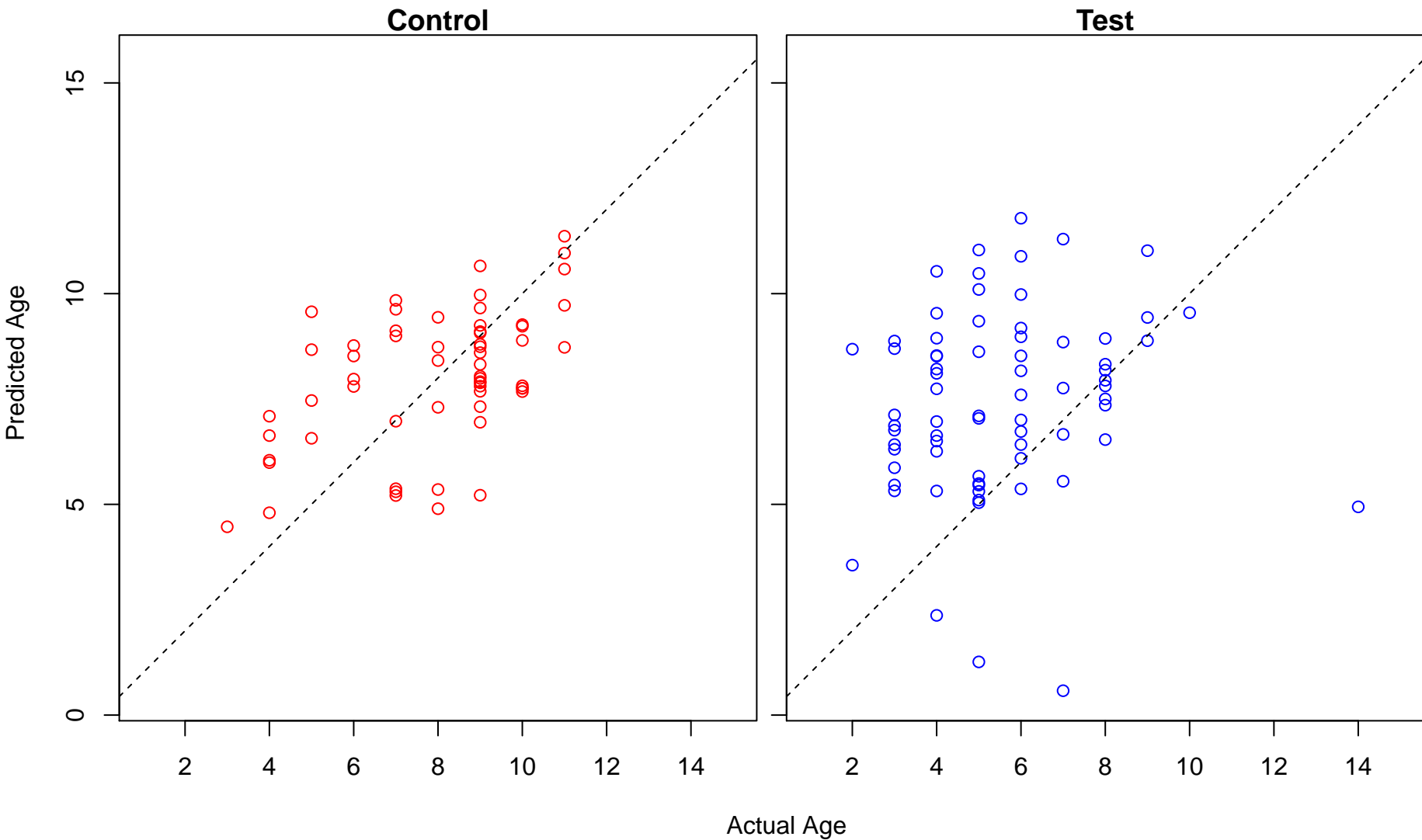
regulation of wound healing (Score: 1.206998)



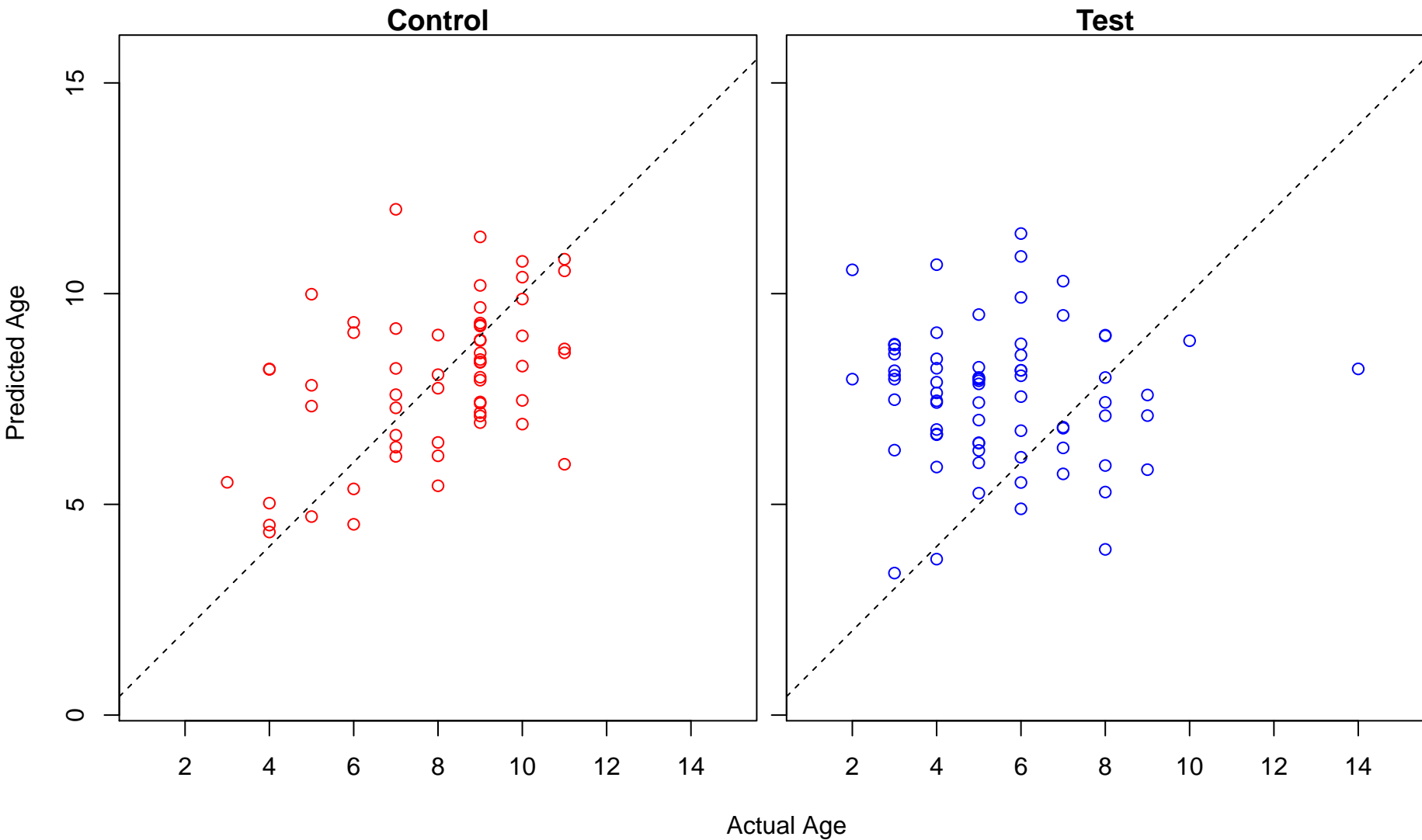
negative regulation of protein dephosphorylation (Score: 1.206149)



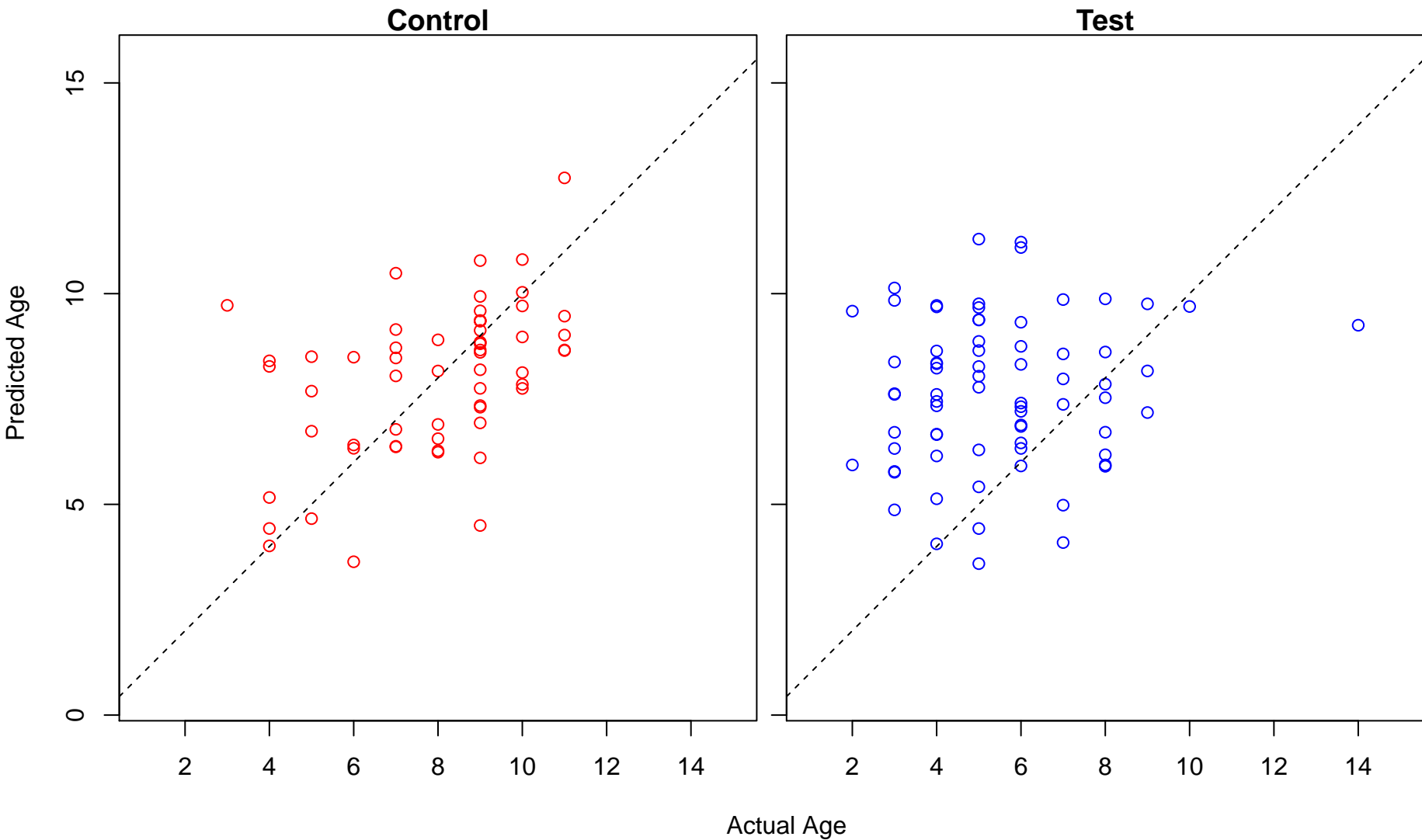
cellular response to endogenous stimulus (Score: 1.204842)



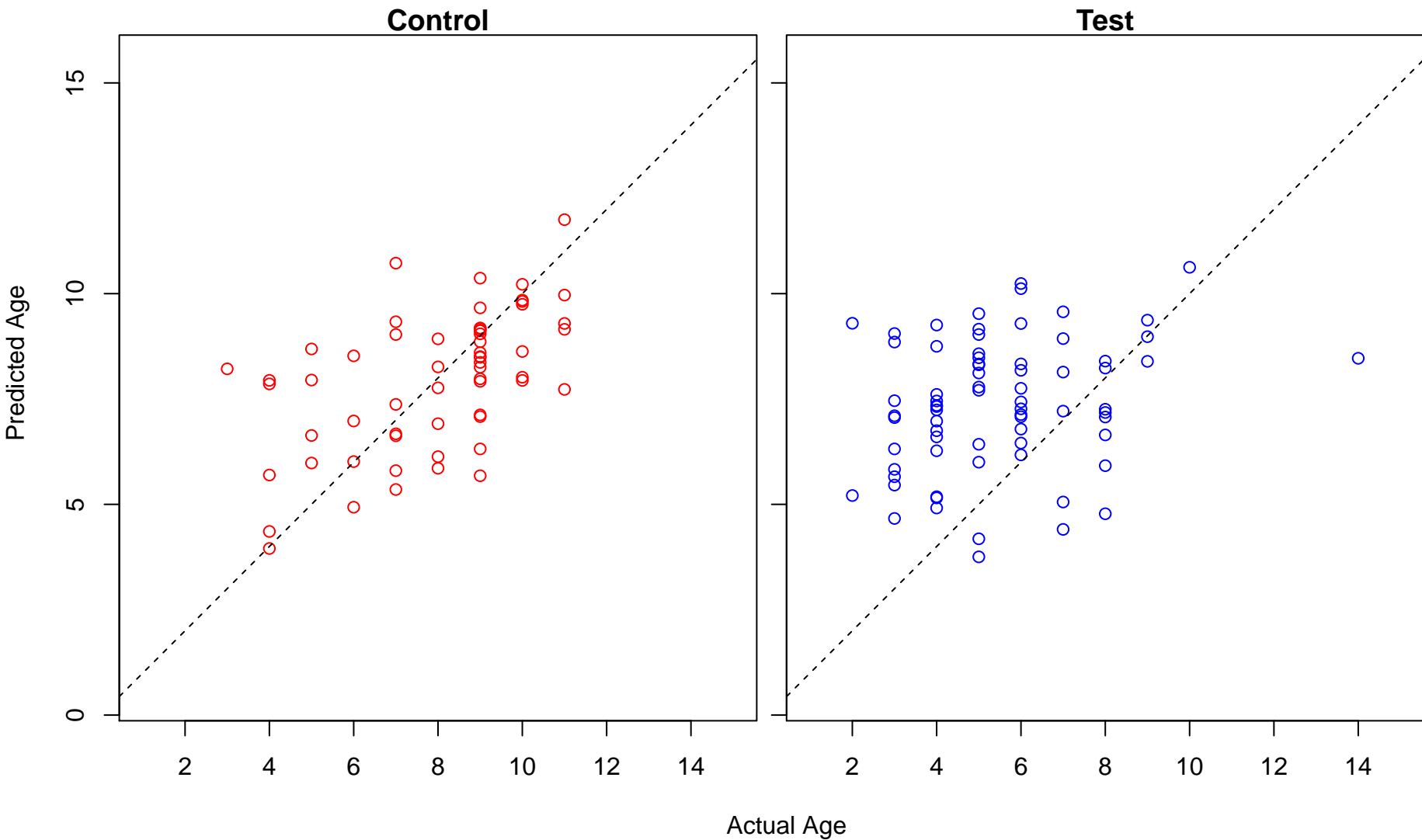
nucleoside monophosphate metabolic process (Score: 1.203535)



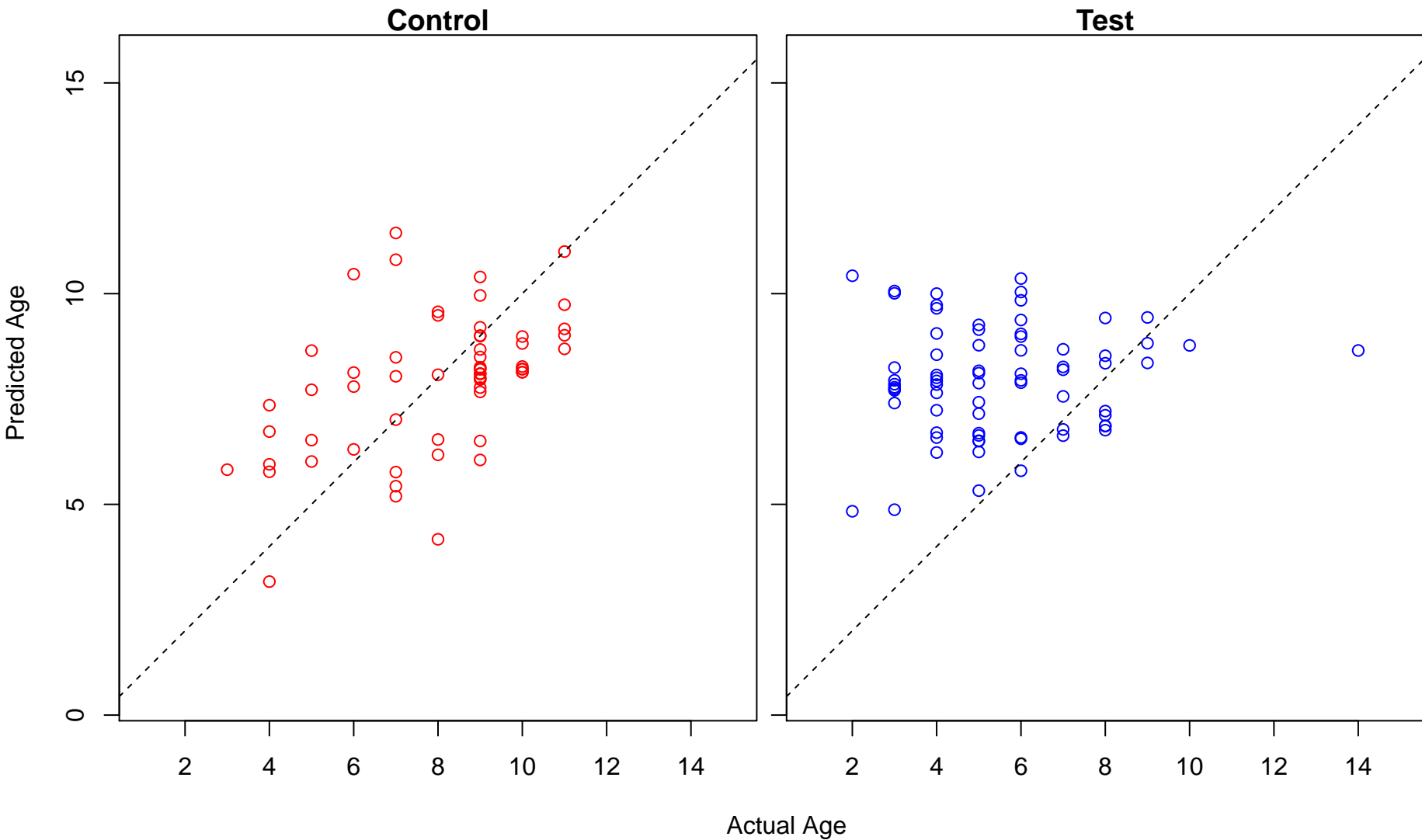
SRP-dependent cotranslational protein targeting to membrane (Score: 1.202372)



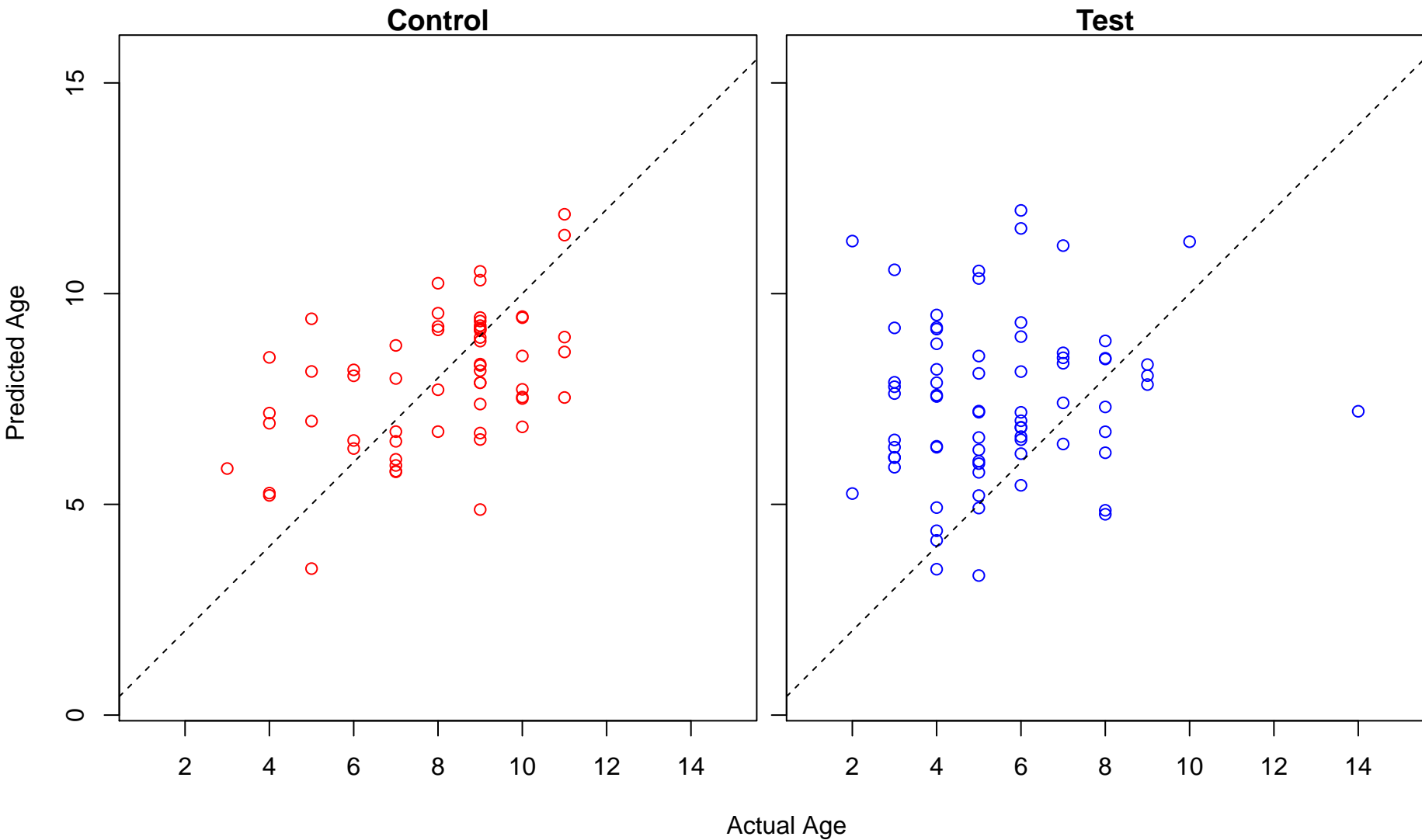
RNA biosynthetic process (Score: 1.200118)



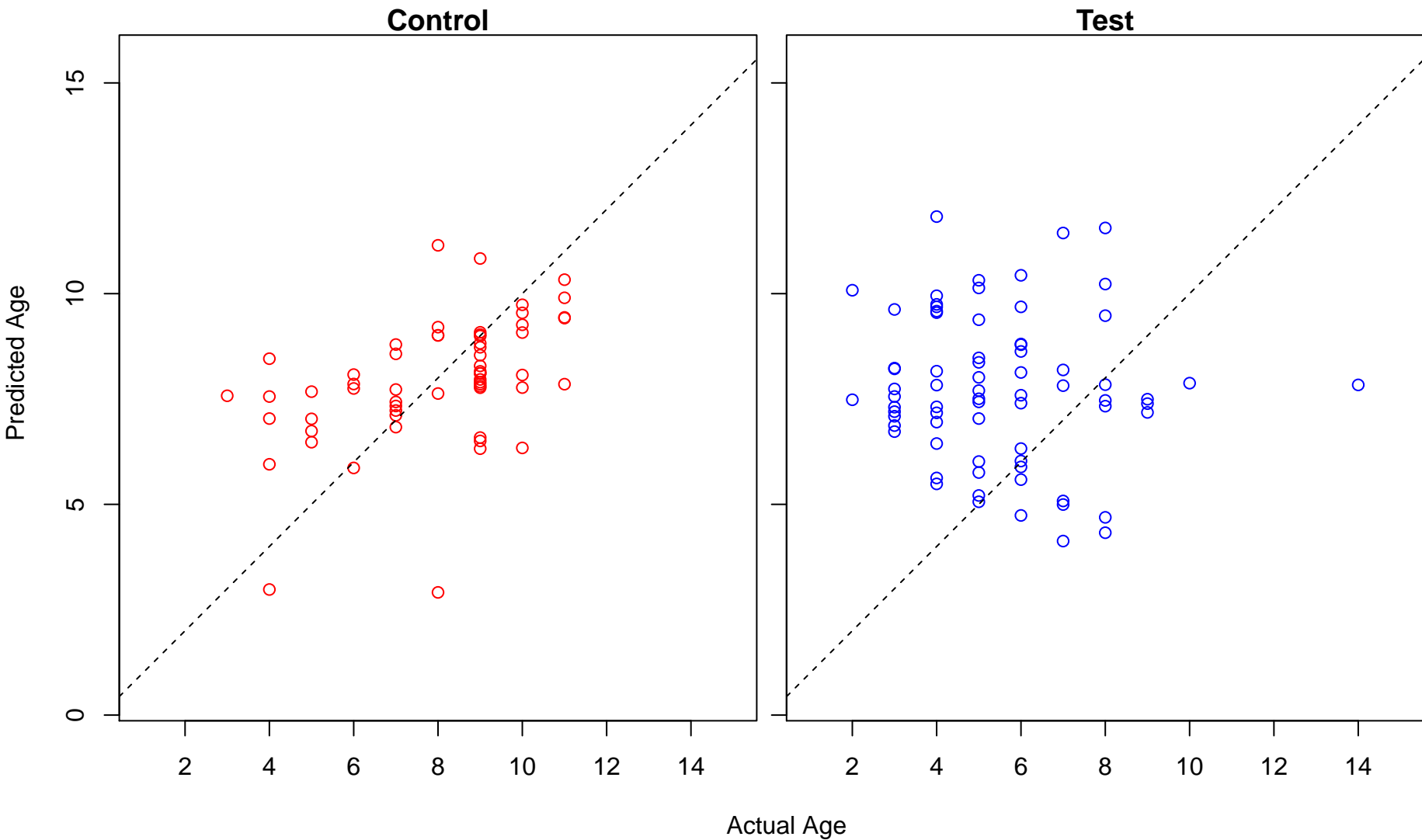
regulation of intracellular transport (Score: 1.199451)



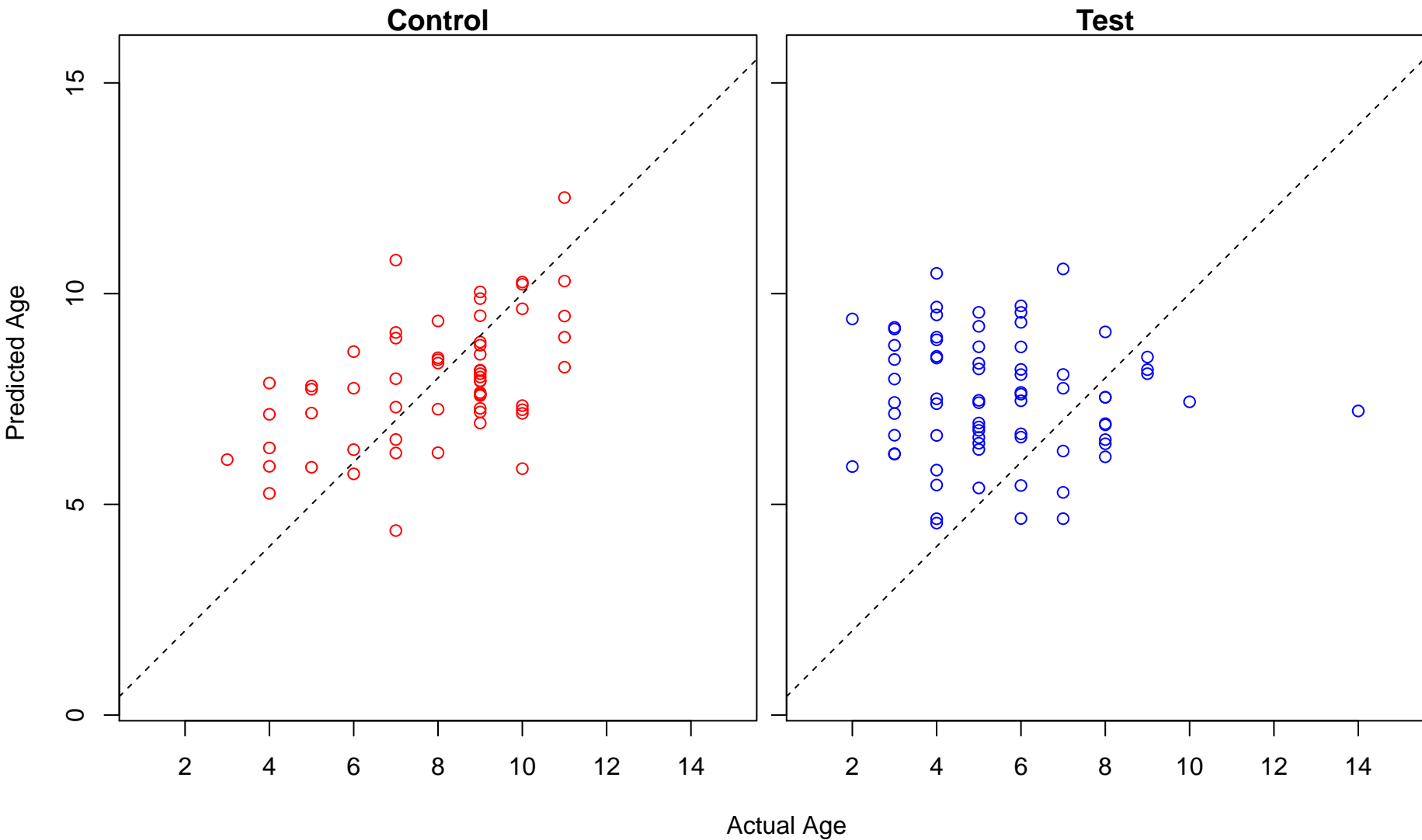
natural killer cell activation (Score: 1.198338)



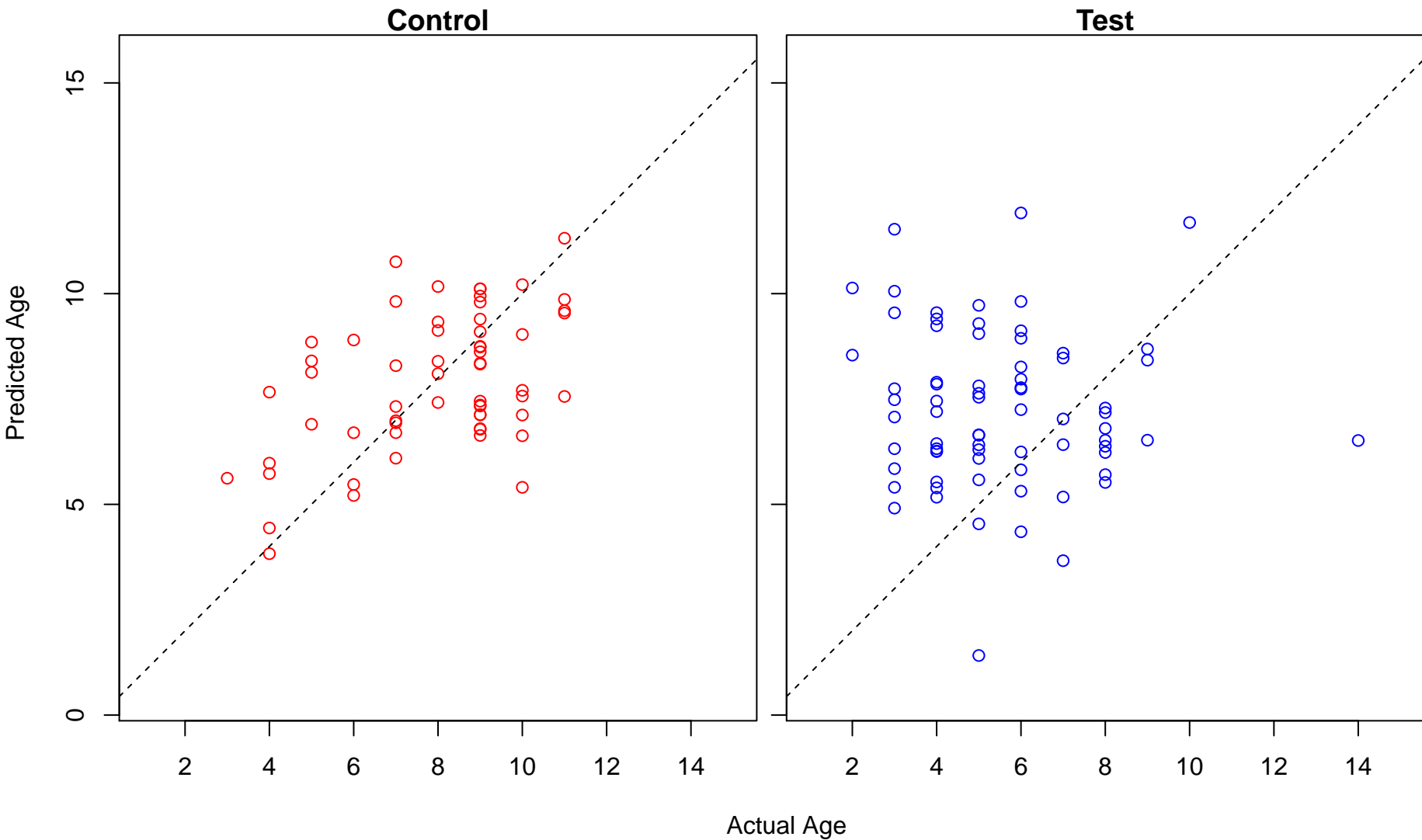
synaptic transmission, dopaminergic (Score: 1.196519)



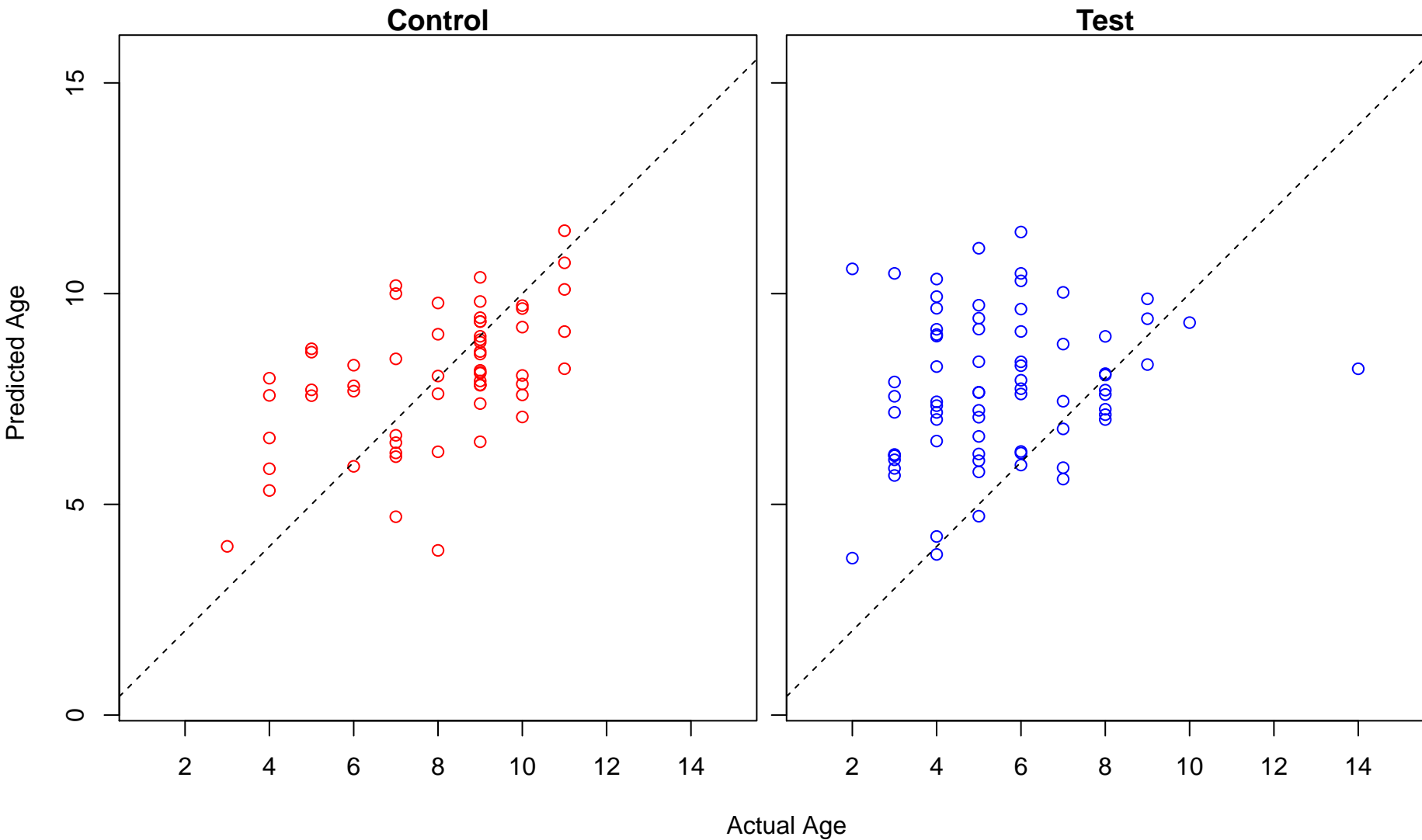
establishment of epithelial cell apical/basal polarity (Score: 1.195890)



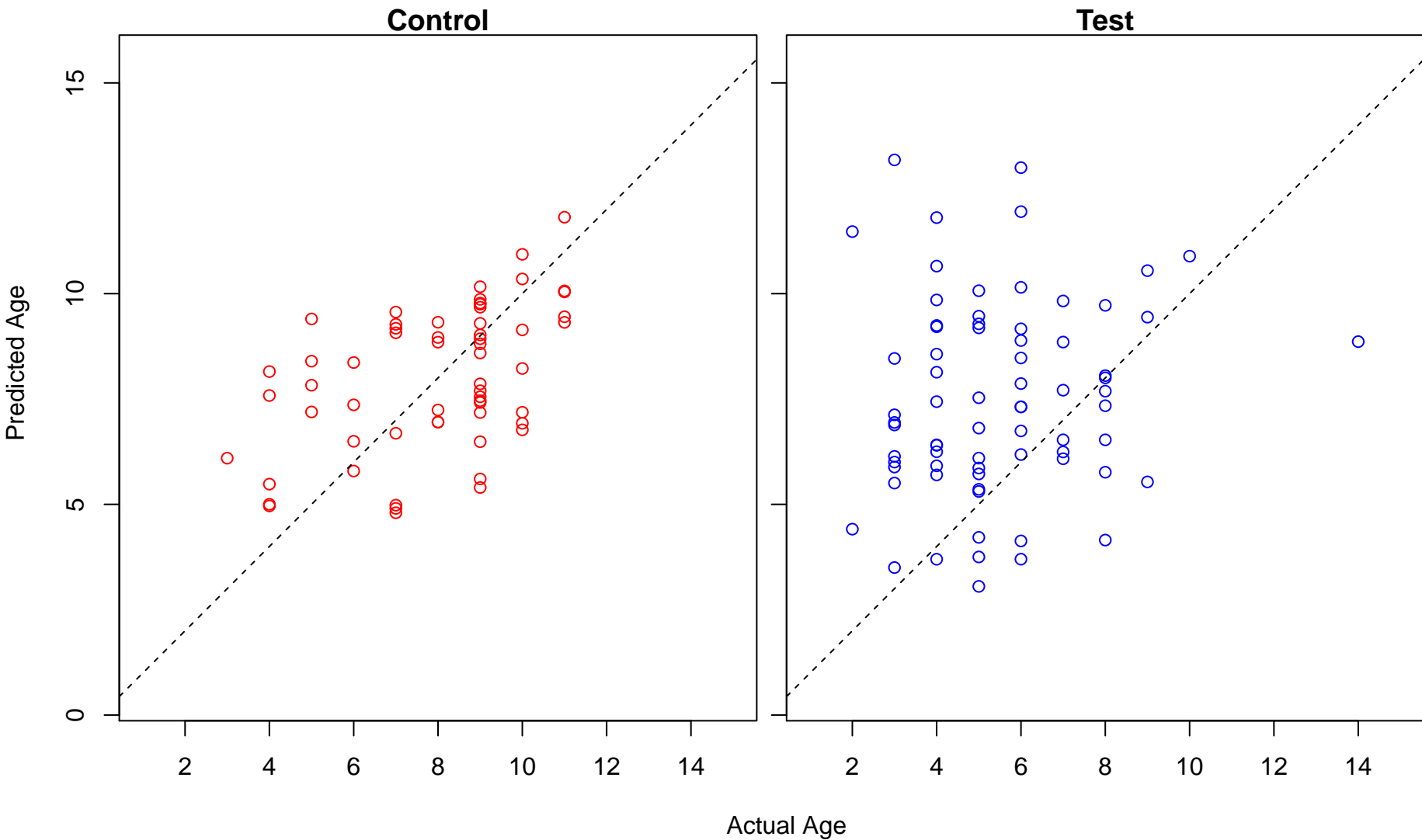
telomere capping (Score: 1.195588)



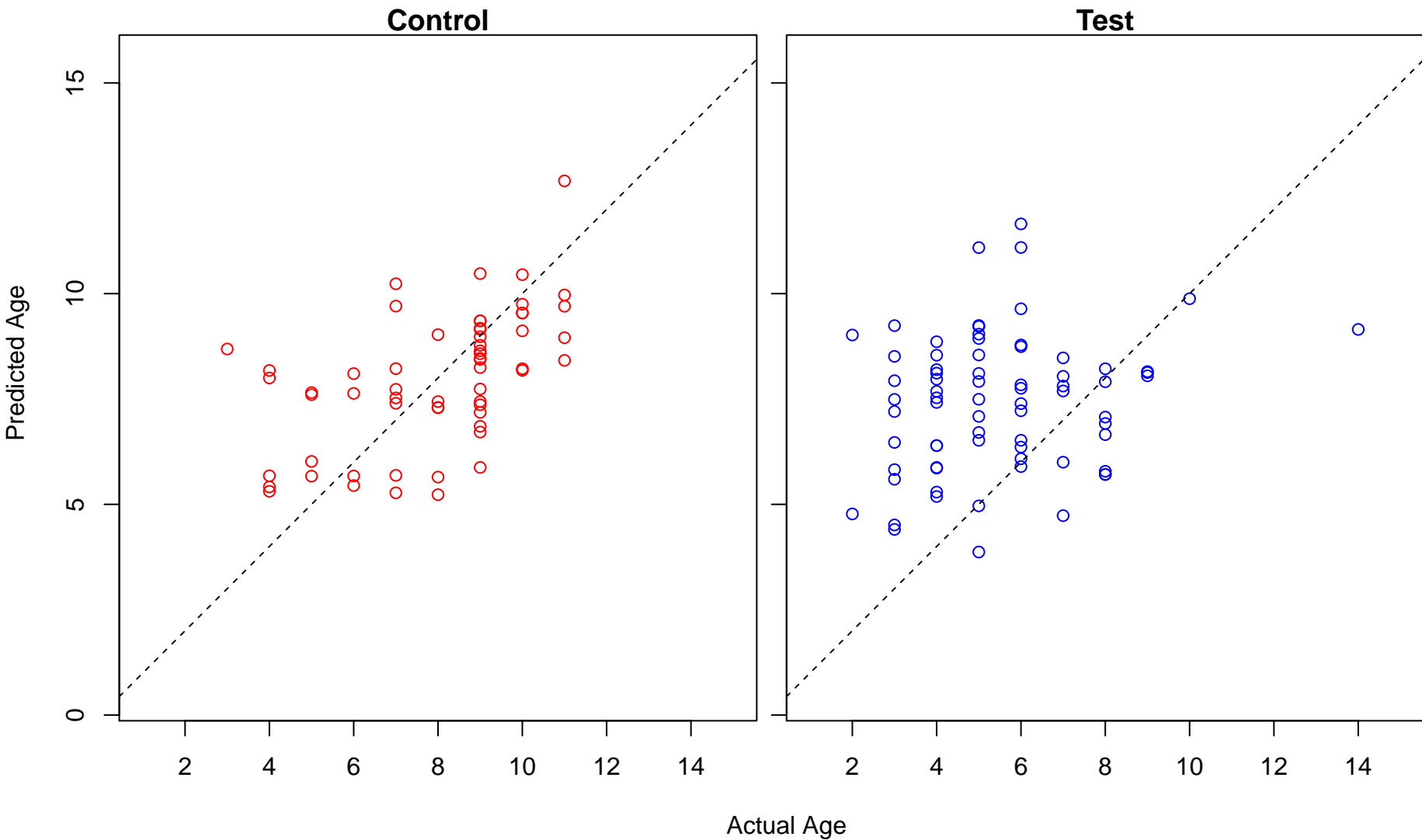
regulation of cell communication (Score: 1.195588)



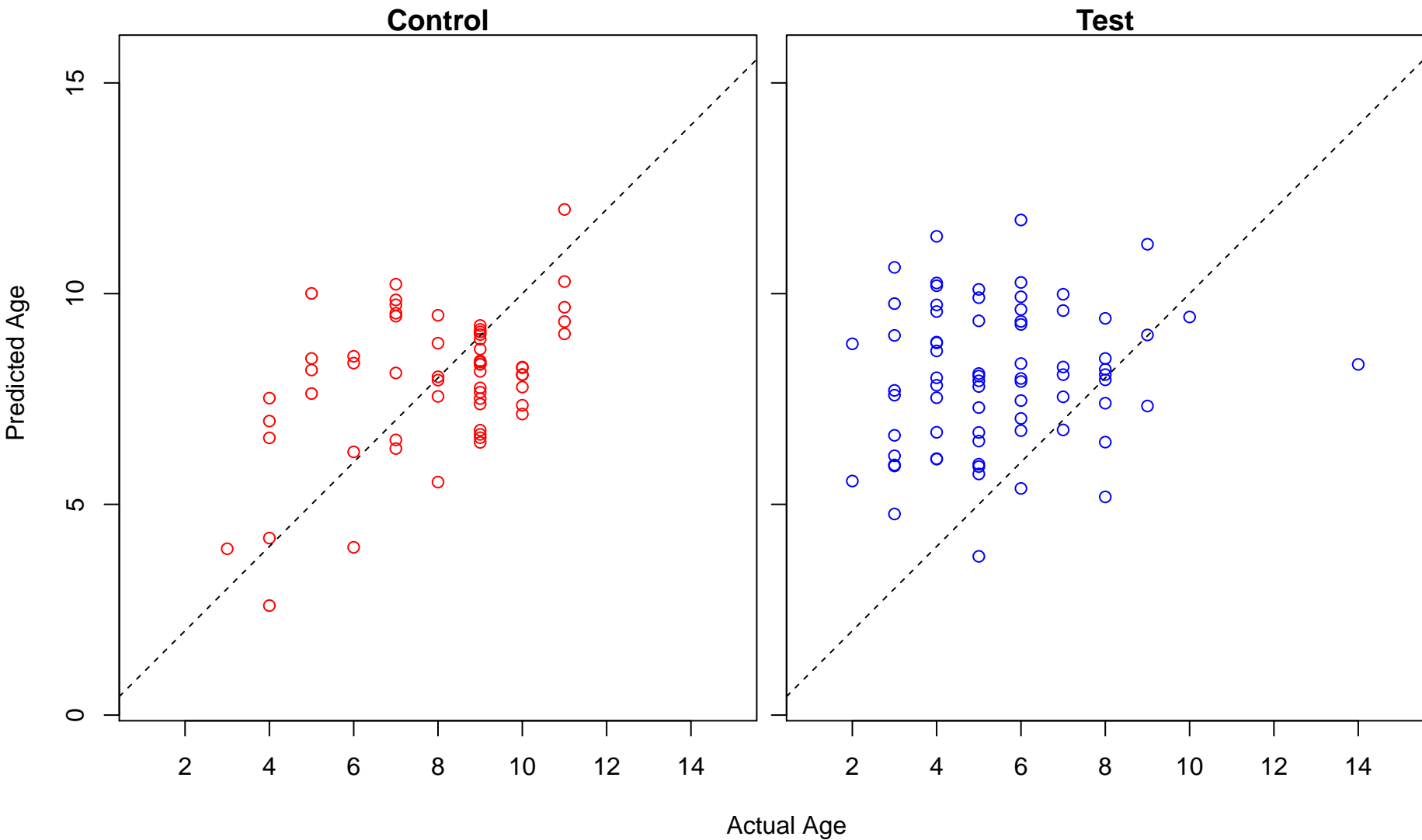
actin filament organization (Score: 1.195372)



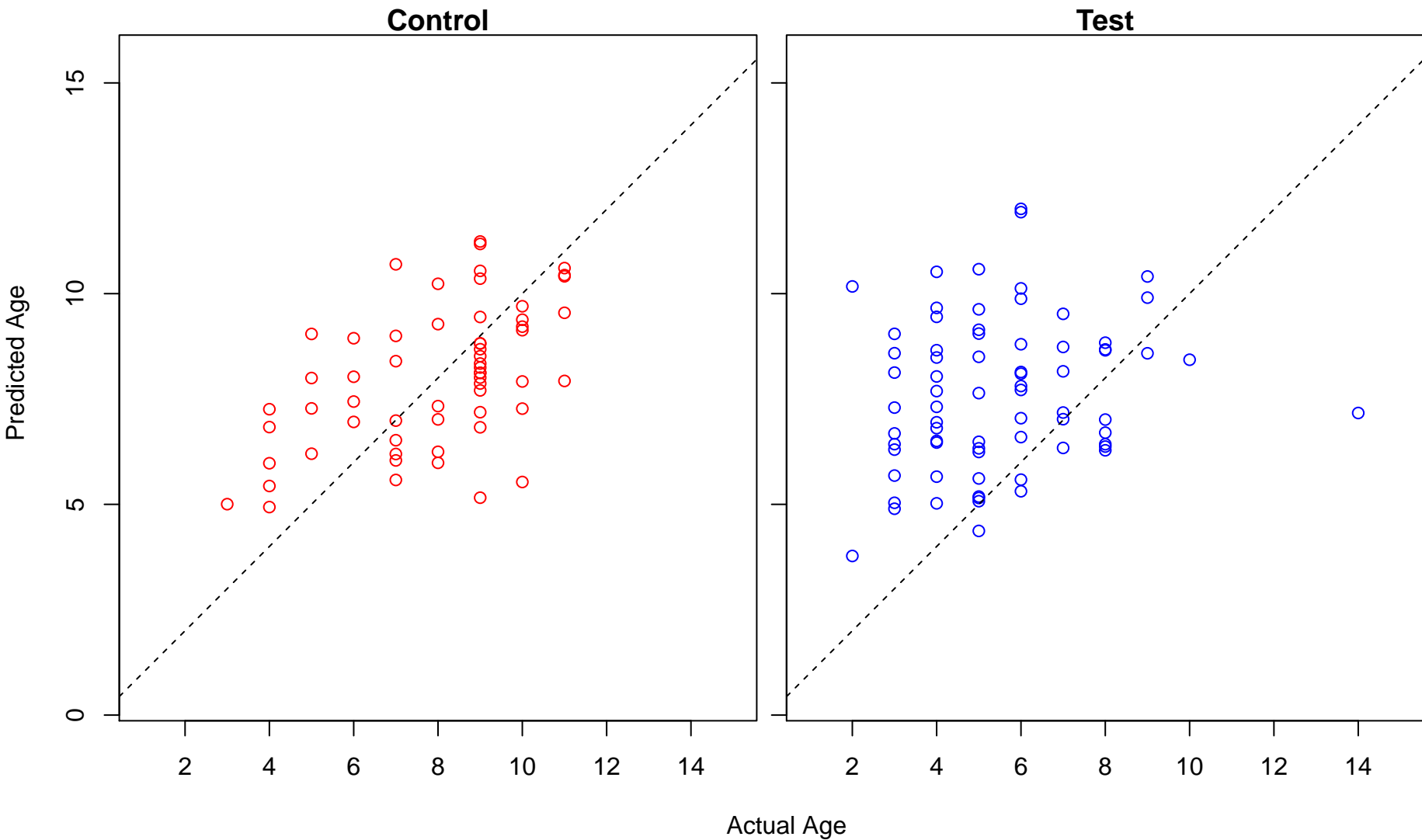
intracellular protein transport (Score: 1.193635)



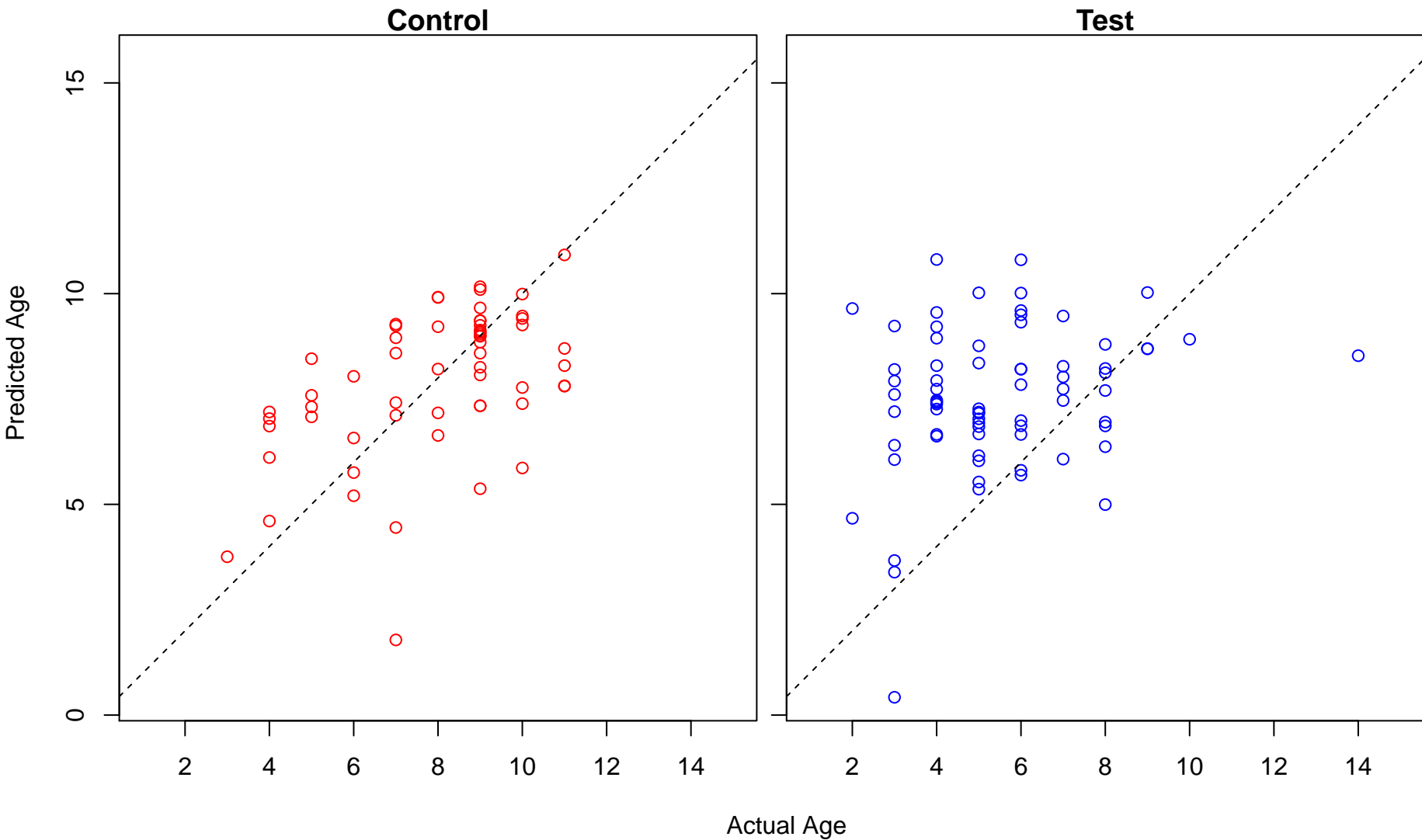
RNA methylation (Score: 1.193606)



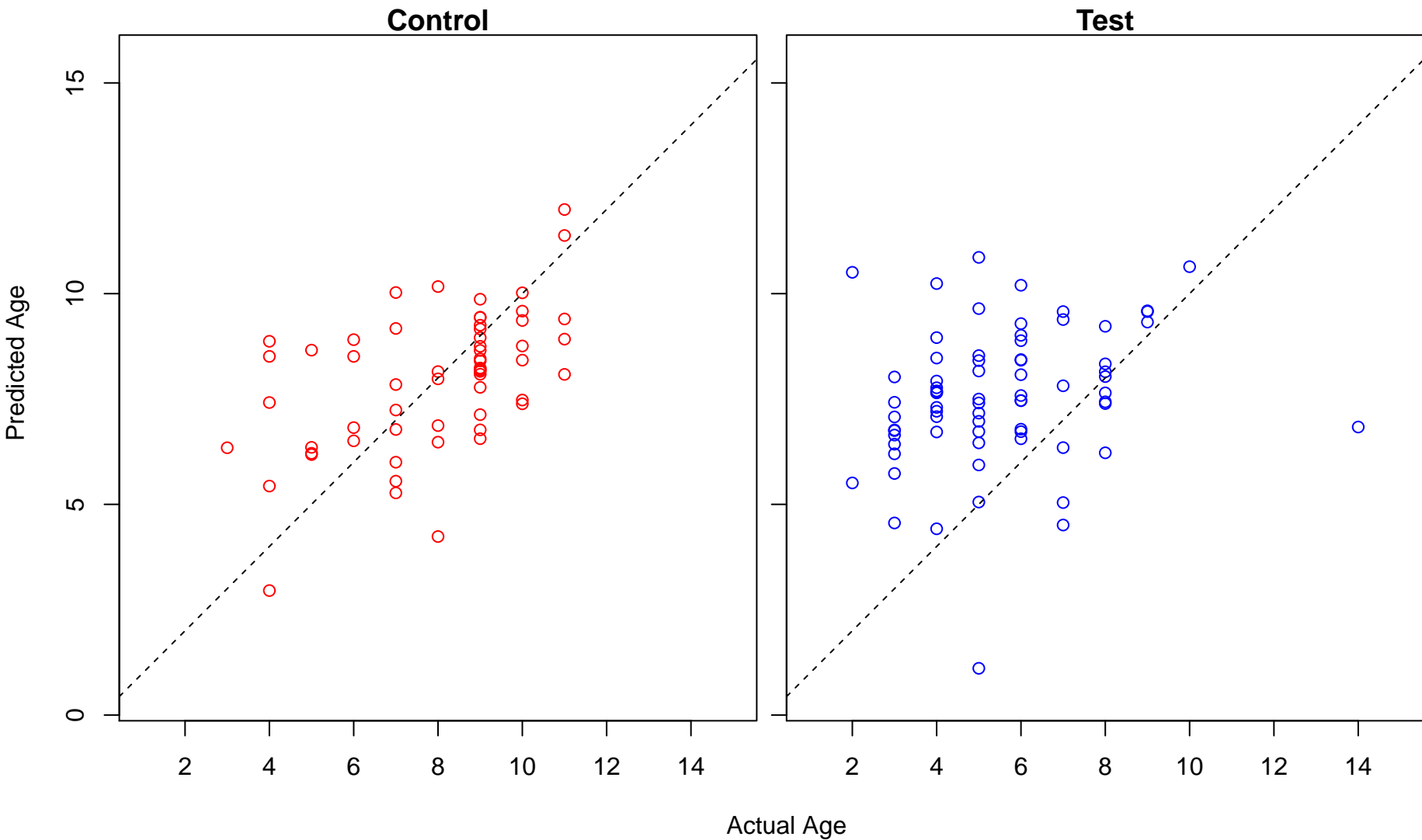
cell development (Score: 1.191368)



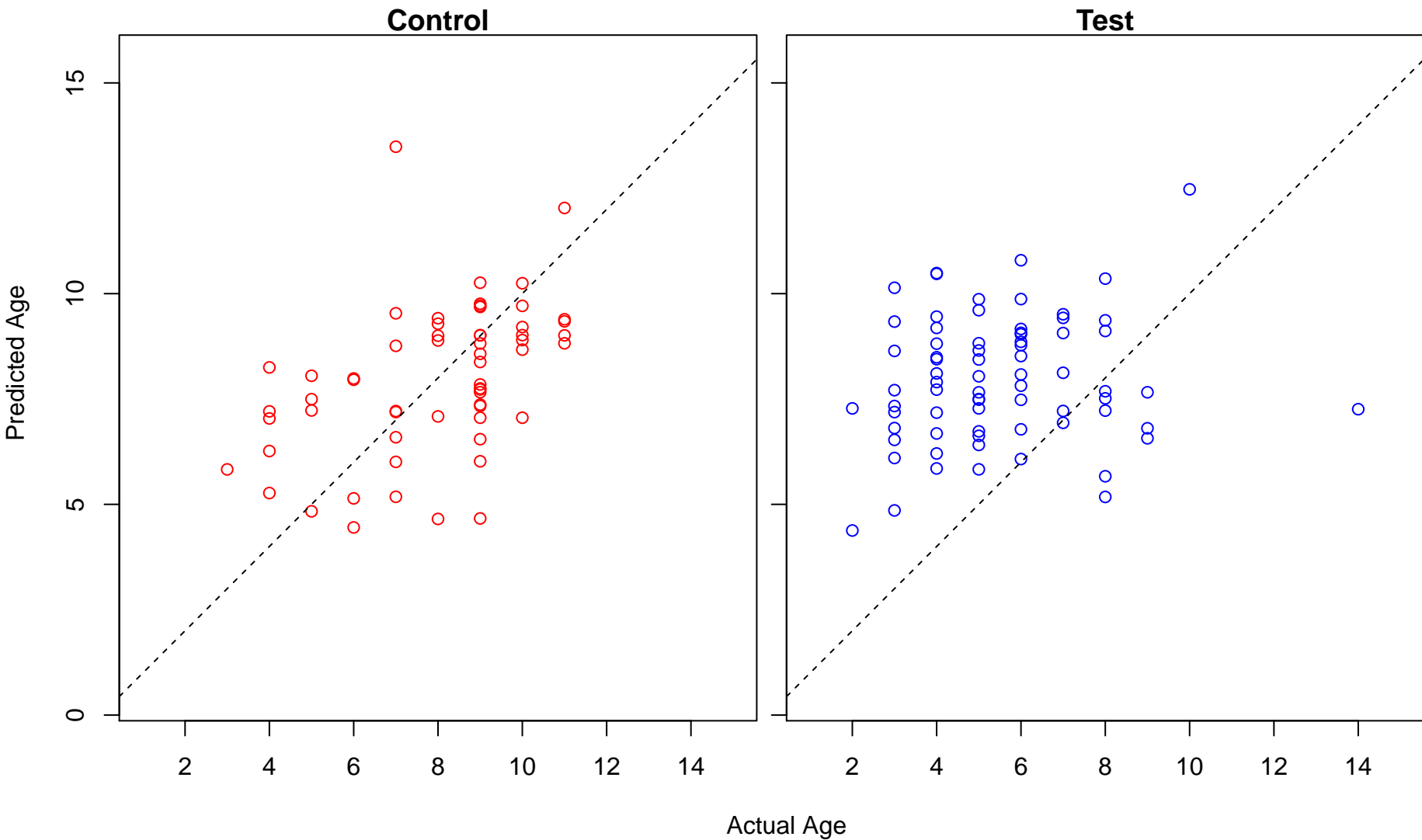
negative regulation of receptor binding (Score: 1.190865)



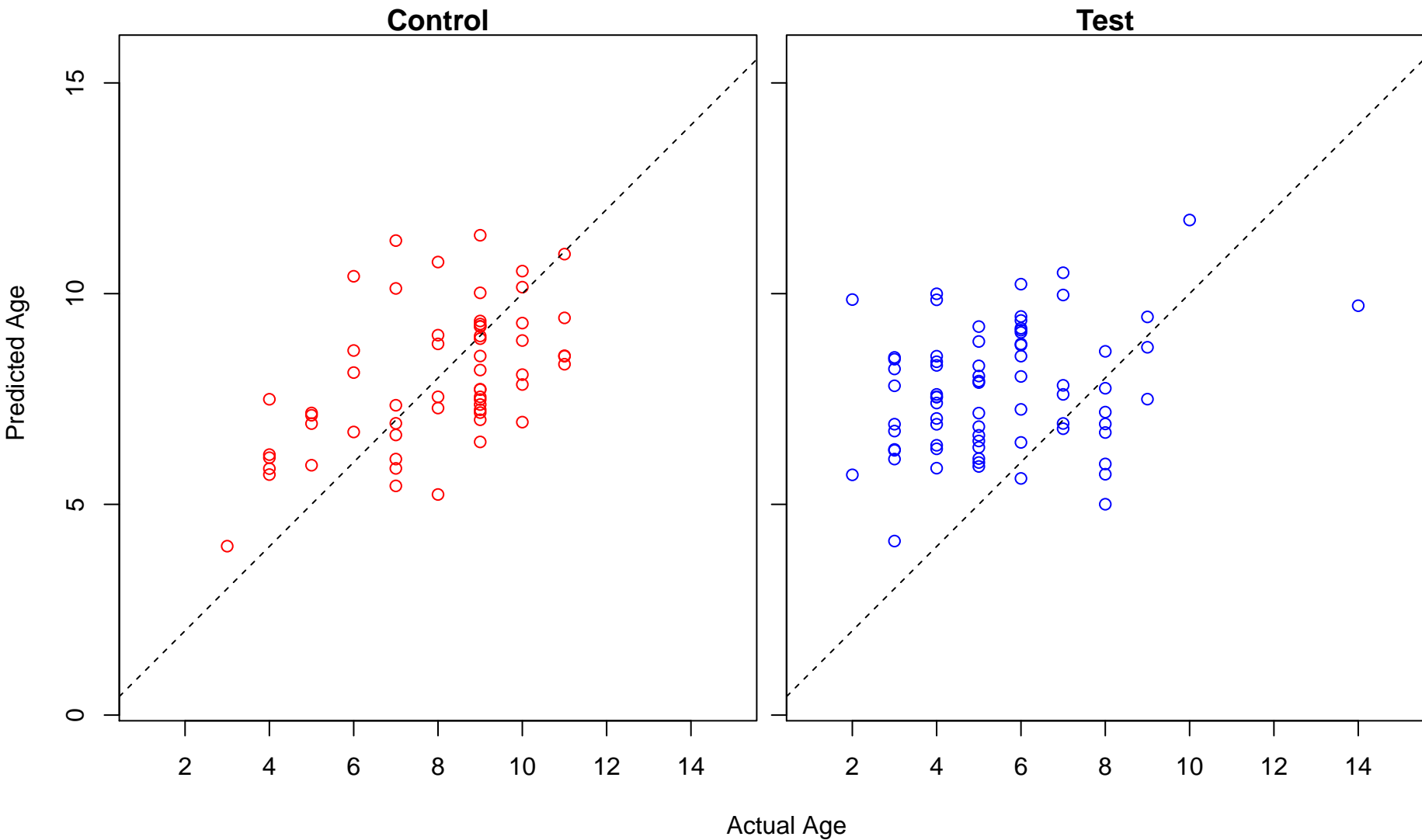
protein metabolic process (Score: 1.190678)



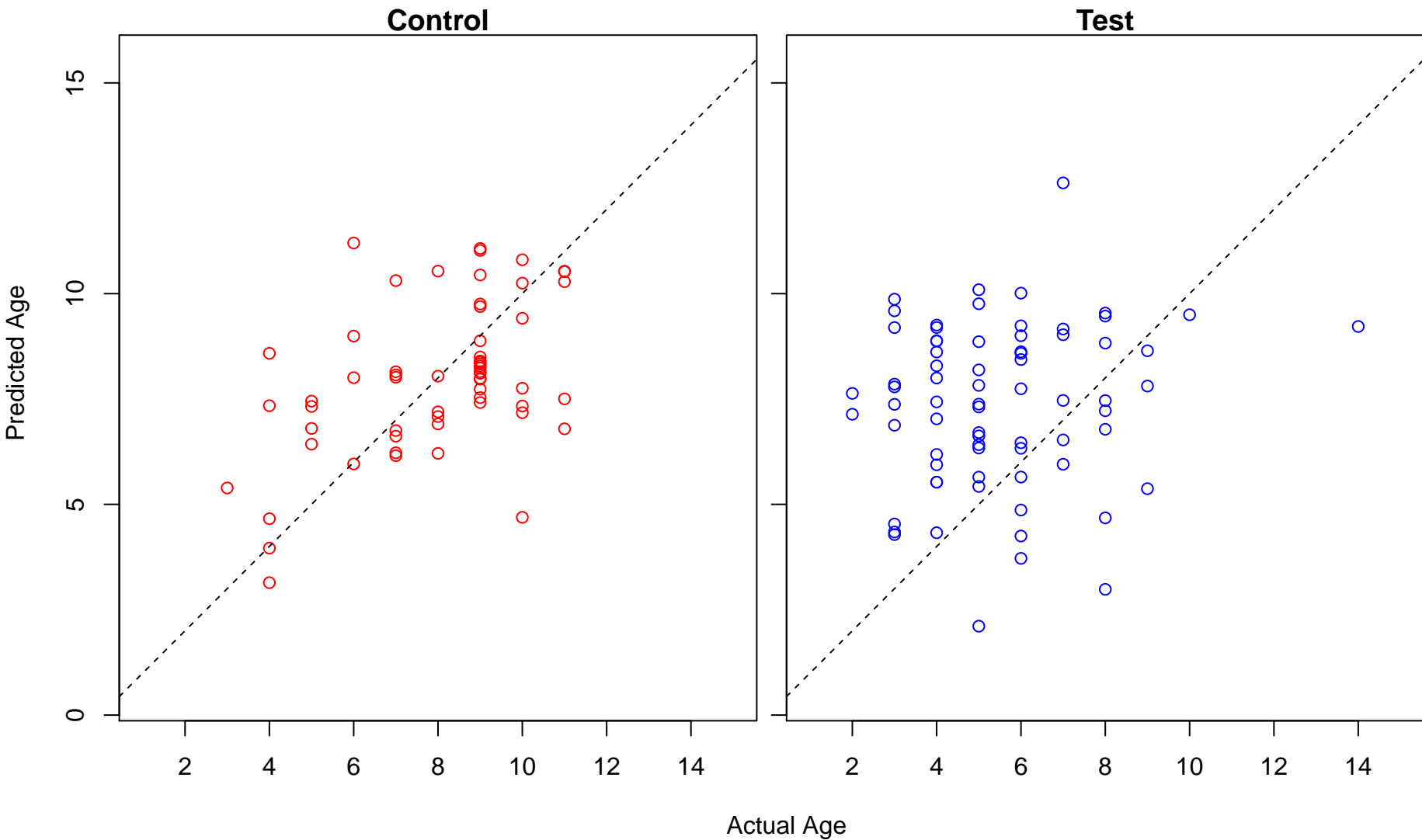
nonmotile primary cilium assembly (Score: 1.190394)



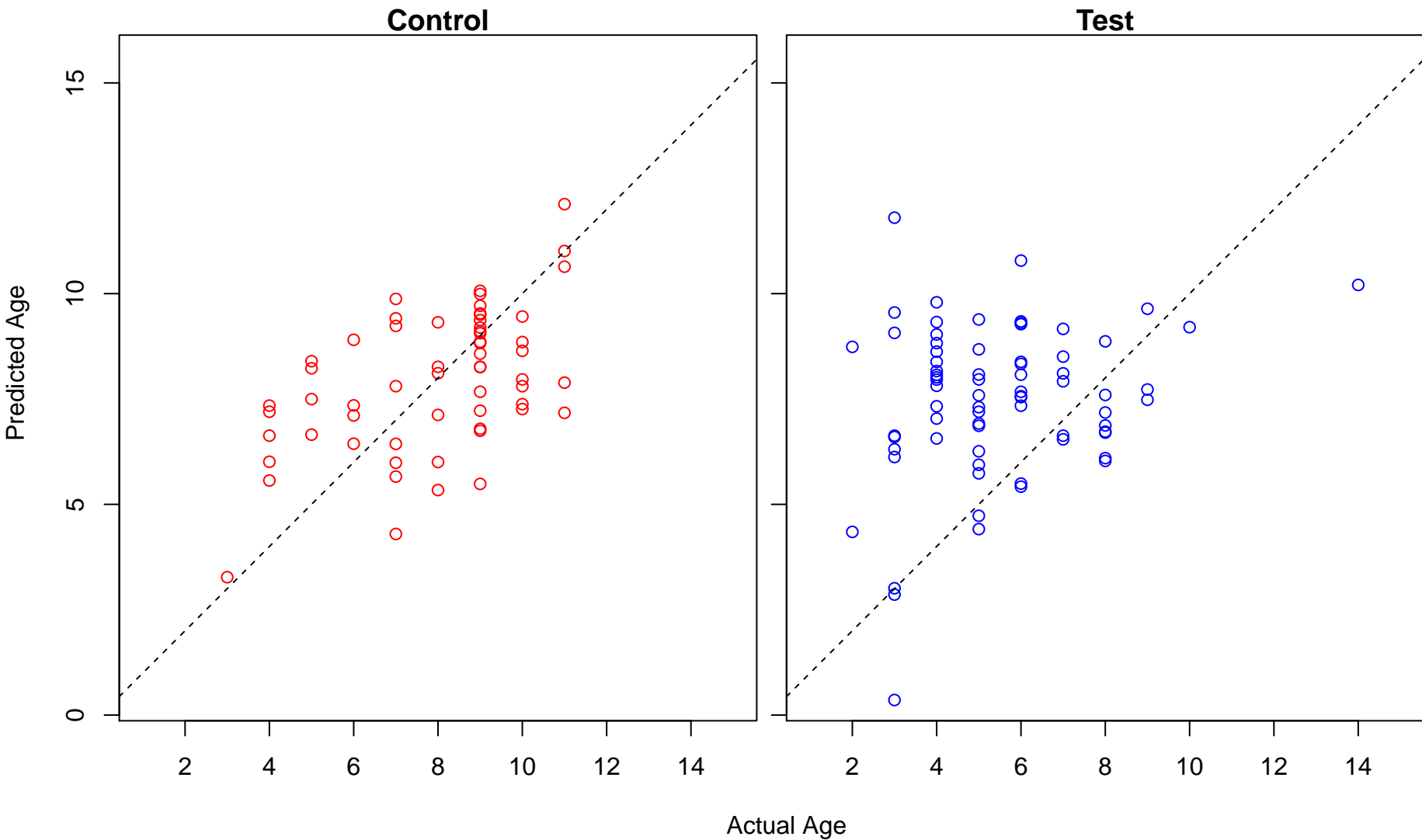
positive regulation of mitochondrion organization (Score: 1.189922)



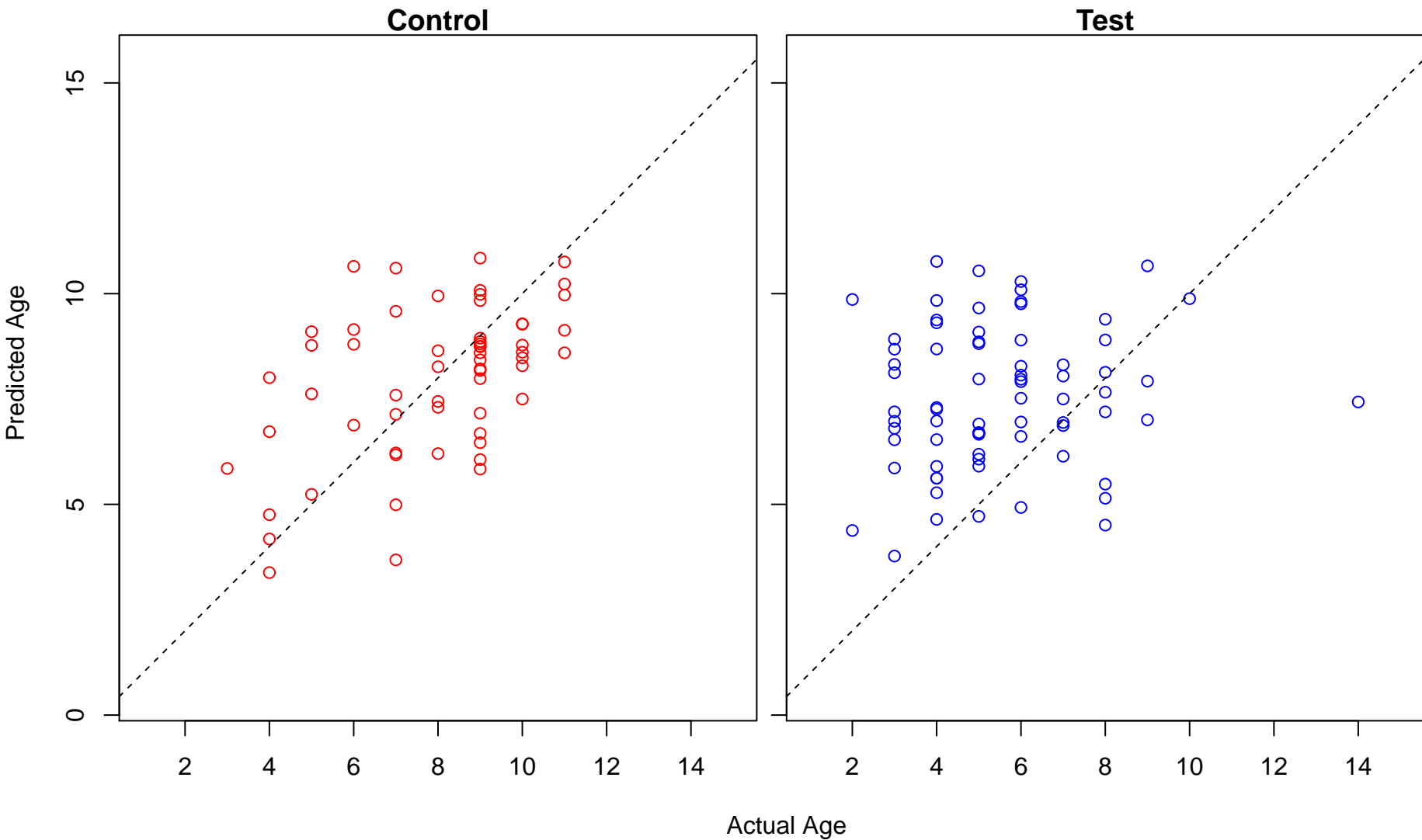
endoplasmic reticulum unfolded protein response (Score: 1.189811)



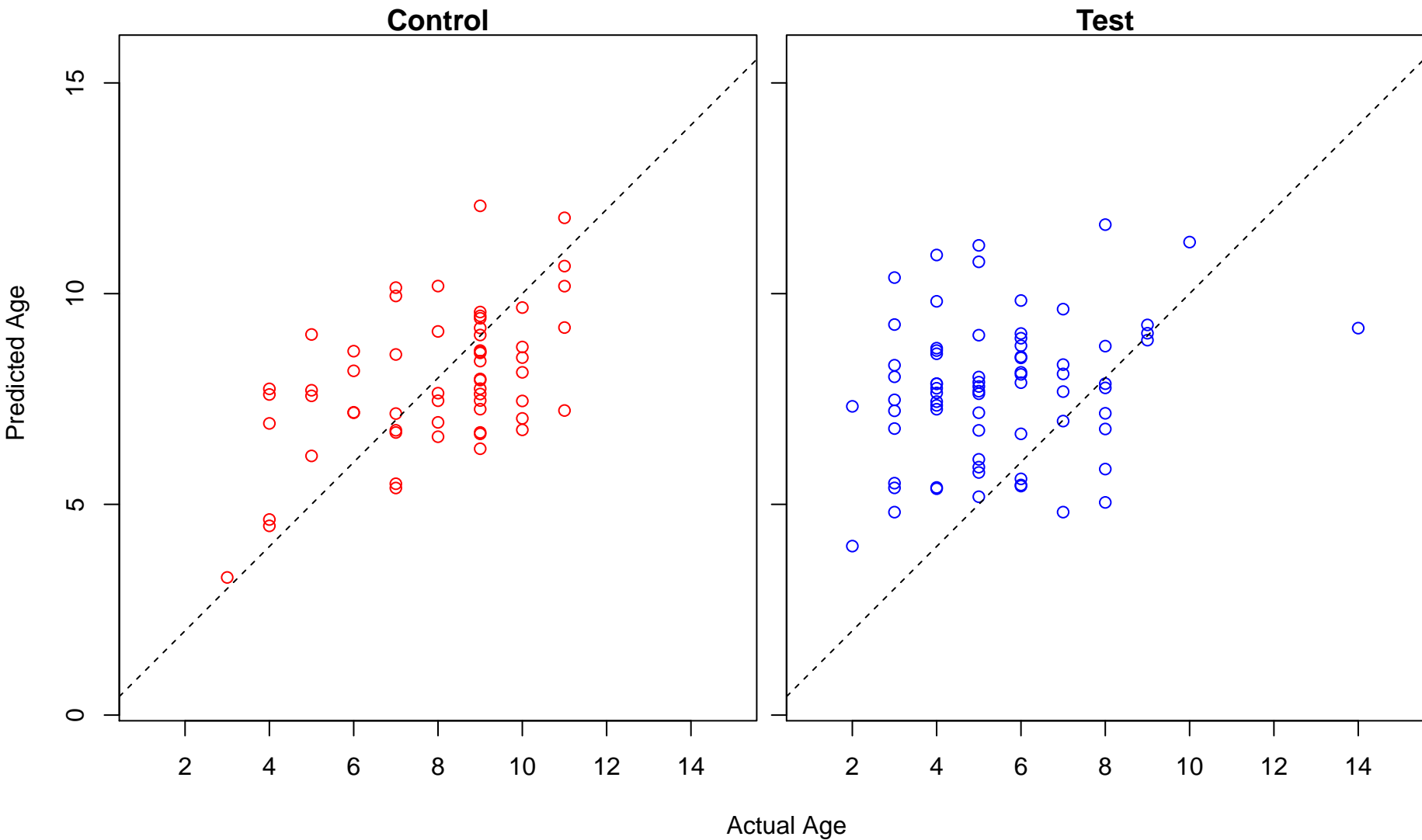
regulation of heart growth (Score: 1.189015)



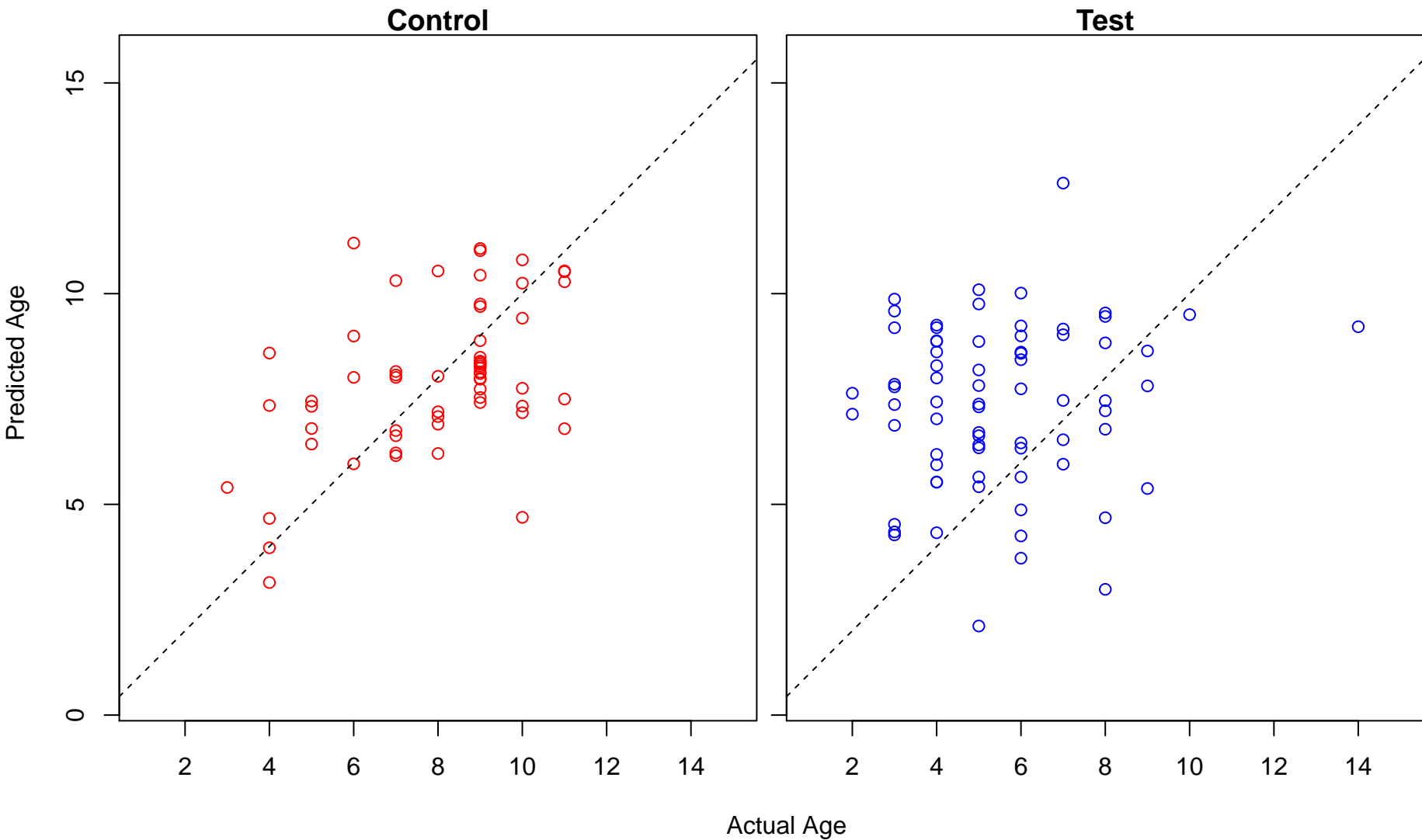
organelle localization (Score: 1.187220)



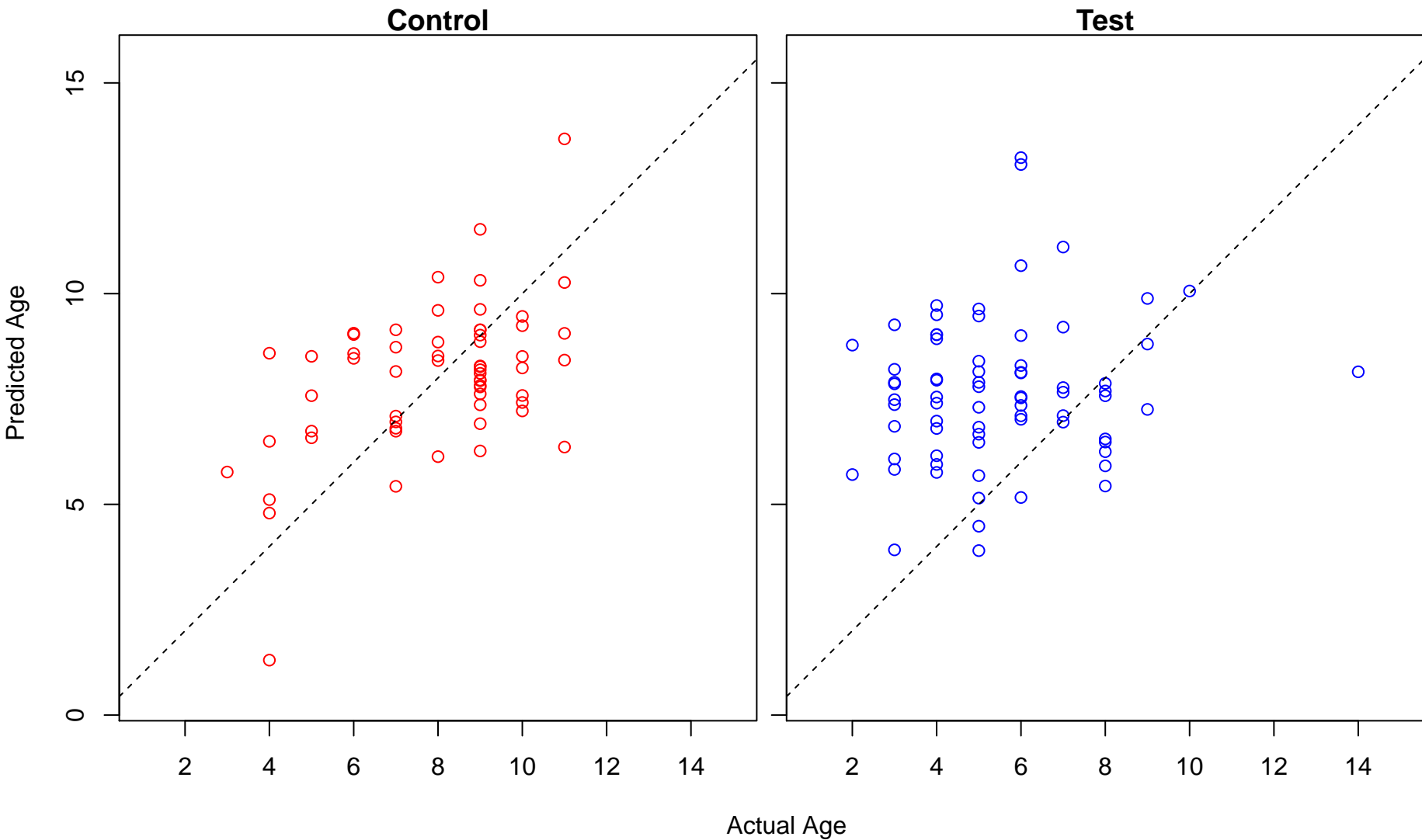
thymic T cell selection (Score: 1.186861)



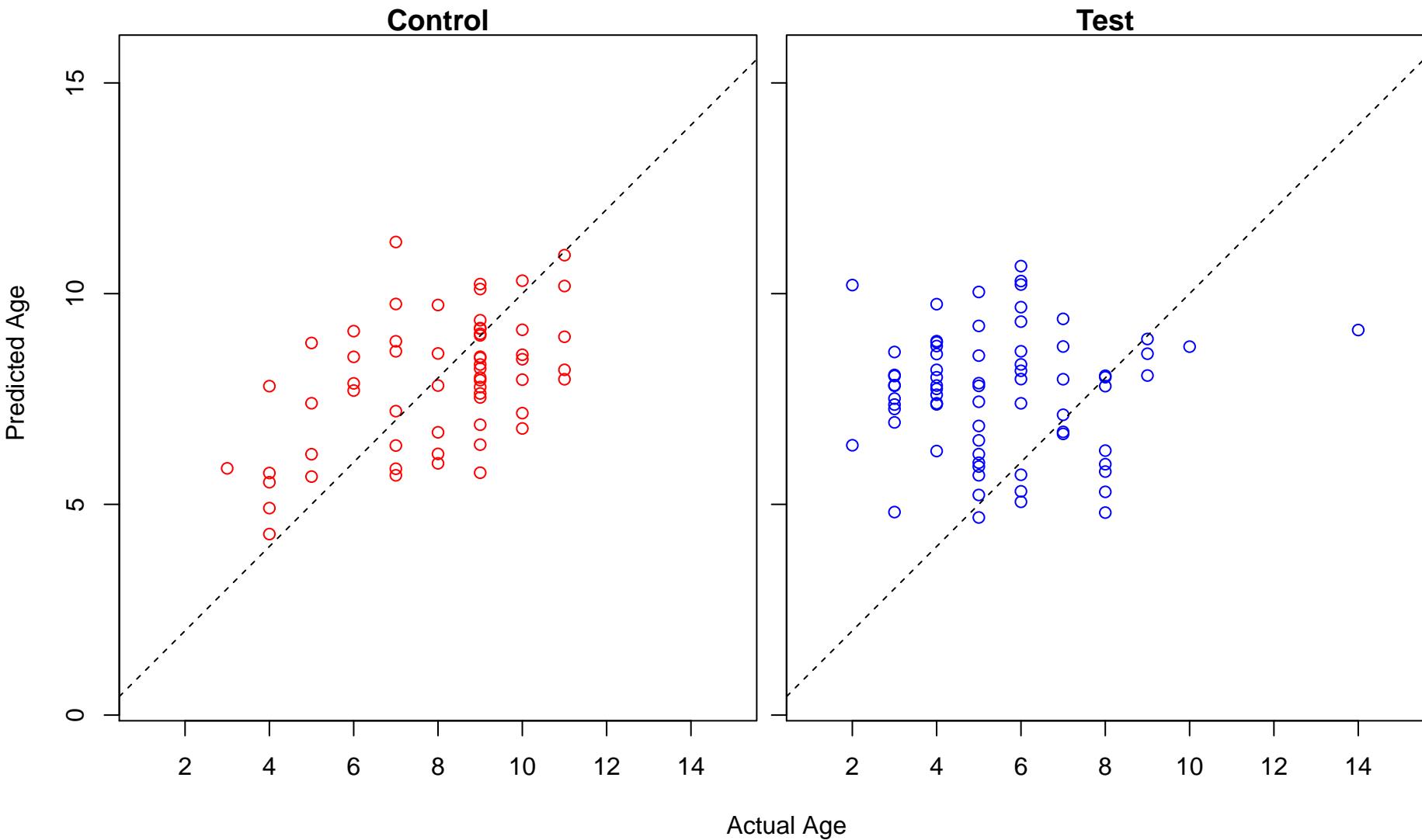
cellular response to unfolded protein (Score: 1.186729)



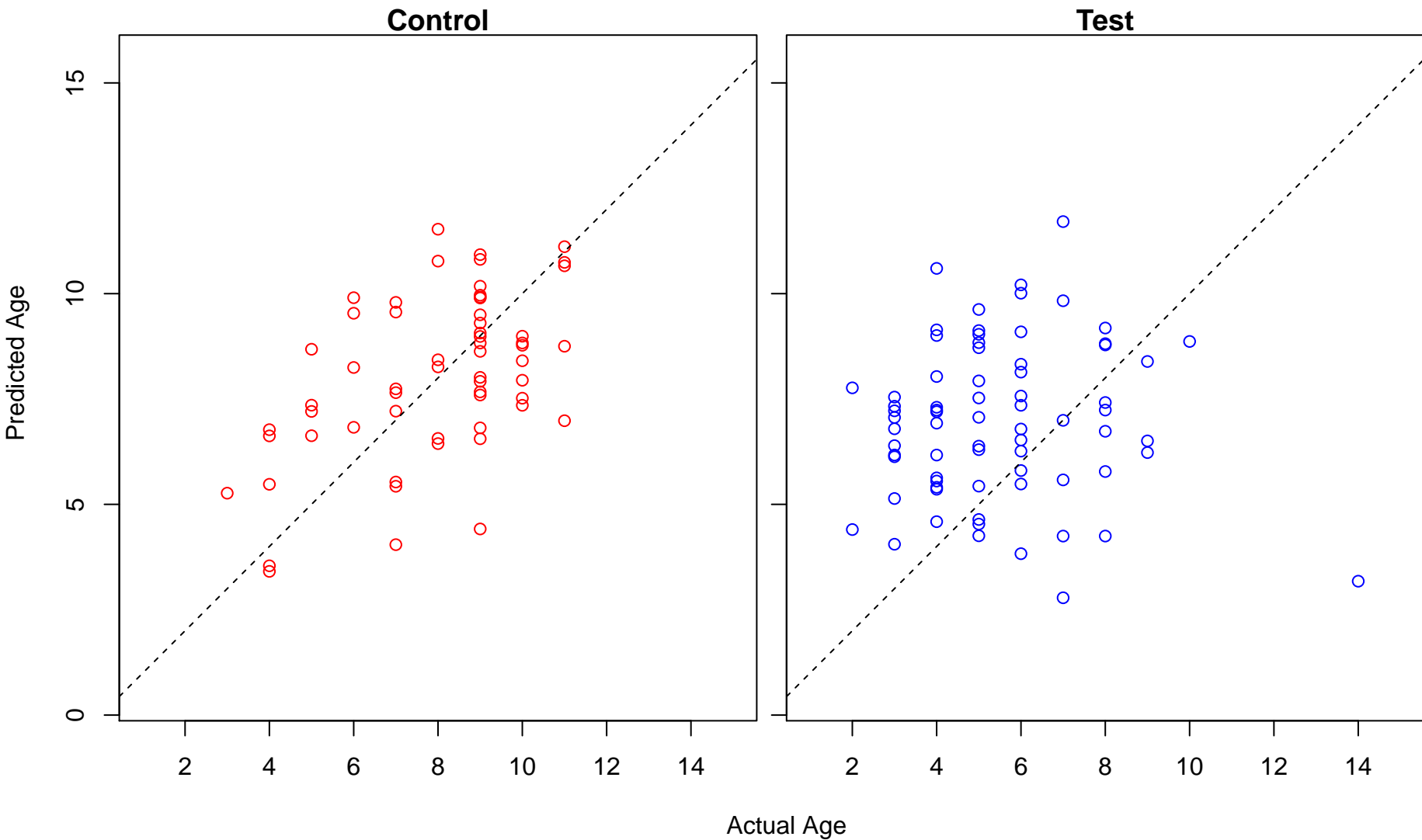
regulation of endocytosis (Score: 1.186728)



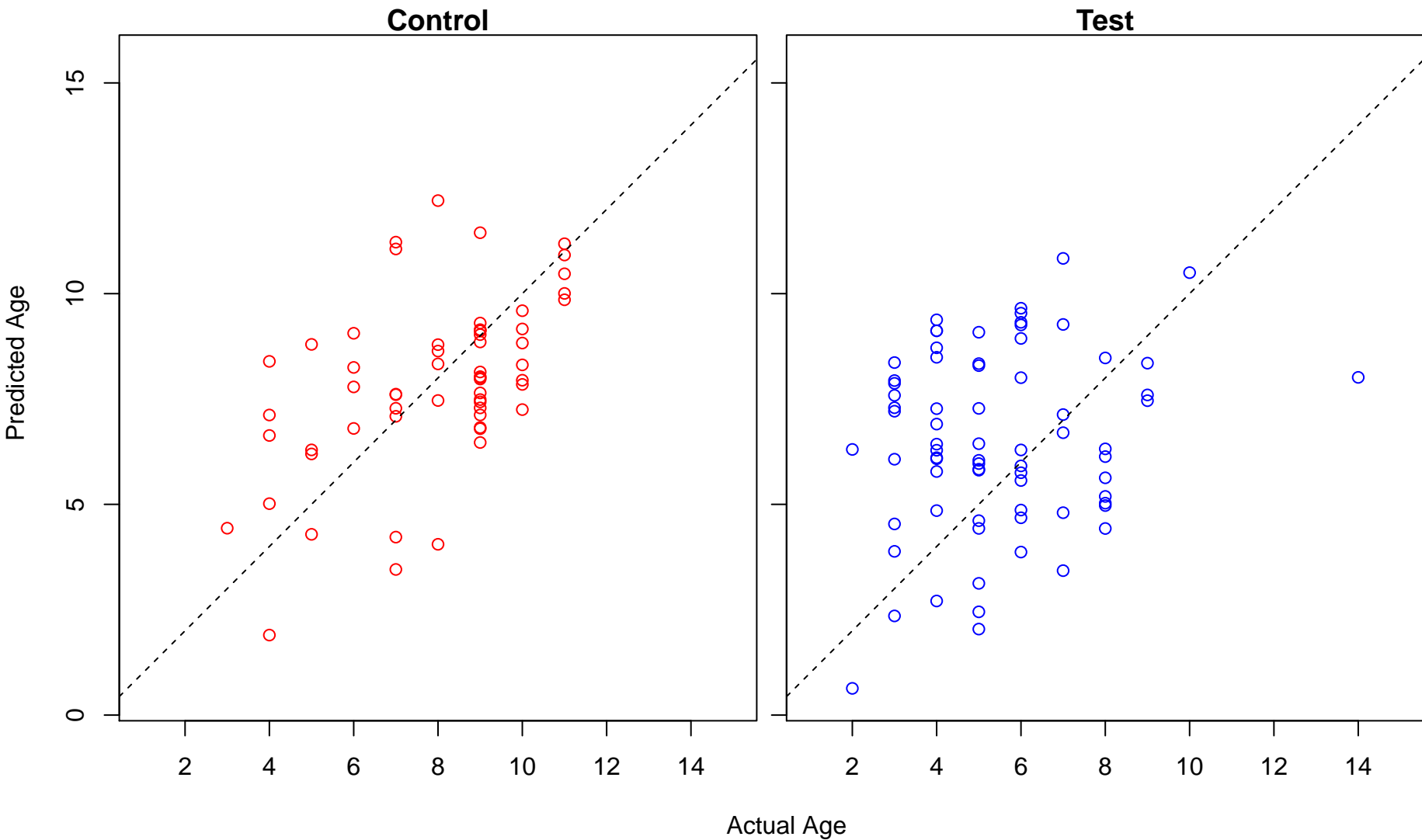
proteolysis (Score: 1.185080)



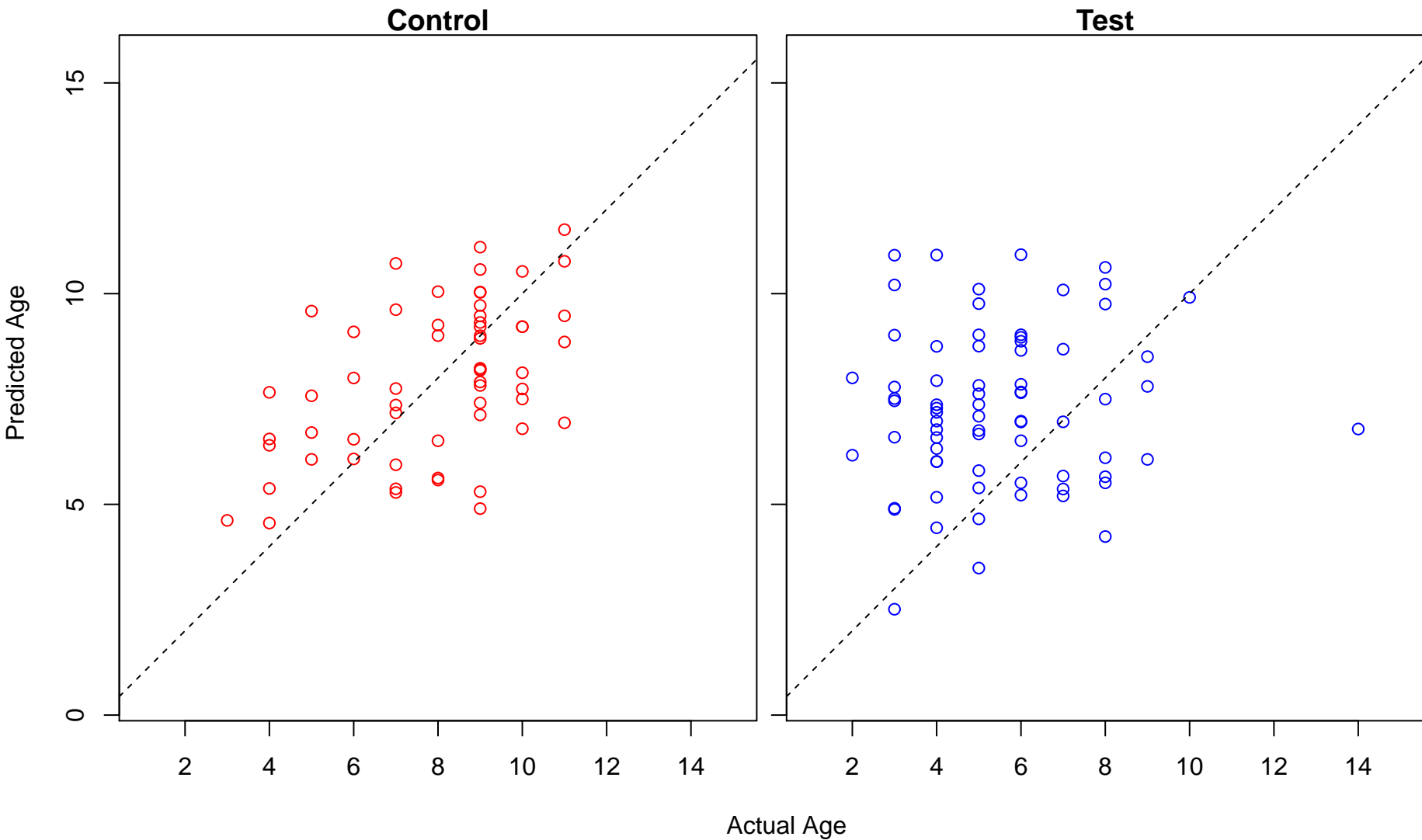
regulation of dephosphorylation (Score: 1.184911)



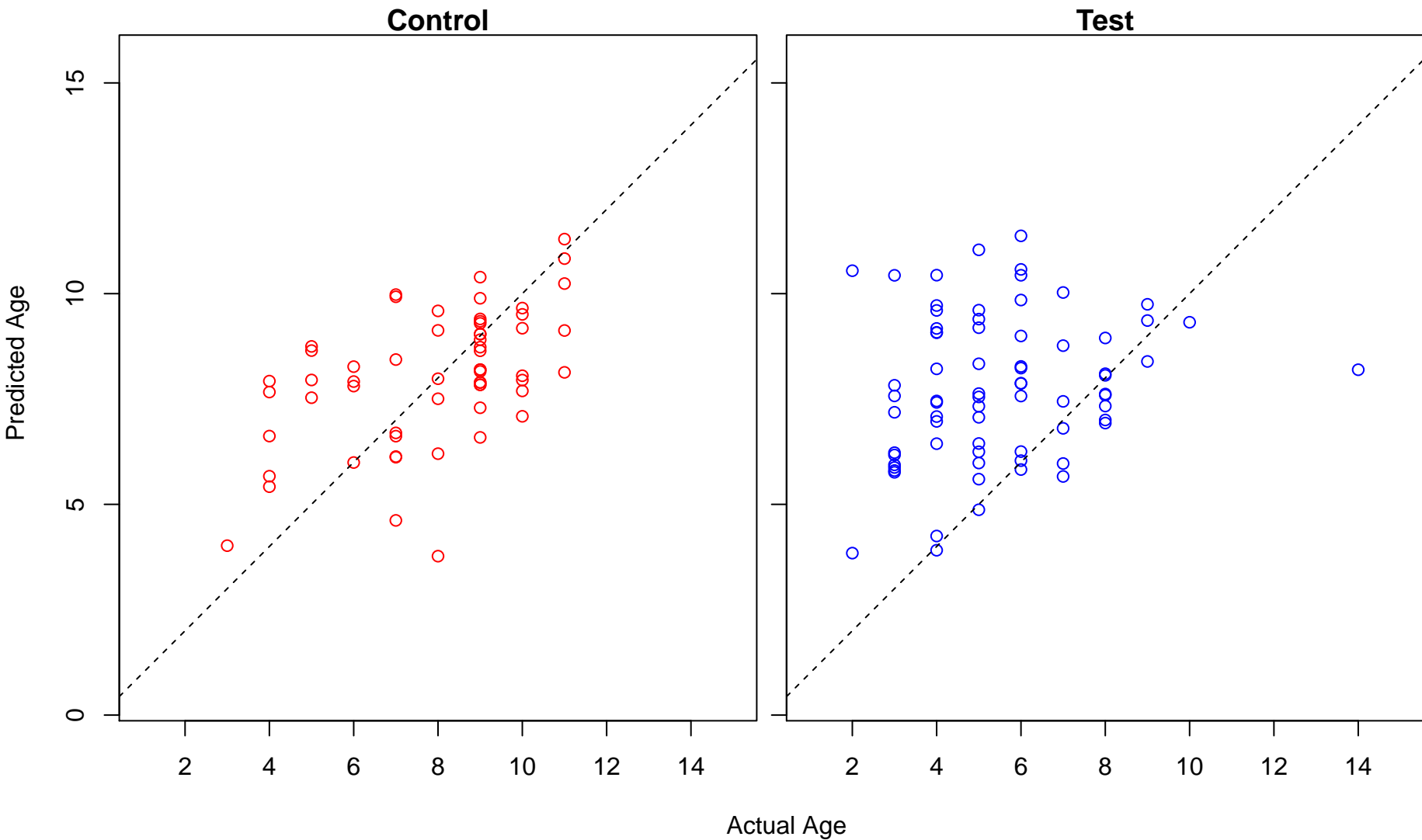
regulation of fatty acid metabolic process (Score: 1.184678)



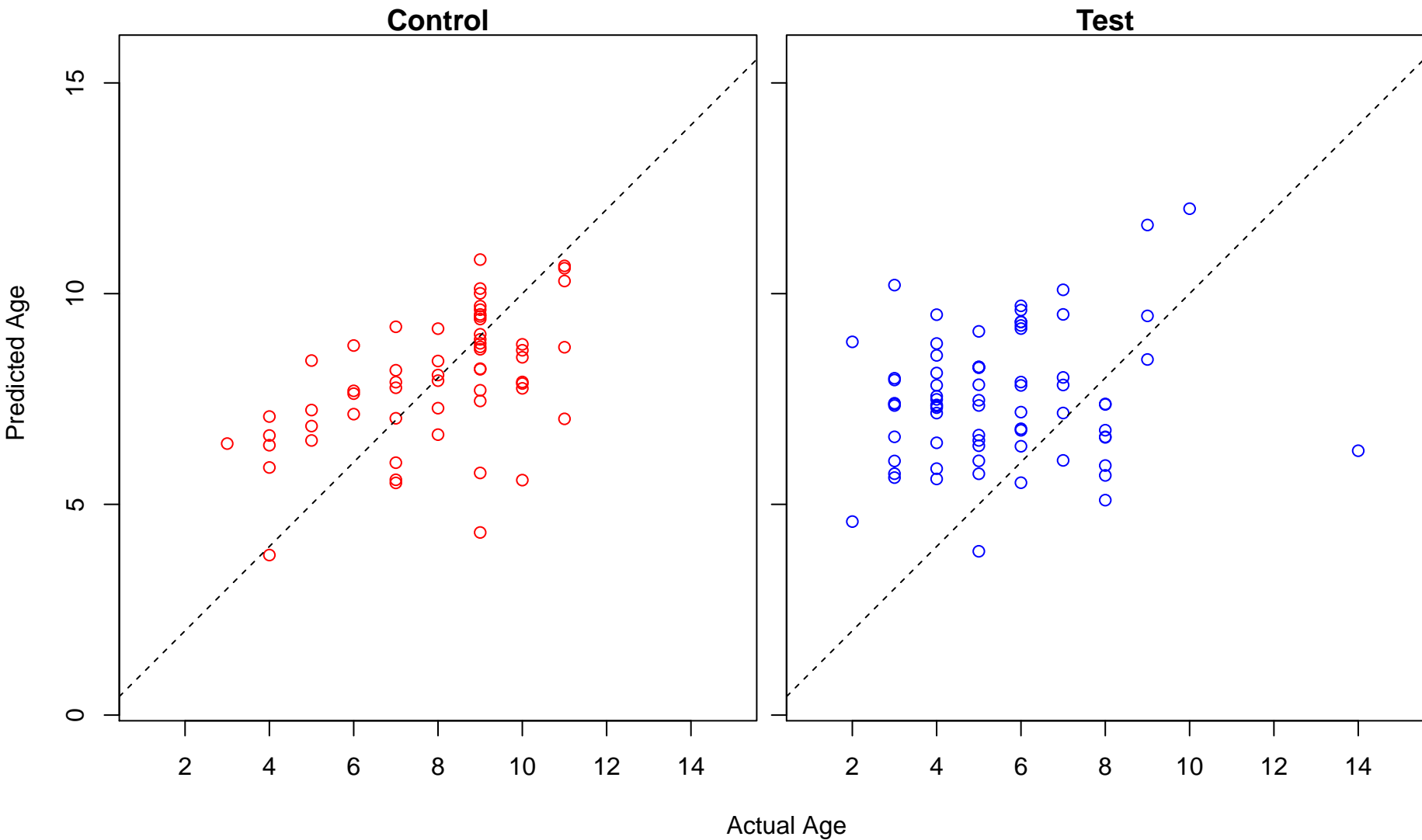
carbohydrate derivative biosynthetic process (Score: 1.182989)



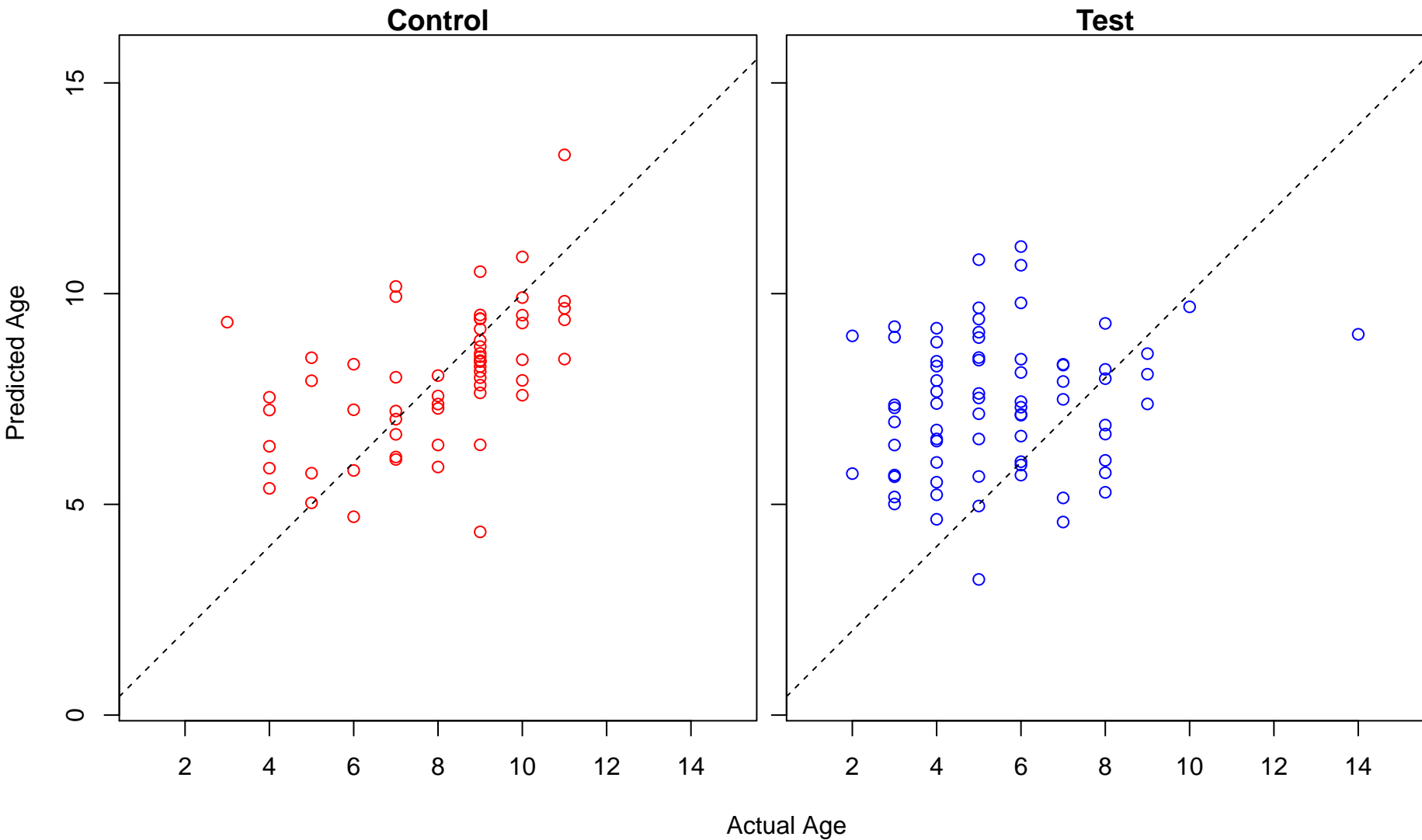
regulation of signaling (Score: 1.182851)



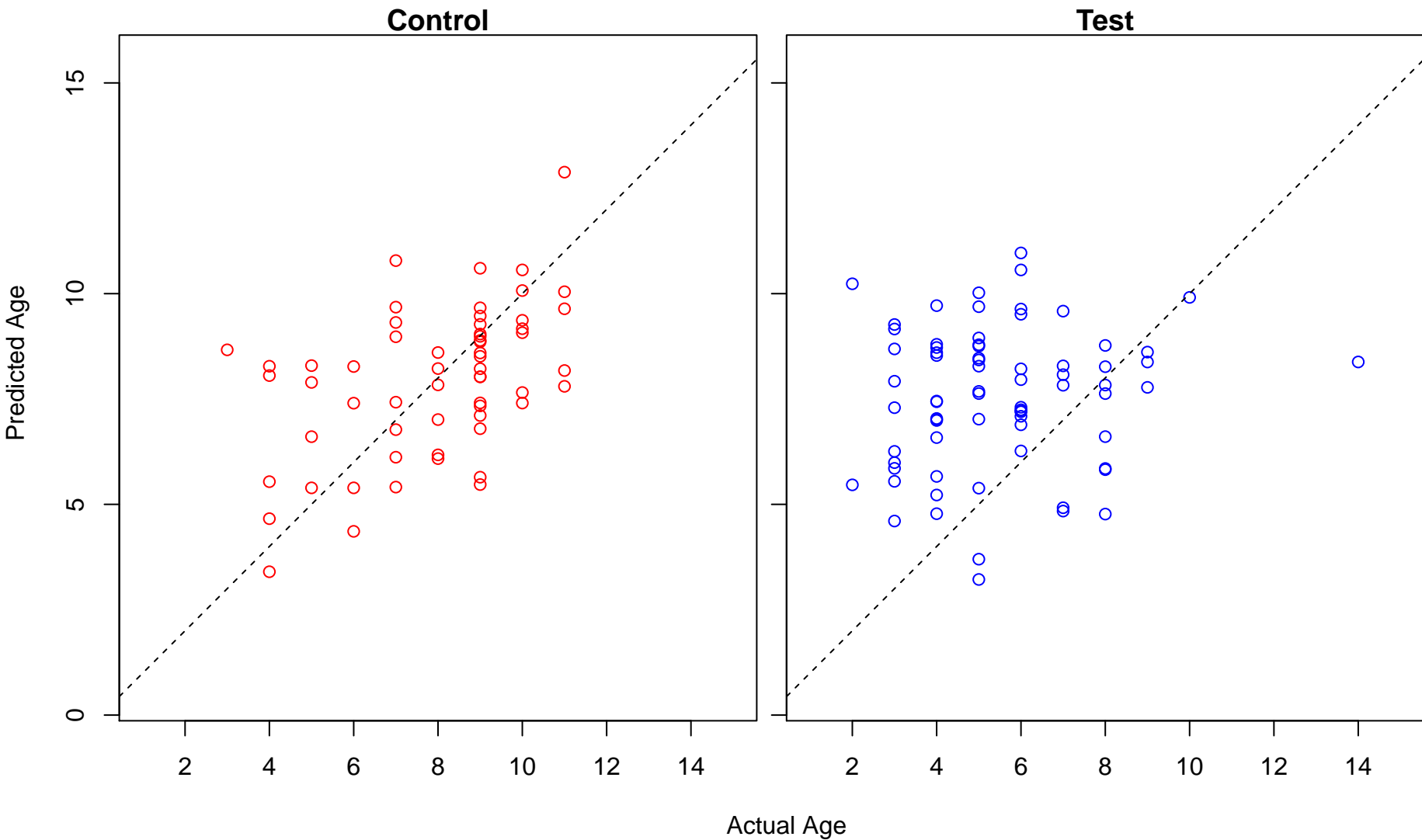
regulation of spindle assembly (Score: 1.180421)



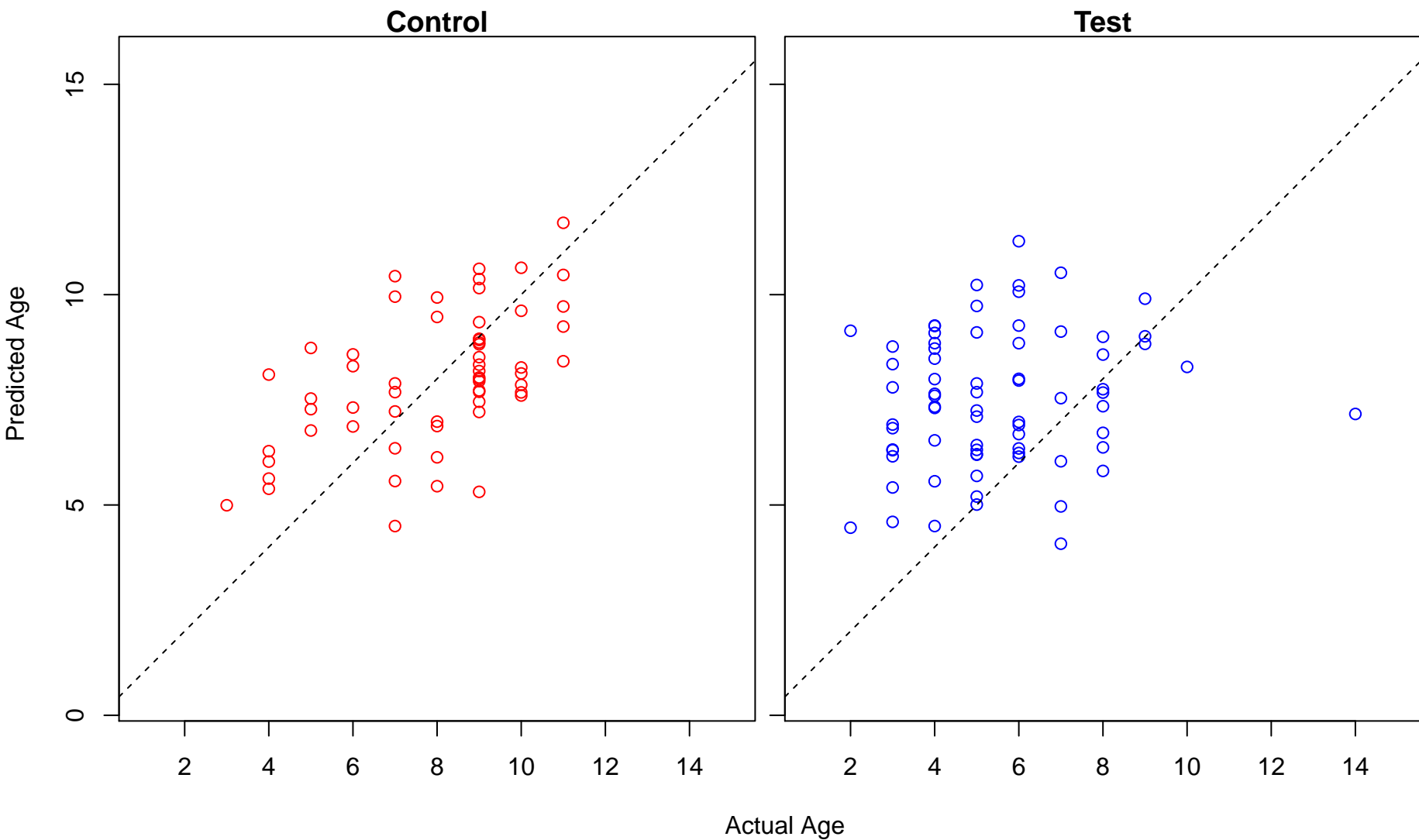
protein targeting to membrane (Score: 1.180107)



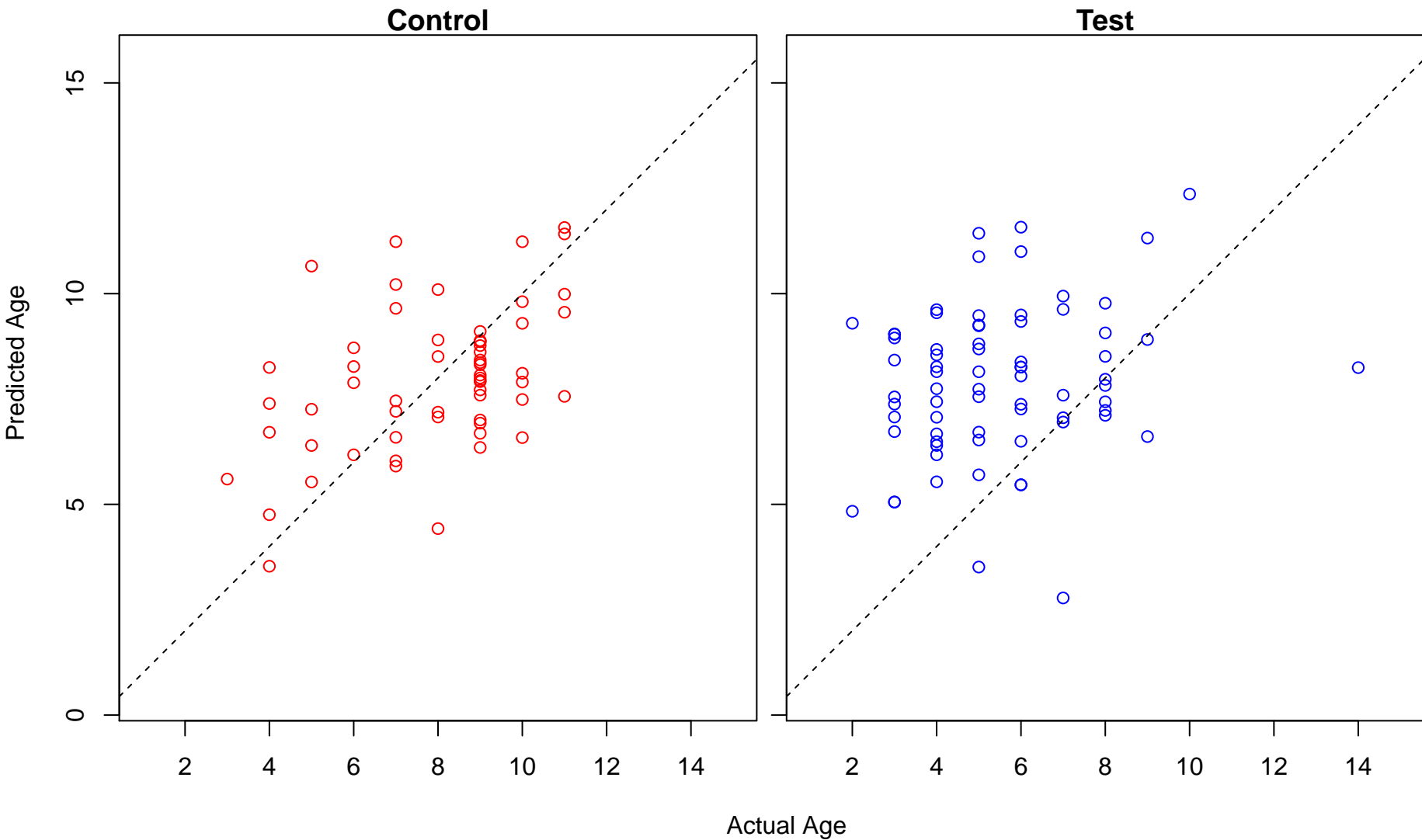
multi-organism cellular process (Score: 1.179511)



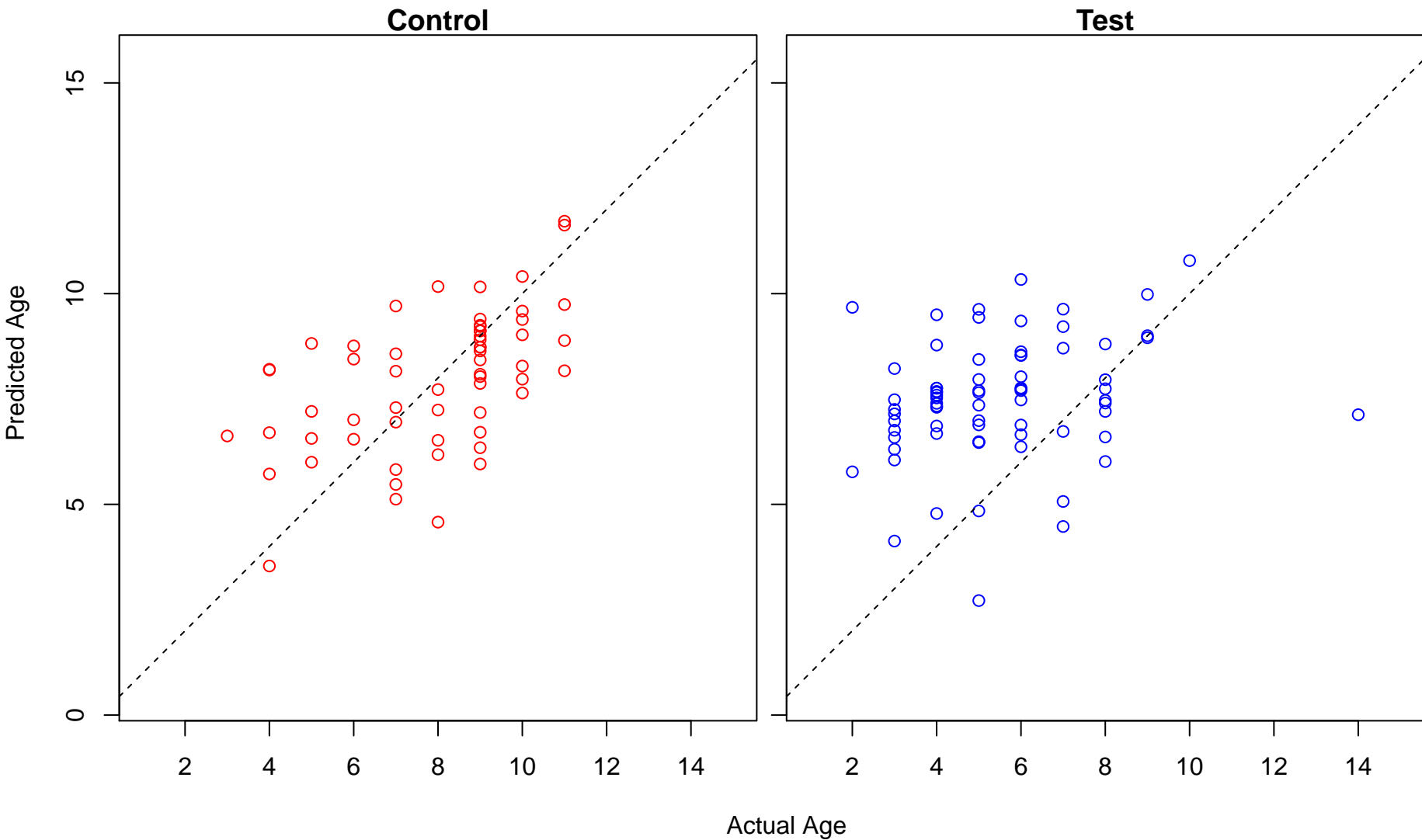
positive regulation of defense response (Score: 1.176083)



cellular iron ion homeostasis (Score: 1.174873)

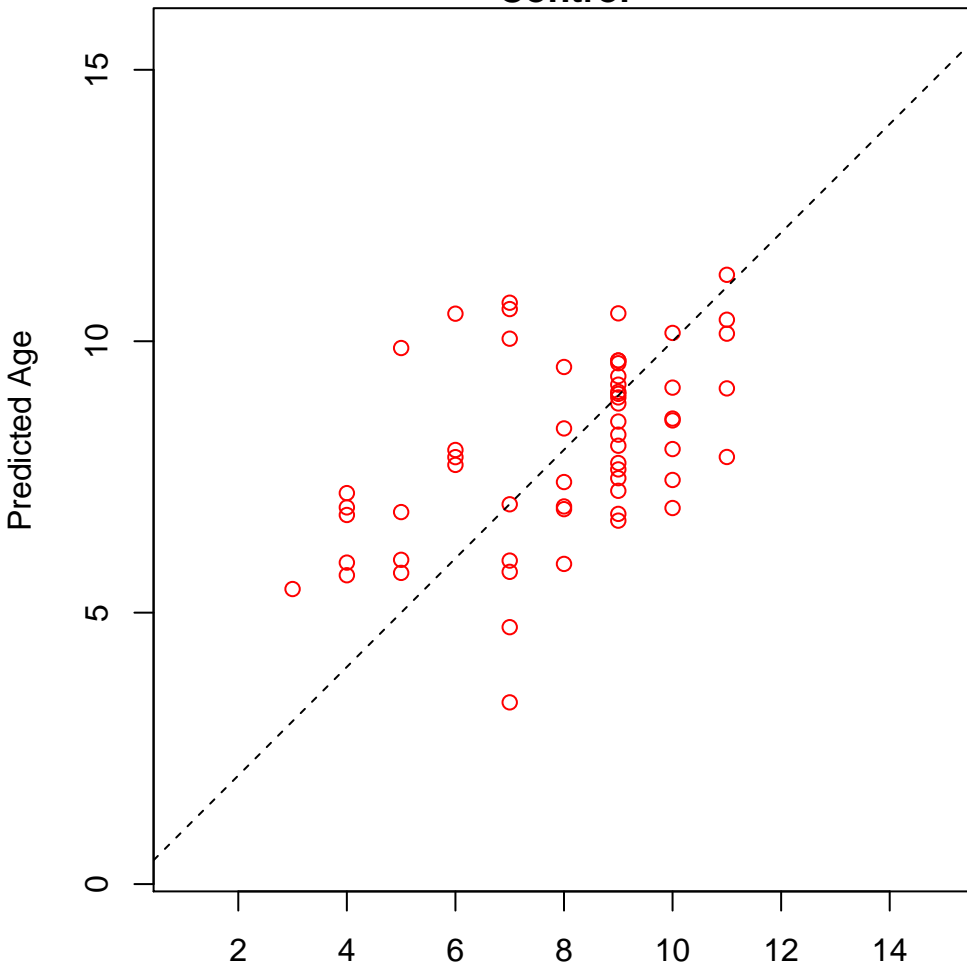


macromolecule metabolic process (Score: 1.174336)

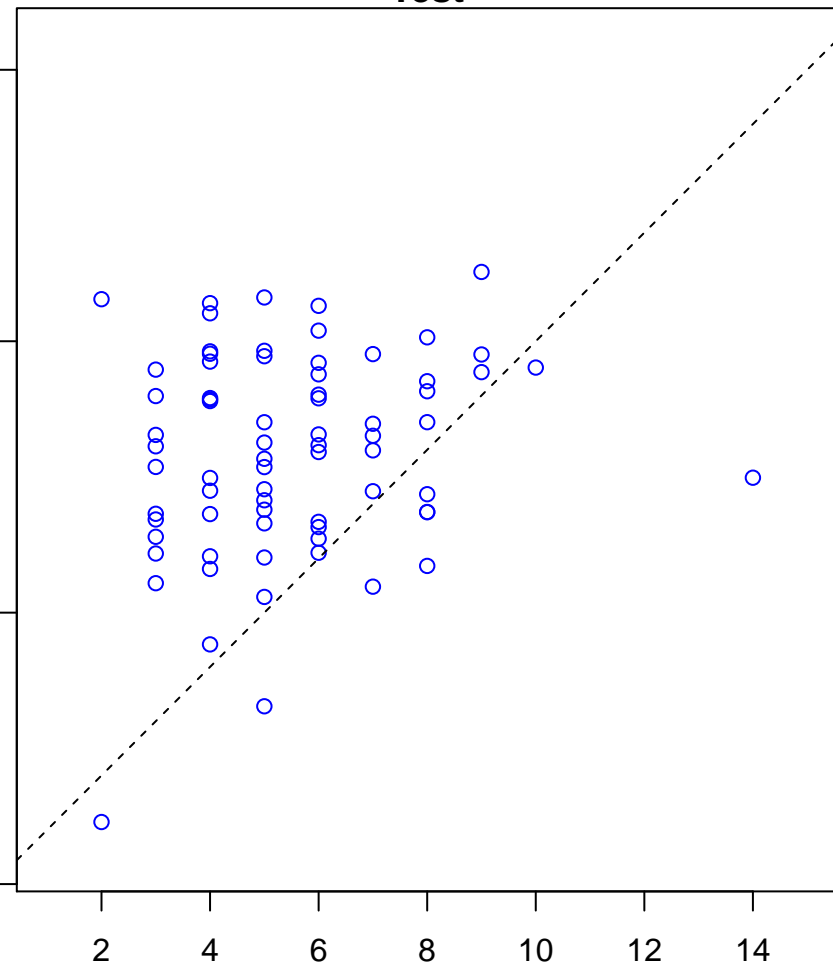


positive regulation of cell differentiation (Score: 1.172681)

Control

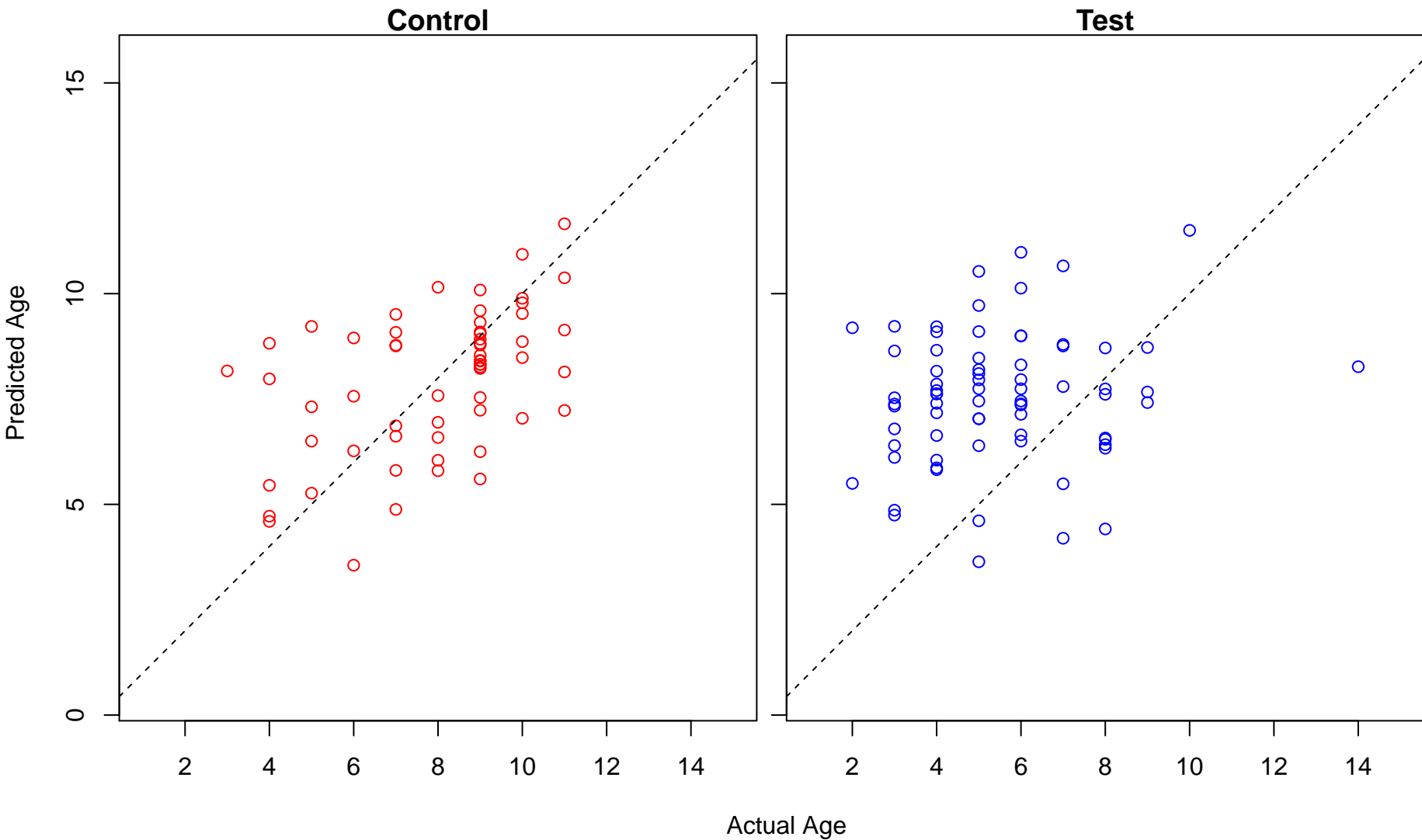


Test

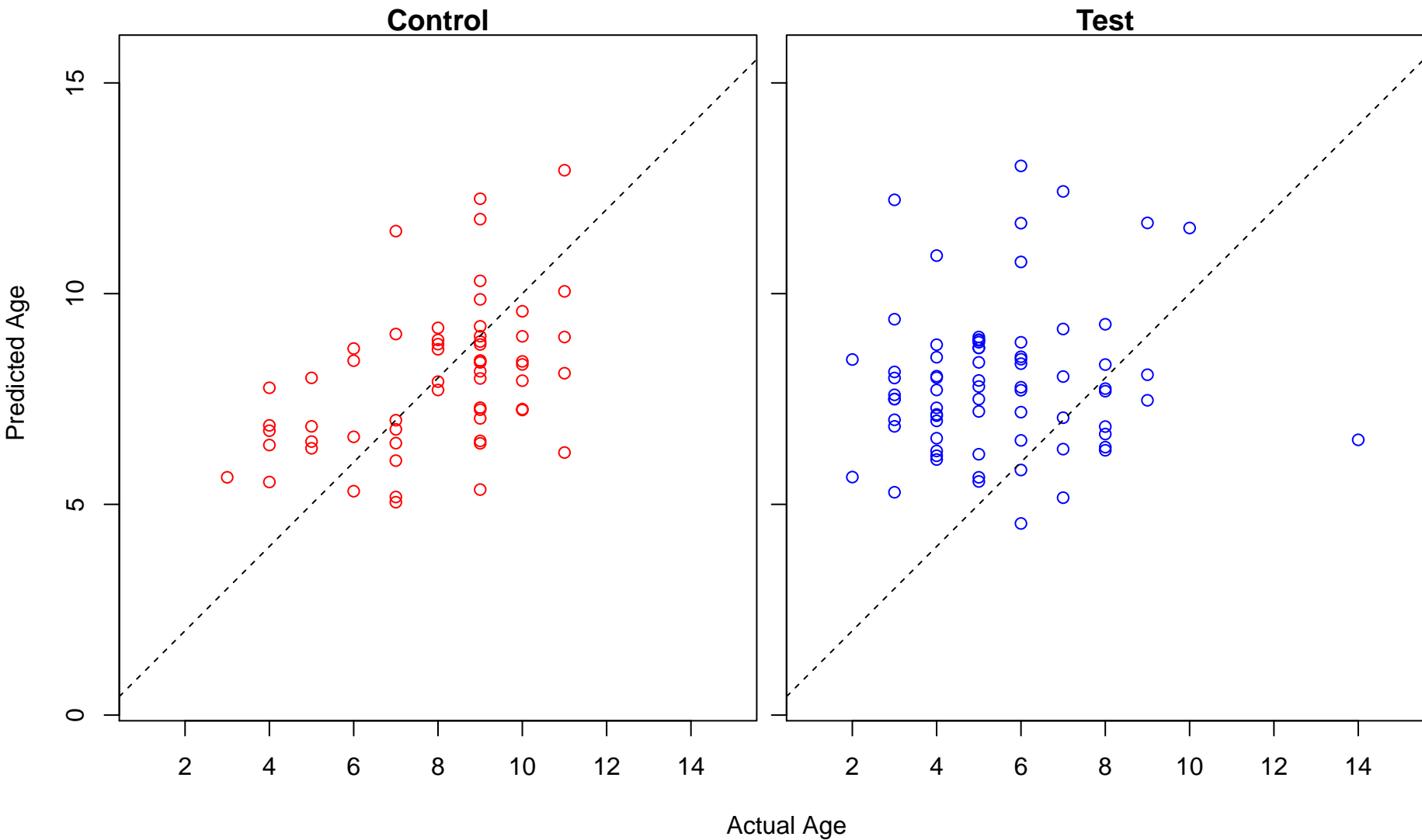


Actual Age

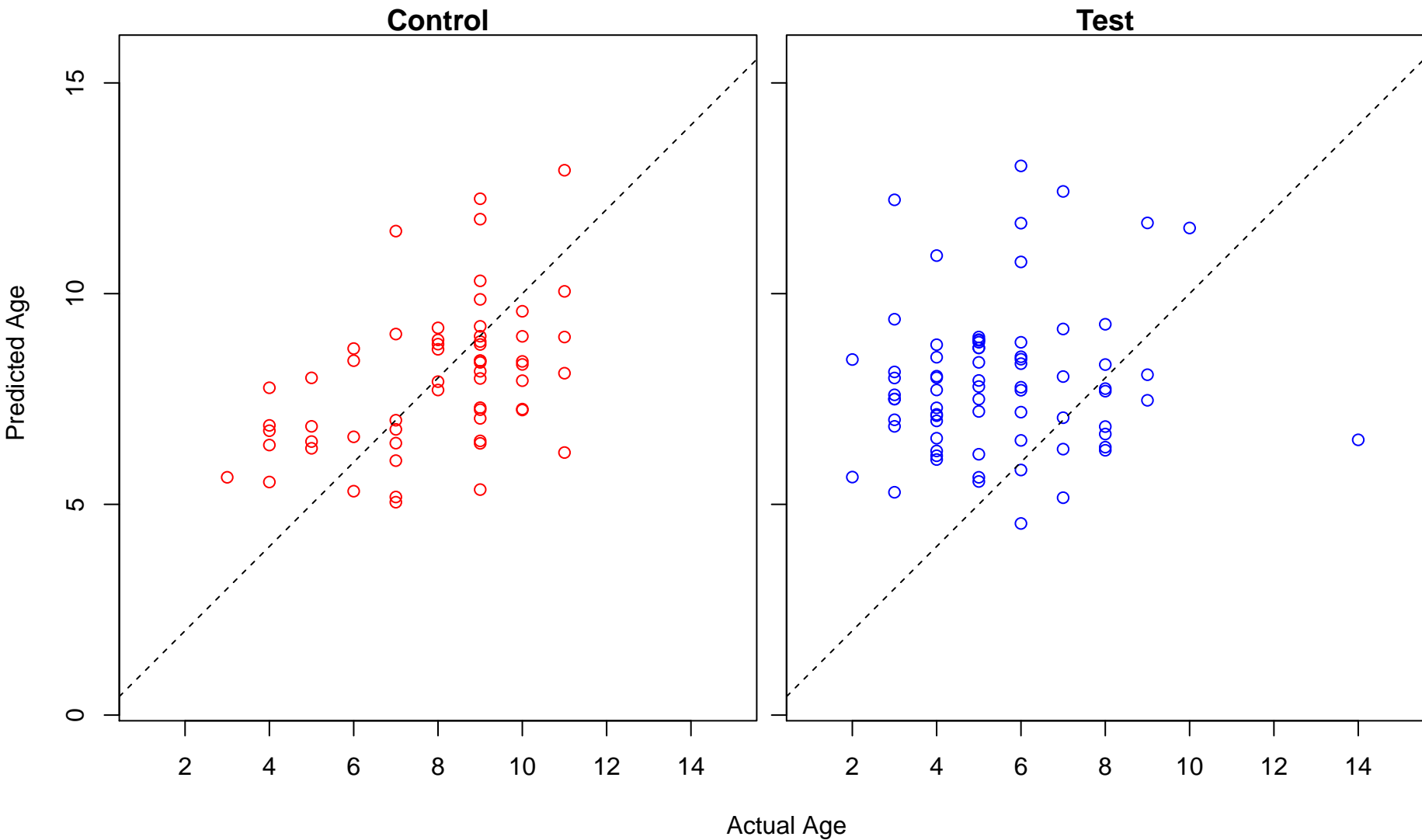
small molecule metabolic process (Score: 1.171364)



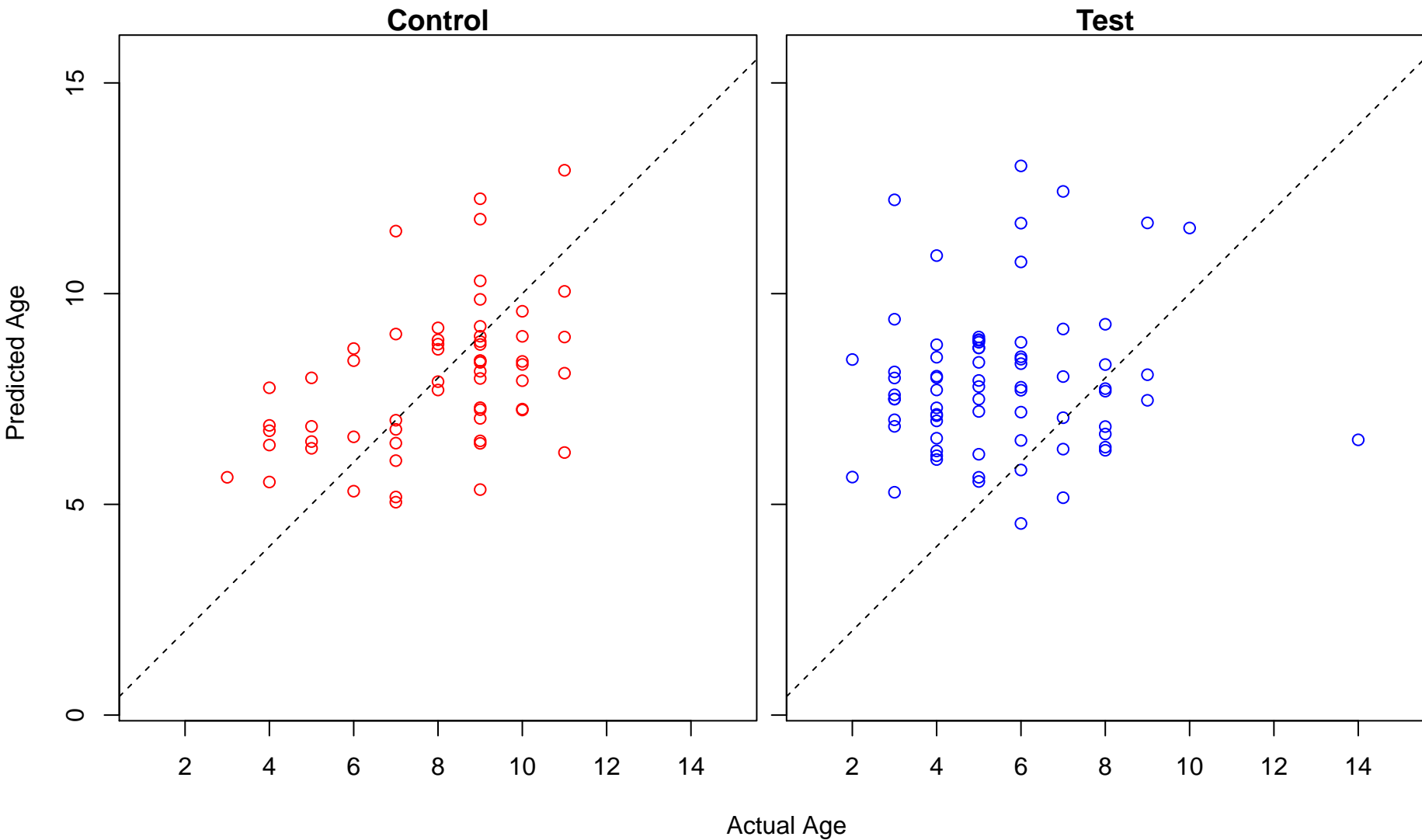
polysaccharide catabolic process (Score: 1.169782)



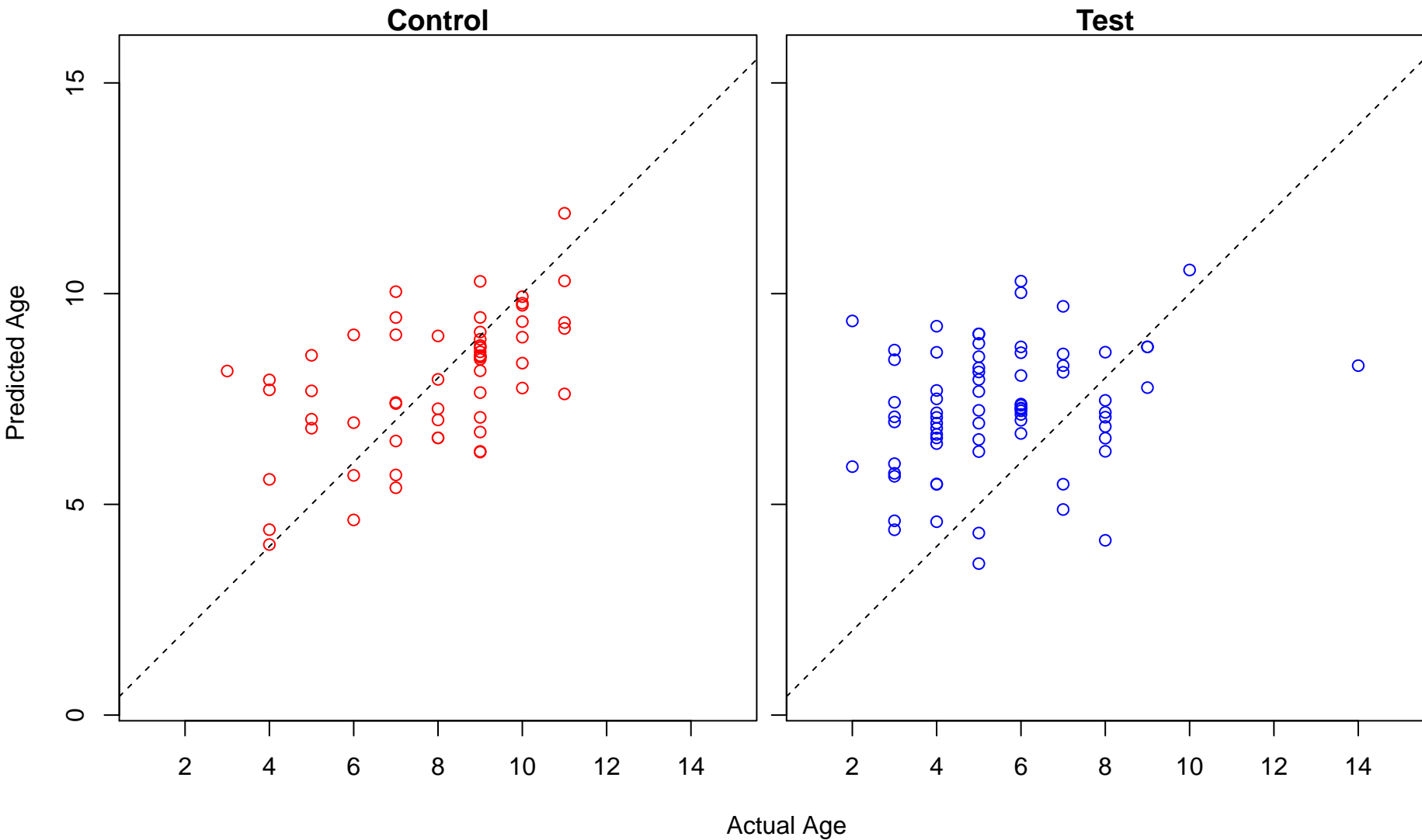
glucan catabolic process (Score: 1.169782)



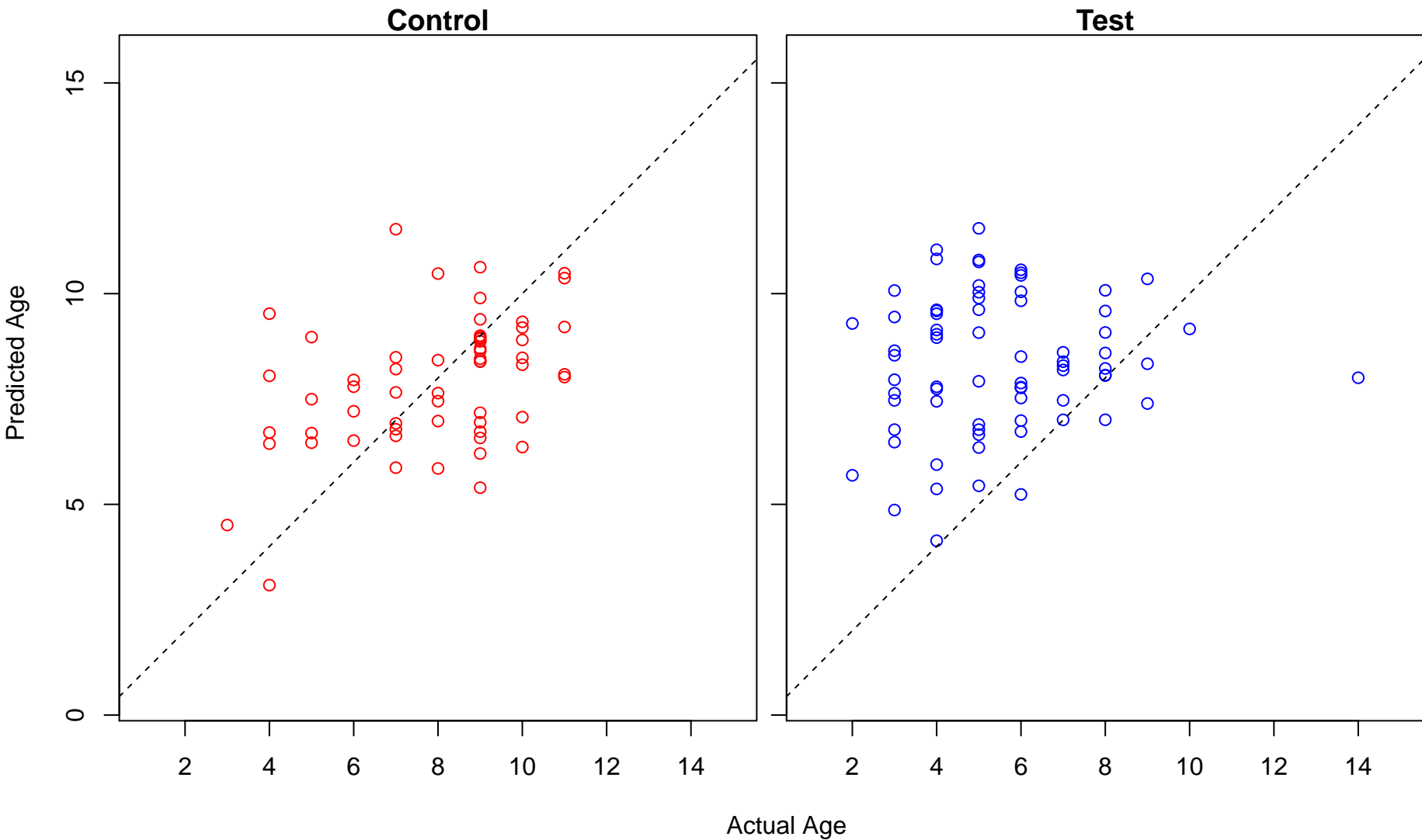
cellular polysaccharide catabolic process (Score: 1.169782)



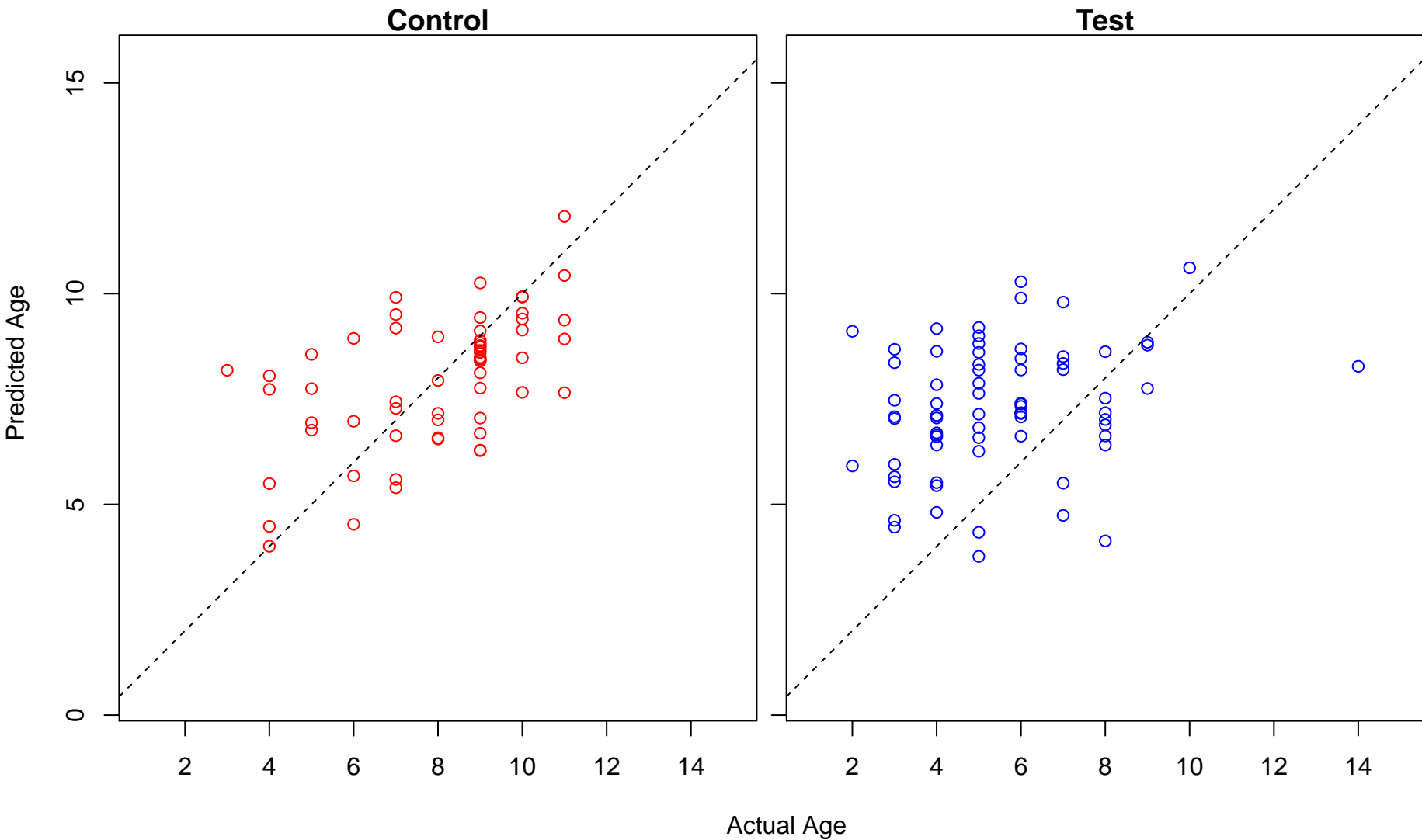
nucleobase-containing compound biosynthetic process (Score: 1.167184)



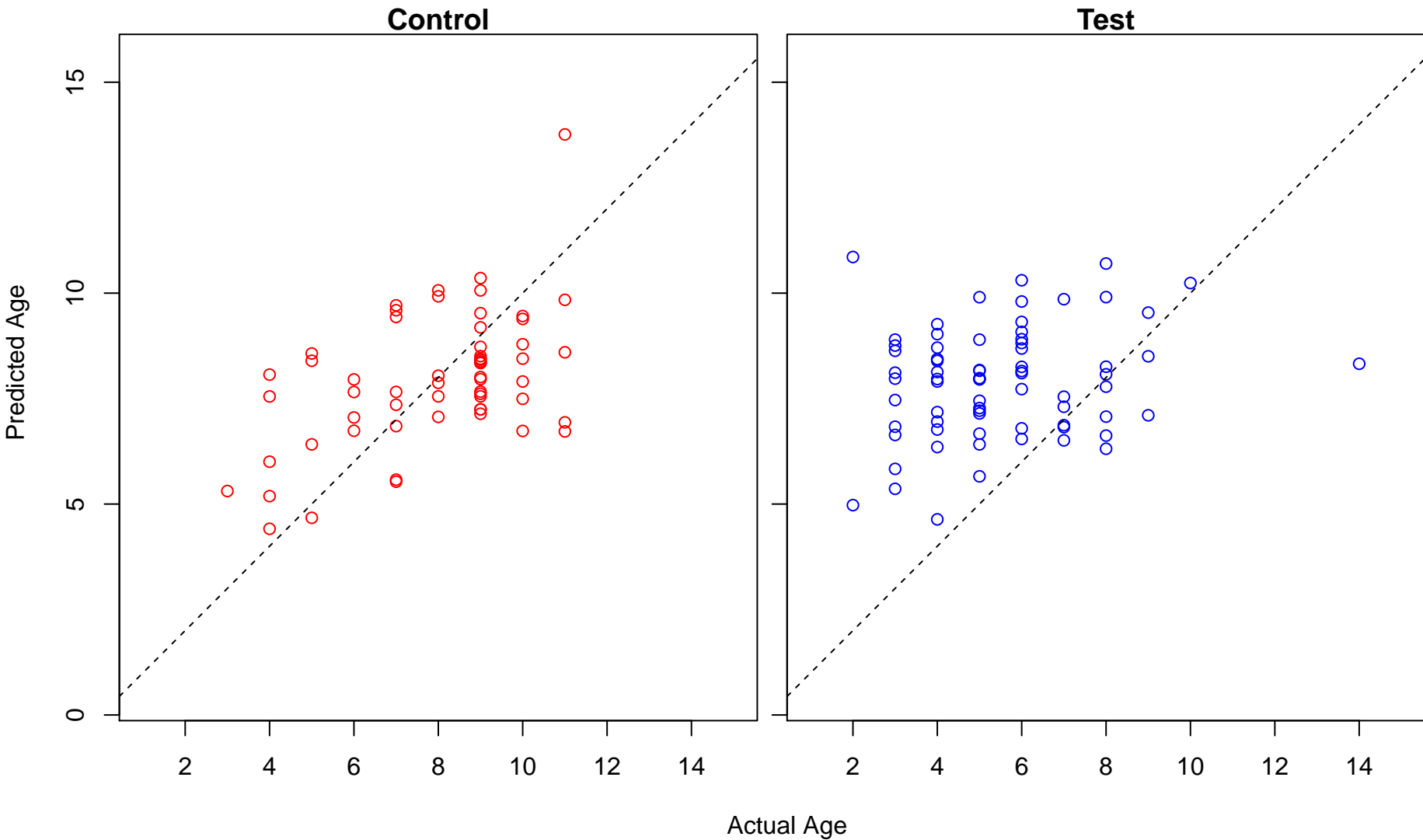
'de novo' protein folding (Score: 1.166179)



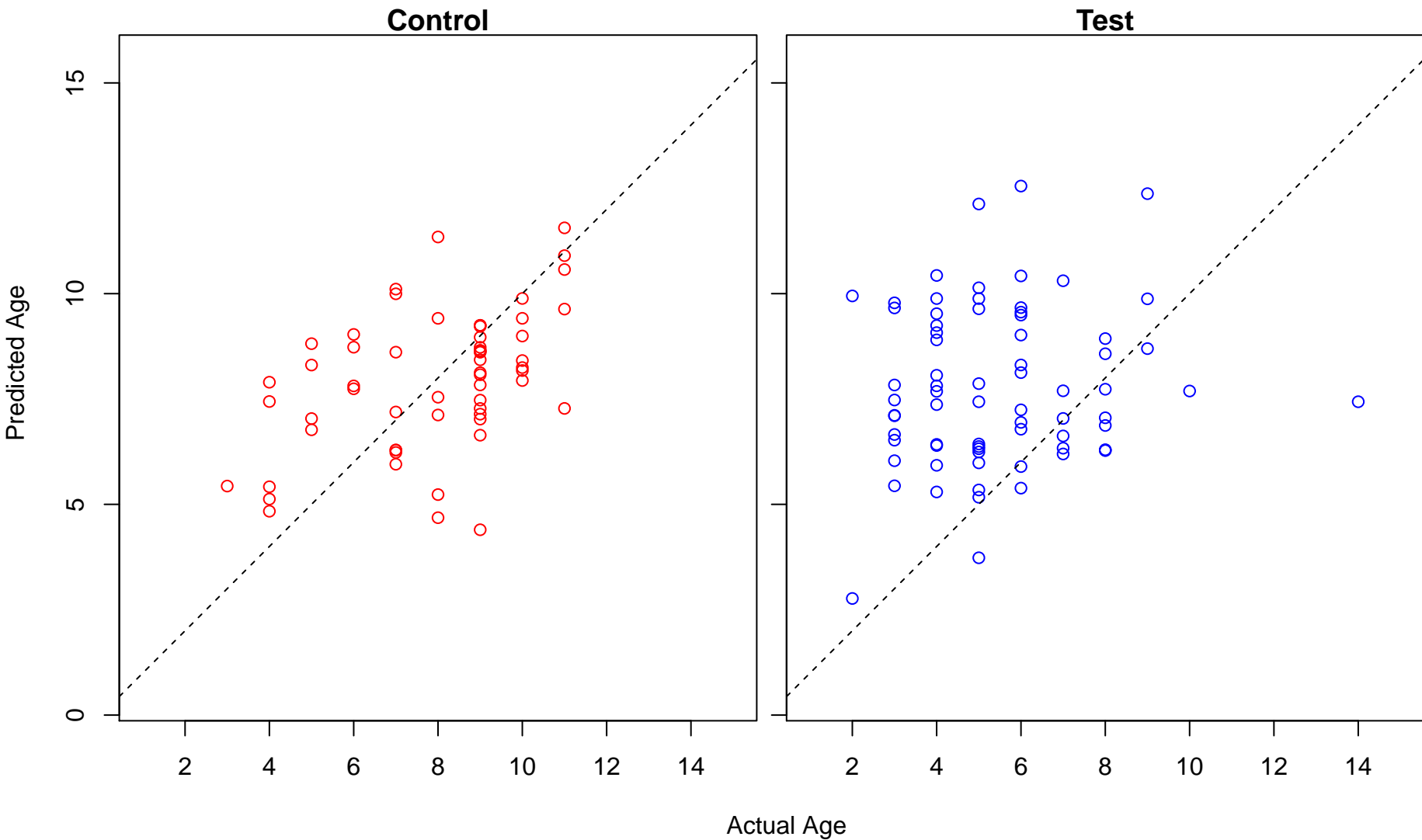
organic cyclic compound biosynthetic process (Score: 1.165339)



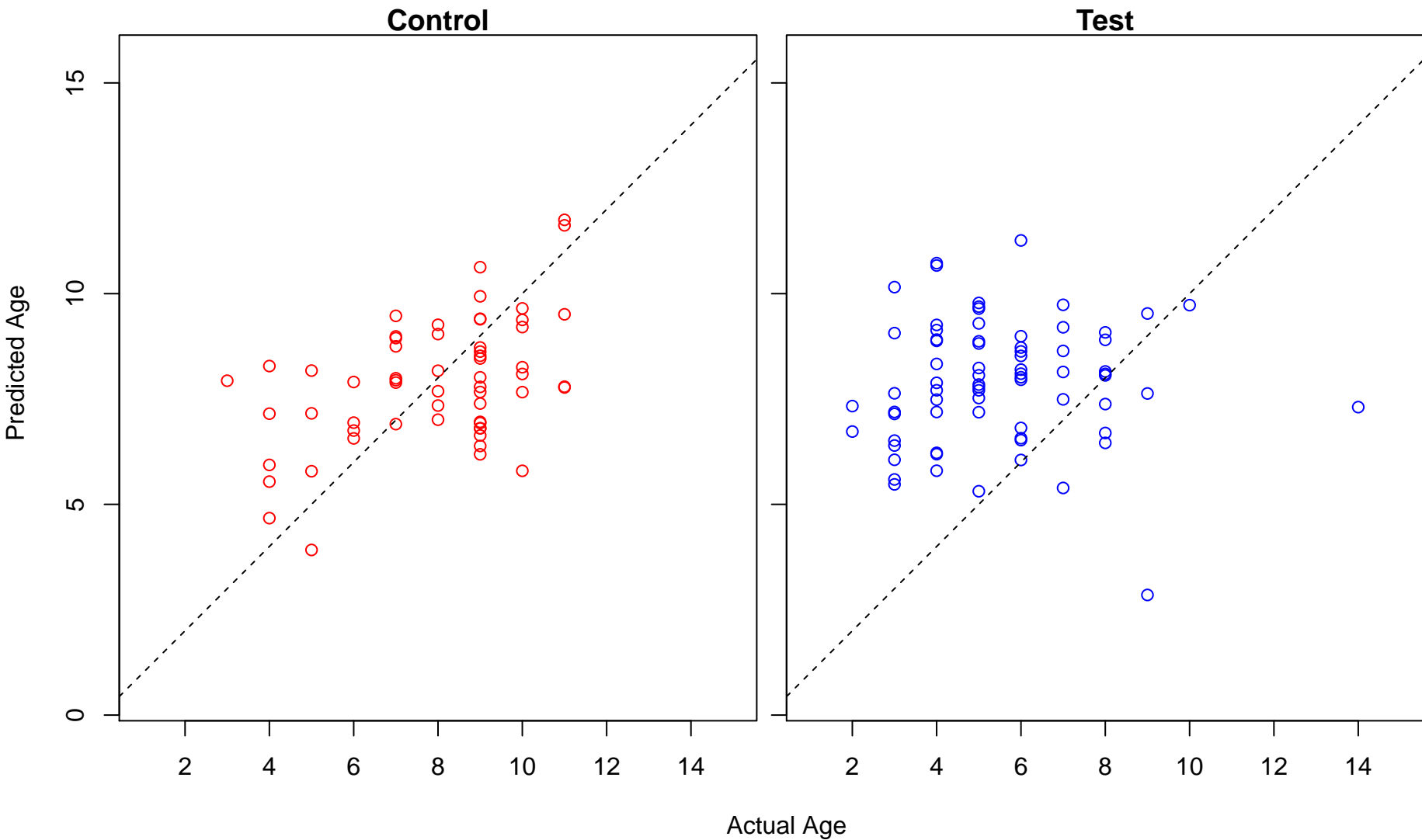
positive regulation of antigen receptor-mediated signaling pathway (Score: 1.164568)



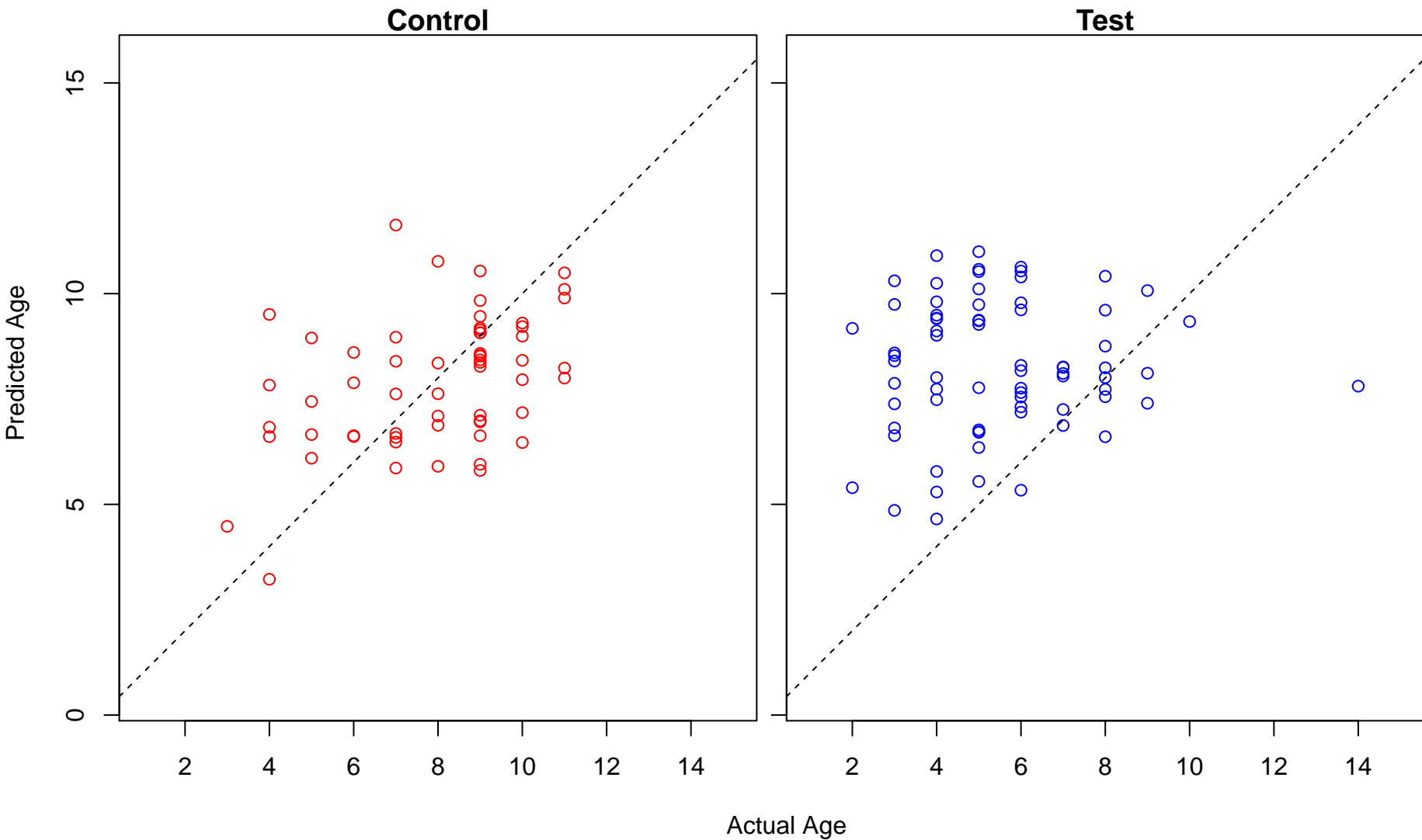
response to peptide (Score: 1.164386)



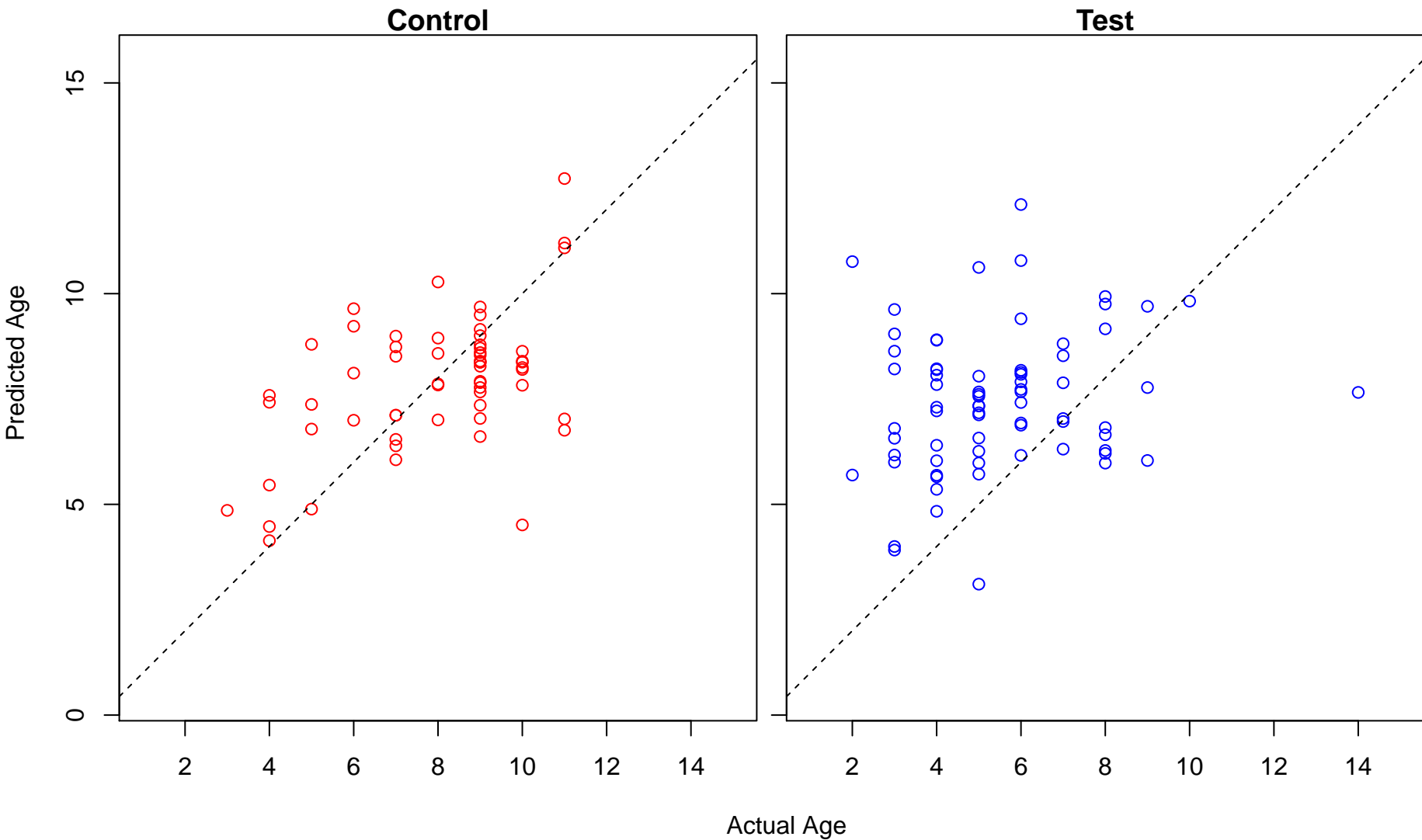
serotonin receptor signaling pathway (Score: 1.164286)



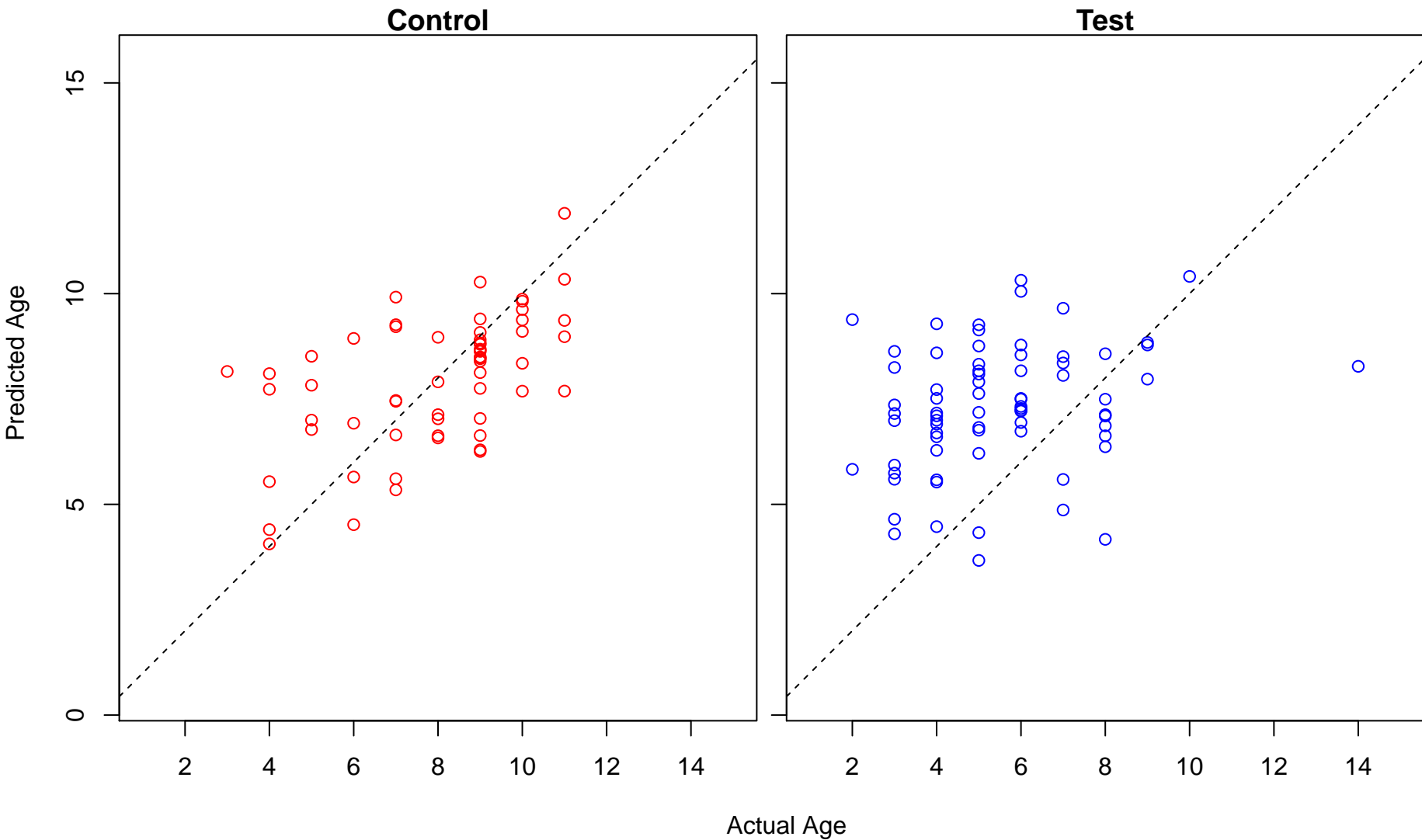
'de novo' posttranslational protein folding (Score: 1.163992)



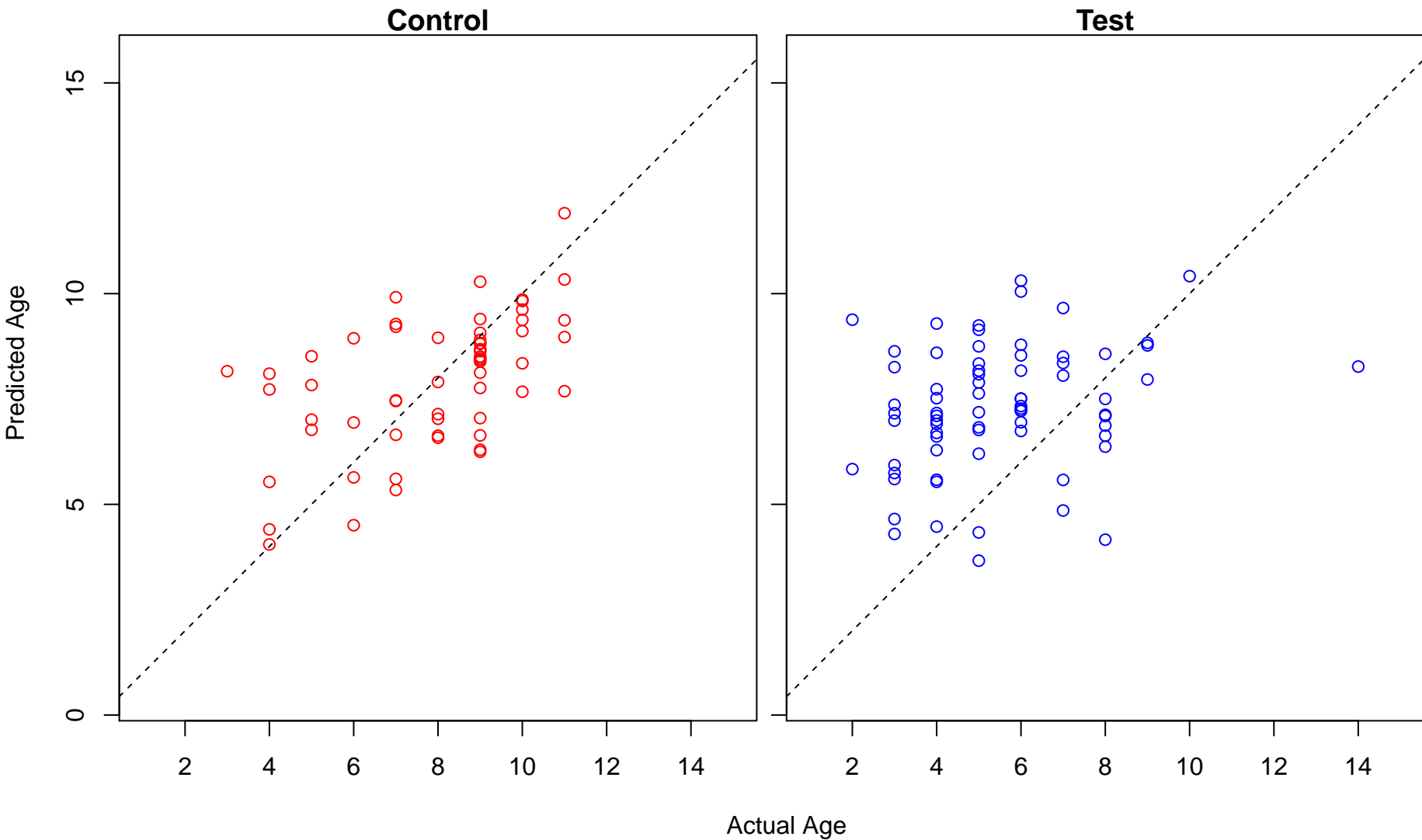
regulation of cellular response to insulin stimulus (Score: 1.161000)



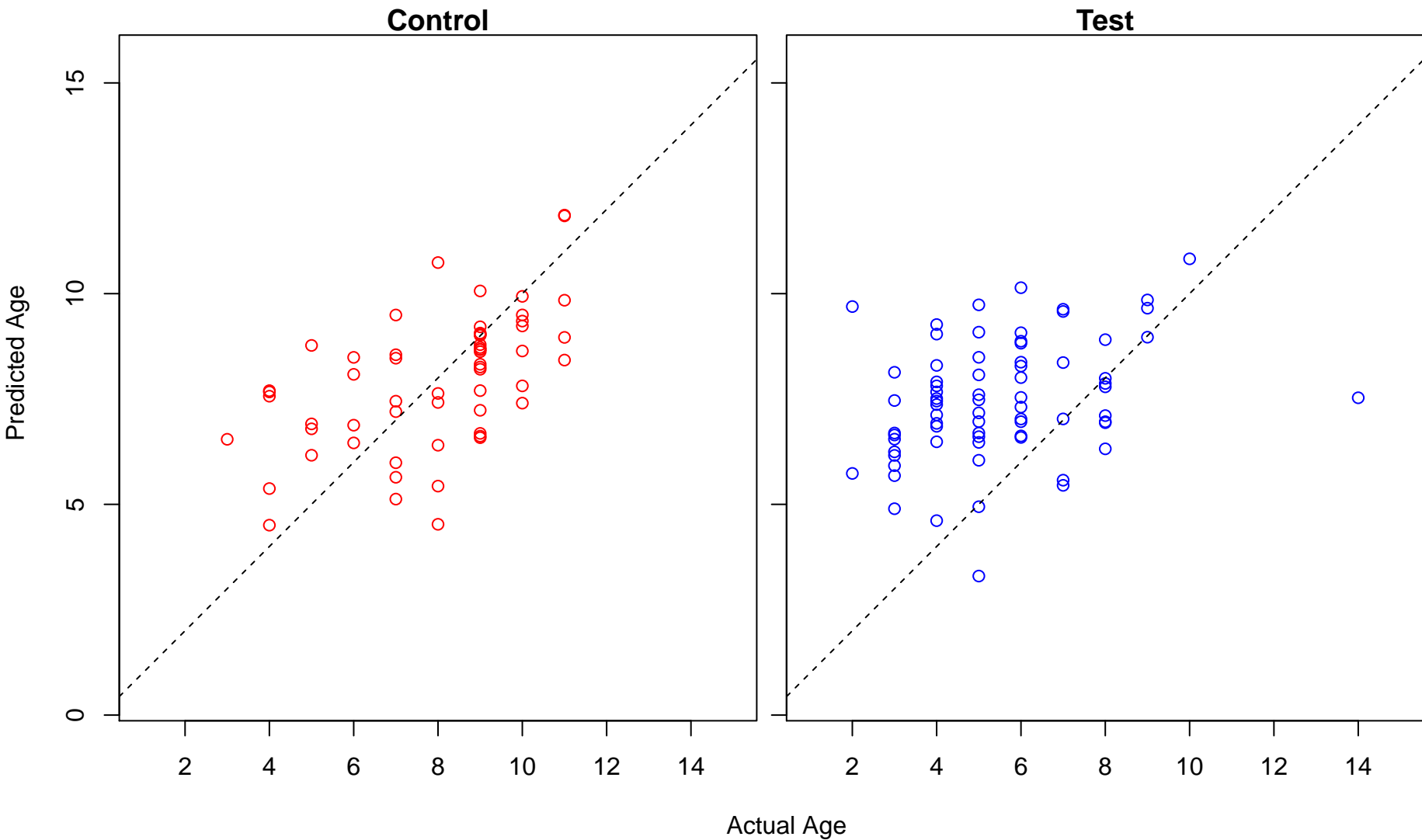
aromatic compound biosynthetic process (Score: 1.160448)



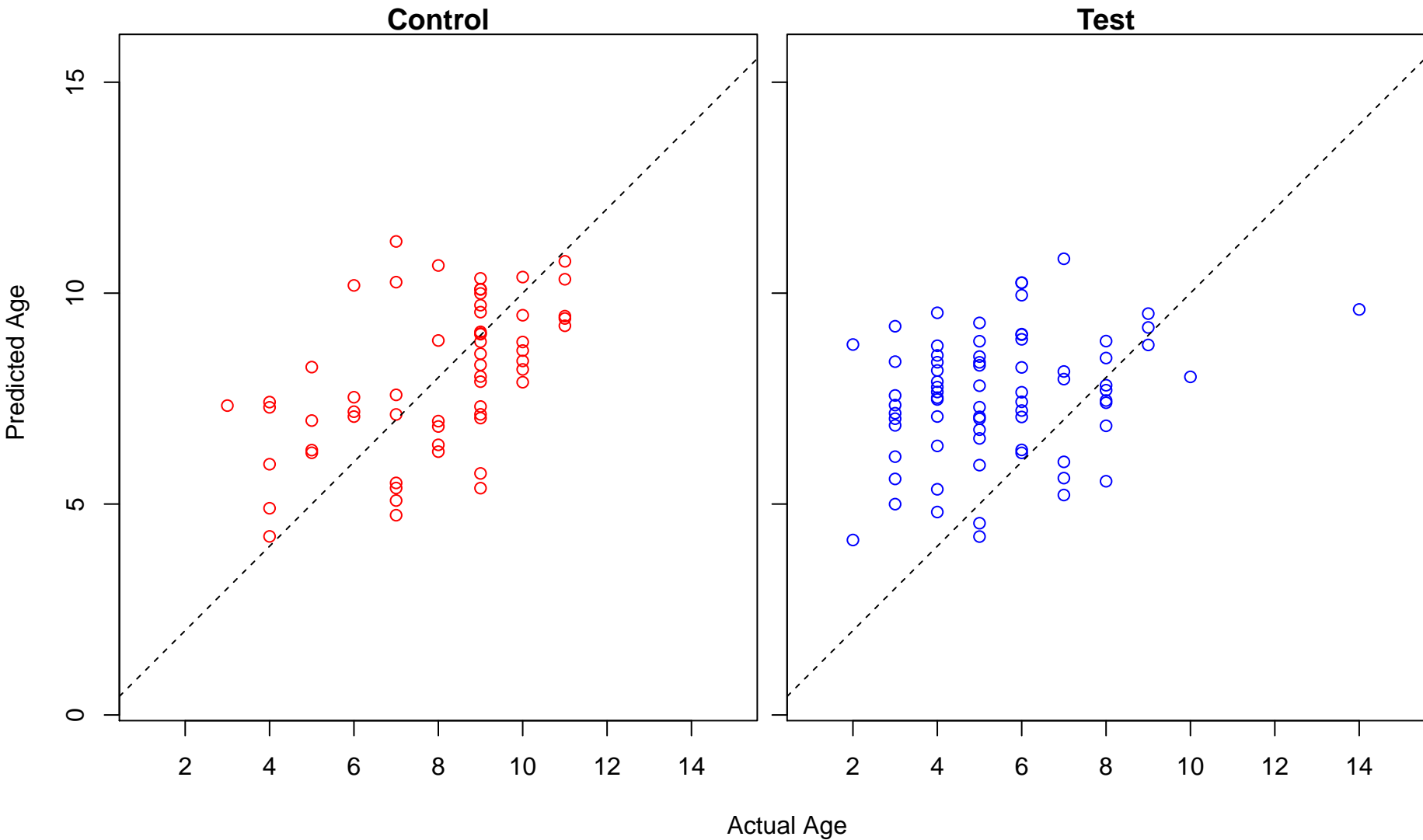
heterocycle biosynthetic process (Score: 1.159935)



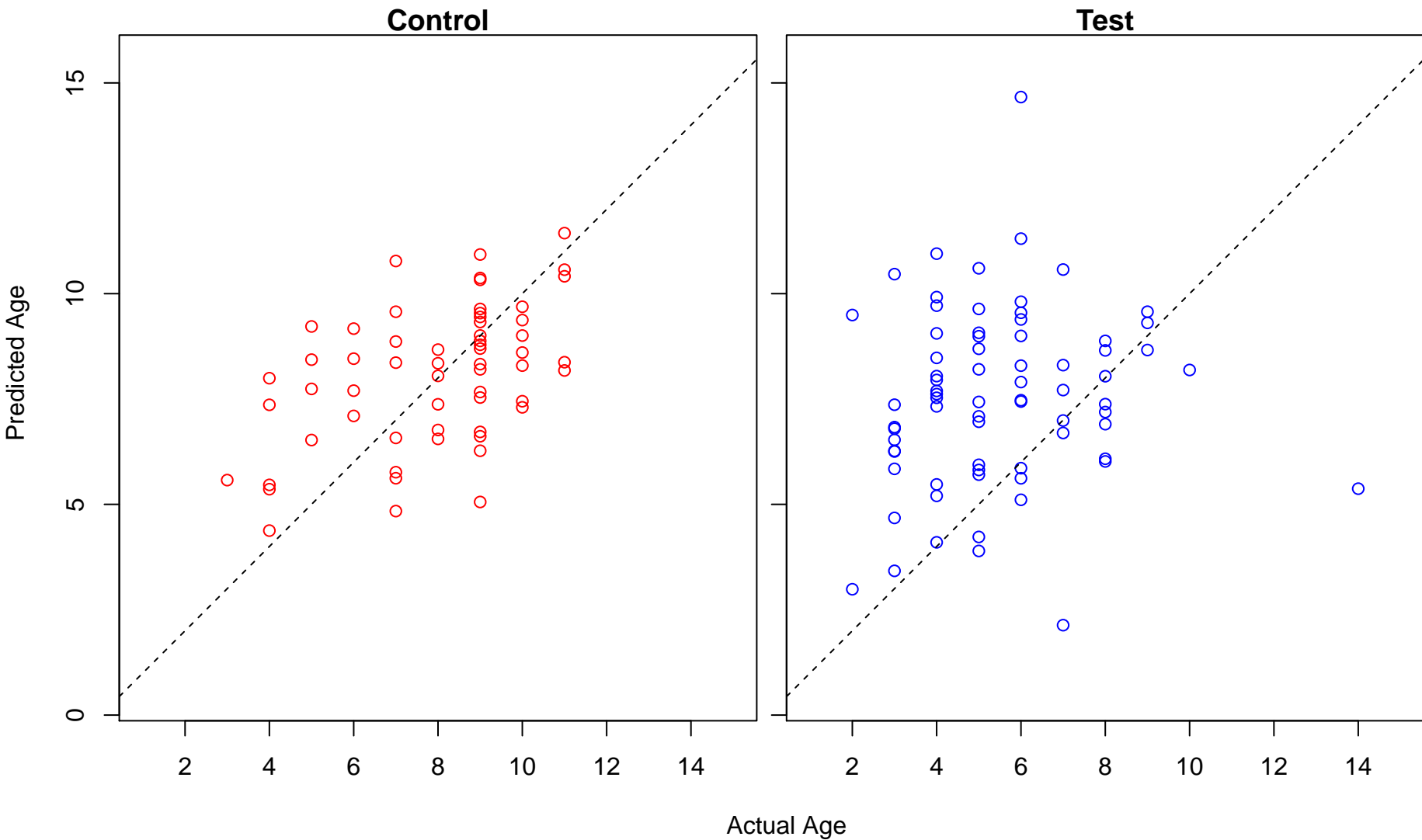
metabolic process (Score: 1.159876)



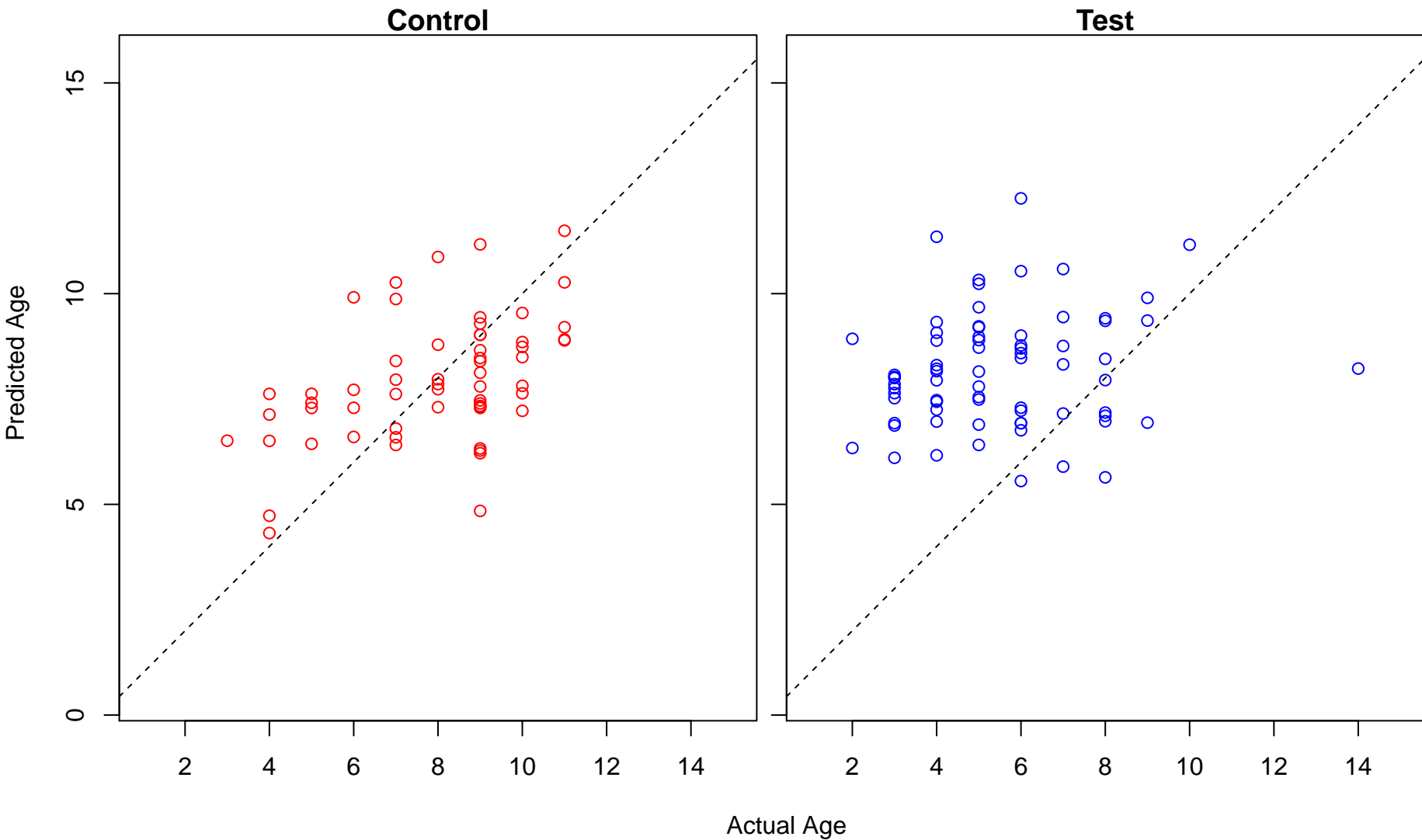
negative regulation of nitrogen compound metabolic process (Score: 1.159421)



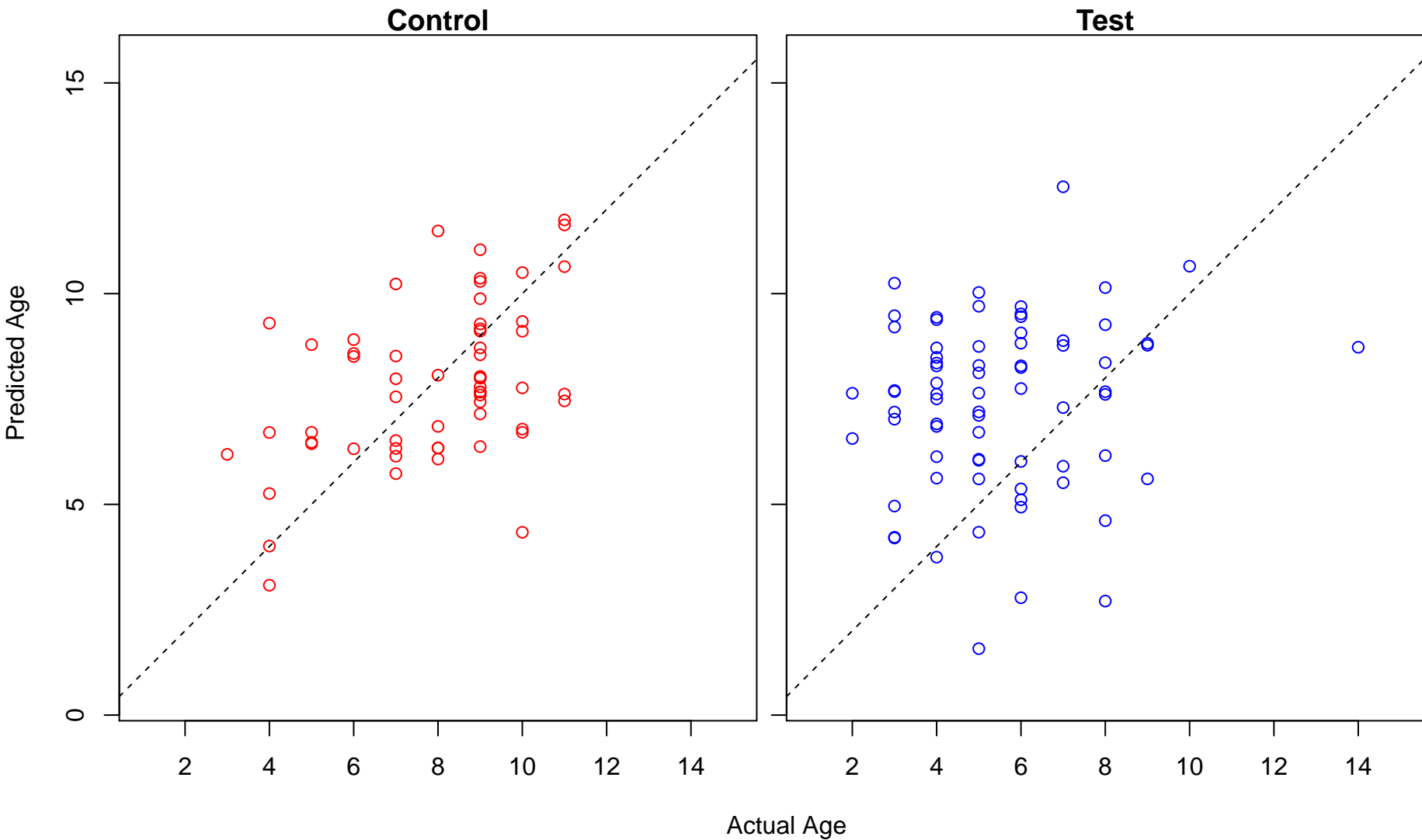
generation of neurons (Score: 1.157480)



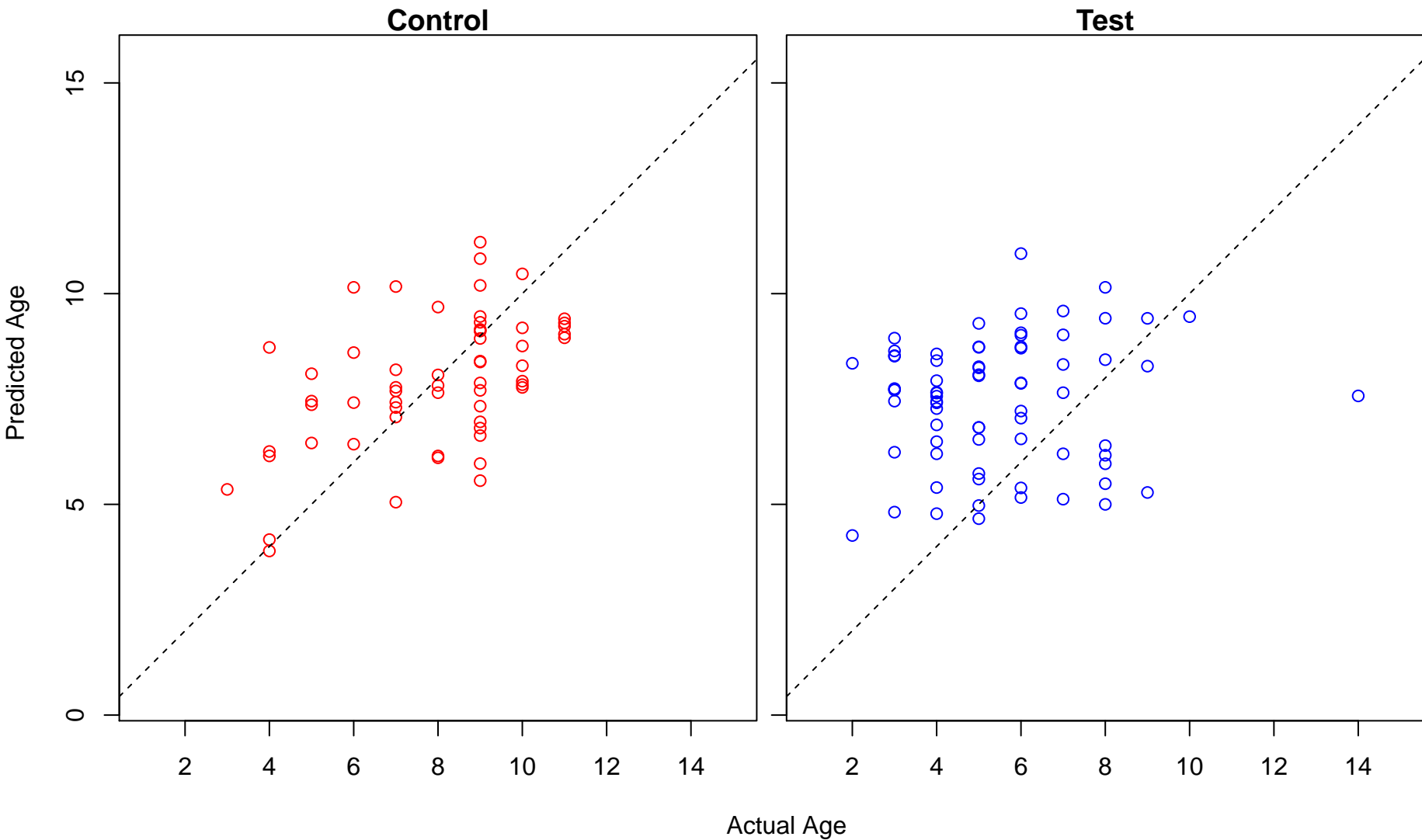
histone H4 deacetylation (Score: 1.157187)



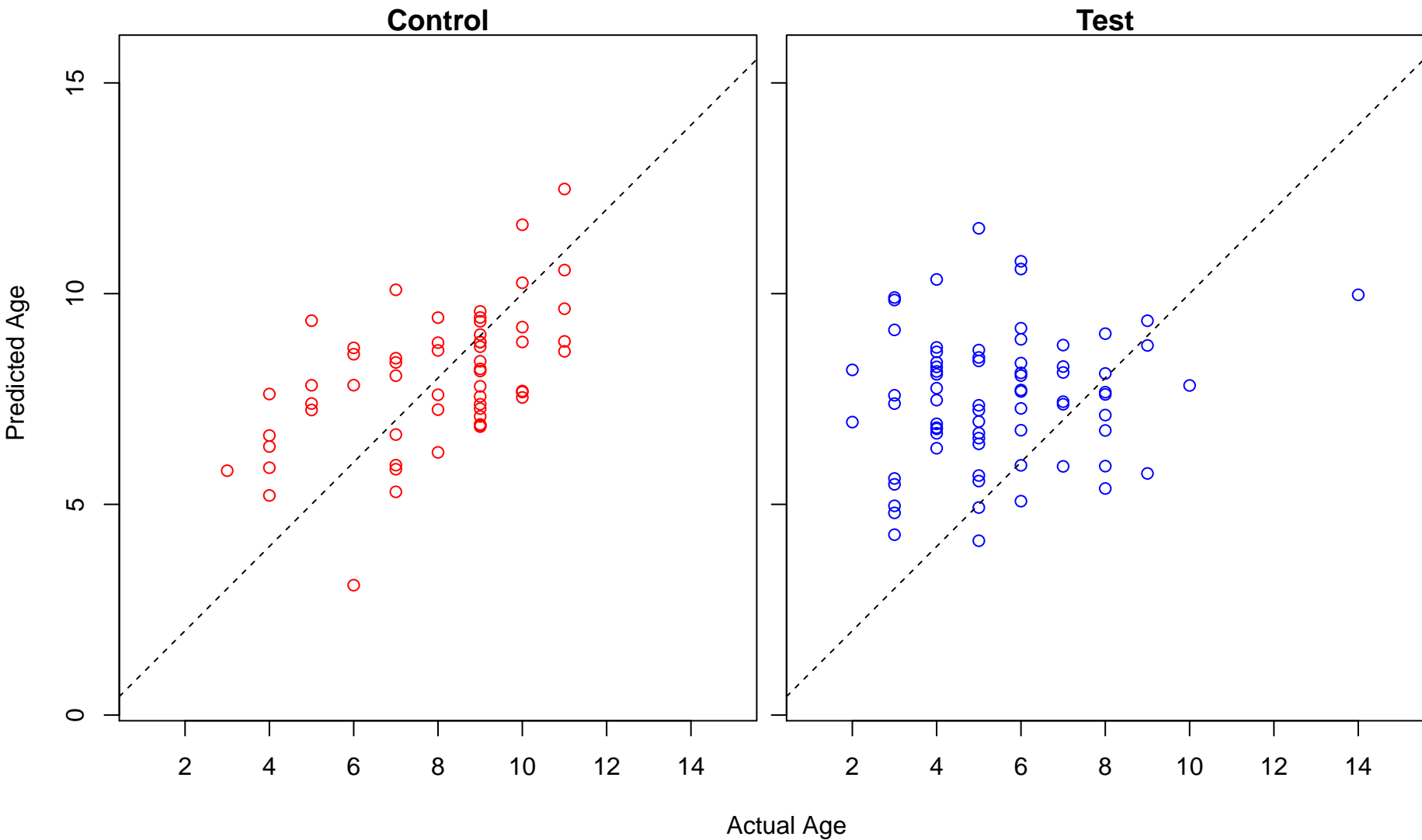
response to topologically incorrect protein (Score: 1.157063)



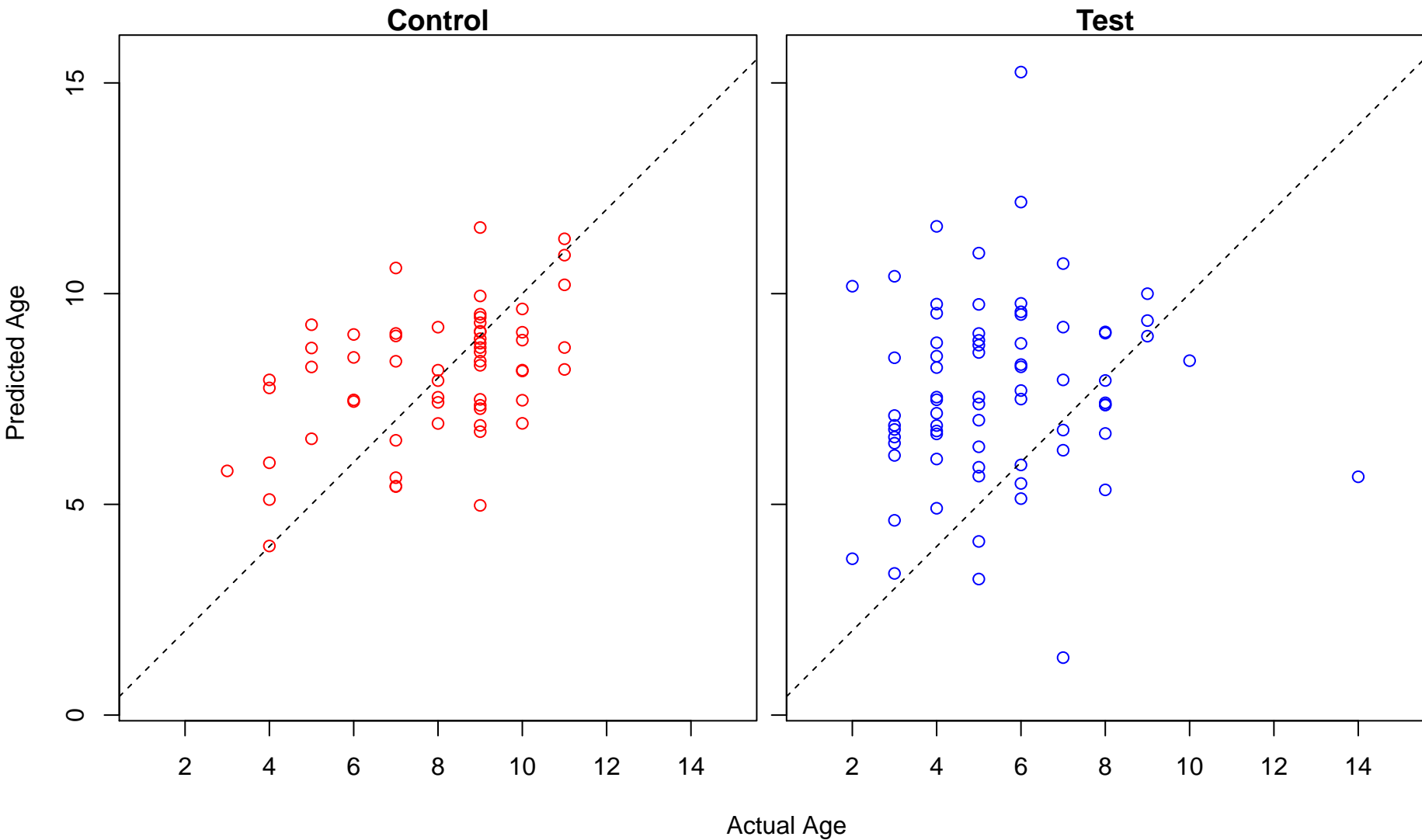
developmental pigmentation (Score: 1.156501)



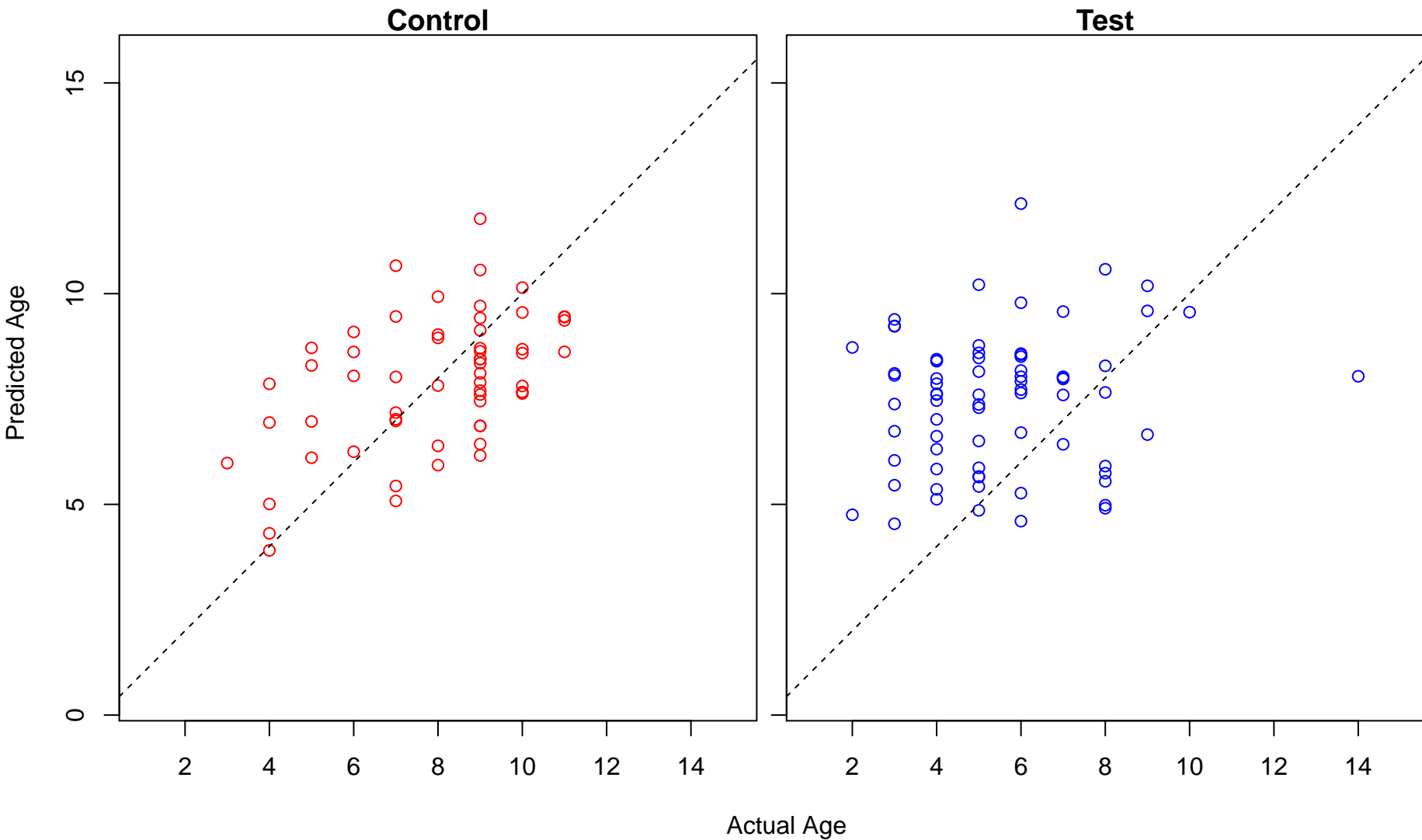
positive regulation of dendritic cell antigen processing and presentation (Score: 1.155804)



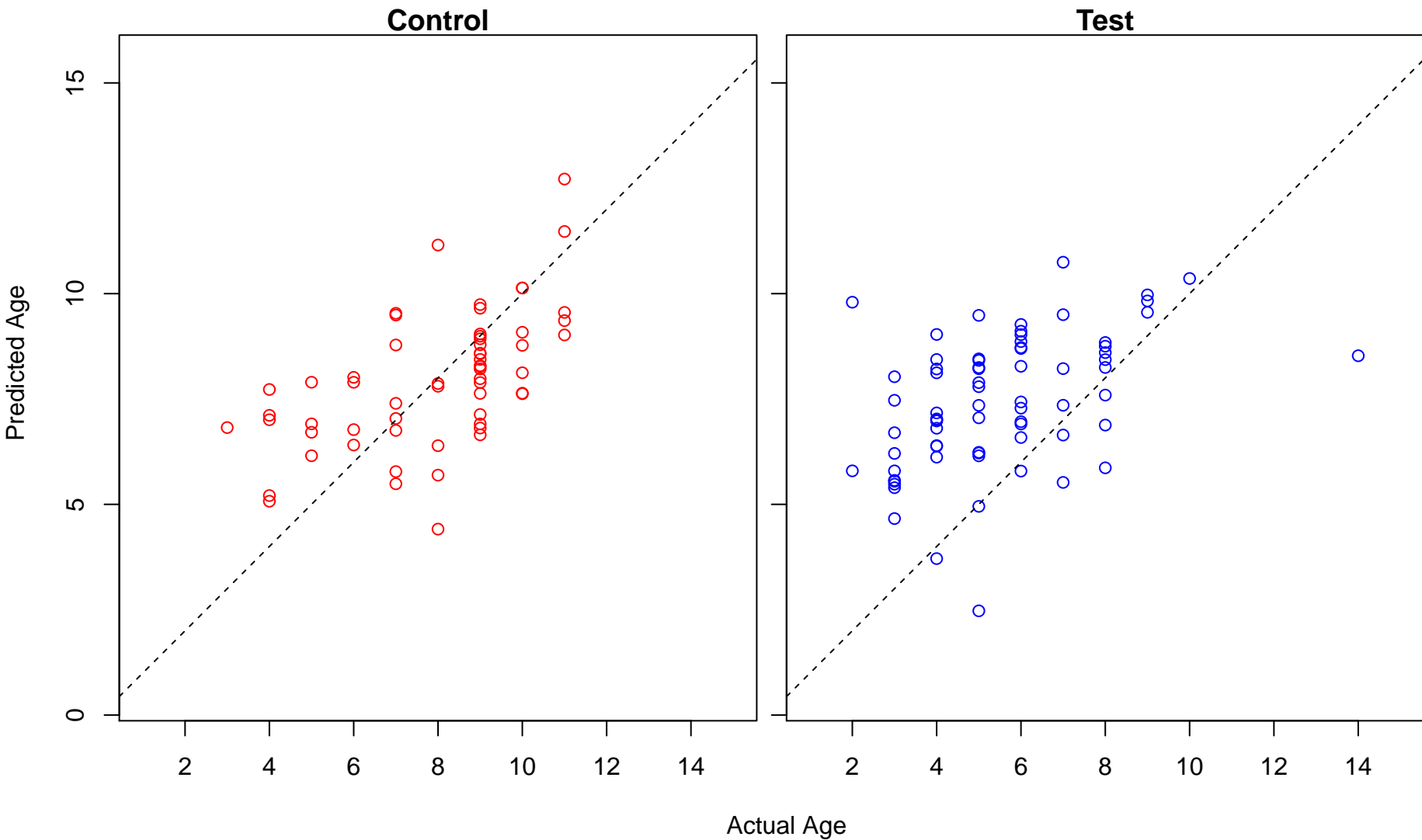
neuron differentiation (Score: 1.154749)



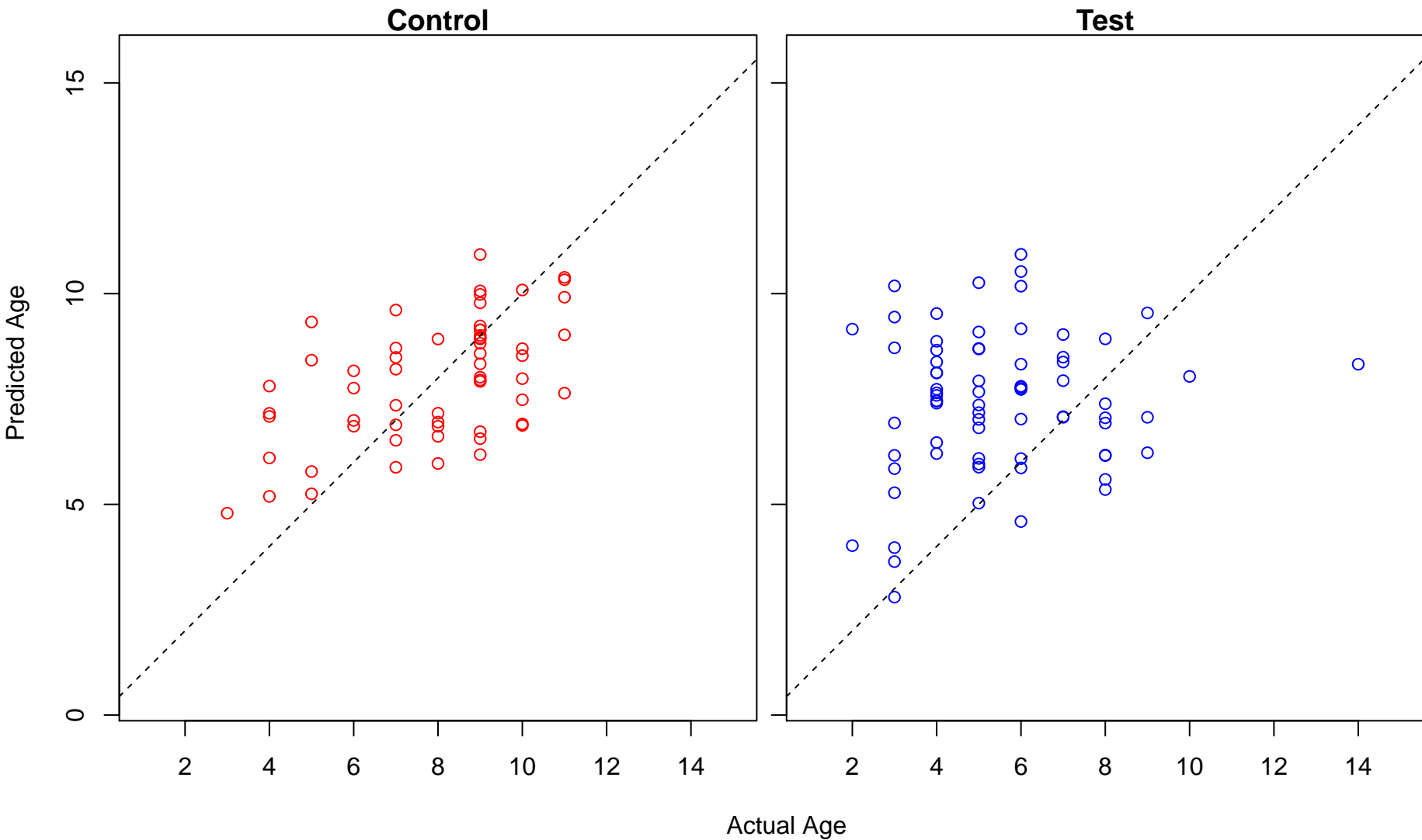
cellular pigmentation (Score: 1.154633)



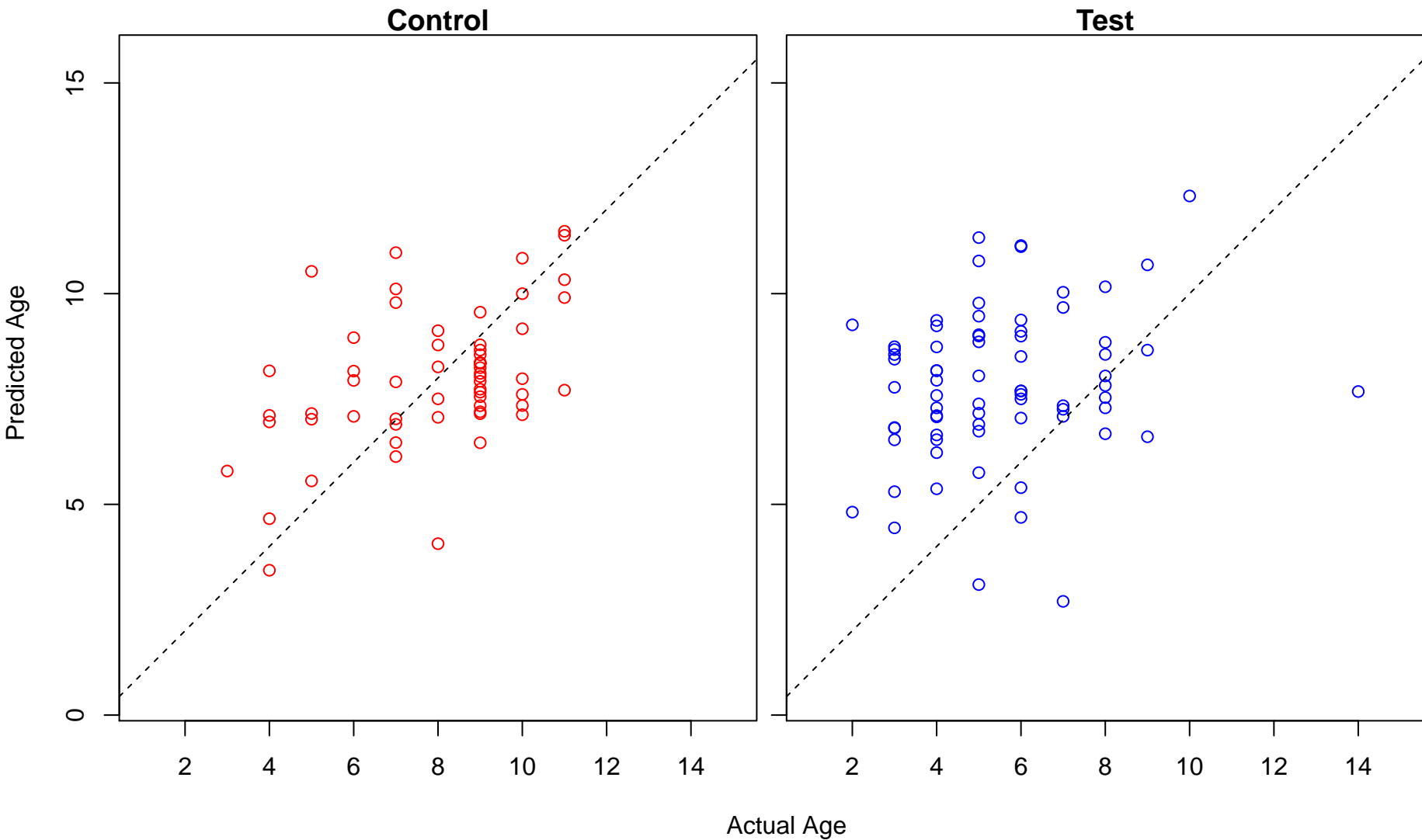
single-organism metabolic process (Score: 1.153980)



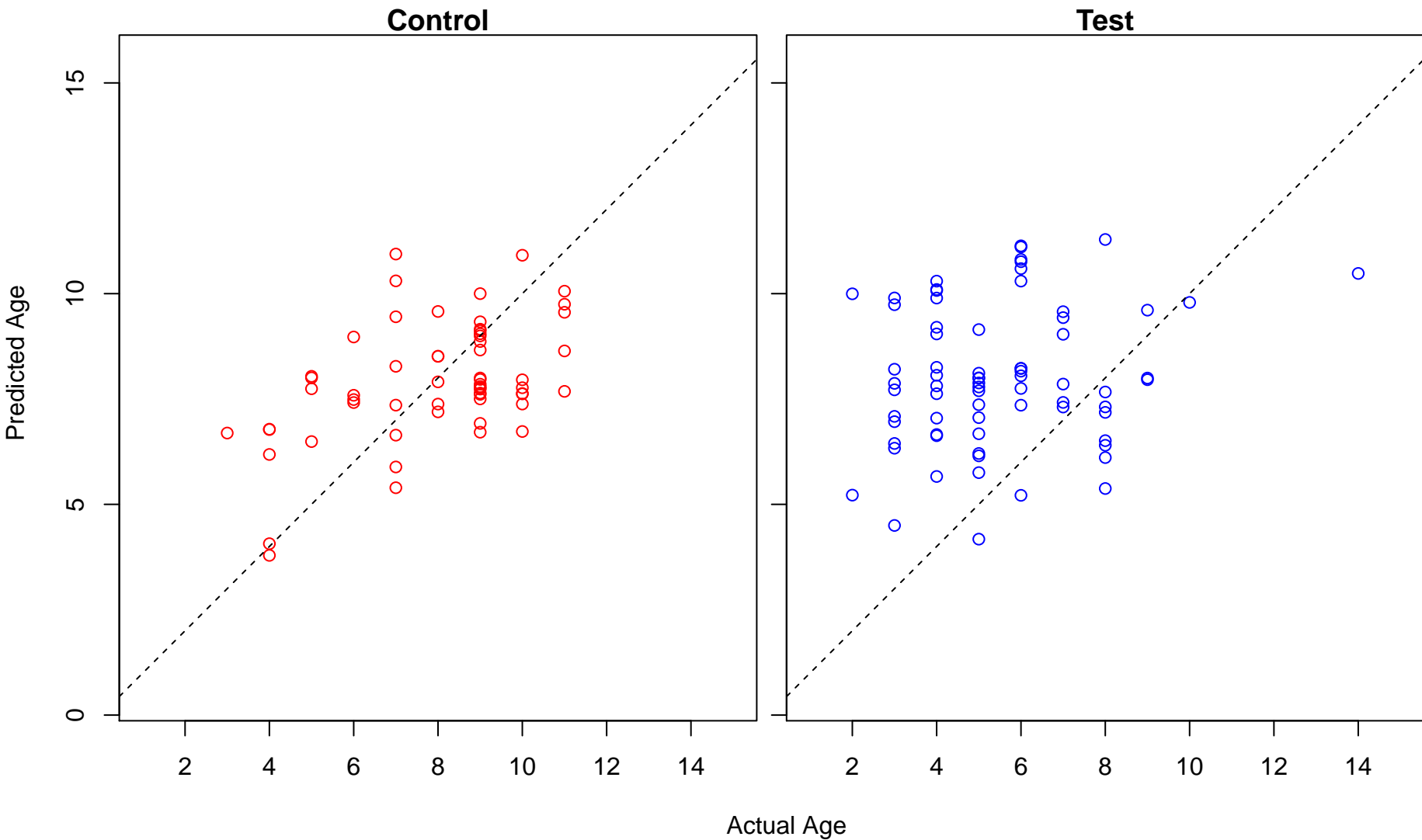
prostatic bud formation (Score: 1.152085)



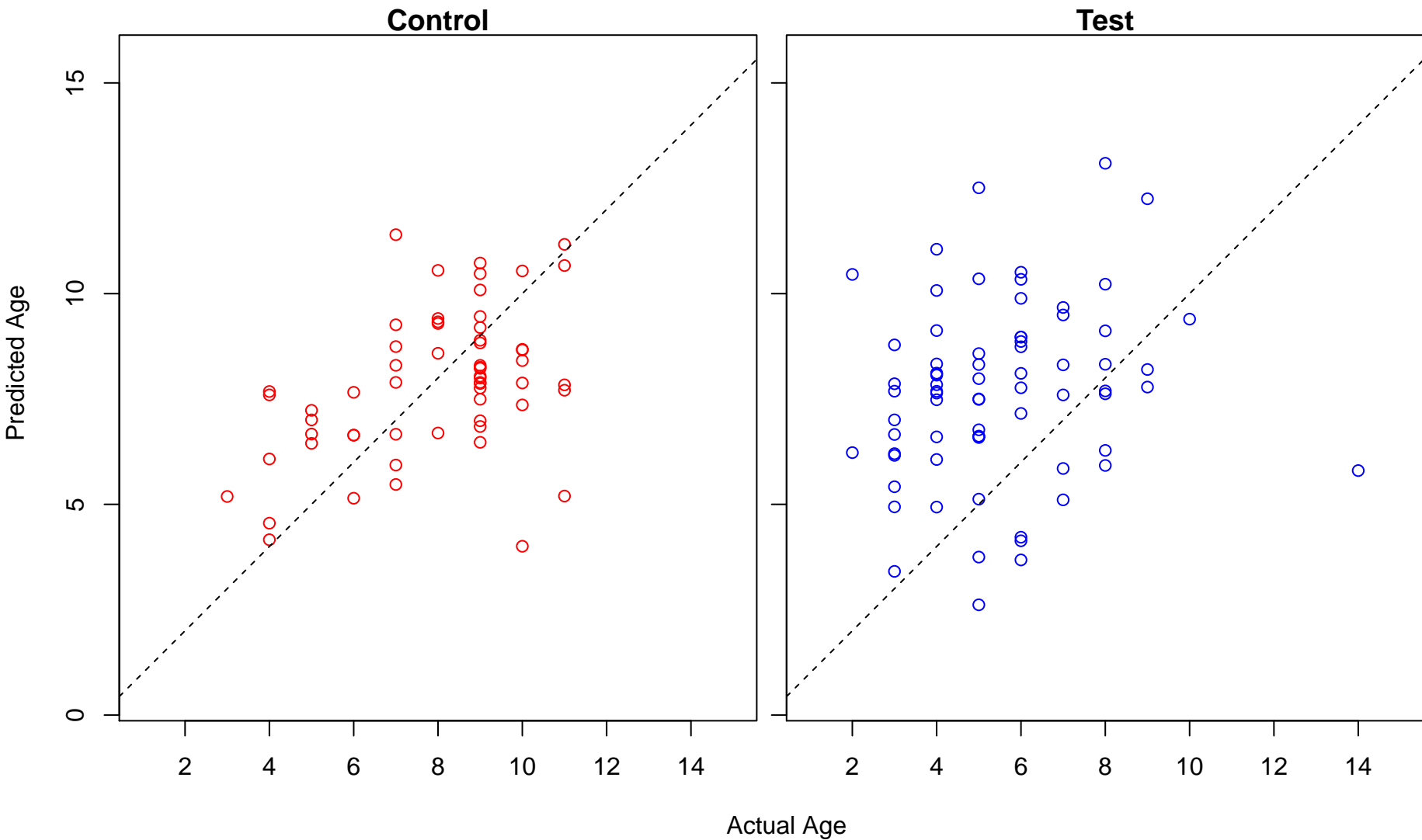
iron ion homeostasis (Score: 1.151663)



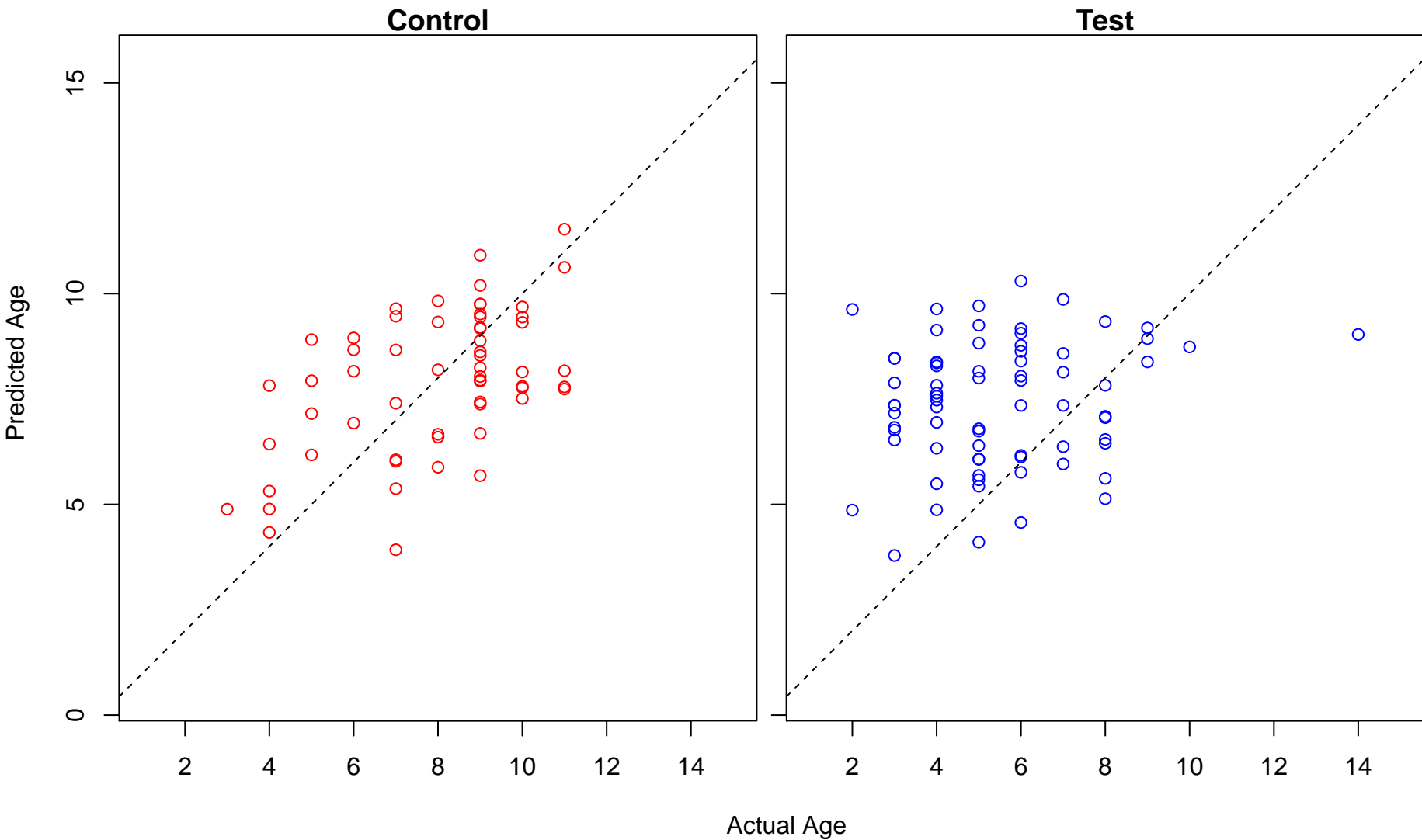
regulation of Ras protein signal transduction (Score: 1.146227)



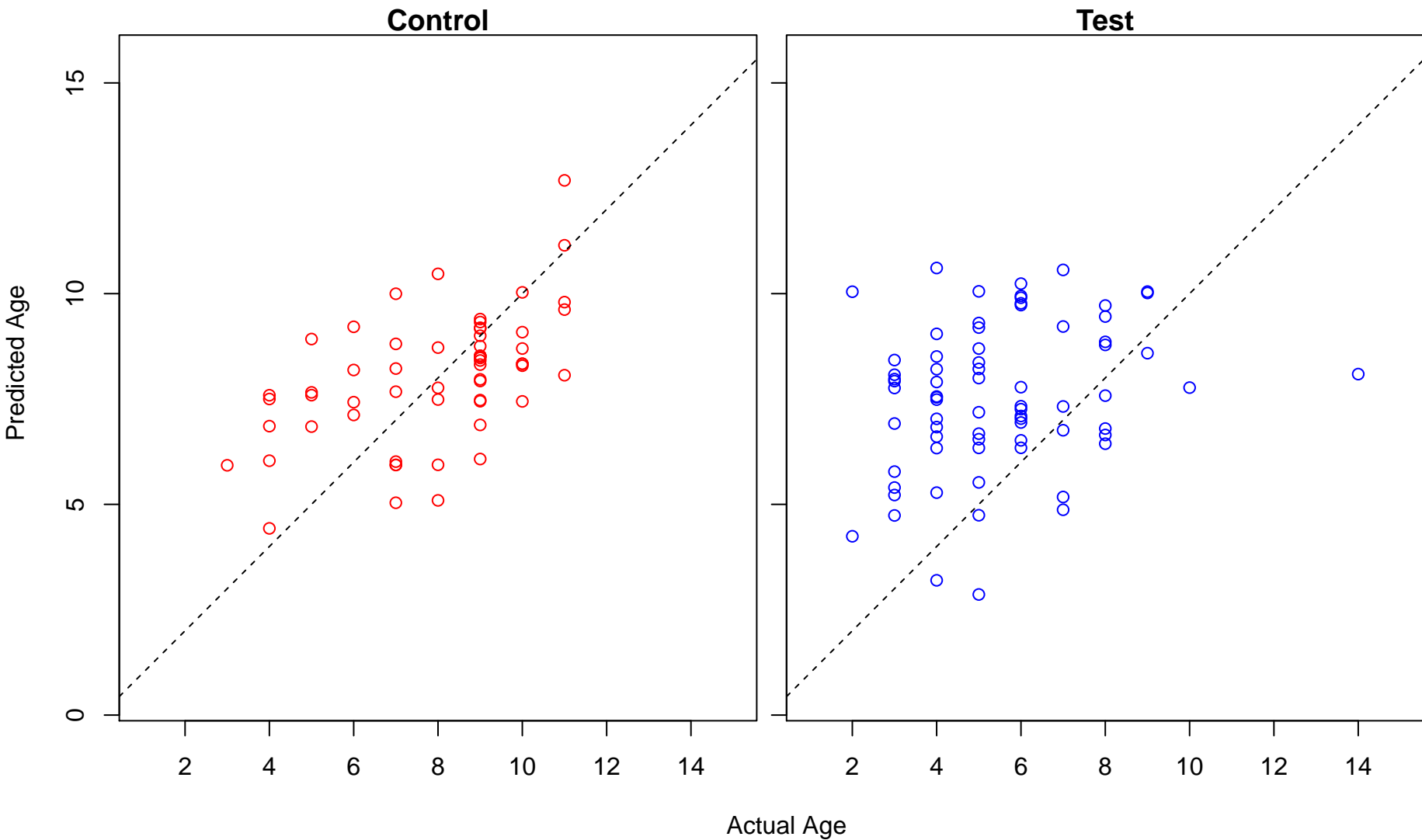
multicellular organismal homeostasis (Score: 1.145871)



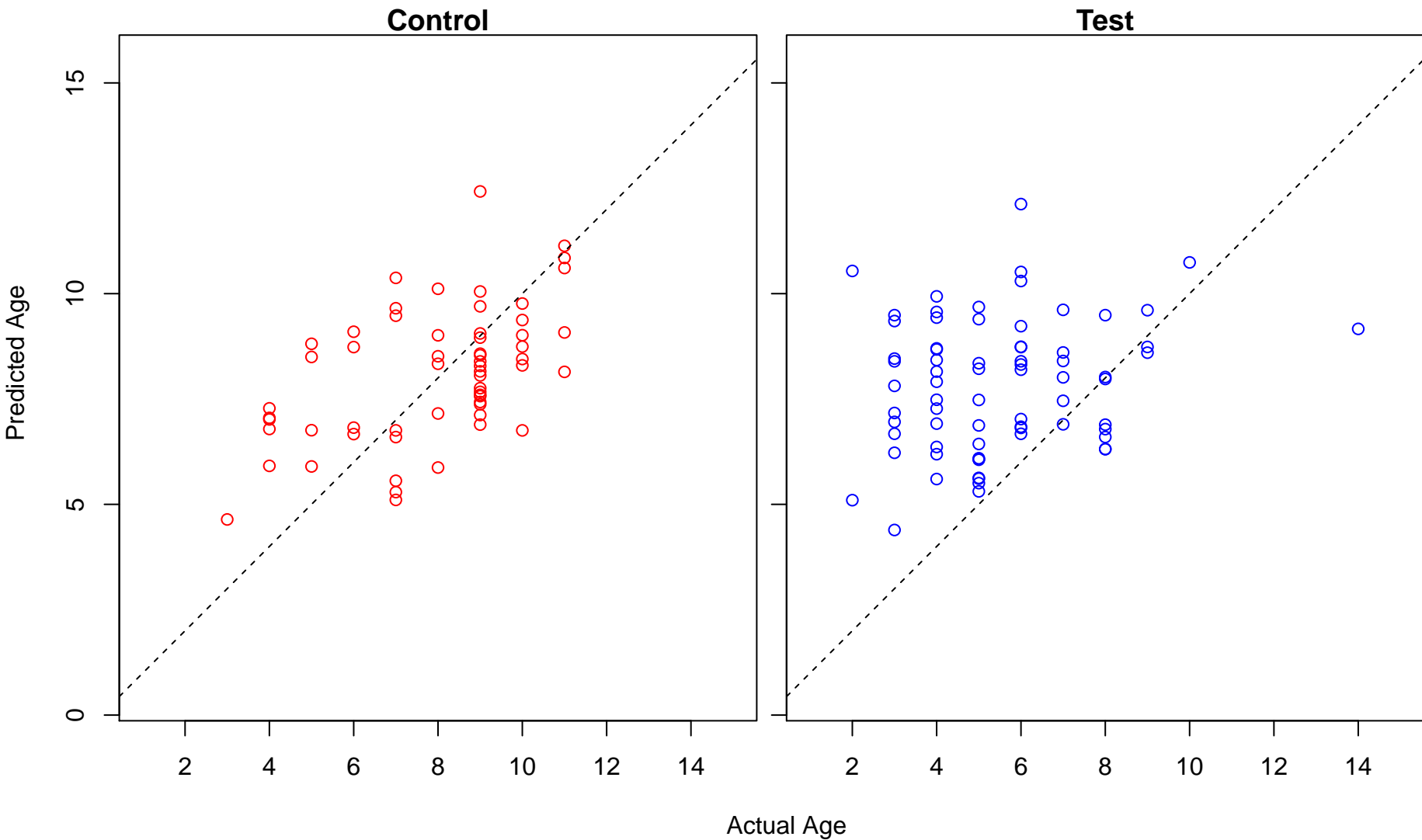
cell-cell adhesion (Score: 1.144496)



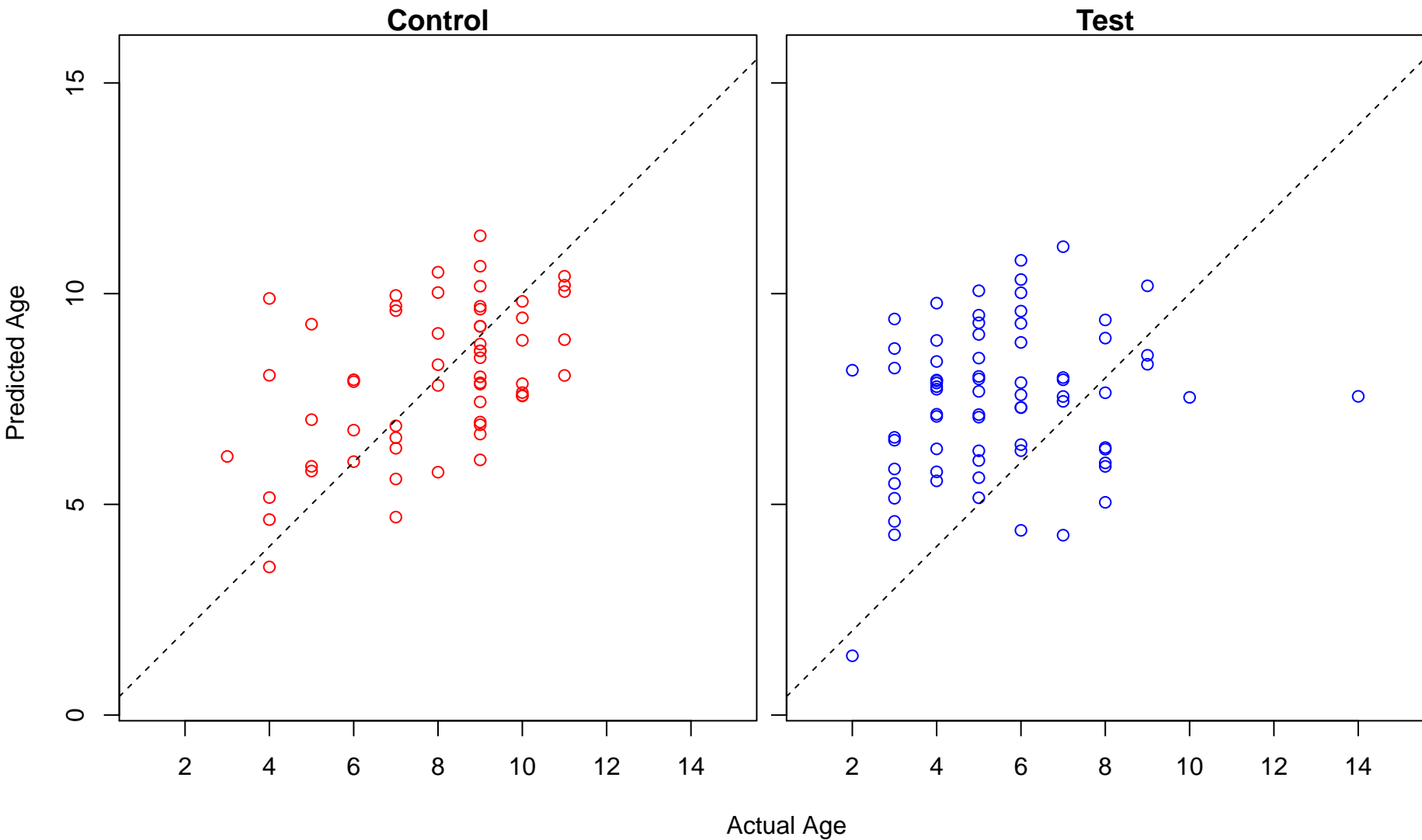
negative regulation of cellular process (Score: 1.144193)



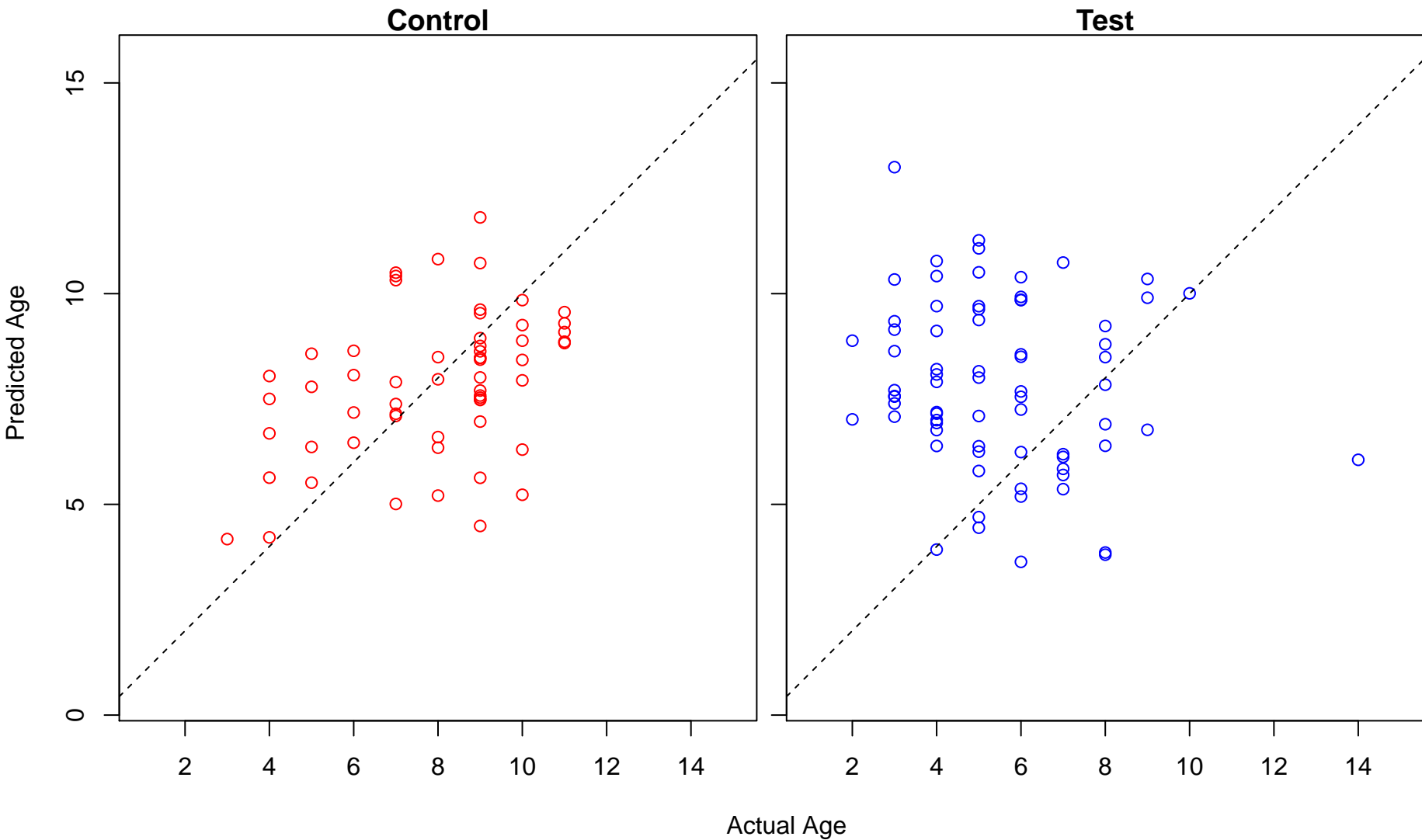
positive regulation of cellular component organization (Score: 1.143293)



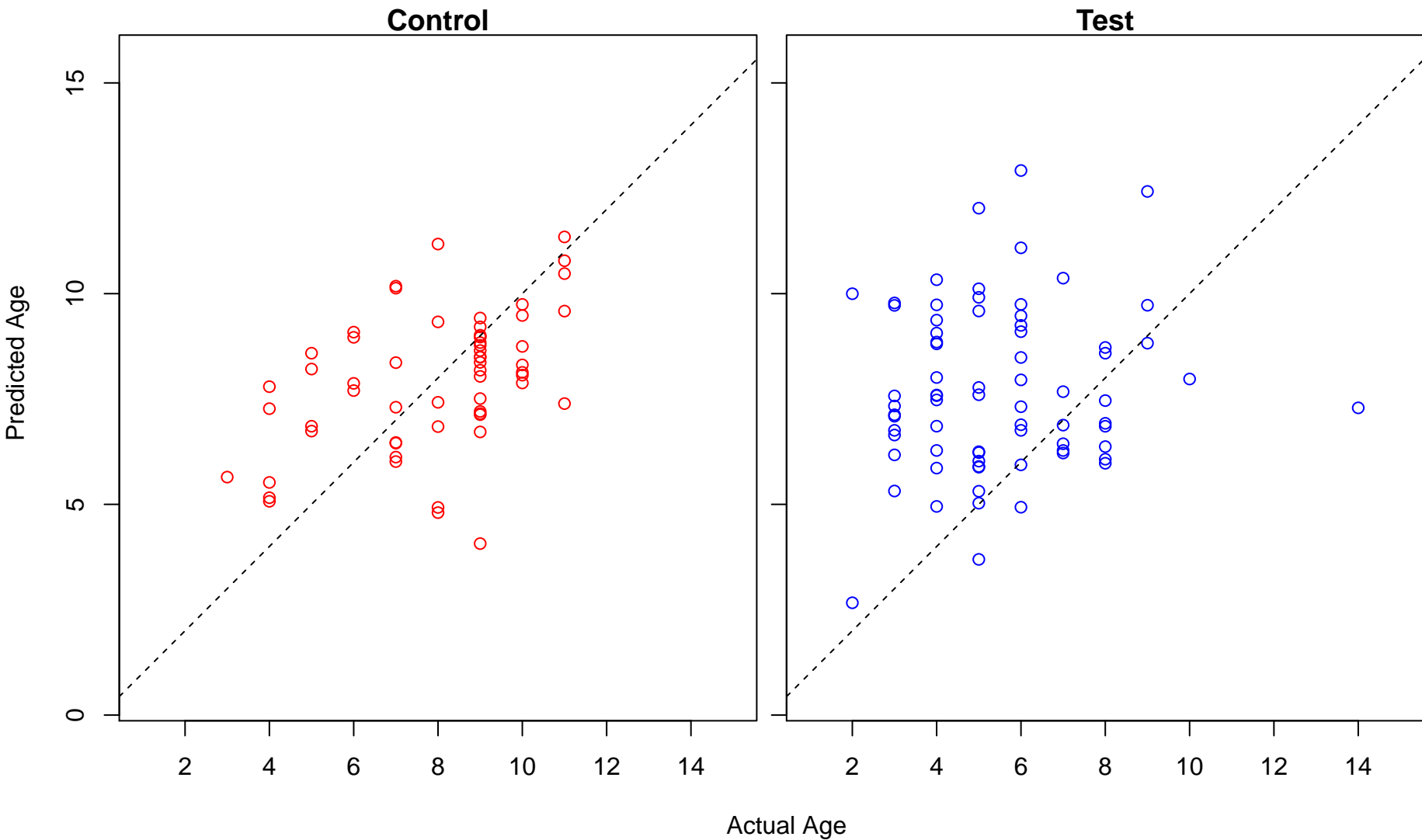
positive regulation of JAK-STAT cascade (Score: 1.142979)



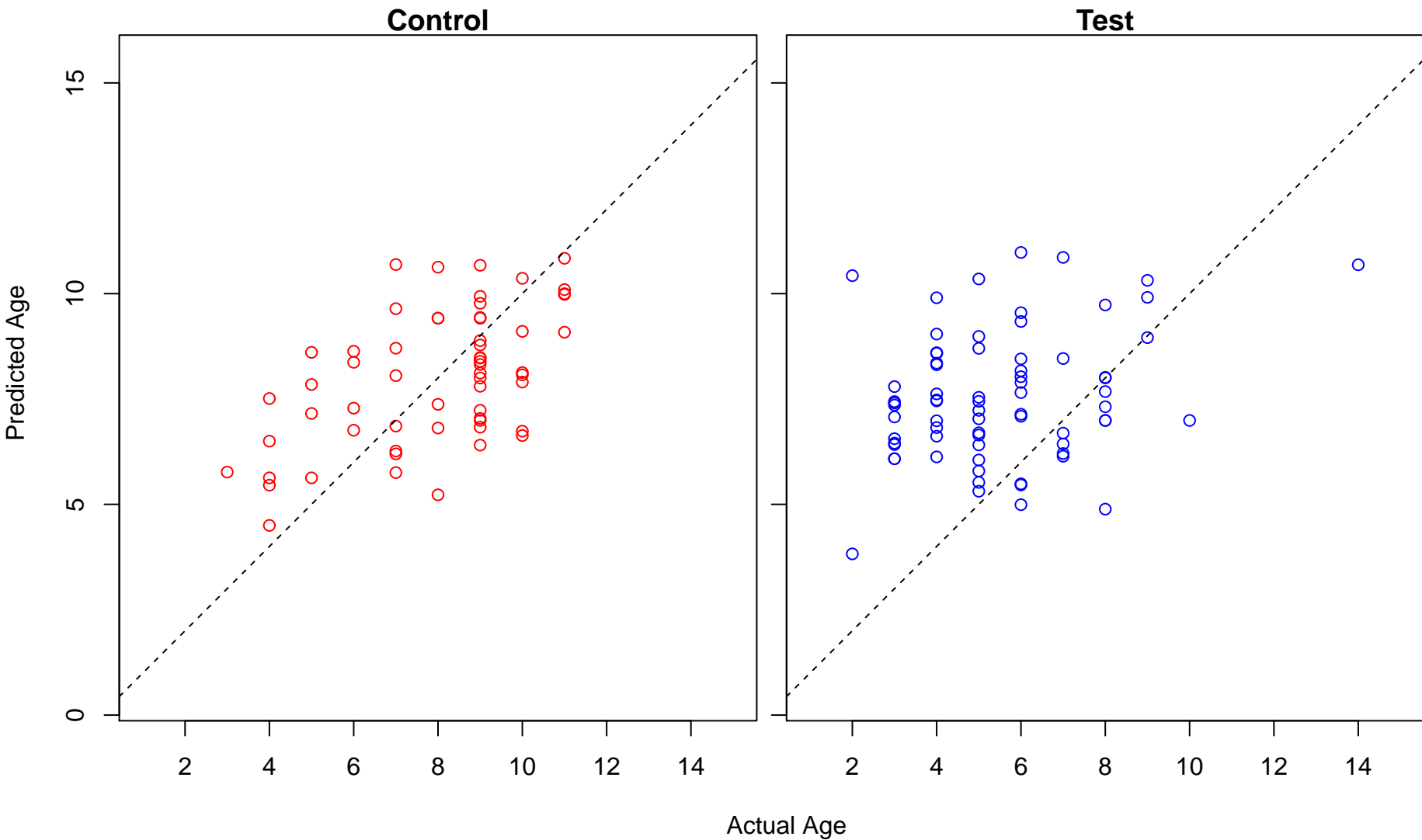
cerebral cortex tangential migration (Score: 1.139501)



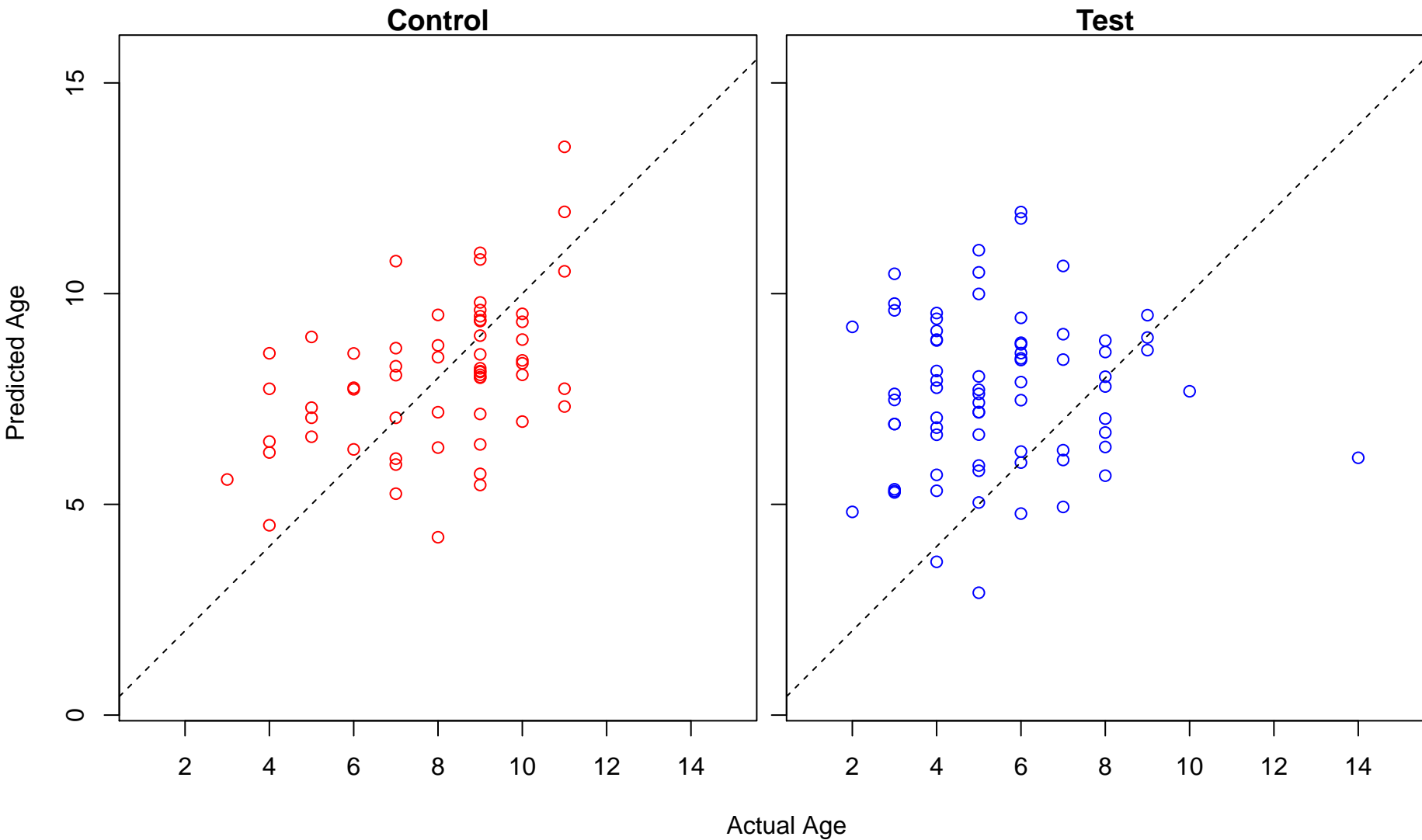
cellular response to peptide (Score: 1.138670)



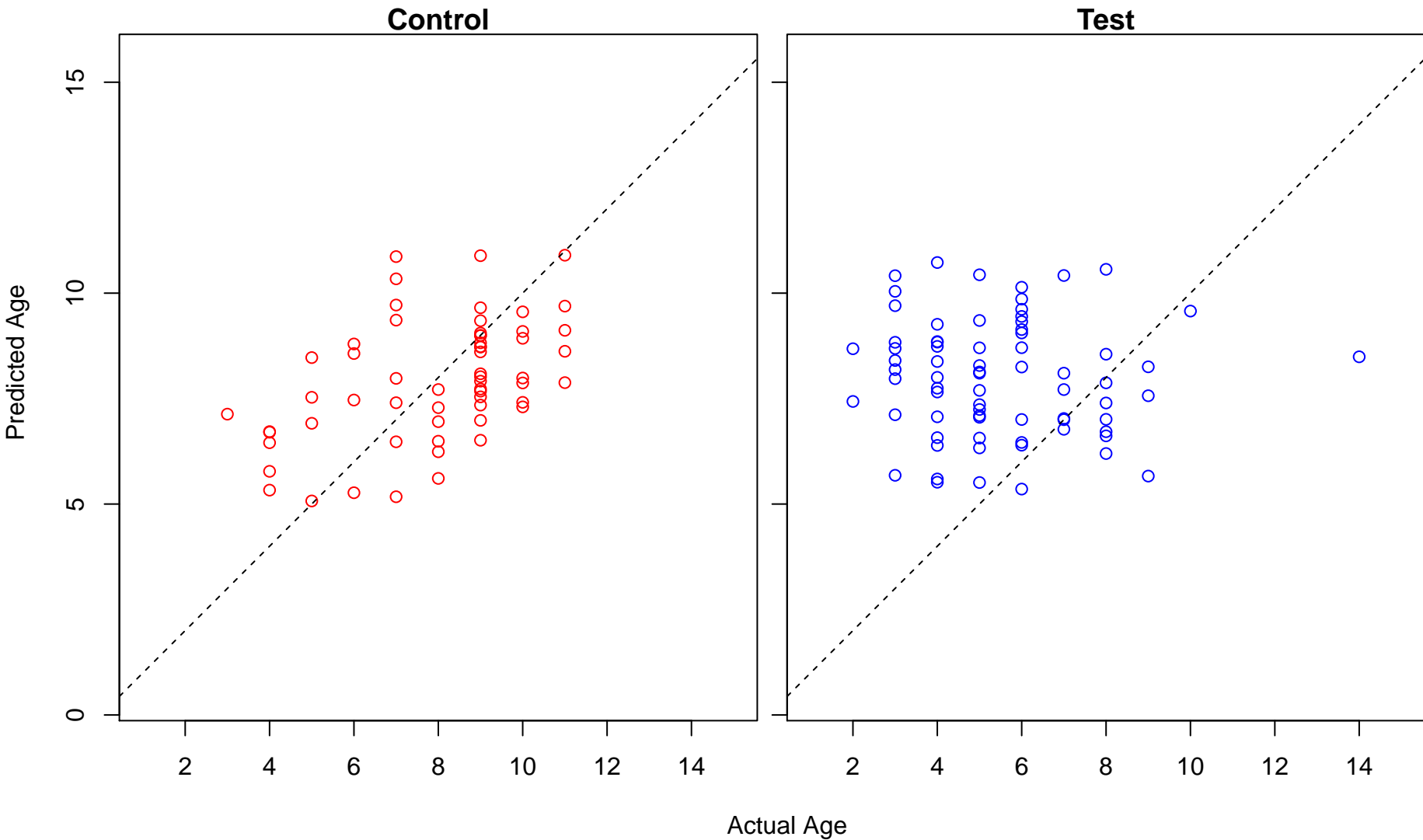
exocytosis (Score: 1.138260)



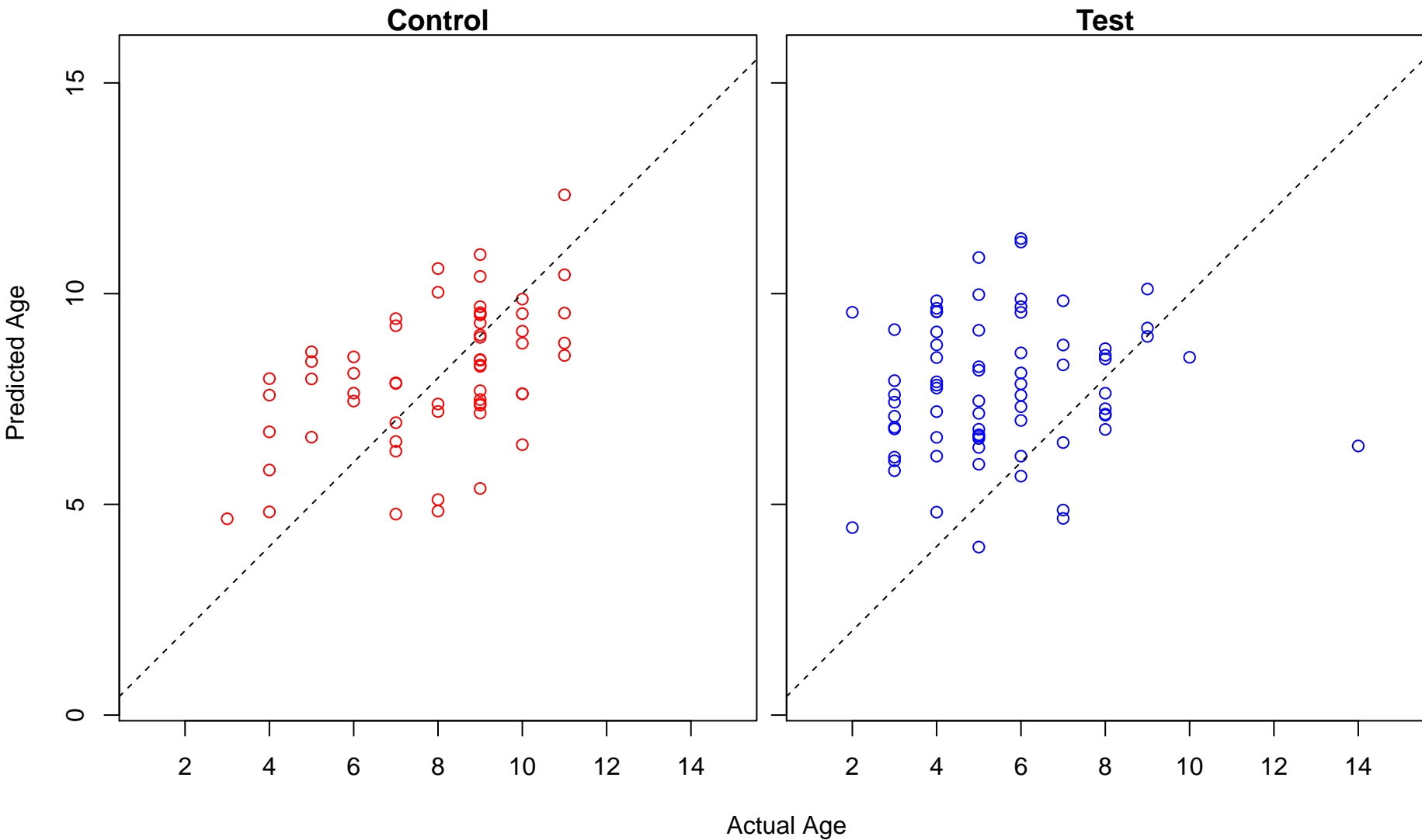
negative regulation of phosphorylation (Score: 1.137679)



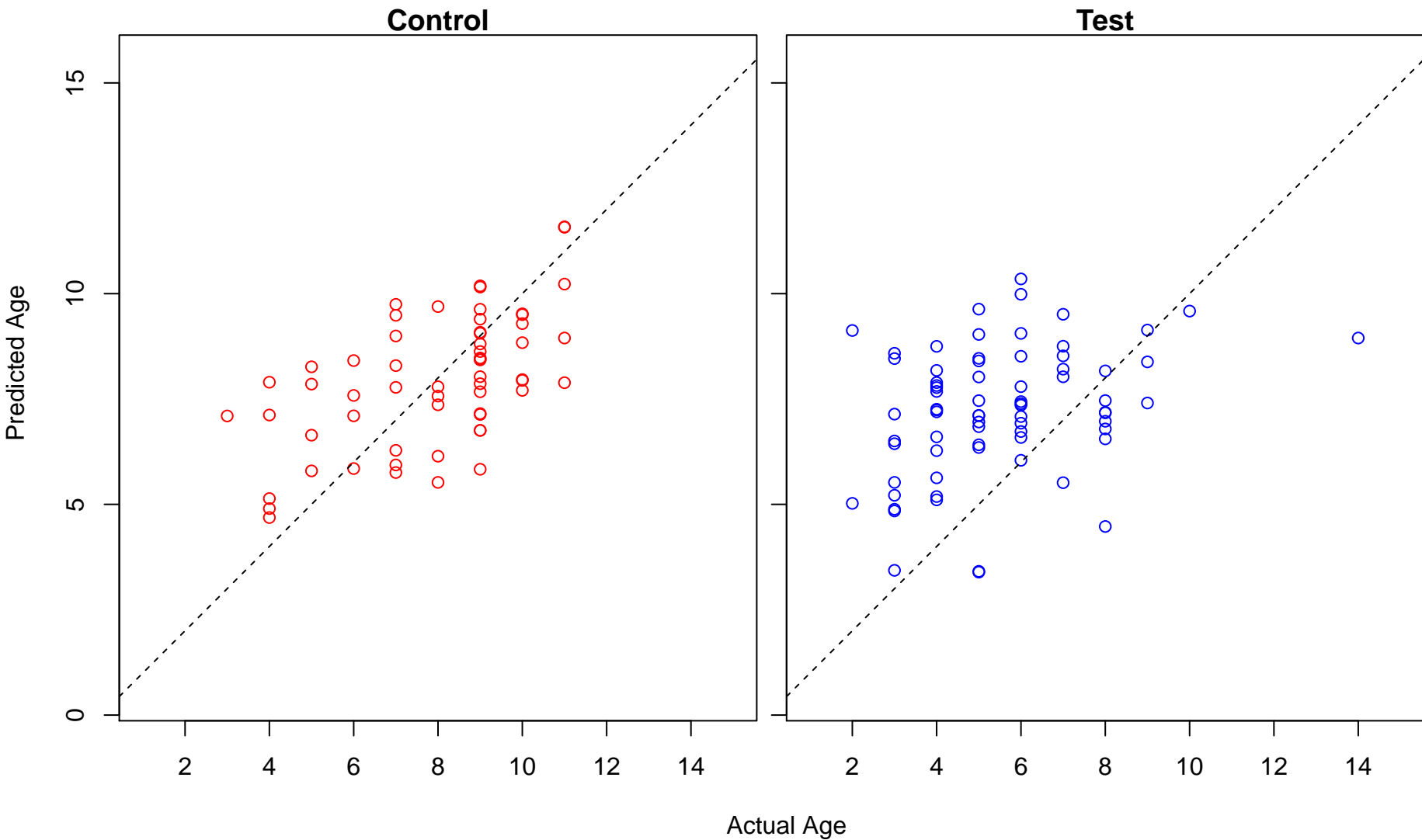
intrinsic apoptotic signaling pathway in response to DNA damage (Score: 1.137453)



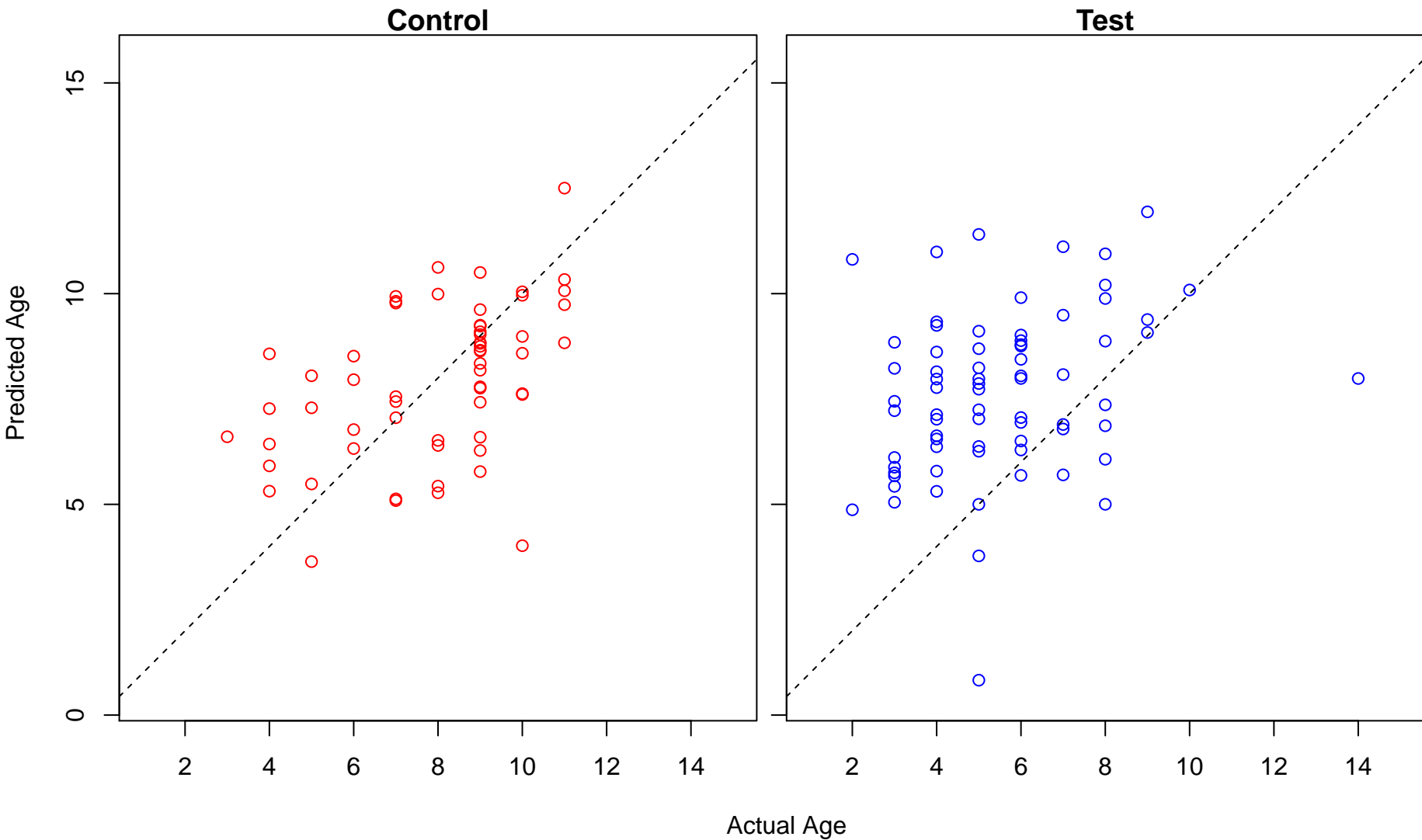
regulation of cellular protein metabolic process (Score: 1.136935)



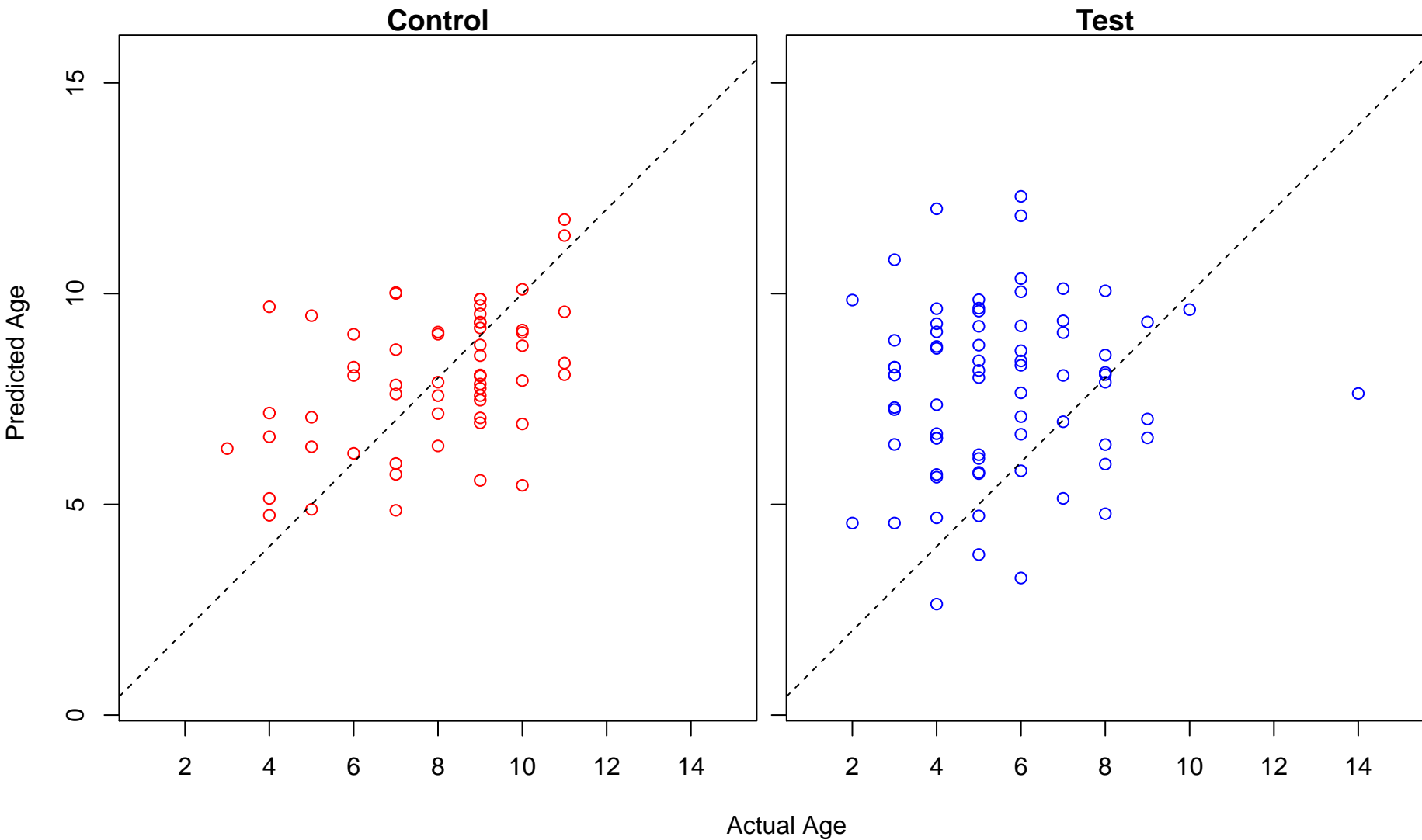
membrane organization (Score: 1.134874)



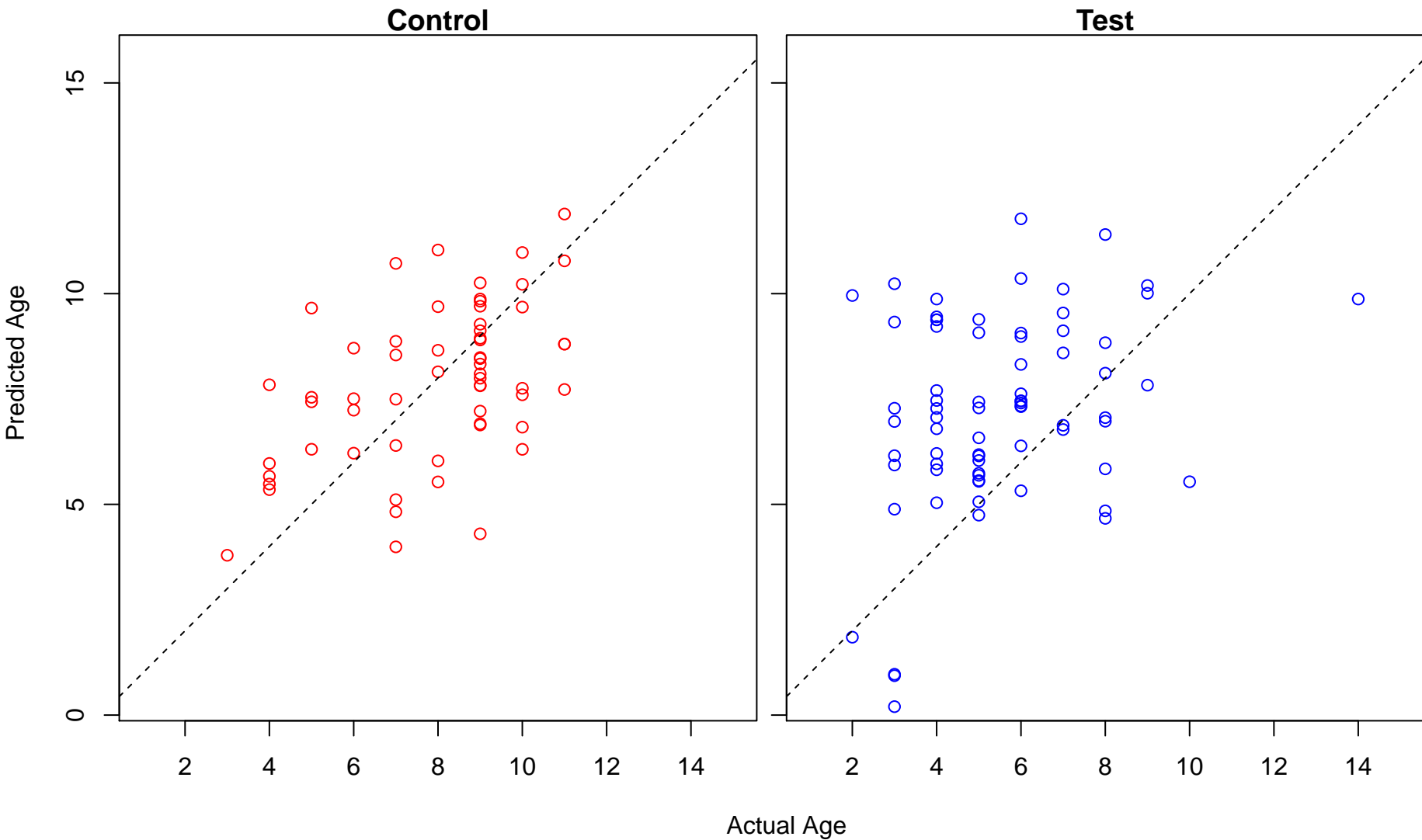
phagocytosis (Score: 1.134476)



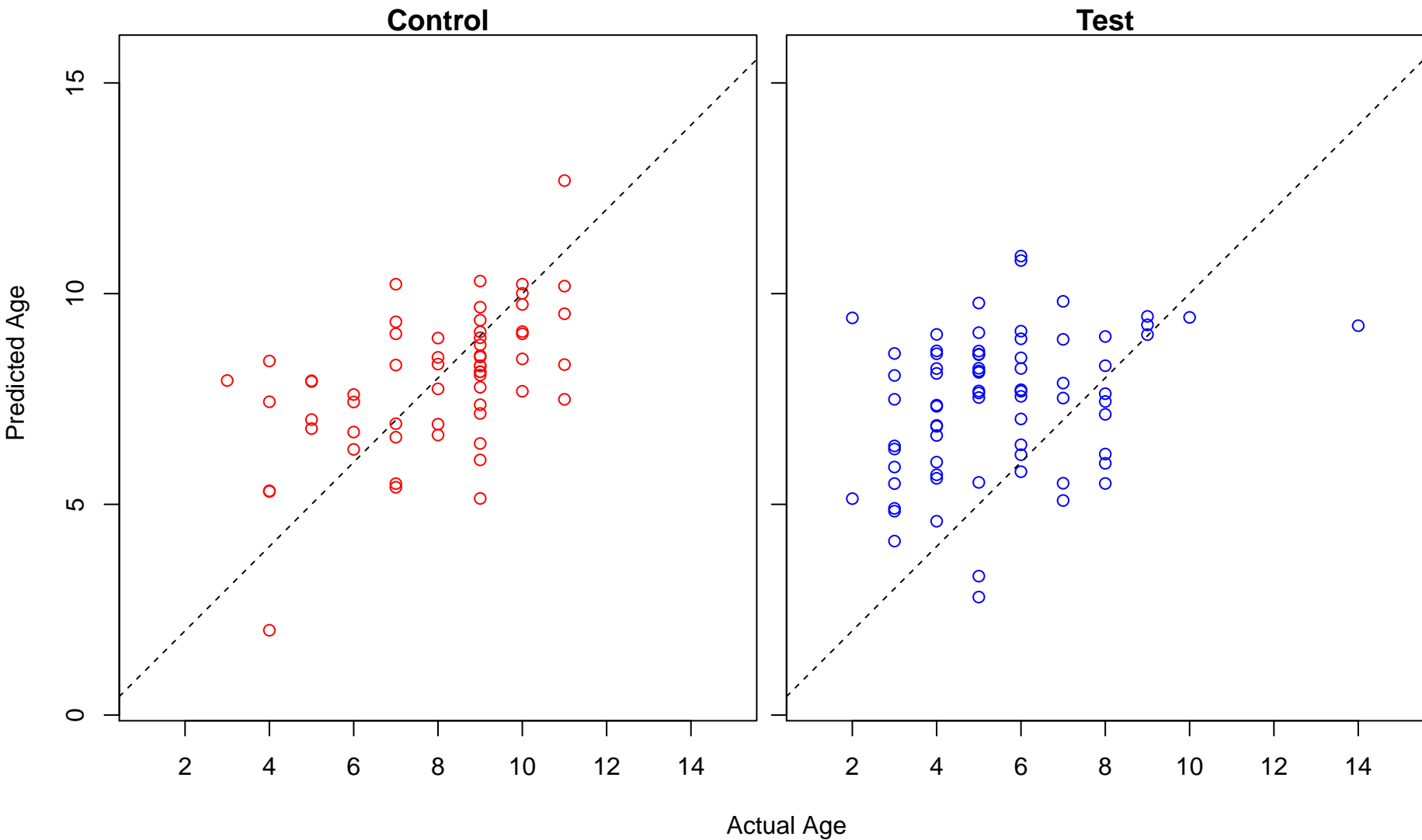
glycerolipid biosynthetic process (Score: 1.134452)



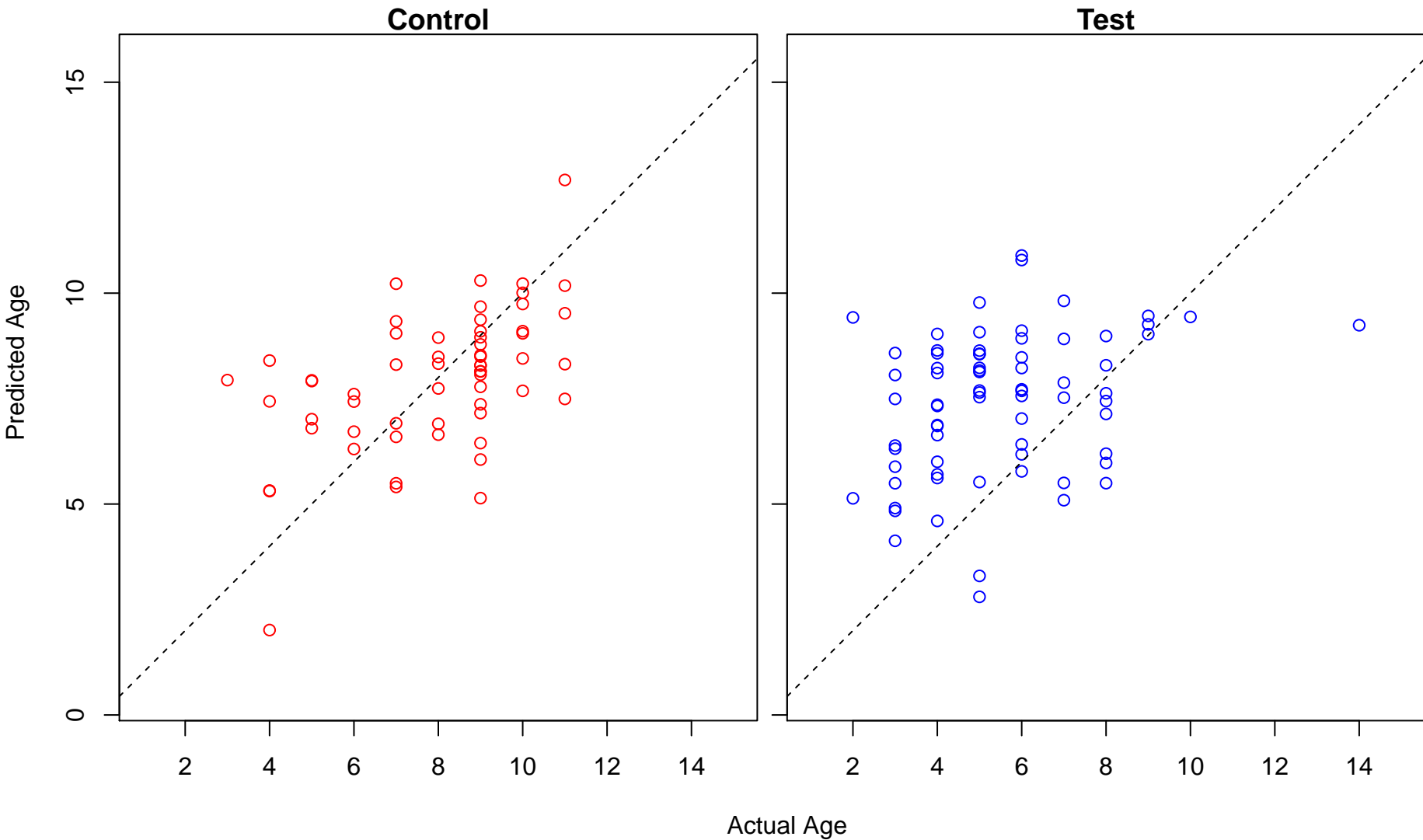
renal tubule morphogenesis (Score: 1.132519)



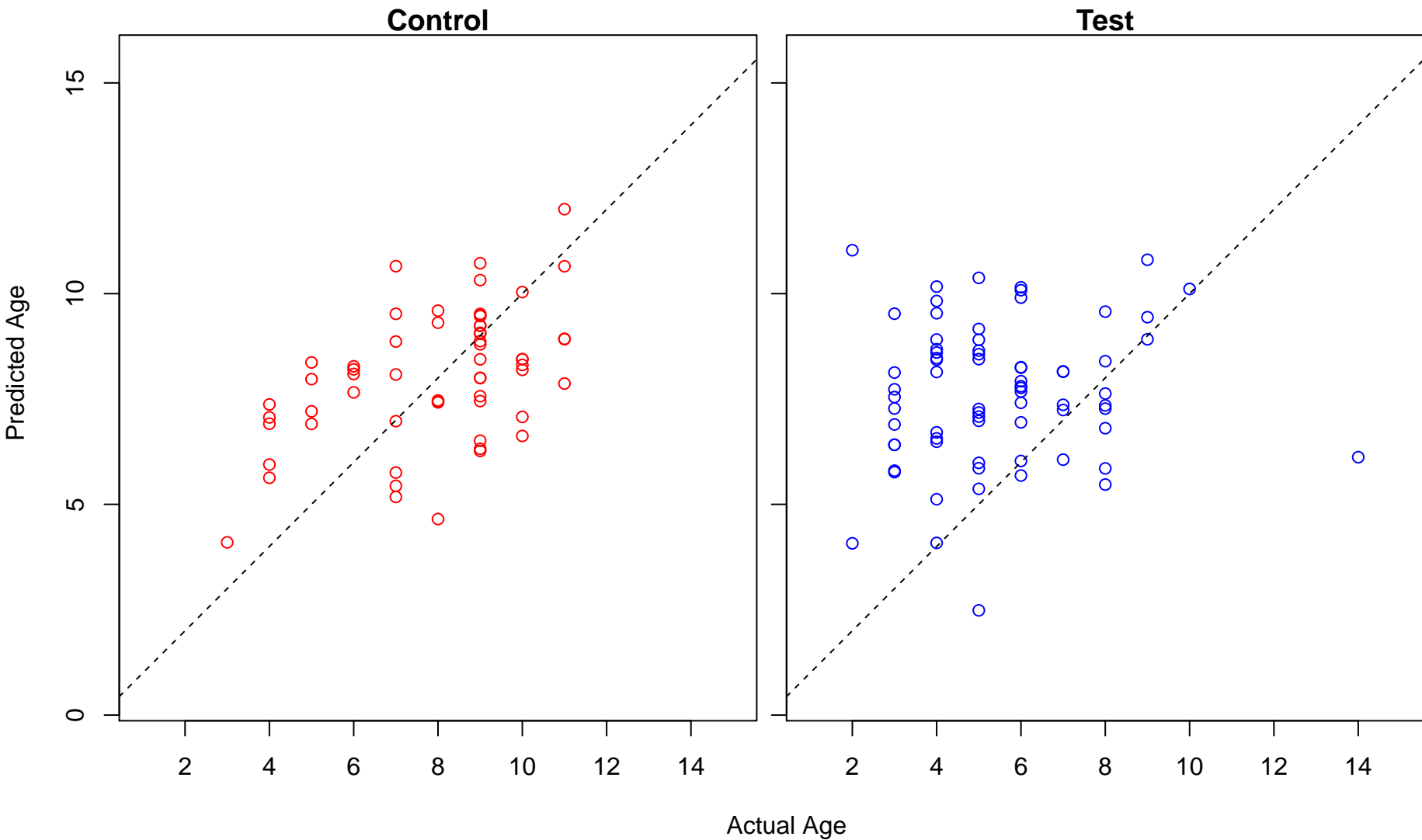
symbiosis, encompassing mutualism through parasitism (Score: 1.132026)



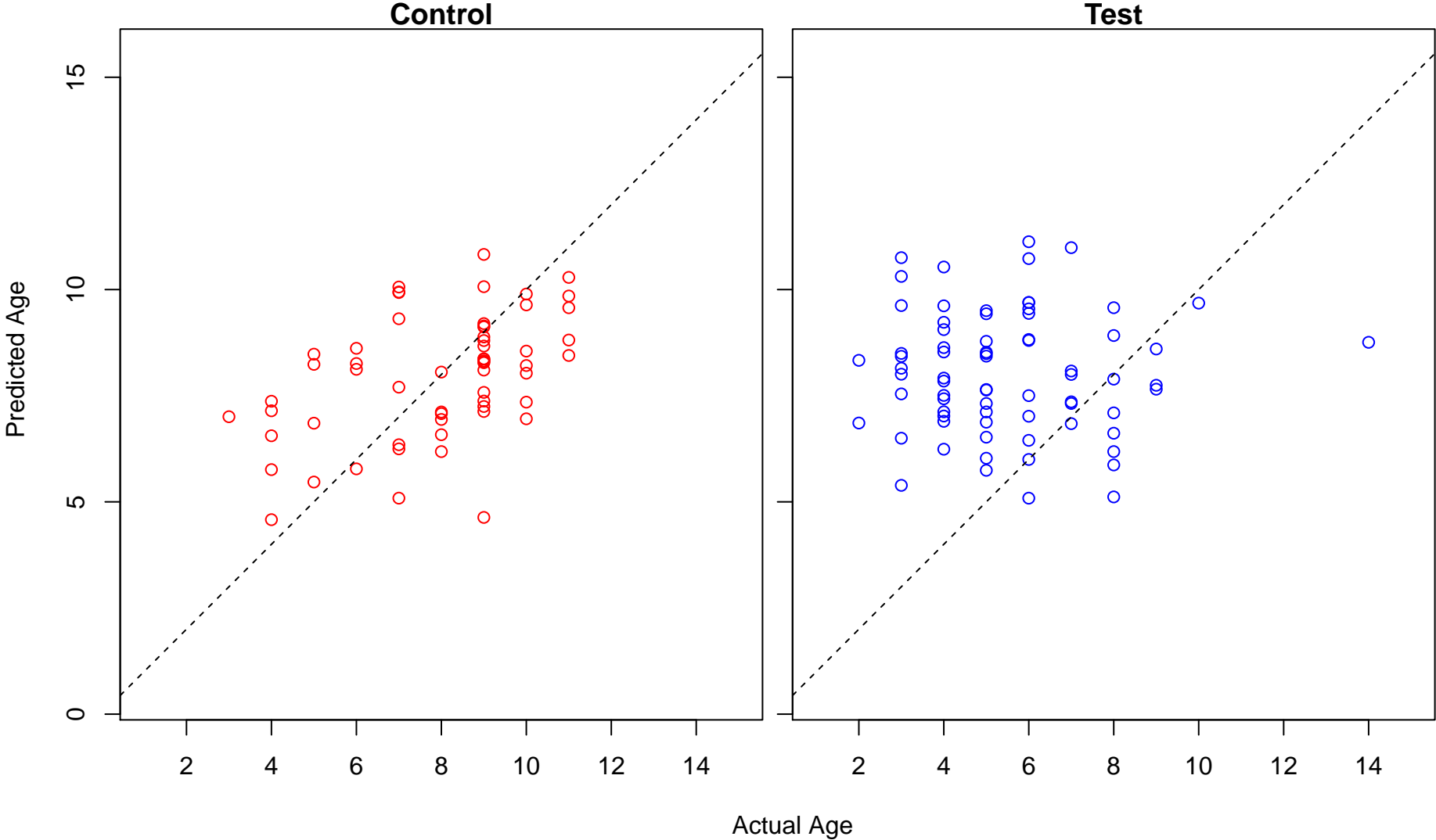
interspecies interaction between organisms (Score: 1.132026)



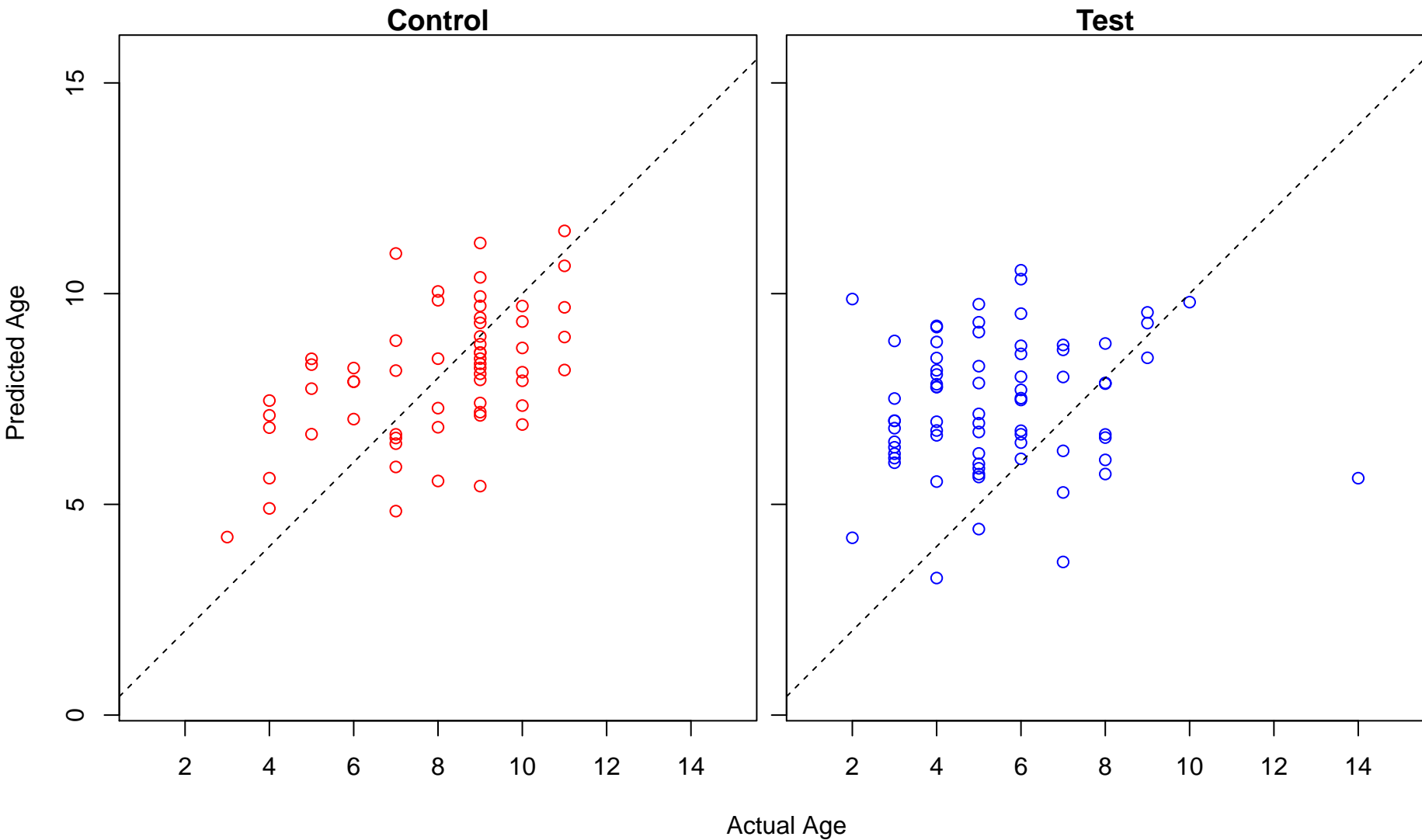
positive regulation of nitrogen compound metabolic process (Score: 1.131312)



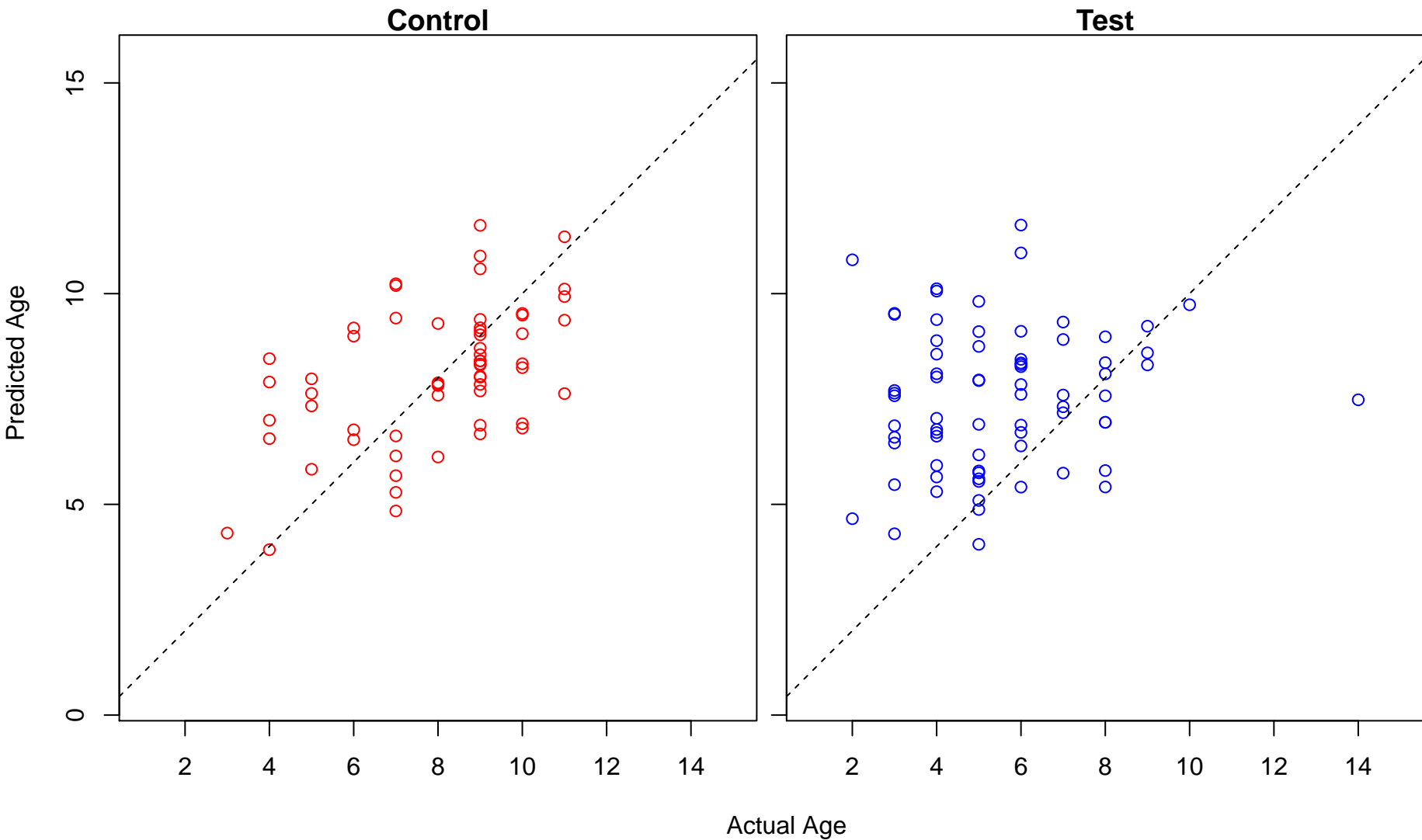
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (Score: 1.131)



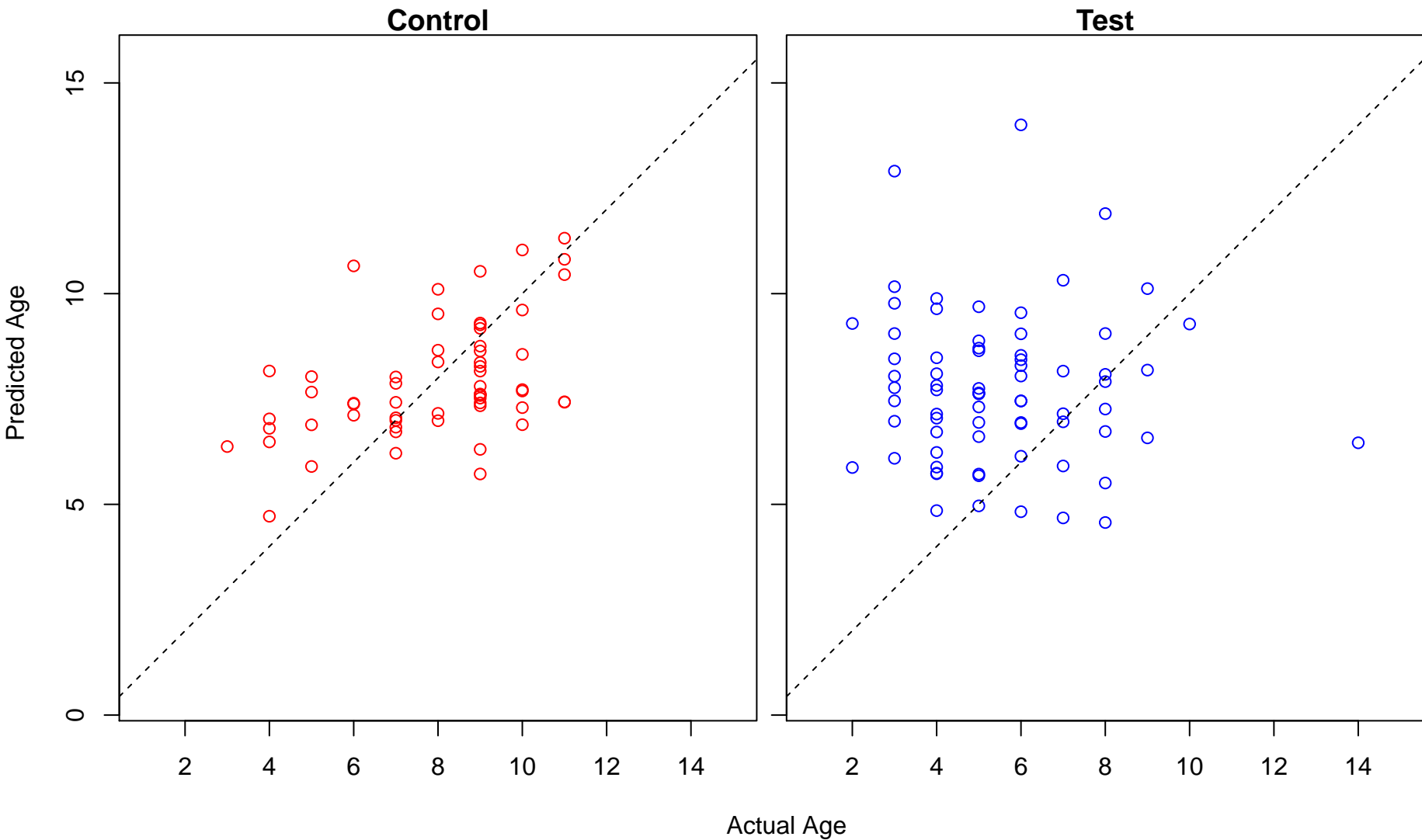
regulation of molecular function (Score: 1.130576)



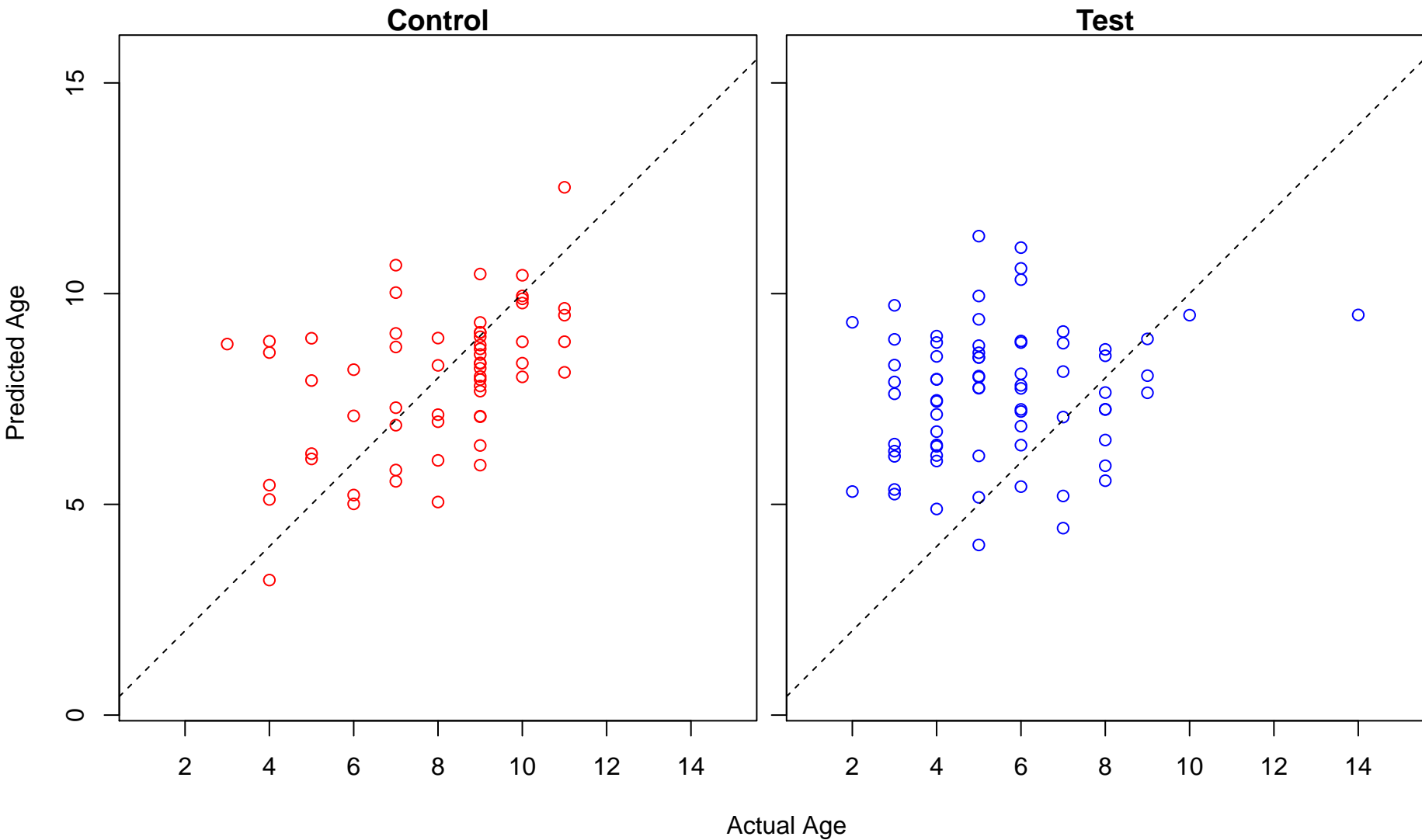
regulation of organelle organization (Score: 1.130296)



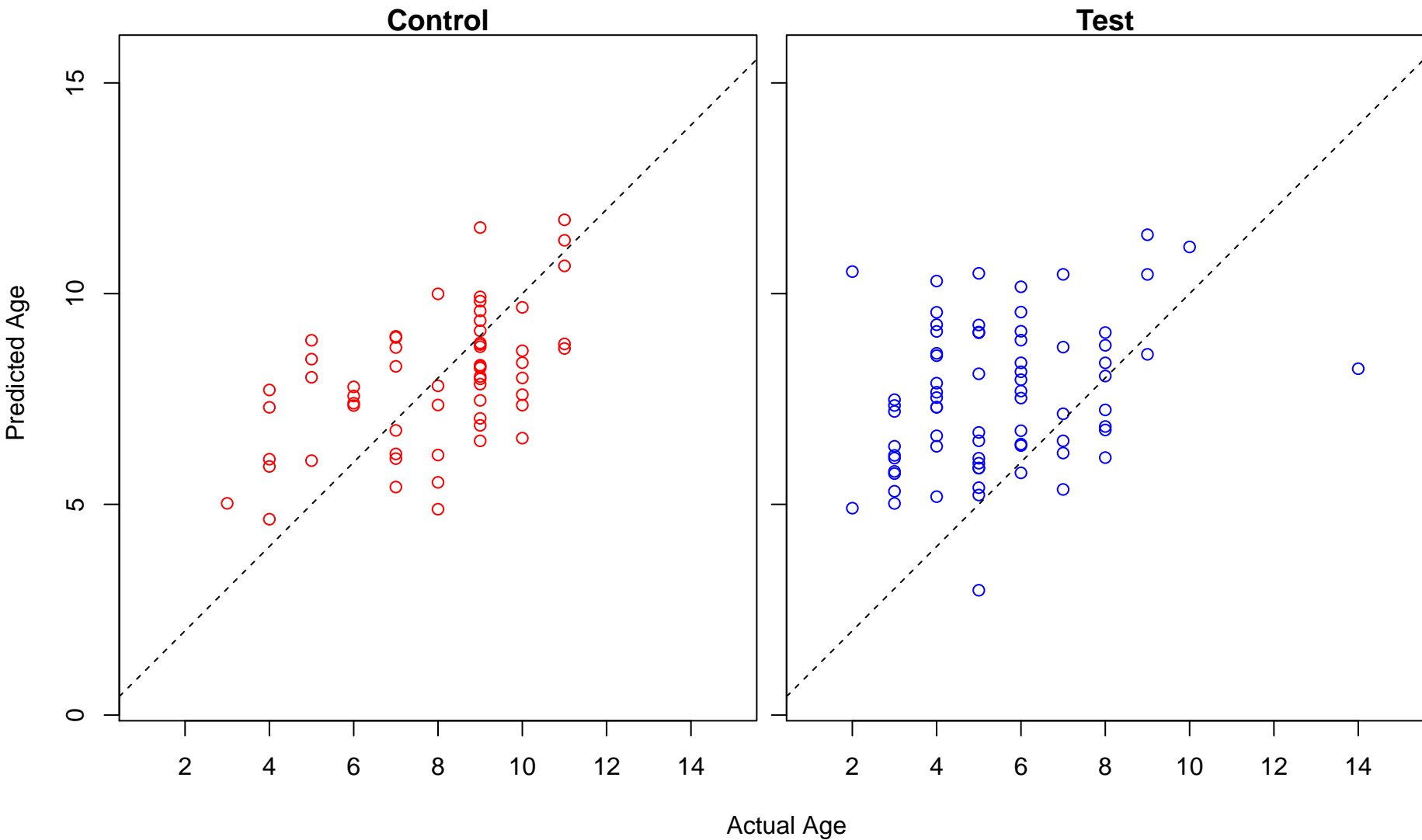
actin filament reorganization (Score: 1.129455)



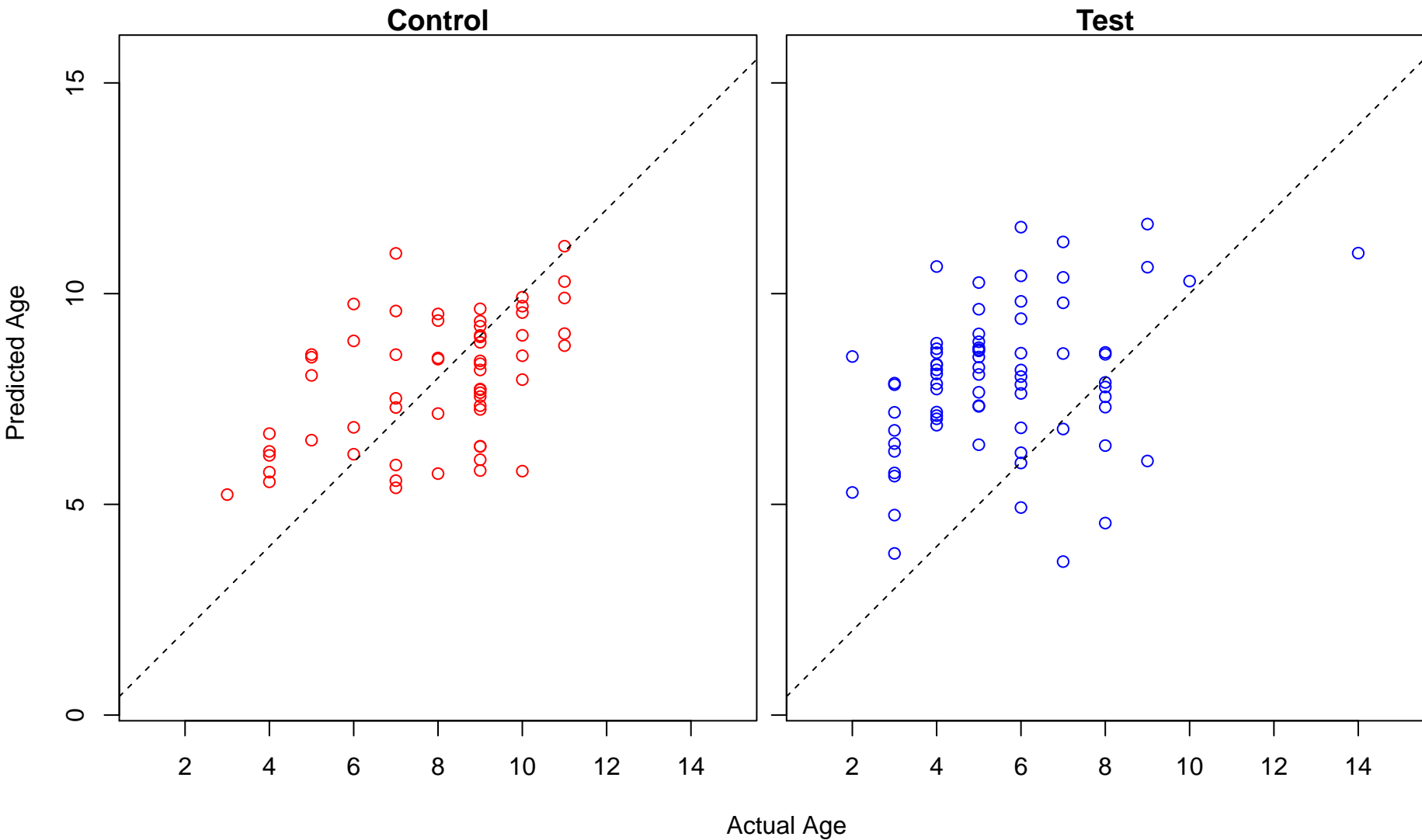
cytoplasmic transport (Score: 1.129262)



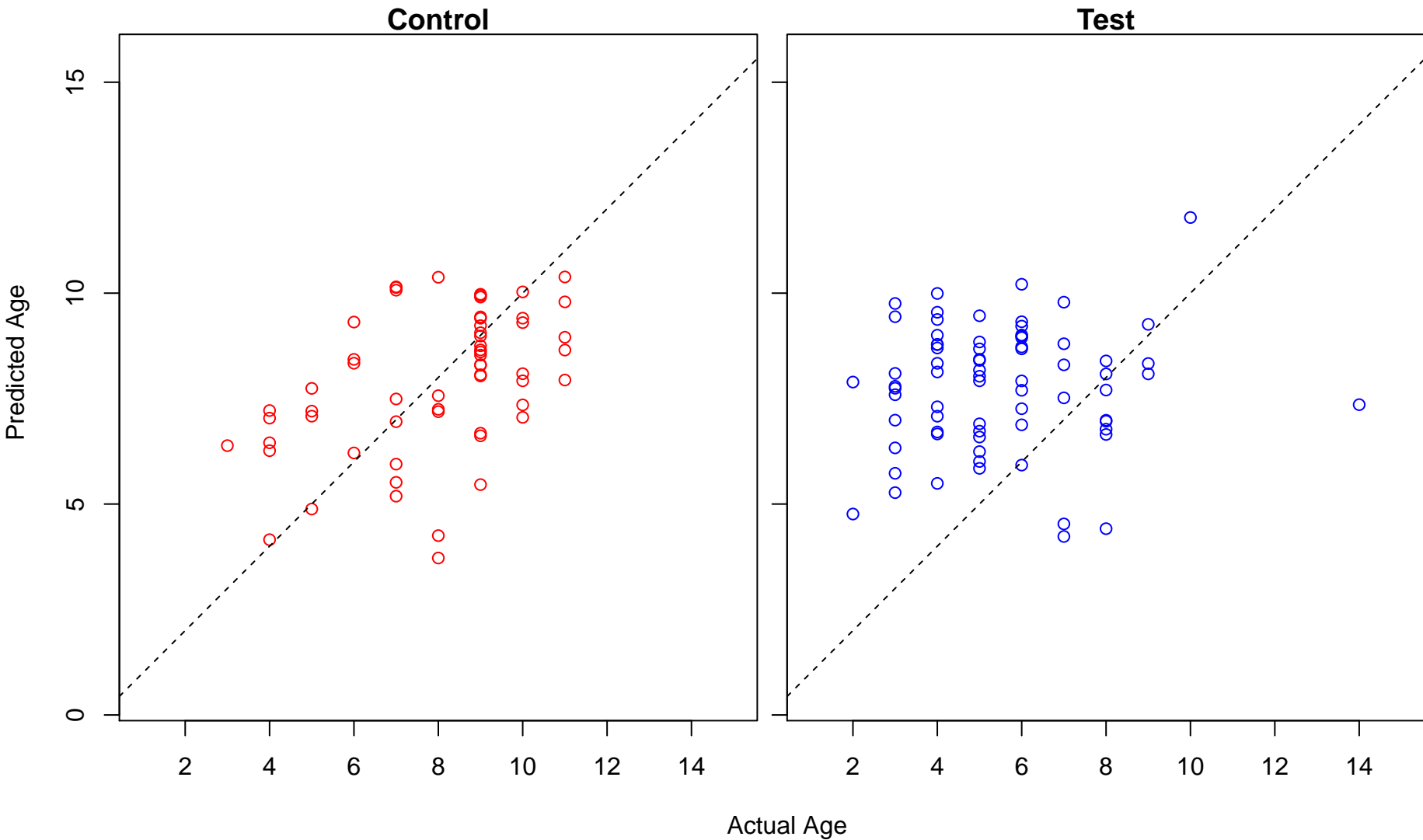
cellular response to stimulus (Score: 1.128682)



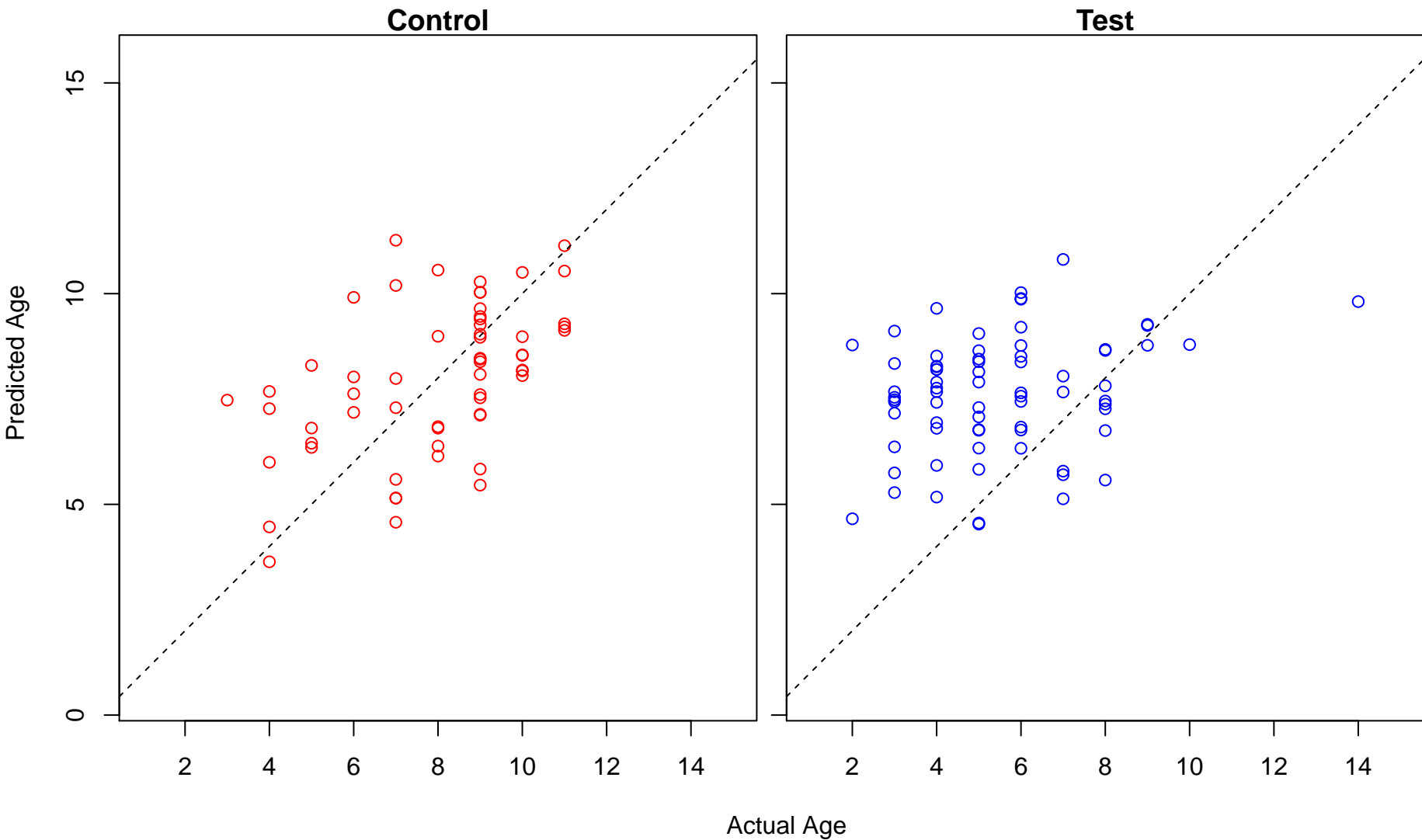
histone H4 acetylation (Score: 1.128631)



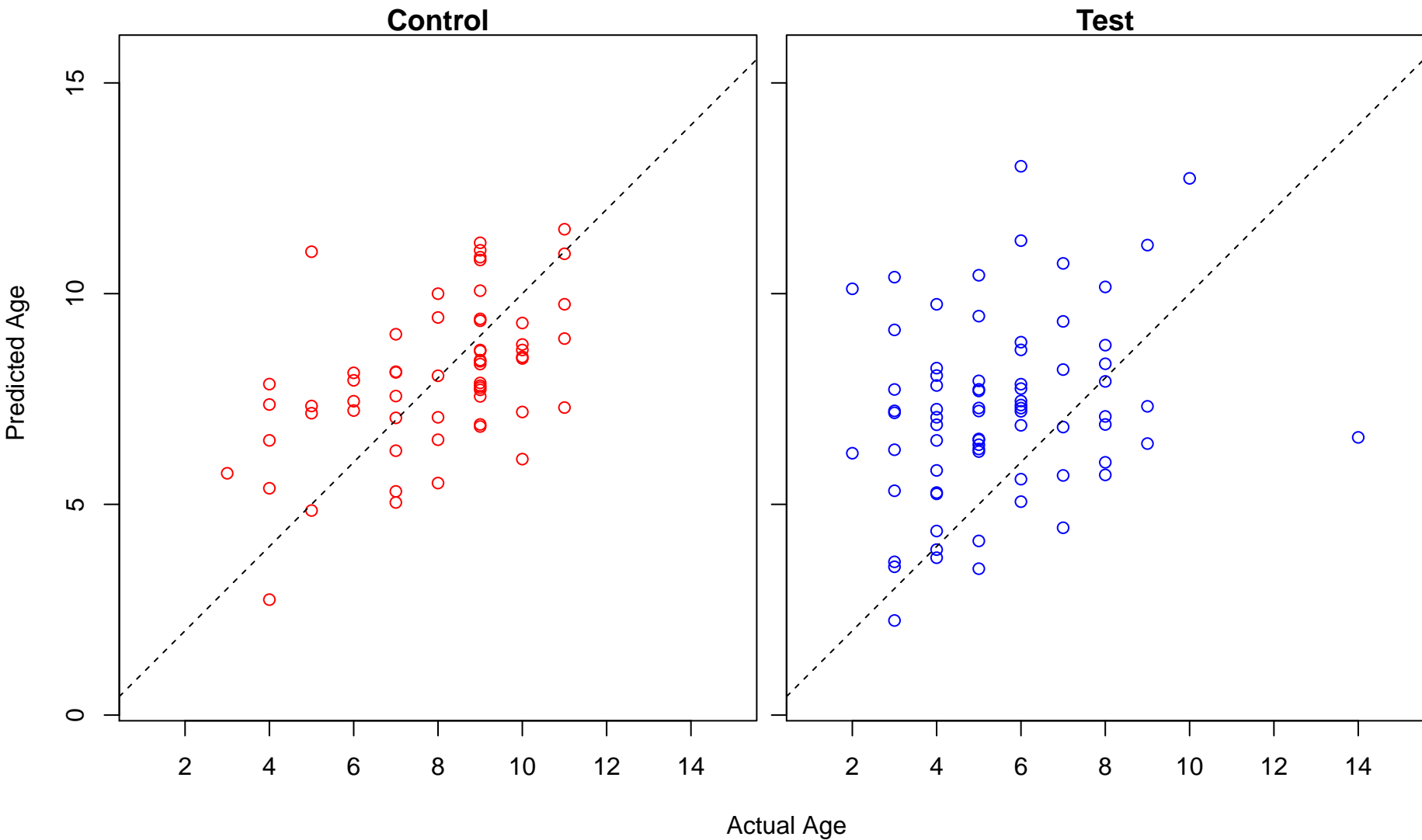
negative regulation of NF-kappaB transcription factor activity (Score: 1.128517)



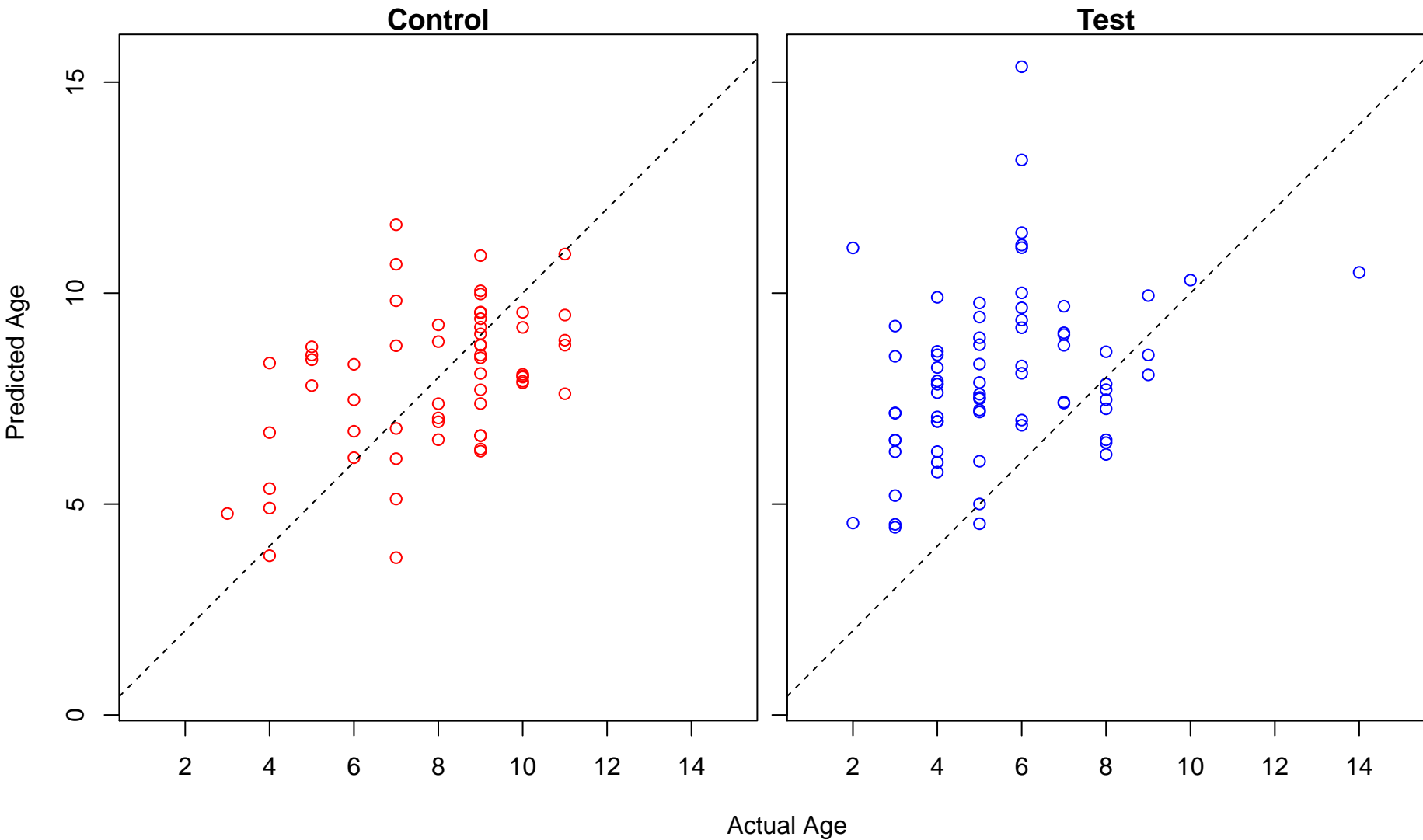
negative regulation of gene expression (Score: 1.127406)



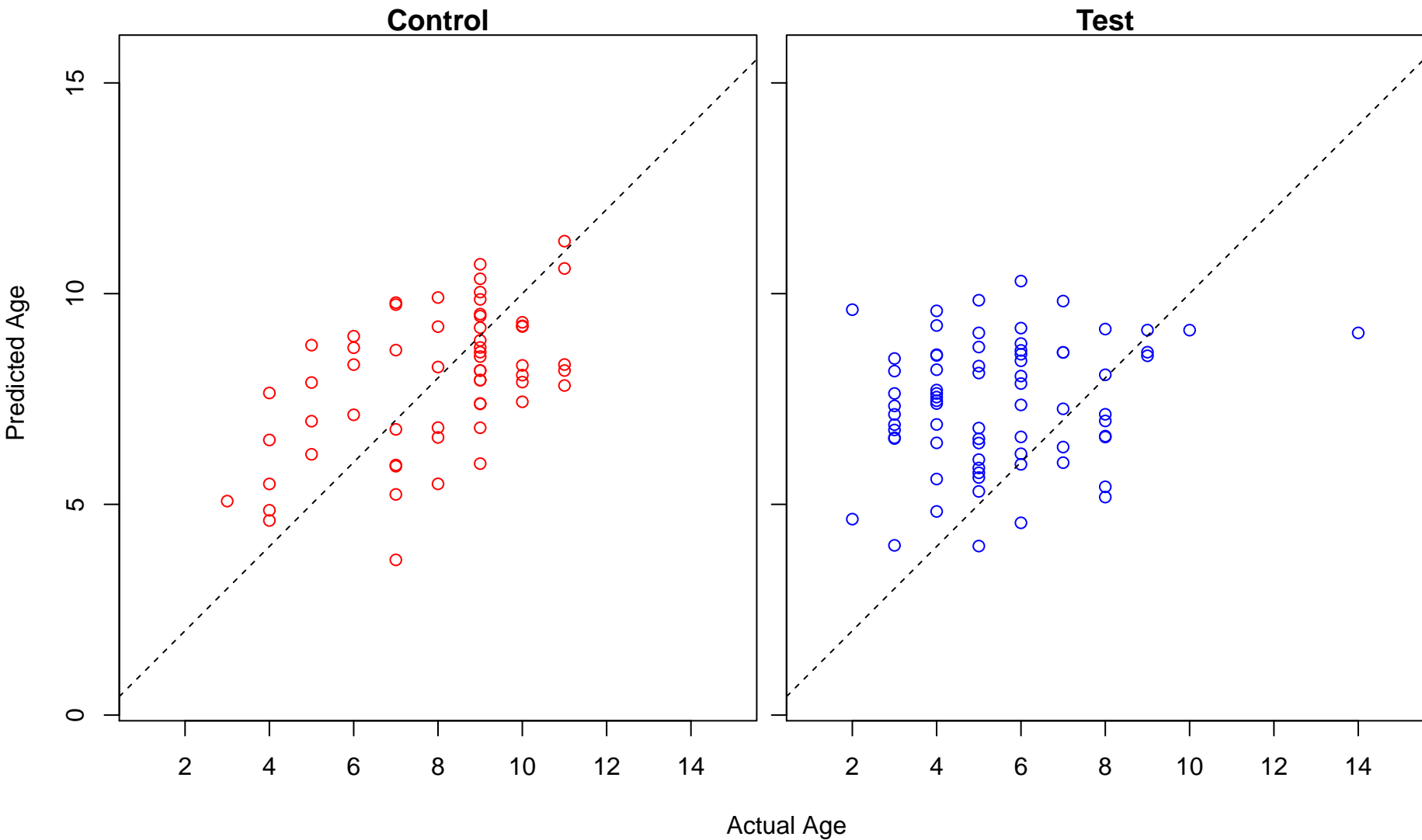
vesicle organization (Score: 1.126475)



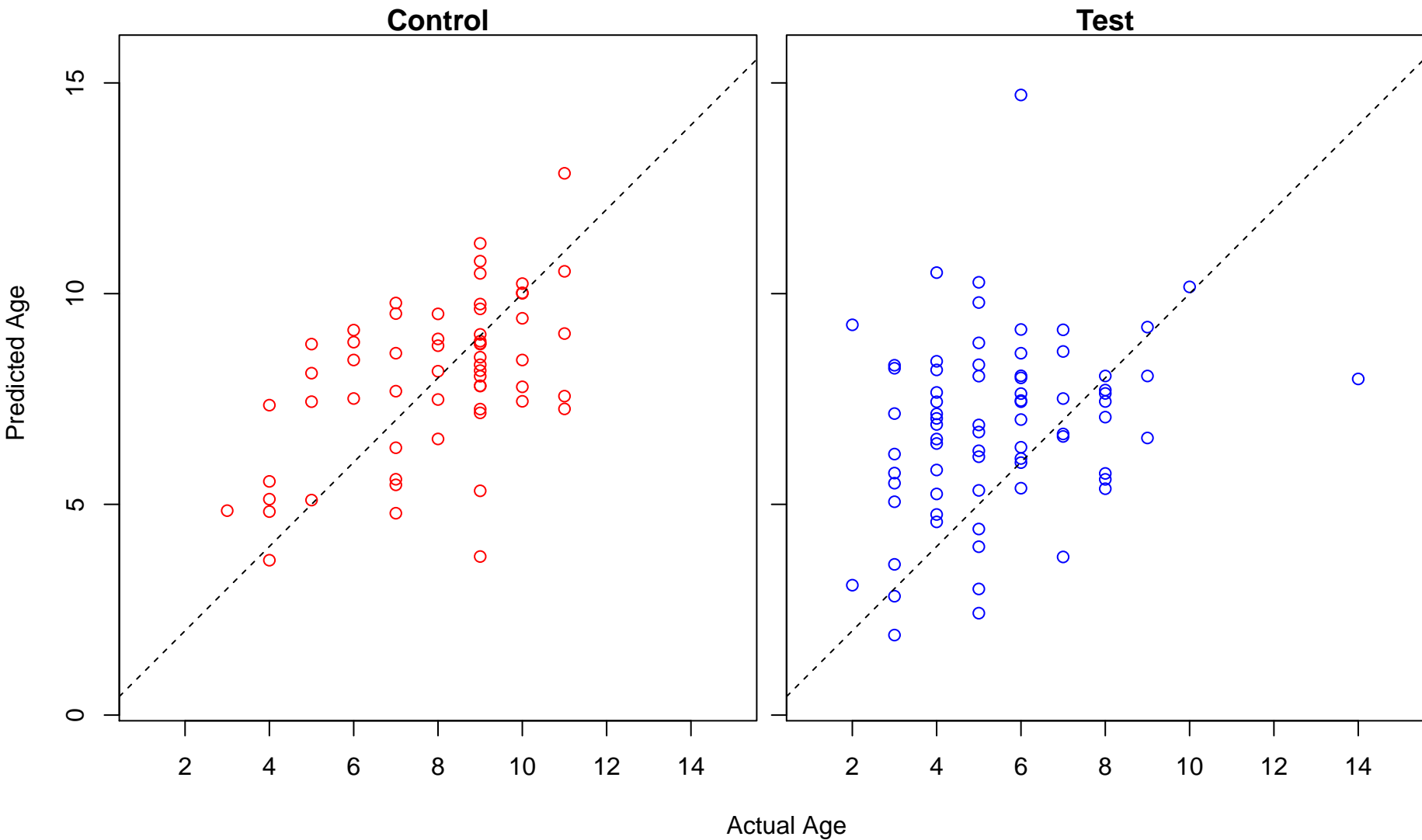
myeloid dendritic cell differentiation (Score: 1.125729)



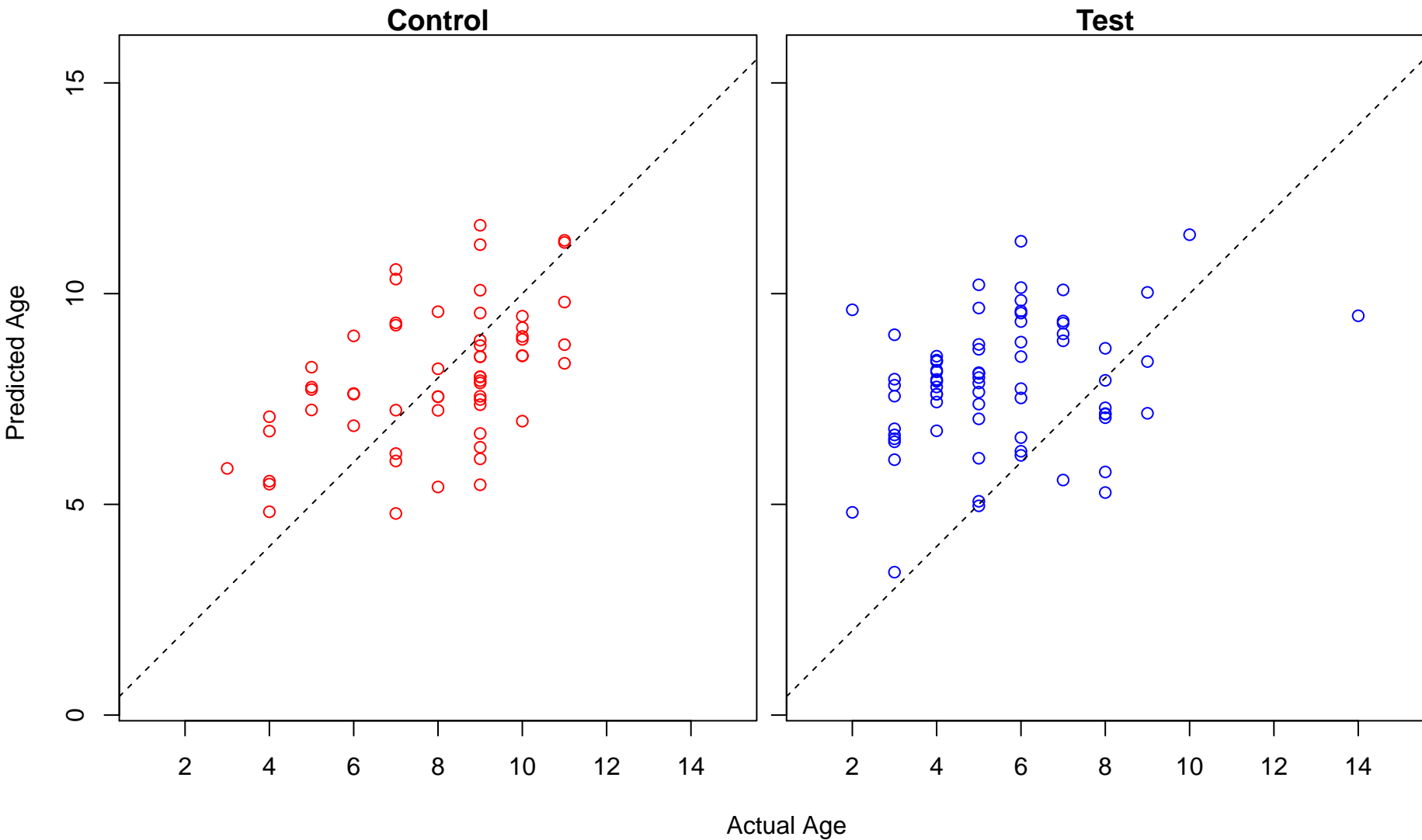
cell adhesion (Score: 1.125512)



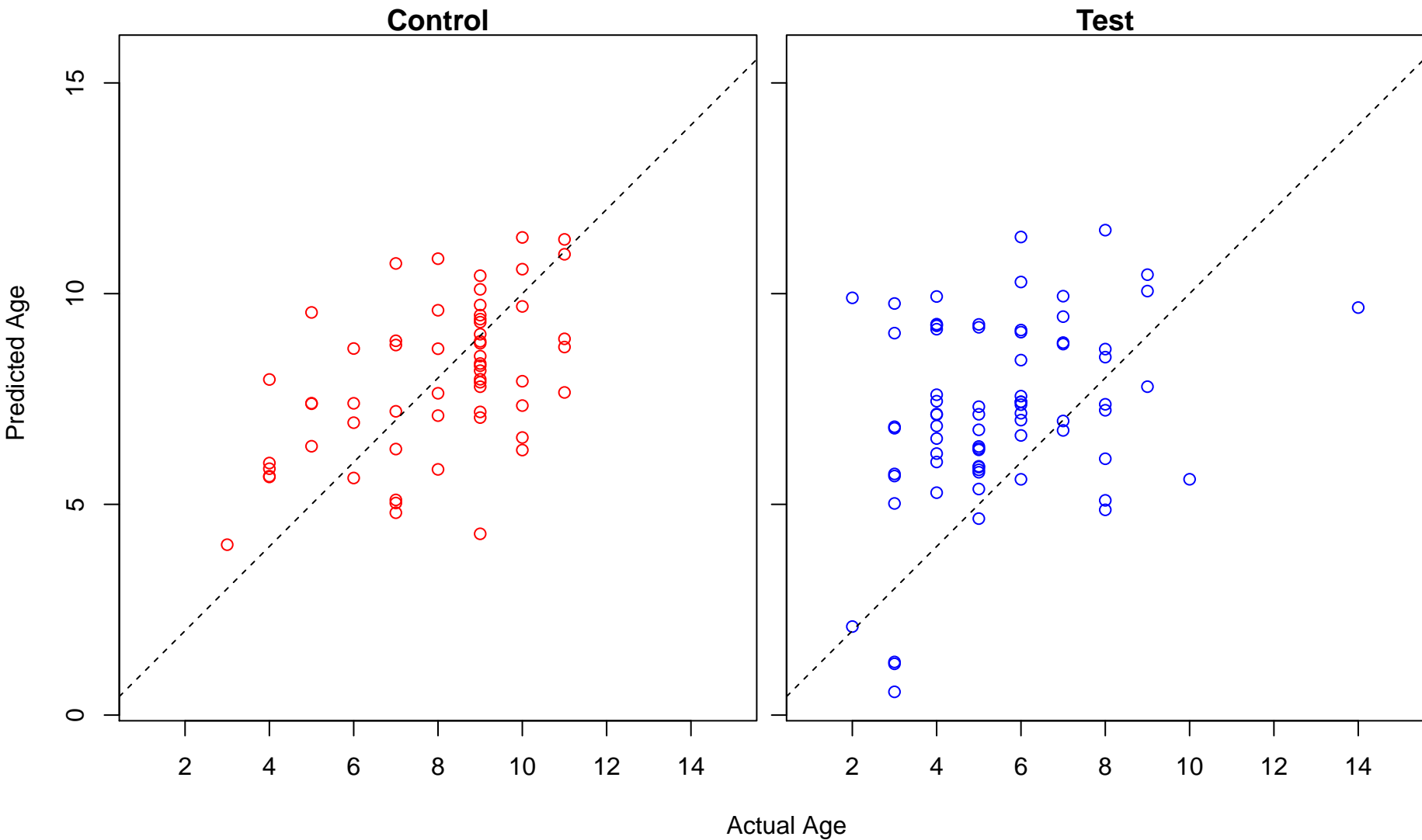
organelle assembly (Score: 1.124535)



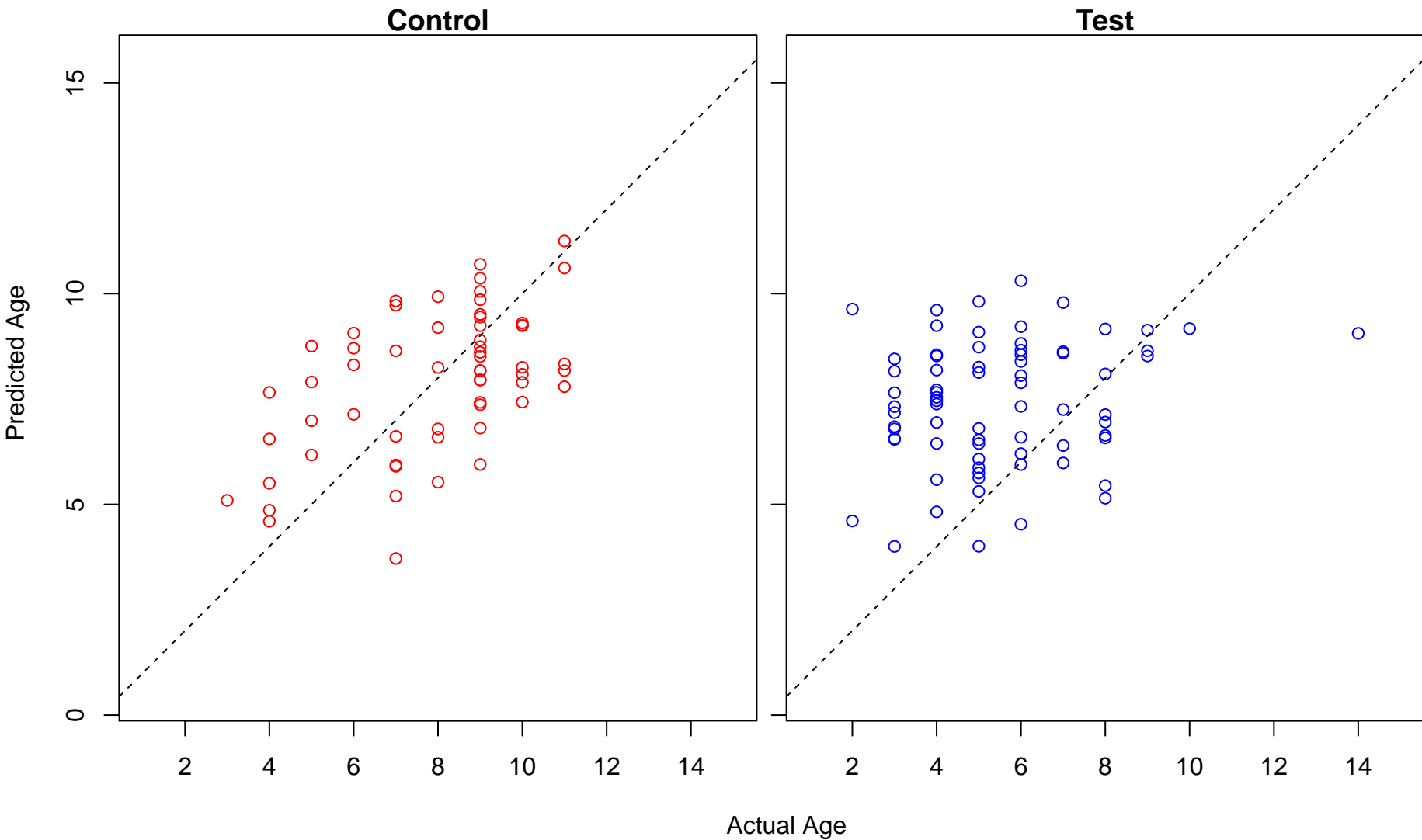
cell division (Score: 1.123587)



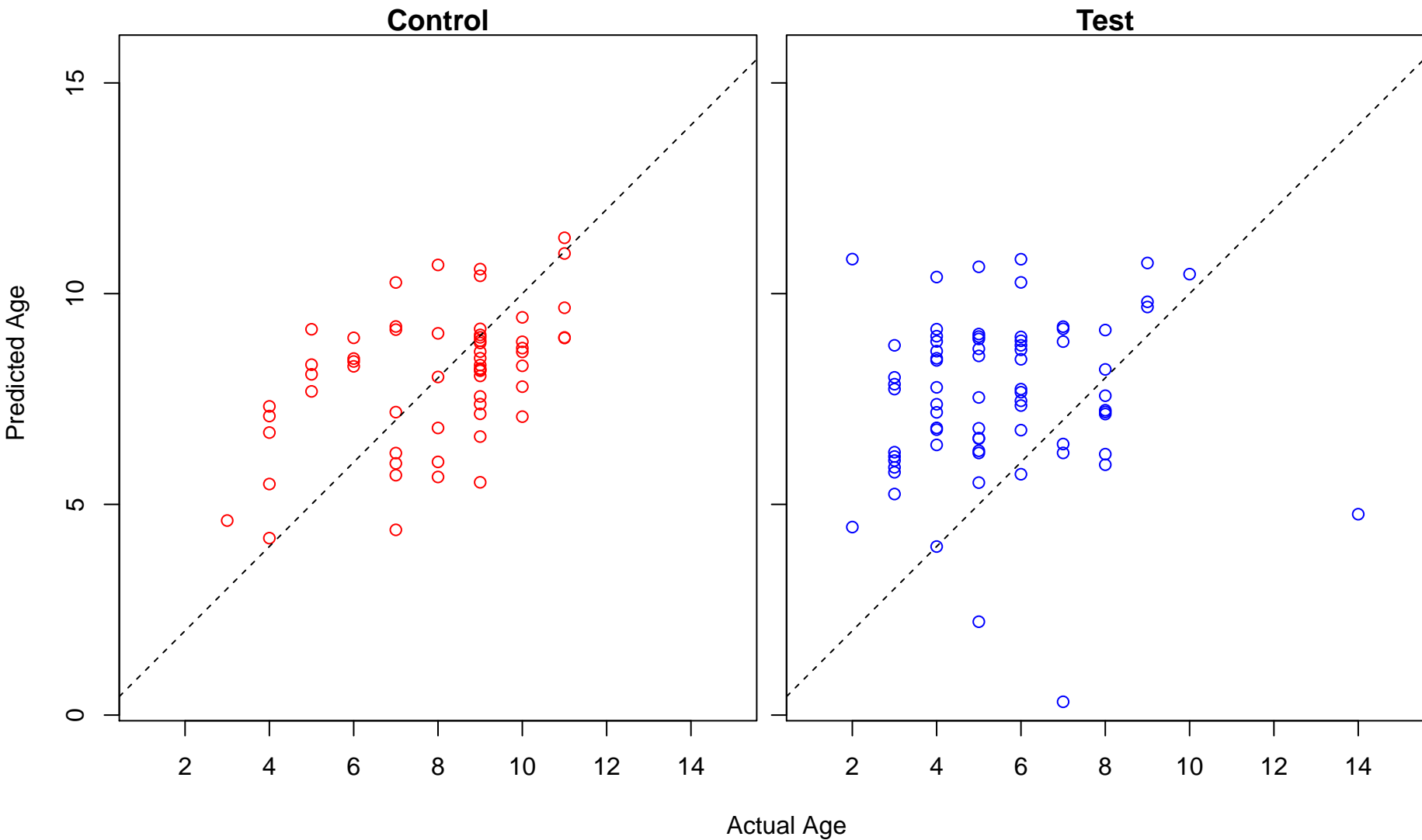
nephron tubule development (Score: 1.121216)



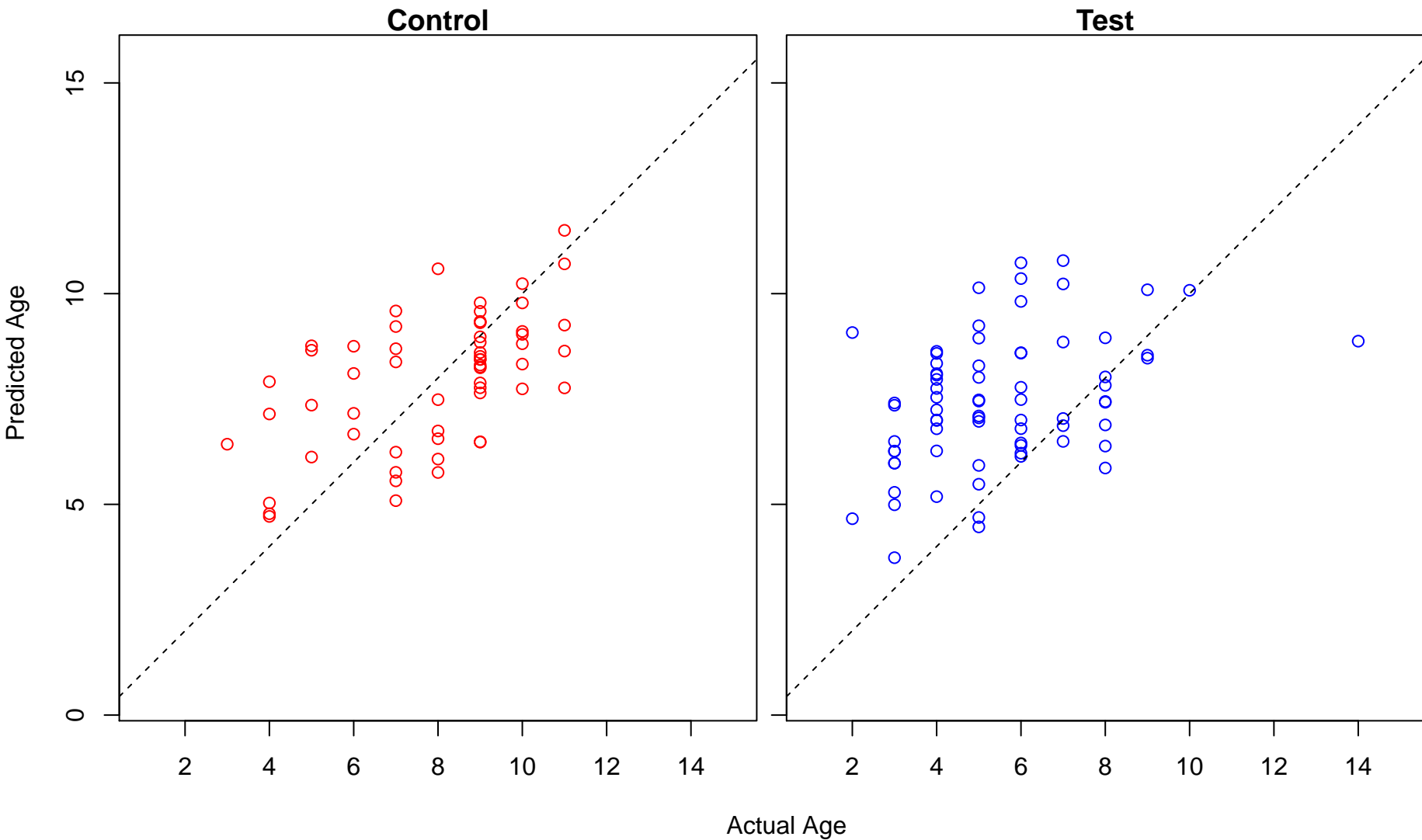
biological adhesion (Score: 1.120686)



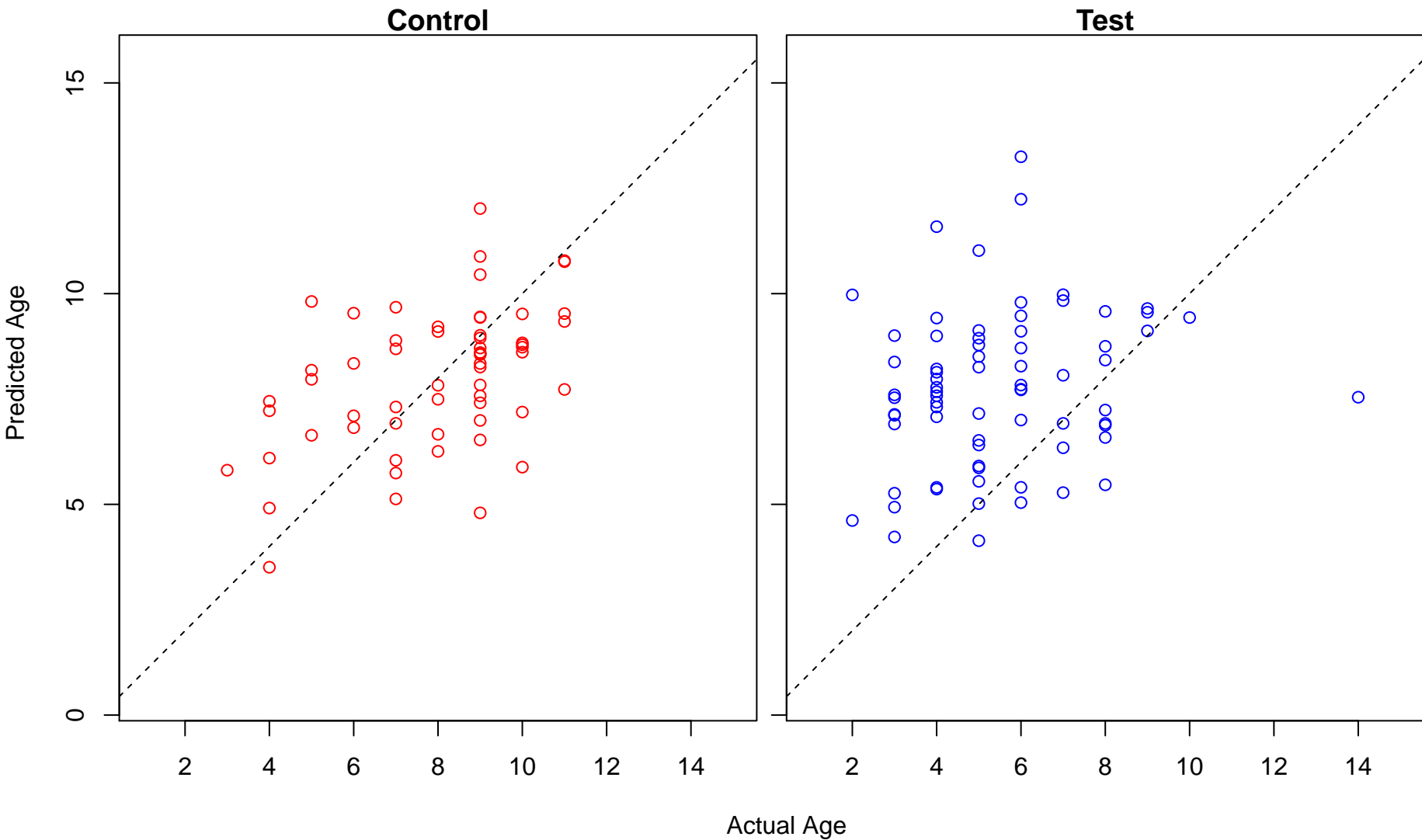
macromolecule modification (Score: 1.120030)



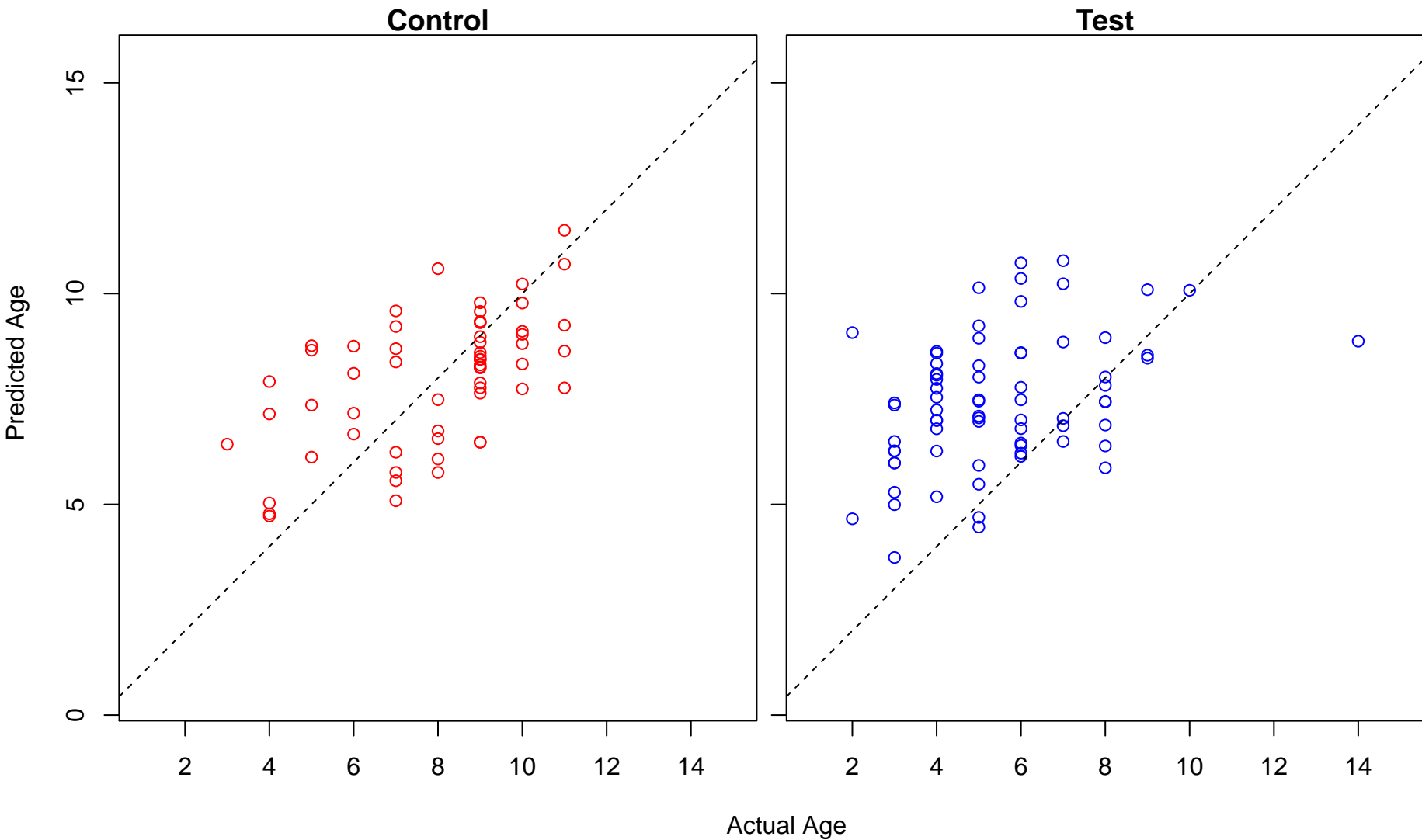
cellular component organization (Score: 1.119727)



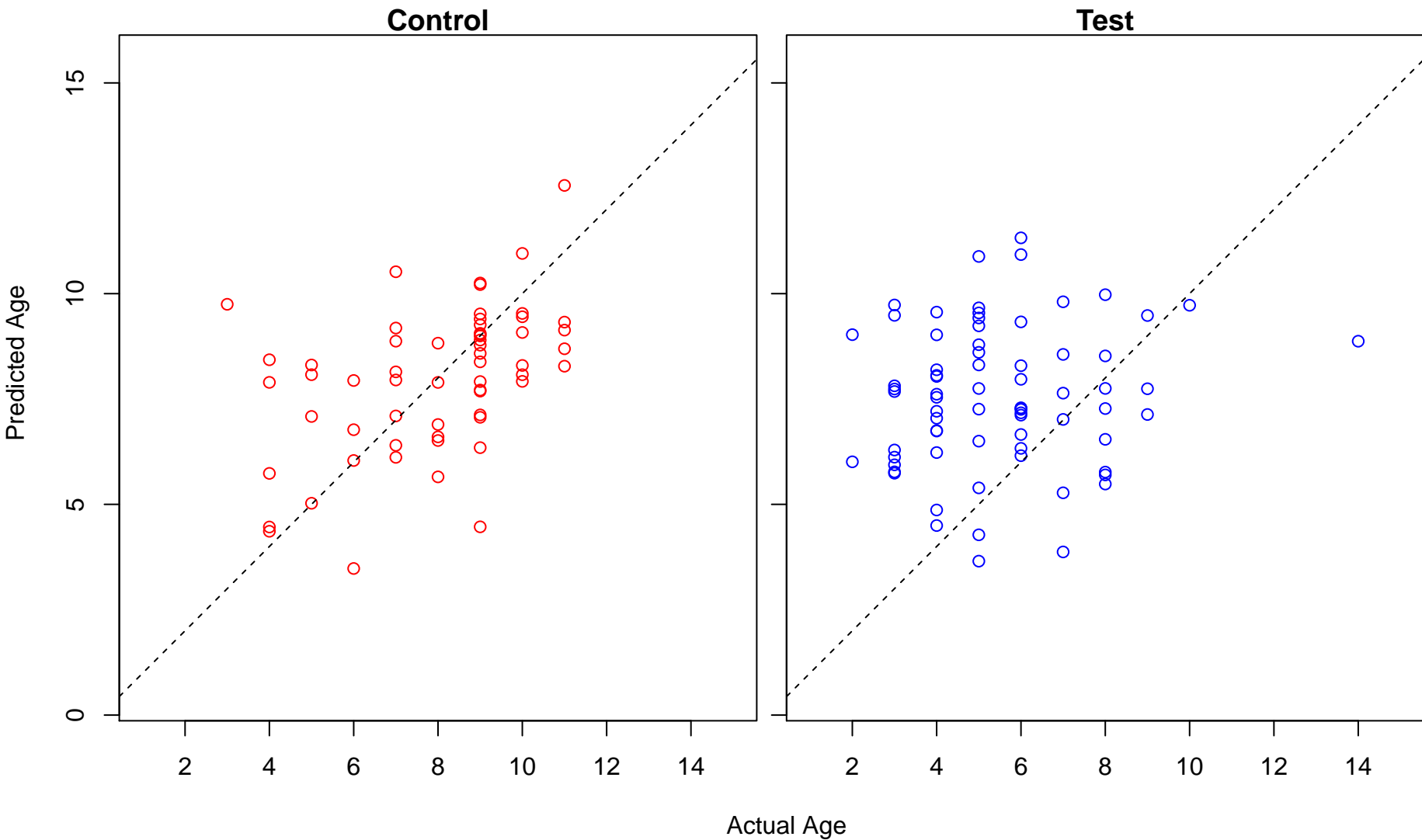
neuron development (Score: 1.119488)



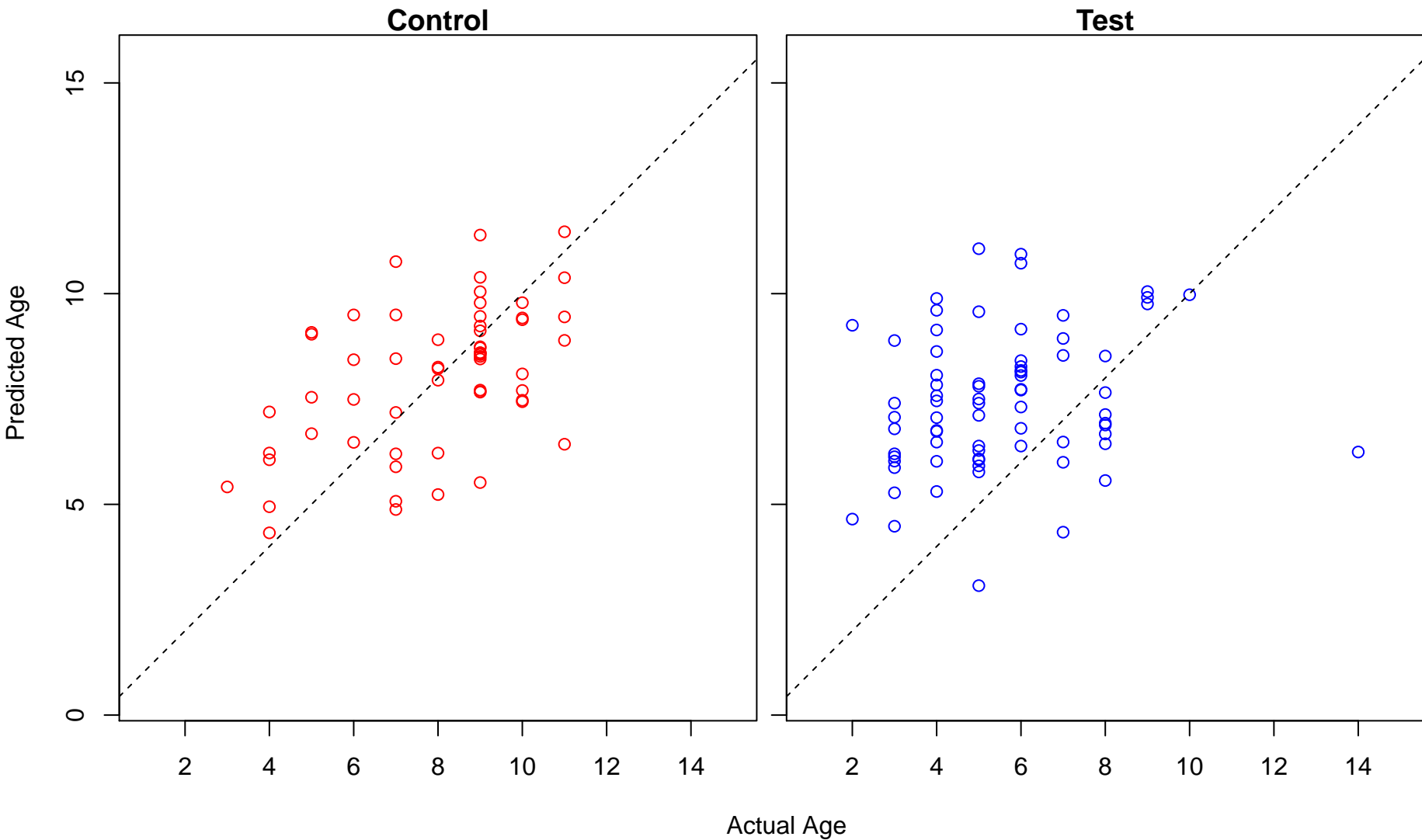
cellular component organization or biogenesis (Score: 1.118376)



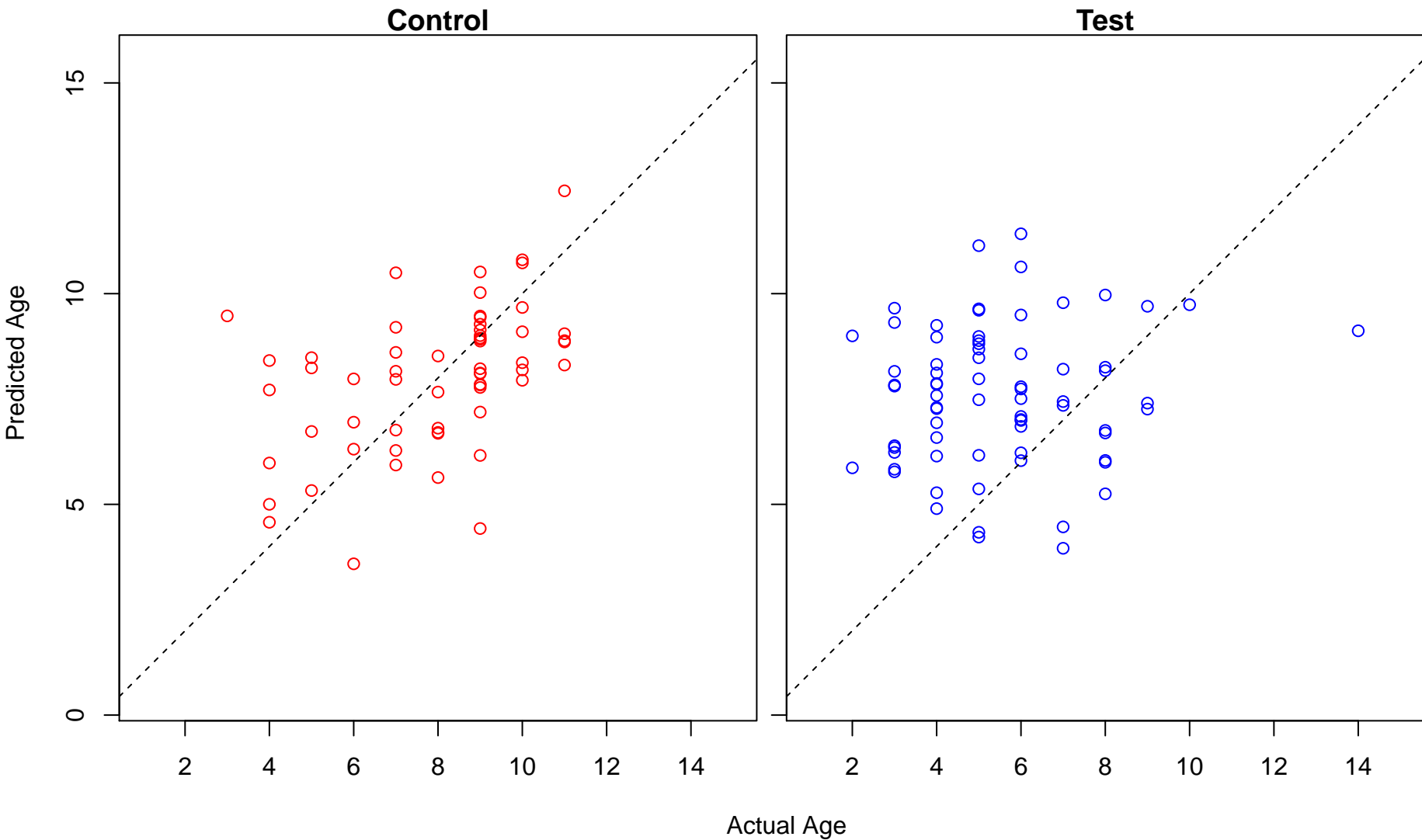
establishment of protein localization to endoplasmic reticulum (Score: 1.117752)



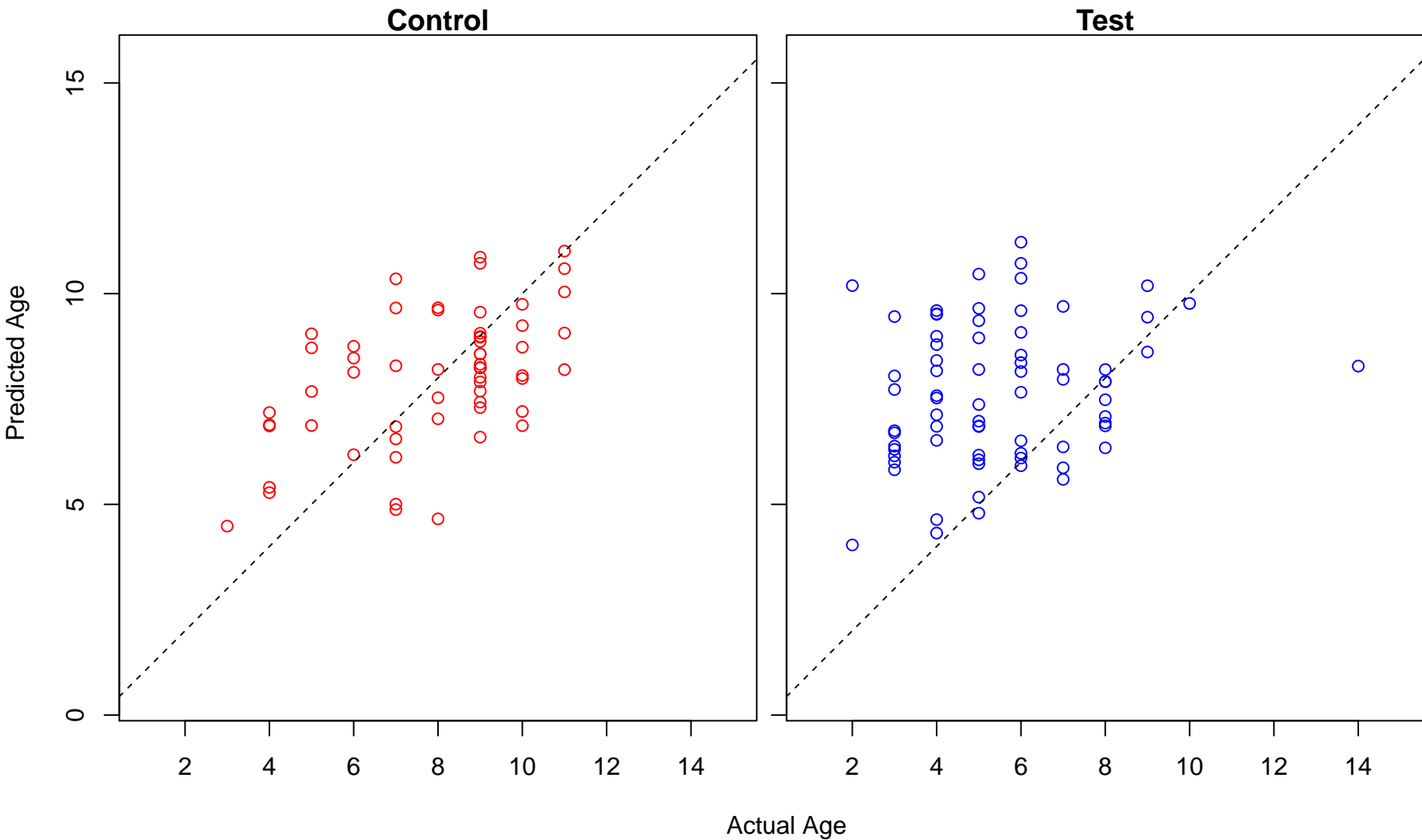
negative regulation of catalytic activity (Score: 1.117653)



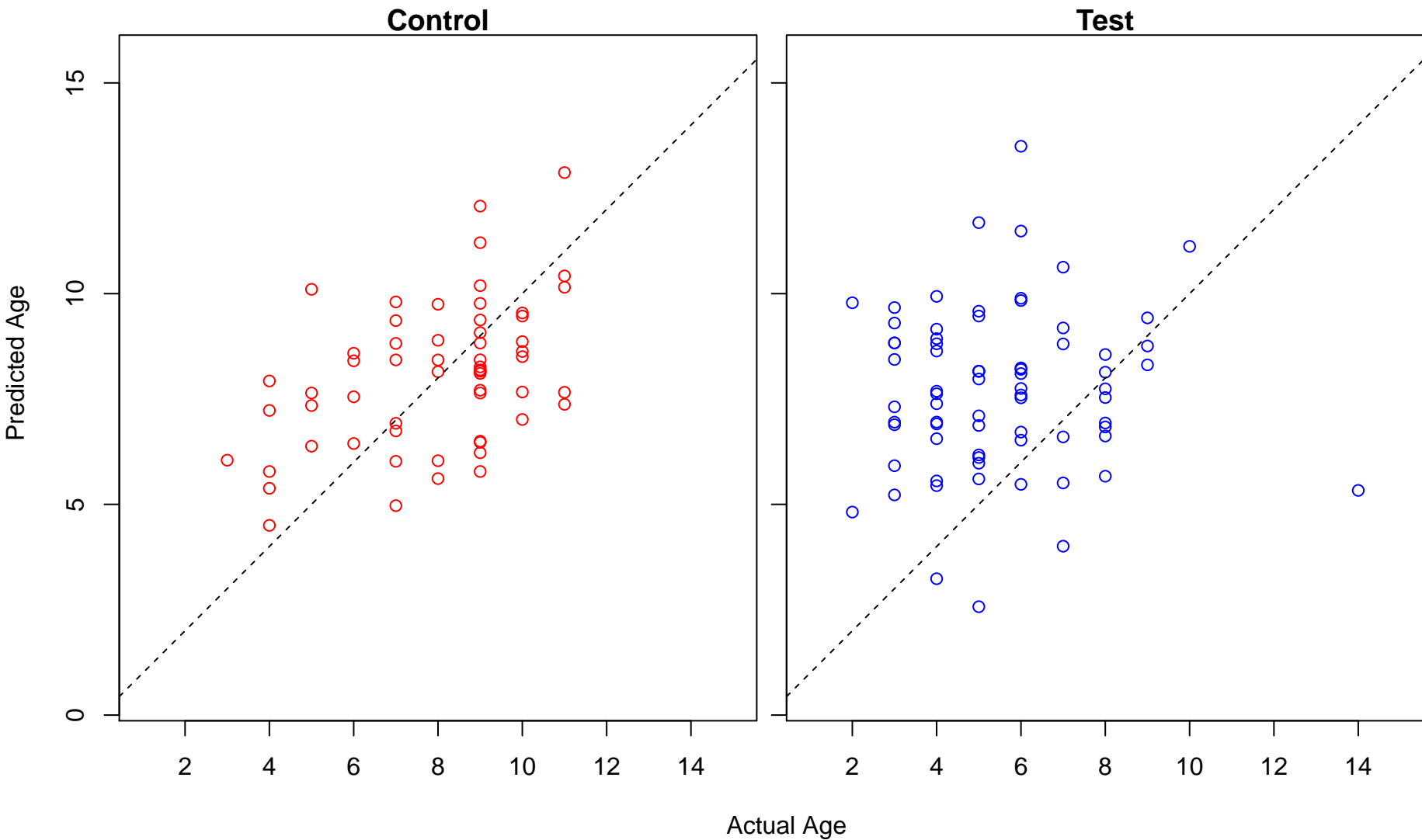
alpha-amino acid metabolic process (Score: 1.117433)



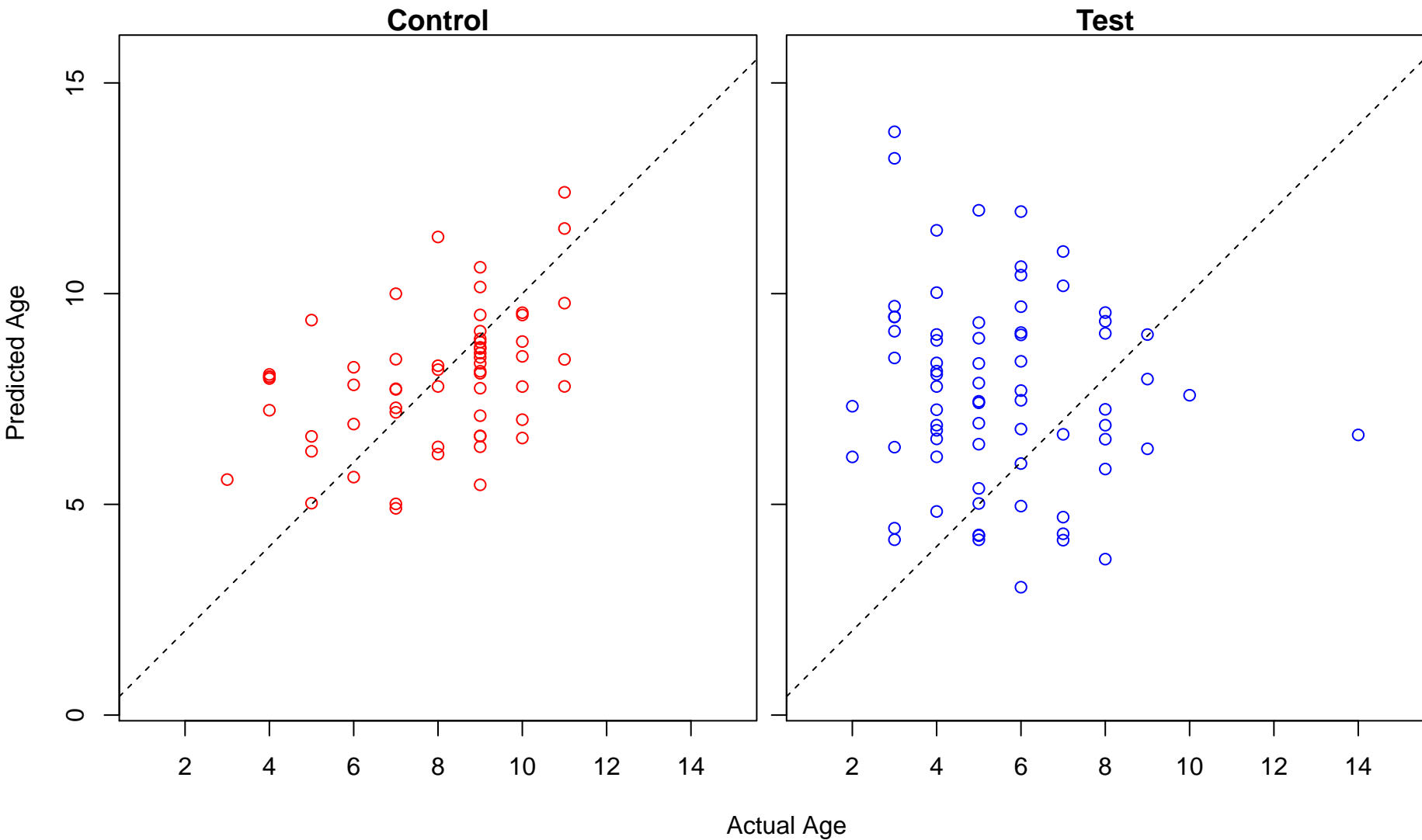
regulation of signal transduction (Score: 1.116818)



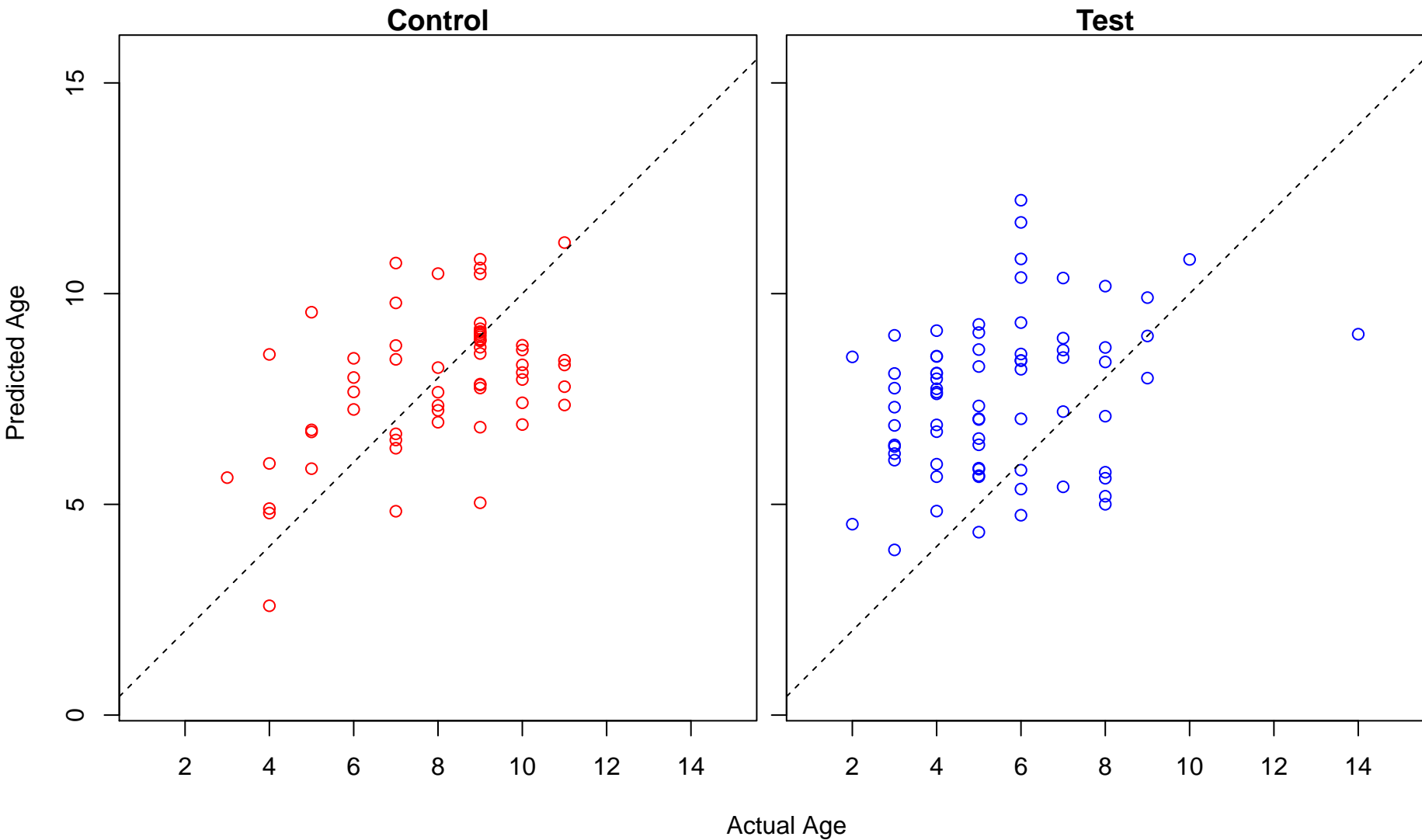
negative regulation of kinase activity (Score: 1.115713)



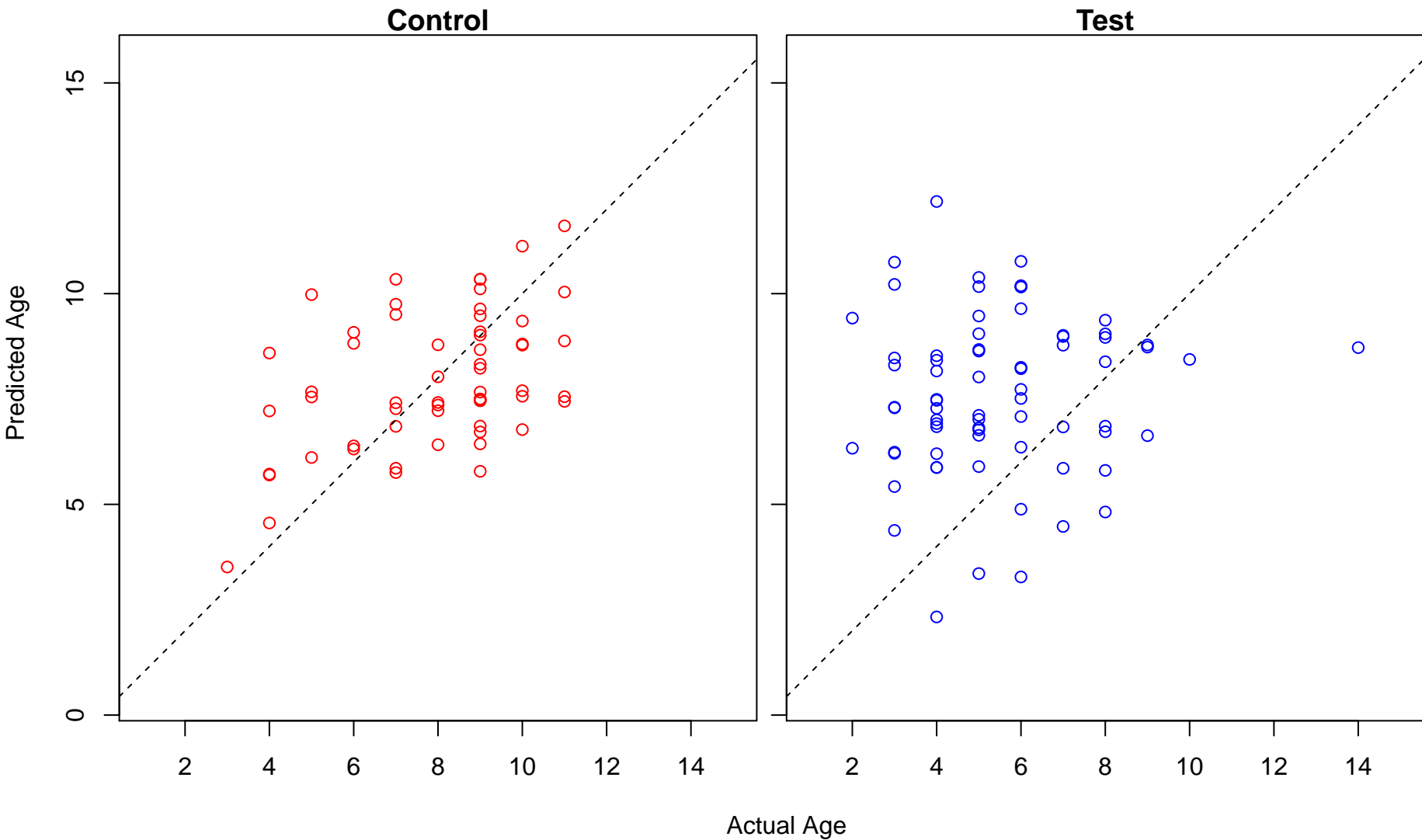
negative regulation of mast cell activation involved in immune response (Score: 1.114869)



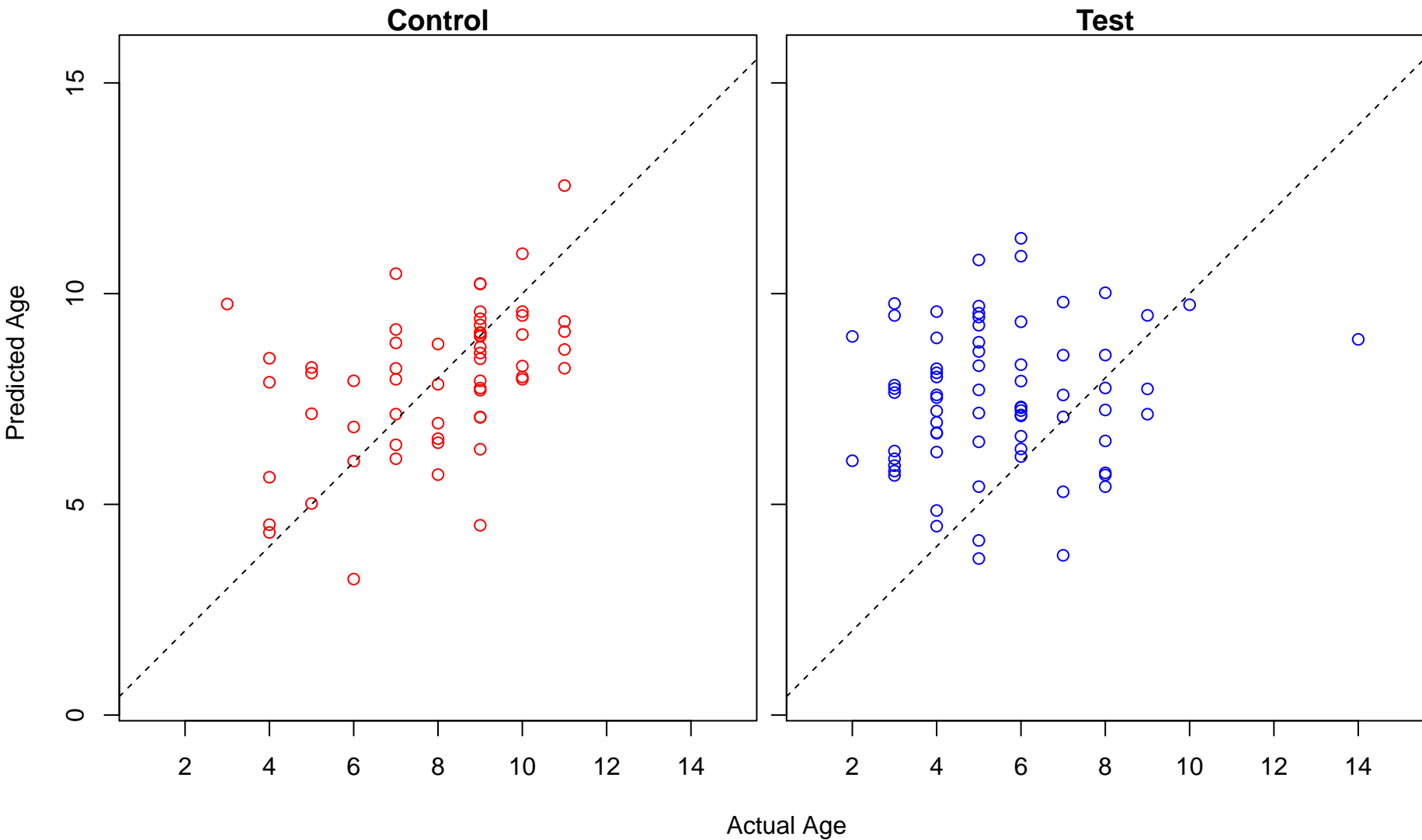
lipid metabolic process (Score: 1.114694)



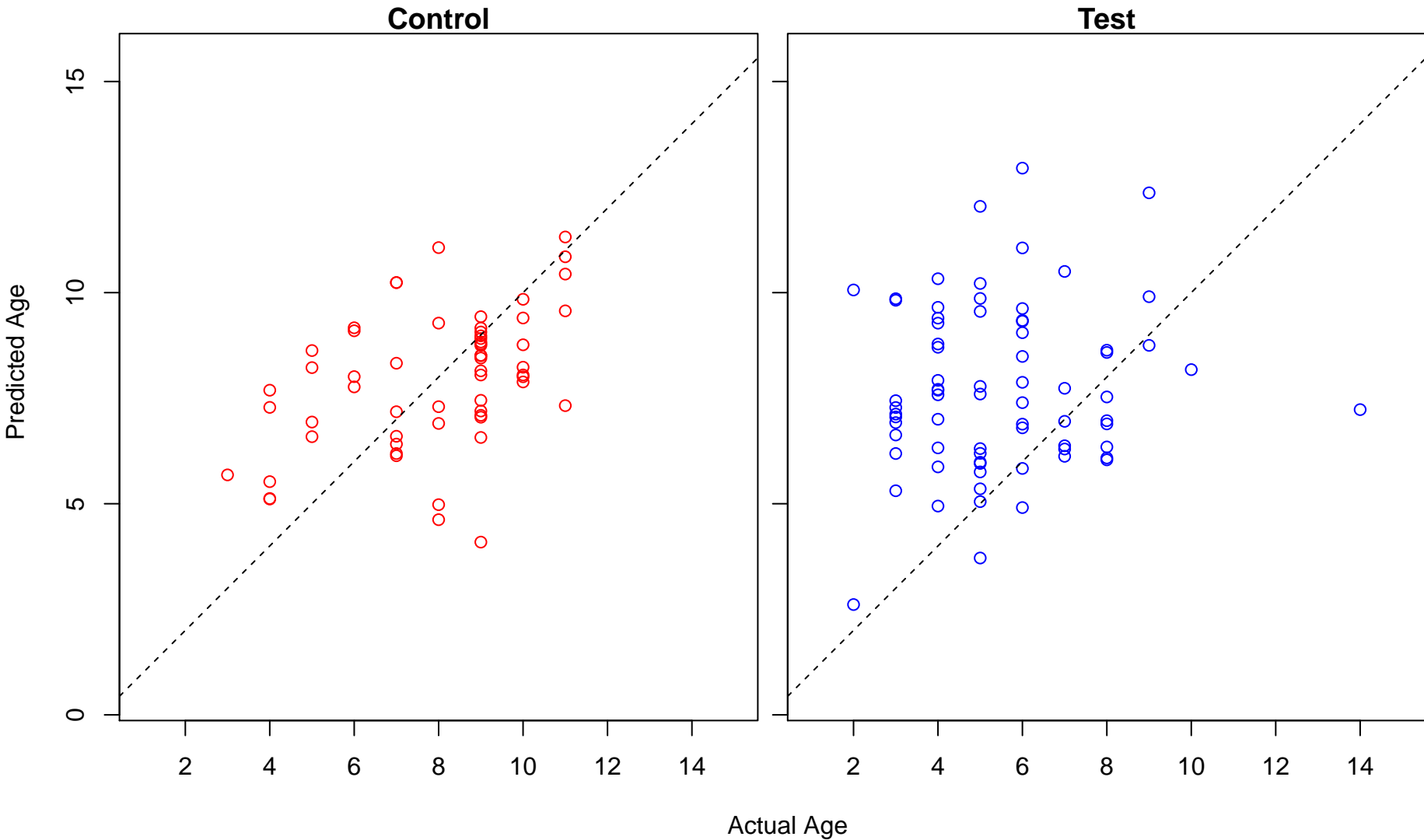
cellular respiration (Score: 1.114575)



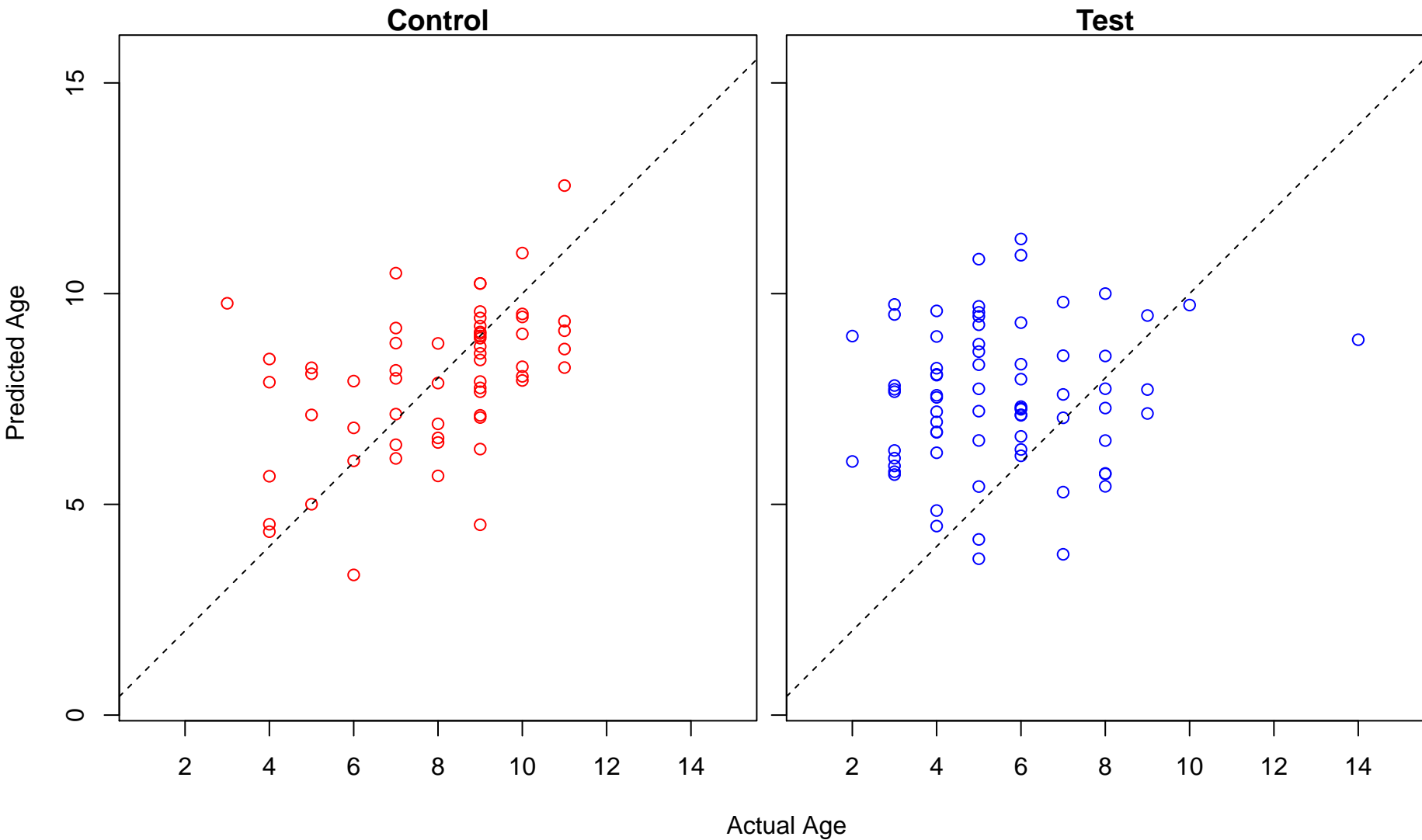
cotranslational protein targeting to membrane (Score: 1.114179)



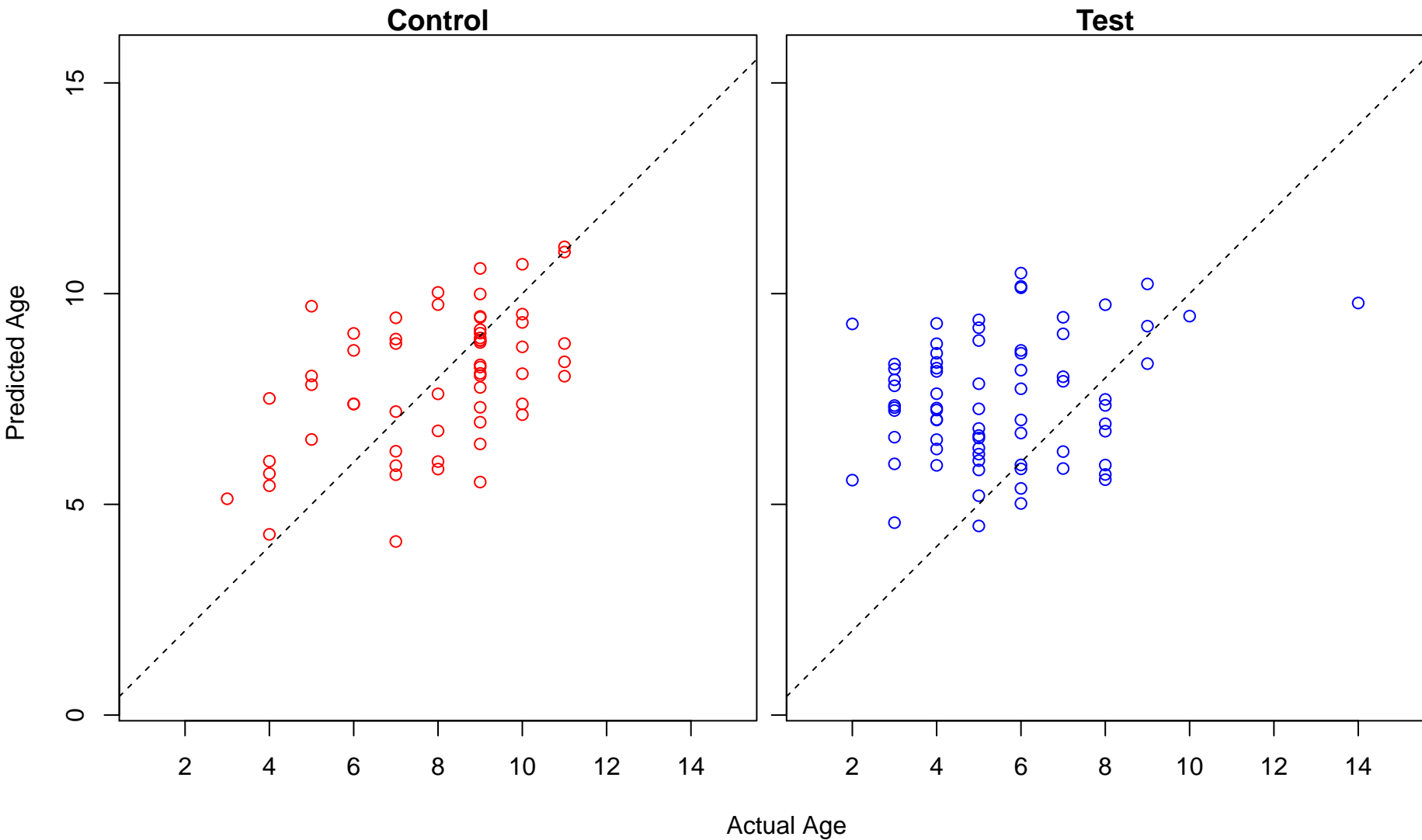
cellular response to peptide hormone stimulus (Score: 1.114137)



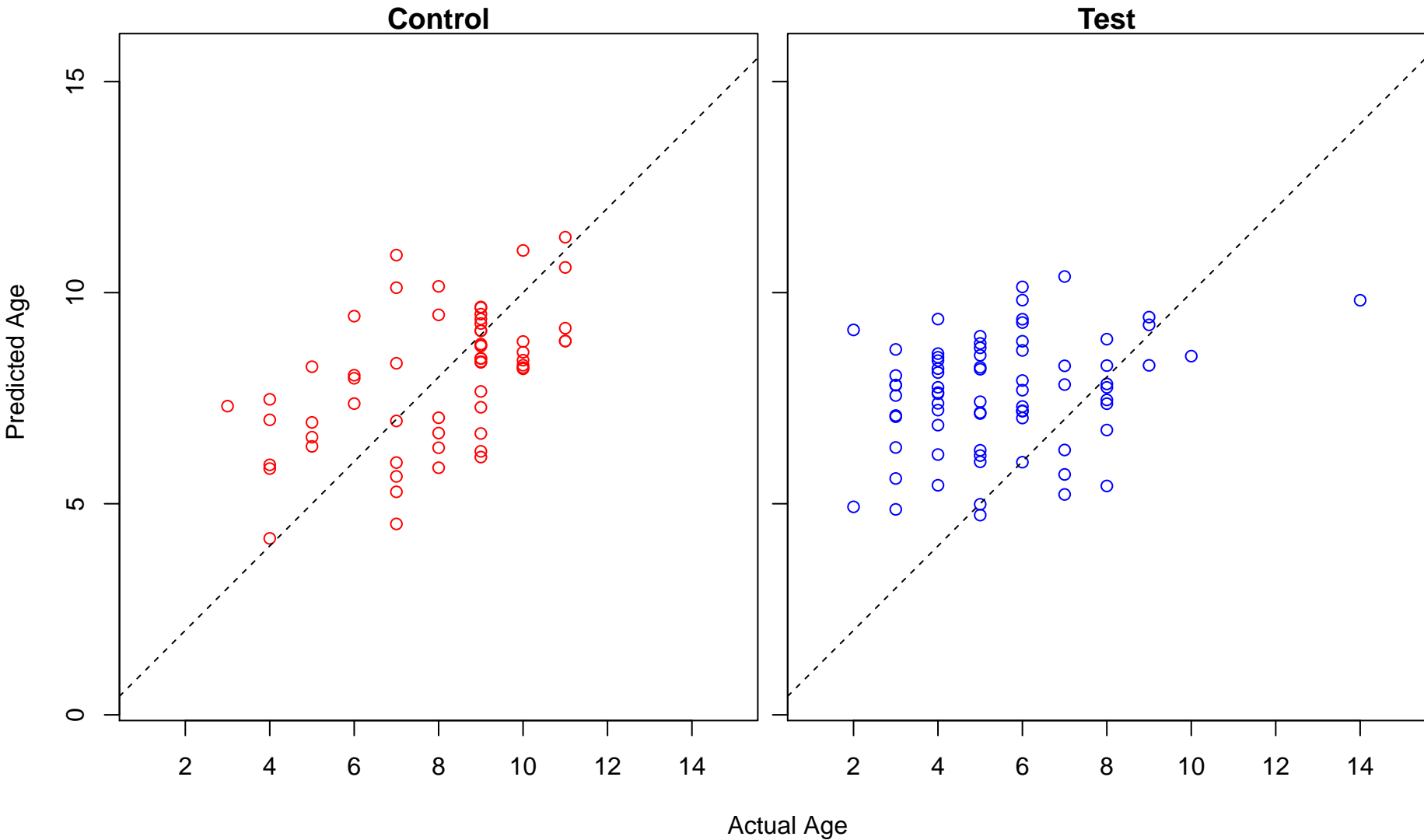
protein targeting to ER (Score: 1.113659)



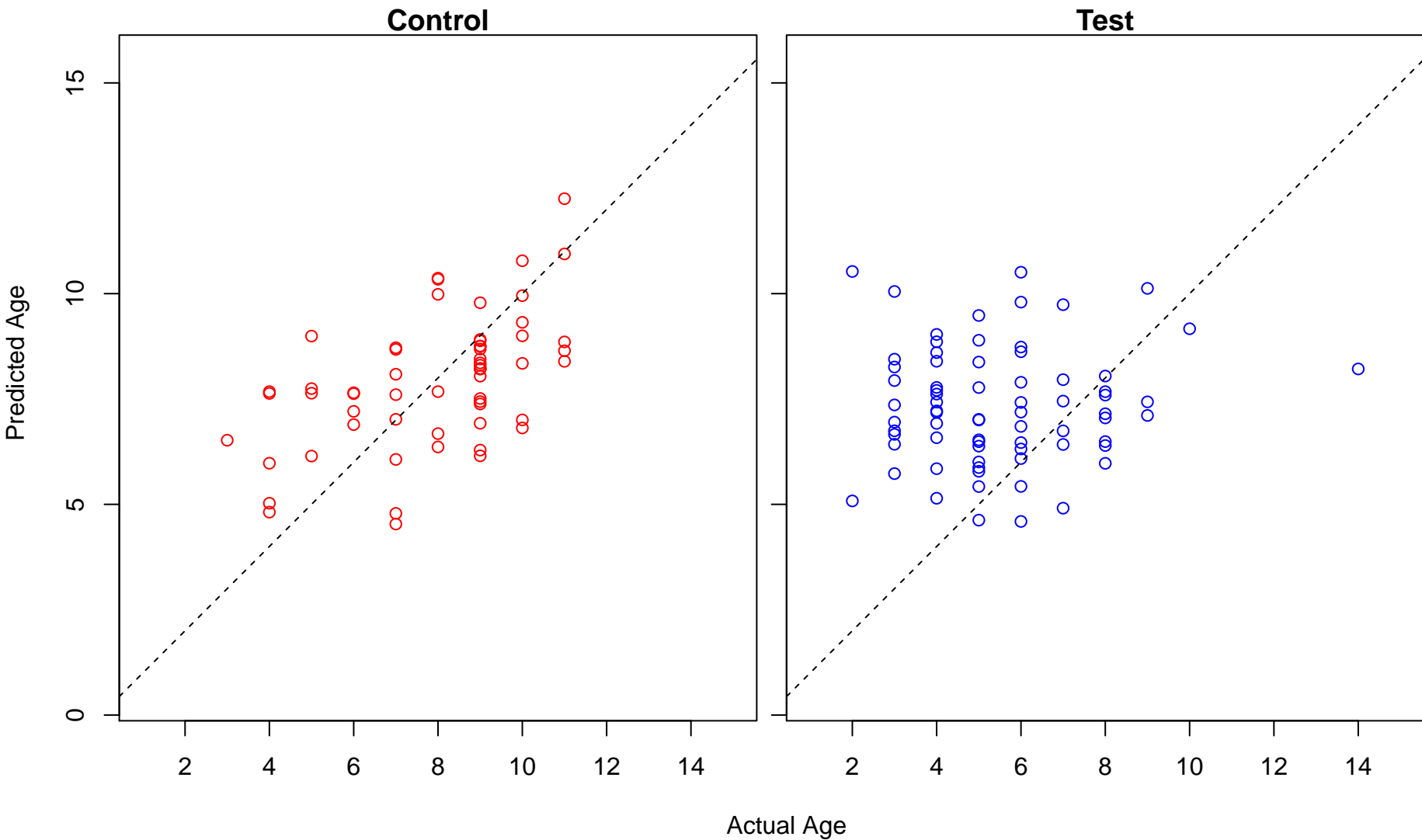
leukocyte cell-cell adhesion (Score: 1.113515)



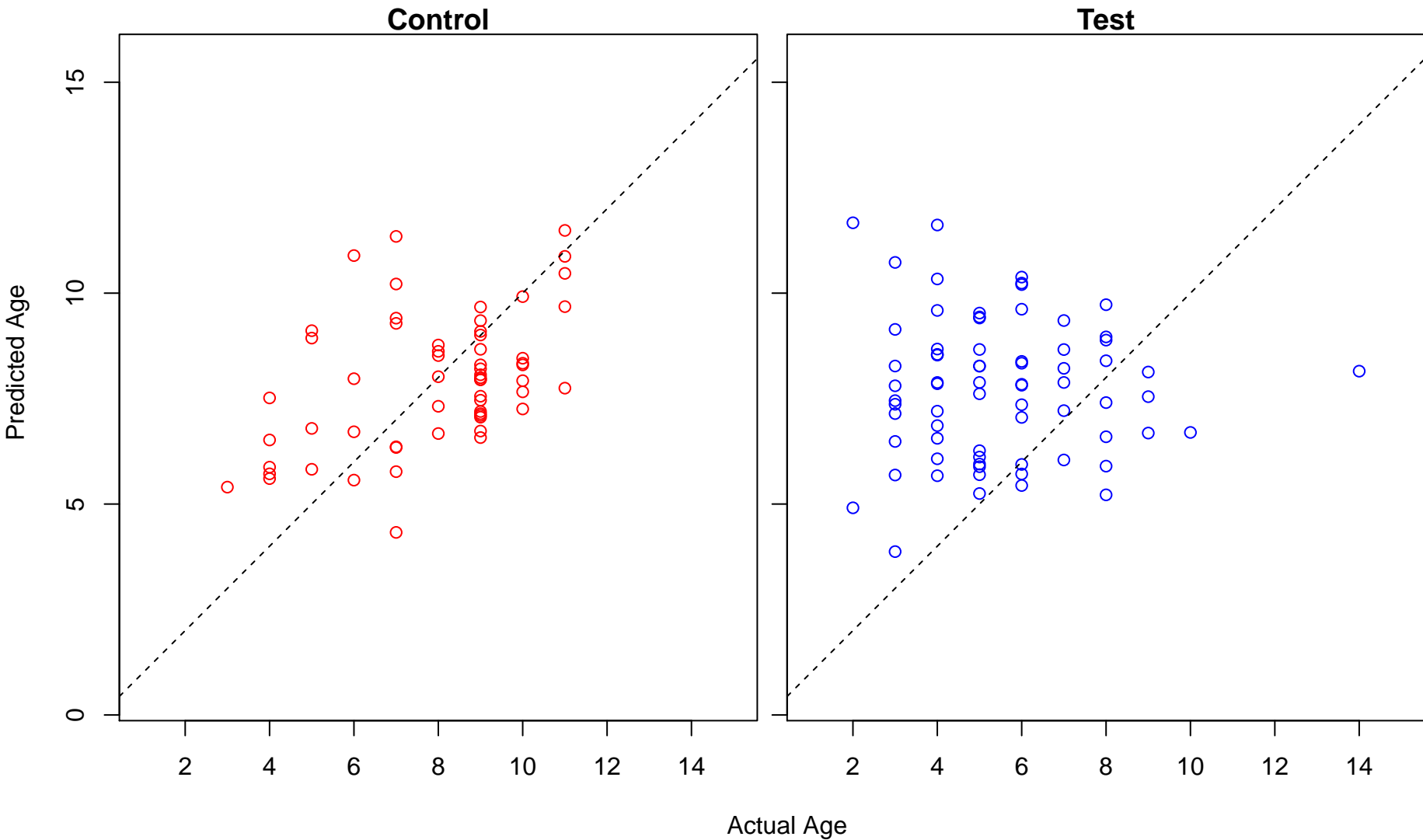
negative regulation of RNA metabolic process (Score: 1.112813)



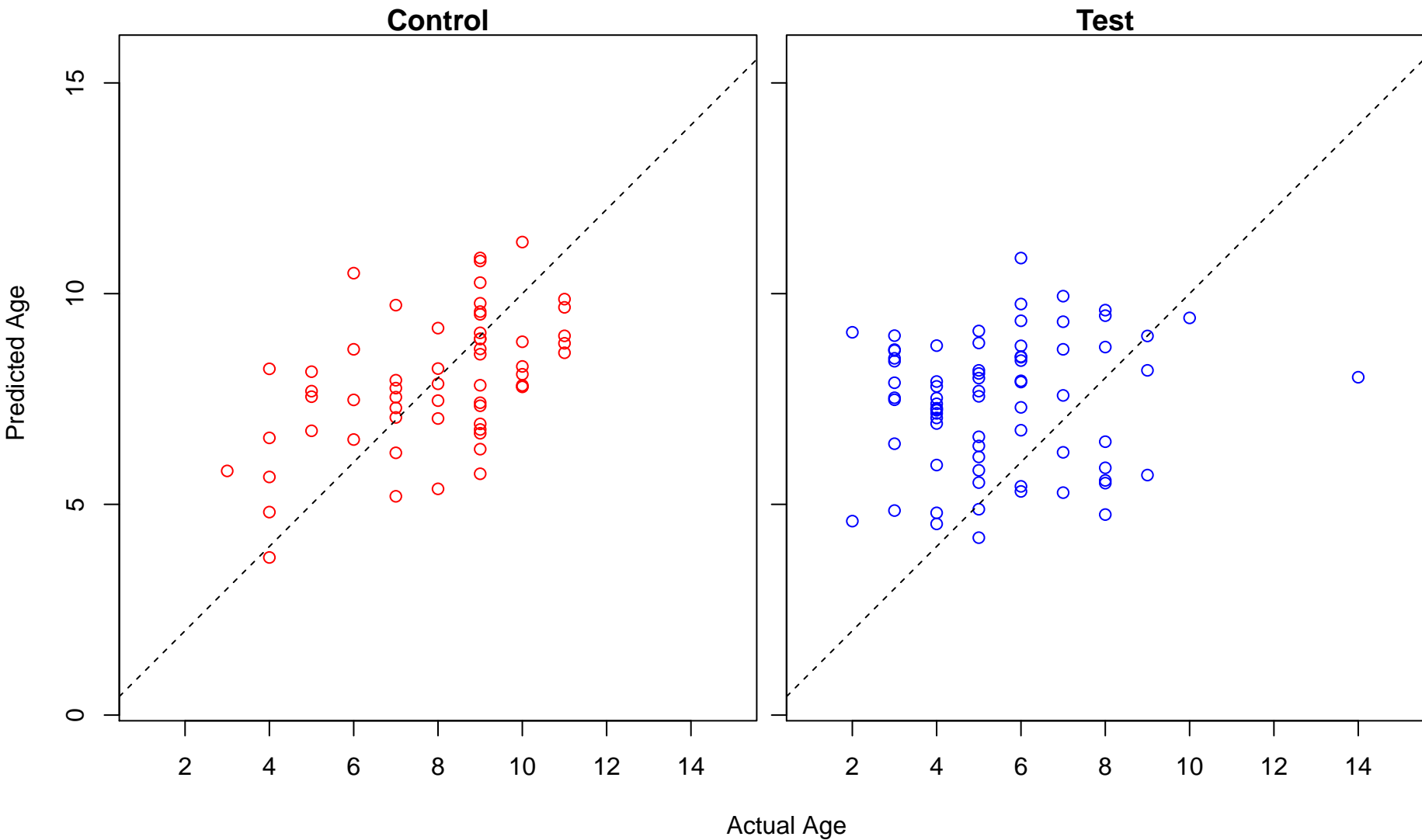
T cell proliferation (Score: 1.112679)



negative regulation of protein catabolic process (Score: 1.111719)

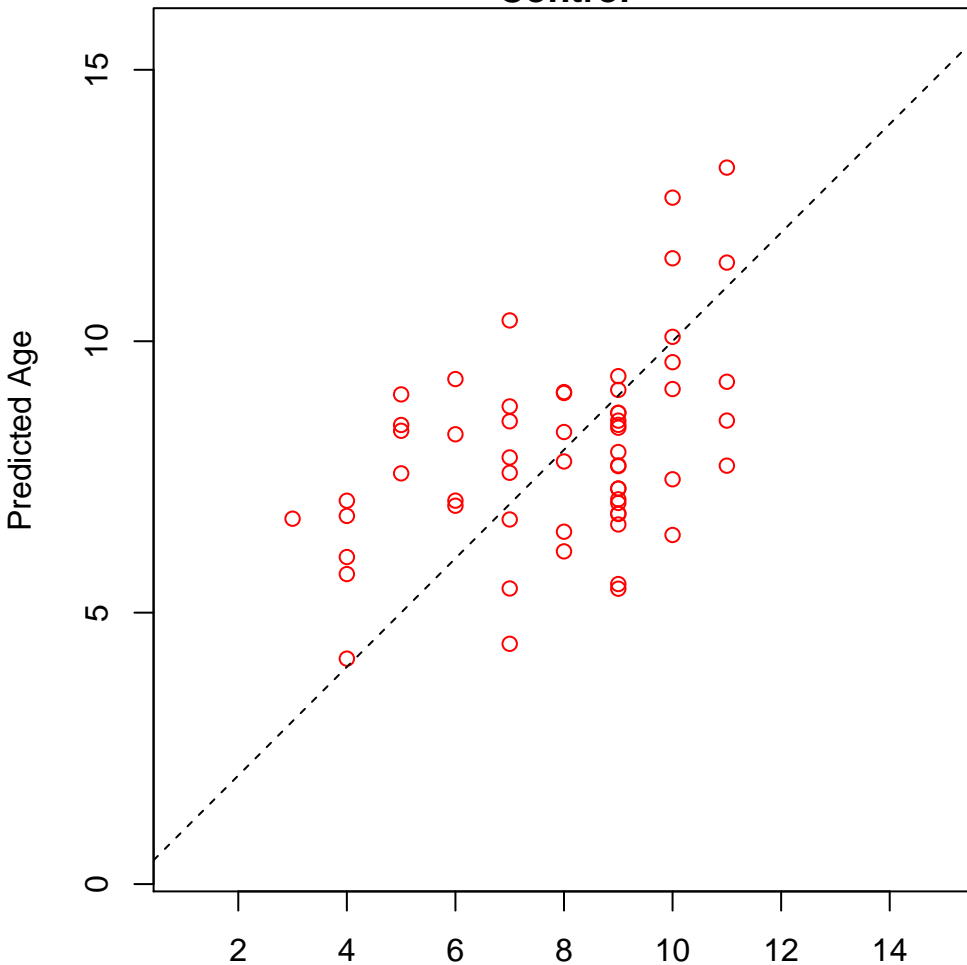


pigmentation (Score: 1.110086)

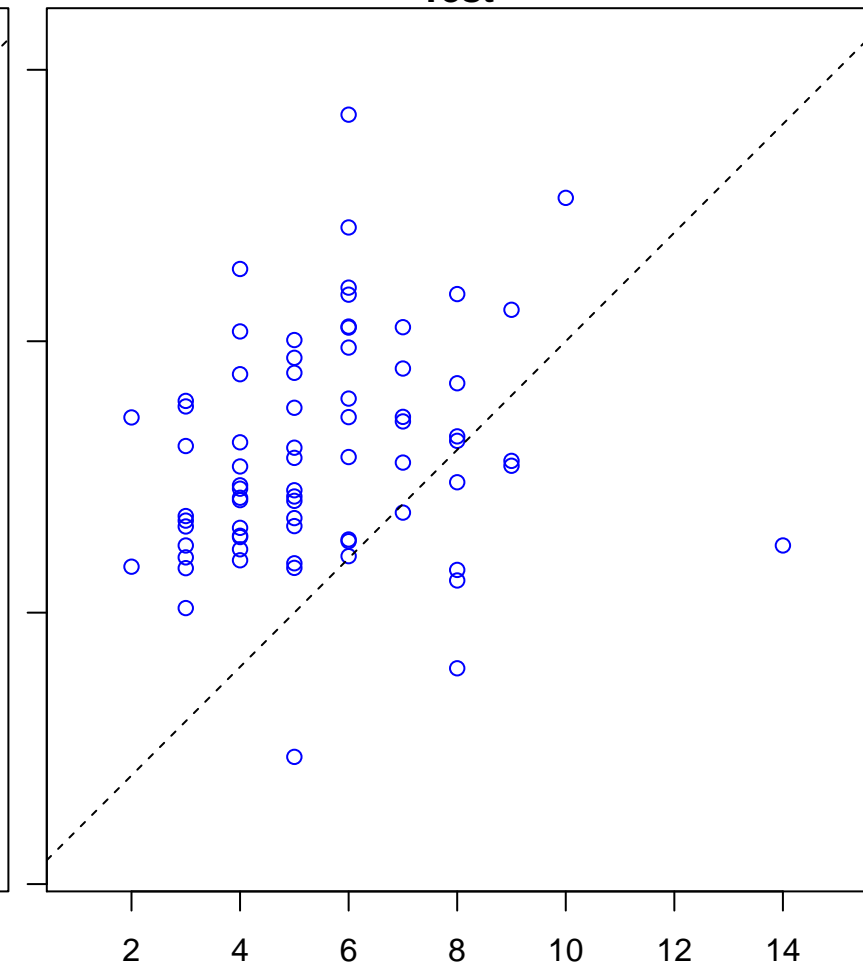


placenta blood vessel development (Score: 1.108701)

Control

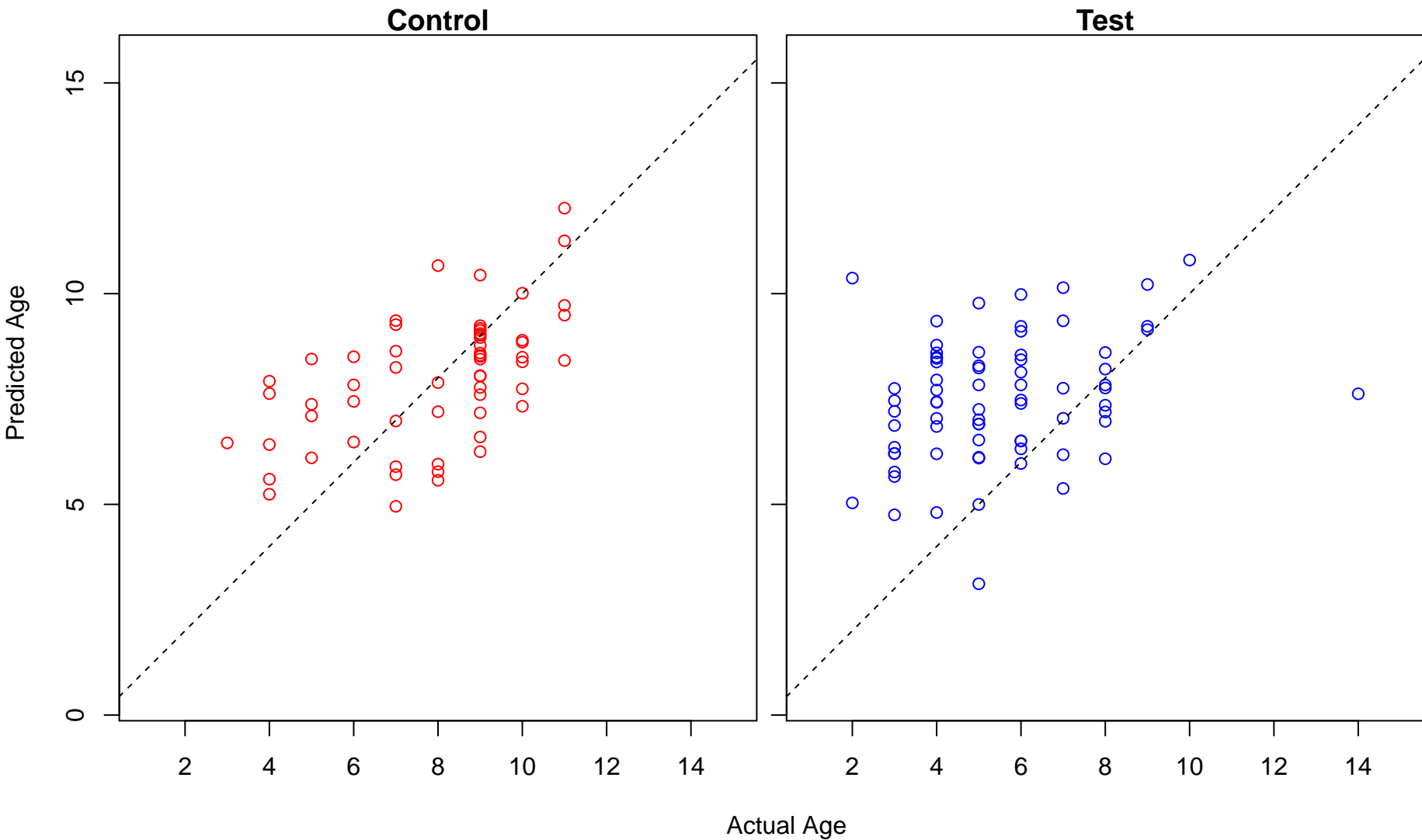


Test

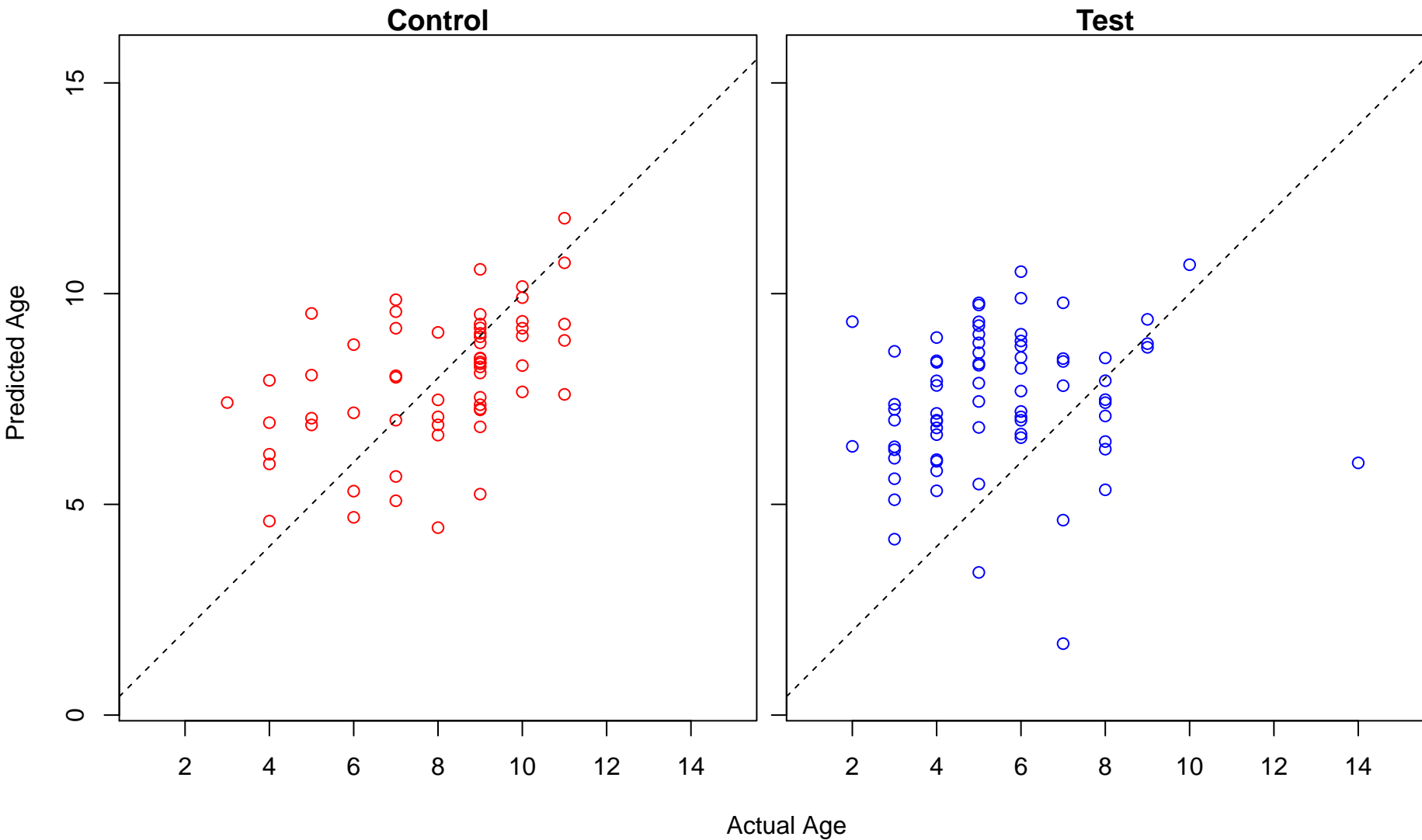


Actual Age

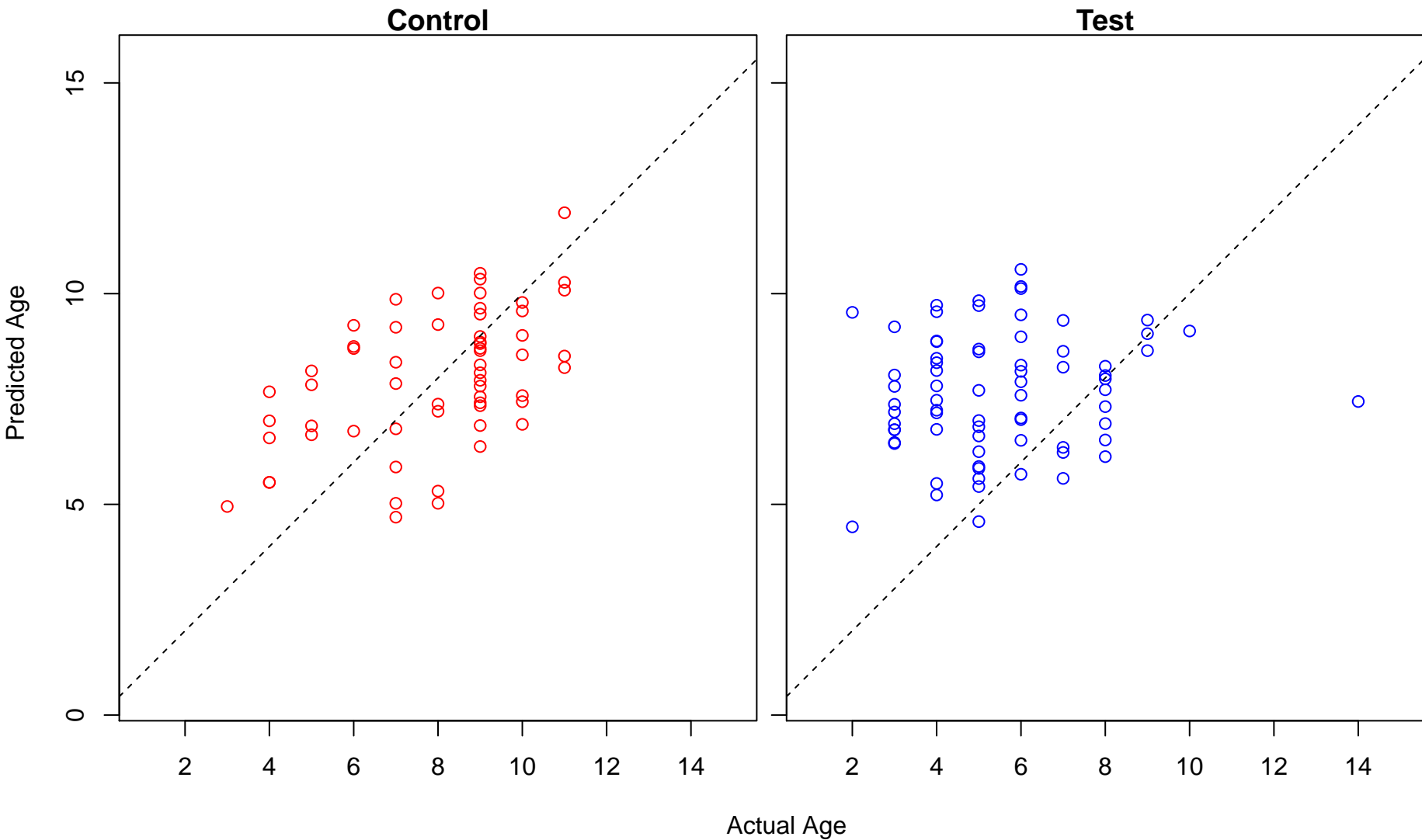
single-organism process (Score: 1.107871)



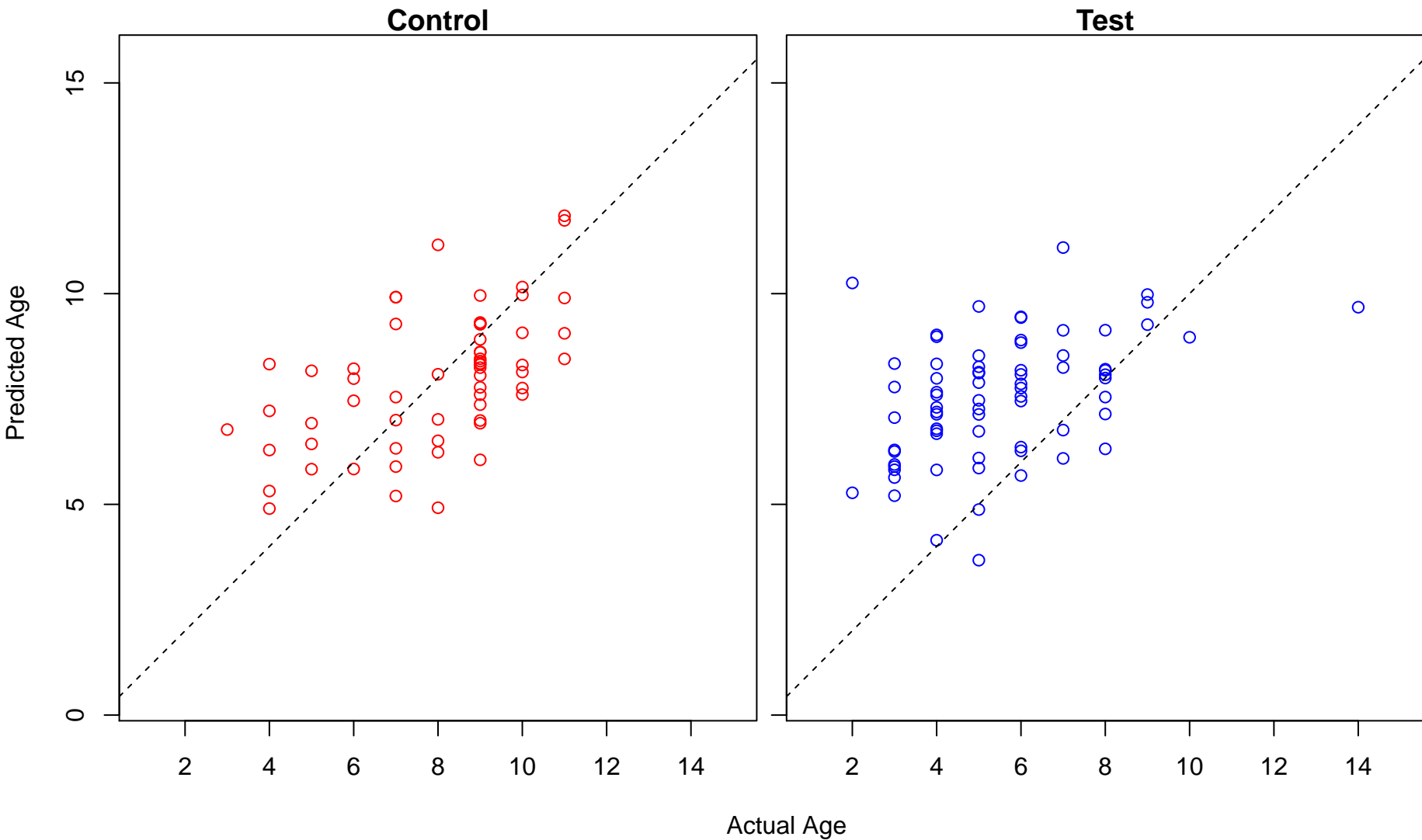
nucleic acid metabolic process (Score: 1.105544)



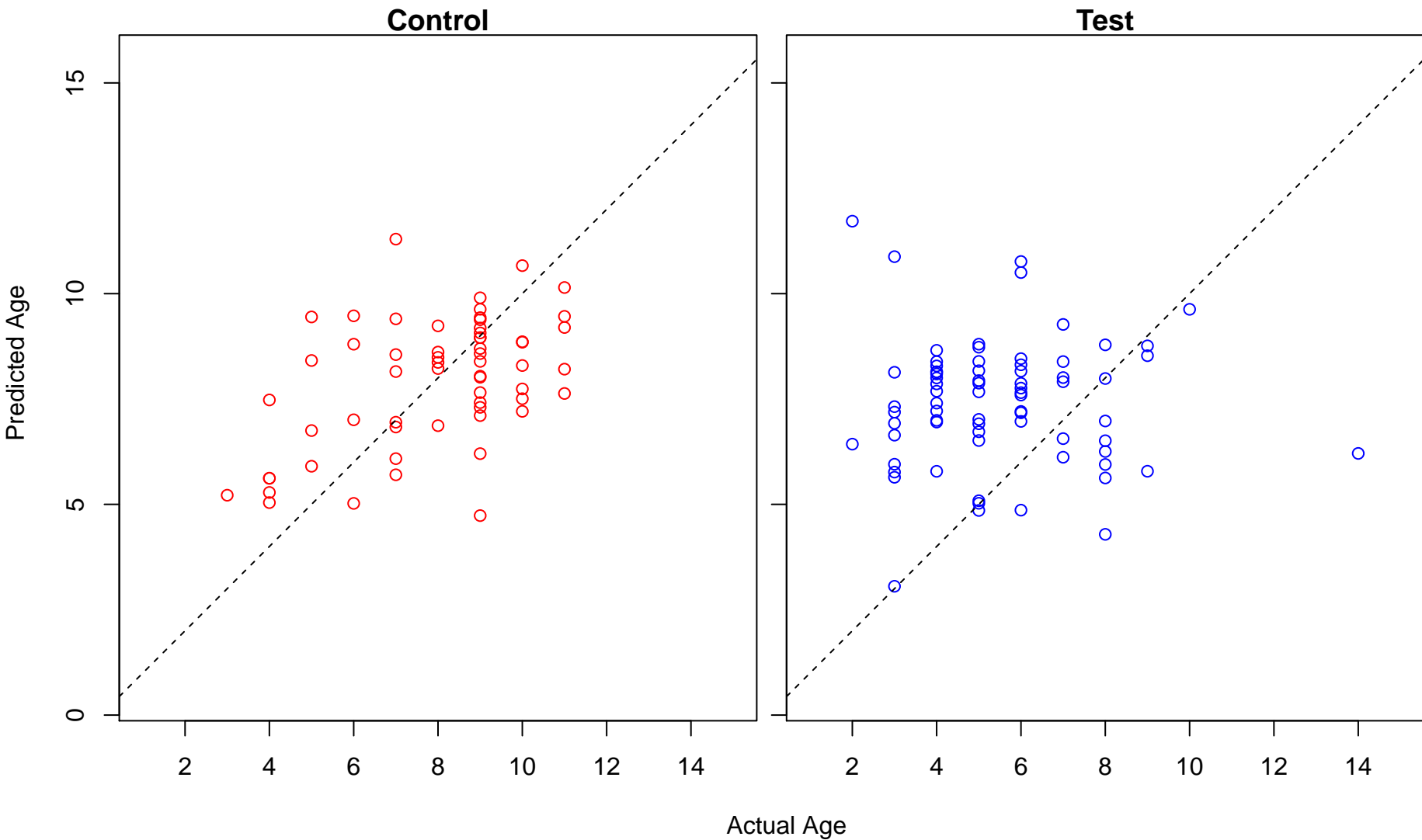
regulation of protein metabolic process (Score: 1.104937)



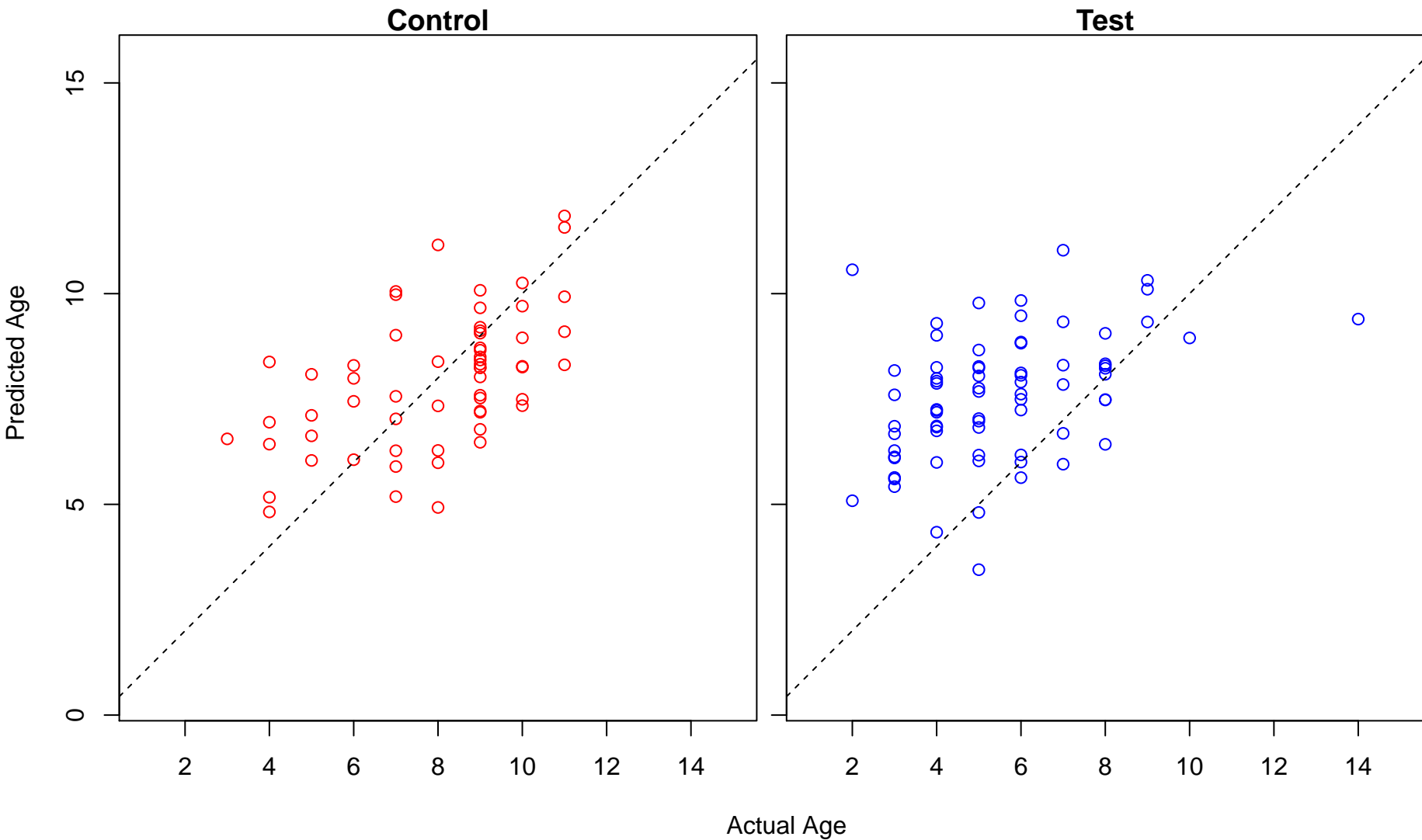
single-organism transport (Score: 1.104564)



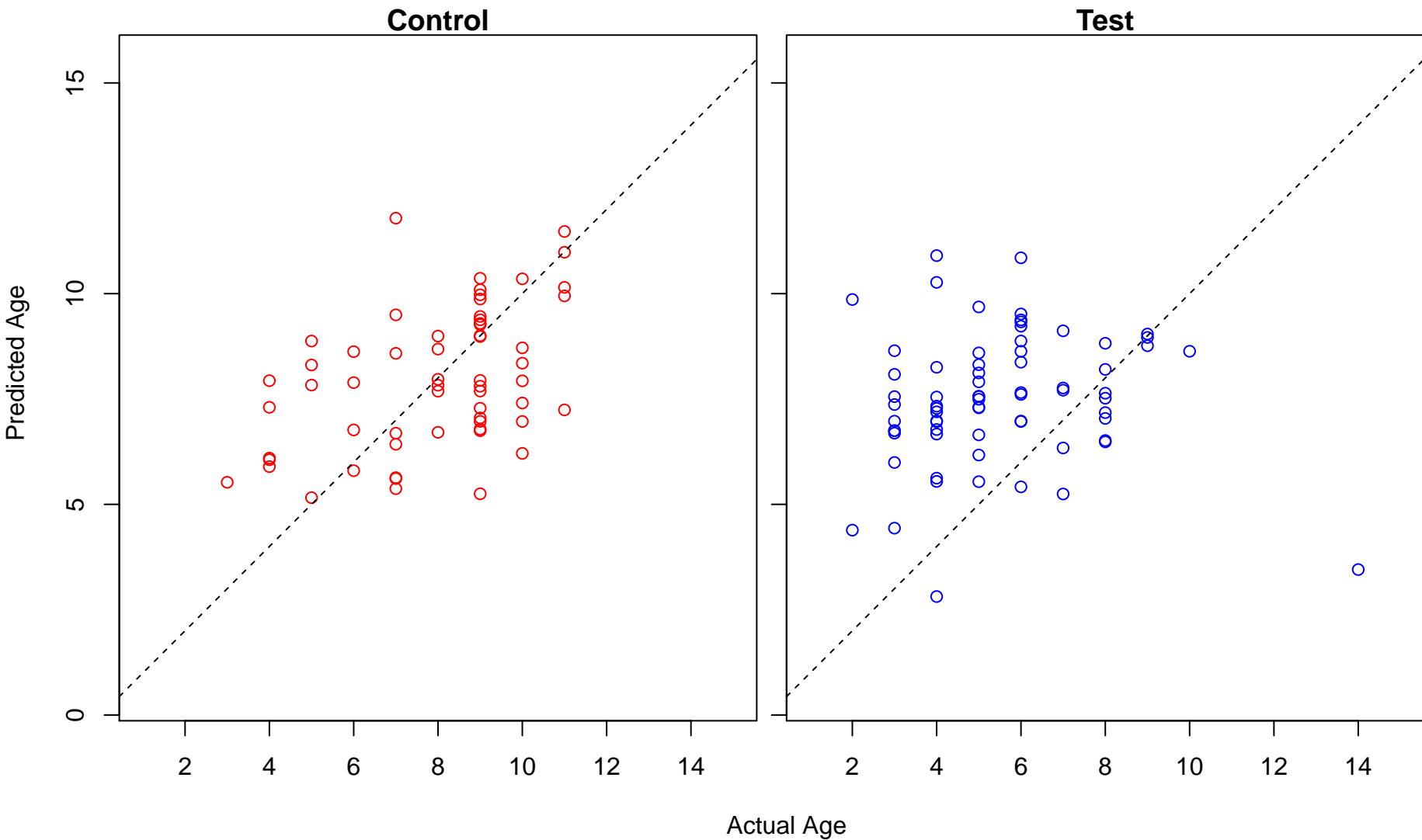
negative regulation of chromosome organization (Score: 1.104501)



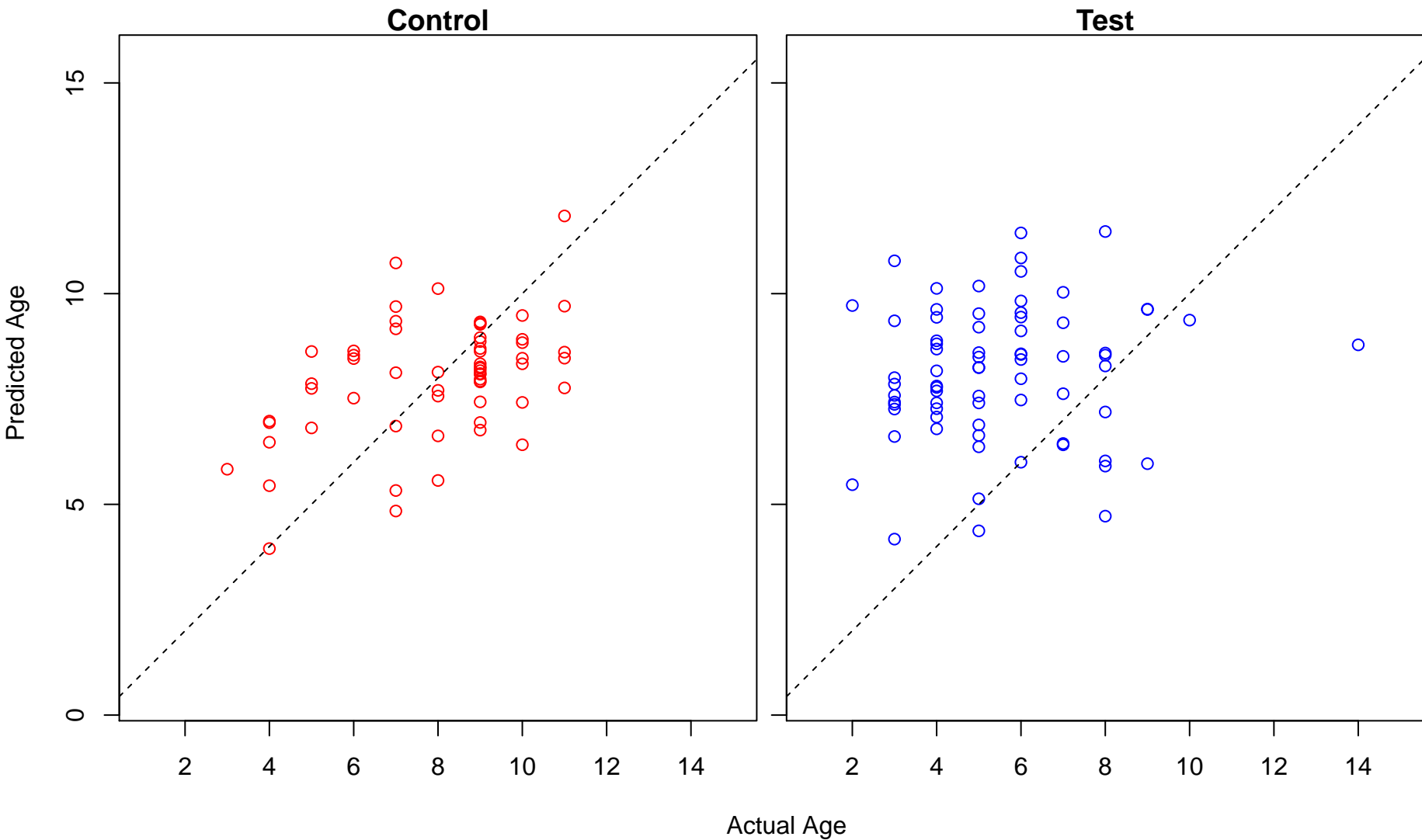
localization (Score: 1.104258)



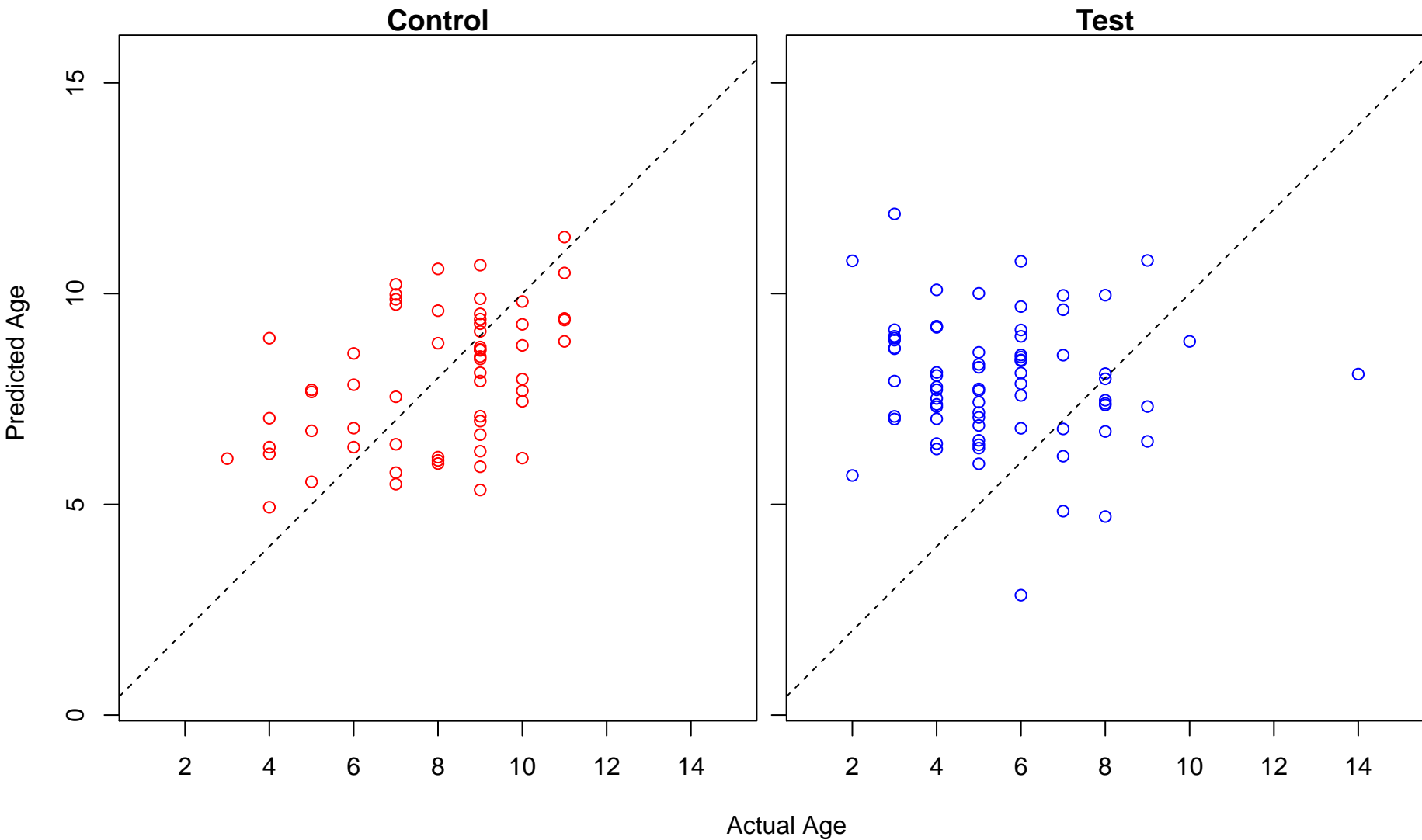
regulation of cellular catabolic process (Score: 1.104091)



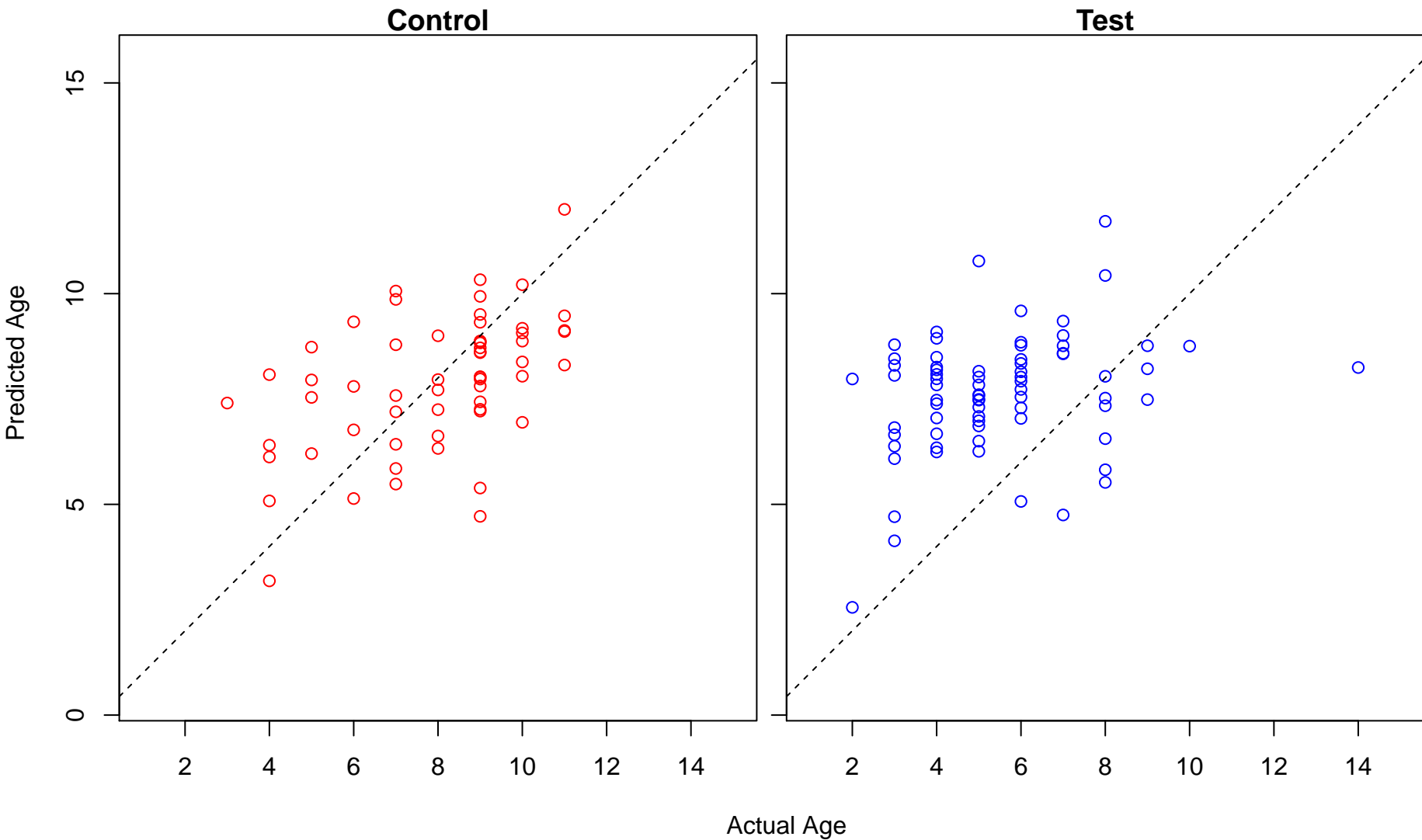
palate development (Score: 1.102820)



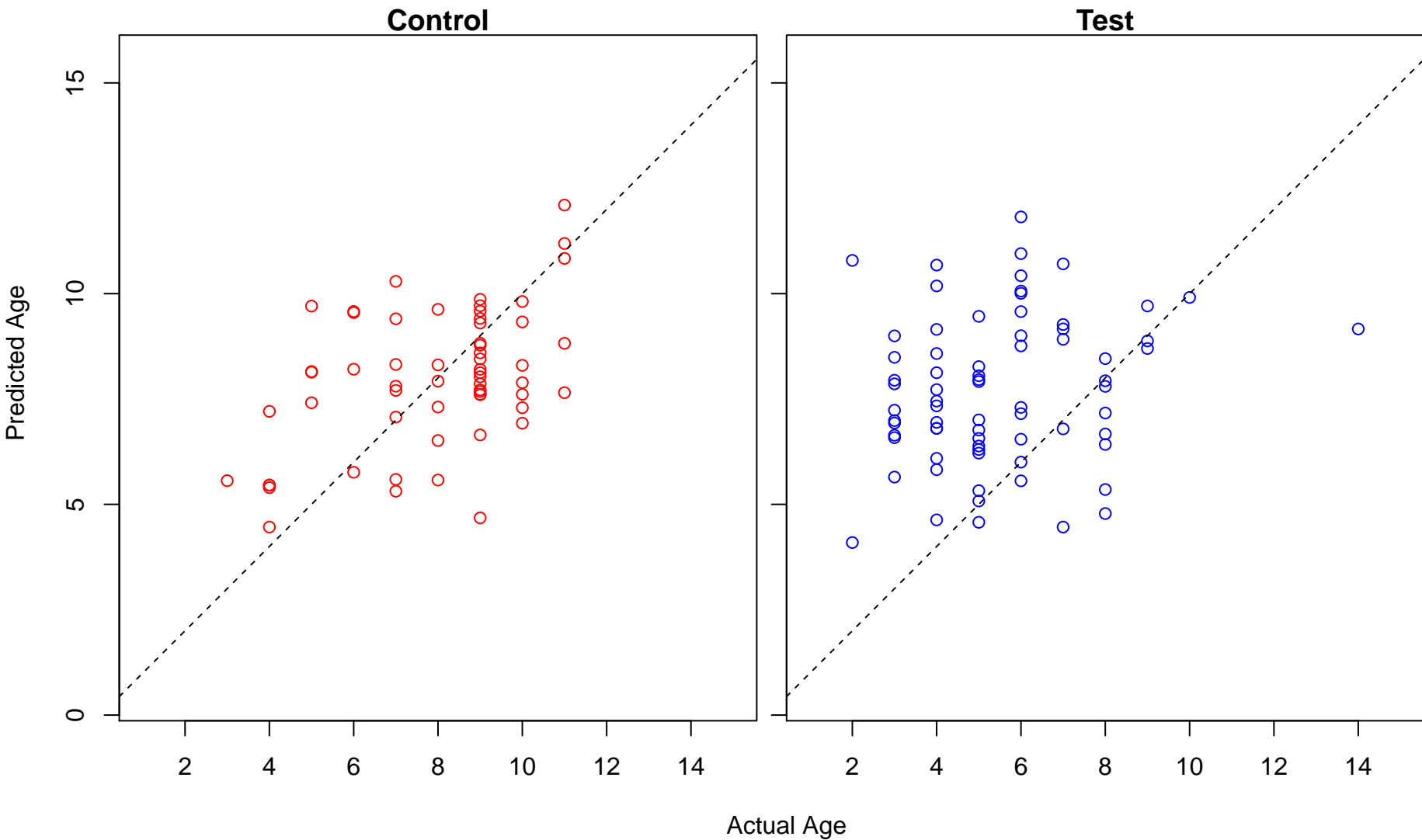
activation of cysteine-type endopeptidase activity (Score: 1.102754)



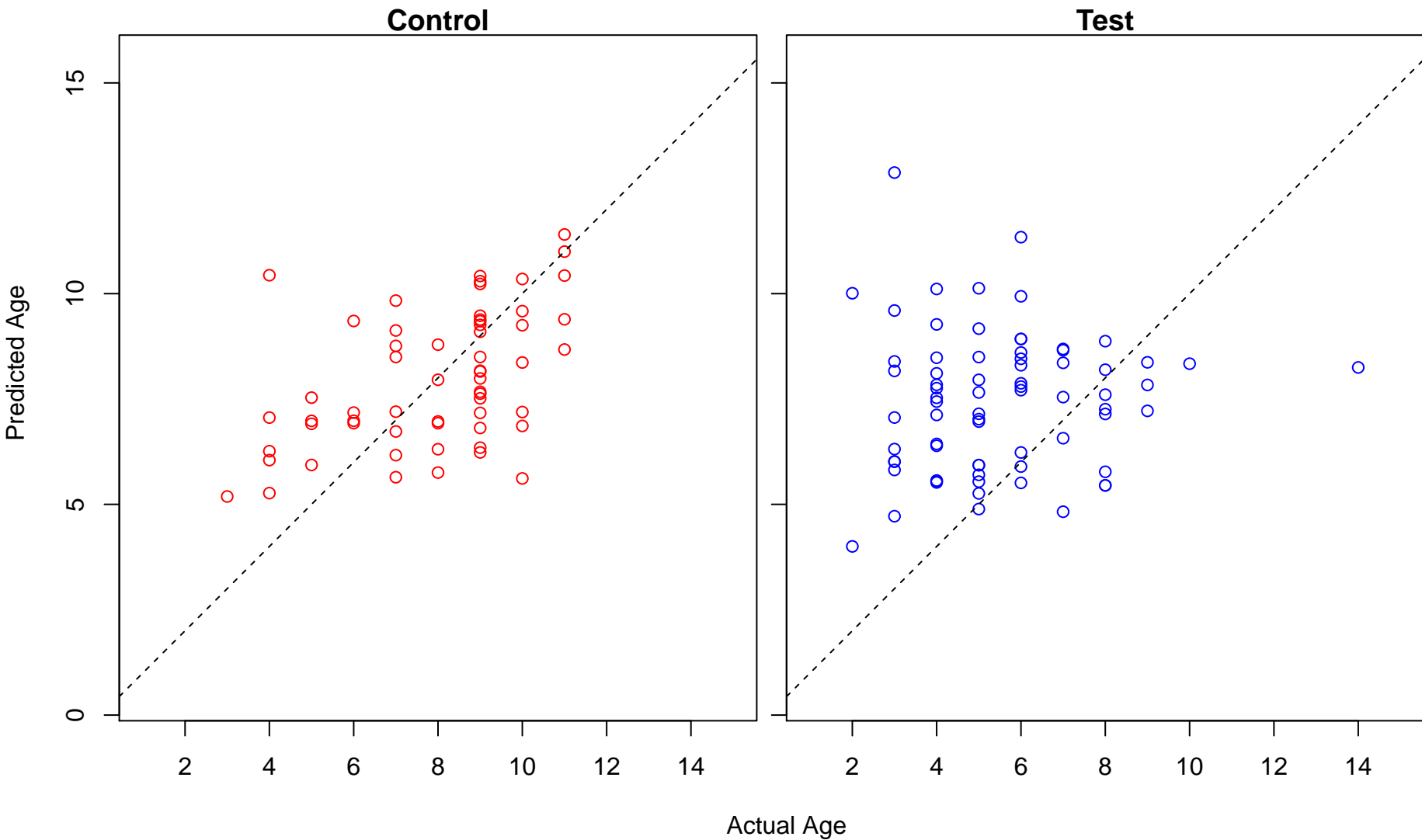
regulation of osteoblast differentiation (Score: 1.102476)



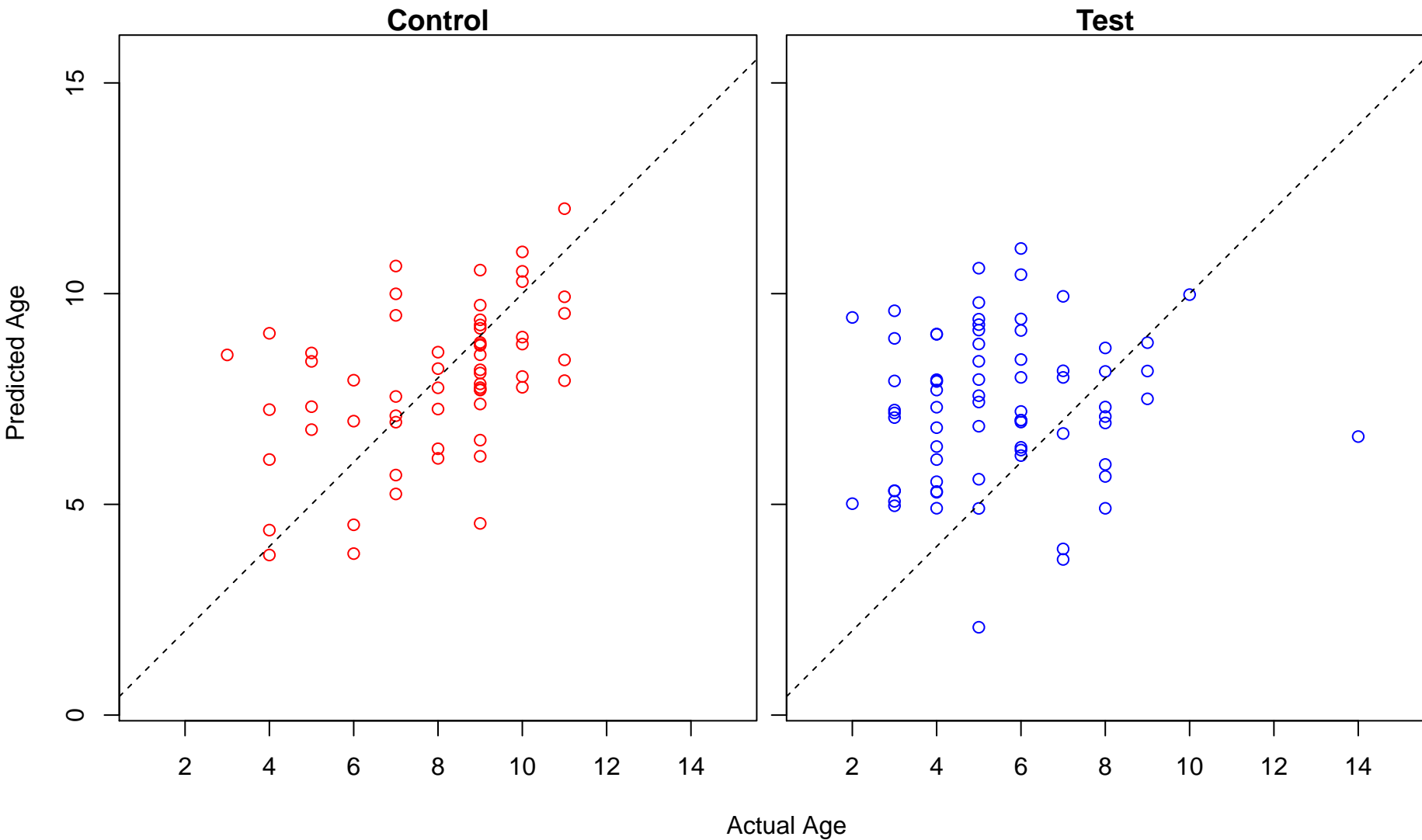
apoptotic signaling pathway (Score: 1.102457)



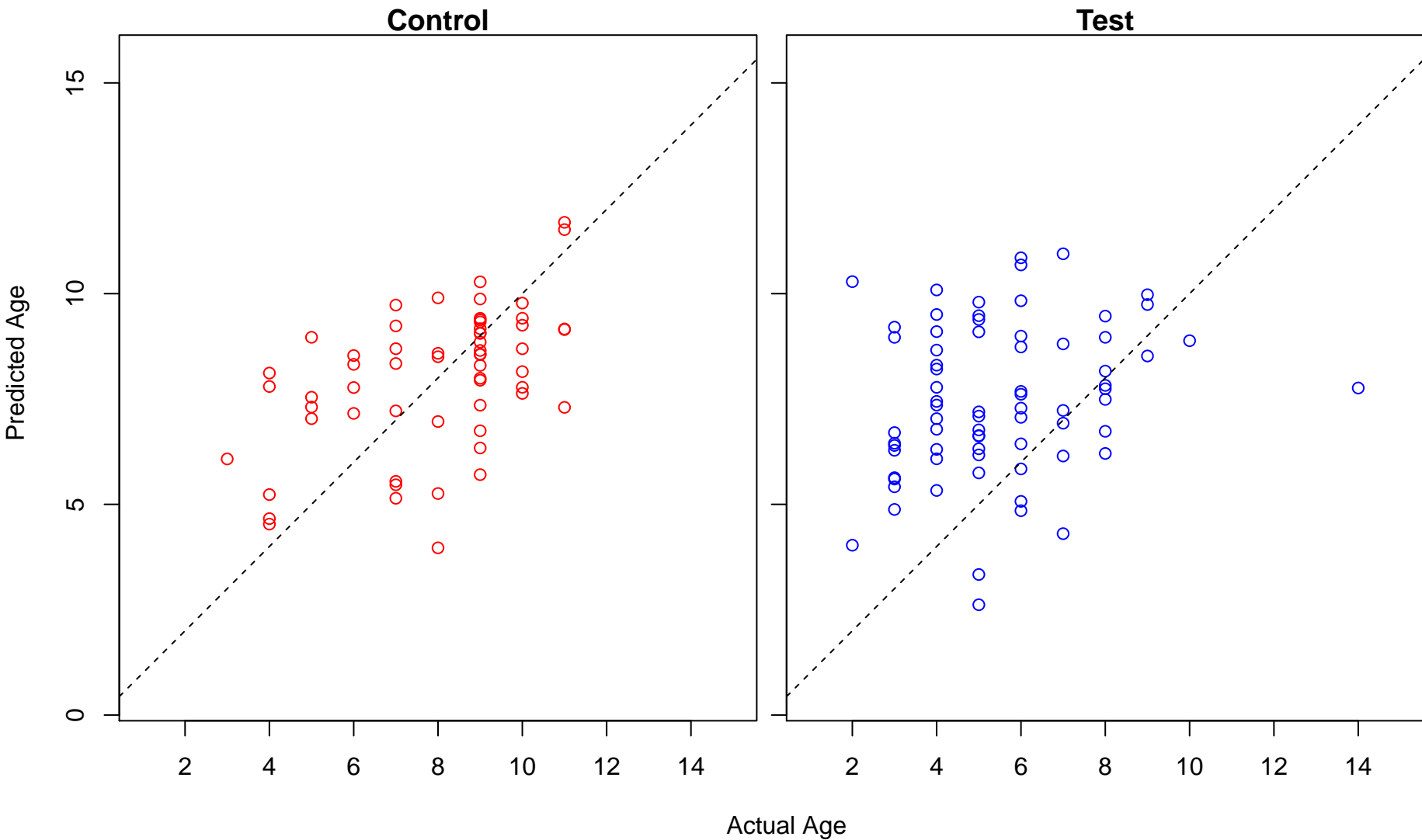
mesenchyme development (Score: 1.102246)



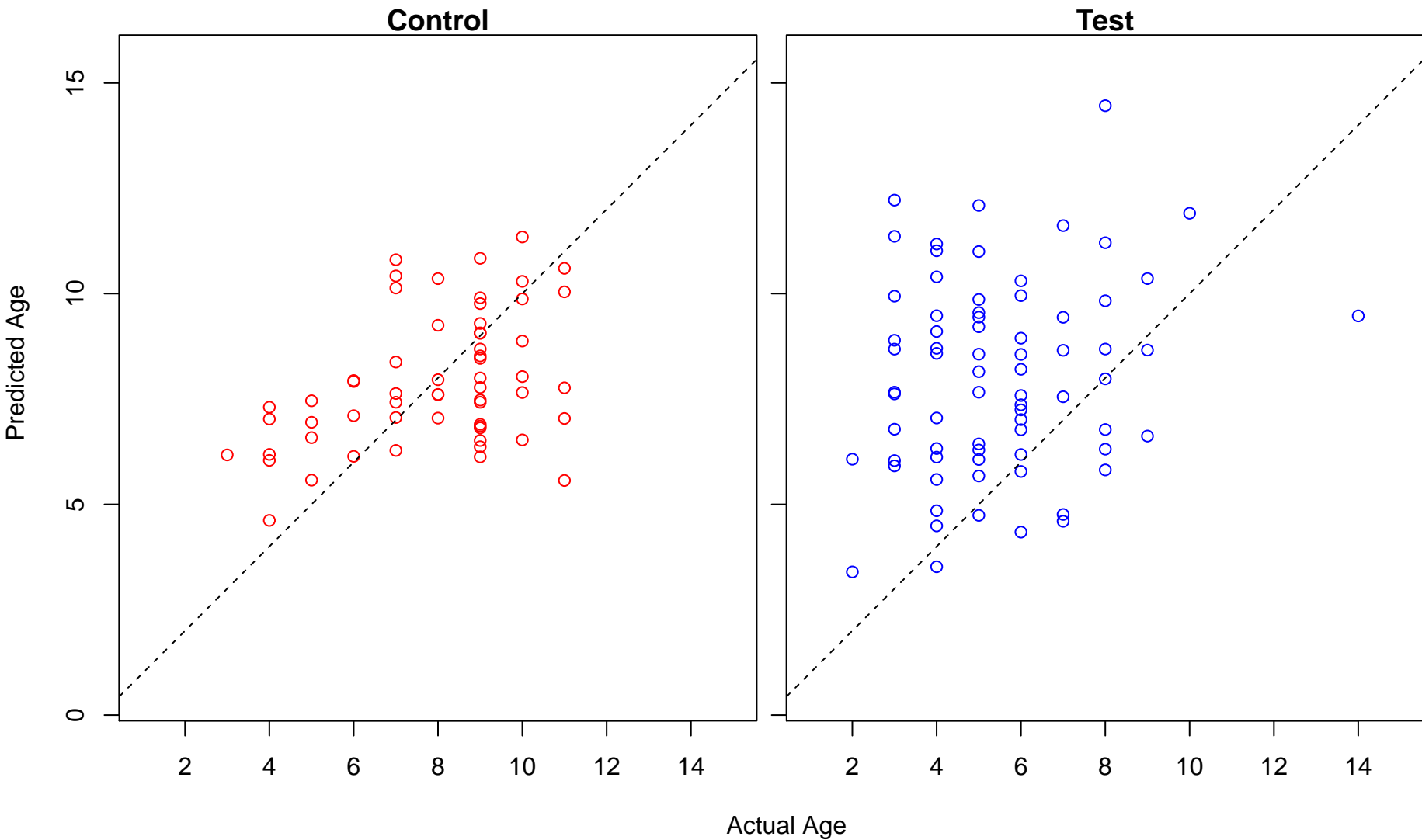
mRNA metabolic process (Score: 1.101744)



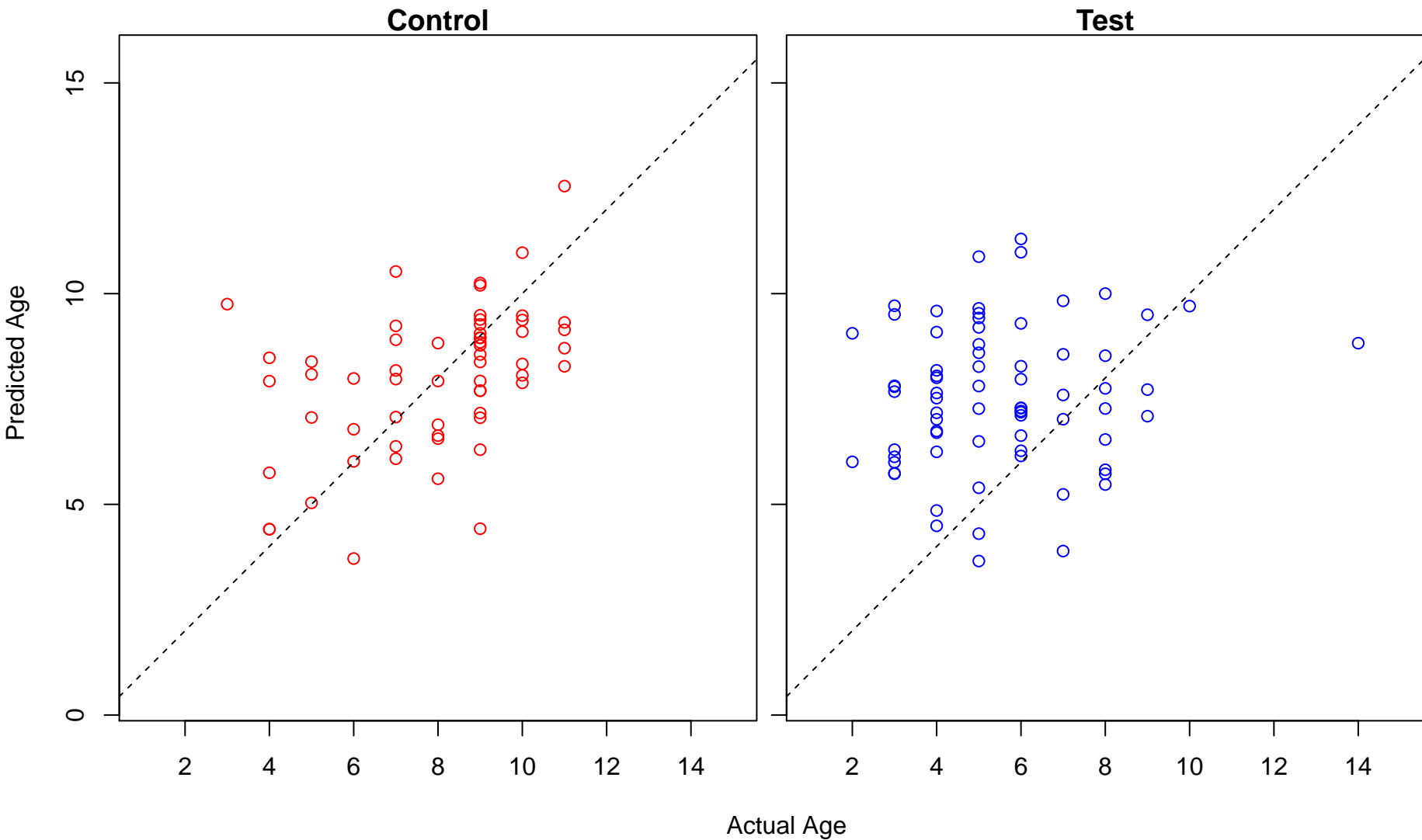
regulation of biological quality (Score: 1.099669)



protein deneddylatn (Score: 1.099062)

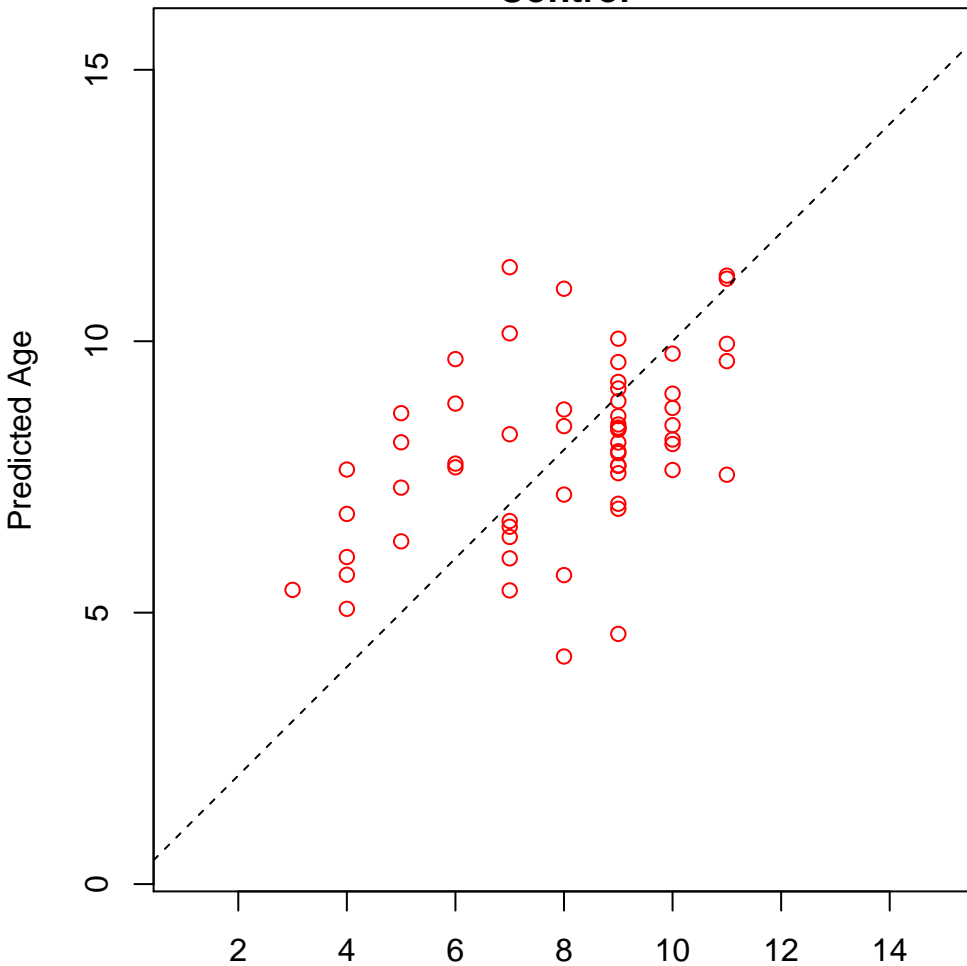


protein localization to endoplasmic reticulum (Score: 1.098226)

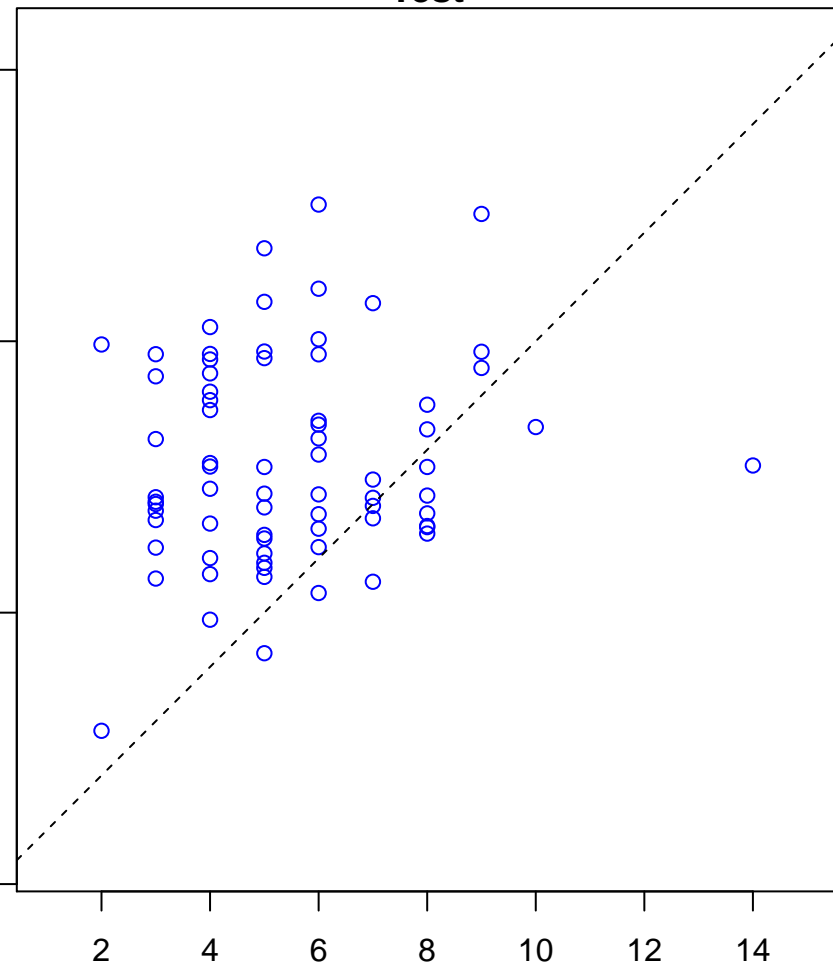


cellular response to nitrogen compound (Score: 1.097579)

Control

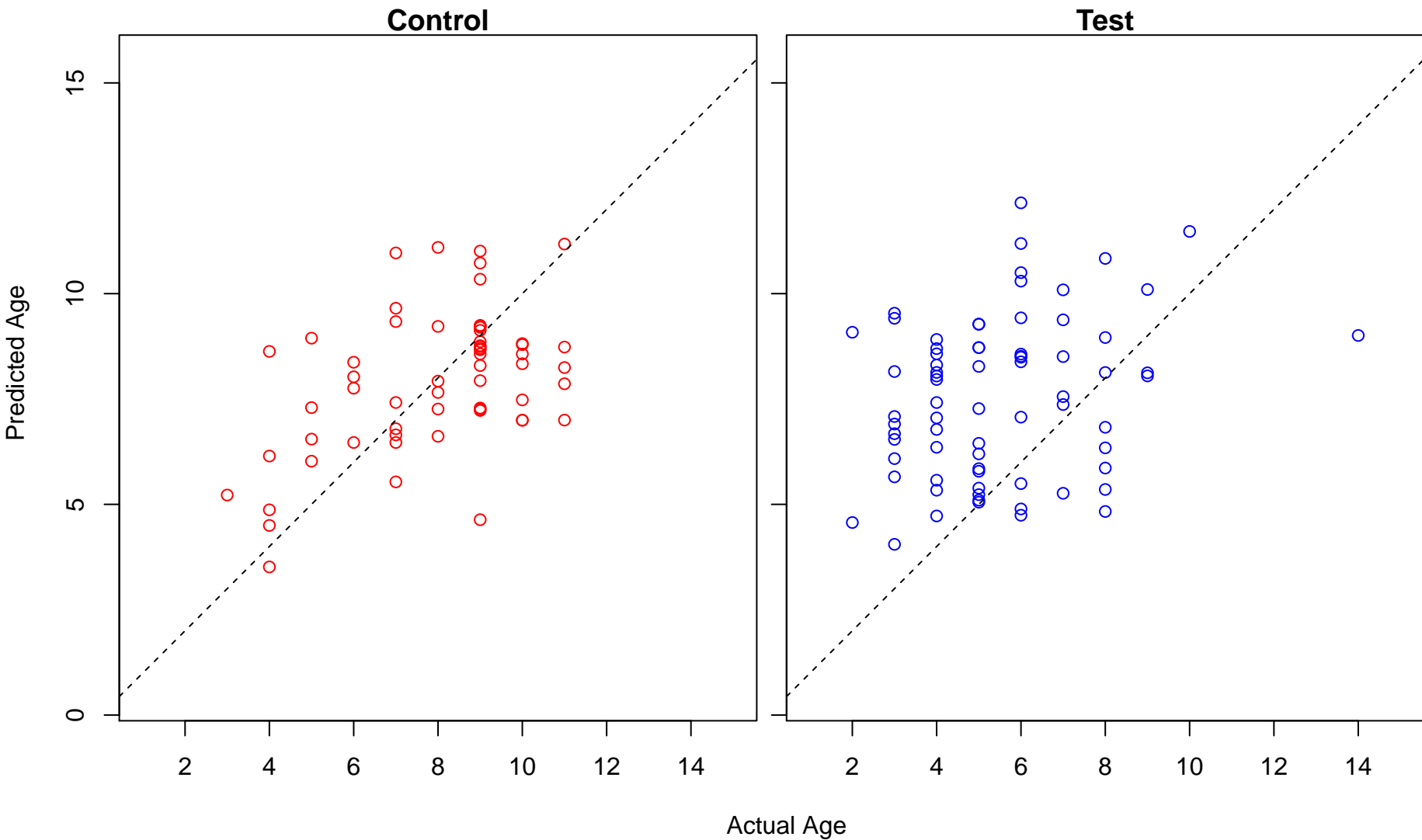


Test

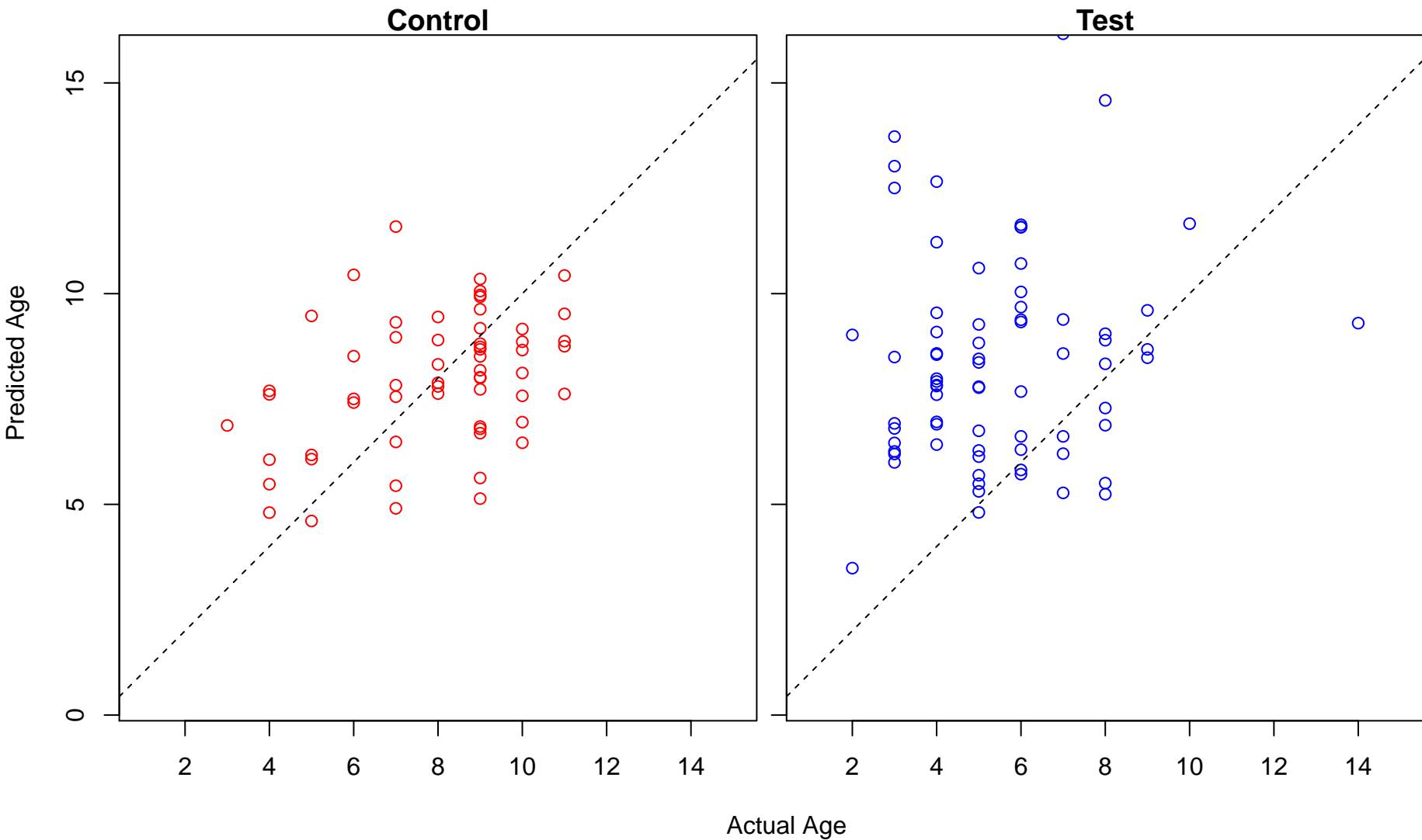


Actual Age

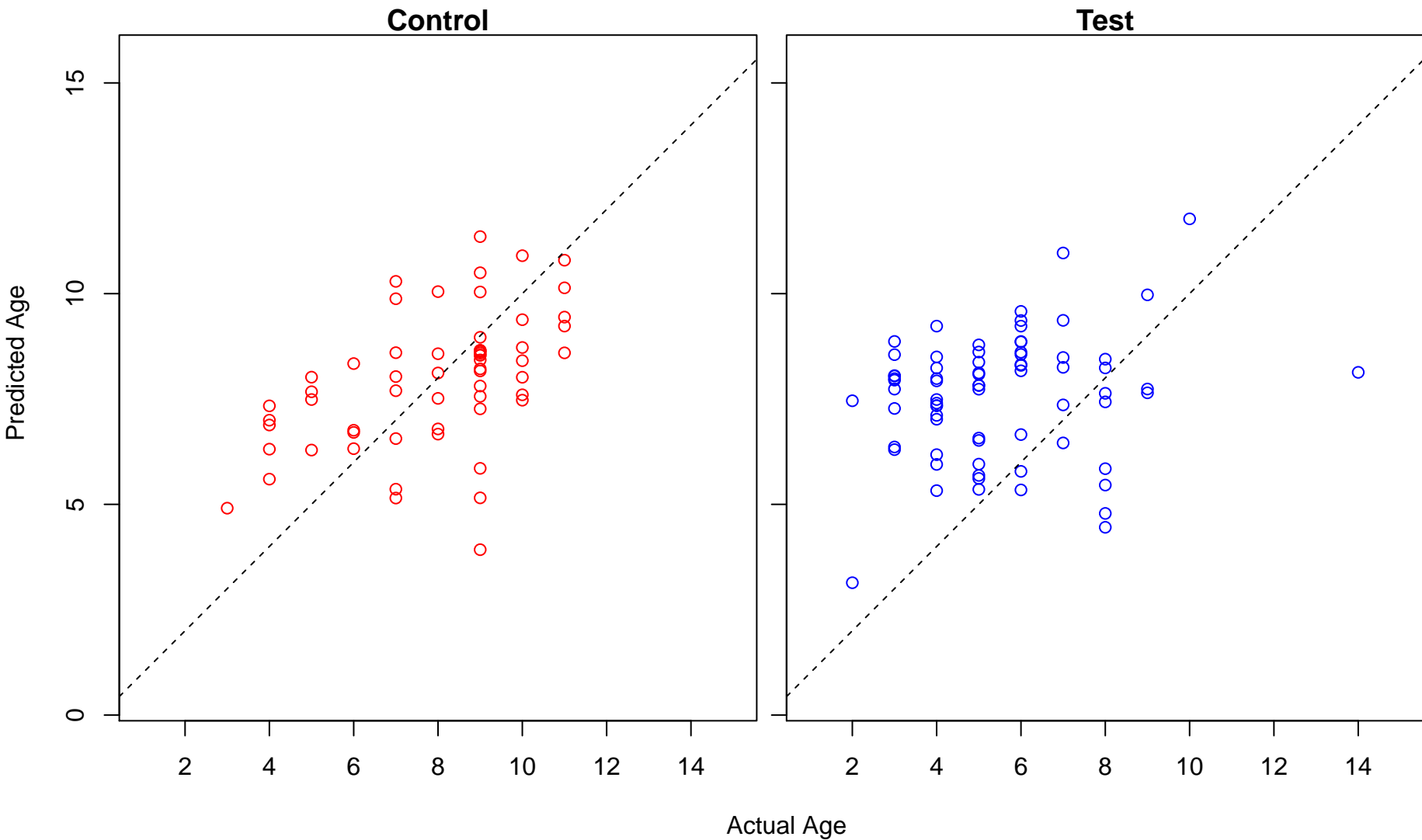
cellular lipid metabolic process (Score: 1.096549)



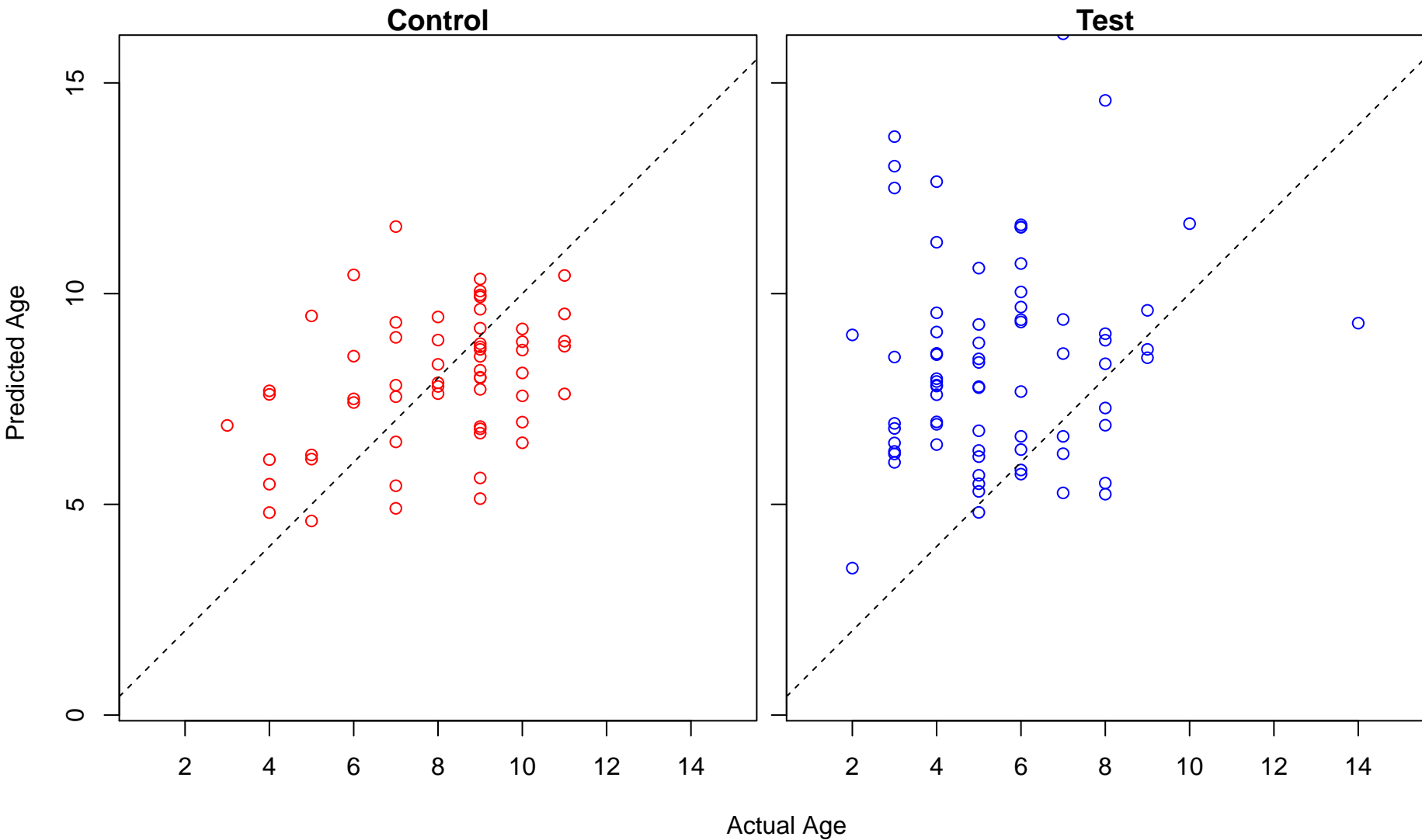
regulation of coagulation (Score: 1.096207)



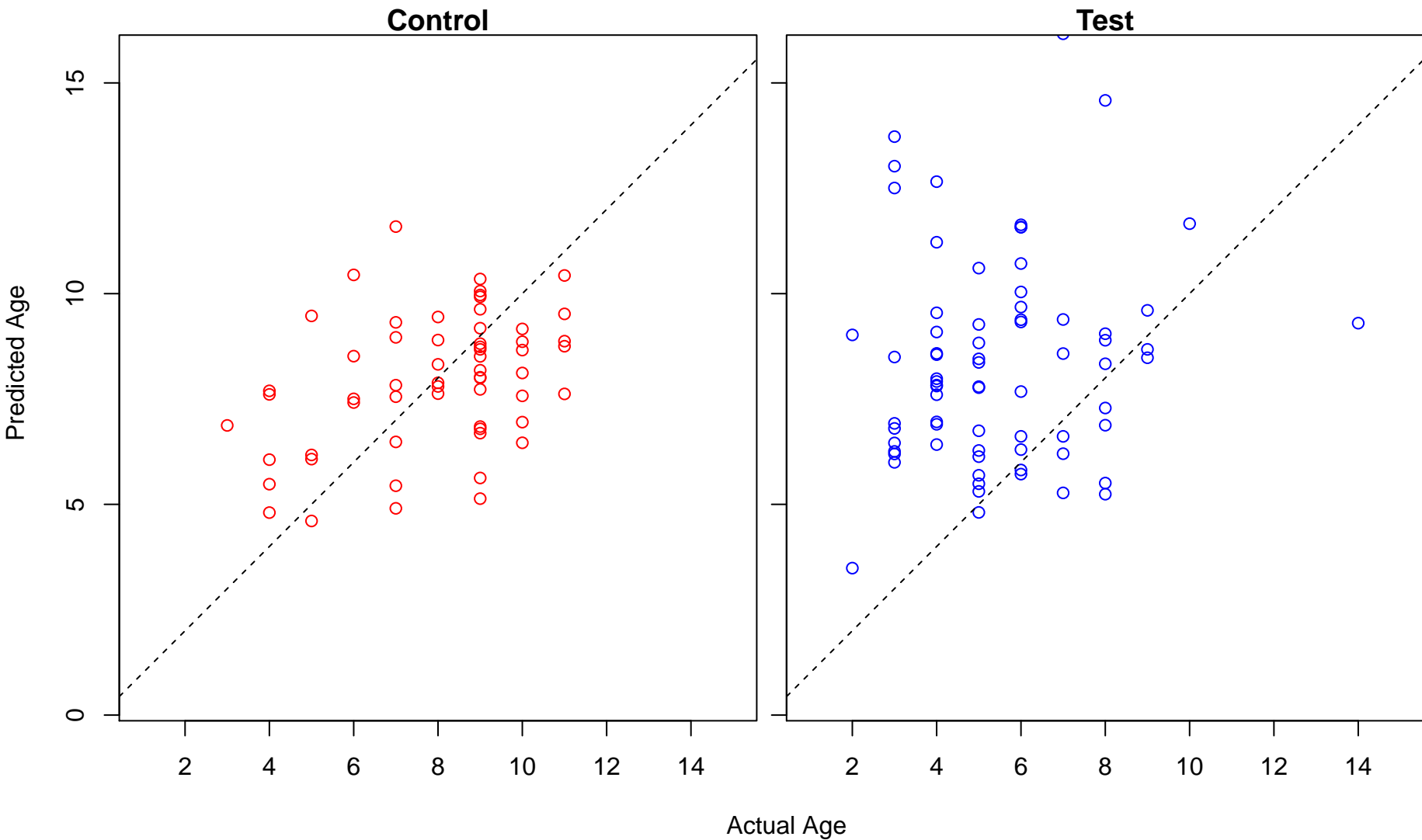
regulation of tyrosine phosphorylation of Stat1 protein (Score: 1.096177)



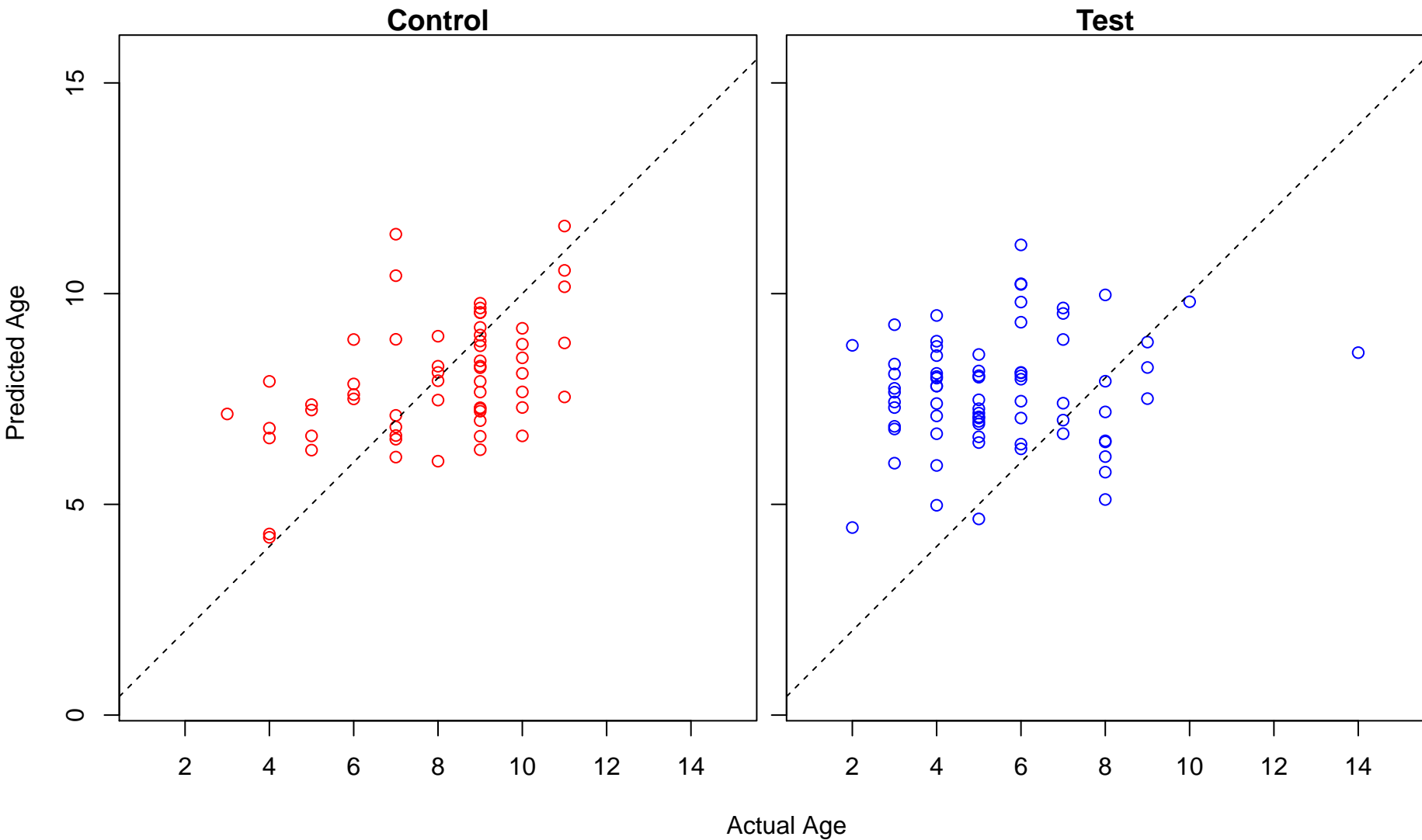
regulation of blood coagulation (Score: 1.095994)



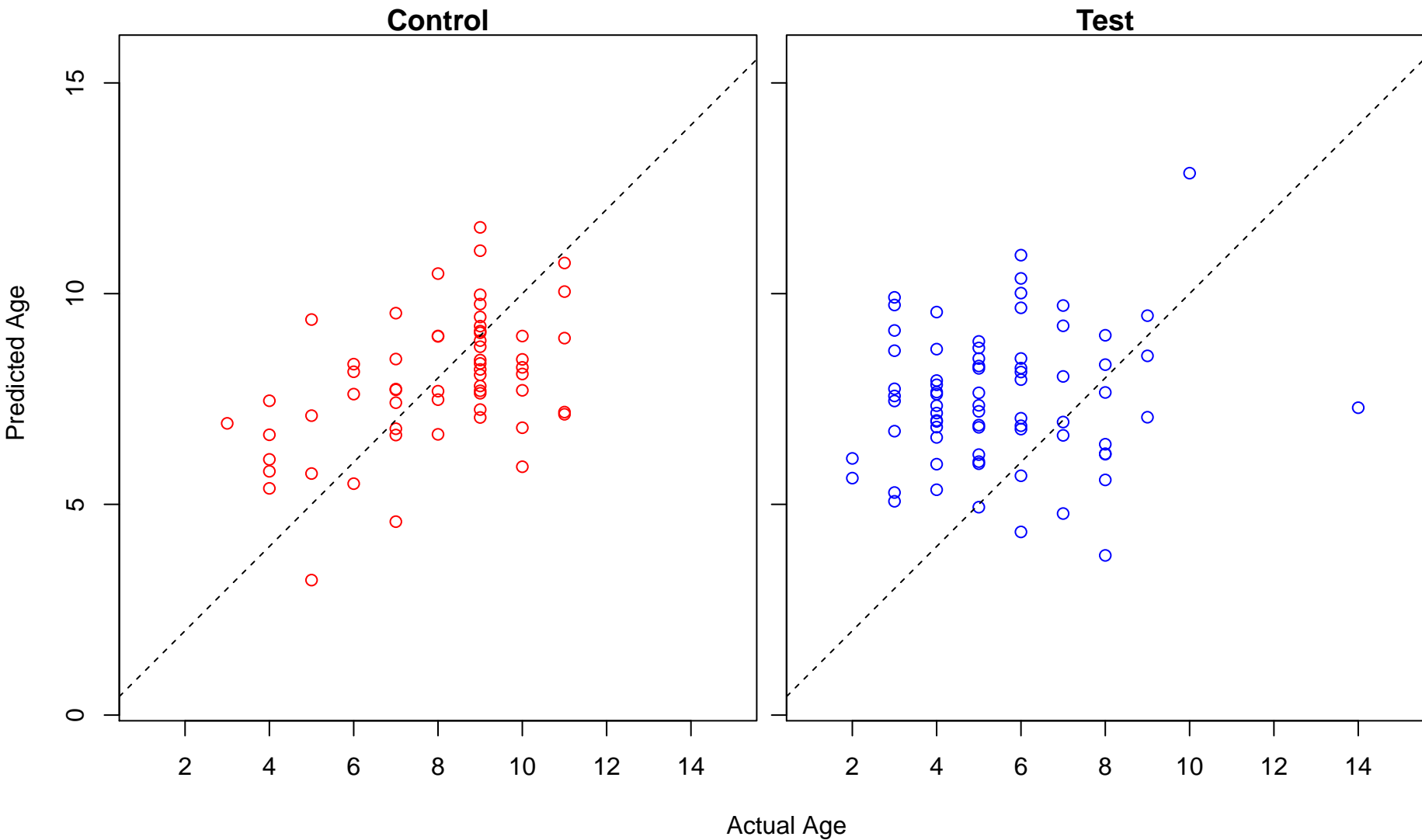
regulation of hemostasis (Score: 1.095994)



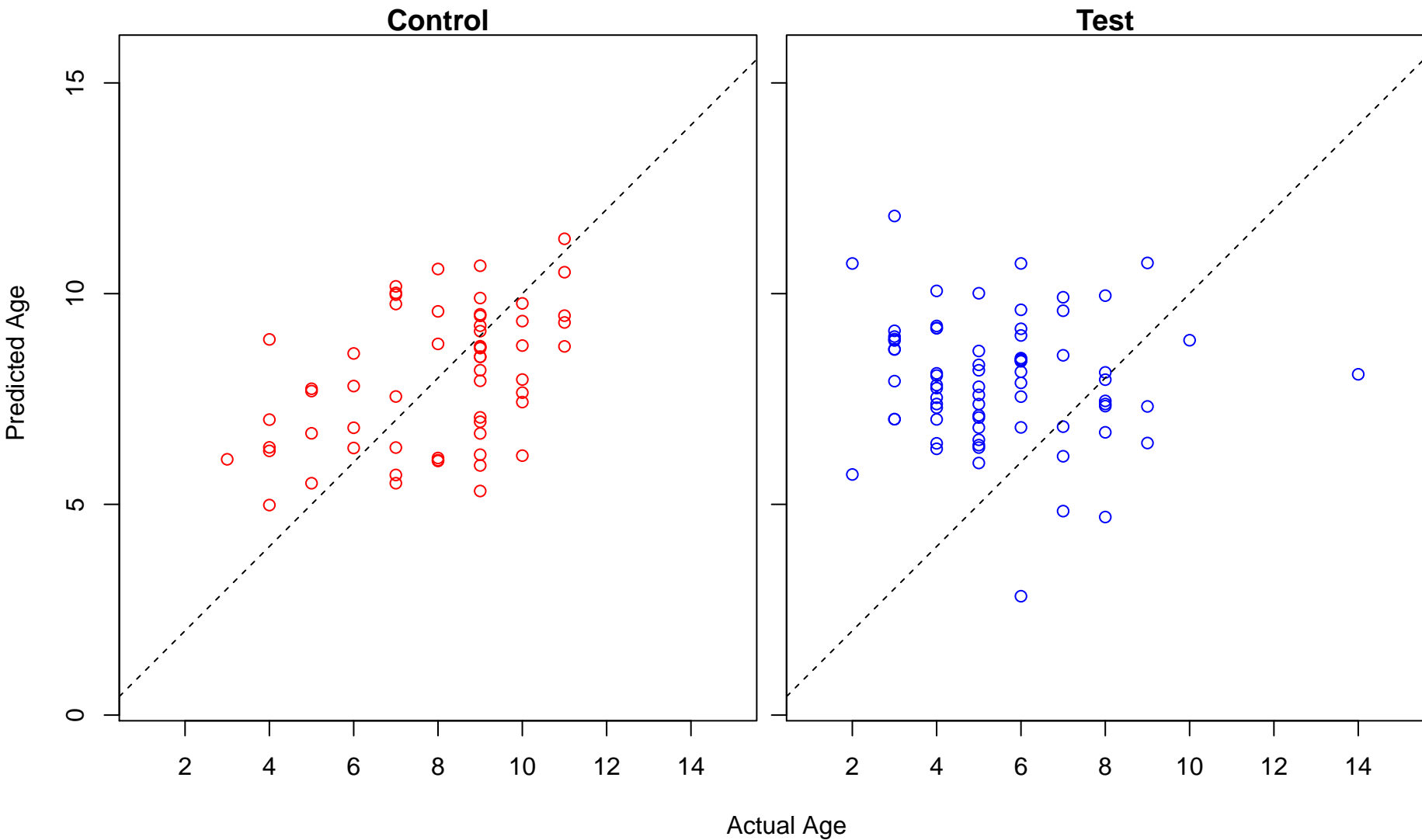
inner ear morphogenesis (Score: 1.095636)



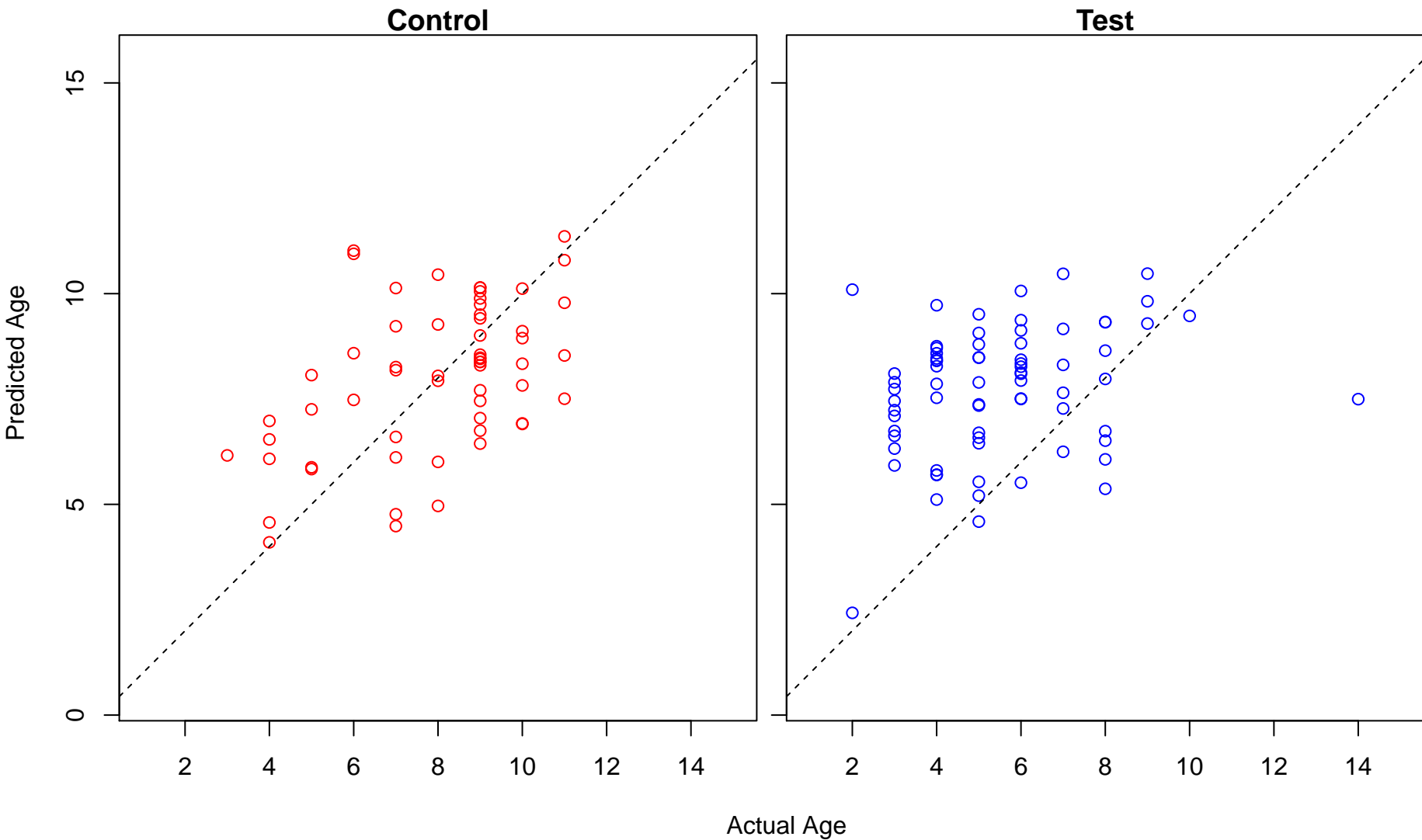
activation of protein kinase B activity (Score: 1.095364)



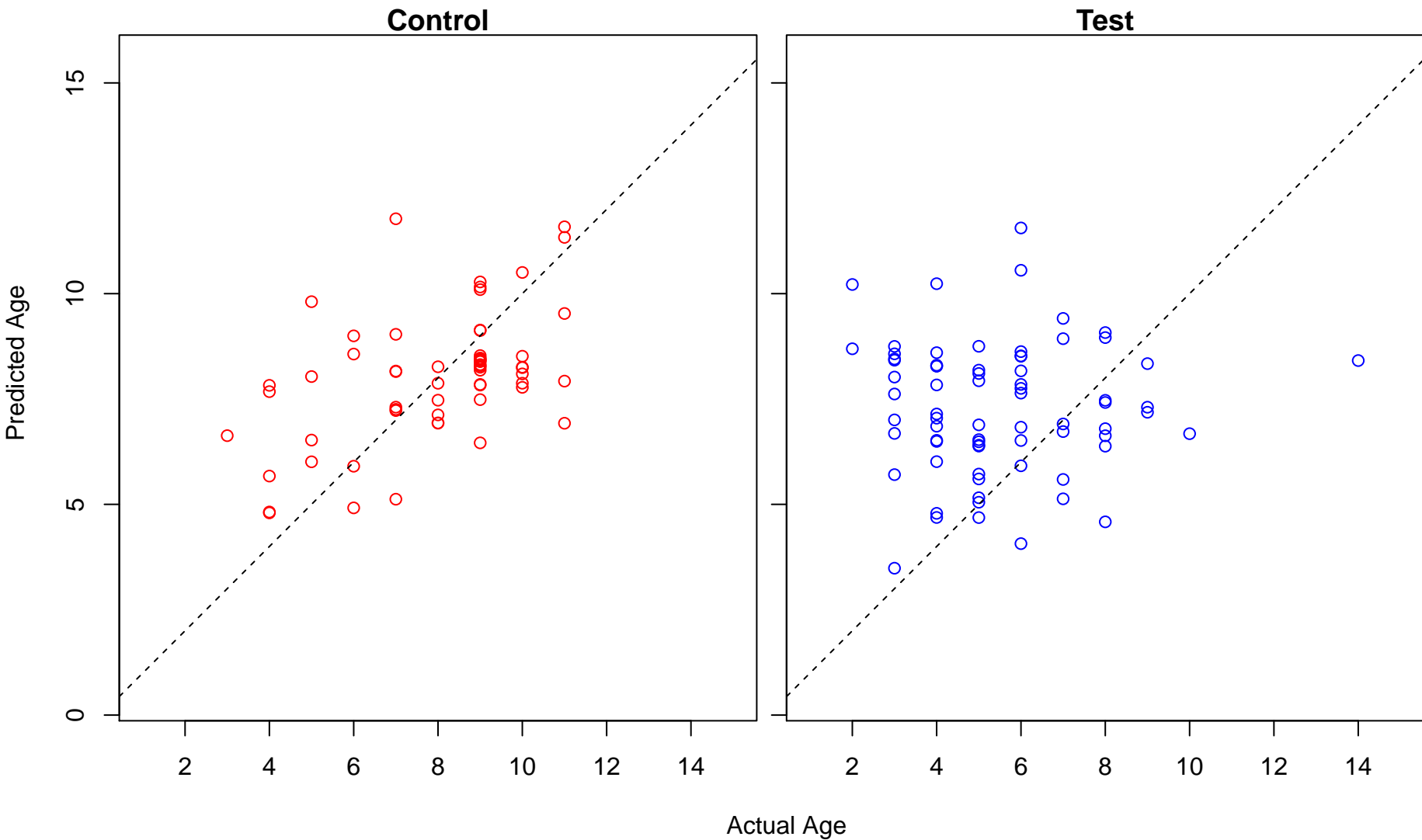
zymogen activation (Score: 1.095140)



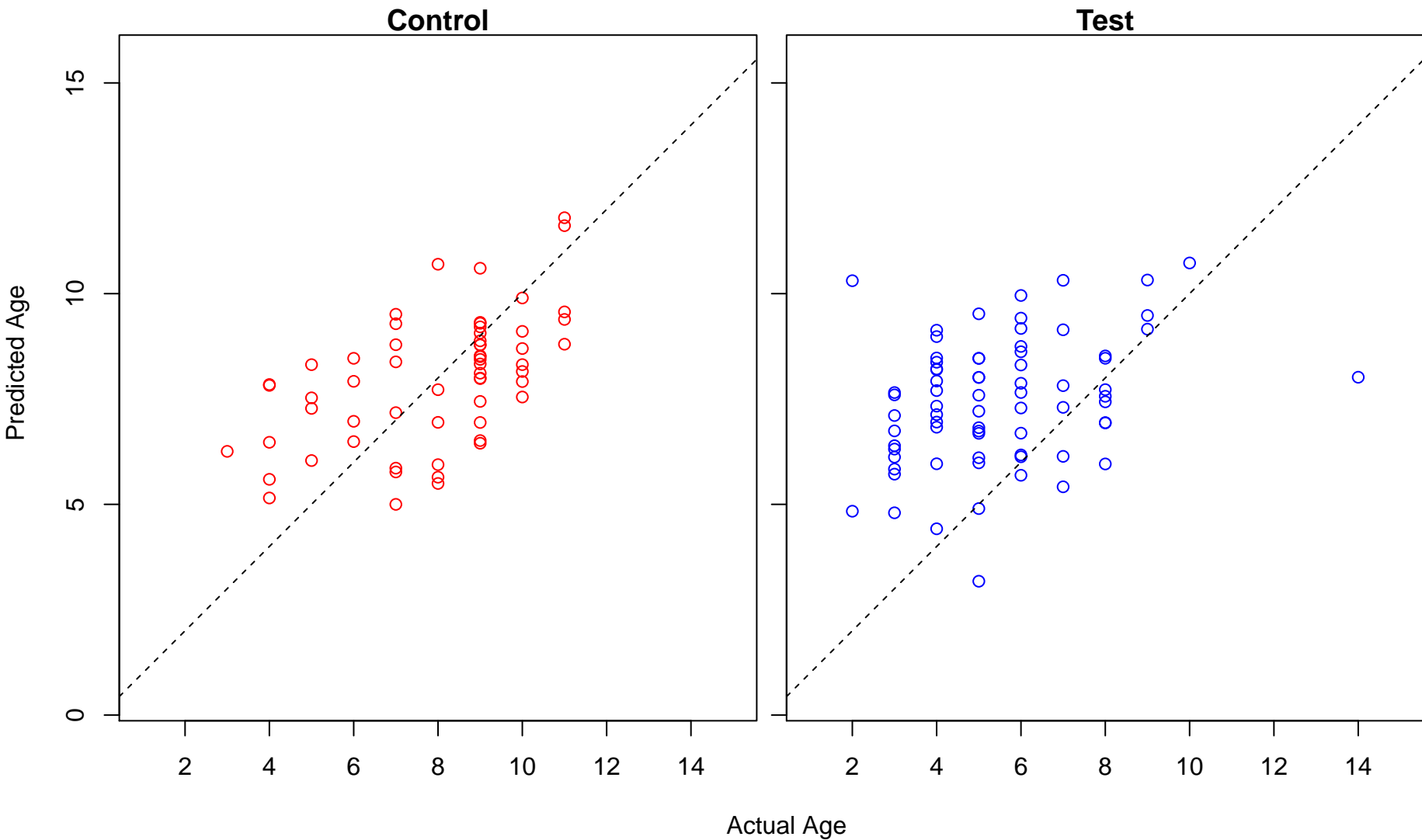
positive regulation of cell development (Score: 1.095062)



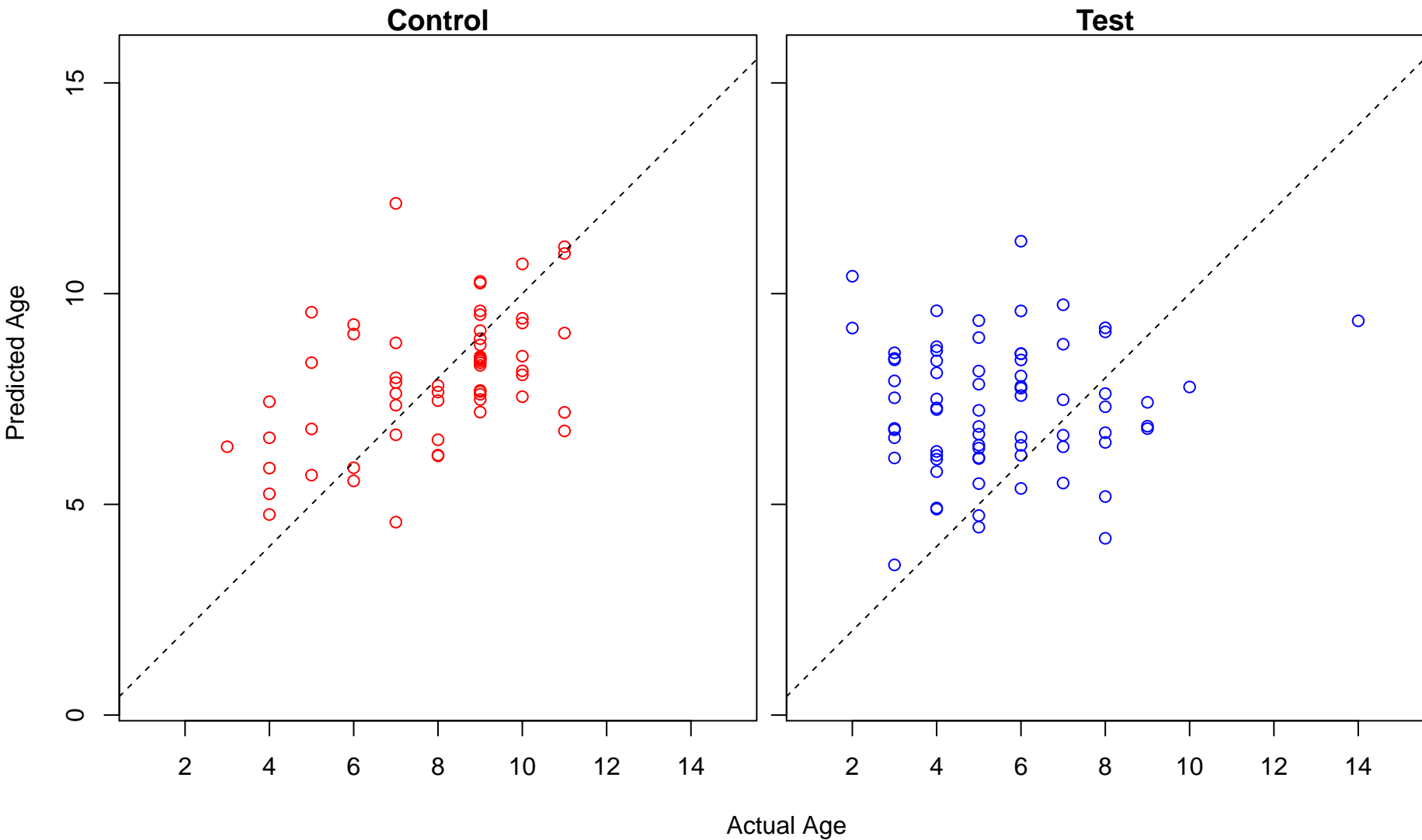
nucleoside triphosphate biosynthetic process (Score: 1.094402)



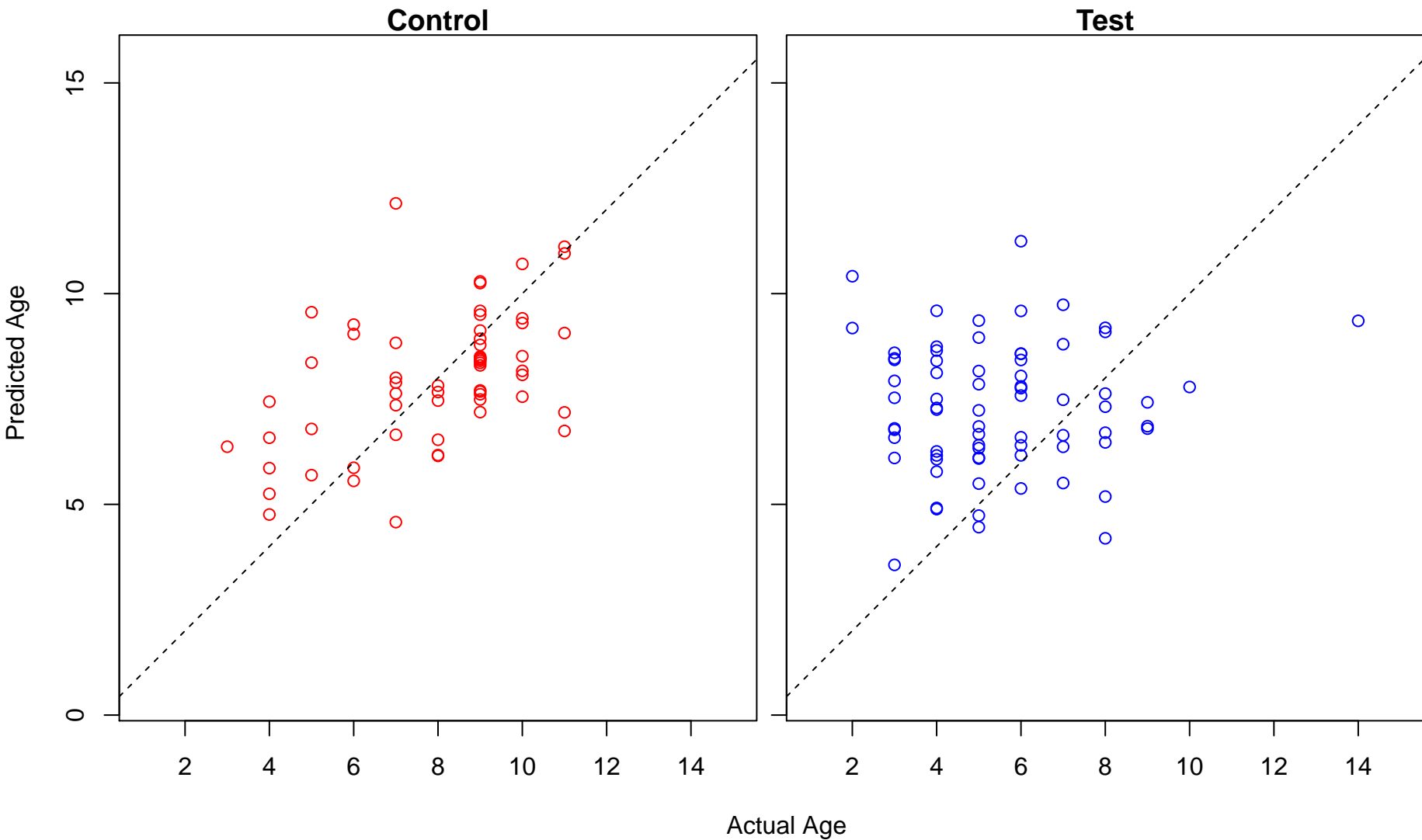
single-organism cellular process (Score: 1.094053)



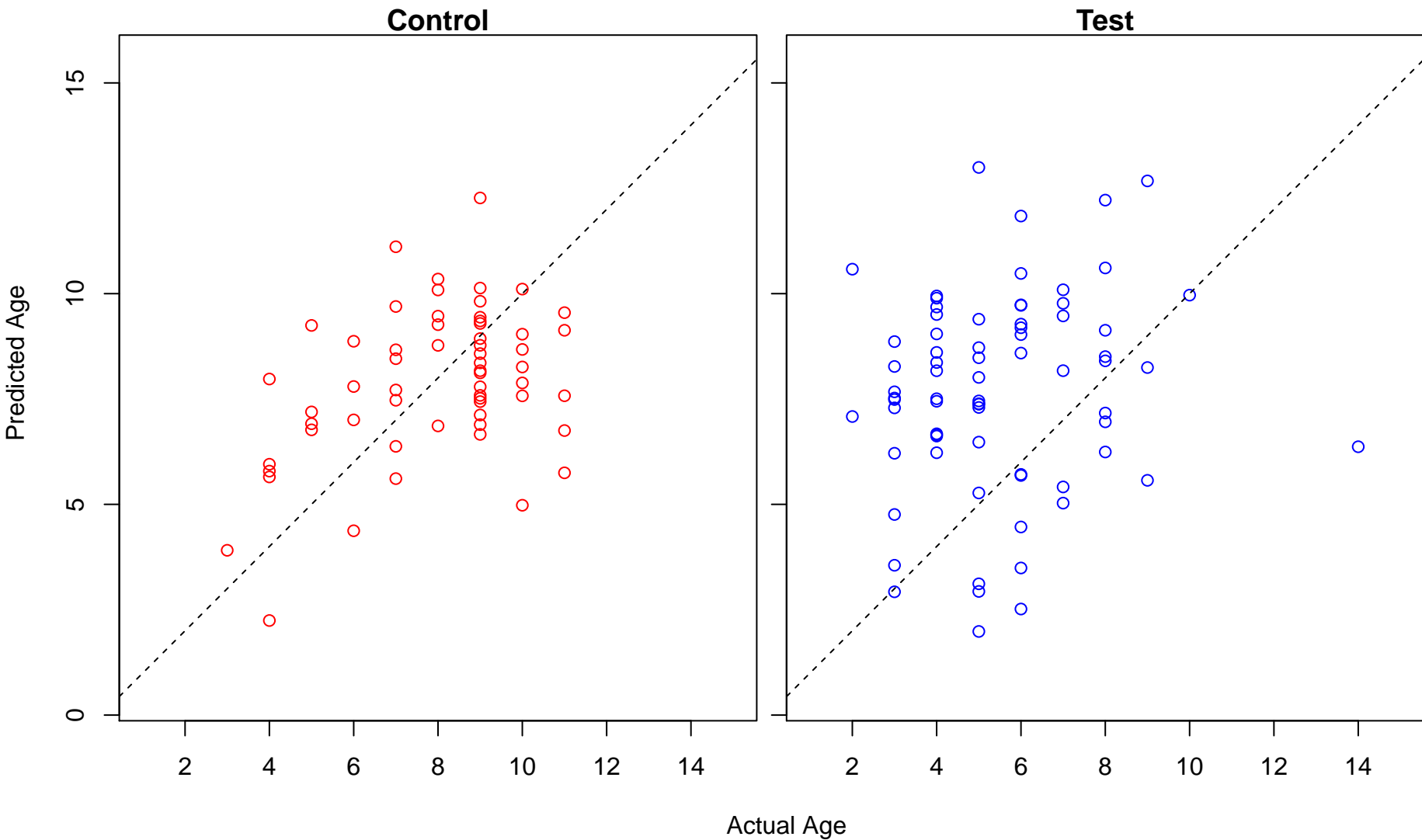
purine nucleoside monophosphate biosynthetic process (Score: 1.093957)



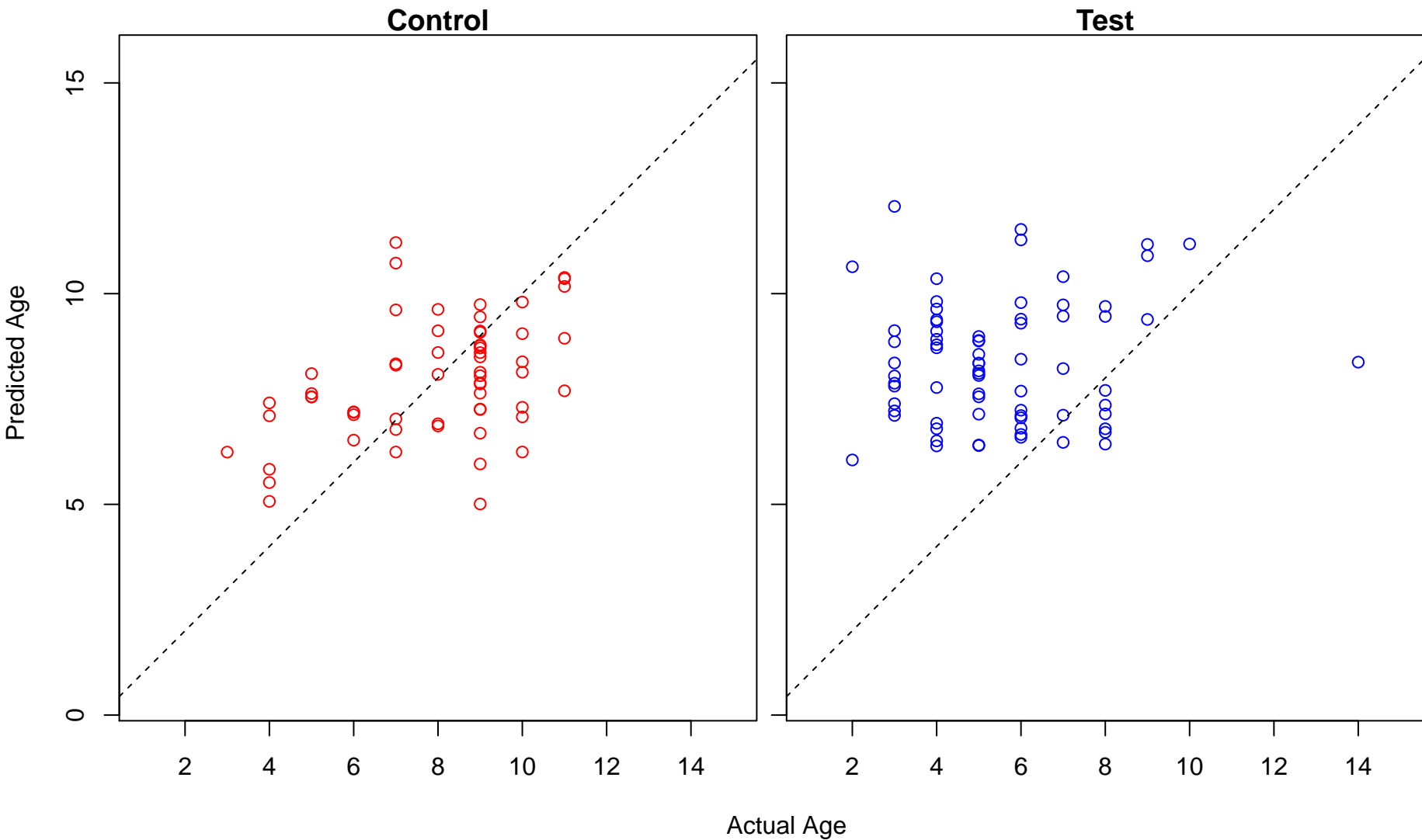
purine ribonucleoside monophosphate biosynthetic process (Score: 1.093957)



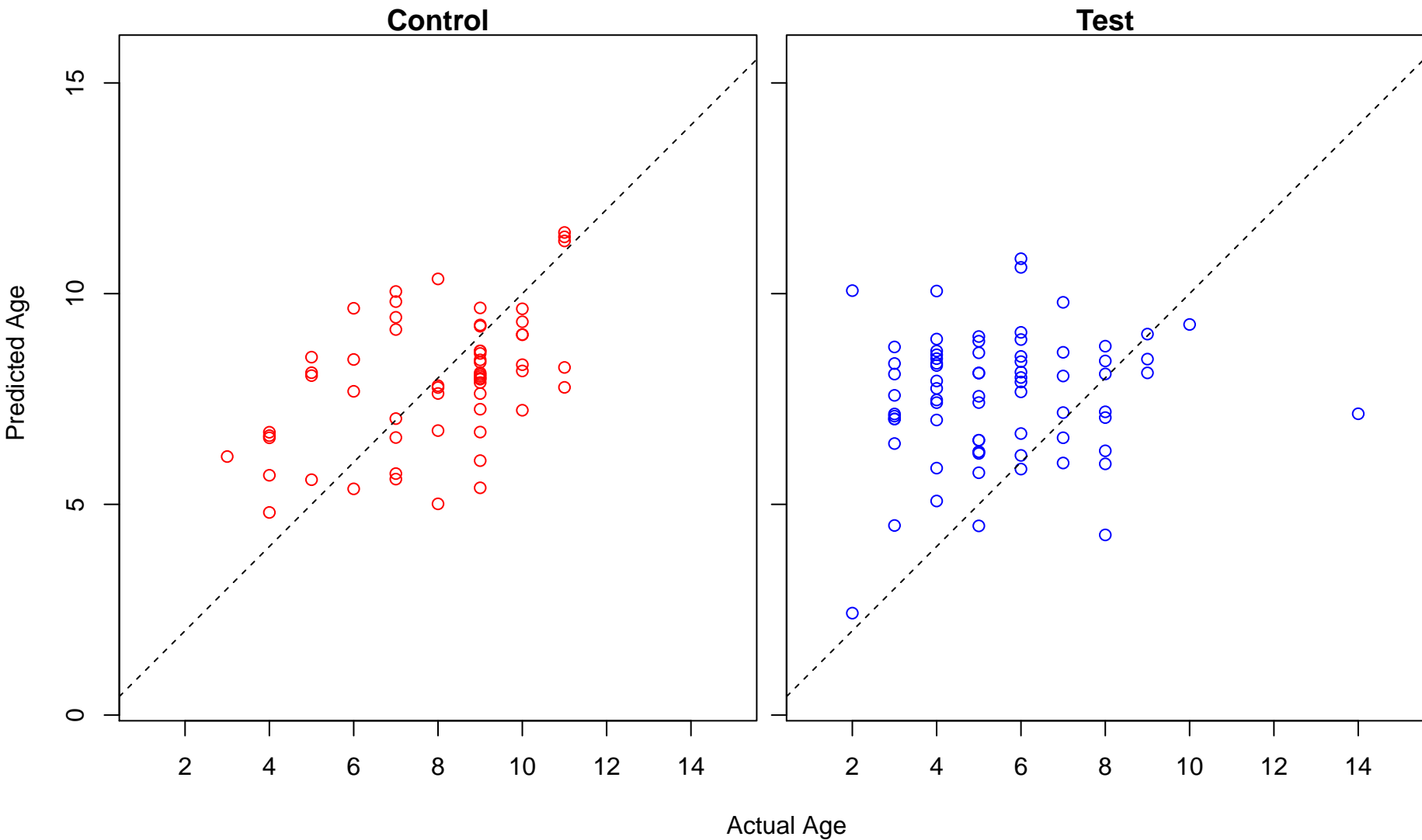
retina homeostasis (Score: 1.093799)



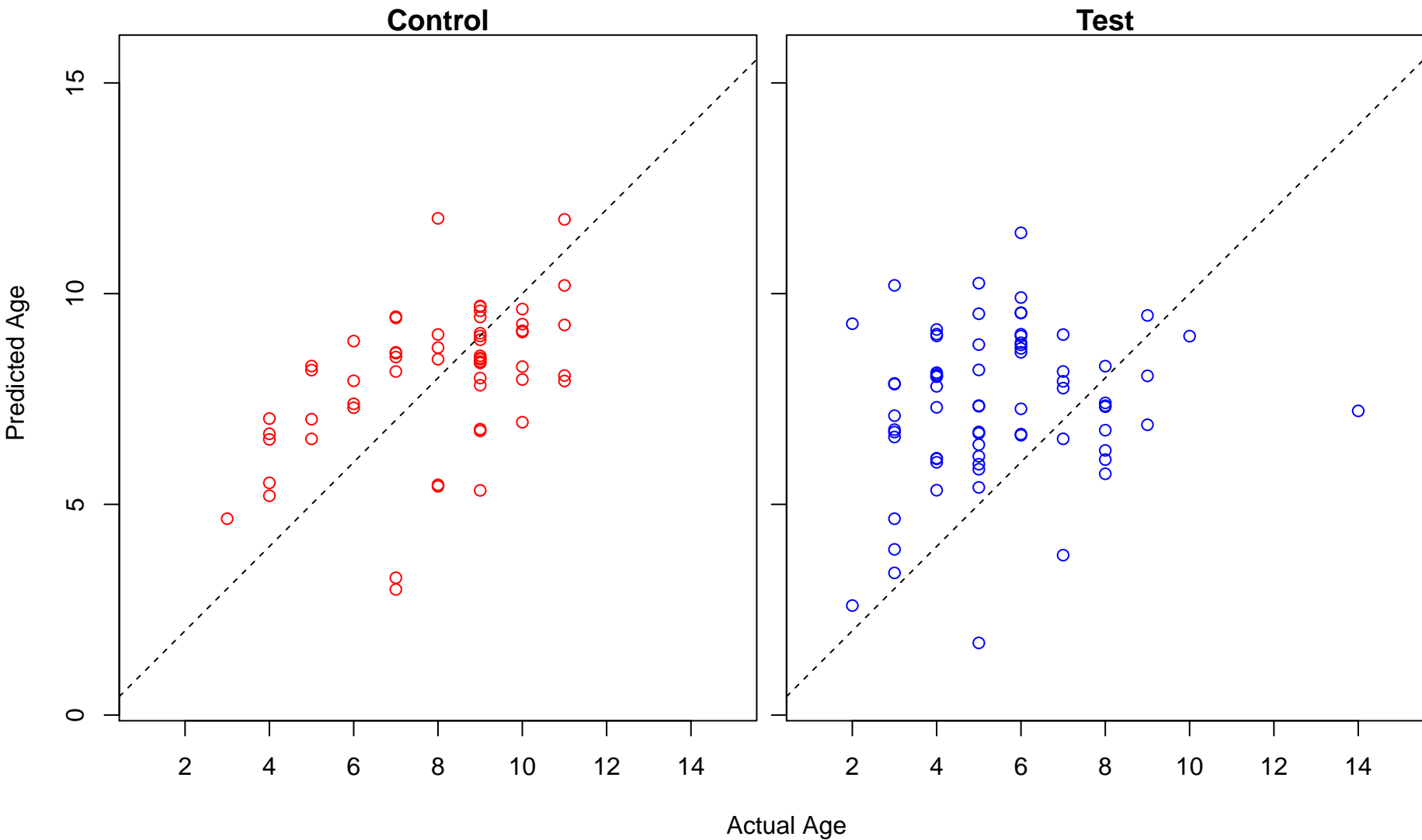
CRD-mediated mRNA stabilization (Score: 1.093537)



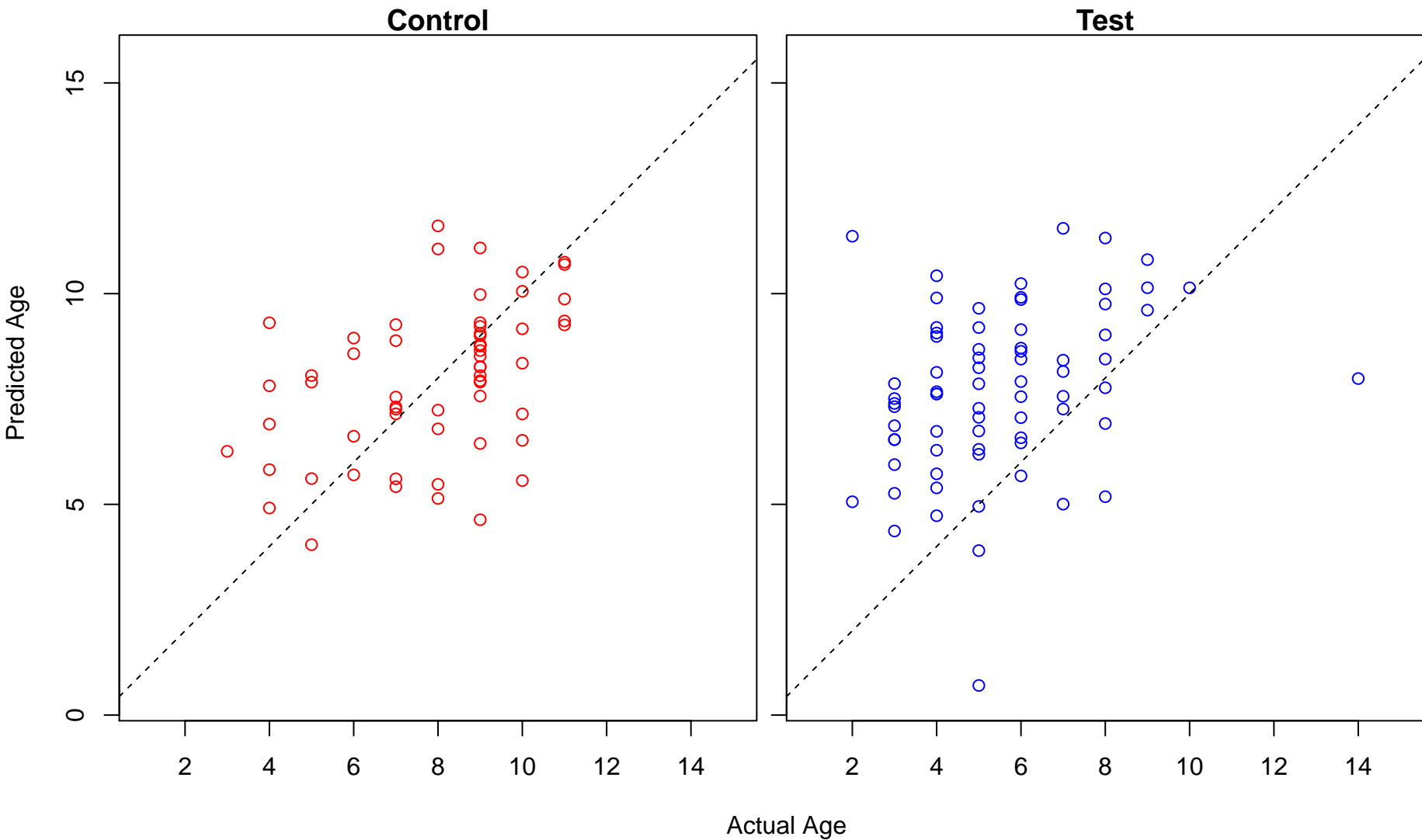
endomembrane system organization (Score: 1.092978)



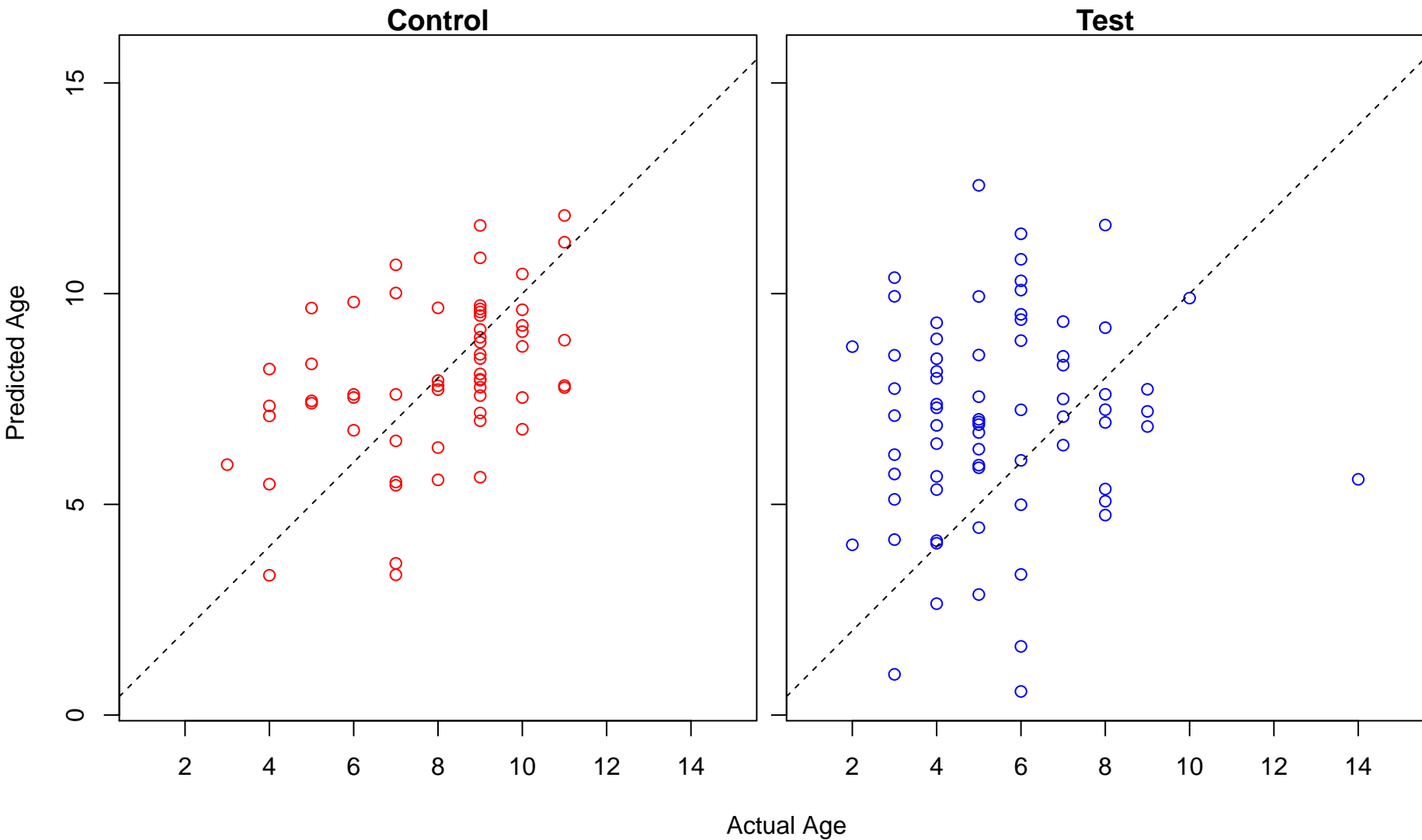
branching morphogenesis of an epithelial tube (Score: 1.092584)



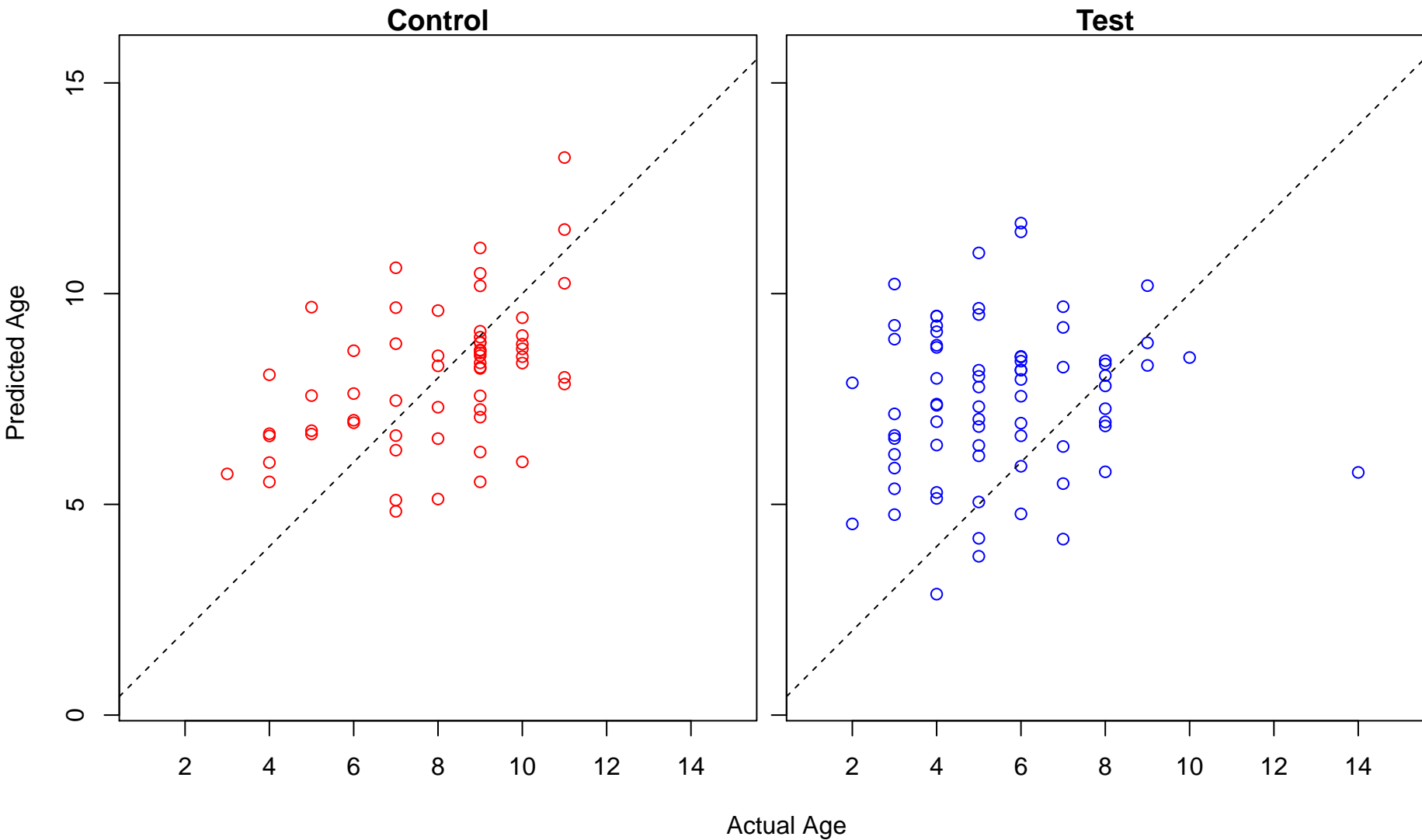
Fc receptor mediated stimulatory signaling pathway (Score: 1.092207)



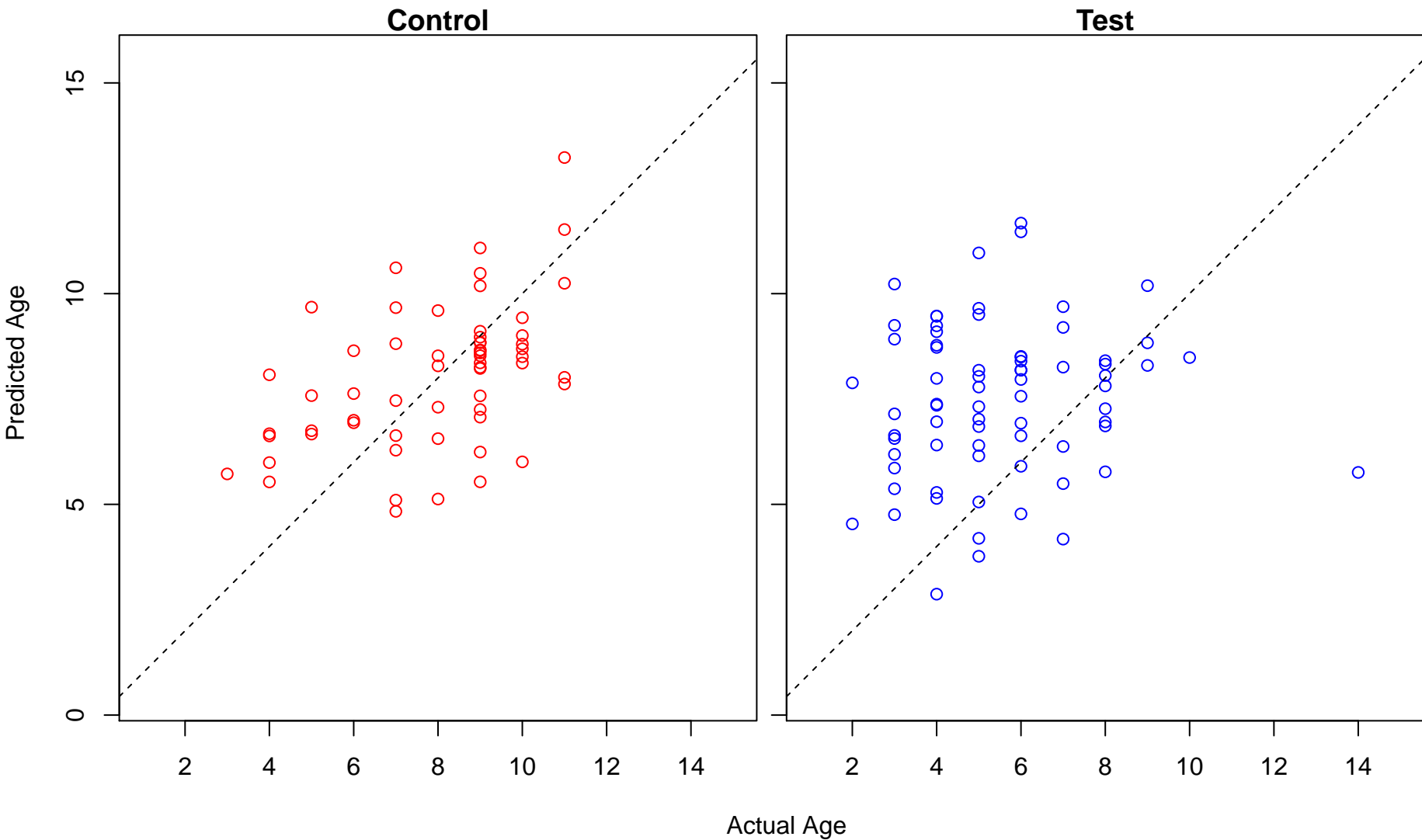
aminoglycan biosynthetic process (Score: 1.092197)



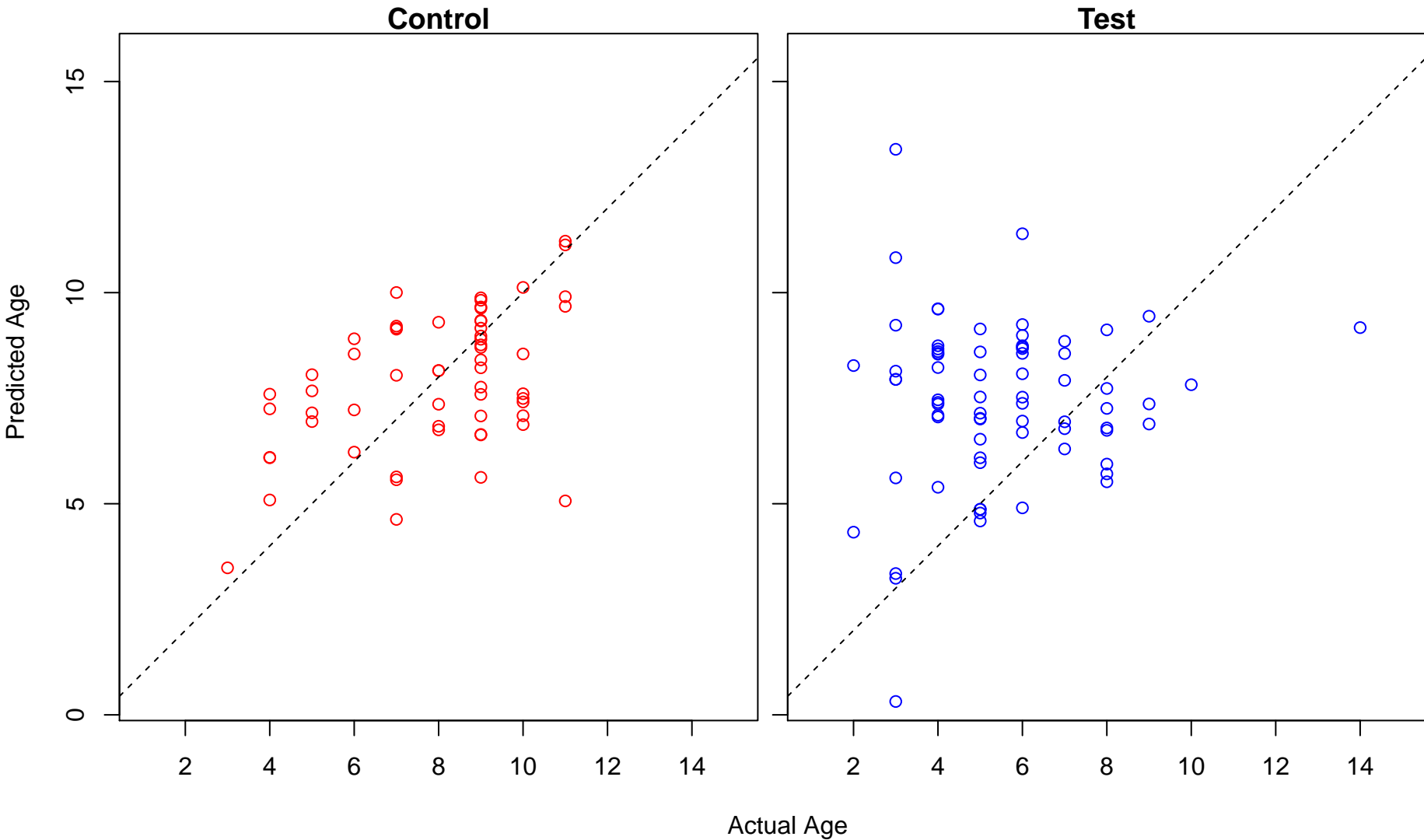
negative regulation of phosphorus metabolic process (Score: 1.091783)



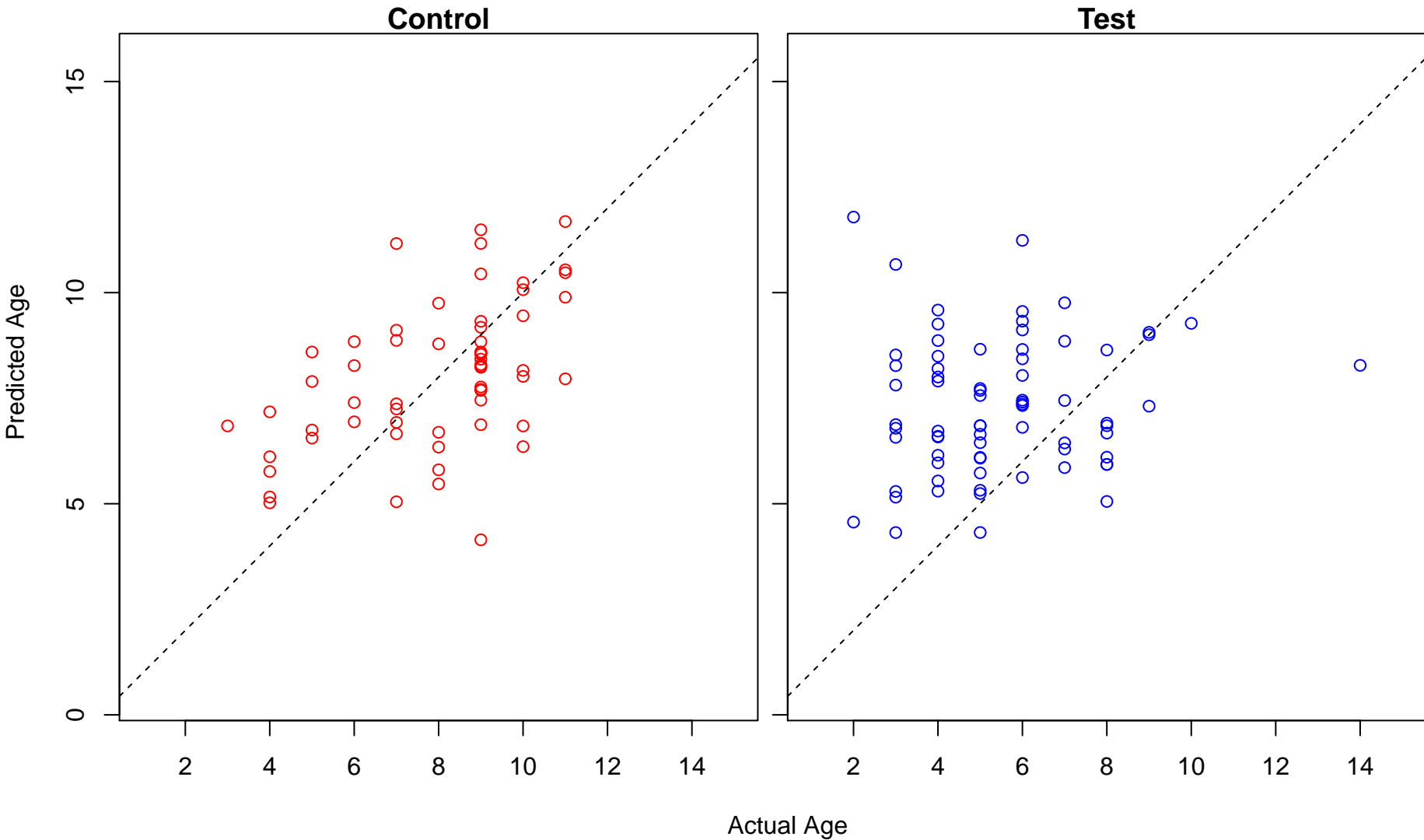
negative regulation of phosphate metabolic process (Score: 1.091783)



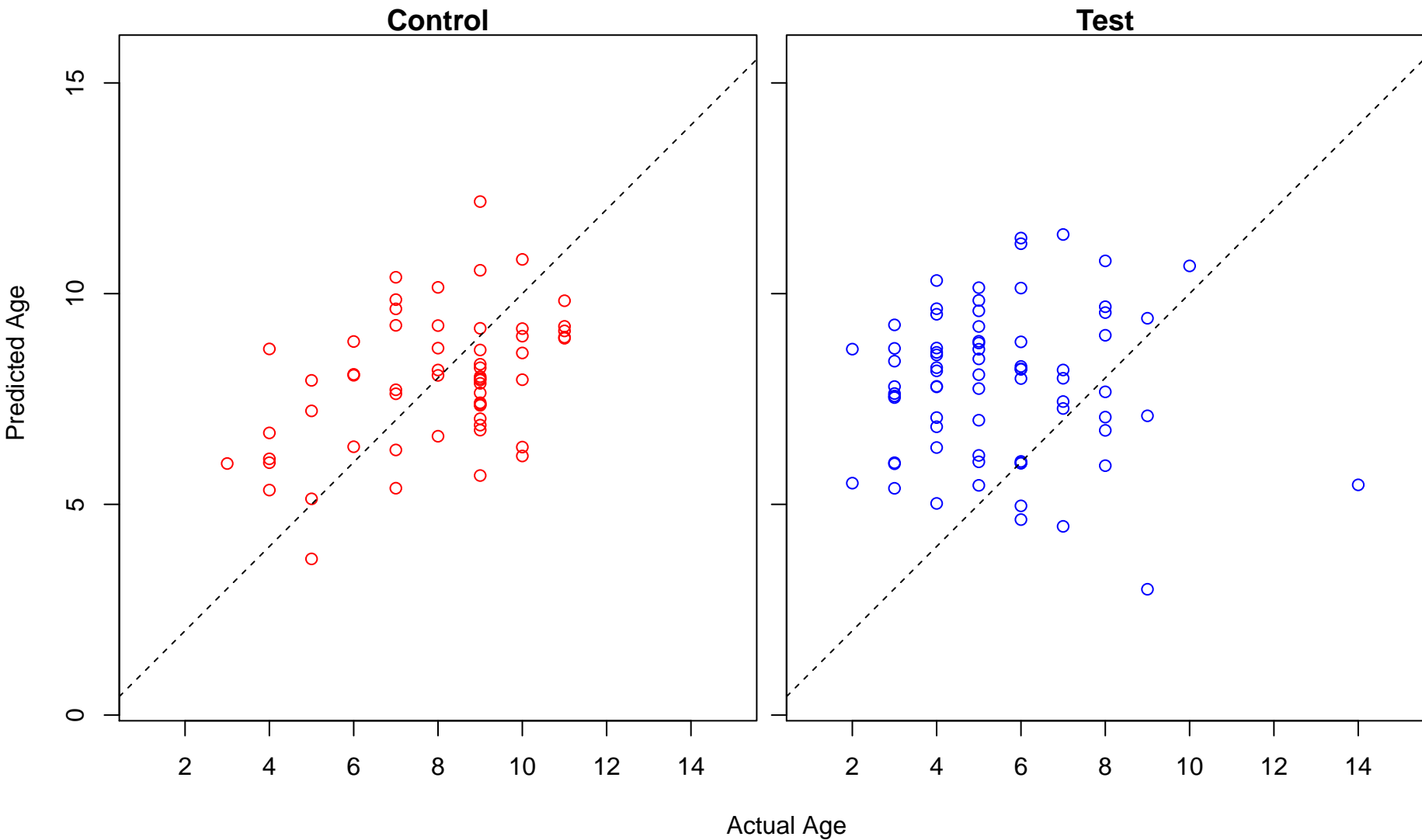
regulation of cardiac muscle tissue development (Score: 1.091711)



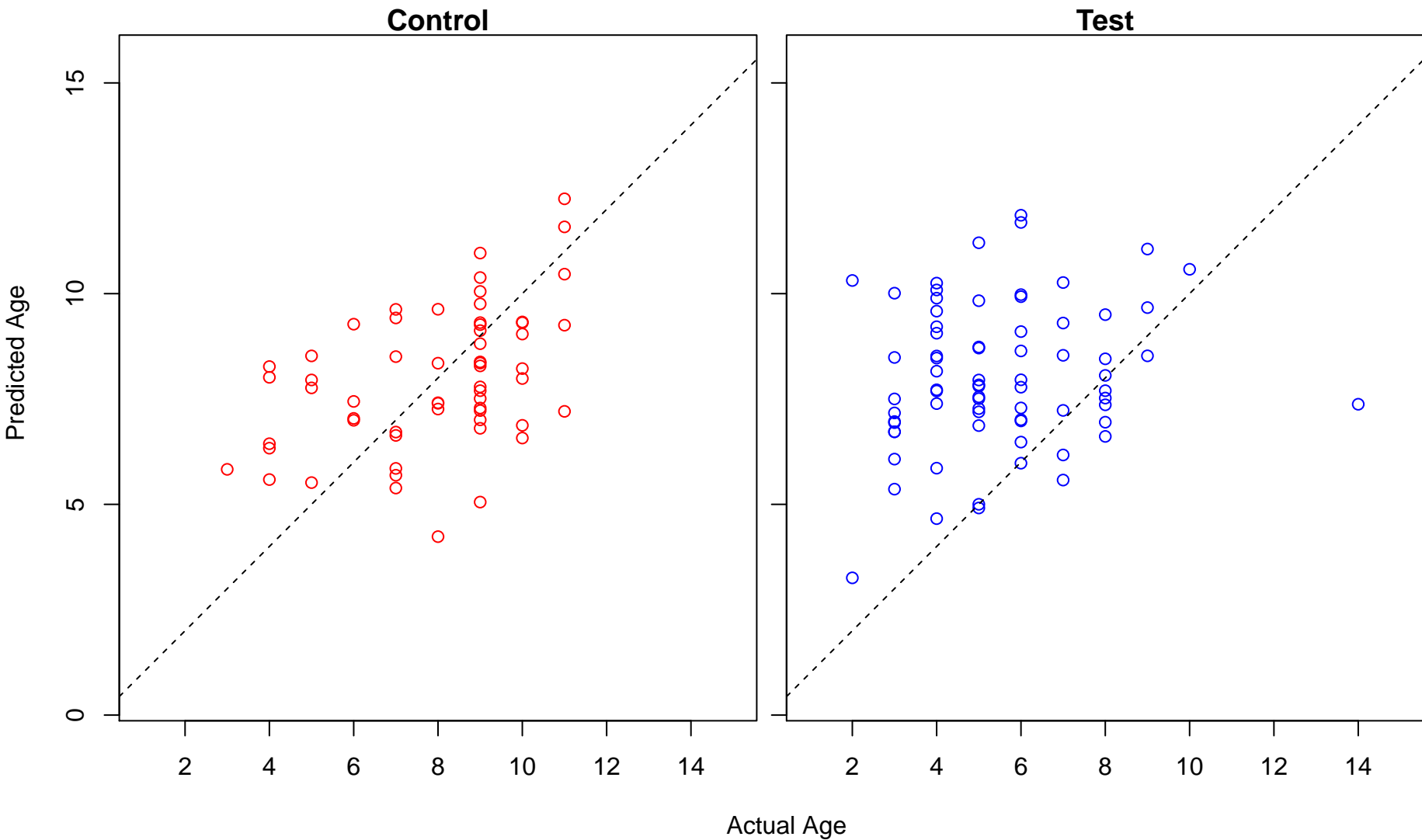
regulation of mitochondrial membrane permeability (Score: 1.091297)



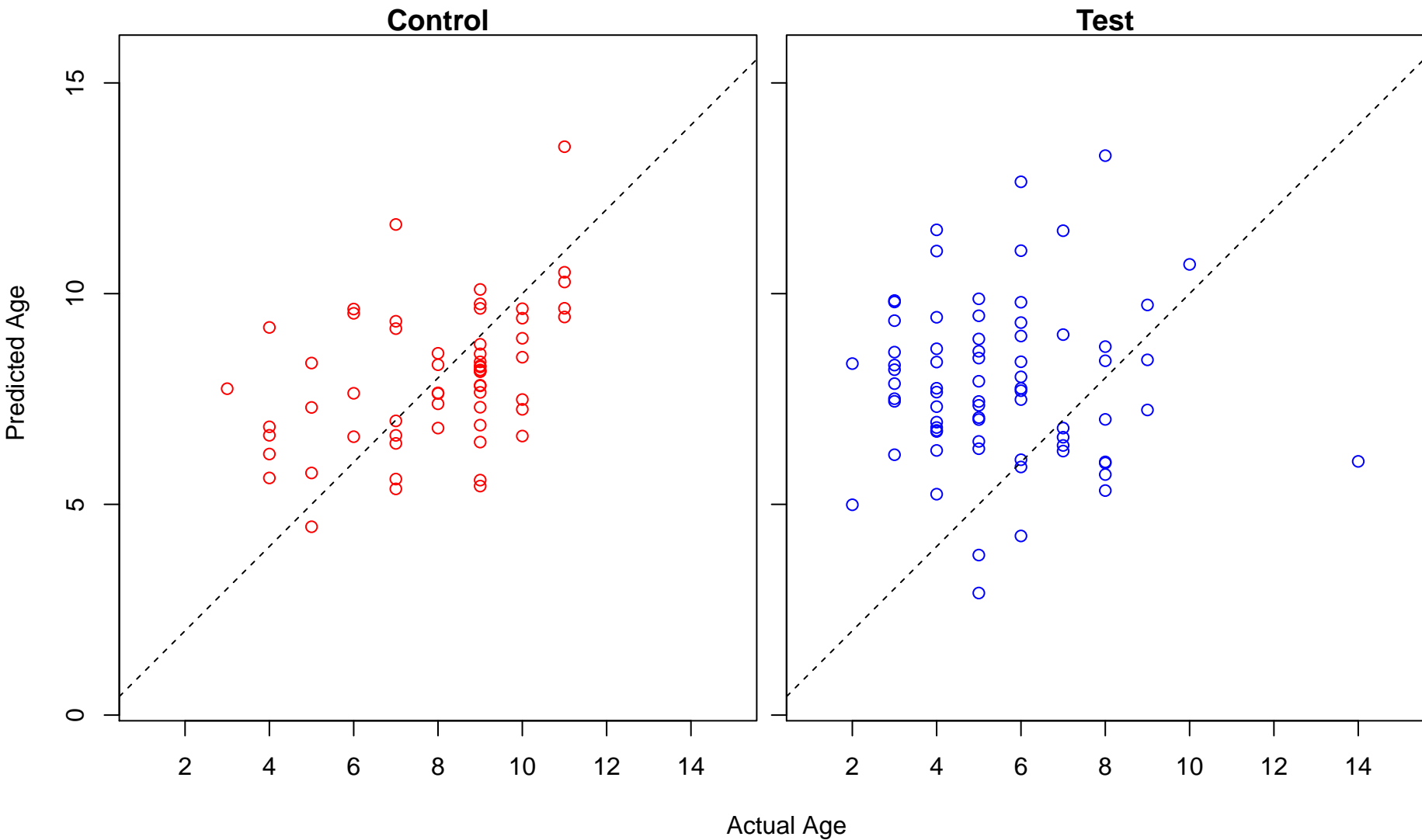
negative regulation of neuron apoptotic process (Score: 1.090396)



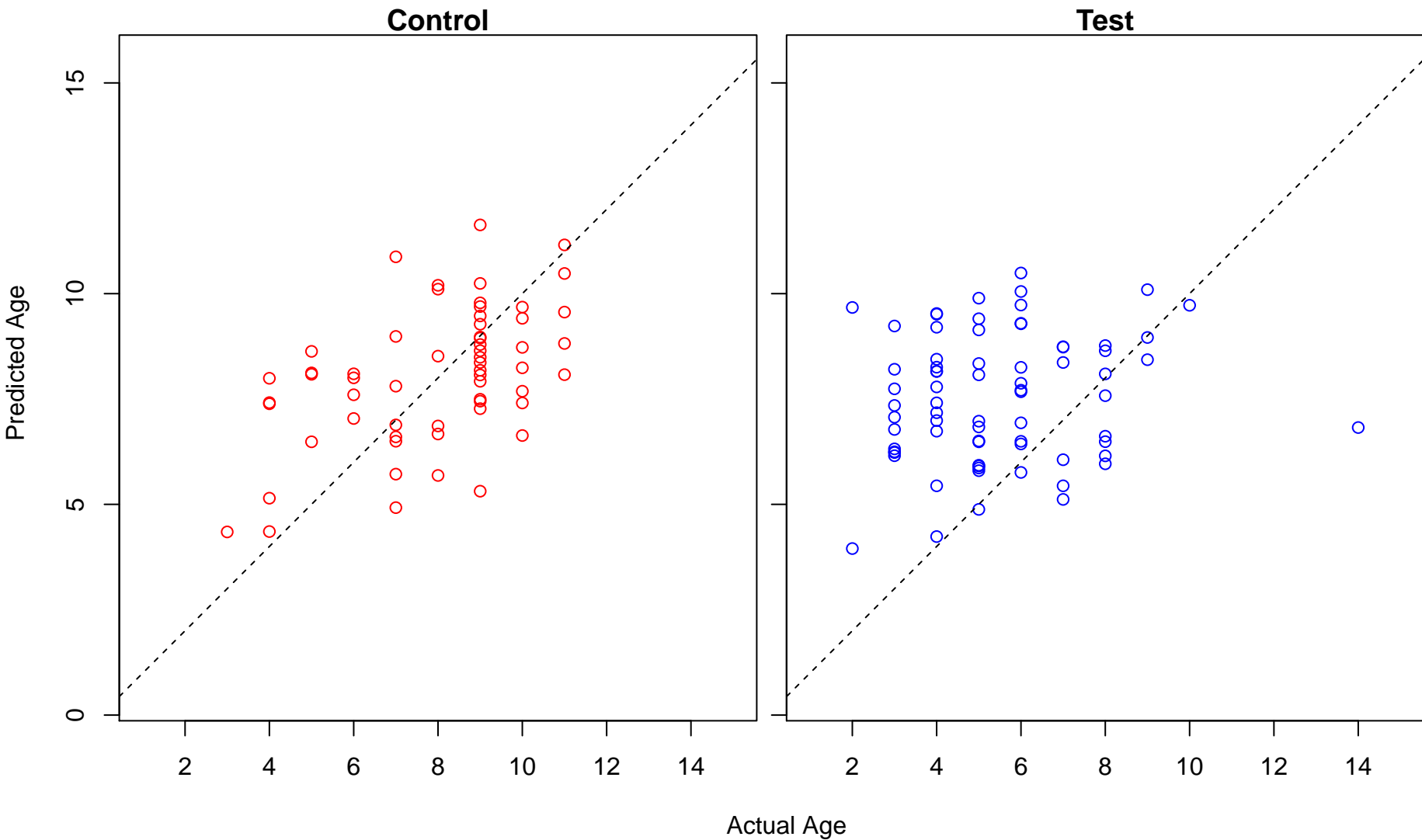
regulation of multicellular organismal process (Score: 1.090387)



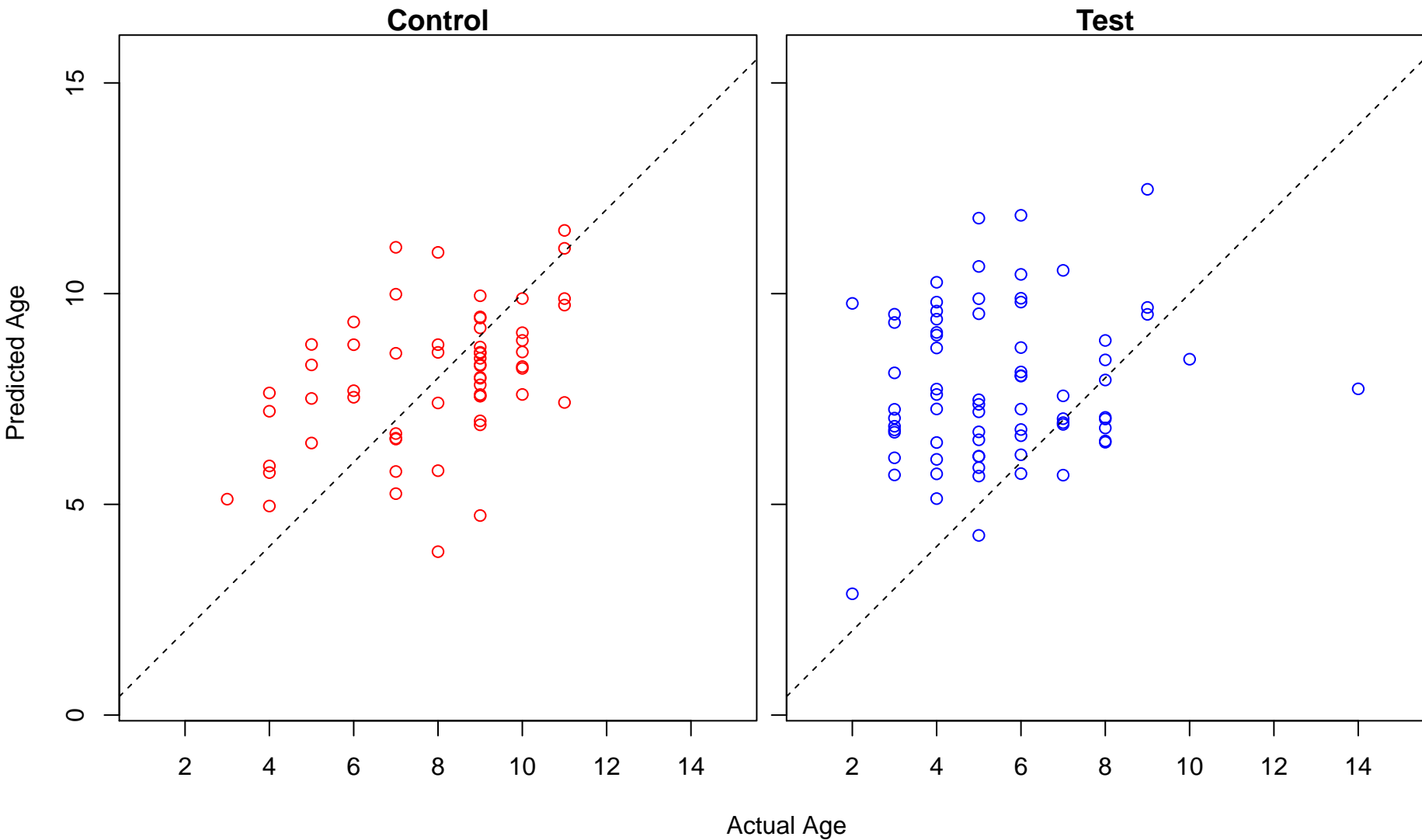
leukocyte homeostasis (Score: 1.089572)



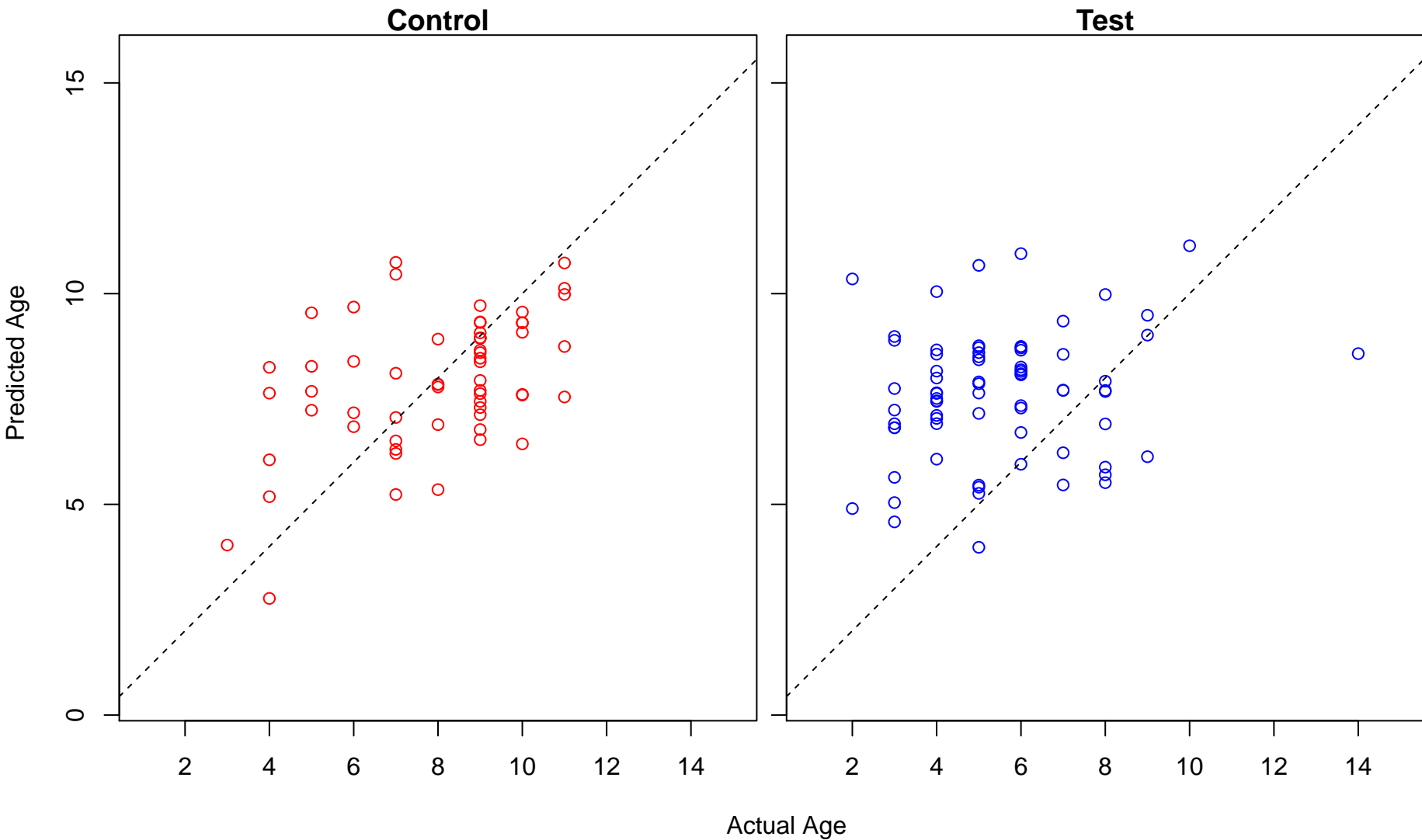
regulation of catalytic activity (Score: 1.088440)



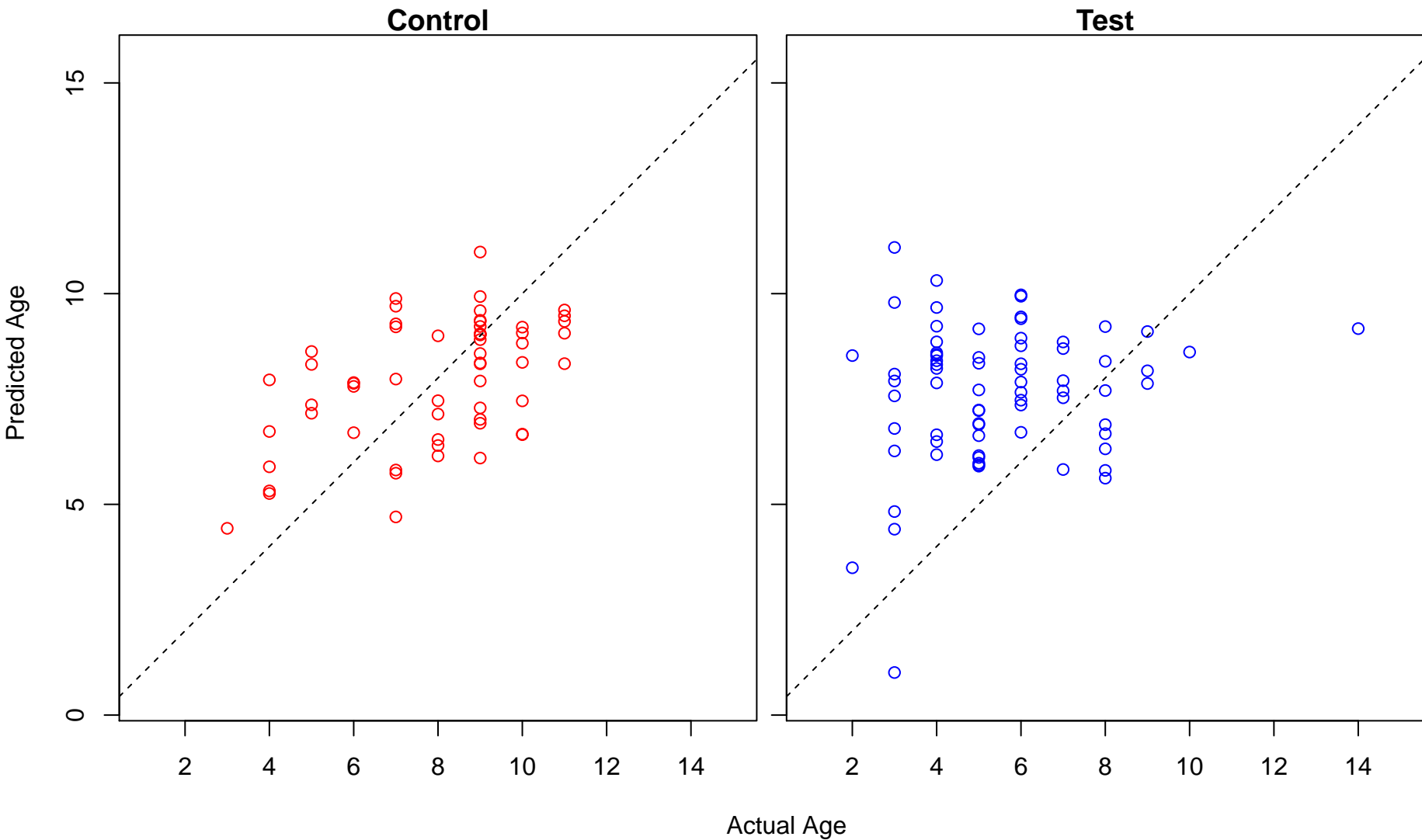
response to nitrogen compound (Score: 1.088219)



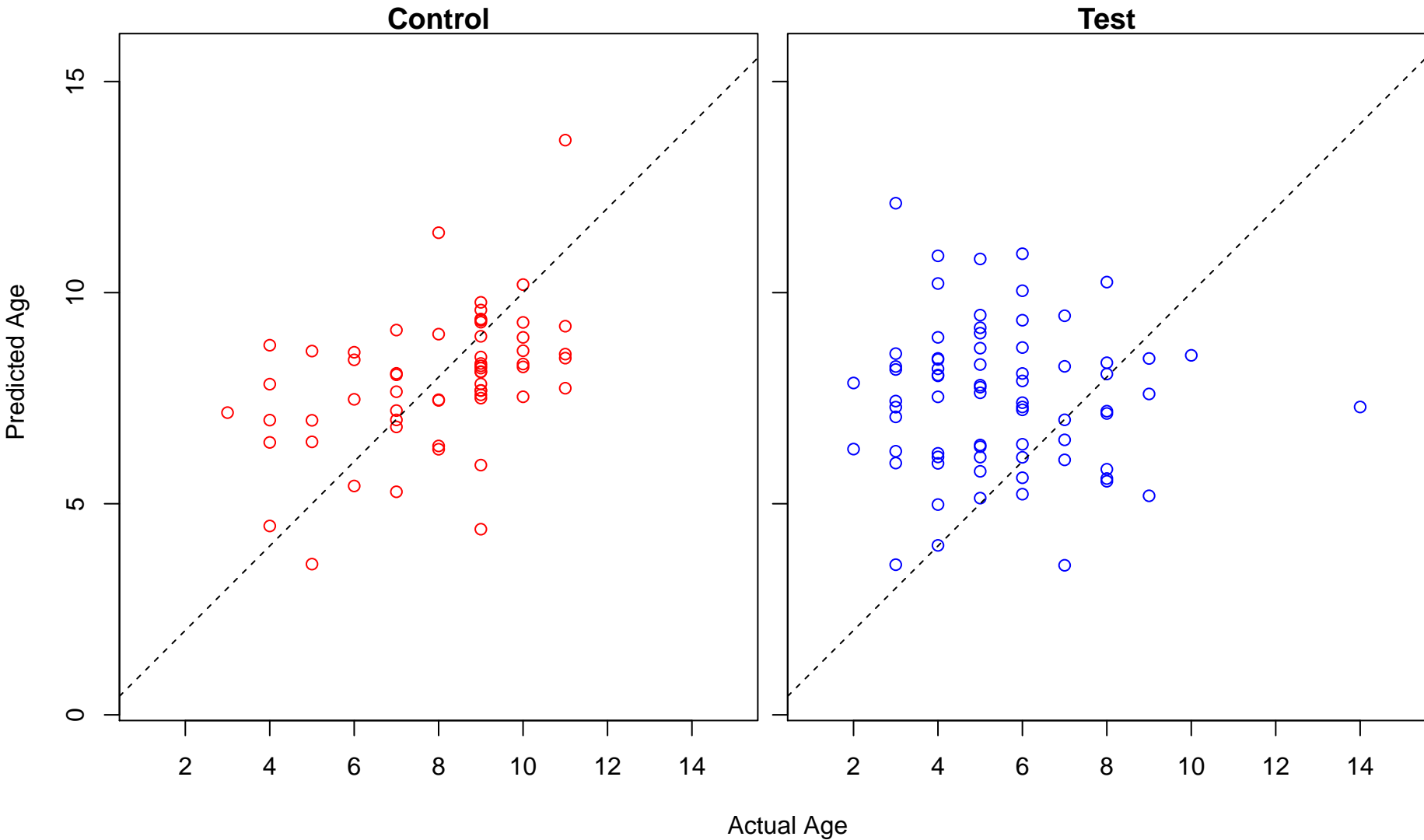
chromatin organization (Score: 1.087733)



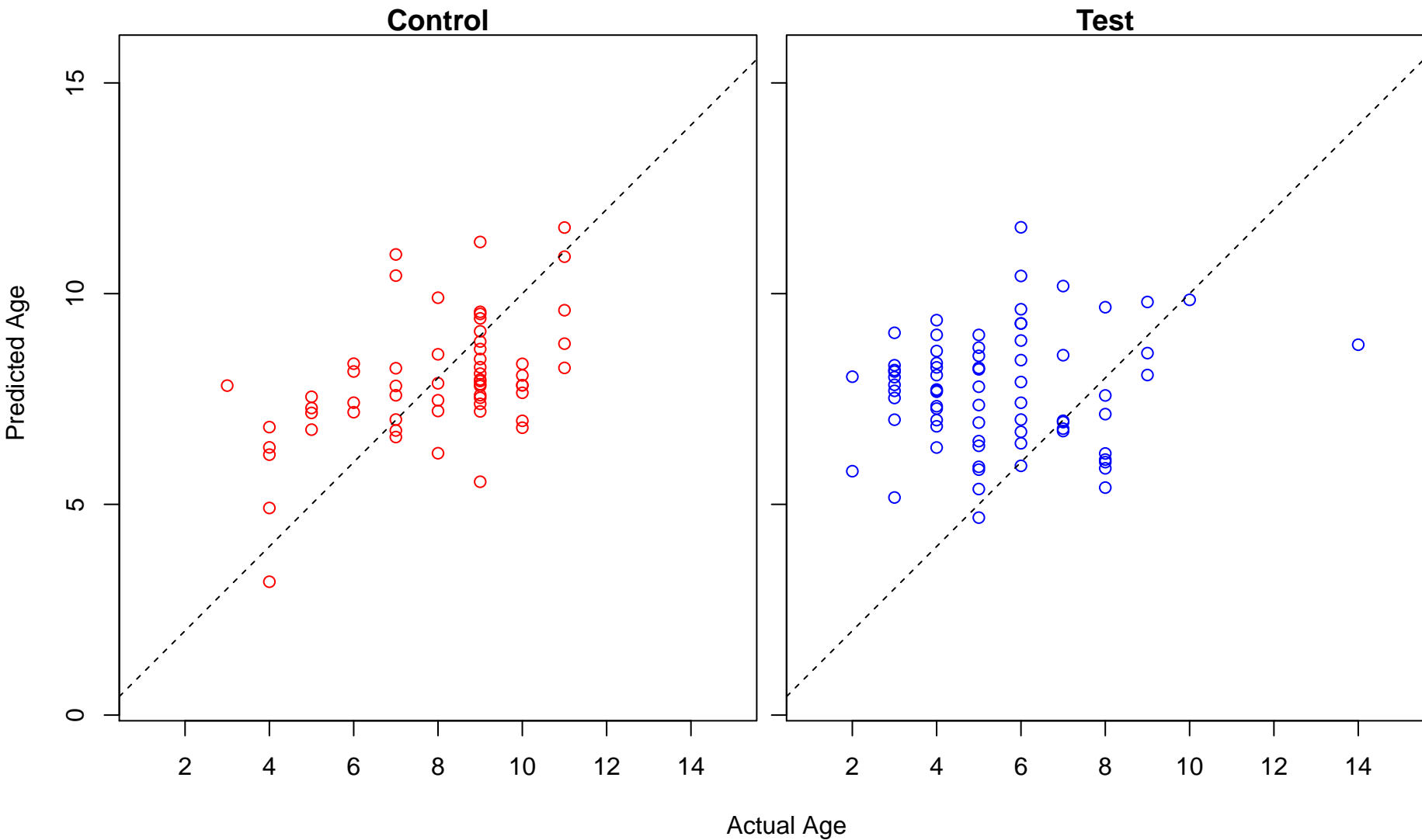
negative regulation of BMP signaling pathway (Score: 1.086067)



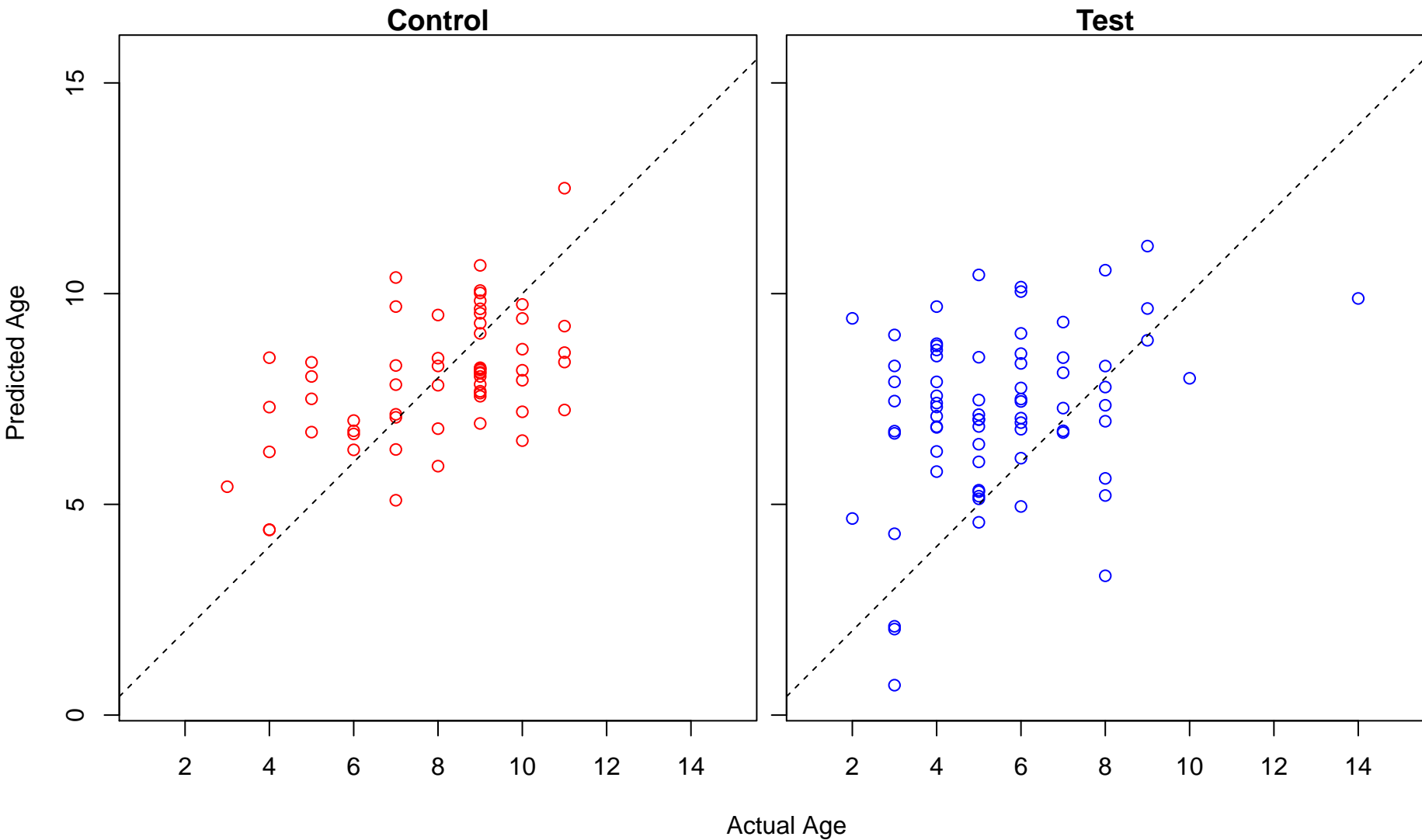
cytoplasmic sequestering of transcription factor (Score: 1.085850)



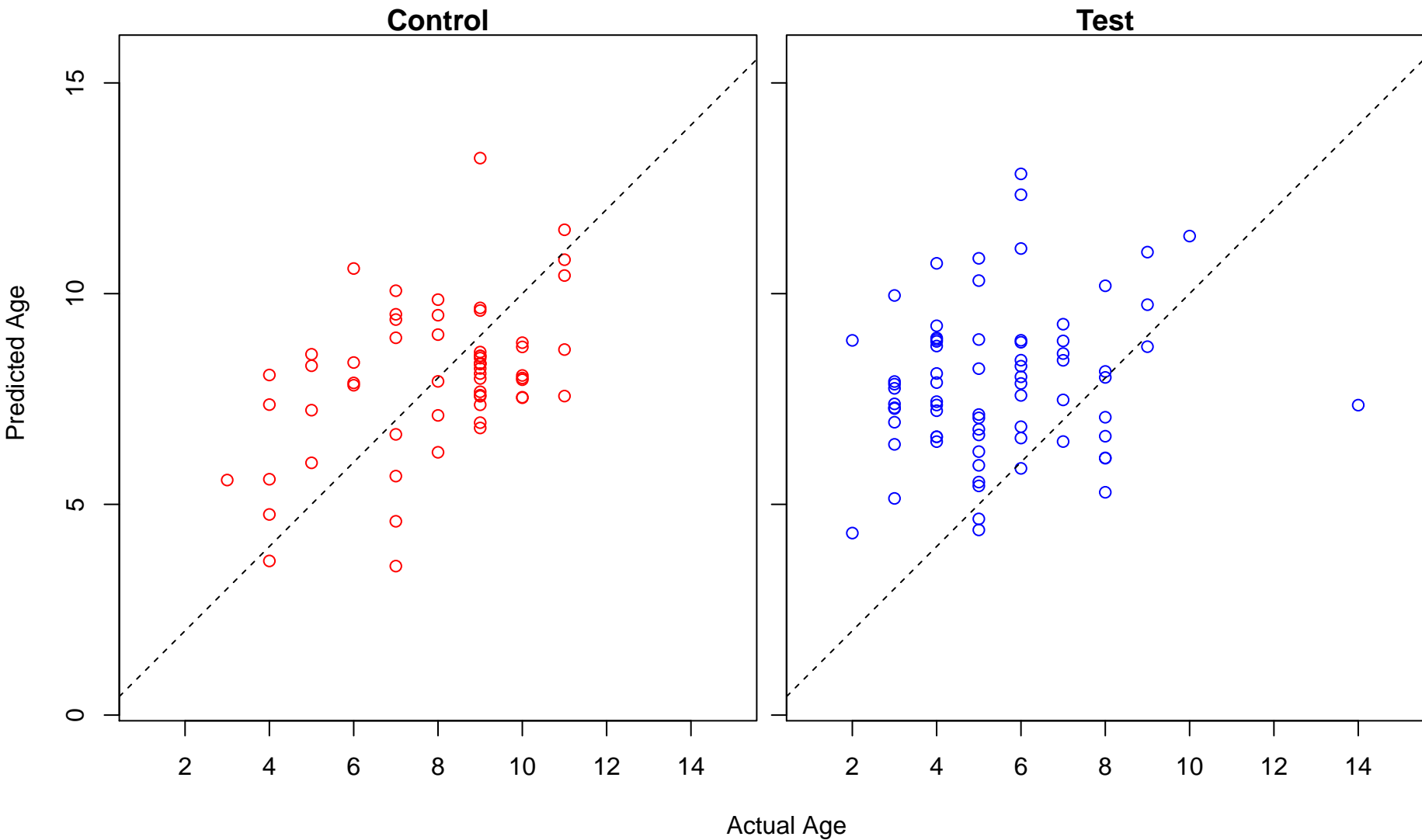
negative regulation of lipid metabolic process (Score: 1.085801)



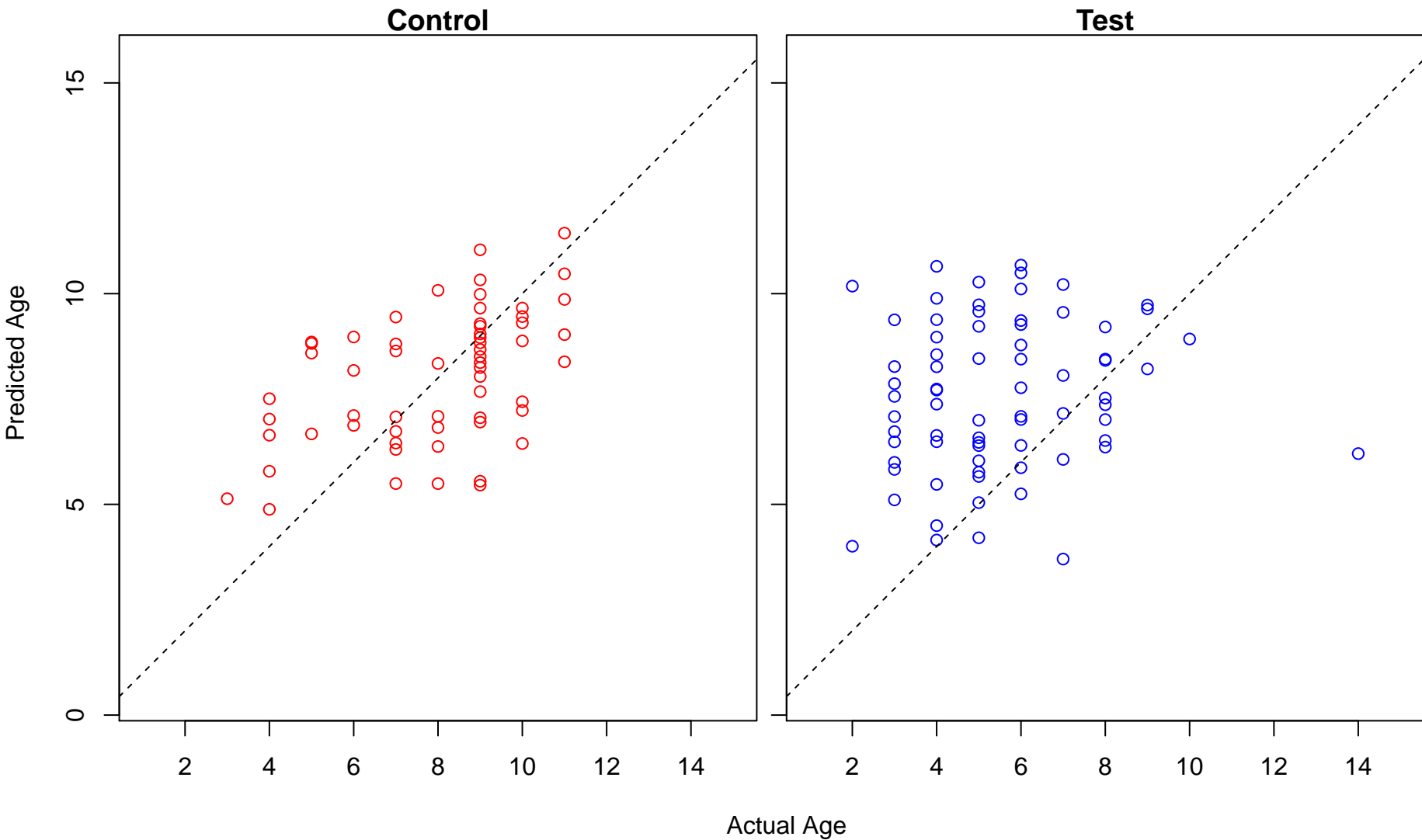
cell differentiation in hindbrain (Score: 1.085275)



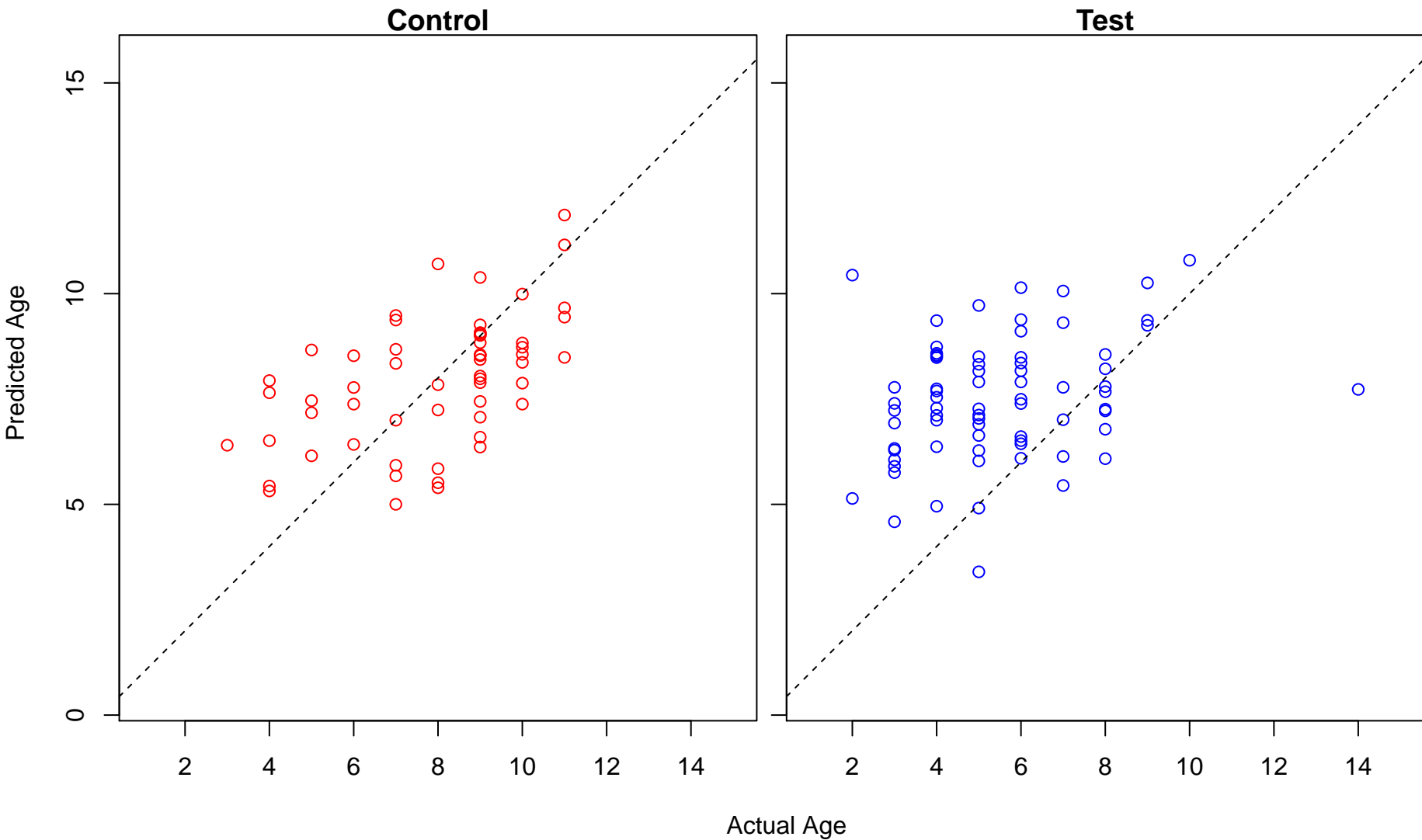
regulation of vesicle-mediated transport (Score: 1.083043)



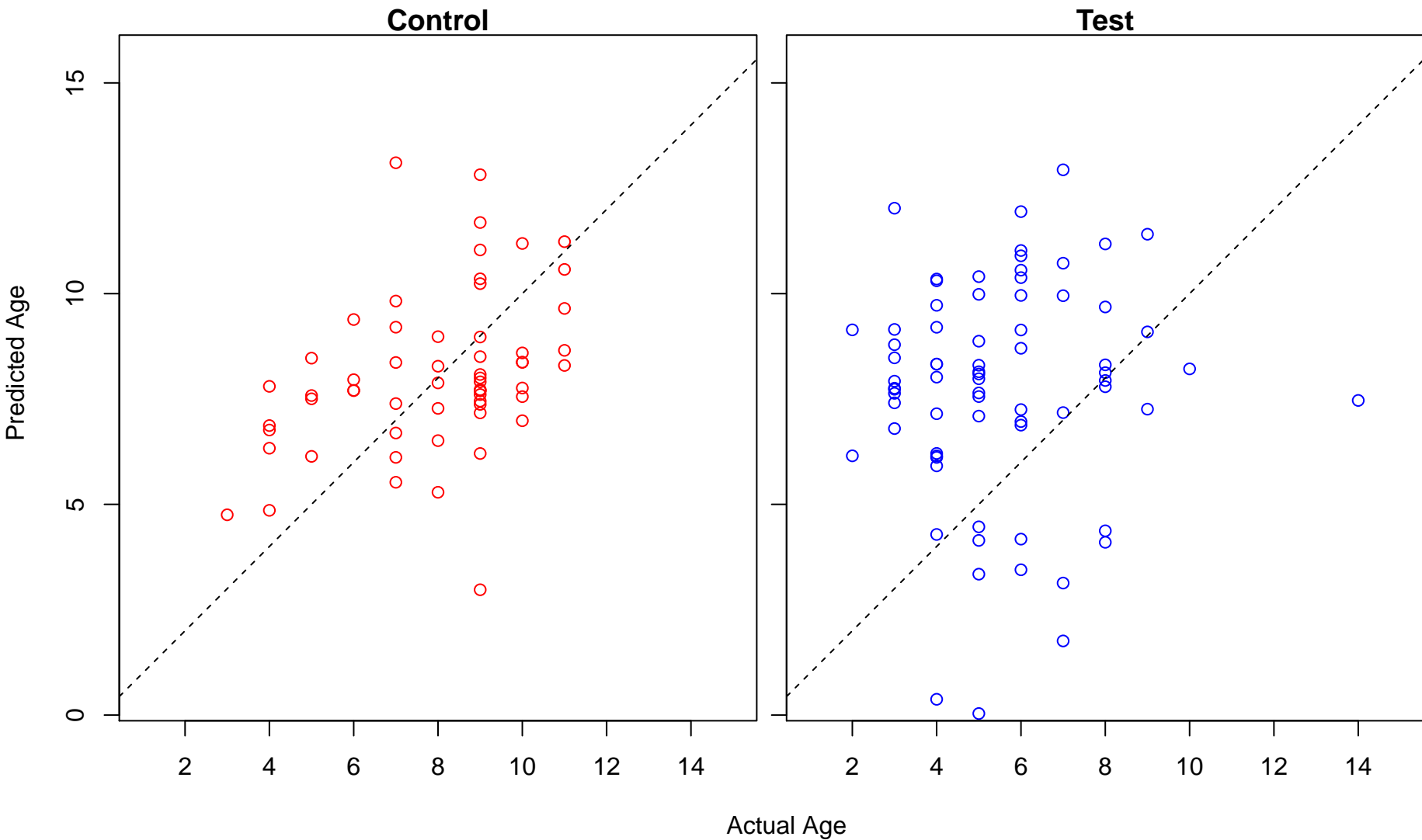
anatomical structure development (Score: 1.082606)



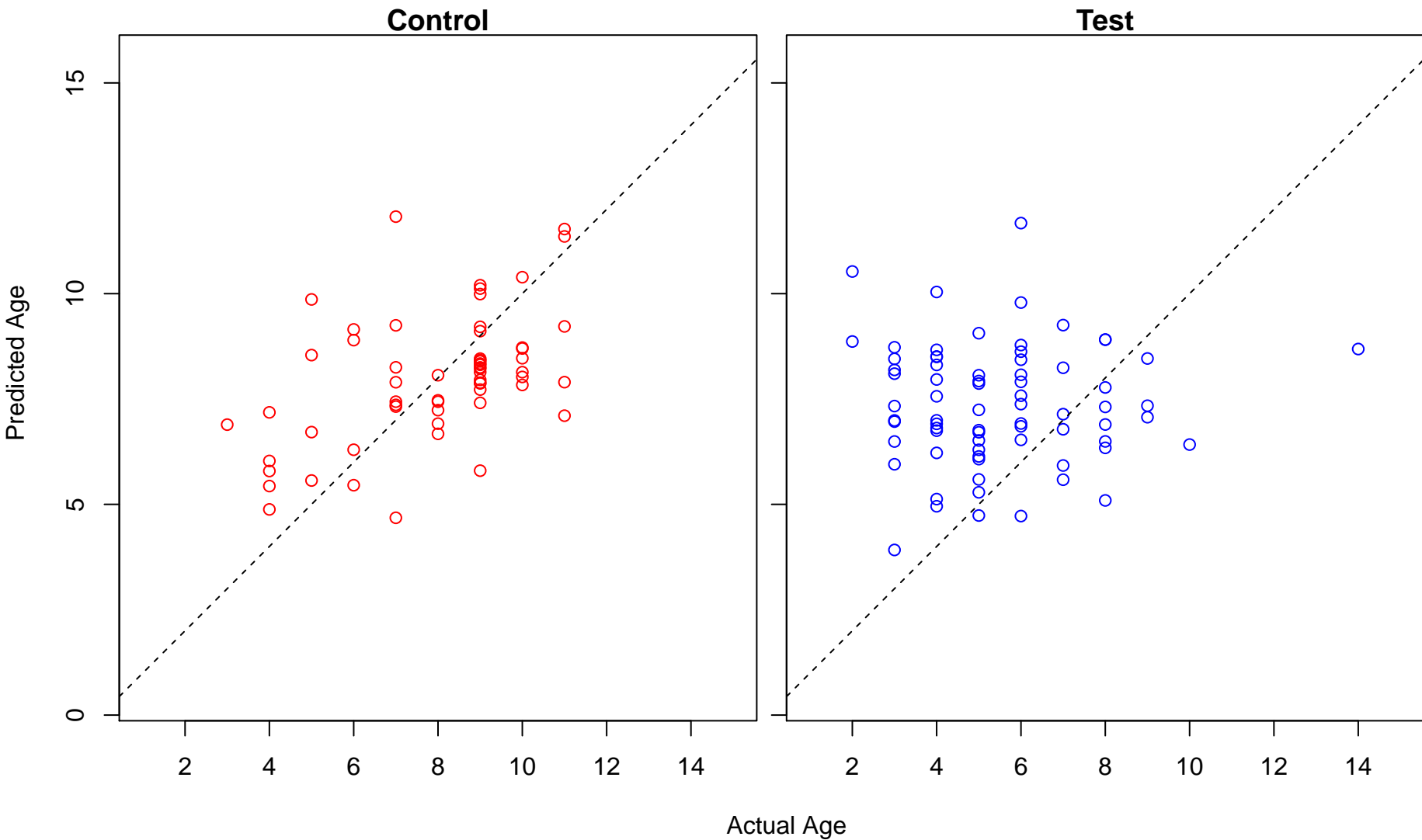
cellular process (Score: 1.082553)



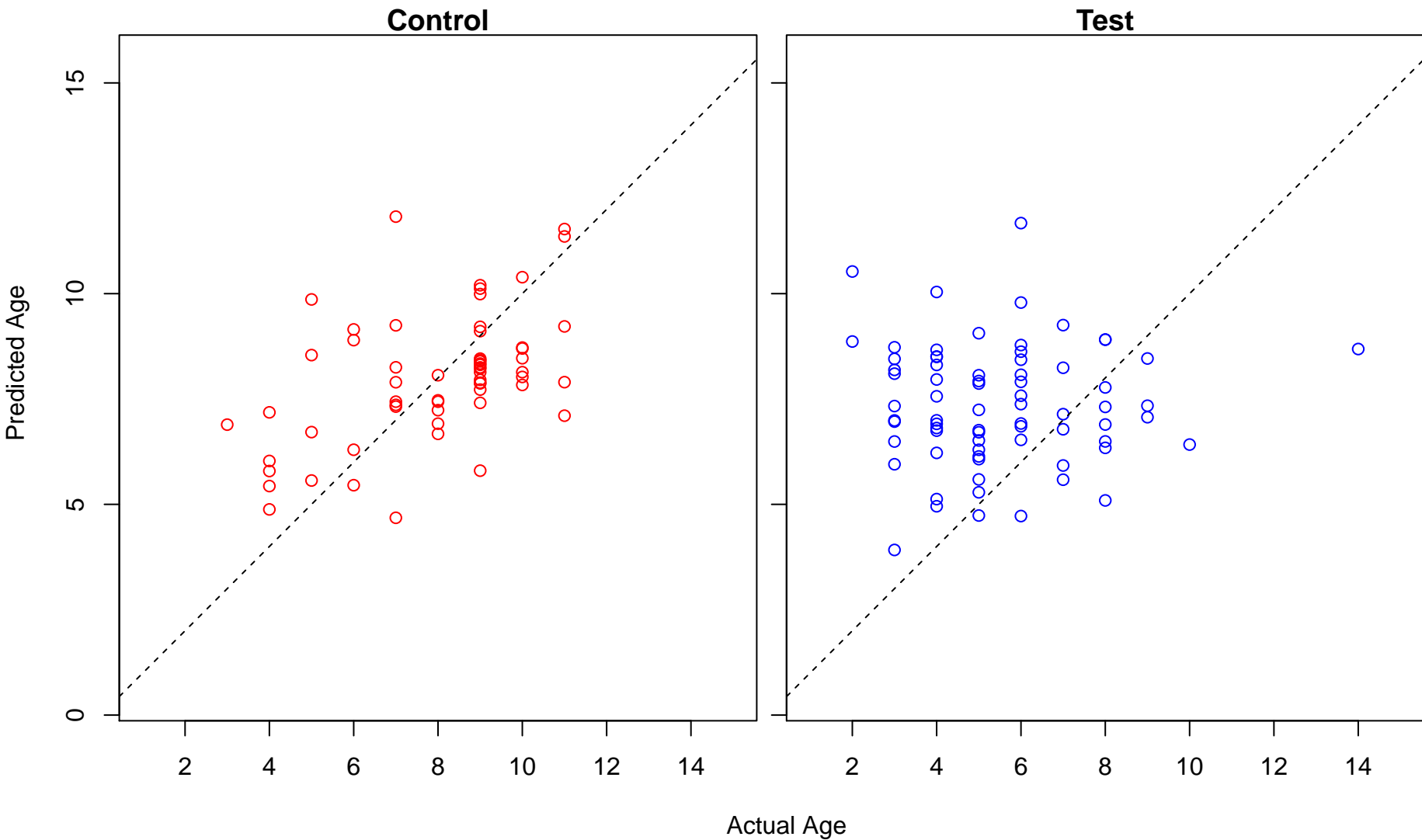
negative regulation of extrinsic apoptotic signaling pathway (Score: 1.082377)



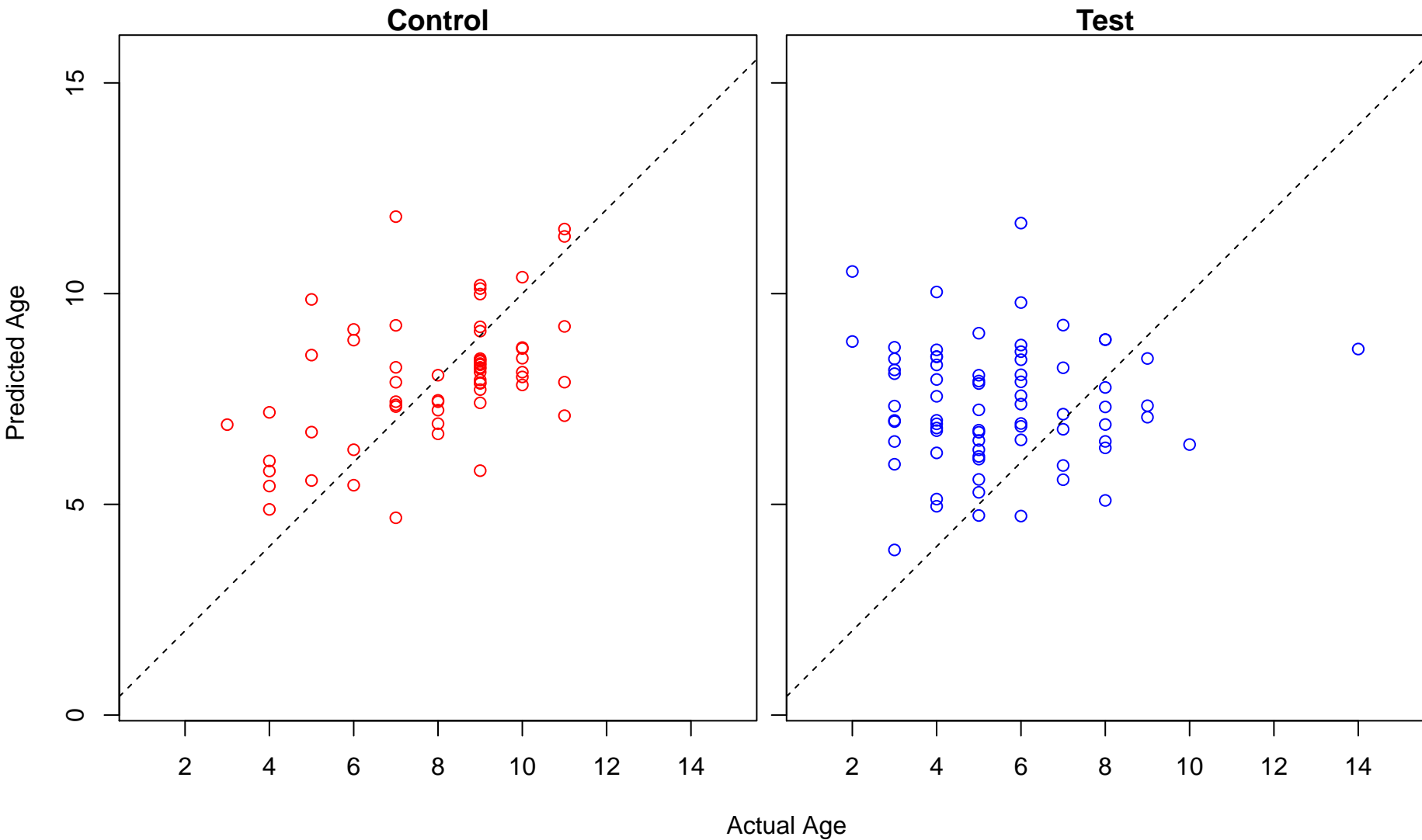
ATP biosynthetic process (Score: 1.082237)



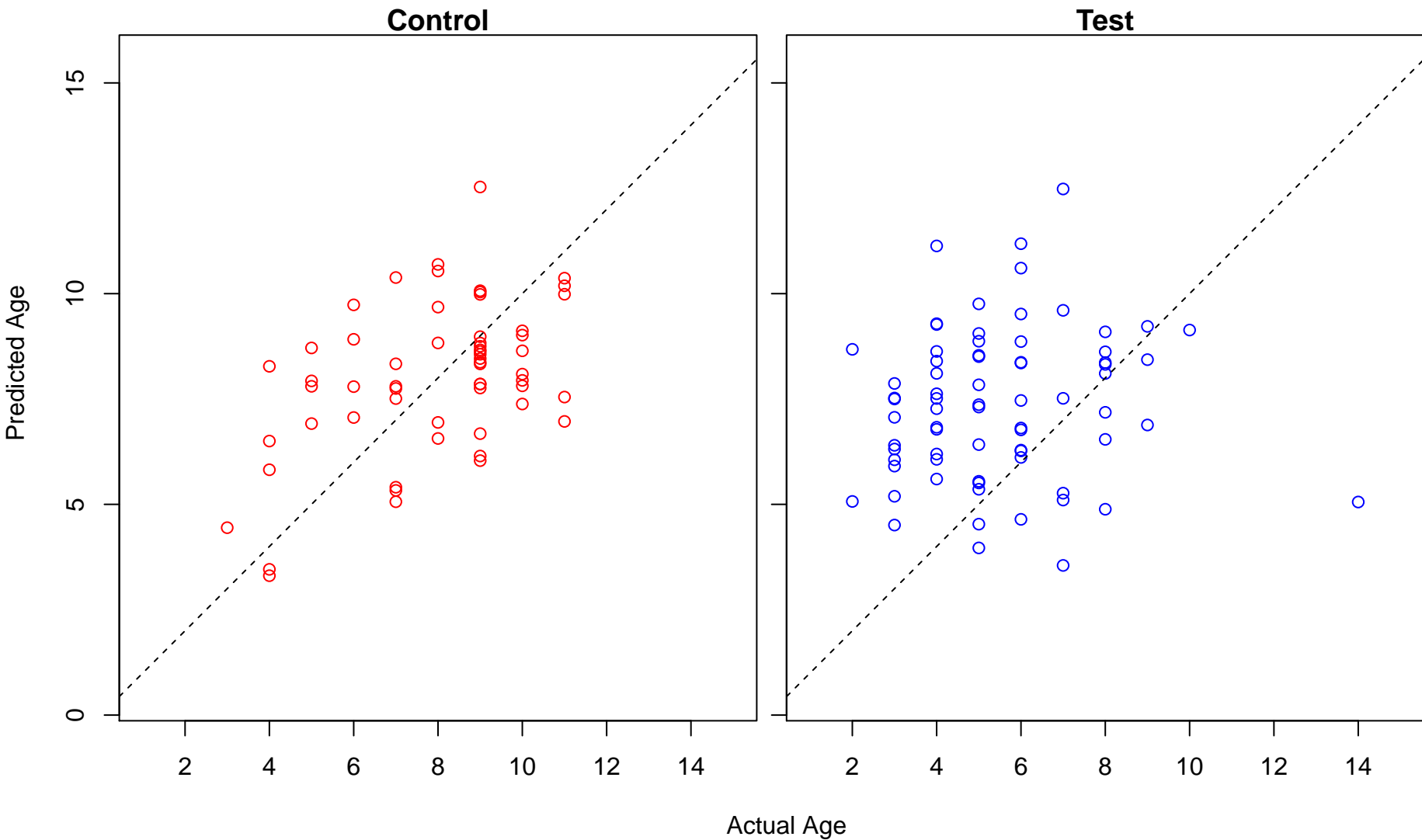
purine nucleoside triphosphate biosynthetic process (Score: 1.082237)



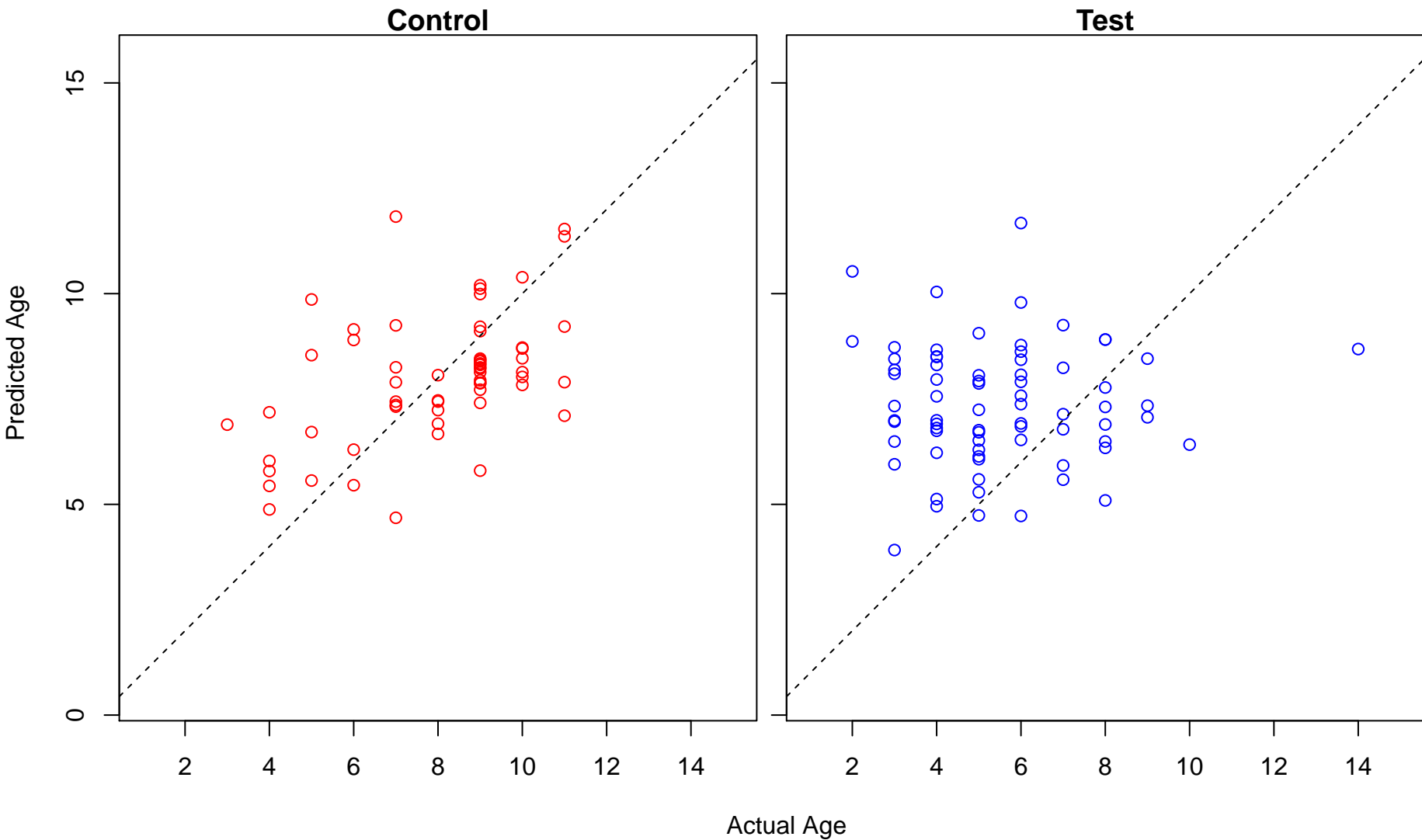
purine ribonucleoside triphosphate biosynthetic process (Score: 1.082237)



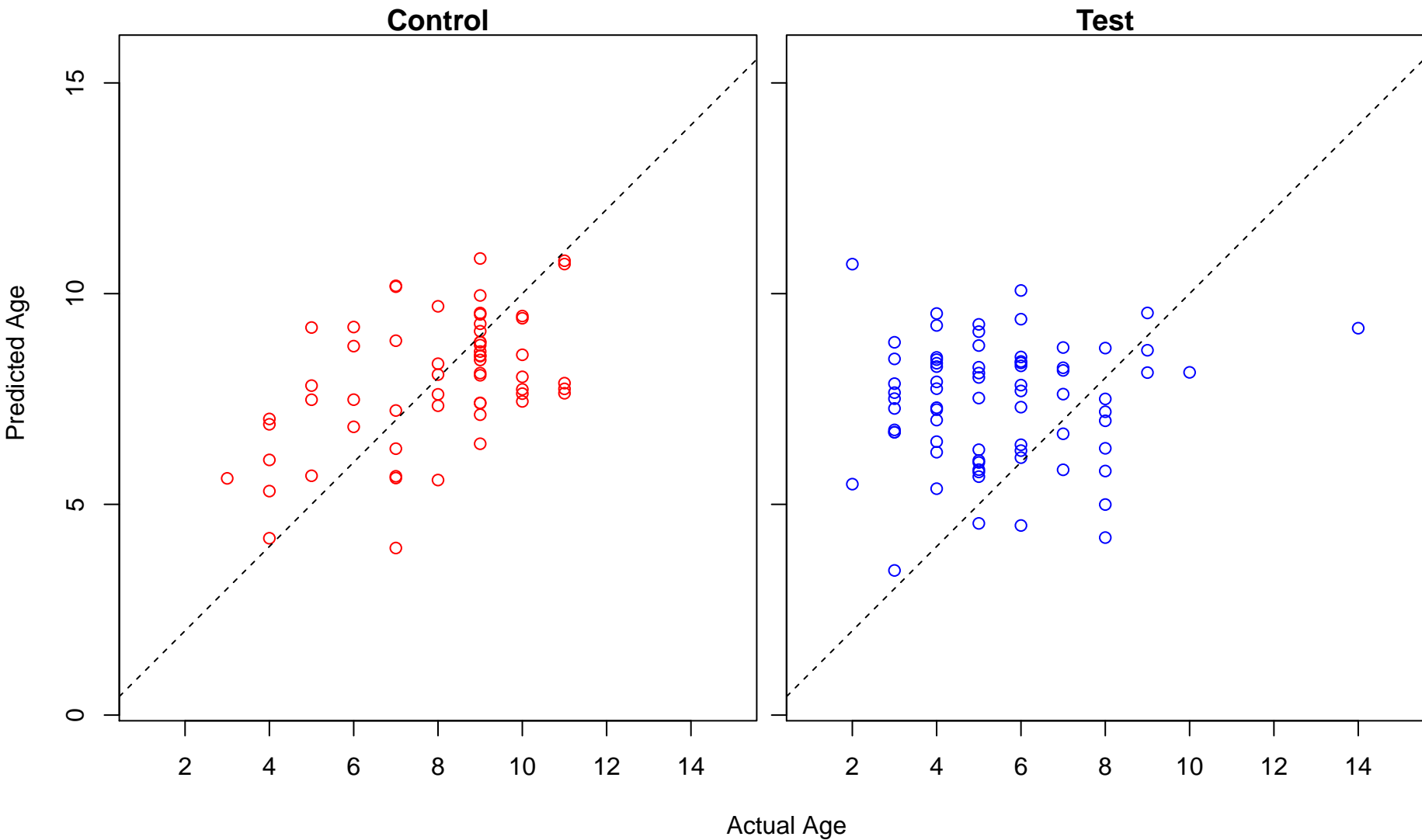
regulation of phosphatase activity (Score: 1.082067)



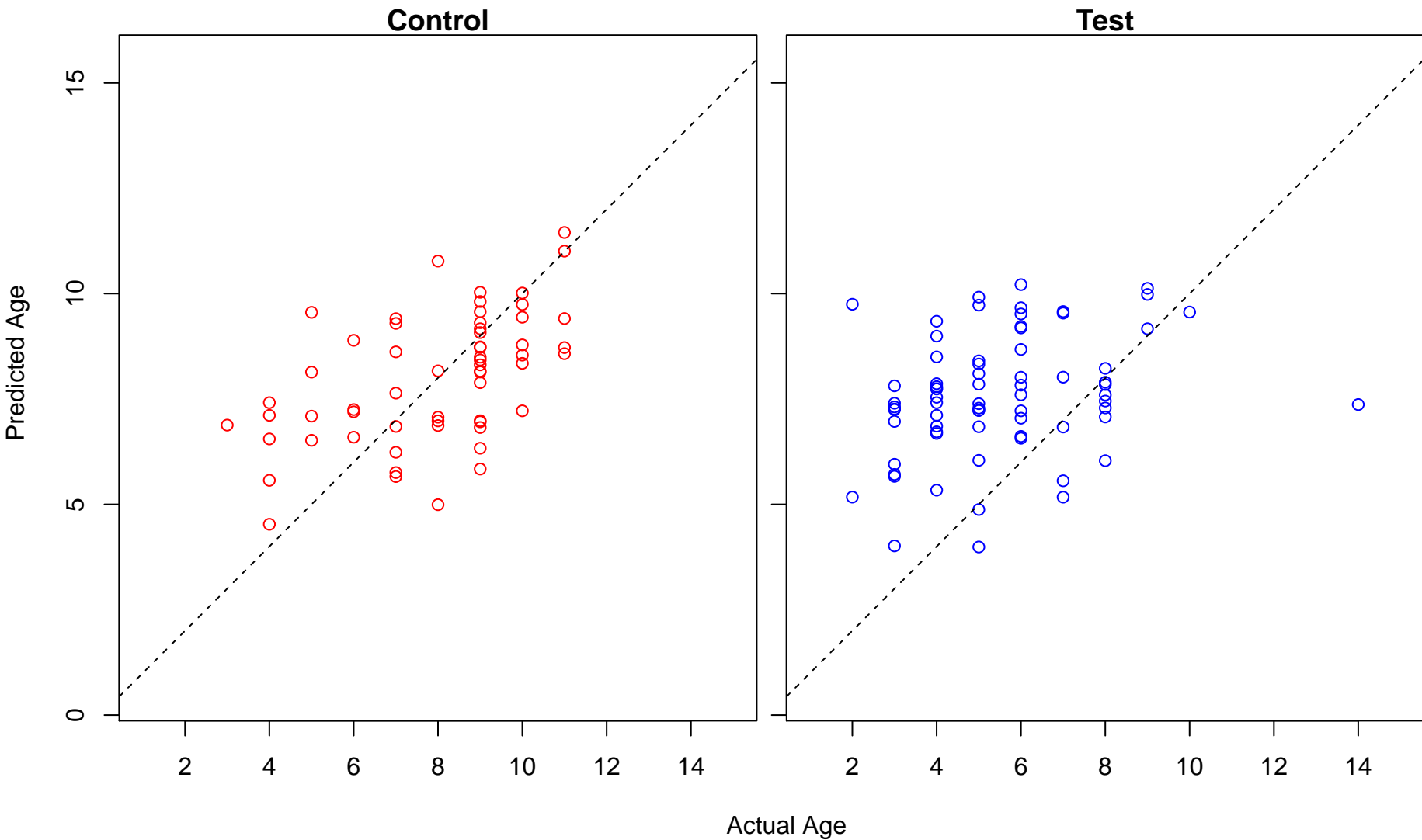
ribonucleoside triphosphate biosynthetic process (Score: 1.081796)



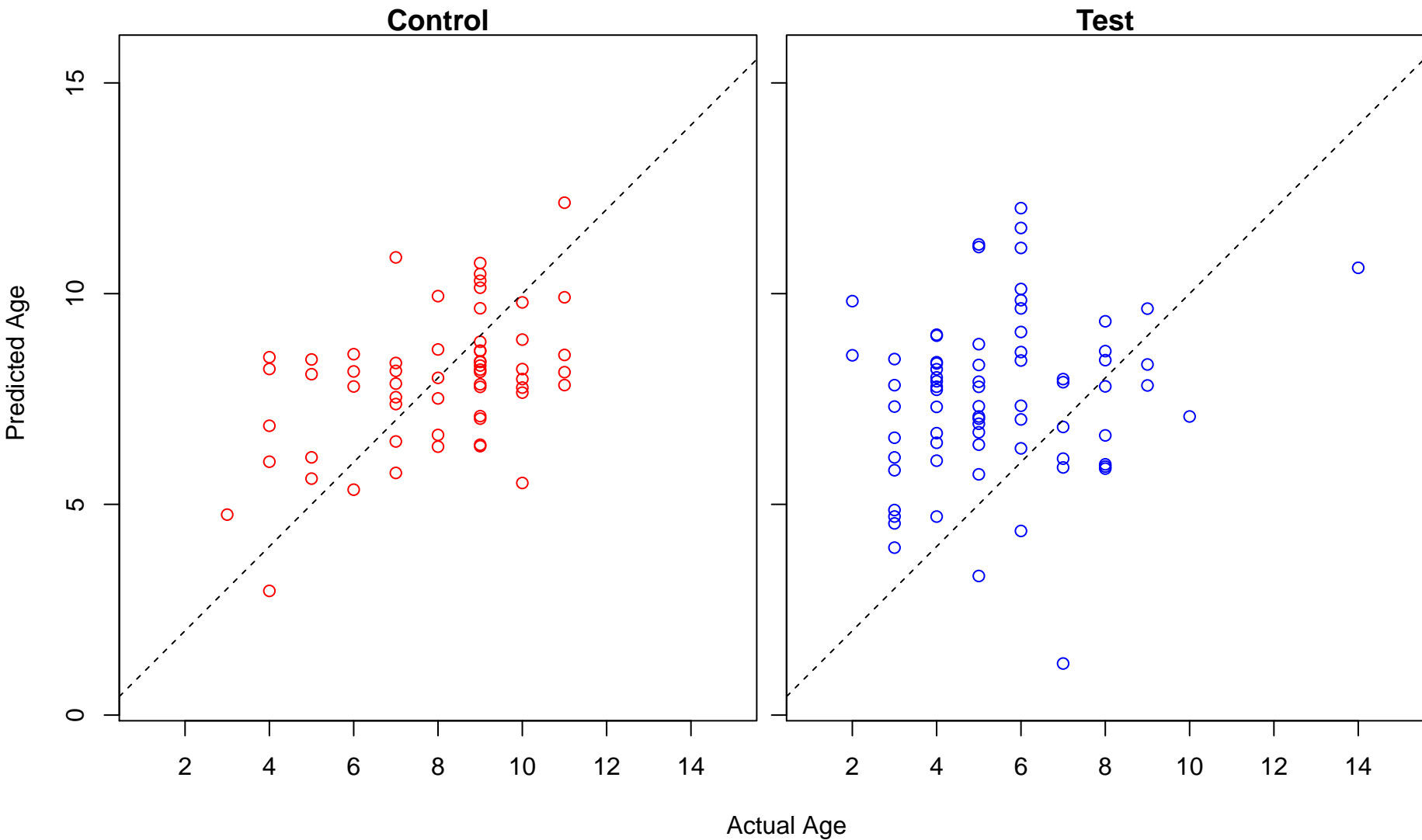
homotypic cell-cell adhesion (Score: 1.081530)



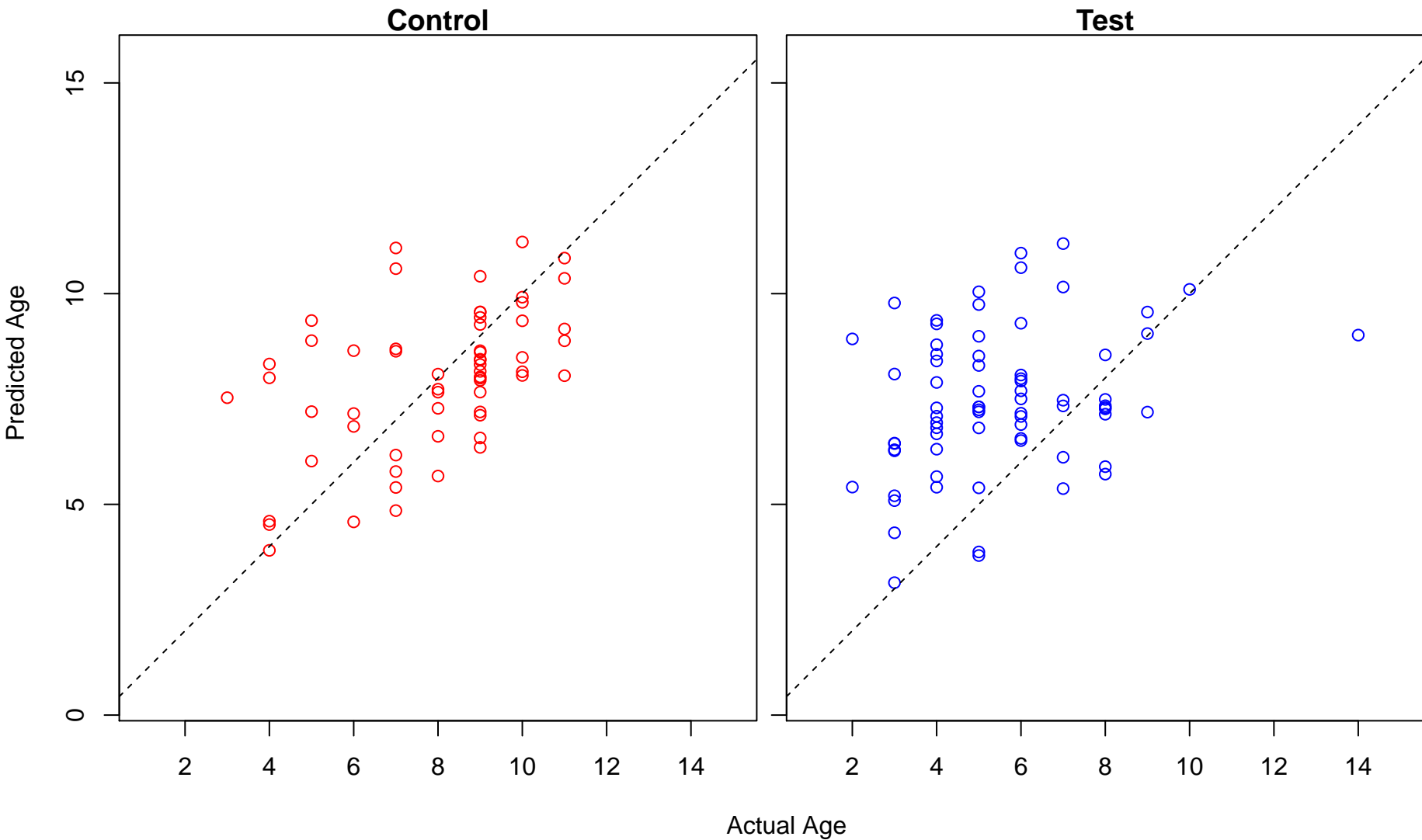
cellular macromolecule metabolic process (Score: 1.081312)



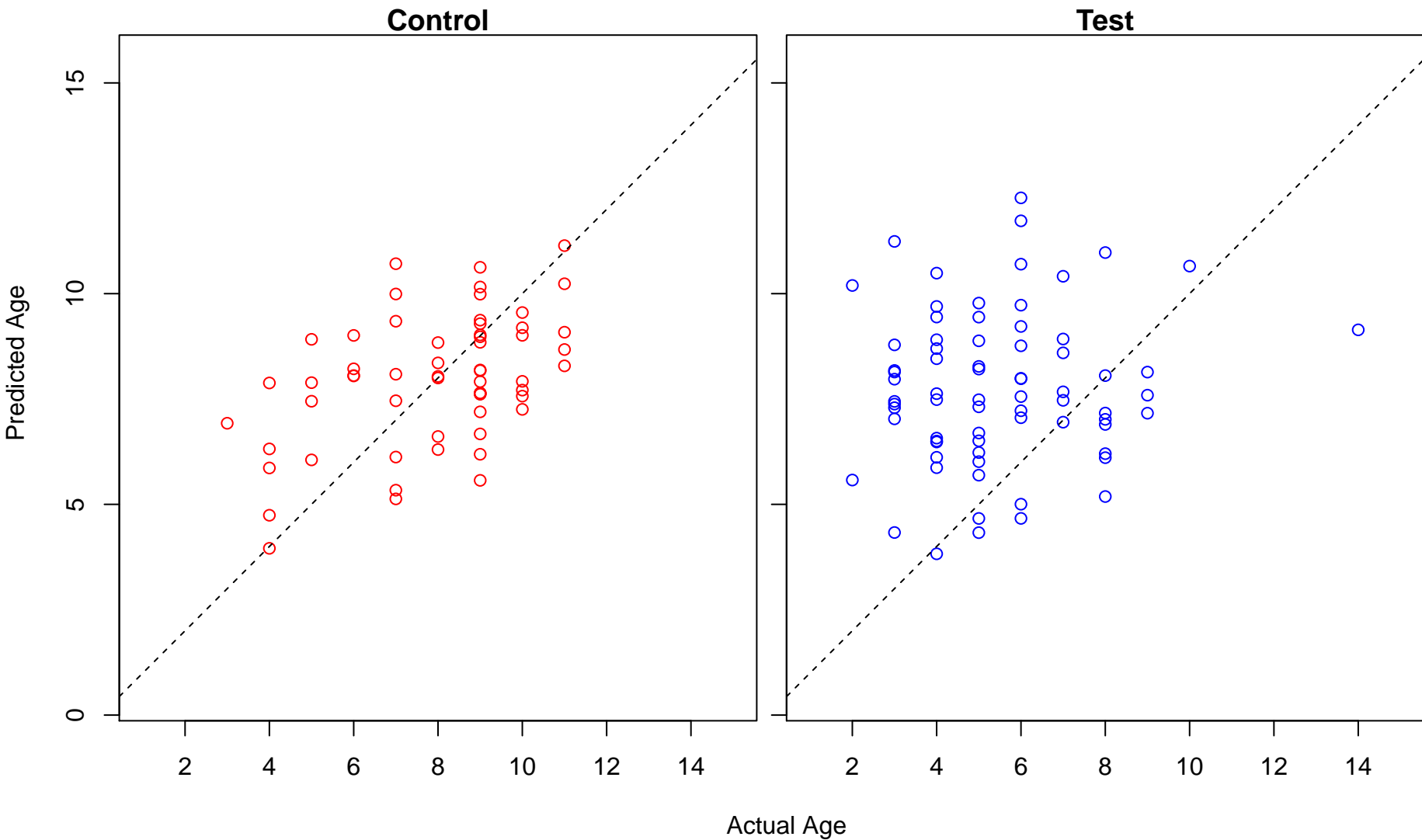
regulation of humoral immune response (Score: 1.081225)



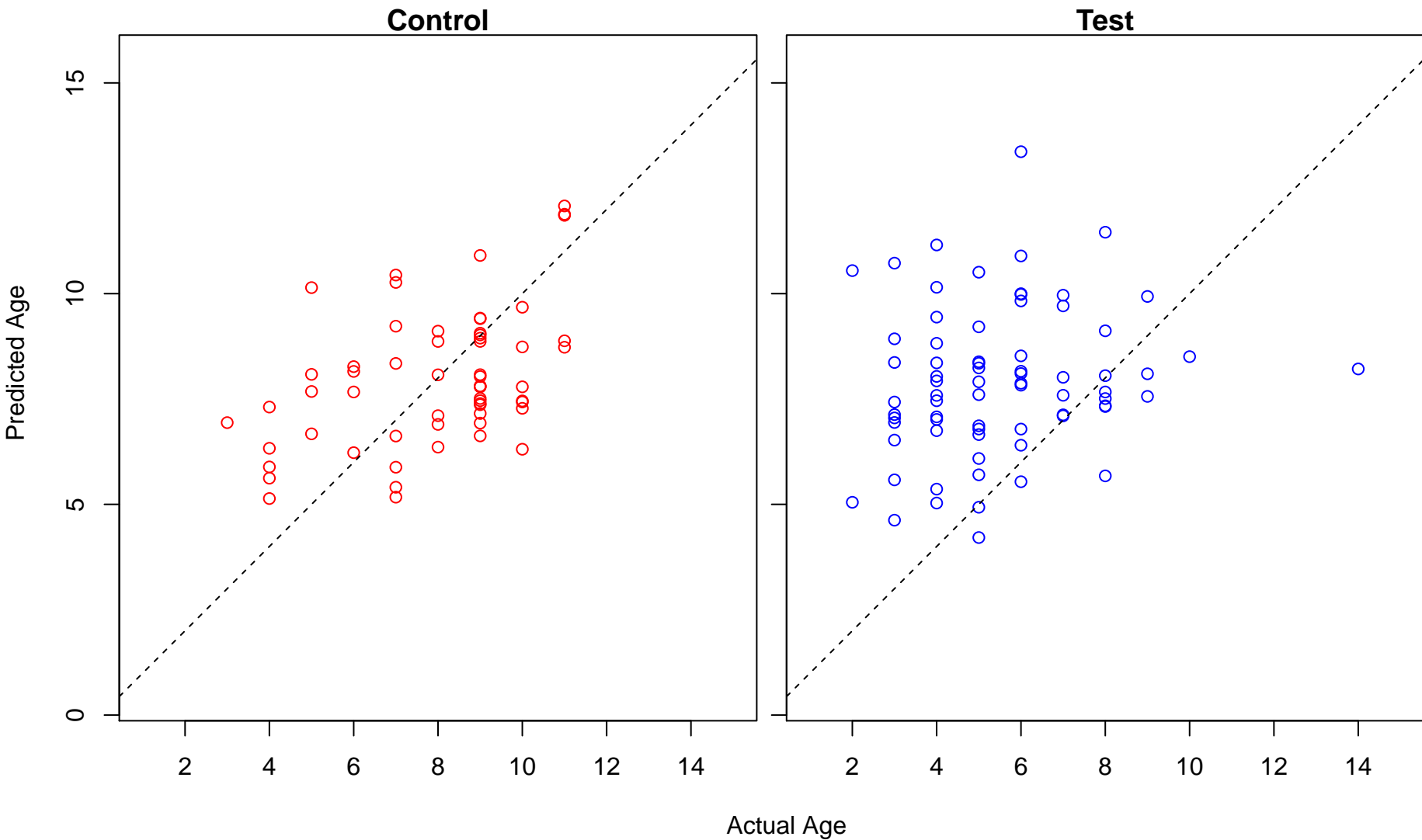
protein complex subunit organization (Score: 1.080278)



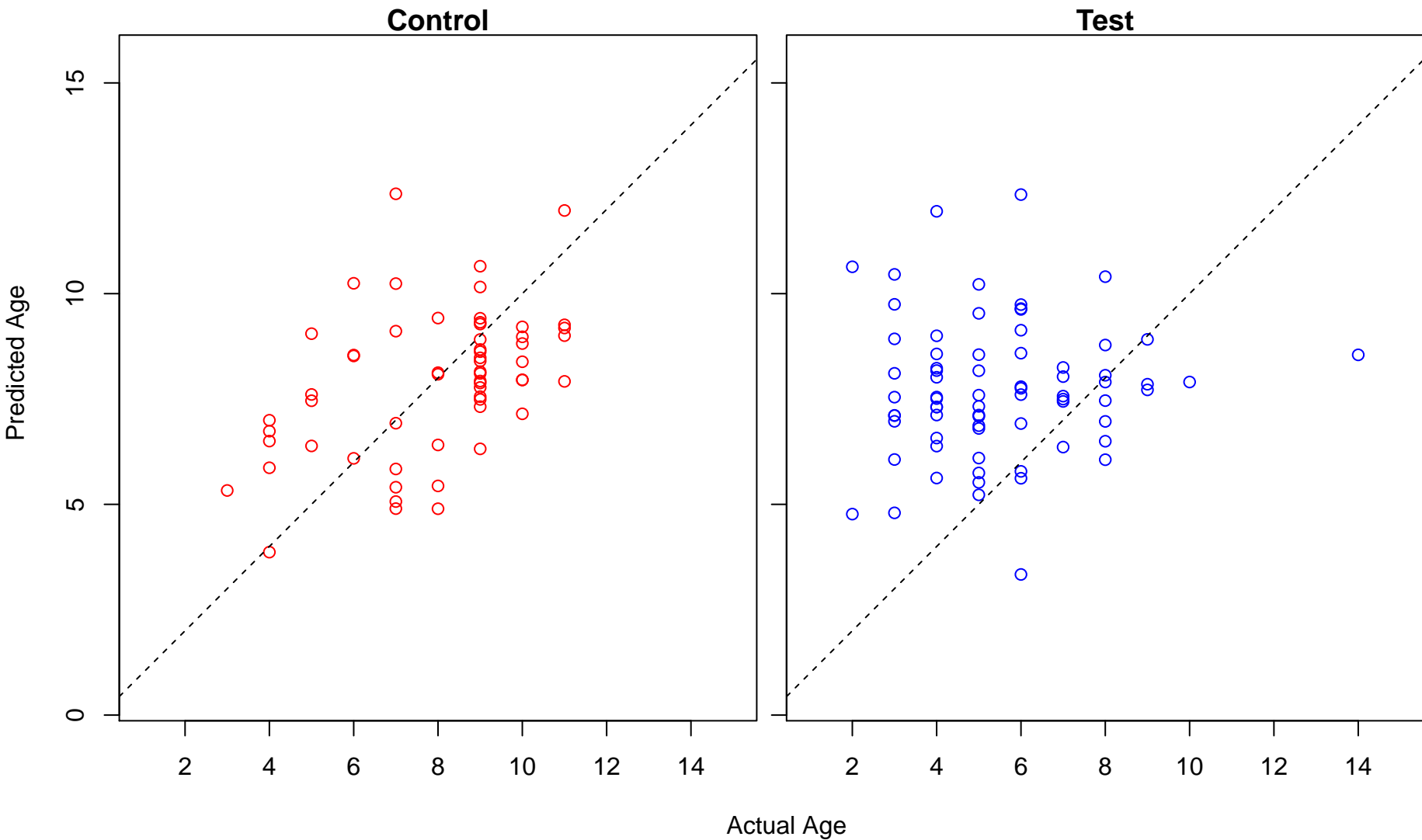
glycerolipid metabolic process (Score: 1.079958)



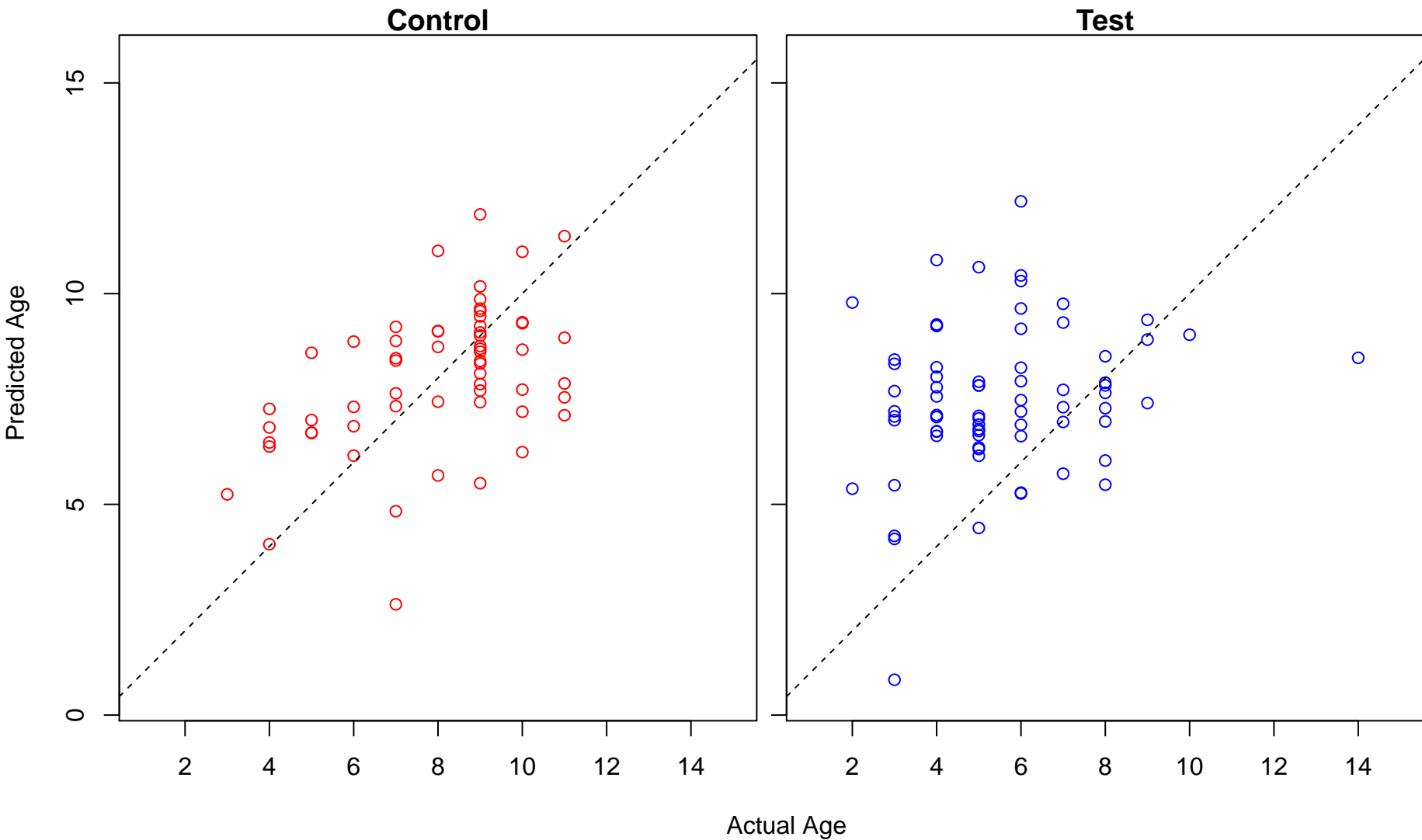
regulation of cell morphogenesis (Score: 1.079586)



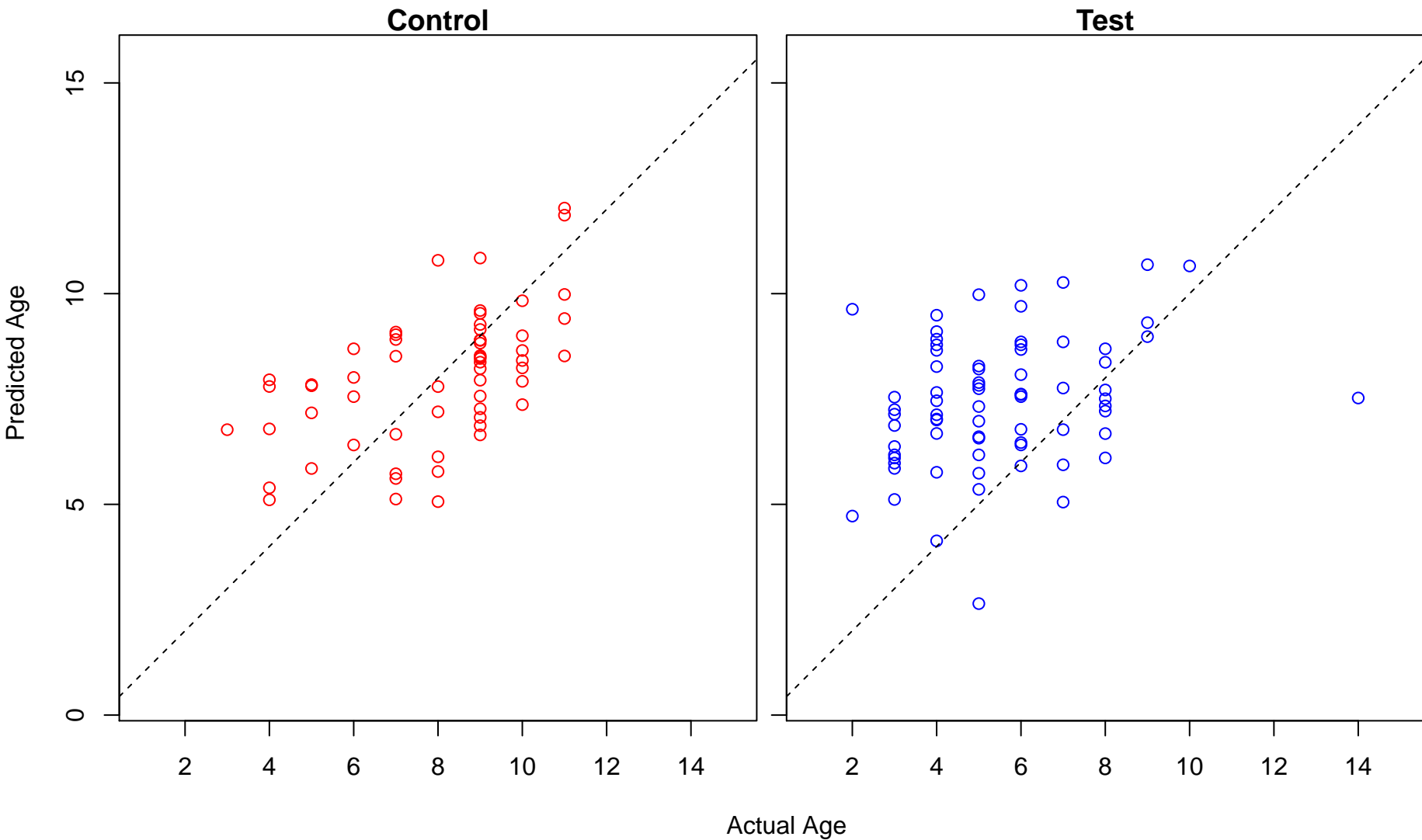
regulation of intracellular protein transport (Score: 1.078844)



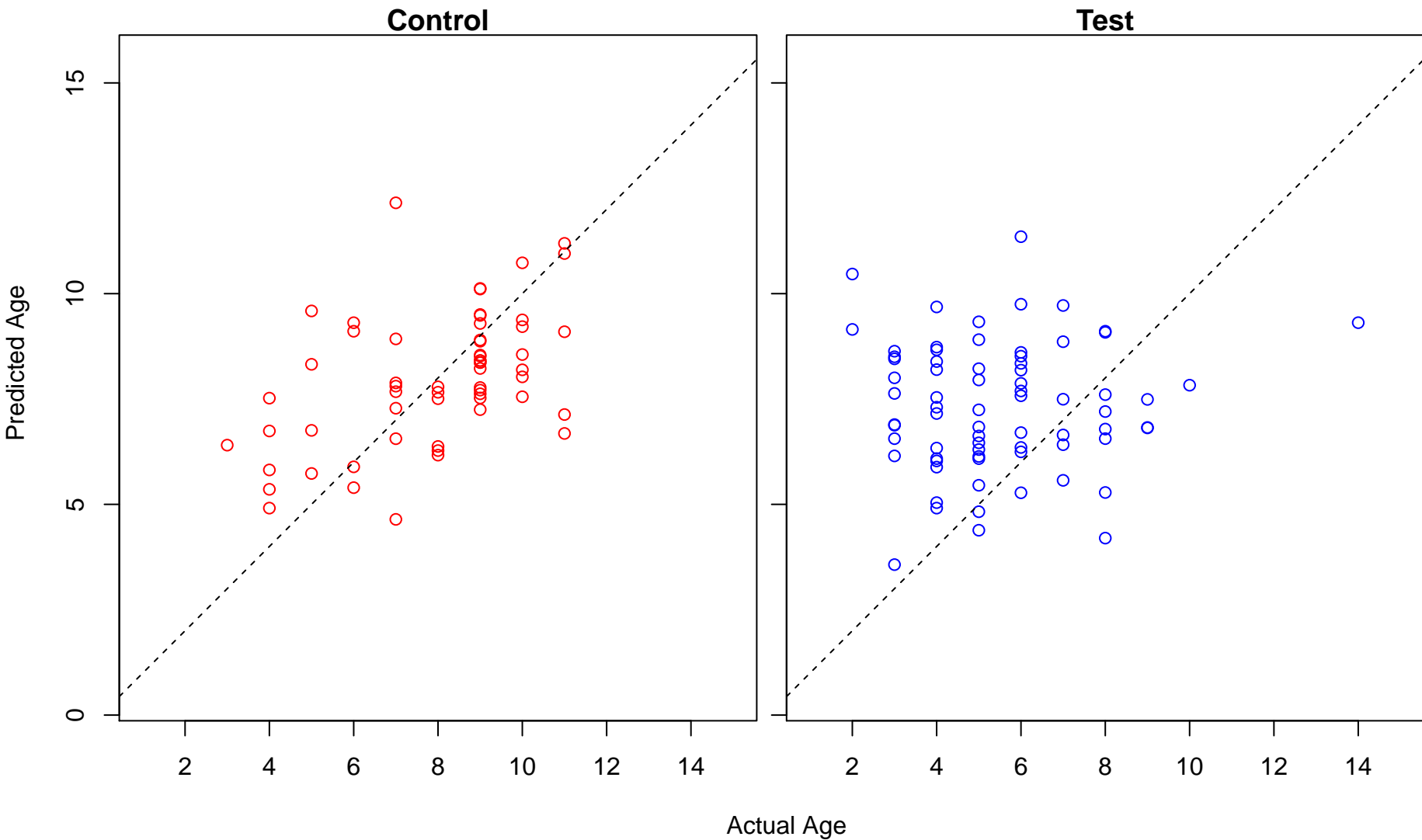
regulation of receptor binding (Score: 1.077362)



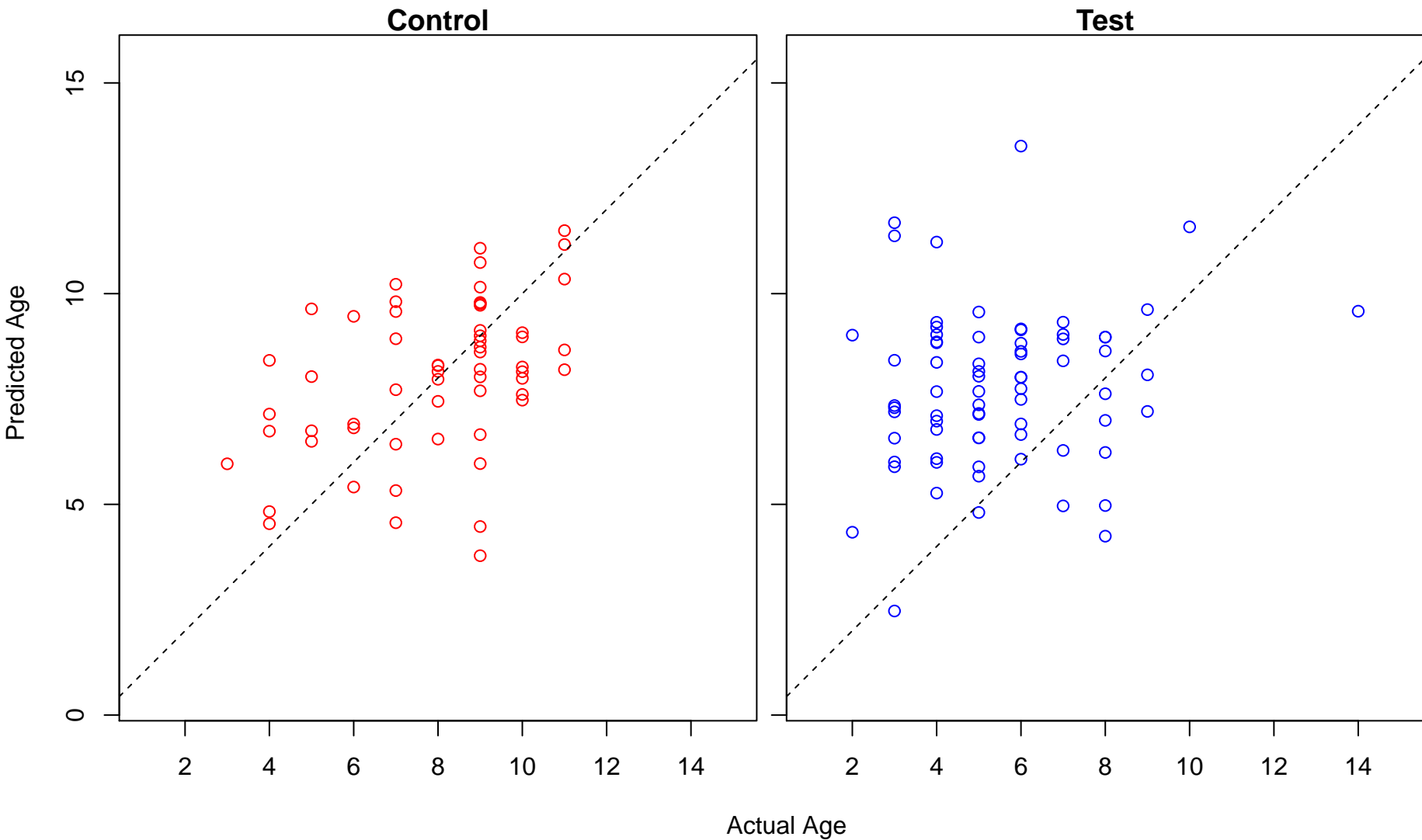
regulation of cellular process (Score: 1.075615)



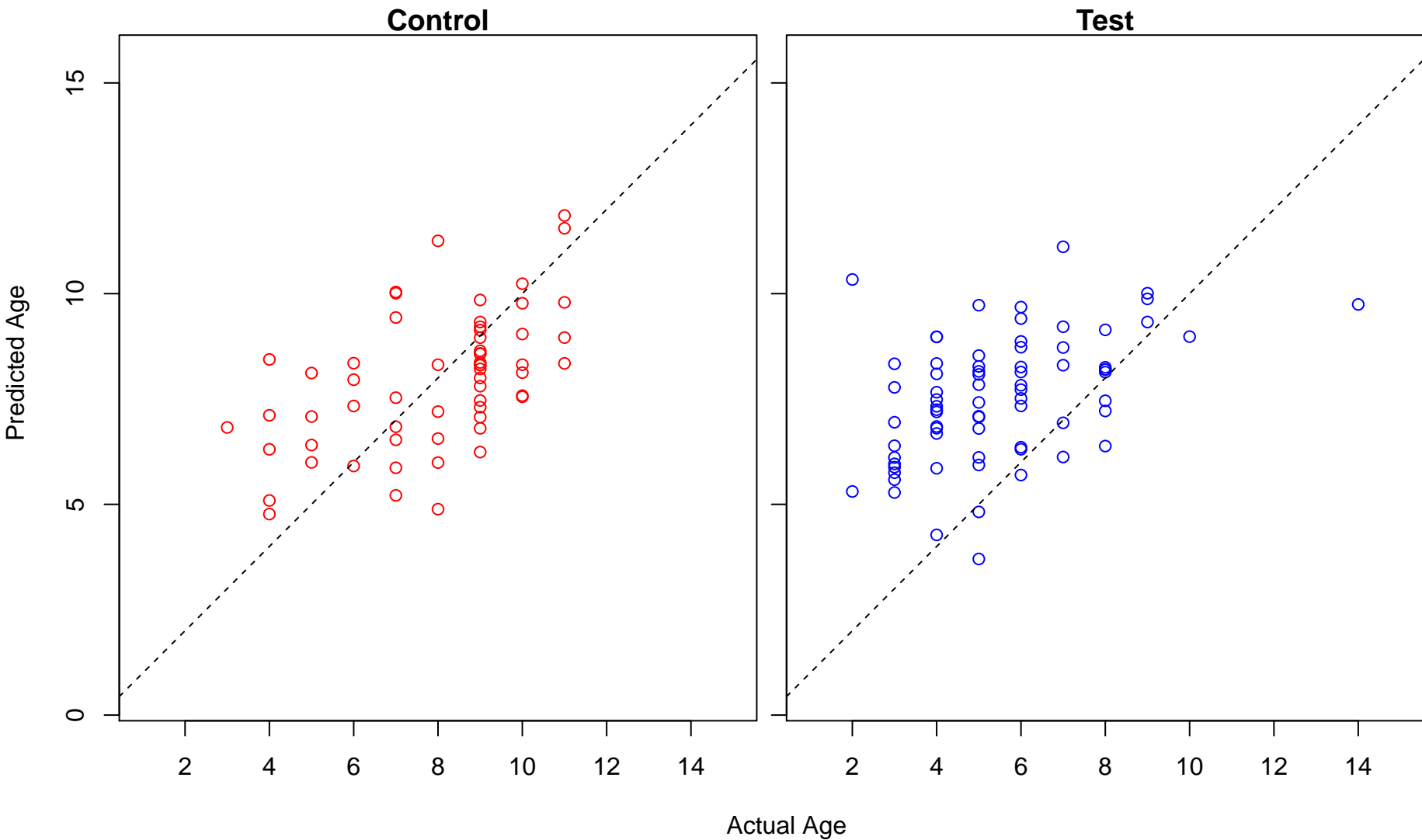
ribonucleoside monophosphate biosynthetic process (Score: 1.075611)



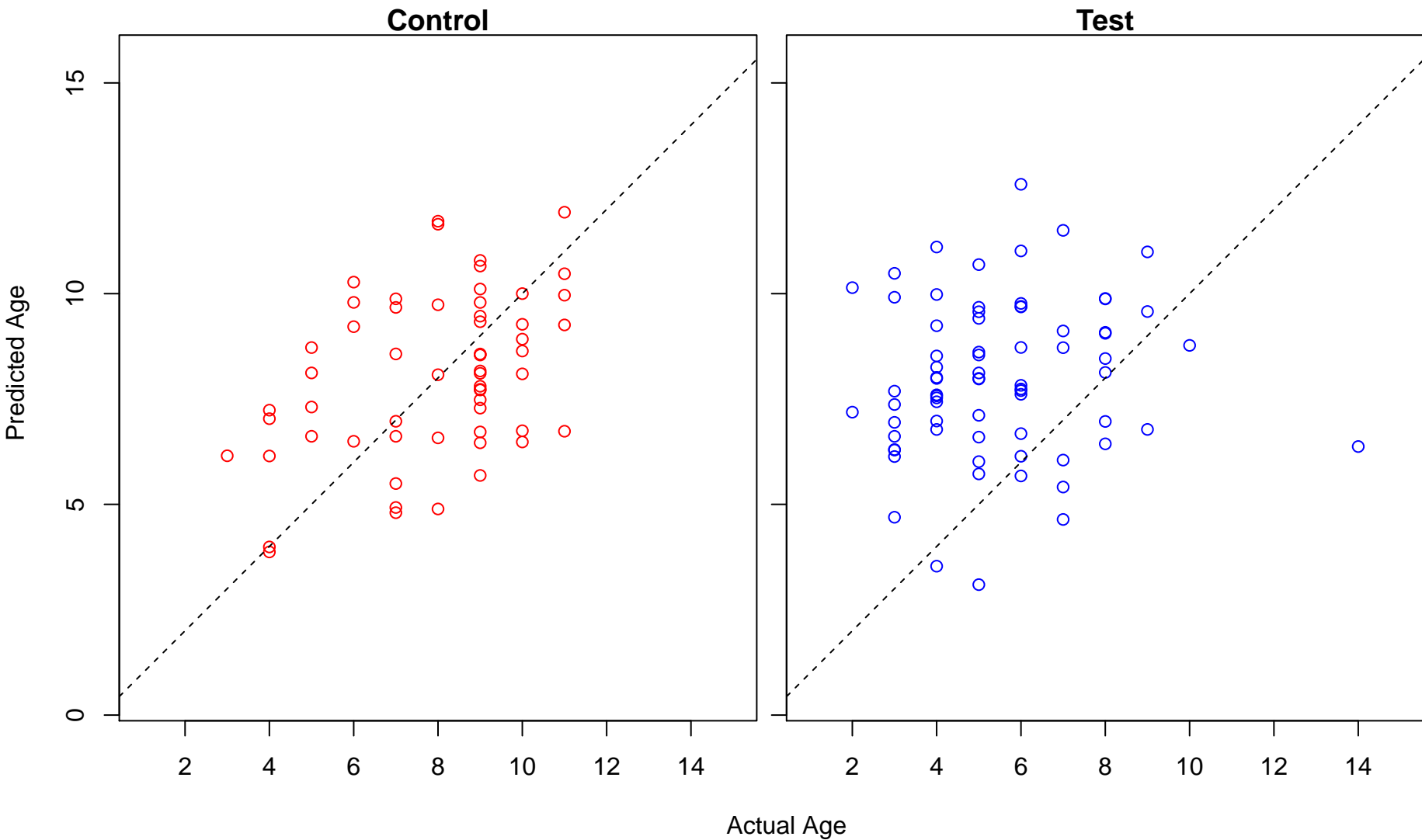
microtubule-based process (Score: 1.073988)



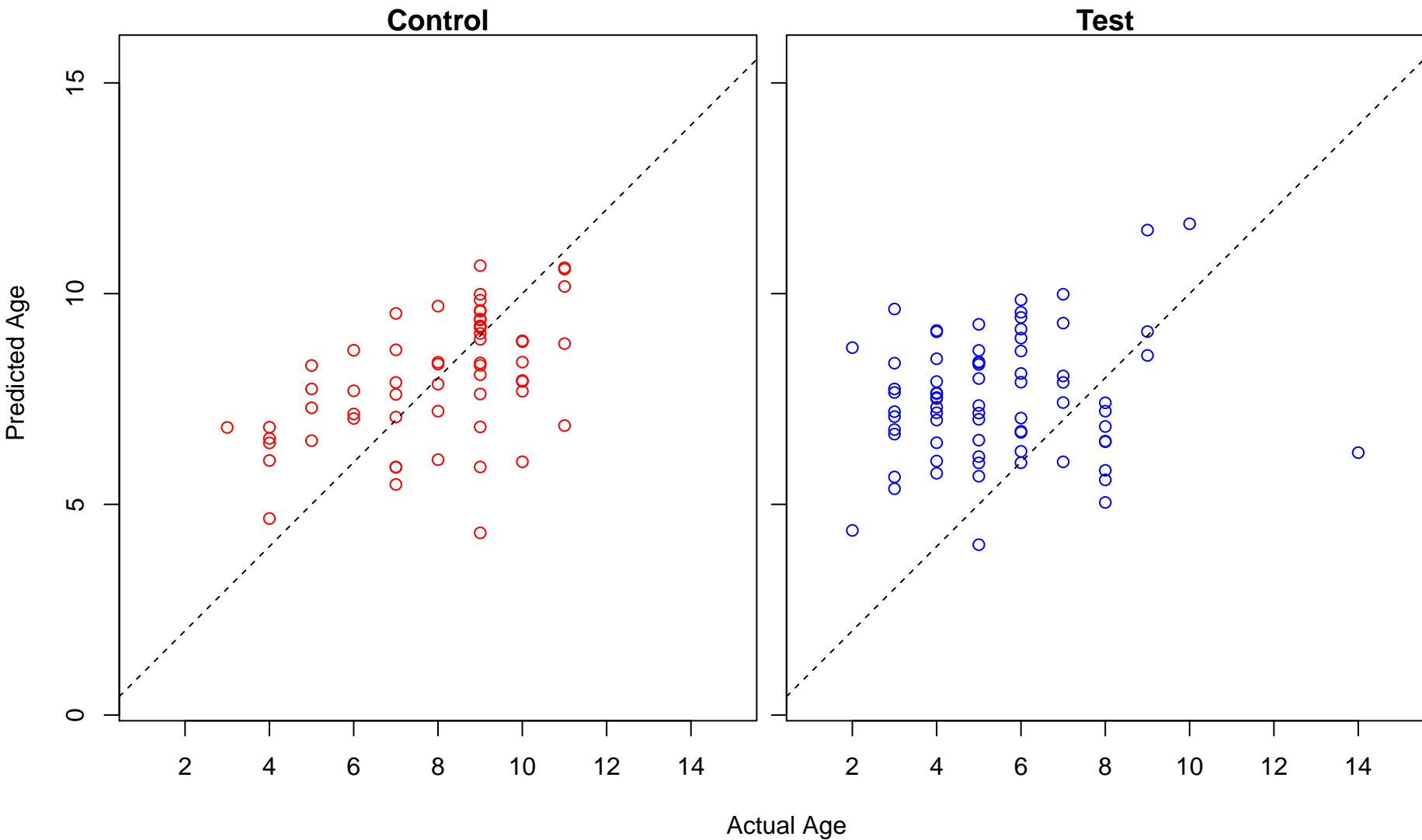
establishment of localization (Score: 1.073732)



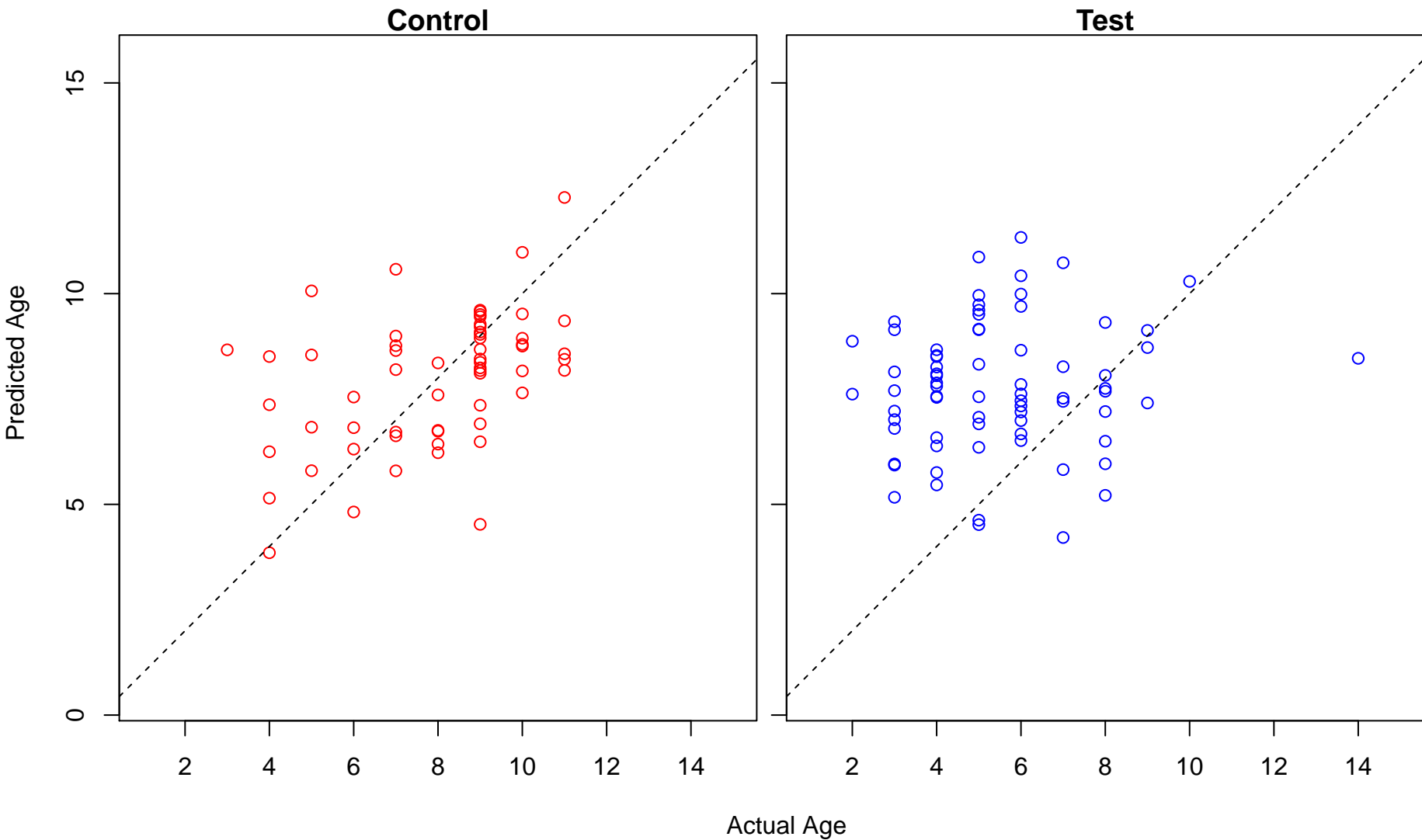
regulation of phosphoprotein phosphatase activity (Score: 1.071296)



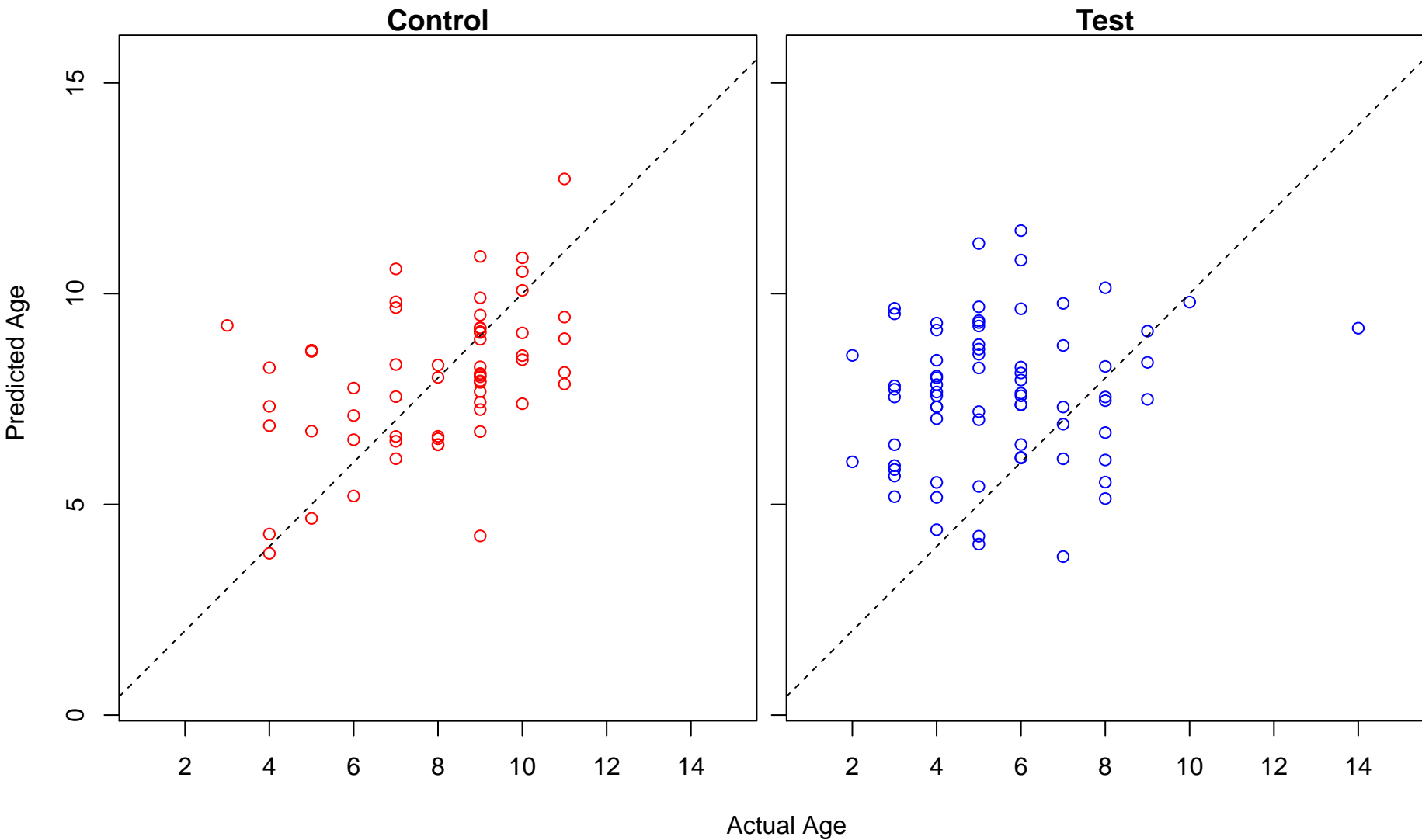
regulation of spindle organization (Score: 1.070431)



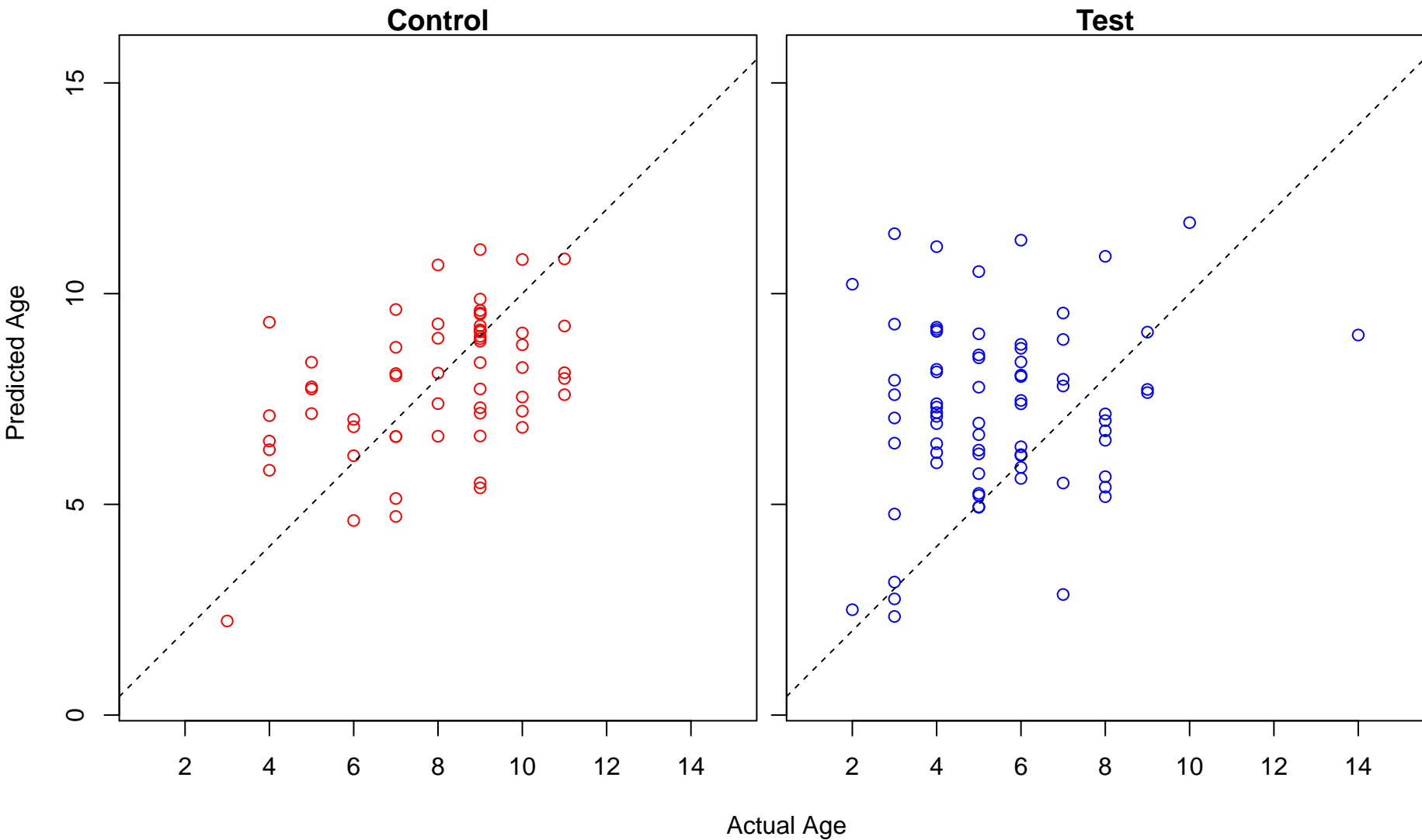
RNA catabolic process (Score: 1.069386)



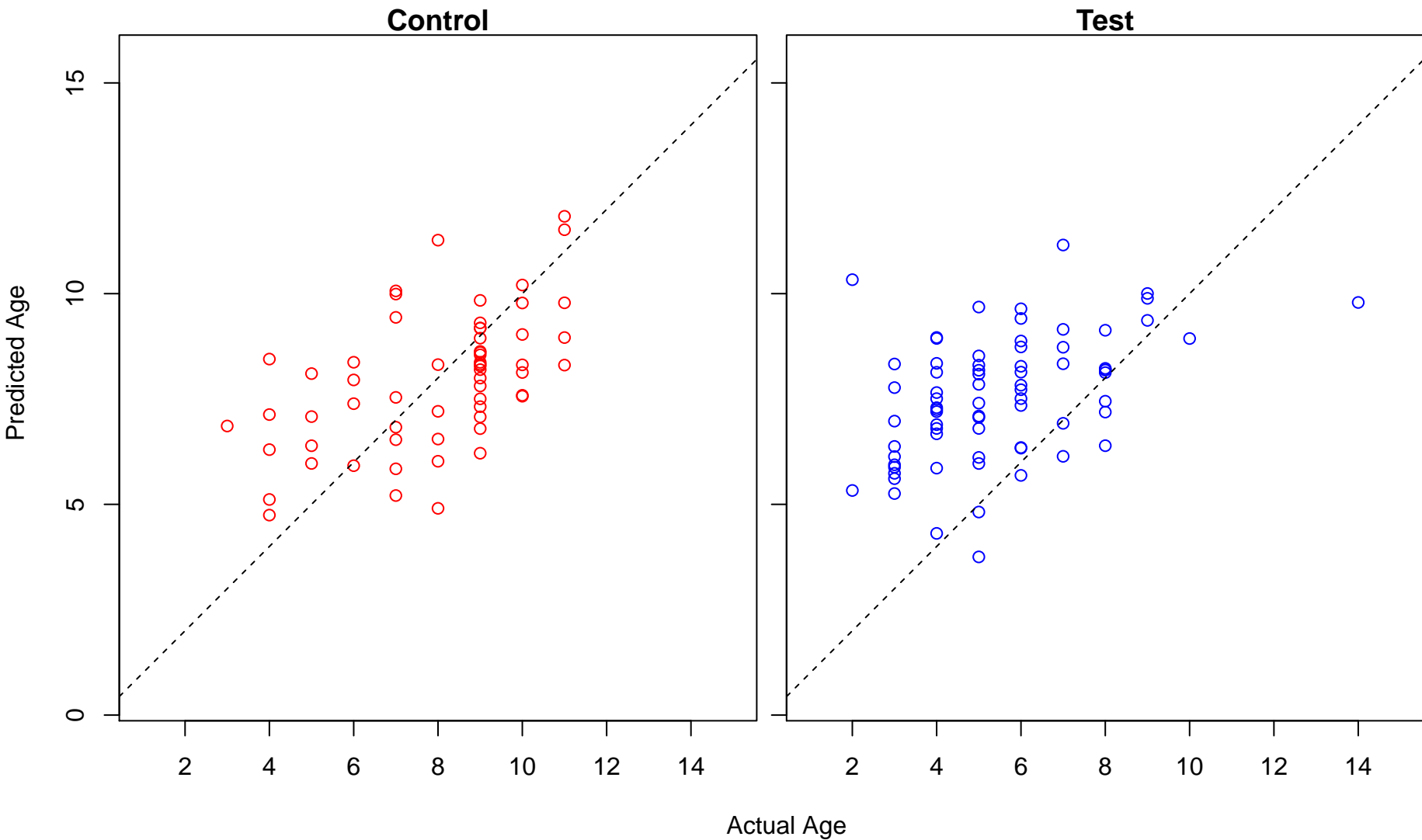
translational elongation (Score: 1.069147)



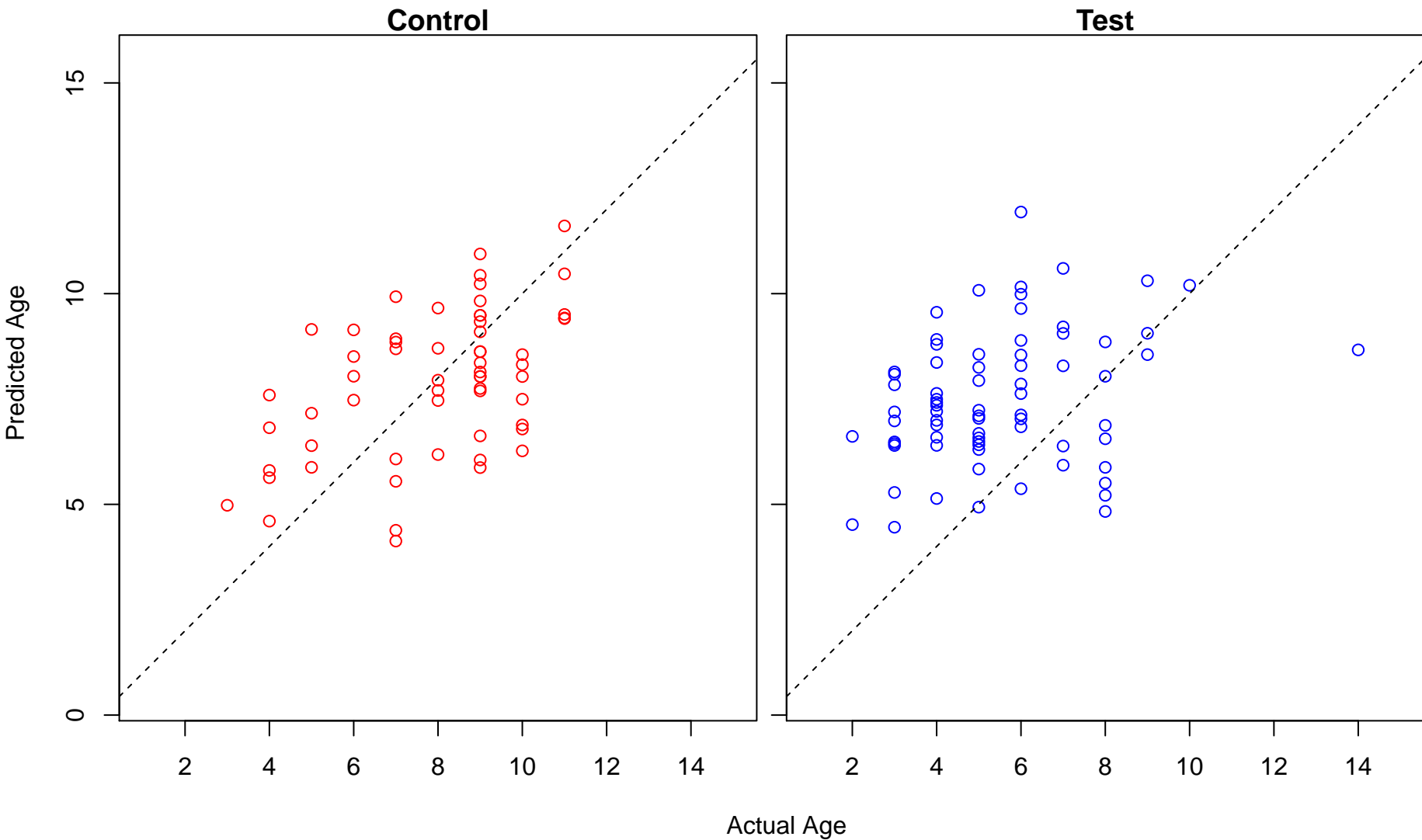
regulation of organ growth (Score: 1.068127)



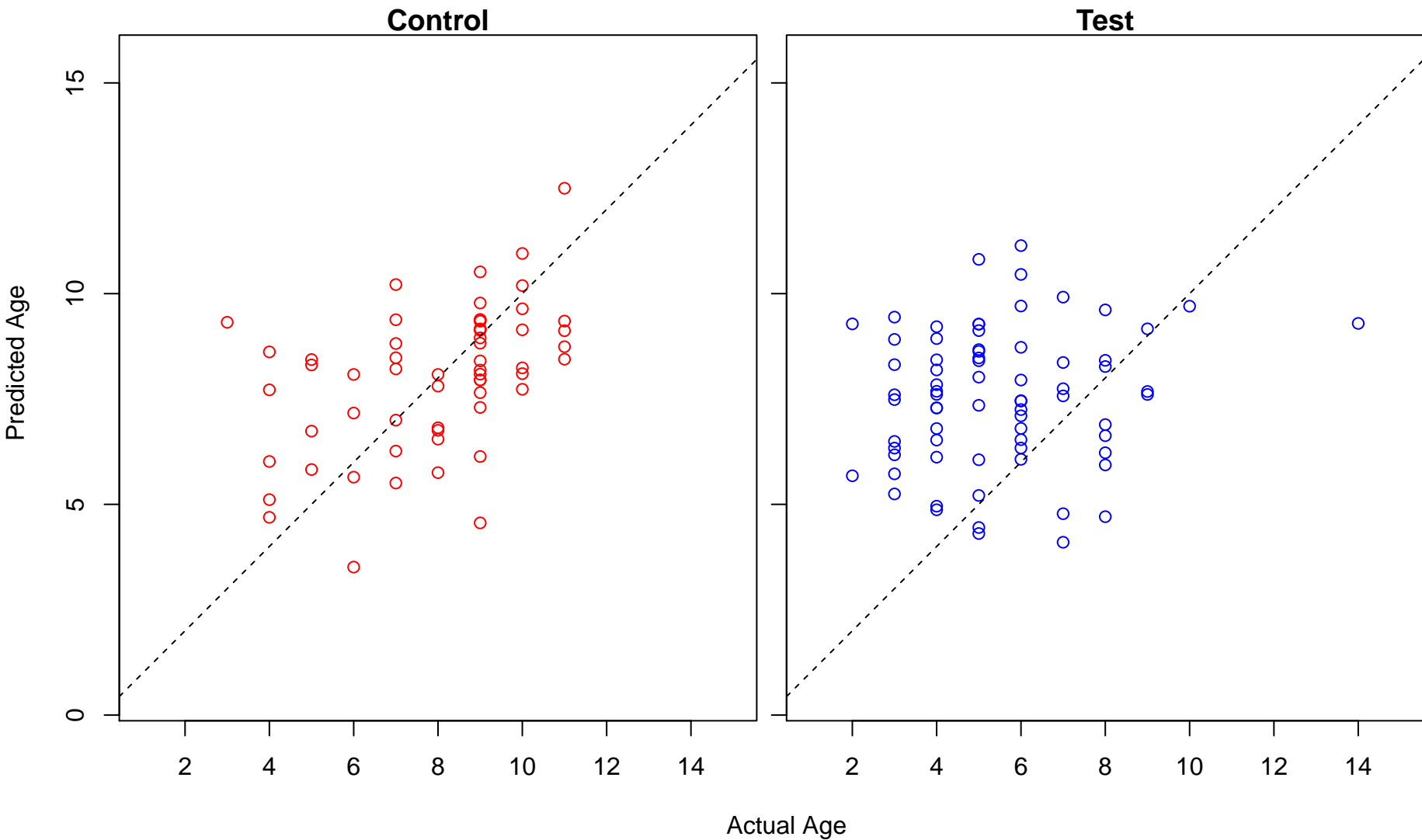
transport (Score: 1.068002)



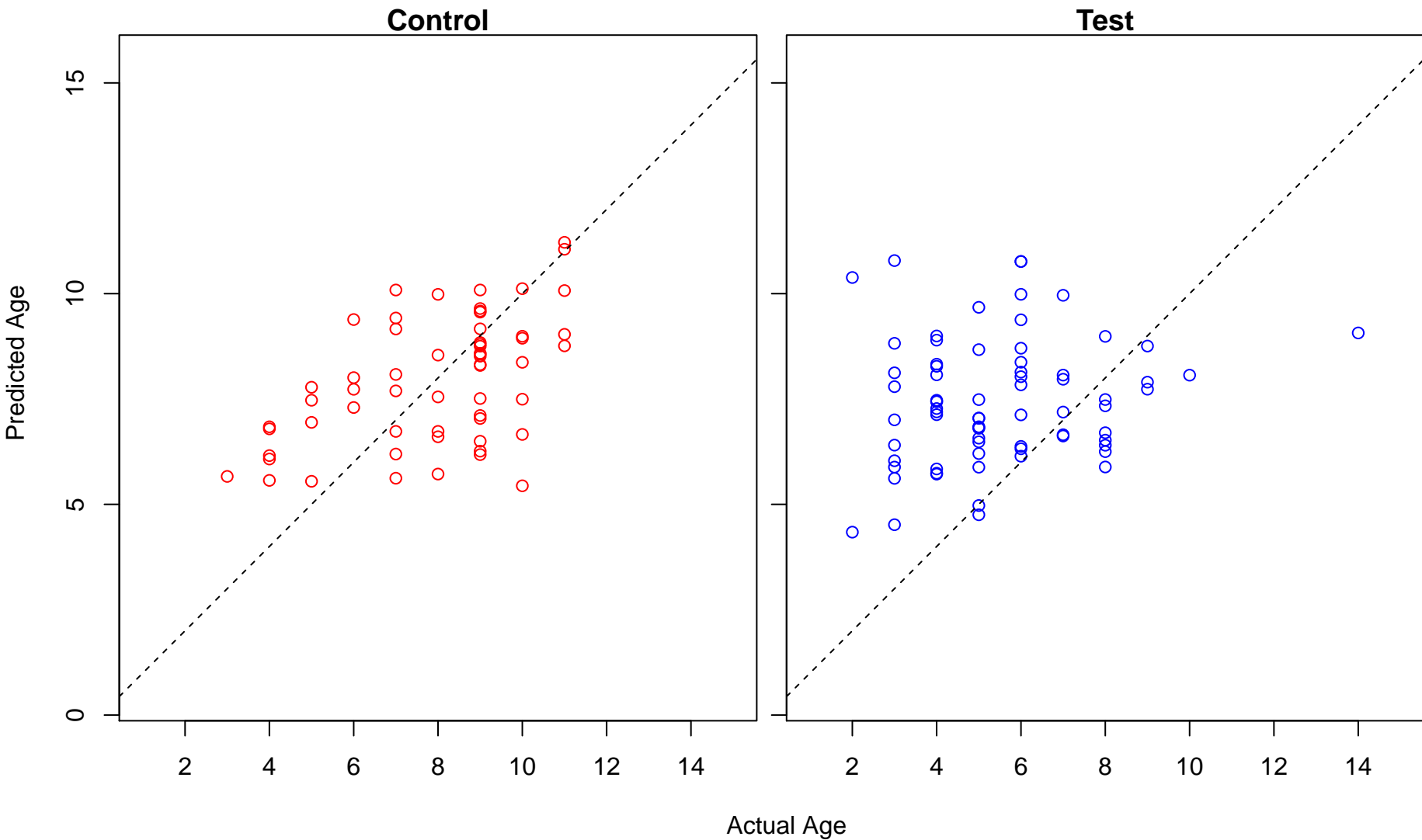
regulation of establishment of protein localization to plasma membrane (Score: 1.067909)



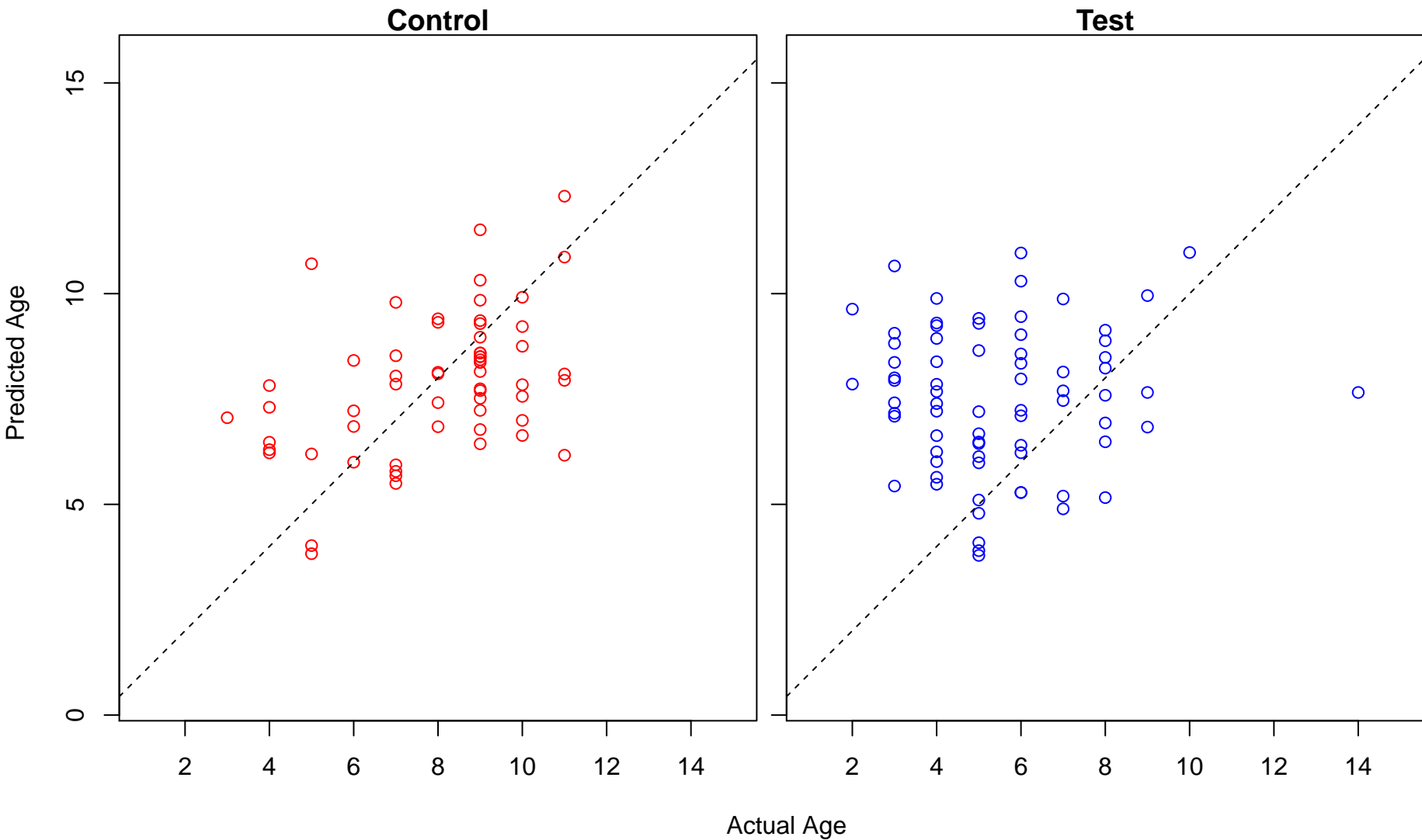
cellular amino acid metabolic process (Score: 1.067808)



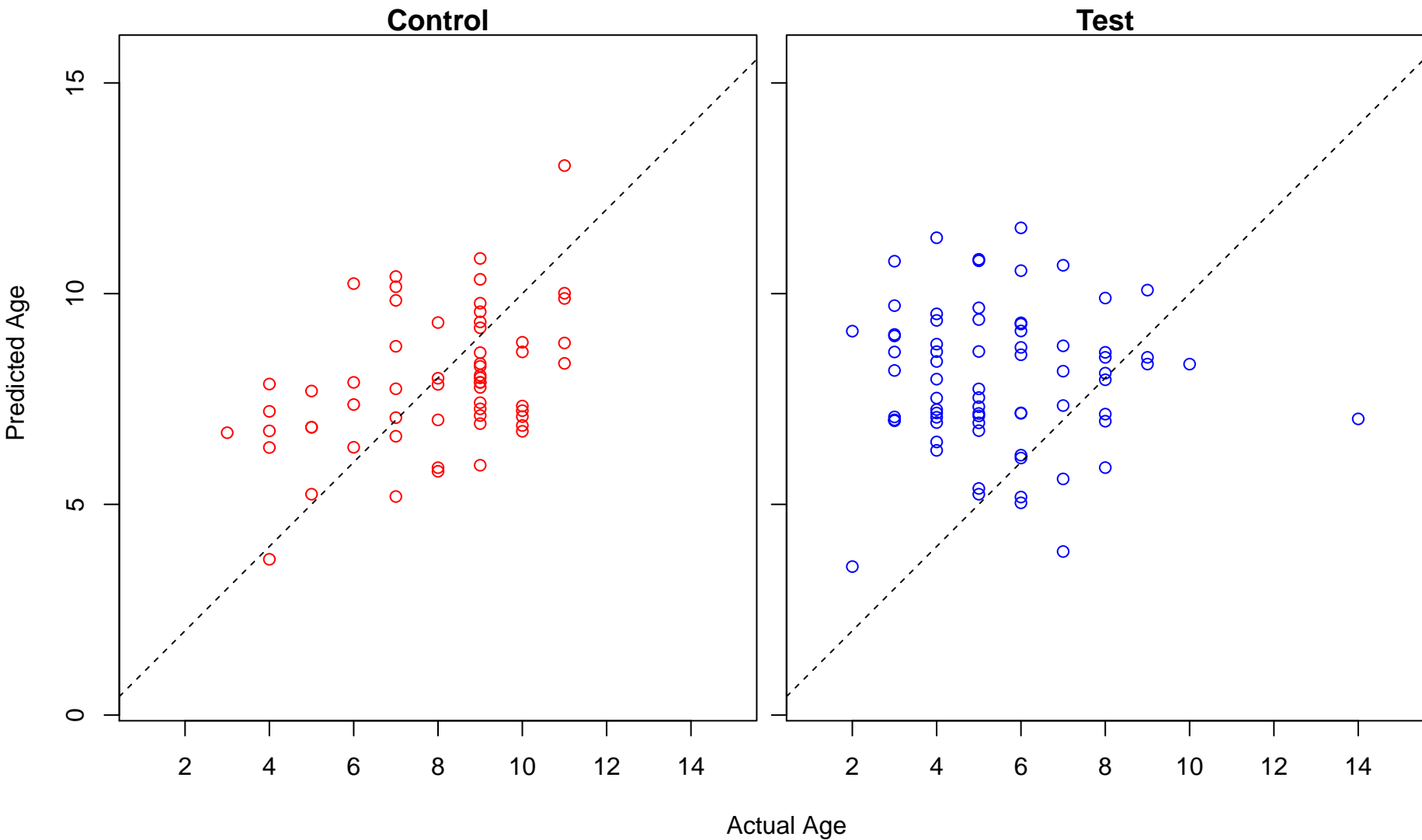
stem cell development (Score: 1.067648)



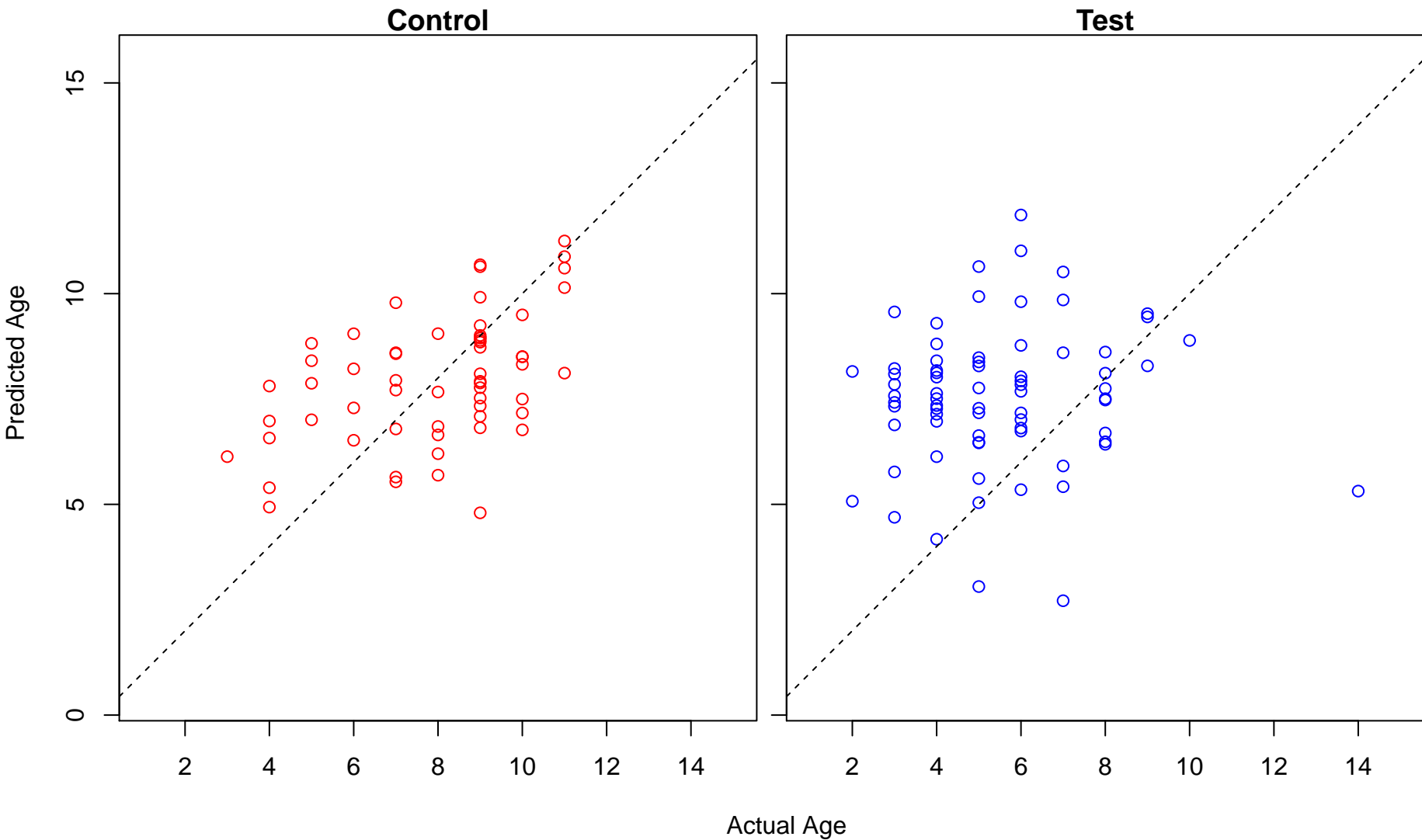
cochlea morphogenesis (Score: 1.067609)



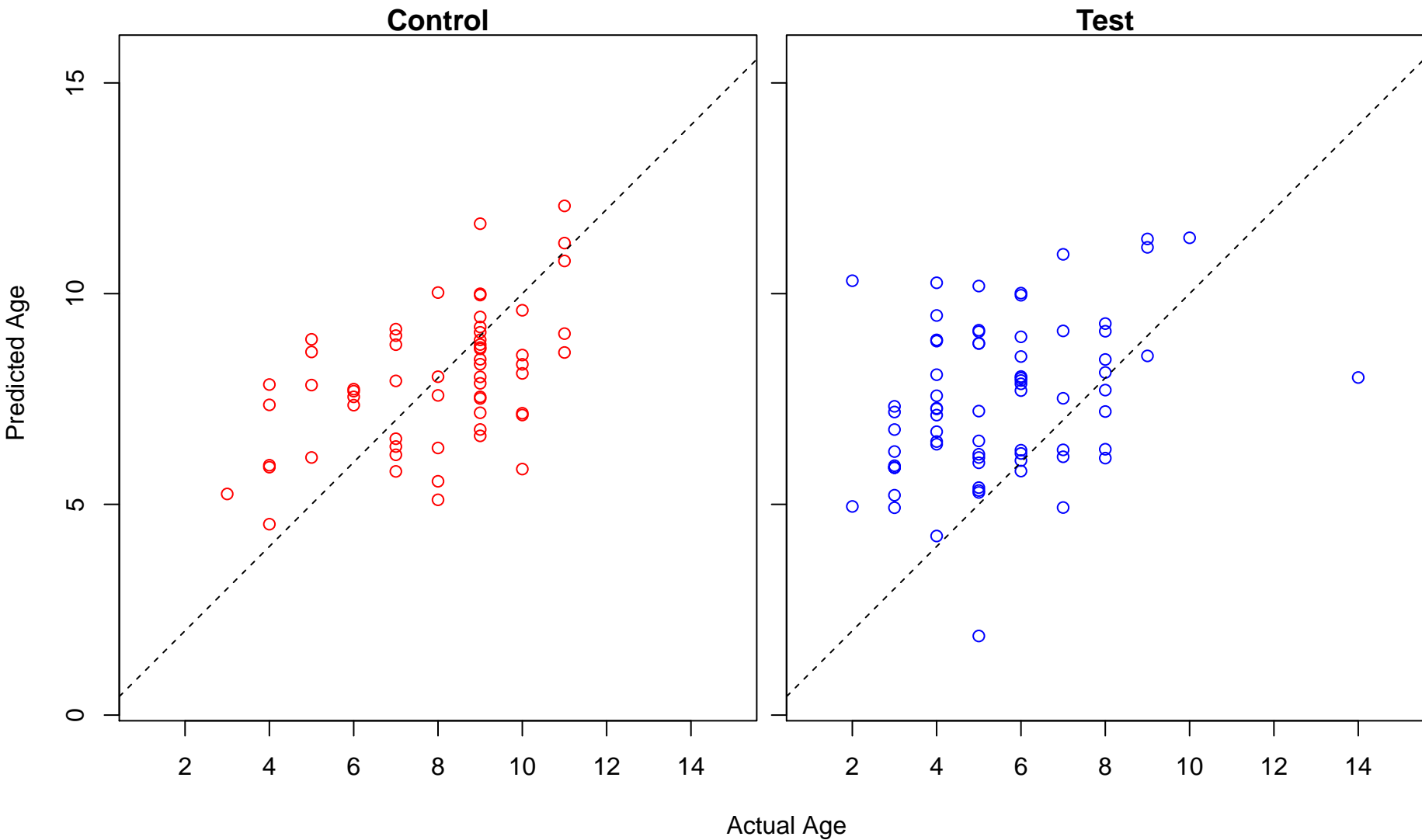
gamete generation (Score: 1.067581)



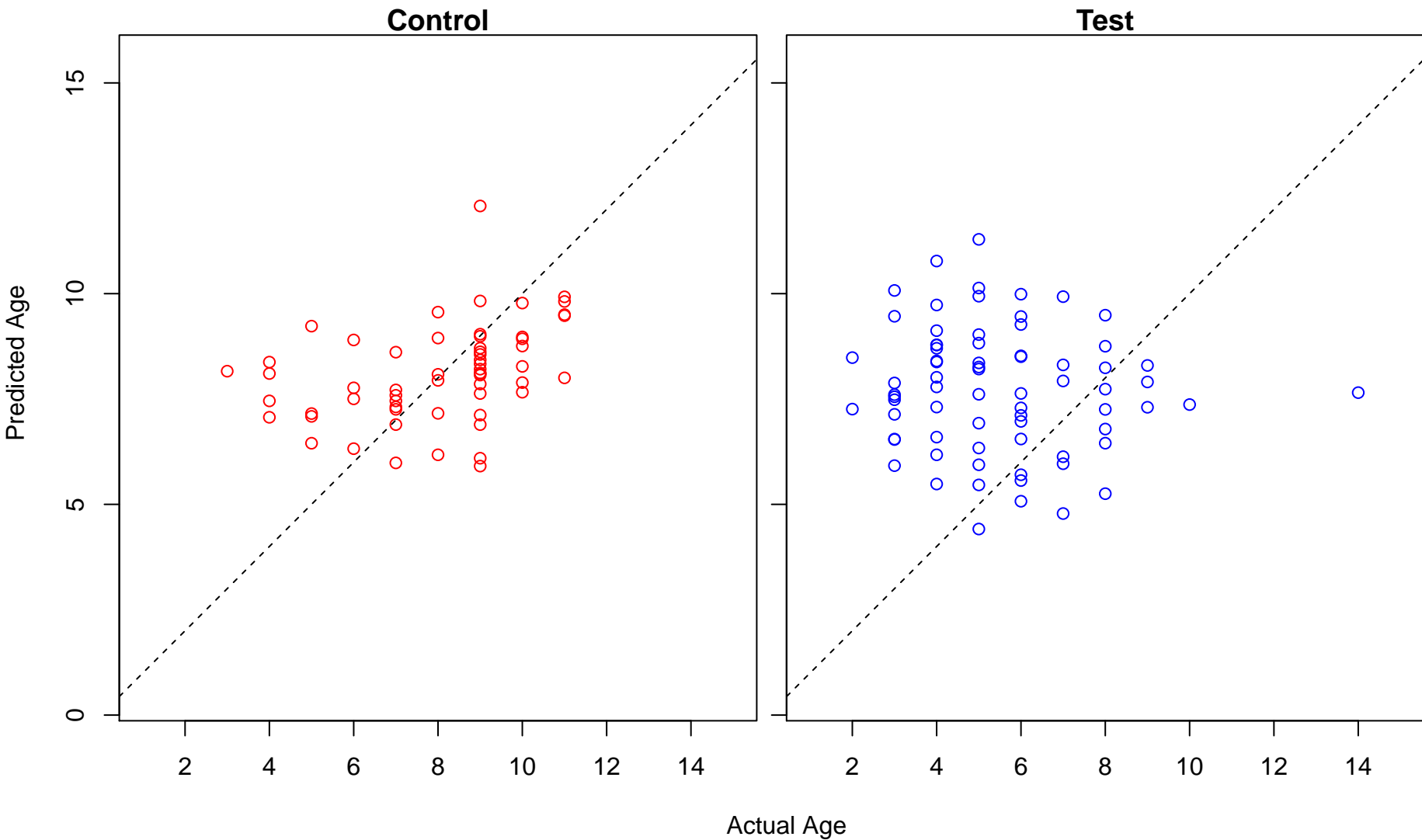
innate immune response-activating signal transduction (Score: 1.067489)



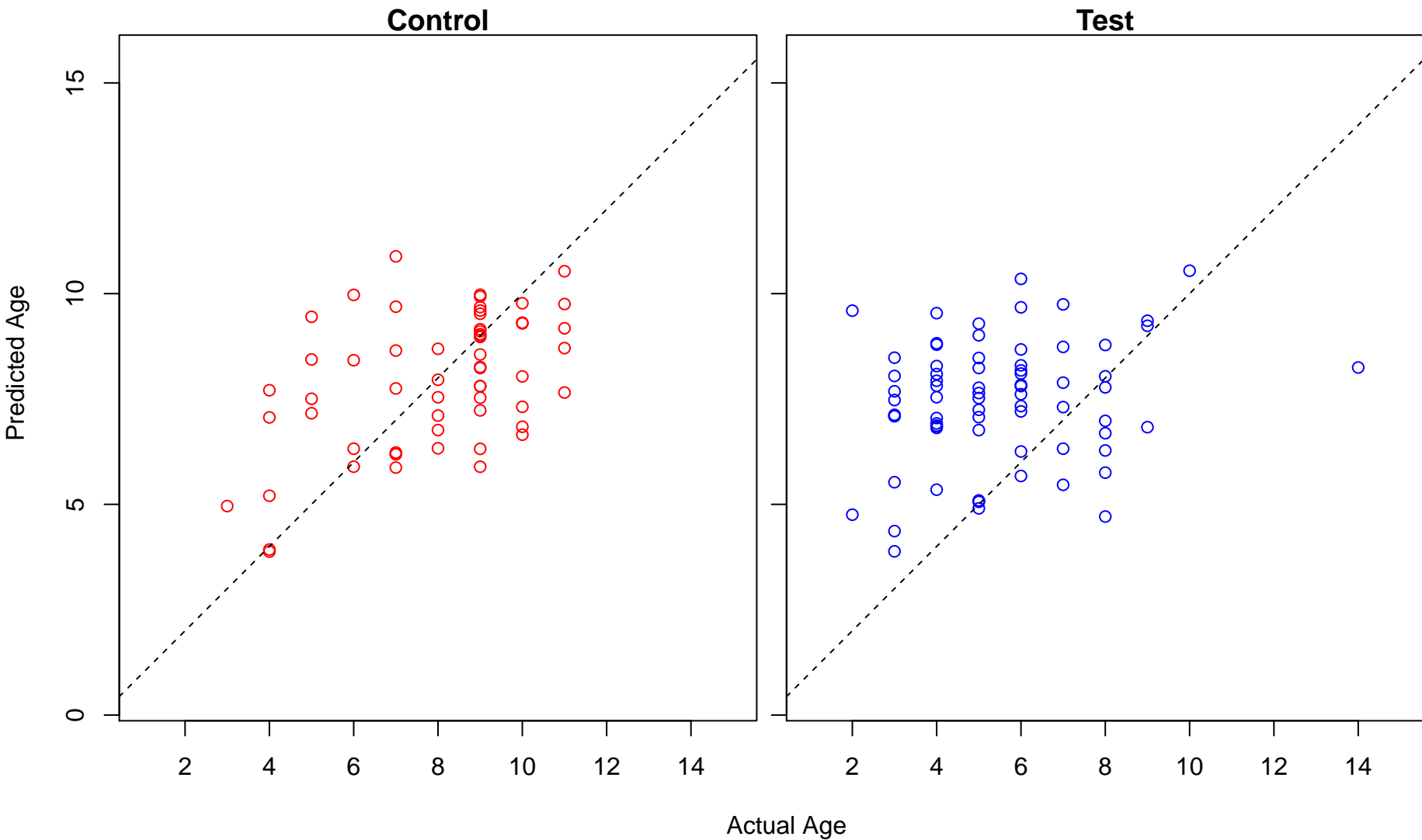
cell communication (Score: 1.066893)



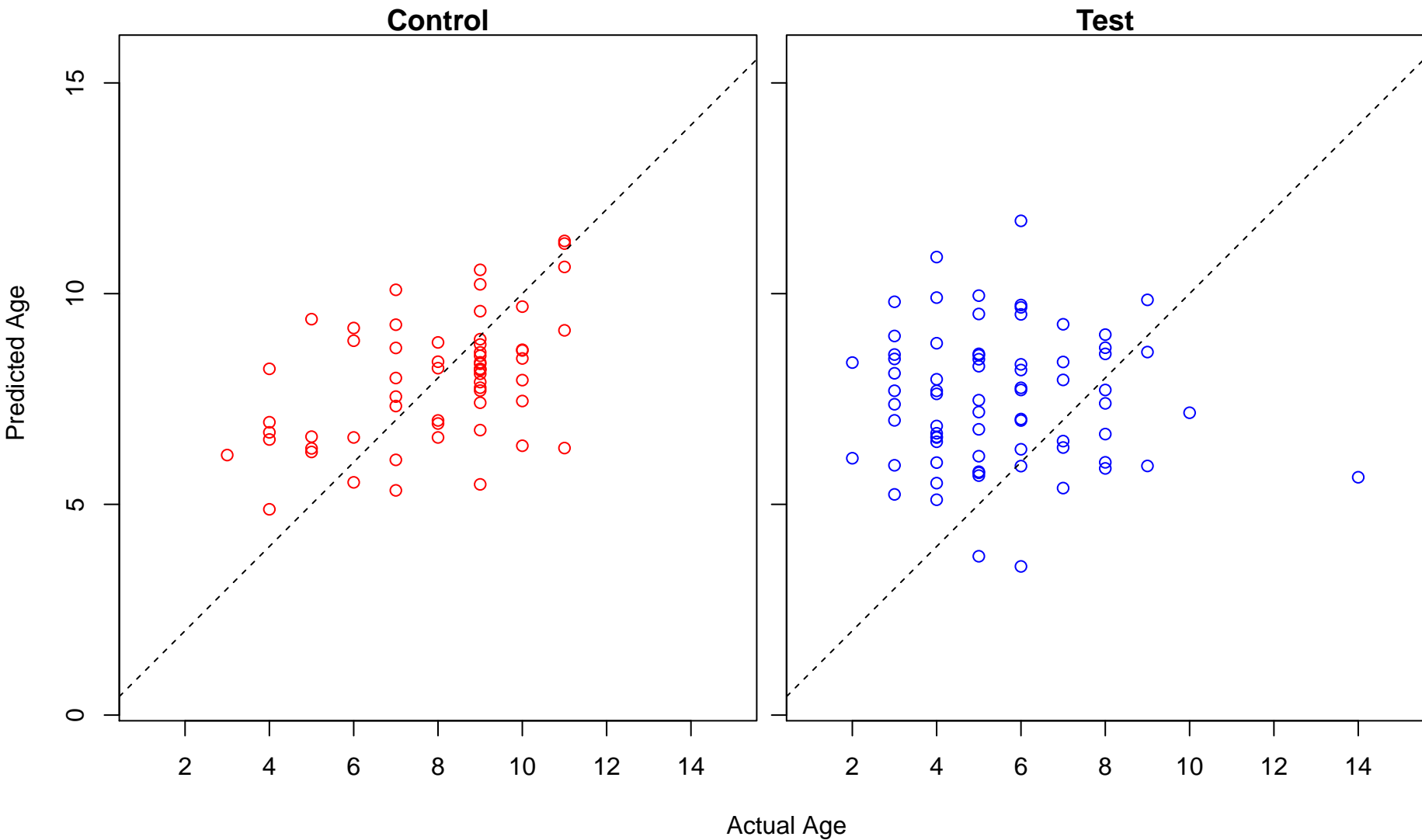
regulation of dopamine secretion (Score: 1.066751)



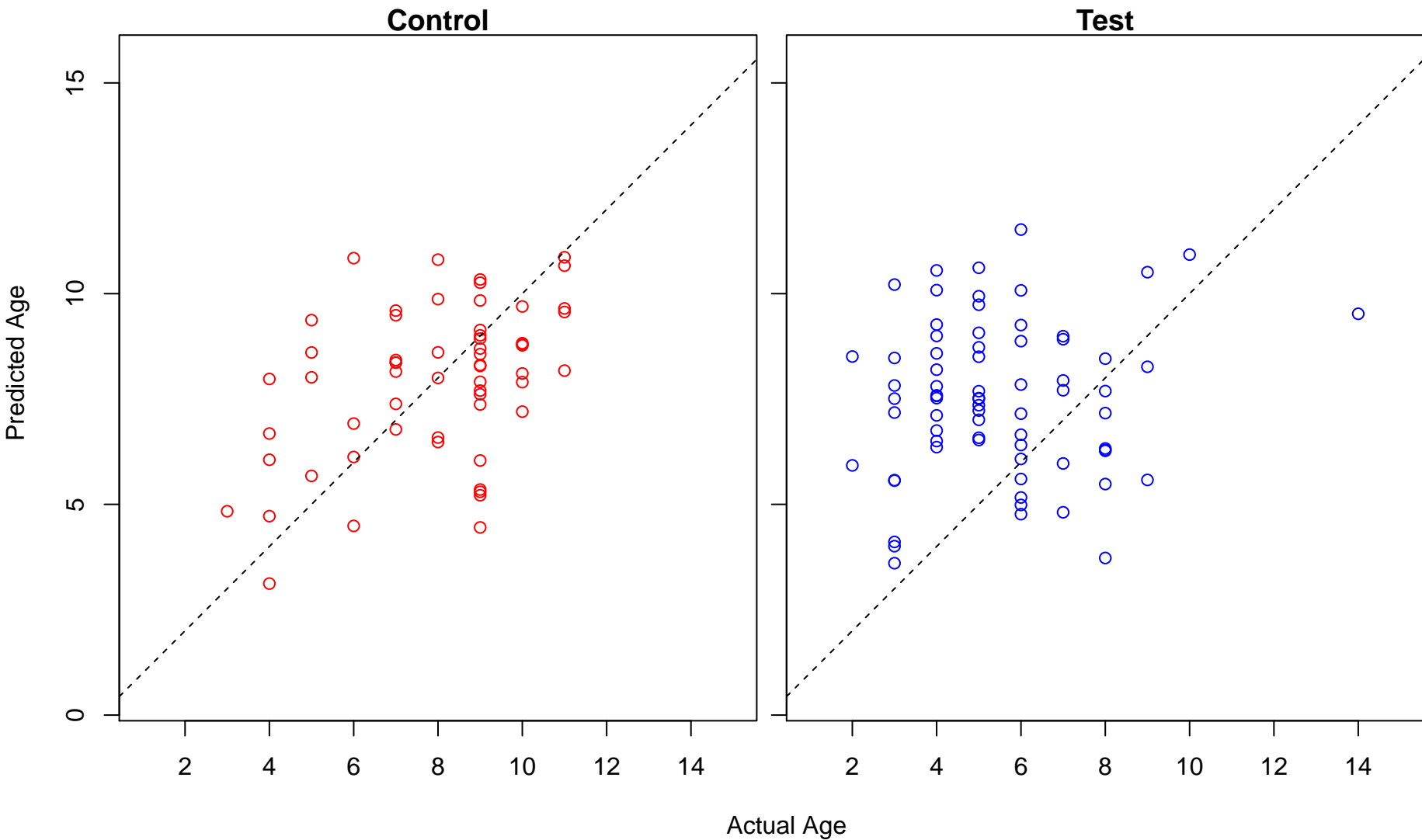
chromosome organization (Score: 1.066581)



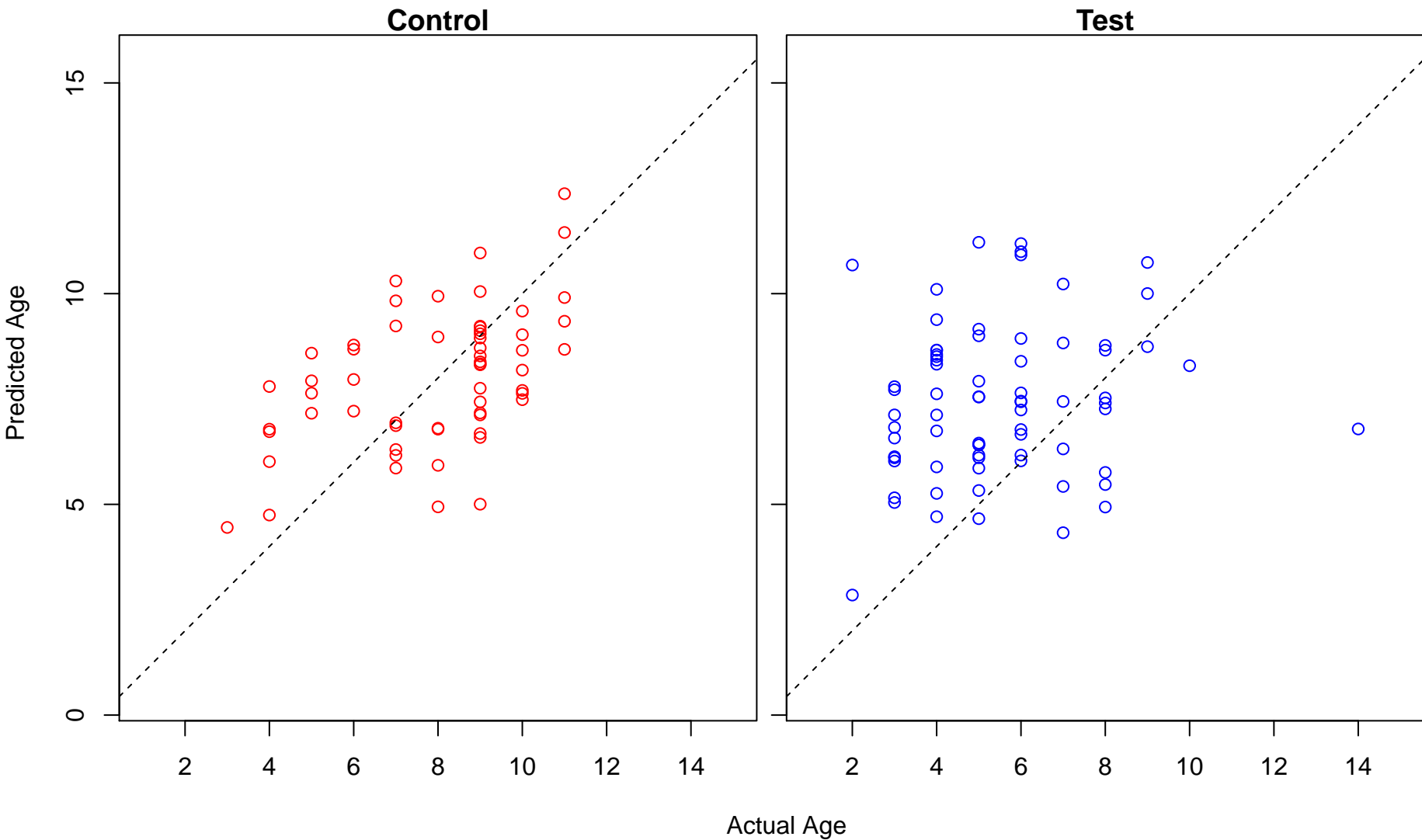
muscle system process (Score: 1.066244)



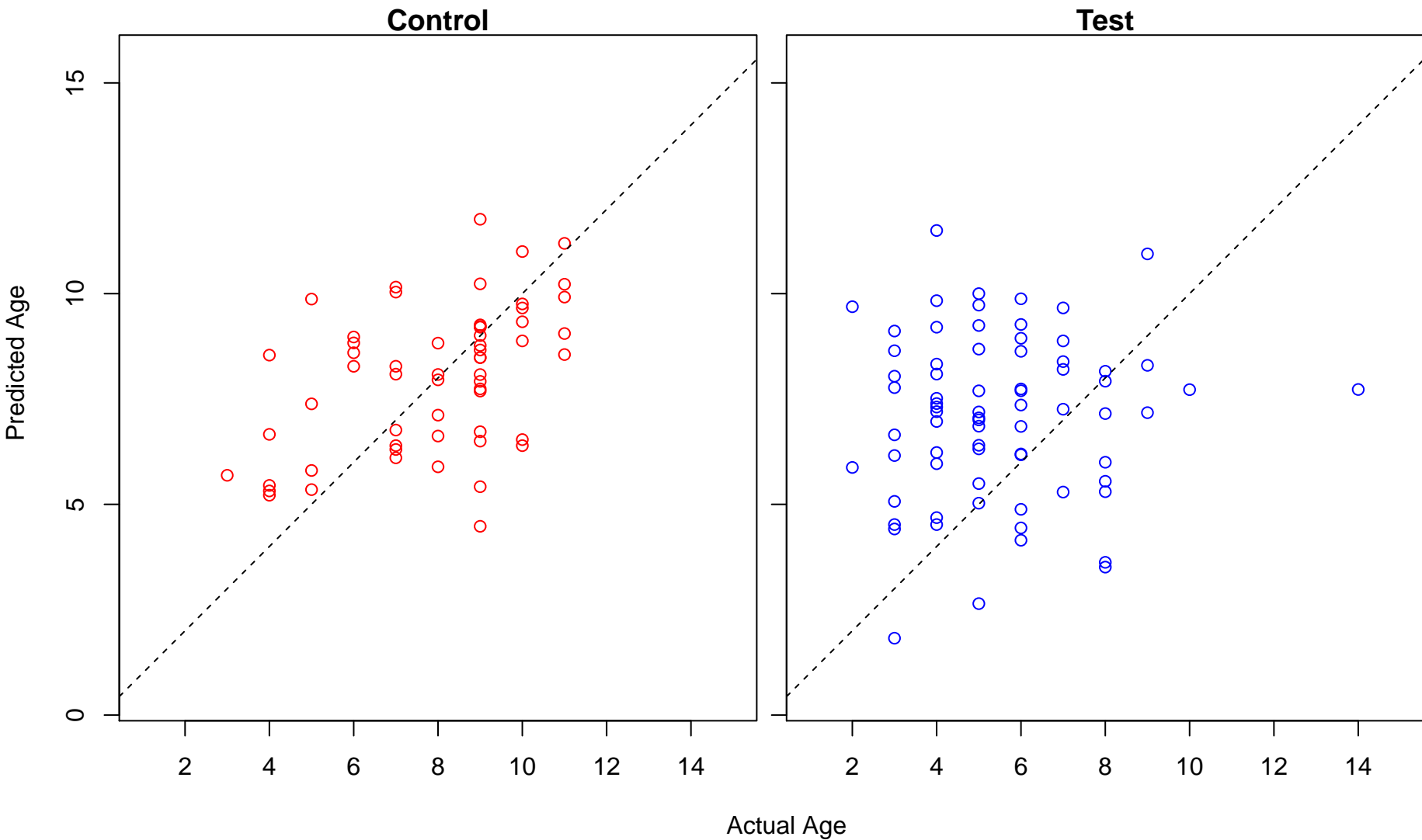
histone deacetylation (Score: 1.065746)



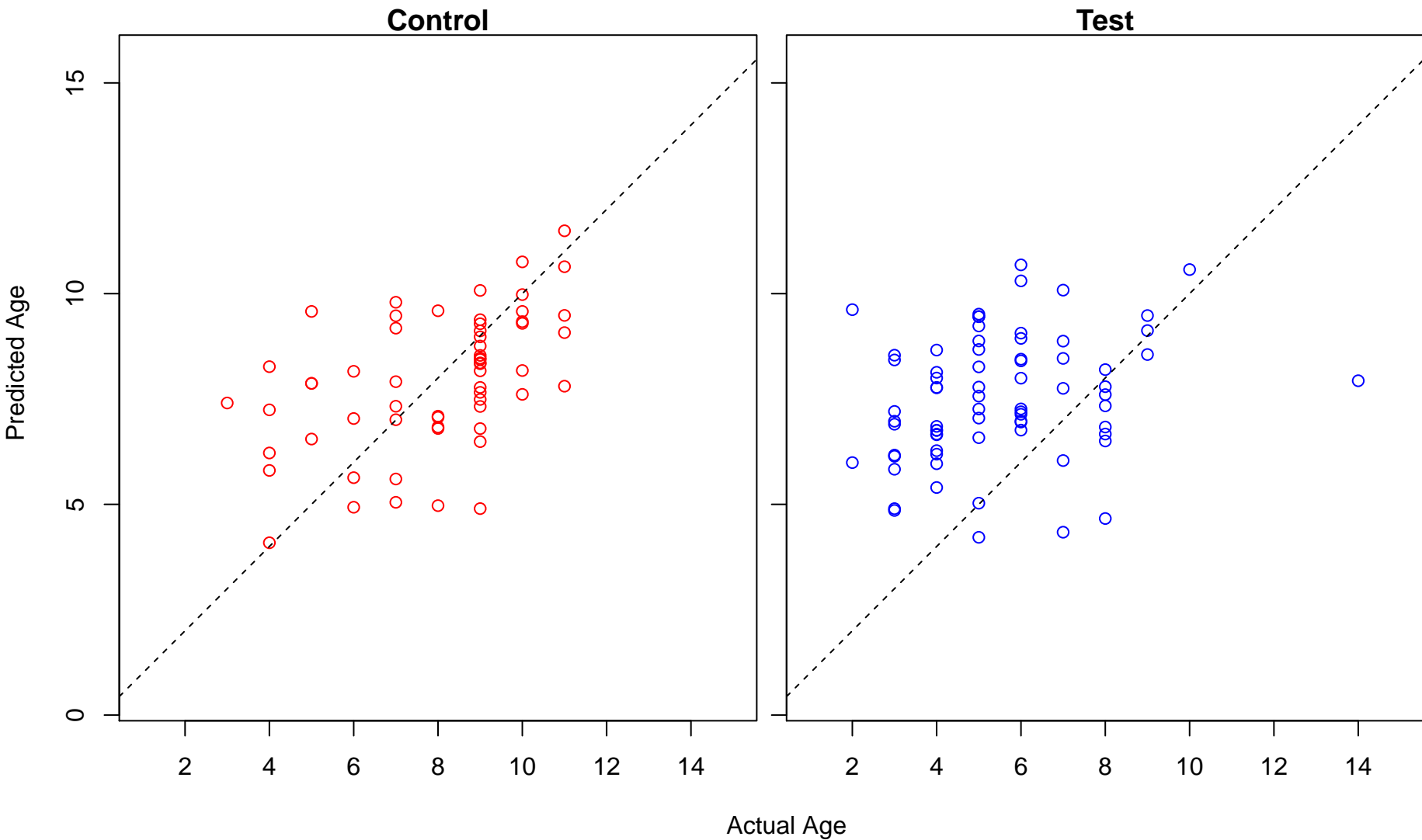
regulation of response to stress (Score: 1.064504)



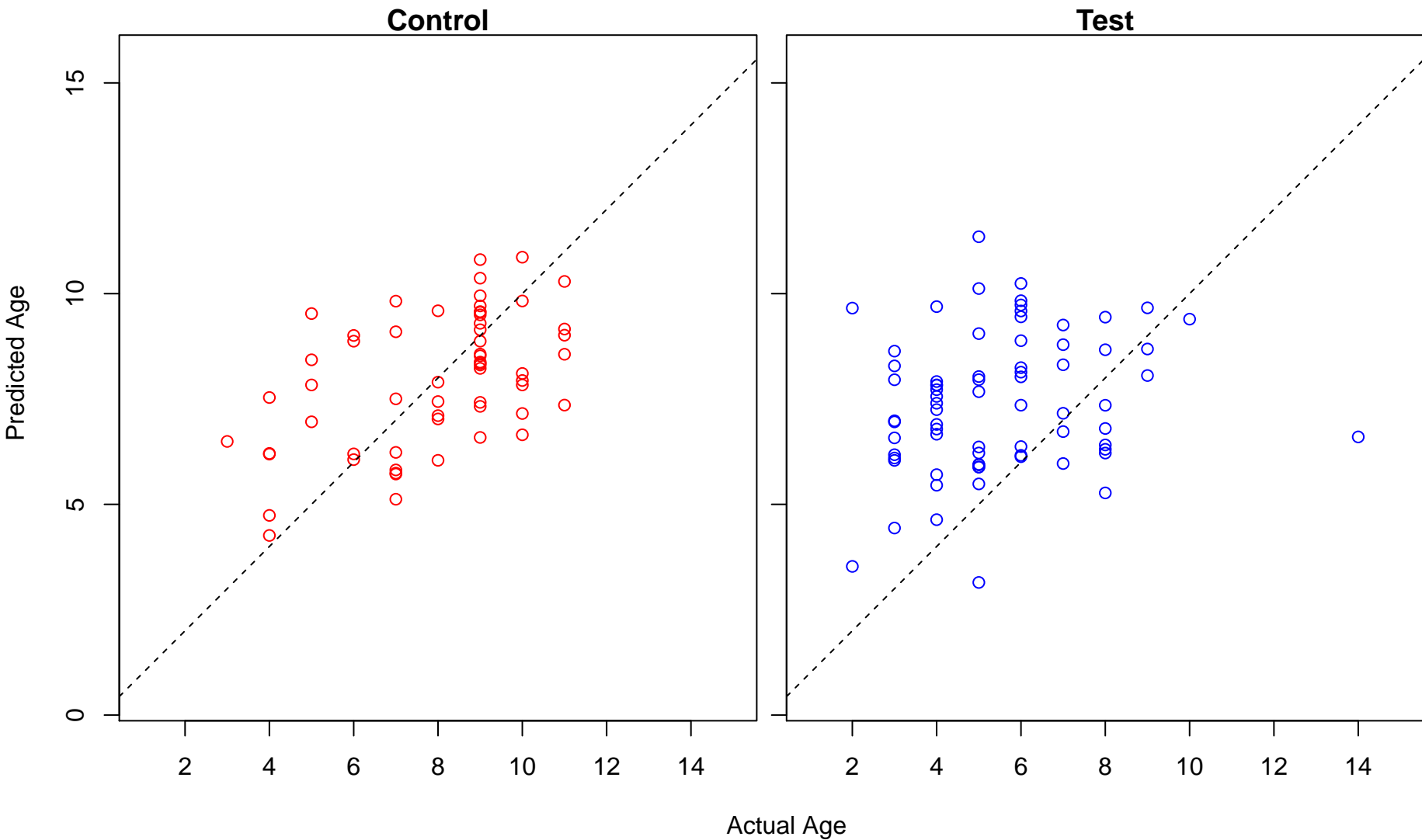
T cell mediated immunity (Score: 1.063788)



RNA metabolic process (Score: 1.063658)

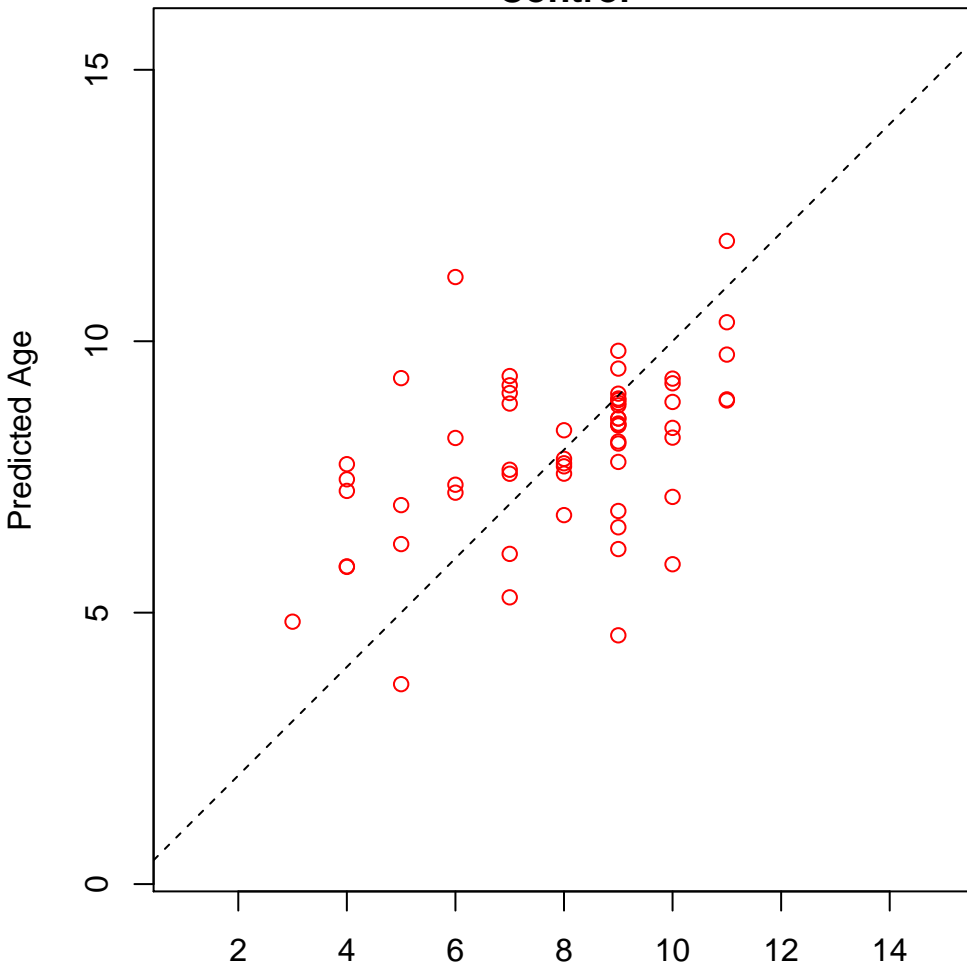


chondroitin sulfate proteoglycan metabolic process (Score: 1.063578)

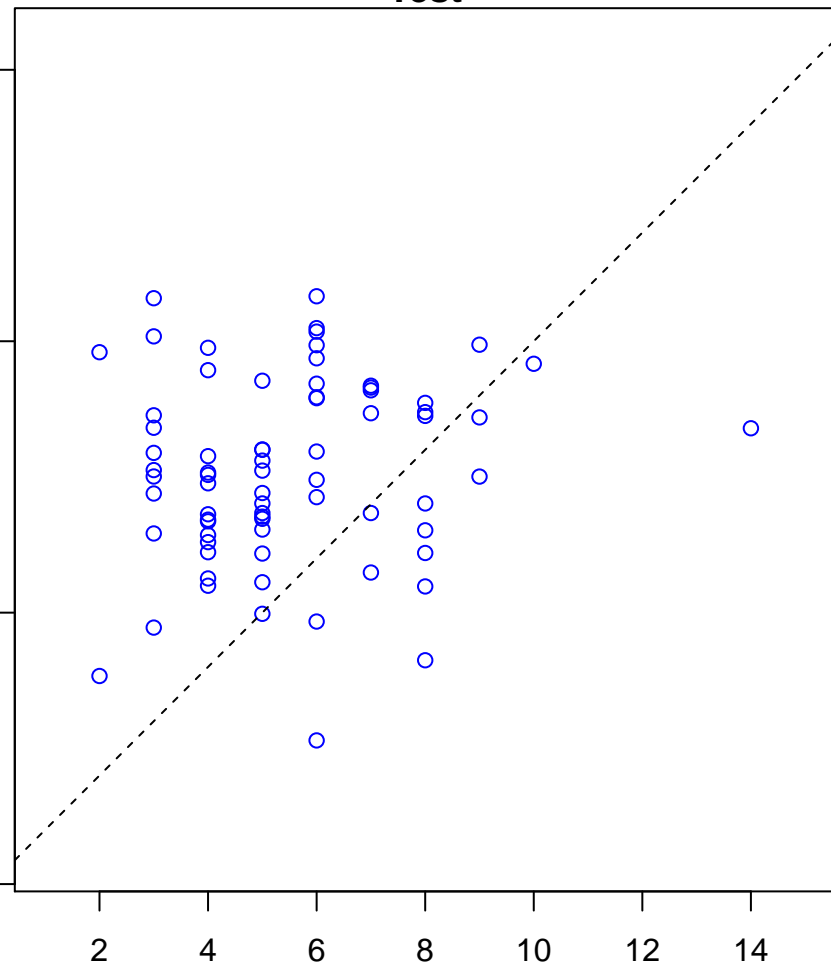


phosphatidylglycerol metabolic process (Score: 1.063549)

Control

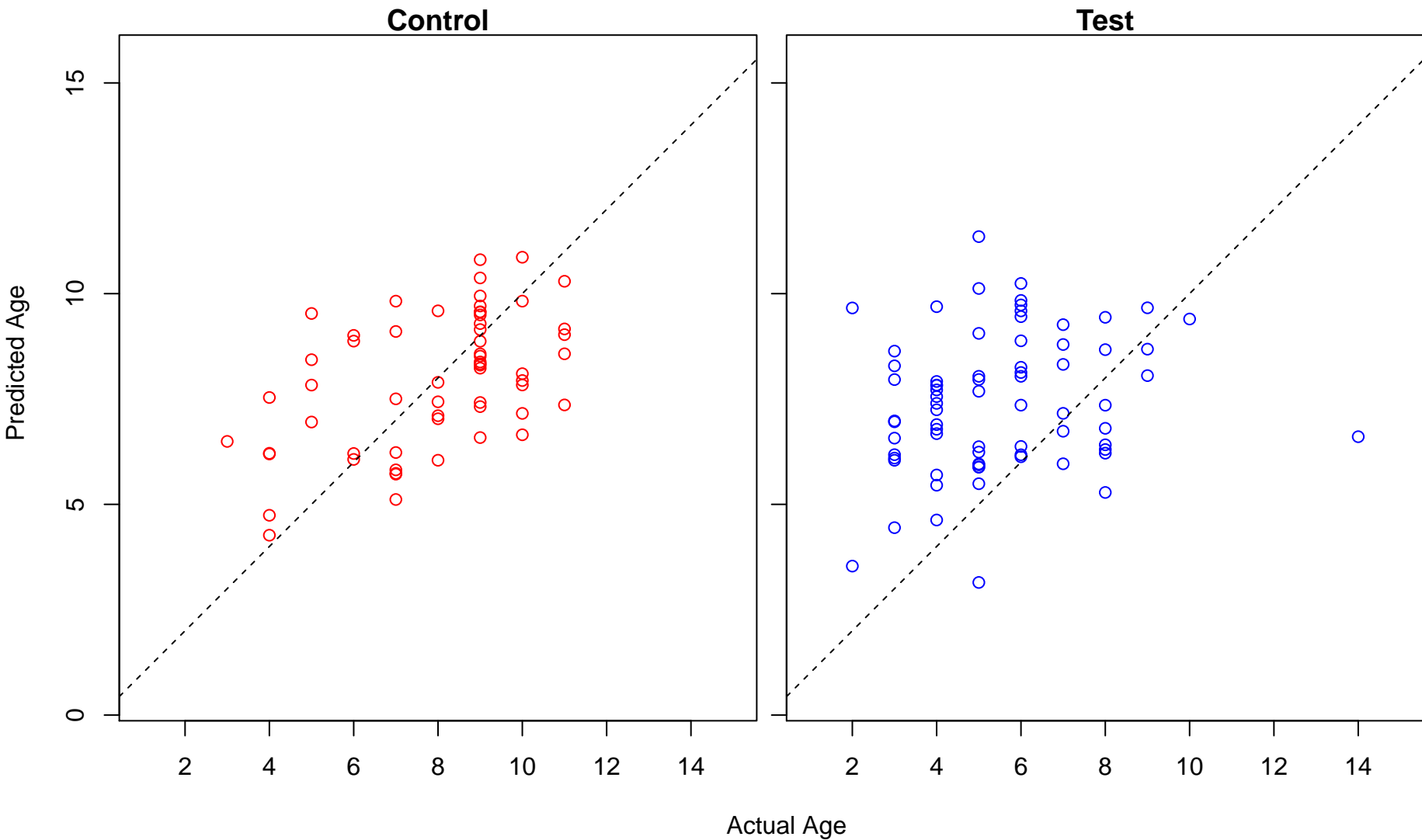


Test

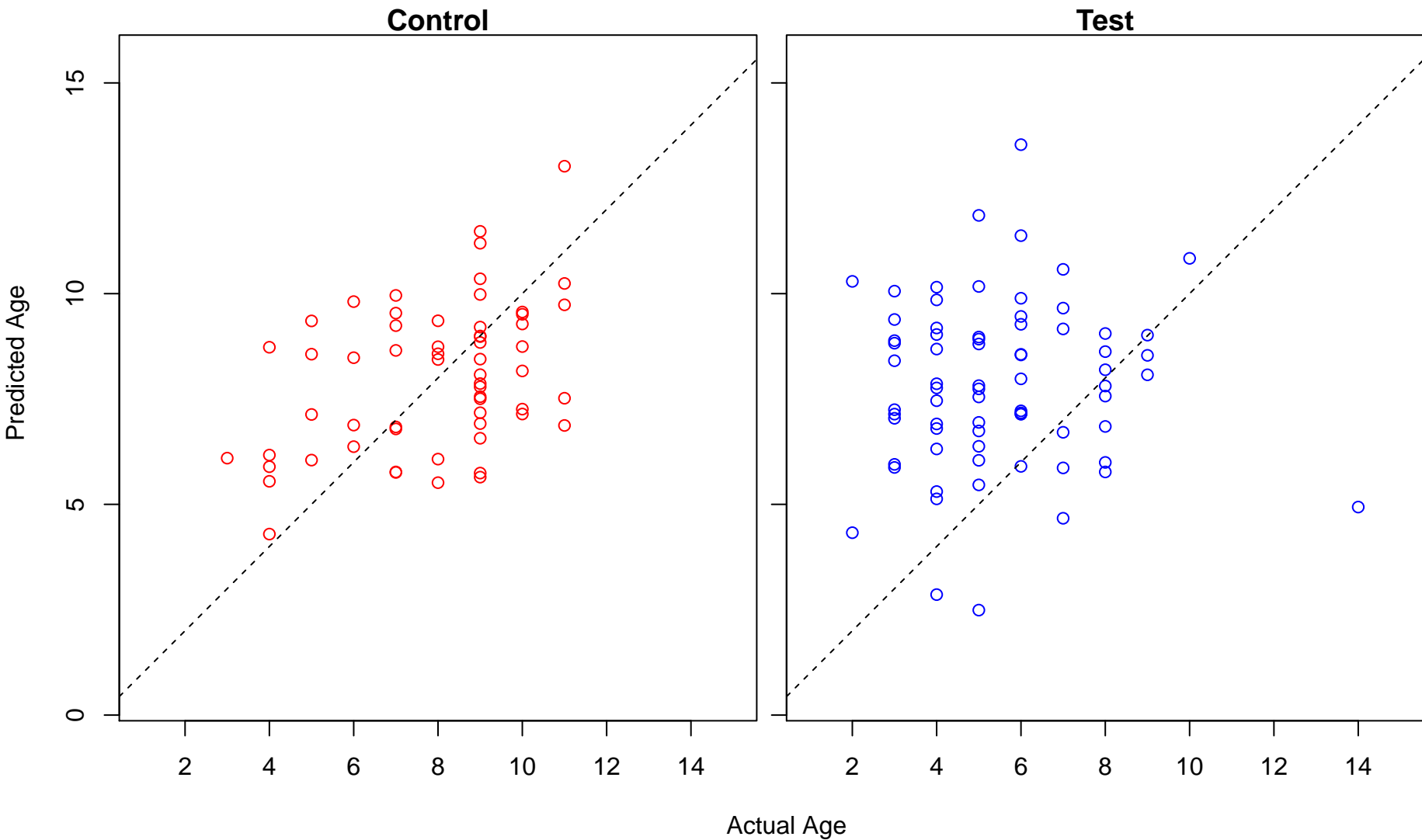


Actual Age

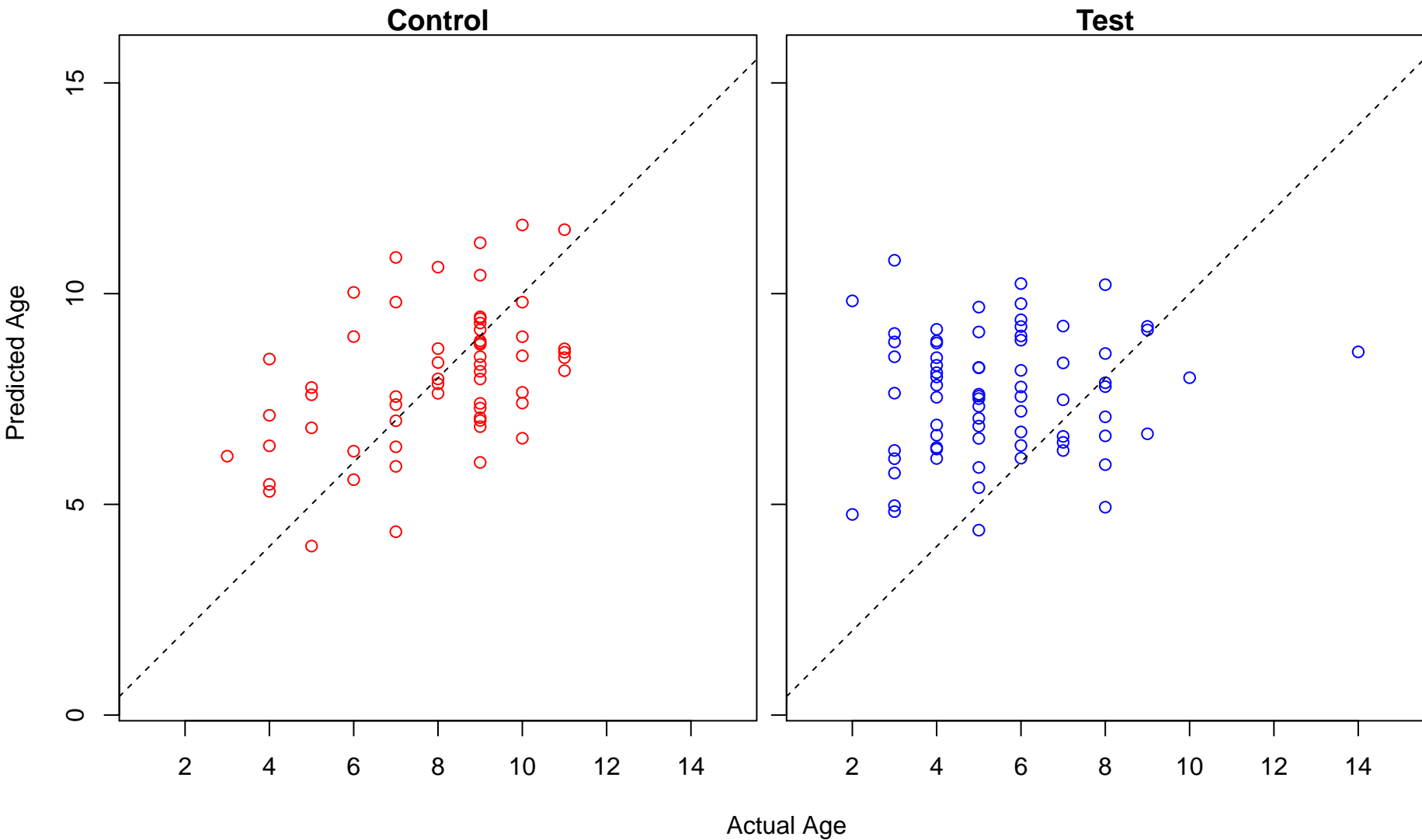
chondroitin sulfate metabolic process (Score: 1.063548)



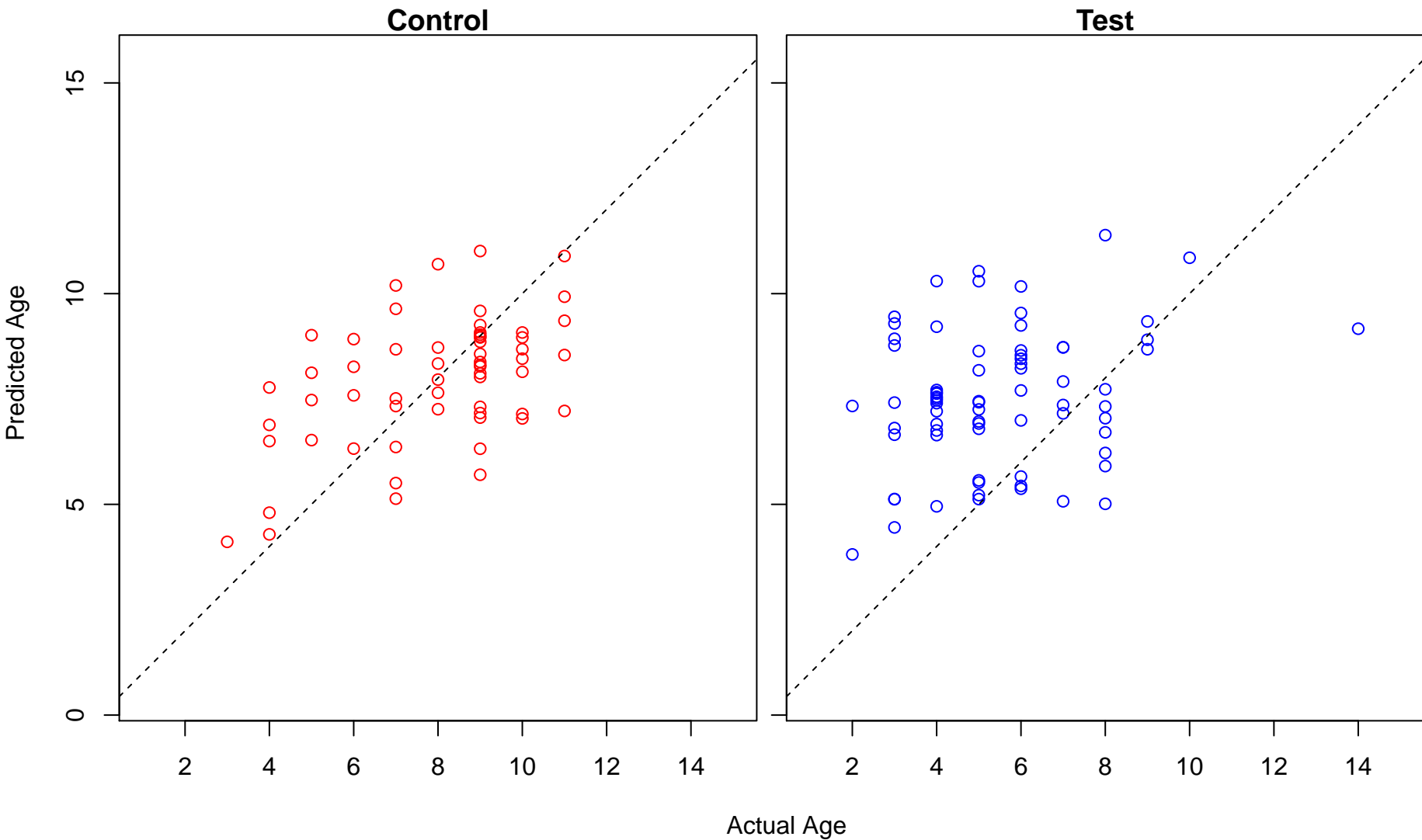
negative regulation of protein kinase activity (Score: 1.062075)



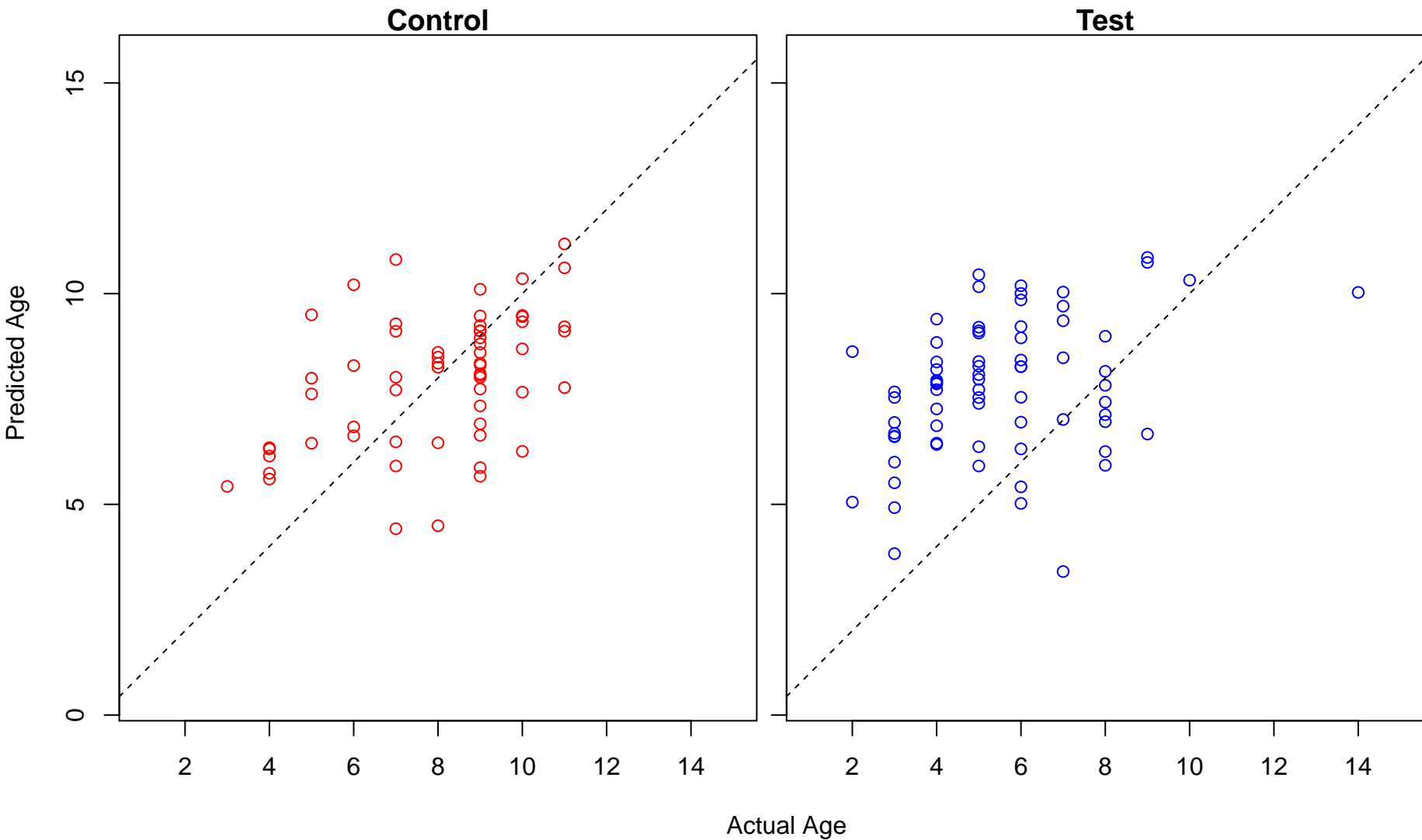
hormone transport (Score: 1.062046)



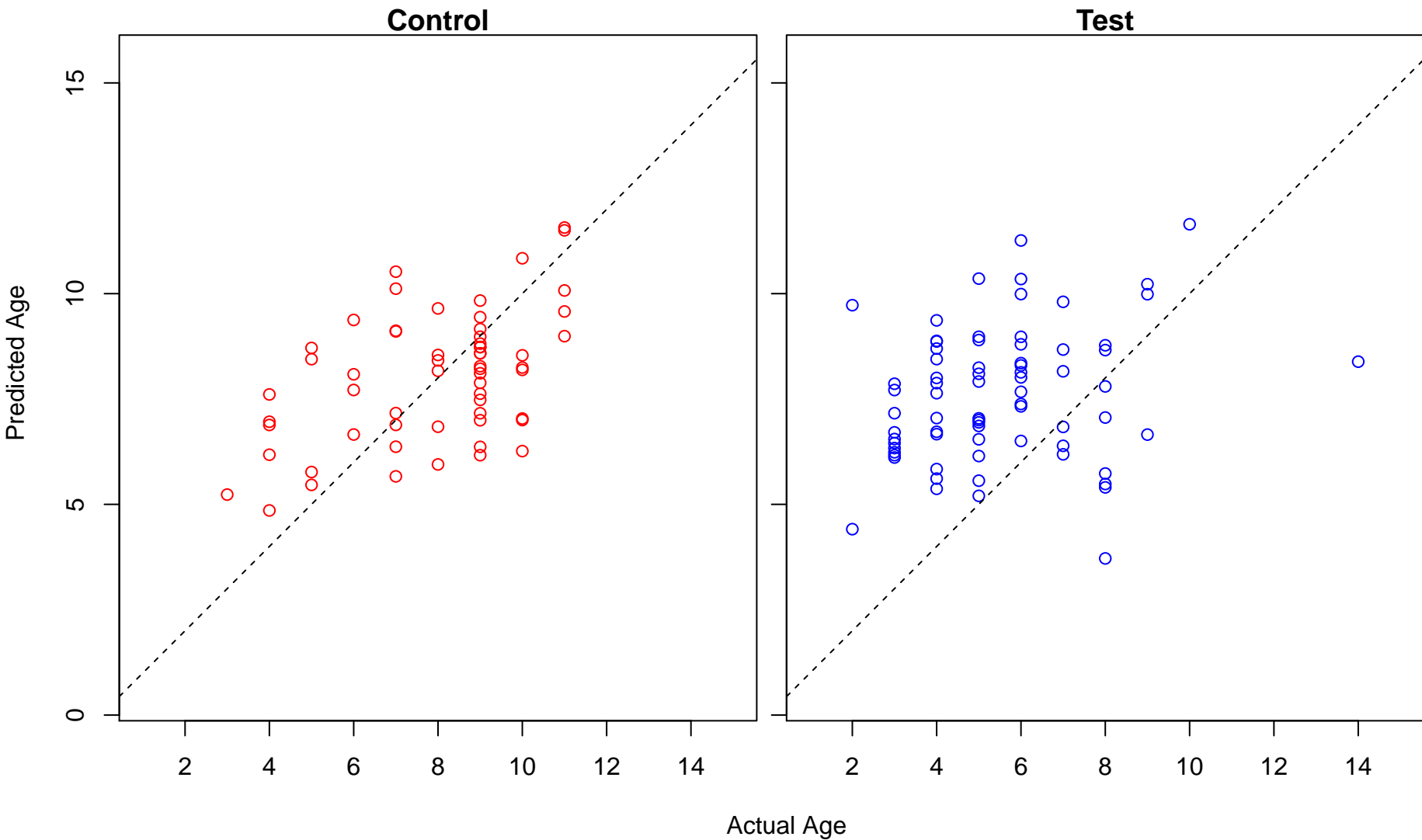
negative thymic T cell selection (Score: 1.061427)



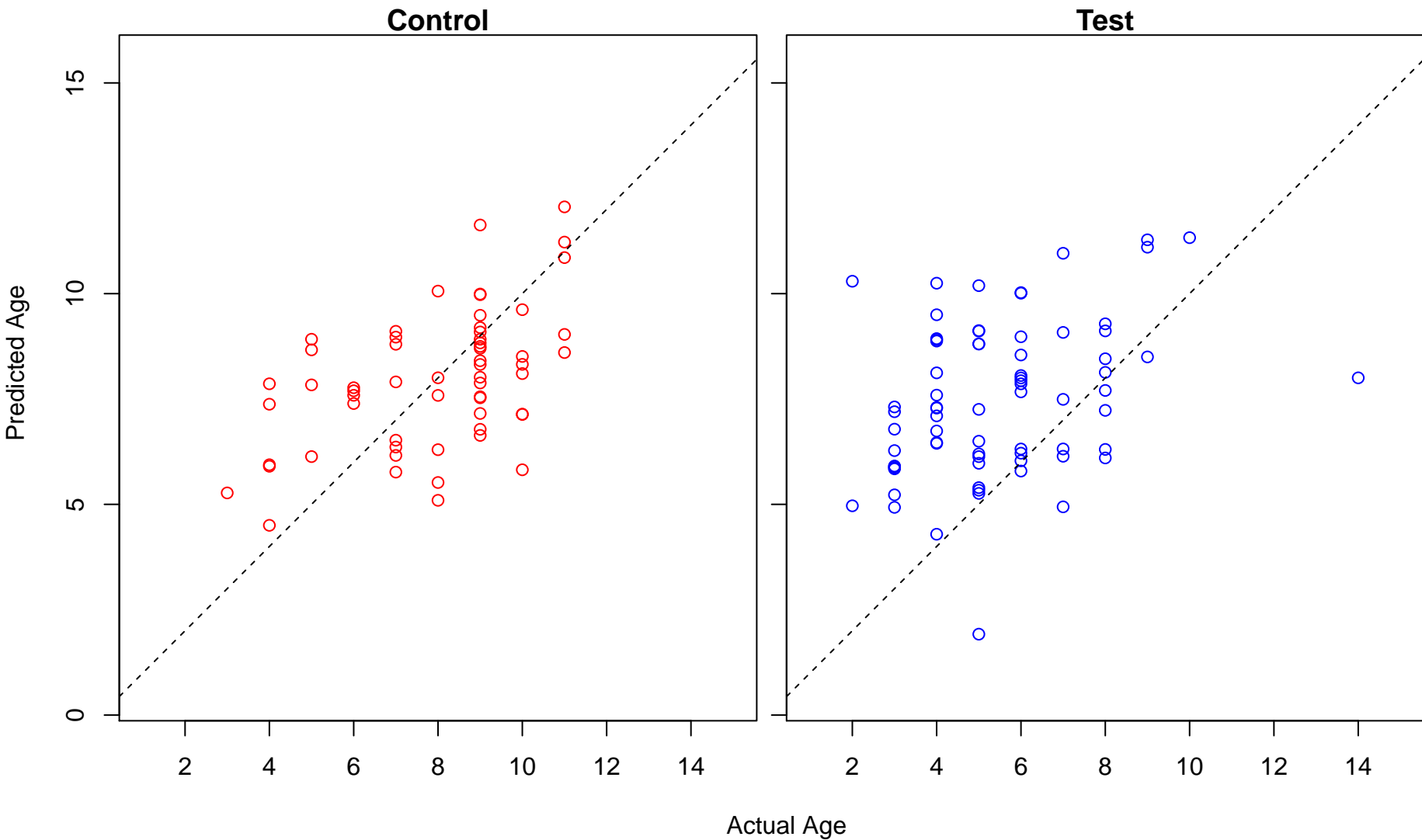
histone acetylation (Score: 1.060682)



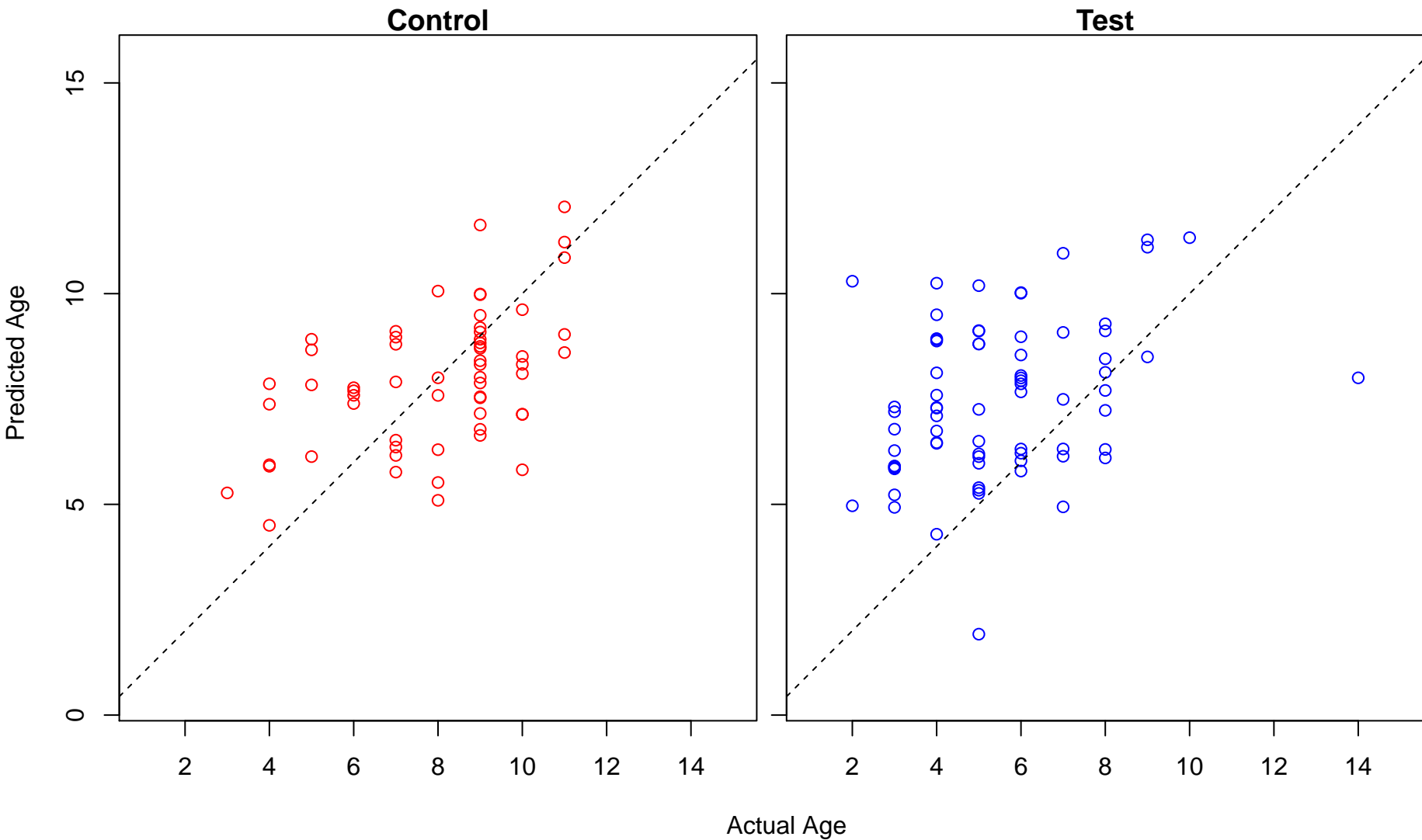
regulation of cellular response to stress (Score: 1.060659)



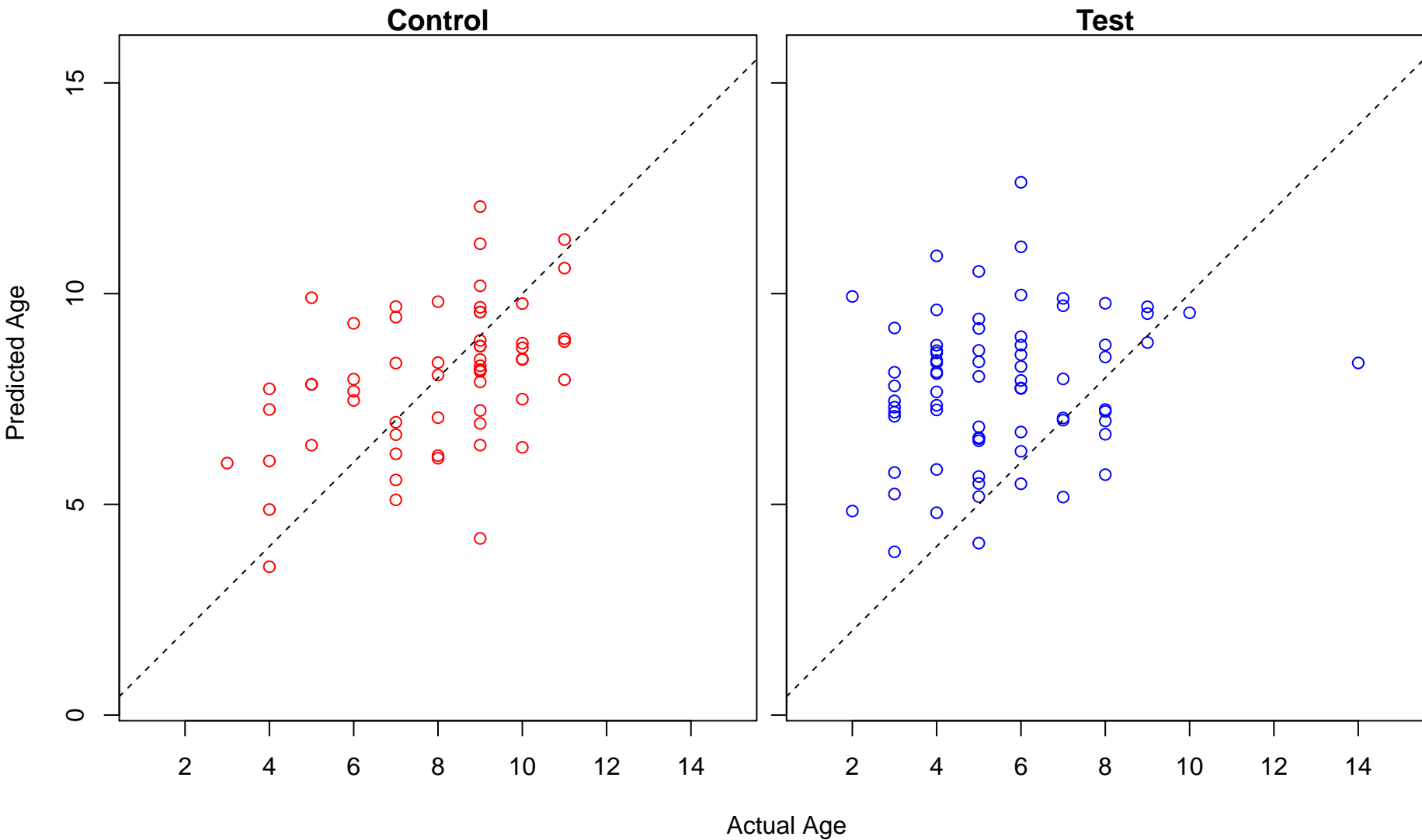
signaling (Score: 1.060380)



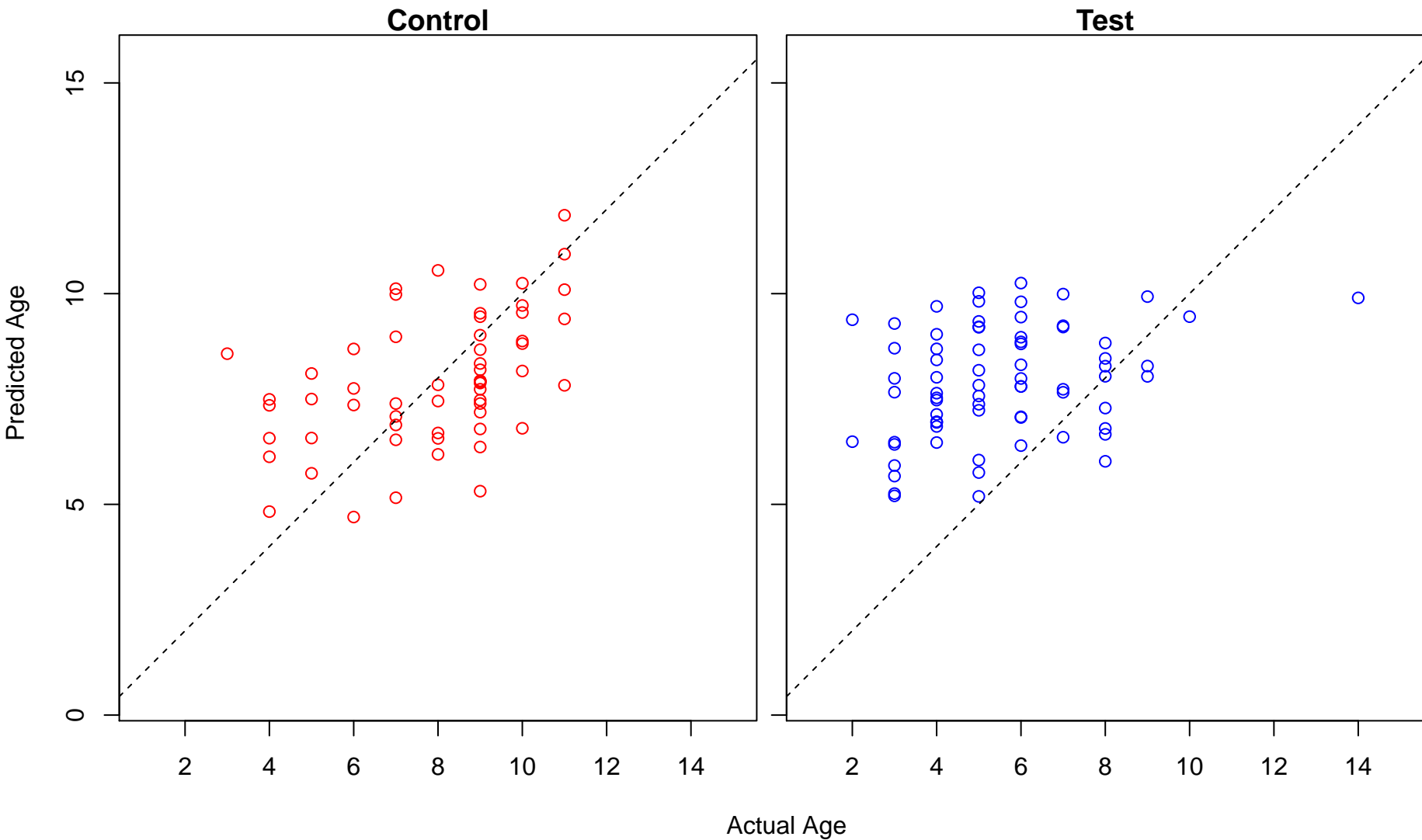
single organism signaling (Score: 1.060380)



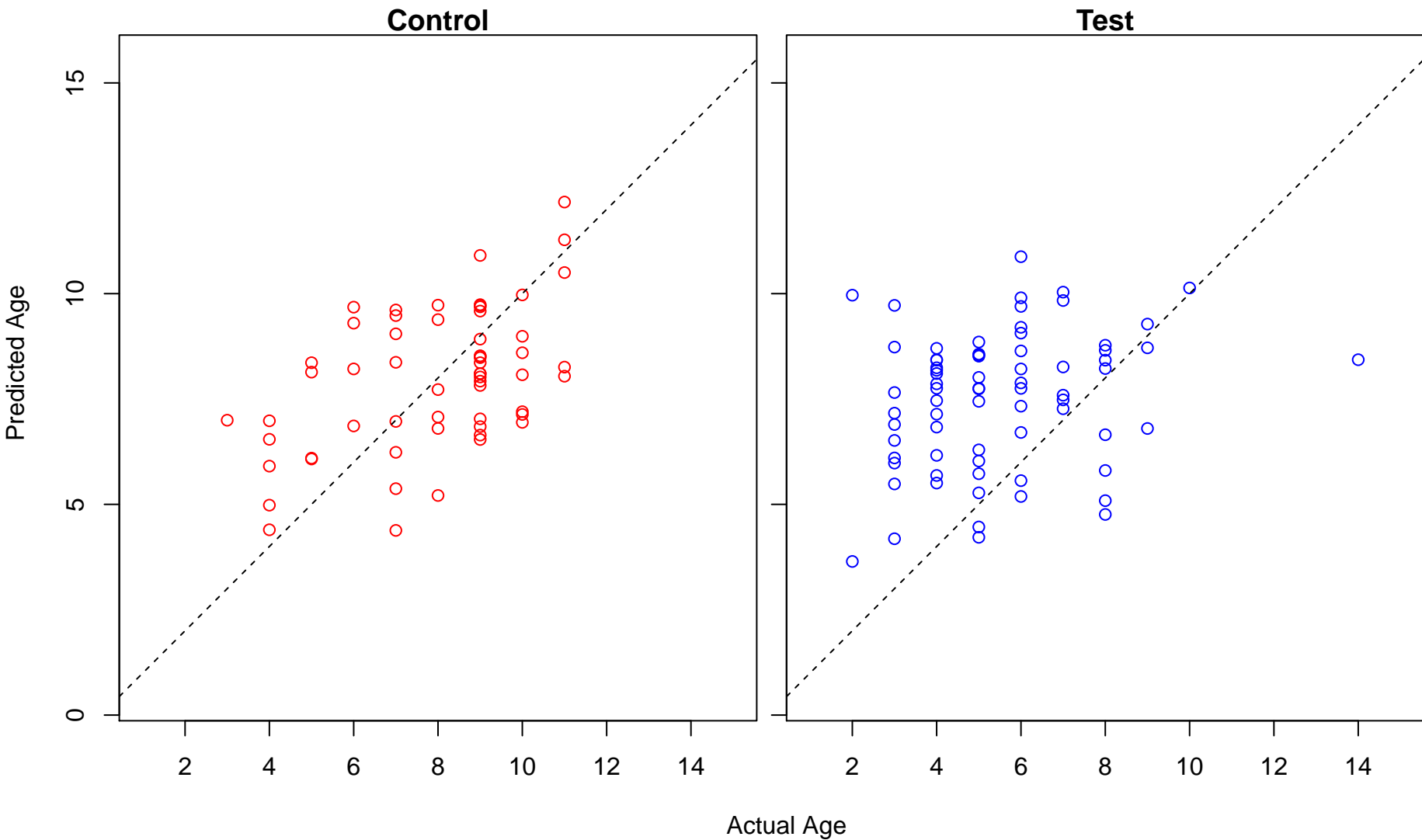
cell projection organization (Score: 1.059901)



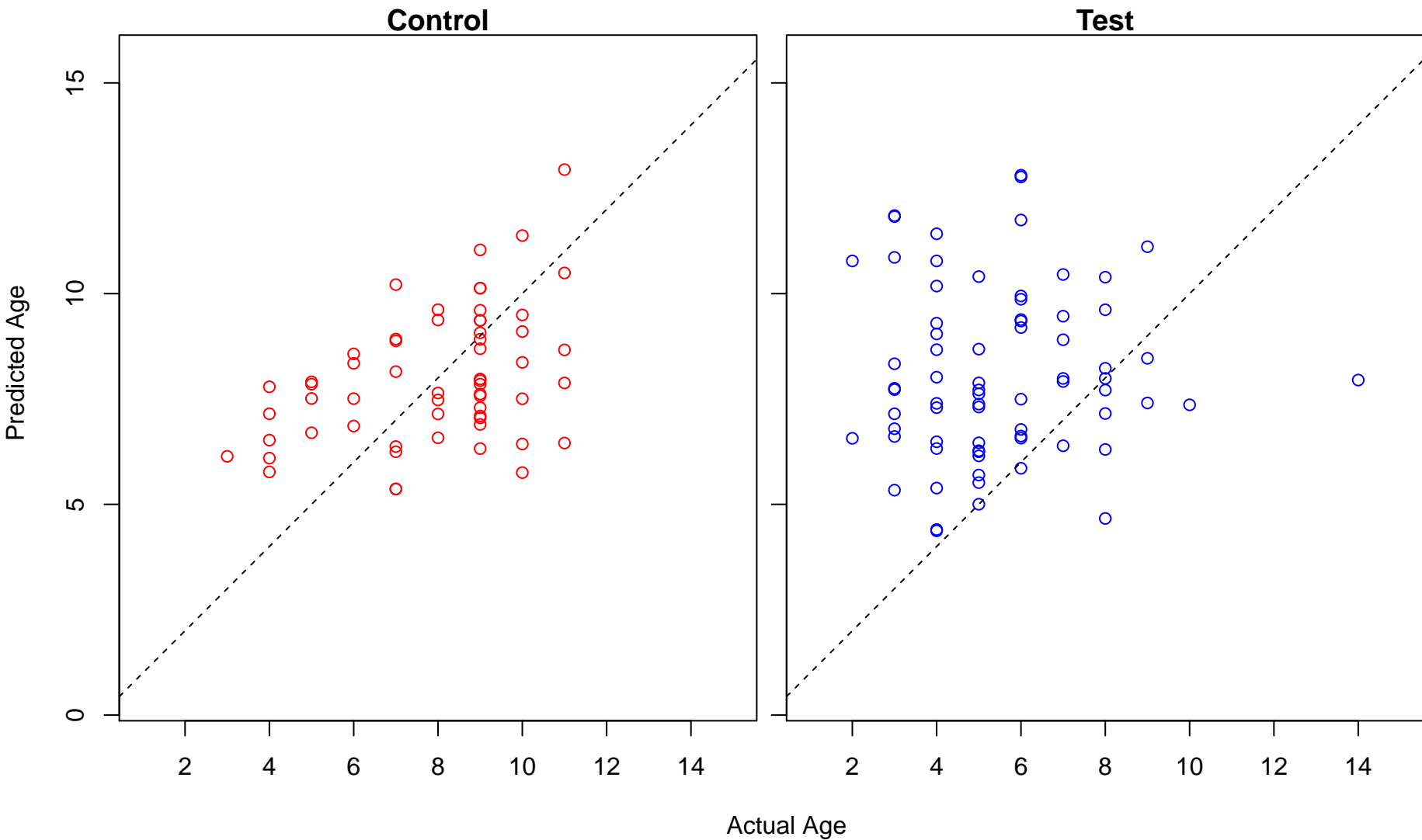
carboxylic acid metabolic process (Score: 1.059000)



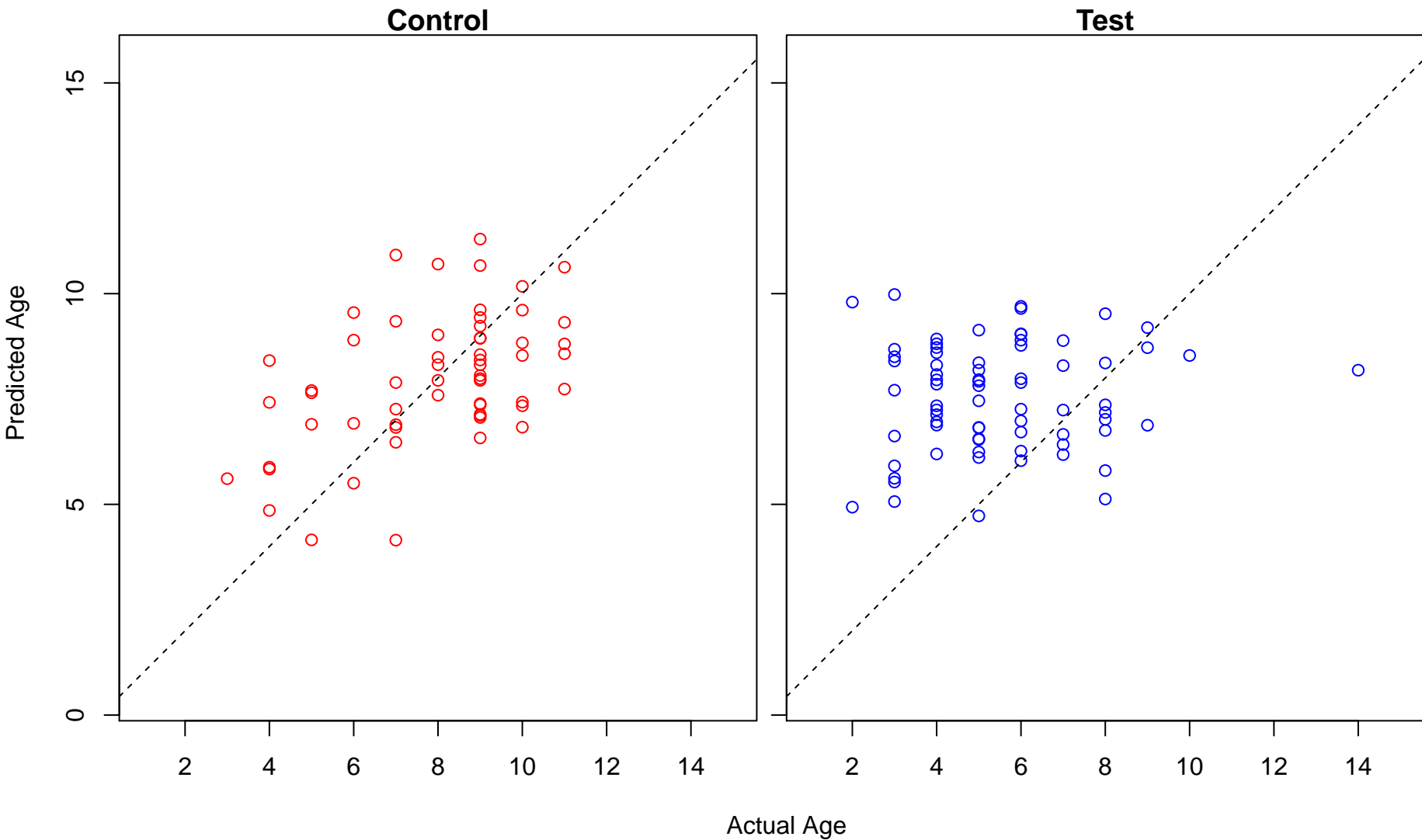
positive regulation of cell morphogenesis involved in differentiation (Score: 1.058512)



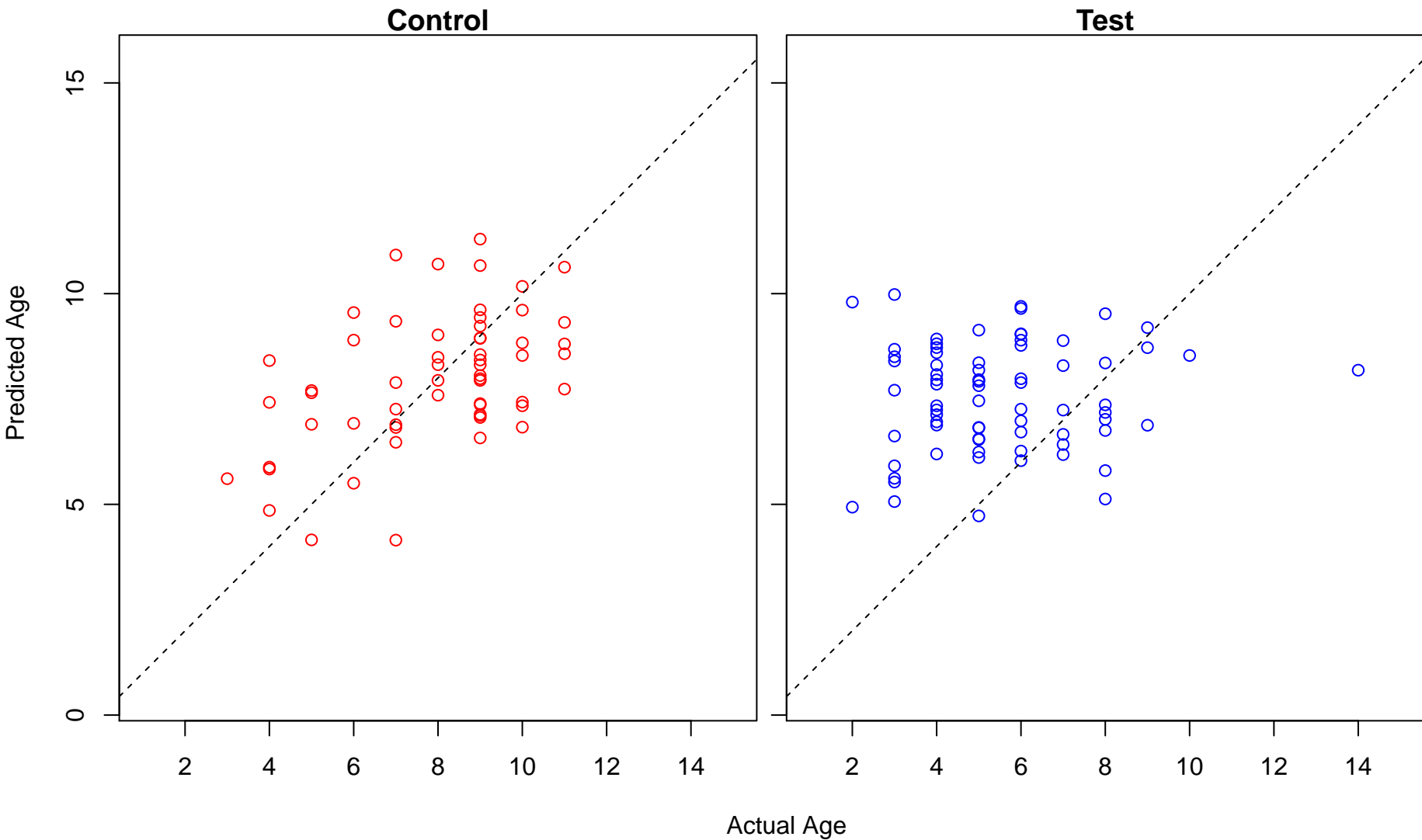
lens development in camera-type eye (Score: 1.058096)



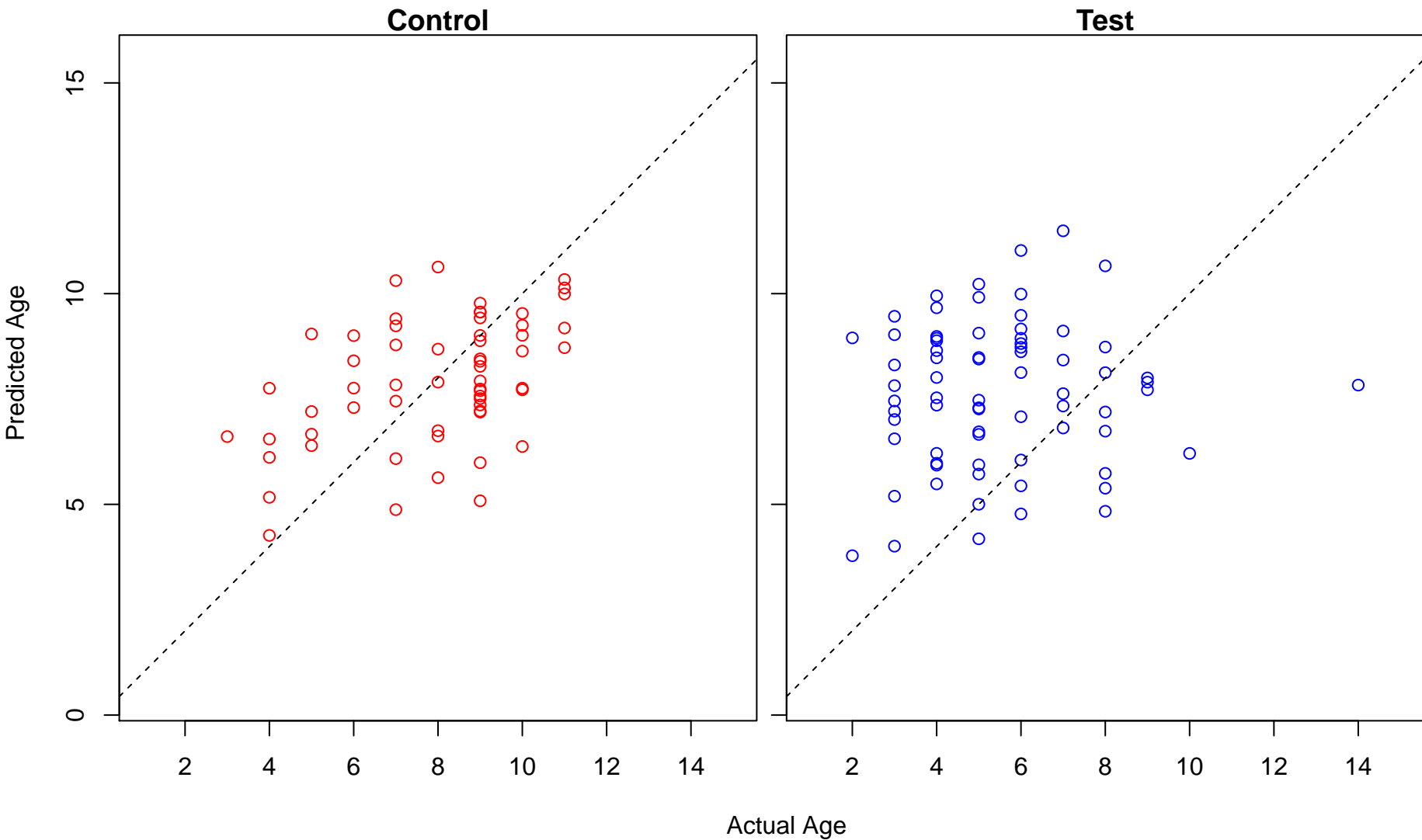
peptide secretion (Score: 1.056546)



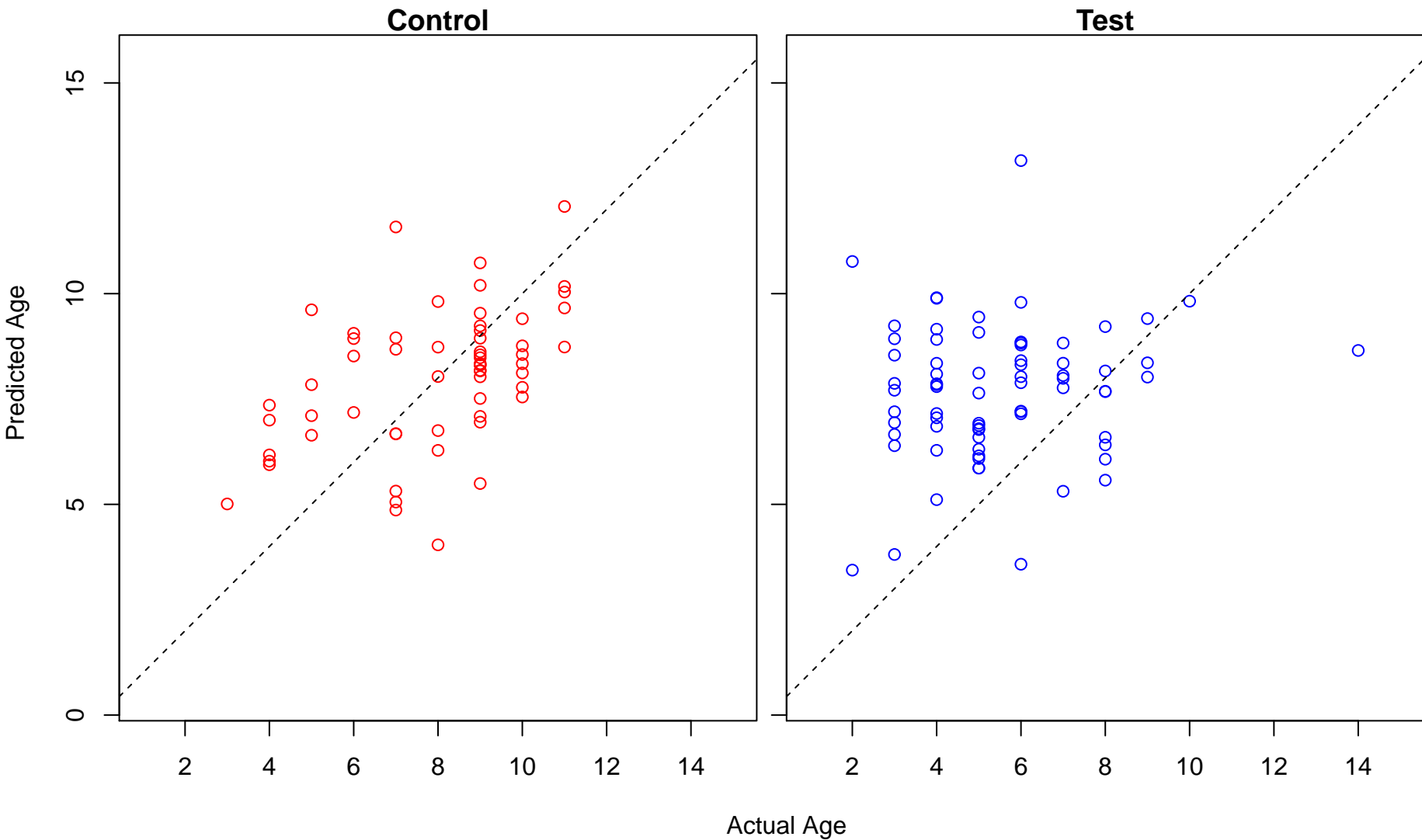
peptide hormone secretion (Score: 1.056546)



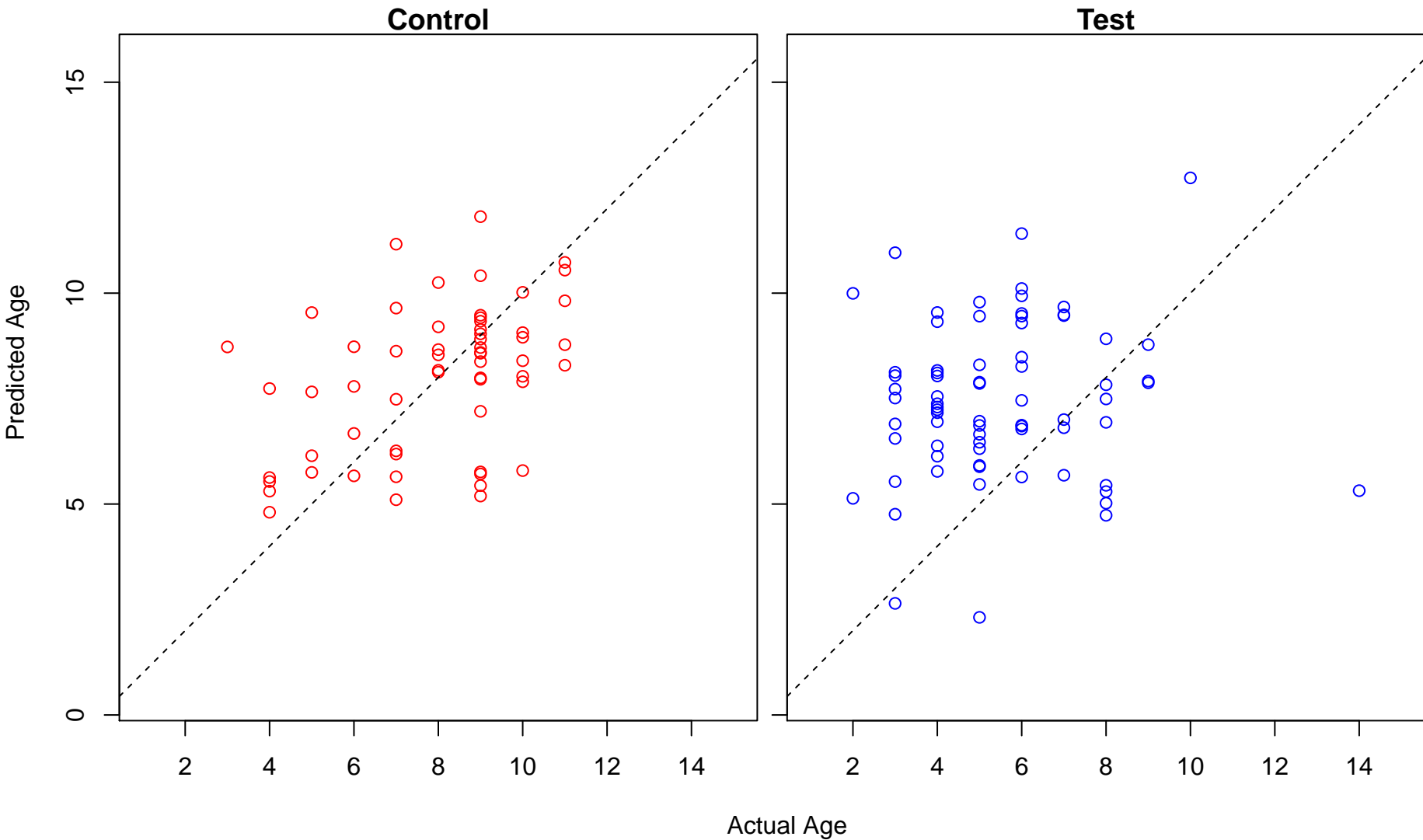
positive regulation of cyclin–dependent protein kinase activity (Score: 1.056145)



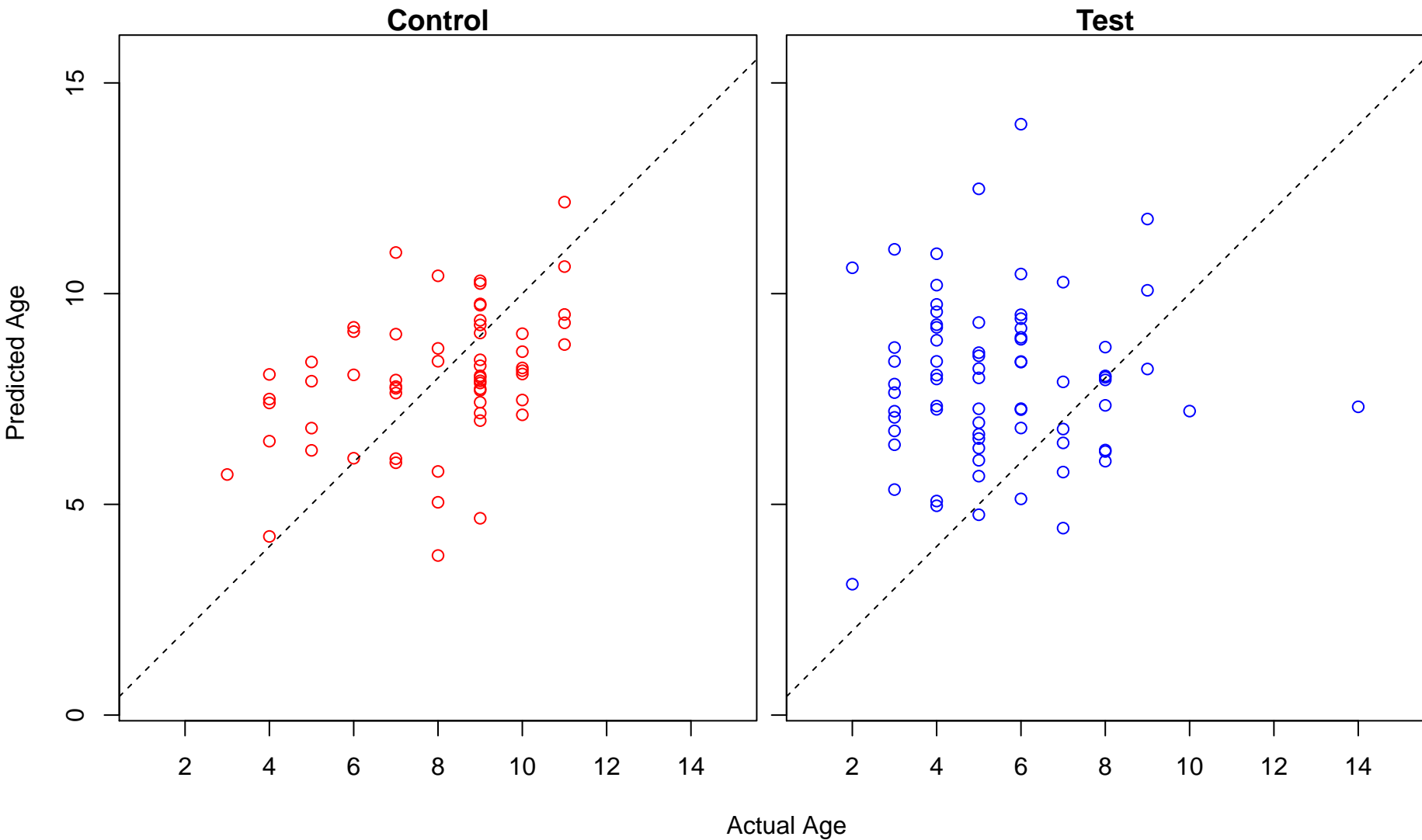
regulation of cellular localization (Score: 1.055809)



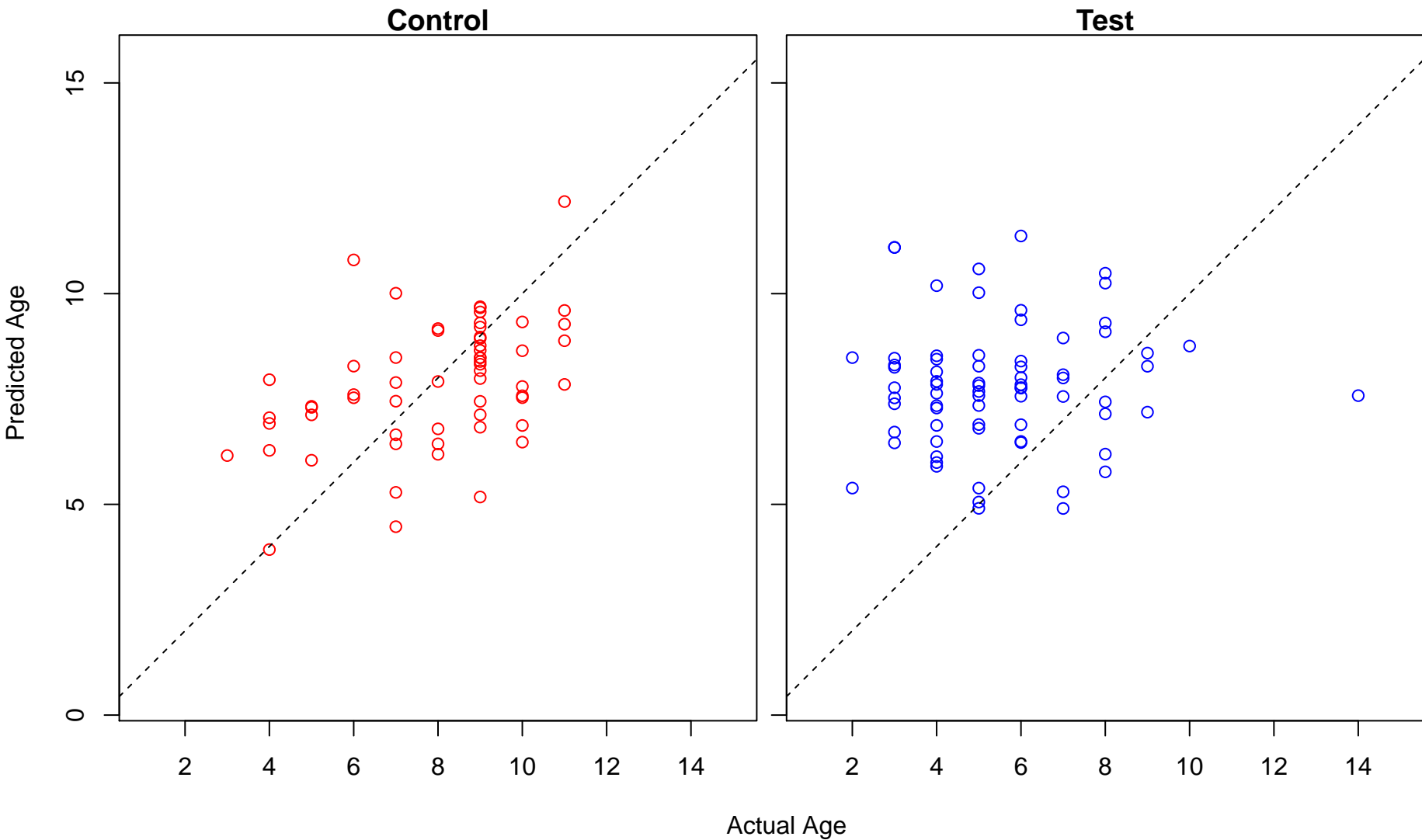
mitotic sister chromatid segregation (Score: 1.055536)



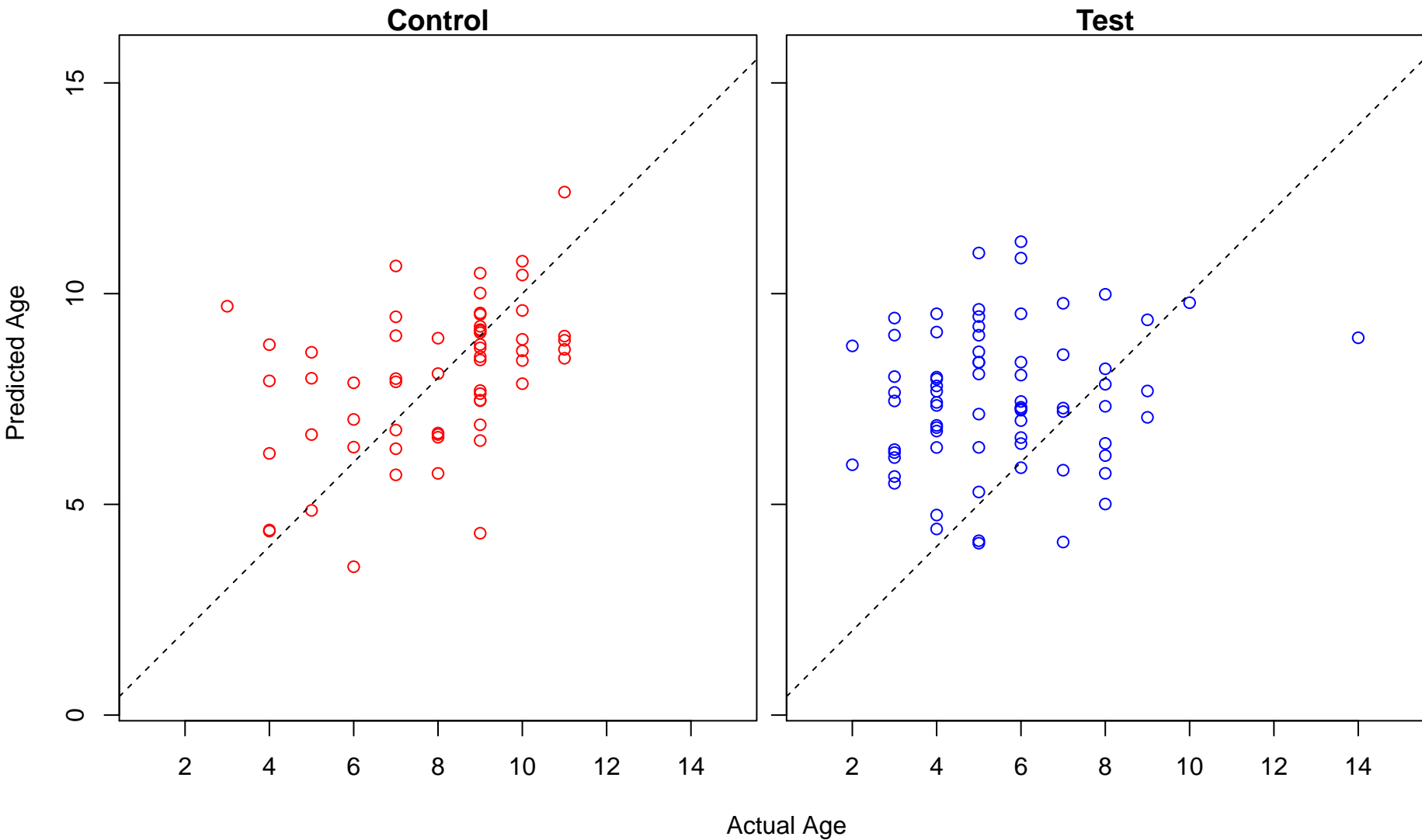
regulation of MAPK cascade (Score: 1.054978)



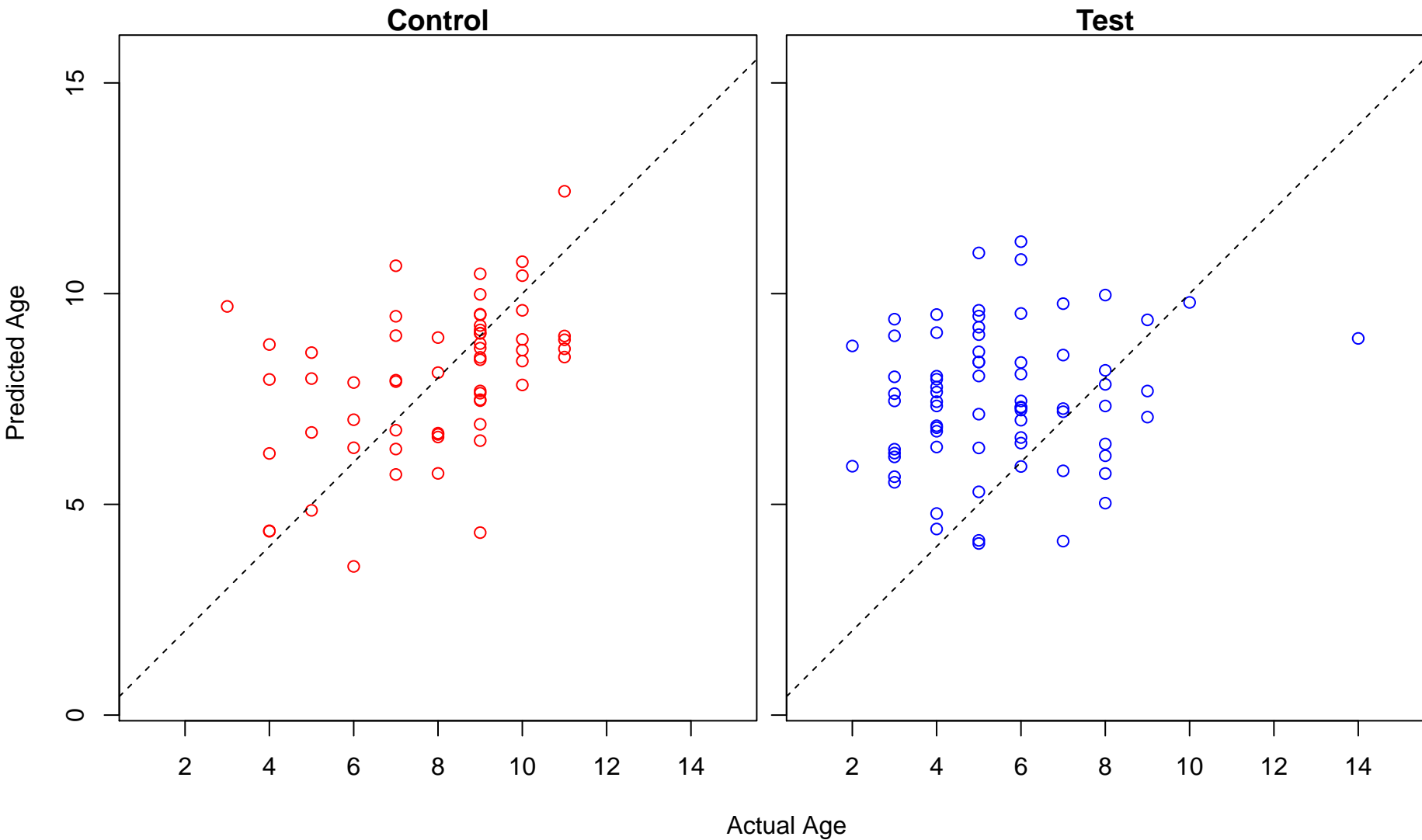
oogenesis (Score: 1.051928)



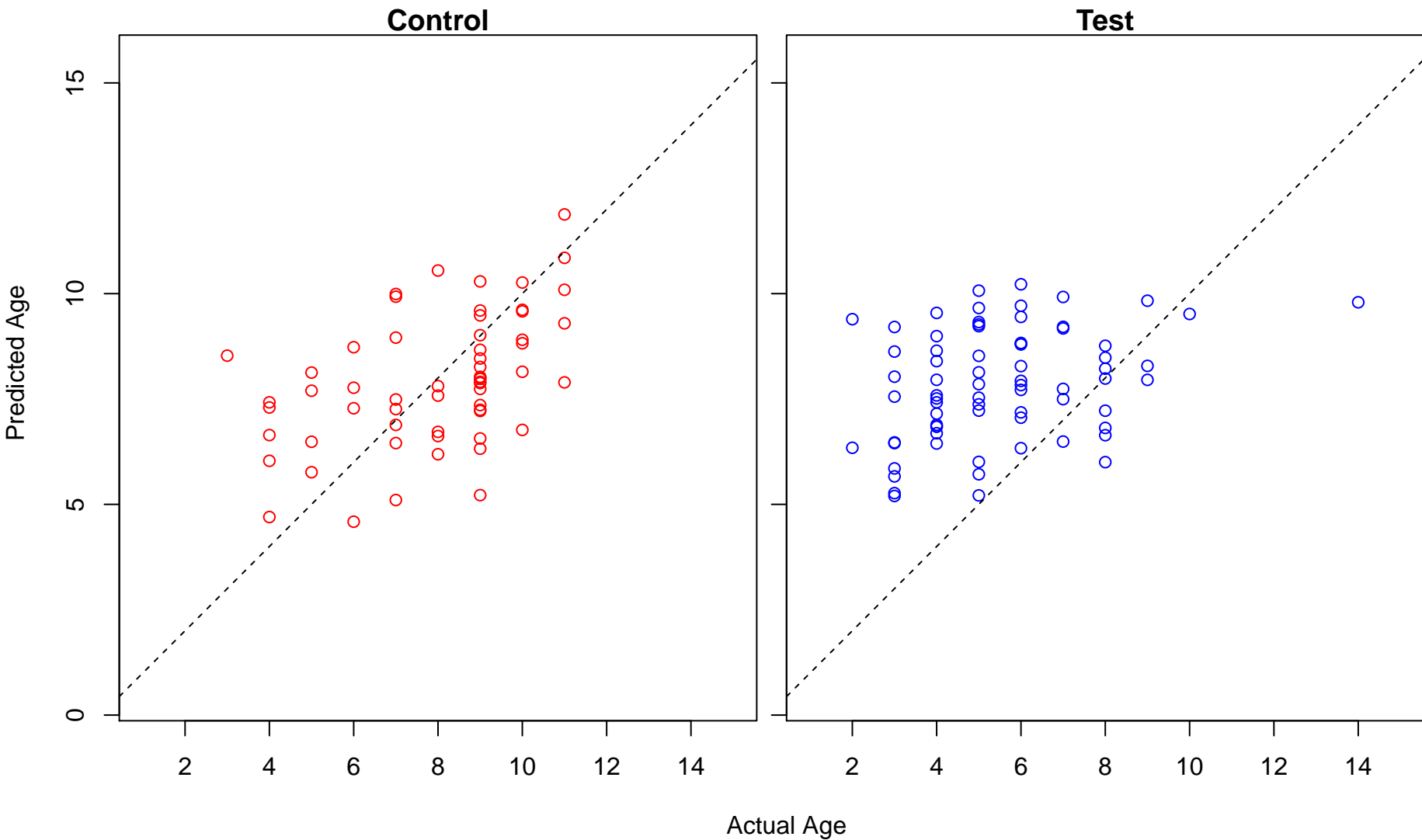
protein complex disassembly (Score: 1.051732)



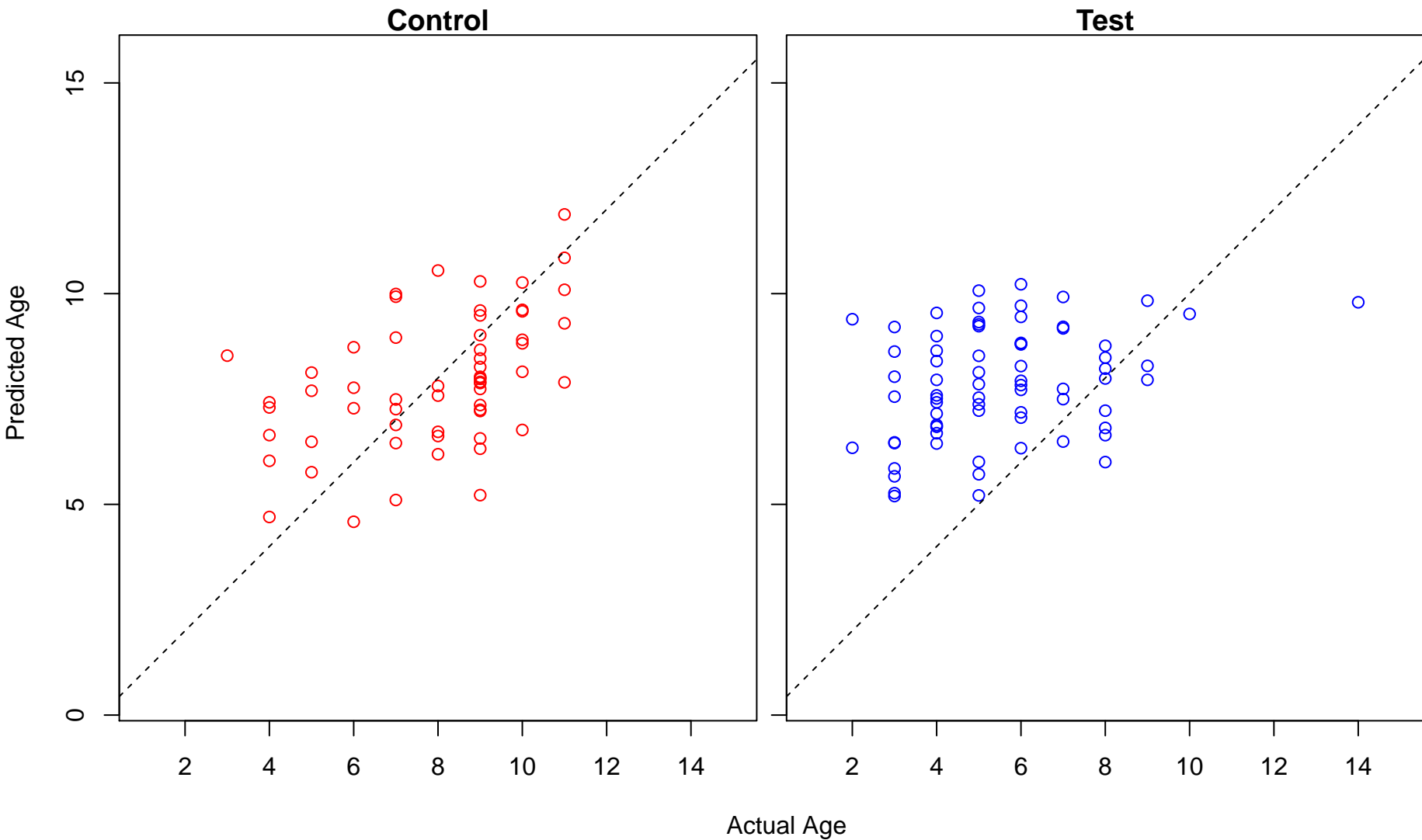
macromolecular complex disassembly (Score: 1.050315)



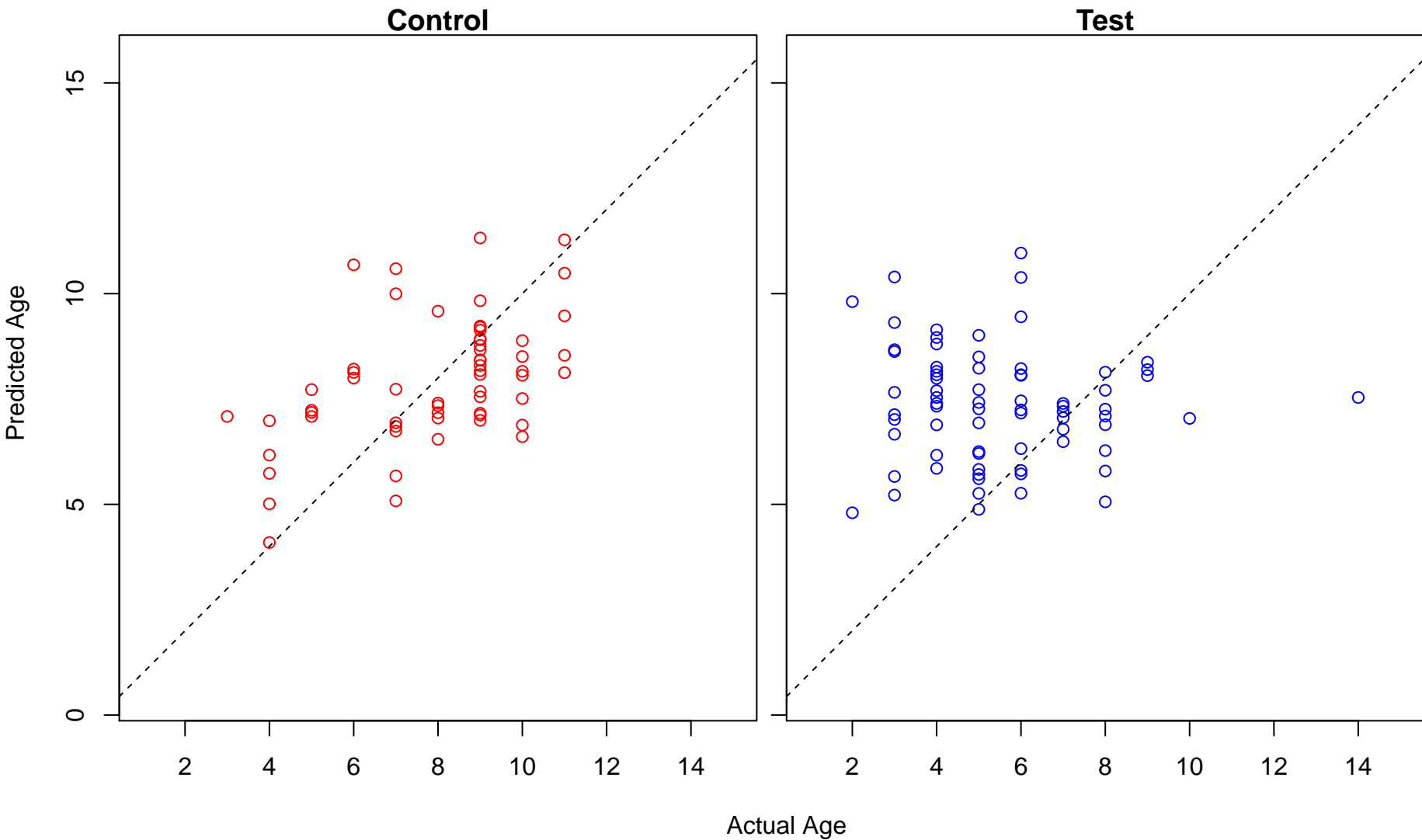
oxoacid metabolic process (Score: 1.049821)



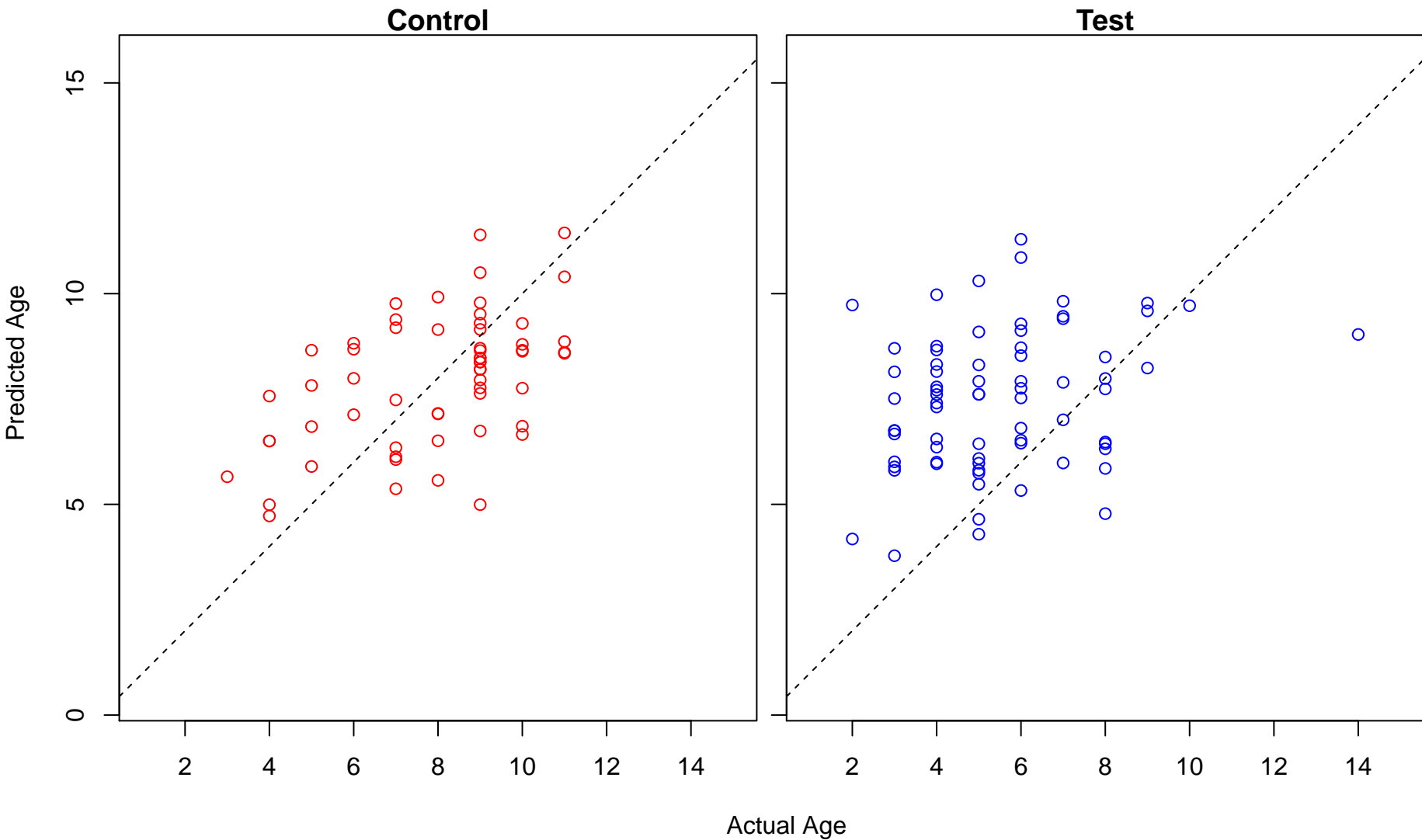
organic acid metabolic process (Score: 1.049727)



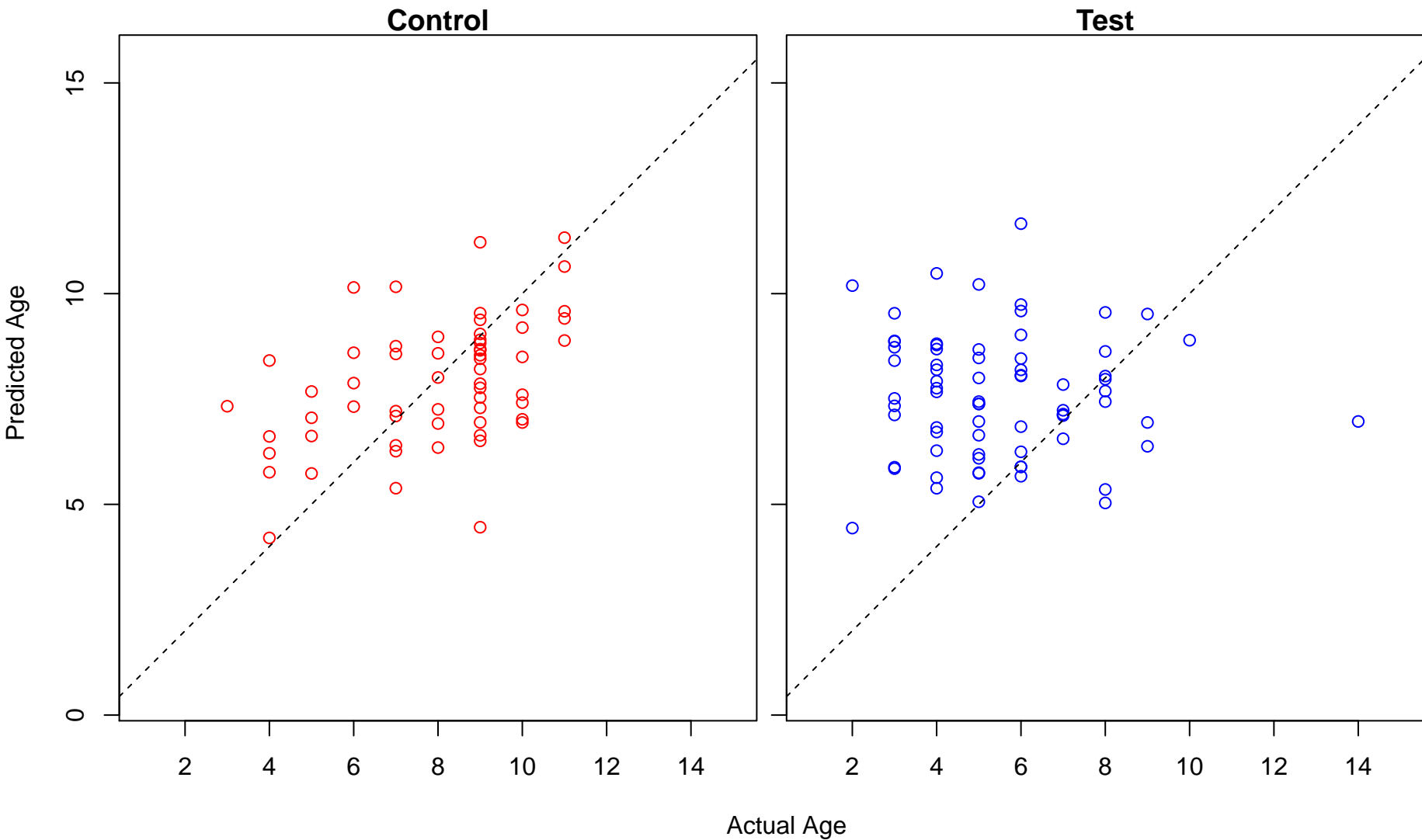
maintenance of location (Score: 1.049434)



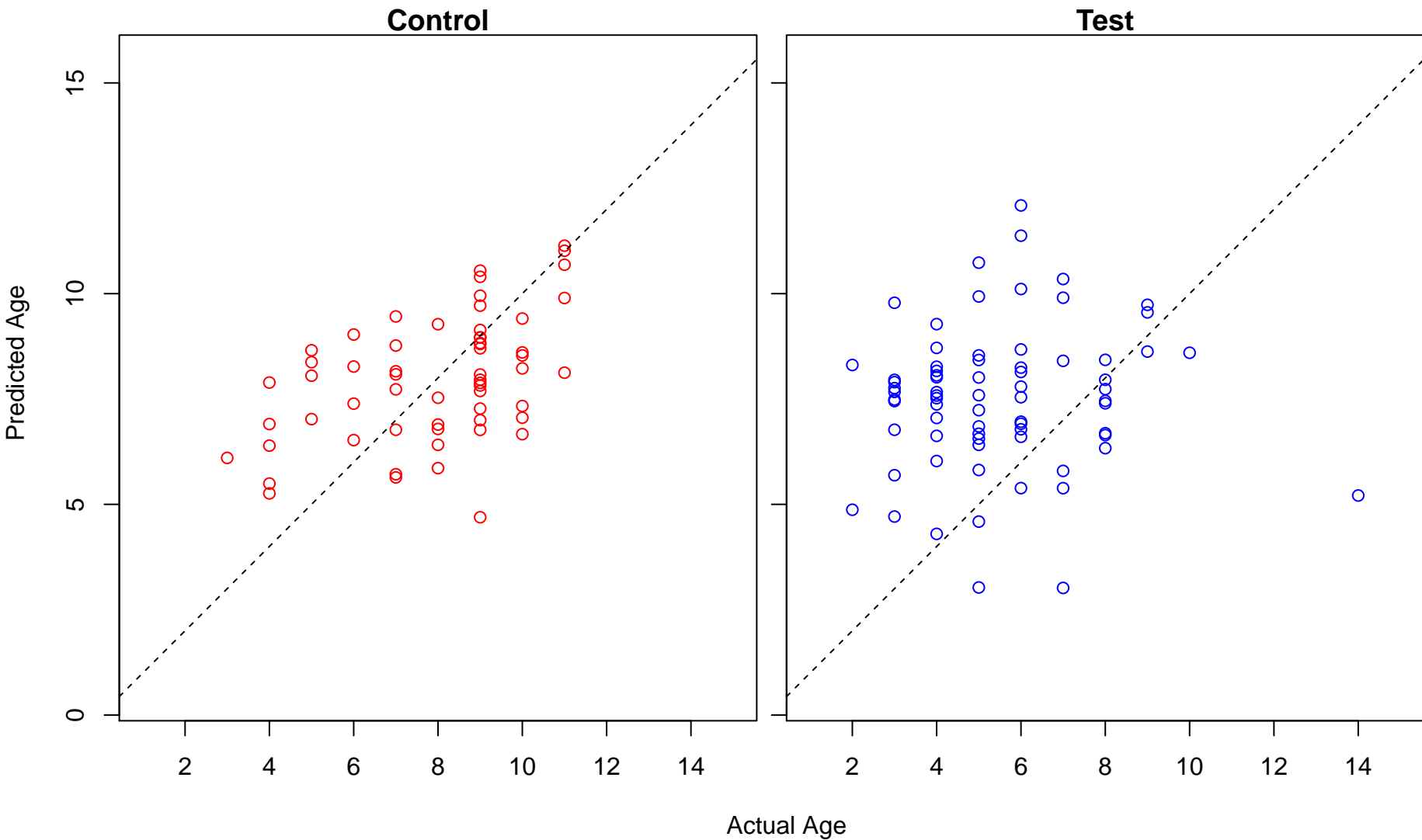
cell morphogenesis involved in differentiation (Score: 1.049233)



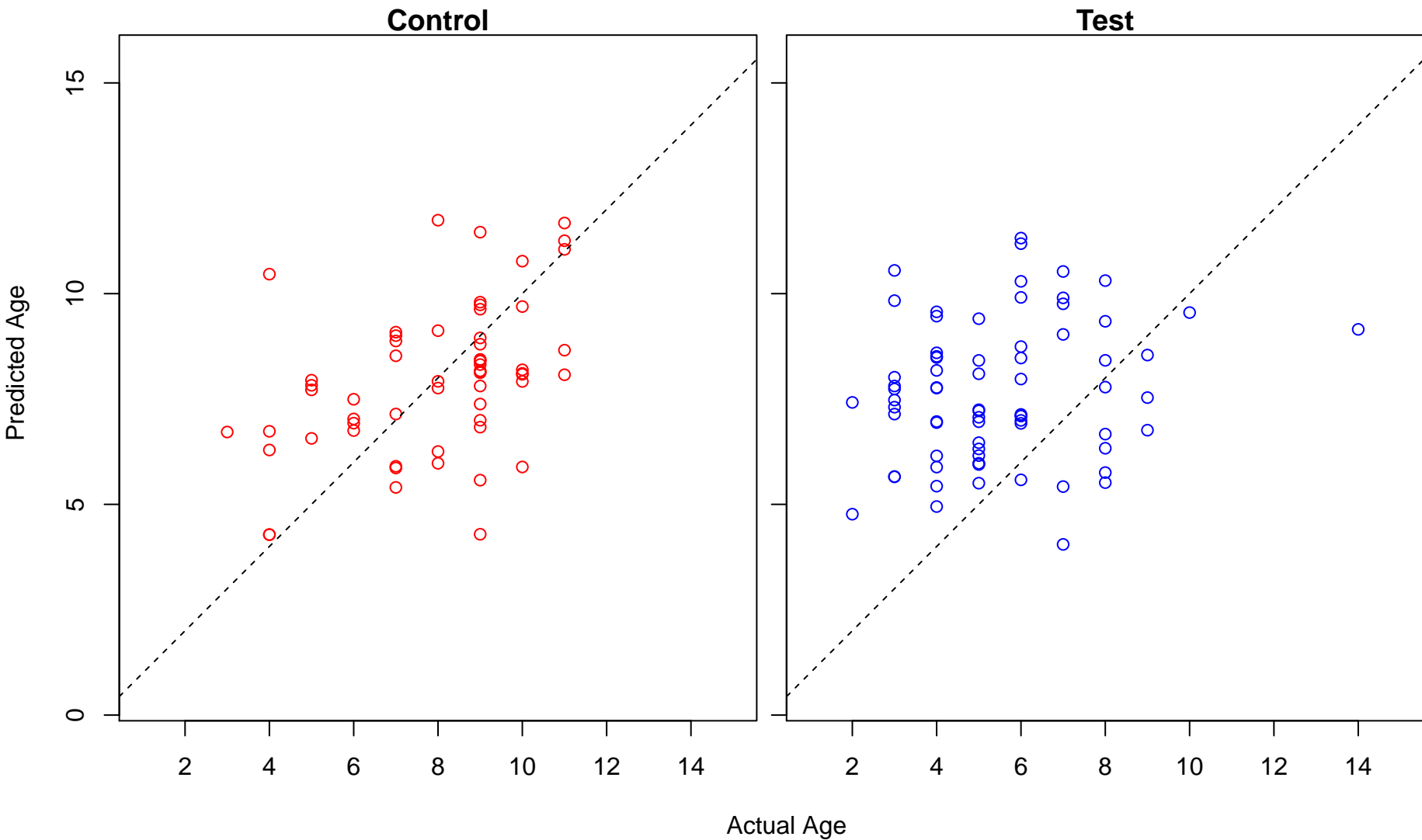
cytoplasmic sequestering of protein (Score: 1.048469)



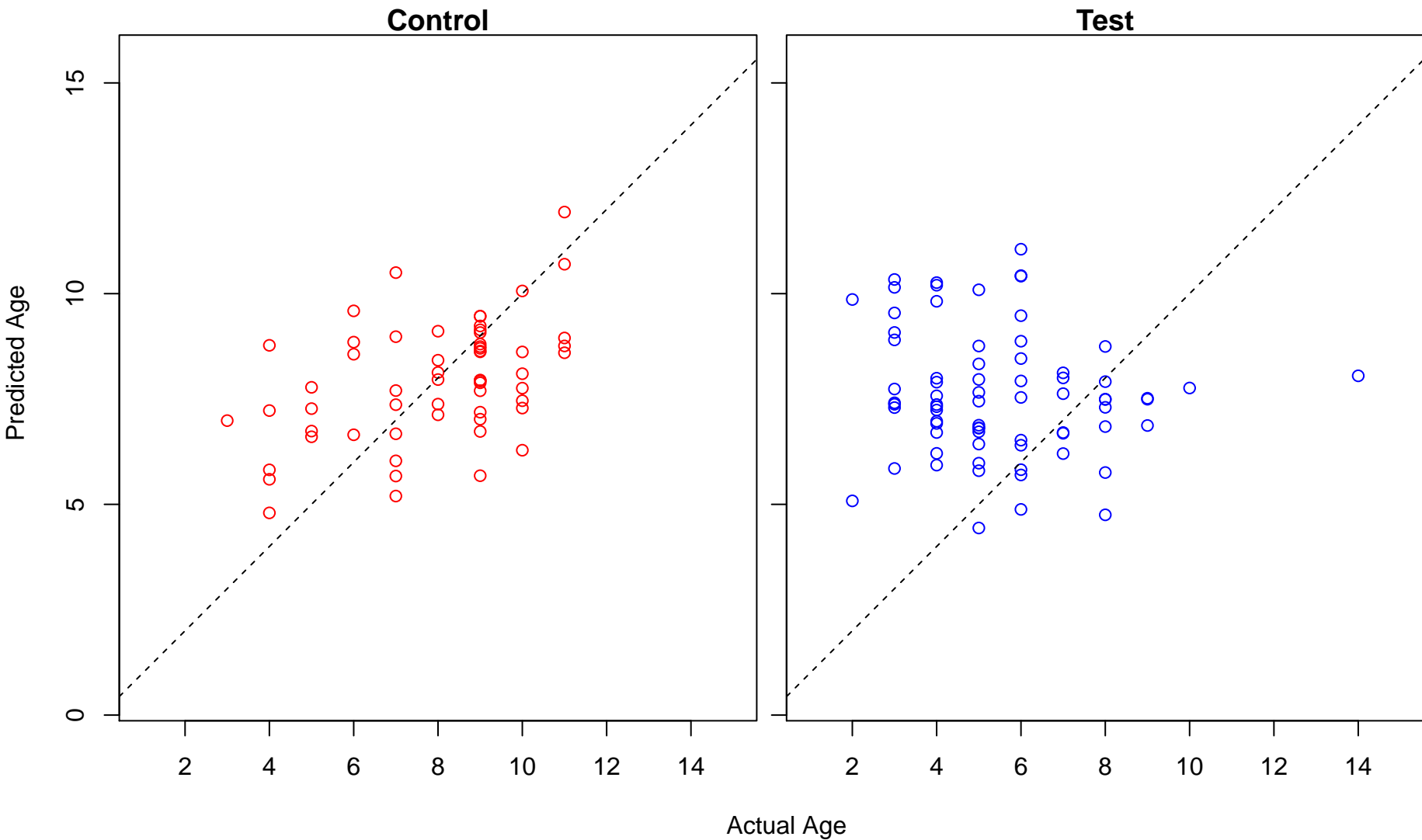
activation of innate immune response (Score: 1.048026)



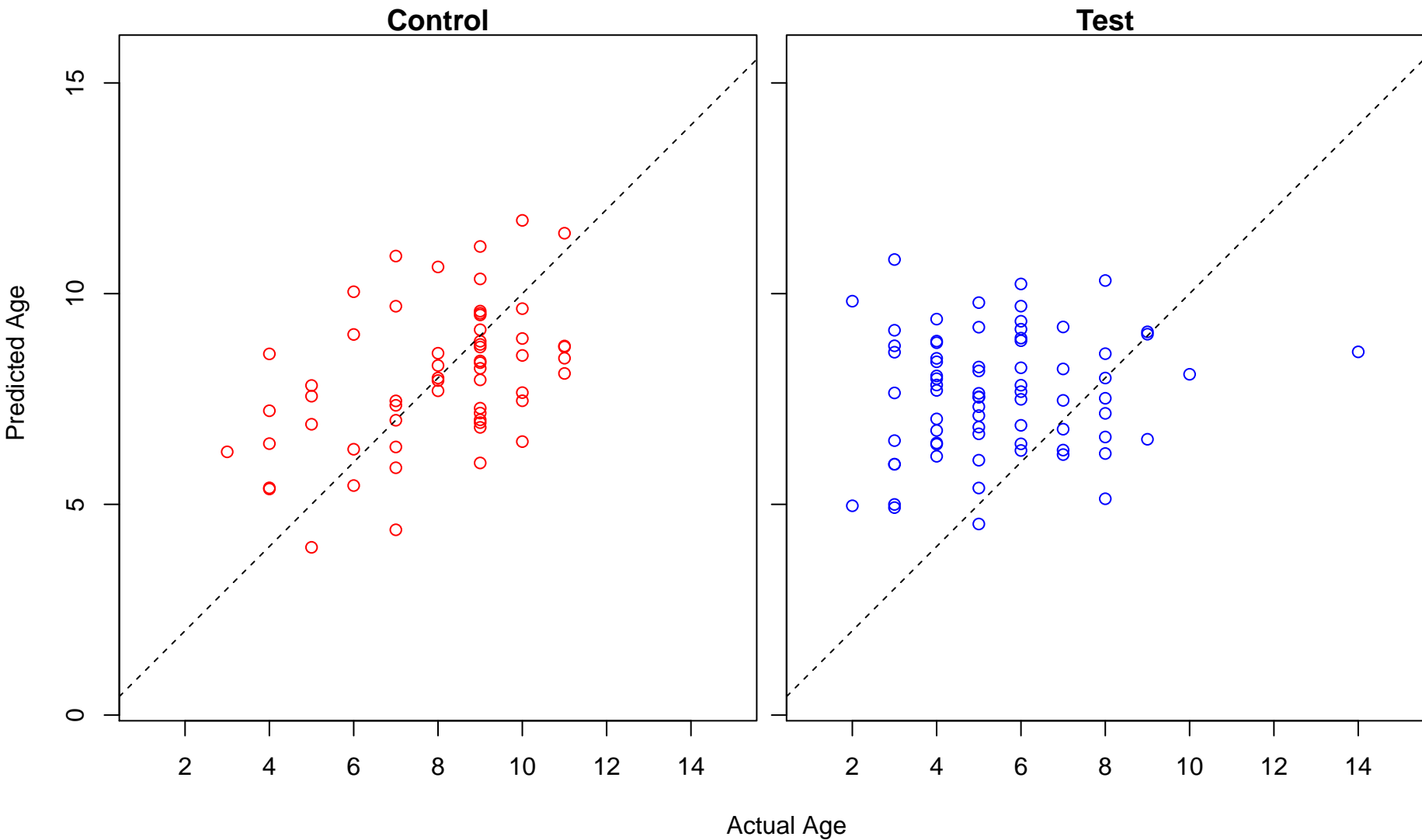
ear development (Score: 1.046640)



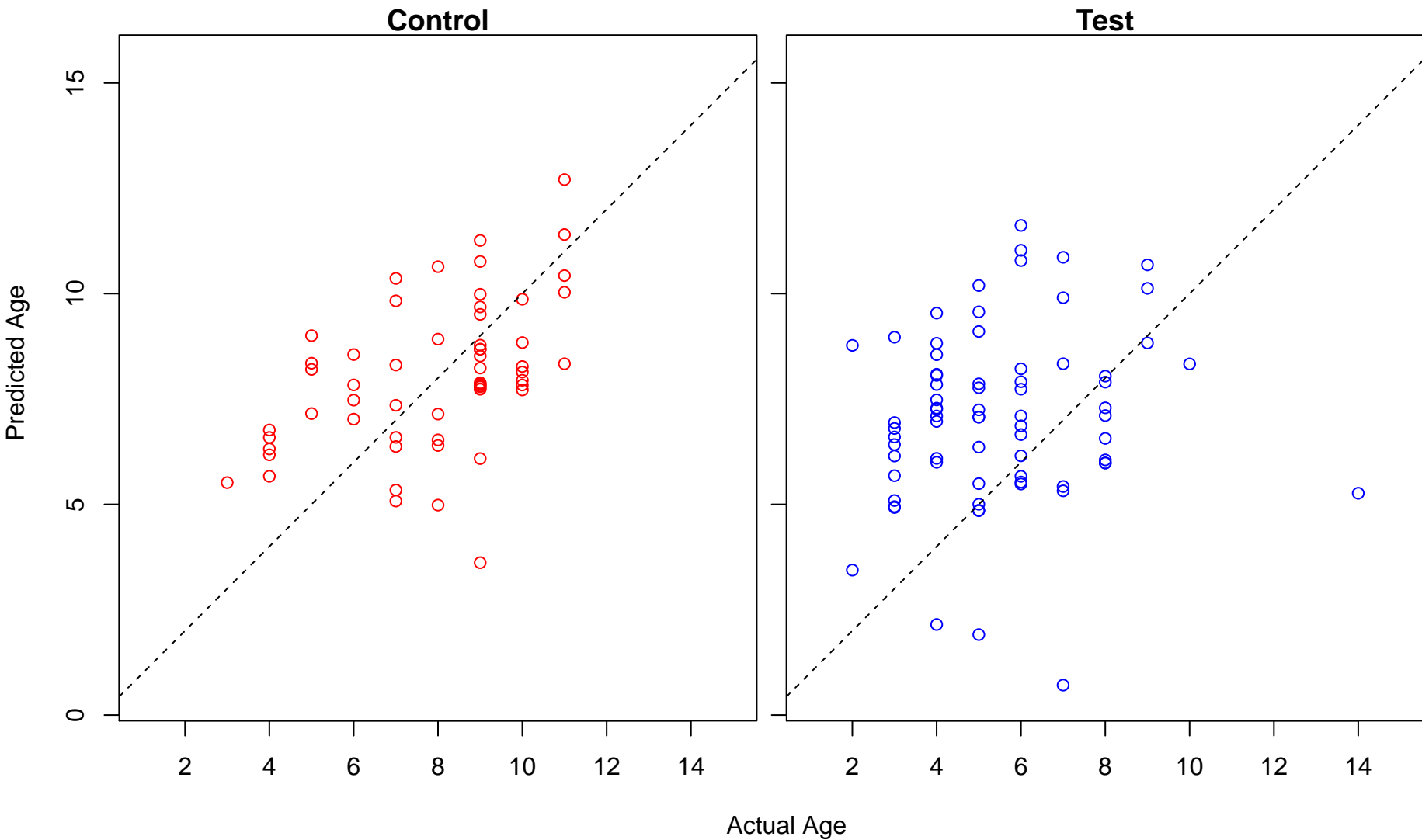
adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway (Score: 1.046260)



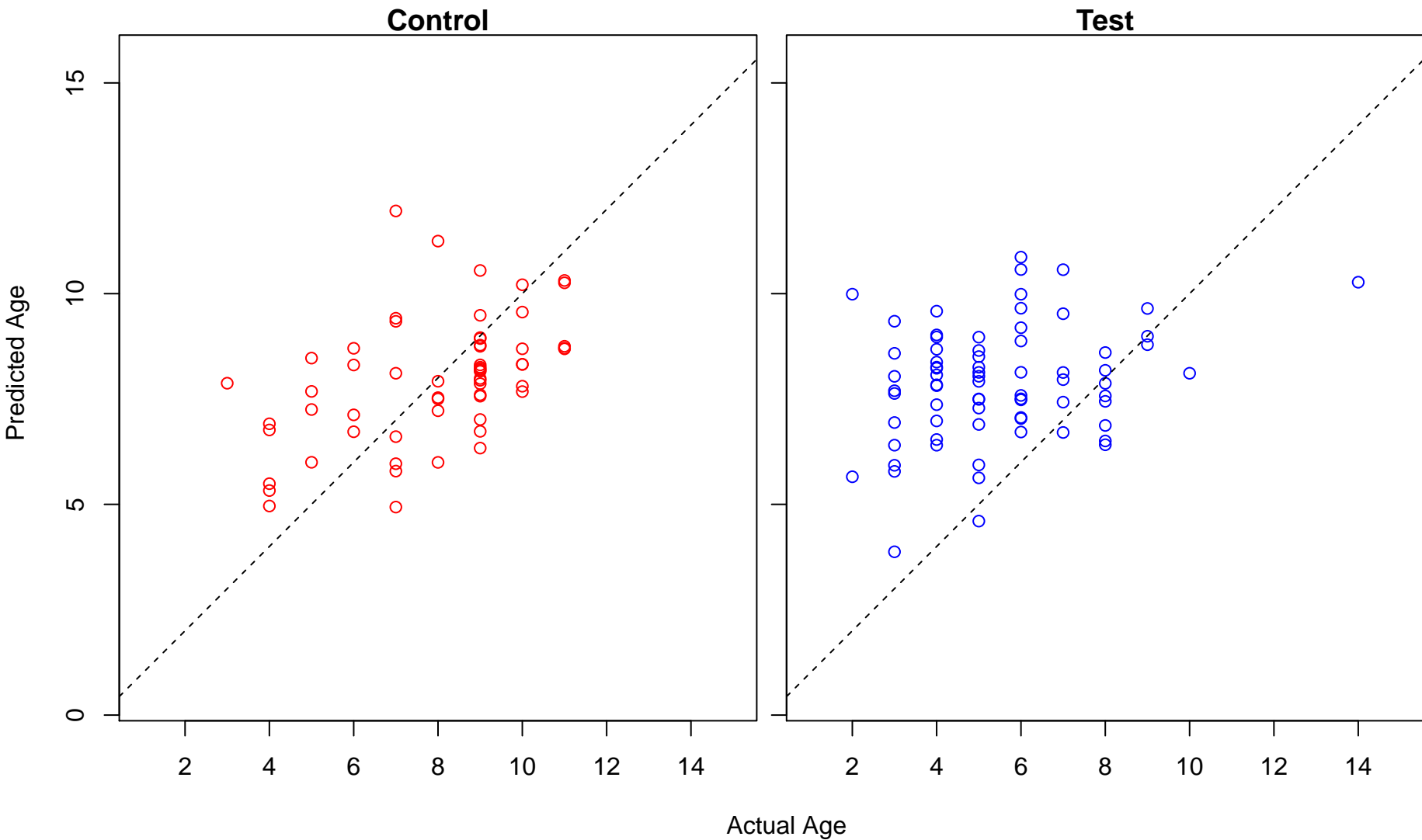
hormone secretion (Score: 1.045548)



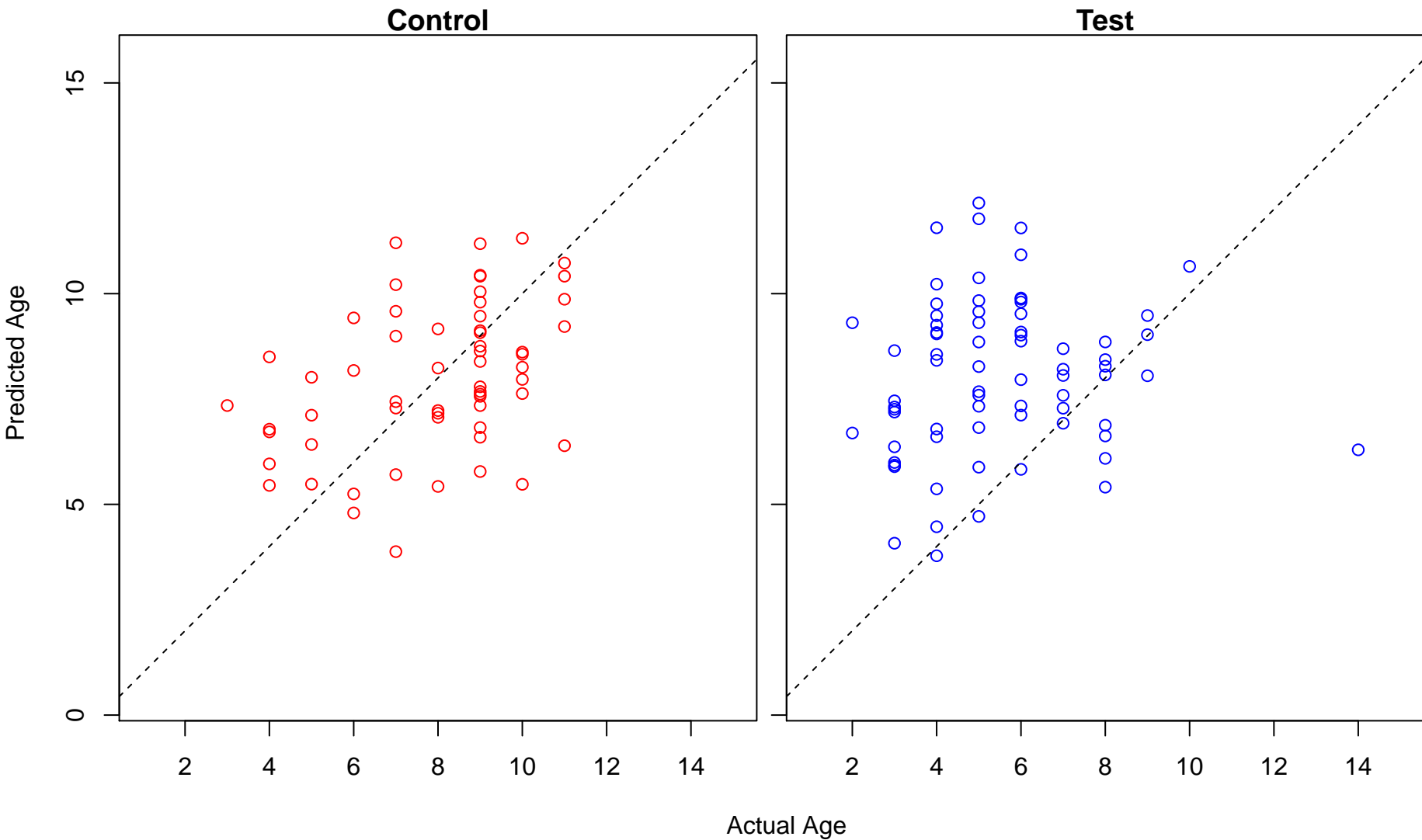
regulation of innate immune response (Score: 1.045329)



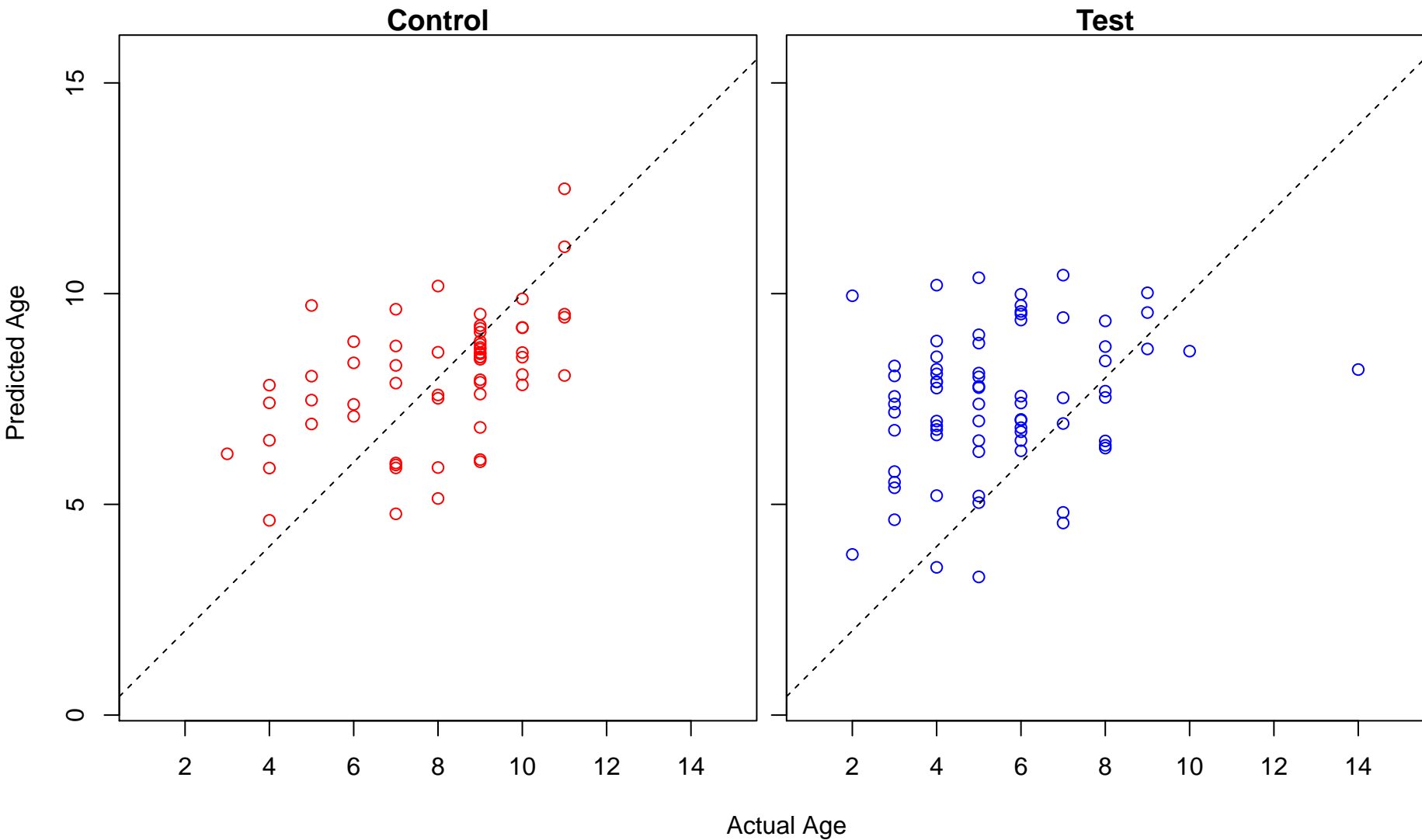
macromolecular complex subunit organization (Score: 1.043987)



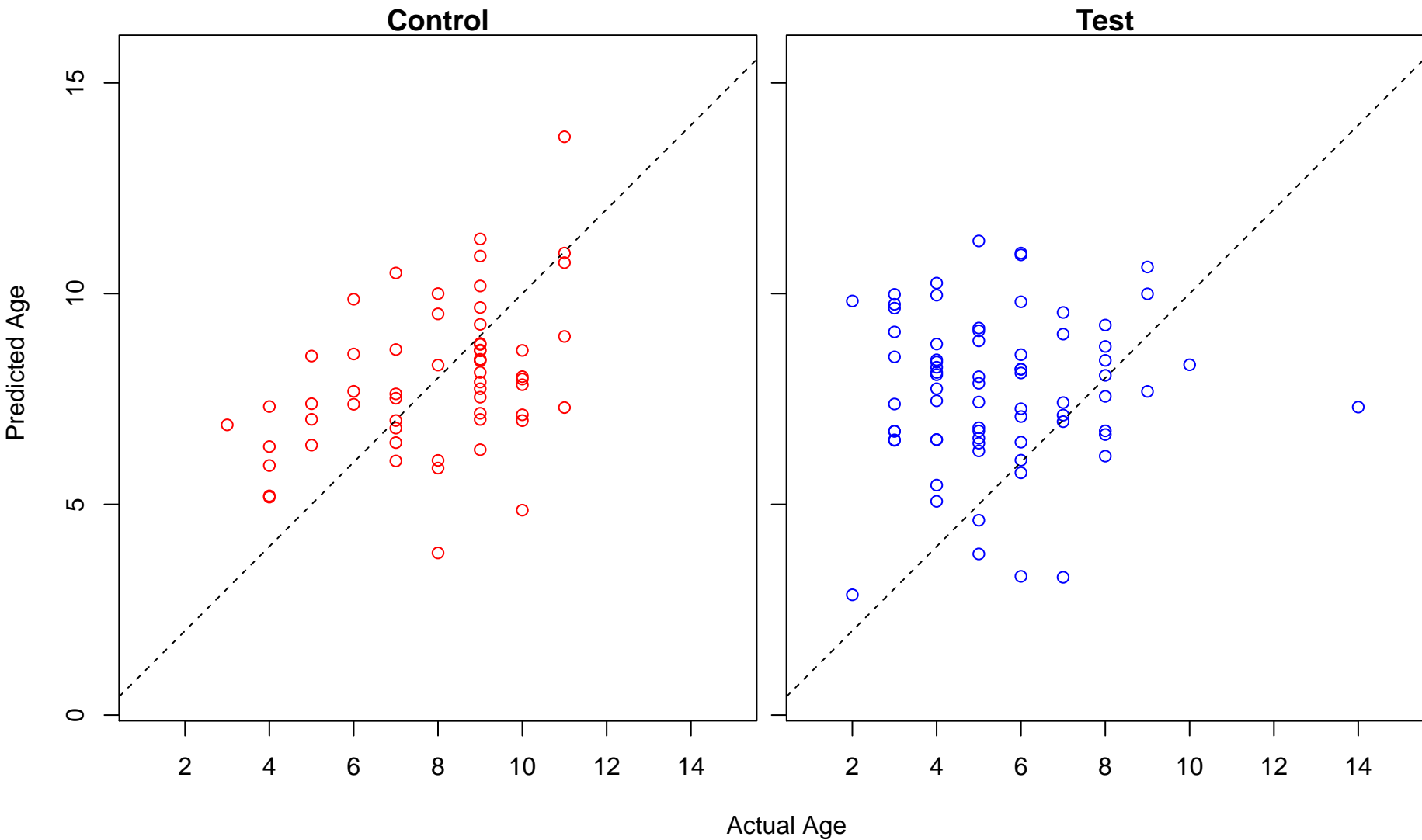
regulation of DNA repair (Score: 1.043880)



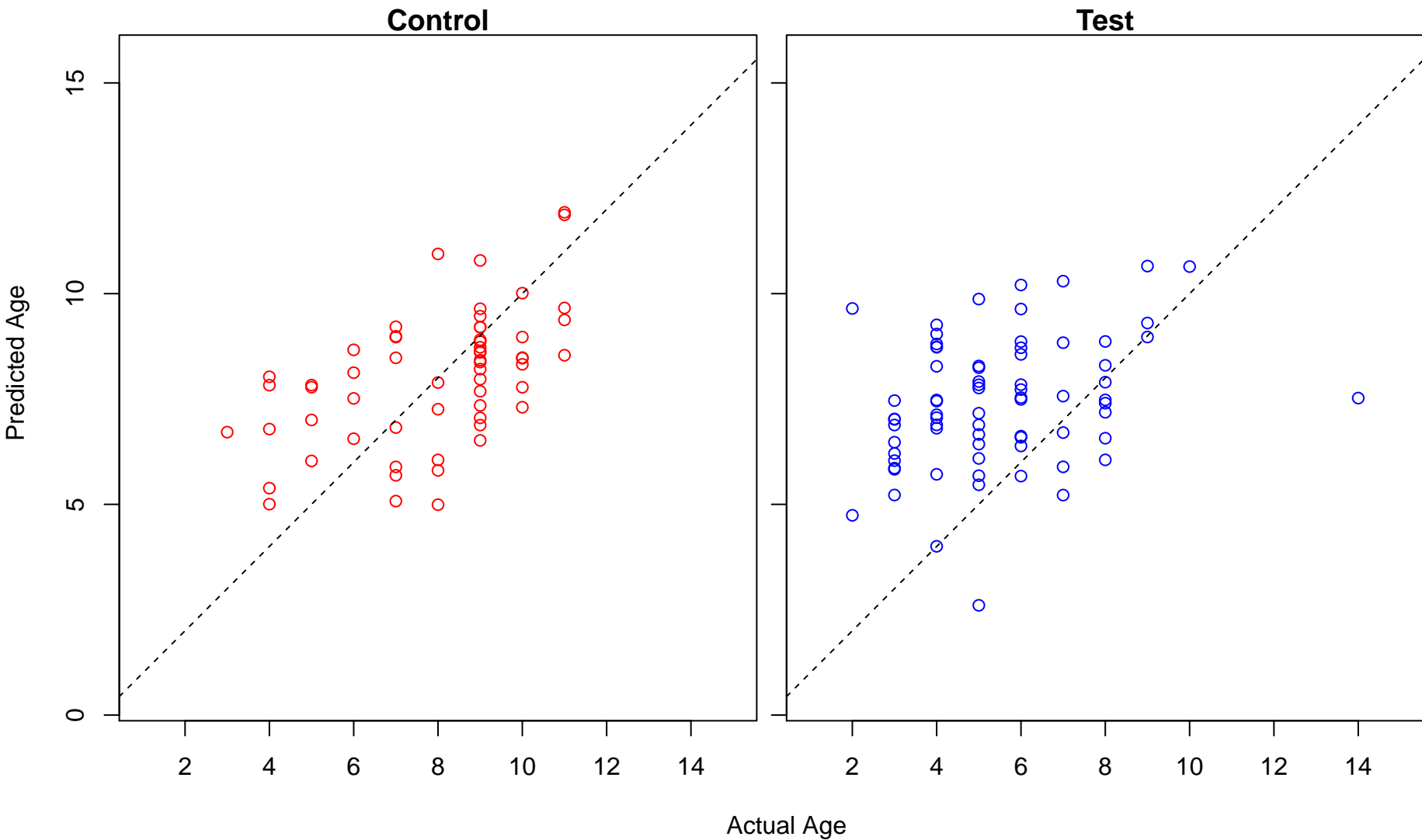
negative regulation of biological process (Score: 1.043757)



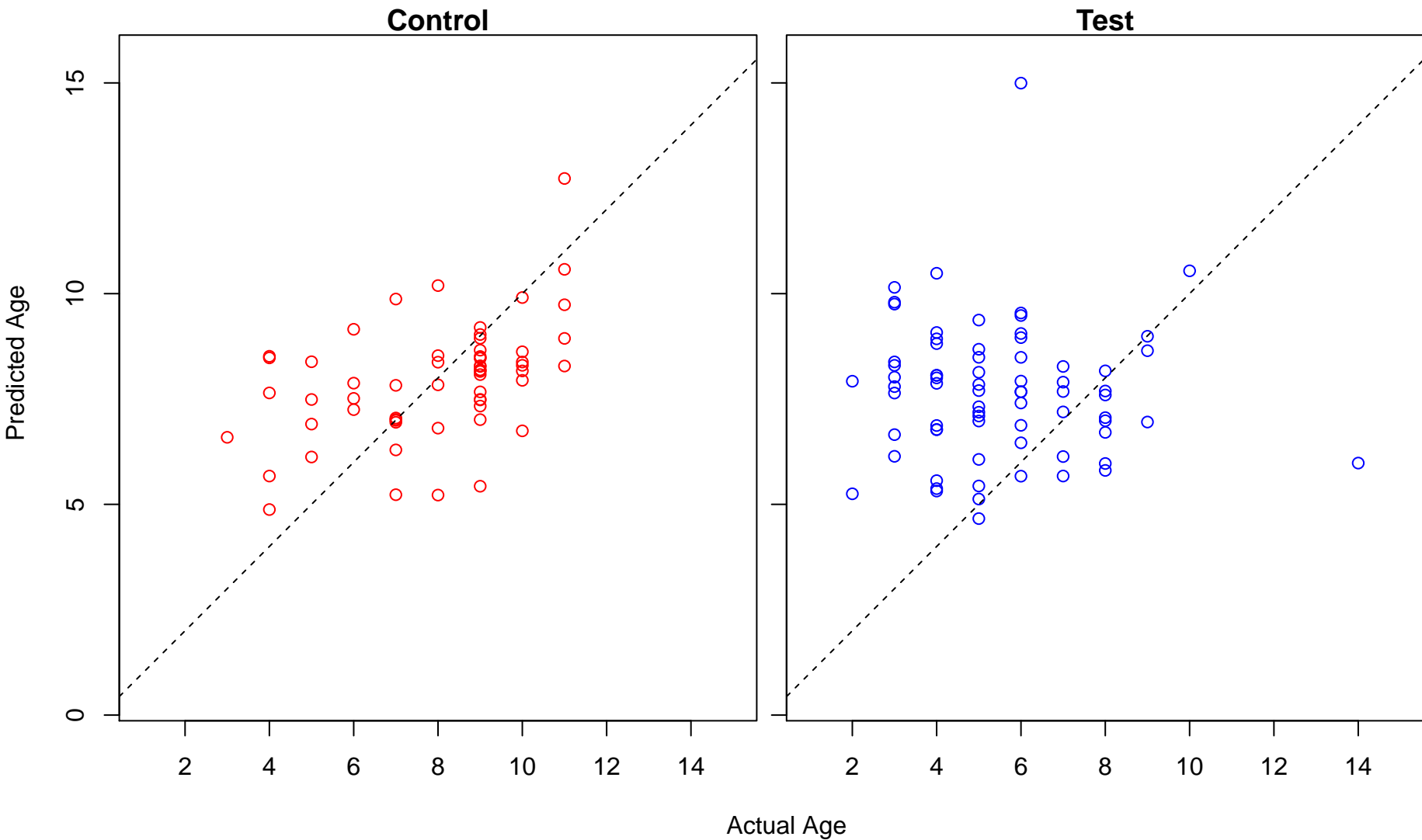
cellular process involved in reproduction in multicellular organism (Score: 1.043679)



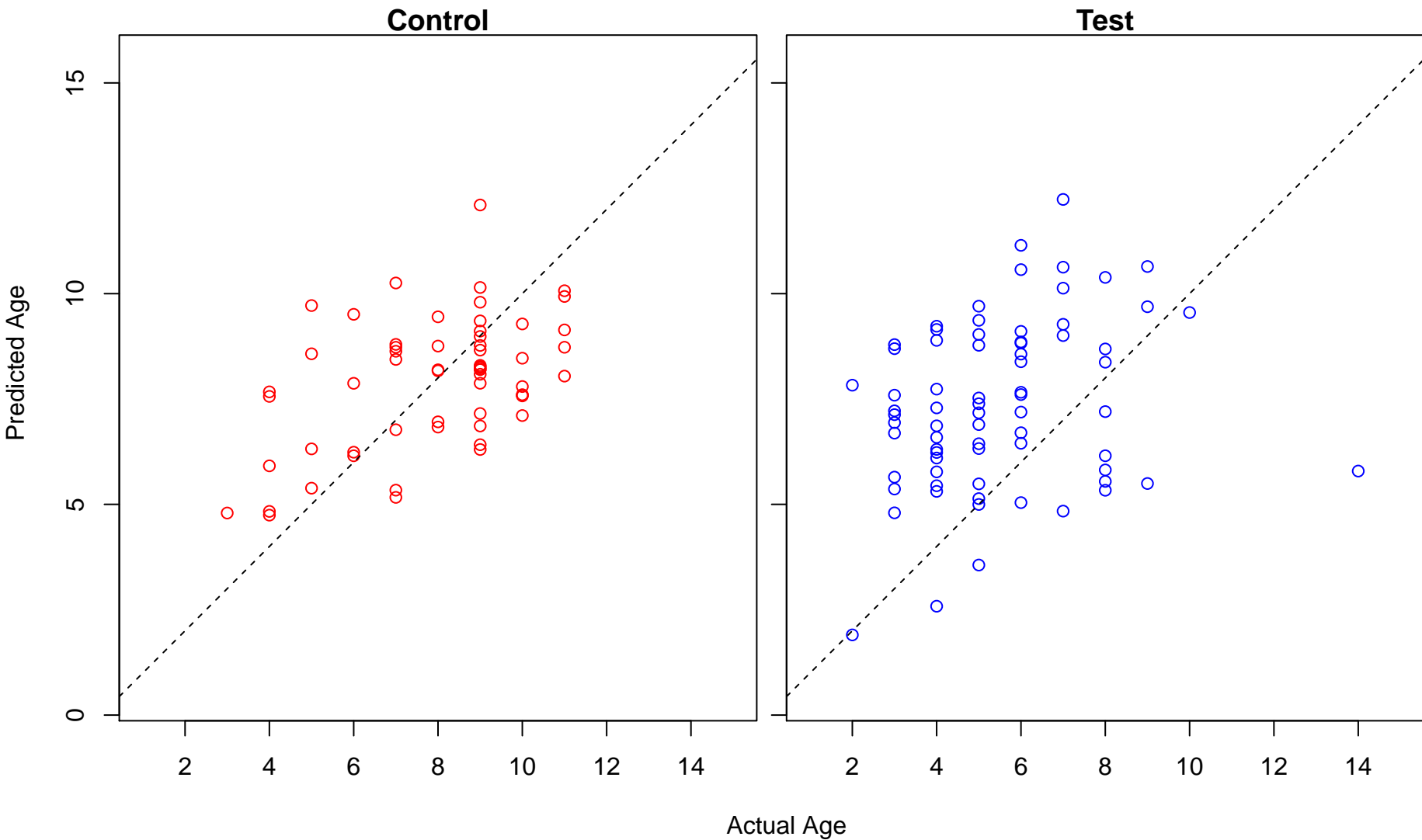
regulation of biological process (Score: 1.043633)



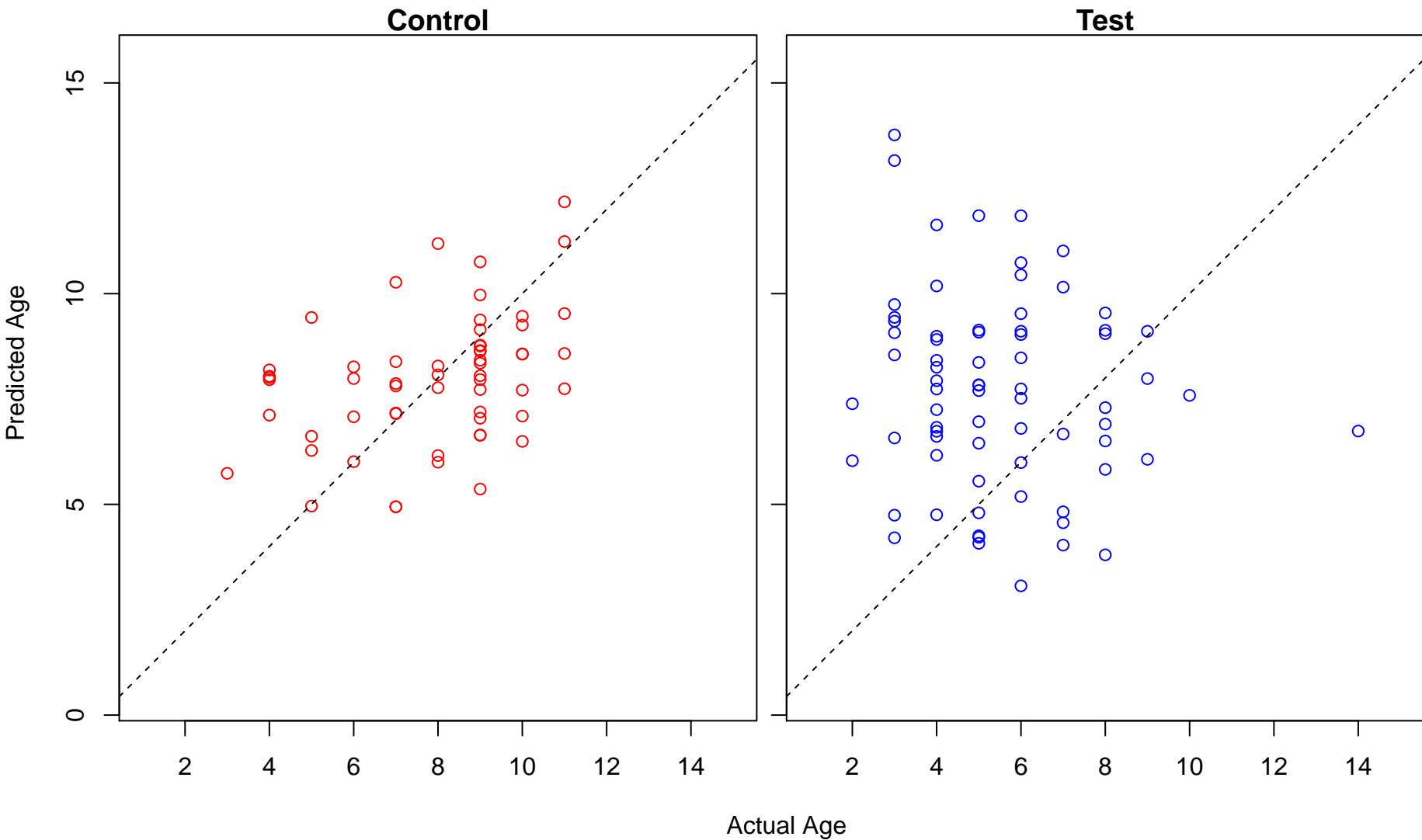
positive regulation of CD4-positive, alpha-beta T cell differentiation (Score: 1.043474)



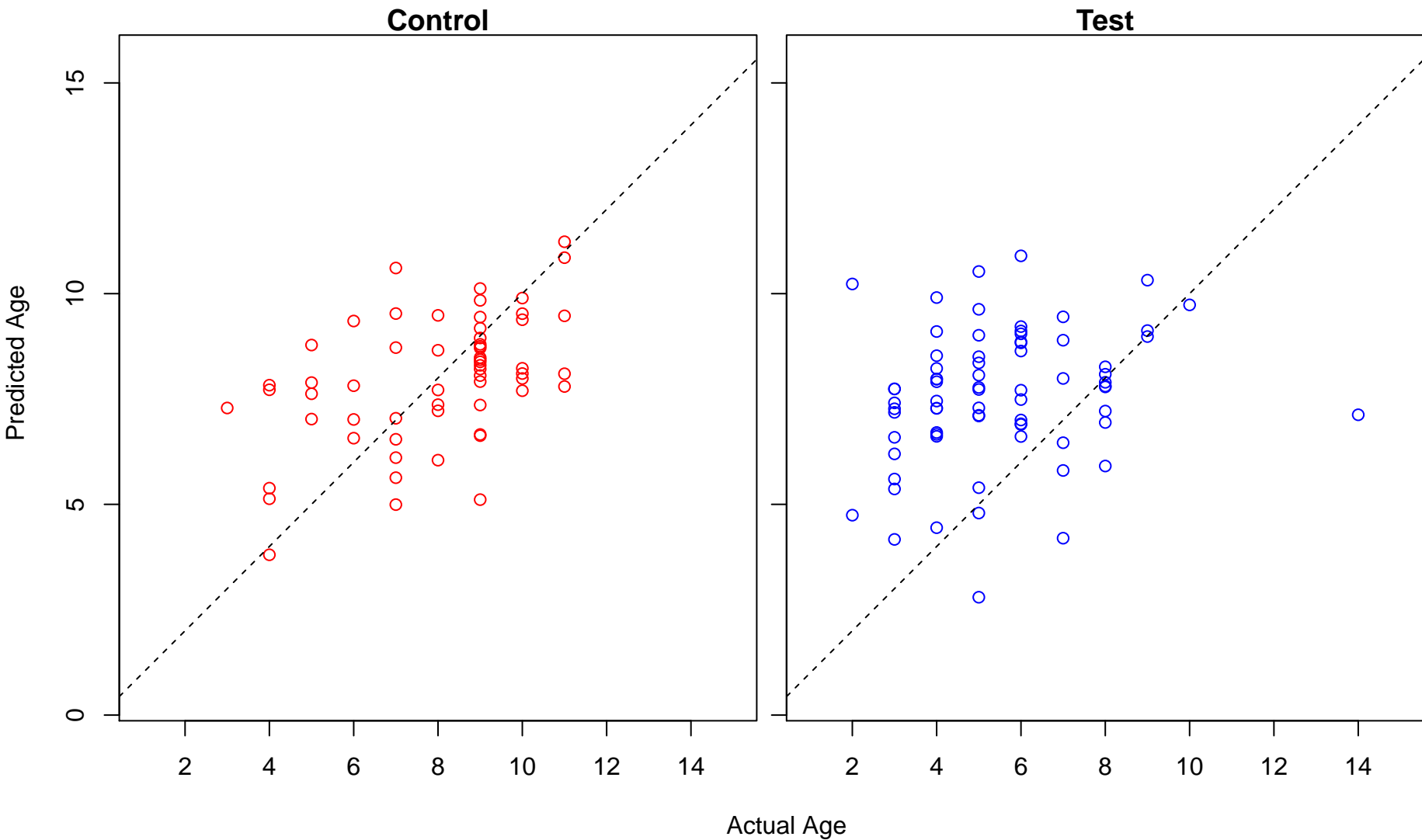
myoblast fusion (Score: 1.042805)



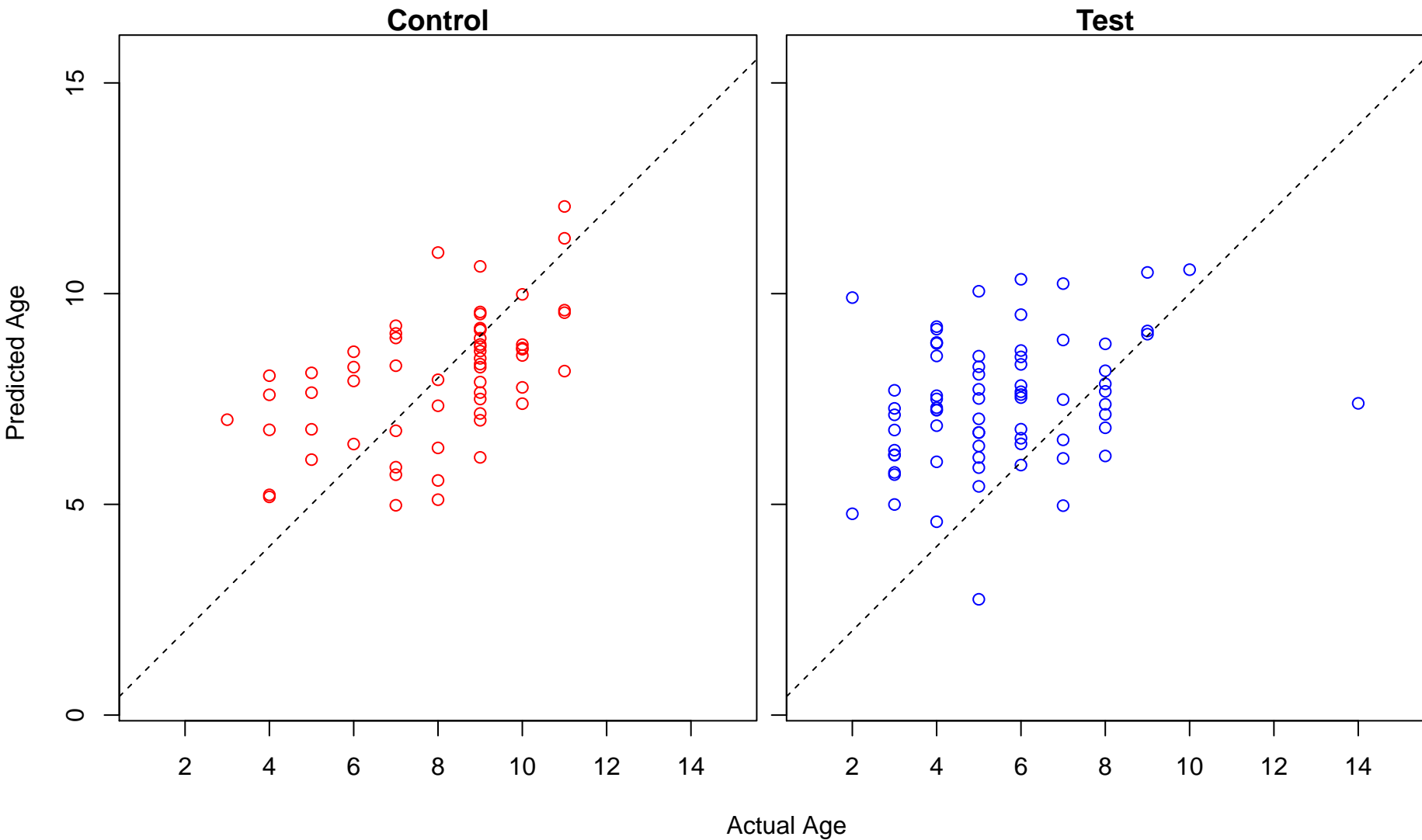
negative regulation of mast cell activation (Score: 1.042429)



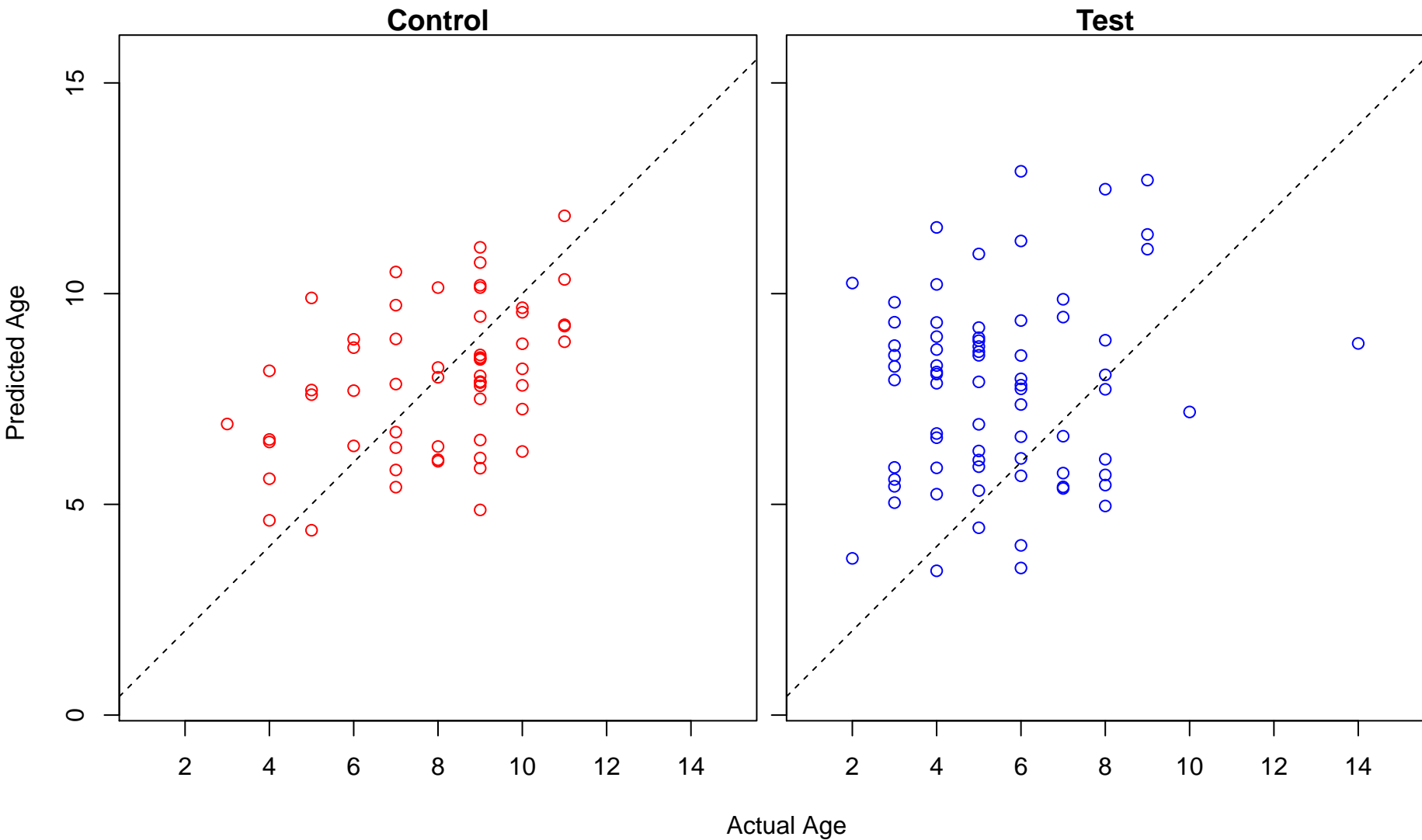
cellular protein metabolic process (Score: 1.042283)



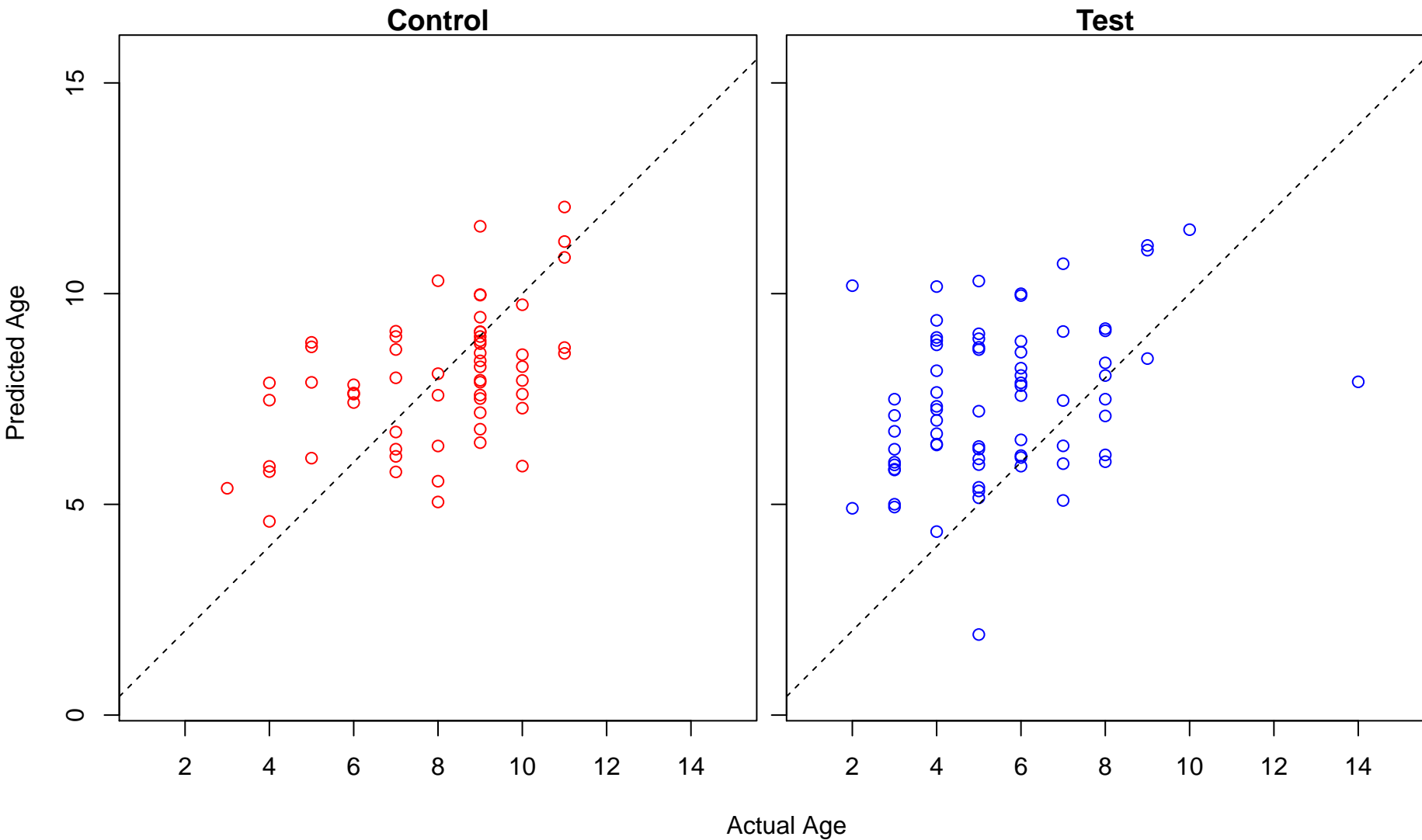
biological regulation (Score: 1.041314)



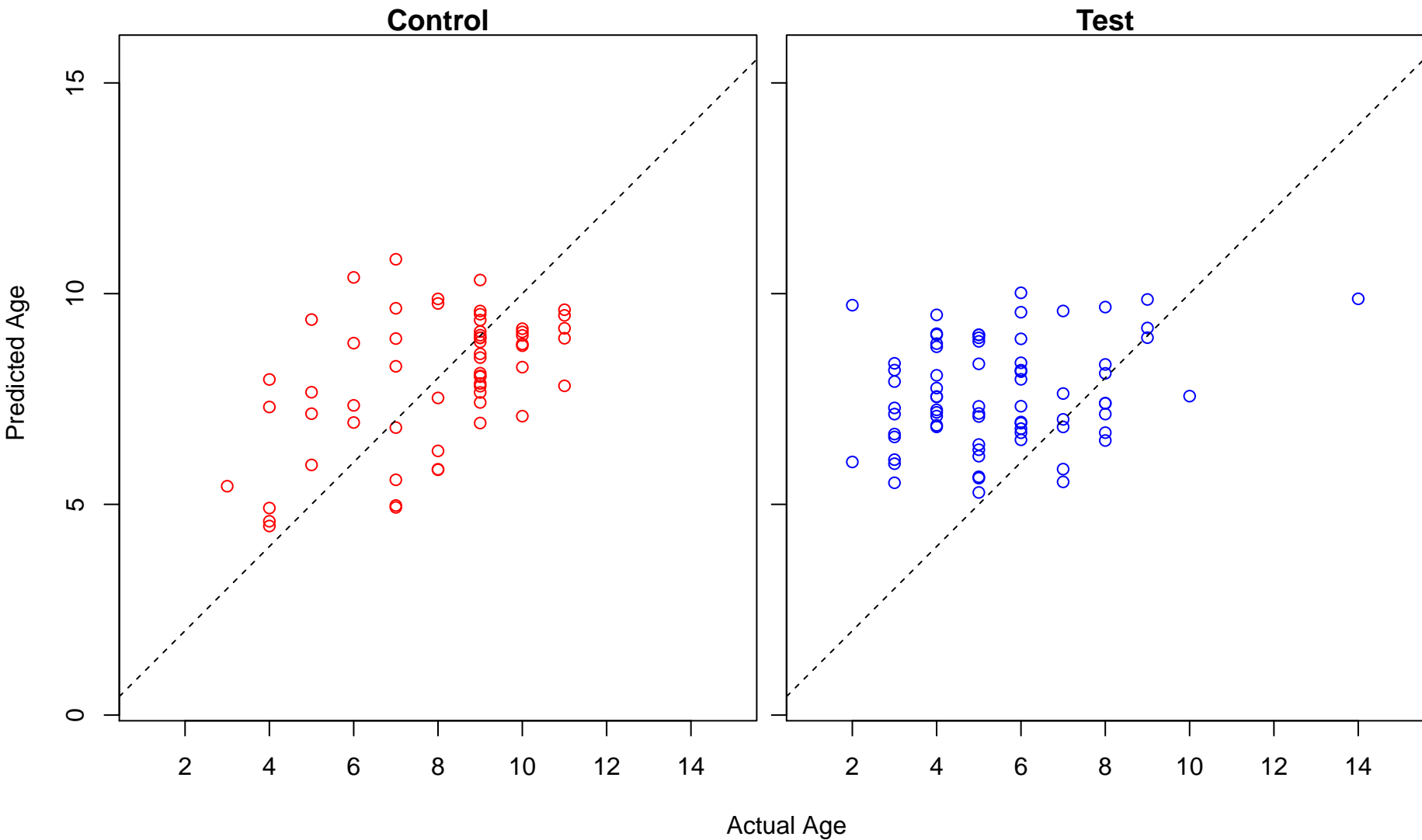
myeloid cell homeostasis (Score: 1.040351)



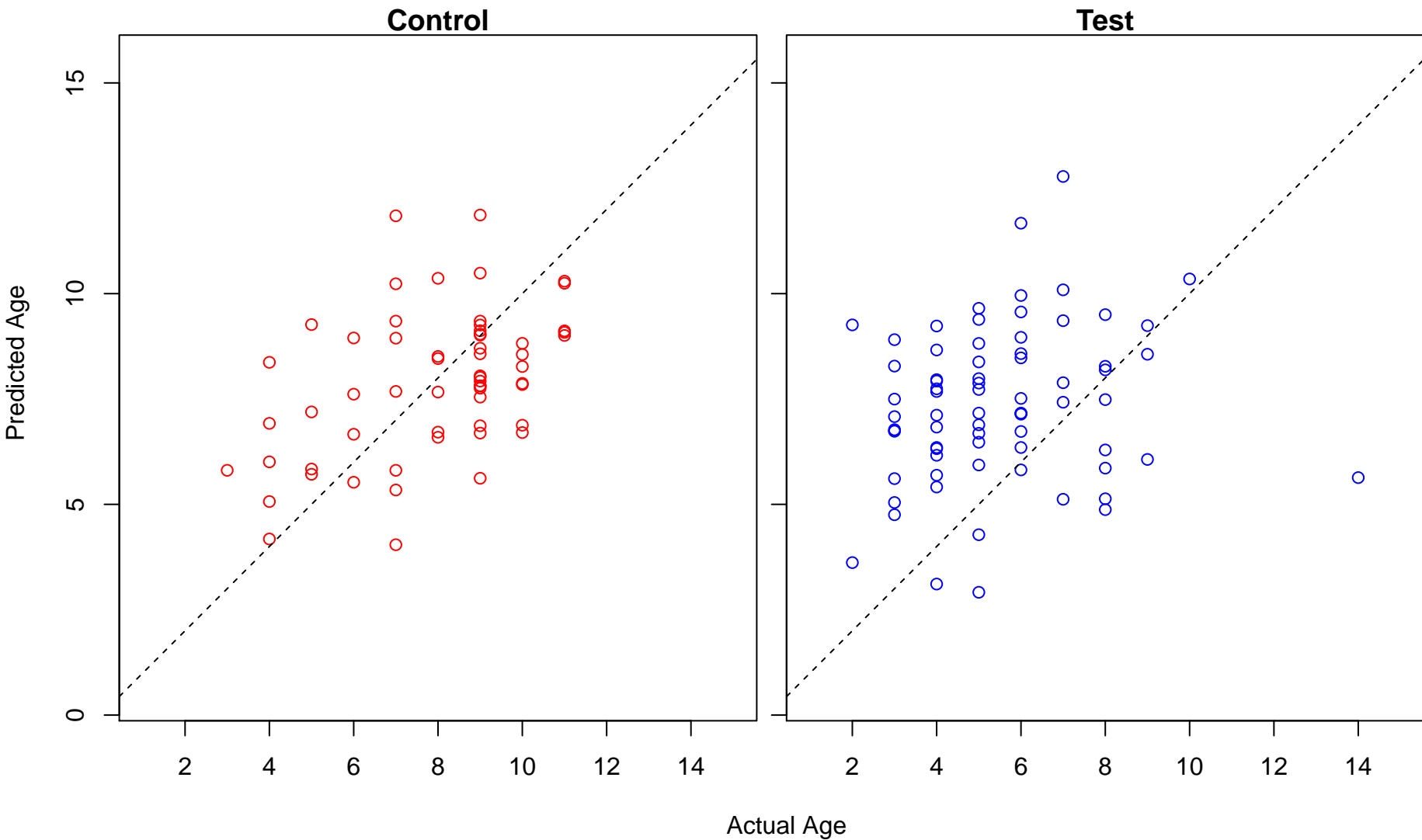
signal transduction (Score: 1.040328)



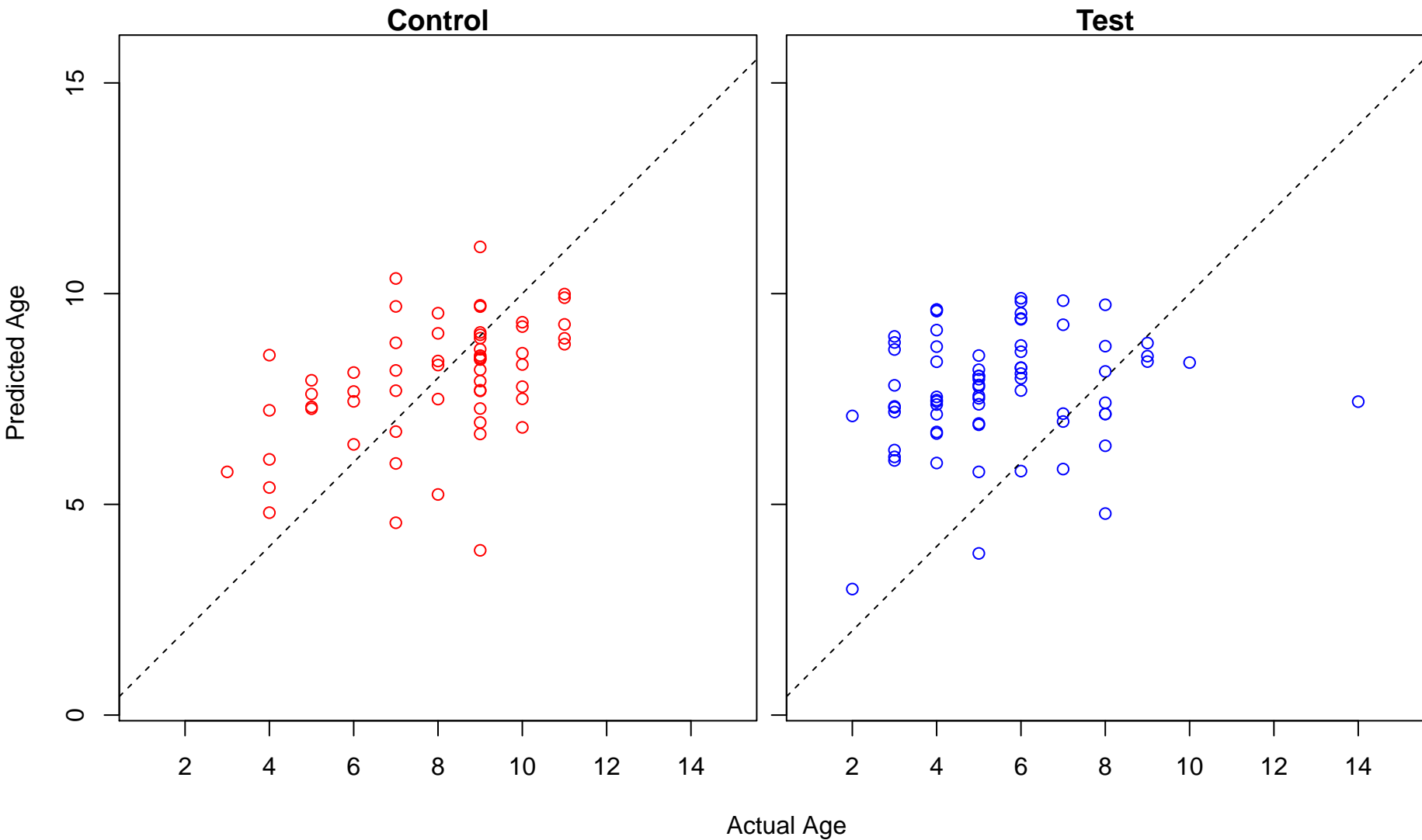
metal ion homeostasis (Score: 1.039748)



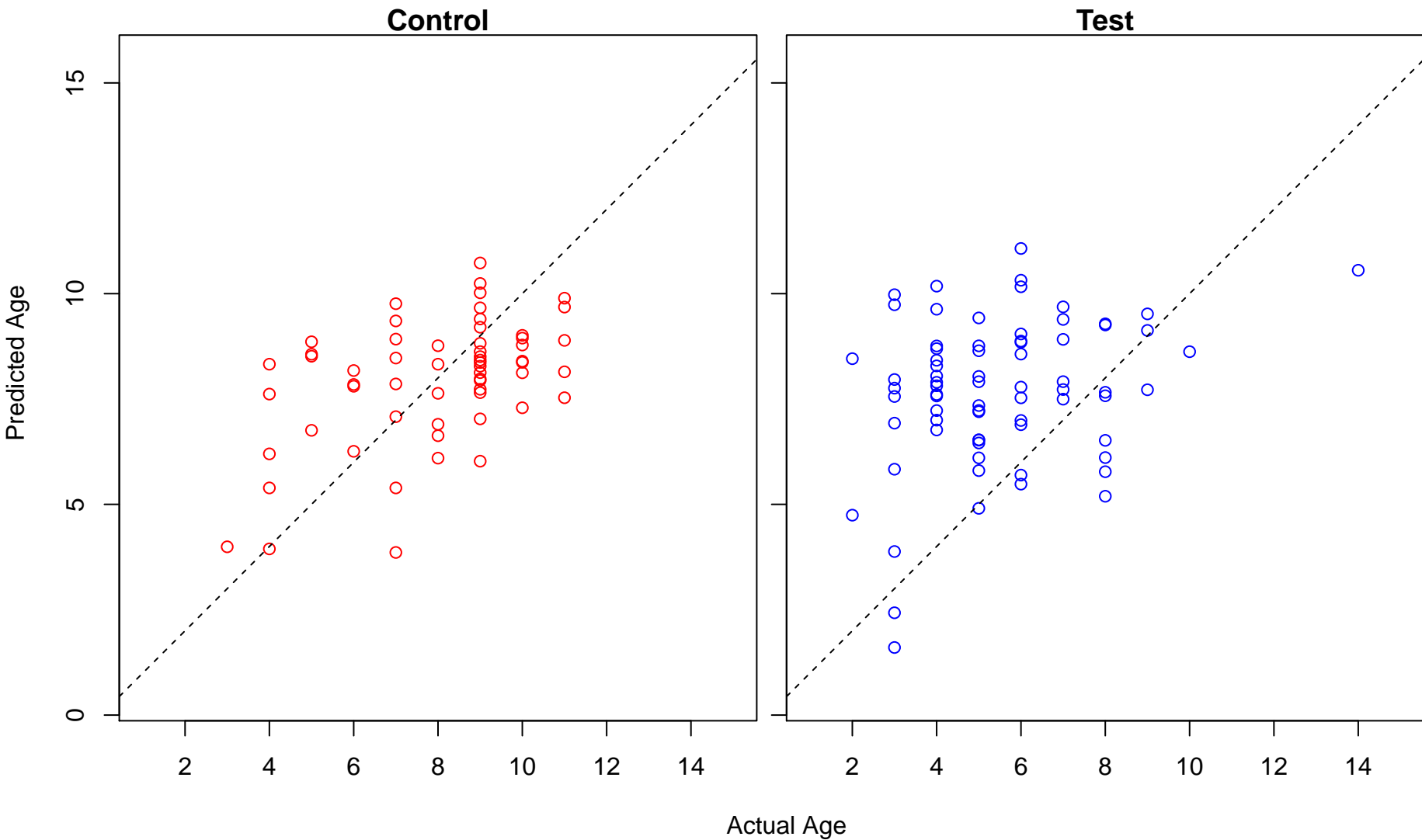
syncytium formation (Score: 1.037943)



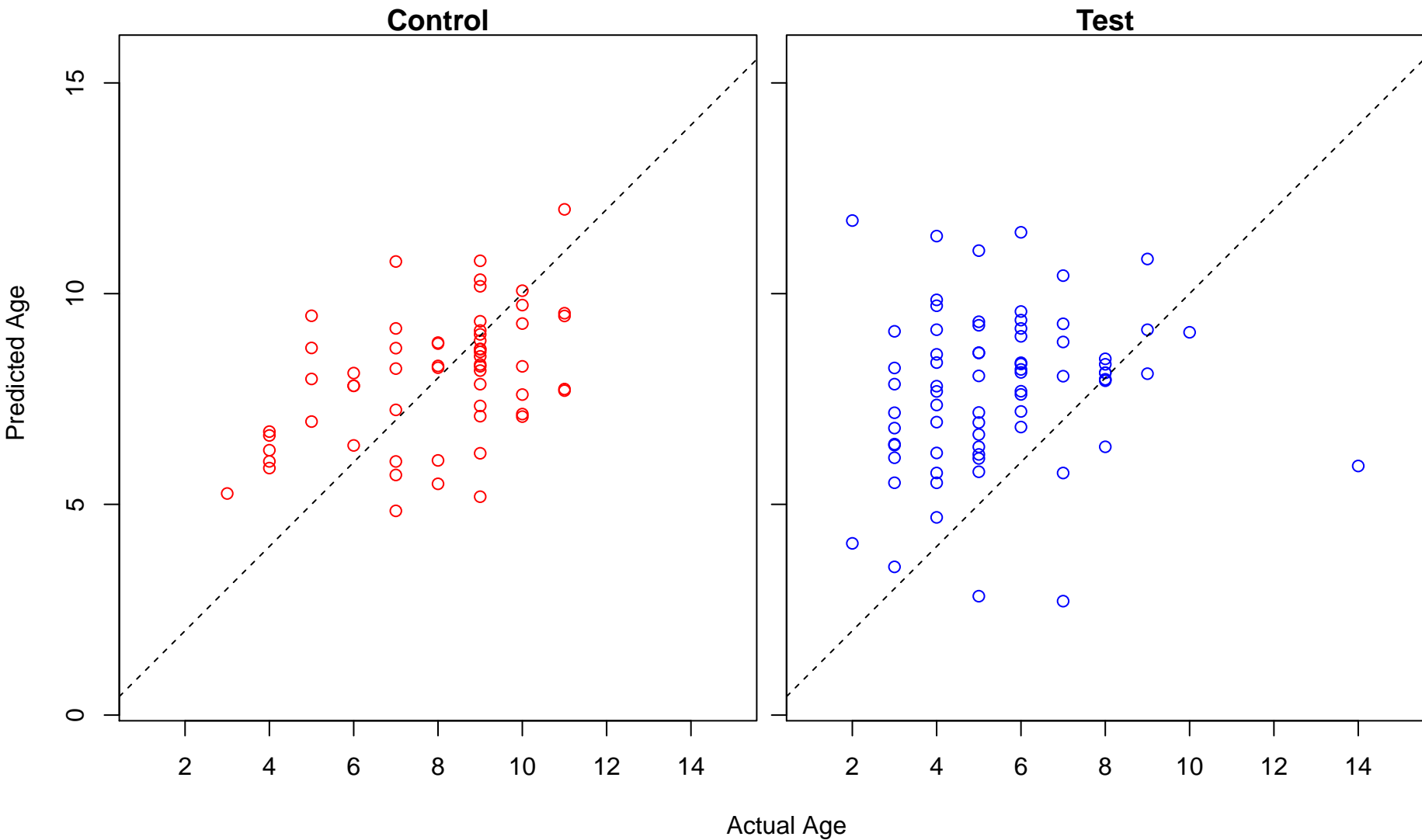
regulation of tyrosine phosphorylation of Stat3 protein (Score: 1.037602)



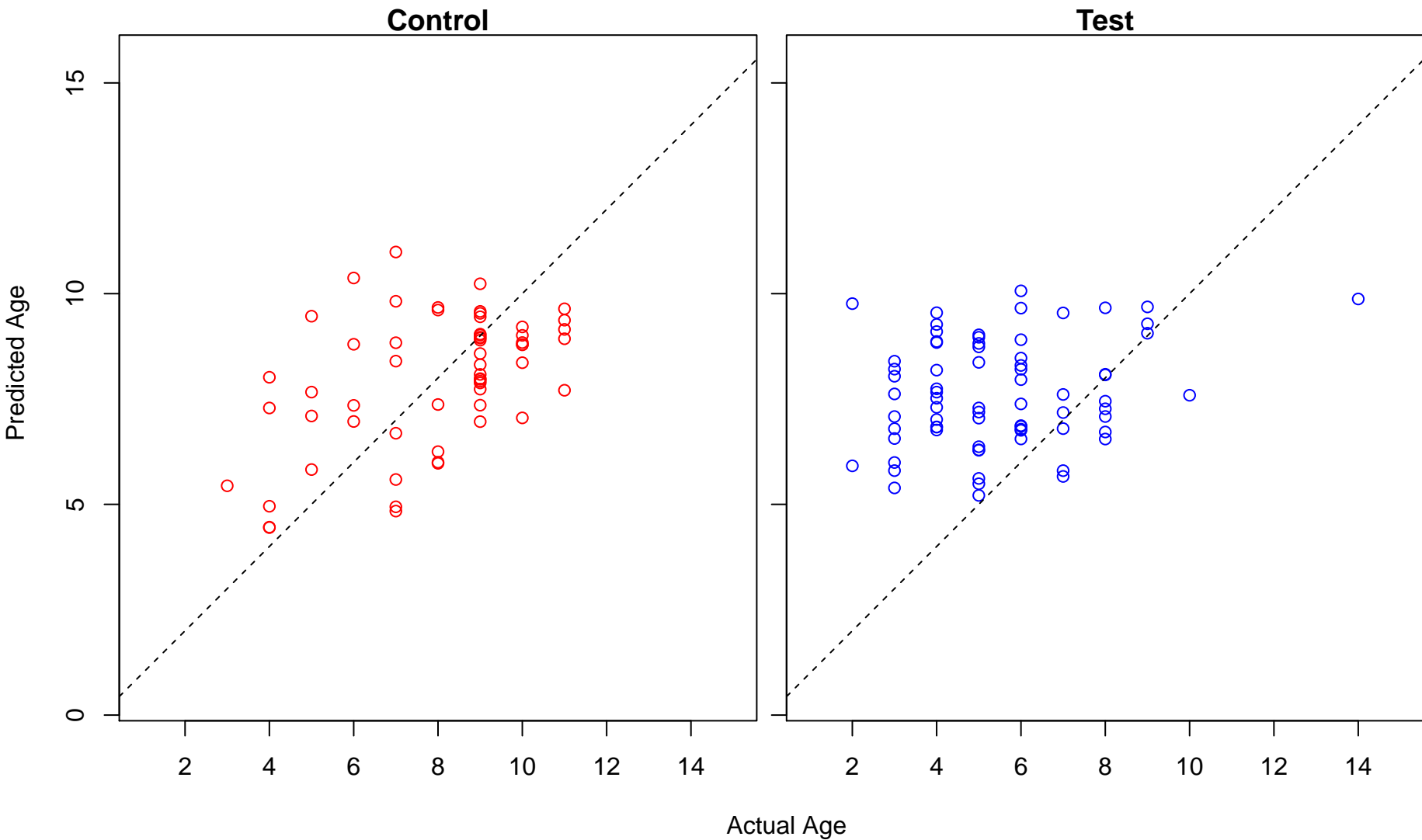
neural plate development (Score: 1.036656)



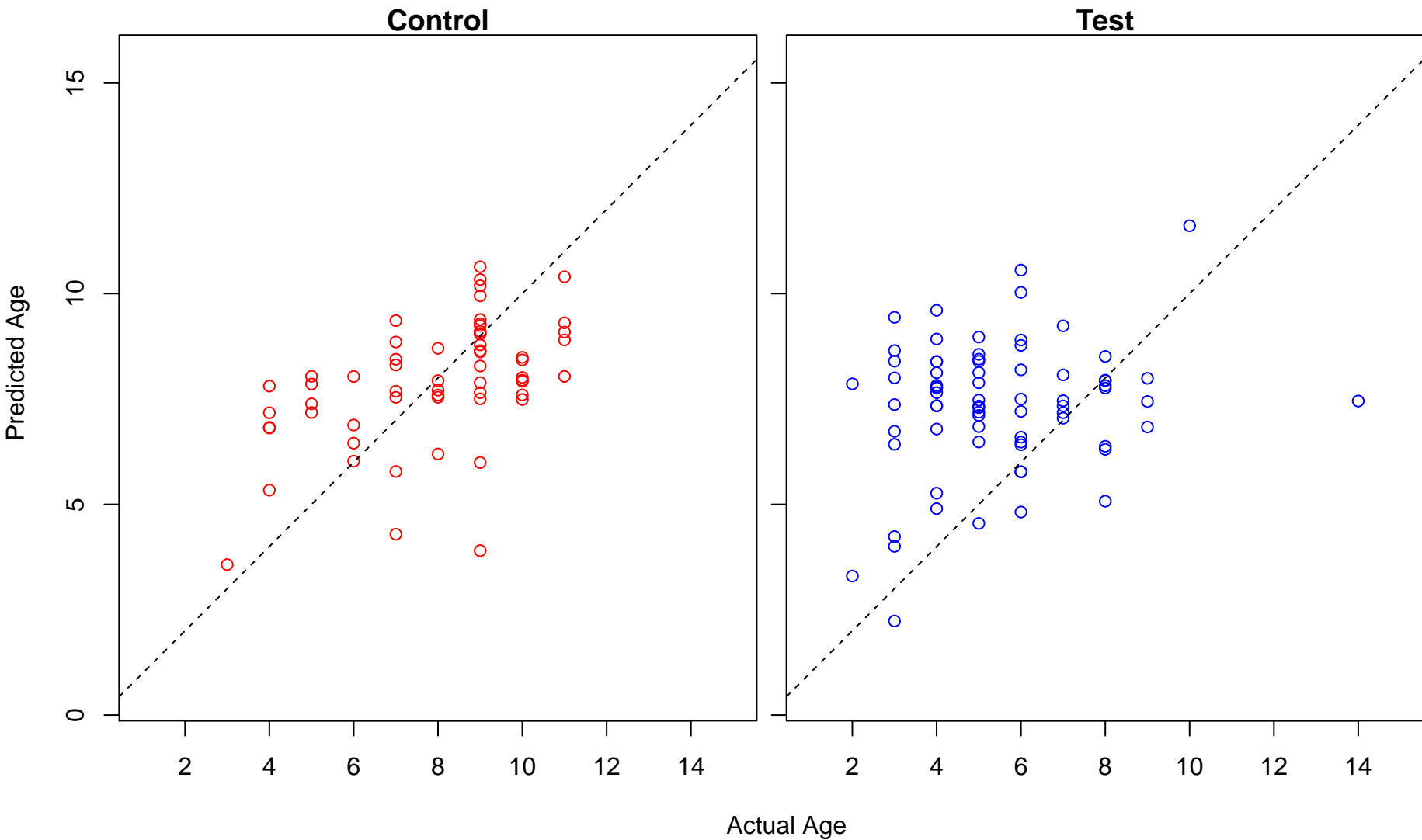
negative regulation of cellular macromolecule biosynthetic process (Score: 1.036269)



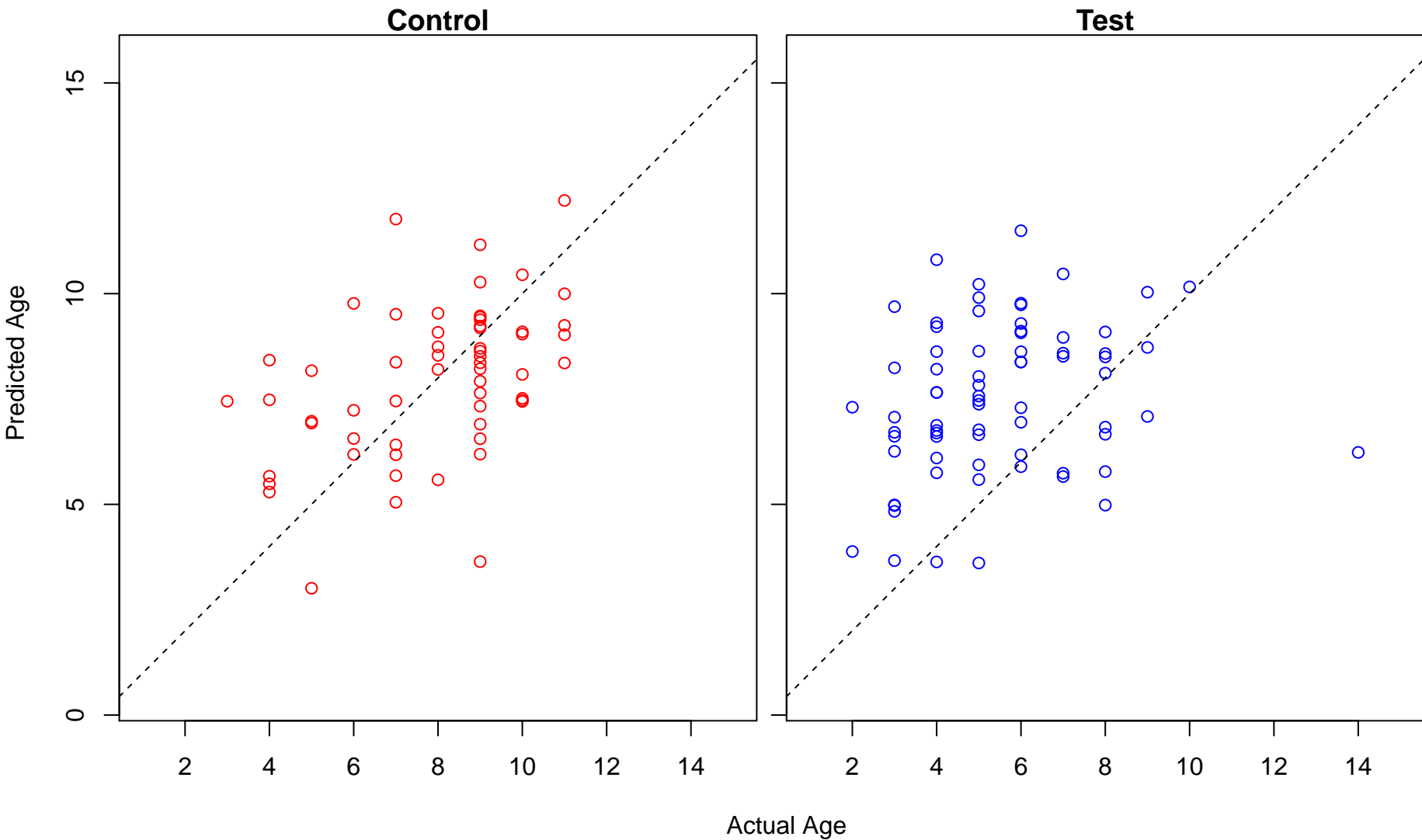
cation homeostasis (Score: 1.036152)



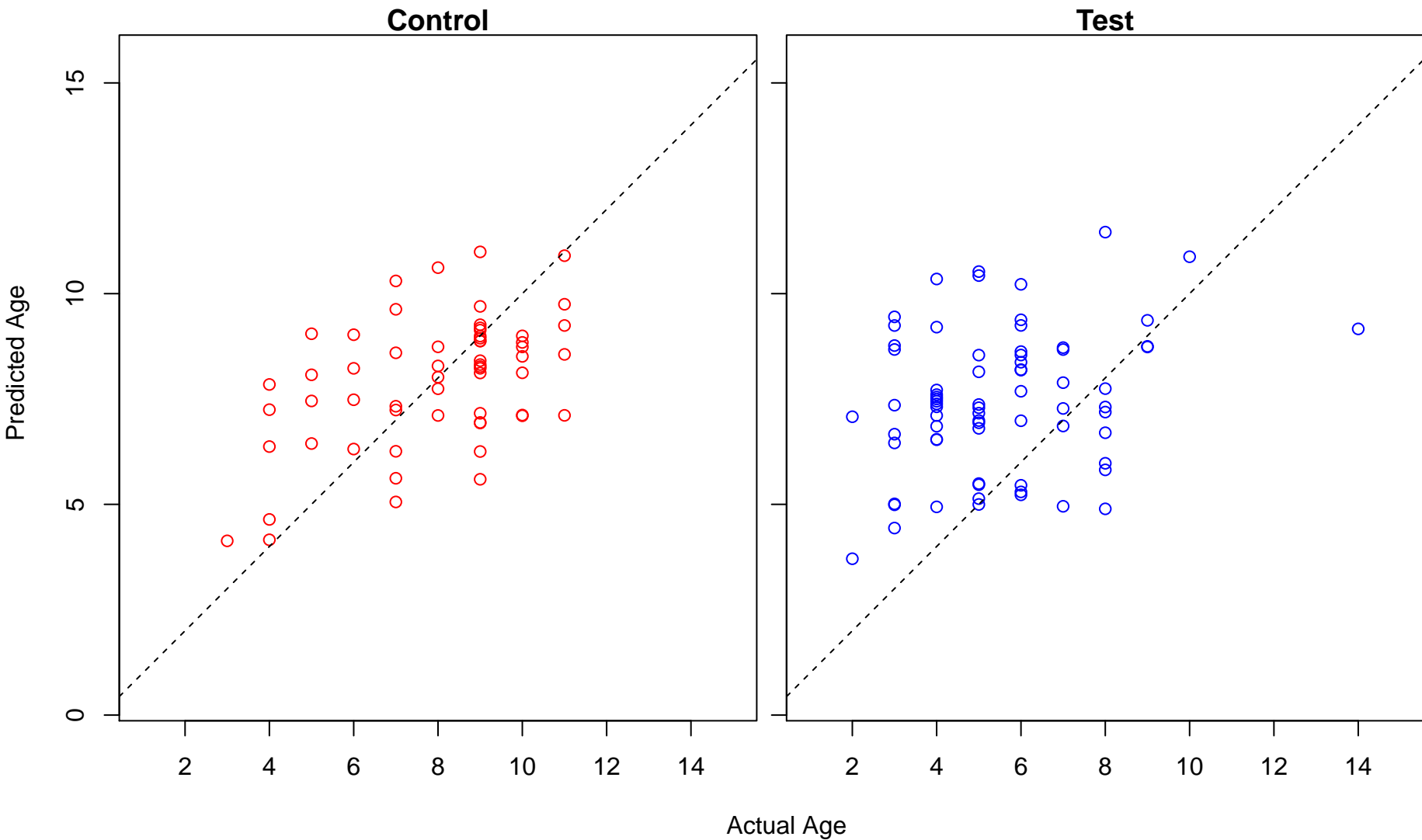
axial mesoderm development (Score: 1.034663)



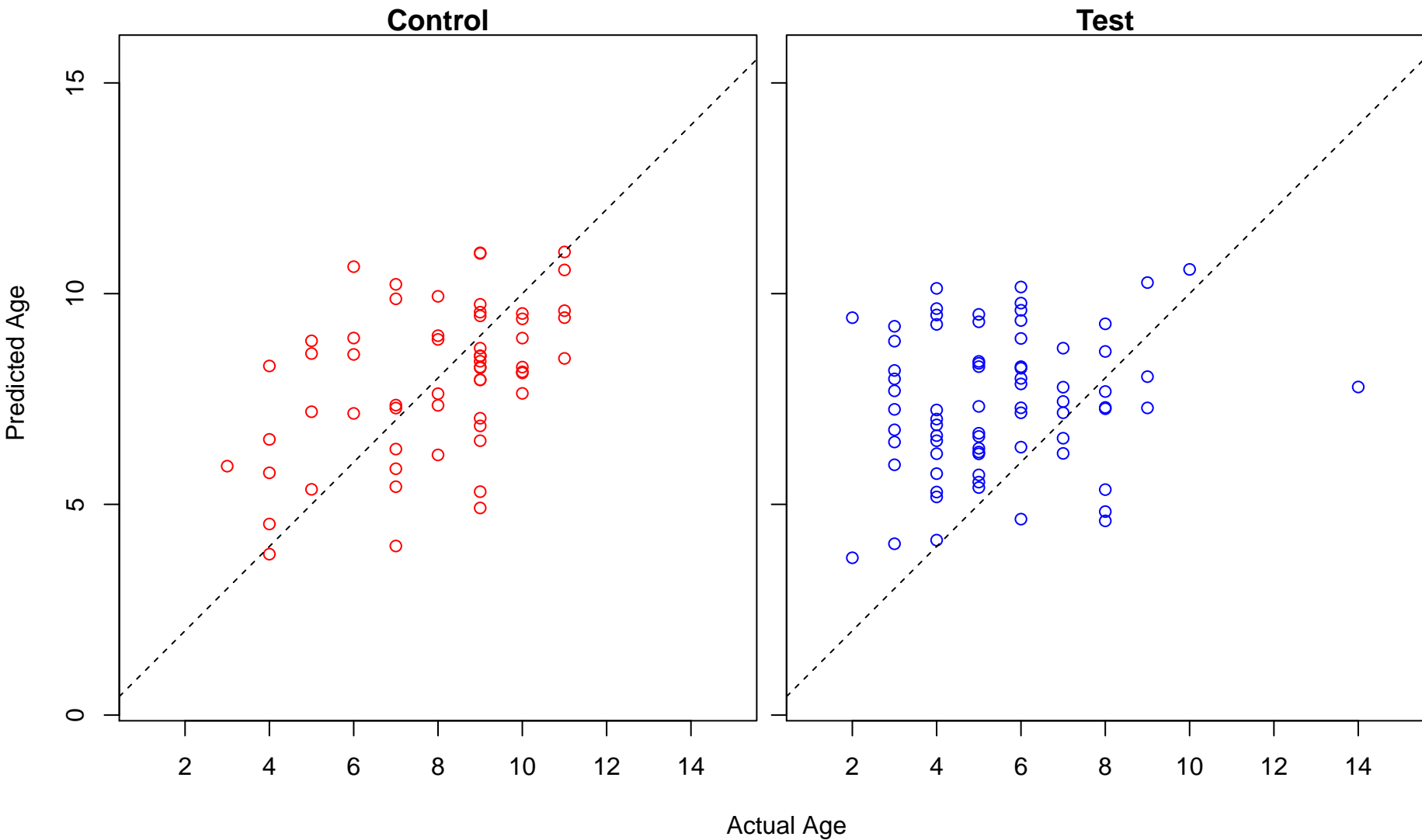
regulation of autophagy (Score: 1.033978)



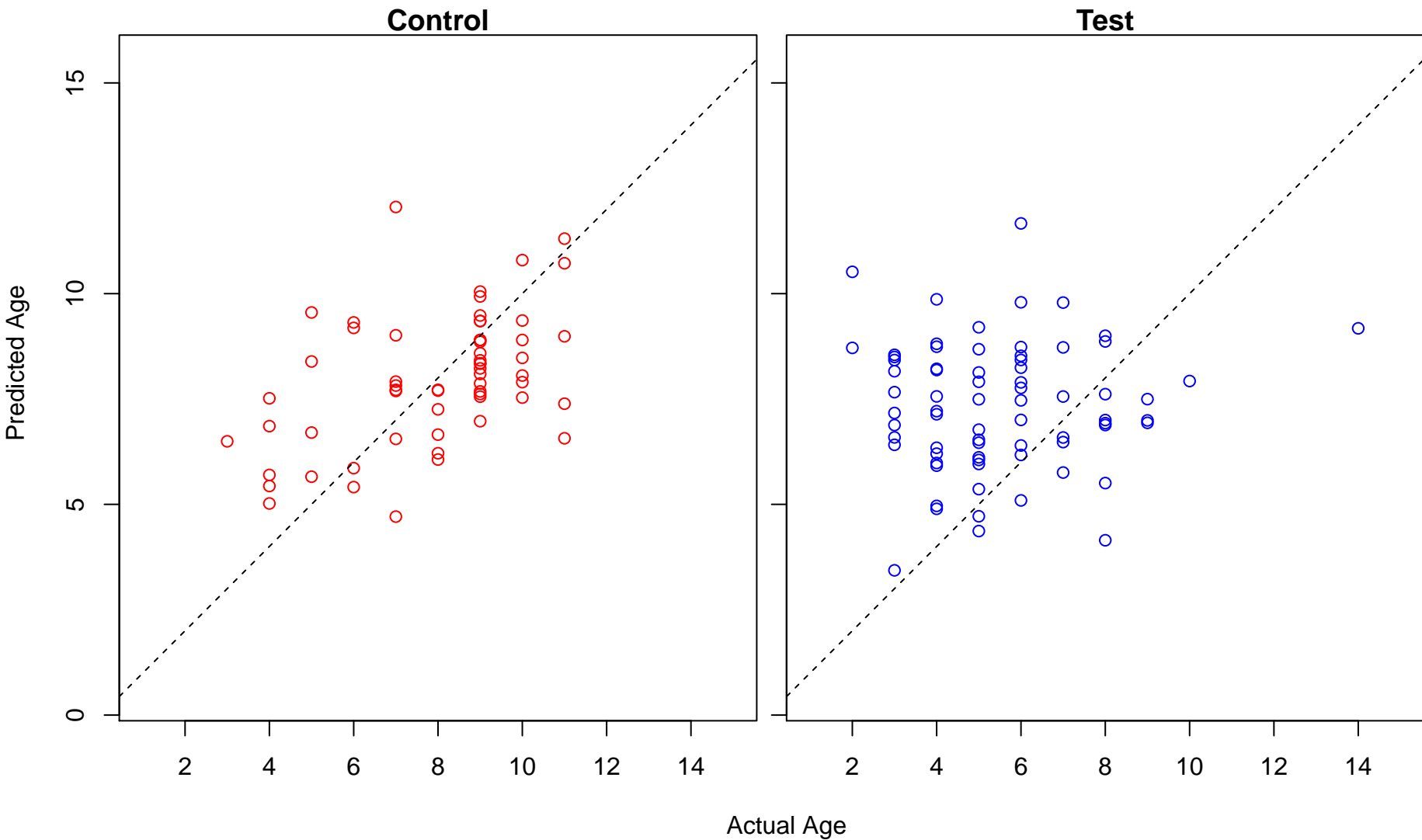
negative T cell selection (Score: 1.033672)



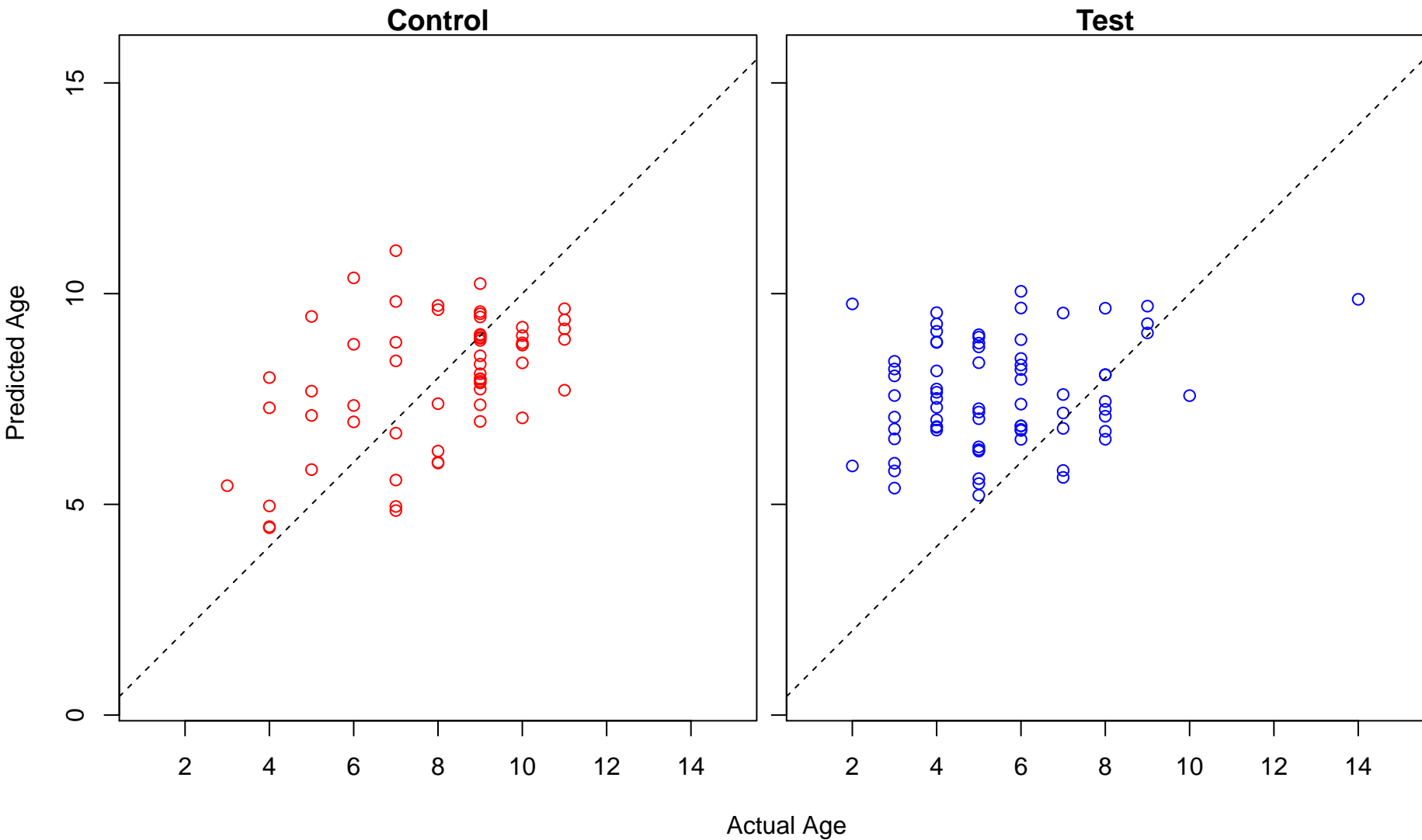
establishment of organelle localization (Score: 1.031990)



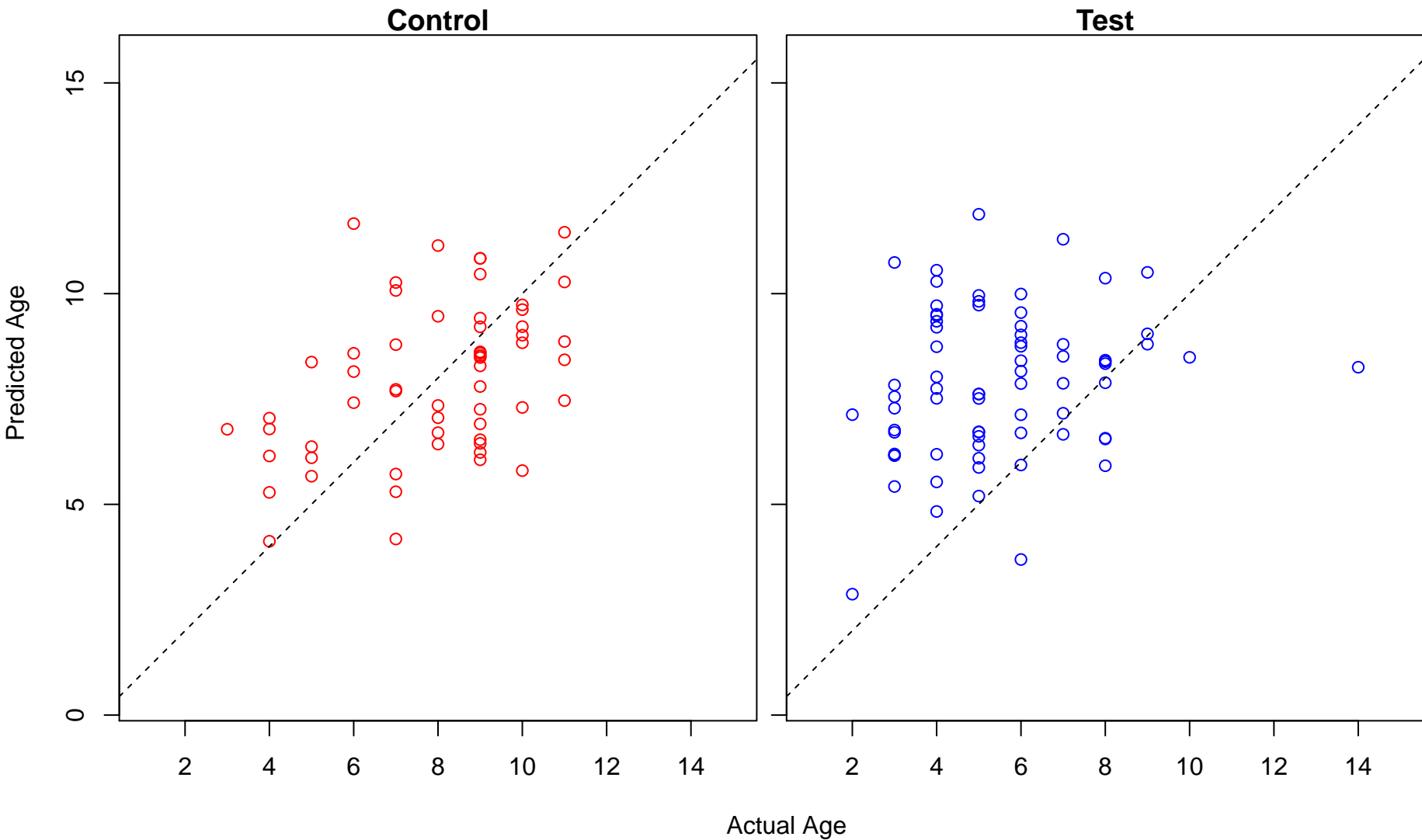
nucleoside monophosphate biosynthetic process (Score: 1.031305)



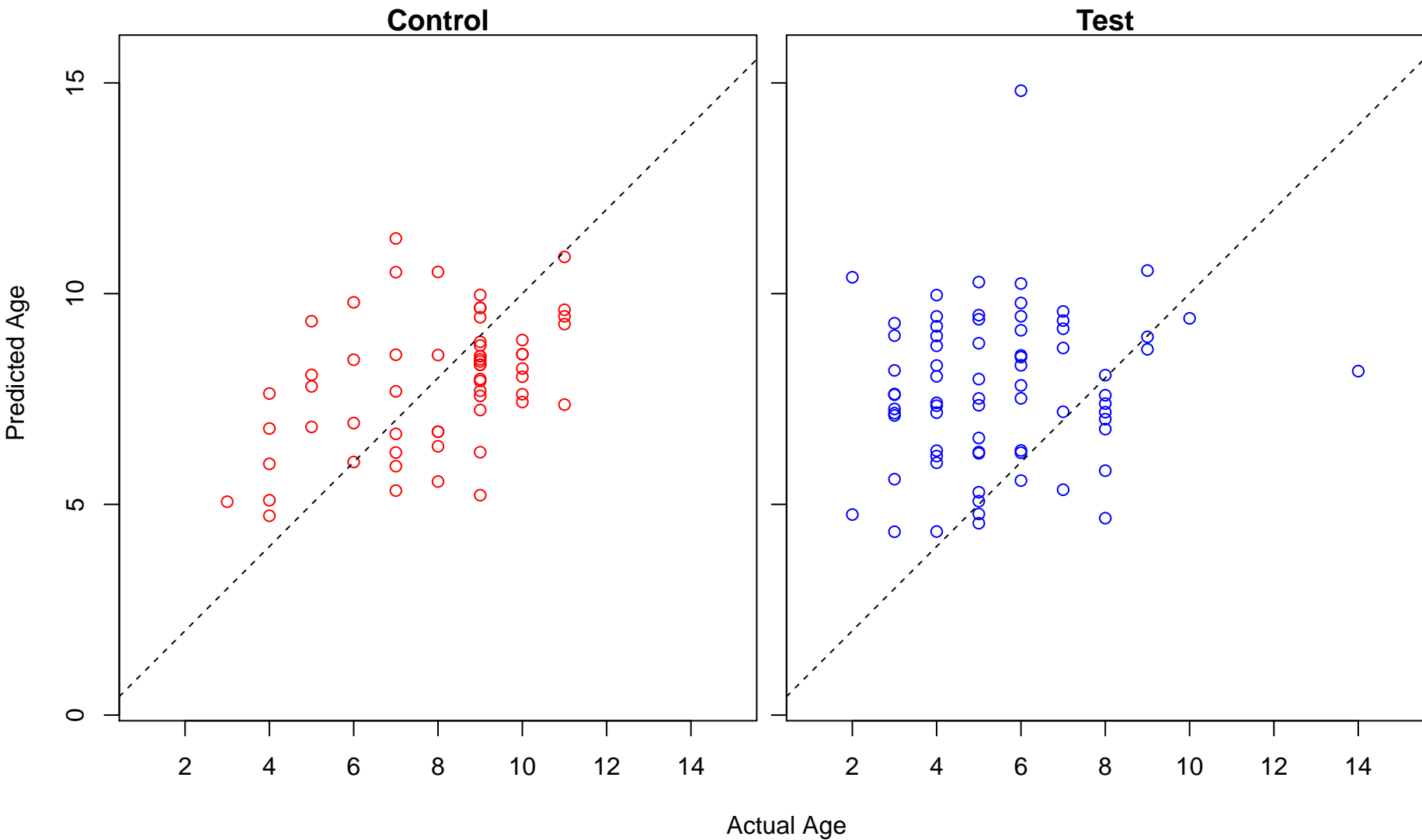
ion homeostasis (Score: 1.030893)



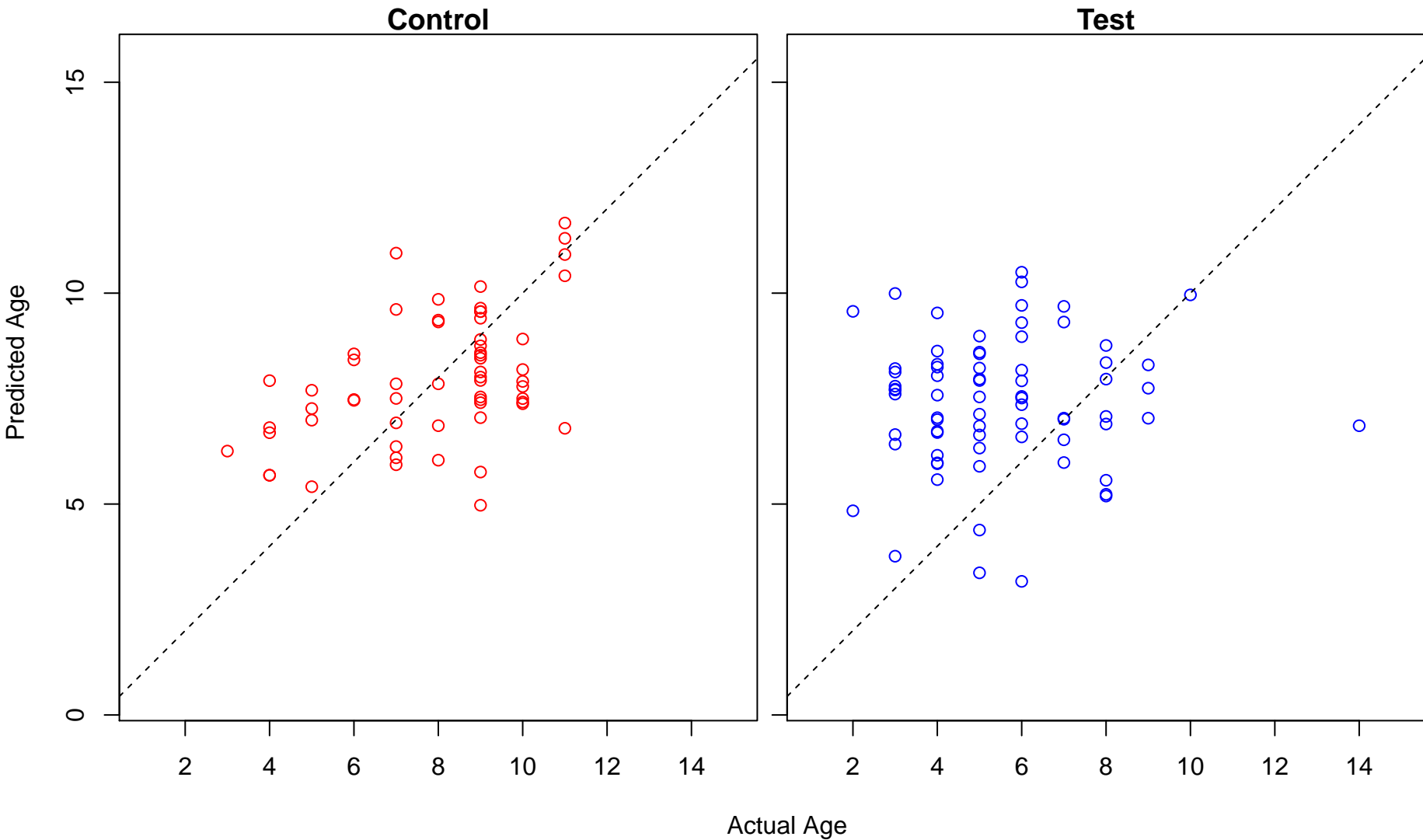
regulation of nervous system development (Score: 1.030659)



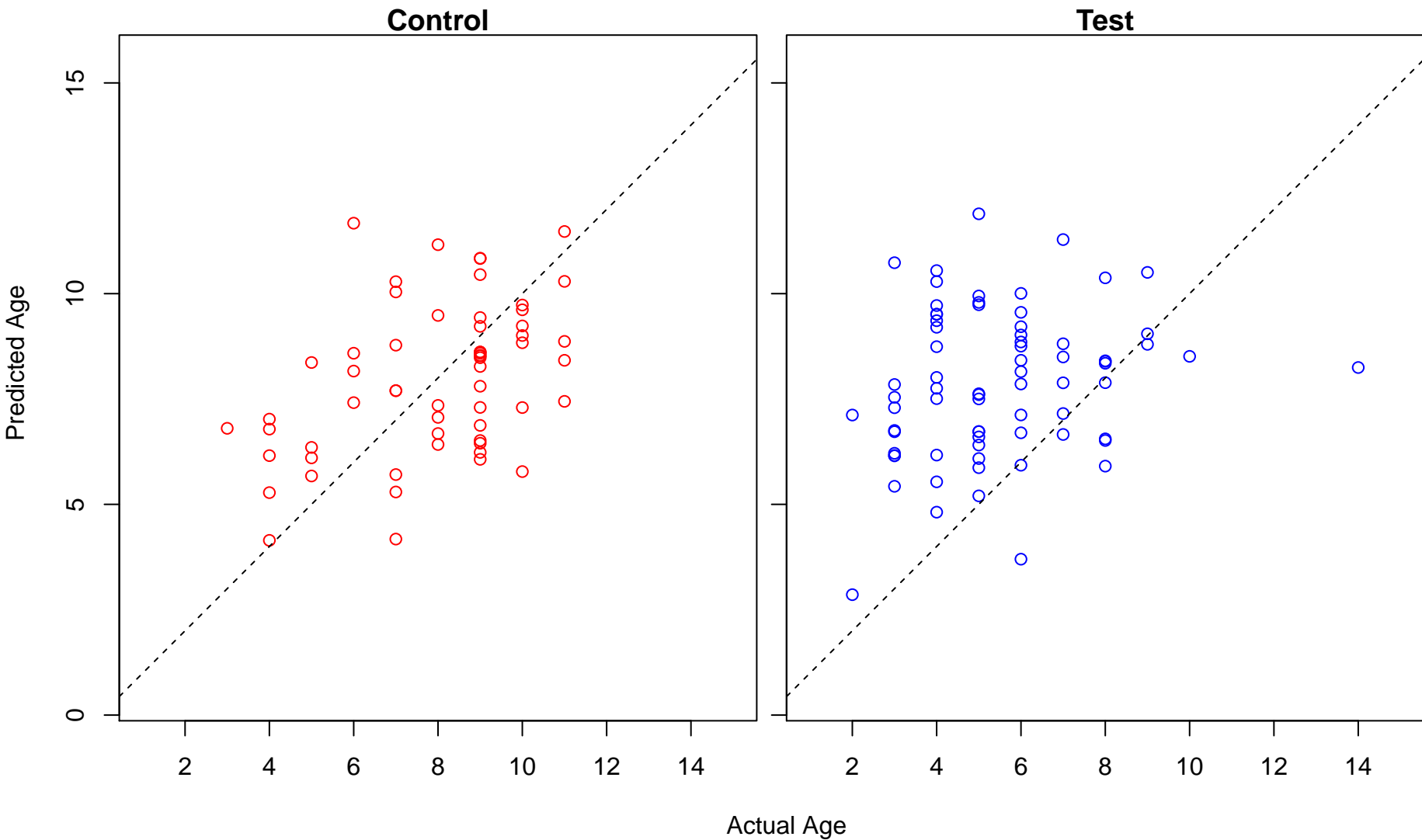
fibroblast growth factor receptor signaling pathway (Score: 1.029582)



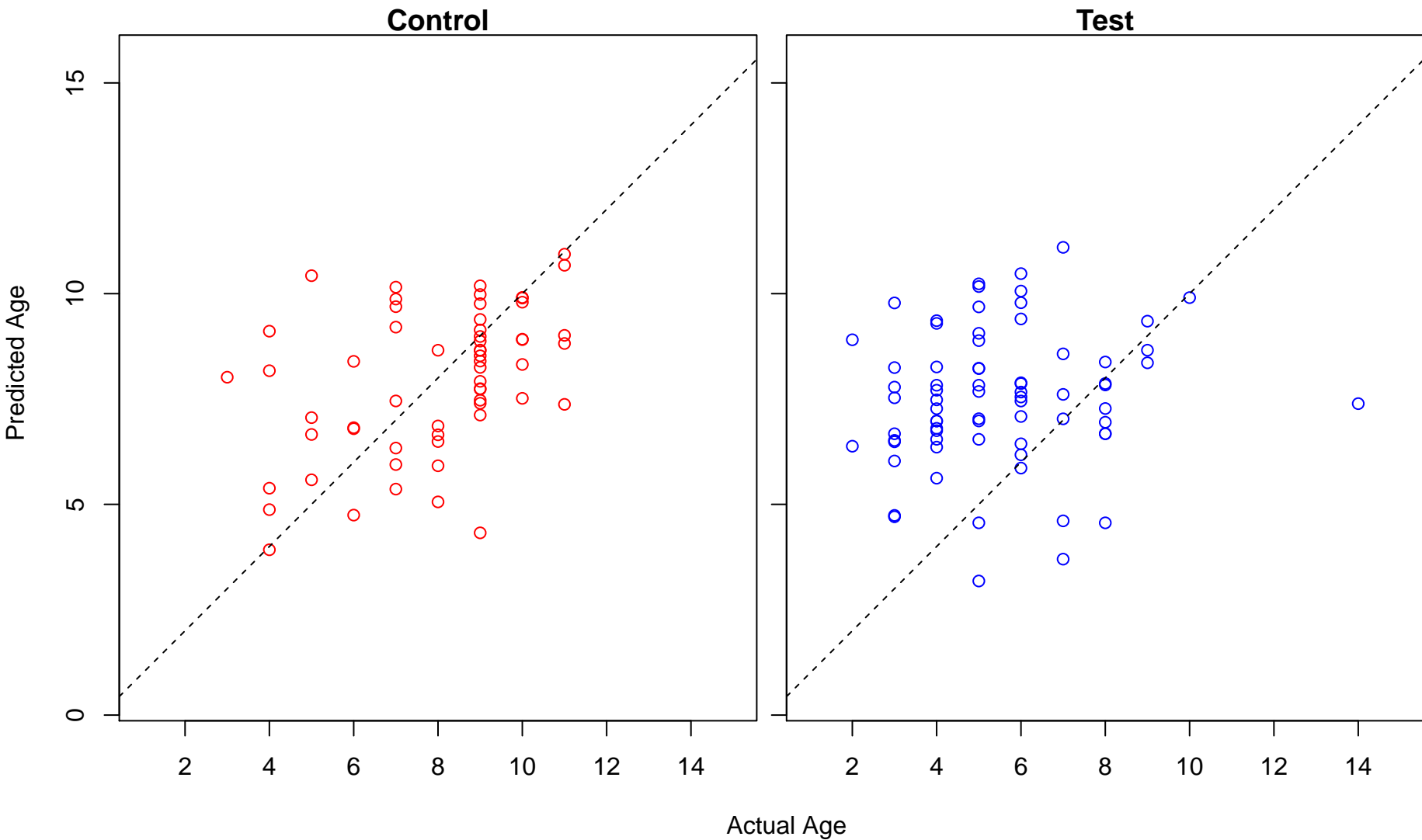
positive regulation of homeostatic process (Score: 1.029471)



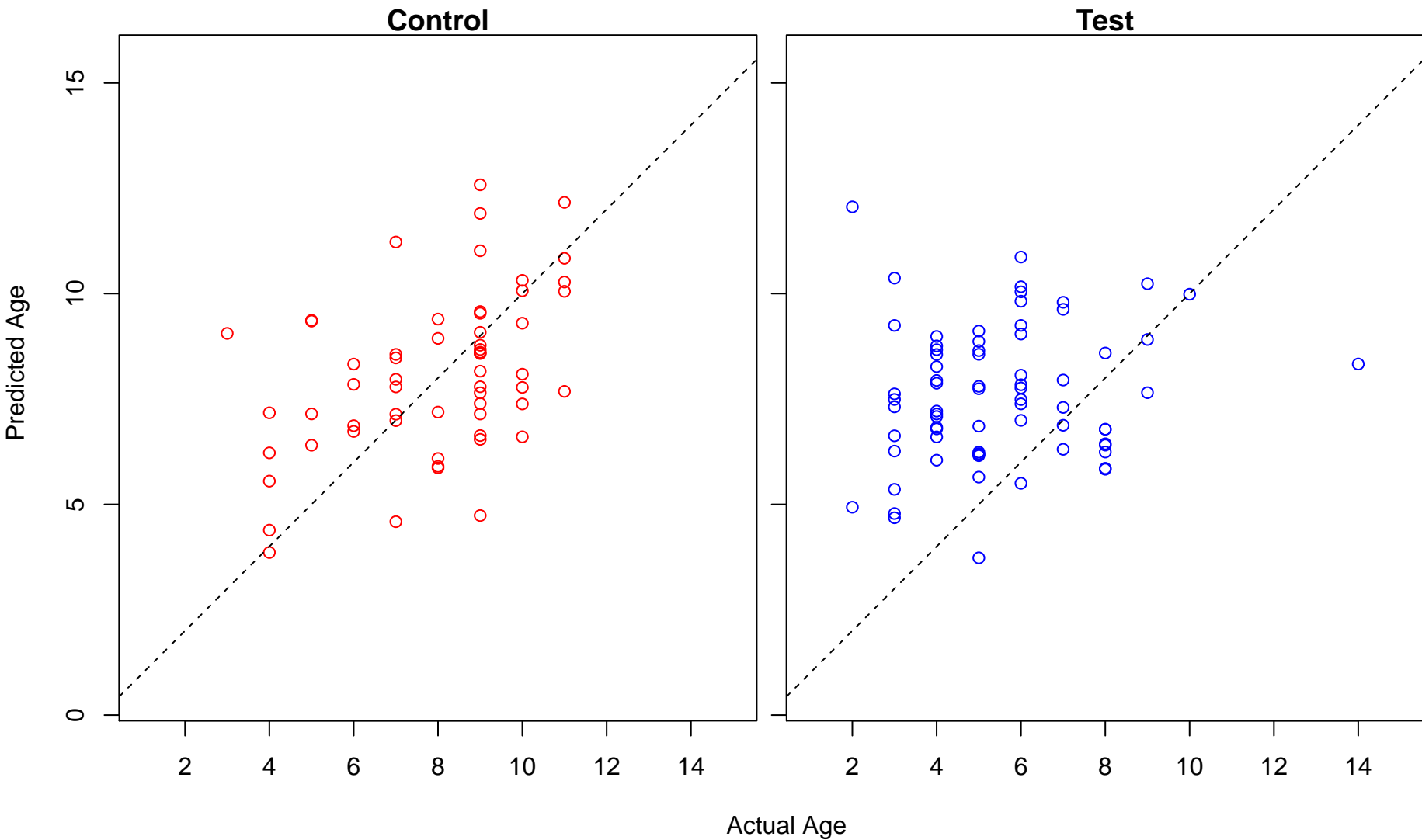
regulation of neurogenesis (Score: 1.029282)



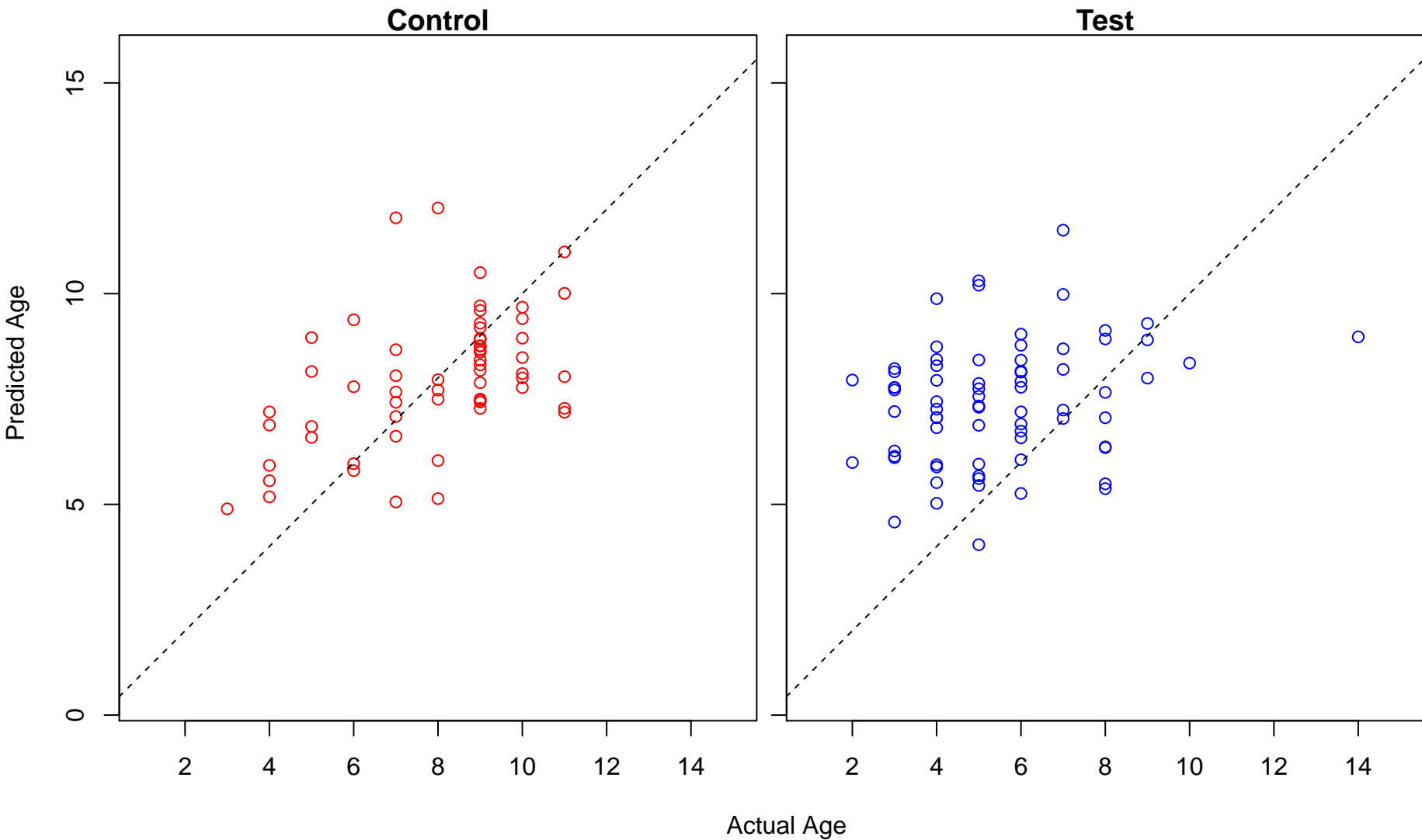
cellular catabolic process (Score: 1.027194)



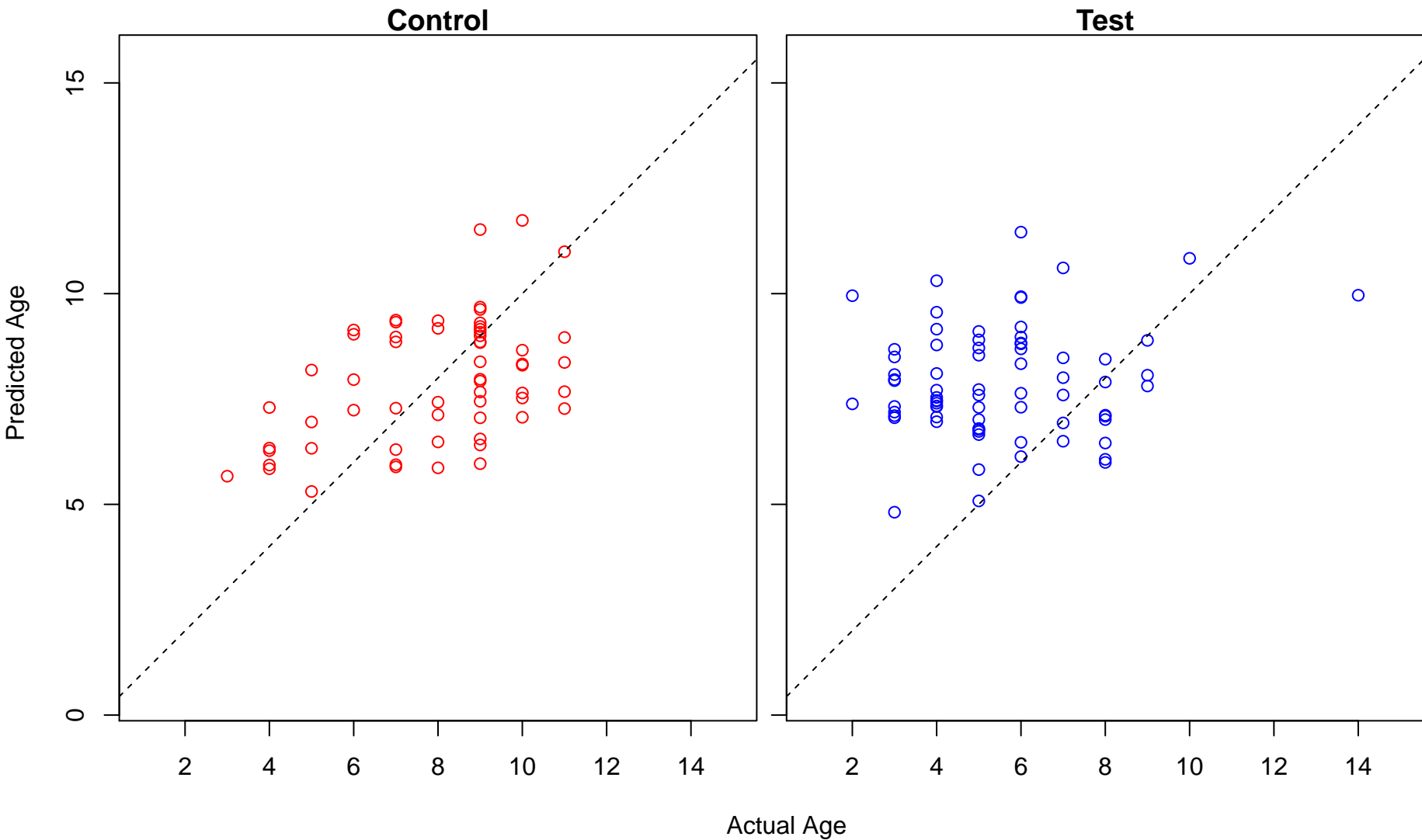
mitochondrial membrane organization (Score: 1.025724)



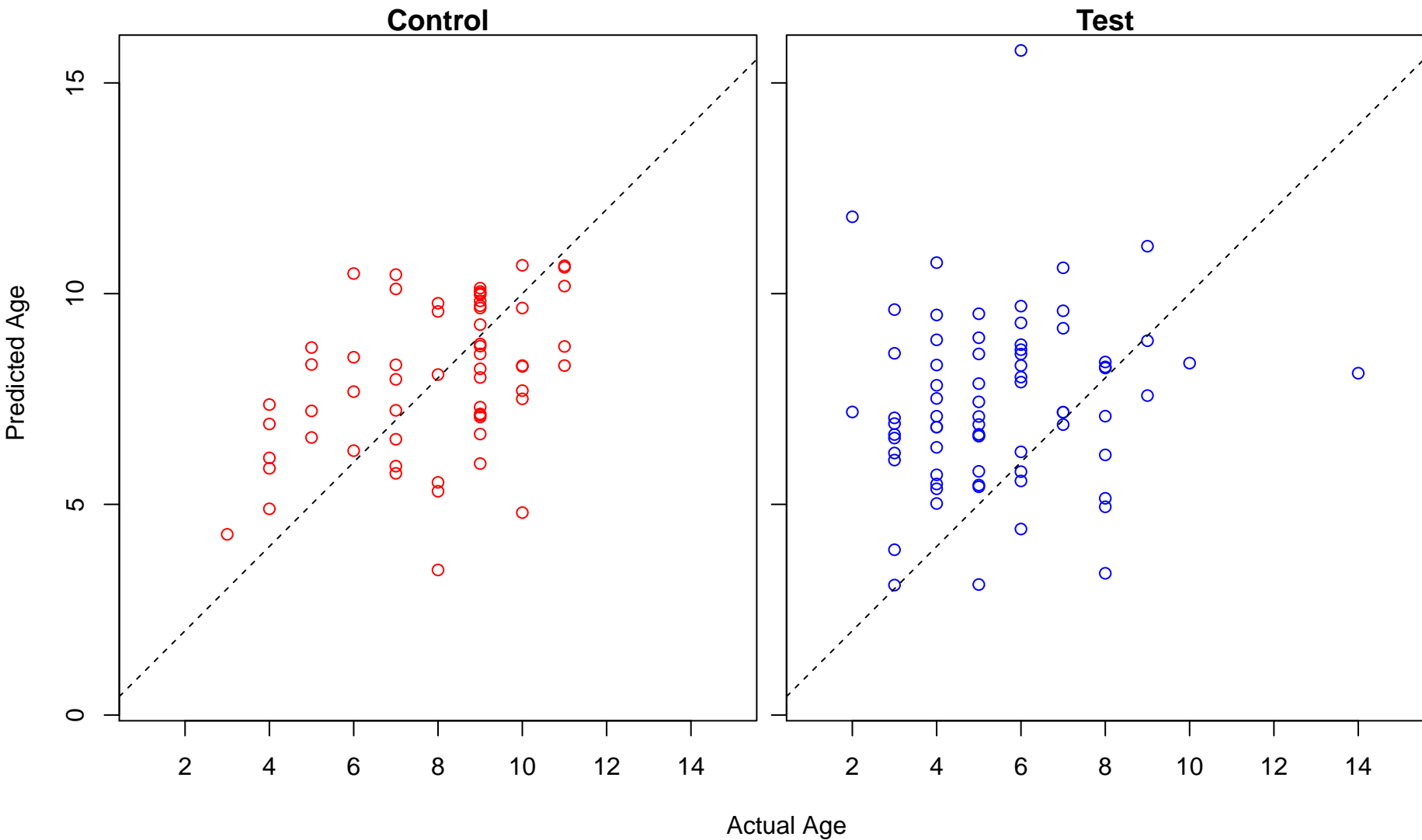
muscle cell proliferation (Score: 1.024684)



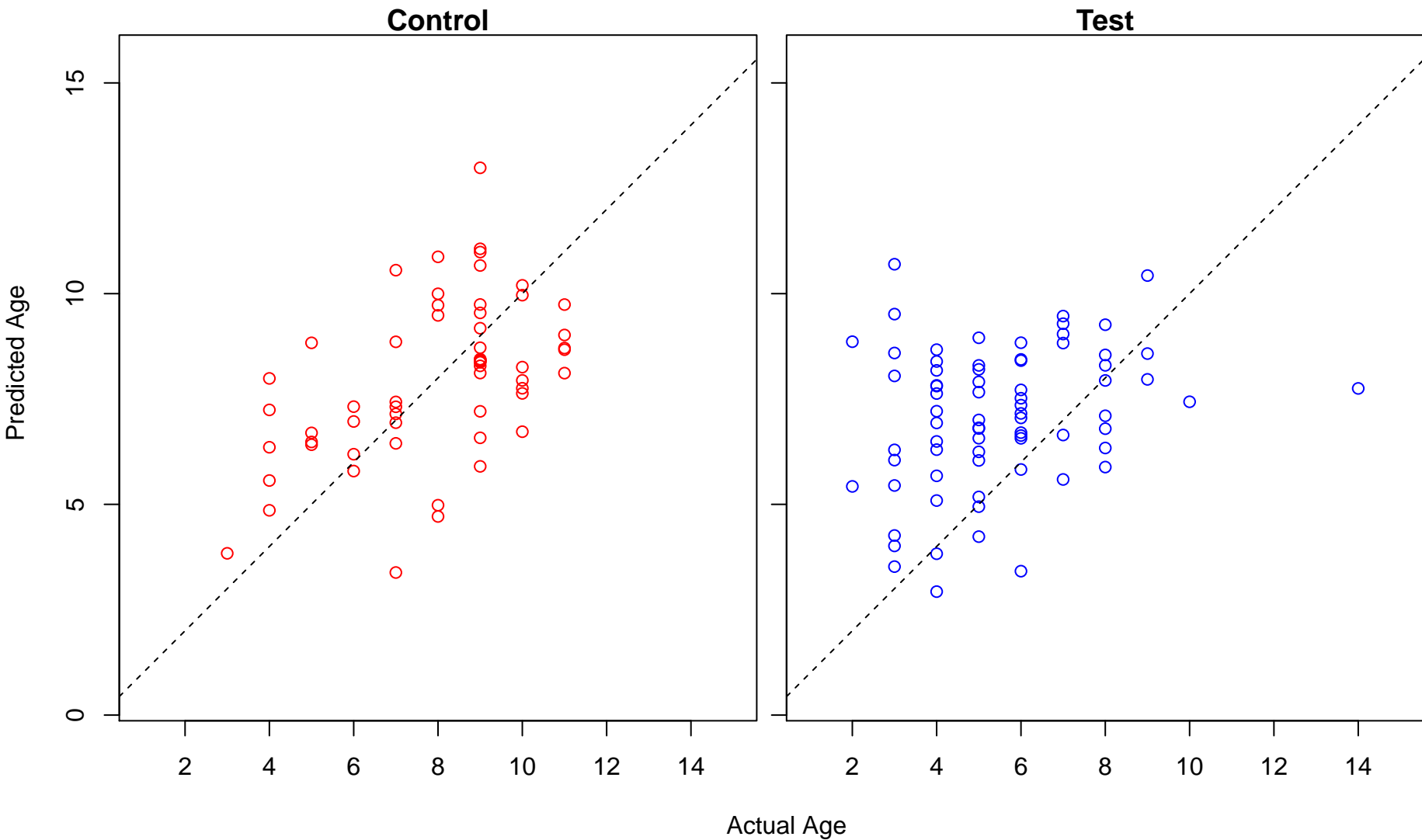
regulation of mitochondrion organization (Score: 1.024443)



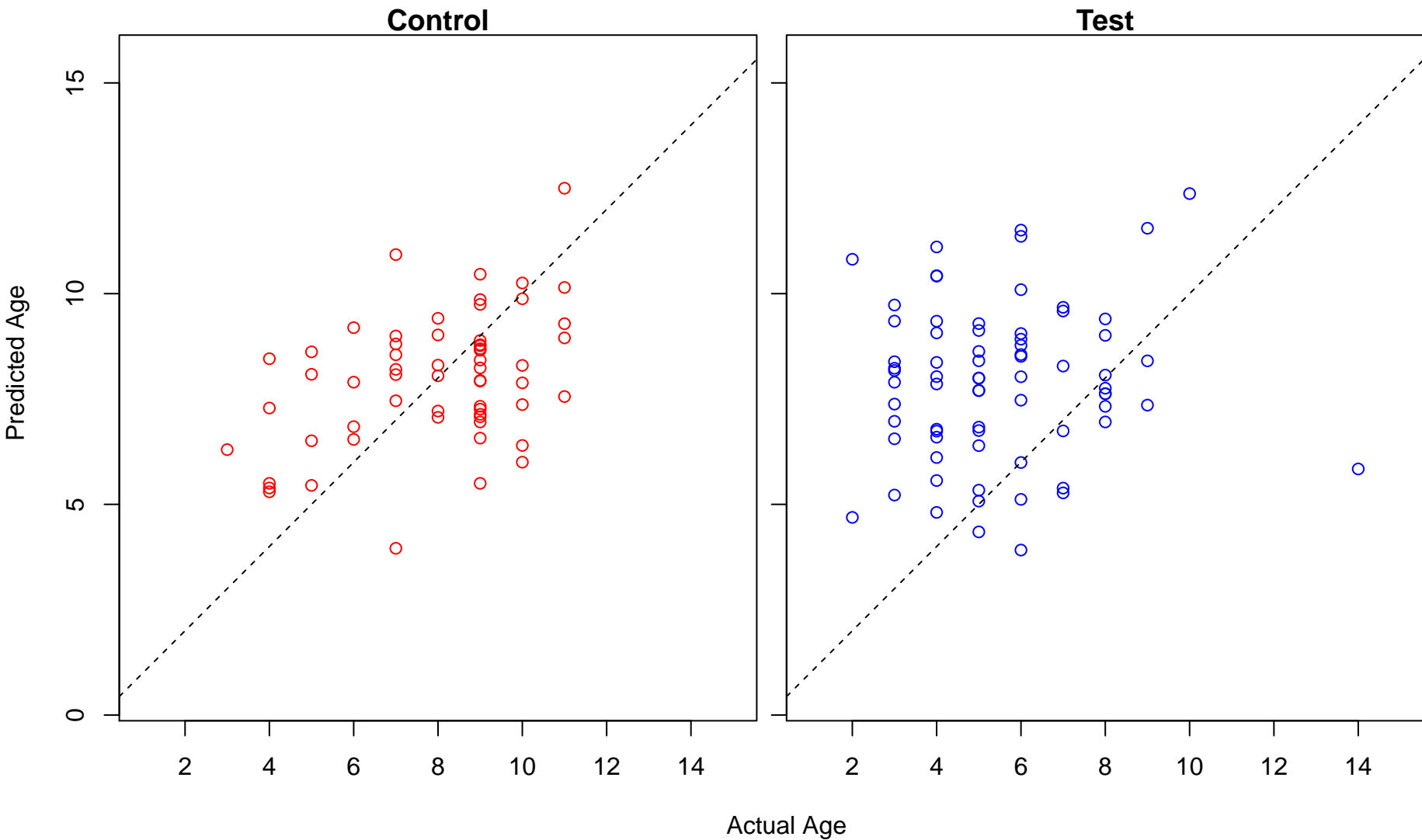
leukocyte mediated immunity (Score: 1.024041)



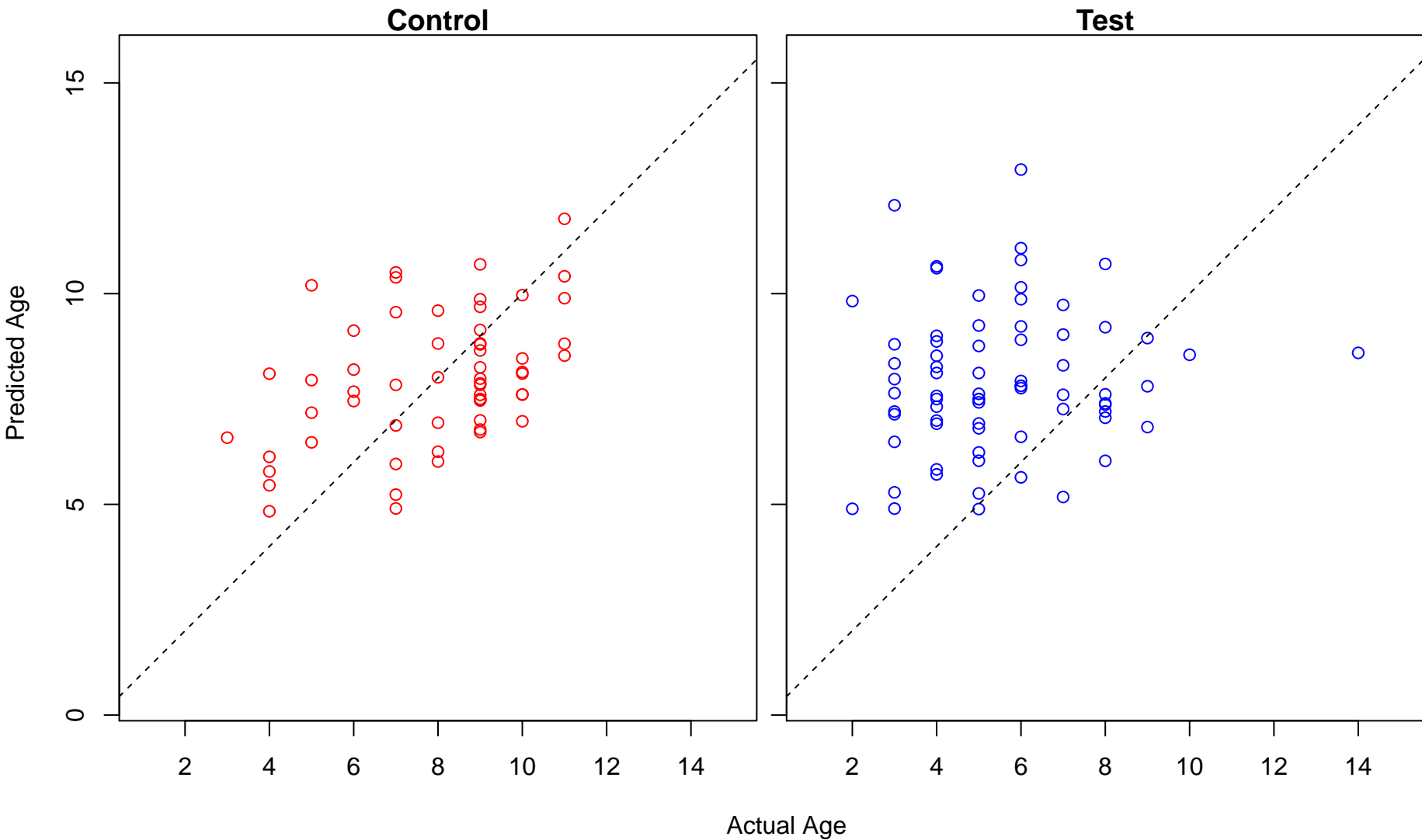
organ growth (Score: 1.024000)



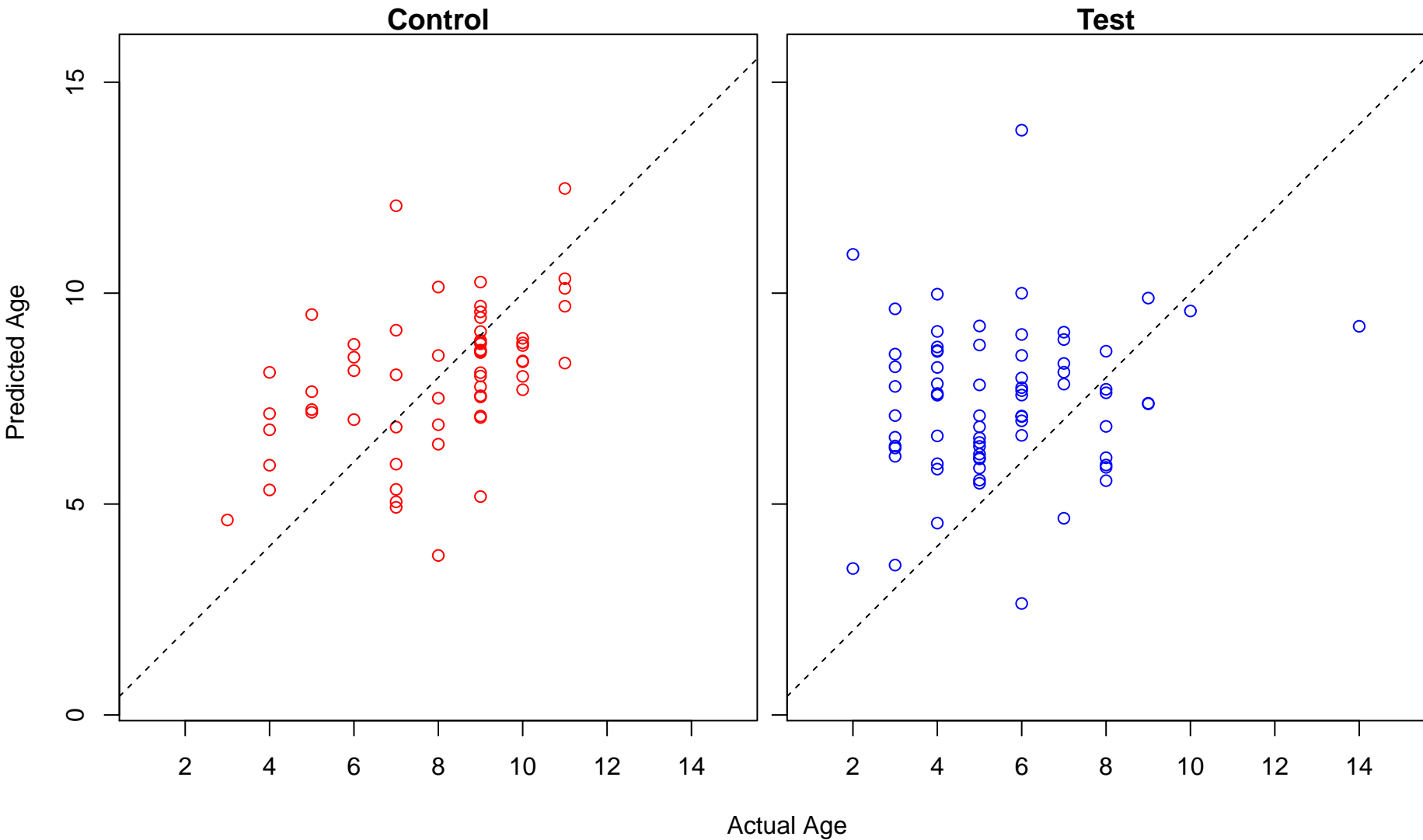
regulation of lymphocyte differentiation (Score: 1.023478)



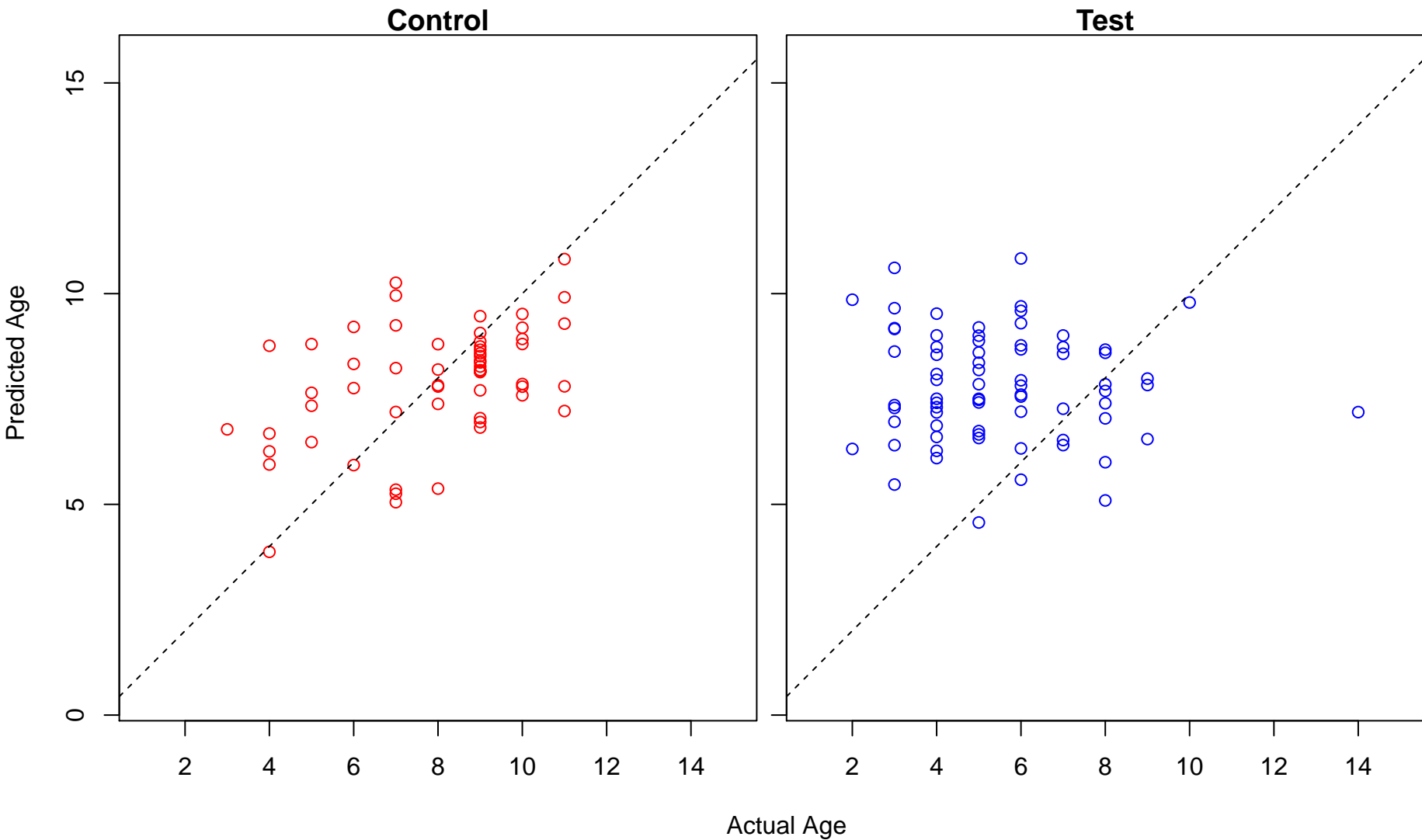
regulation of cell morphogenesis involved in differentiation (Score: 1.023172)



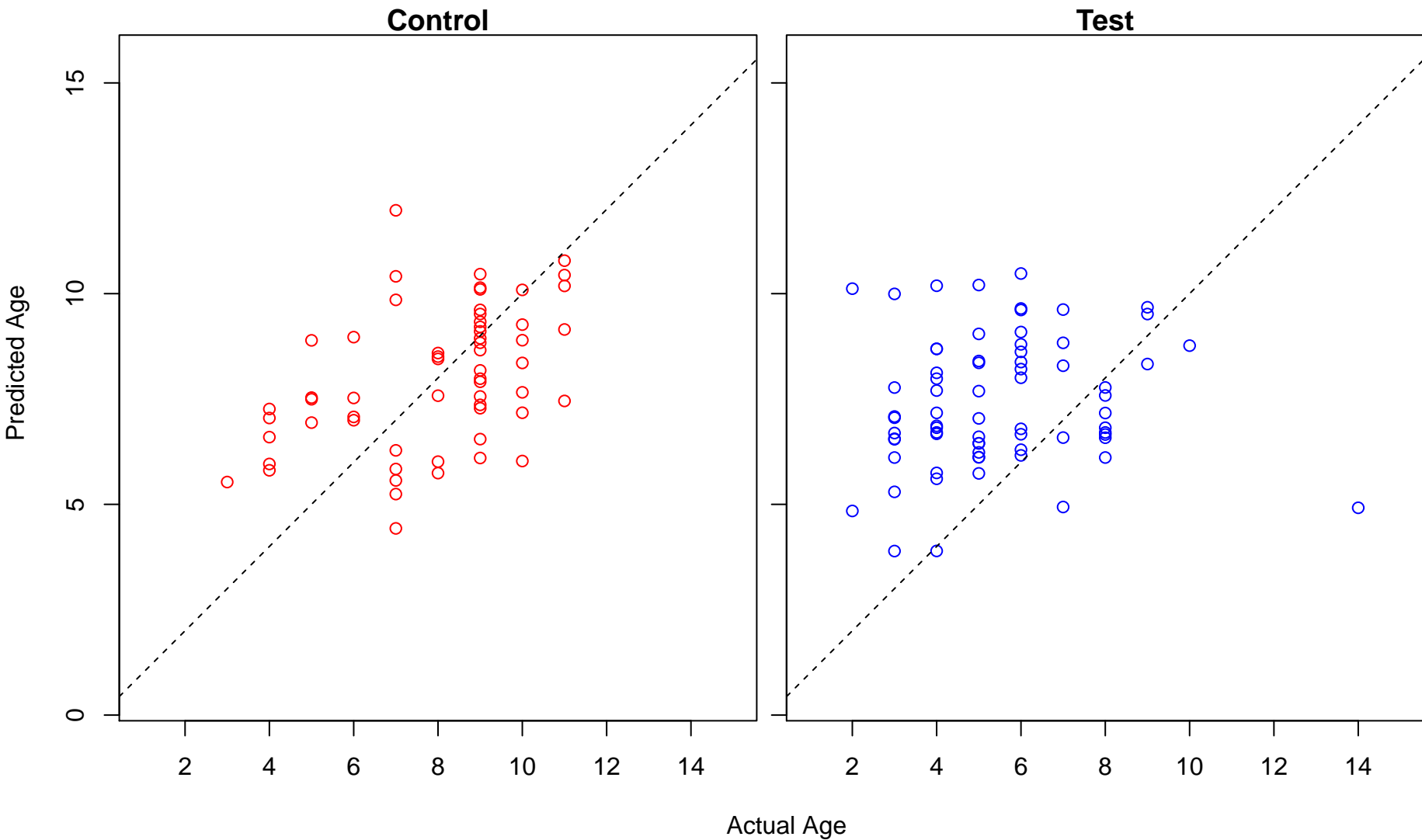
regulation of establishment of protein localization (Score: 1.022905)



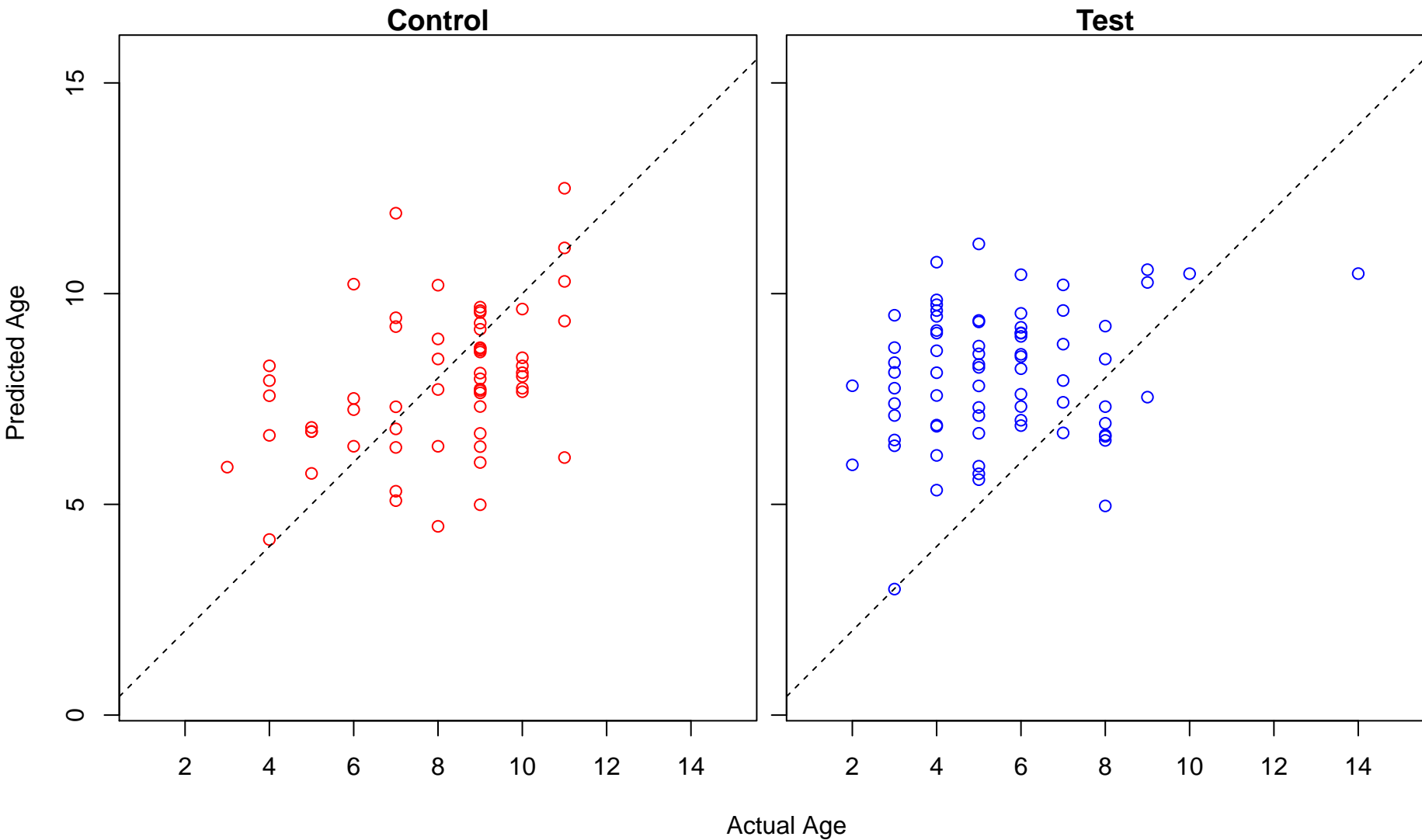
mRNA splice site selection (Score: 1.022474)



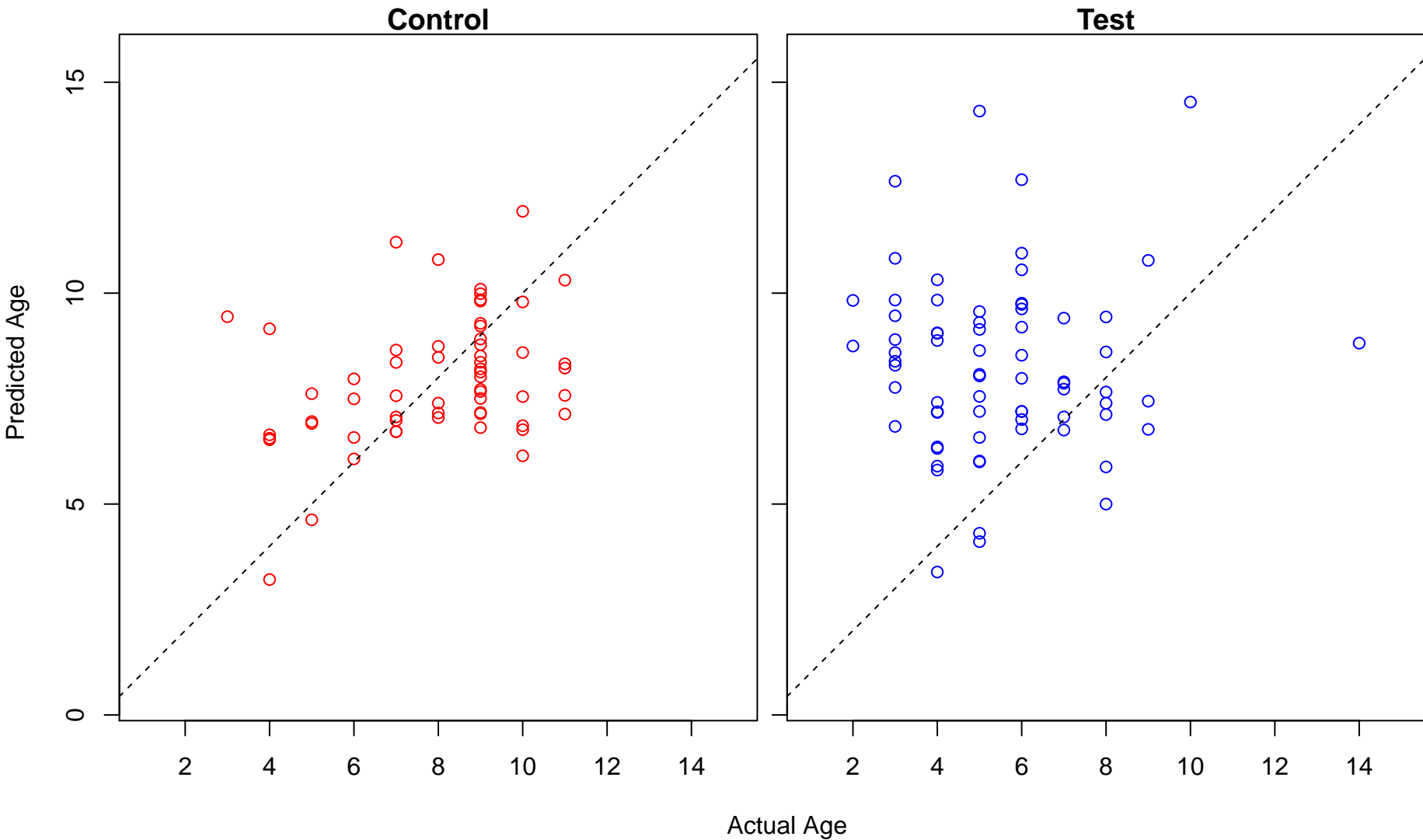
positive regulation of catabolic process (Score: 1.022290)



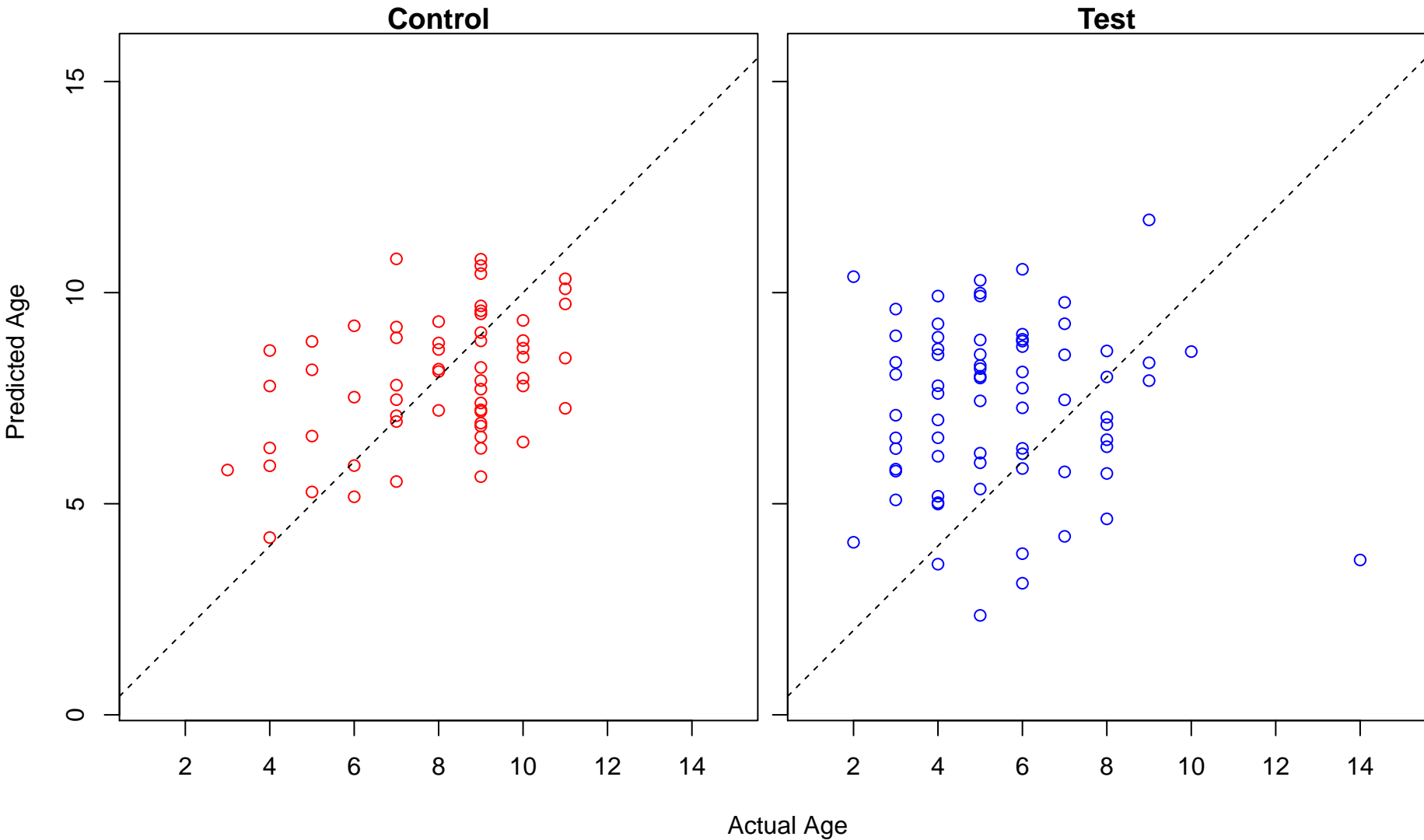
protein K11-linked ubiquitination (Score: 1.022196)



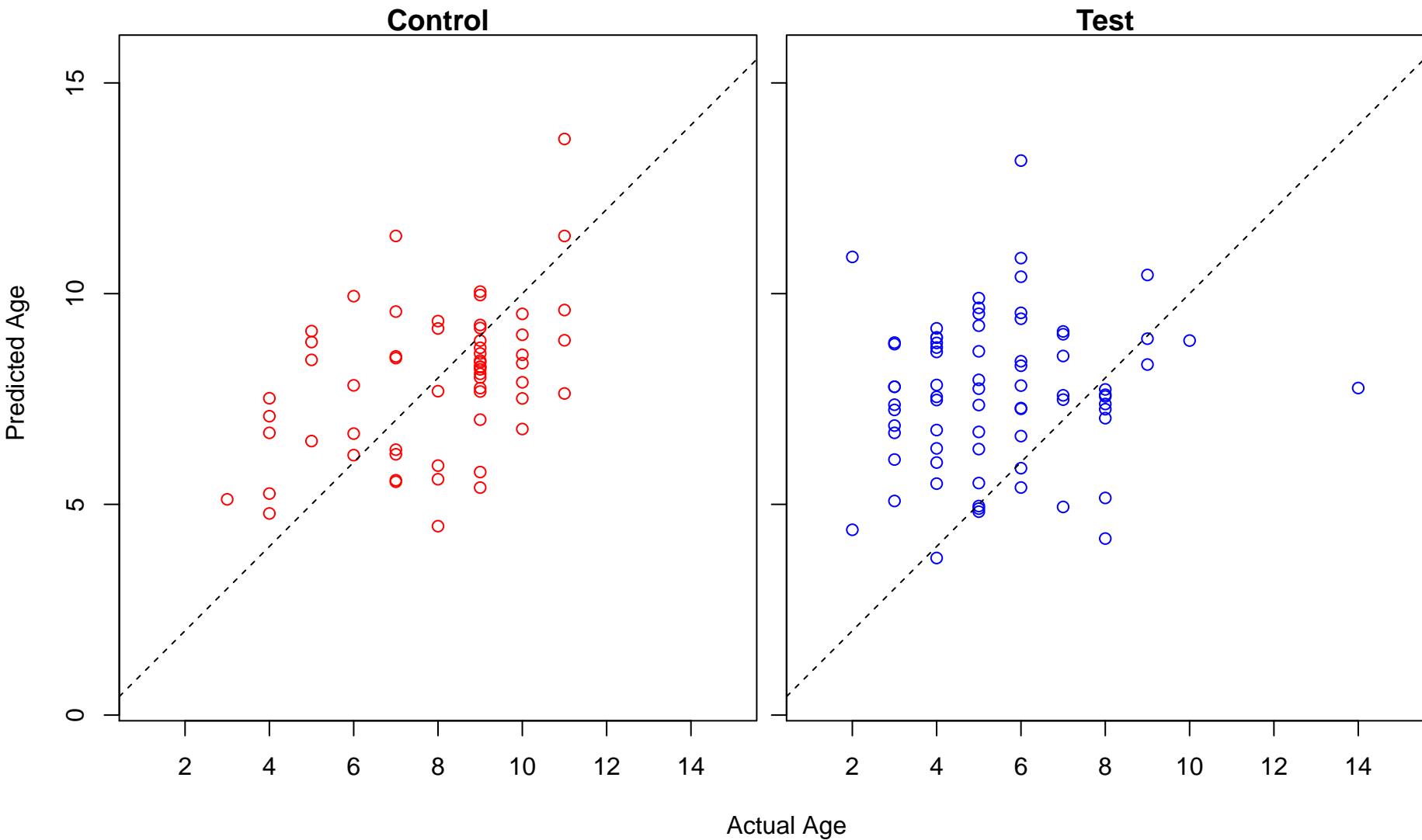
protein kinase C-activating G-protein coupled receptor signaling pathway (Score: 1.021929)



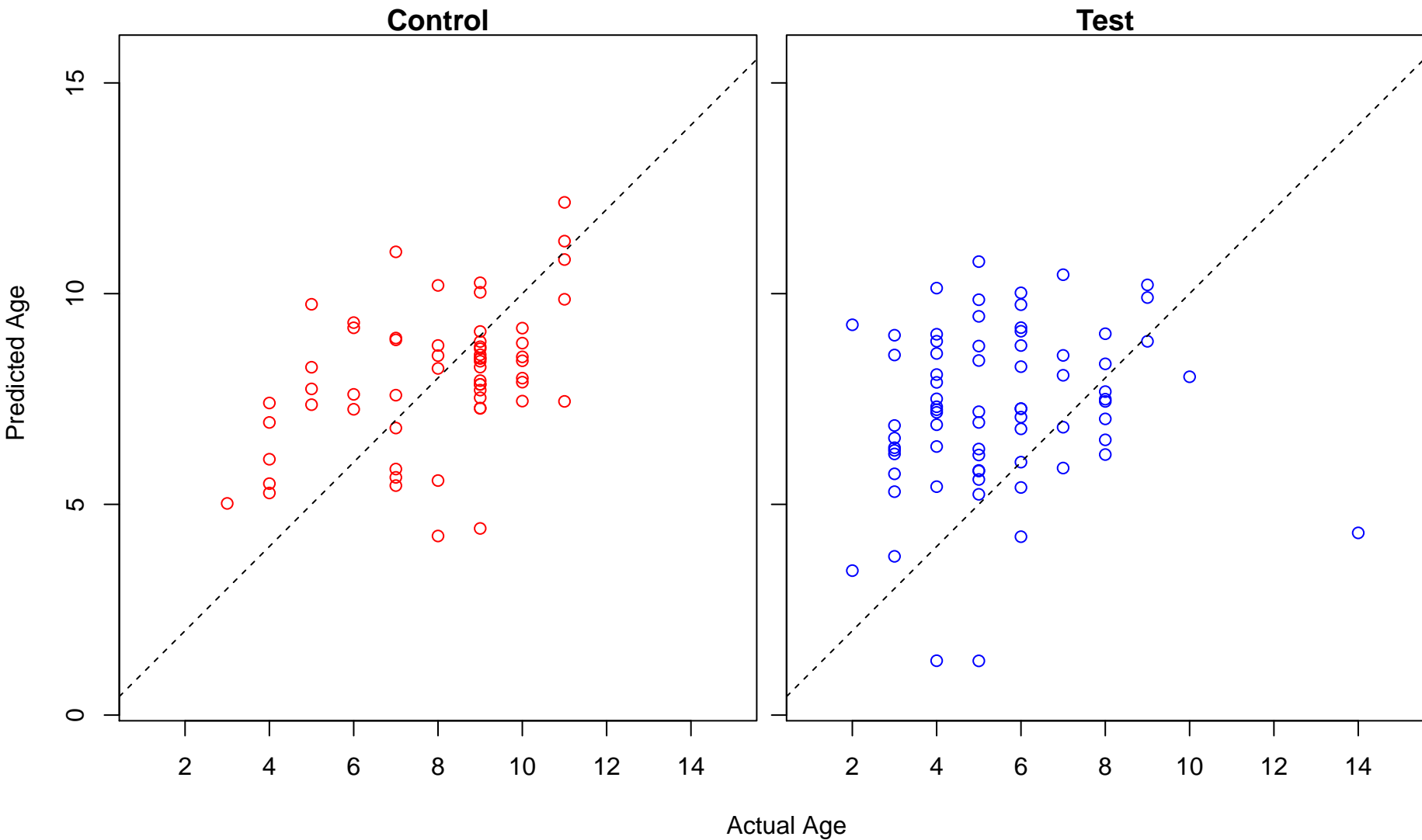
cytoplasmic mRNA processing body assembly (Score: 1.021233)



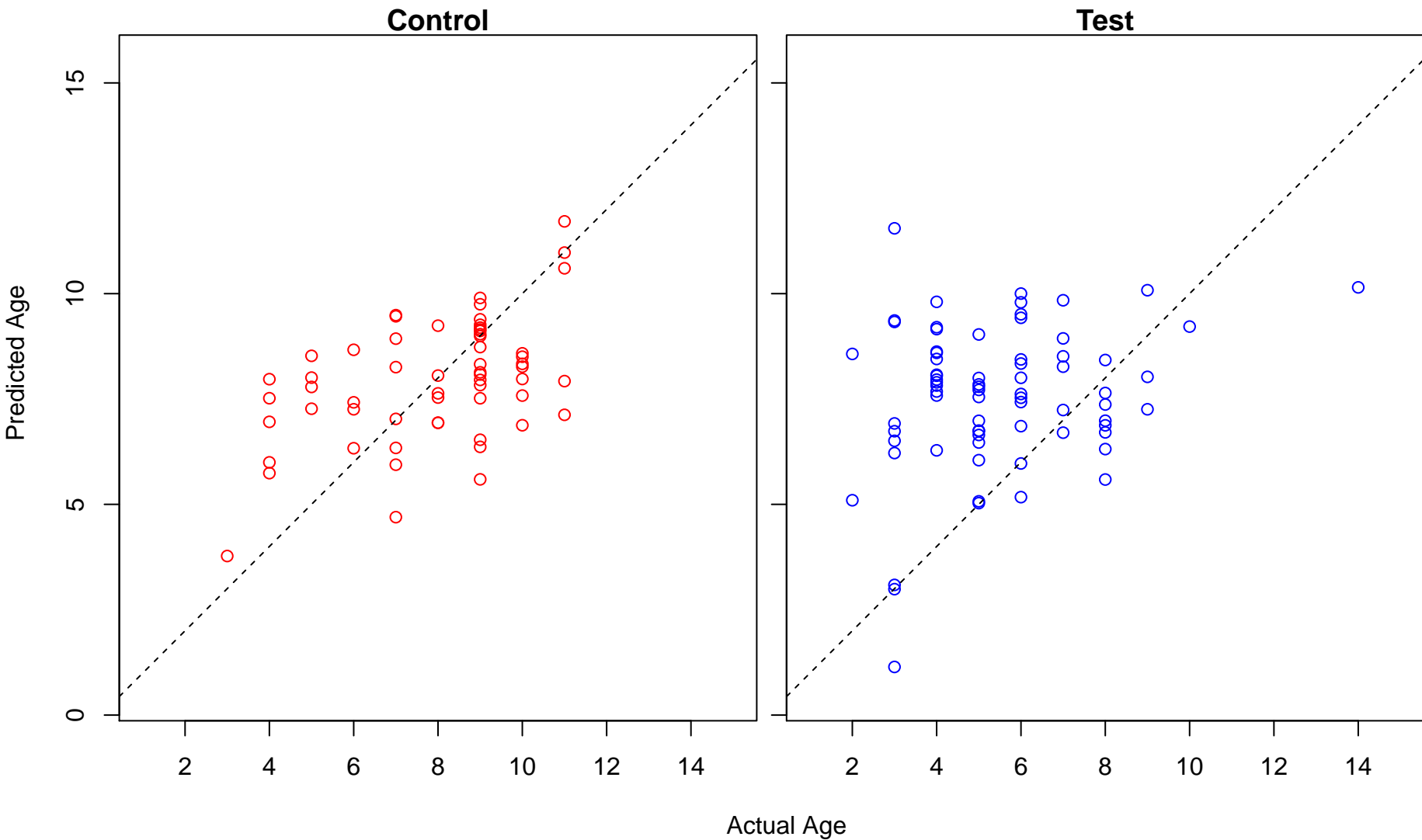
epidermal growth factor receptor signaling pathway (Score: 1.021209)



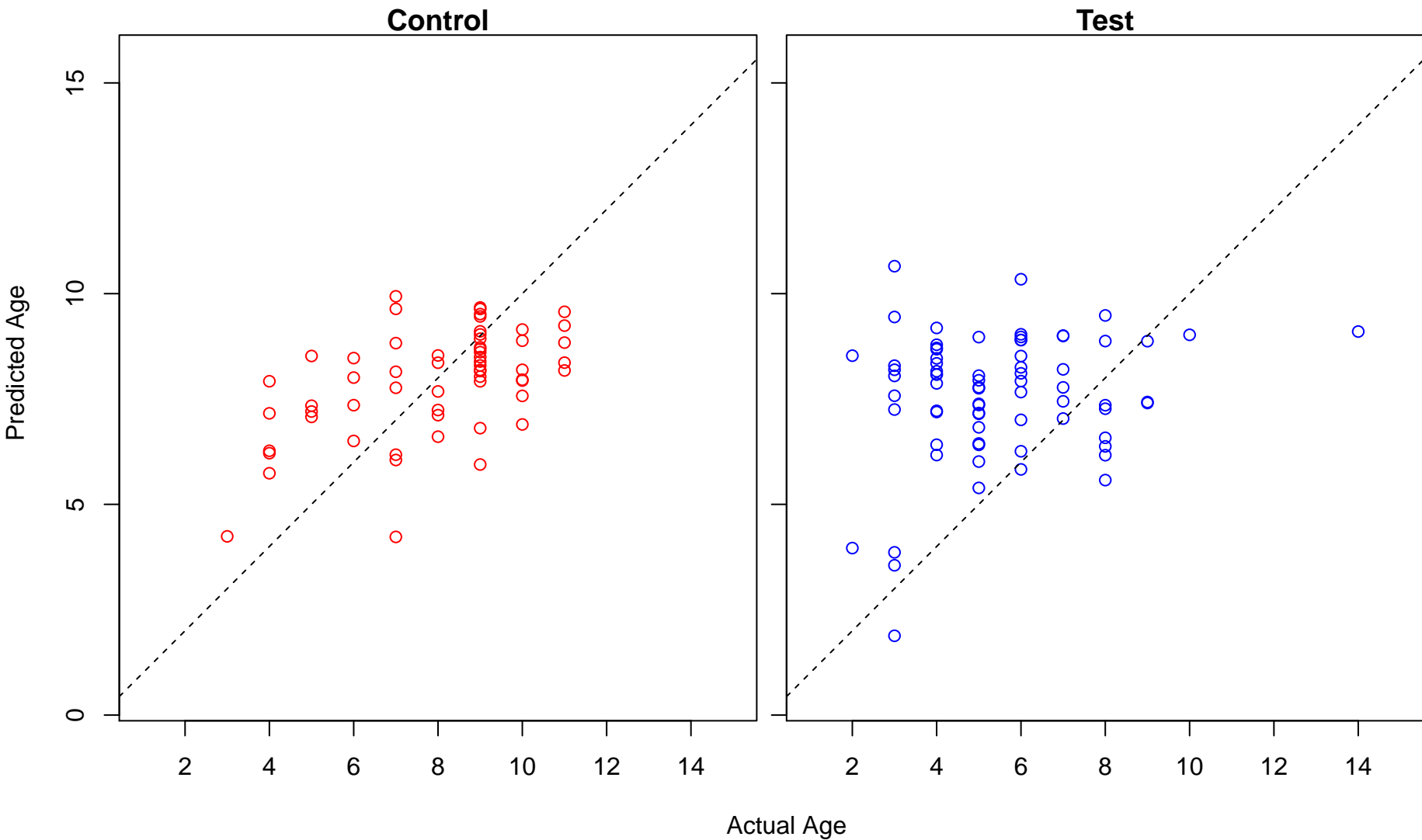
cellular response to oxygen-containing compound (Score: 1.019612)



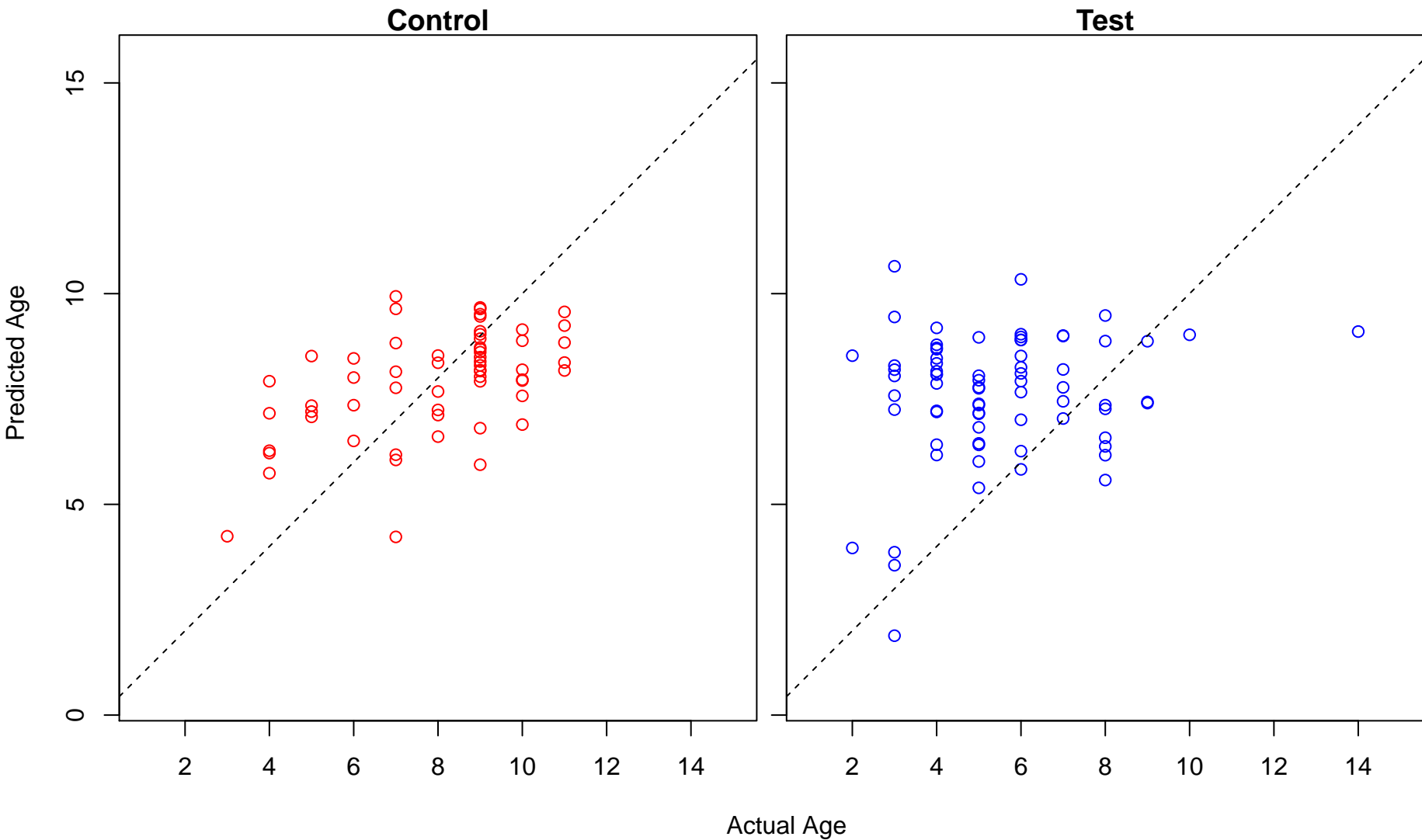
regulation of cardiac muscle cell proliferation (Score: 1.018328)



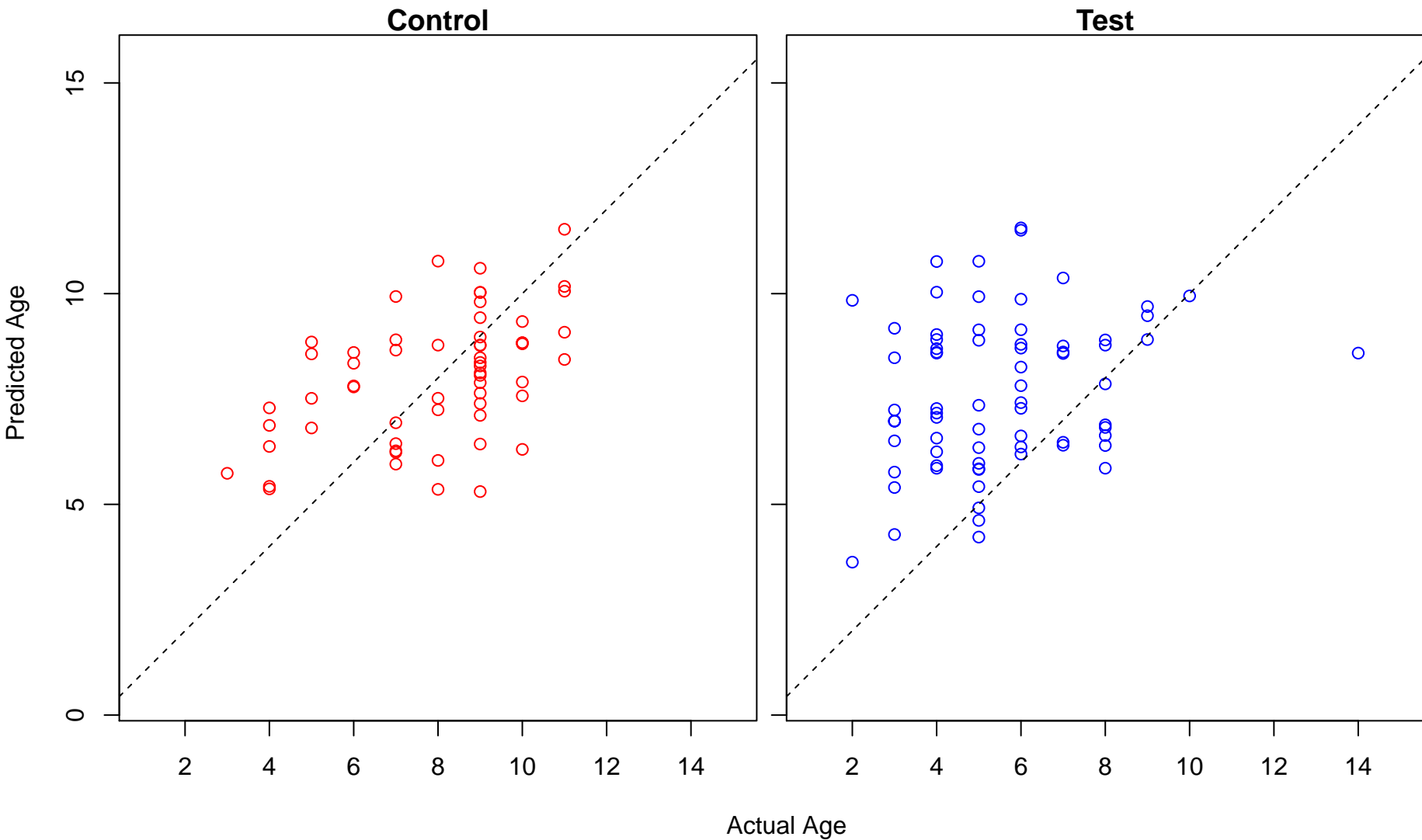
neural plate regionalization (Score: 1.017552)



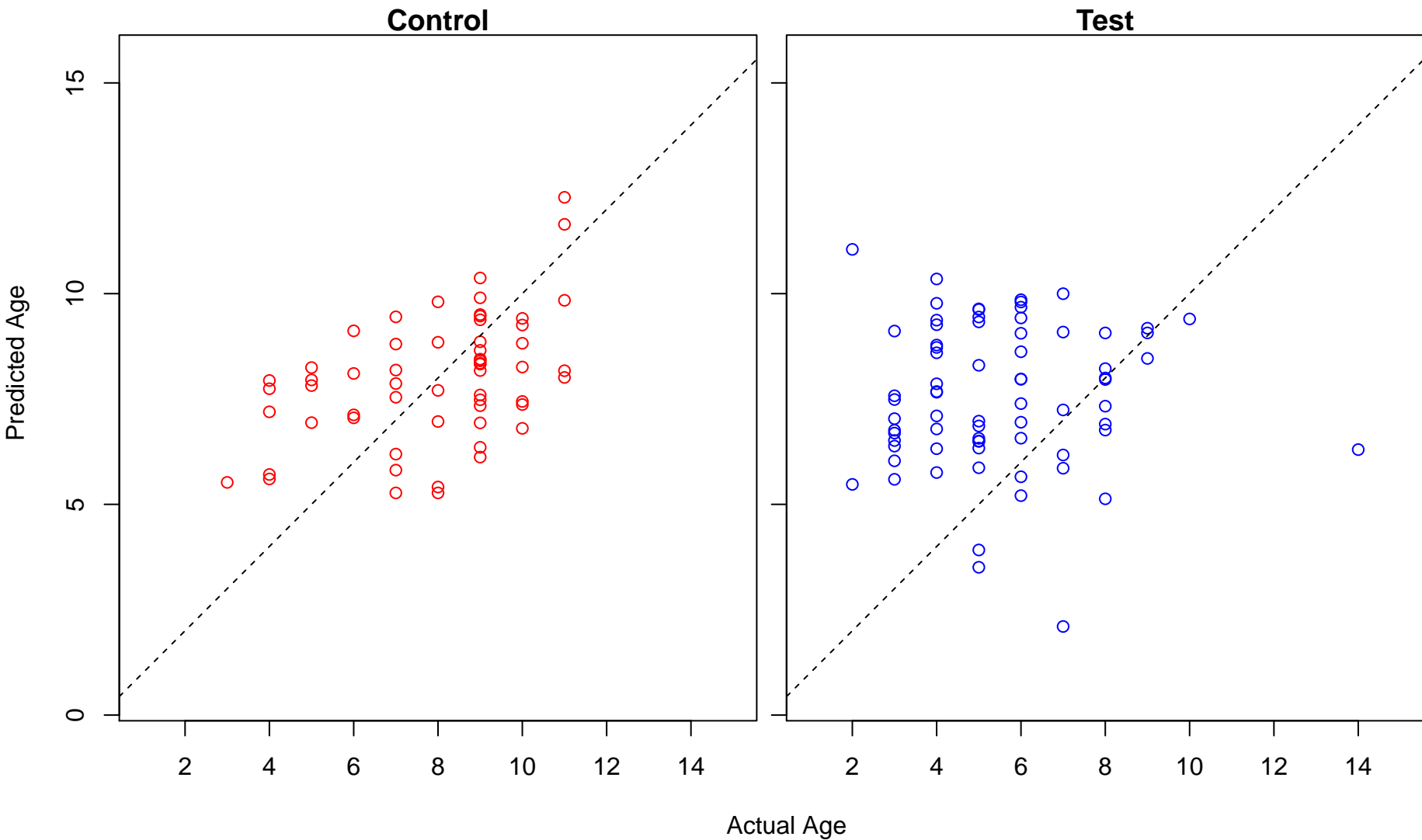
neural plate anterior/posterior regionalization (Score: 1.017131)



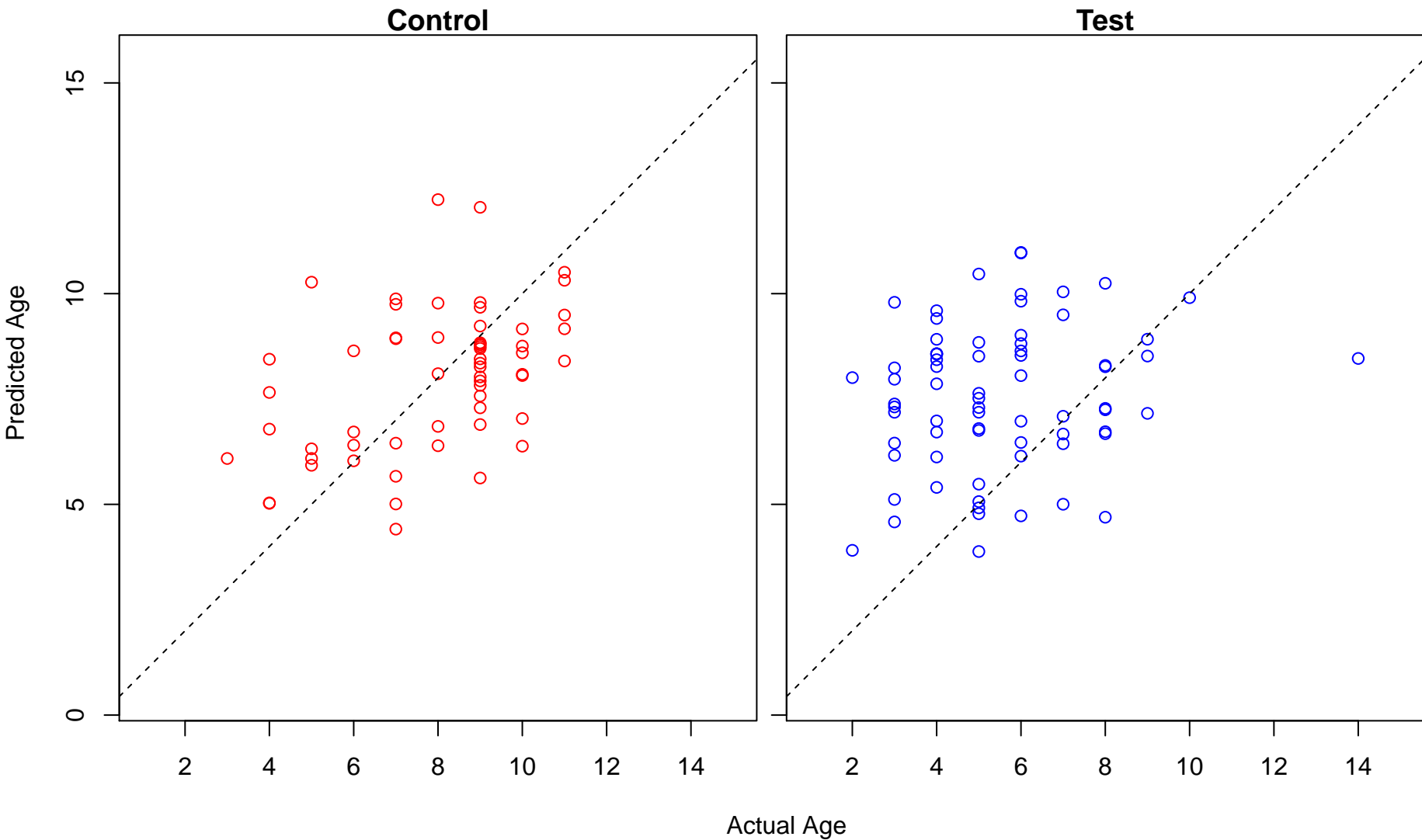
anatomical structure morphogenesis (Score: 1.017015)



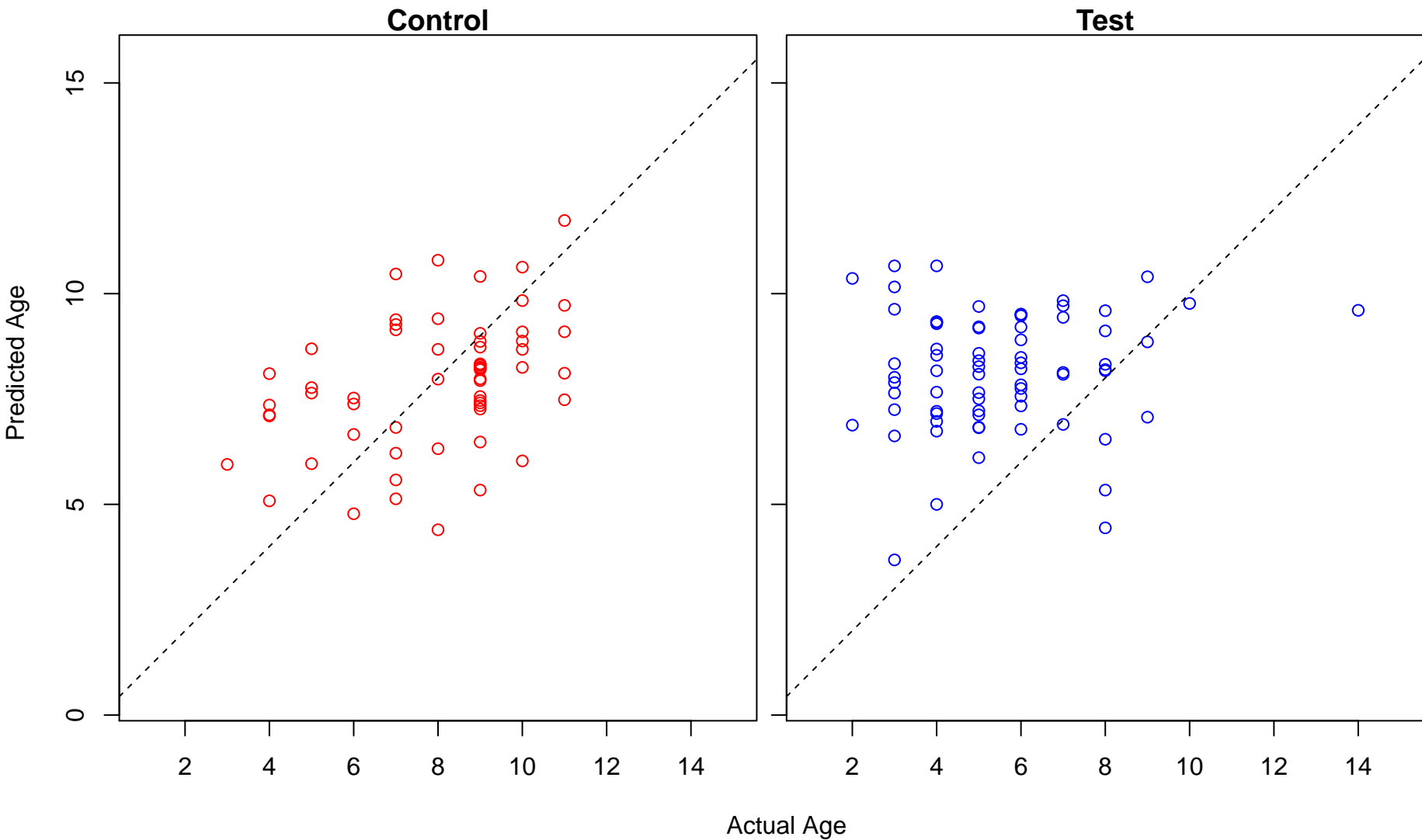
single-multicellular organism process (Score: 1.016745)



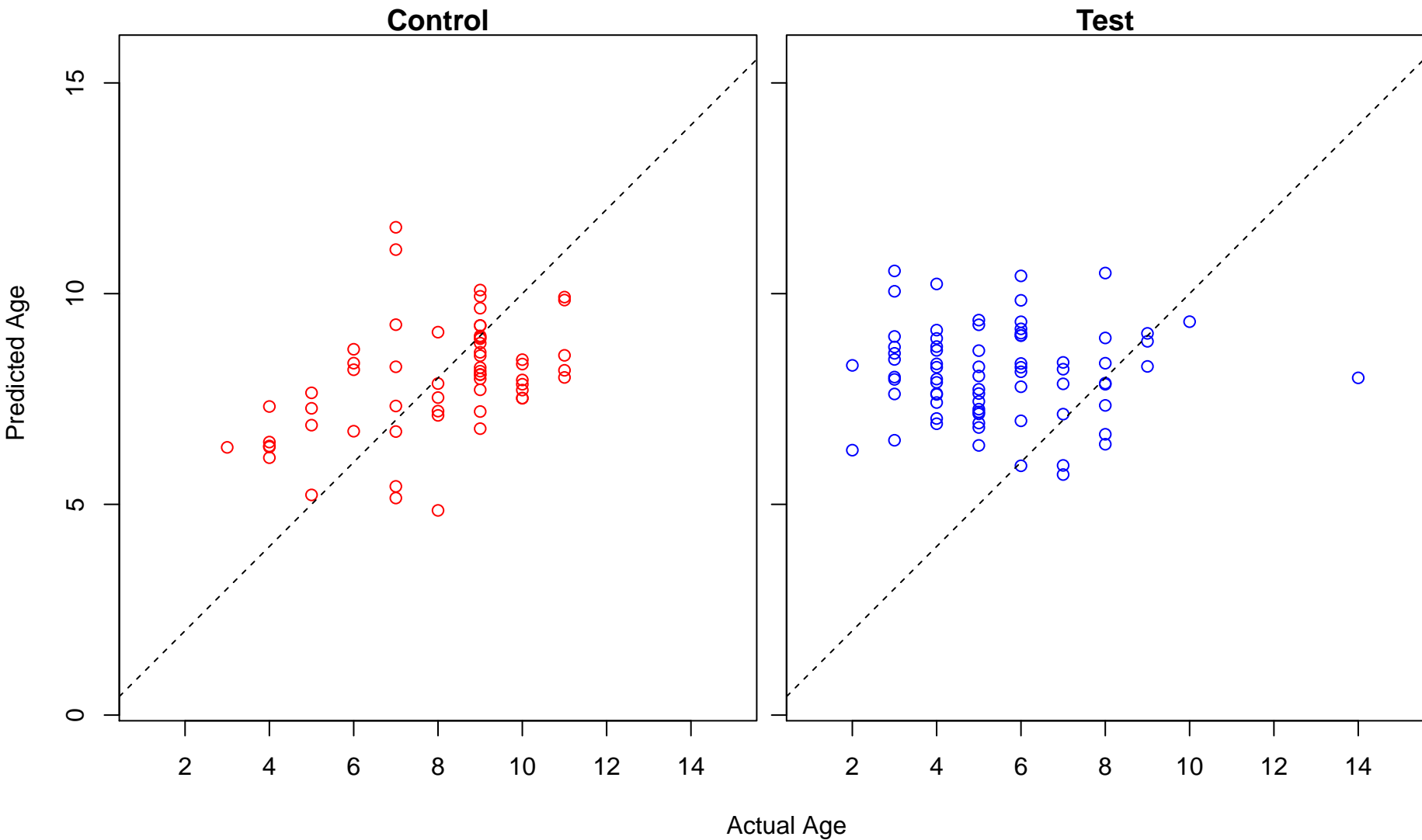
regulation of cell projection organization (Score: 1.016697)



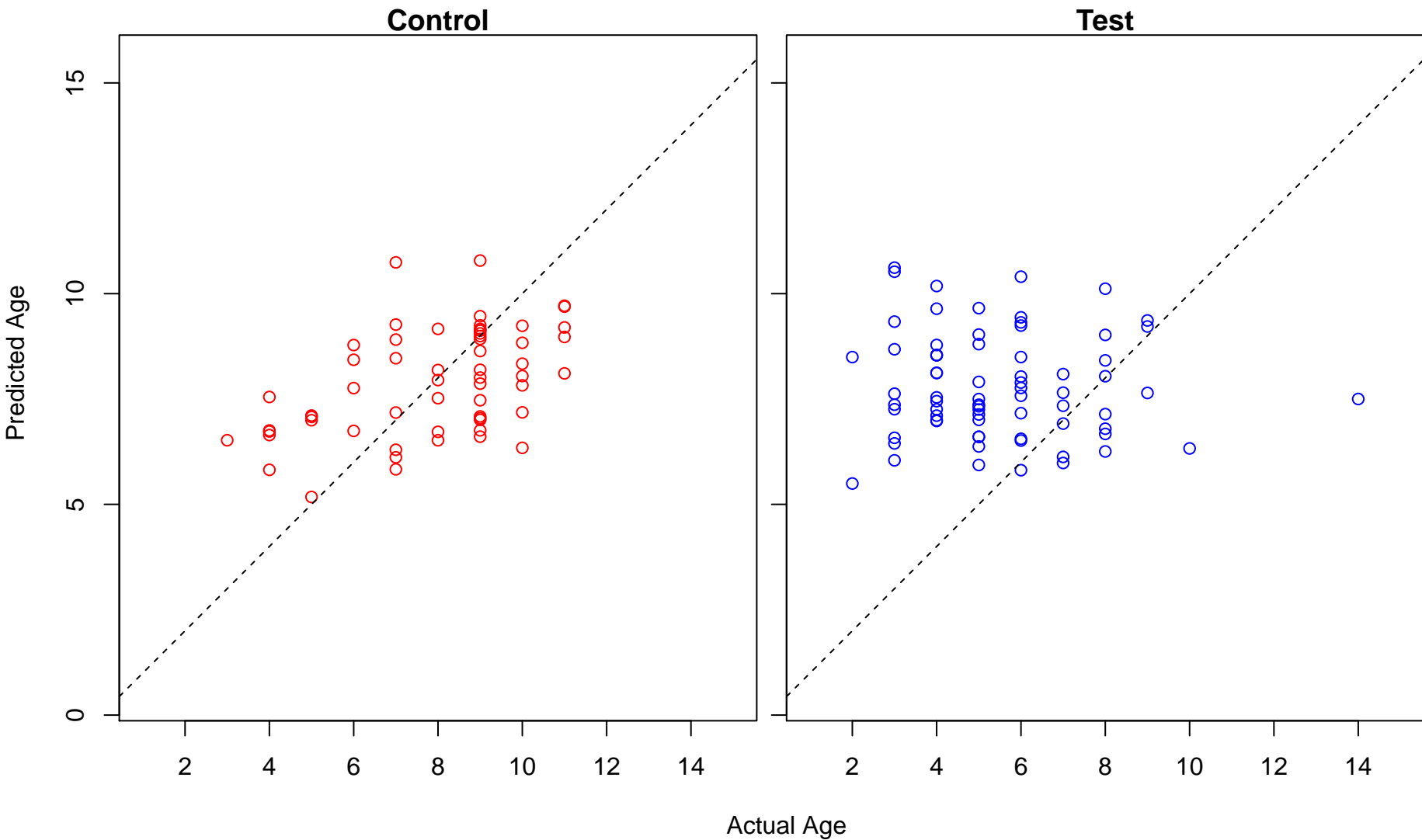
chromosome separation (Score: 1.015699)



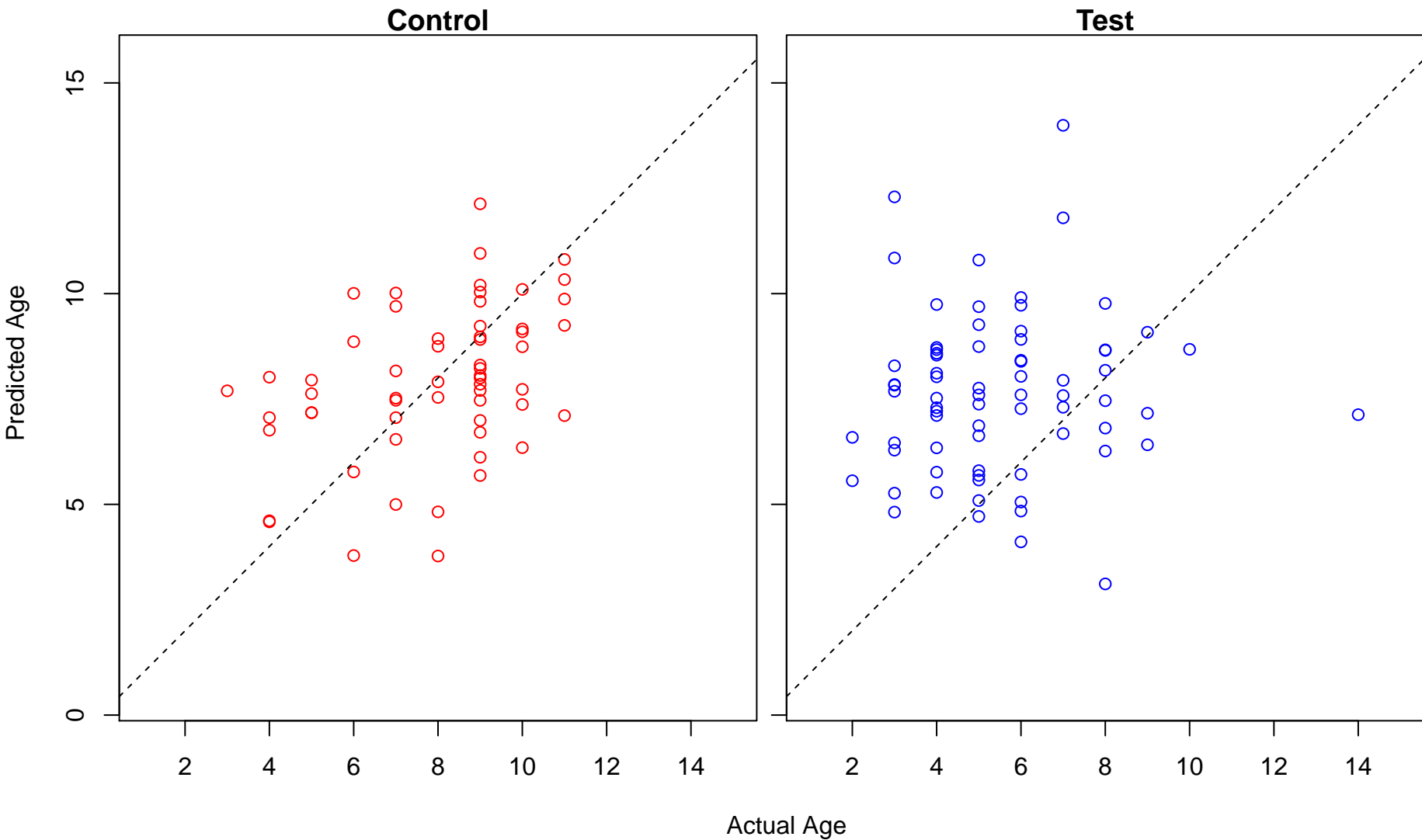
regulation of exocytosis (Score: 1.015224)



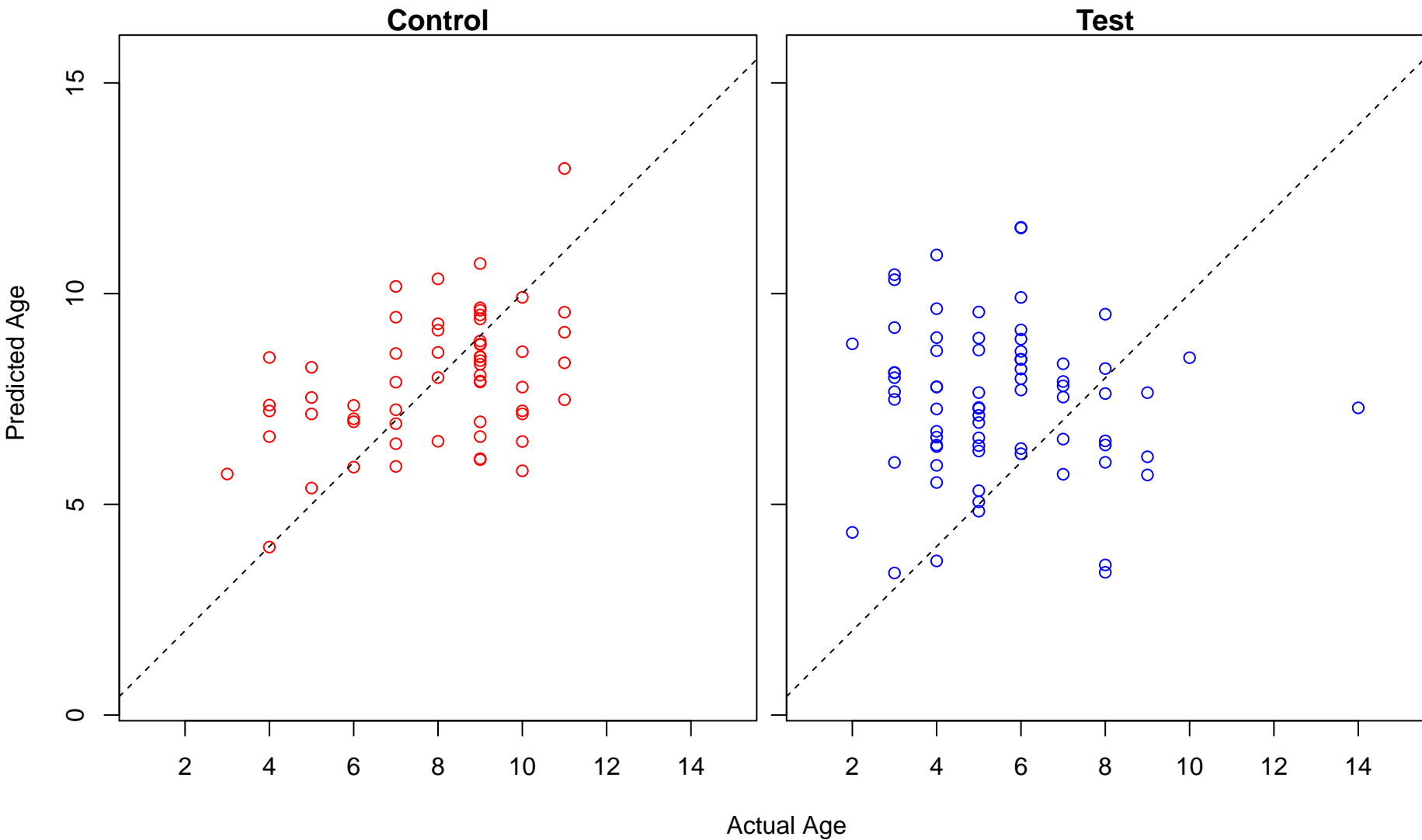
JAK-STAT cascade (Score: 1.014999)



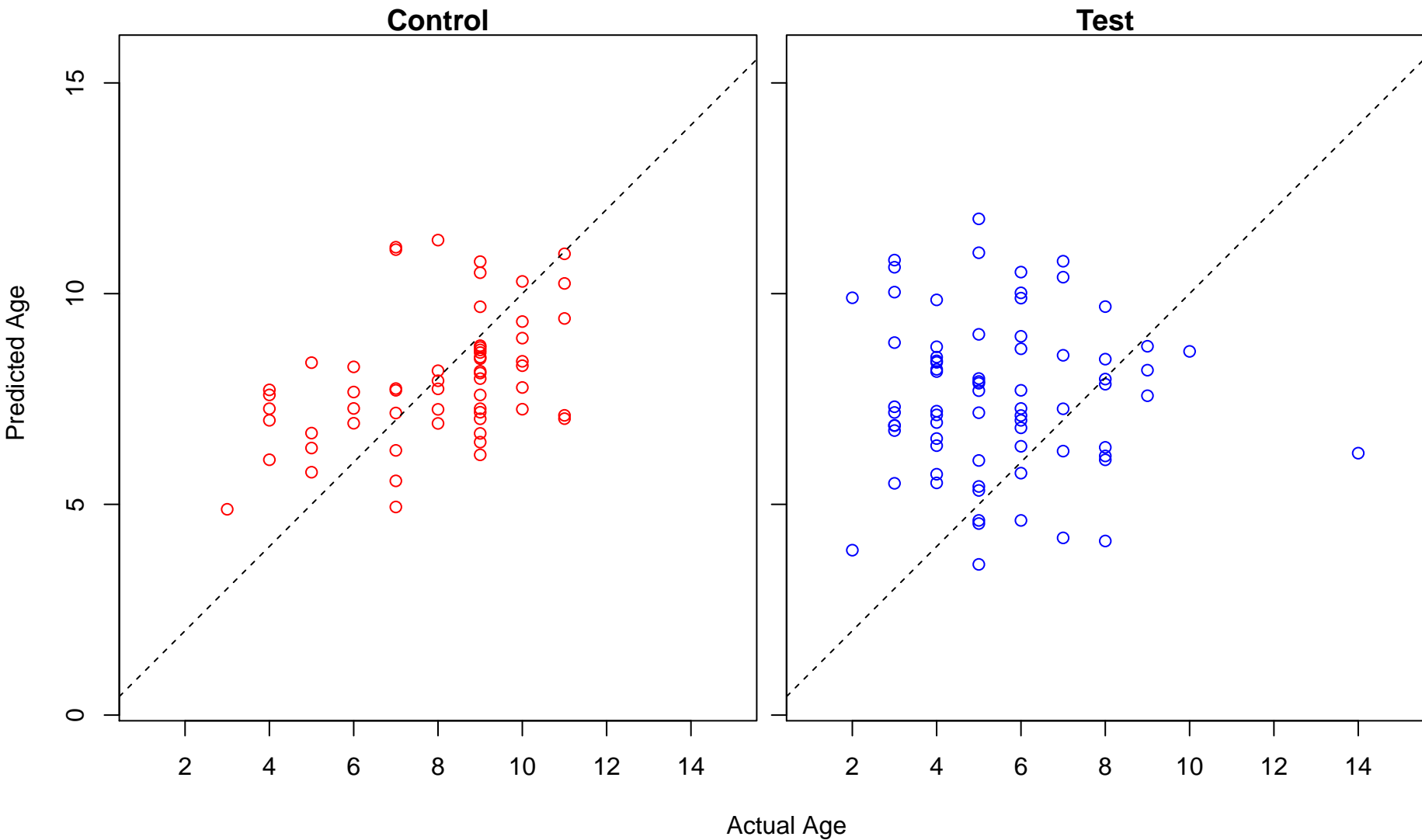
endocrine pancreas development (Score: 1.014870)



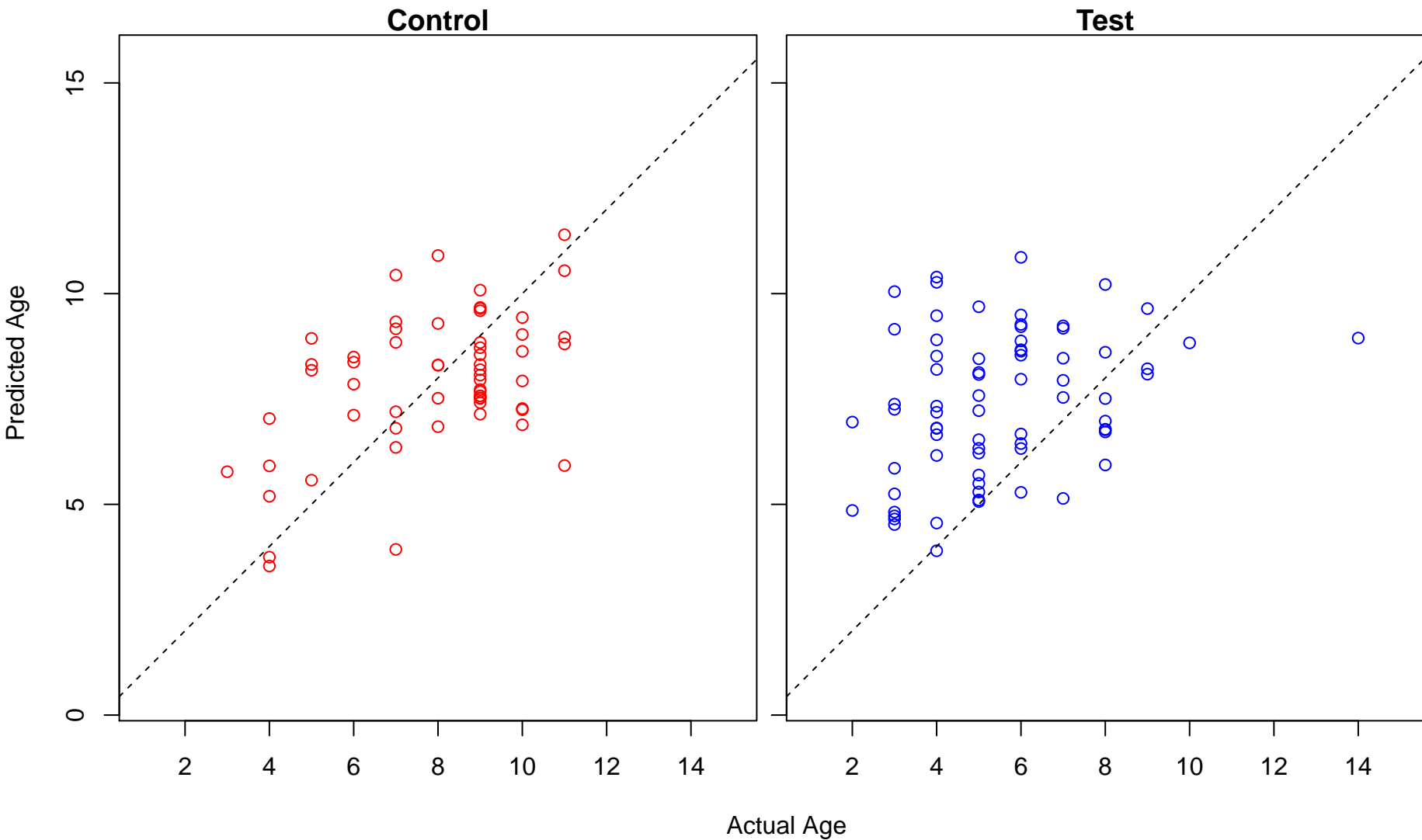
regulation of phosphatidylinositol 3-kinase activity (Score: 1.014329)



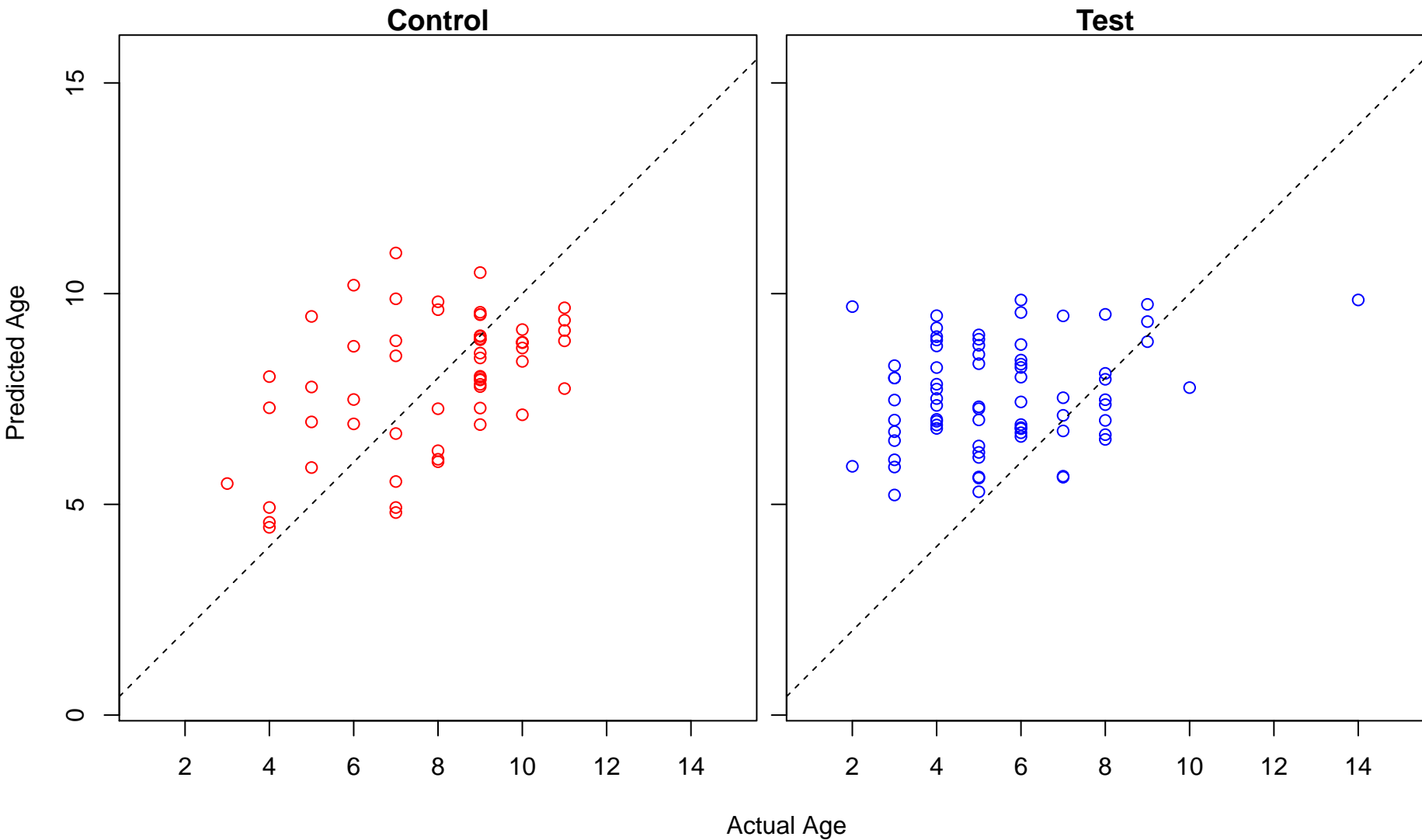
negative regulation of viral entry into host cell (Score: 1.014206)



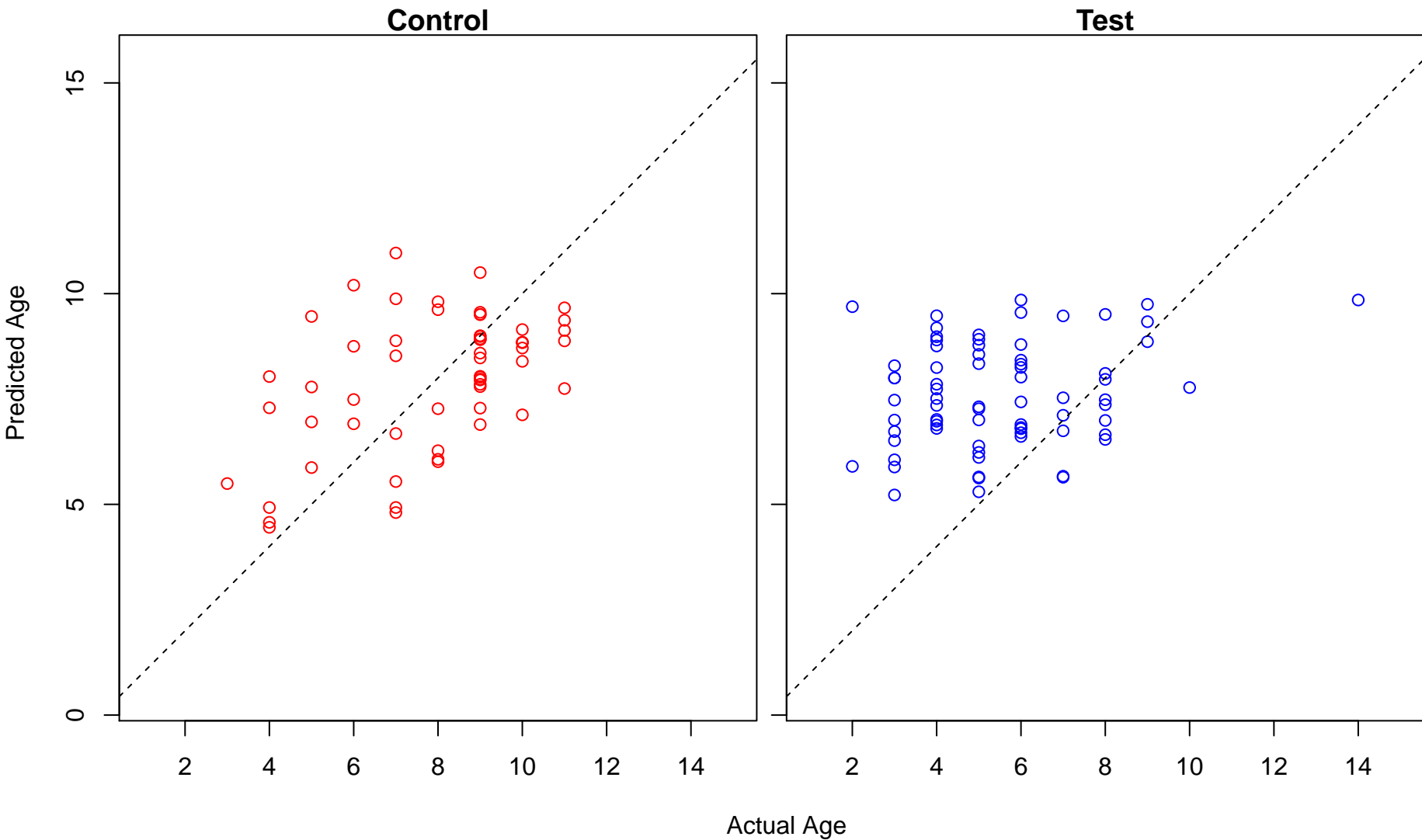
regulation of cellular carbohydrate metabolic process (Score: 1.014115)



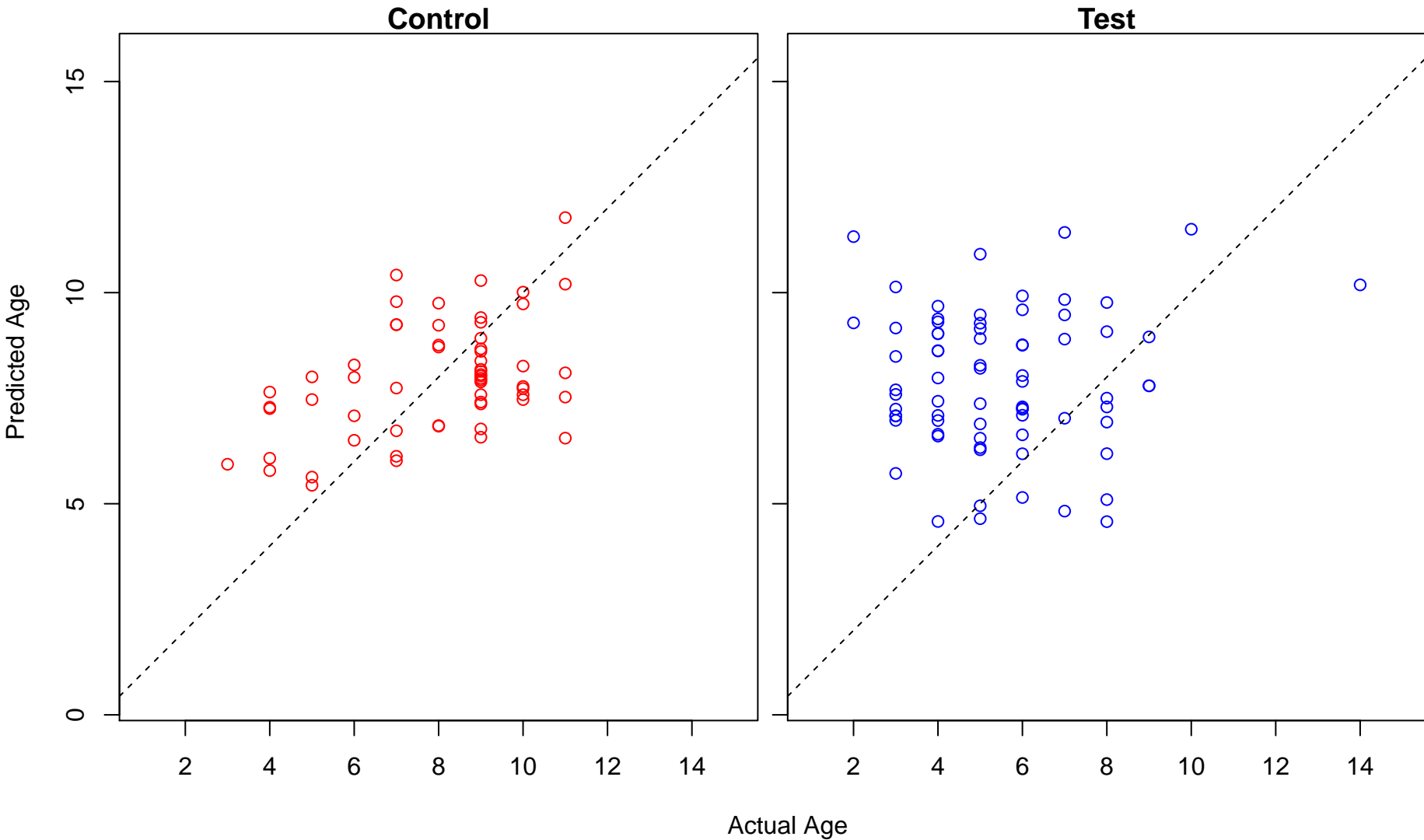
cellular cation homeostasis (Score: 1.012575)



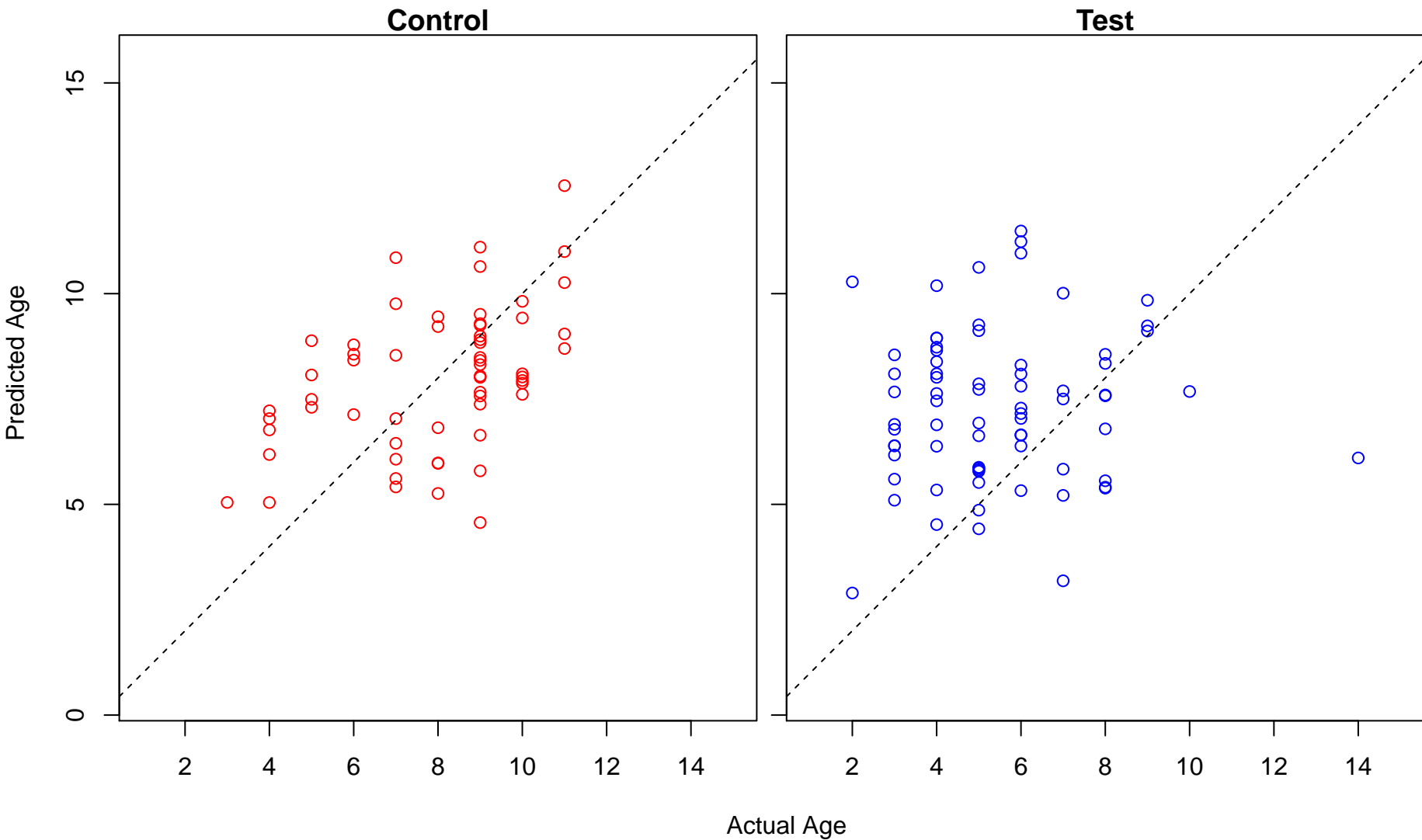
cellular ion homeostasis (Score: 1.012534)



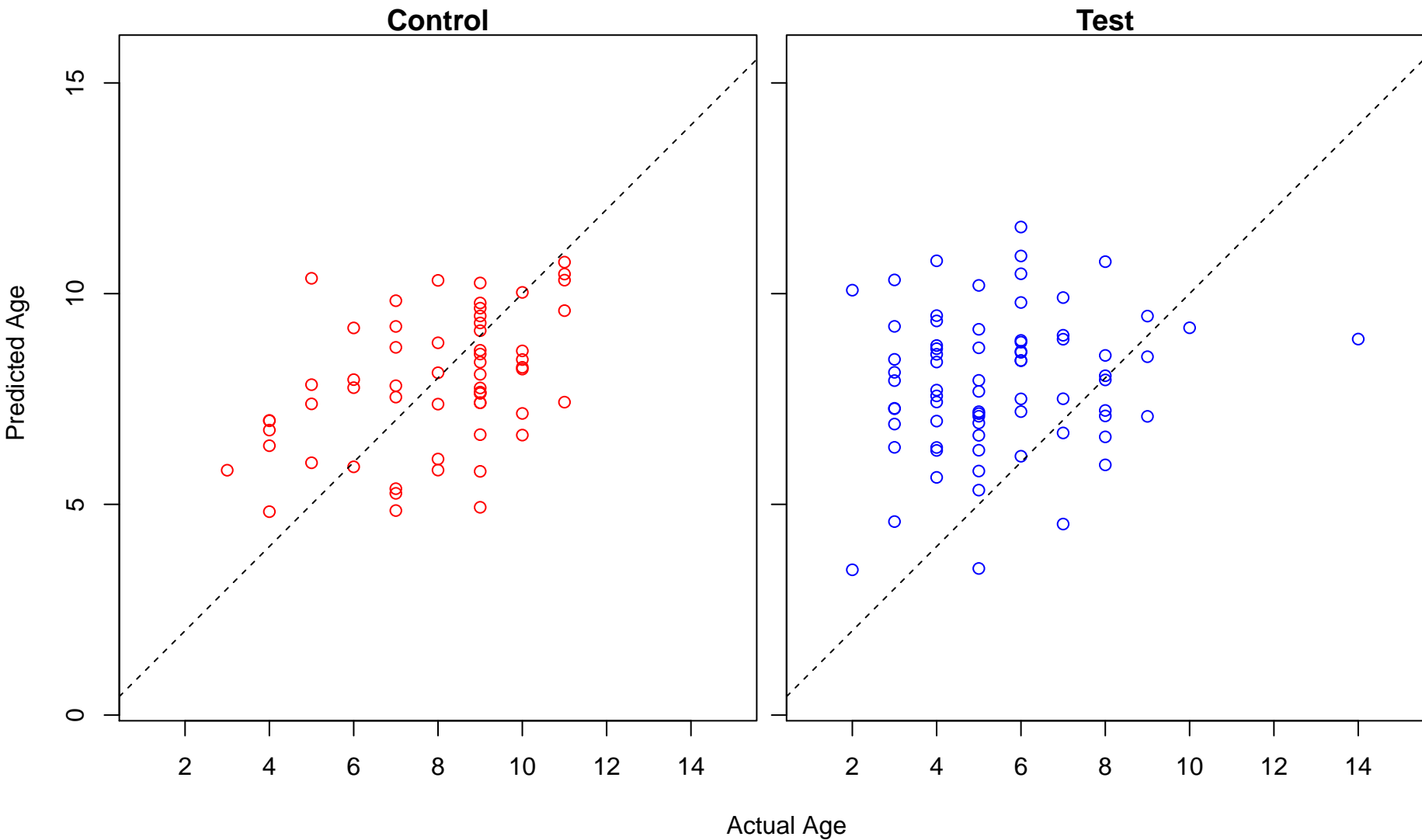
transcription from RNA polymerase III promoter (Score: 1.012300)



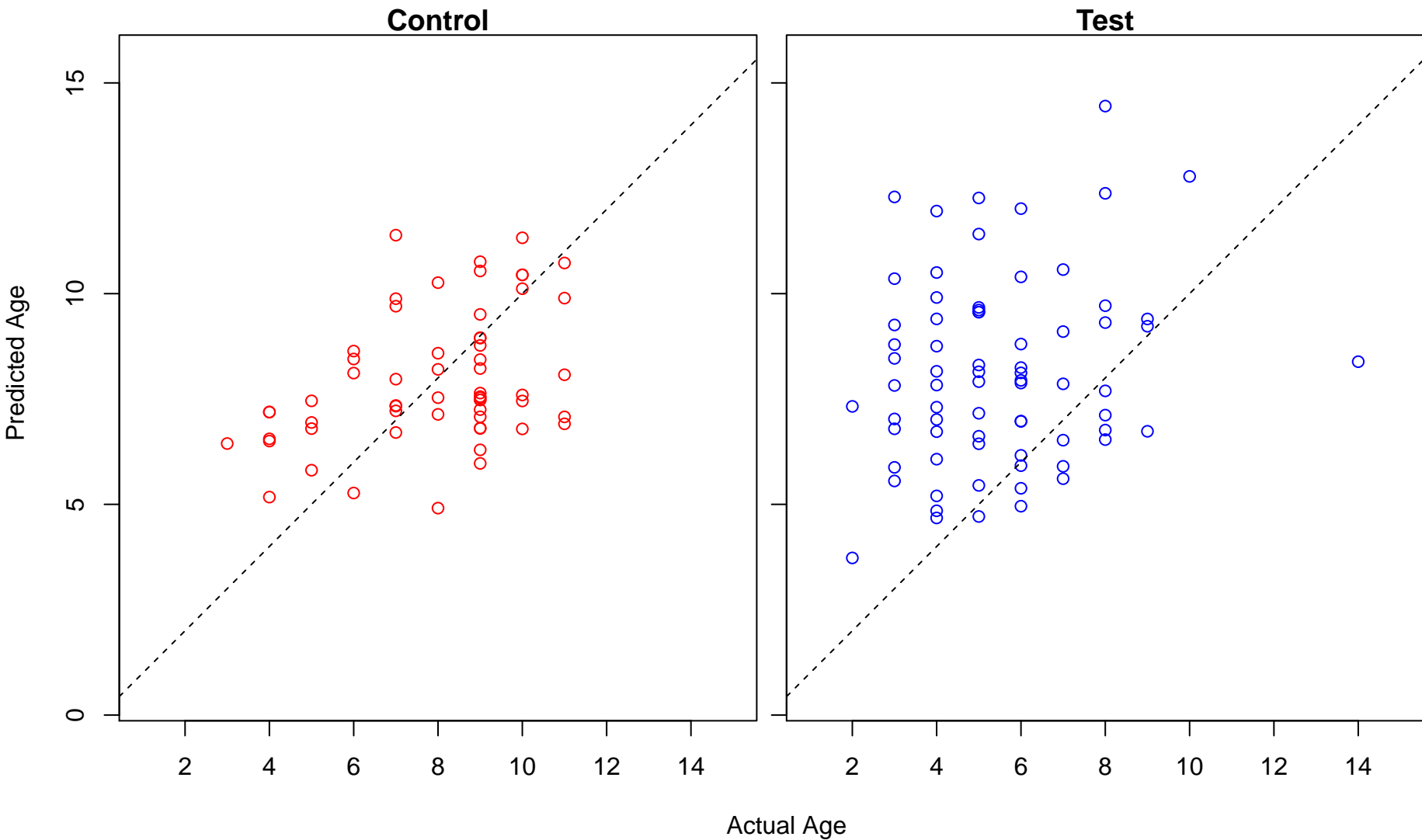
regulation of defense response (Score: 1.011398)



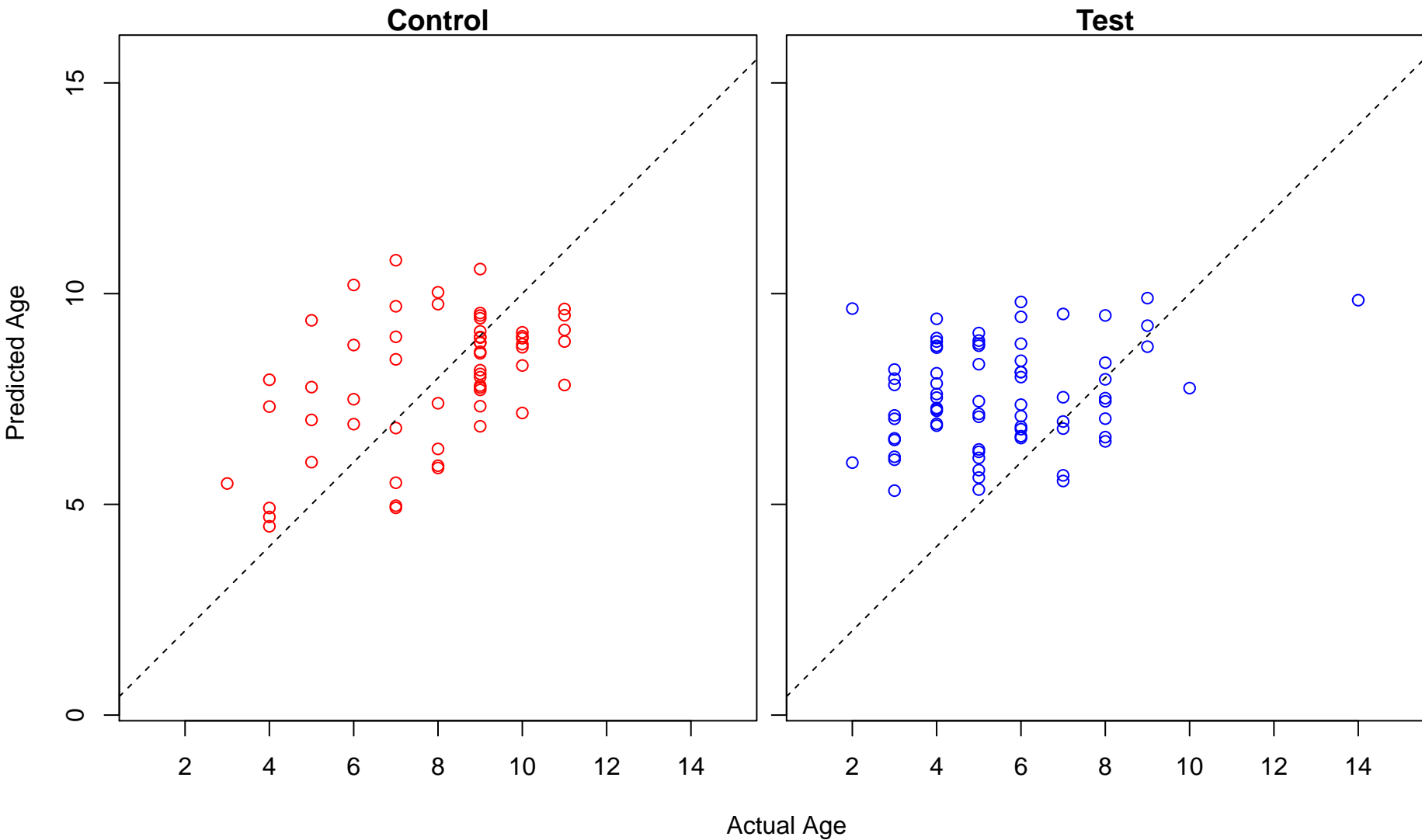
morphogenesis of an epithelium (Score: 1.011355)



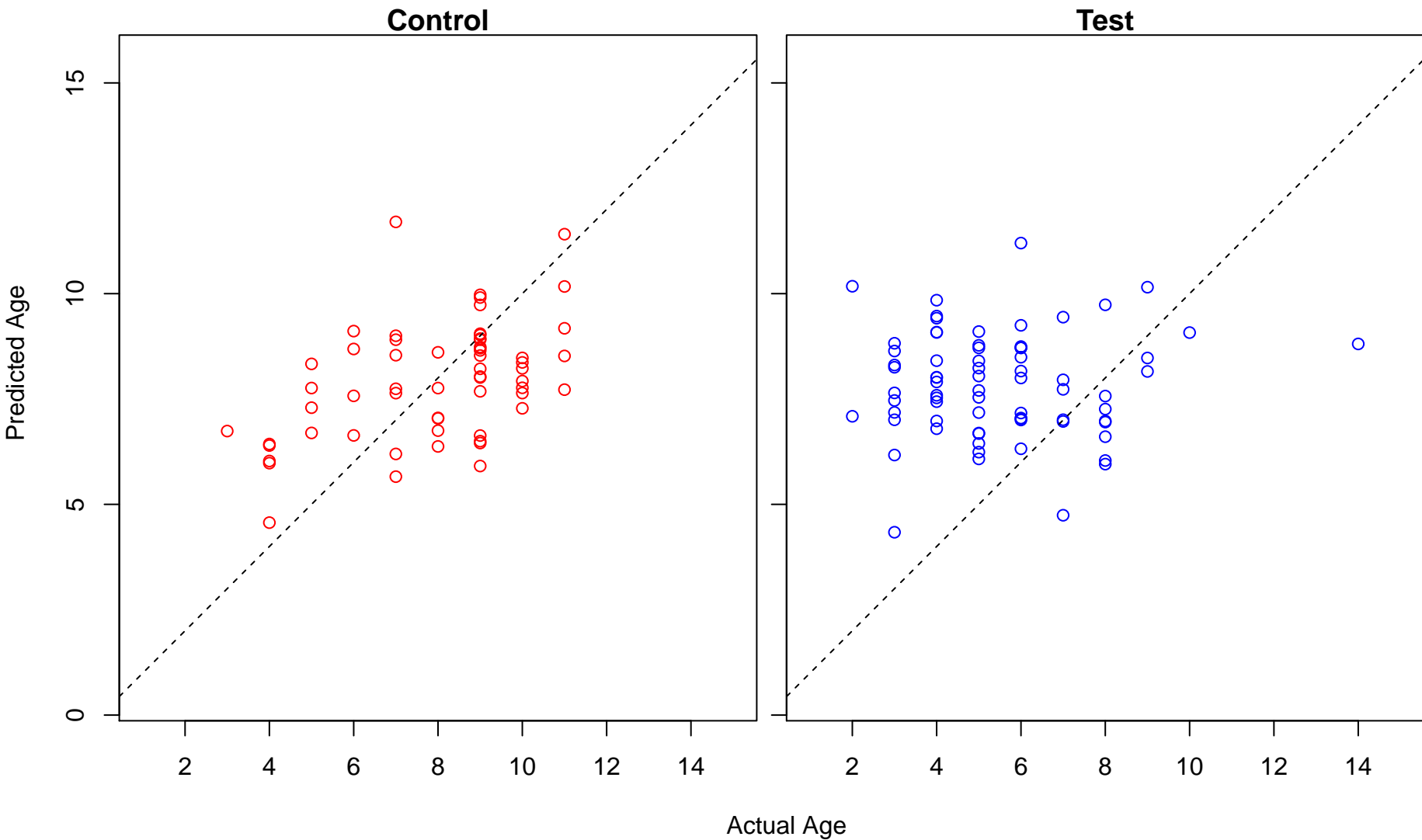
cullin deneddylation (Score: 1.010618)



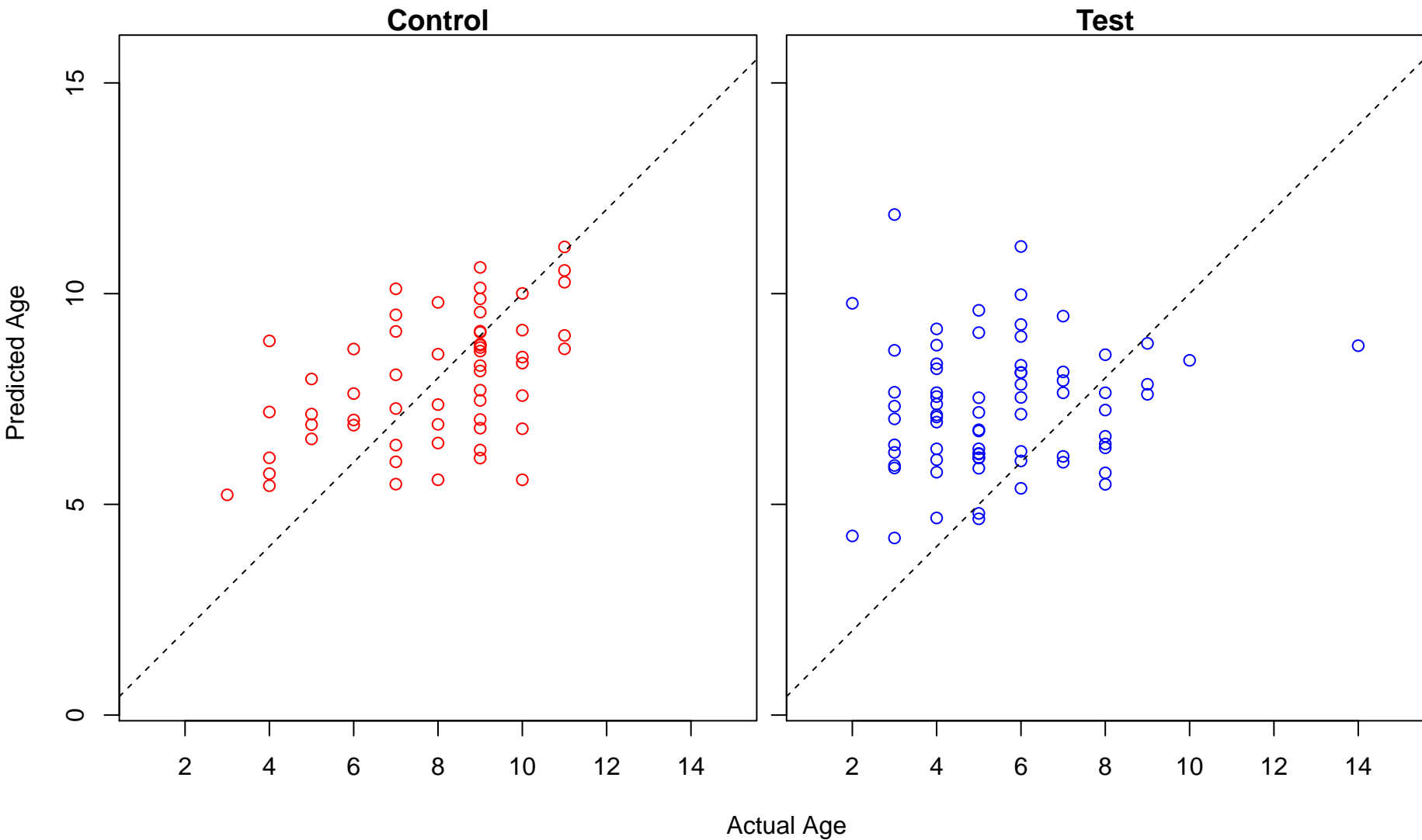
cellular metal ion homeostasis (Score: 1.009987)



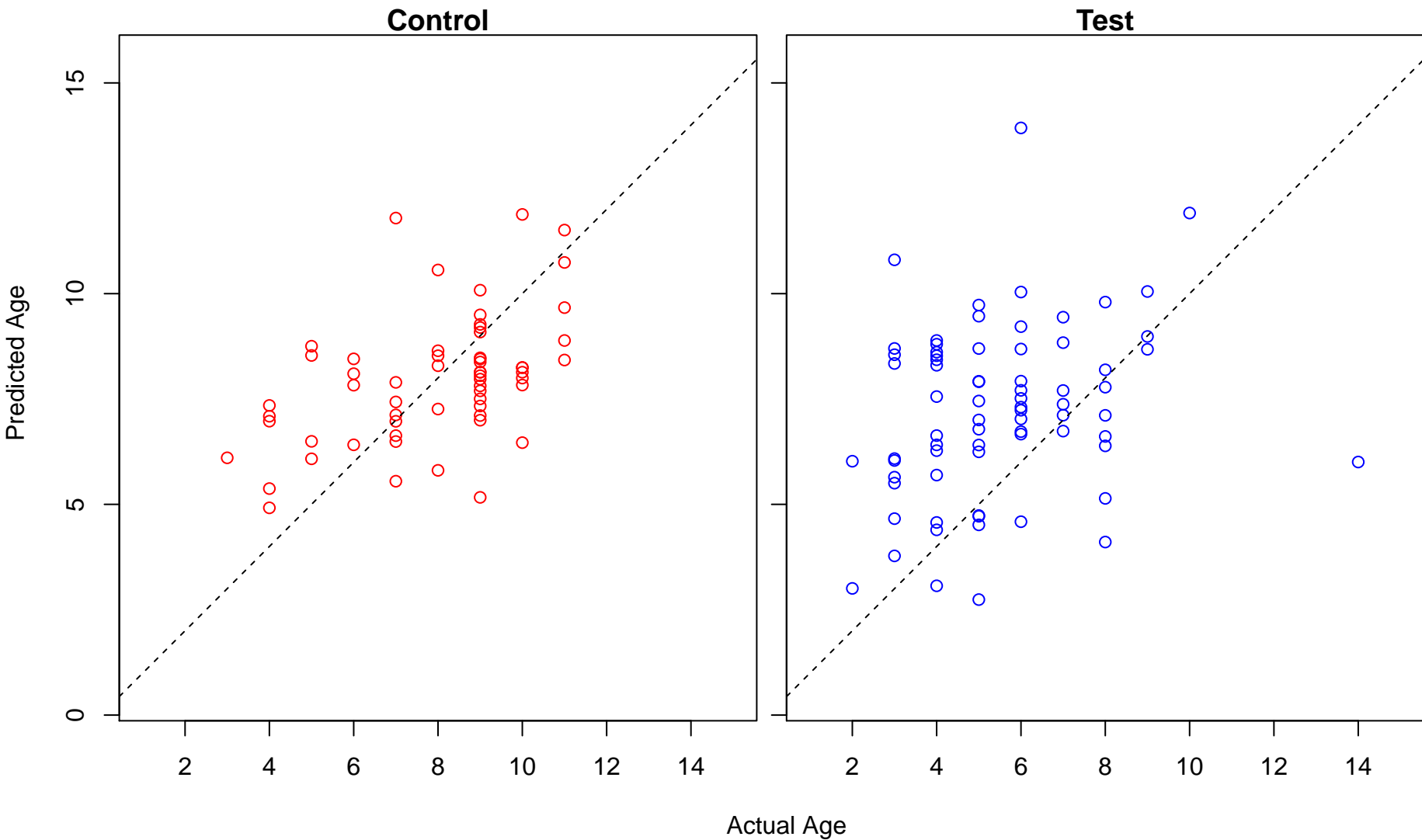
alpha-beta T cell differentiation (Score: 1.009692)



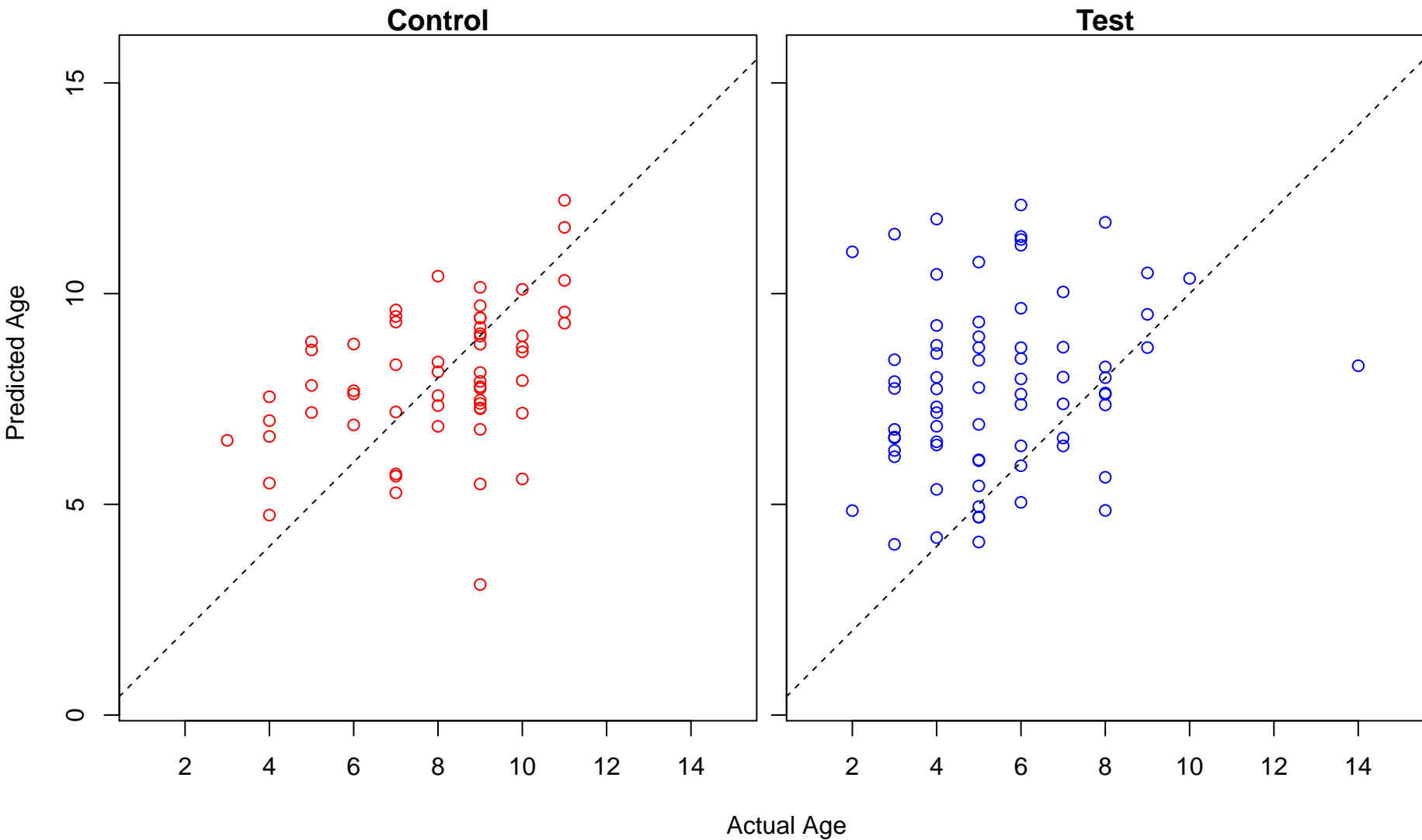
stem cell differentiation (Score: 1.008870)



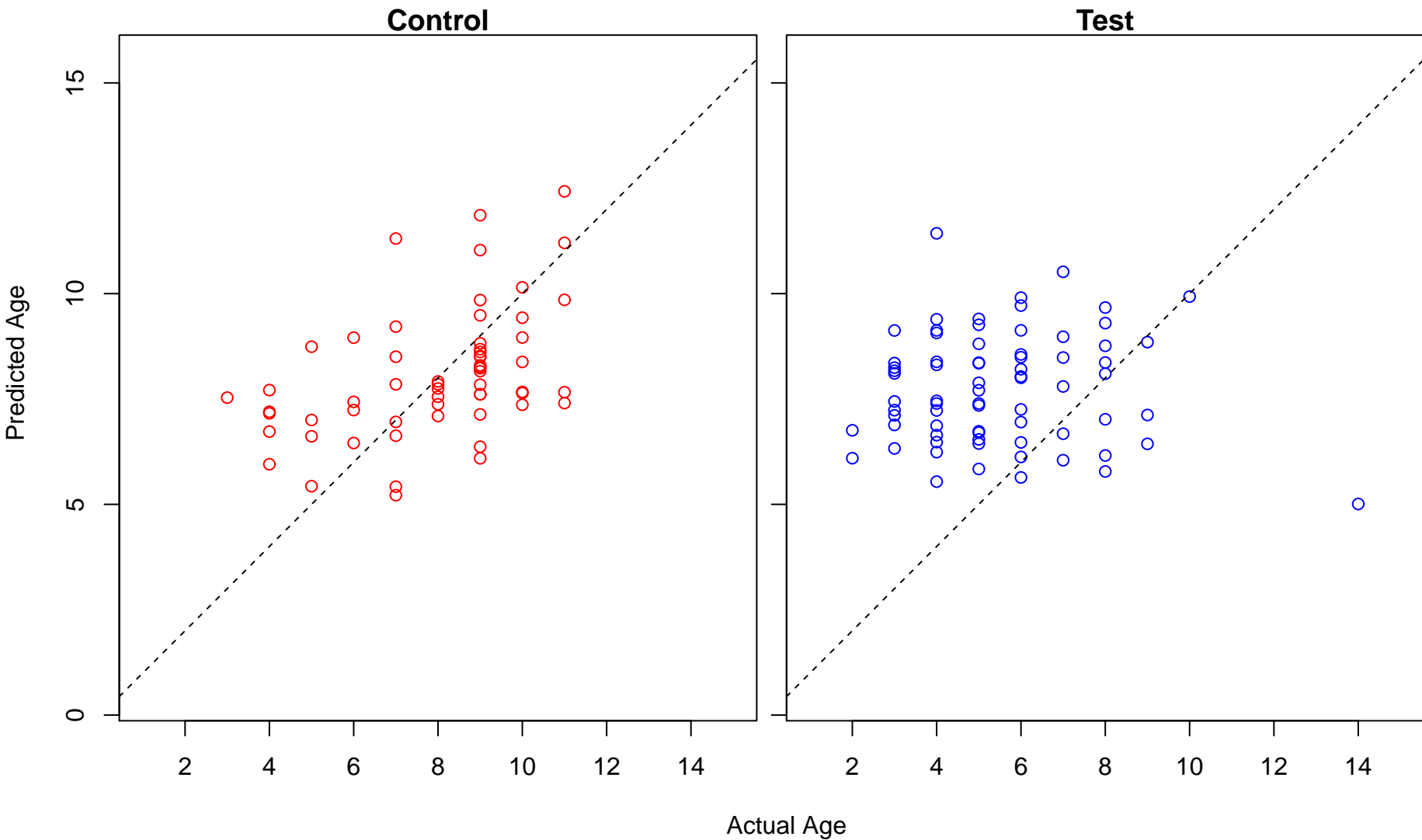
regulation of T-helper cell differentiation (Score: 1.008236)



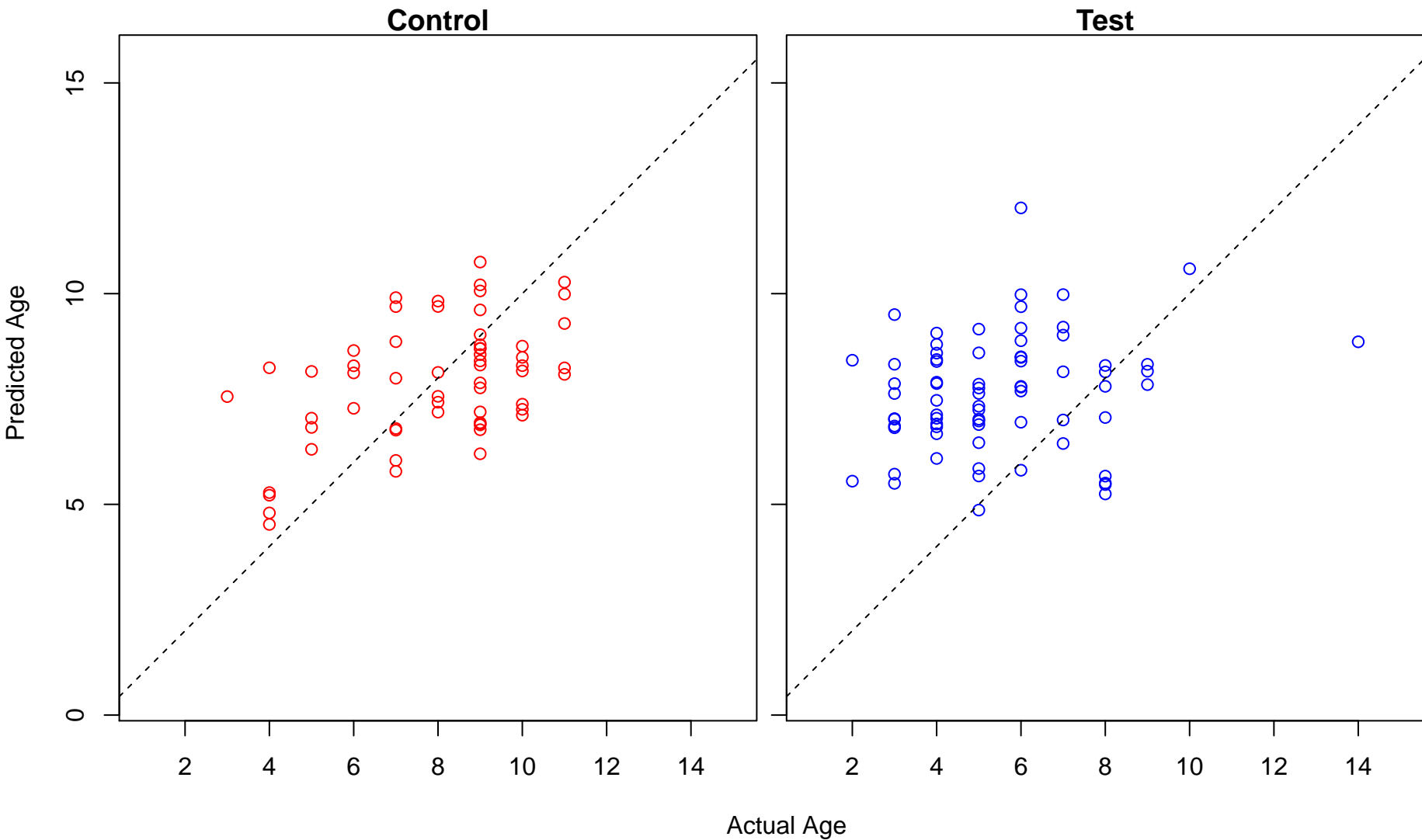
actin cytoskeleton organization (Score: 1.008027)



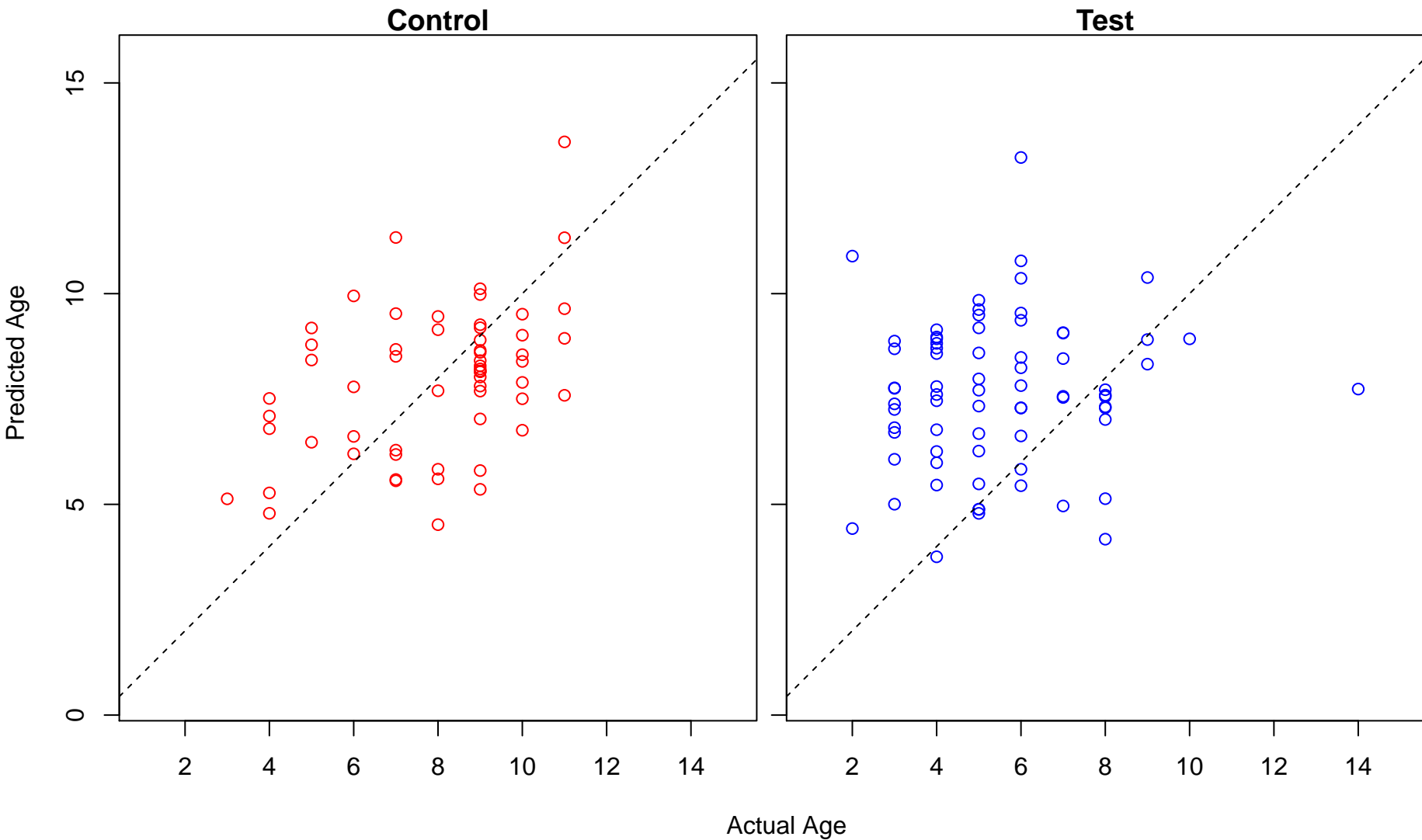
collagen biosynthetic process (Score: 1.007794)



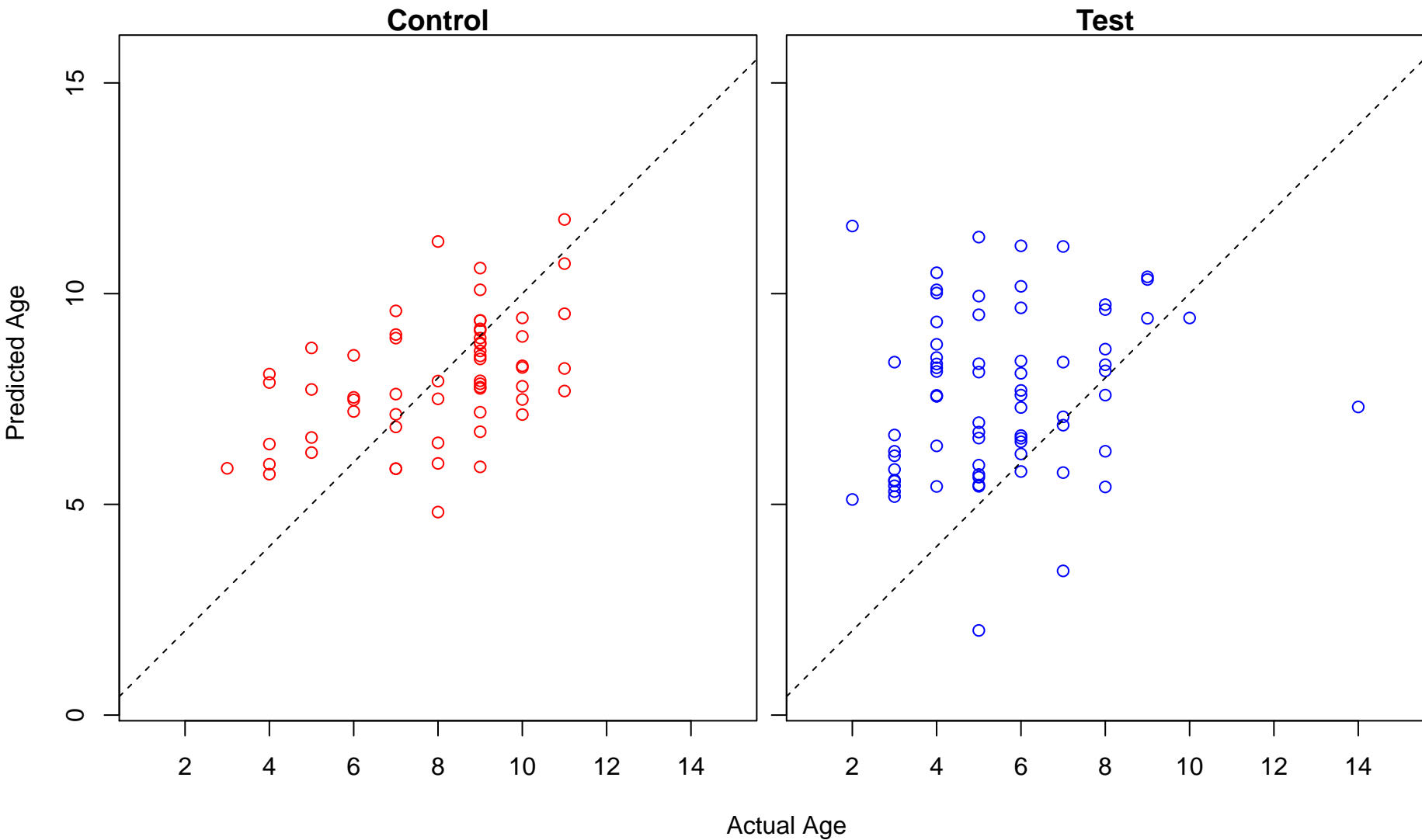
neuroepithelial cell differentiation (Score: 1.007681)



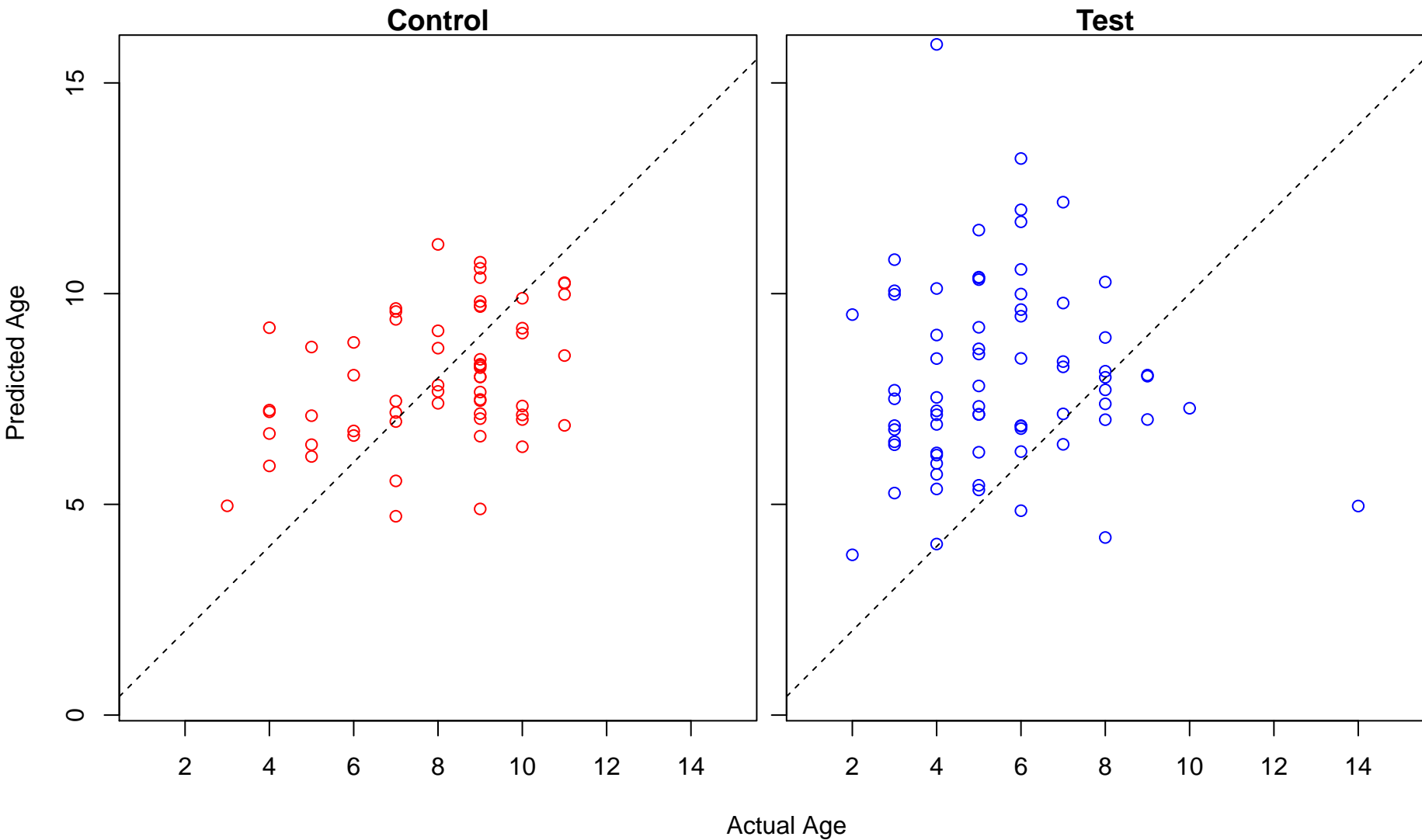
ERBB signaling pathway (Score: 1.007663)



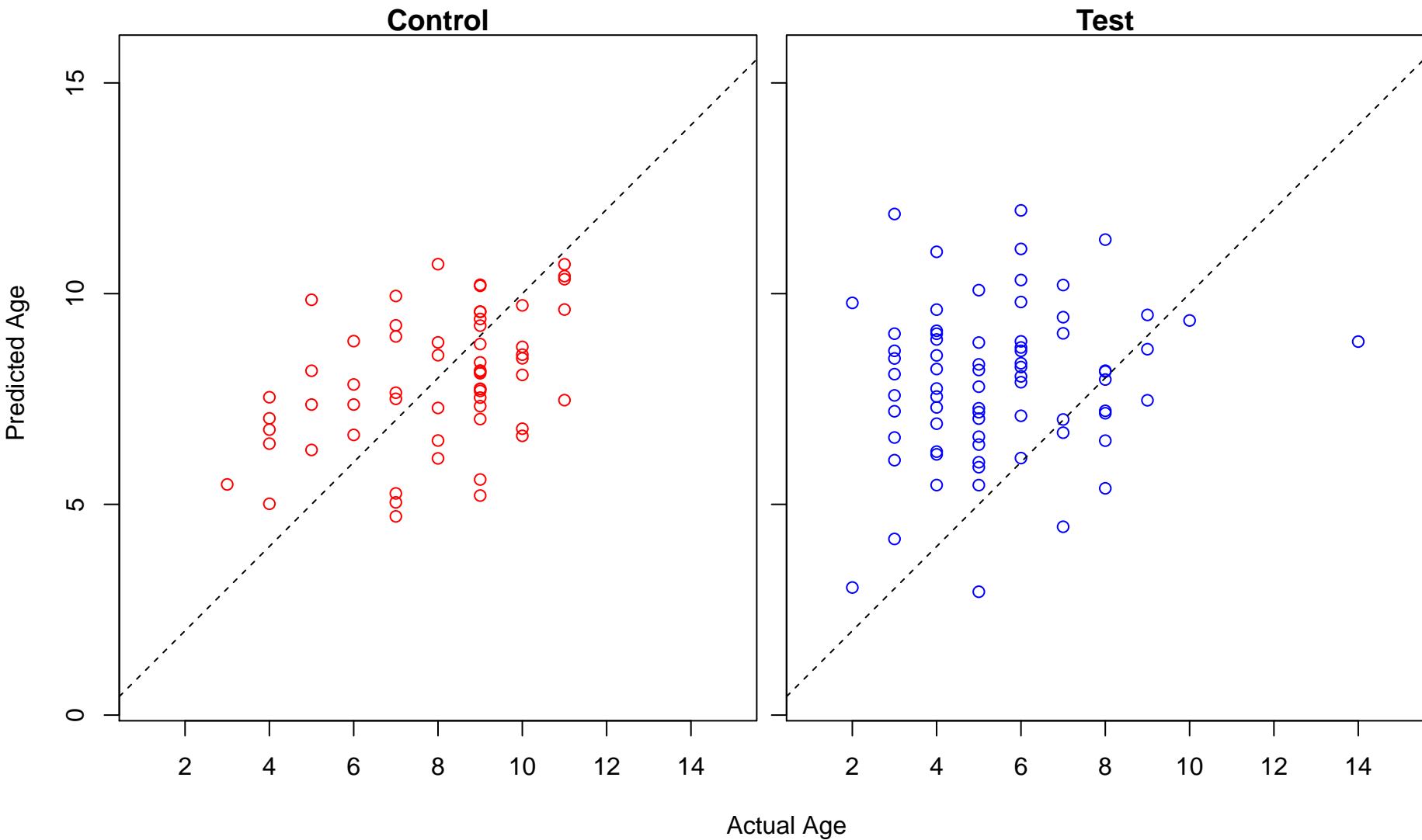
response to stress (Score: 1.006845)



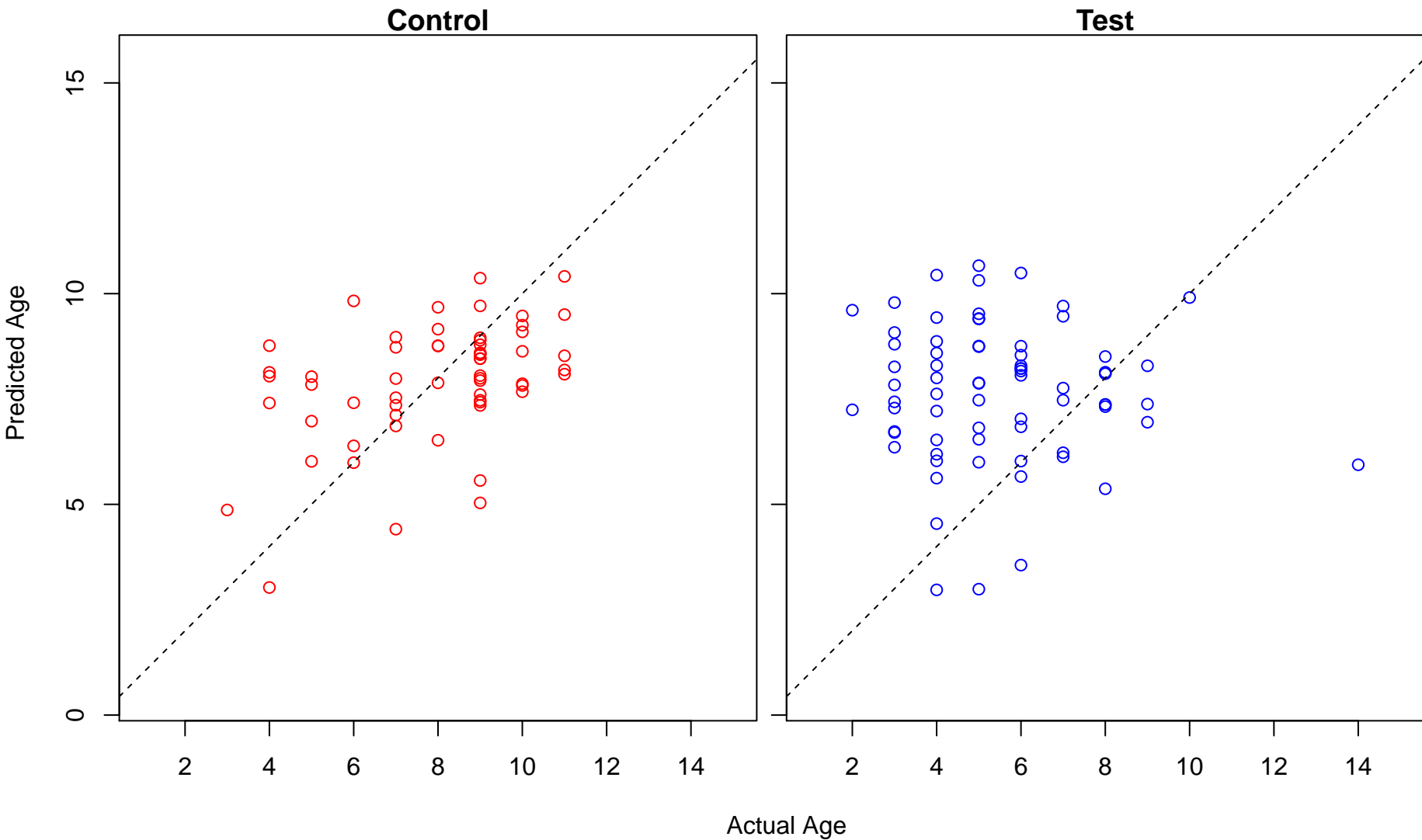
regulation of hormone metabolic process (Score: 1.006414)



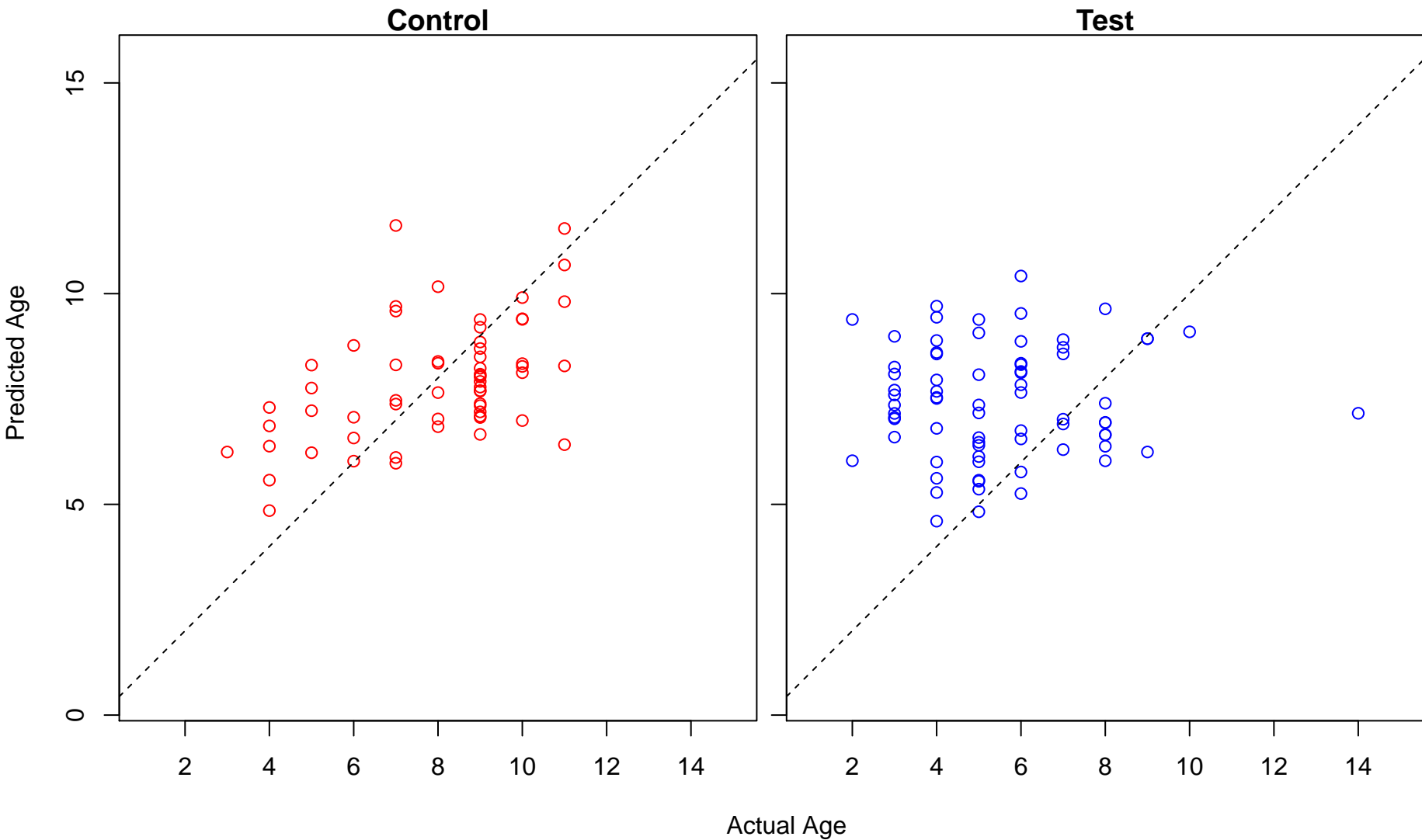
tissue morphogenesis (Score: 1.005772)



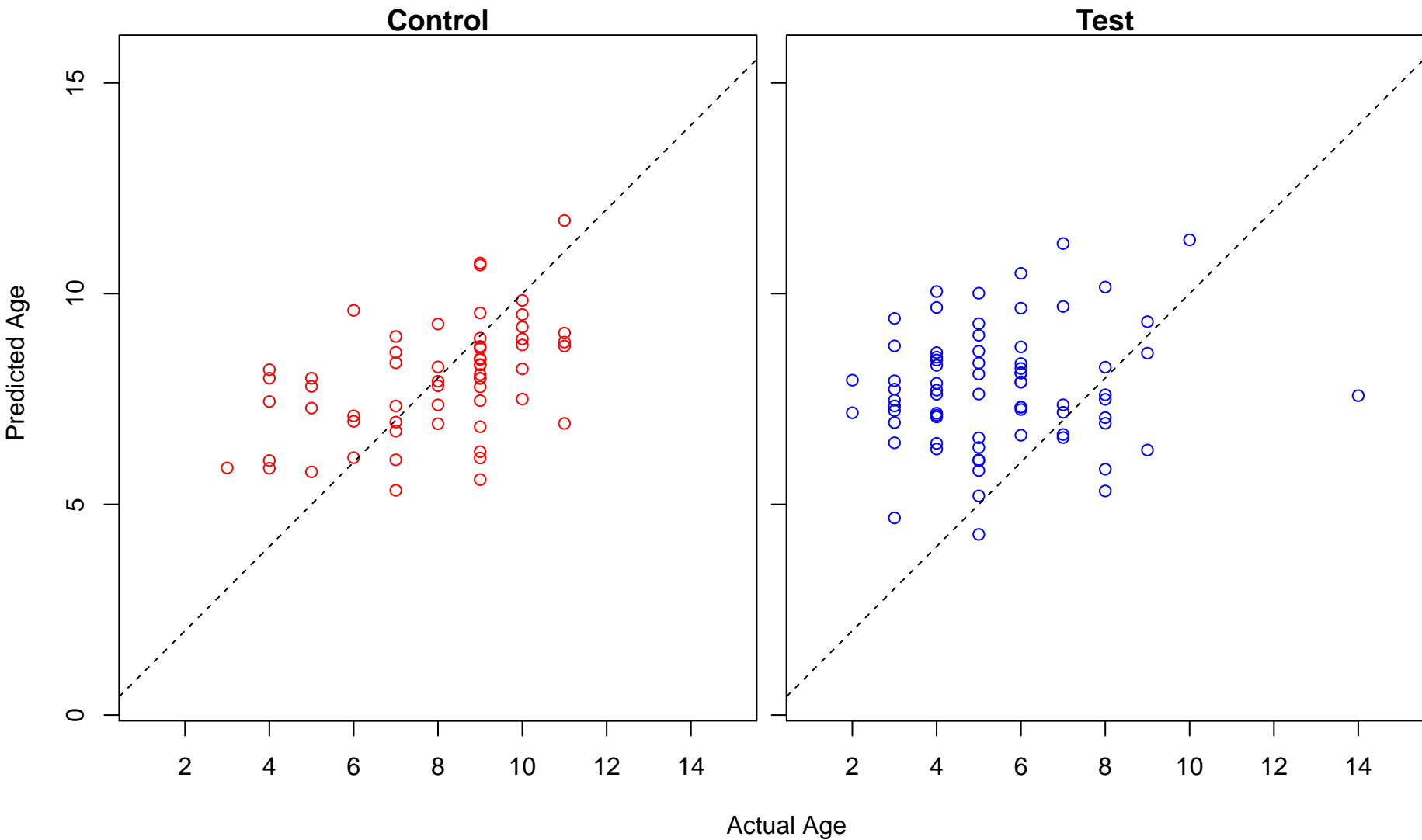
oxidative DNA demethylation (Score: 1.005149)



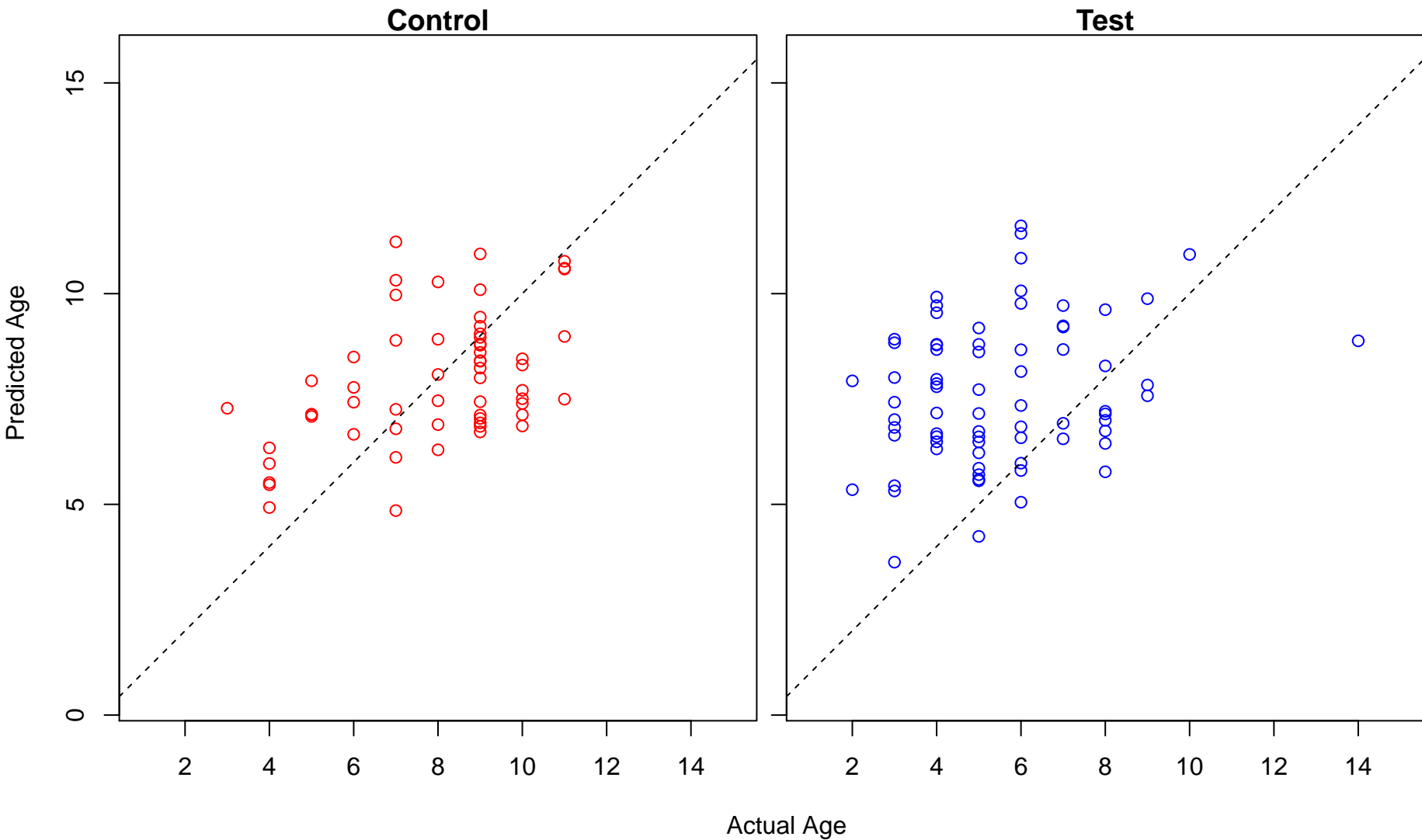
establishment of apical/basal cell polarity (Score: 1.004945)



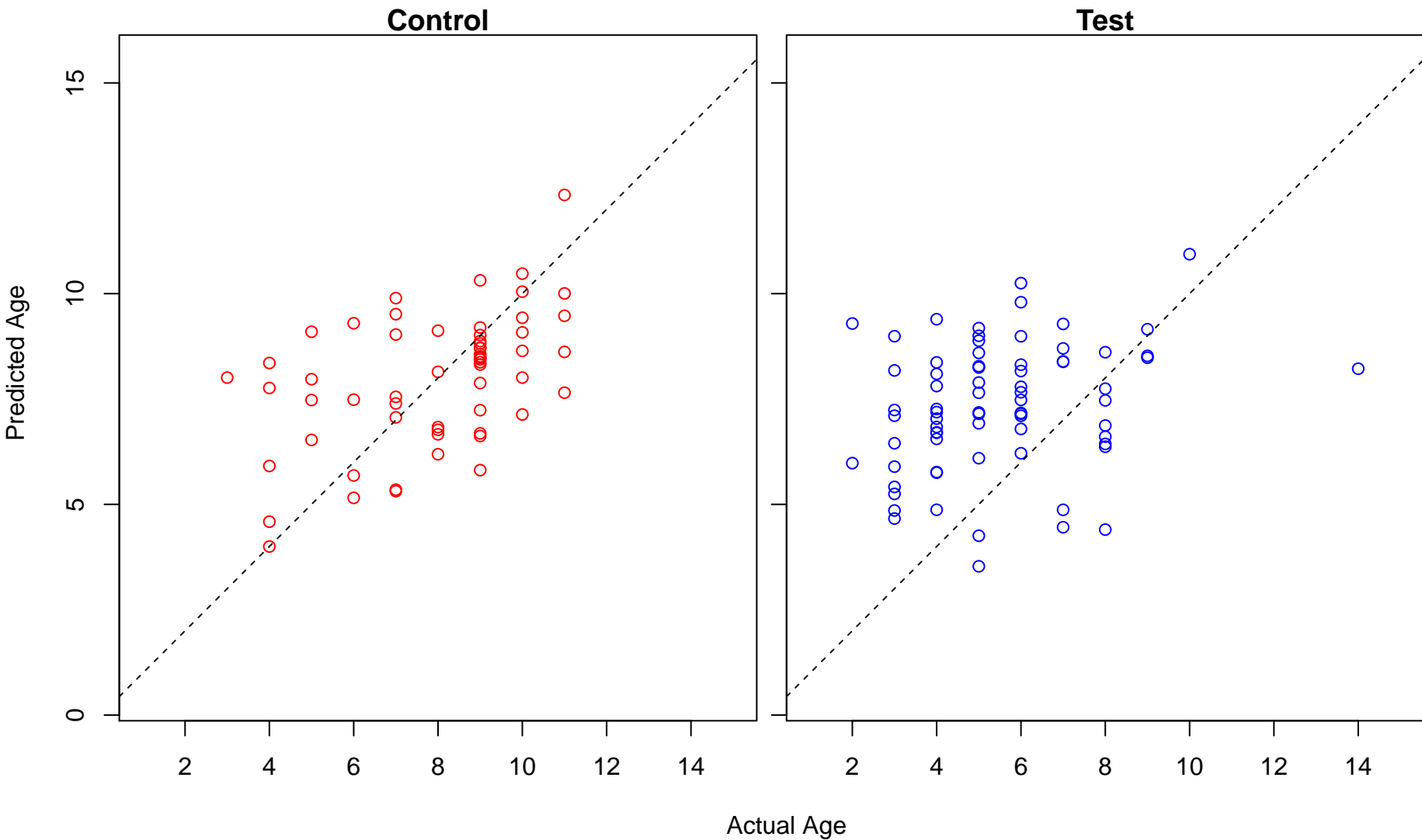
response to calcium ion (Score: 1.004319)



endodermal cell differentiation (Score: 1.004244)

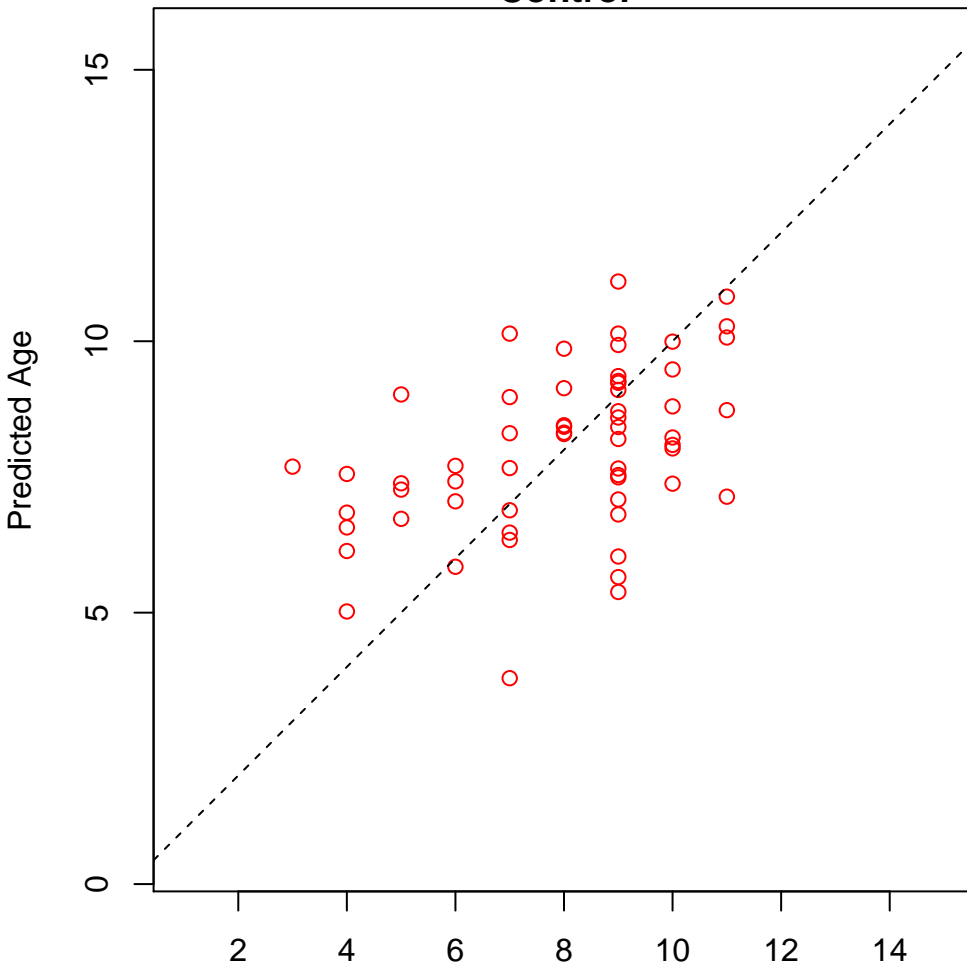


cellular nitrogen compound biosynthetic process (Score: 1.004166)

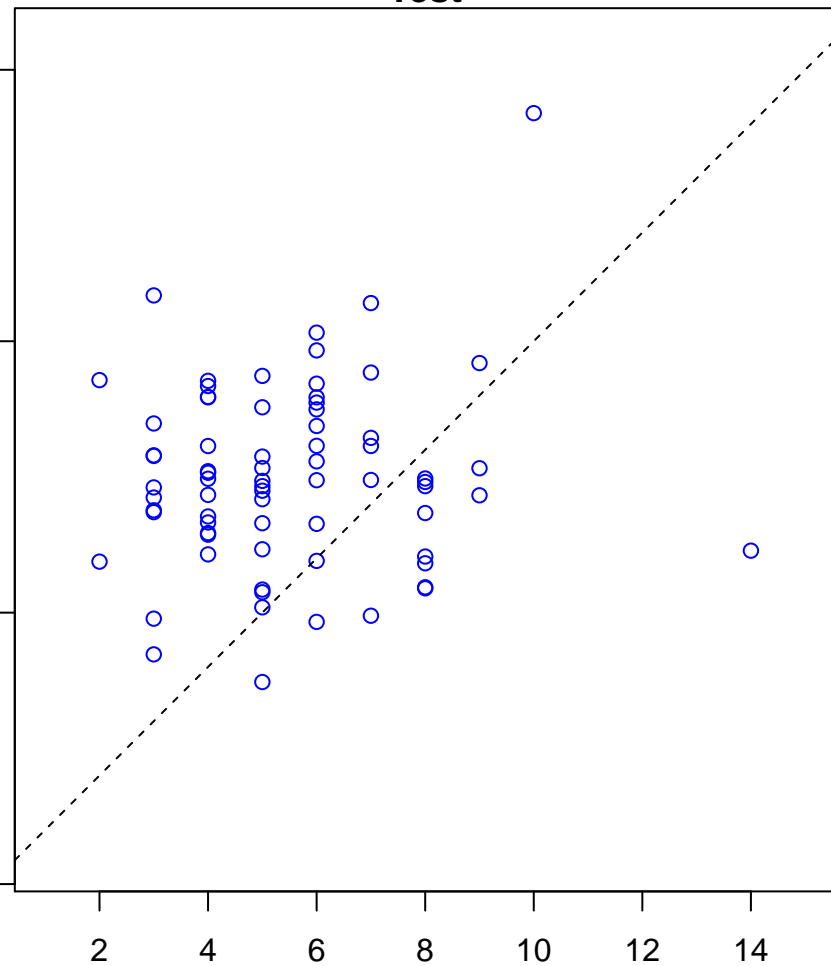


mitotic metaphase plate congruence (Score: 1.004144)

Control

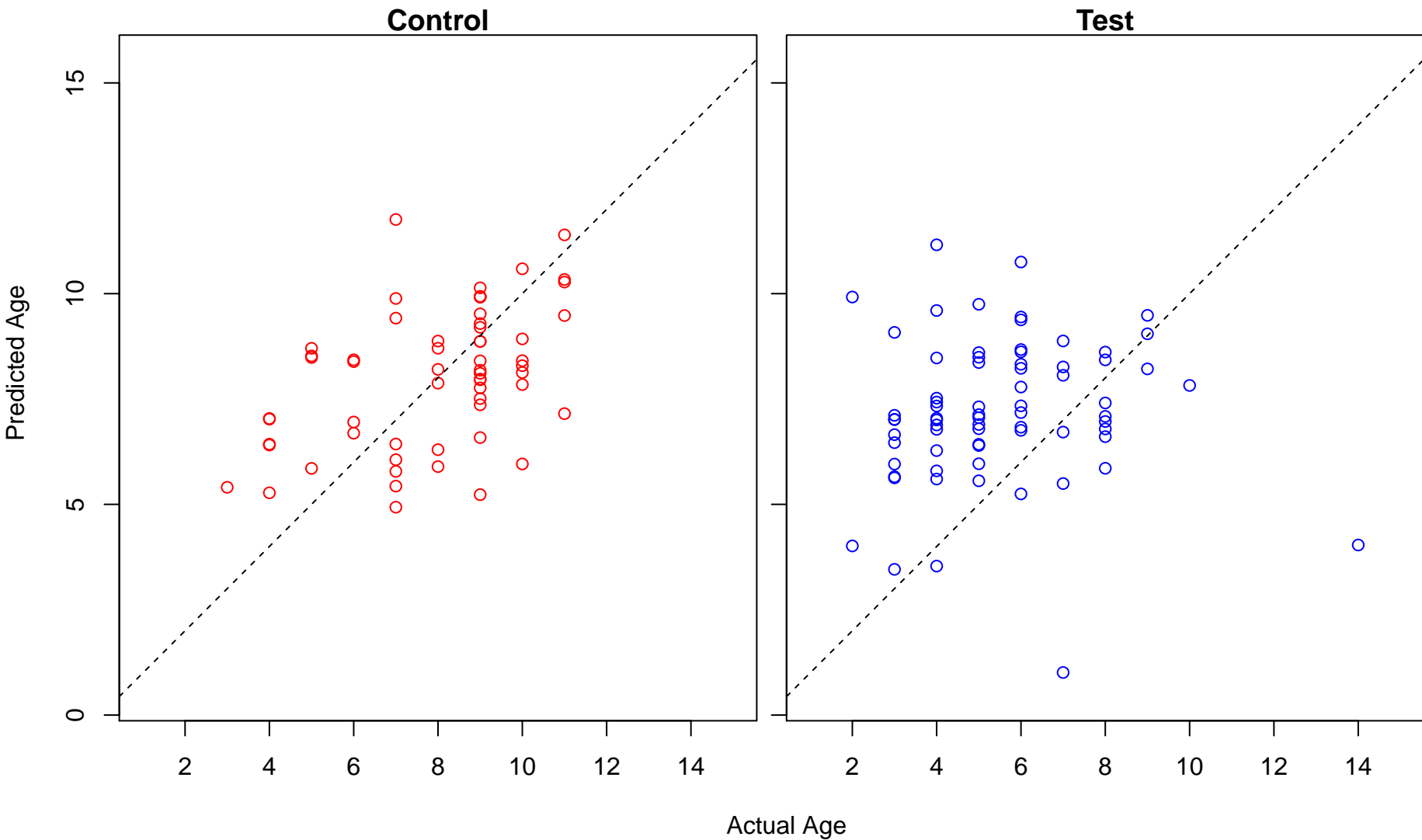


Test

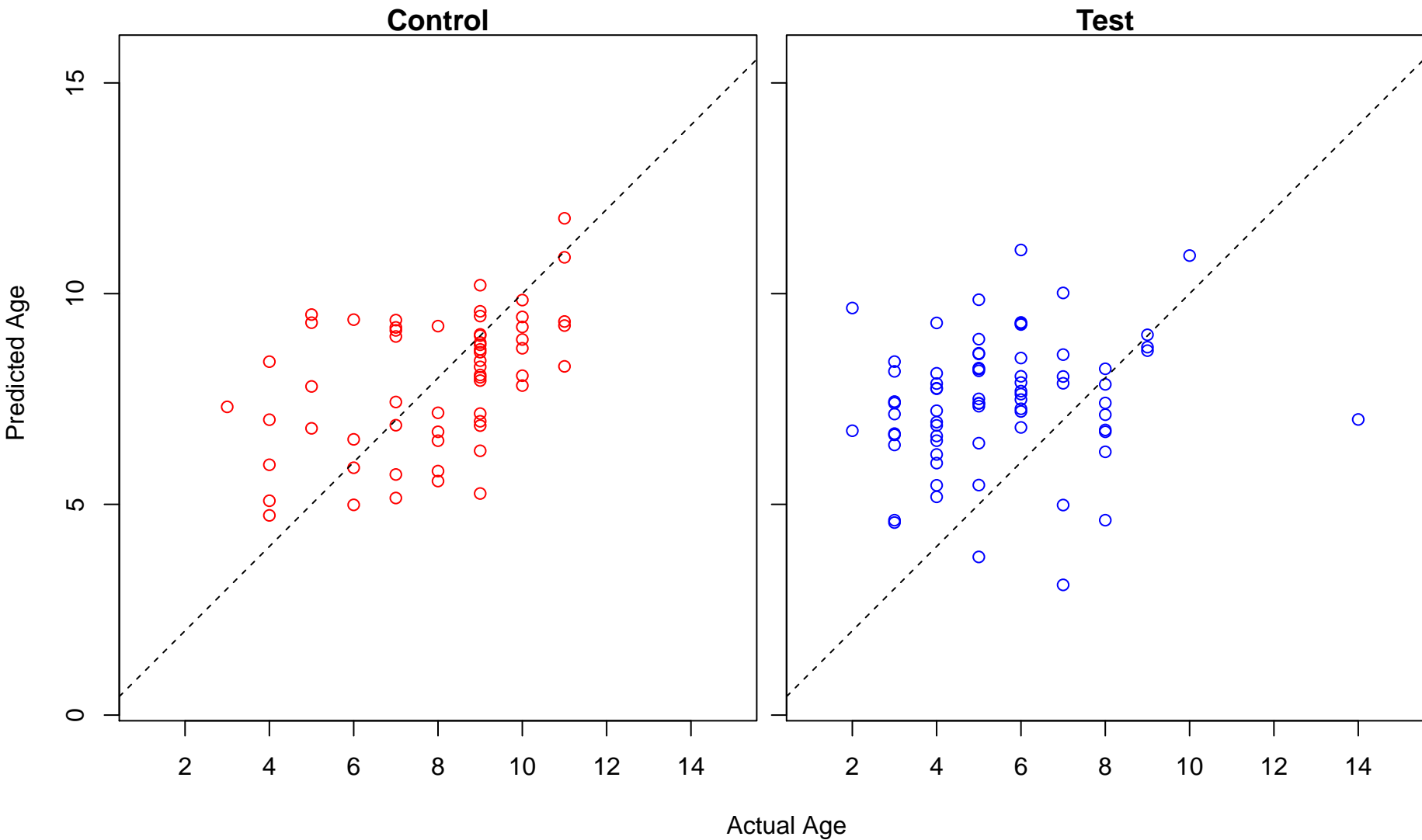


Actual Age

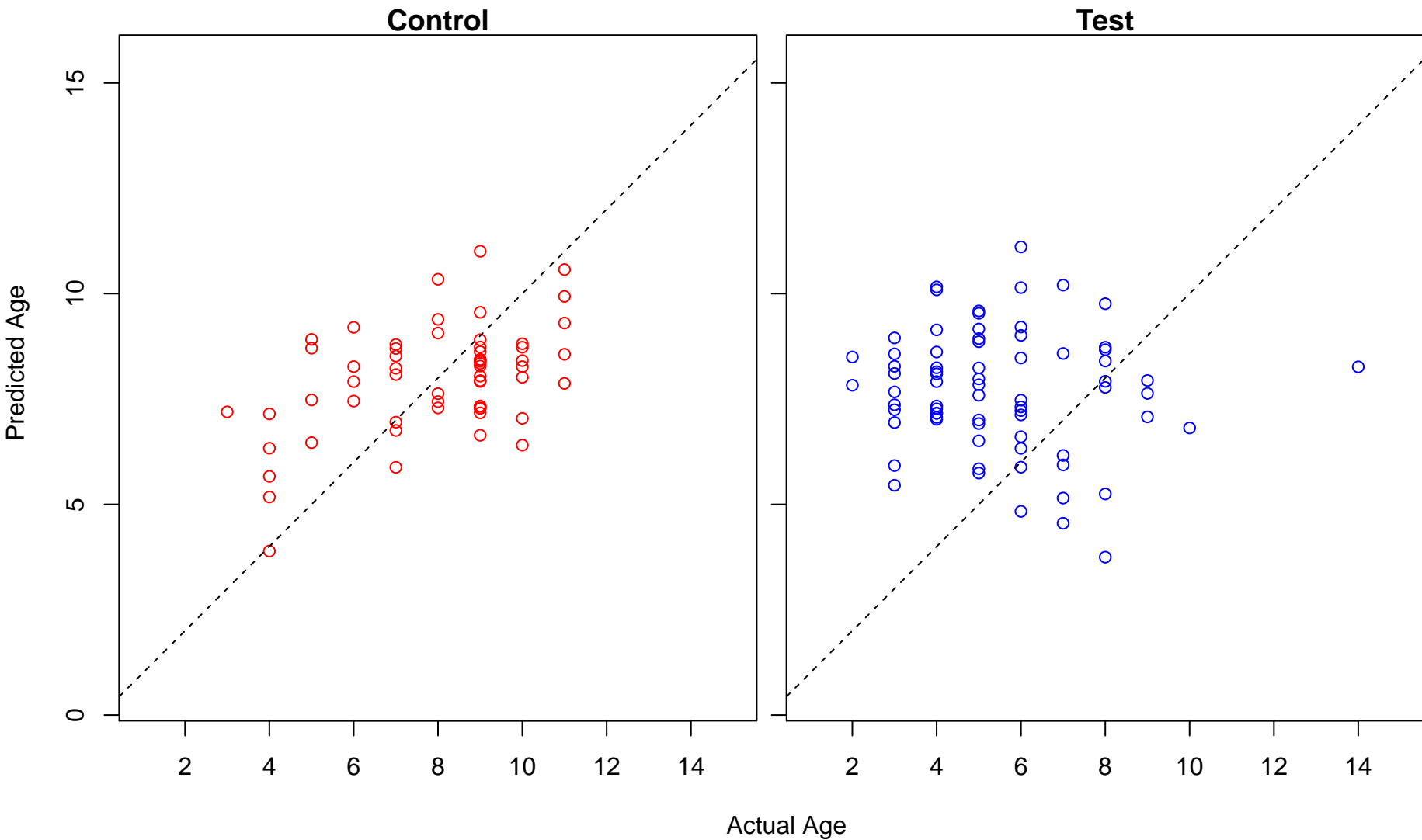
regulation of catabolic process (Score: 1.003955)



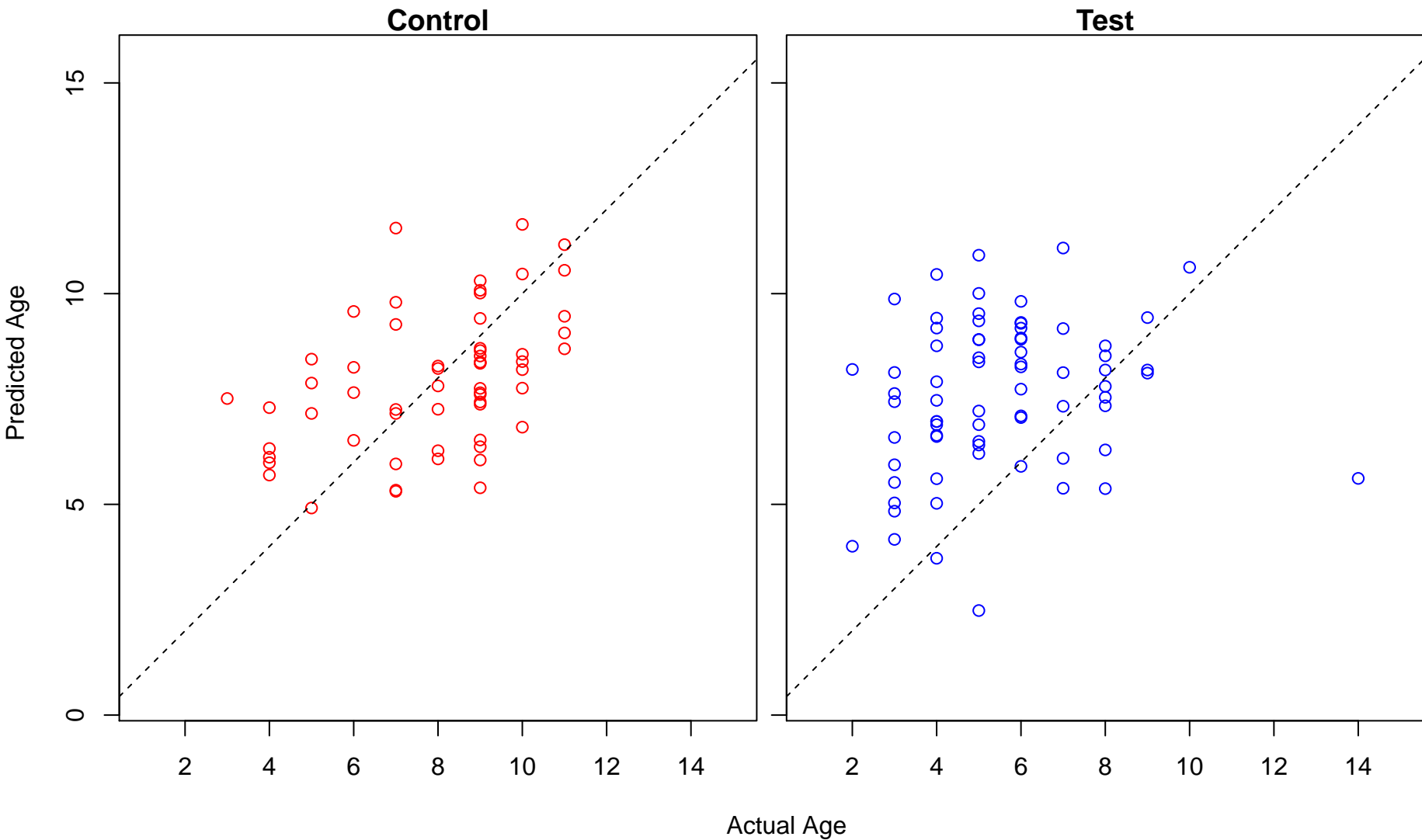
cellular aromatic compound metabolic process (Score: 1.003764)



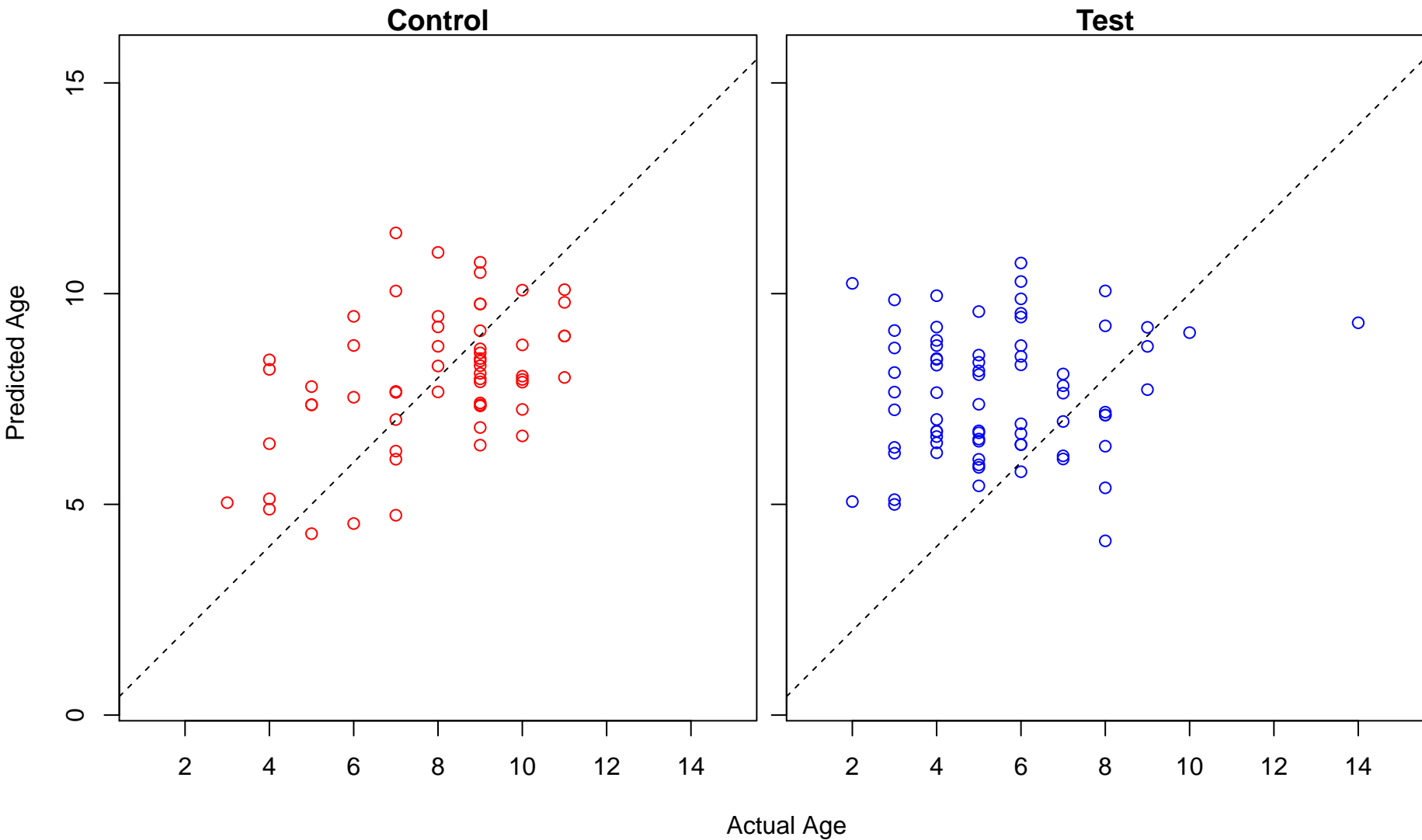
negative regulation of neurotransmitter transport (Score: 1.003096)



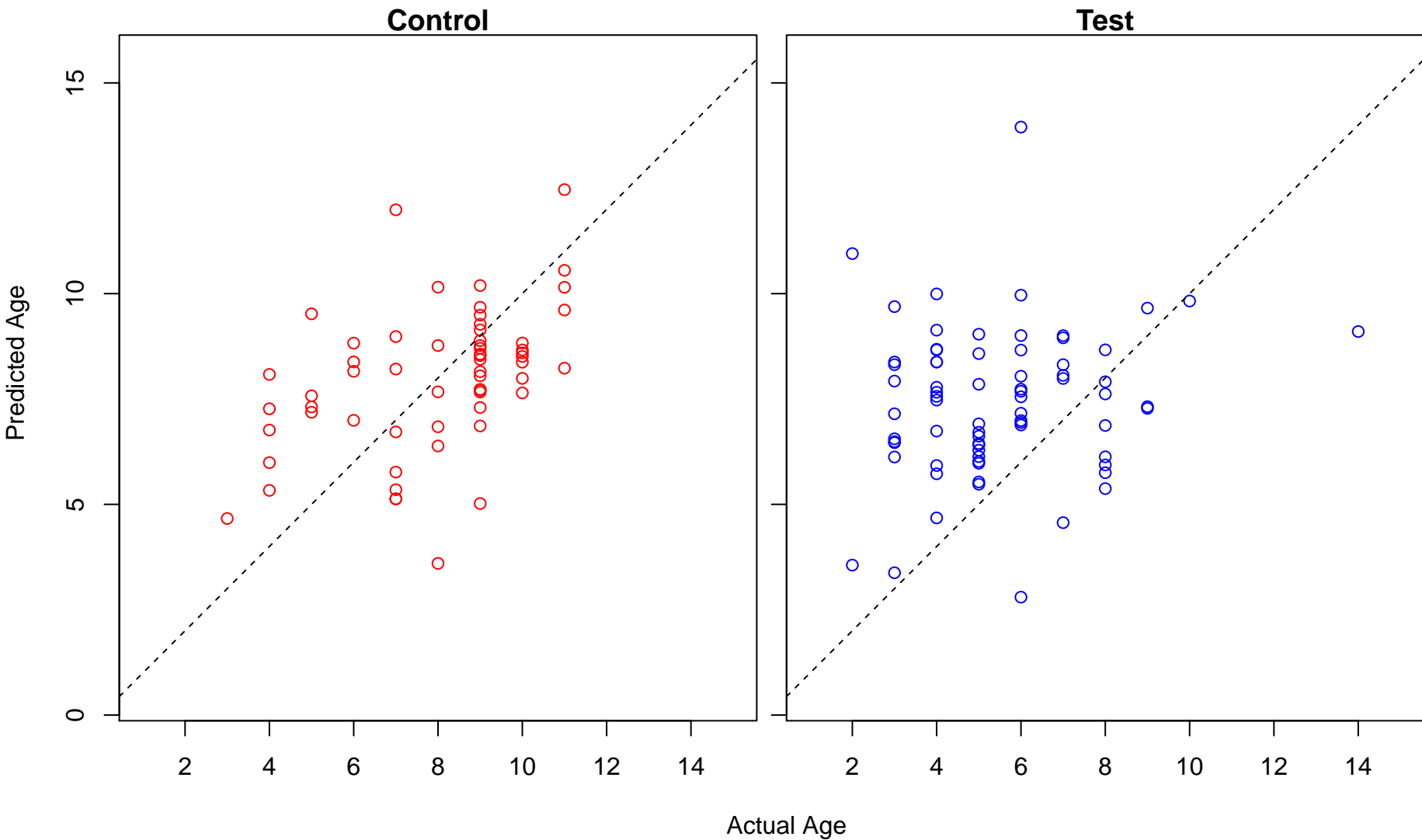
regulation of response to nutrient levels (Score: 1.002892)



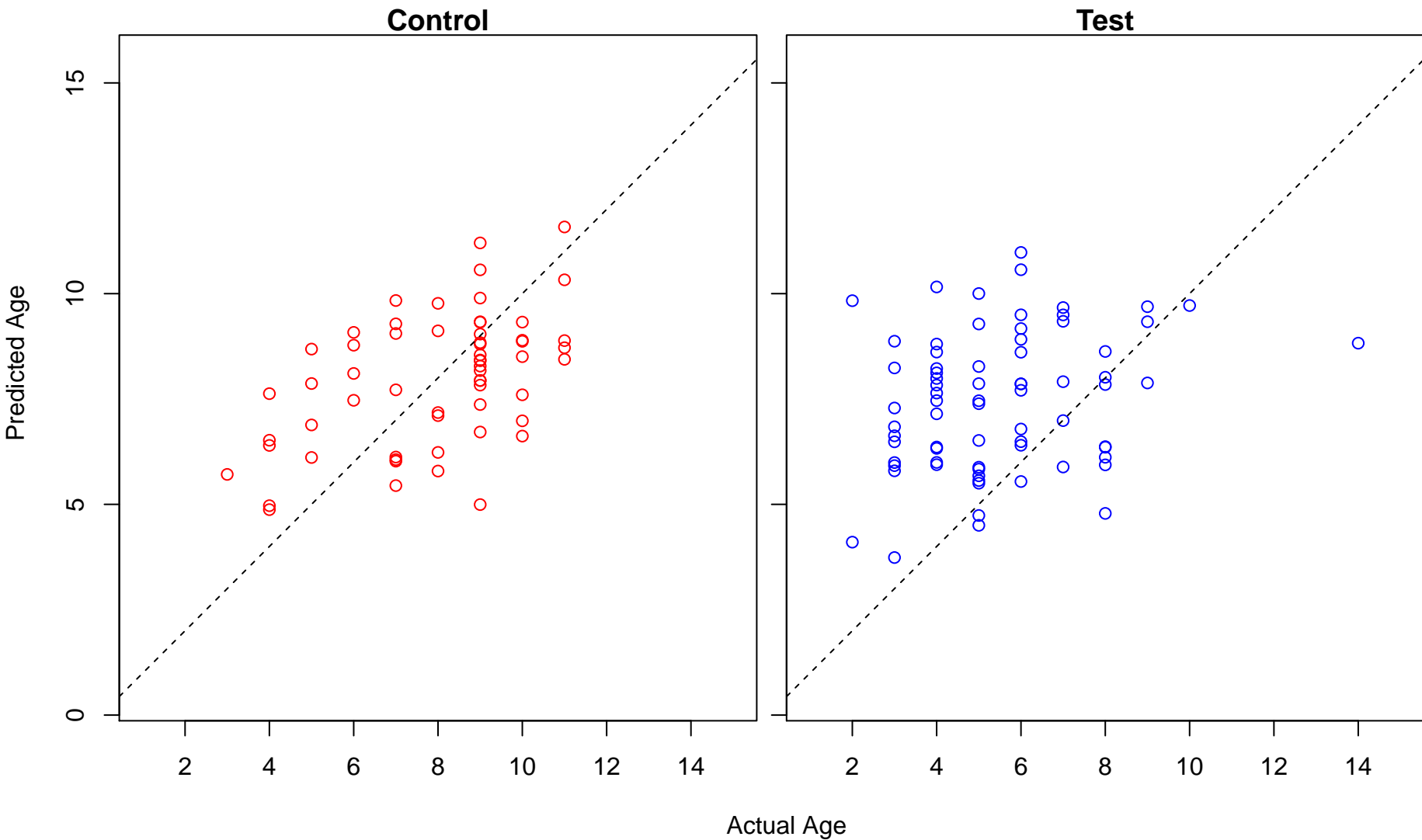
peptide transport (Score: 1.002769)



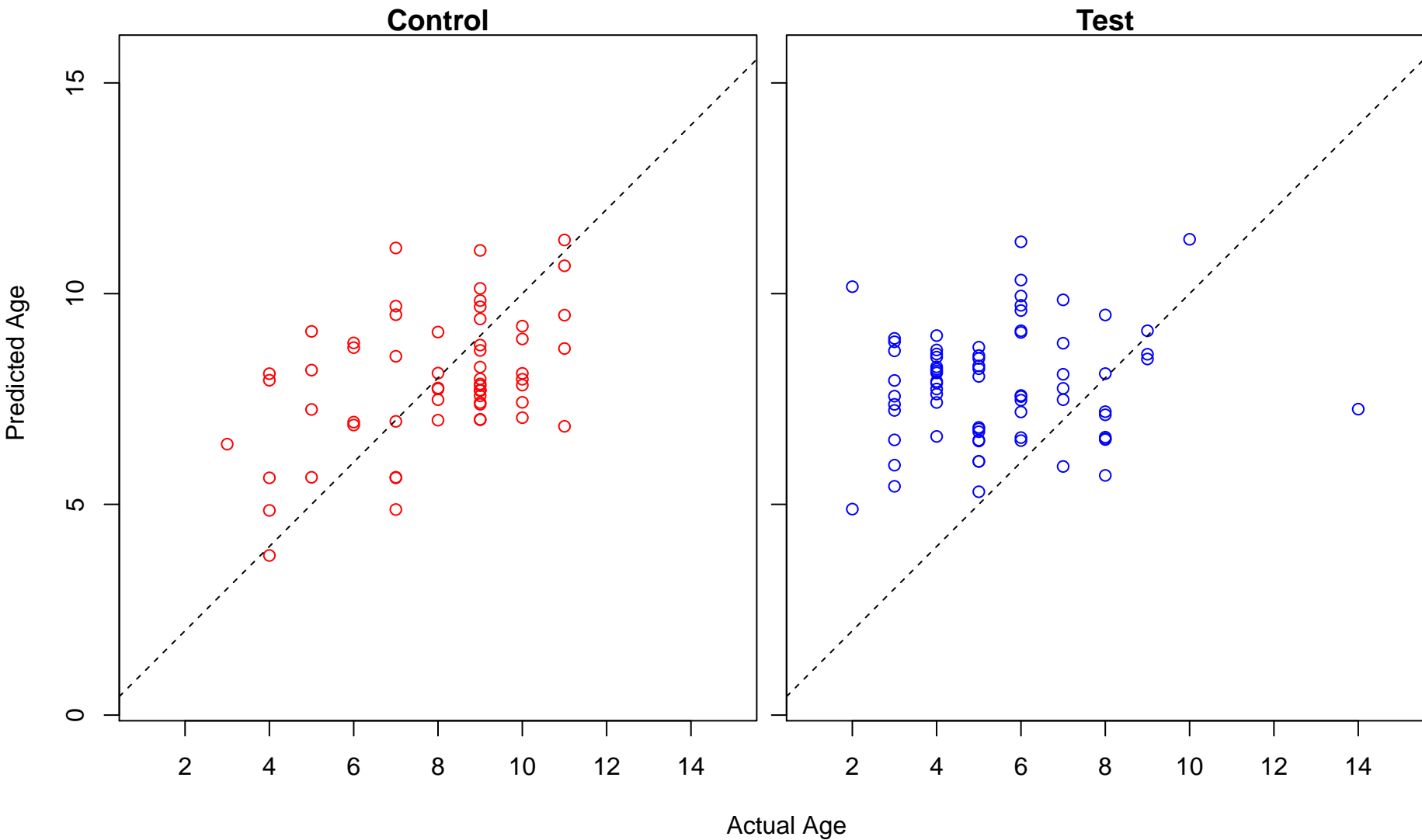
regulation of protein localization (Score: 1.002644)



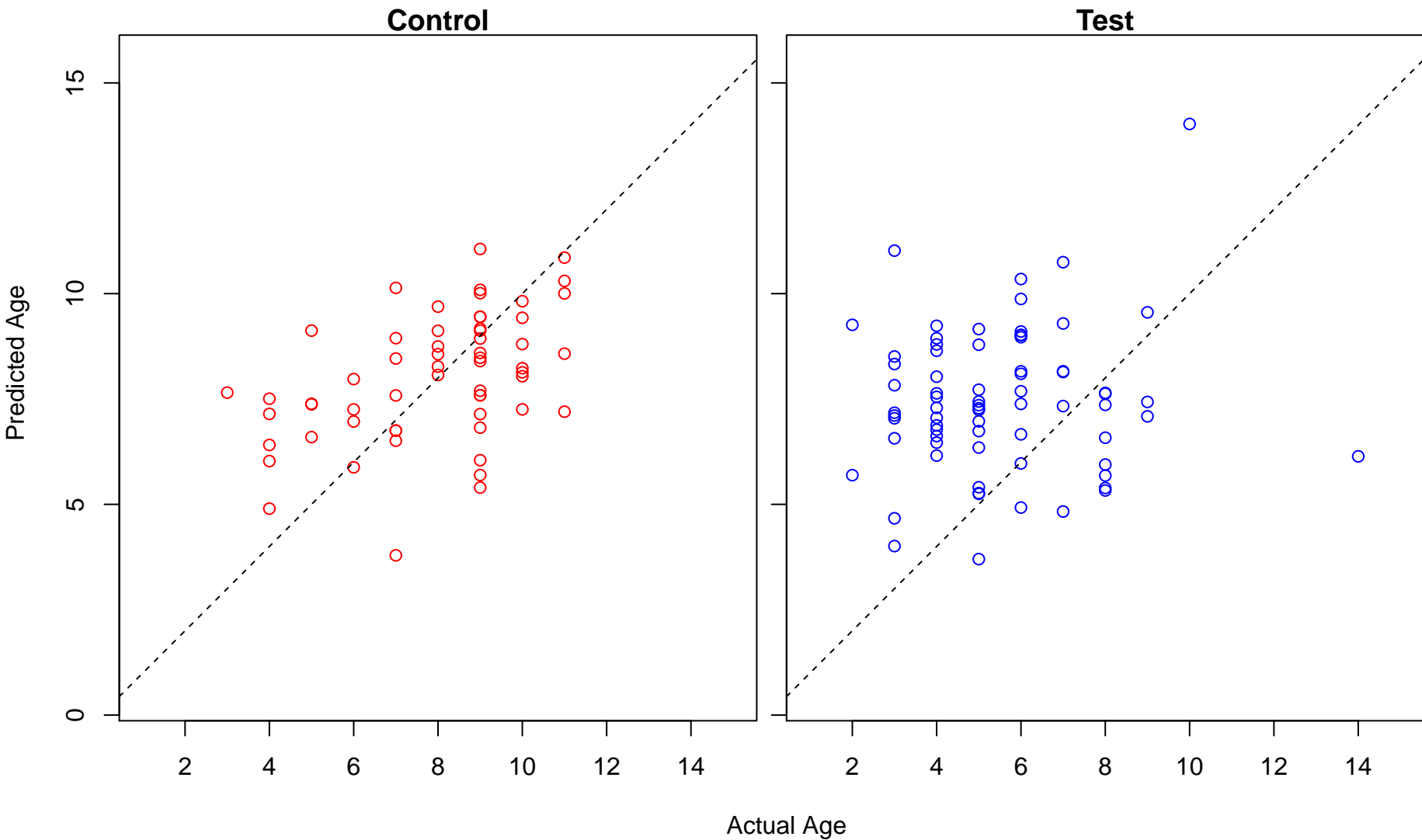
cell morphogenesis (Score: 1.002056)



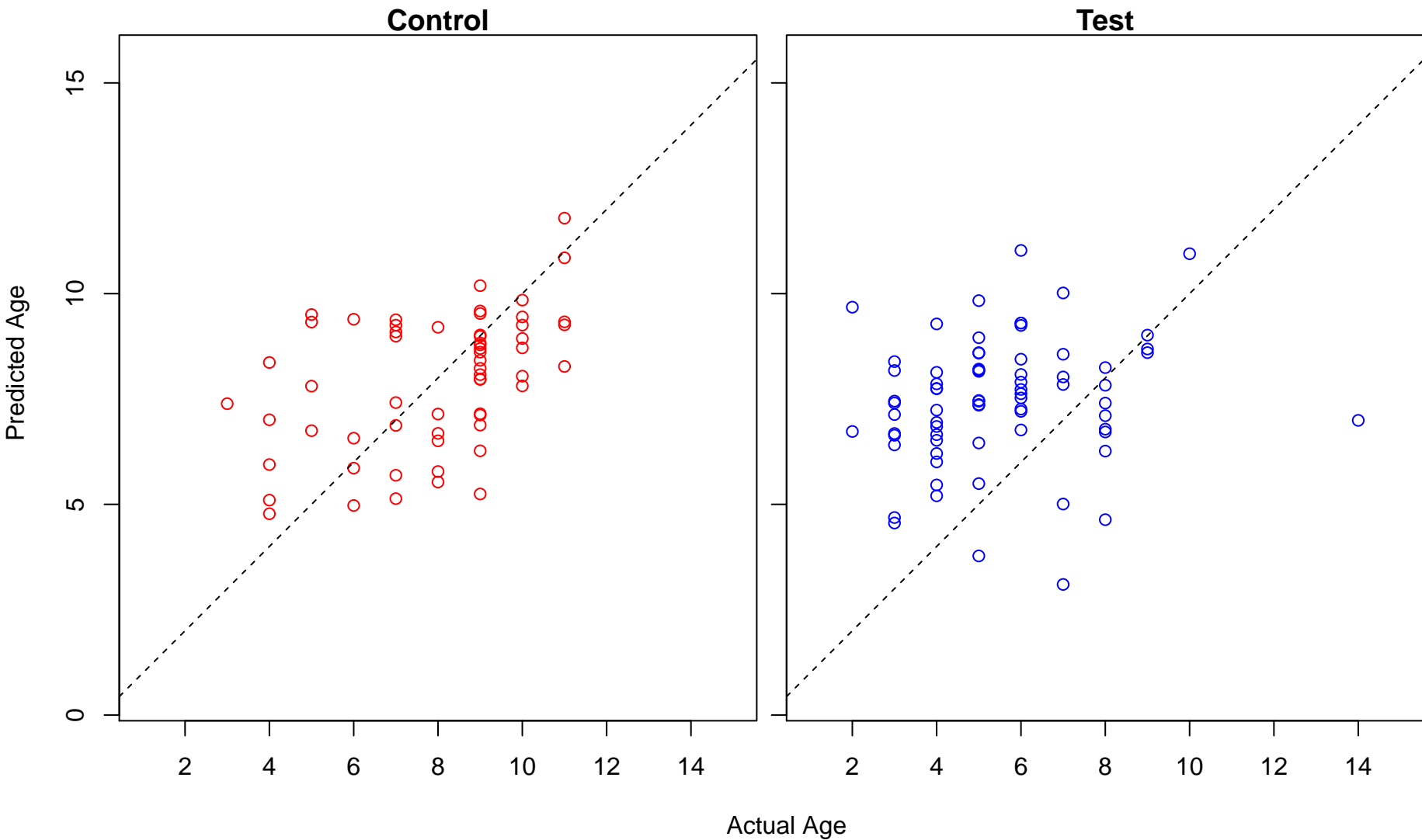
epidermal cell differentiation (Score: 1.001462)



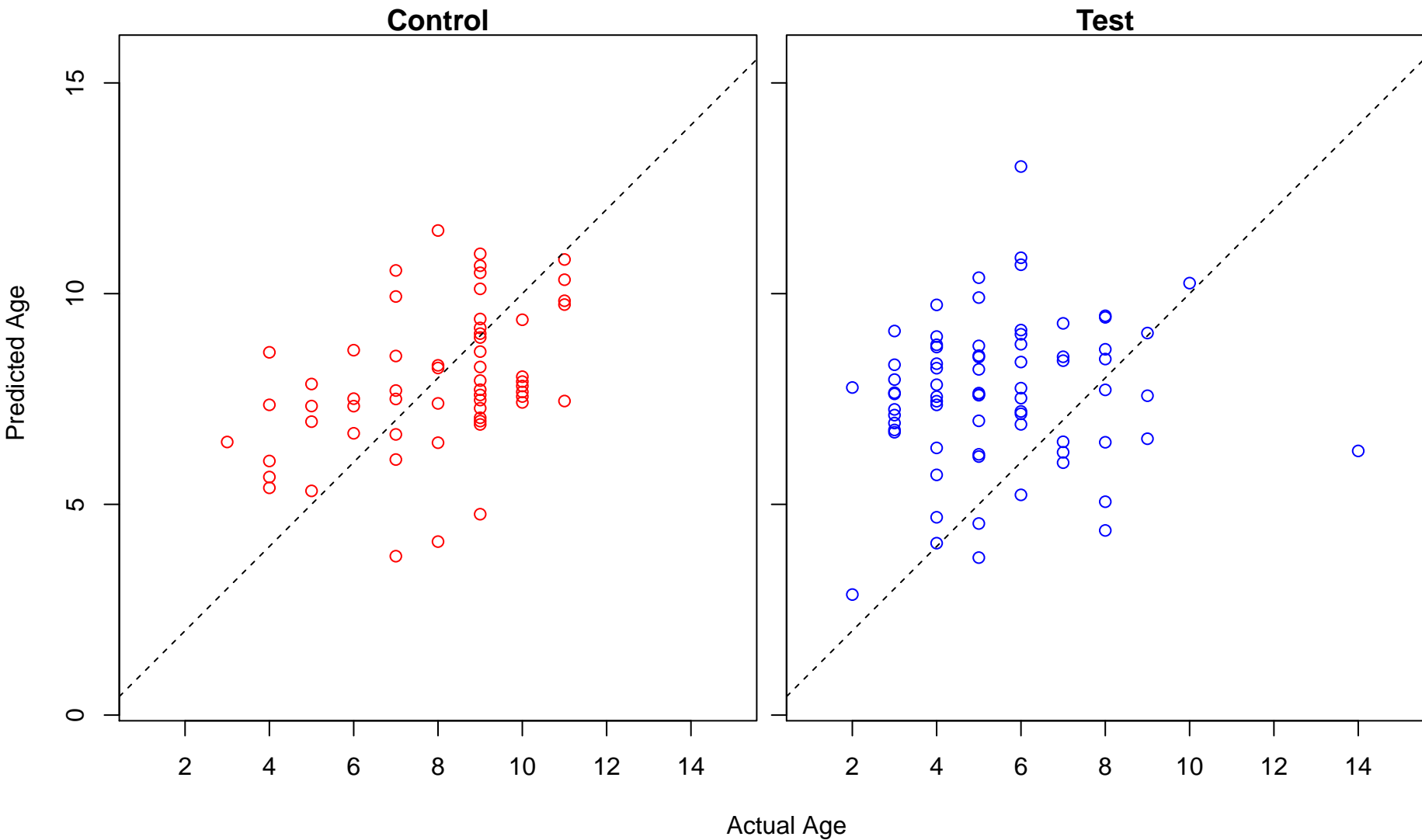
metaphase plate congression (Score: 1.001329)



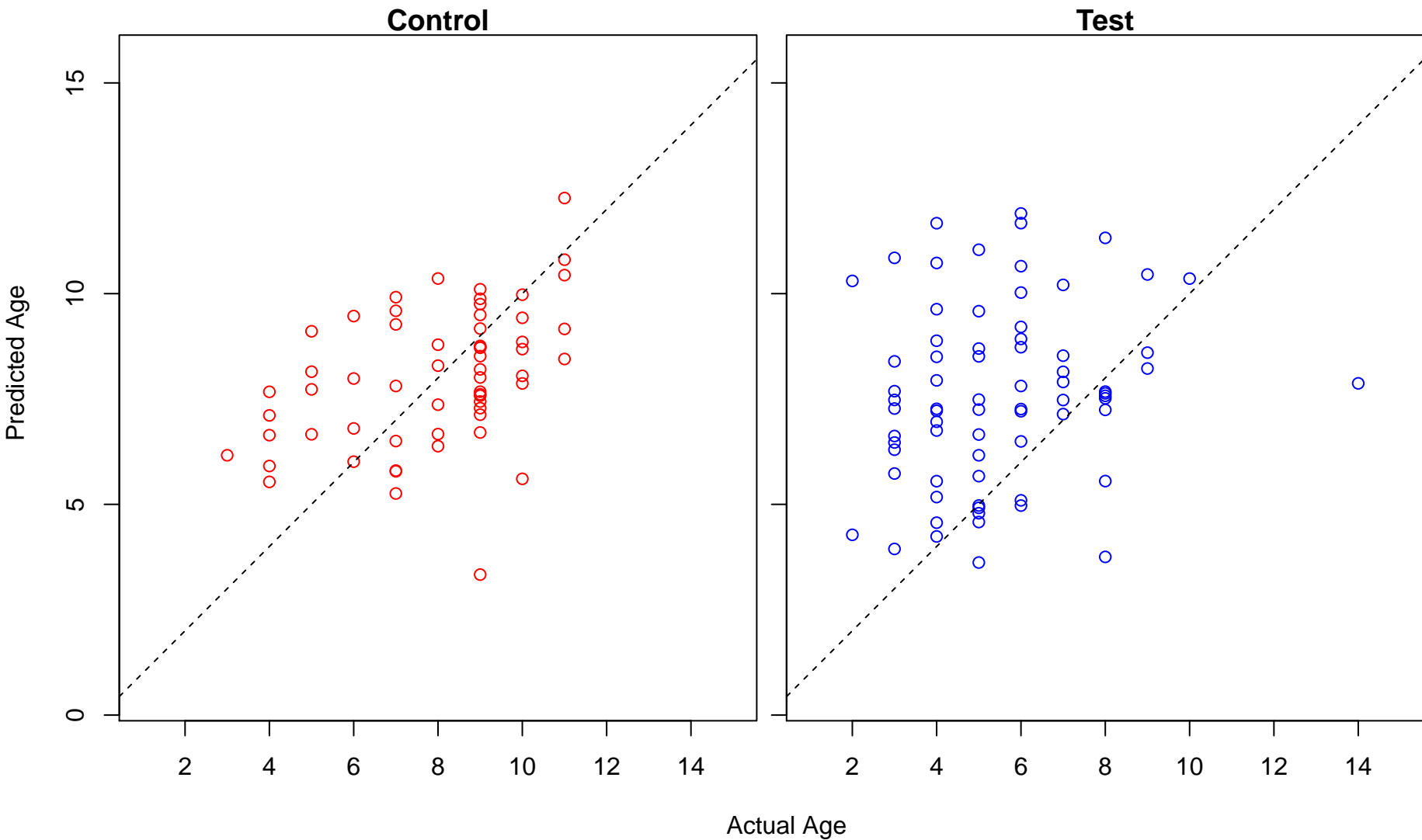
heterocycle metabolic process (Score: 1.000874)



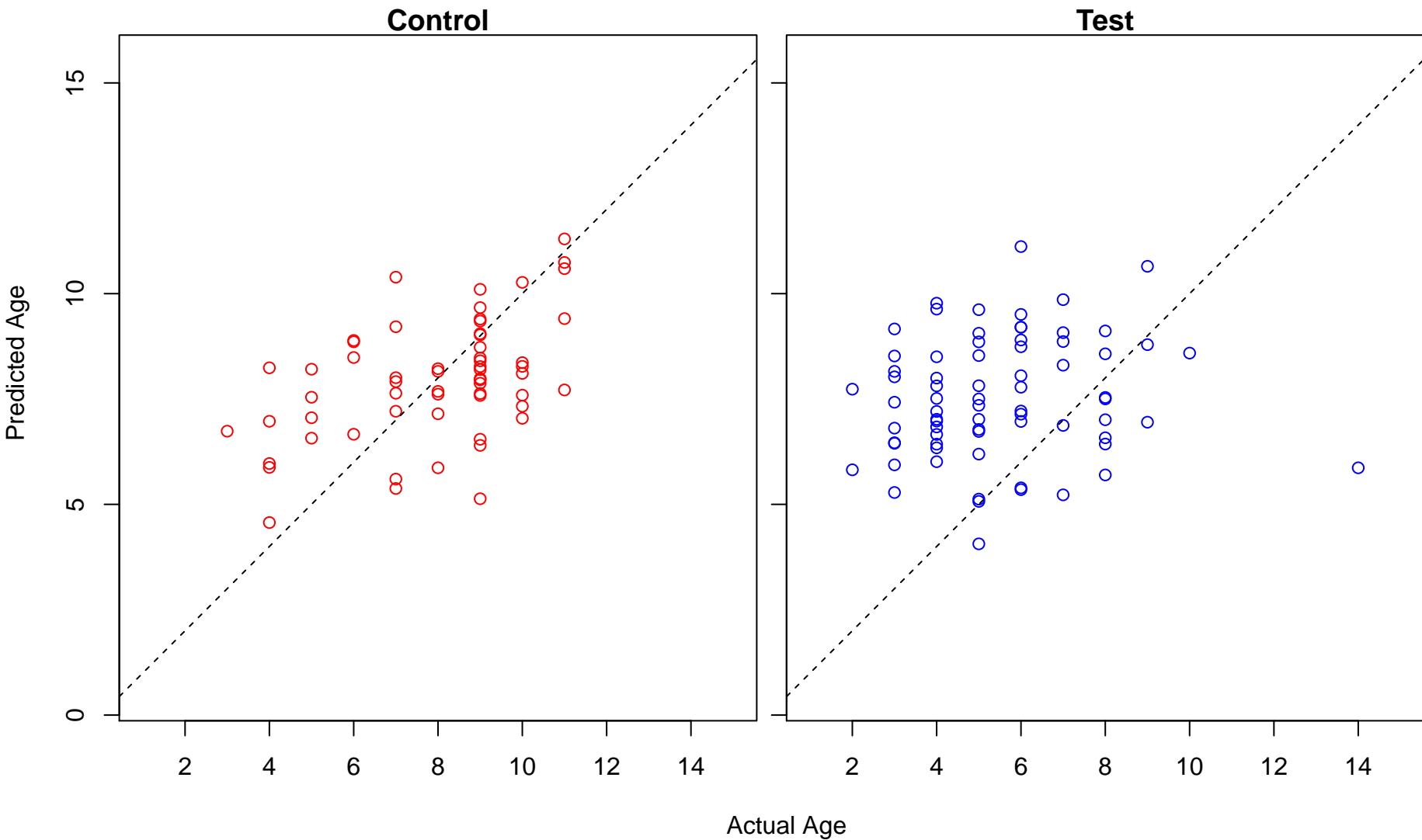
regulation of dendrite development (Score: 0.999040)



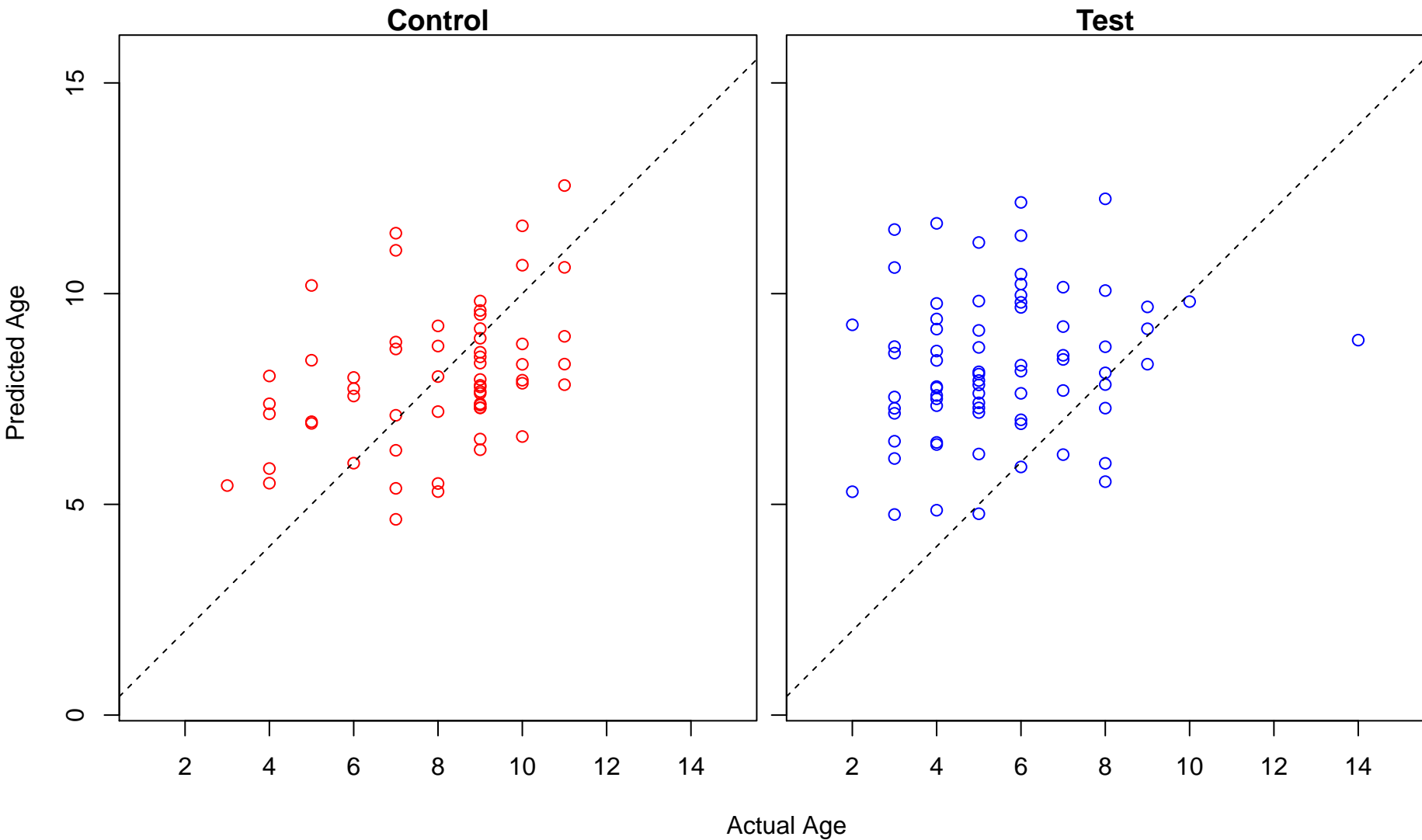
actin filament-based process (Score: 0.997632)



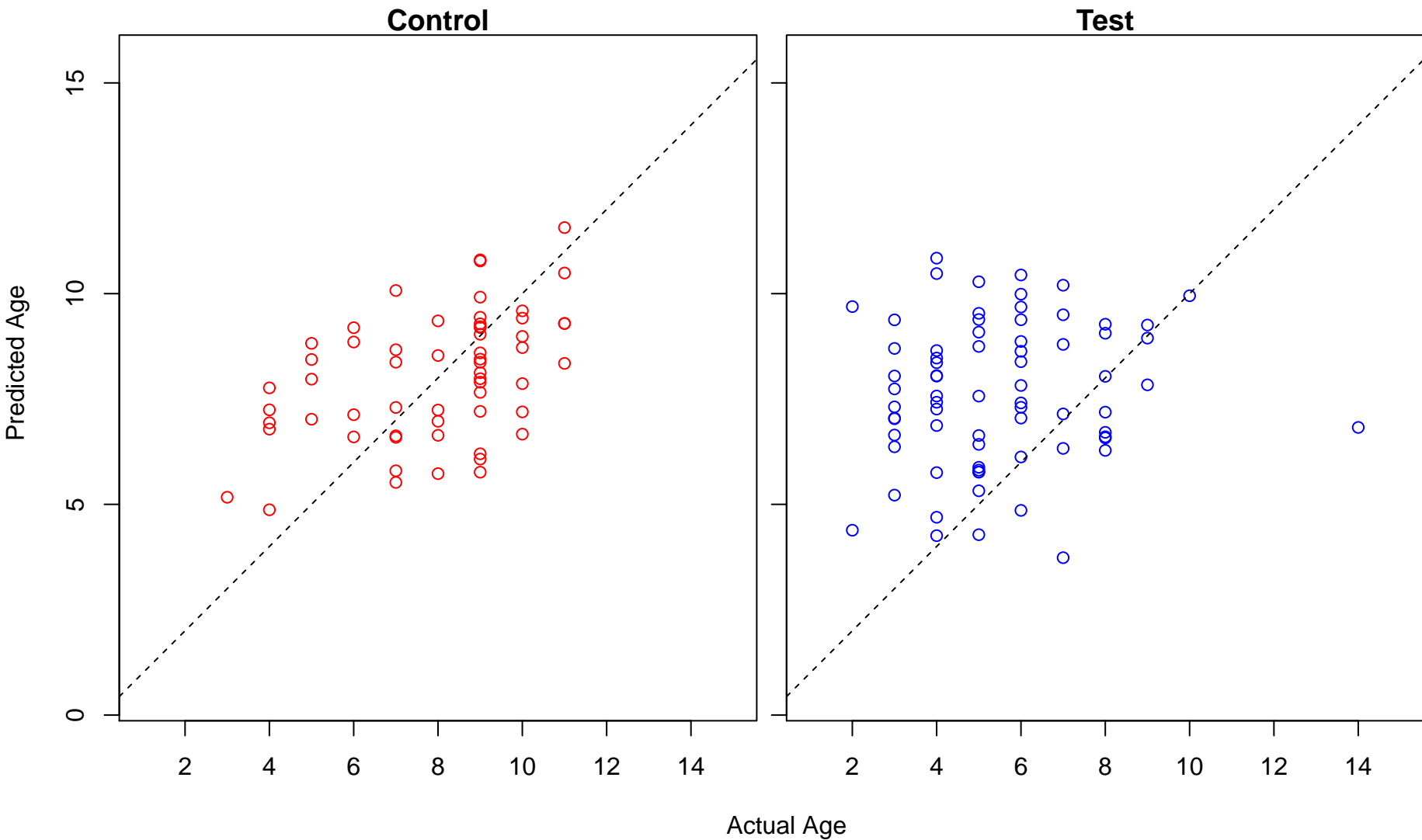
muscle contraction (Score: 0.997528)



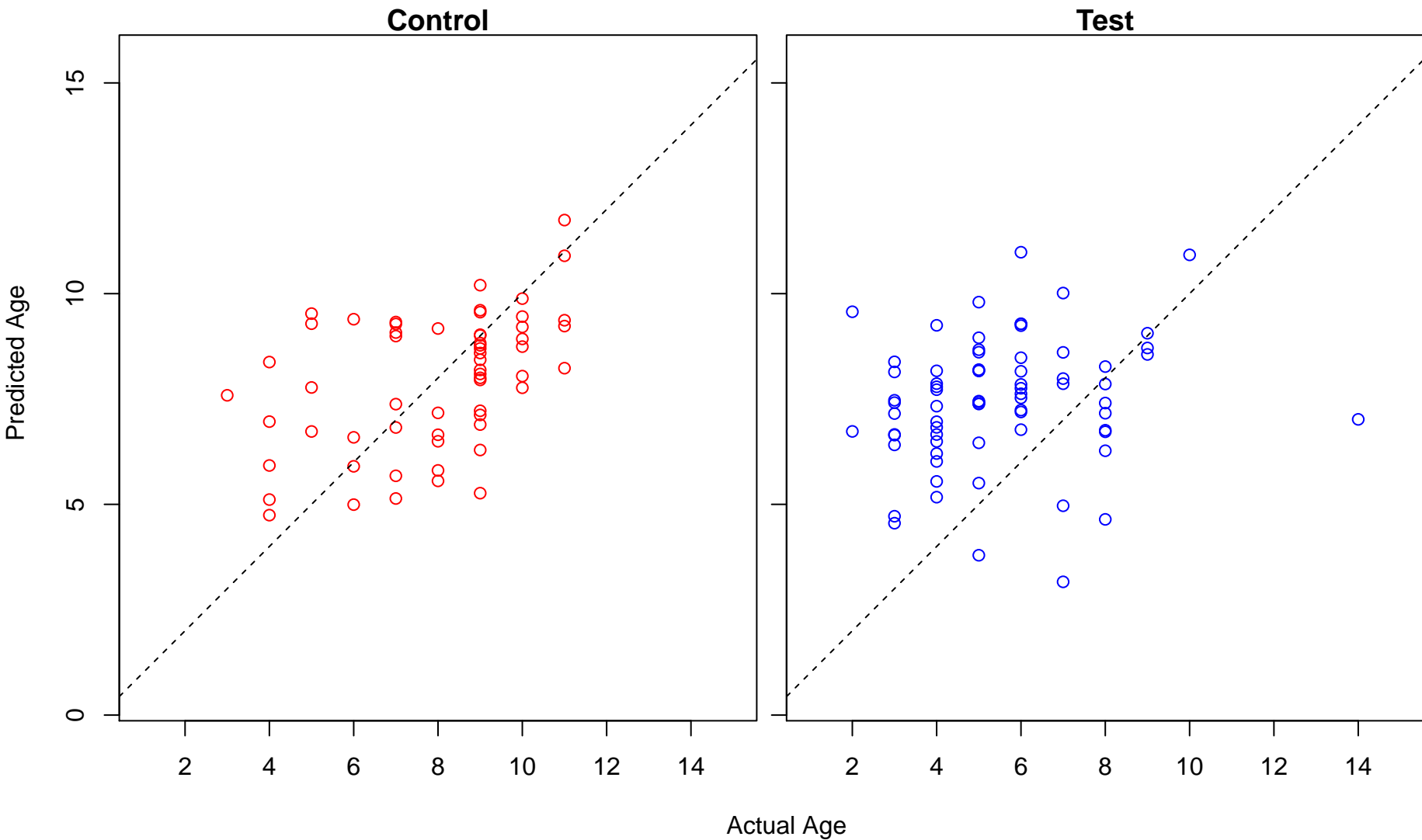
eye development (Score: 0.996365)



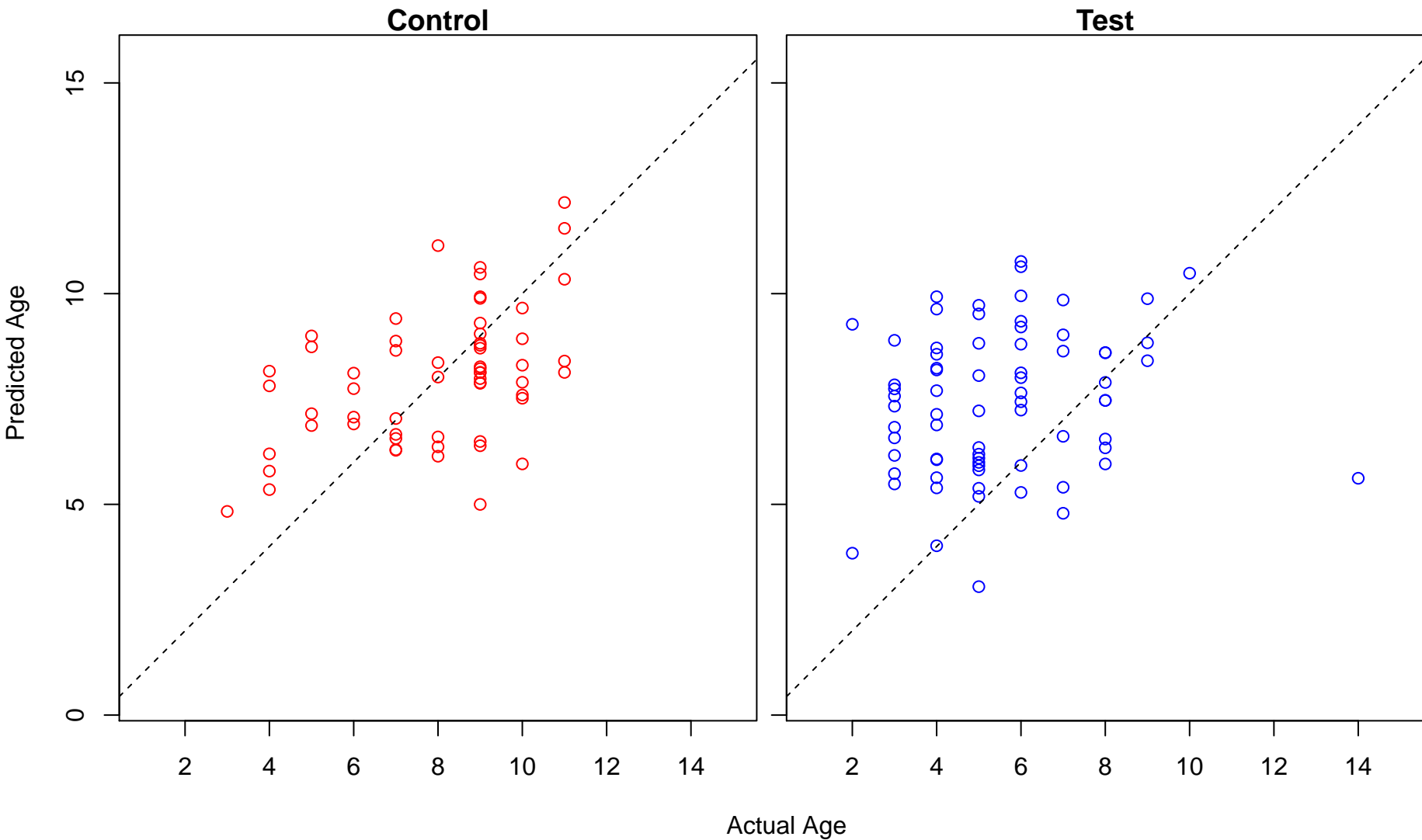
multicellular organismal development (Score: 0.995707)



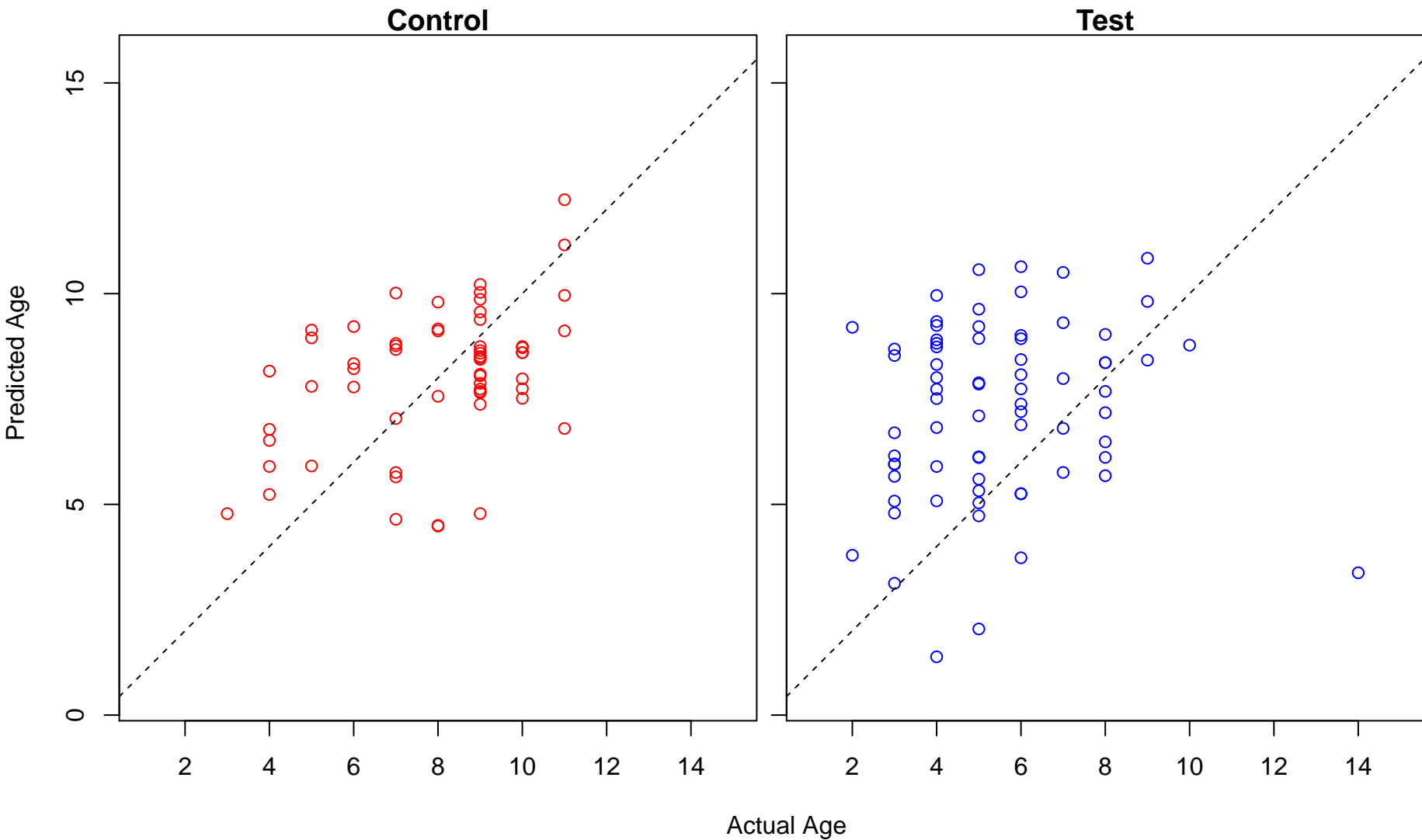
organic cyclic compound metabolic process (Score: 0.994976)



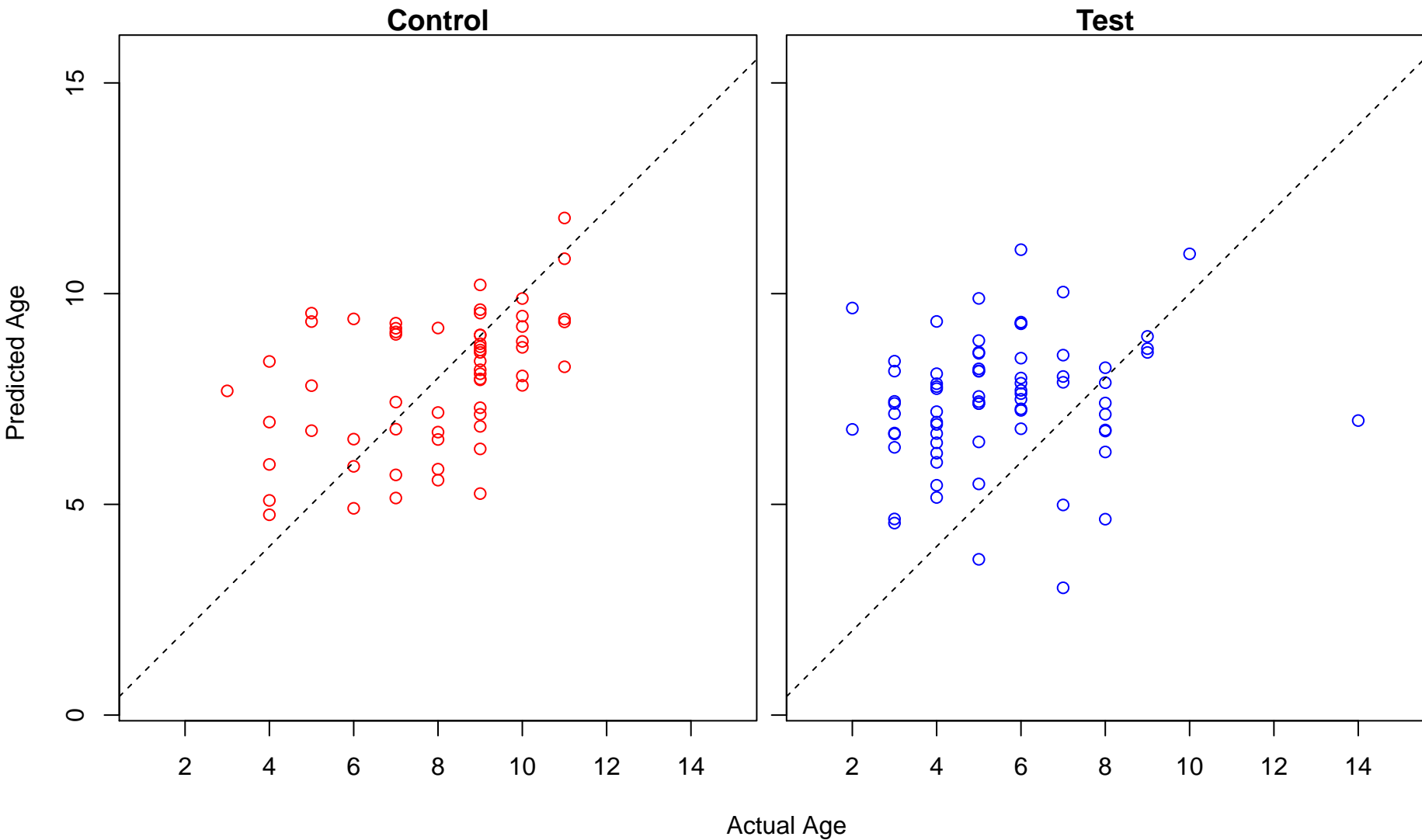
tissue development (Score: 0.993338)



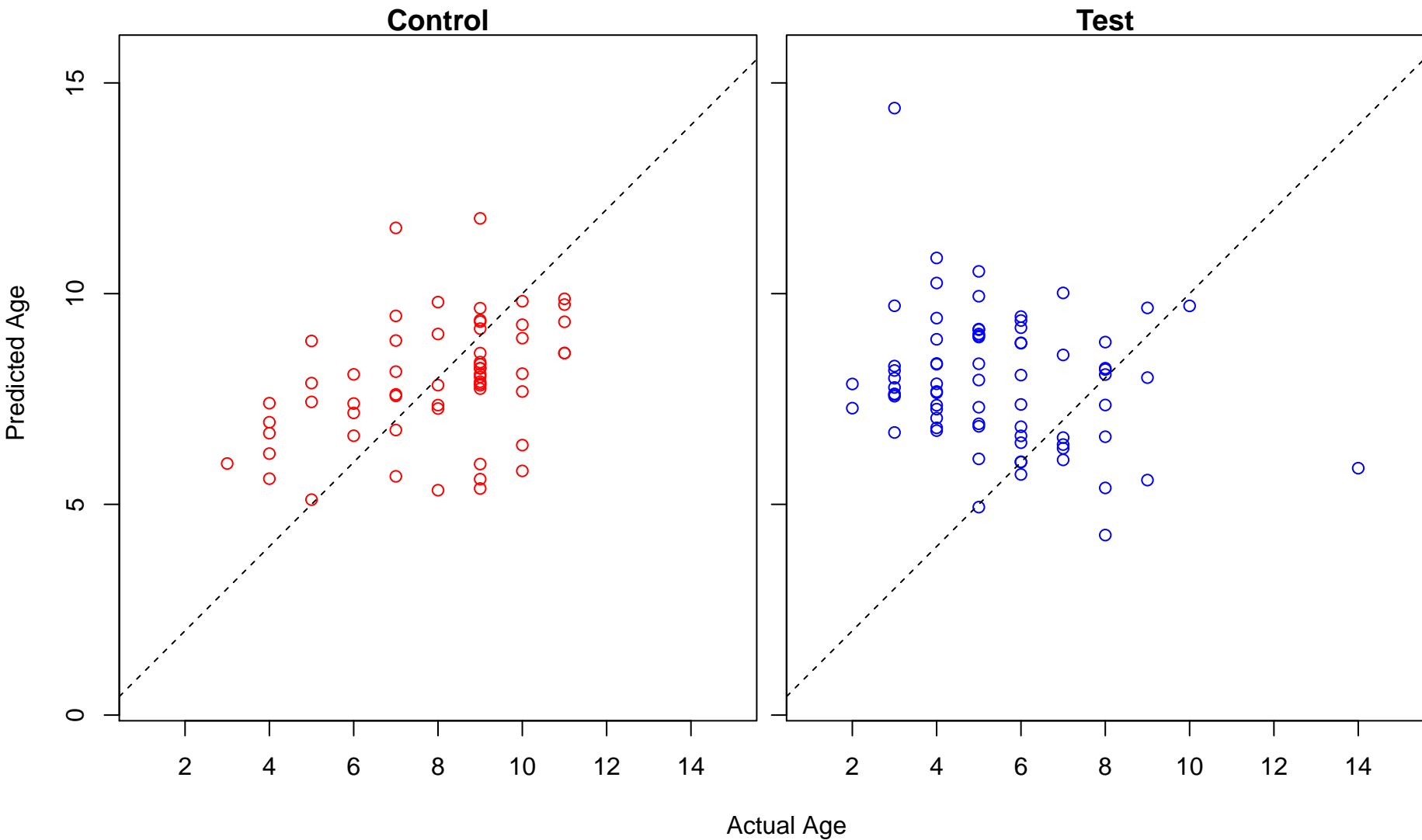
response to oxygen-containing compound (Score: 0.992994)



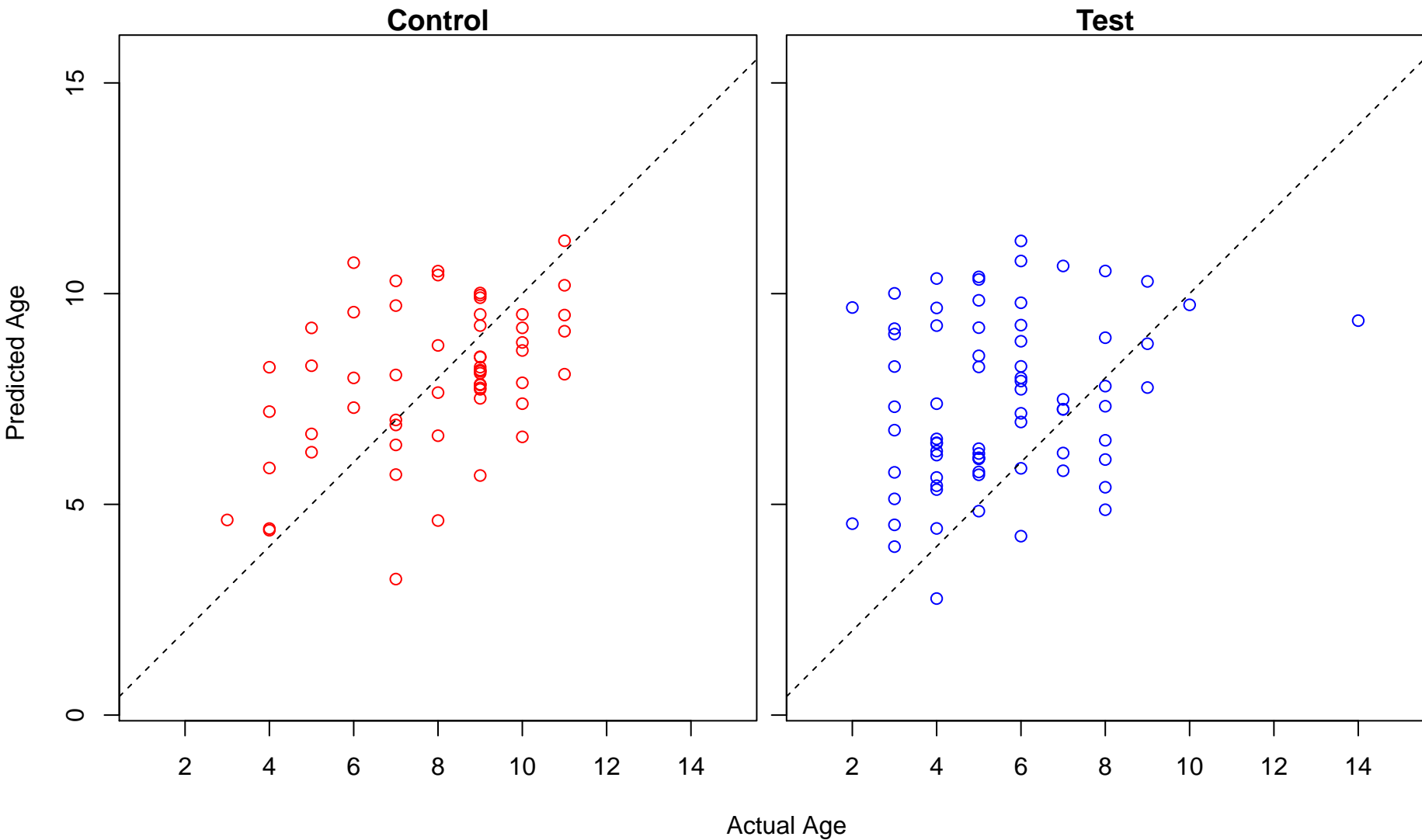
nucleobase-containing compound metabolic process (Score: 0.992138)



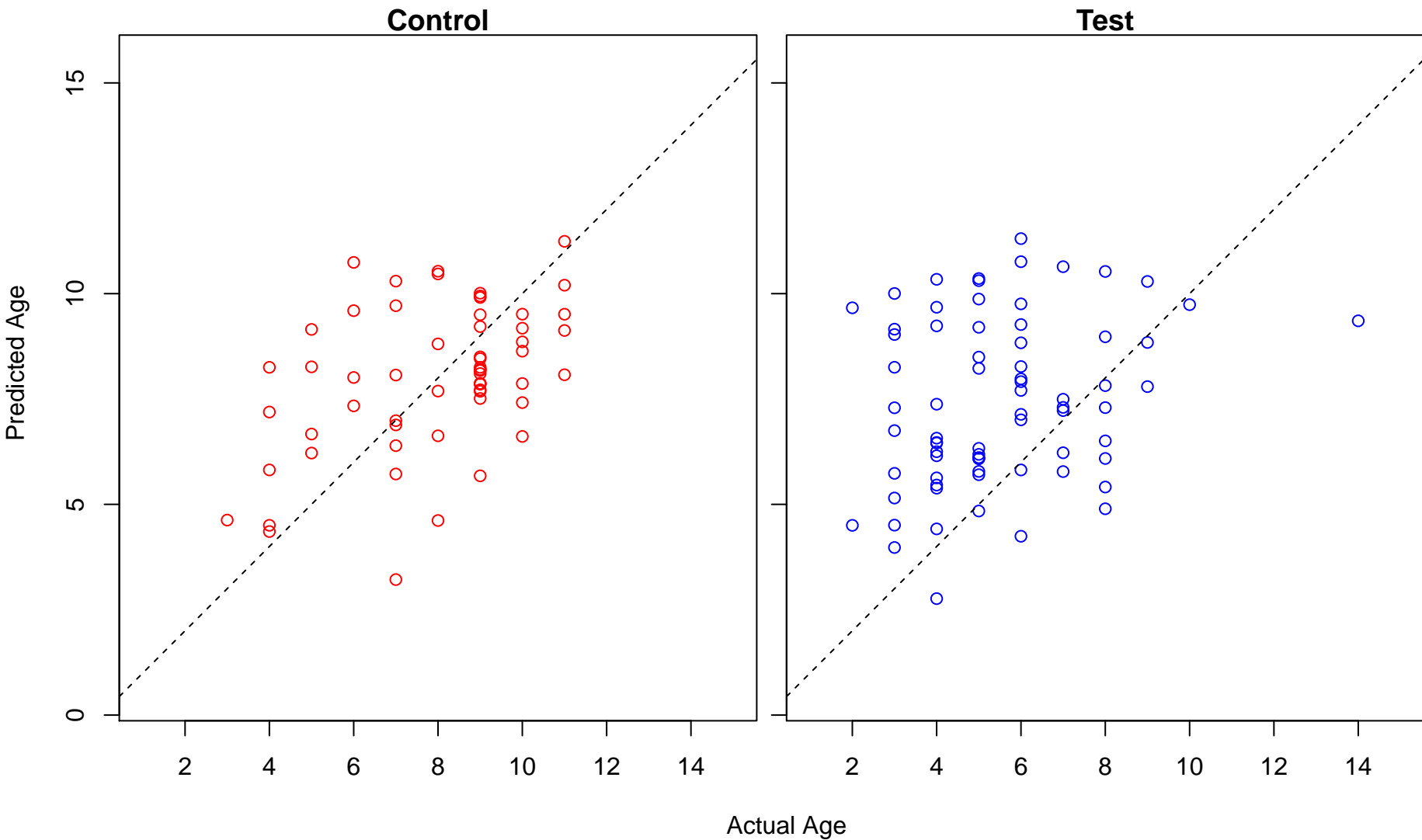
substrate-dependent cerebral cortex tangential migration (Score: 0.991987)



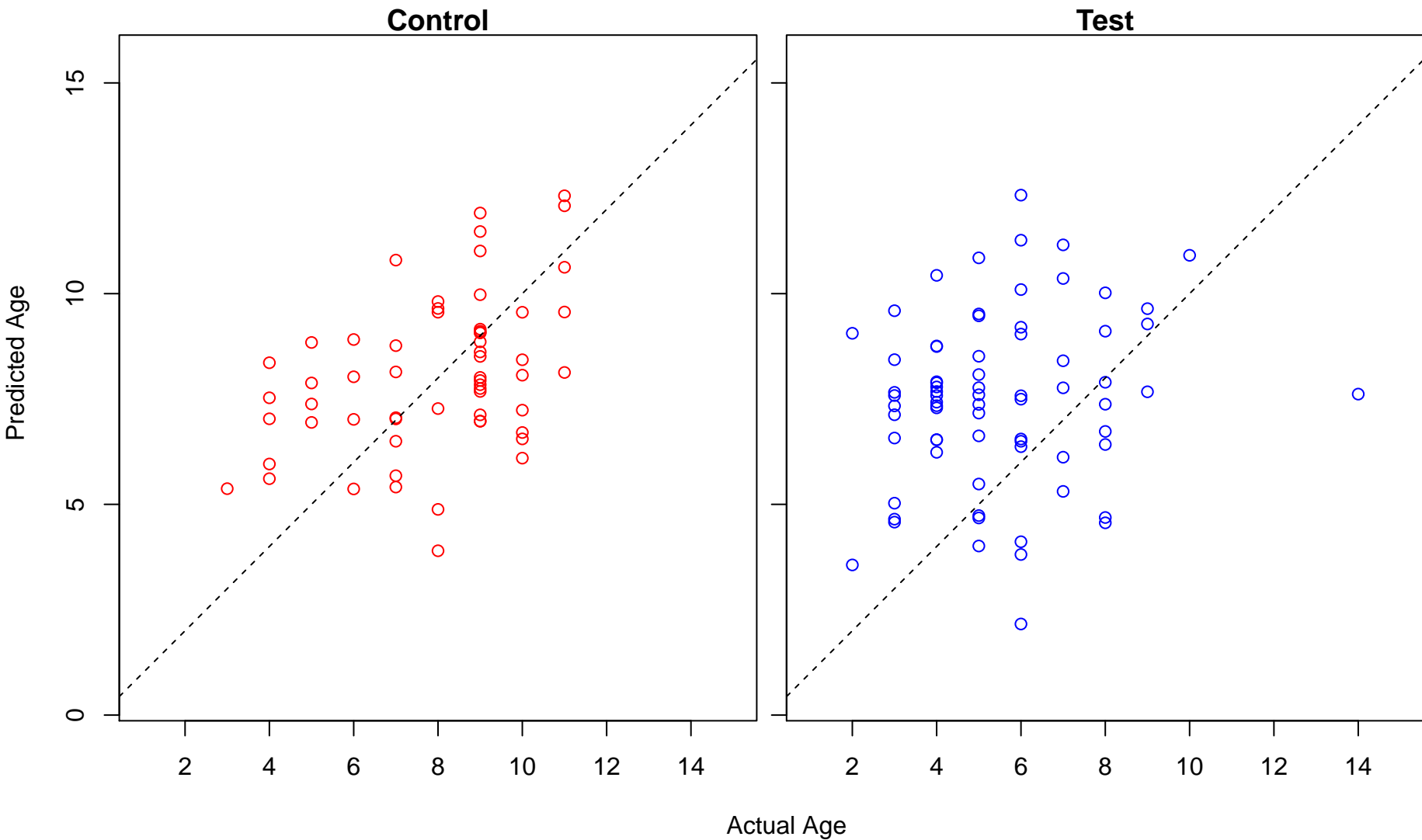
establishment of vesicle localization (Score: 0.991228)



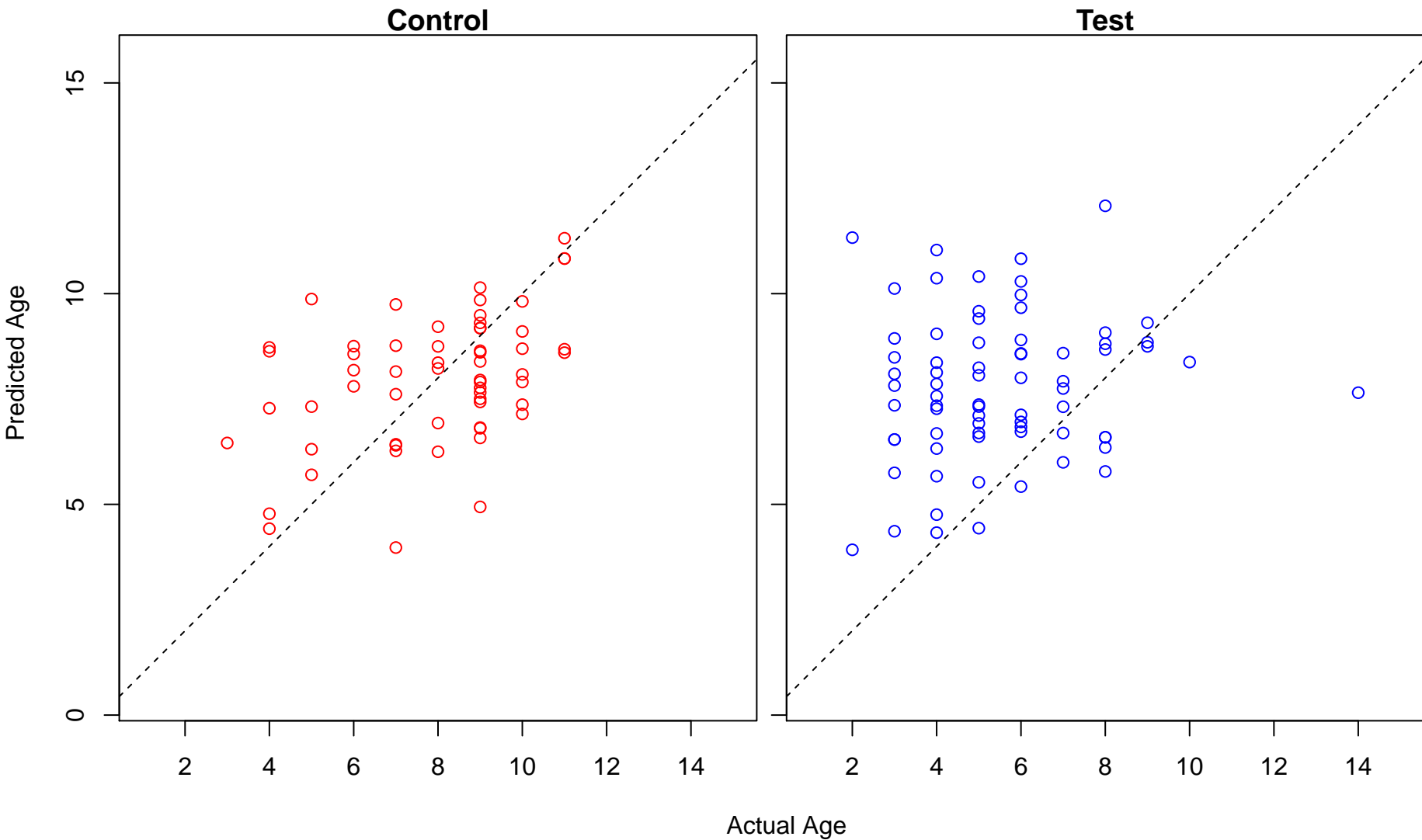
vesicle localization (Score: 0.991080)



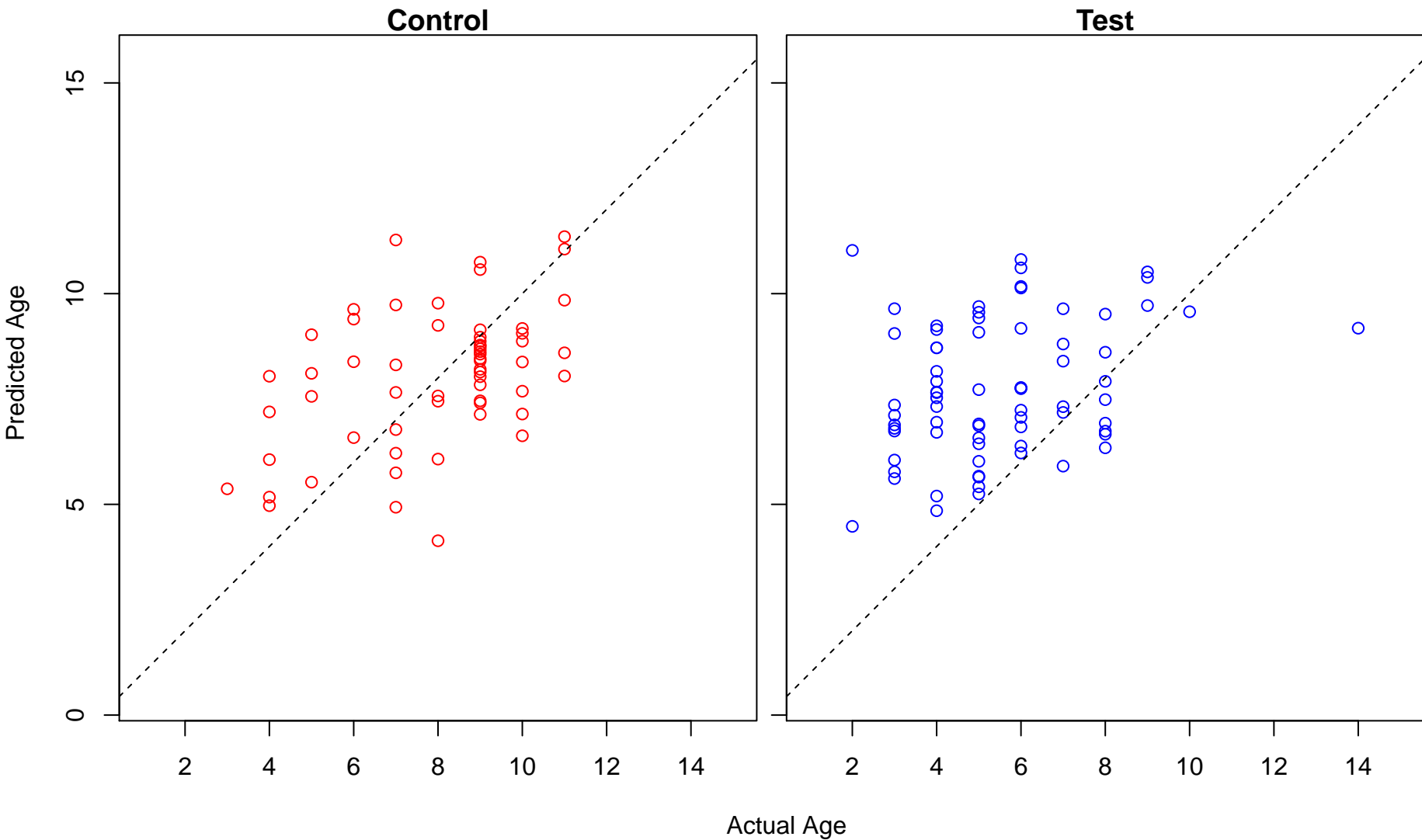
cellular response to UV (Score: 0.989616)



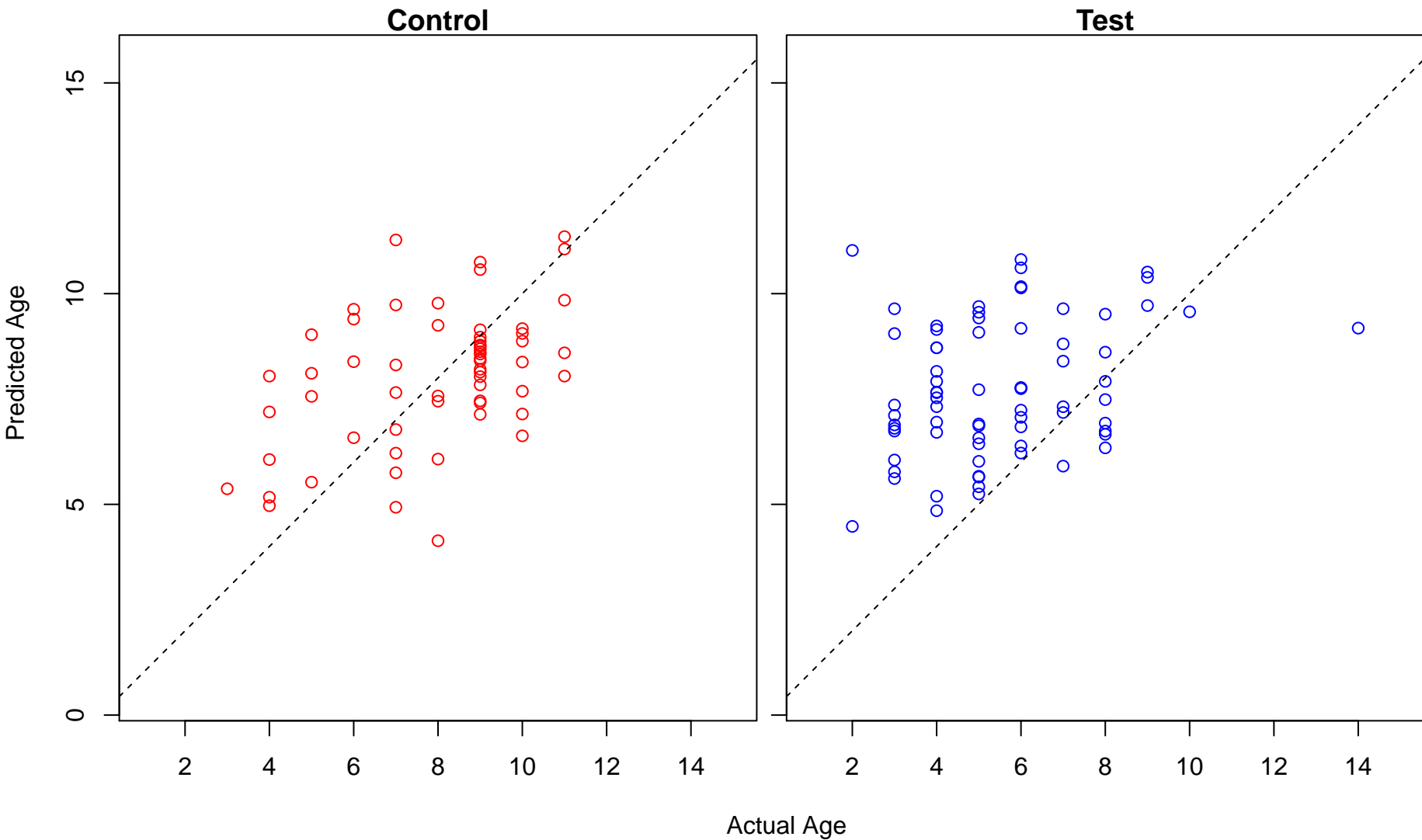
B cell activation (Score: 0.988174)



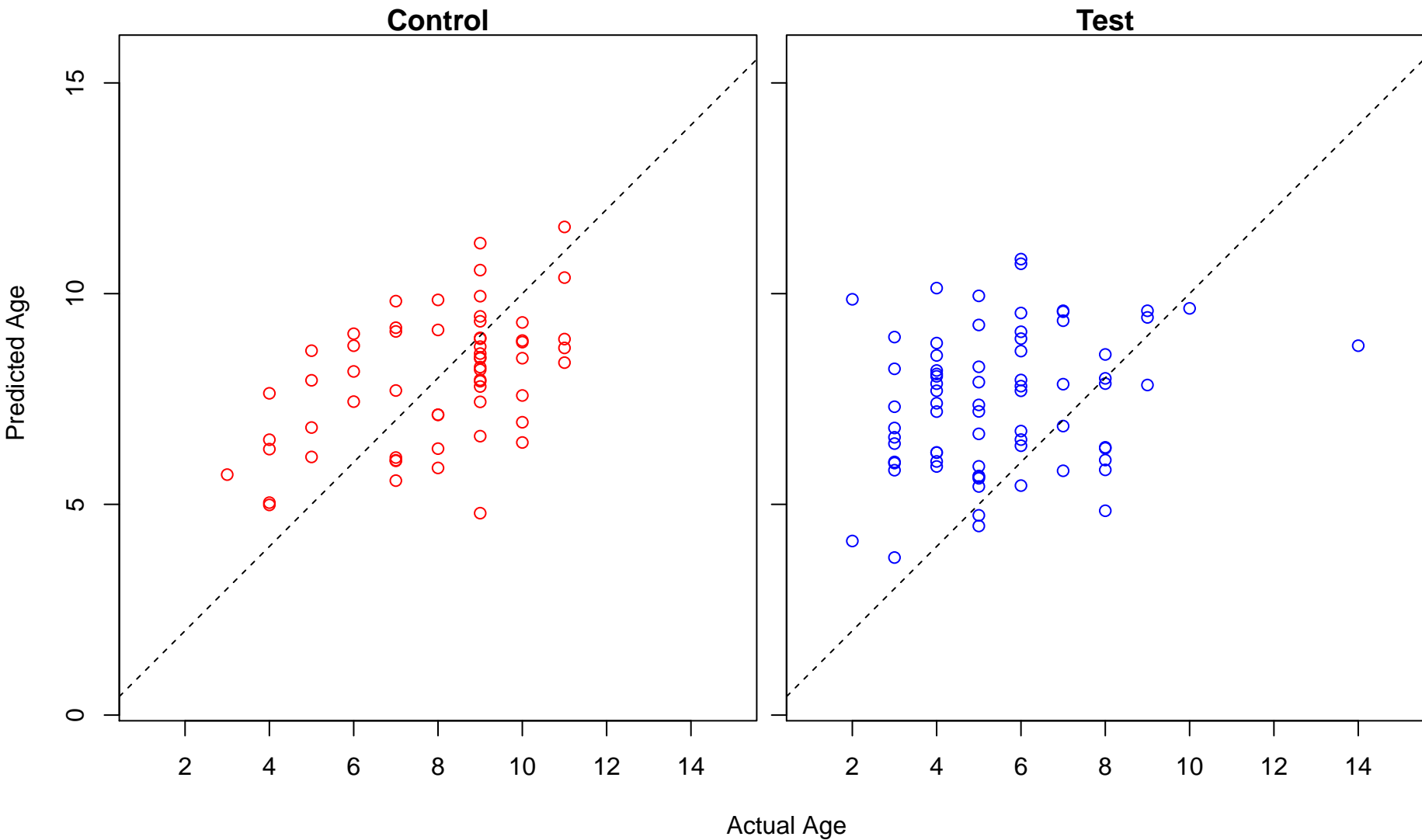
regulation of programmed cell death (Score: 0.987993)



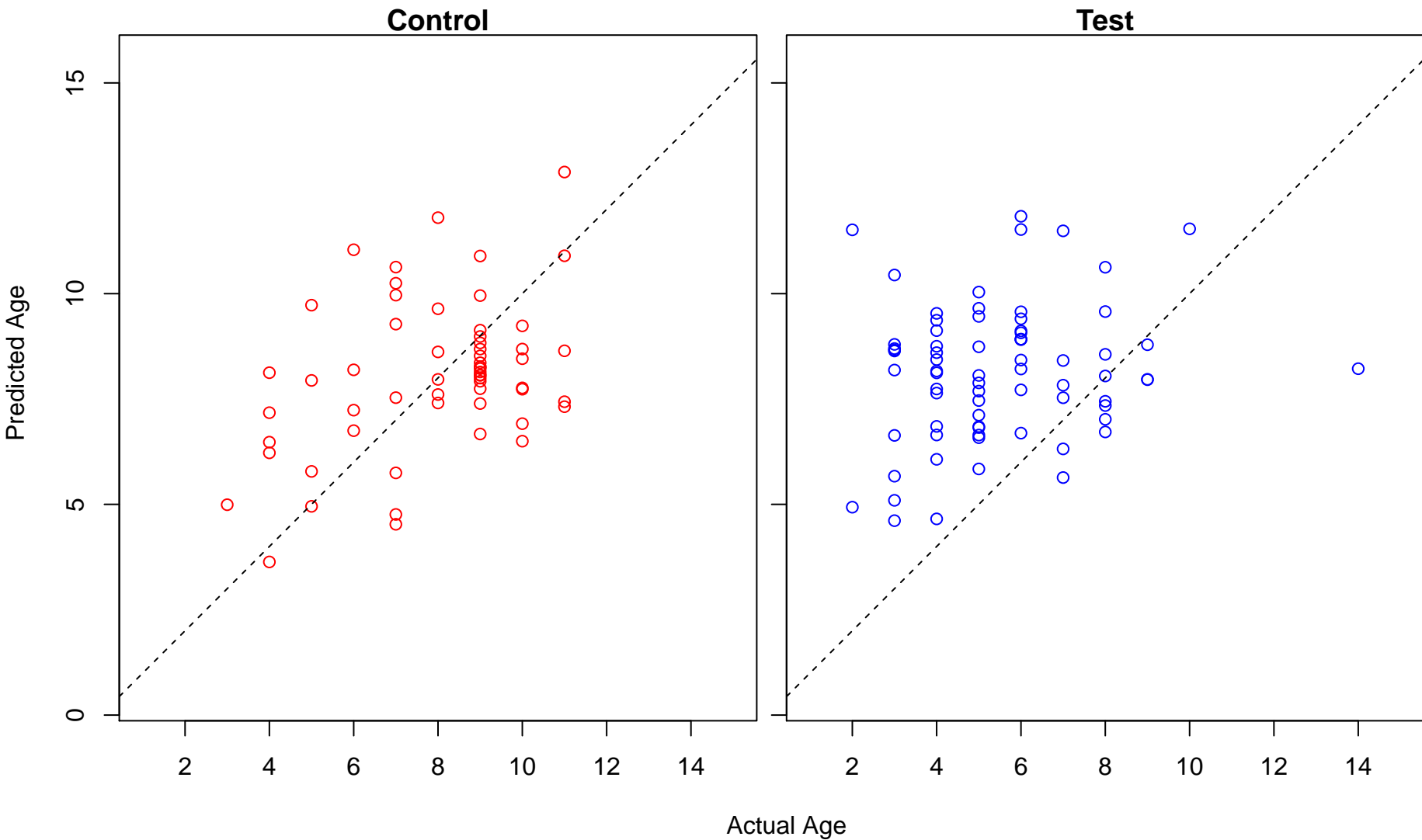
regulation of apoptotic process (Score: 0.987483)



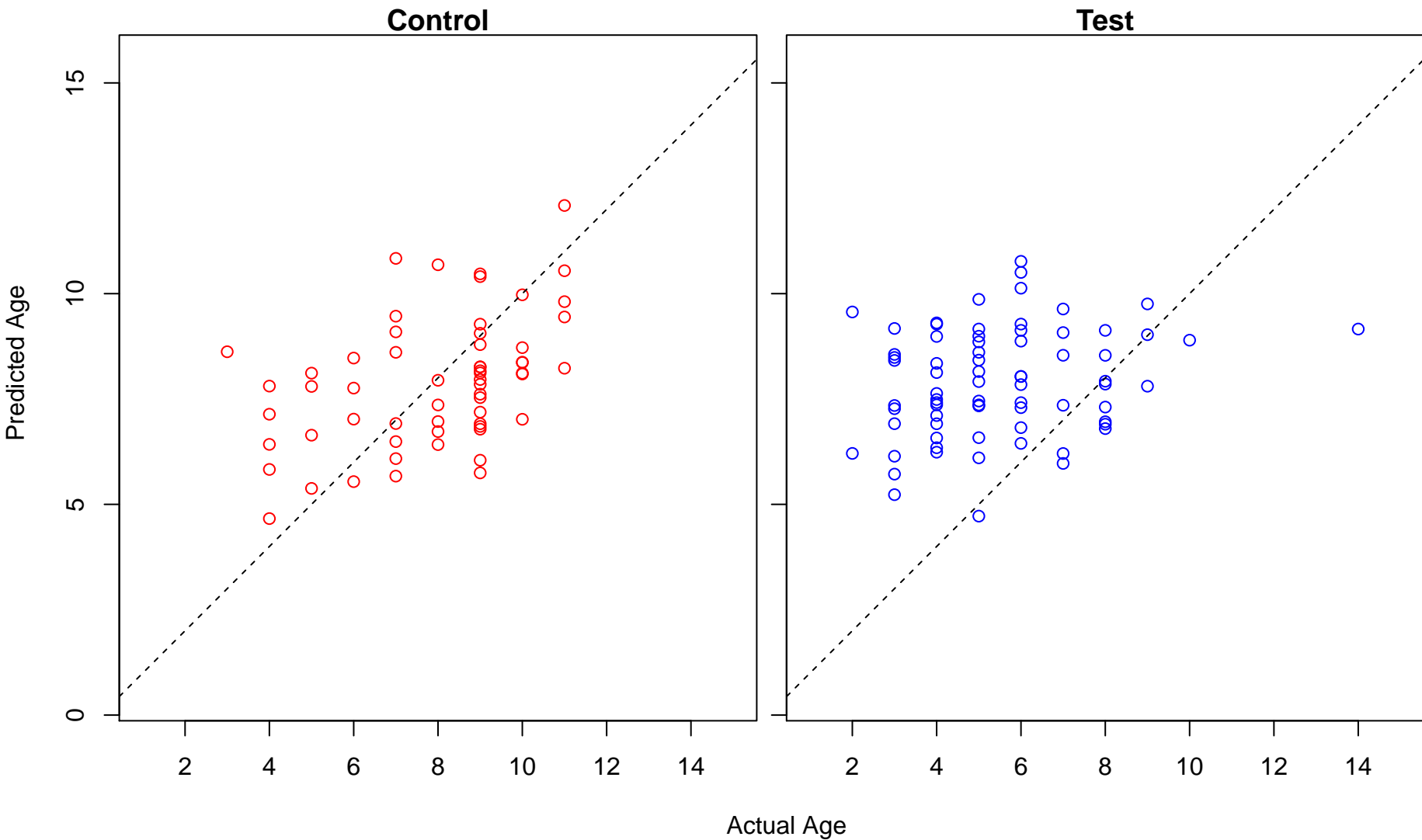
cellular component morphogenesis (Score: 0.987405)



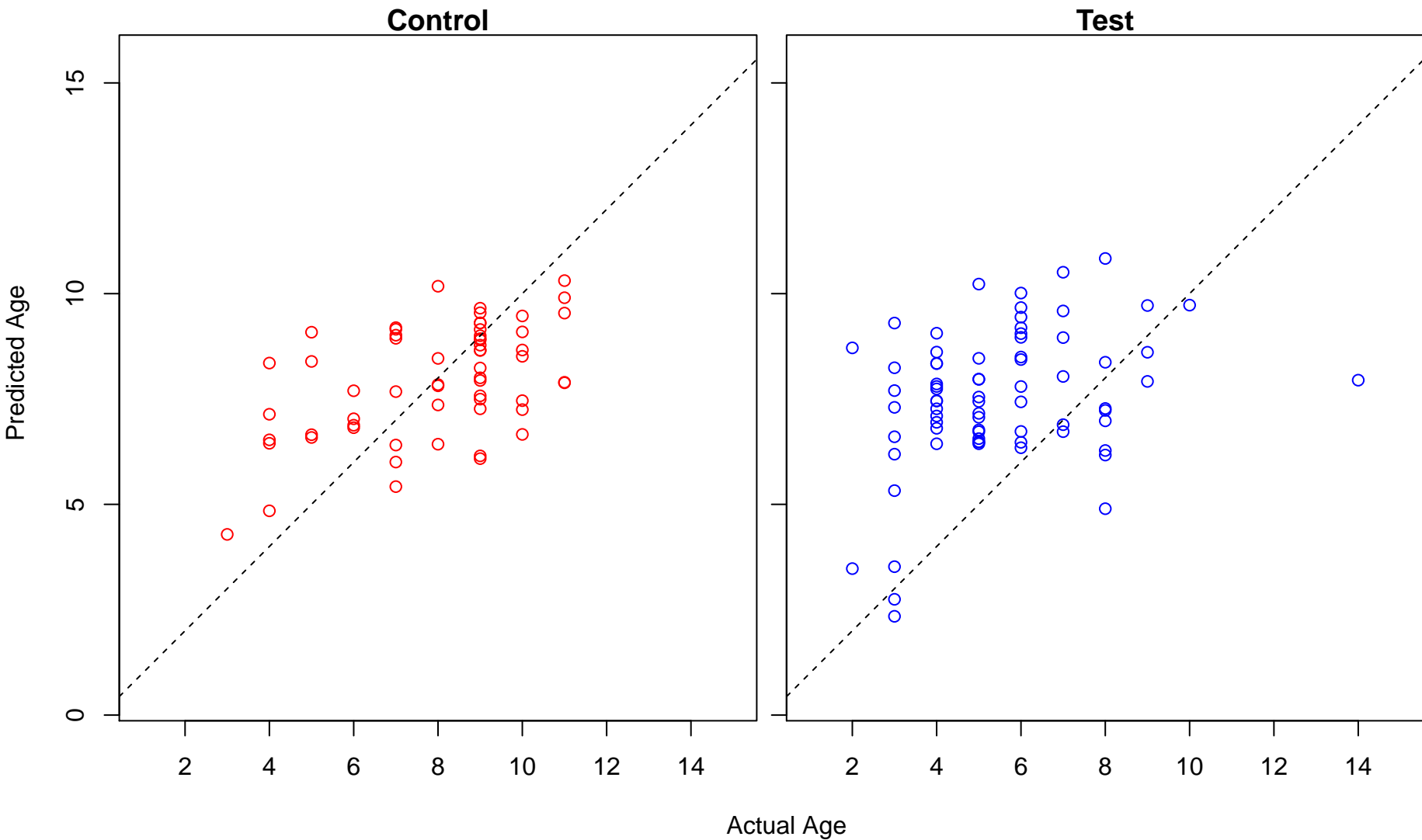
regulation of antigen receptor-mediated signaling pathway (Score: 0.987071)



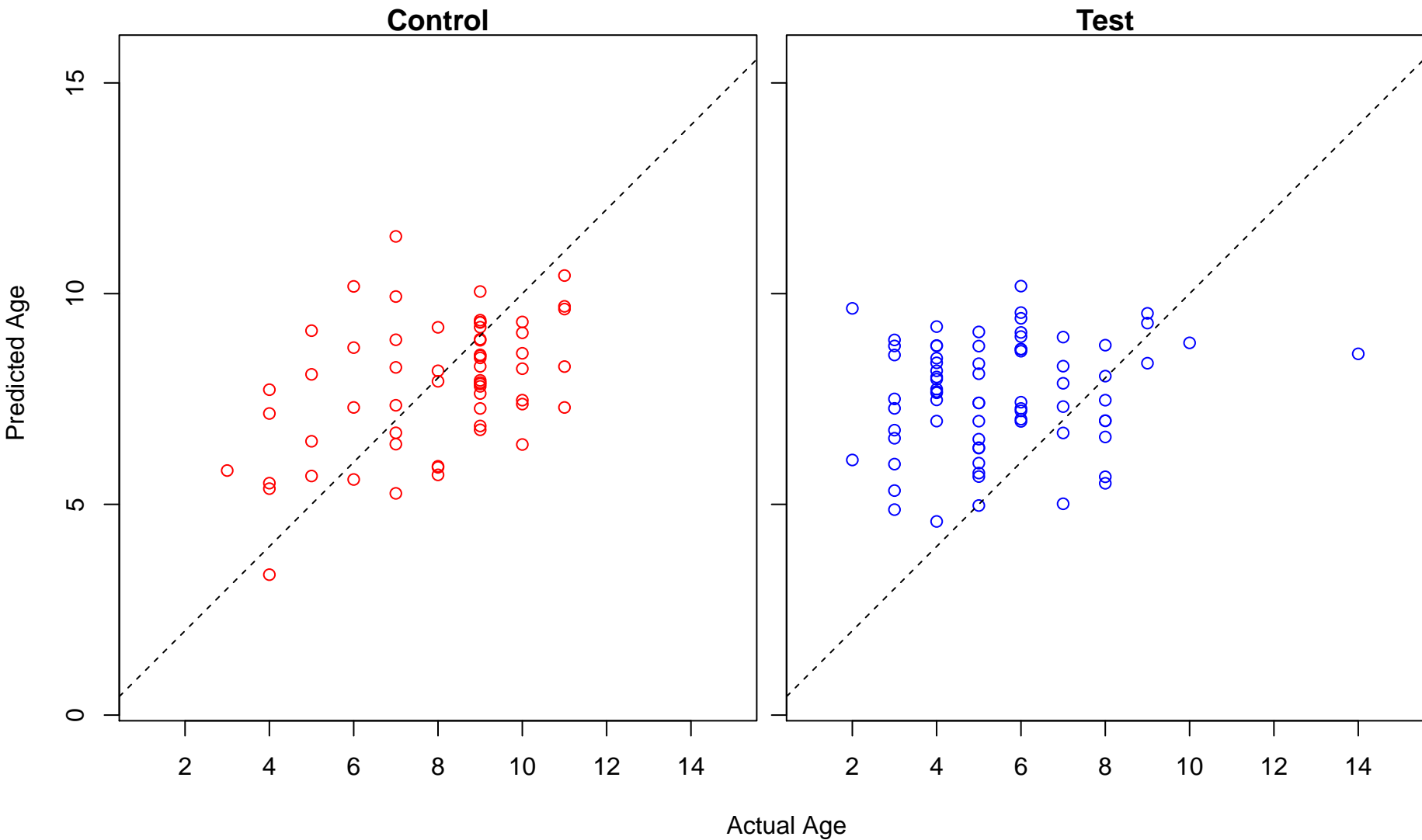
organonitrogen compound metabolic process (Score: 0.986836)



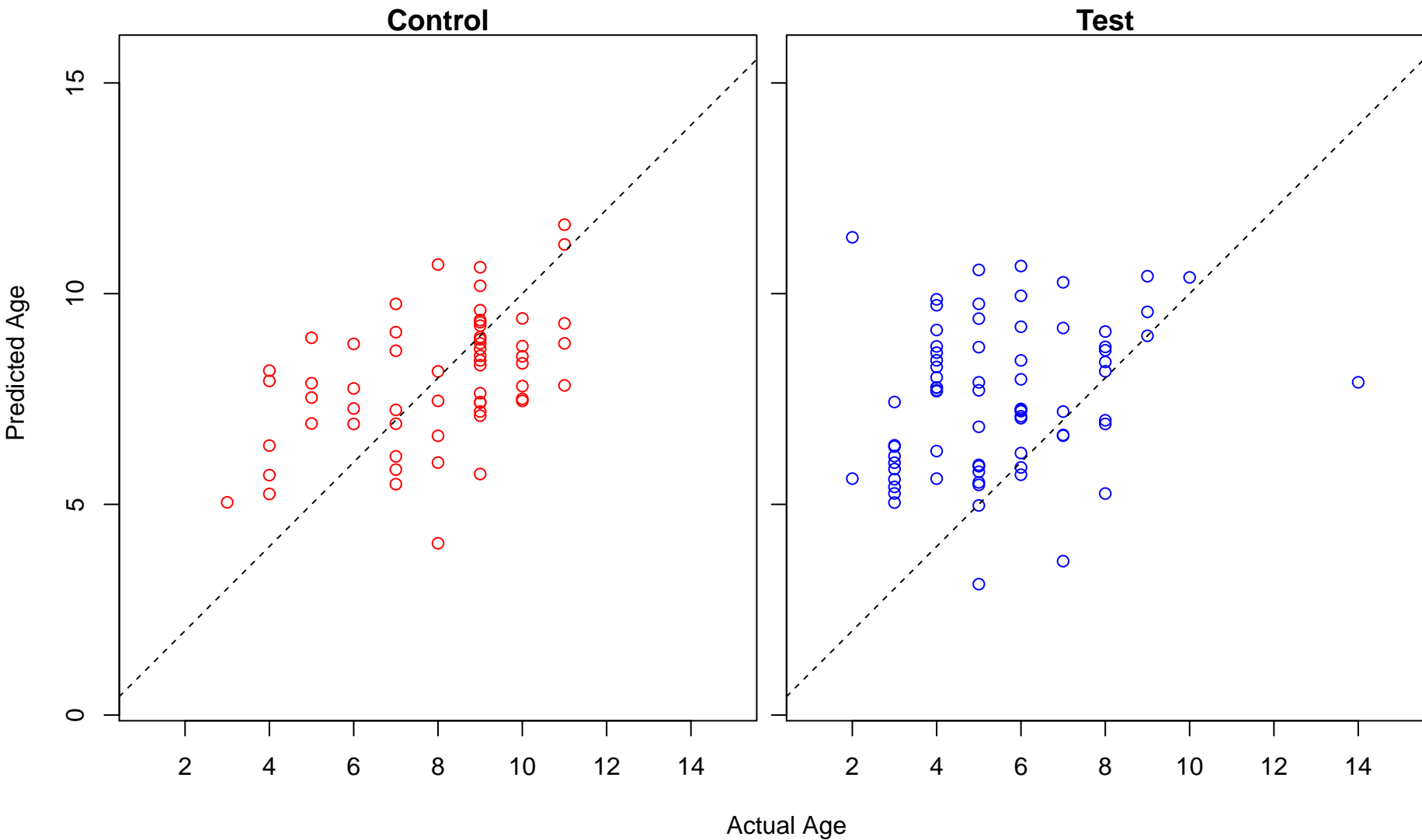
regulation of fibroblast growth factor receptor signaling pathway (Score: 0.986238)



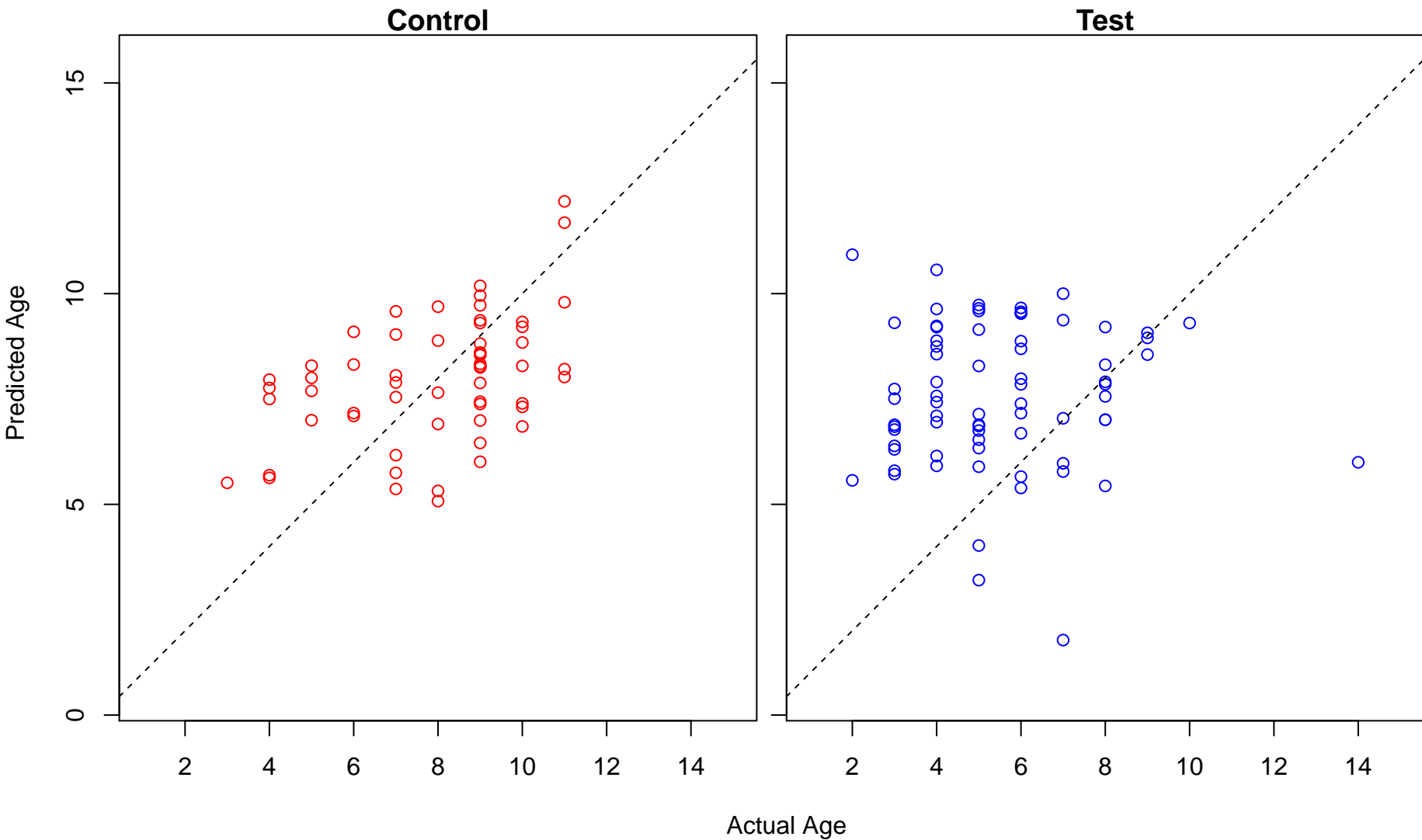
protein modification by small protein conjugation or removal (Score: 0.985591)



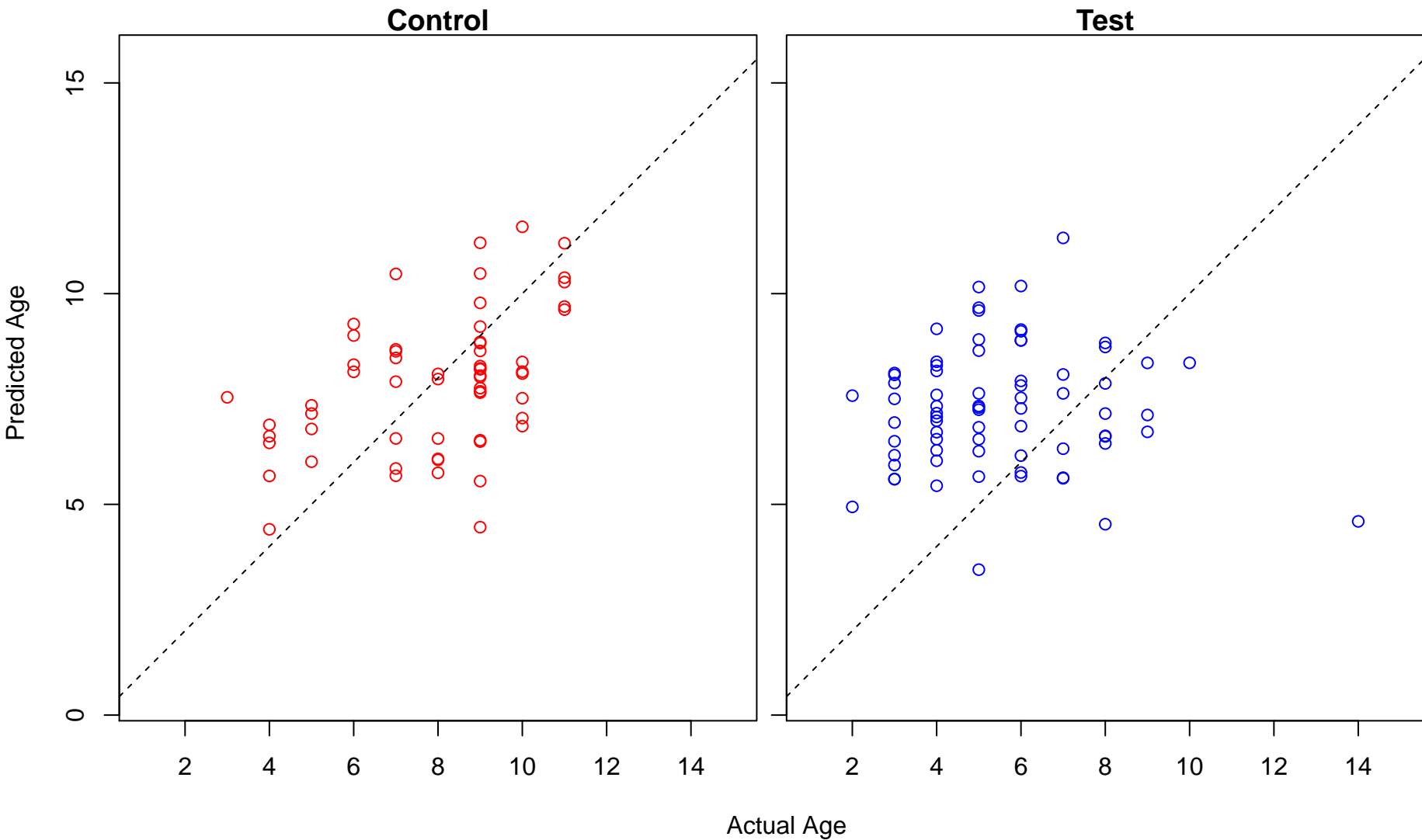
response to stimulus (Score: 0.984488)



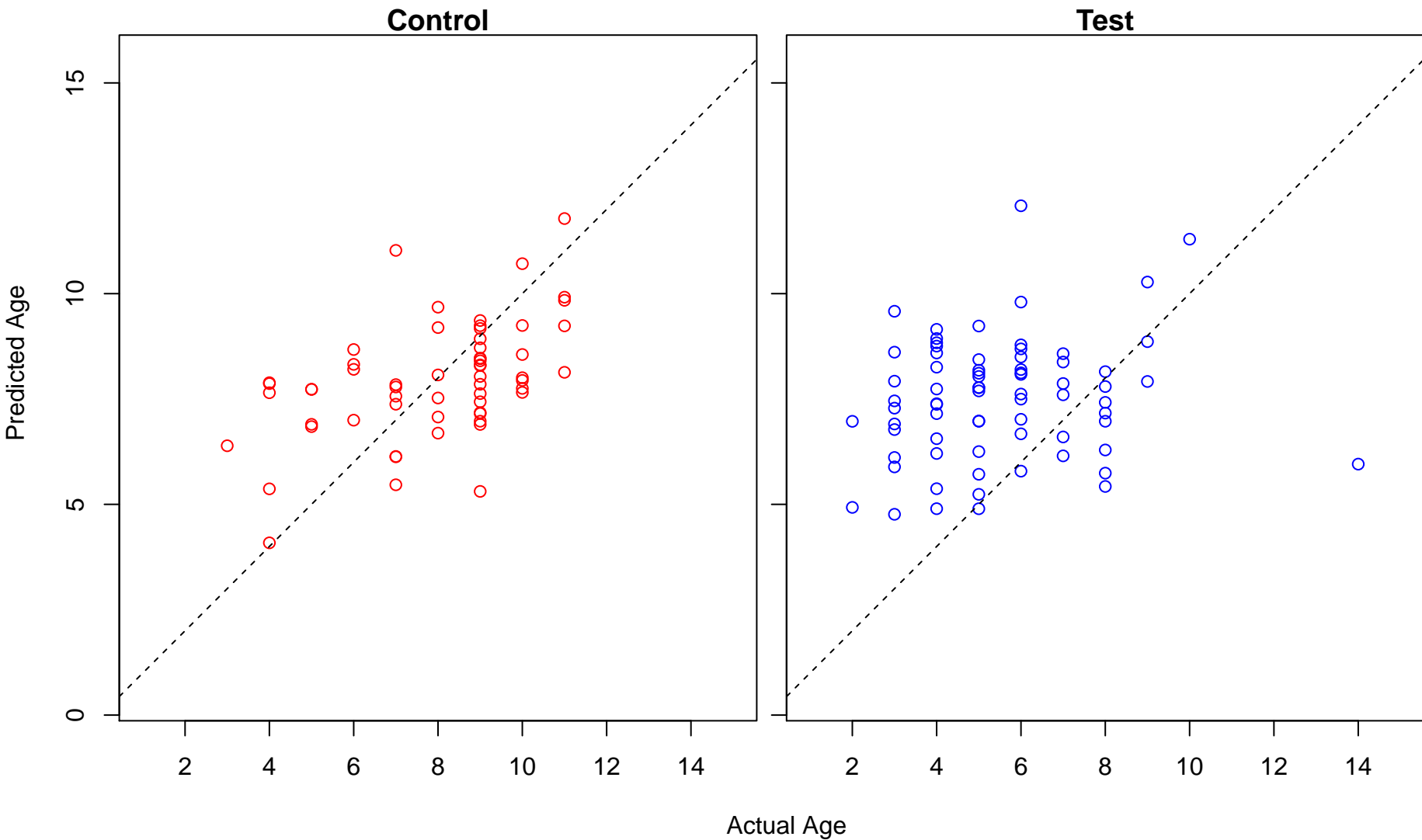
multicellular organismal process (Score: 0.983795)



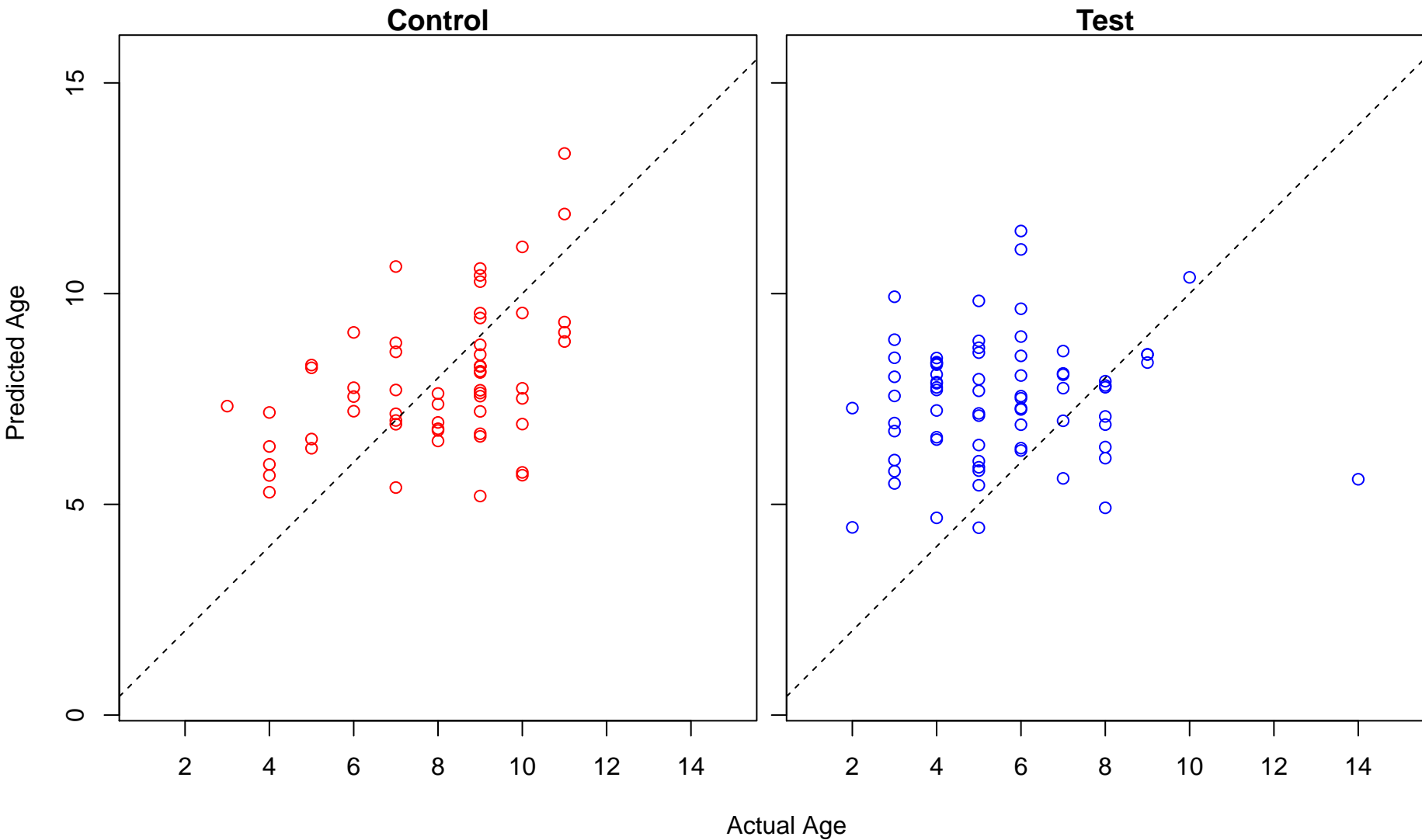
negative regulation of autophagy (Score: 0.983671)



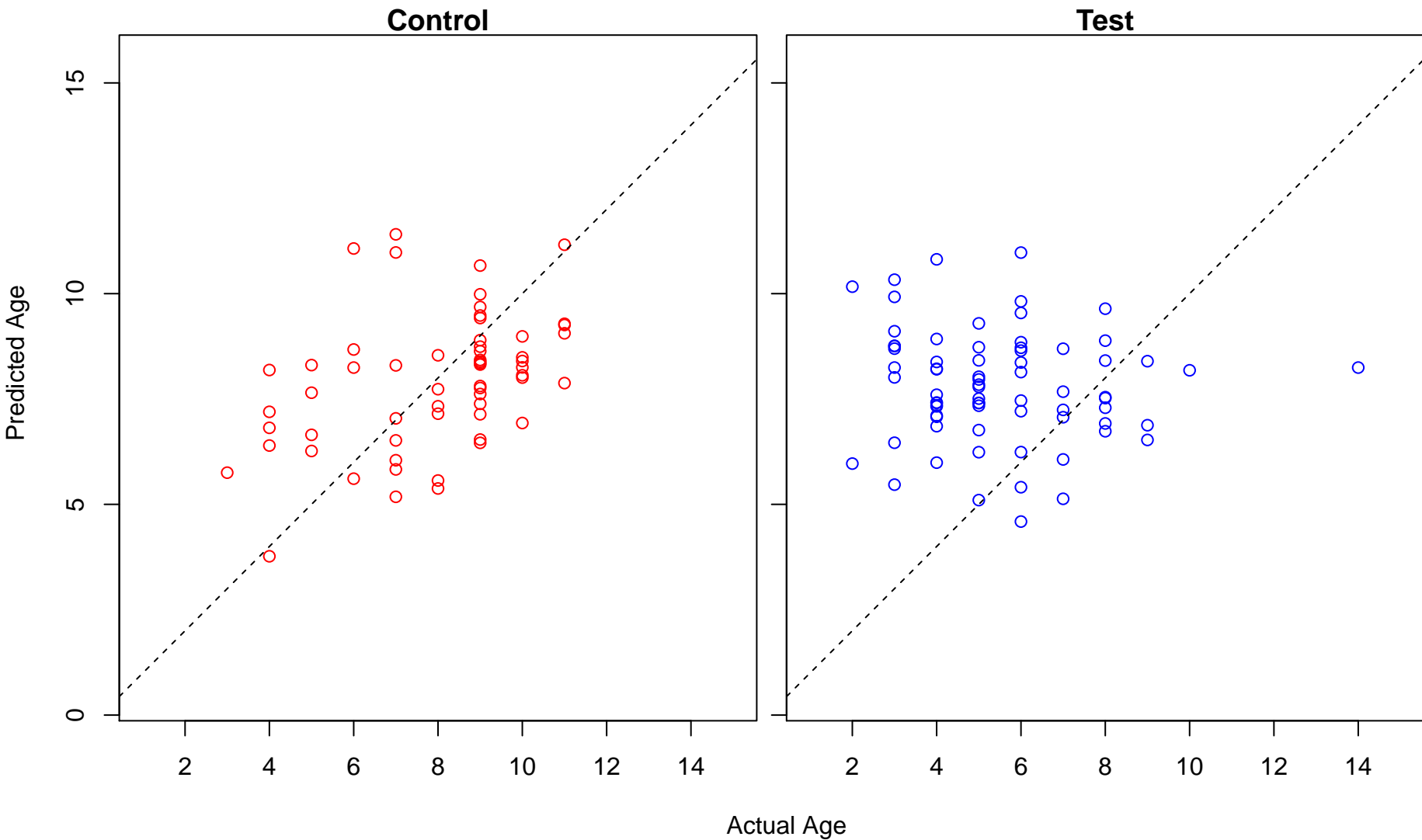
positive regulation of T-helper cell differentiation (Score: 0.983510)



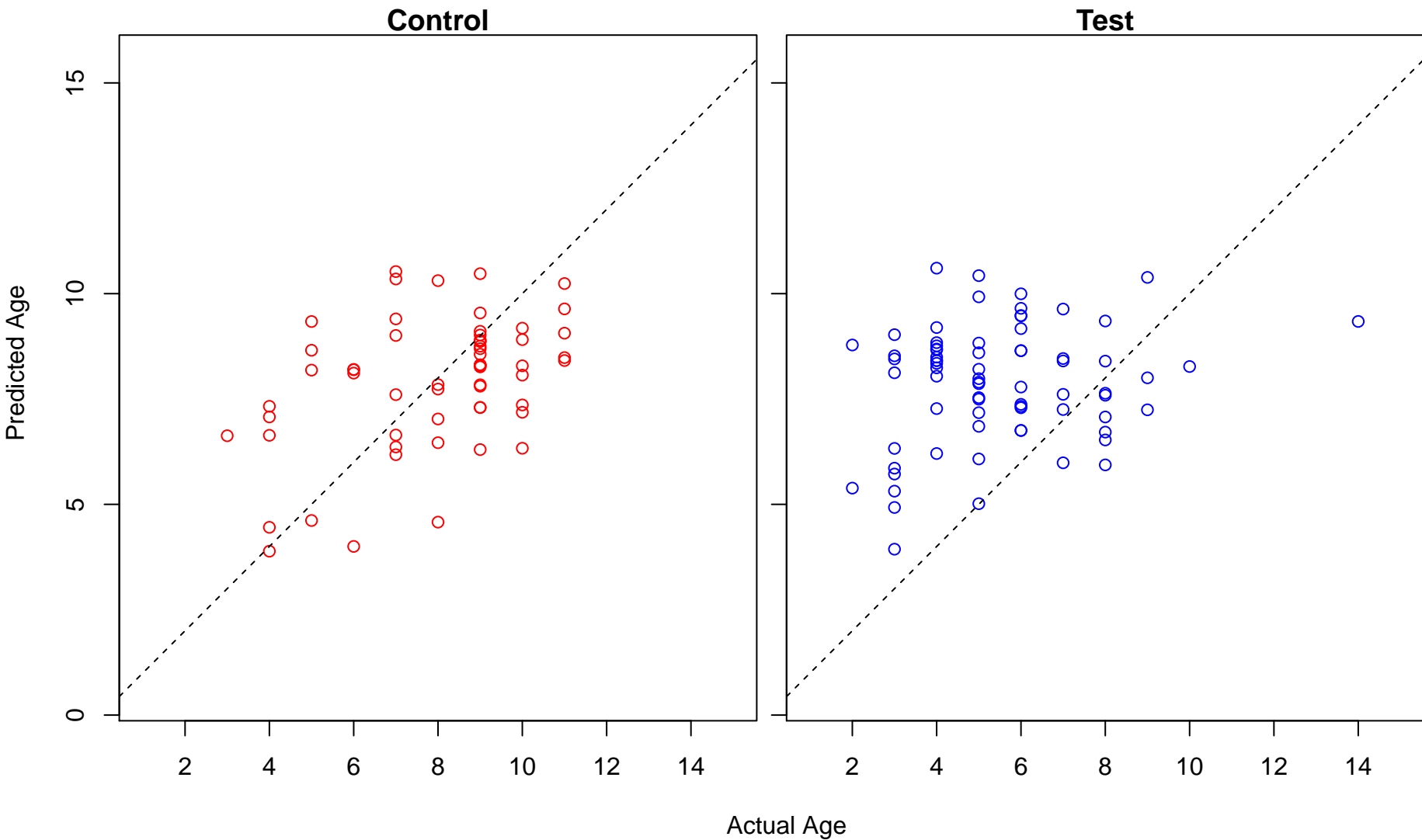
anatomical structure regression (Score: 0.980247)



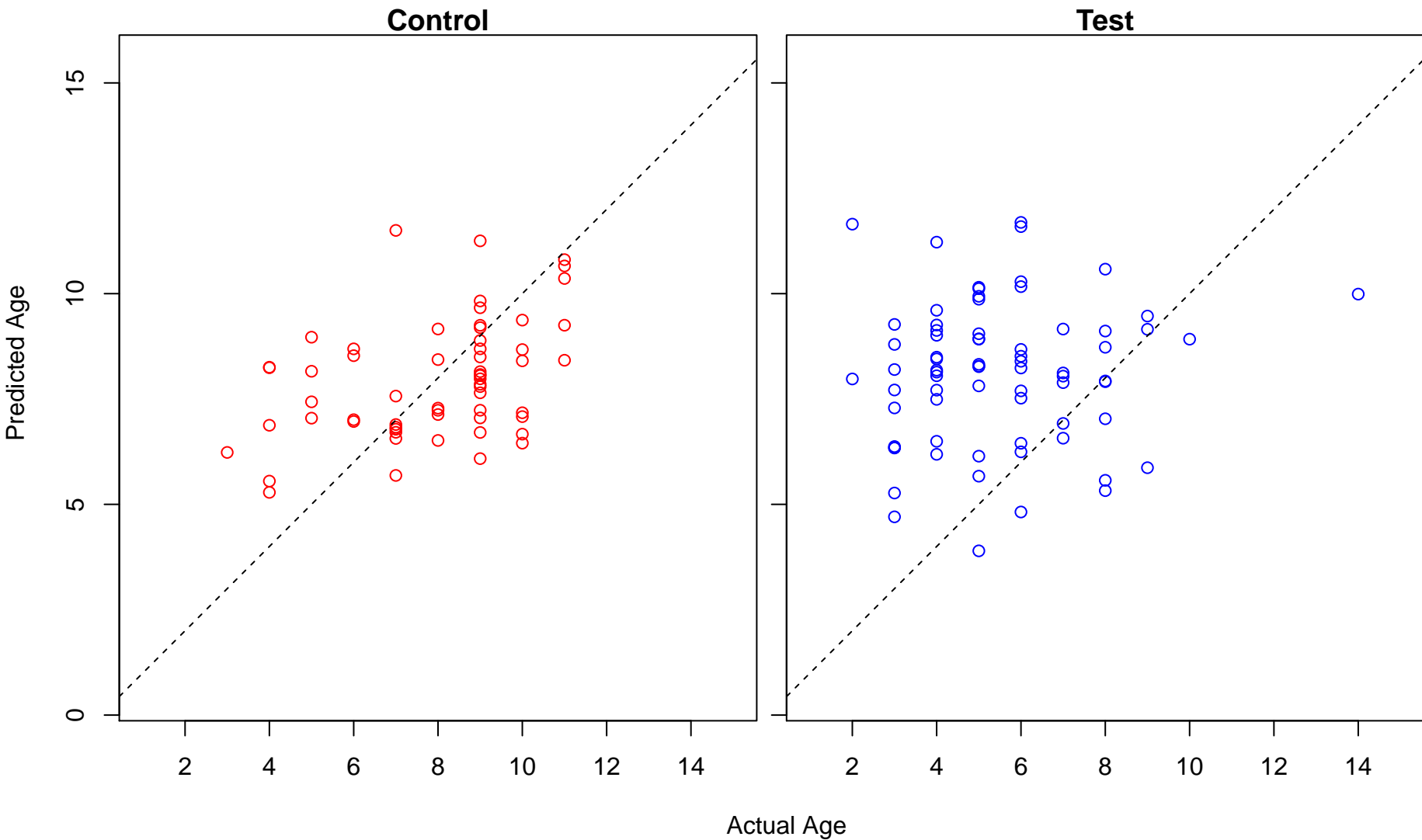
positive regulation of intracellular protein transport (Score: 0.980138)



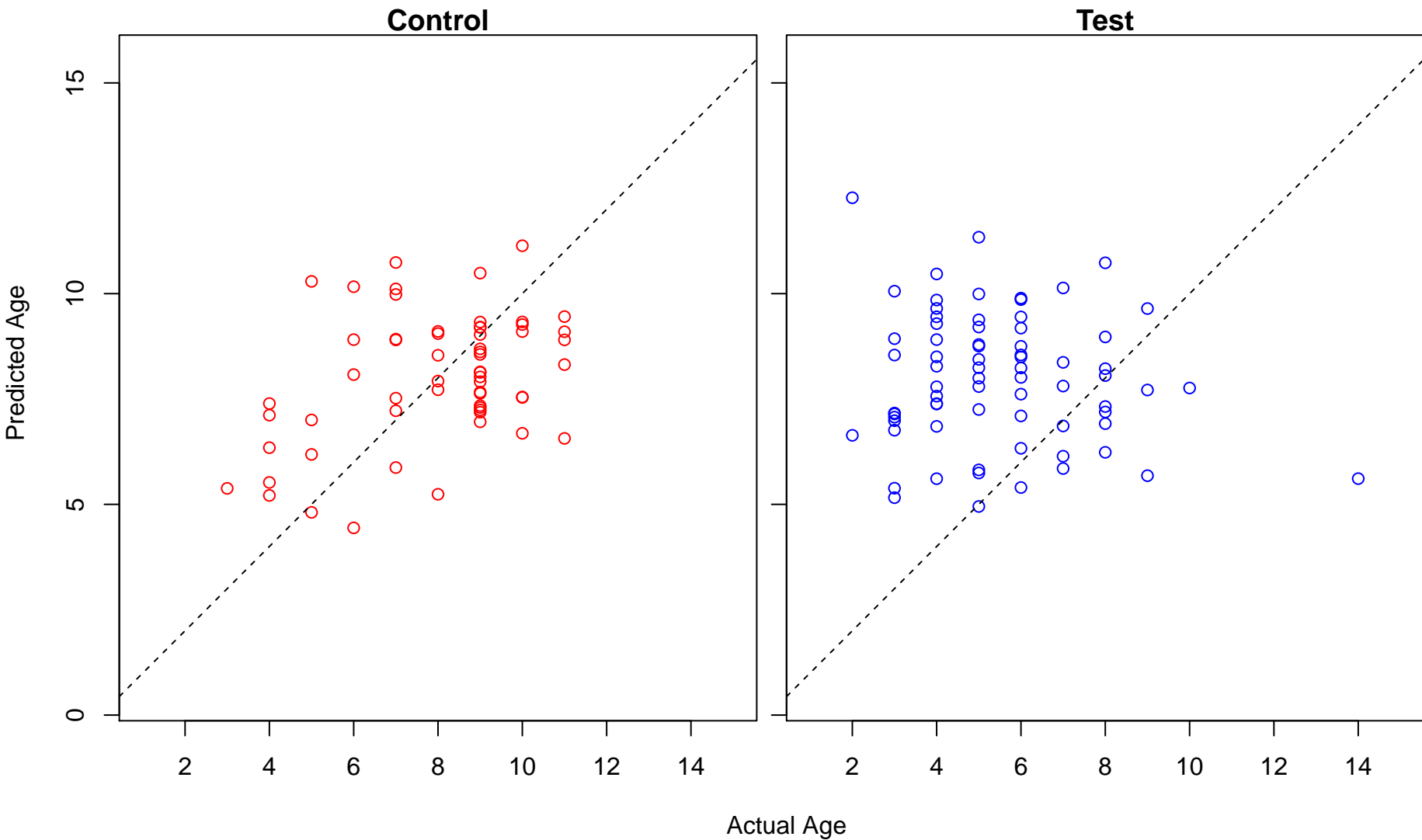
cell recognition (Score: 0.979899)



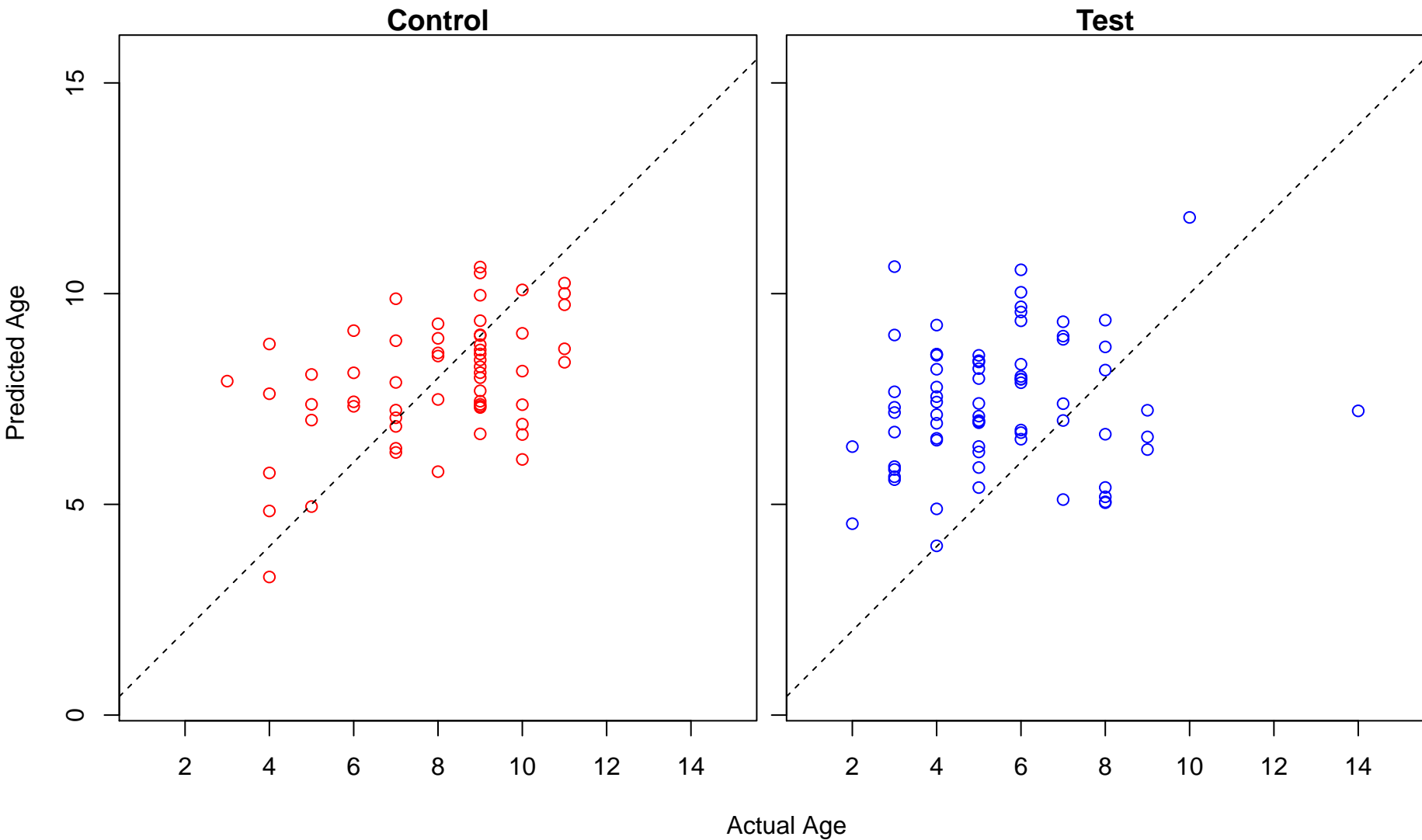
chorion development (Score: 0.978531)



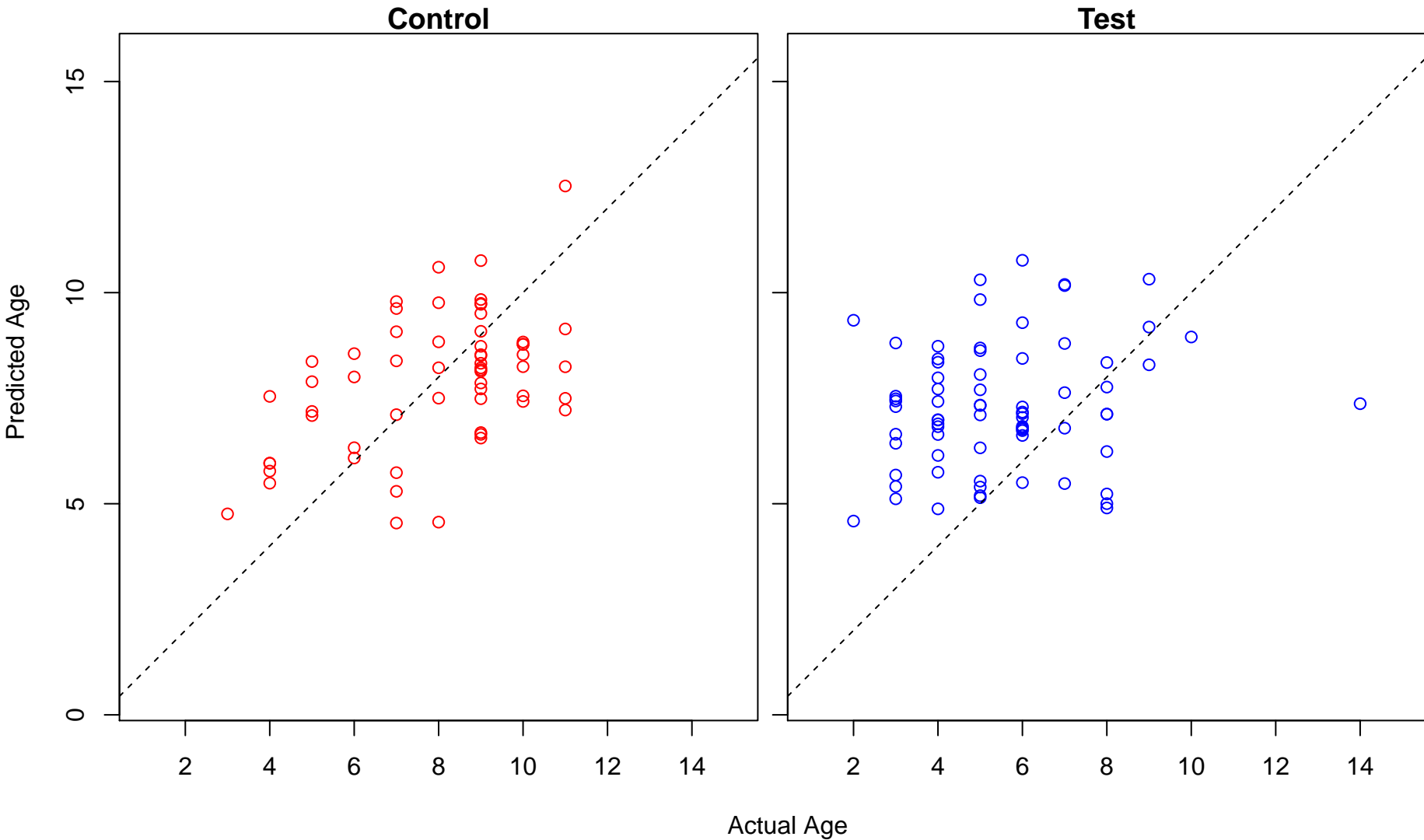
regulation of protein acetylation (Score: 0.977012)



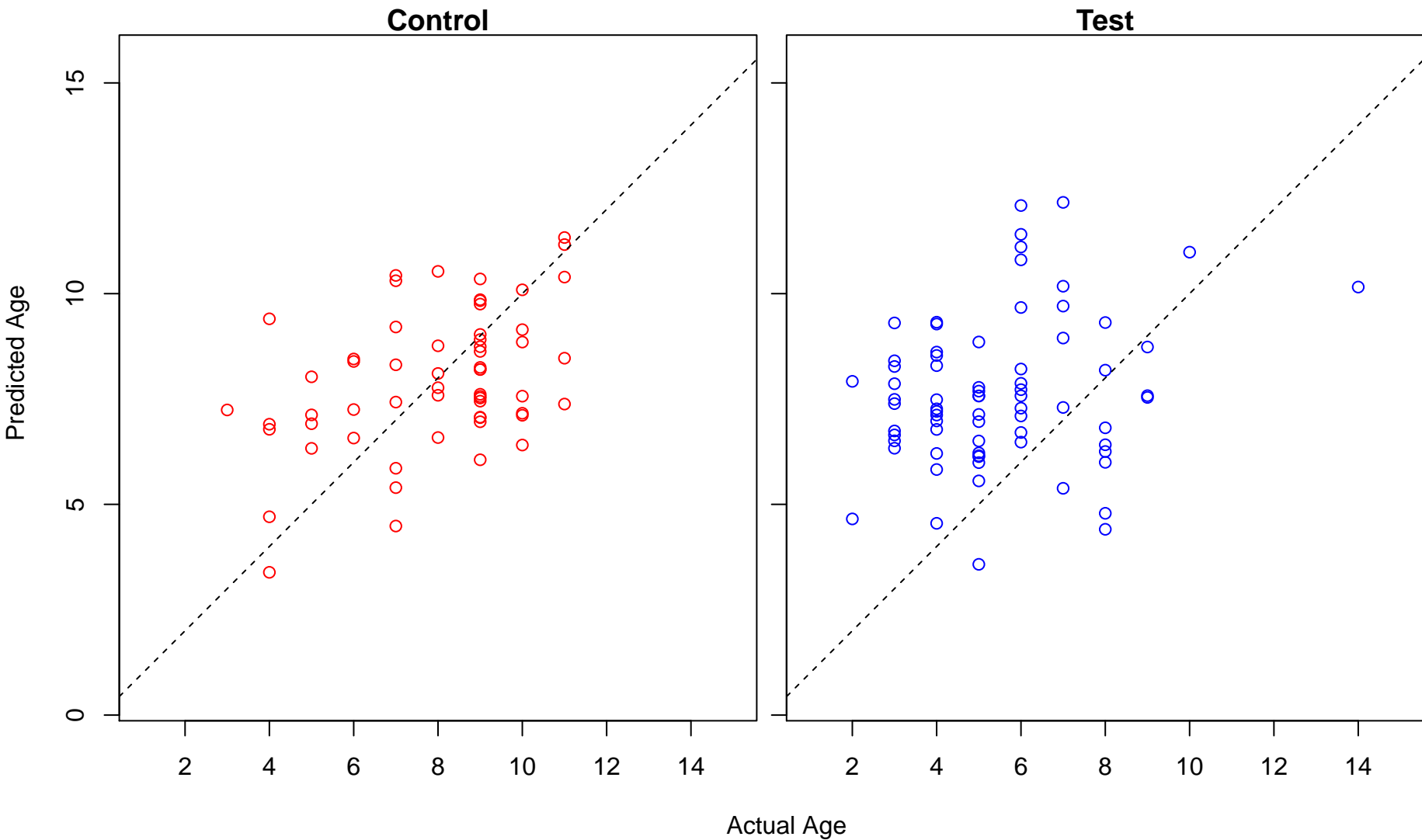
columnar/cuboidal epithelial cell development (Score: 0.976008)



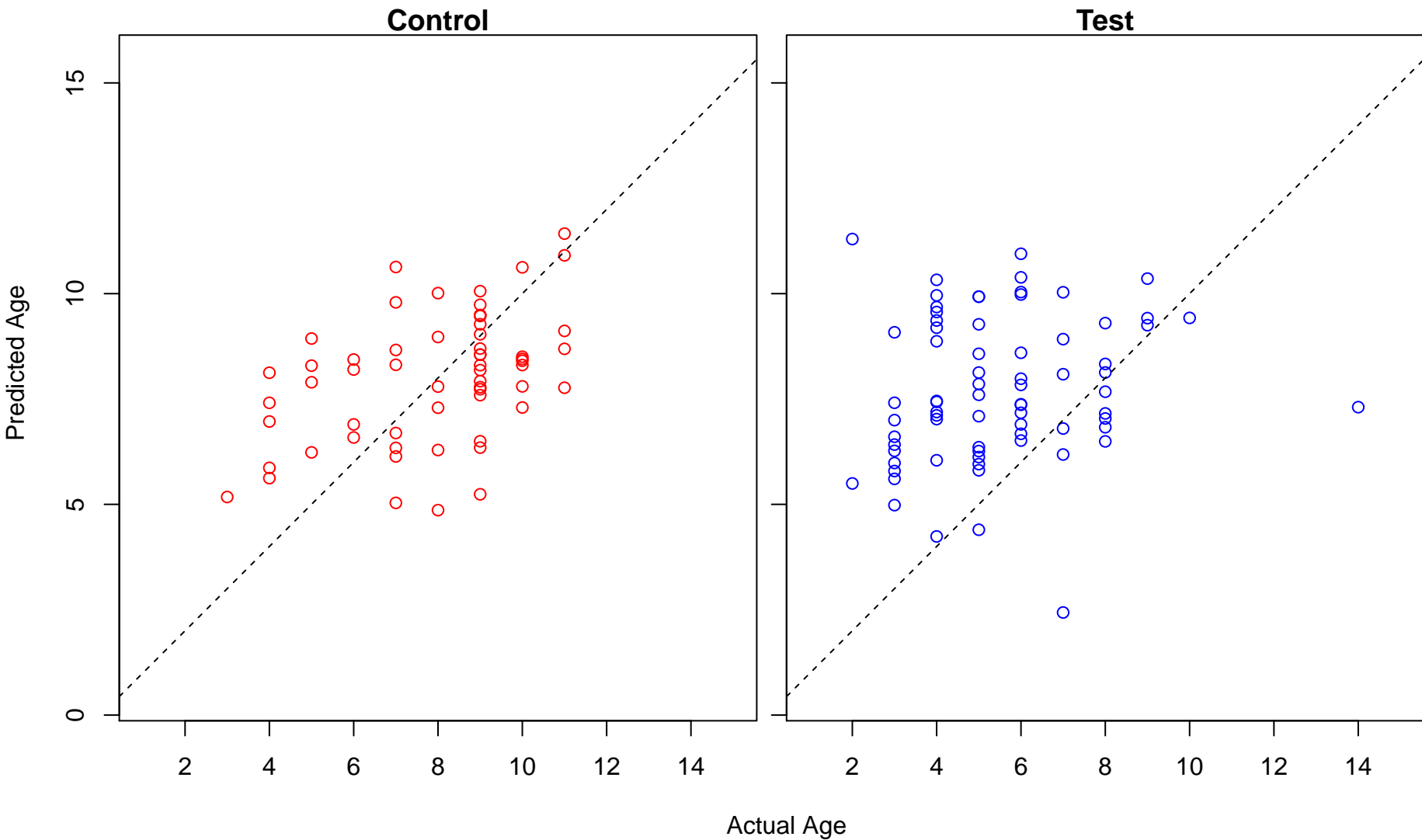
negative regulation of phosphatase activity (Score: 0.975650)



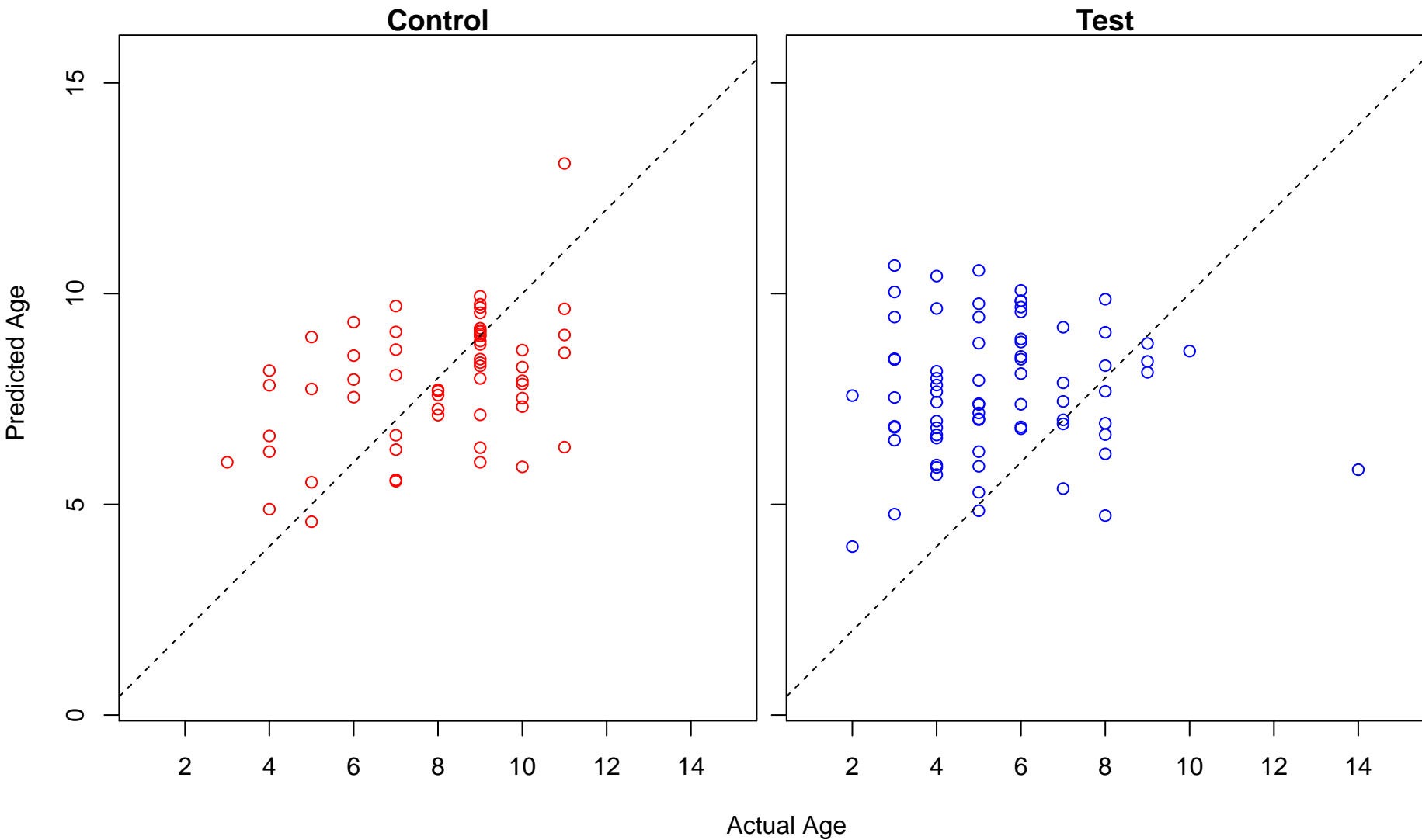
inner ear development (Score: 0.975437)



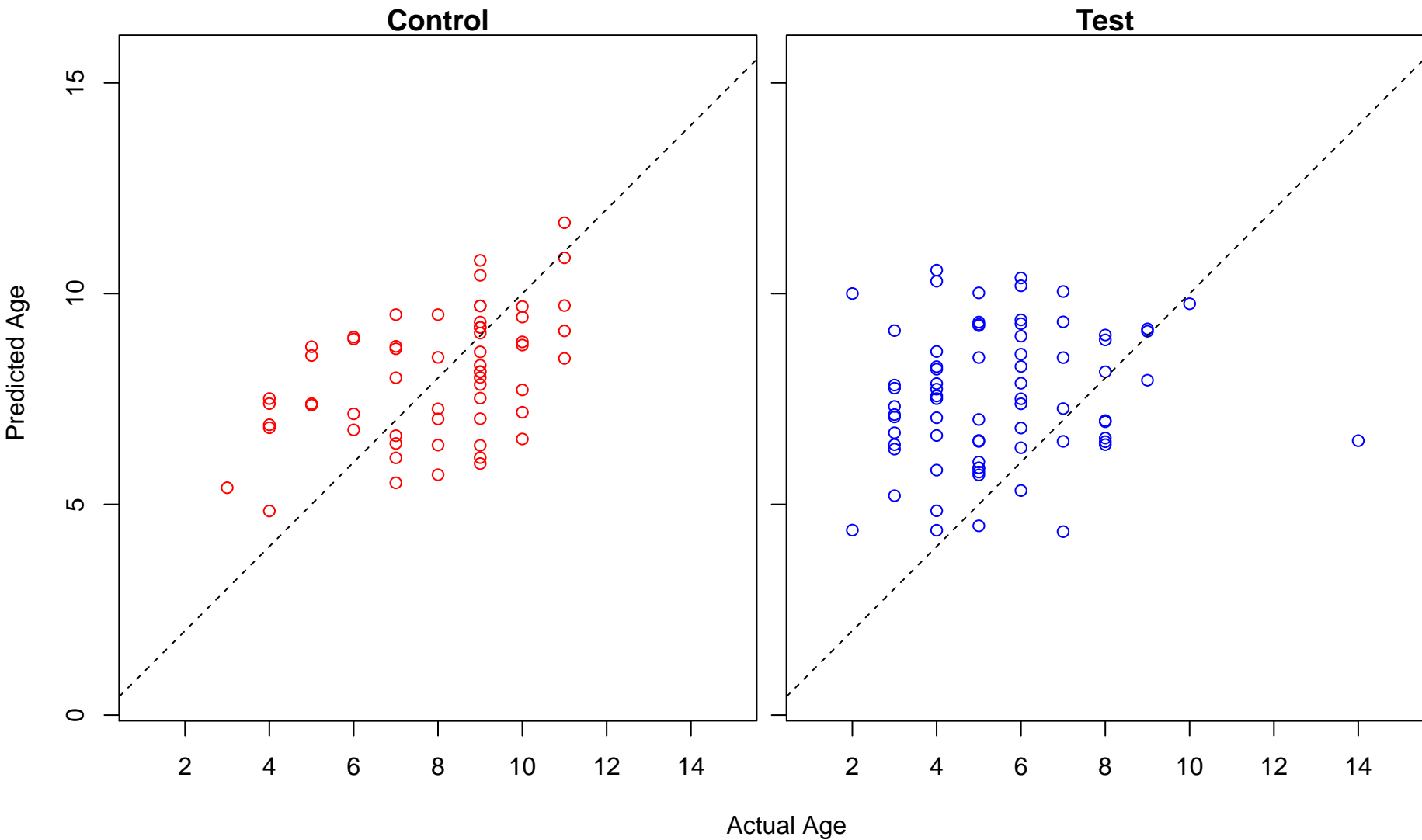
positive regulation of cellular process (Score: 0.974080)



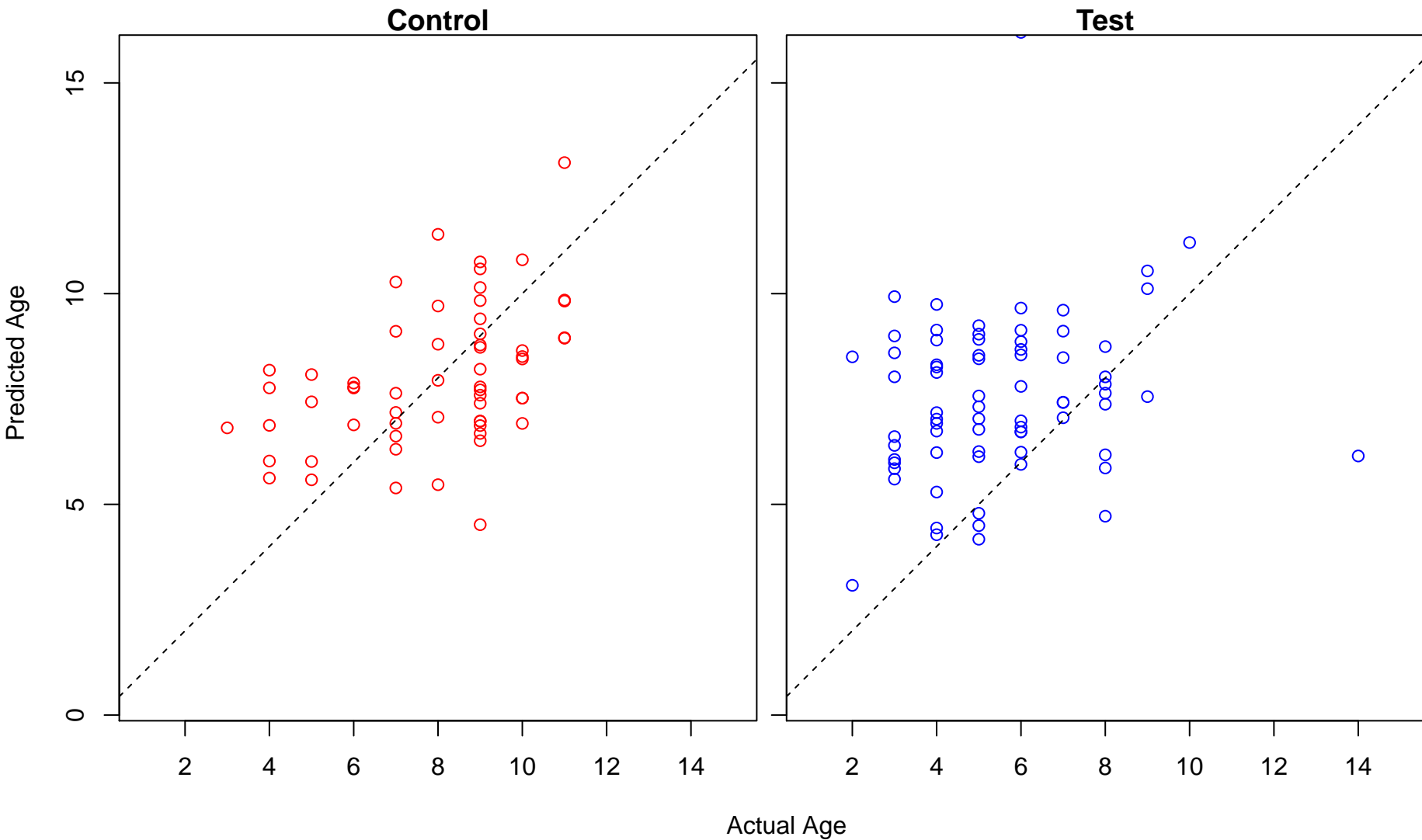
aminoglycan catabolic process (Score: 0.973900)



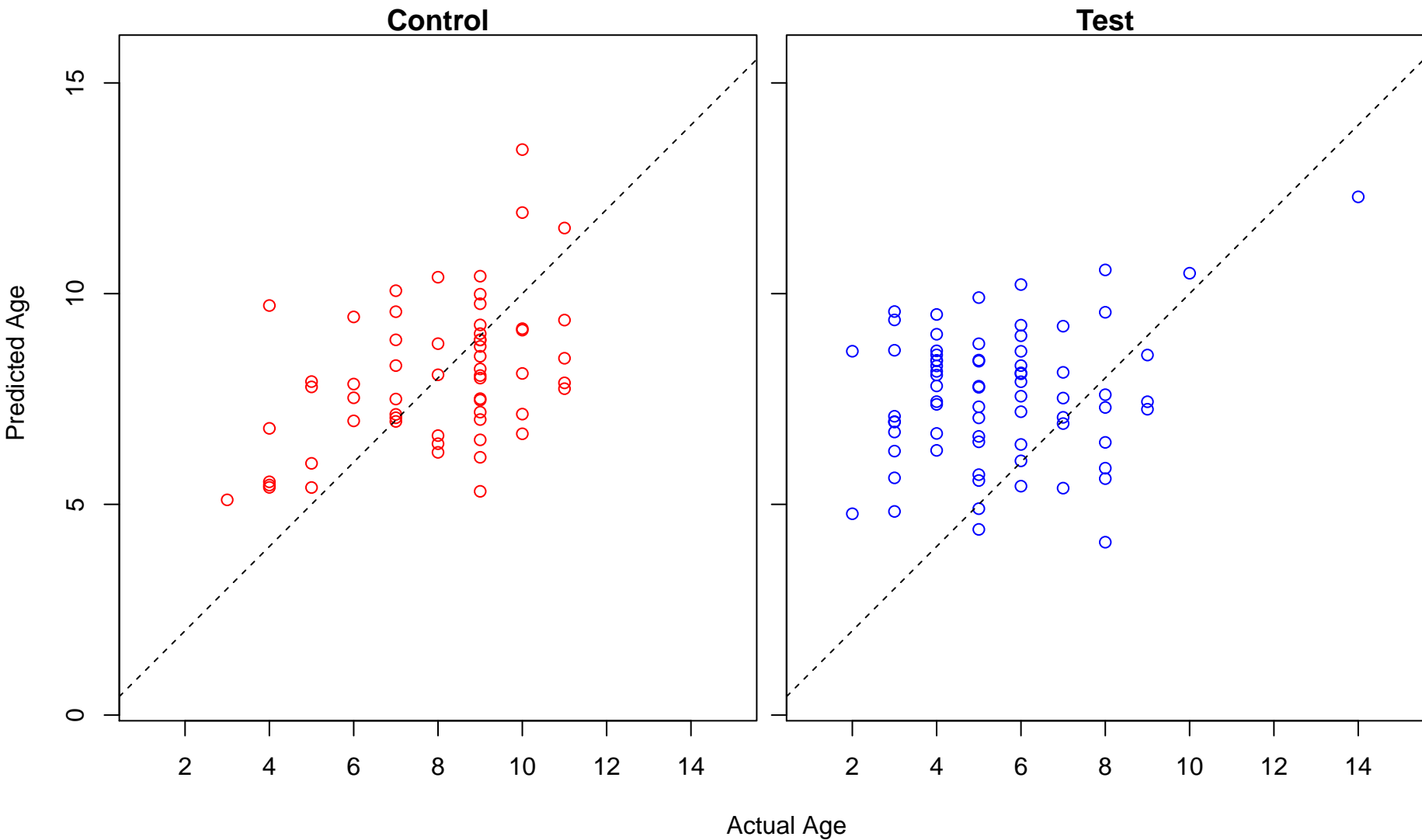
developmental process (Score: 0.973772)



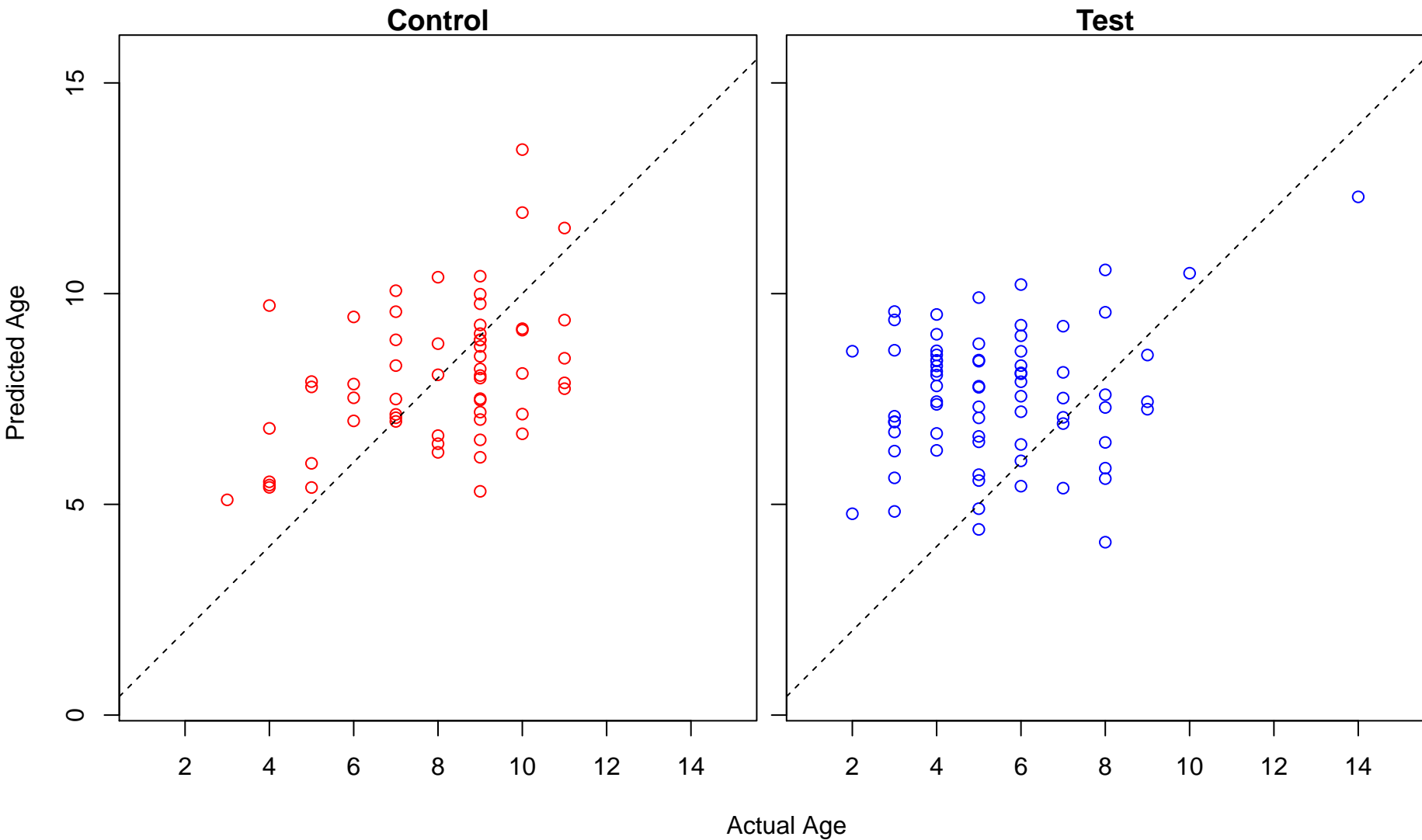
regulation of CD4-positive, alpha-beta T cell differentiation (Score: 0.973757)



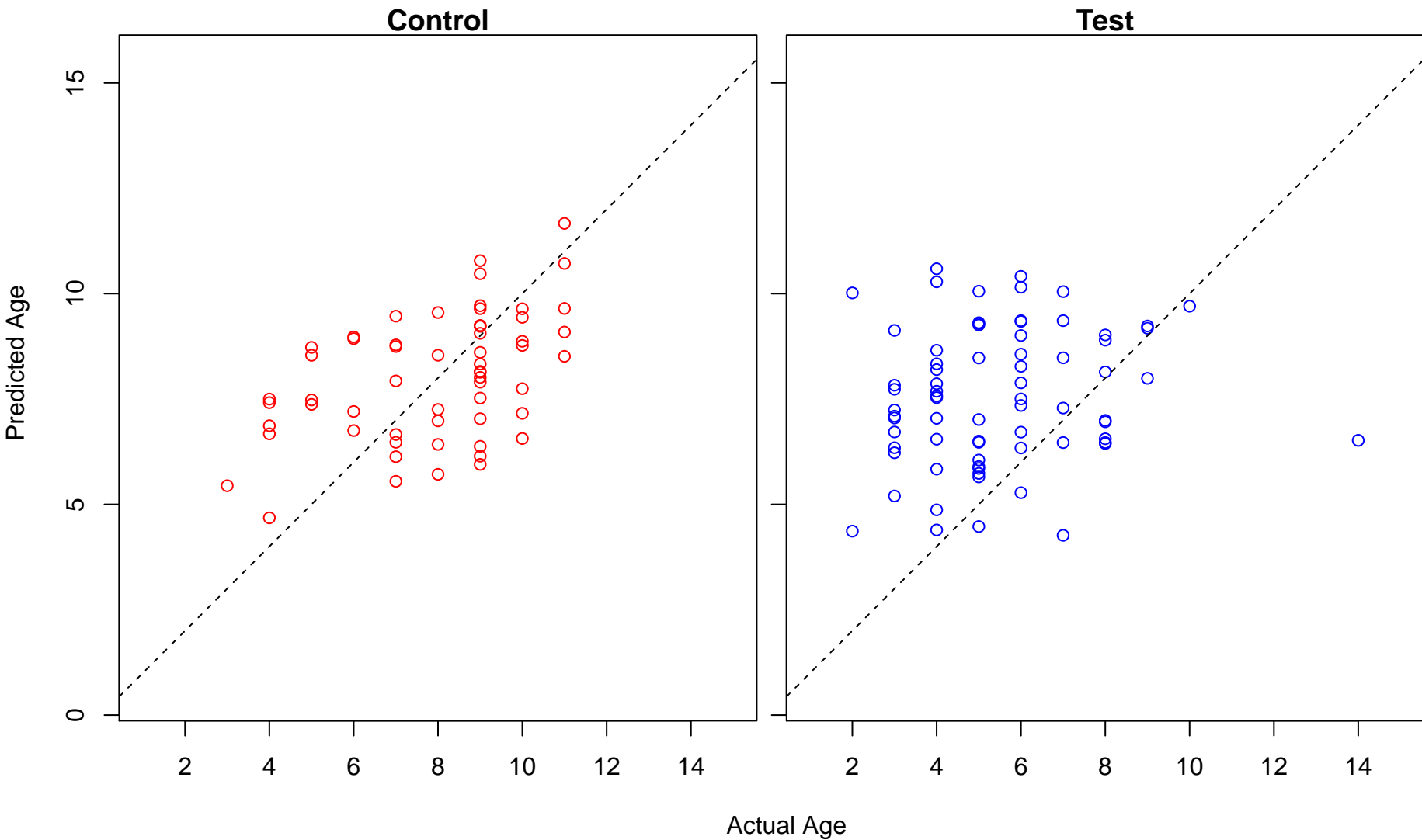
extracellular regulation of signal transduction (Score: 0.973733)



extracellular negative regulation of signal transduction (Score: 0.973733)

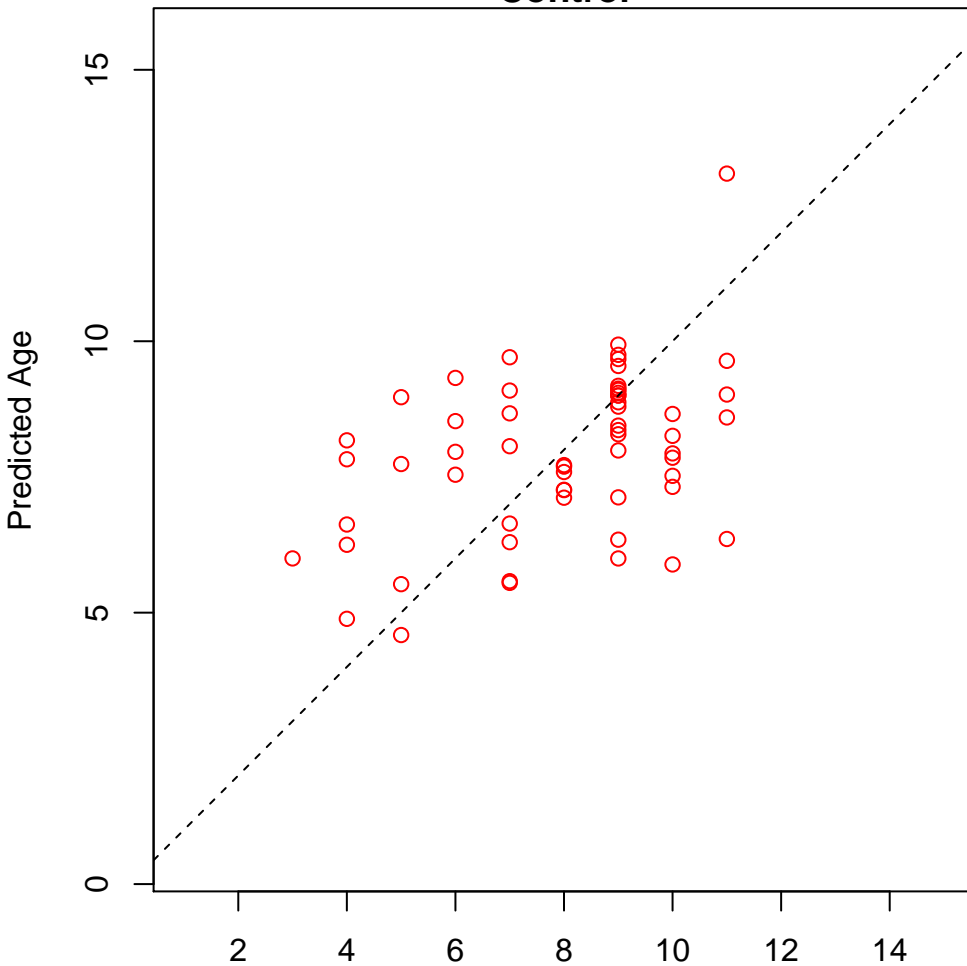


single-organism developmental process (Score: 0.973725)

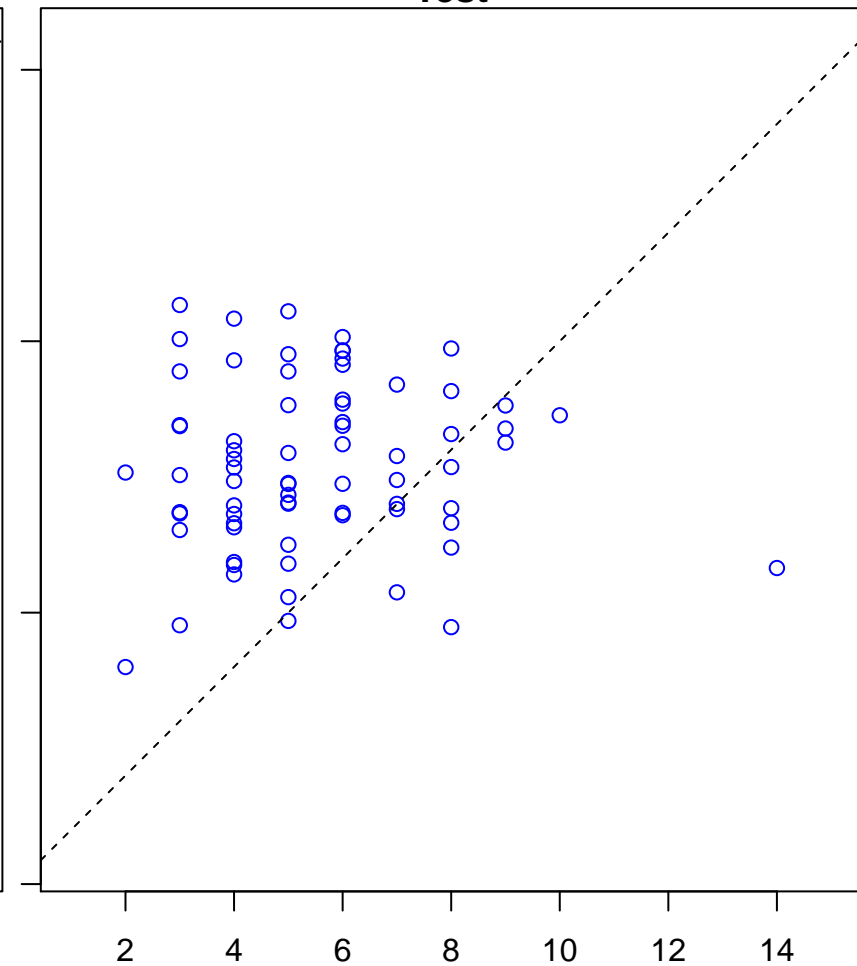


glycosaminoglycan catabolic process (Score: 0.973718)

Control

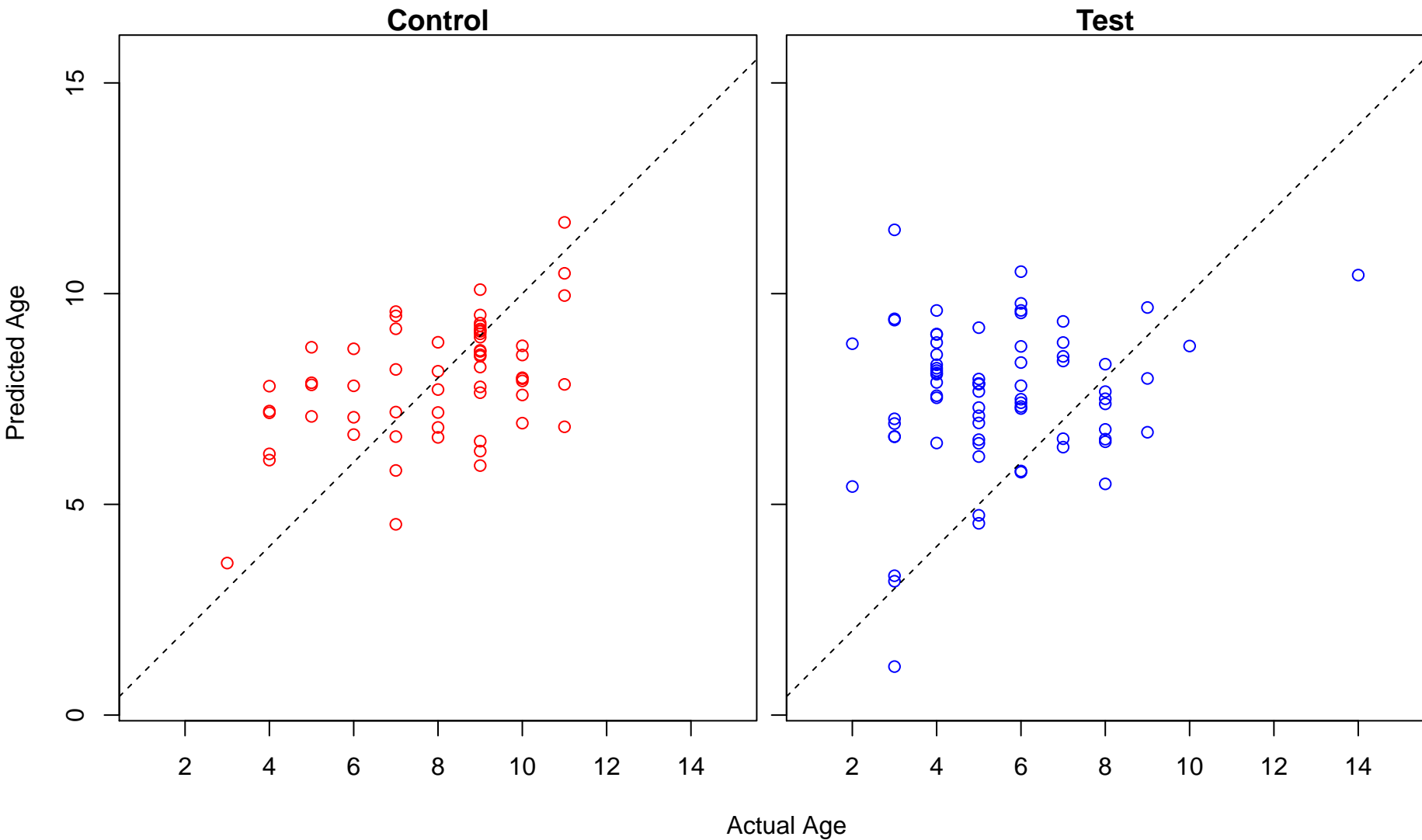


Test

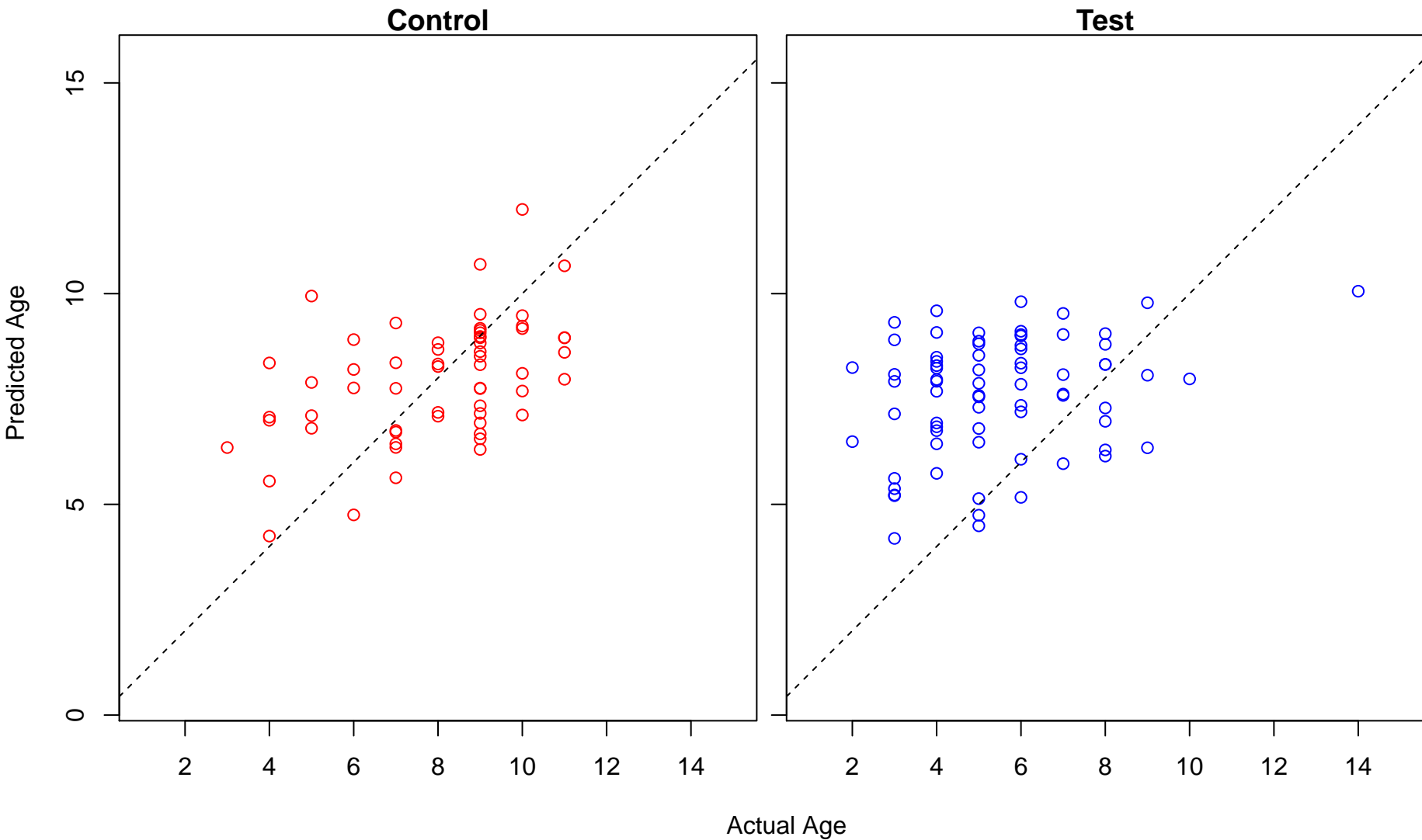


Actual Age

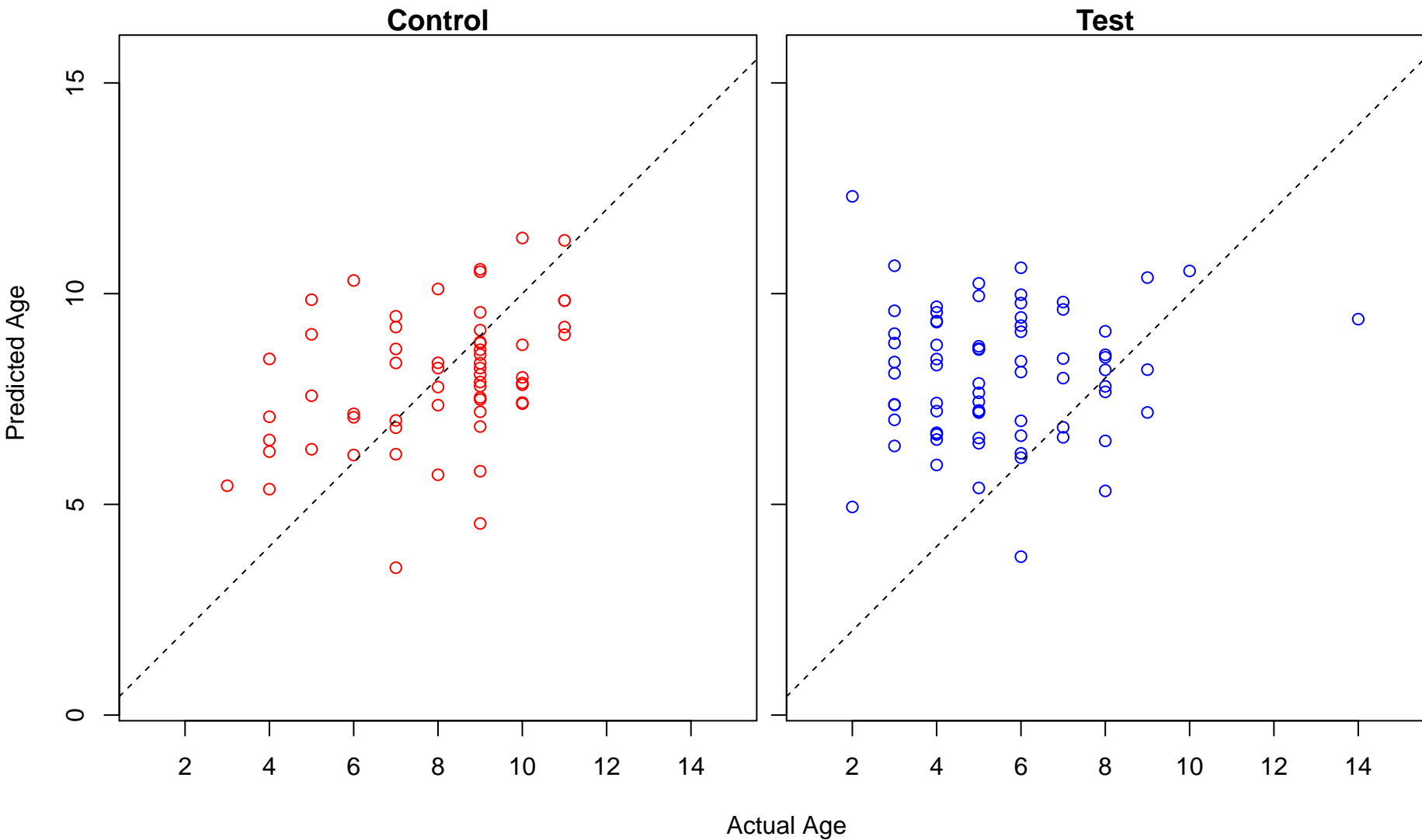
regulation of cardiac muscle tissue growth (Score: 0.970782)



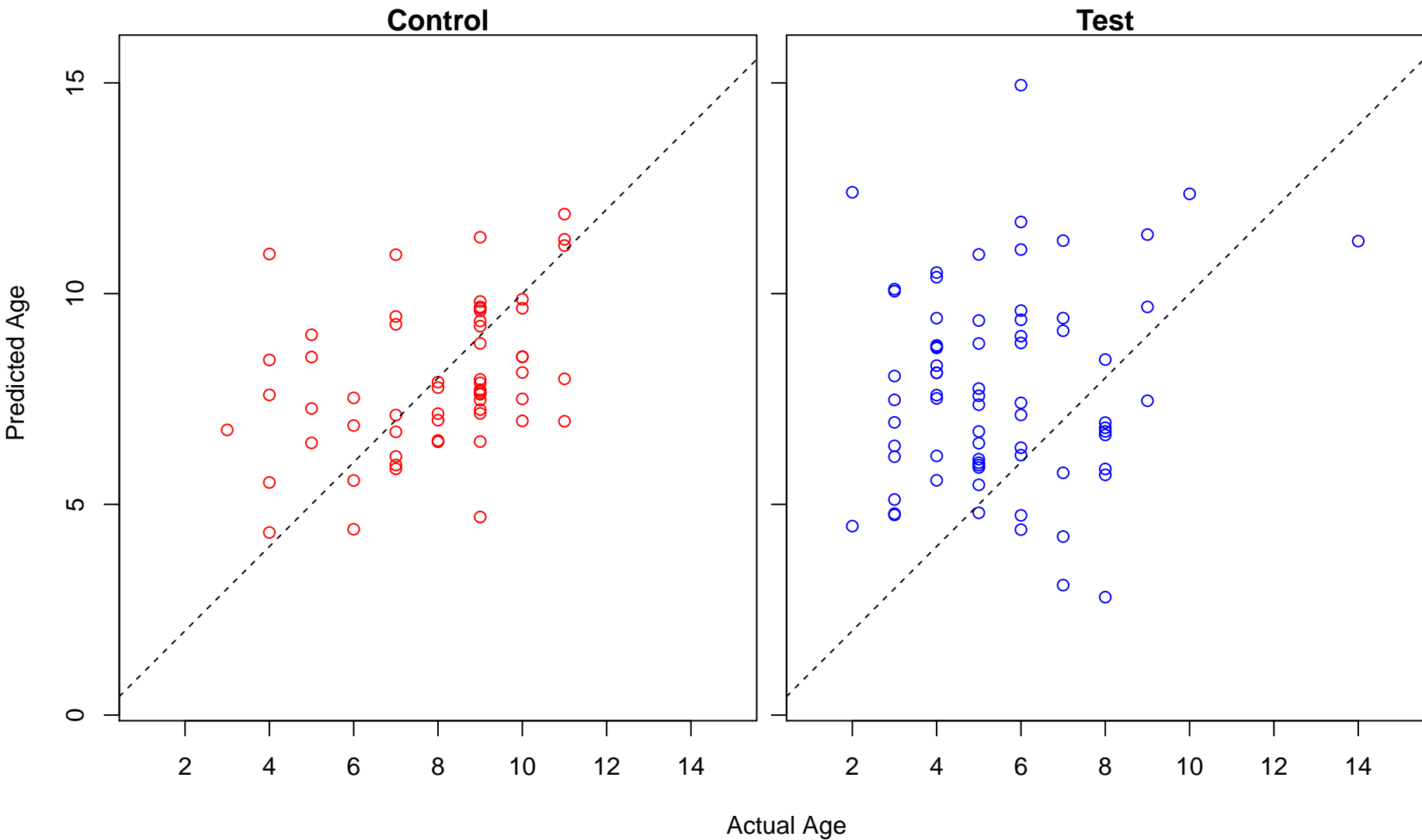
regulation of dendritic cell antigen processing and presentation (Score: 0.970108)



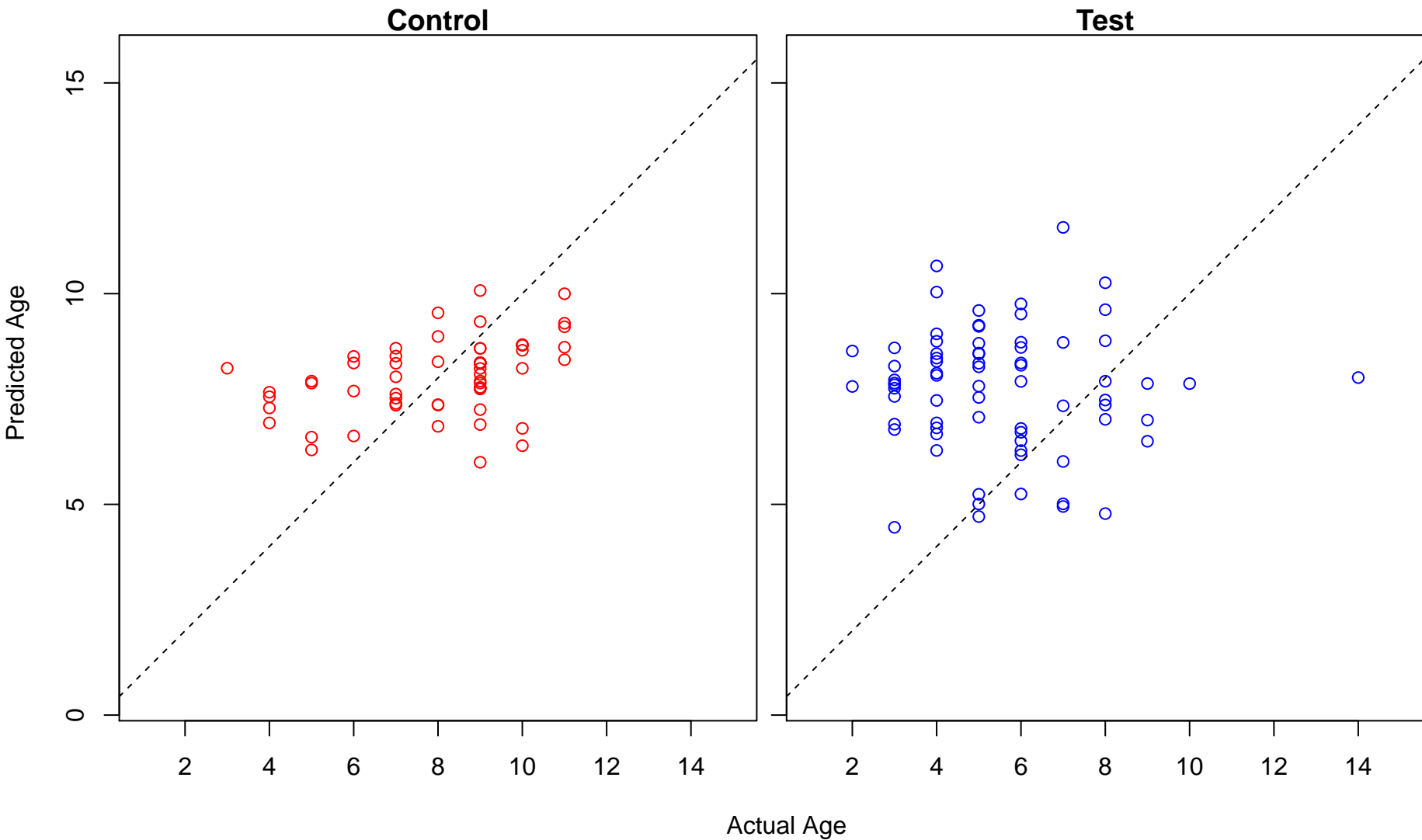
regulation of filopodium assembly (Score: 0.969860)



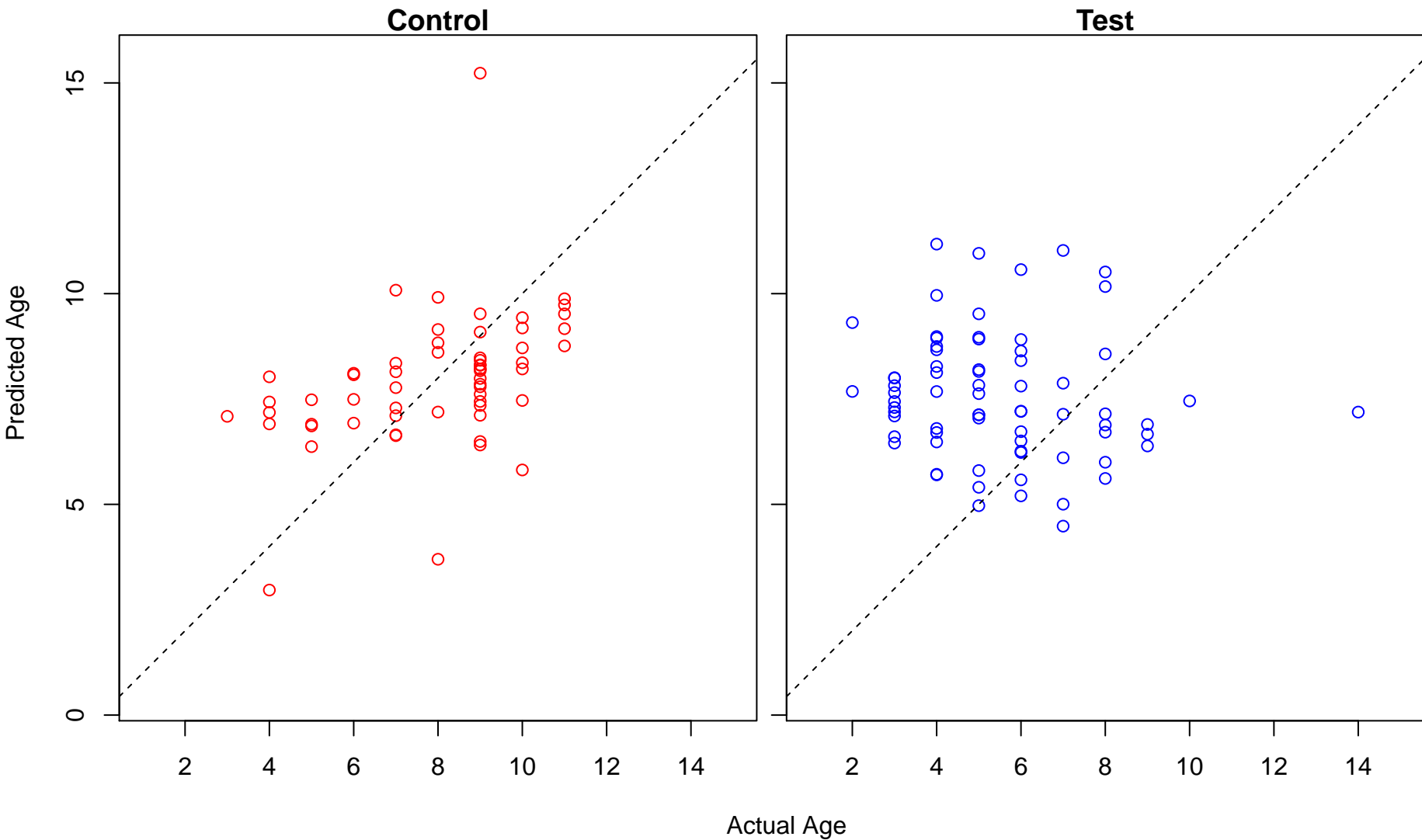
ncRNA metabolic process (Score: 0.969763)



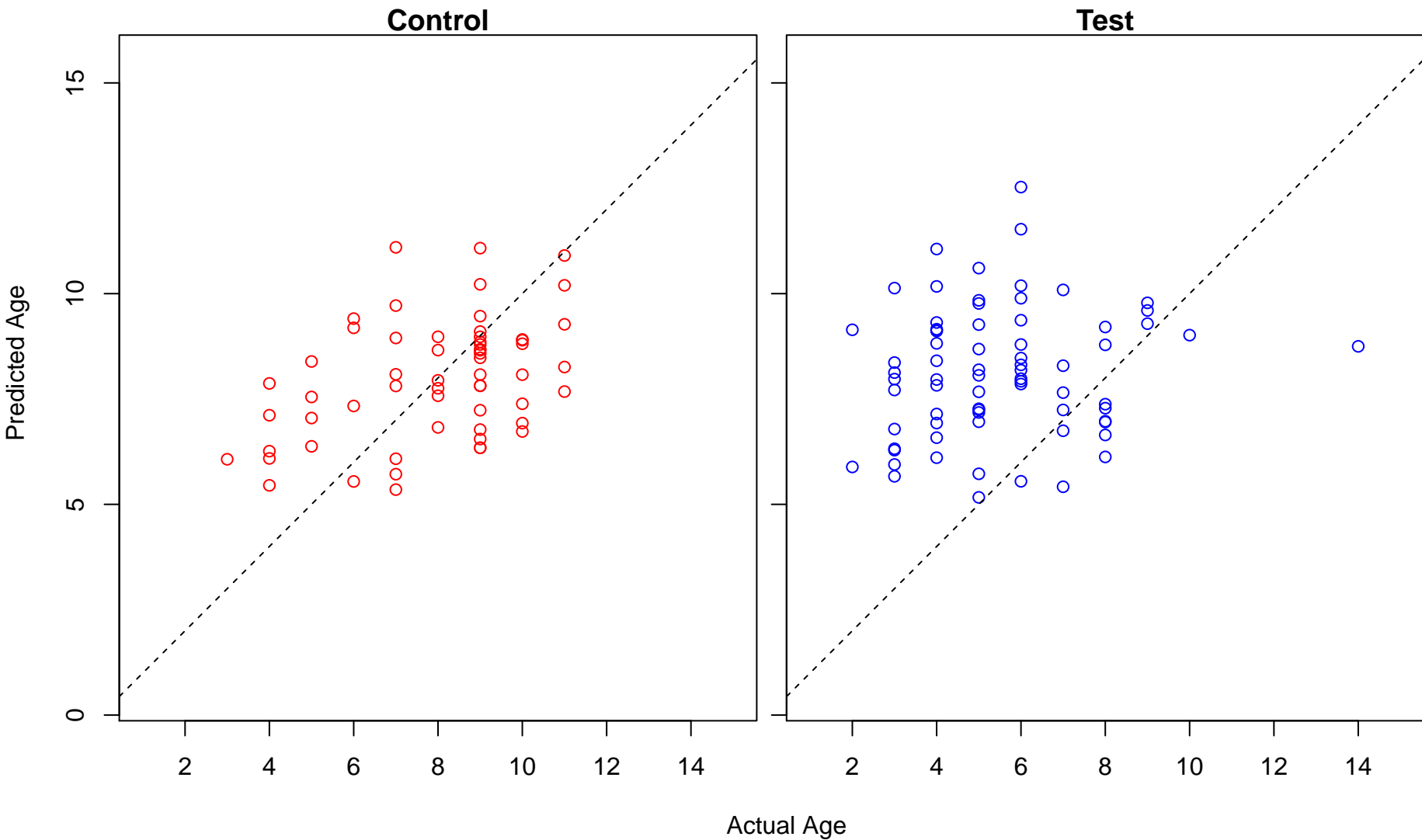
dopamine biosynthetic process (Score: 0.969383)



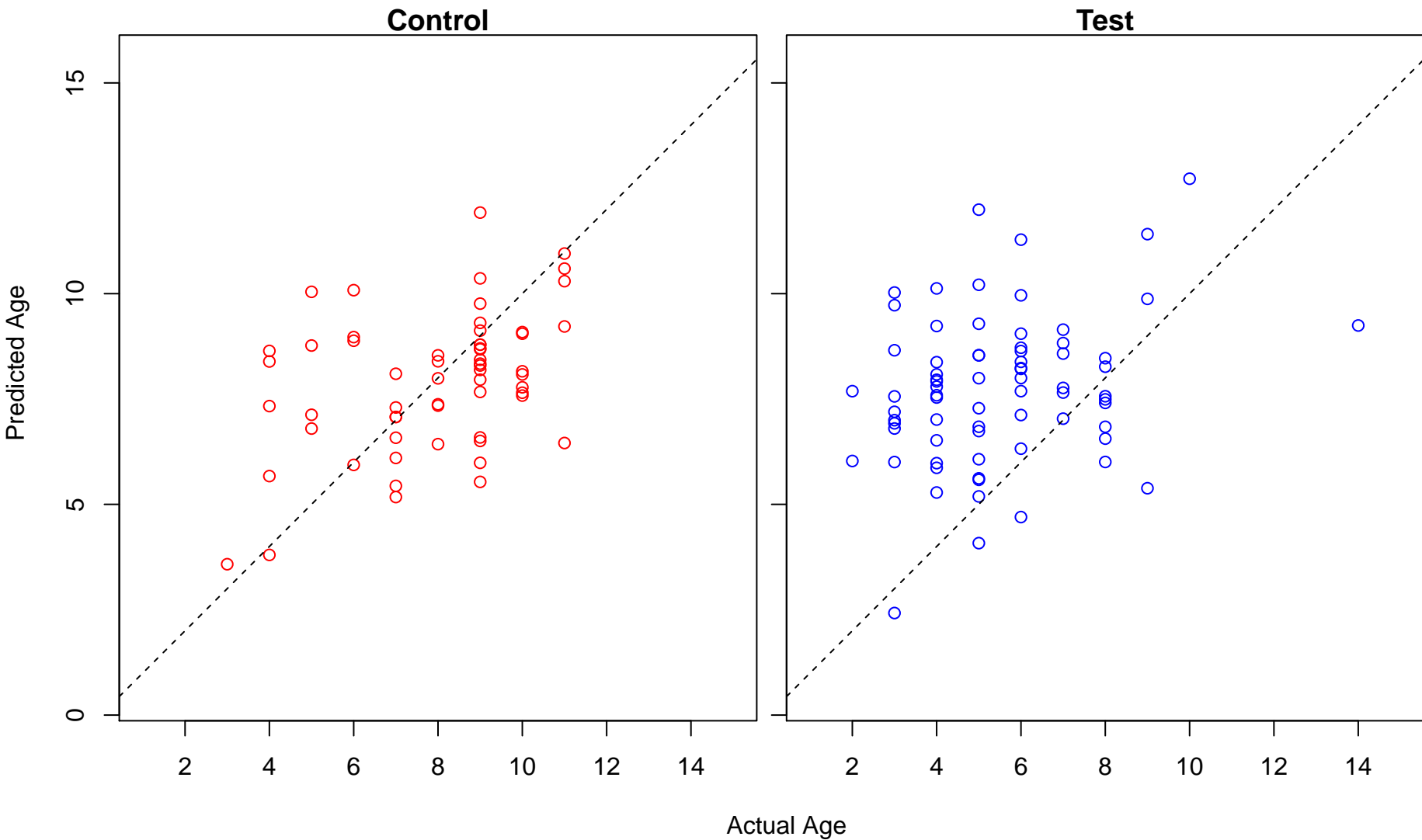
negative regulation of amine transport (Score: 0.969374)



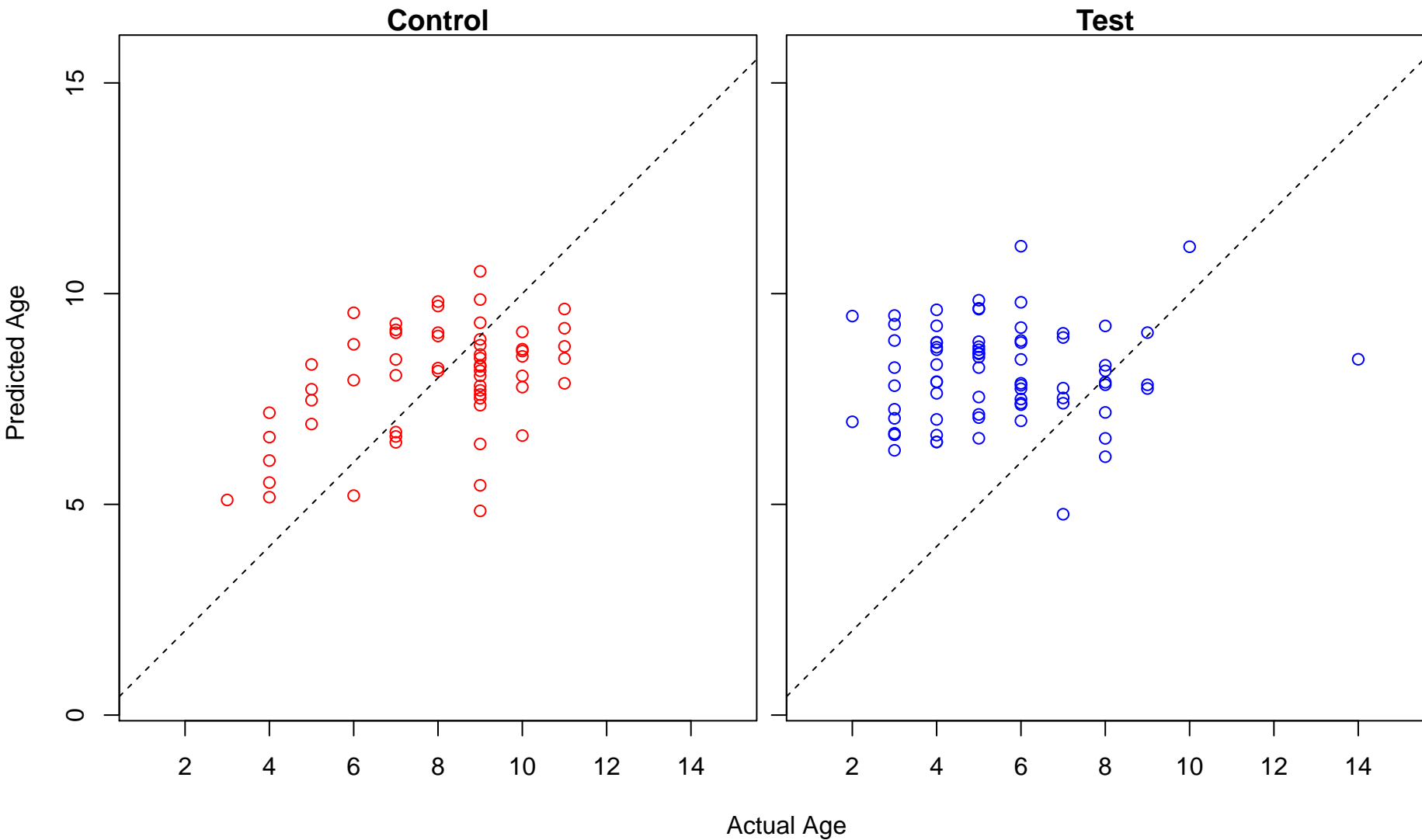
memory (Score: 0.968838)



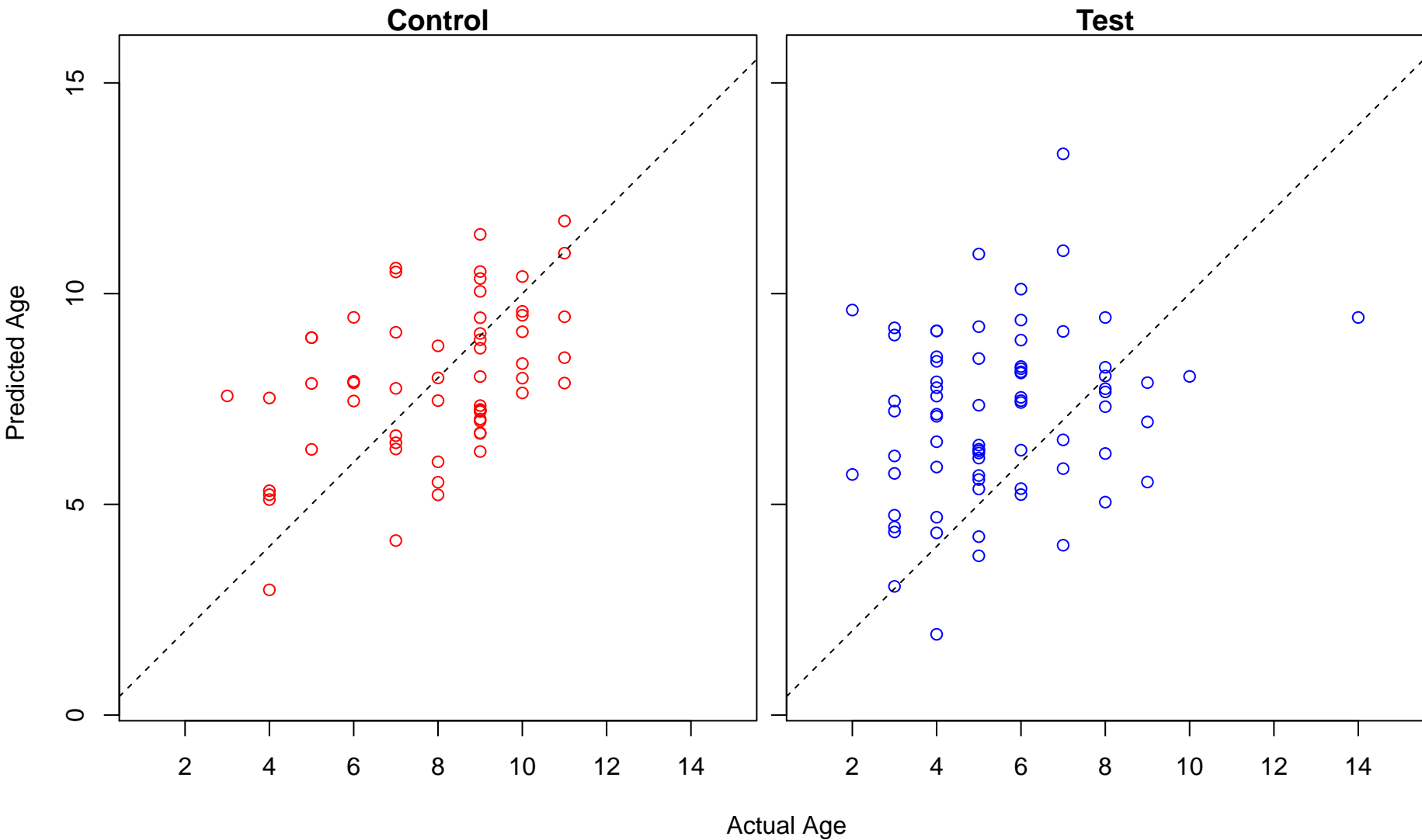
muscle fiber development (Score: 0.967716)



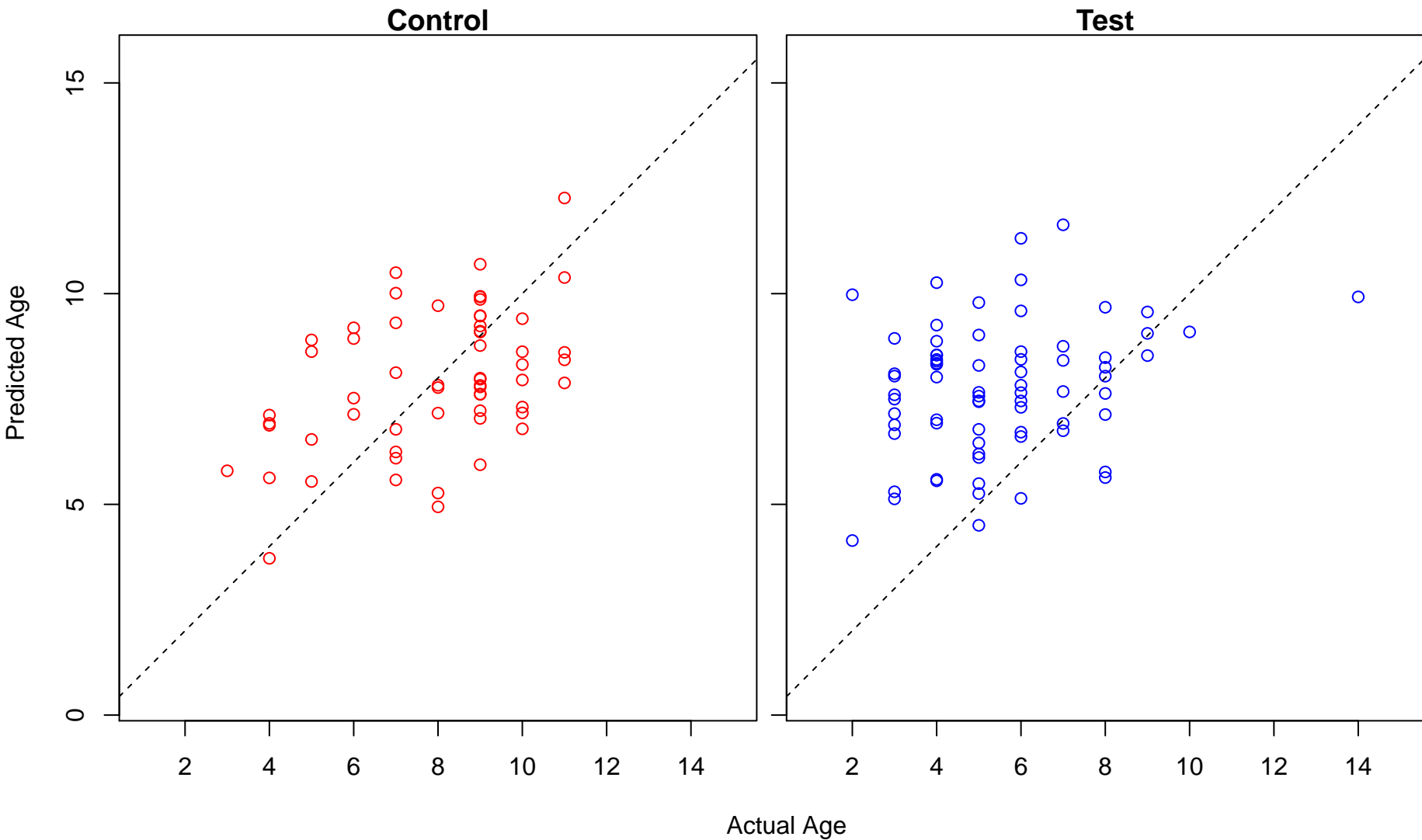
very-low-density lipoprotein particle assembly (Score: 0.966874)



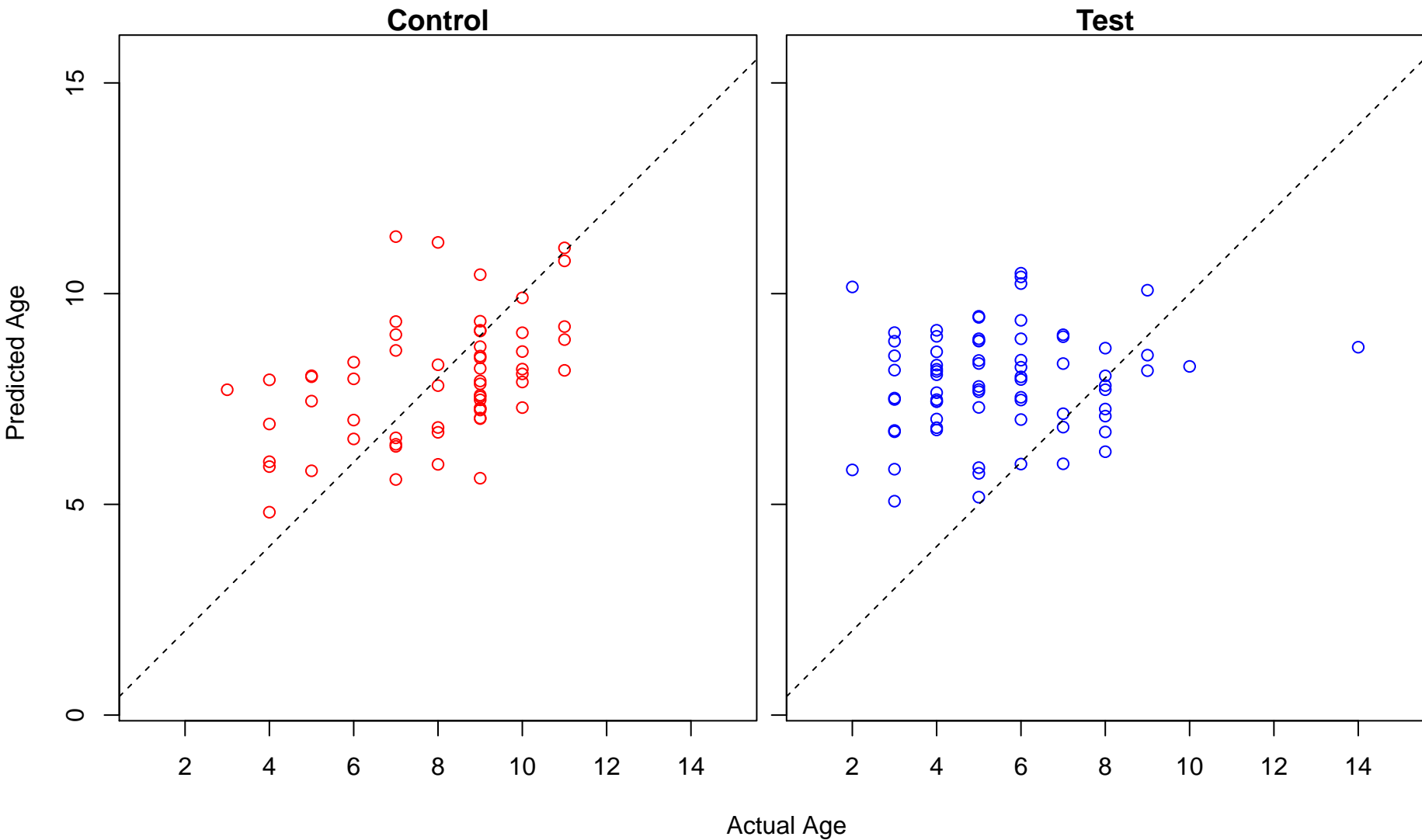
mitotic DNA damage checkpoint (Score: 0.966165)



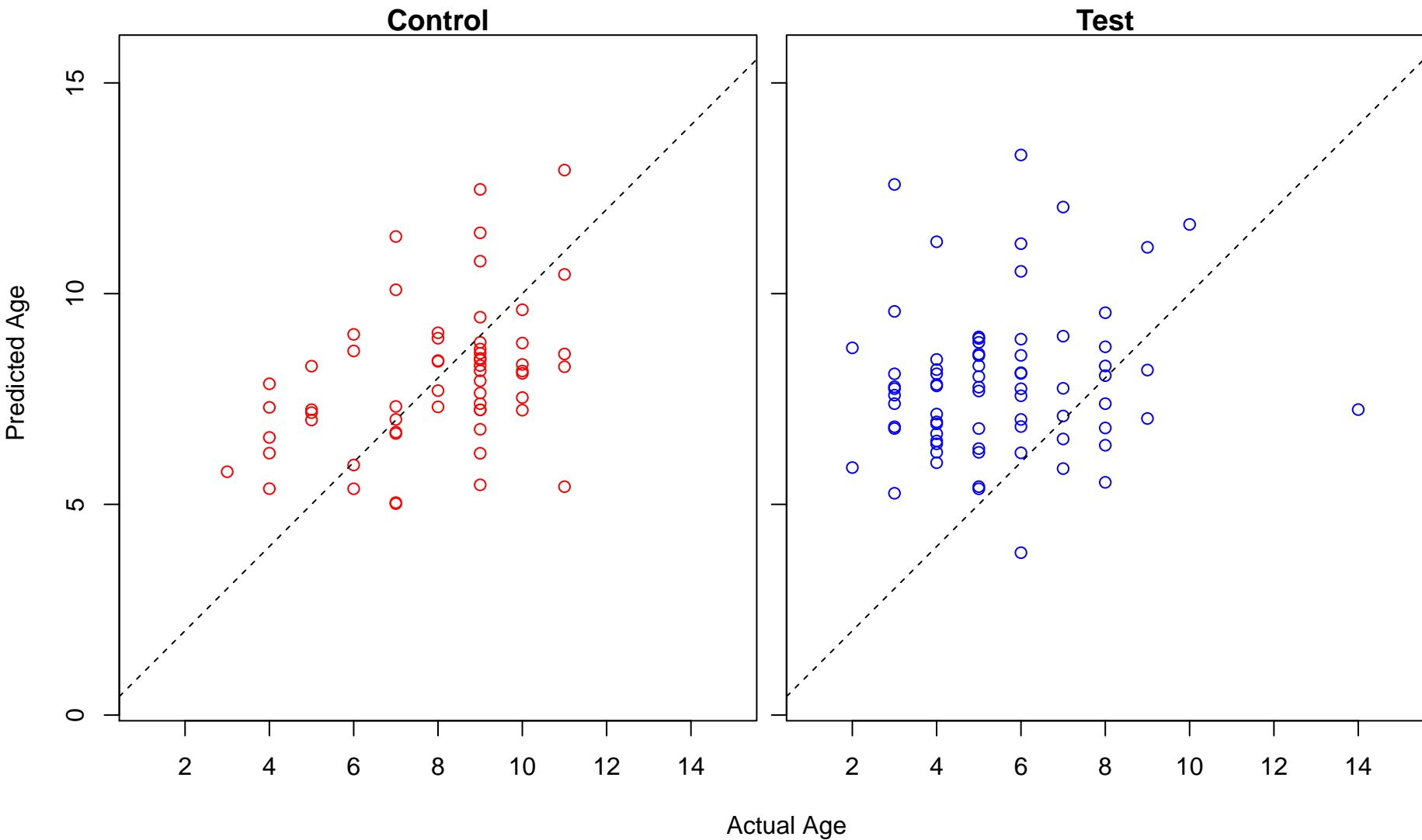
response to wounding (Score: 0.965160)



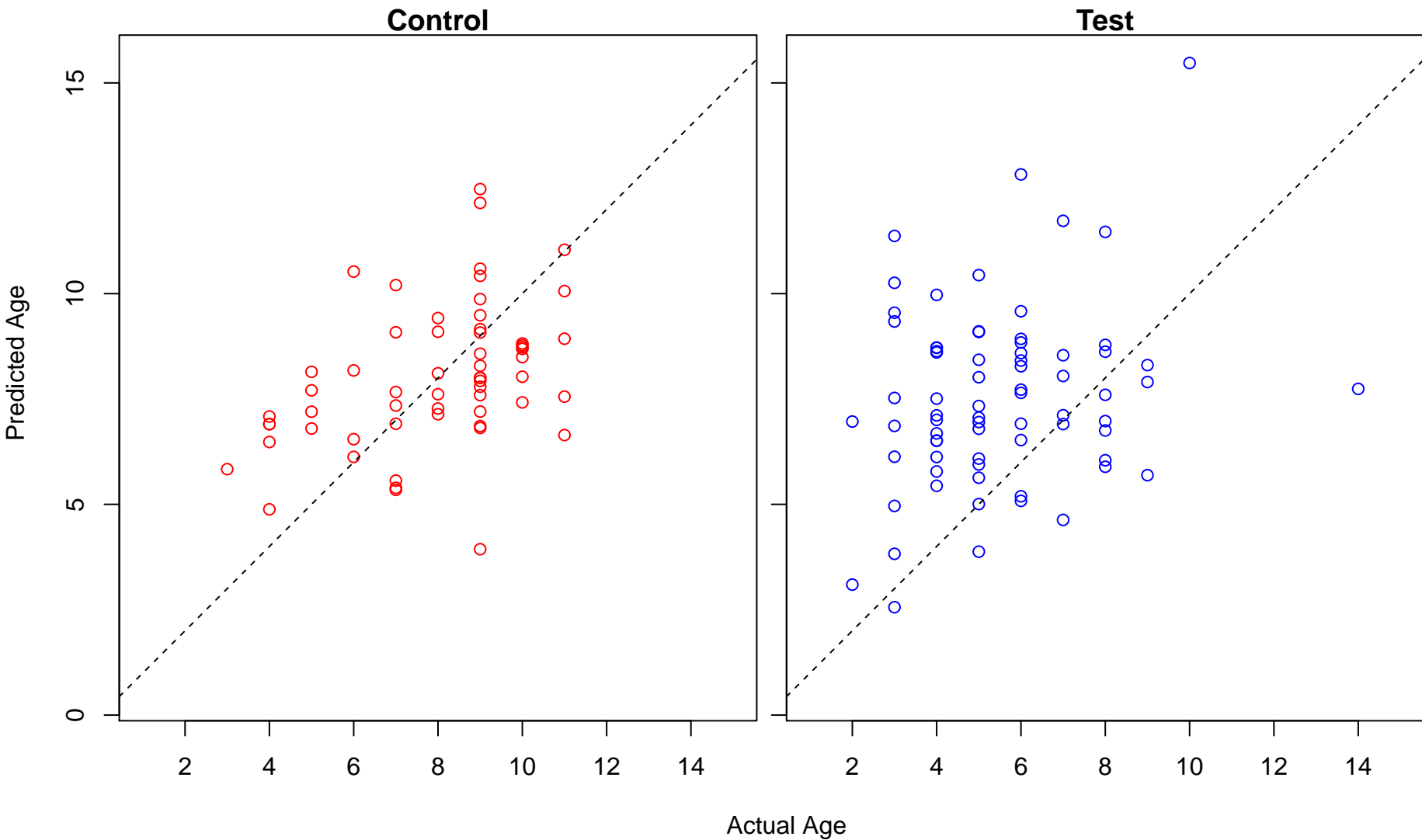
gene expression (Score: 0.964623)



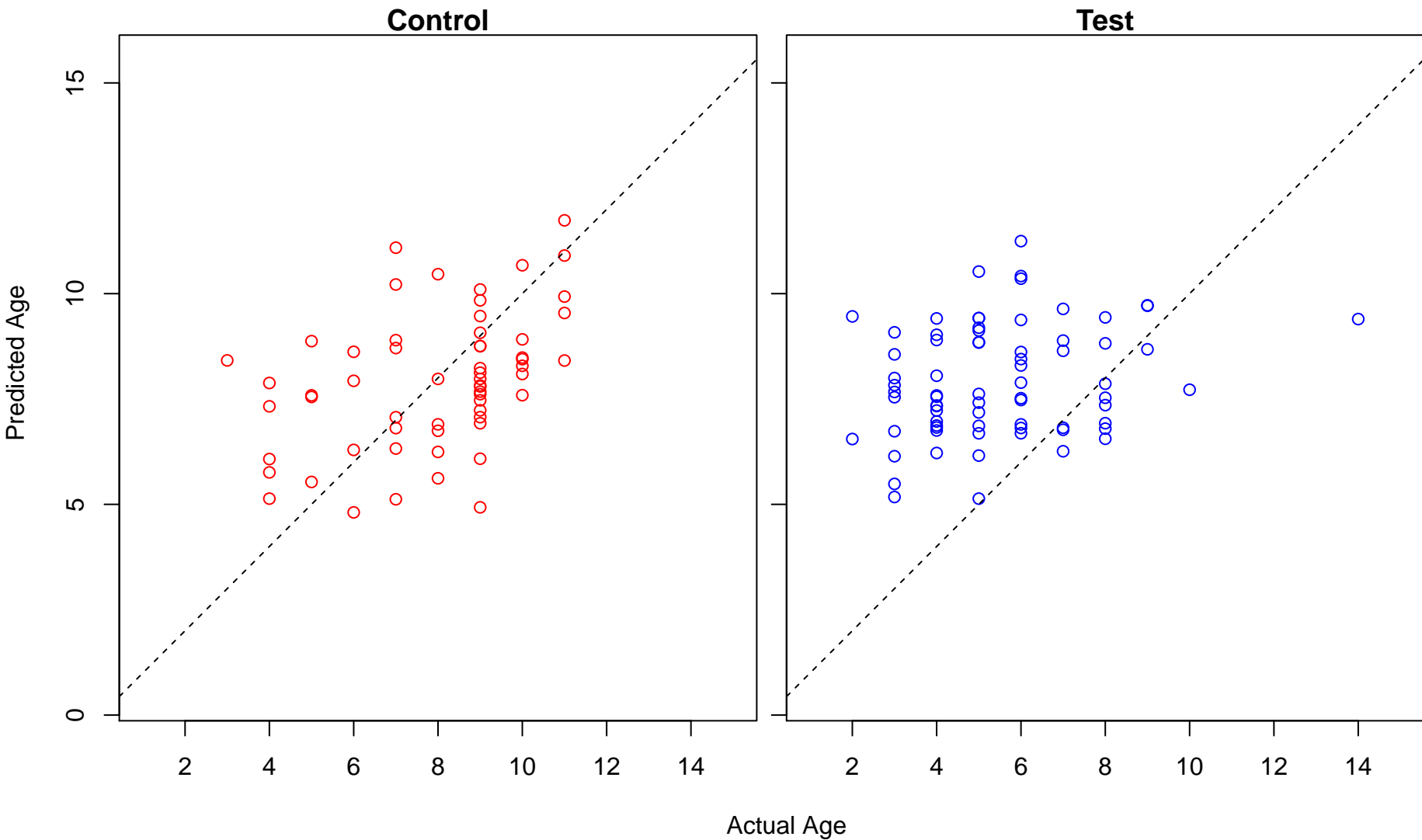
cellular carbohydrate catabolic process (Score: 0.964468)



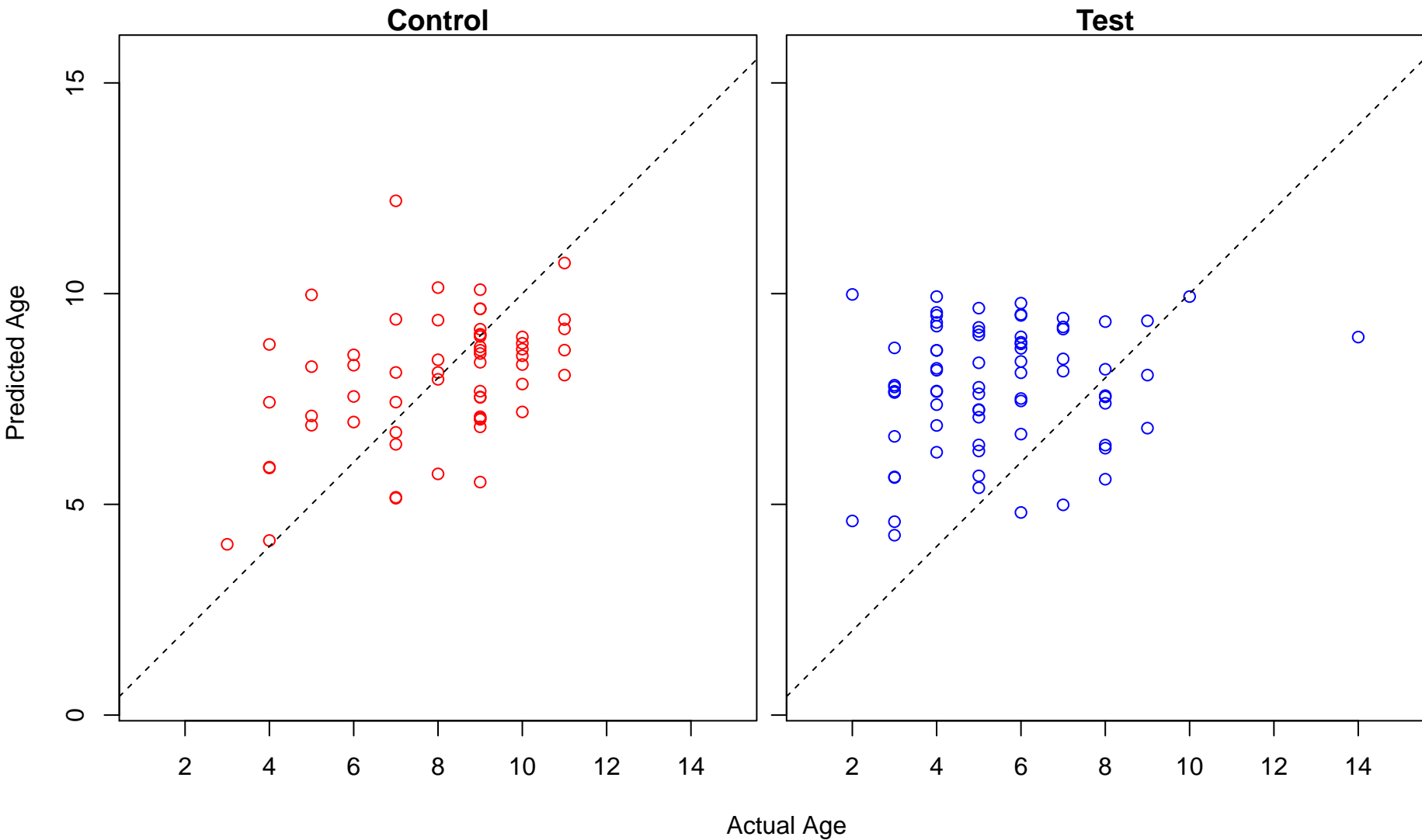
positive regulation of activated T cell proliferation (Score: 0.963772)



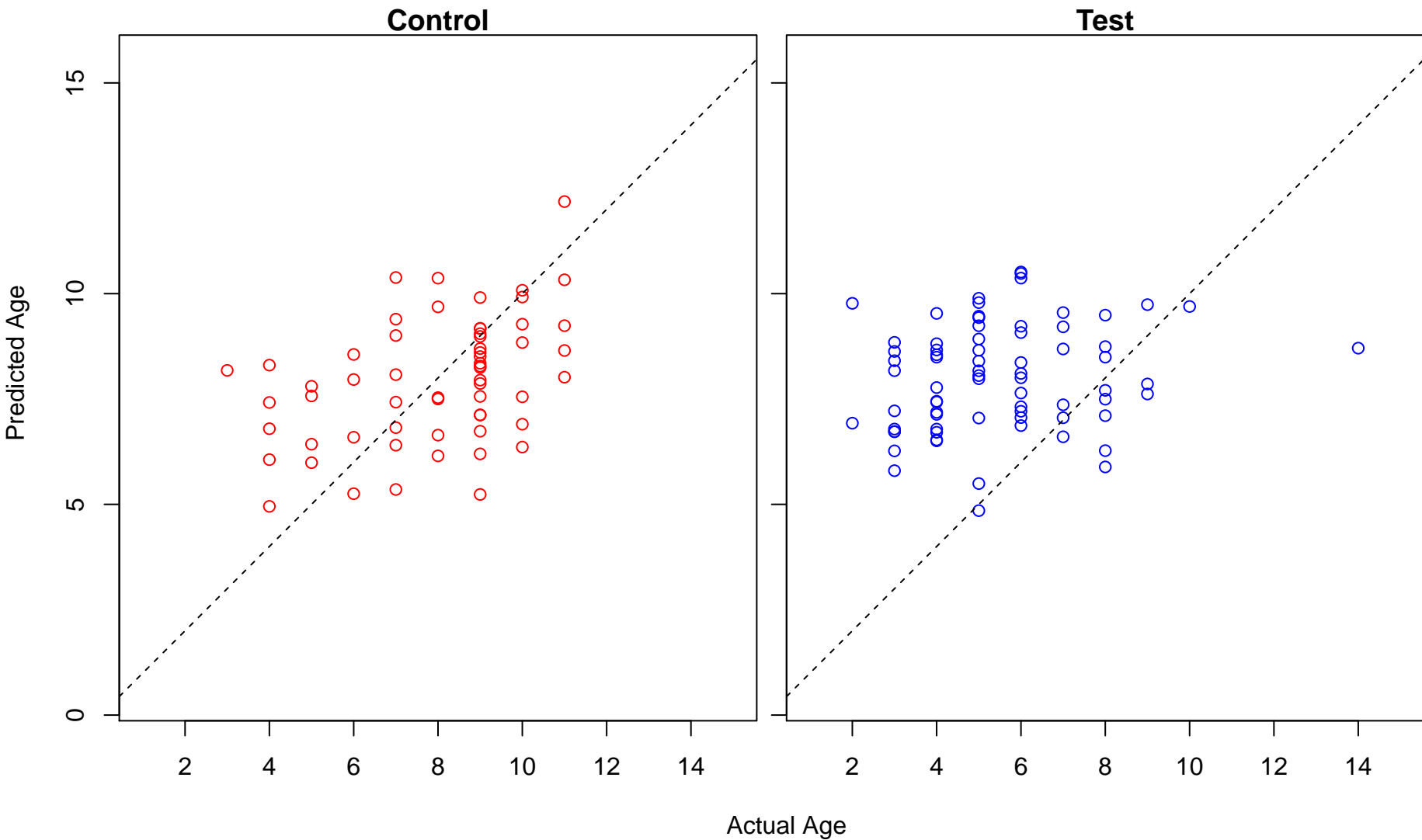
organic substance catabolic process (Score: 0.963005)



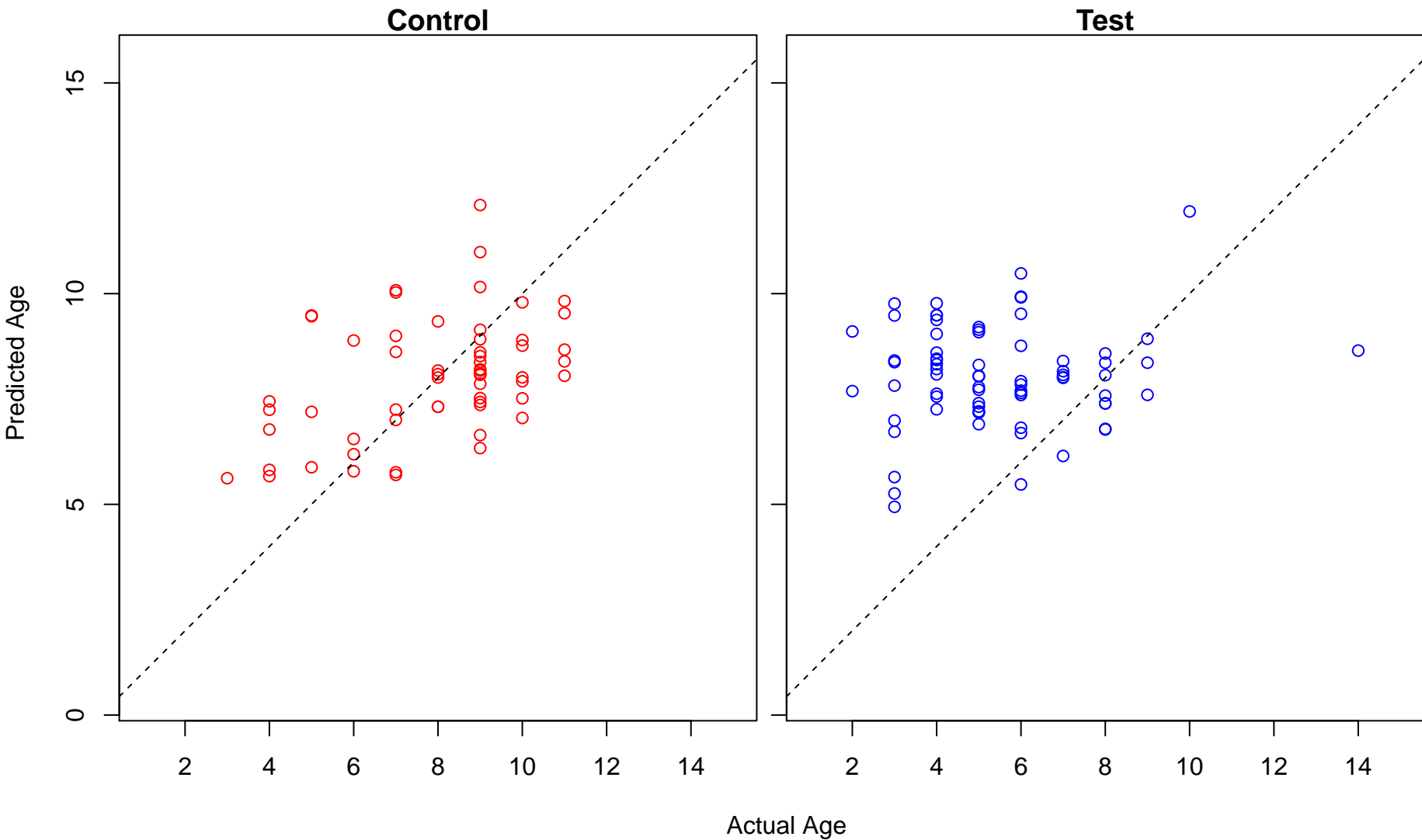
mesoderm development (Score: 0.962953)



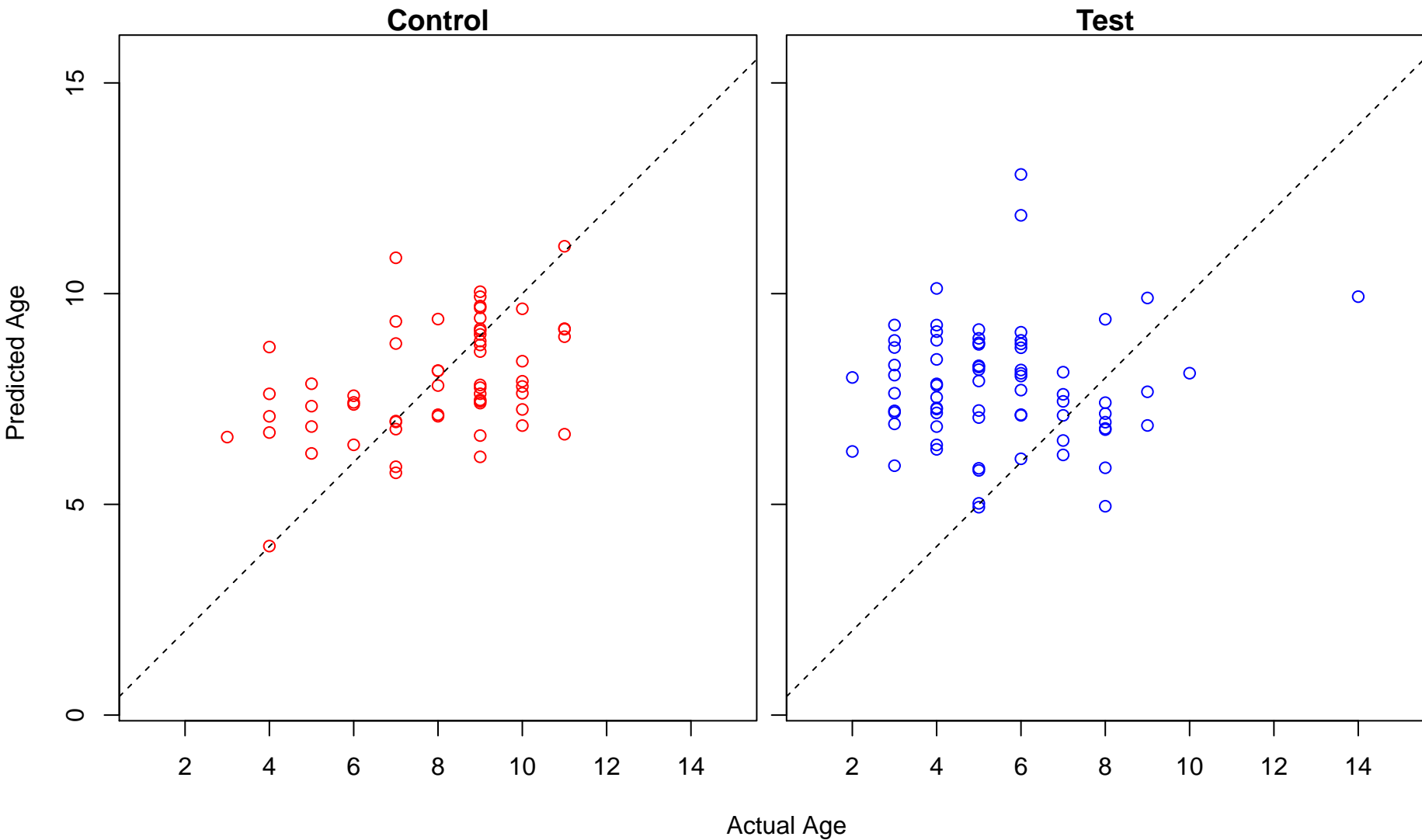
cellular modified amino acid metabolic process (Score: 0.962554)



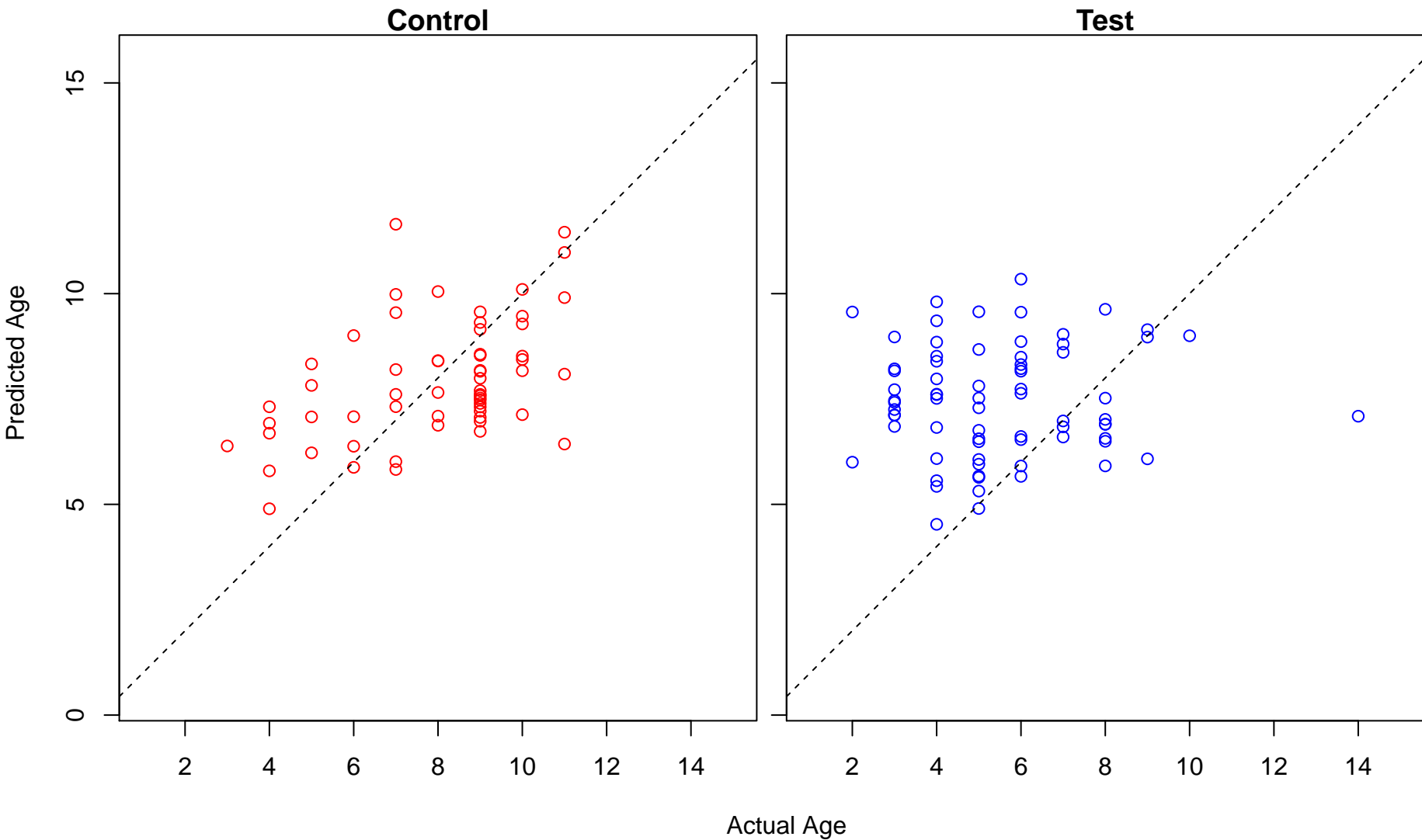
Rac protein signal transduction (Score: 0.962449)



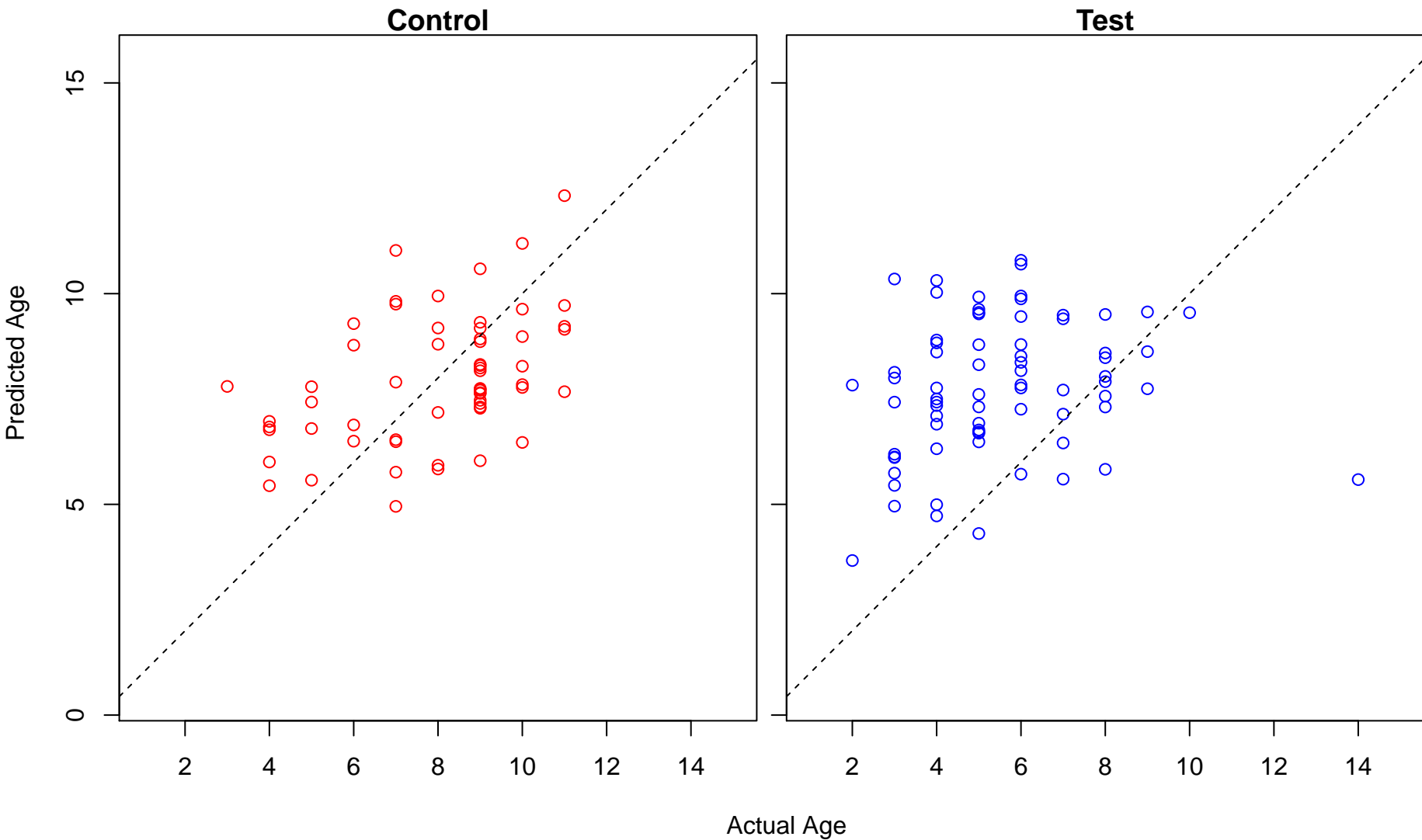
regulation of lipid kinase activity (Score: 0.962130)



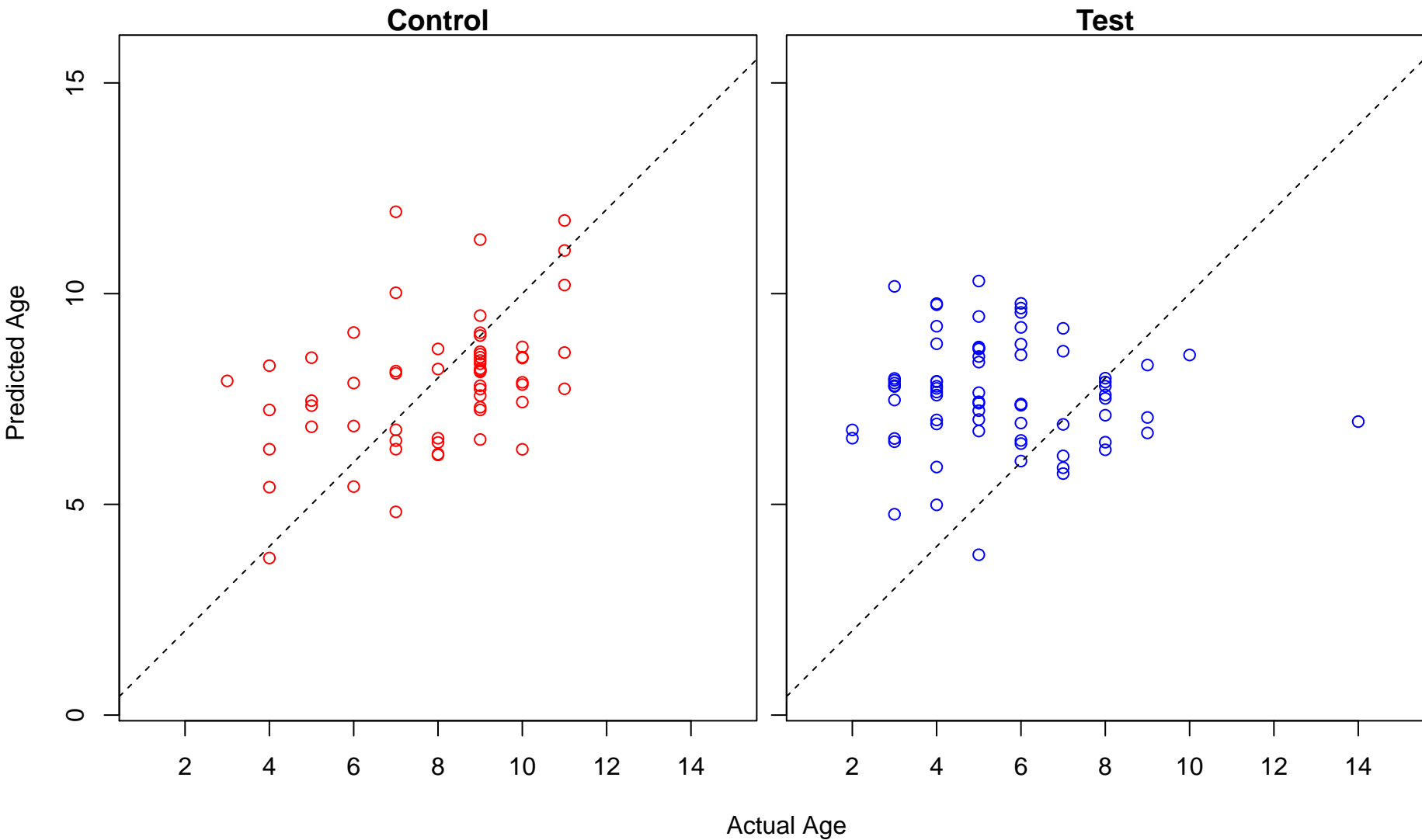
establishment of monopolar cell polarity (Score: 0.961065)



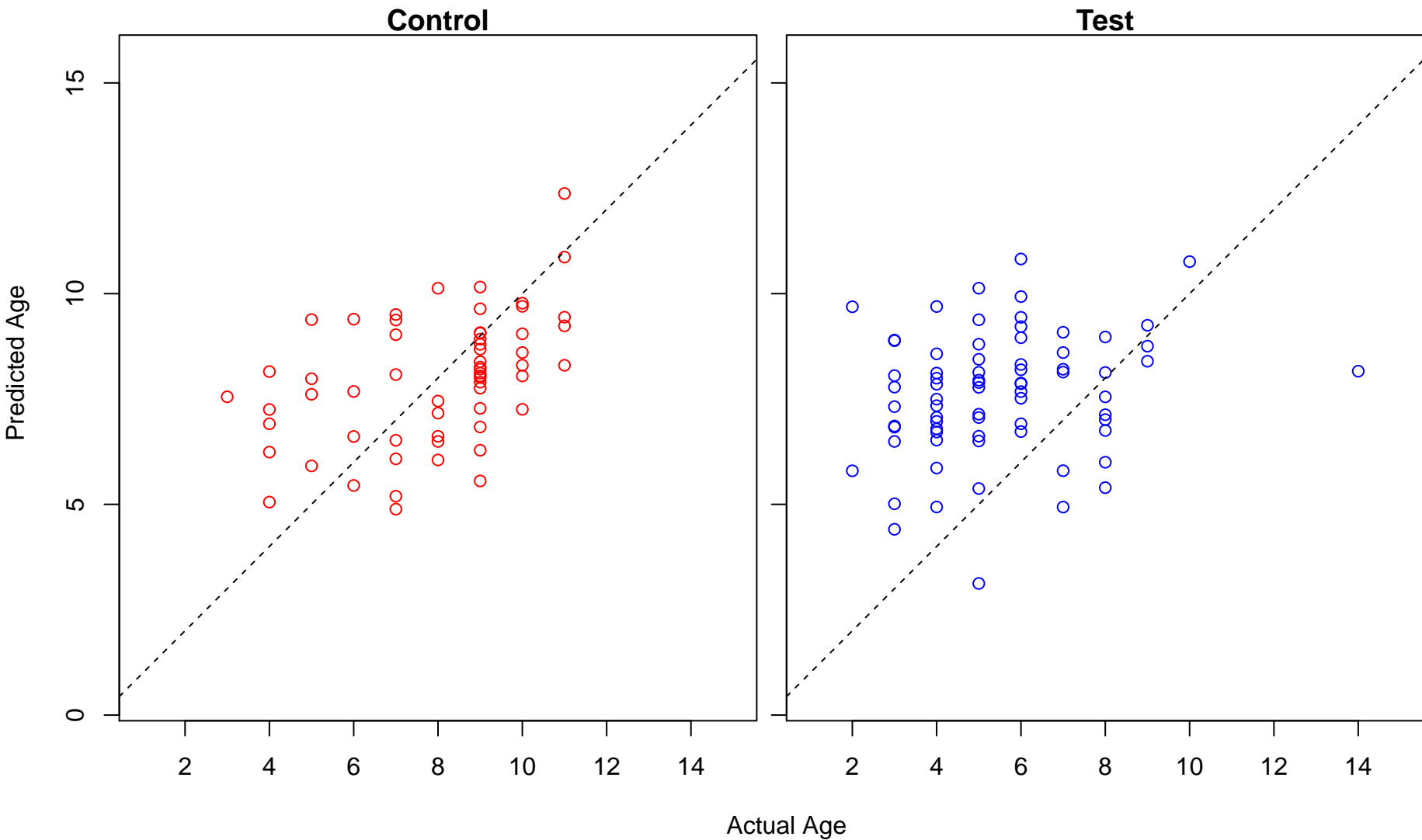
regulation of vacuole organization (Score: 0.960847)



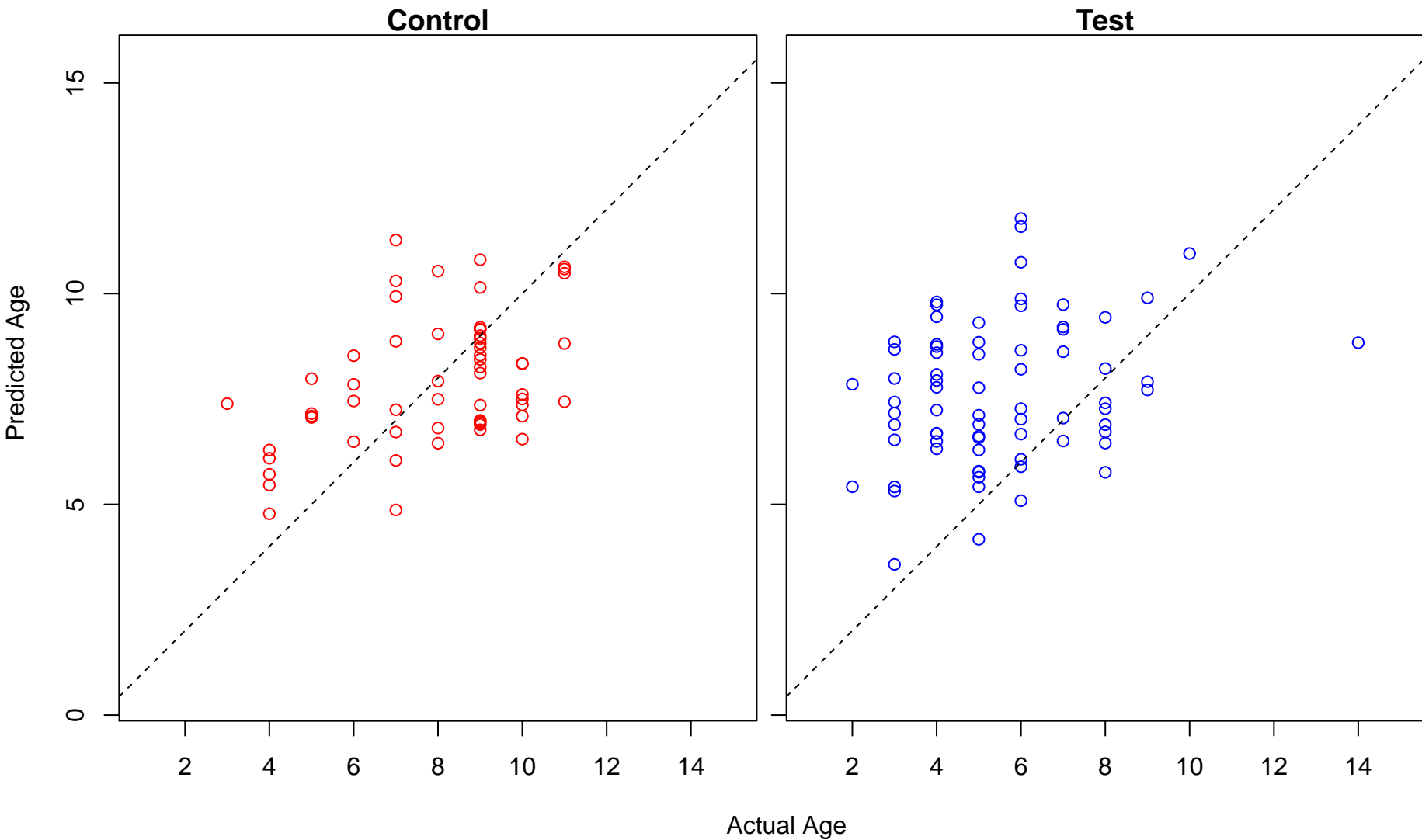
hormone metabolic process (Score: 0.960683)



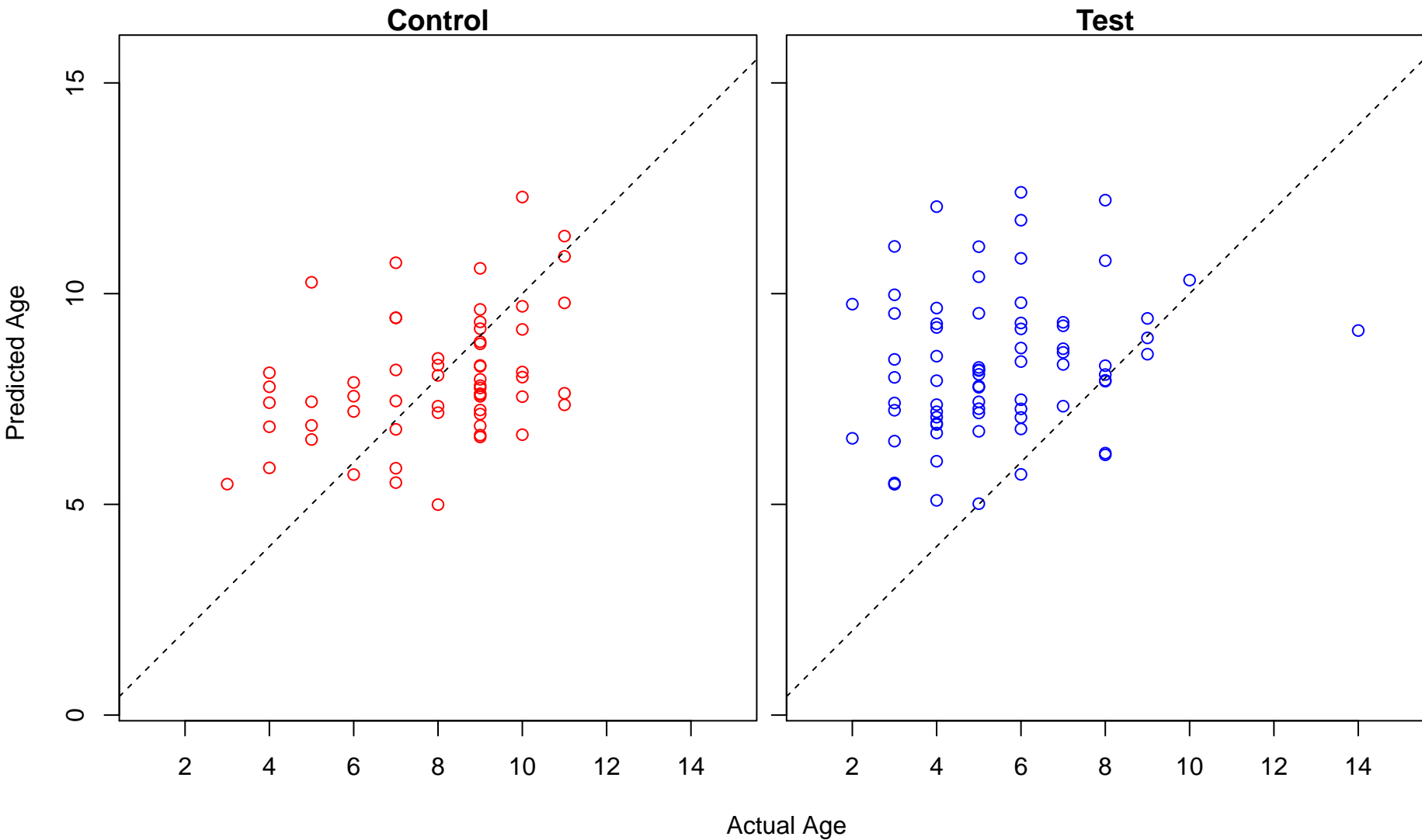
organic substance biosynthetic process (Score: 0.960189)



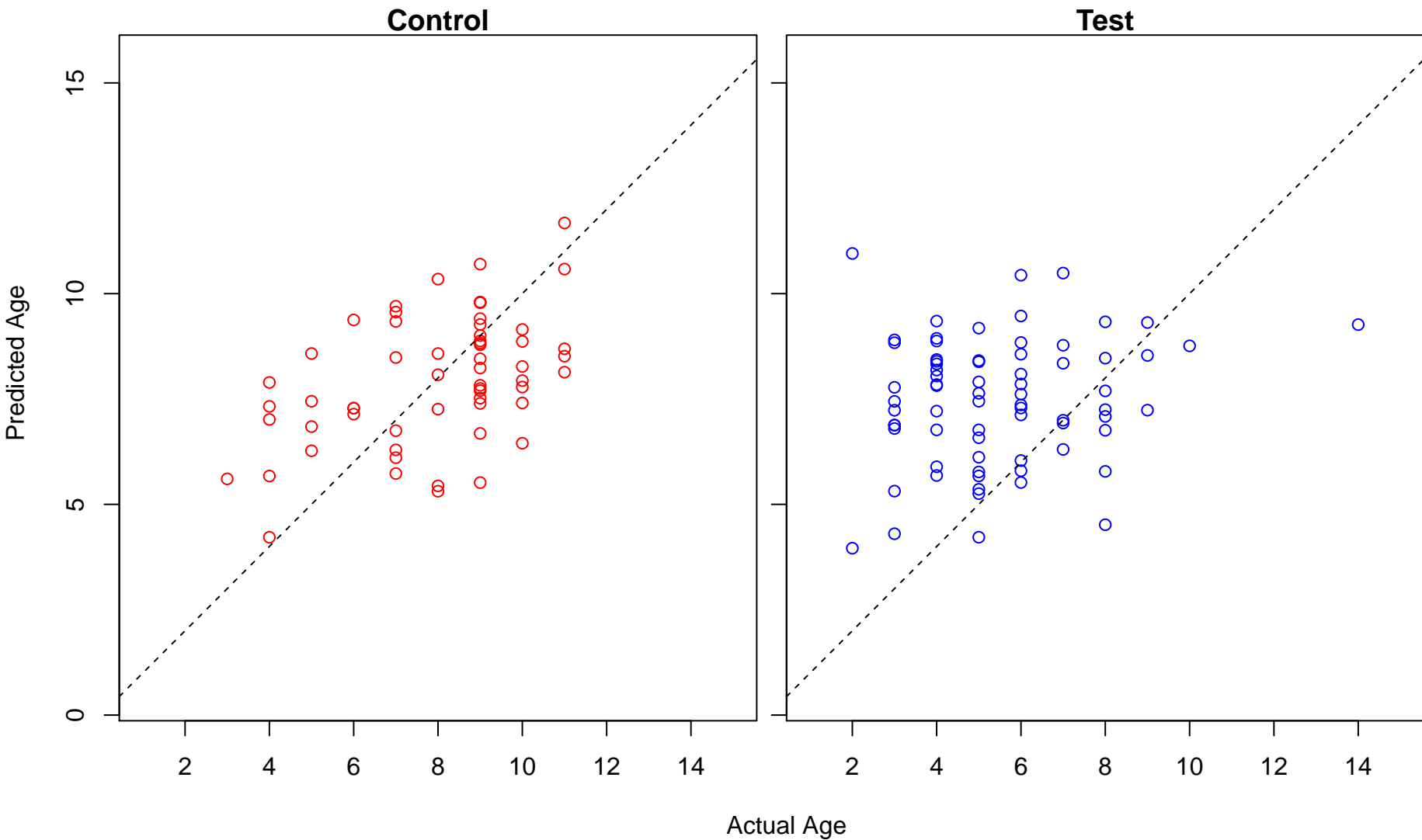
endoderm formation (Score: 0.959384)



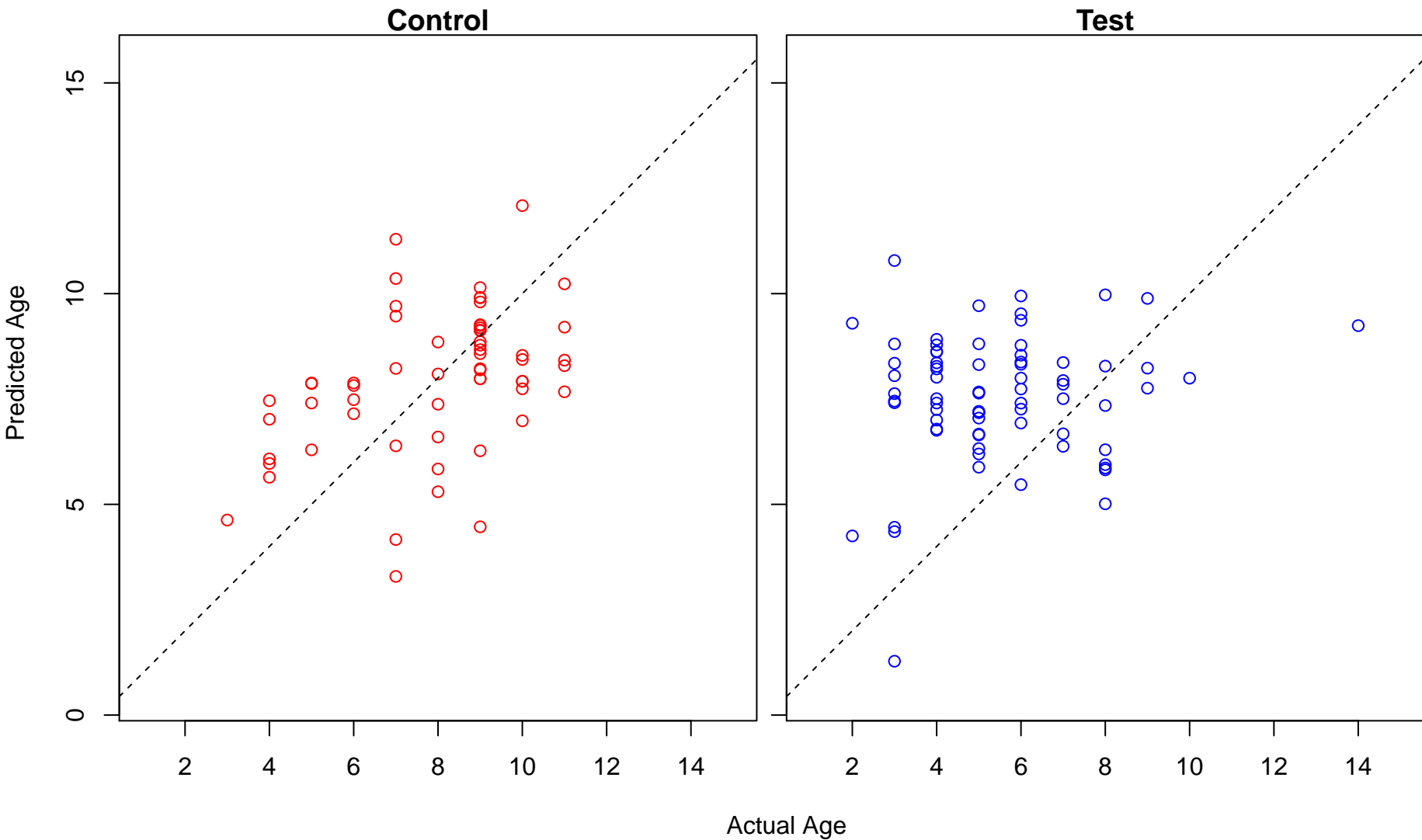
camera-type eye development (Score: 0.959345)



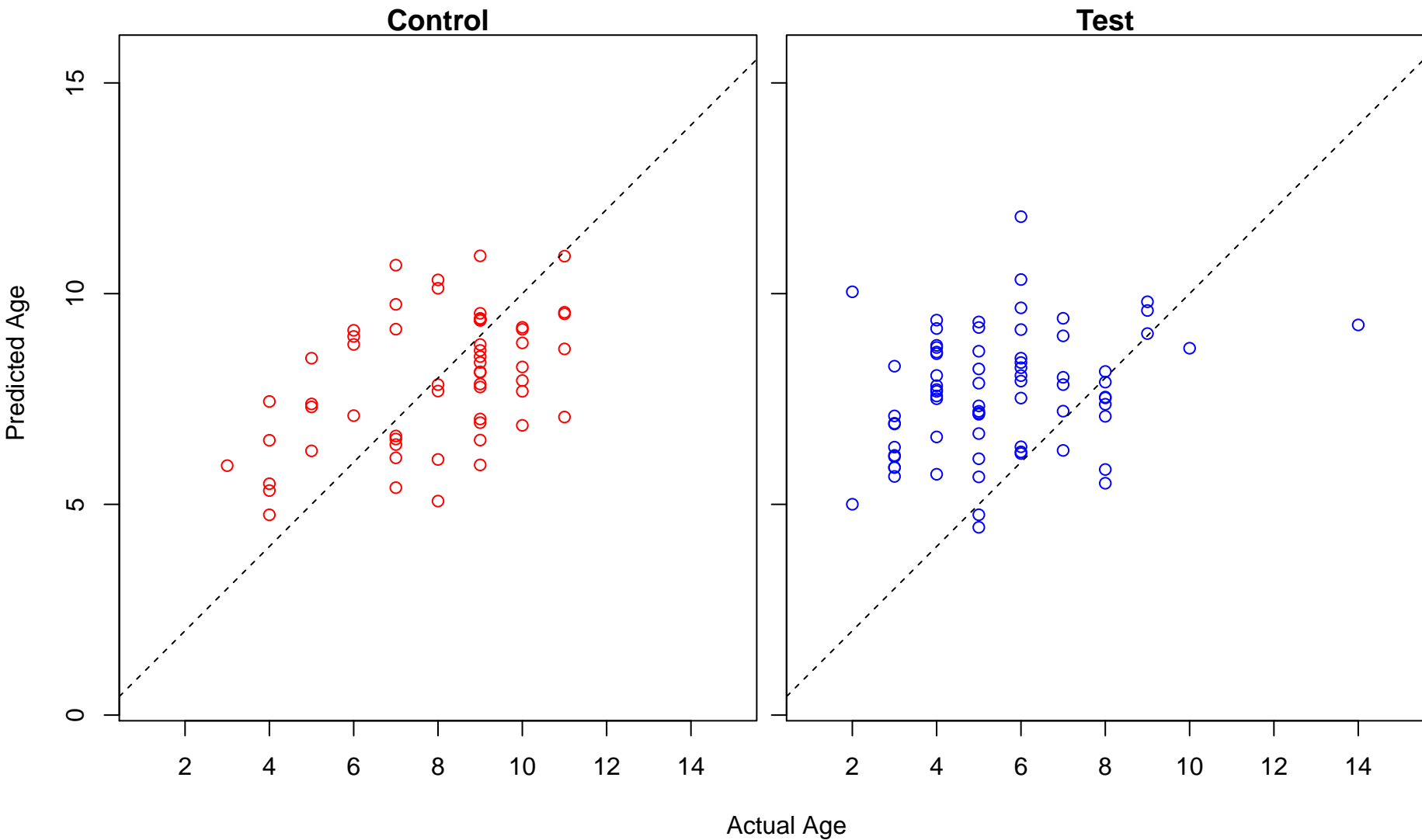
platelet activation (Score: 0.957957)



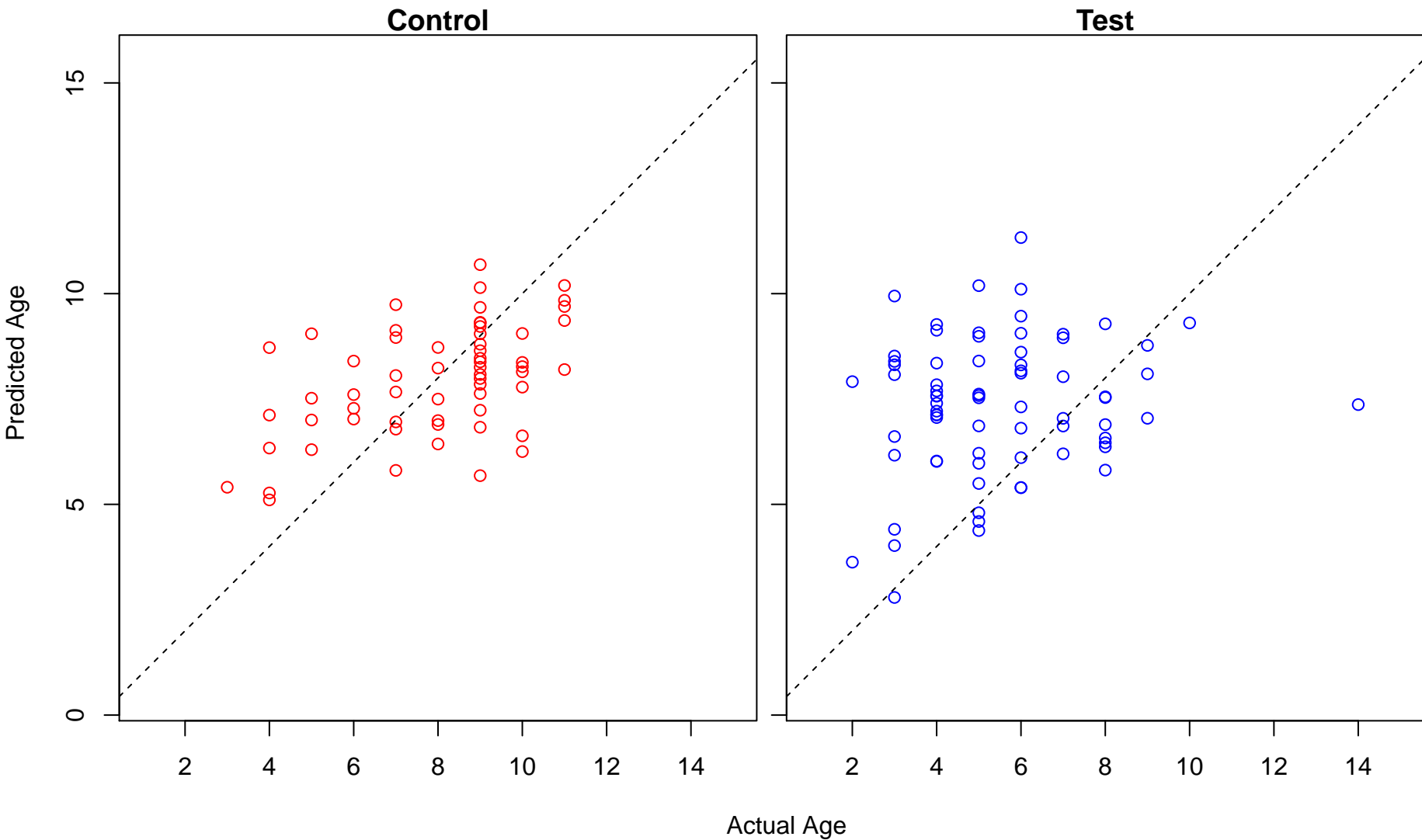
regulation of astrocyte differentiation (Score: 0.957885)



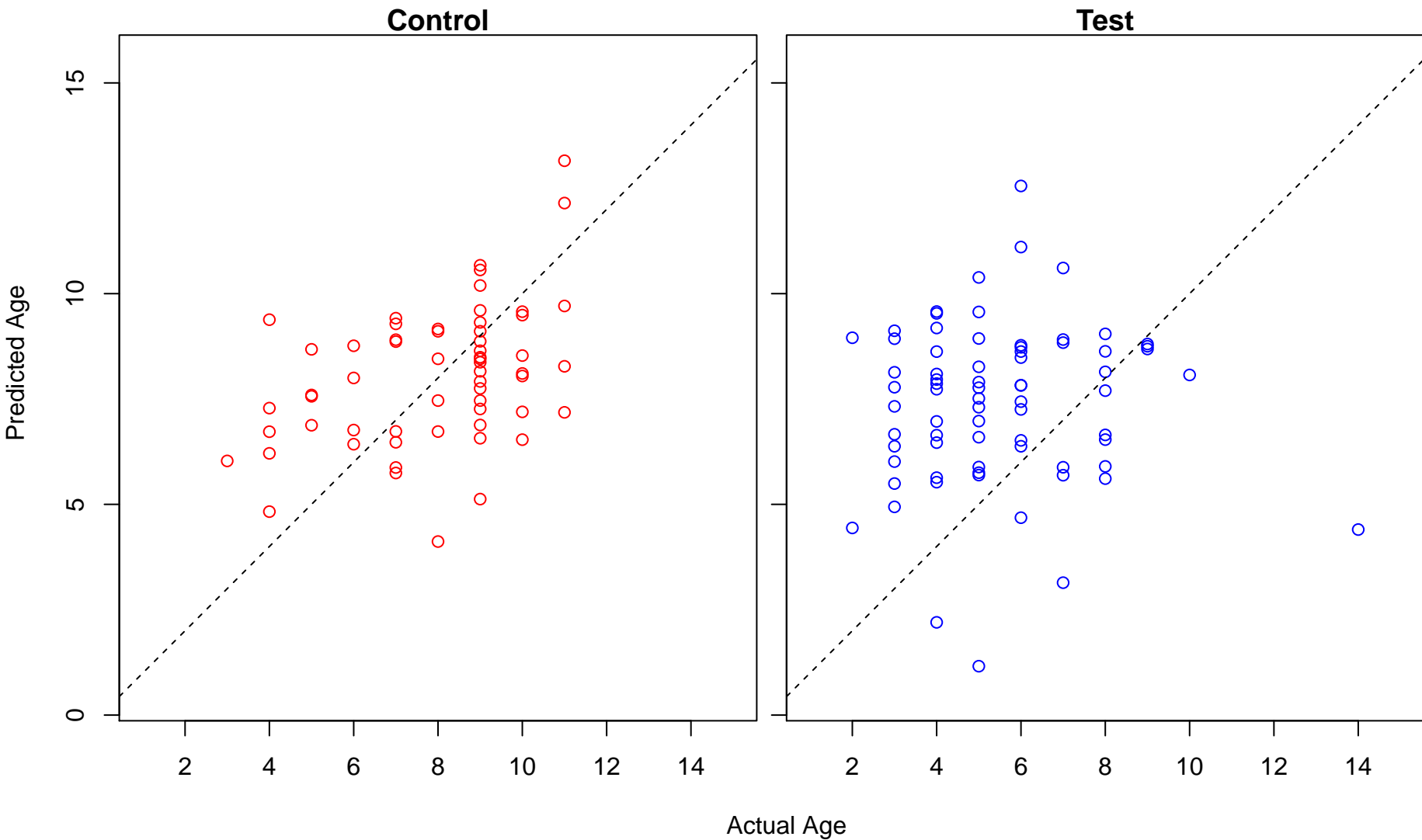
positive regulation of protein metabolic process (Score: 0.956182)



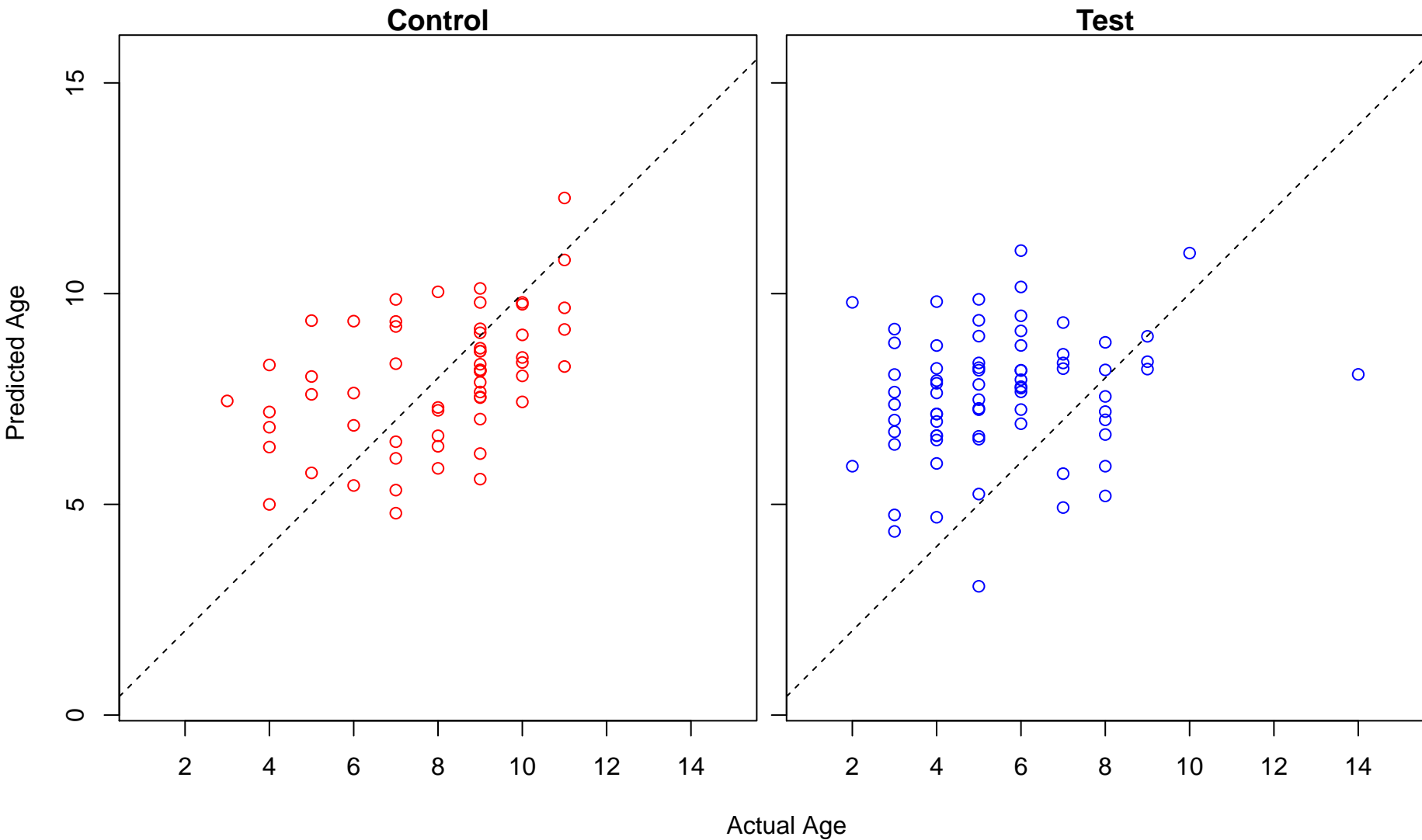
notochord morphogenesis (Score: 0.955939)



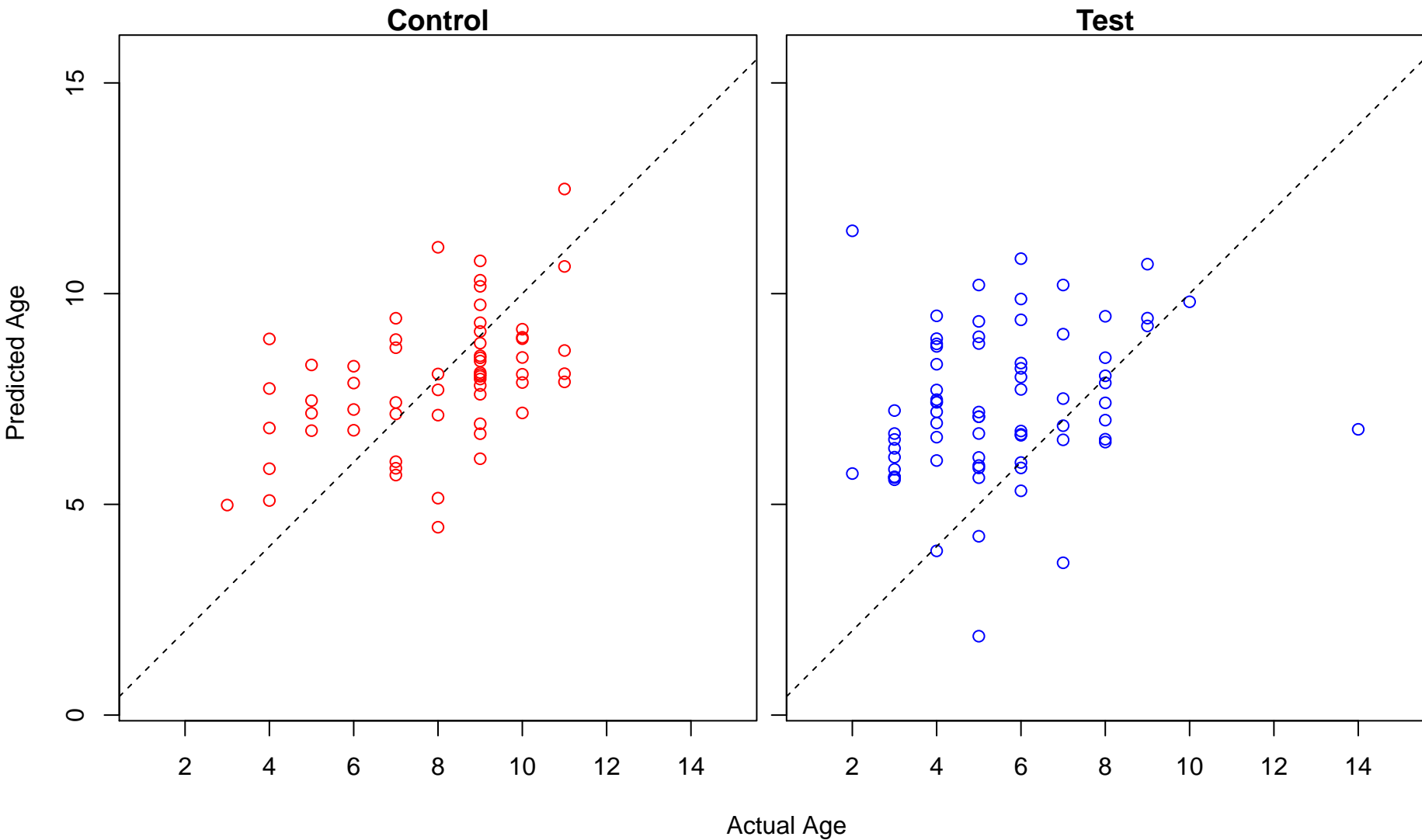
negative regulation of protein phosphorylation (Score: 0.954495)



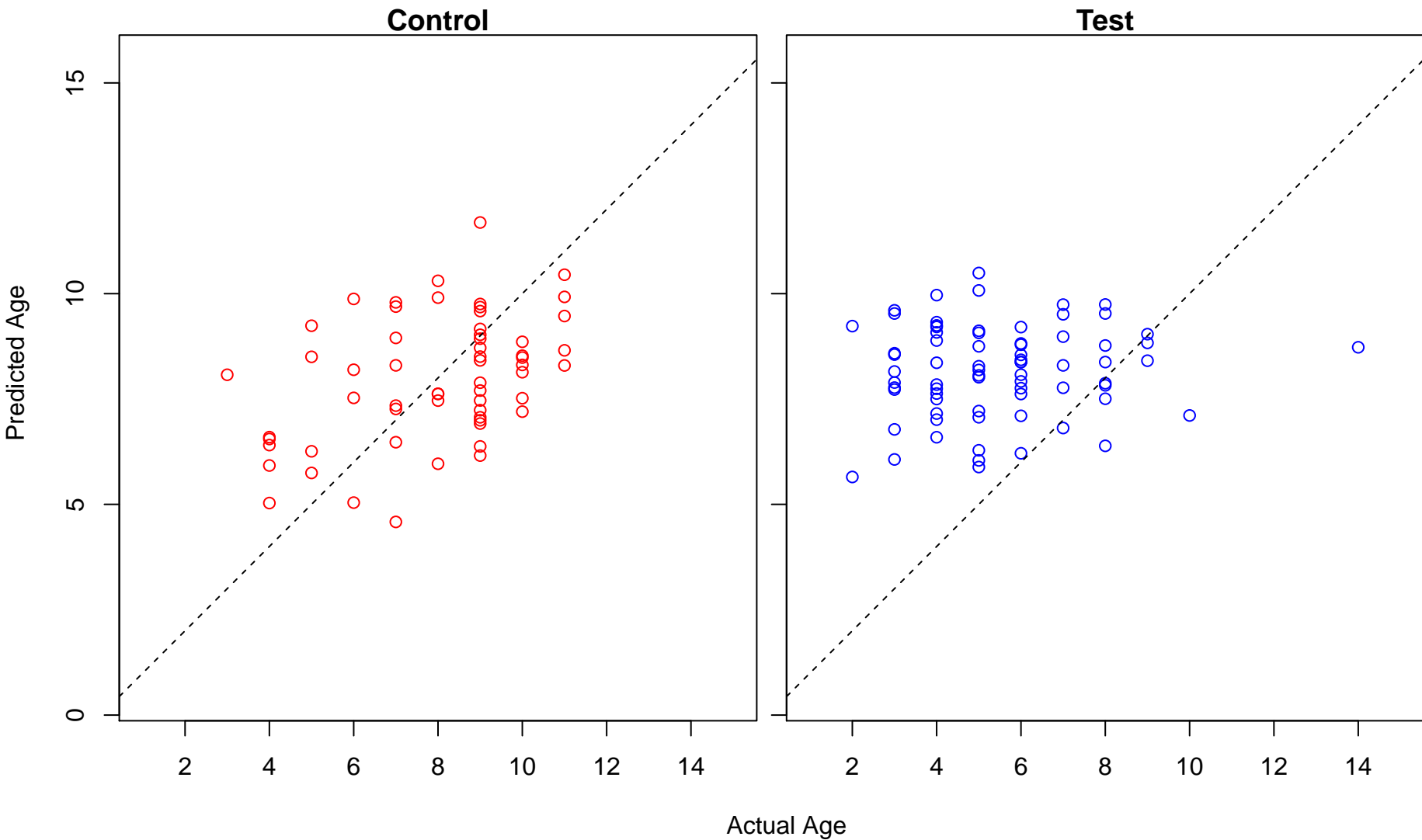
cellular biosynthetic process (Score: 0.954256)



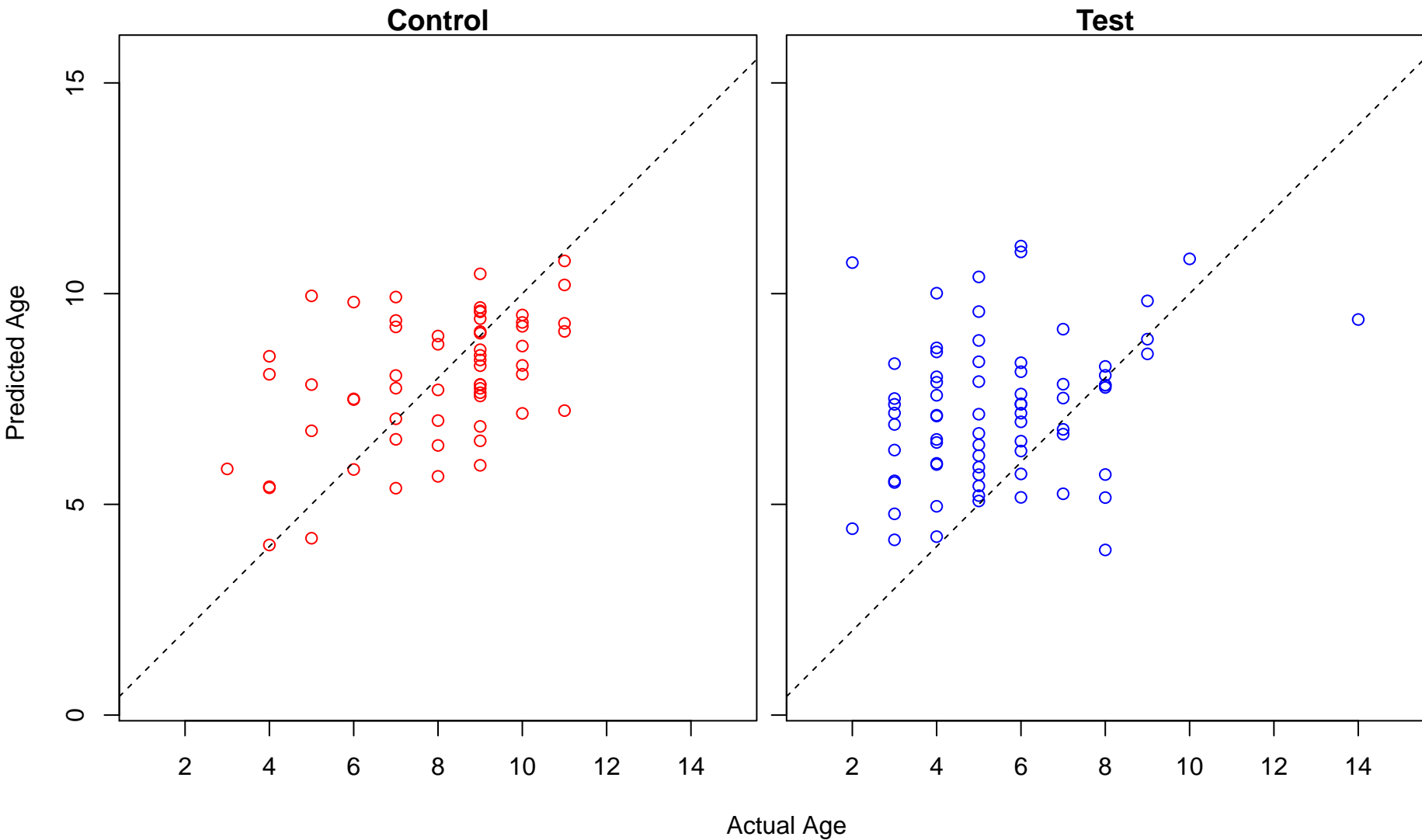
positive regulation of biological process (Score: 0.953352)



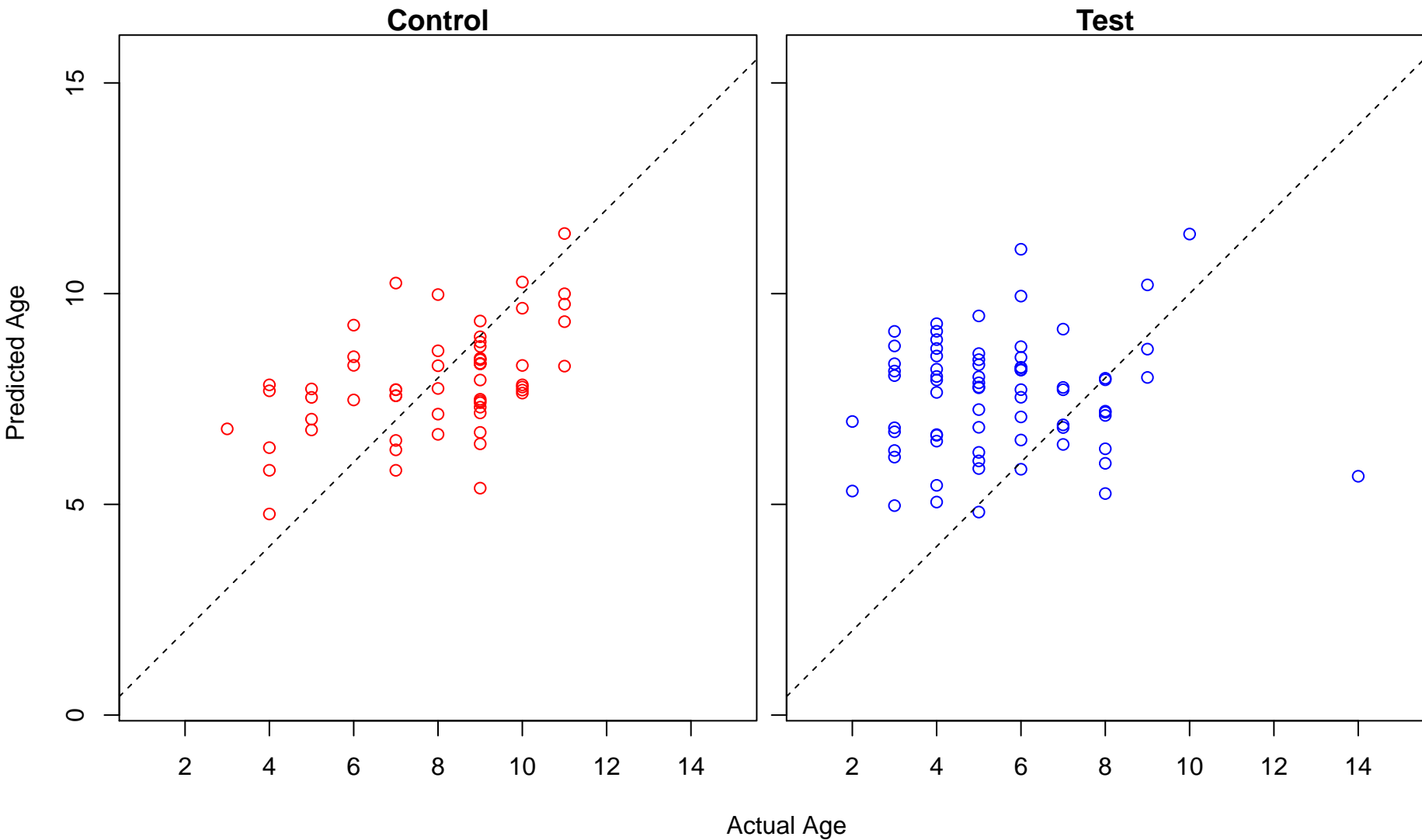
regulation of cellular senescence (Score: 0.953112)



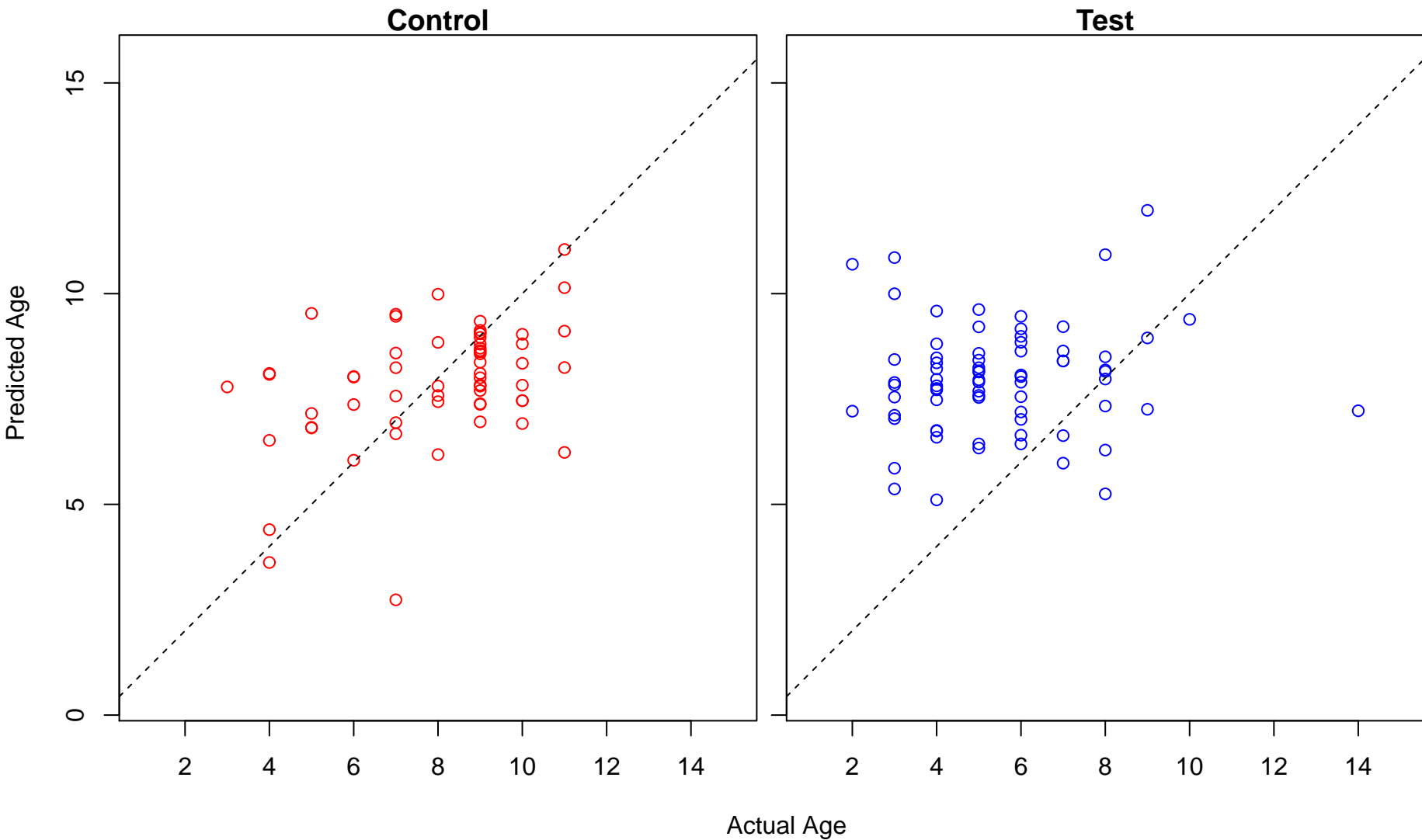
ion transmembrane transport (Score: 0.951980)



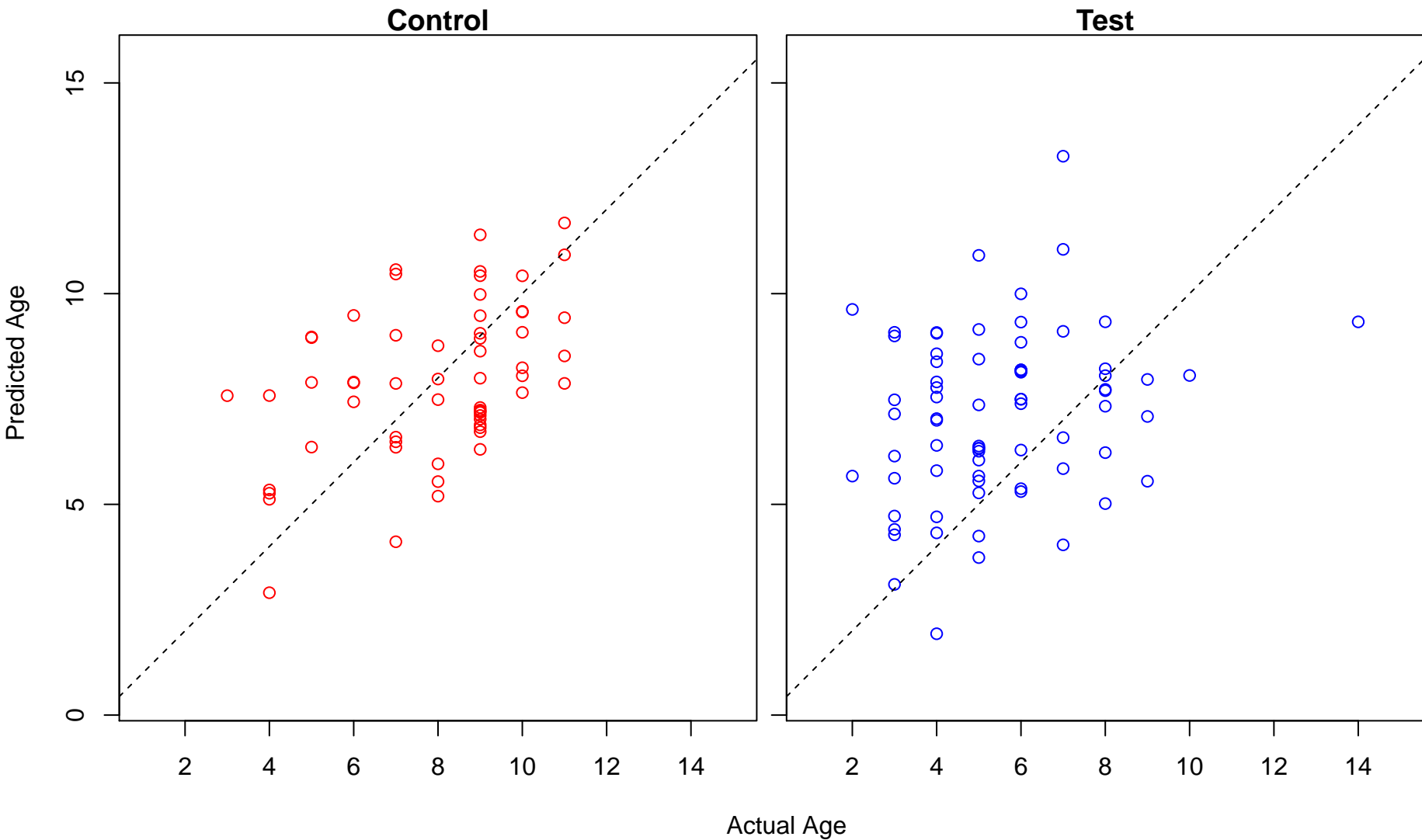
regulation of T-helper 2 cell differentiation (Score: 0.951737)



Leydig cell differentiation (Score: 0.950273)

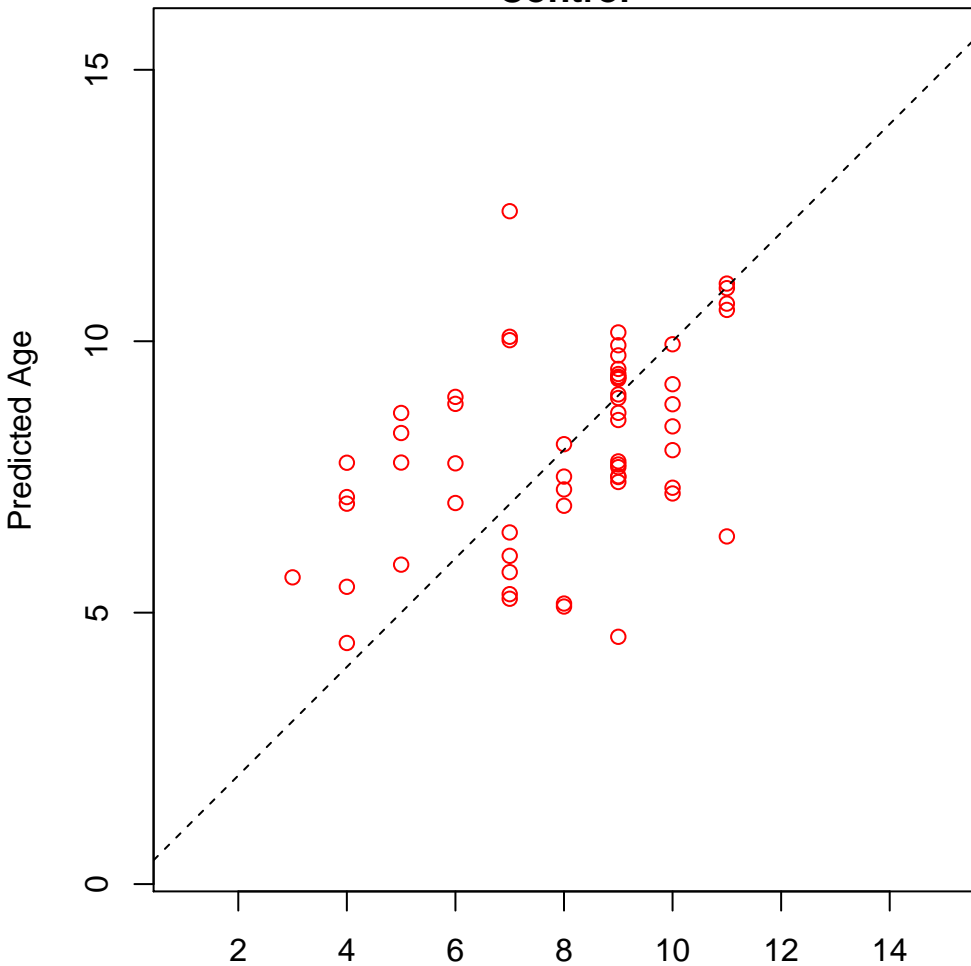


mitotic DNA integrity checkpoint (Score: 0.949550)

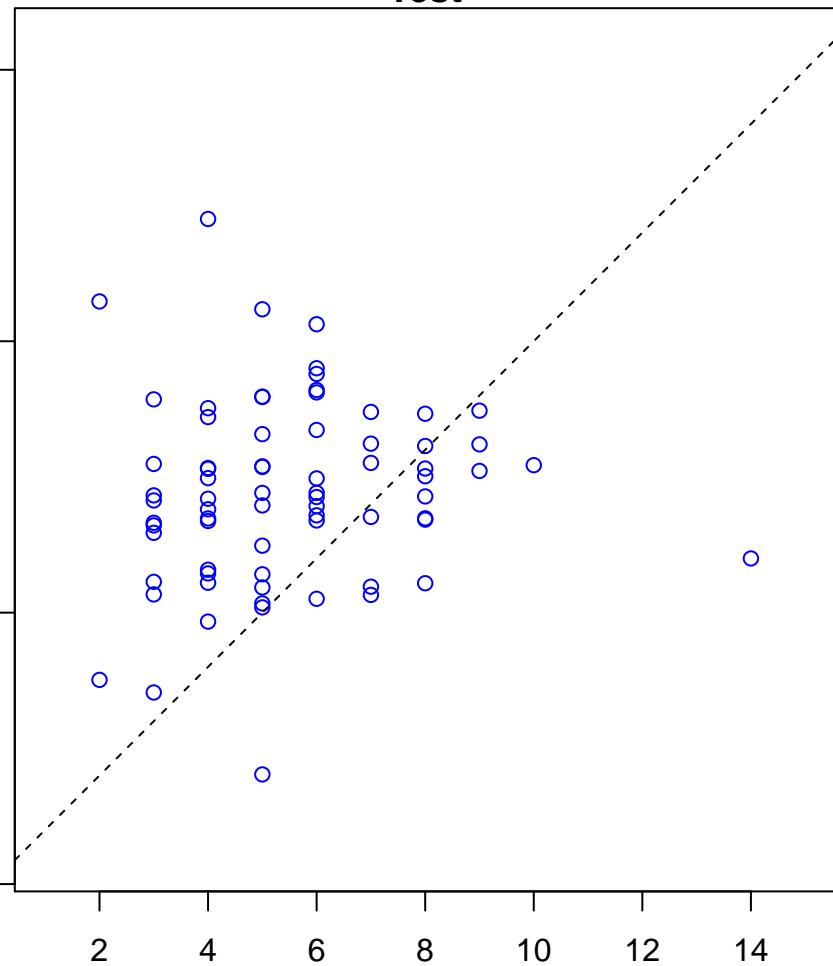


regulation of protein catabolic process (Score: 0.949313)

Control

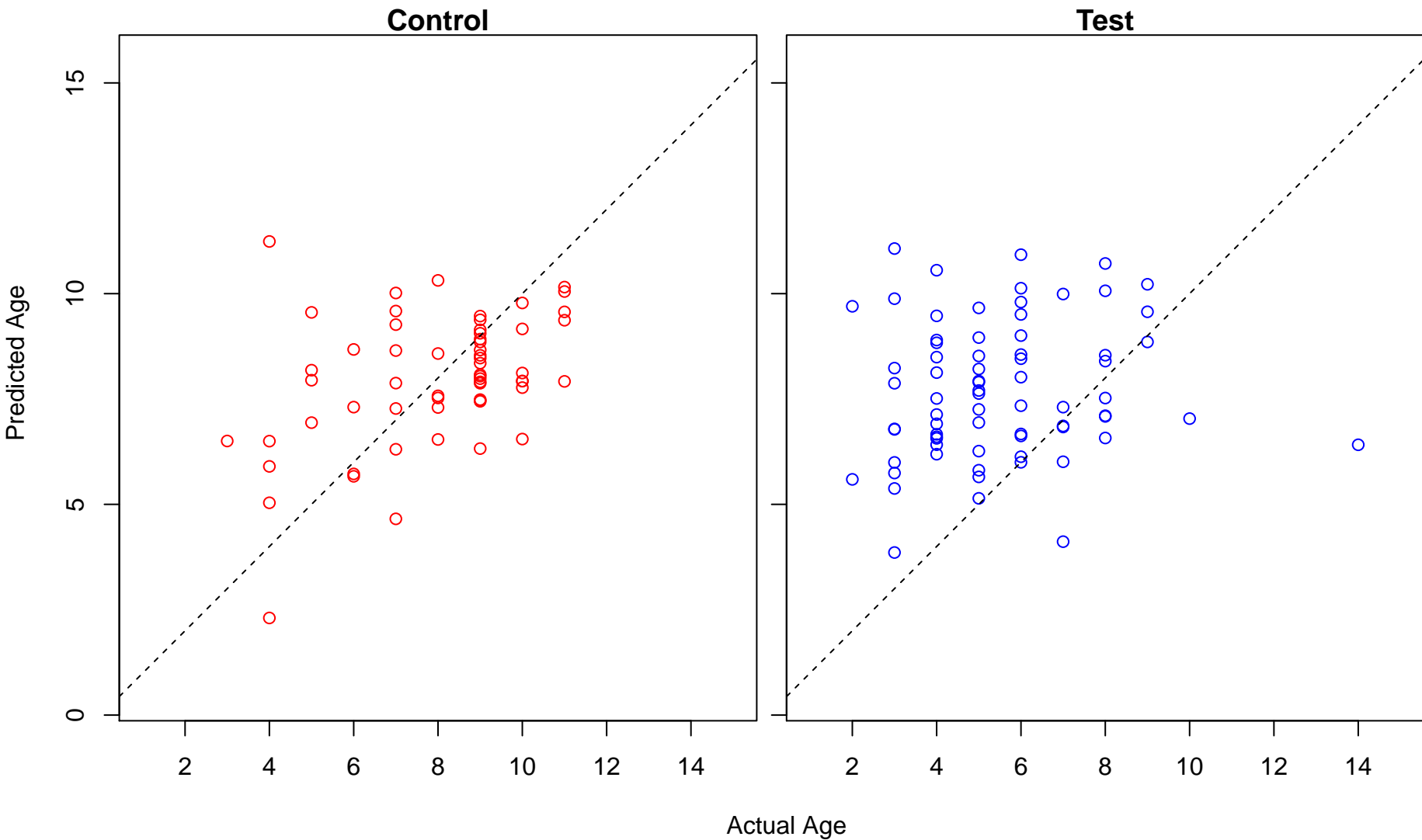


Test

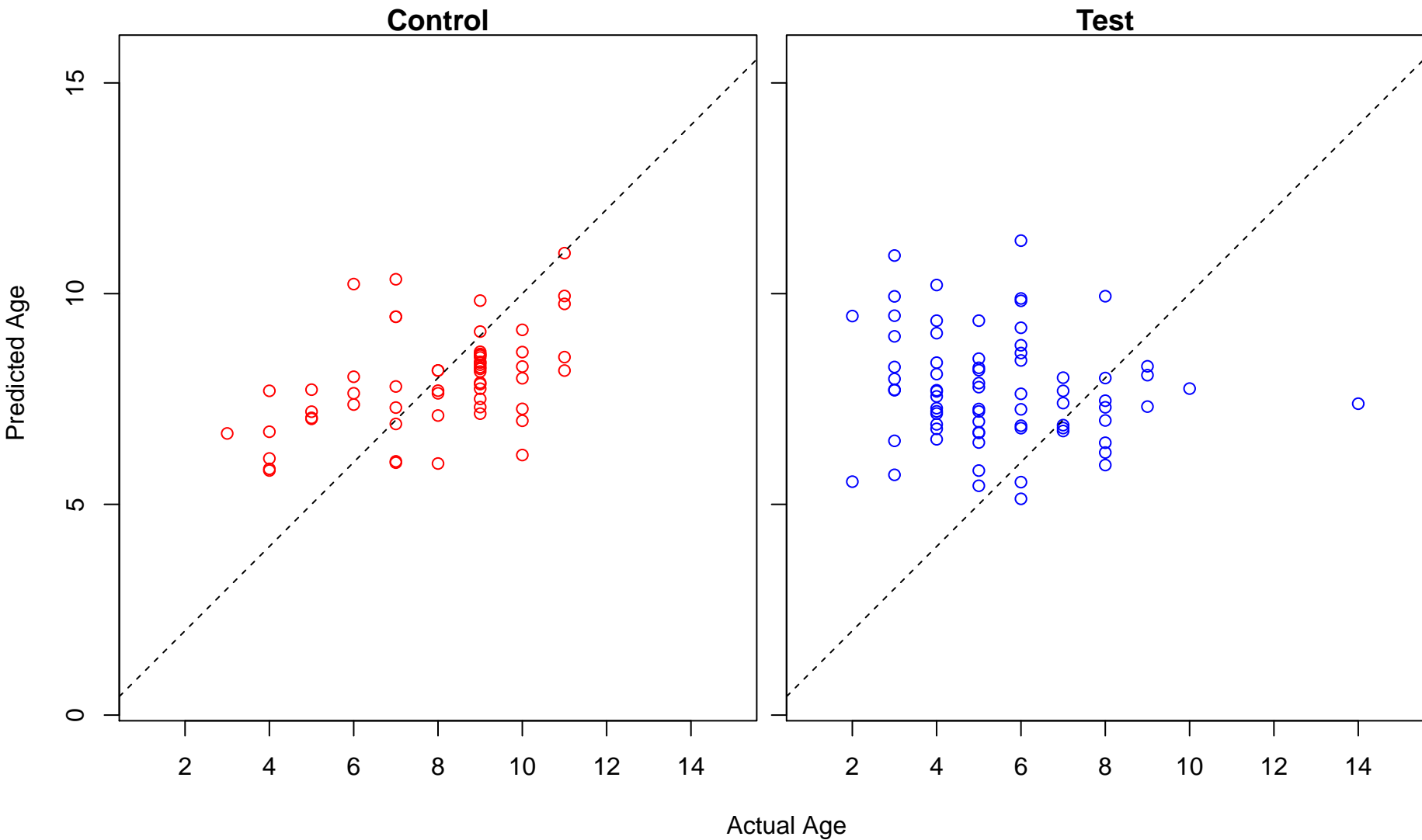


Actual Age

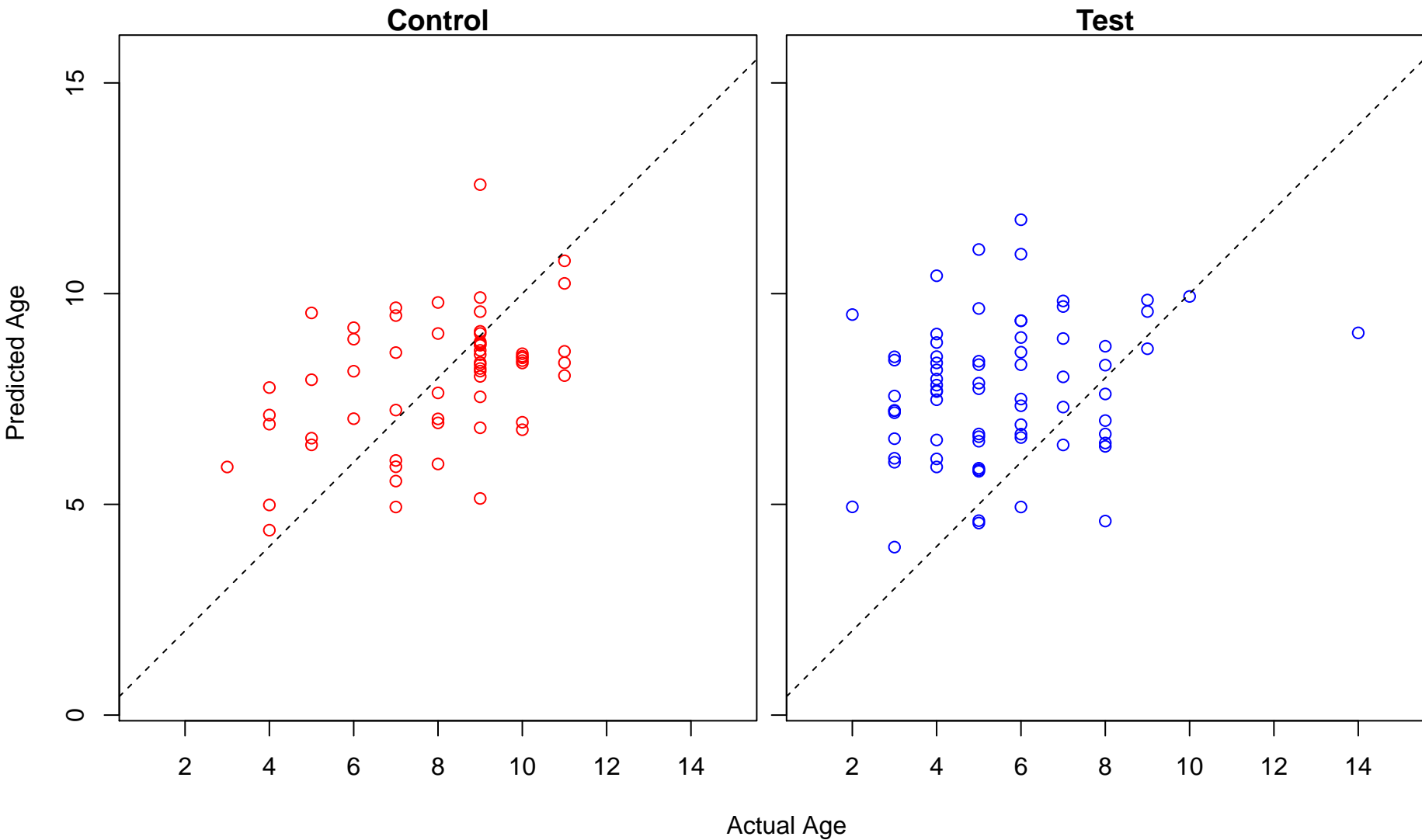
negative regulation of fat cell differentiation (Score: 0.949173)



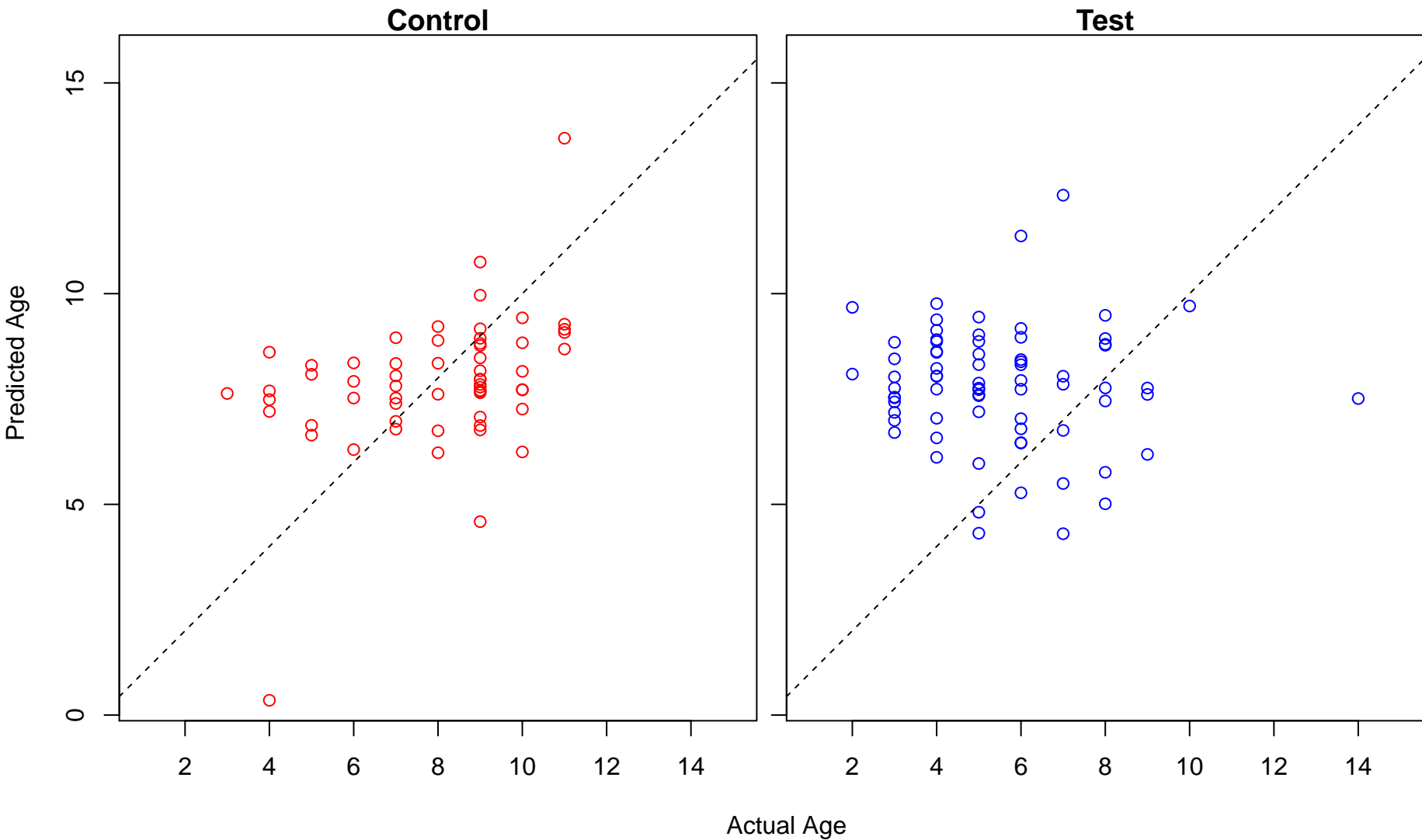
actin cytoskeleton reorganization (Score: 0.948985)



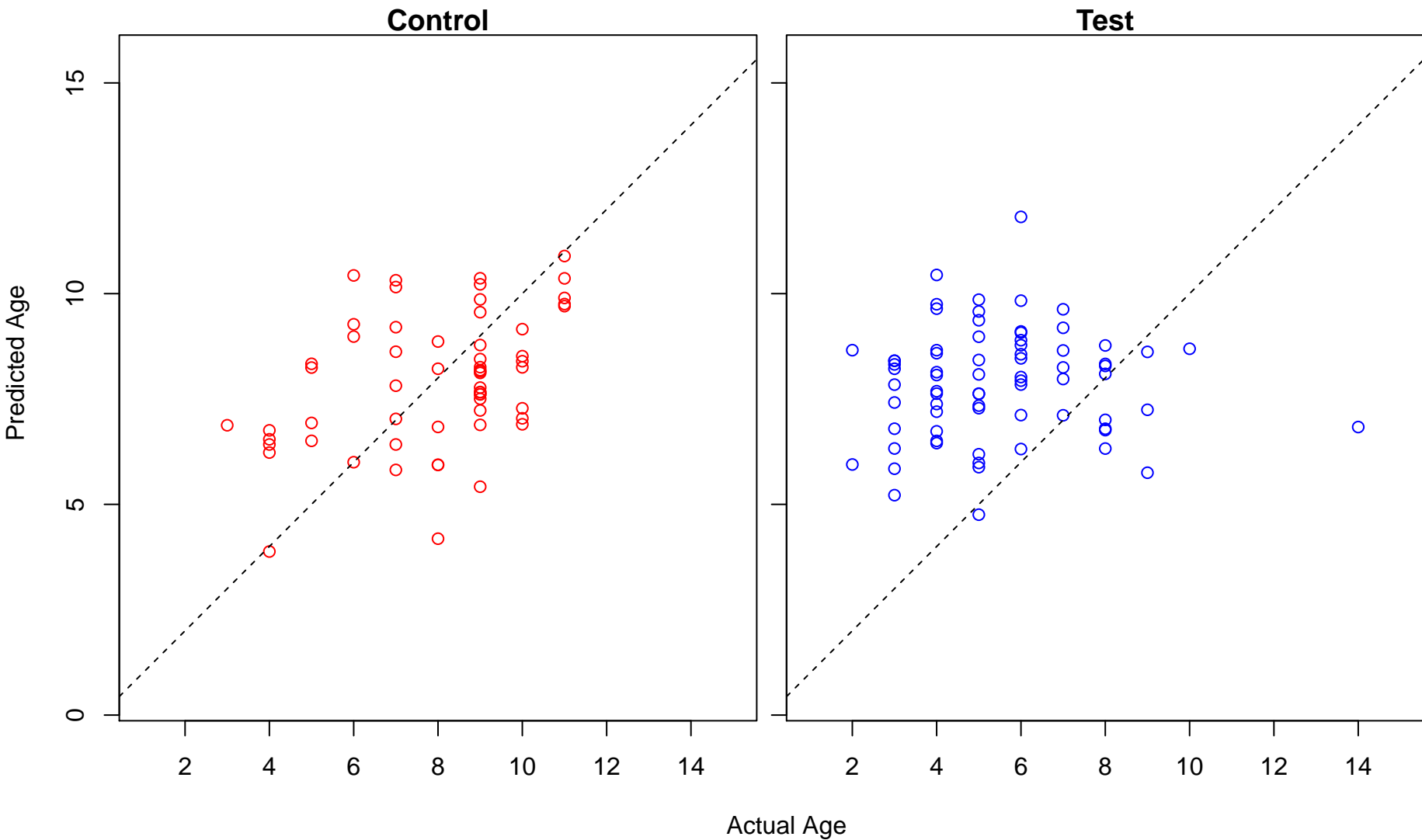
axonogenesis (Score: 0.948222)



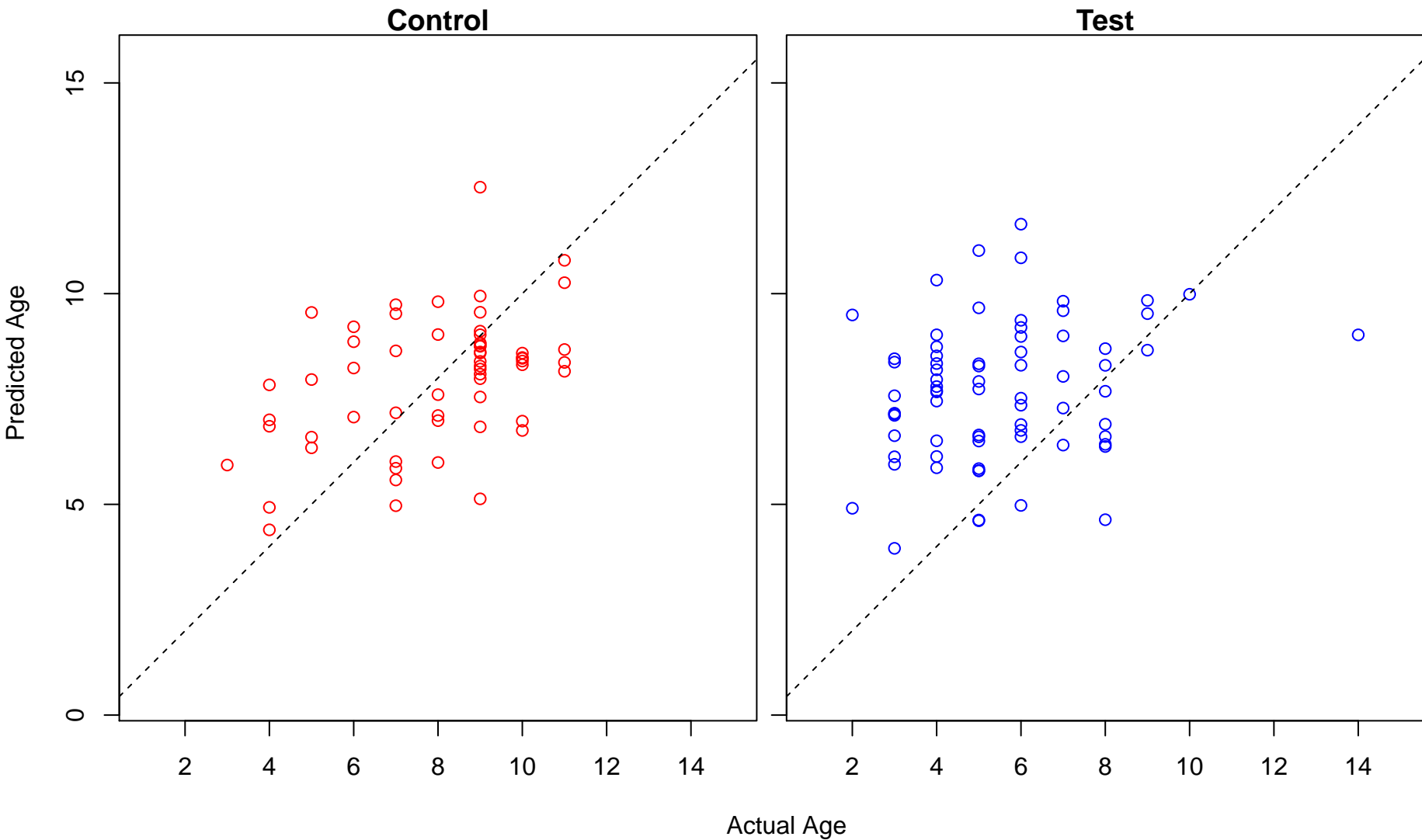
dopamine metabolic process (Score: 0.947013)



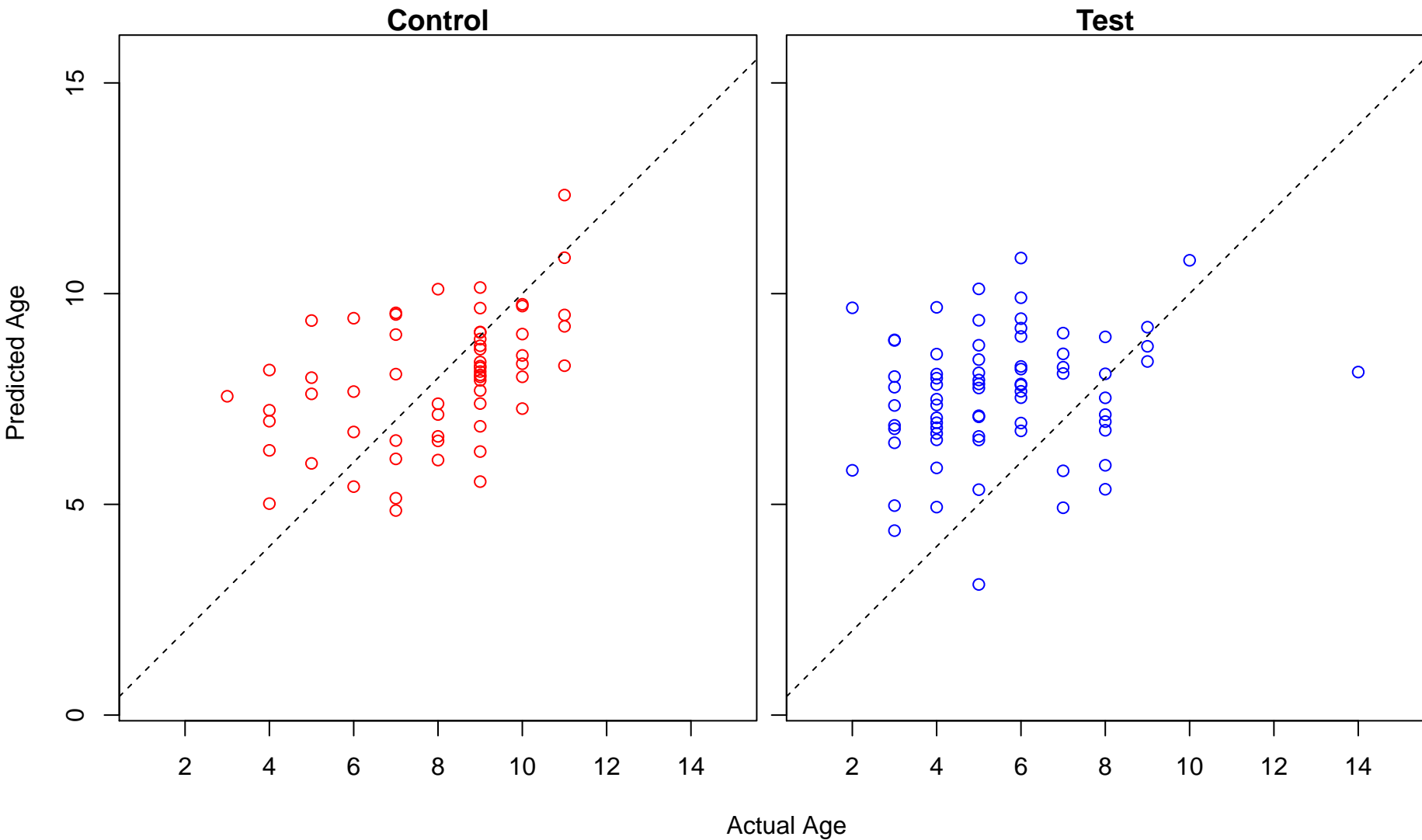
cell proliferation in forebrain (Score: 0.946620)



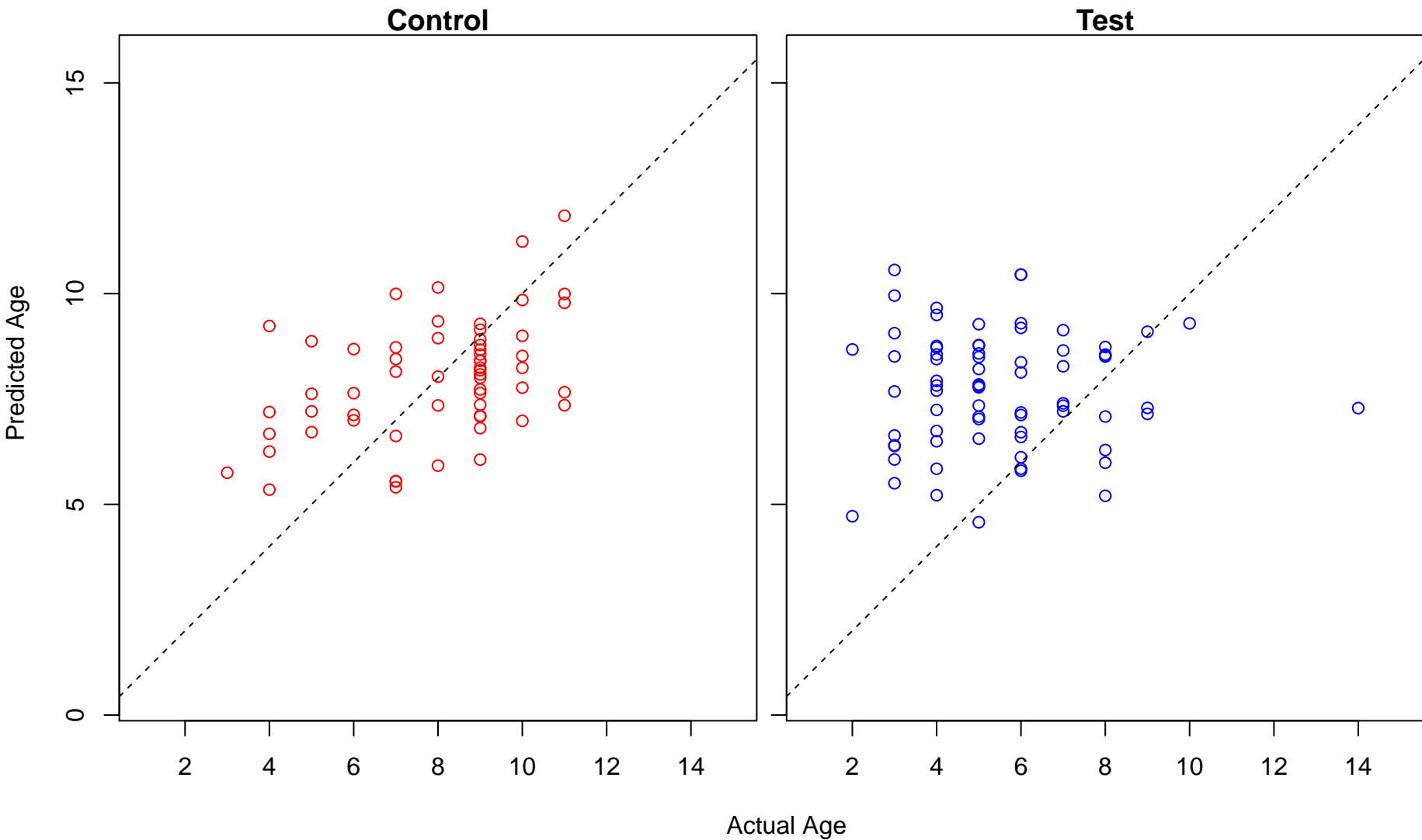
cell morphogenesis involved in neuron differentiation (Score: 0.945550)



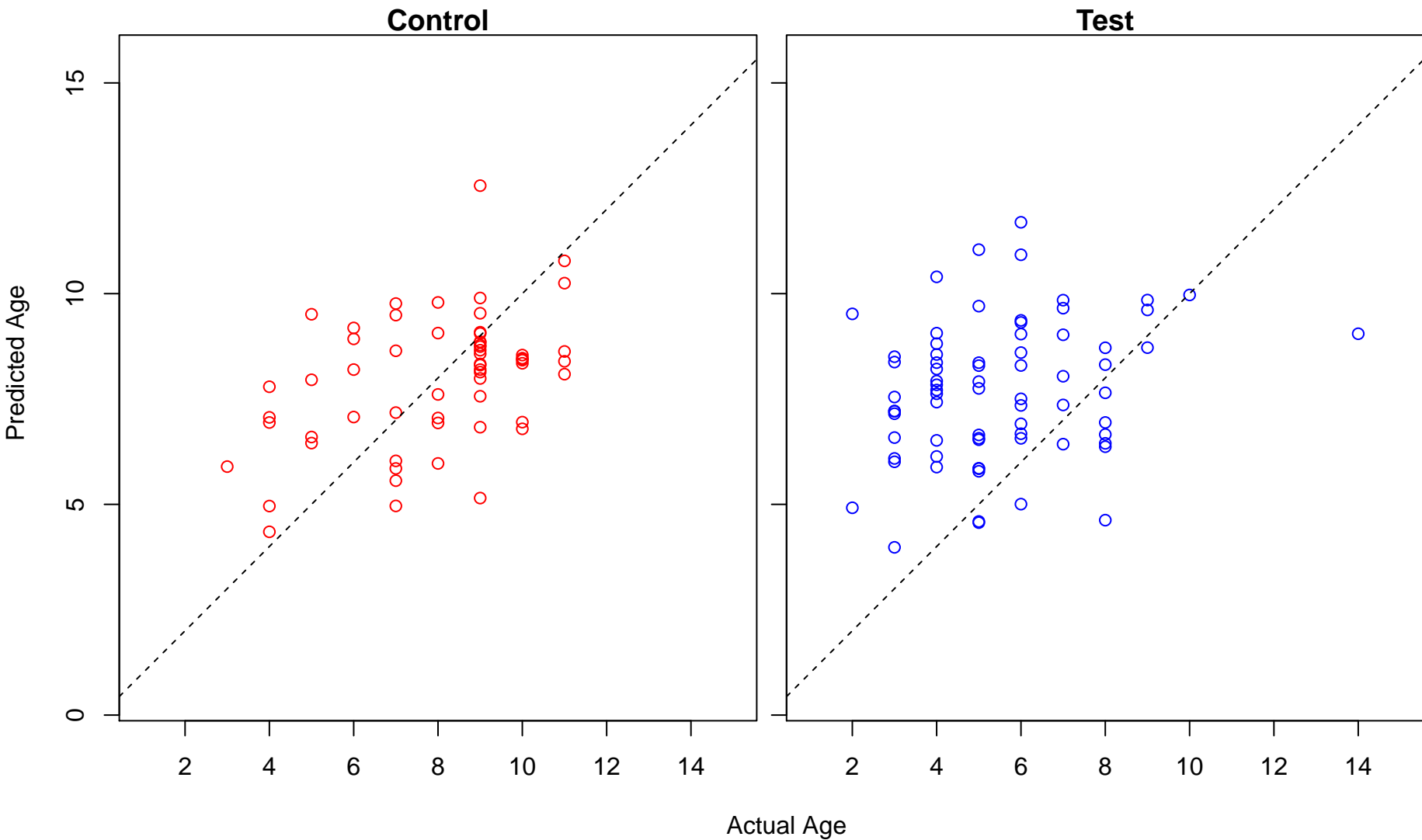
biosynthetic process (Score: 0.943700)



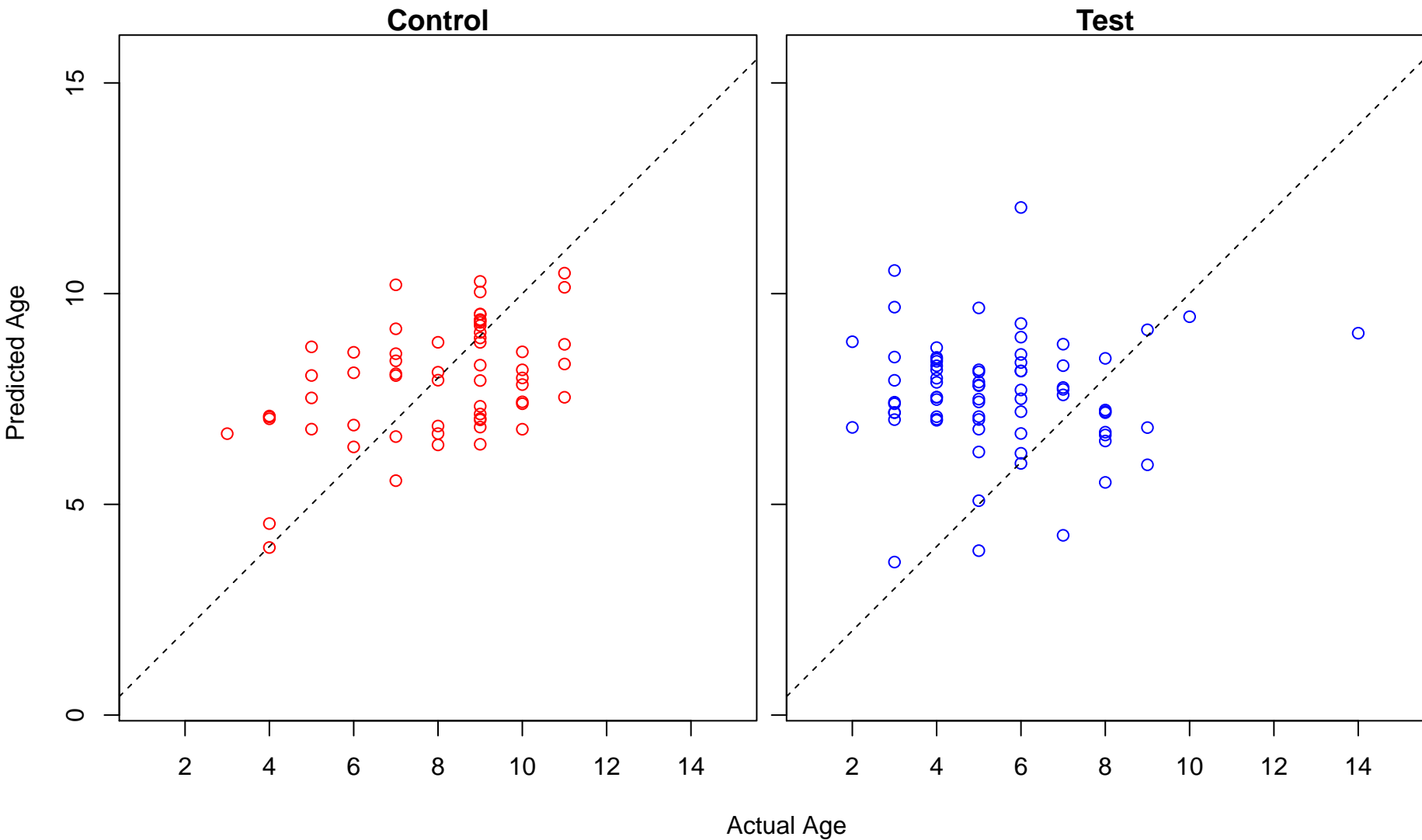
peptidyl-lysine trimethylation (Score: 0.943688)



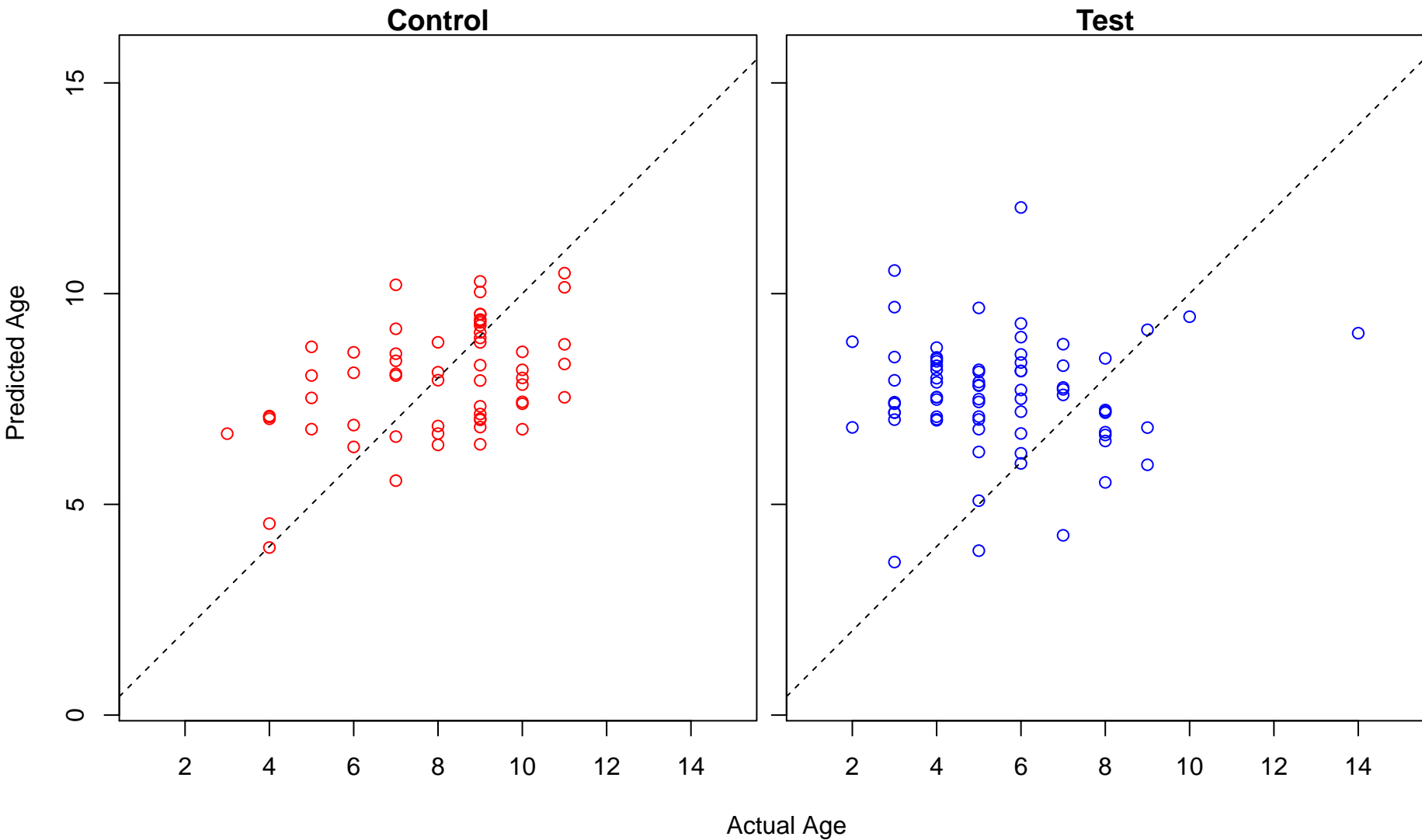
neuron projection morphogenesis (Score: 0.943434)



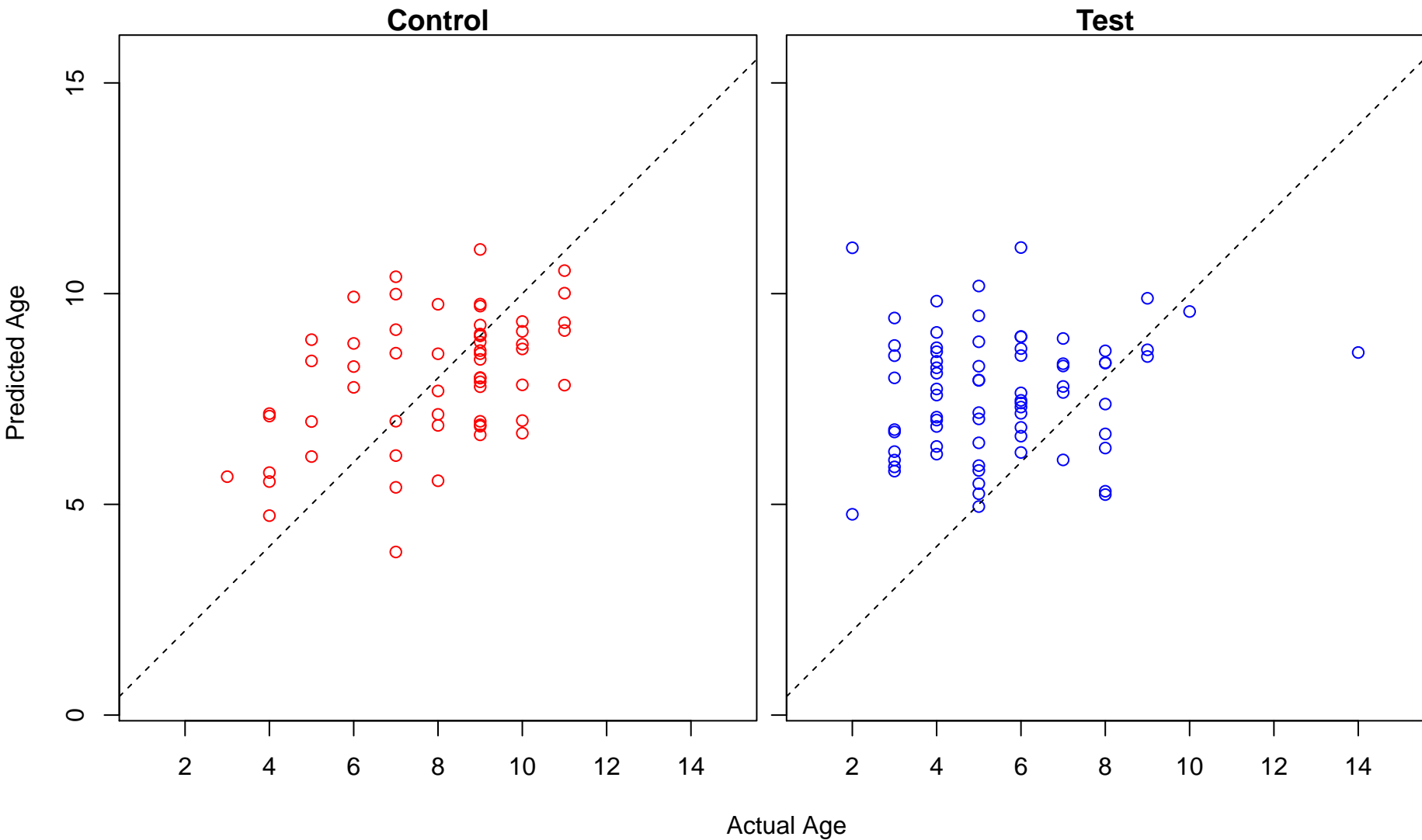
regulation of dendritic cell chemotaxis (Score: 0.943361)



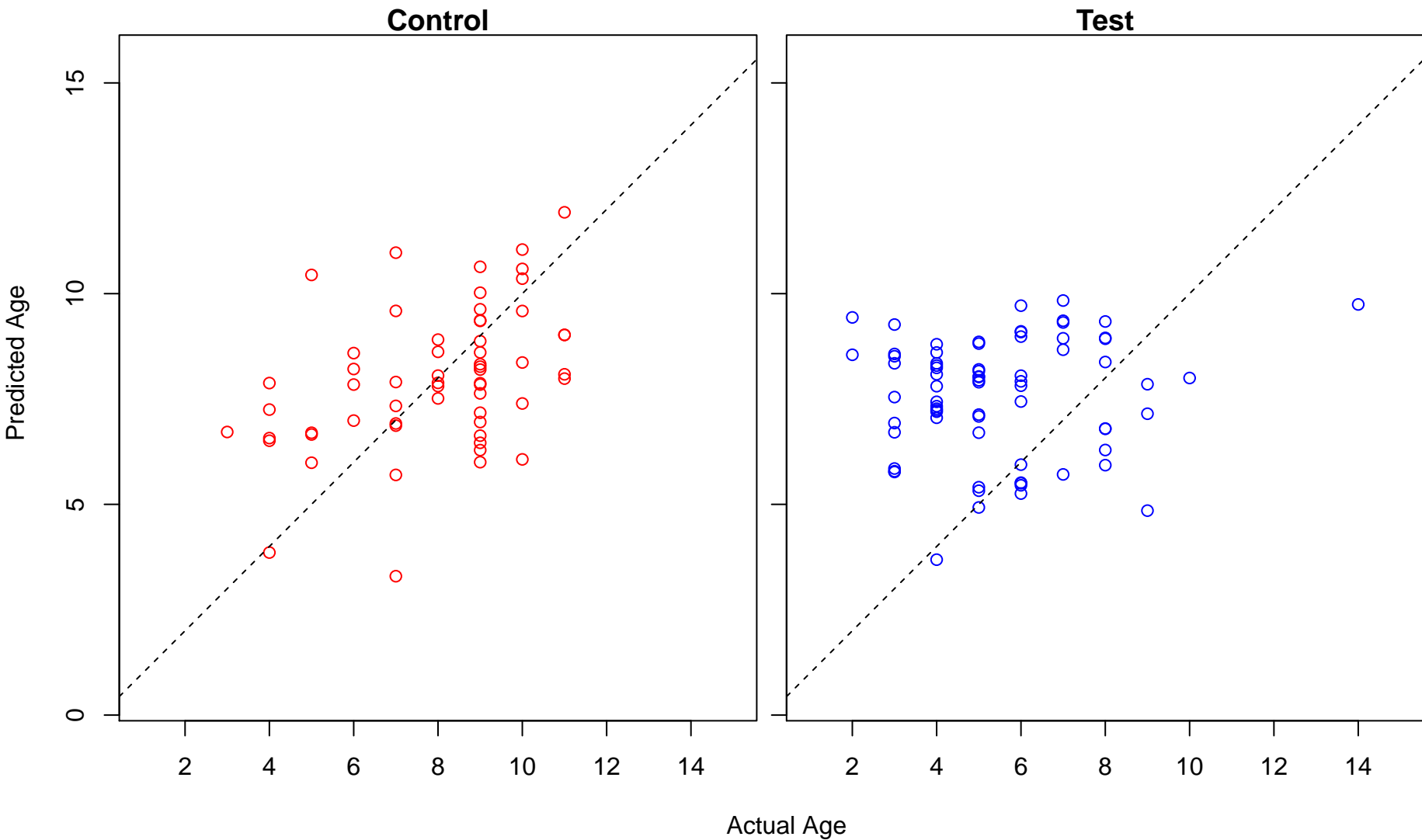
positive regulation of dendritic cell chemotaxis (Score: 0.943361)



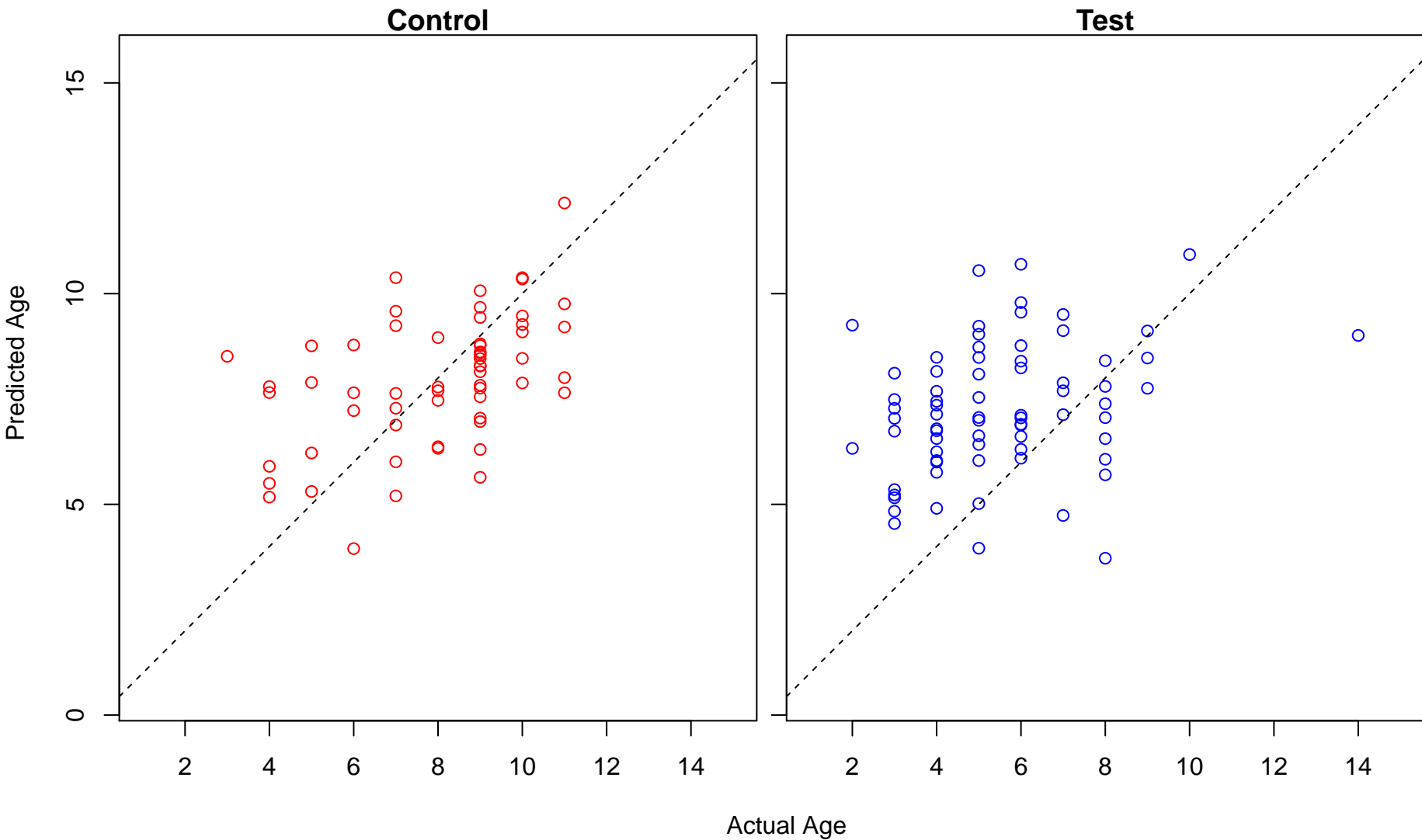
peptidyl-amino acid modification (Score: 0.943289)



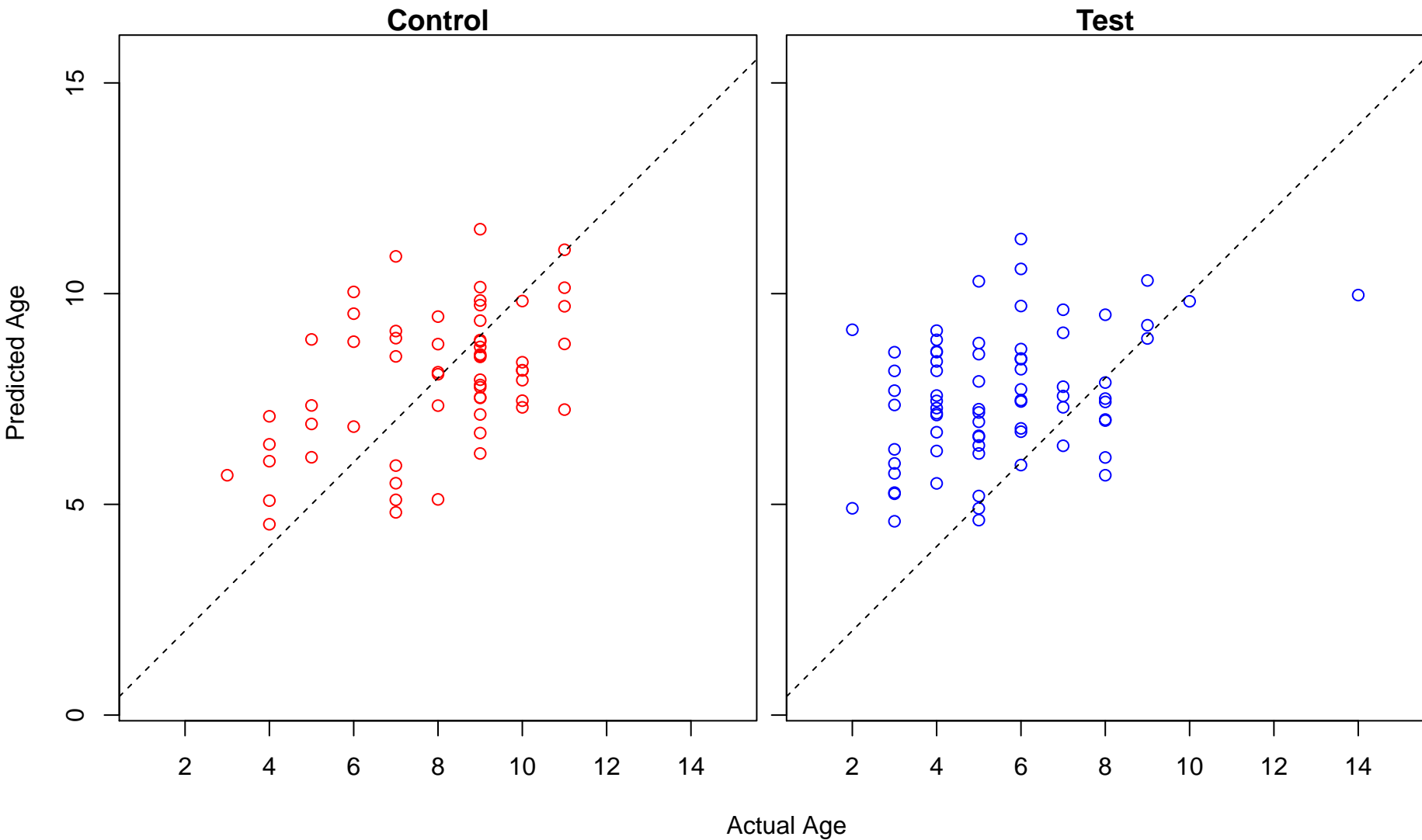
vacuolar acidification (Score: 0.942722)



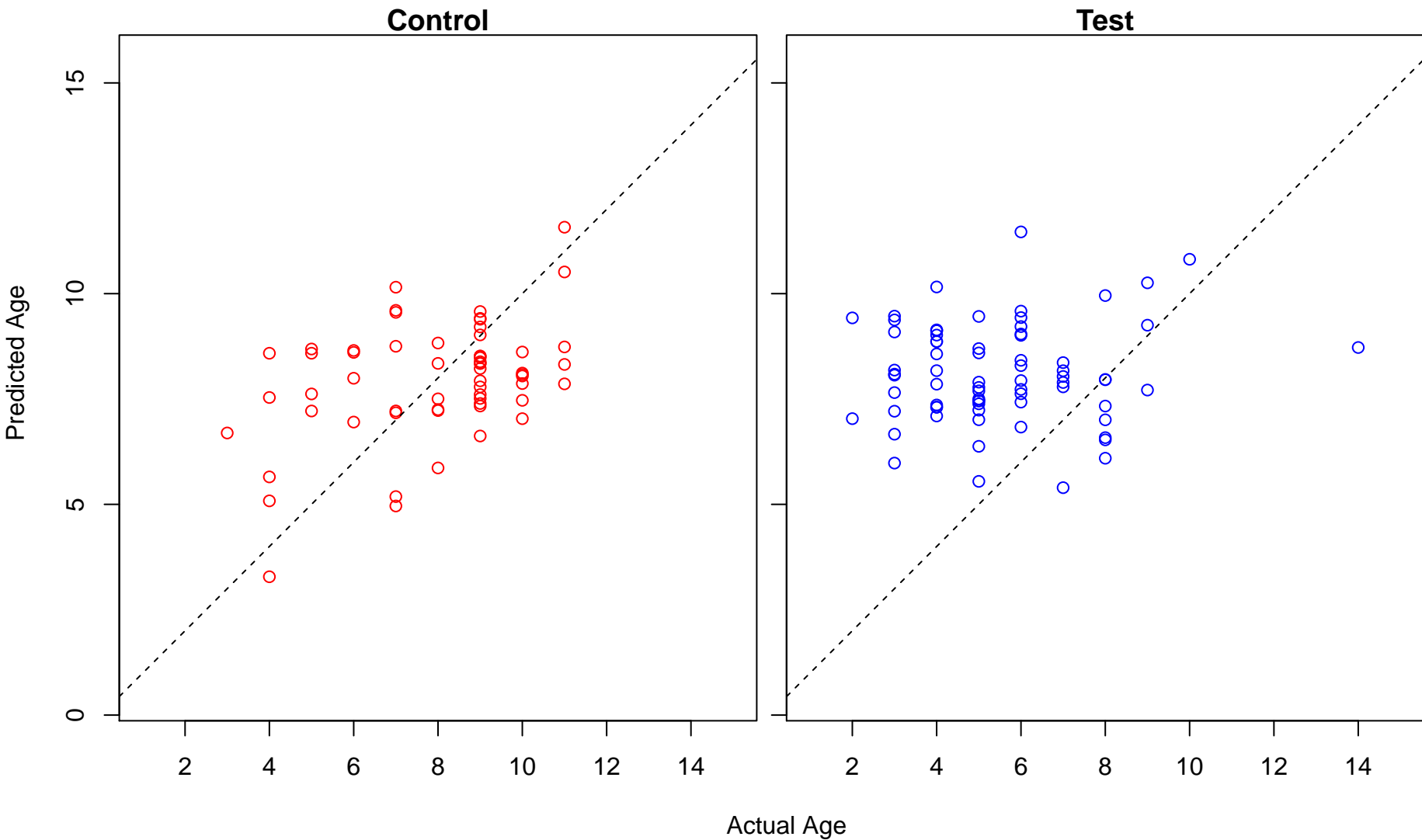
cellular component disassembly (Score: 0.941783)



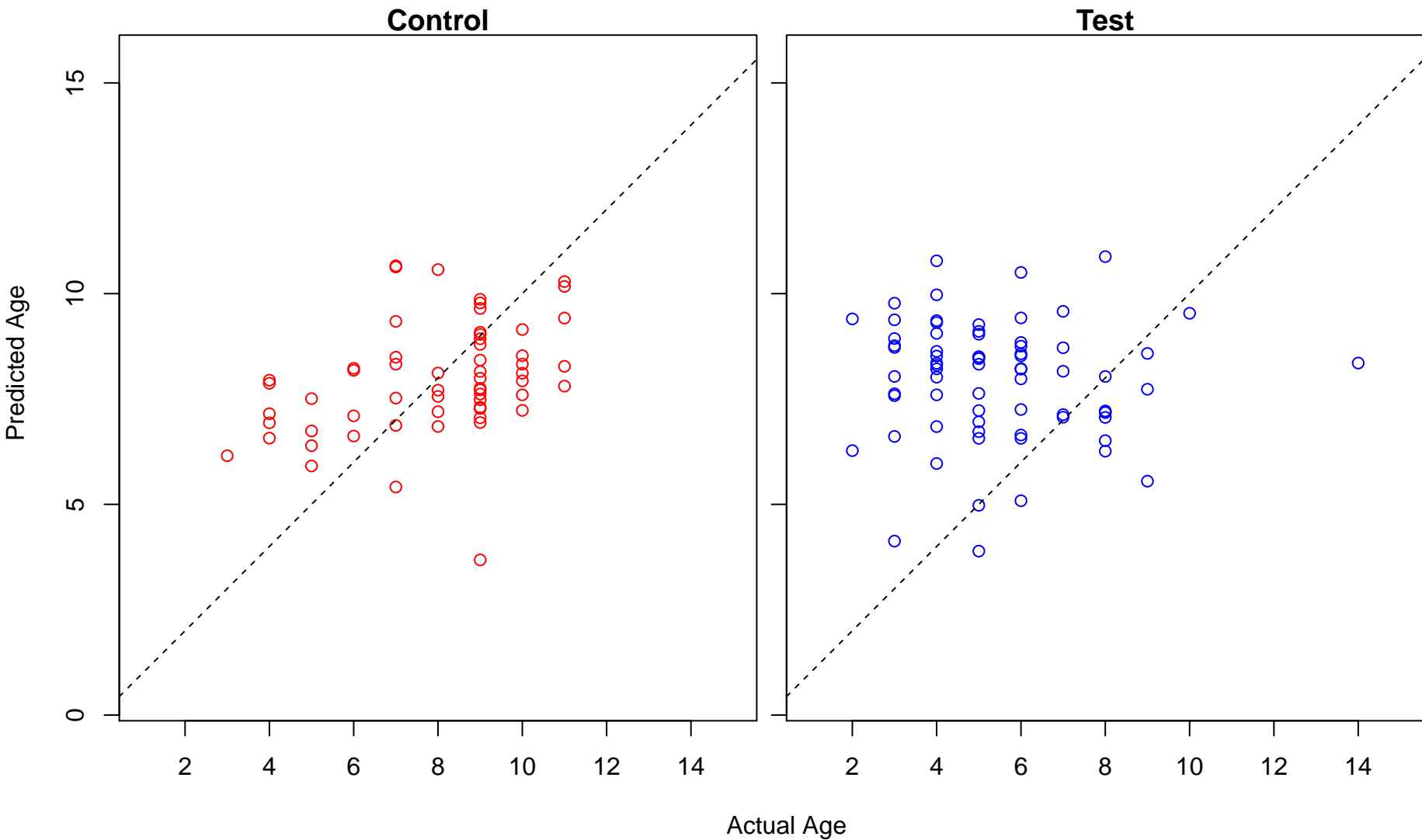
regulation of cell migration (Score: 0.941529)



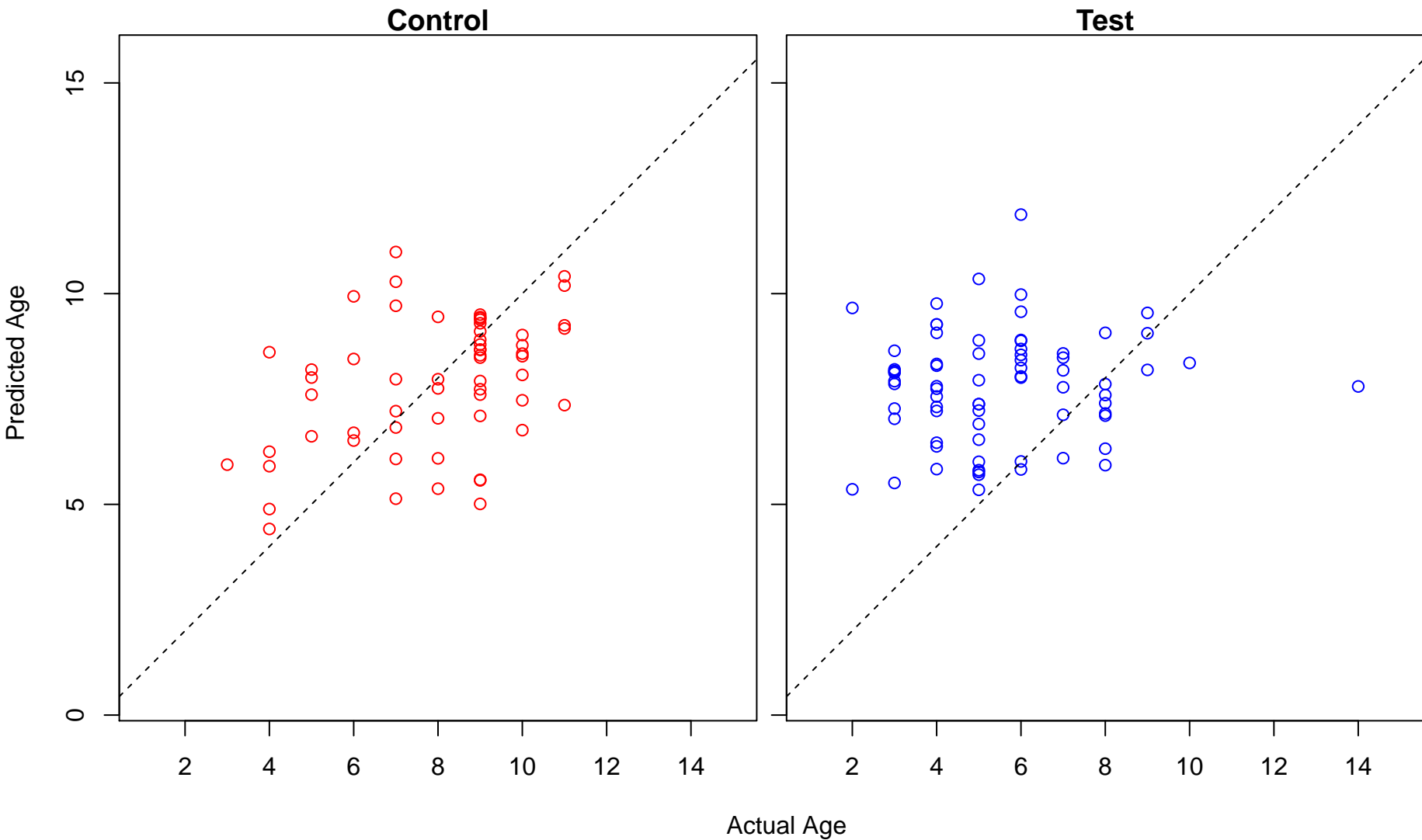
keratinocyte differentiation (Score: 0.940548)



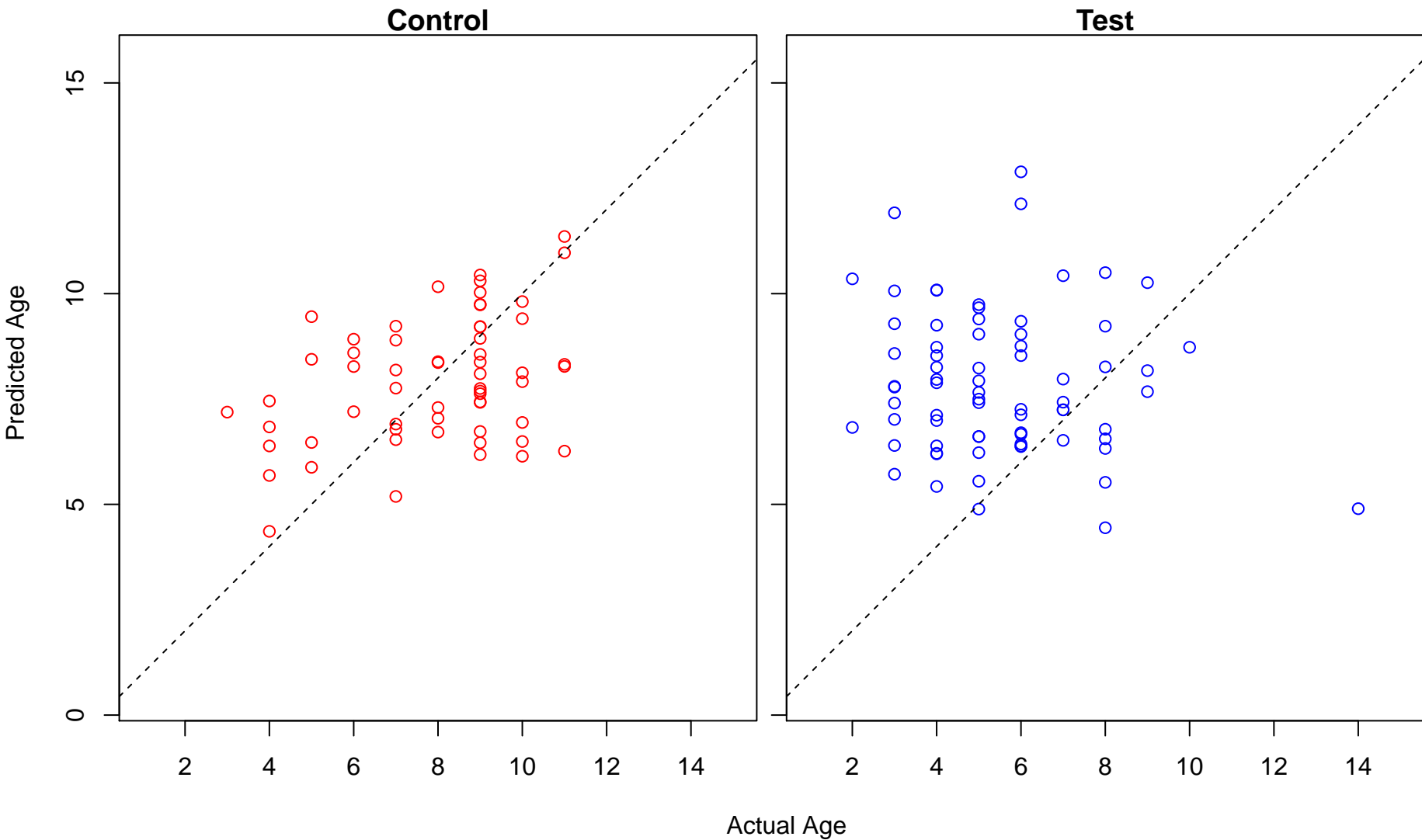
mitotic cell cycle arrest (Score: 0.940301)



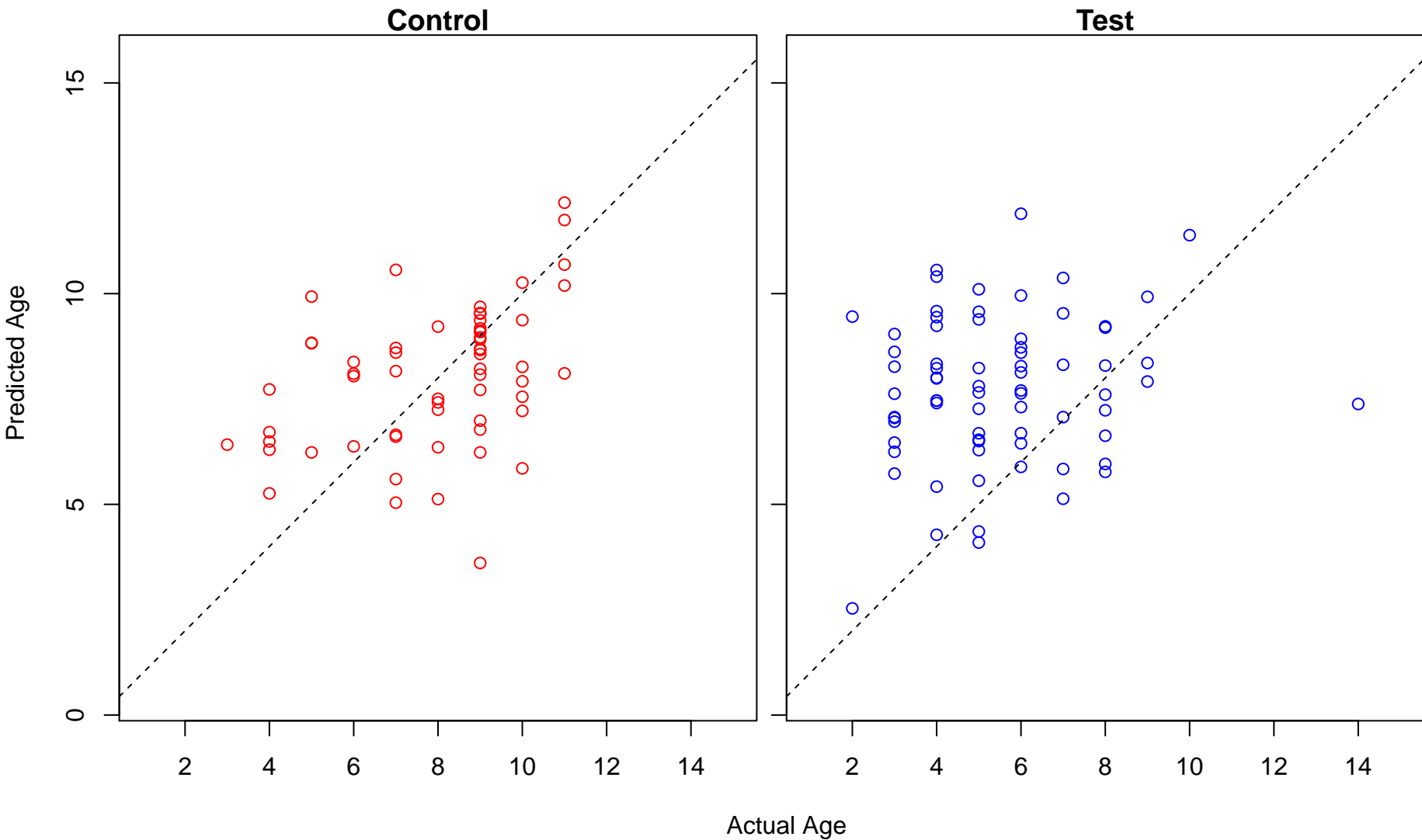
activation of MAPKK activity (Score: 0.940039)



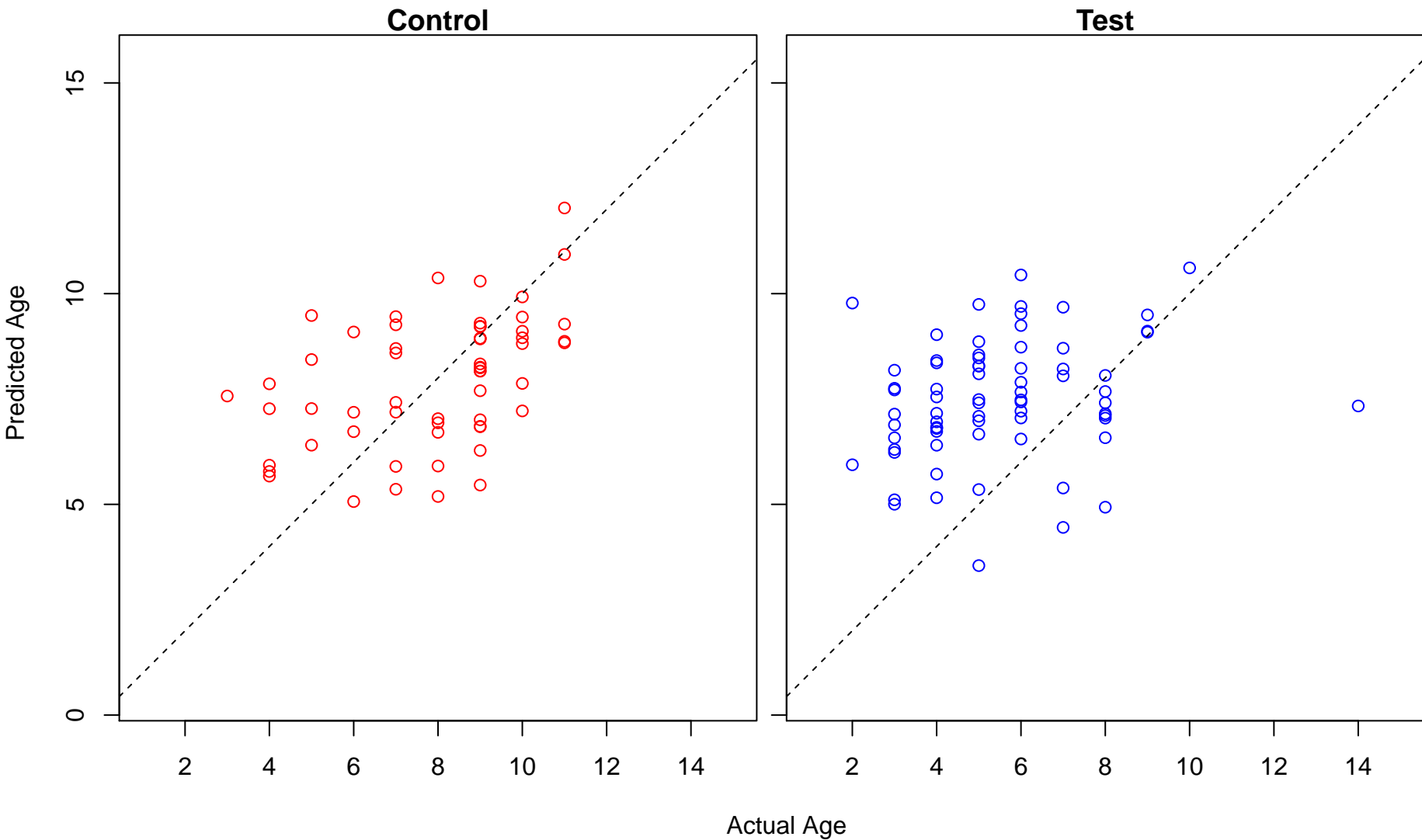
actin filament severing (Score: 0.939928)



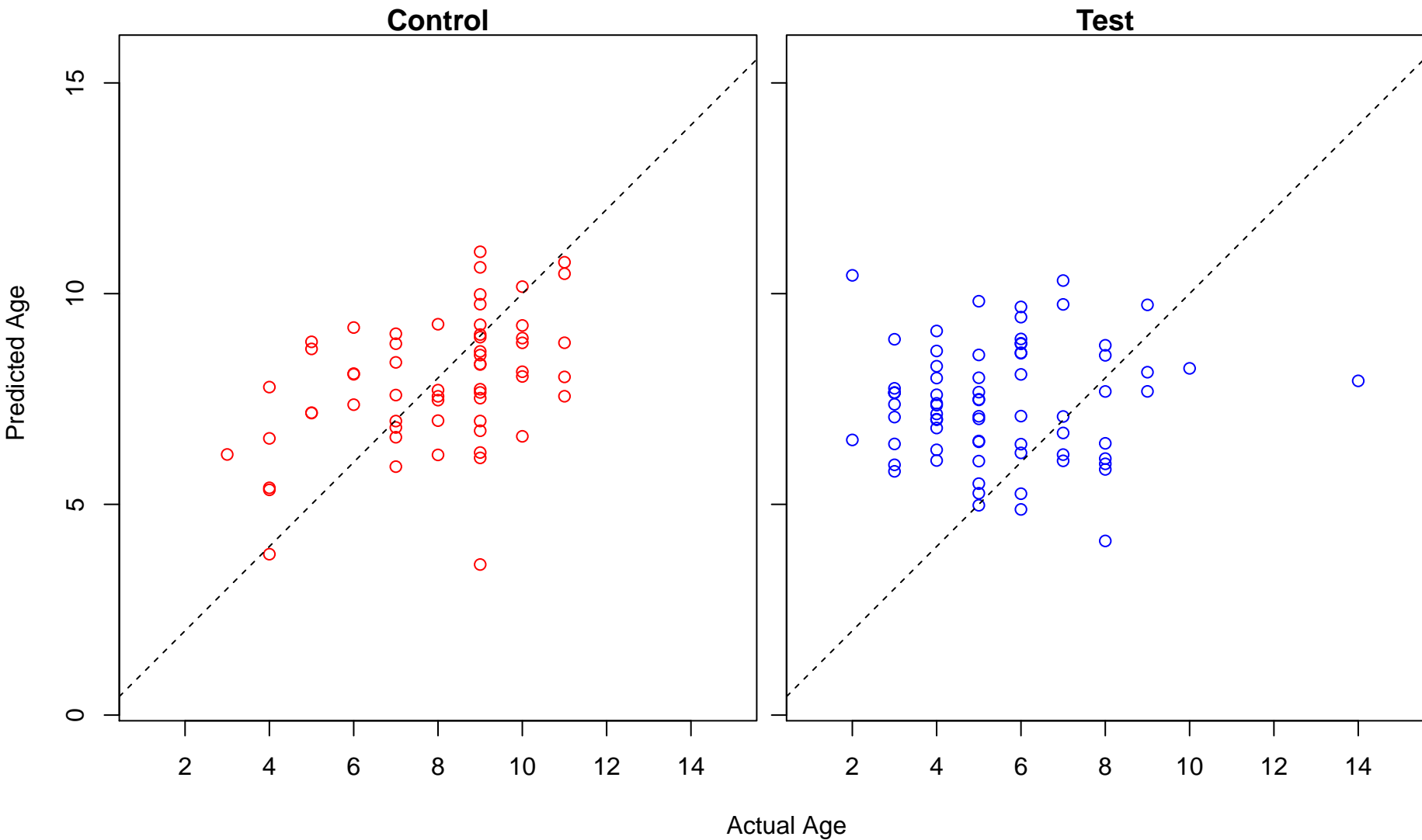
regulation of developmental process (Score: 0.939894)



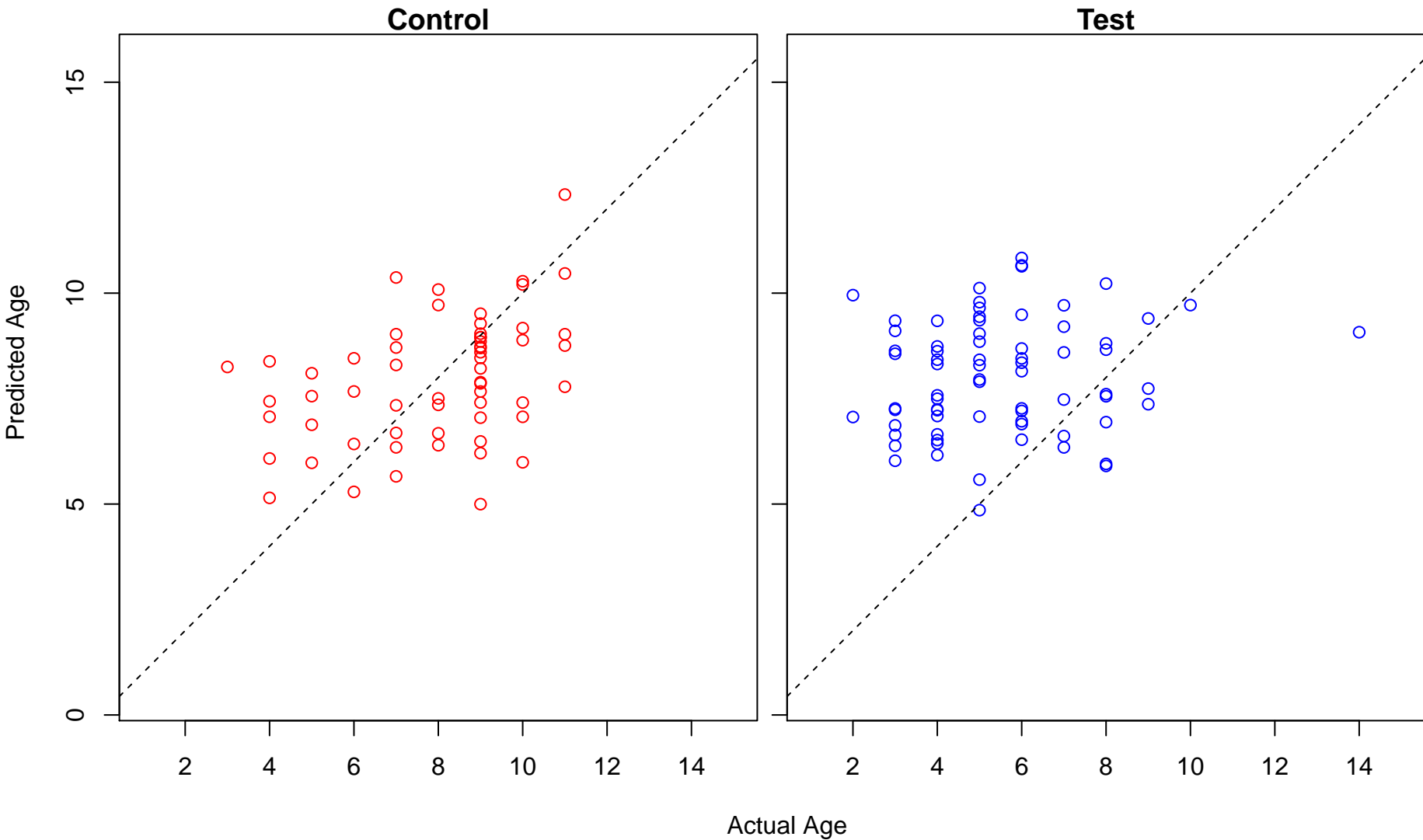
nitrogen compound metabolic process (Score: 0.939815)



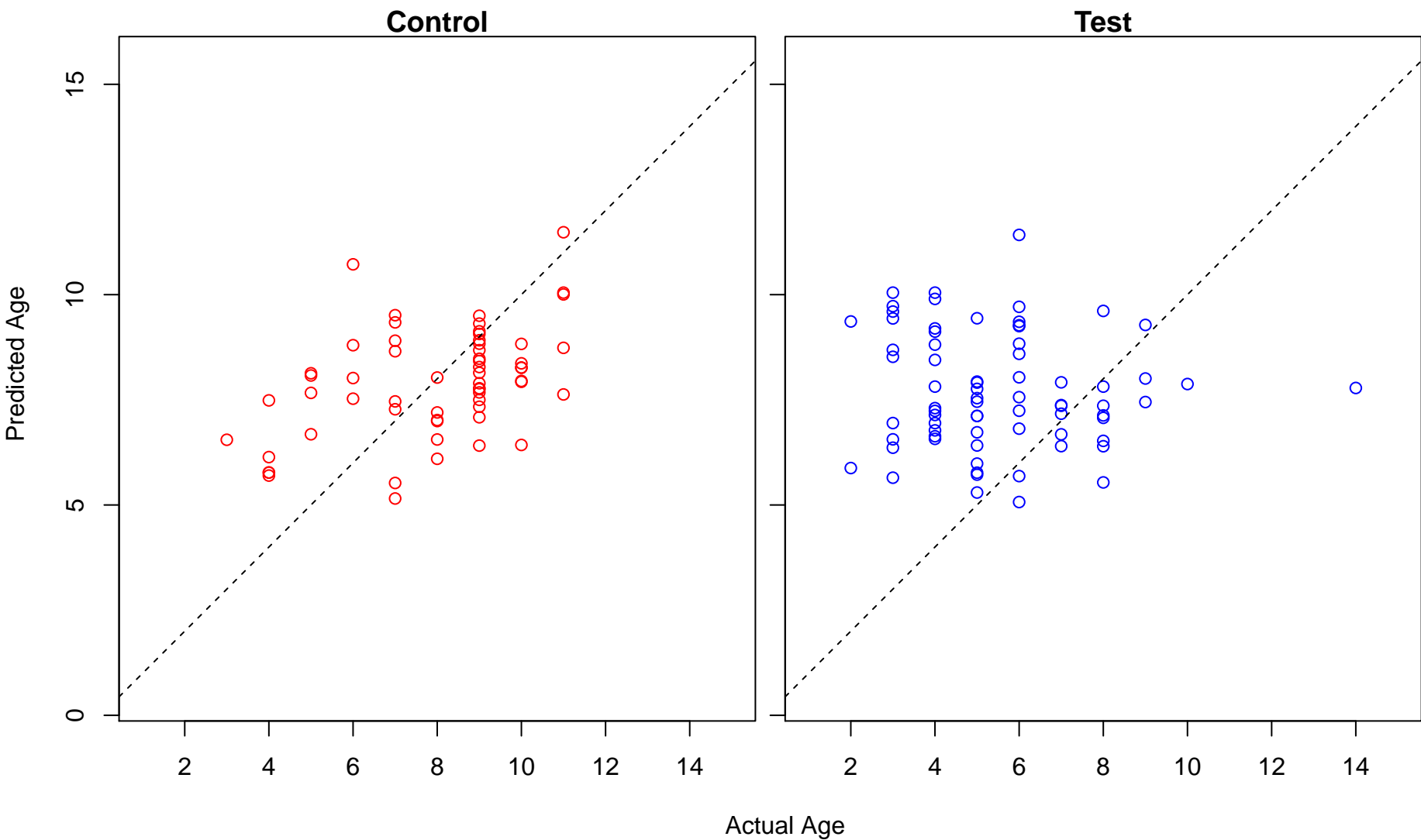
protein processing (Score: 0.939406)



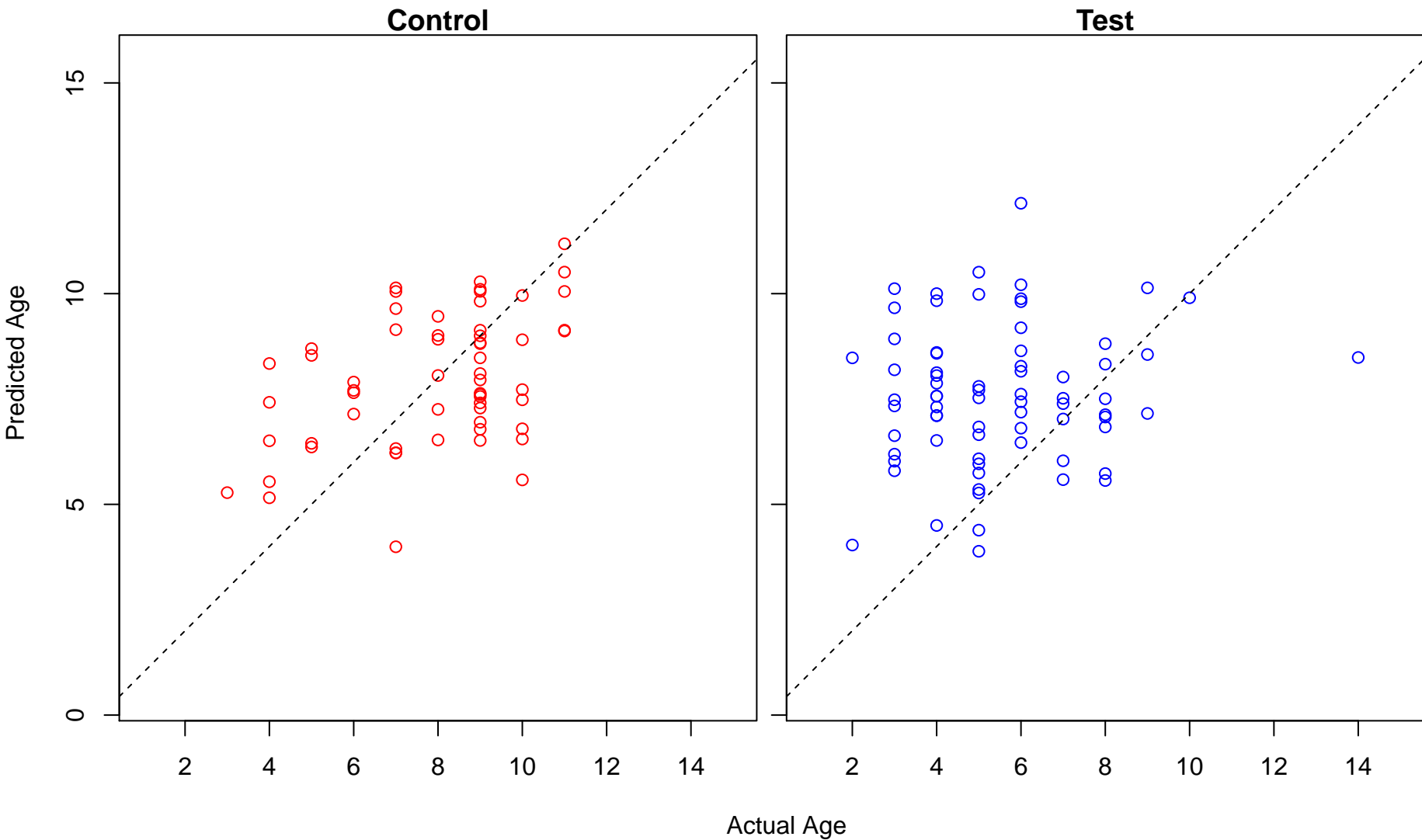
serine family amino acid metabolic process (Score: 0.939119)



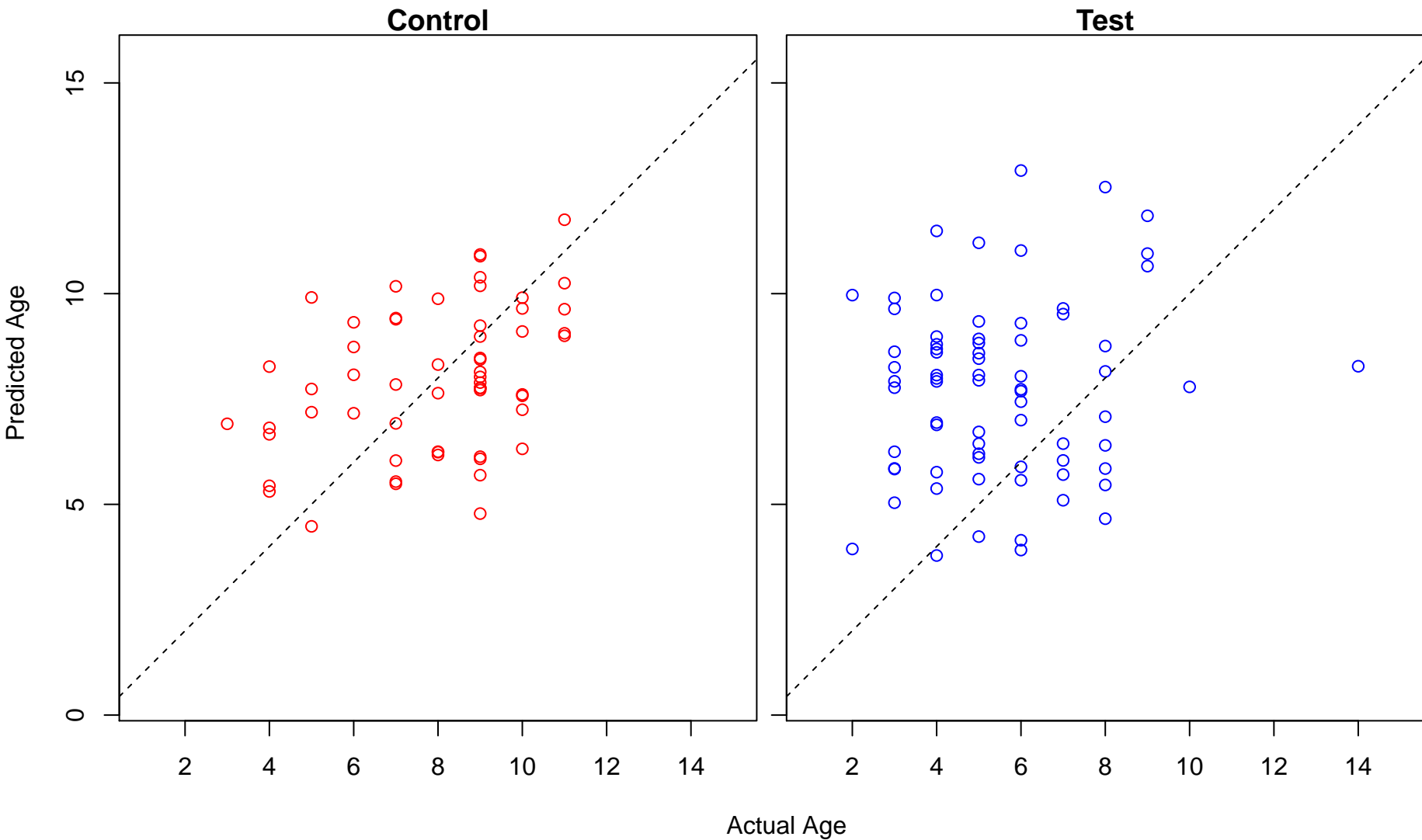
G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (Score: 0.0)



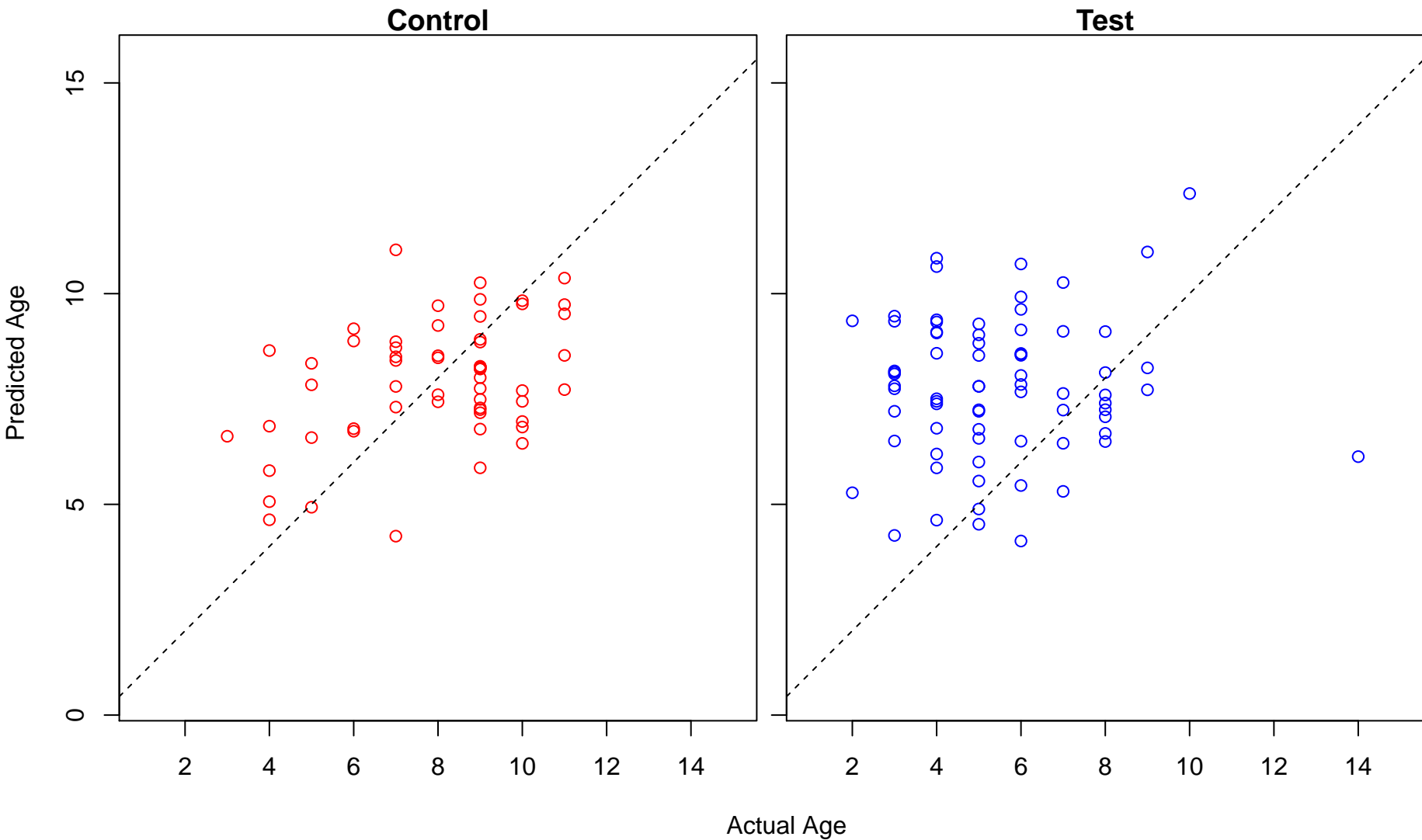
protein autophosphorylation (Score: 0.937482)



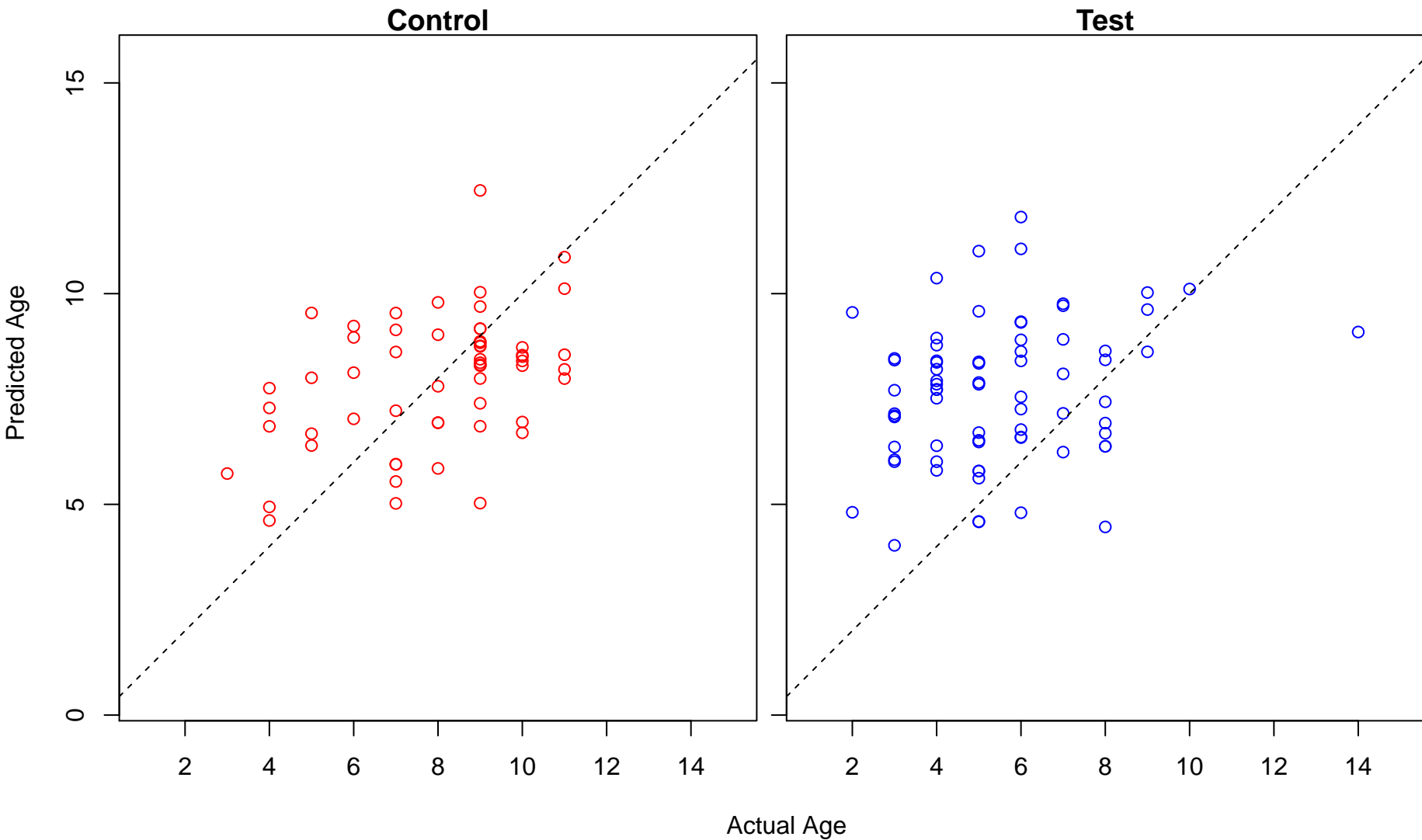
homeostasis of number of cells (Score: 0.935404)



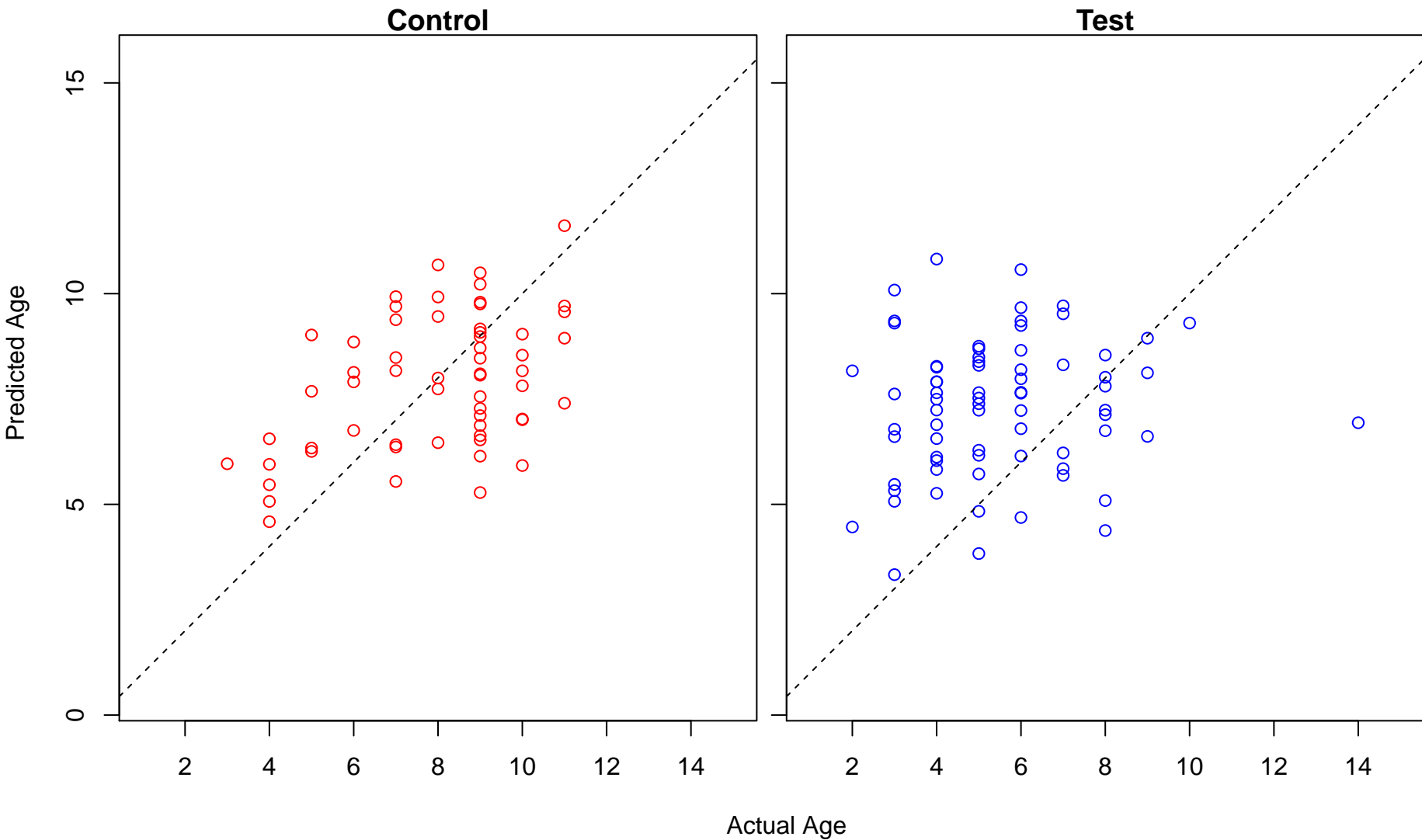
positive regulation of lymphocyte differentiation (Score: 0.932570)



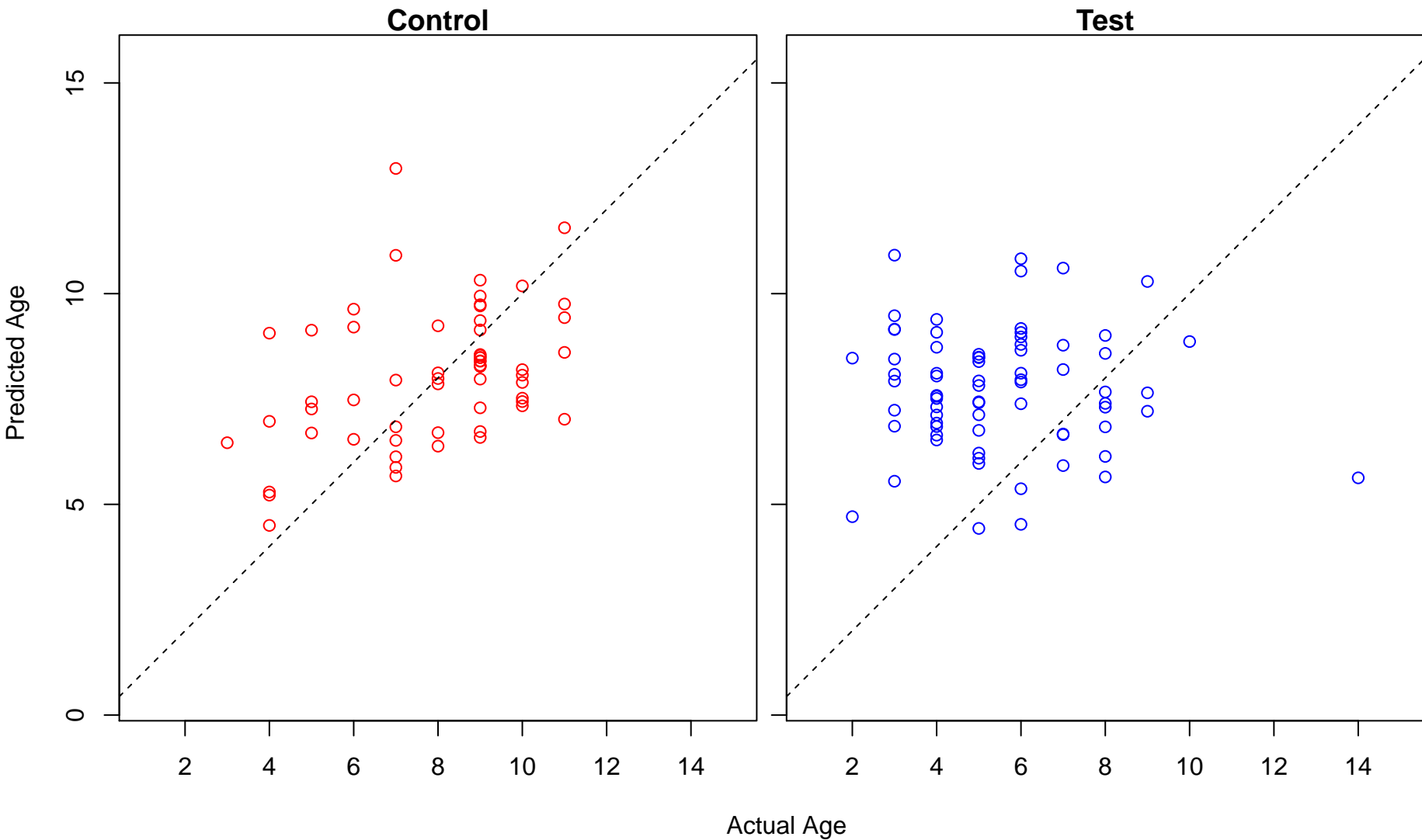
axon guidance (Score: 0.932567)



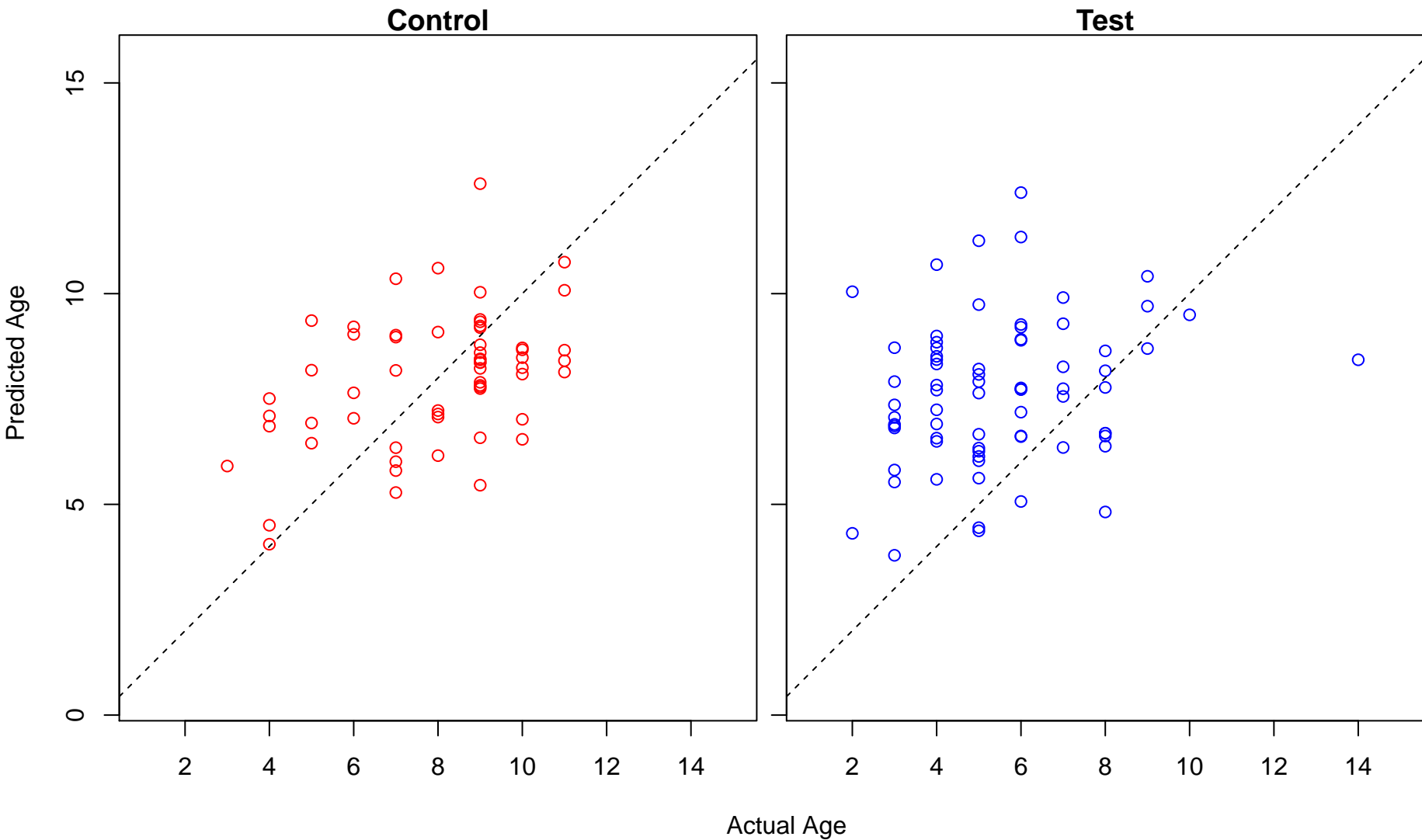
cofactor catabolic process (Score: 0.932206)



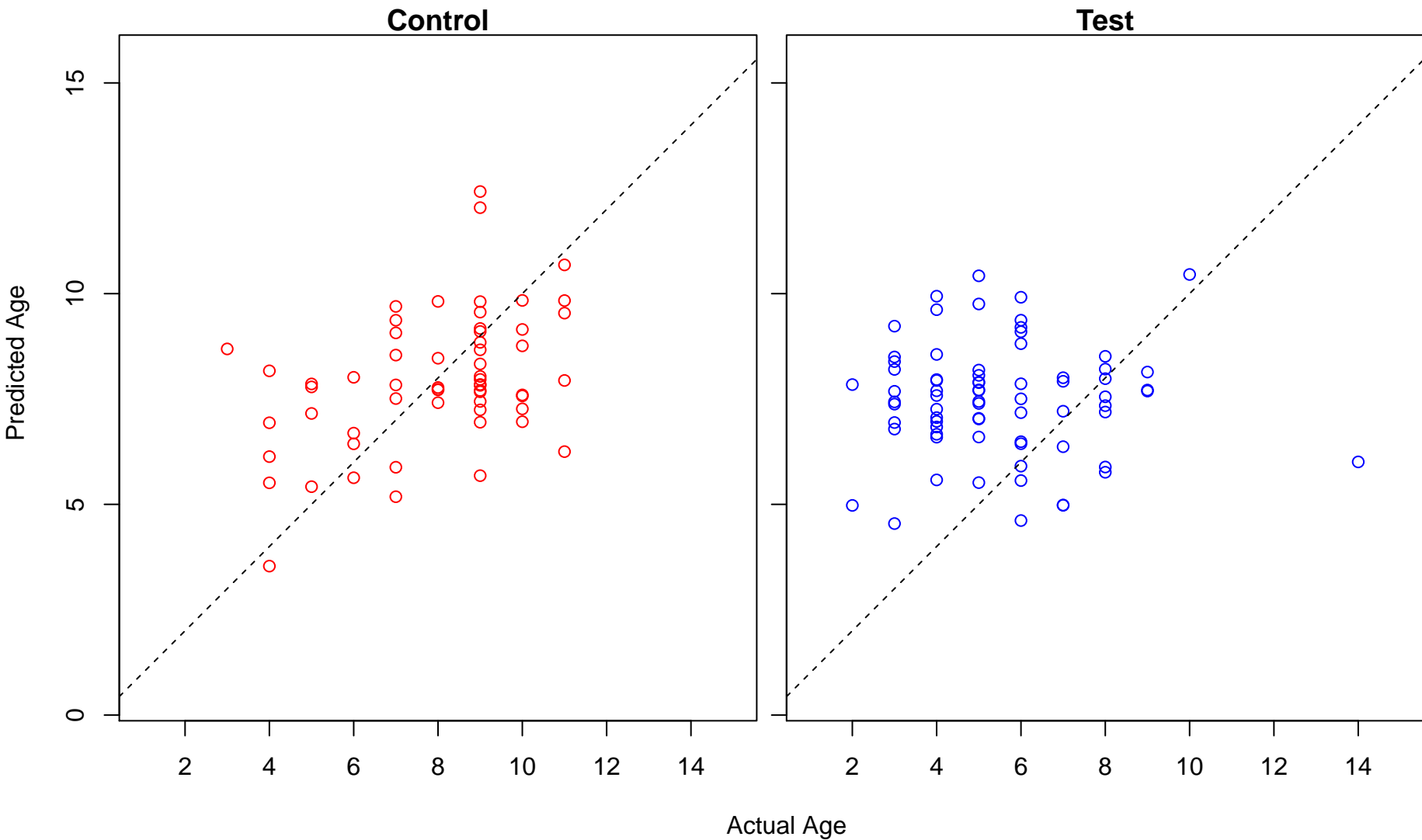
positive regulation of calcium ion transmembrane transporter activity (Score: 0.932034)



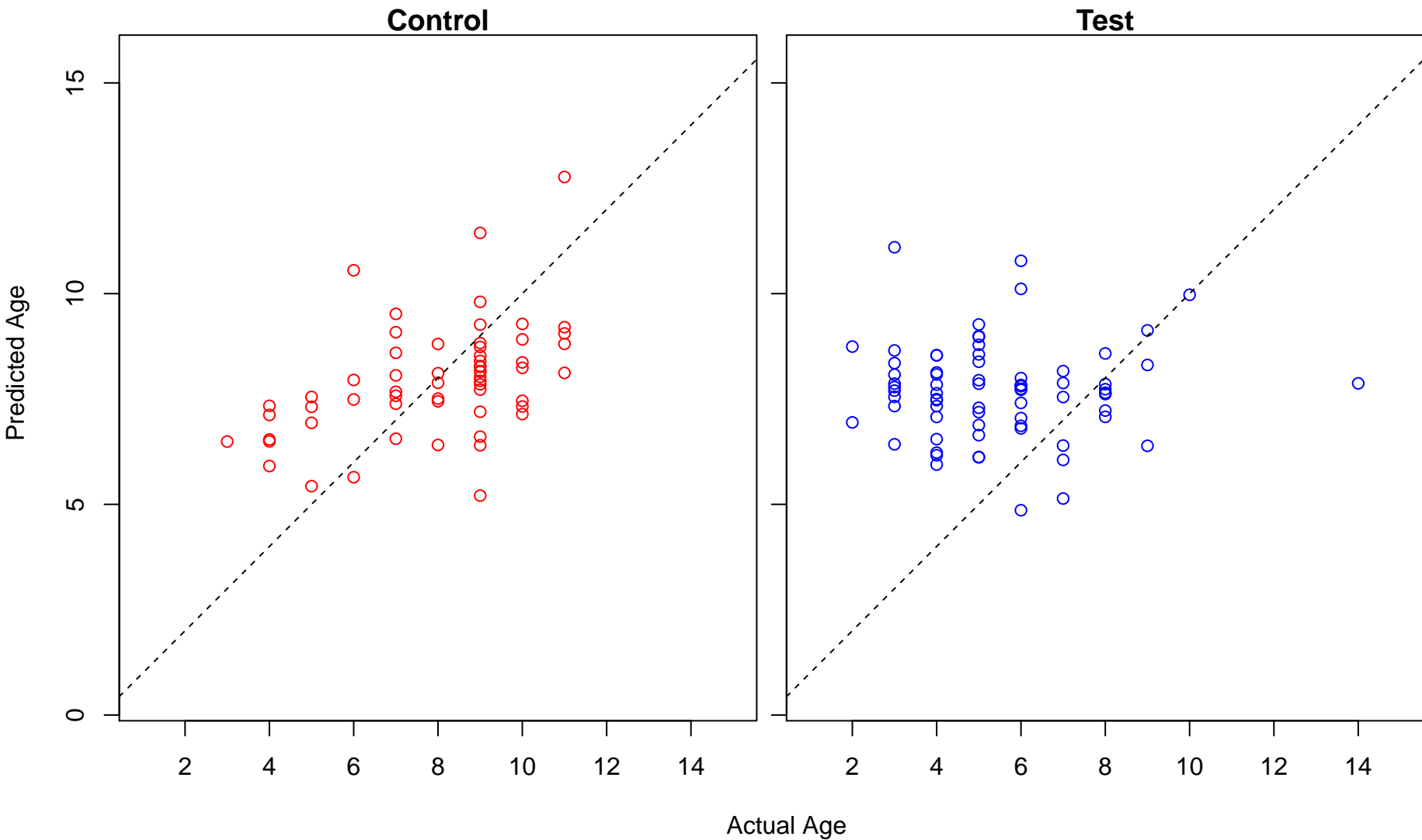
neuron projection development (Score: 0.931413)



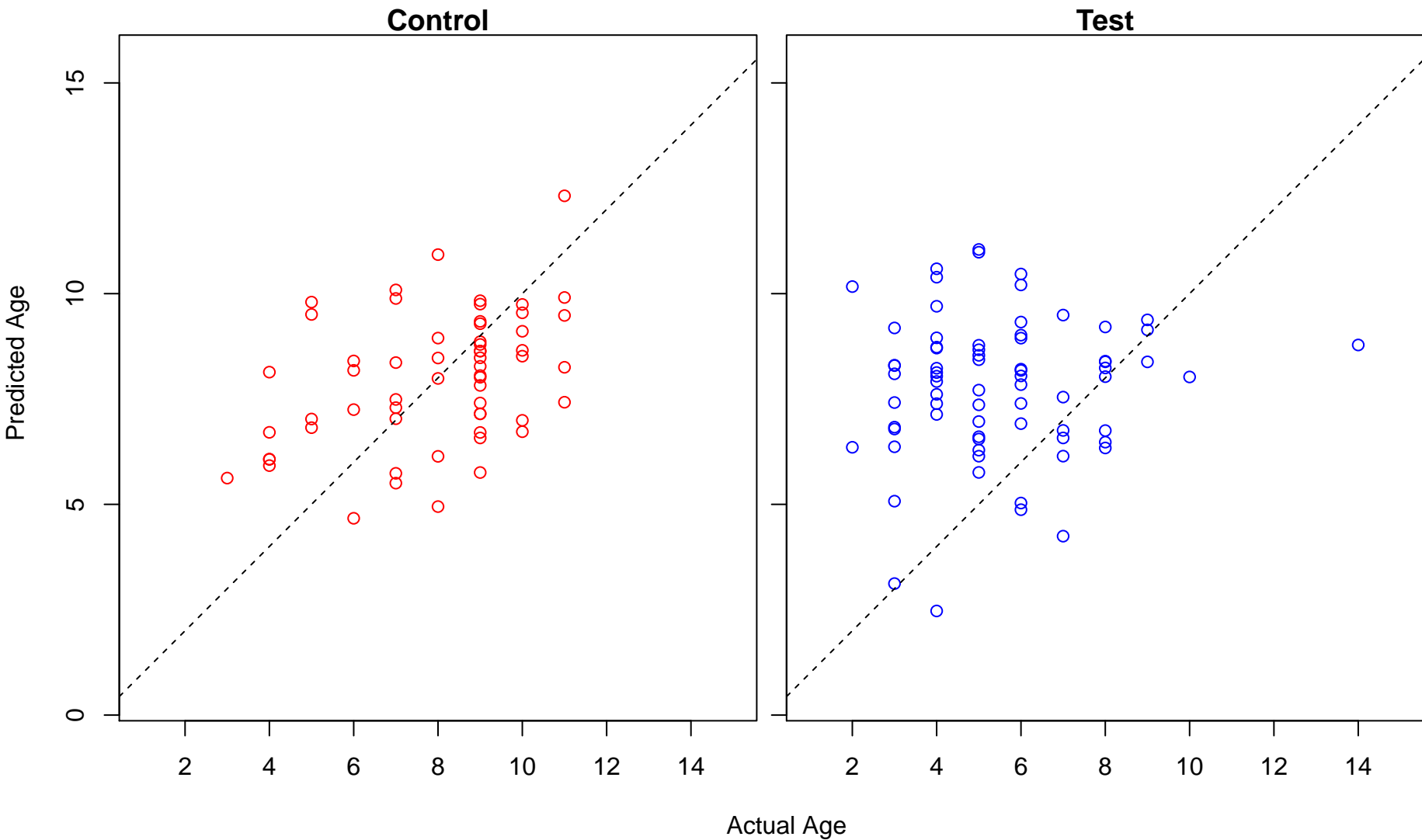
stress granule assembly (Score: 0.931079)



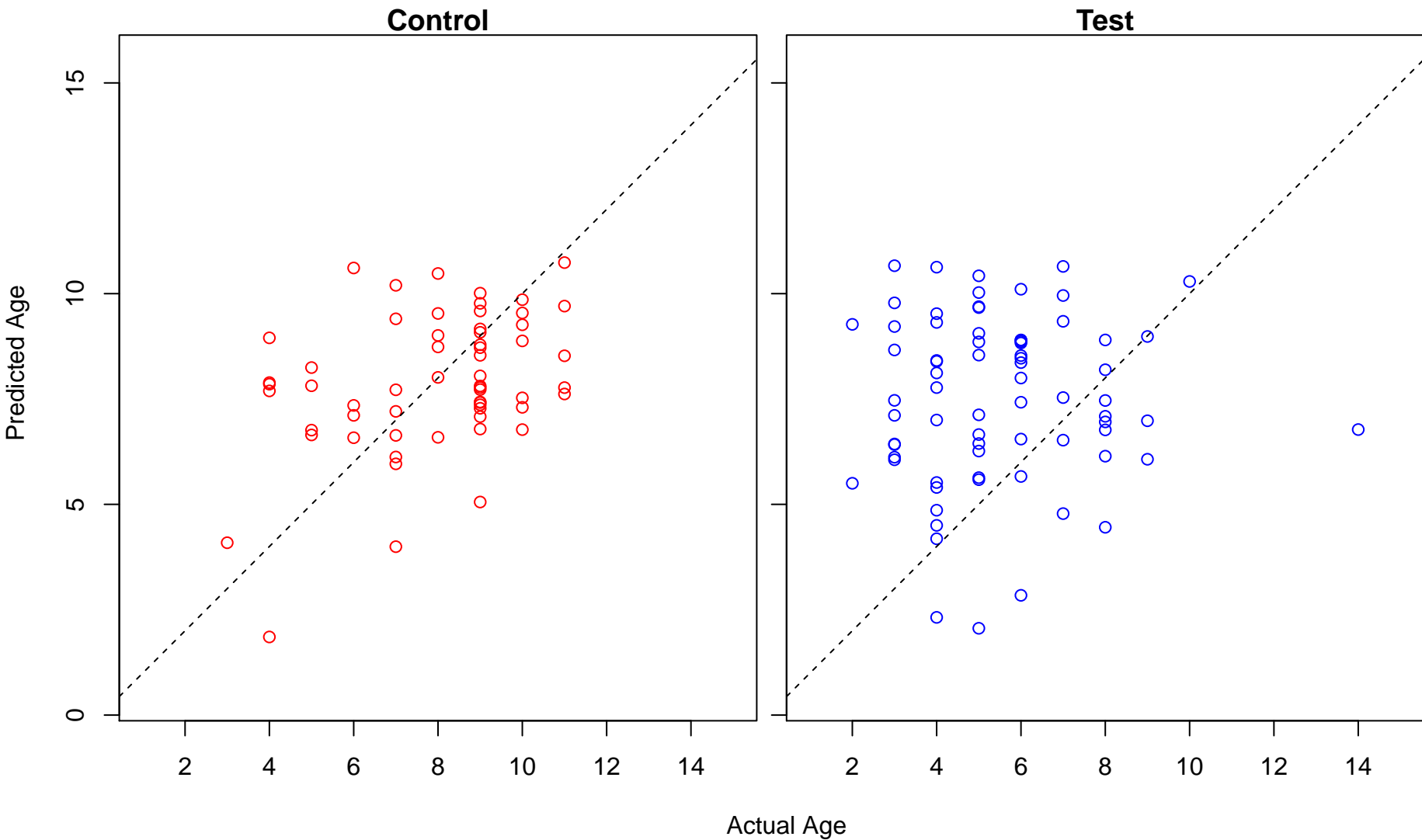
peroxisome proliferator activated receptor signaling pathway (Score: 0.928937)



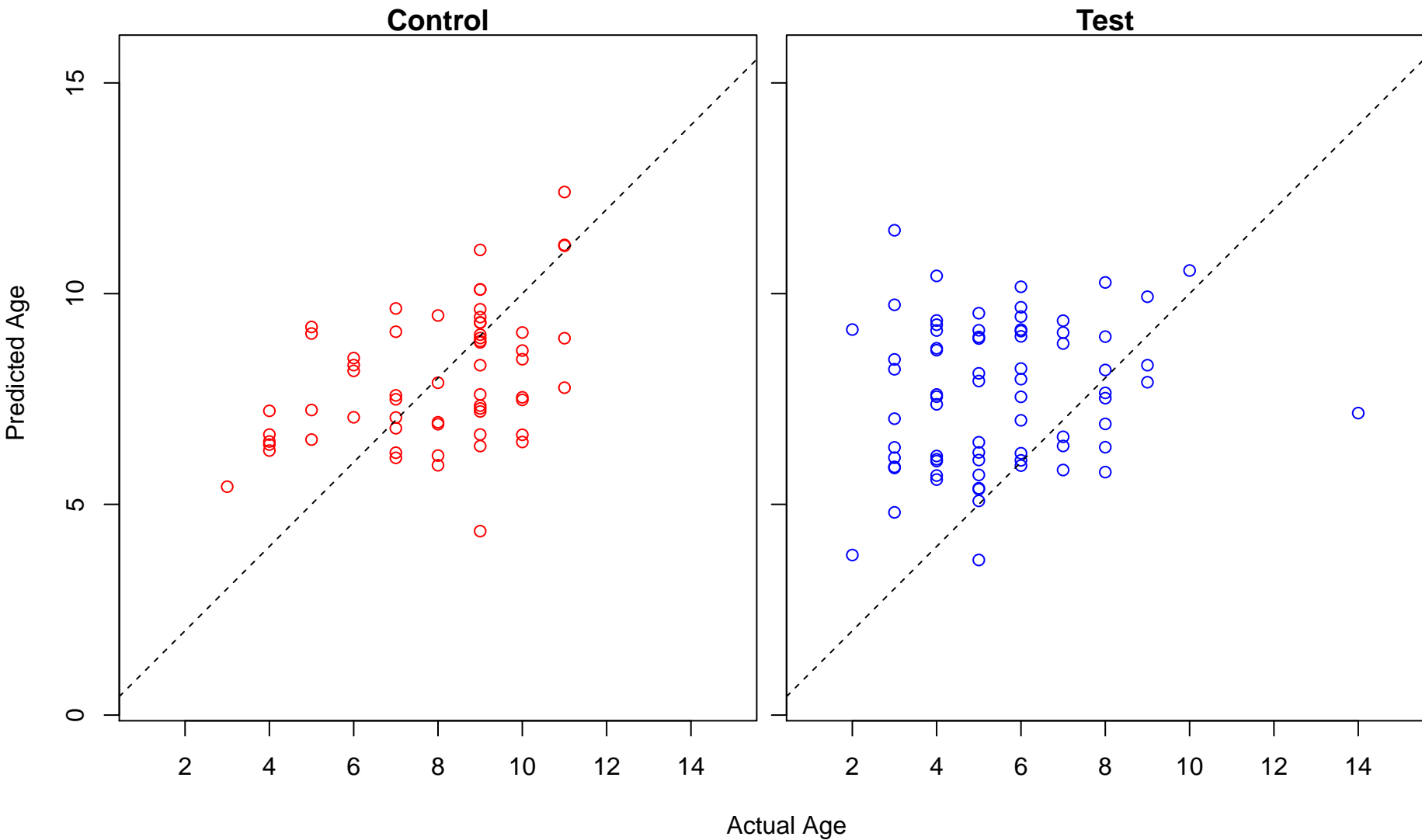
cellular glucose homeostasis (Score: 0.928828)



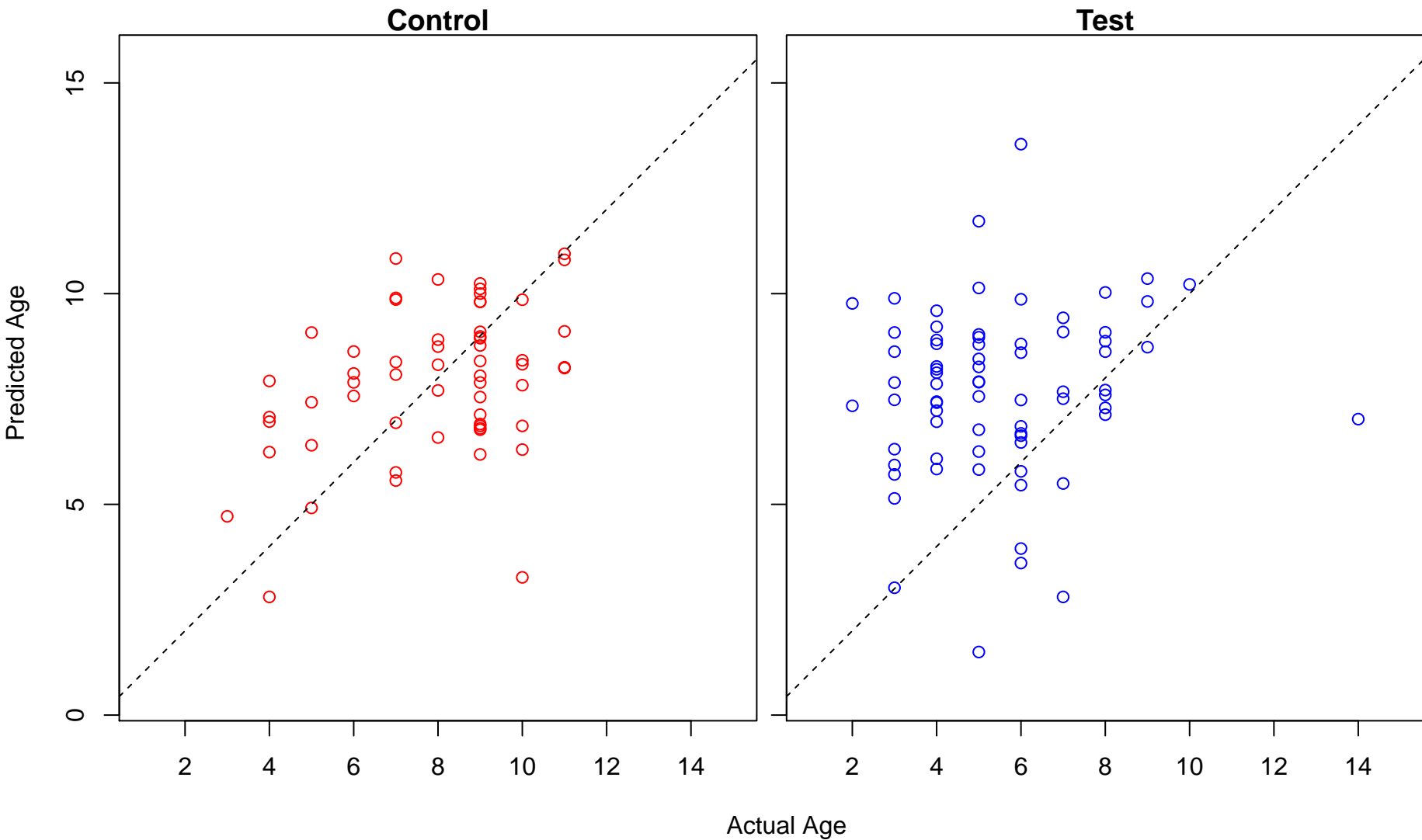
DNA demethylation (Score: 0.927883)



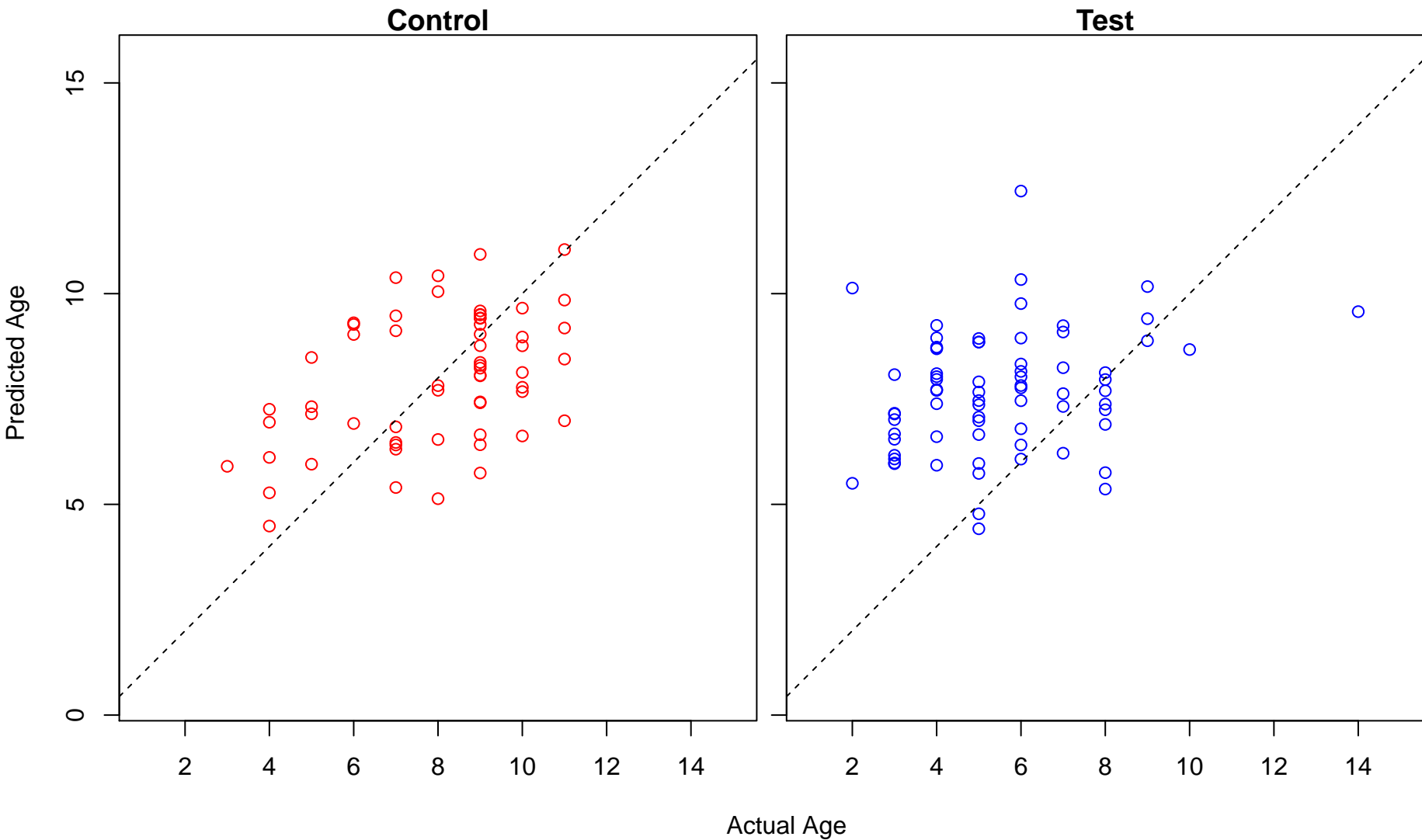
embryo development (Score: 0.927657)



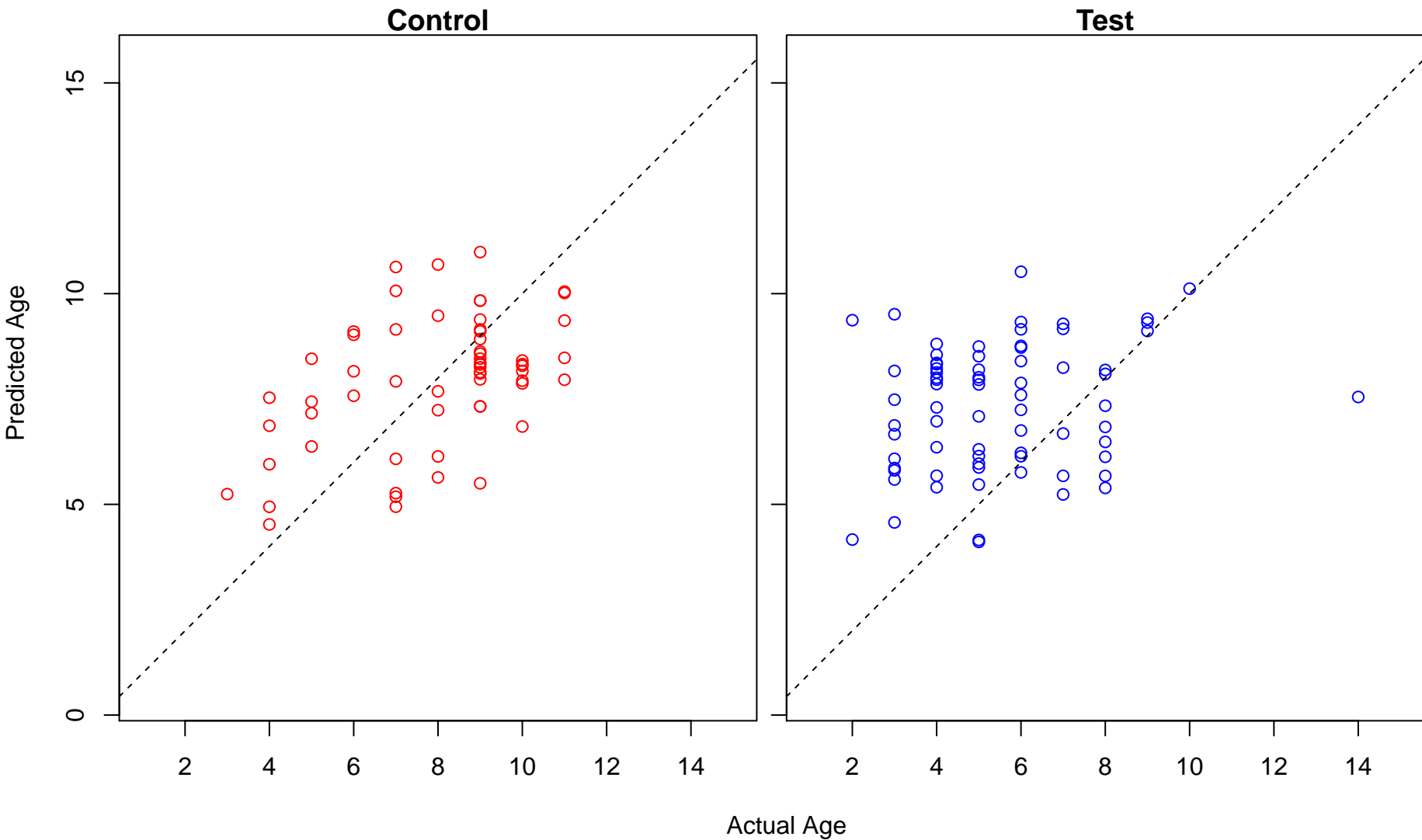
chaperone-mediated protein folding (Score: 0.926663)



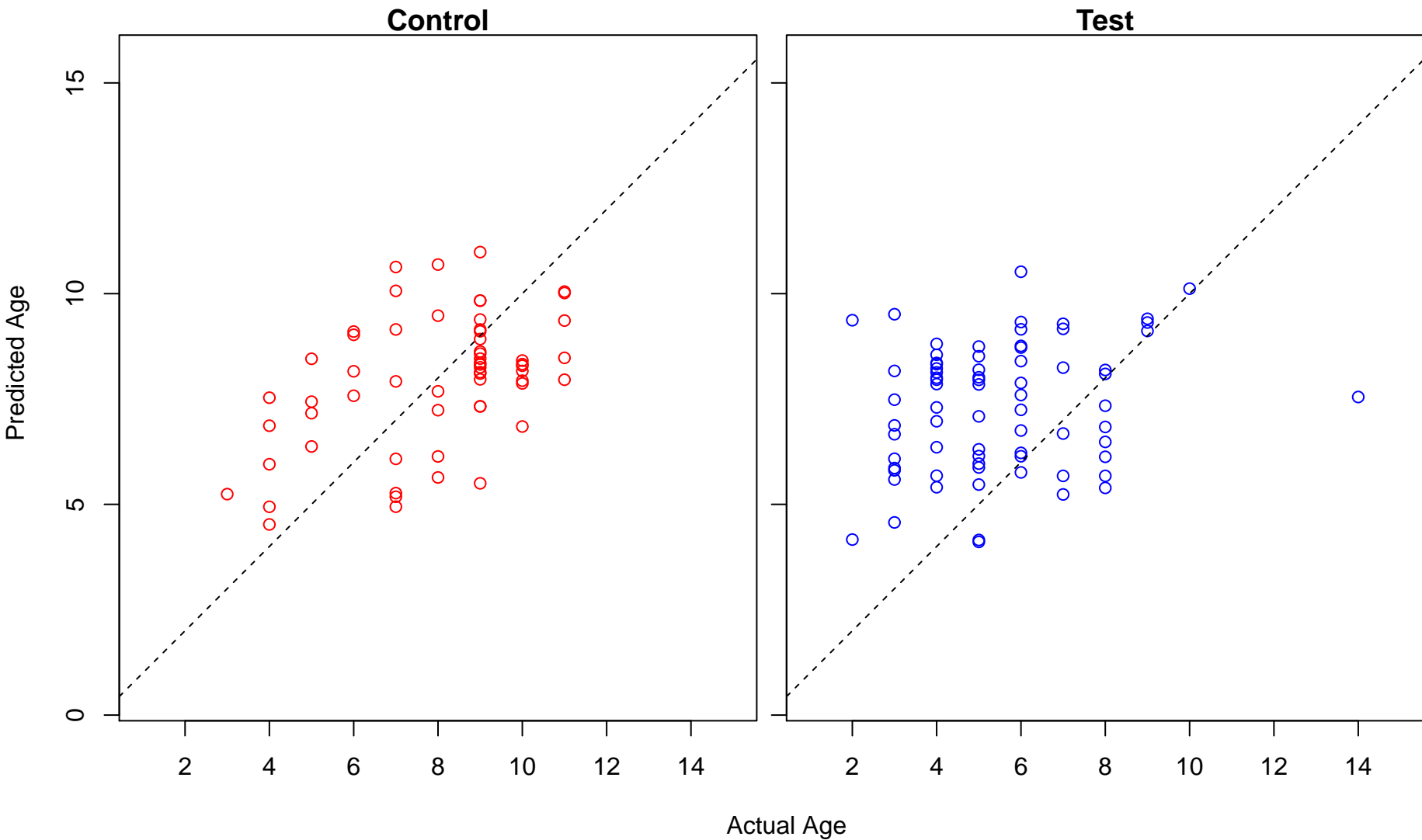
positive regulation of cellular protein metabolic process (Score: 0.926079)



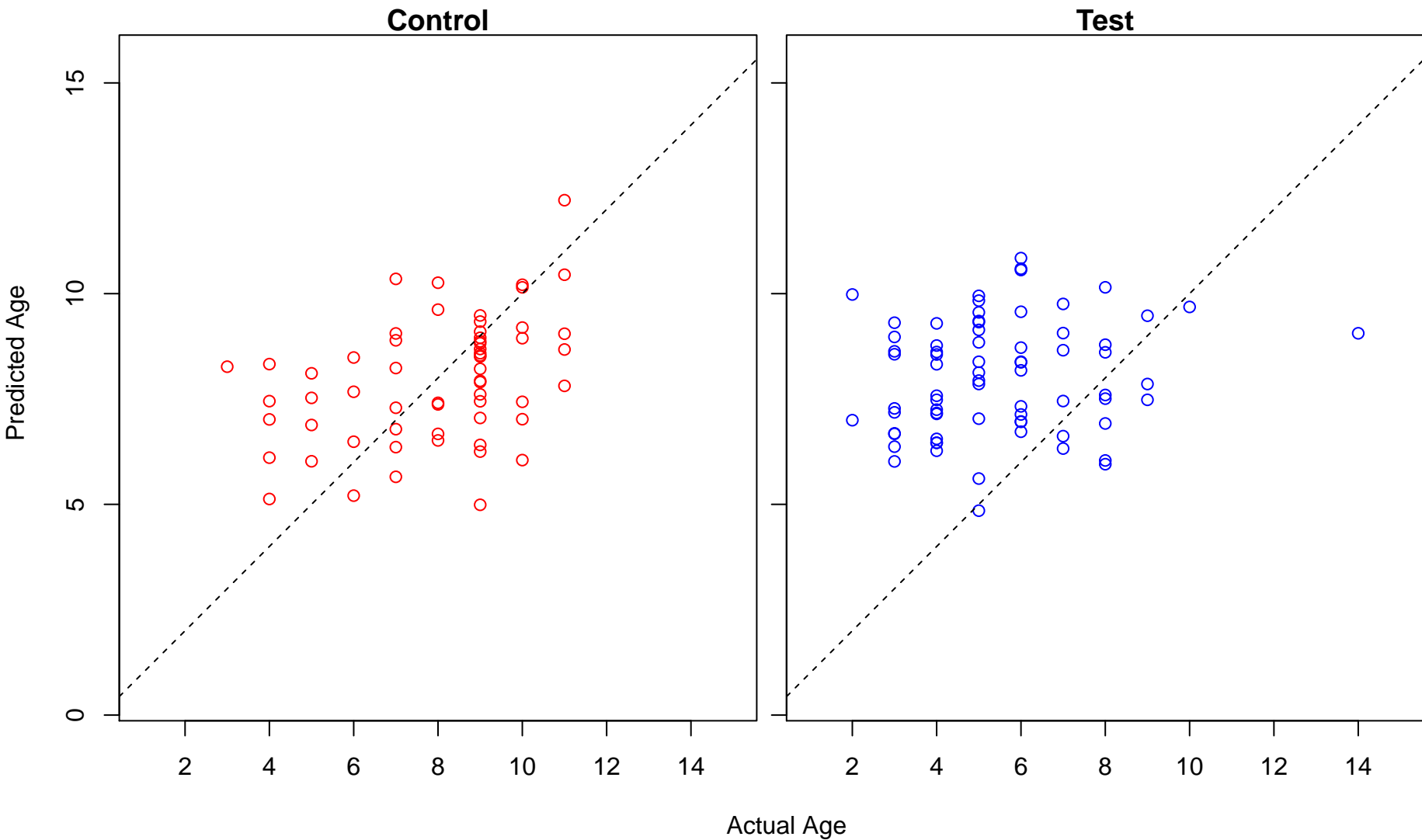
cellular protein modification process (Score: 0.925850)



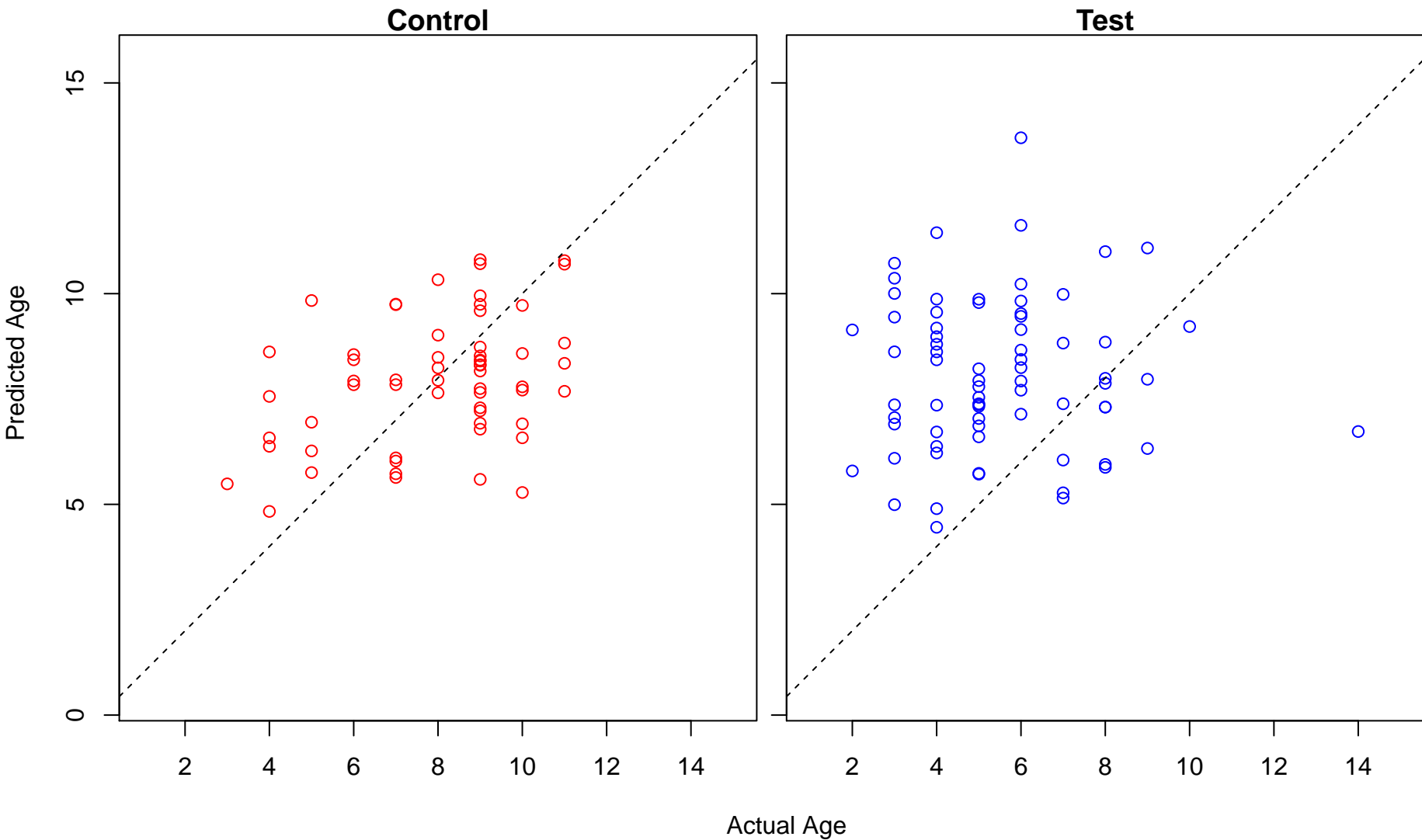
protein modification process (Score: 0.925850)



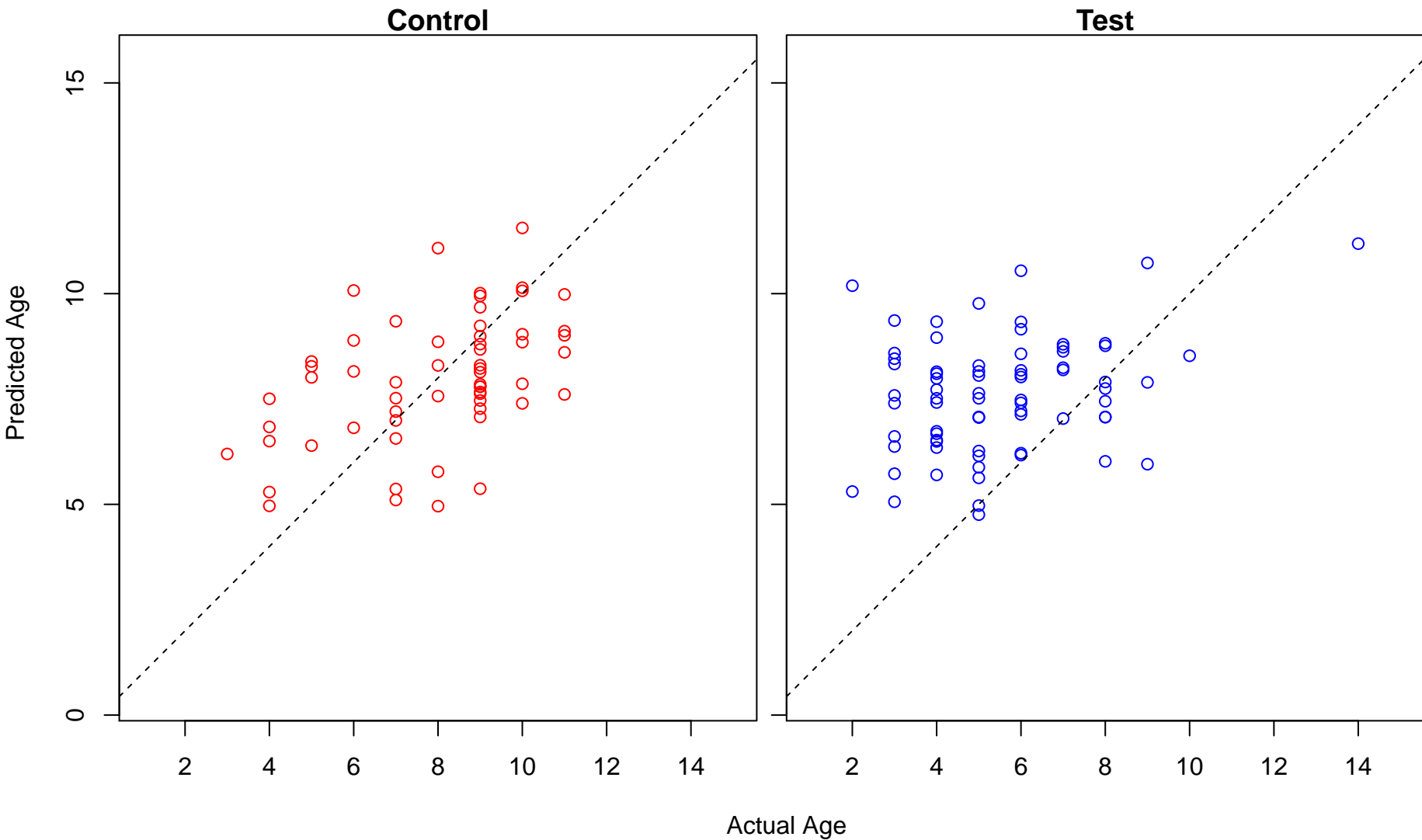
viral transcription (Score: 0.925701)



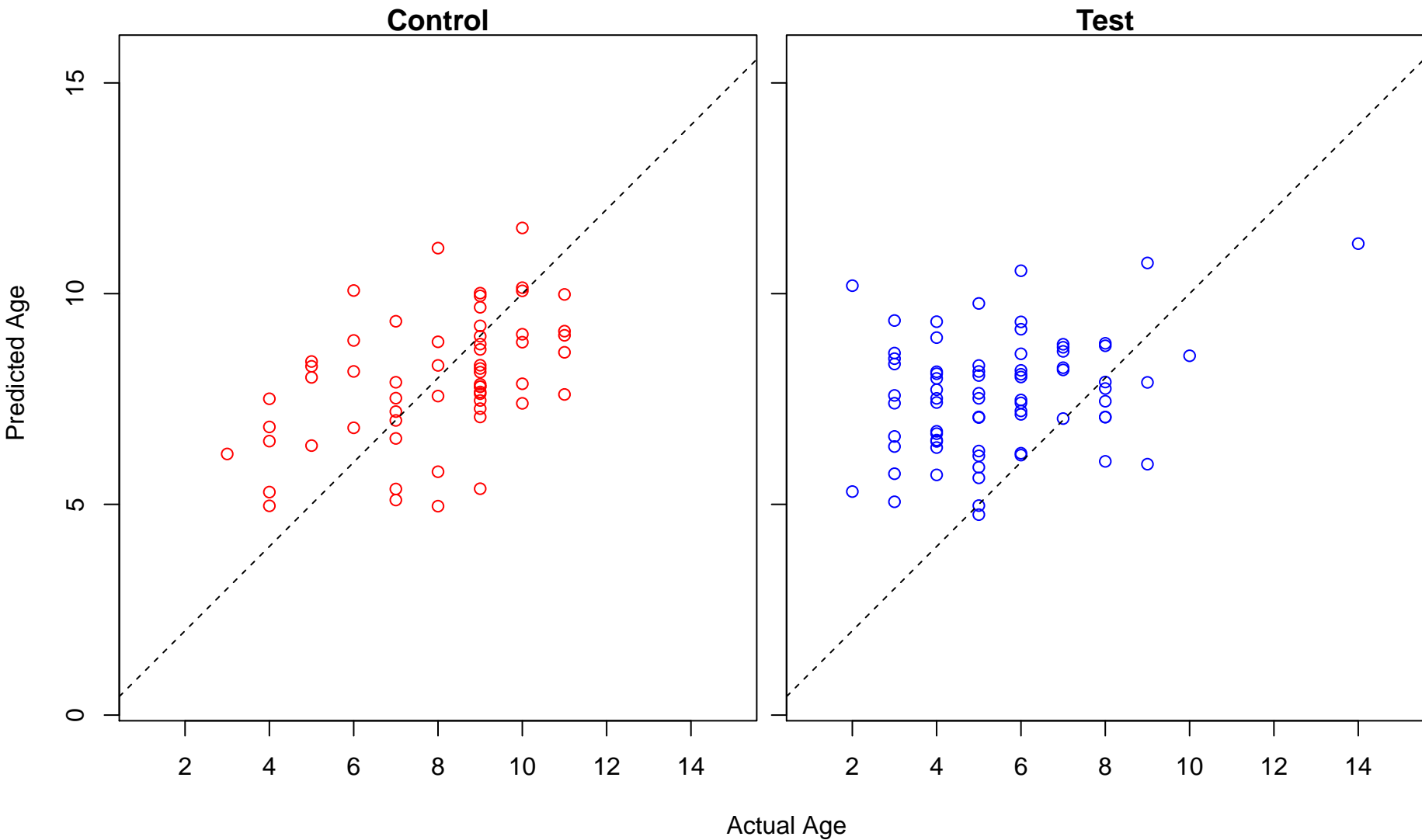
learning or memory (Score: 0.925160)



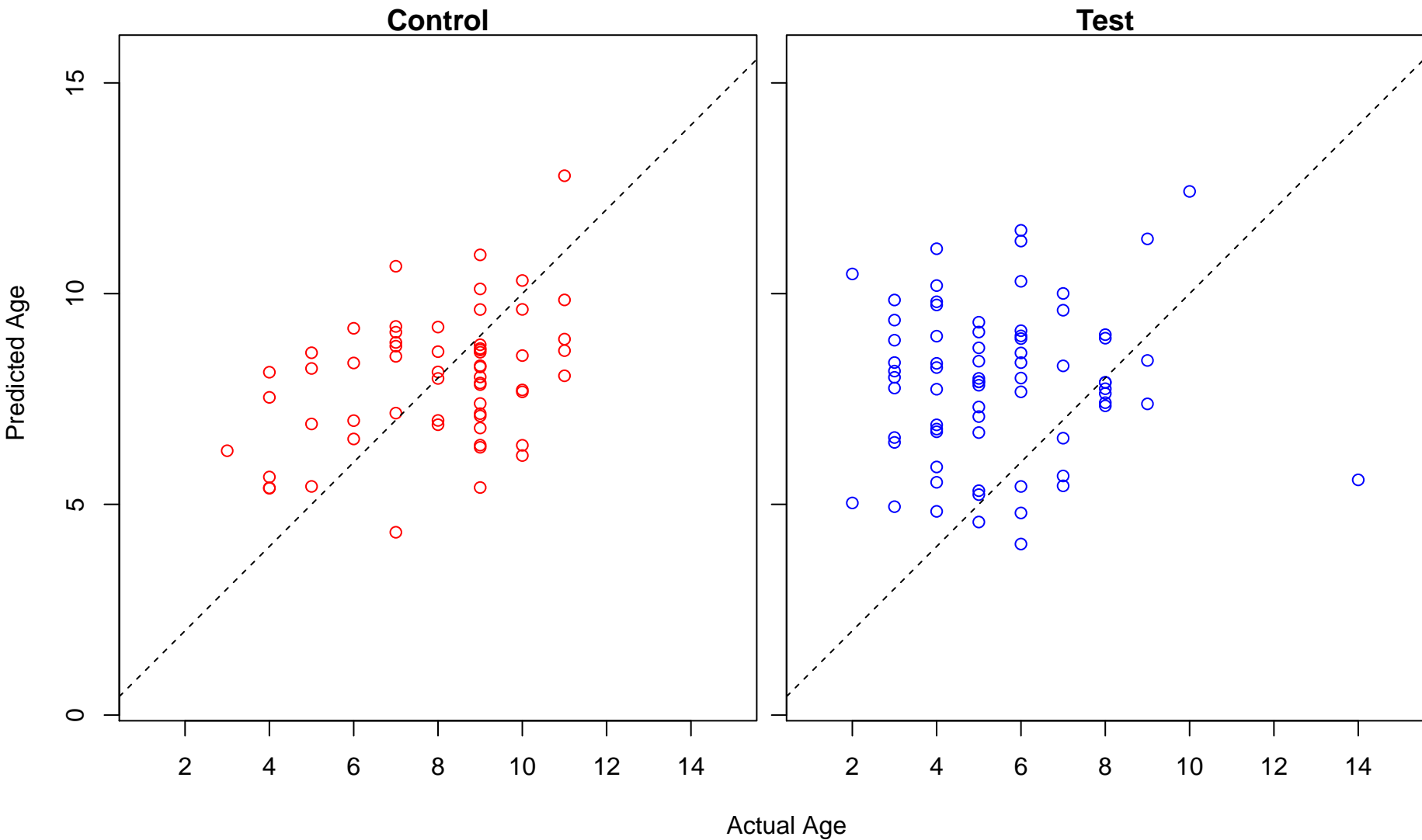
response to protozoan (Score: 0.921989)



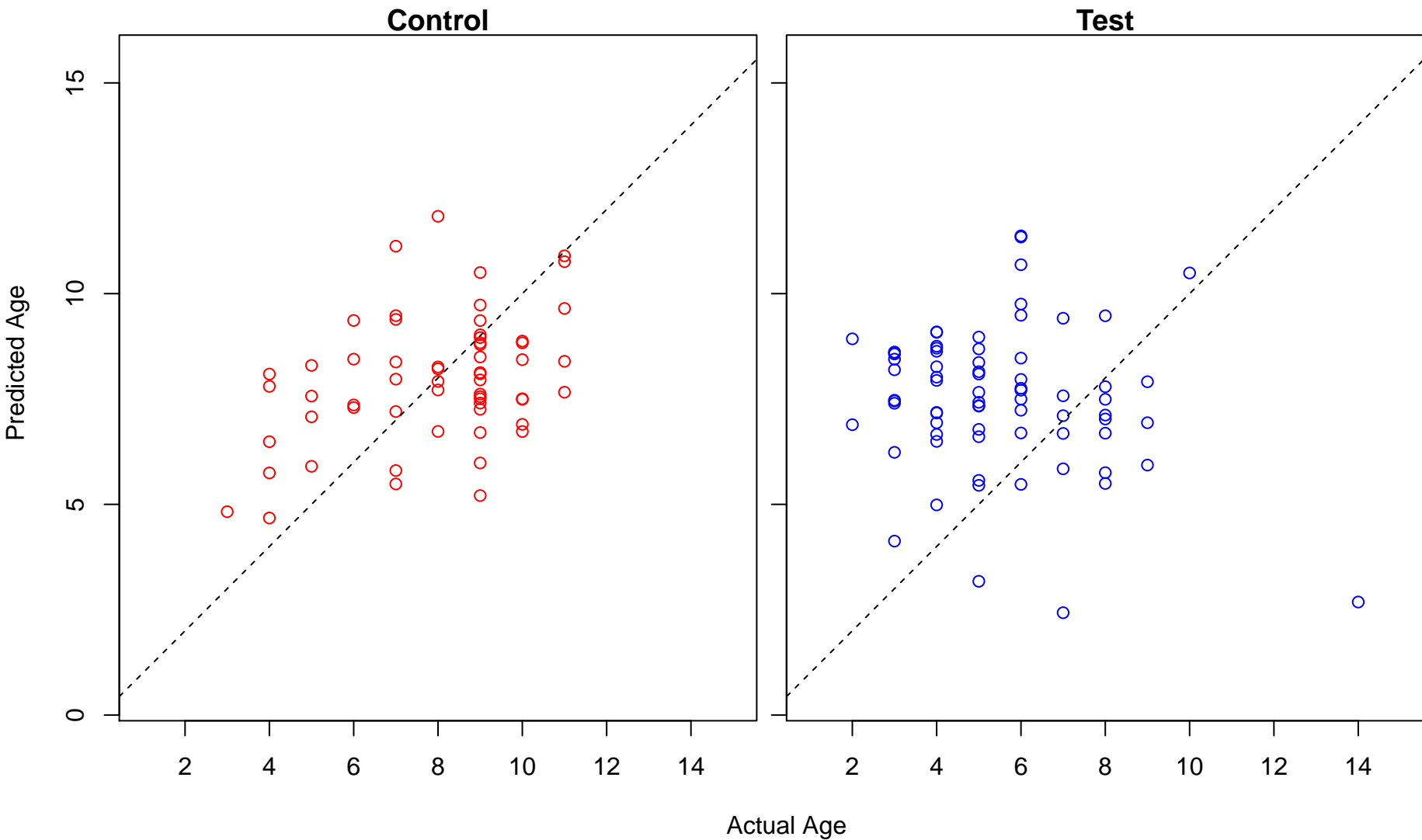
defense response to protozoan (Score: 0.921989)



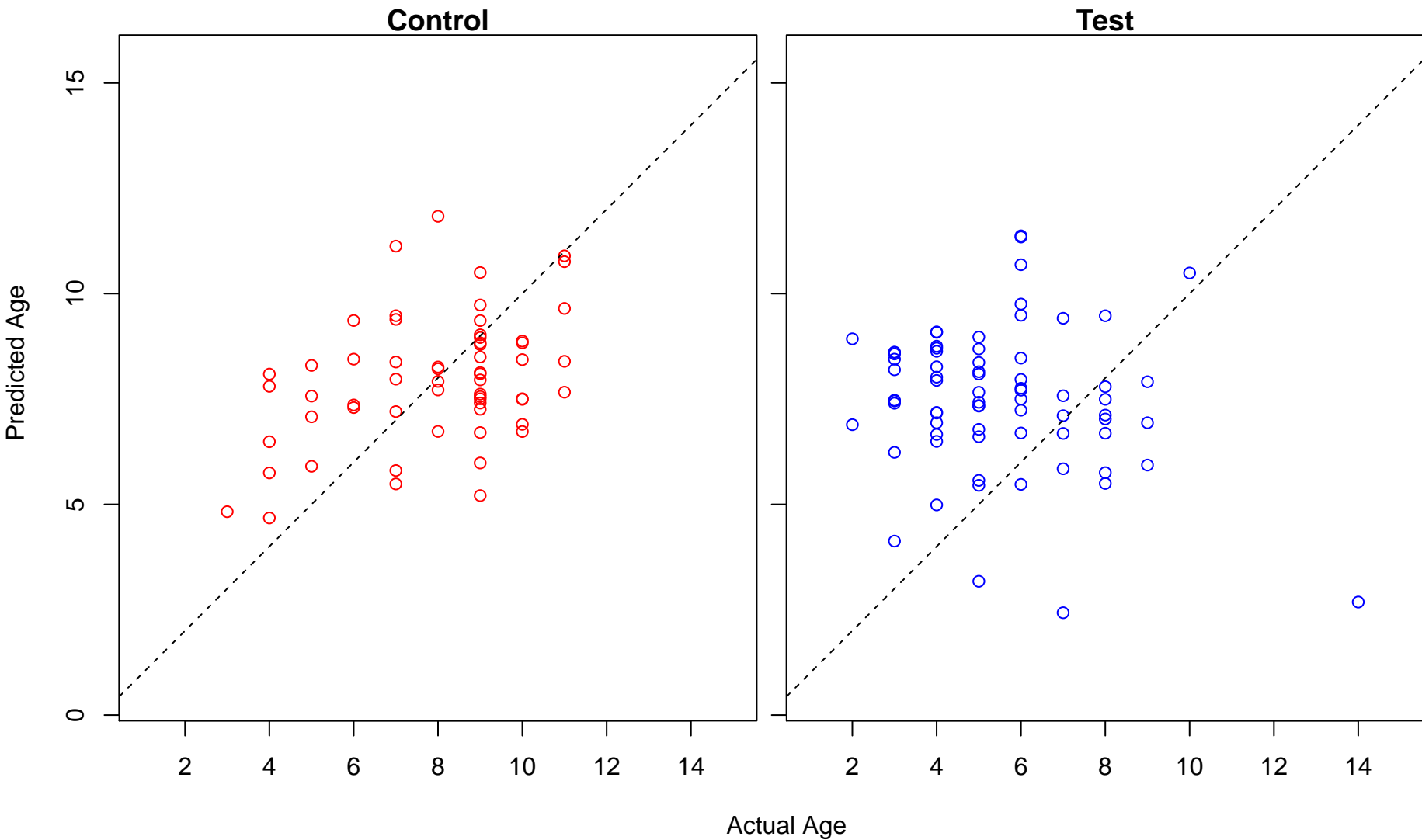
regulation of T cell differentiation (Score: 0.920899)



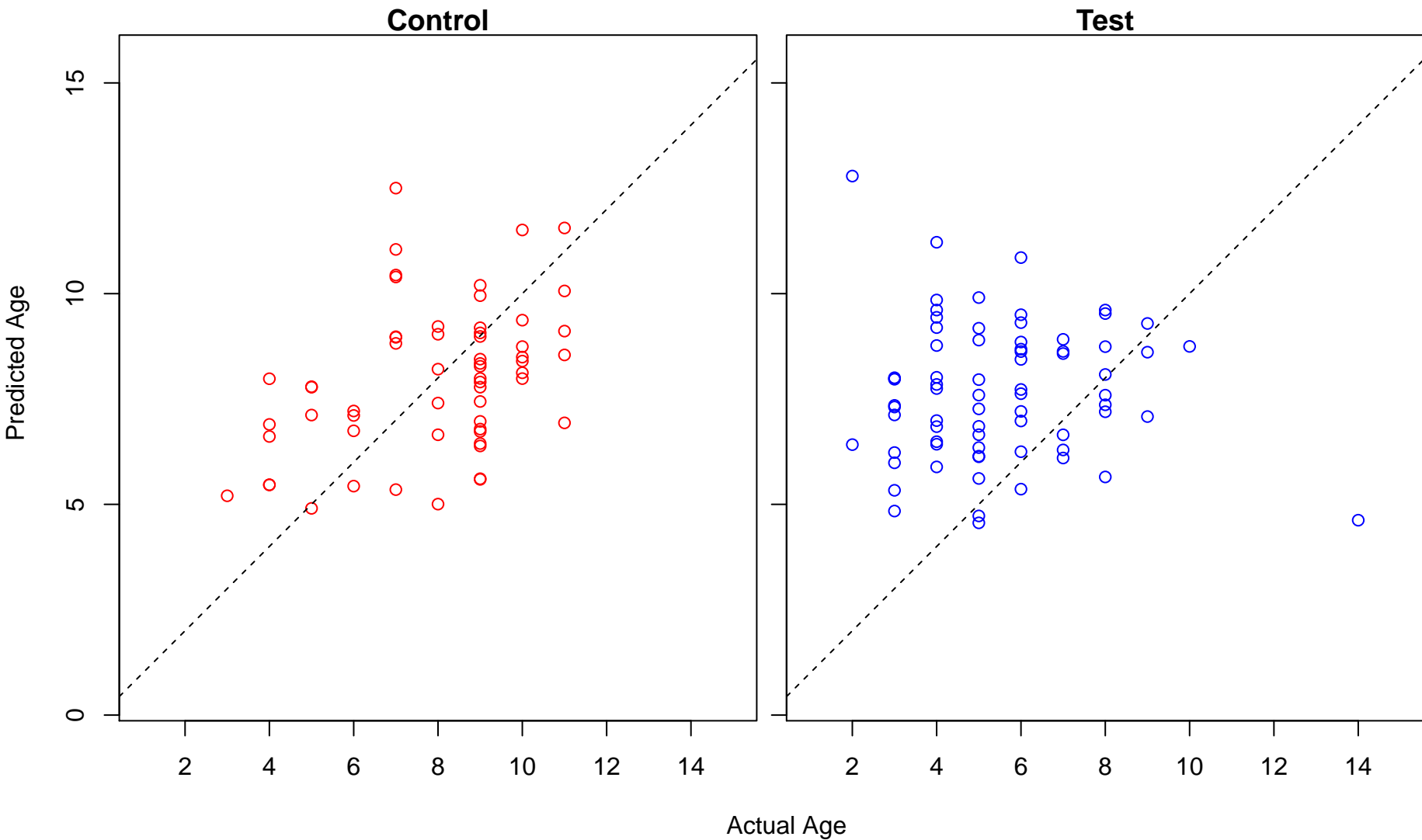
negative regulation of translation, ncRNA-mediated (Score: 0.920220)



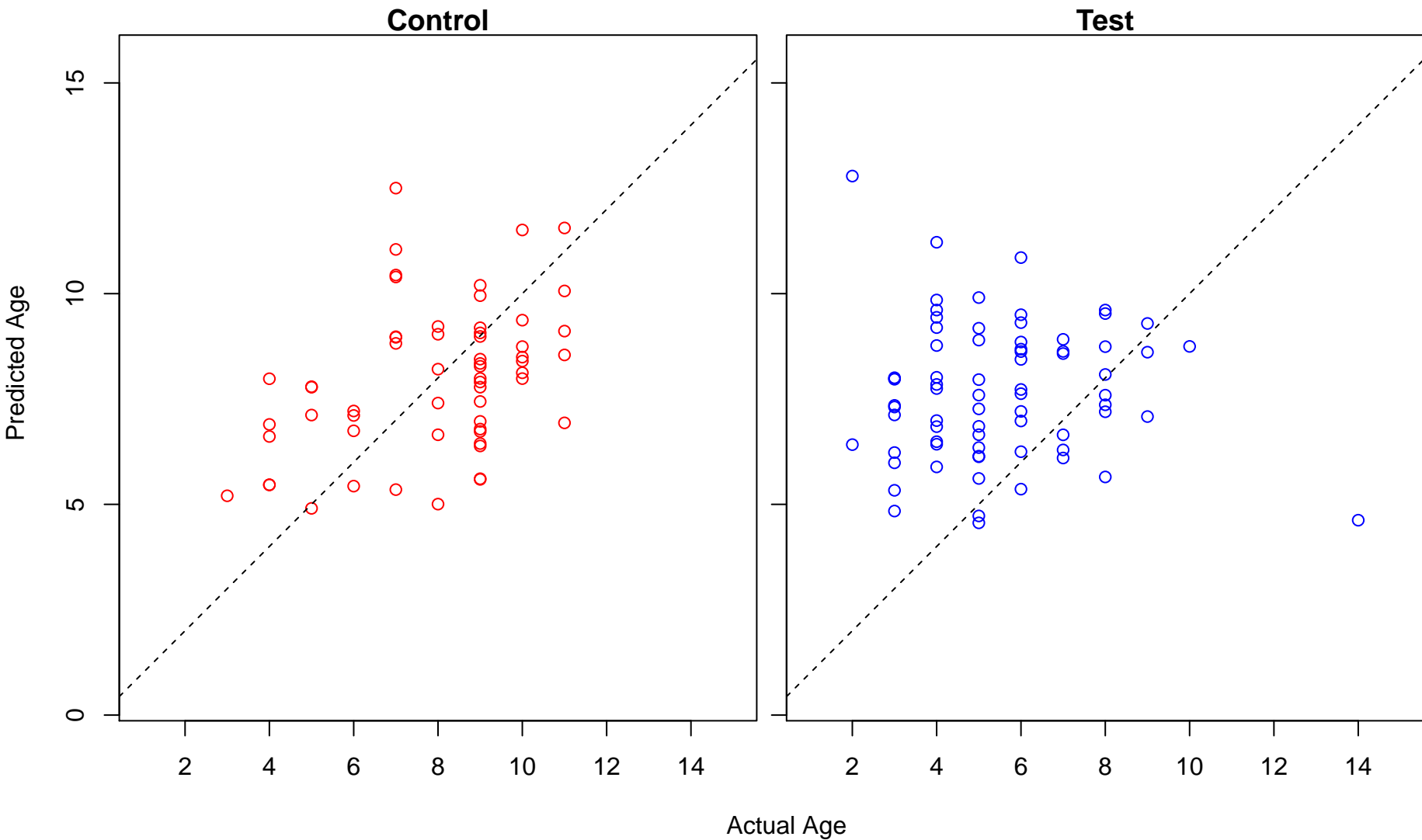
regulation of translation, ncRNA-mediated (Score: 0.920220)



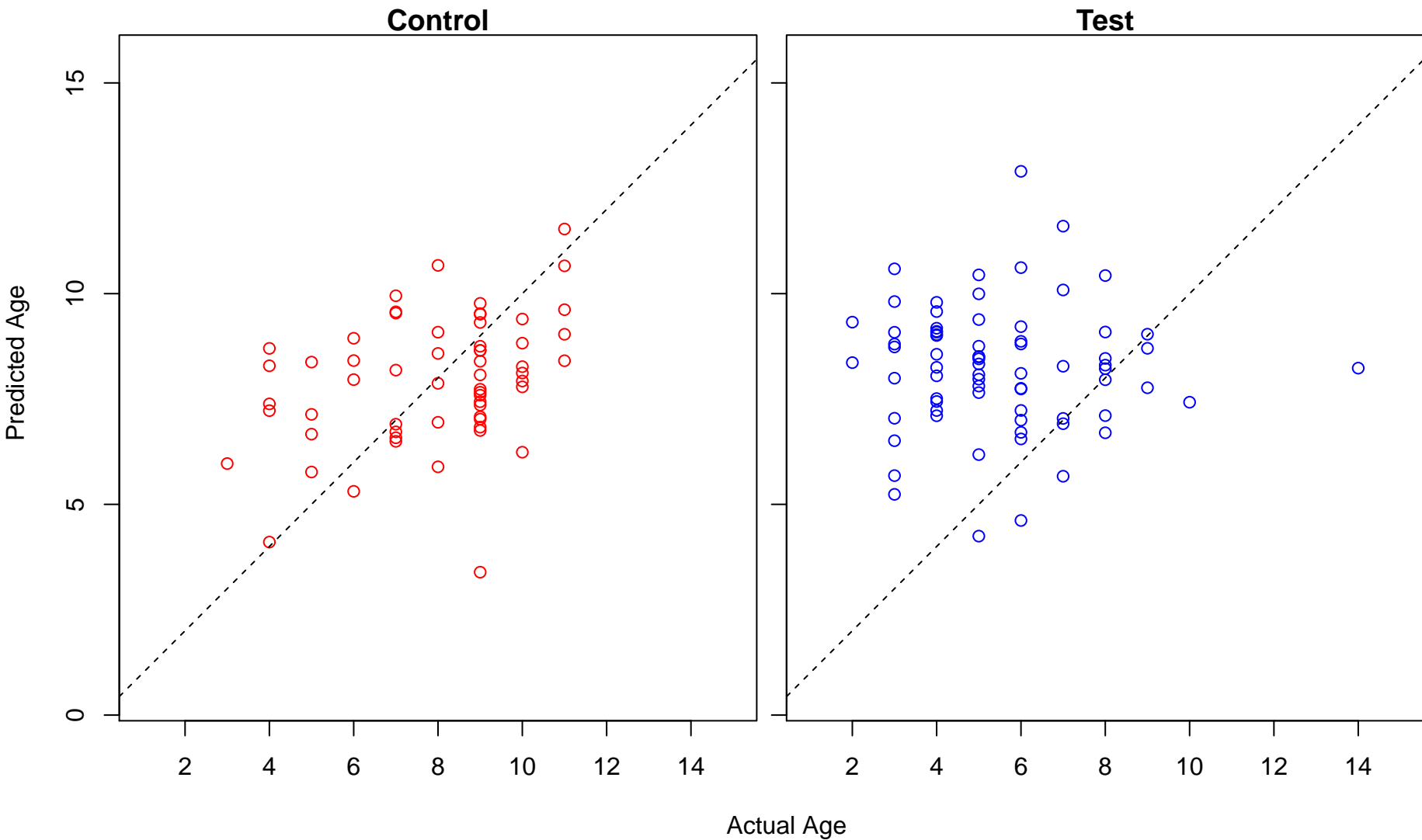
negative regulation of mononuclear cell proliferation (Score: 0.920209)



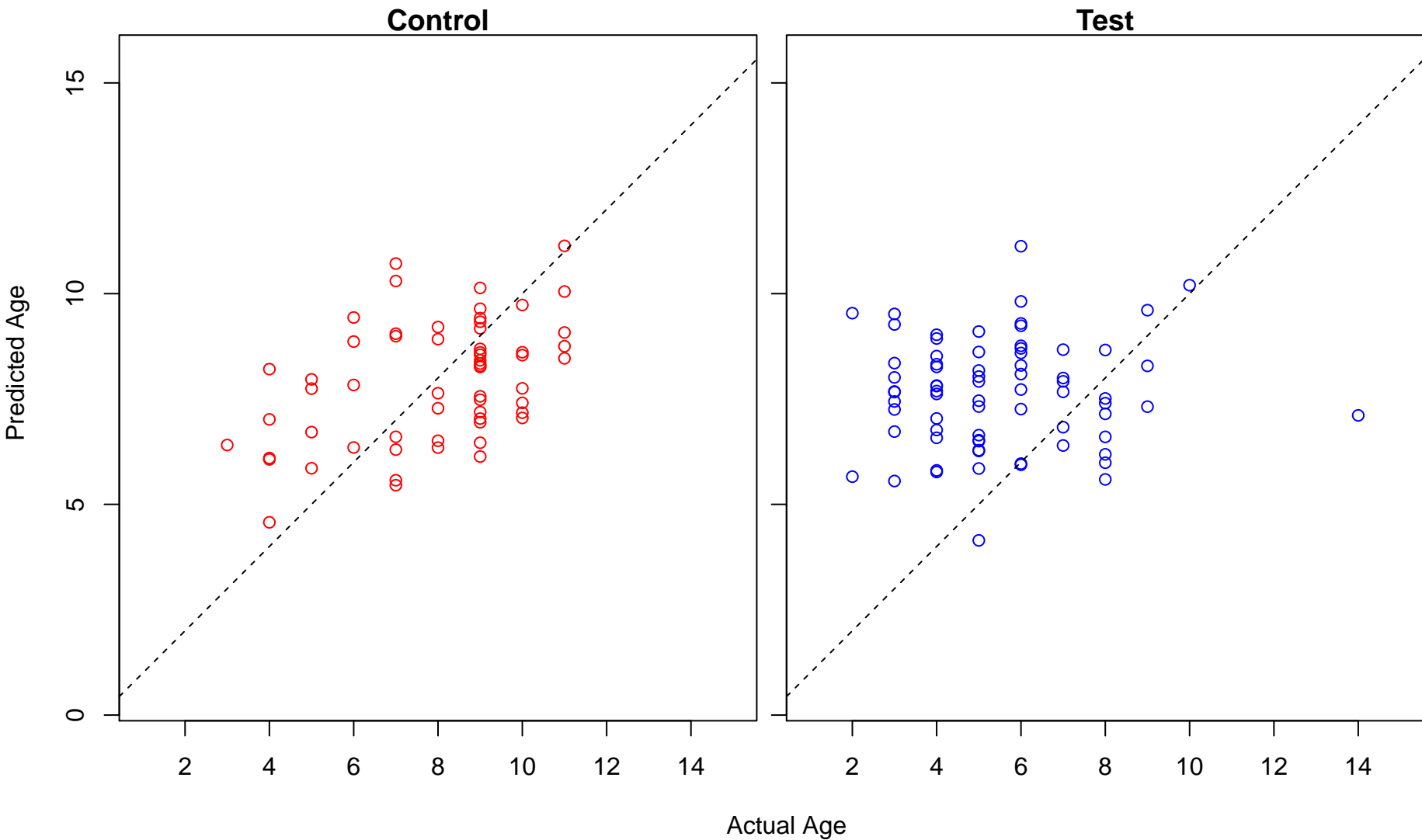
negative regulation of lymphocyte proliferation (Score: 0.920209)



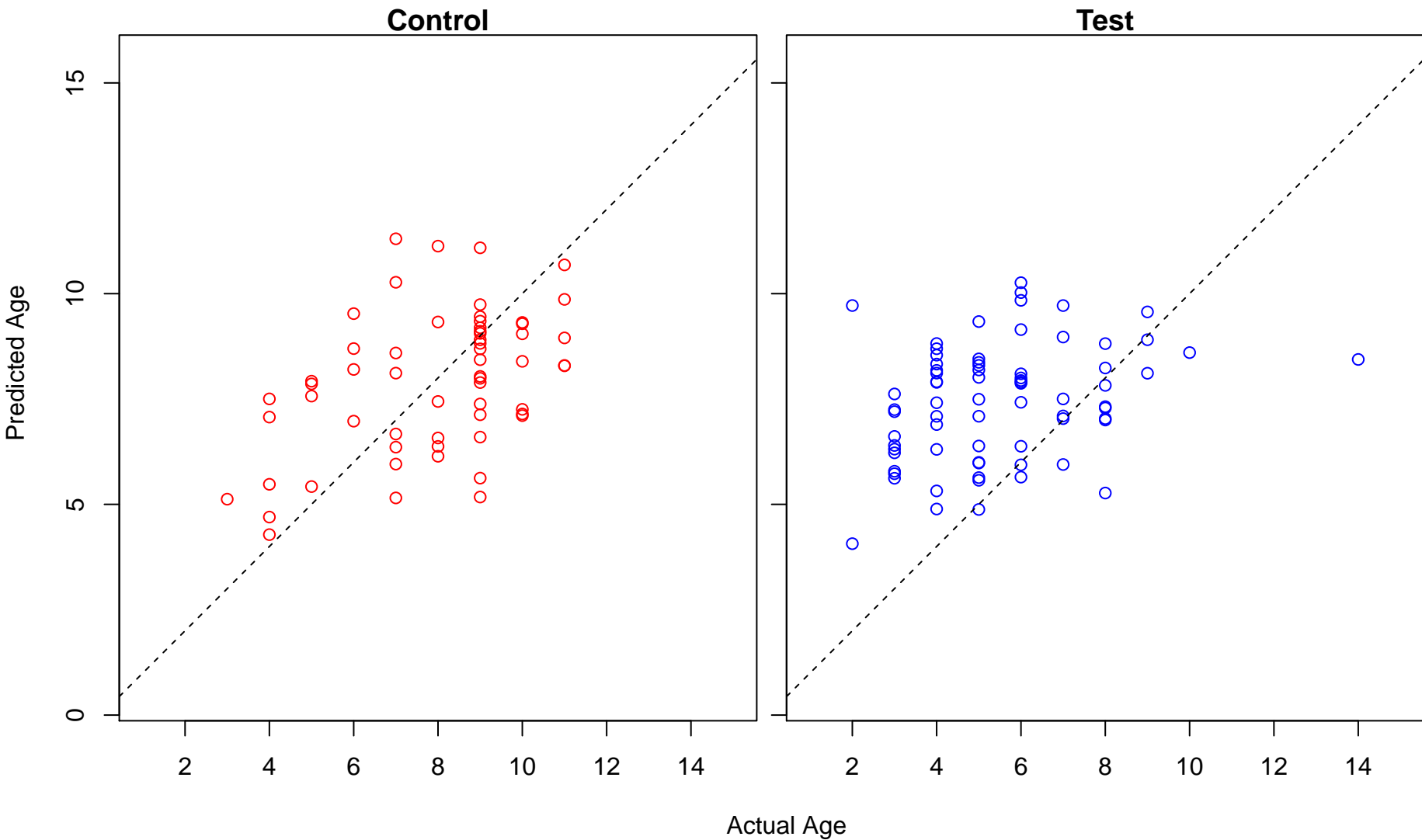
phospholipid catabolic process (Score: 0.919939)



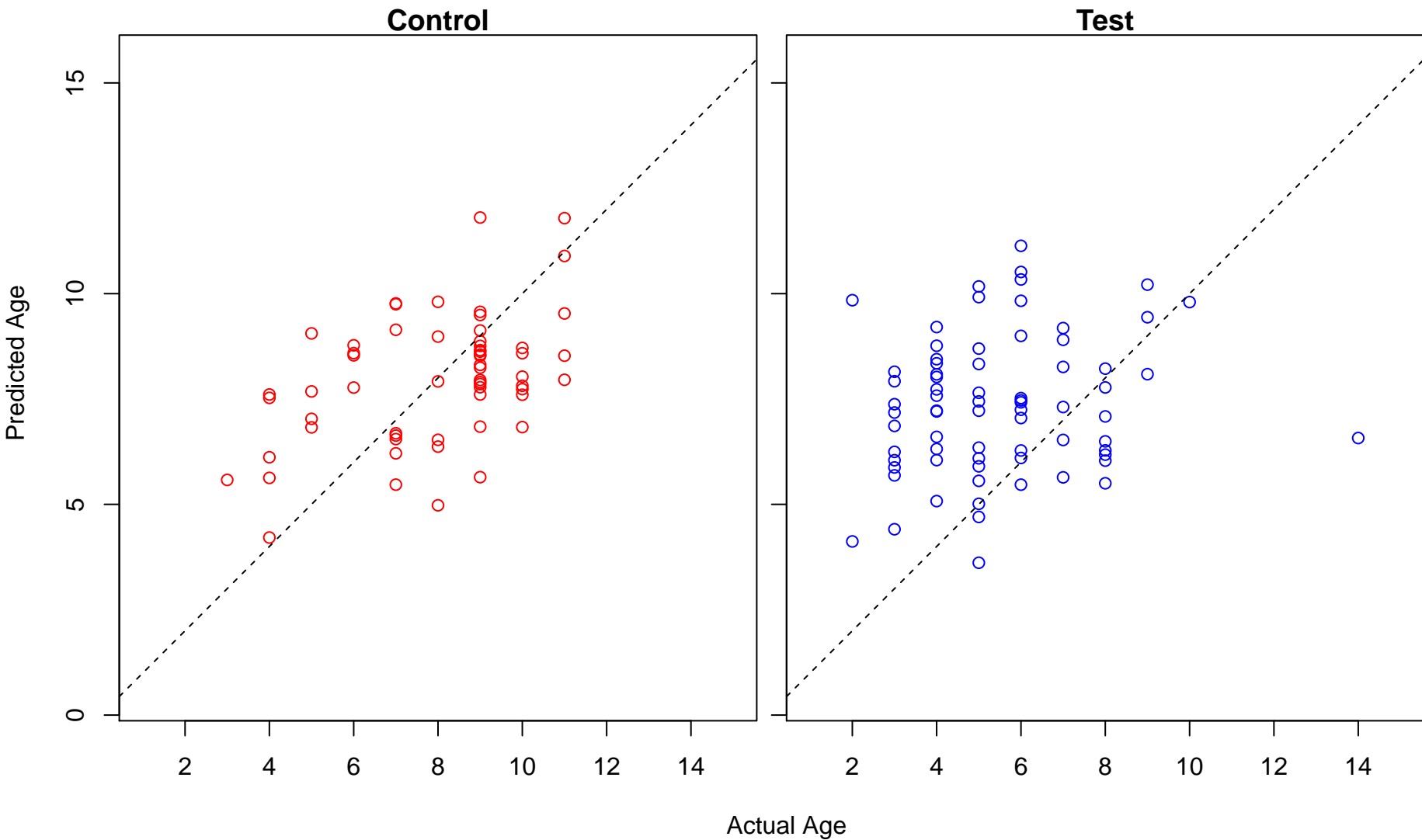
peptidyl-serine modification (Score: 0.919671)



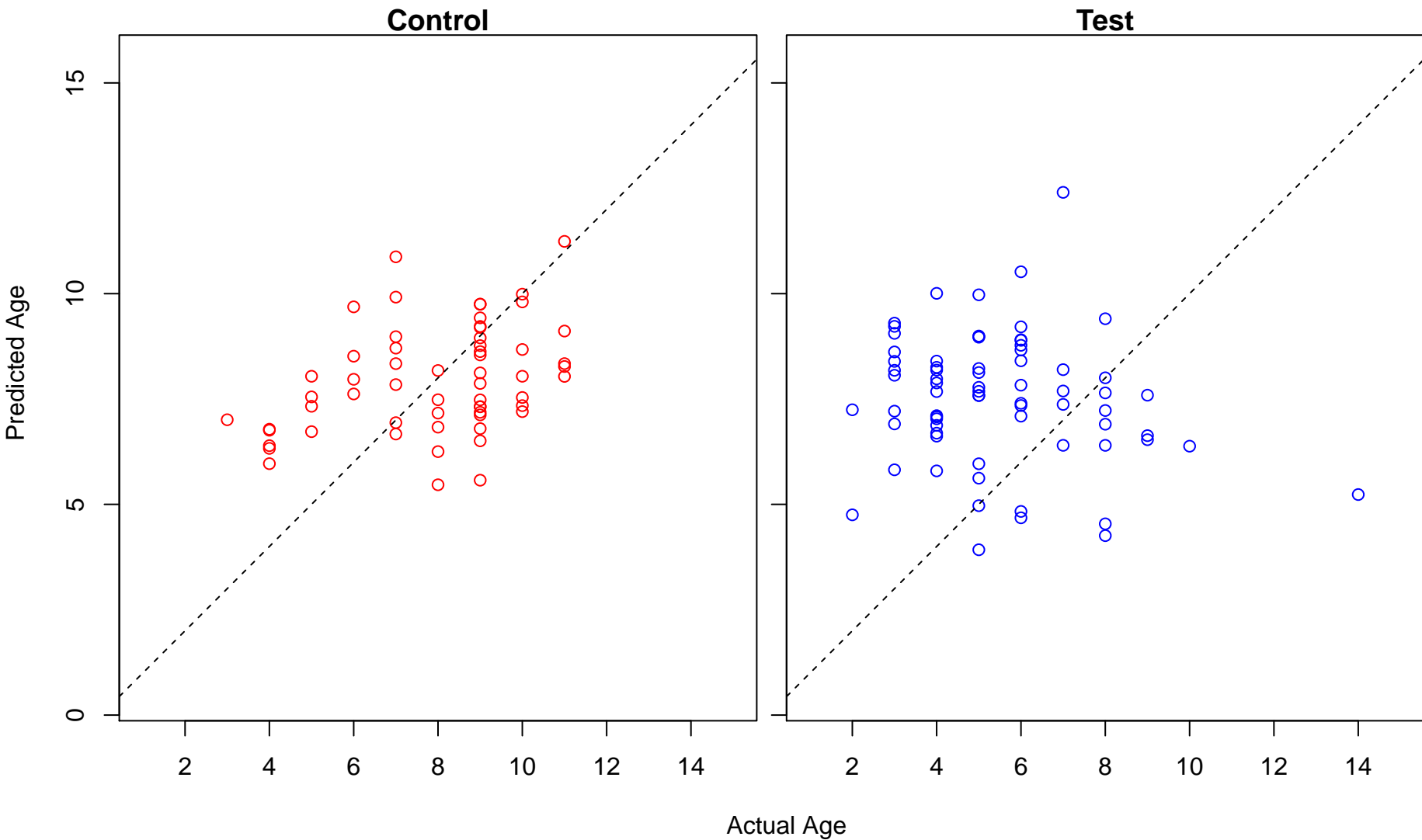
positive regulation of catalytic activity (Score: 0.919347)



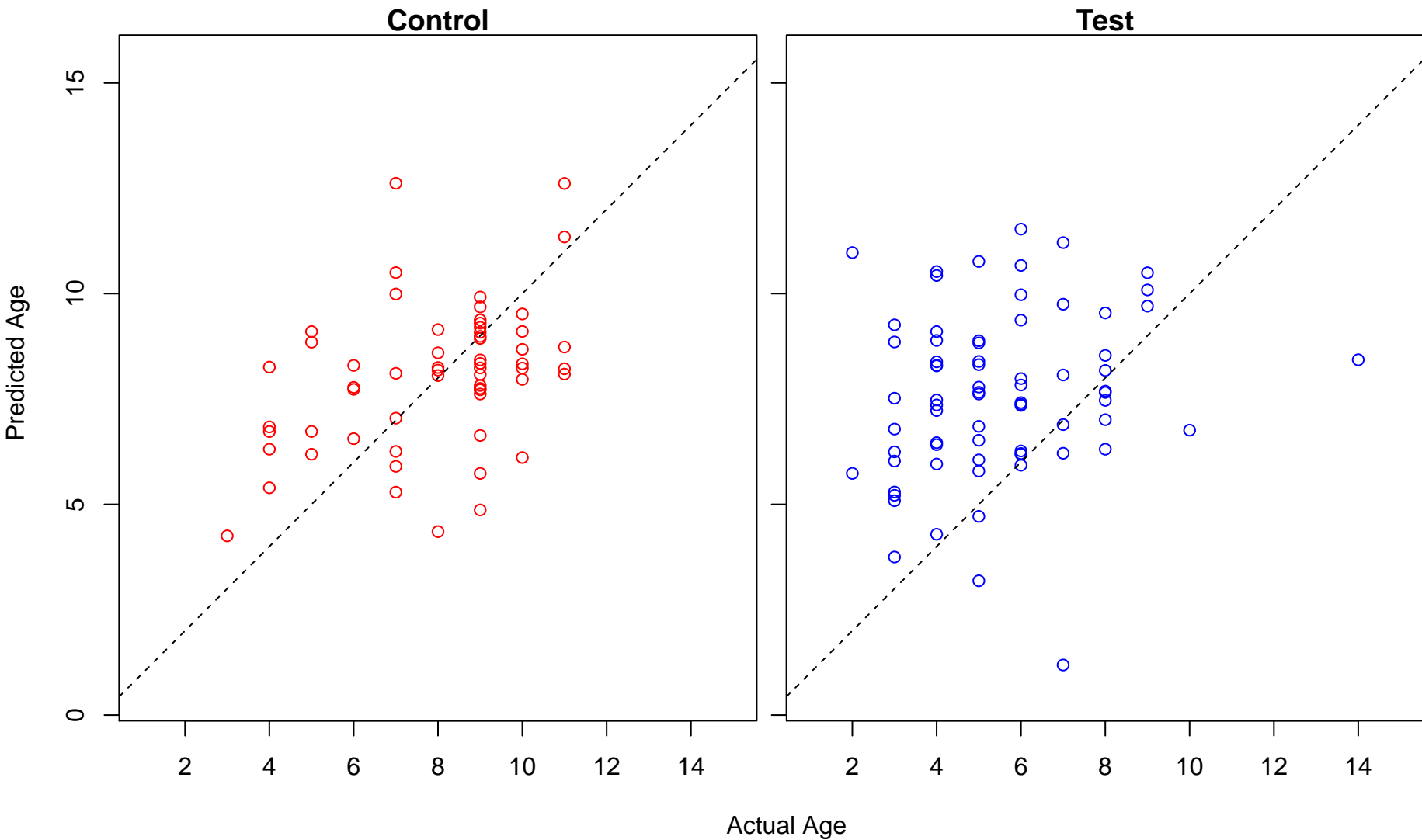
enzyme linked receptor protein signaling pathway (Score: 0.919179)



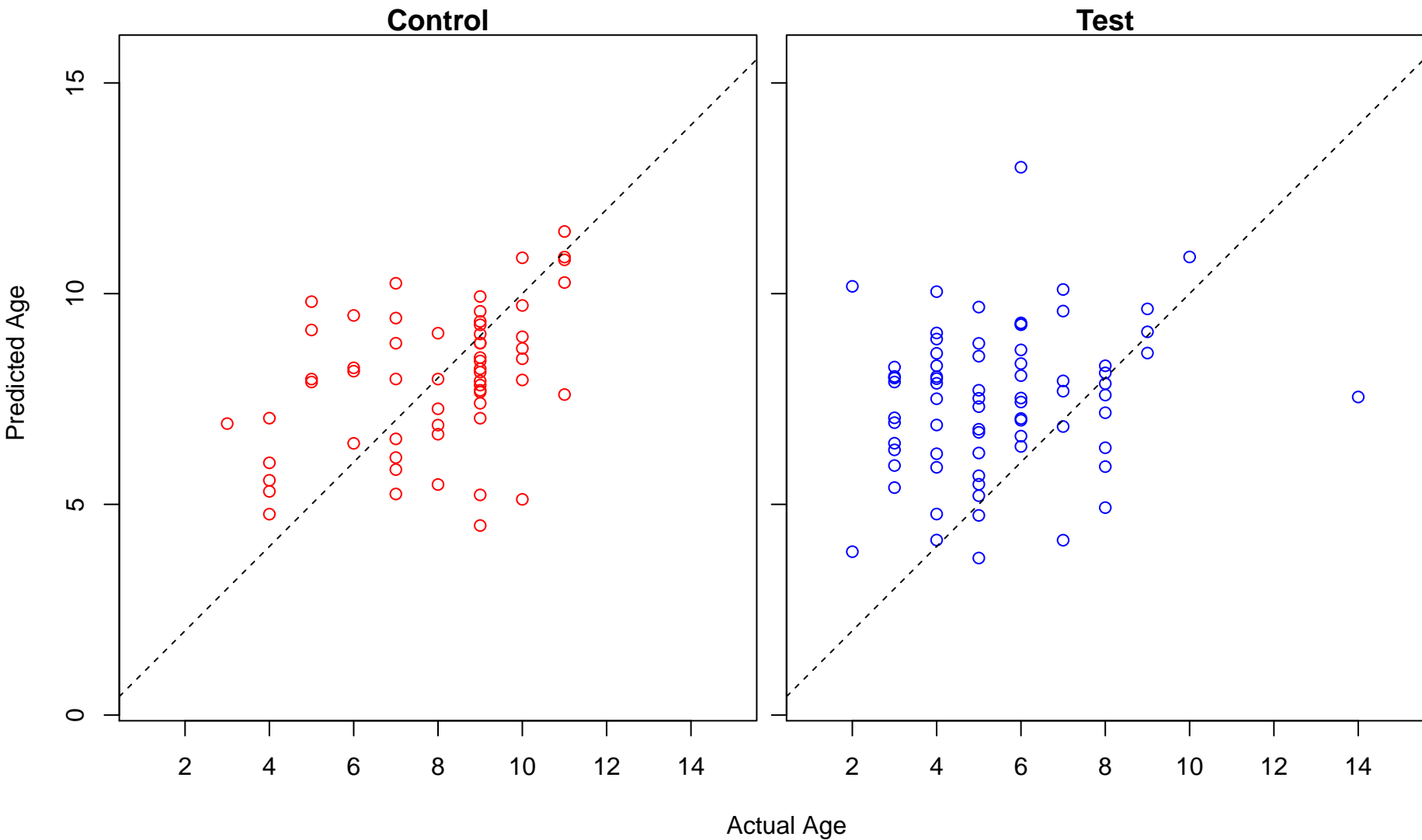
anagen (Score: 0.918308)



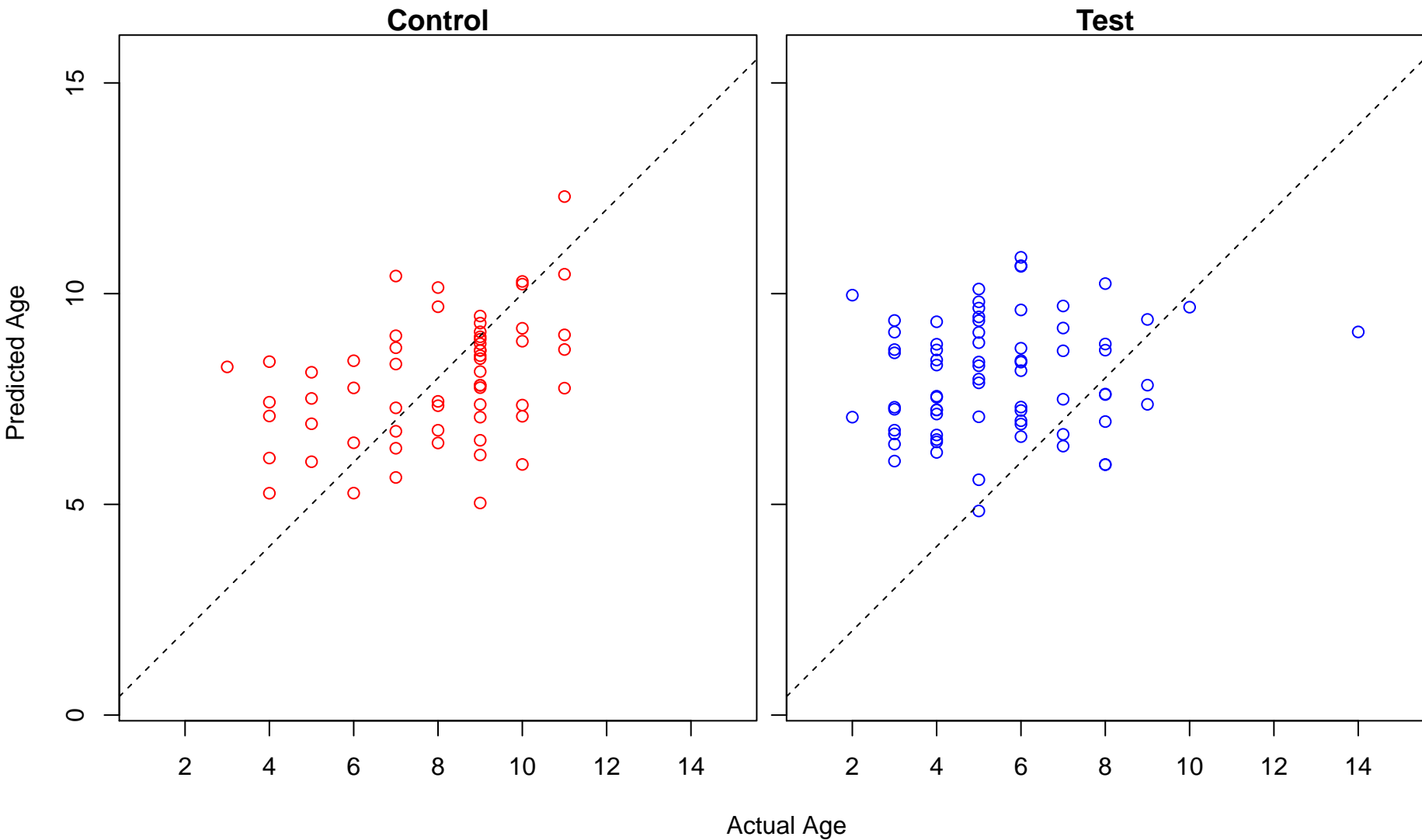
regulation of cell proliferation (Score: 0.918067)



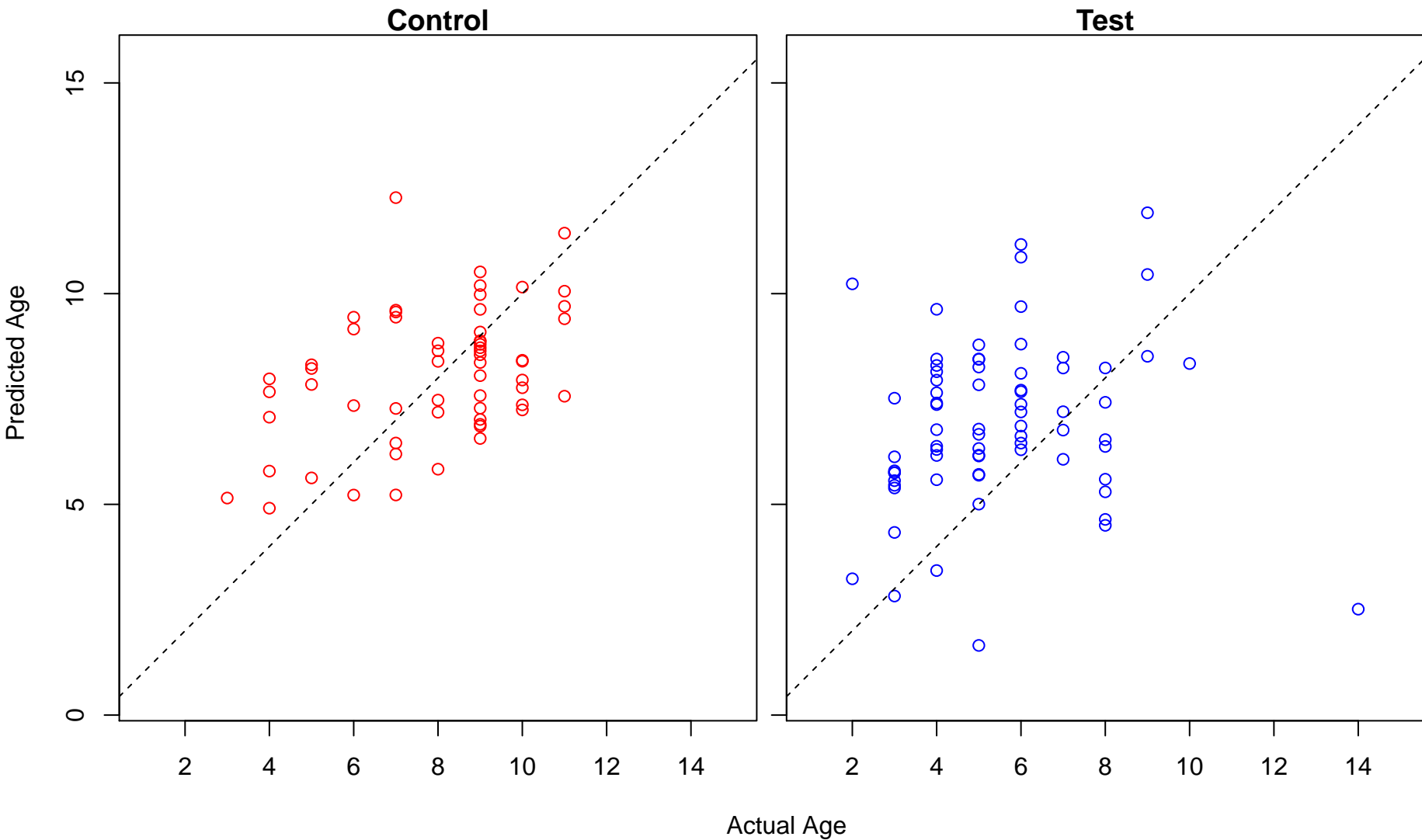
negative regulation of multicellular organismal process (Score: 0.917915)



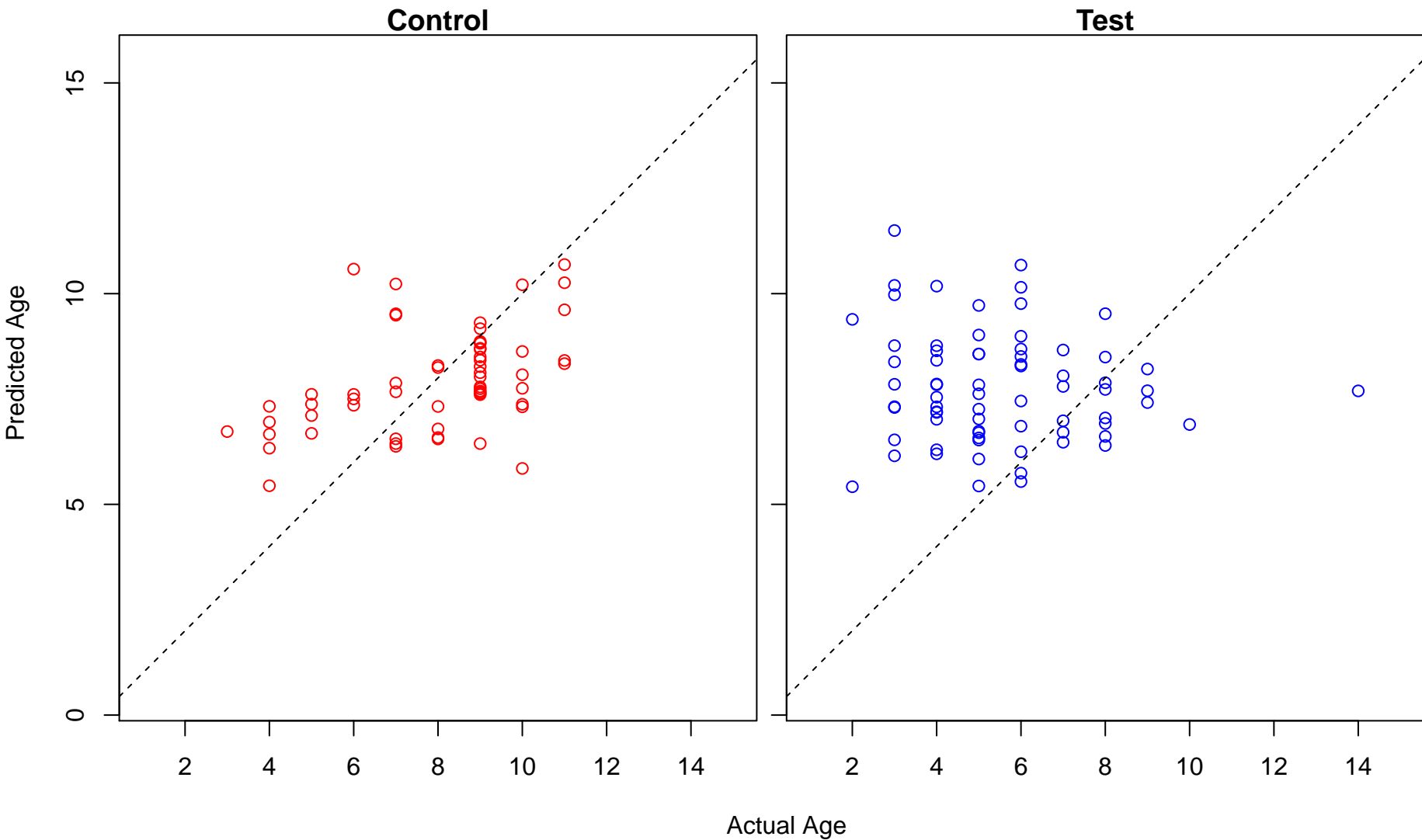
translational termination (Score: 0.916423)



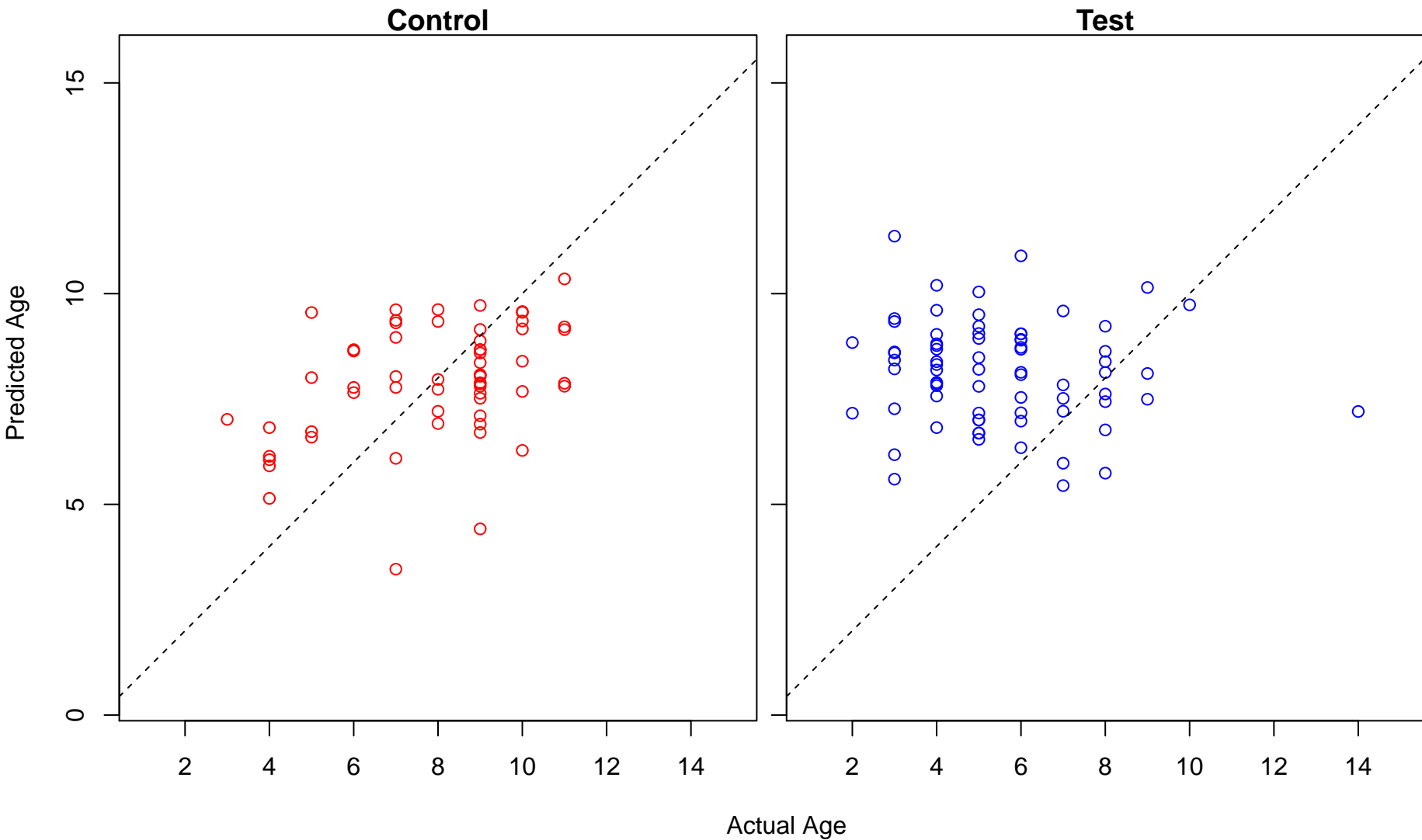
cellular response to stress (Score: 0.916089)



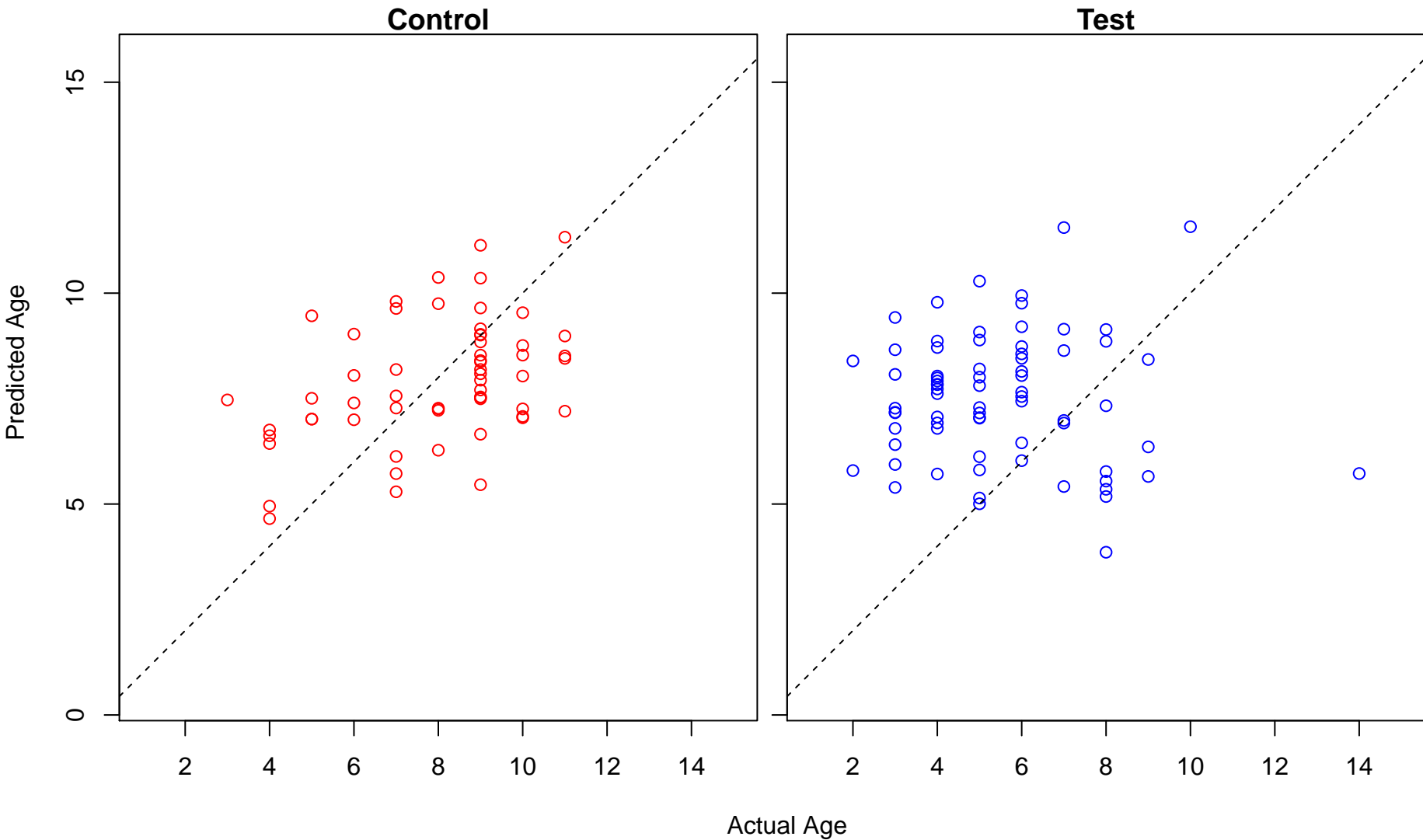
receptor clustering (Score: 0.916065)



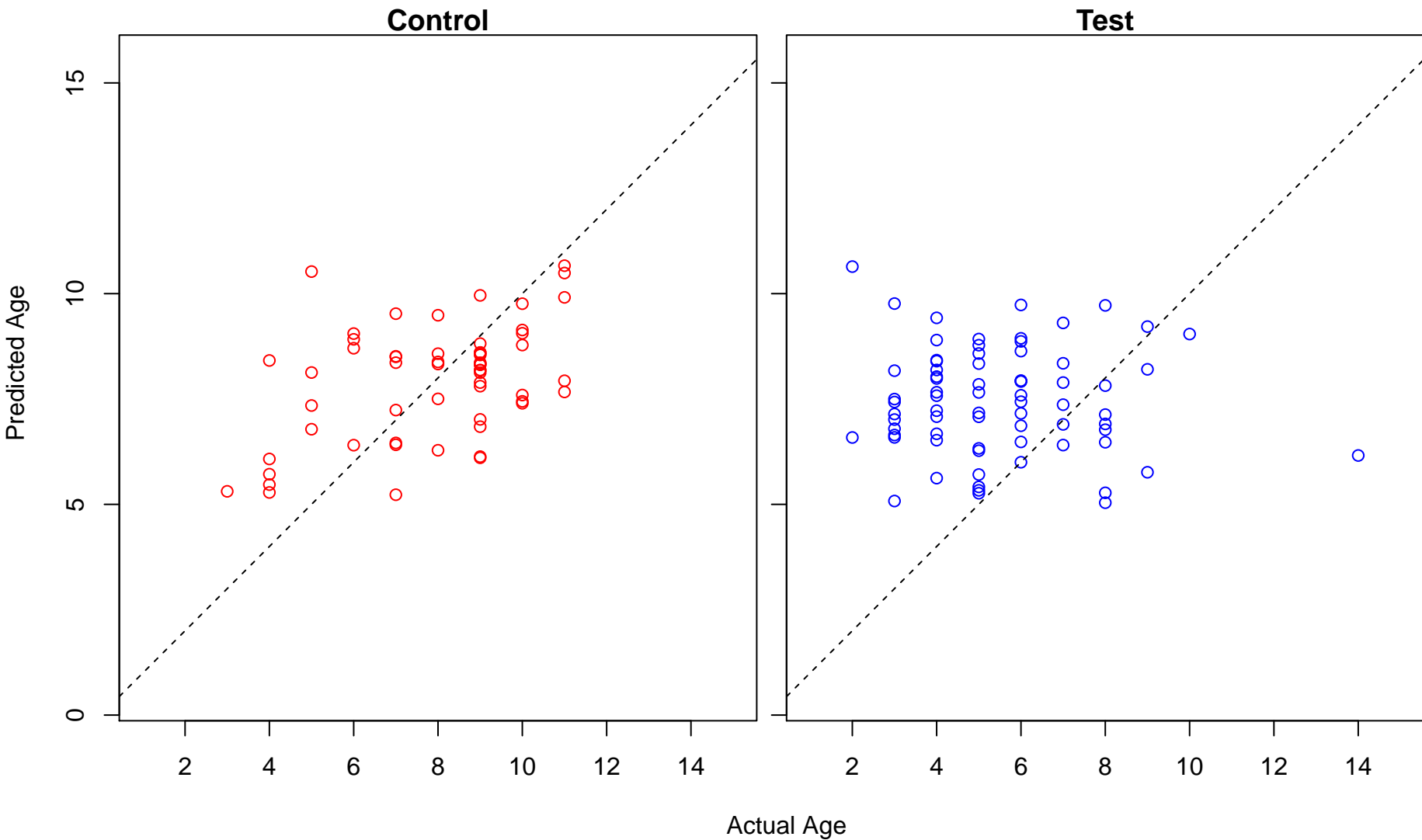
SCF complex assembly (Score: 0.915950)



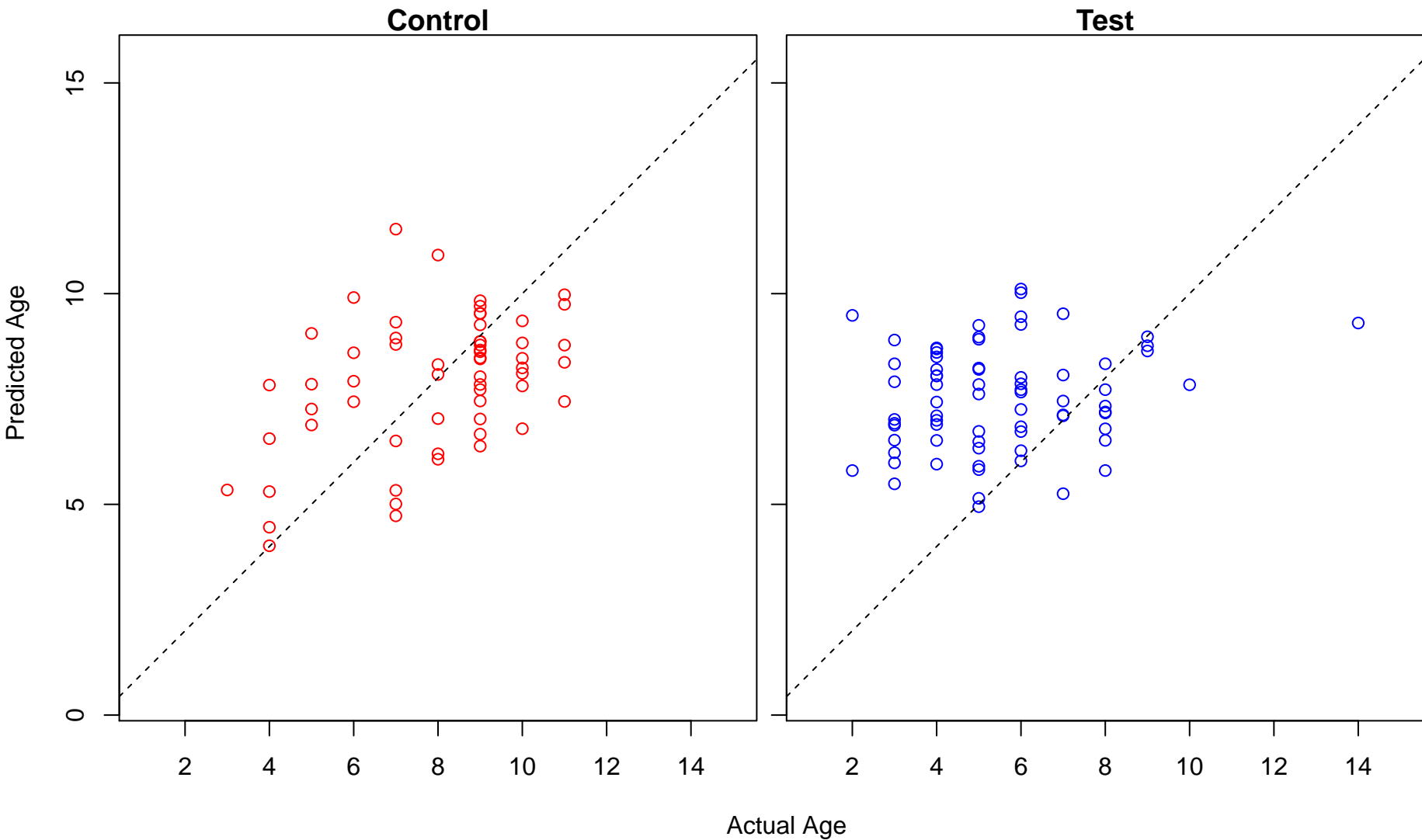
positive regulation of developmental growth (Score: 0.914828)



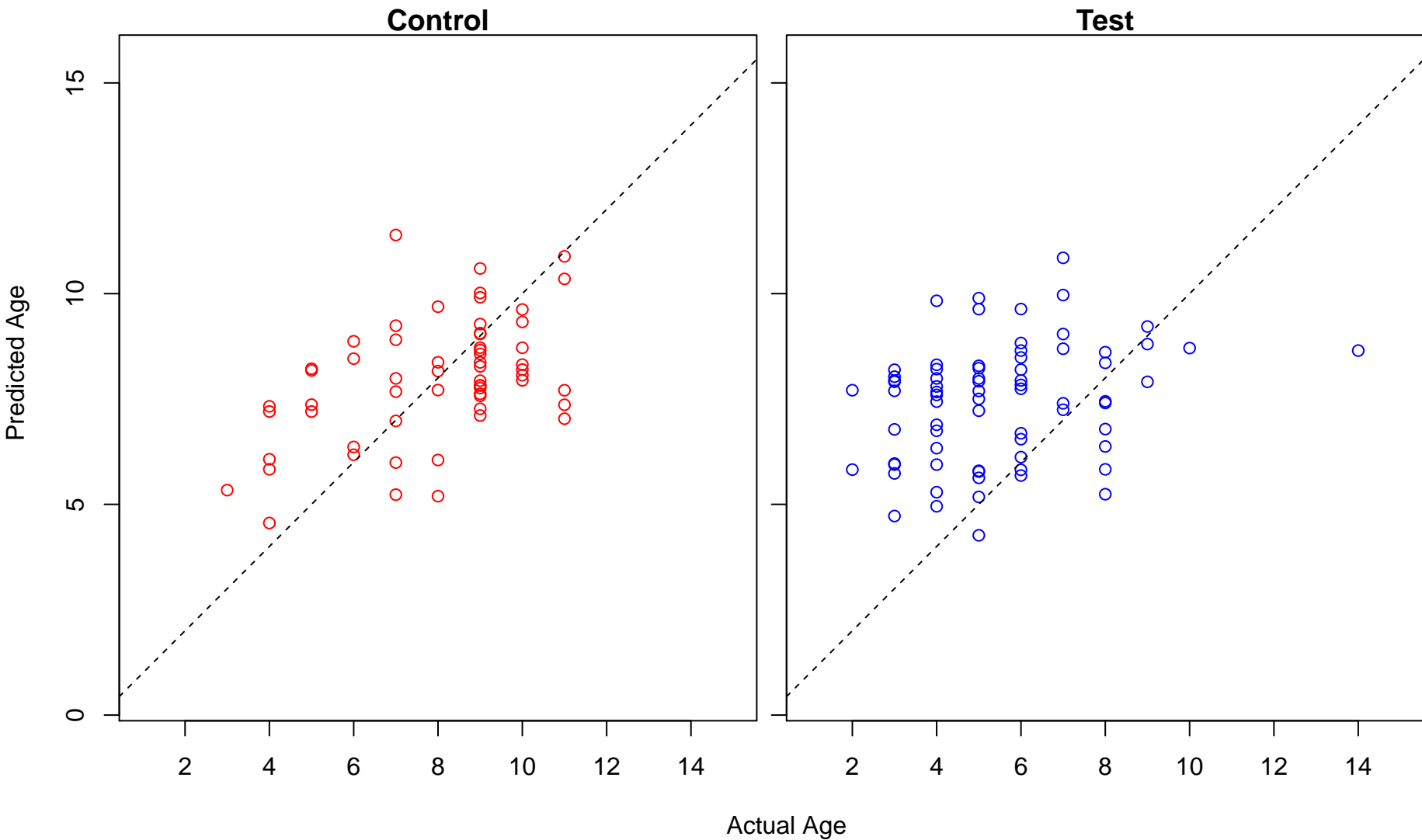
positive regulation of histone modification (Score: 0.913813)



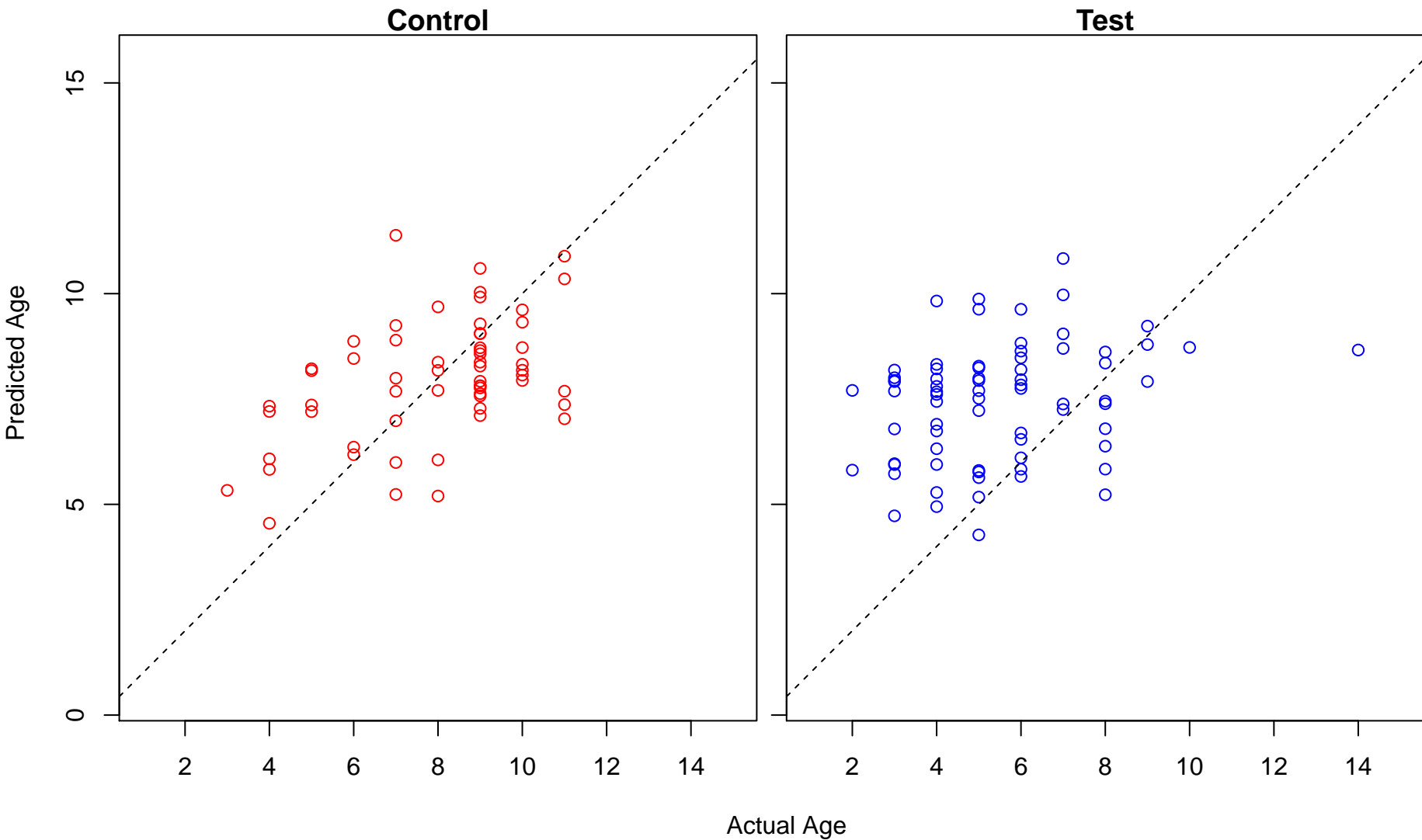
chemical homeostasis (Score: 0.913247)



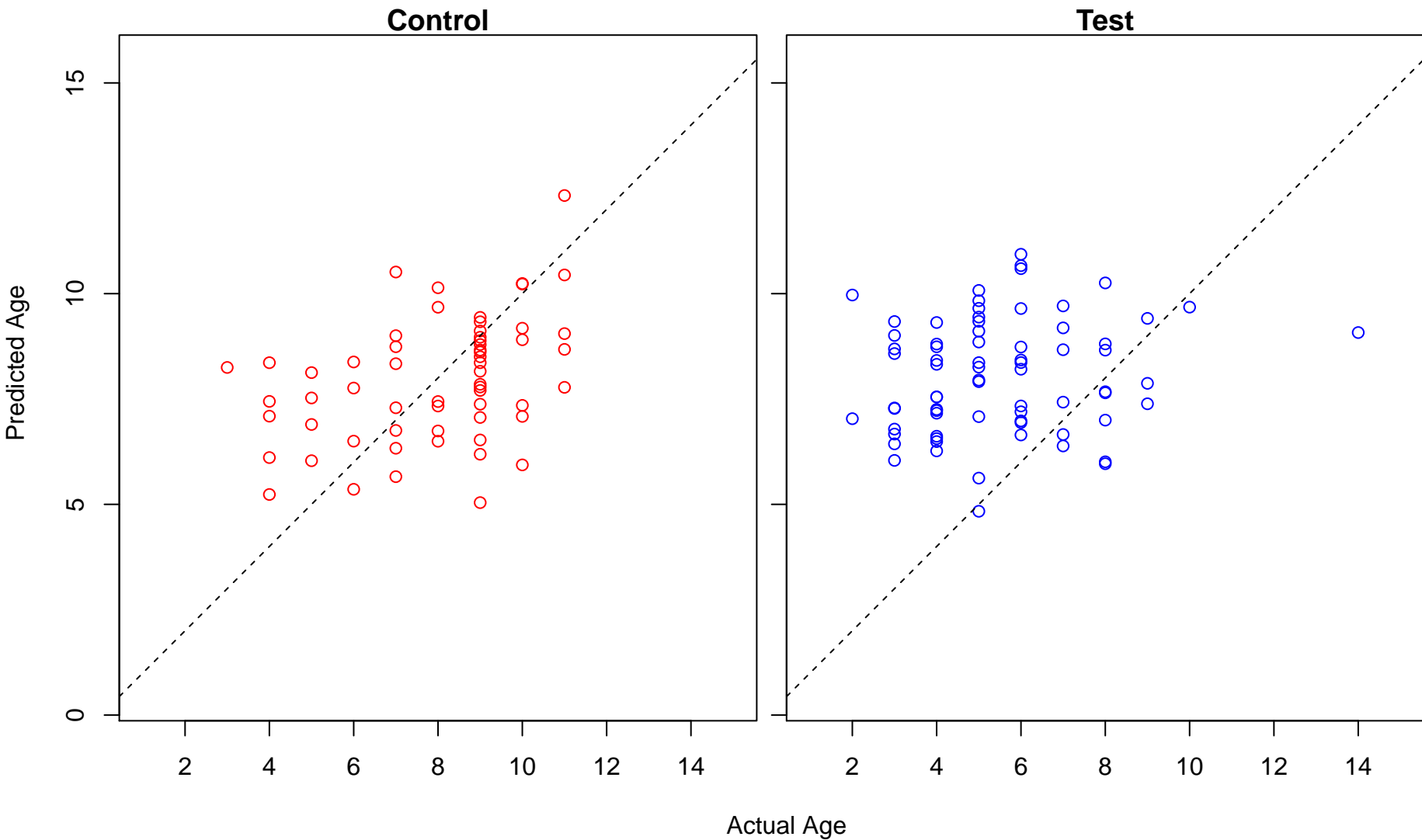
cardiac muscle cell proliferation (Score: 0.913009)



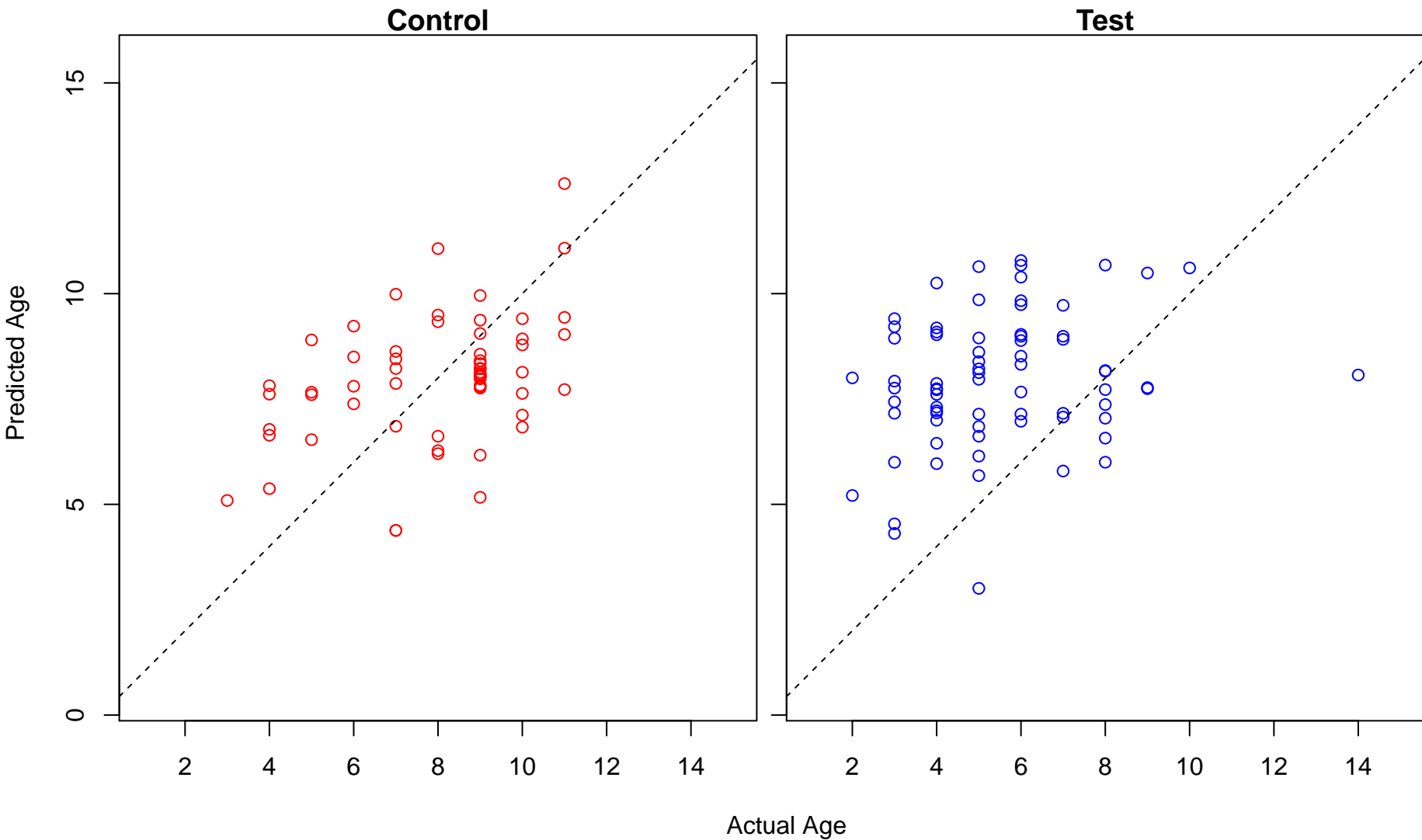
striated muscle cell proliferation (Score: 0.911945)



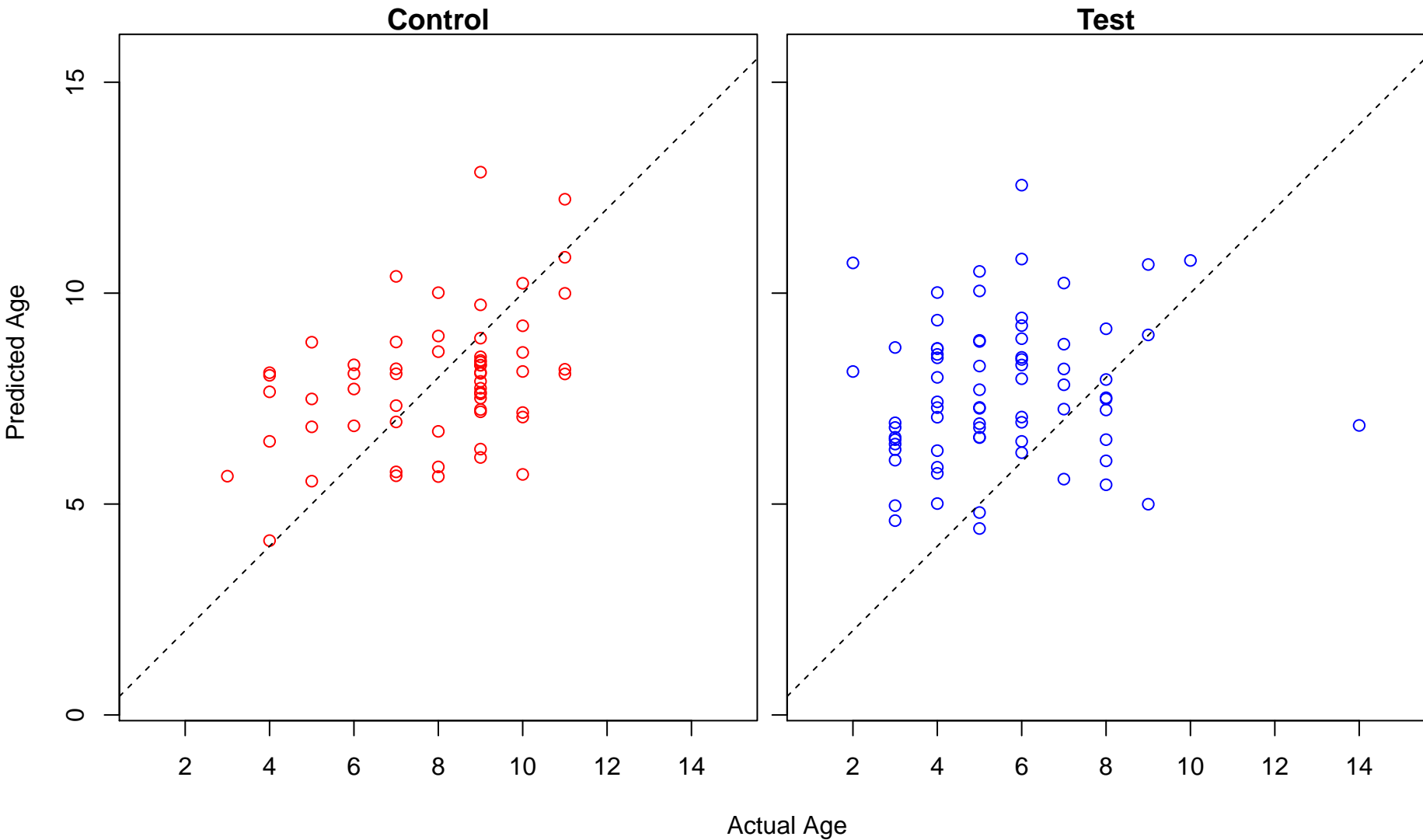
cellular protein complex disassembly (Score: 0.911895)



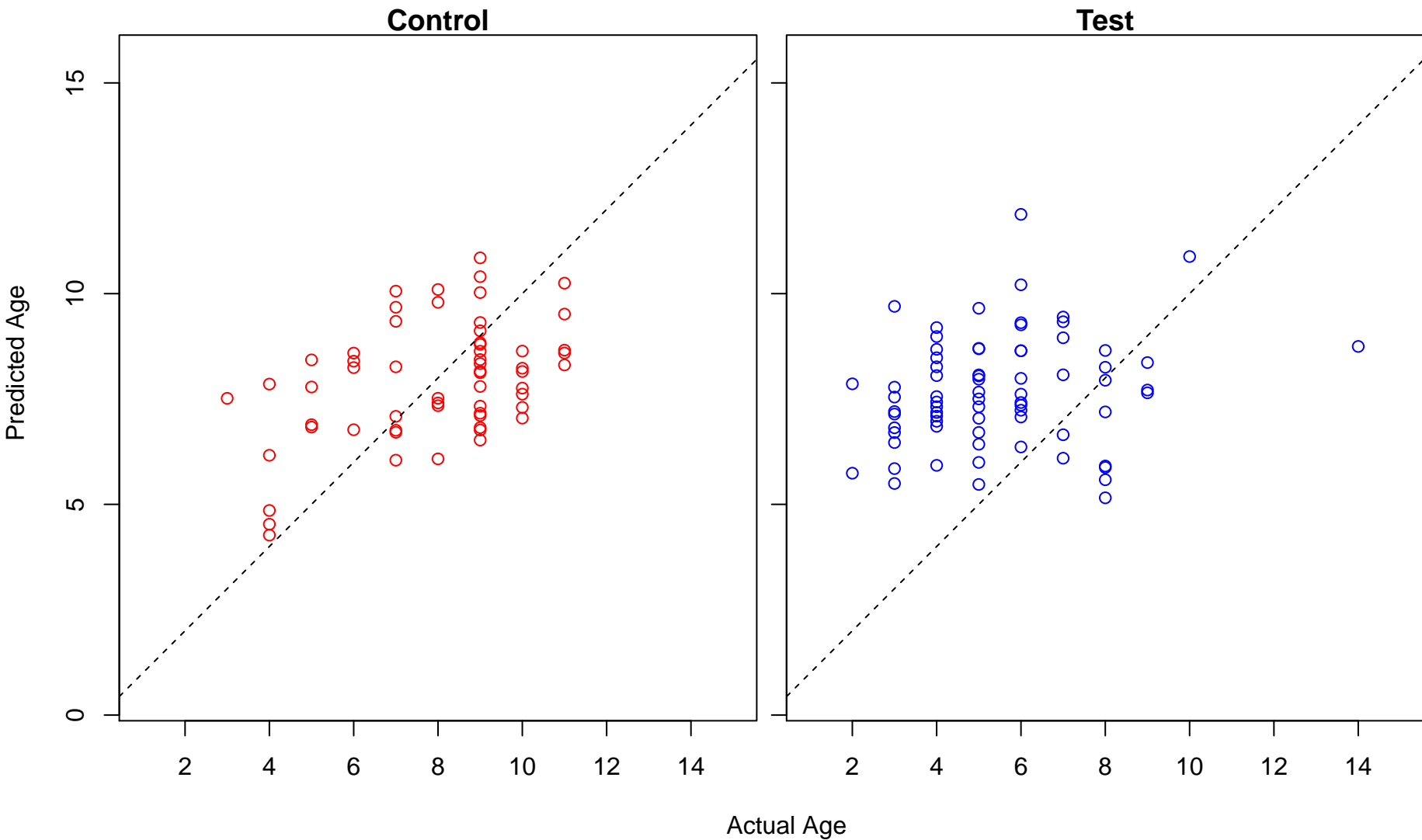
patterning of blood vessels (Score: 0.911711)



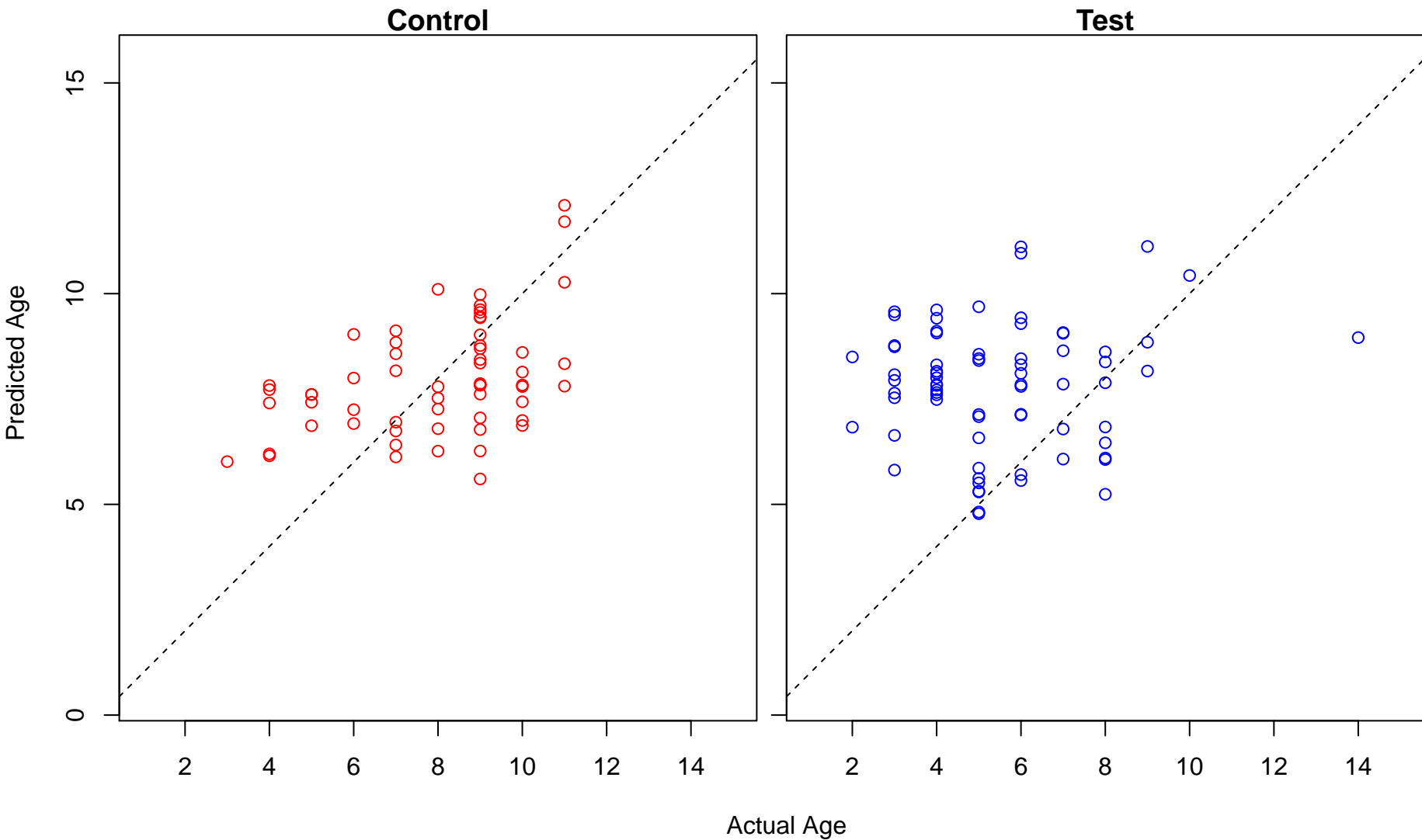
negative regulation of intrinsic apoptotic signaling pathway (Score: 0.911028)



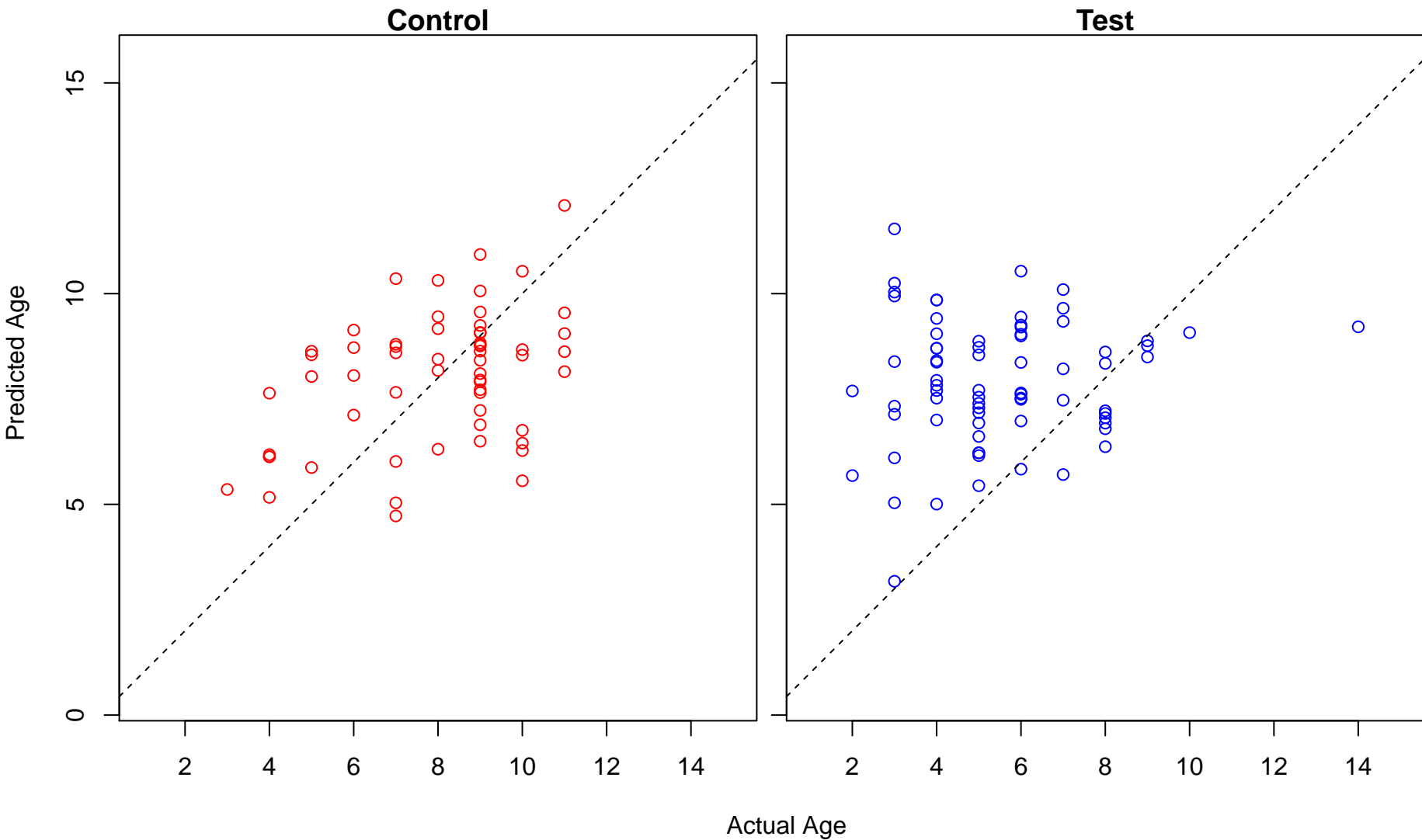
columnar/cuboidal epithelial cell differentiation (Score: 0.910549)



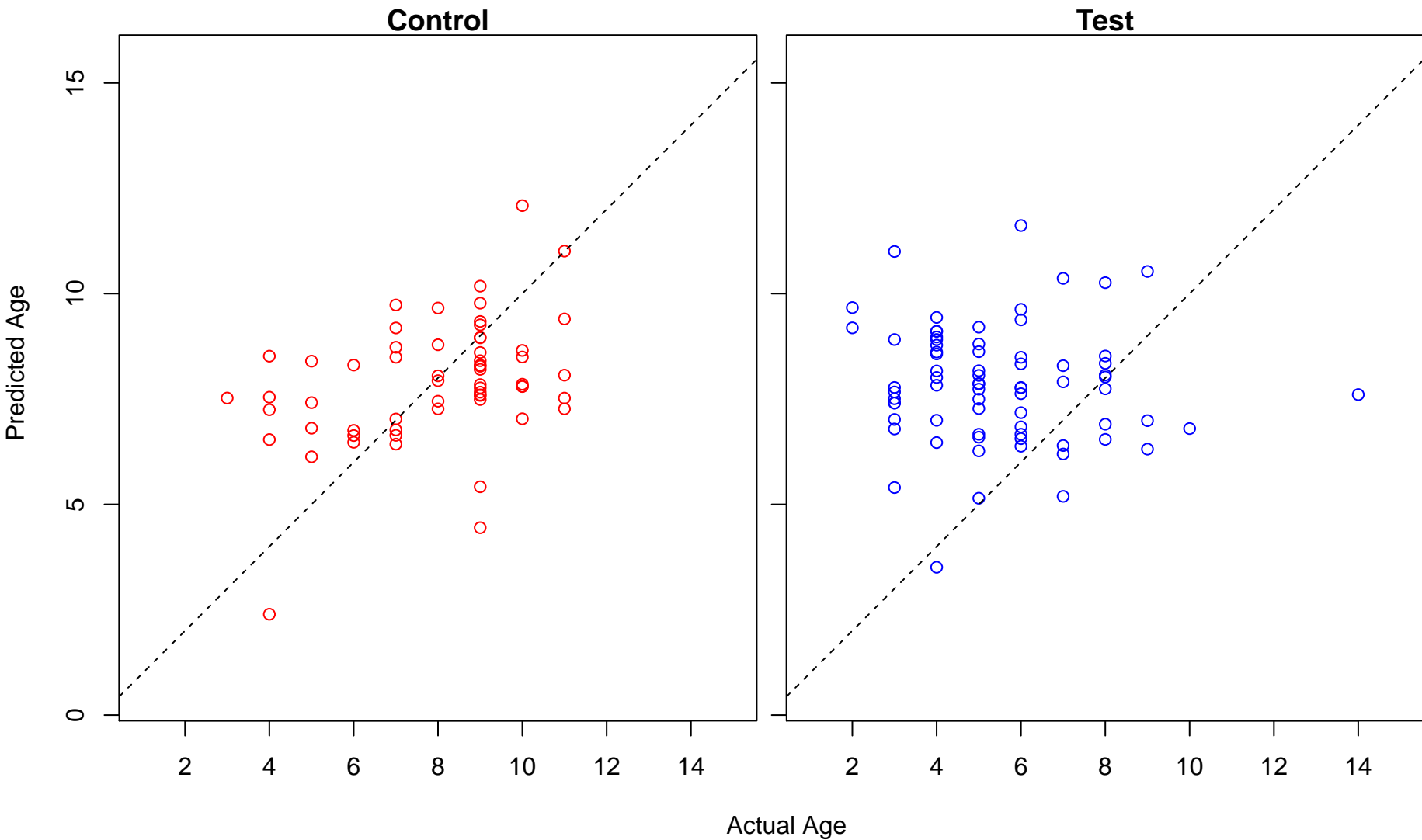
cellular modified amino acid biosynthetic process (Score: 0.910320)



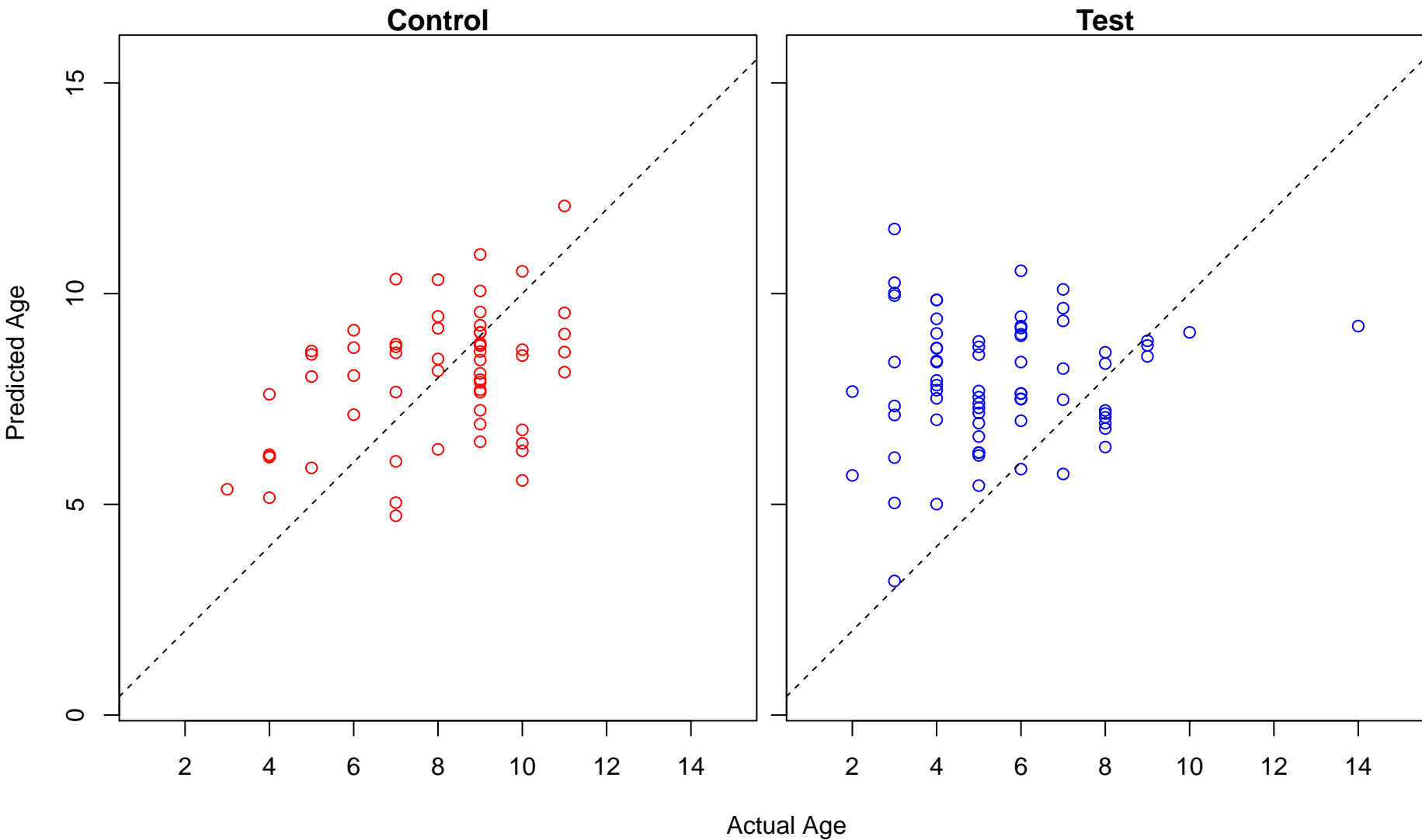
regulation of muscle tissue development (Score: 0.910084)



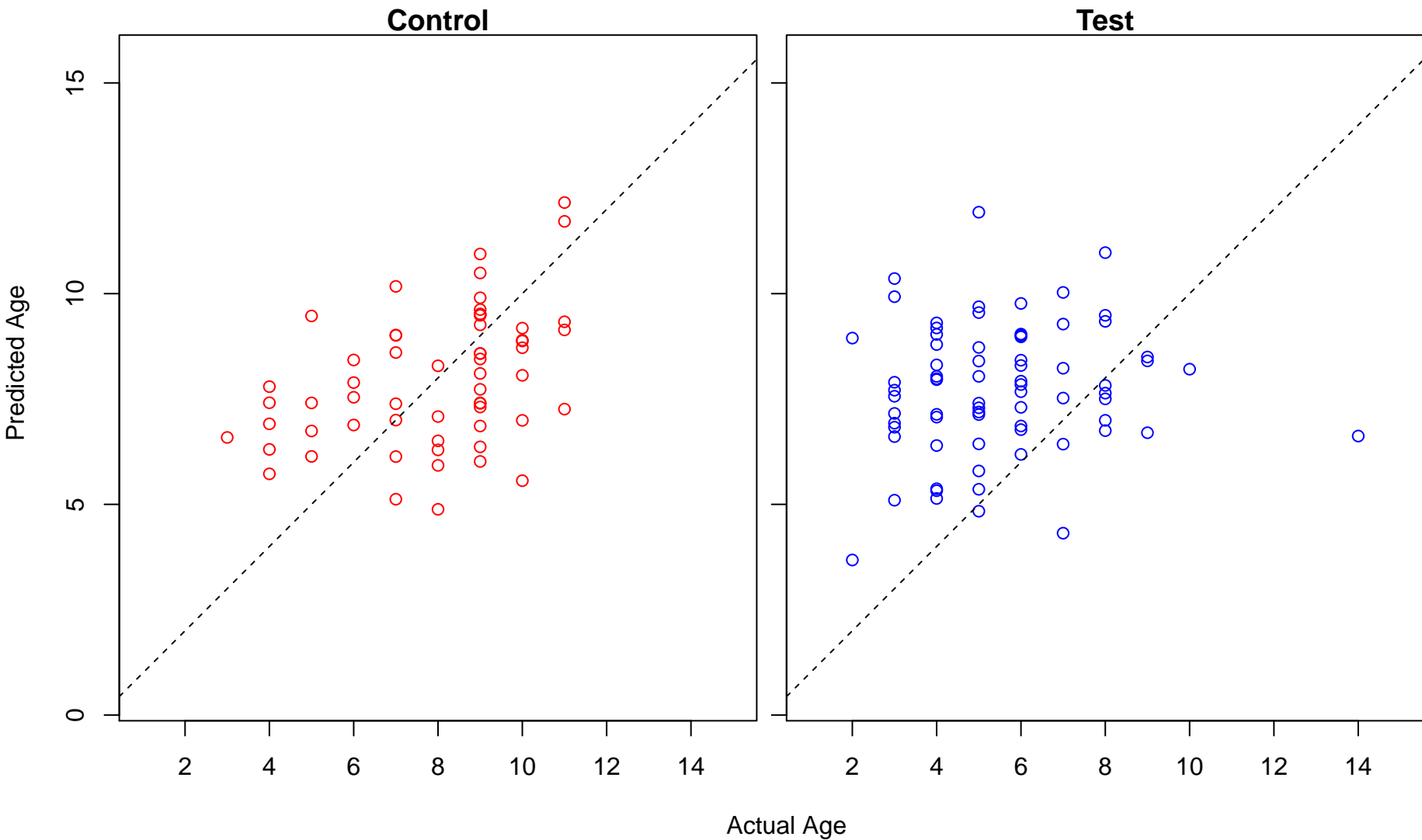
axon regeneration (Score: 0.909973)



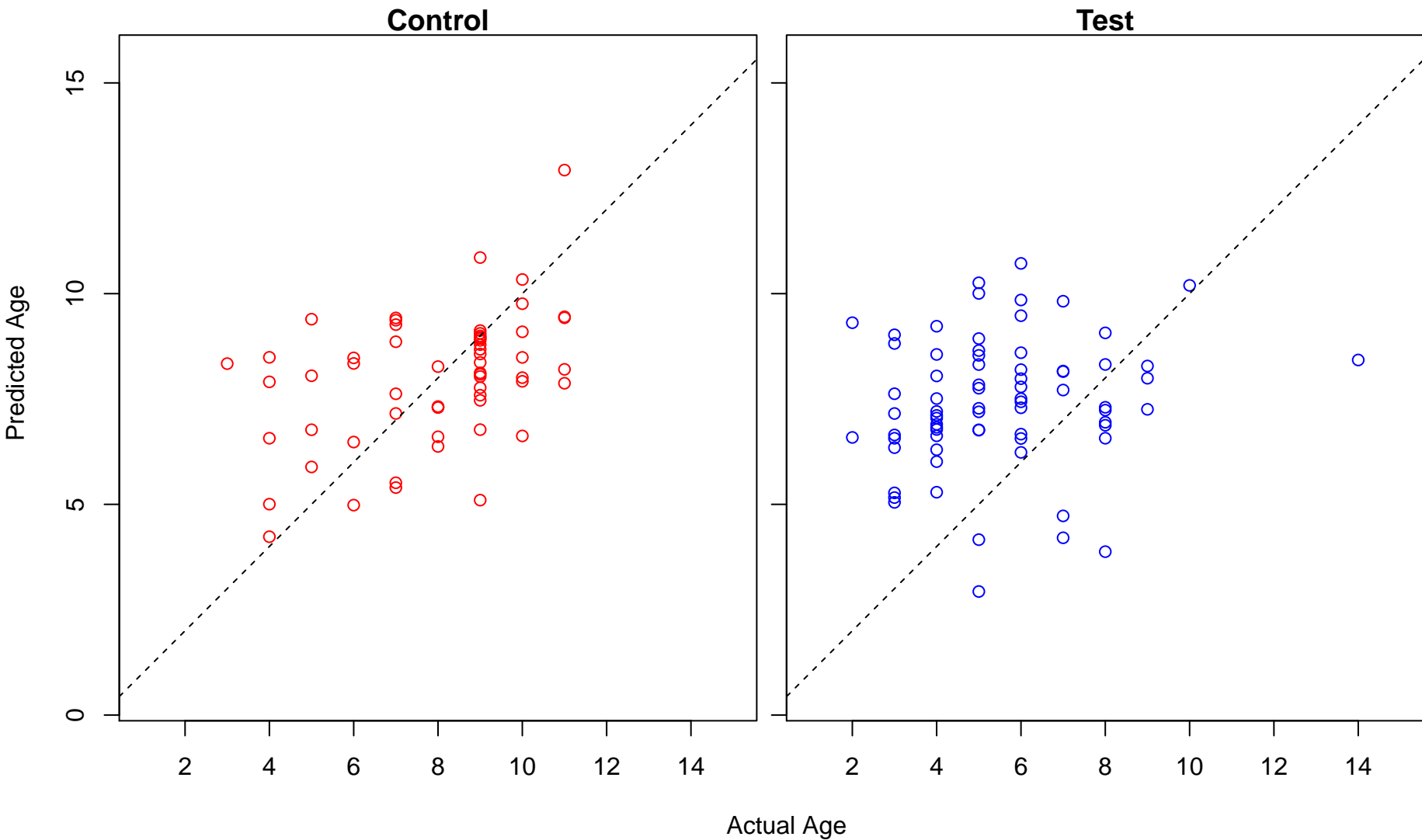
regulation of striated muscle tissue development (Score: 0.909868)



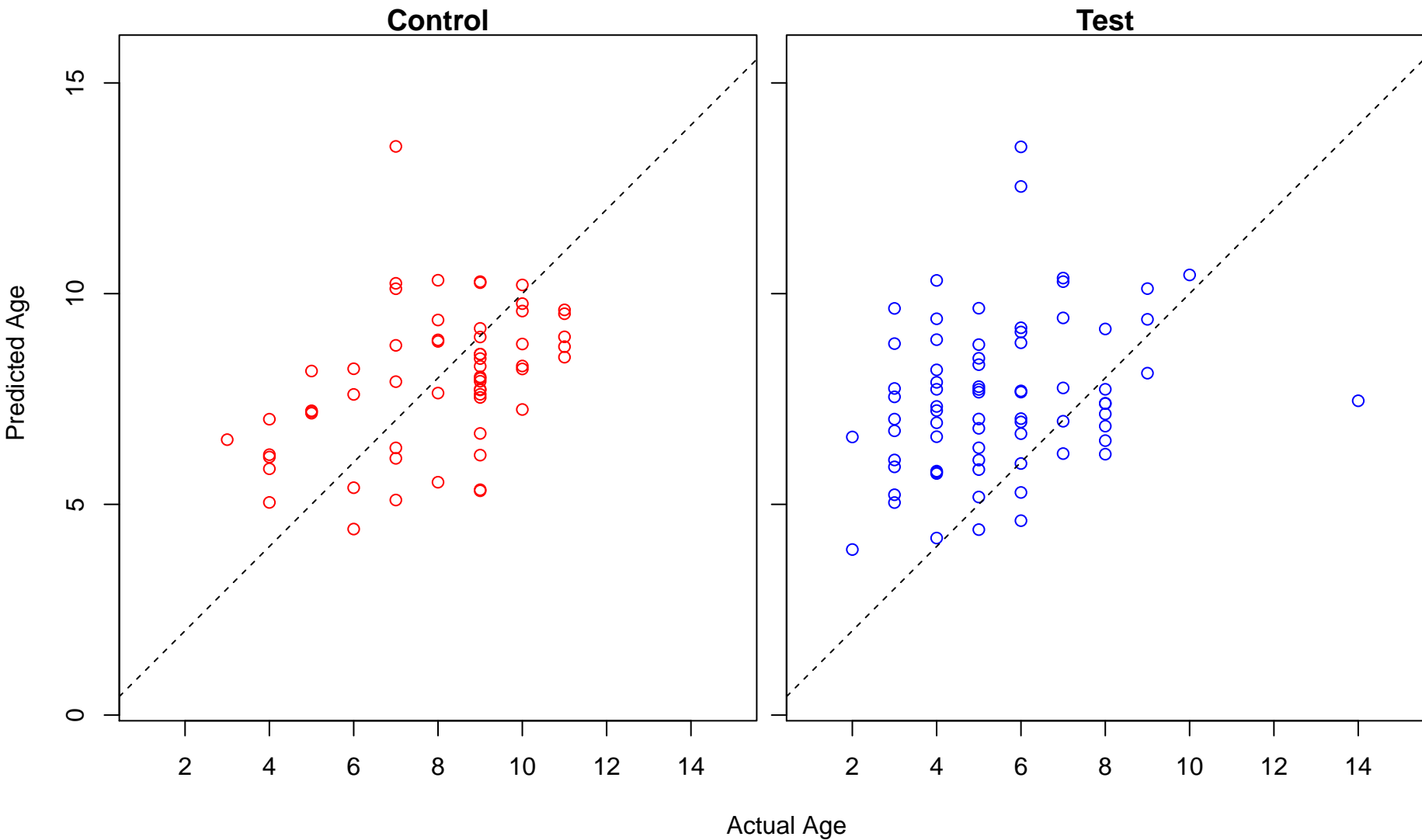
glycosphingolipid metabolic process (Score: 0.909793)



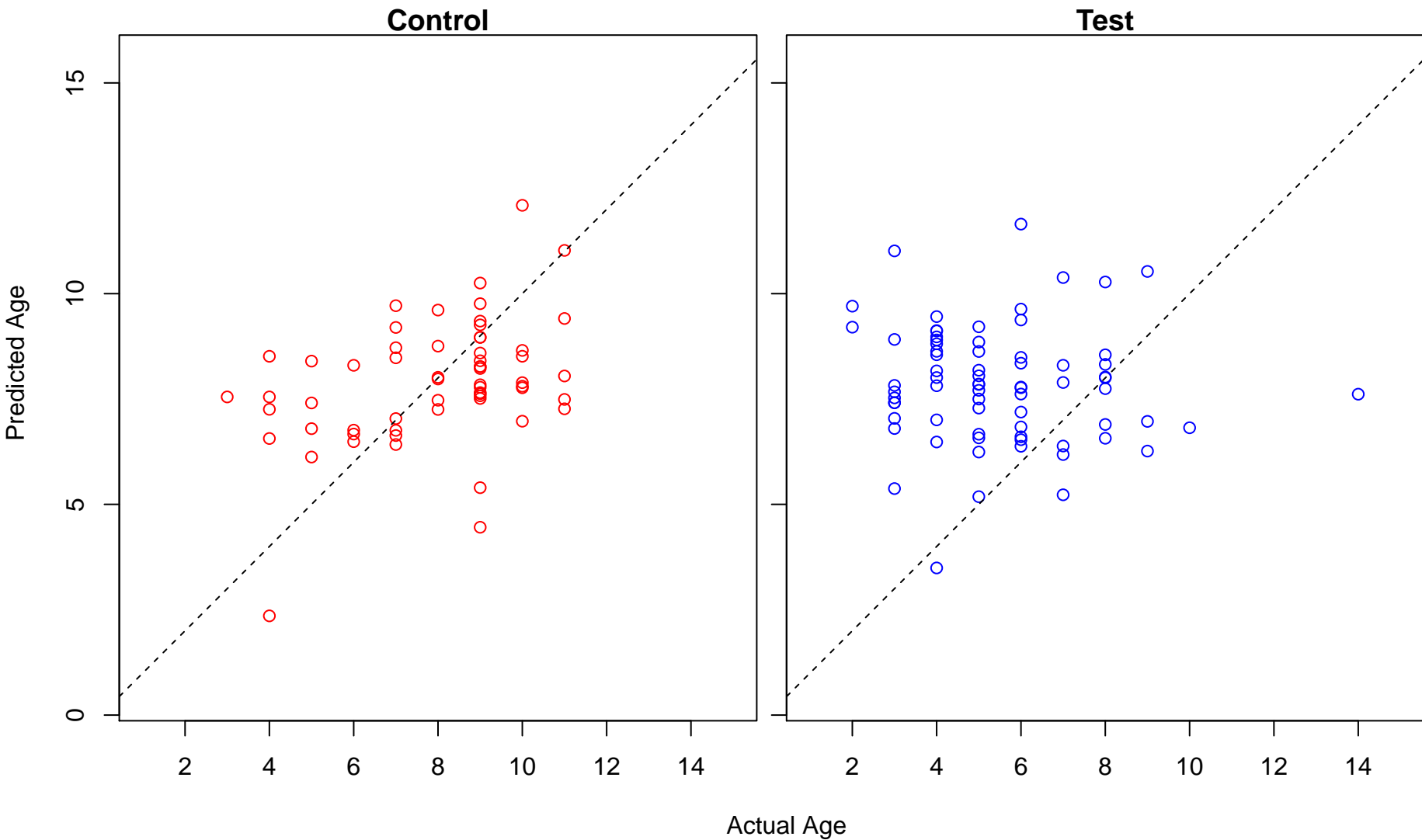
organonitrogen compound biosynthetic process (Score: 0.908622)



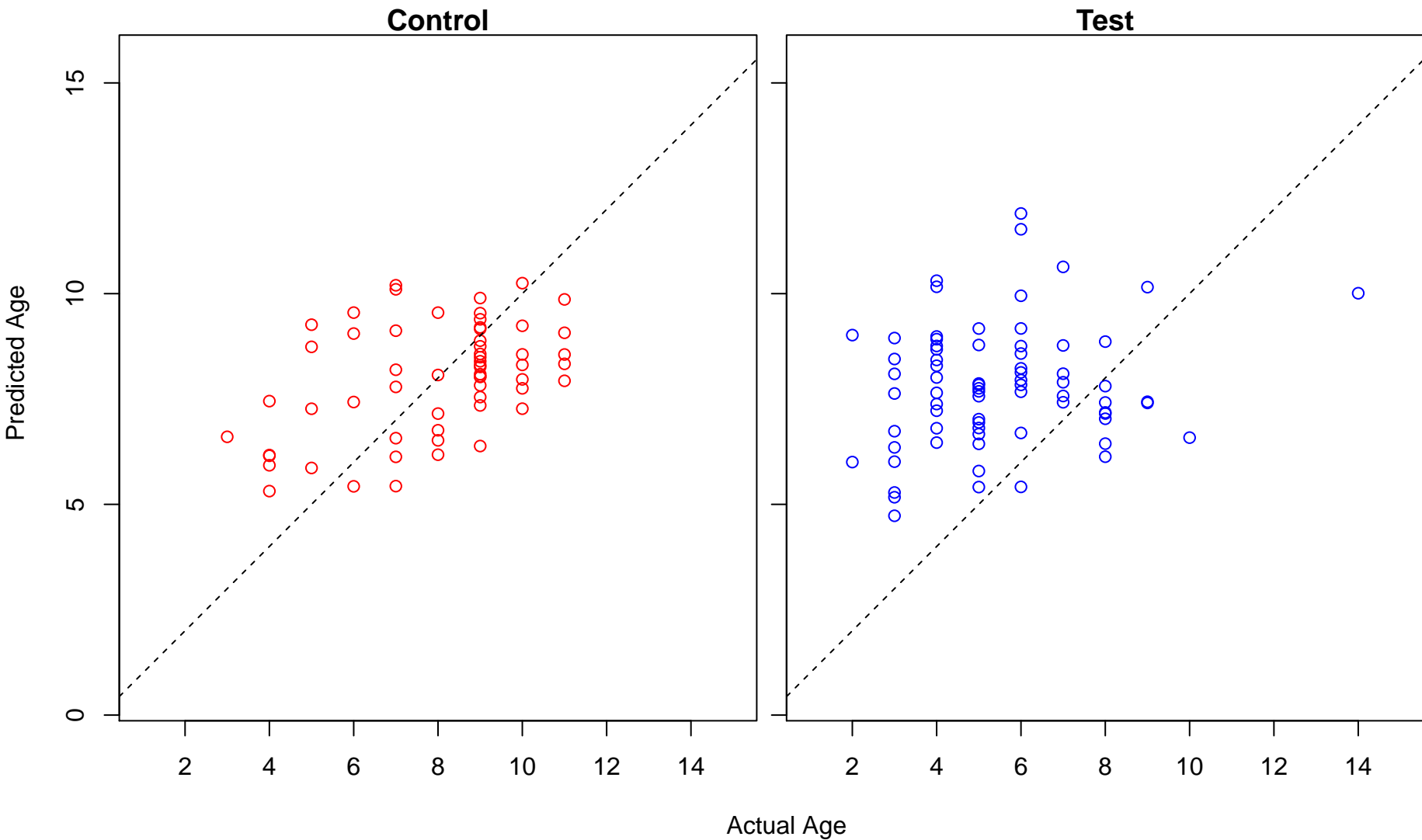
substrate adhesion-dependent cell spreading (Score: 0.908402)



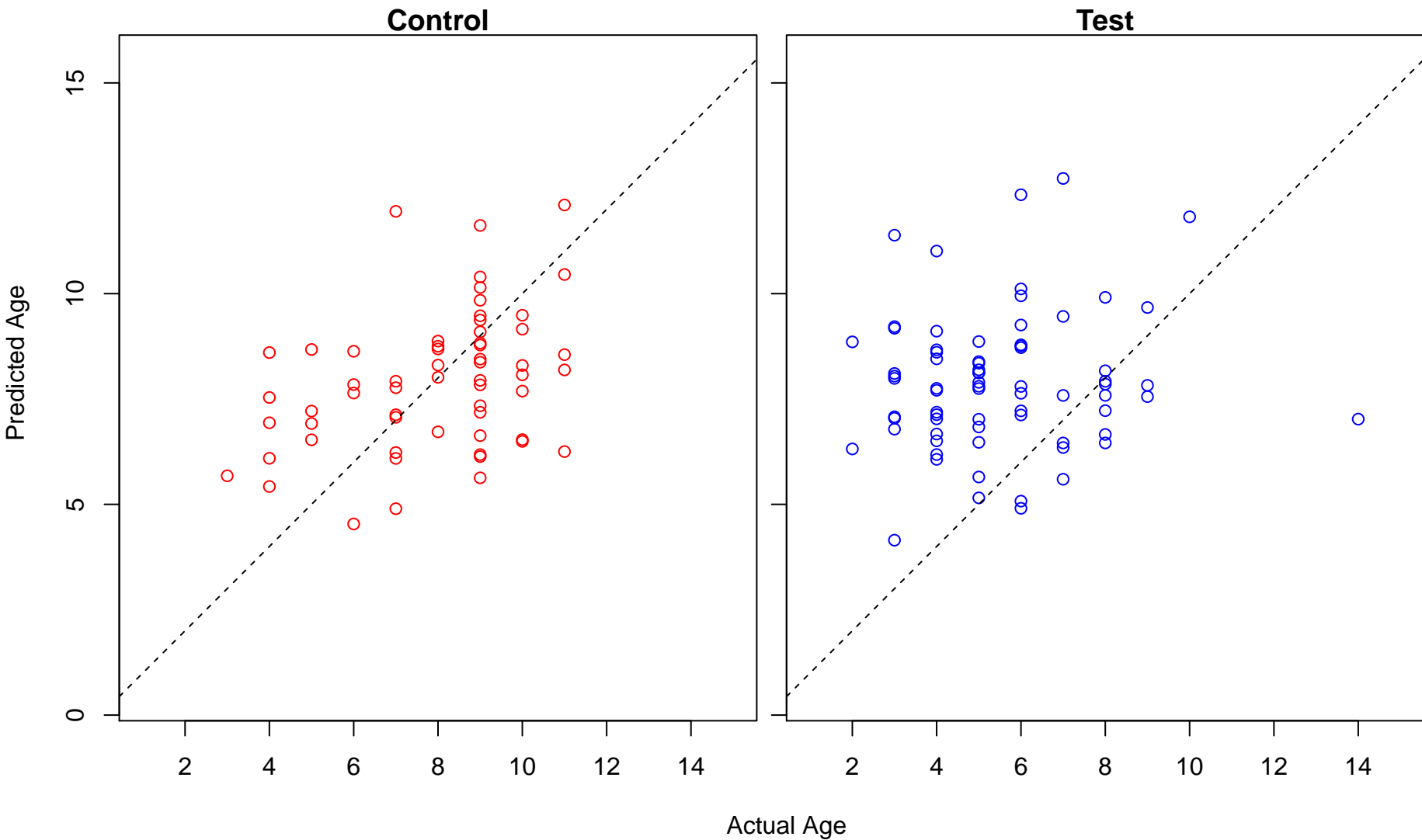
neuron projection regeneration (Score: 0.908230)



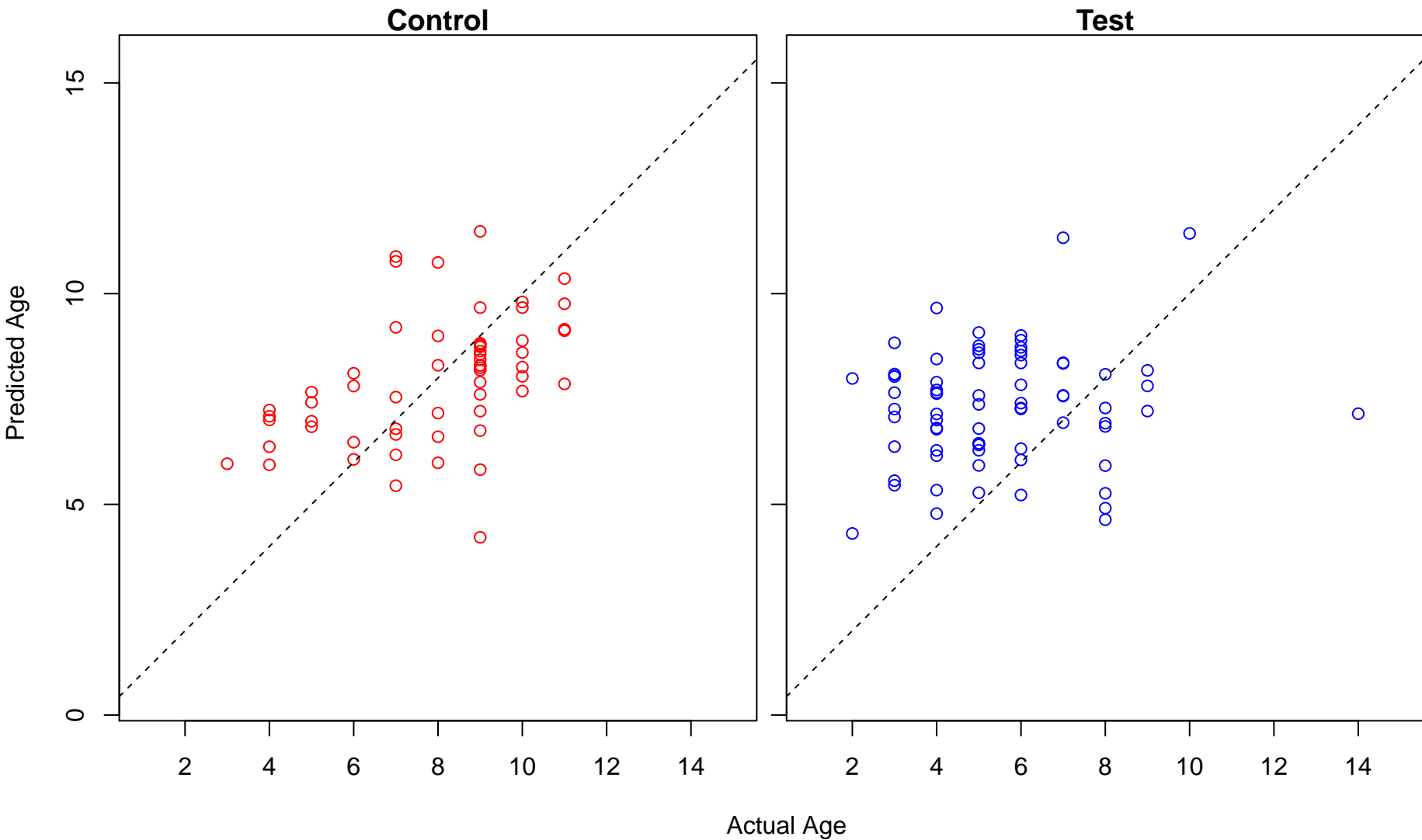
chemokine-mediated signaling pathway (Score: 0.907646)



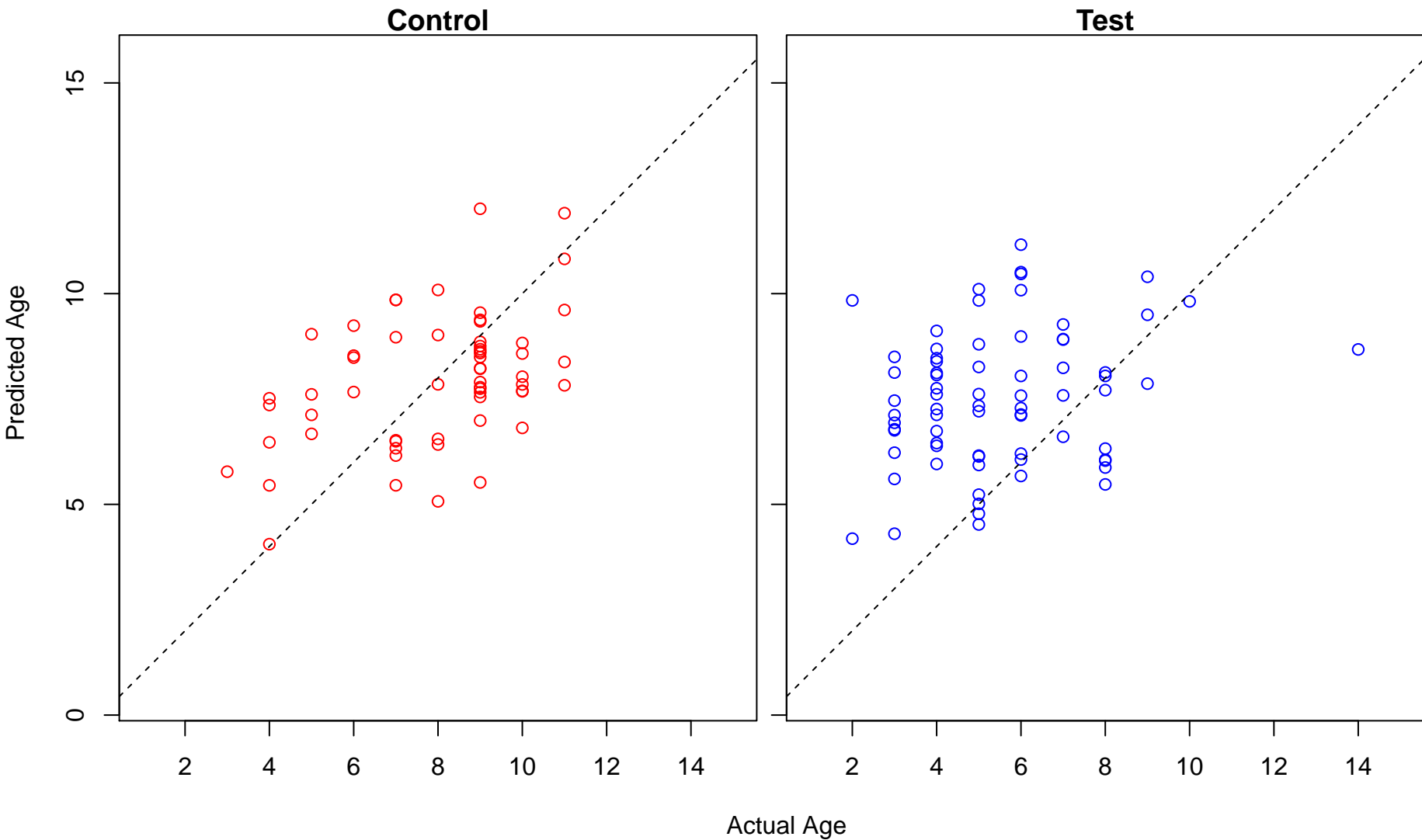
glycogen catabolic process (Score: 0.907251)



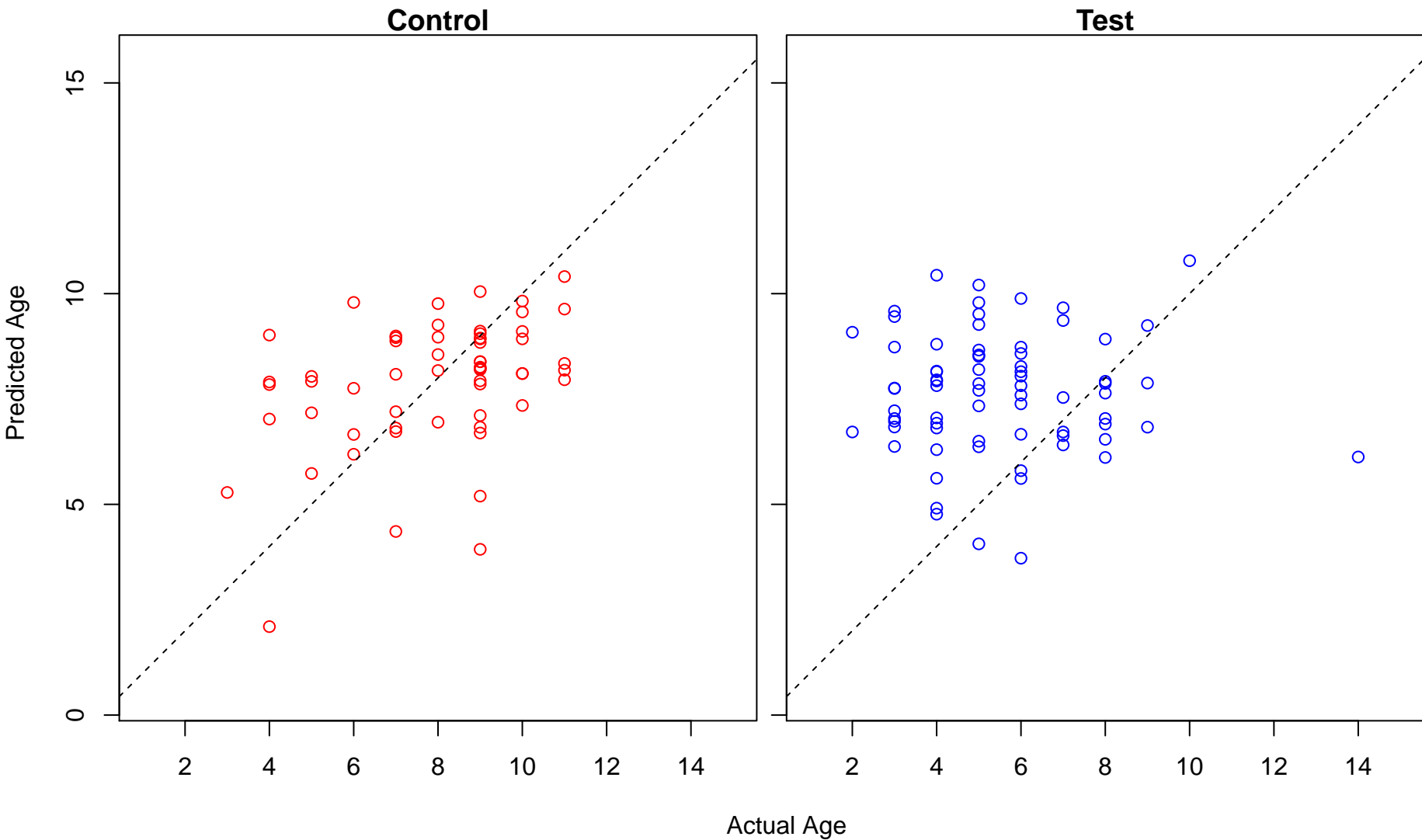
positive regulation of tyrosine phosphorylation of Stat1 protein (Score: 0.906403)



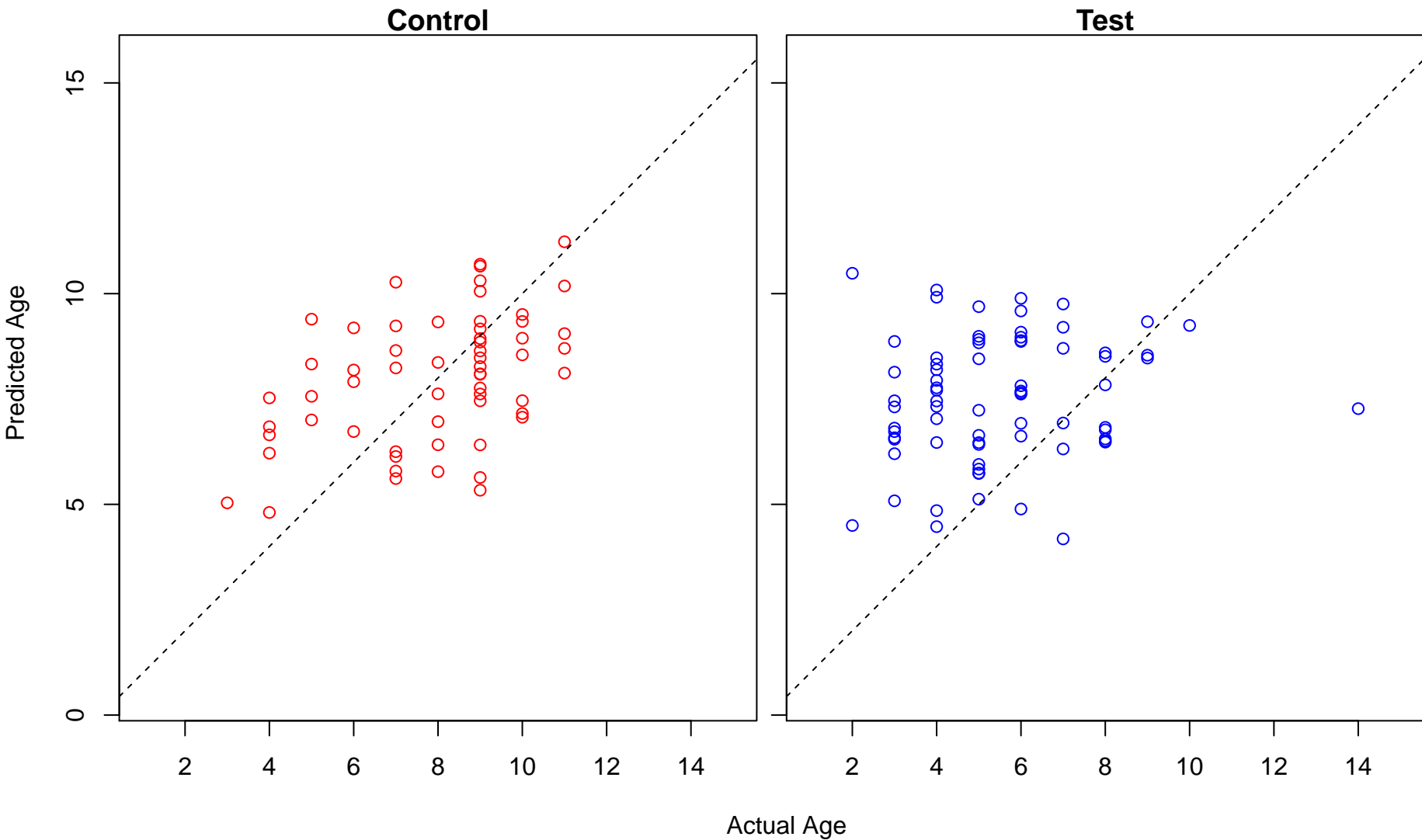
transmembrane receptor protein tyrosine kinase signaling pathway (Score: 0.906217)



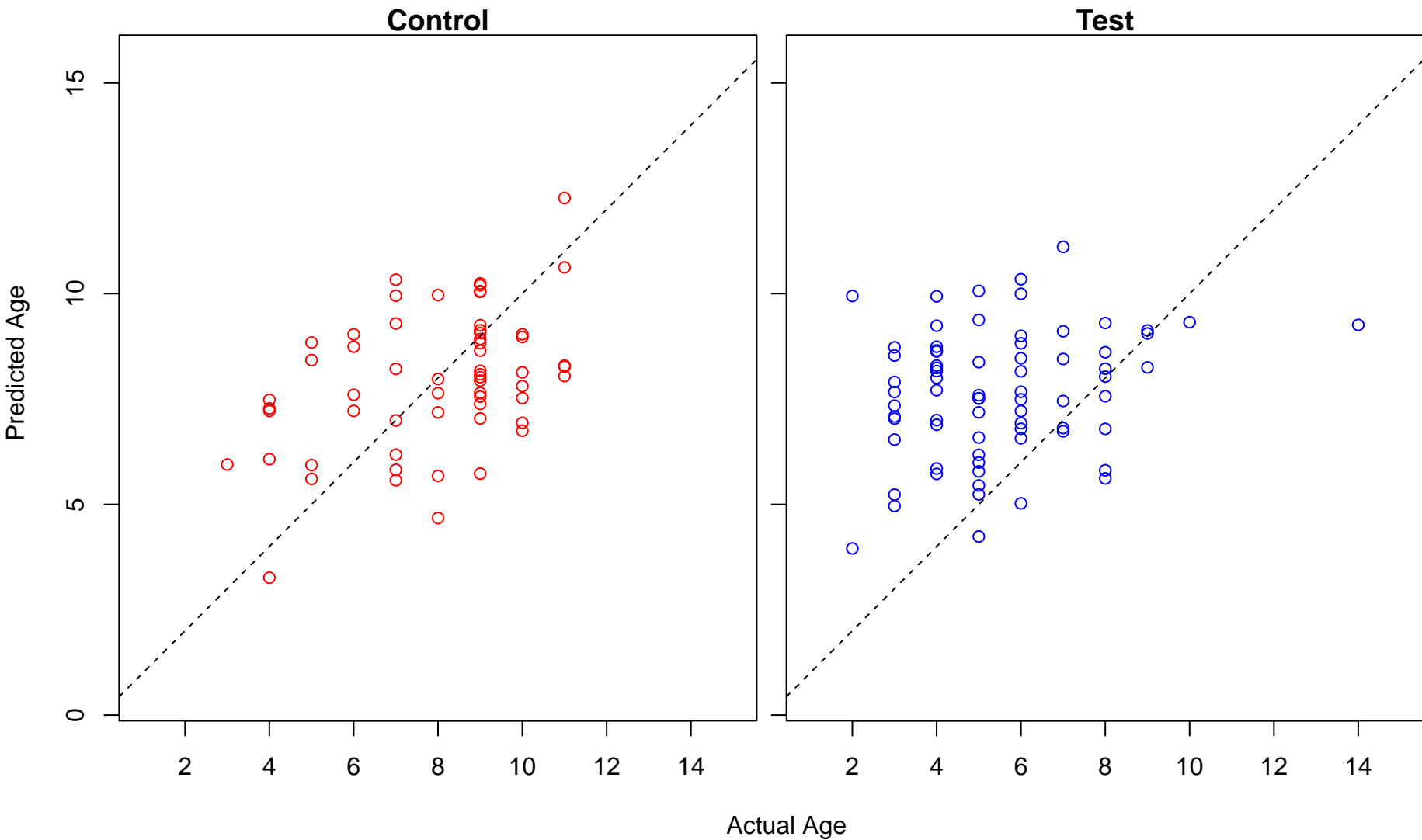
oxidative demethylation (Score: 0.905294)



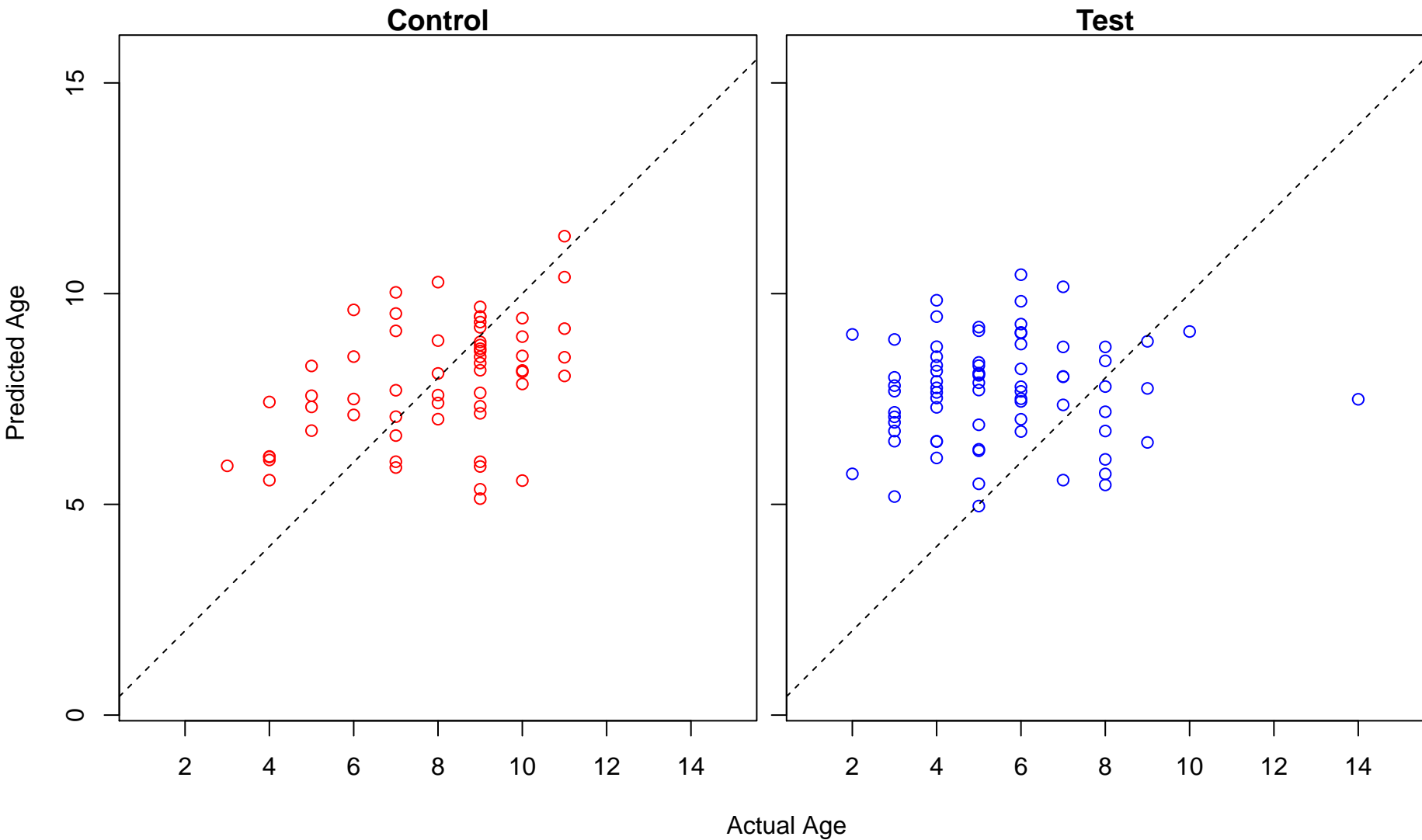
system development (Score: 0.905037)



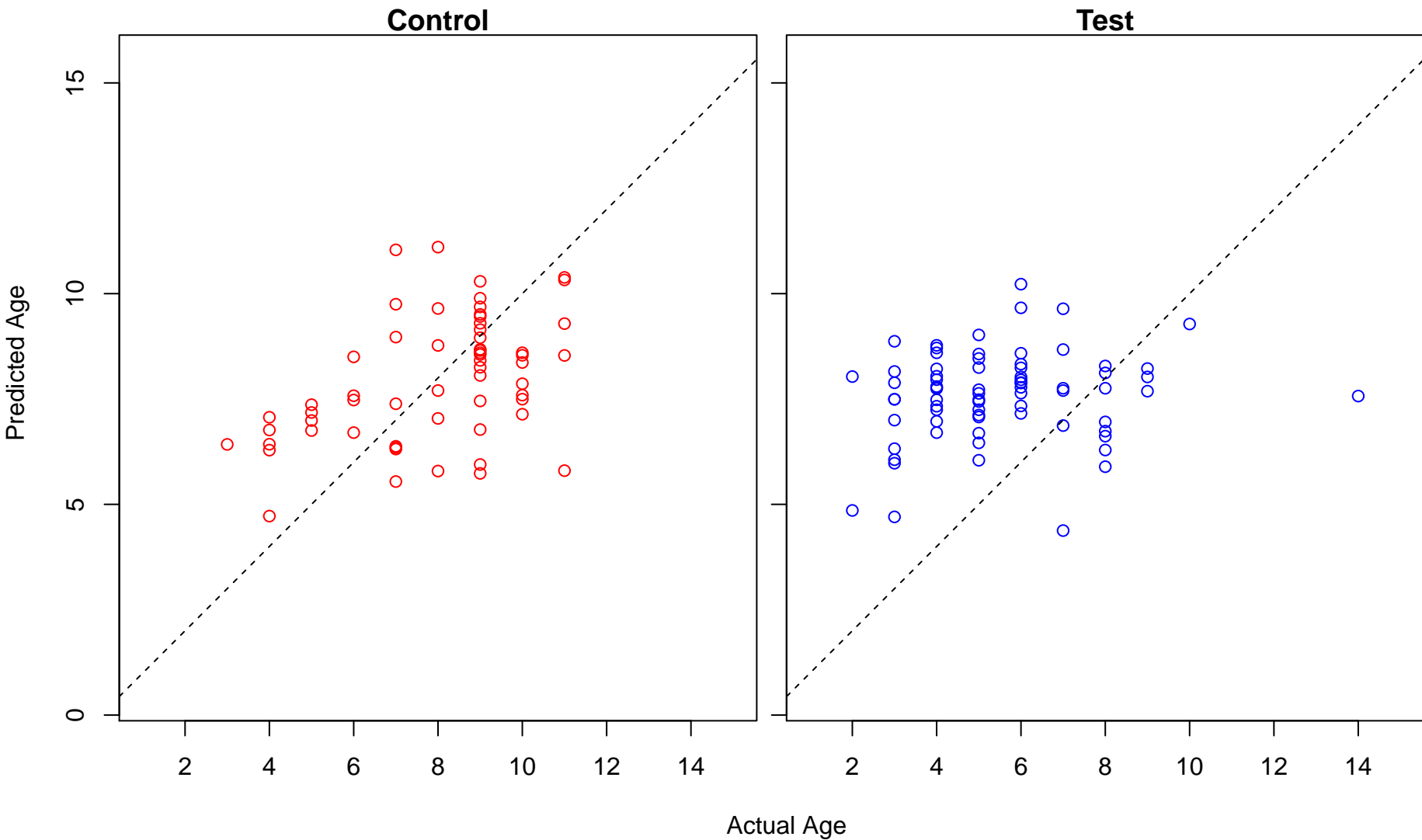
wound healing (Score: 0.904978)



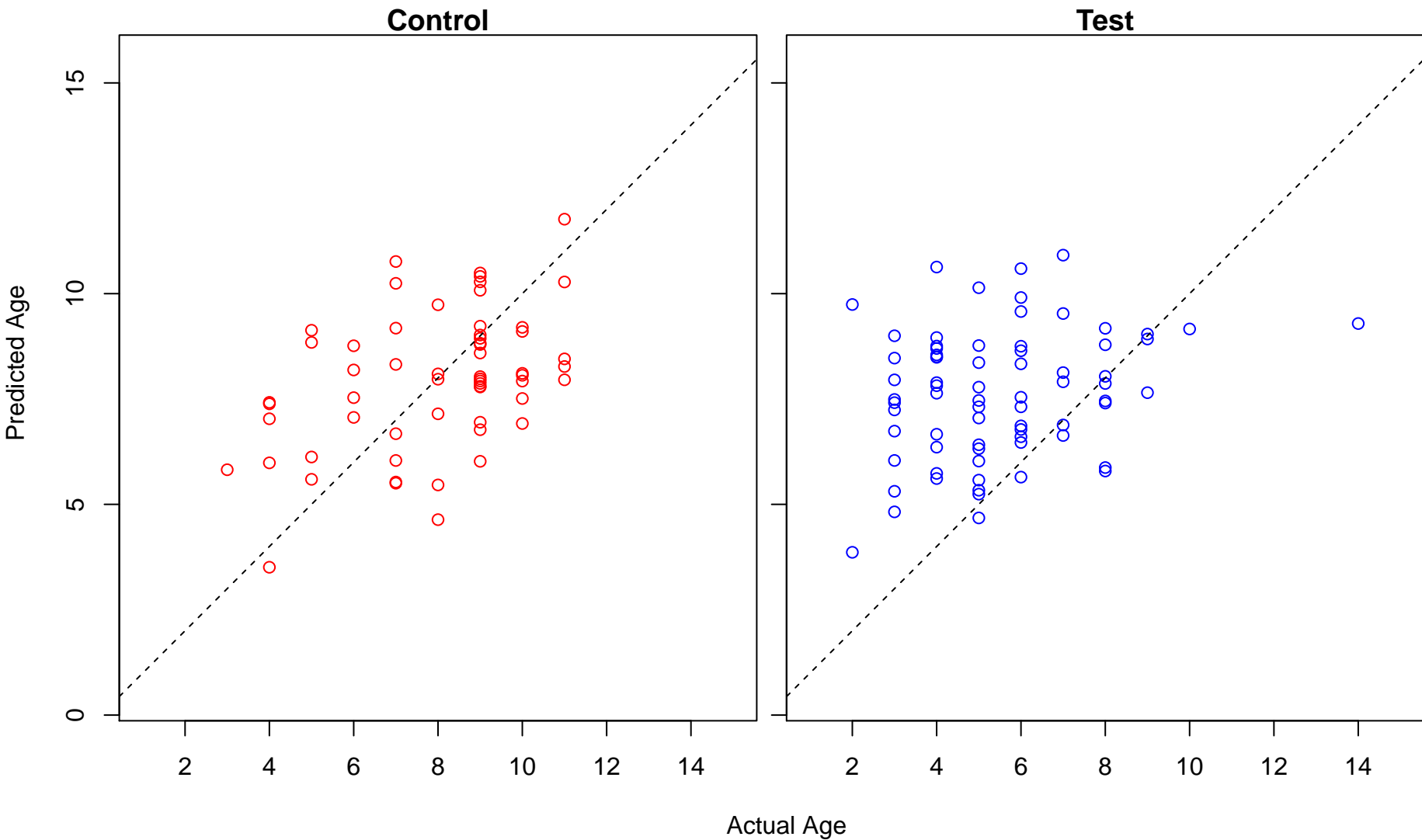
body morphogenesis (Score: 0.904317)



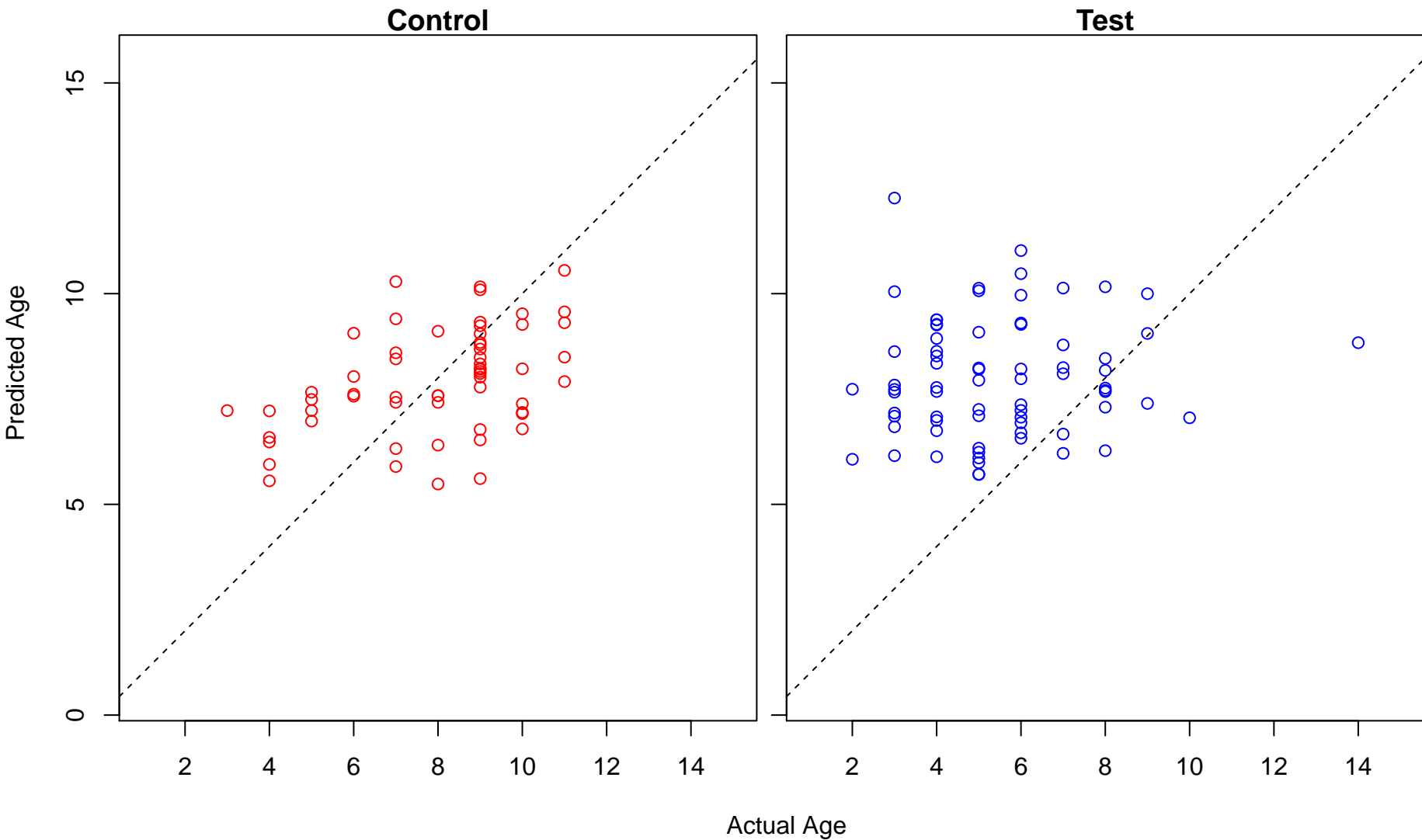
negative regulation of transcription factor import into nucleus (Score: 0.903507)



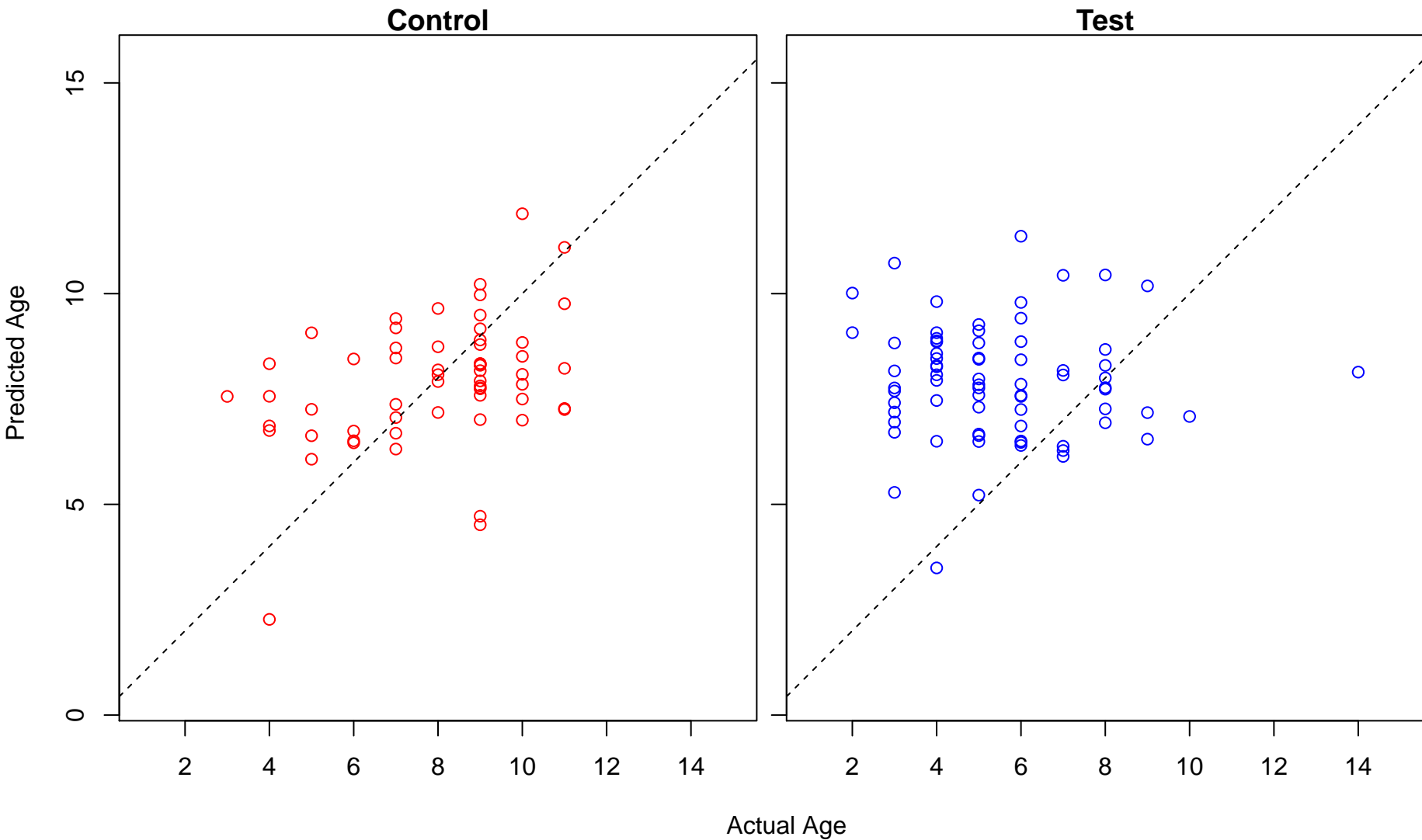
regulation of body fluid levels (Score: 0.902806)



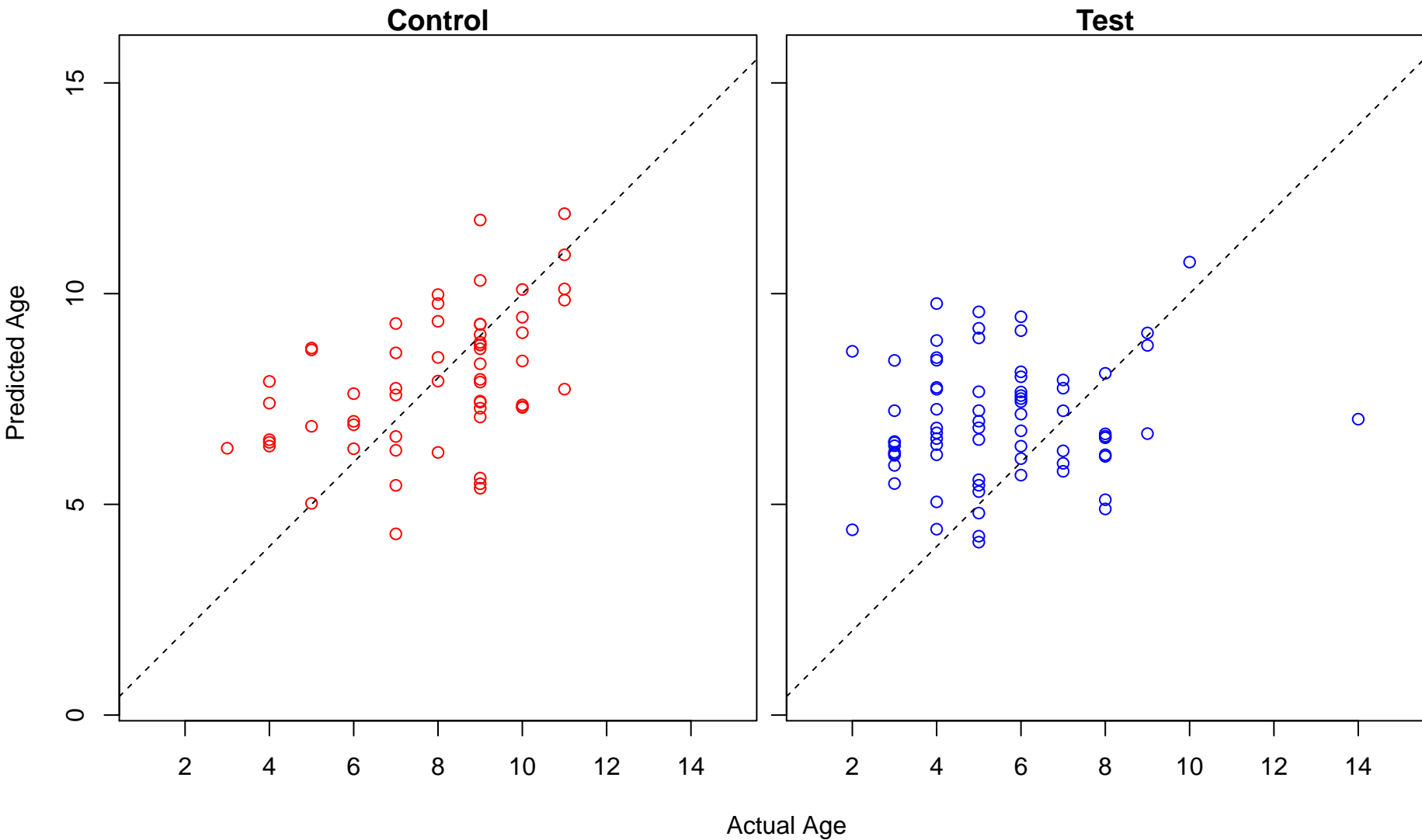
cell-matrix adhesion (Score: 0.902683)



response to axon injury (Score: 0.902478)

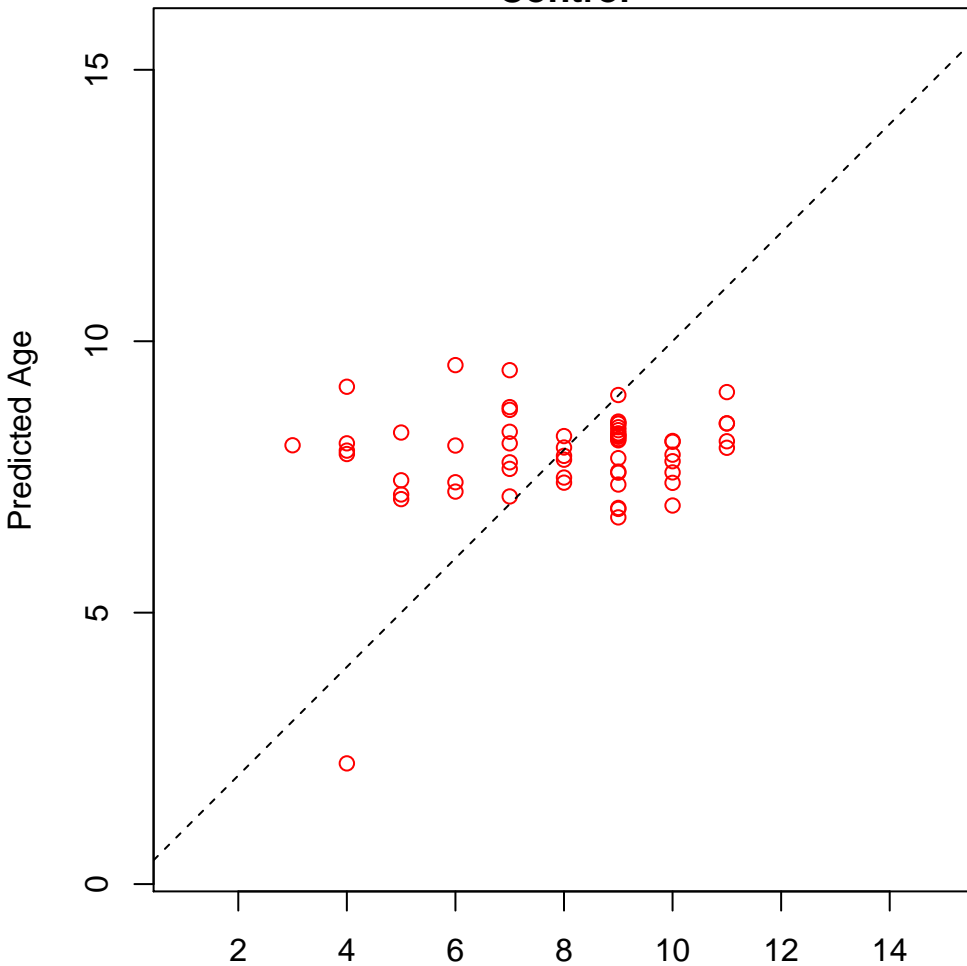


positive regulation of cellular response to insulin stimulus (Score: 0.902239)

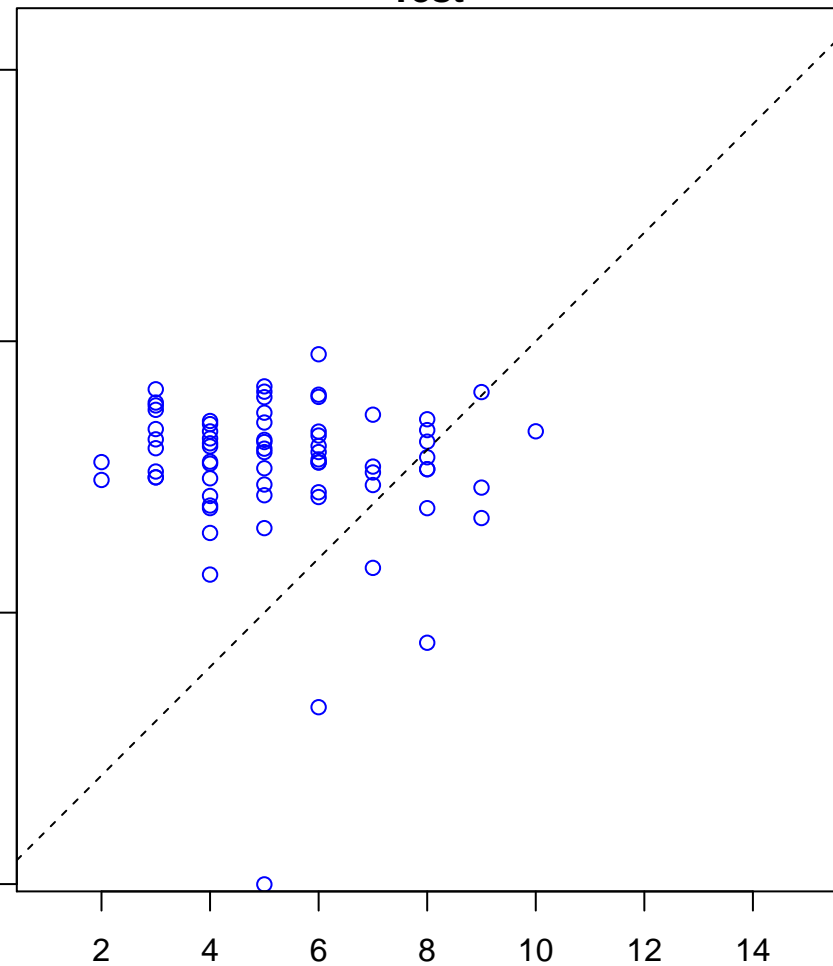


central nervous system segmentation (Score: 0.902071)

Control

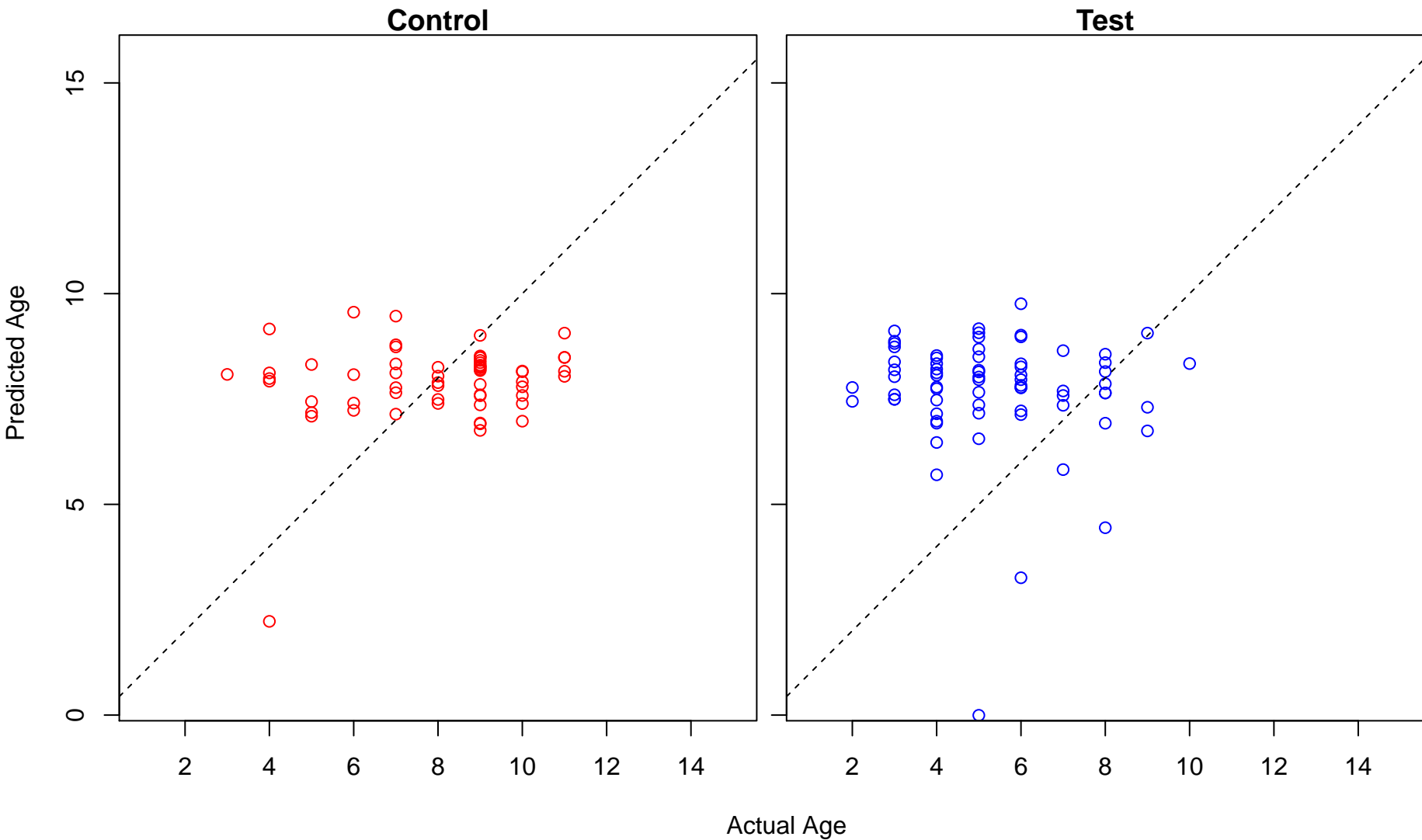


Test

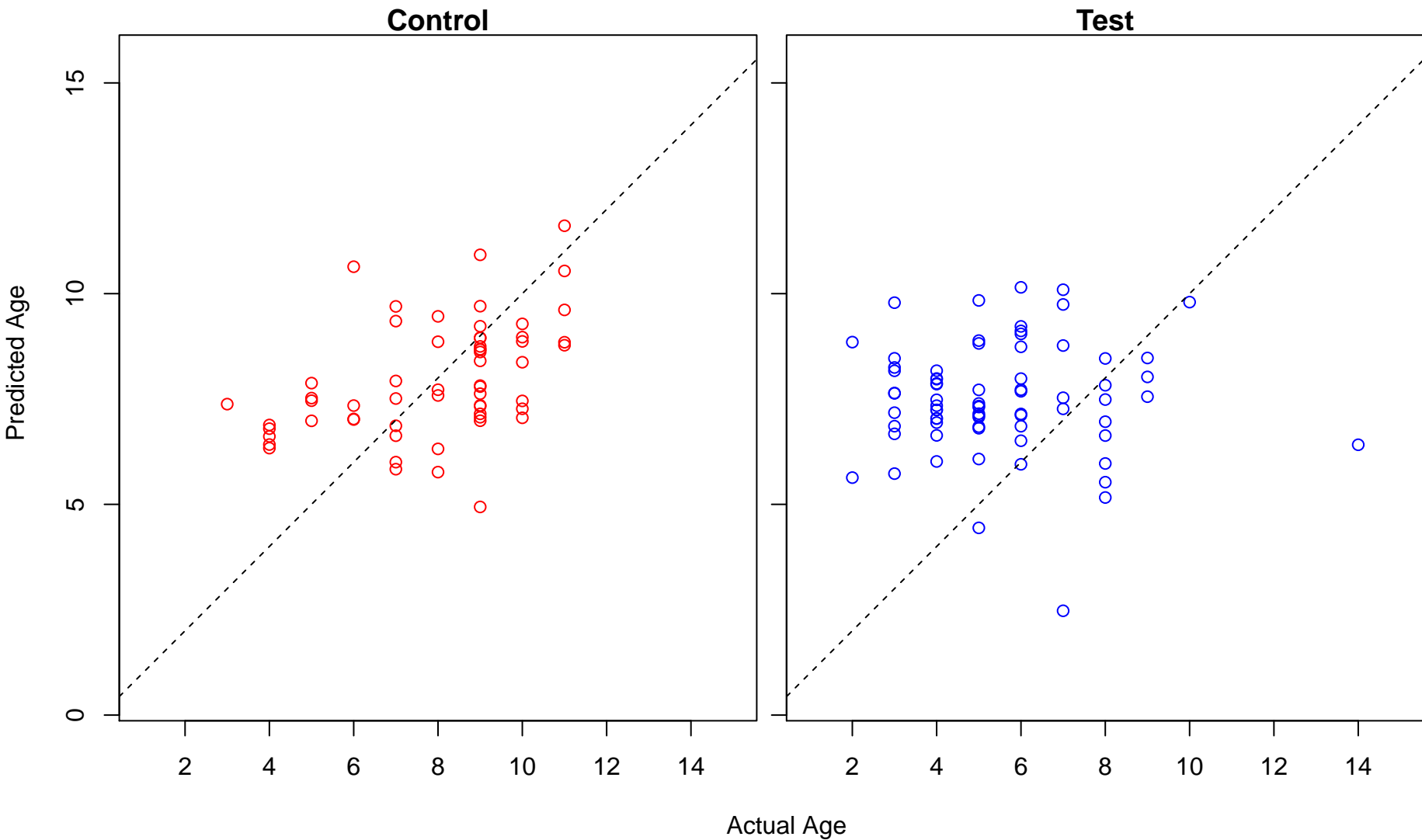


Actual Age

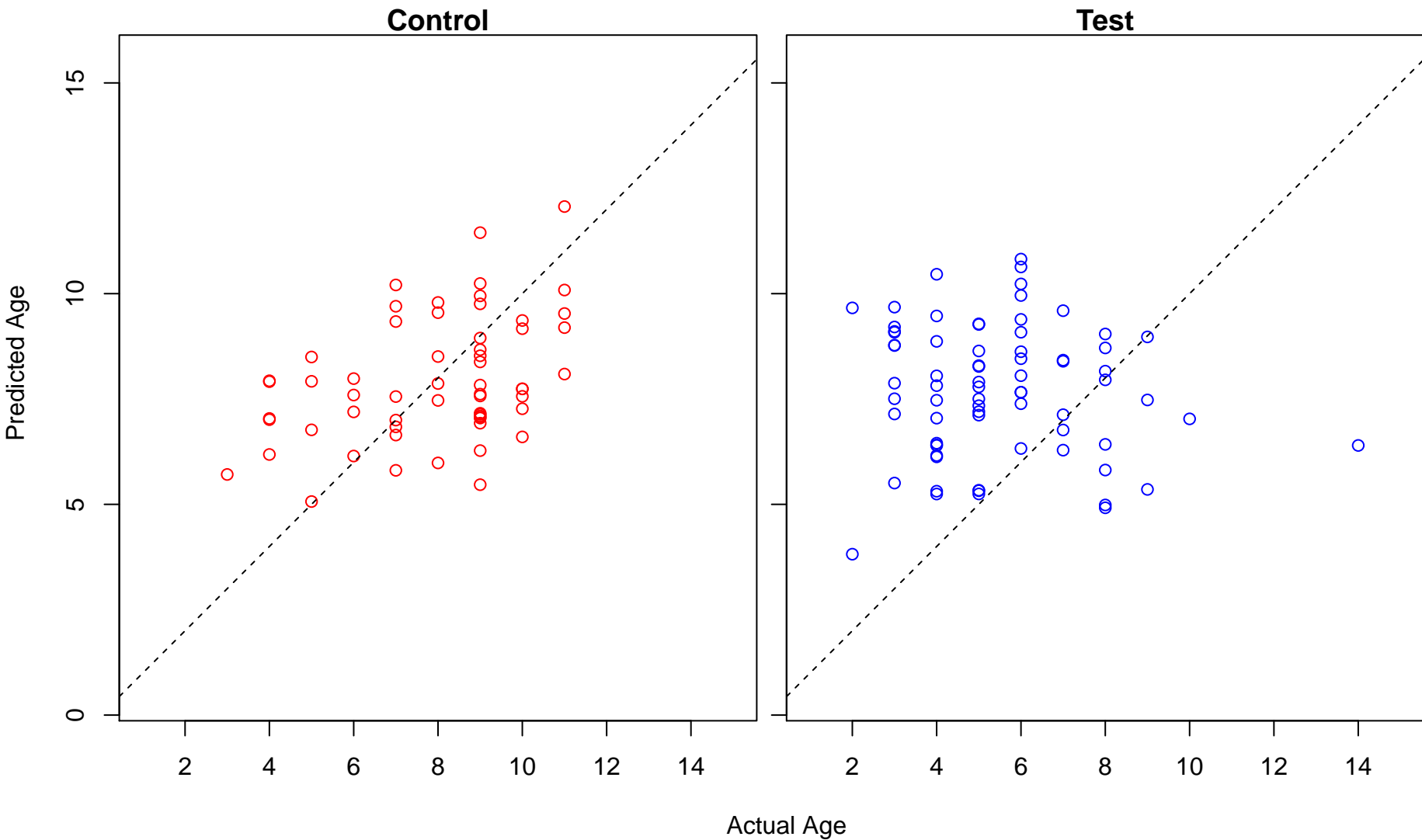
brain segmentation (Score: 0.902071)



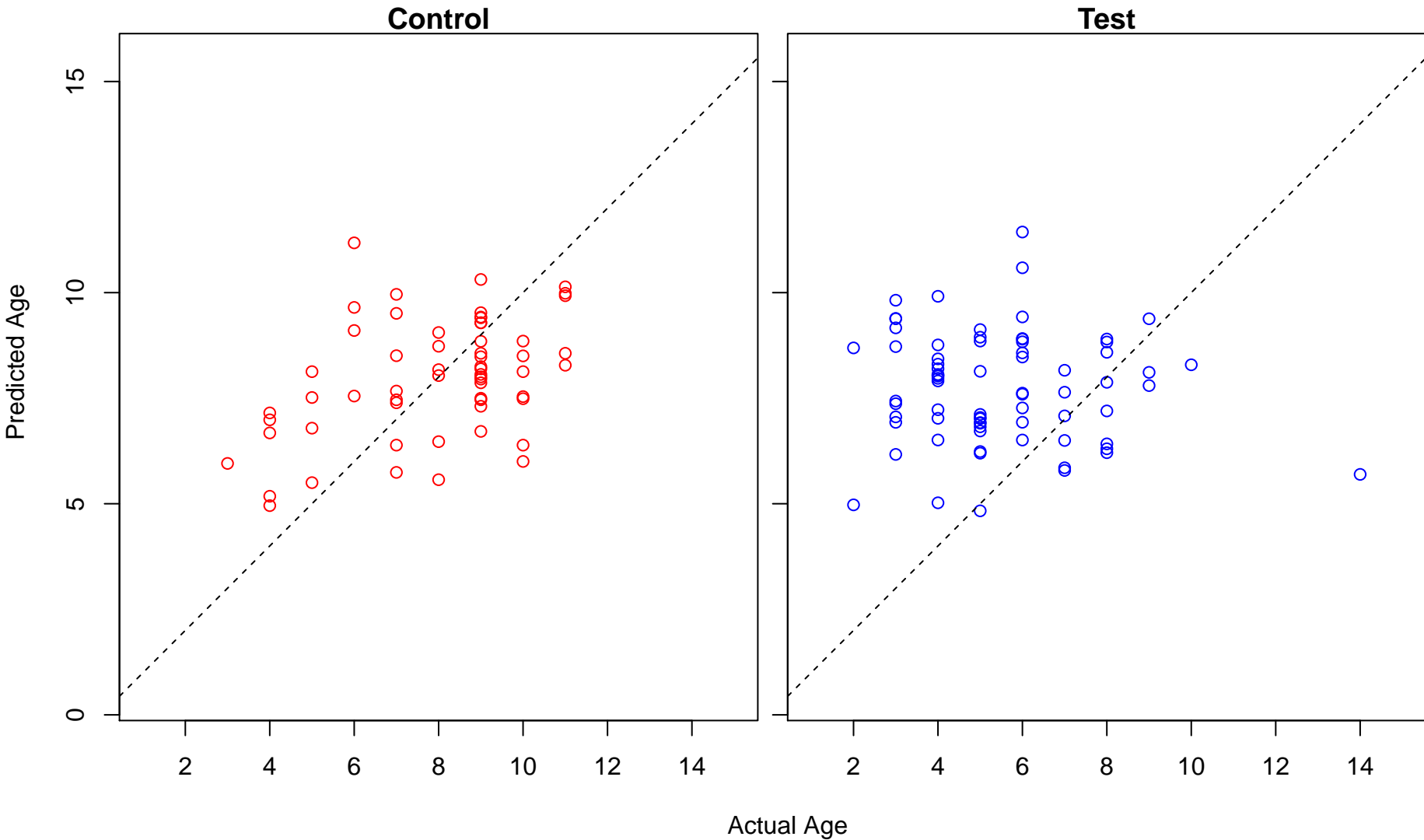
anatomical structure maturation (Score: 0.901459)



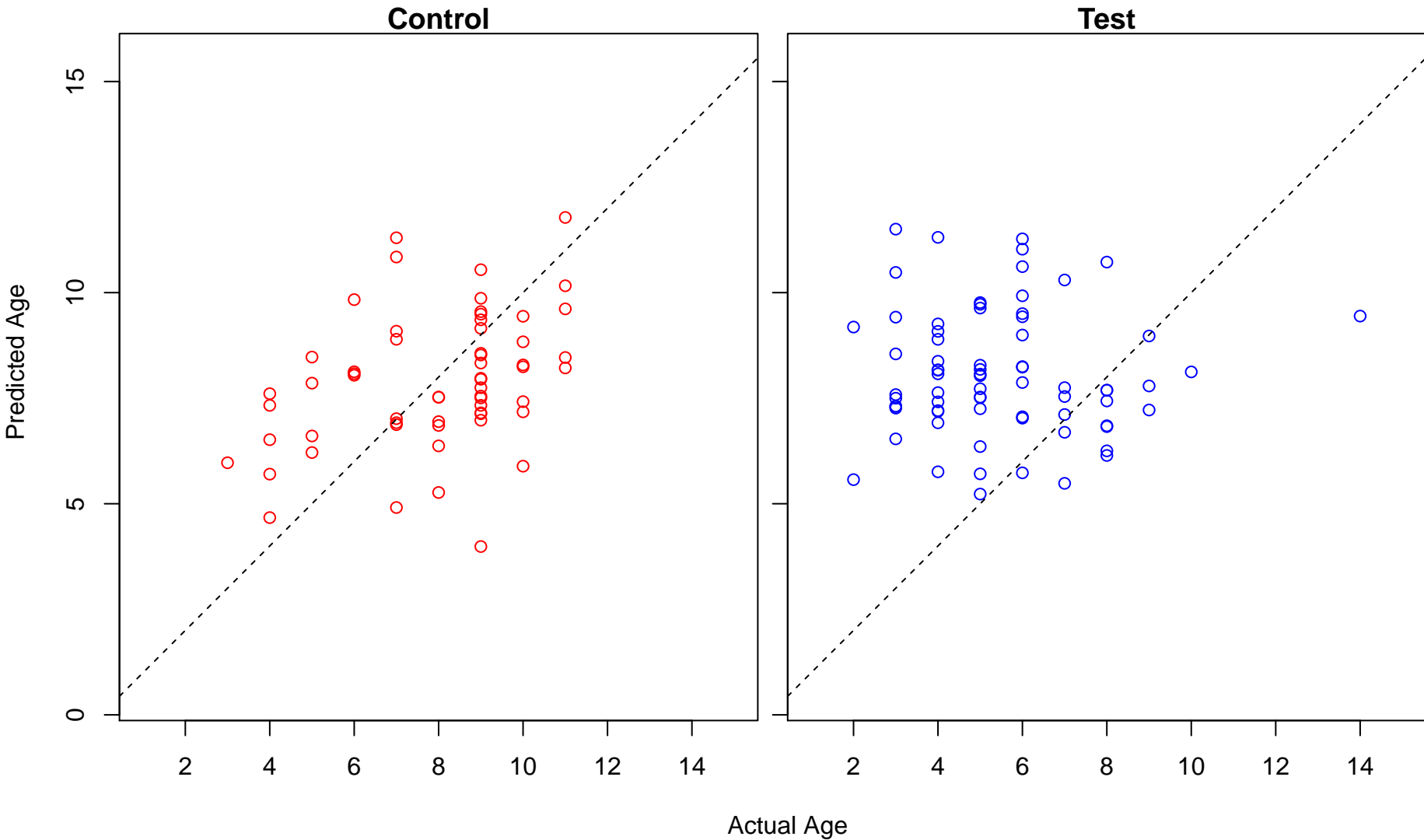
positive regulation of phosphatidylinositol 3-kinase activity (Score: 0.901441)



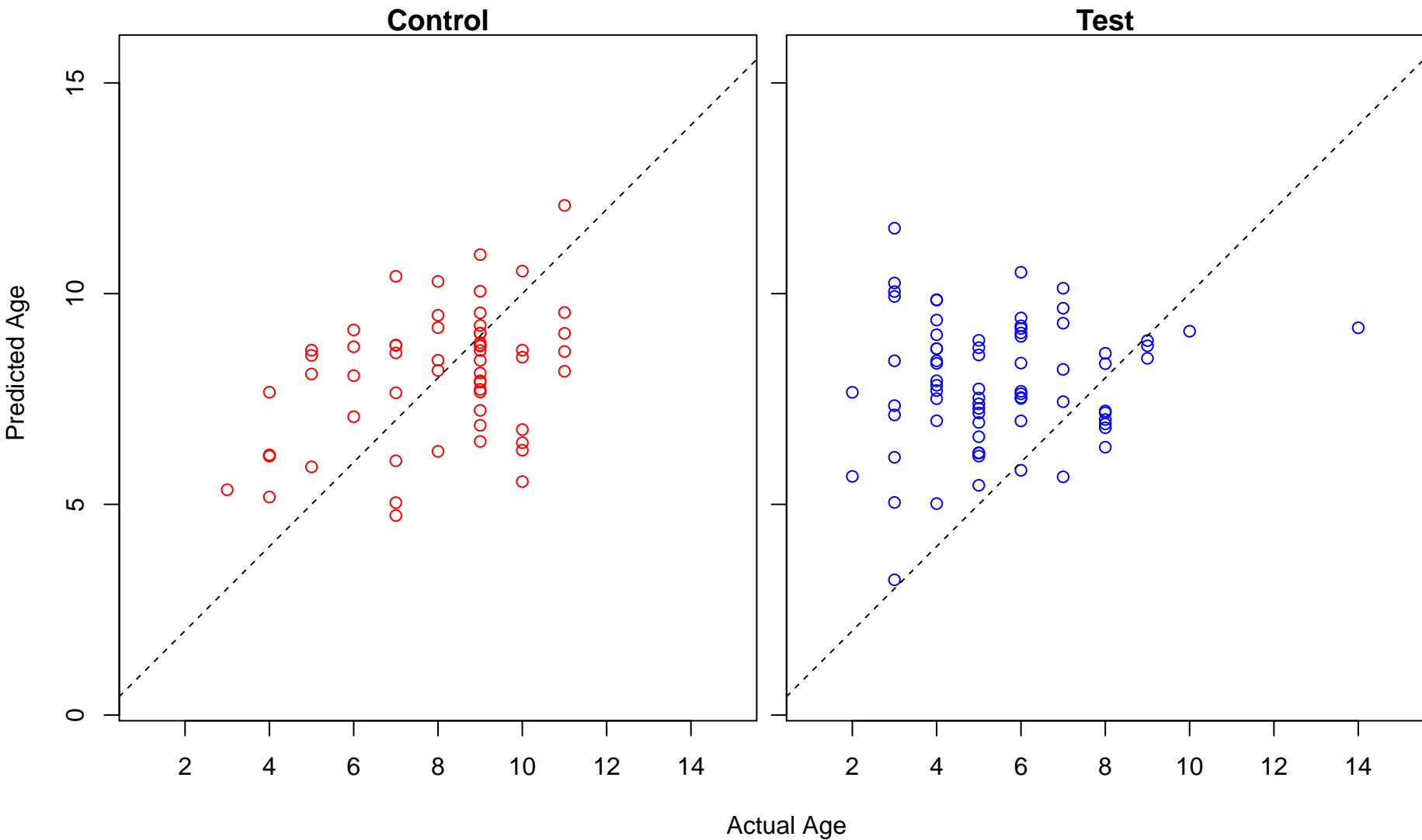
regulation of cytokine biosynthetic process (Score: 0.901158)



signal transduction by p53 class mediator (Score: 0.900402)

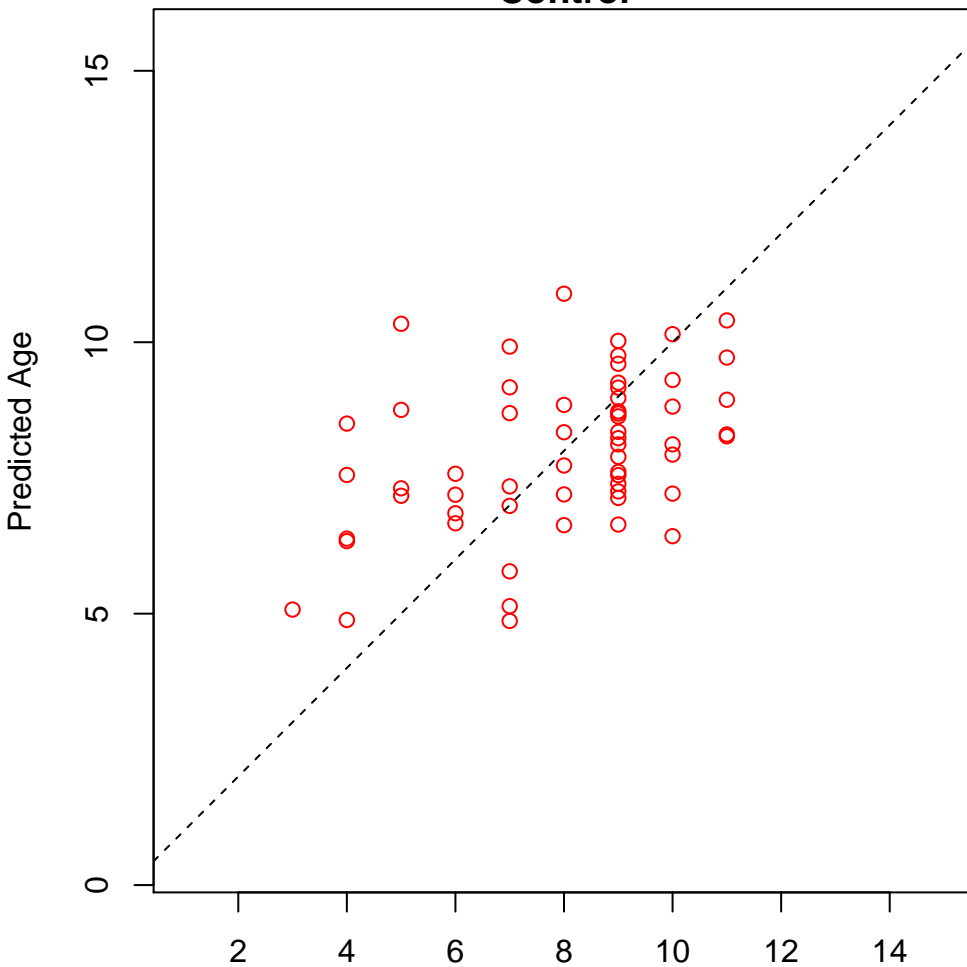


regulation of muscle organ development (Score: 0.900347)

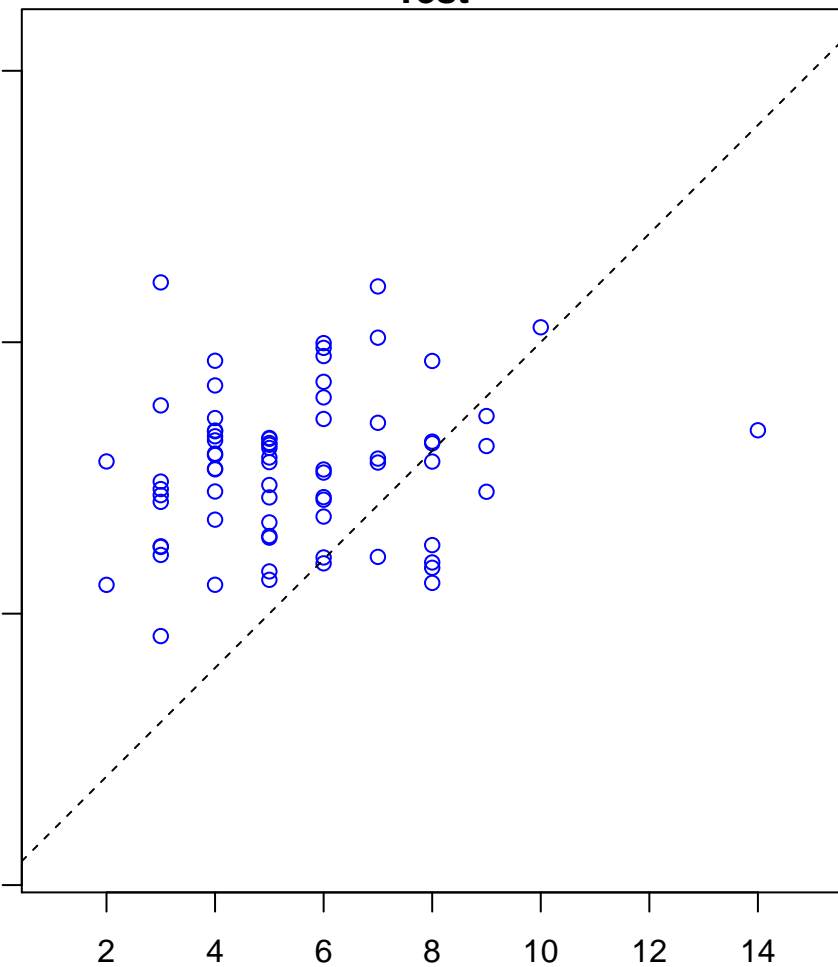


regulation of histone H3-K4 methylation (Score: 0.900119)

Control

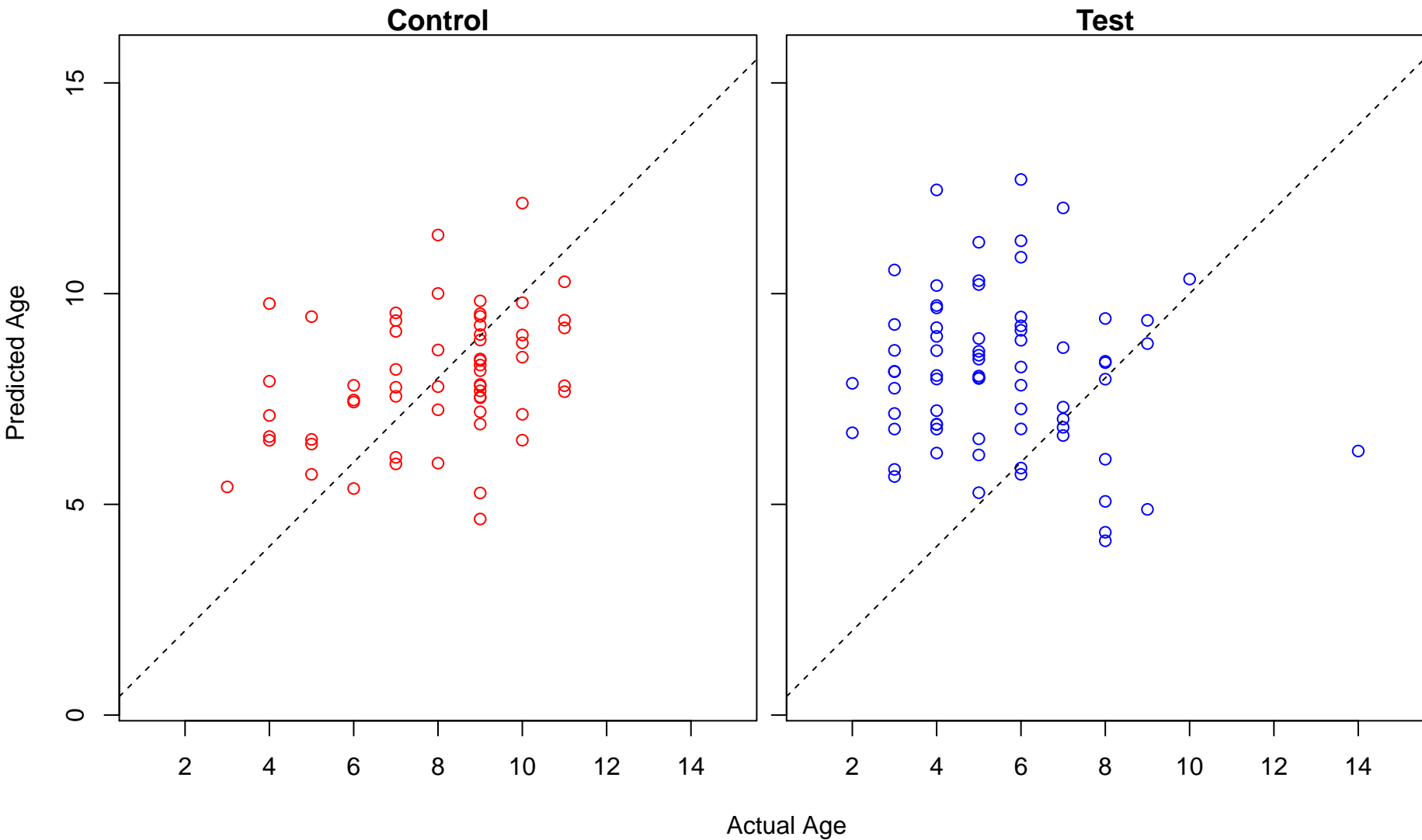


Test

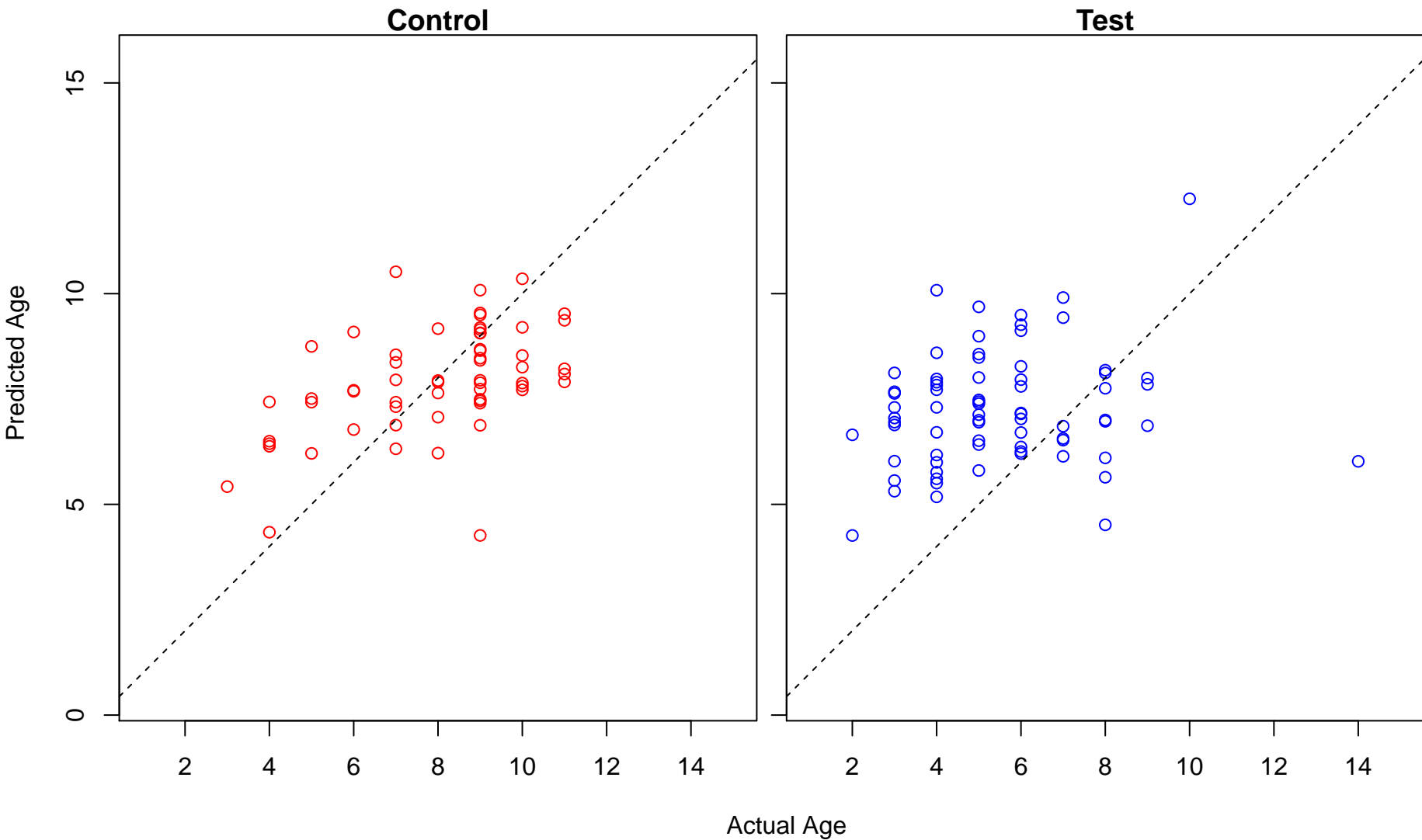


Actual Age

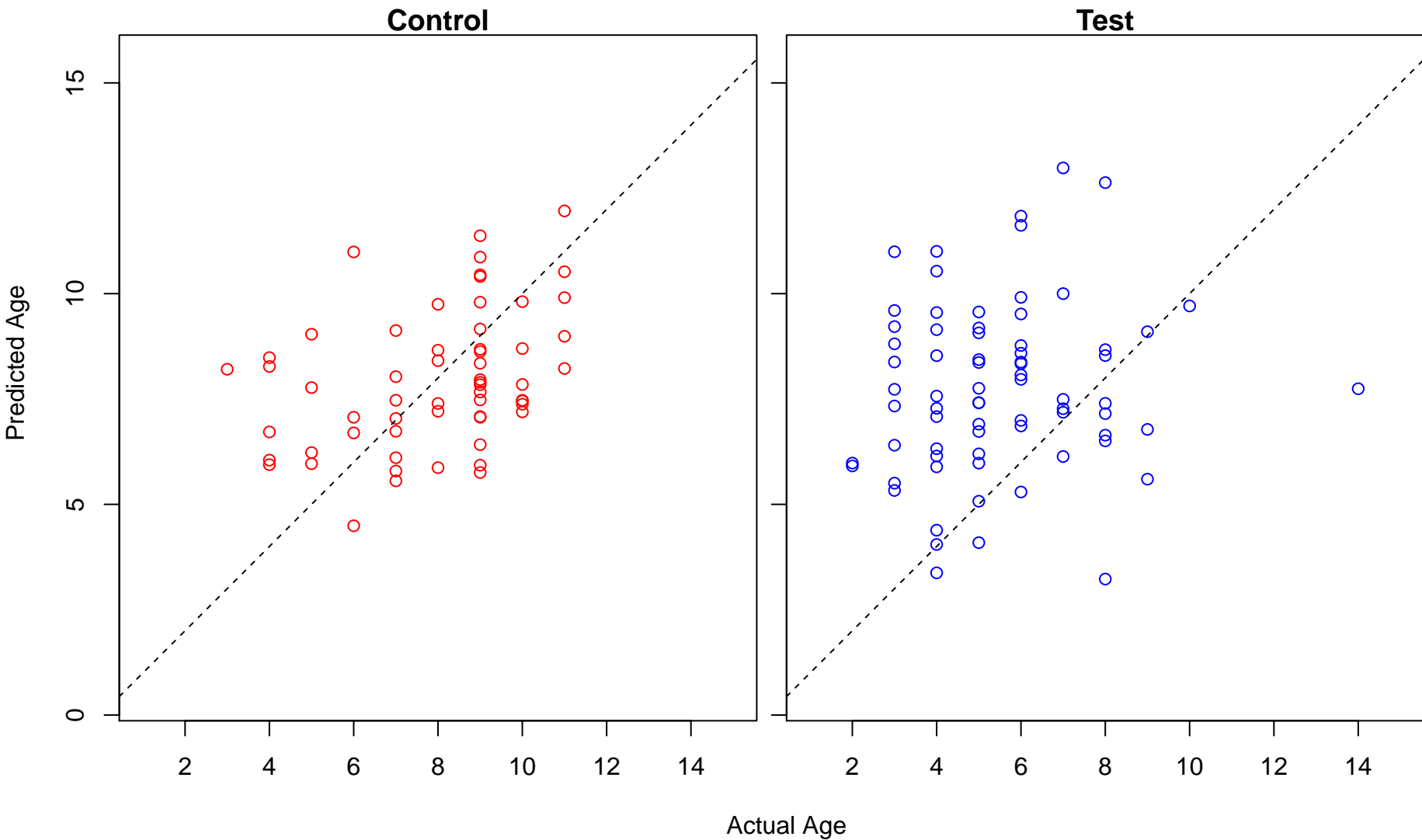
ureter development (Score: 0.898792)



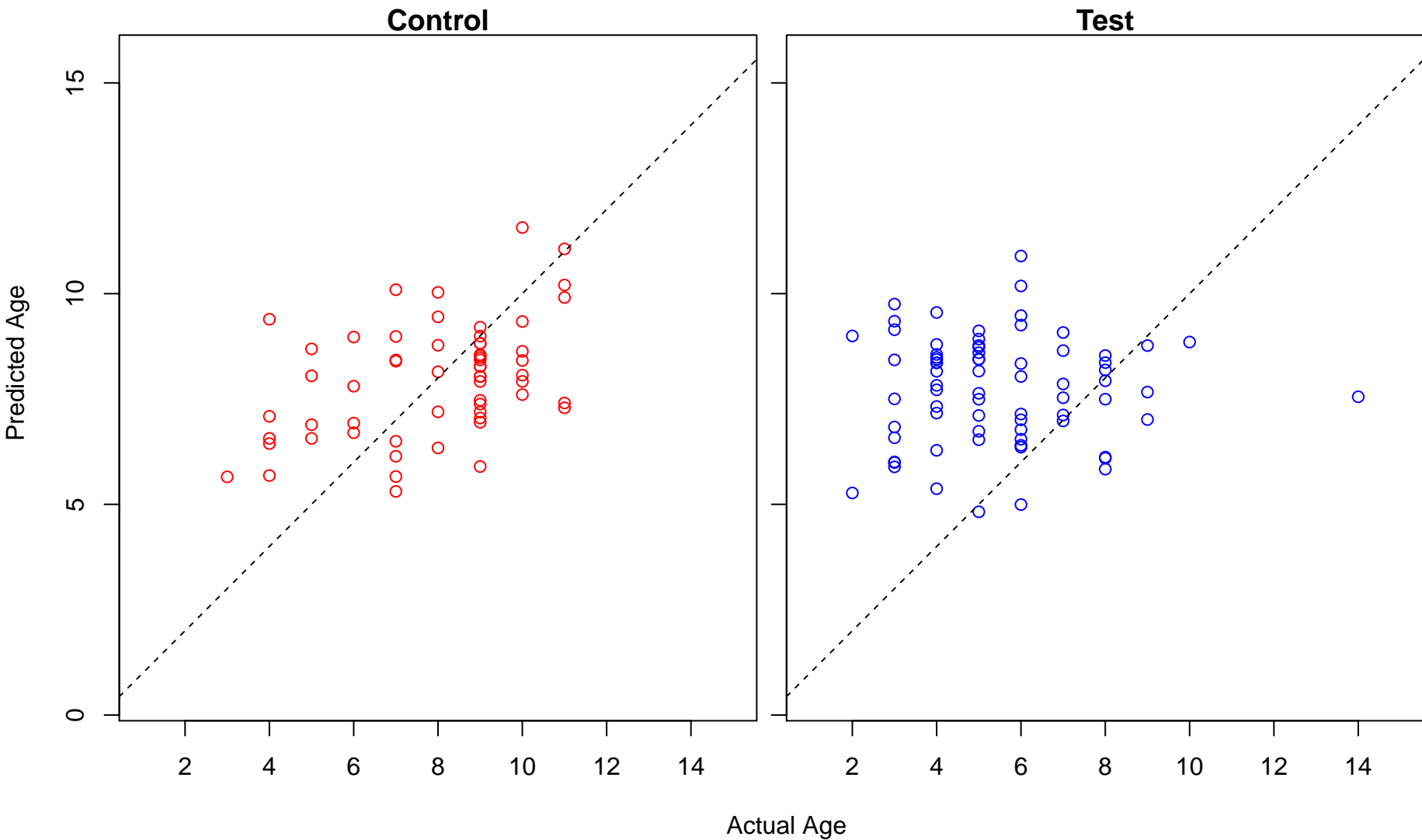
myeloid dendritic cell activation involved in immune response (Score: 0.897757)



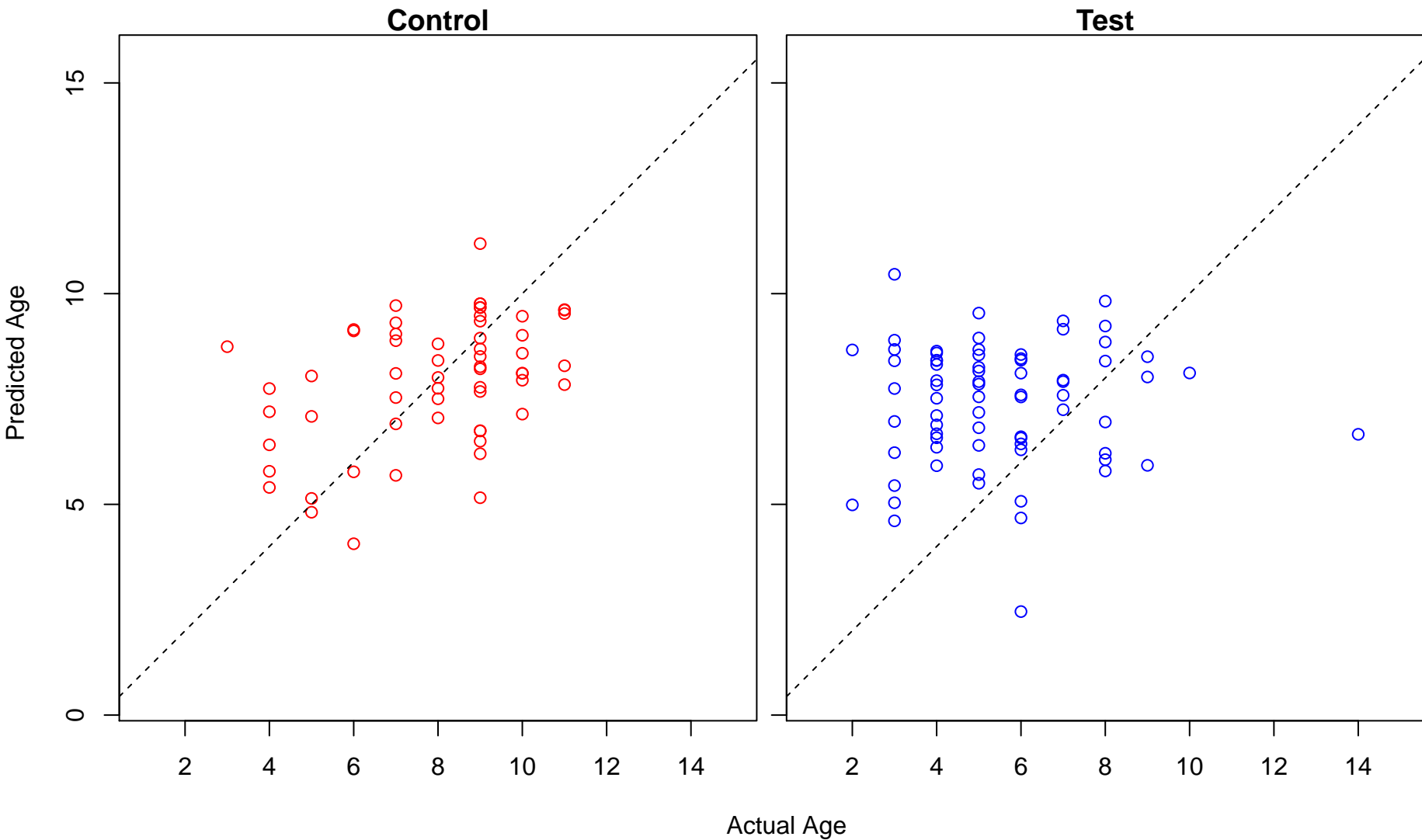
regulation of cardiac muscle contraction by calcium ion signaling (Score: 0.896596)



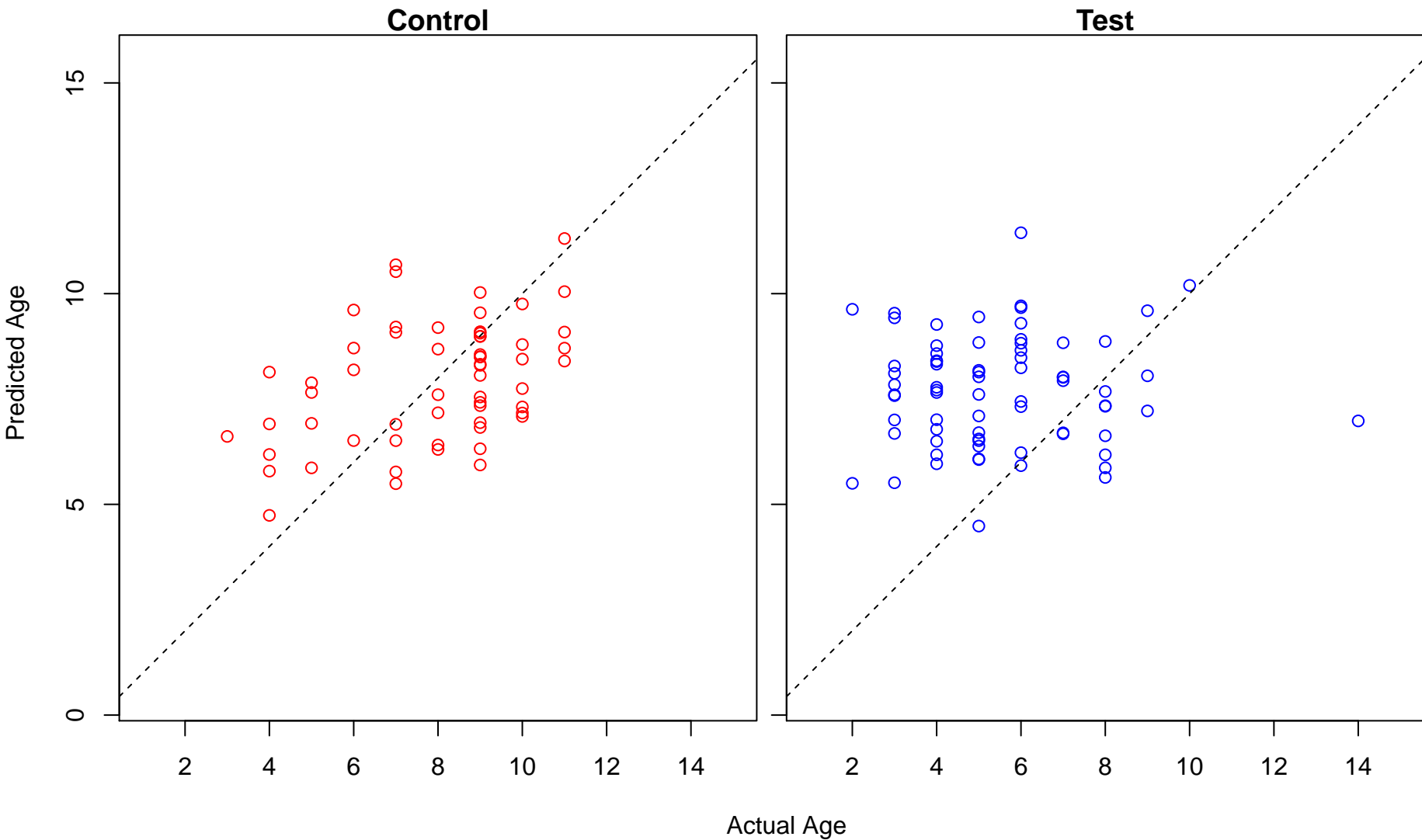
histone H3-K4 trimethylation (Score: 0.895909)



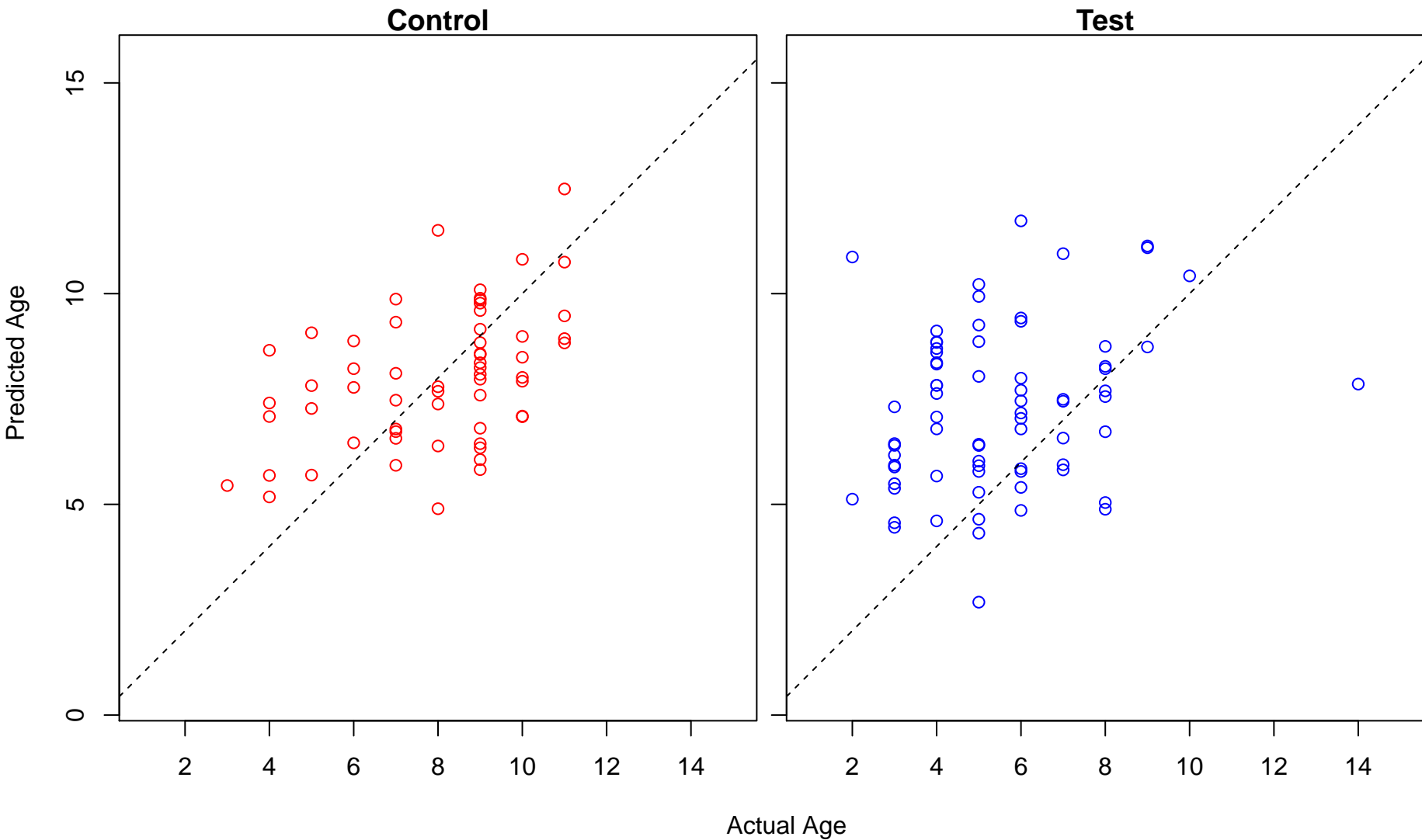
apoptotic nuclear changes (Score: 0.894617)



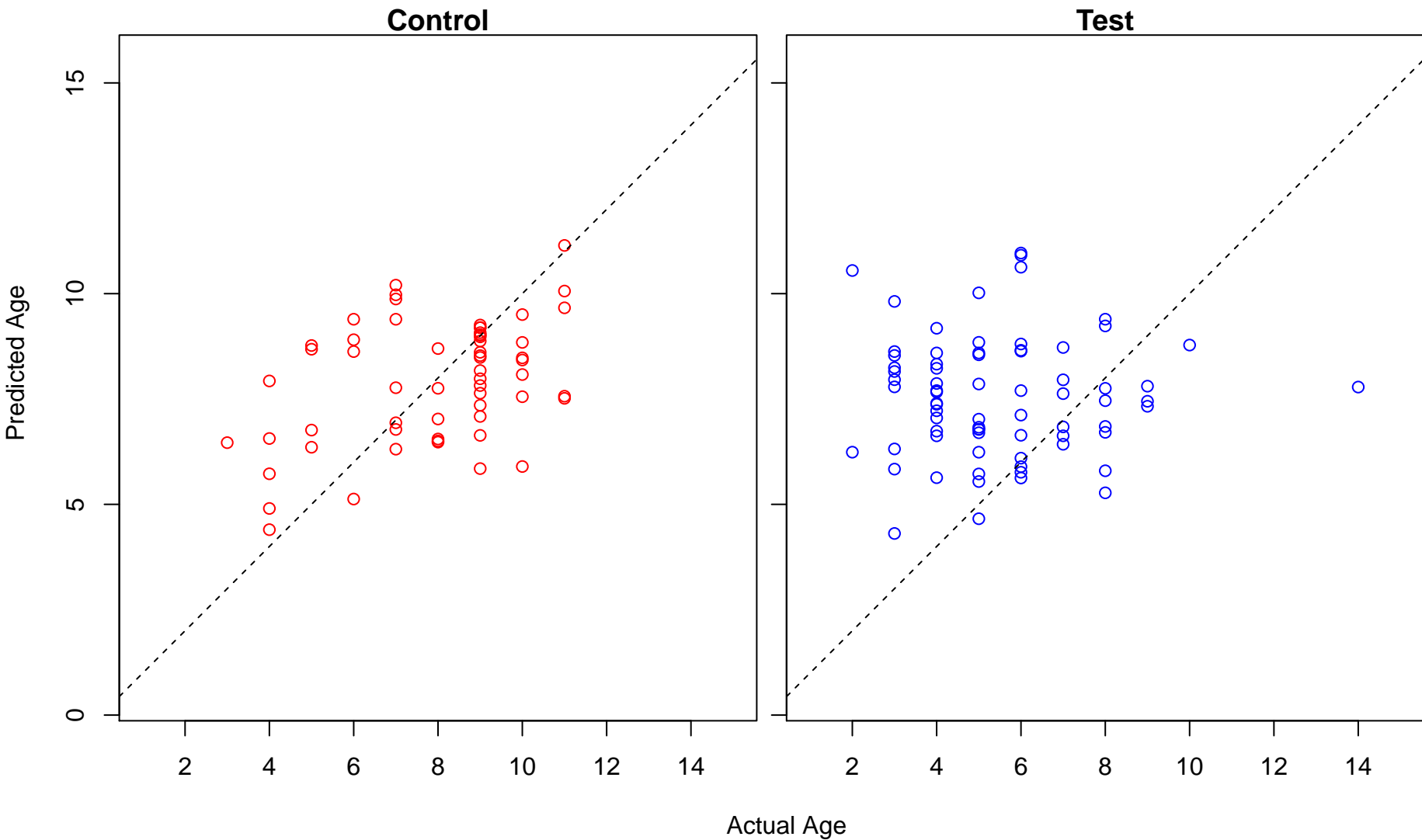
peptidyl-serine phosphorylation (Score: 0.893587)



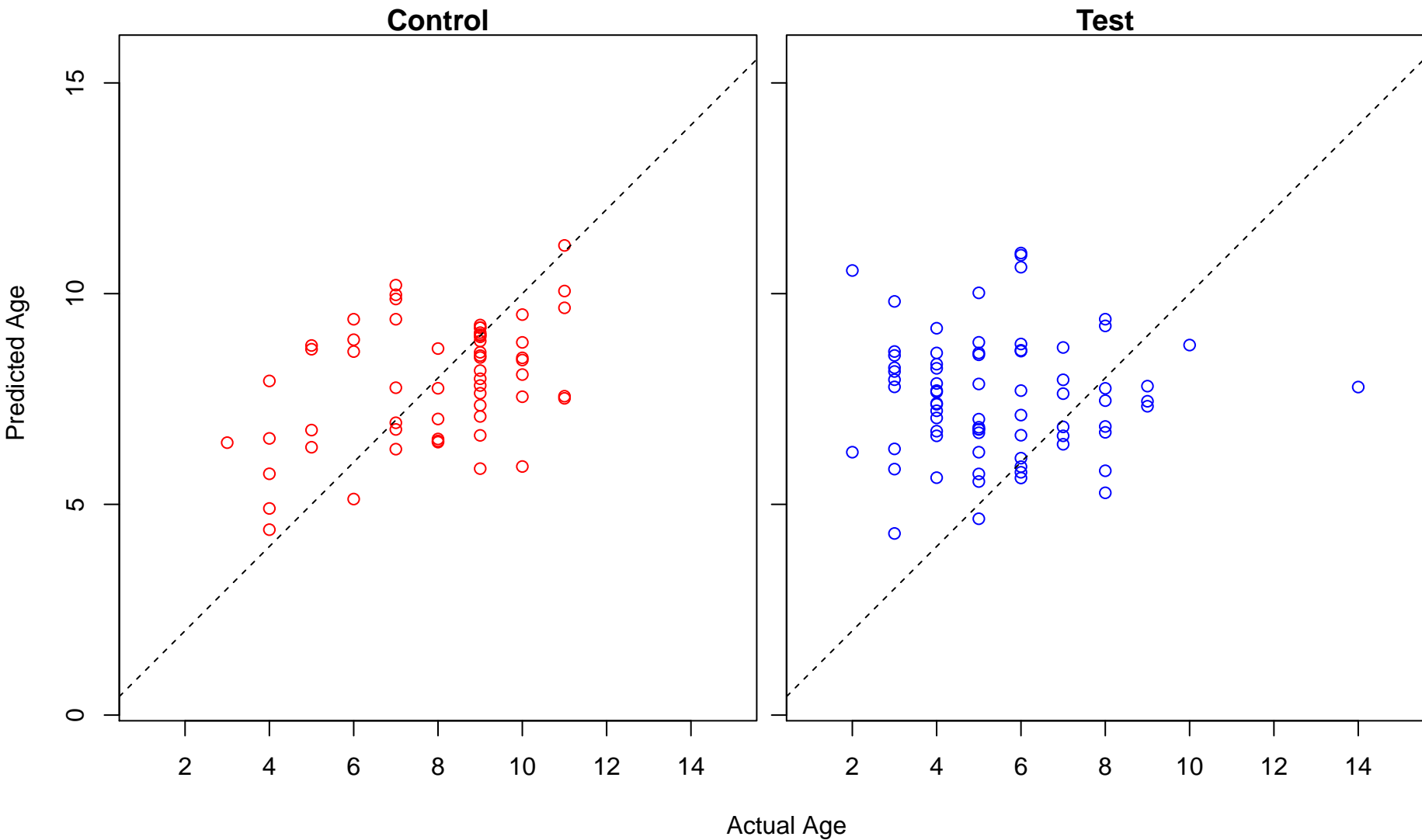
innate immune response (Score: 0.892132)



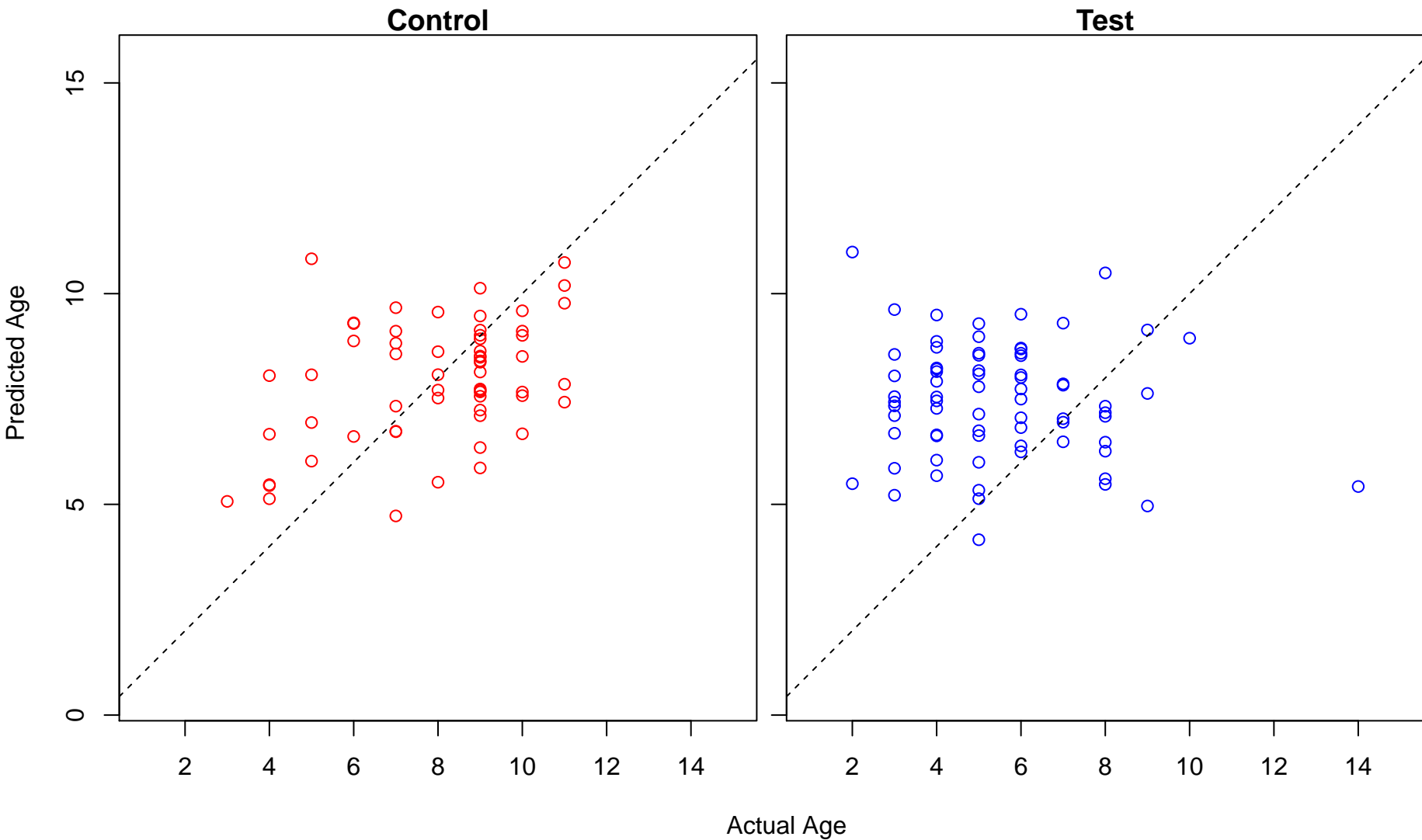
proton transport (Score: 0.891848)



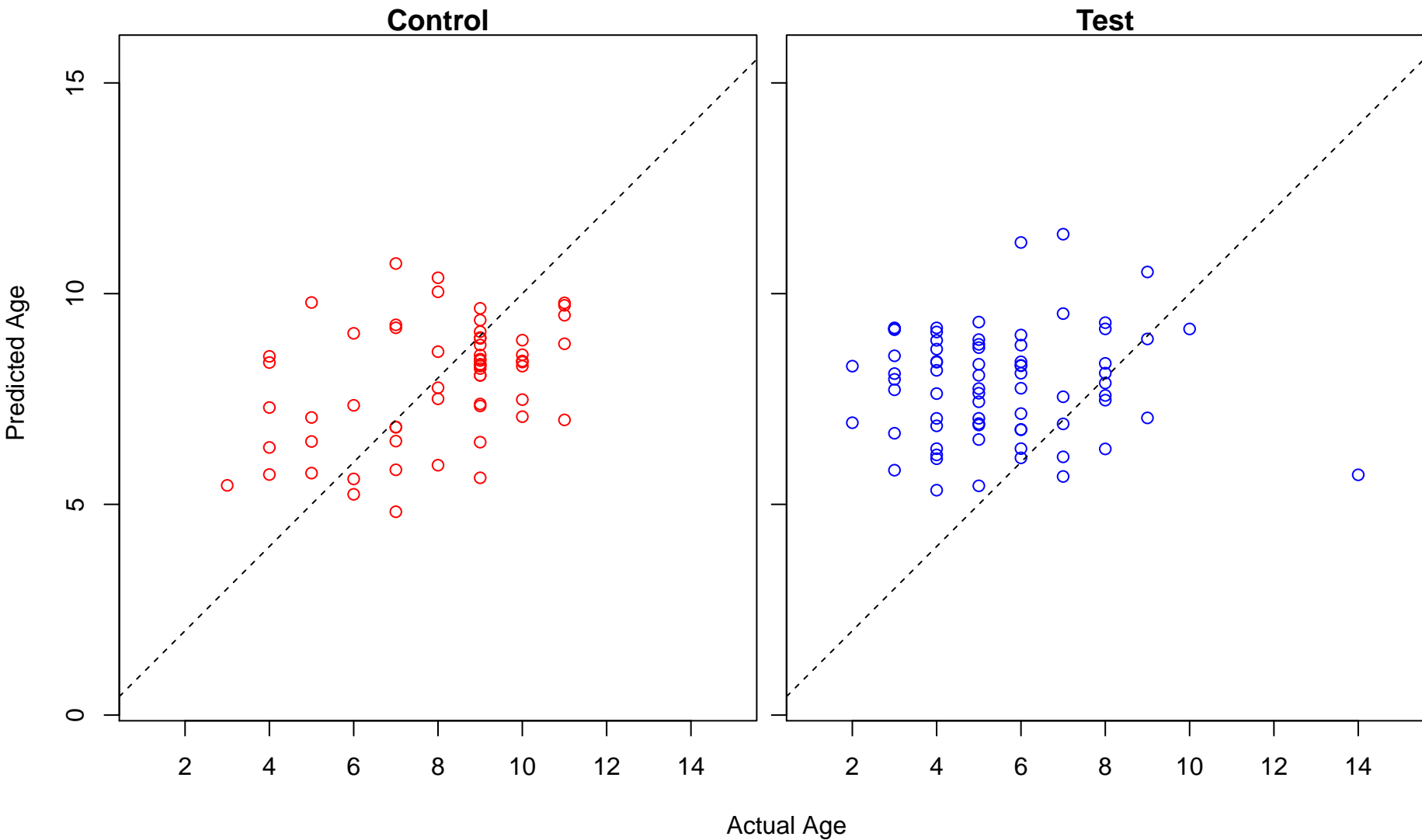
hydrogen transport (Score: 0.891709)



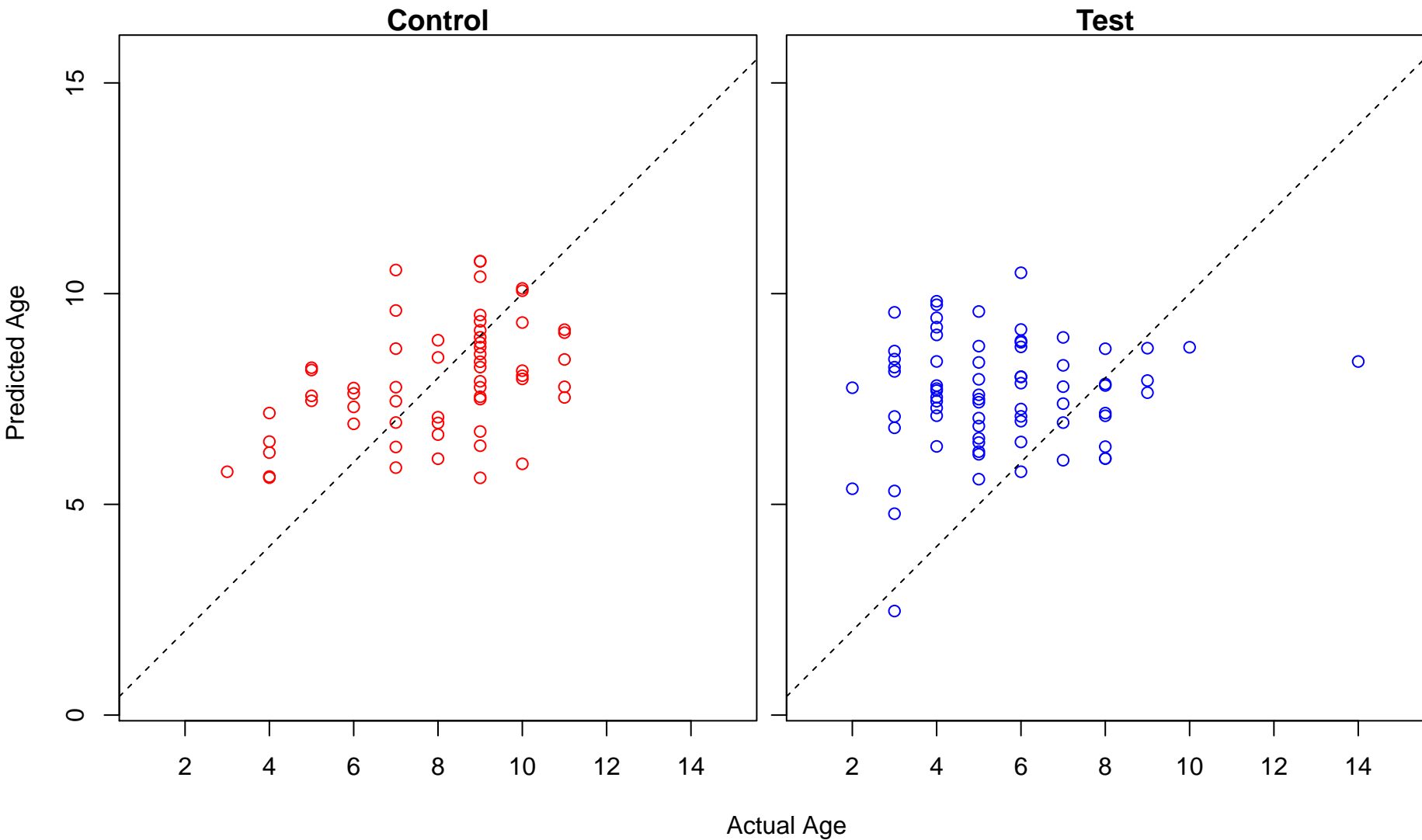
regulation of histone modification (Score: 0.891081)



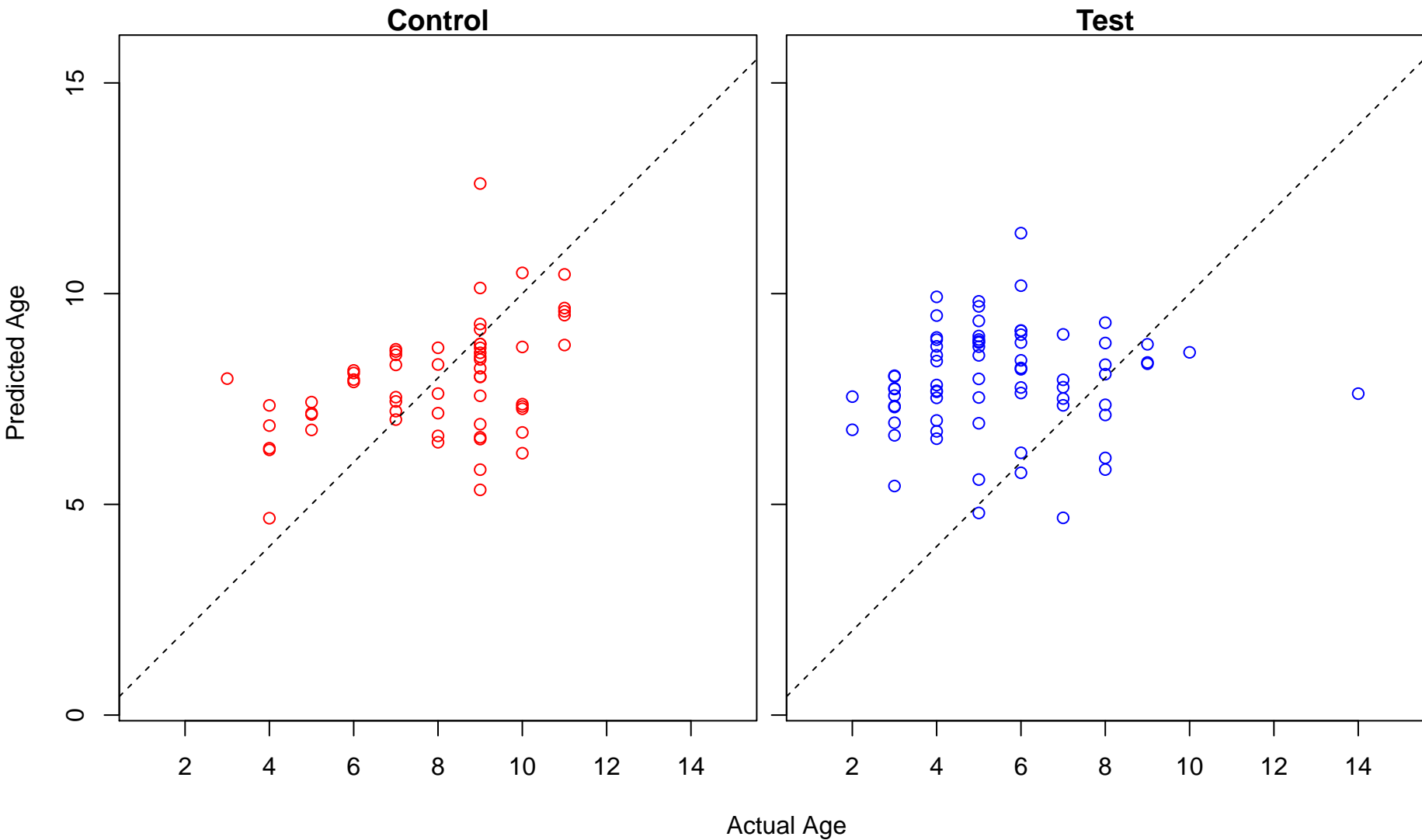
positive regulation of receptor activity (Score: 0.891034)



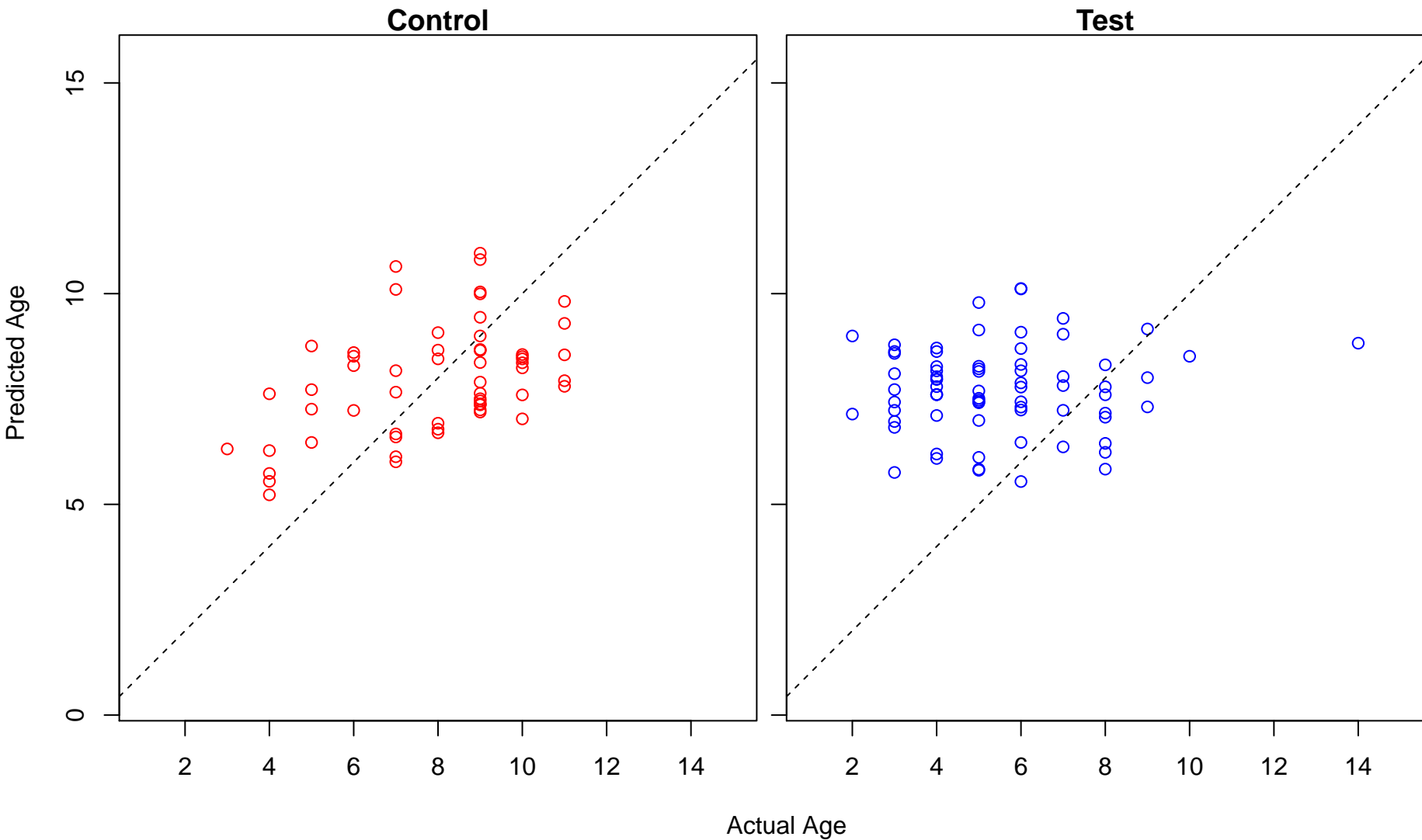
regulation of morphogenesis of a branching structure (Score: 0.889419)



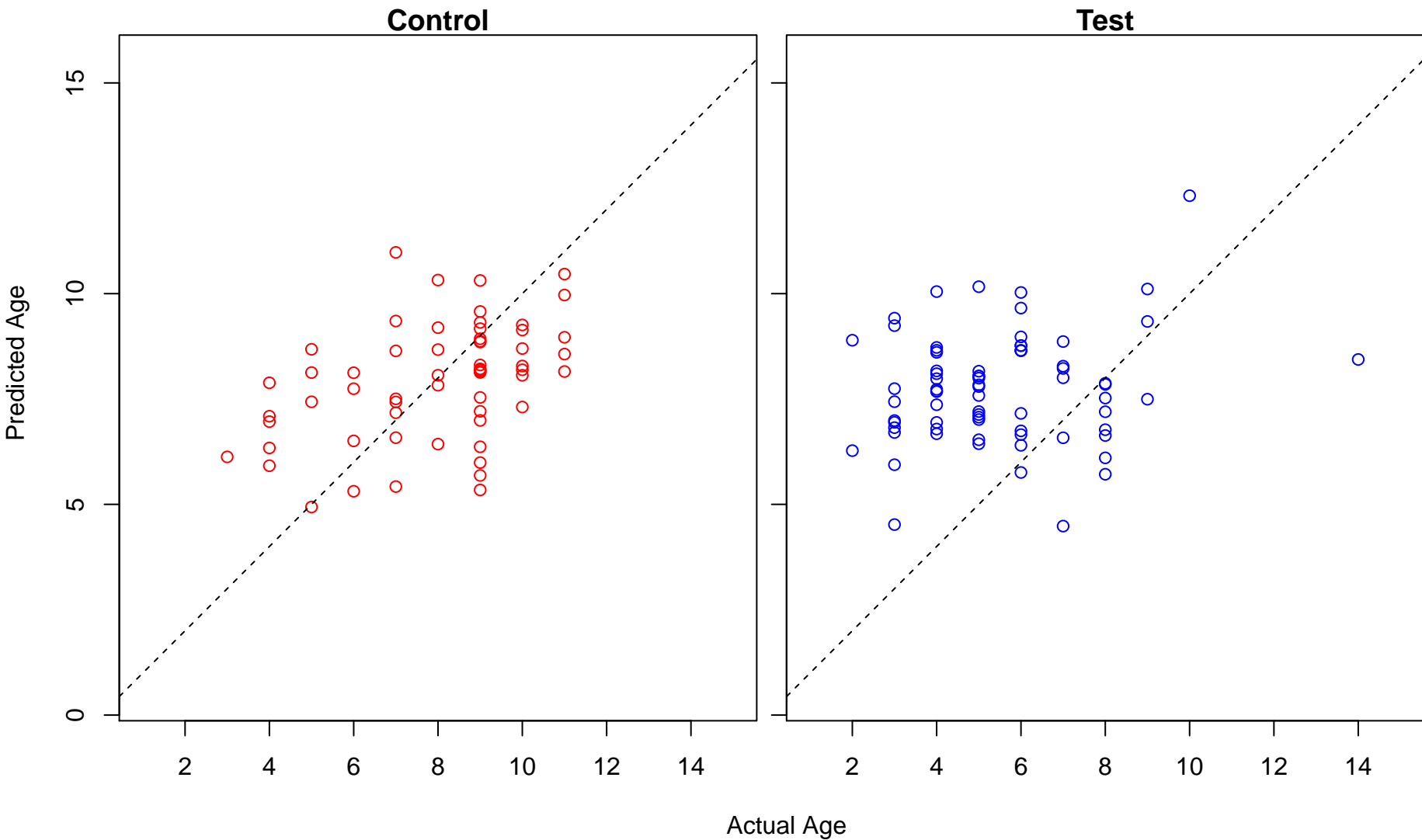
negative regulation of macroautophagy (Score: 0.888573)



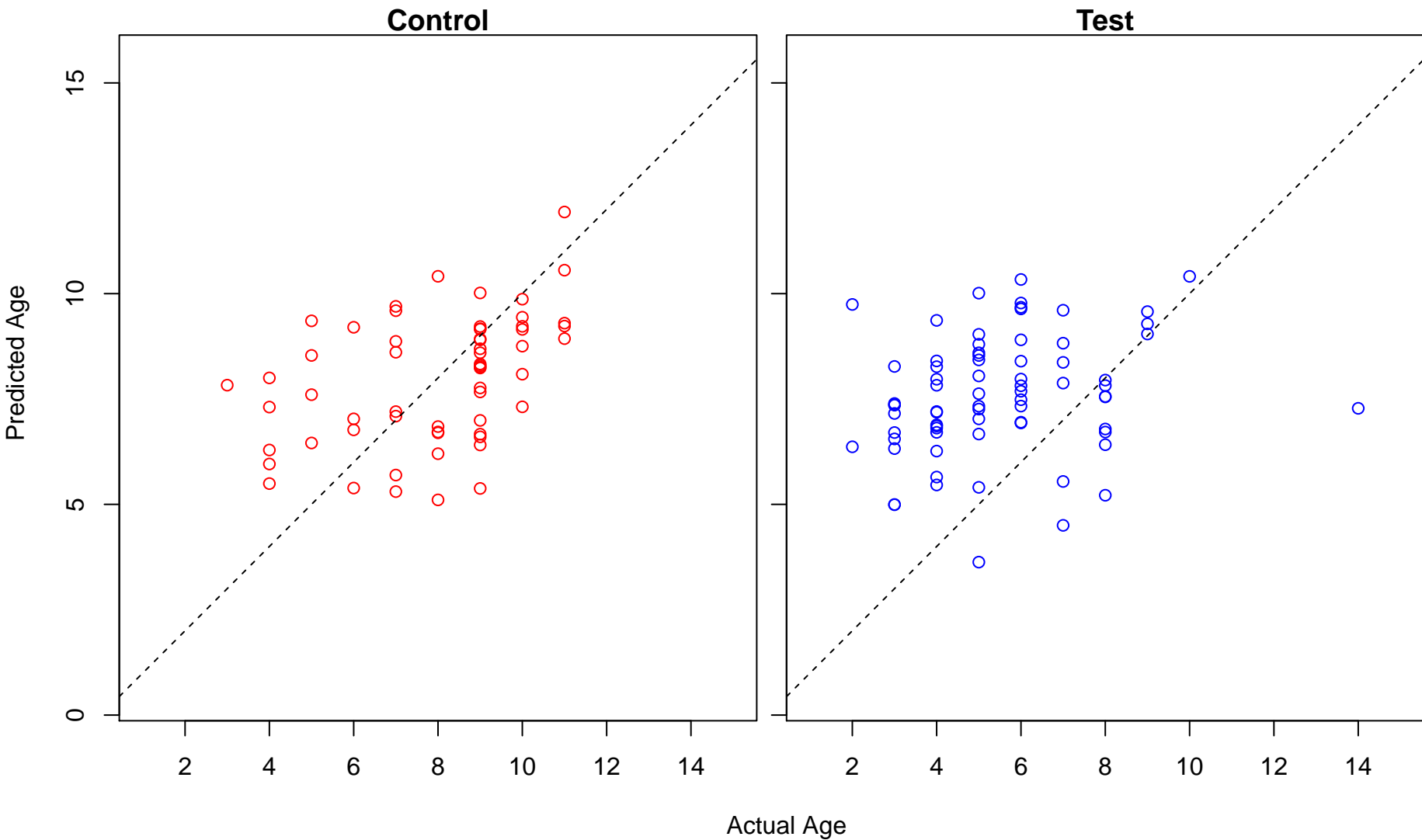
synaptic vesicle transport (Score: 0.888017)



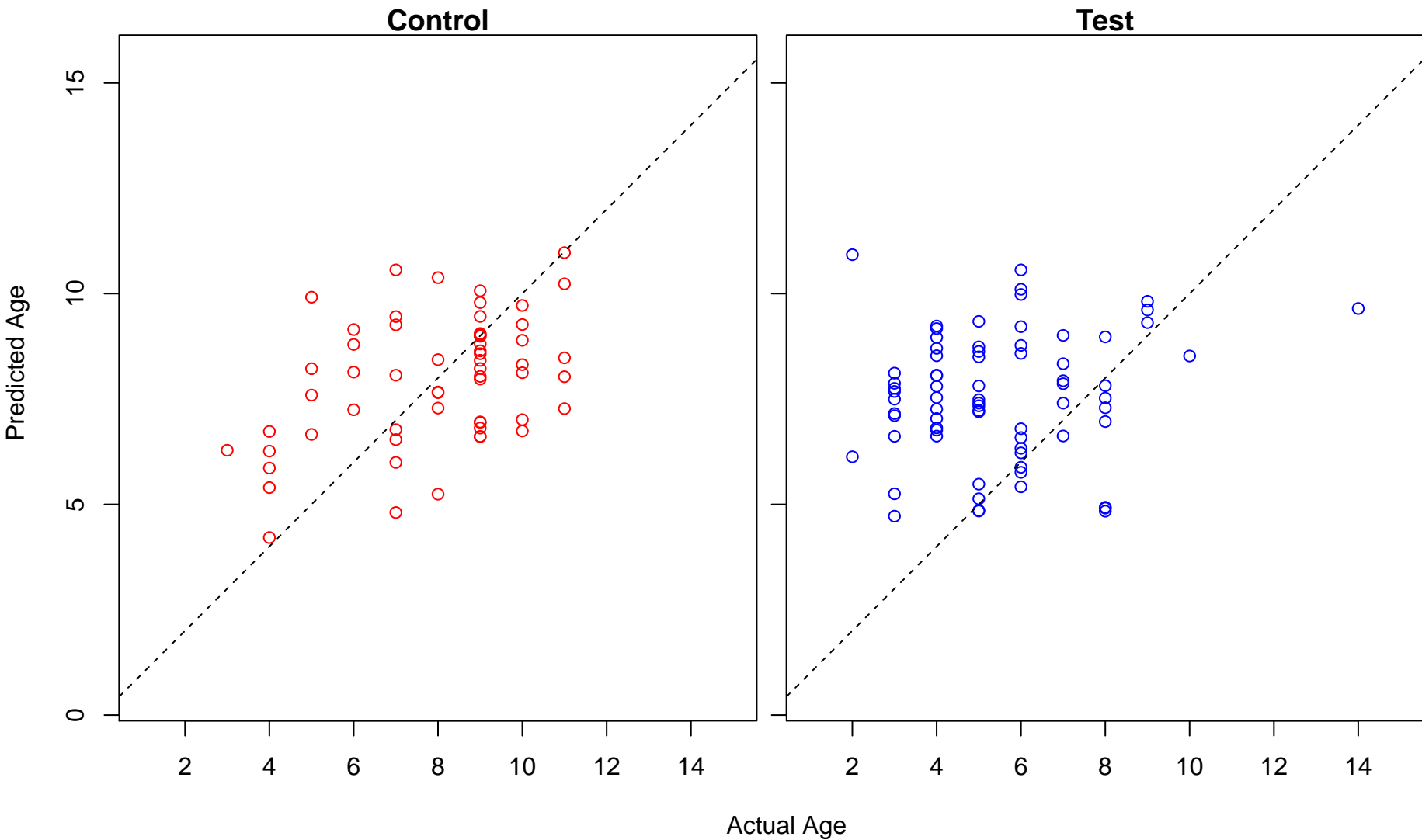
substrate-dependent cell migration (Score: 0.887386)



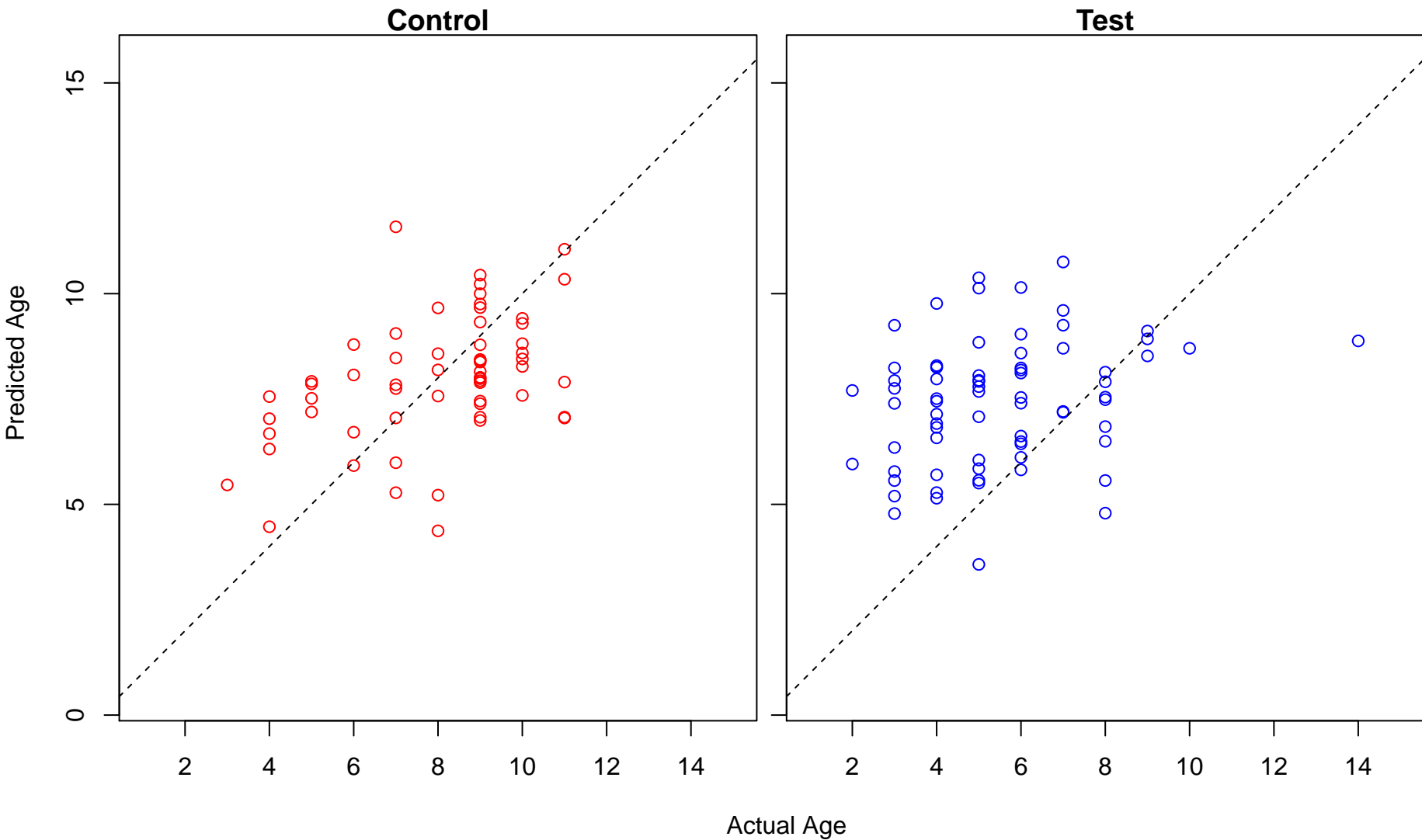
cellular nitrogen compound metabolic process (Score: 0.886630)



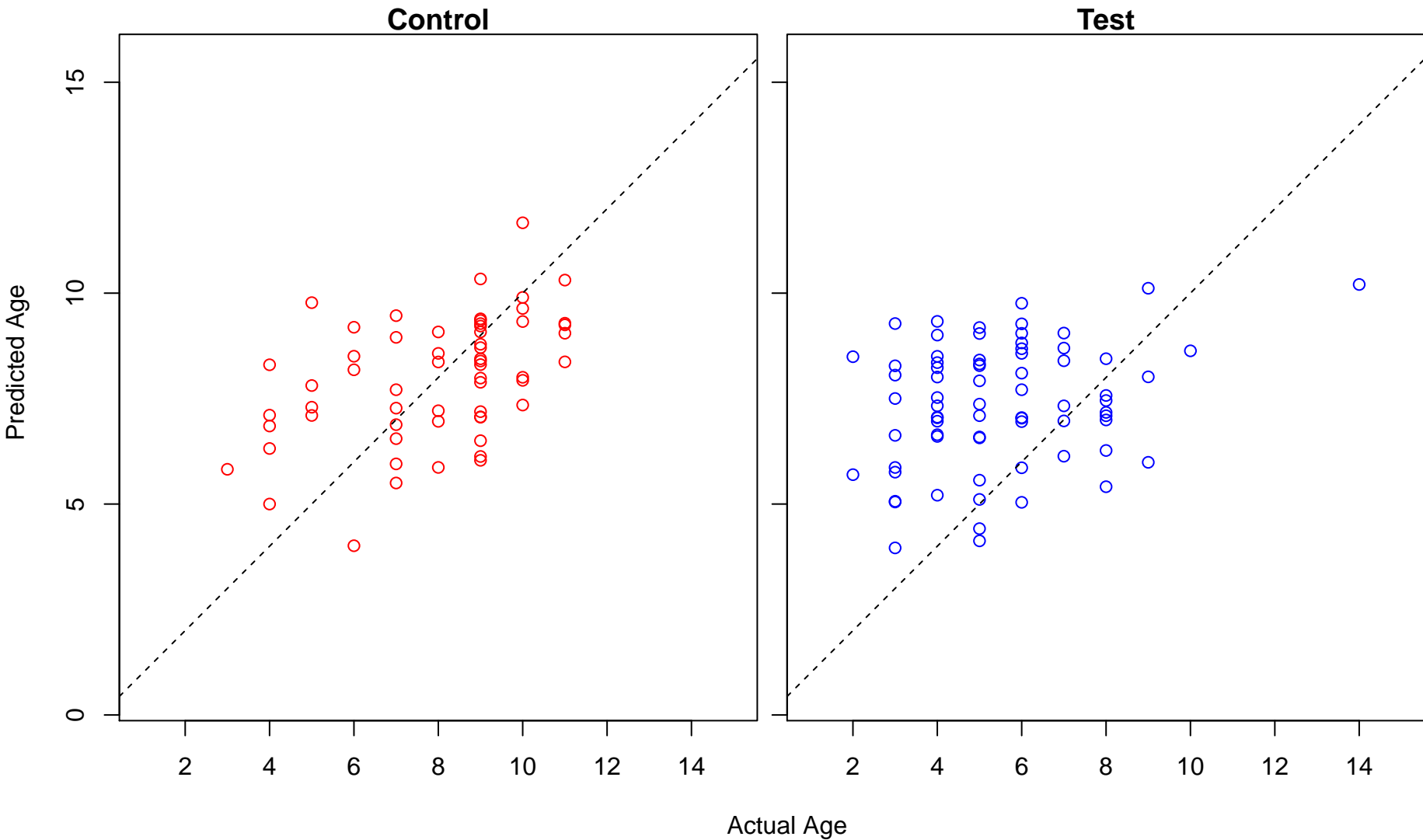
leukocyte aggregation (Score: 0.885574)



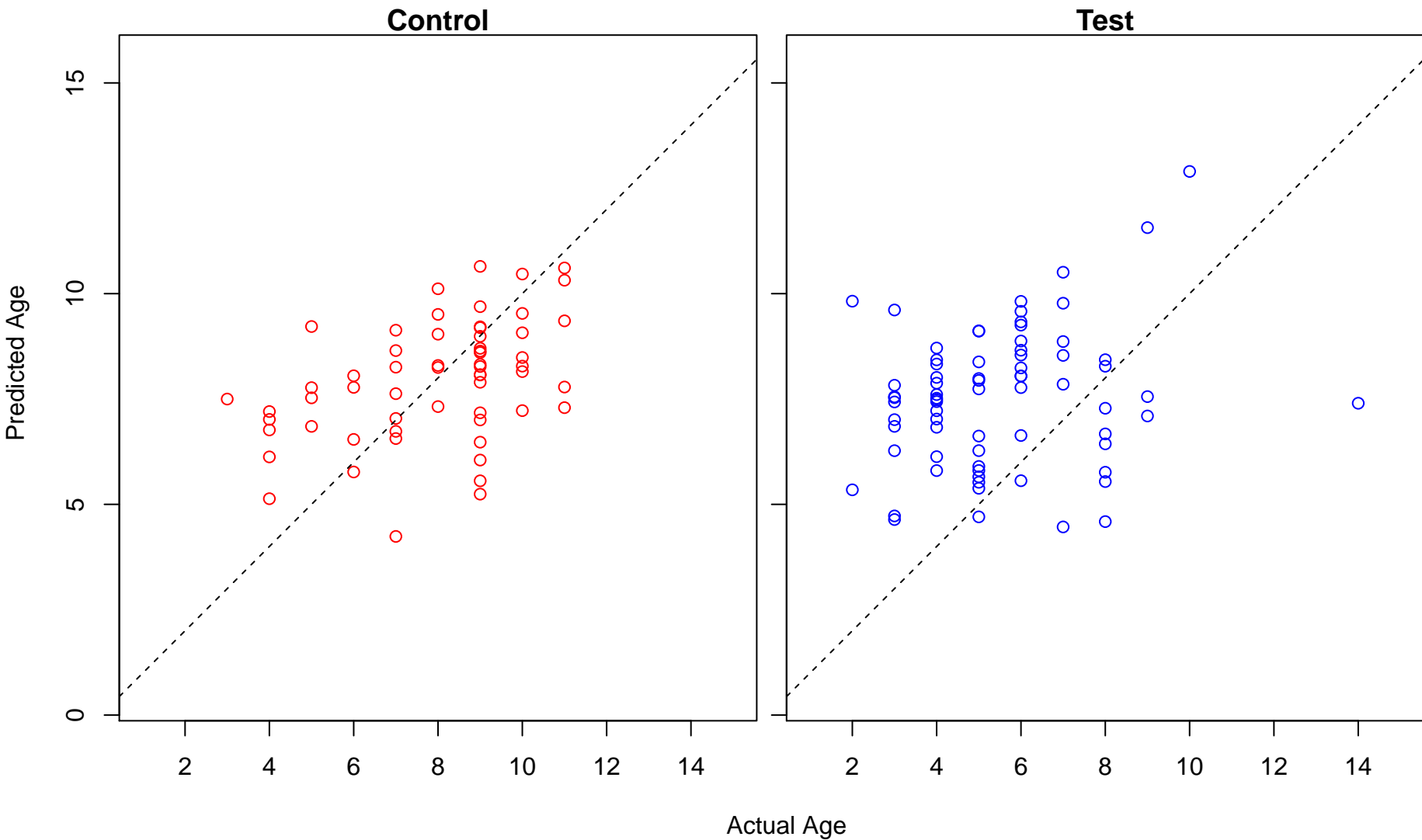
cardiac muscle tissue growth (Score: 0.885381)



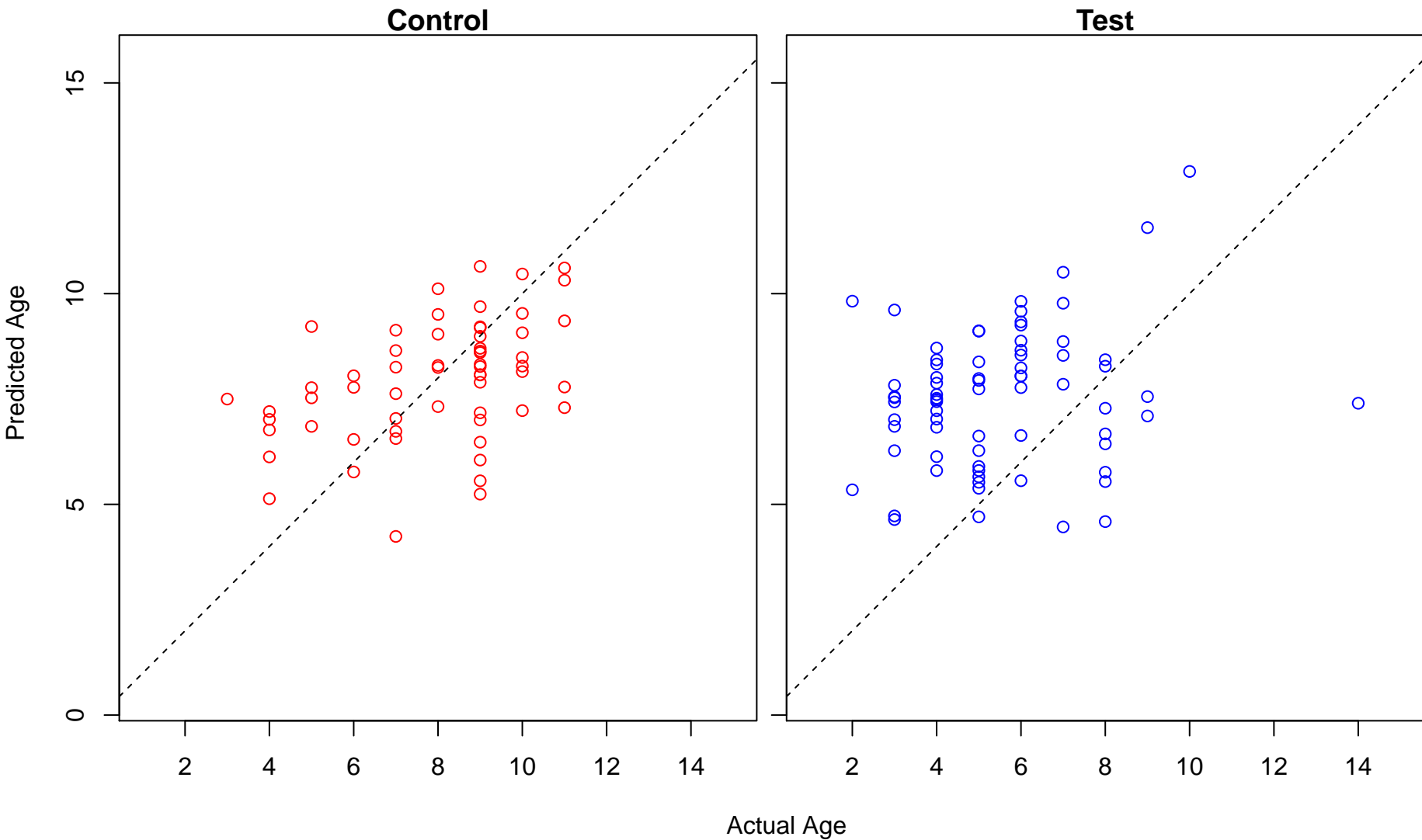
positive regulation of antigen processing and presentation (Score: 0.884376)



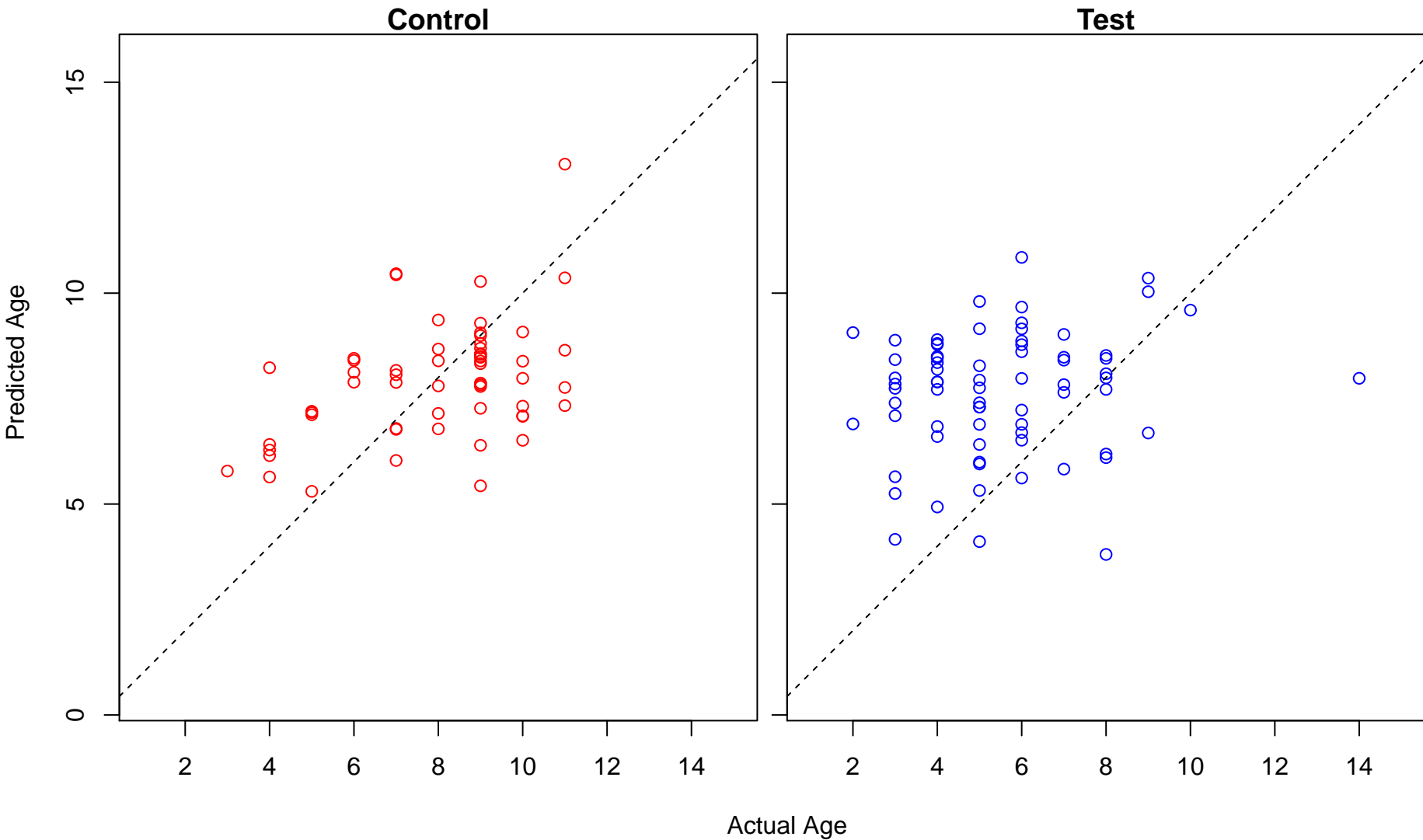
chromosome localization (Score: 0.883946)



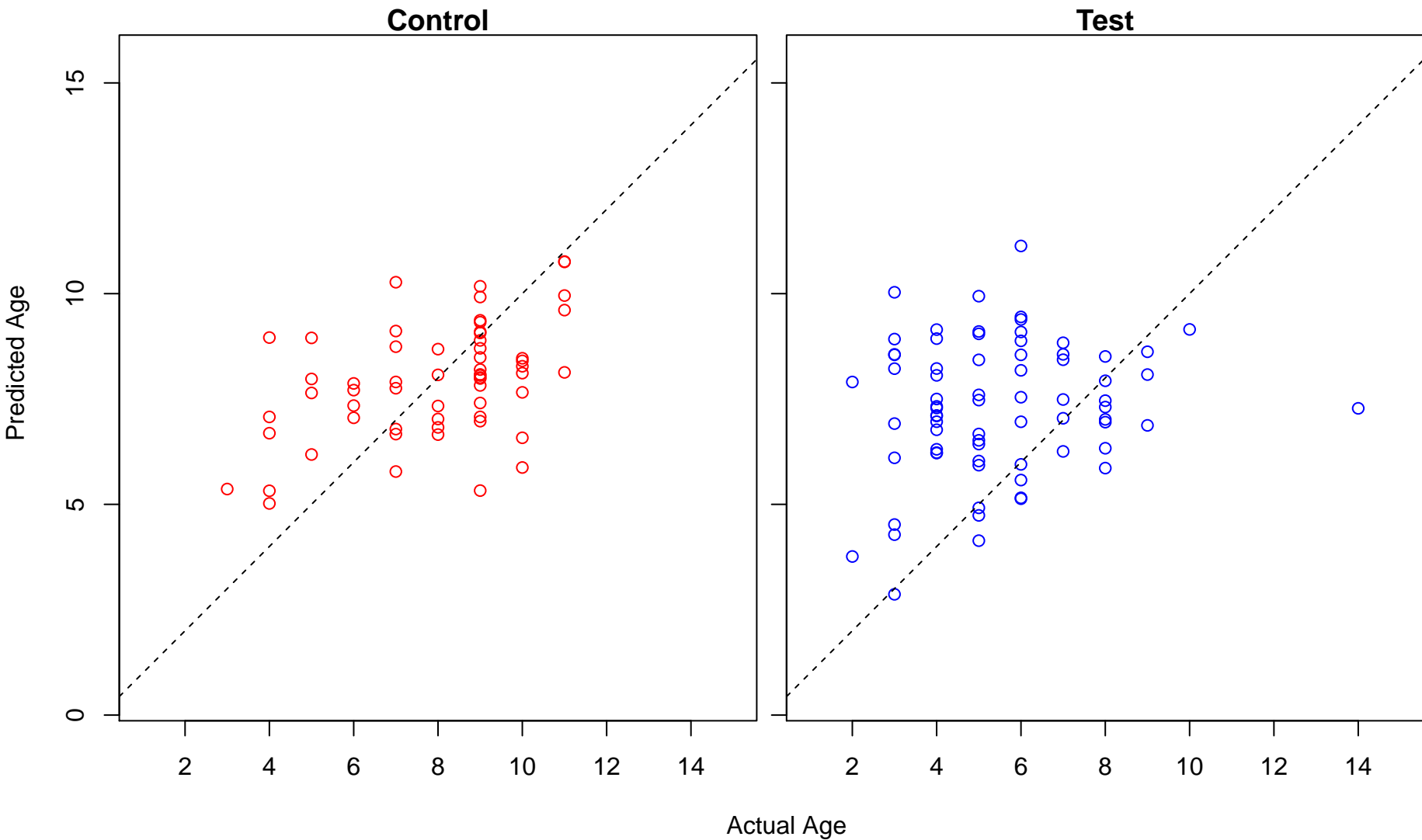
establishment of chromosome localization (Score: 0.883946)



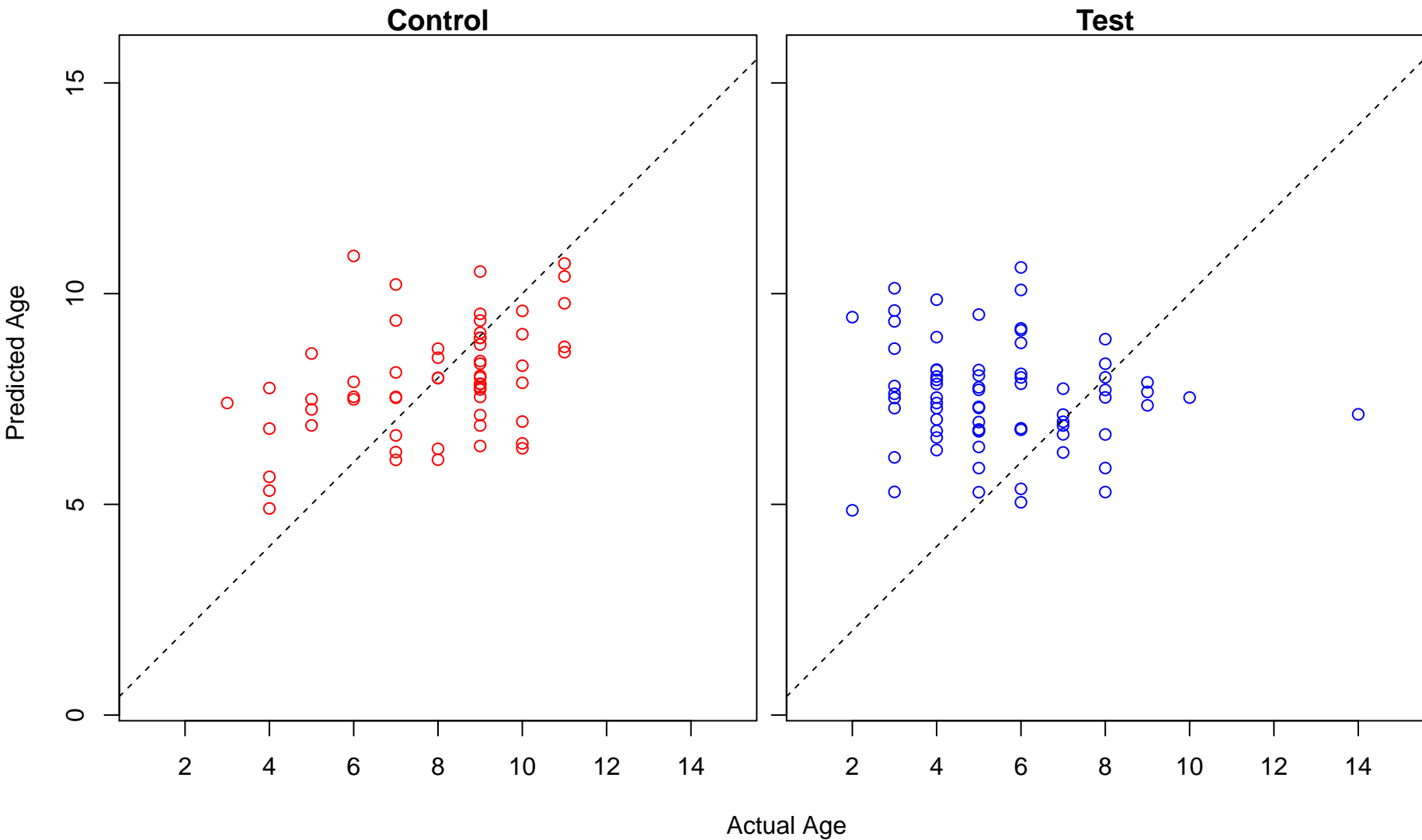
positive regulation of interleukin-2 production (Score: 0.883221)



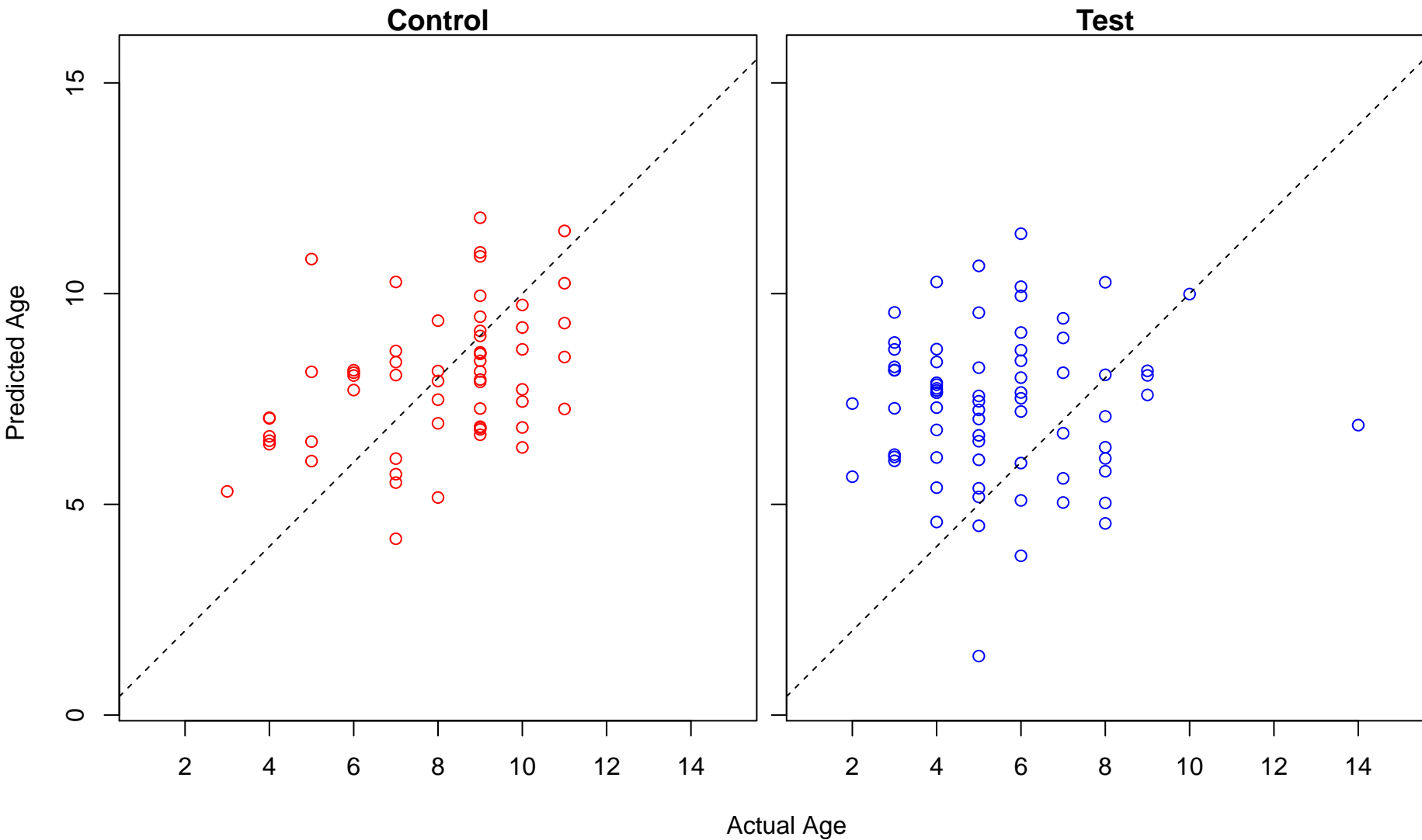
notochord development (Score: 0.882965)



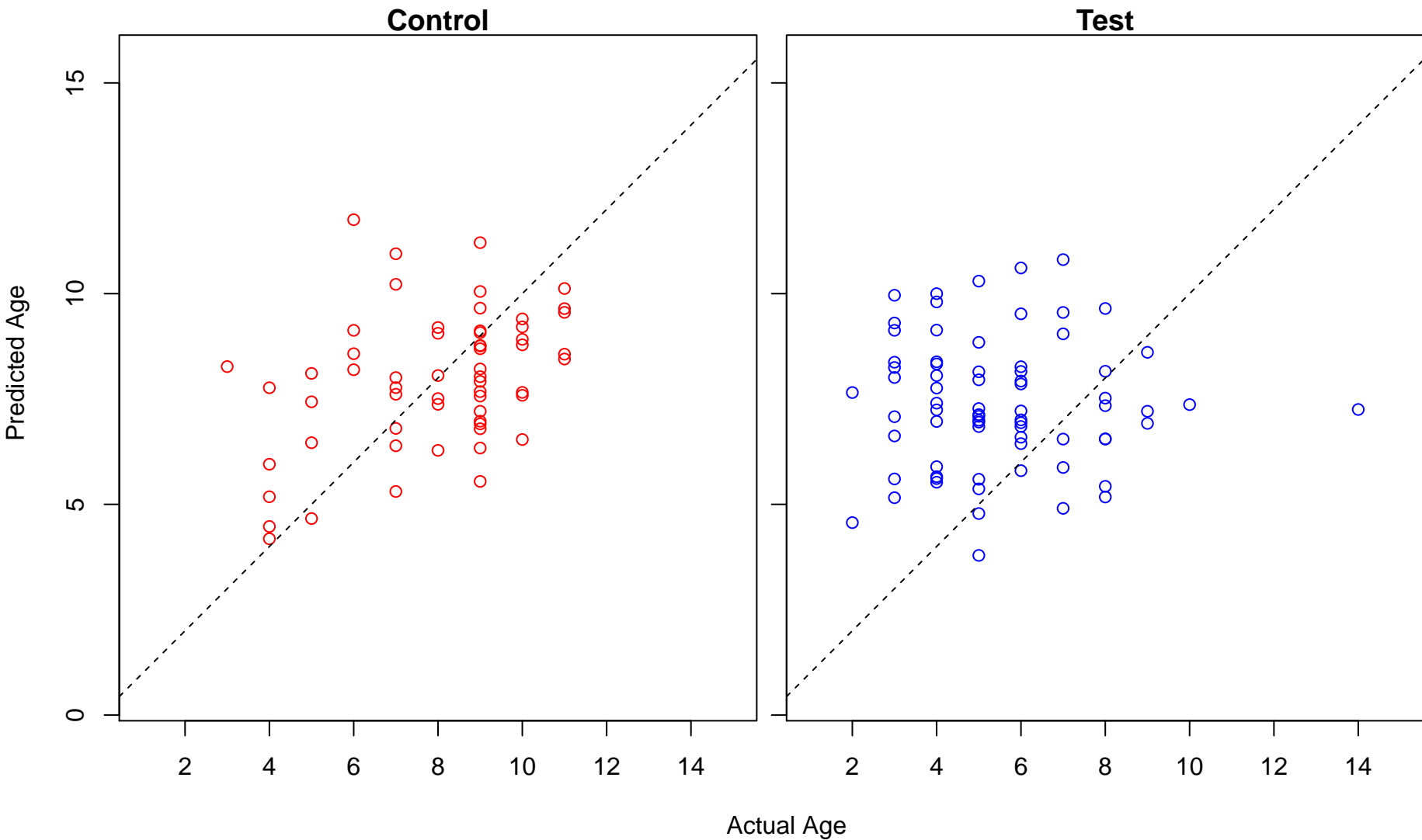
maintenance of protein location in cell (Score: 0.882729)



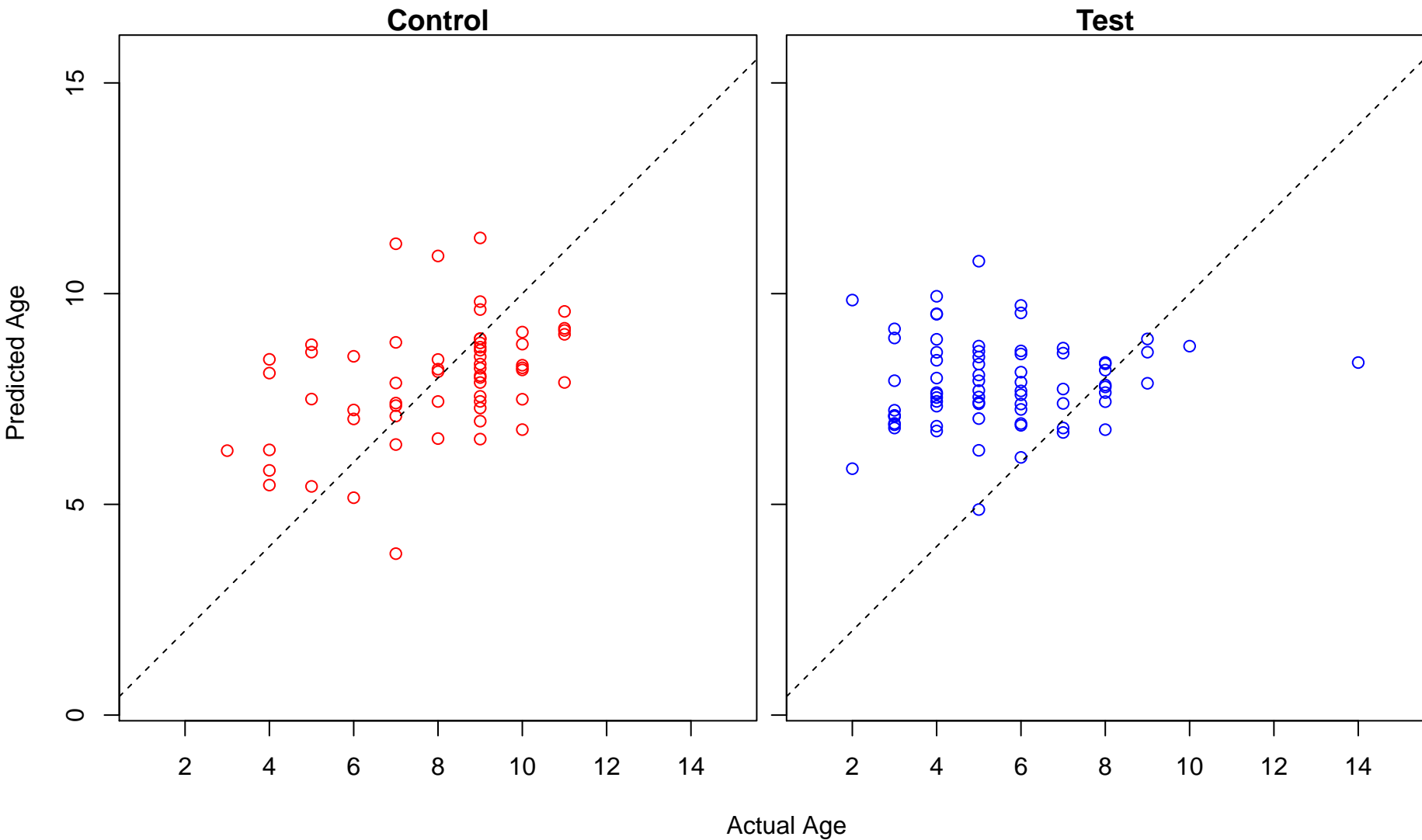
O-glycan processing (Score: 0.881616)



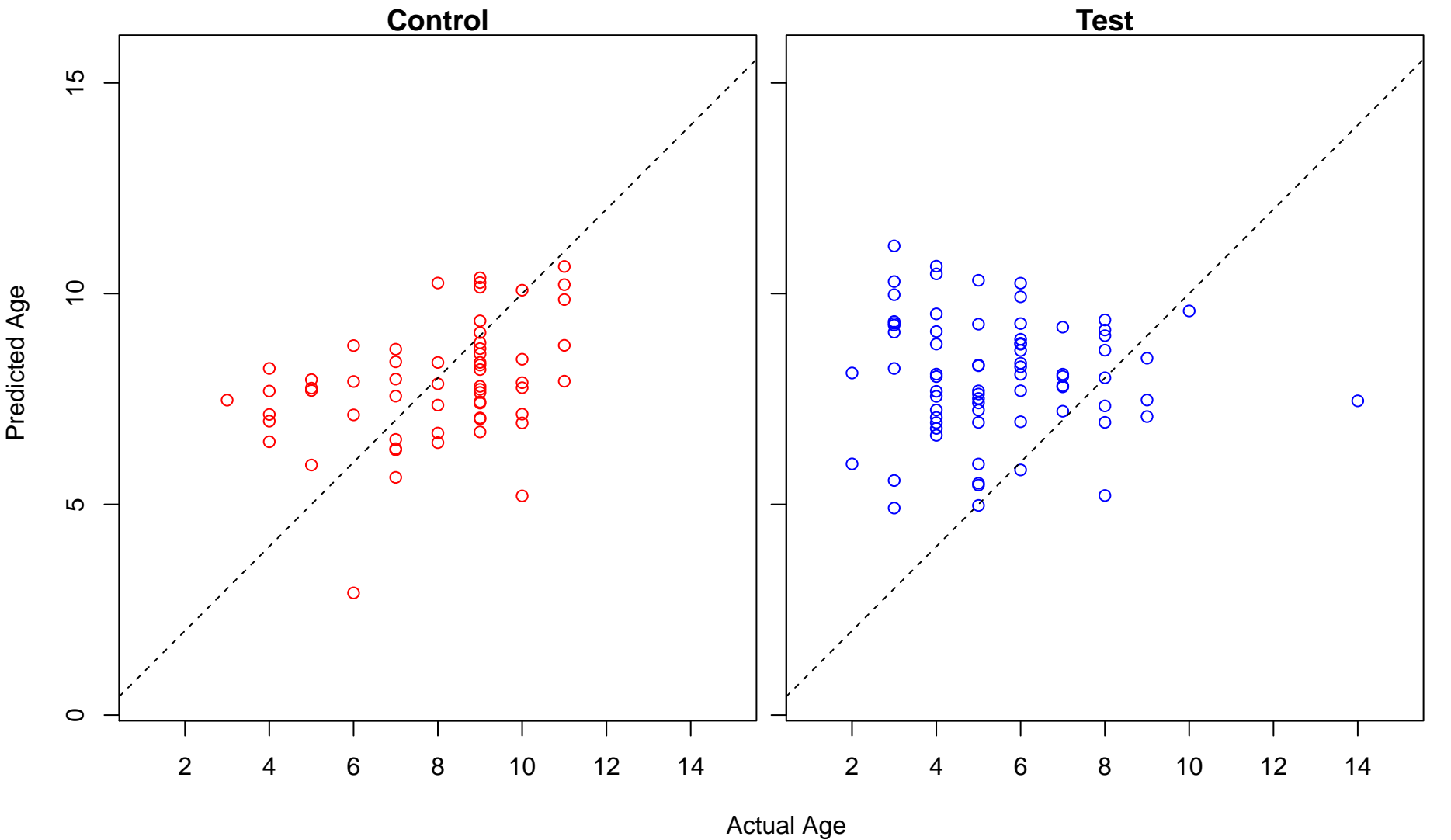
tetrapyrrole metabolic process (Score: 0.880056)



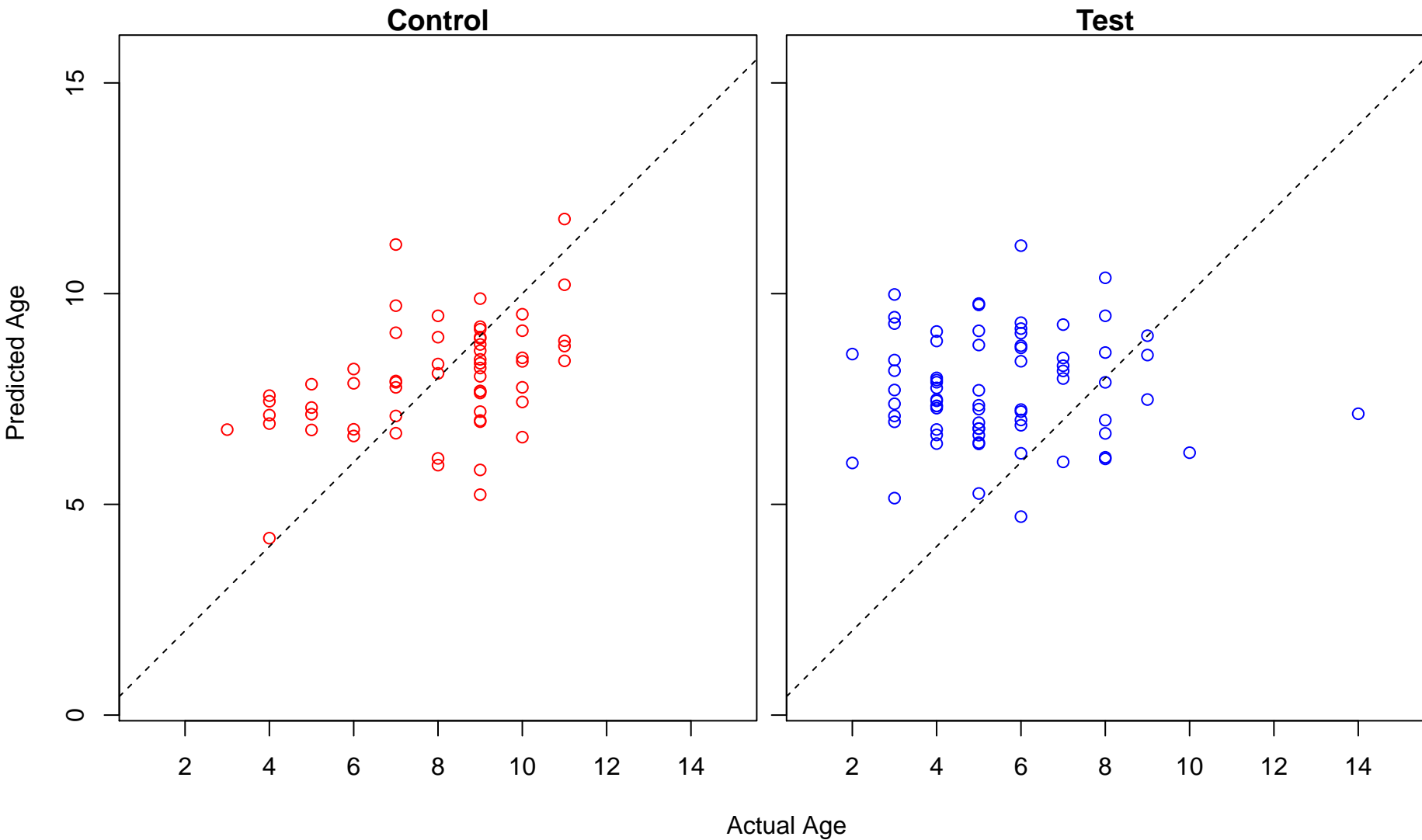
insulin secretion (Score: 0.878981)



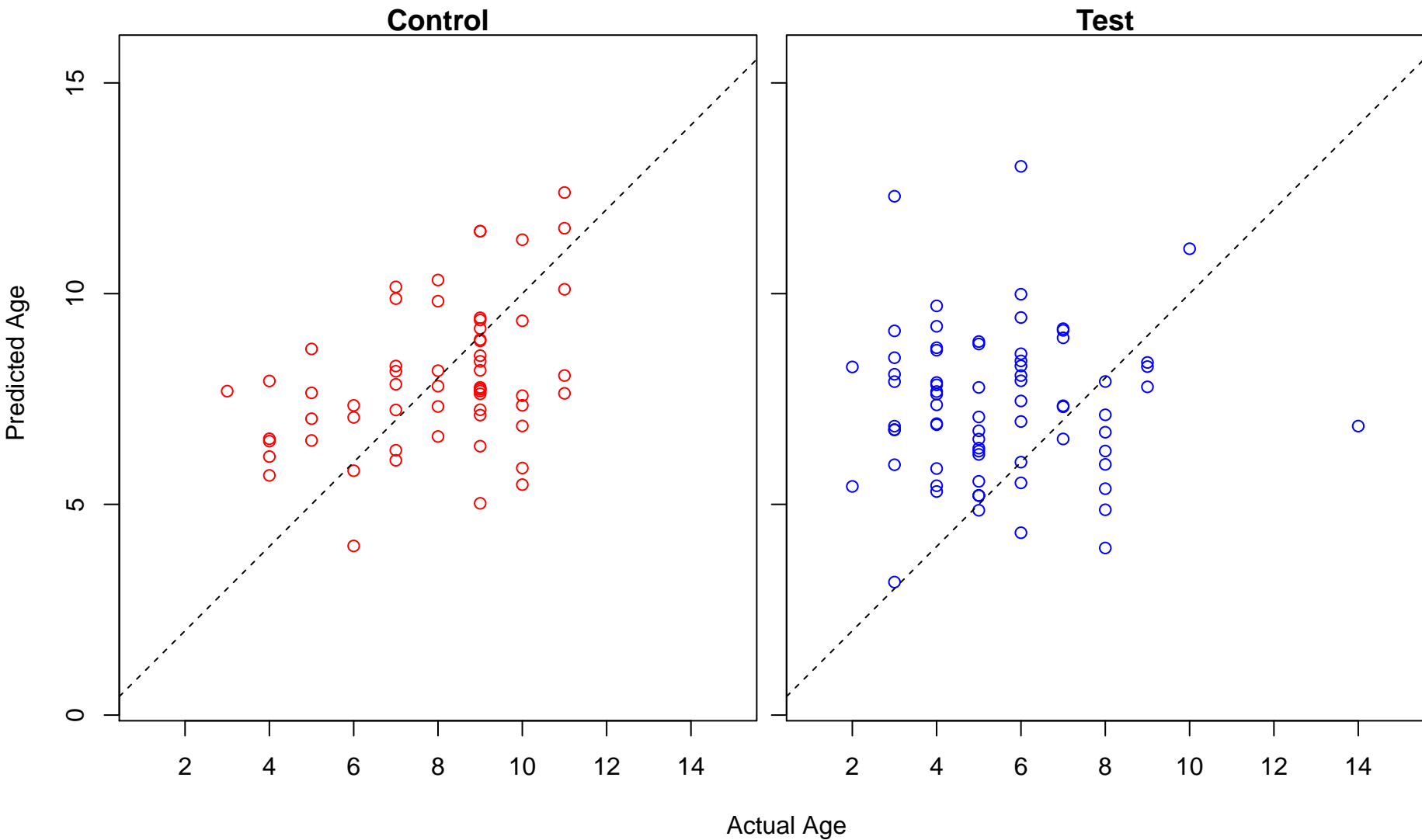
Regulation of lipid transport by positive regulation of transcription from RNA polymerase II promoter (Score)



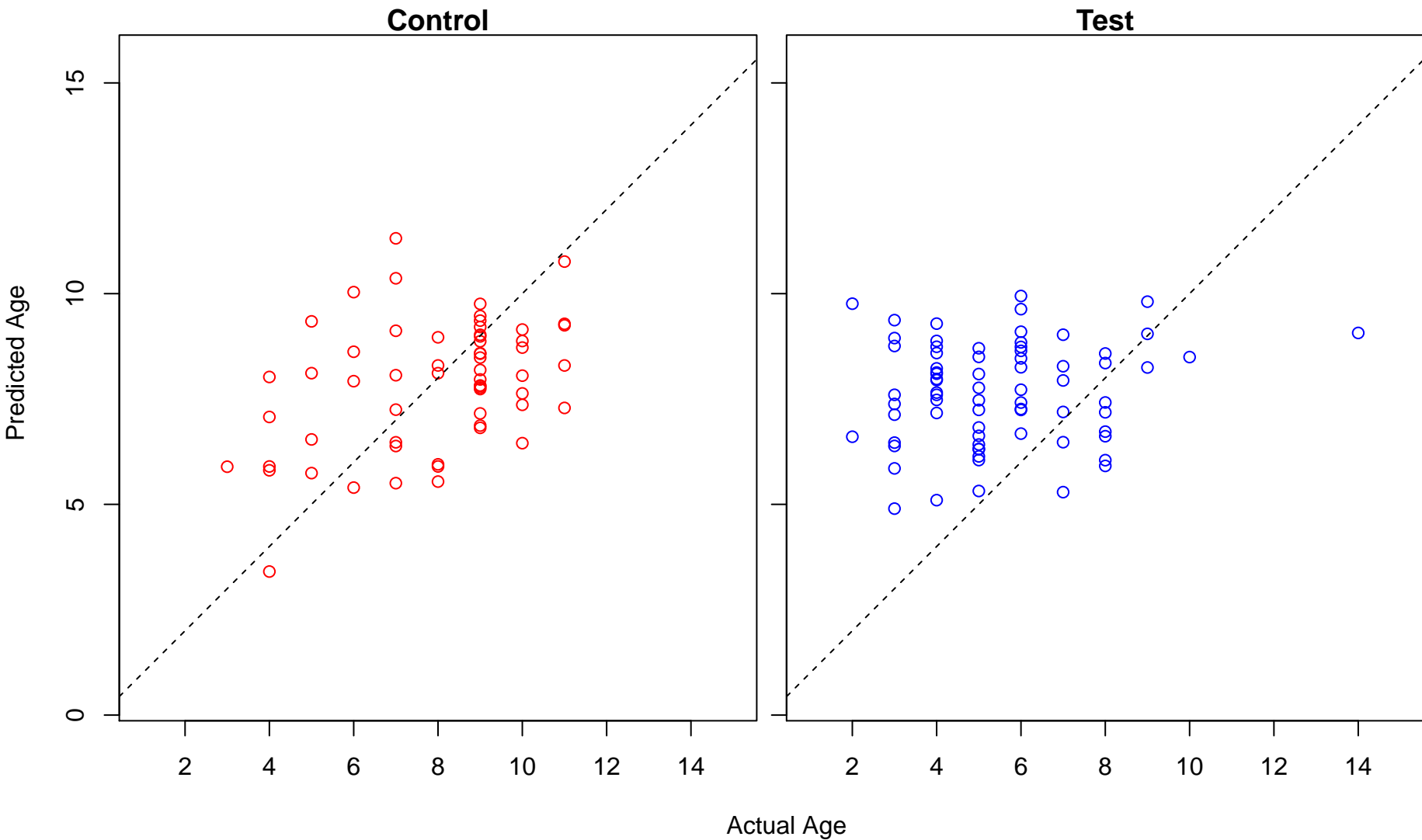
negative regulation of peptidyl-tyrosine phosphorylation (Score: 0.877888)



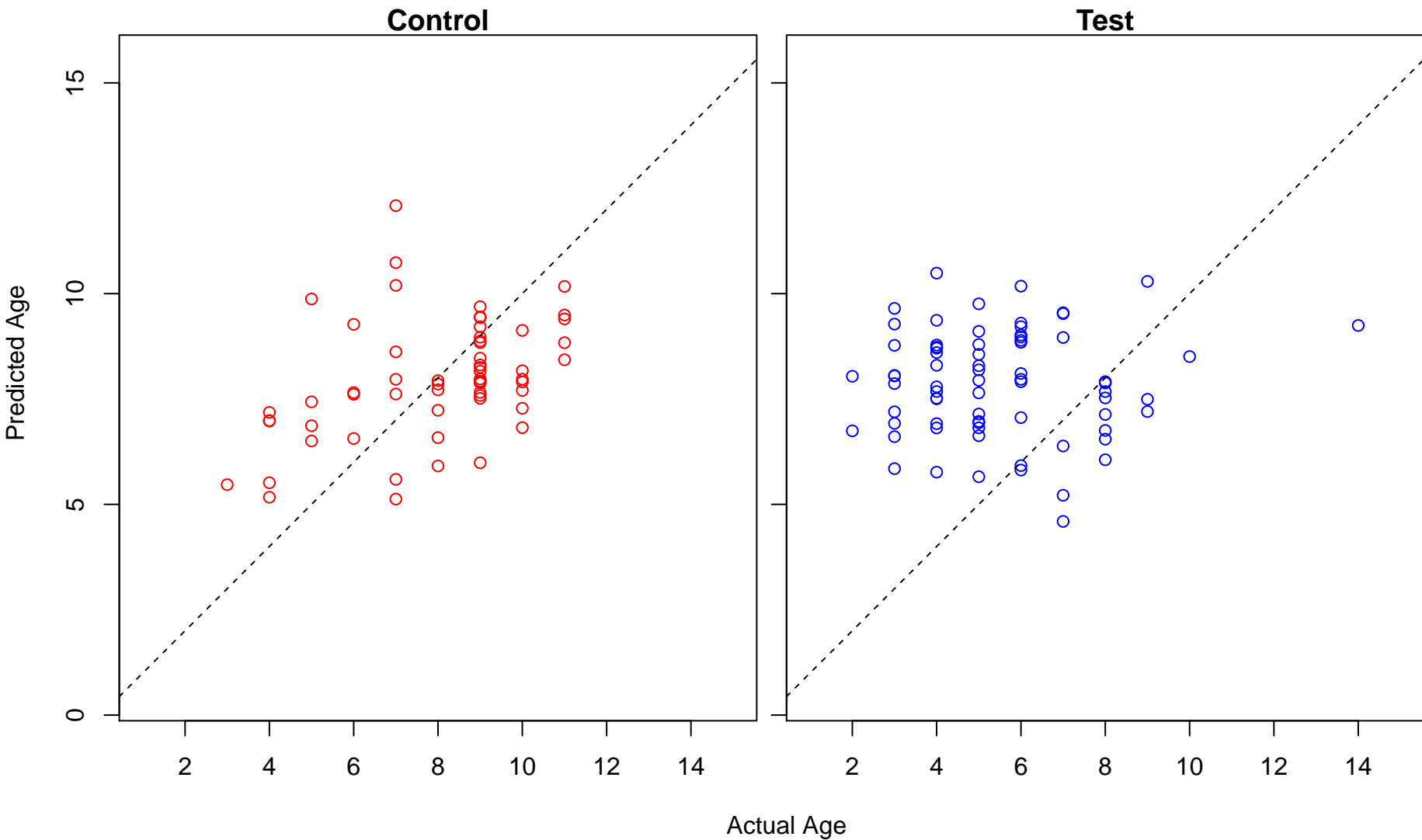
positive regulation of fatty acid metabolic process (Score: 0.877835)



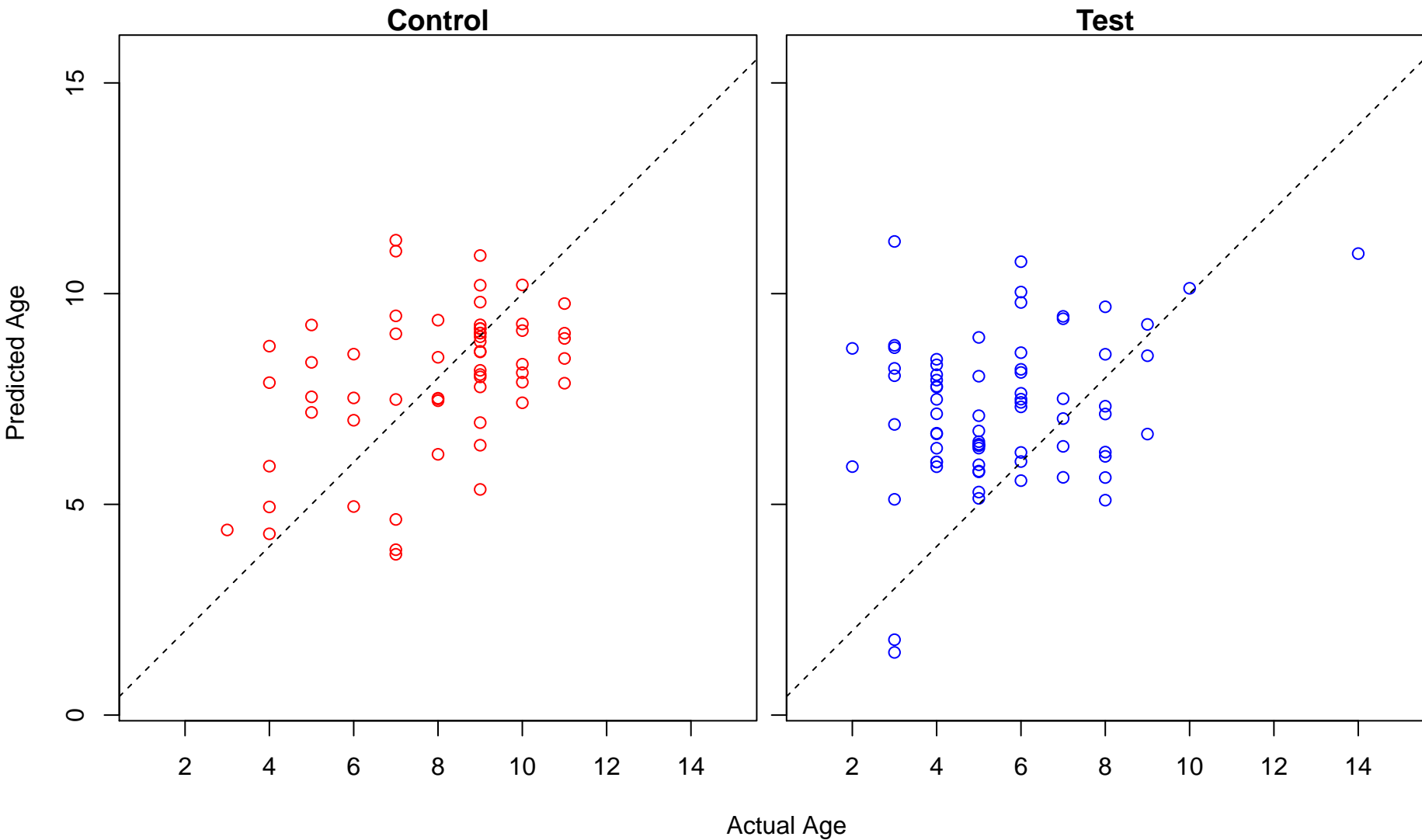
protein modification by small protein conjugation (Score: 0.877623)



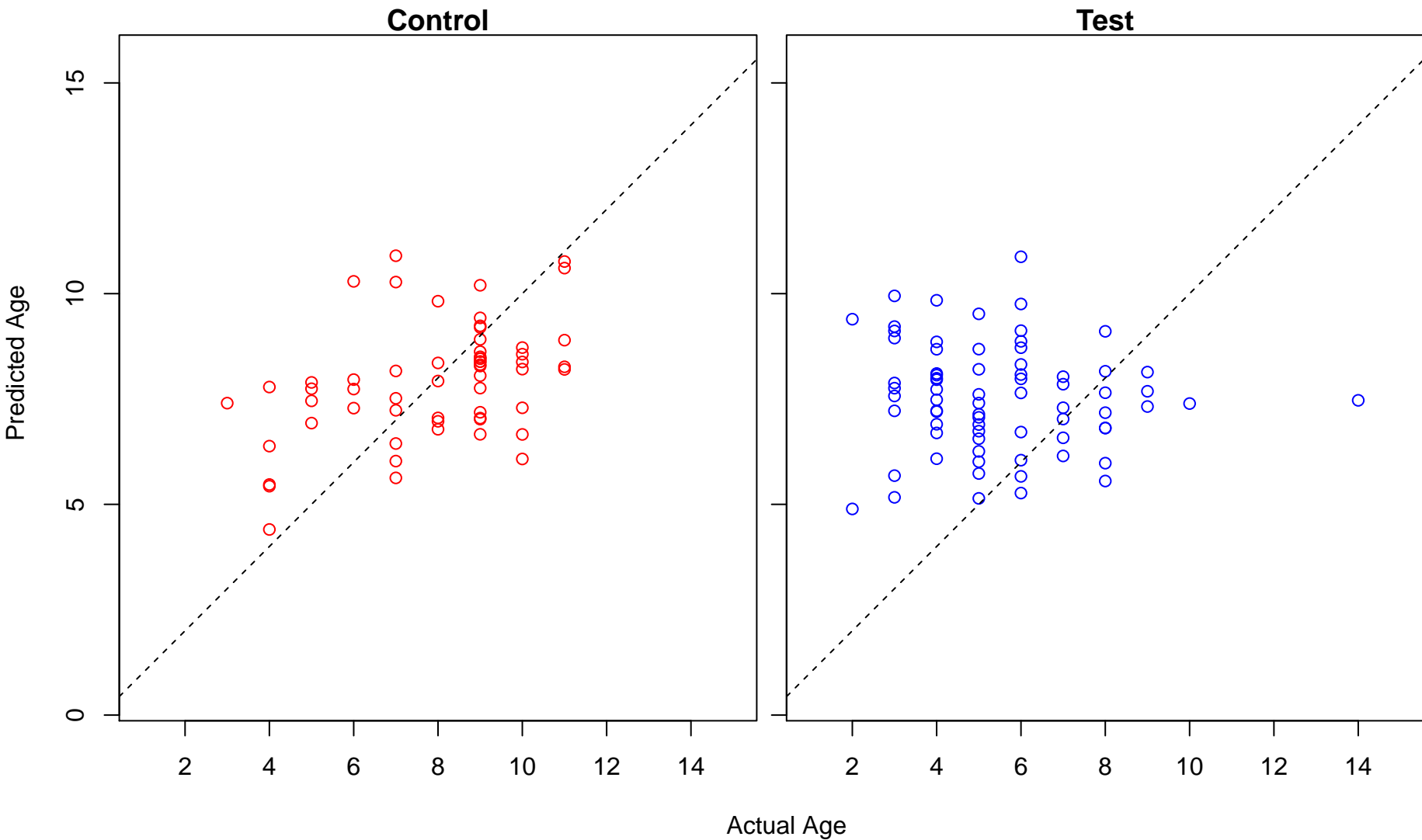
bile acid metabolic process (Score: 0.877196)



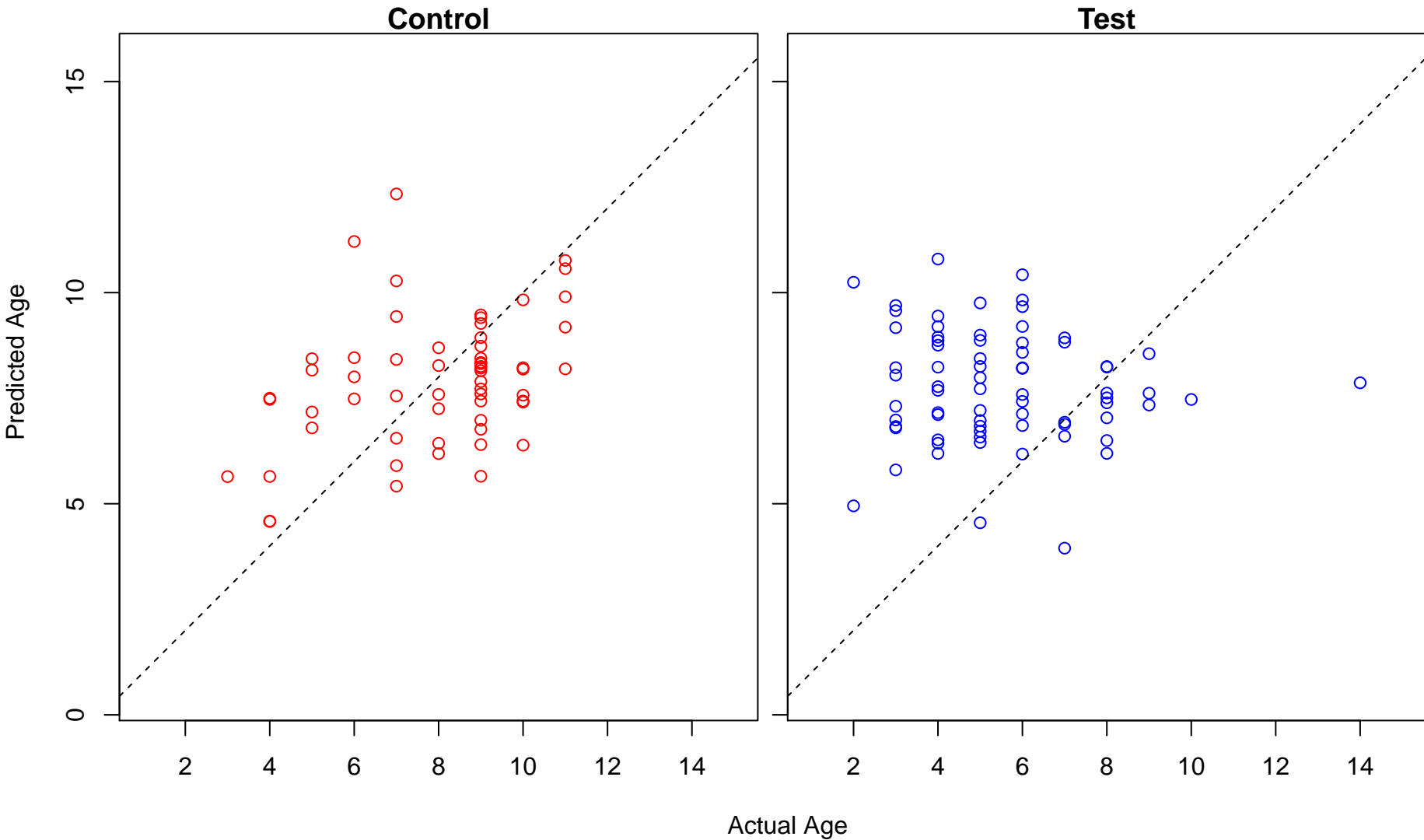
motor neuron axon guidance (Score: 0.877007)



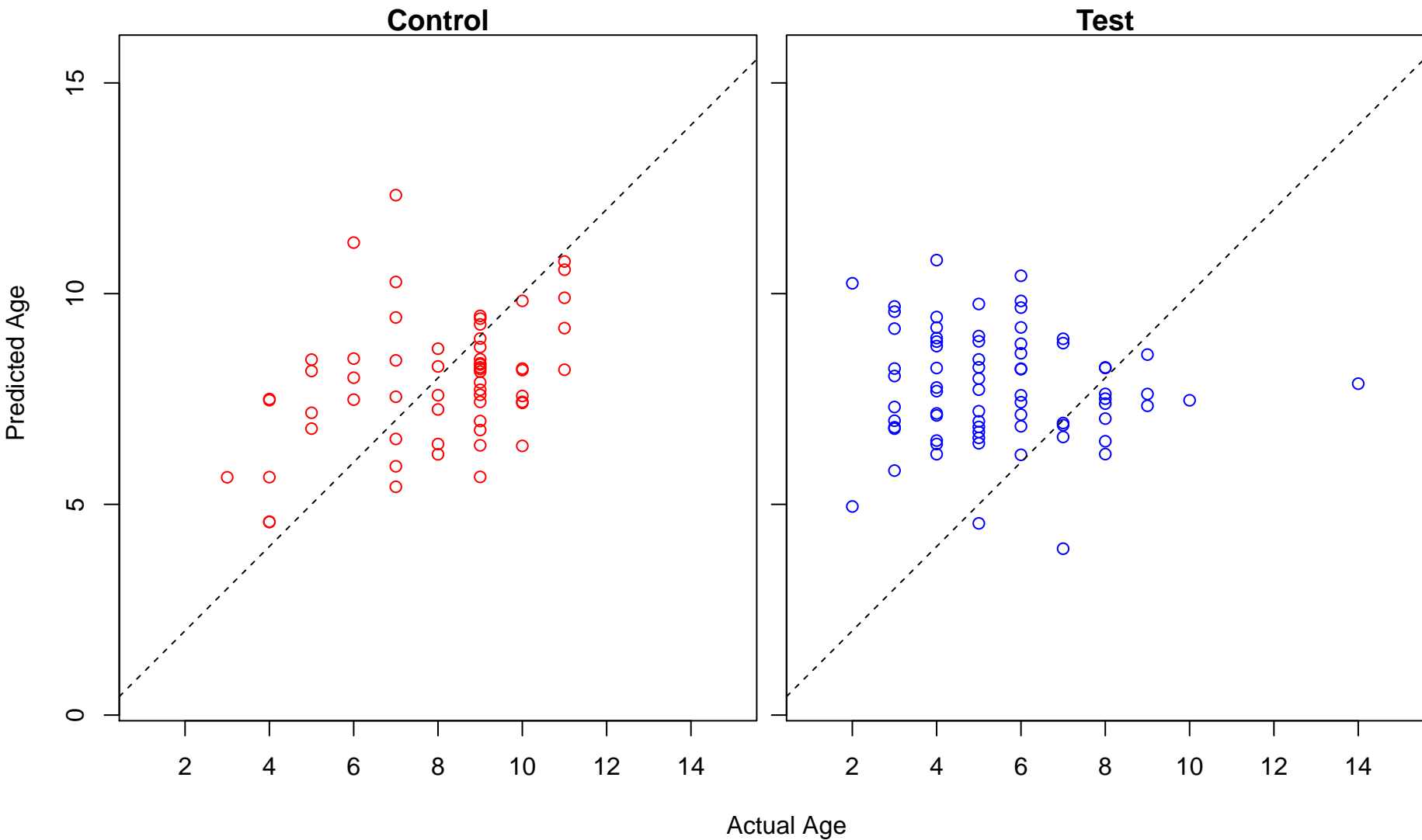
maintenance of location in cell (Score: 0.875227)



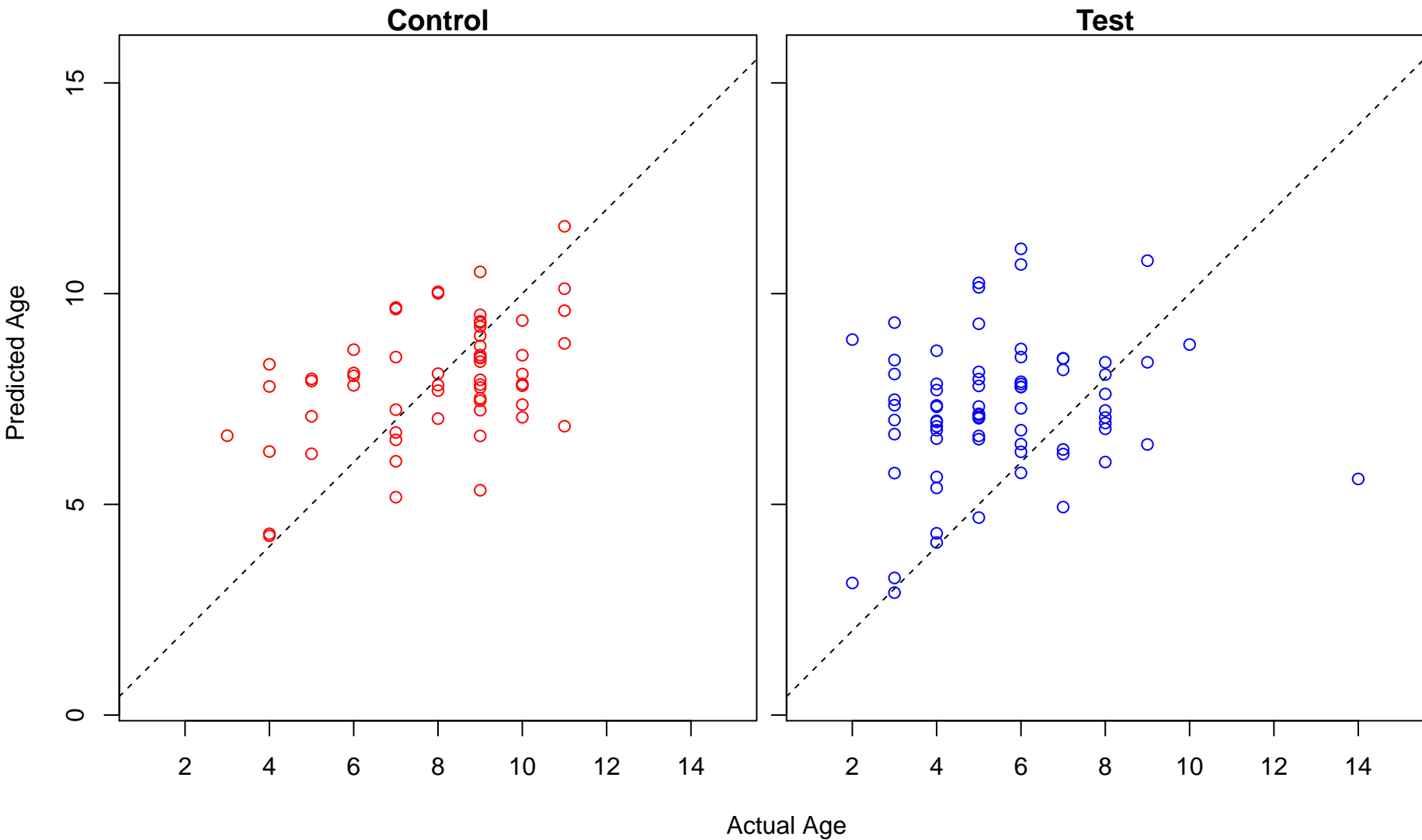
cardiovascular system development (Score: 0.874665)



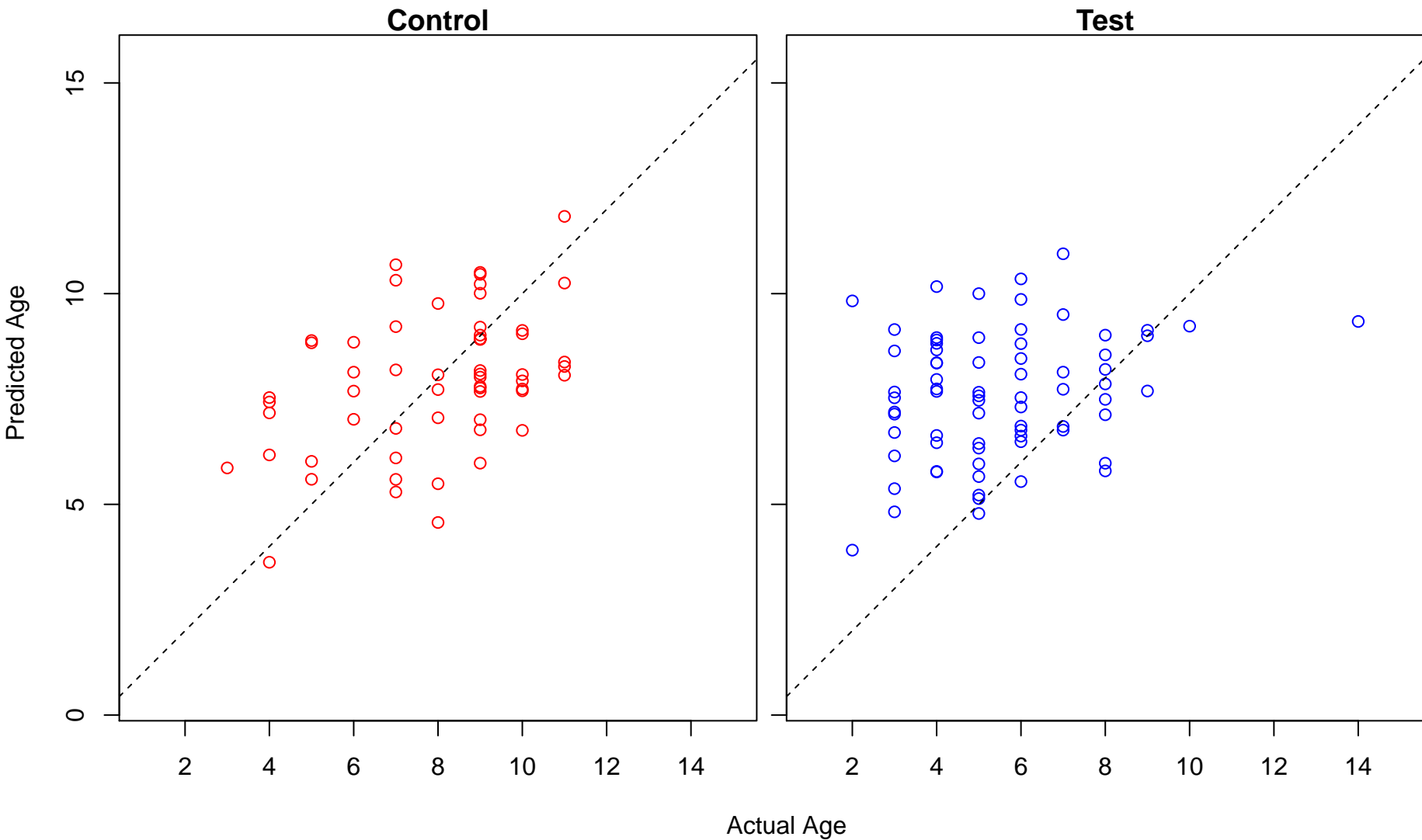
circulatory system development (Score: 0.874665)



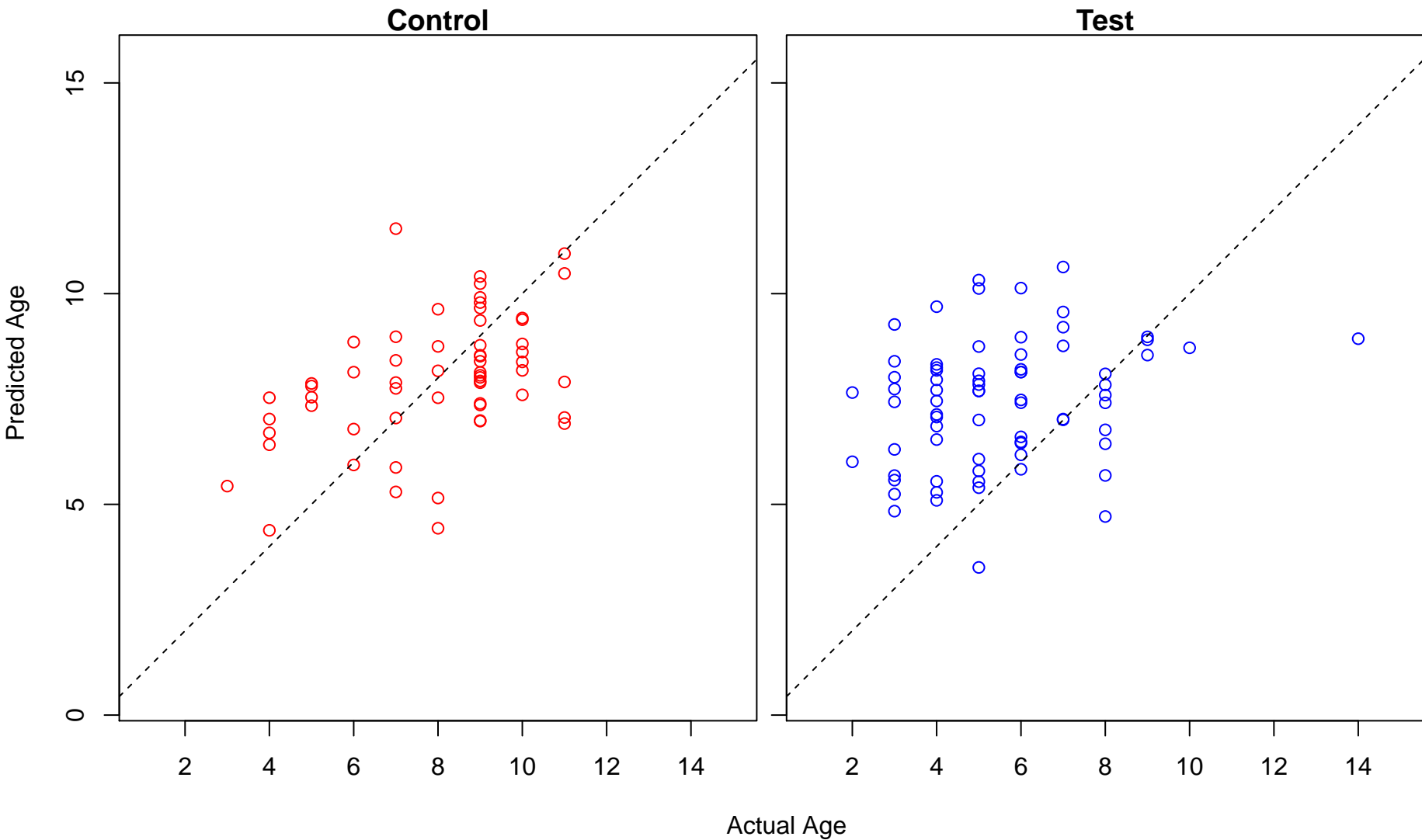
myeloid cell activation involved in immune response (Score: 0.874490)



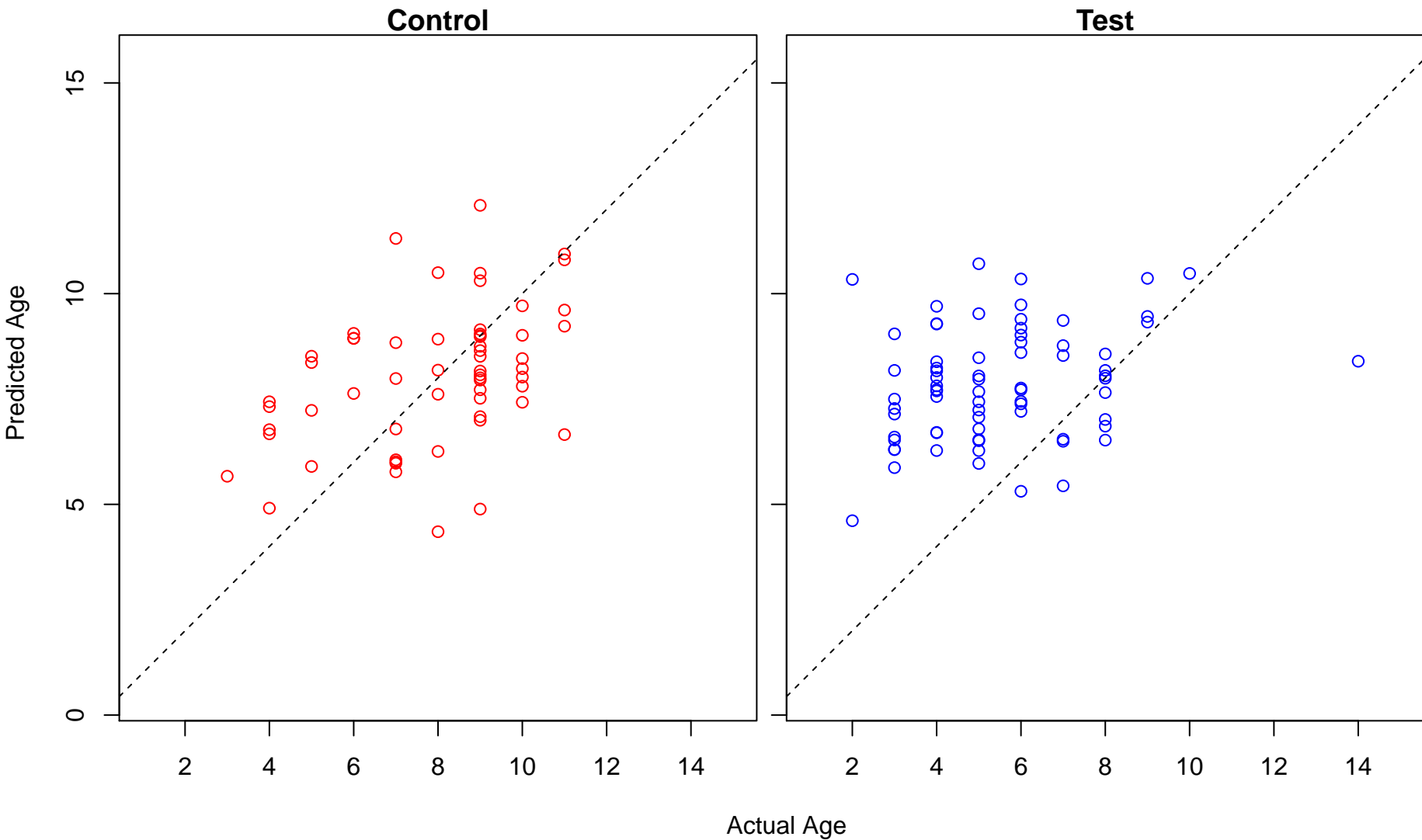
hemostasis (Score: 0.873847)



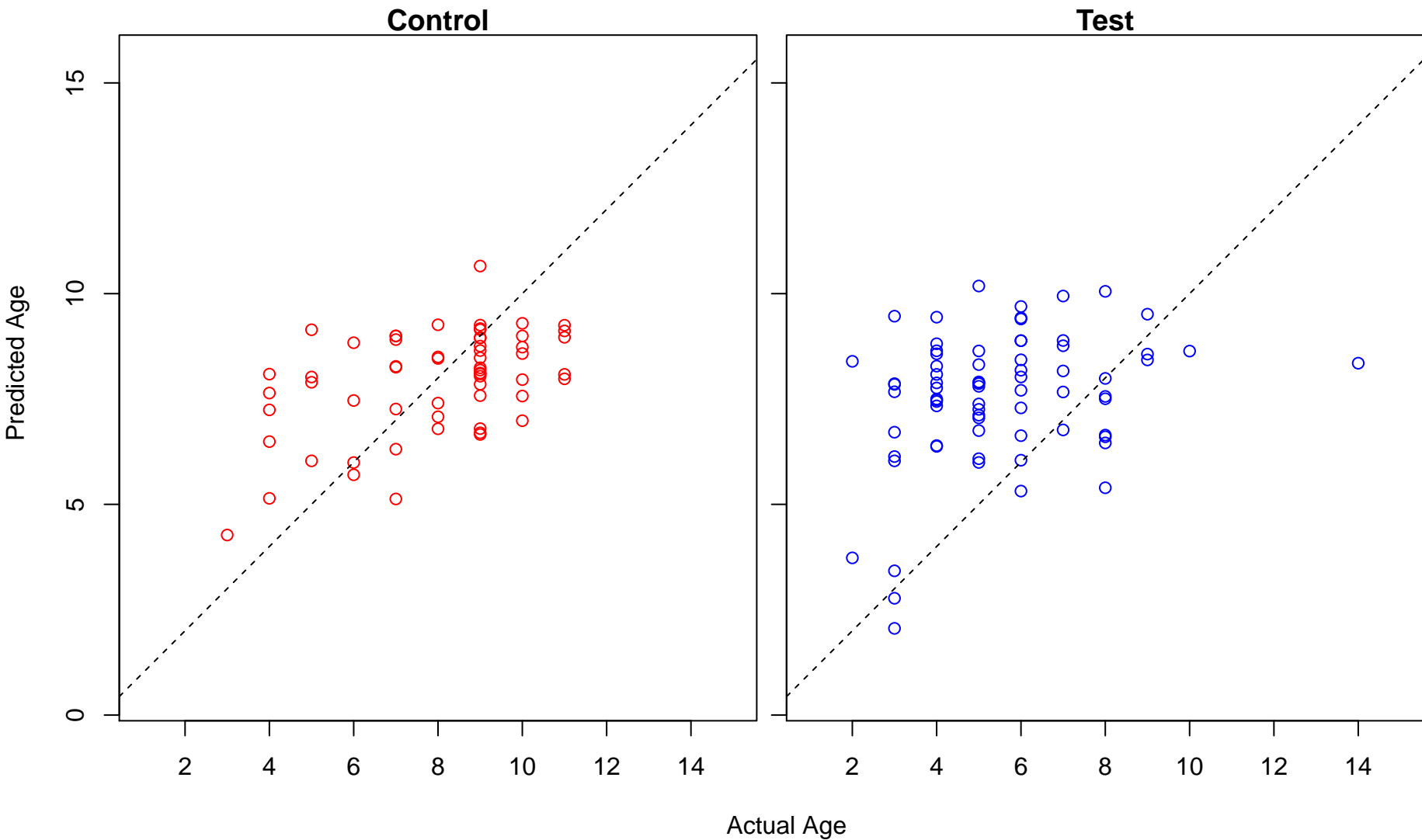
heart growth (Score: 0.873323)



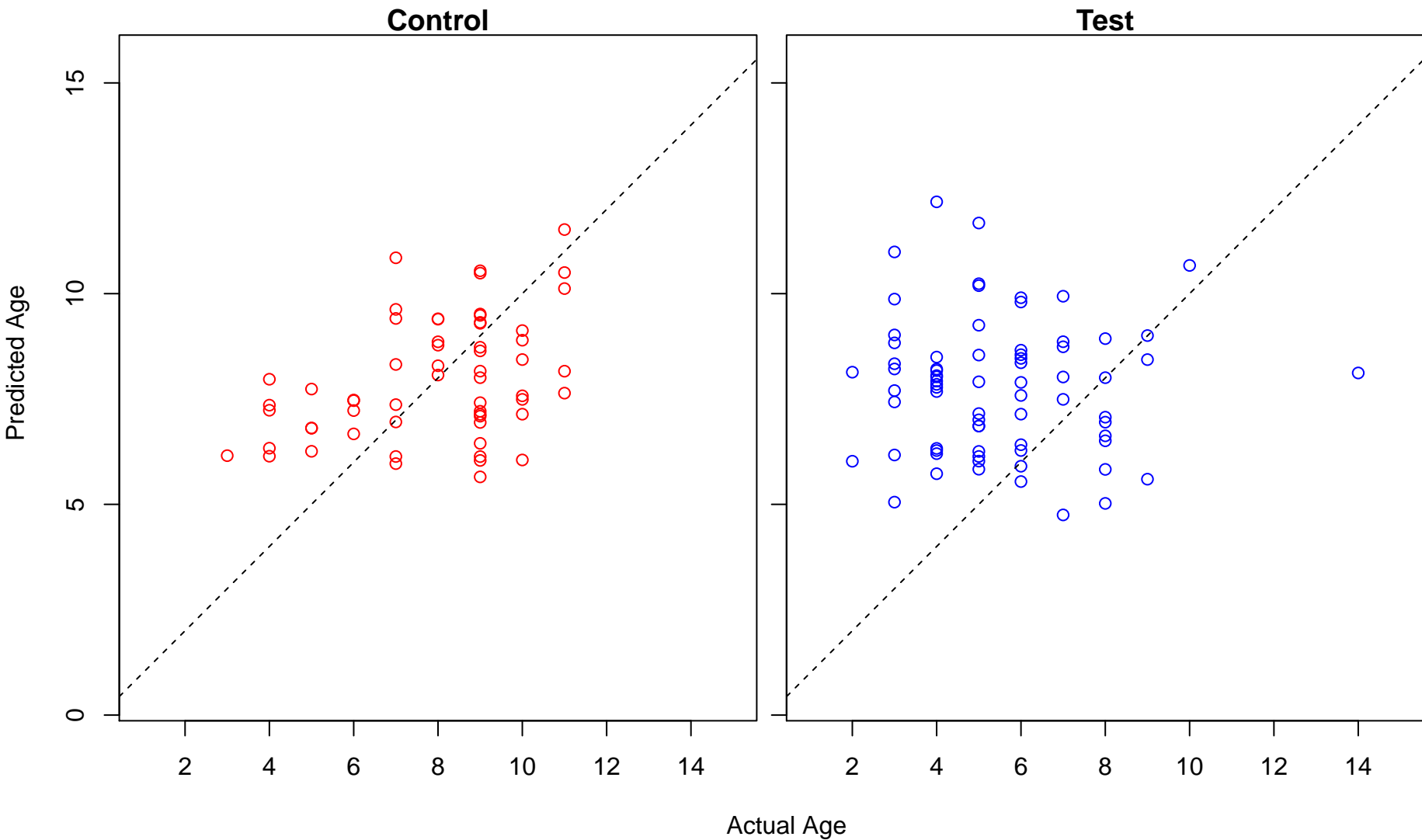
positive regulation of multicellular organismal process (Score: 0.873175)



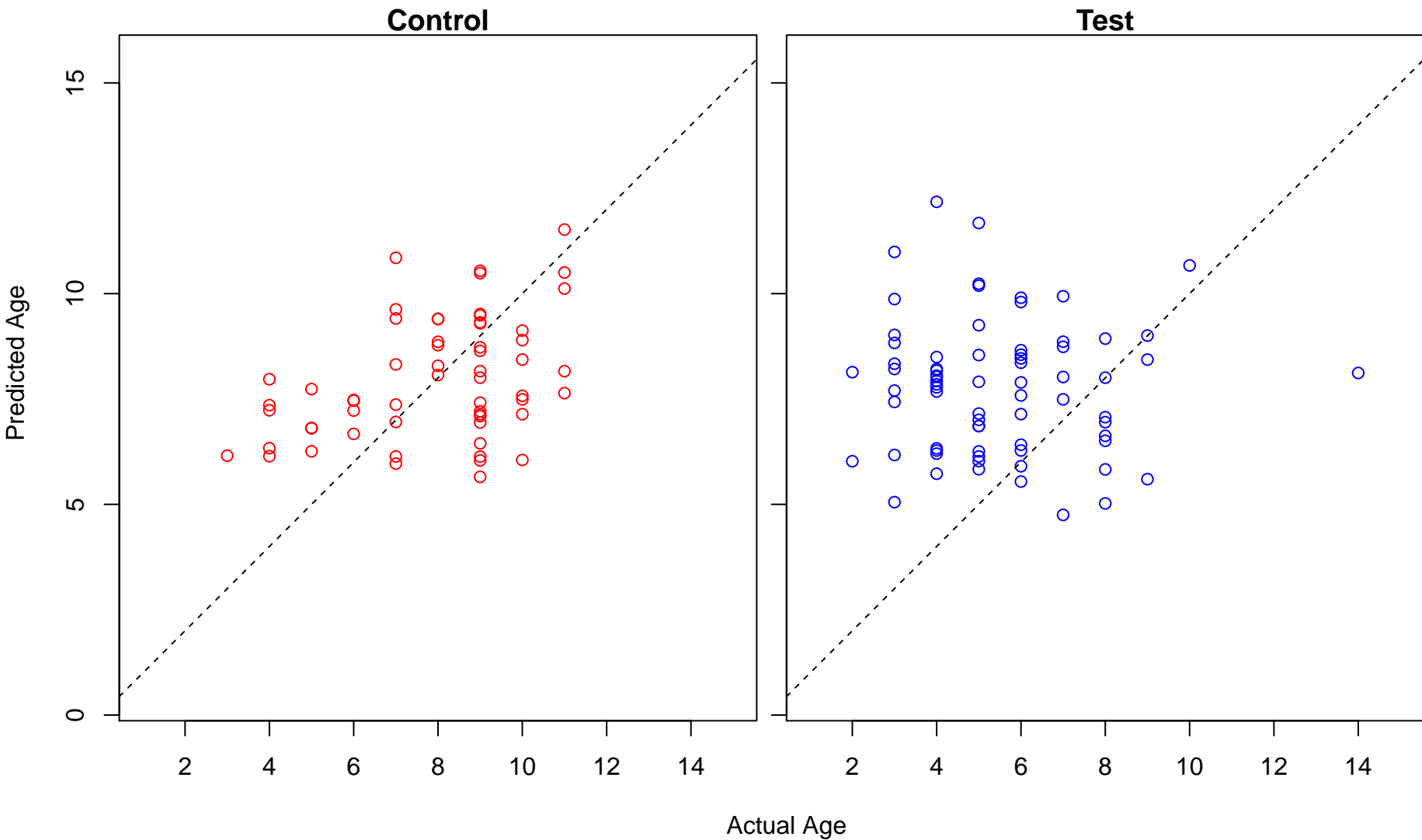
mesonephric tubule formation (Score: 0.872933)



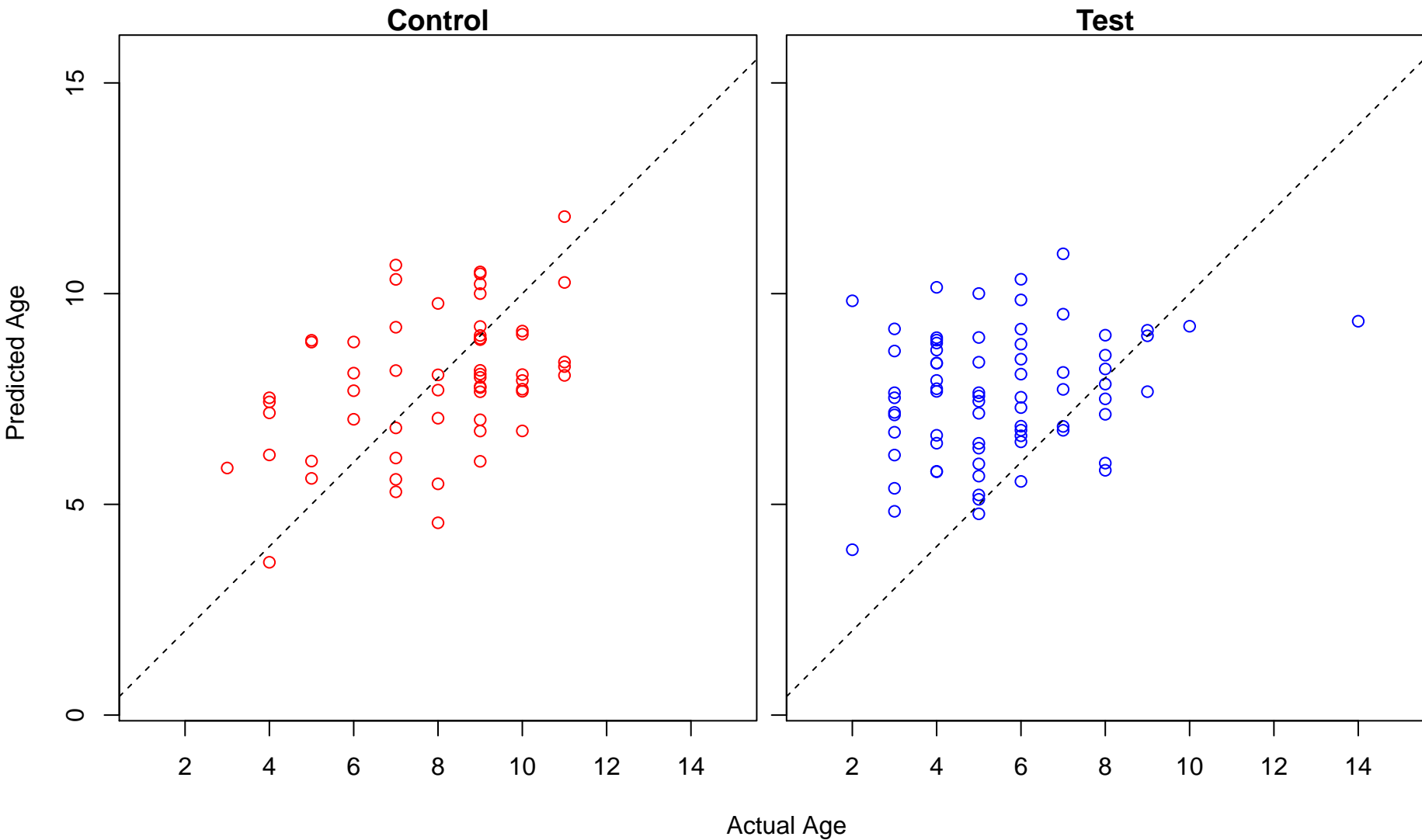
mitochondrial respiratory chain complex IV assembly (Score: 0.872319)



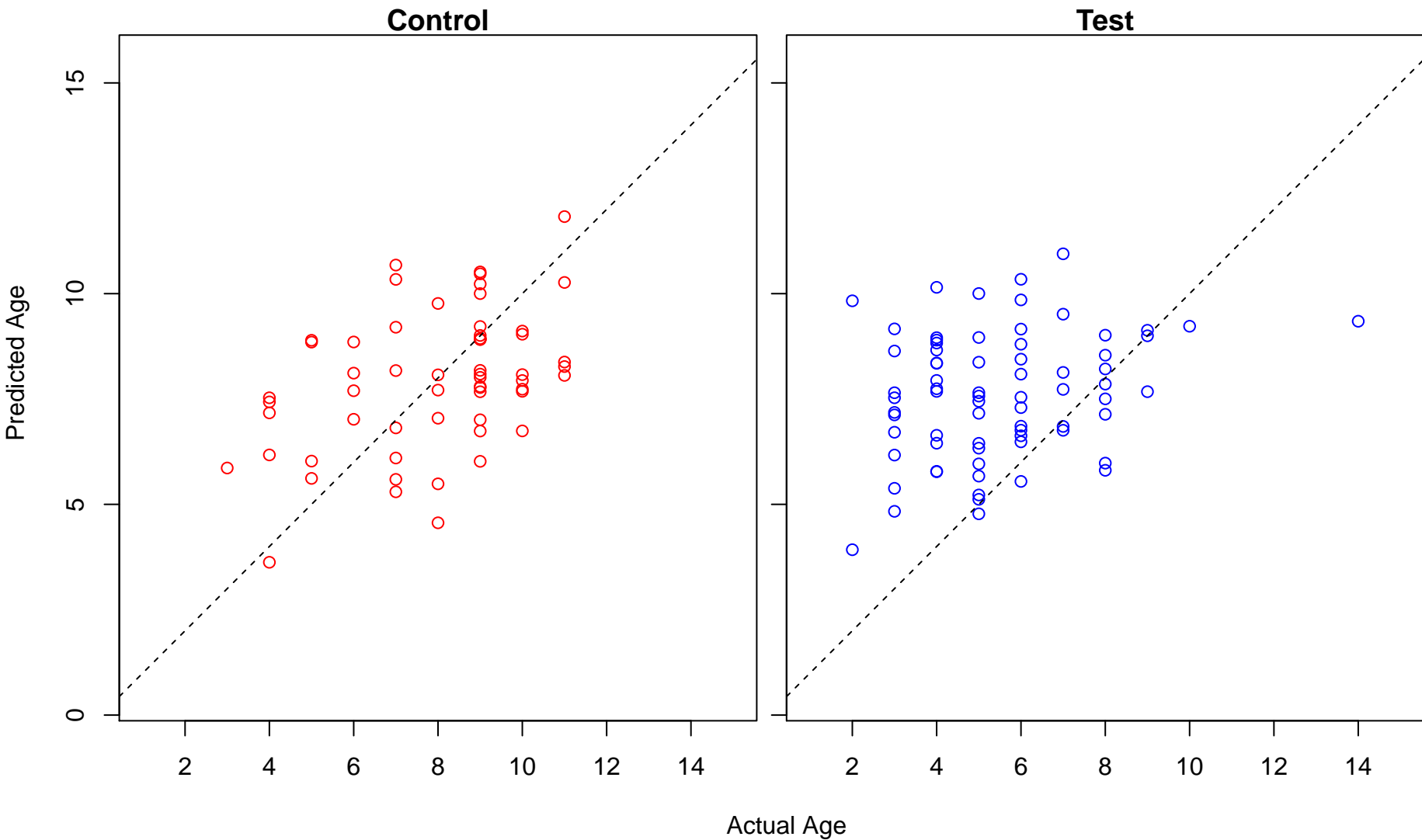
mitochondrial respiratory chain complex IV biogenesis (Score: 0.872319)



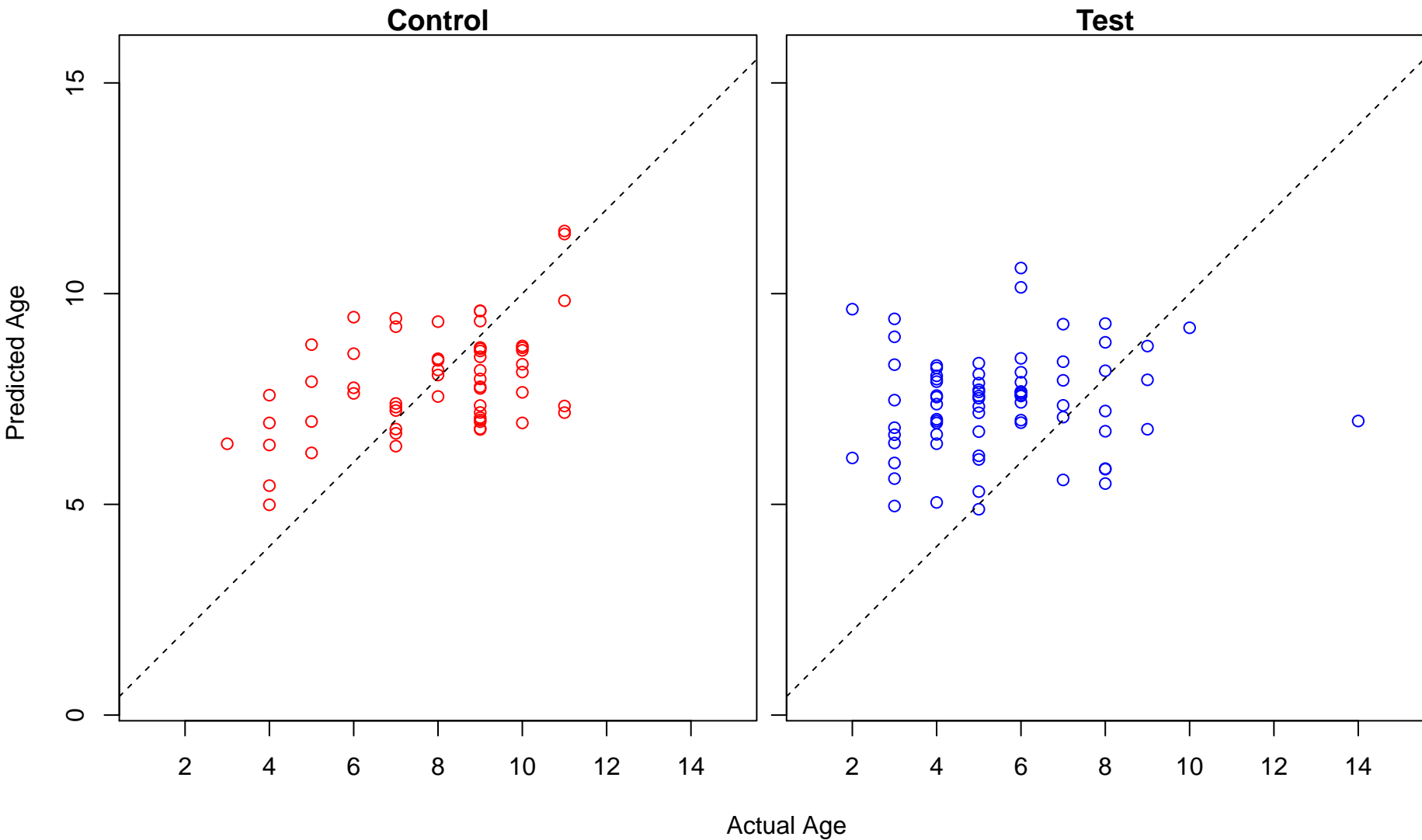
blood coagulation (Score: 0.871057)



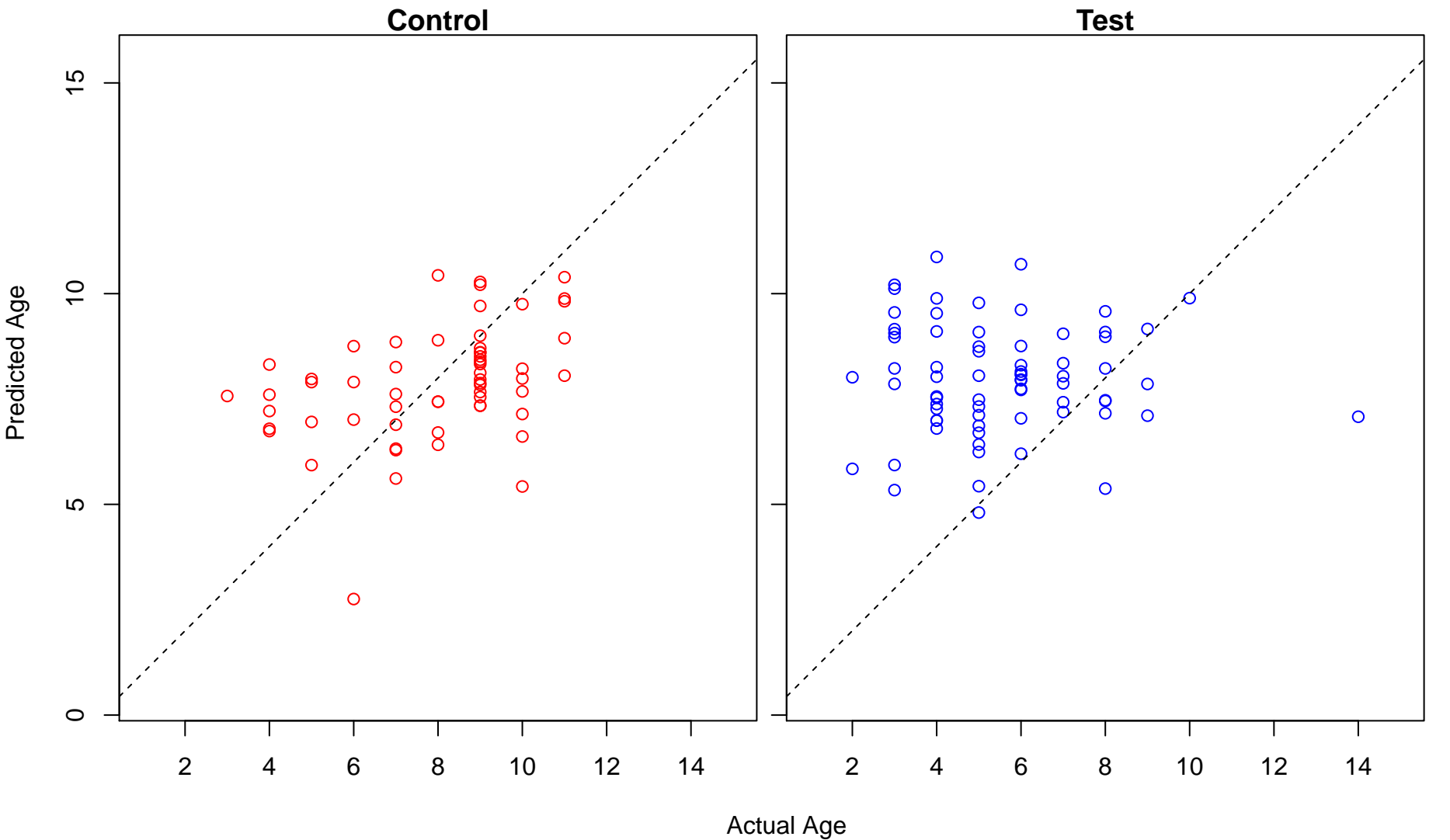
coagulation (Score: 0.871057)



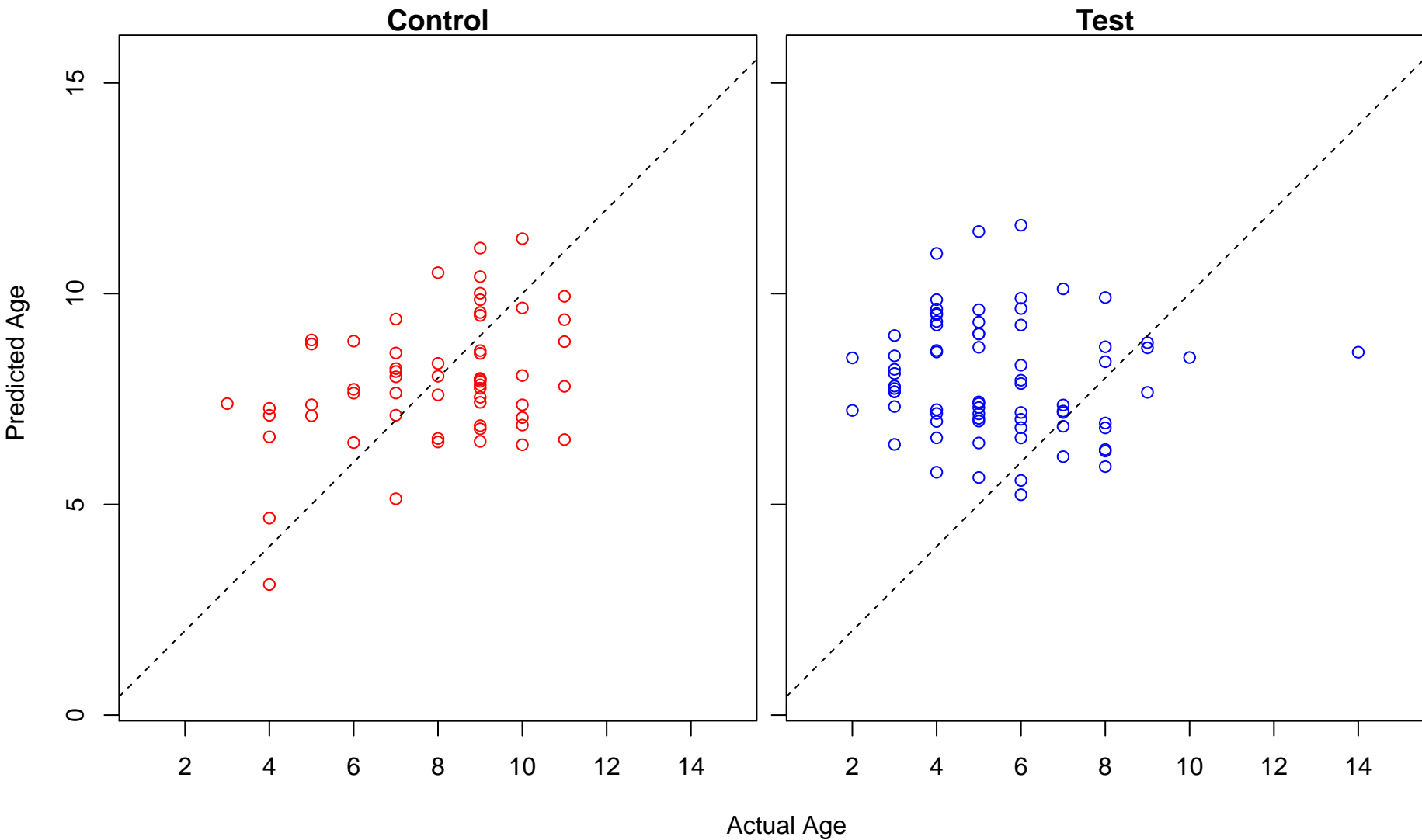
regulation of insulin receptor signaling pathway (Score: 0.870853)



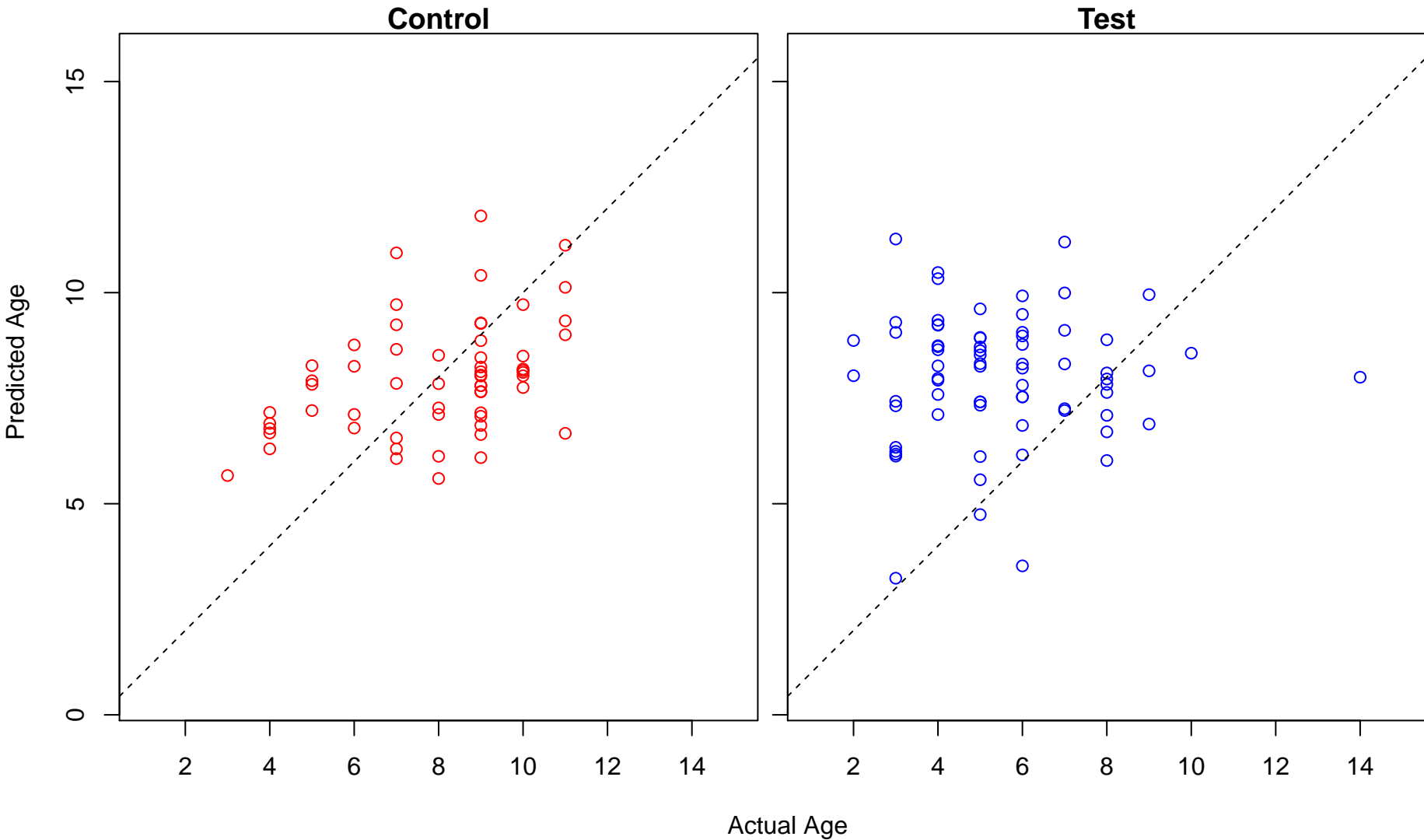
of cellular ketone metabolic process by positive regulation of transcription from RNA polymerase II promot



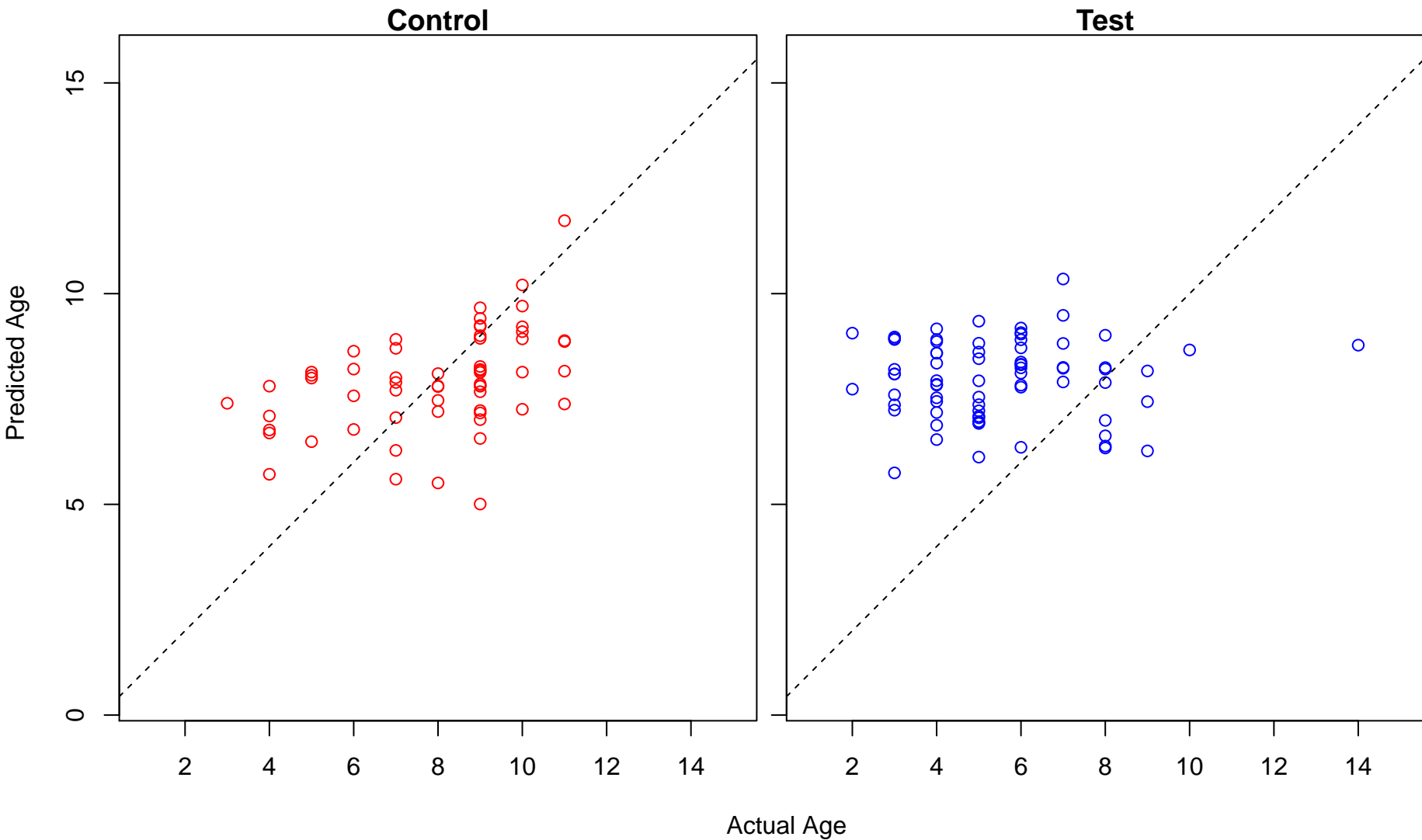
negative regulation of microtubule polymerization (Score: 0.870293)



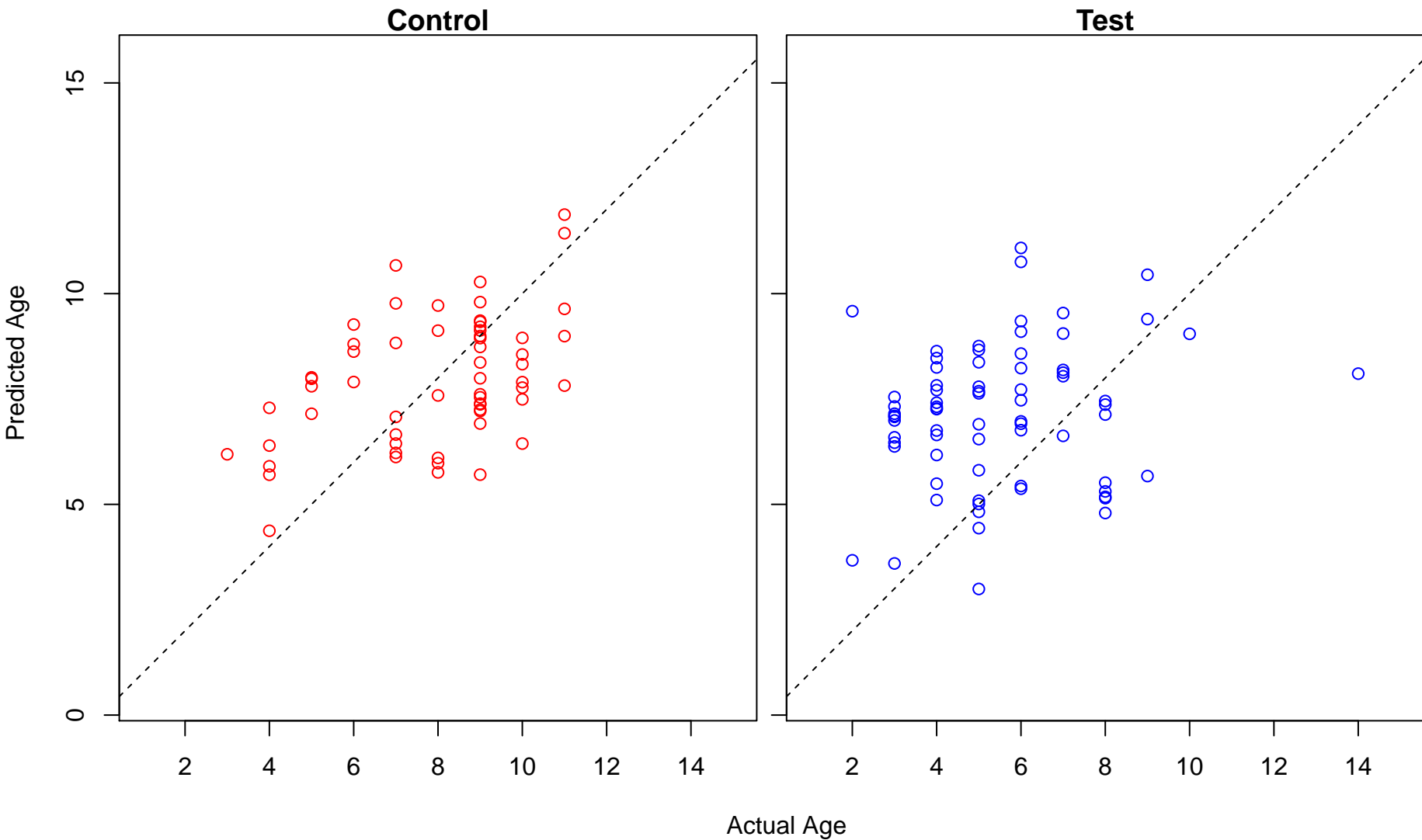
negative regulation of mitochondrial fusion (Score: 0.870189)



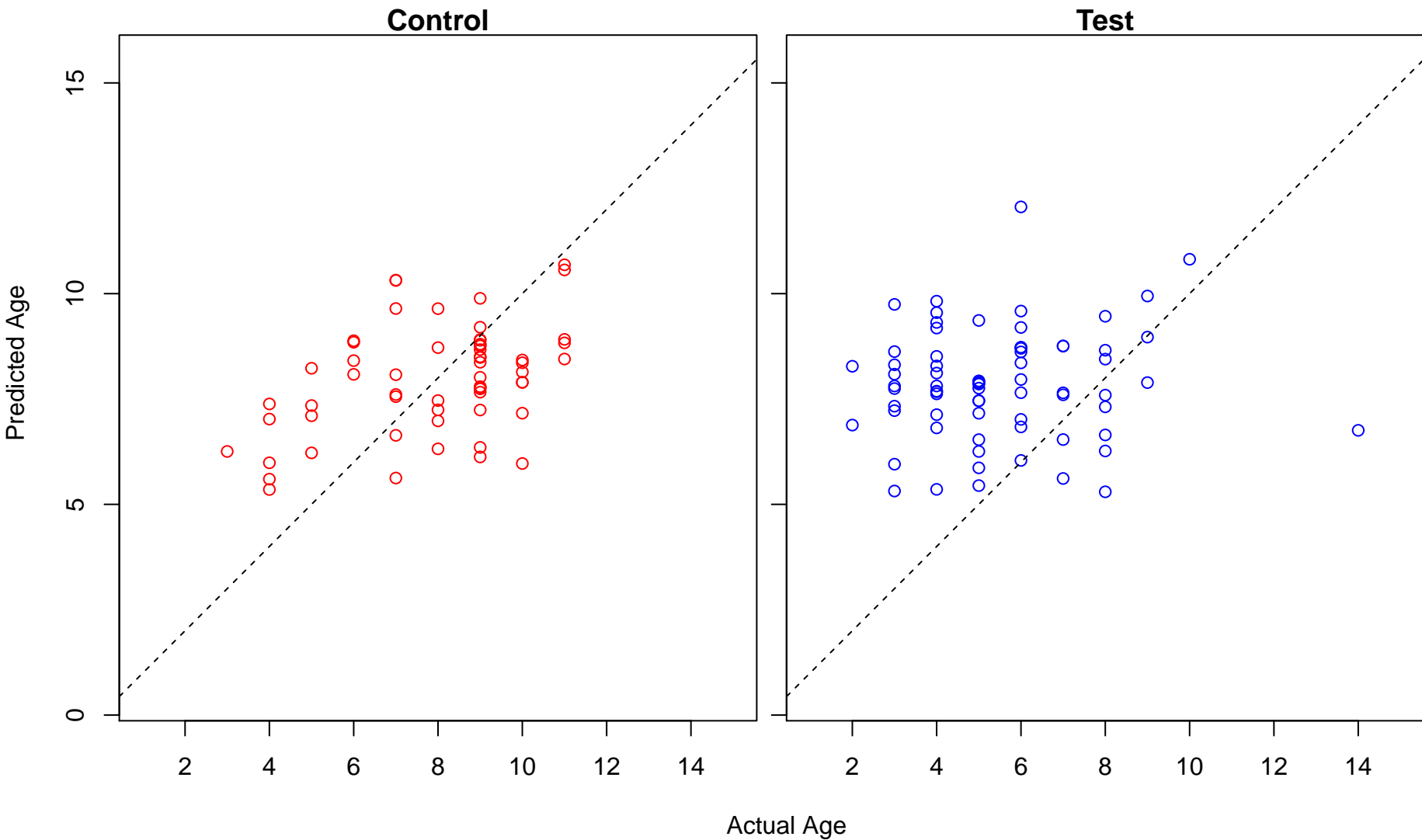
smoothened signaling pathway involved in dorsal/ventral neural tube patterning (Score: 0.869257)



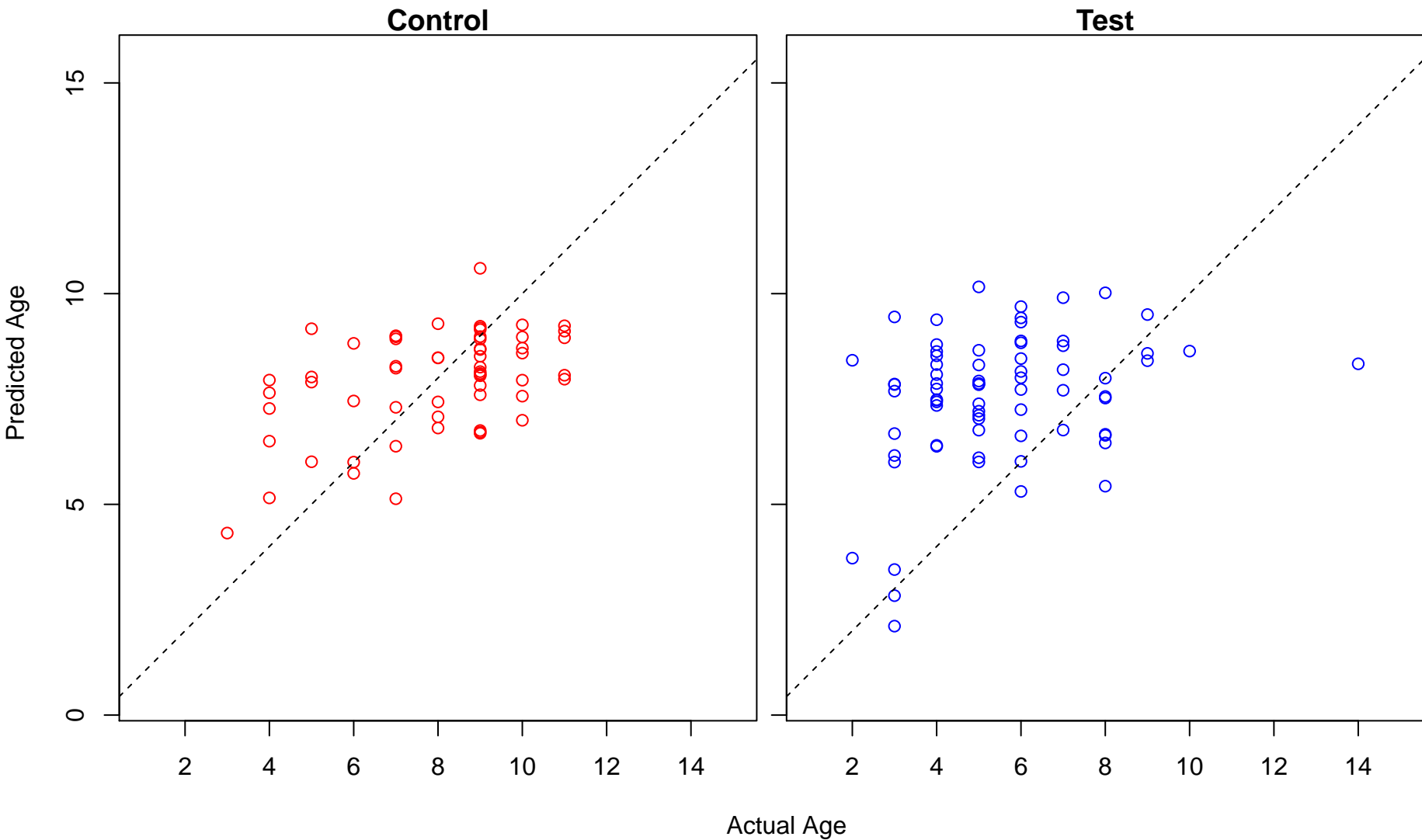
vascular endothelial growth factor receptor signaling pathway (Score: 0.869243)



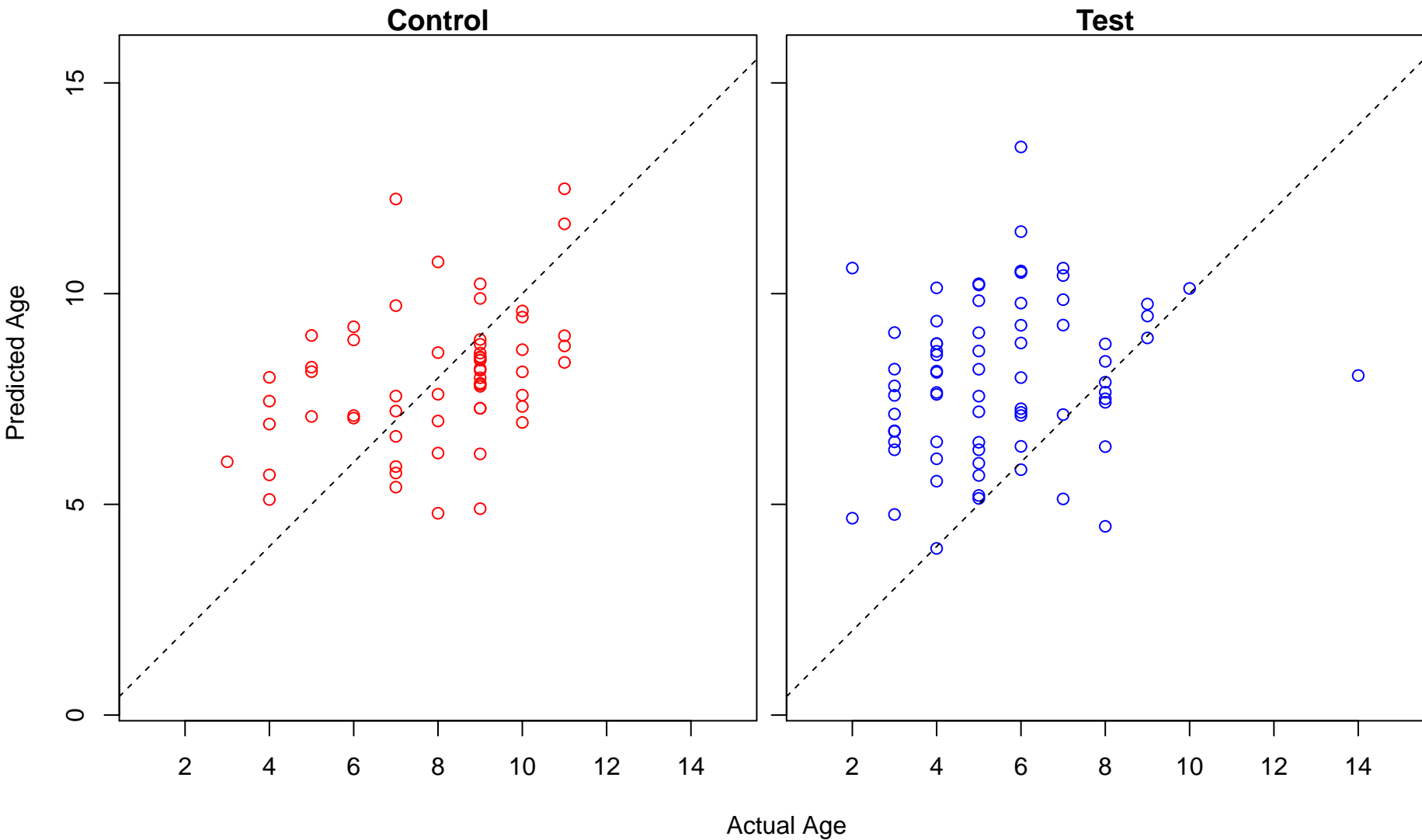
regulation of interleukin-2 production (Score: 0.868266)



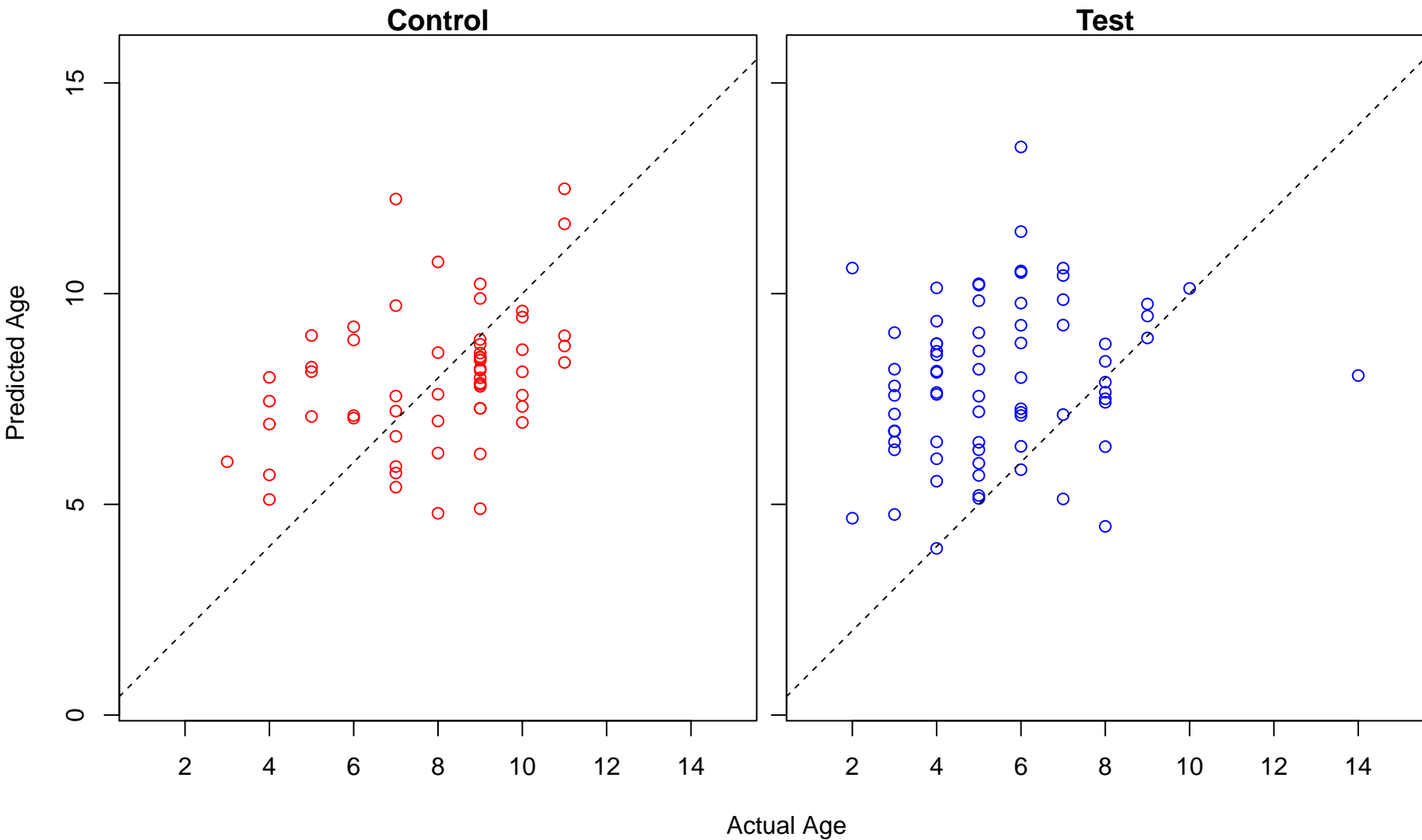
ureteric bud formation (Score: 0.866704)



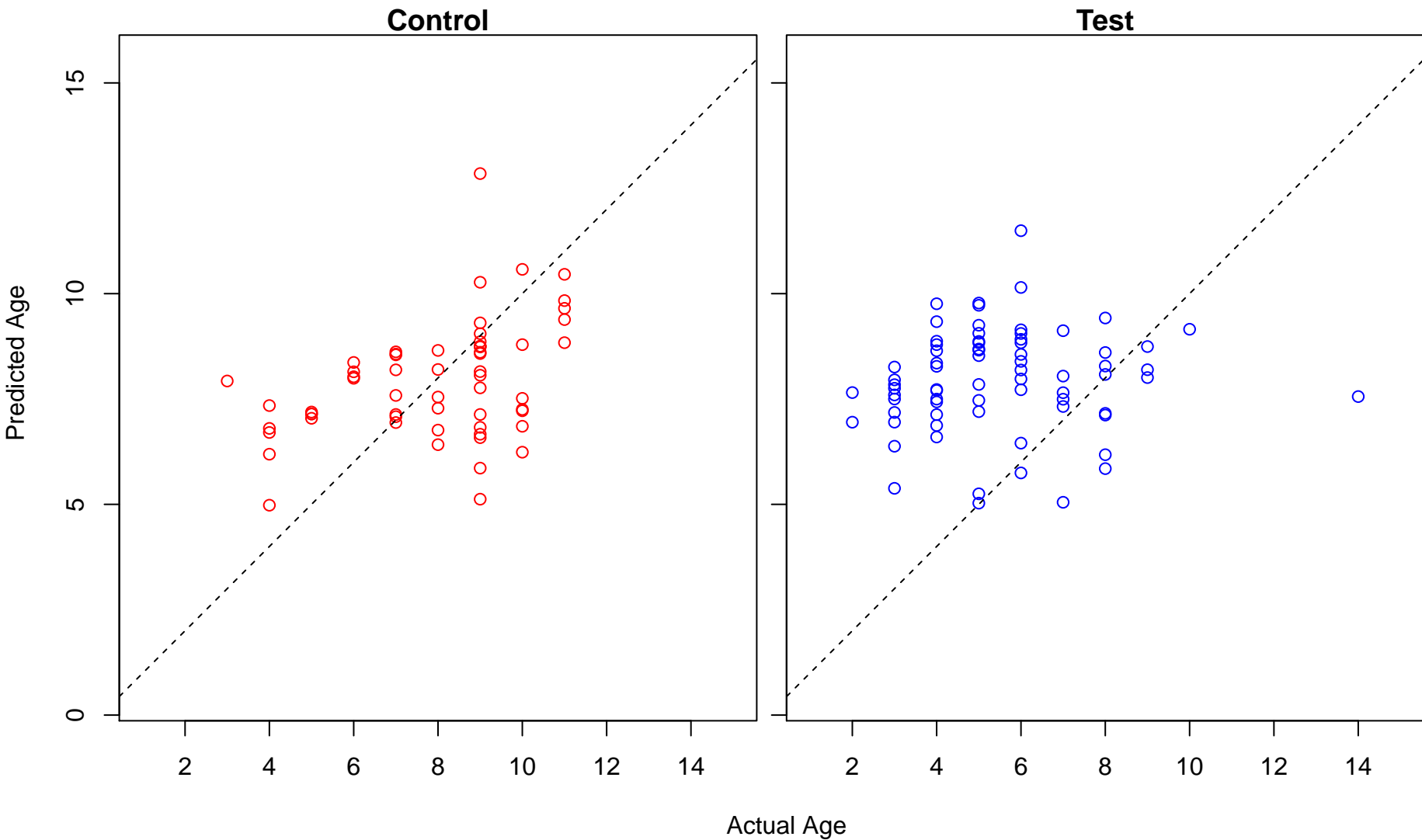
neurotrophin TRK receptor signaling pathway (Score: 0.865629)



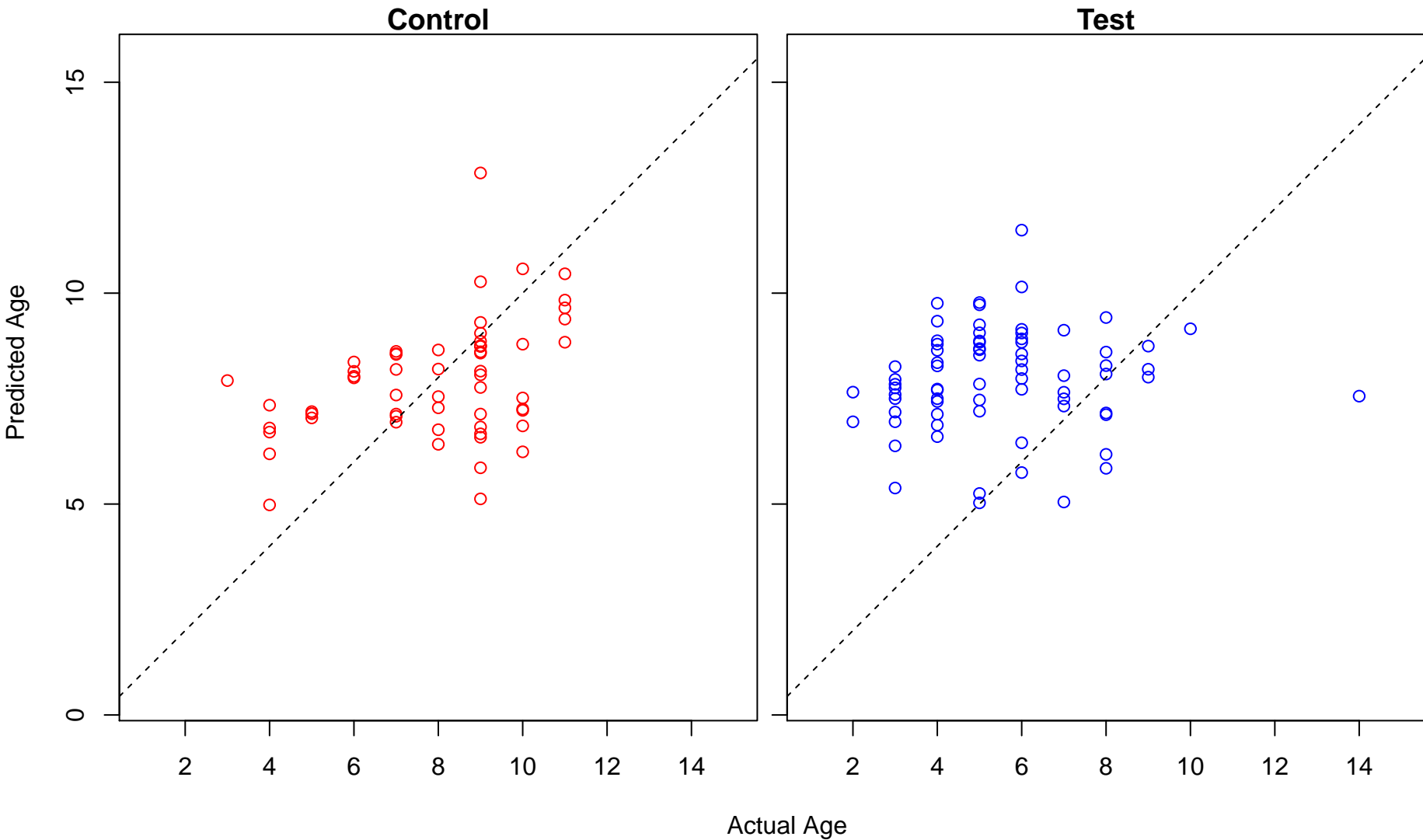
neurotrophin signaling pathway (Score: 0.865584)



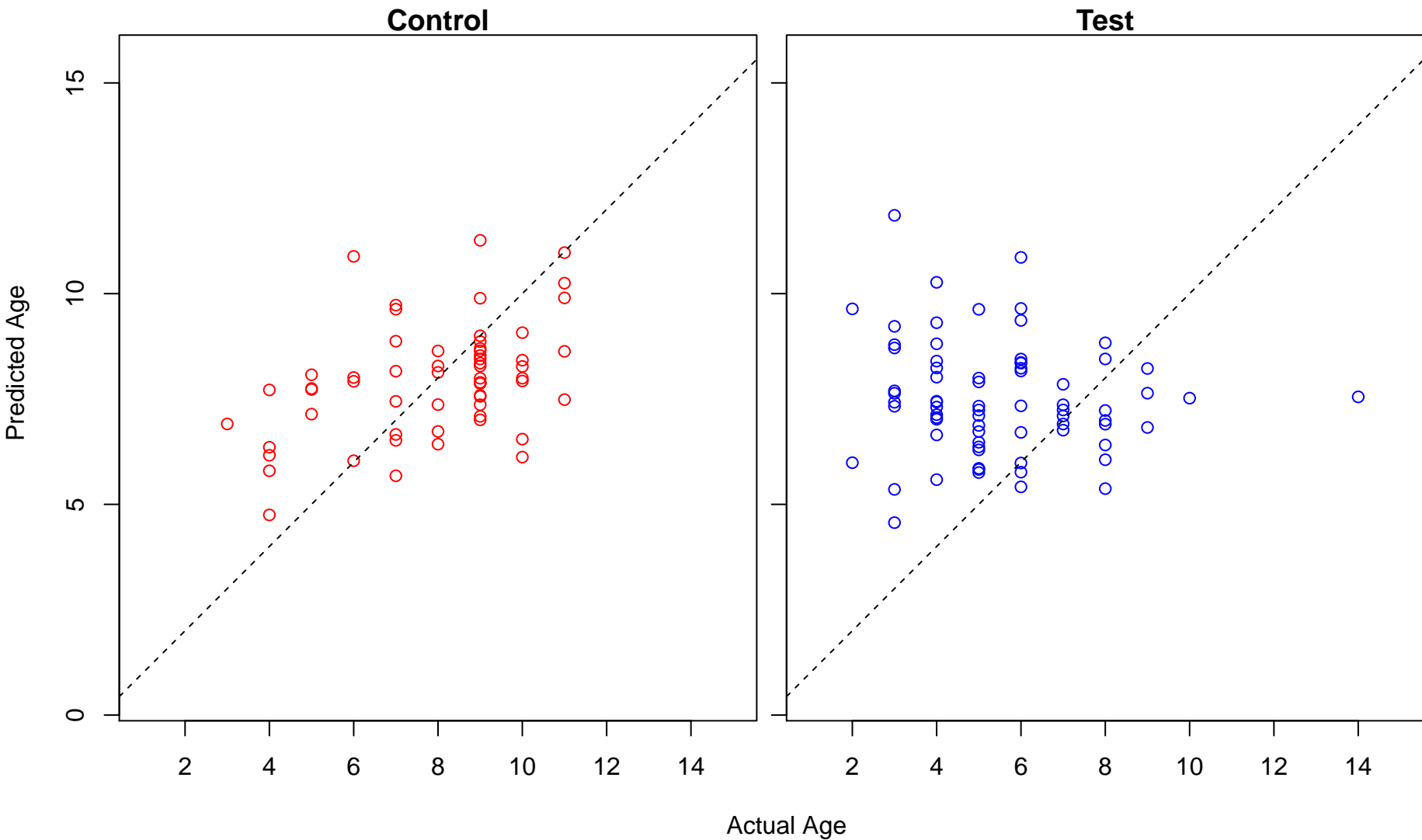
negative regulation of response to extracellular stimulus (Score: 0.864363)



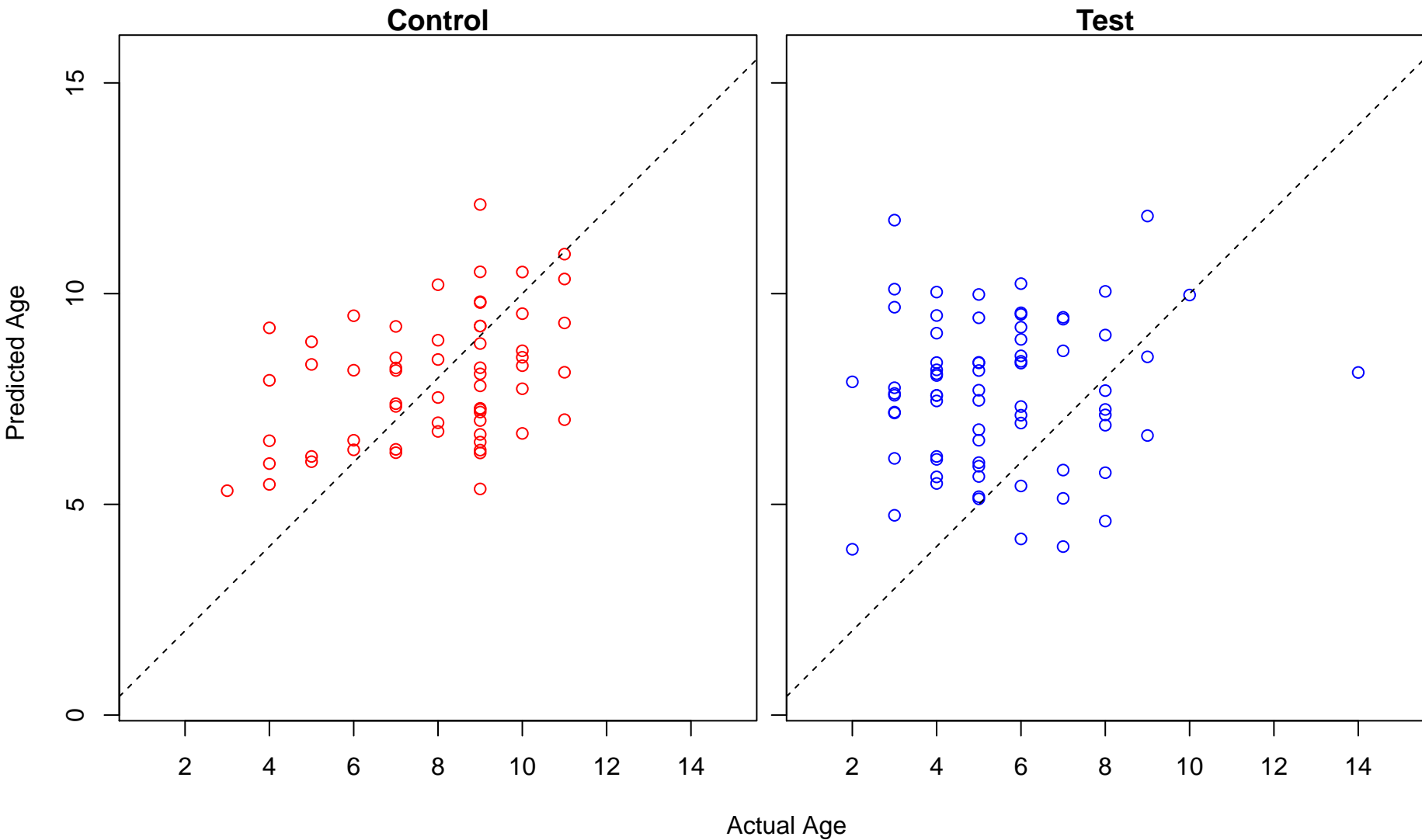
negative regulation of response to nutrient levels (Score: 0.864363)



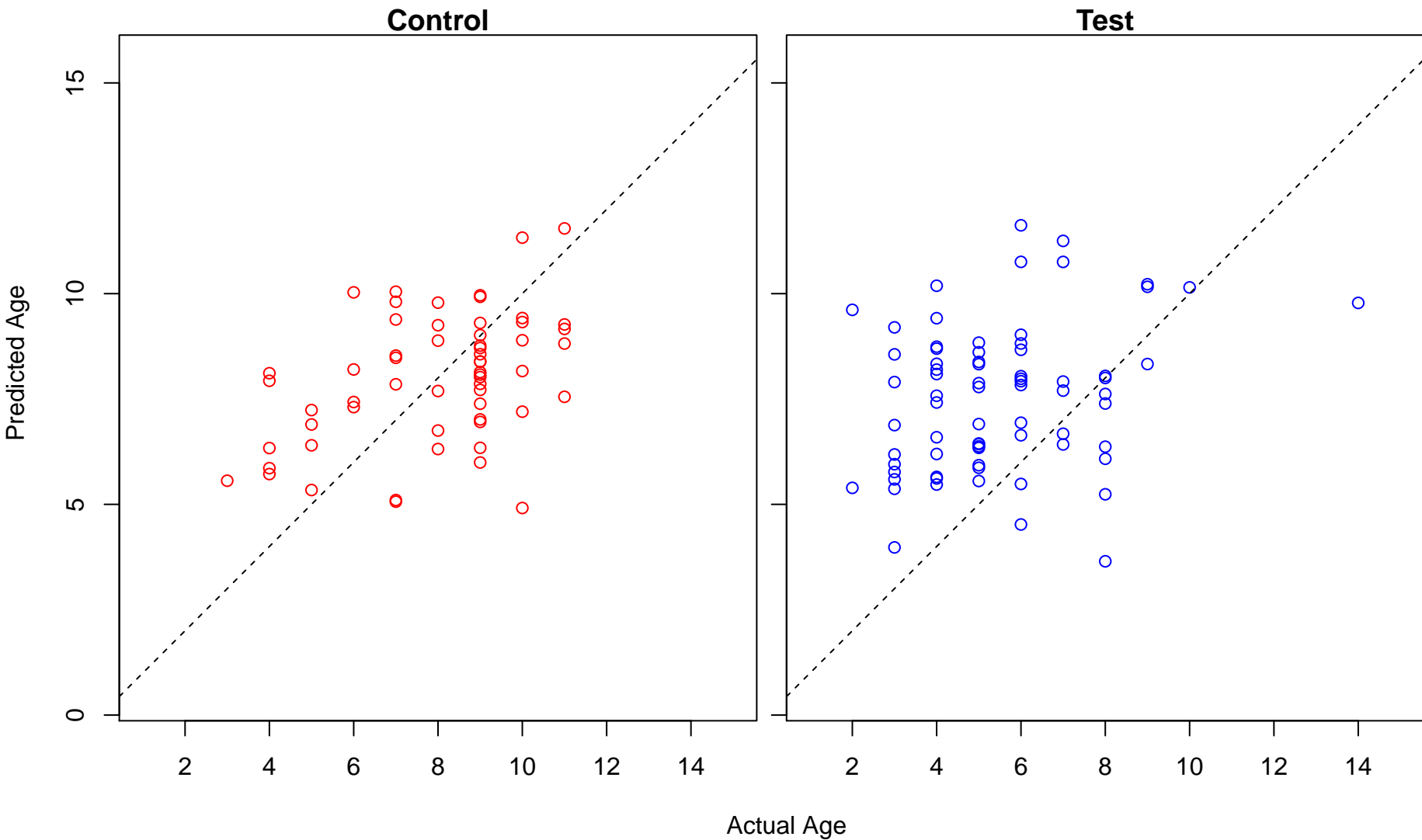
mitotic spindle organization (Score: 0.862528)



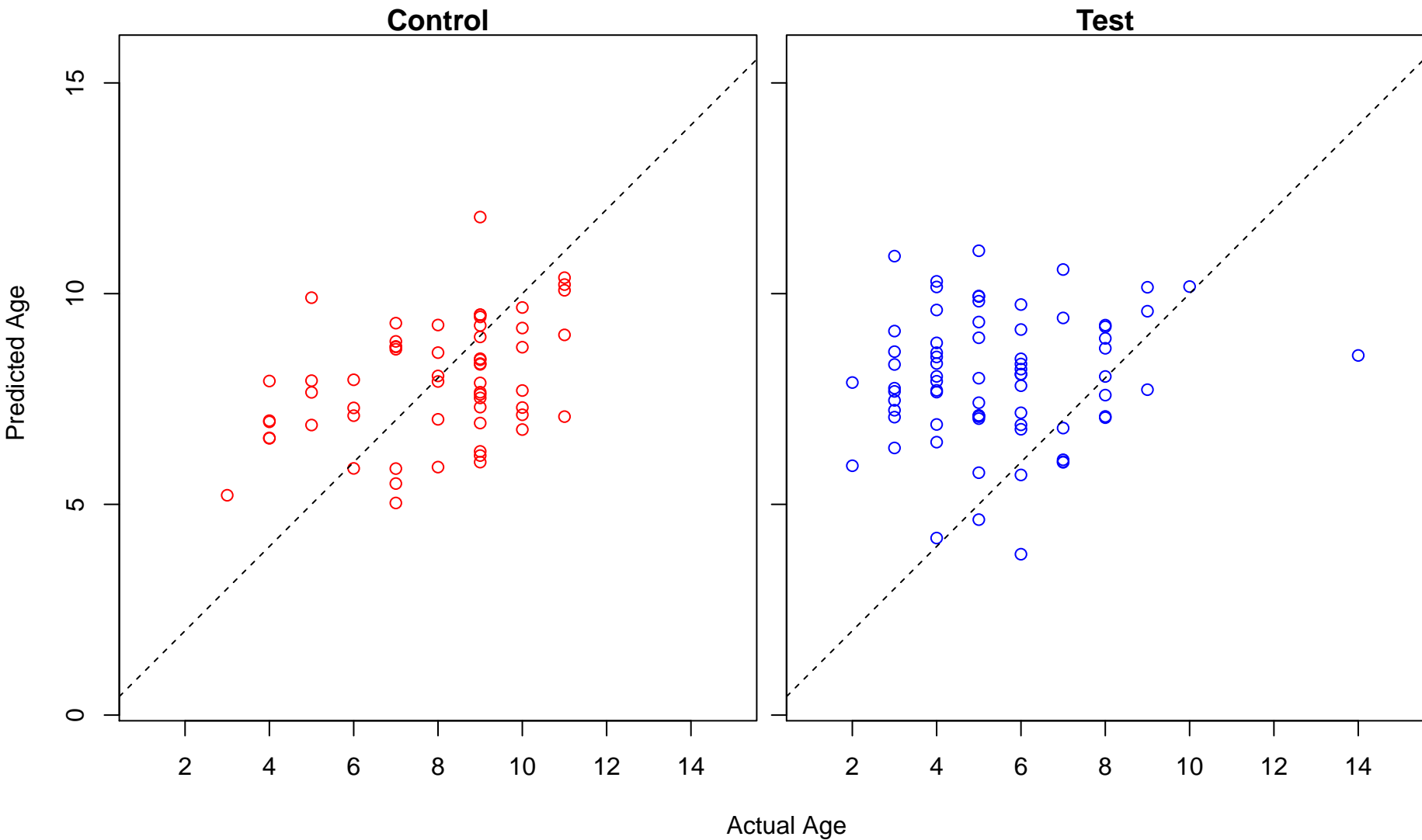
positive regulation of axon extension (Score: 0.862089)



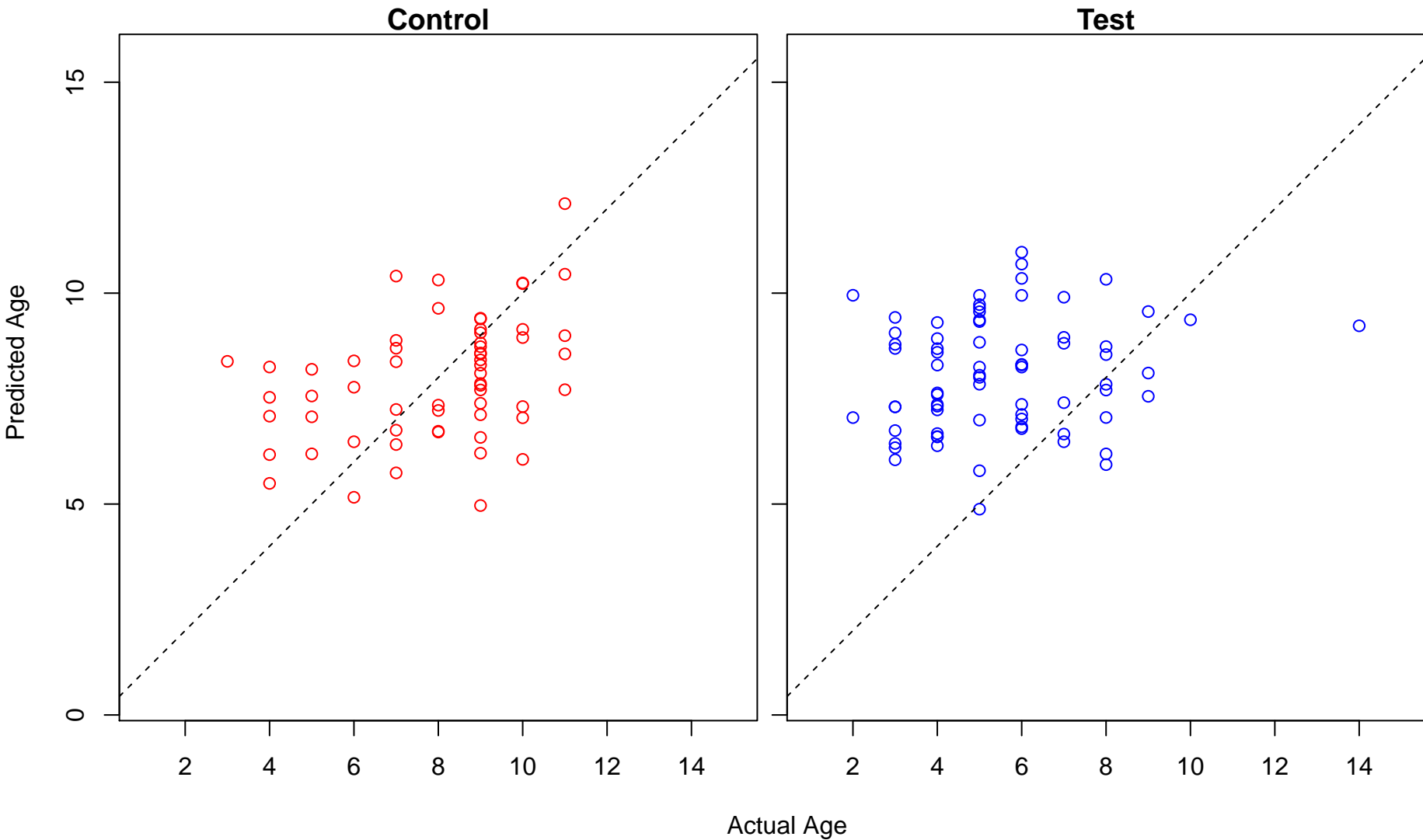
protein targeting to plasma membrane (Score: 0.860897)



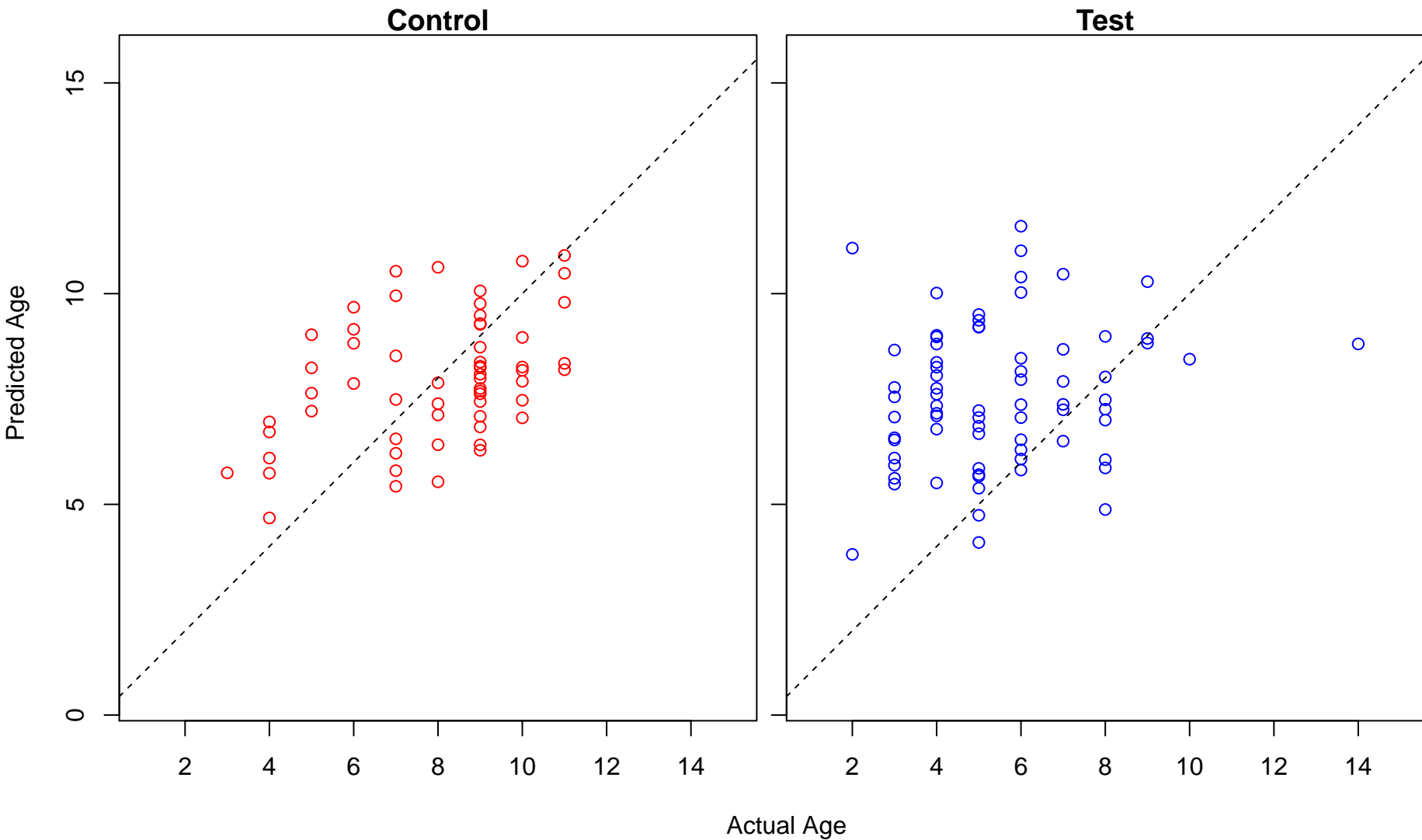
positive thymic T cell selection (Score: 0.860086)



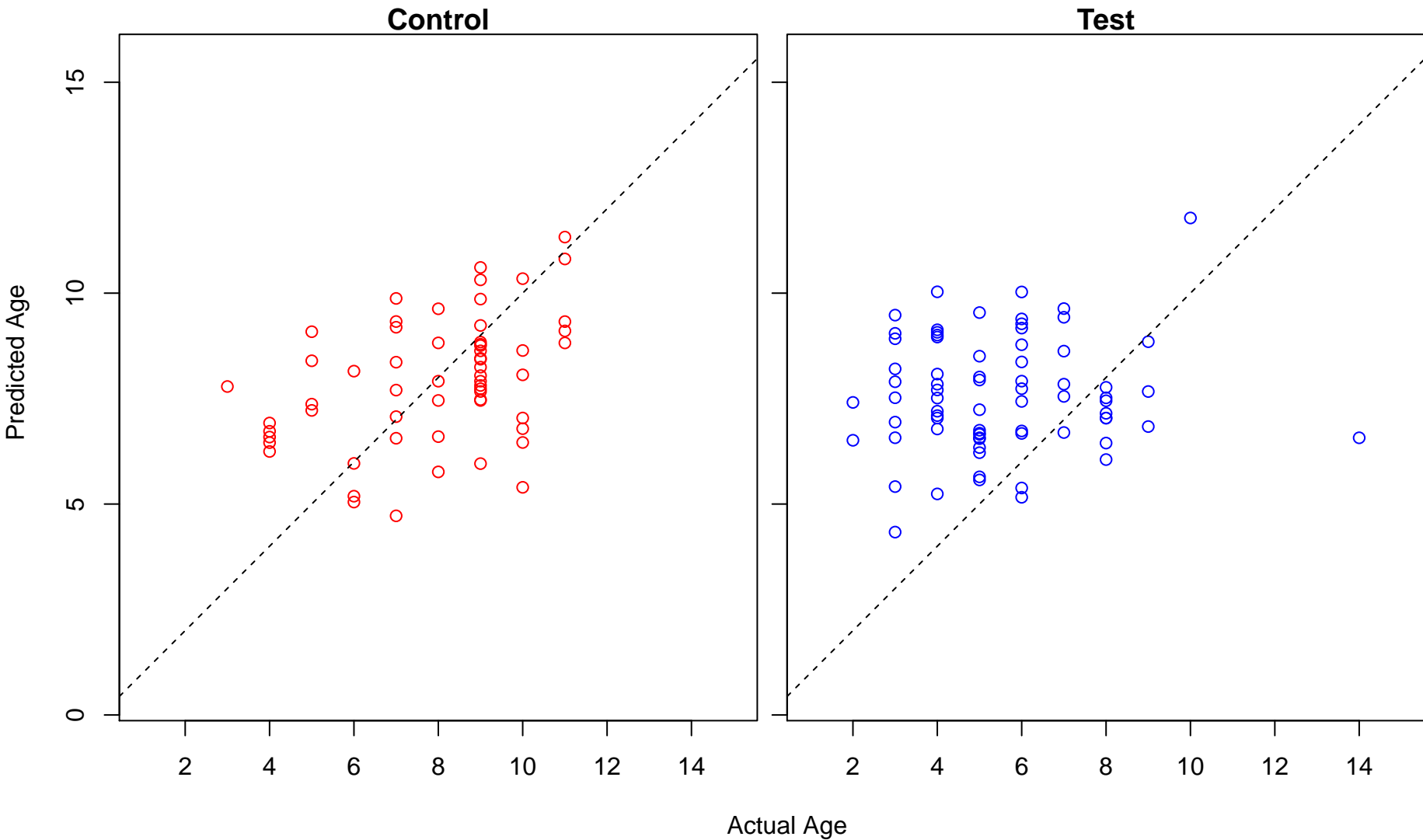
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (Score: 0.859910)



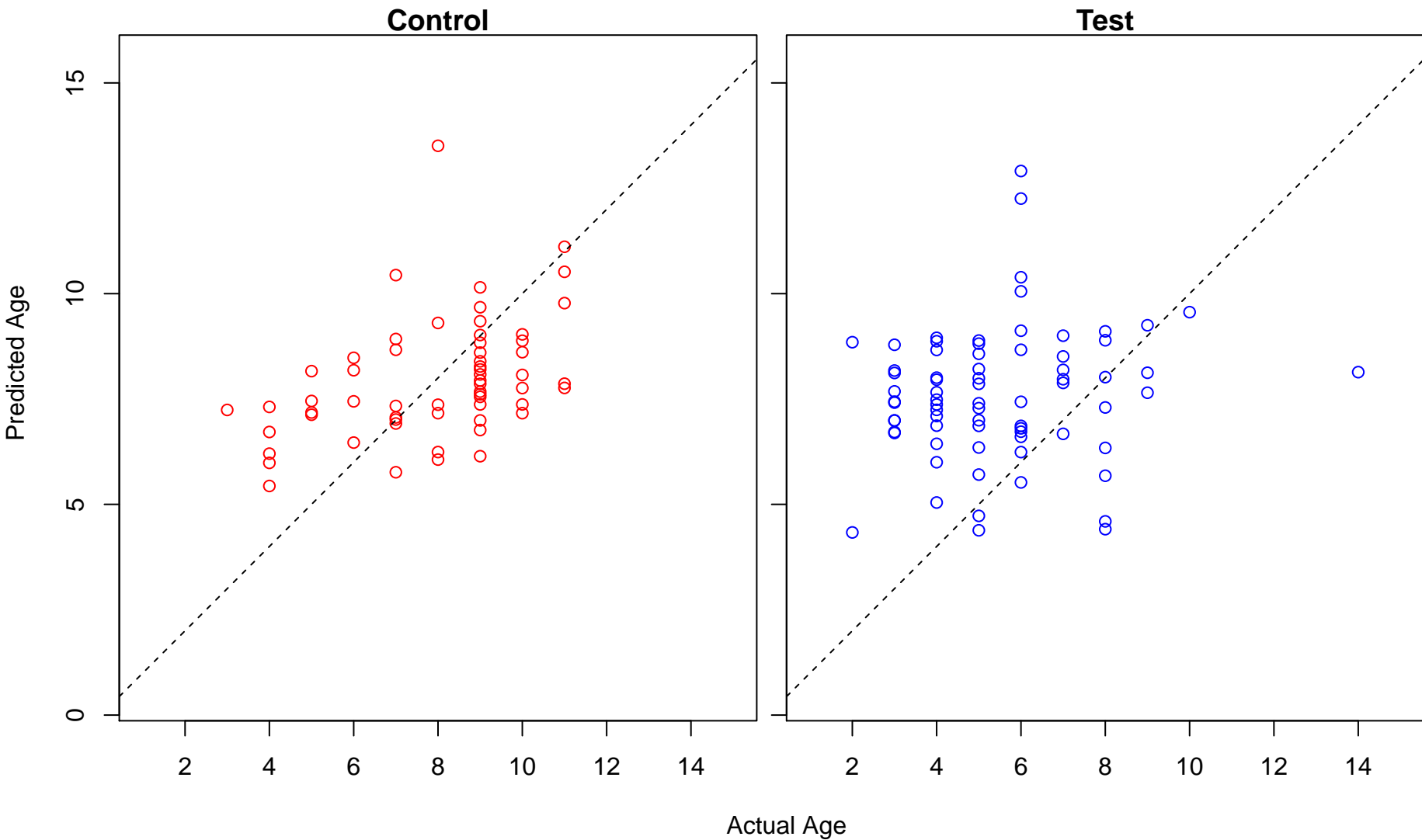
cellular response to chemical stimulus (Score: 0.859494)



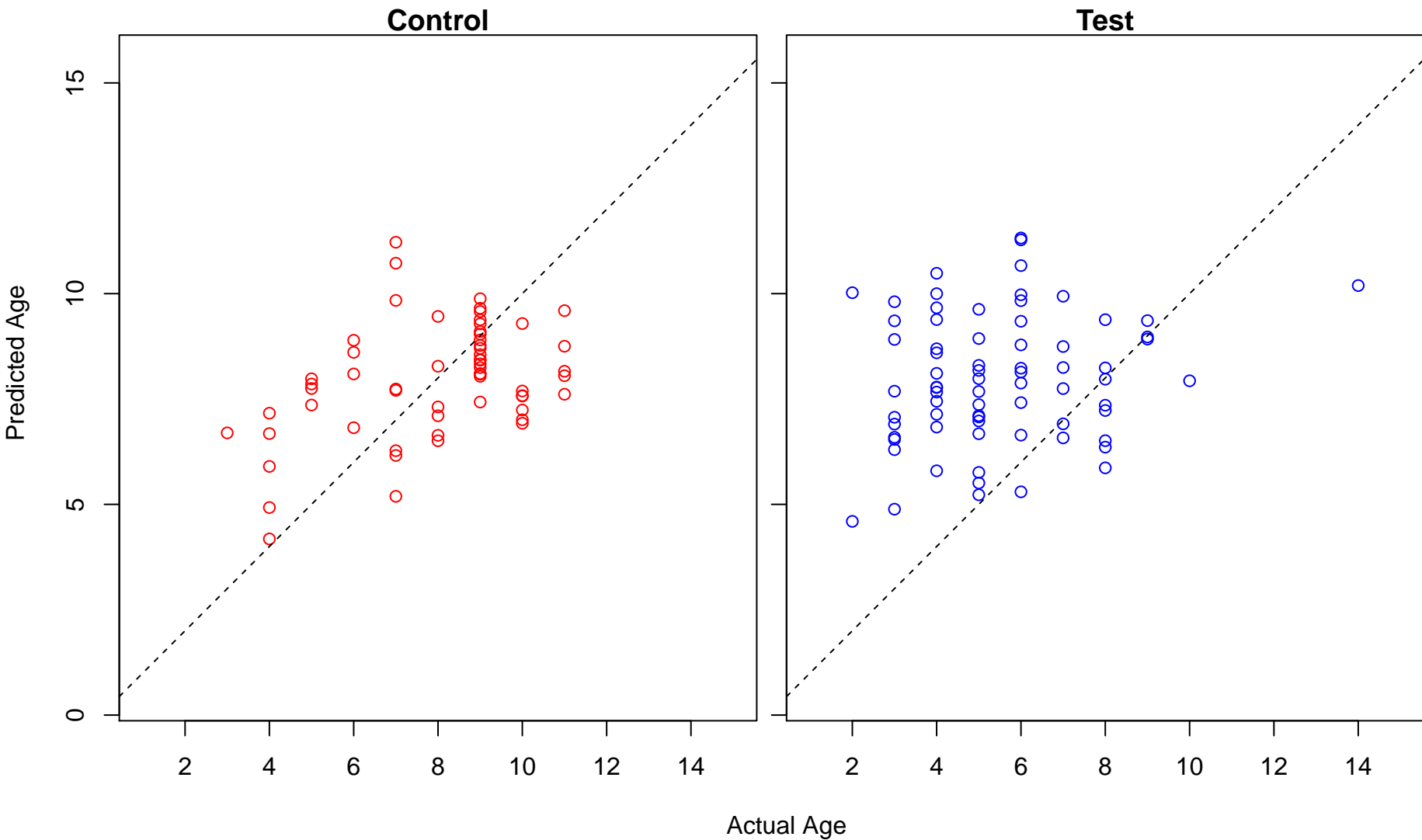
positive regulation of fatty acid beta-oxidation (Score: 0.858056)



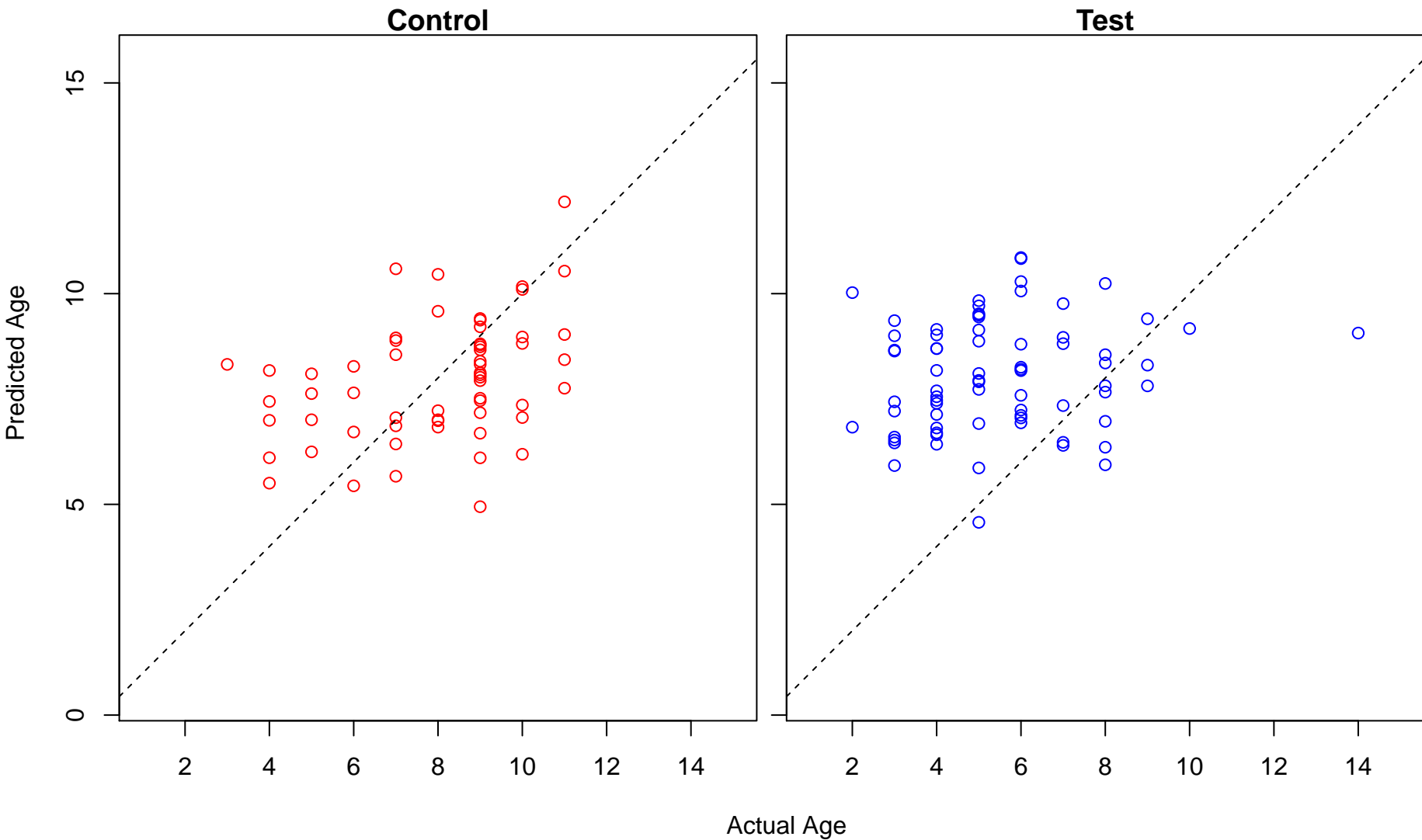
regulation of dendrite morphogenesis (Score: 0.857824)



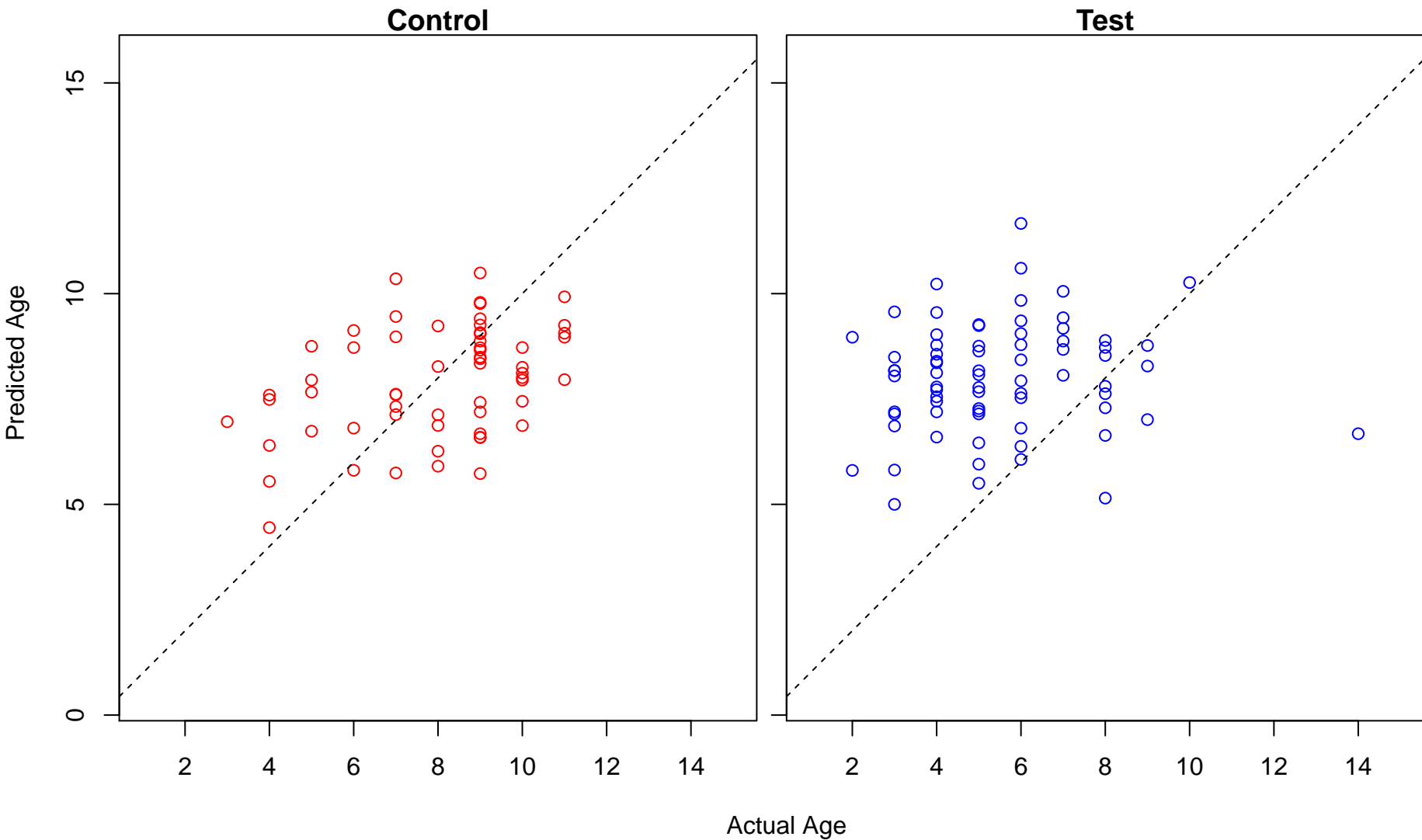
glial cell migration (Score: 0.857820)



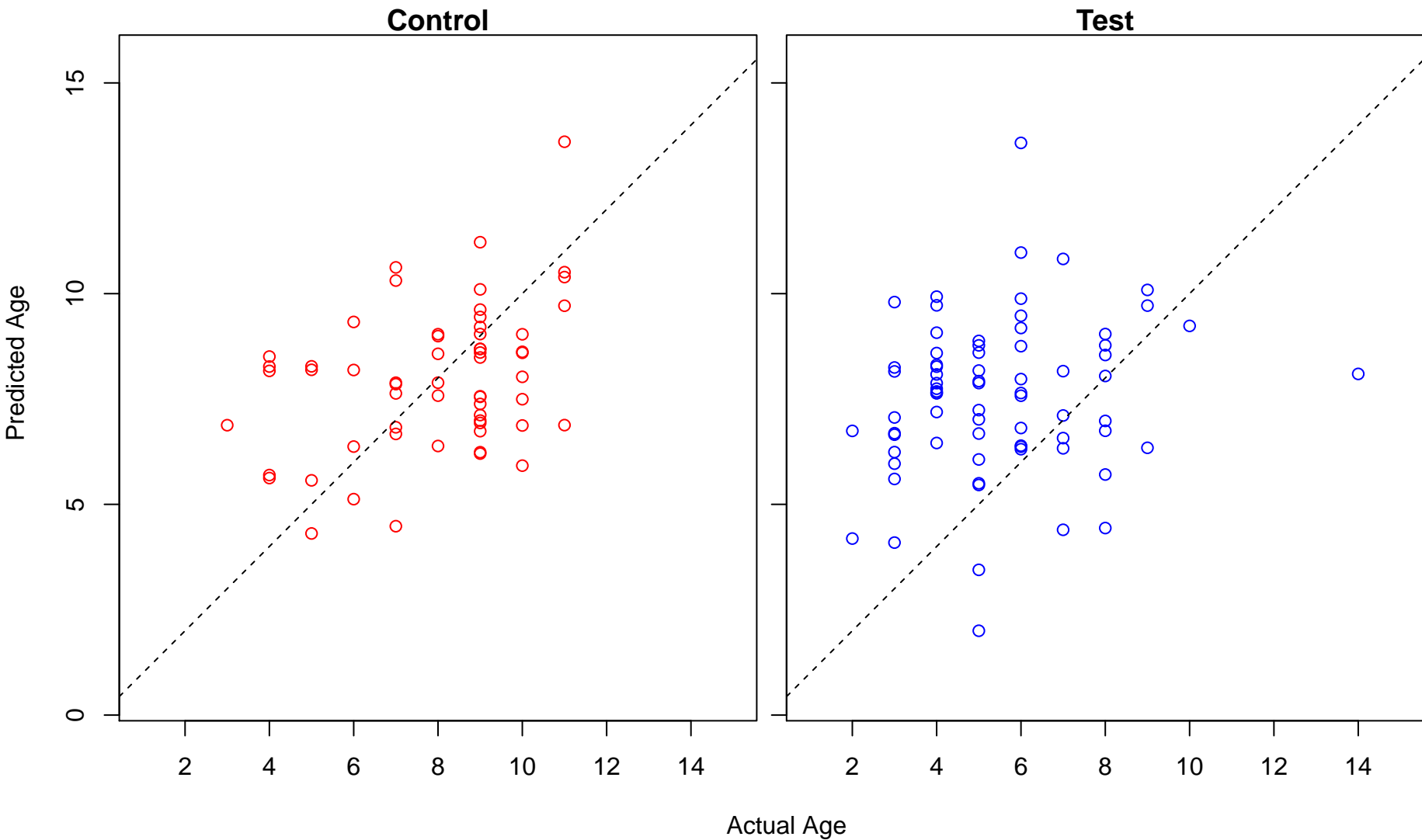
mRNA catabolic process (Score: 0.857044)



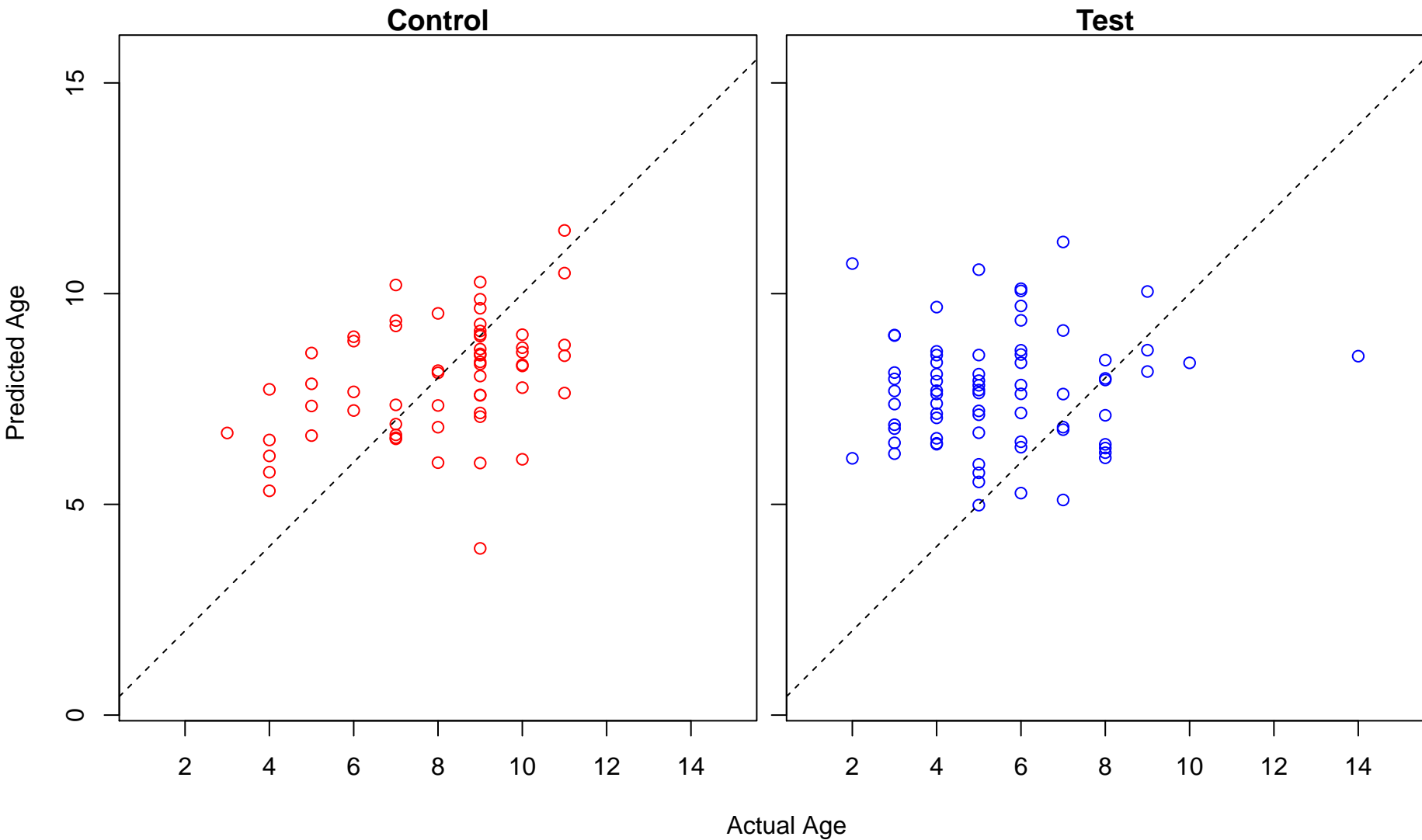
interkinetic nuclear migration (Score: 0.856632)



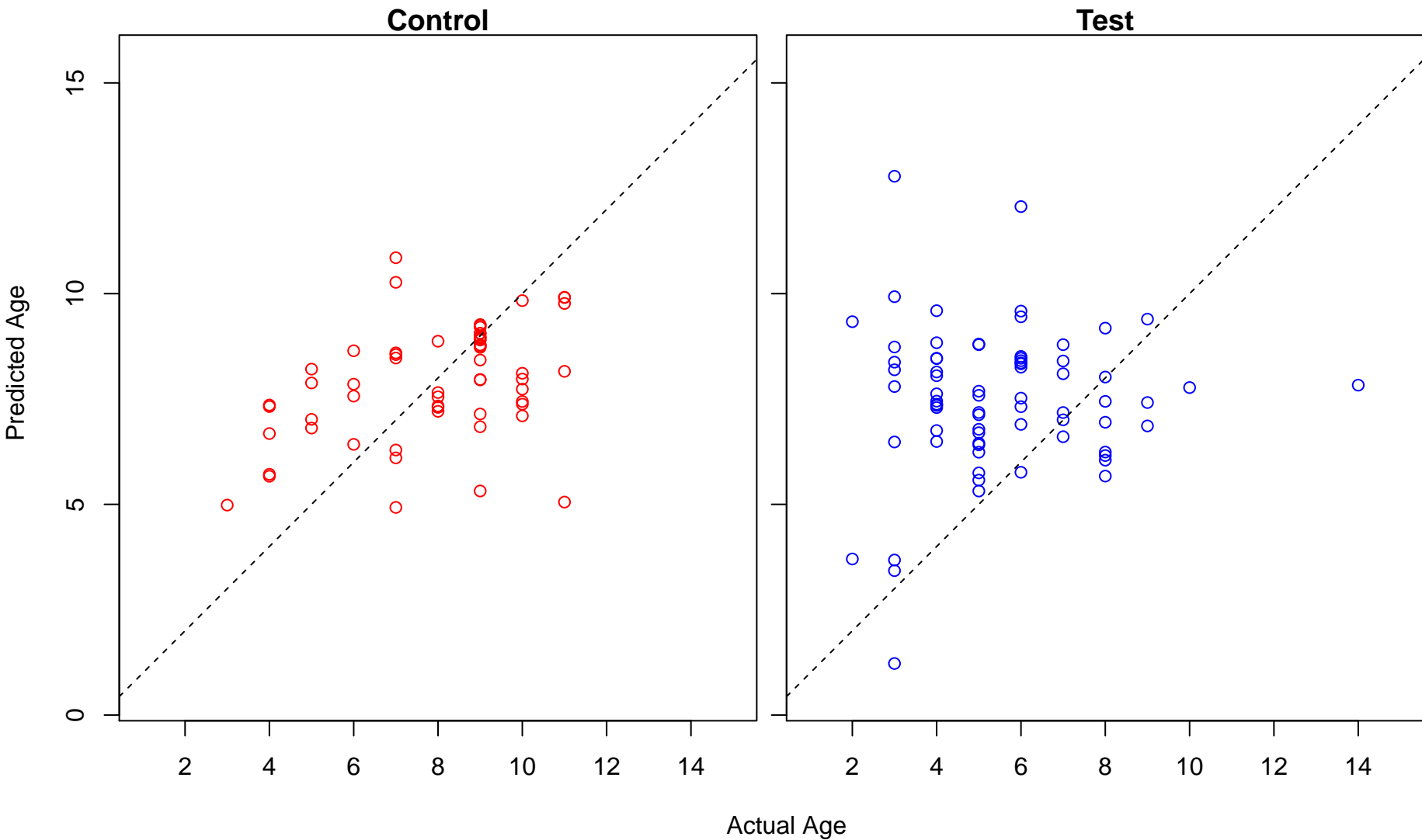
microtubule anchoring (Score: 0.855930)



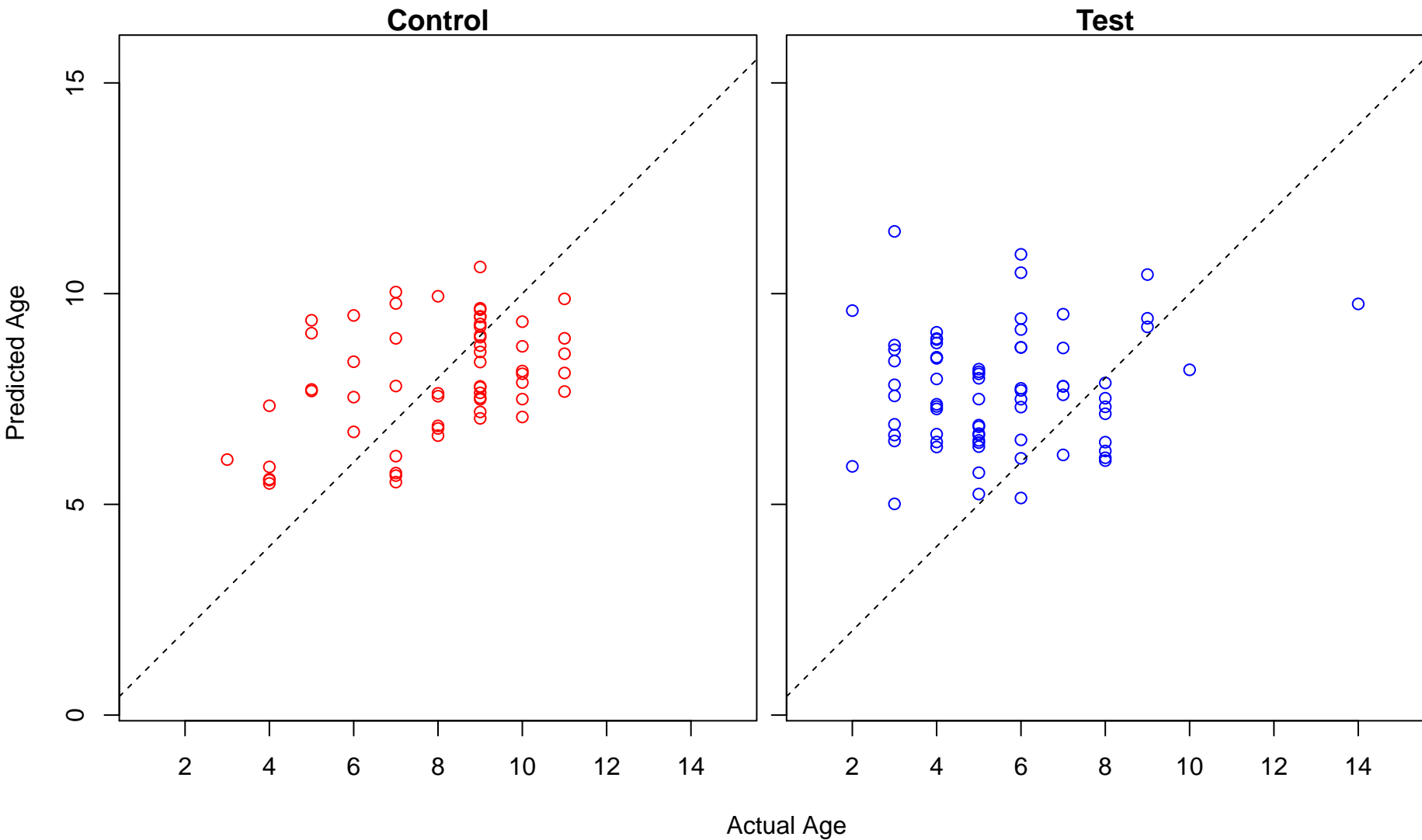
positive regulation of proteolysis (Score: 0.853759)



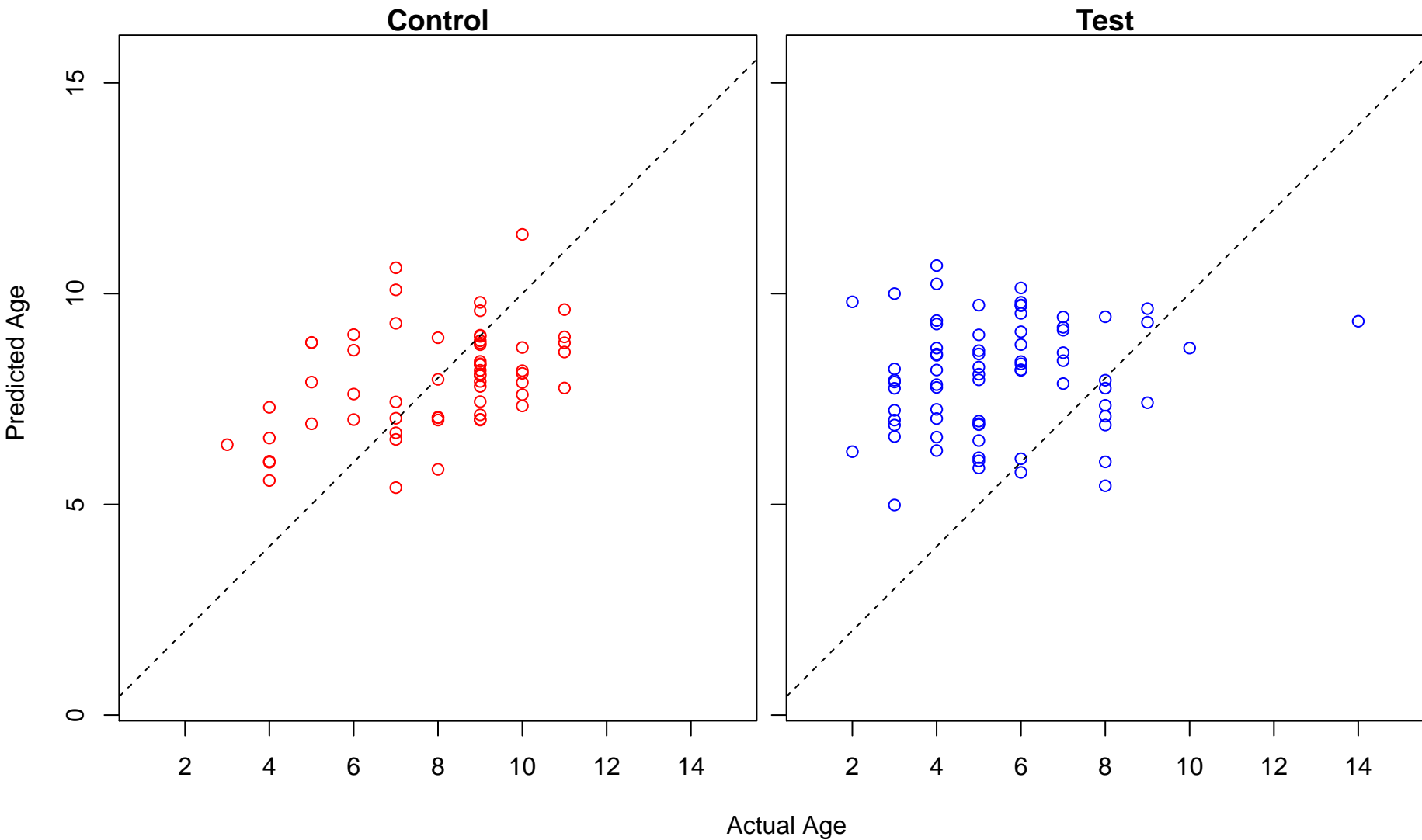
negative regulation of striated muscle tissue development (Score: 0.853125)



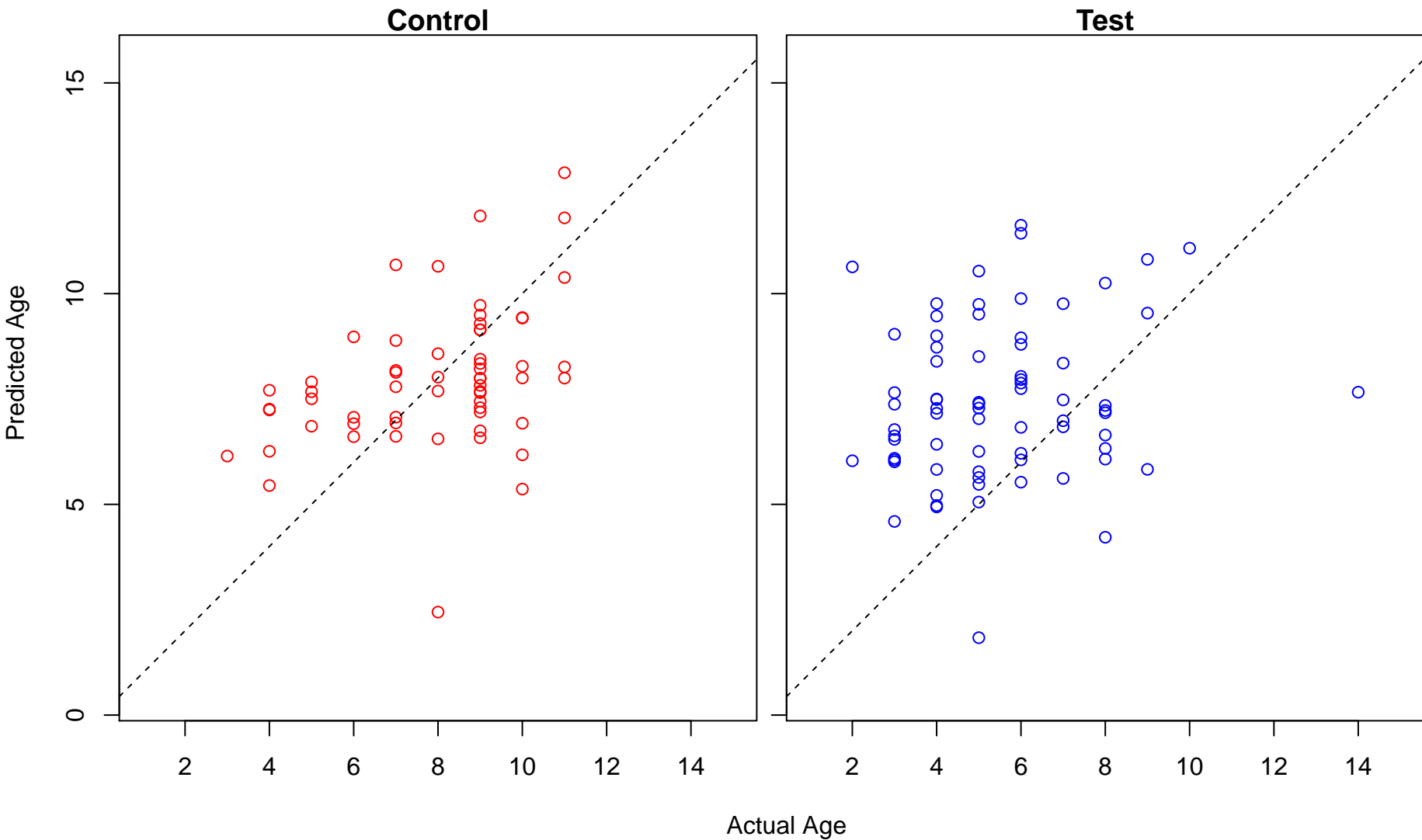
defense response to virus (Score: 0.848224)



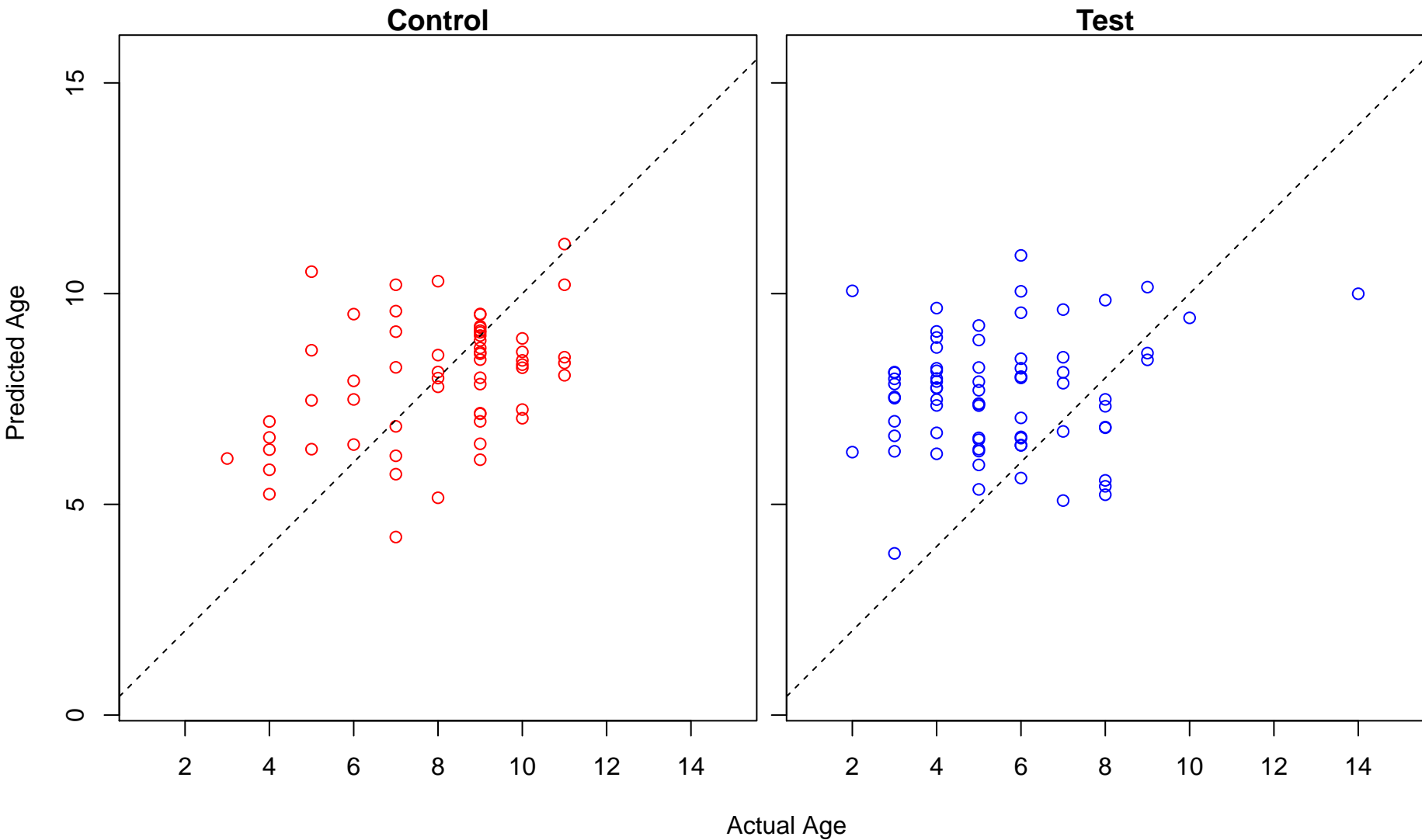
protein homooligomerization (Score: 0.848177)



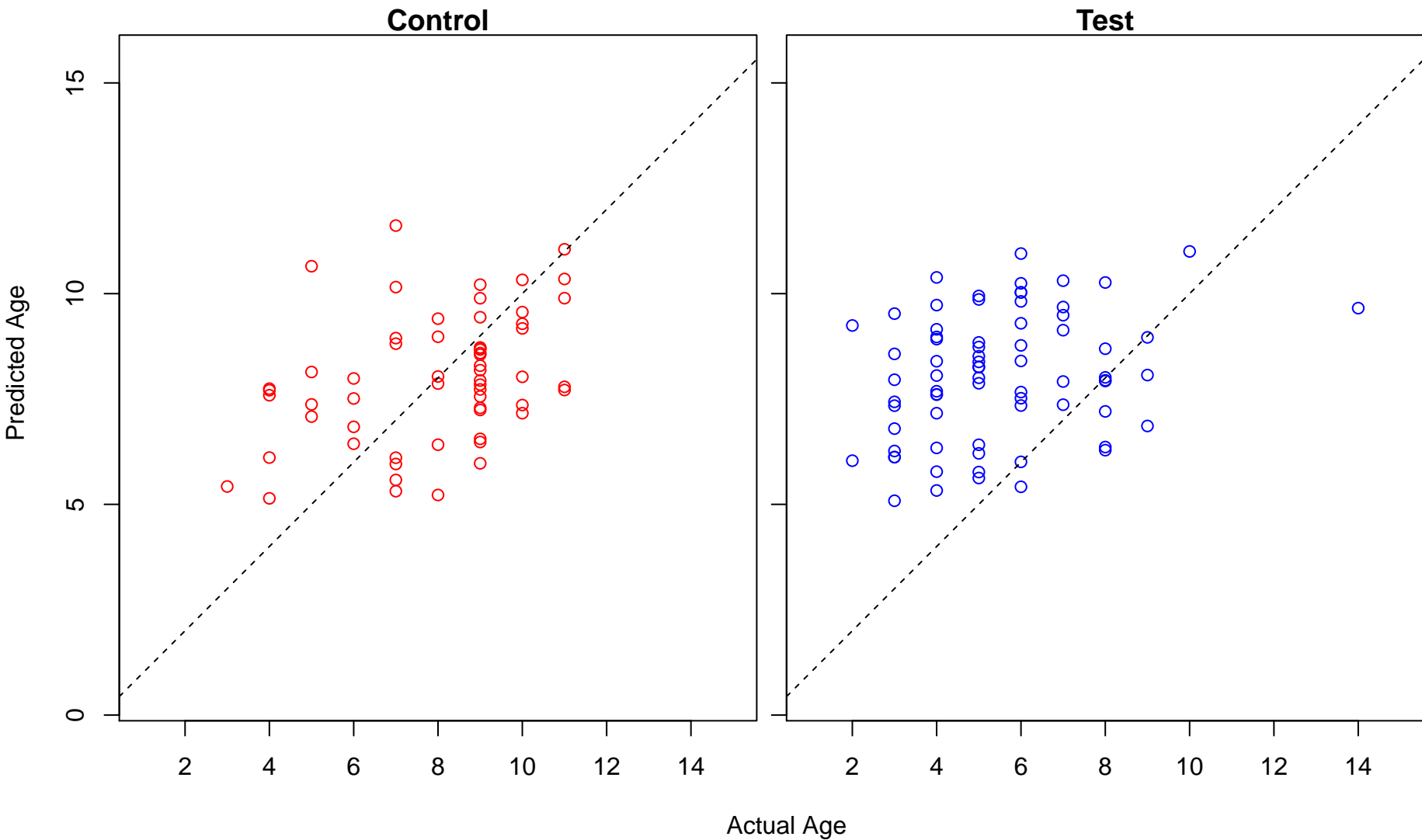
negative regulation of apoptotic signaling pathway (Score: 0.846582)



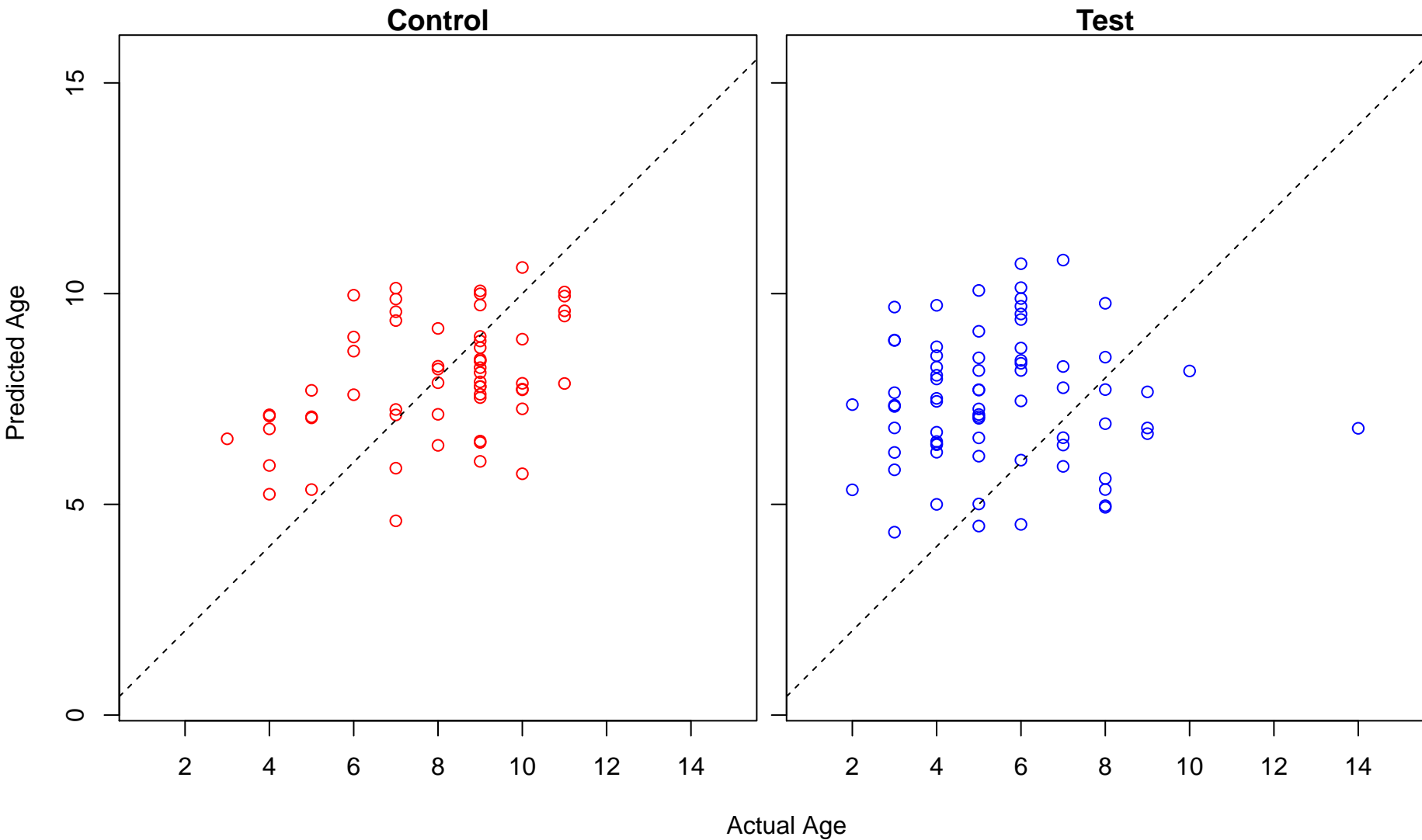
T cell differentiation (Score: 0.845505)



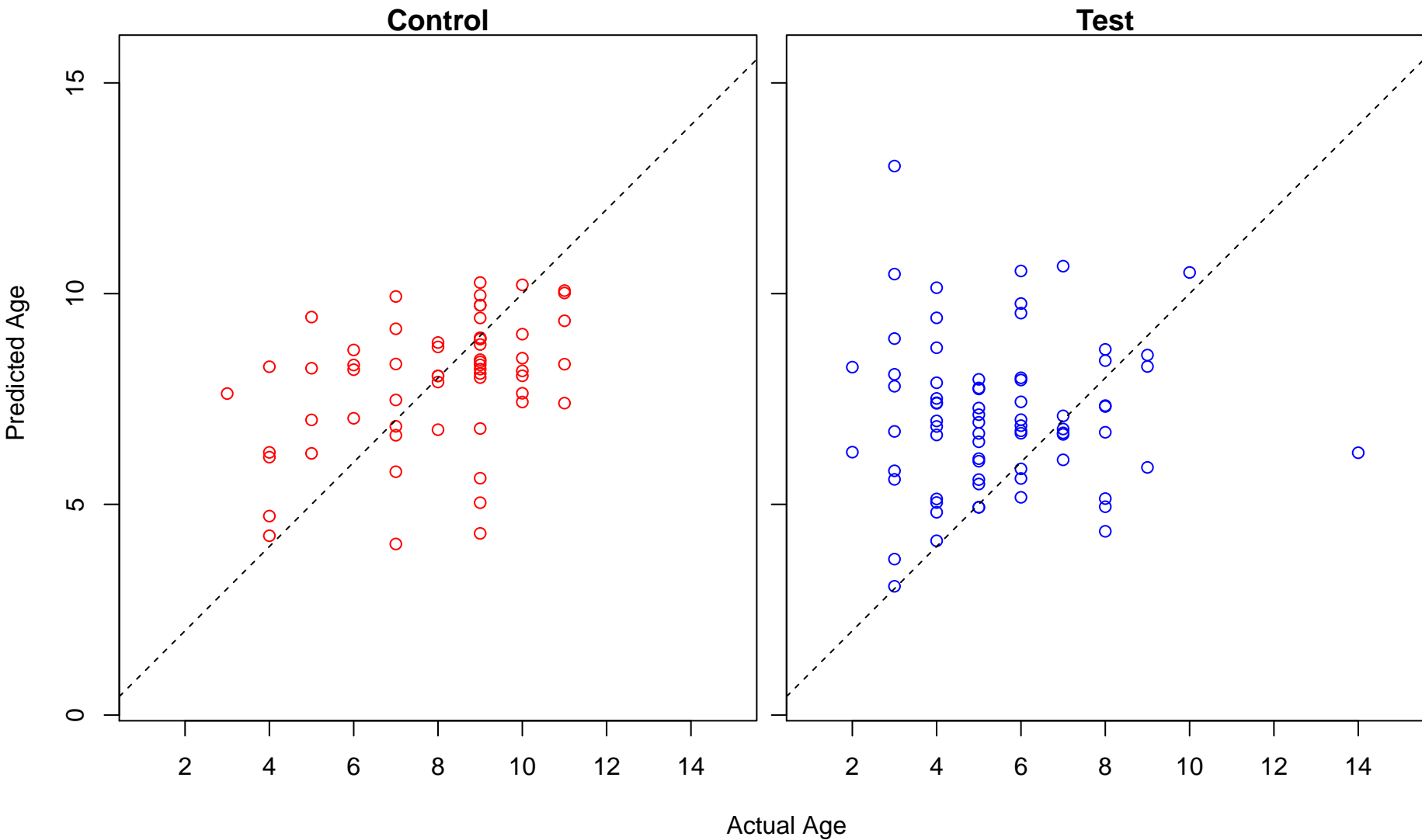
sensory organ development (Score: 0.845422)



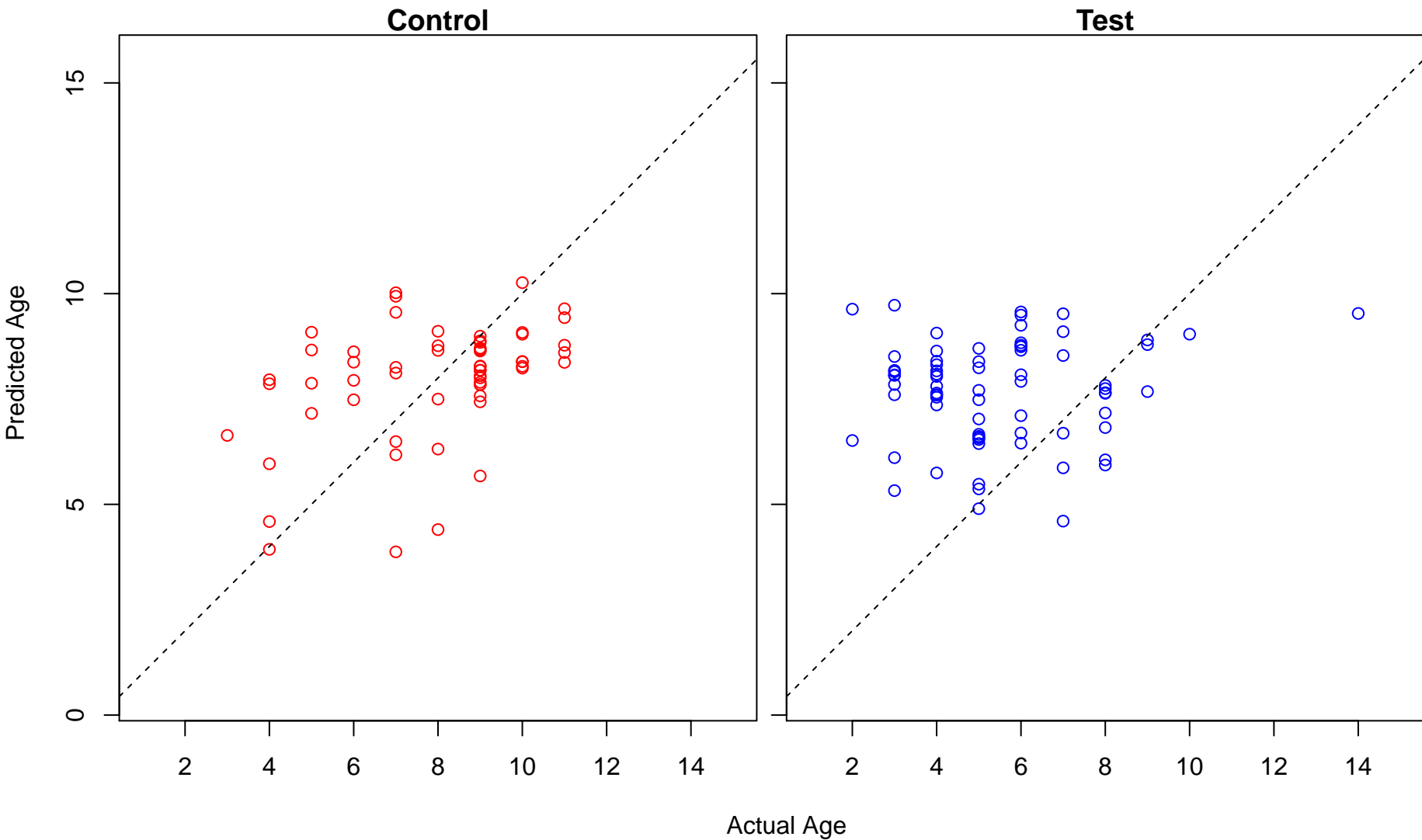
positive regulation of carbohydrate metabolic process (Score: 0.844563)



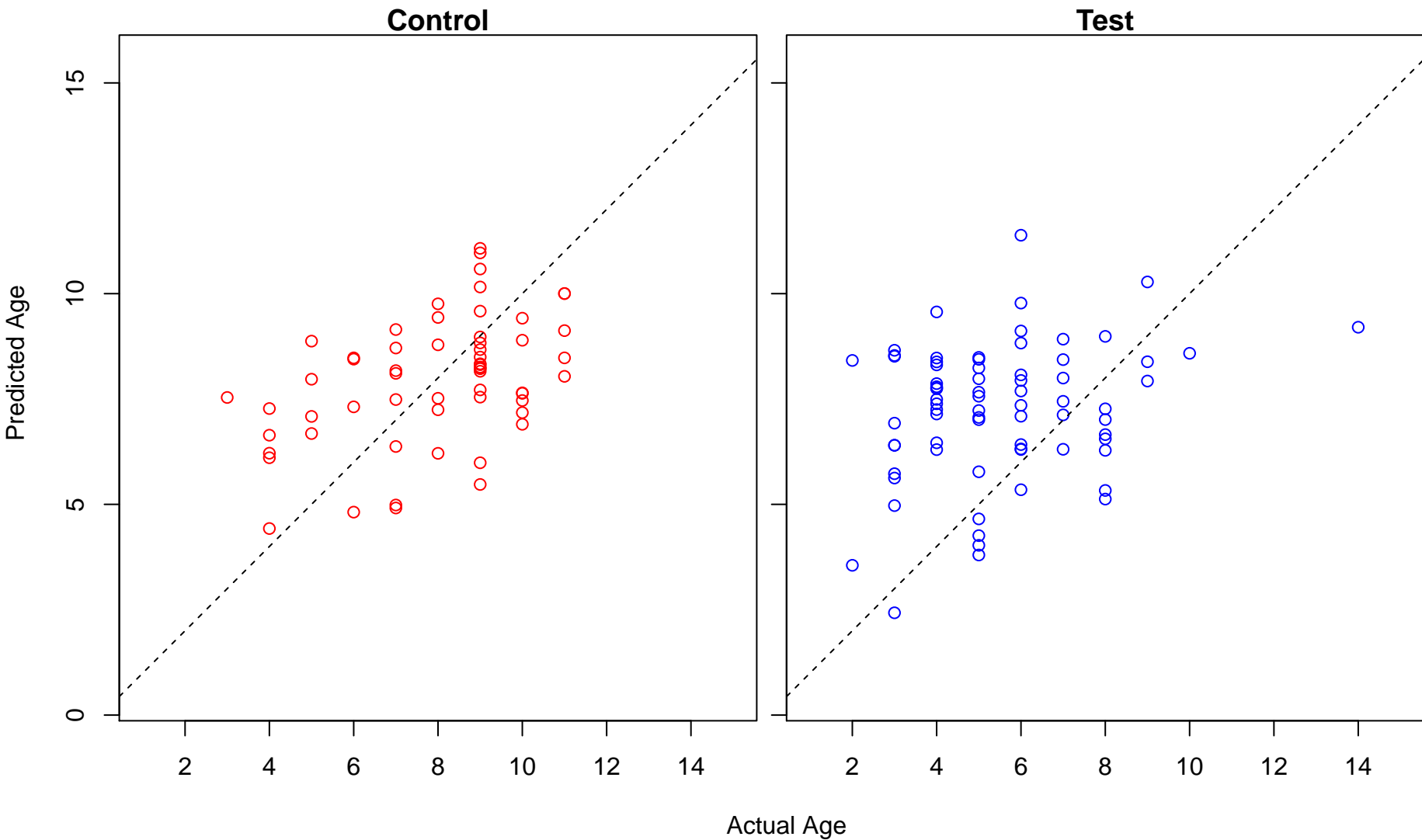
mismatch repair (Score: 0.842053)



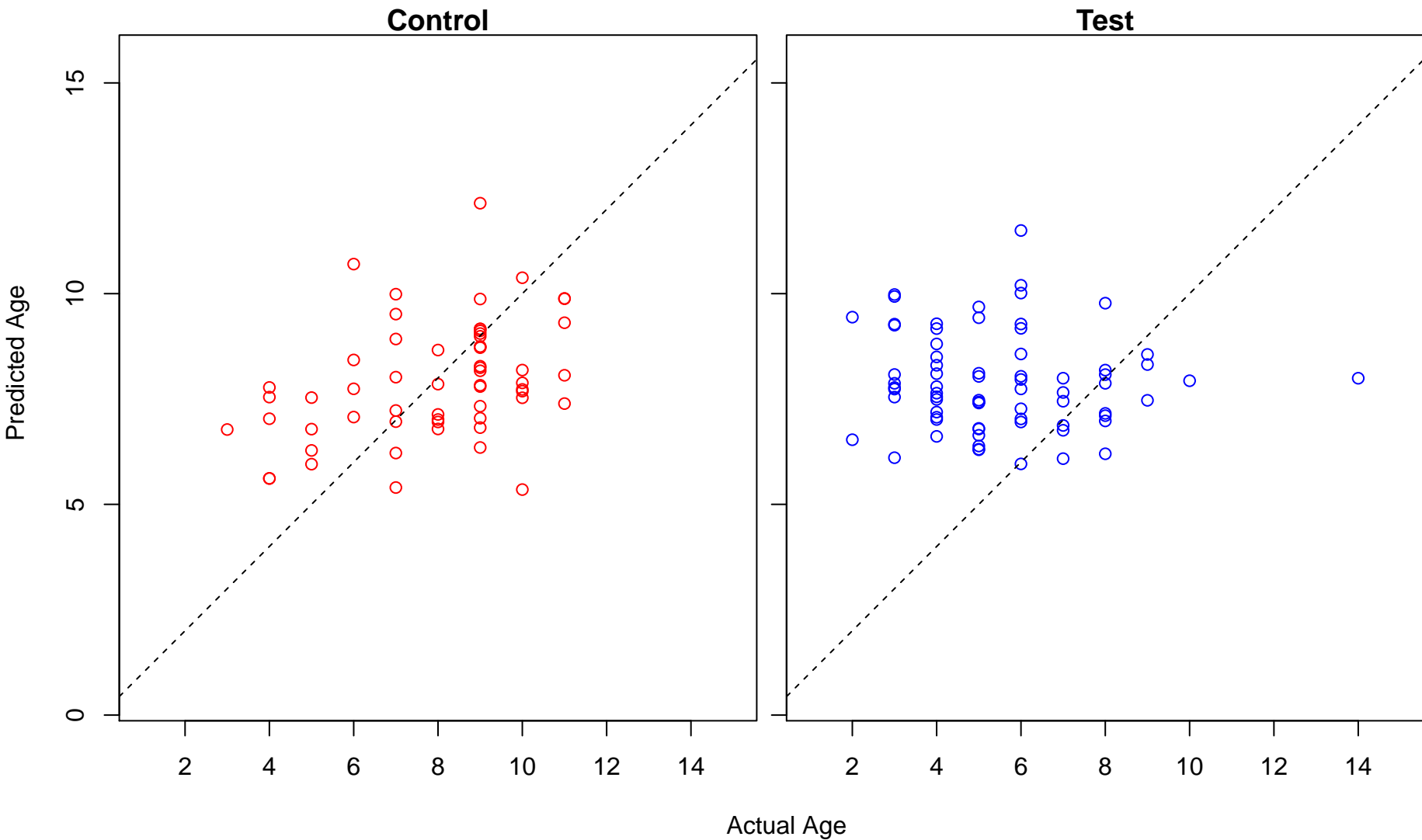
negative regulation of epithelial to mesenchymal transition (Score: 0.841710)



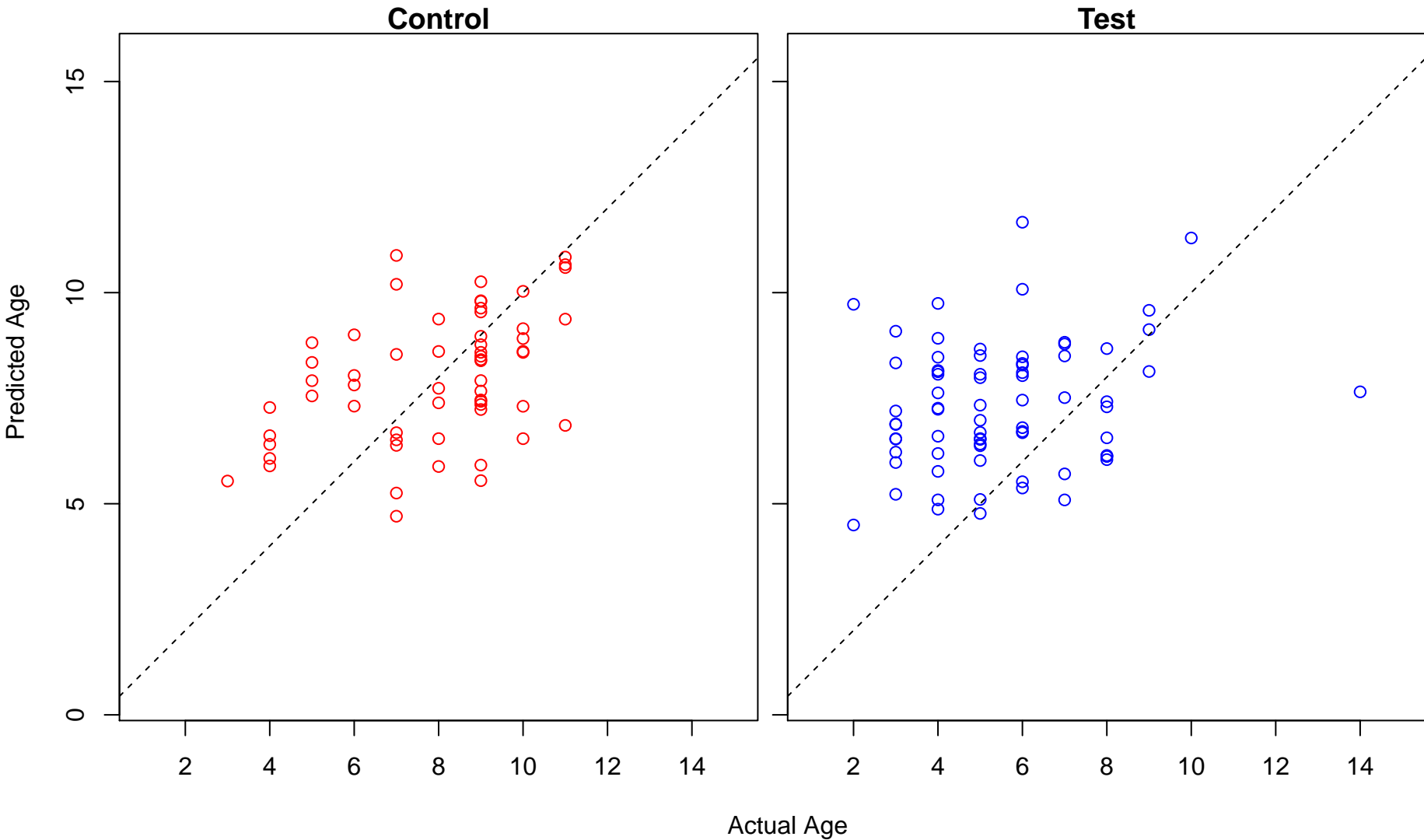
regulation of oxidoreductase activity (Score: 0.841586)



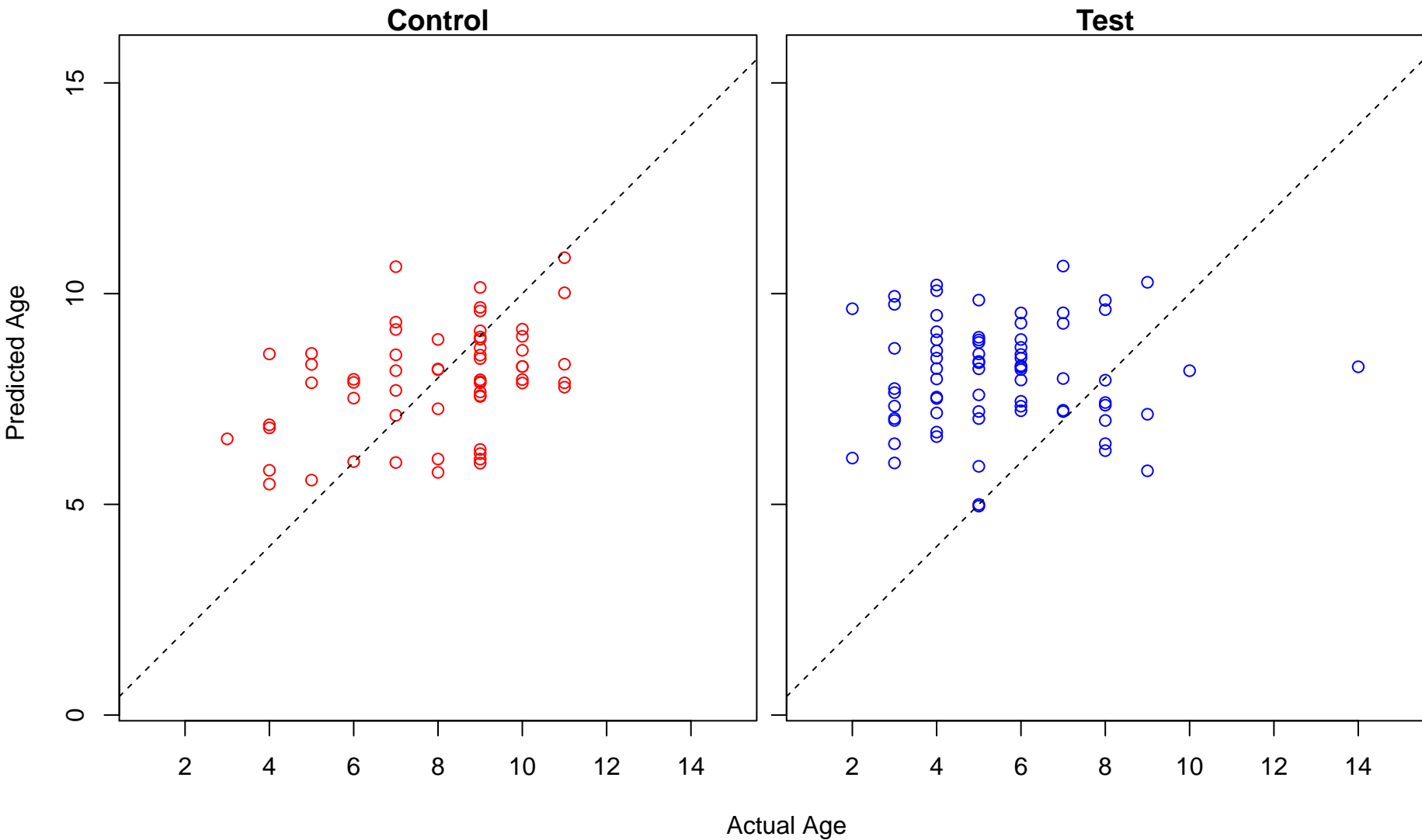
ephrin receptor signaling pathway (Score: 0.840995)



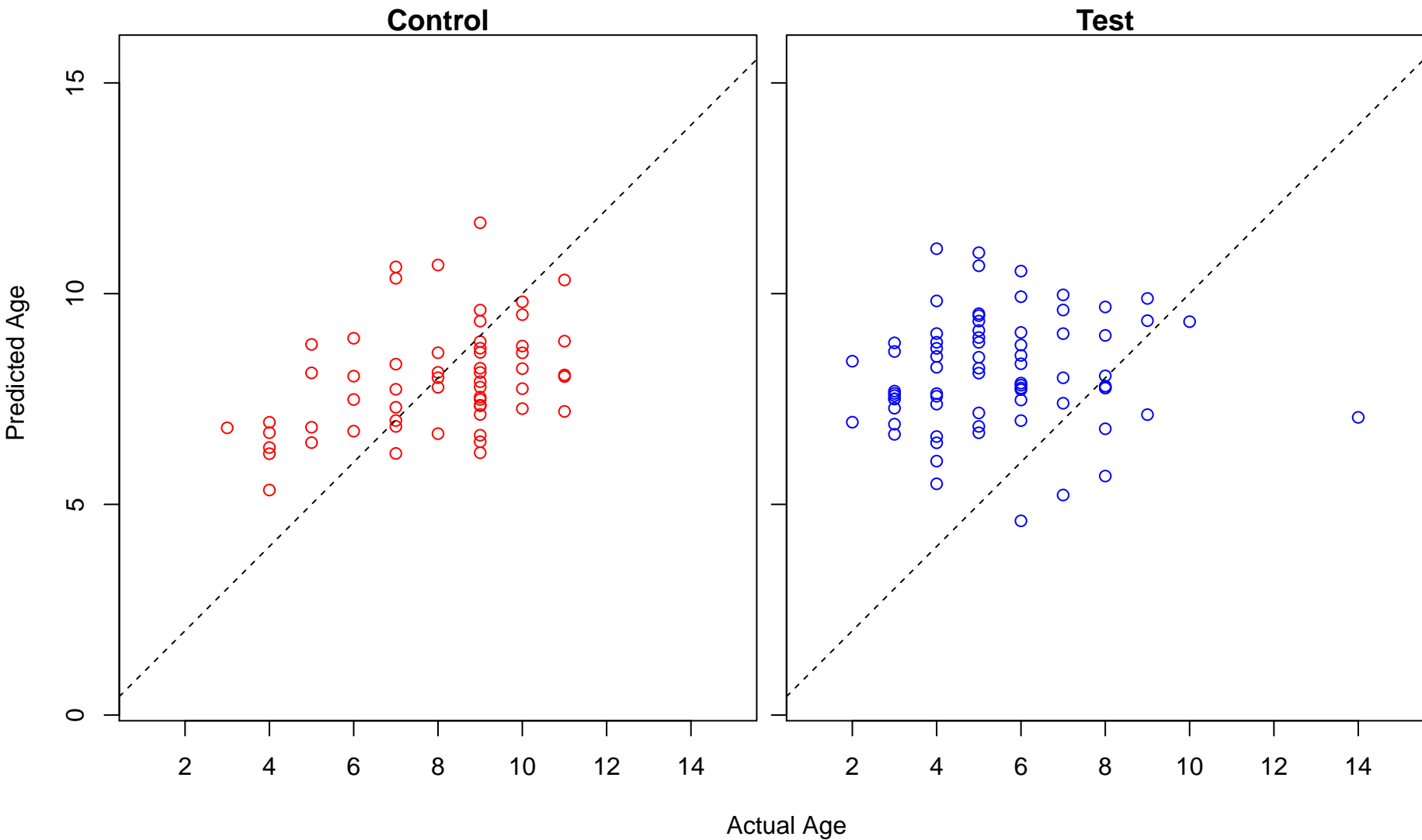
transcription from RNA polymerase II promoter (Score: 0.840144)



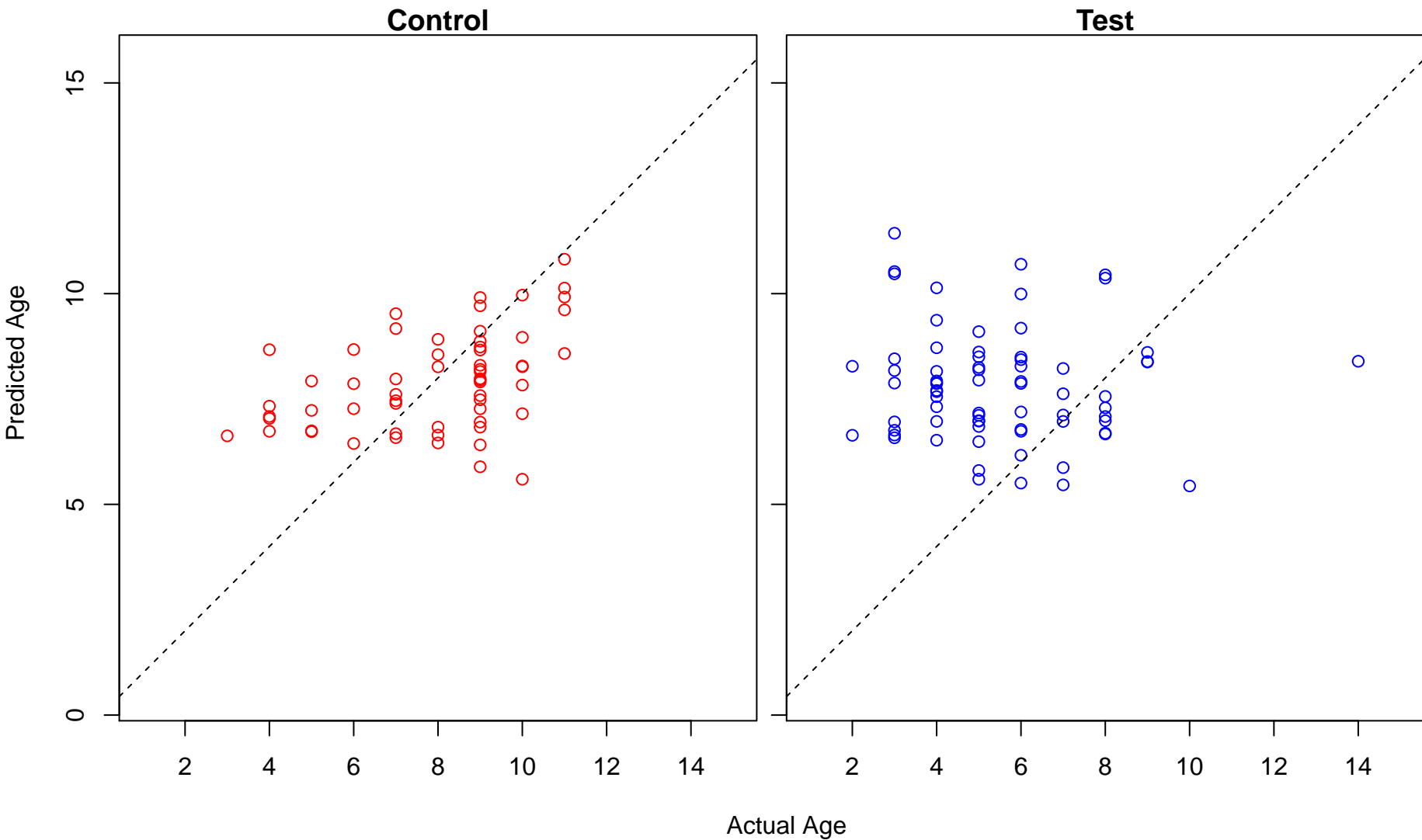
ribosome disassembly (Score: 0.839488)



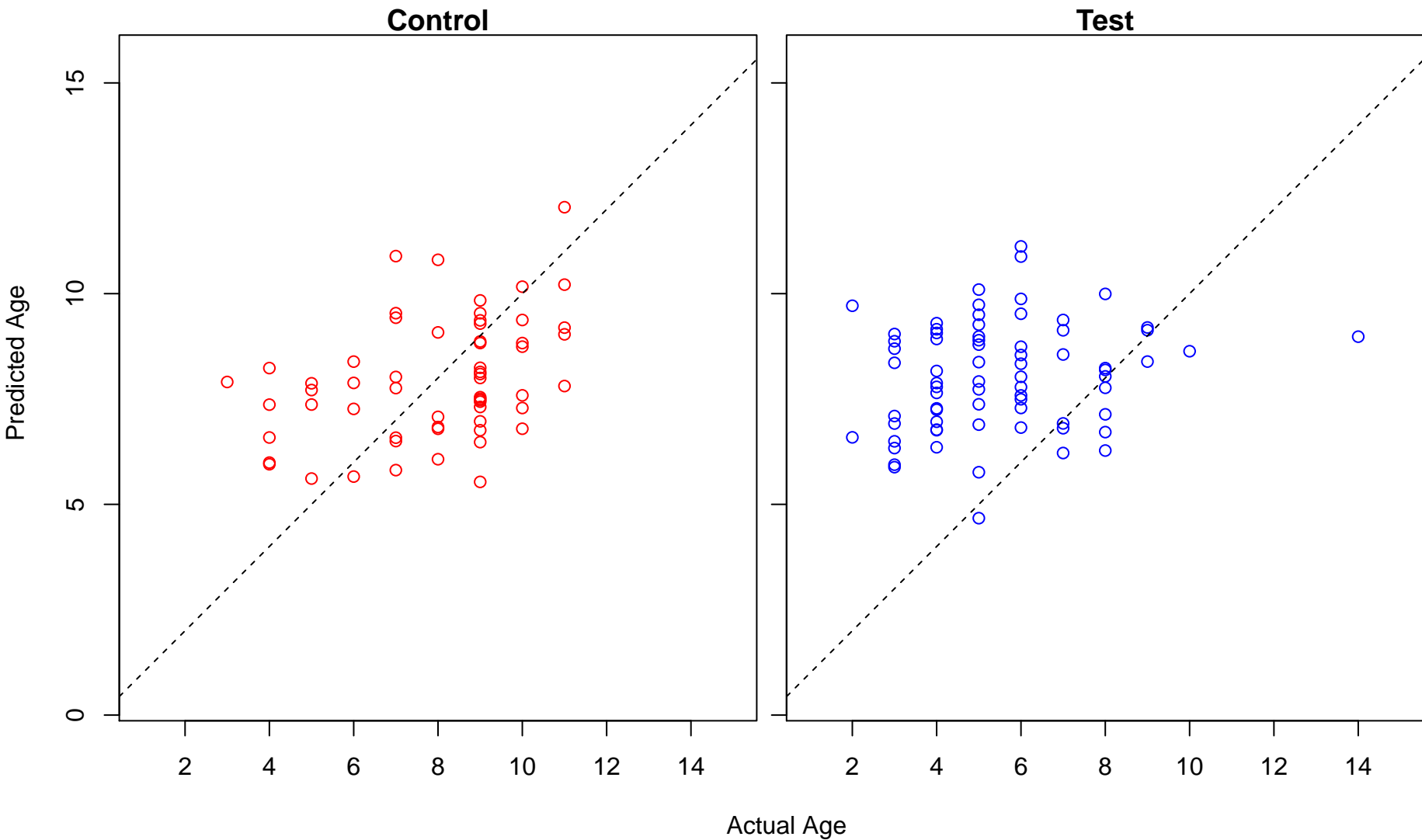
peptidyl-lysine deacetylation (Score: 0.839125)



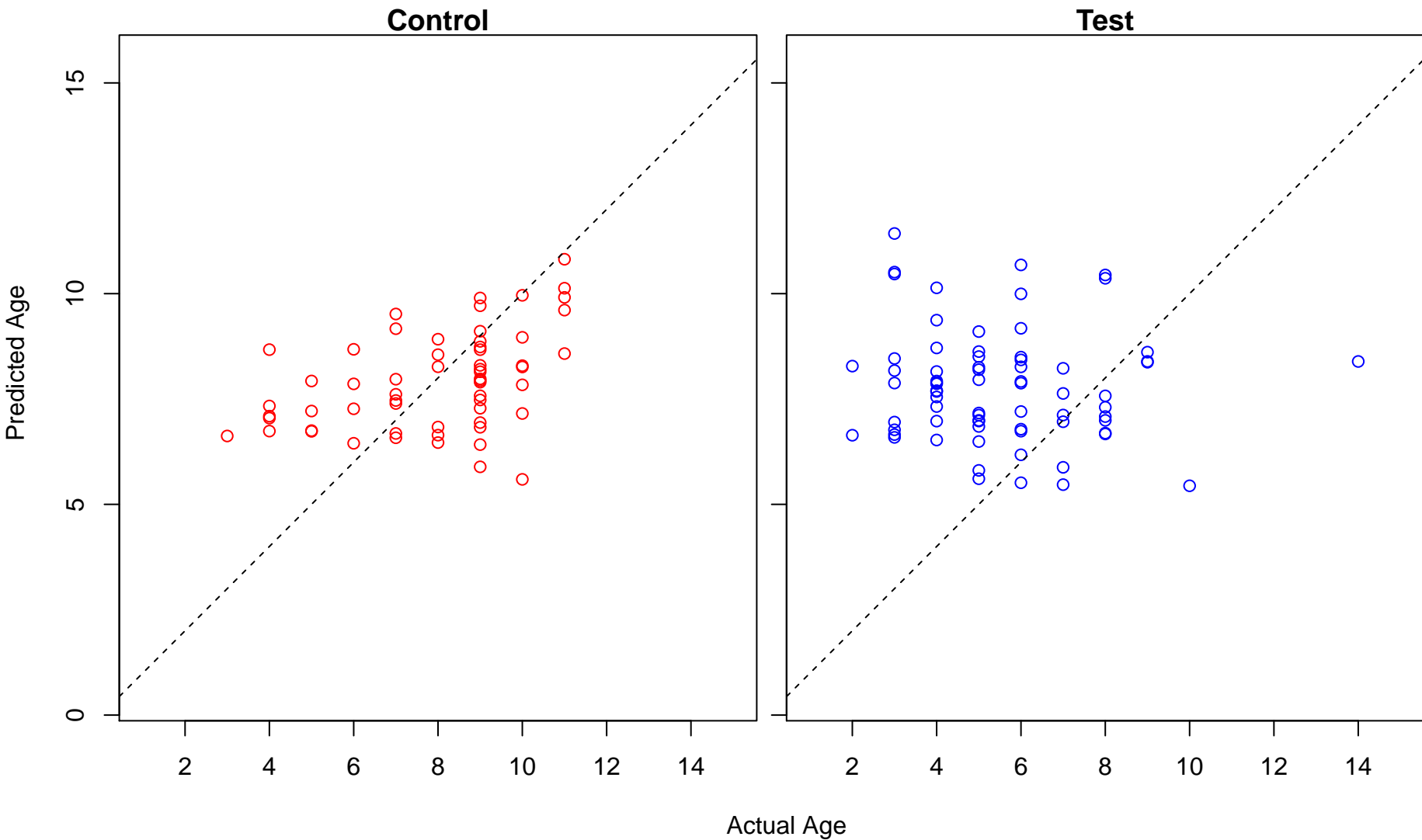
platelet morphogenesis (Score: 0.837427)



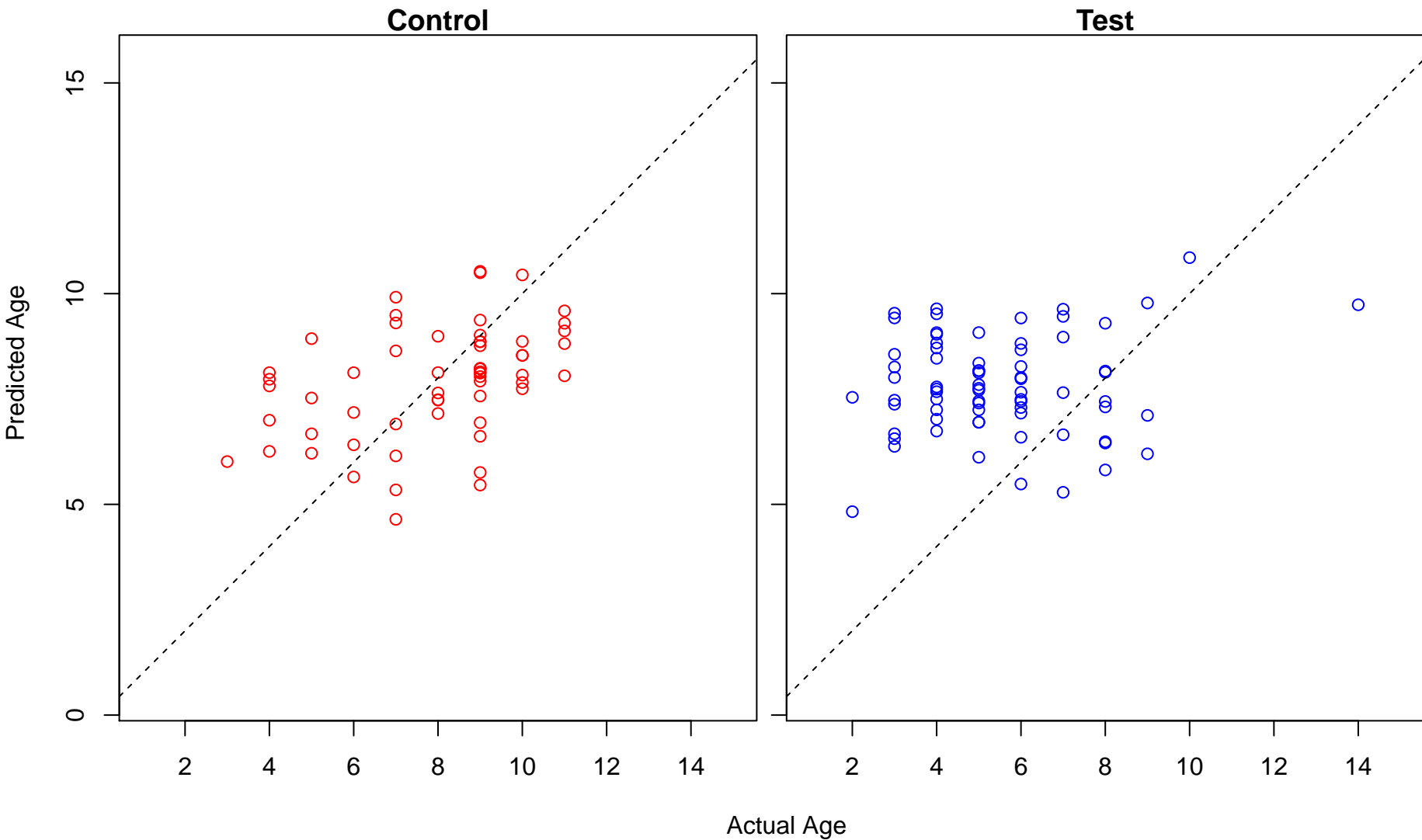
cellular amide metabolic process (Score: 0.836410)



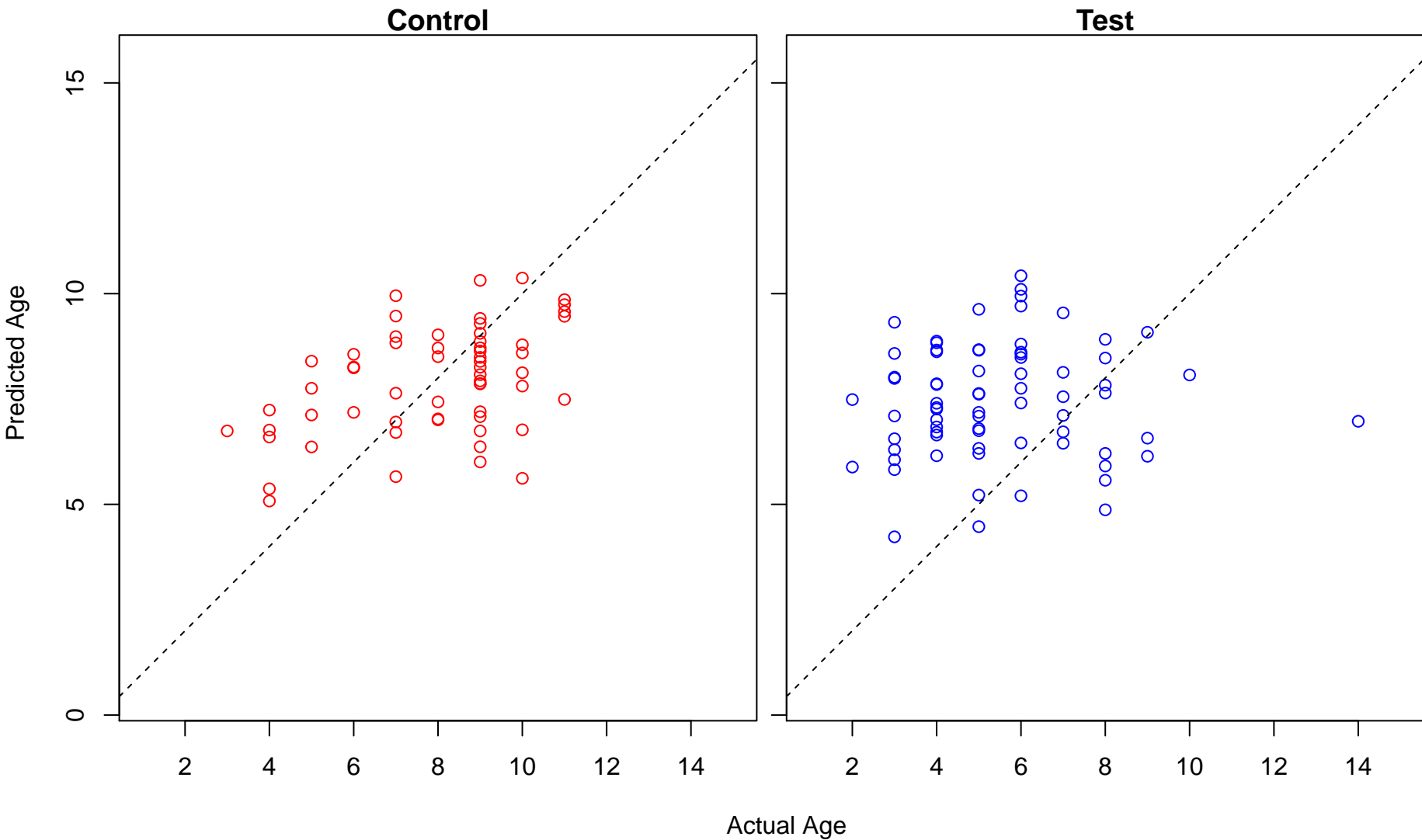
platelet formation (Score: 0.834984)



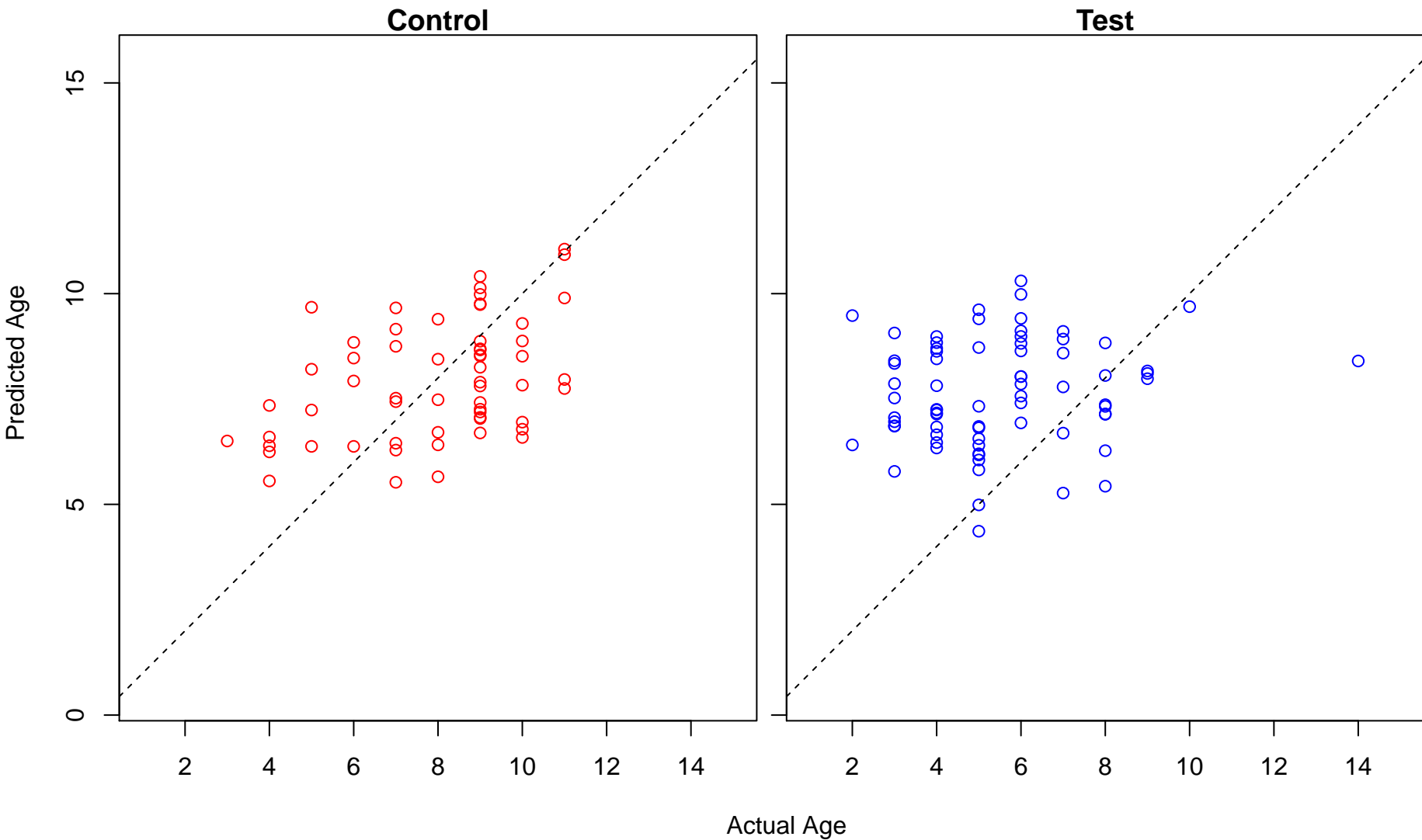
regulation of interleukin-6-mediated signaling pathway (Score: 0.834347)



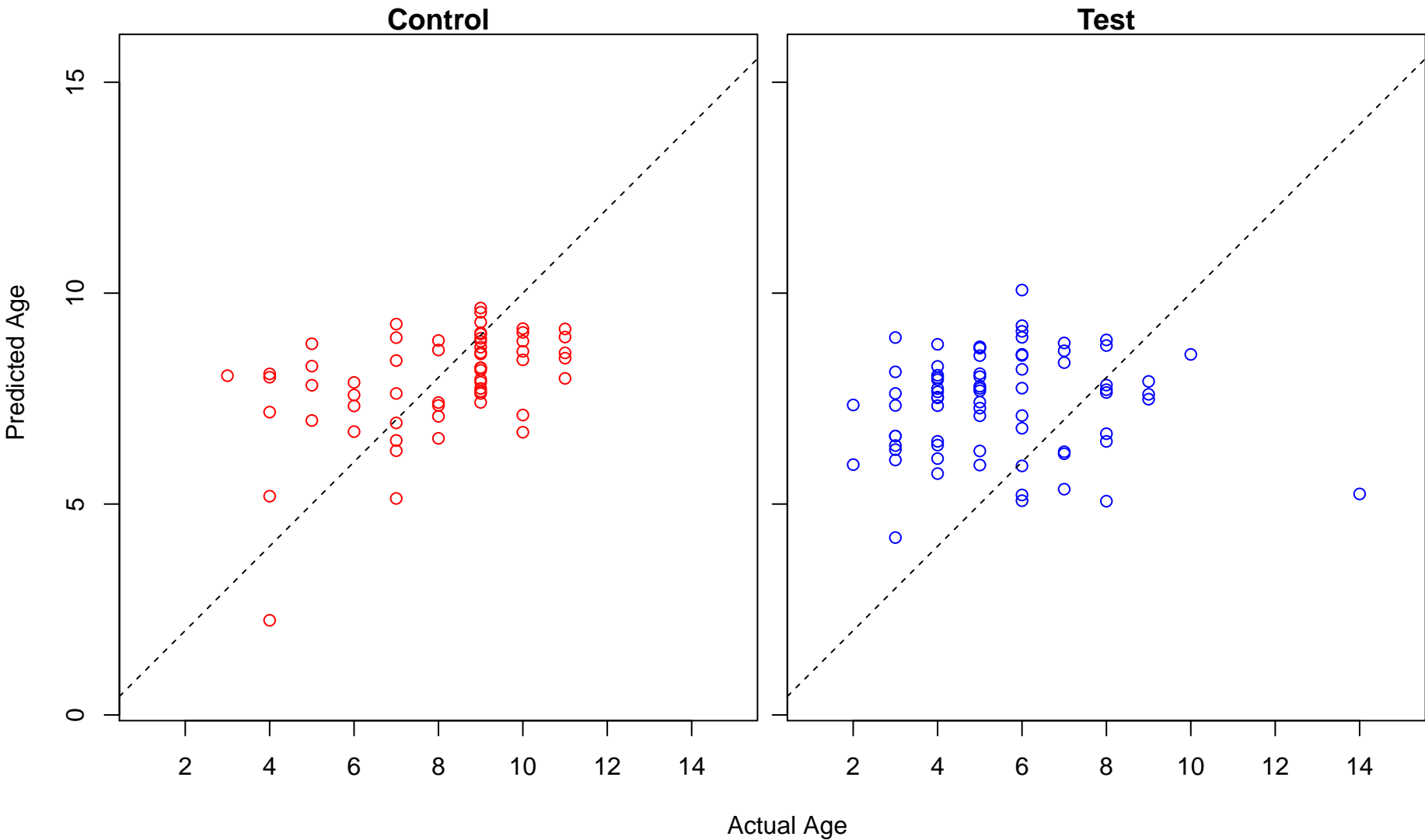
positive regulation of glucose metabolic process (Score: 0.833181)



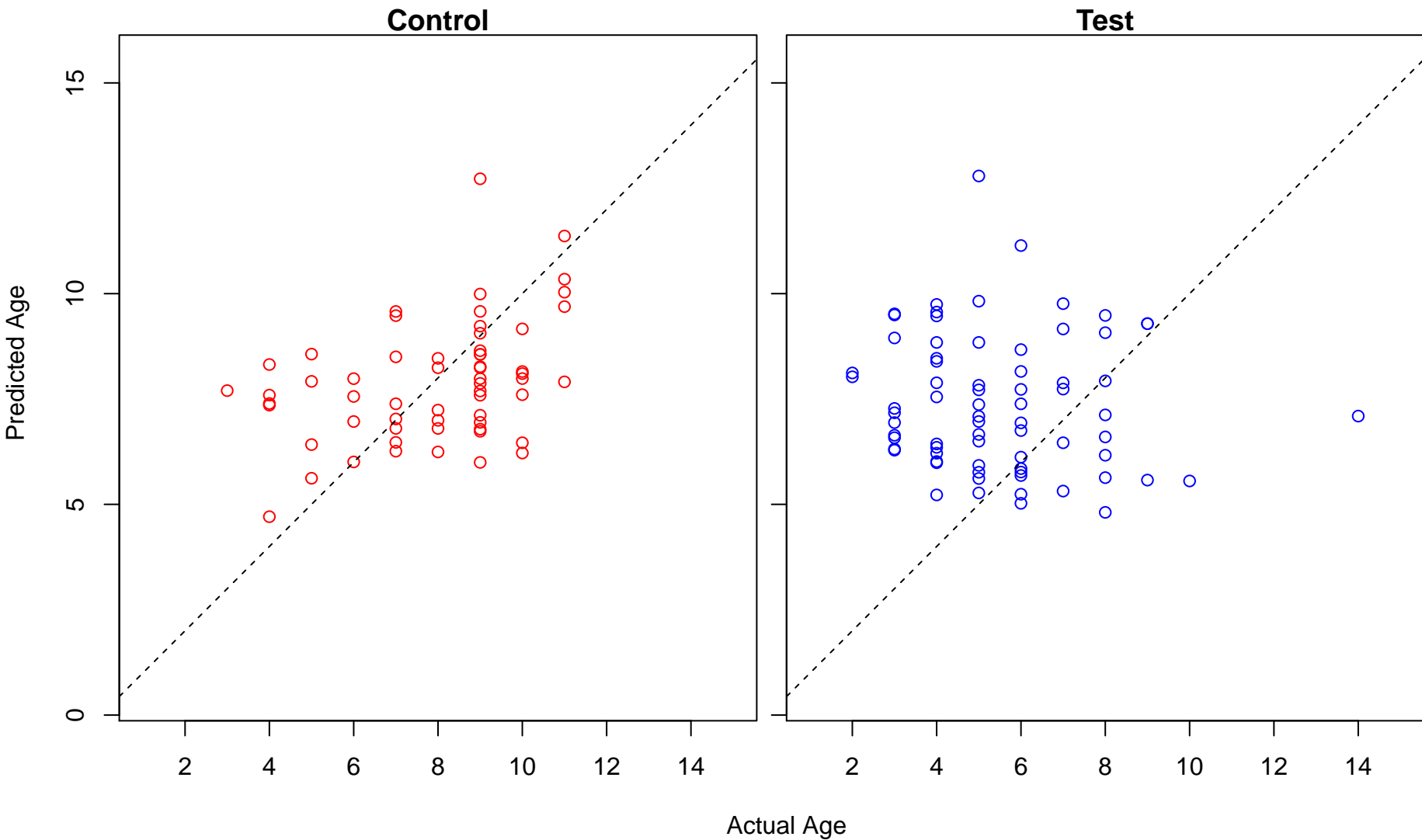
embryonic digit morphogenesis (Score: 0.832622)



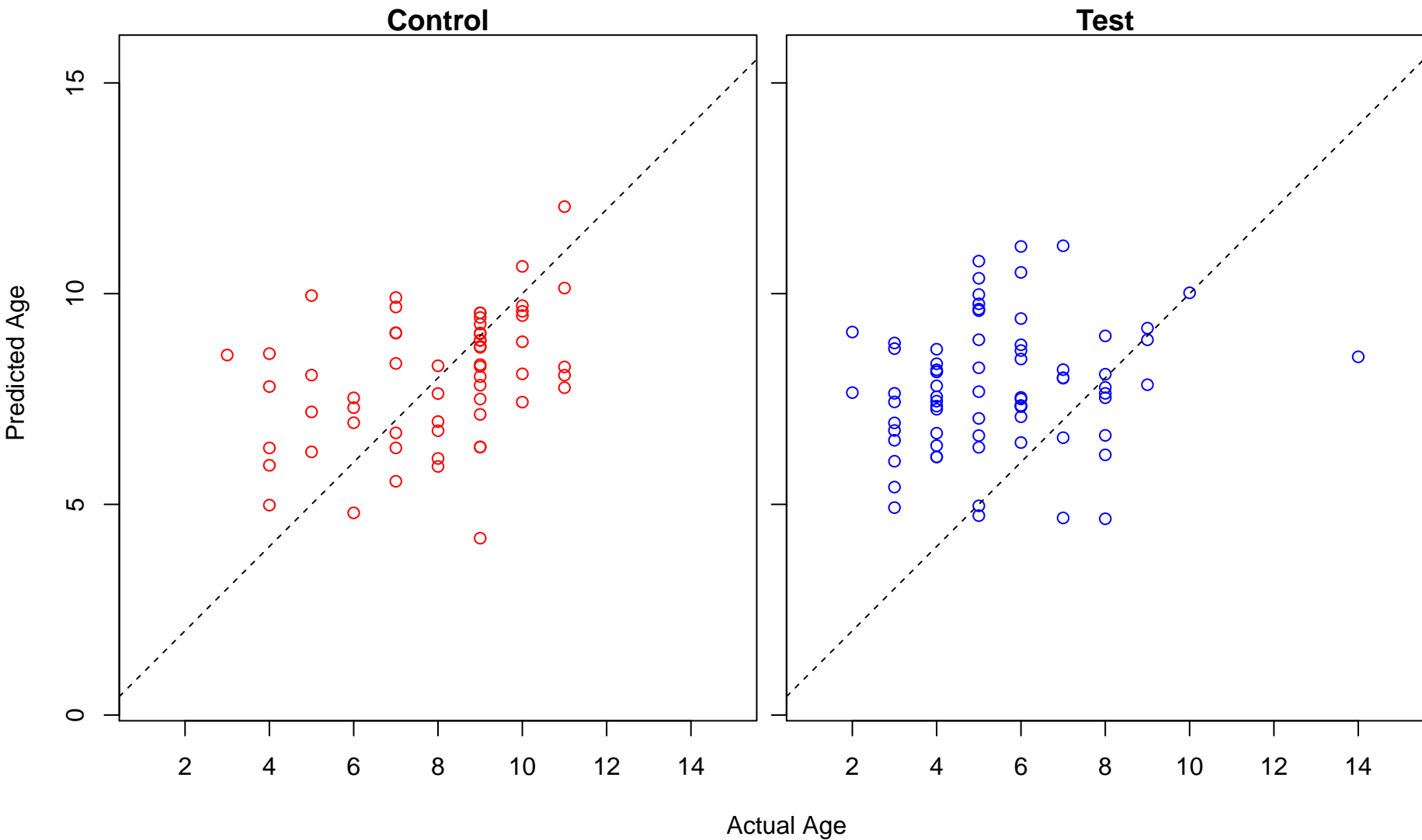
regulation of peroxisome proliferator activated receptor signaling pathway (Score: 0.832398)



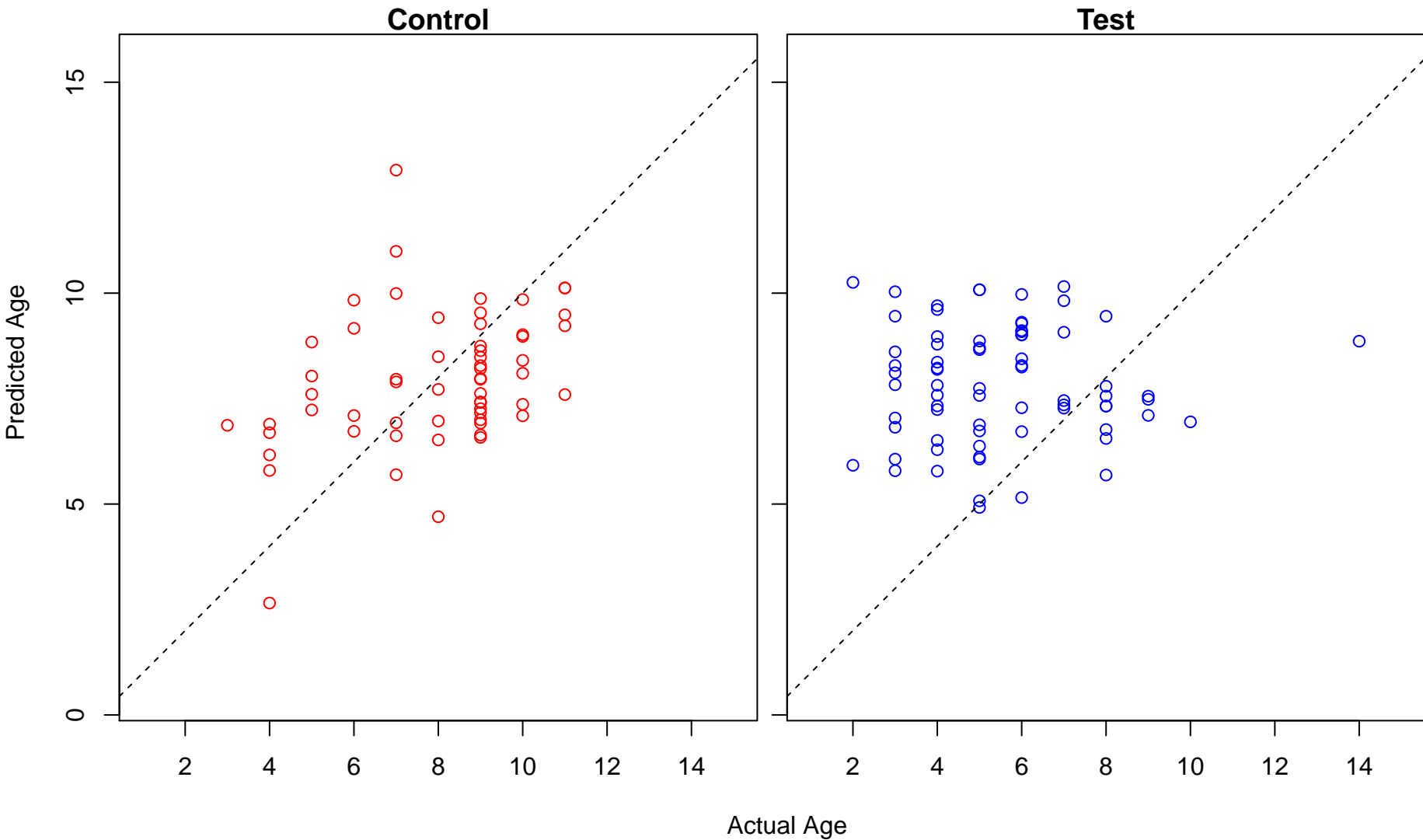
thalamus development (Score: 0.832338)



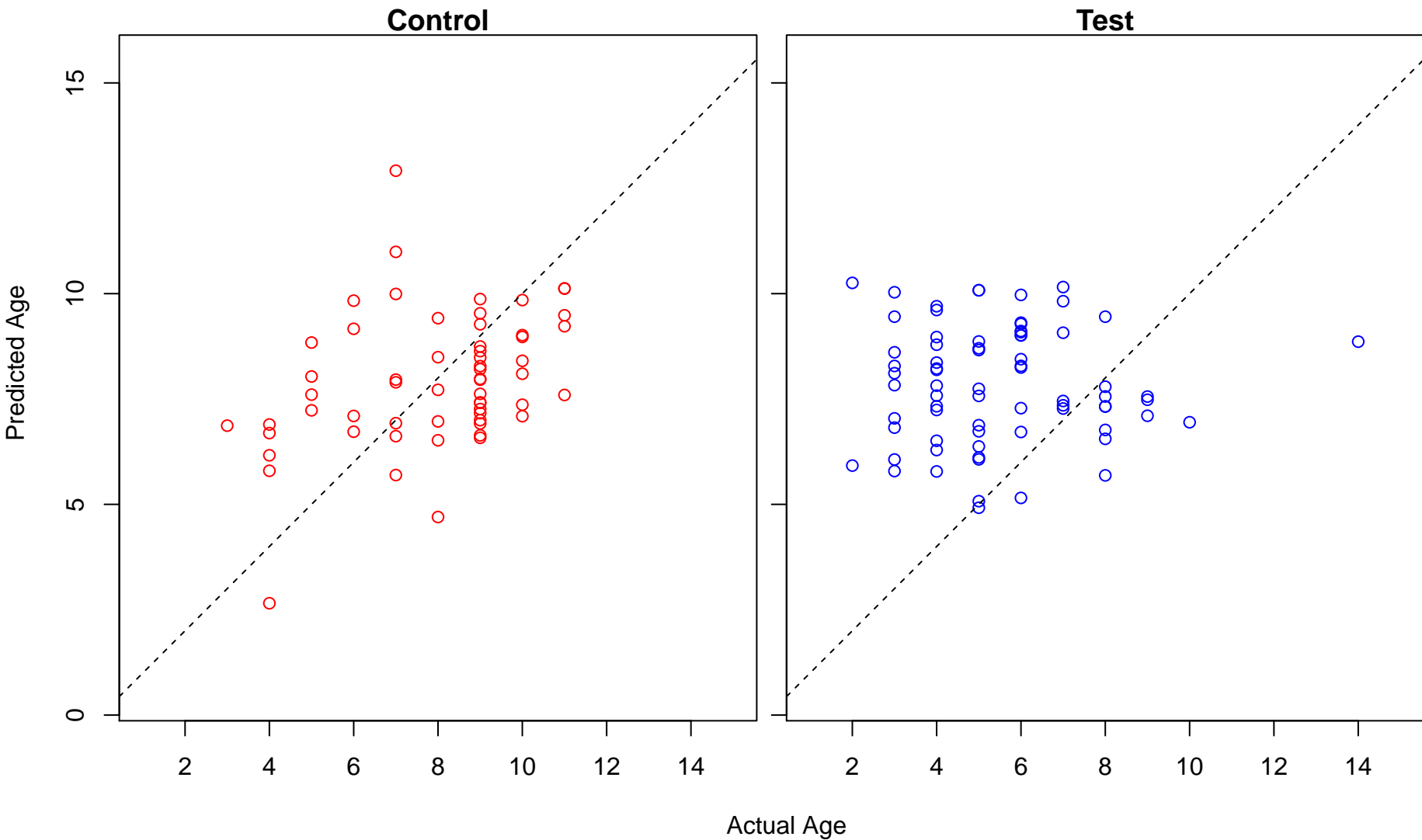
organic cyclic compound catabolic process (Score: 0.831152)



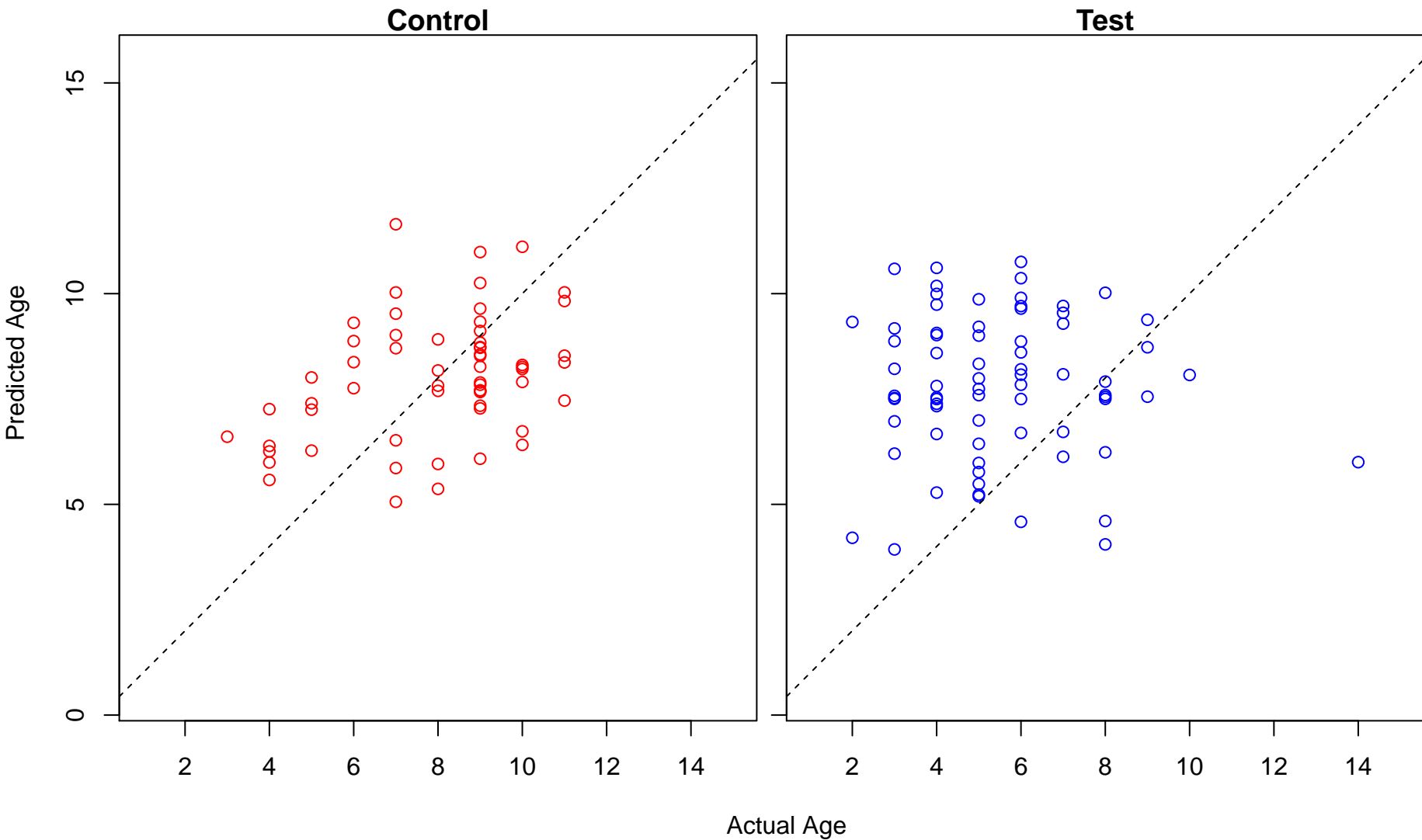
cellular biogenic amine metabolic process (Score: 0.829982)



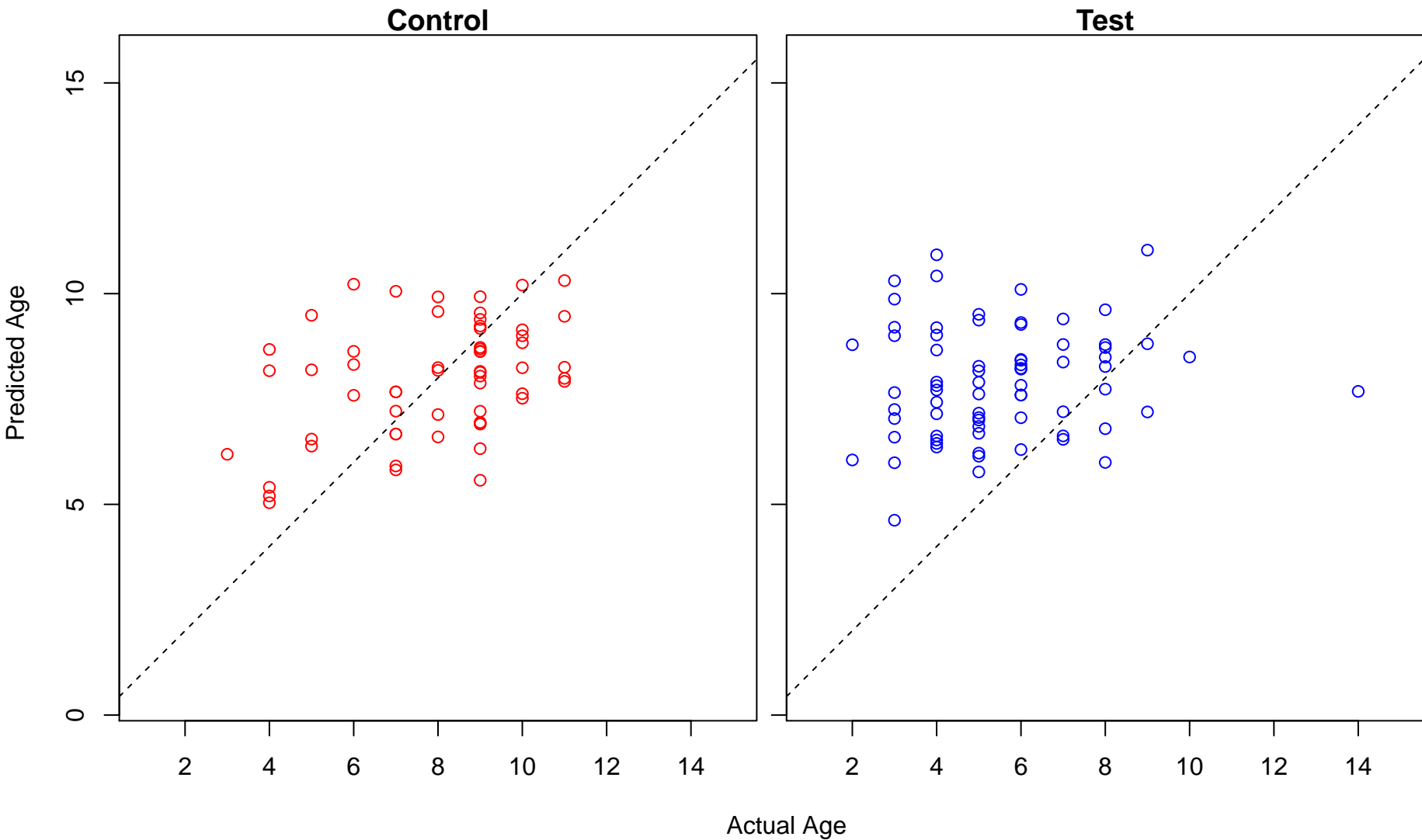
cellular amine metabolic process (Score: 0.829982)



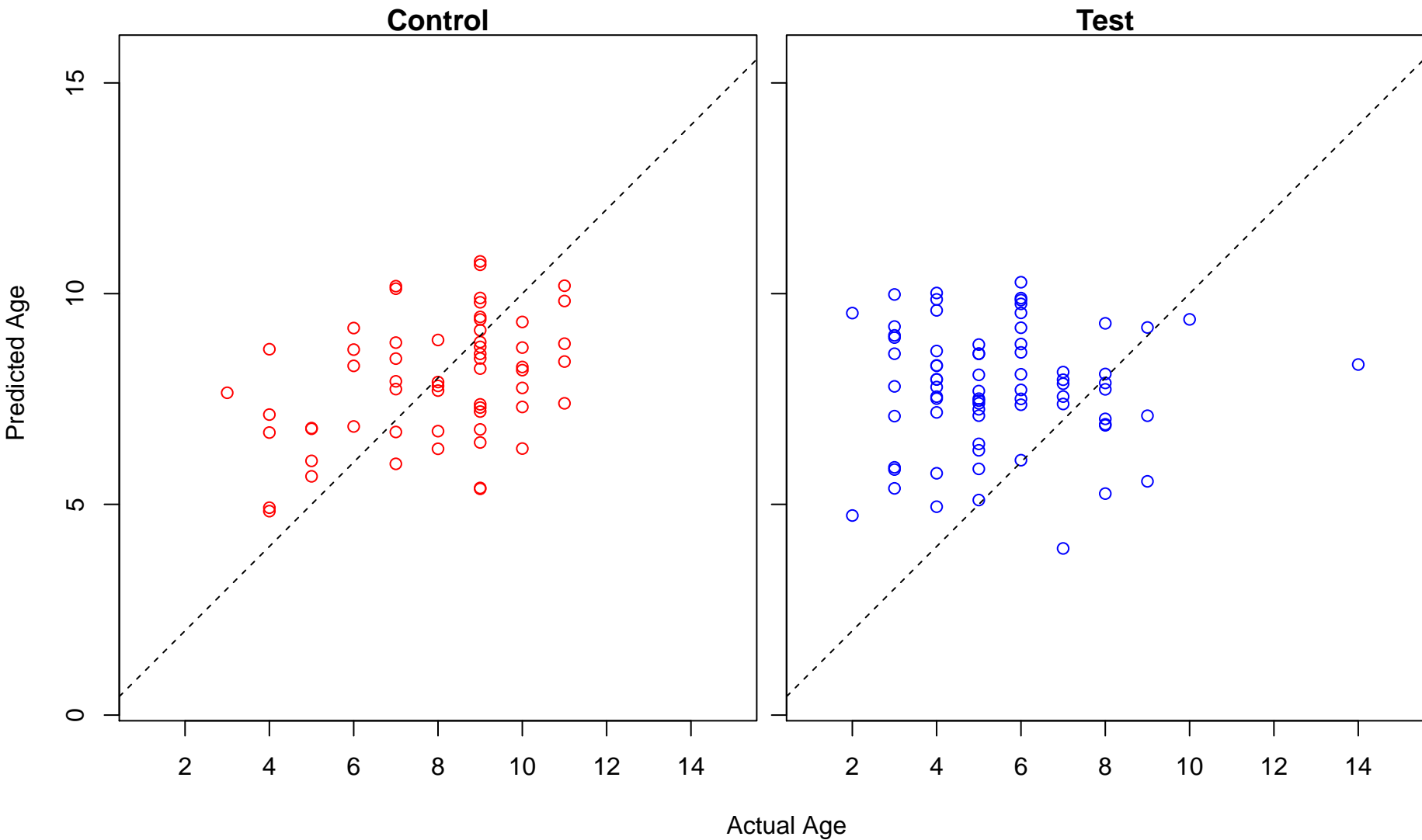
regulation of epithelial cell proliferation (Score: 0.829152)



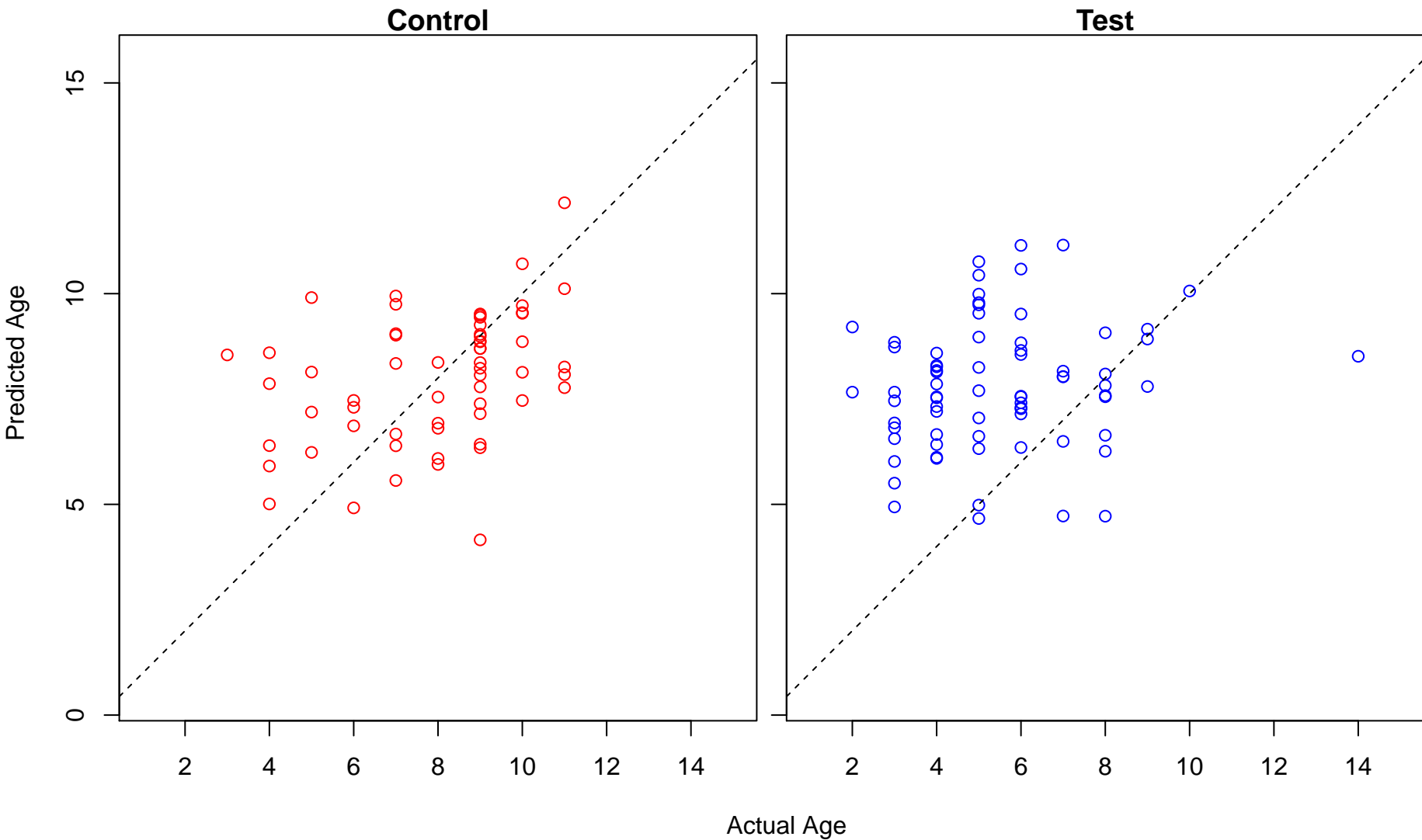
positive regulation of T-helper 1 type immune response (Score: 0.829117)



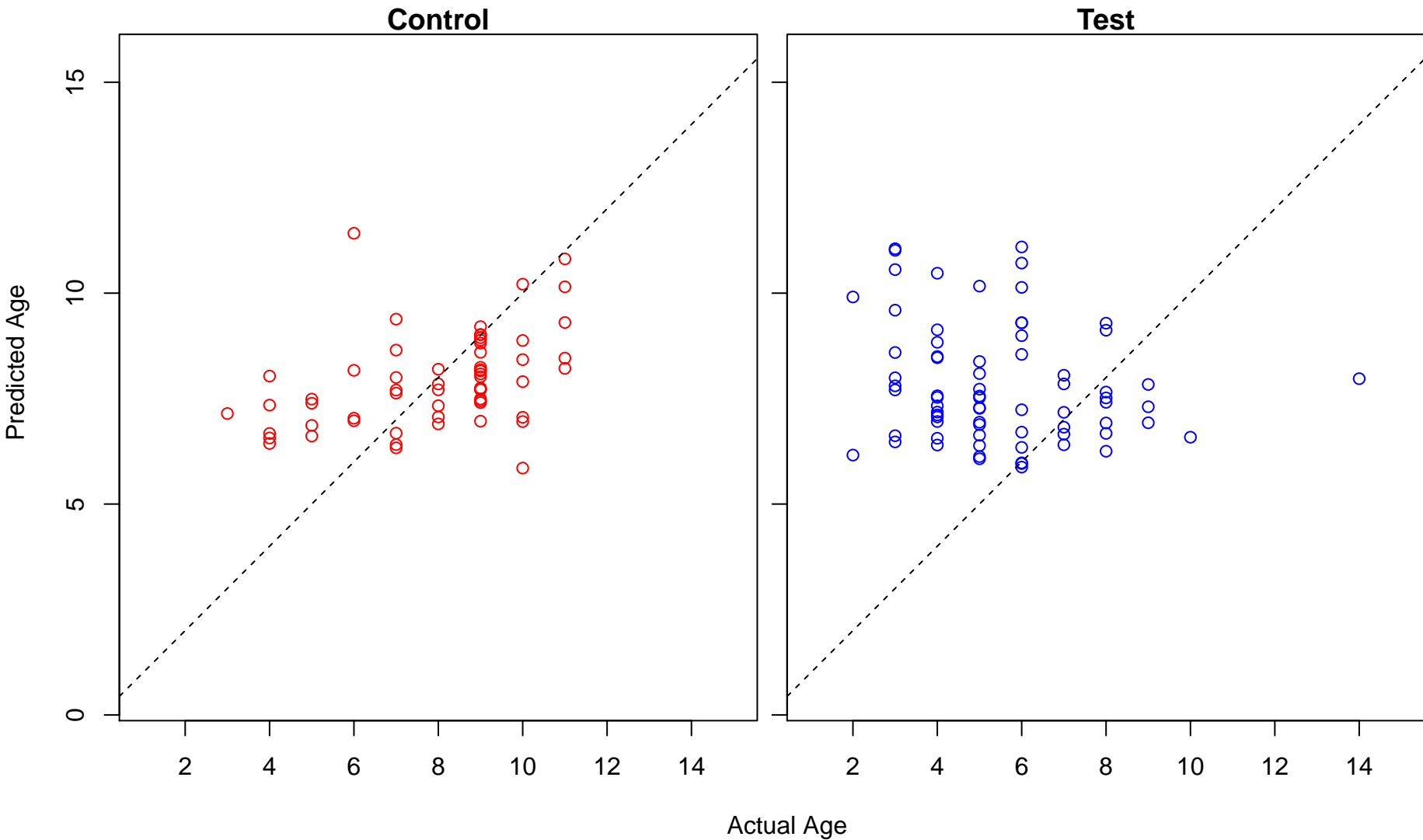
positive regulation of stress fiber assembly (Score: 0.829084)



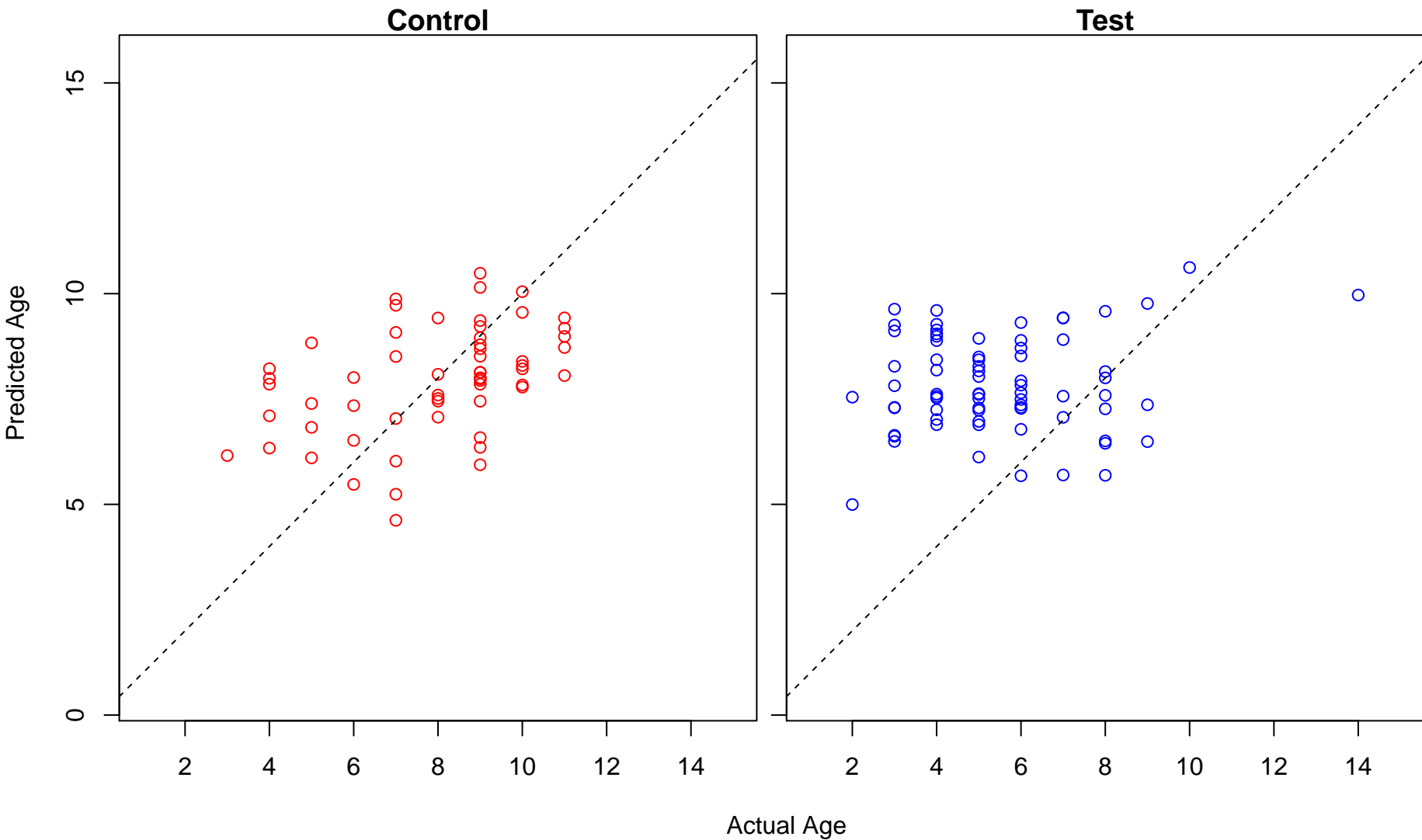
nucleobase-containing compound catabolic process (Score: 0.828713)



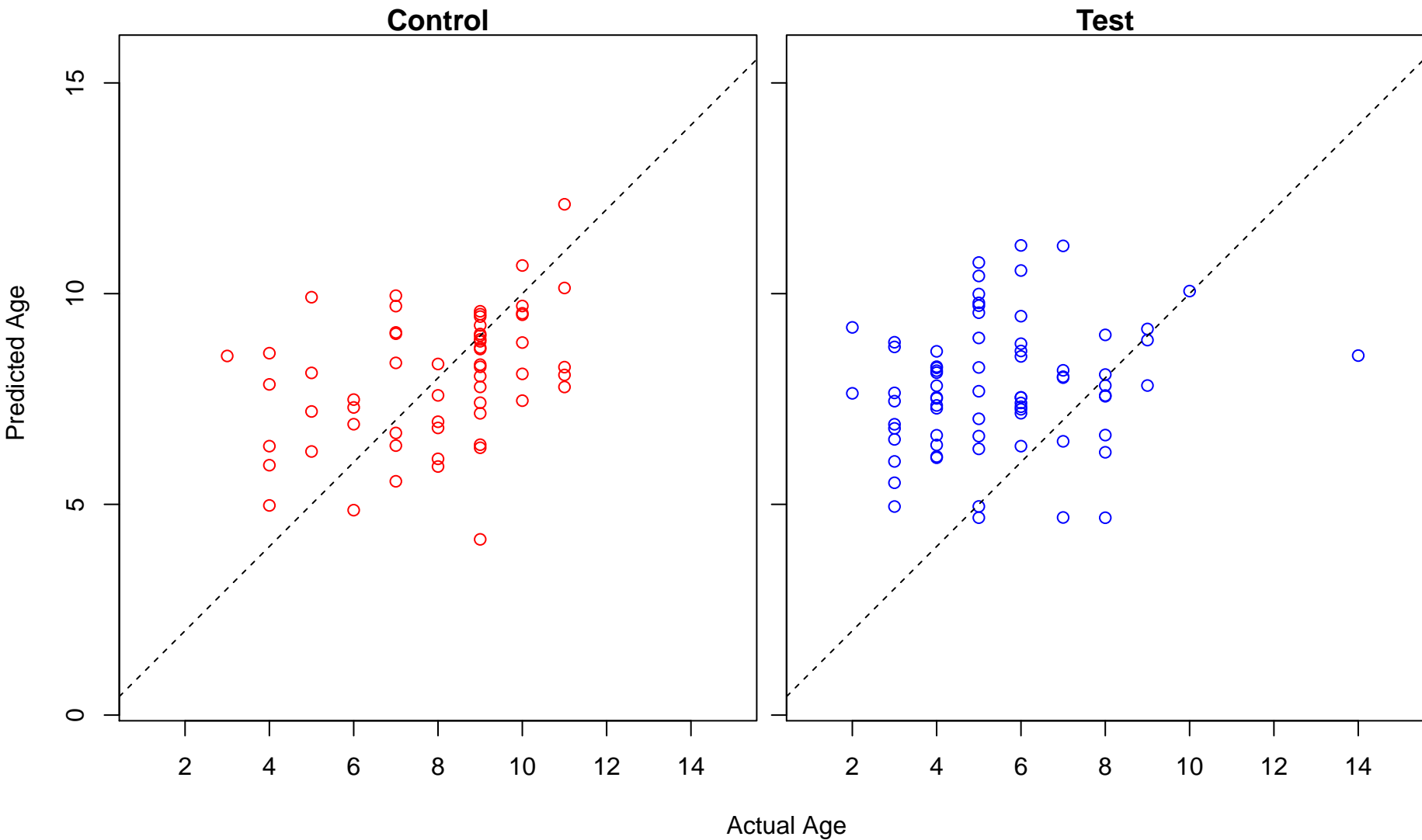
adenylate cyclase-inhibiting dopamine receptor signaling pathway (Score: 0.828172)



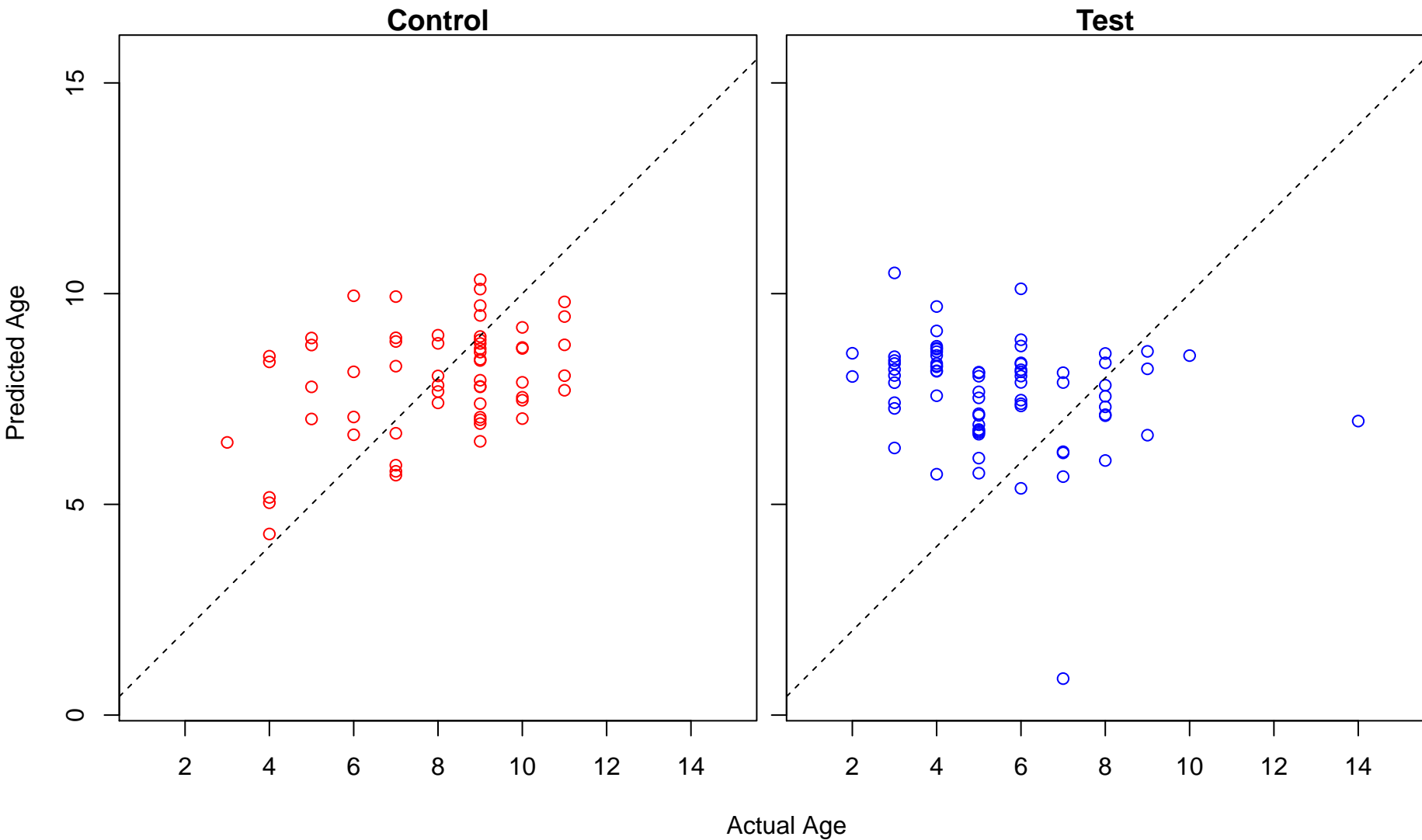
negative regulation of interleukin-6-mediated signaling pathway (Score: 0.827455)



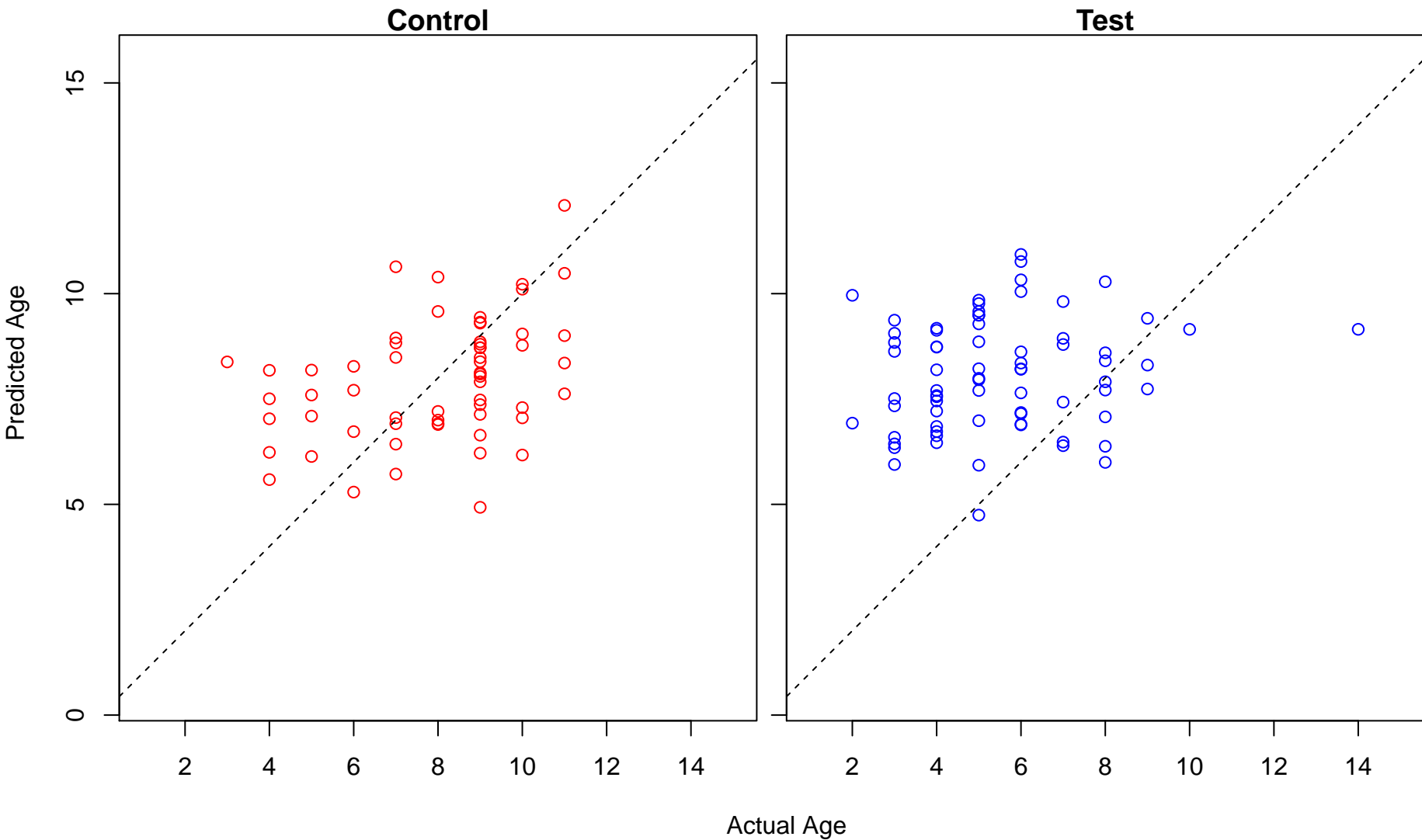
heterocycle catabolic process (Score: 0.826929)



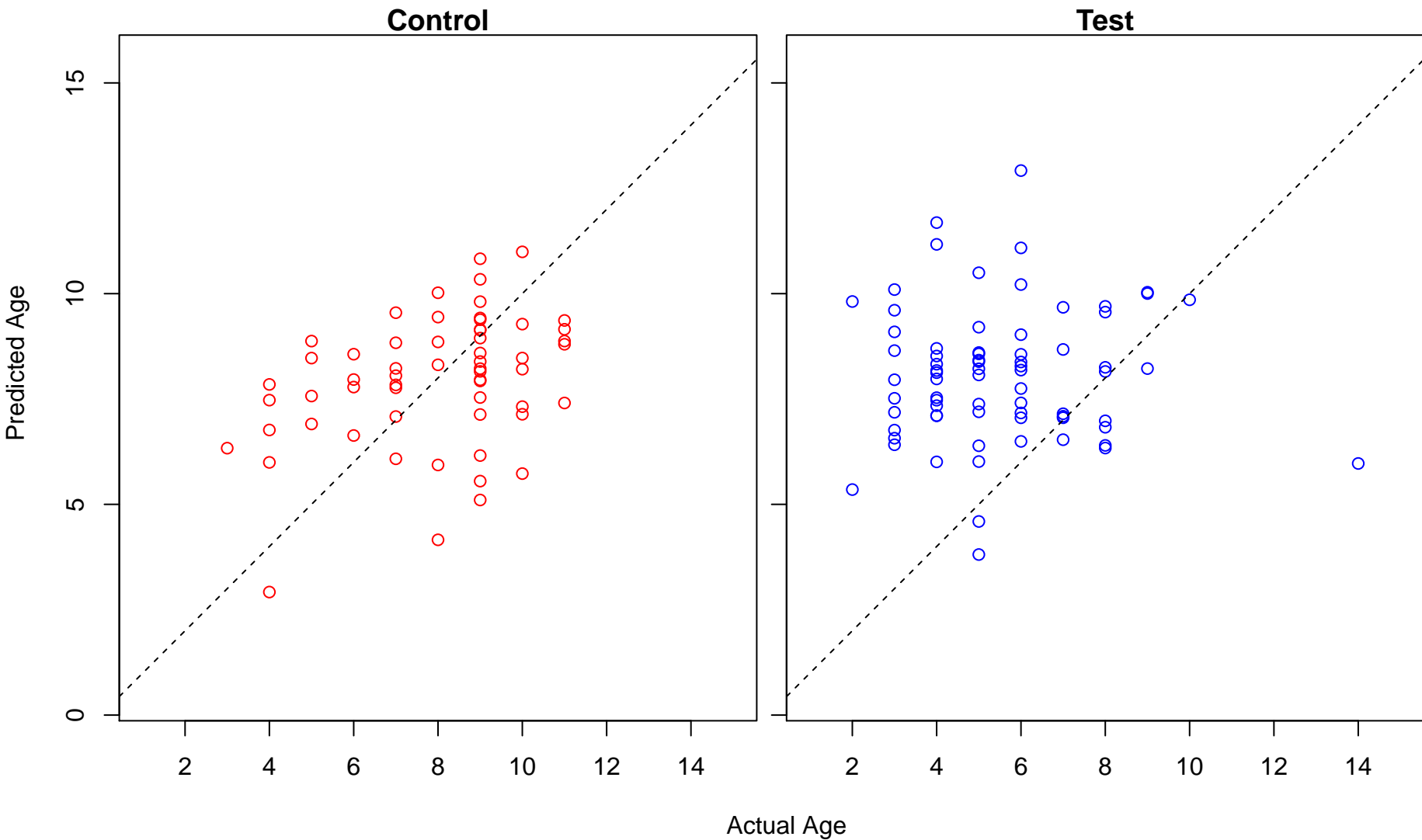
negative regulation of biomineral tissue development (Score: 0.826655)



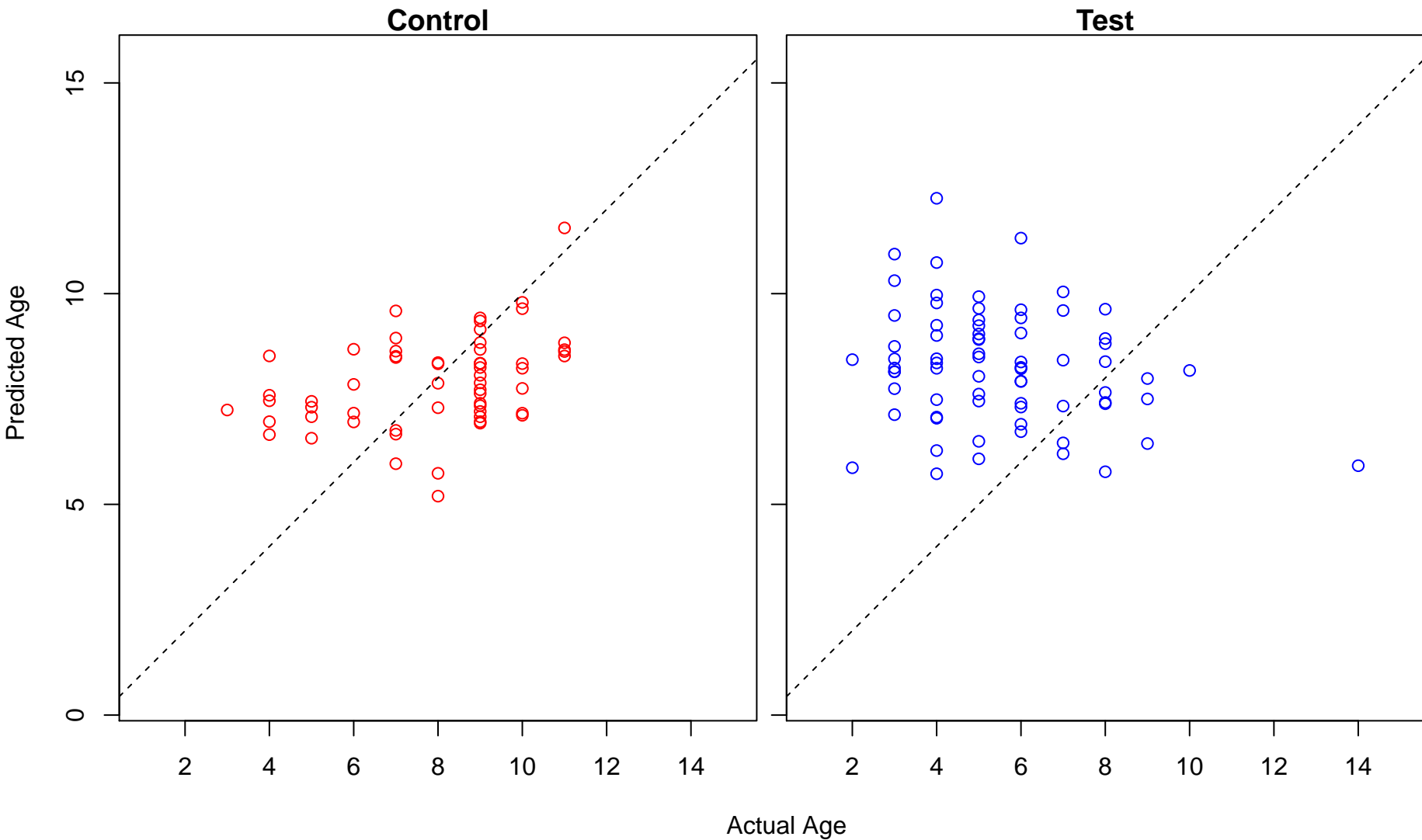
nuclear-transcribed mRNA catabolic process (Score: 0.826099)



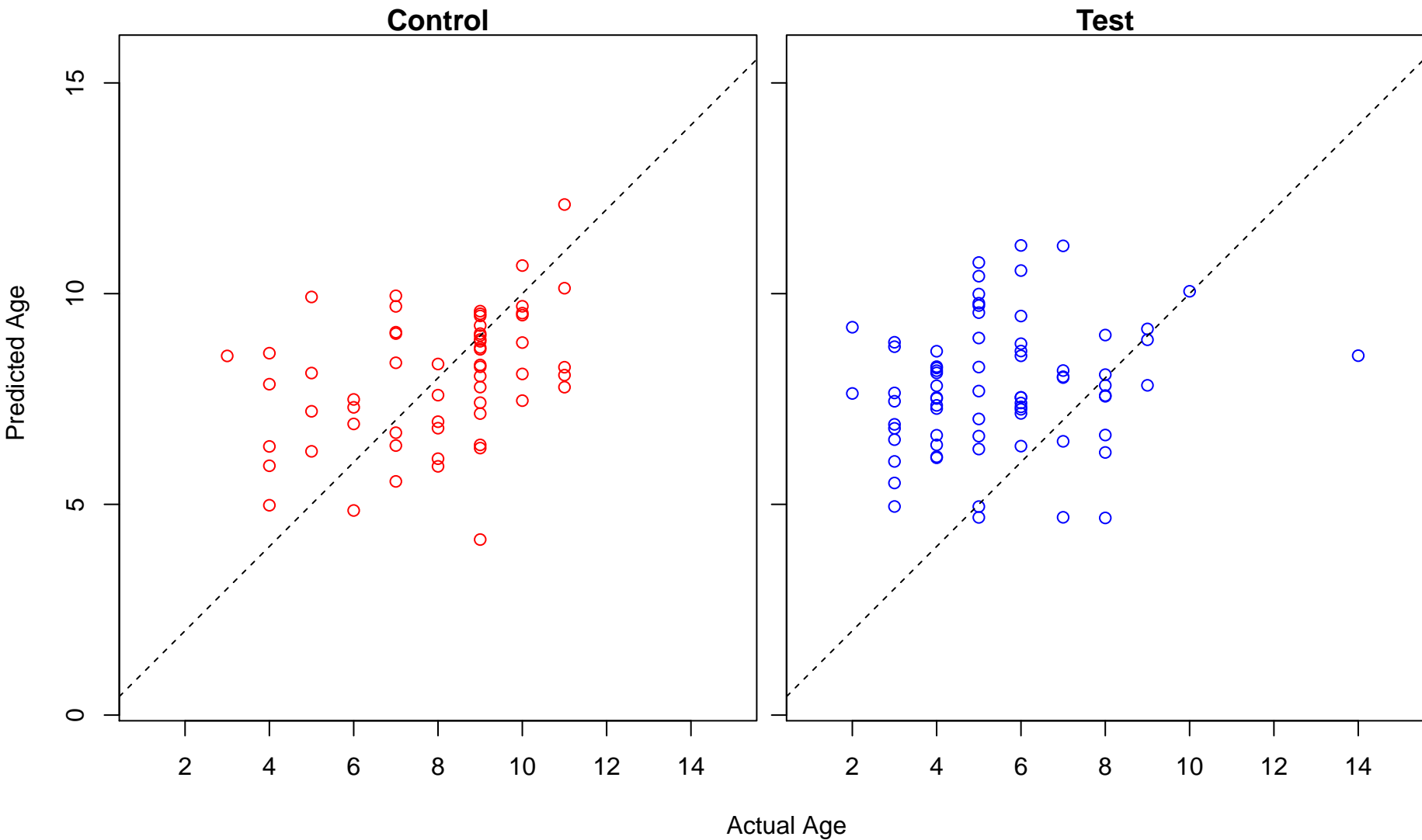
isoprenoid metabolic process (Score: 0.825743)



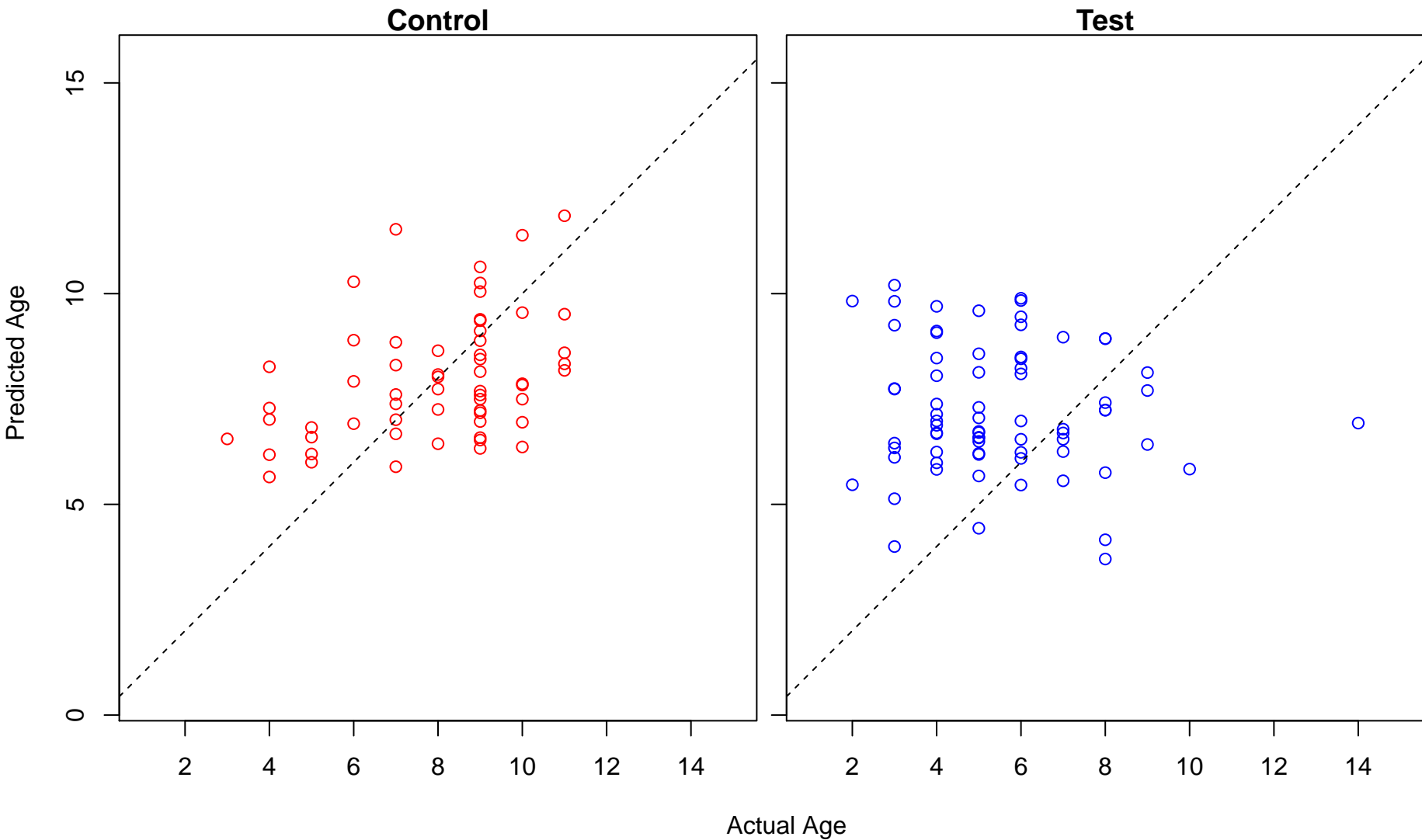
soft palate development (Score: 0.825502)



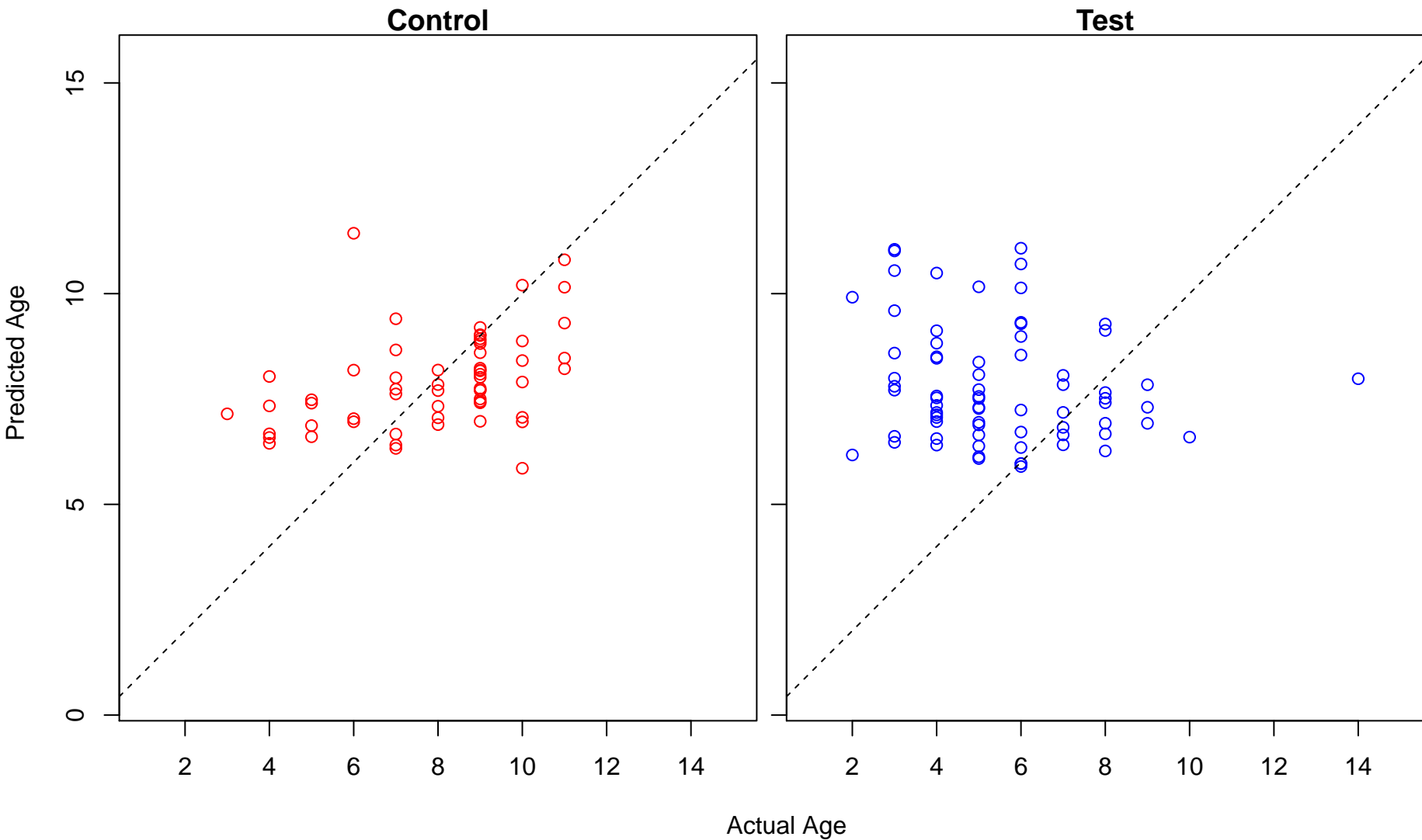
aromatic compound catabolic process (Score: 0.825211)



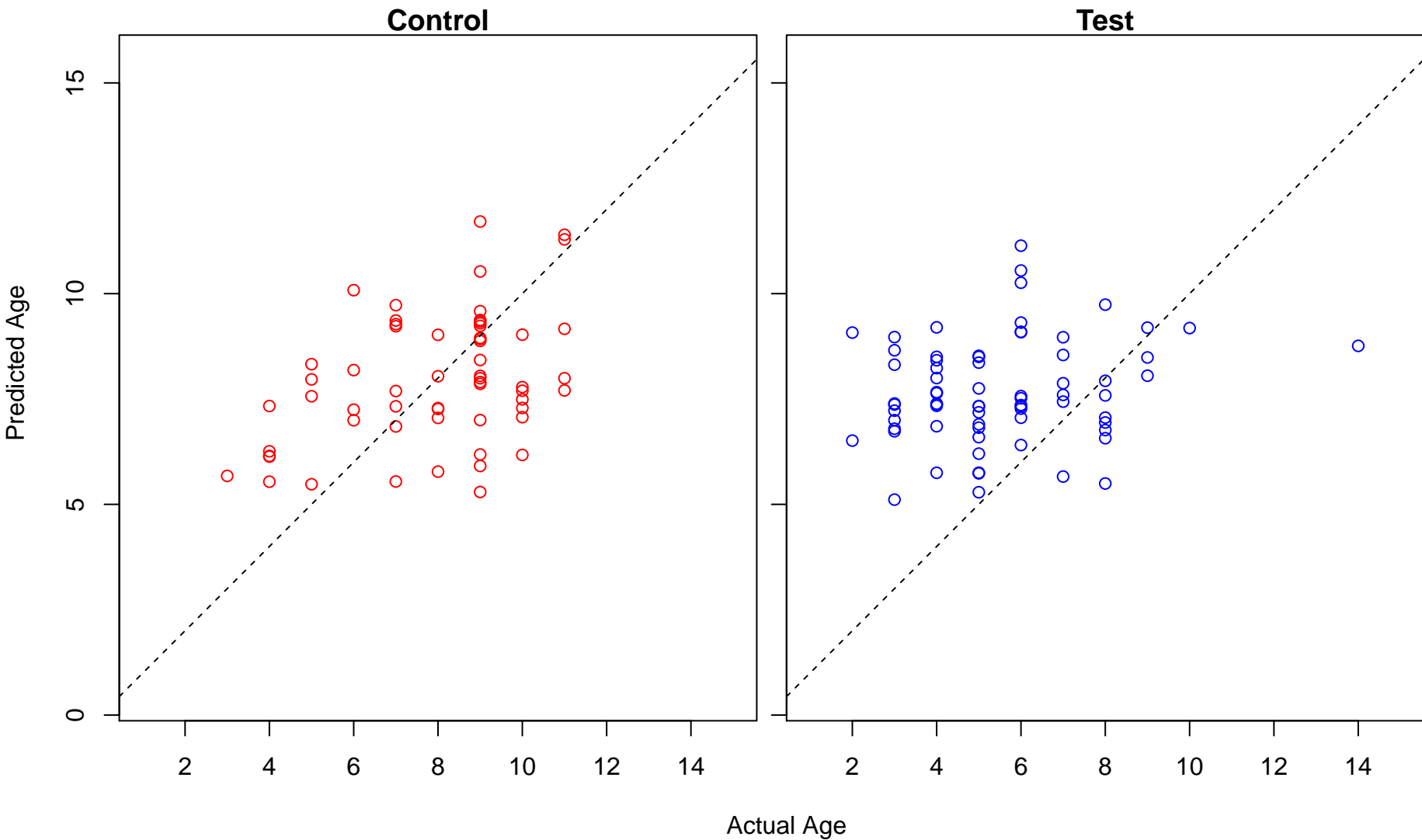
growth hormone secretion (Score: 0.824899)



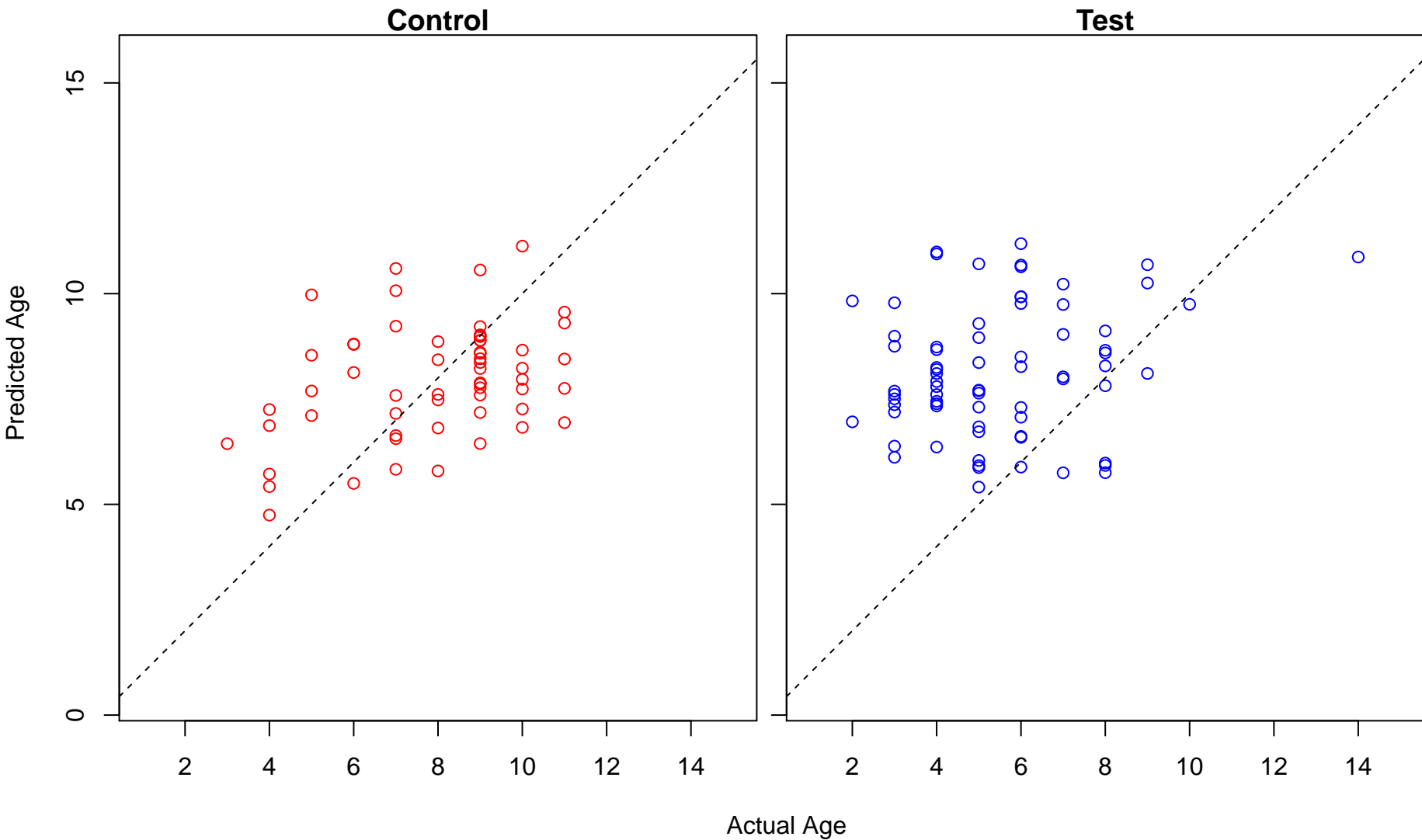
actin crosslink formation (Score: 0.824353)



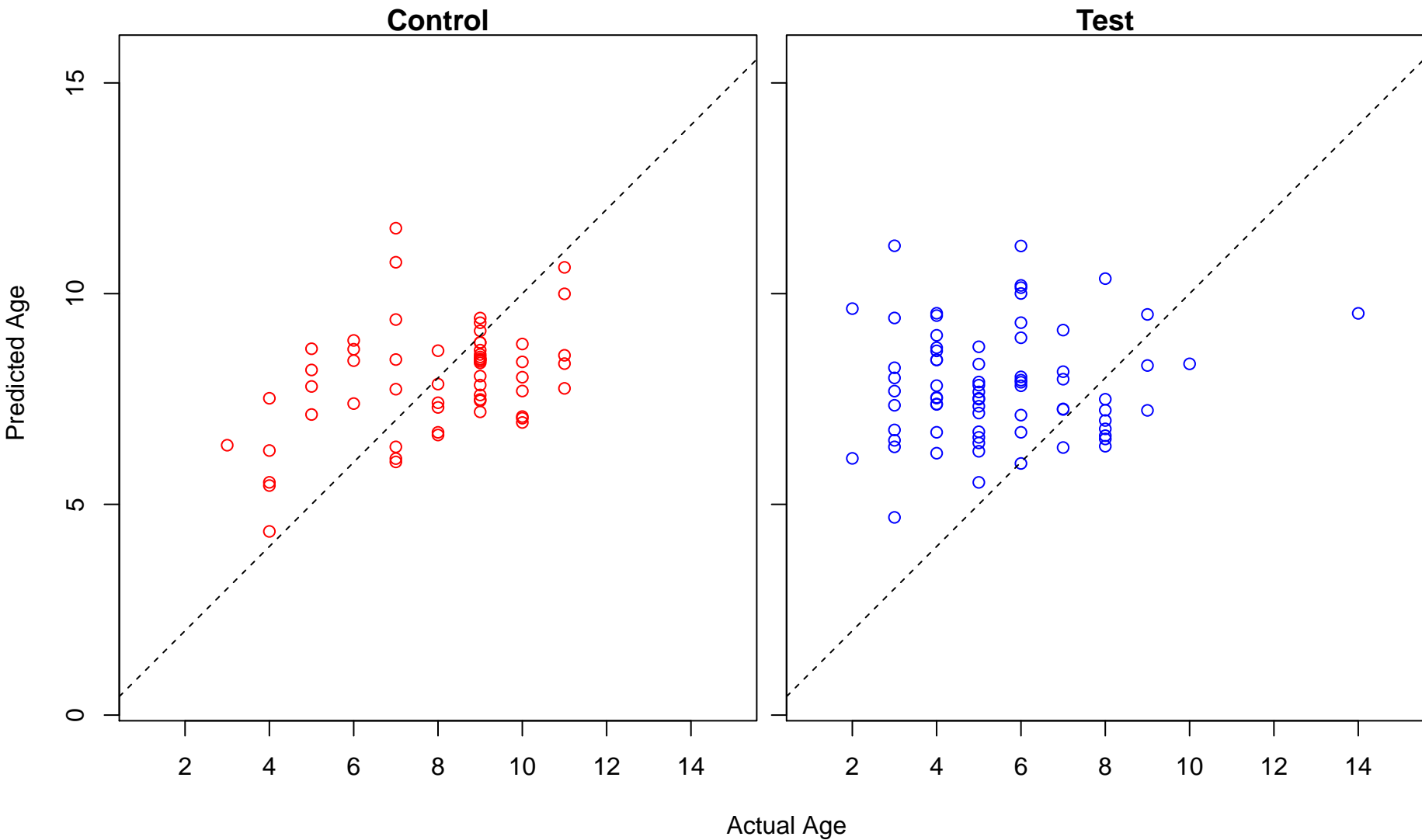
lipid localization (Score: 0.823940)



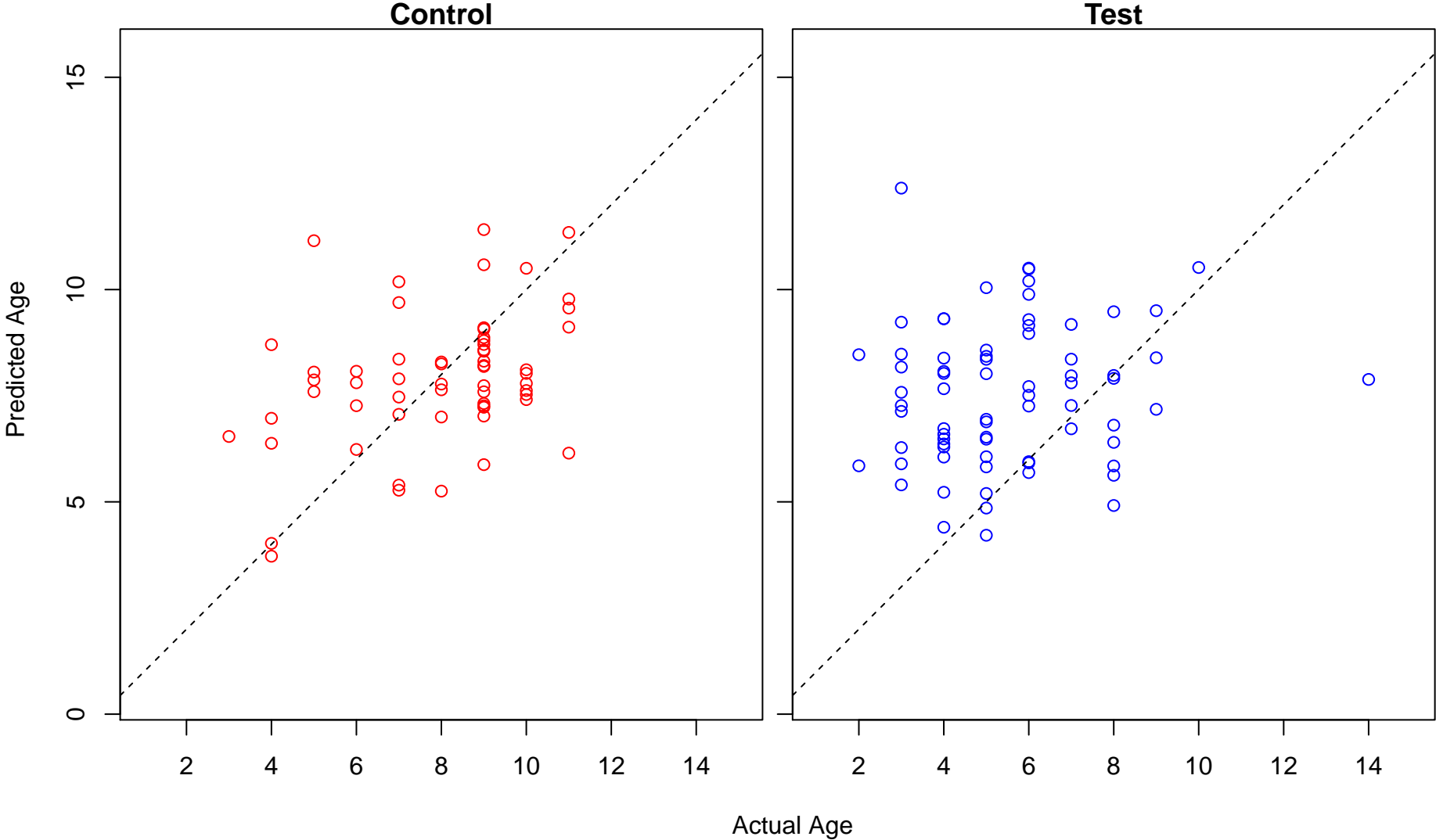
Notch signaling pathway (Score: 0.823116)



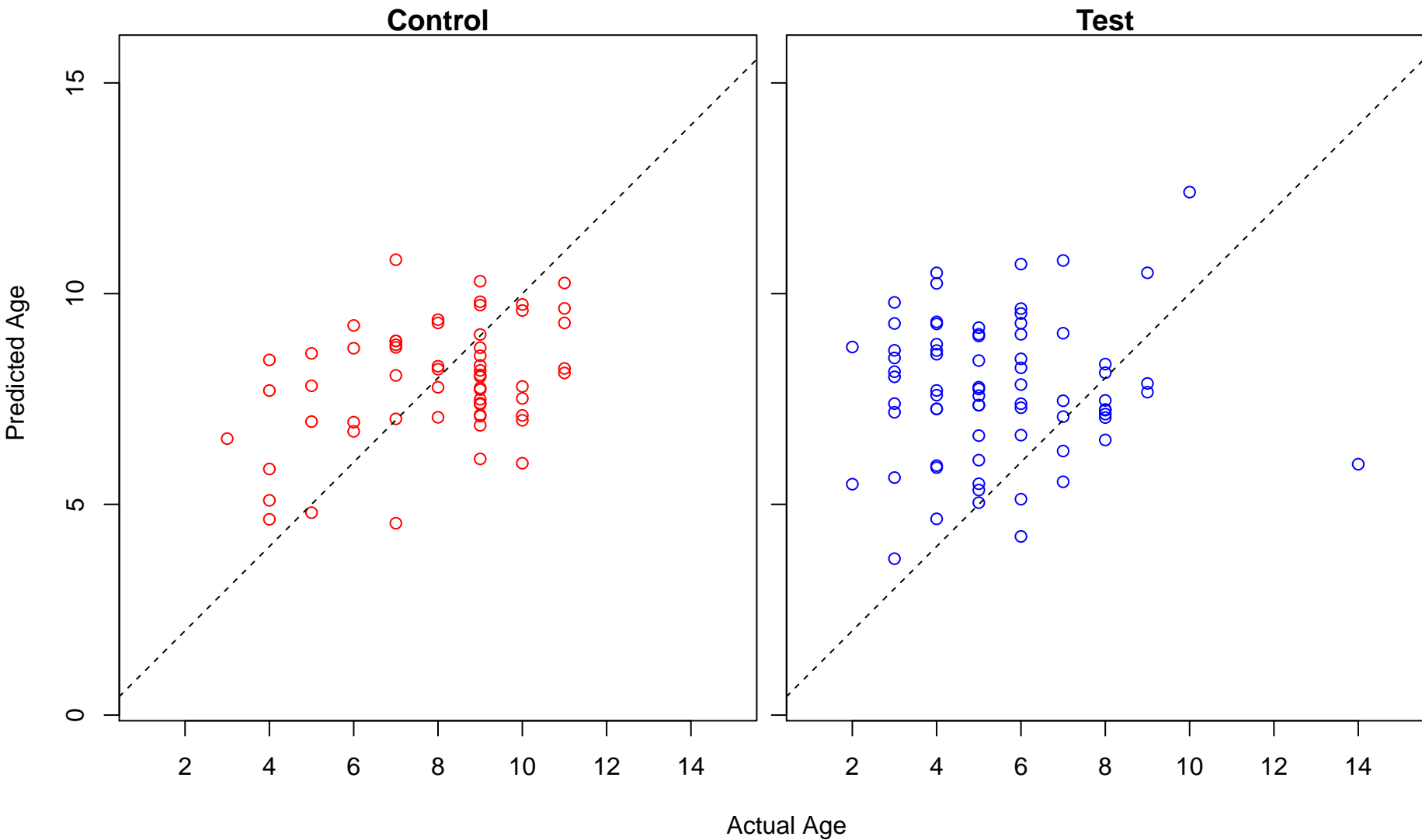
forebrain development (Score: 0.822611)



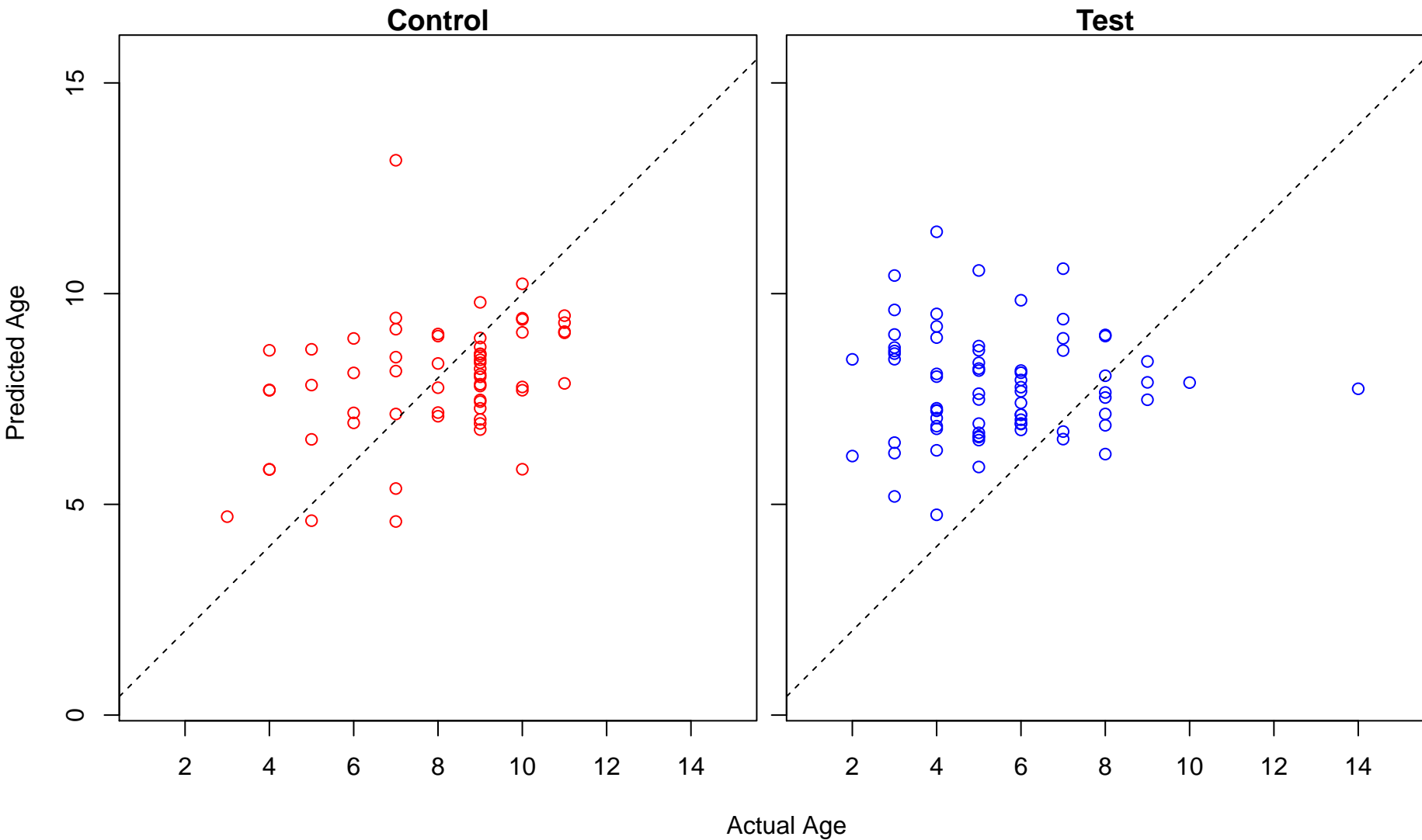
cytoplasmic pattern recognition receptor signaling pathway (Score: 0.822189)



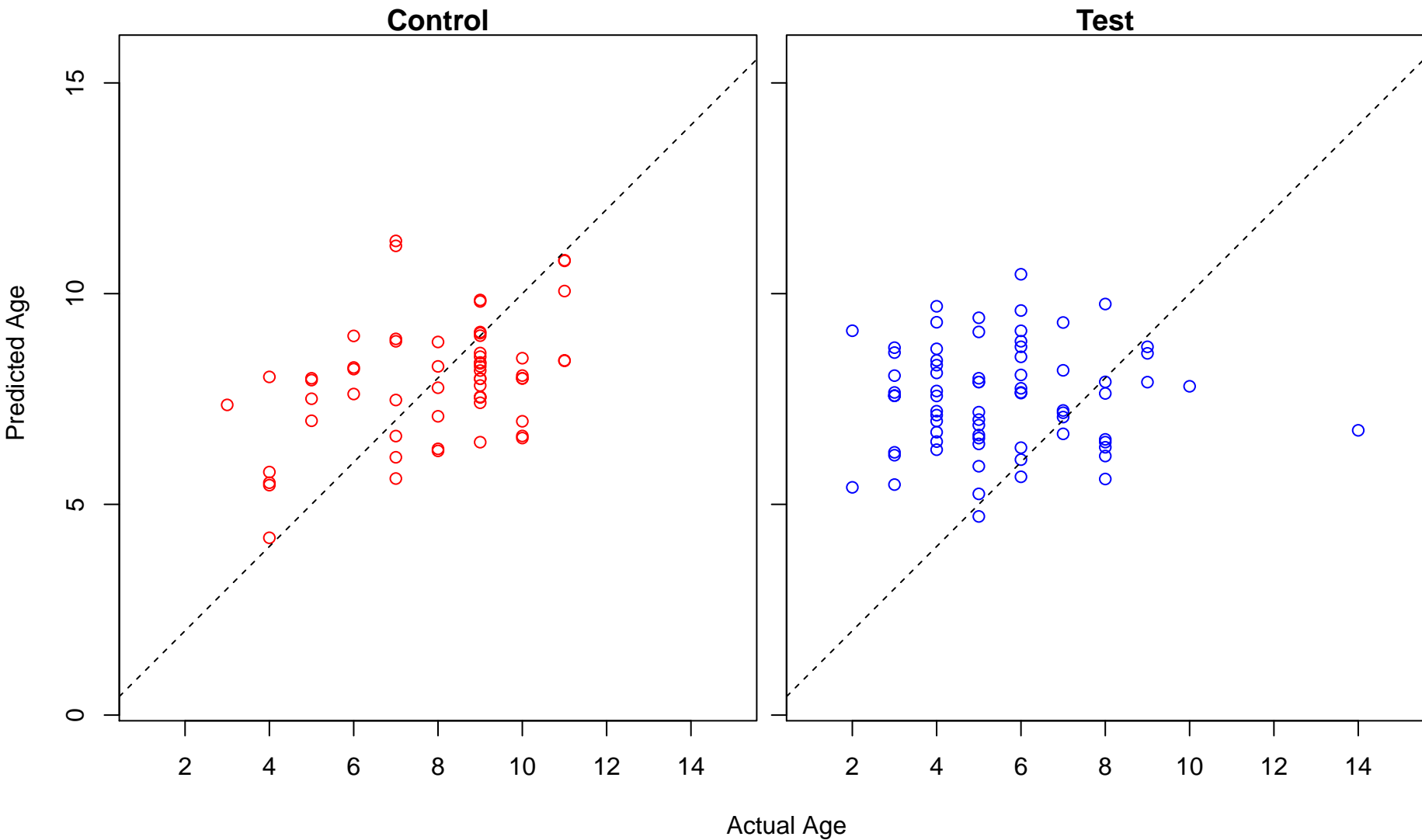
positive regulation of T cell differentiation (Score: 0.822103)



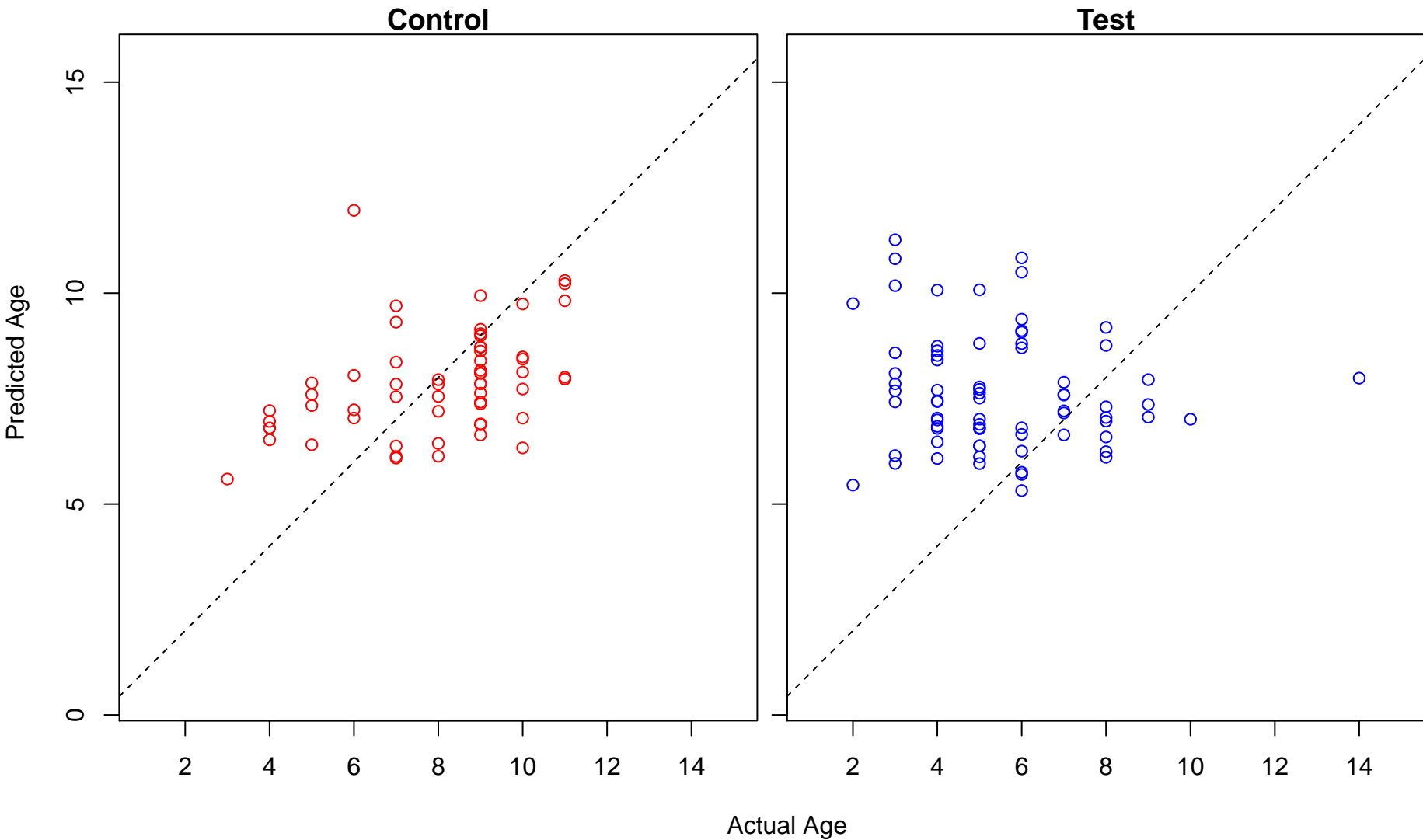
positive regulation of syncytium formation by plasma membrane fusion (Score: 0.821507)



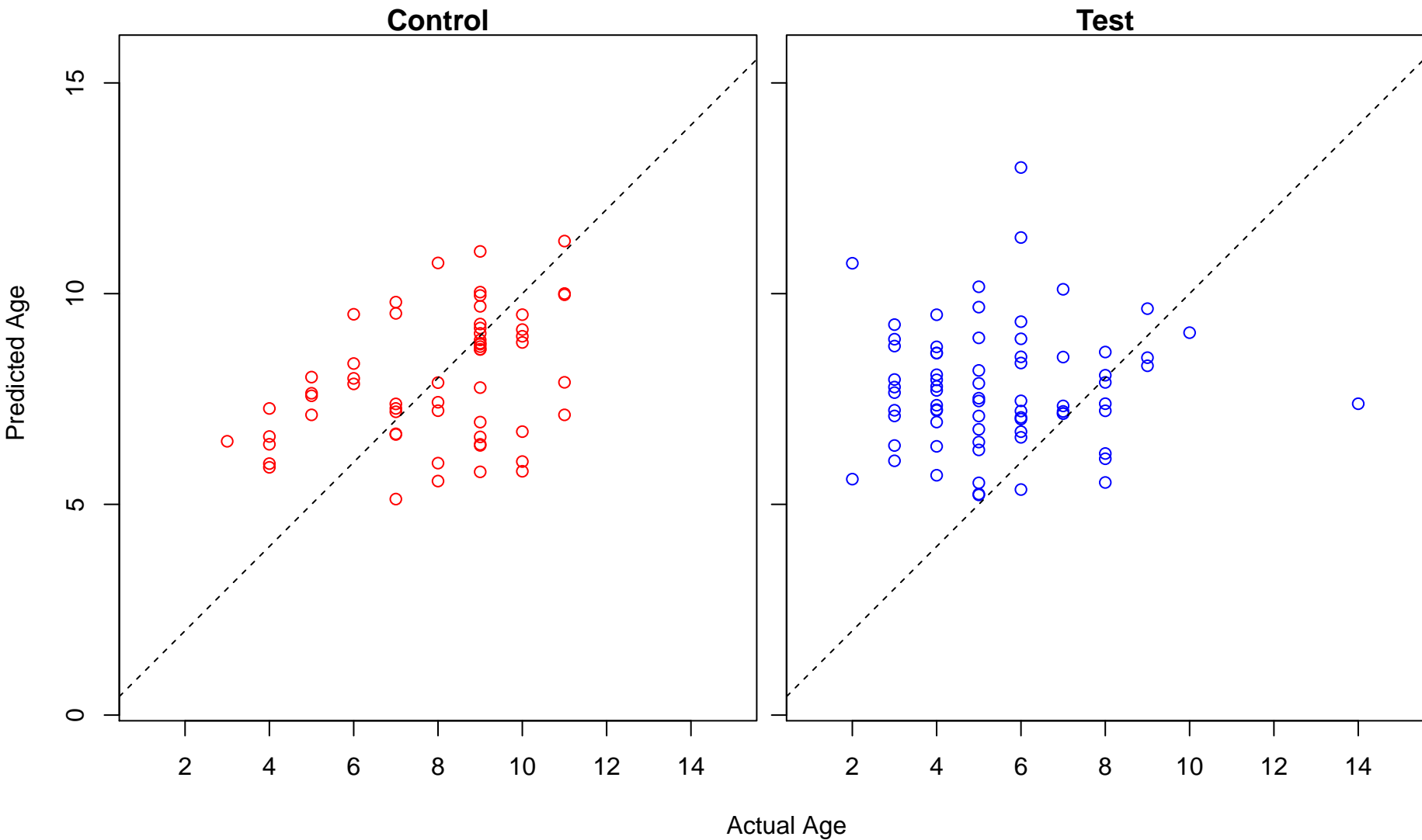
regulation of cell shape (Score: 0.821122)



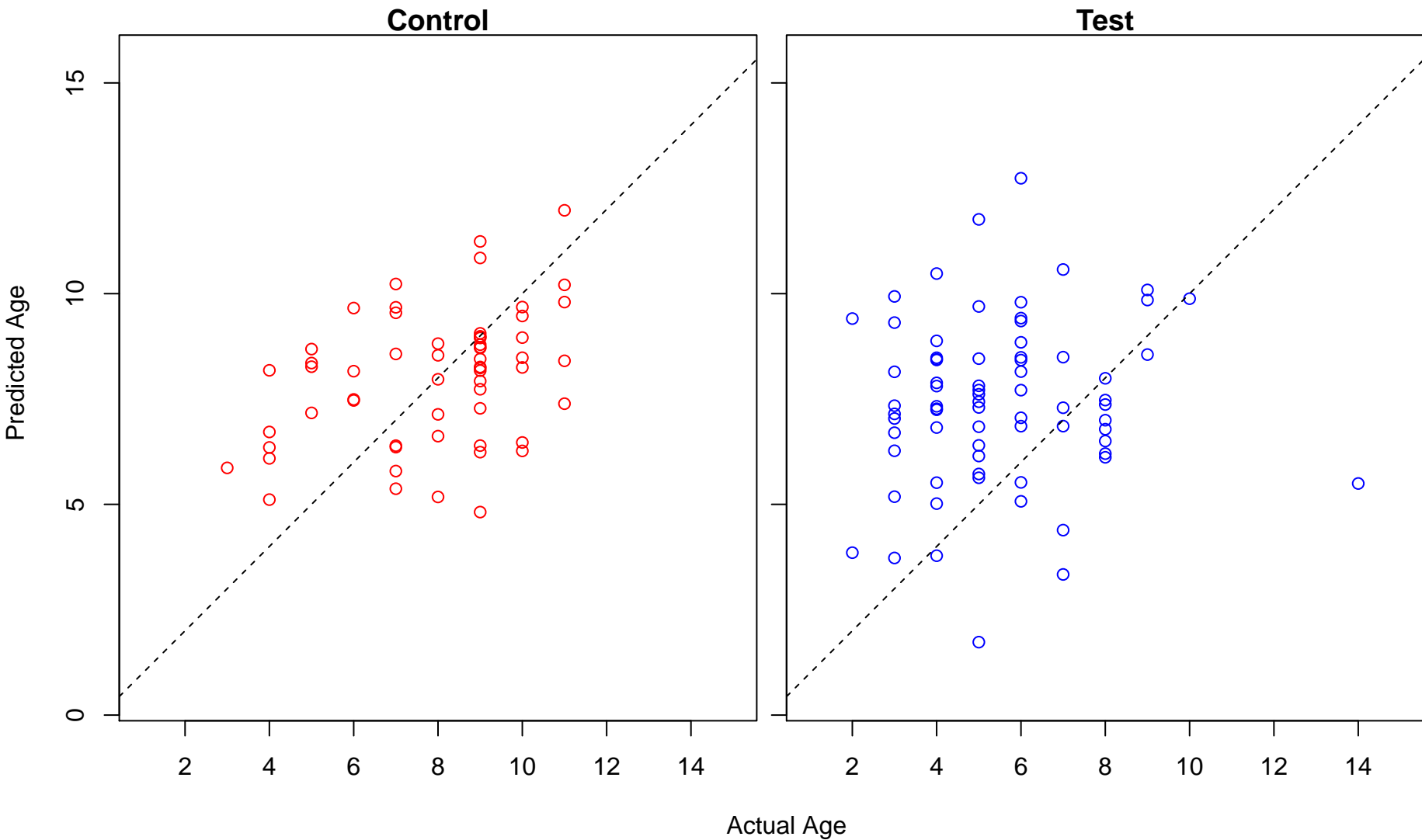
adenylate cyclase–modulating G–protein coupled receptor signaling pathway (Score: 0.820134)



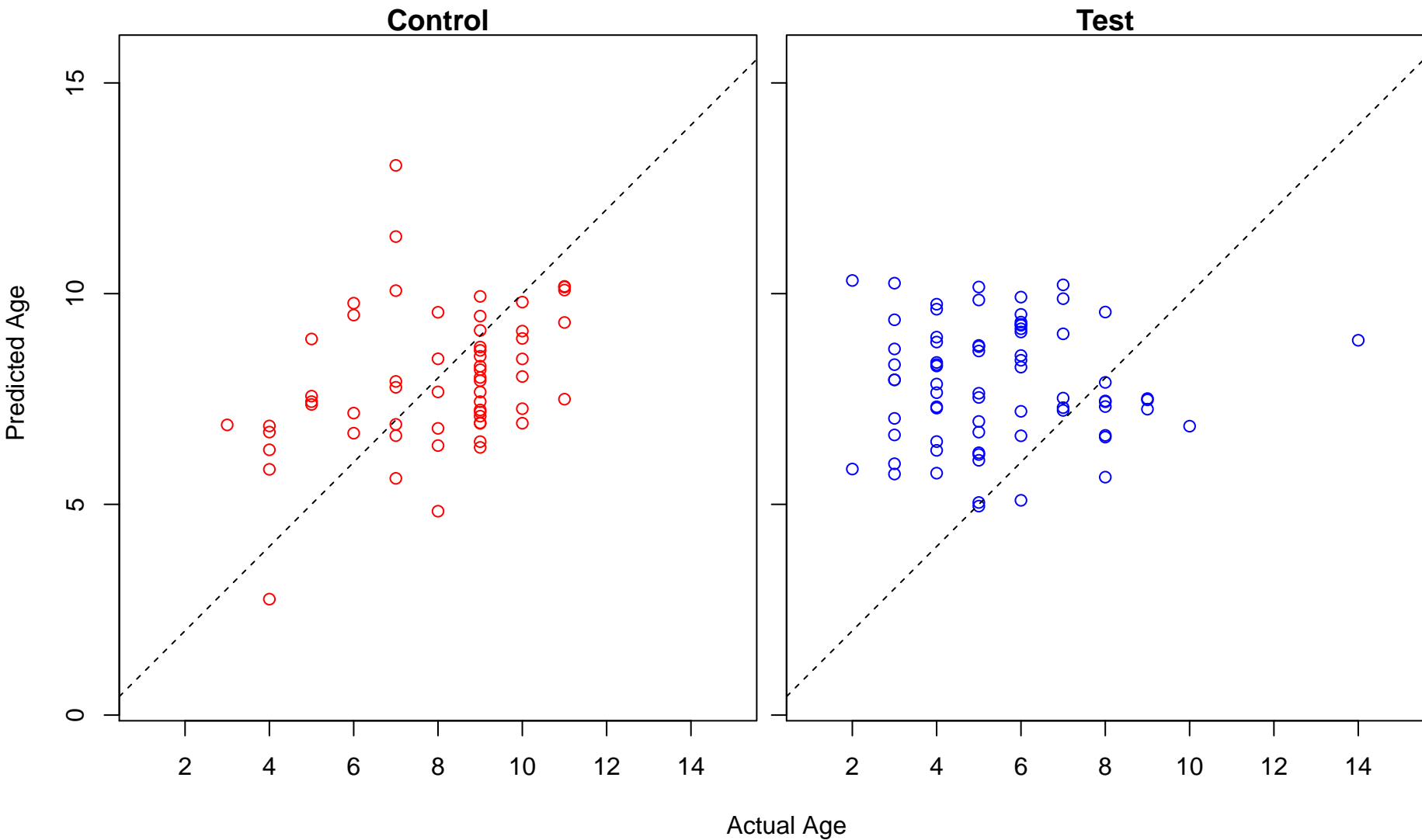
regulation of endopeptidase activity (Score: 0.819683)



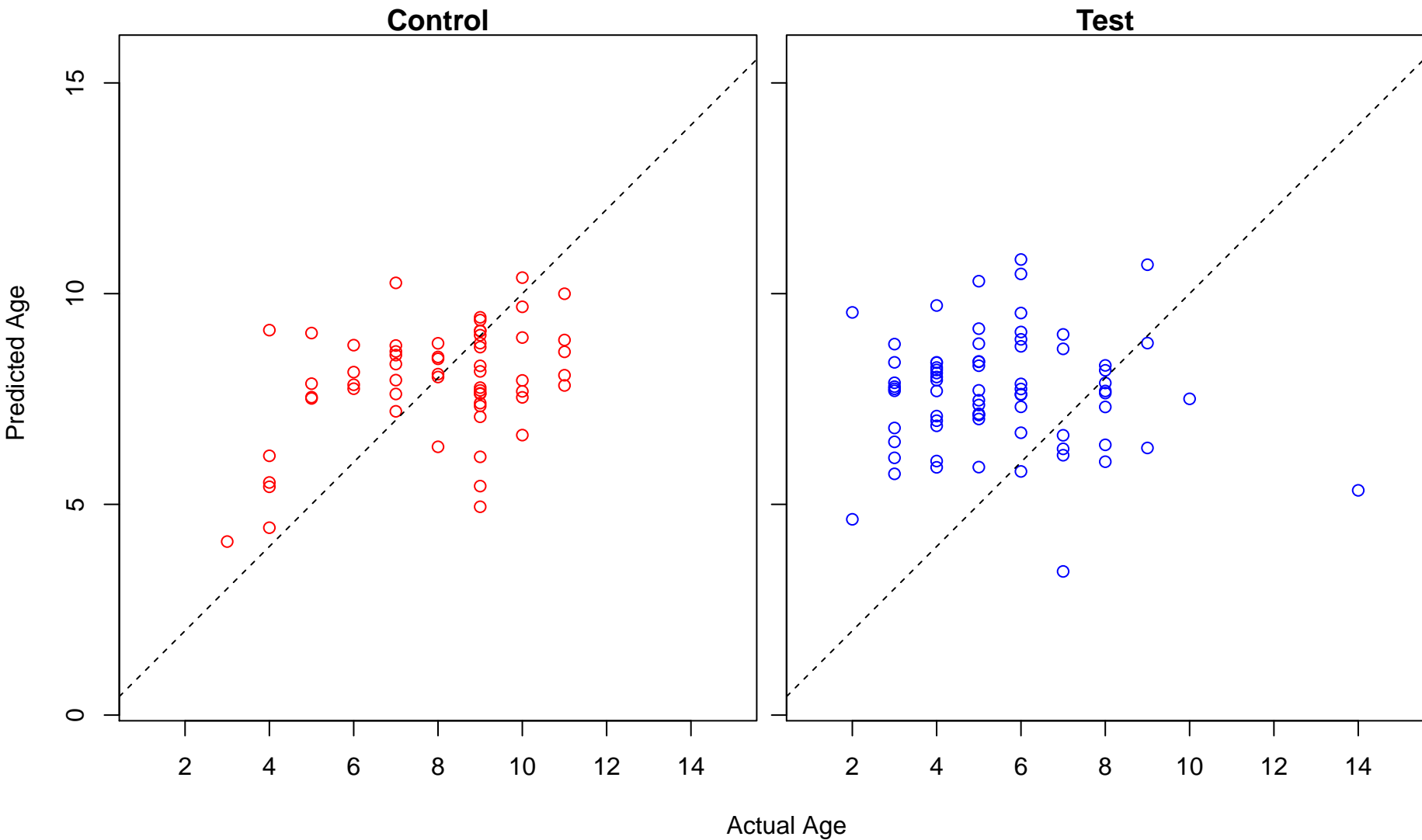
negative regulation of transferase activity (Score: 0.819174)



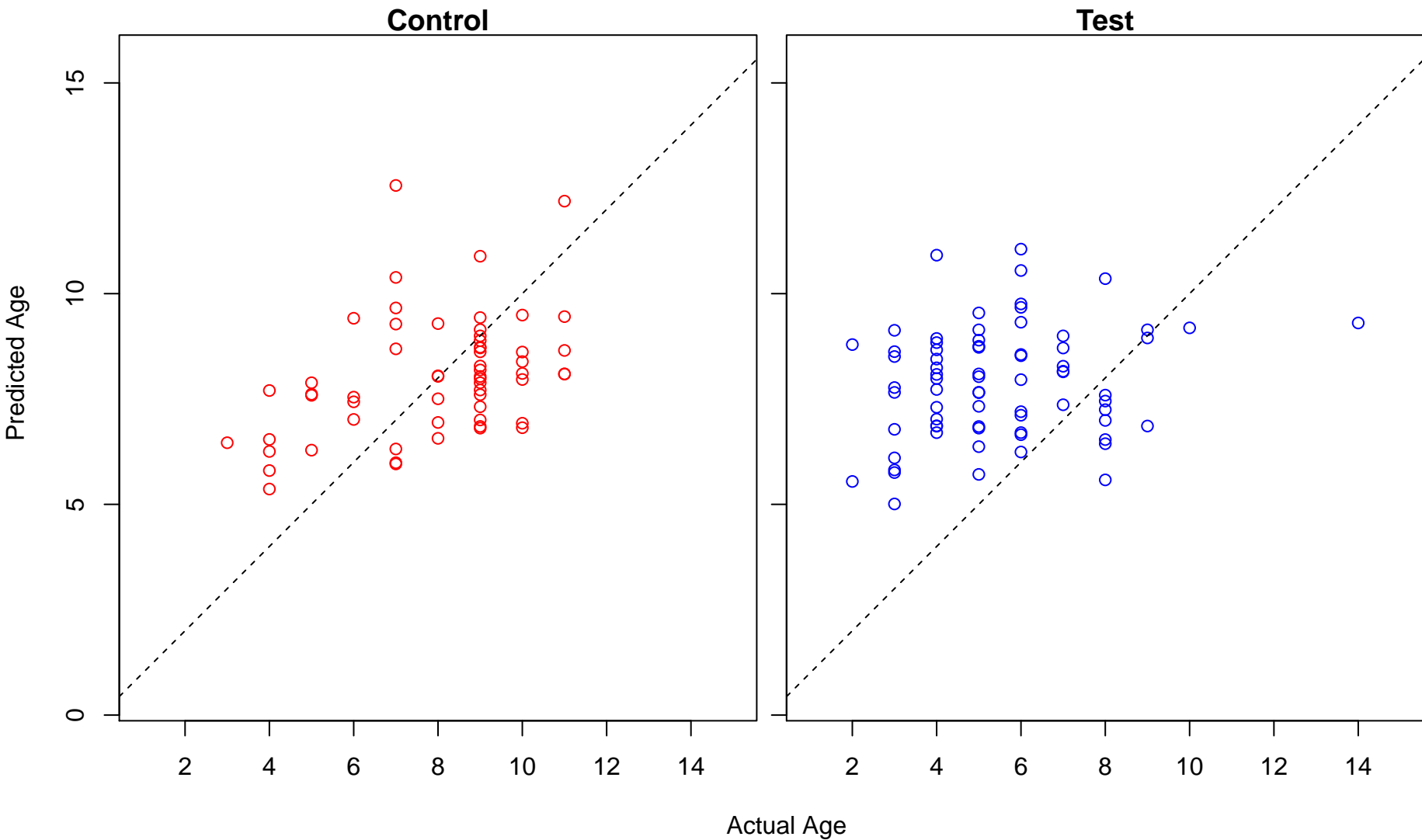
amine metabolic process (Score: 0.819055)



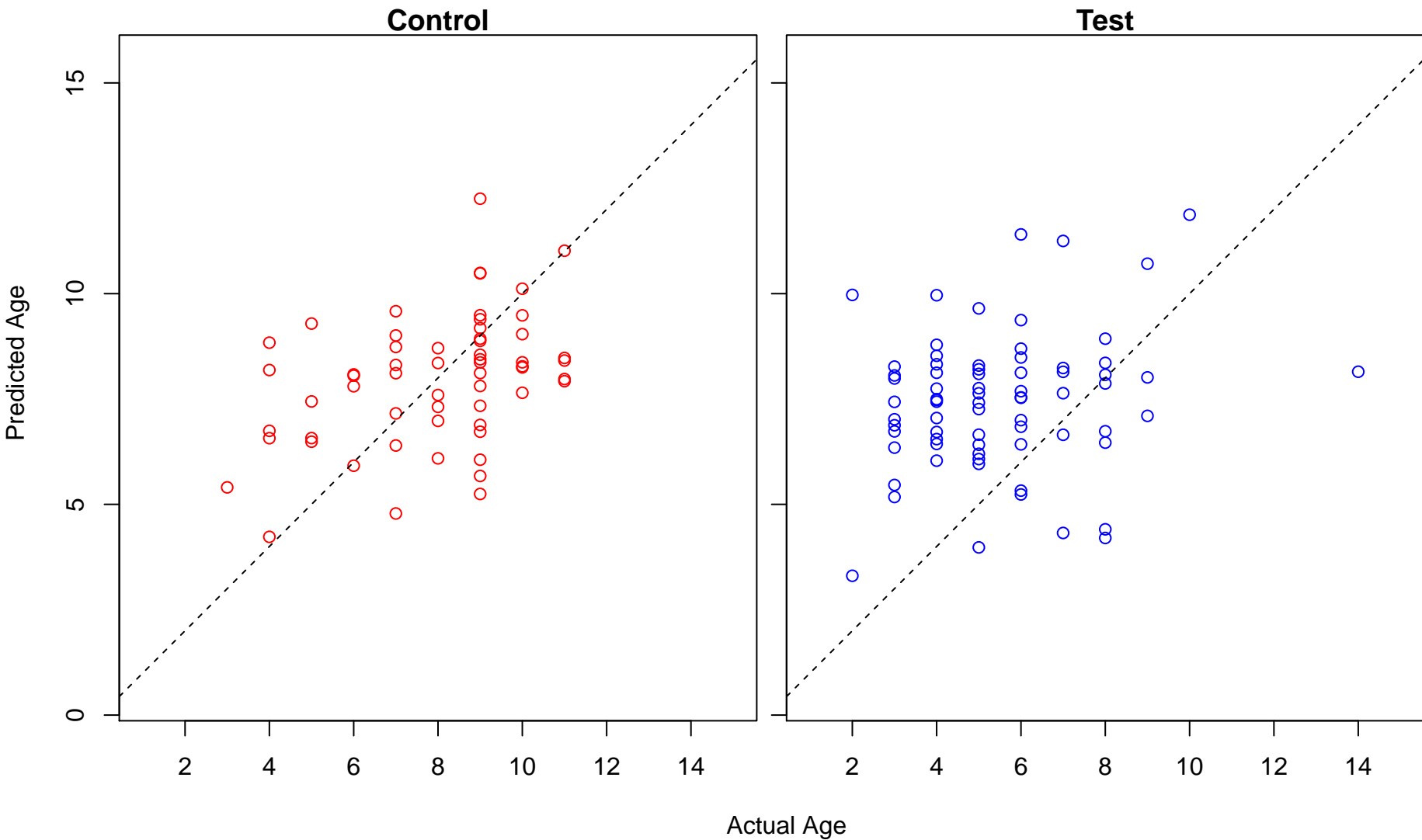
regulation of ATP biosynthetic process (Score: 0.818844)



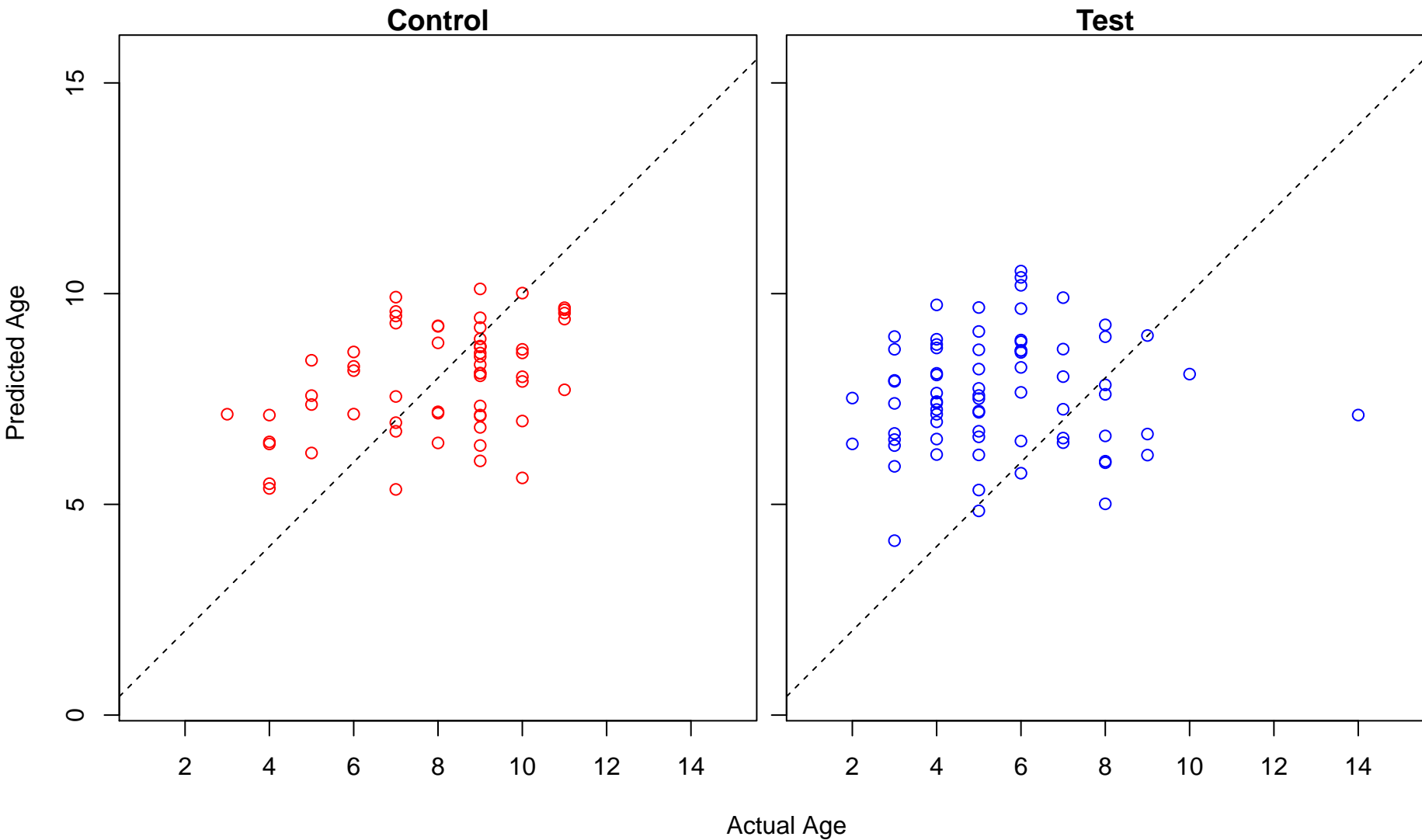
hindbrain radial glia guided cell migration (Score: 0.818742)



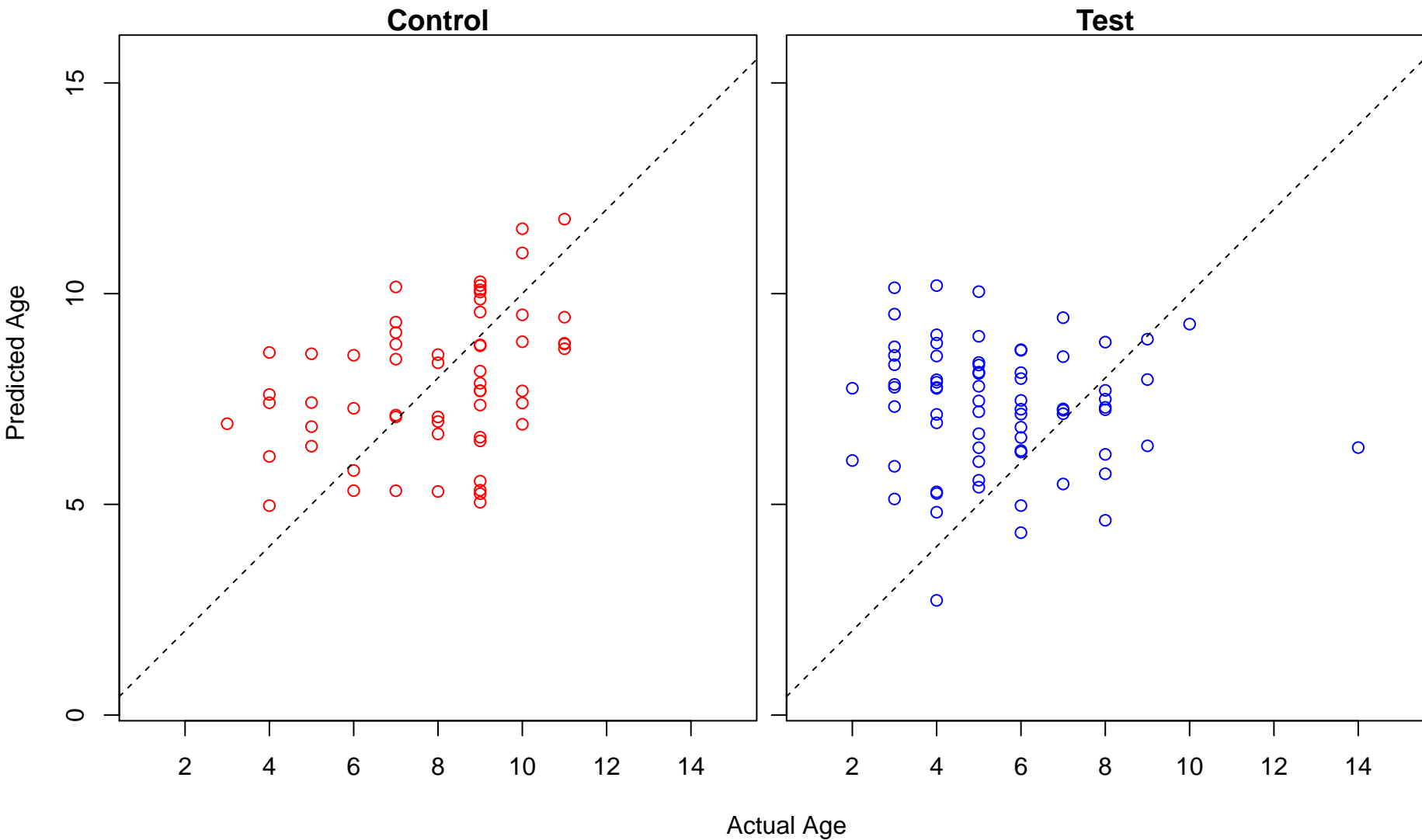
regulation of interleukin-12 production (Score: 0.816312)



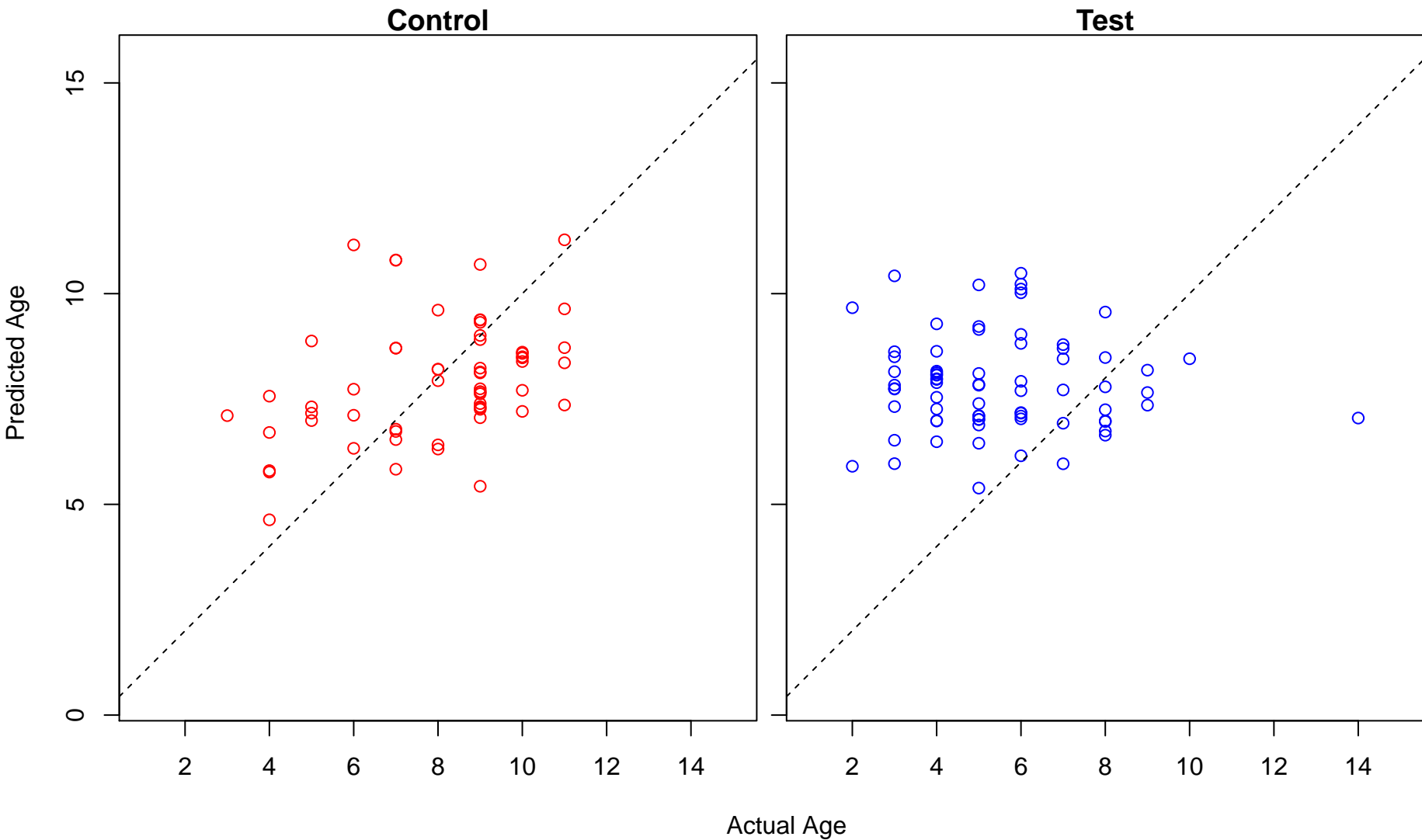
positive regulation of cellular carbohydrate metabolic process (Score: 0.816070)



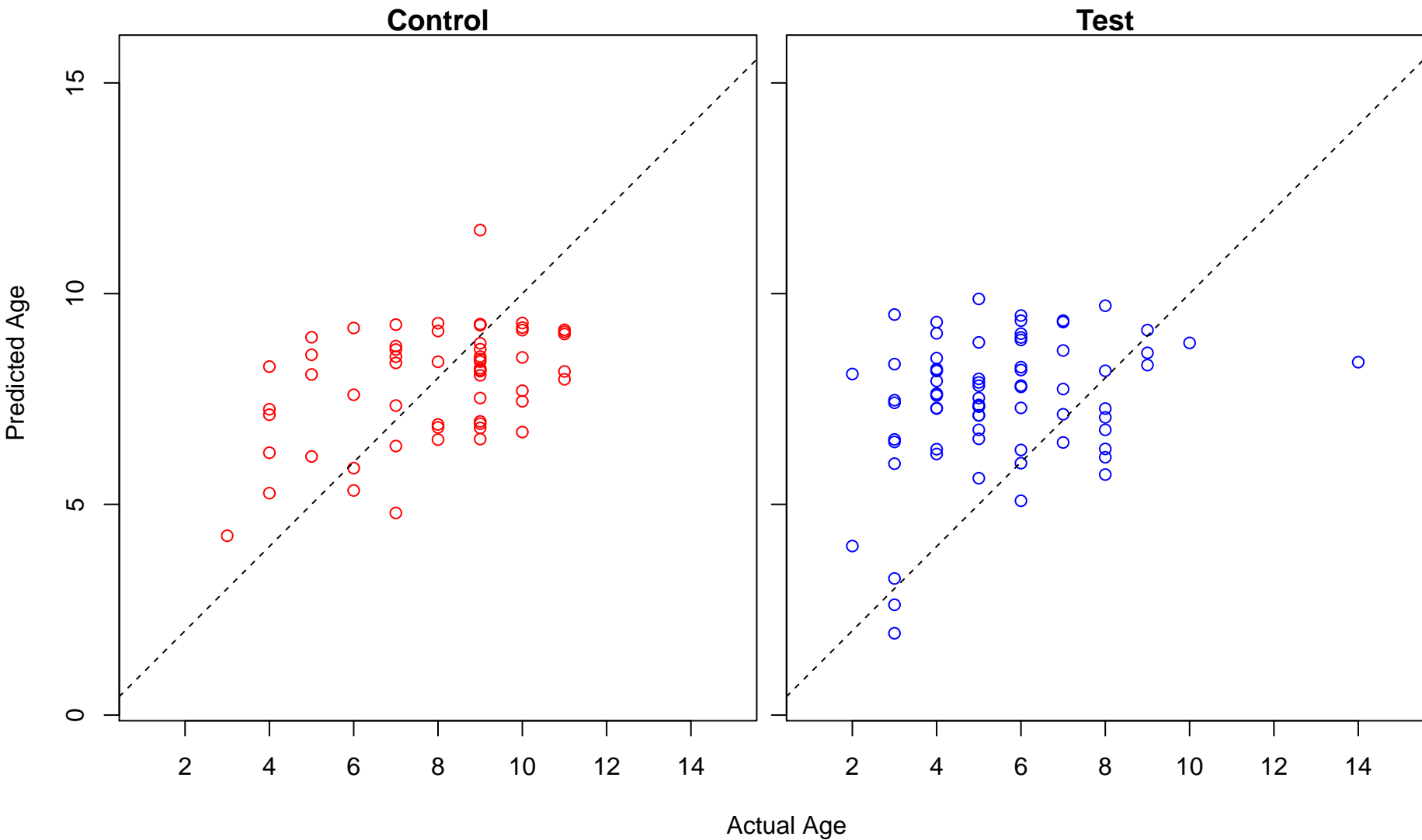
polysaccharide biosynthetic process (Score: 0.815389)



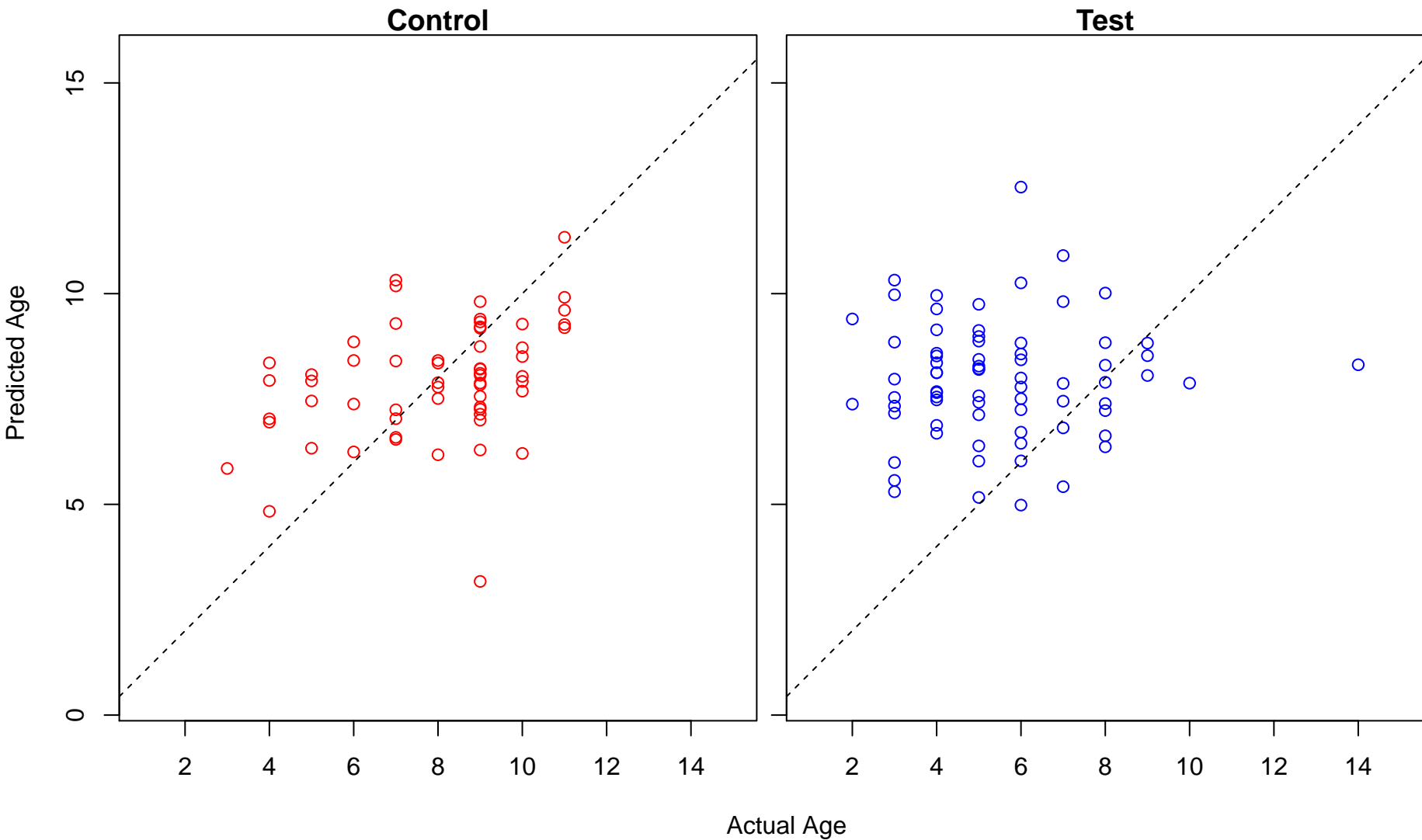
regulation of axonogenesis (Score: 0.815192)



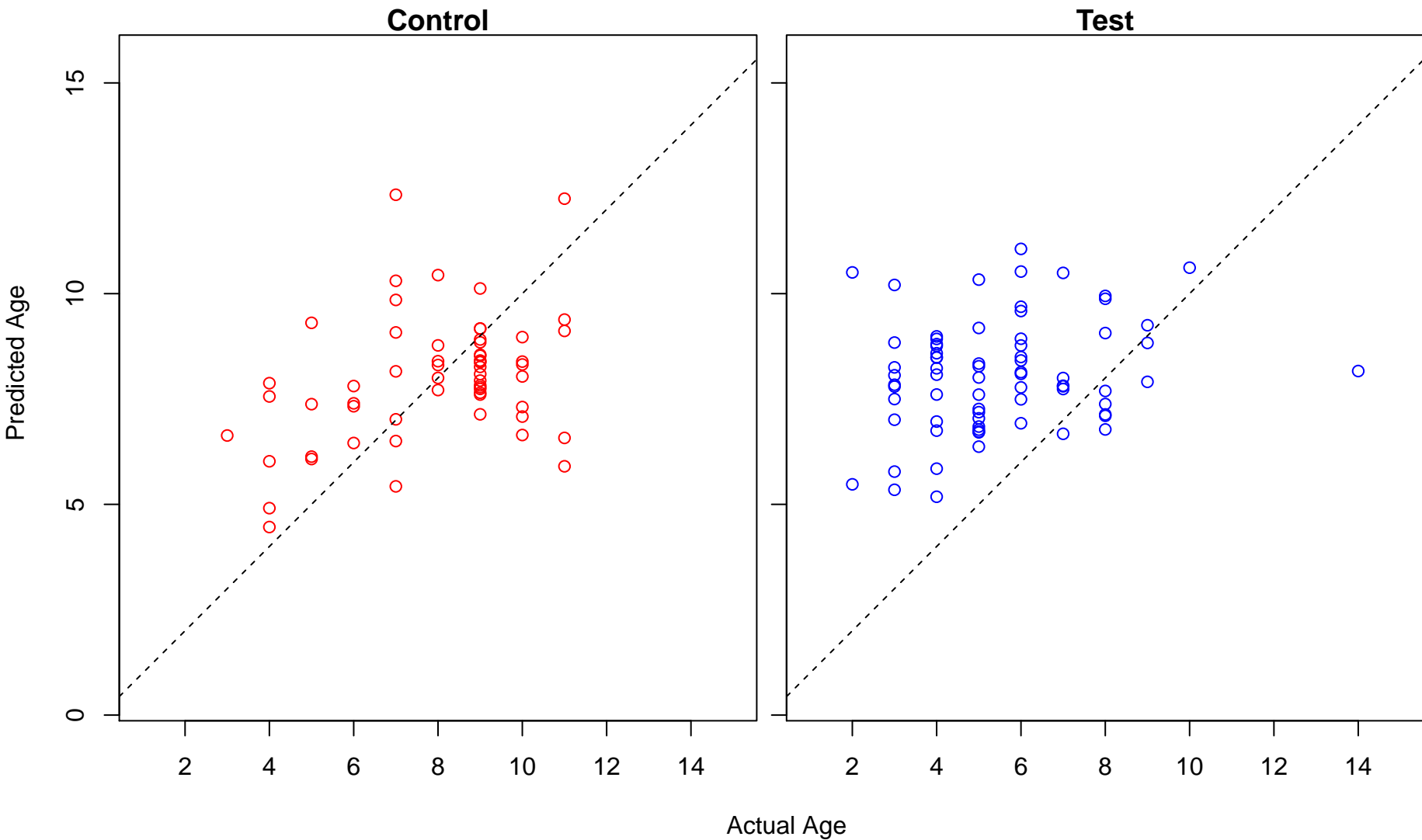
nephron tubule formation (Score: 0.814804)



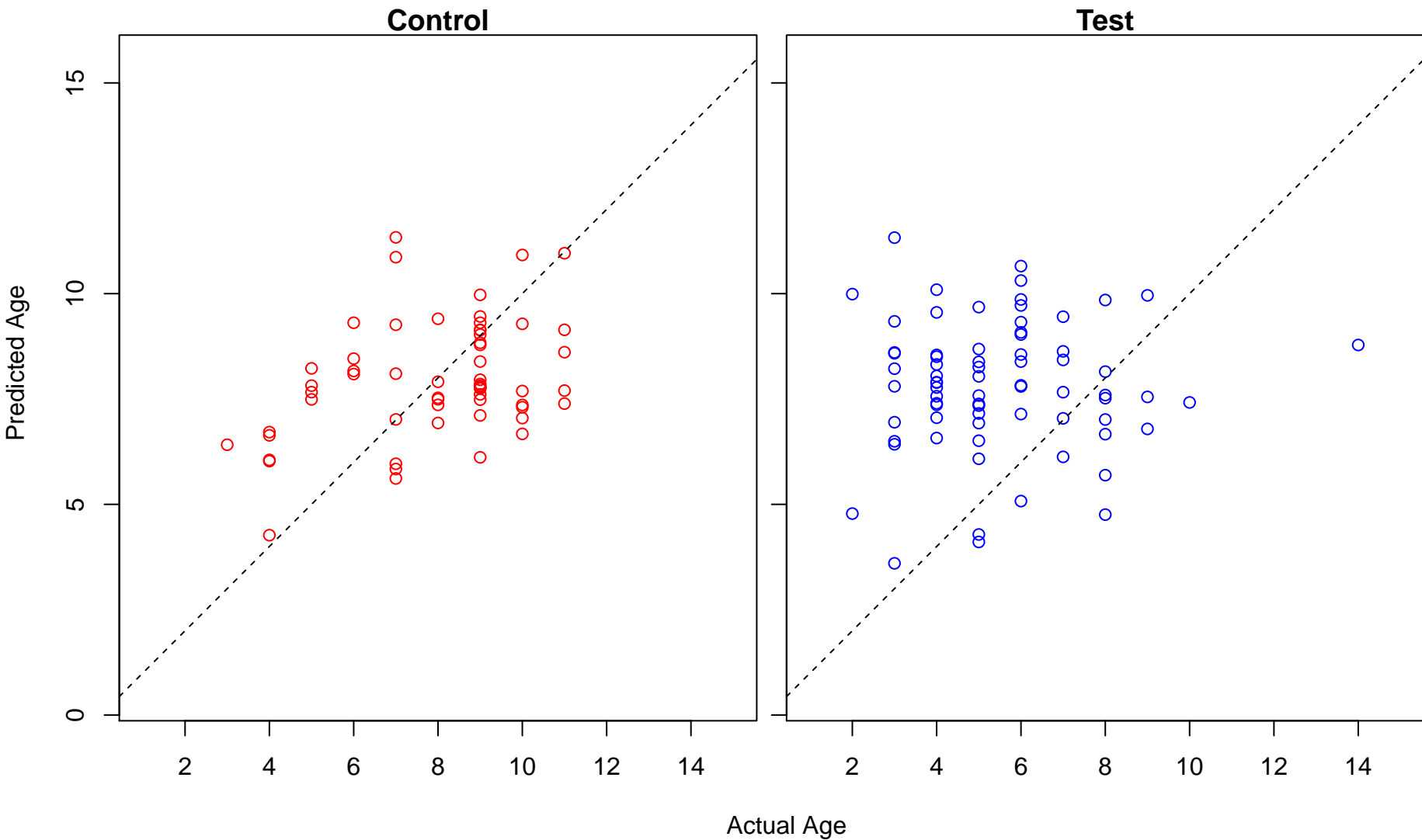
glycerophospholipid catabolic process (Score: 0.814769)



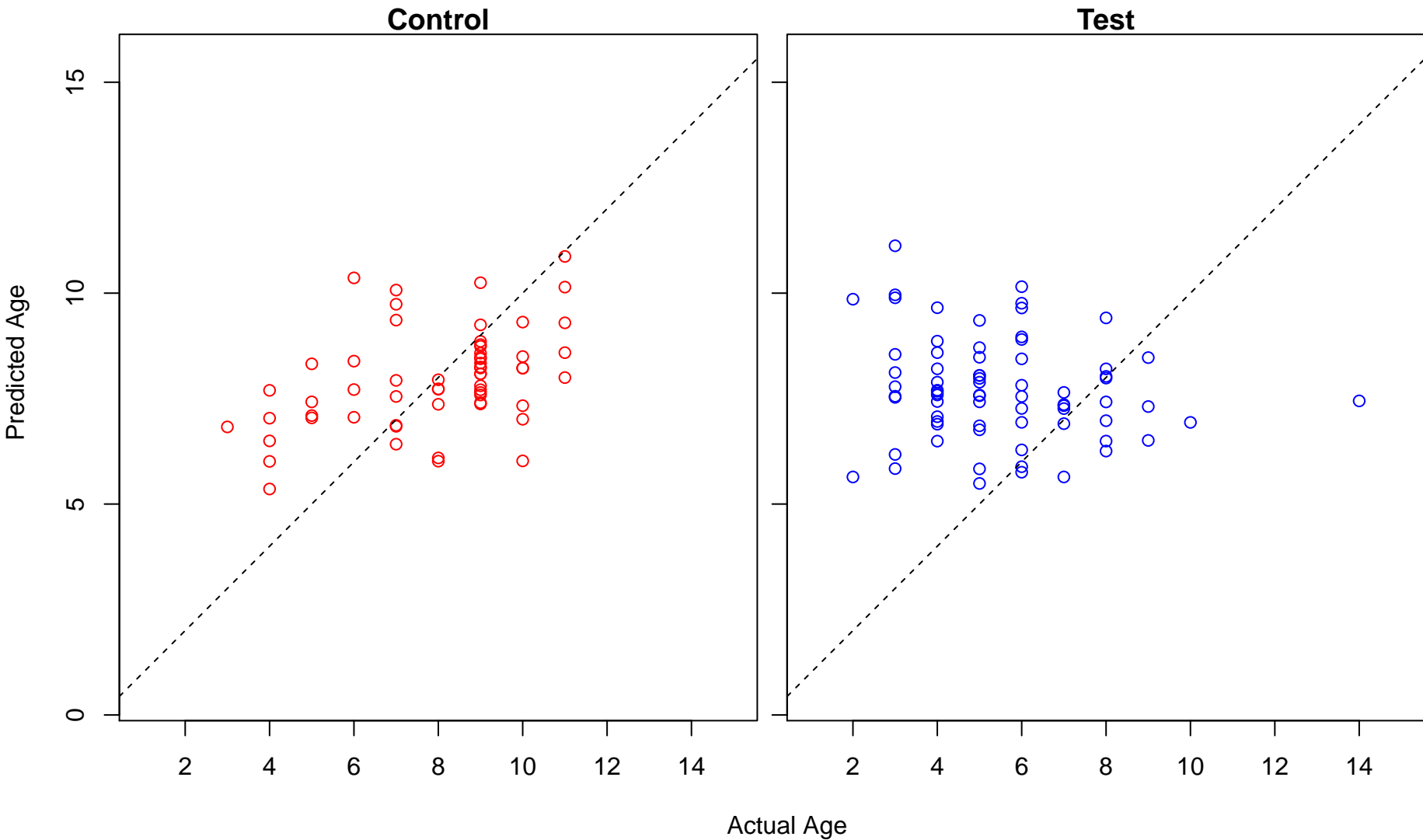
regulation of B cell receptor signaling pathway (Score: 0.814532)



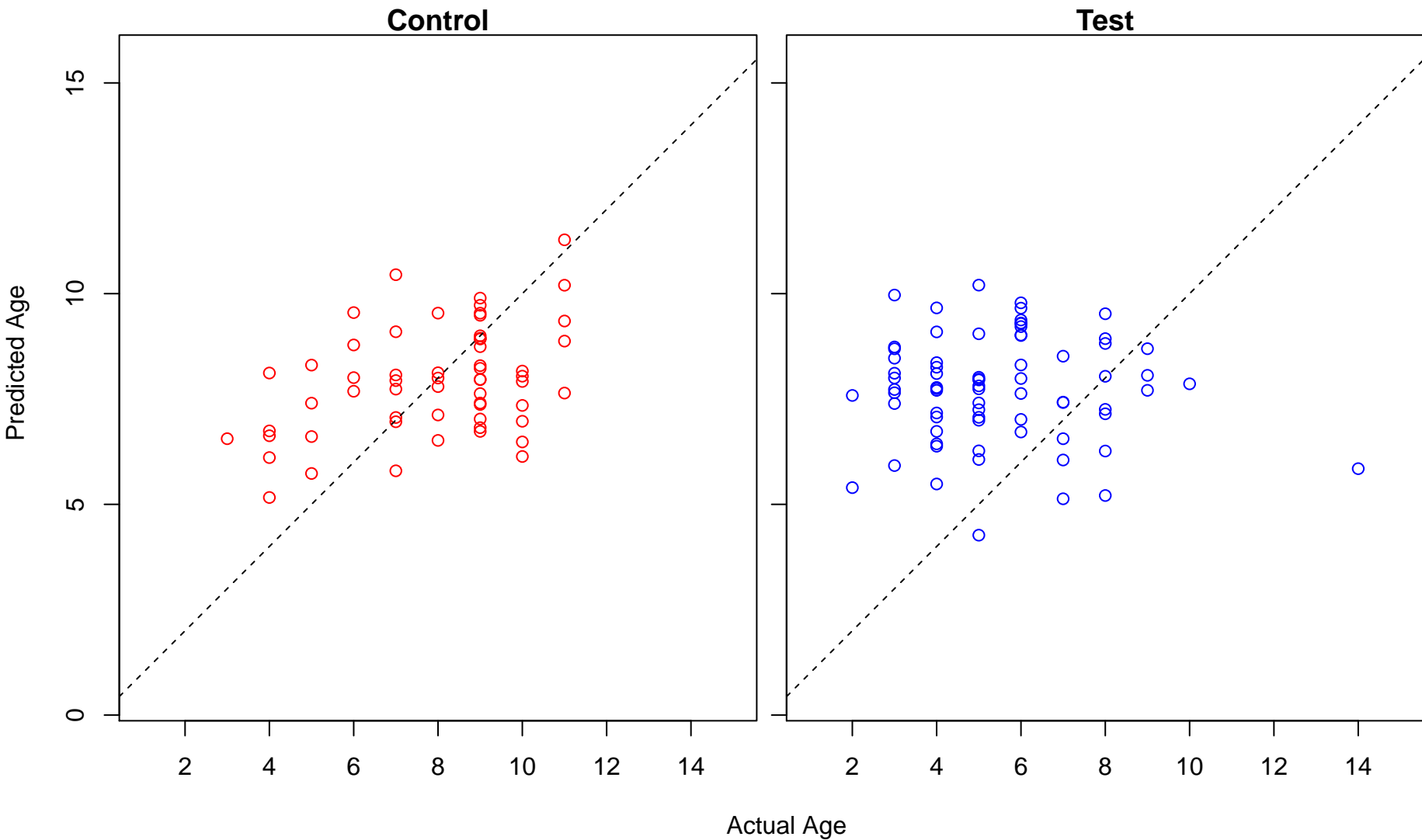
regulation of epithelial to mesenchymal transition (Score: 0.814490)



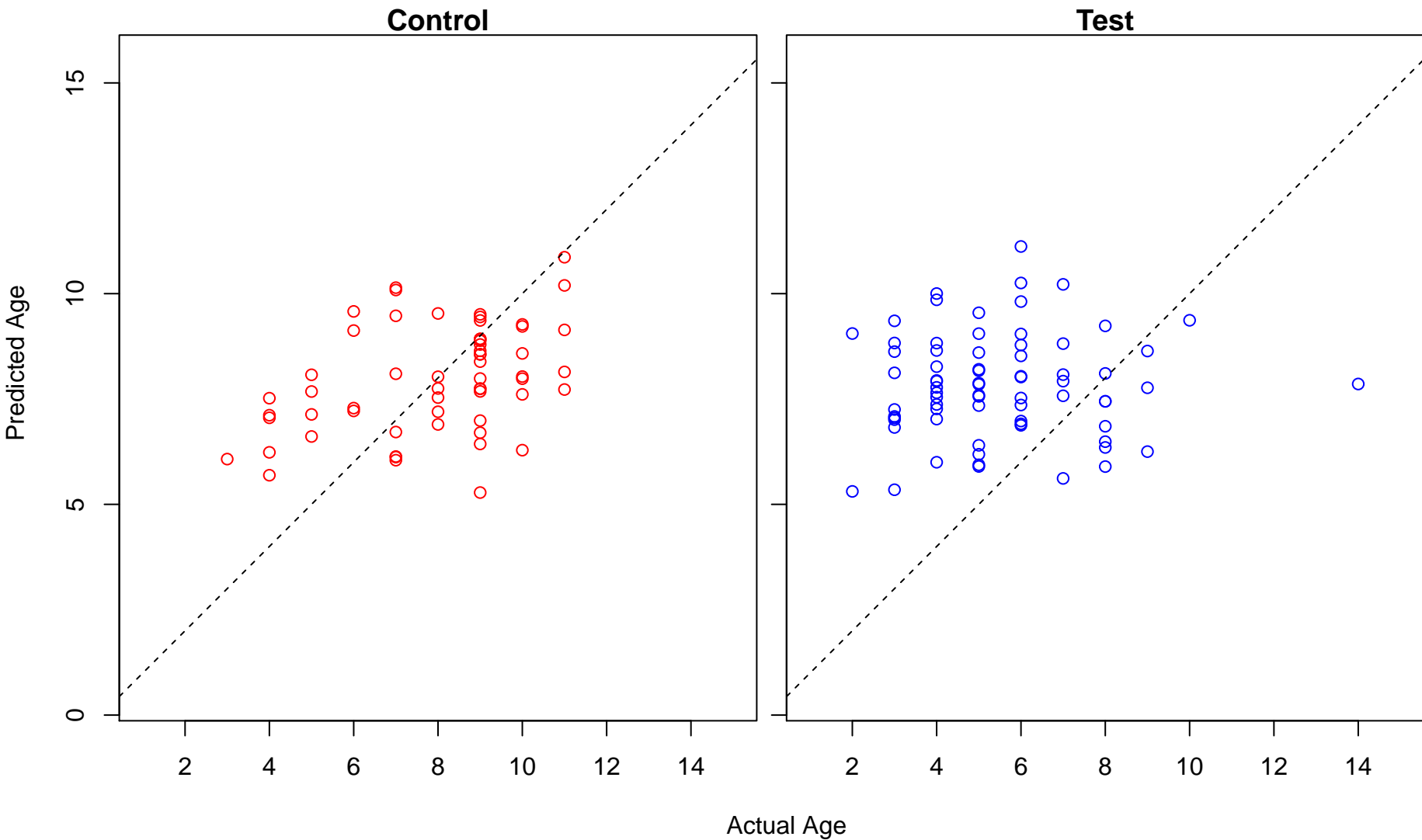
positive regulation of transcription factor import into nucleus (Score: 0.814007)



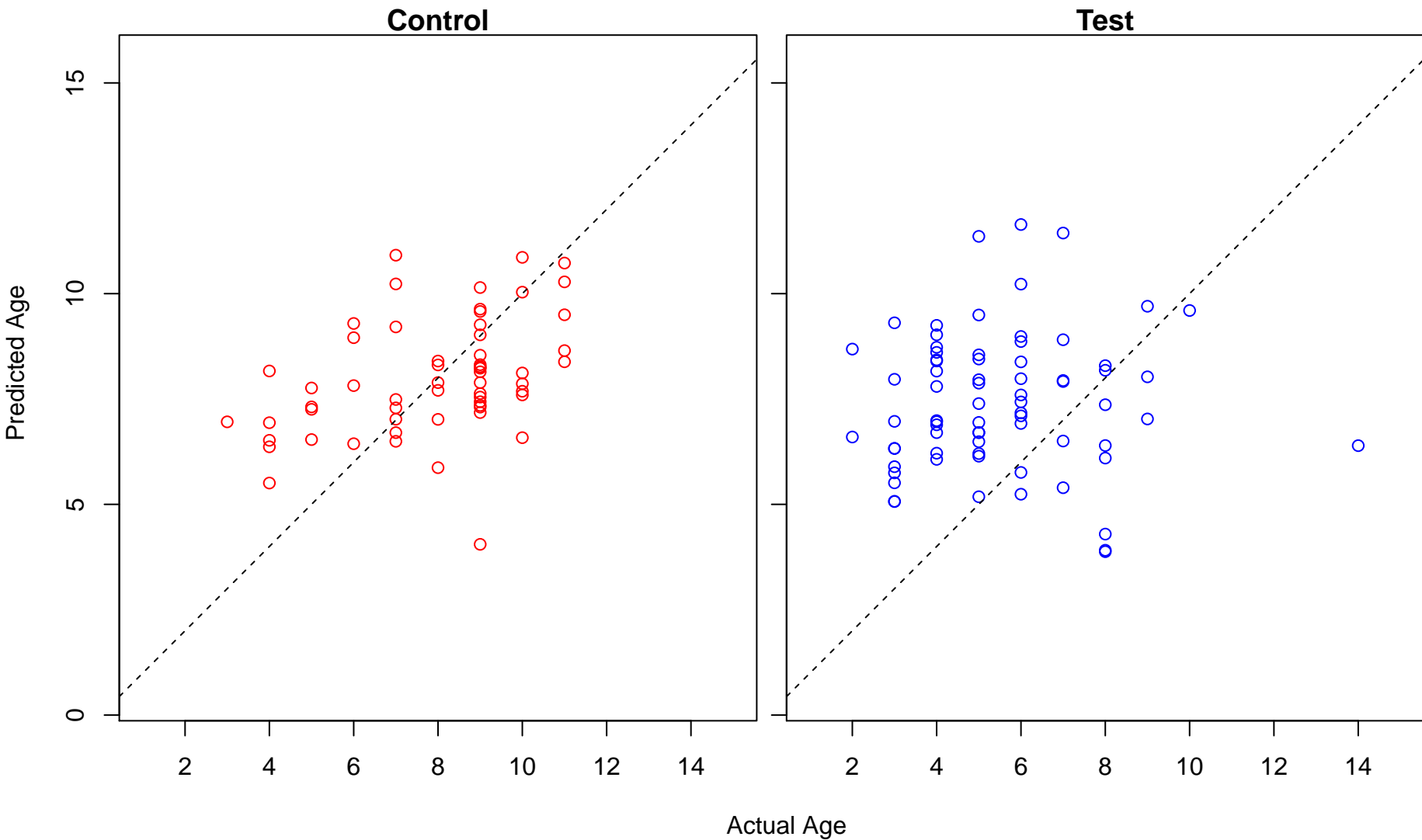
hyaluronan metabolic process (Score: 0.813071)



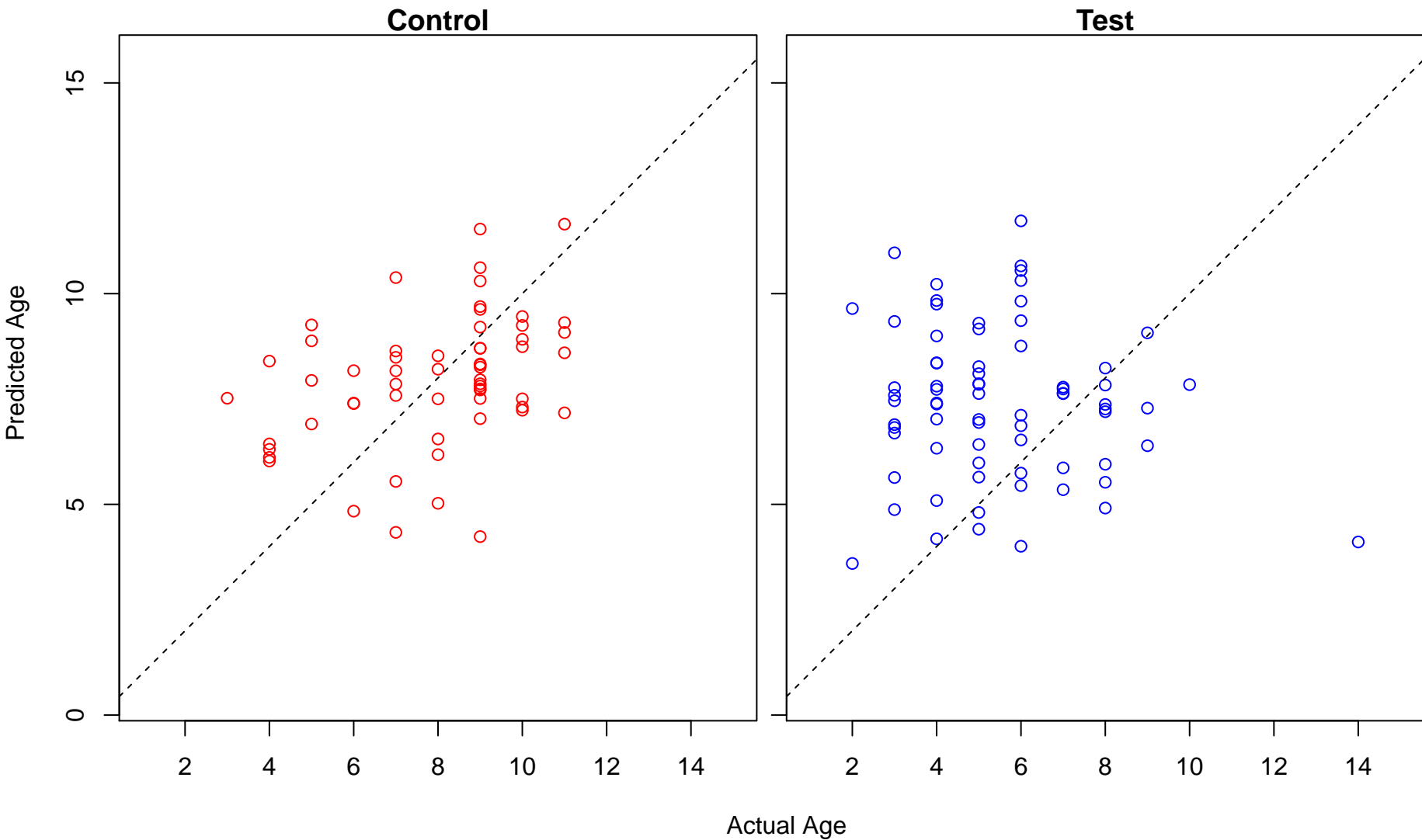
face development (Score: 0.812742)



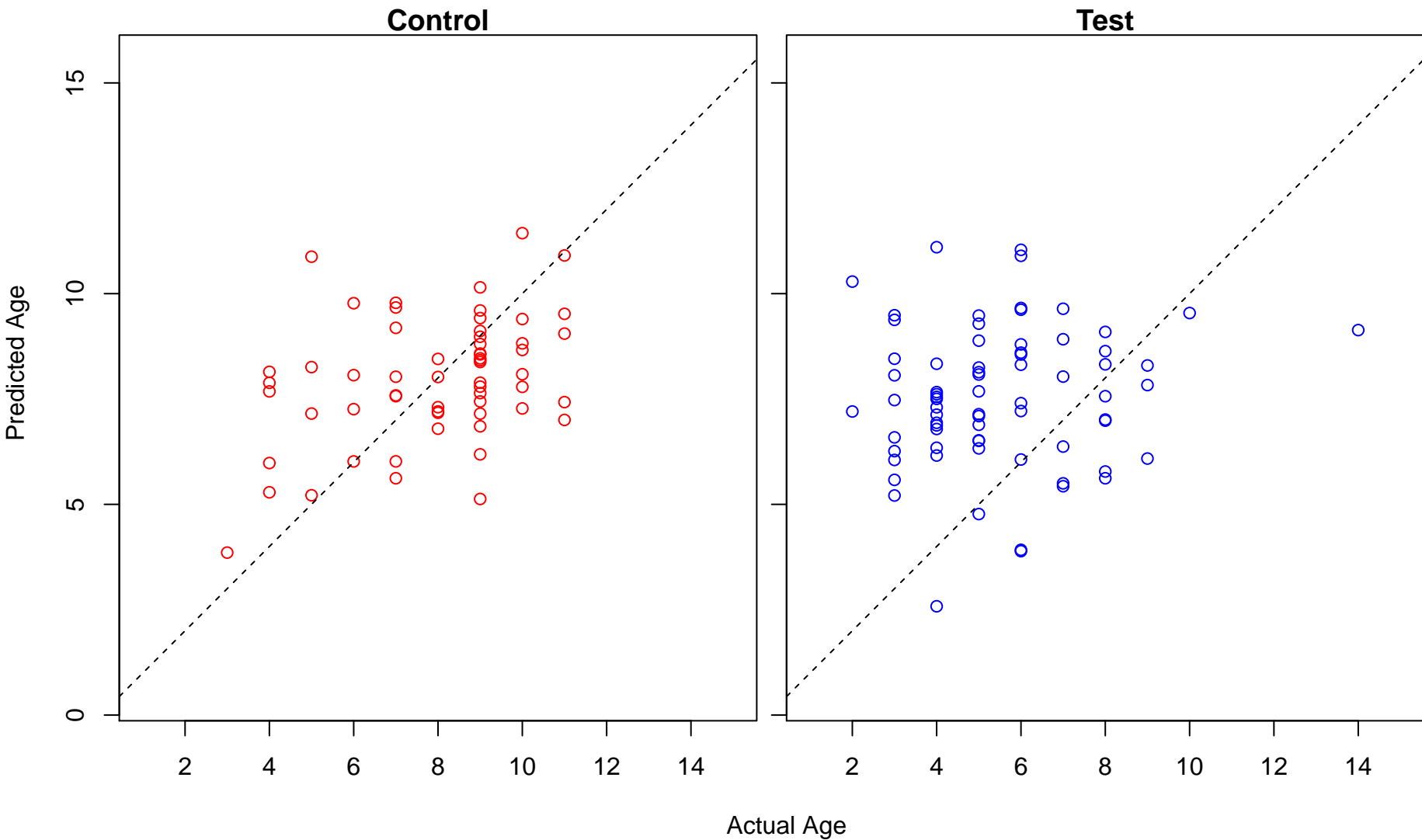
positive regulation of epithelial cell proliferation (Score: 0.810585)



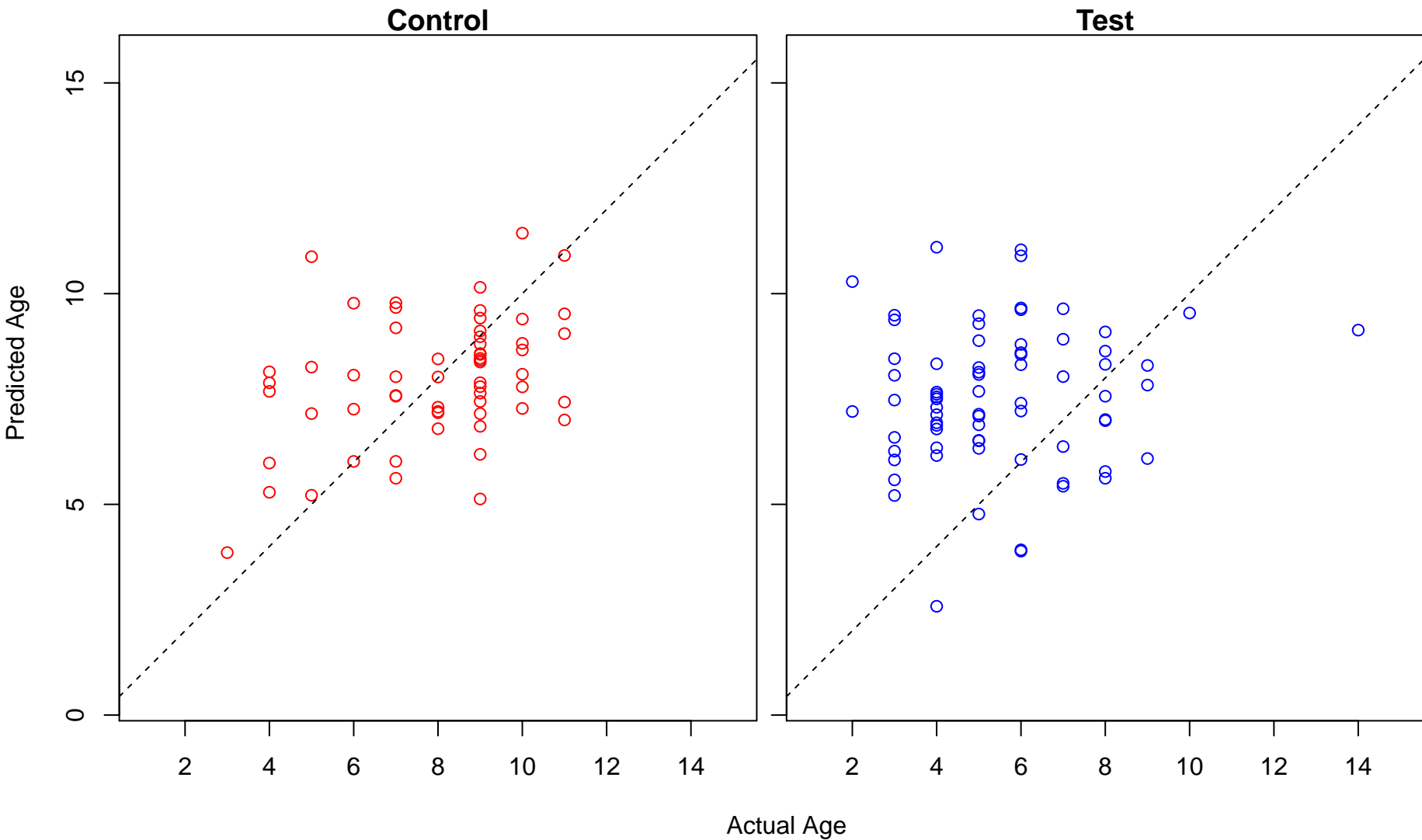
positive regulation of DNA repair (Score: 0.810581)



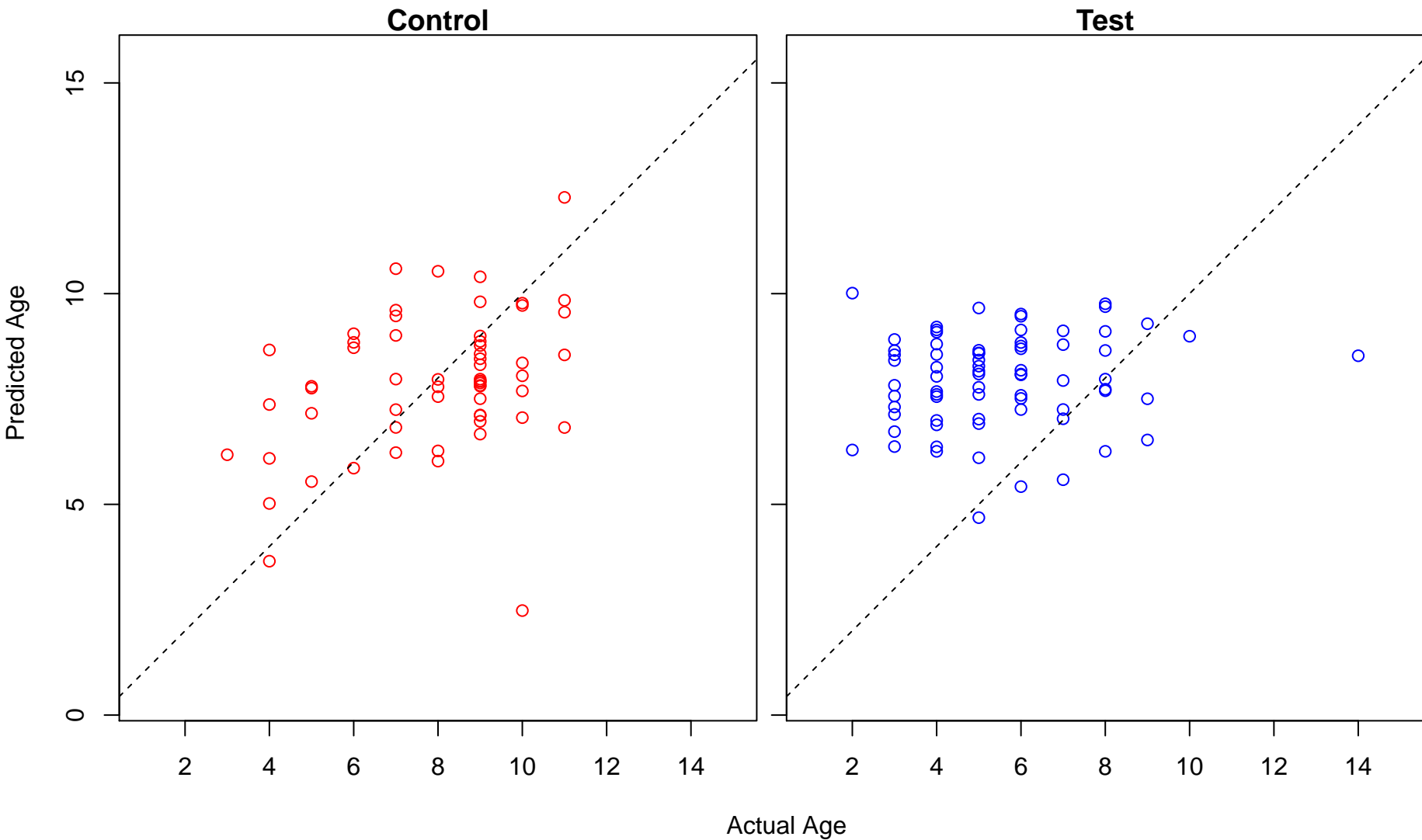
electron transport chain (Score: 0.810485)



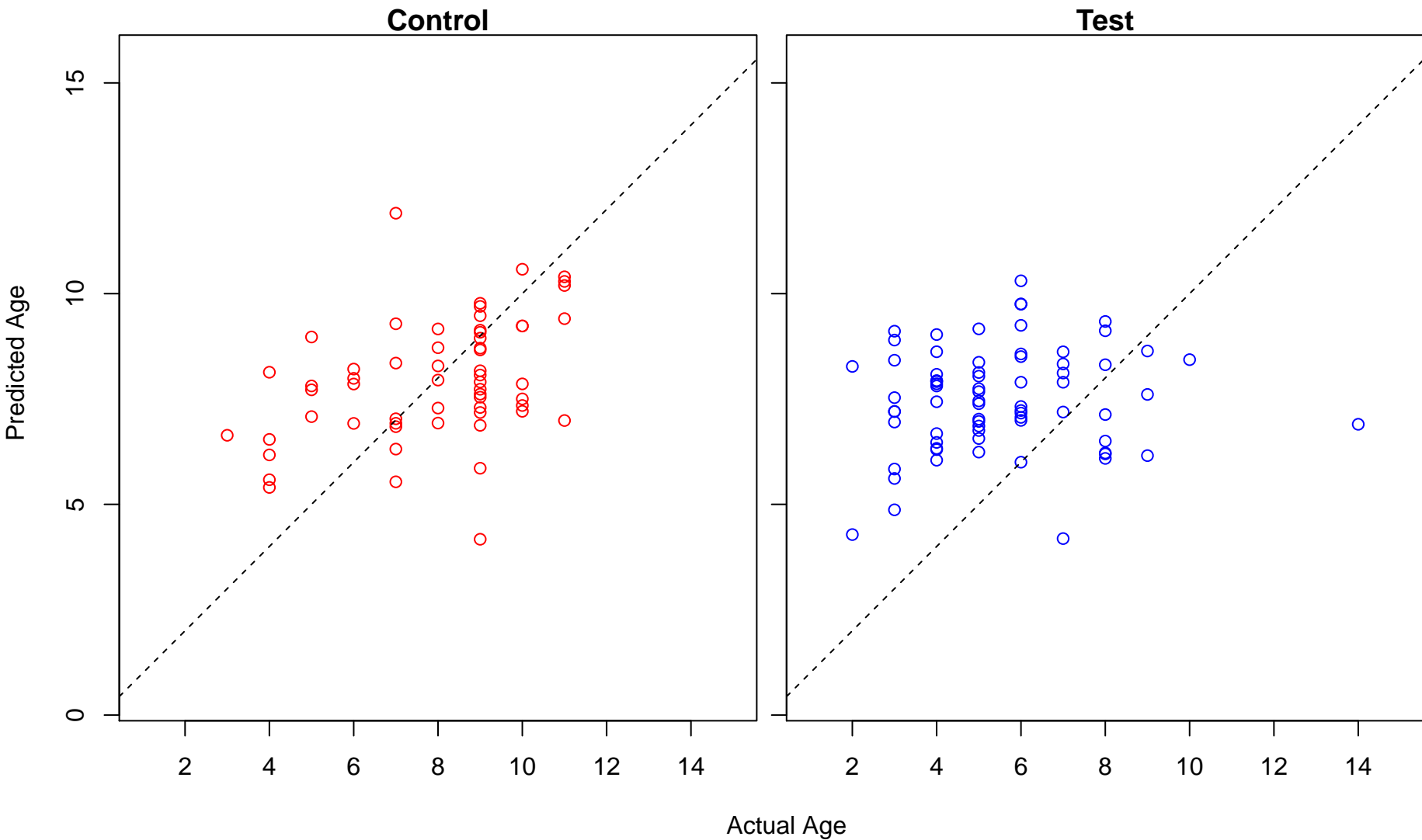
respiratory electron transport chain (Score: 0.810485)



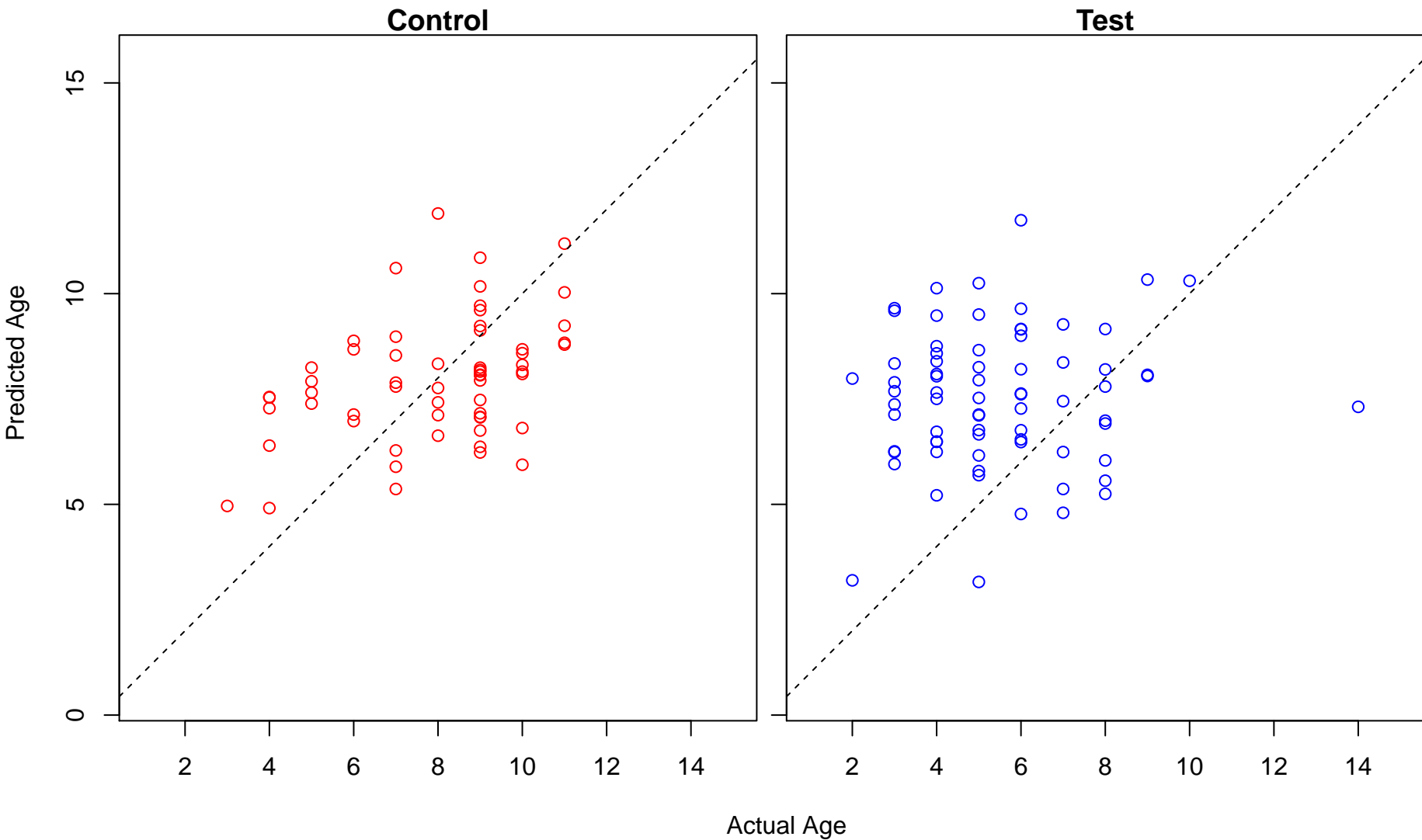
negative regulation of glucose transport (Score: 0.810249)



positive regulation of ossification (Score: 0.809929)

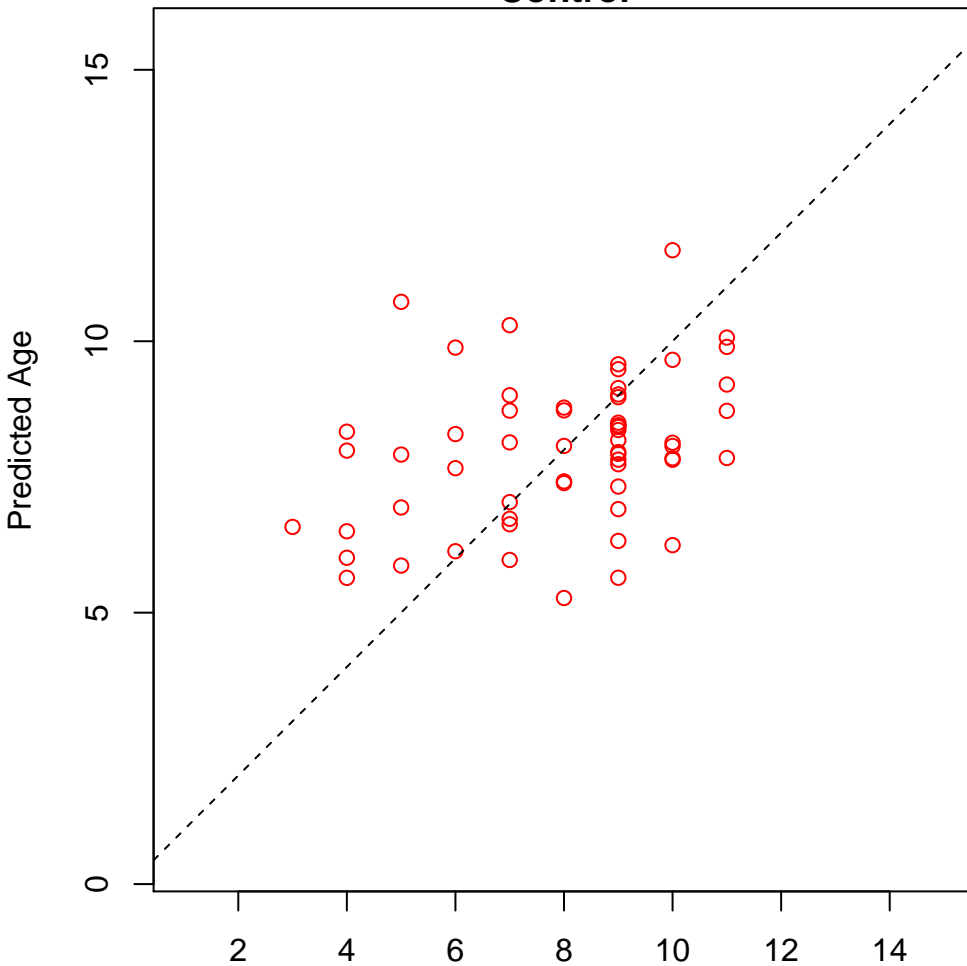


regulation of acyl-CoA biosynthetic process (Score: 0.808811)

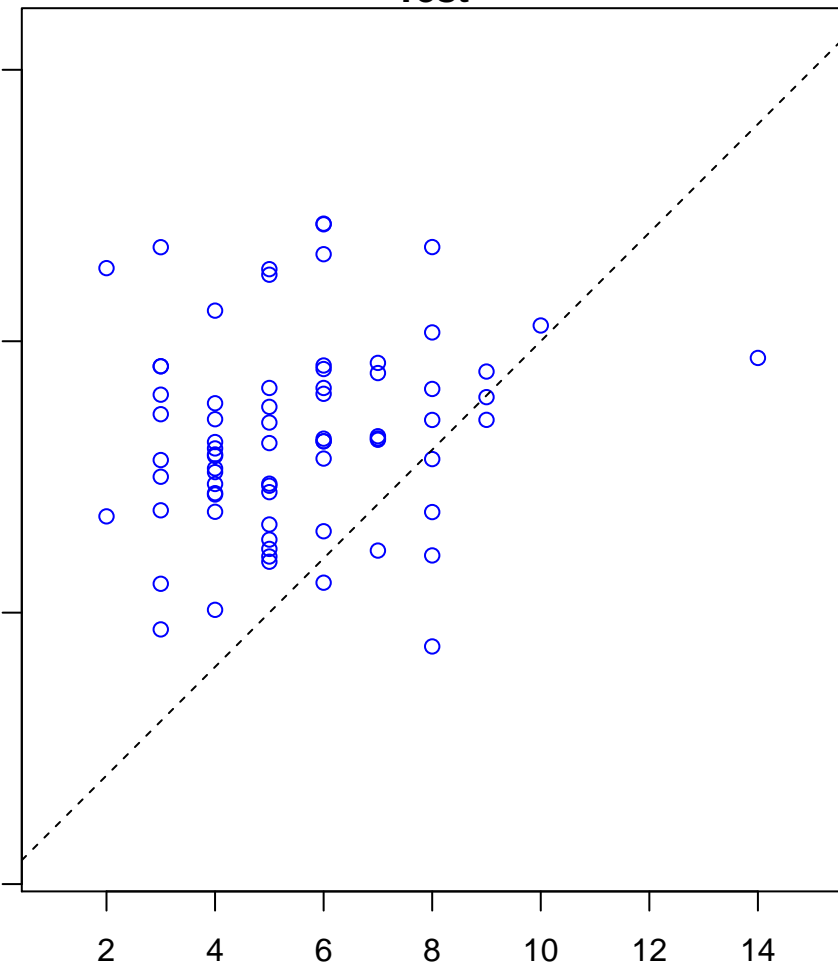


retina development in camera-type eye (Score: 0.807174)

Control

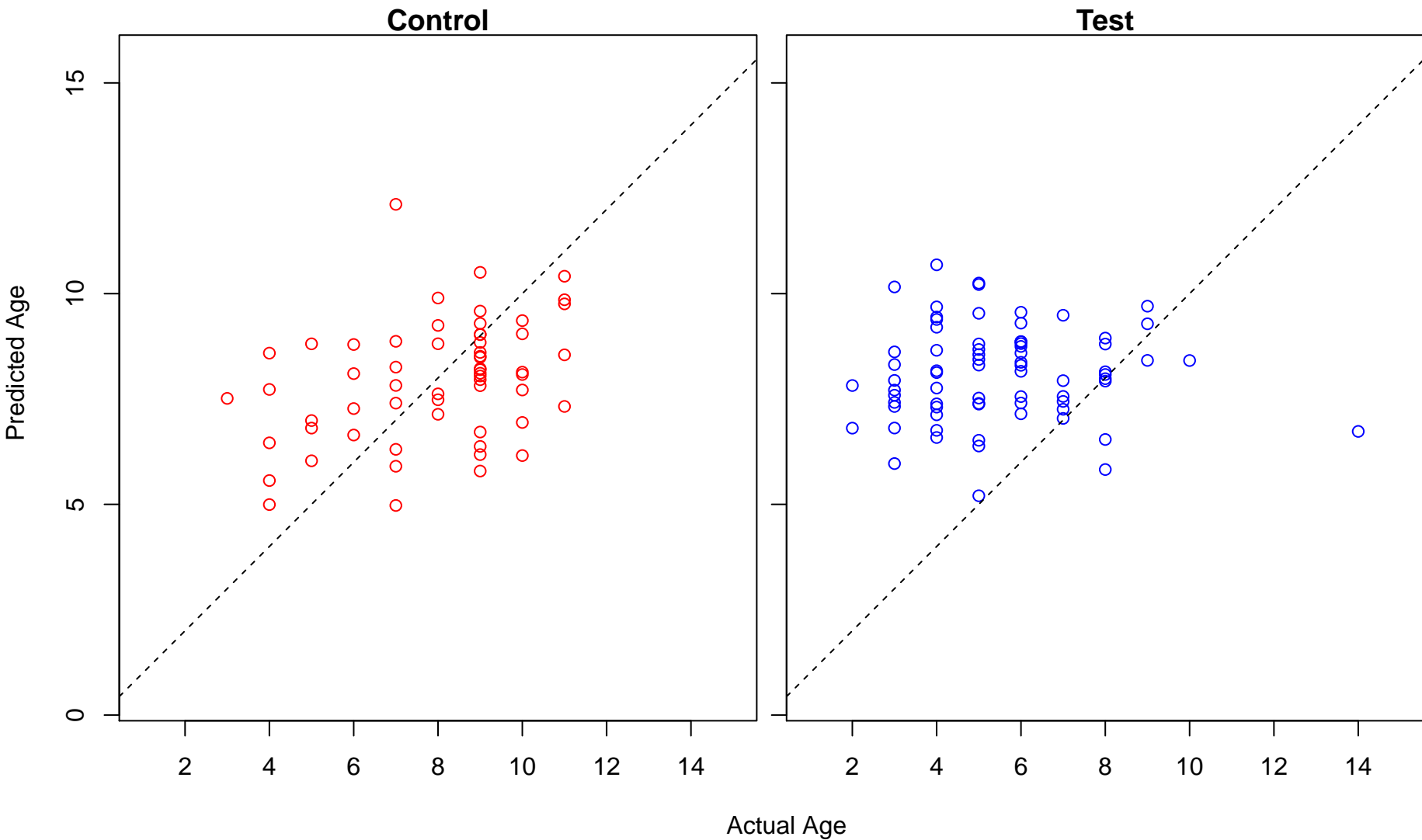


Test

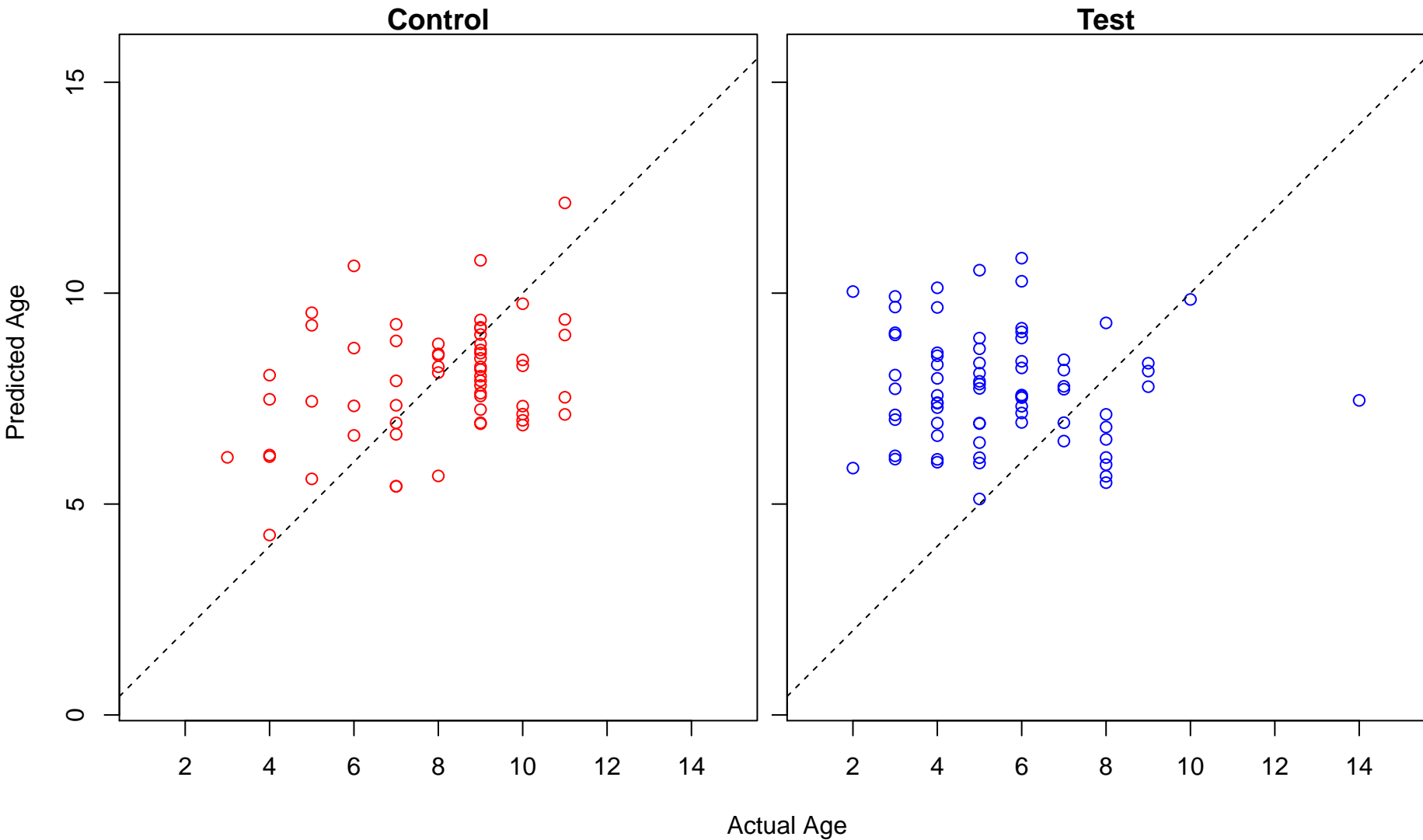


Actual Age

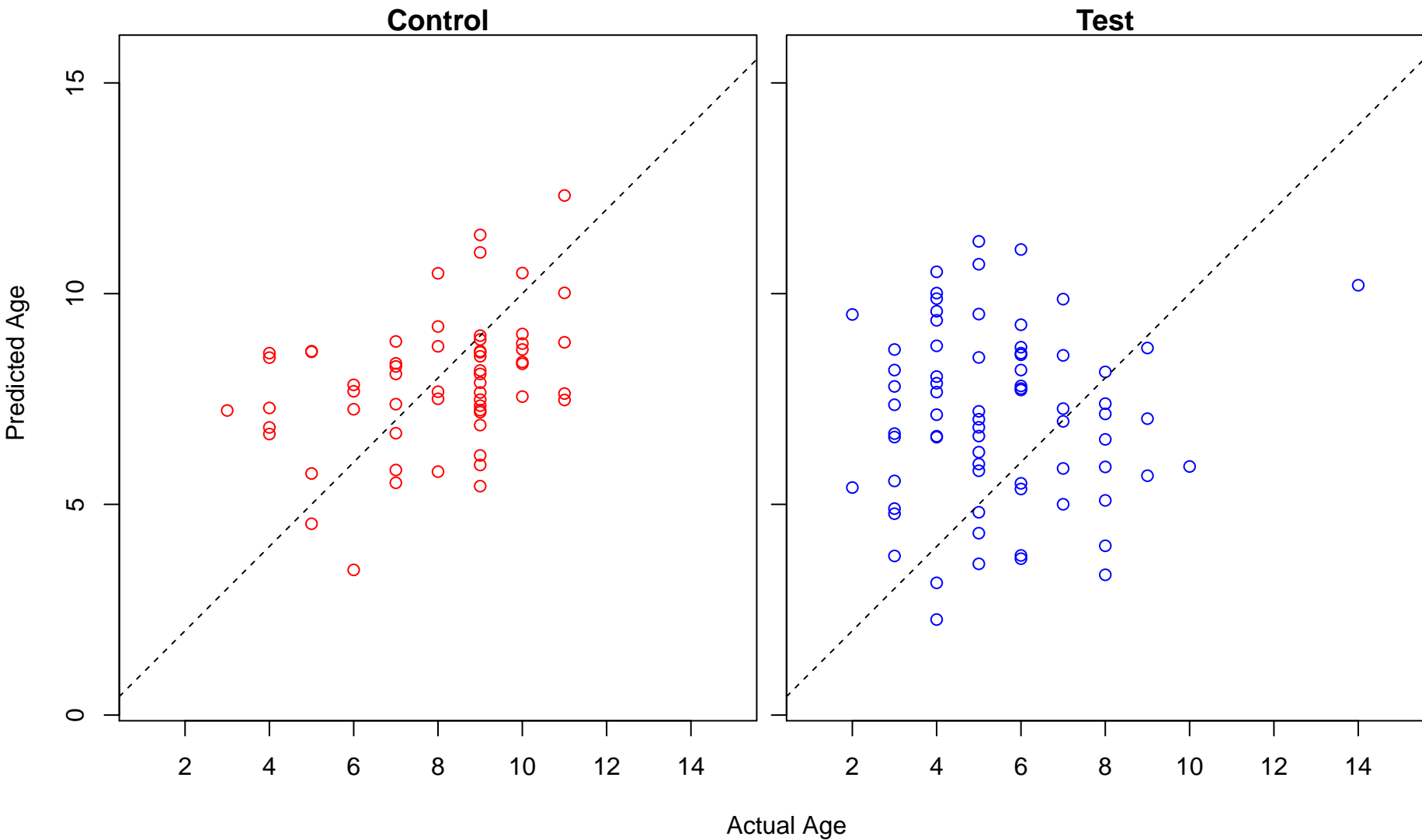
cellular hormone metabolic process (Score: 0.806884)



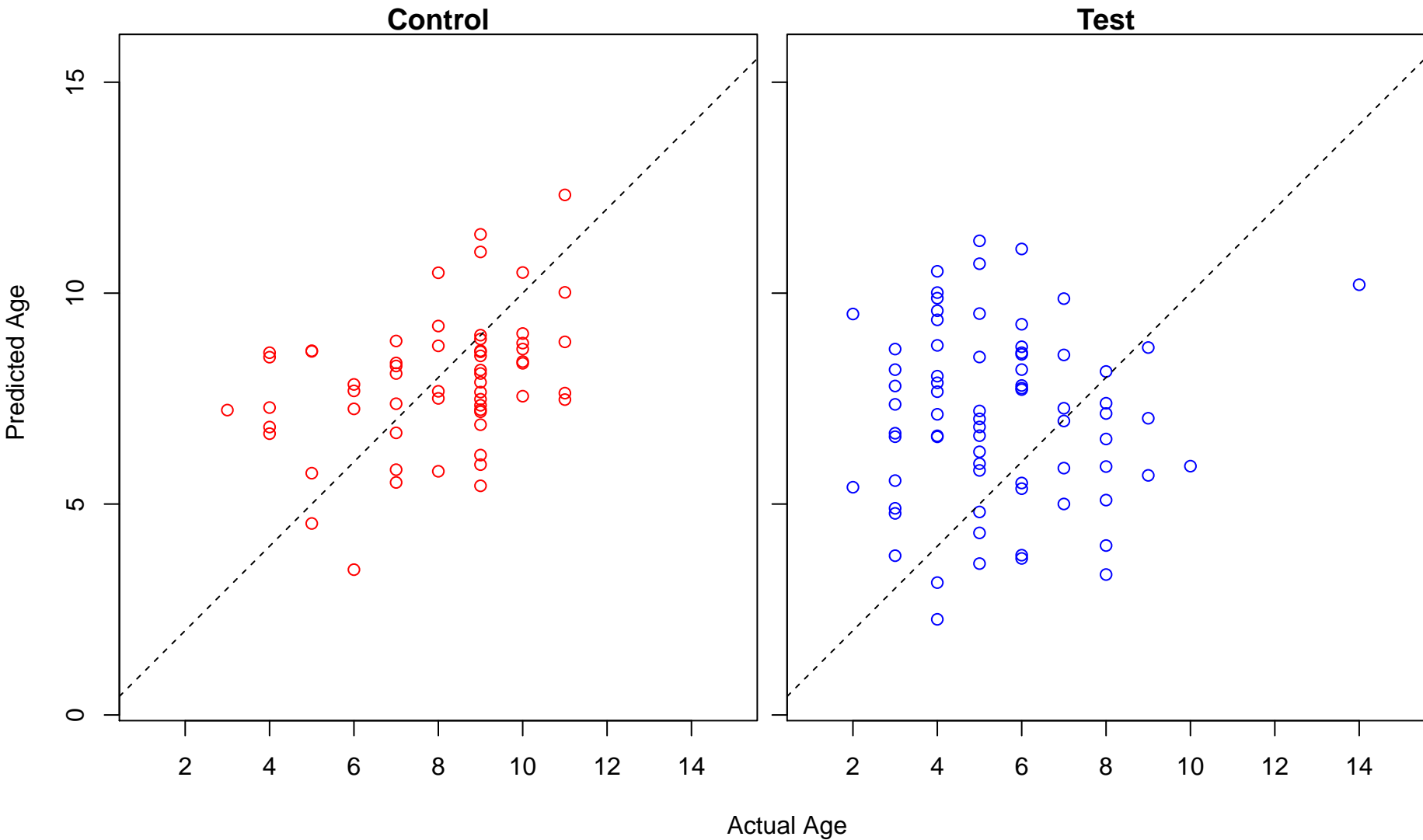
regulation of microtubule-based movement (Score: 0.806696)



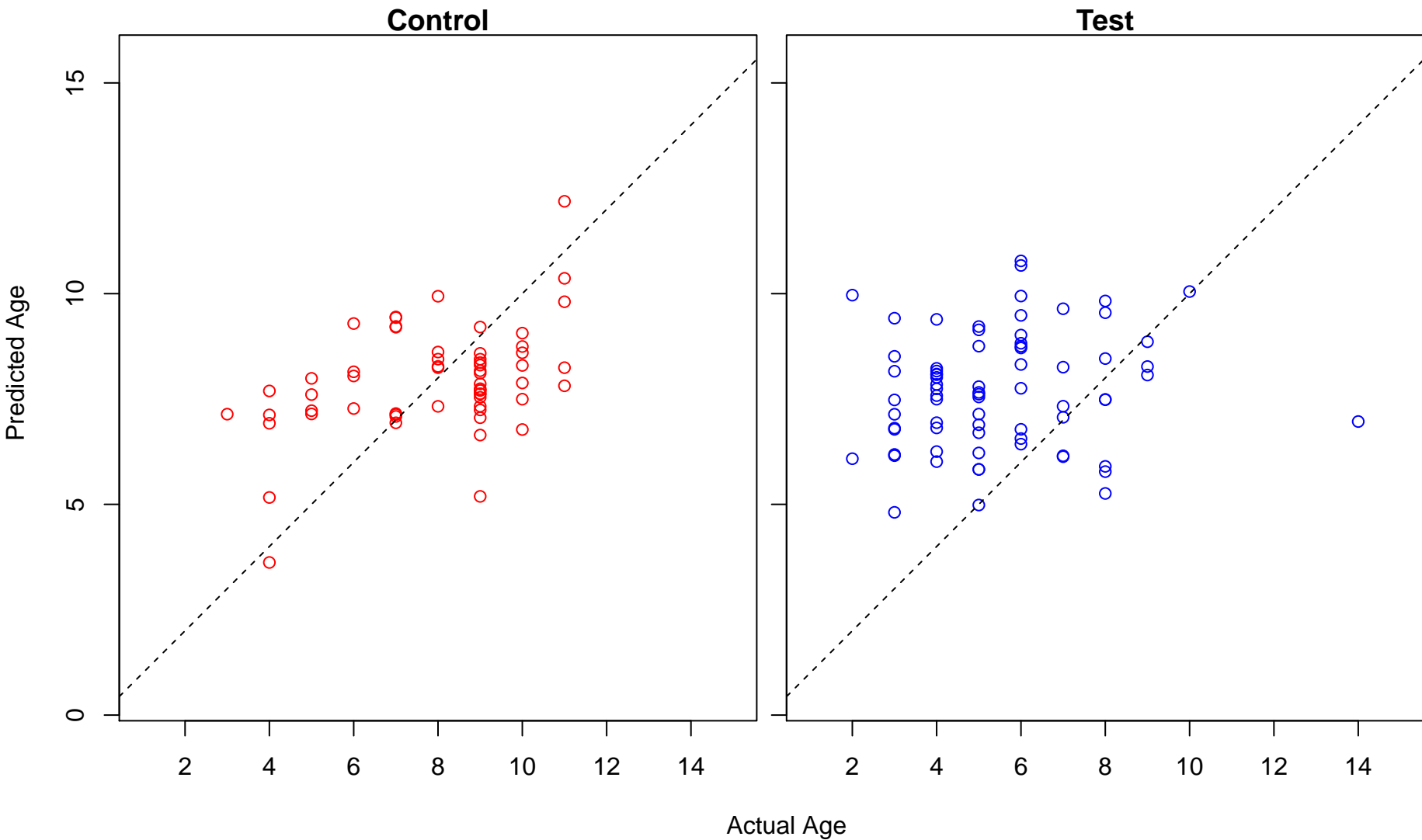
negative regulation of sterol transport (Score: 0.805860)



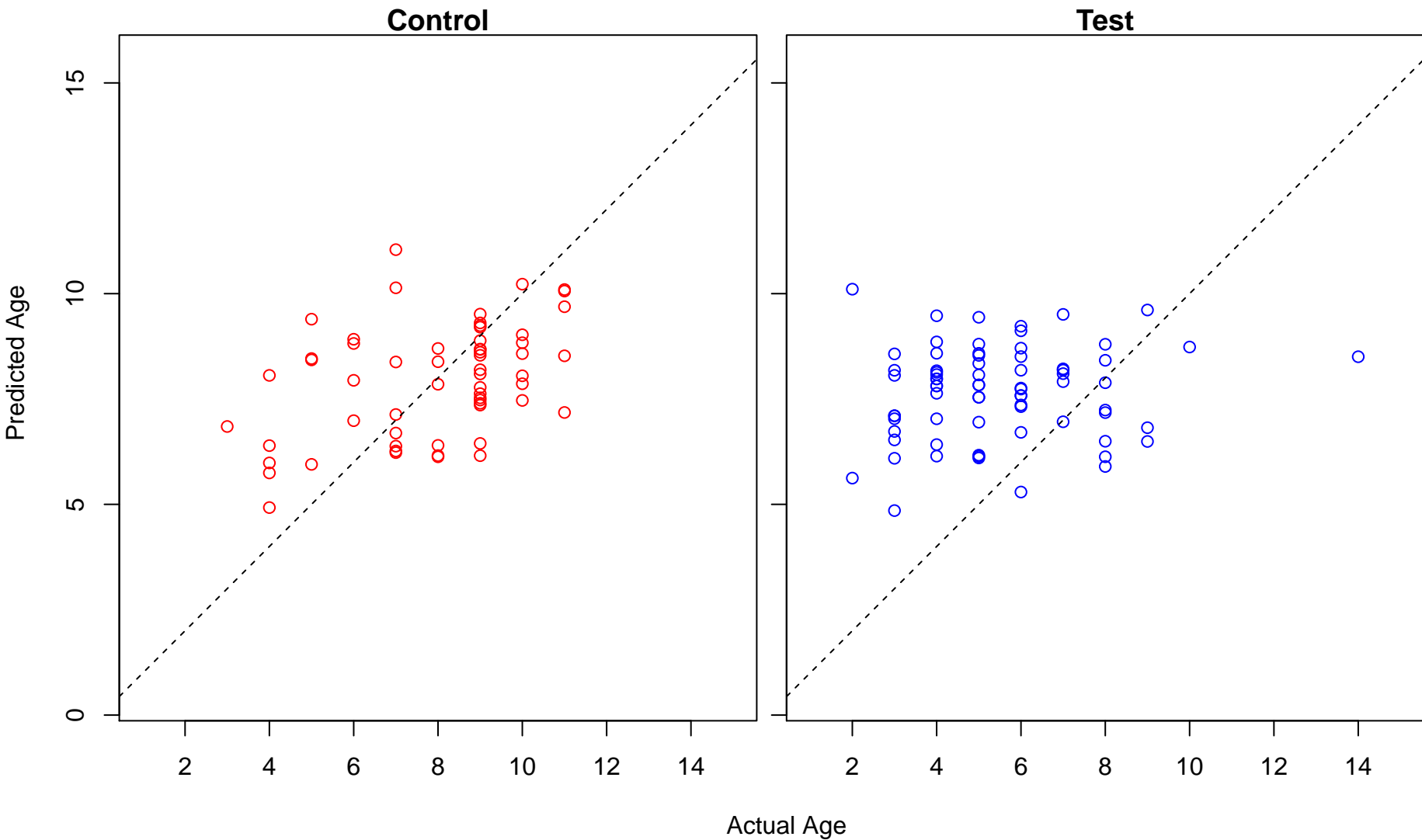
negative regulation of cholesterol transport (Score: 0.805860)



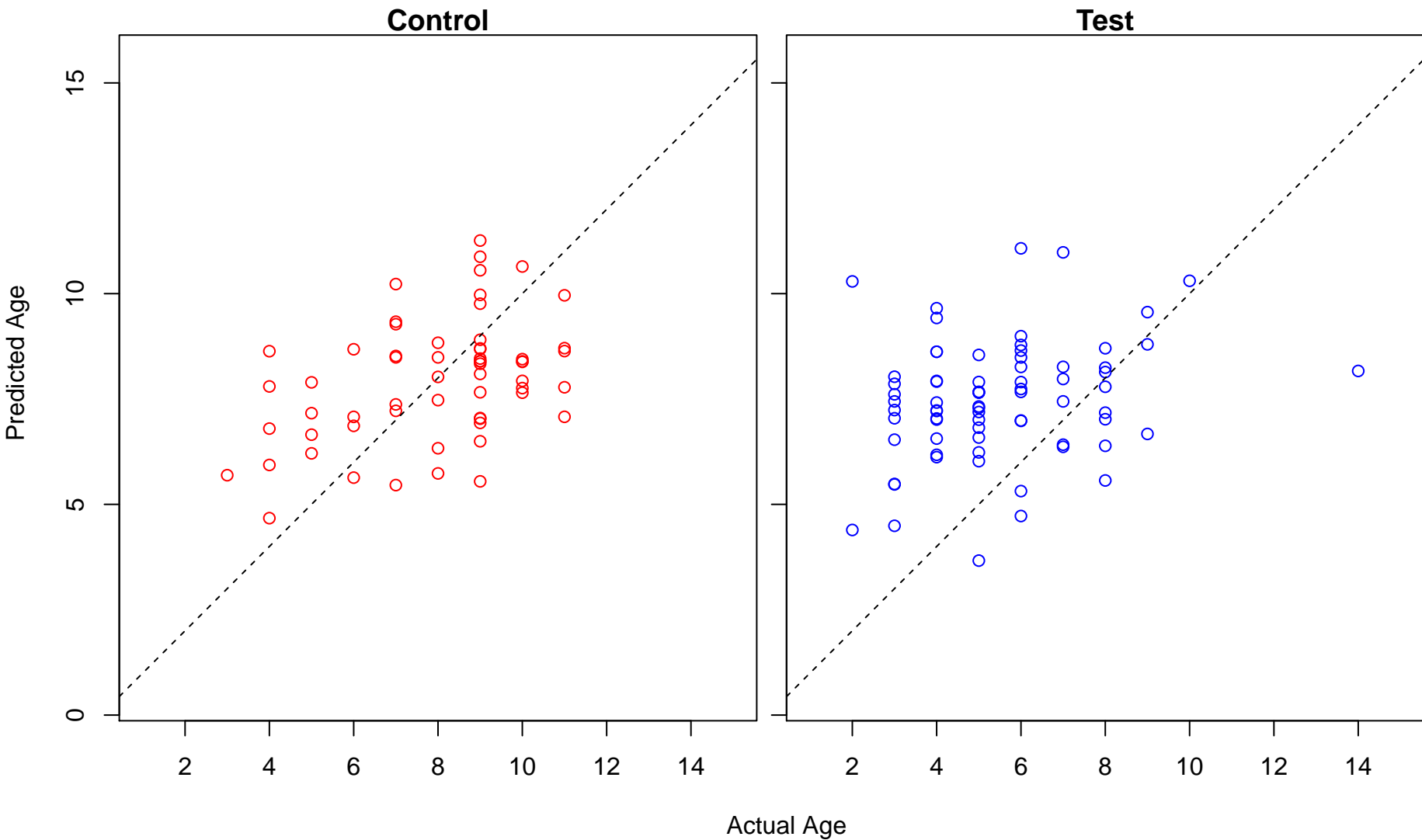
regulation of vascular endothelial growth factor receptor signaling pathway (Score: 0.804948)



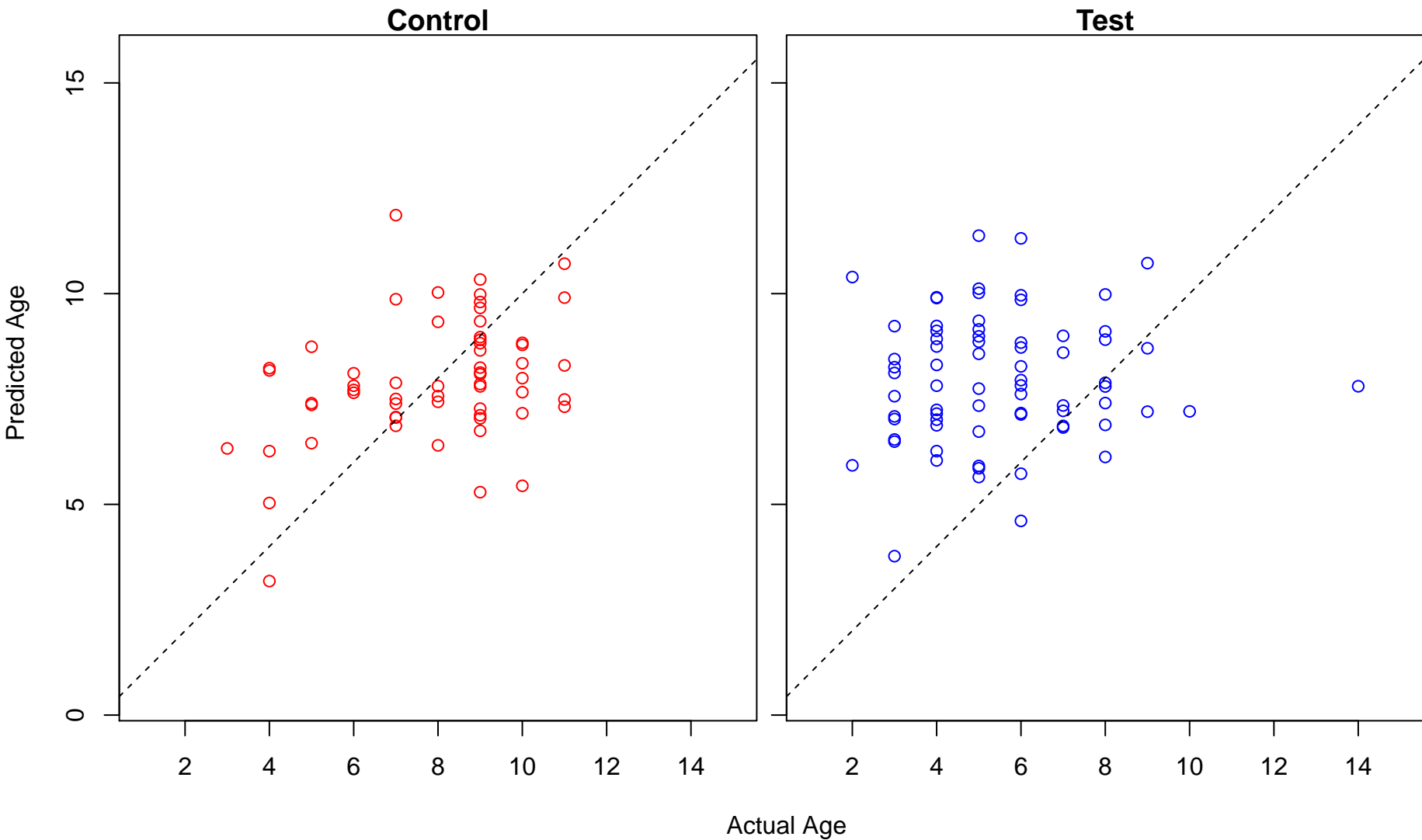
positive regulation of myeloid cell differentiation (Score: 0.804757)



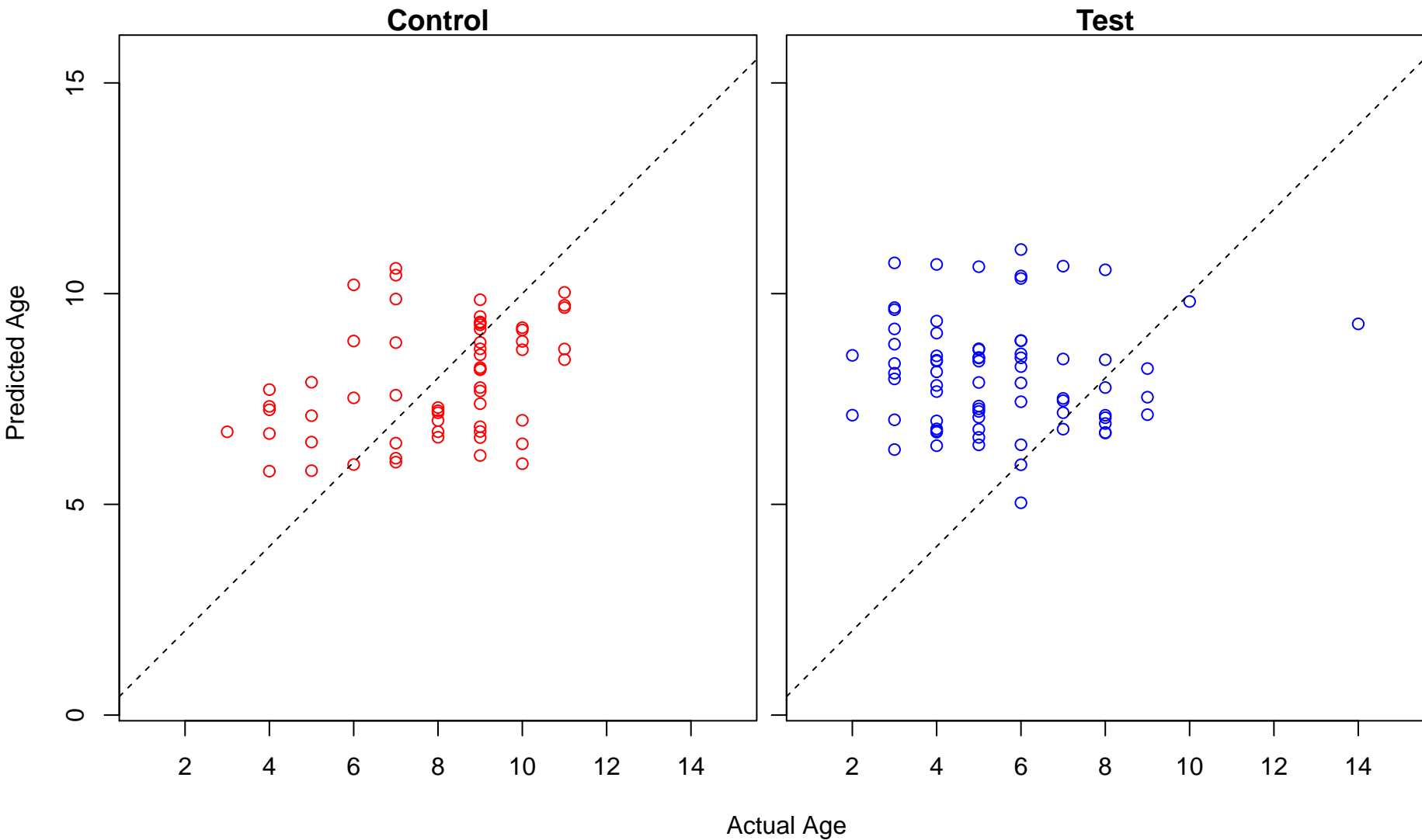
positive regulation of interleukin-12 production (Score: 0.804688)



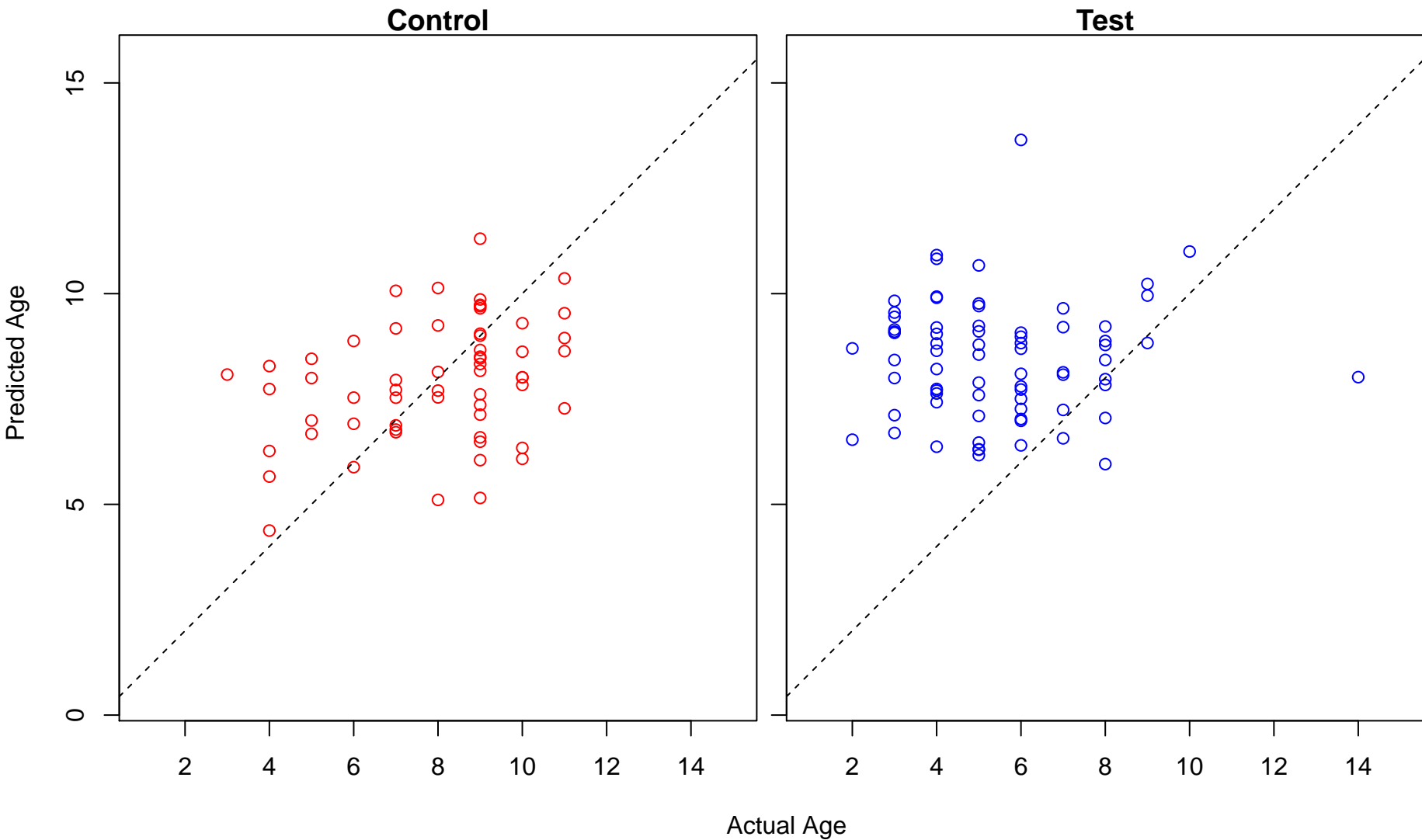
protein folding (Score: 0.803315)



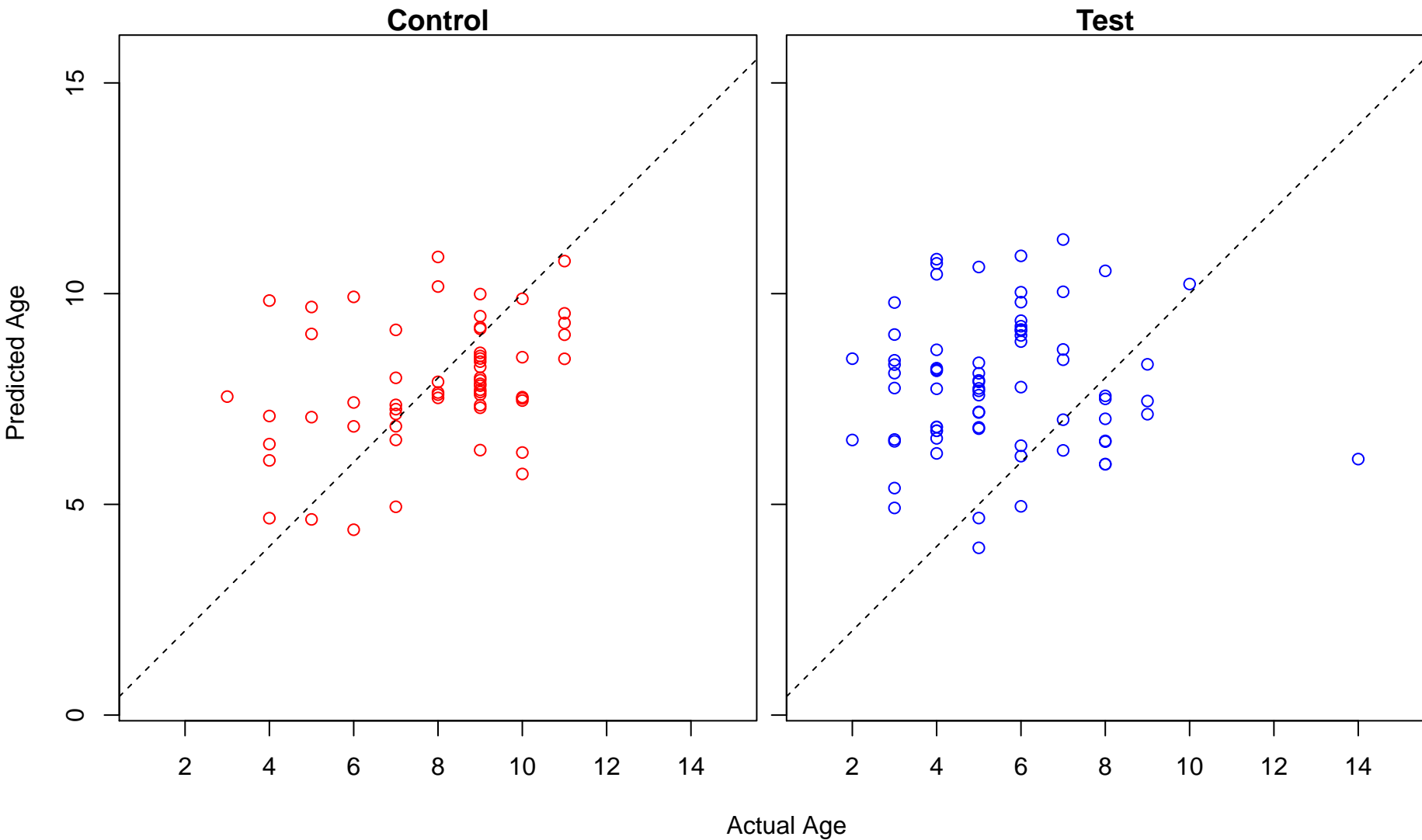
intrinsic apoptotic signaling pathway by p53 class mediator (Score: 0.803005)



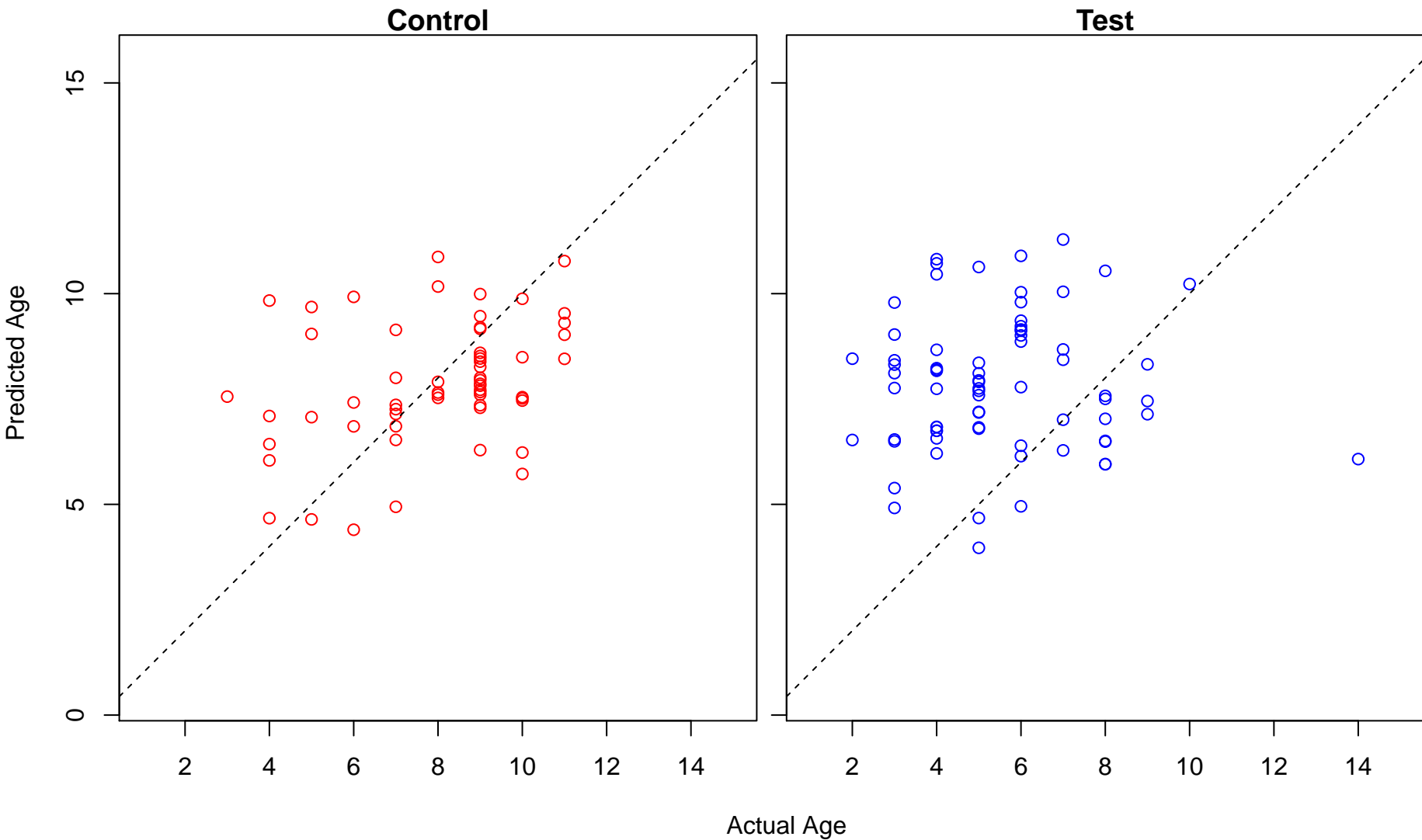
galactose metabolic process (Score: 0.802889)



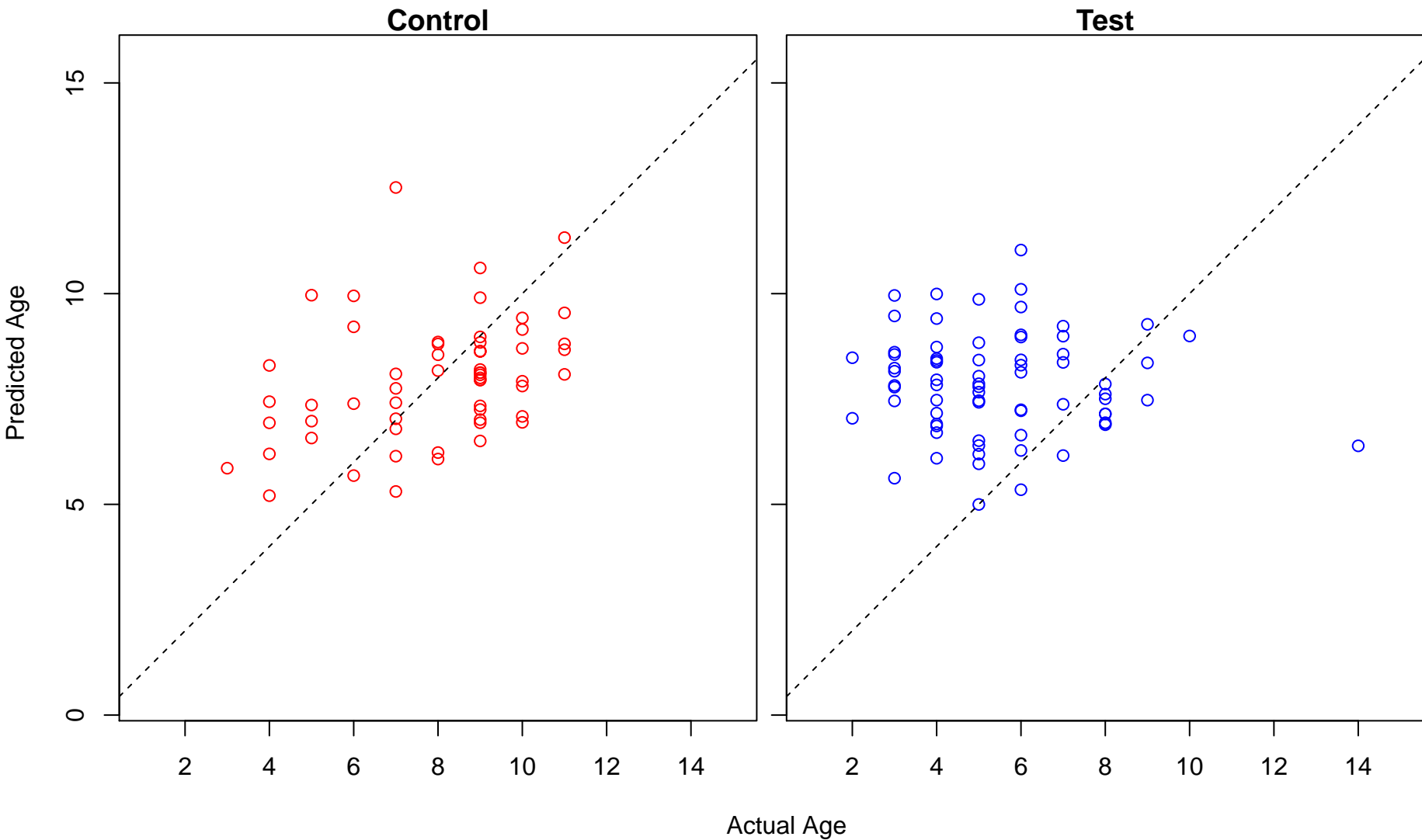
negative regulation of response to food (Score: 0.802055)



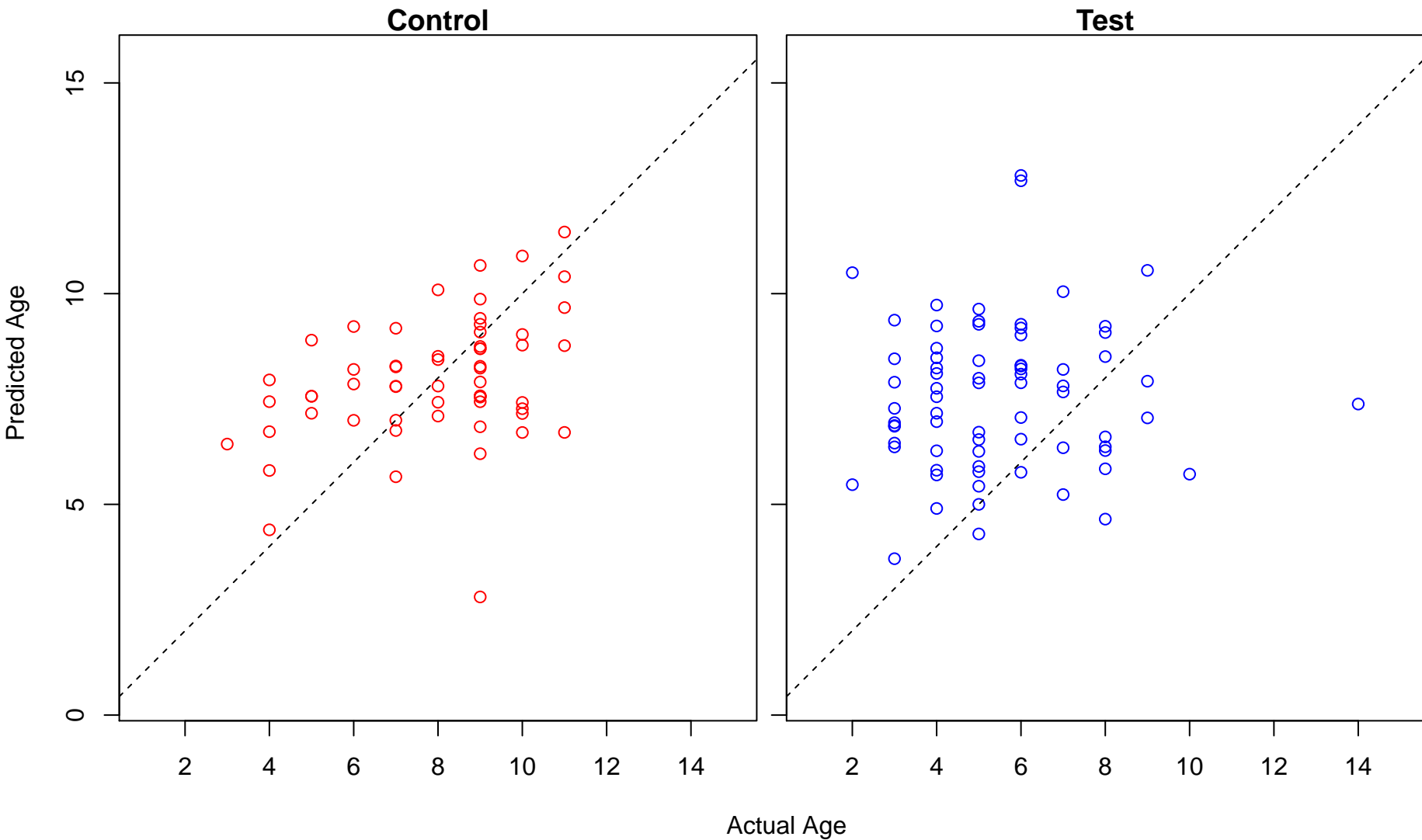
negative regulation of appetite (Score: 0.802055)



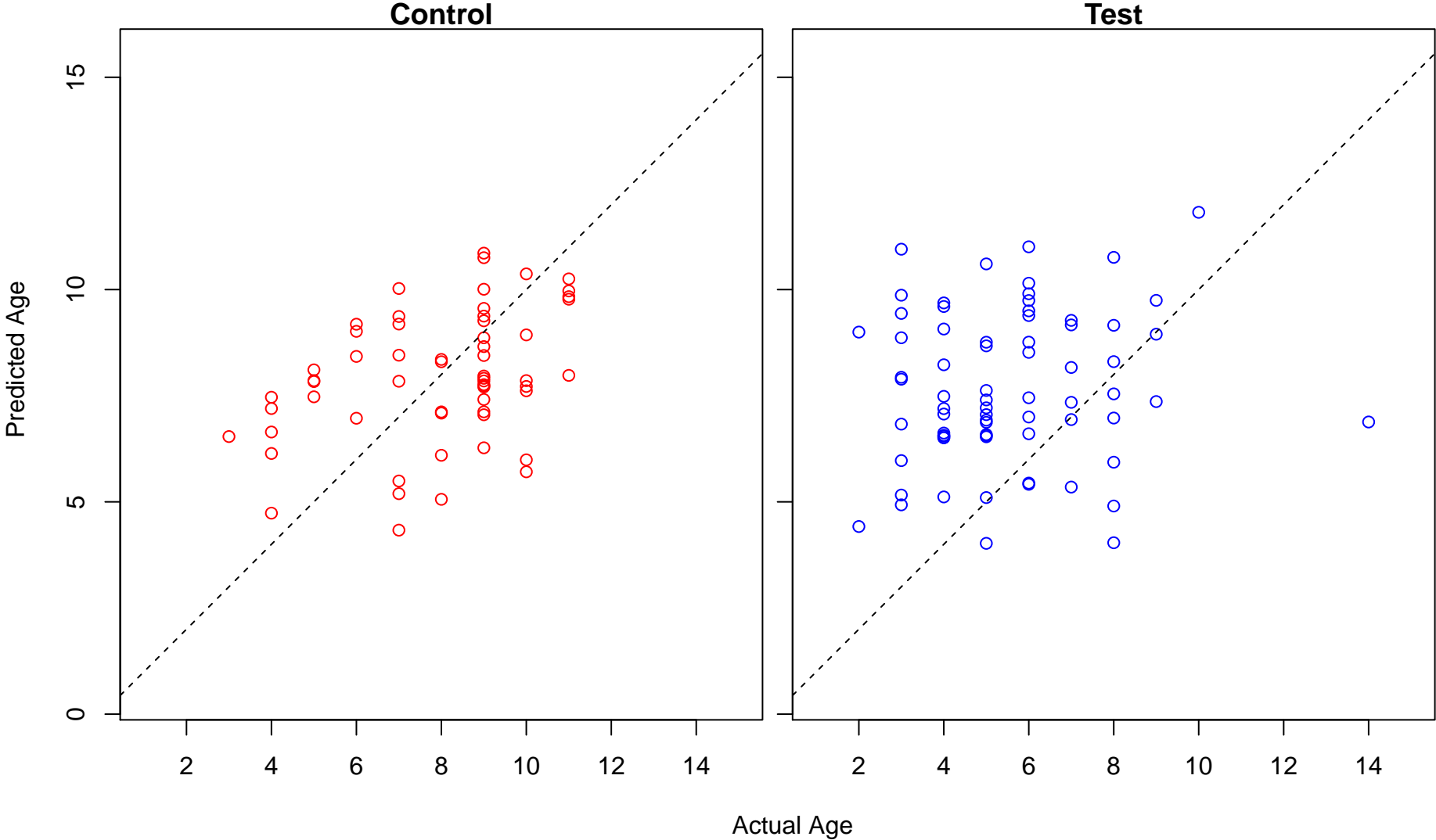
negative regulation of peptidyl–threonine phosphorylation (Score: 0.801821)



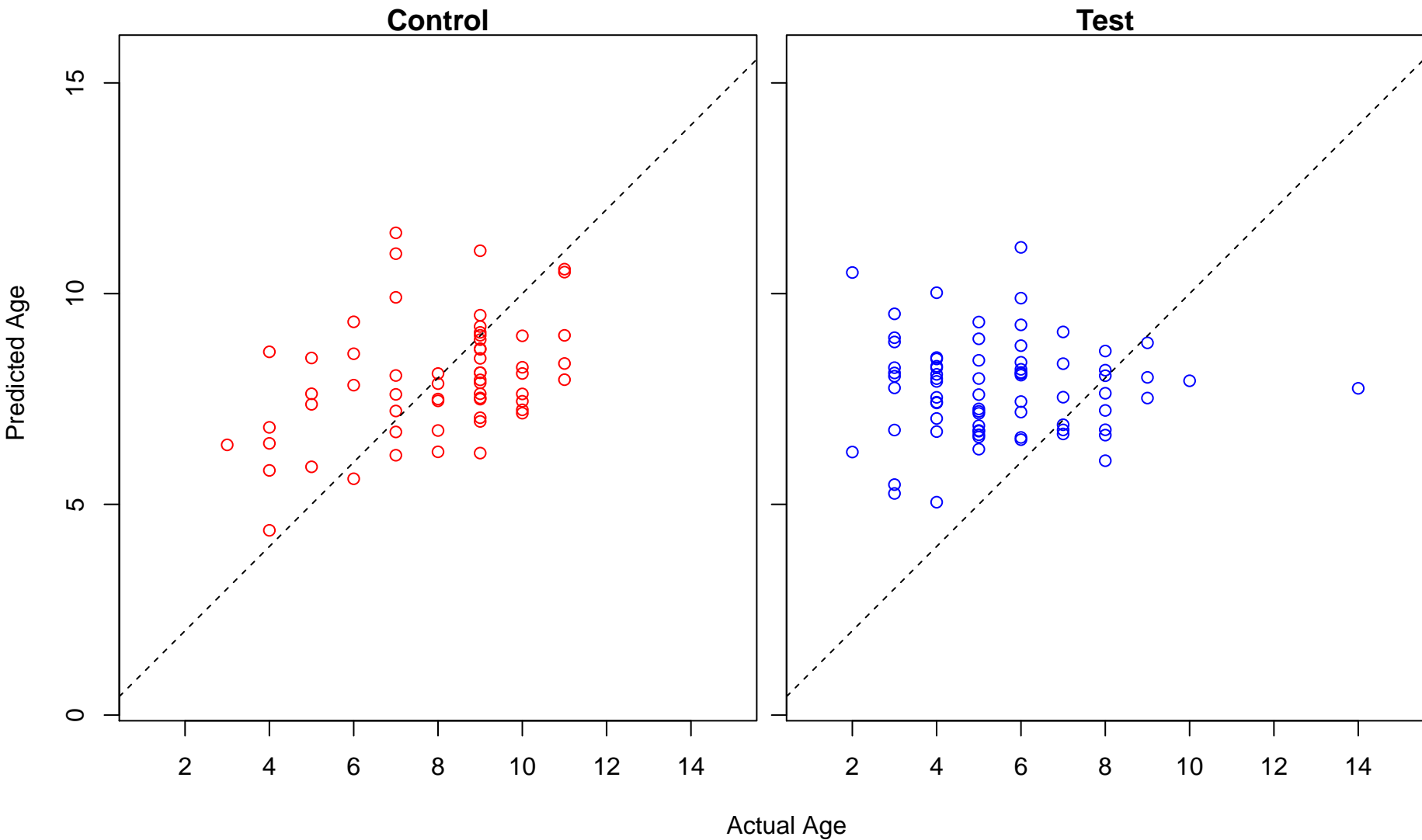
myofibril assembly (Score: 0.801758)



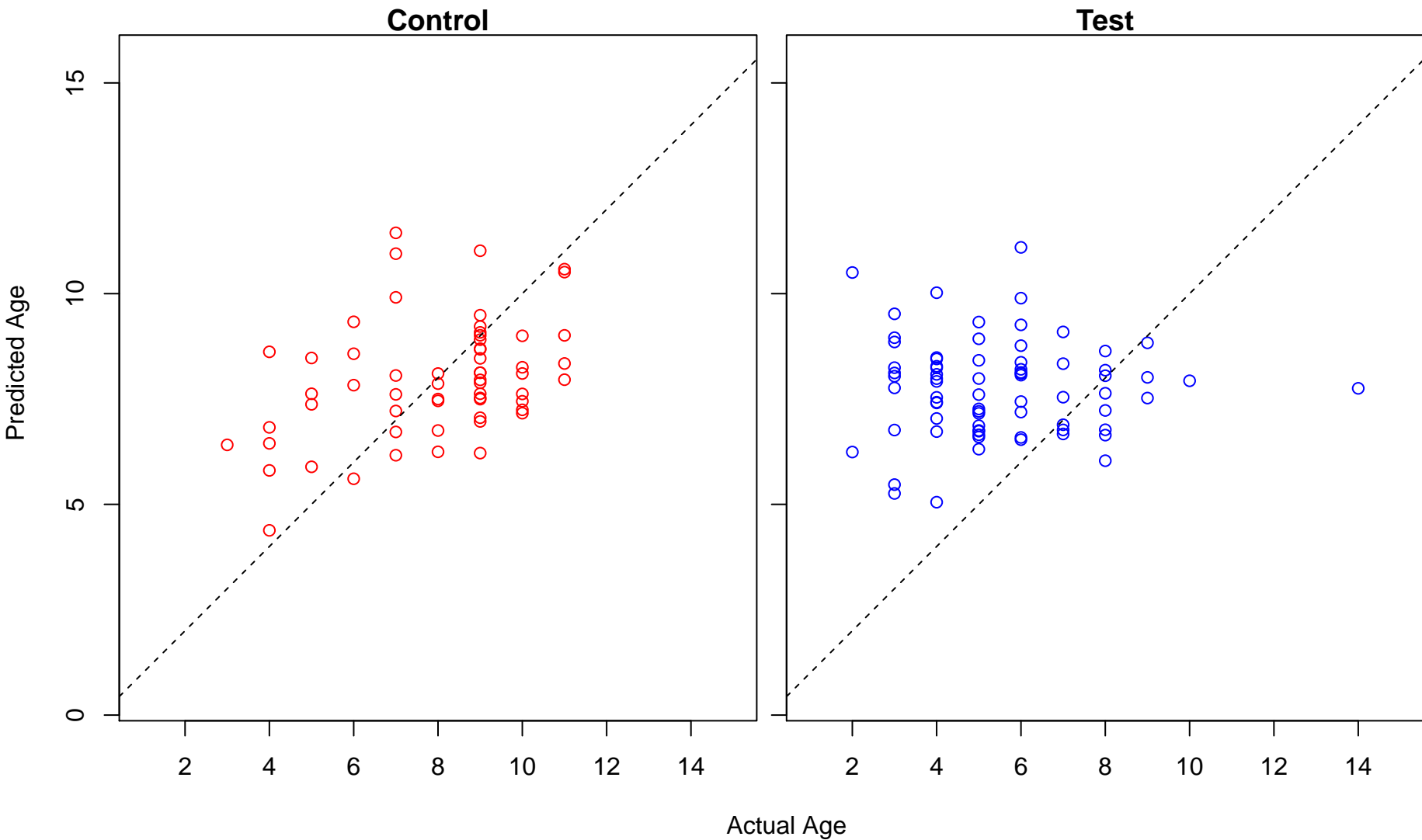
regulation of intracellular steroid hormone receptor signaling pathway (Score: 0.801521)



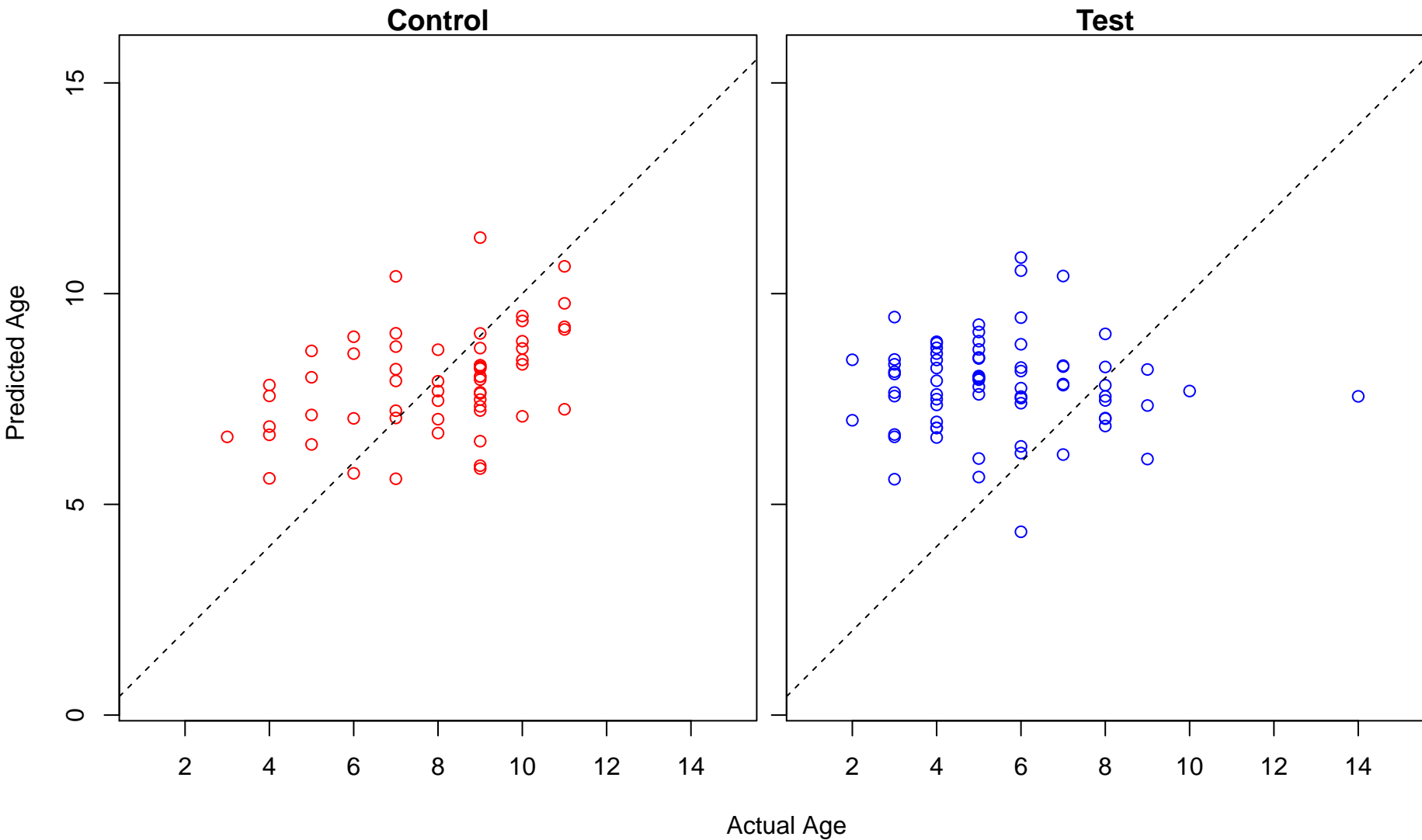
purine nucleoside monophosphate metabolic process (Score: 0.801230)



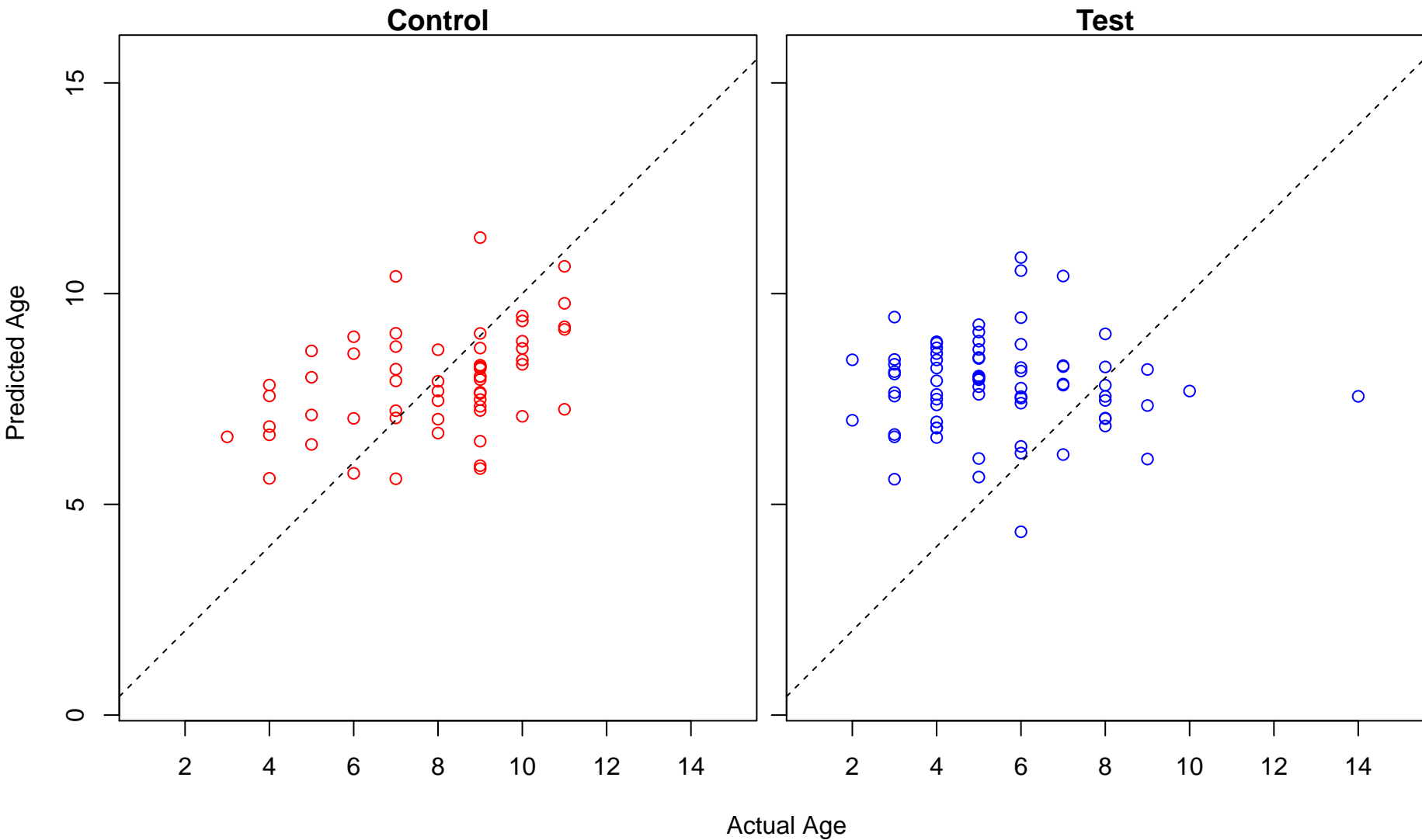
purine ribonucleoside monophosphate metabolic process (Score: 0.801230)



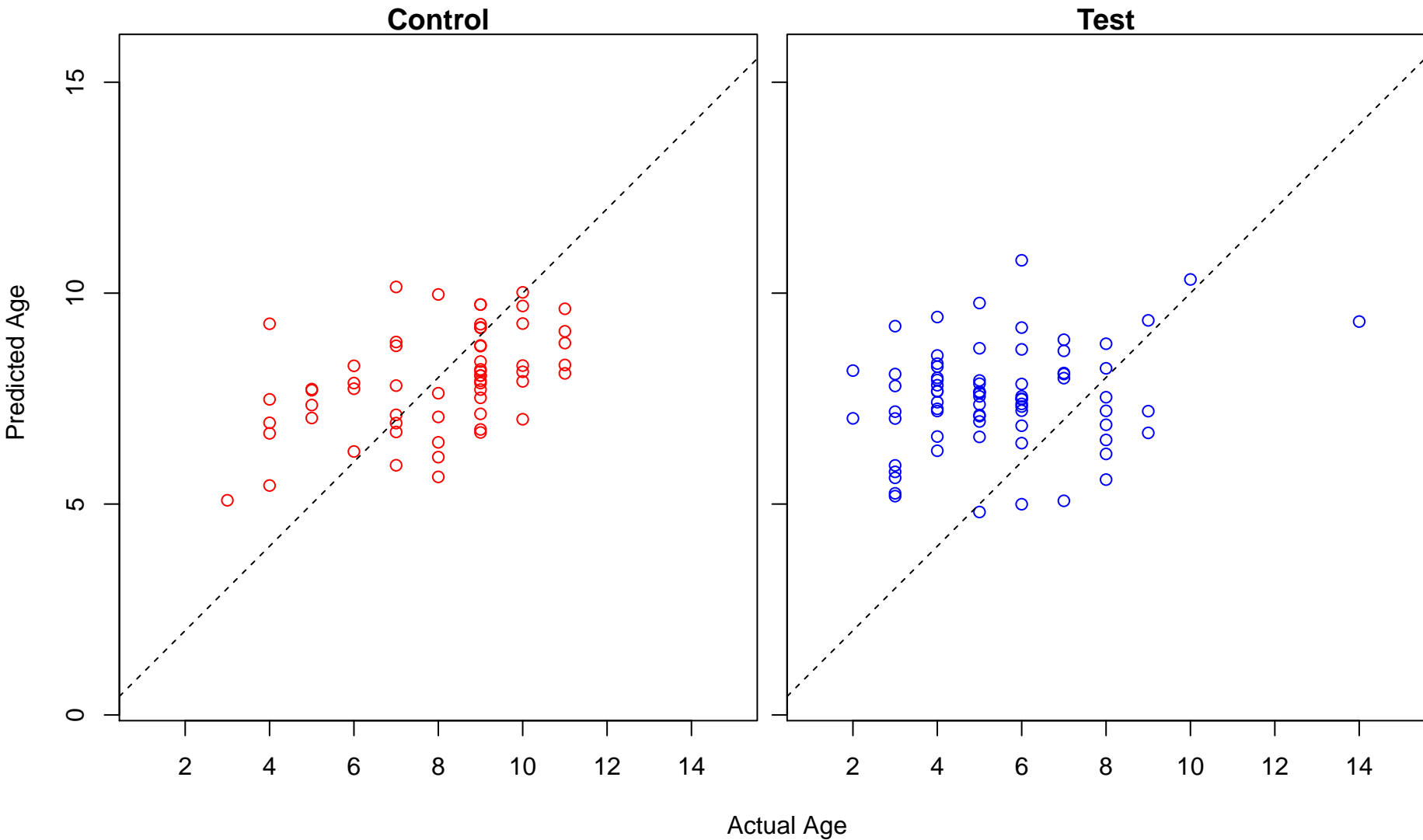
cardiac muscle adaptation (Score: 0.800791)



cardiac muscle hypertrophy in response to stress (Score: 0.800791)

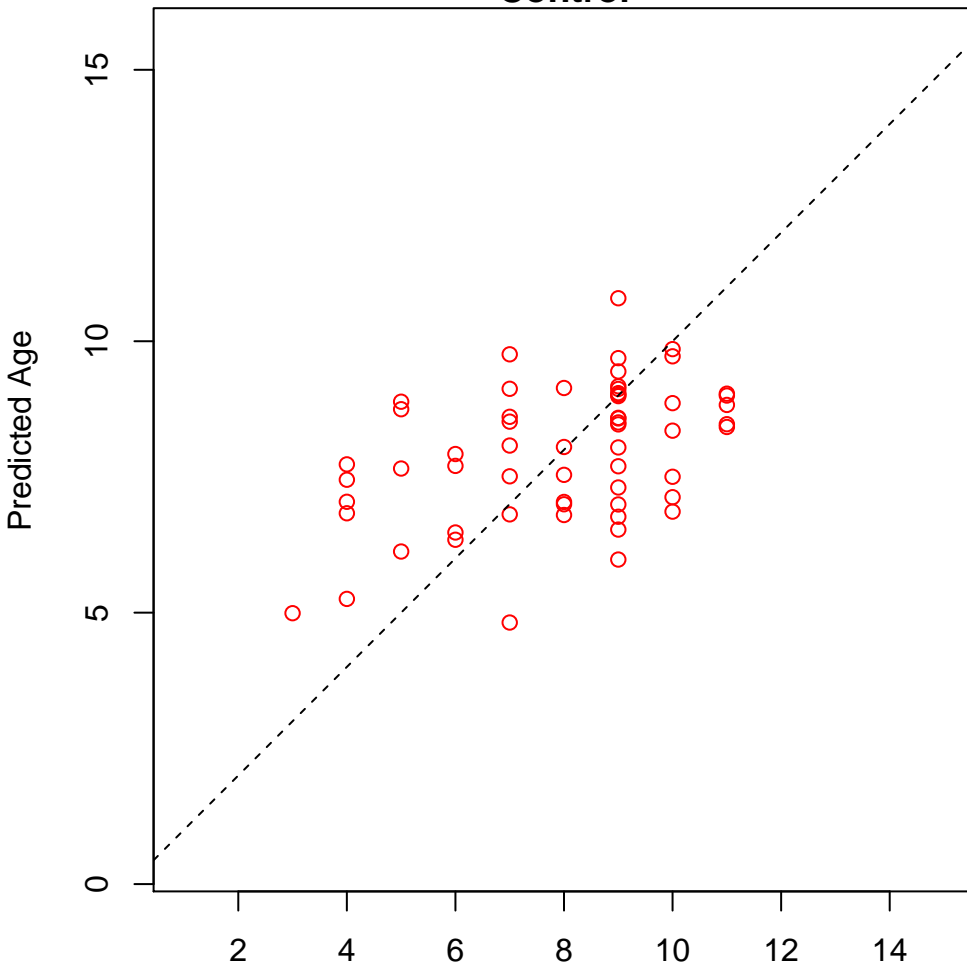


positive regulation of humoral immune response (Score: 0.800676)

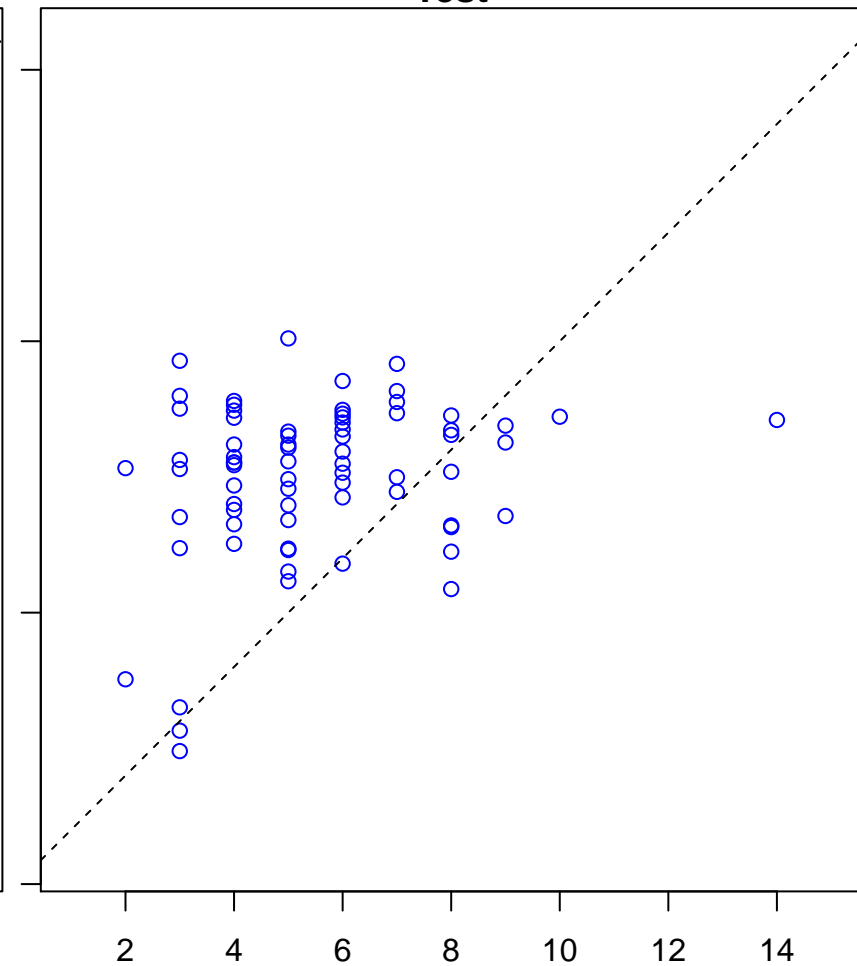


embryonic skeletal joint morphogenesis (Score: 0.800522)

Control

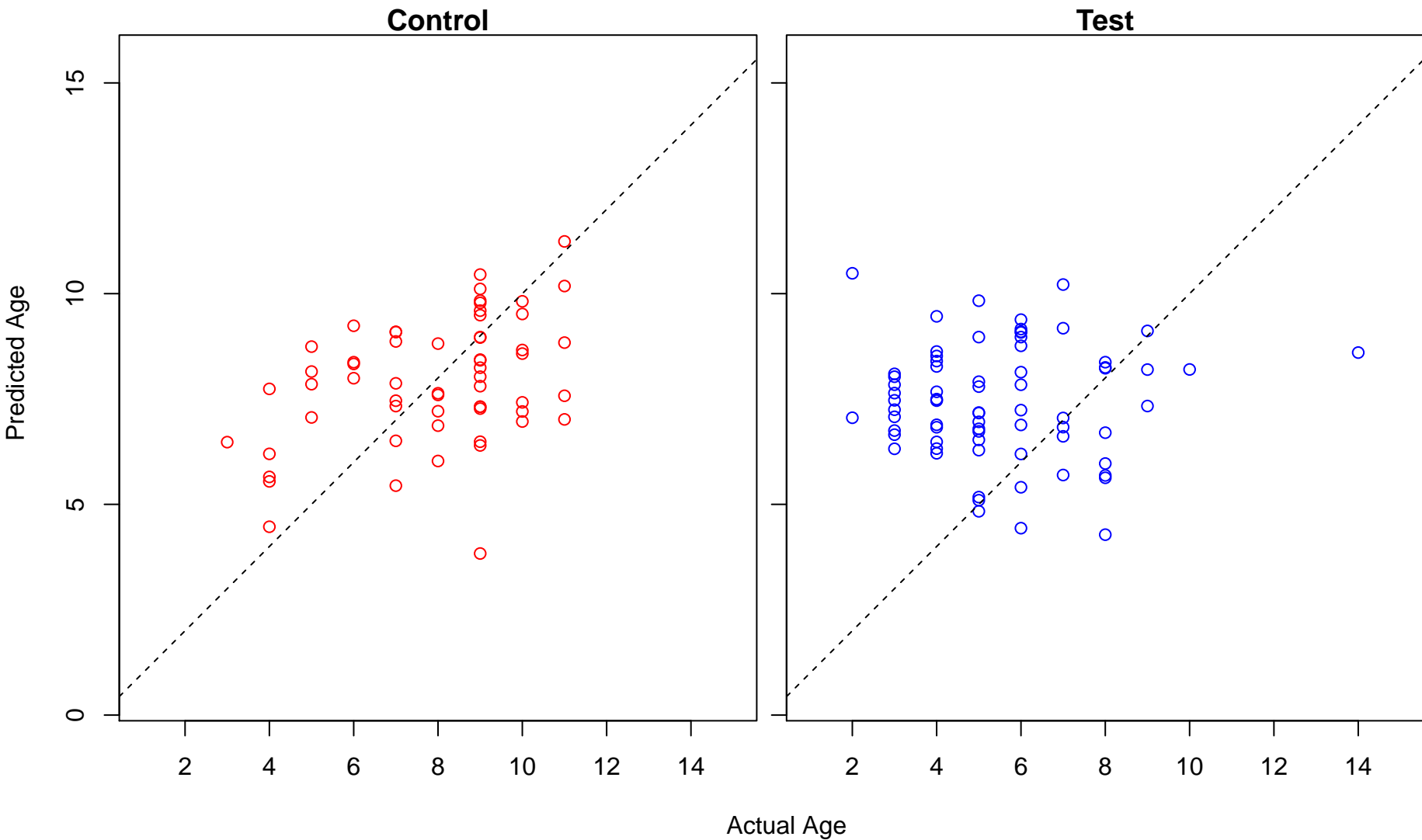


Test



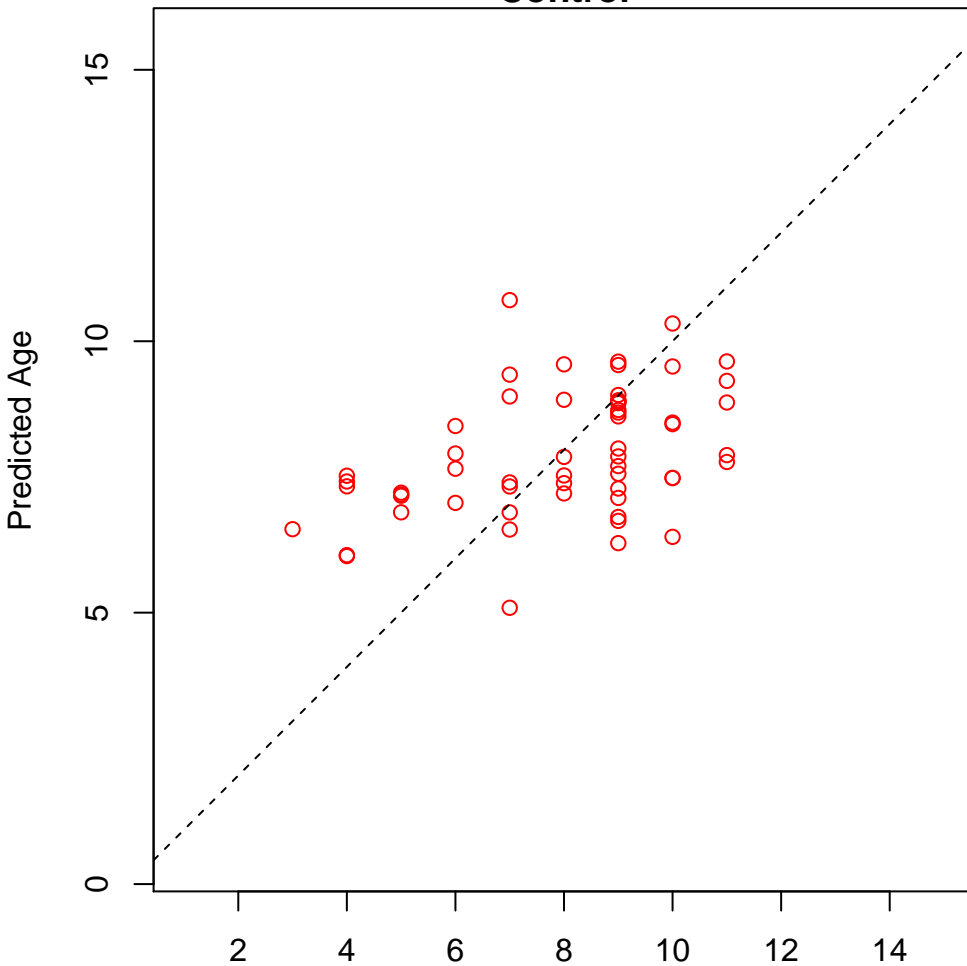
Actual Age

protein maturation (Score: 0.800509)

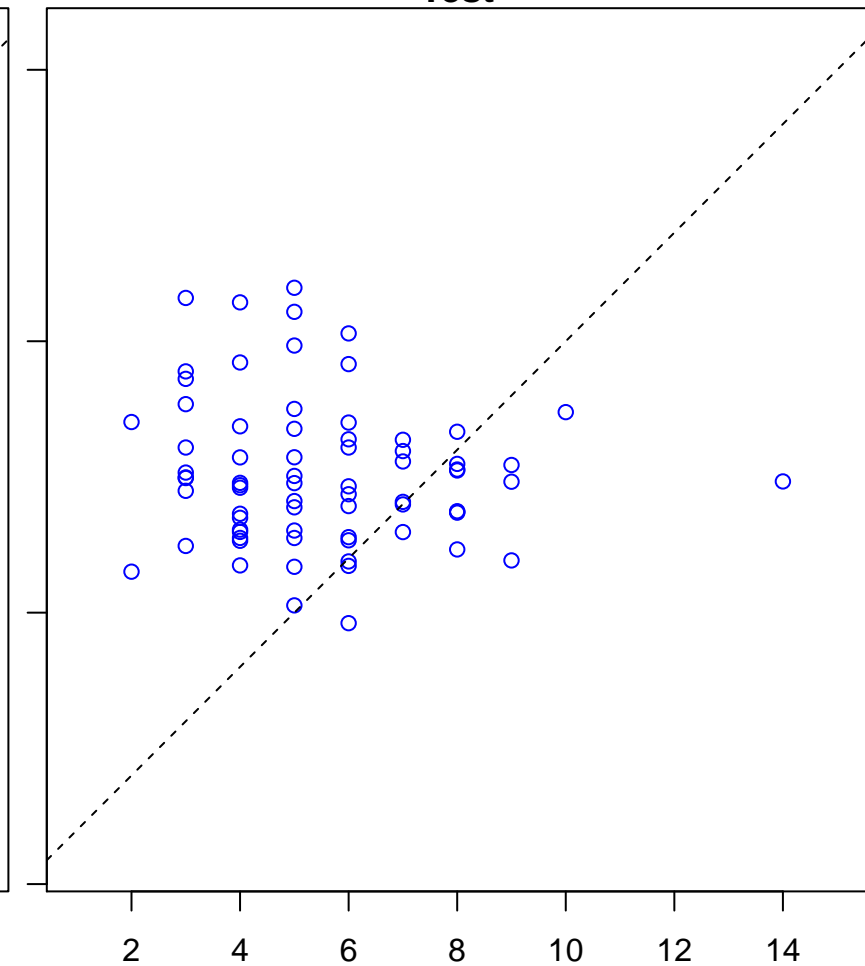


protein import into mitochondrial matrix (Score: 0.800334)

Control

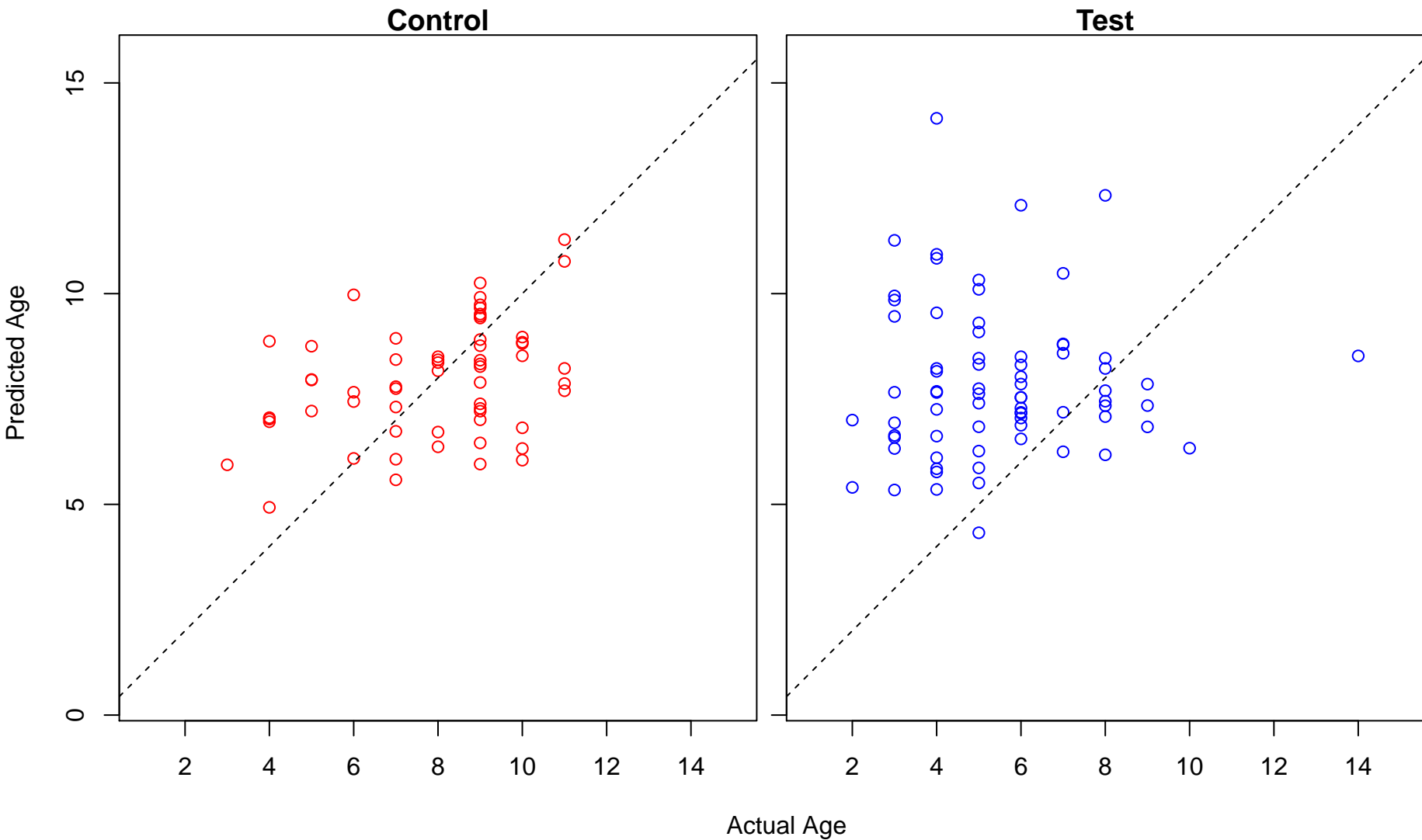


Test

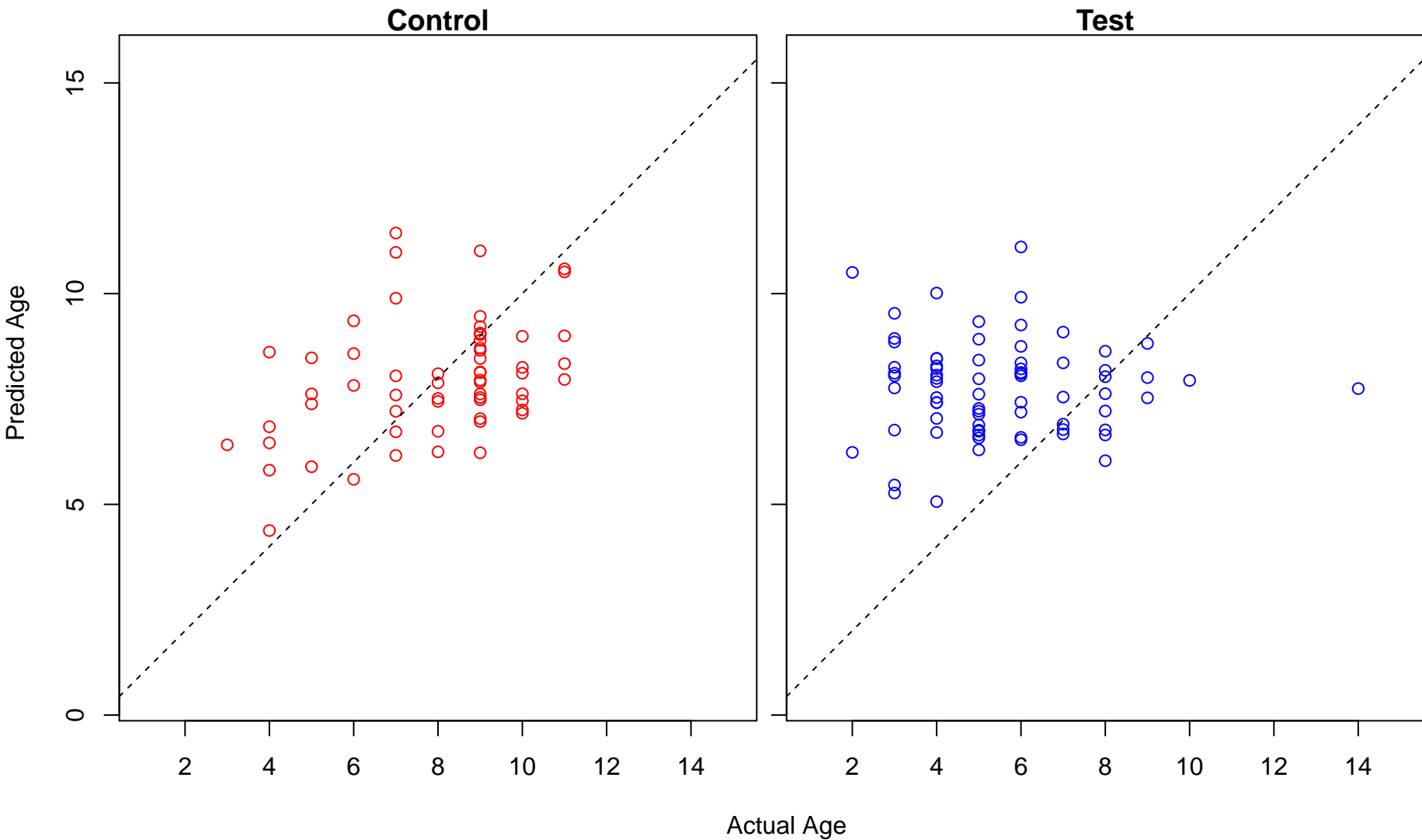


Actual Age

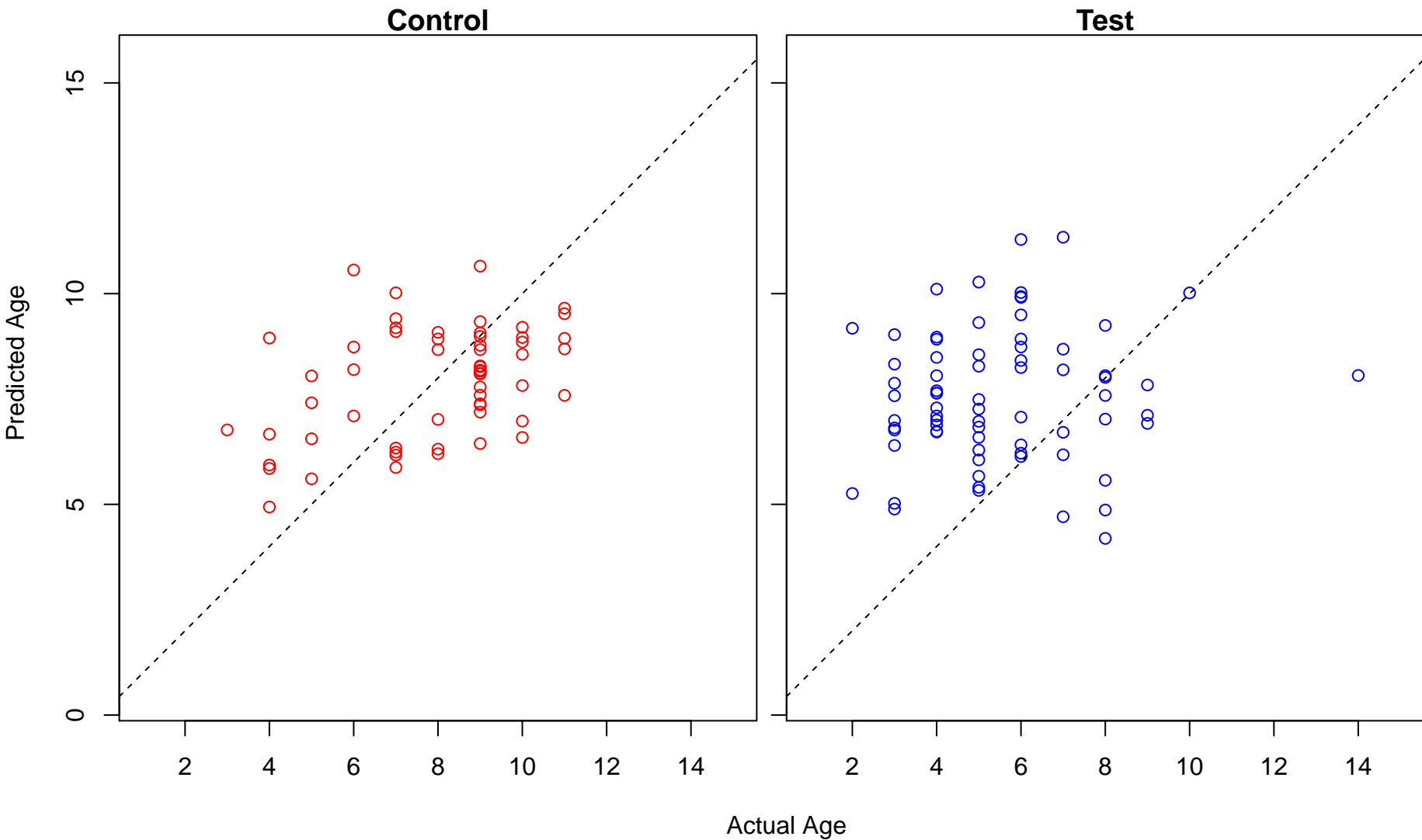
regulation of T-helper 17 type immune response (Score: 0.799955)



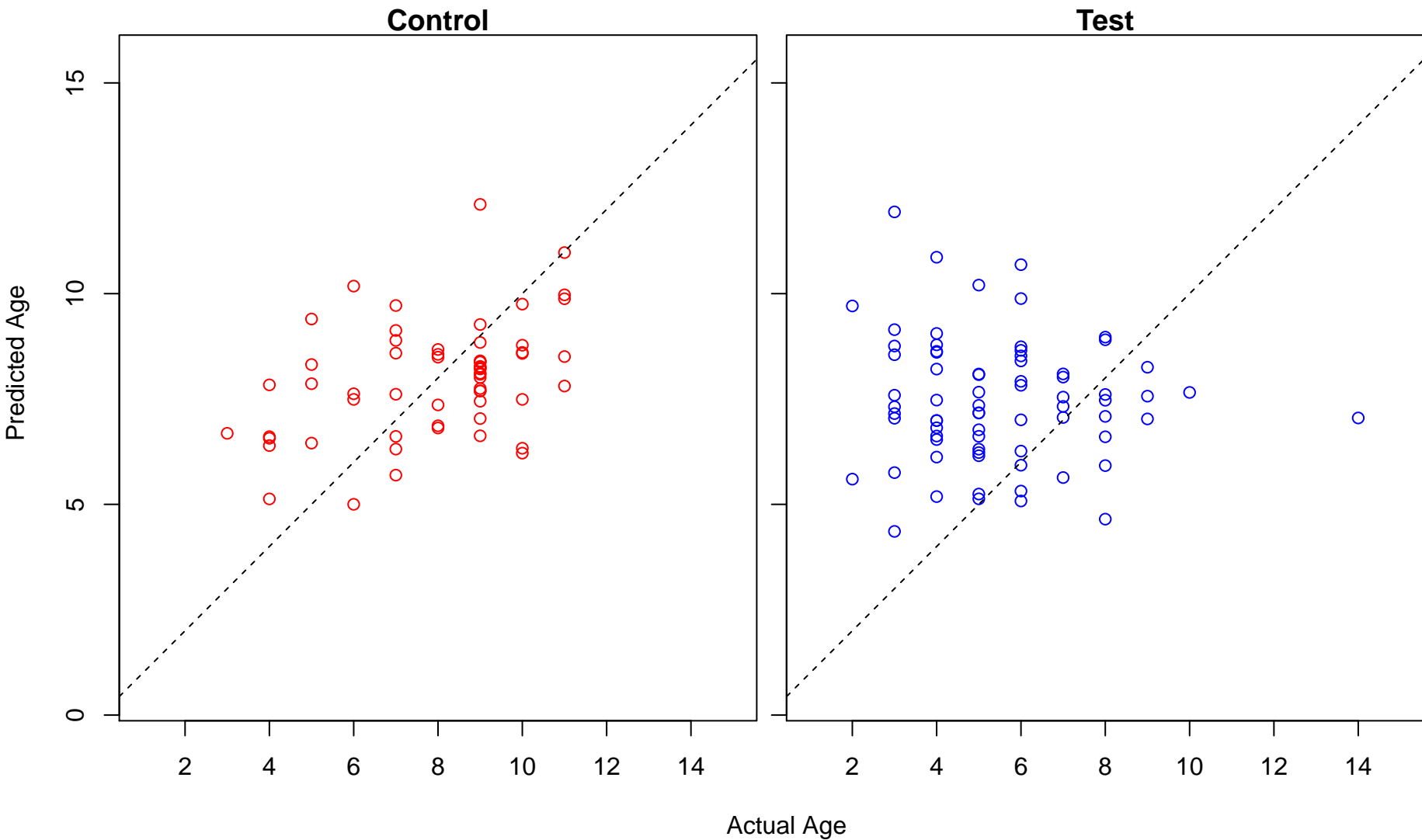
ribonucleoside monophosphate metabolic process (Score: 0.798734)



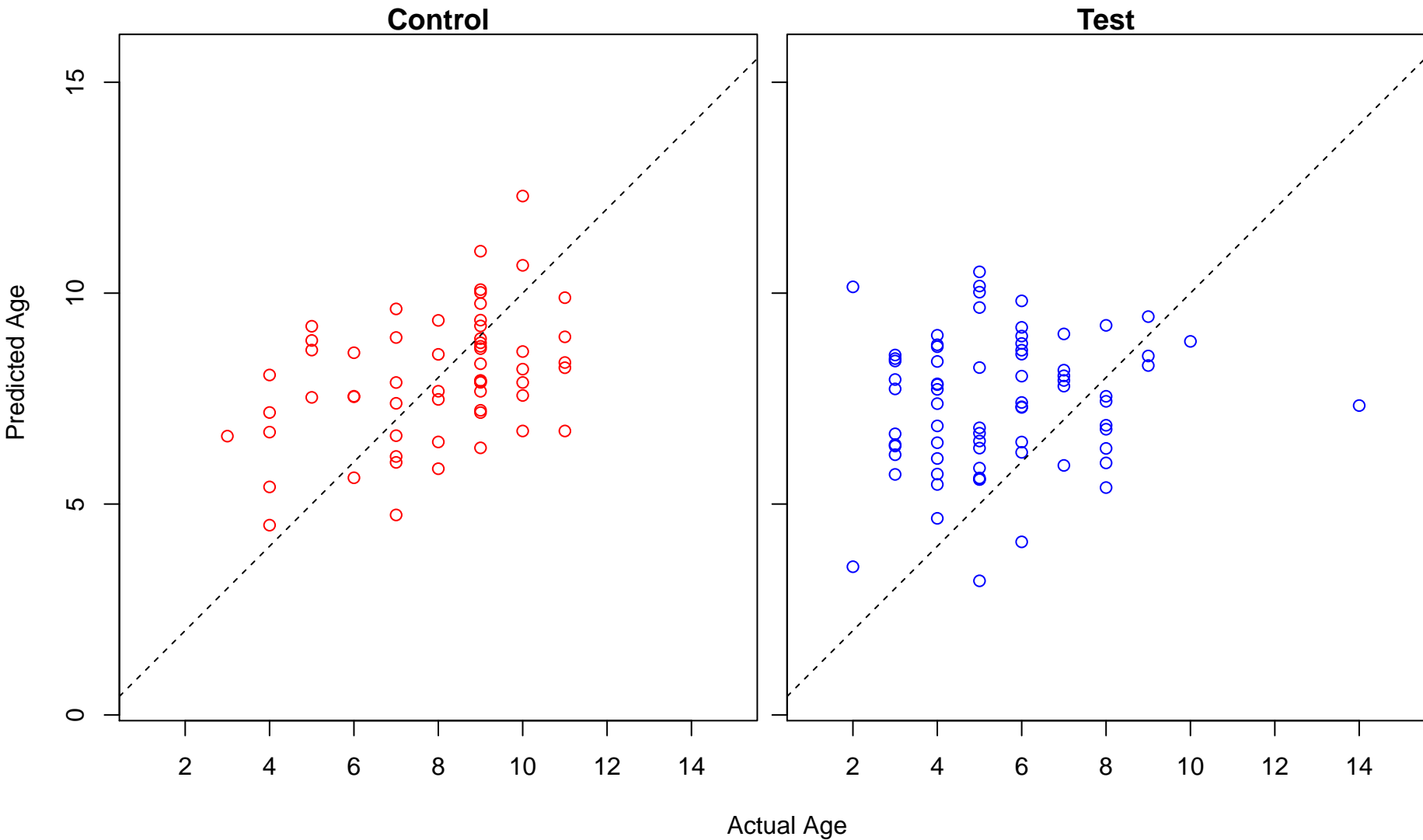
positive regulation of ATPase activity (Score: 0.797896)



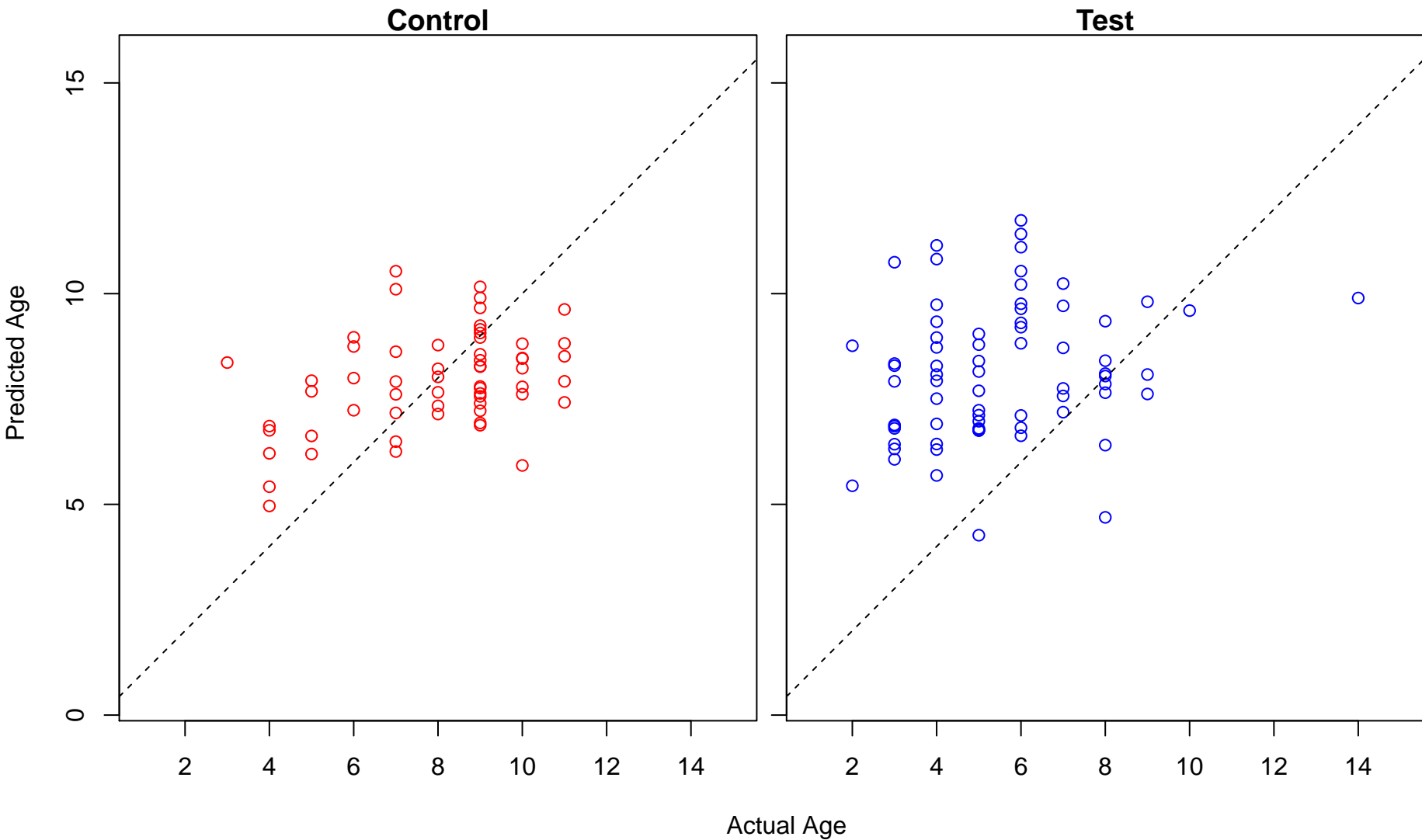
spindle assembly (Score: 0.796396)



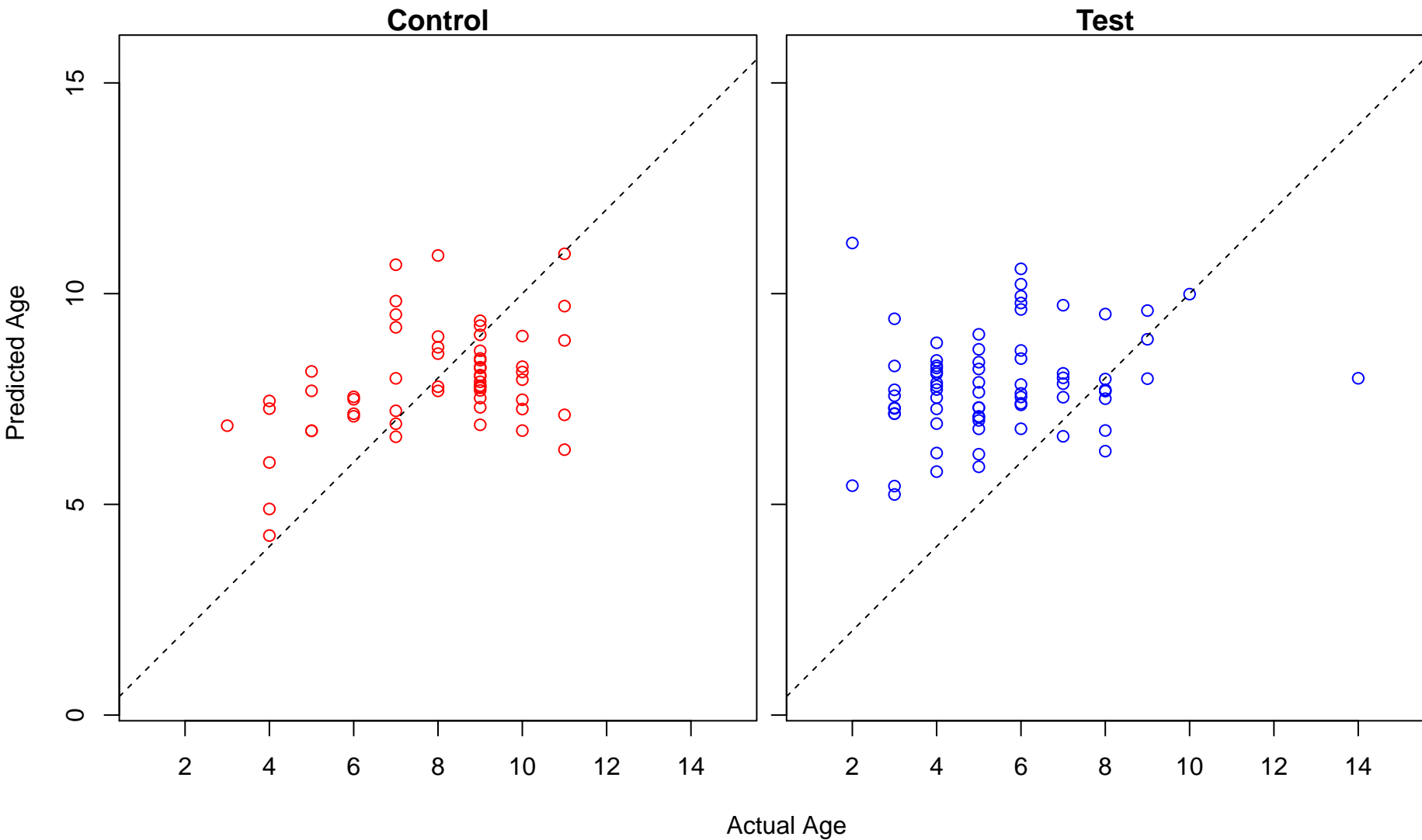
chondroitin sulfate proteoglycan biosynthetic process (Score: 0.796032)



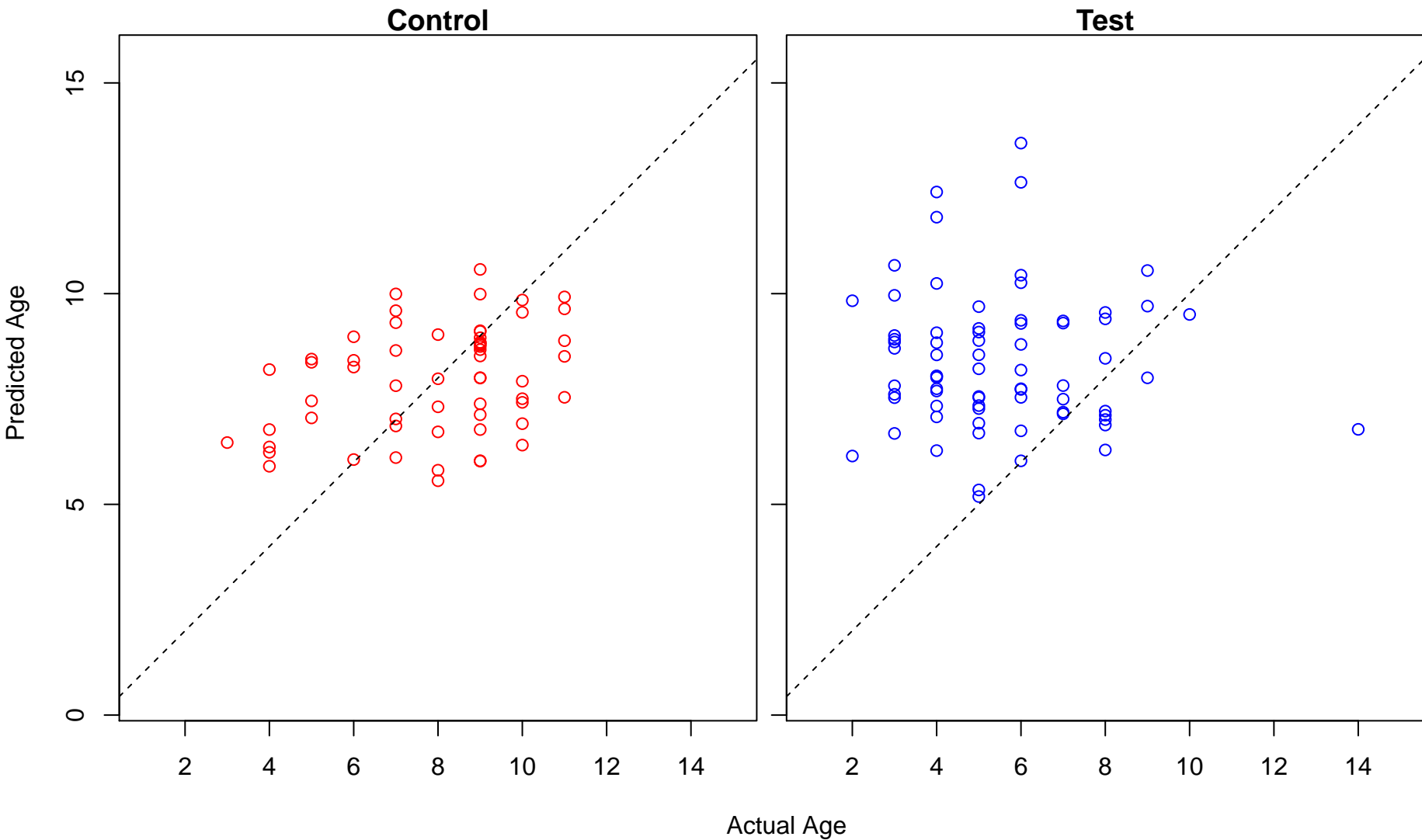
positive regulation of Rho protein signal transduction (Score: 0.794202)



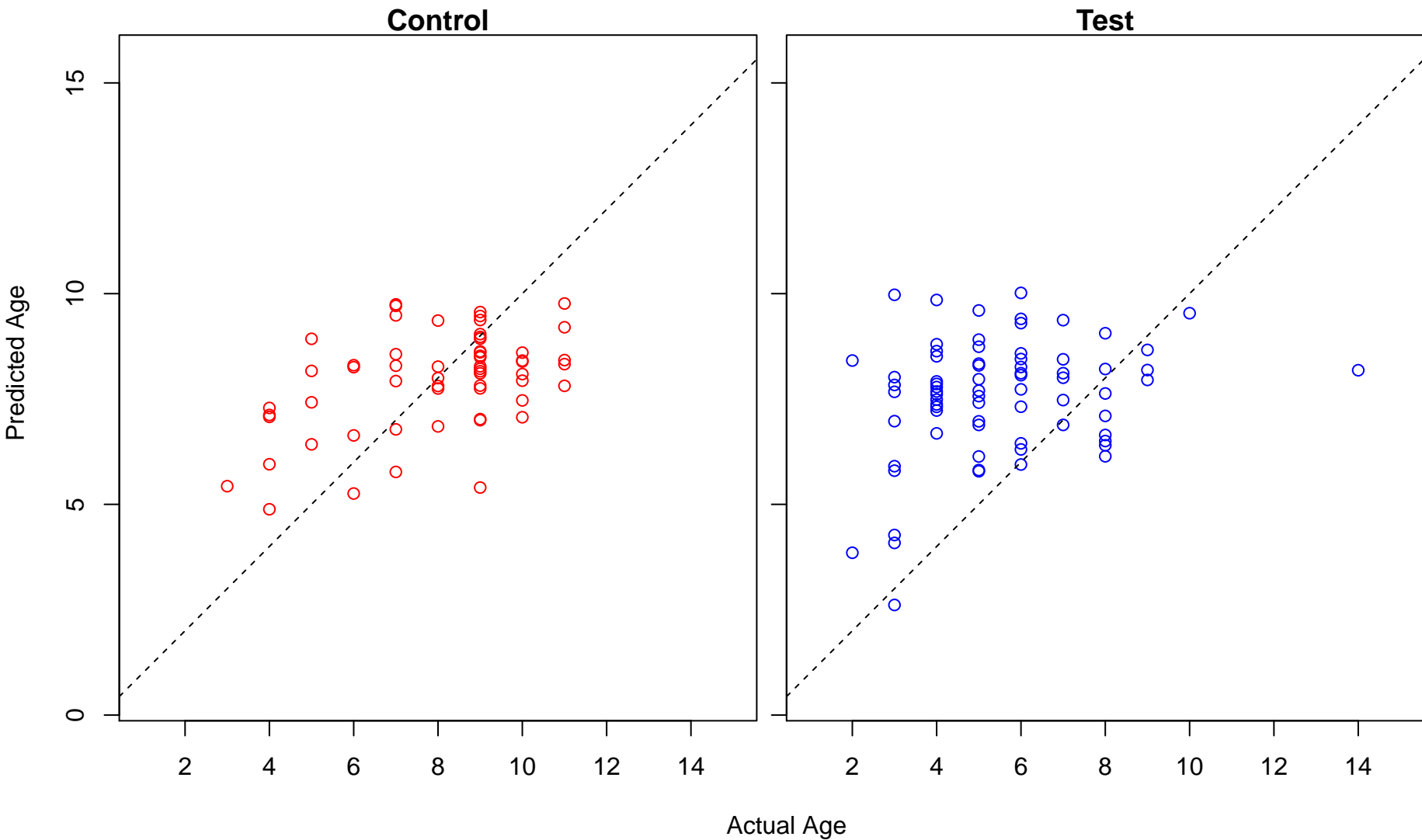
positive regulation of B cell receptor signaling pathway (Score: 0.794139)



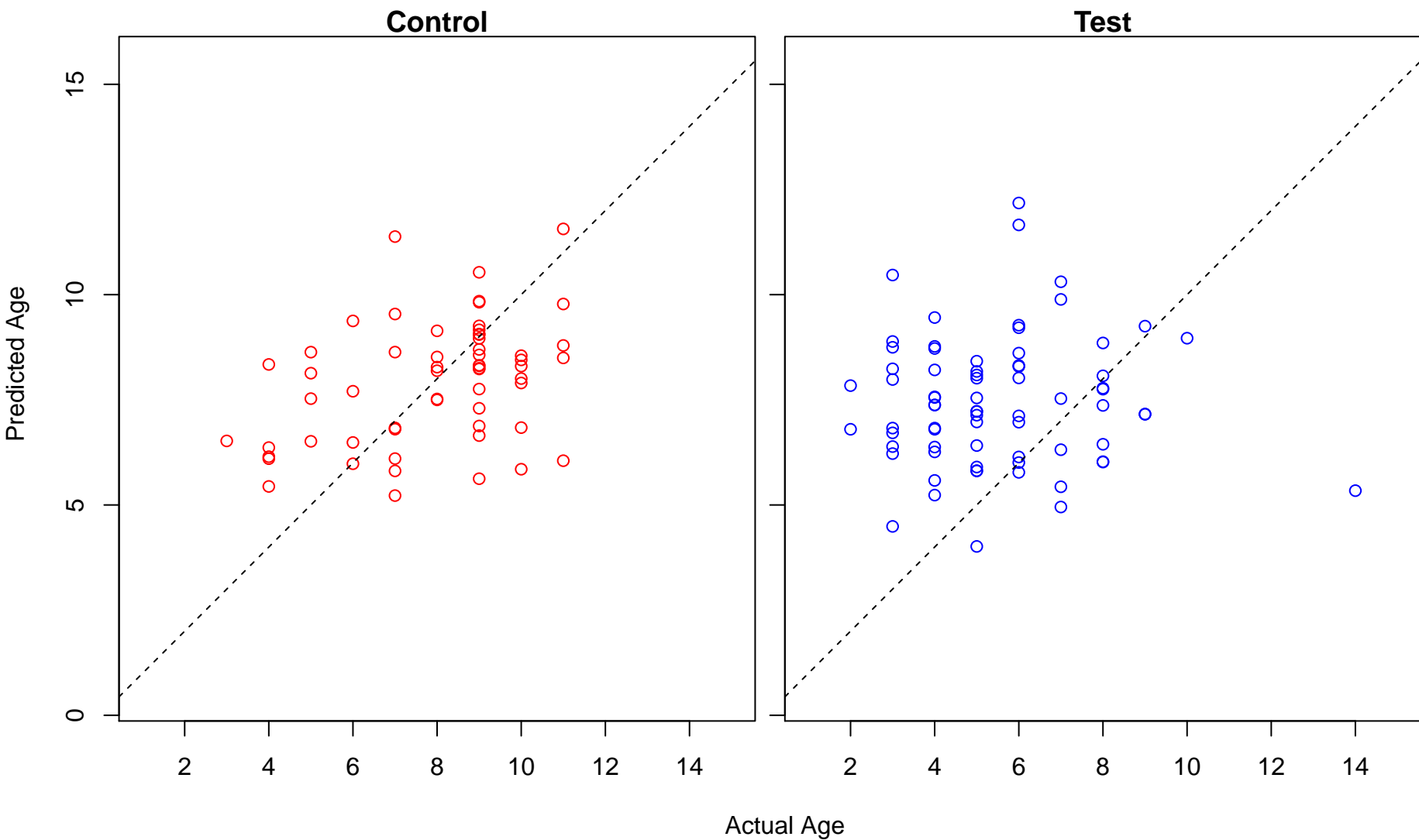
retinoid metabolic process (Score: 0.793801)



negative regulation of astrocyte differentiation (Score: 0.792727)

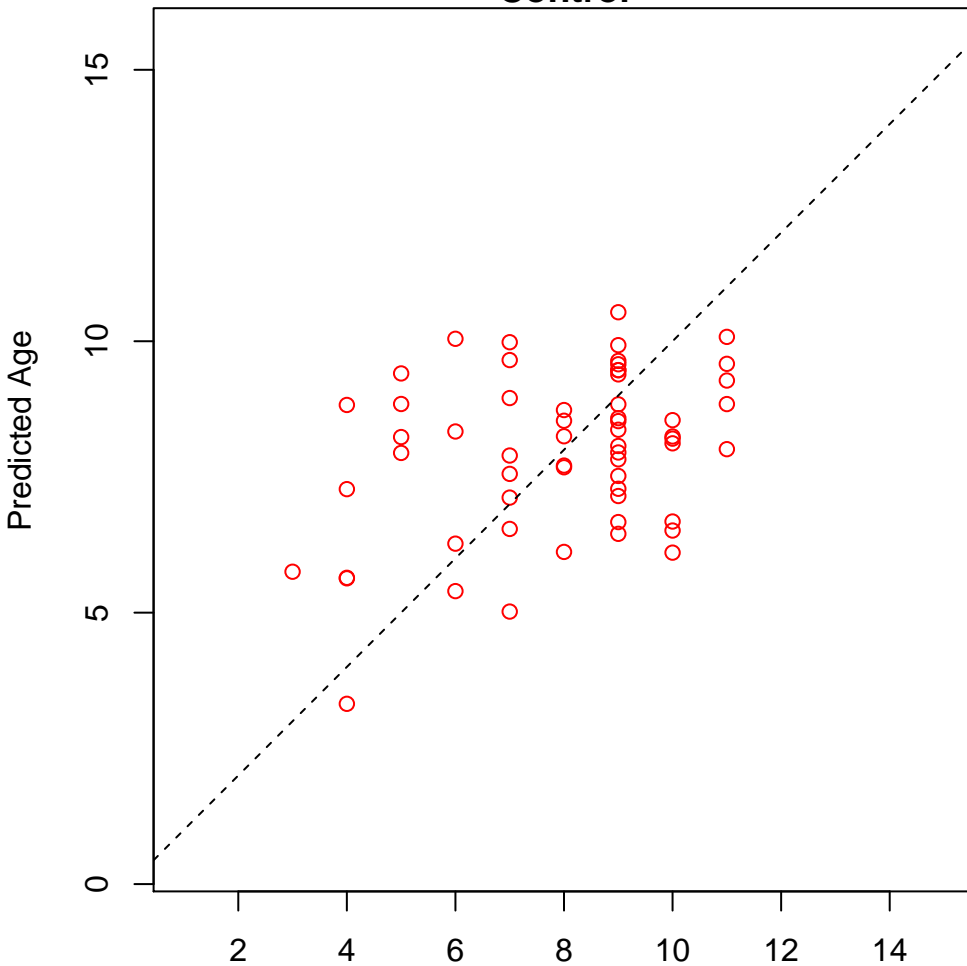


positive regulation of protein autophosphorylation (Score: 0.792244)

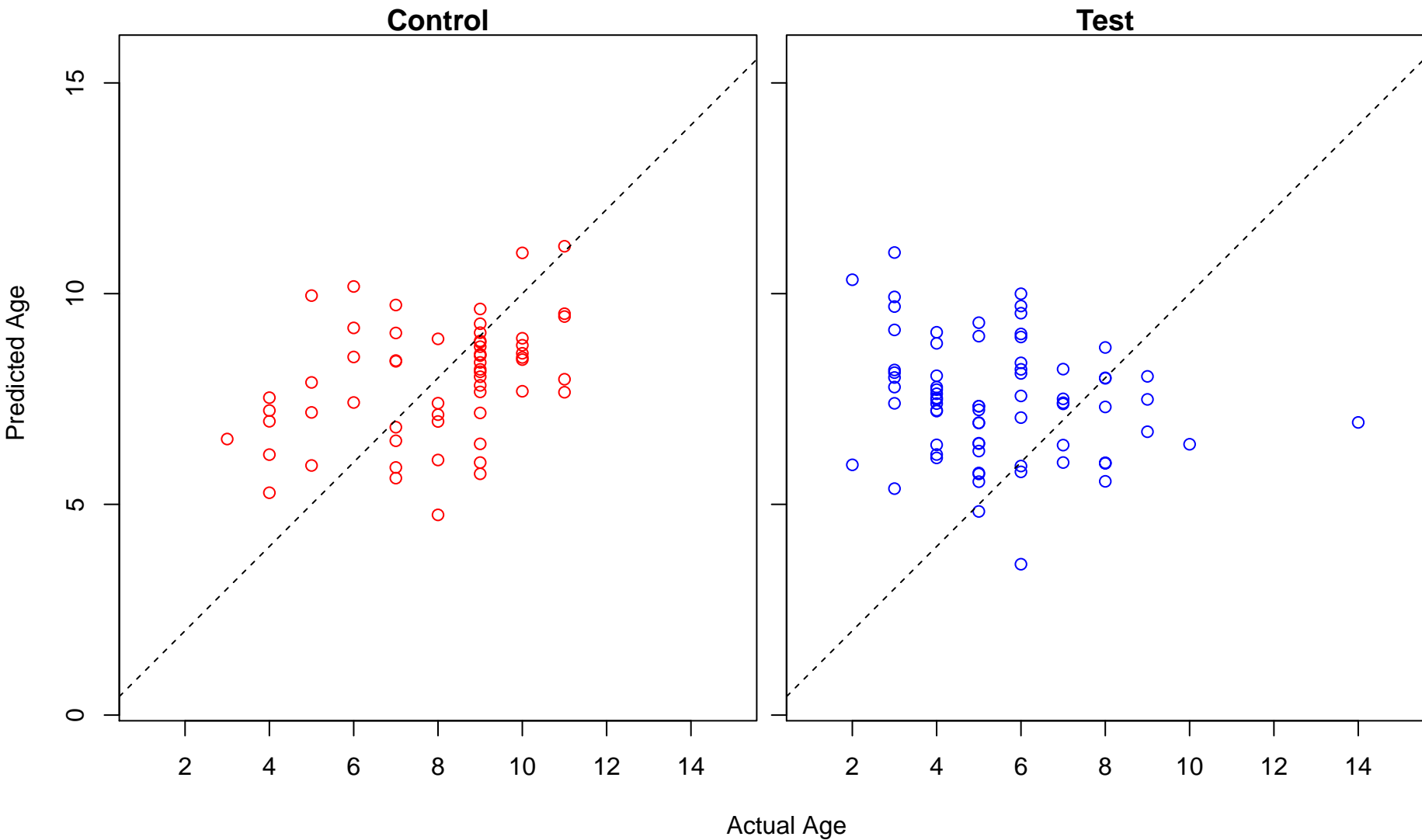


nucleoside phosphate catabolic process (Score: 0.791132)

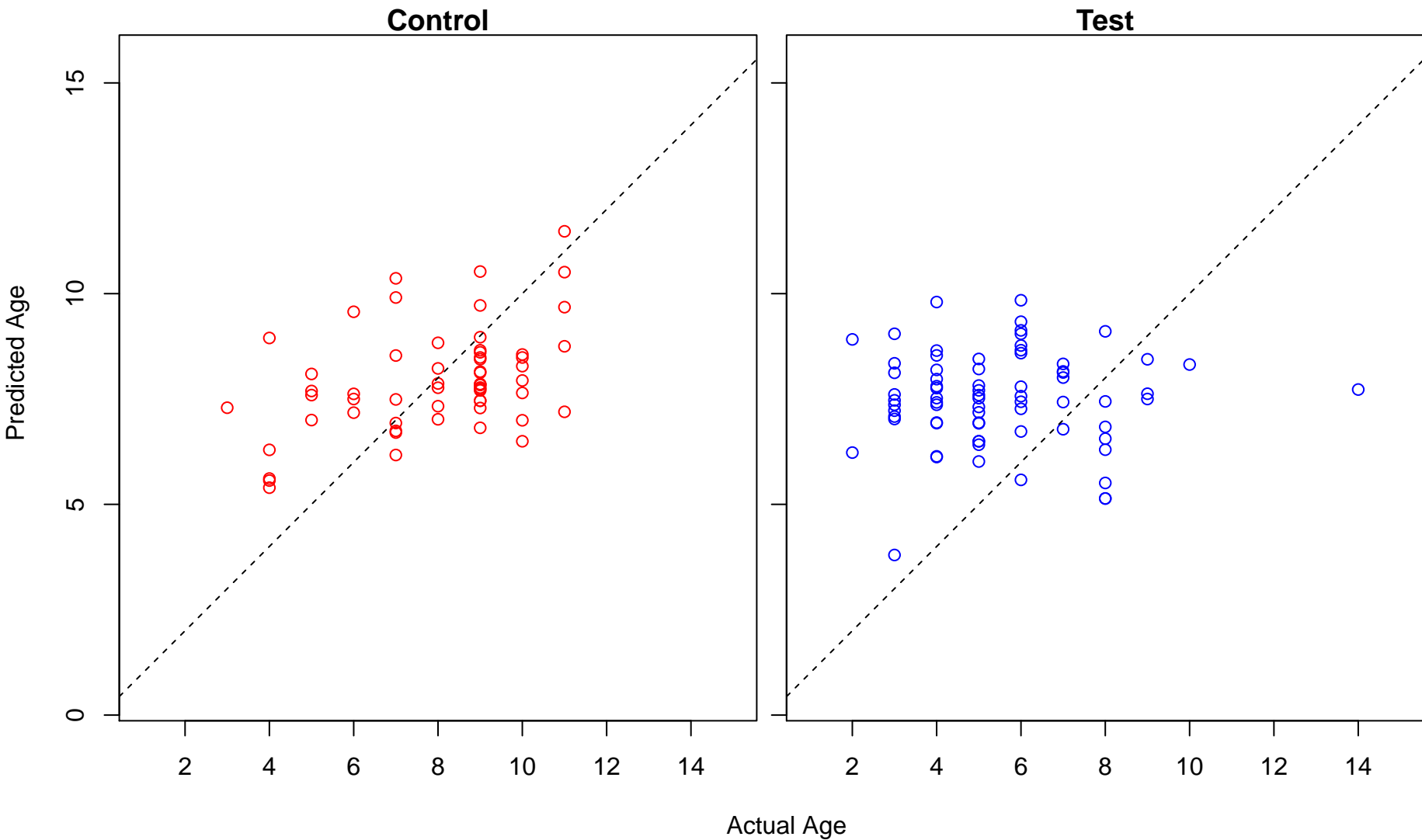
Control



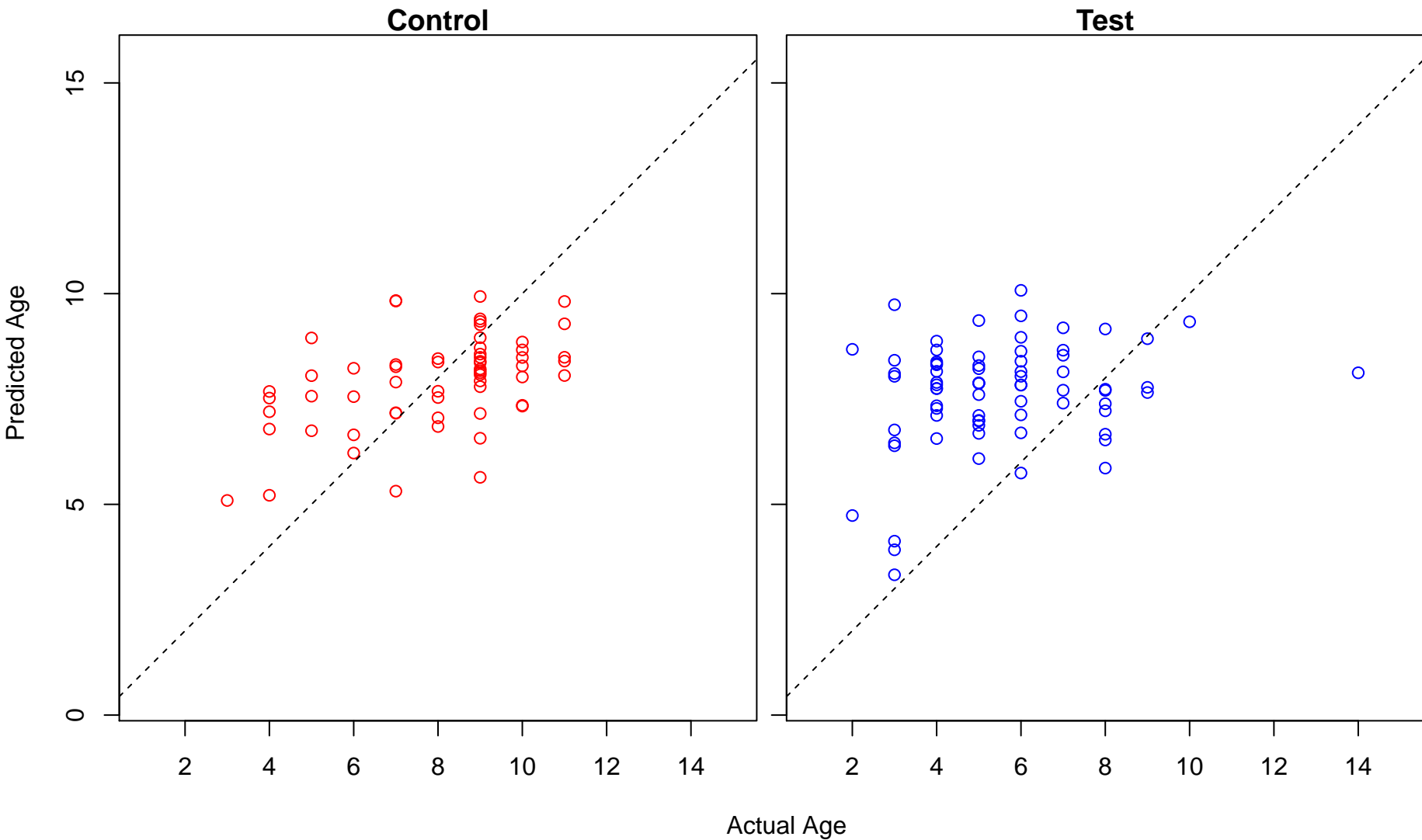
regulation of viral entry into host cell (Score: 0.790720)



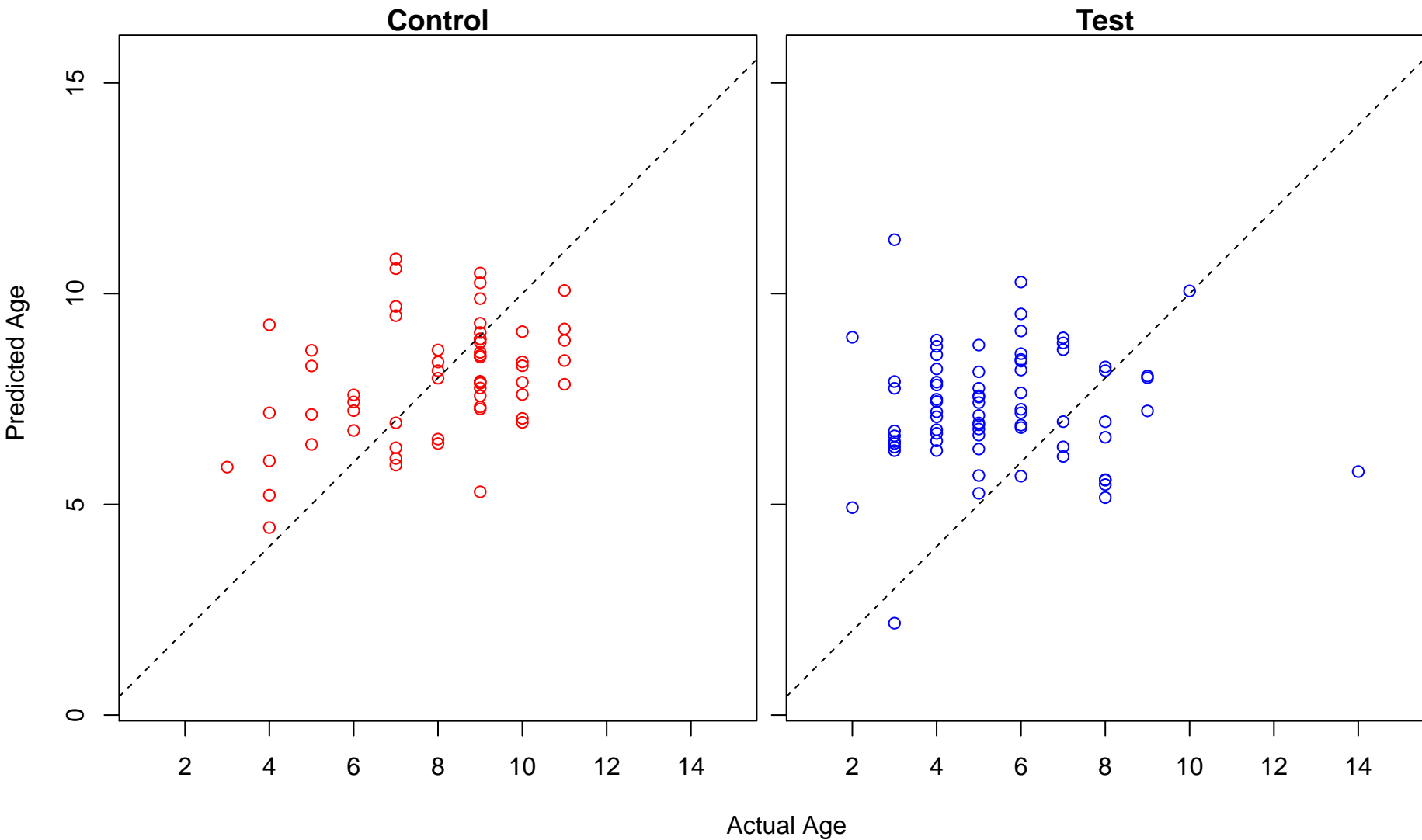
auditory receptor cell stereocilium organization (Score: 0.790590)



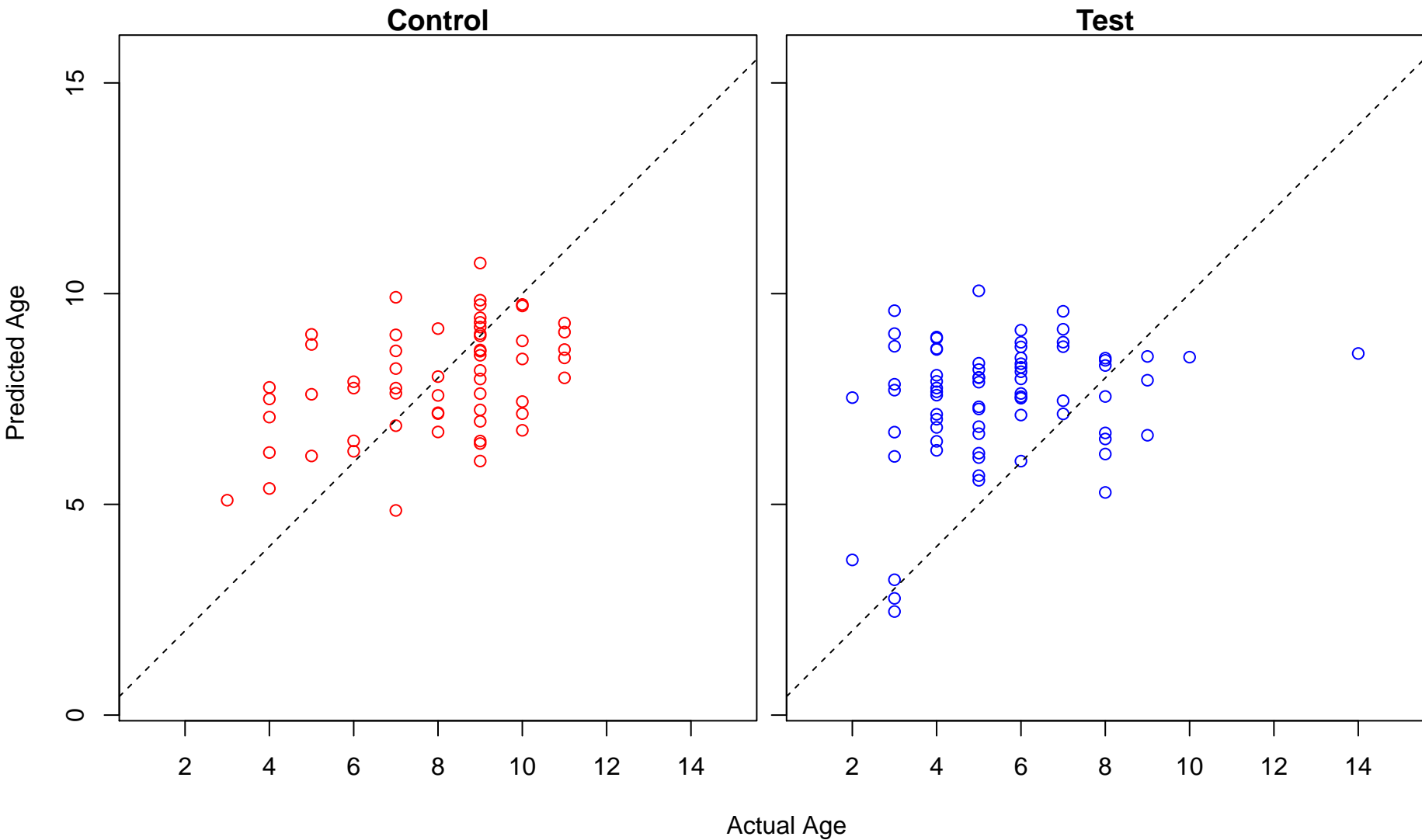
lateral sprouting from an epithelium (Score: 0.789384)



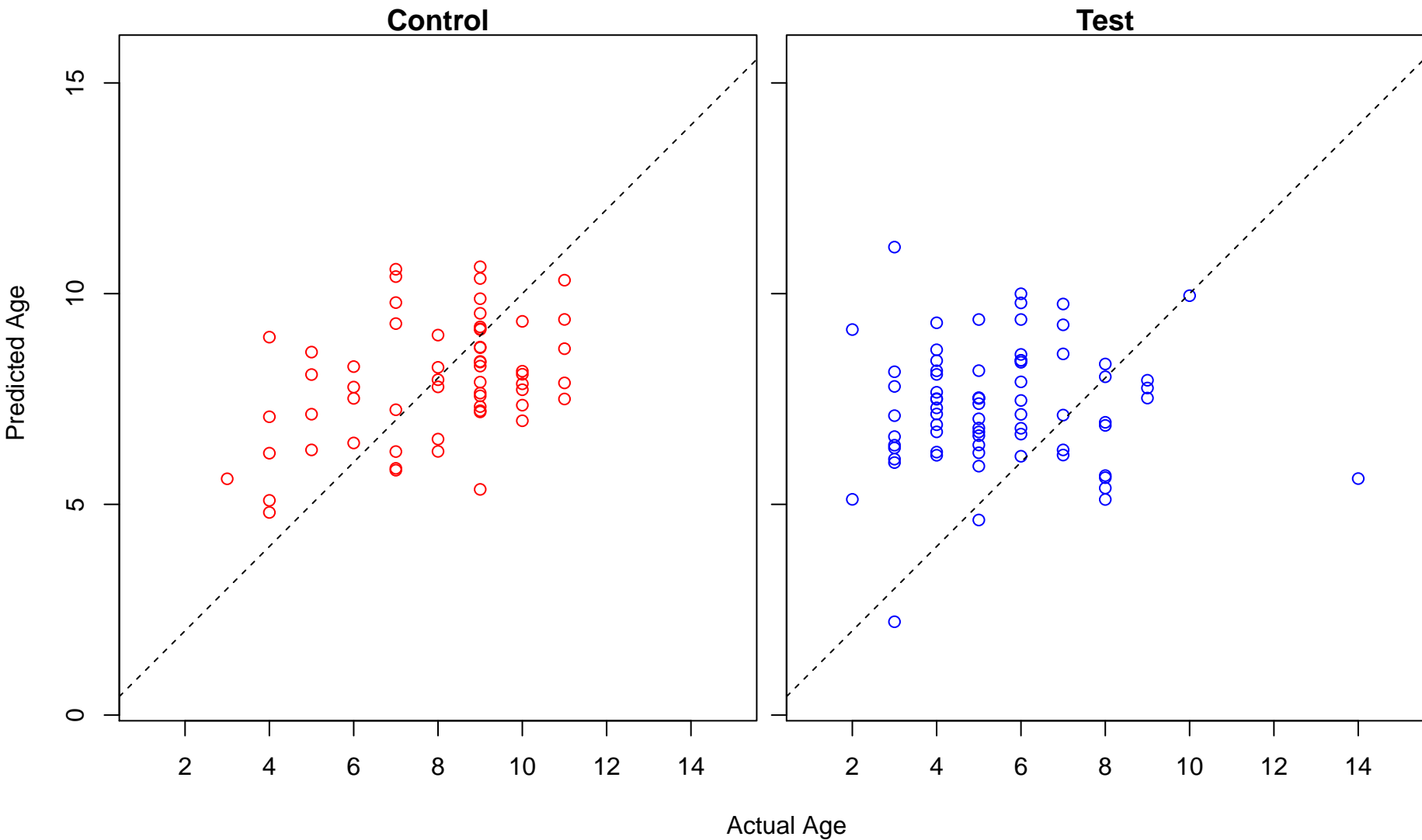
organelle membrane fusion (Score: 0.788394)



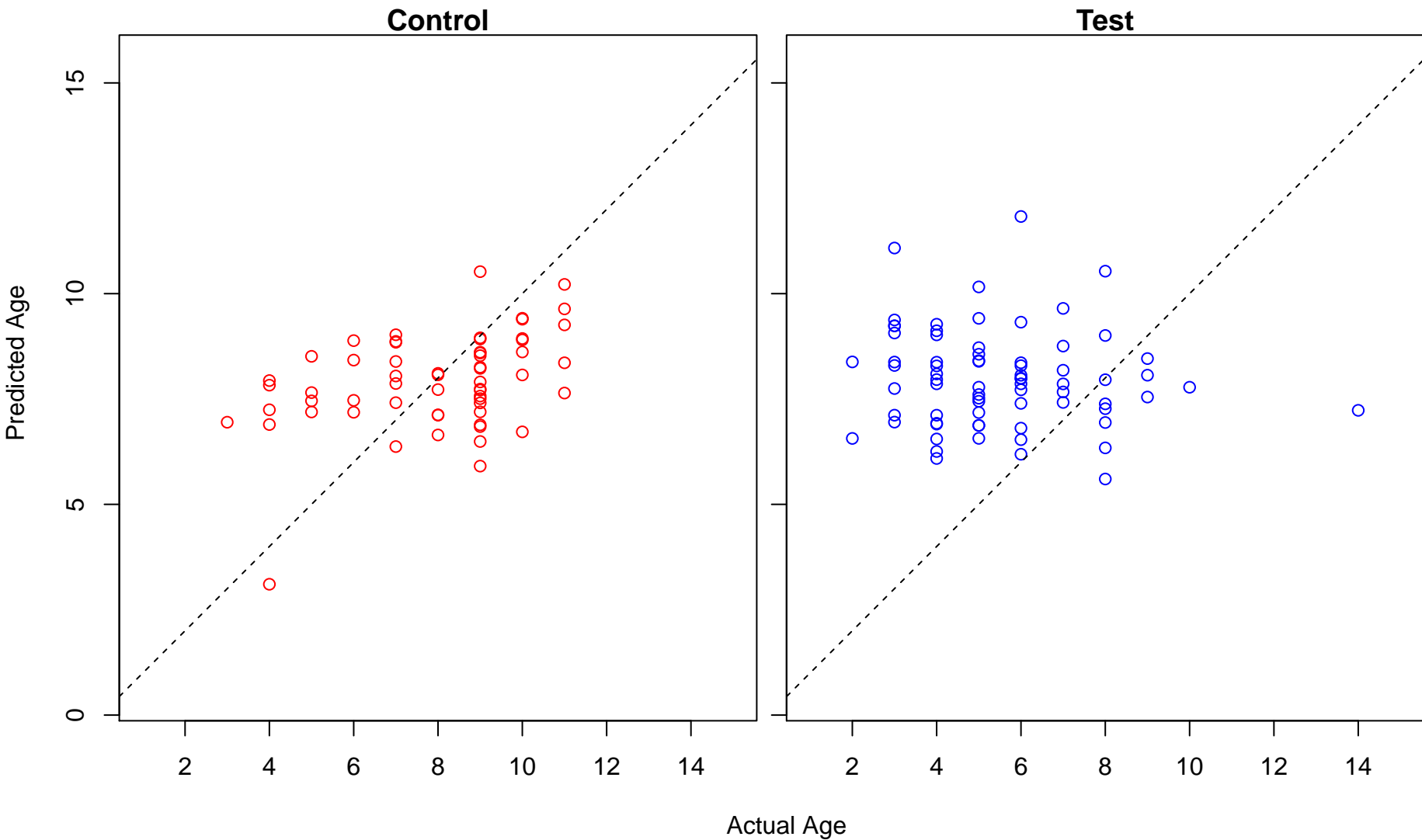
embryonic skeletal joint development (Score: 0.787996)



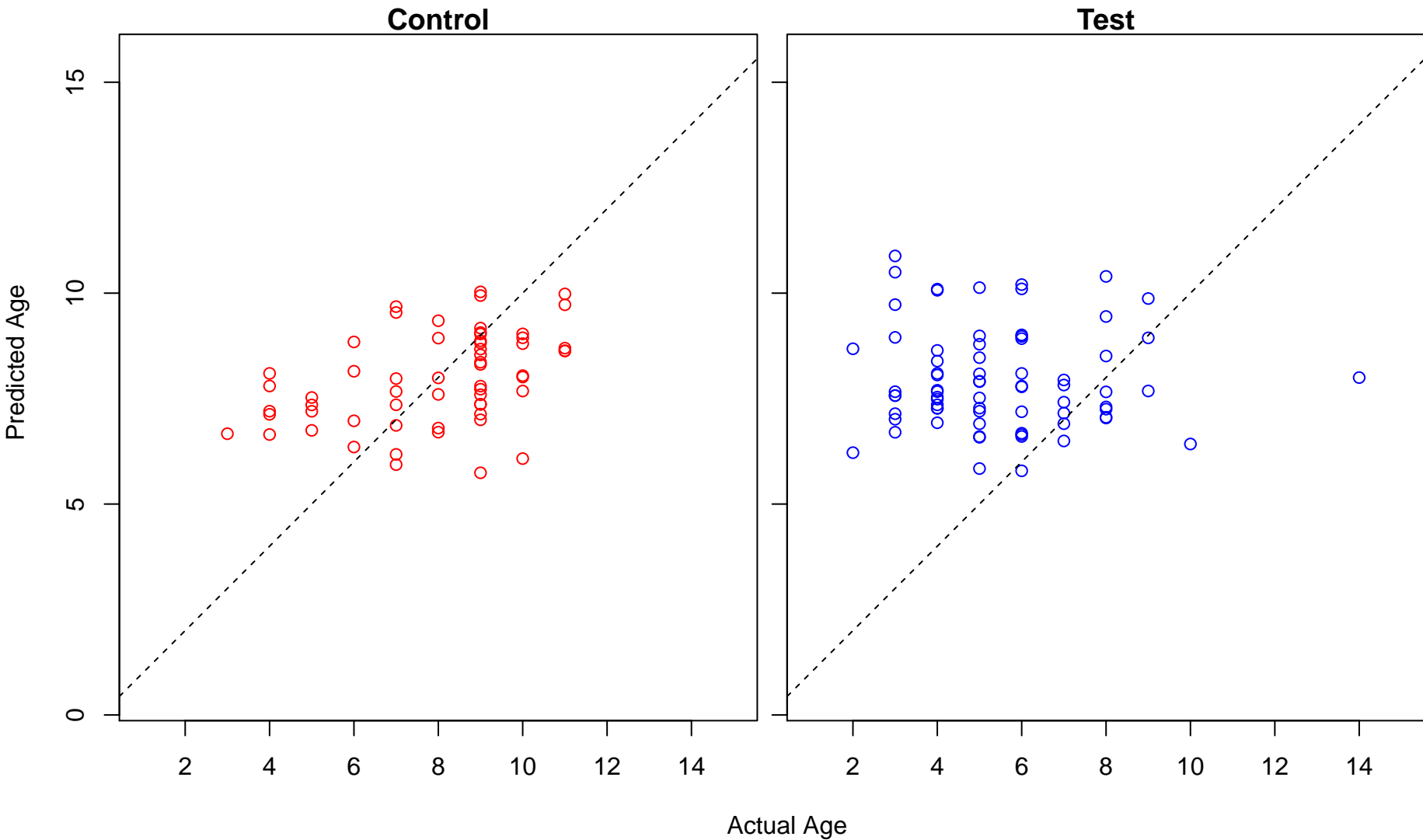
organelle fusion (Score: 0.787723)



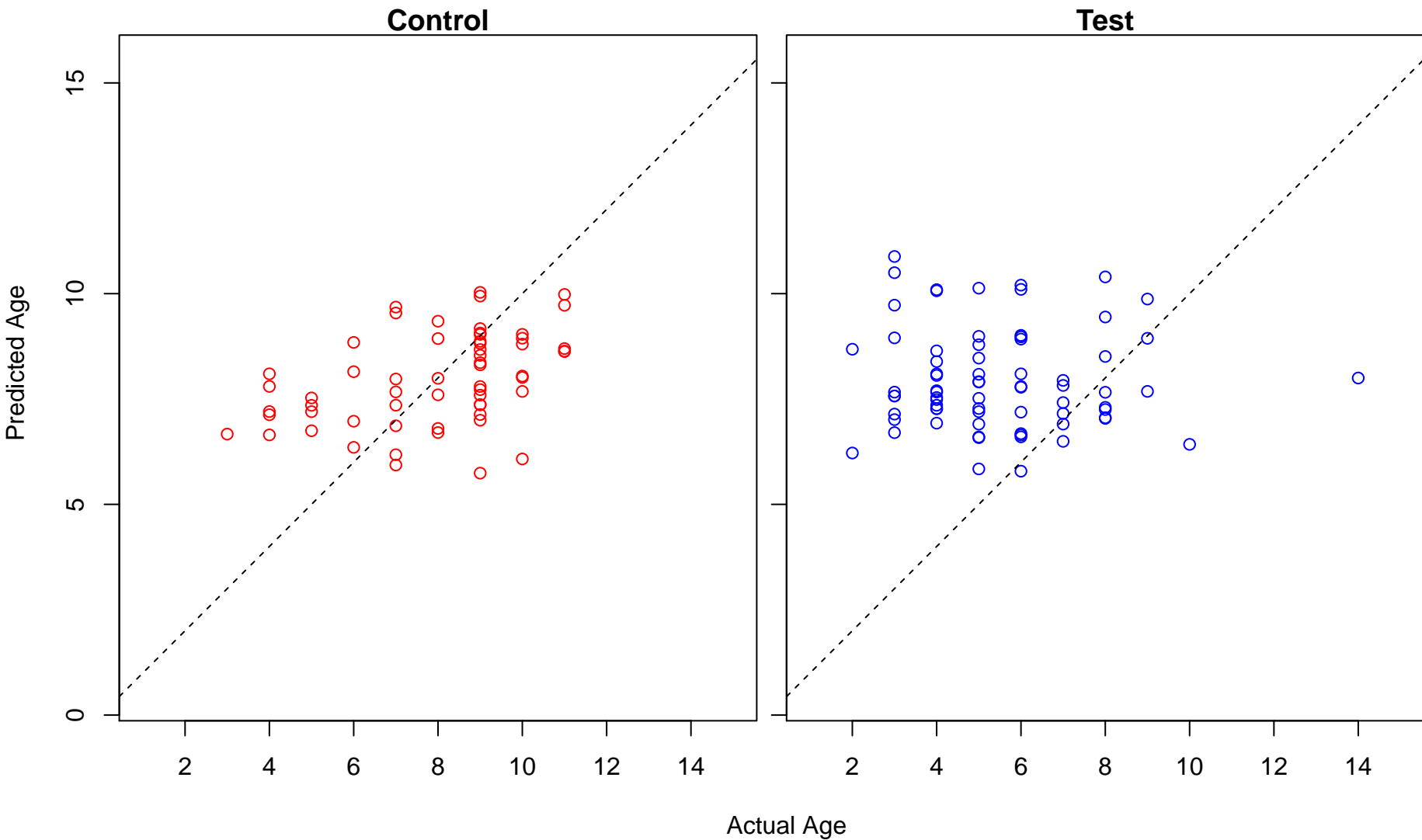
medulla oblongata development (Score: 0.786823)



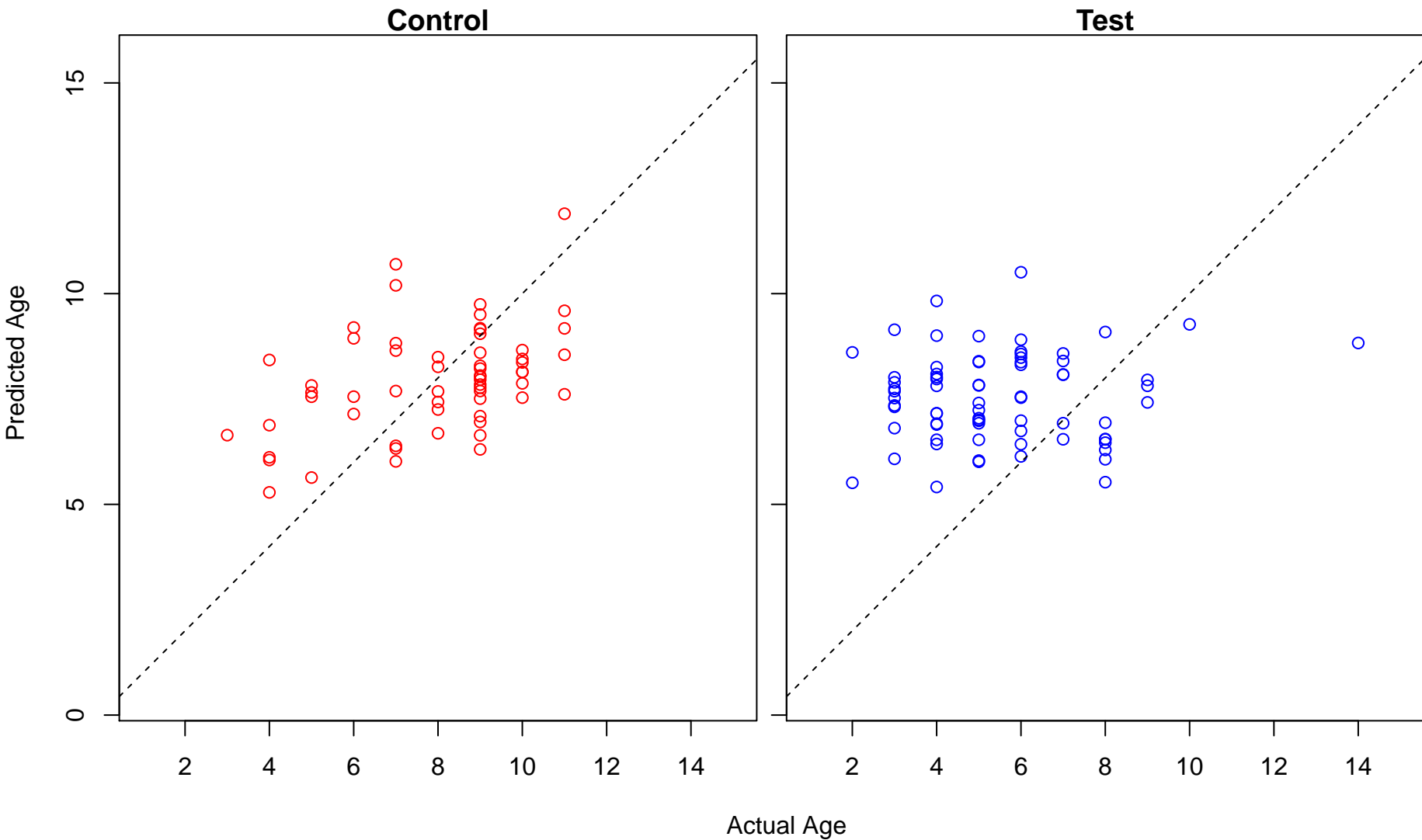
growth hormone receptor signaling pathway (Score: 0.785507)



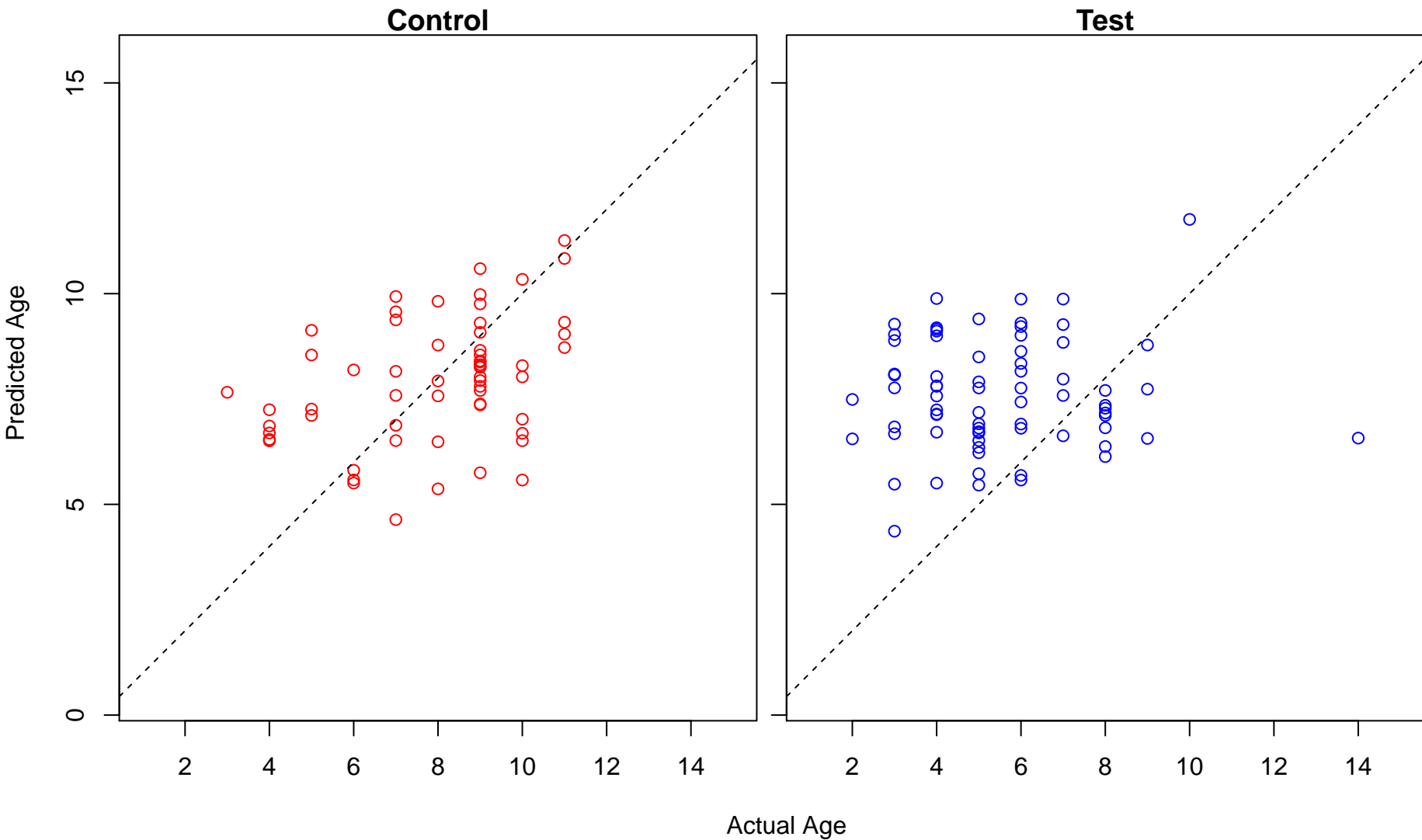
cellular response to growth hormone stimulus (Score: 0.785507)



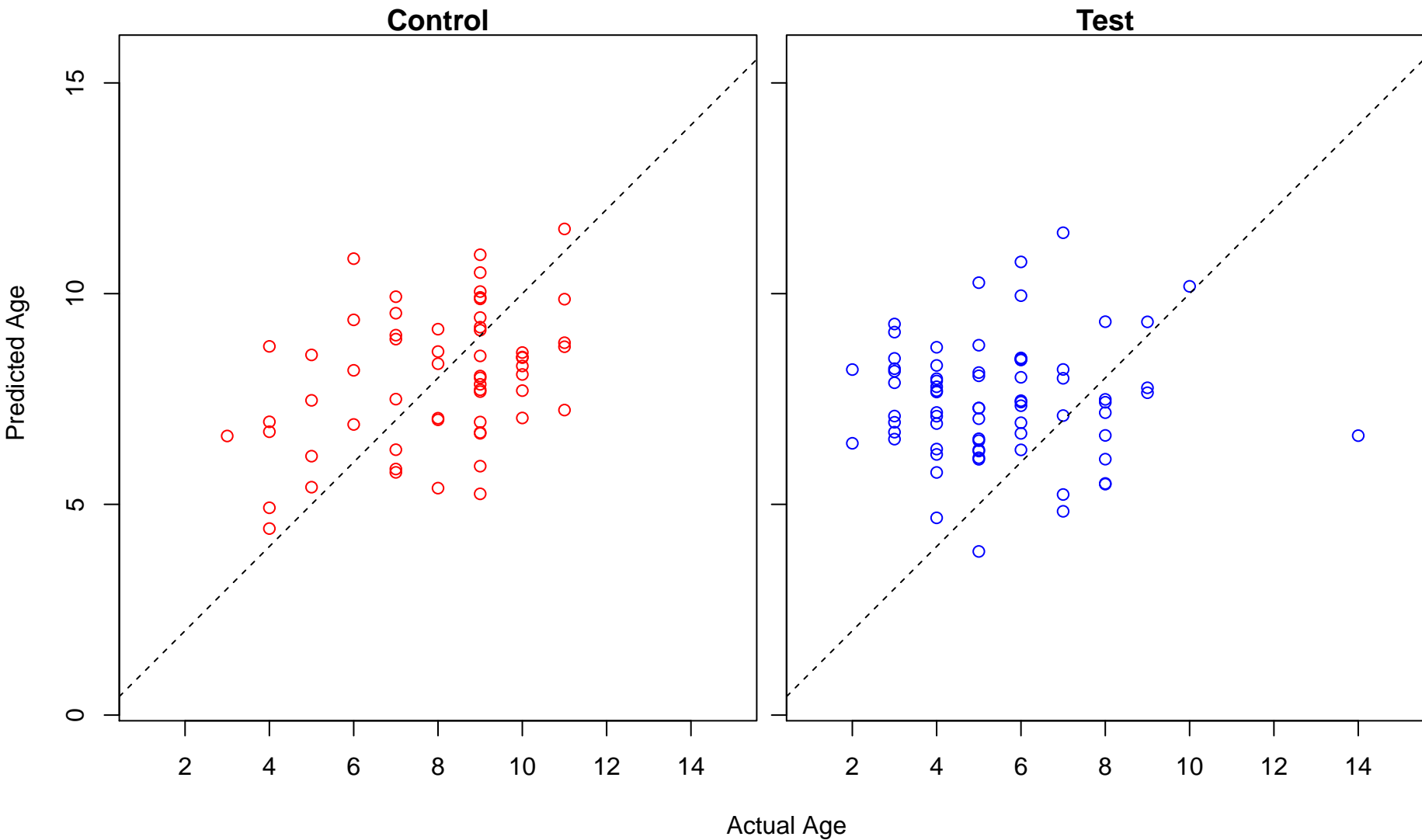
bile acid and bile salt transport (Score: 0.784614)



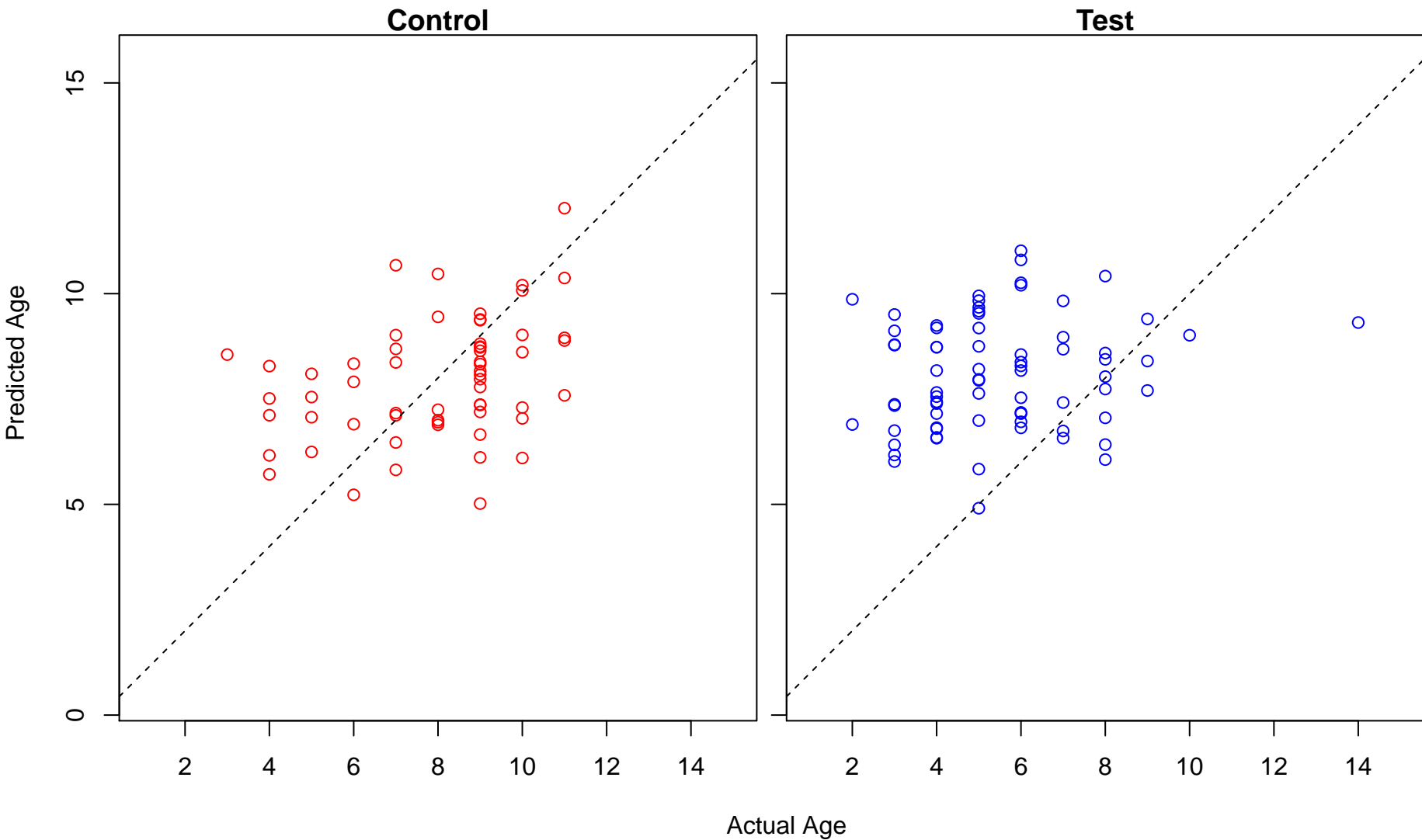
positive regulation of fatty acid oxidation (Score: 0.783815)



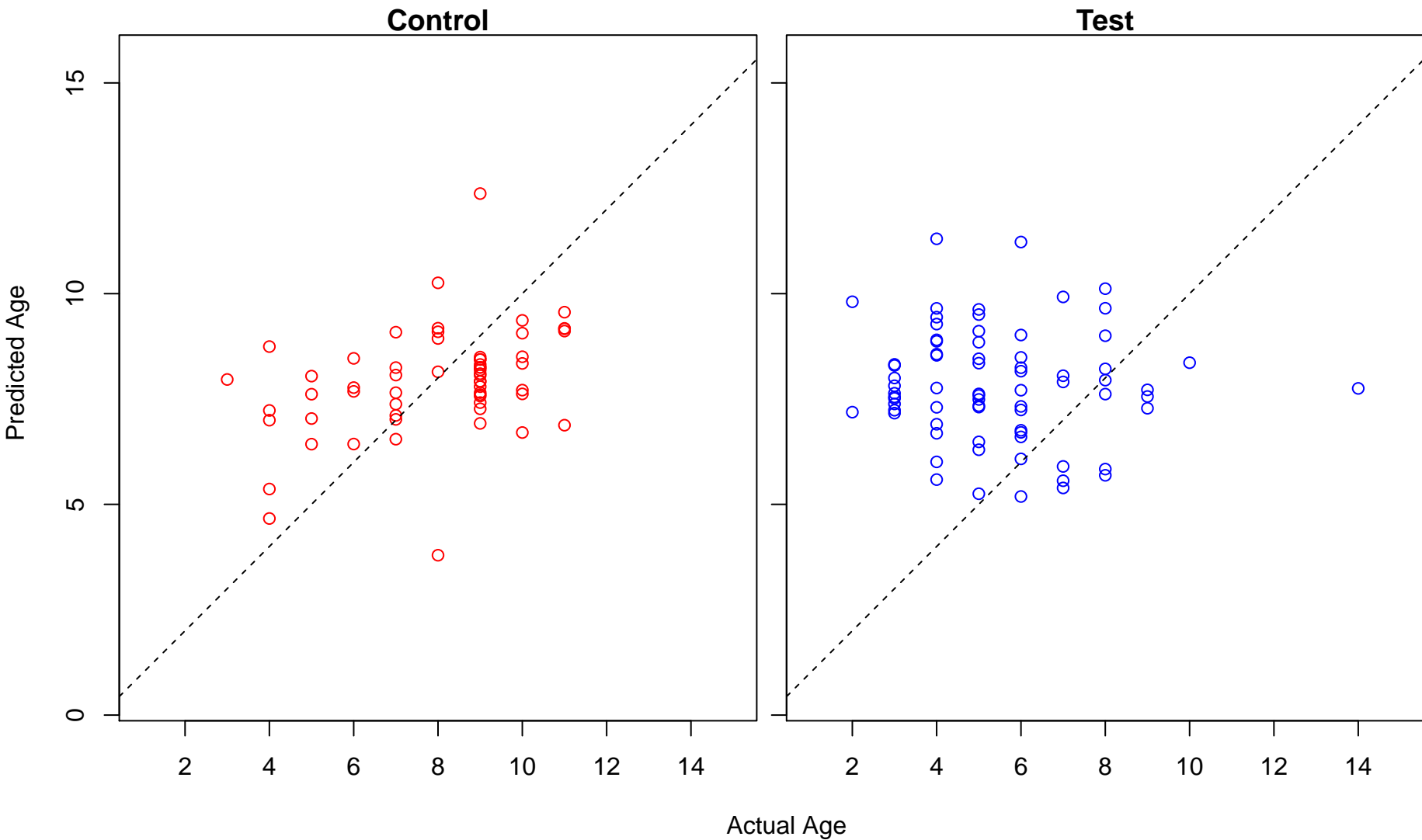
negative regulation of protein serine/threonine kinase activity (Score: 0.783312)



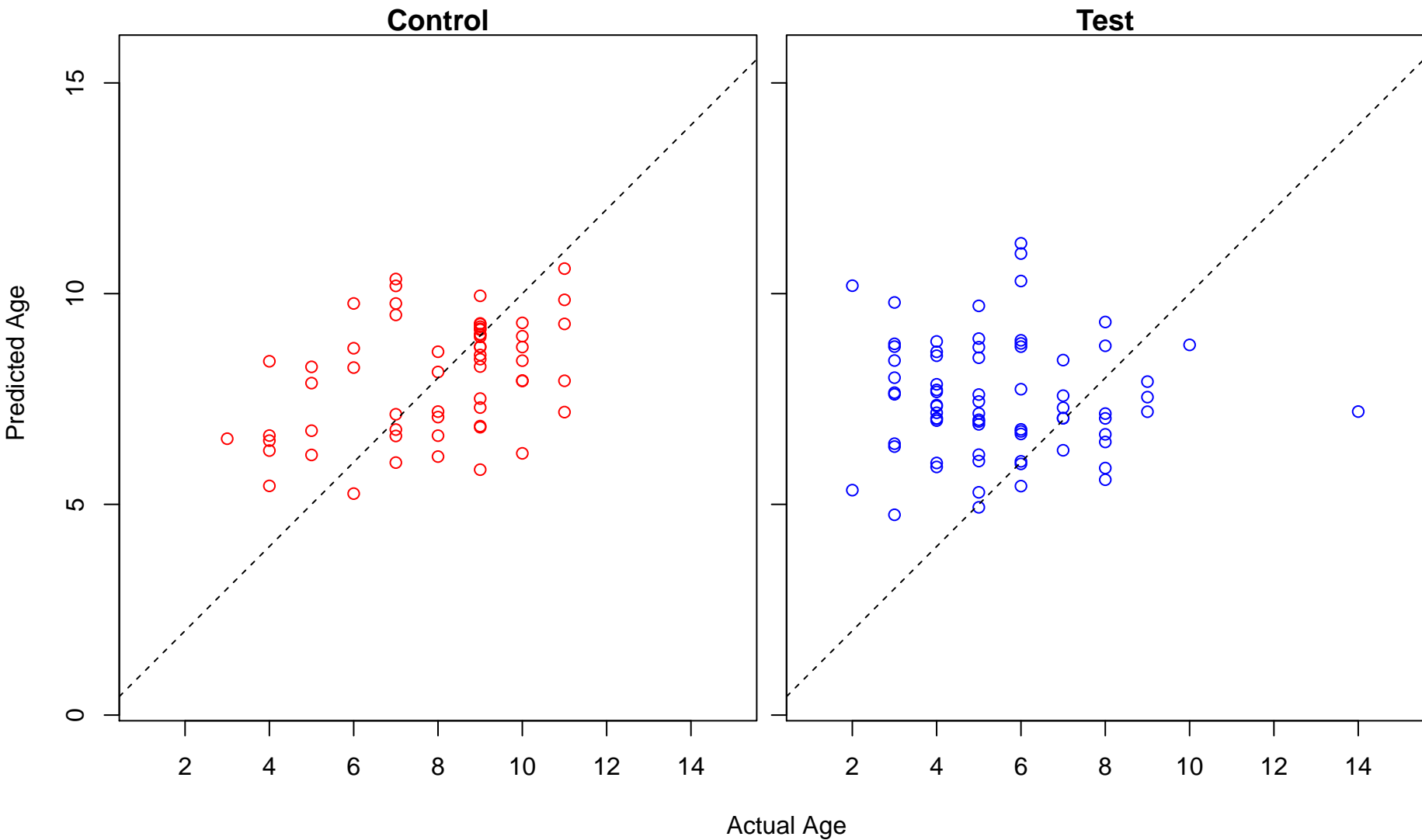
translational initiation (Score: 0.783278)



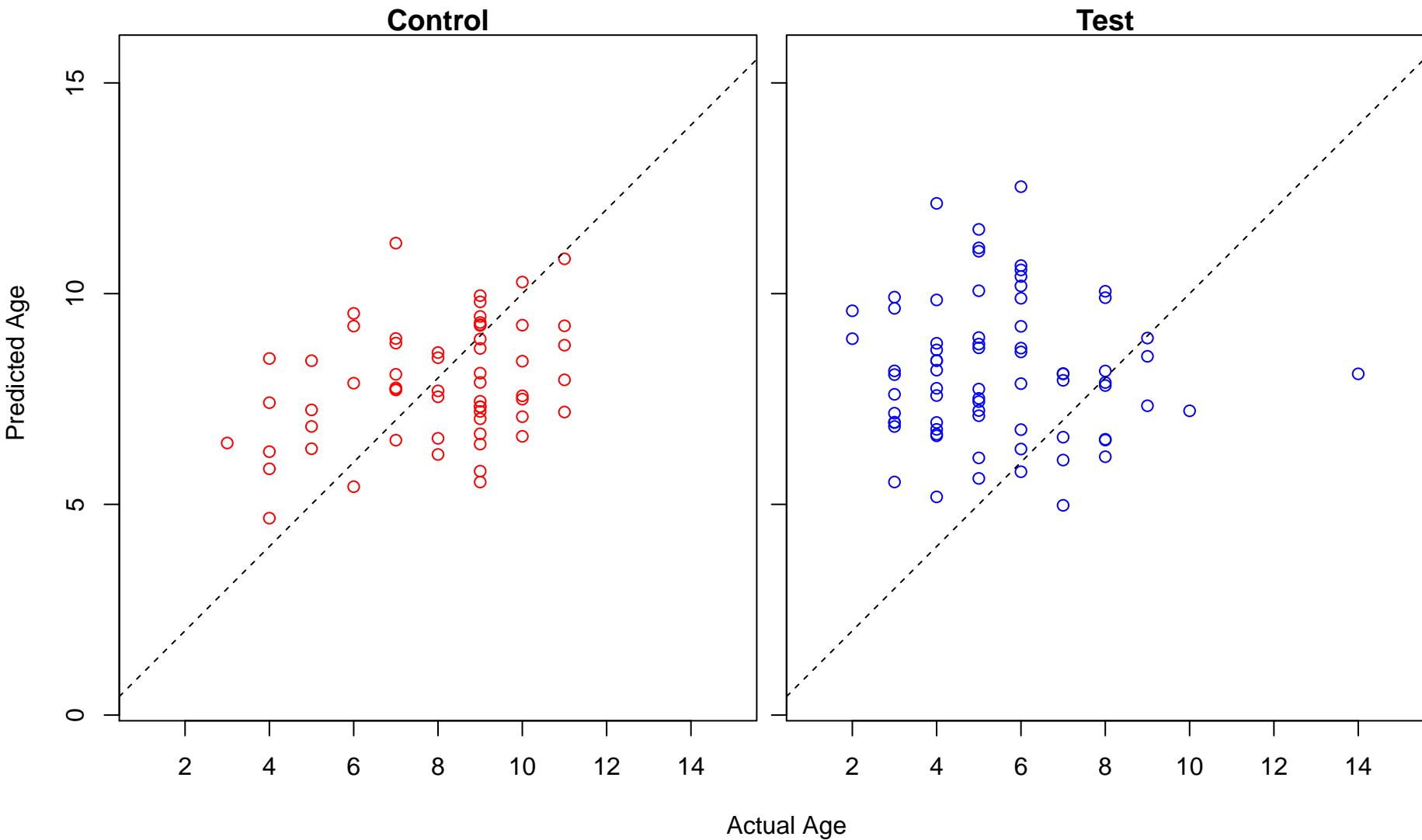
response to iron(II) ion (Score: 0.783076)



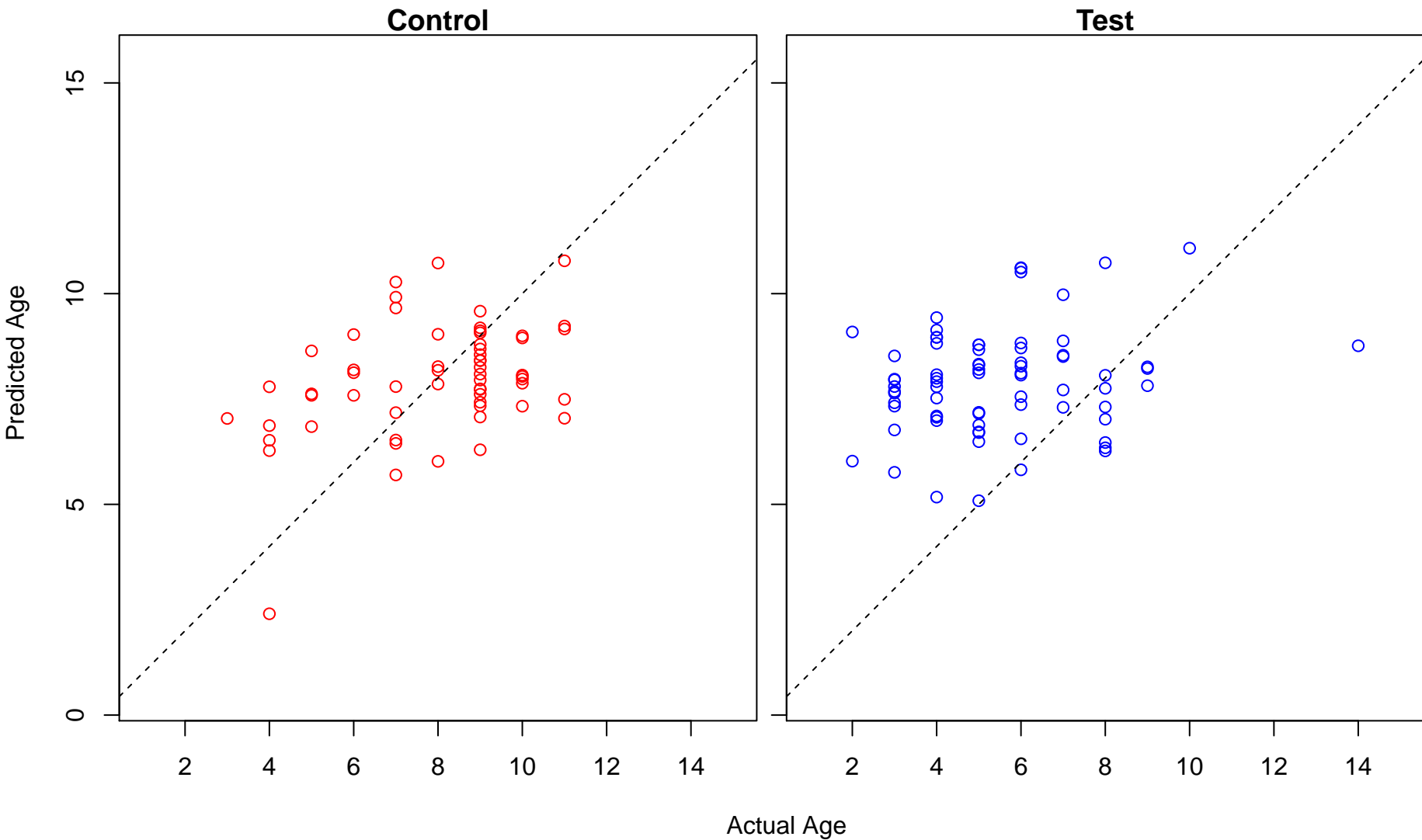
monovalent inorganic cation transport (Score: 0.781719)



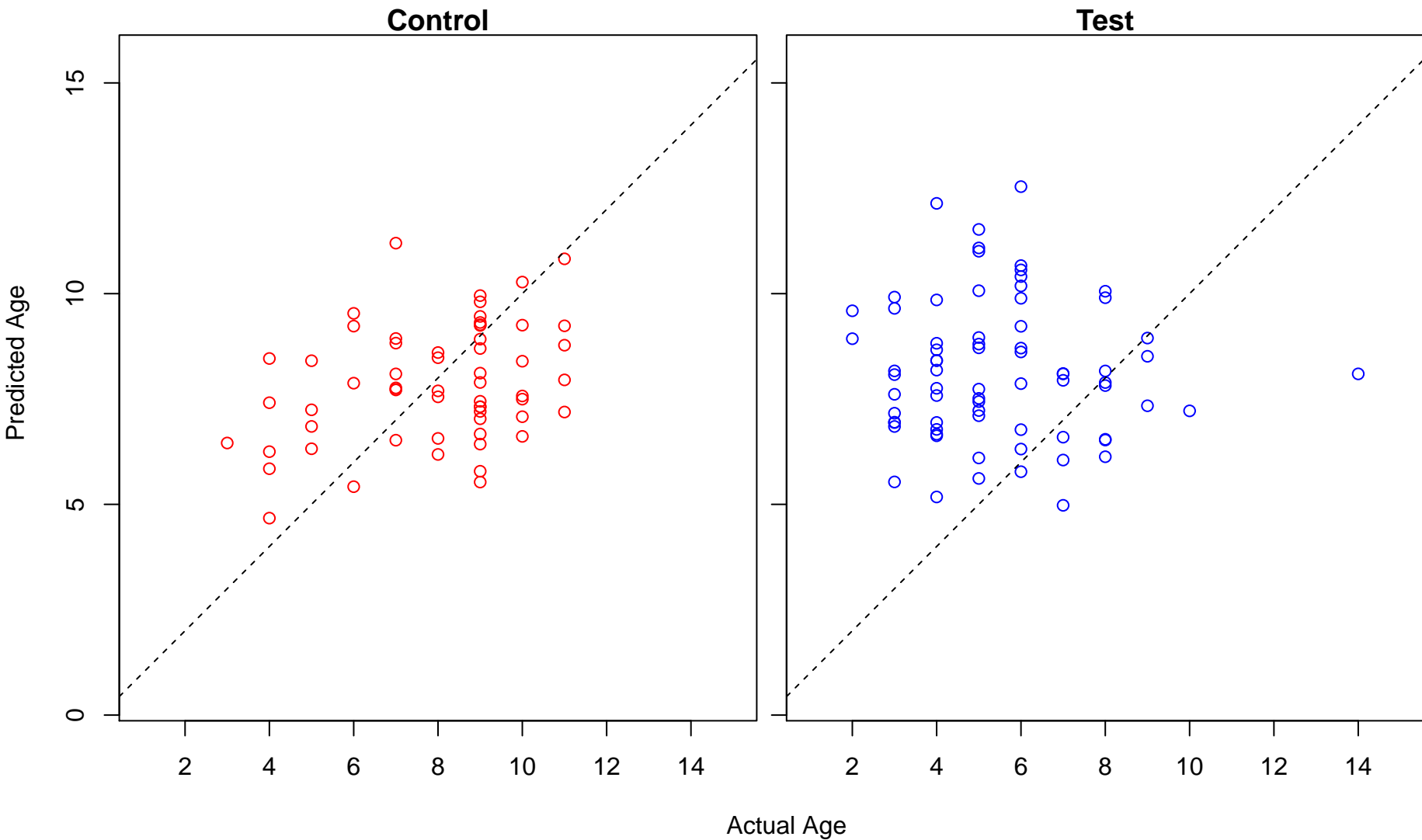
regulation of complement activation (Score: 0.780749)



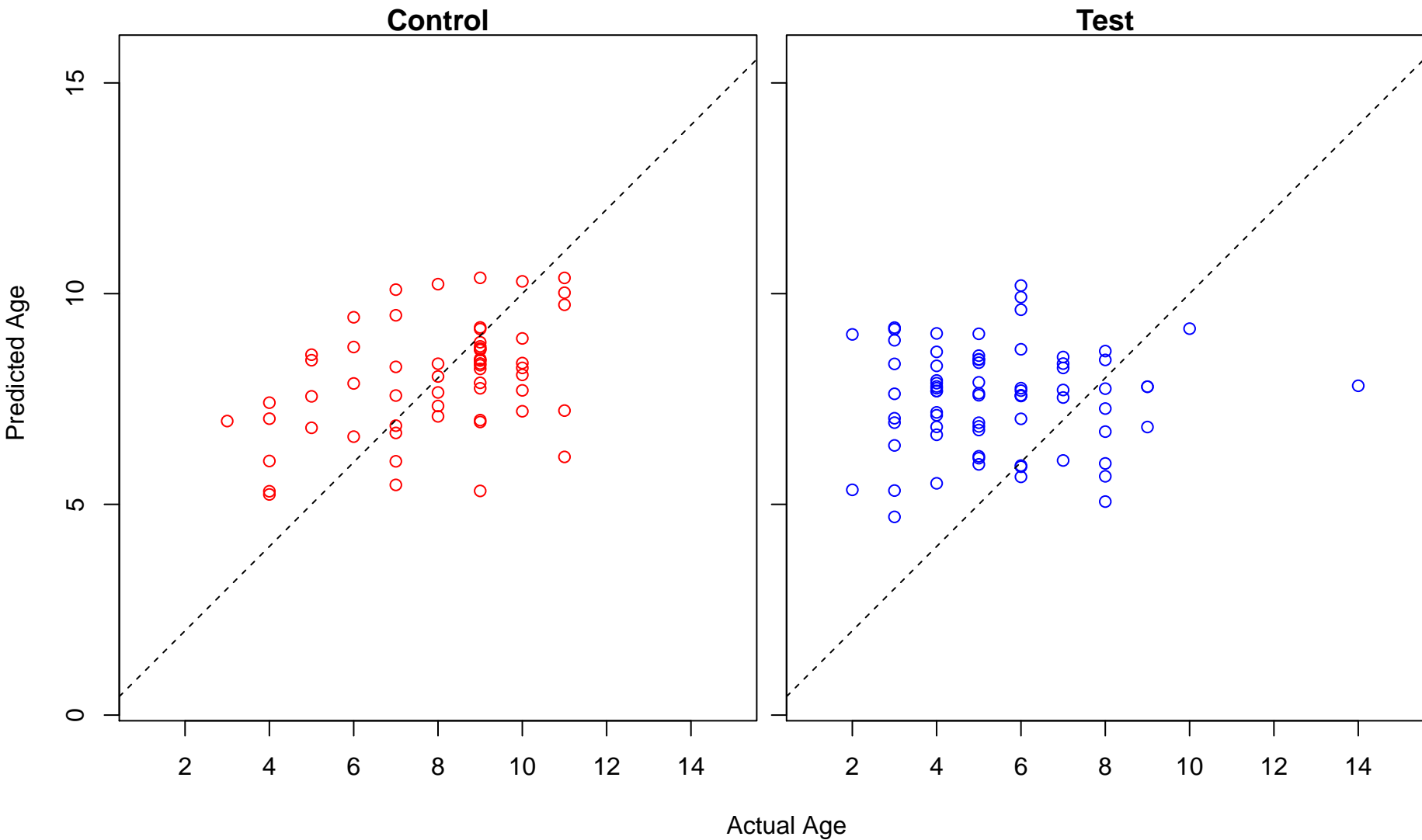
regulation of cell size (Score: 0.780087)



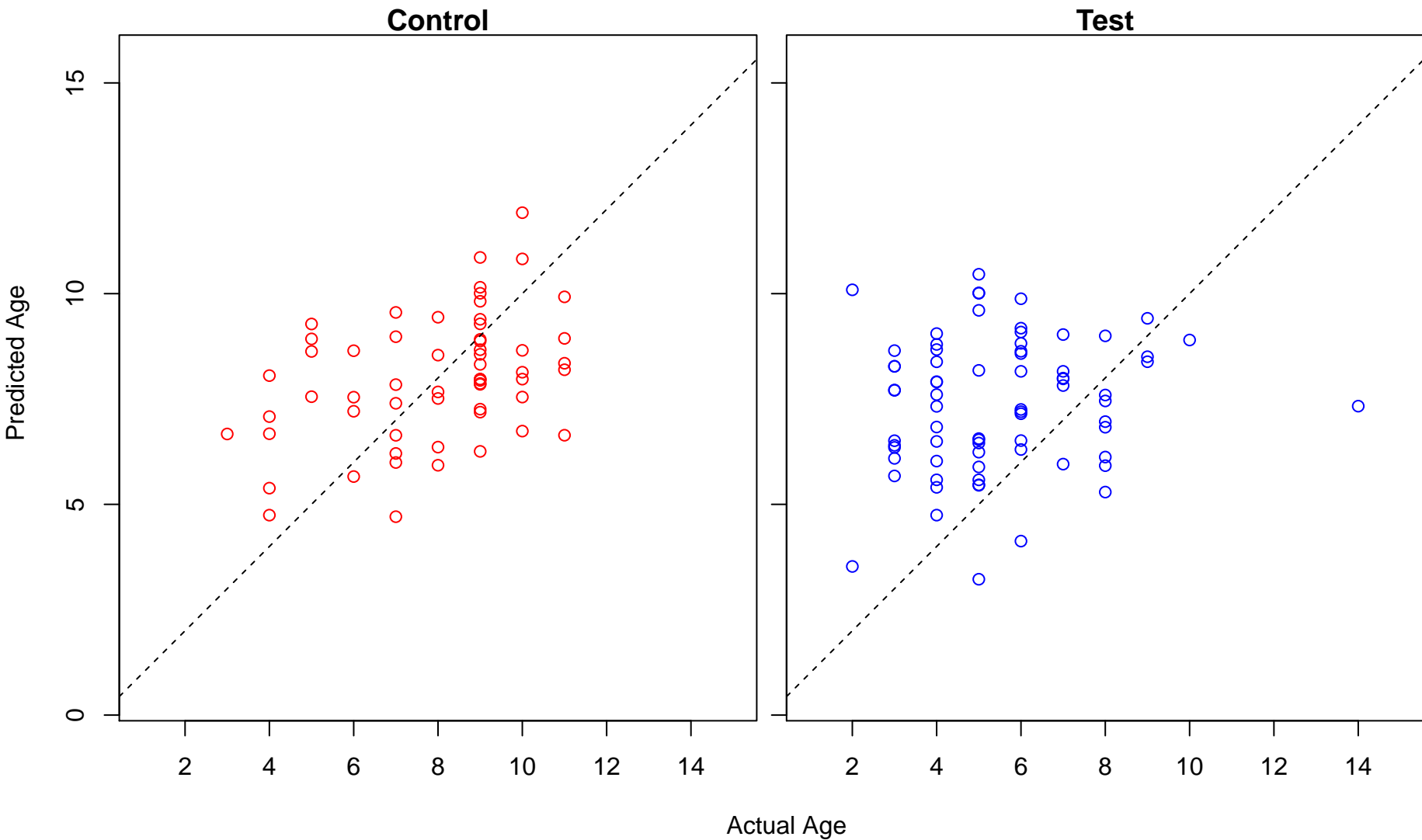
regulation of protein activation cascade (Score: 0.779713)



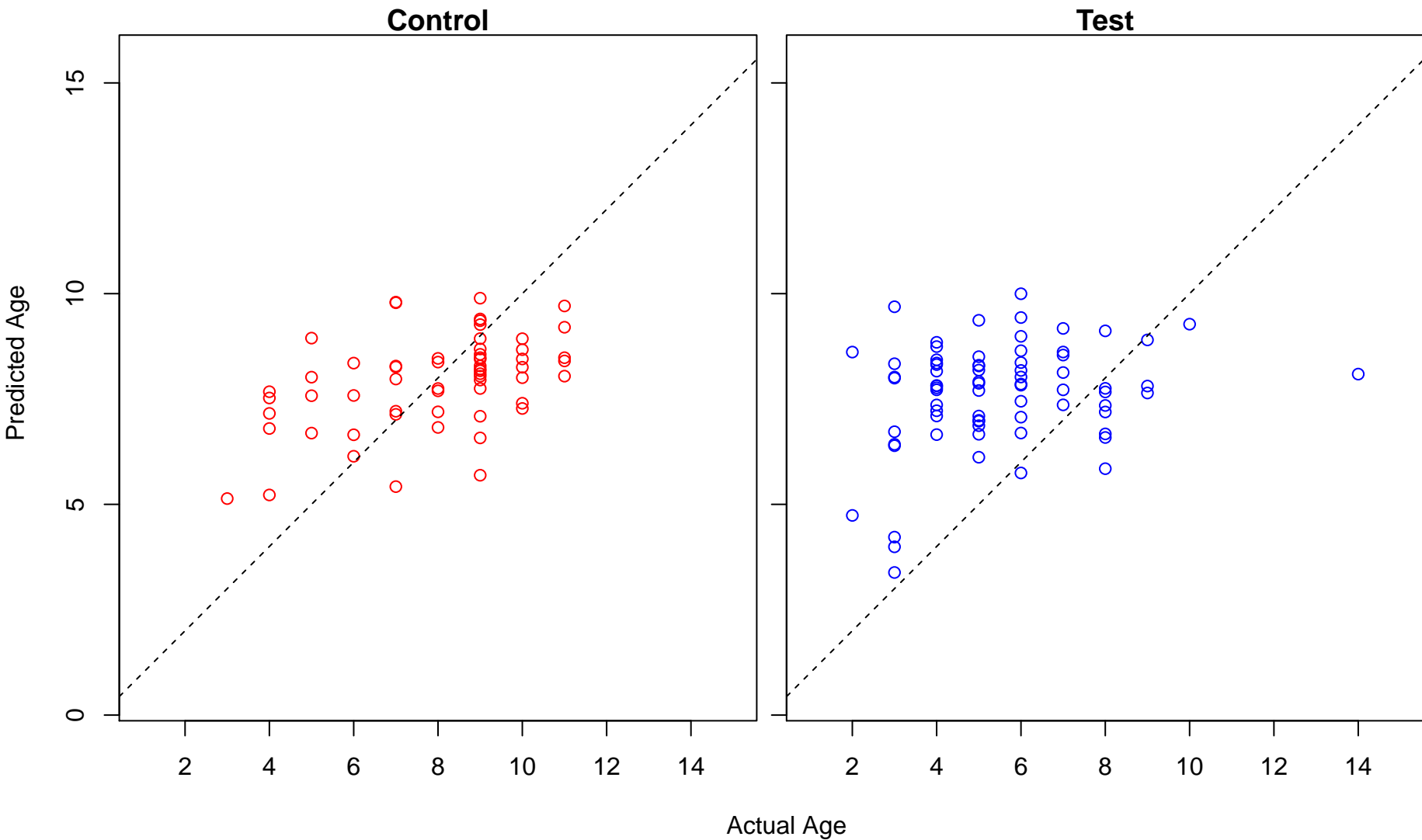
histone H3-K4 methylation (Score: 0.779644)



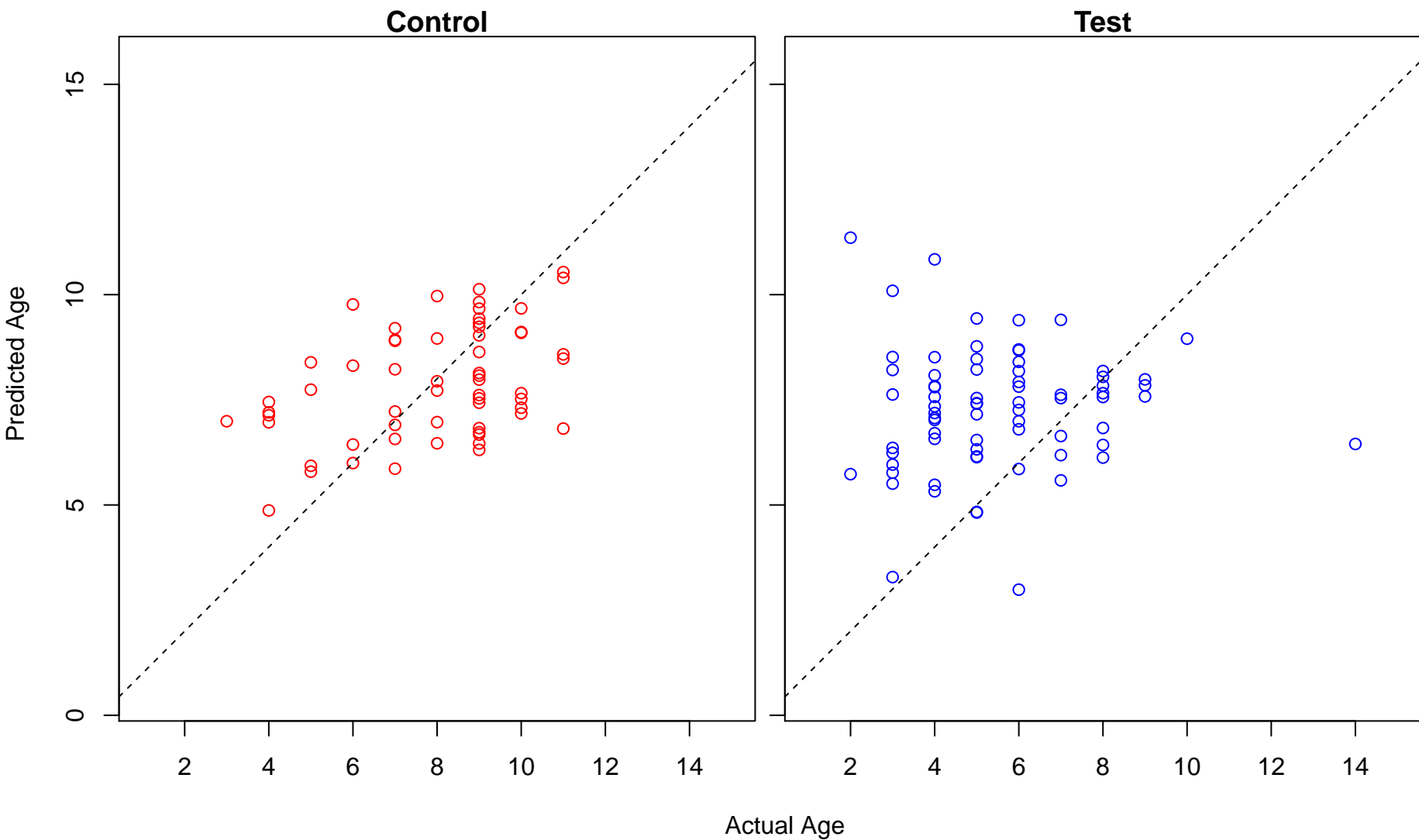
chondroitin sulfate biosynthetic process (Score: 0.779331)



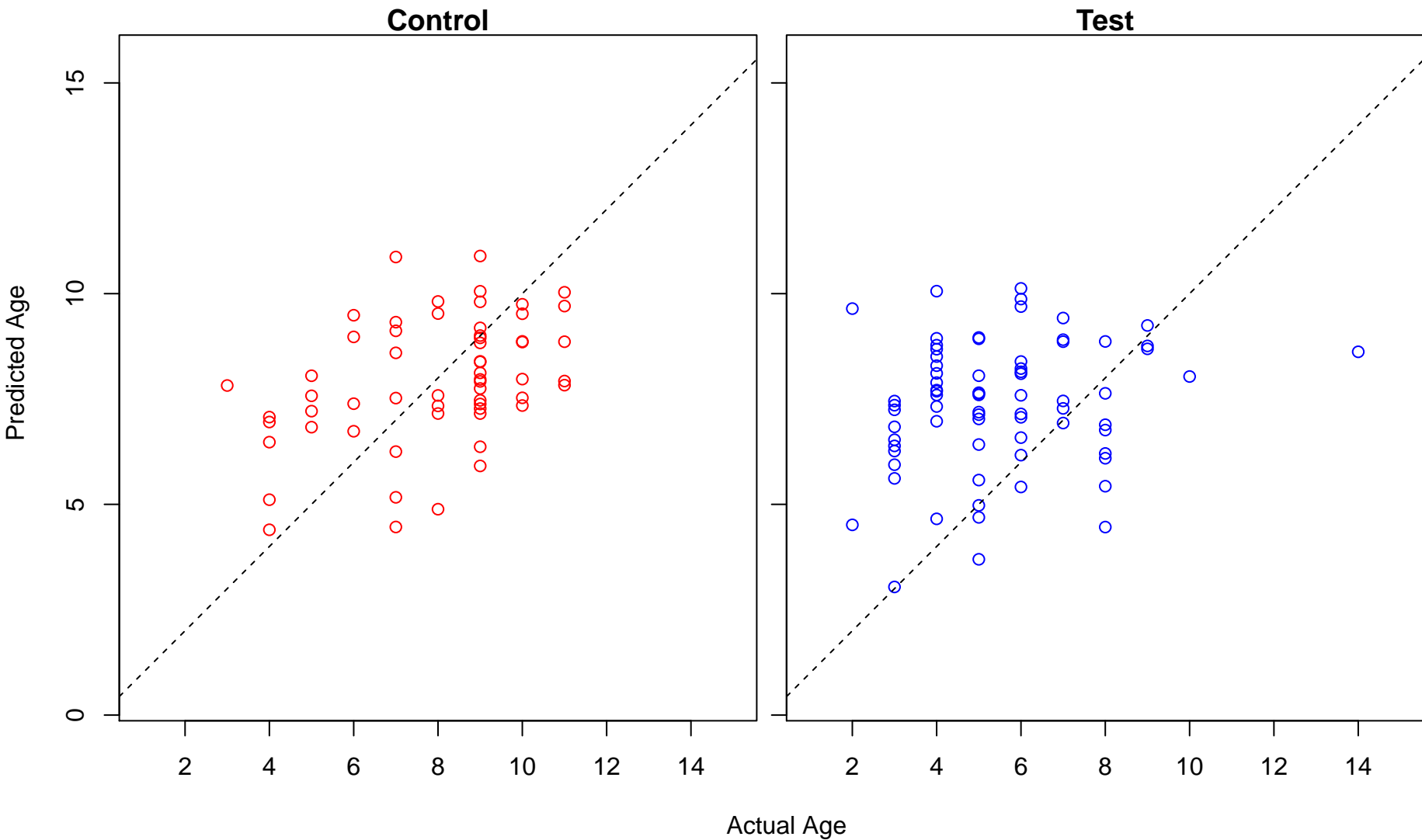
regulation of cytokine activity (Score: 0.779320)



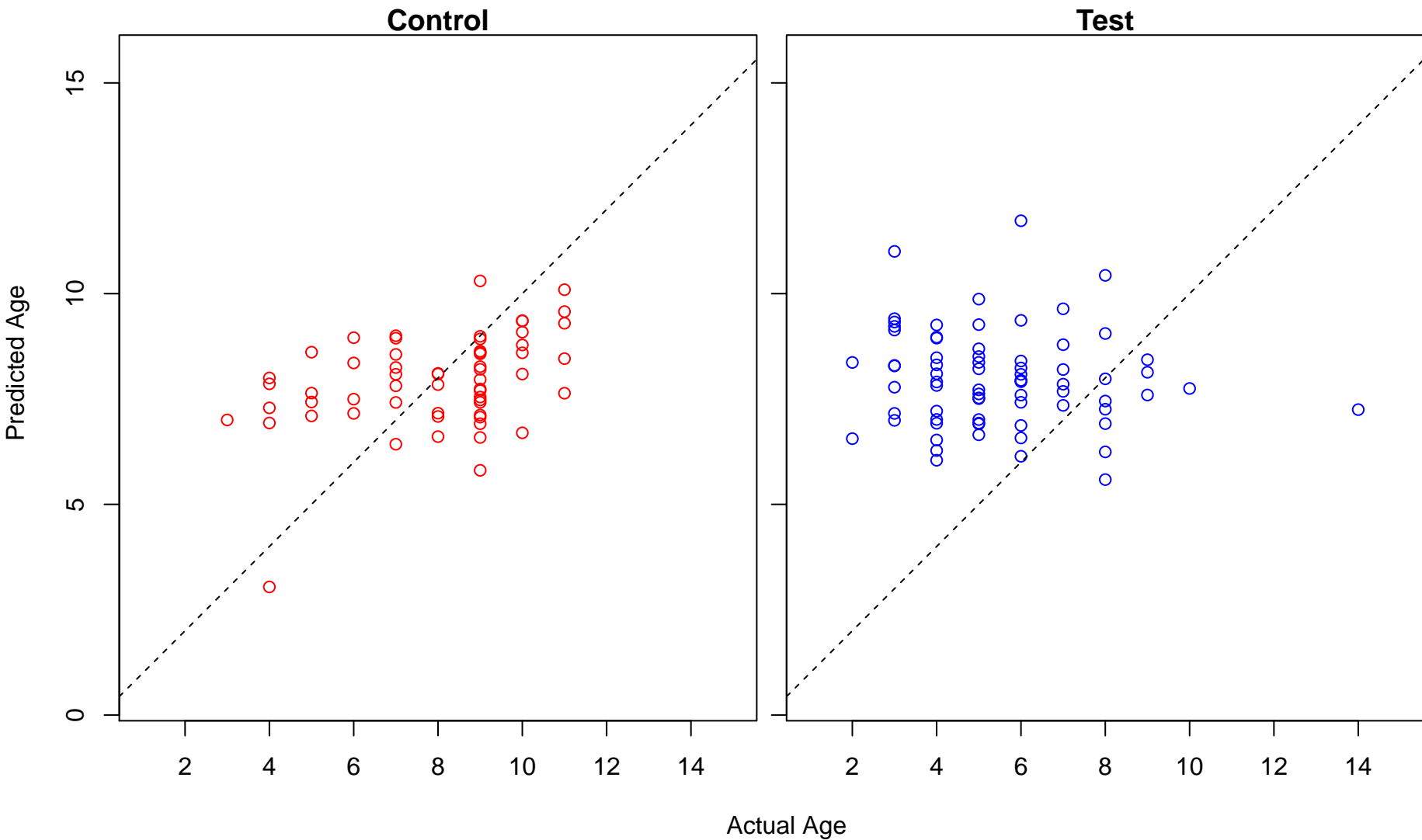
positive regulation of tolerance induction (Score: 0.778838)



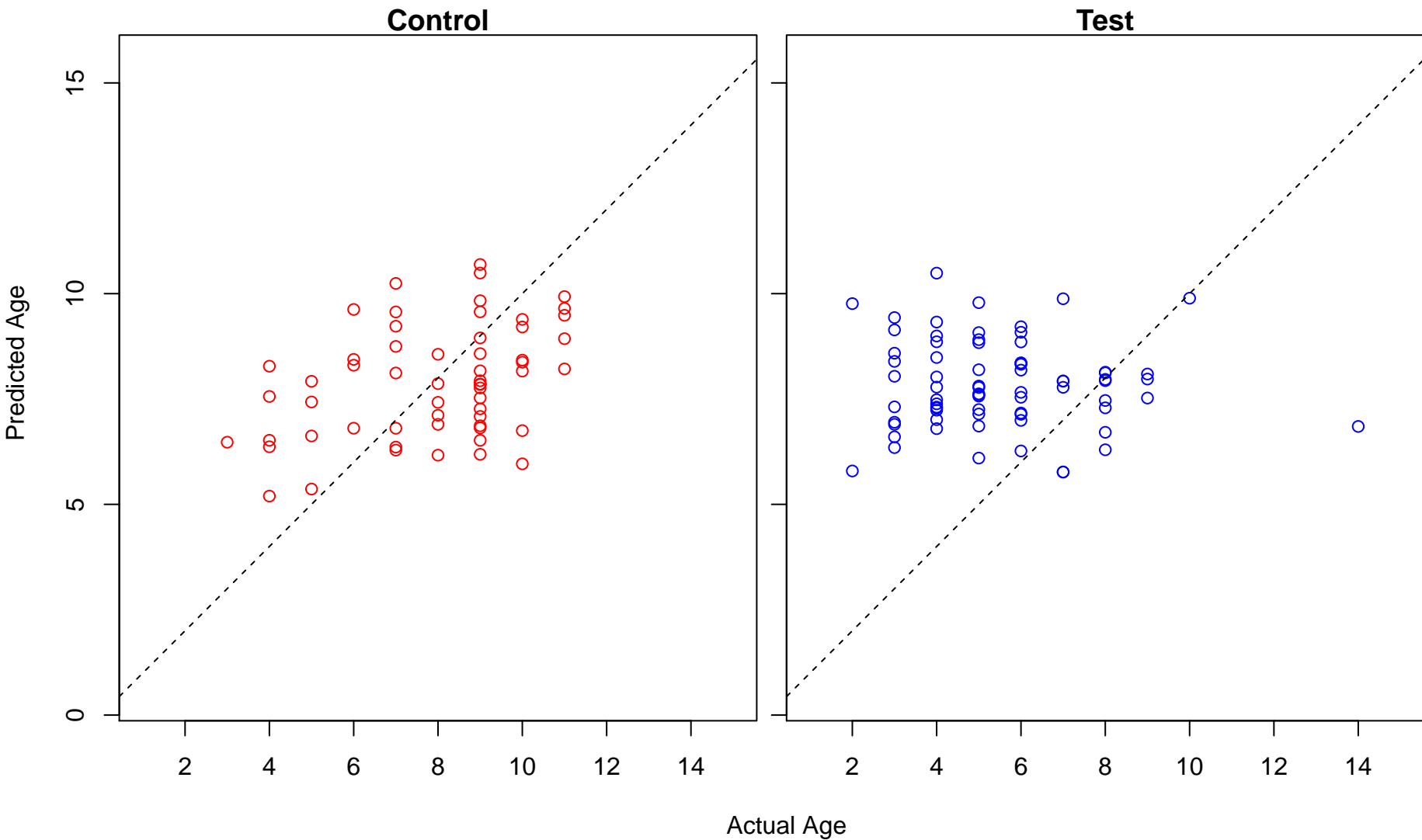
reactive nitrogen species metabolic process (Score: 0.778615)



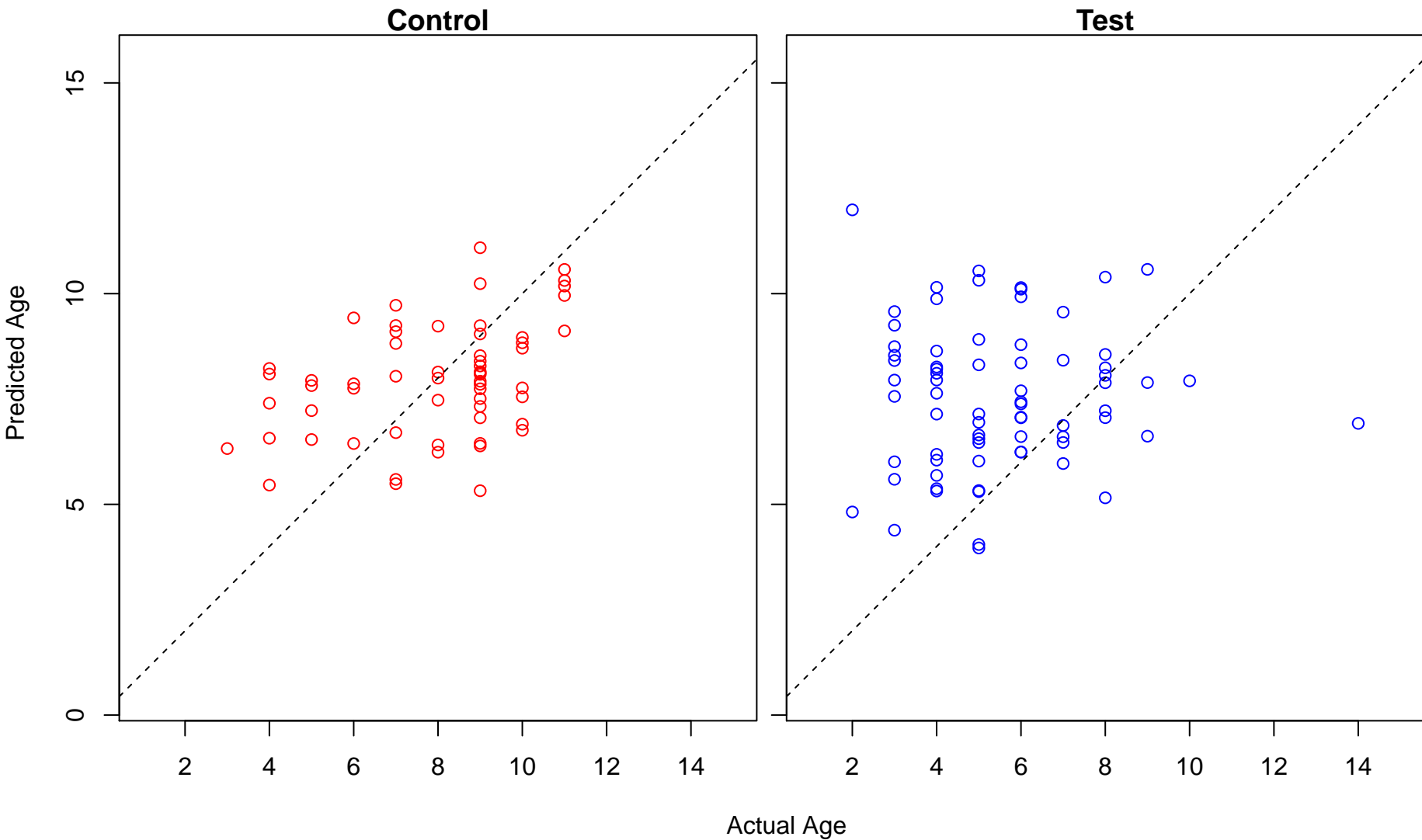
vestibular nucleus development (Score: 0.778364)



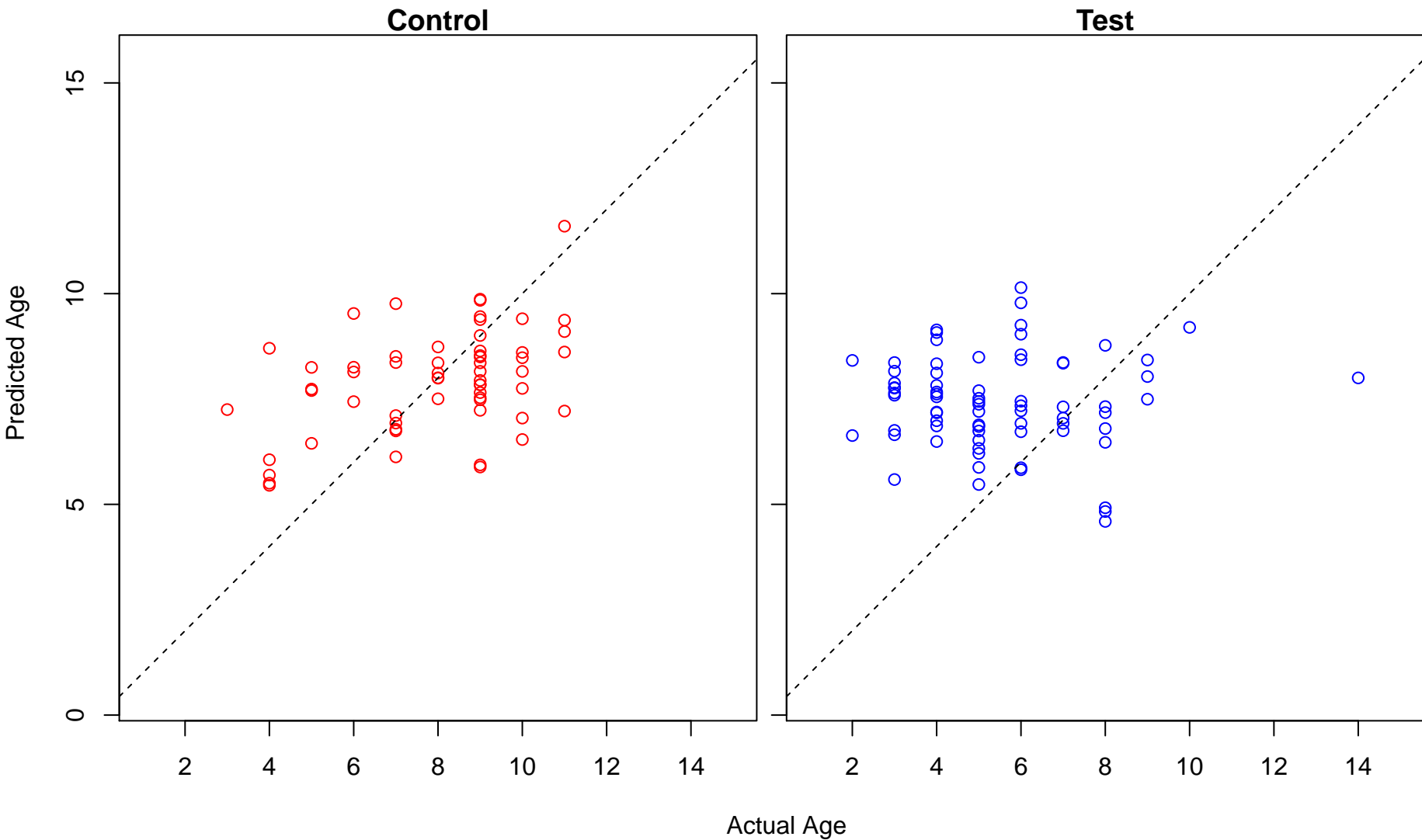
positive regulation of neural precursor cell proliferation (Score: 0.776856)



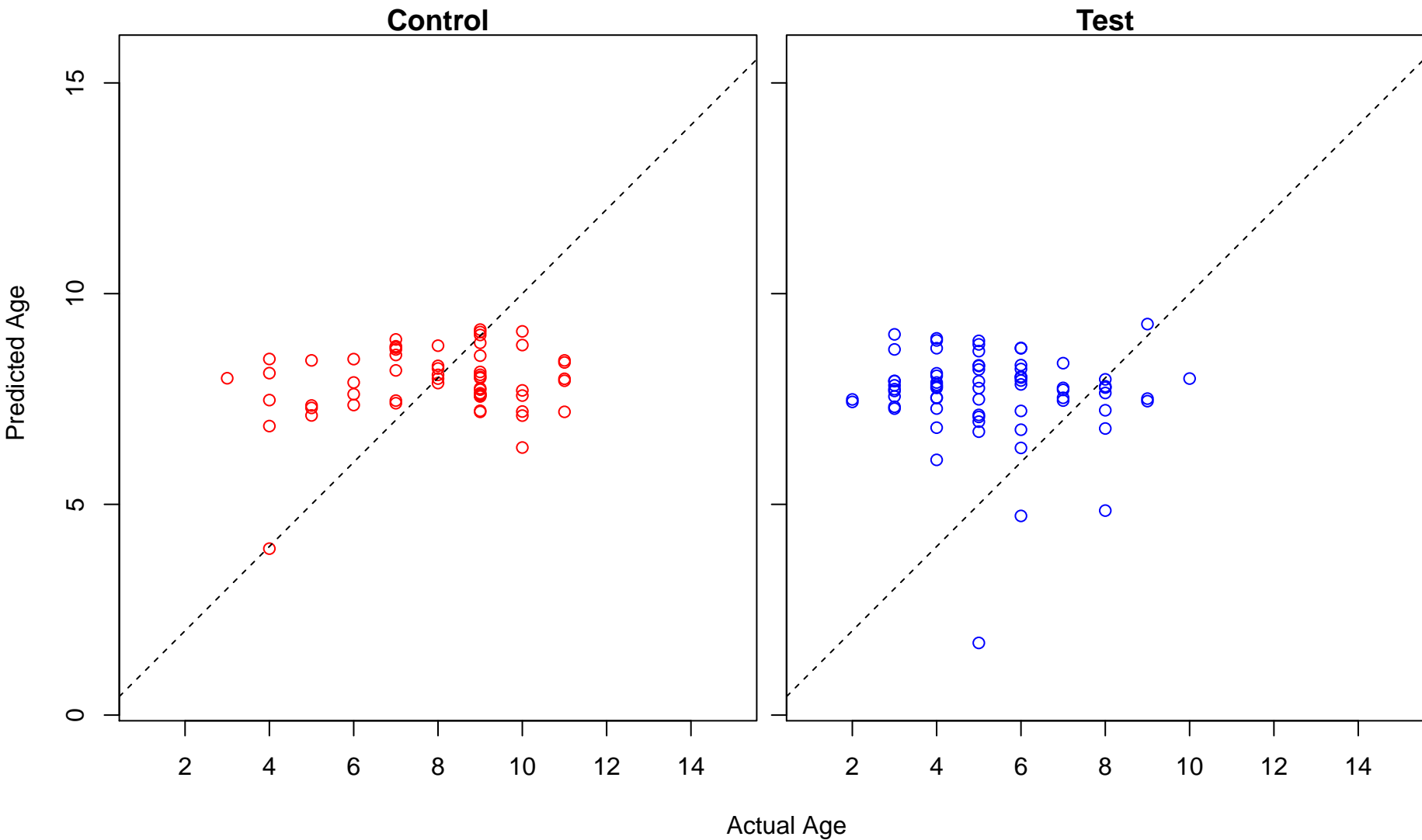
germlinal center formation (Score: 0.776508)



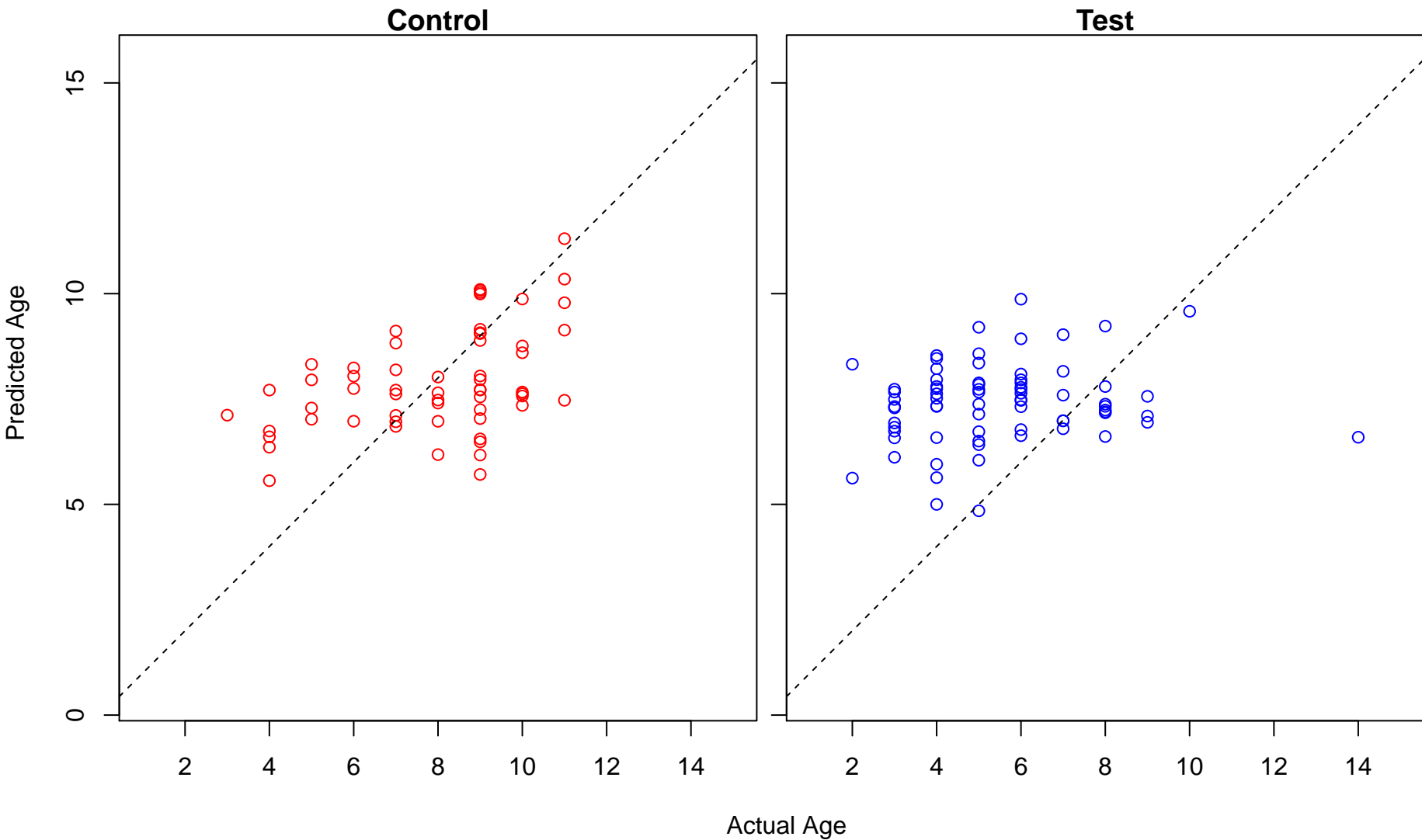
inner ear receptor stereocilium organization (Score: 0.775867)



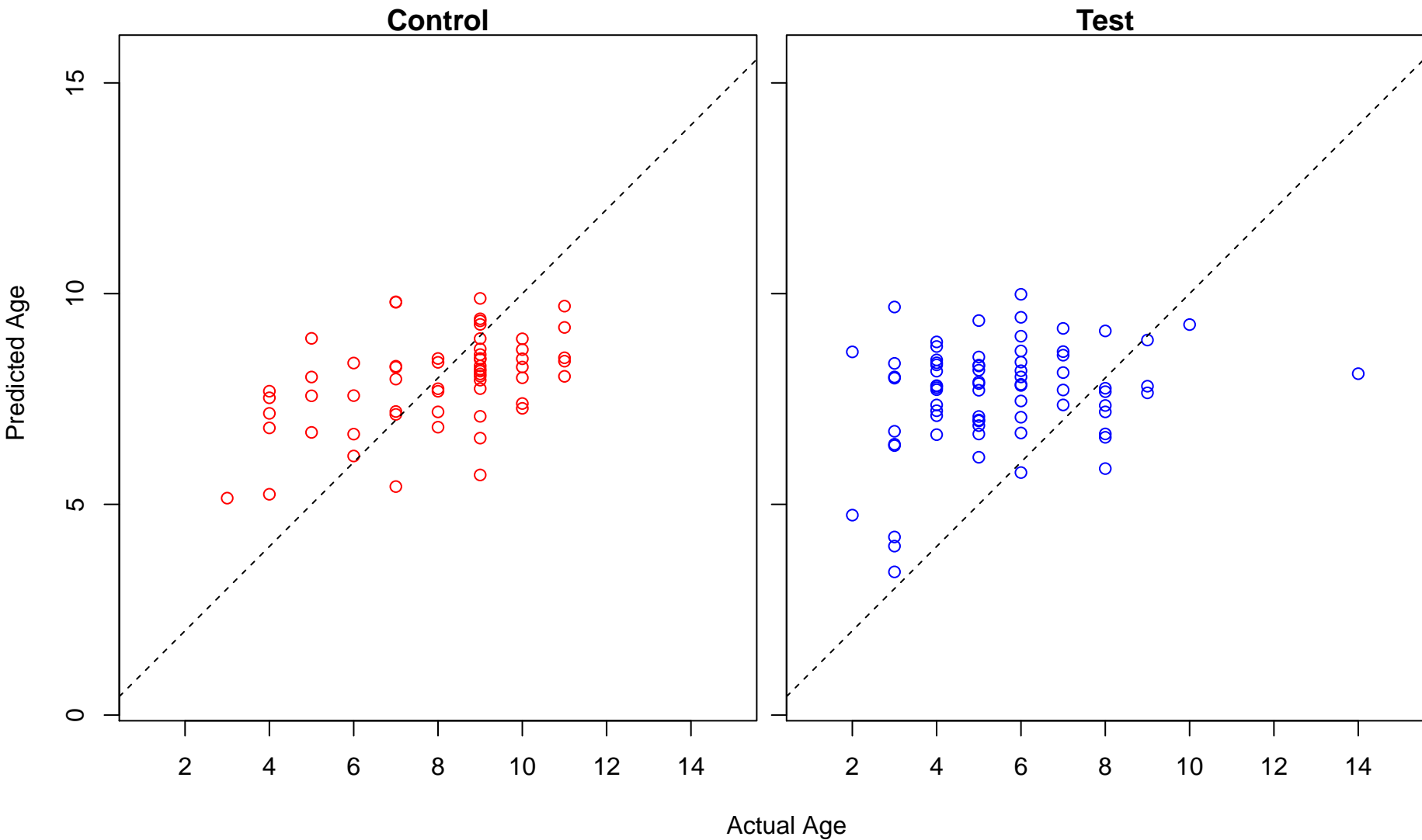
rhombomere 3 development (Score: 0.775713)



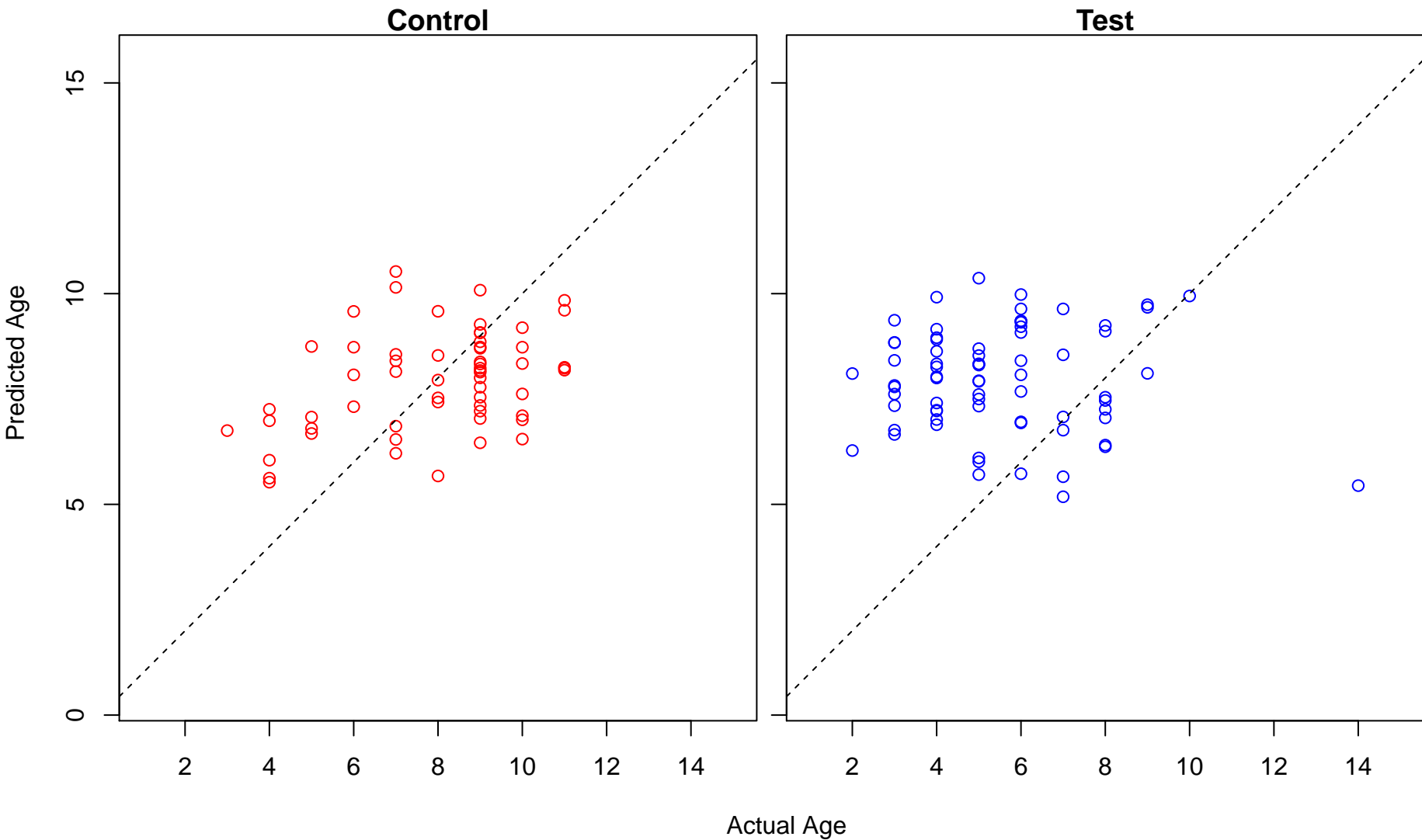
diacylglycerol metabolic process (Score: 0.774181)



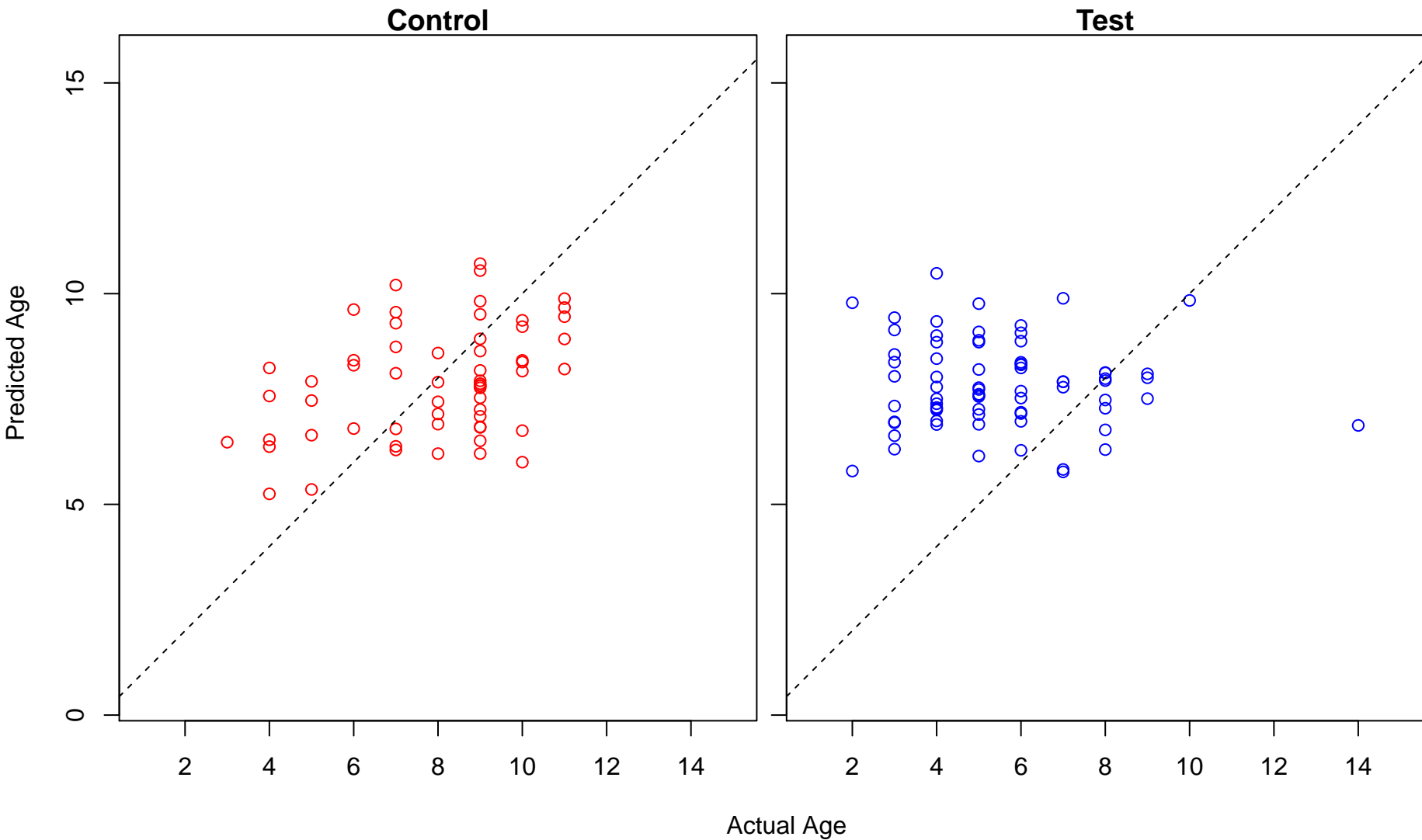
negative regulation of cardiac muscle cell proliferation (Score: 0.773314)



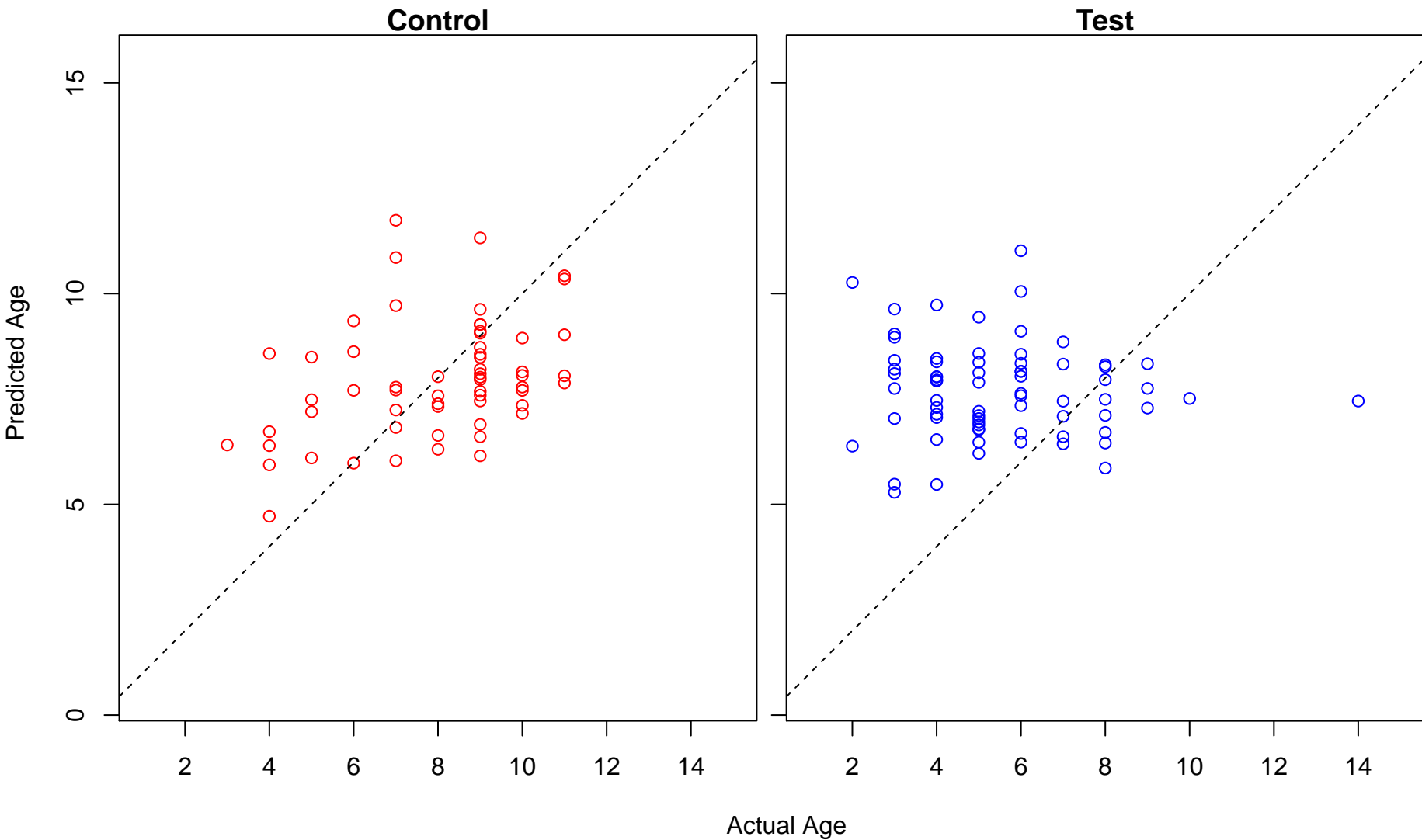
negative regulation of interleukin-8 production (Score: 0.772783)



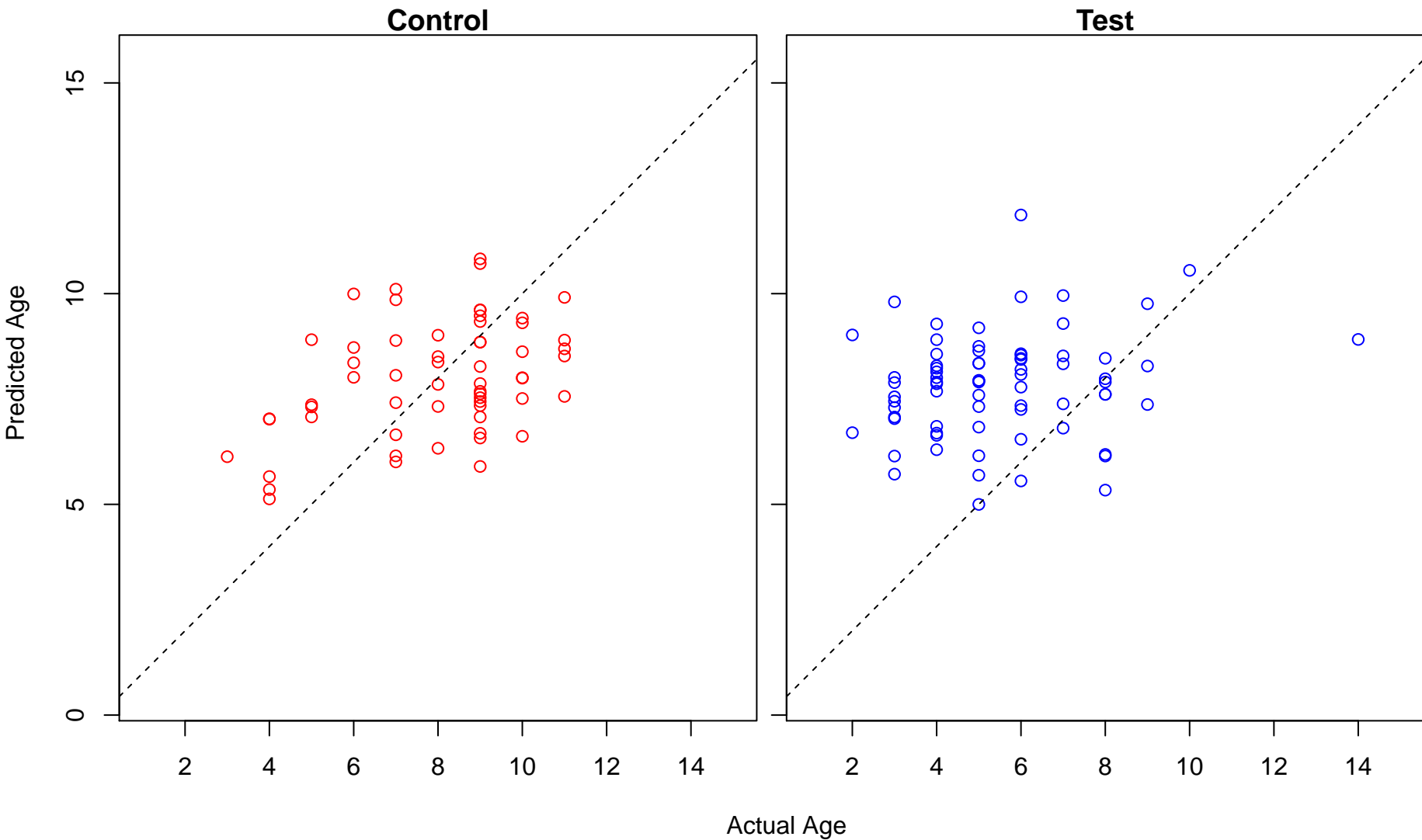
positive regulation of neuroblast proliferation (Score: 0.771885)



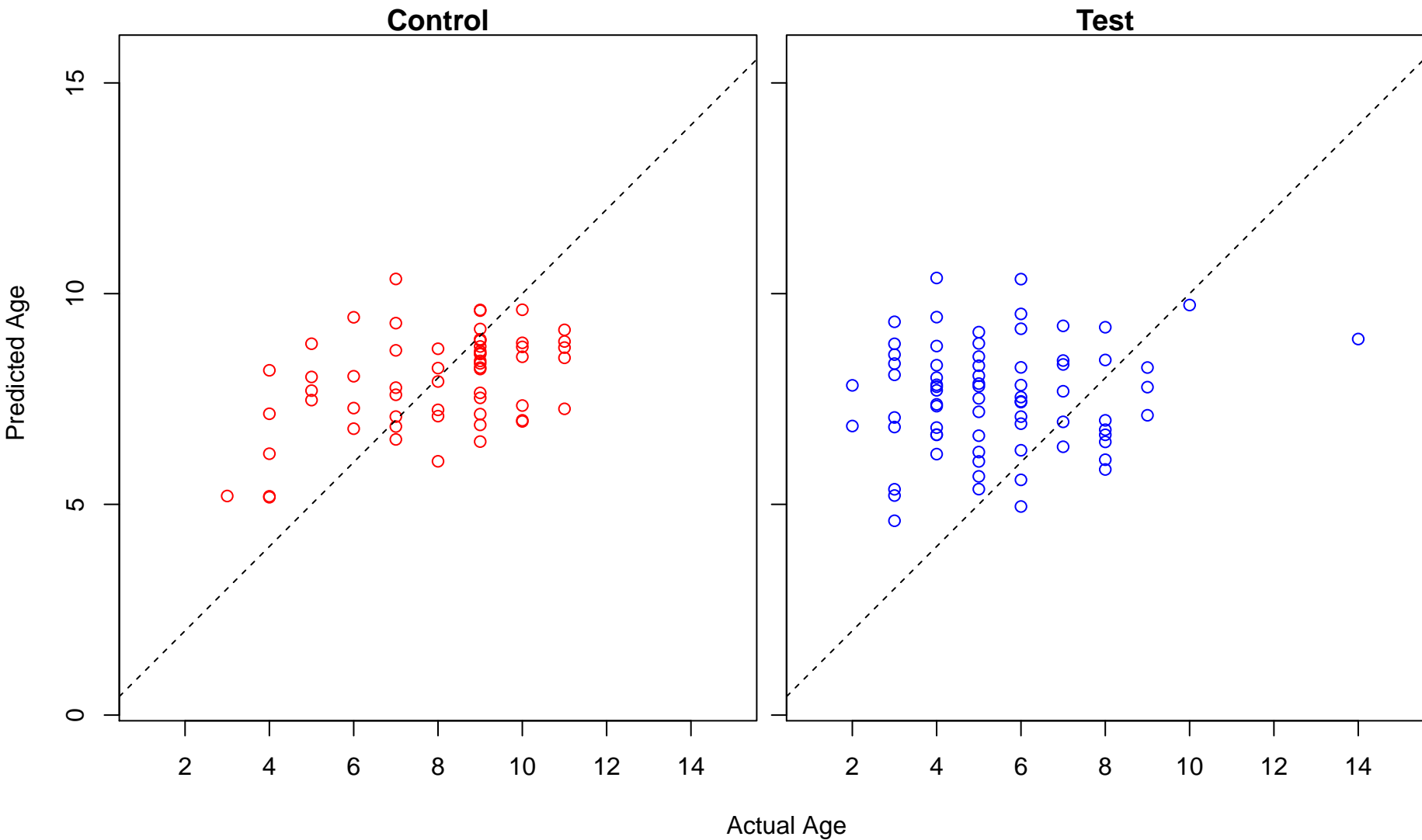
ATP metabolic process (Score: 0.771153)



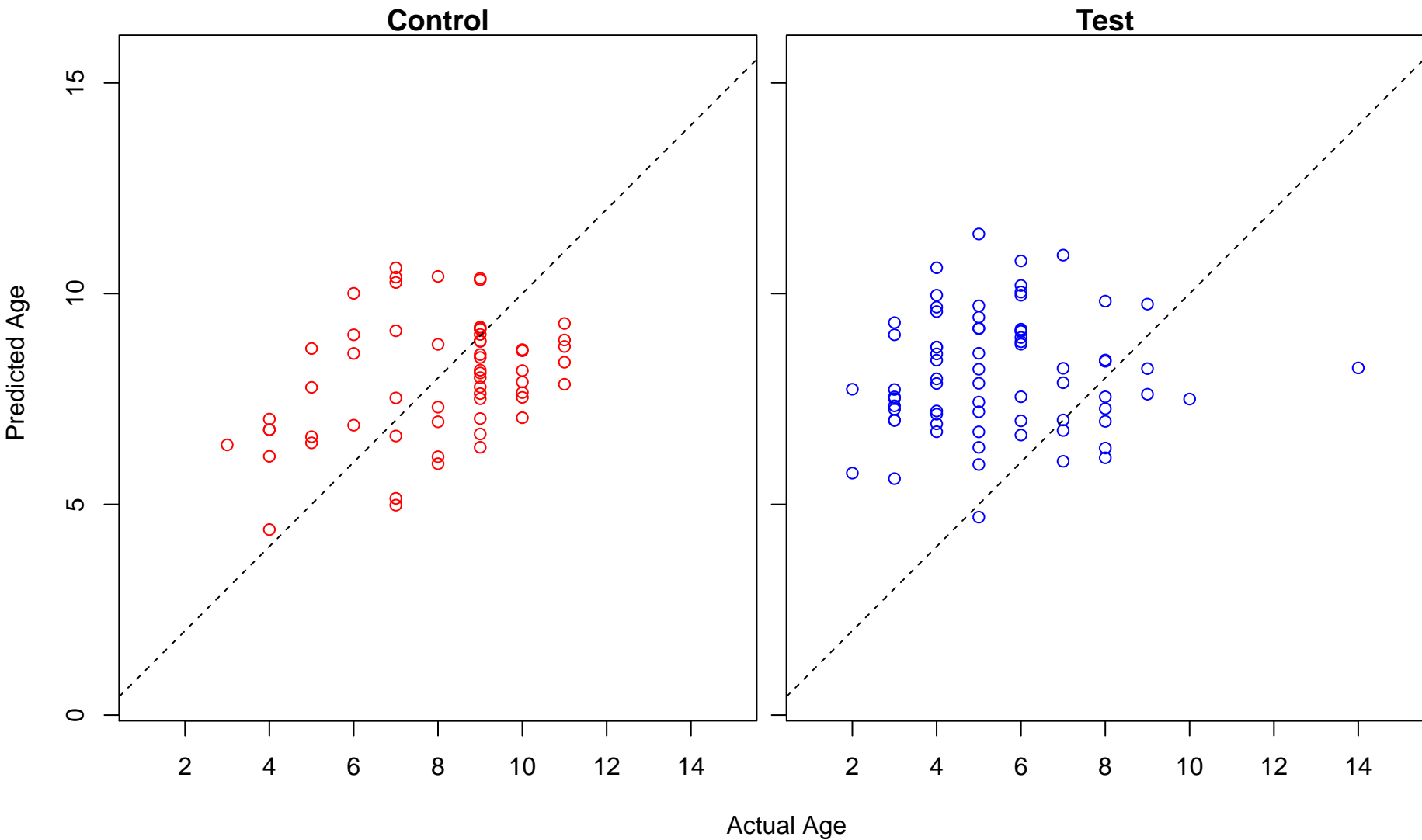
endosome organization (Score: 0.770974)



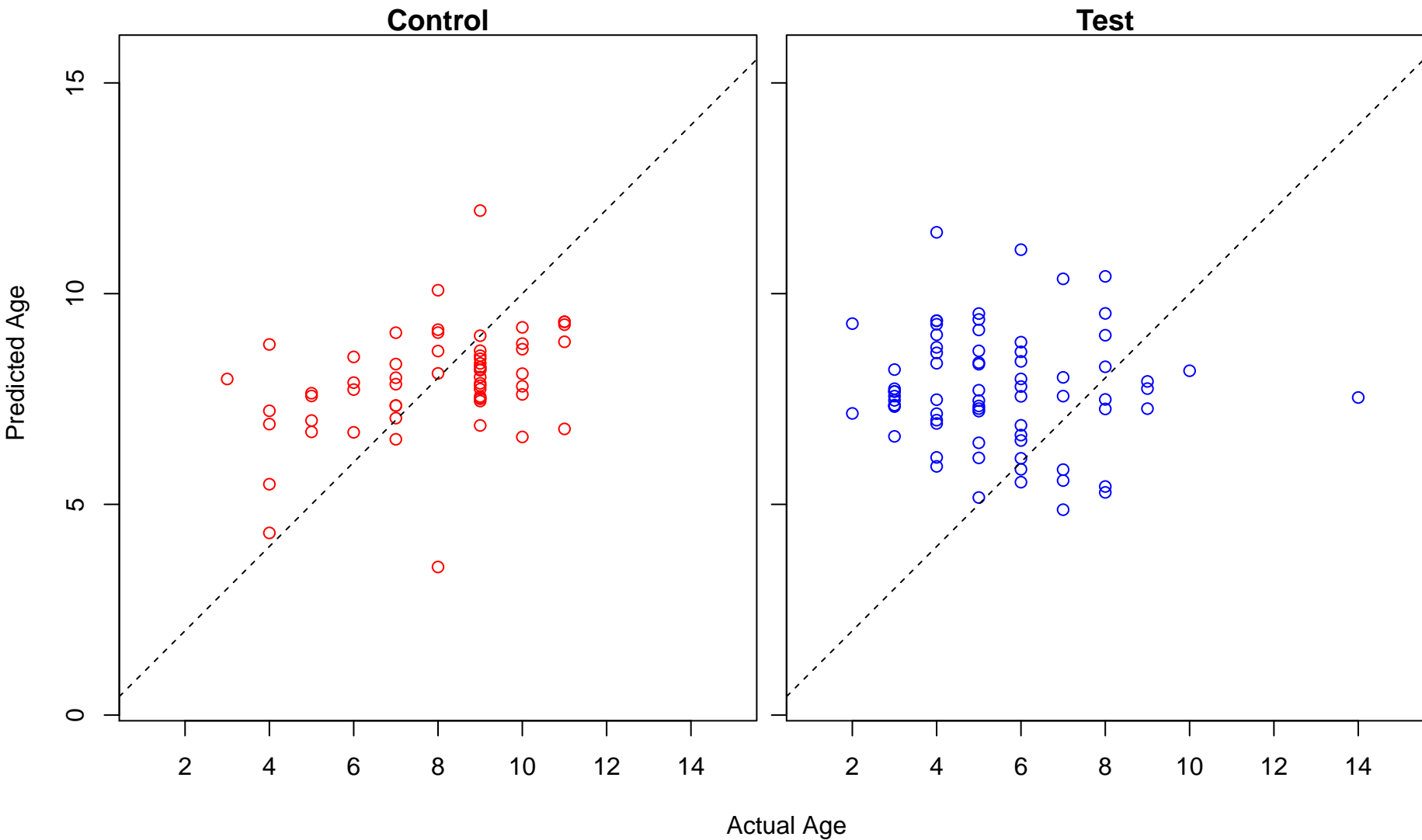
regulation of dendritic cell dendrite assembly (Score: 0.770207)



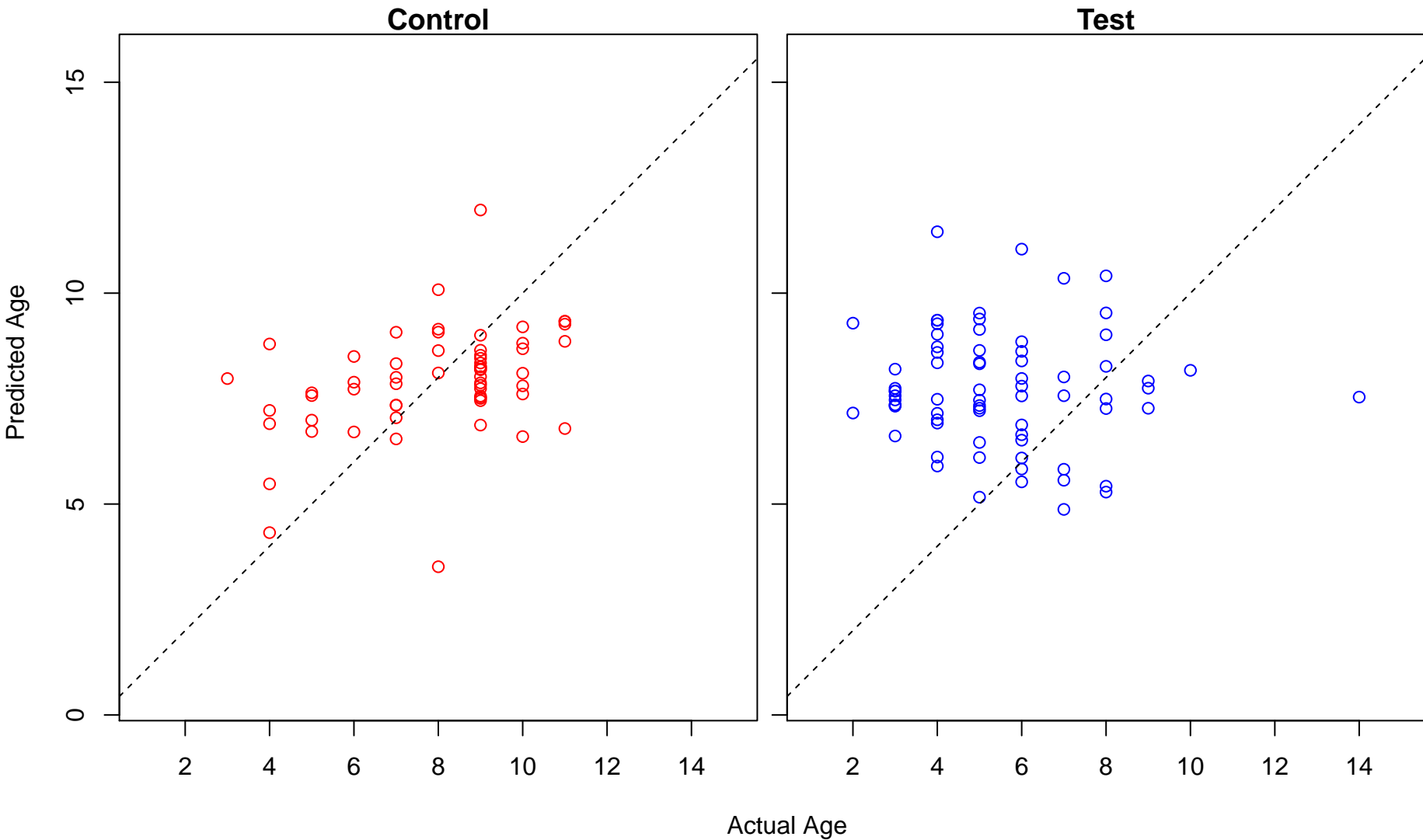
regulation of synaptic plasticity (Score: 0.769934)



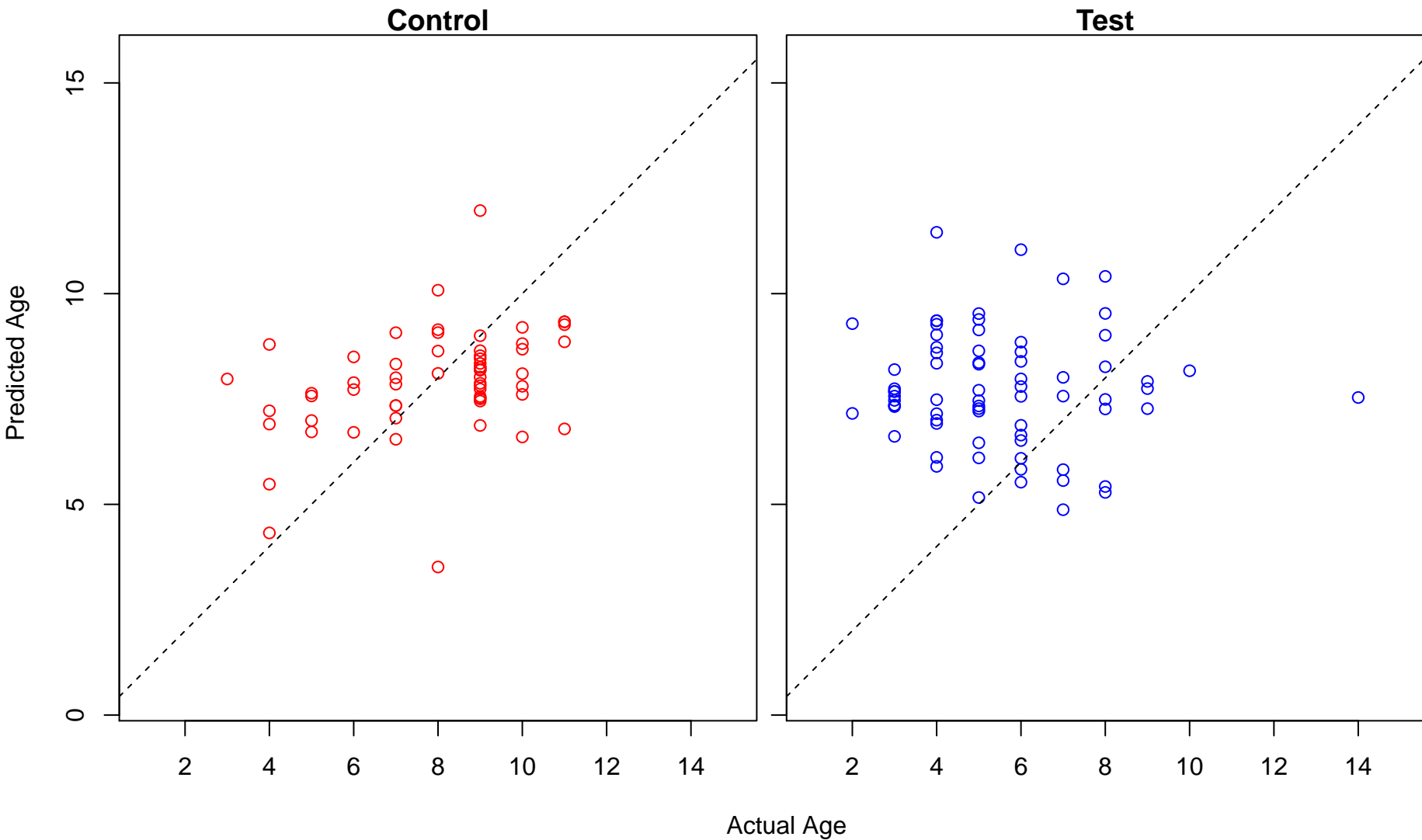
dopamine uptake involved in synaptic transmission (Score: 0.768783)



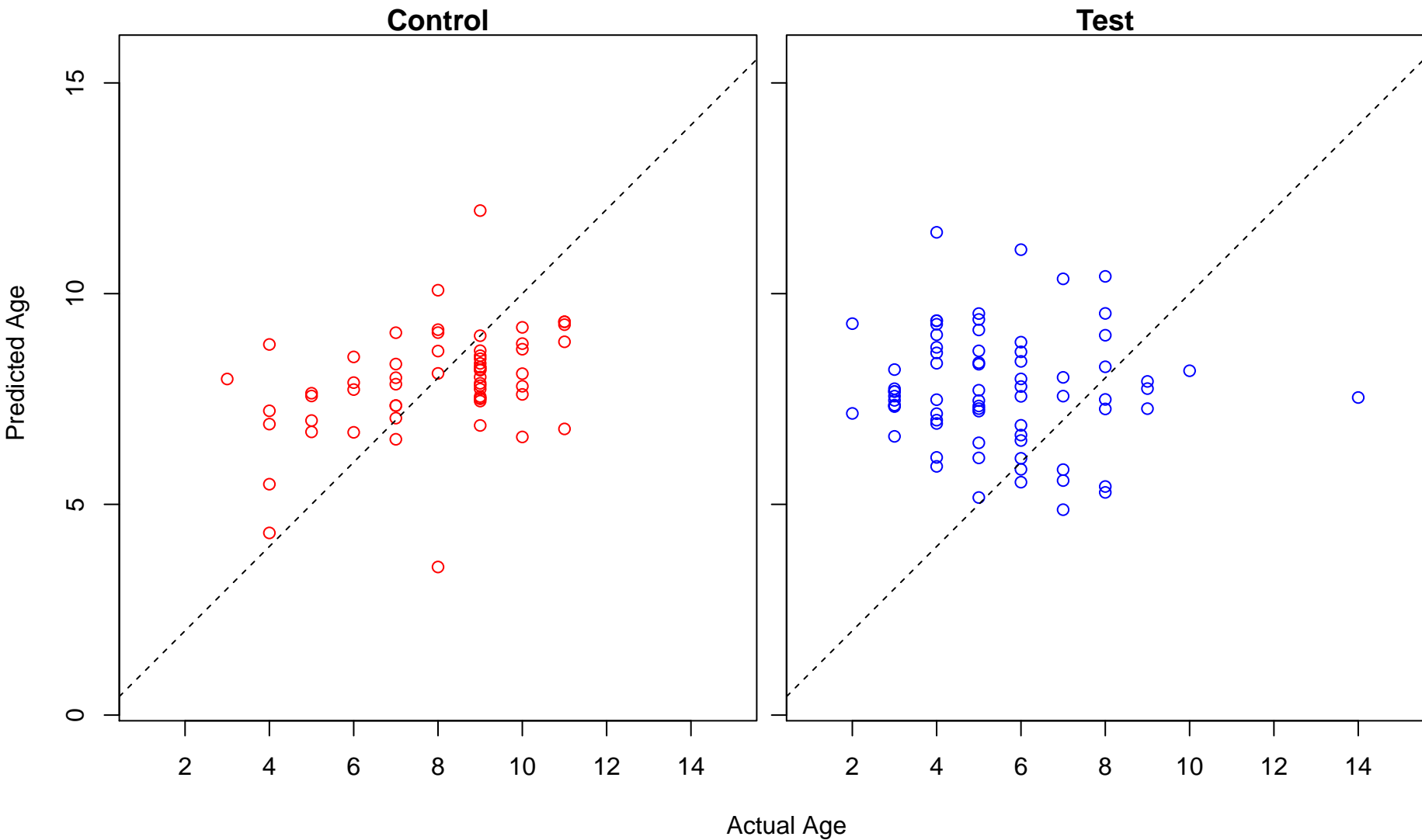
negative regulation of dopamine uptake involved in synaptic transmission (Score: 0.768783)



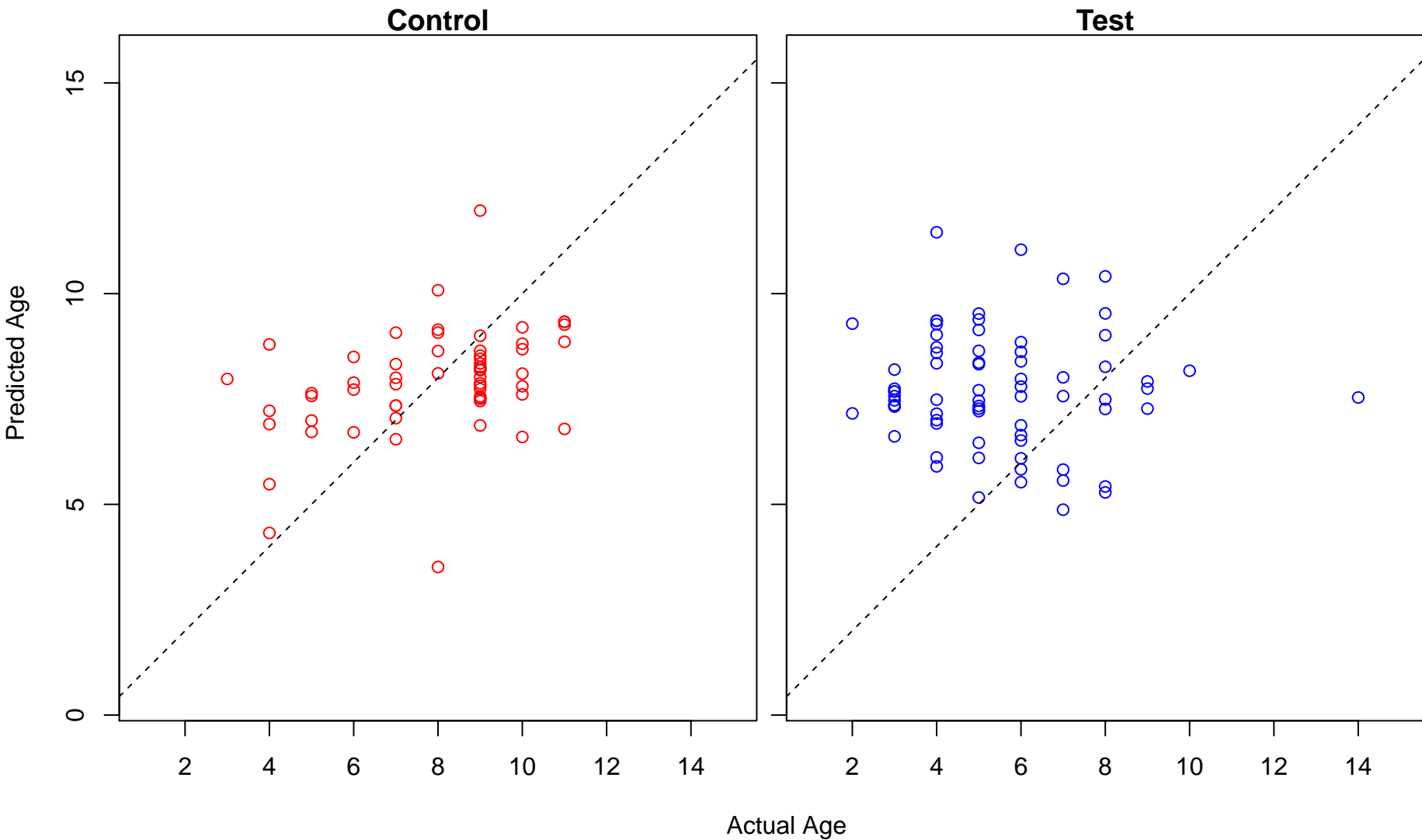
regulation of norepinephrine uptake (Score: 0.768783)



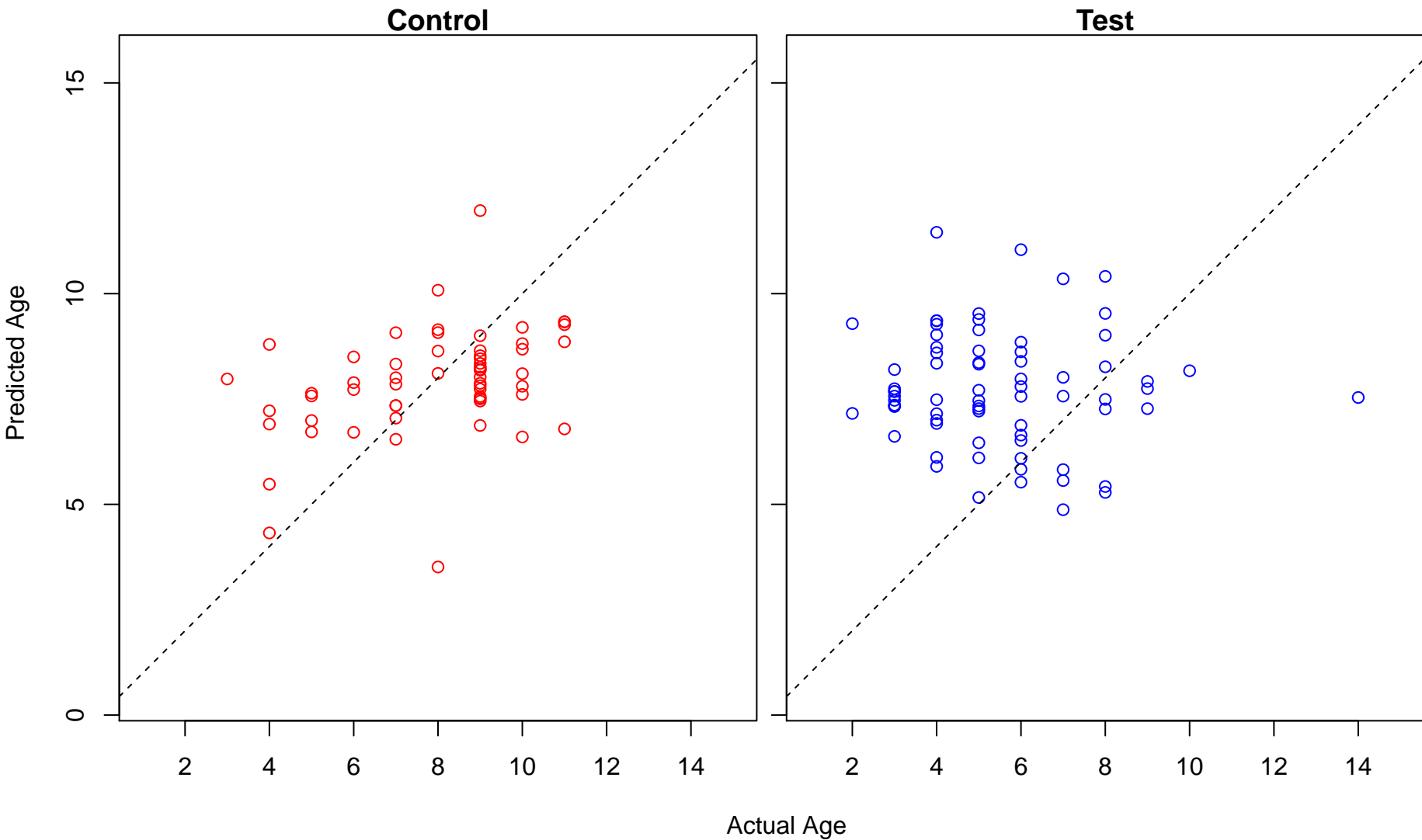
negative regulation of norepinephrine uptake (Score: 0.768783)



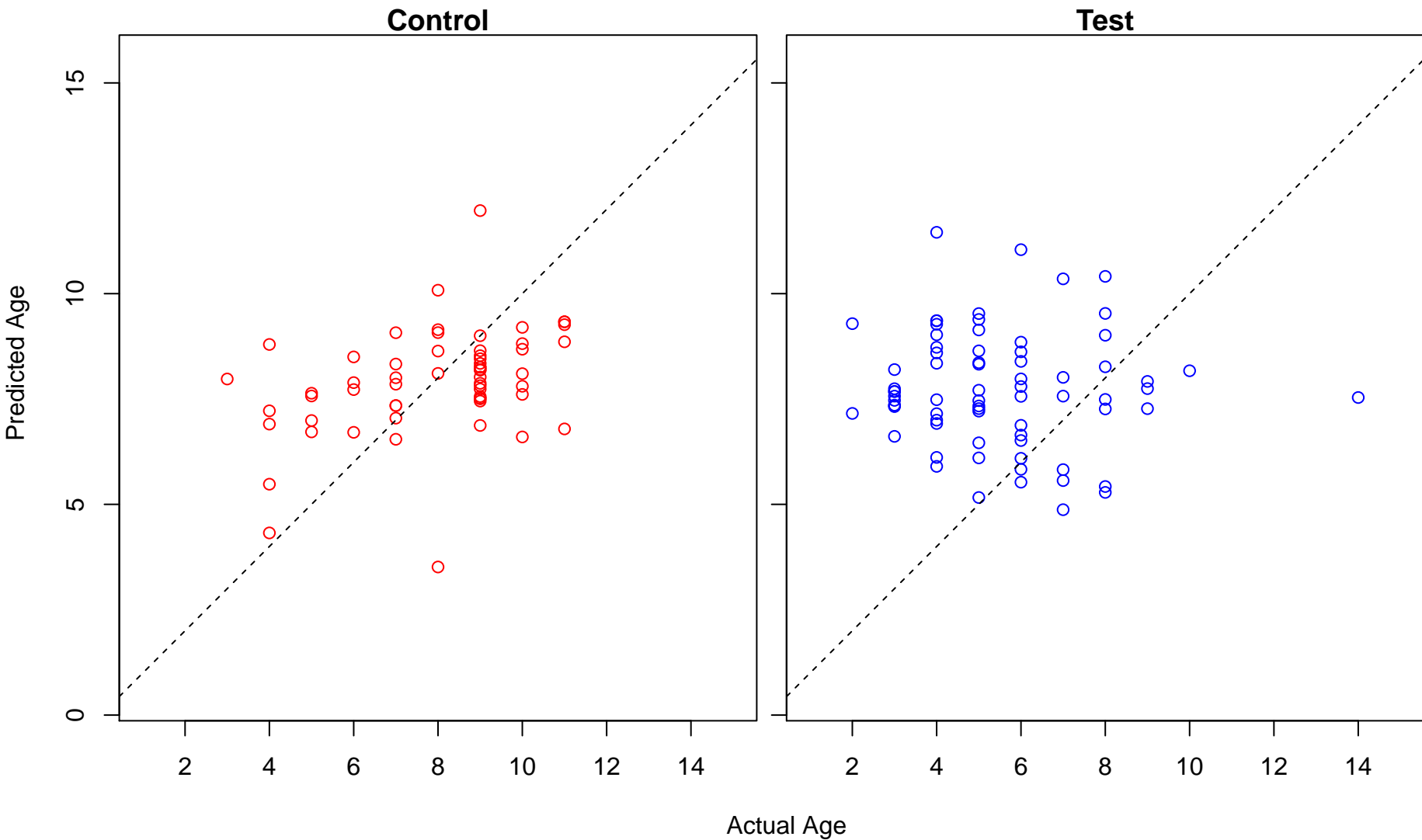
catecholamine uptake involved in synaptic transmission (Score: 0.768783)



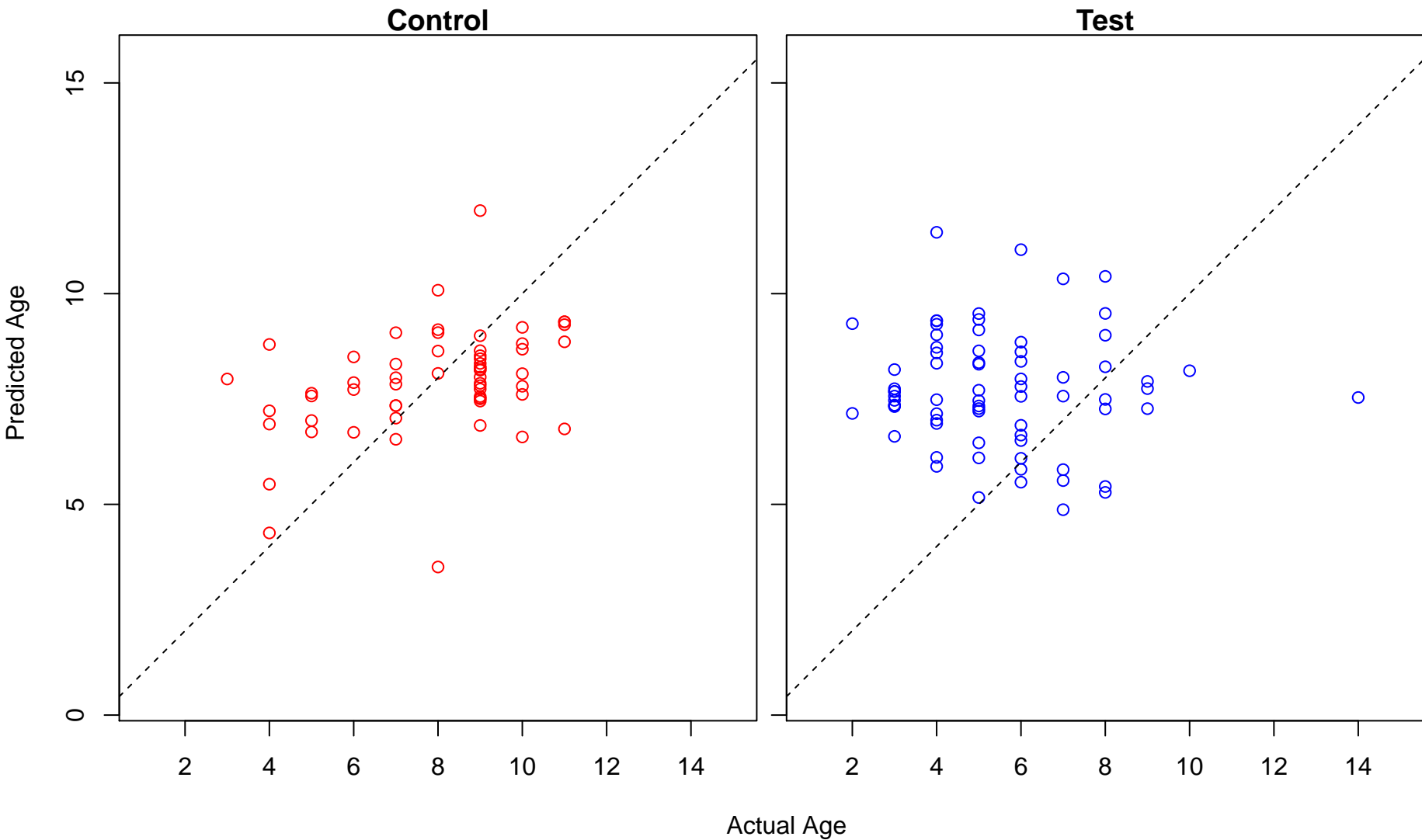
negative regulation of catecholamine uptake involved in synaptic transmission (Score: 0.768783)



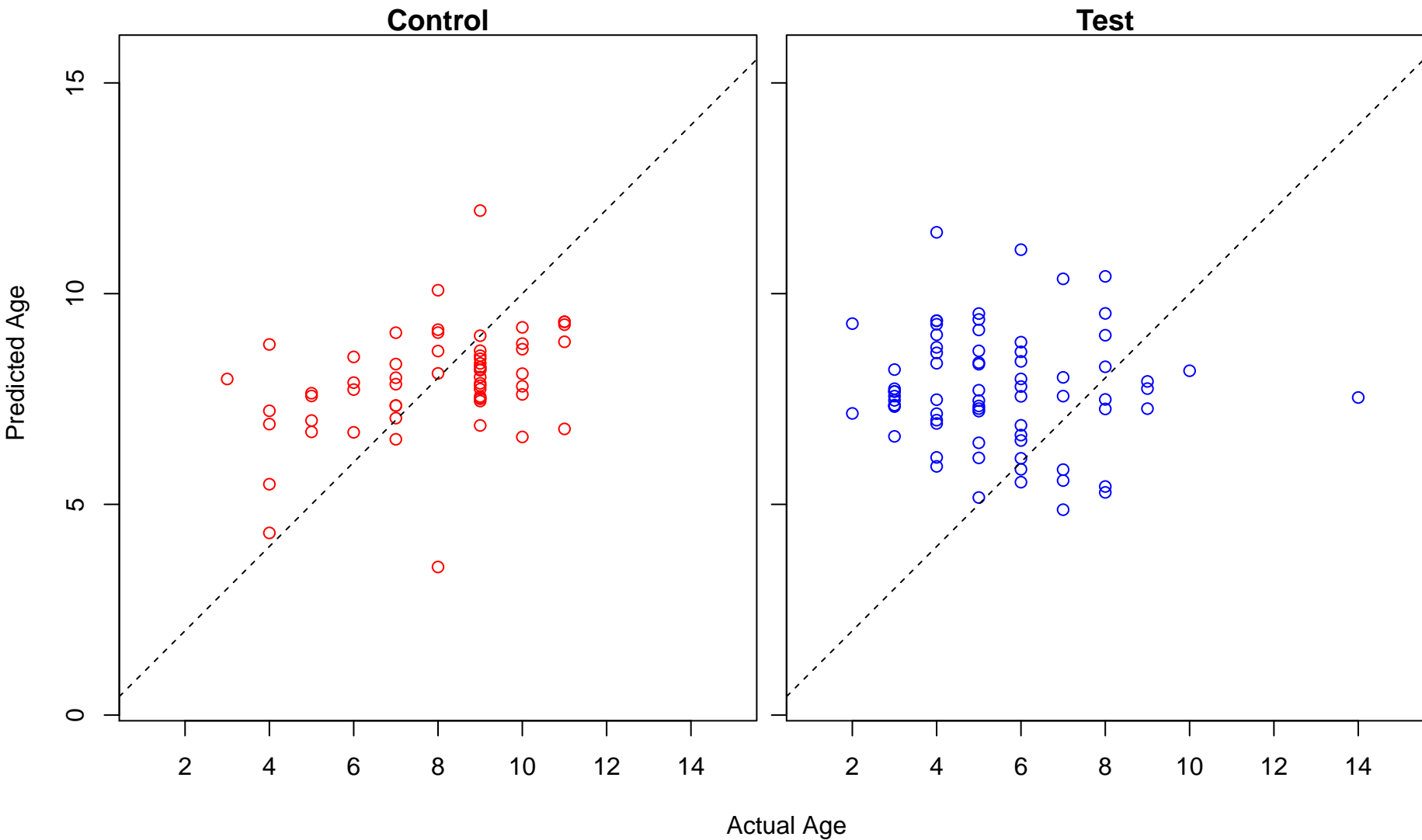
regulation of thrombin receptor signaling pathway (Score: 0.768783)



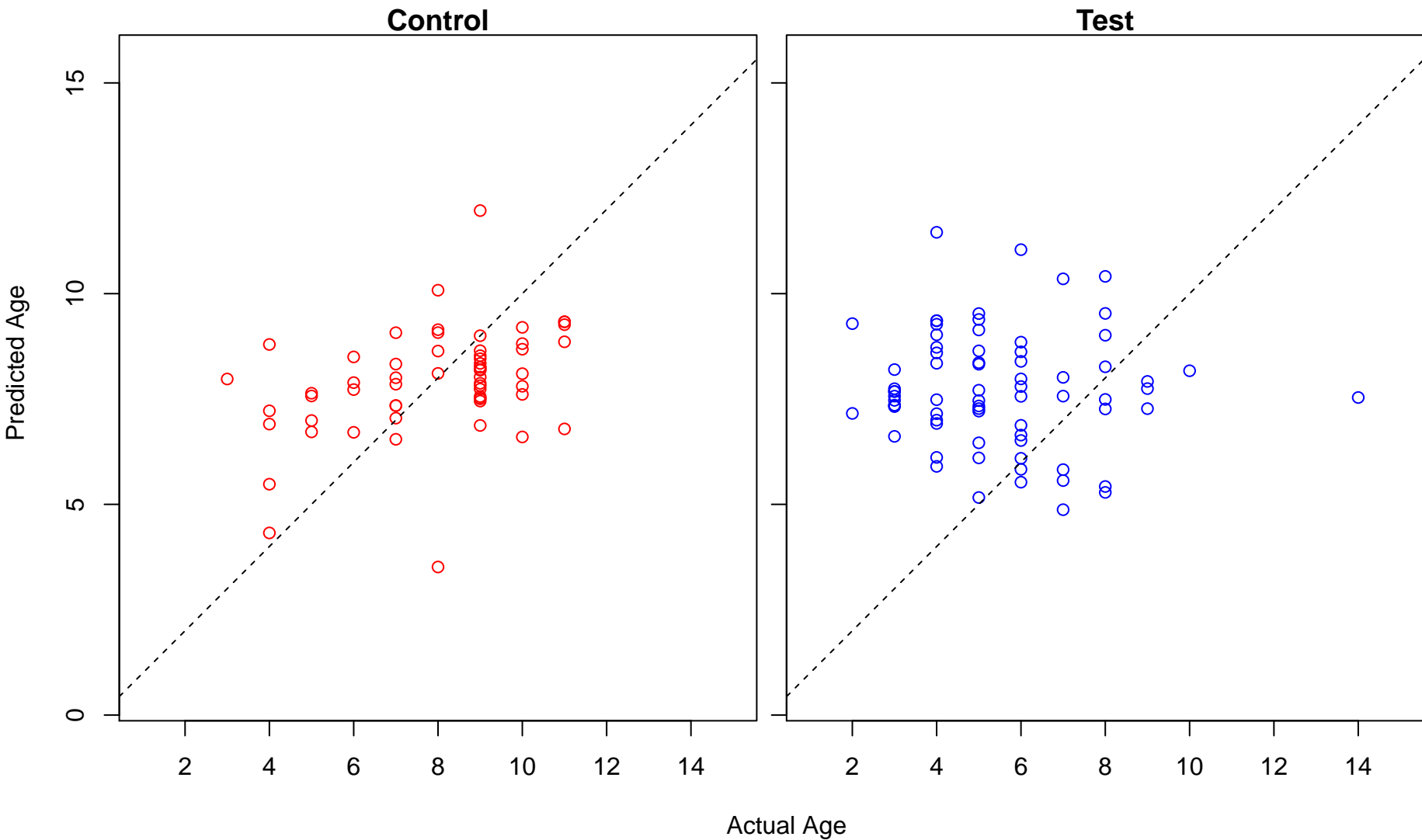
negative regulation of thrombin receptor signaling pathway (Score: 0.768783)



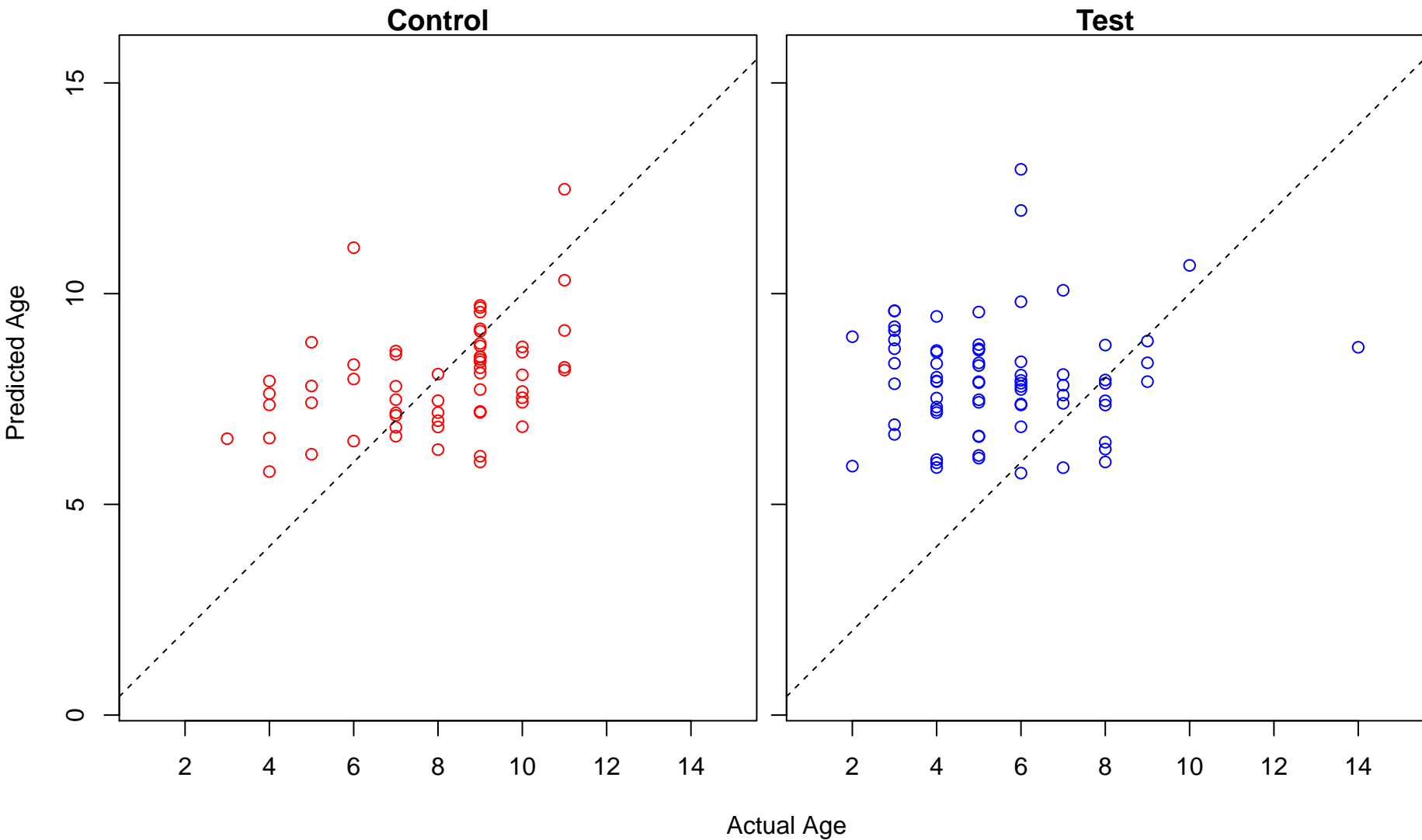
catecholamine uptake (Score: 0.768783)



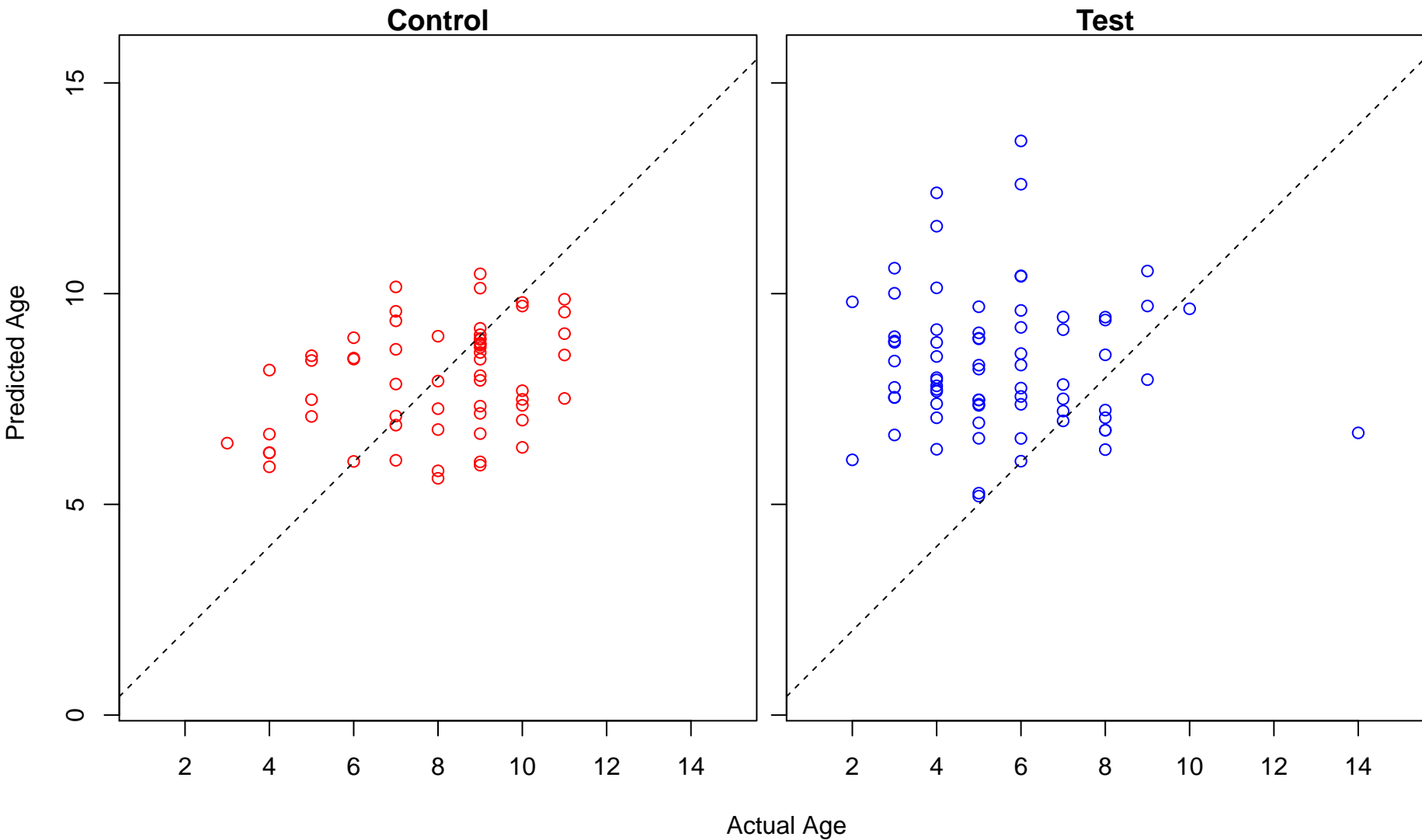
dopamine uptake (Score: 0.768783)



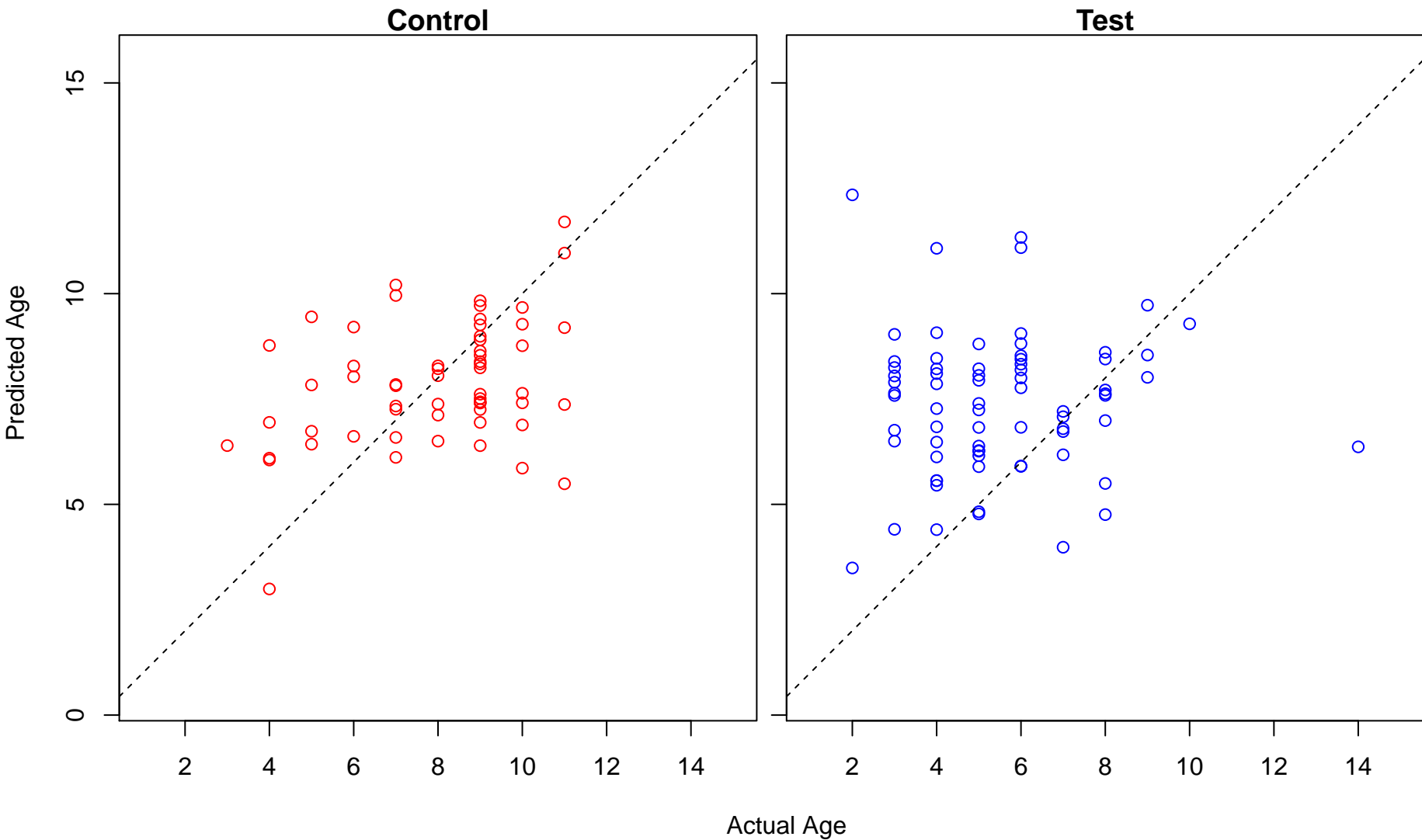
negative regulation of interferon-beta production (Score: 0.768656)



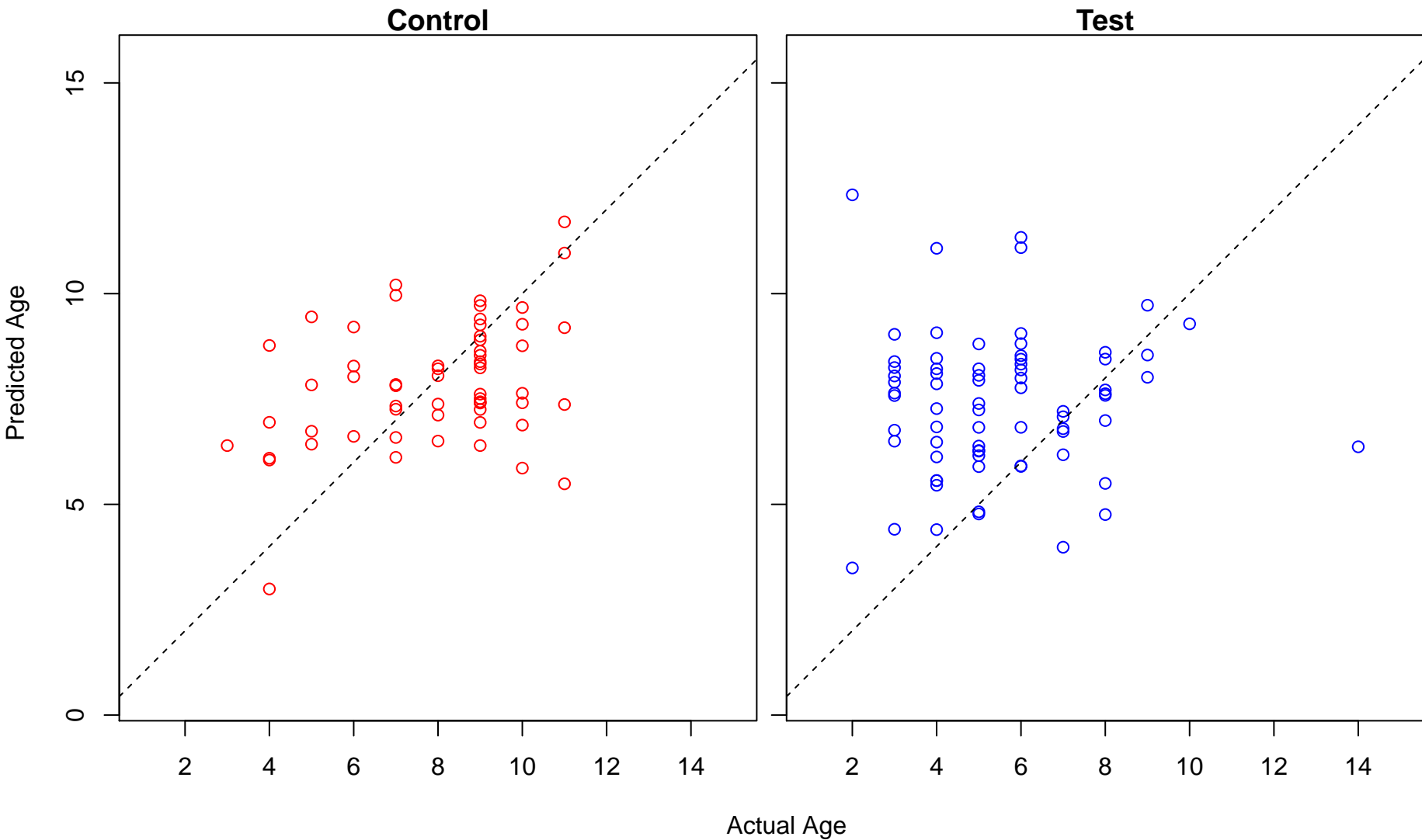
terpenoid metabolic process (Score: 0.768372)



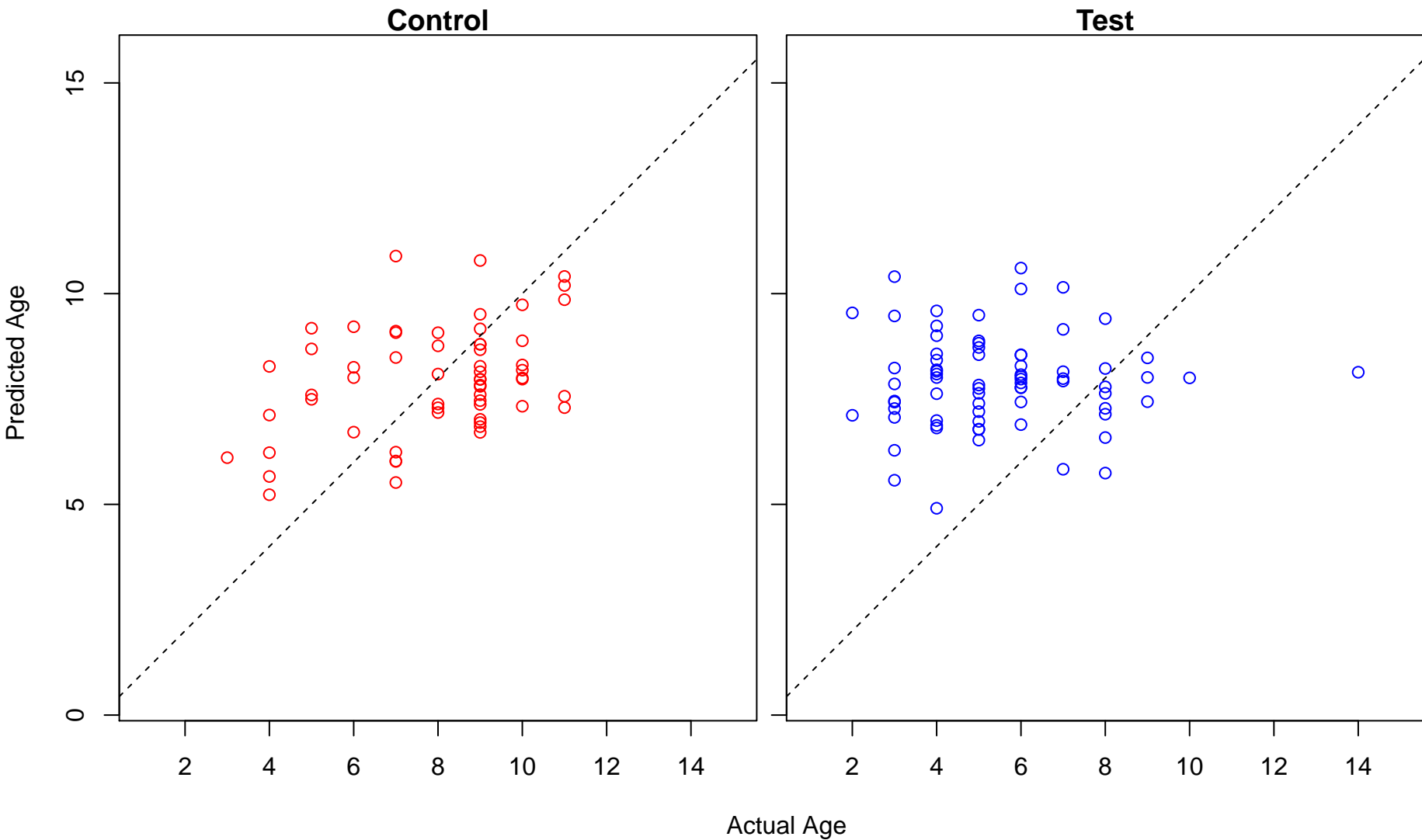
negative regulation of epidermal growth factor receptor signaling pathway (Score: 0.766126)



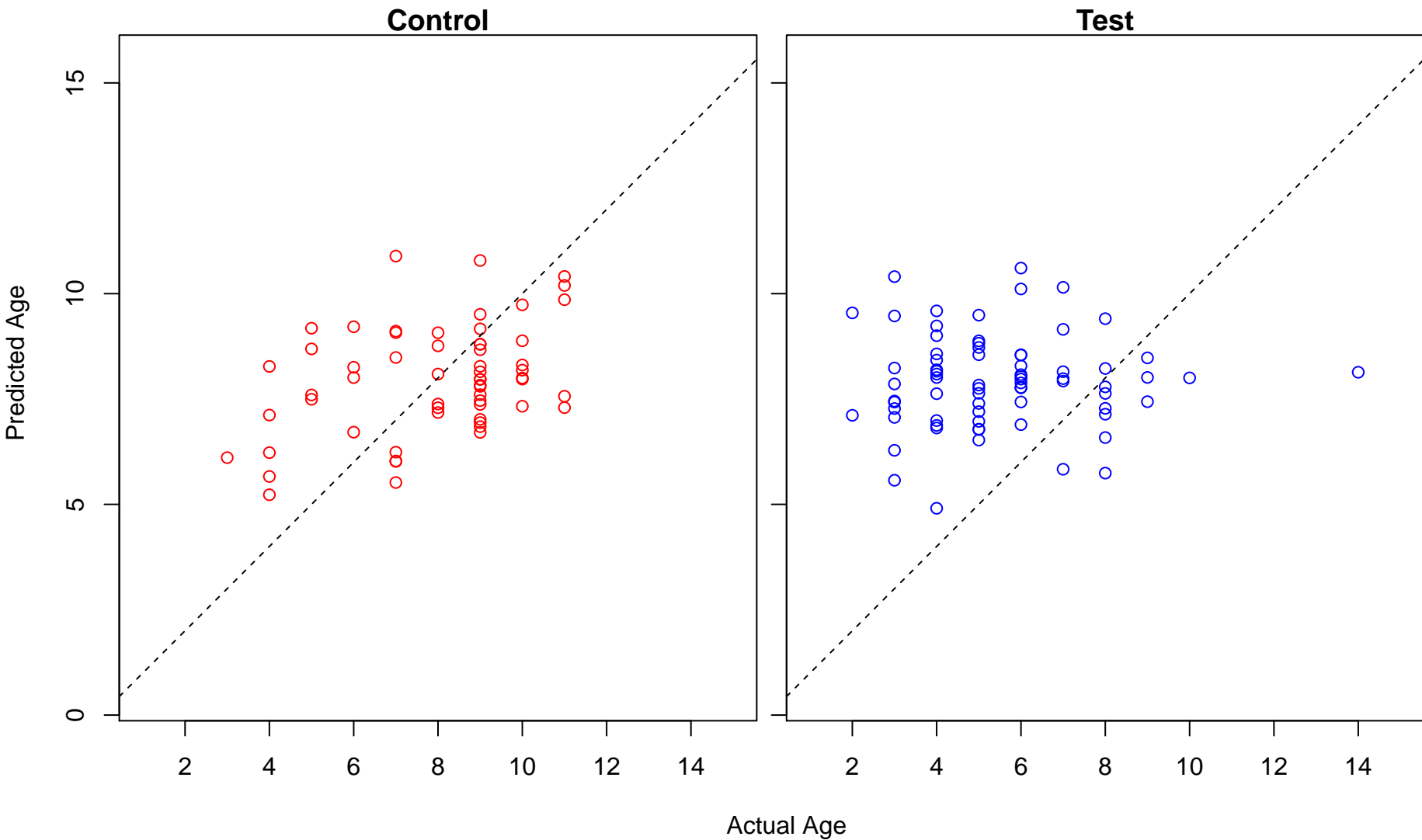
negative regulation of ERBB signaling pathway (Score: 0.765952)



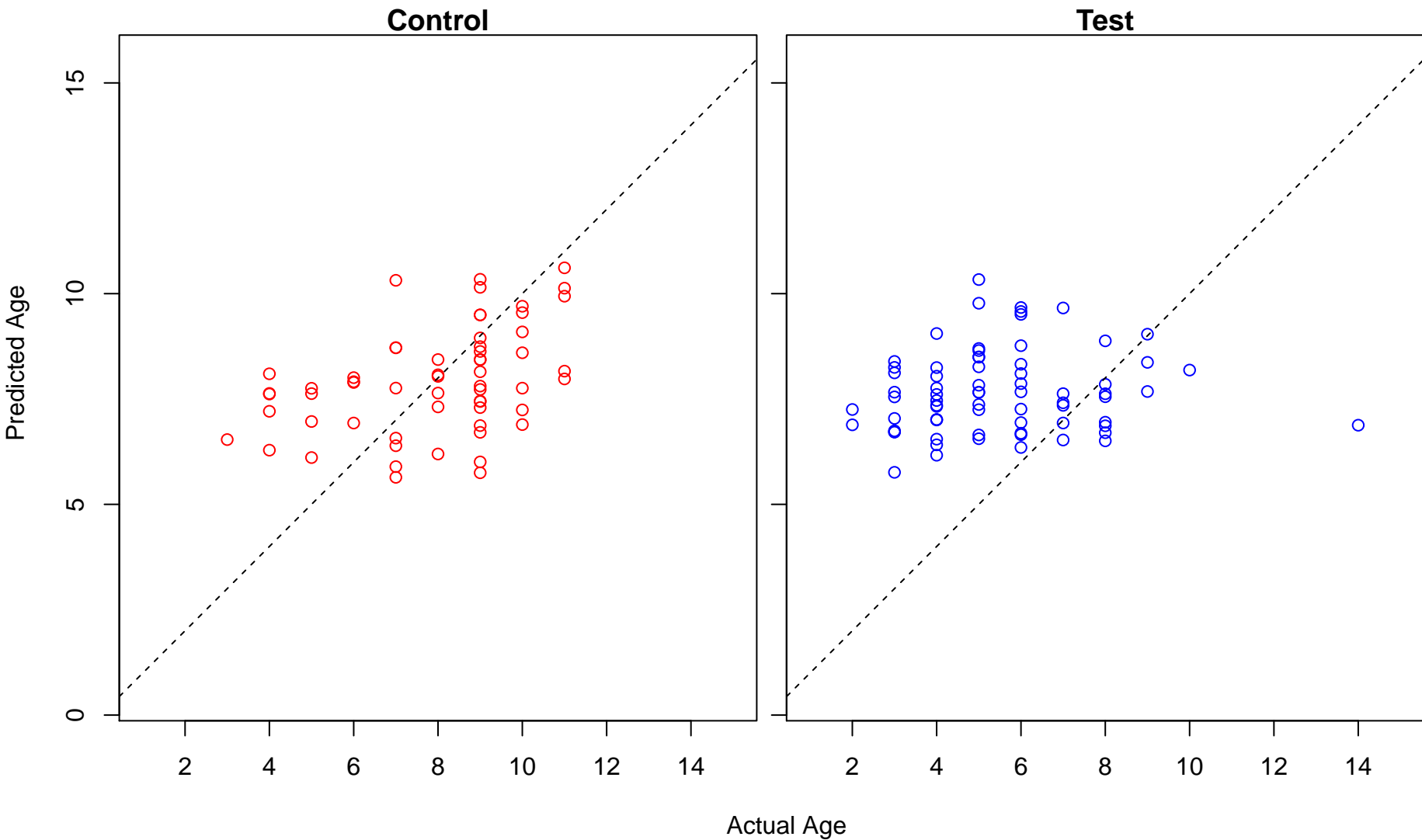
phosphatidylinositol-mediated signaling (Score: 0.765520)



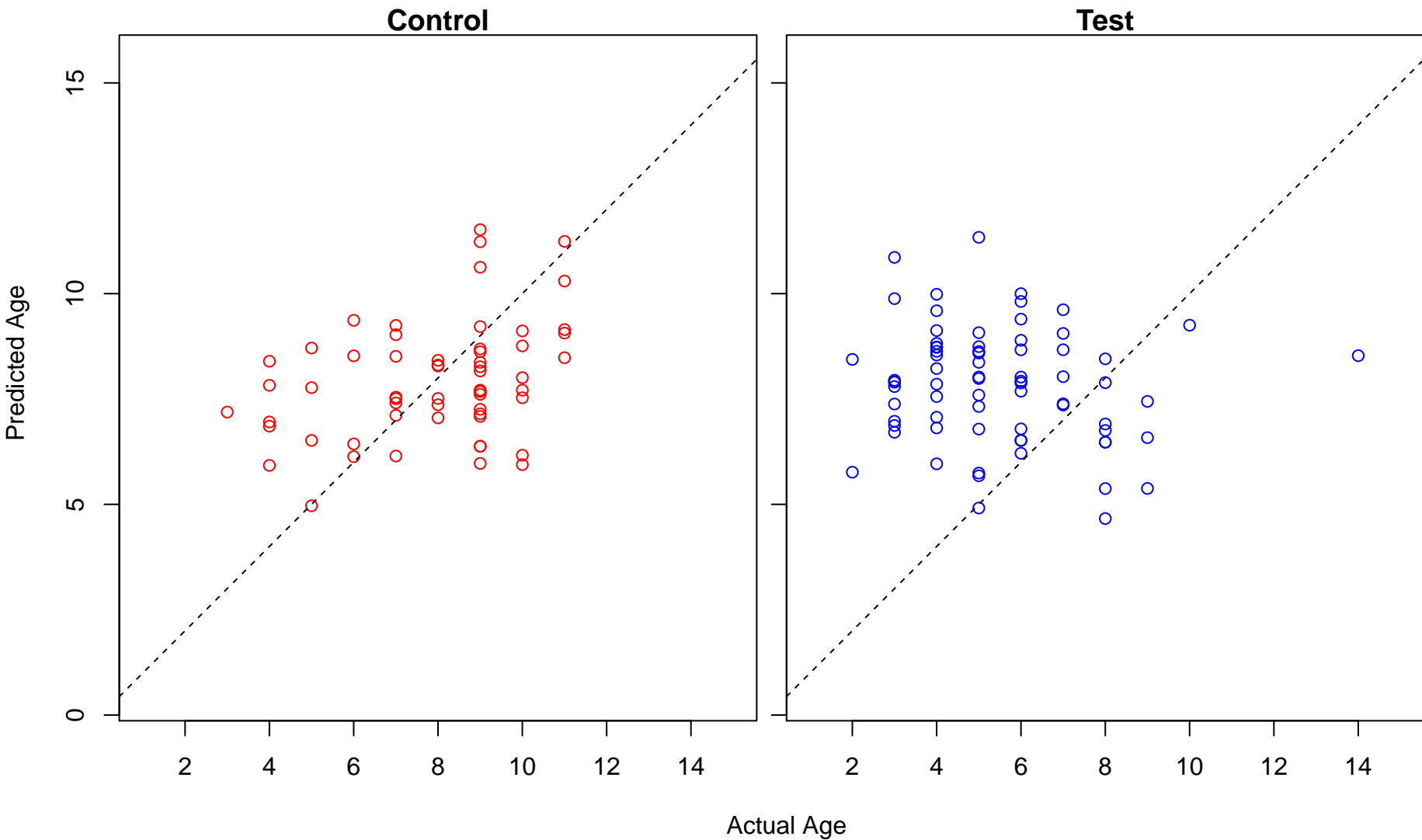
inositol lipid-mediated signaling (Score: 0.765520)



regulation of blood vessel remodeling (Score: 0.765293)

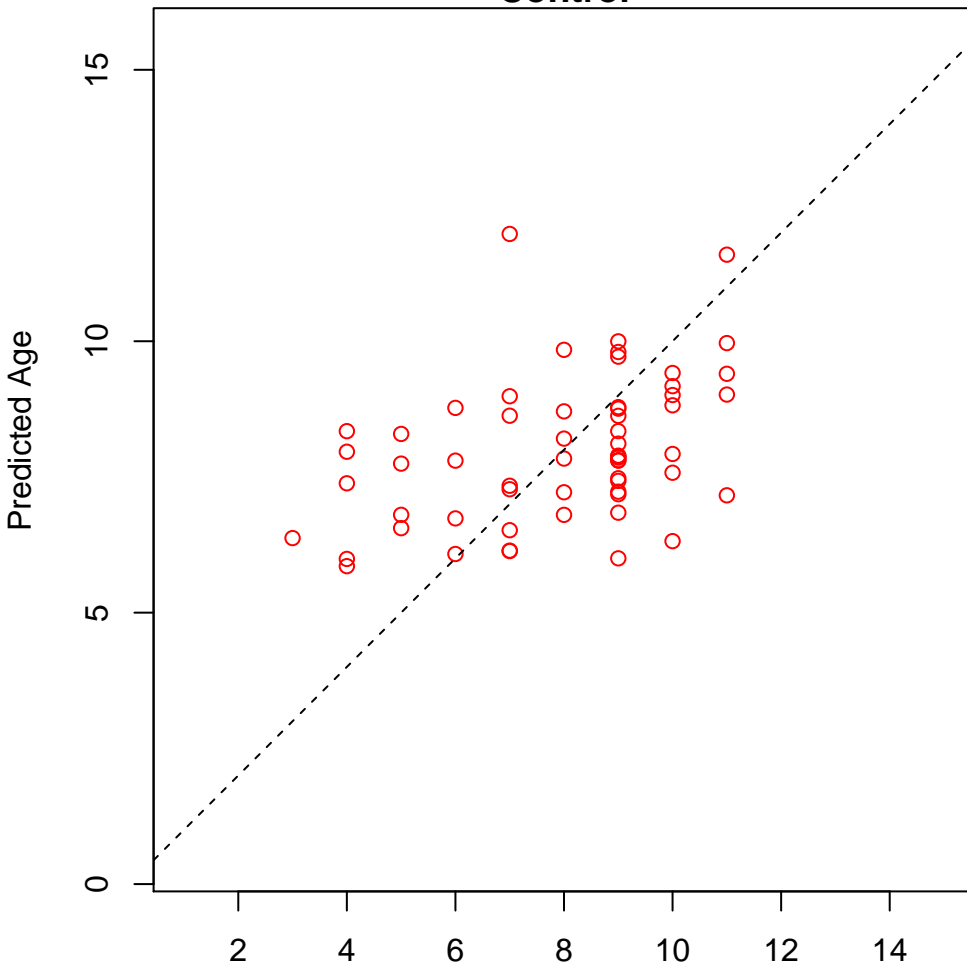


positive regulation of T cell differentiation in thymus (Score: 0.764943)

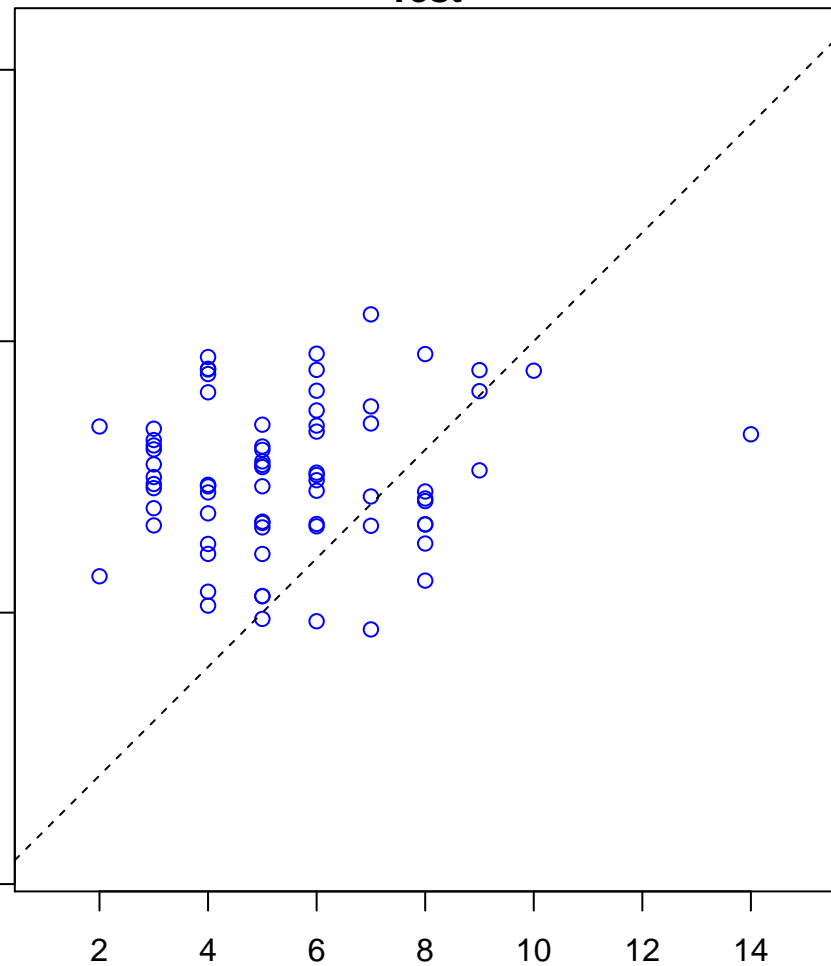


polarized epithelial cell differentiation (Score: 0.764685)

Control

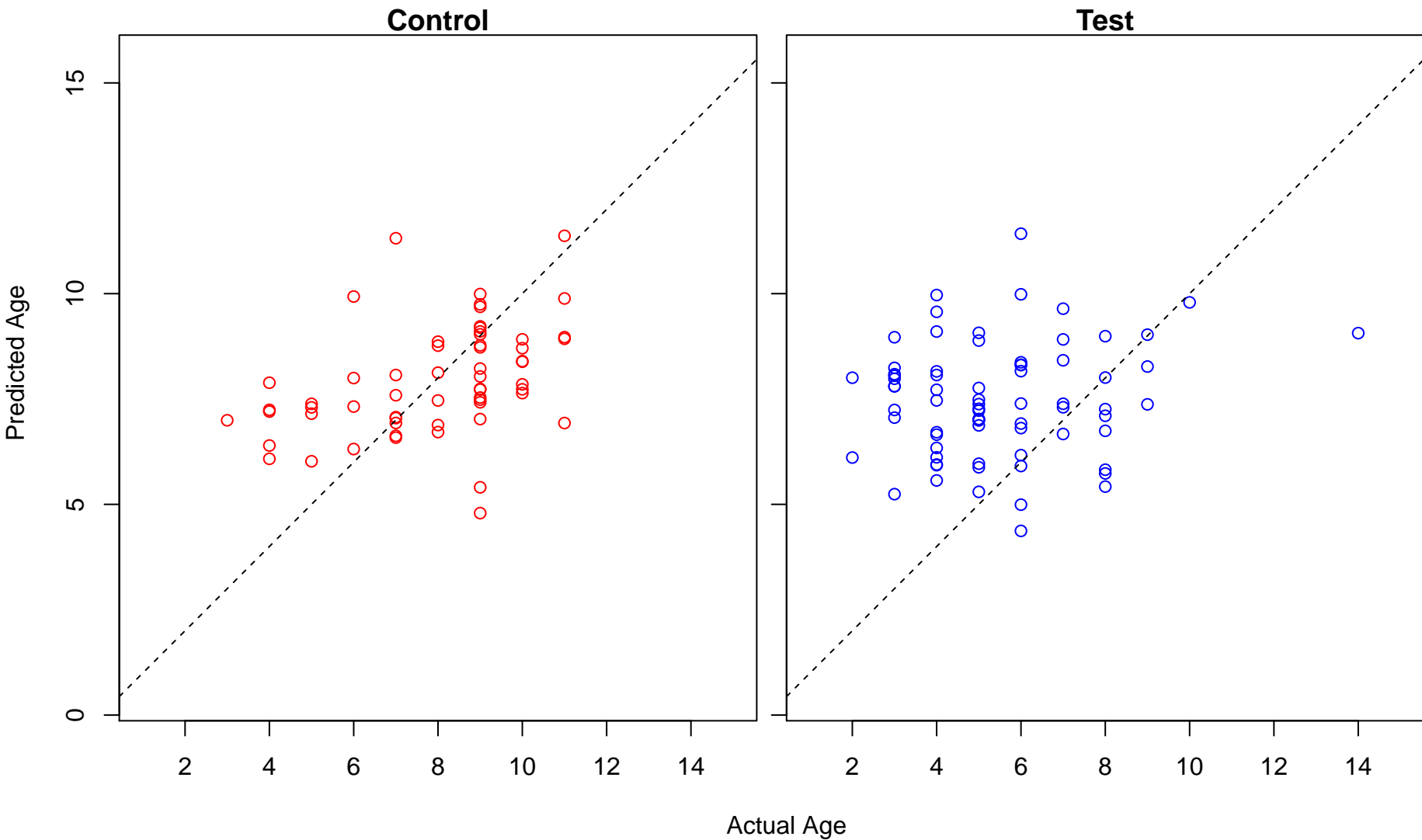


Test

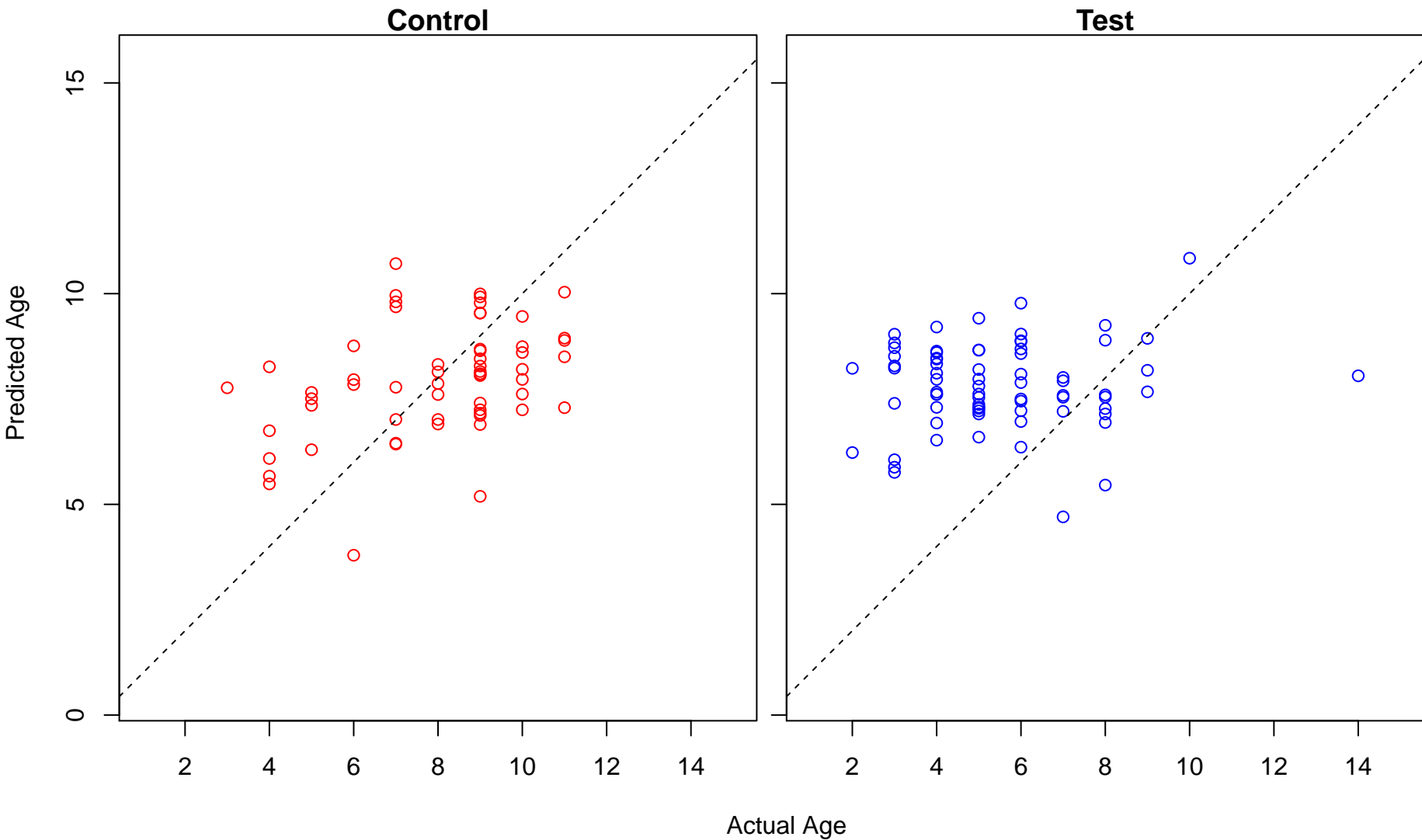


Actual Age

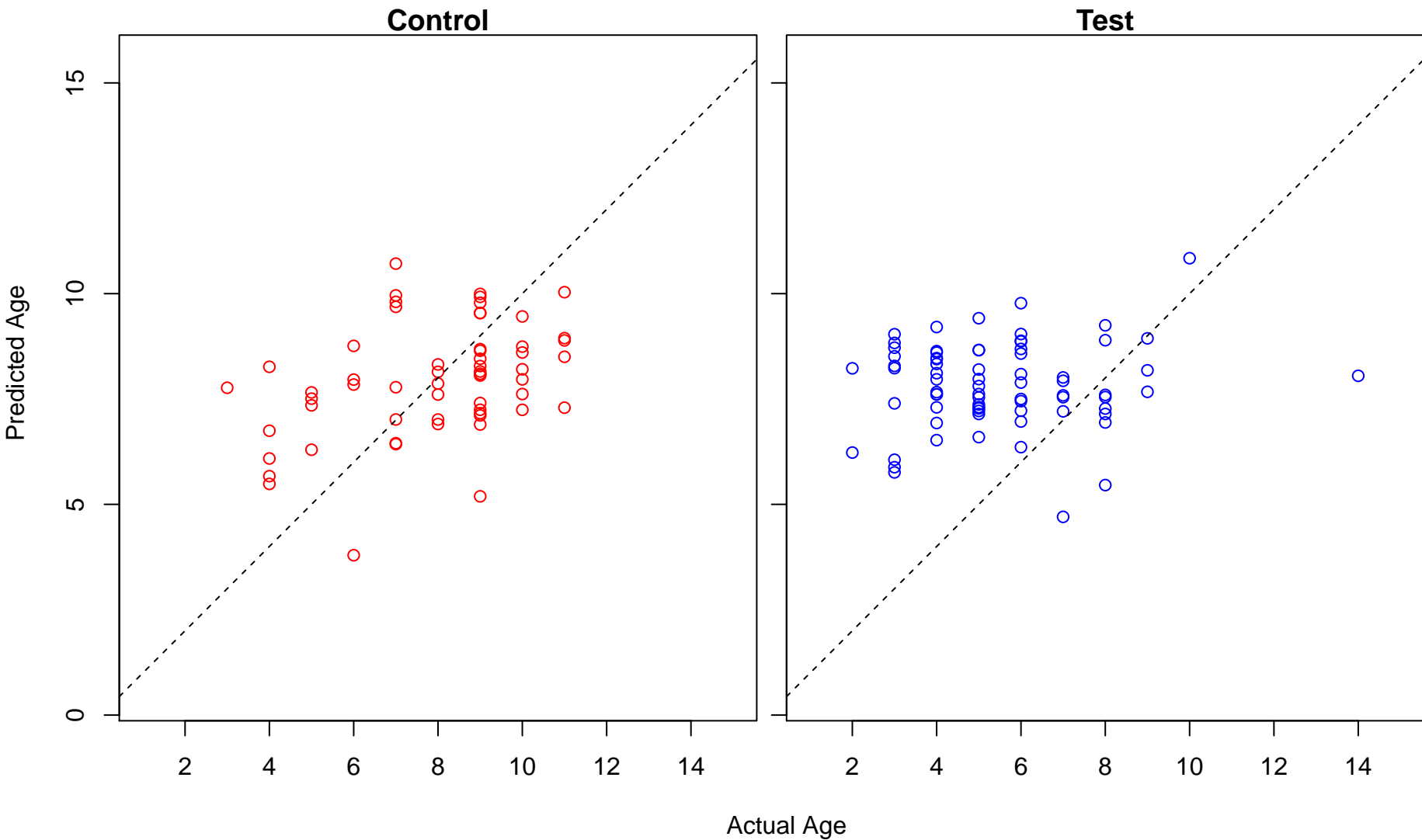
establishment of Golgi localization (Score: 0.761597)



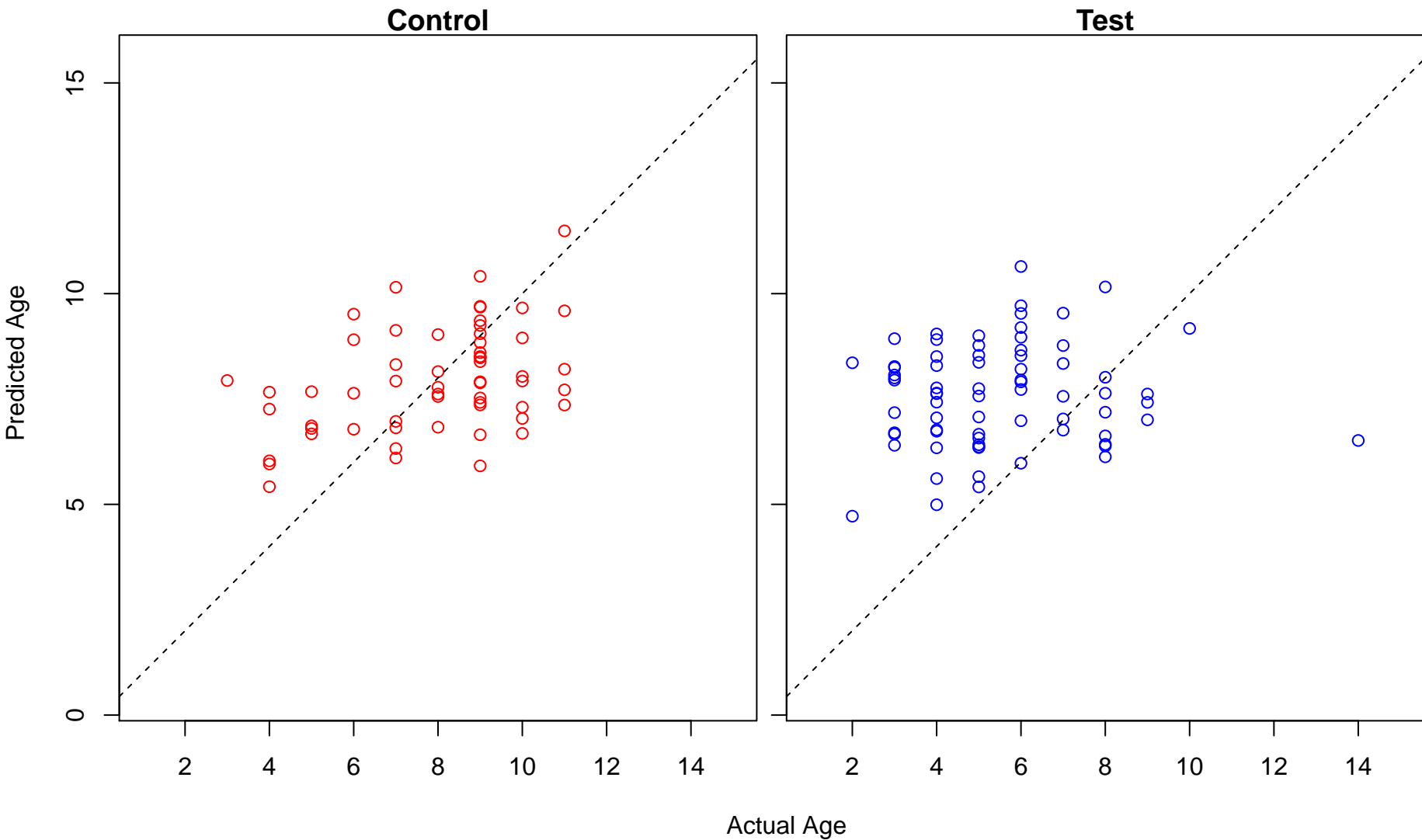
nucleotide-sugar transport (Score: 0.759536)



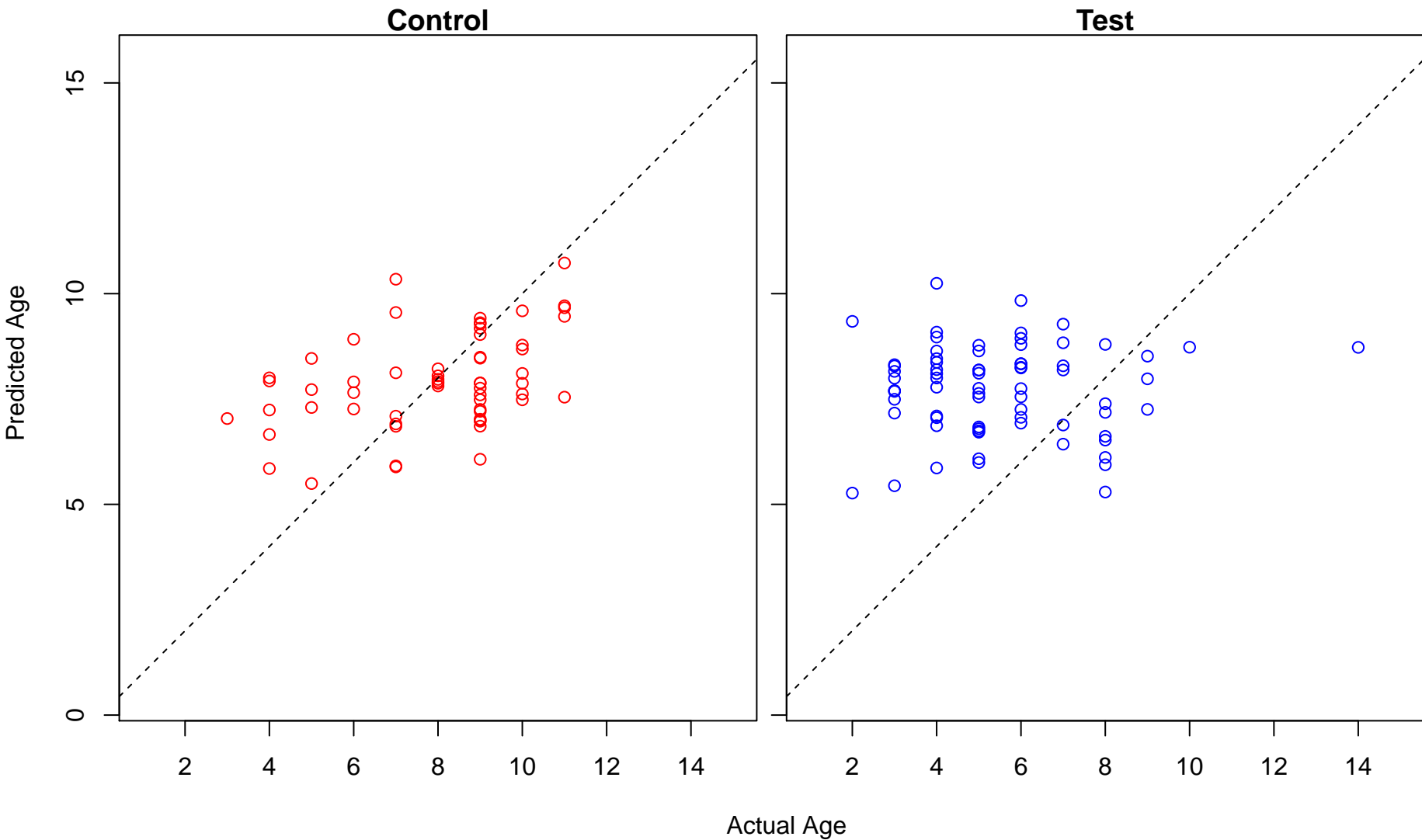
pyrimidine nucleotide–sugar transport (Score: 0.759536)



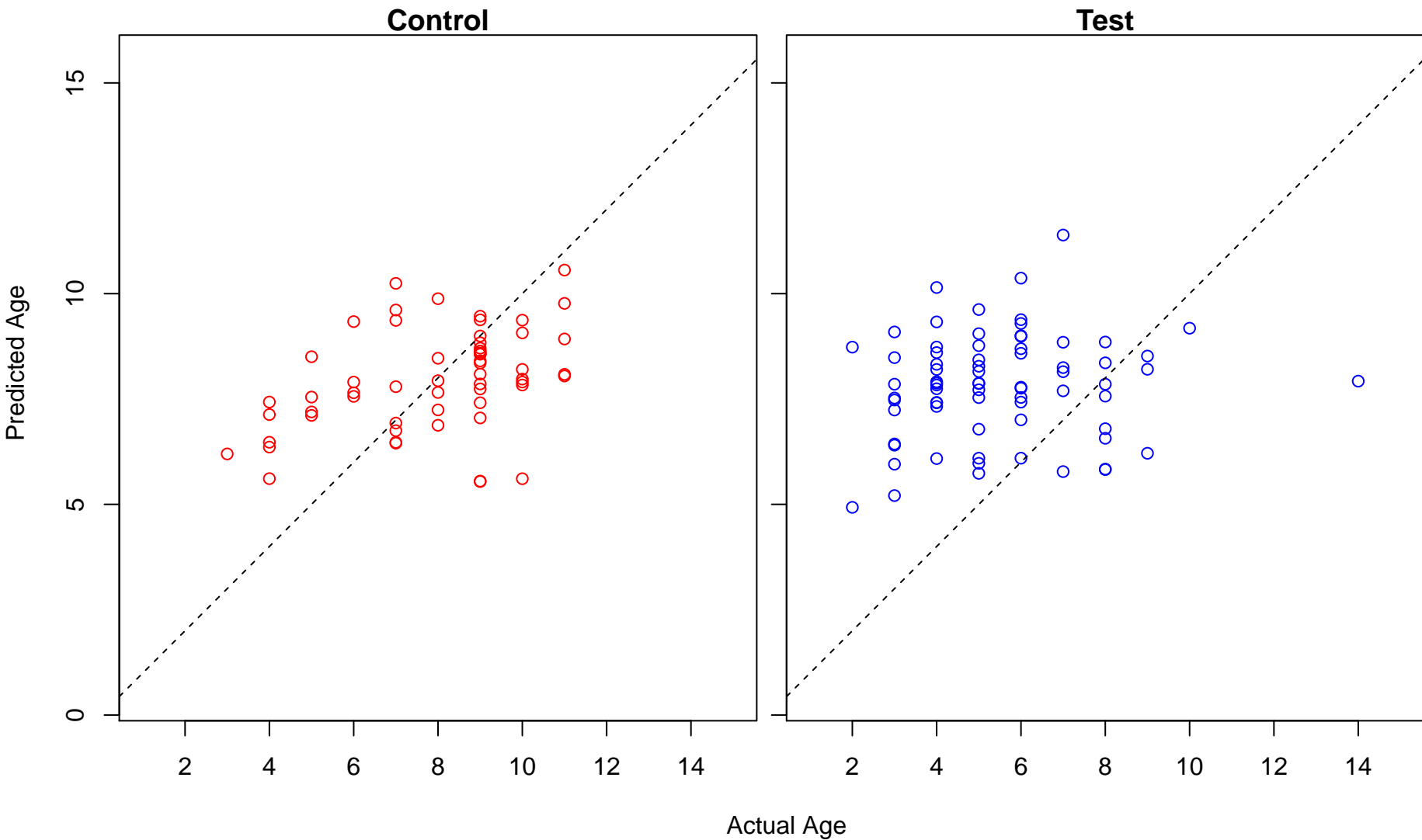
semaphorin-plexin signaling pathway (Score: 0.758667)



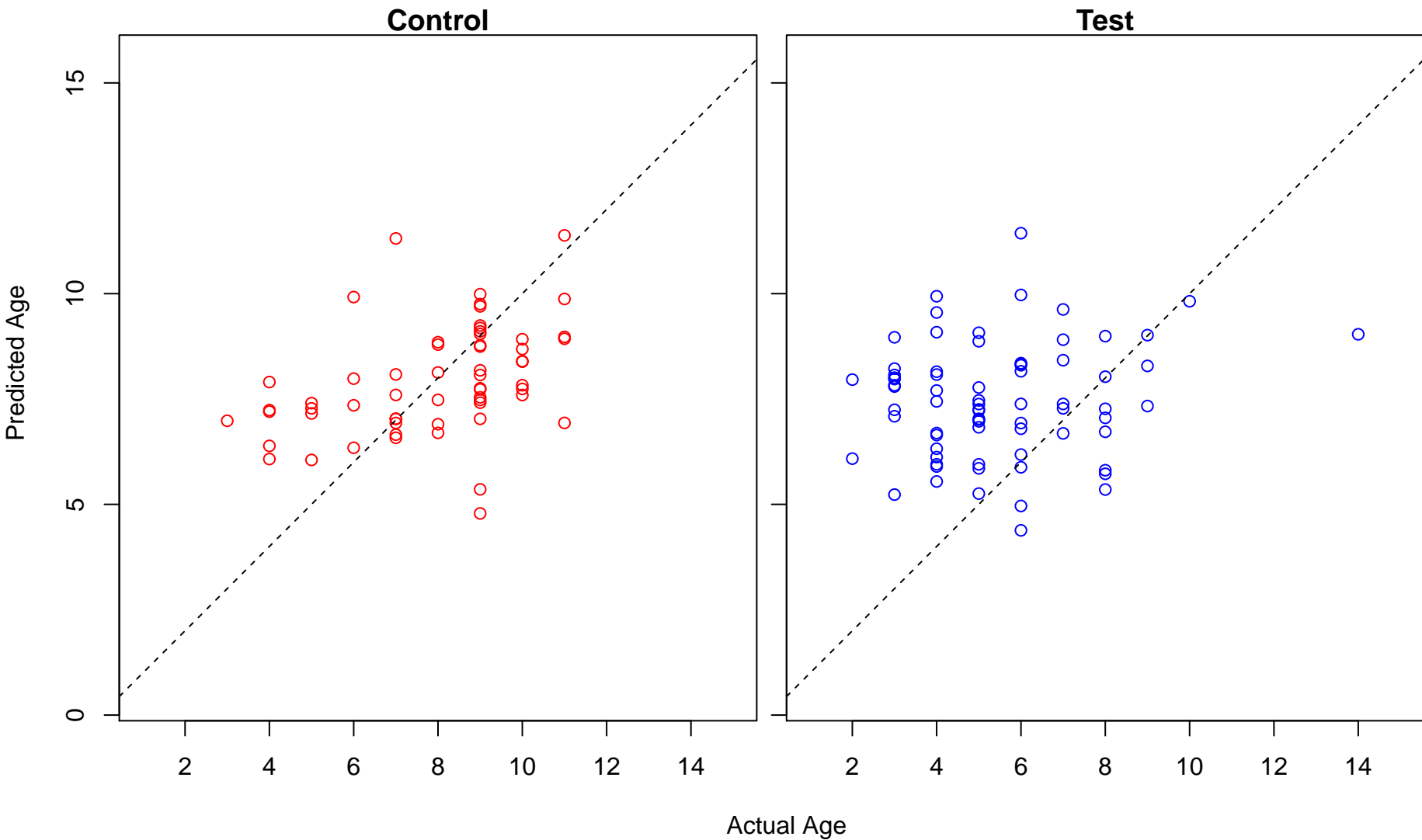
negative regulation of catenin import into nucleus (Score: 0.757989)



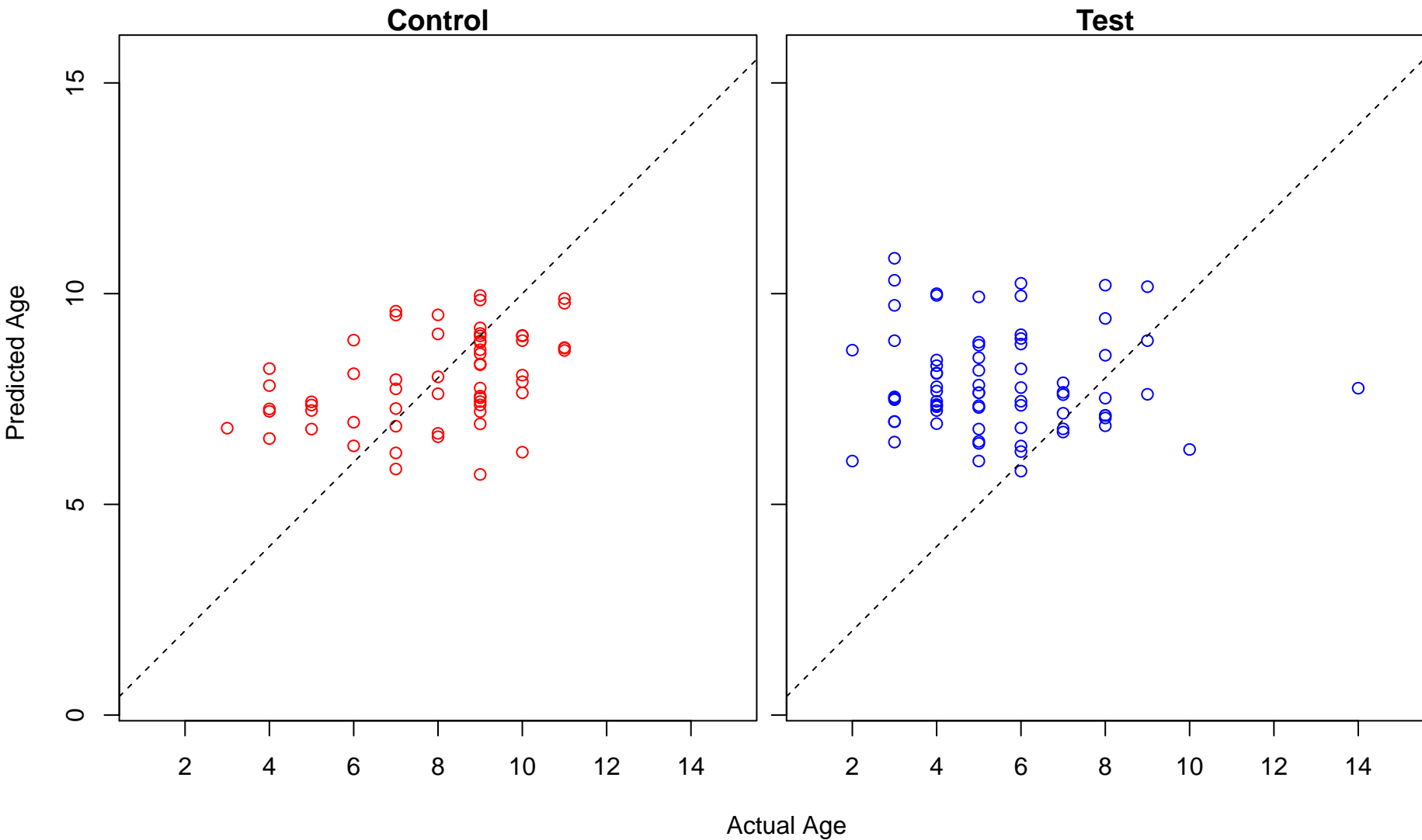
head morphogenesis (Score: 0.757686)



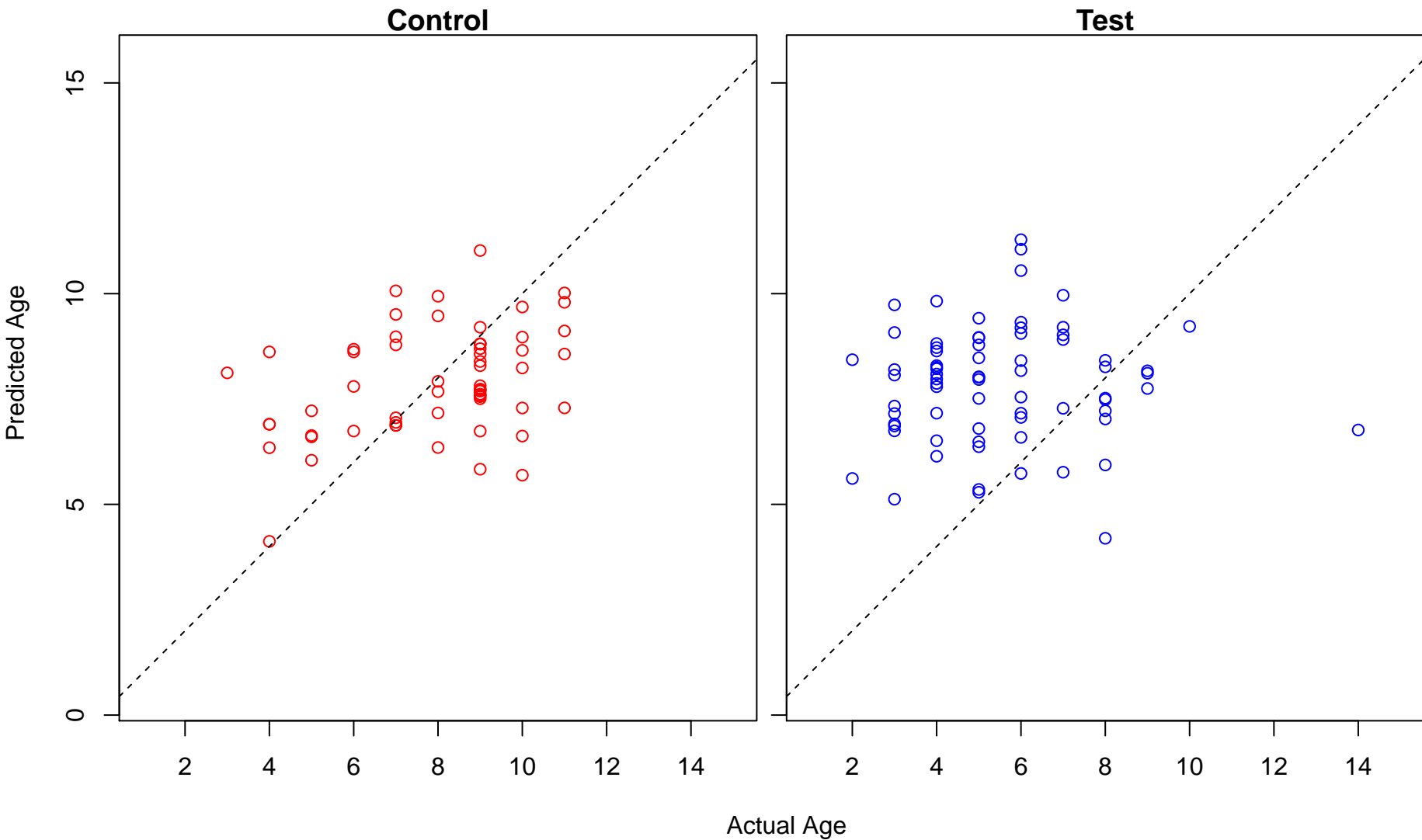
Golgi localization (Score: 0.757268)



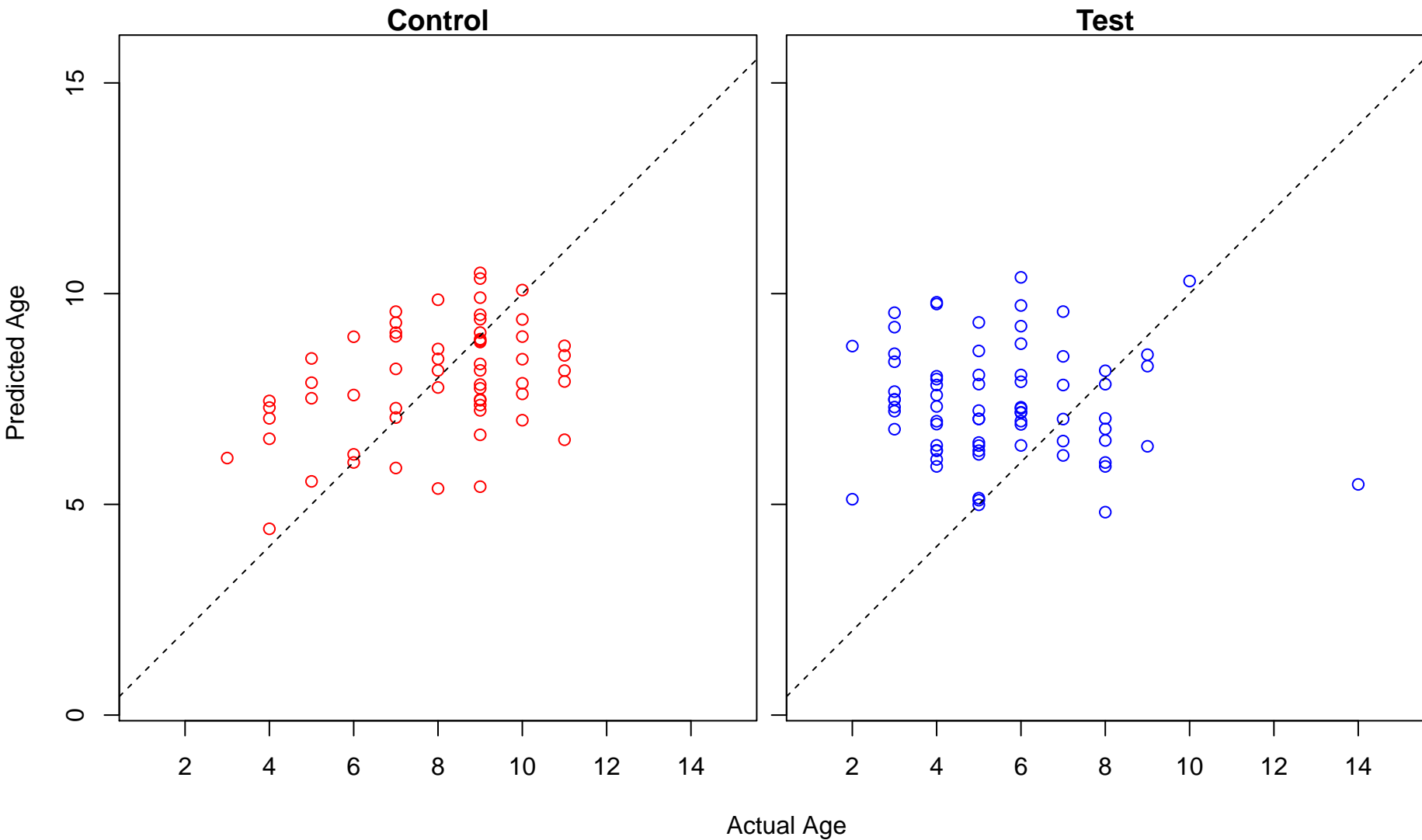
JAK-STAT cascade involved in growth hormone signaling pathway (Score: 0.756458)



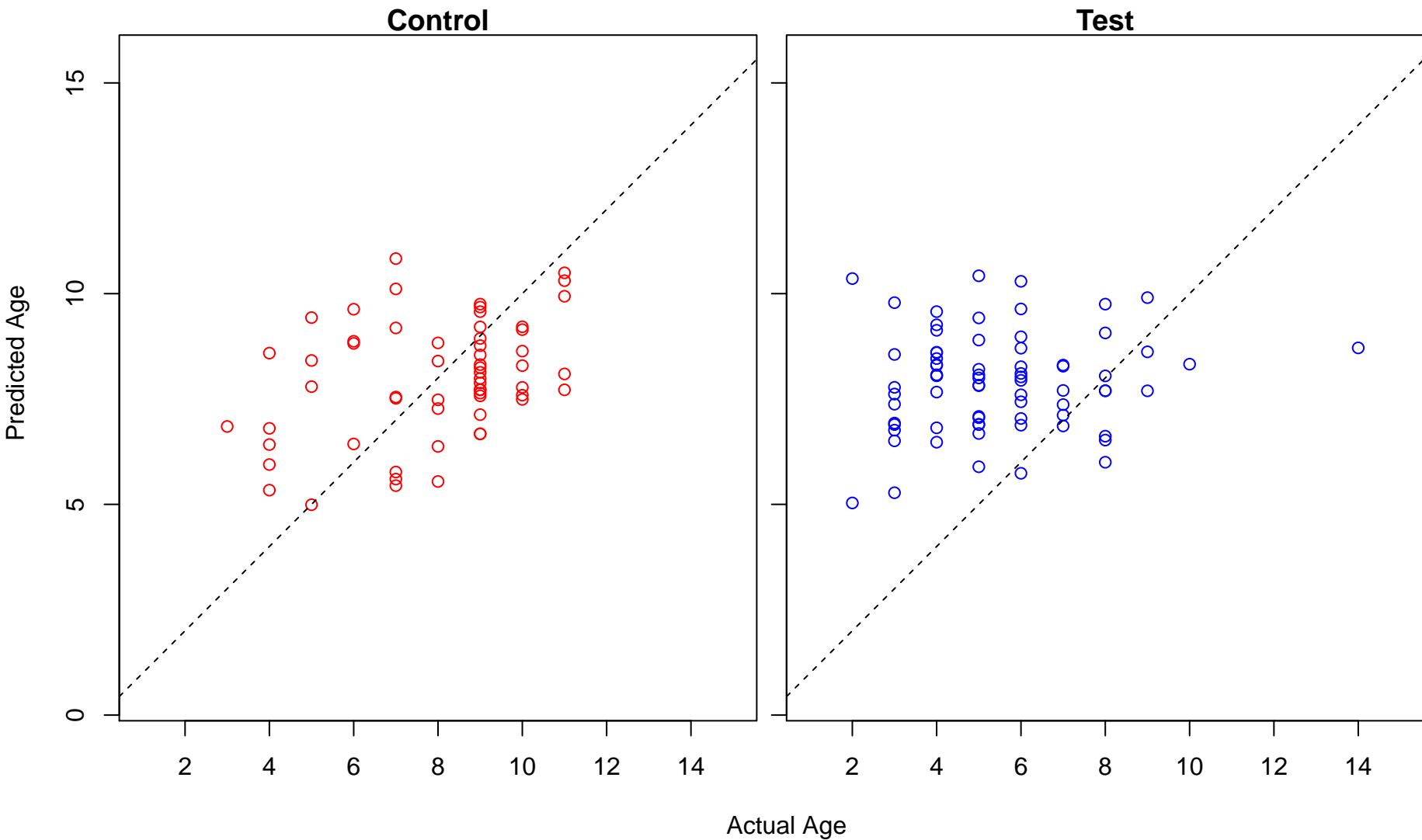
cerebral cortex GABAergic interneuron differentiation (Score: 0.755592)



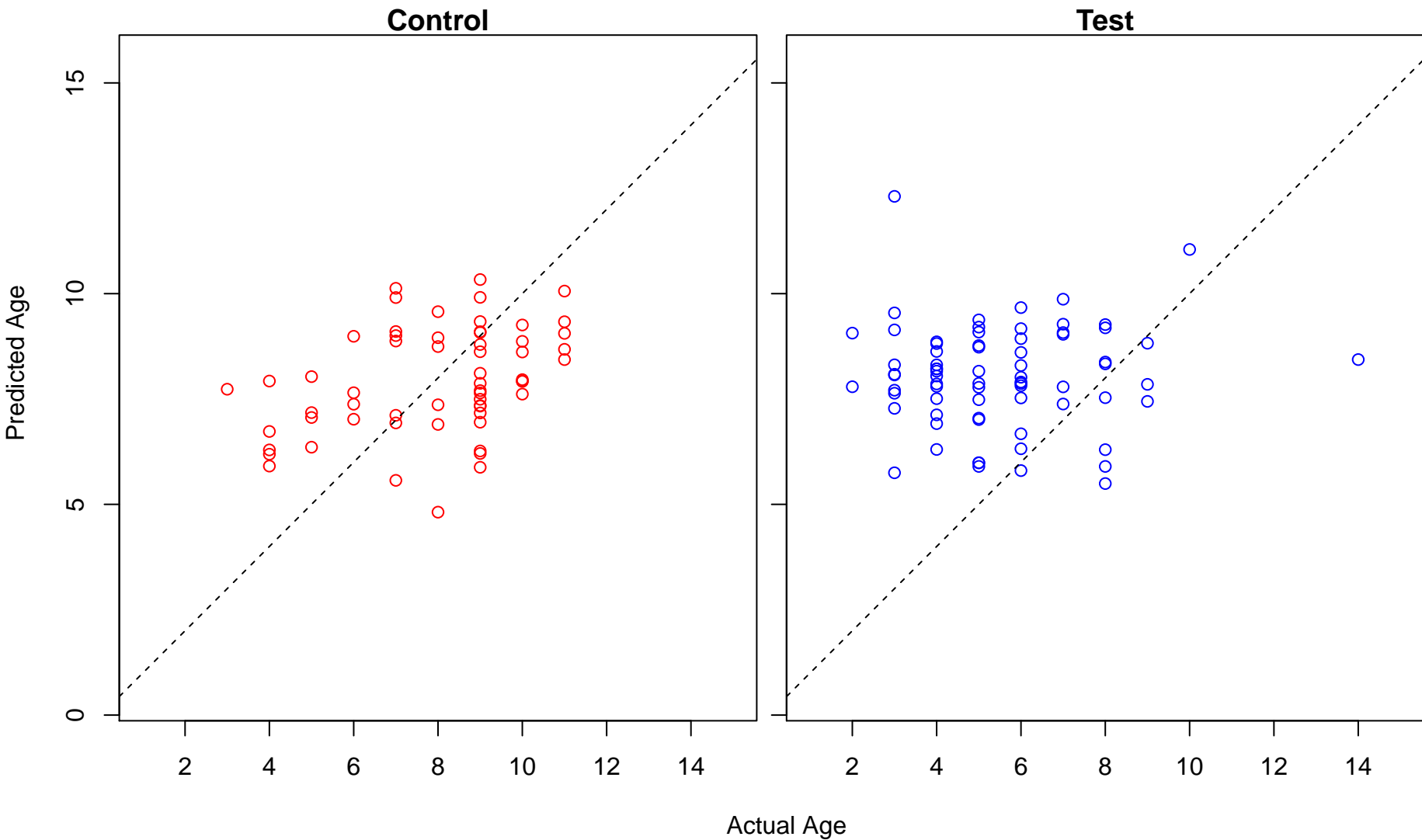
positive regulation of regulatory T cell differentiation (Score: 0.755286)



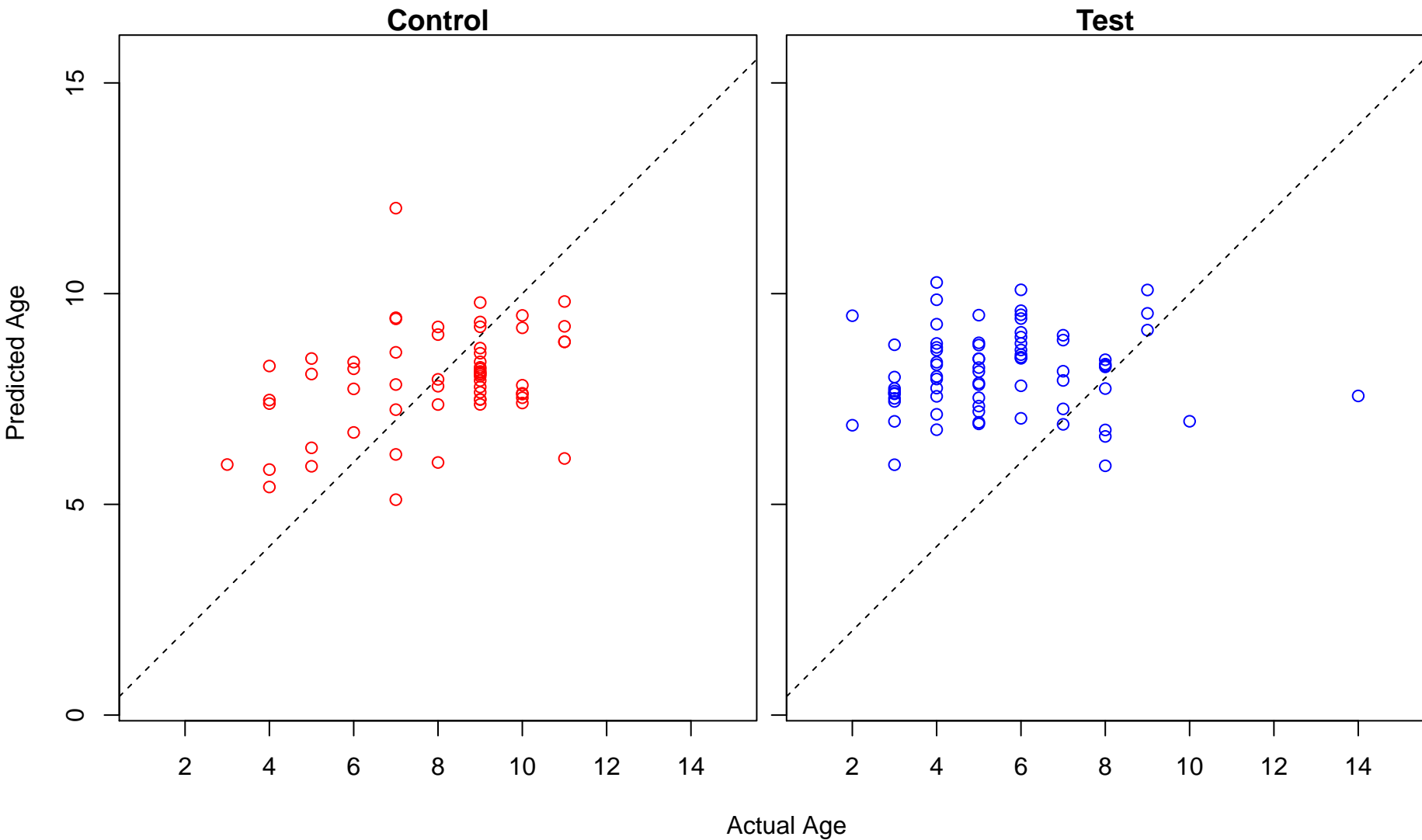
regulation of myeloid cell differentiation (Score: 0.754688)



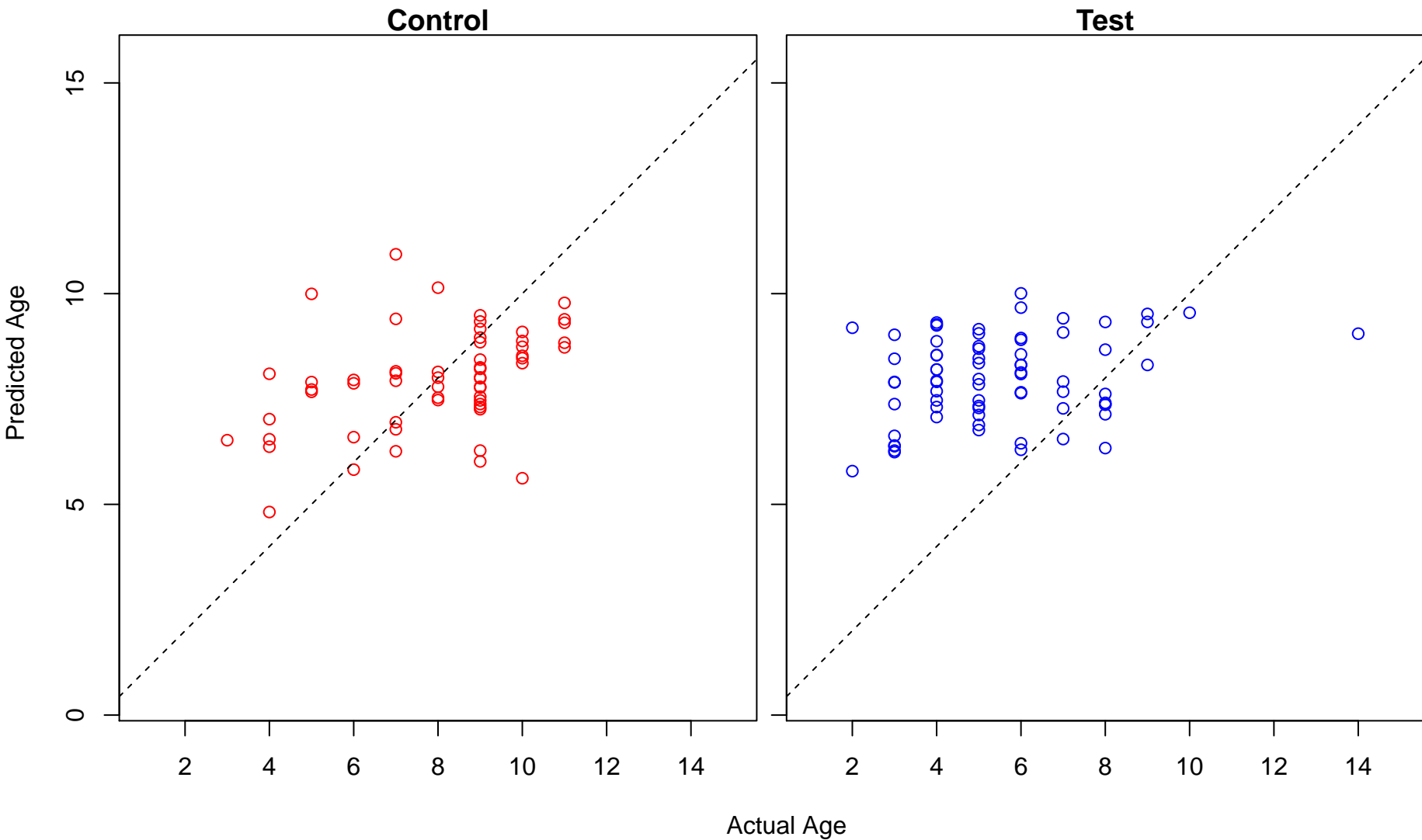
regulation of mesenchymal stem cell differentiation (Score: 0.754588)



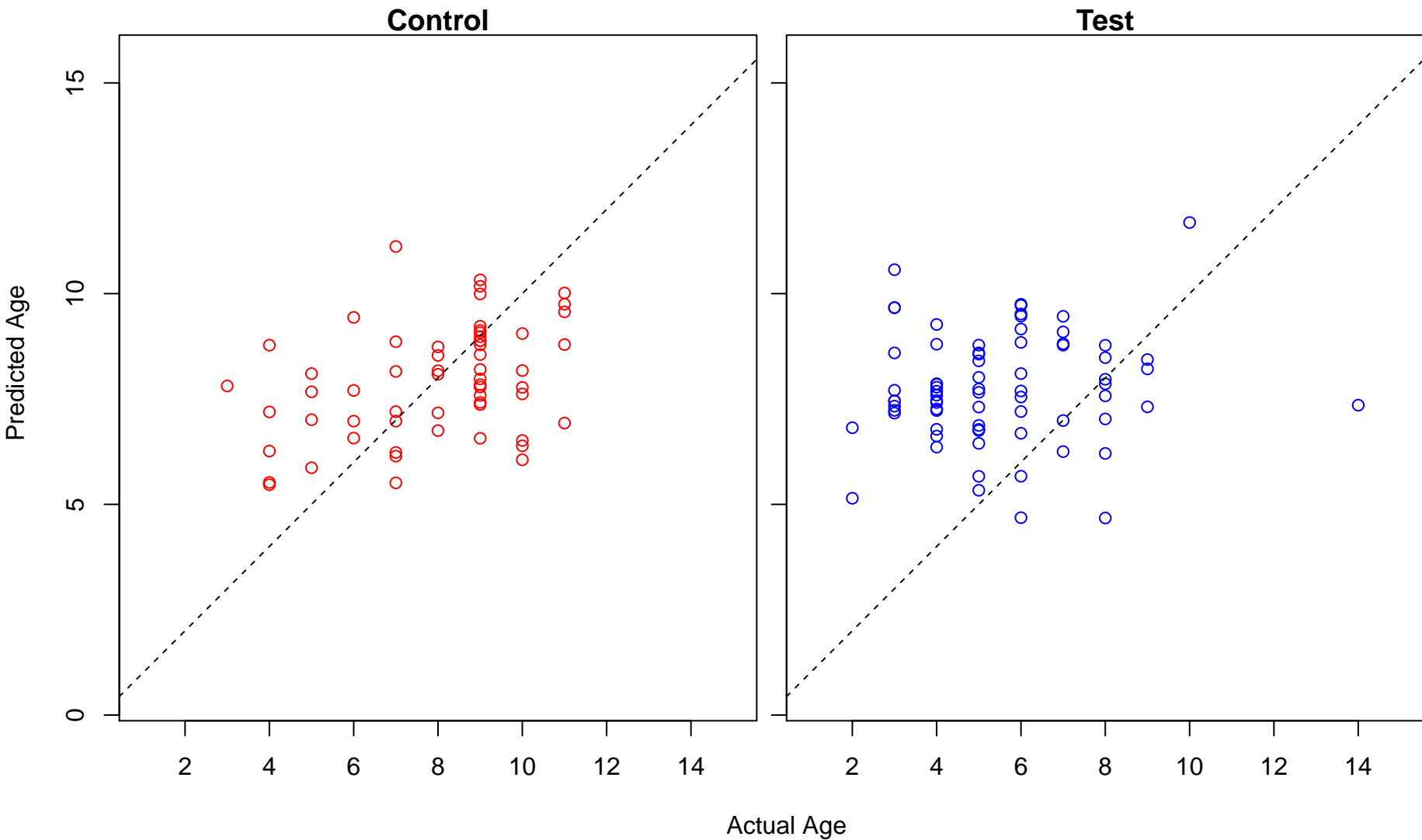
negative regulation of calcium-mediated signaling (Score: 0.754314)



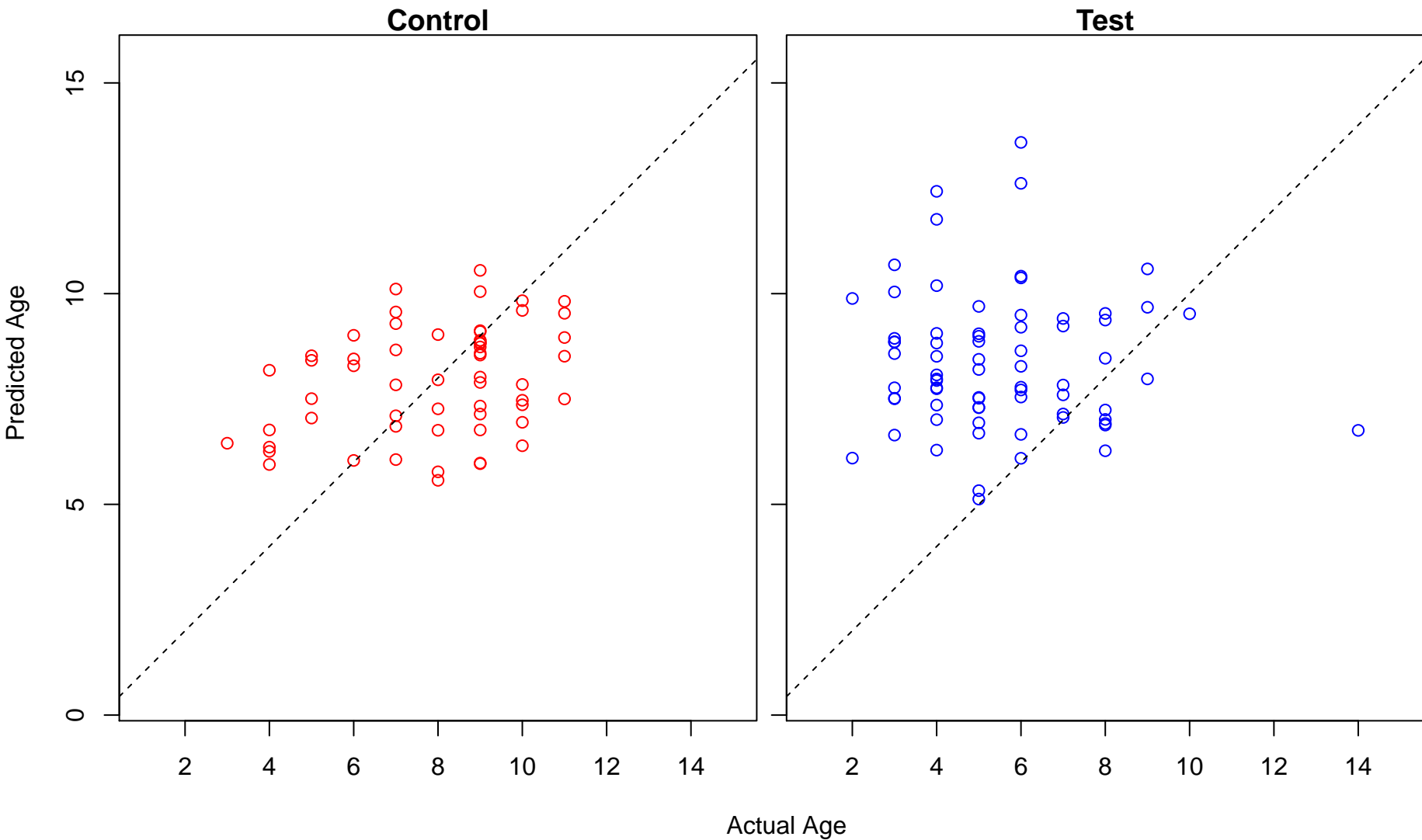
detection of virus (Score: 0.754083)



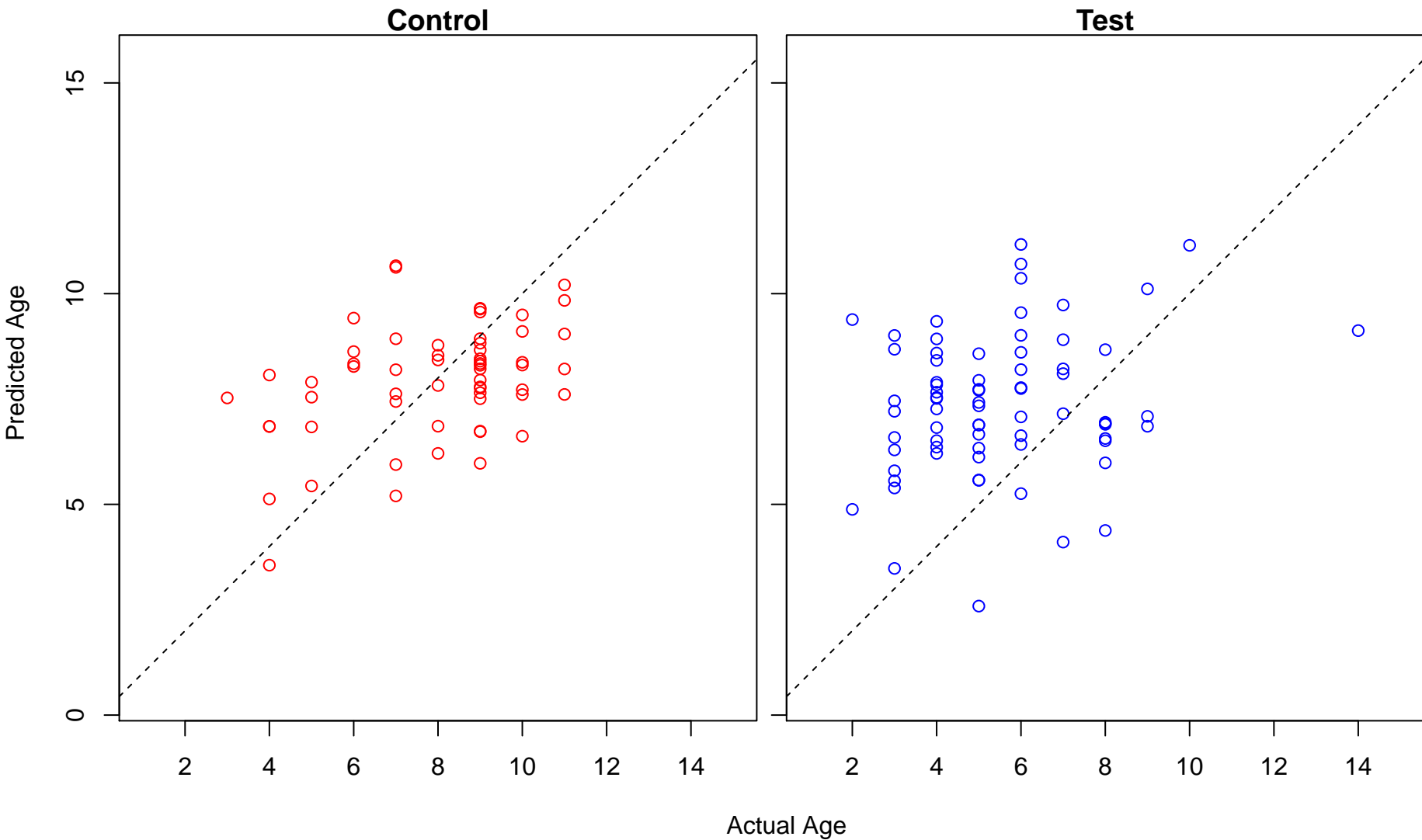
type B pancreatic cell differentiation (Score: 0.754081)



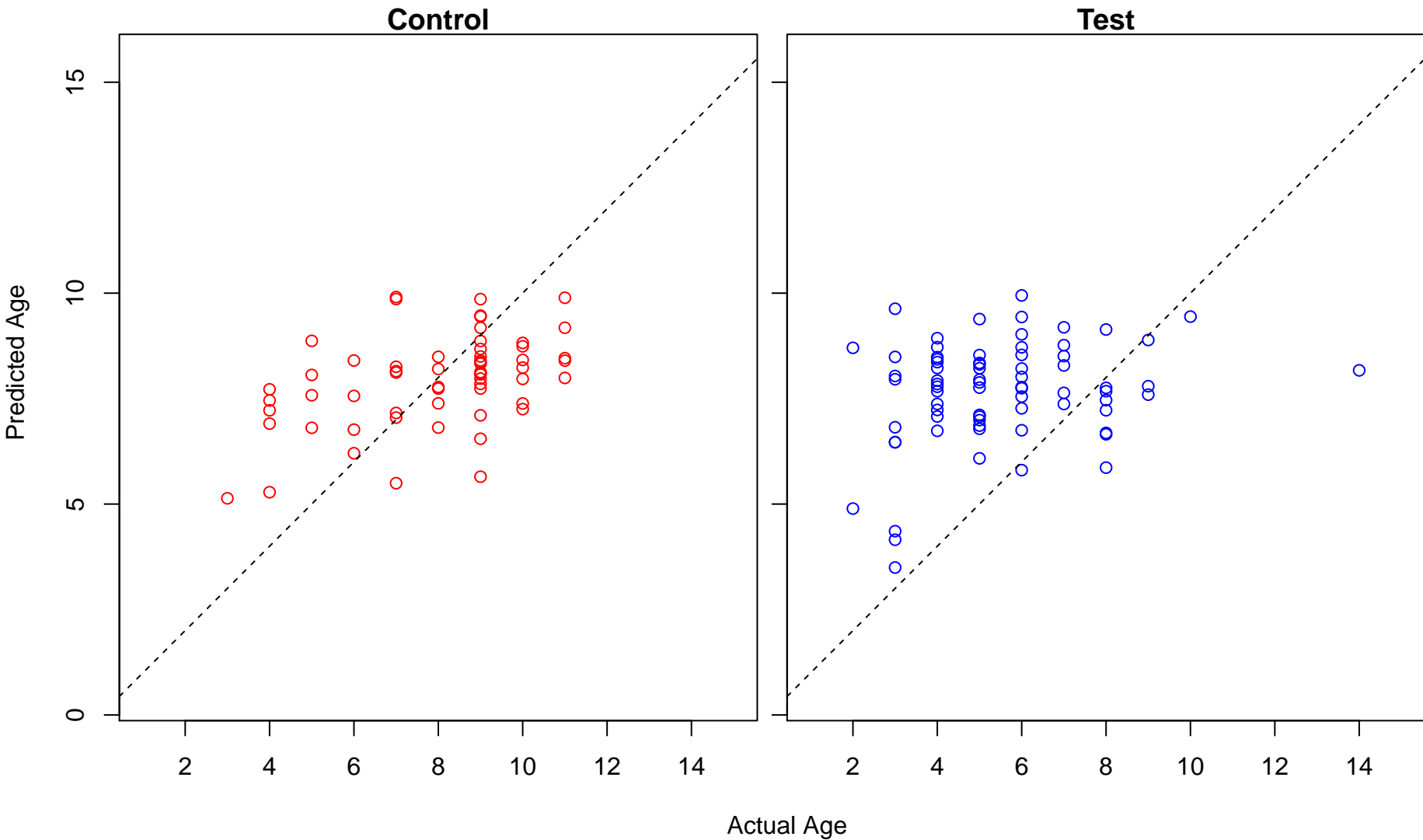
diterpenoid metabolic process (Score: 0.753864)



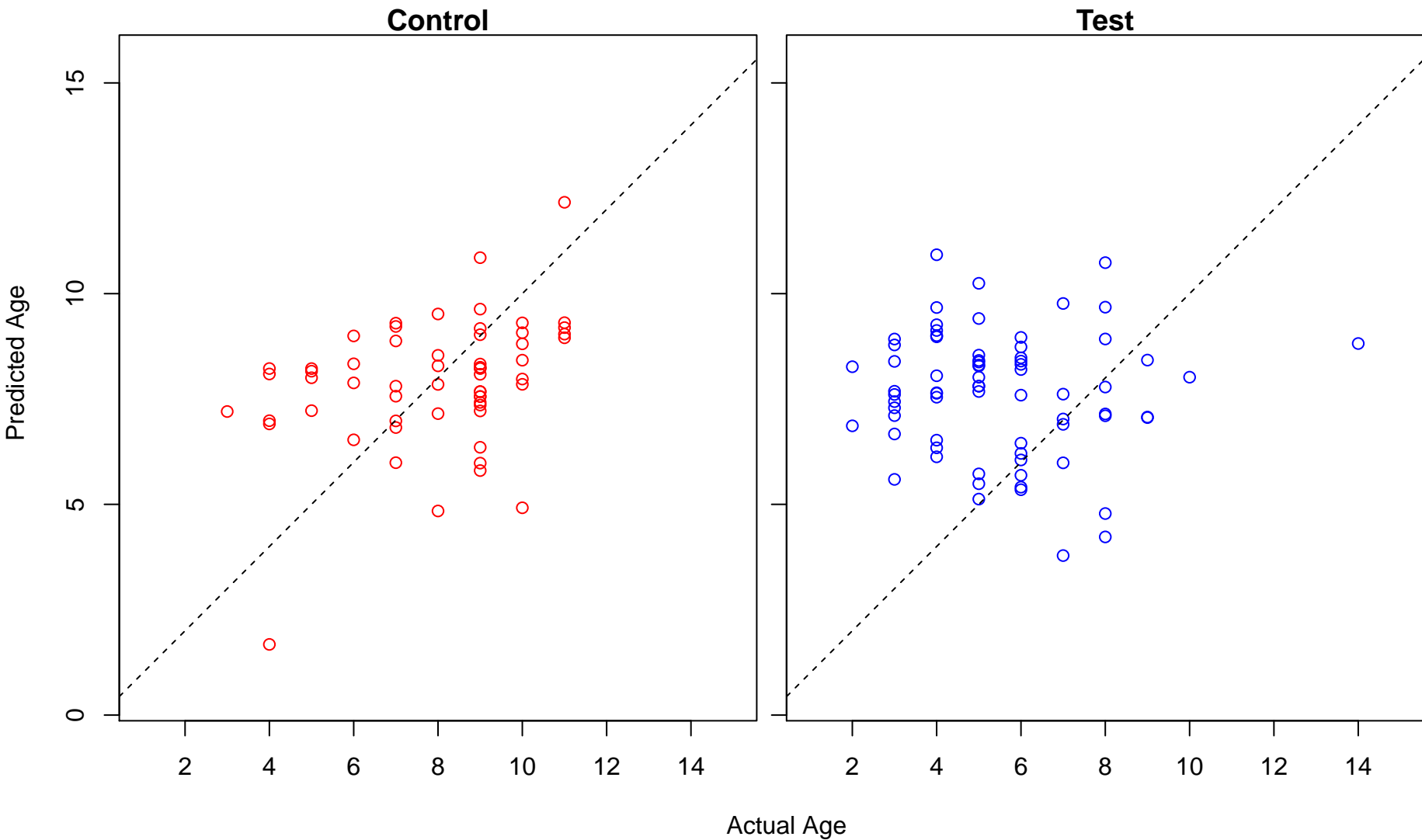
regulation of neutrophil chemotaxis (Score: 0.753651)



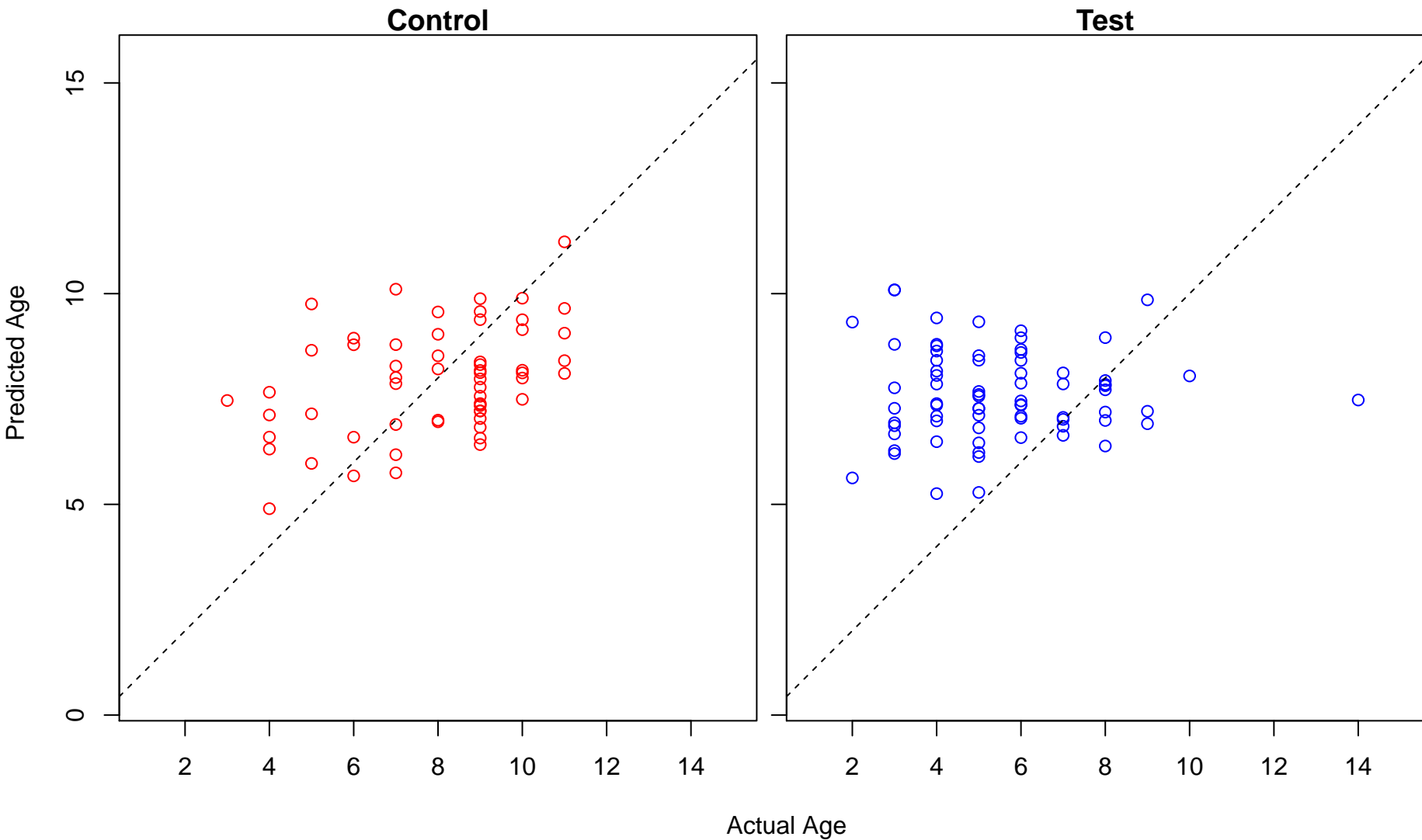
positive regulation of branching involved in ureteric bud morphogenesis (Score: 0.753406)



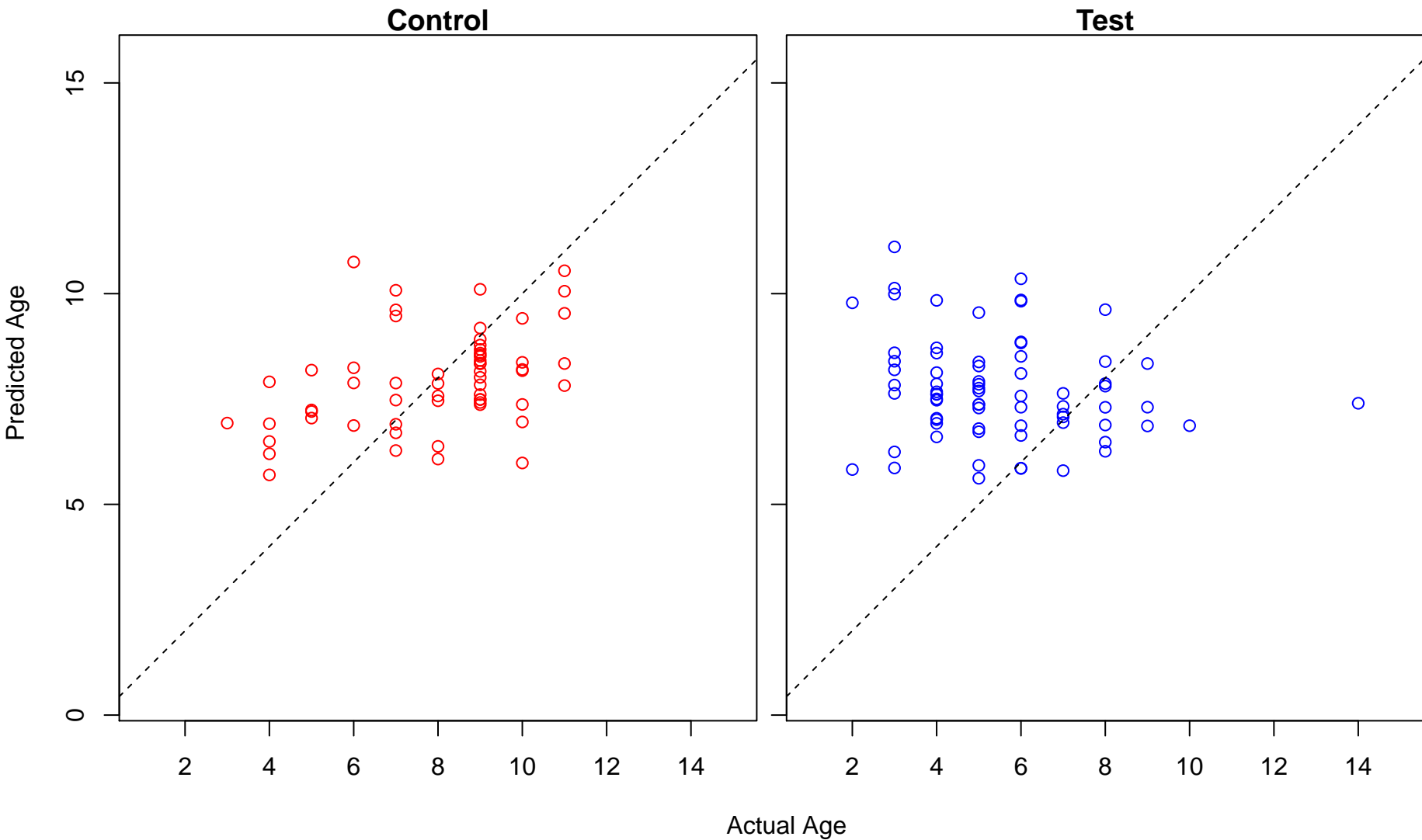
cellular response to copper ion (Score: 0.752397)



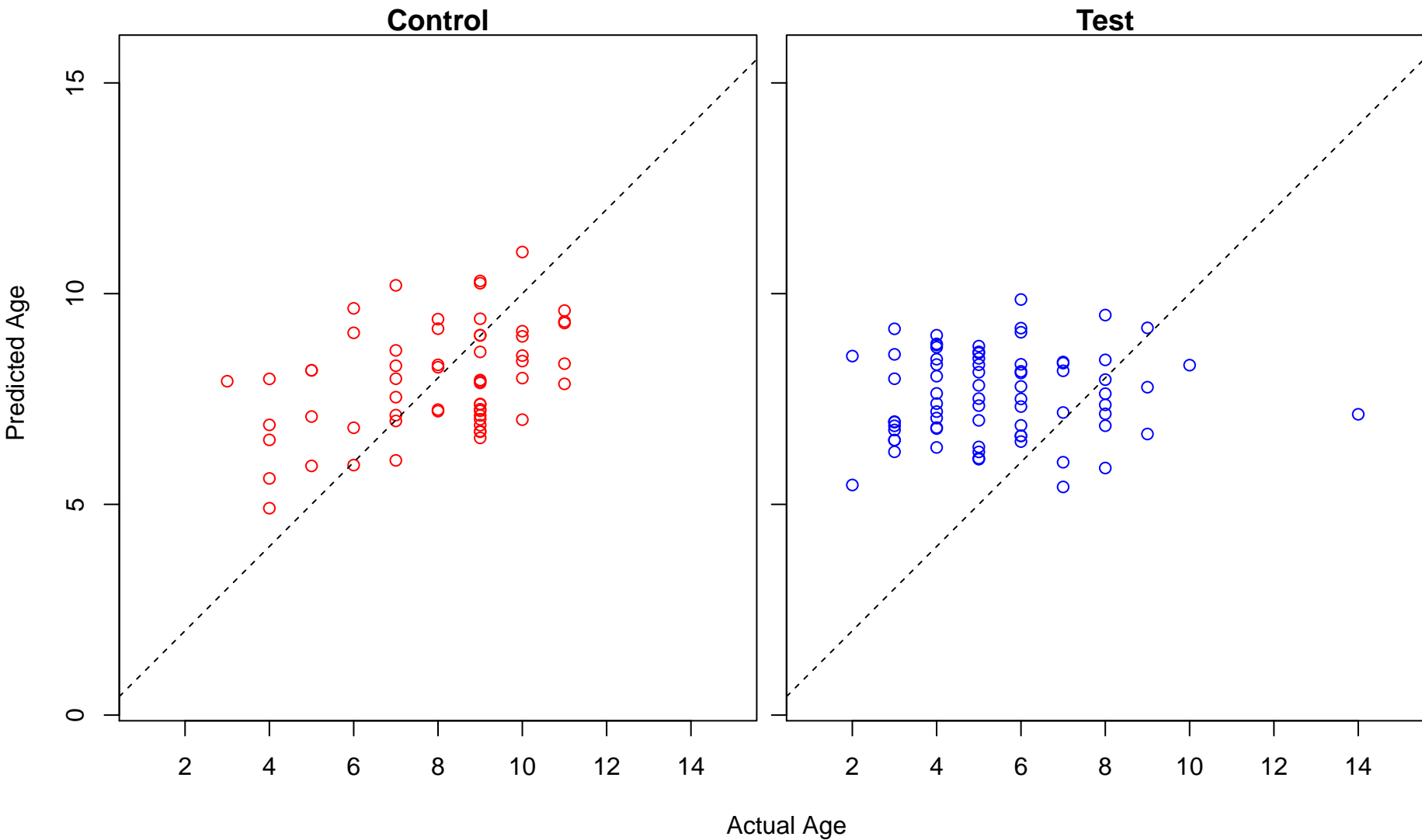
T cell proliferation involved in immune response (Score: 0.751411)



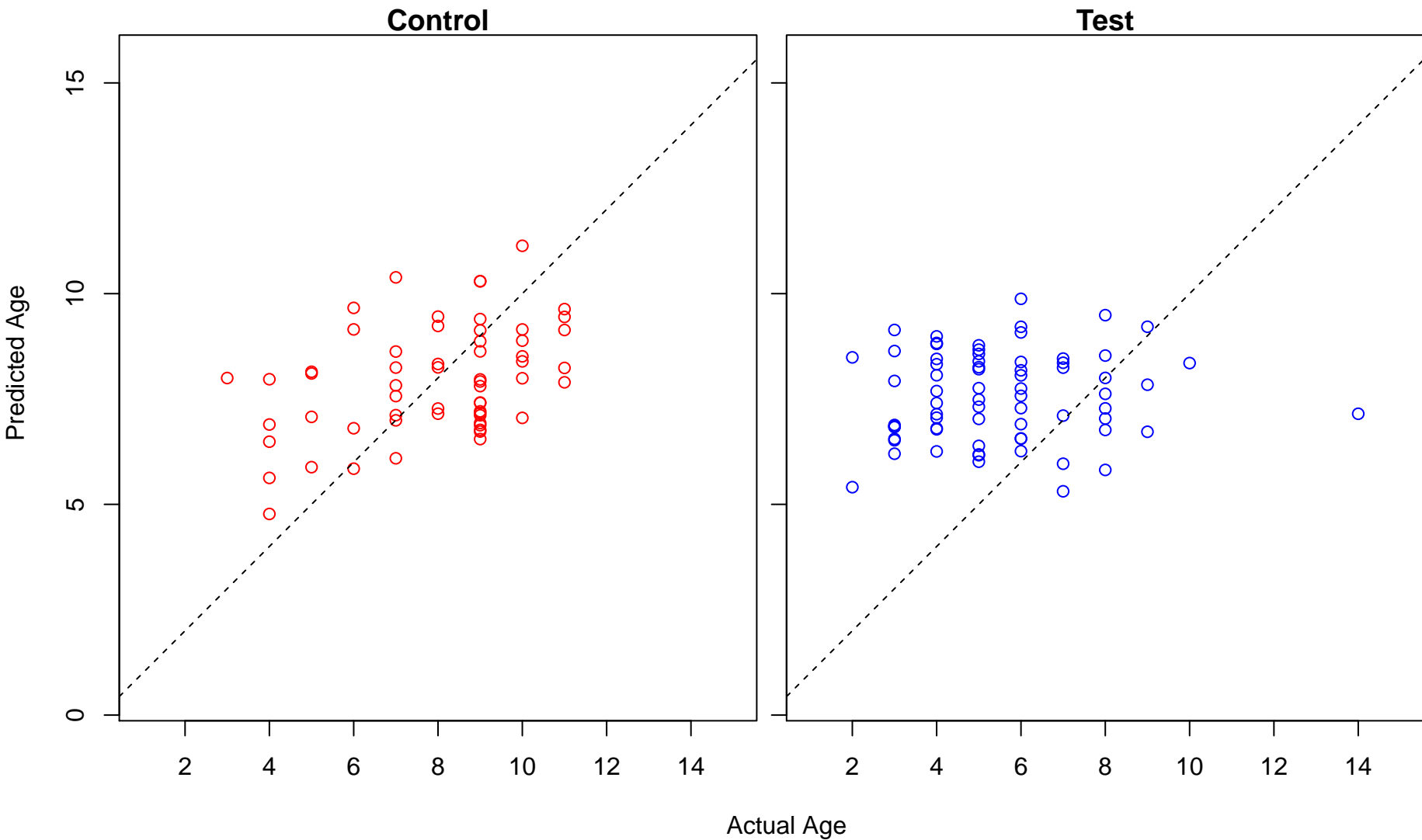
positive regulation of protein import into nucleus (Score: 0.751268)



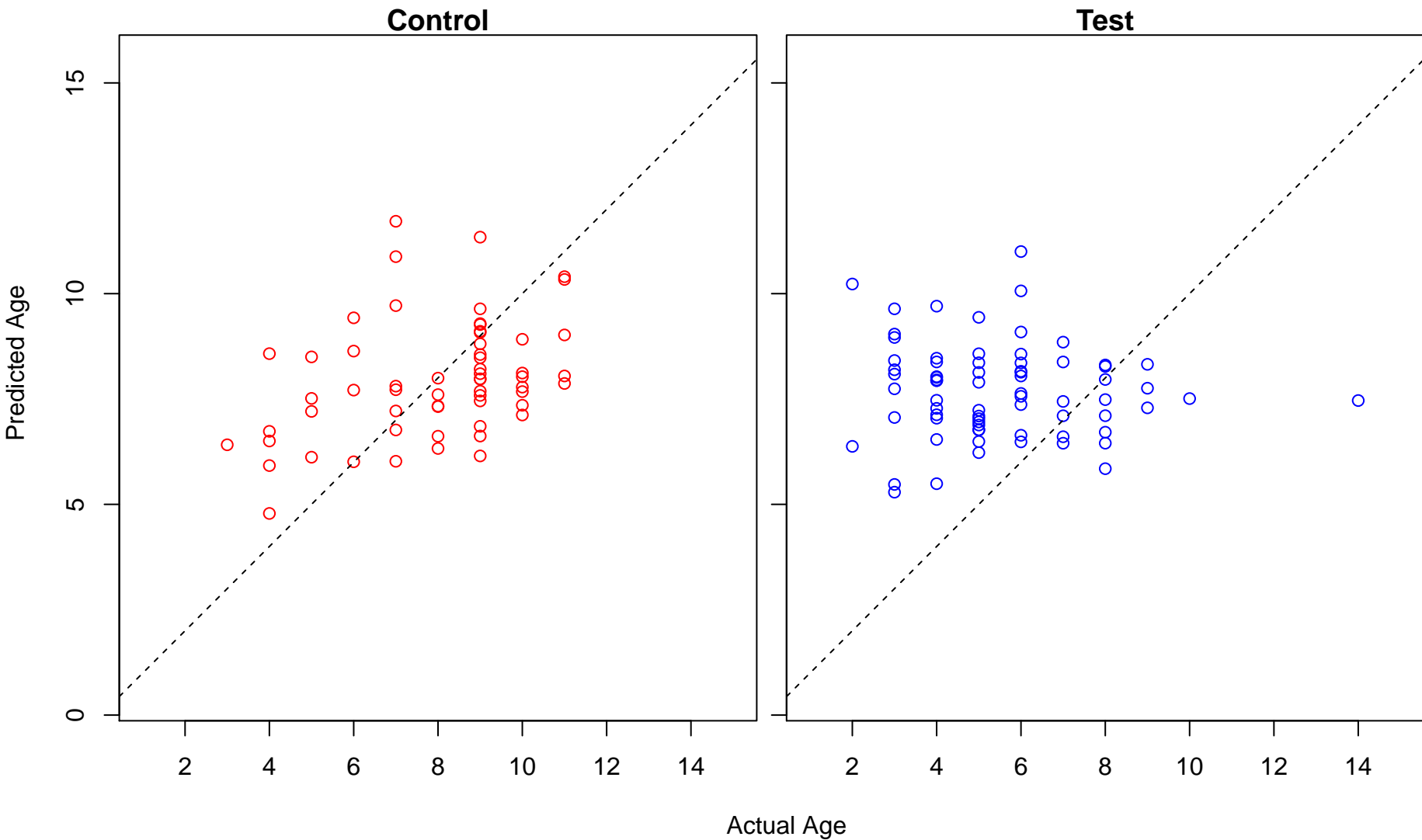
arginine transport (Score: 0.750441)



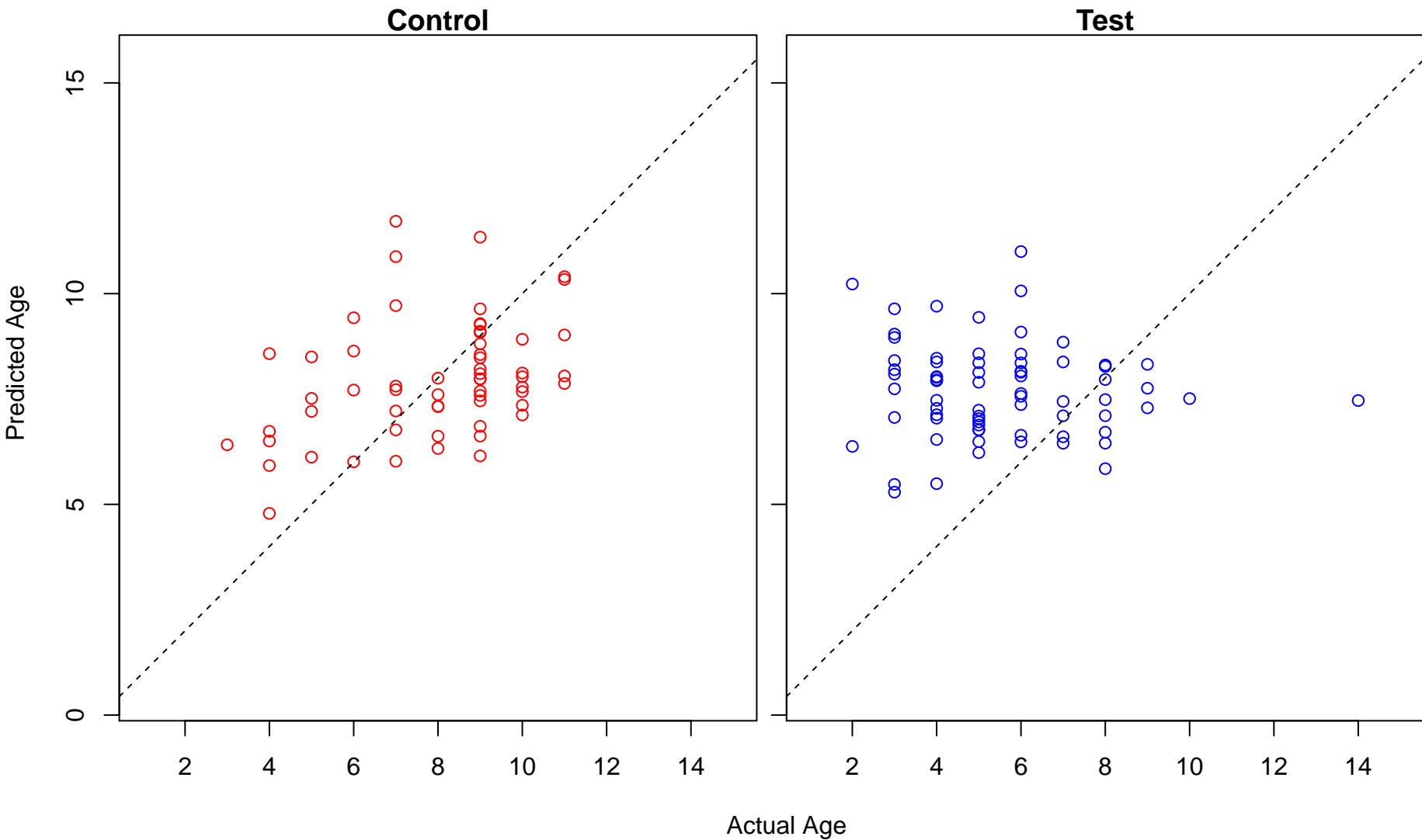
basic amino acid transport (Score: 0.749781)



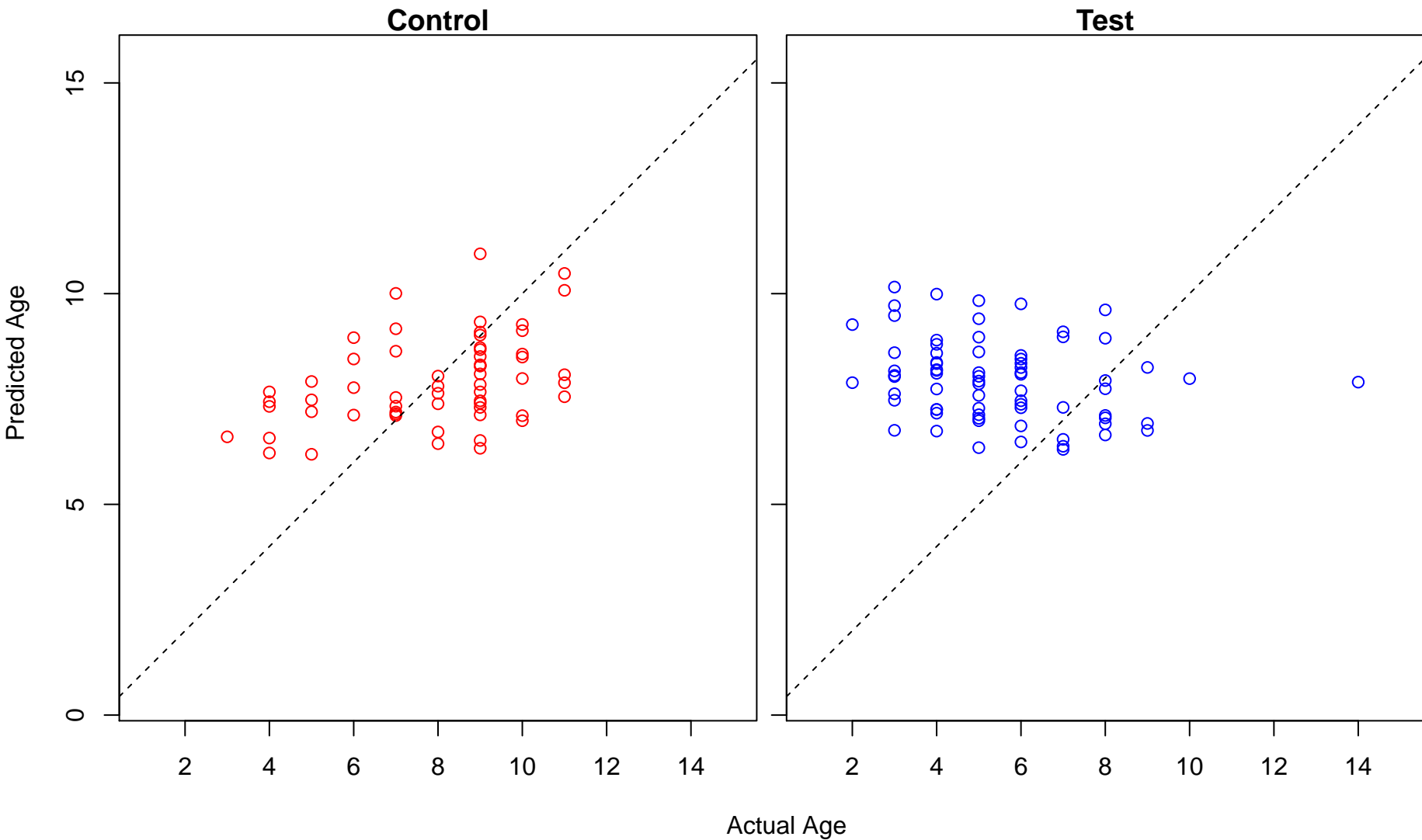
ribonucleoside triphosphate metabolic process (Score: 0.749413)



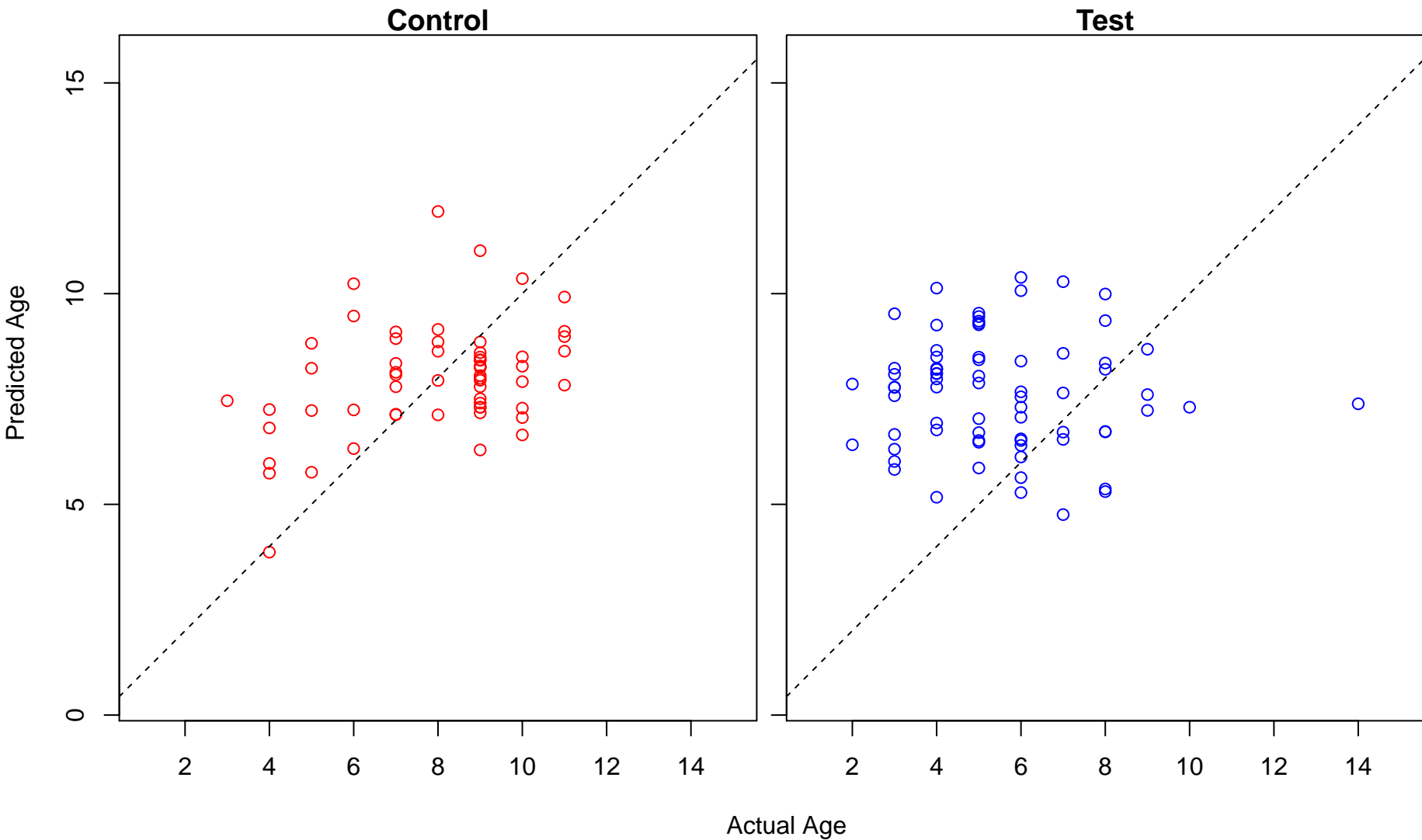
purine ribonucleoside triphosphate metabolic process (Score: 0.749261)



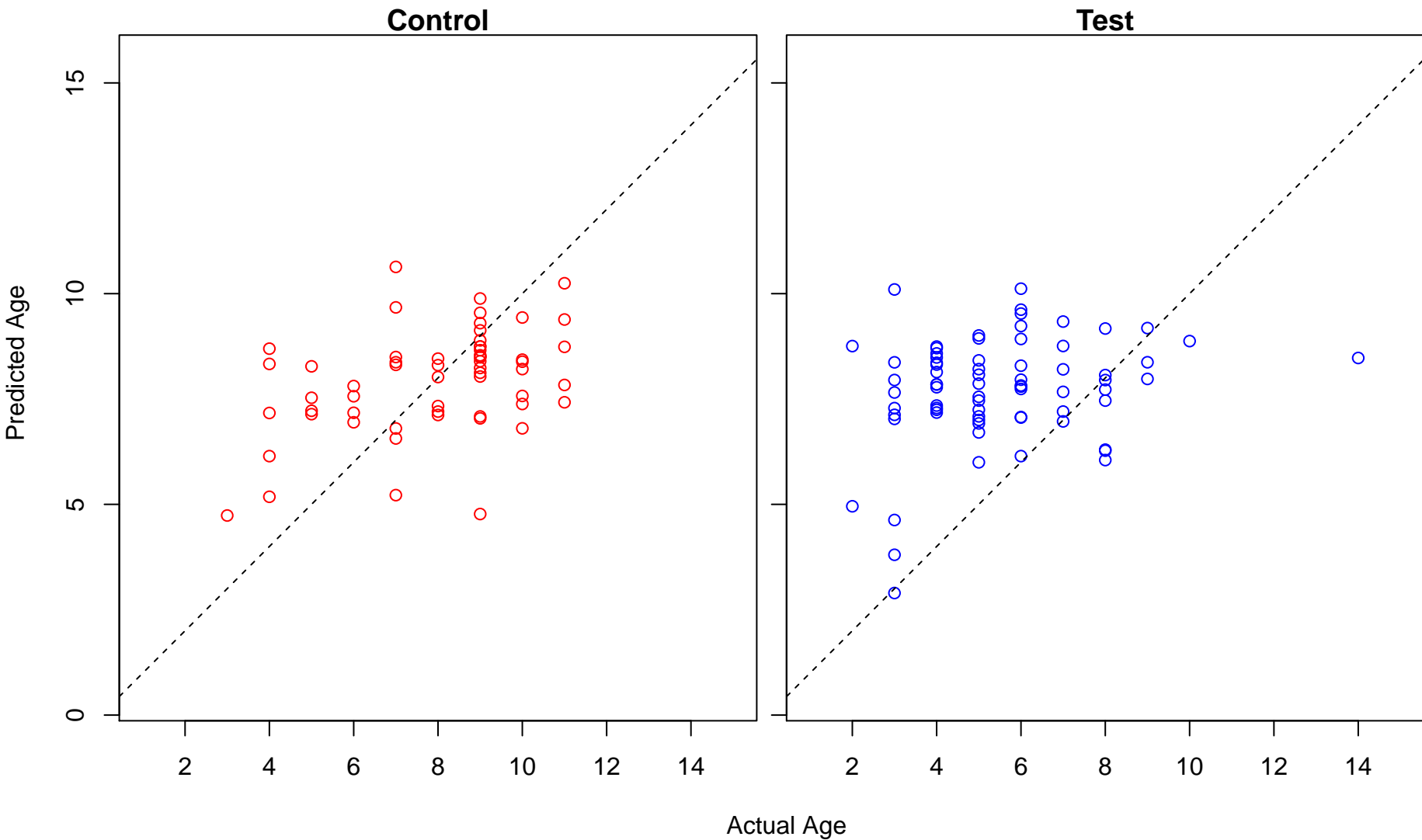
aldehyde catabolic process (Score: 0.748288)



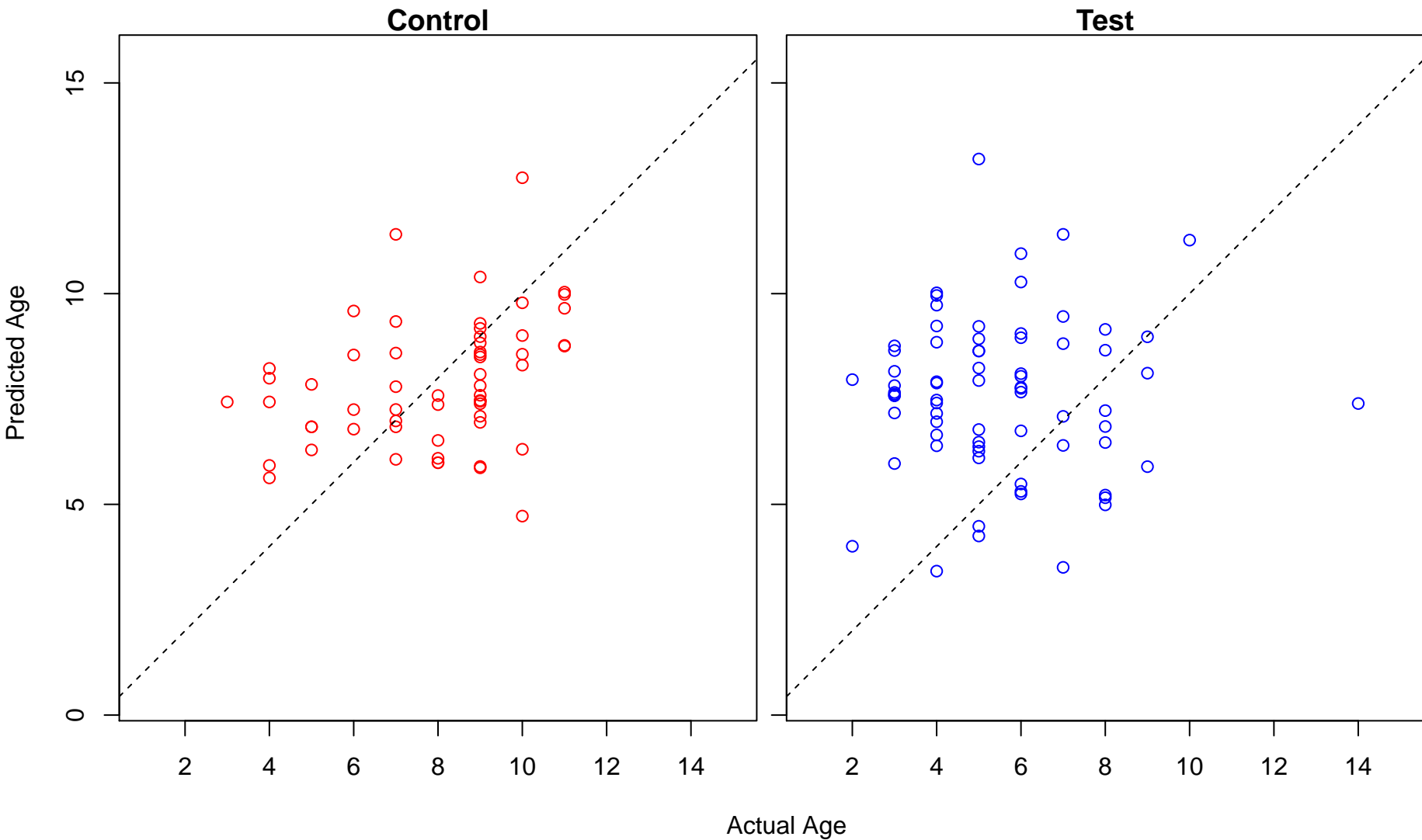
regulation of neurotransmitter uptake (Score: 0.747317)



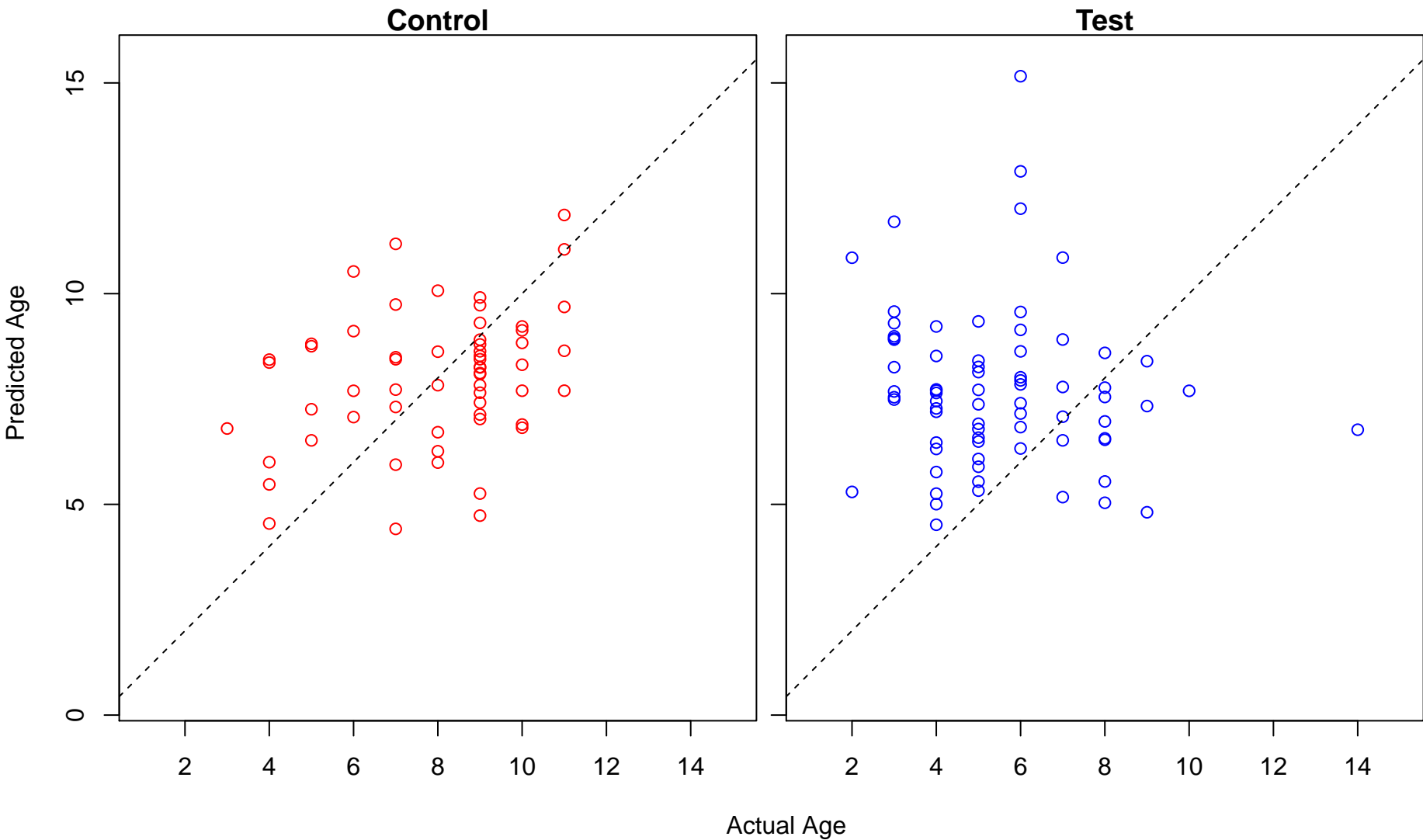
neural plate morphogenesis (Score: 0.745221)



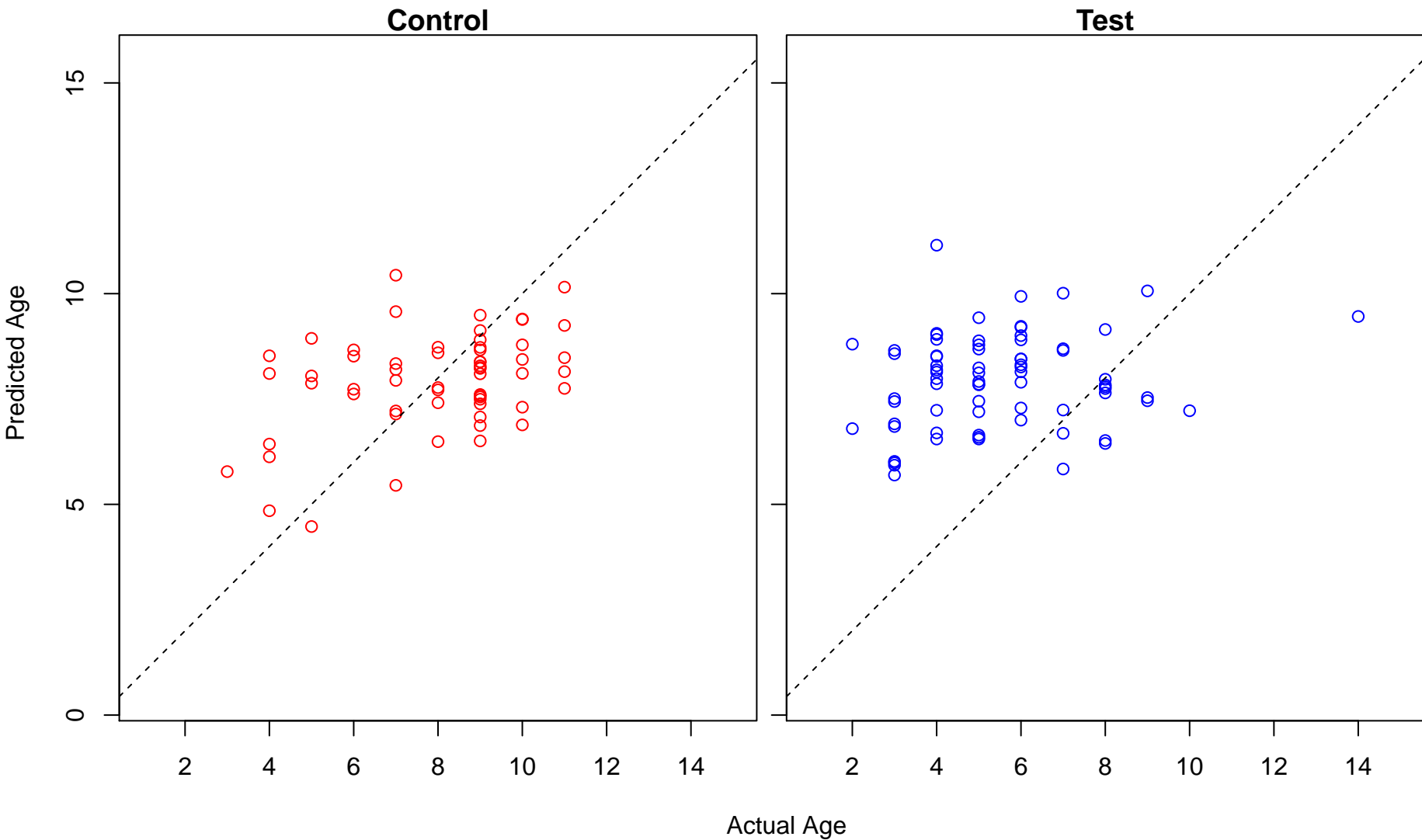
cartilage morphogenesis (Score: 0.745129)



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

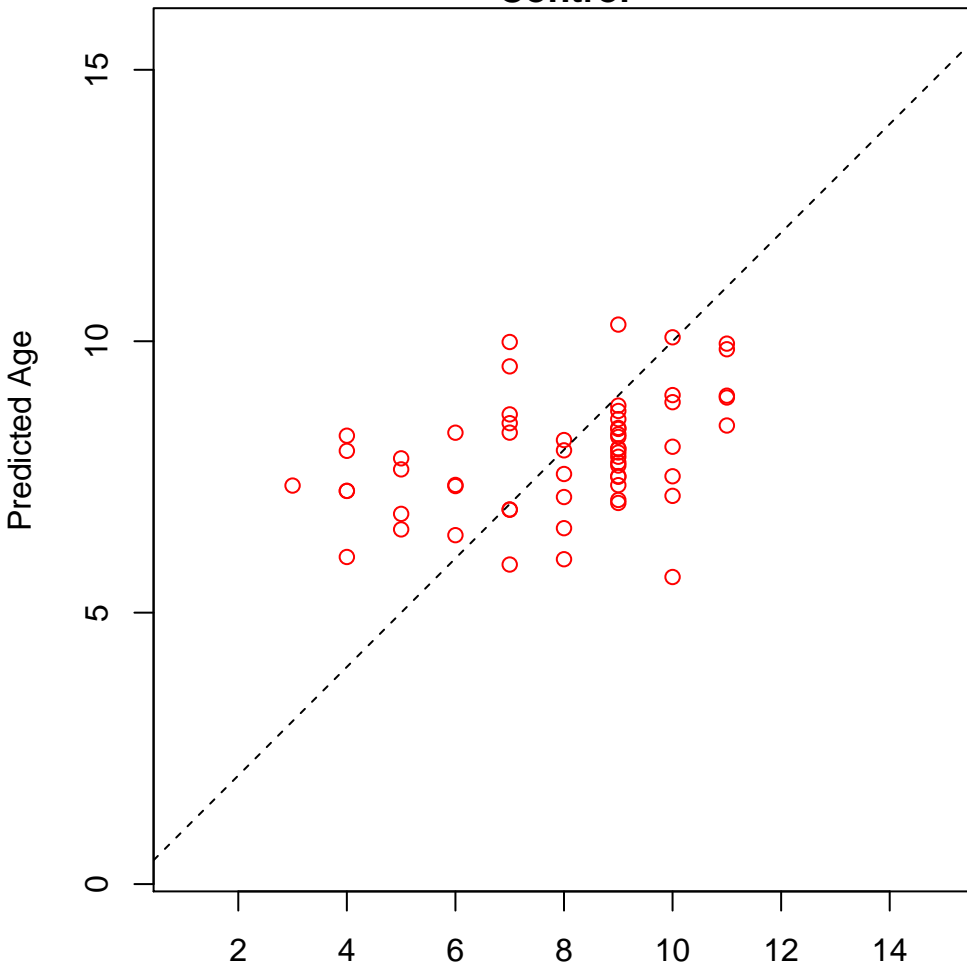


sprouting angiogenesis (Score: 0.742276)

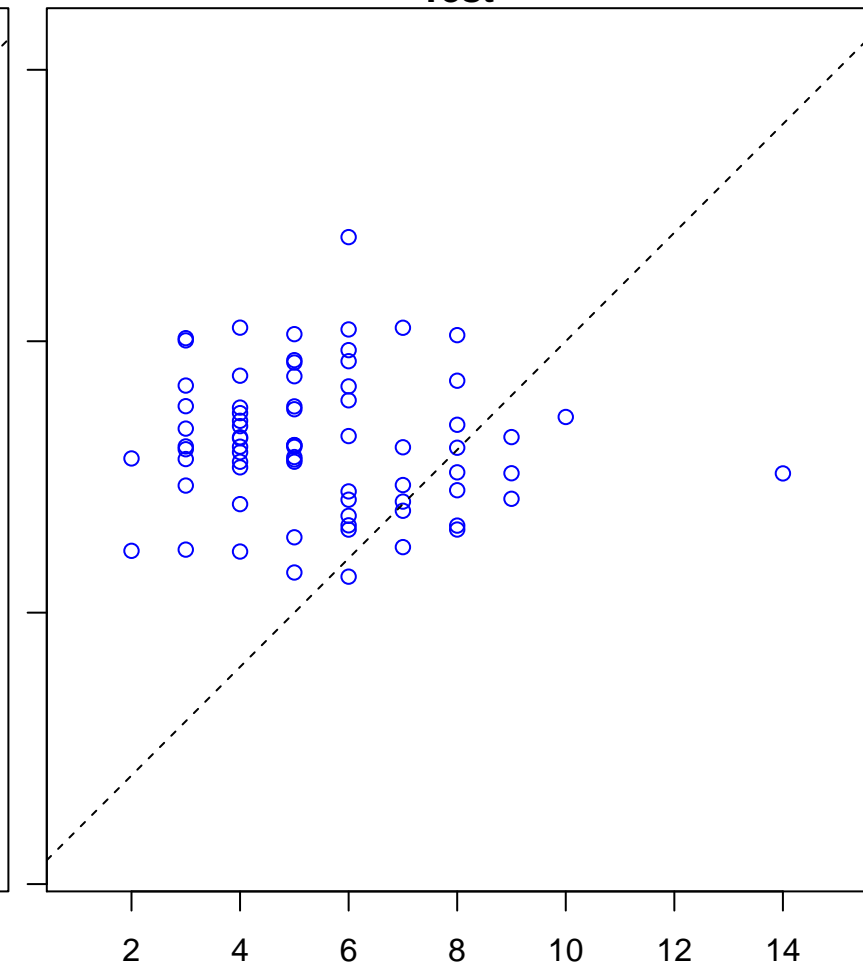


protein insertion into ER membrane (Score: 0.741669)

Control

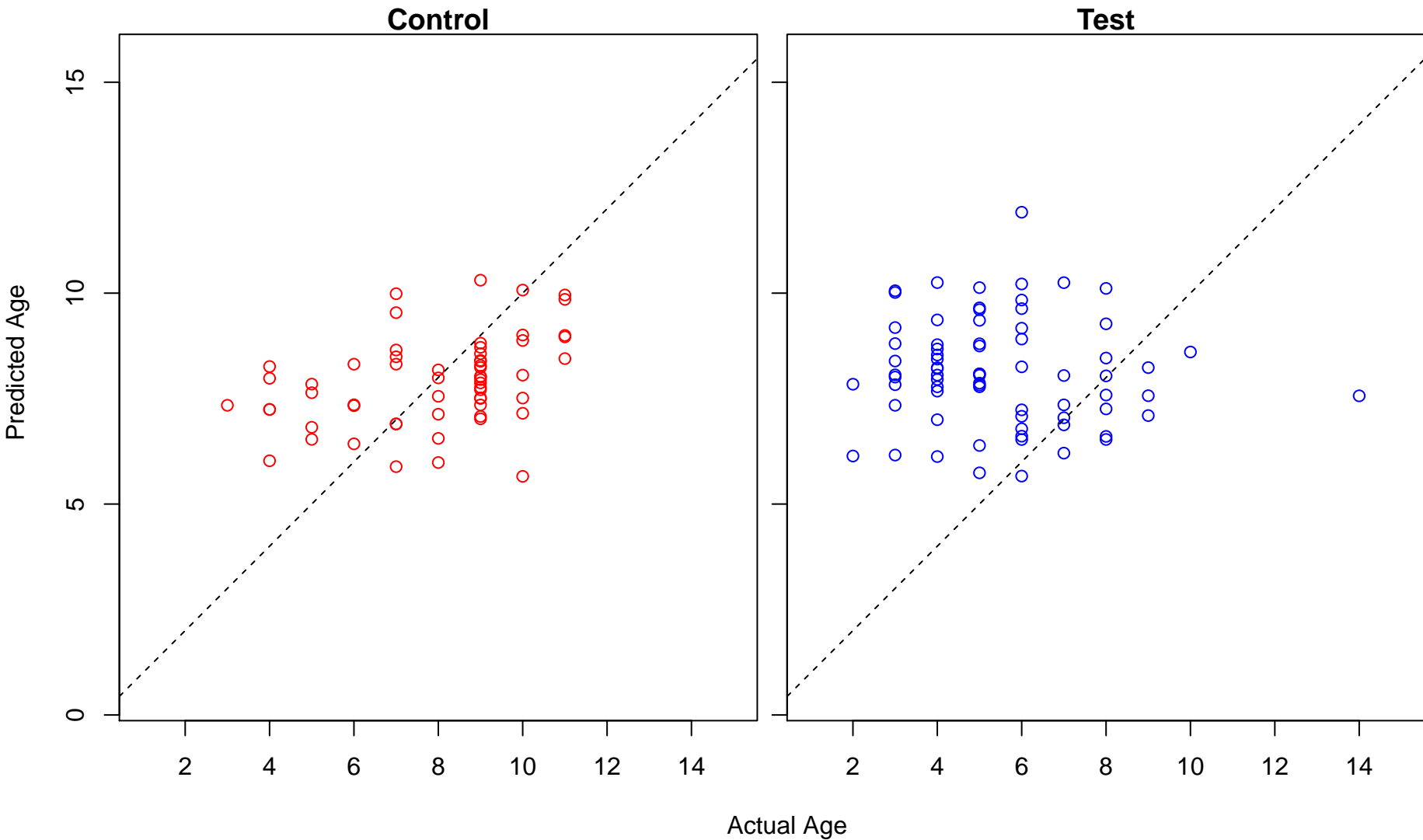


Test

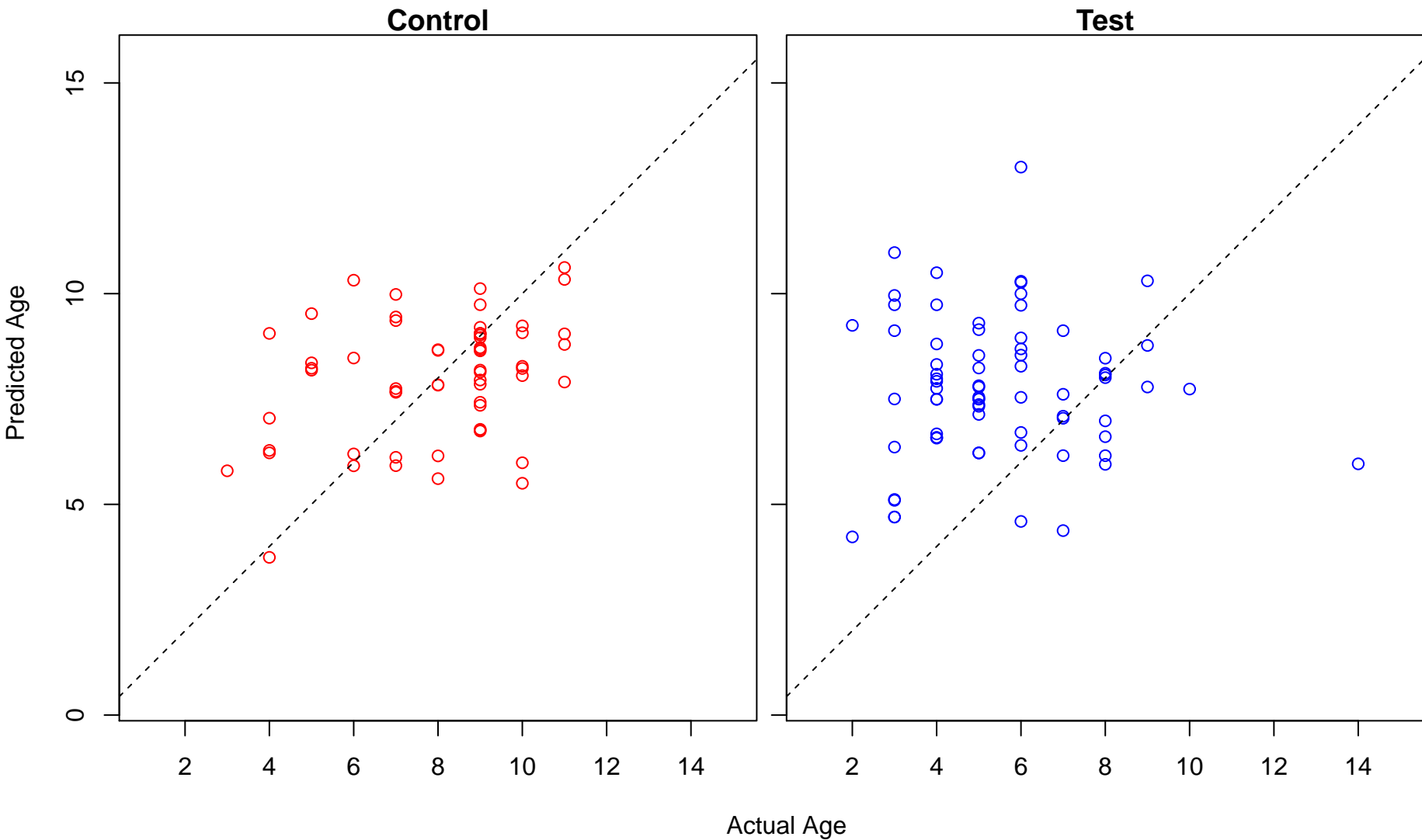


Actual Age

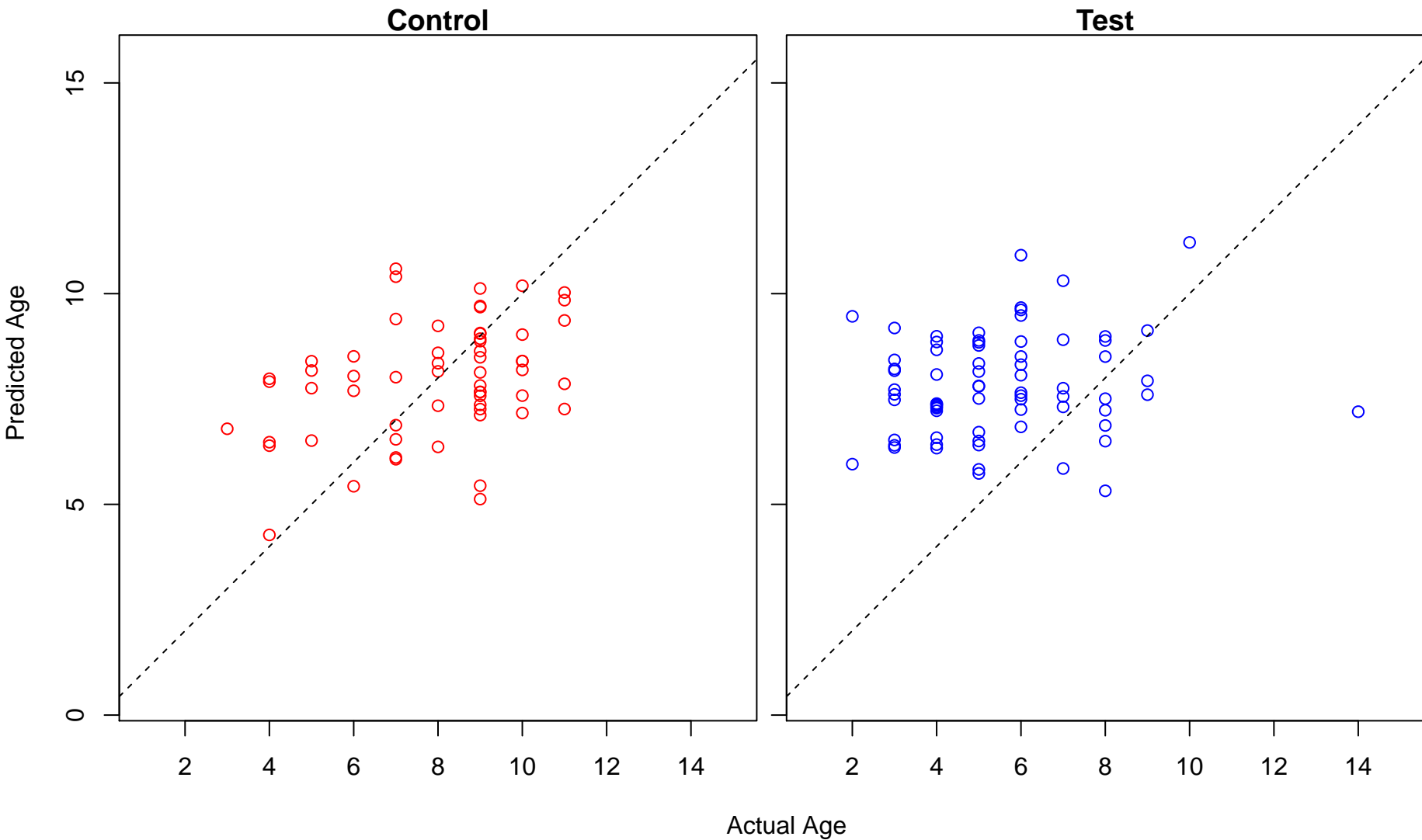
tail-anchored membrane protein insertion into ER membrane (Score: 0.741669)



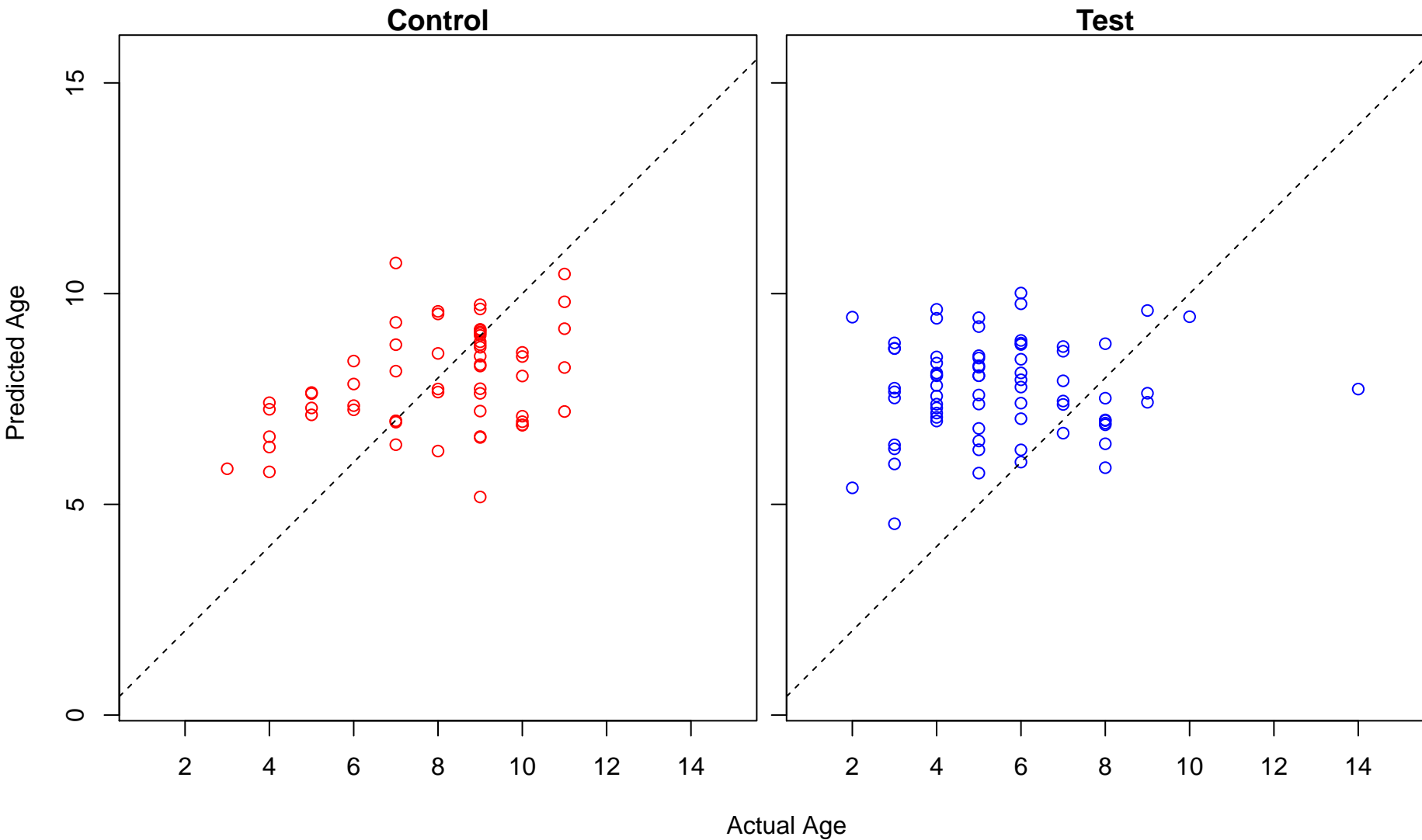
nucleotide catabolic process (Score: 0.740430)



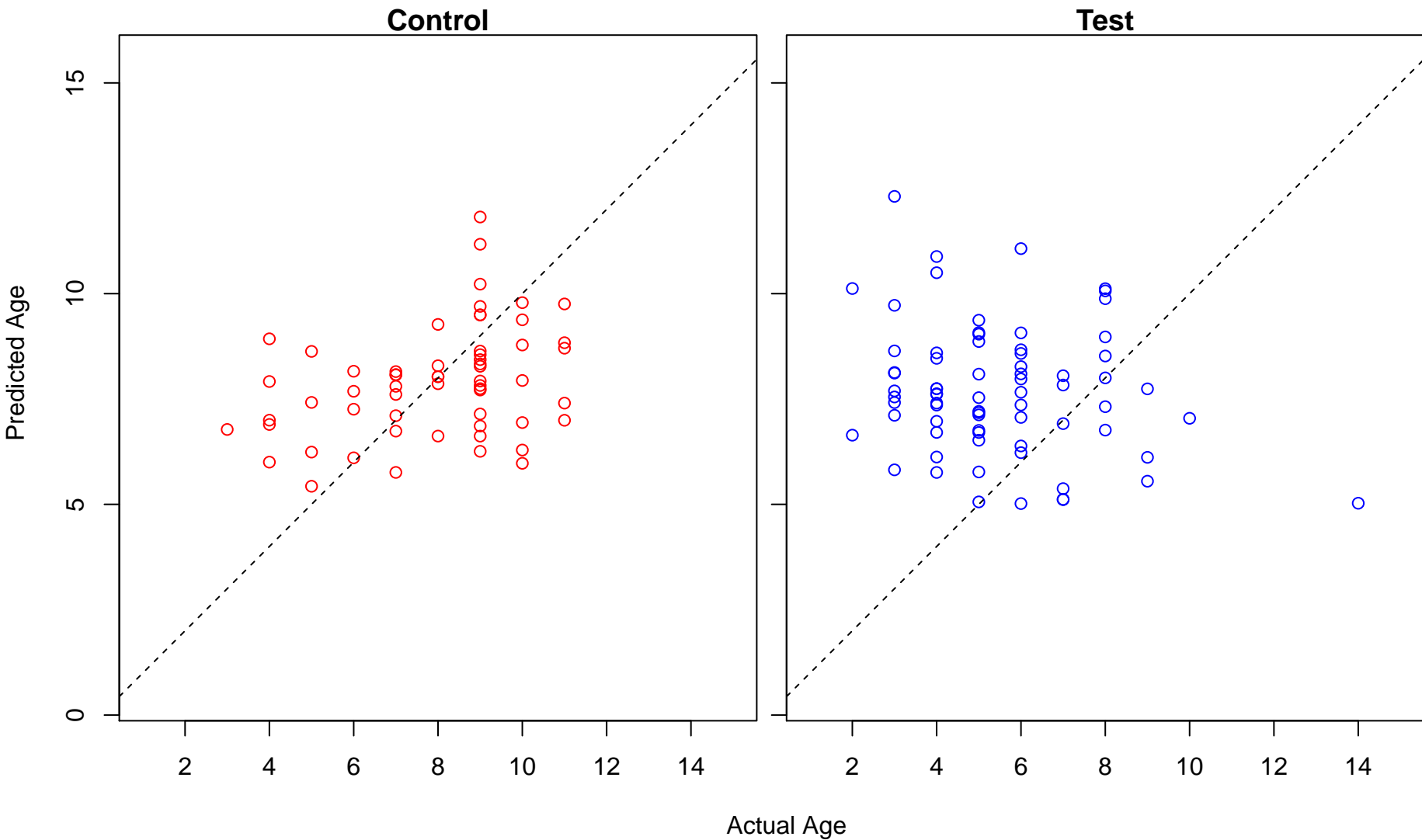
membrane invagination (Score: 0.739828)



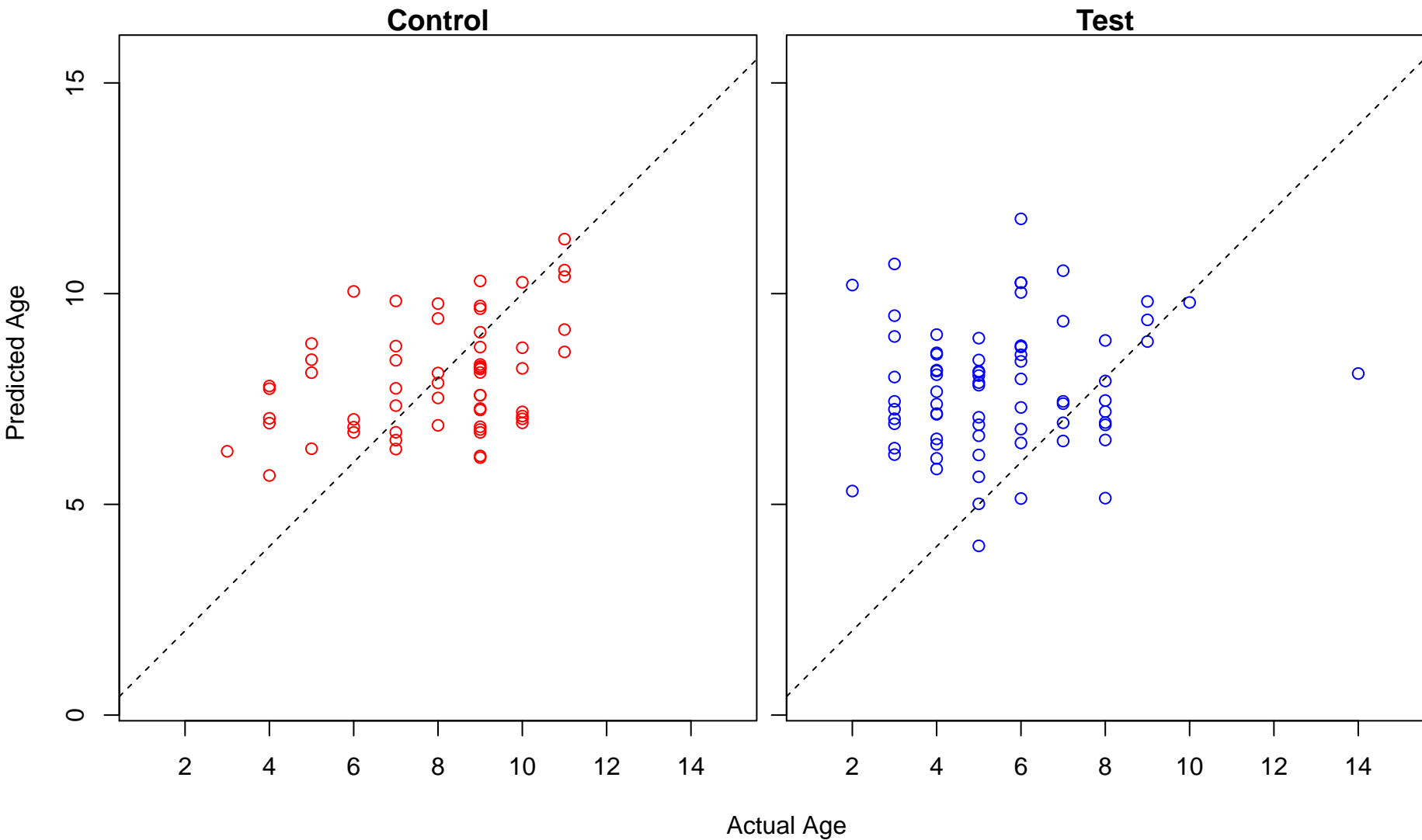
negative regulation of NFAT protein import into nucleus (Score: 0.739301)



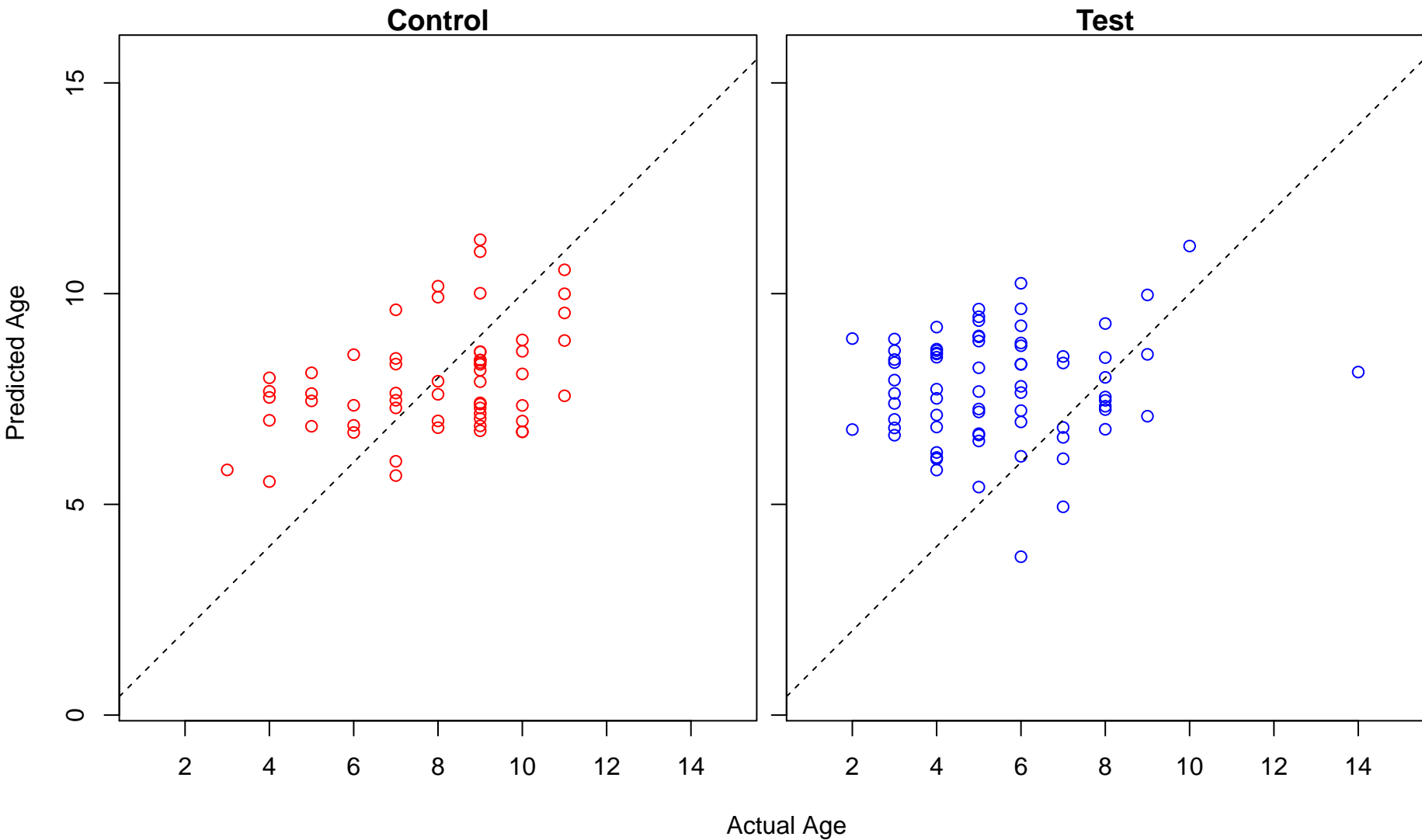
negative regulation of mitochondrial depolarization (Score: 0.739264)



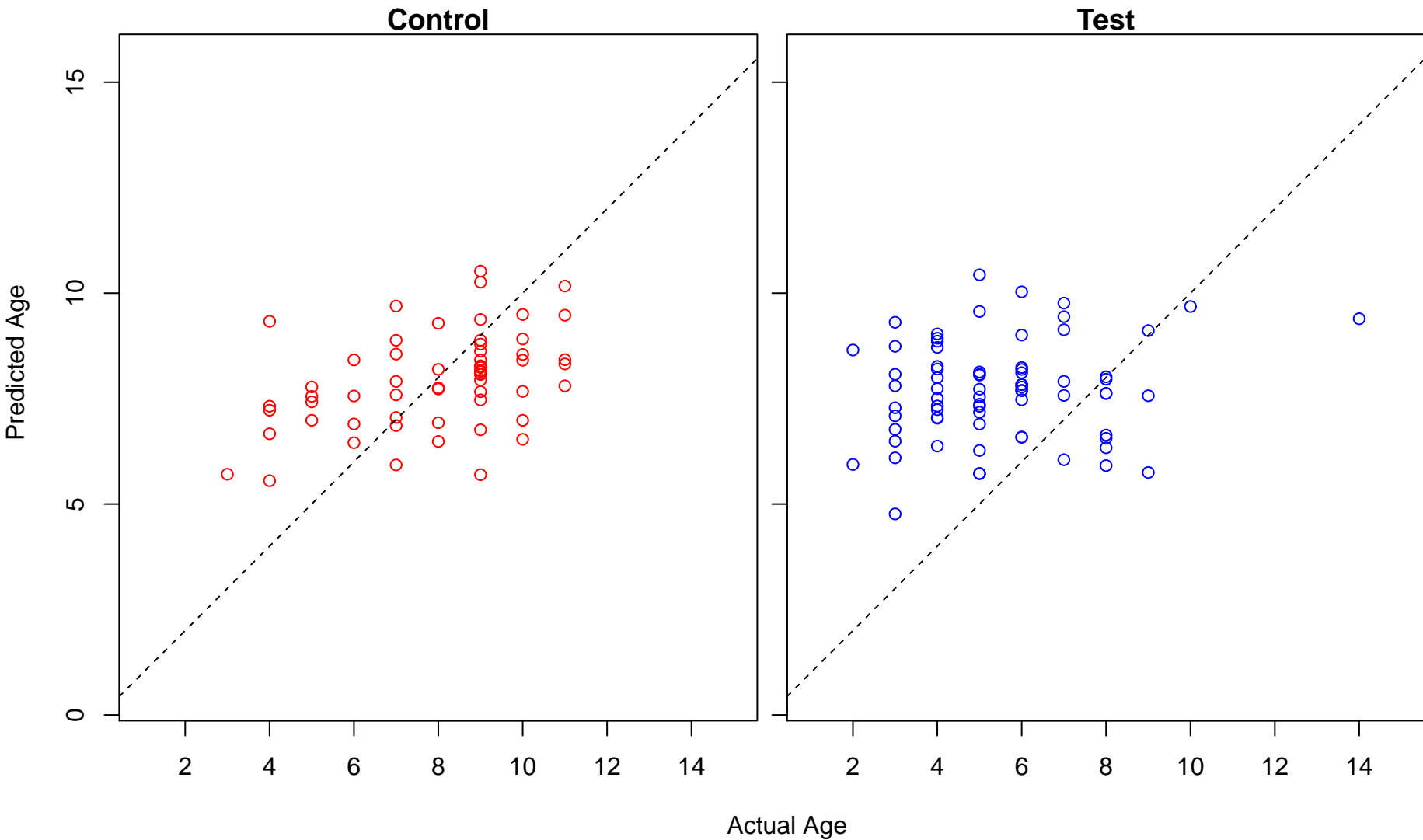
definitive hemopoiesis (Score: 0.739015)



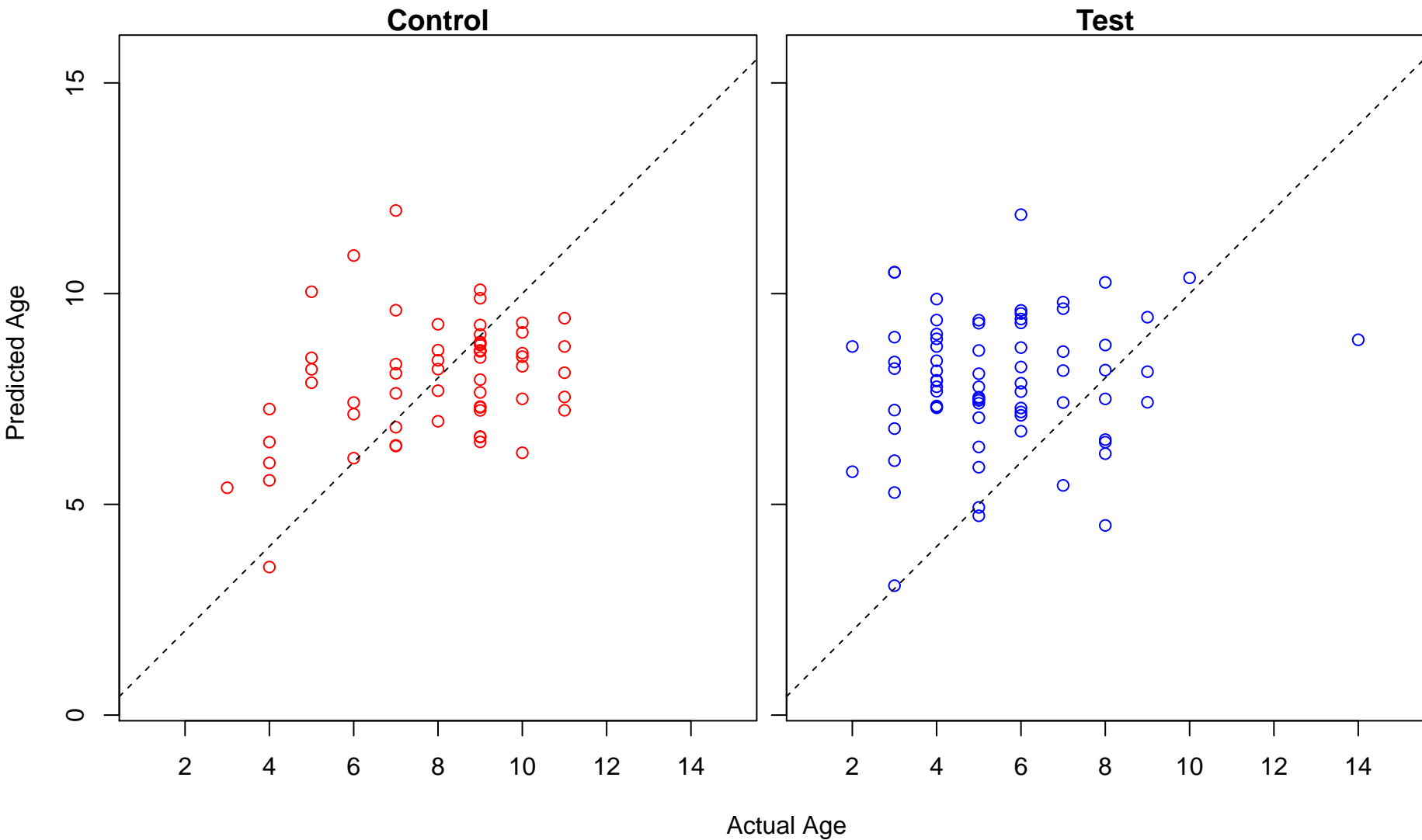
hypoxia-inducible factor-1alpha signaling pathway (Score: 0.738767)



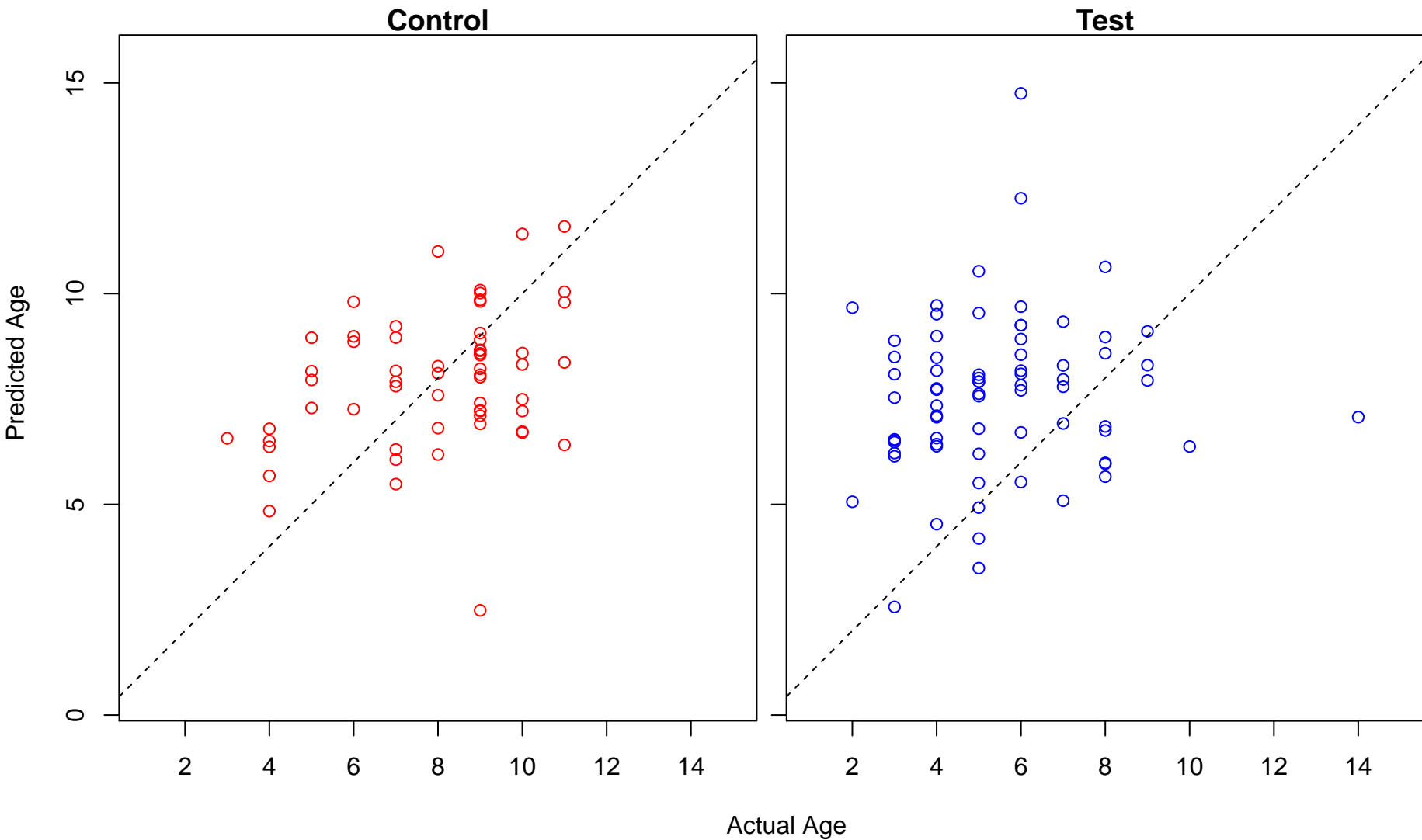
lymphocyte migration into lymphoid organs (Score: 0.738044)



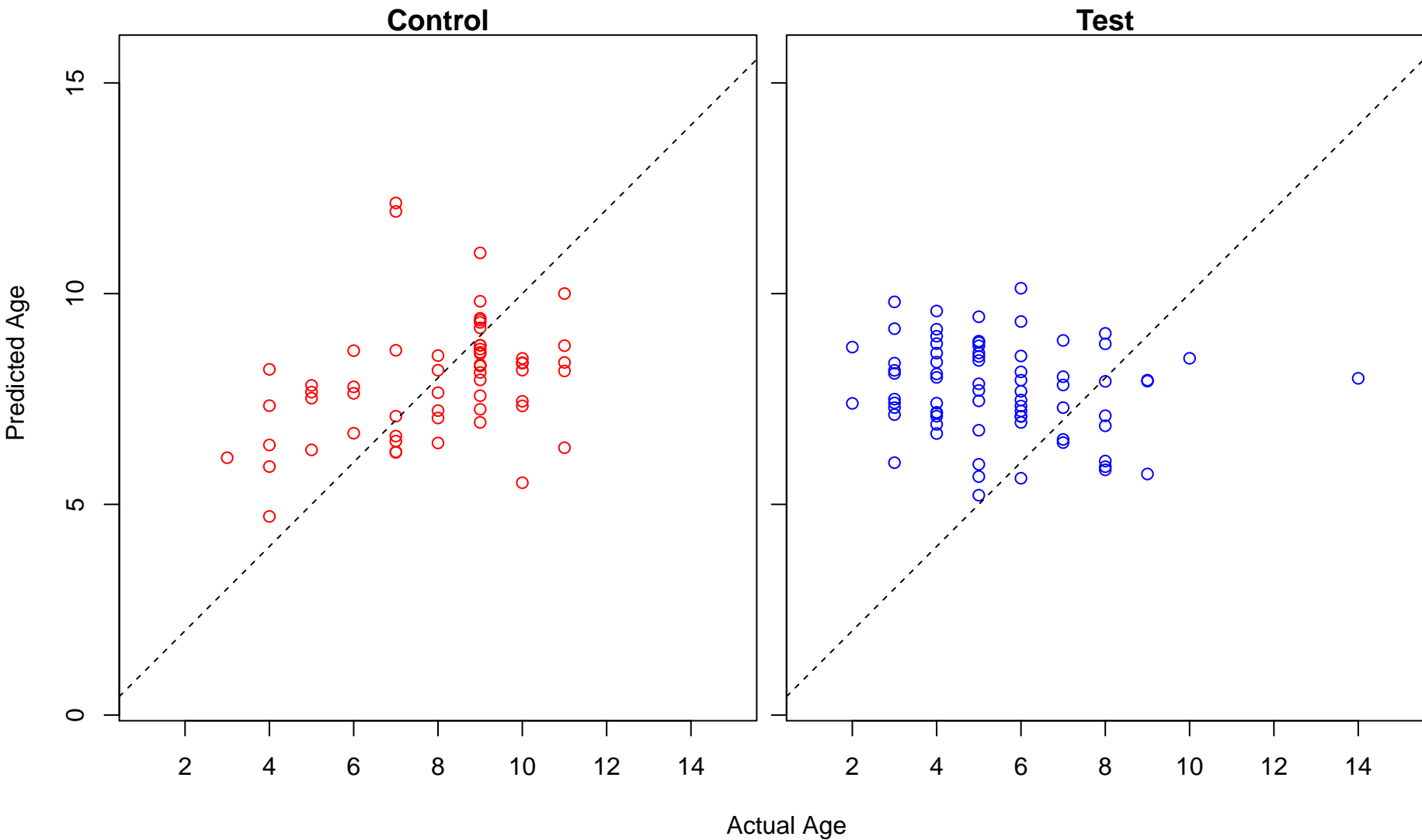
heart valve development (Score: 0.735776)



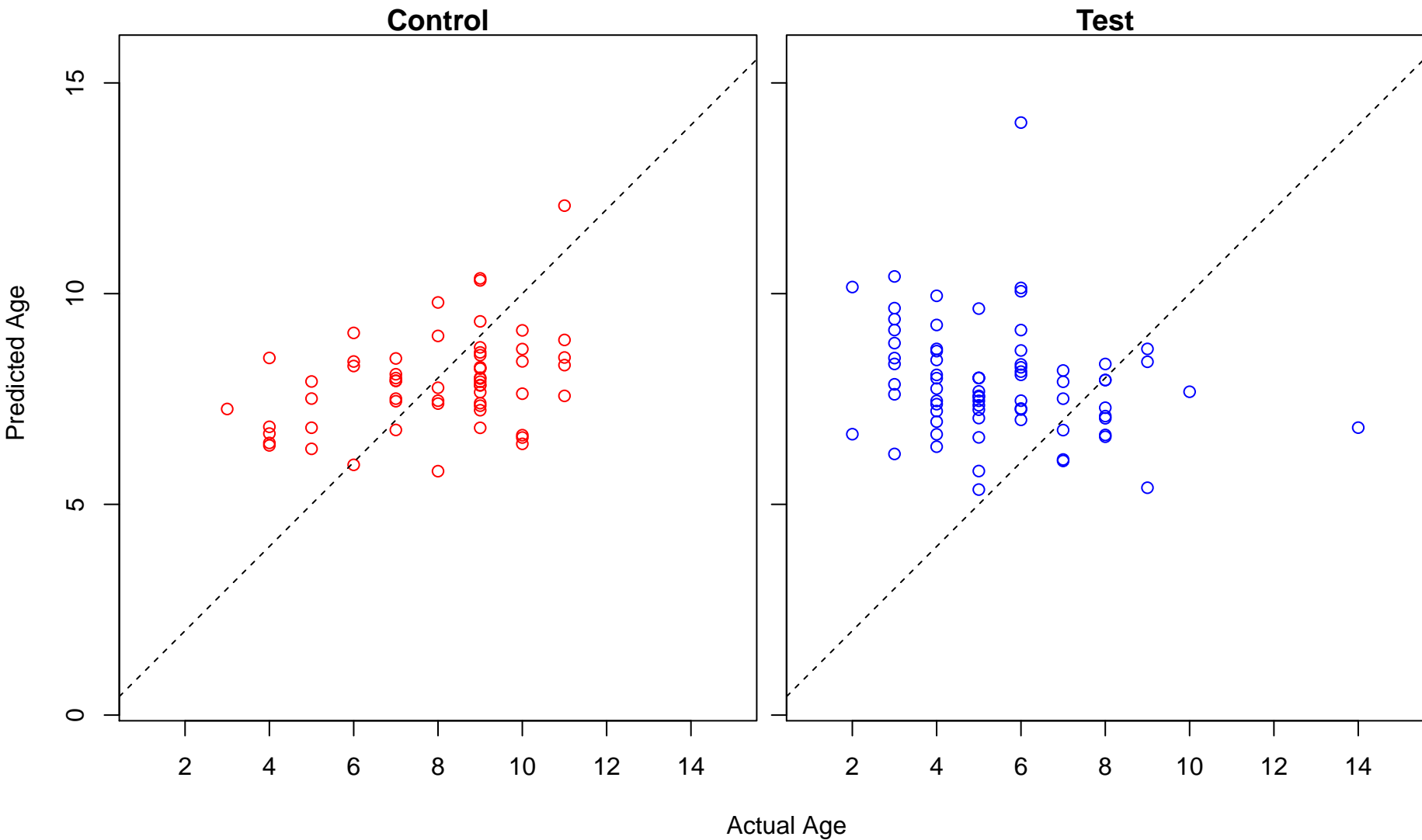
muscle cell development (Score: 0.735650)



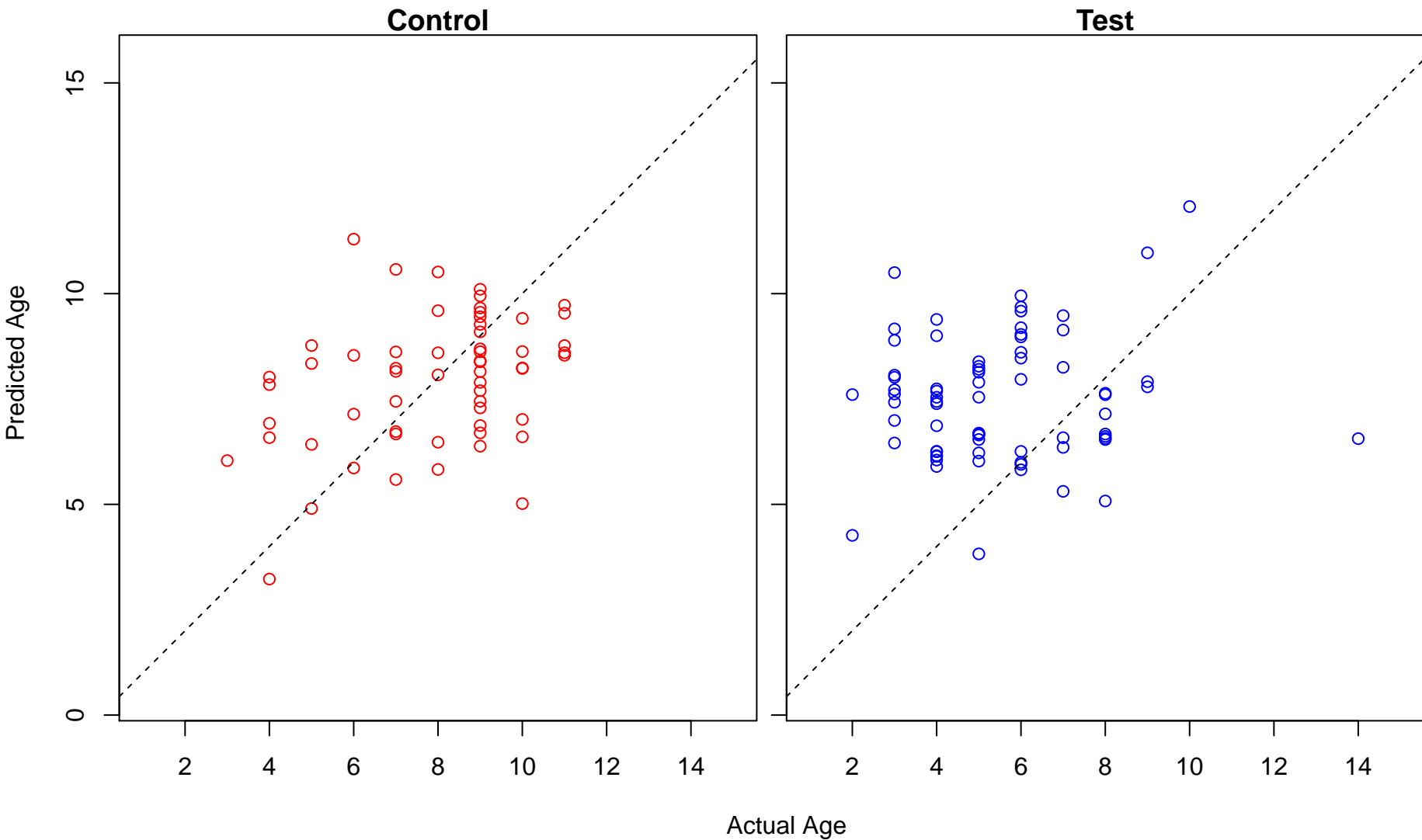
positive regulation of gene expression, epigenetic (Score: 0.735648)



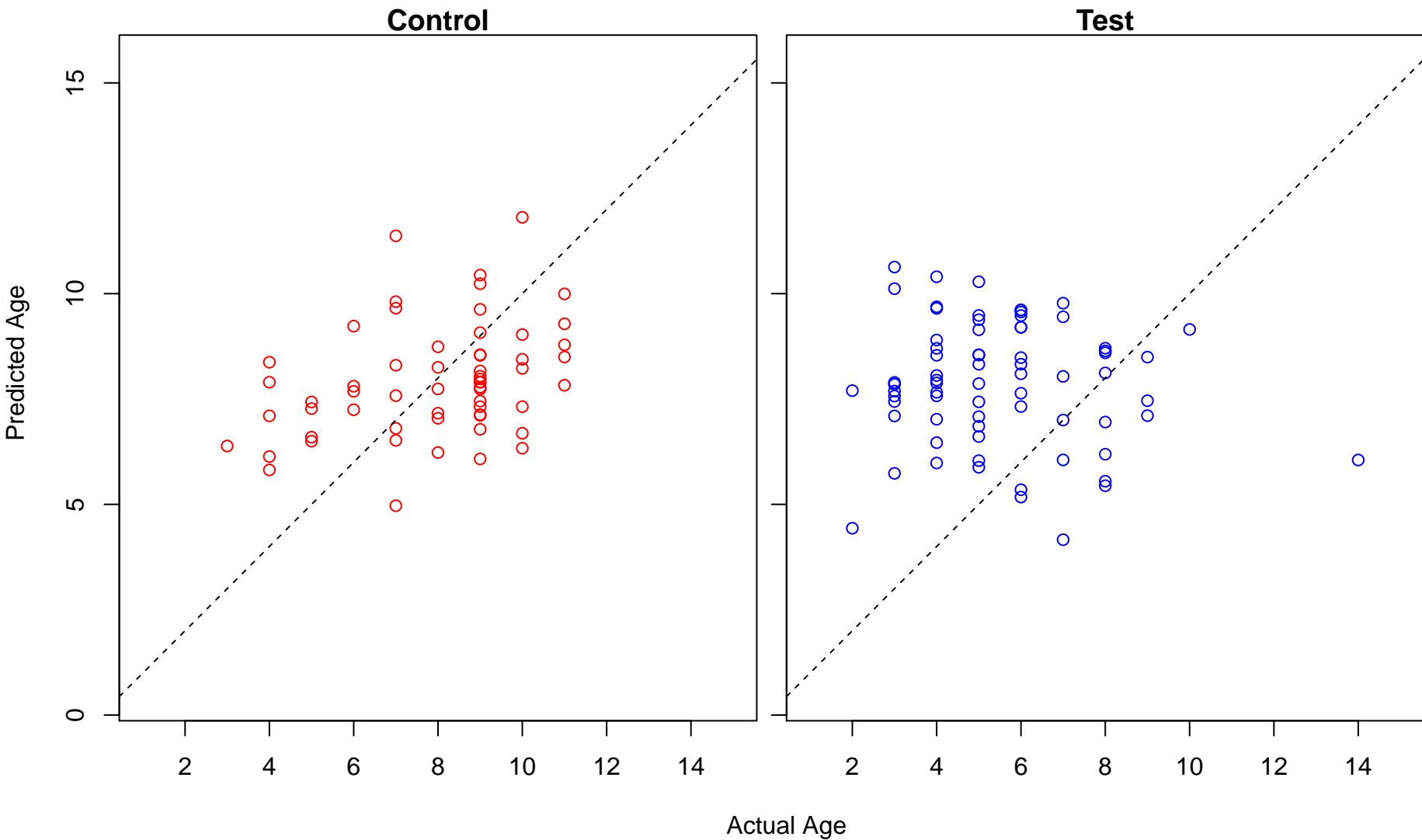
negative regulation of activated T cell proliferation (Score: 0.734179)



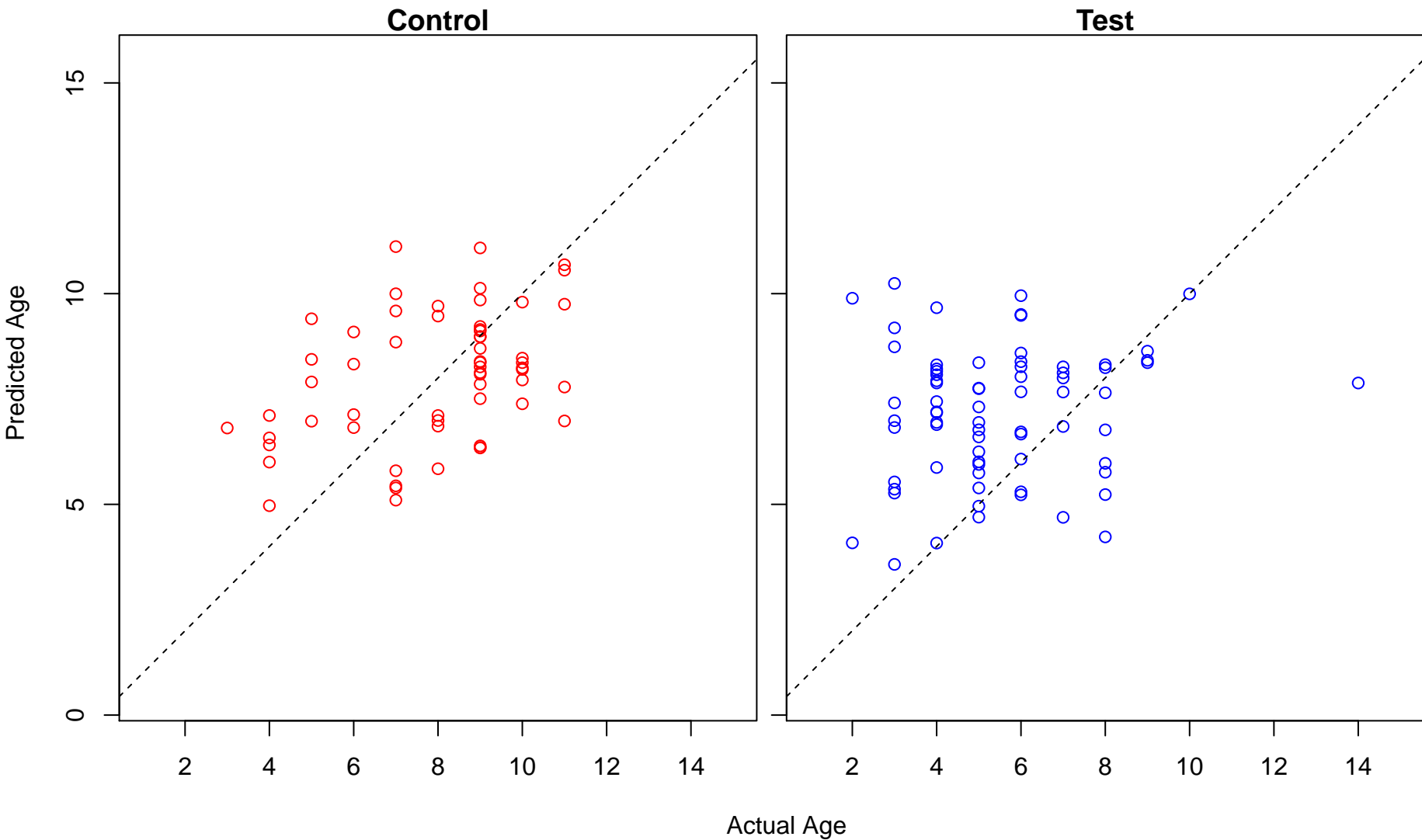
cellular response to epidermal growth factor stimulus (Score: 0.732812)



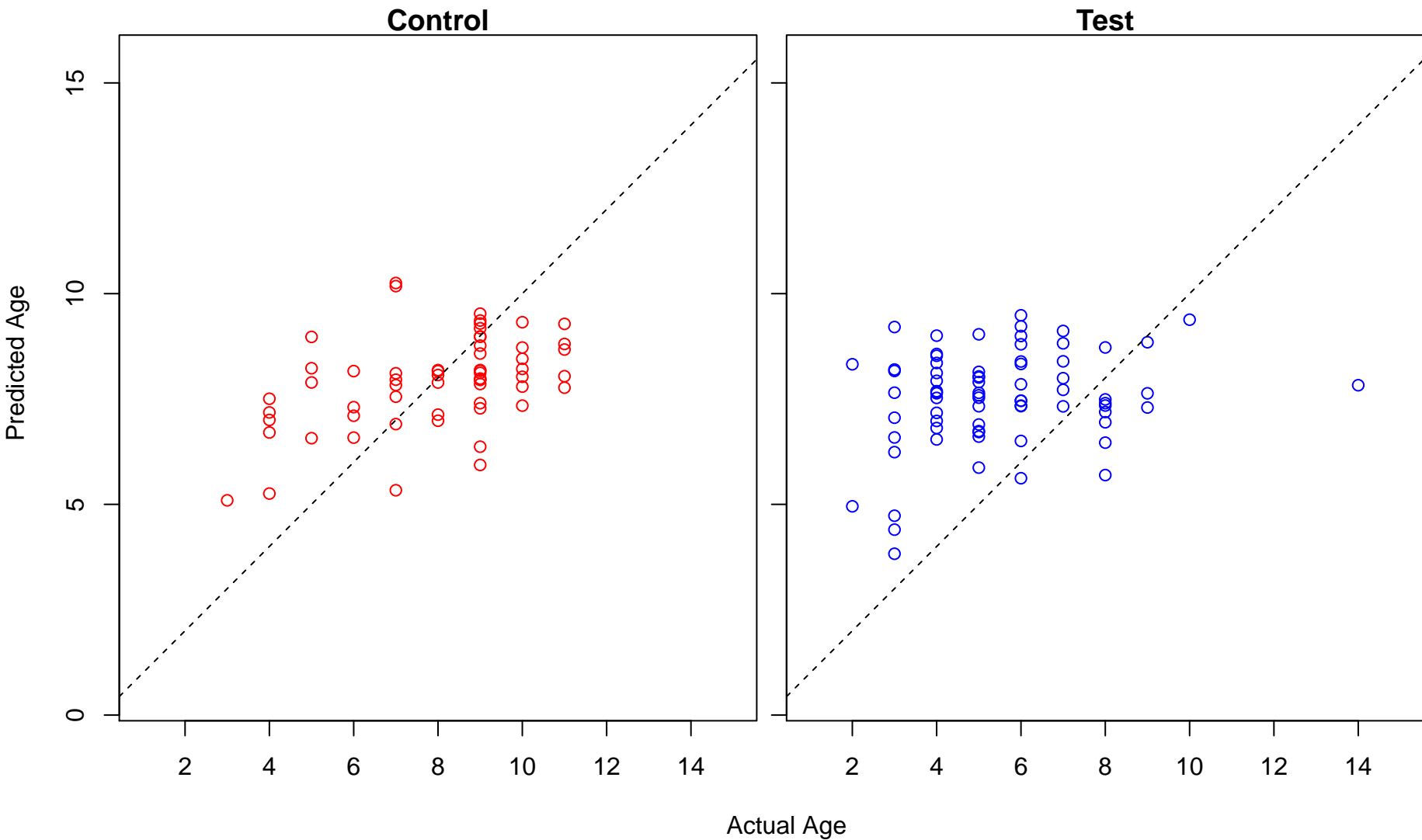
amelogenesis (Score: 0.730653)



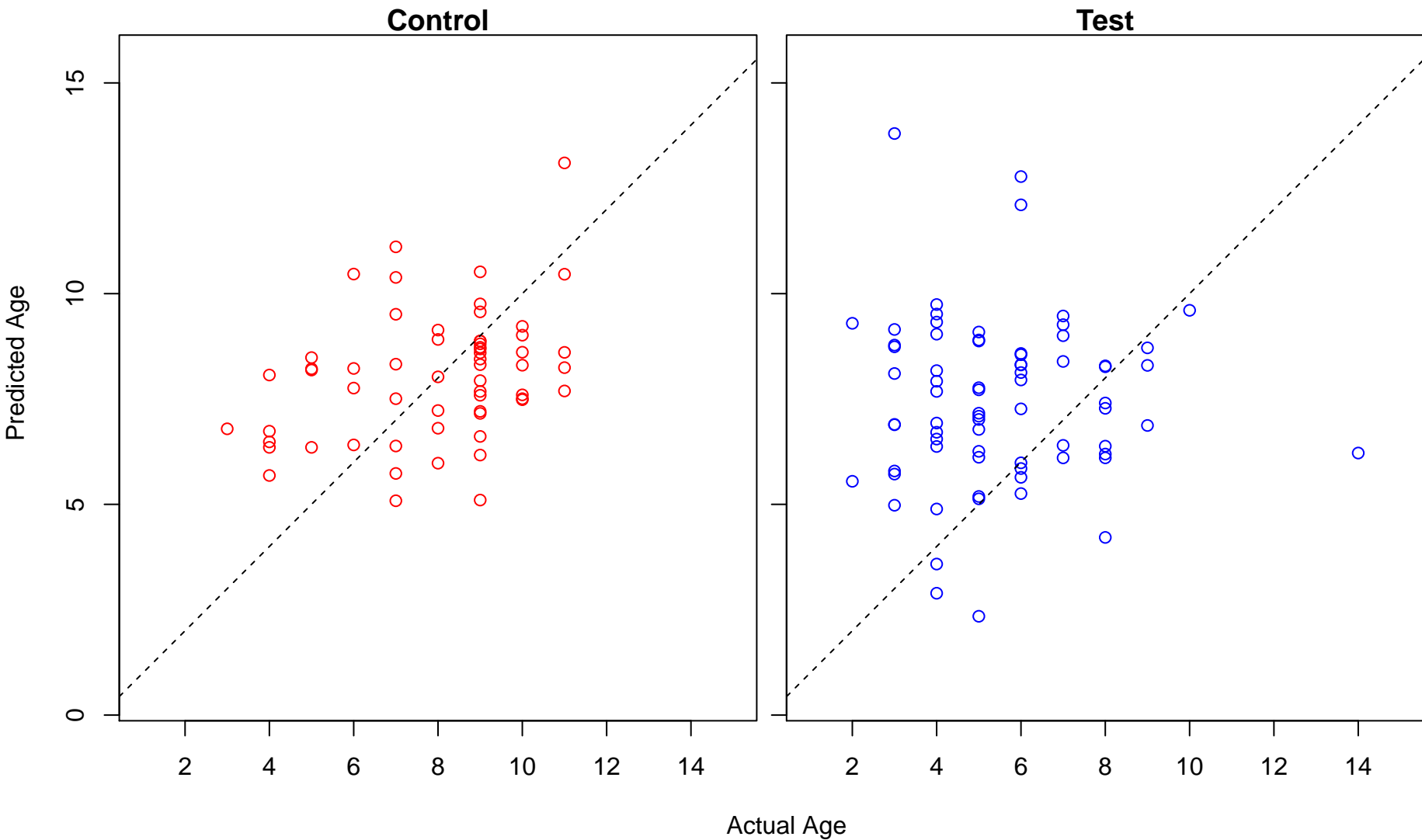
vacuolar transport (Score: 0.728657)



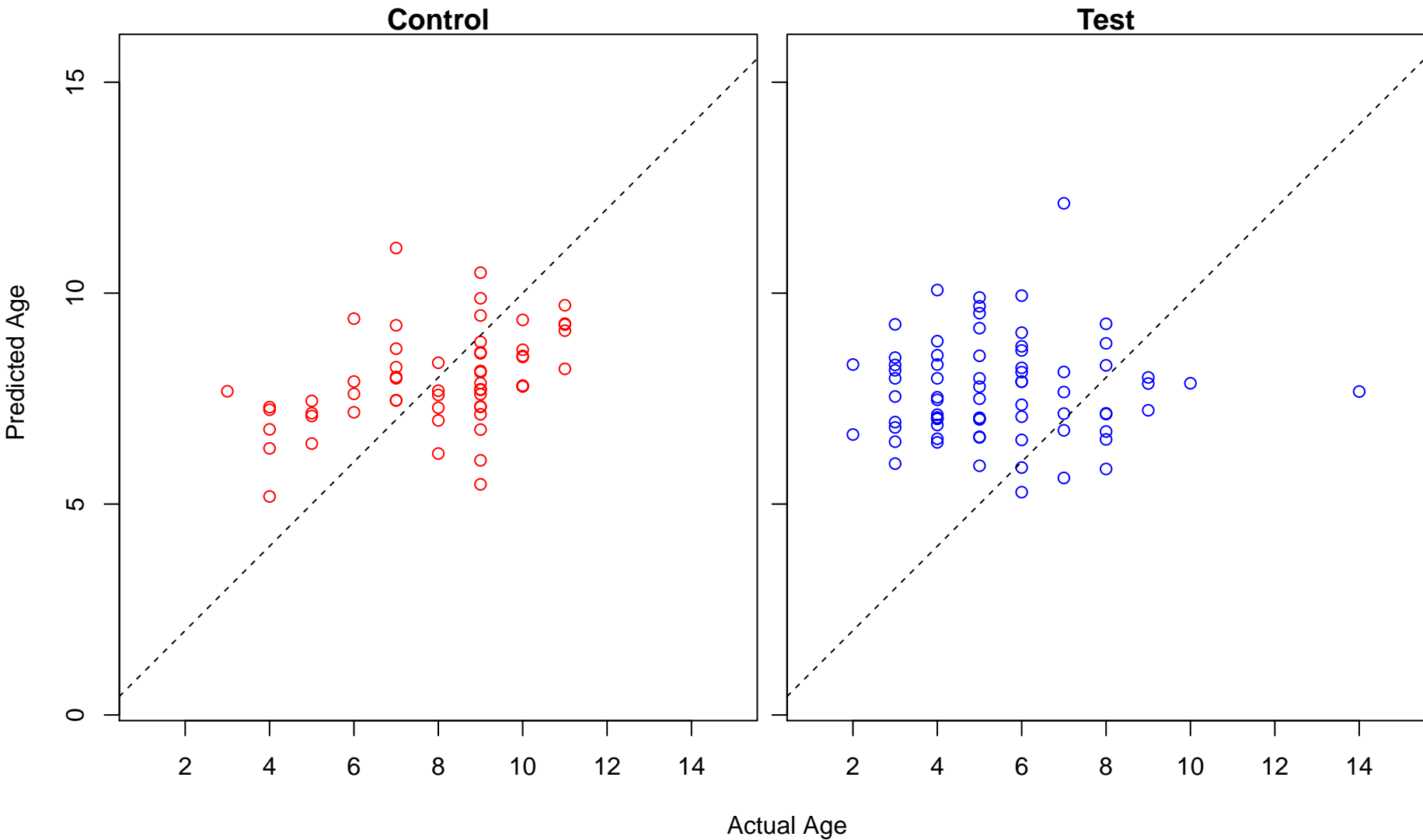
regulation of branching involved in ureteric bud morphogenesis (Score: 0.728389)



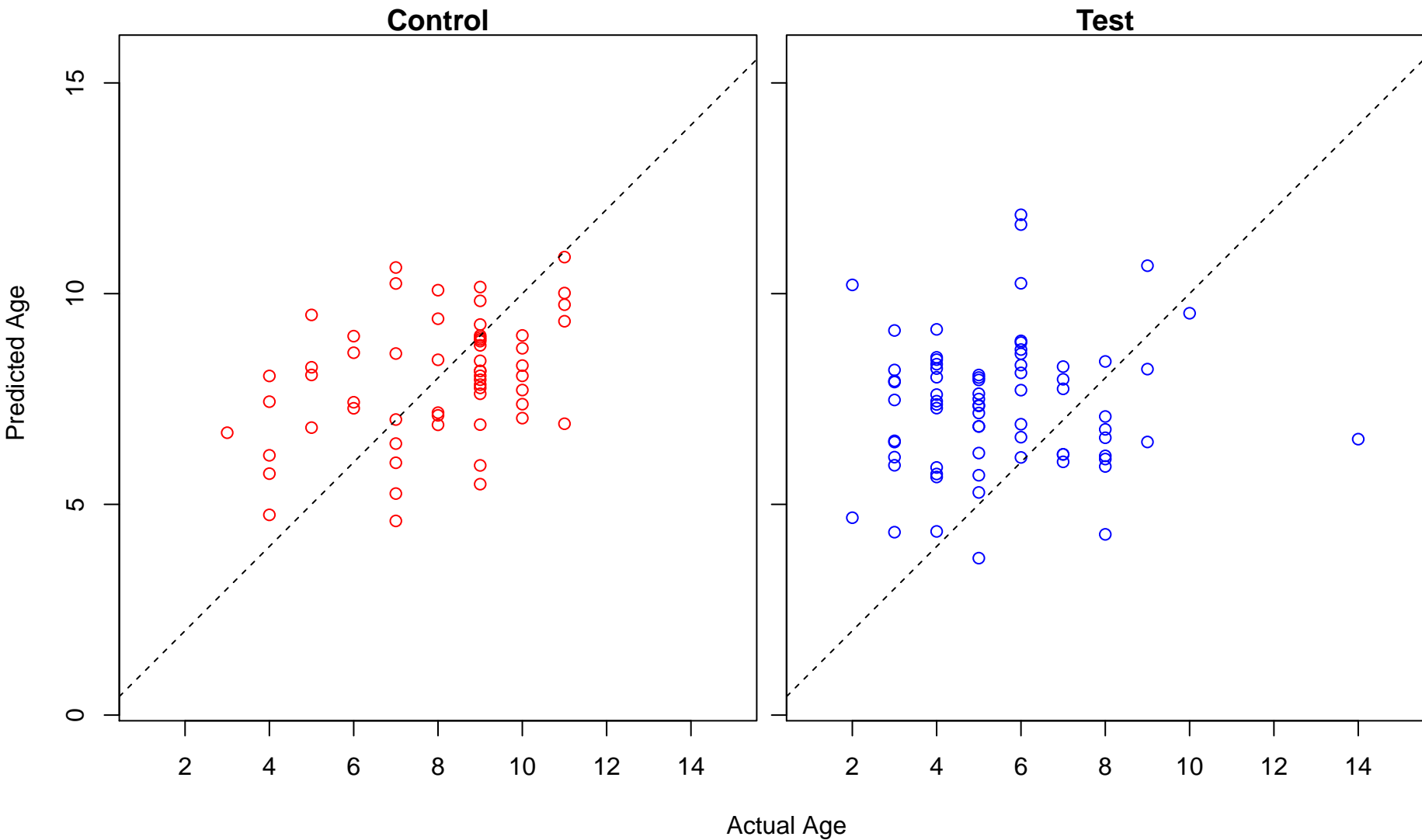
negative regulation of MAPK cascade (Score: 0.726235)



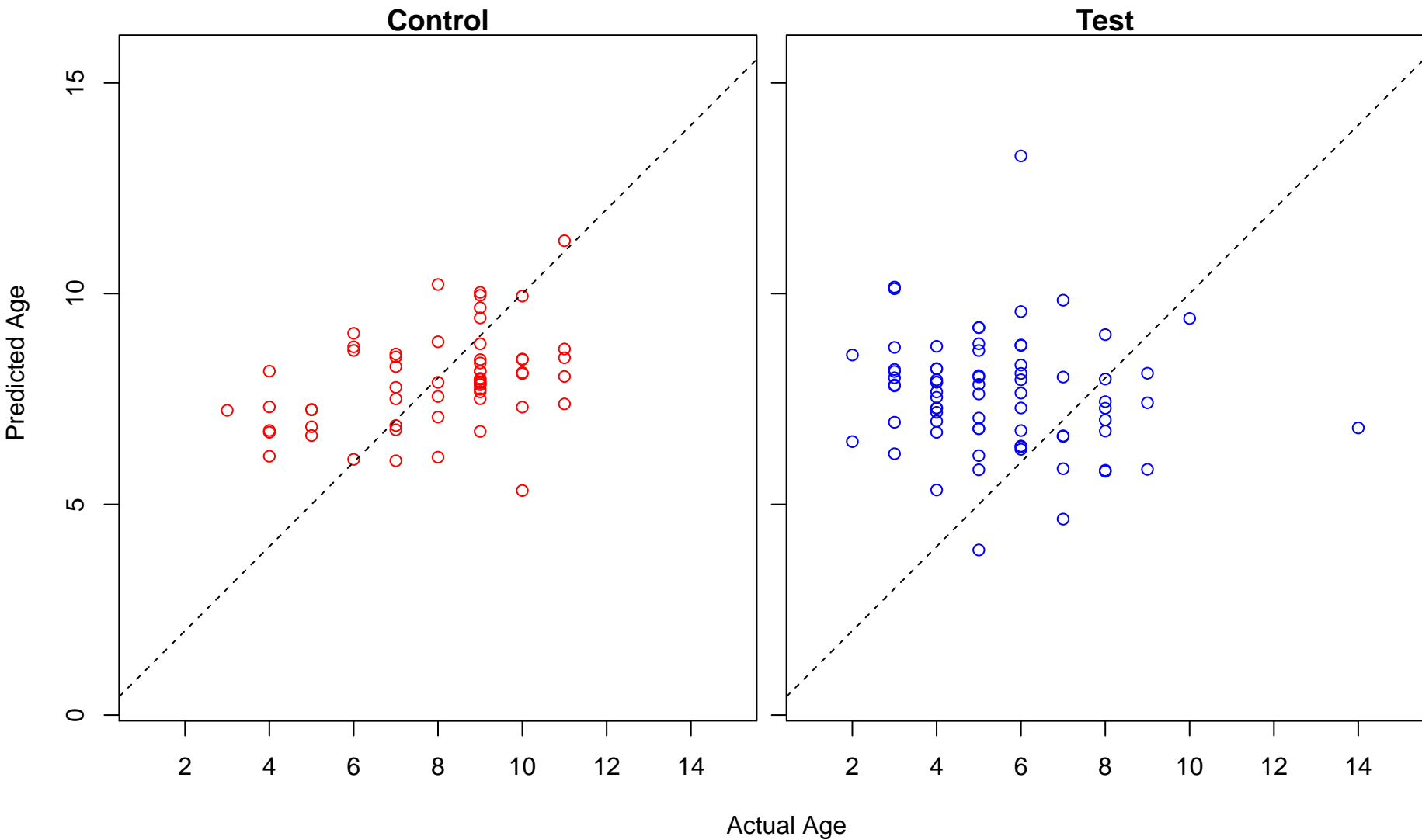
peripheral nervous system myelin maintenance (Score: 0.723714)



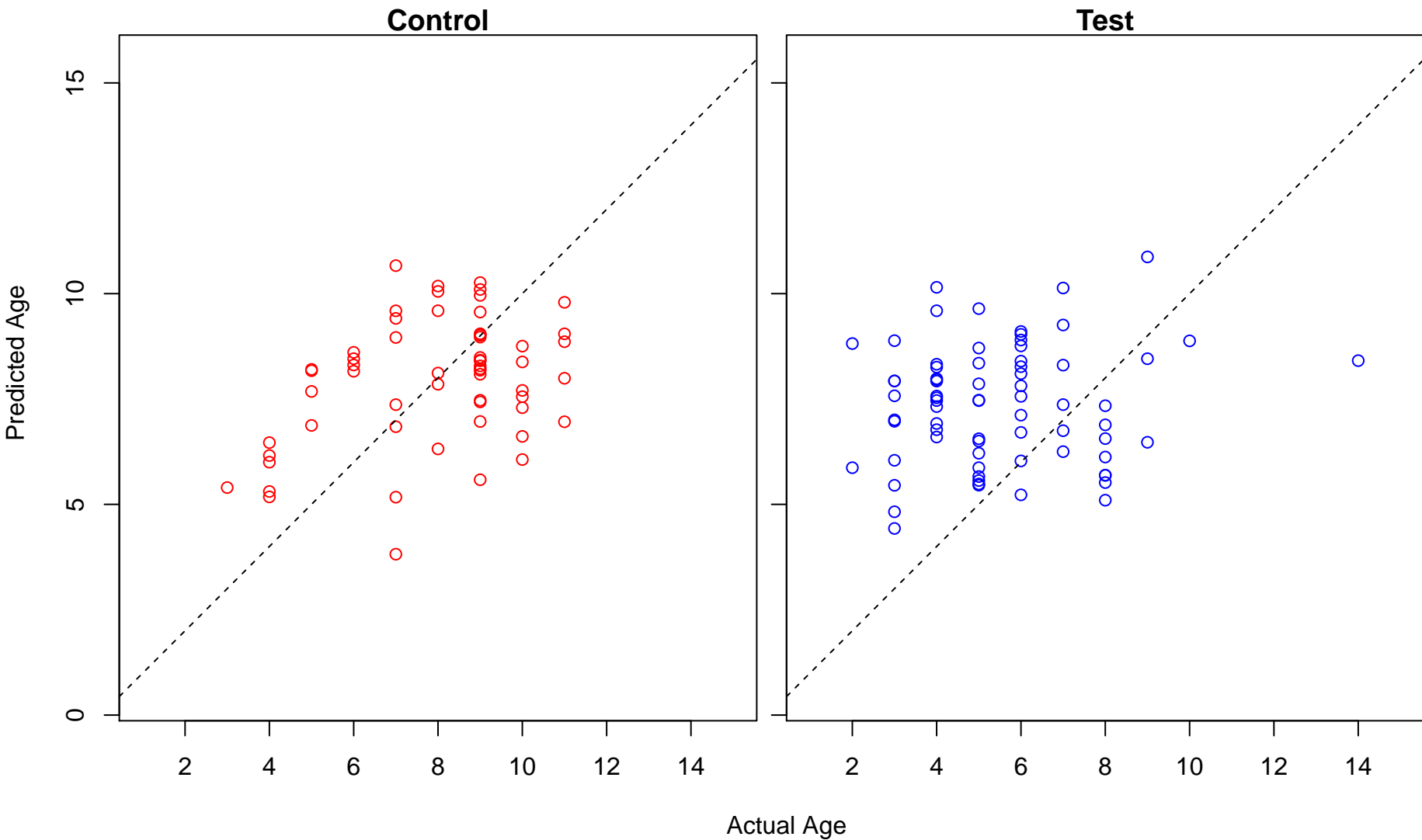
regulation of epithelial cell differentiation (Score: 0.723639)



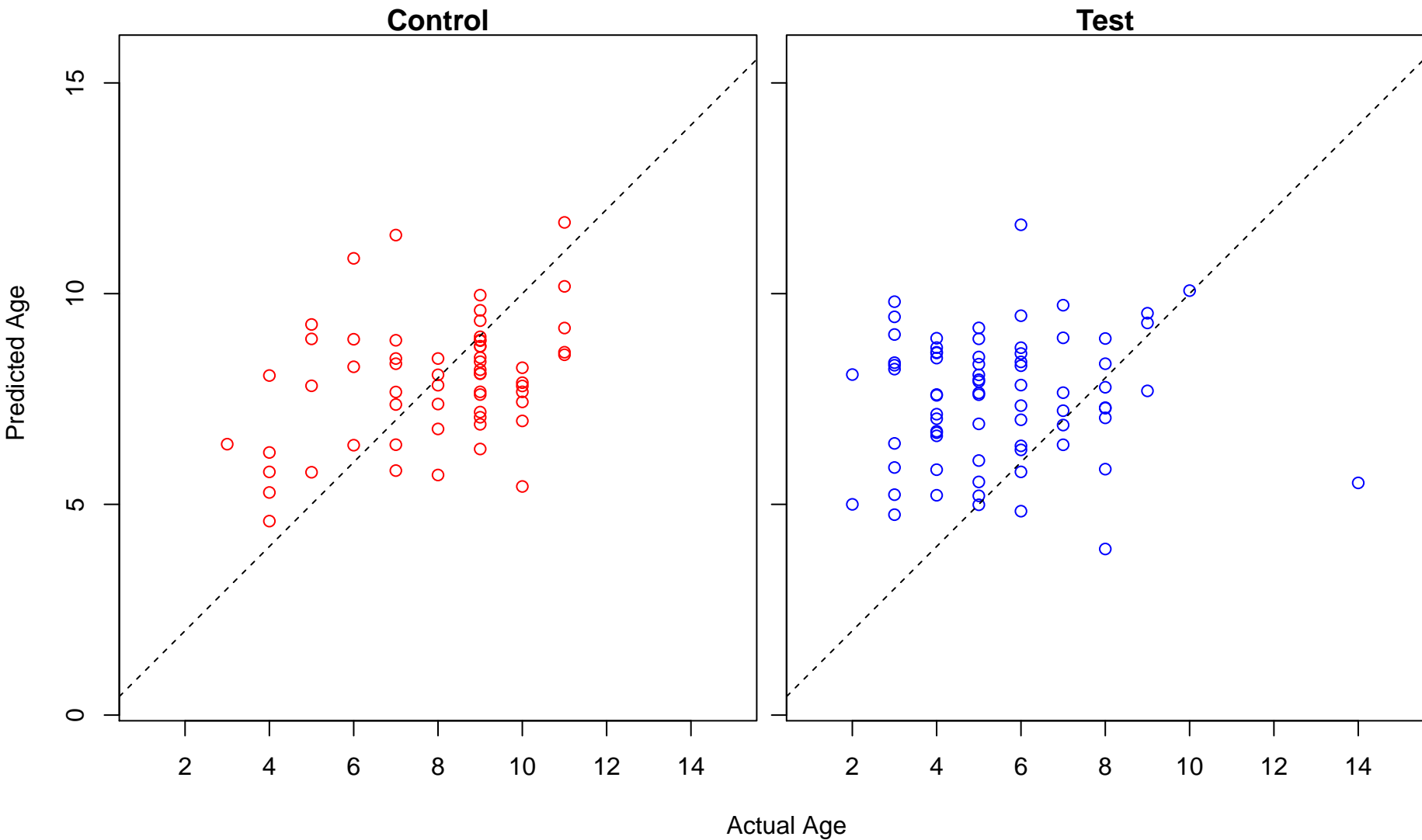
regulation of monocyte chemotactic protein-1 production (Score: 0.721615)



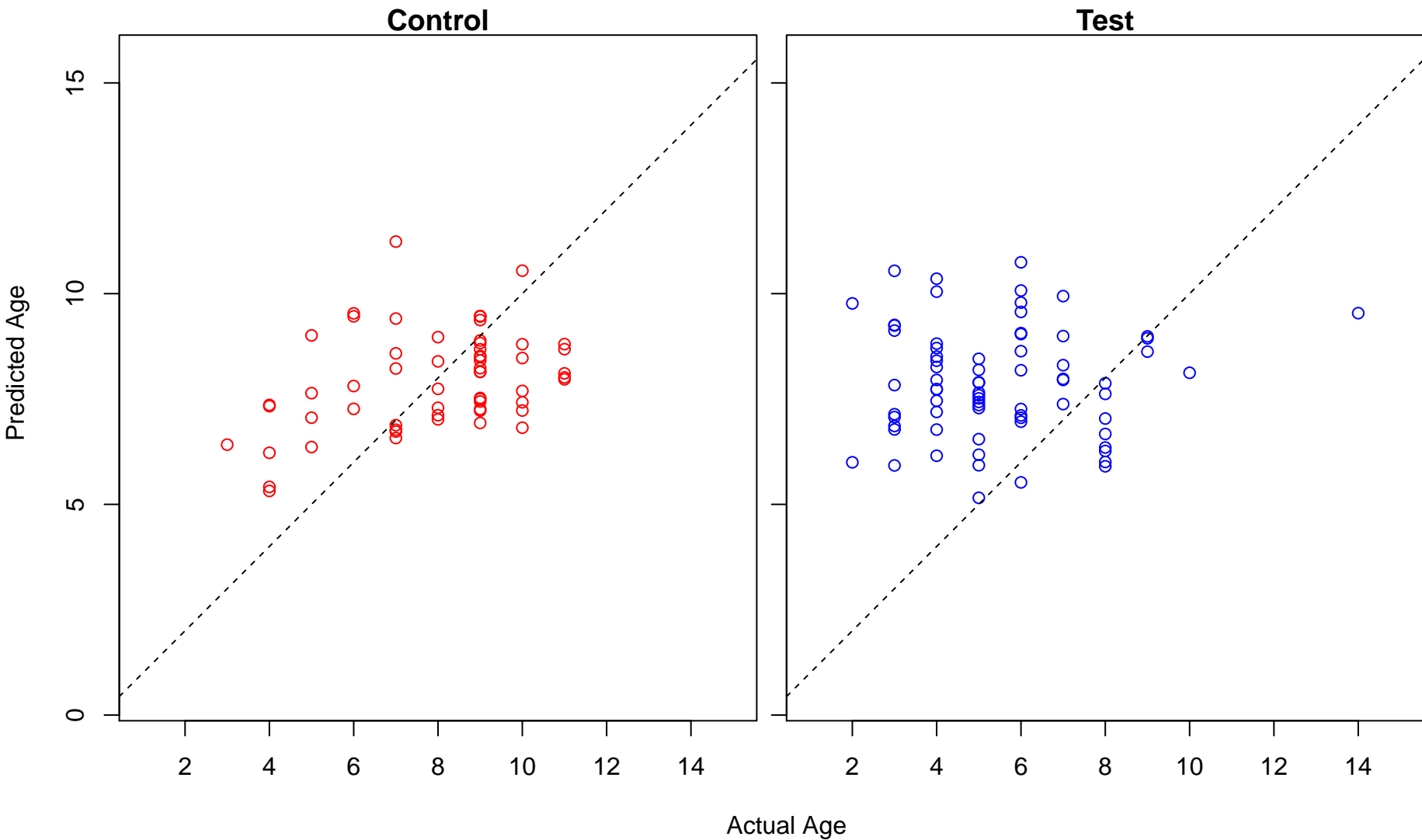
diencephalon development (Score: 0.721106)



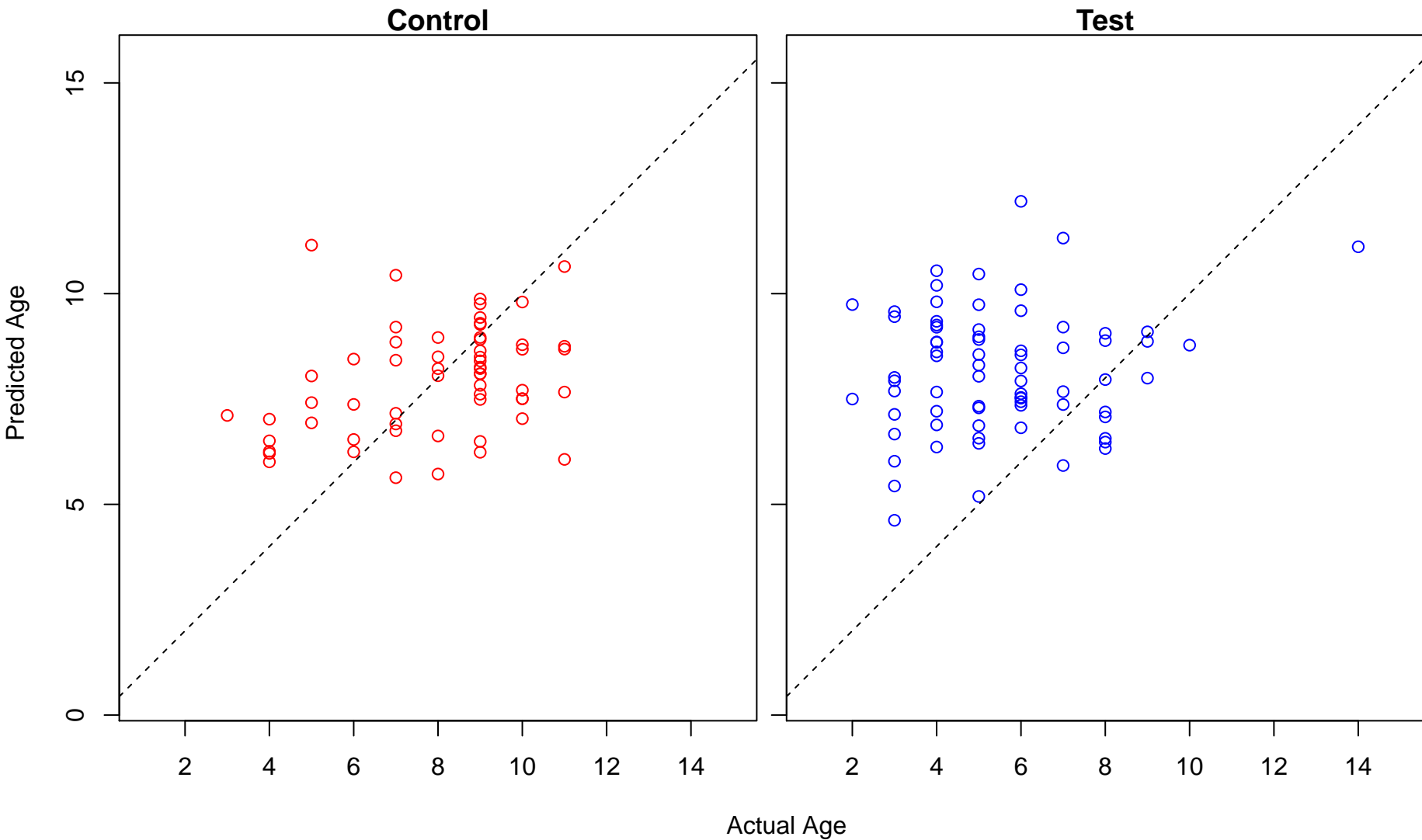
cellular response to glucocorticoid stimulus (Score: 0.720906)



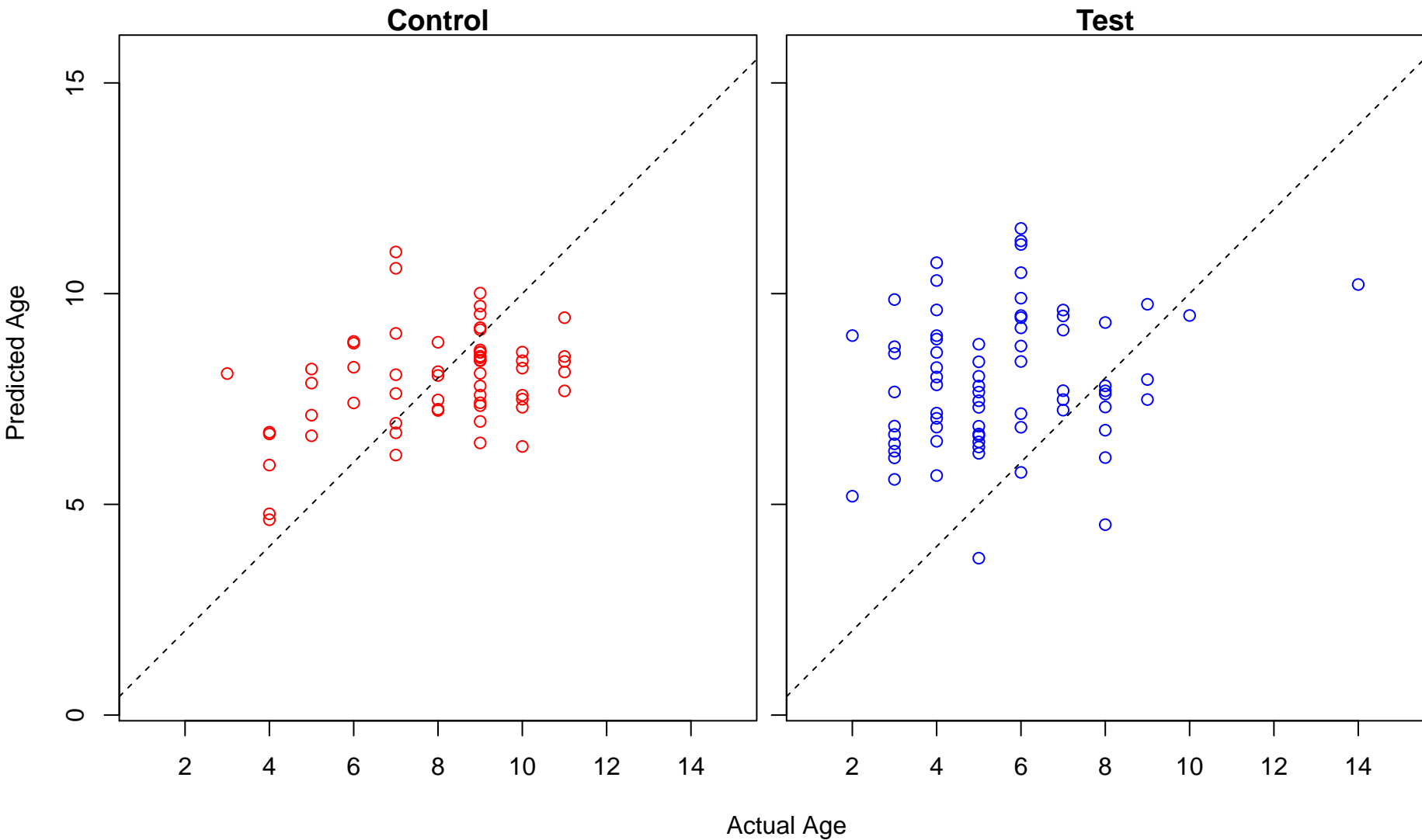
cell killing (Score: 0.719454)



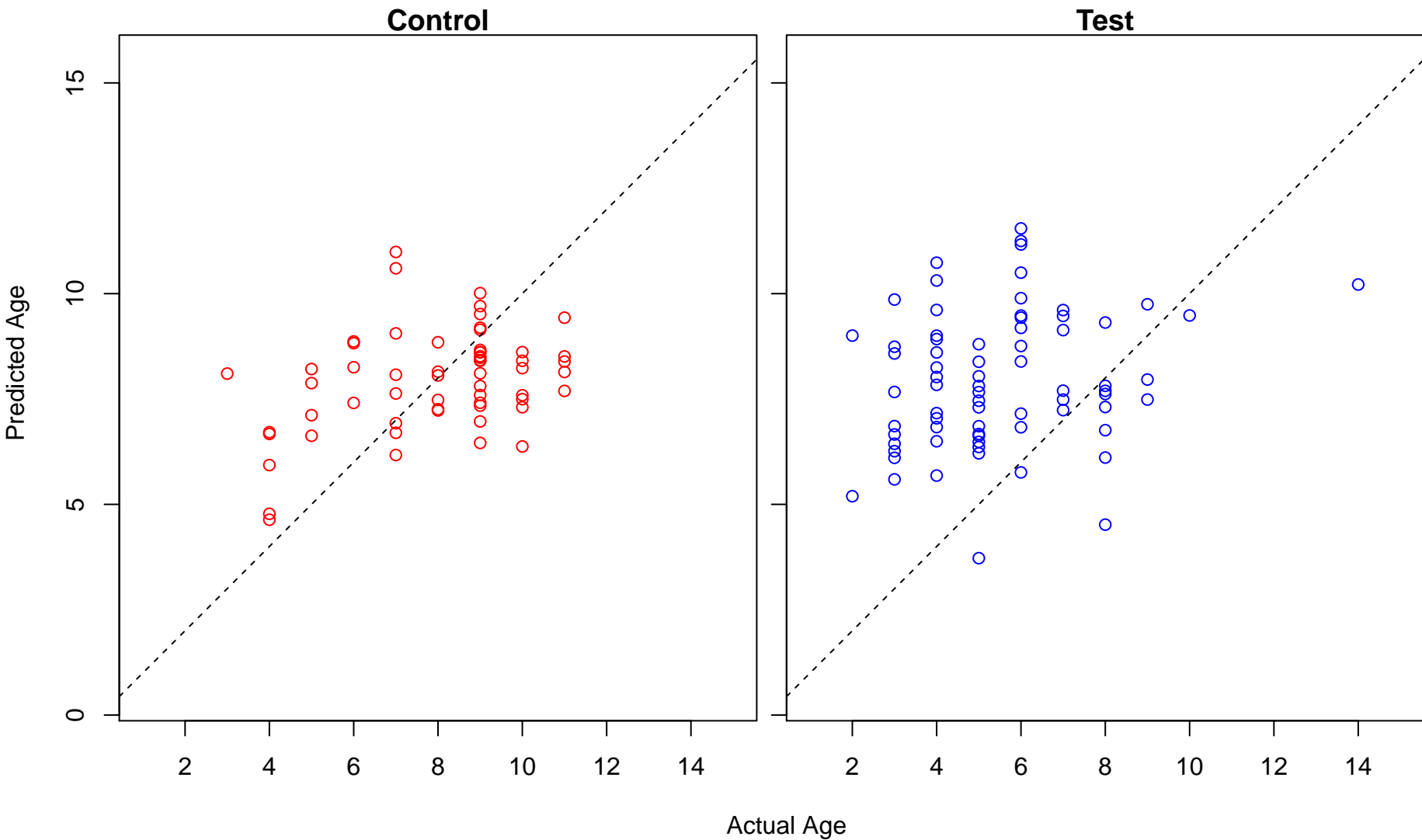
forebrain regionalization (Score: 0.718615)



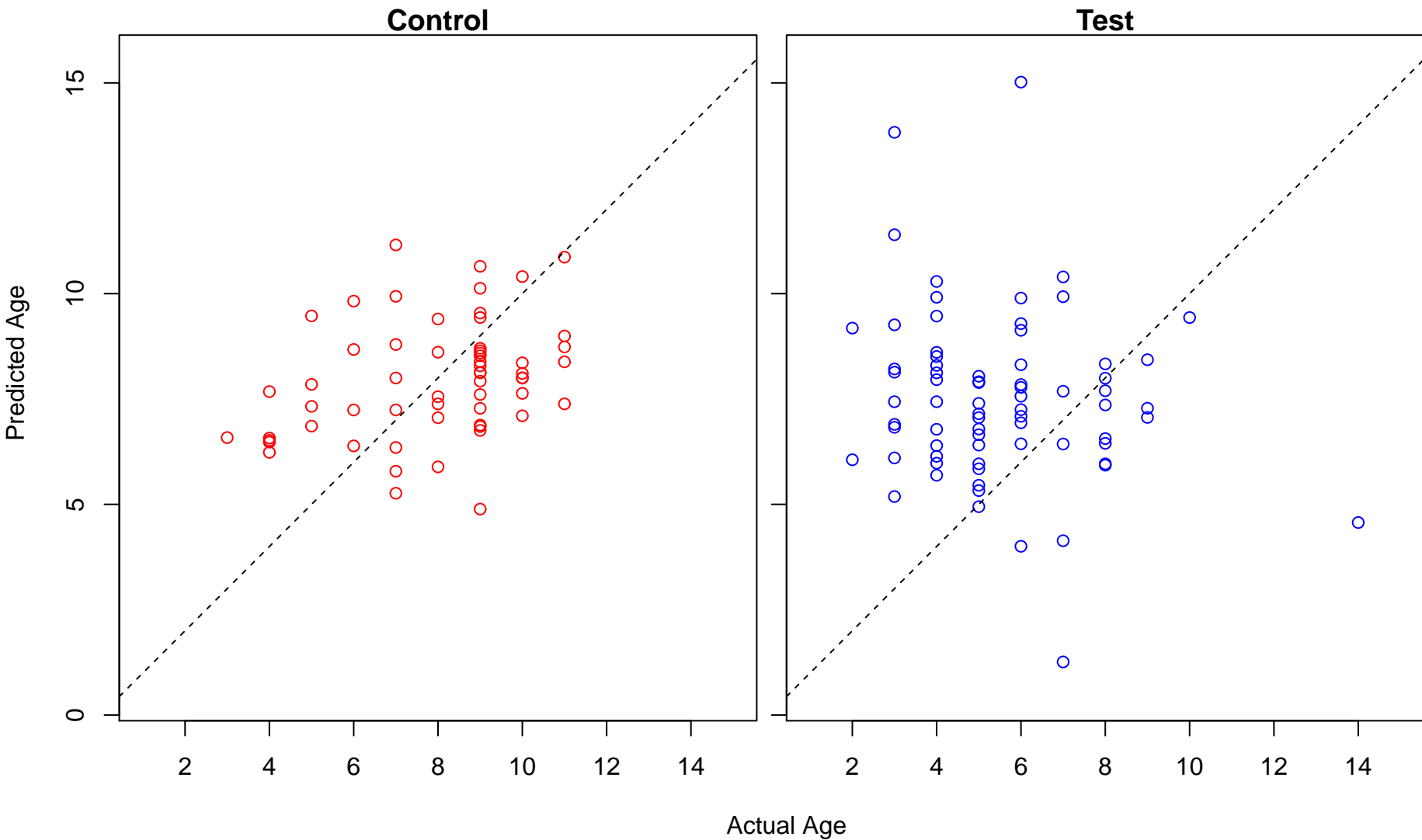
positive regulation of Ras protein signal transduction (Score: 0.717870)



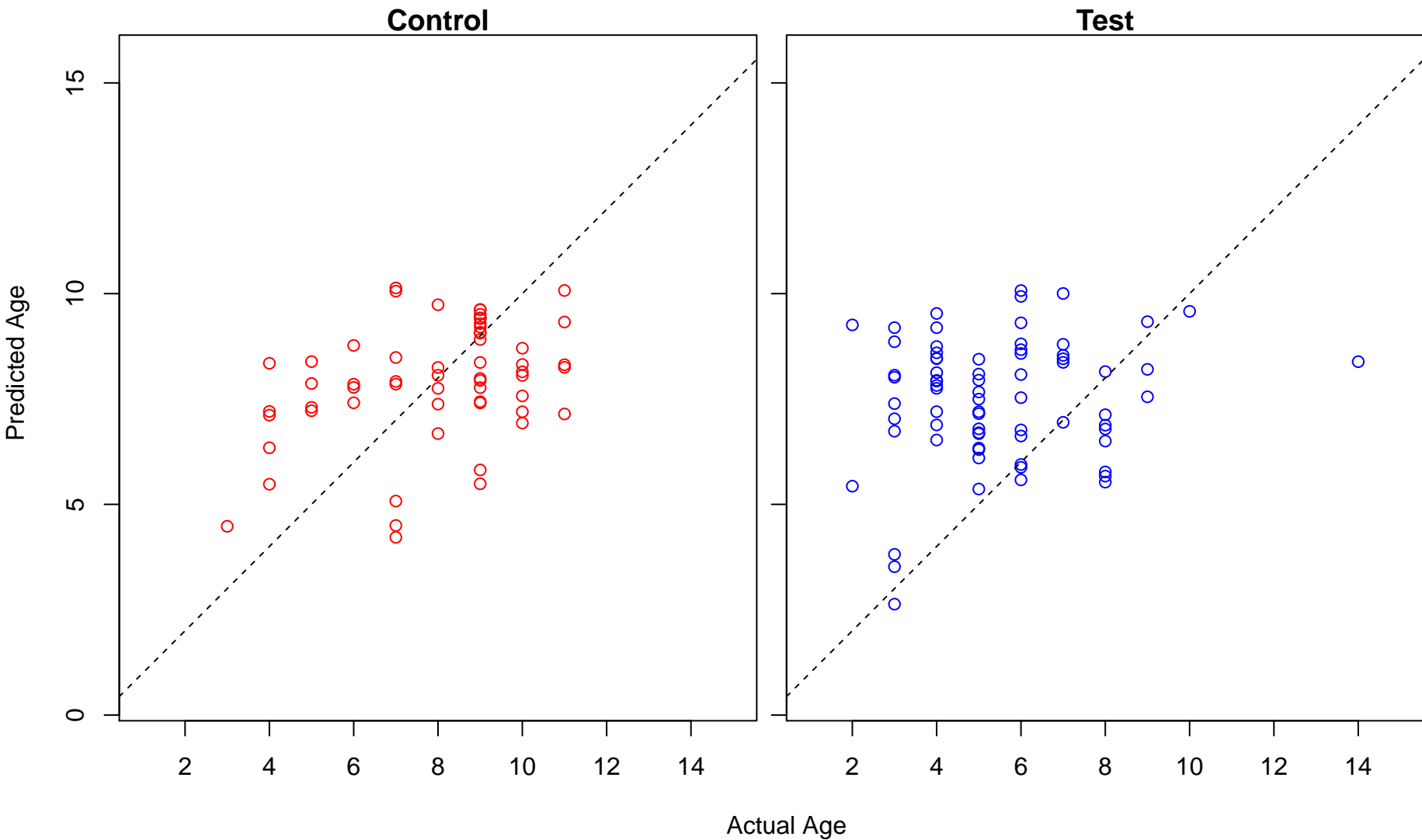
positive regulation of small GTPase mediated signal transduction (Score: 0.717851)



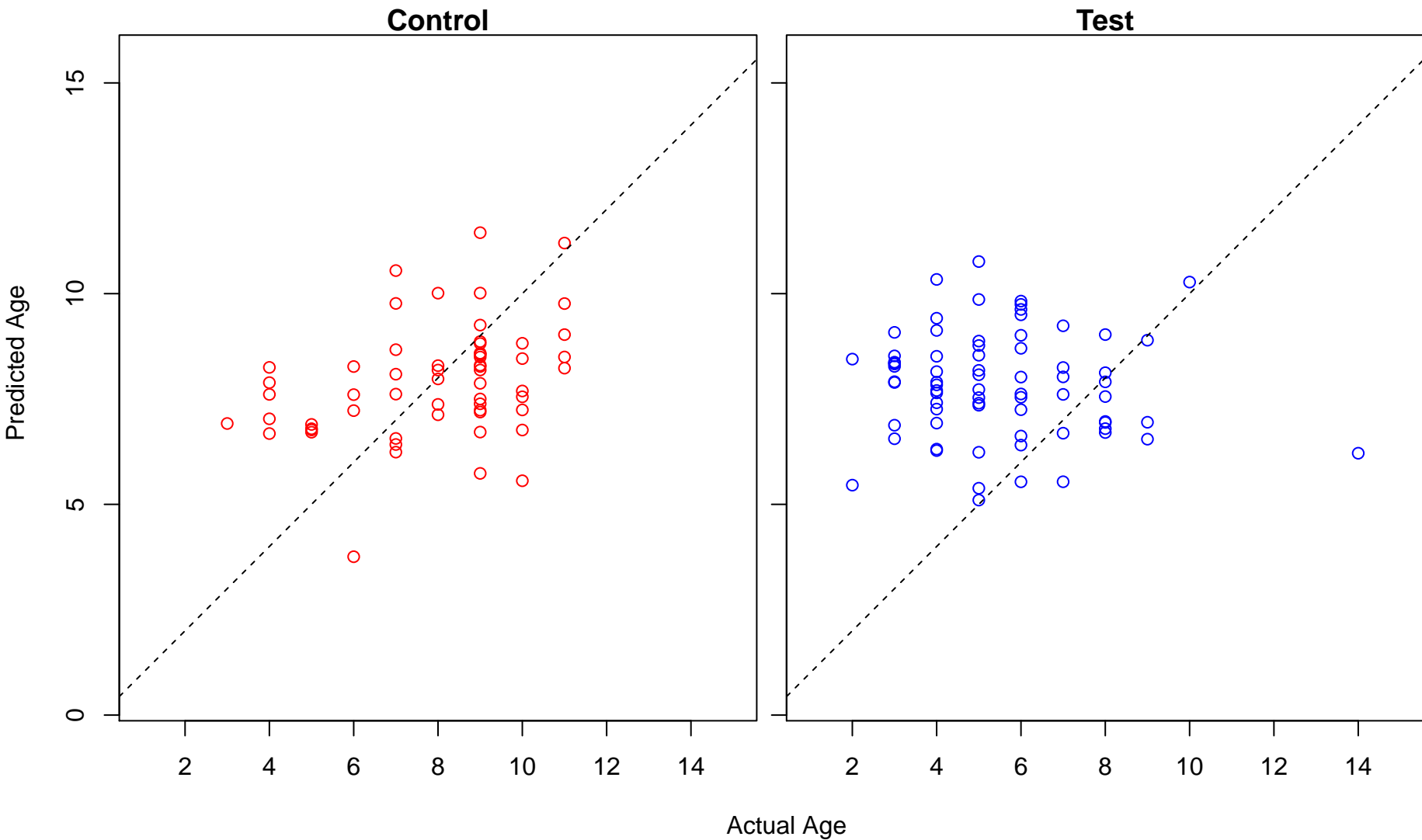
regulation of alpha-beta T cell proliferation (Score: 0.716800)



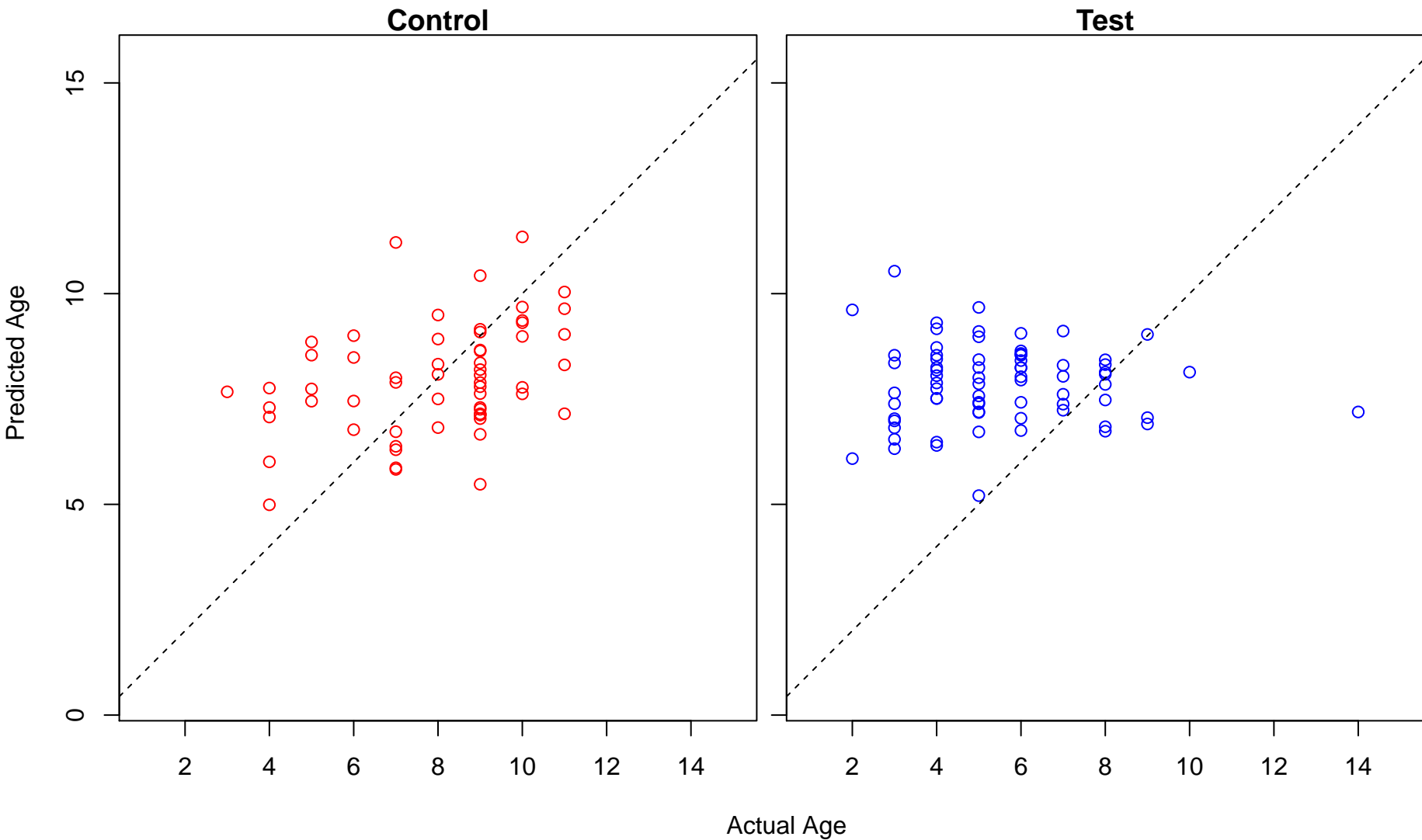
pituitary gland development (Score: 0.716132)



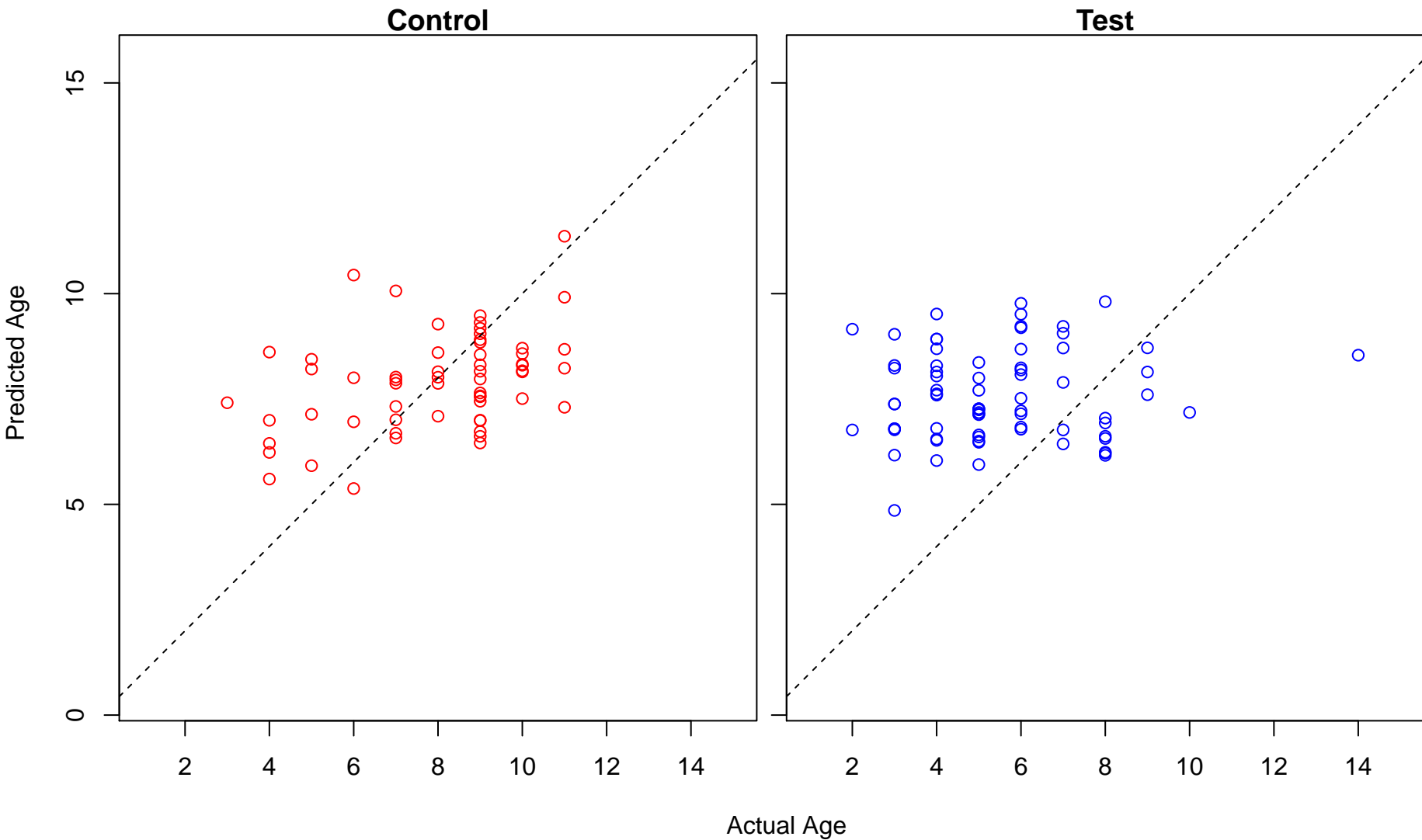
on of cellular ketone metabolic process by regulation of transcription from RNA polymerase II promoter (S



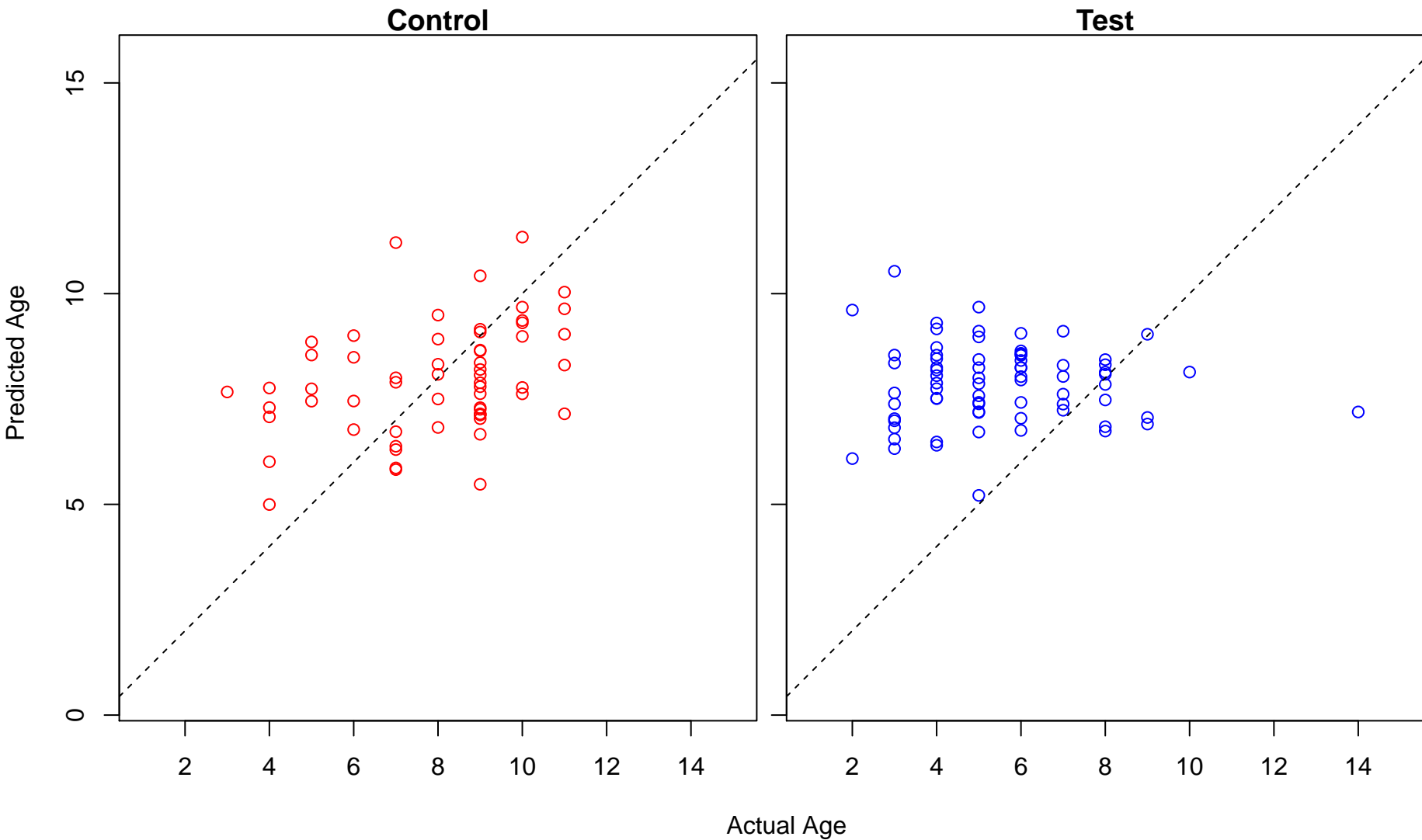
manganese ion transport (Score: 0.714983)



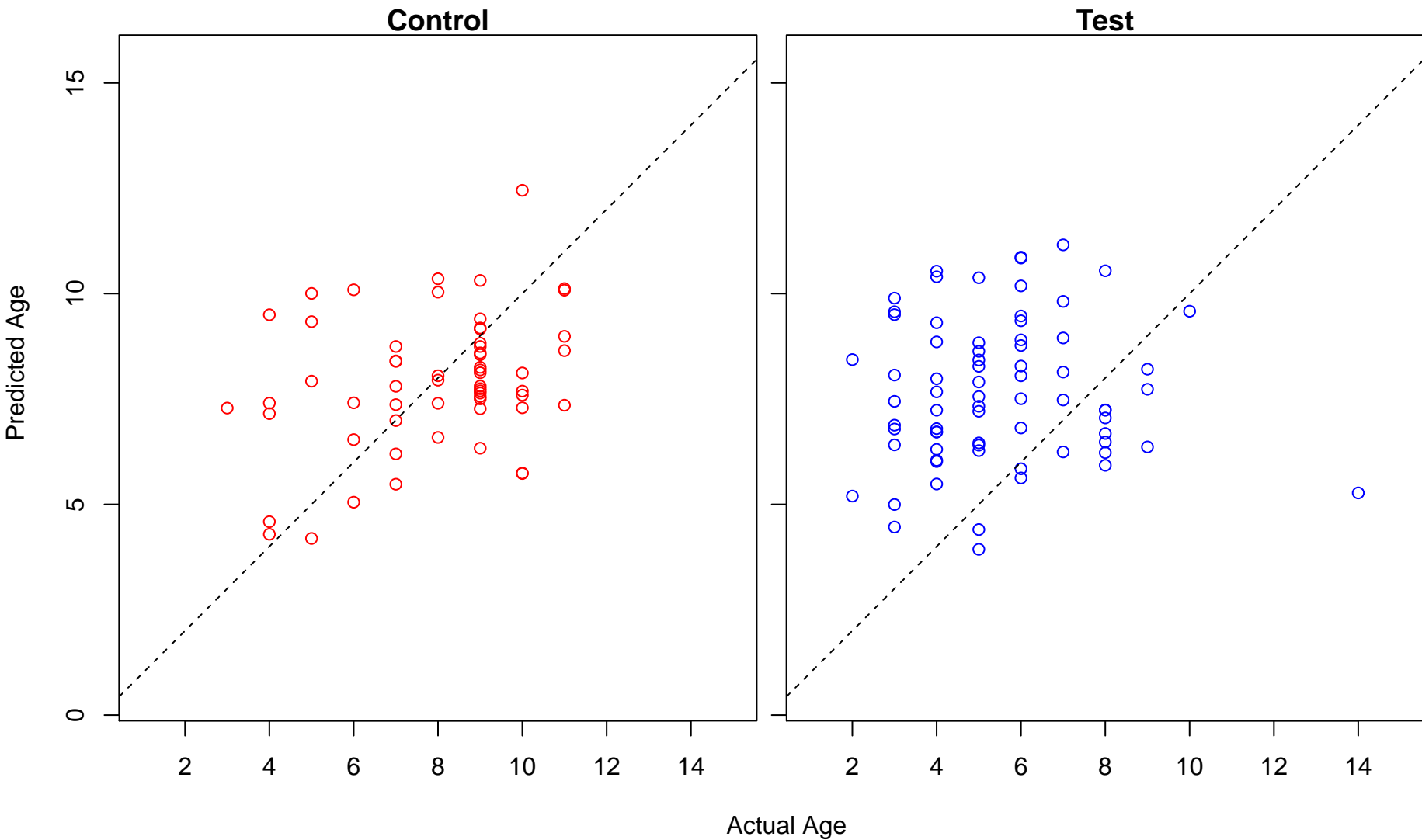
establishment or maintenance of monopolar cell polarity (Score: 0.714730)



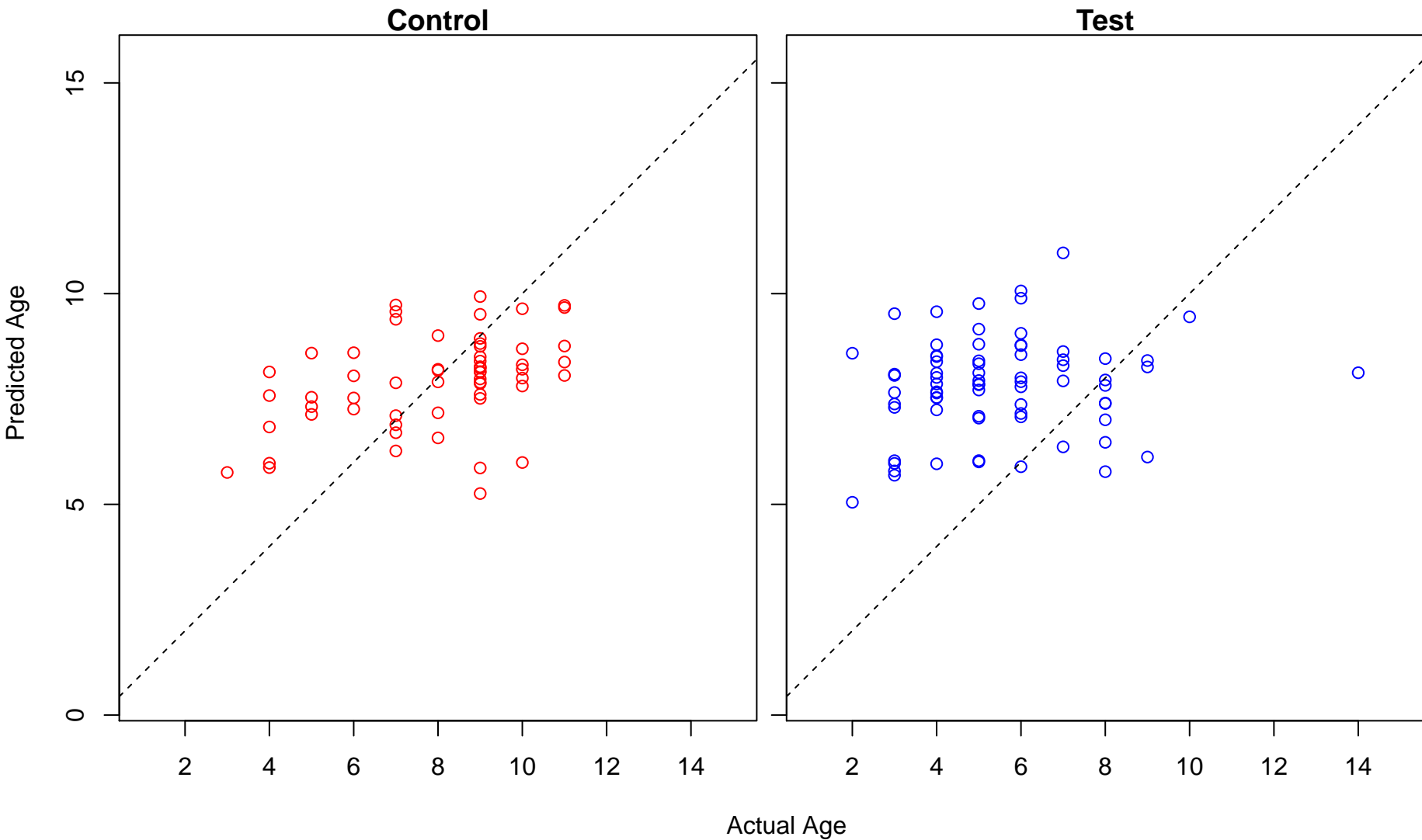
manganese ion transmembrane transport (Score: 0.713709)



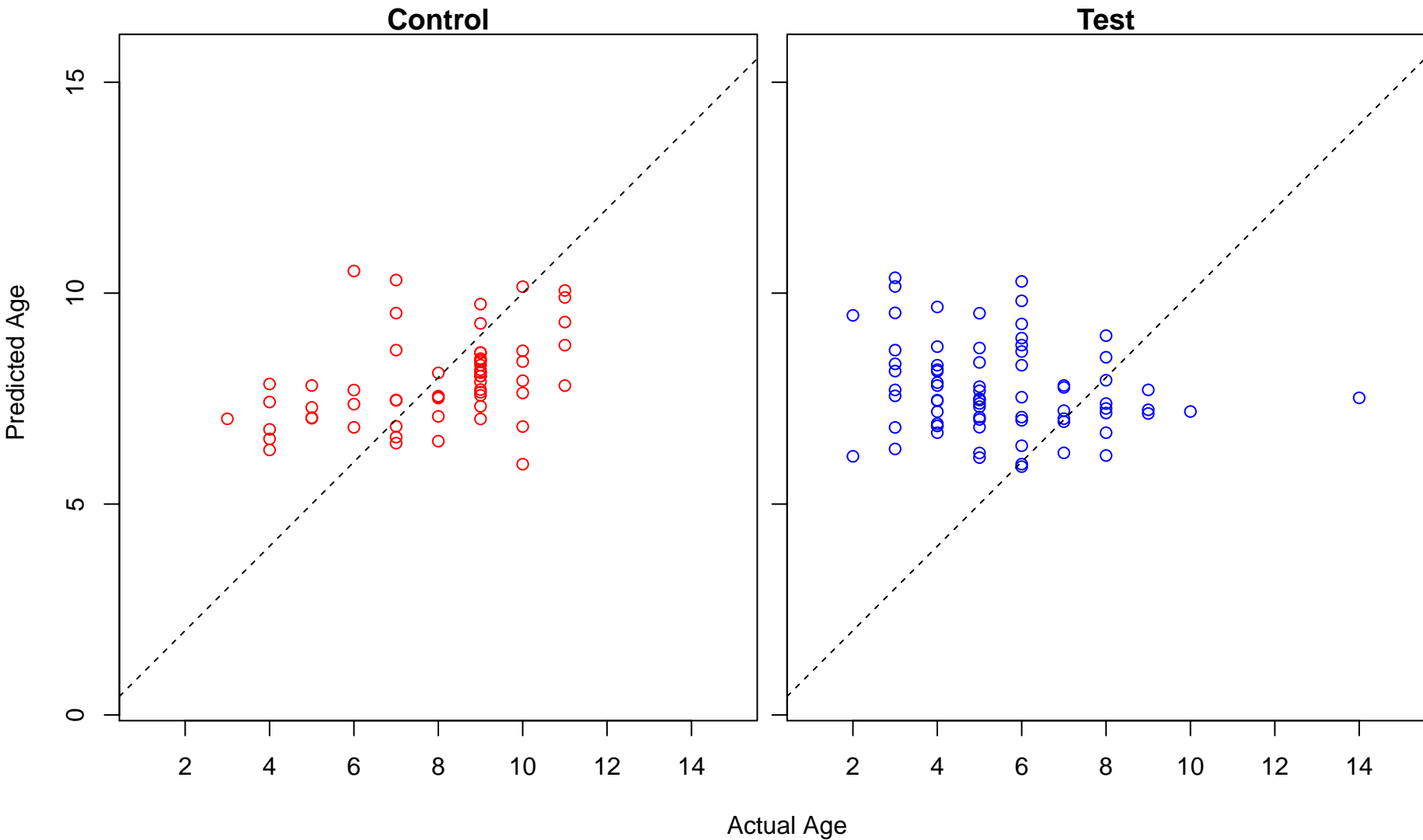
regulation of appetite (Score: 0.713079)



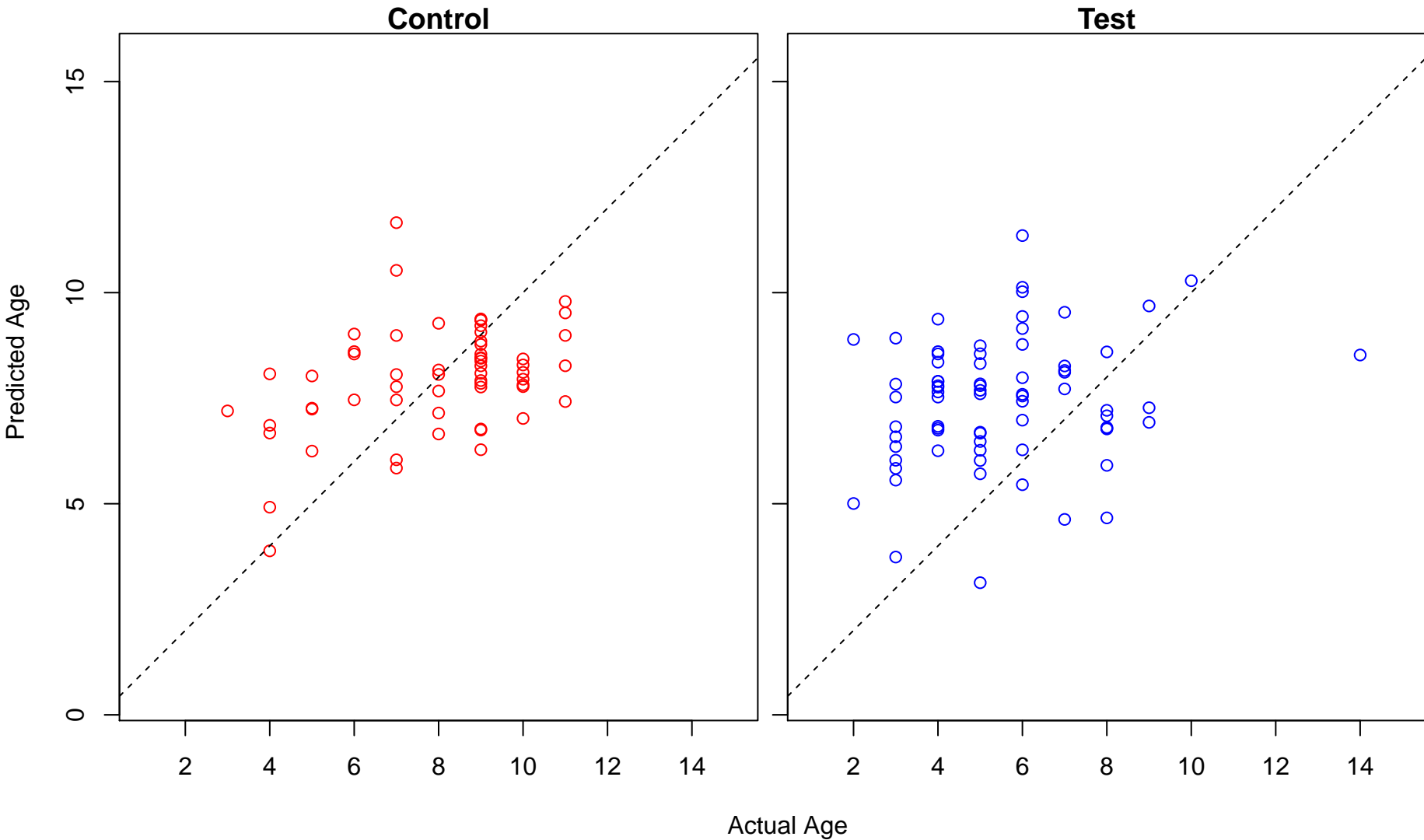
face morphogenesis (Score: 0.711100)



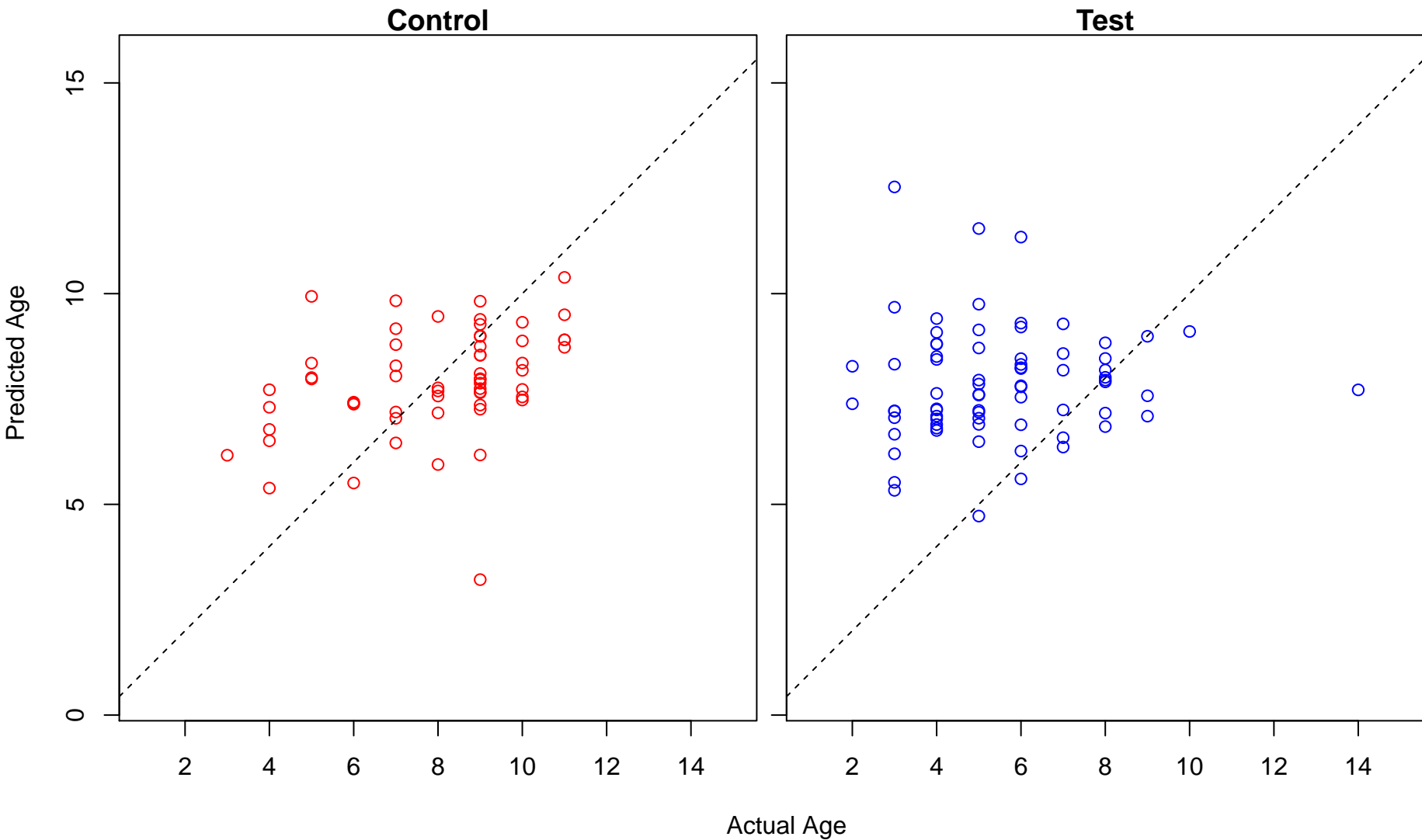
regulation of transcription from RNA polymerase I promoter (Score: 0.710419)



positive regulation of neutrophil chemotaxis (Score: 0.707827)

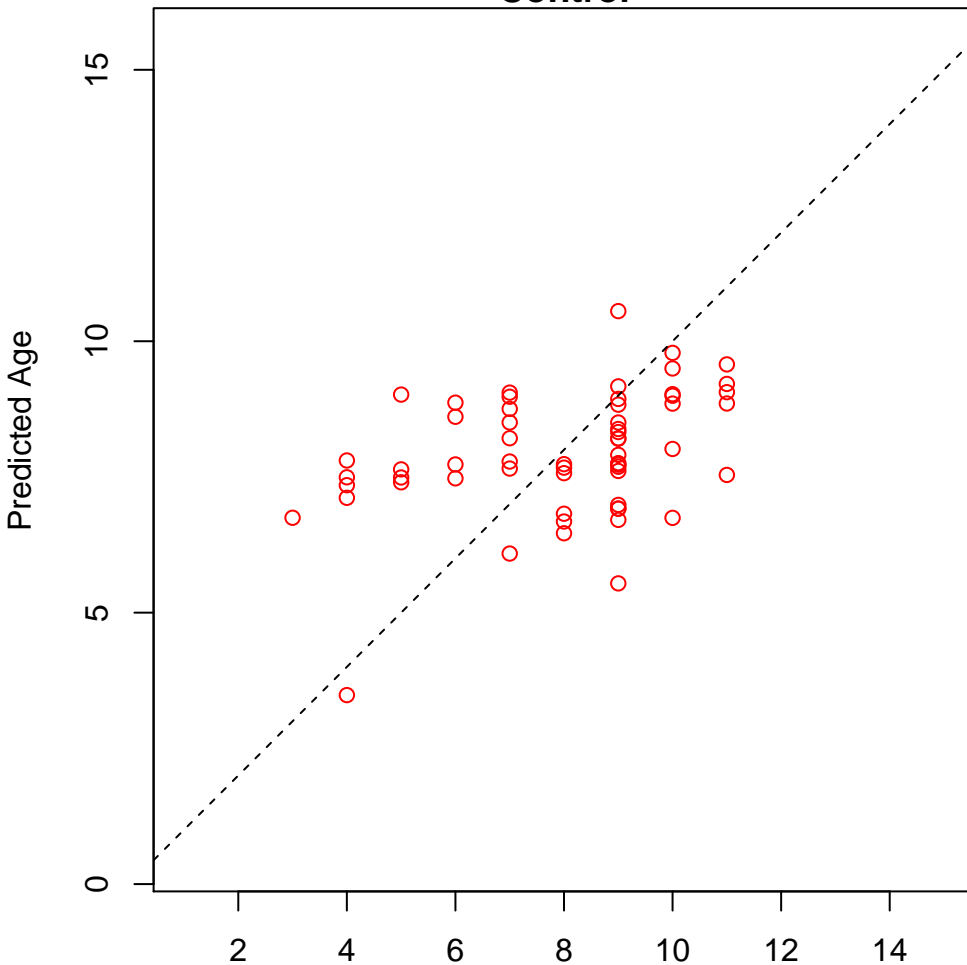


phosphatidylcholine catabolic process (Score: 0.707082)

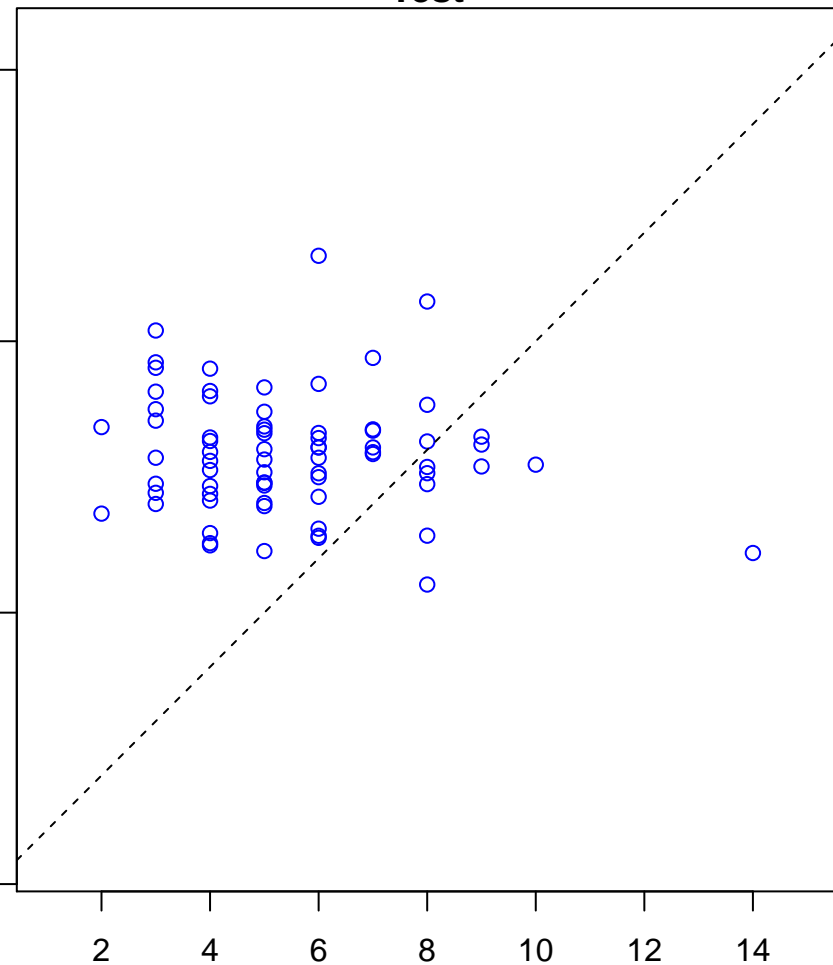


cerebellar molecular layer development (Score: 0.706780)

Control

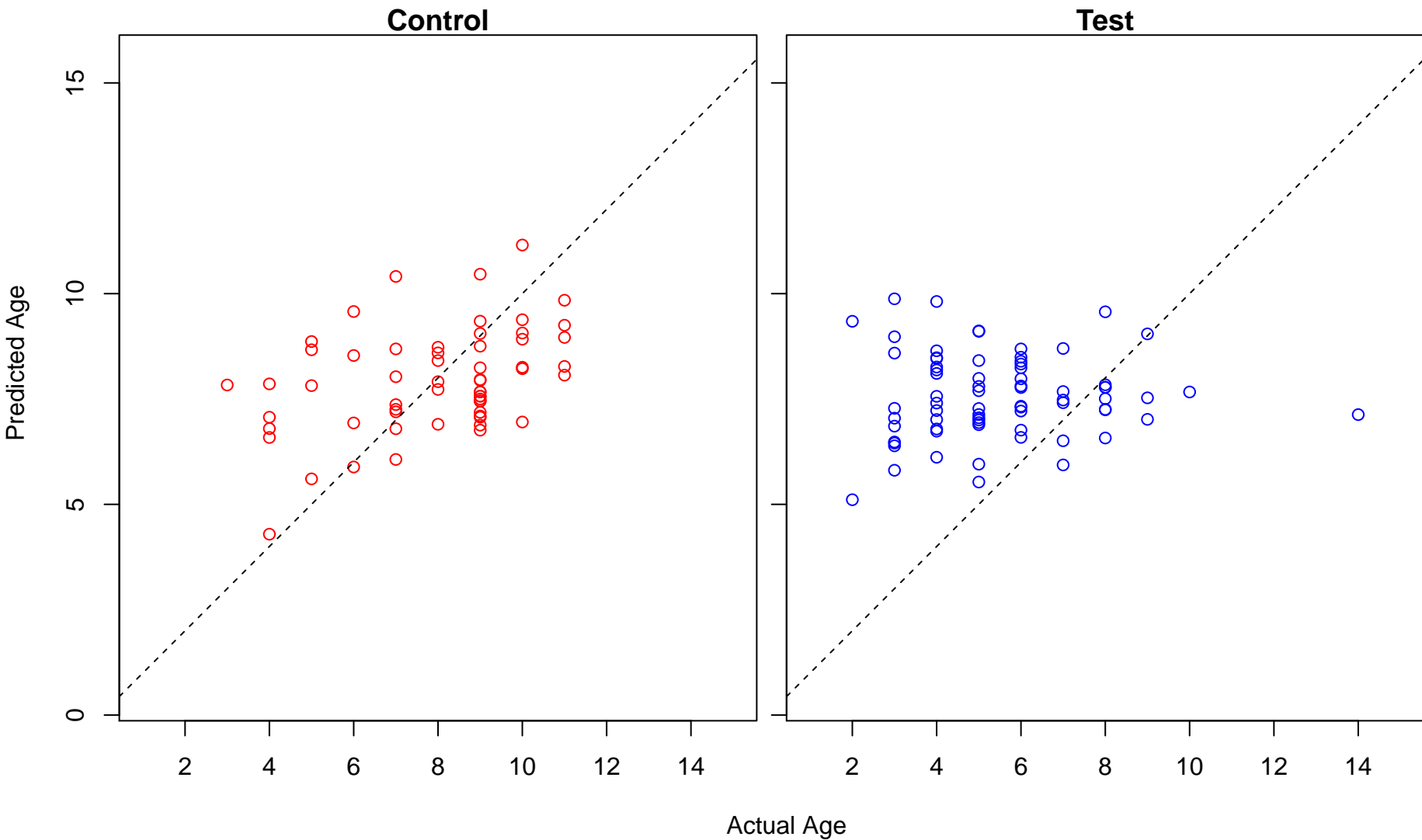


Test

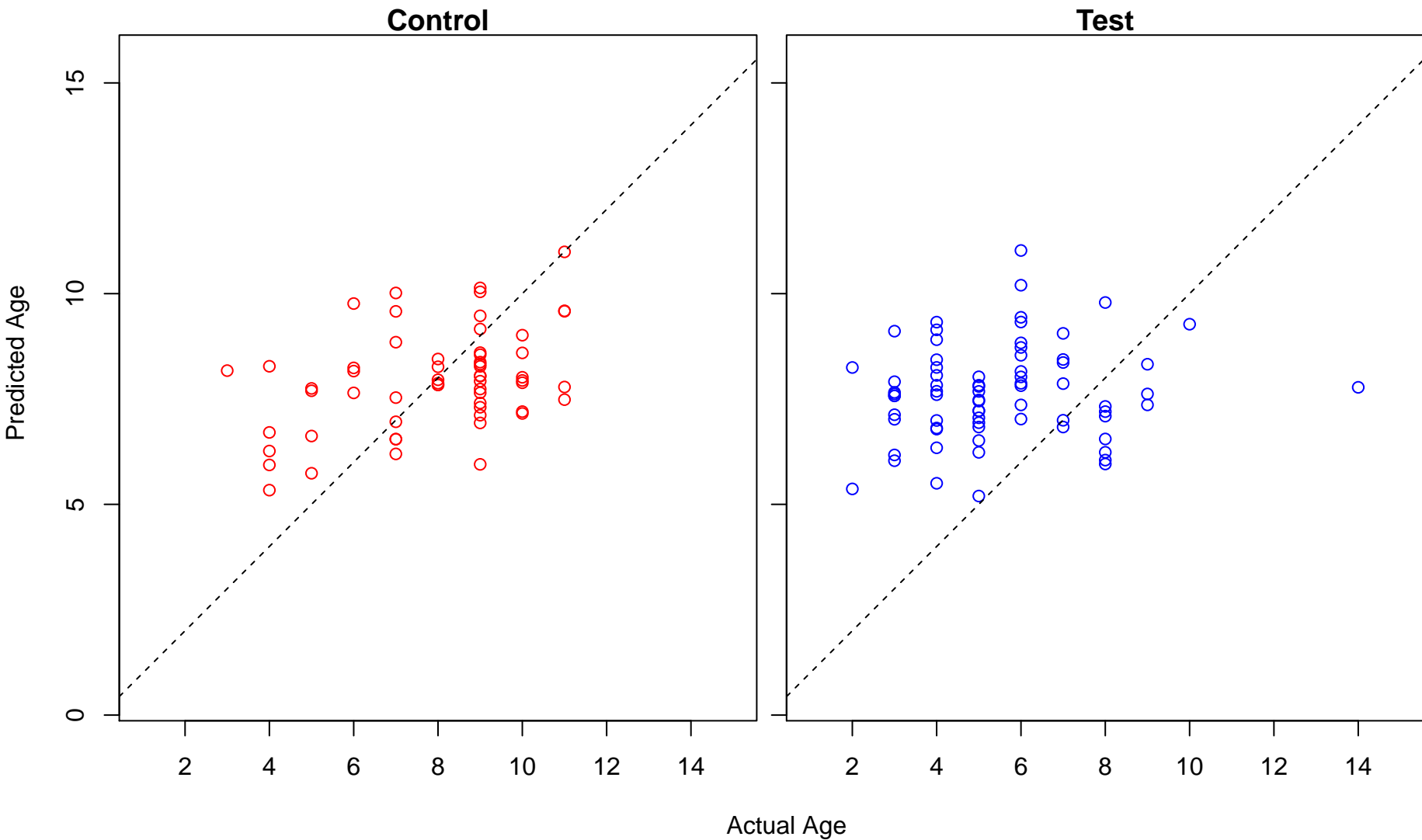


Actual Age

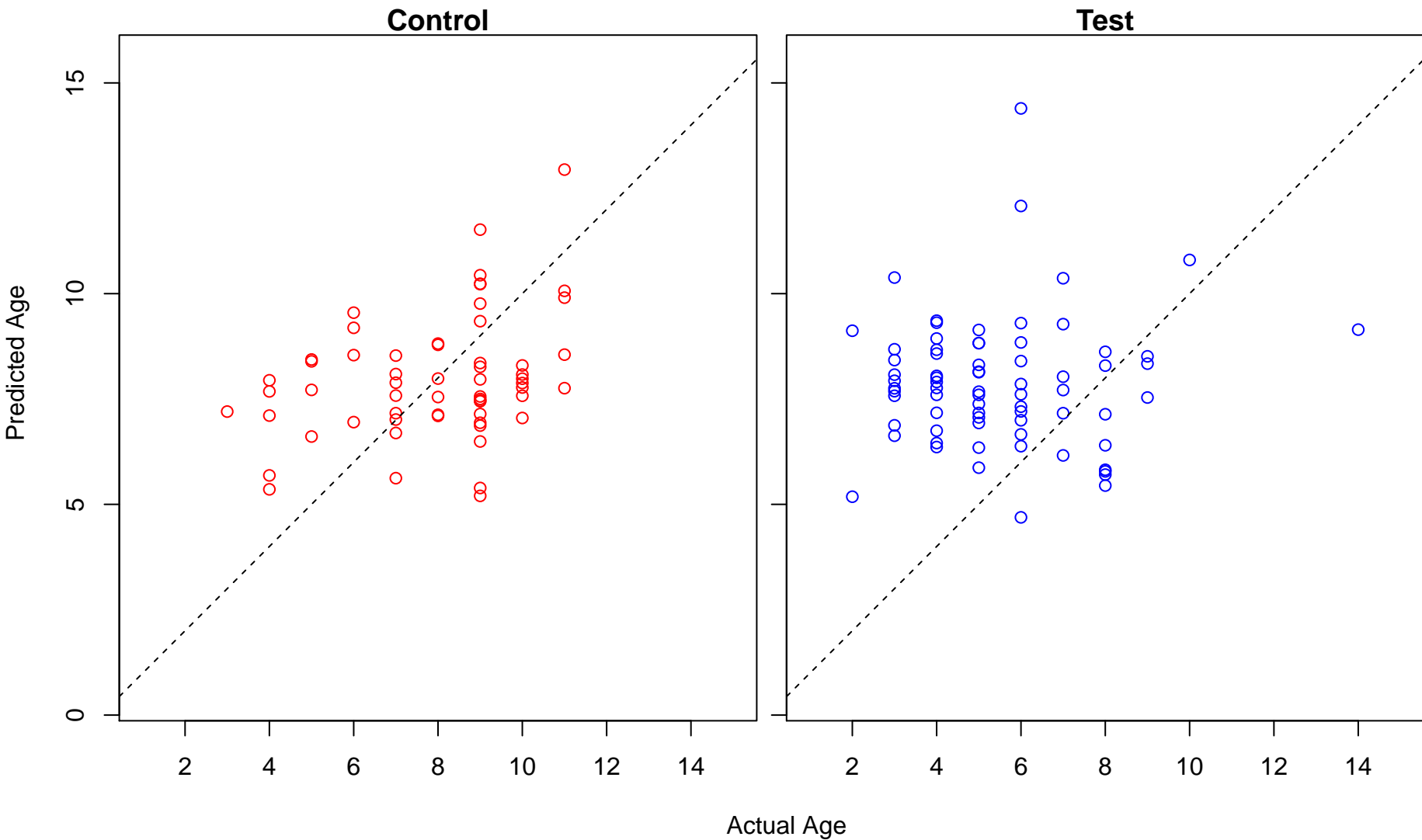
amino acid import (Score: 0.706700)



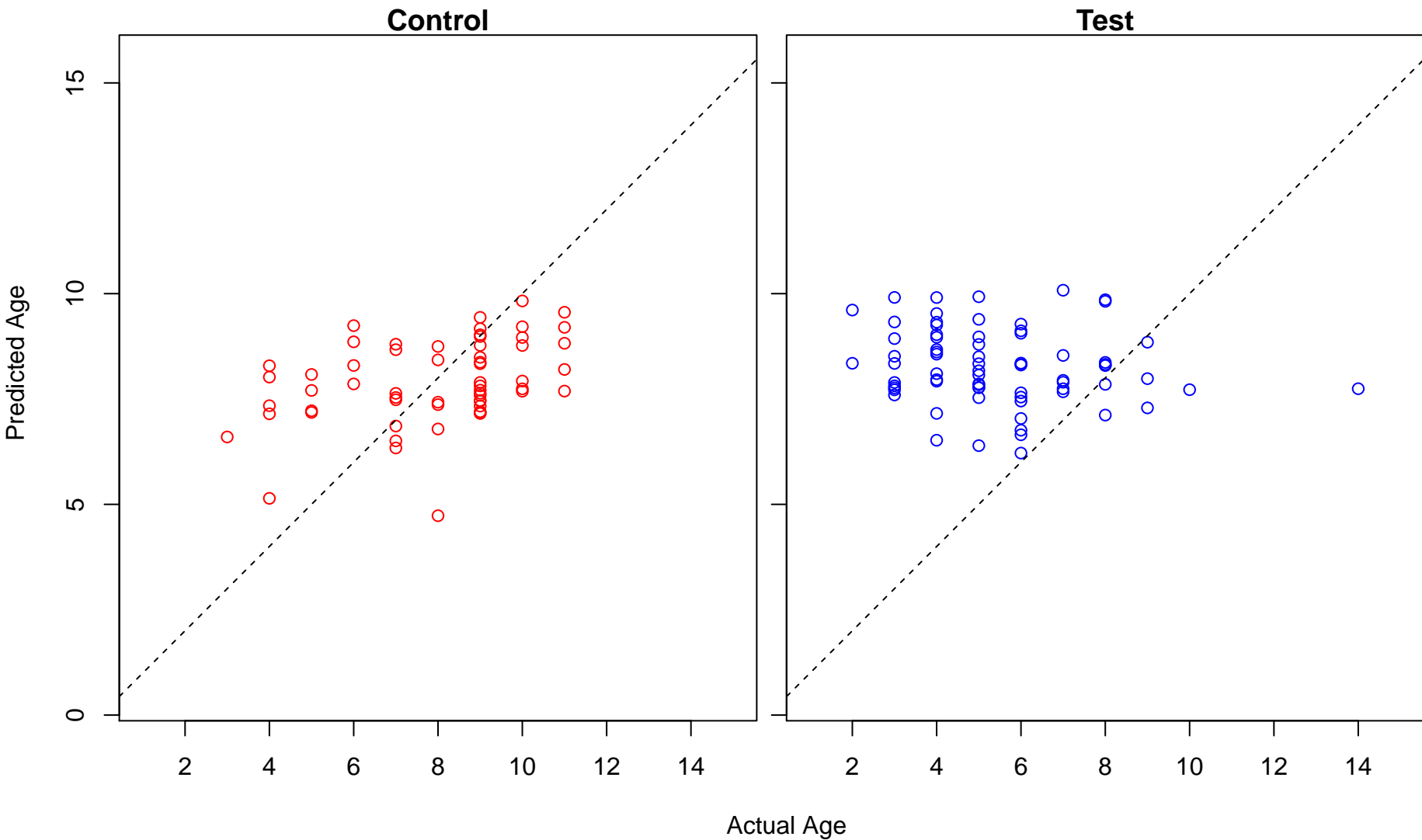
auditory receptor cell morphogenesis (Score: 0.706381)



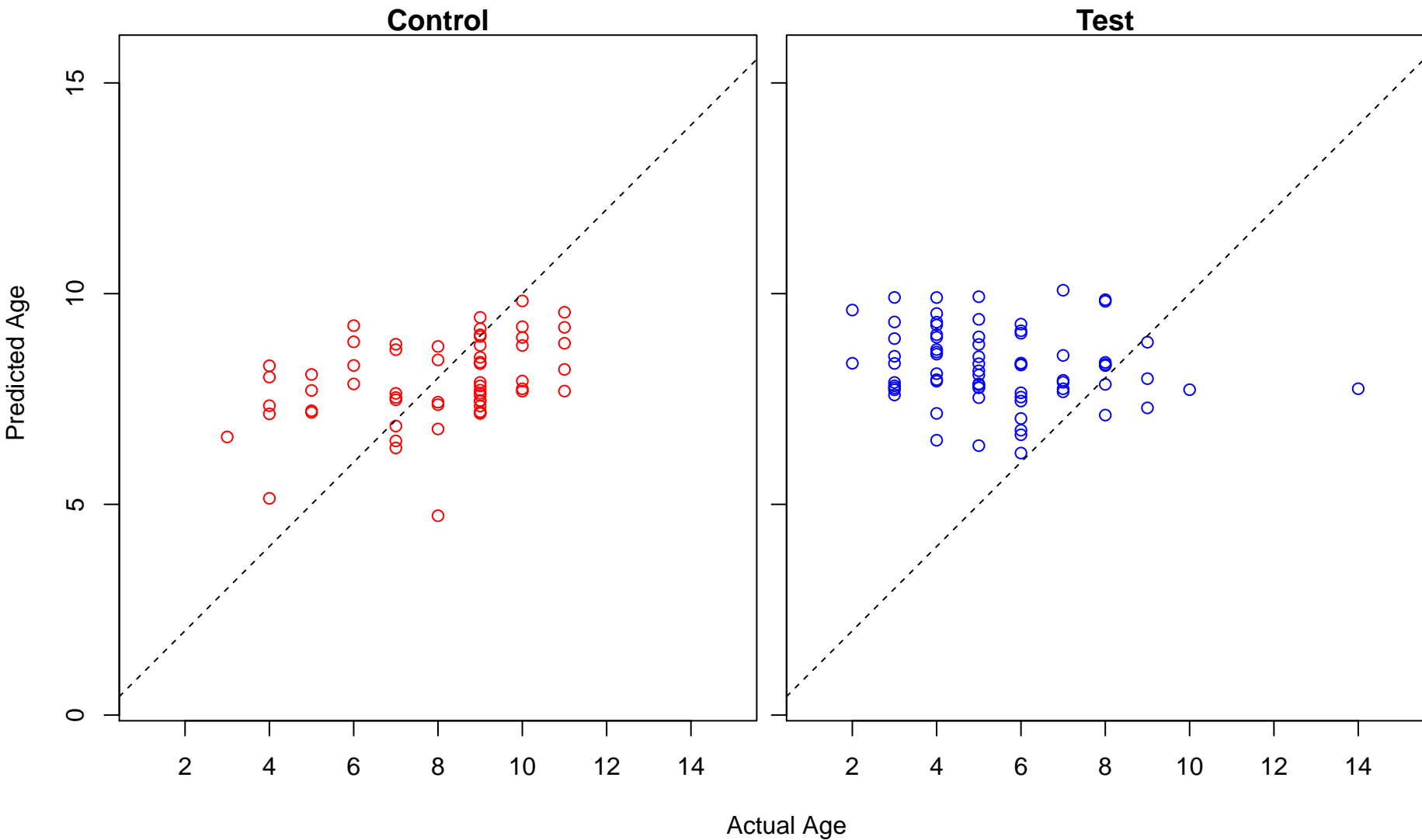
regulation of interleukin-6 production (Score: 0.706080)



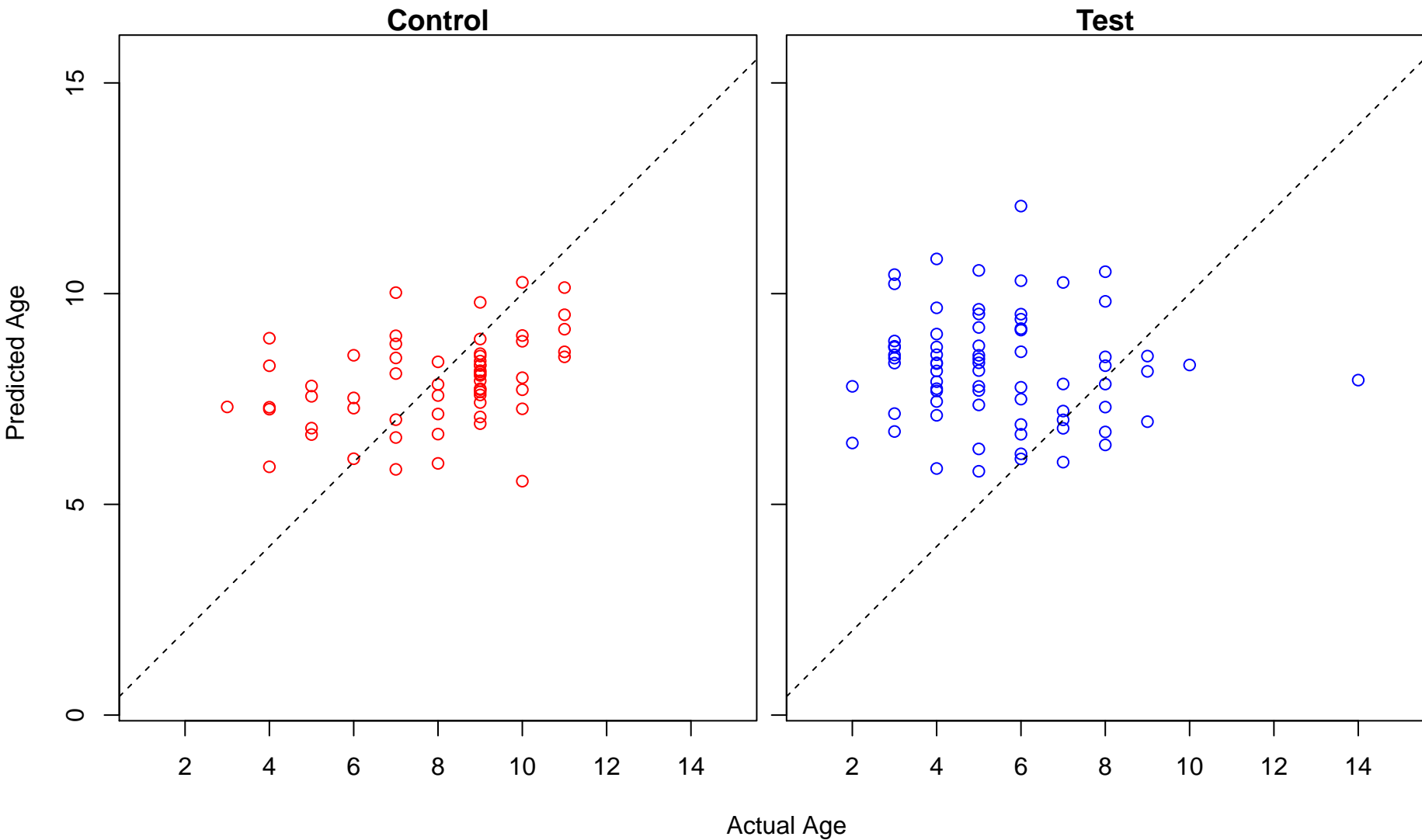
hemoglobin metabolic process (Score: 0.705504)



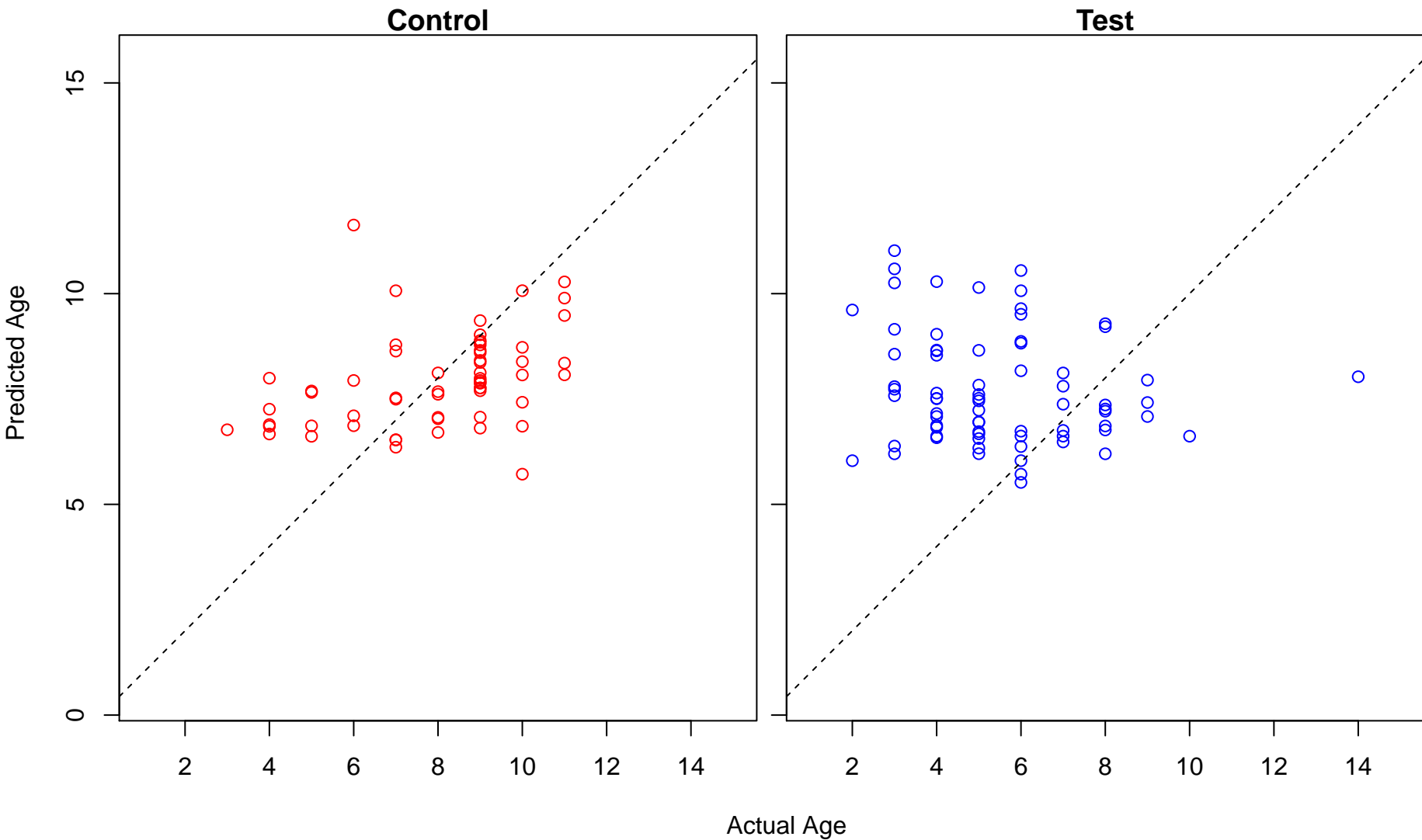
hemoglobin biosynthetic process (Score: 0.705504)



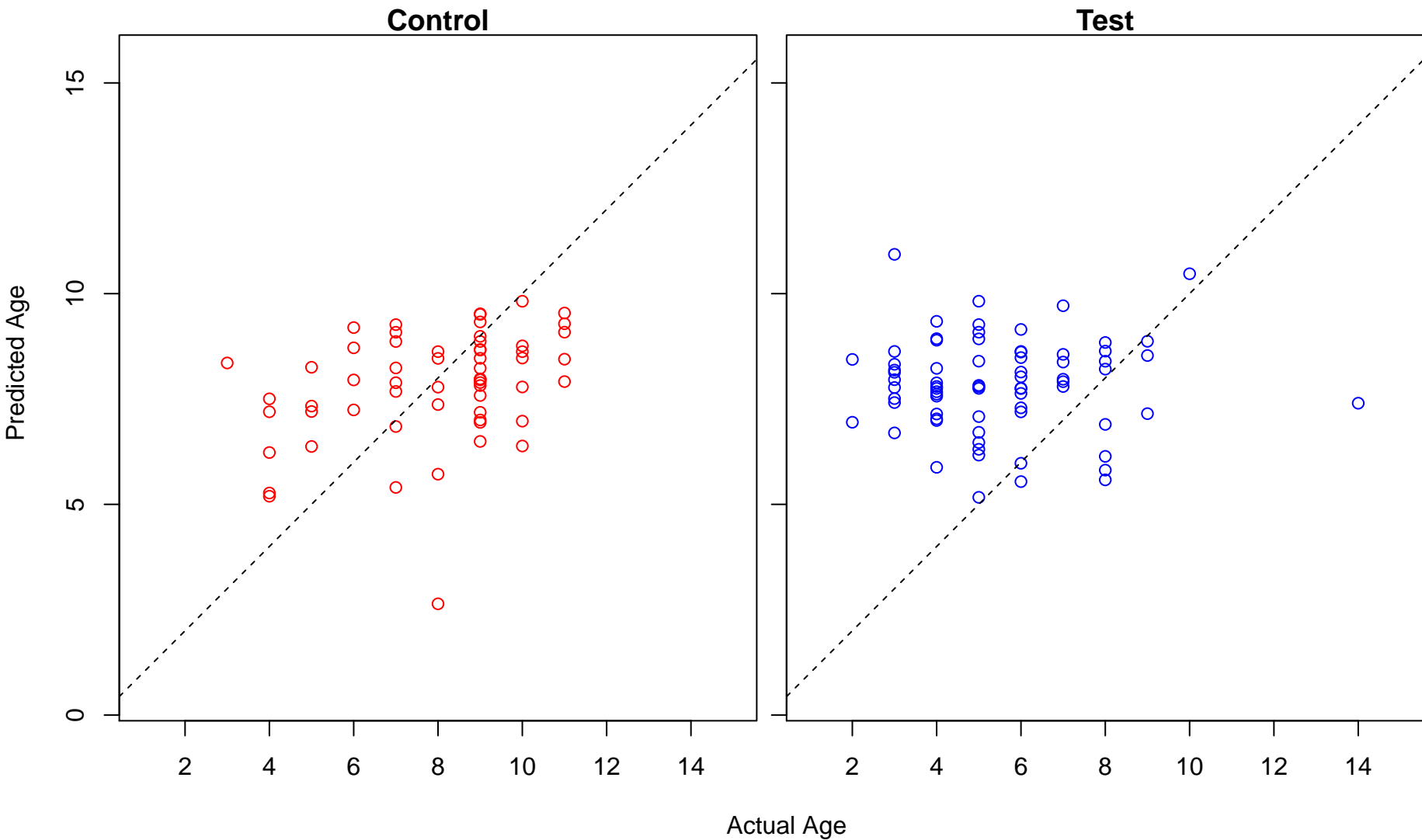
protein insertion into membrane (Score: 0.704601)



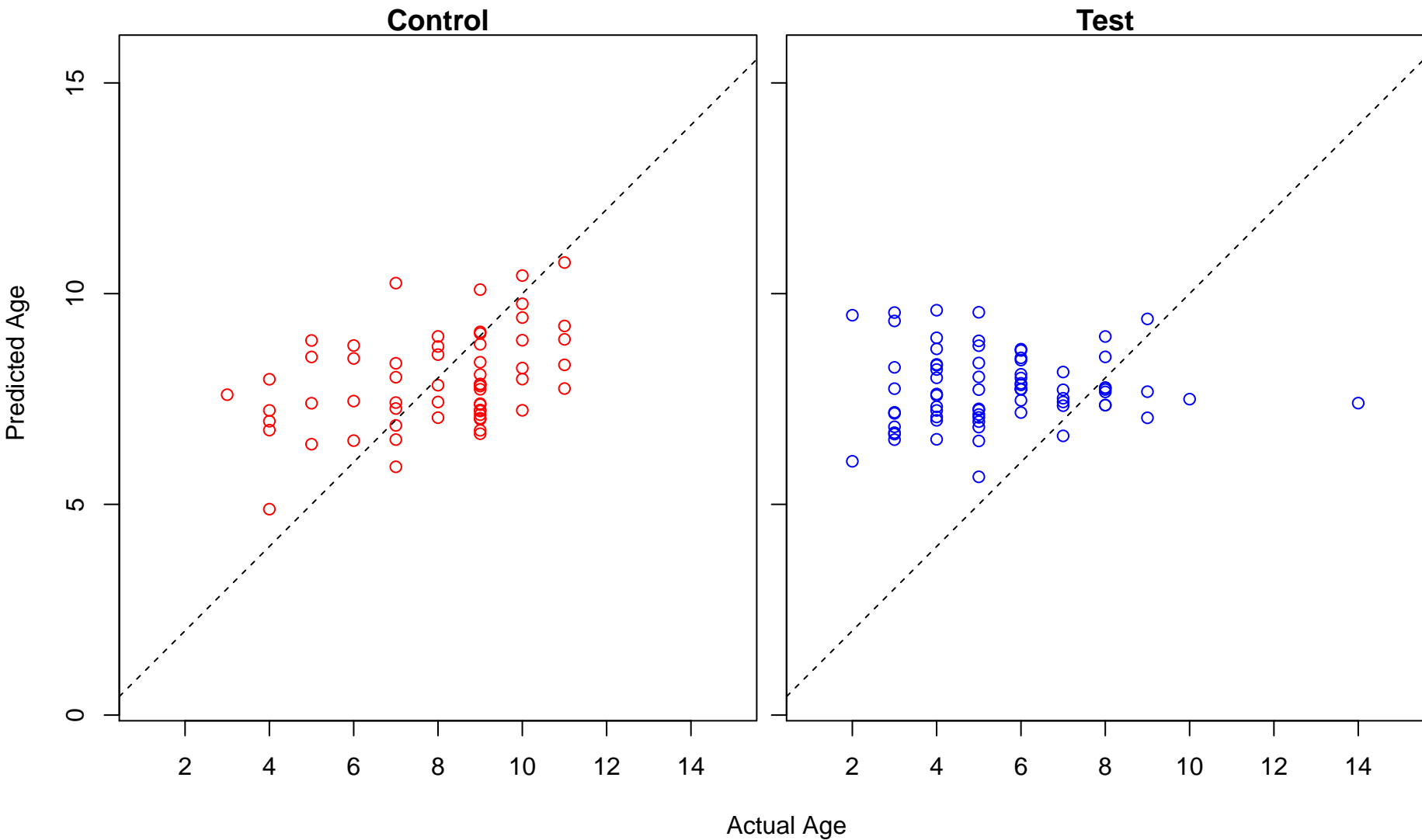
dopamine receptor signaling pathway (Score: 0.703767)



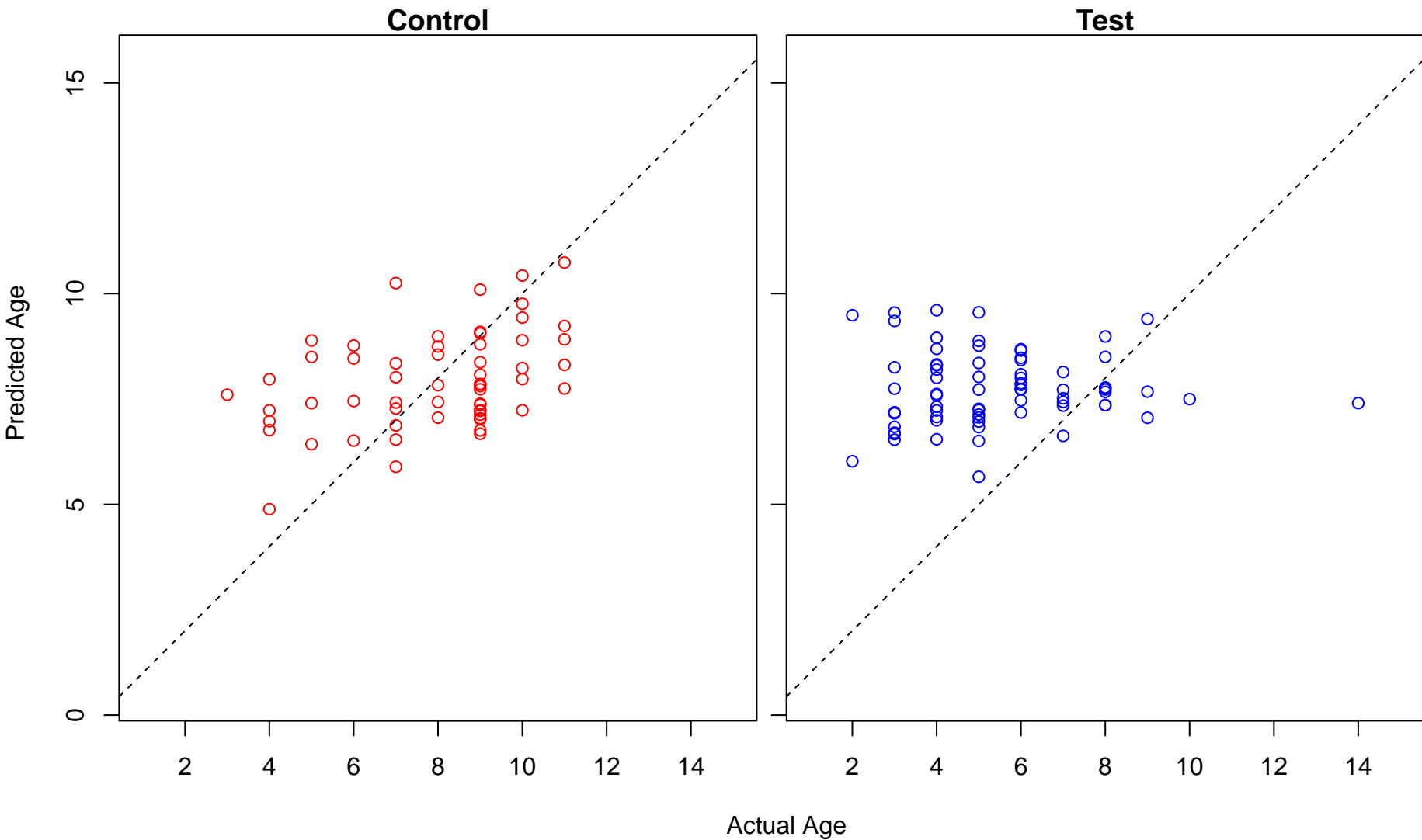
positive regulation of mesenchymal stem cell differentiation (Score: 0.703610)



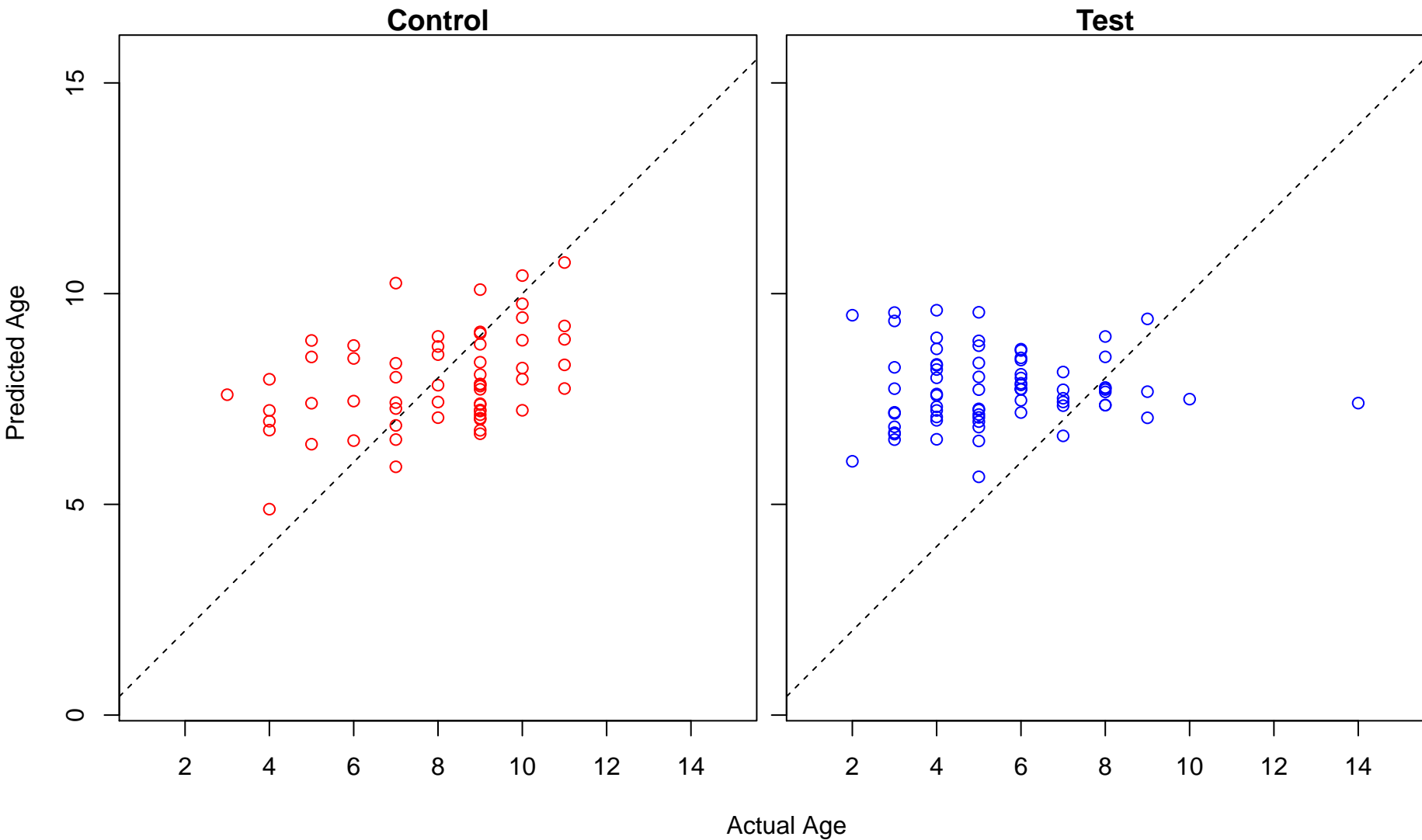
cellular cadmium ion homeostasis (Score: 0.703065)



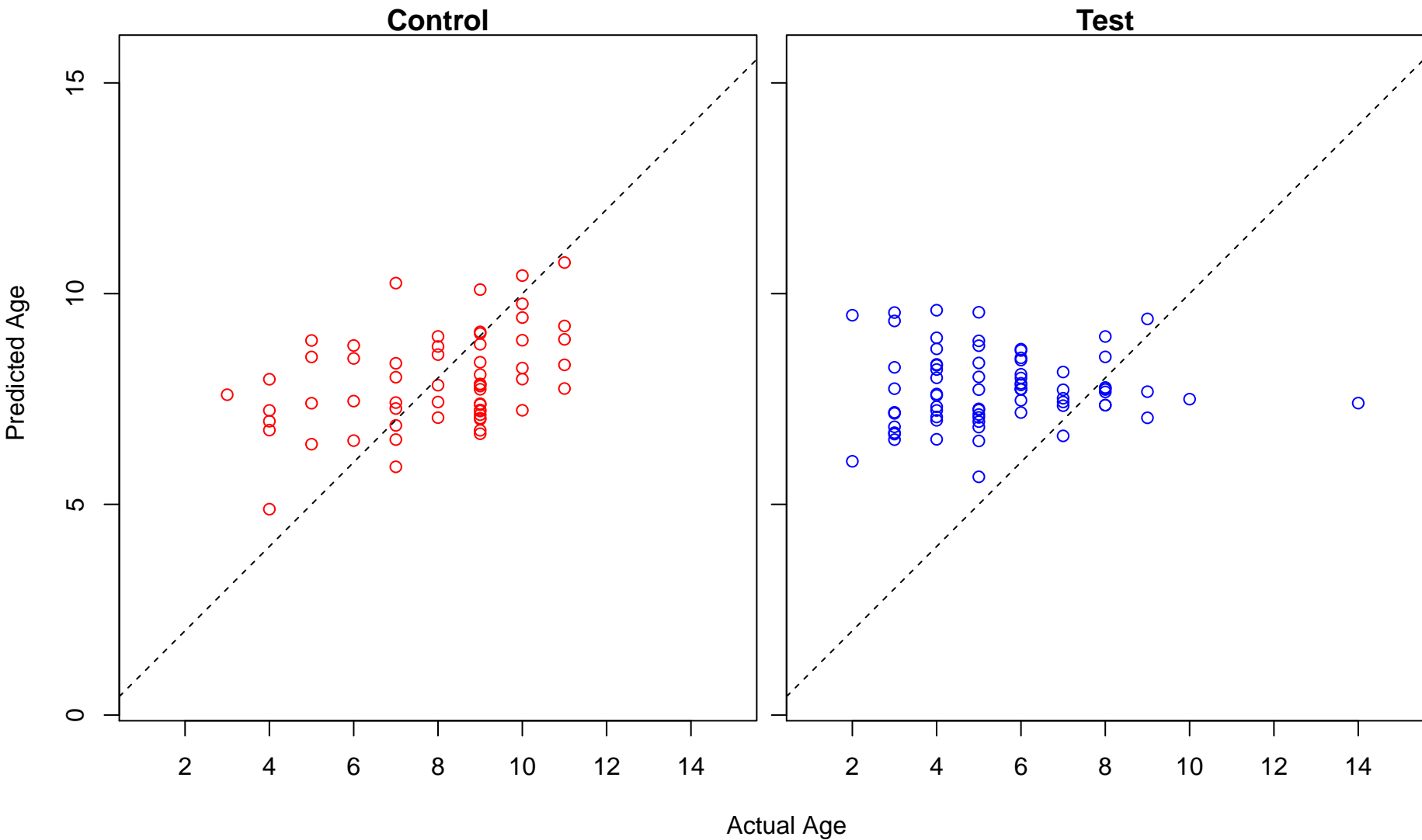
nitrite transport (Score: 0.703065)



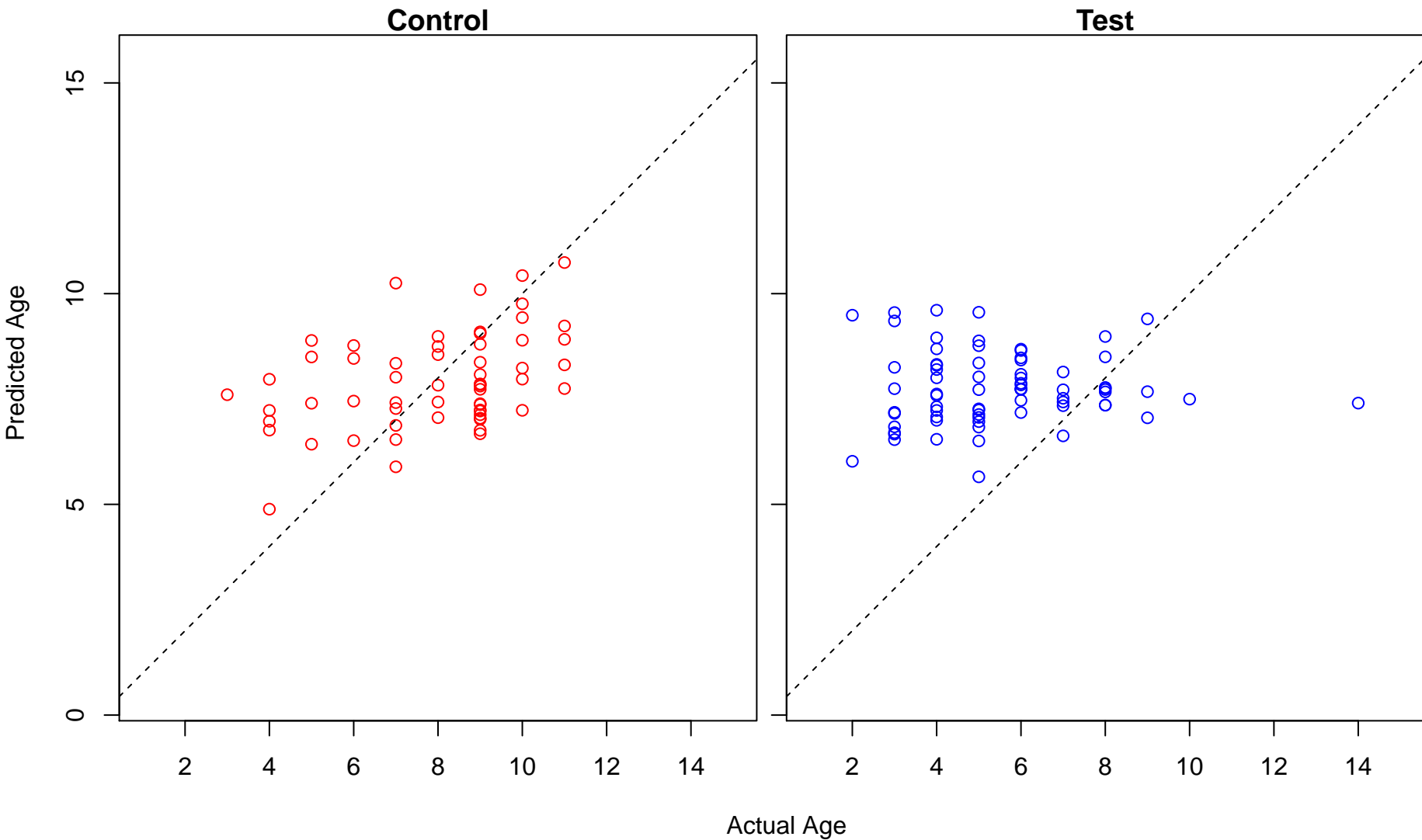
interleukin-3 production (Score: 0.703065)



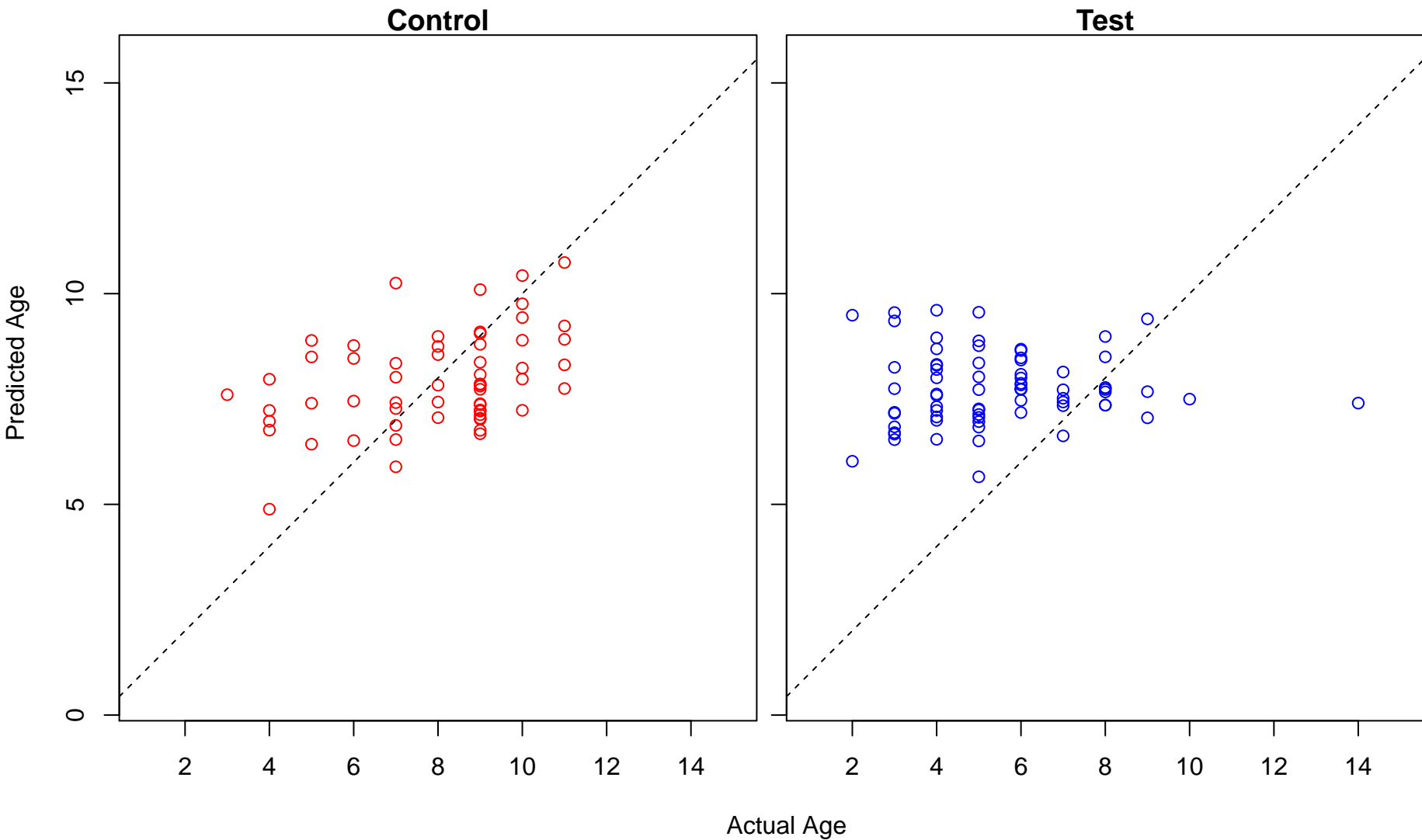
L-arginine import (Score: 0.703065)



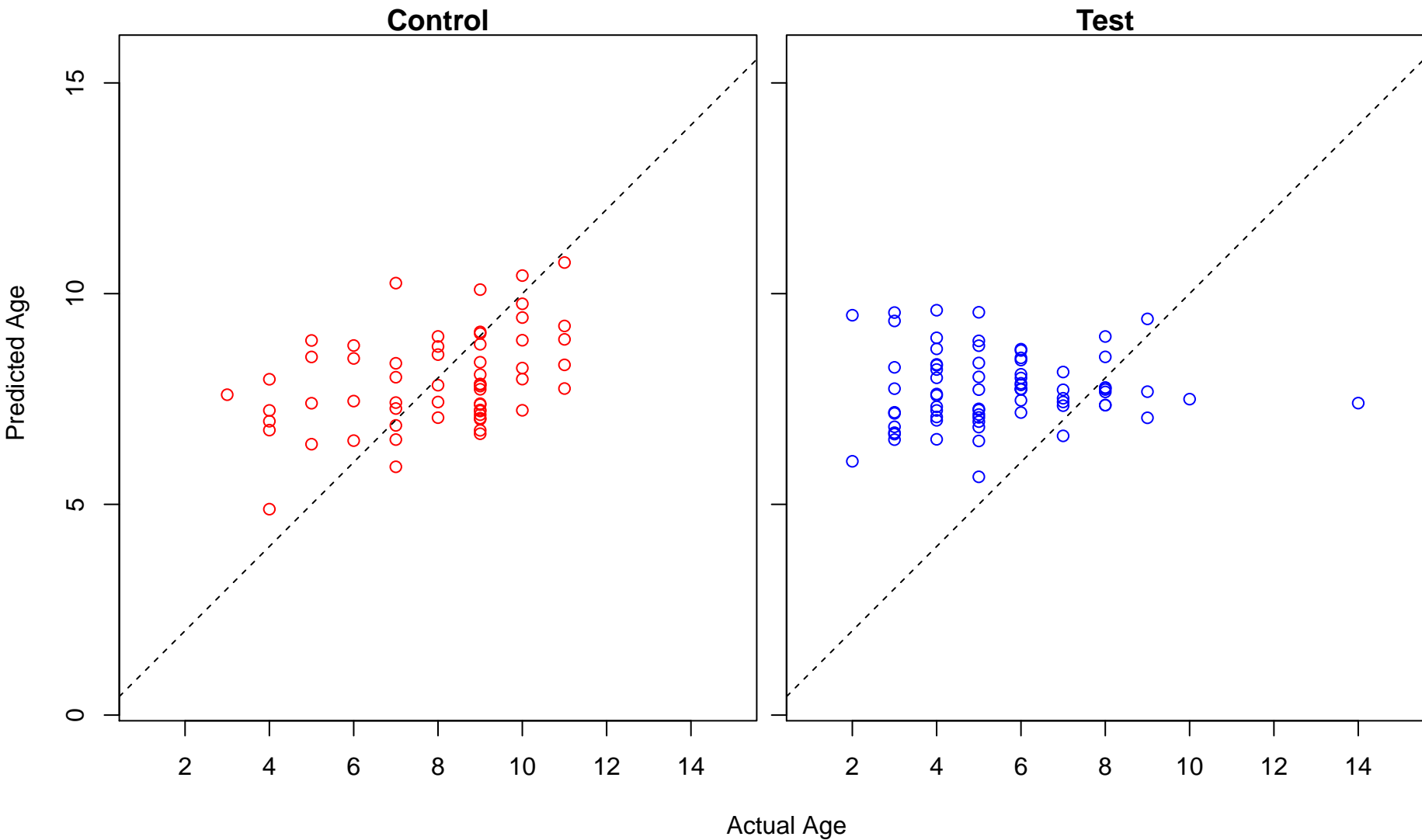
MHC class II biosynthetic process (Score: 0.703065)



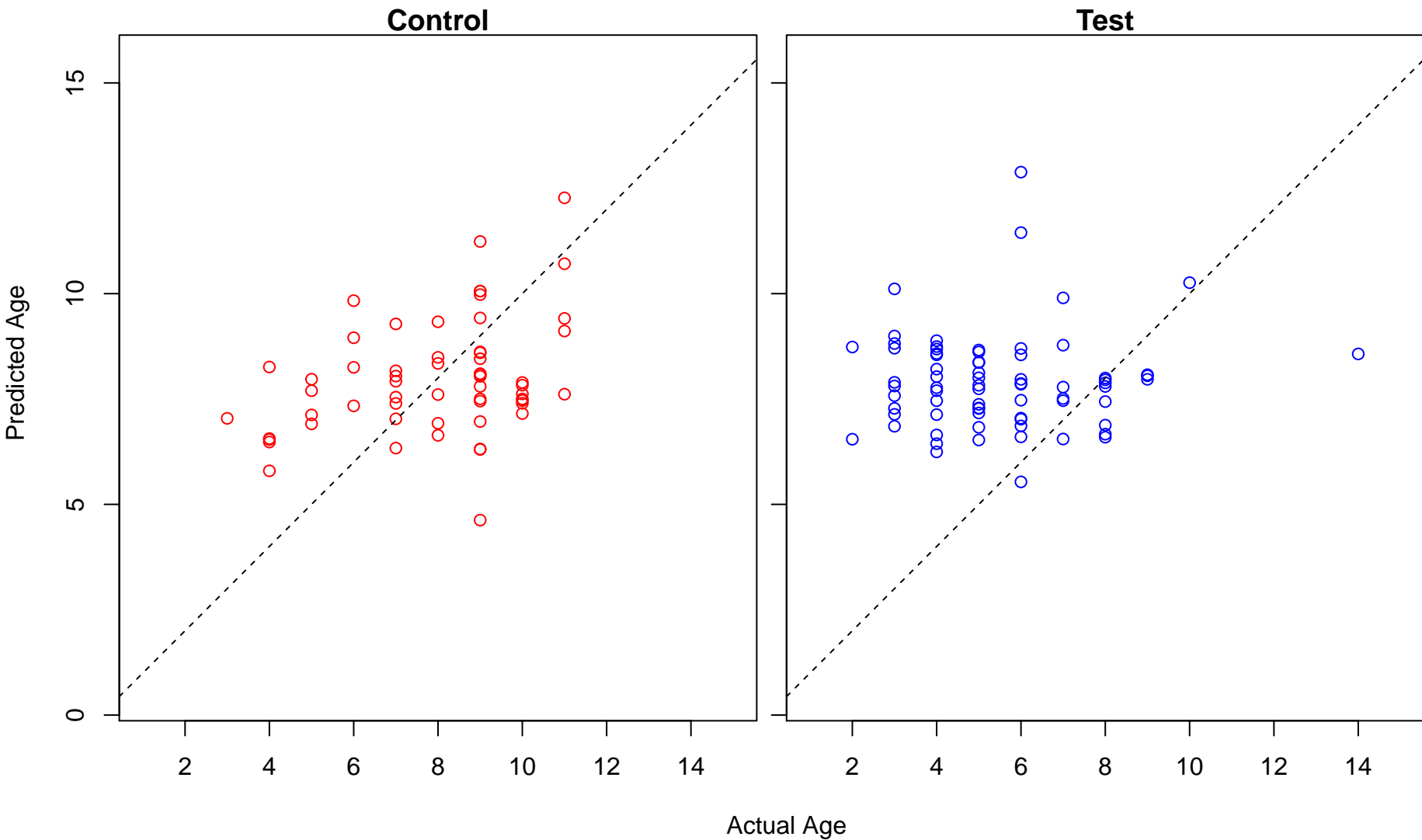
arginine import (Score: 0.703065)



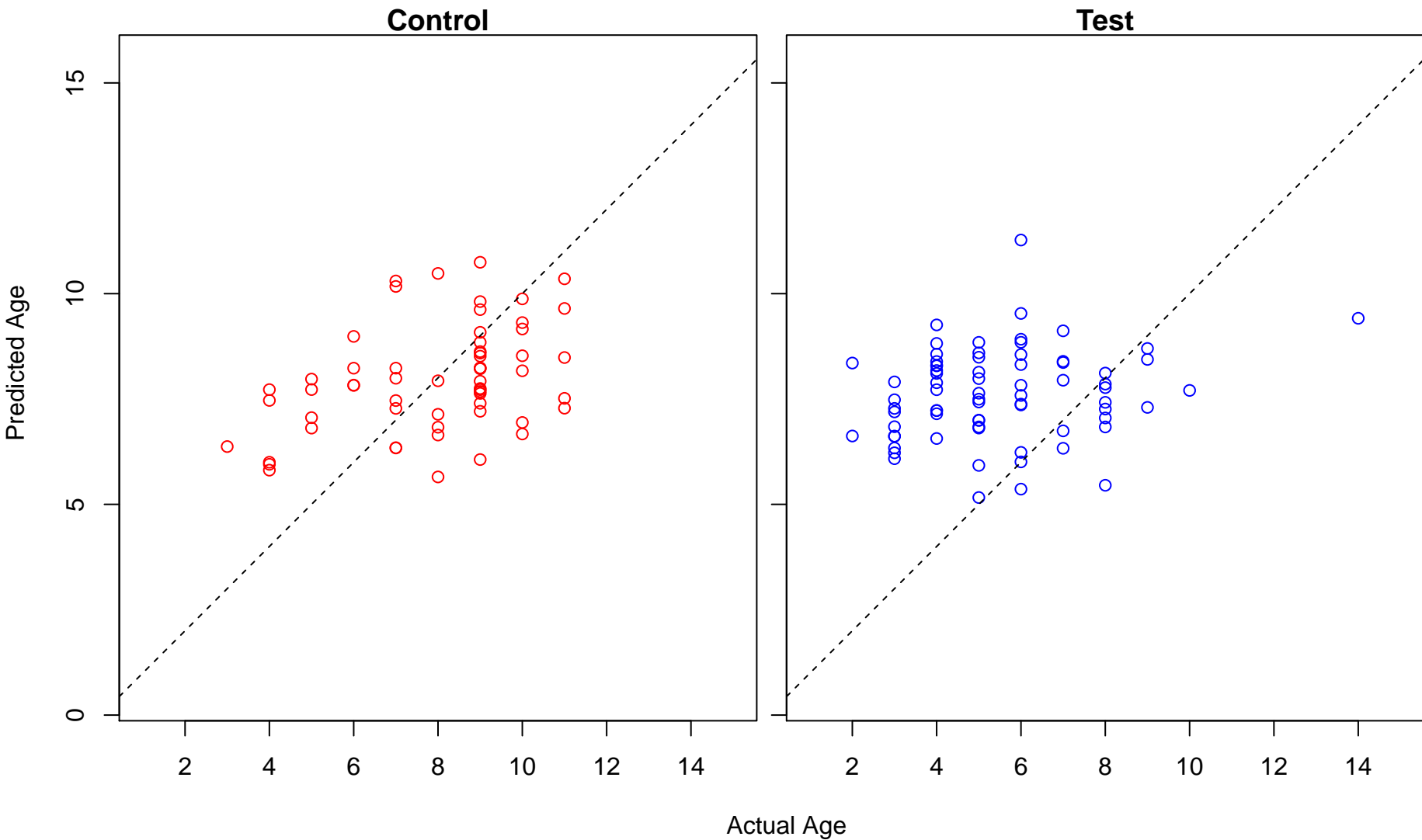
L-arginine transport (Score: 0.703065)



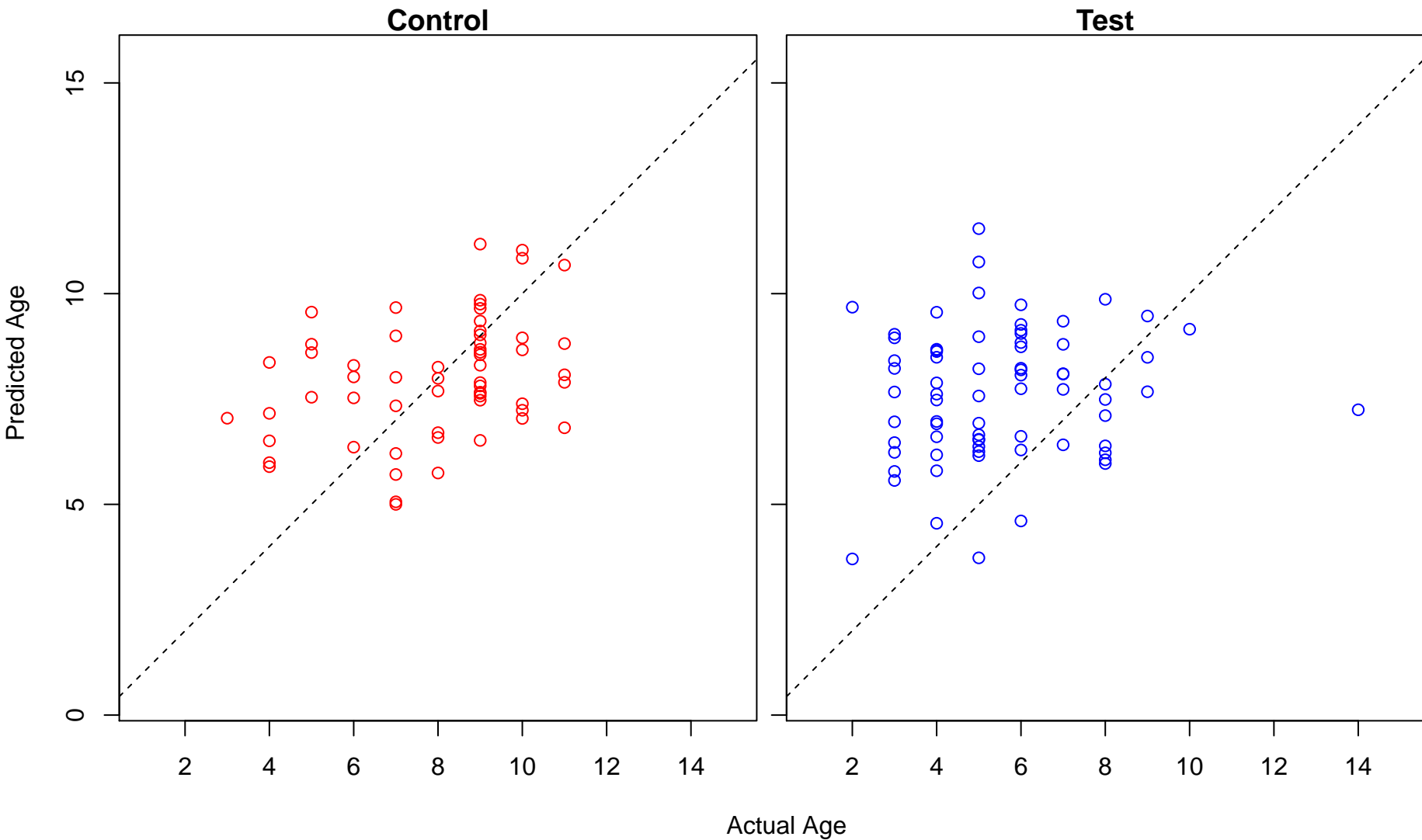
positive regulation of interleukin-6 production (Score: 0.701296)



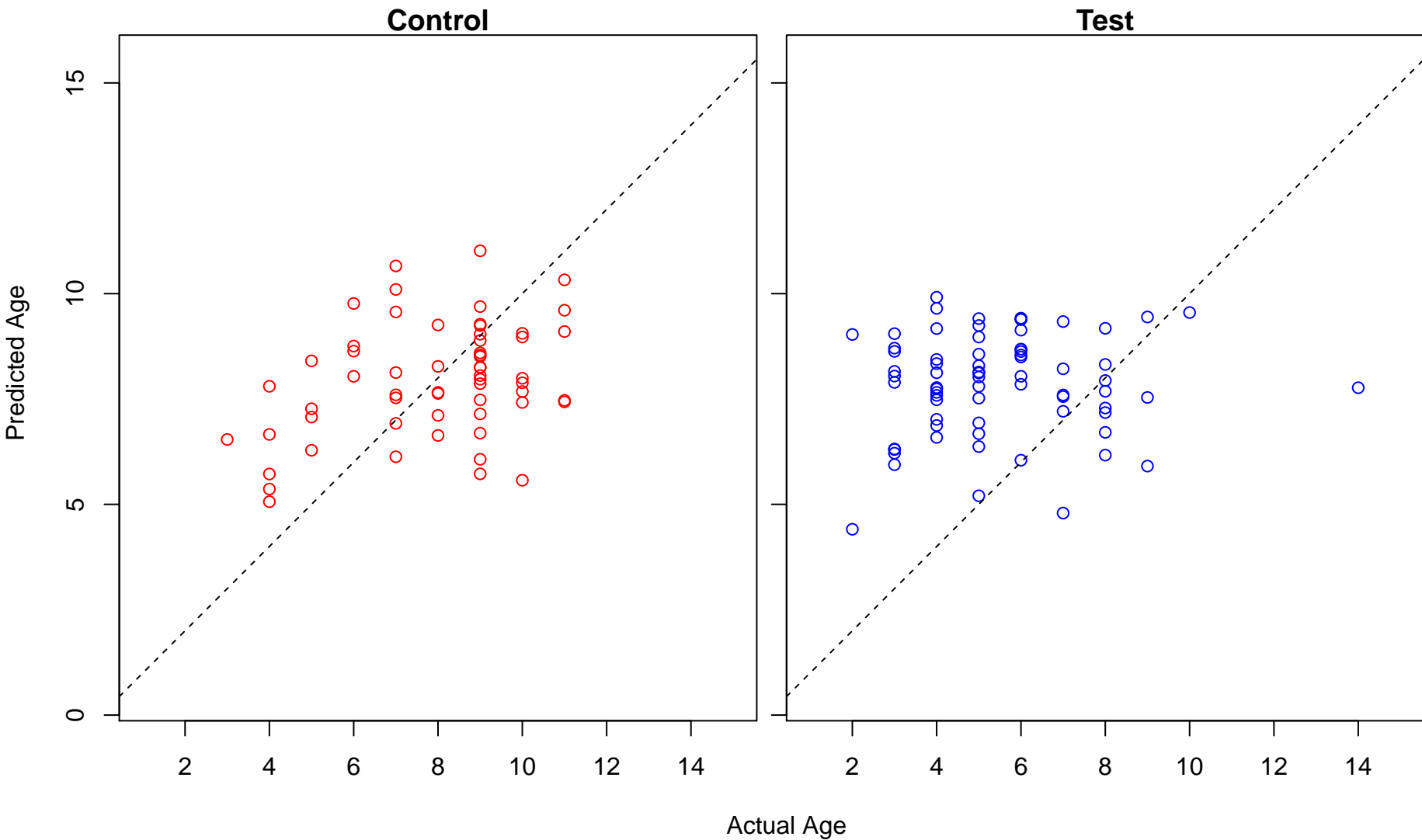
cell chemotaxis (Score: 0.700985)



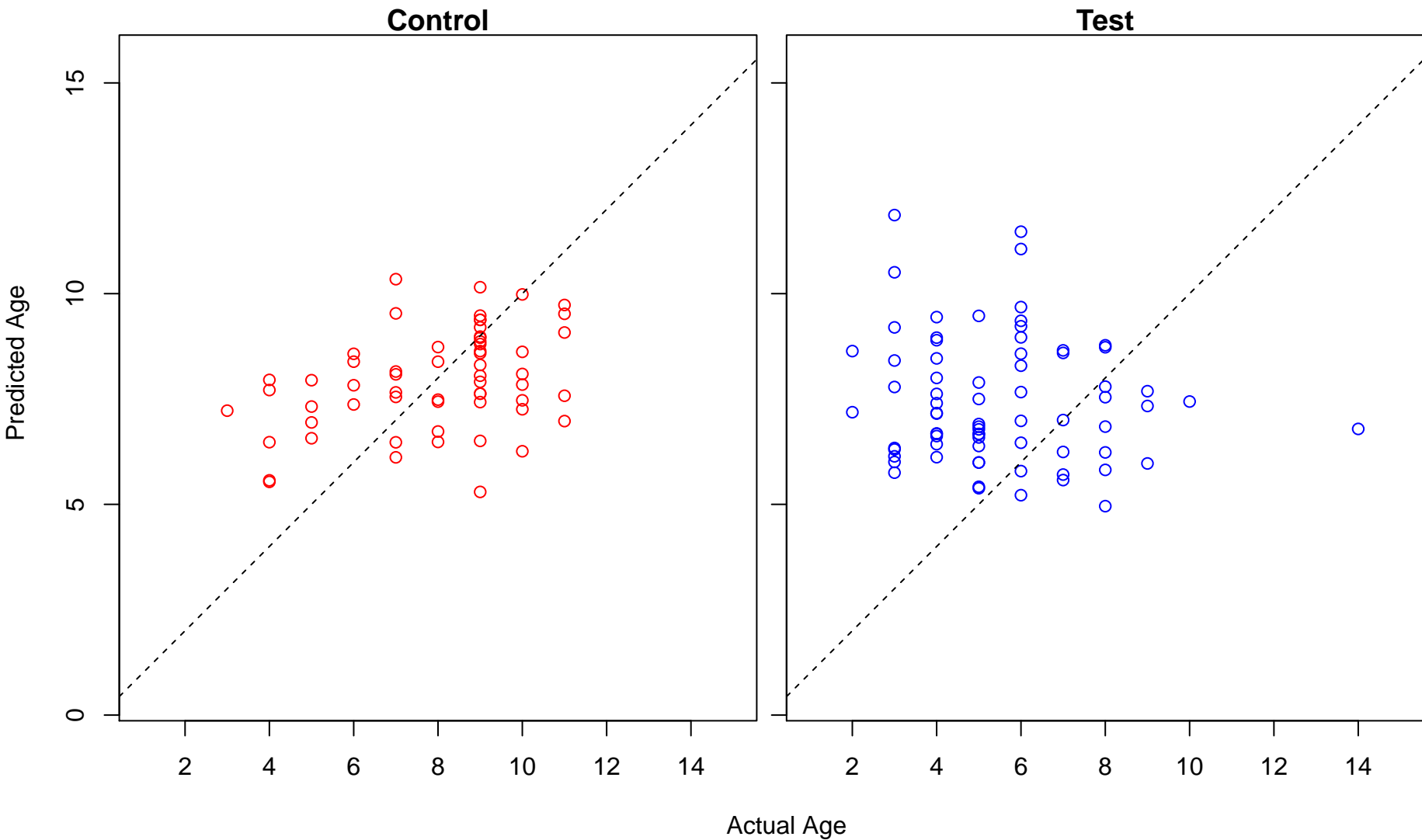
proteoglycan biosynthetic process (Score: 0.700688)



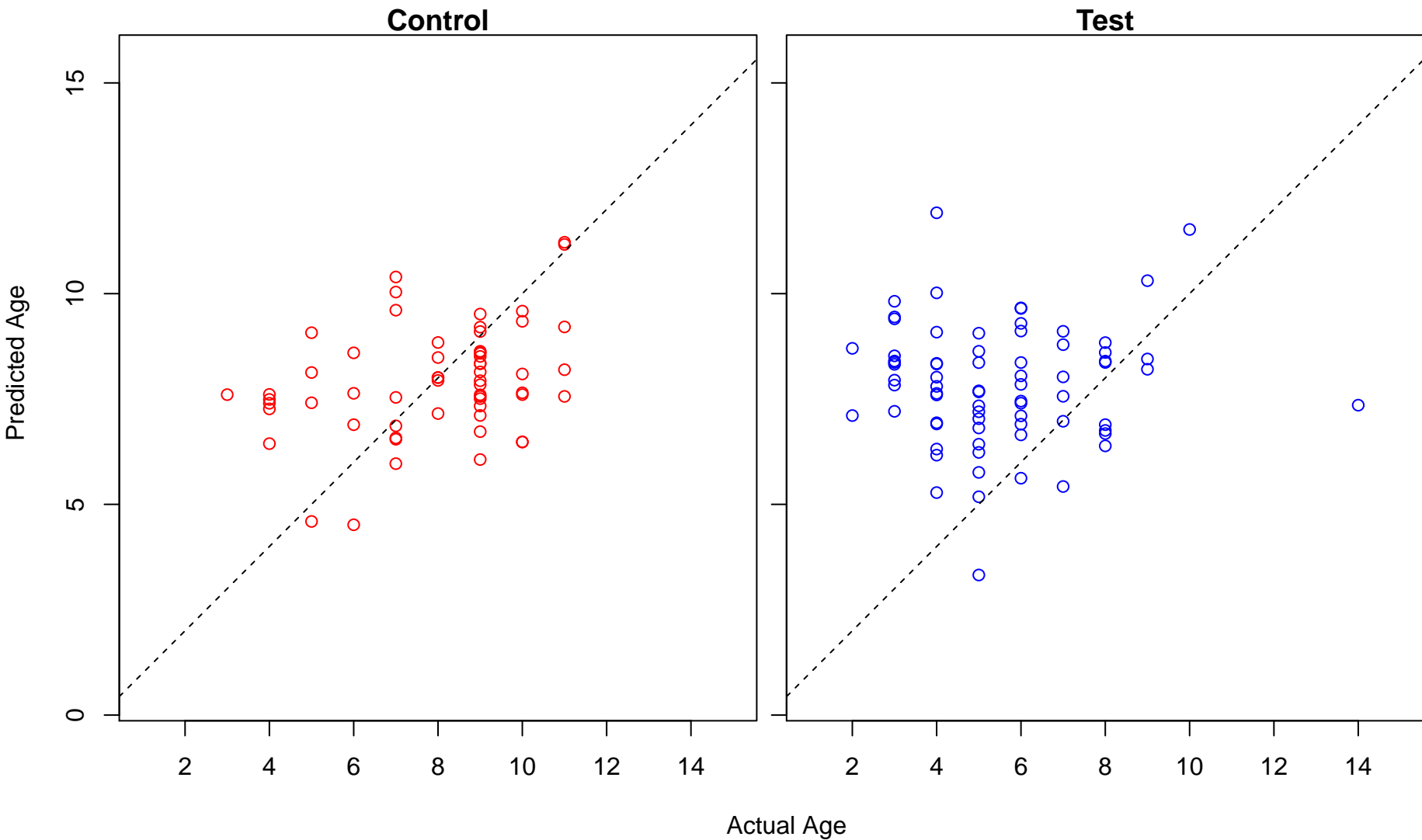
positive regulation of actin filament bundle assembly (Score: 0.698920)



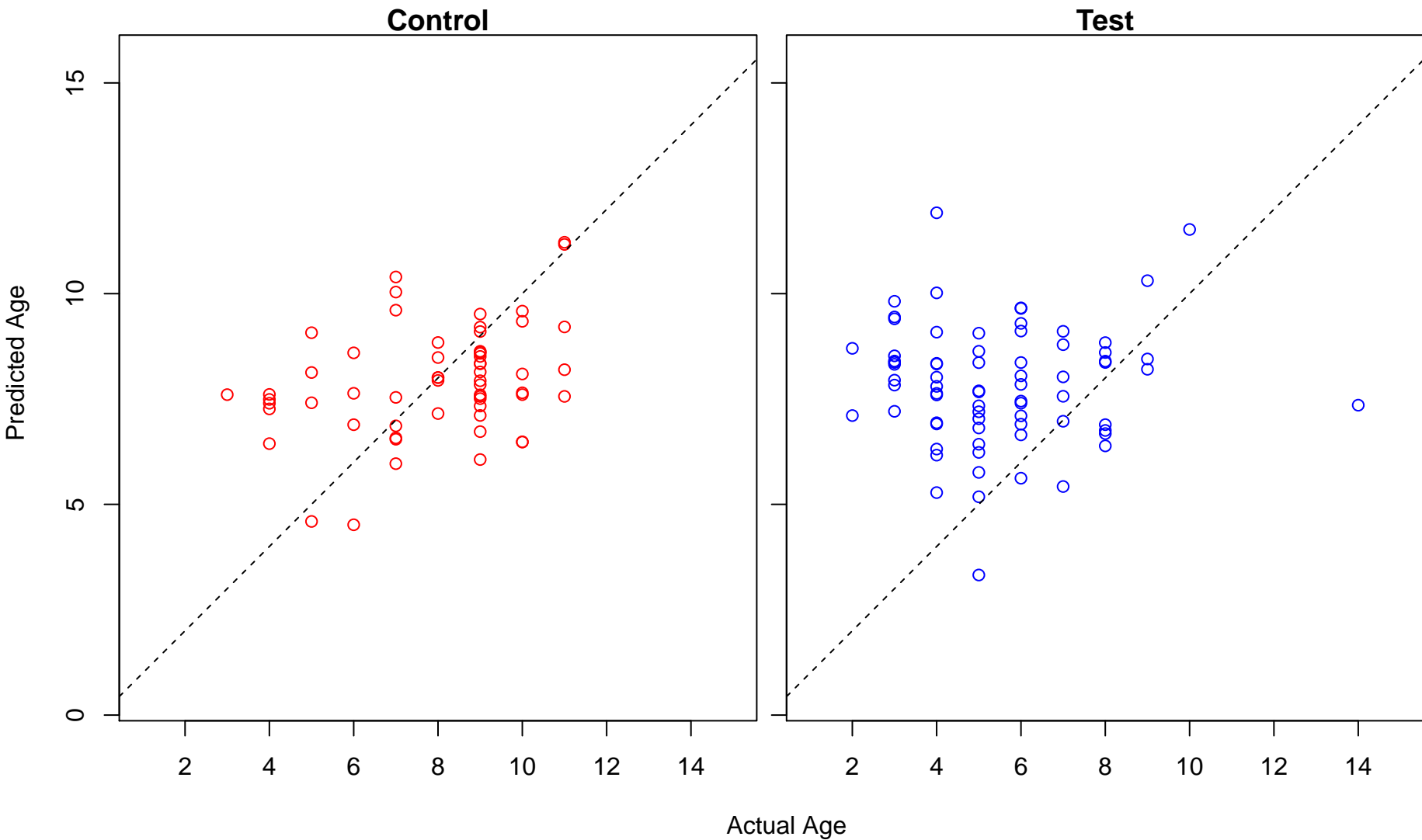
regulation of fibroblast migration (Score: 0.698594)



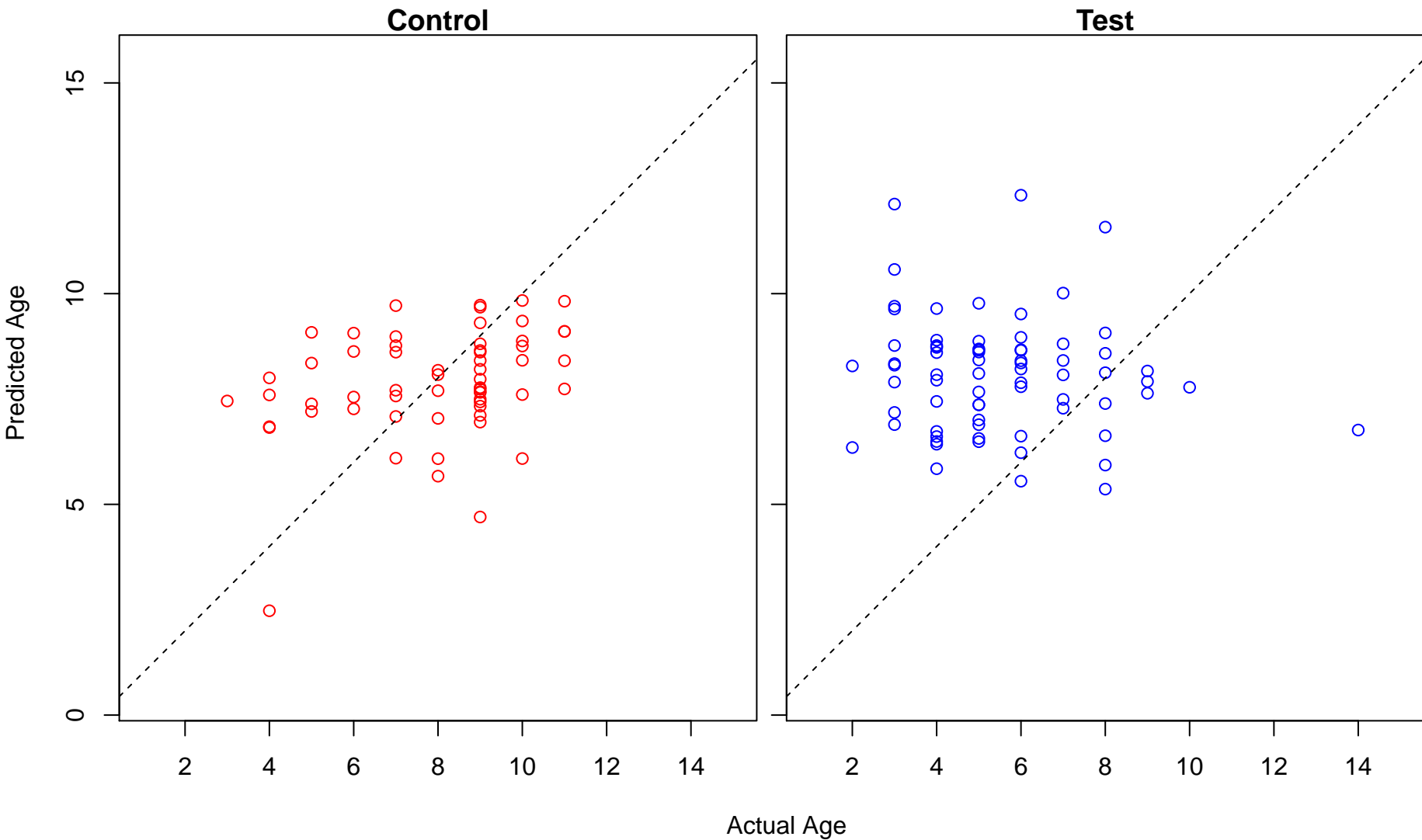
regulation of pseudopodium assembly (Score: 0.697160)



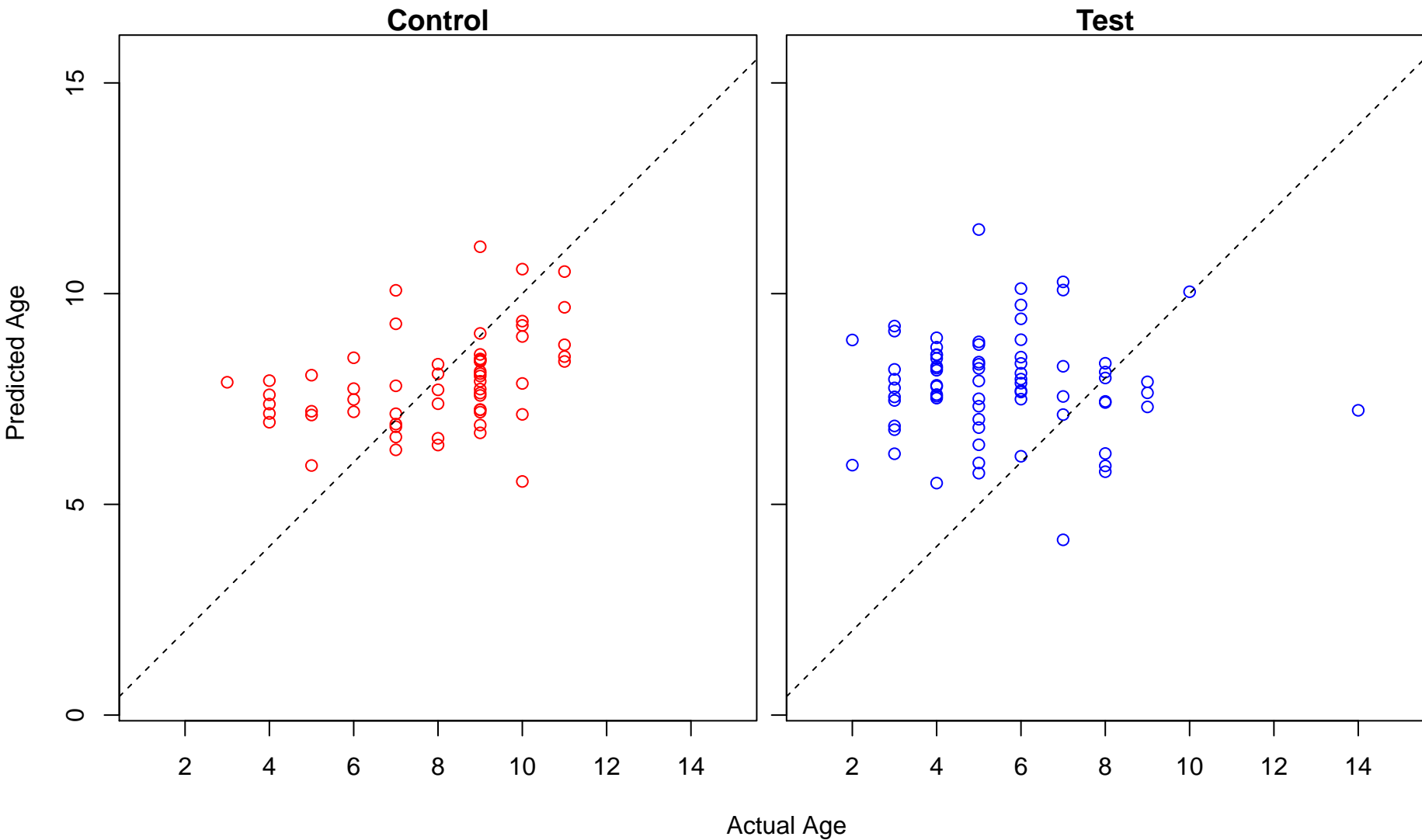
positive regulation of pseudopodium assembly (Score: 0.697160)



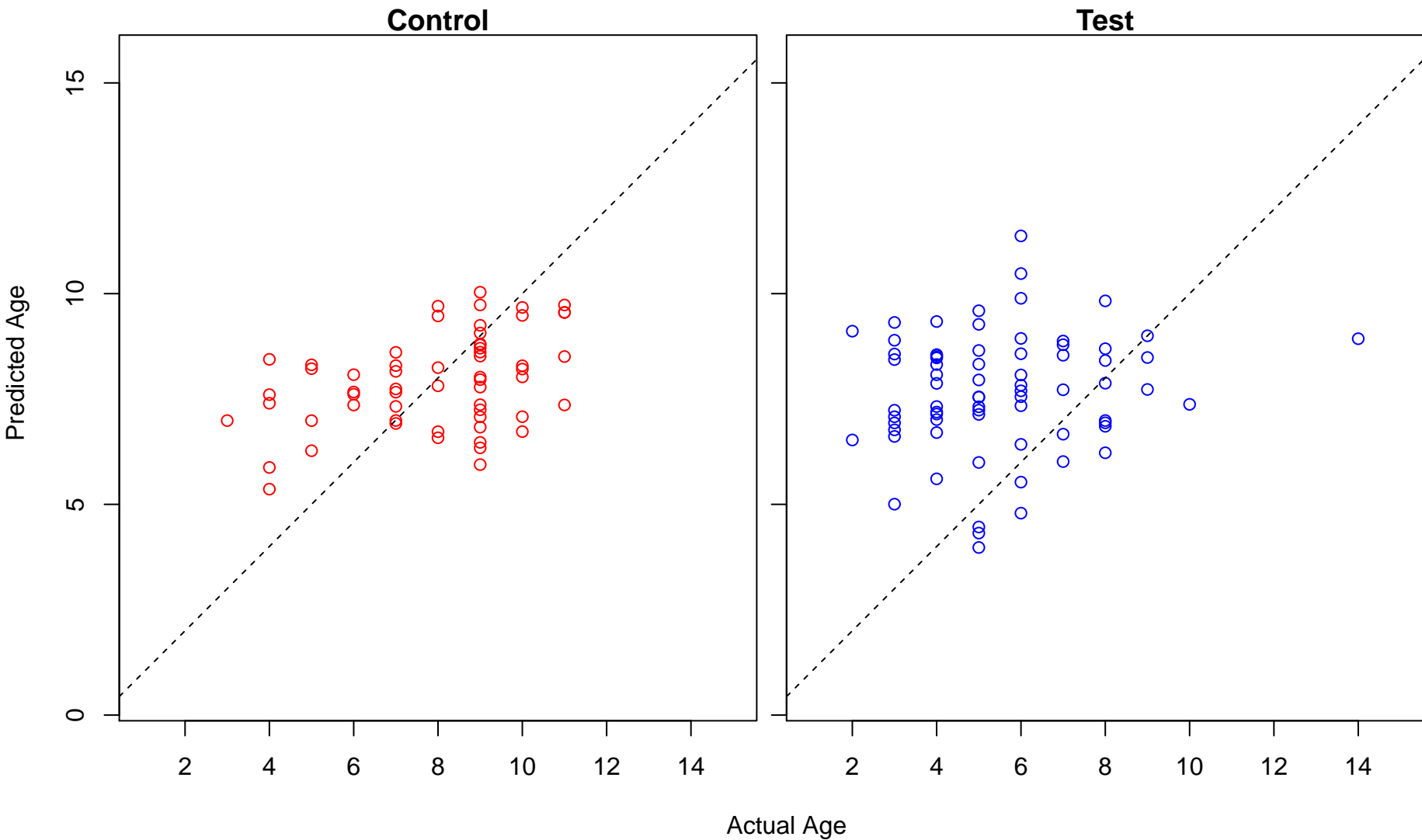
cerebellum maturation (Score: 0.696807)



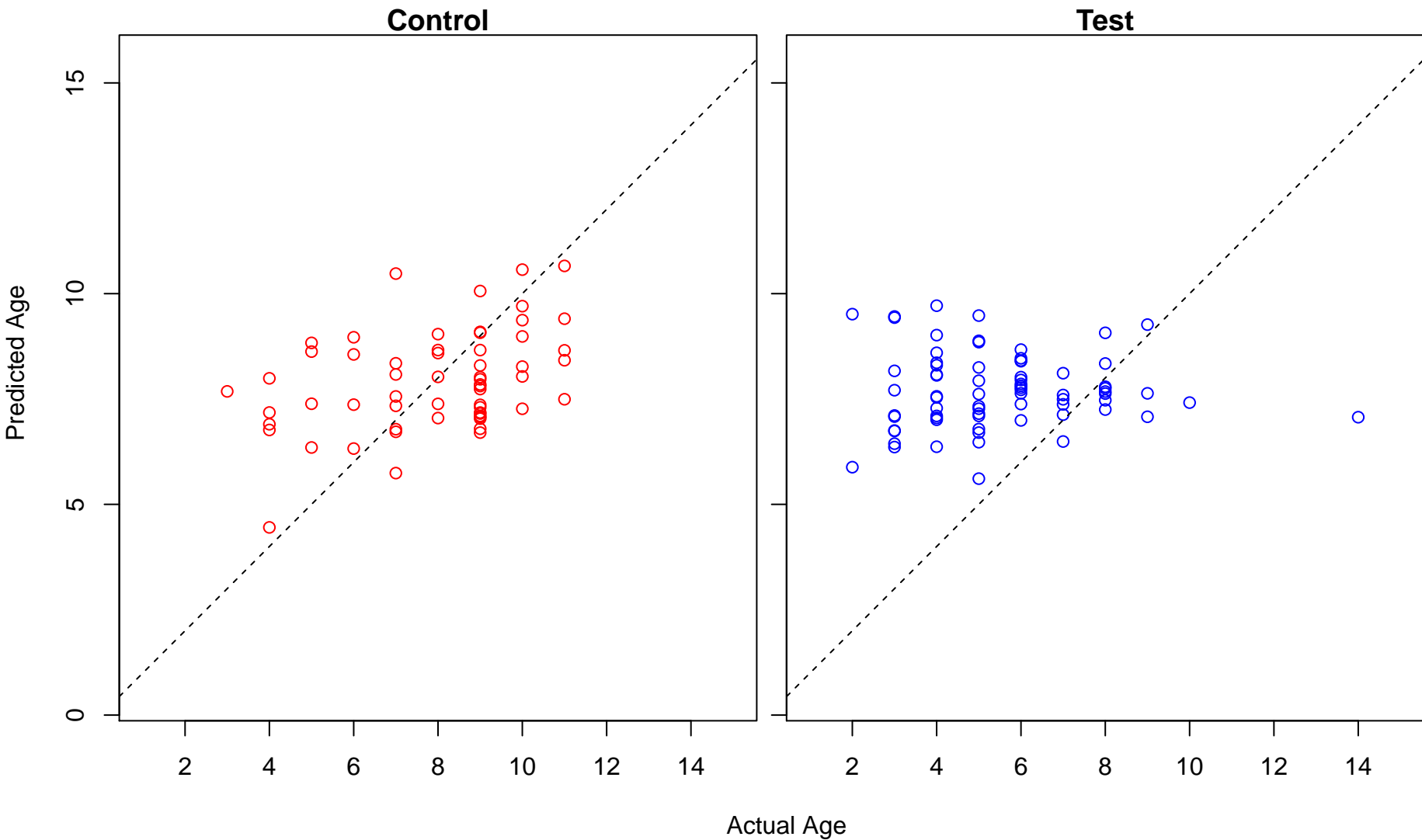
trachea cartilage morphogenesis (Score: 0.696469)



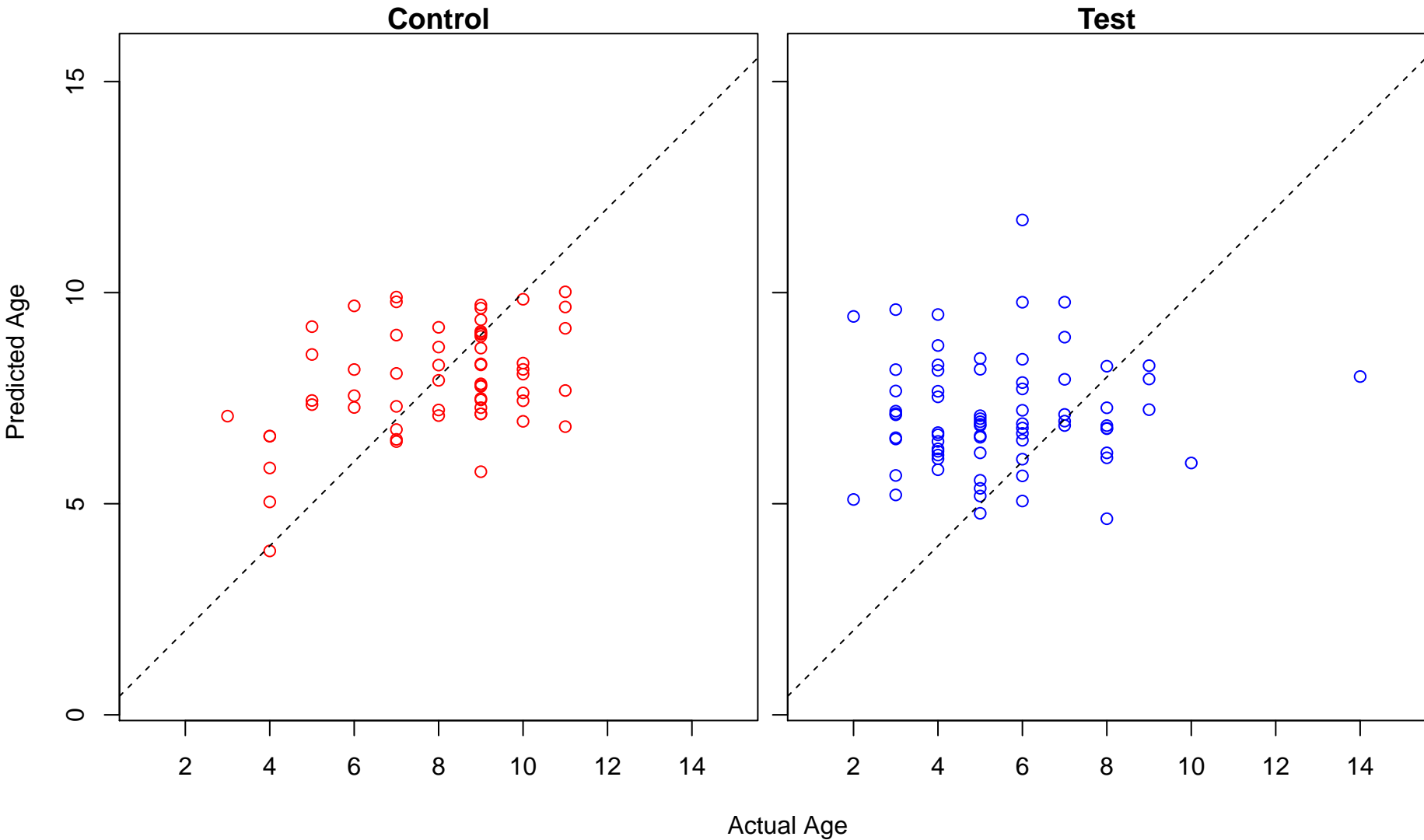
notochord formation (Score: 0.695389)



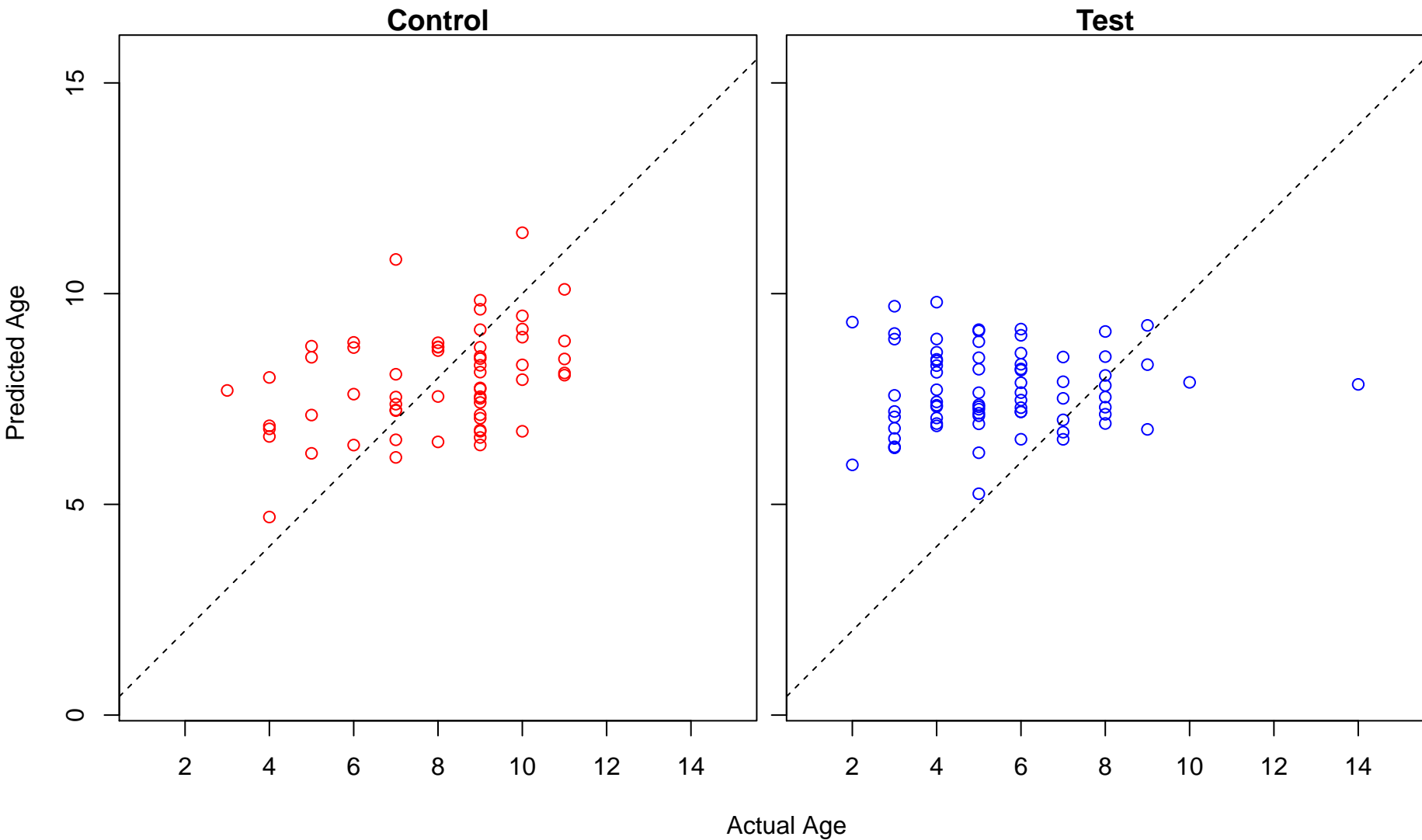
L-amino acid import (Score: 0.694931)



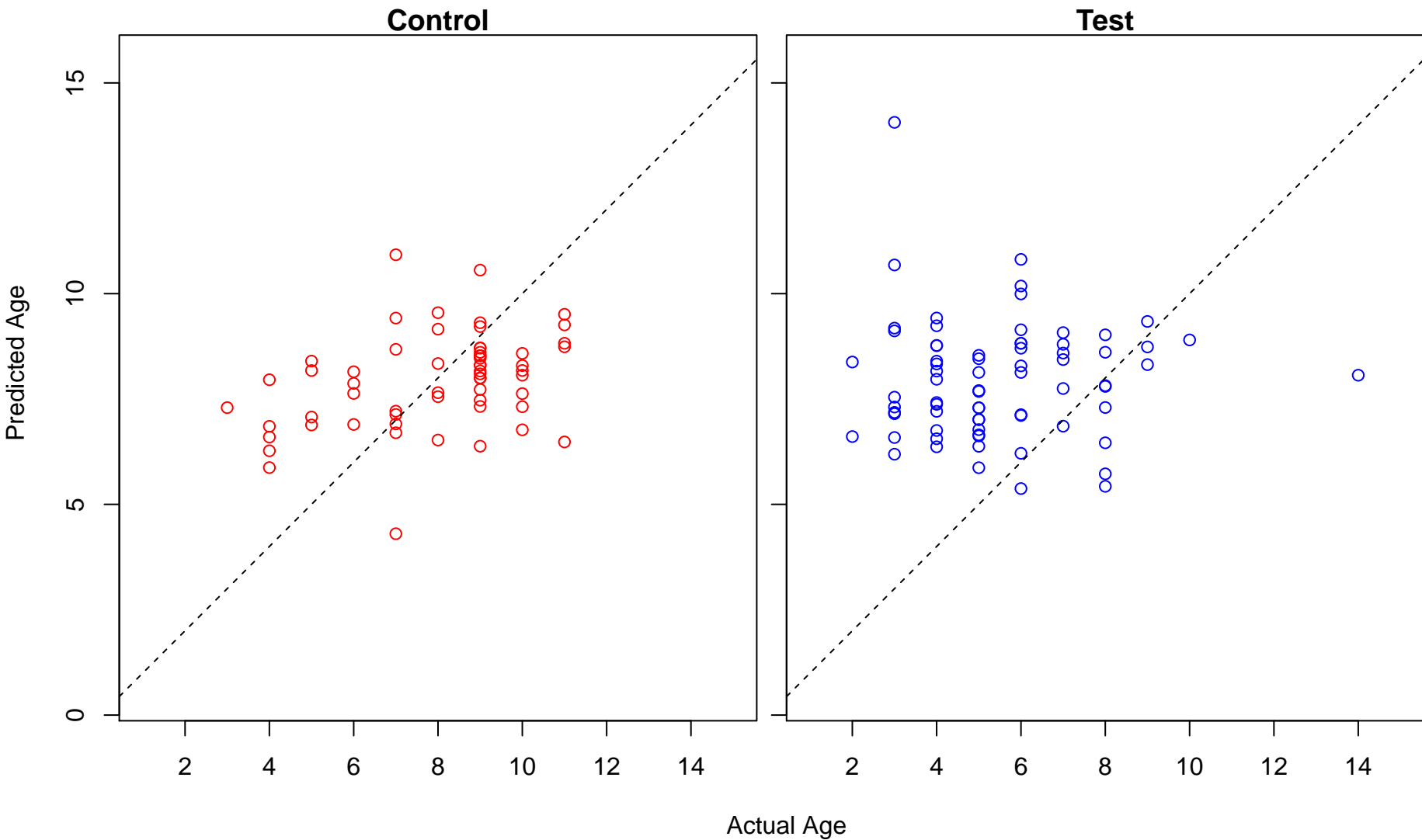
negative regulation of stress fiber assembly (Score: 0.692599)



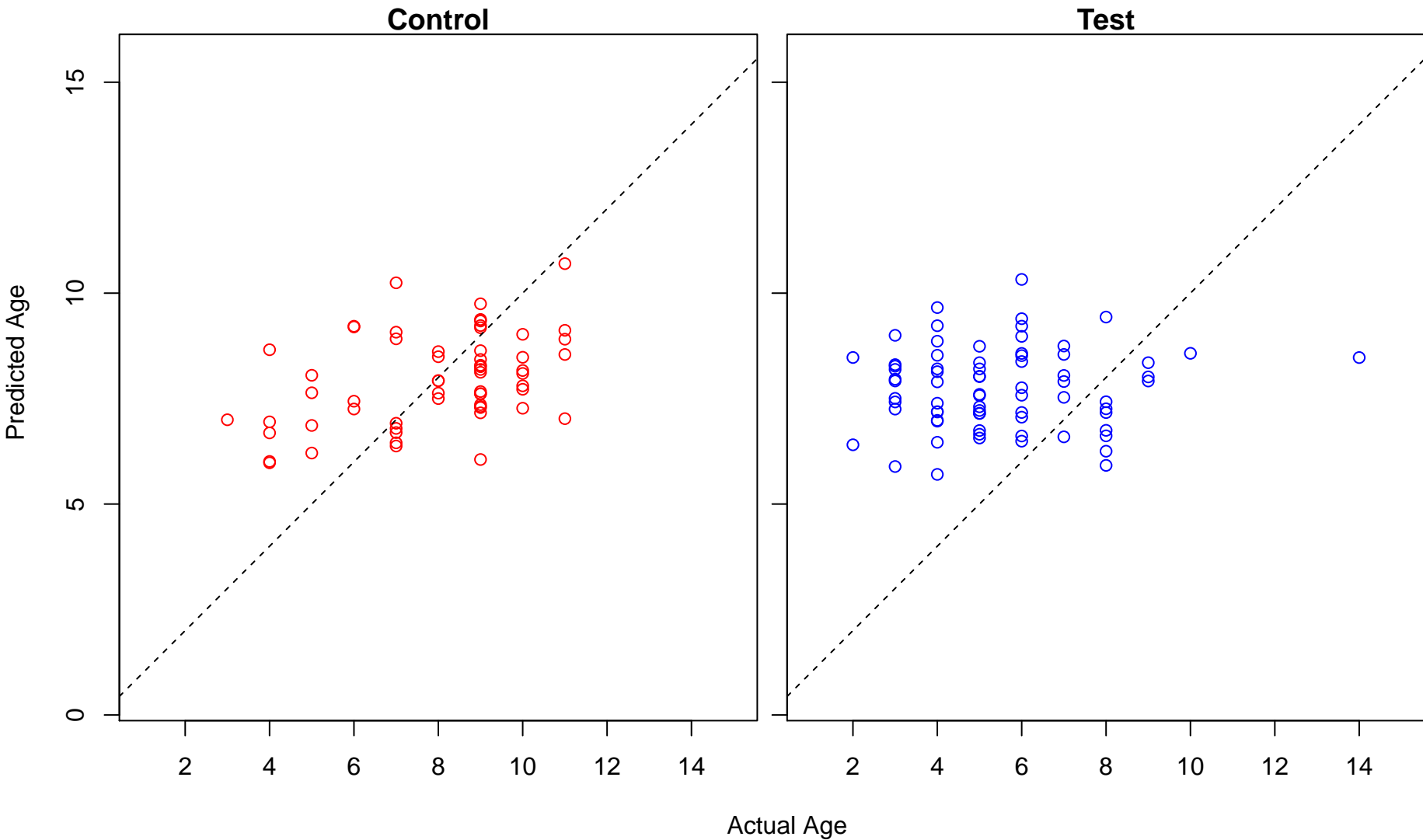
interleukin-2 production (Score: 0.690443)



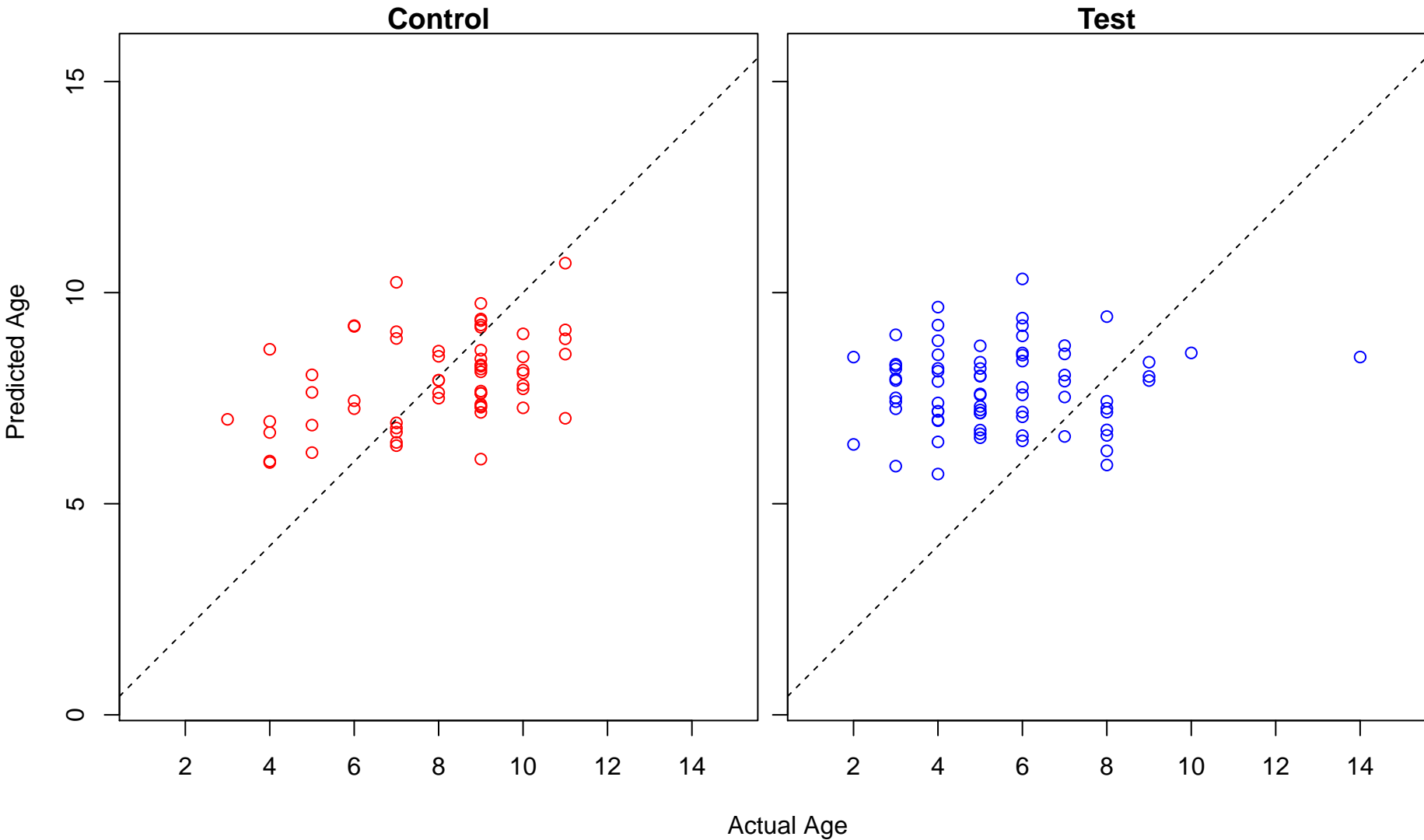
cell migration involved in vasculogenesis (Score: 0.688849)



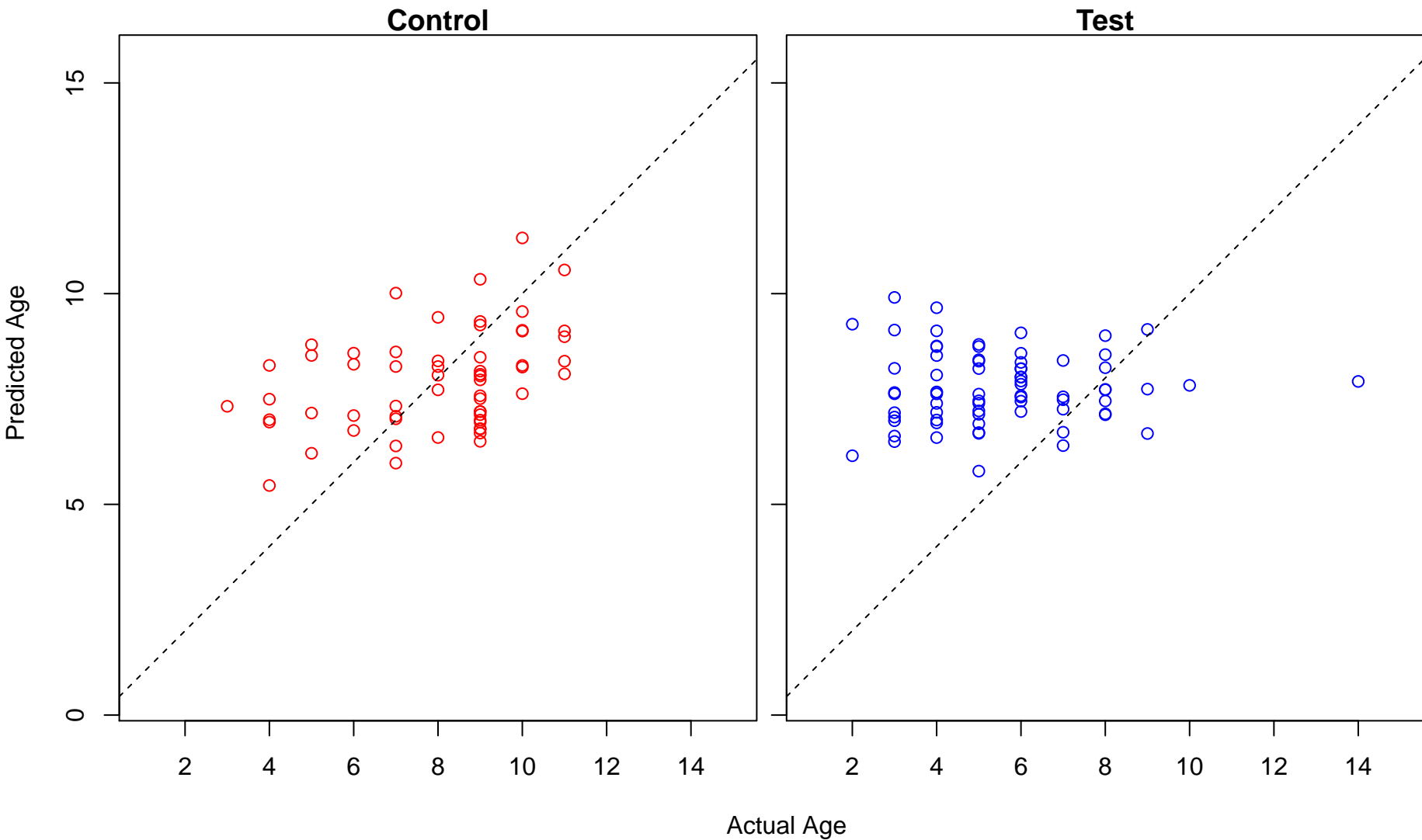
regulation of platelet-derived growth factor receptor signaling pathway (Score: 0.688260)



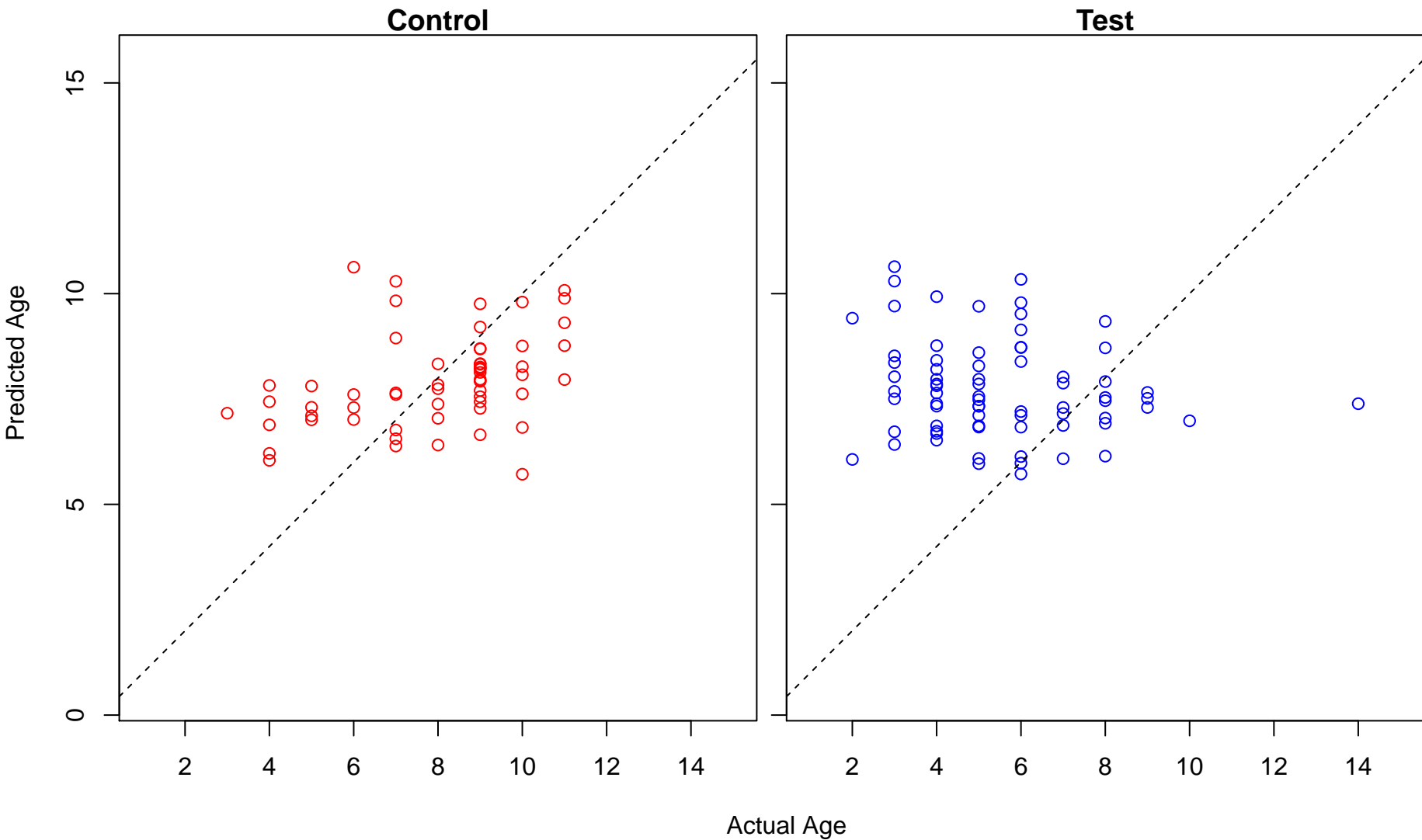
negative regulation of platelet-derived growth factor receptor signaling pathway (Score: 0.688151)



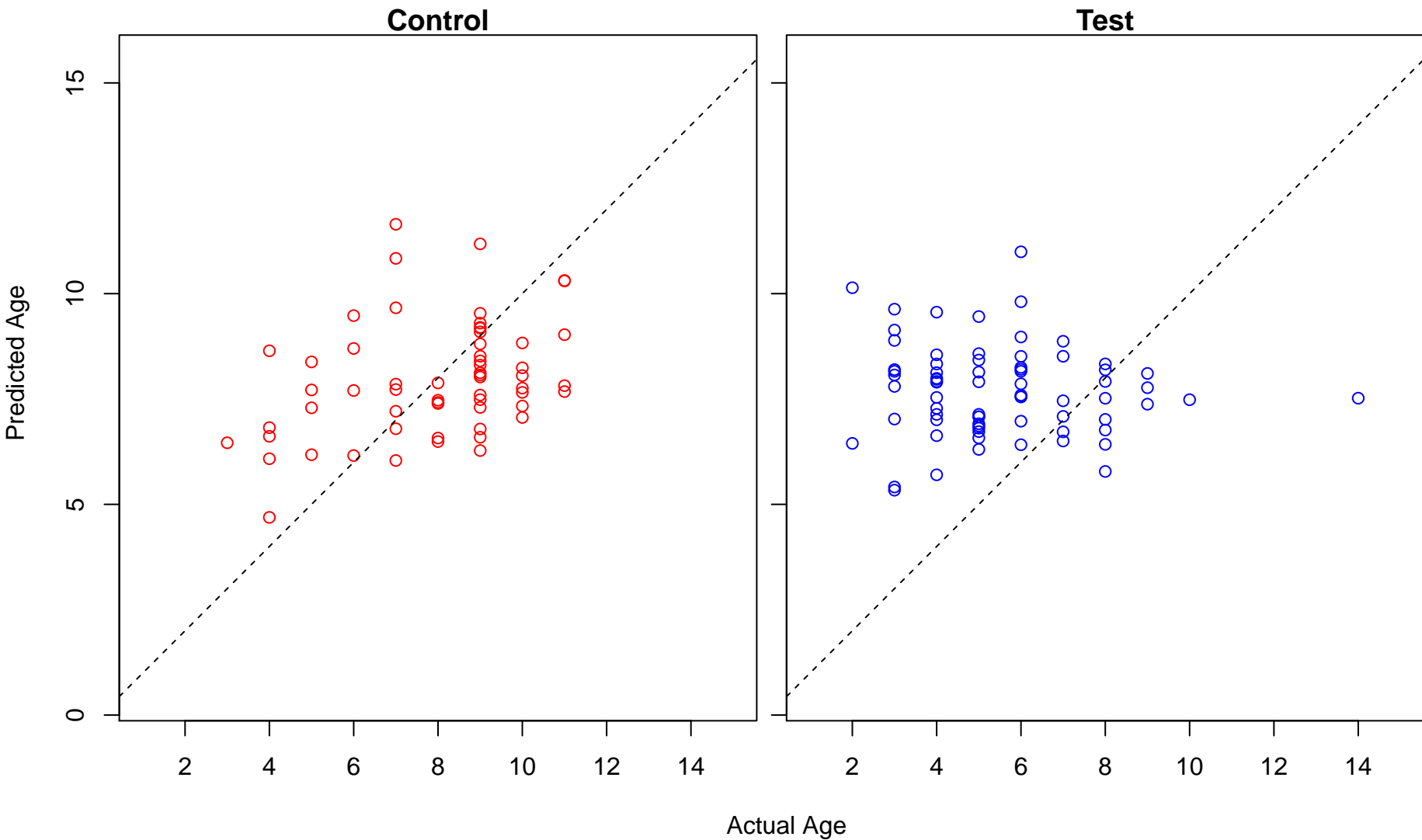
divalent metal ion export (Score: 0.687904)



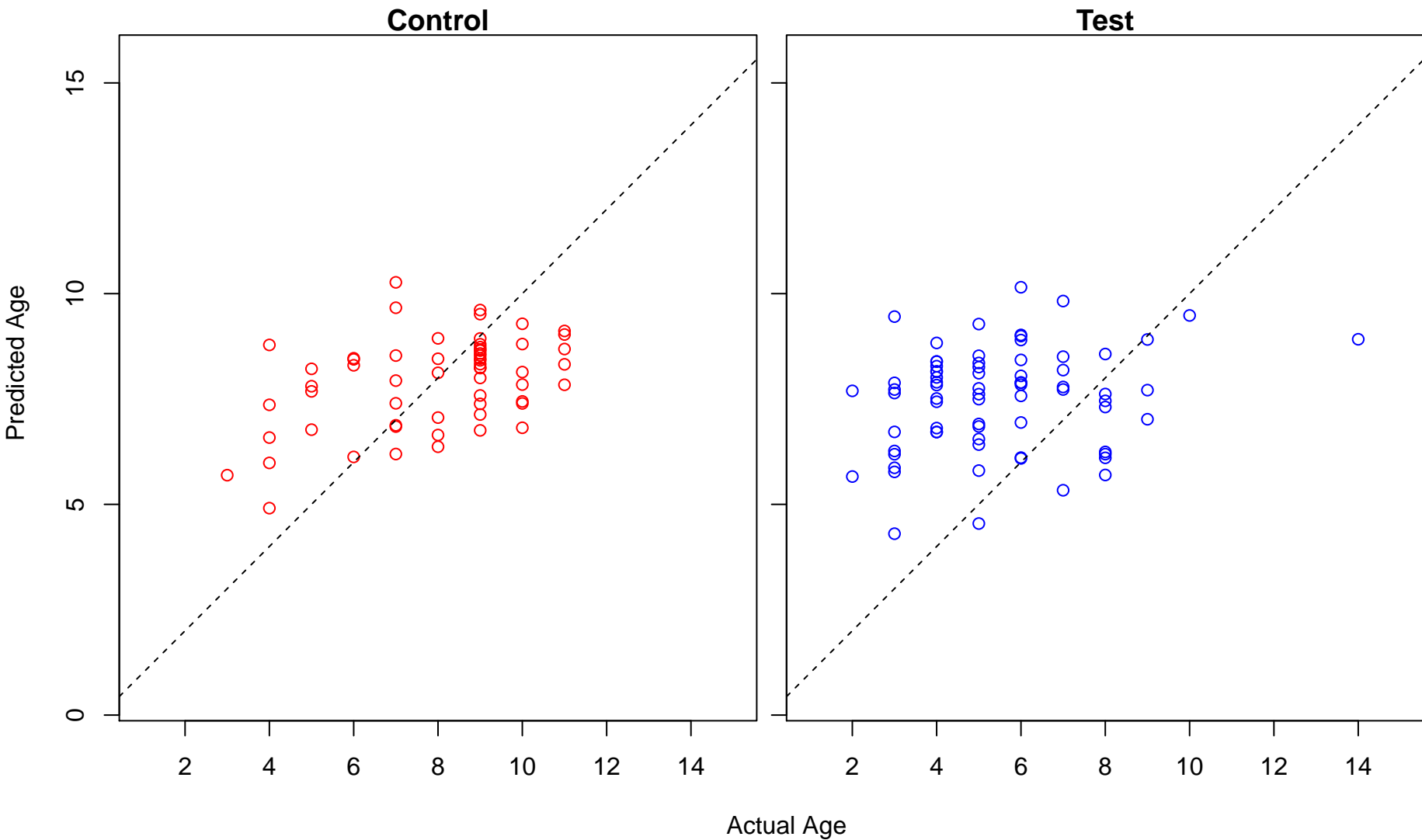
protein localization to cell surface (Score: 0.687684)



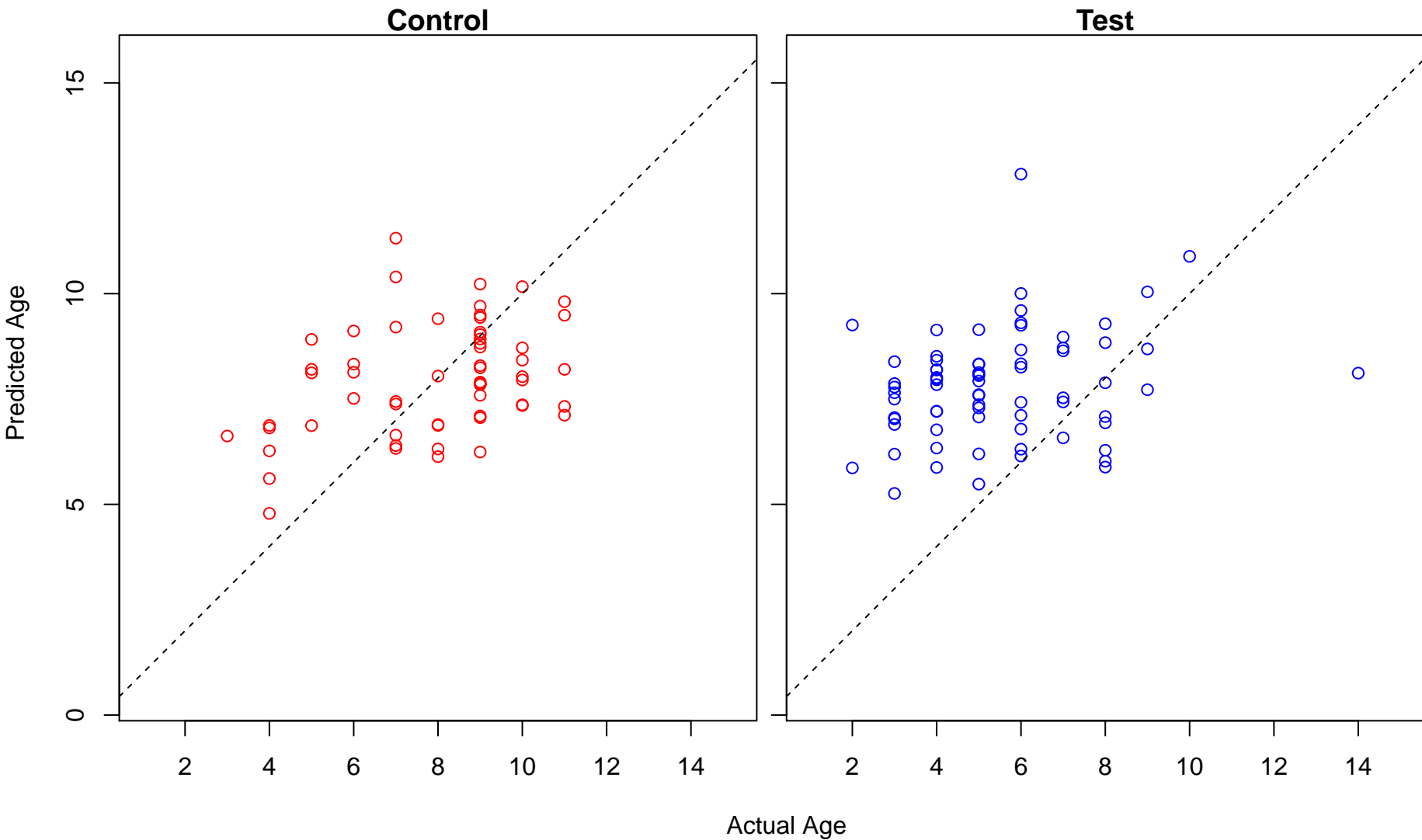
purine nucleoside triphosphate metabolic process (Score: 0.686677)



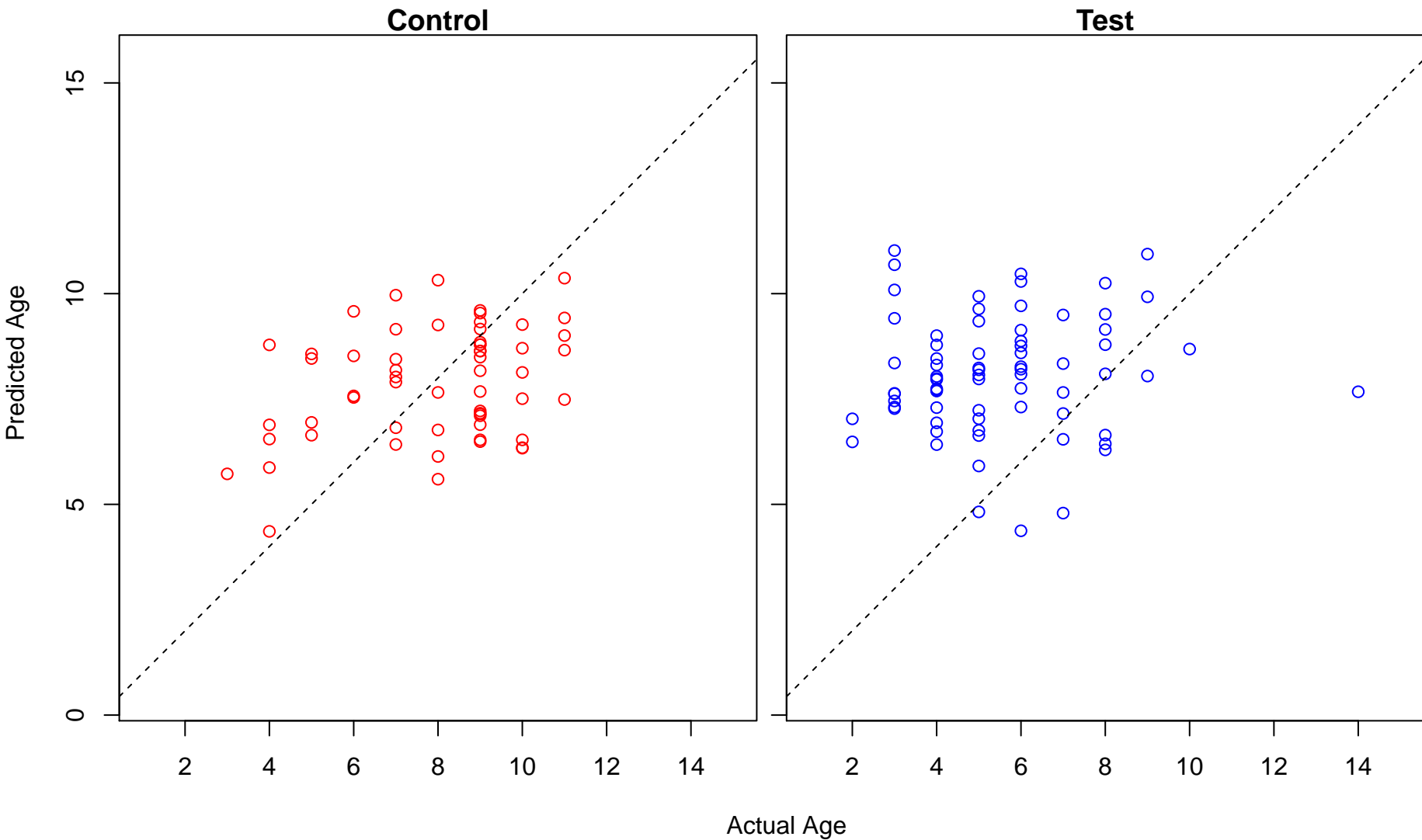
positive regulation of glycoprotein biosynthetic process (Score: 0.685659)



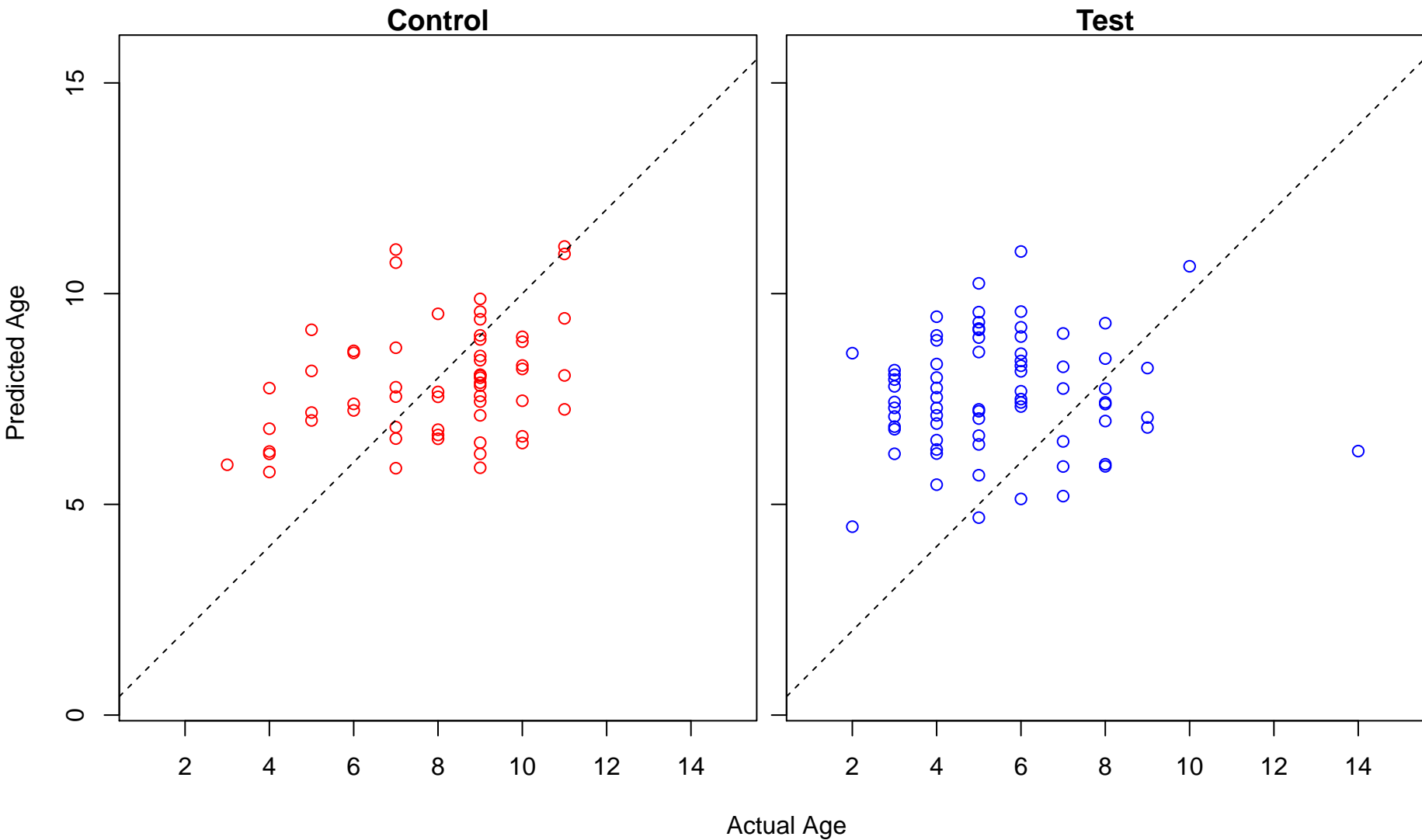
positive regulation of exocytosis (Score: 0.685575)



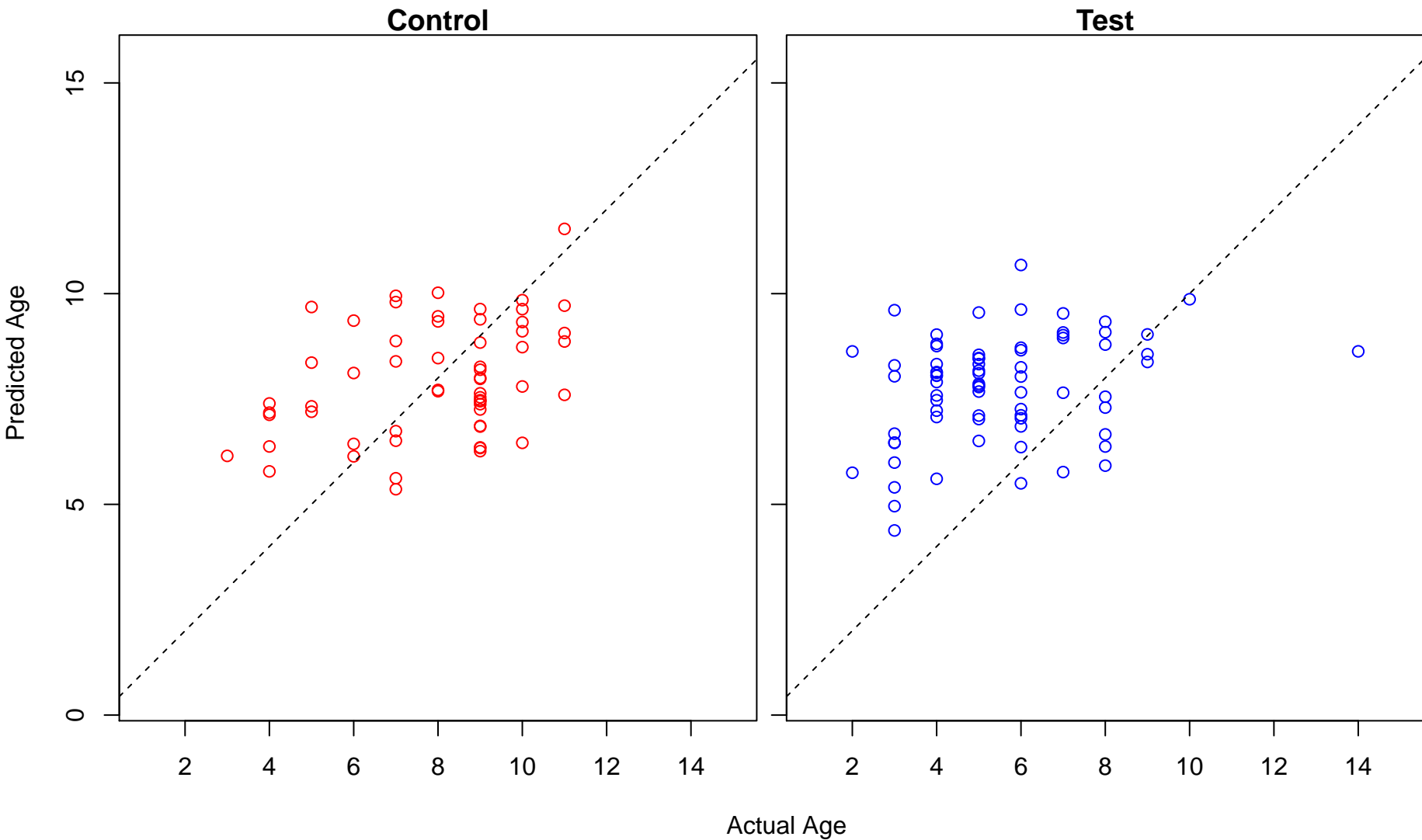
cardiolipin acyl-chain remodeling (Score: 0.685549)



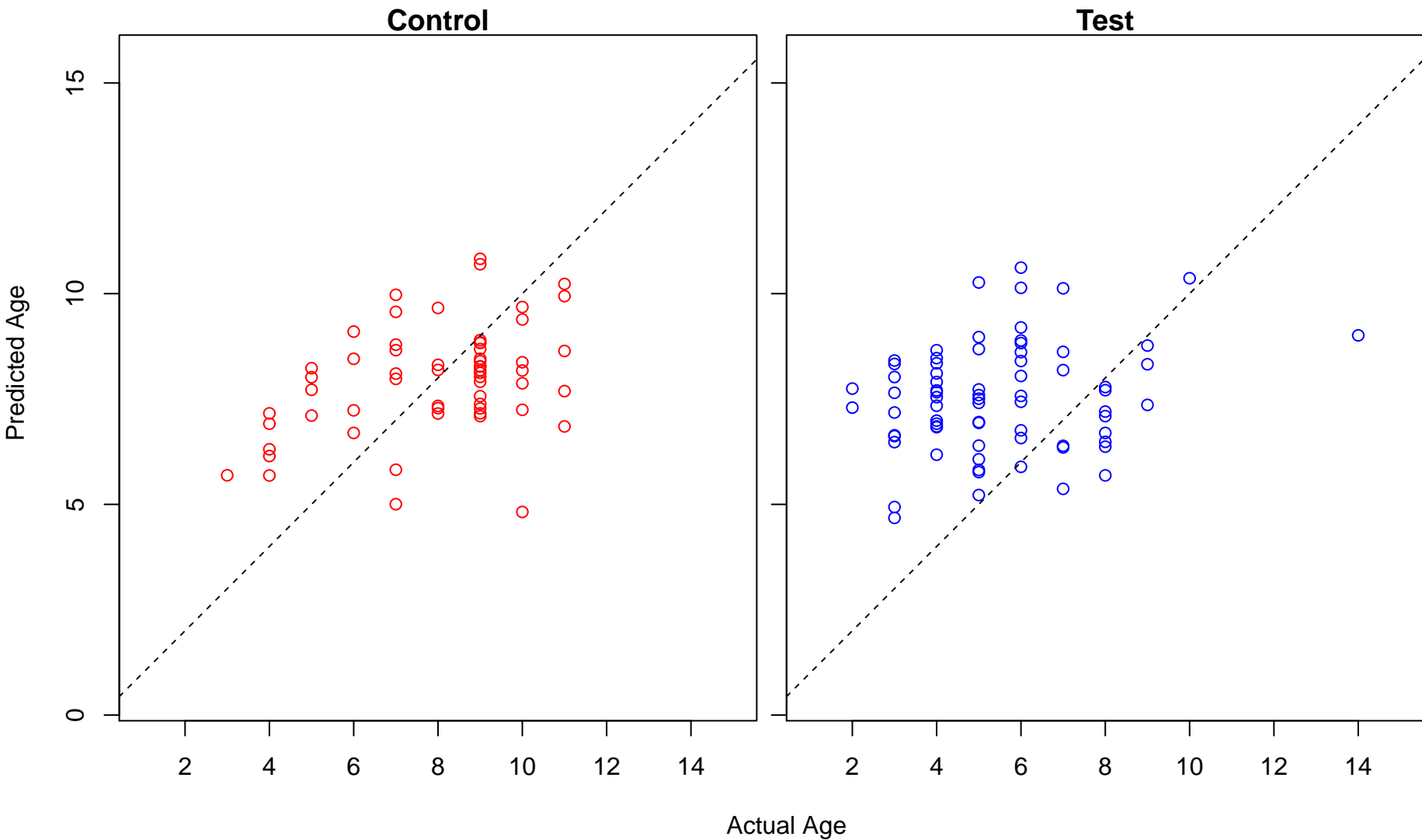
hepaticobiliary system development (Score: 0.685543)



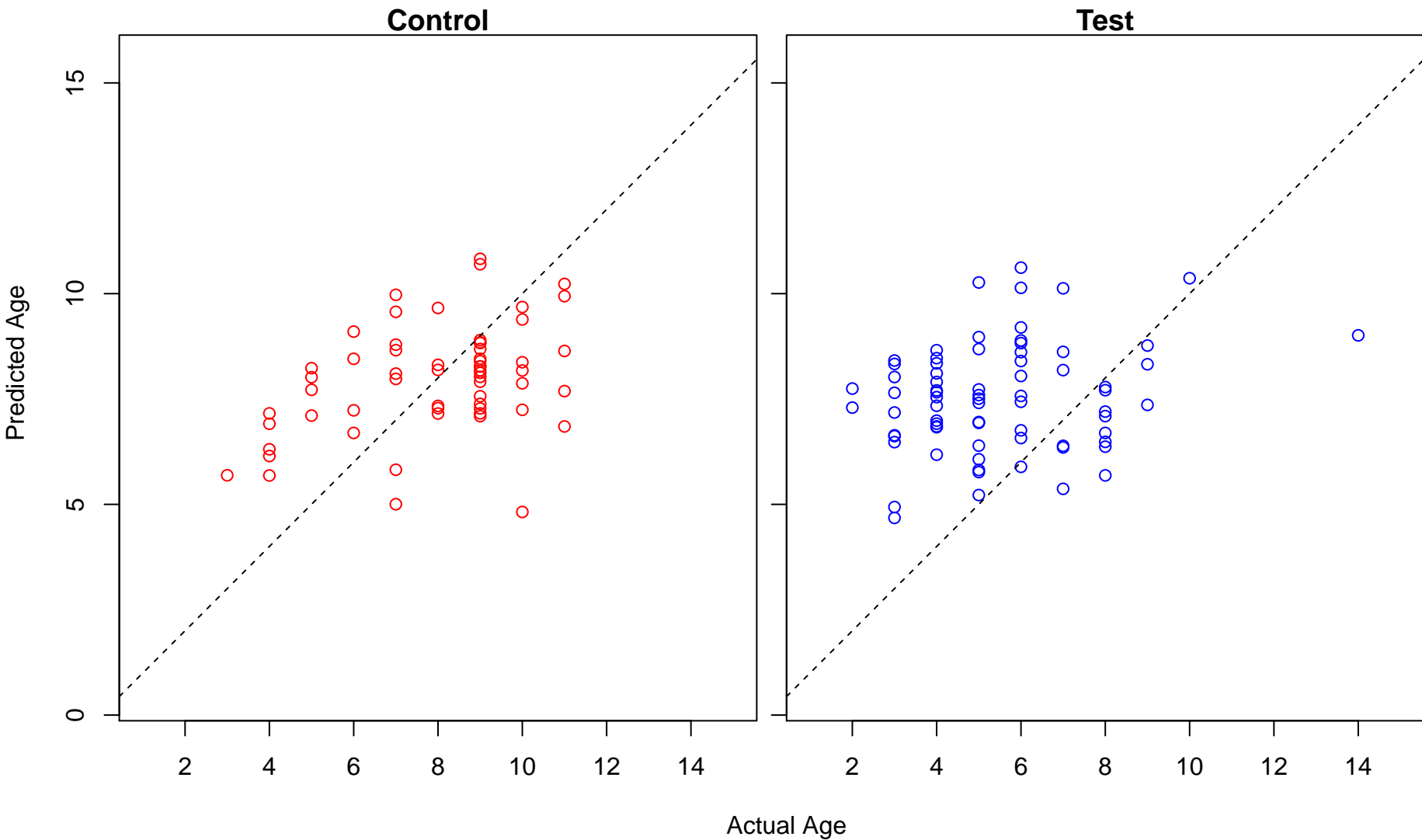
histone H4-K16 acetylation (Score: 0.685177)



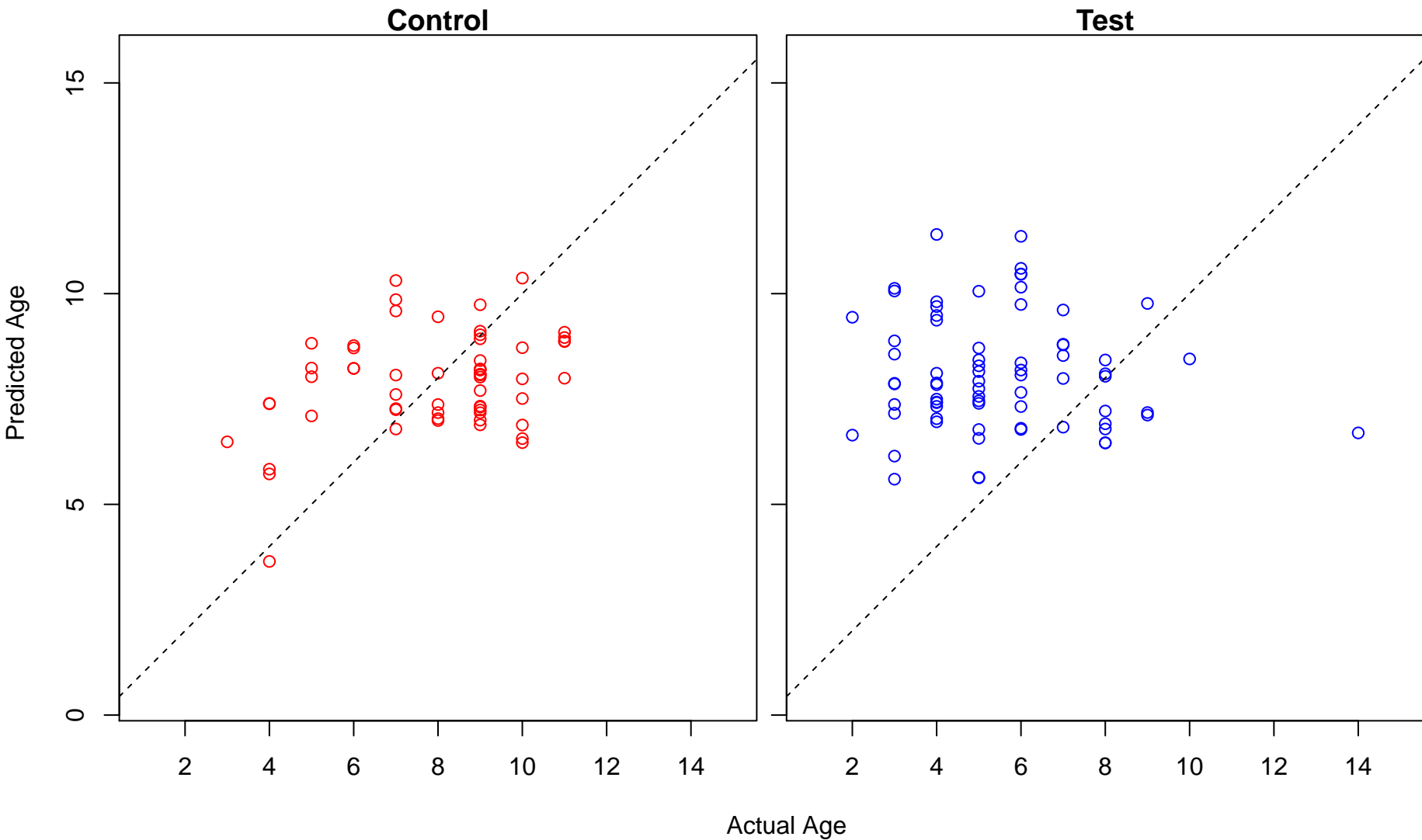
intracellular sterol transport (Score: 0.684818)



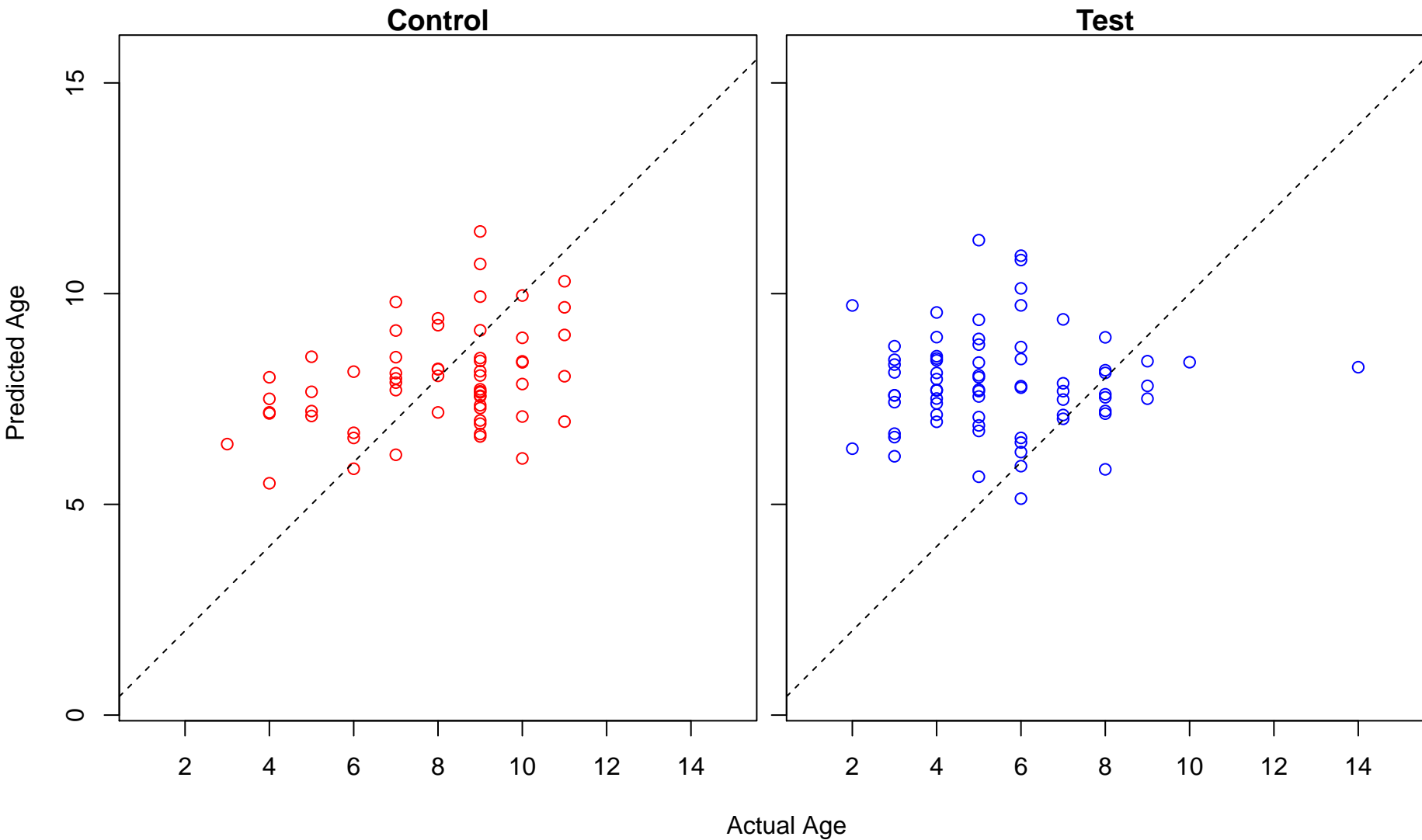
intracellular cholesterol transport (Score: 0.684818)

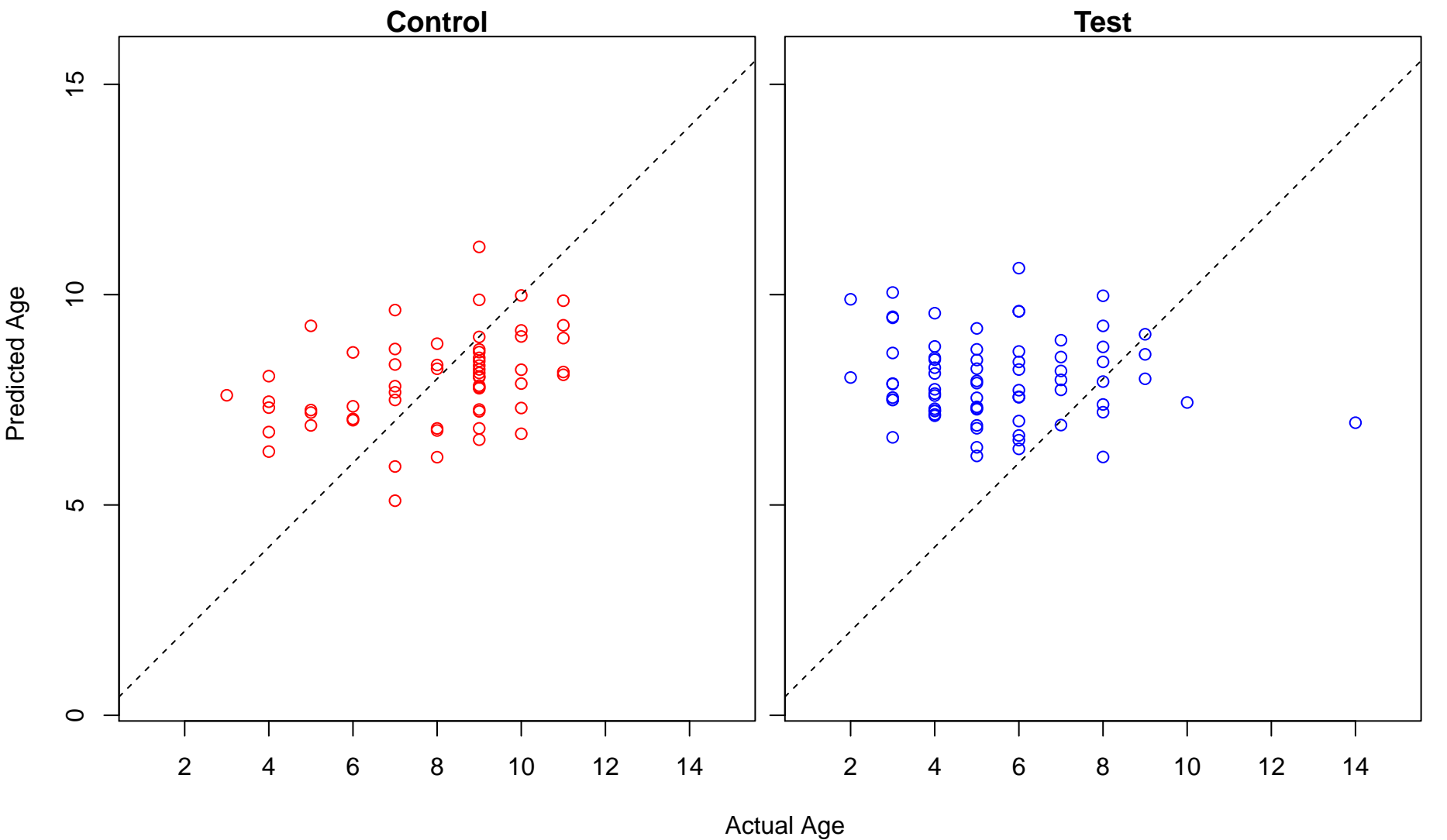


secondary metabolic process (Score: 0.682696)

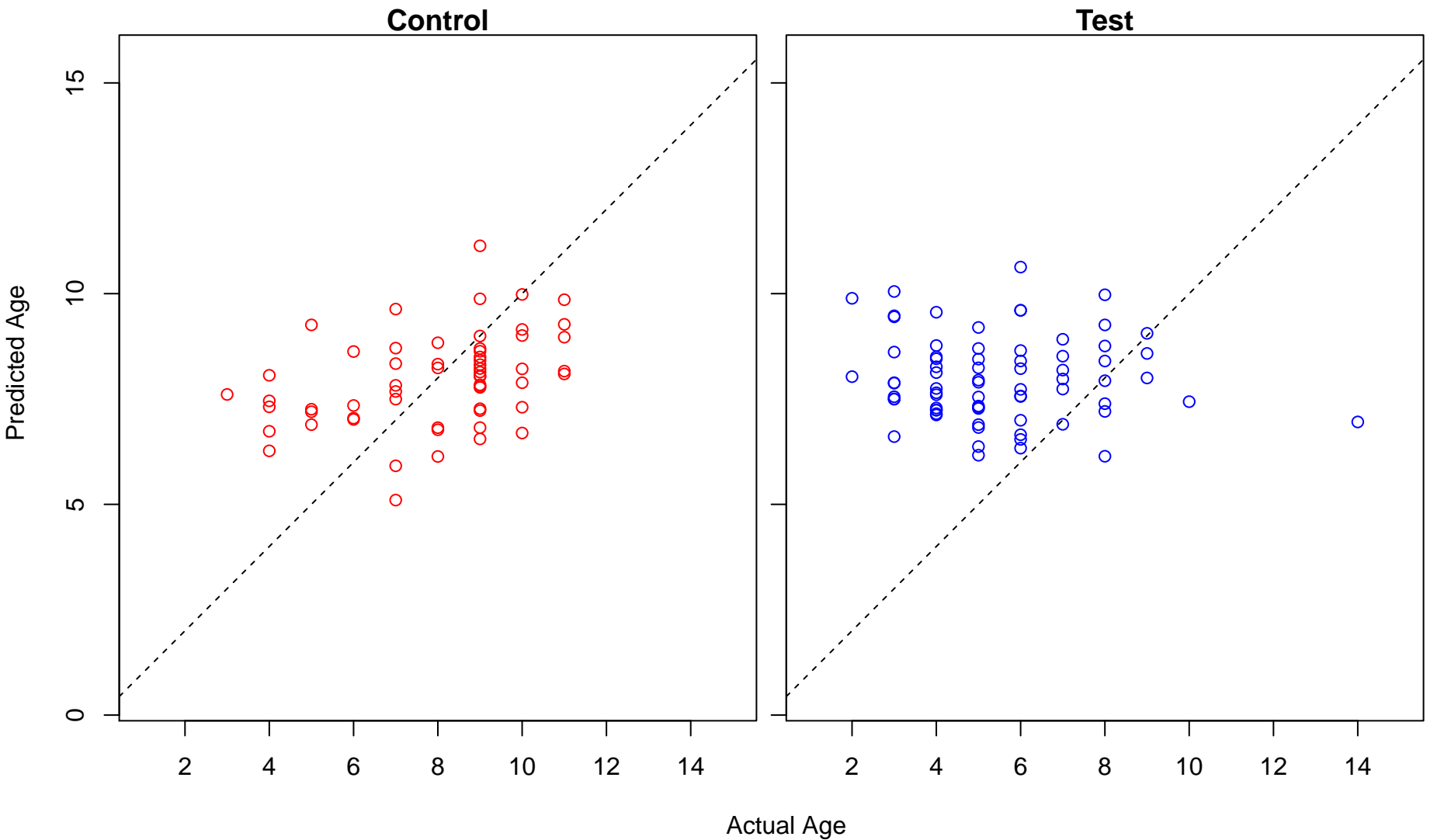


protein import into mitochondrial inner membrane (Score: 0.681516)

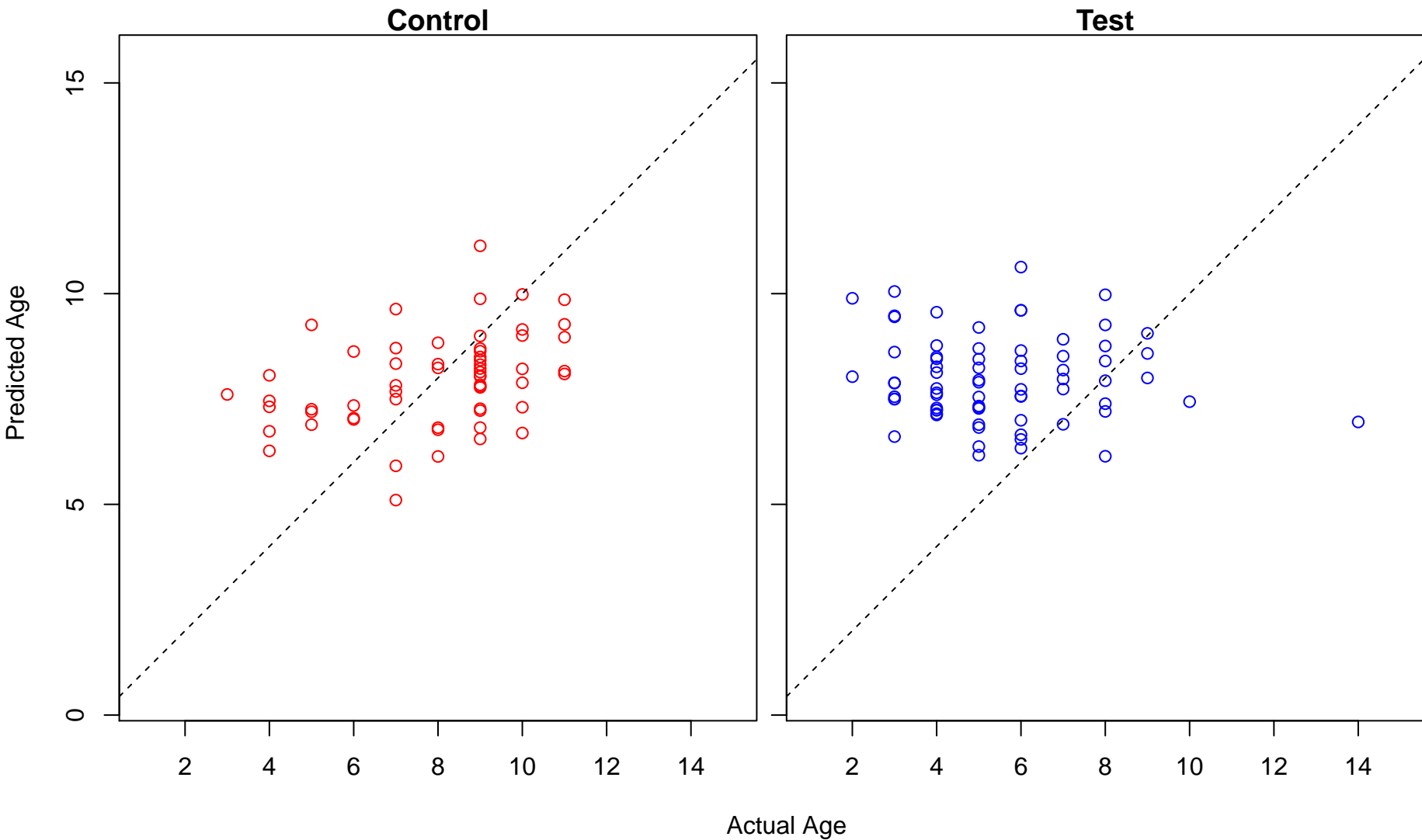




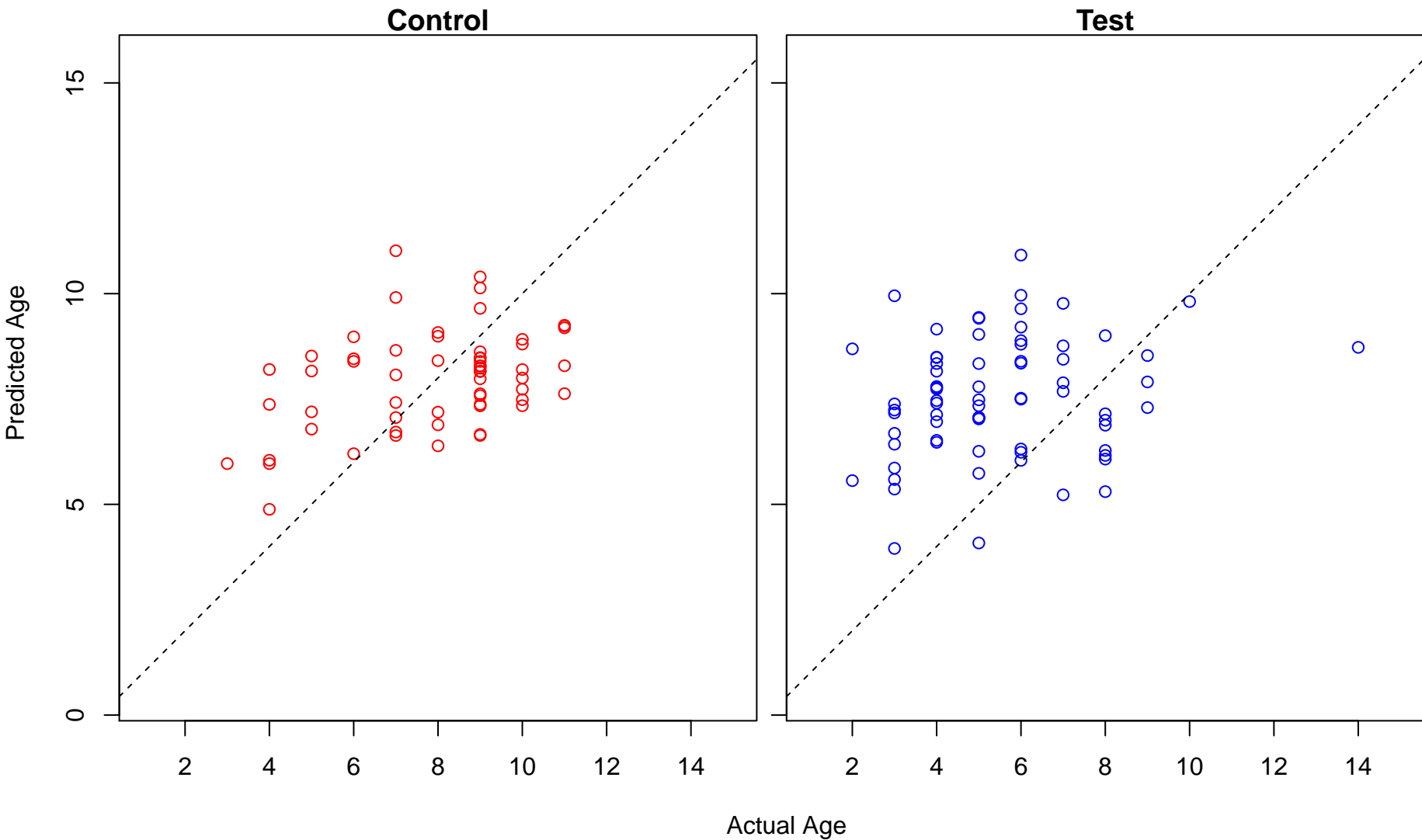
tension of a leading process involved in cell motility in cerebral cortex radial glia guided migration (Score



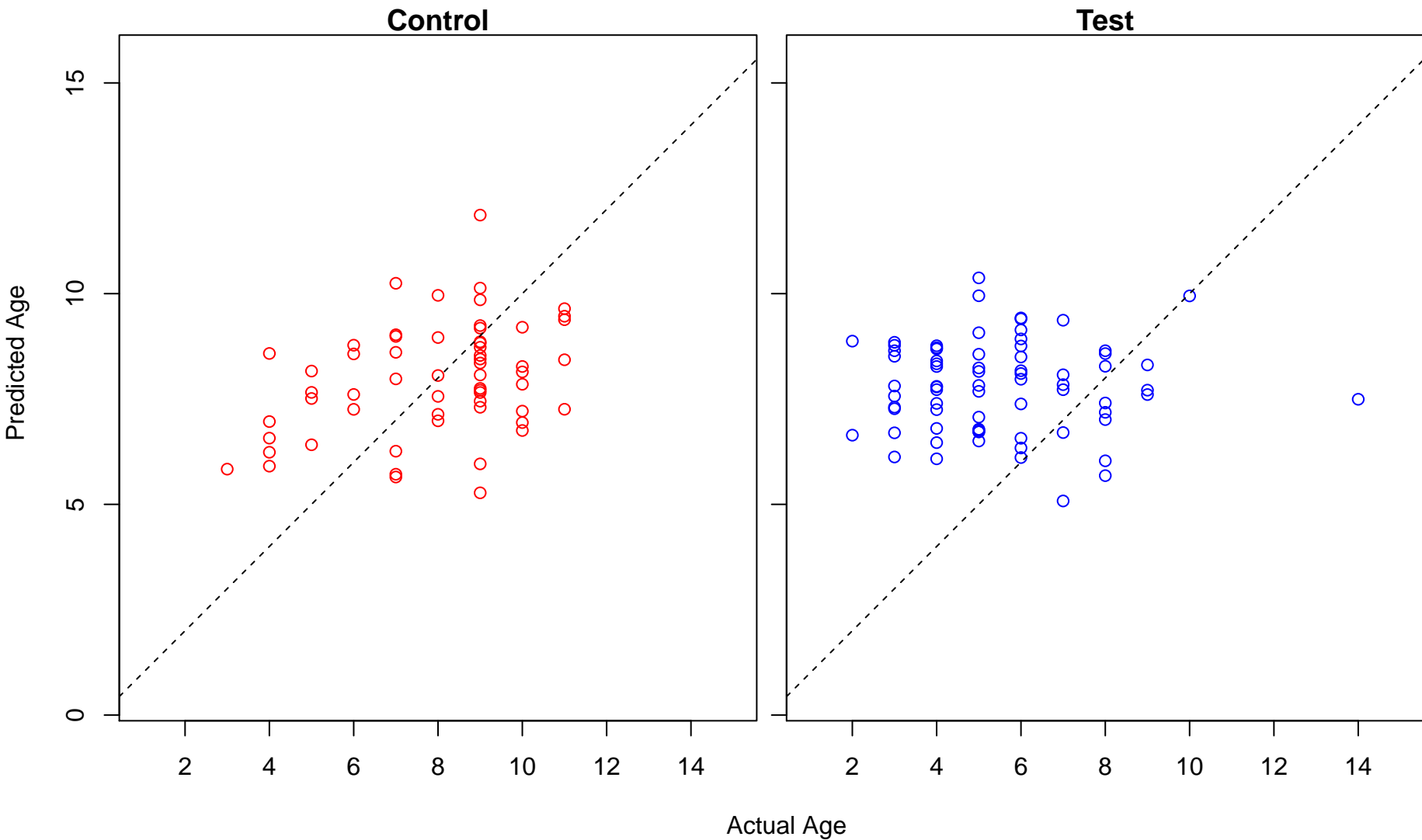
pseudopodium assembly (Score: 0.680542)



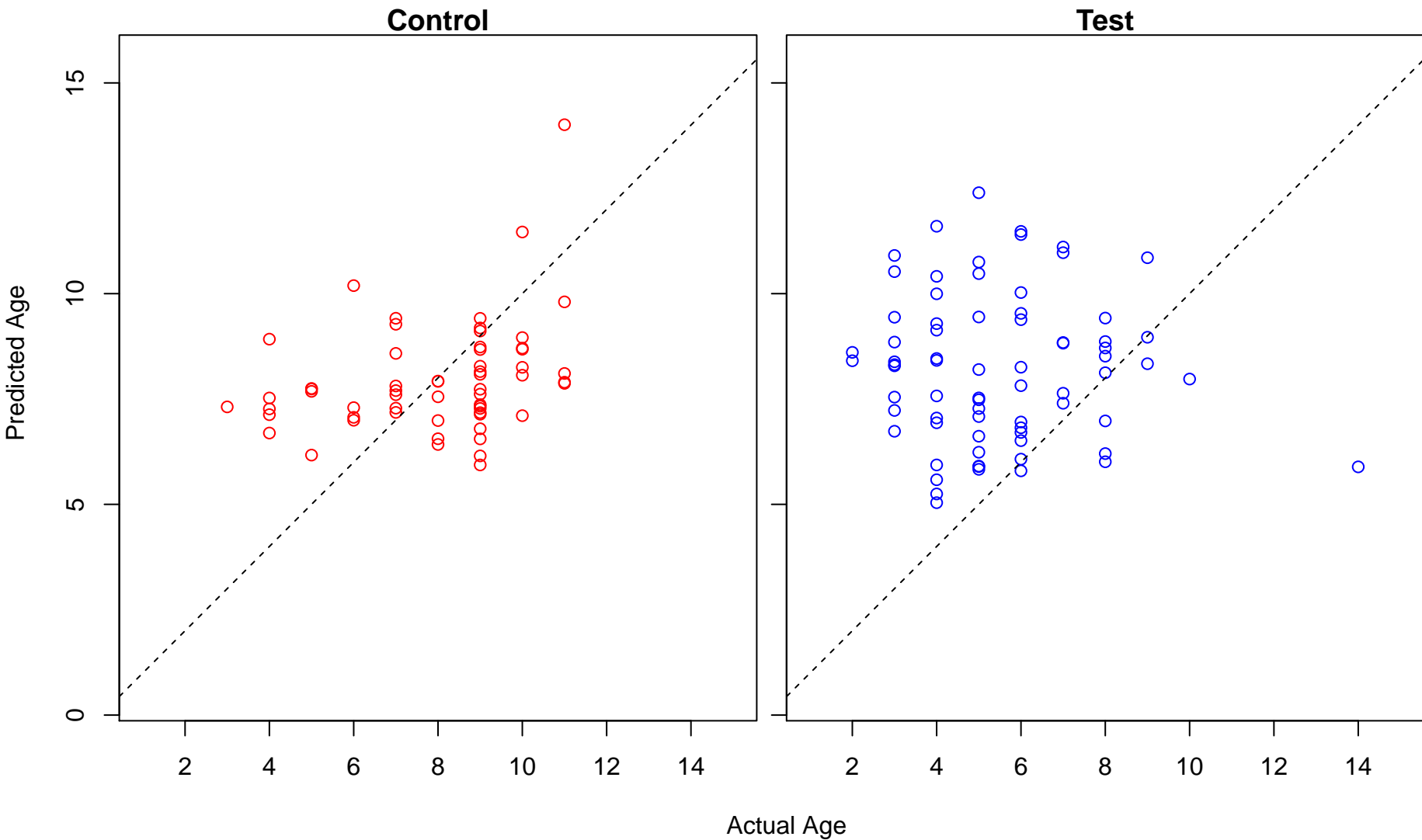
regulation of glycoprotein biosynthetic process (Score: 0.679834)



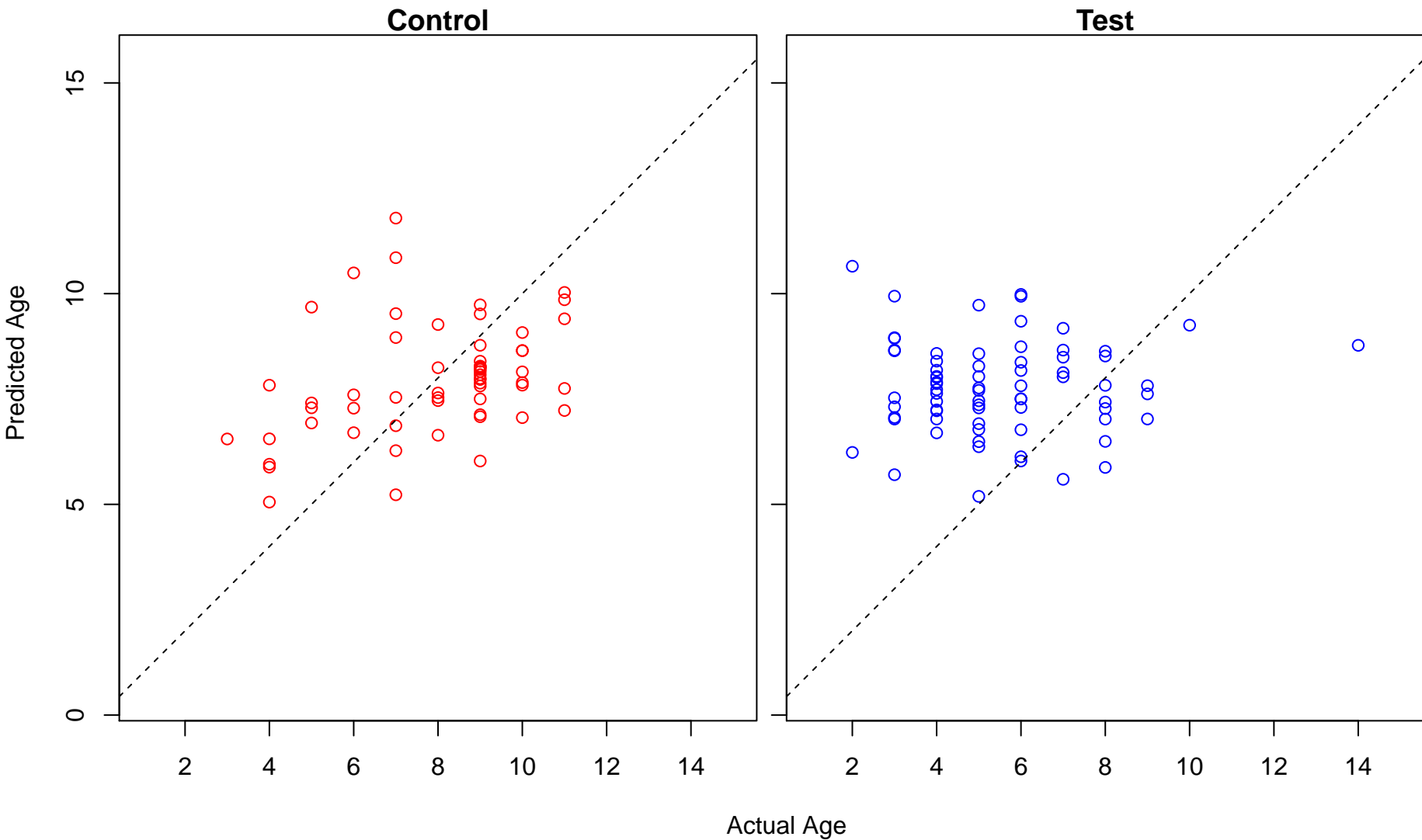
synapse assembly (Score: 0.679787)



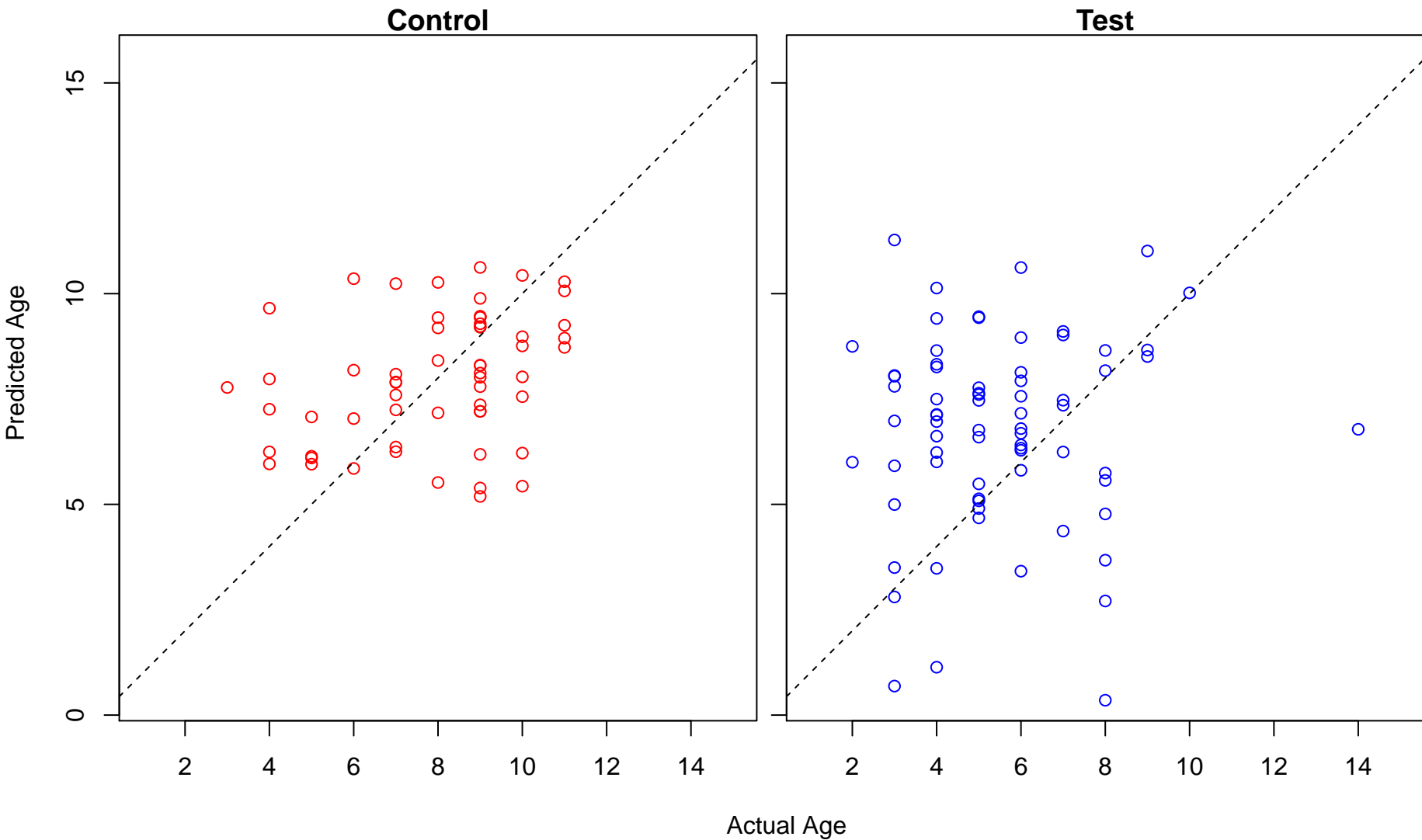
negative regulation of hormone metabolic process (Score: 0.677232)



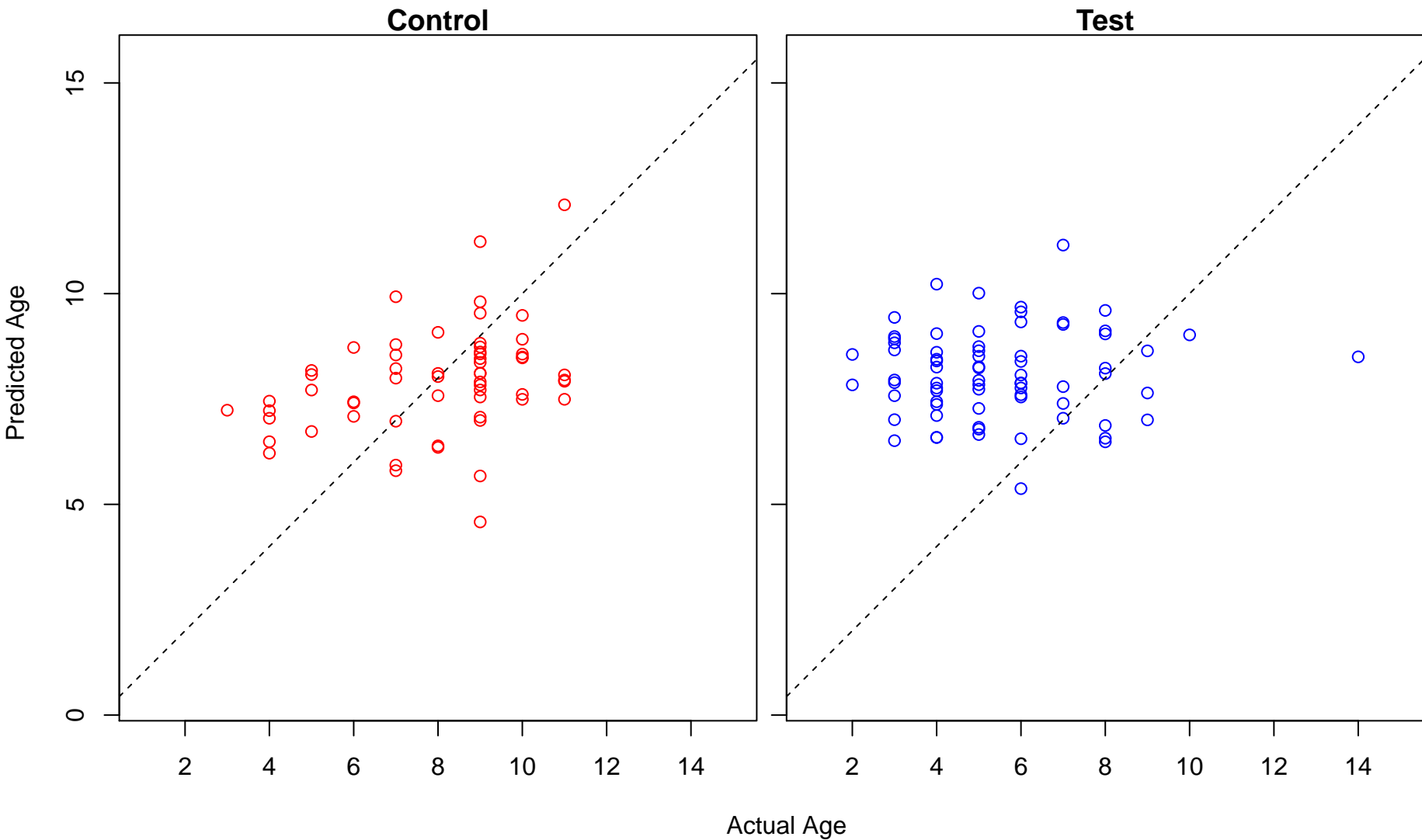
positive regulation of filopodium assembly (Score: 0.676916)



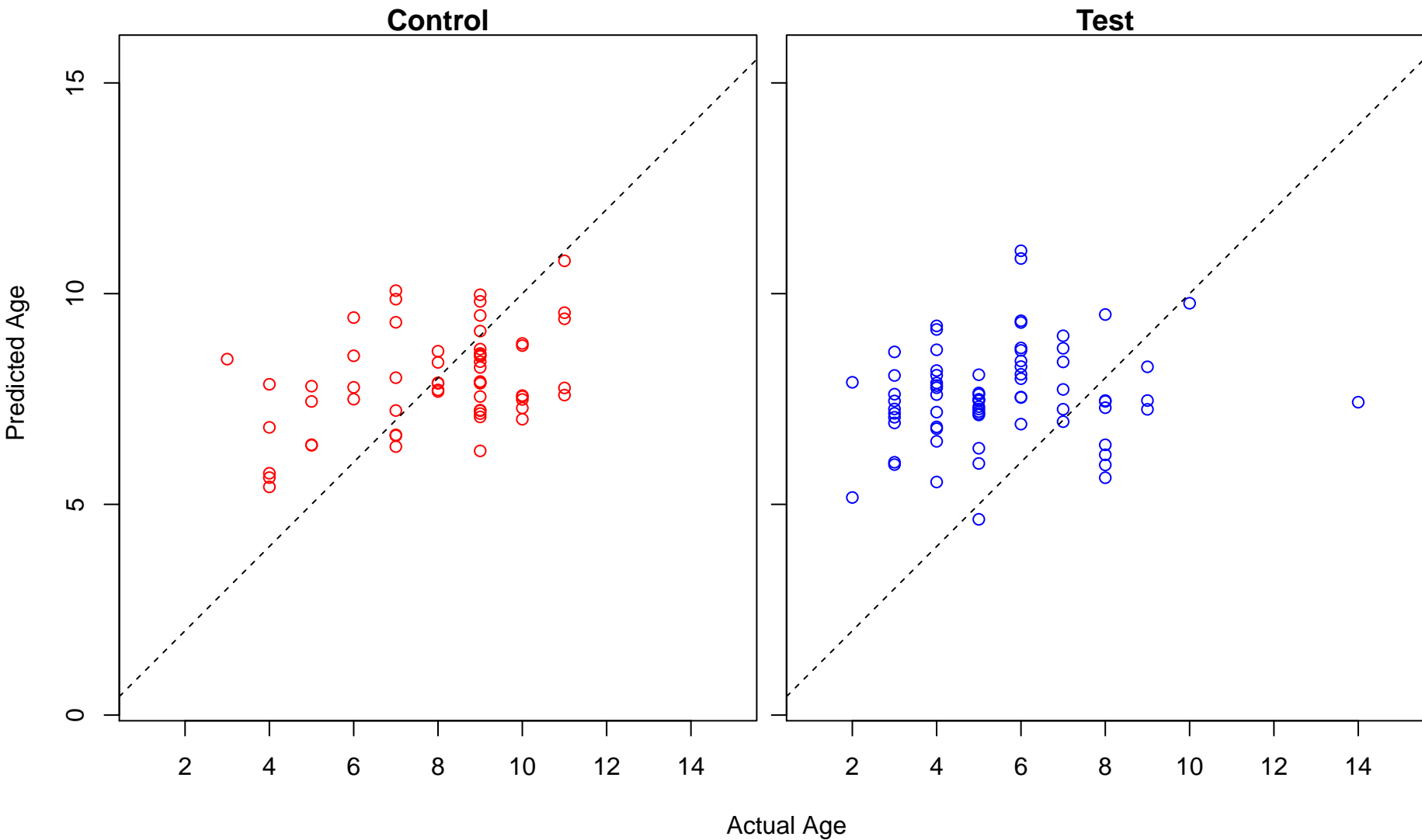
regulation of hair cycle (Score: 0.676826)



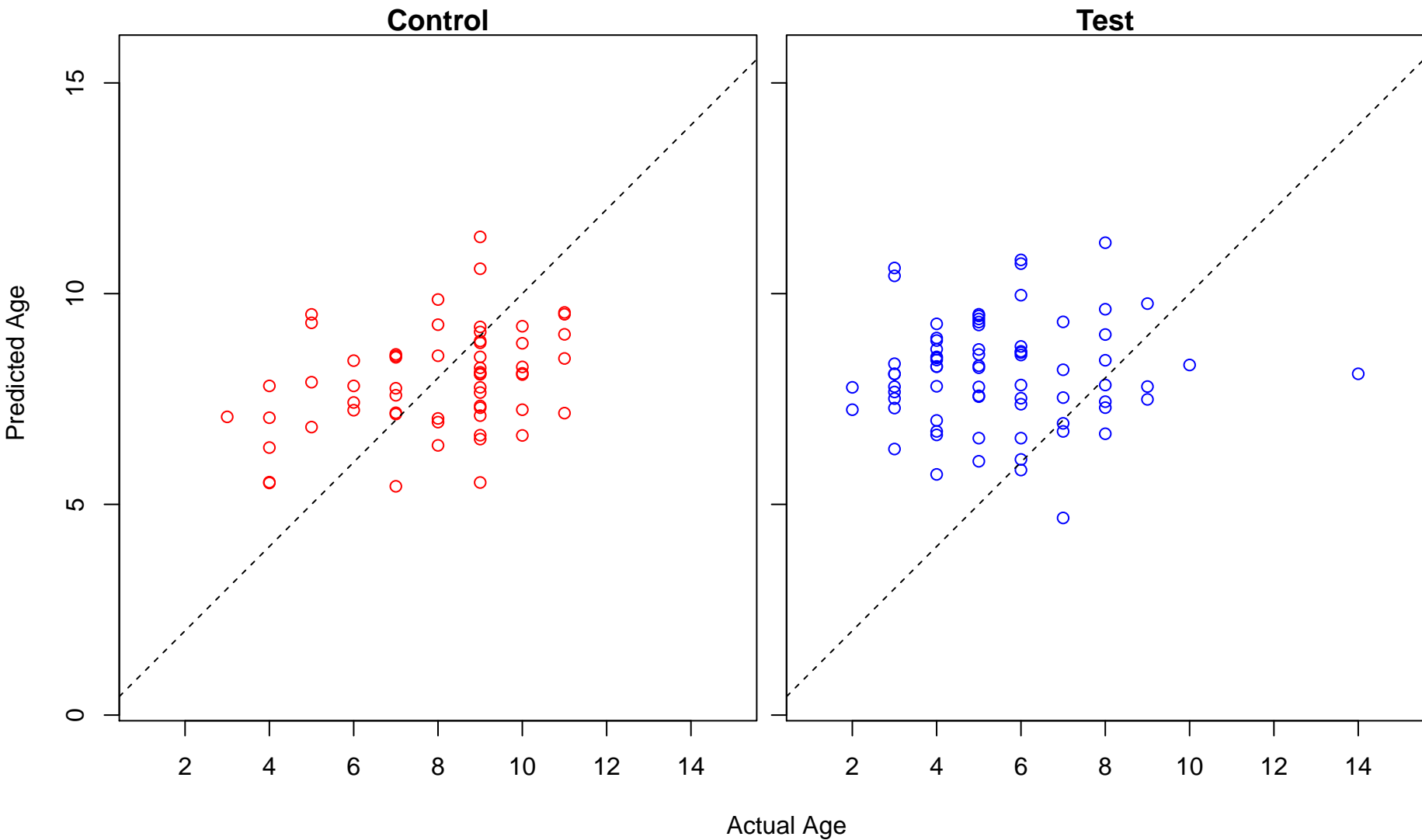
negative regulation of smoothened signaling pathway (Score: 0.674501)



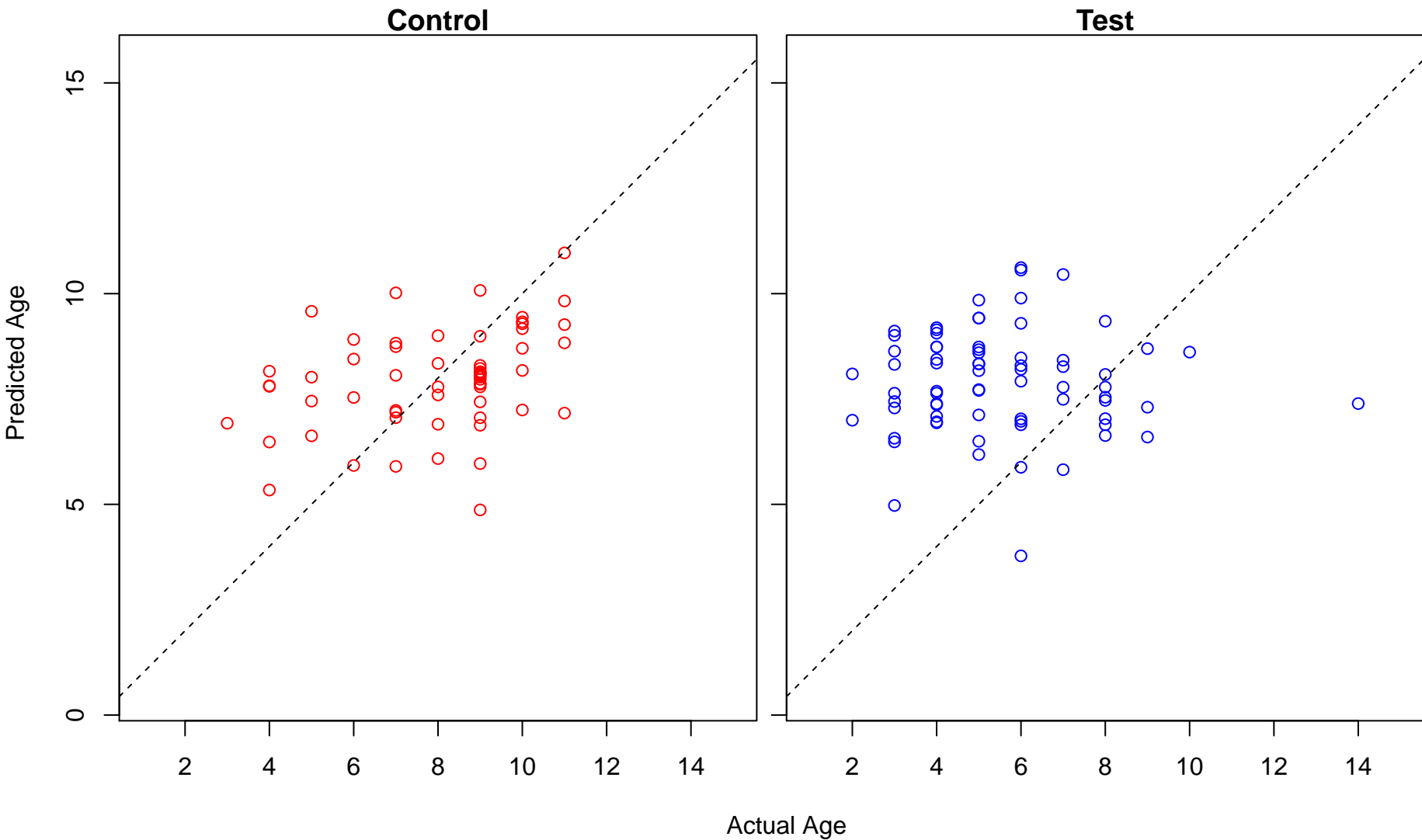
auditory receptor cell development (Score: 0.674469)



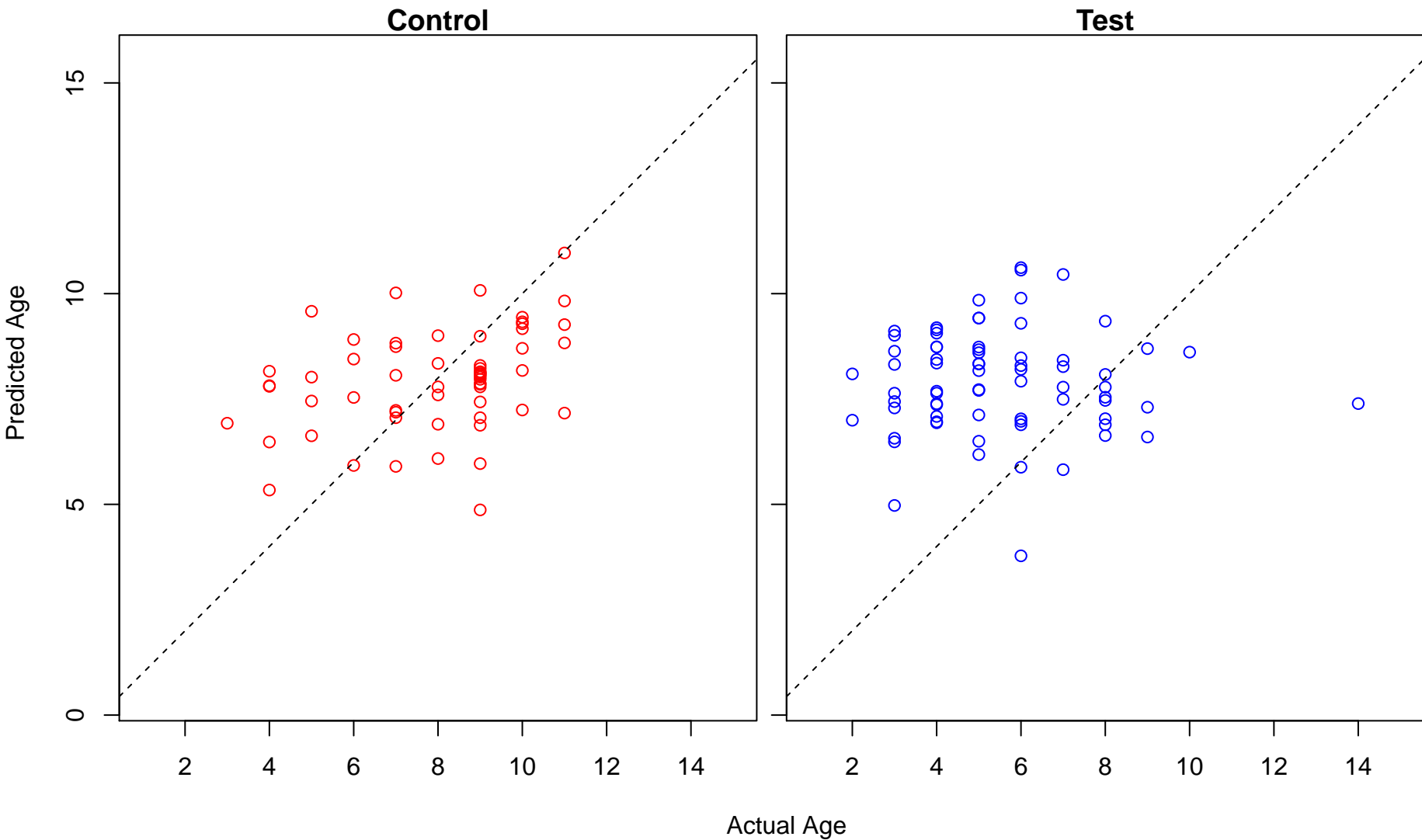
production of molecular mediator involved in inflammatory response (Score: 0.672555)



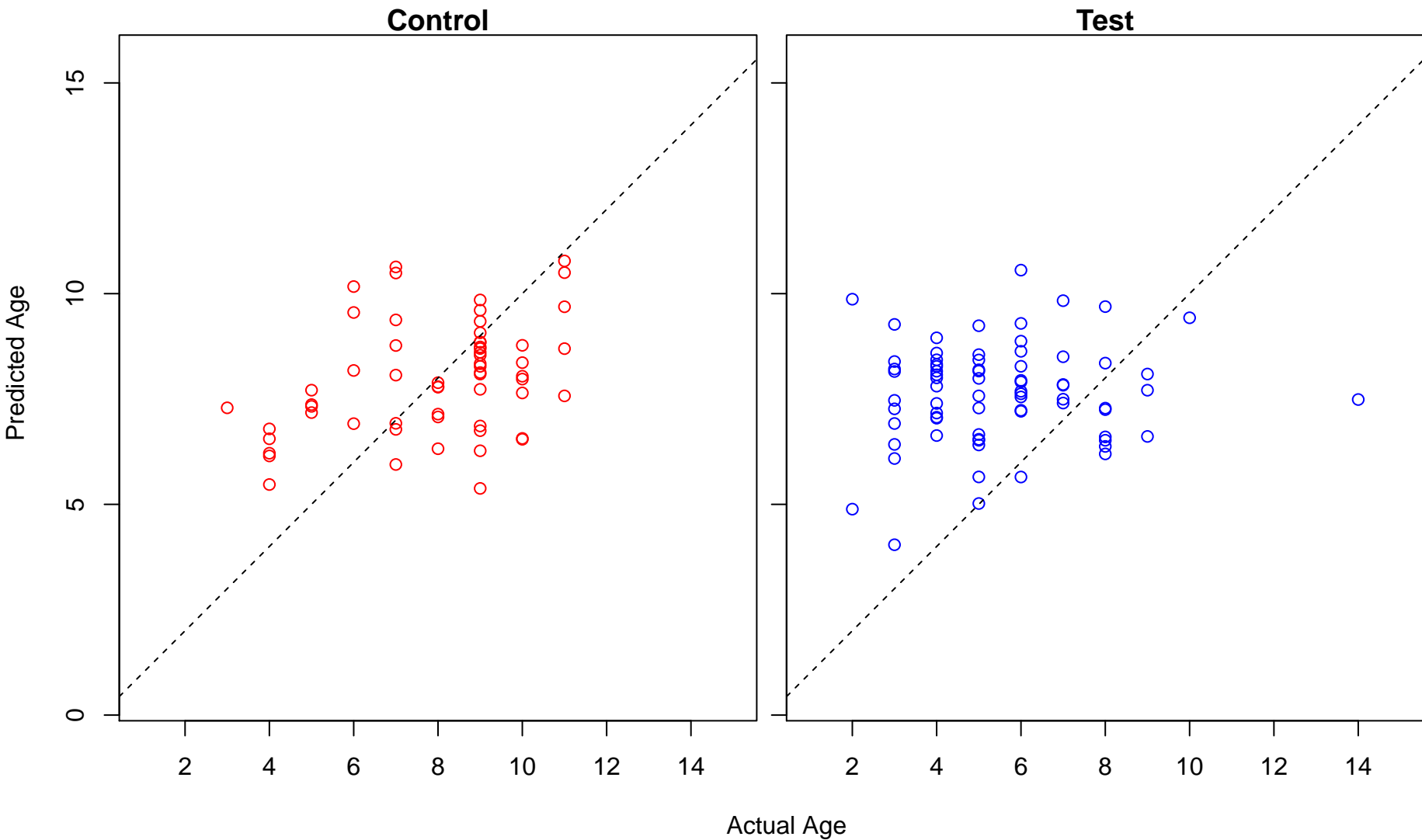
cardiac muscle hypertrophy (Score: 0.671620)



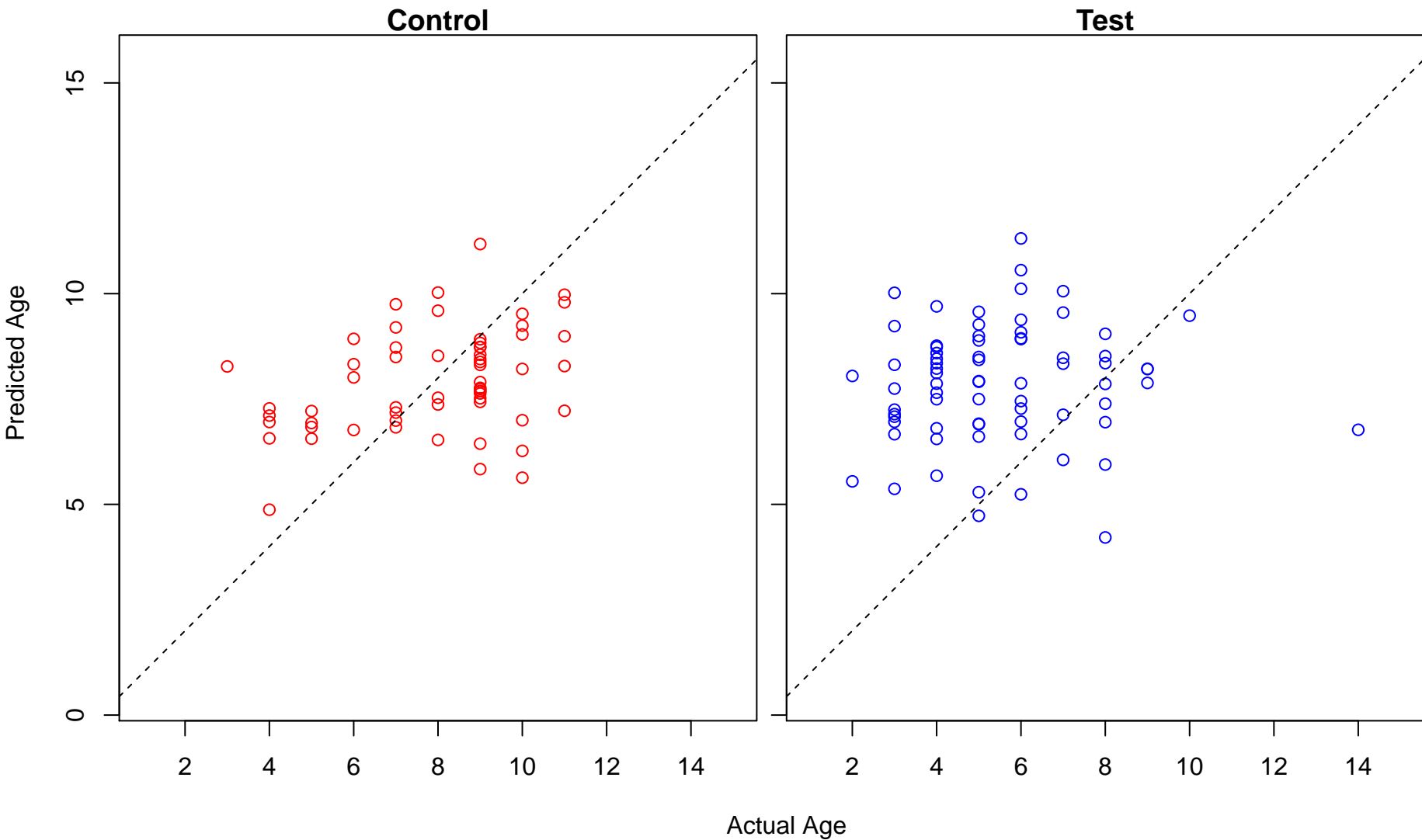
striated muscle hypertrophy (Score: 0.671318)



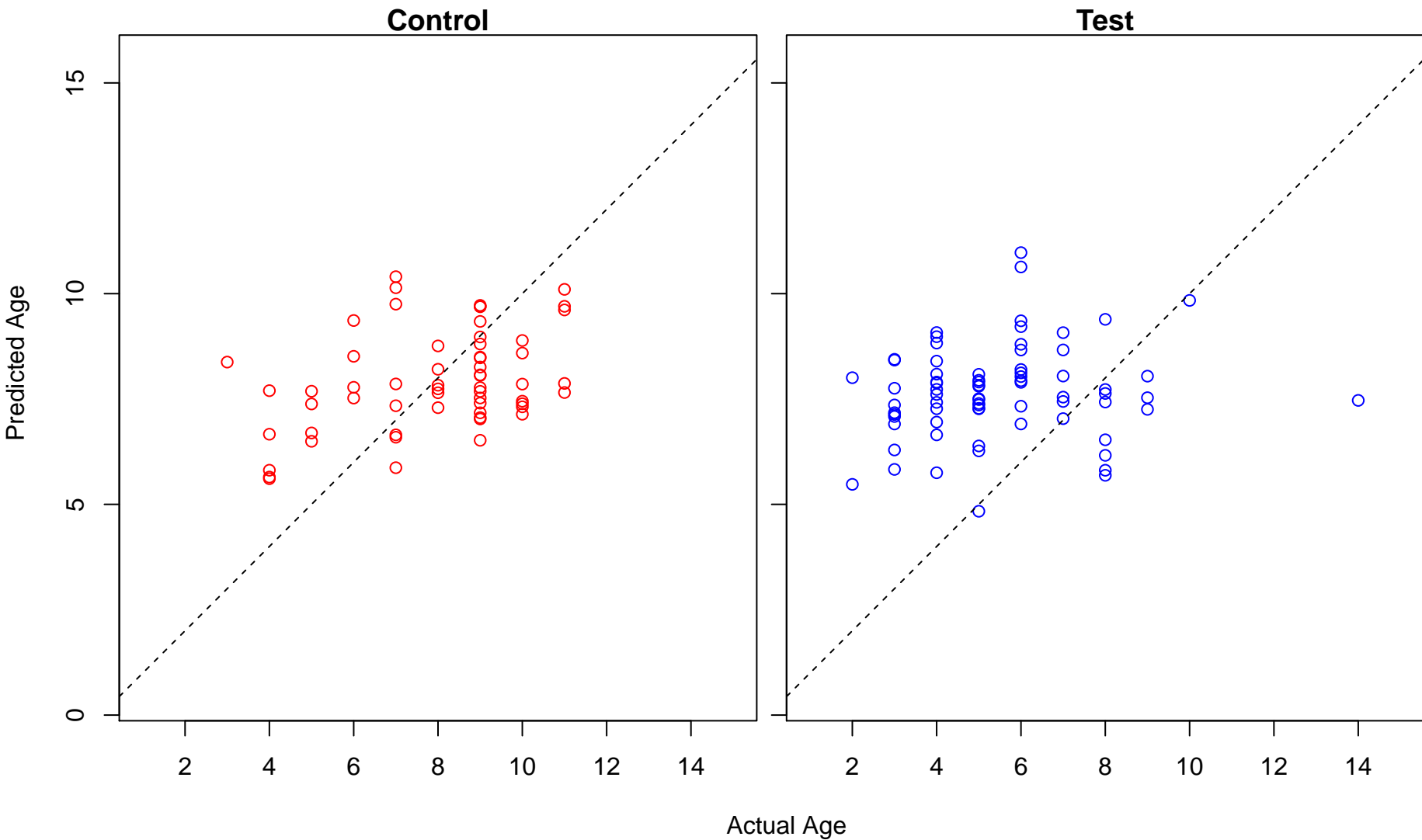
regulation of endothelial cell proliferation (Score: 0.671216)



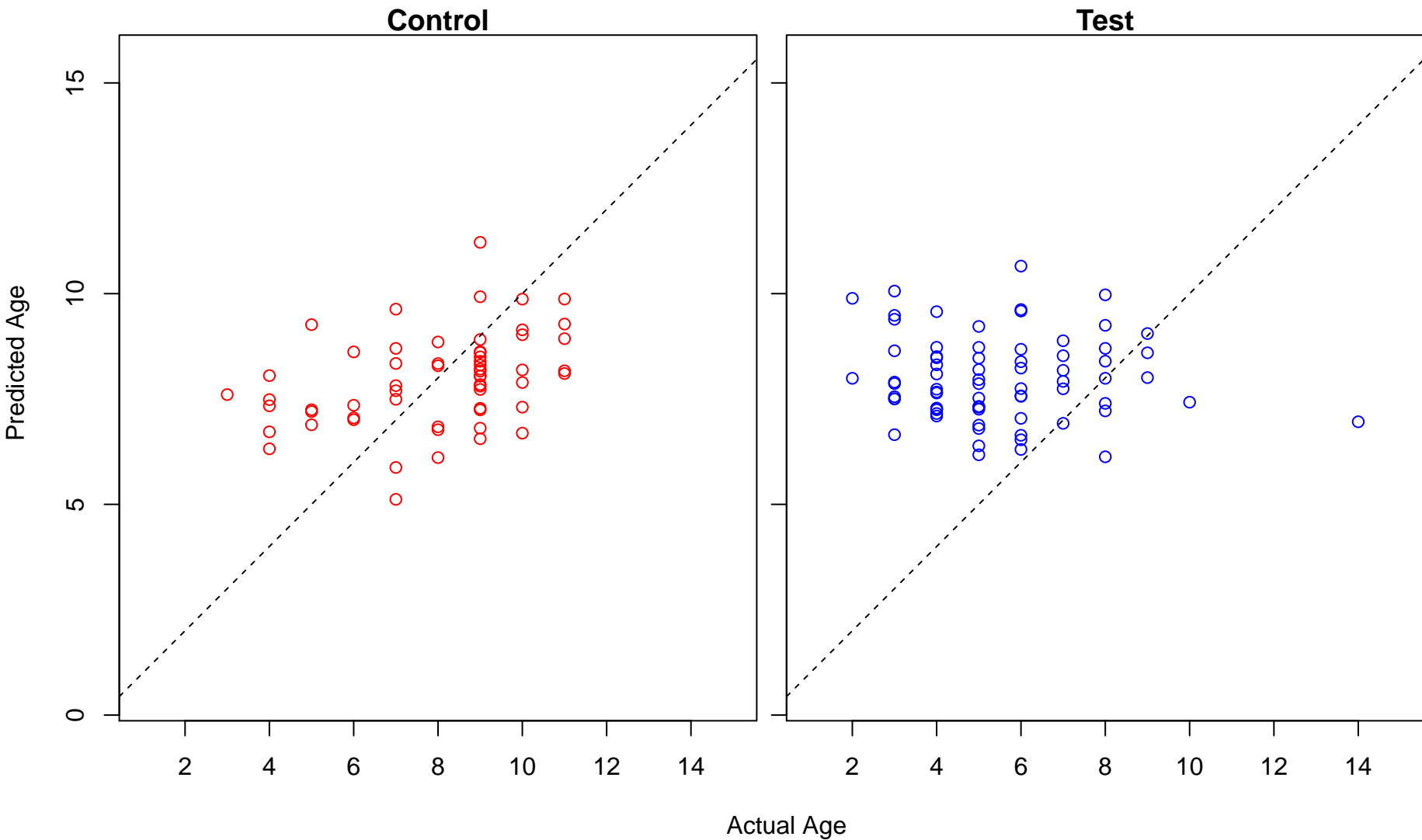
cerebral cortex GABAergic interneuron development (Score: 0.671103)



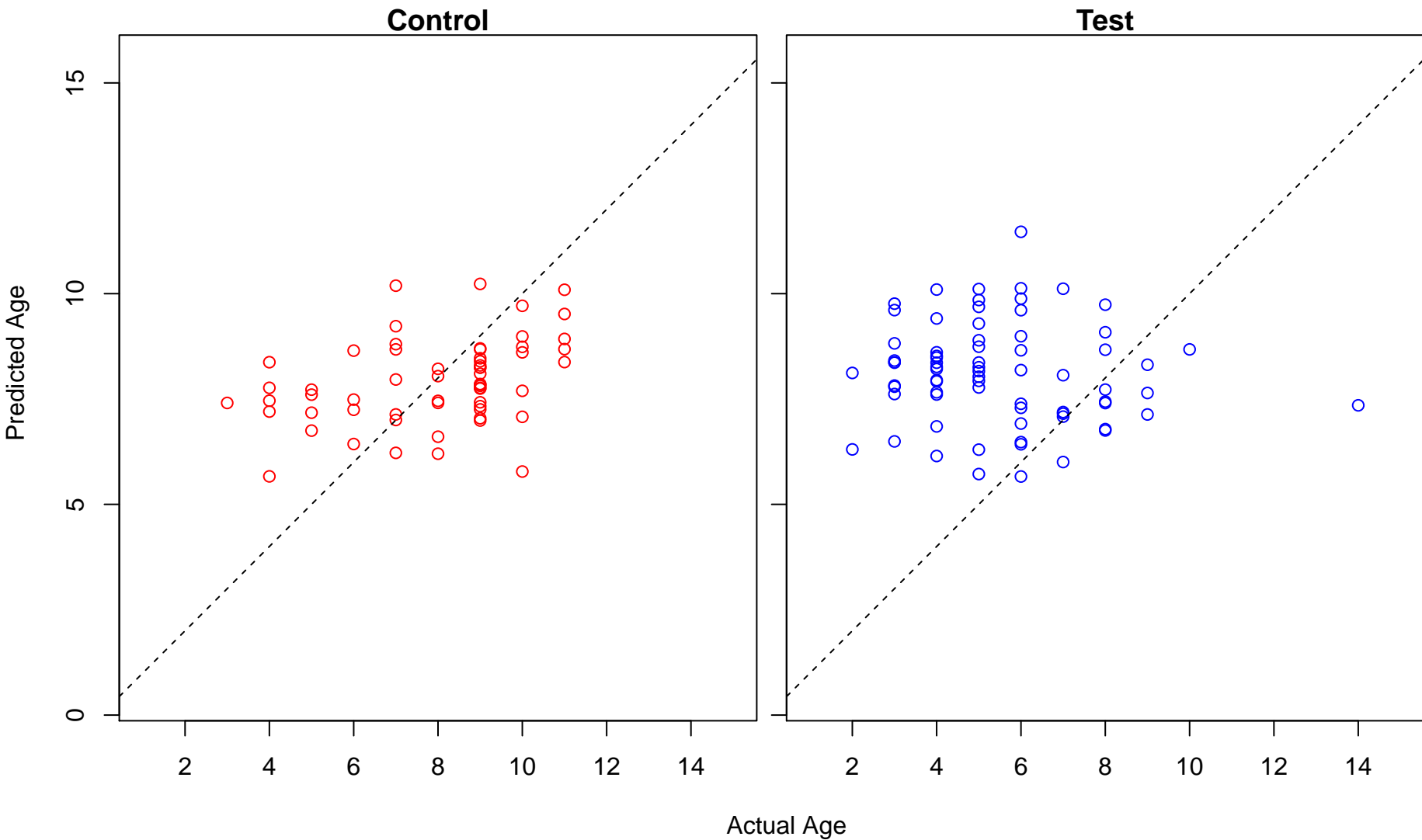
inner ear receptor cell development (Score: 0.670409)



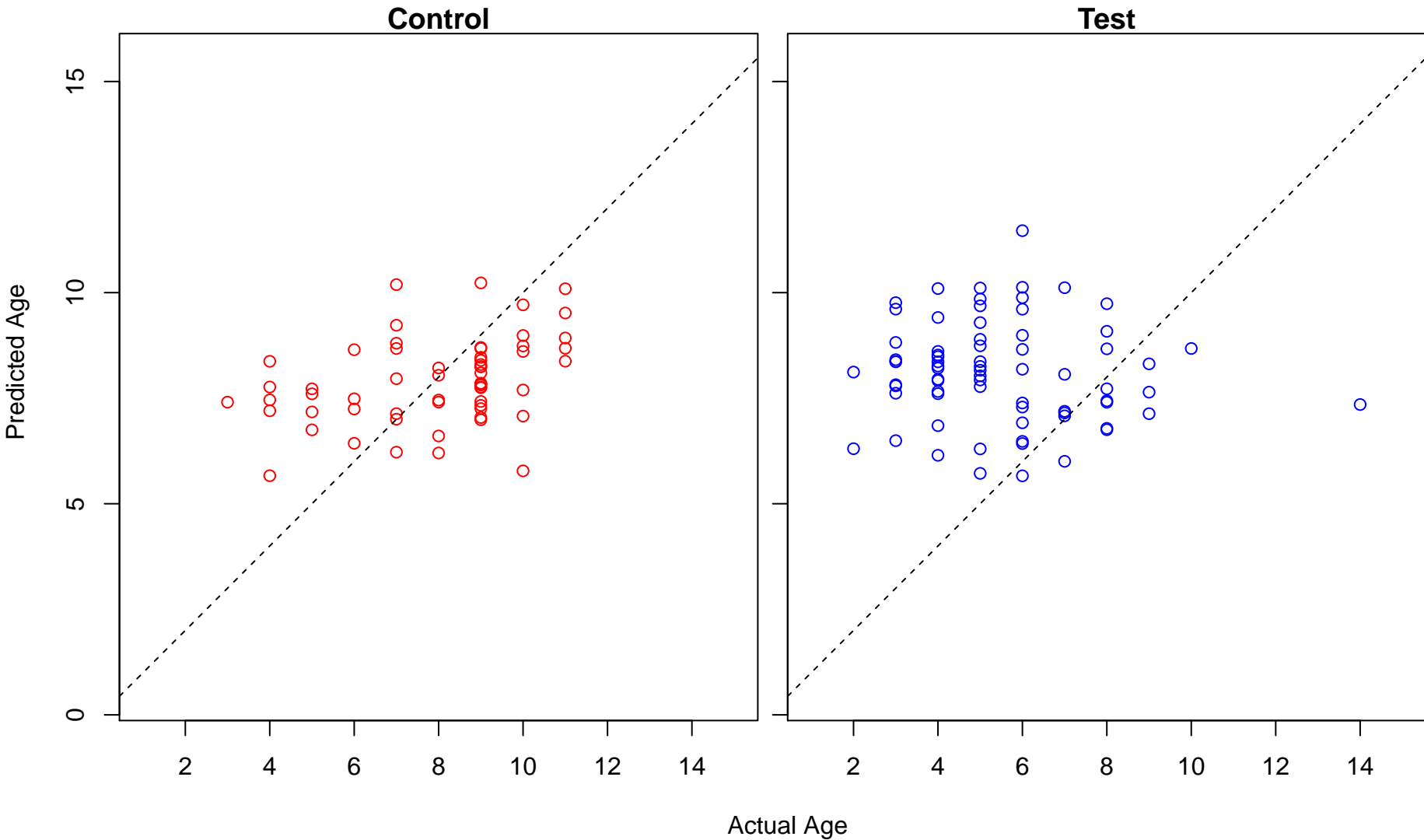
pseudopodium organization (Score: 0.670228)



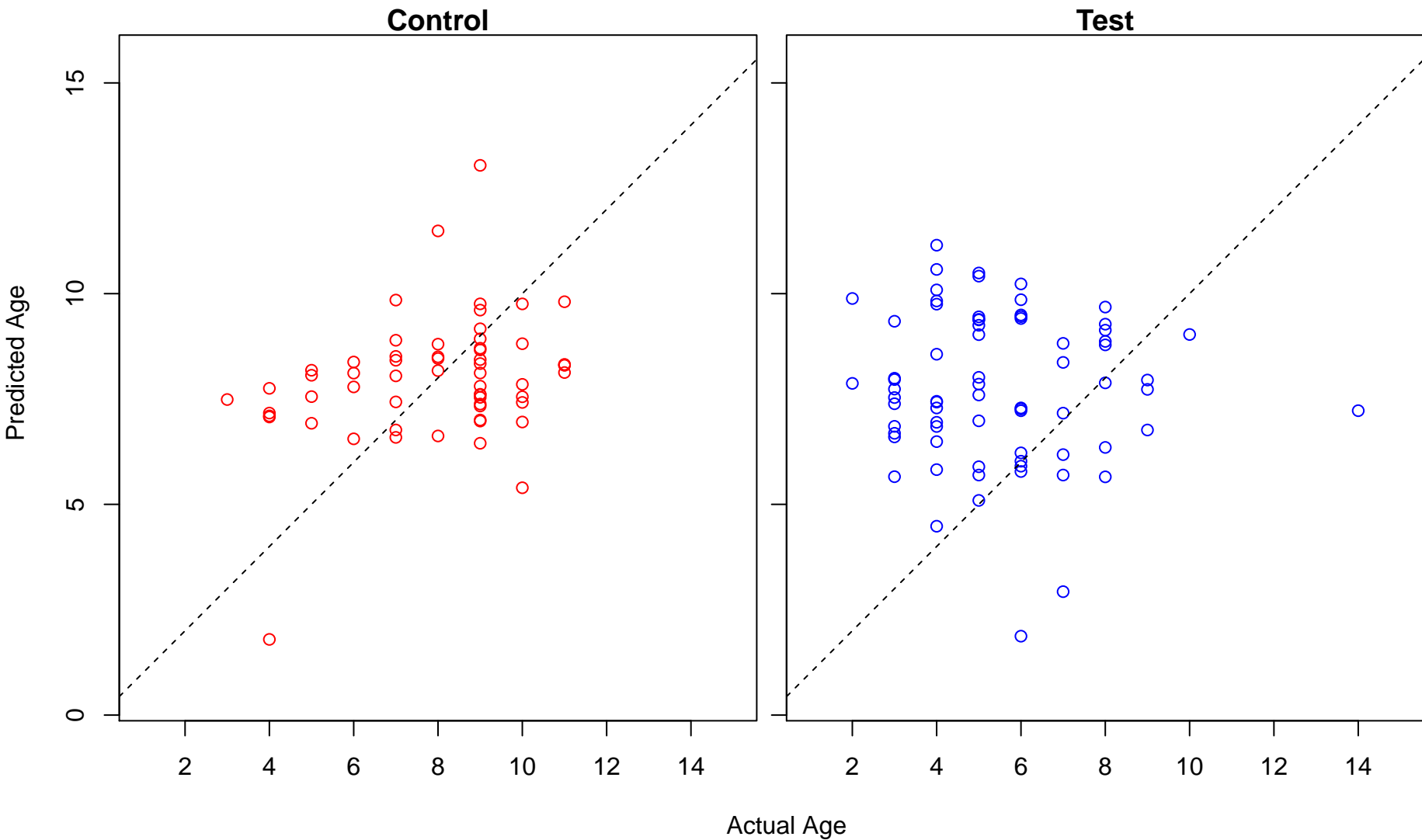
synaptonemal complex assembly (Score: 0.669622)



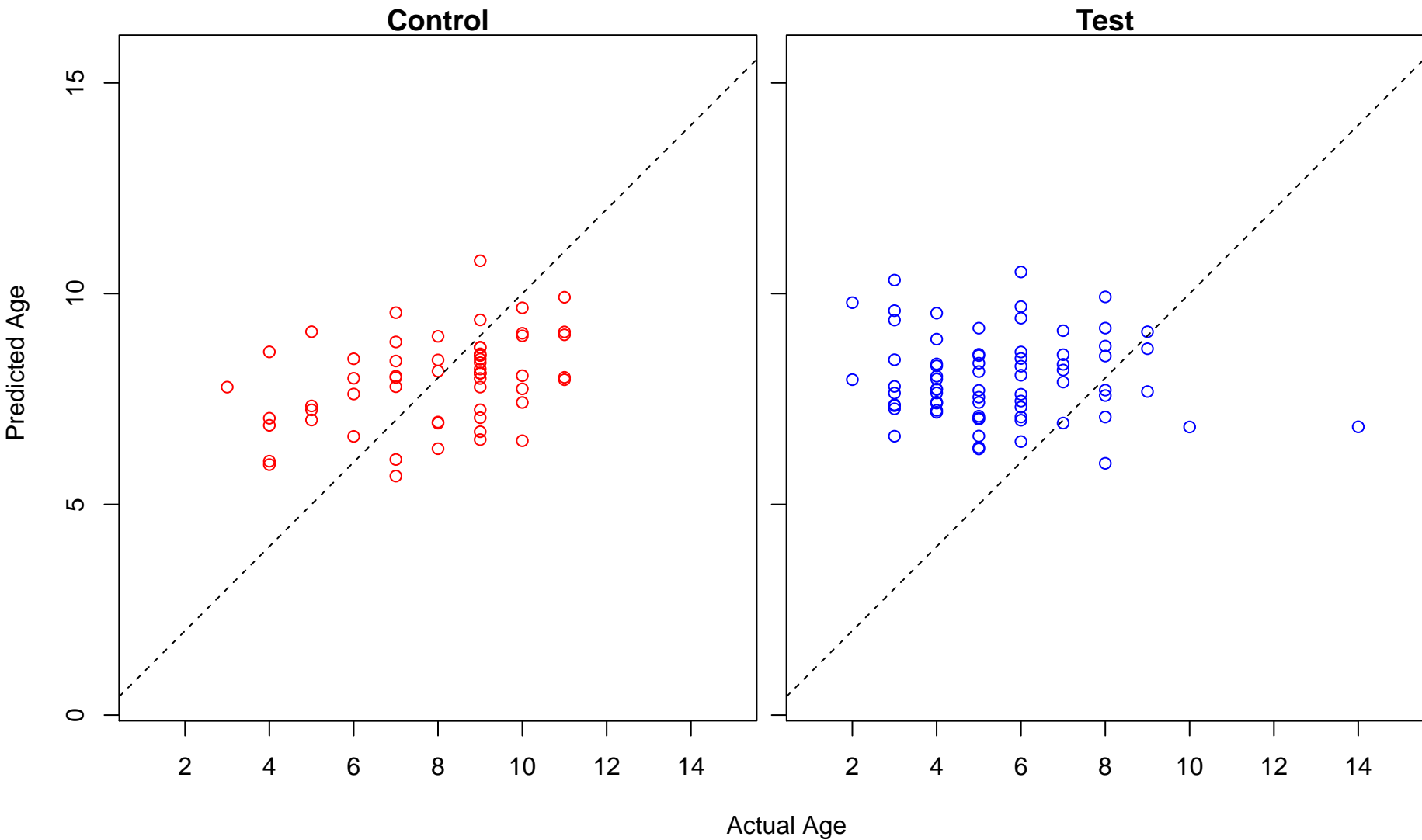
synaptonemal complex organization (Score: 0.669622)



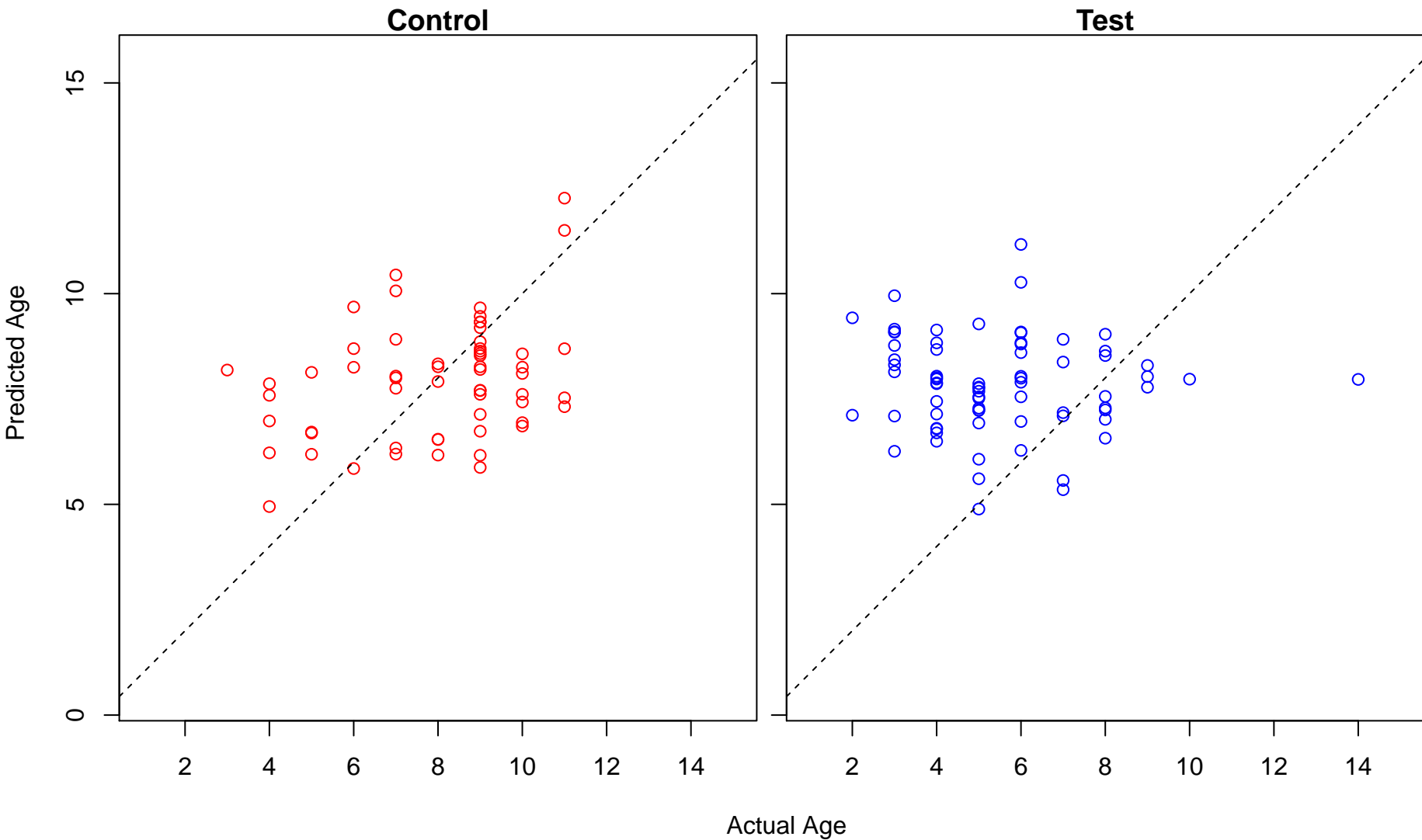
neurotransmitter uptake (Score: 0.666103)



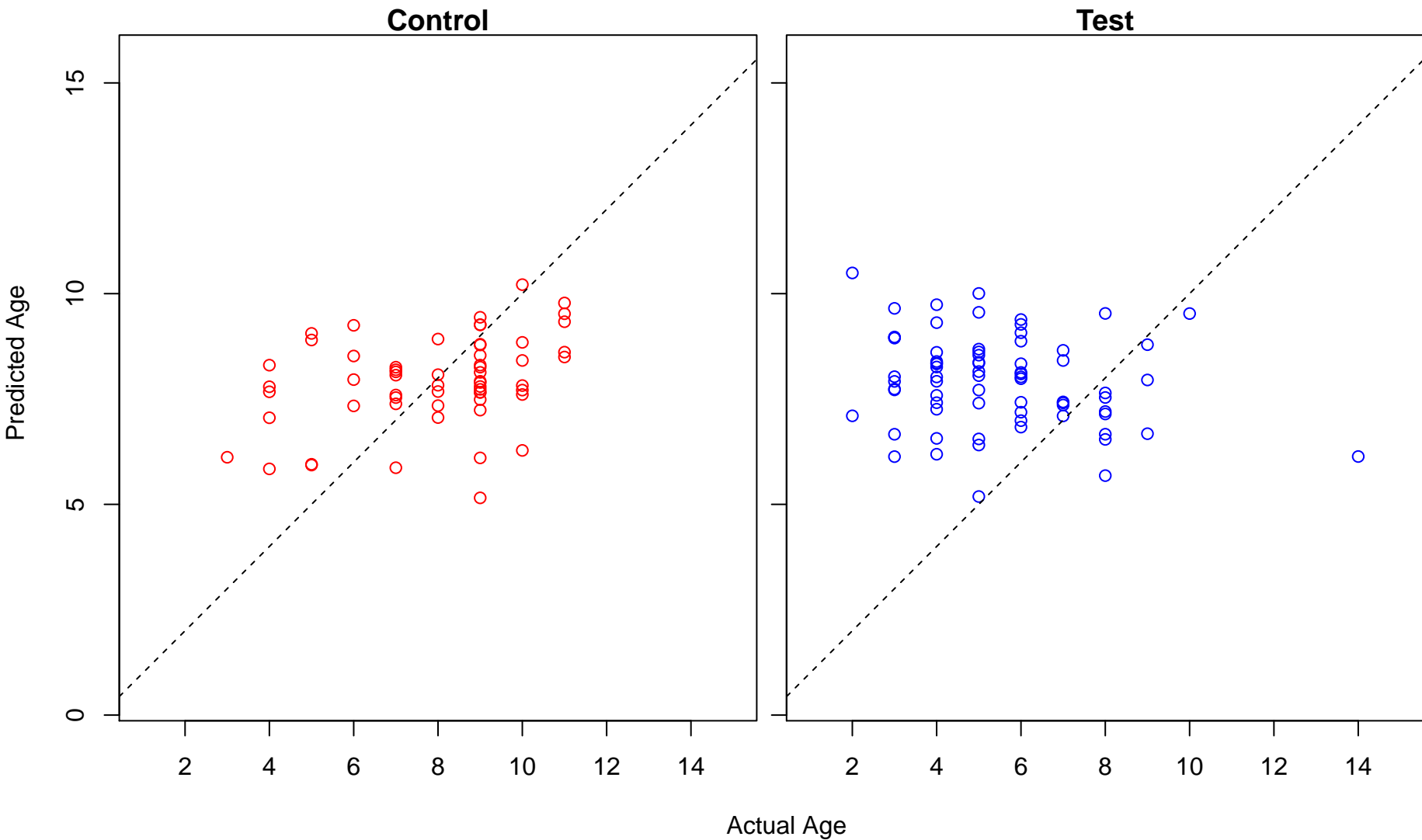
lamellipodium assembly involved in ameboidal cell migration (Score: 0.665692)



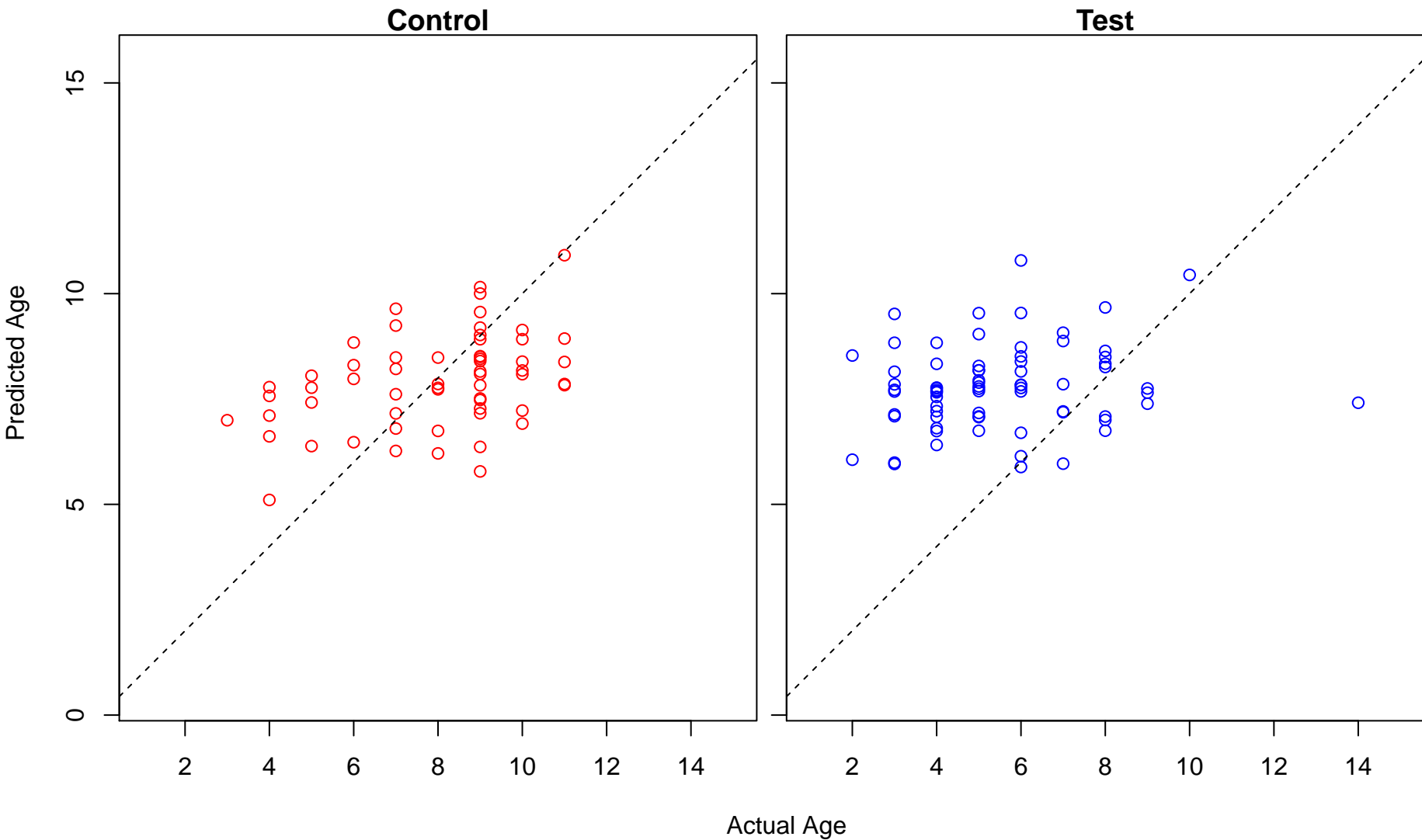
regulation of anion transport (Score: 0.665505)



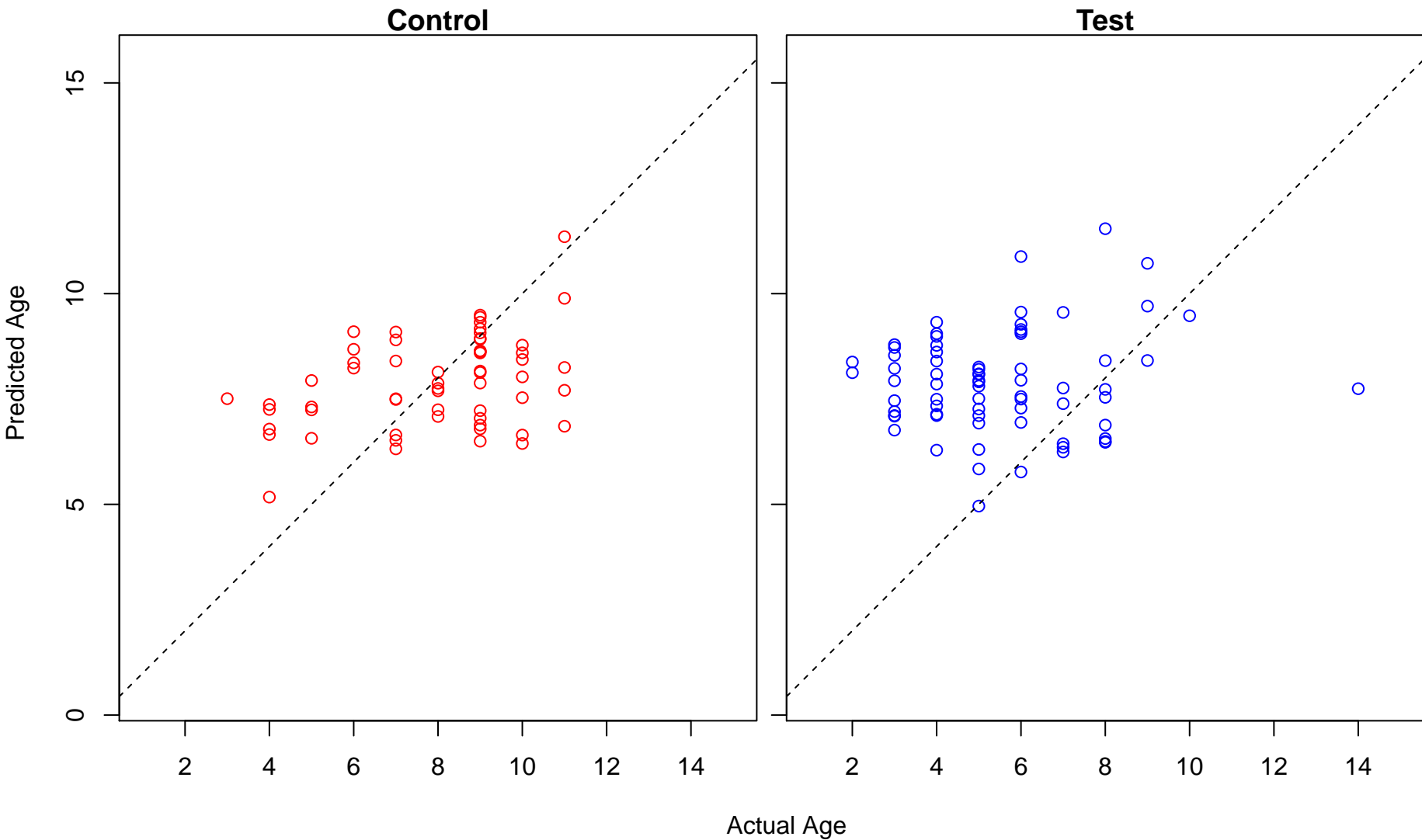
viral genome replication (Score: 0.664833)



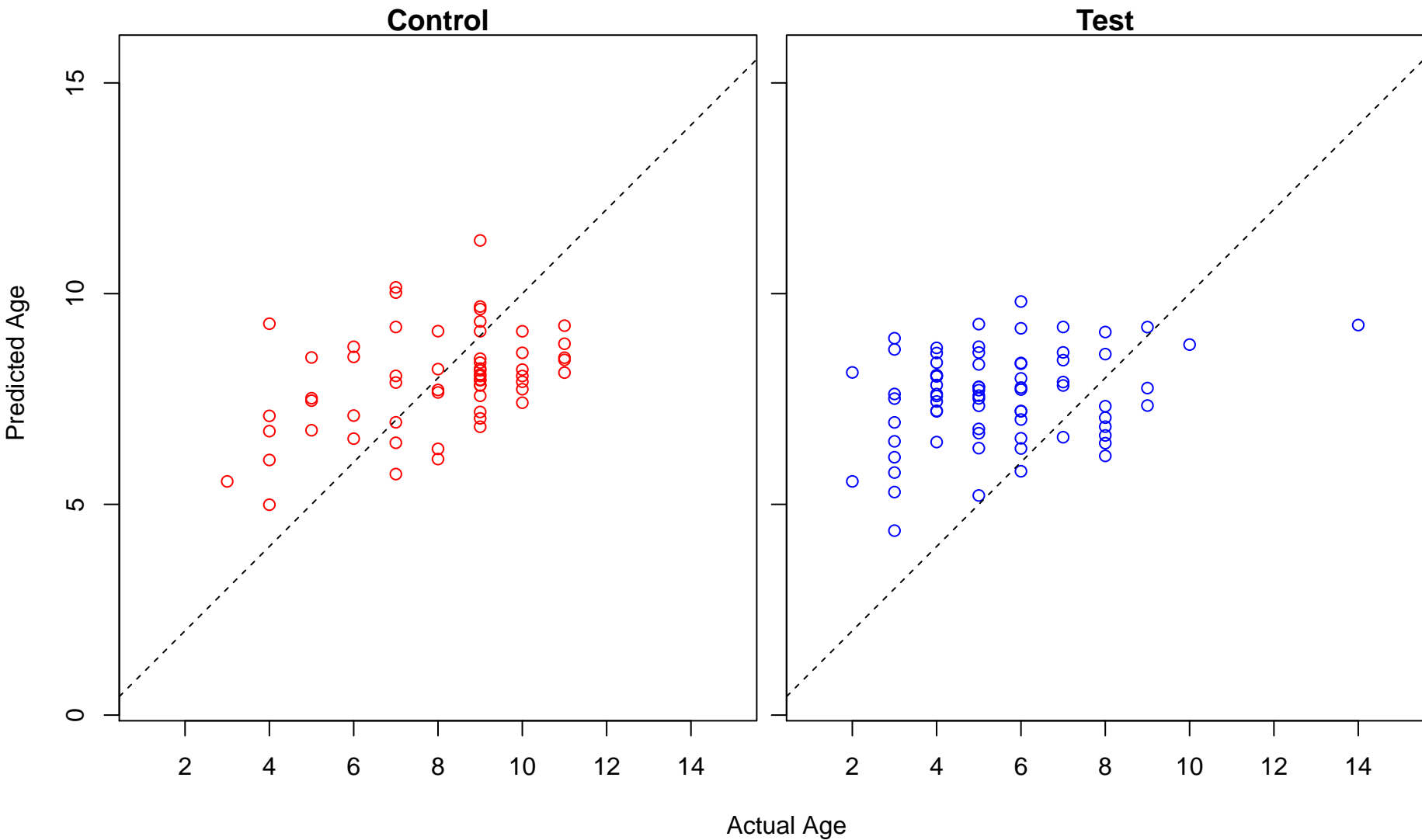
calcium-mediated signaling using intracellular calcium source (Score: 0.664697)



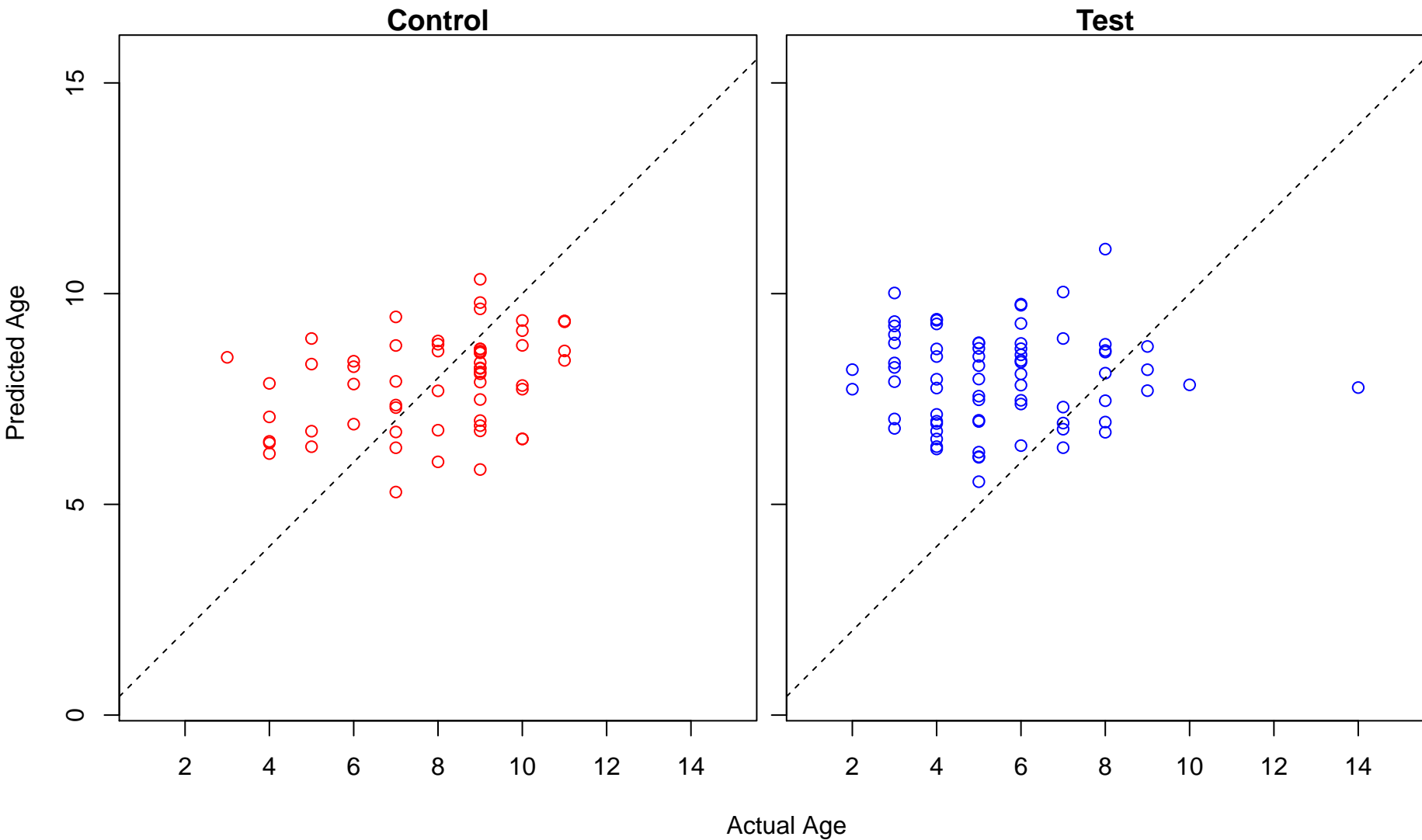
peptide cross-linking (Score: 0.664686)



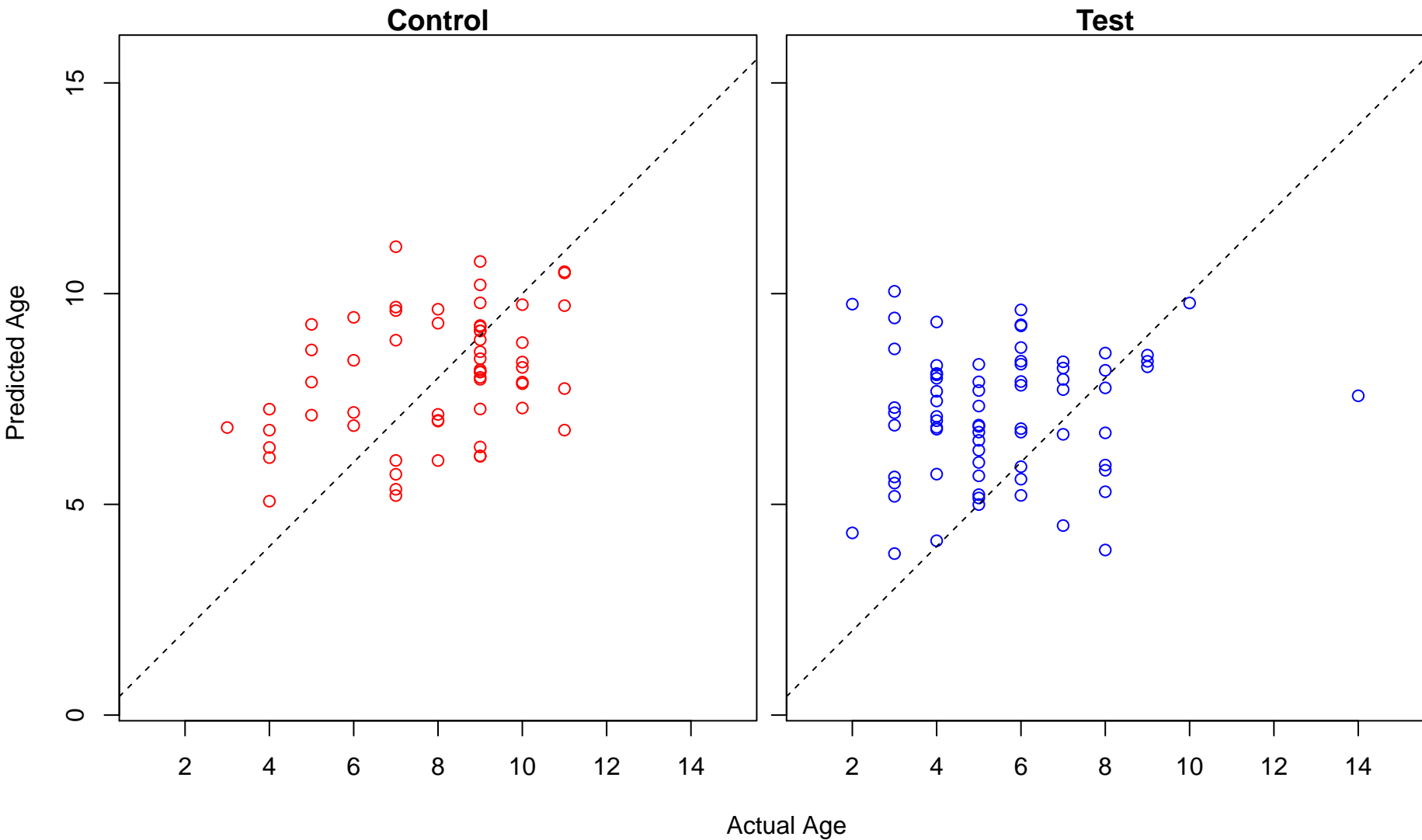
immunological synapse formation (Score: 0.664448)



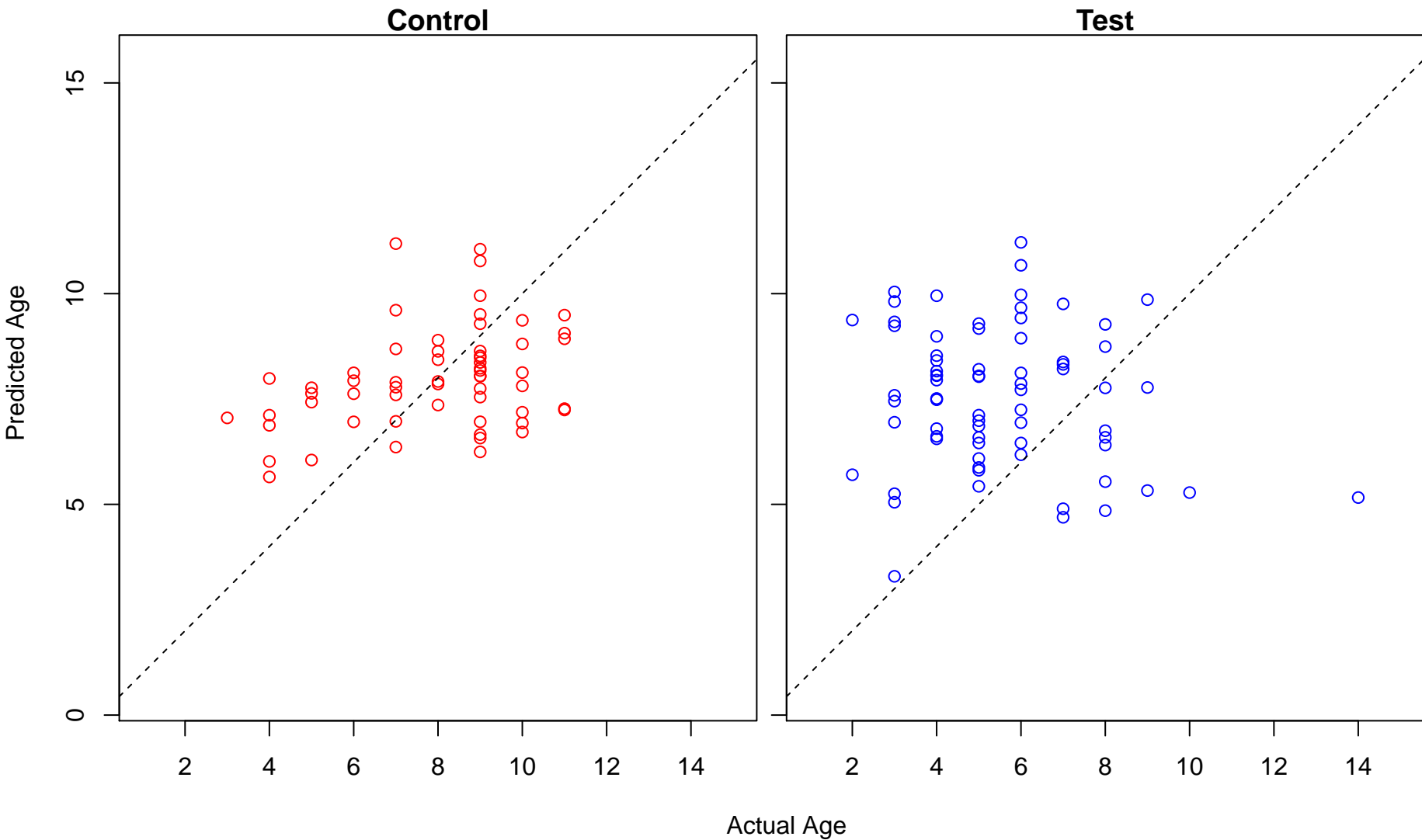
adherens junction assembly (Score: 0.661385)



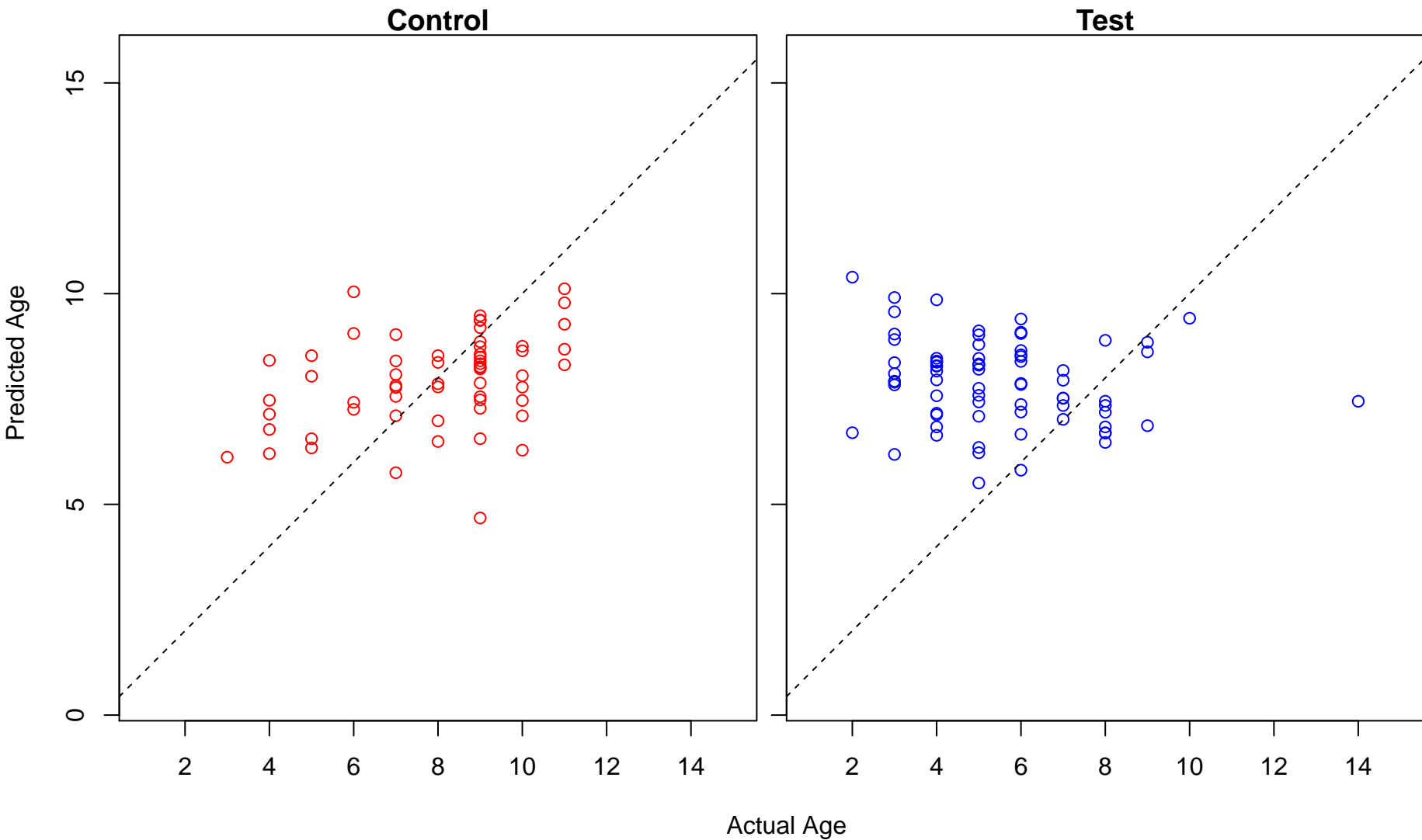
lysosomal transport (Score: 0.658538)



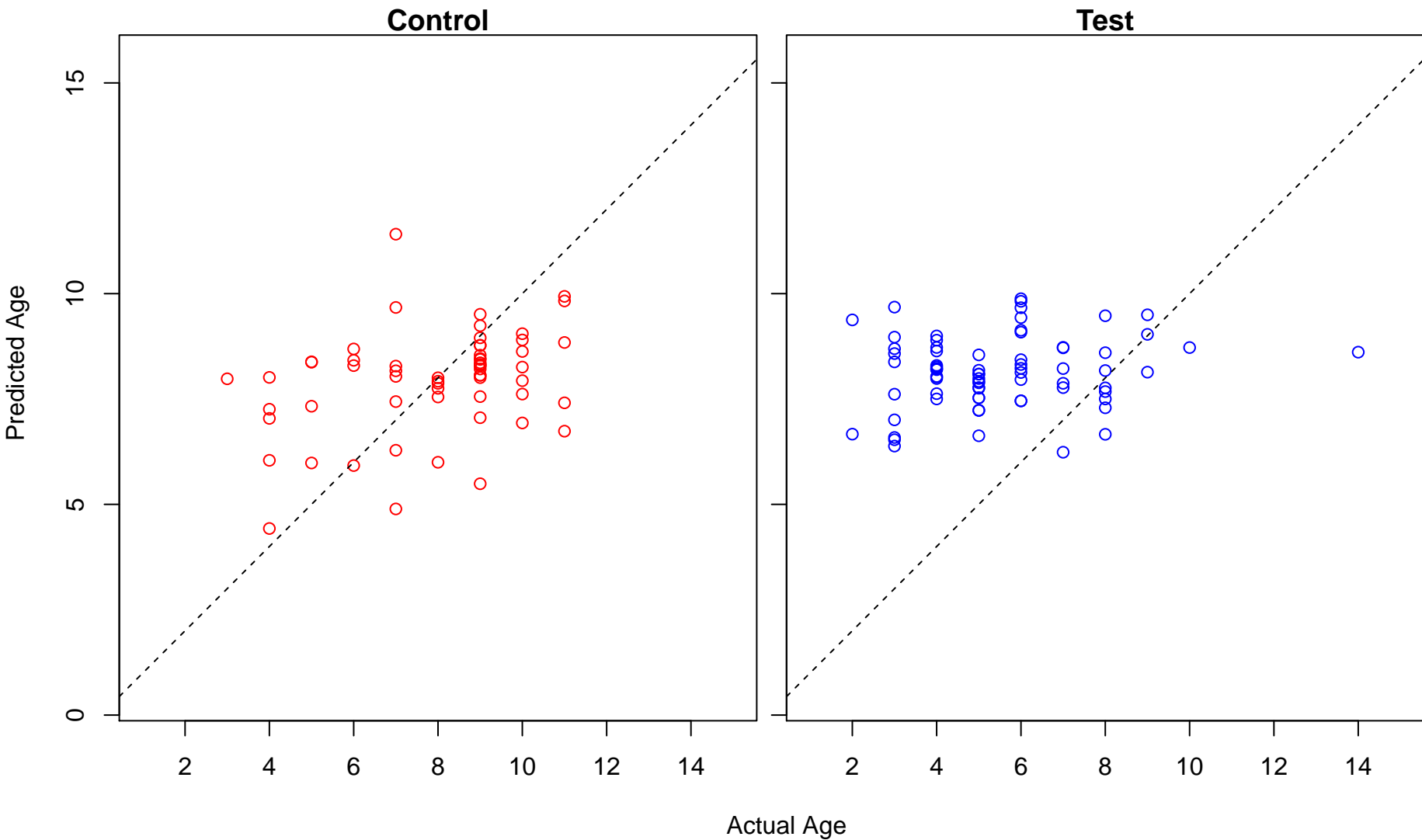
positive regulation of SMAD protein import into nucleus (Score: 0.657861)



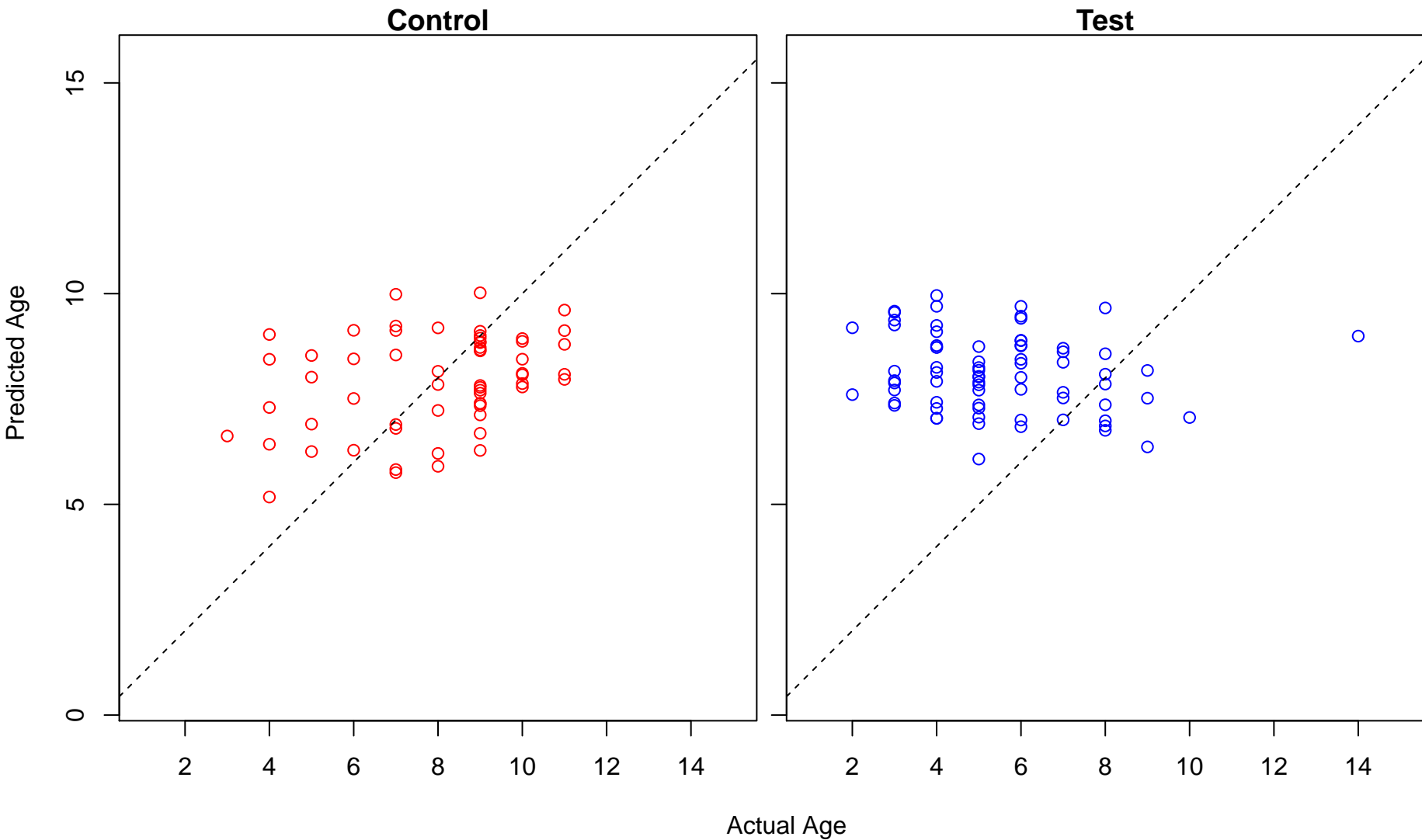
white fat cell differentiation (Score: 0.656261)



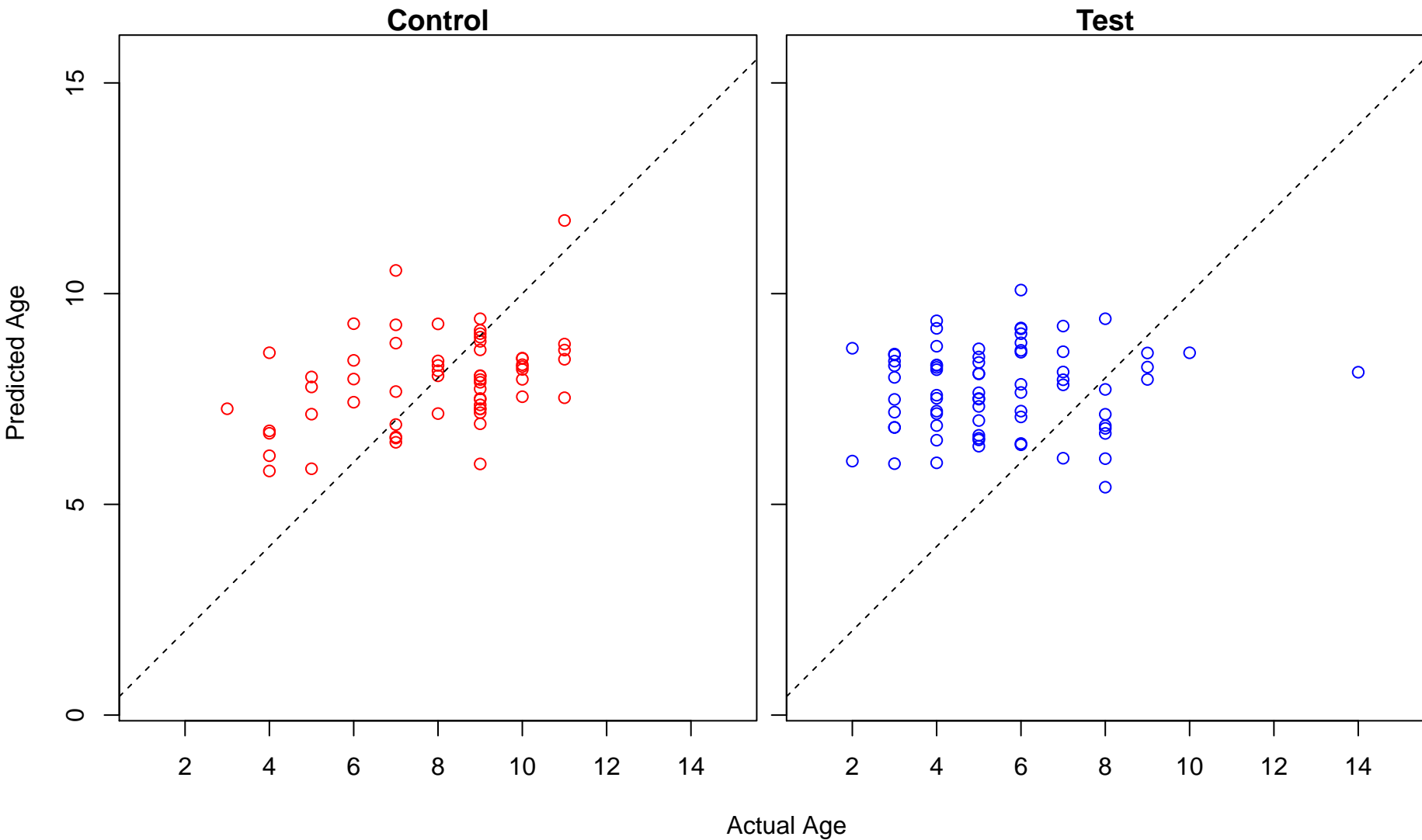
epithelial cell morphogenesis (Score: 0.655417)



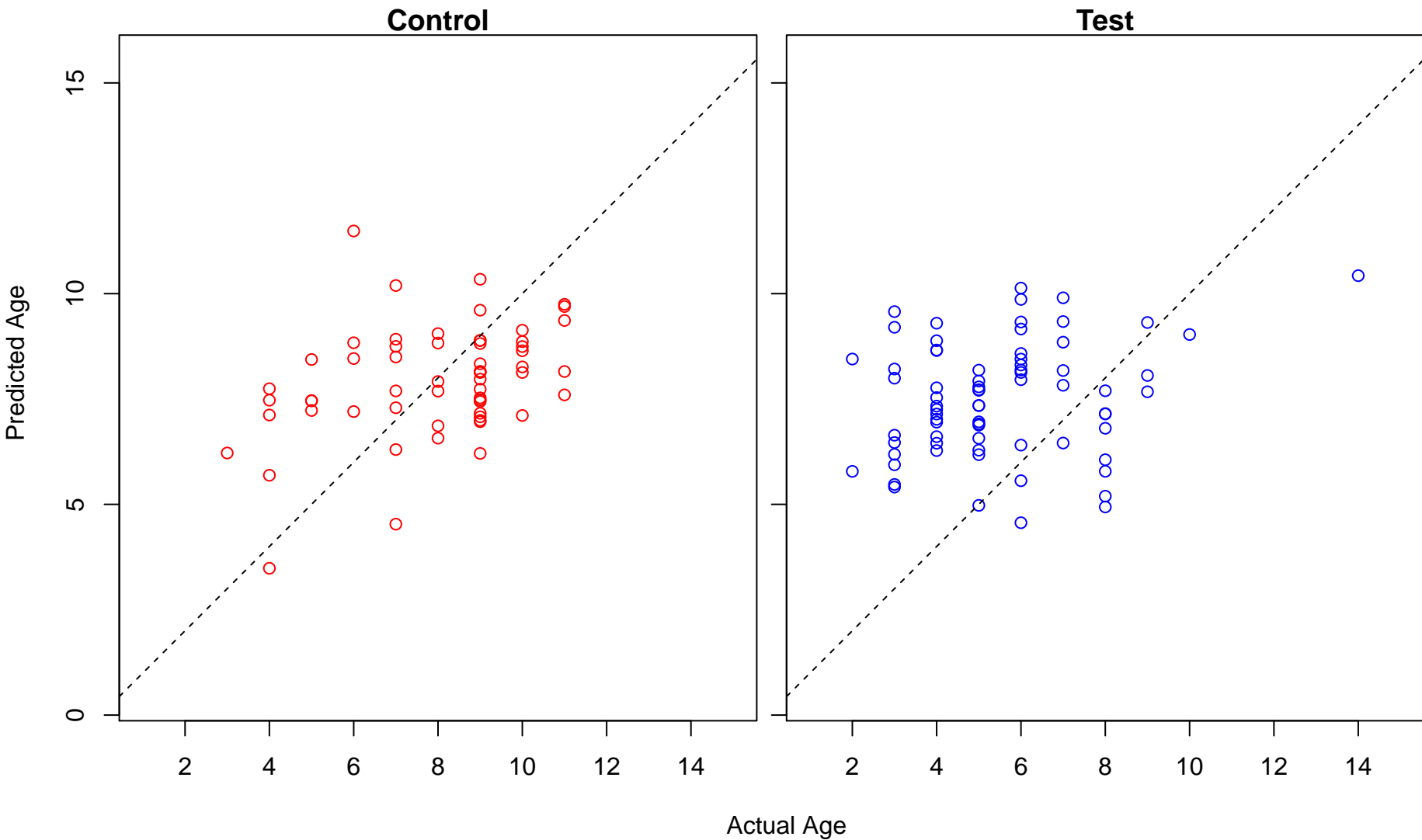
negative regulation of tyrosine phosphorylation of STAT protein (Score: 0.655167)



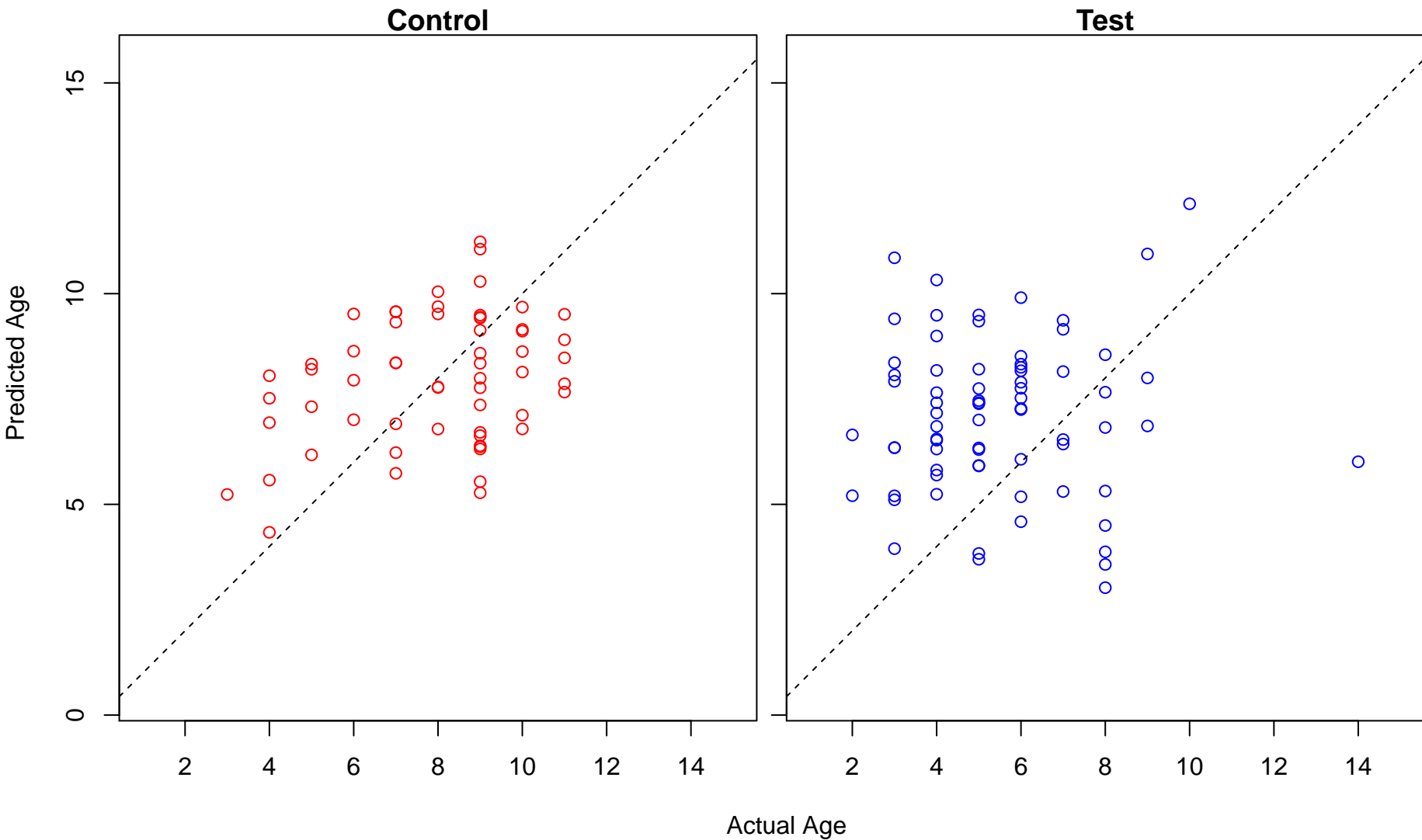
regulation of catenin import into nucleus (Score: 0.652809)



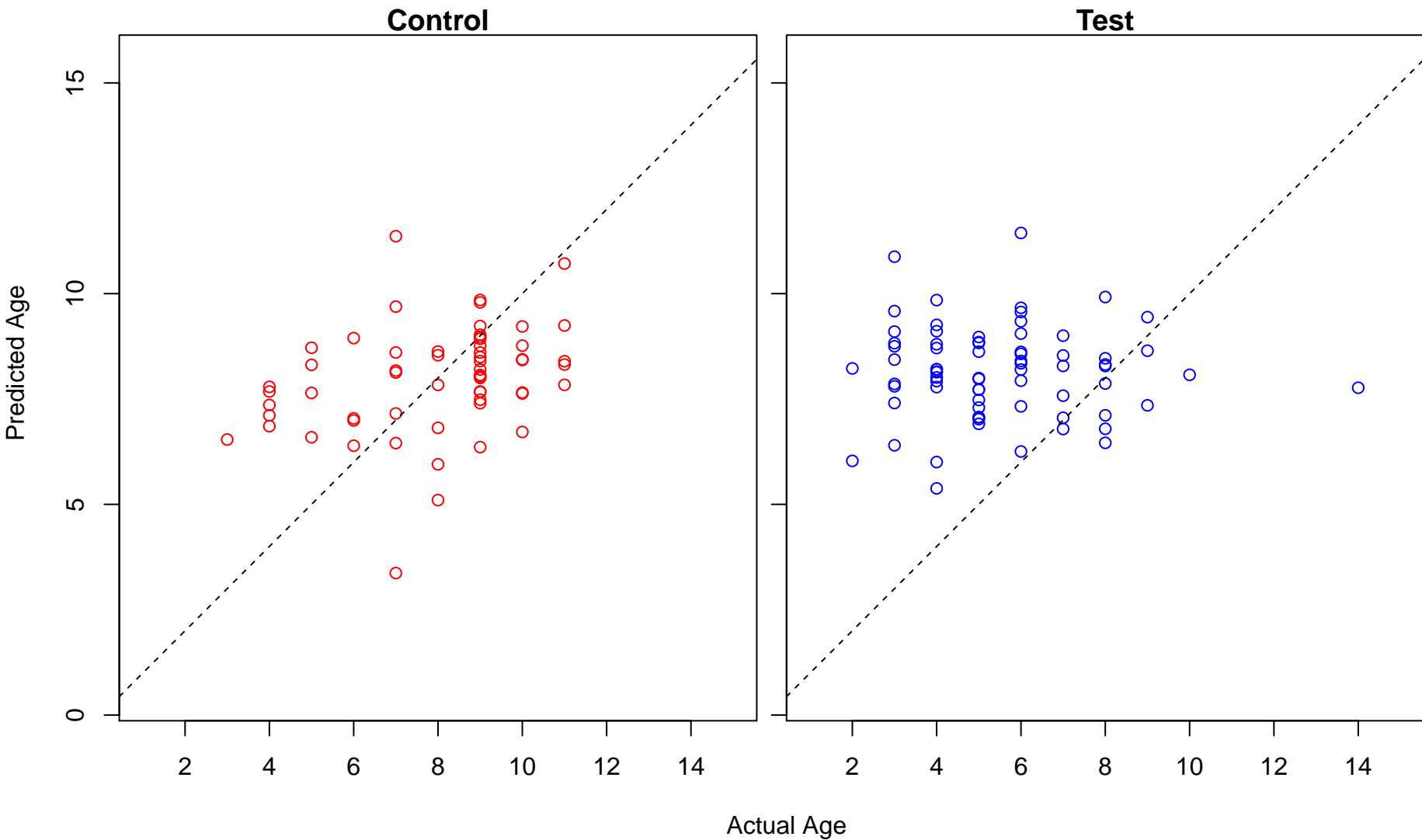
rRNA transcription (Score: 0.652567)



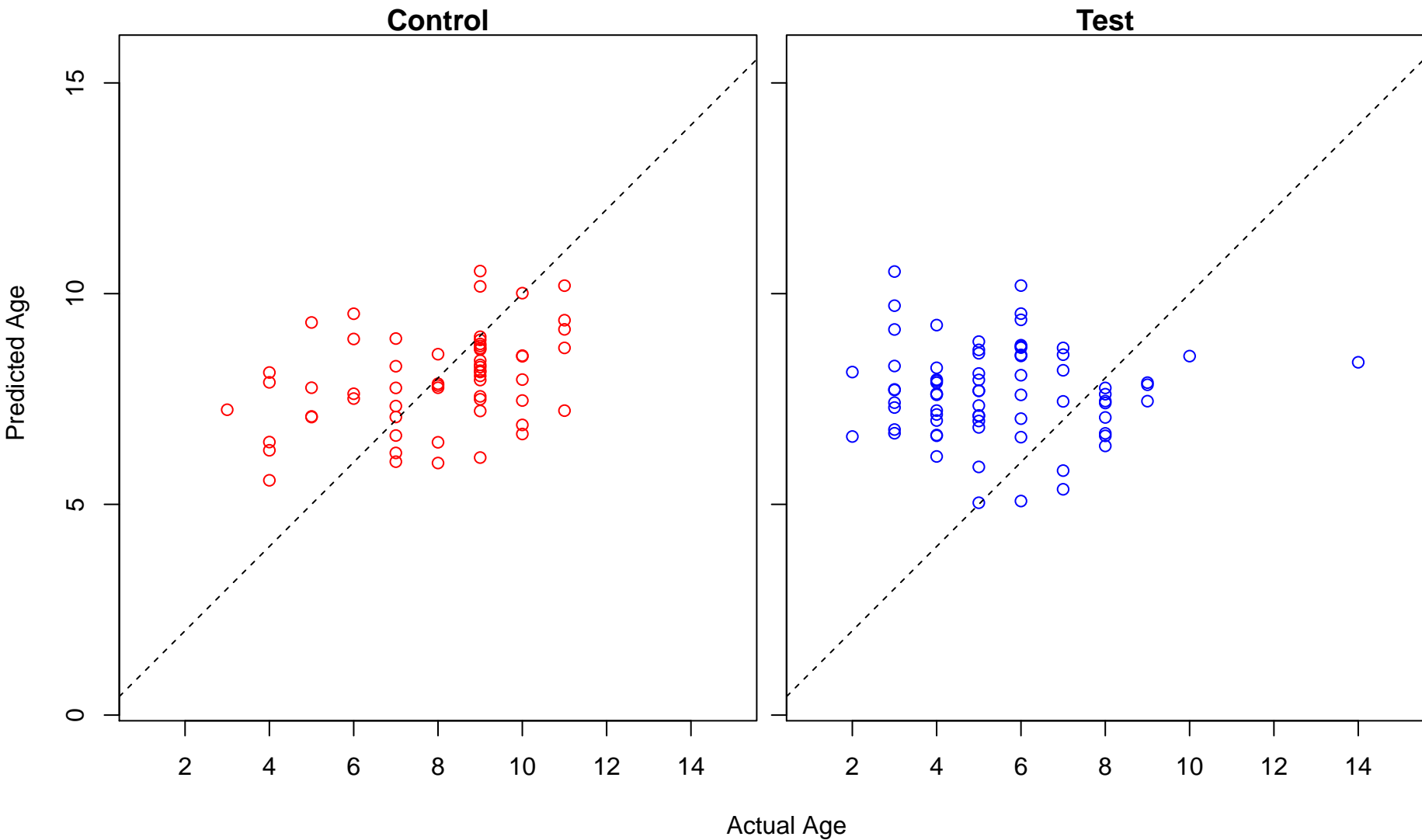
eye photoreceptor cell differentiation (Score: 0.651577)



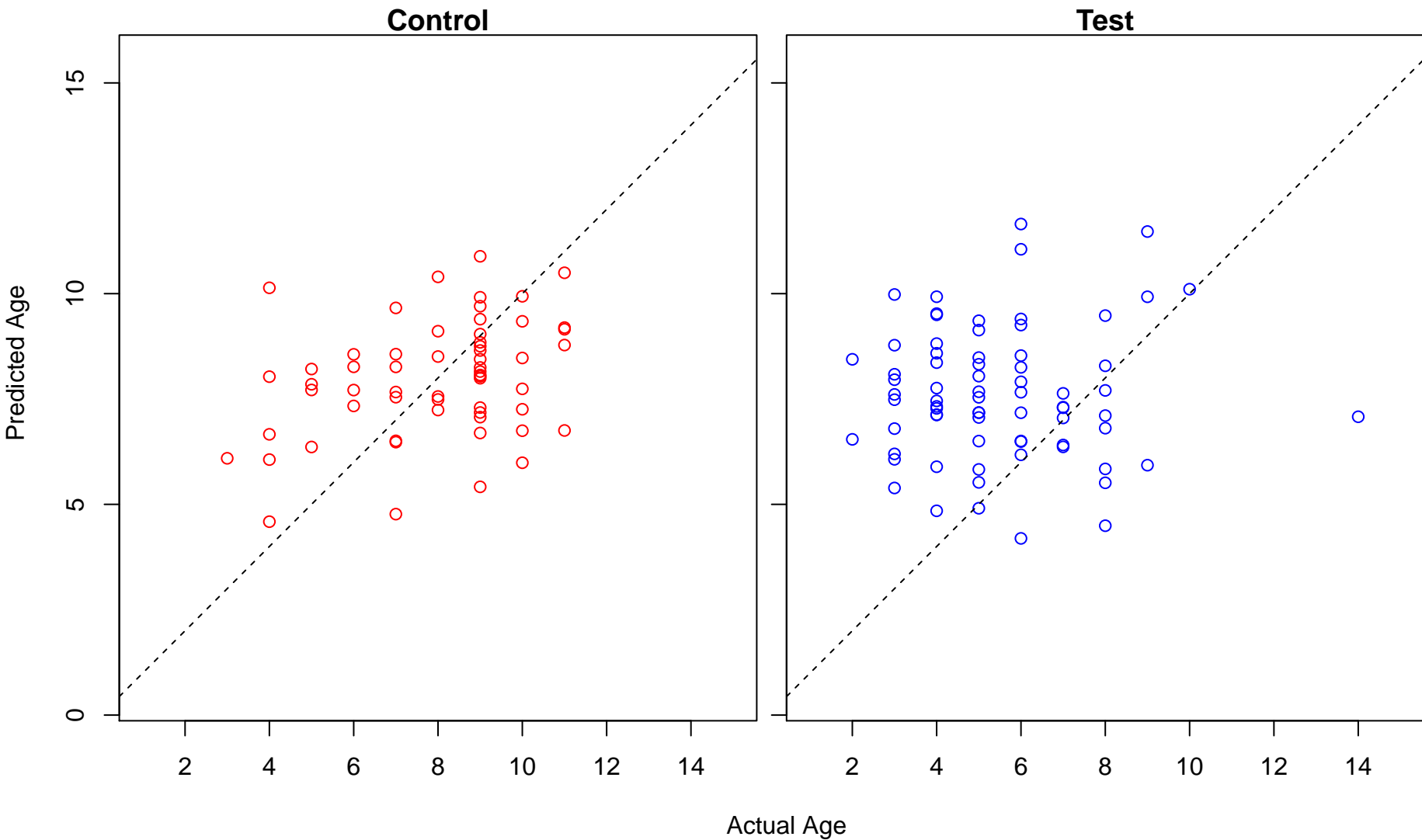
positive regulation of keratinocyte differentiation (Score: 0.651462)



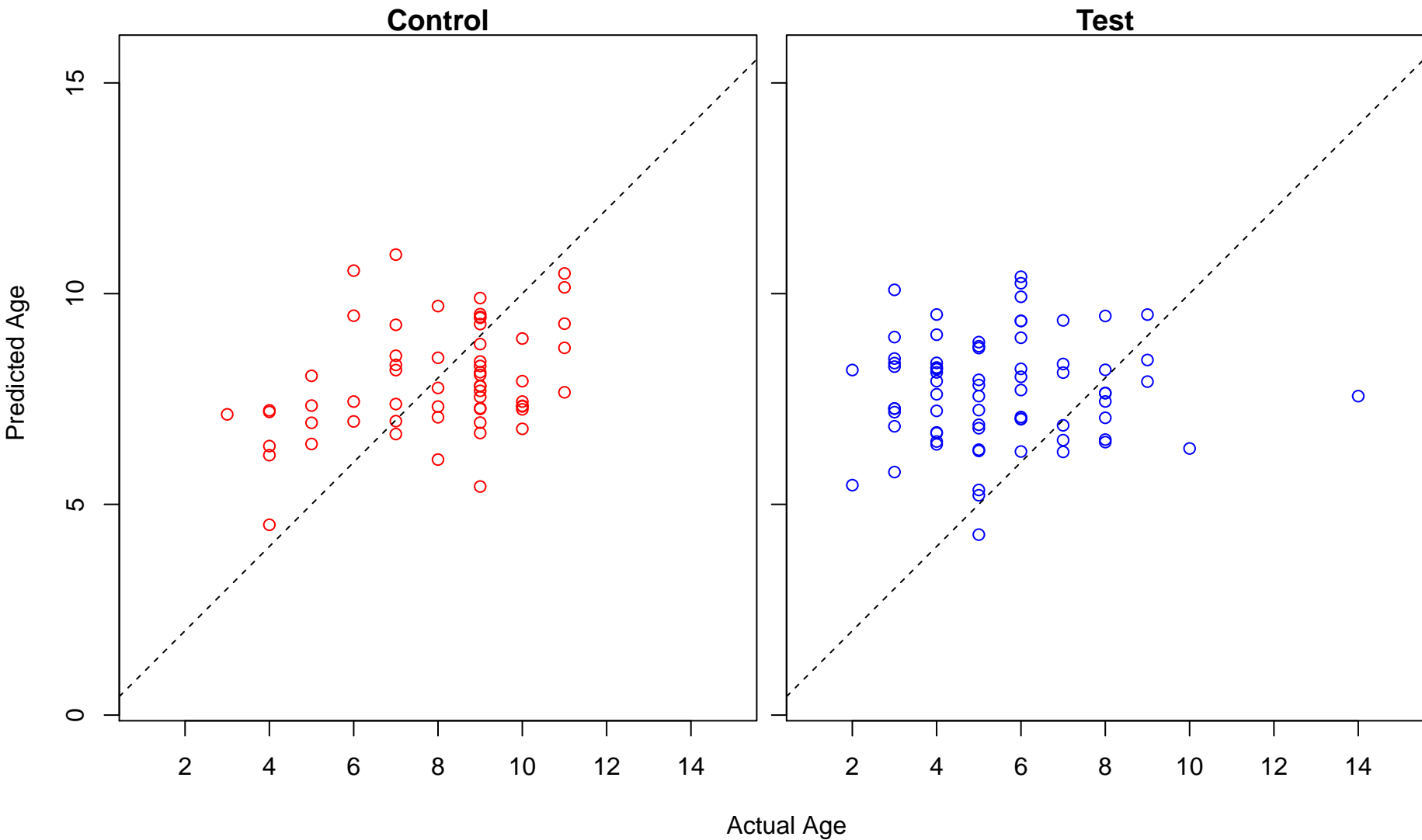
protein O-linked glycosylation via serine (Score: 0.650691)



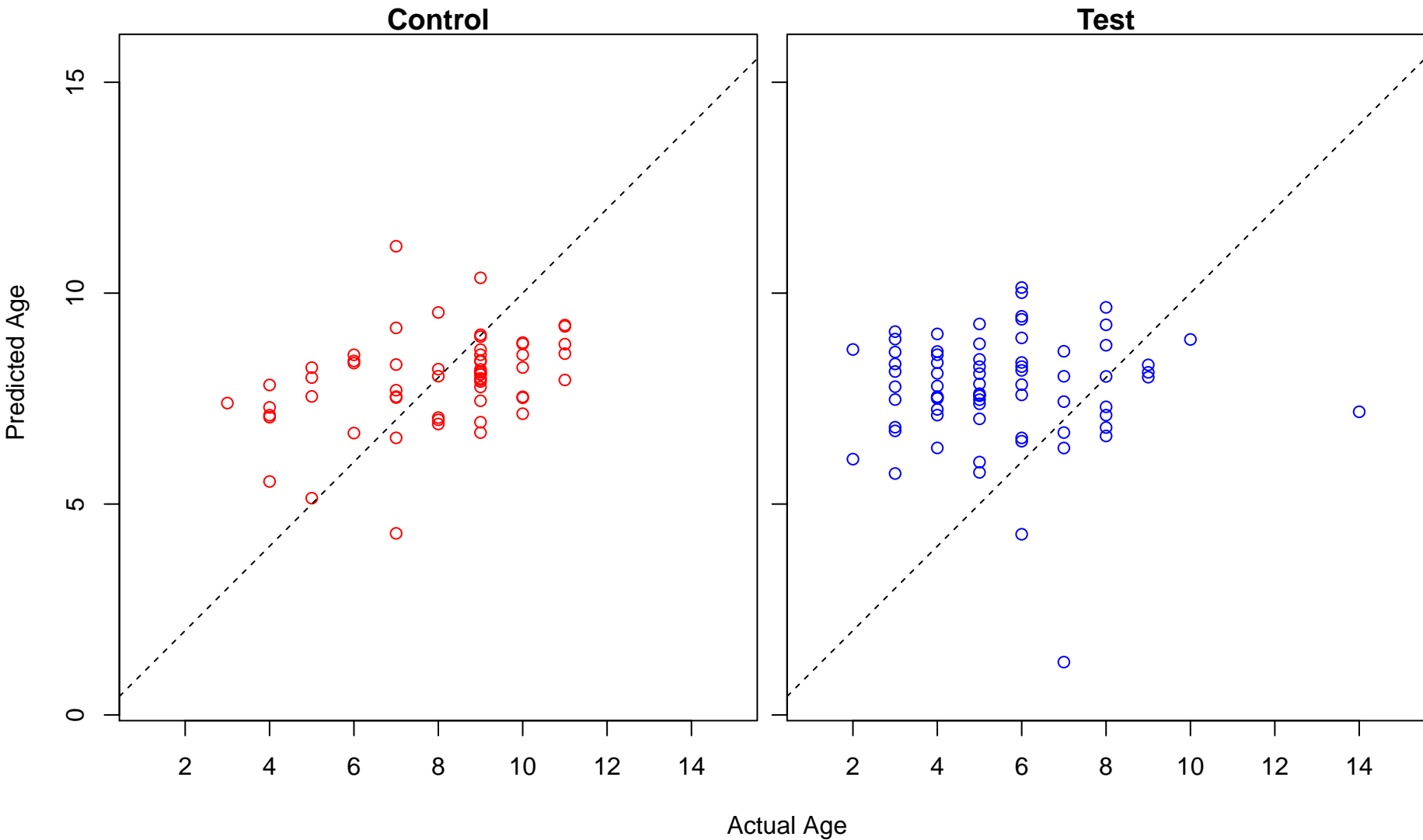
negative regulation of cellular response to oxidative stress (Score: 0.649276)



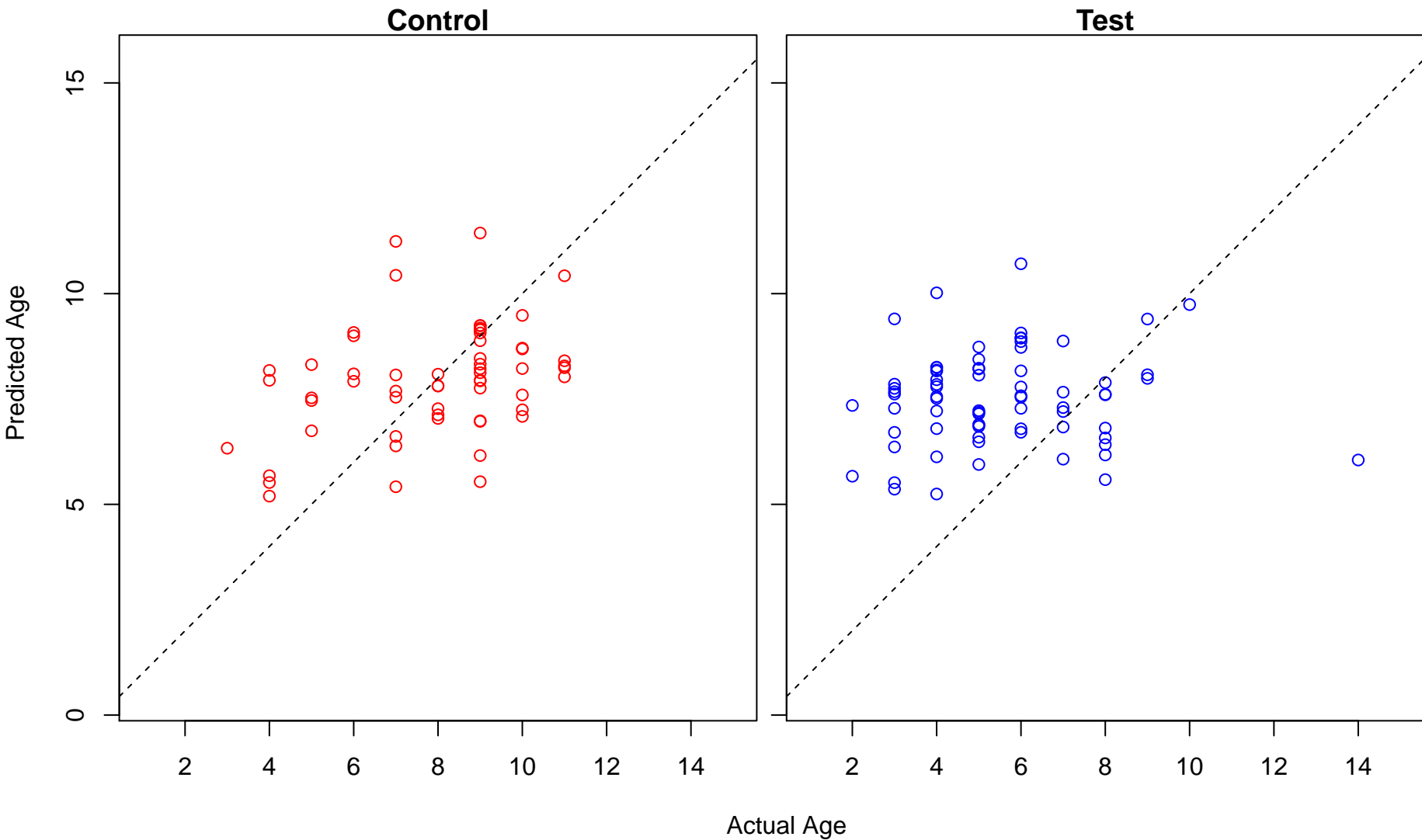
receptor metabolic process (Score: 0.648766)



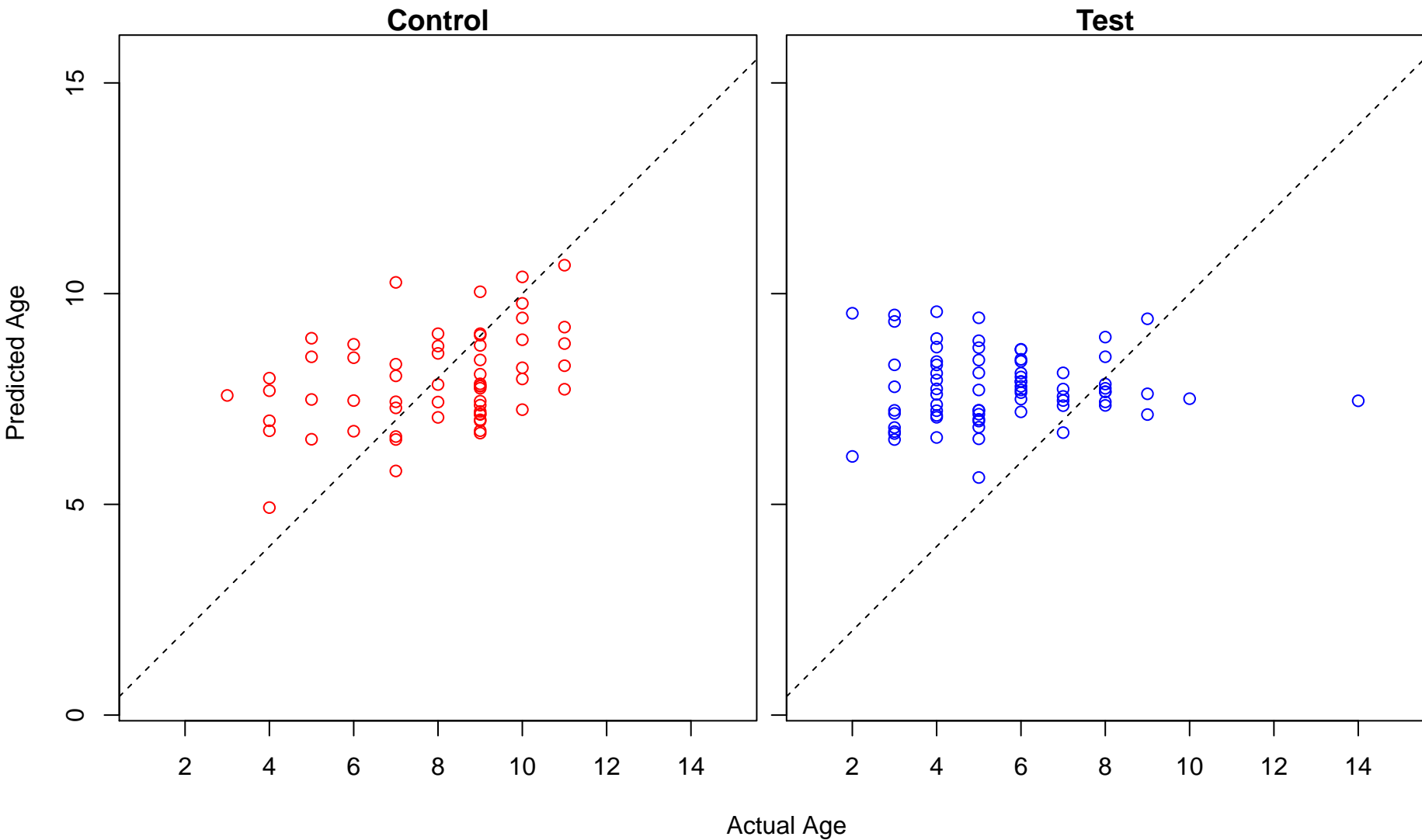
positive regulation of osteoclast differentiation (Score: 0.647205)



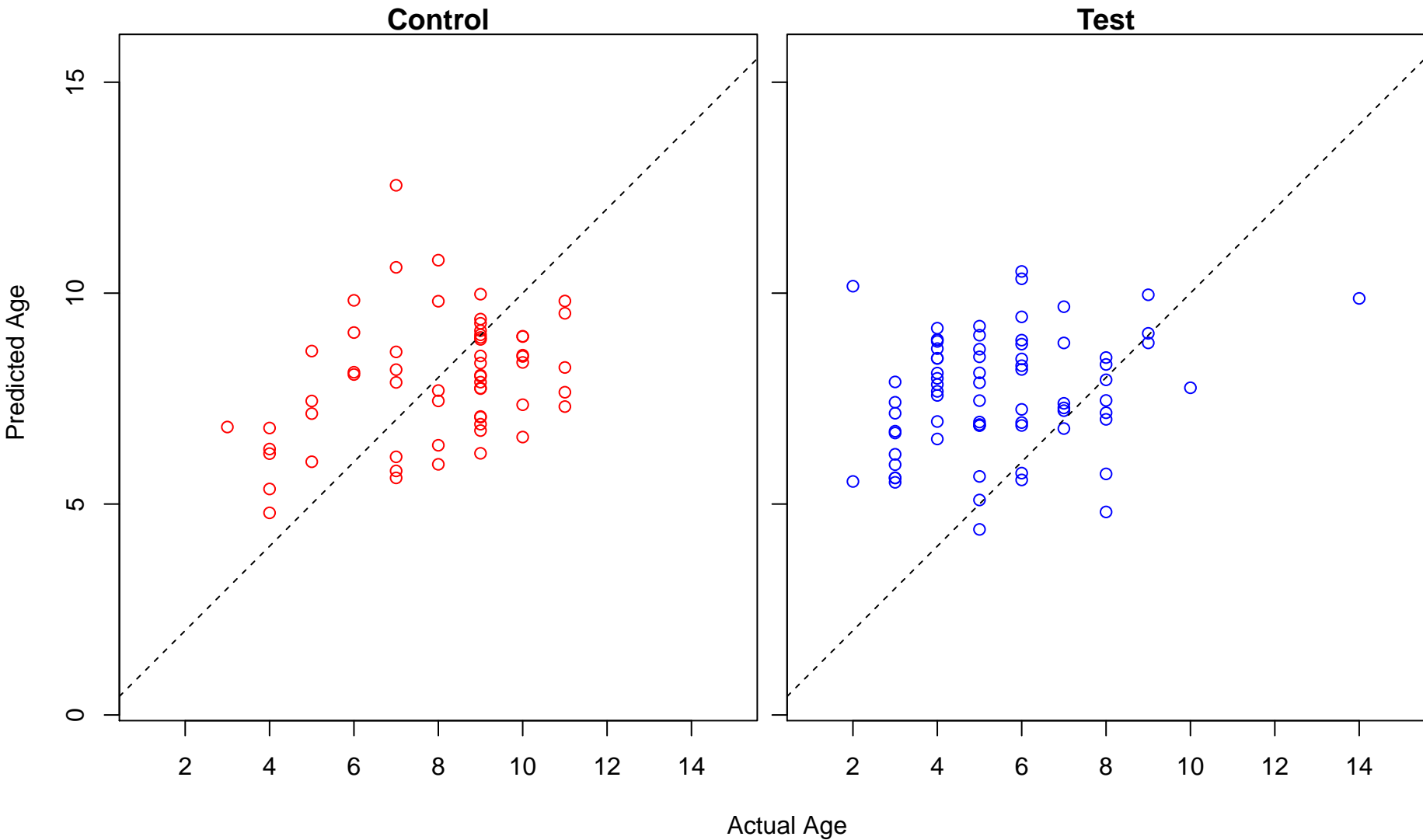
regulation of type 2 immune response (Score: 0.647109)



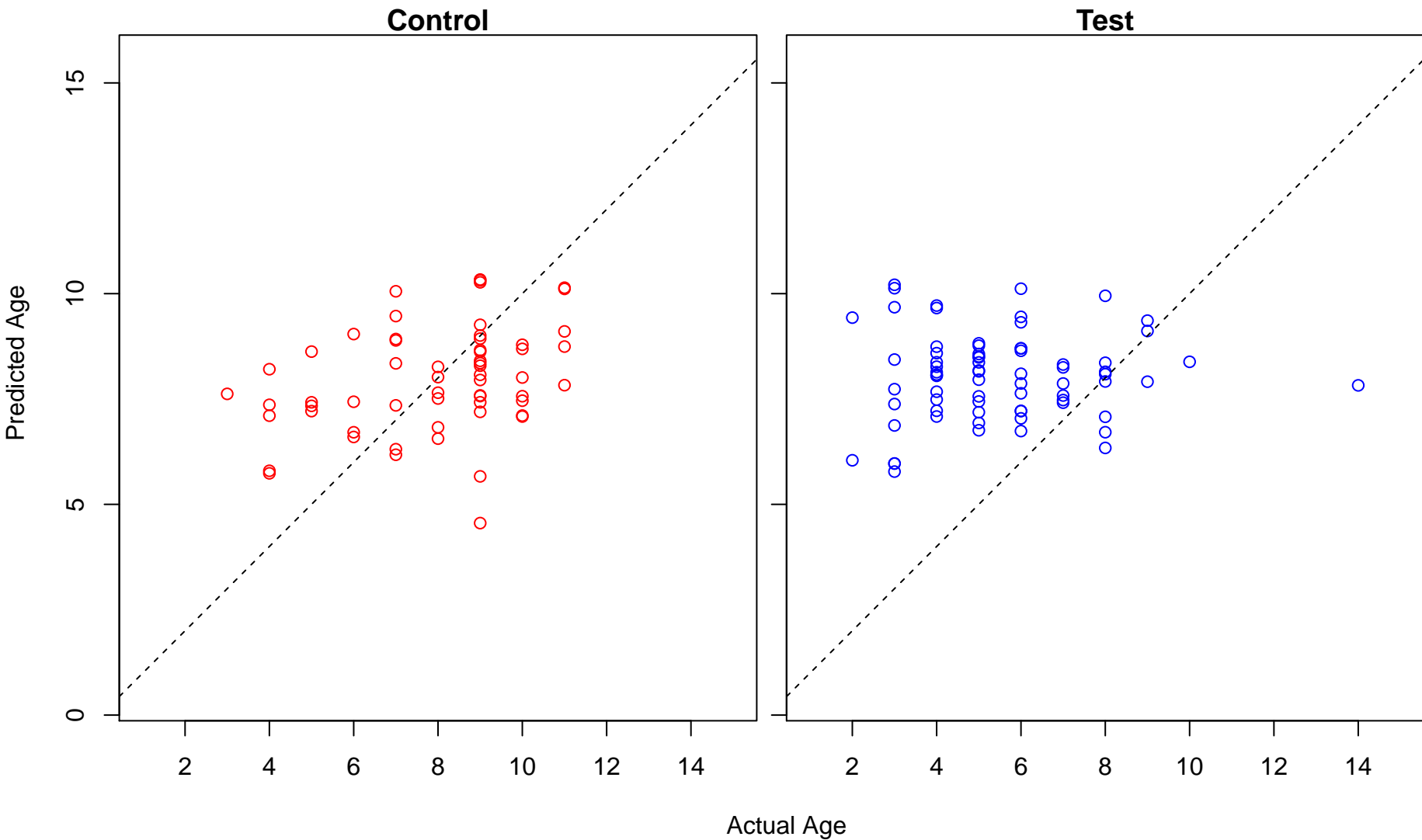
cadmium ion homeostasis (Score: 0.645935)



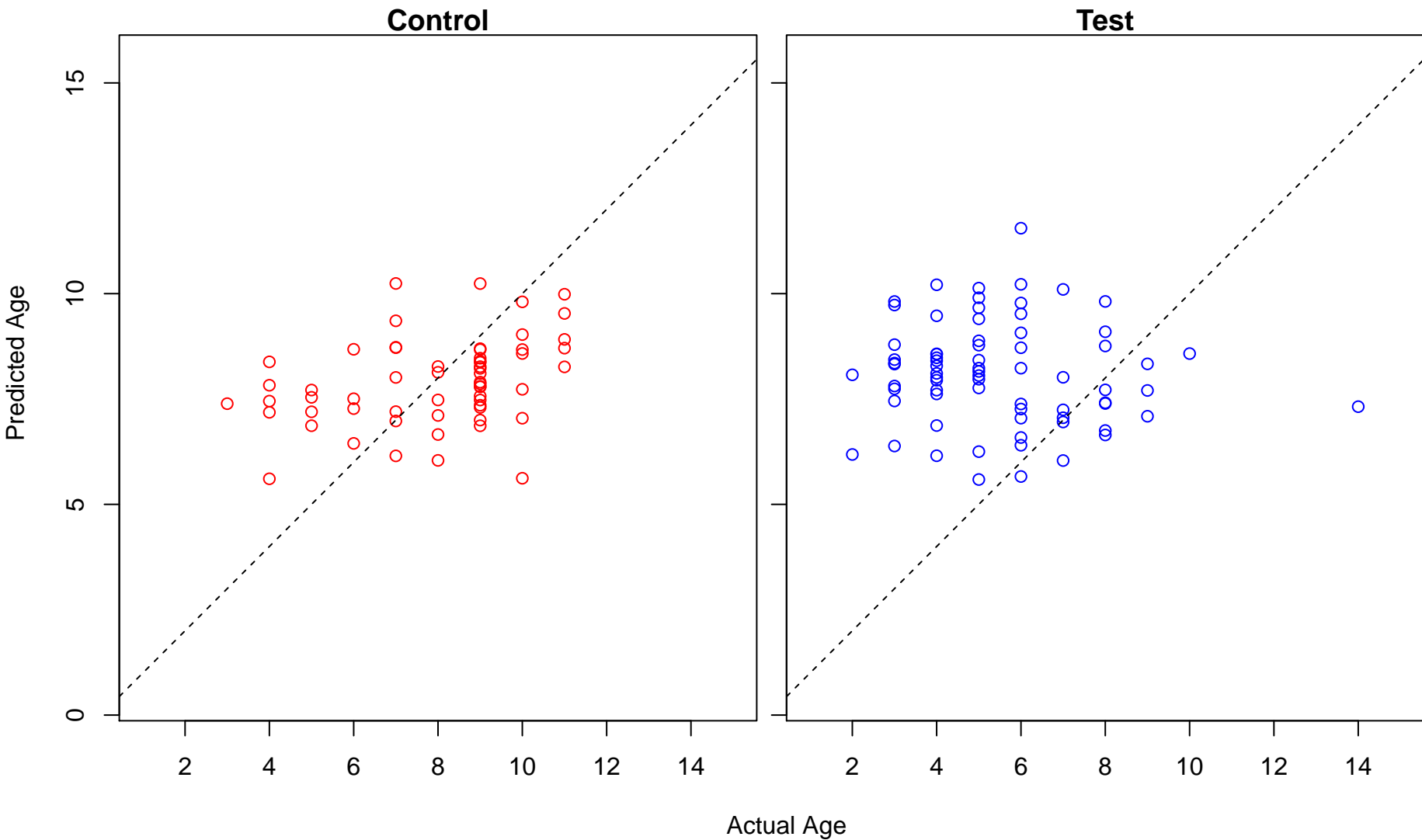
regulation of response to external stimulus (Score: 0.645793)



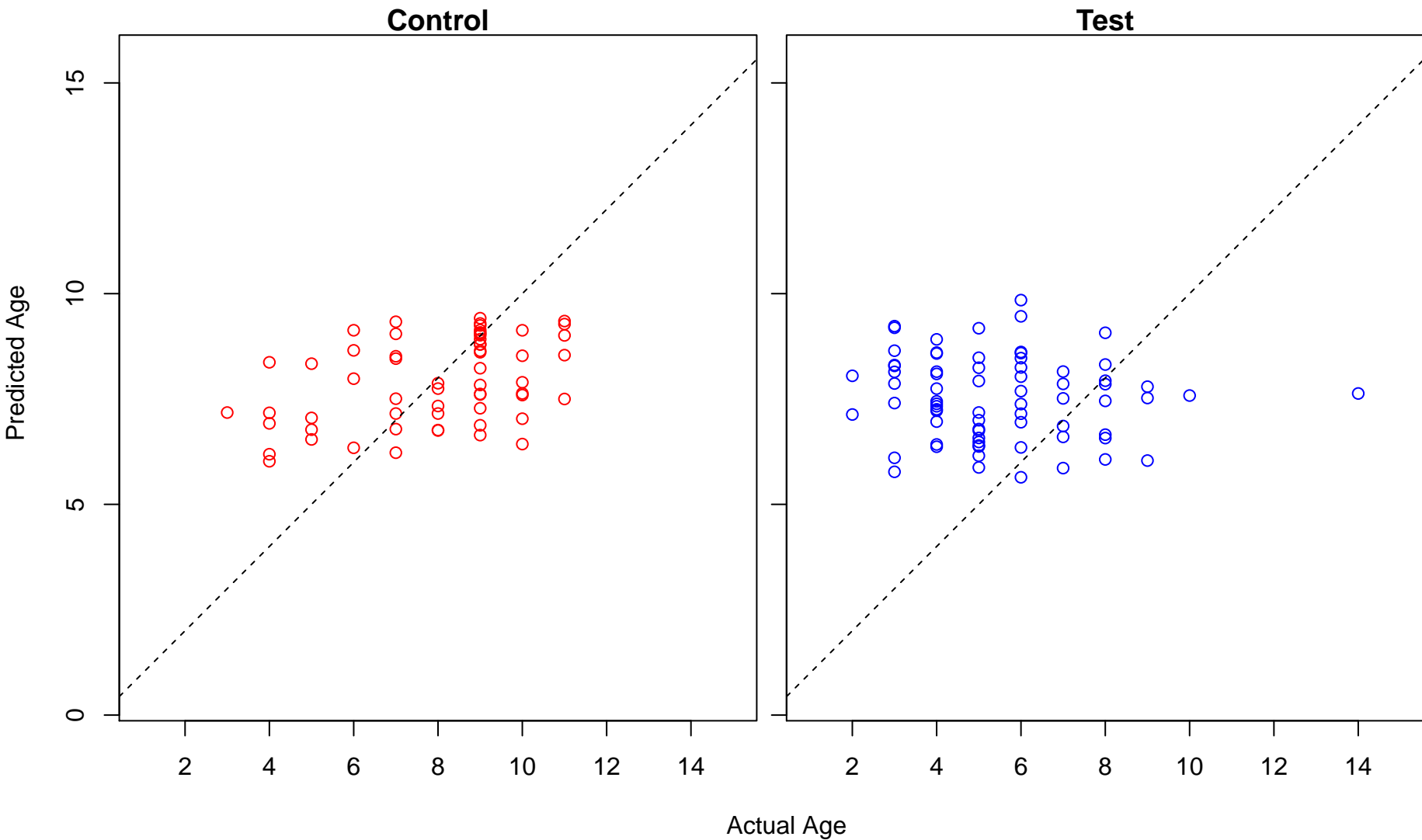
V(D)J recombination (Score: 0.644618)



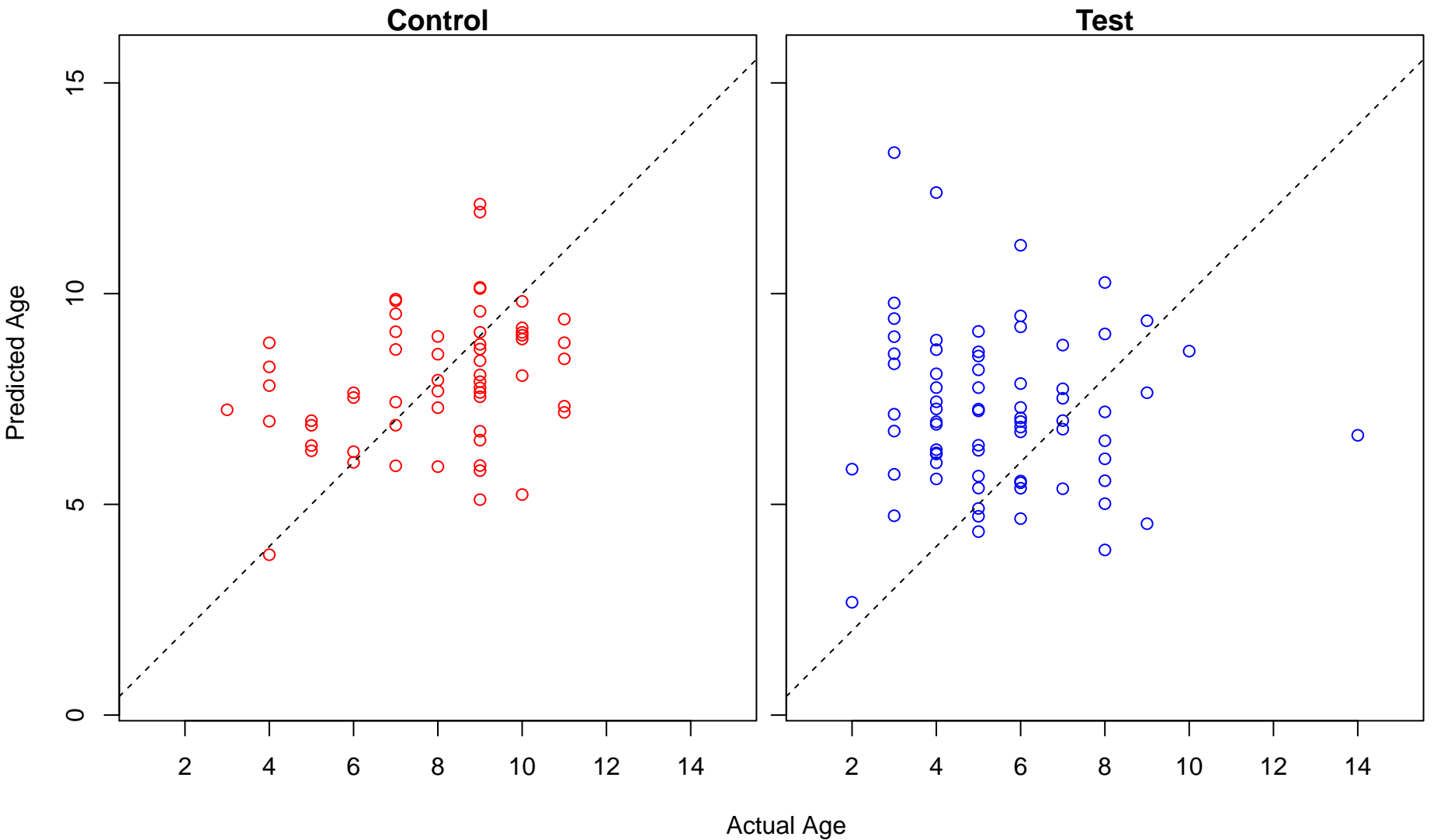
meiotic chromosome segregation (Score: 0.644218)



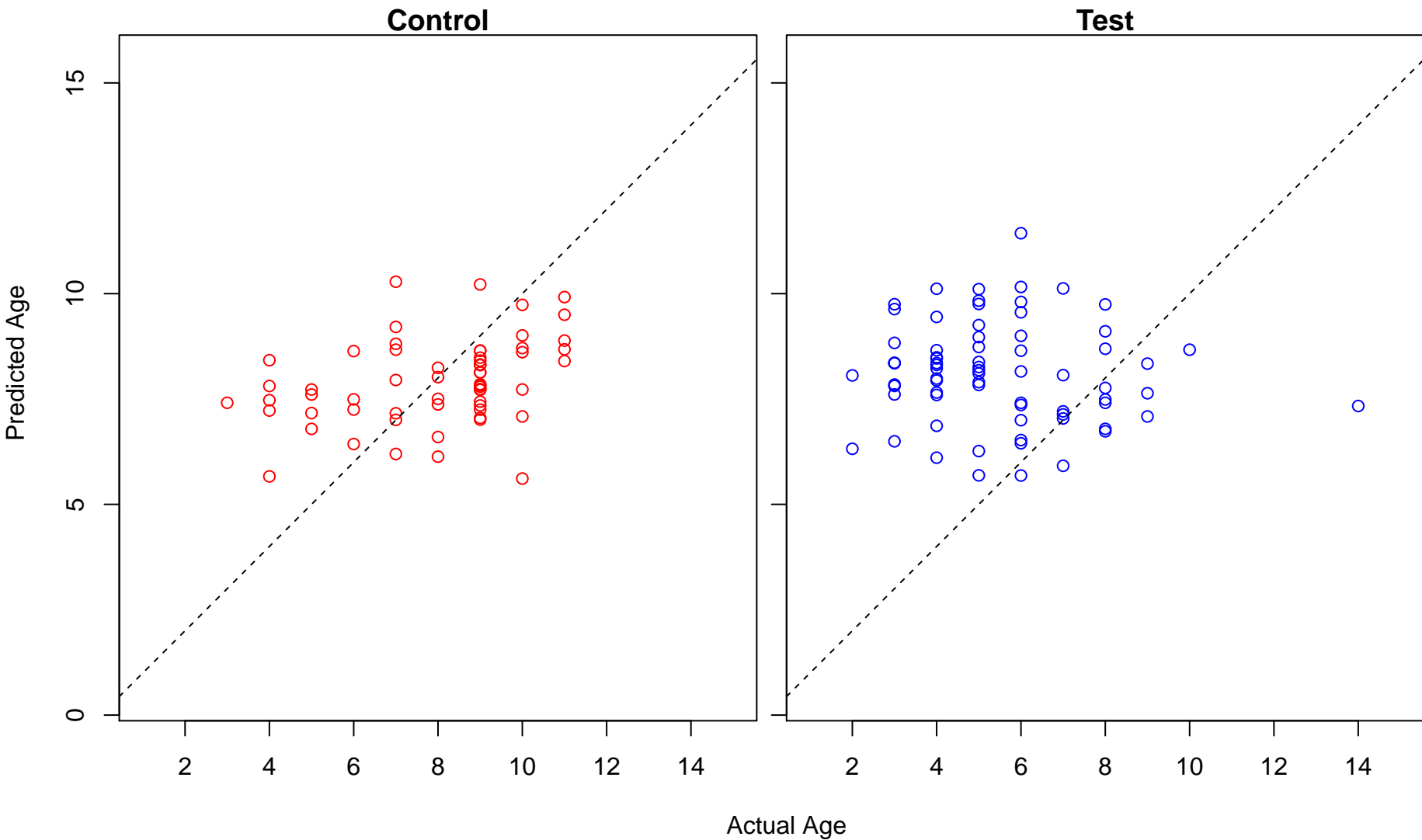
regulation of actin filament depolymerization (Score: 0.642579)



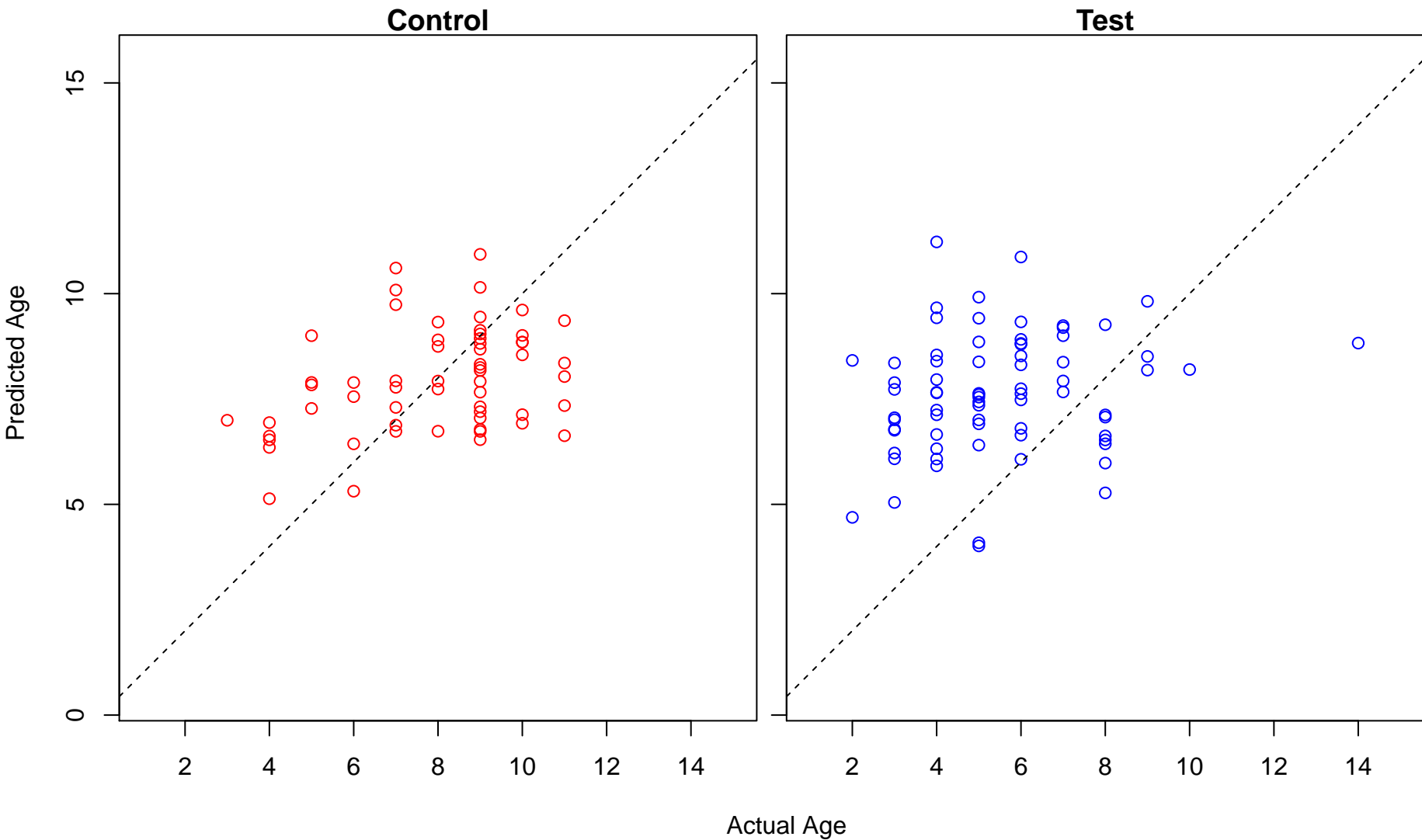
Regulatory regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score)



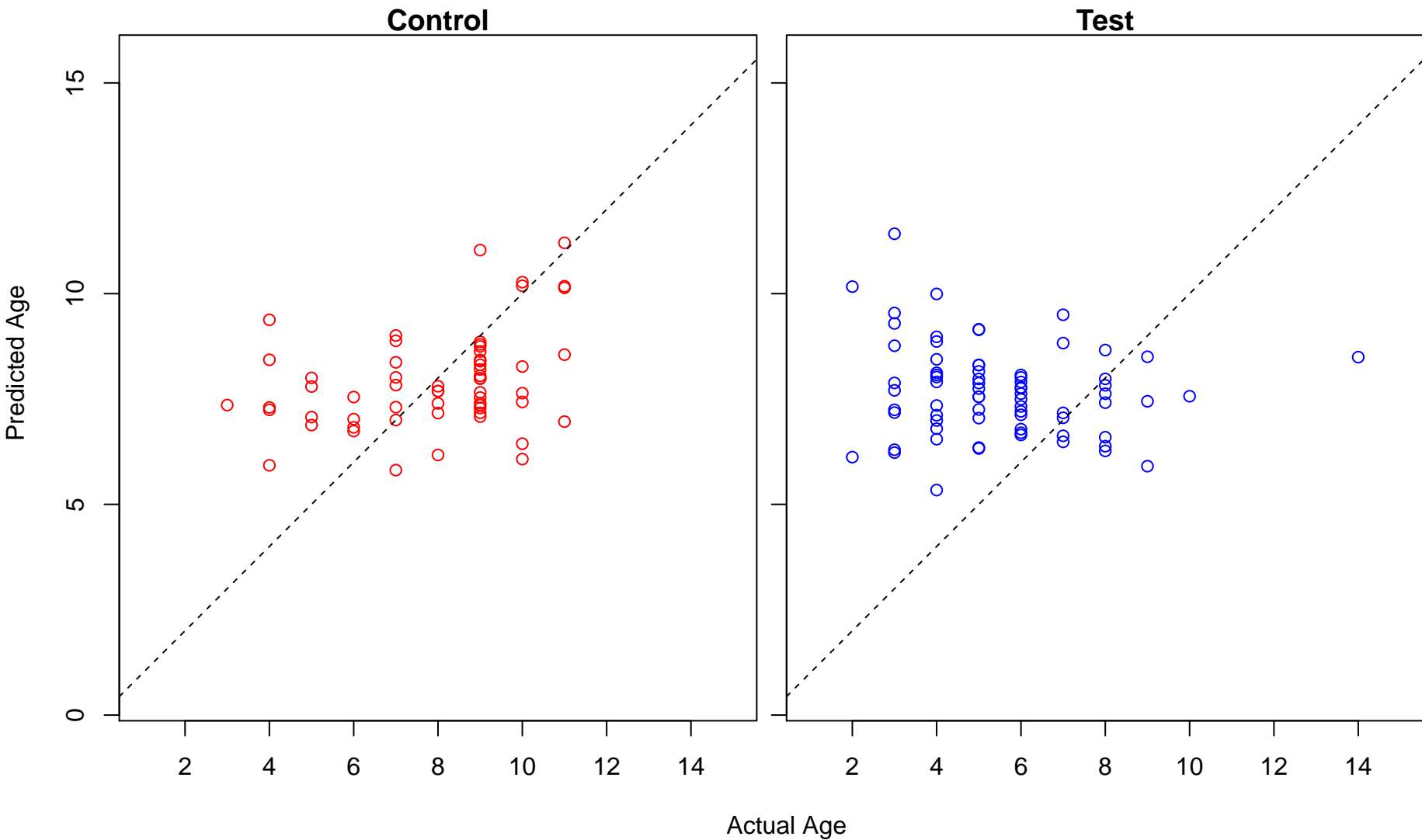
synapsis (Score: 0.640778)



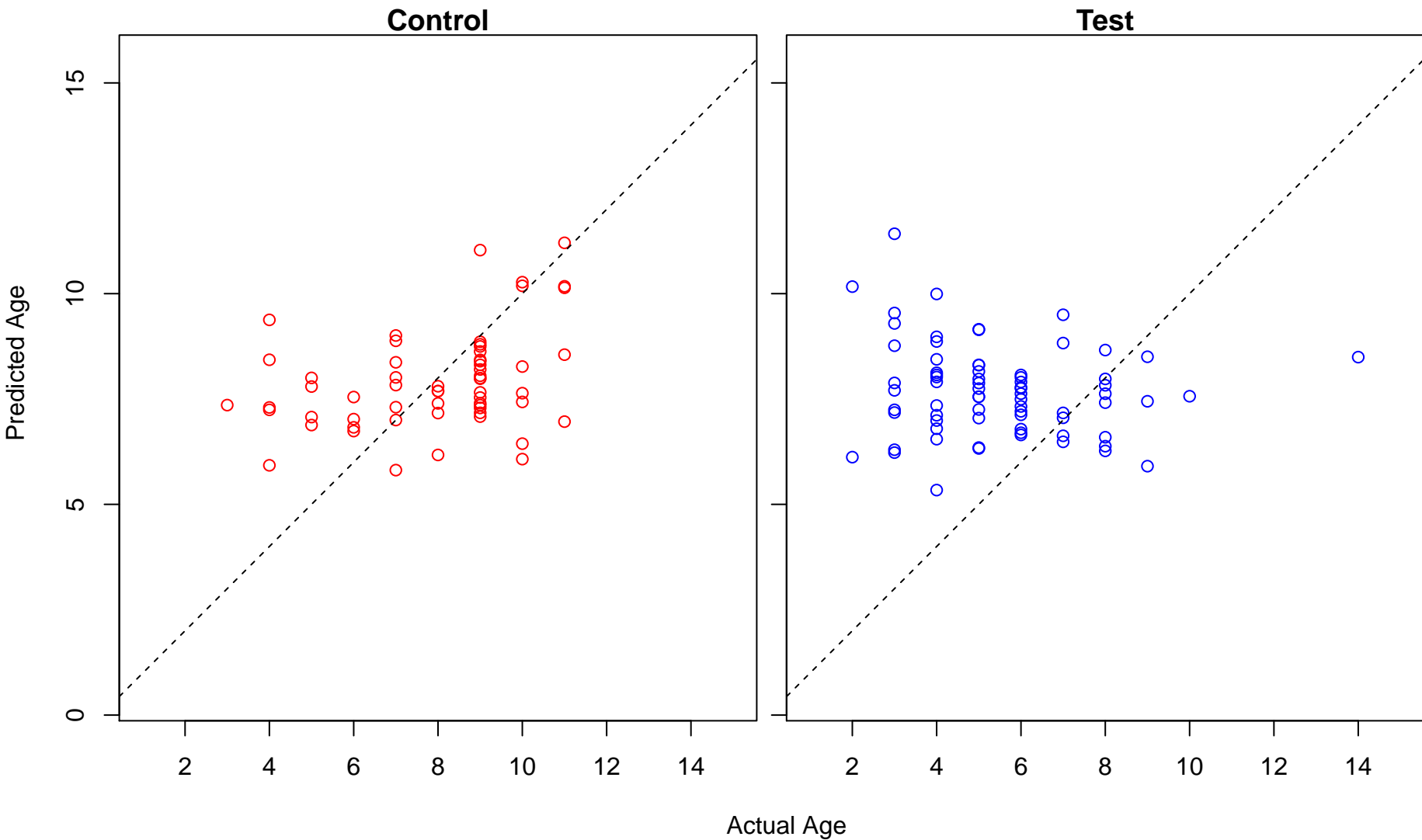
tRNA splicing, via endonucleolytic cleavage and ligation (Score: 0.638785)



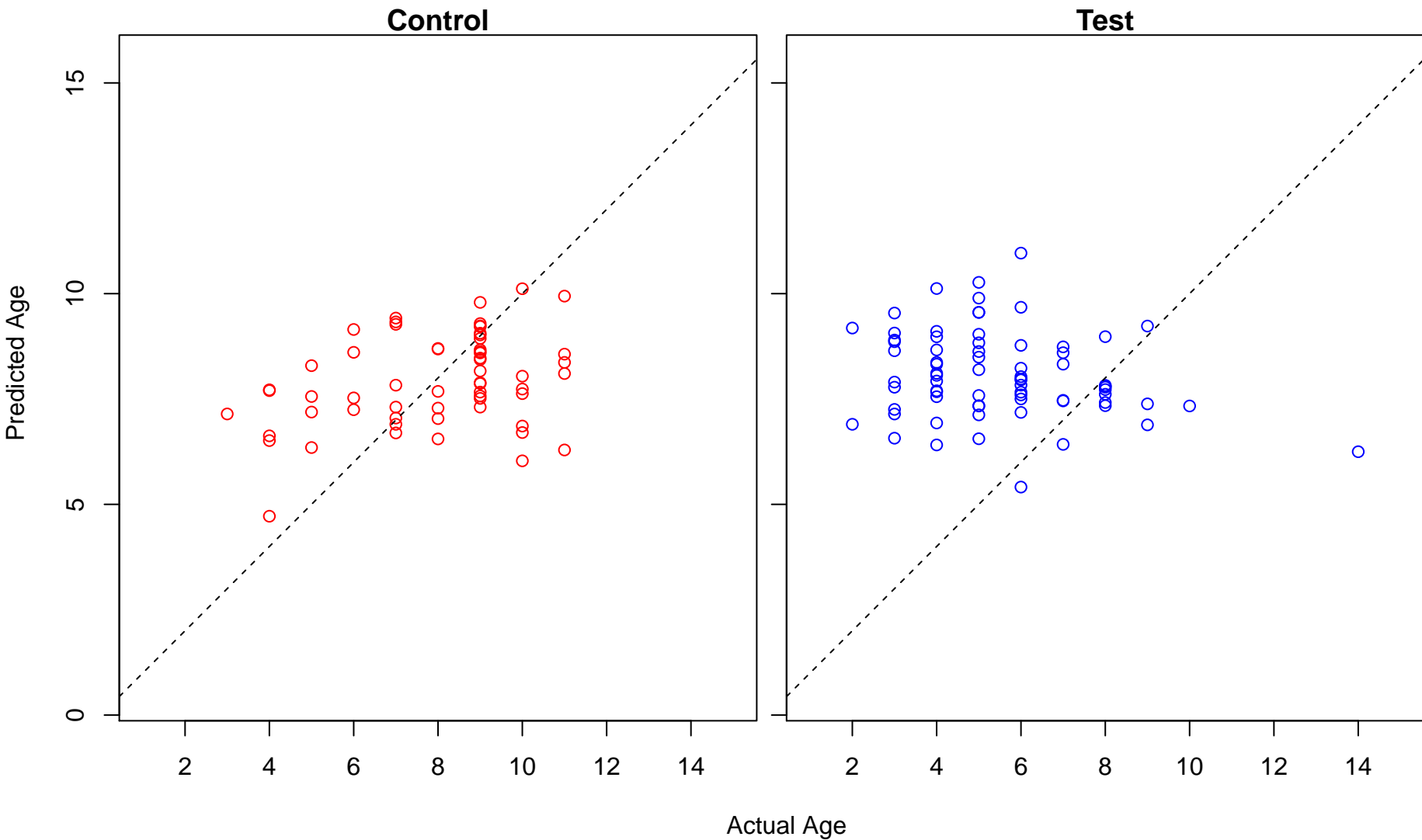
inclusion body assembly (Score: 0.637490)



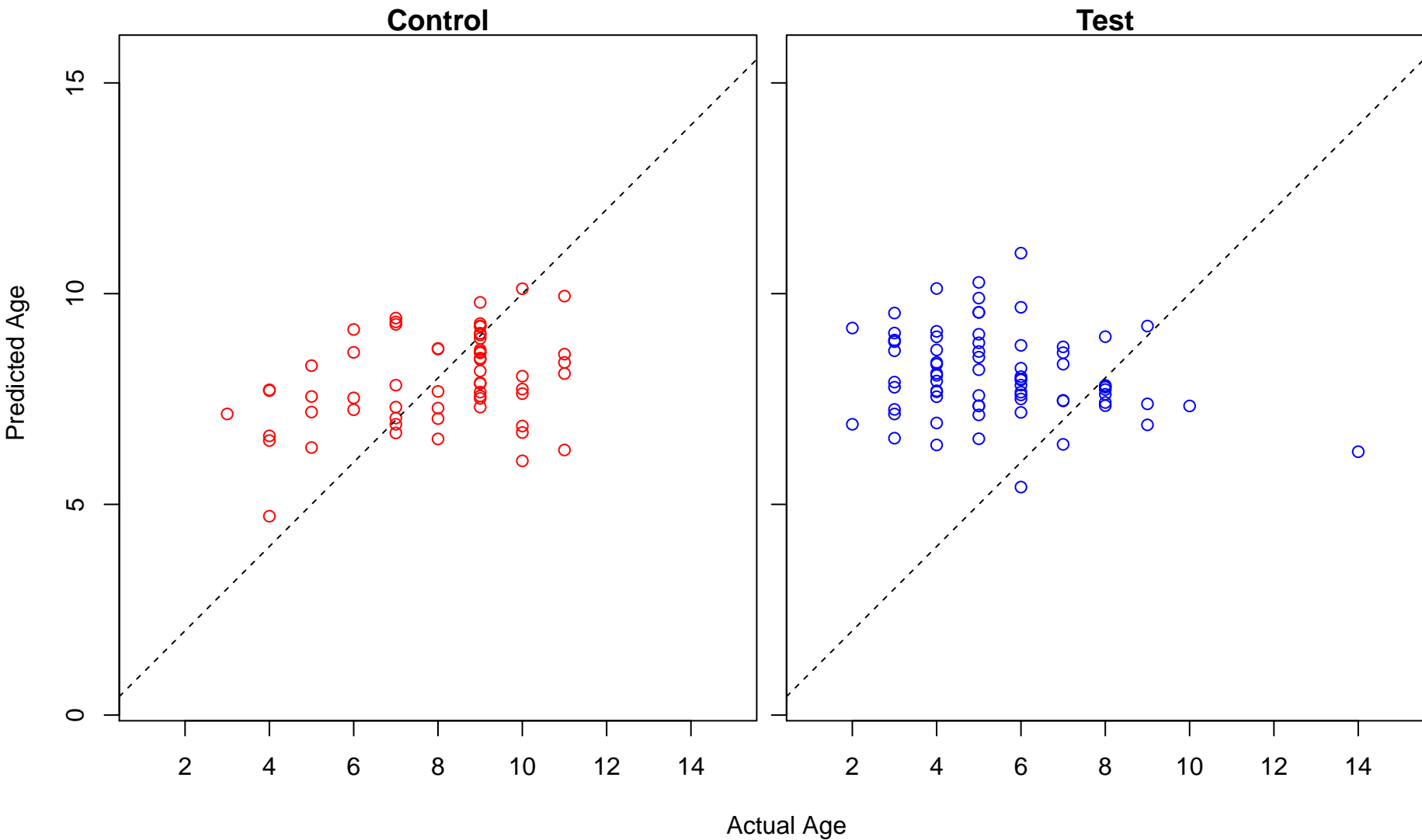
aggresome assembly (Score: 0.637490)



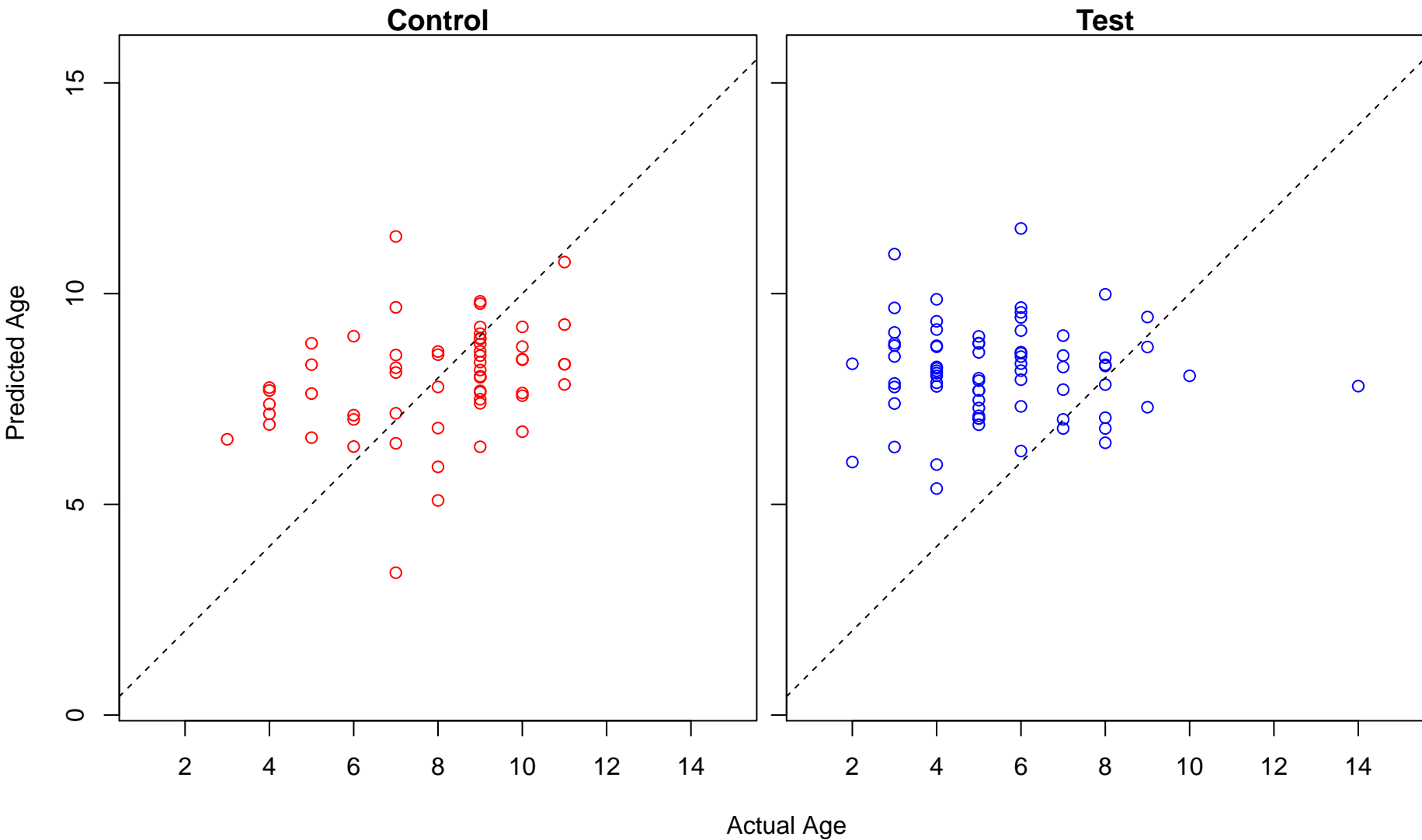
response to isoquinoline alkaloid (Score: 0.636744)



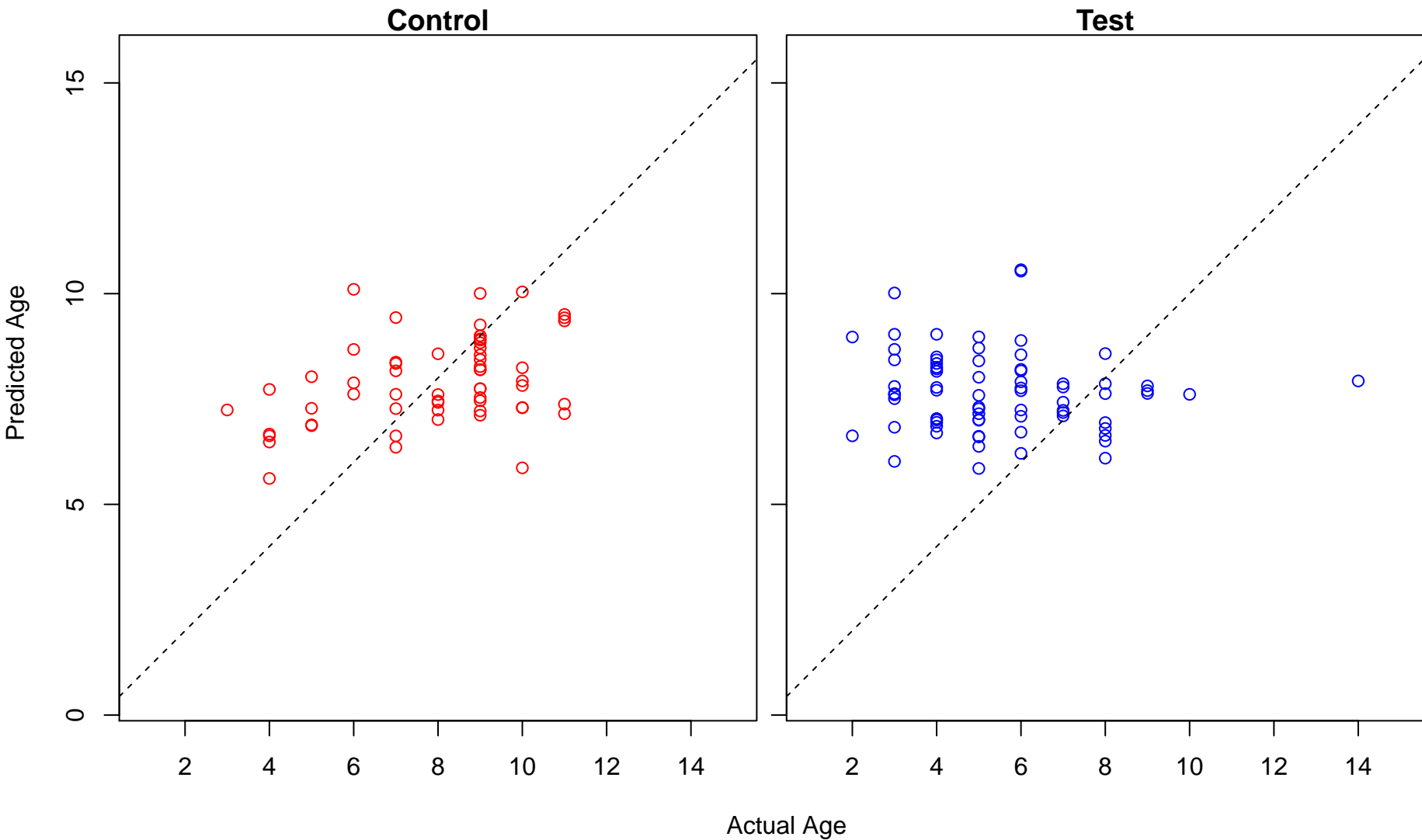
response to morphine (Score: 0.636744)



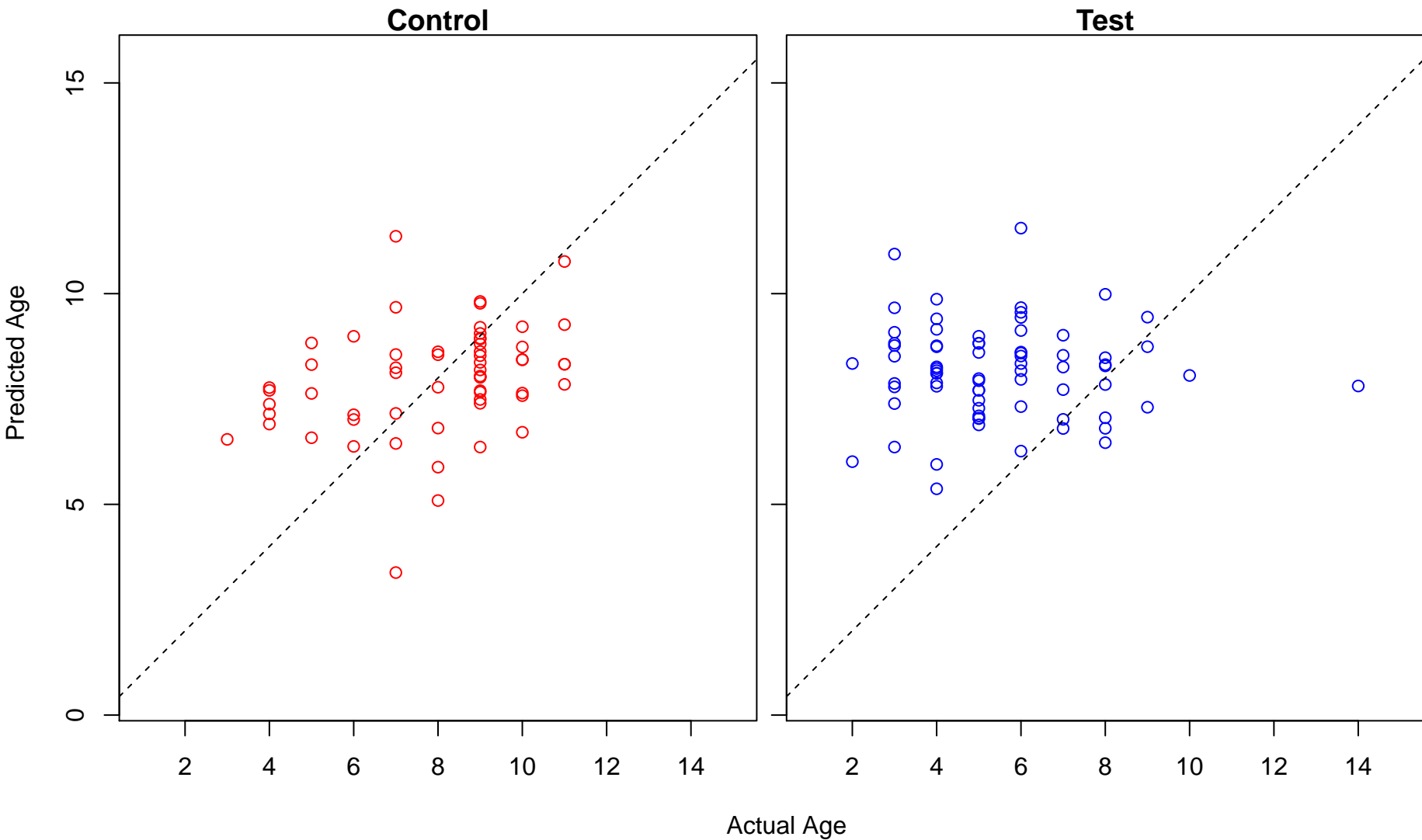
positive regulation of epidermal cell differentiation (Score: 0.636120)



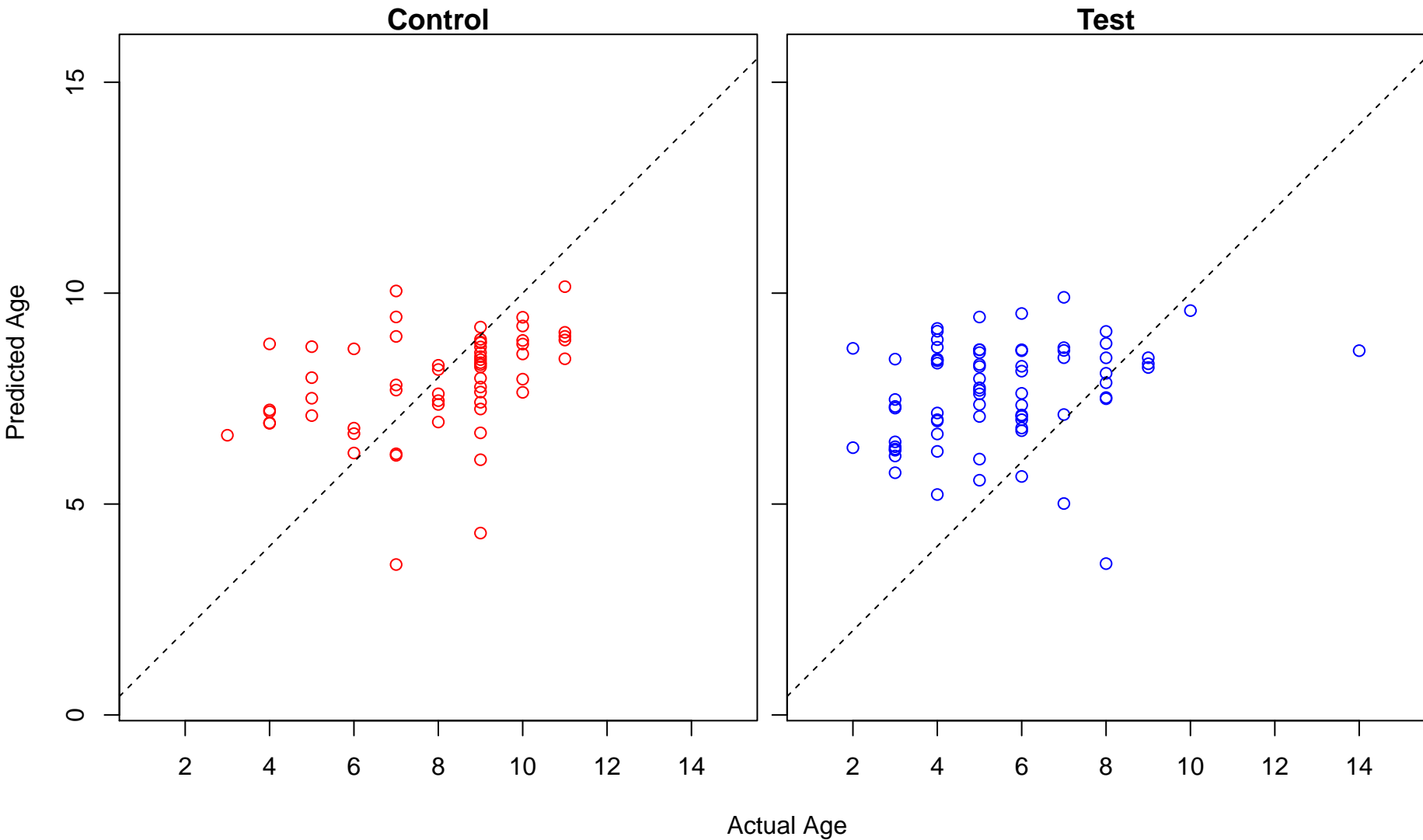
positive regulation of epithelial cell migration (Score: 0.635275)



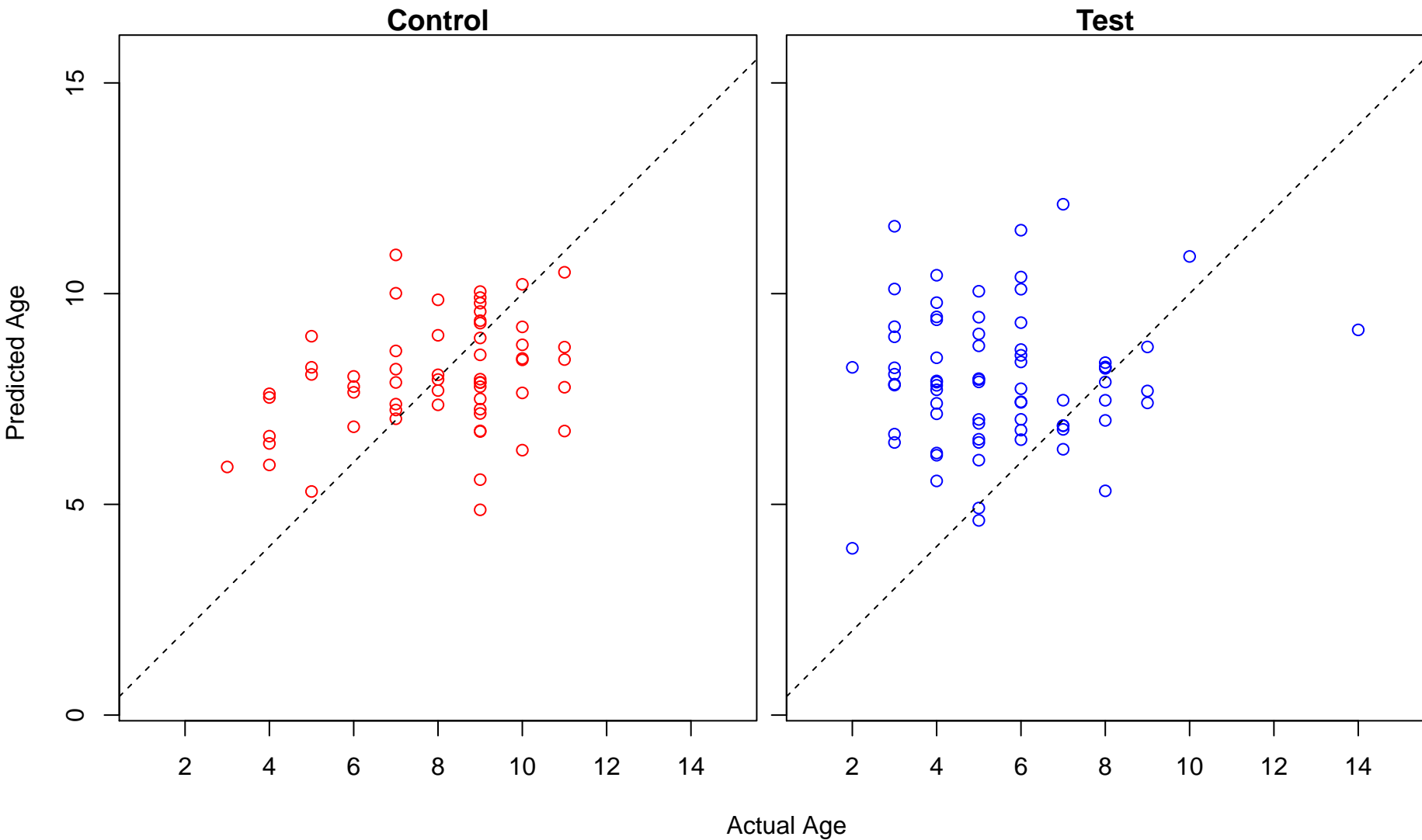
positive regulation of epidermis development (Score: 0.634657)



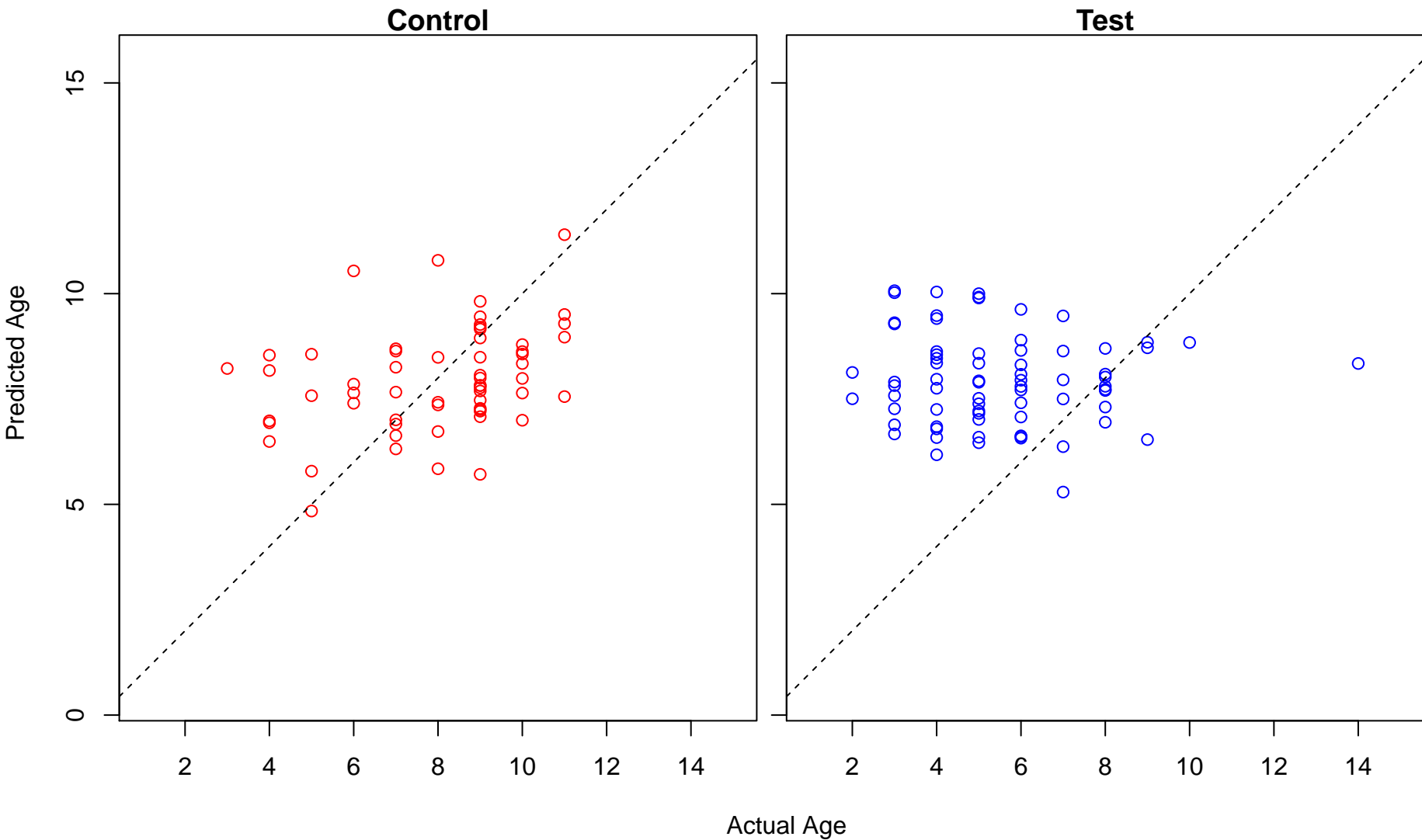
interleukin-27-mediated signaling pathway (Score: 0.634419)



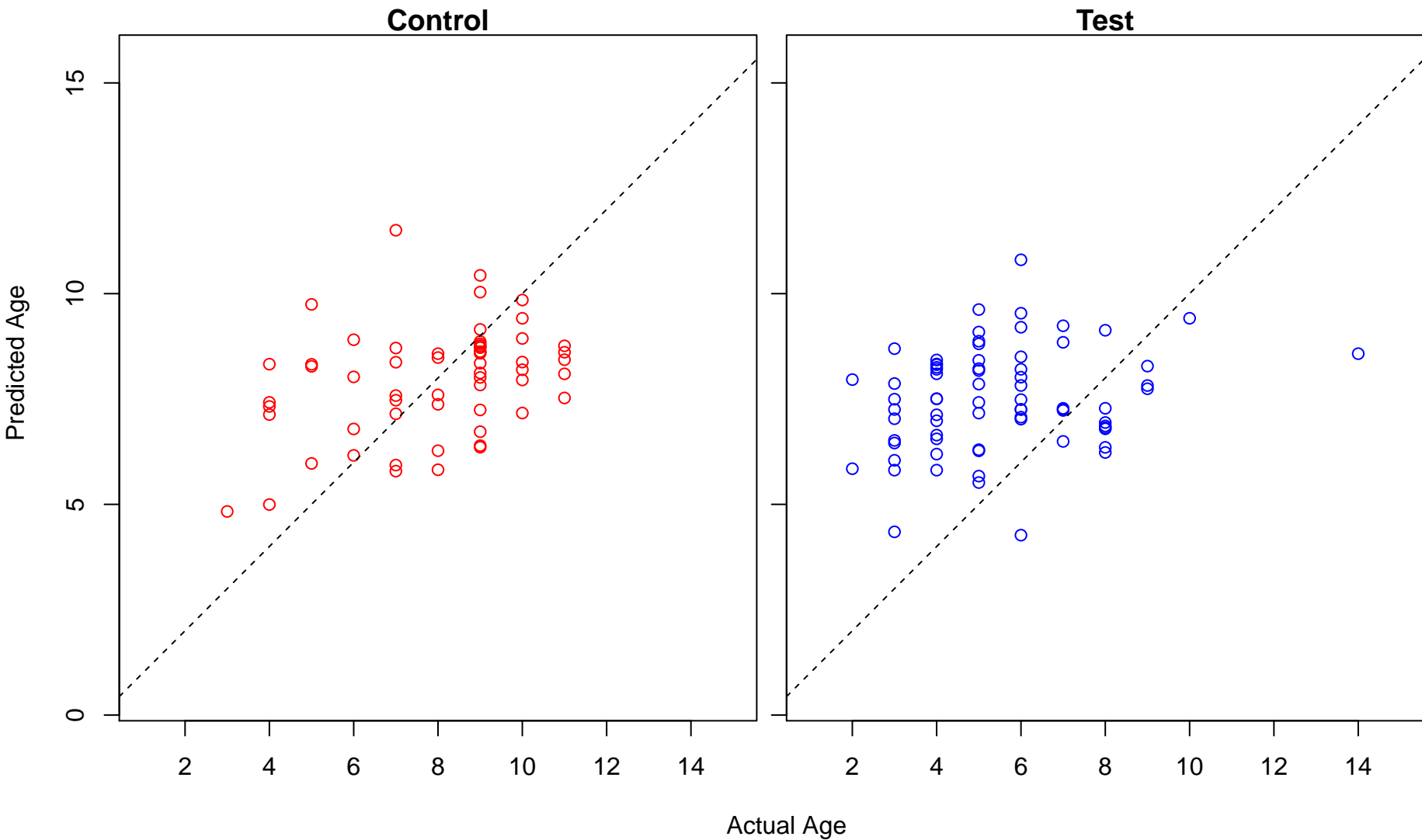
positive regulation of smooth muscle contraction (Score: 0.634283)



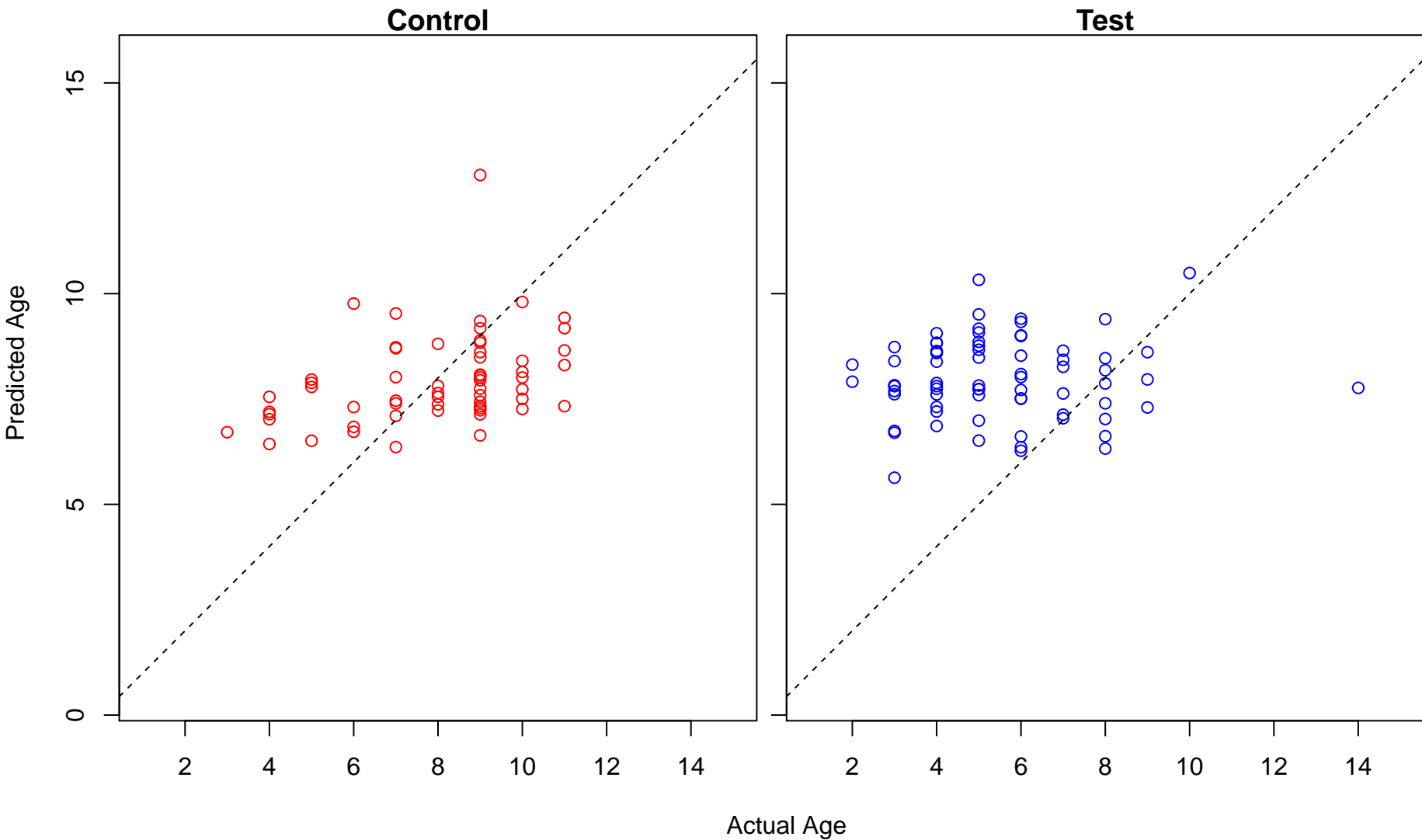
cytoplasmic sequestering of NF-kappaB (Score: 0.633513)



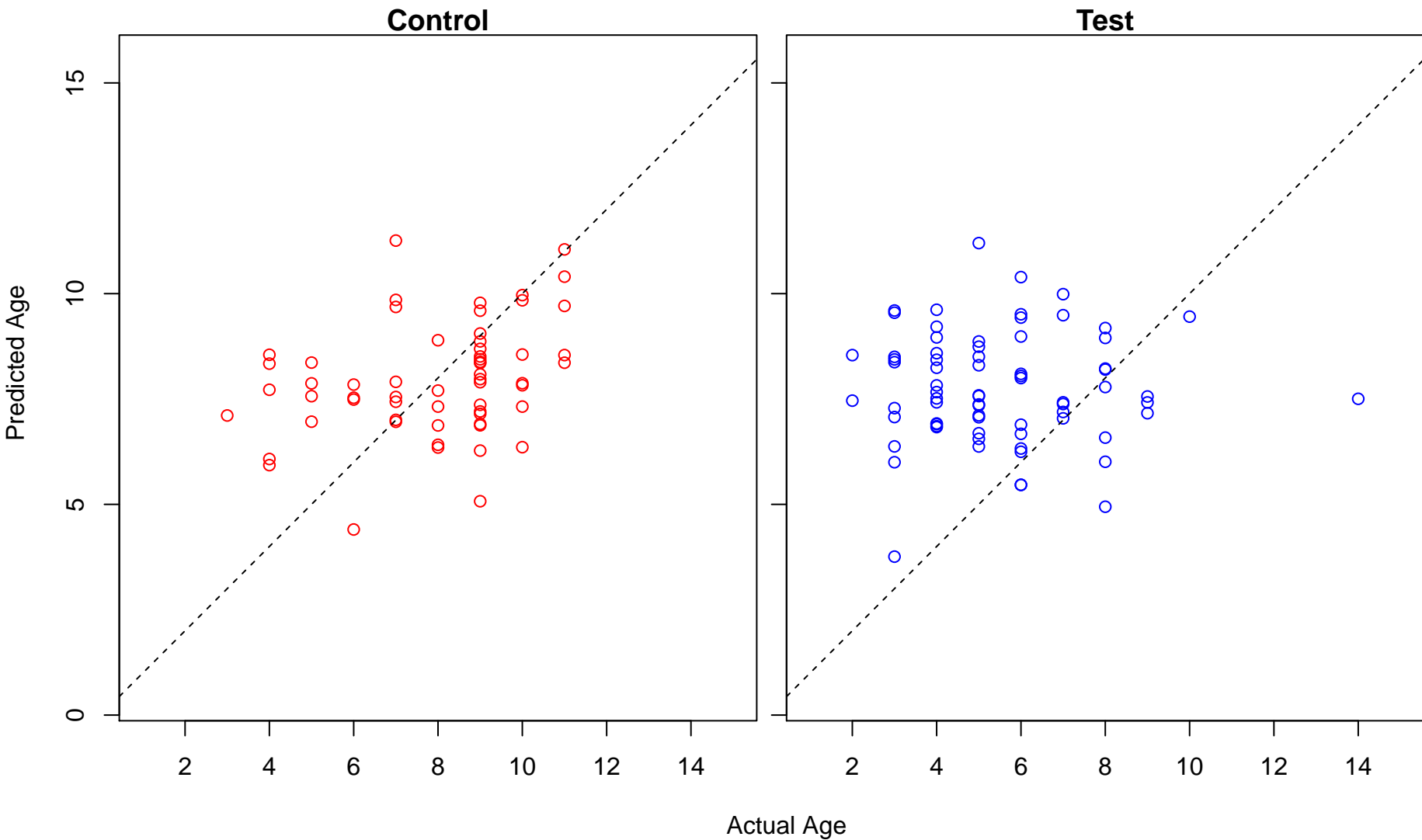
regulation of antigen processing and presentation (Score: 0.633347)



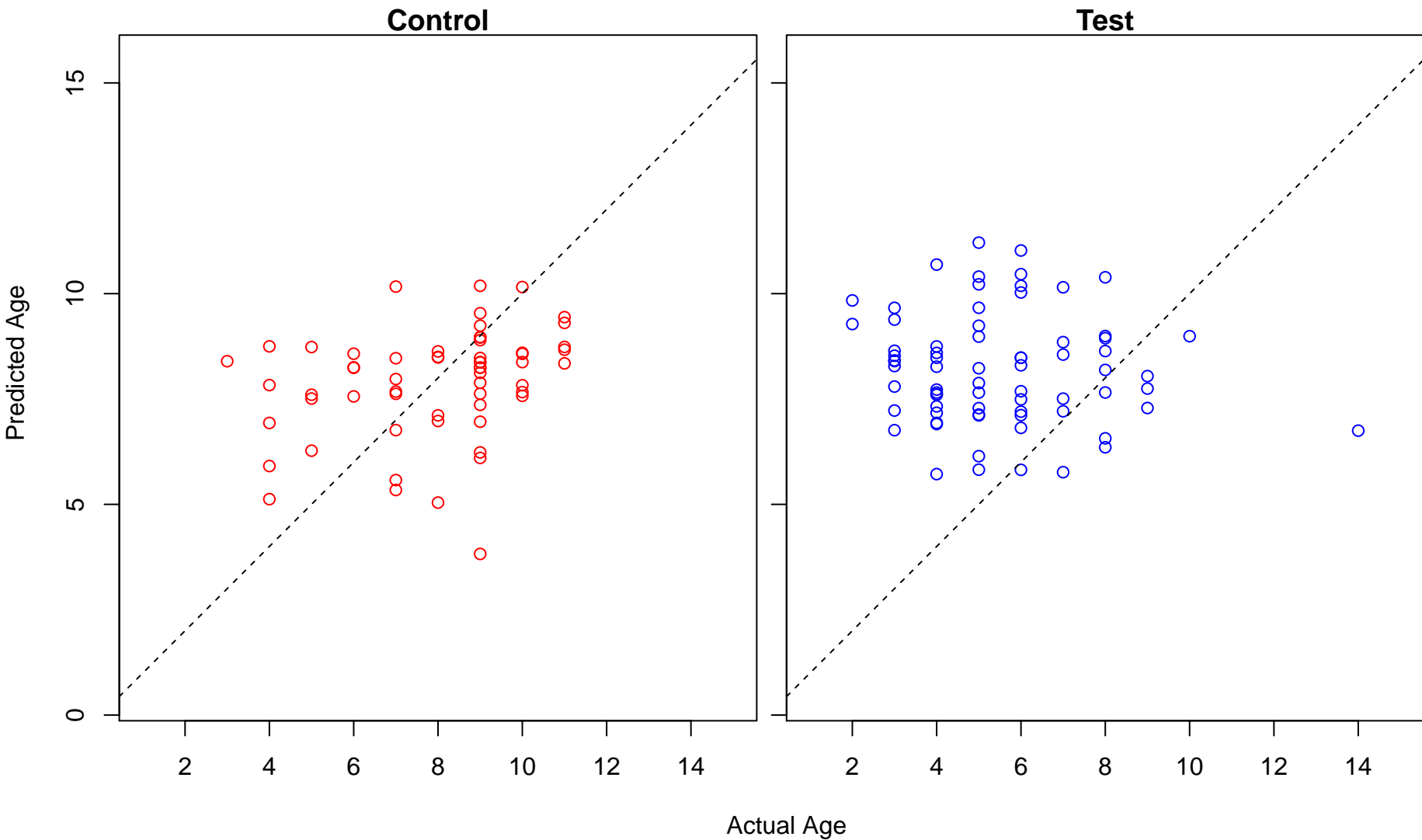
podosome assembly (Score: 0.632919)



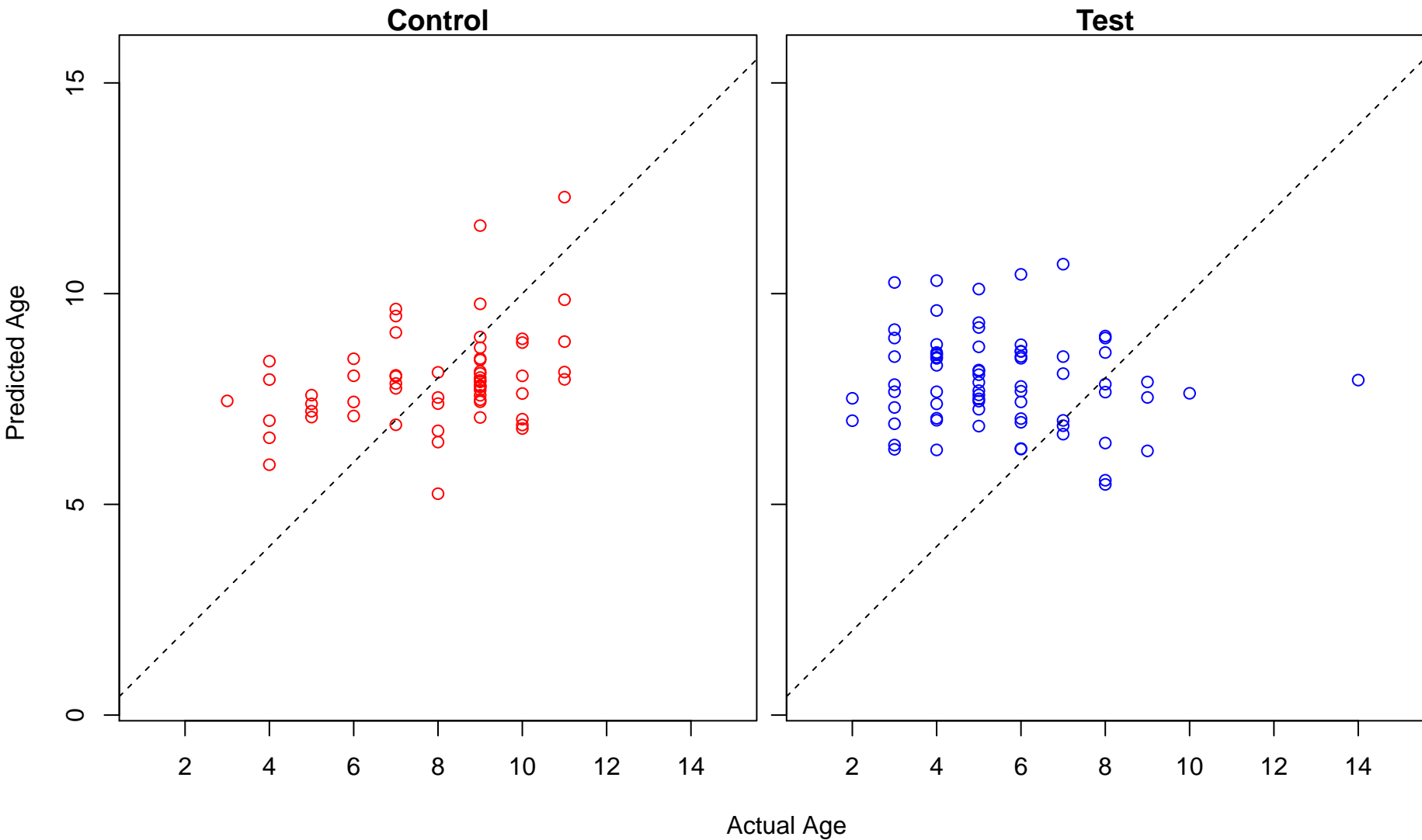
cytochrome complex assembly (Score: 0.632835)



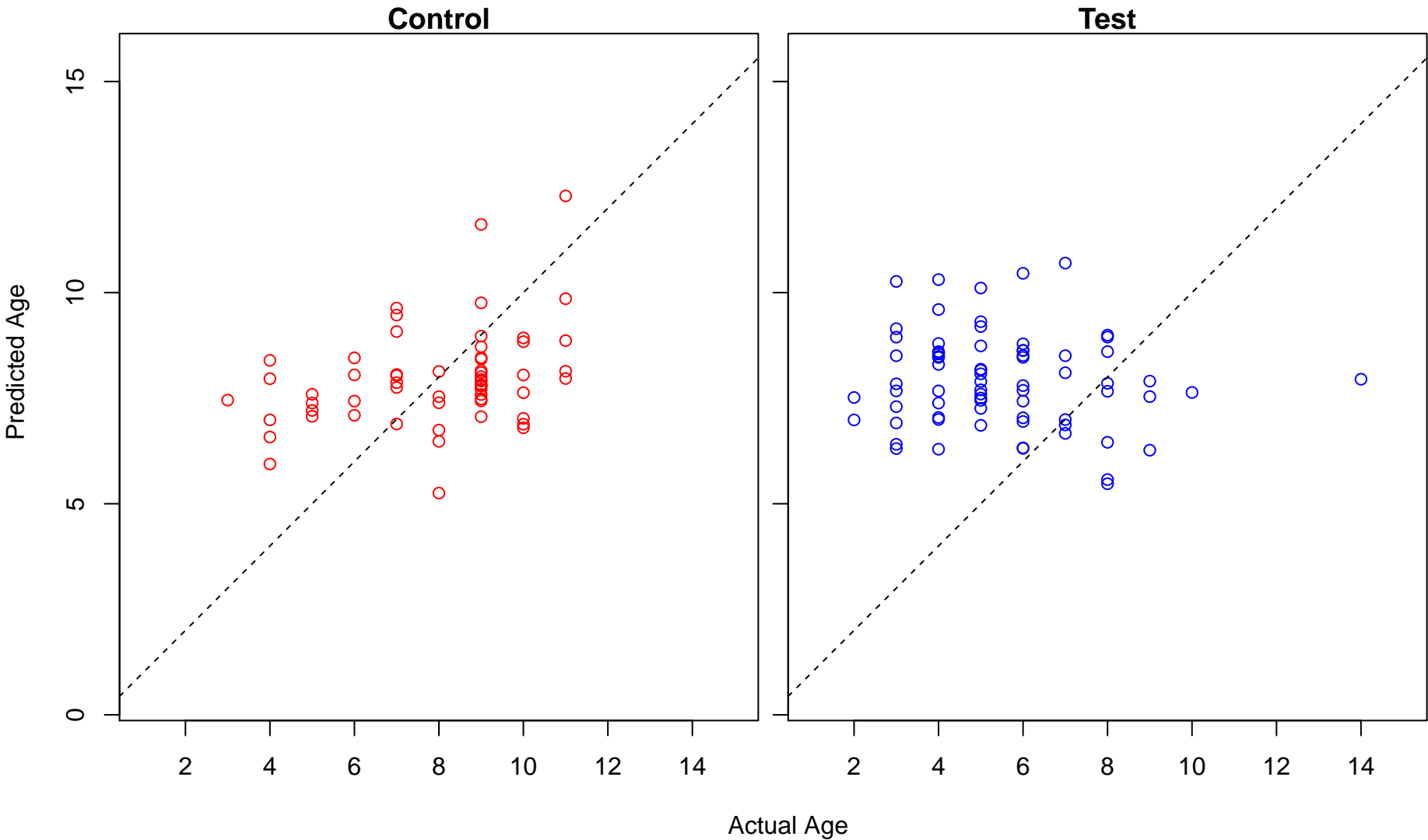
aspartate transport (Score: 0.631644)



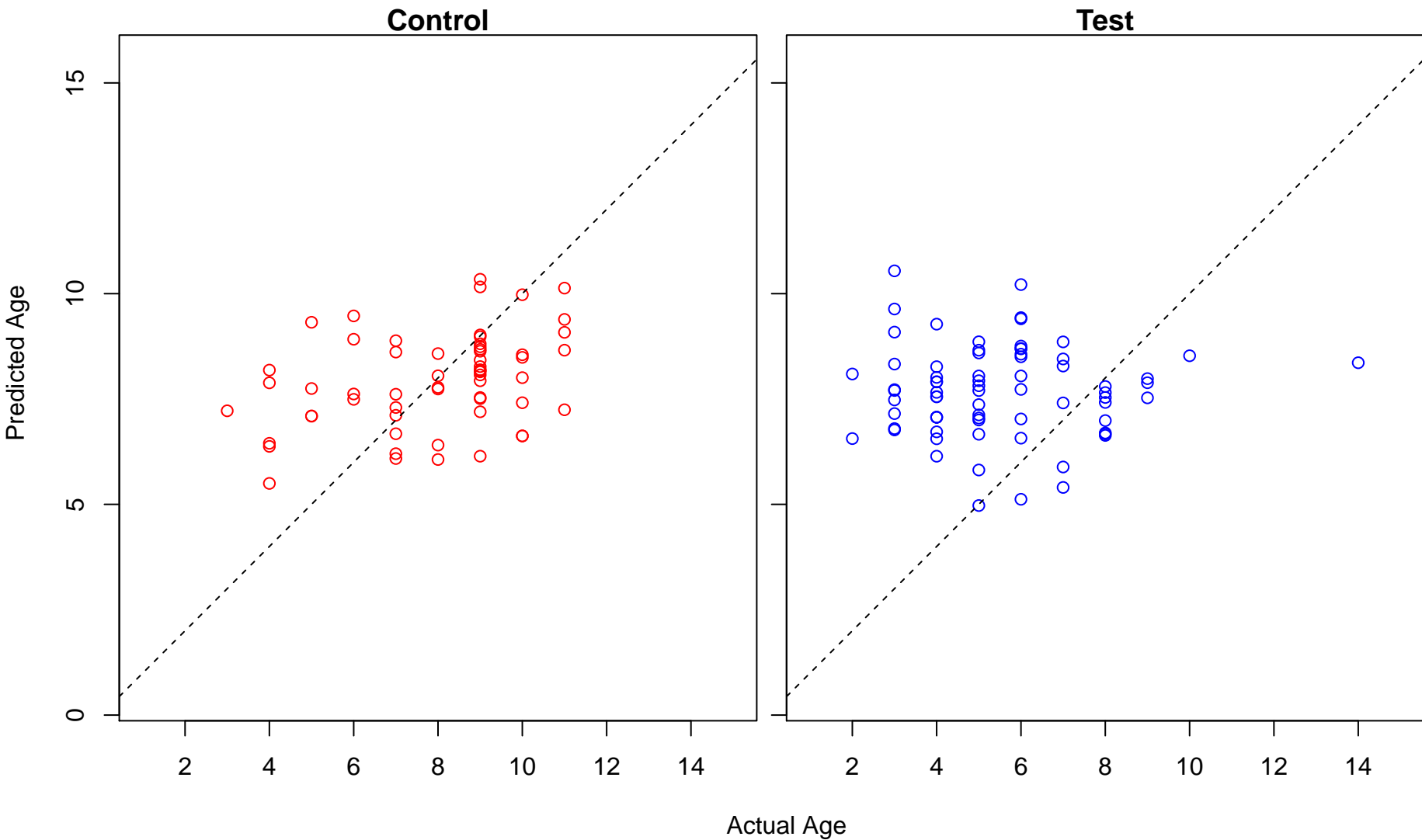
smoothened signaling pathway involved in ventral spinal cord interneuron specification (Score: 0.628)



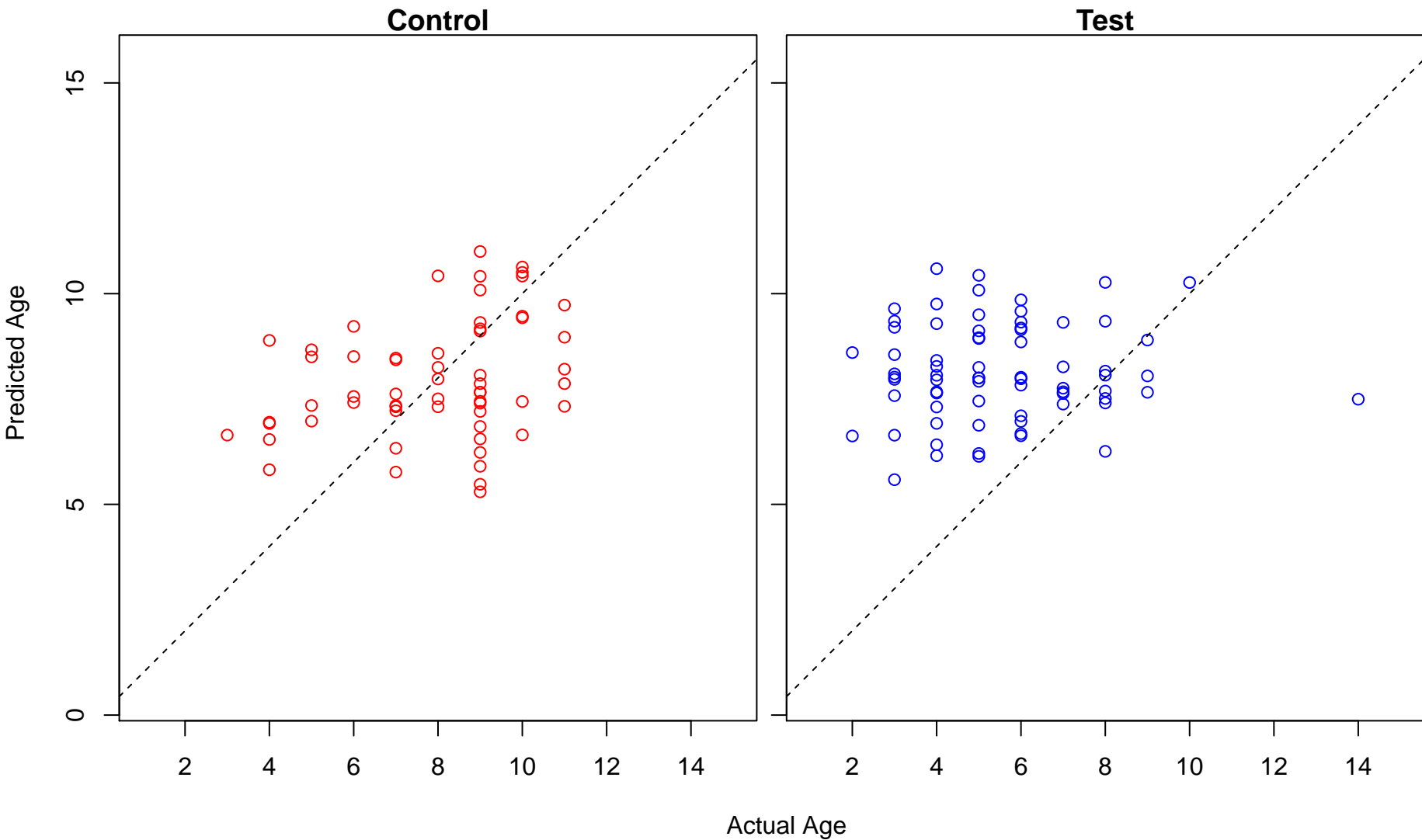
smoothened signaling pathway involved in spinal cord motor neuron cell fate specification (Score: 0.62)



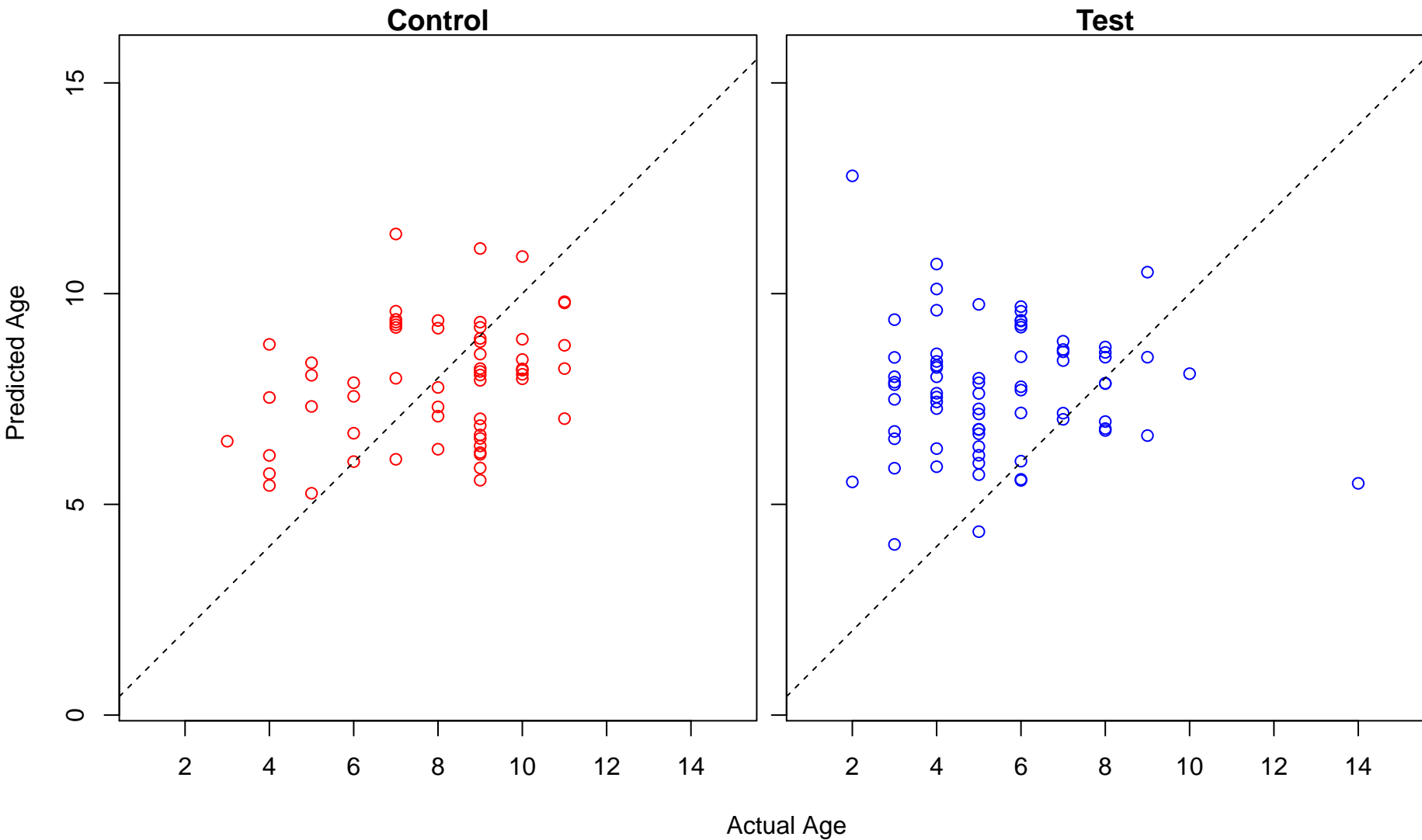
protein O-linked glycosylation via threonine (Score: 0.627589)



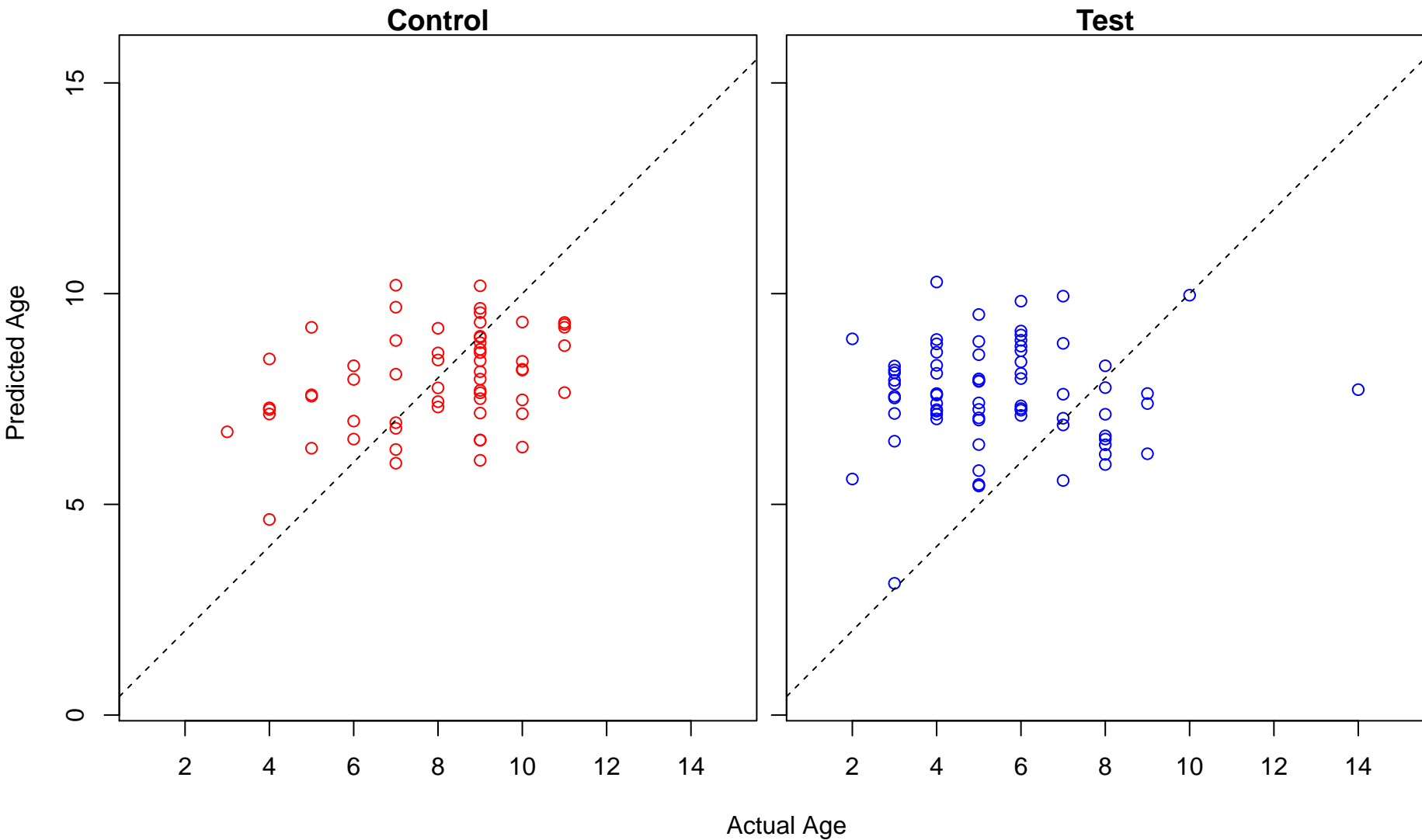
cytokine production involved in immune response (Score: 0.626702)



negative regulation of T cell proliferation (Score: 0.626652)

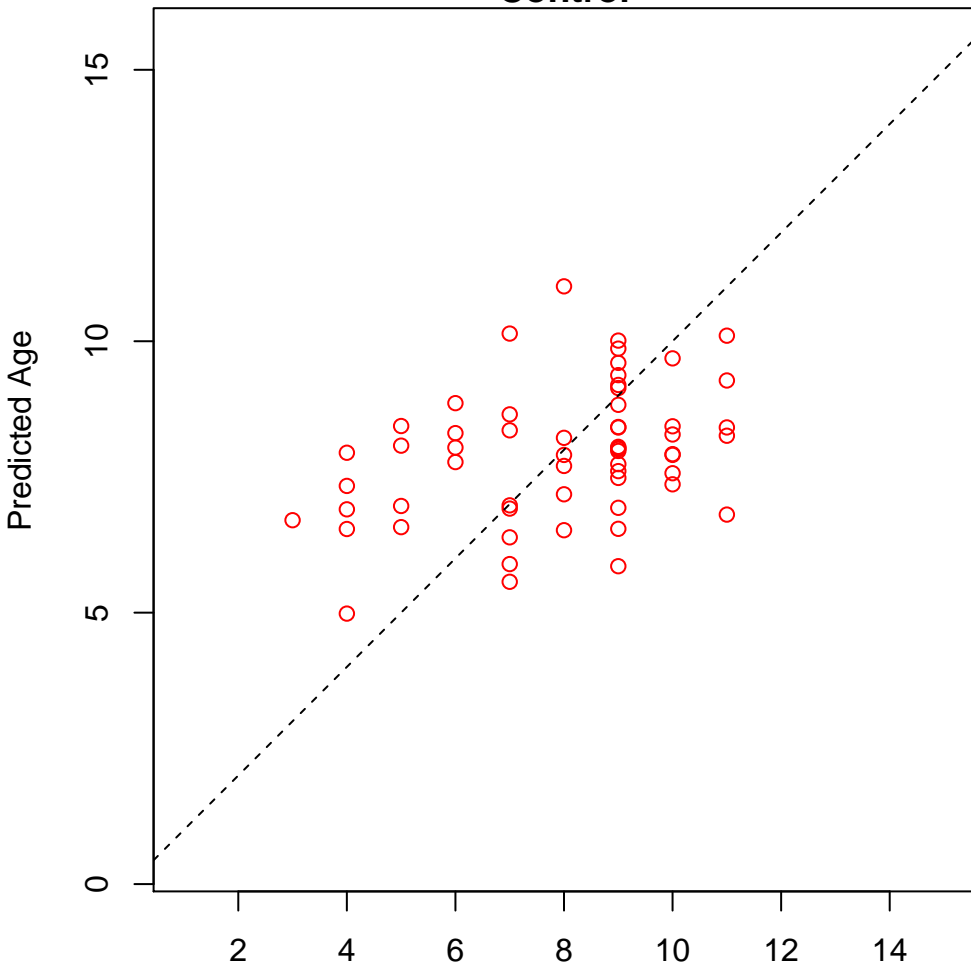


cytoplasmic microtubule organization (Score: 0.626411)

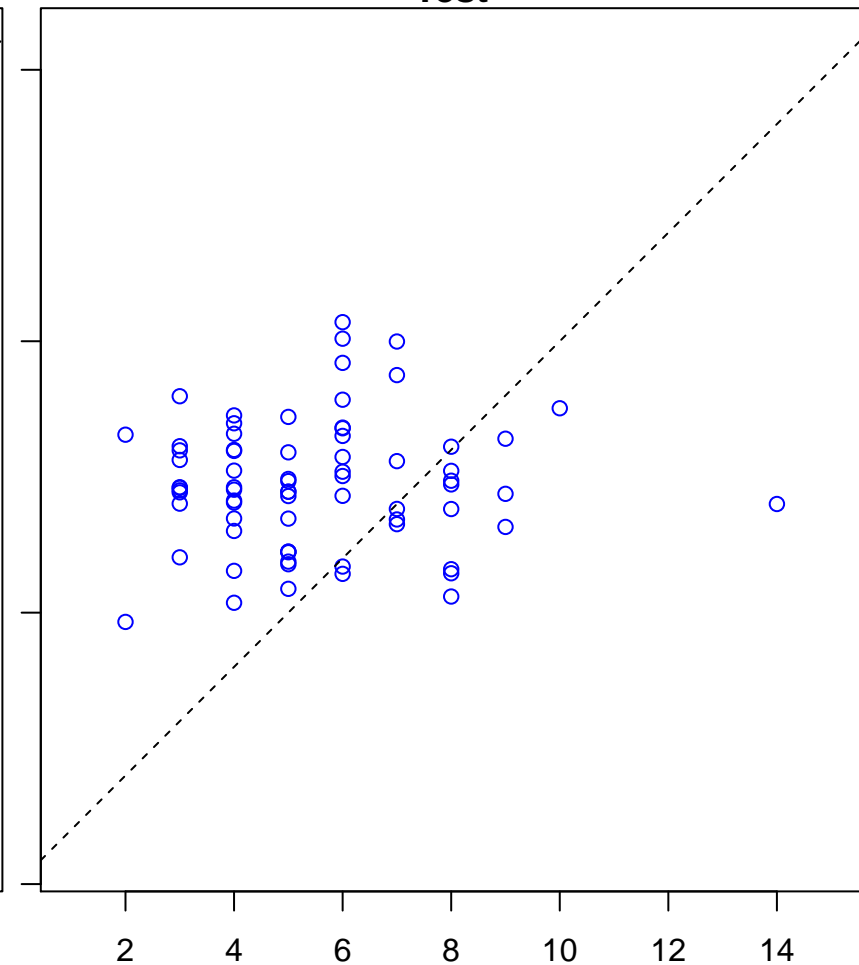


vesicle transport along actin filament (Score: 0.626220)

Control

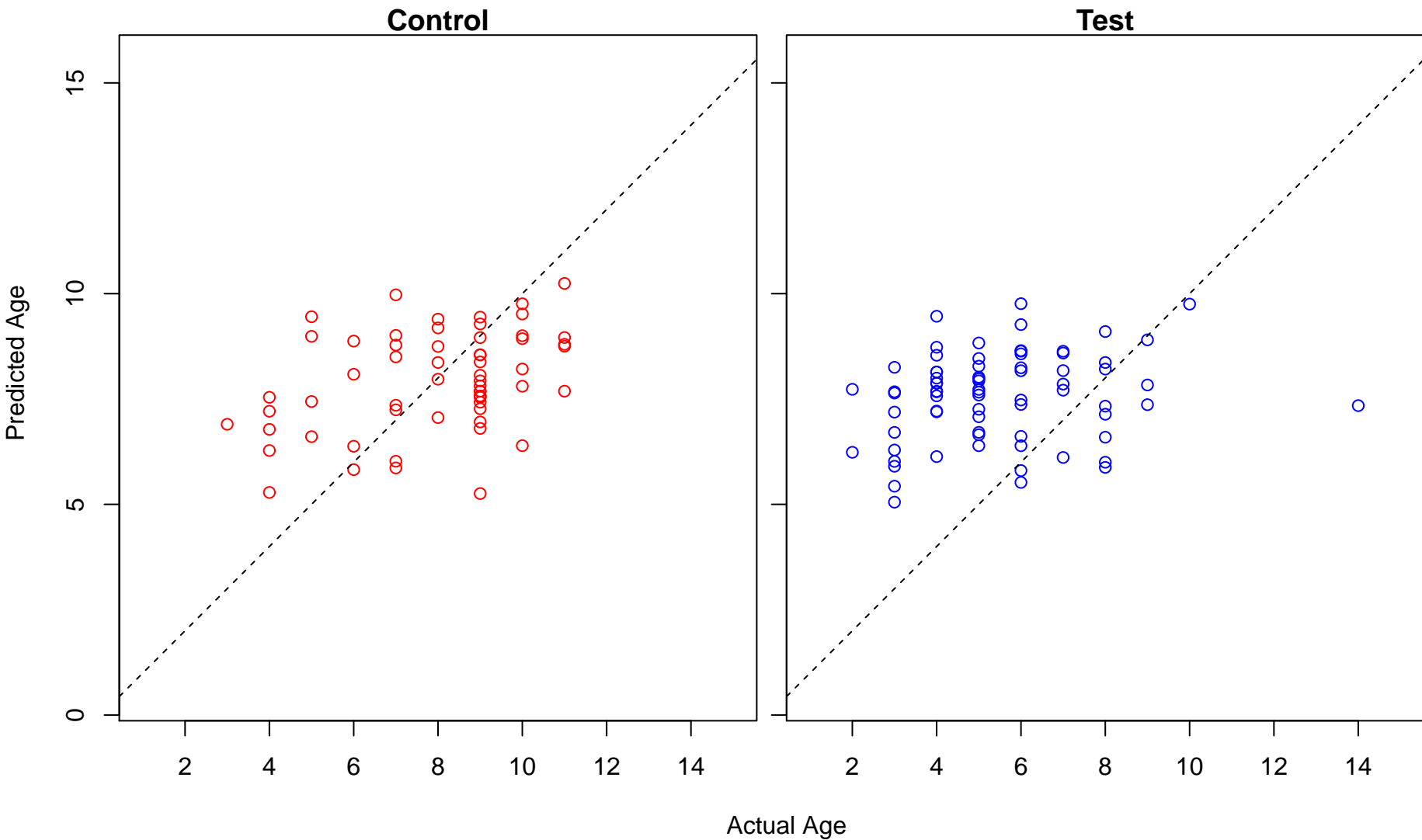


Test

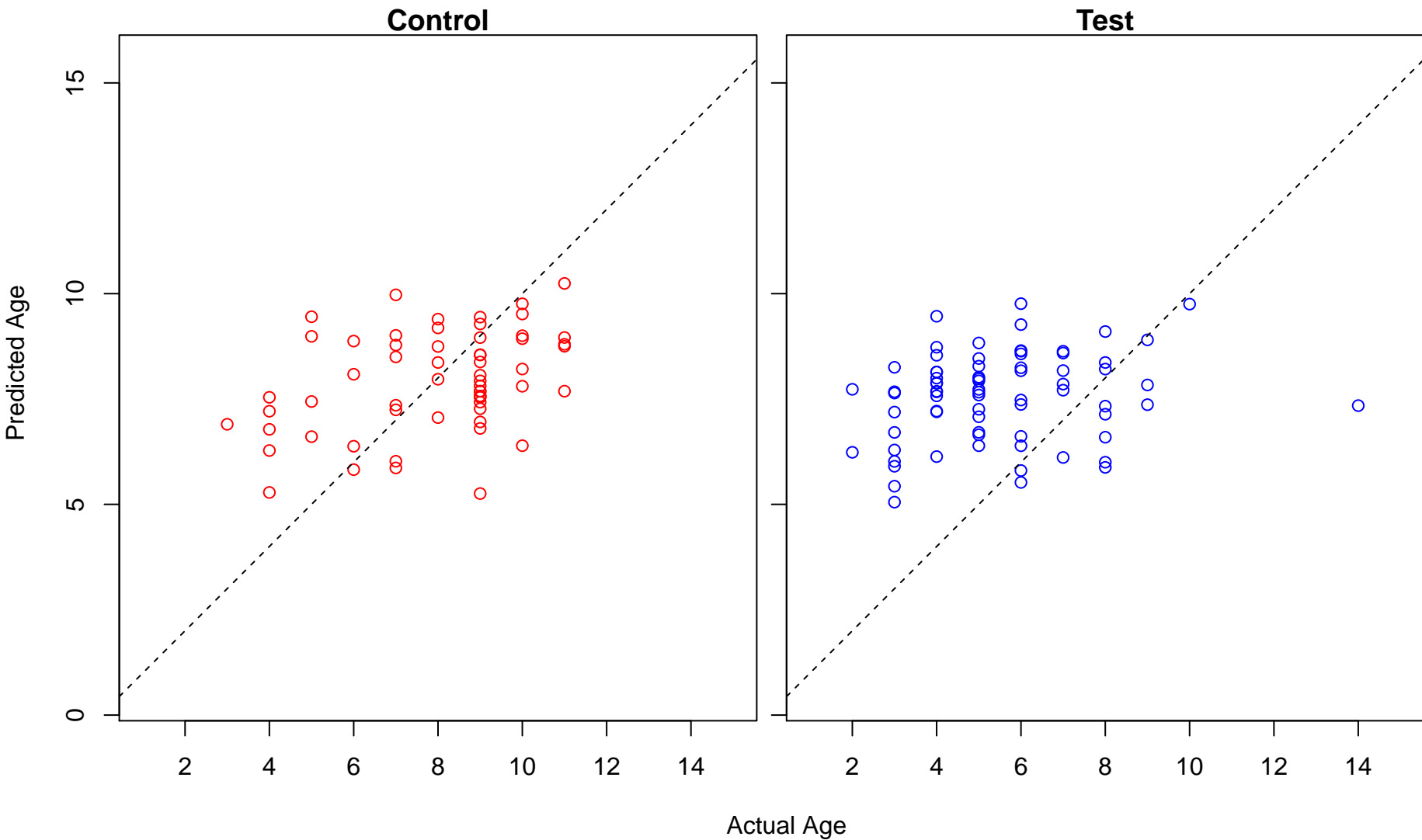


Actual Age

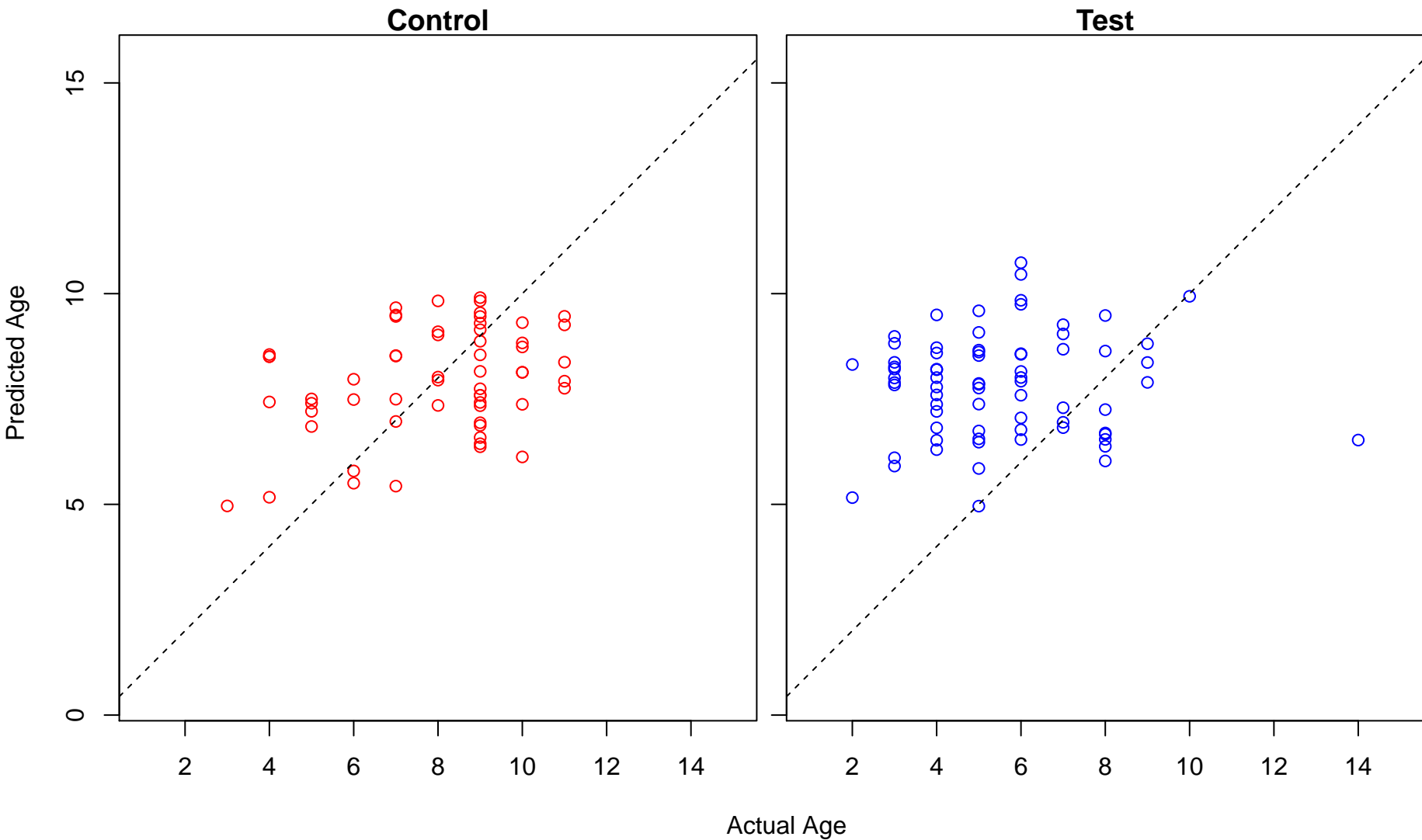
histone H4-K5 acetylation (Score: 0.624348)



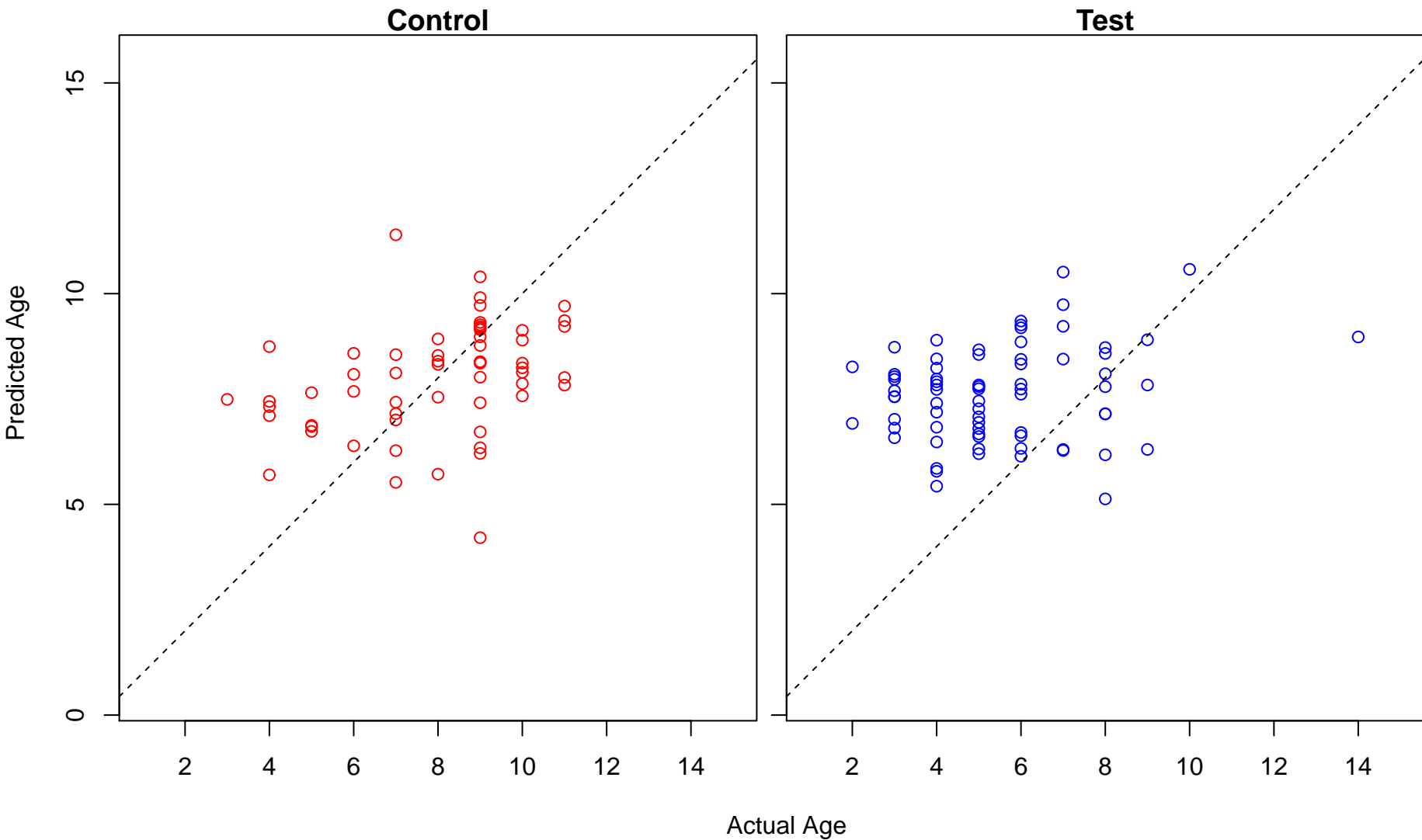
histone H4-K8 acetylation (Score: 0.624348)



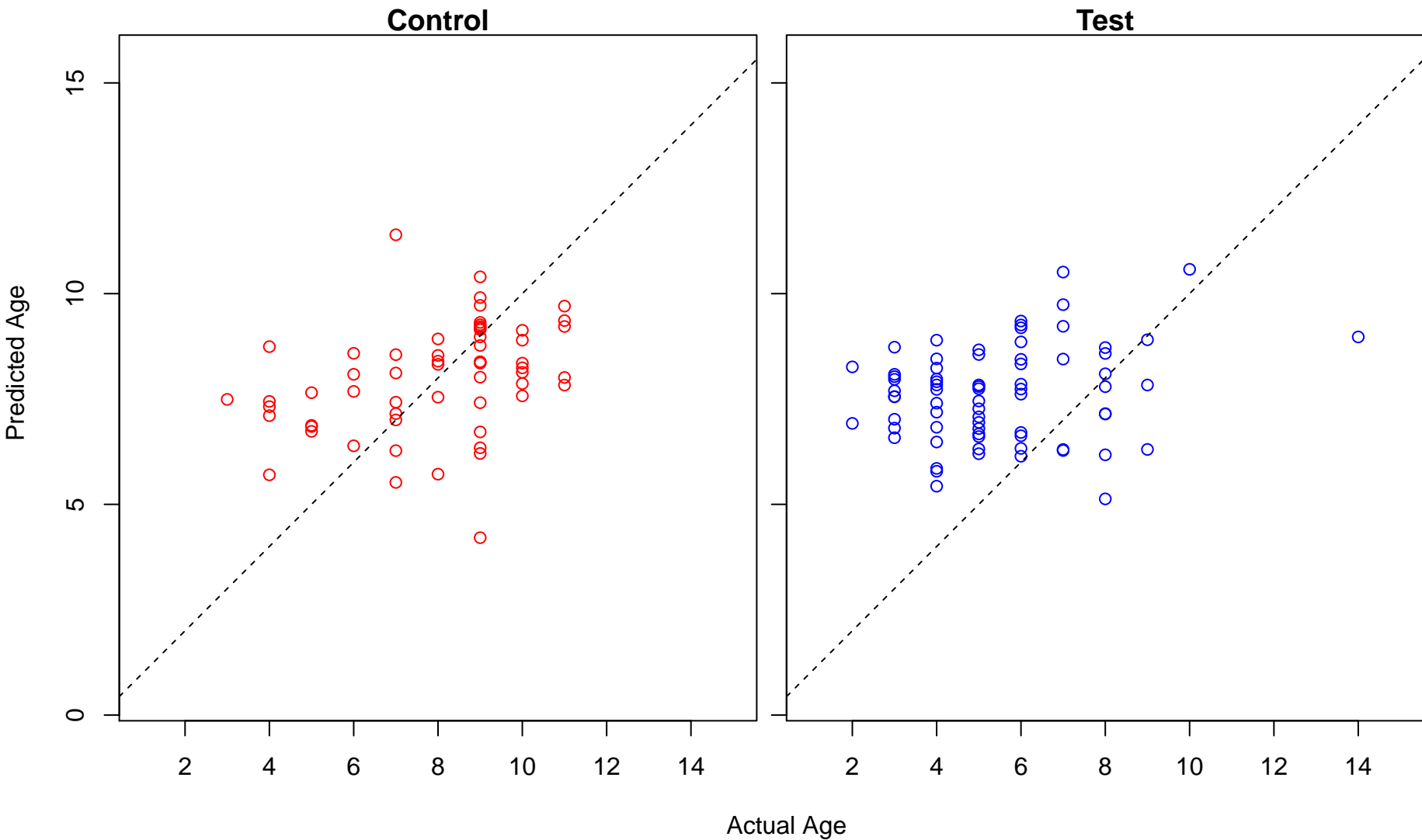
DNA dealkylation involved in DNA repair (Score: 0.624043)



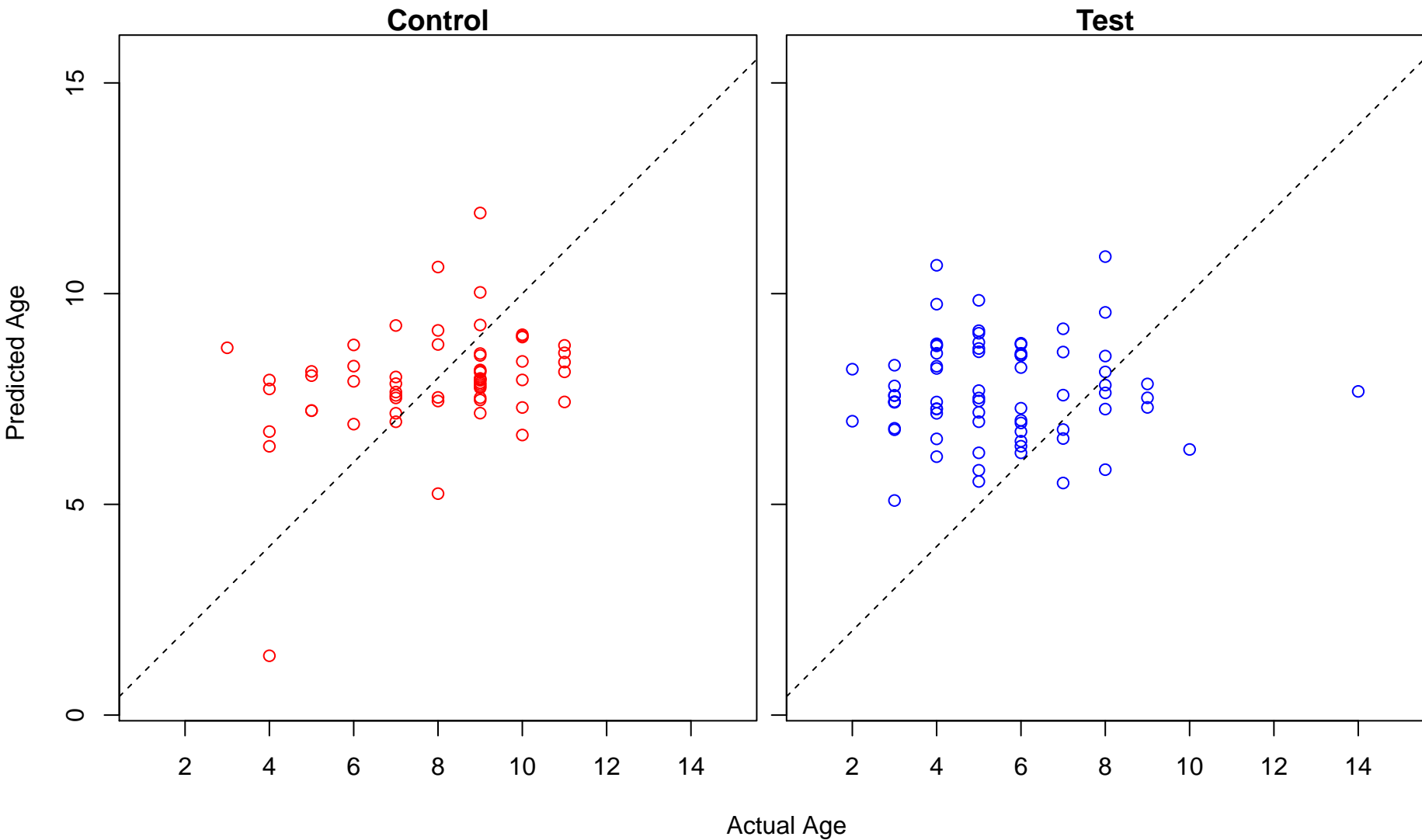
ovulation cycle process (Score: 0.623357)



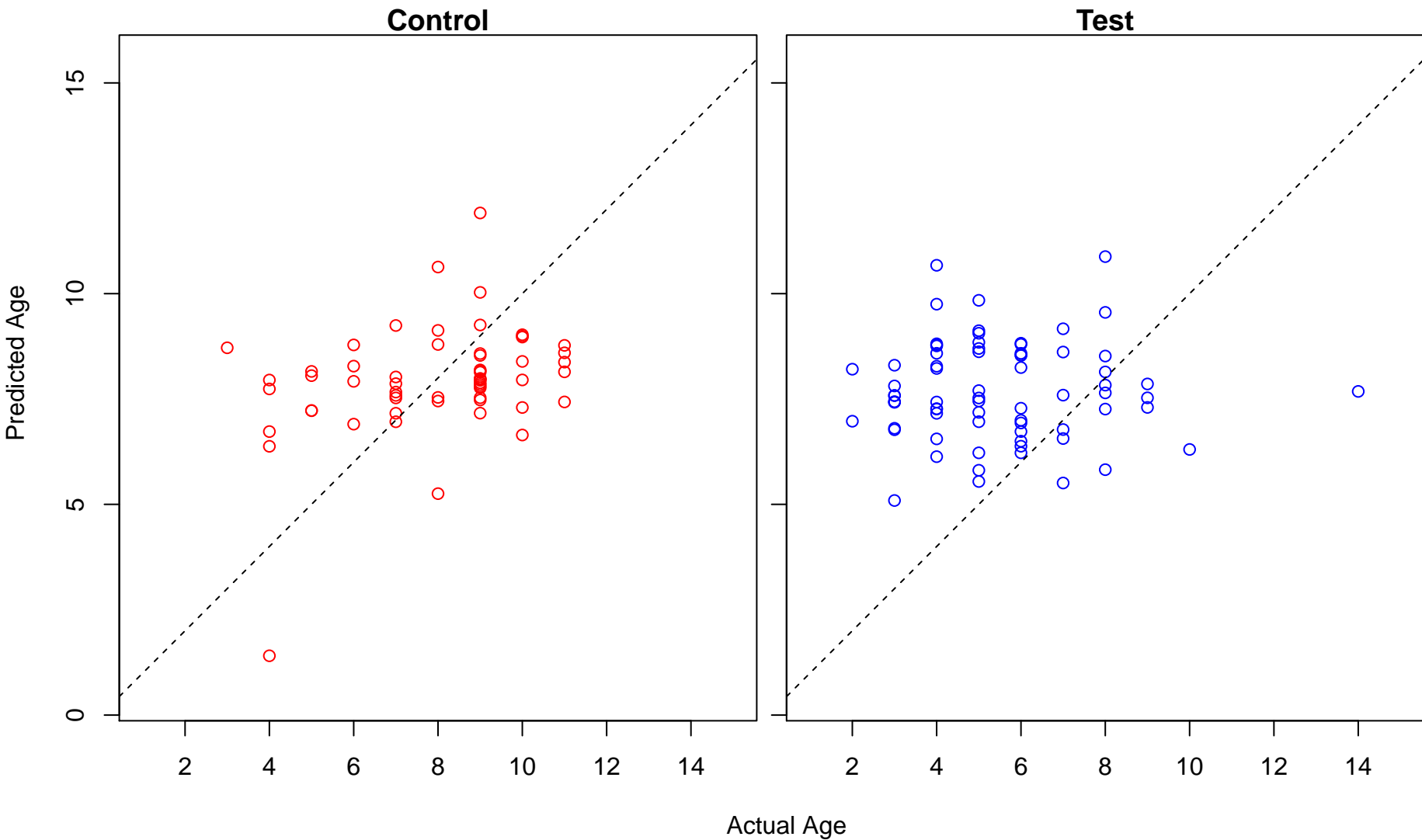
ovulation cycle (Score: 0.62352)



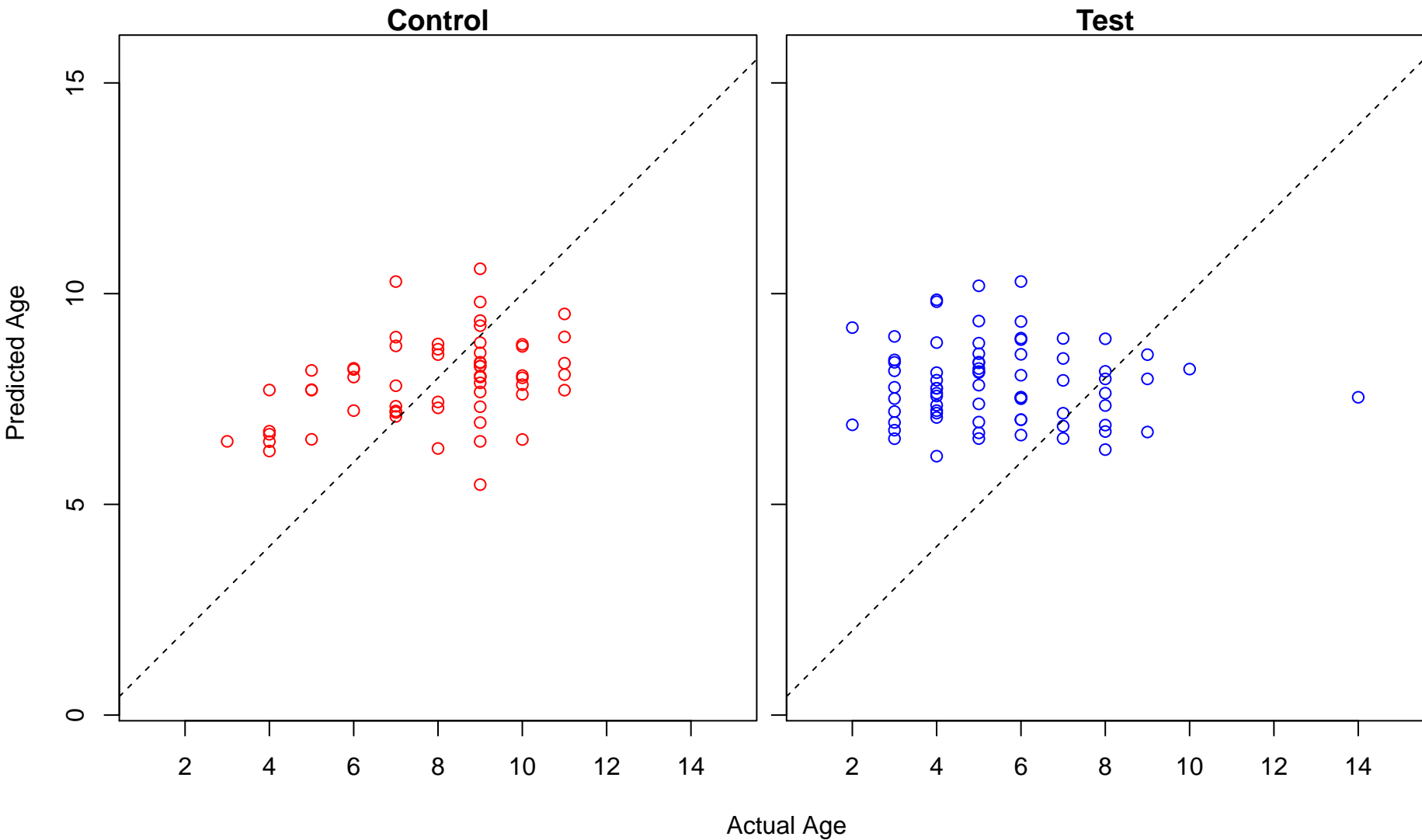
dopamine transport (Score: 0.623270)



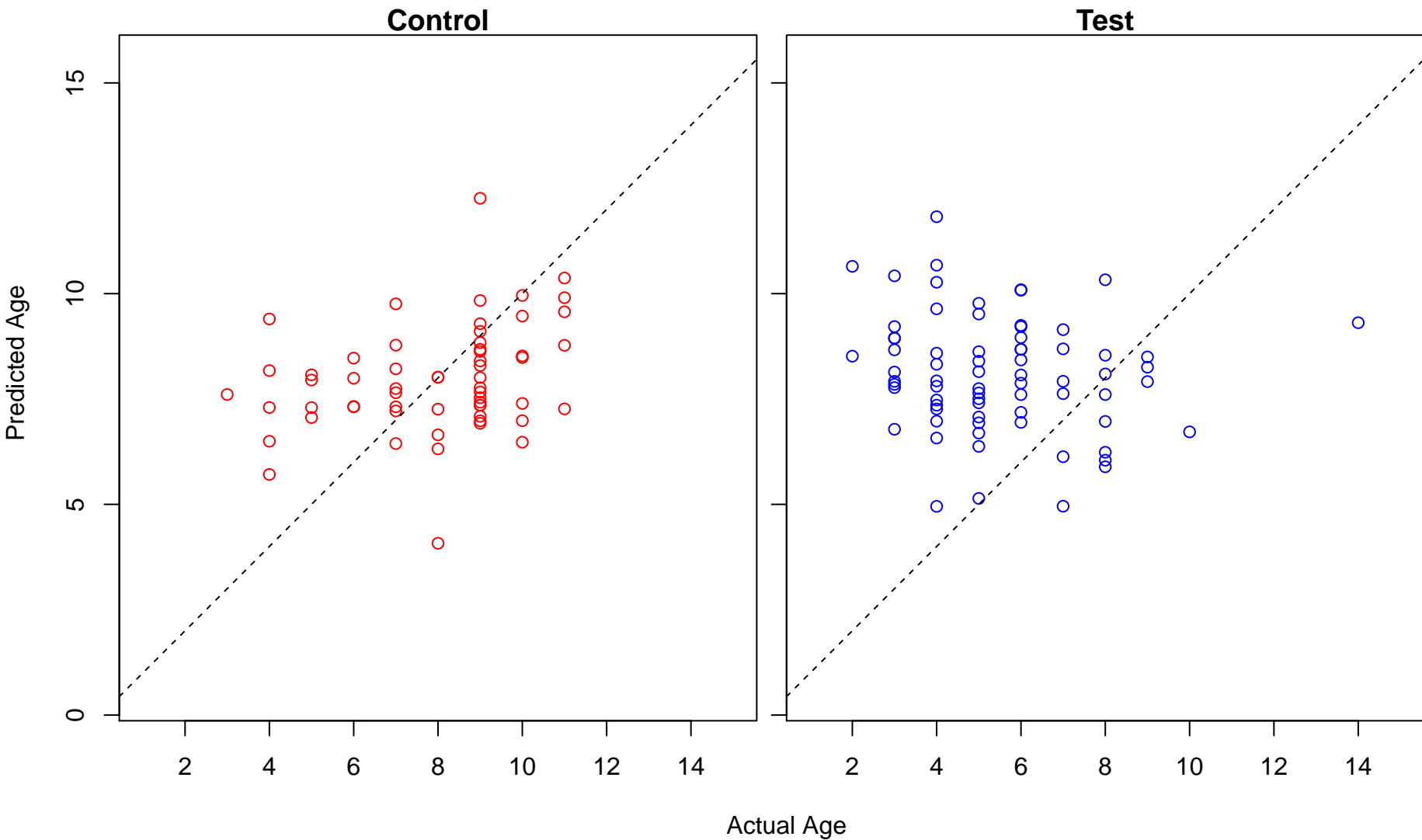
catecholamine transport (Score: 0.623270)



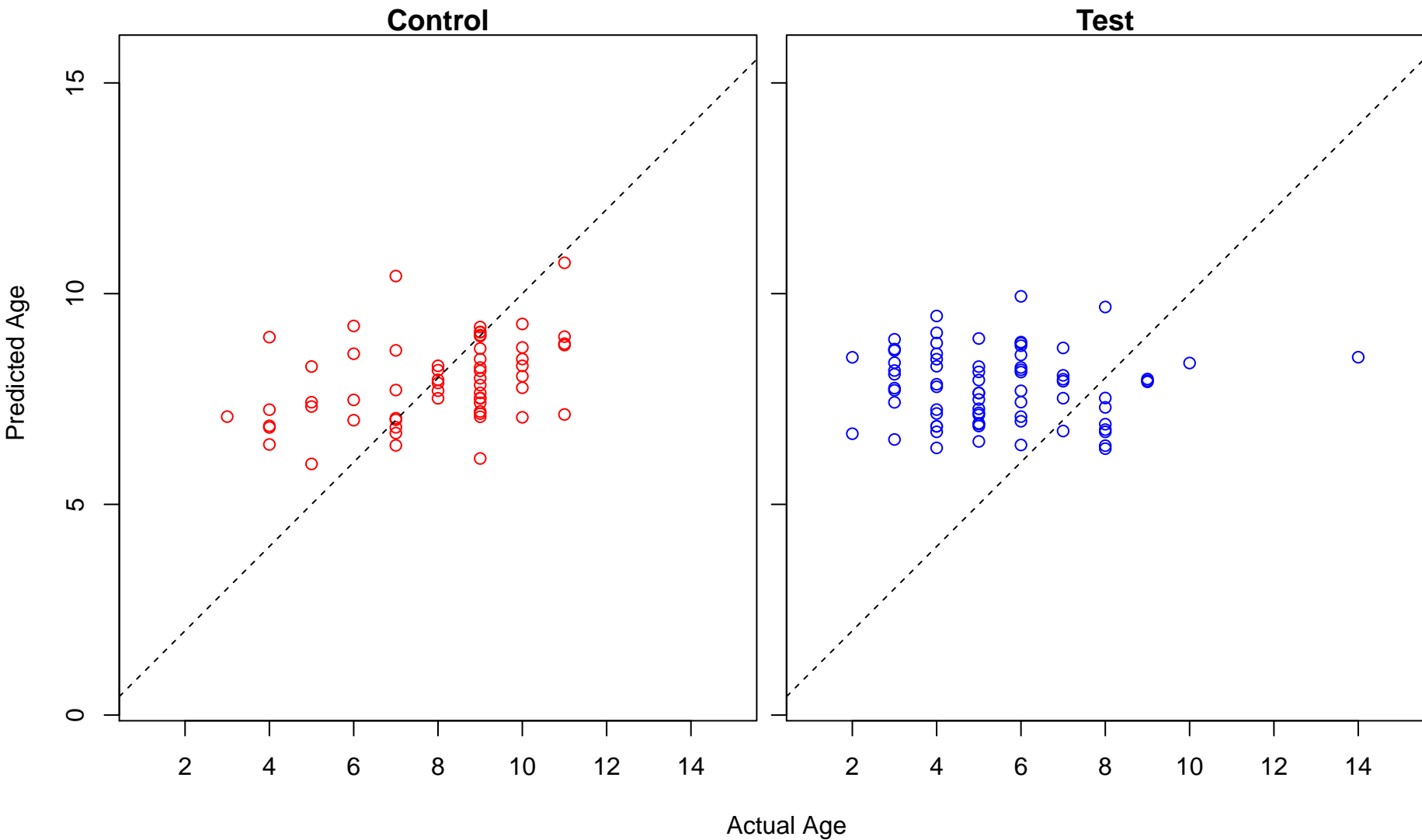
mast cell activation (Score: 0.622521)



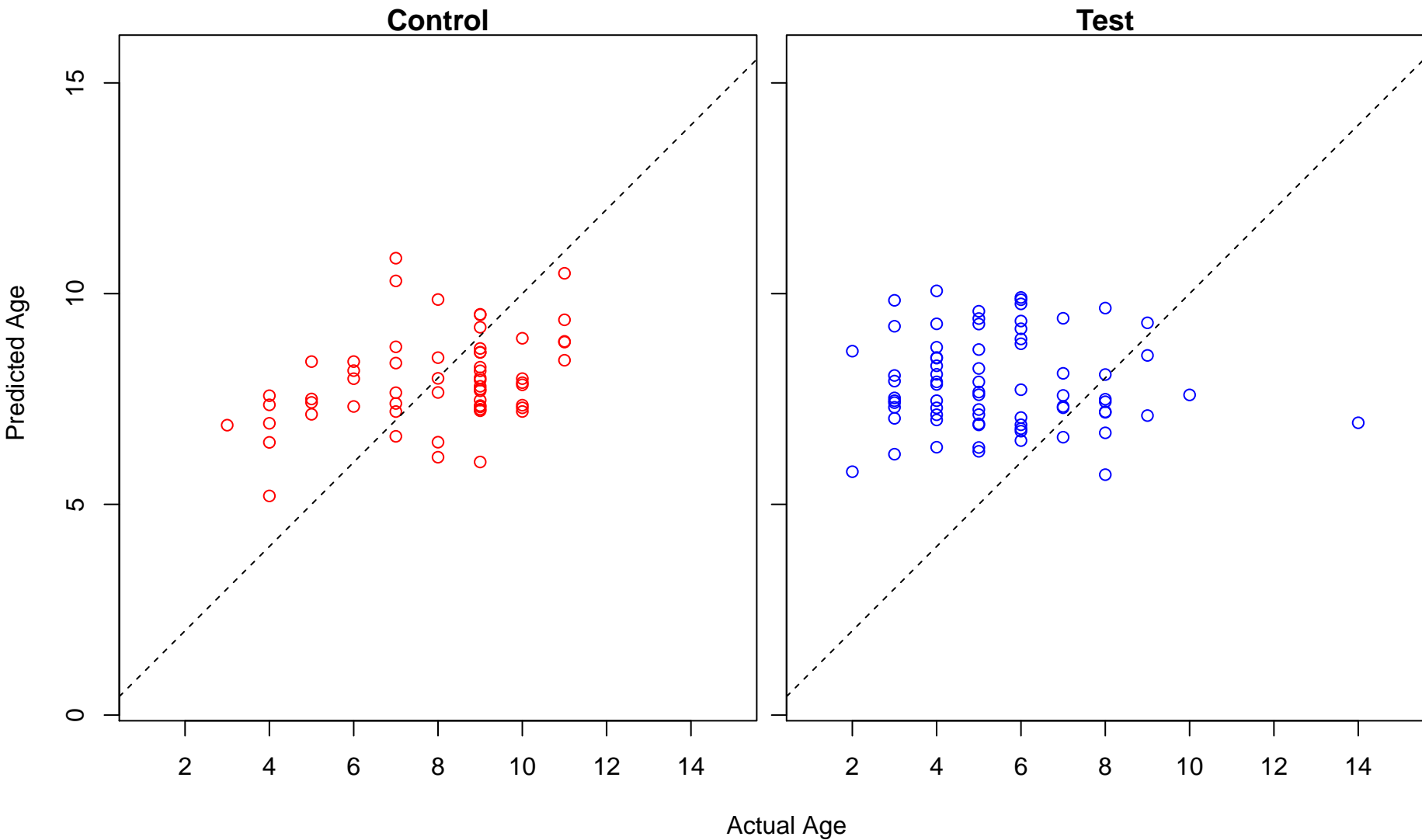
negative regulation of translational initiation in response to stress (Score: 0.621761)



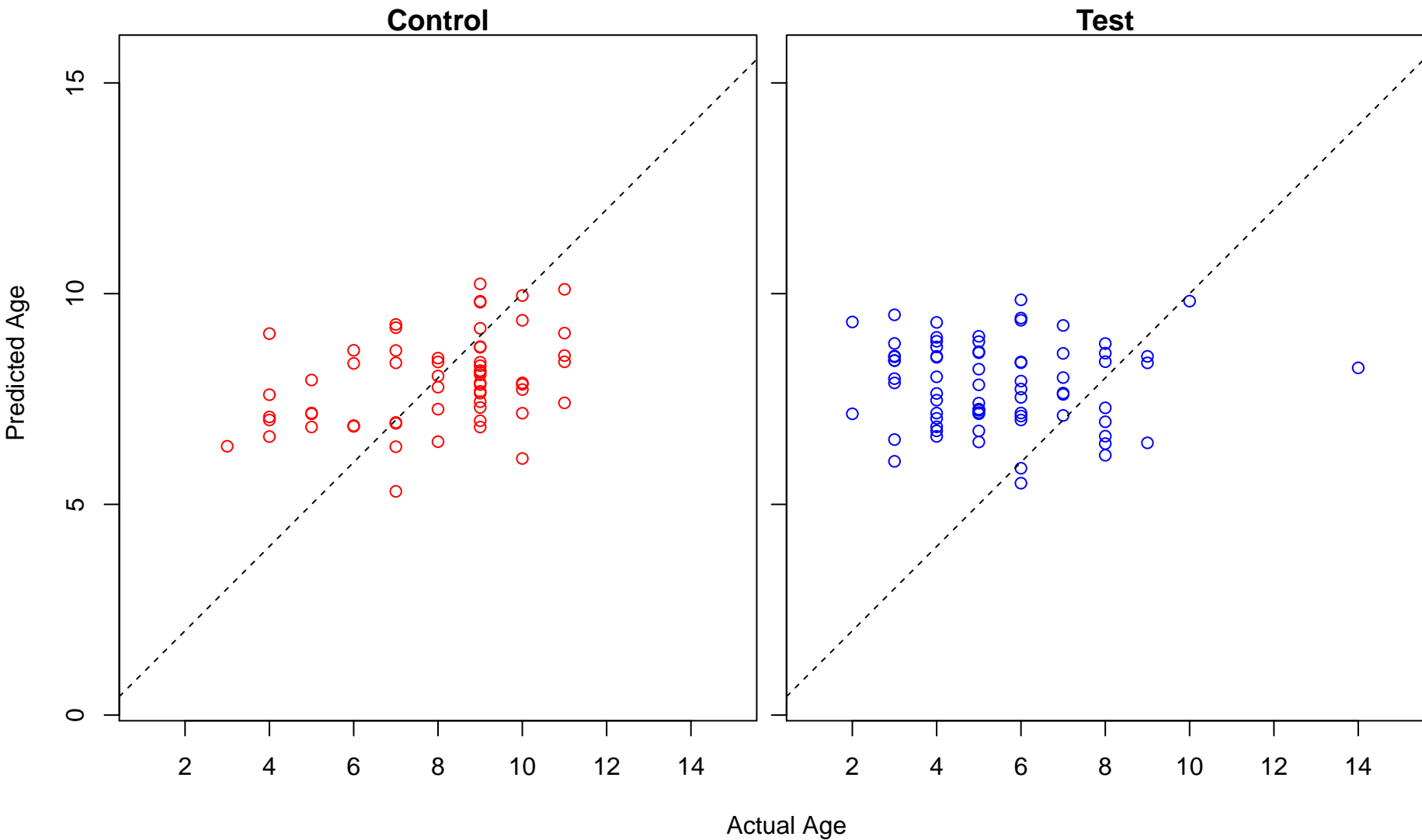
sulfur compound transport (Score: 0.621401)



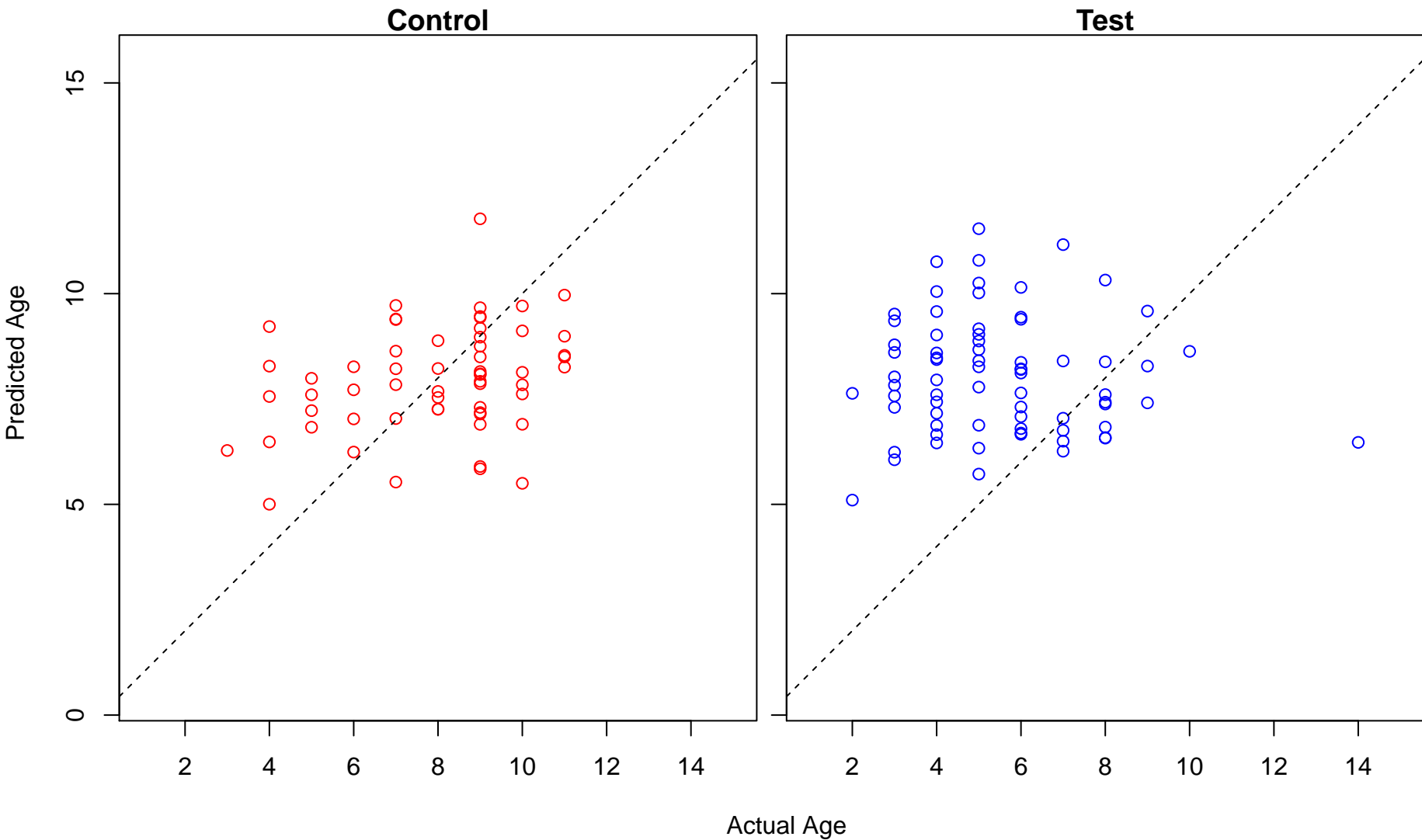
endoplasmic reticulum organization (Score: 0.619234)



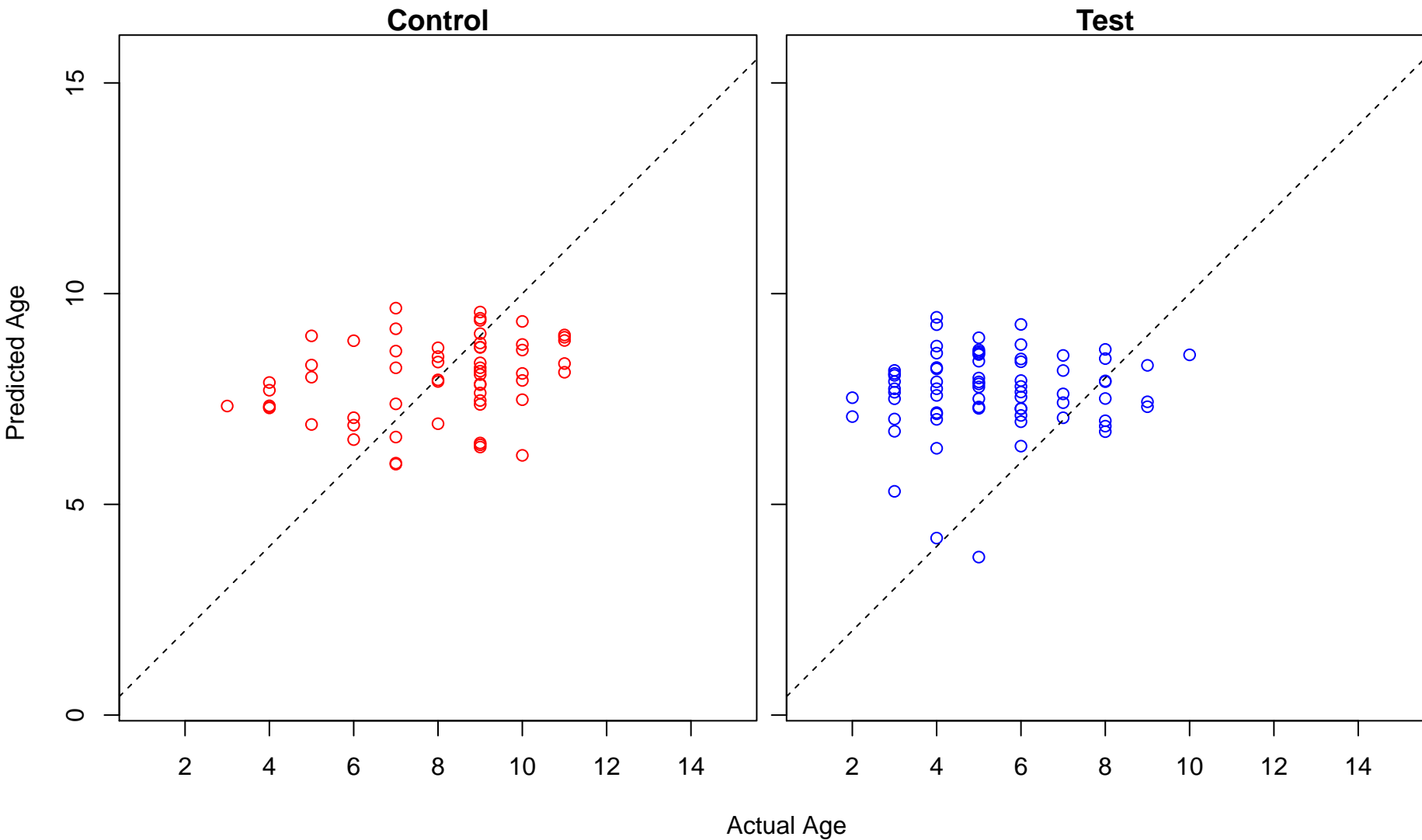
telomere assembly (Score: 0.618930)



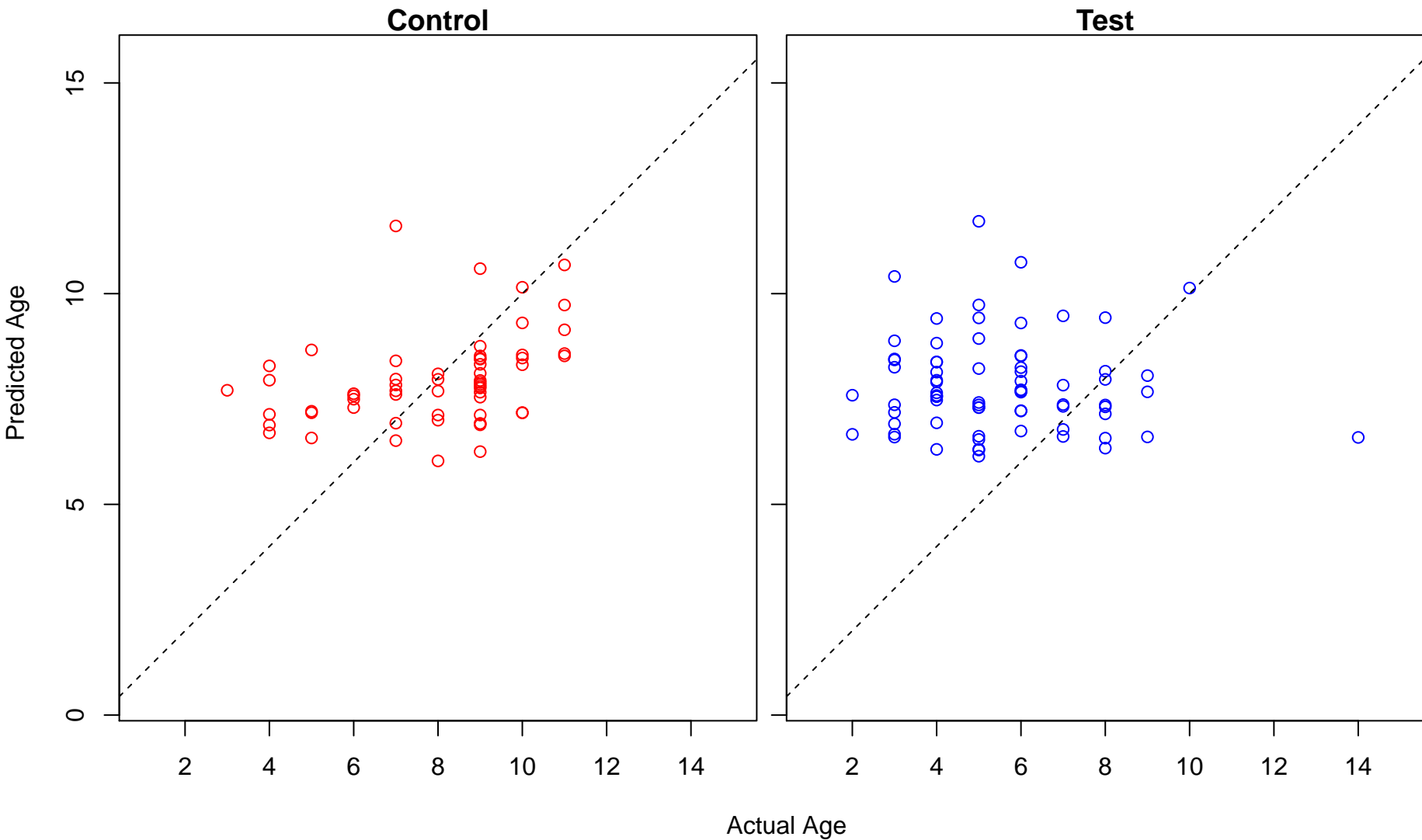
heparan sulfate proteoglycan metabolic process (Score: 0.618722)



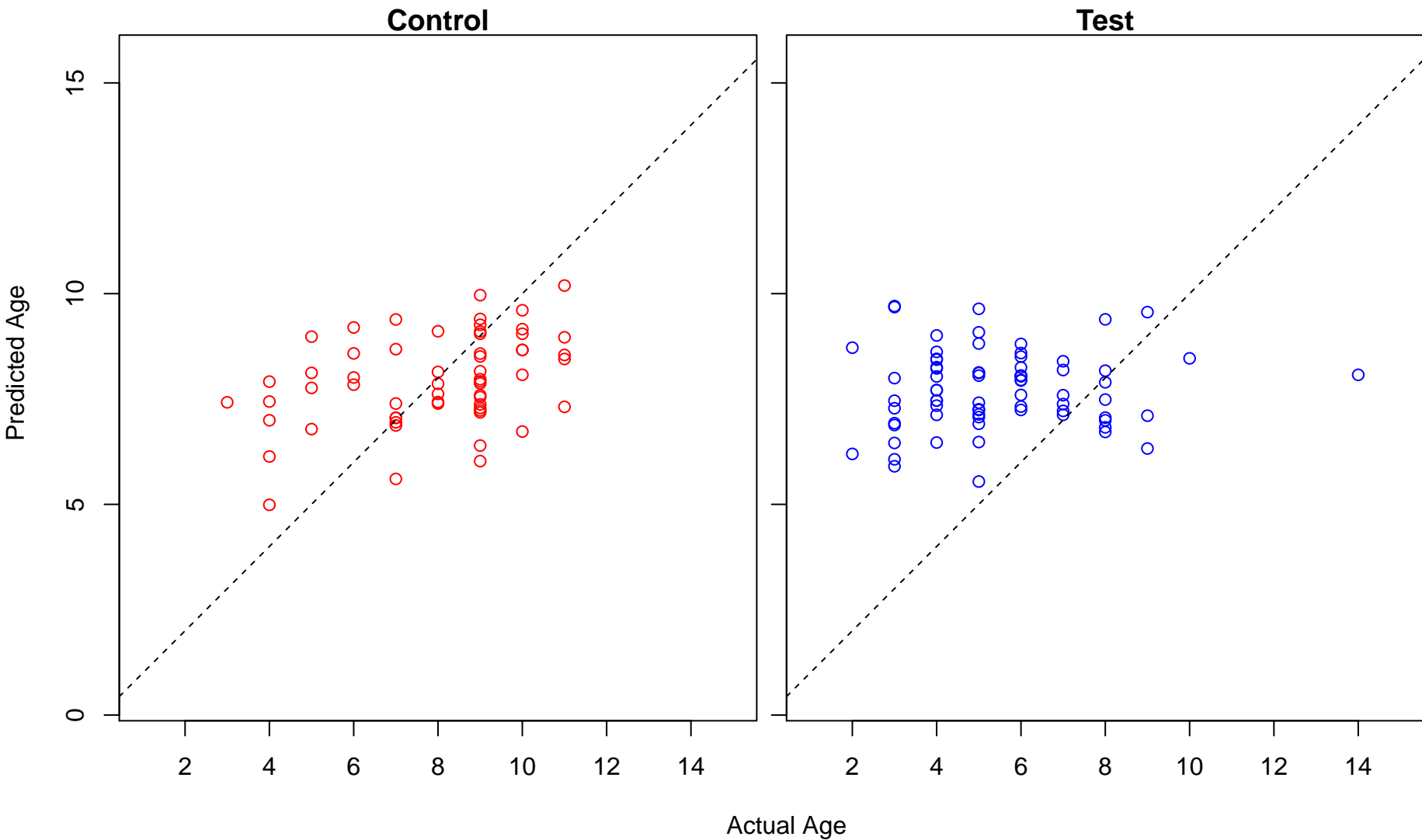
regulation of protein sumoylation (Score: 0.616397)



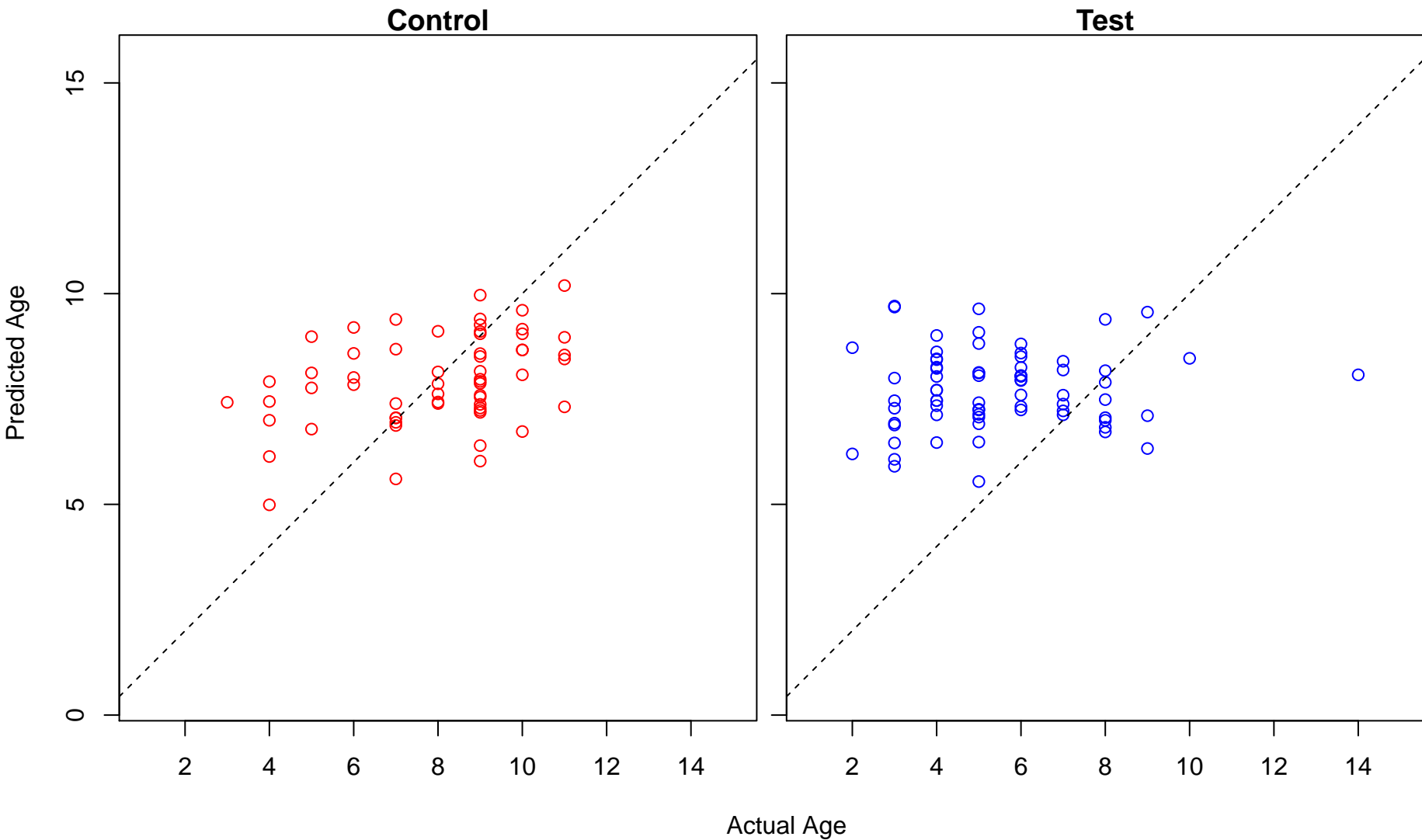
inner medullary collecting duct development (Score: 0.616307)



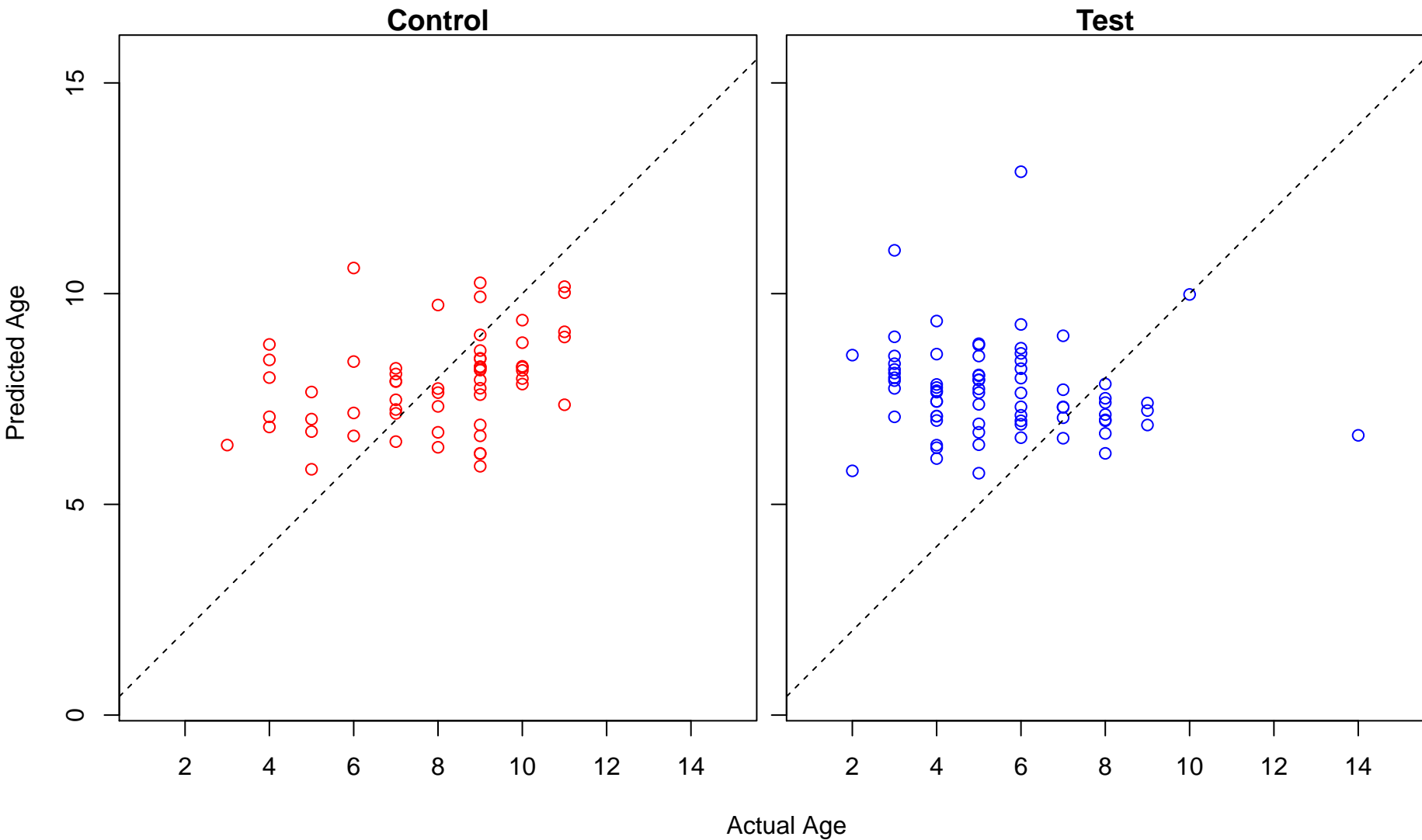
cadmium ion transport (Score: 0.616208)



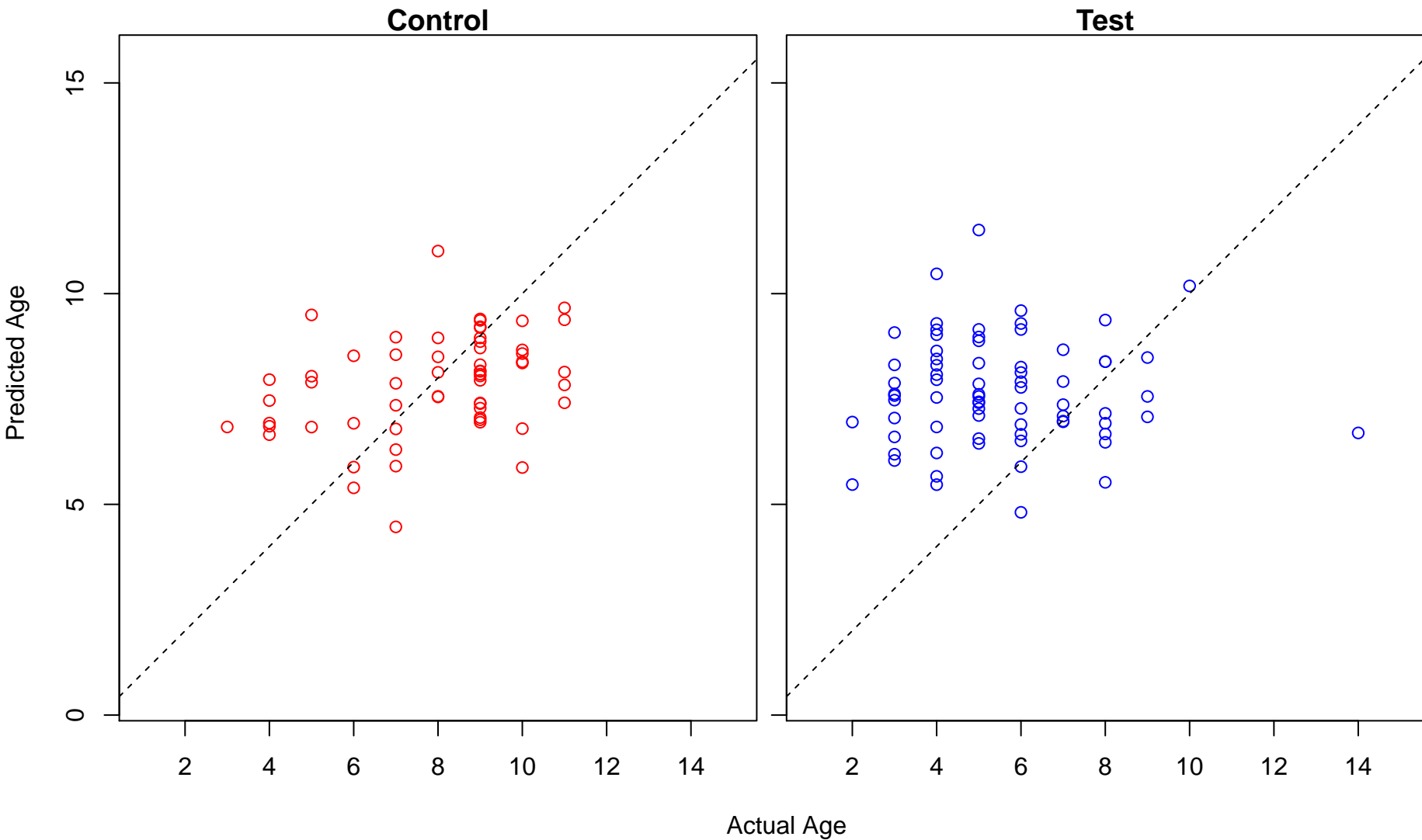
cadmium ion transmembrane transport (Score: 0.616208)



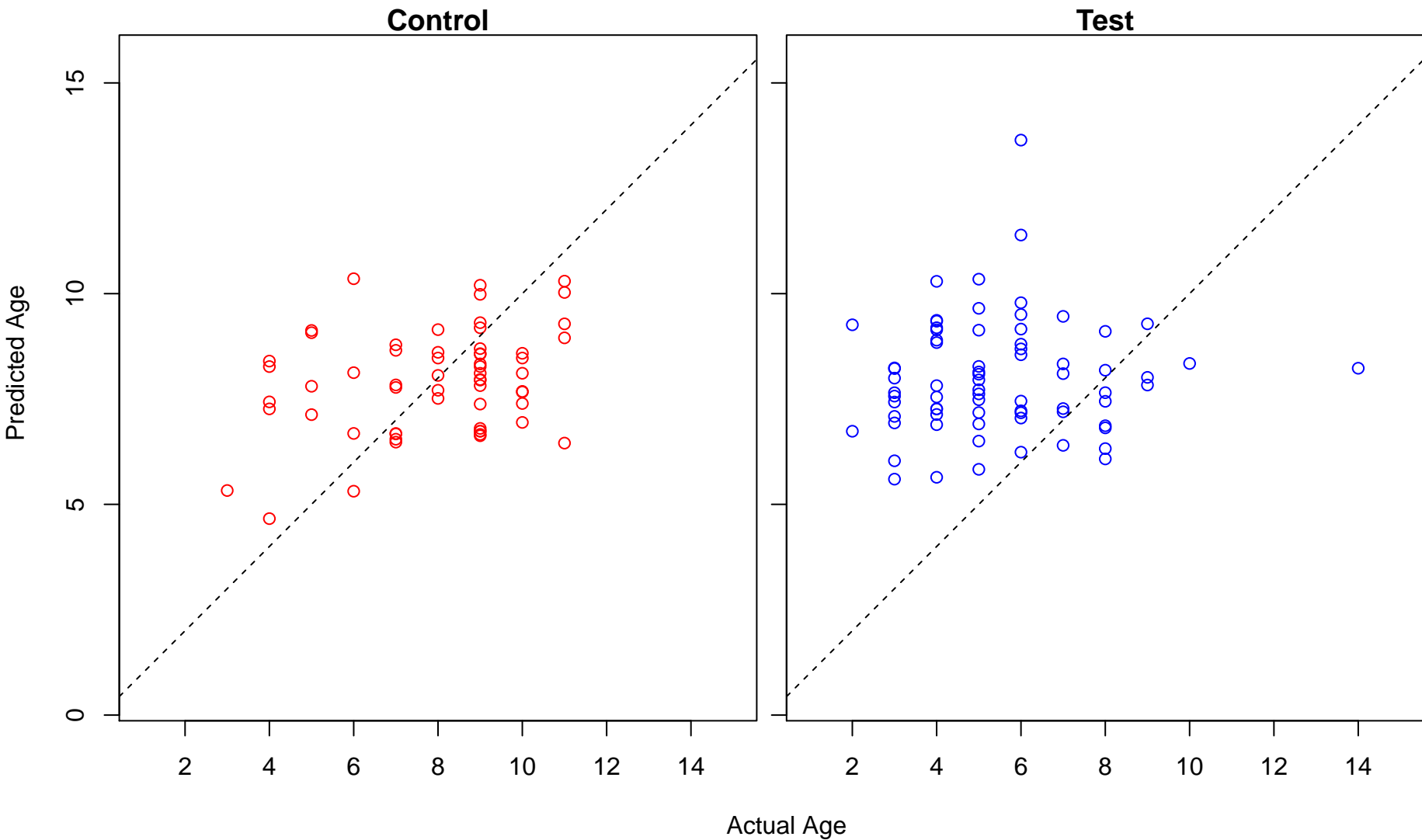
positive regulation of interleukin-10 secretion (Score: 0.616125)



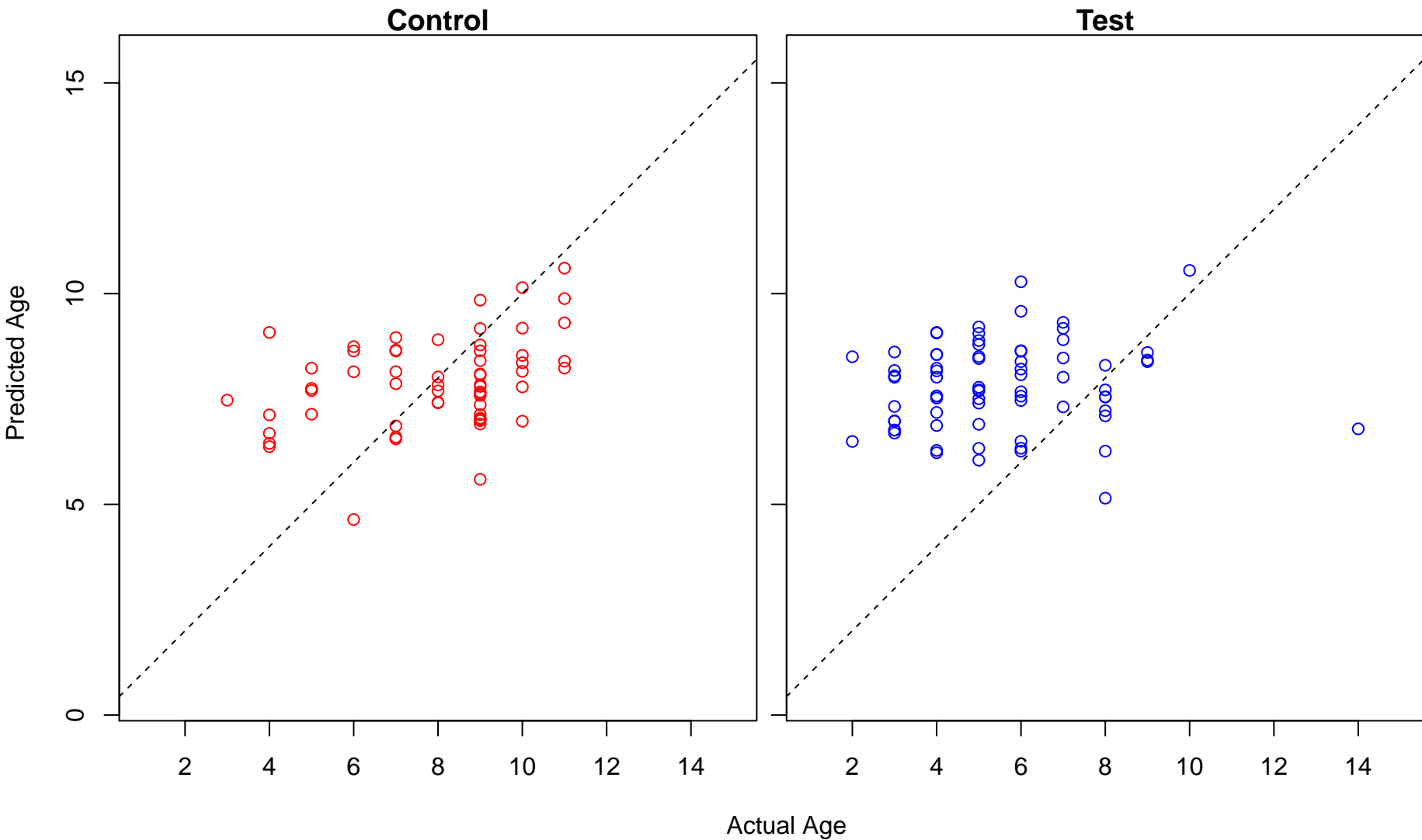
UDP-glucosylation (Score: 0.615810)



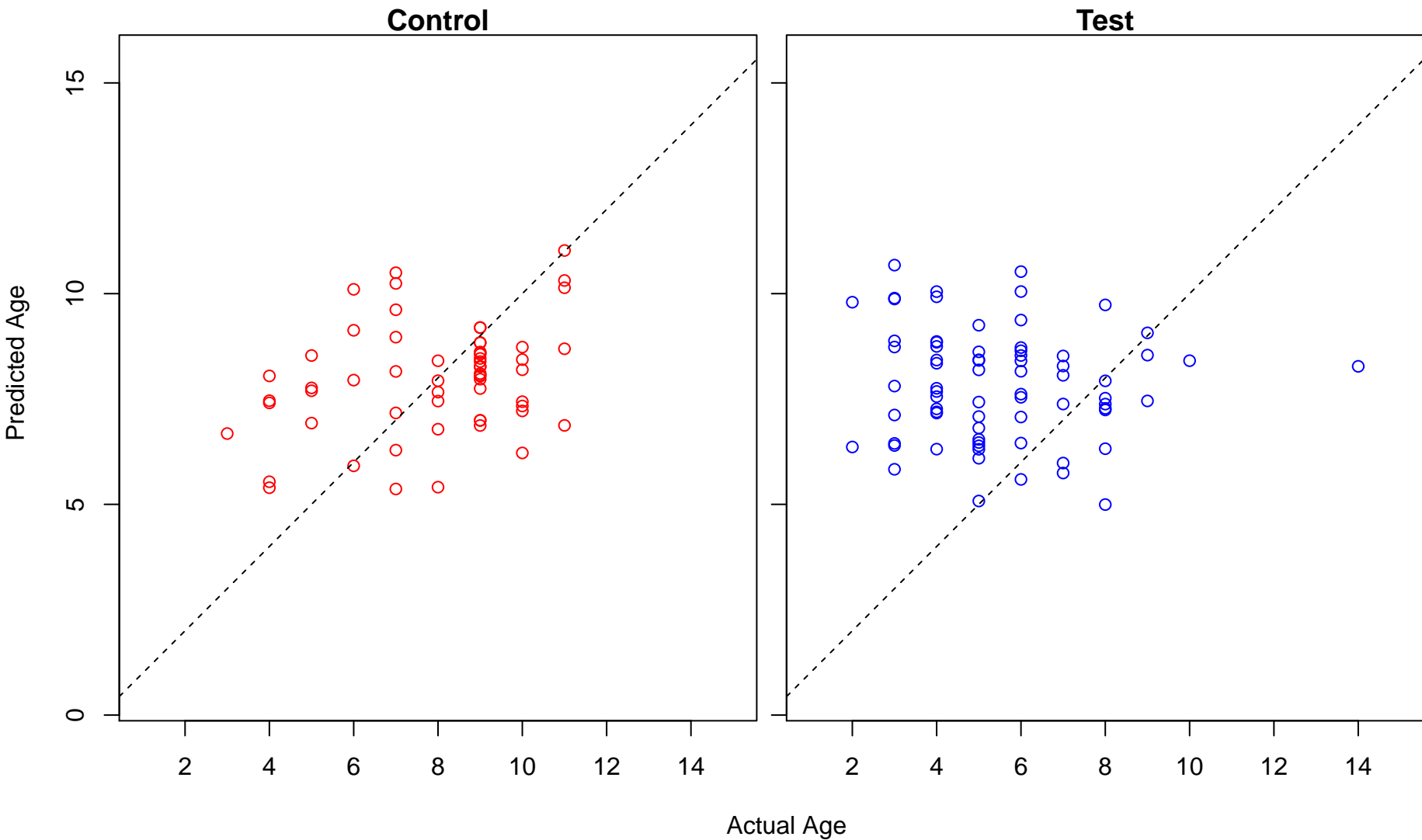
arachidonic acid secretion (Score: 0.615797)



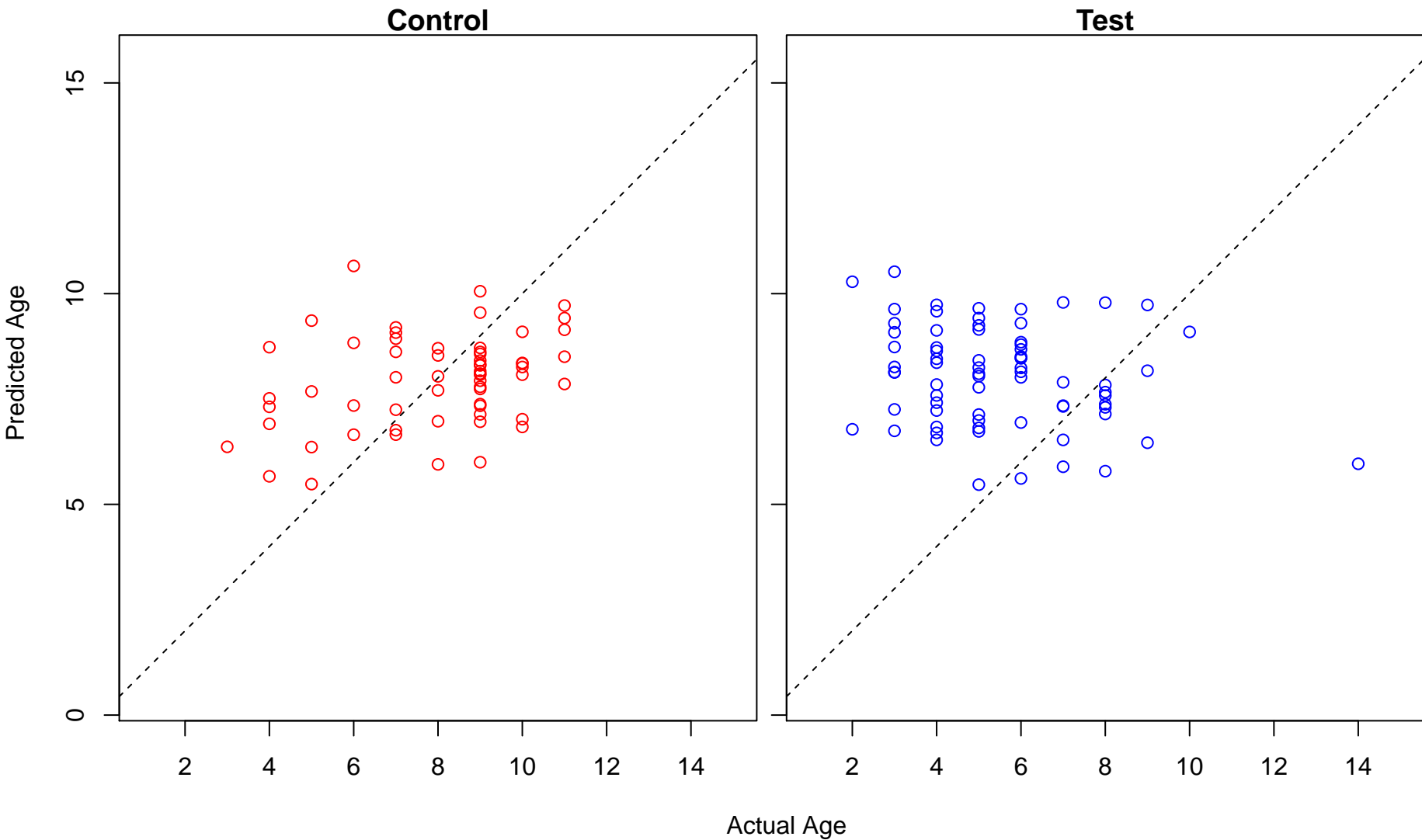
positive regulation of insulin receptor signaling pathway (Score: 0.615565)



lung epithelial cell differentiation (Score: 0.614644)

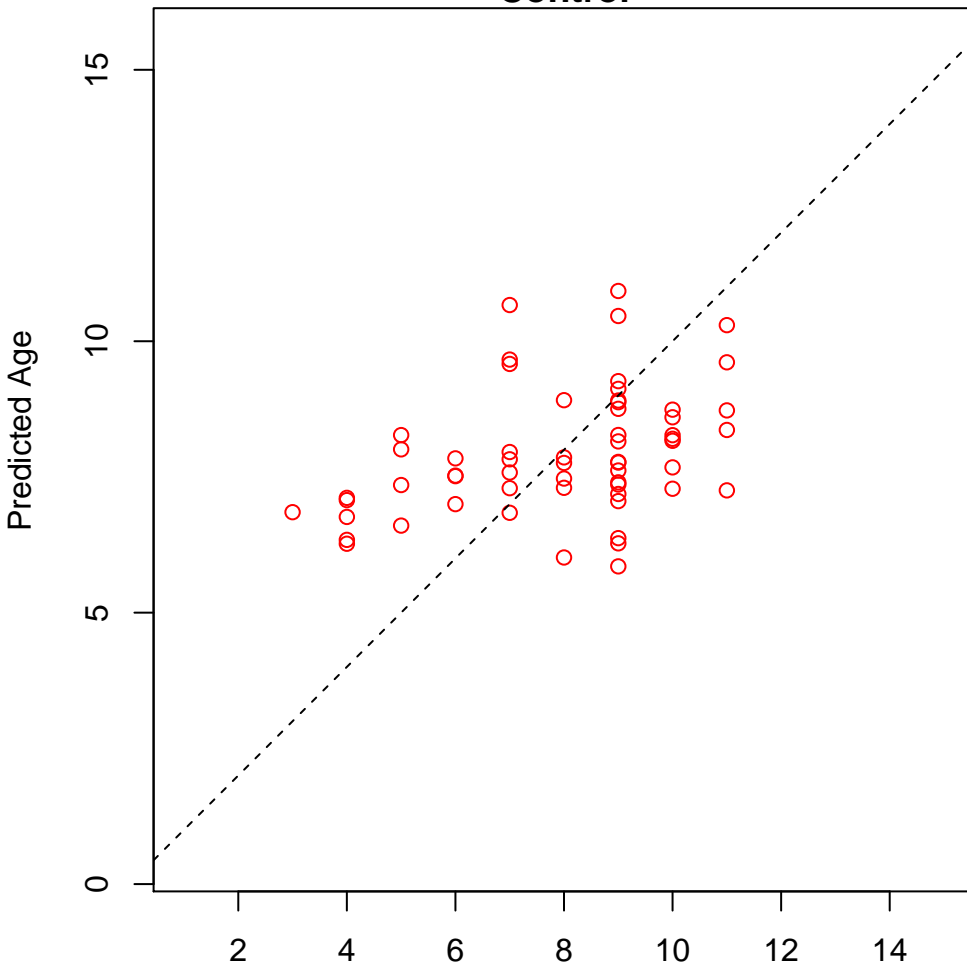


regulation of histone H4 acetylation (Score: 0.612625)

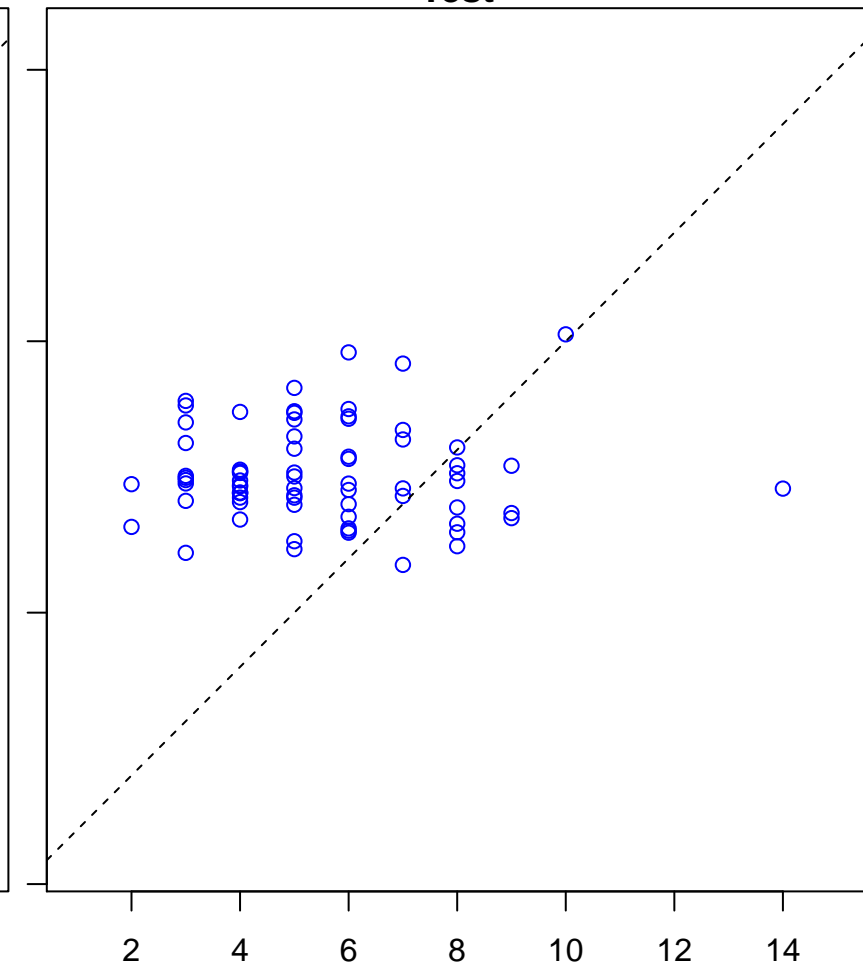


prostate glandular acinus development (Score: 0.612486)

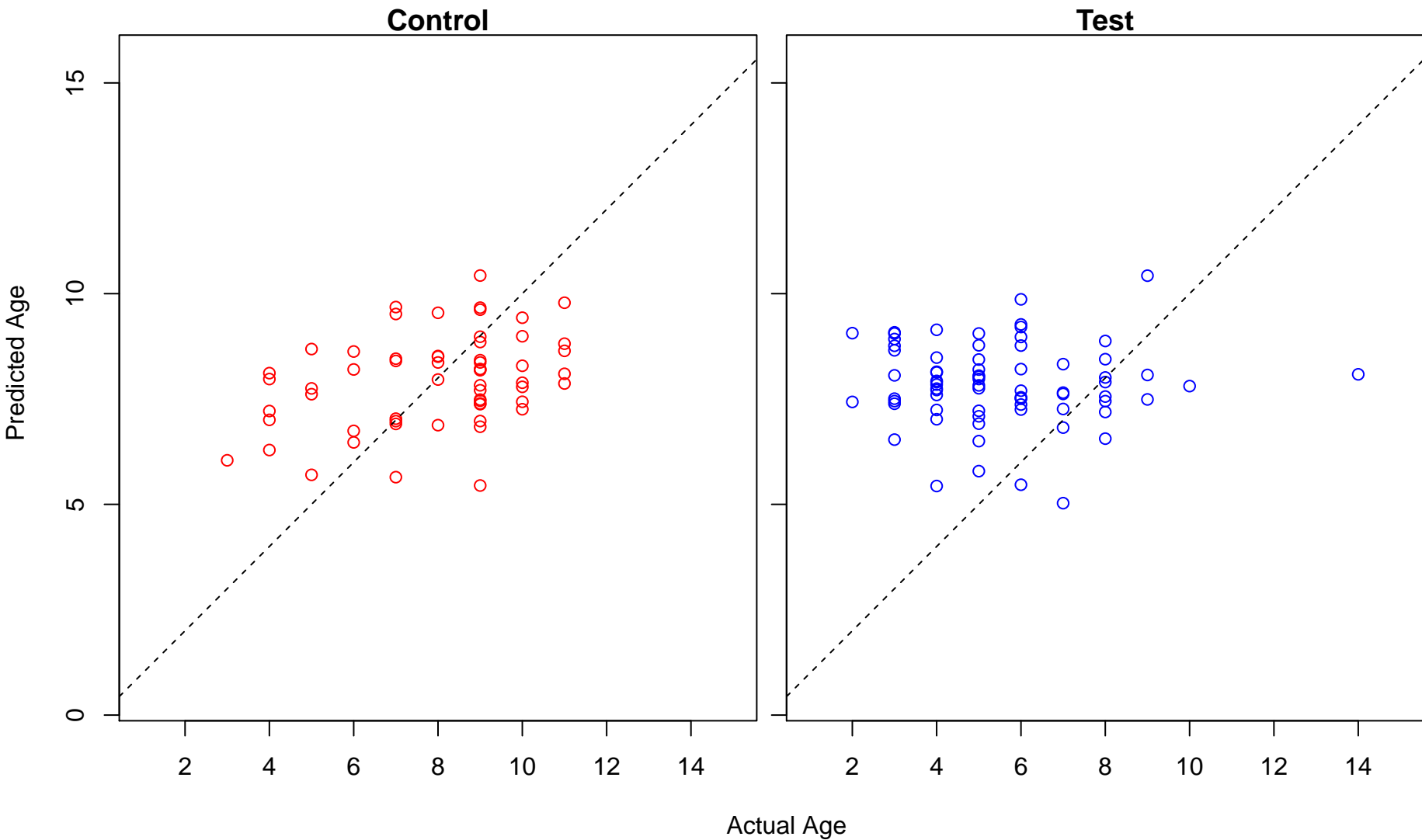
Control



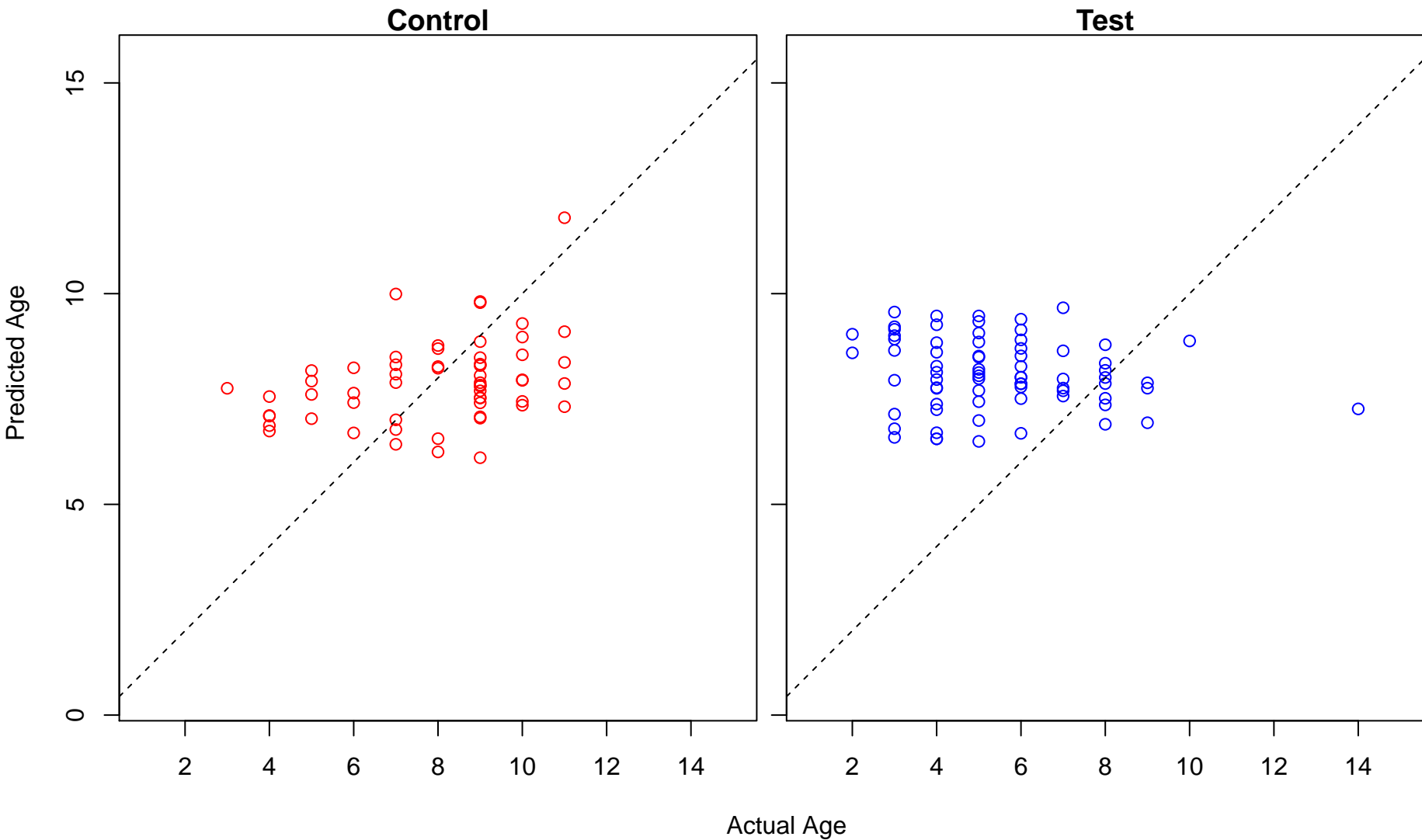
Test



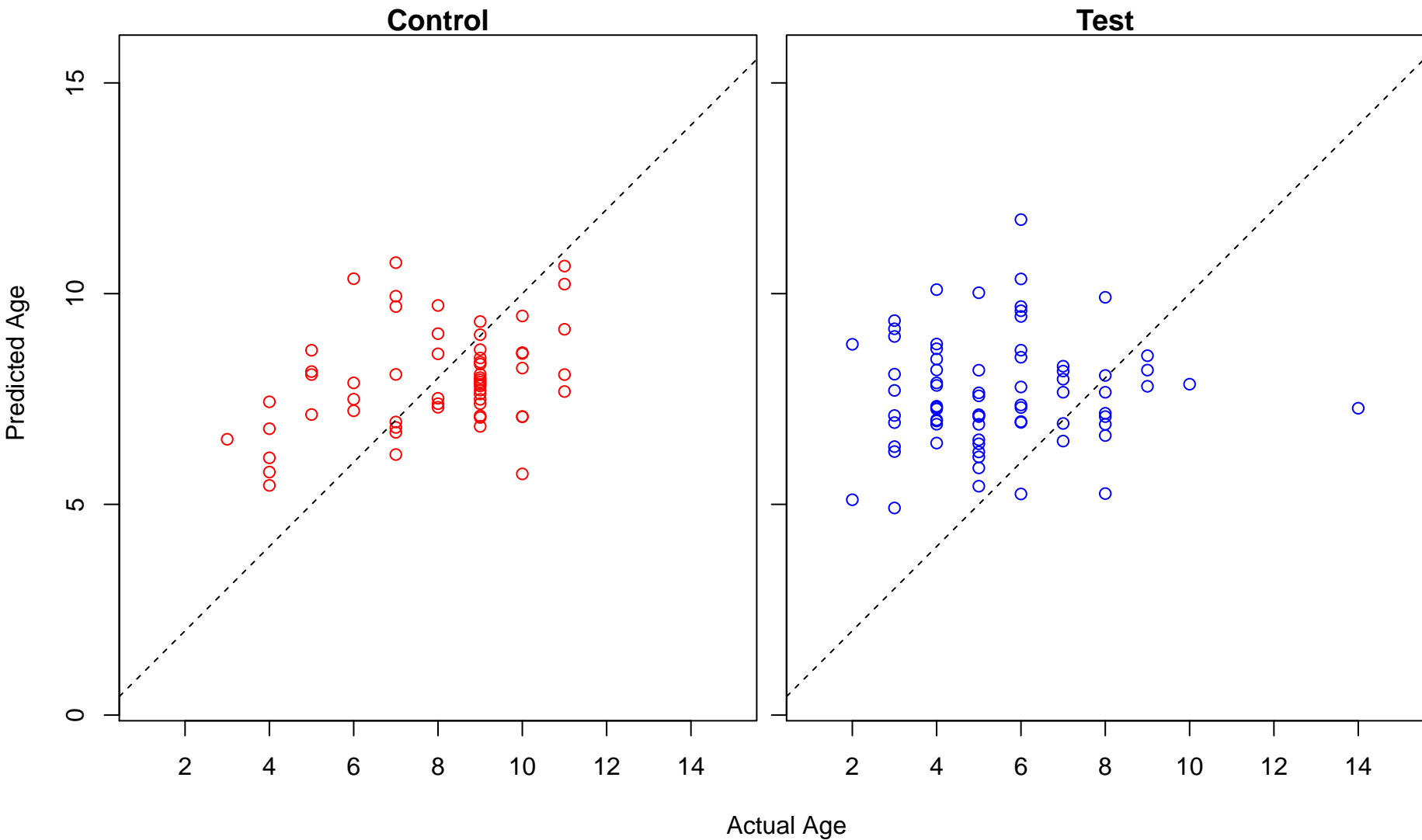
regulation of response to drug (Score: 0.607863)



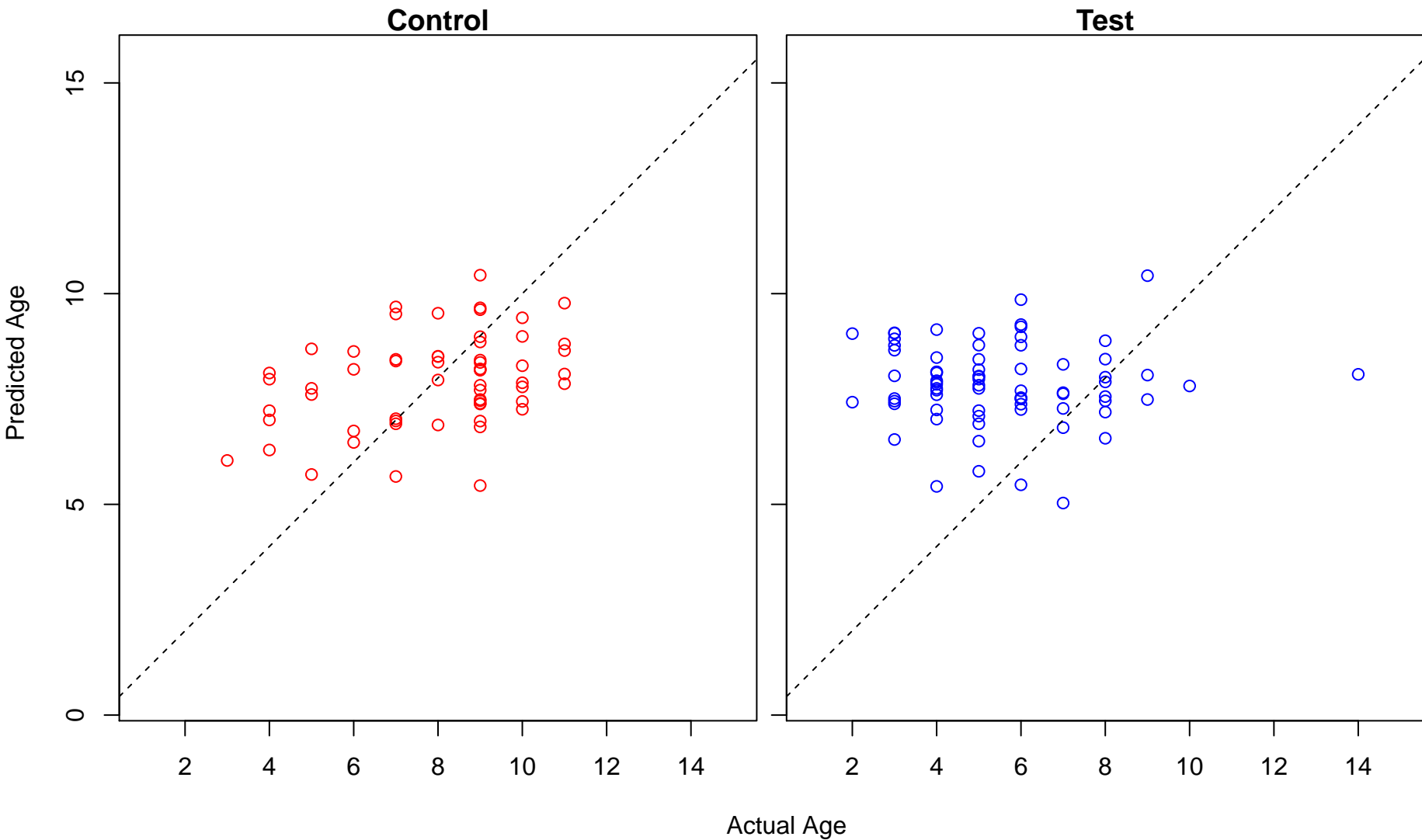
negative regulation of smoothened signaling pathway involved in ventral spinal cord patterning (Score: 0)



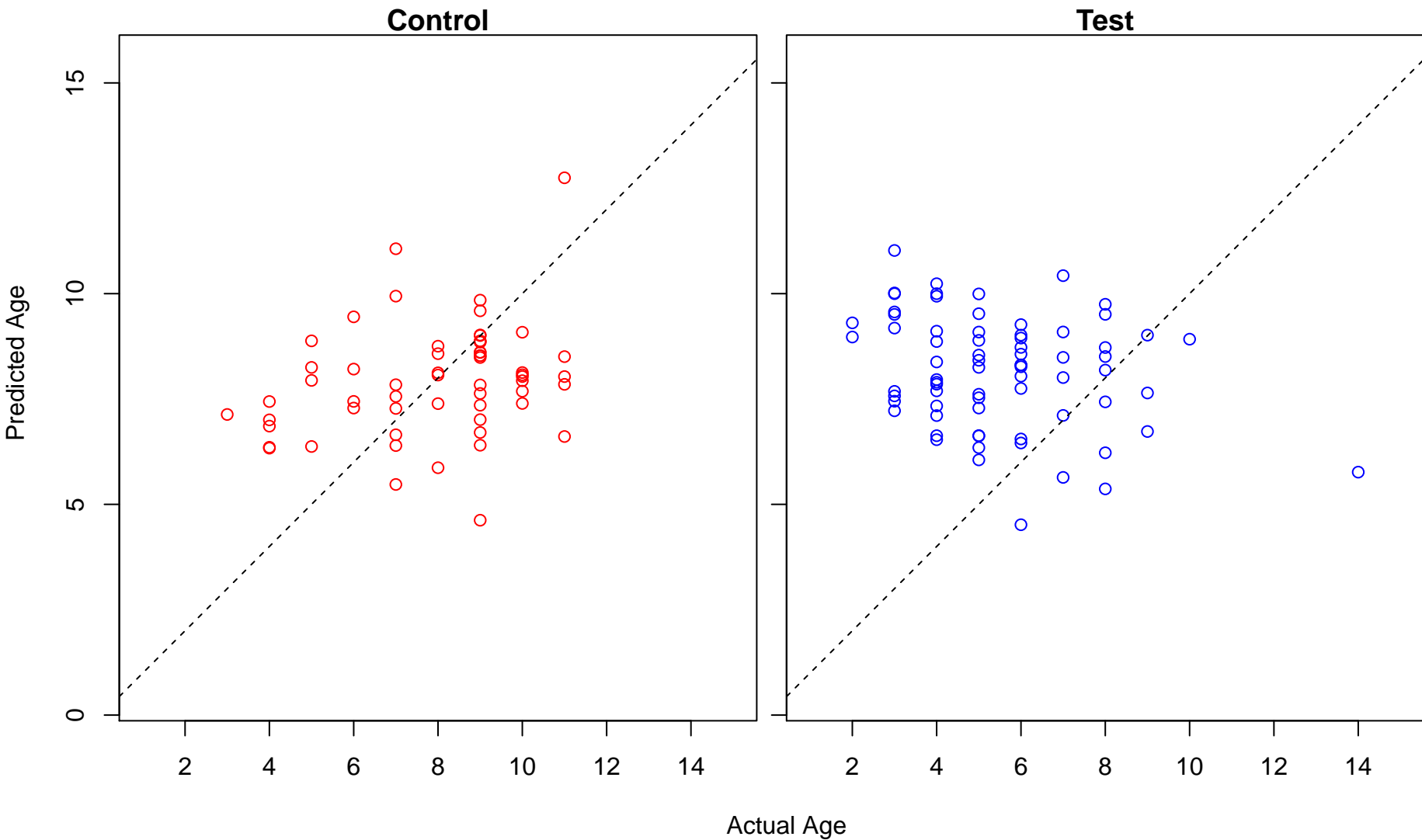
cell fate specification (Score: 0.607550)



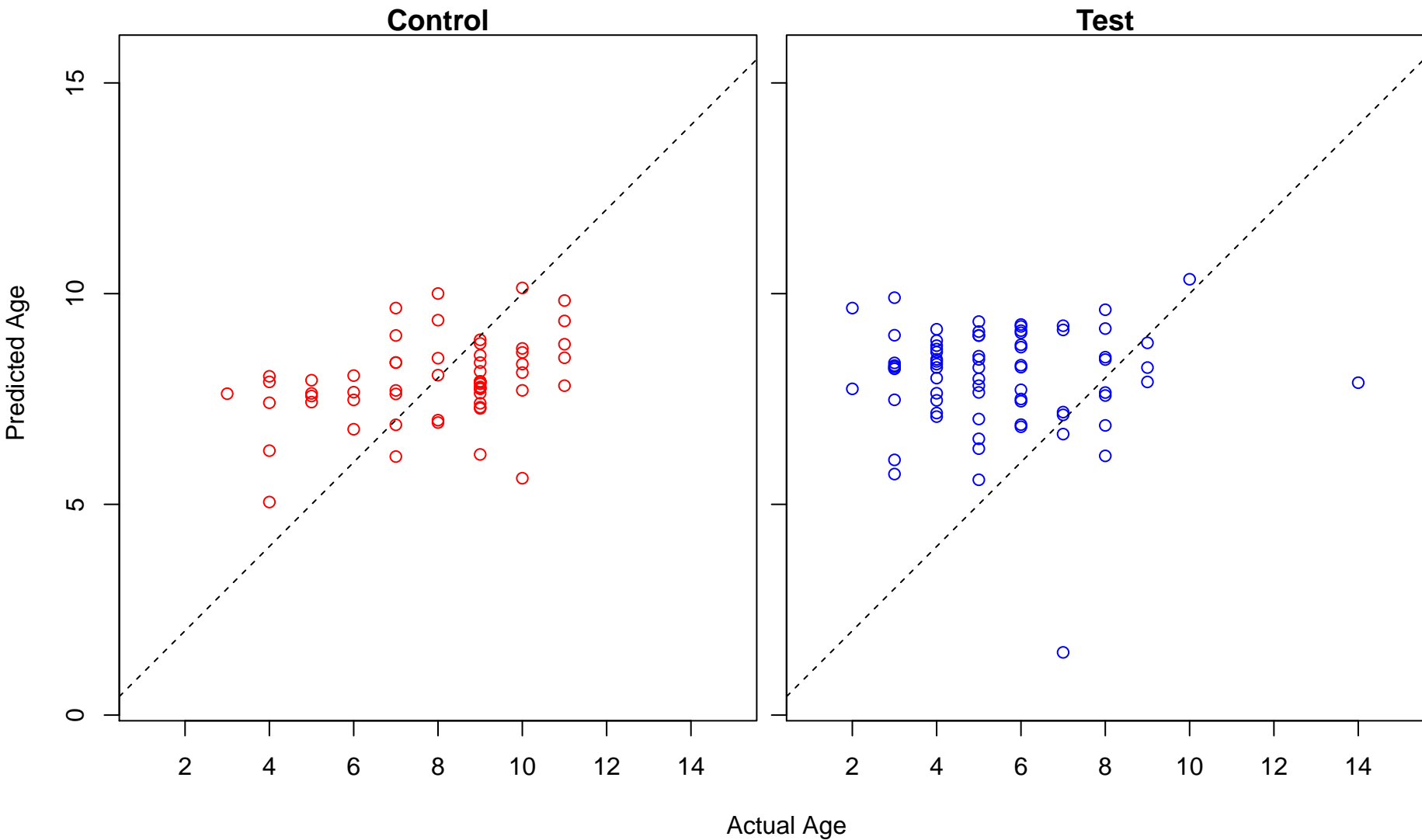
regulation of cellular response to drug (Score: 0.606941)



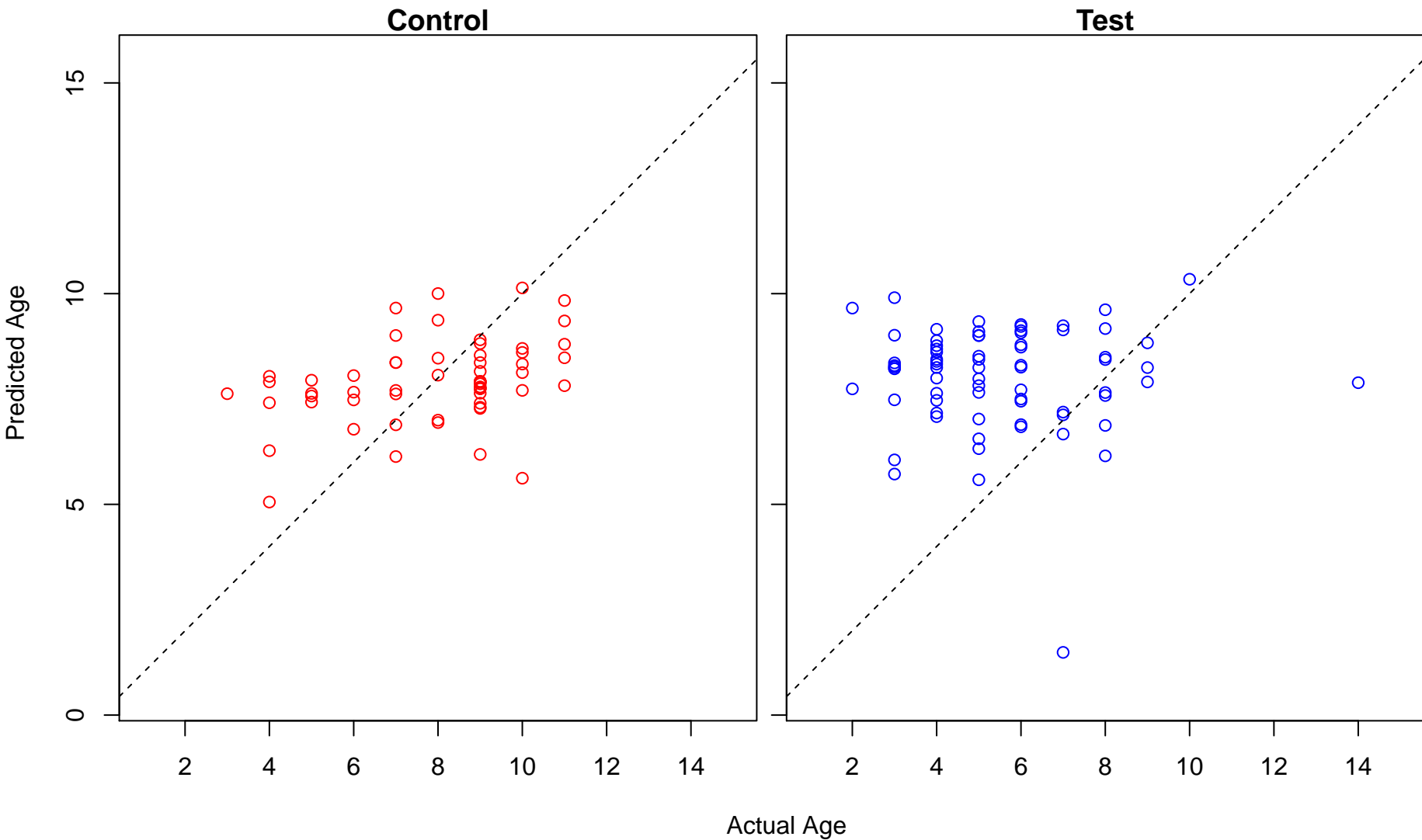
hypothalamus cell differentiation (Score: 0.606351)



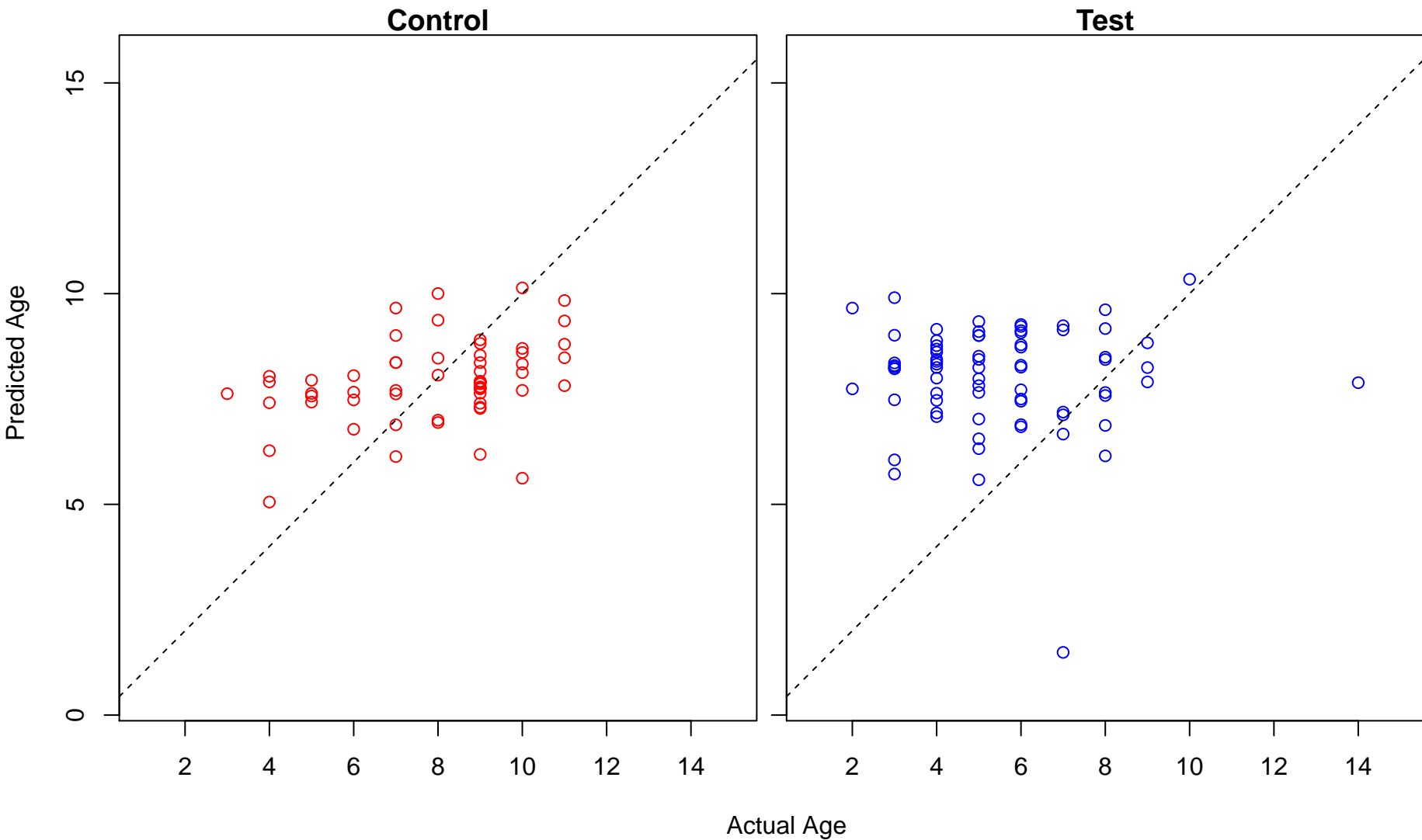
peptidyl-lysine hydroxylation (Score: 0.604451)



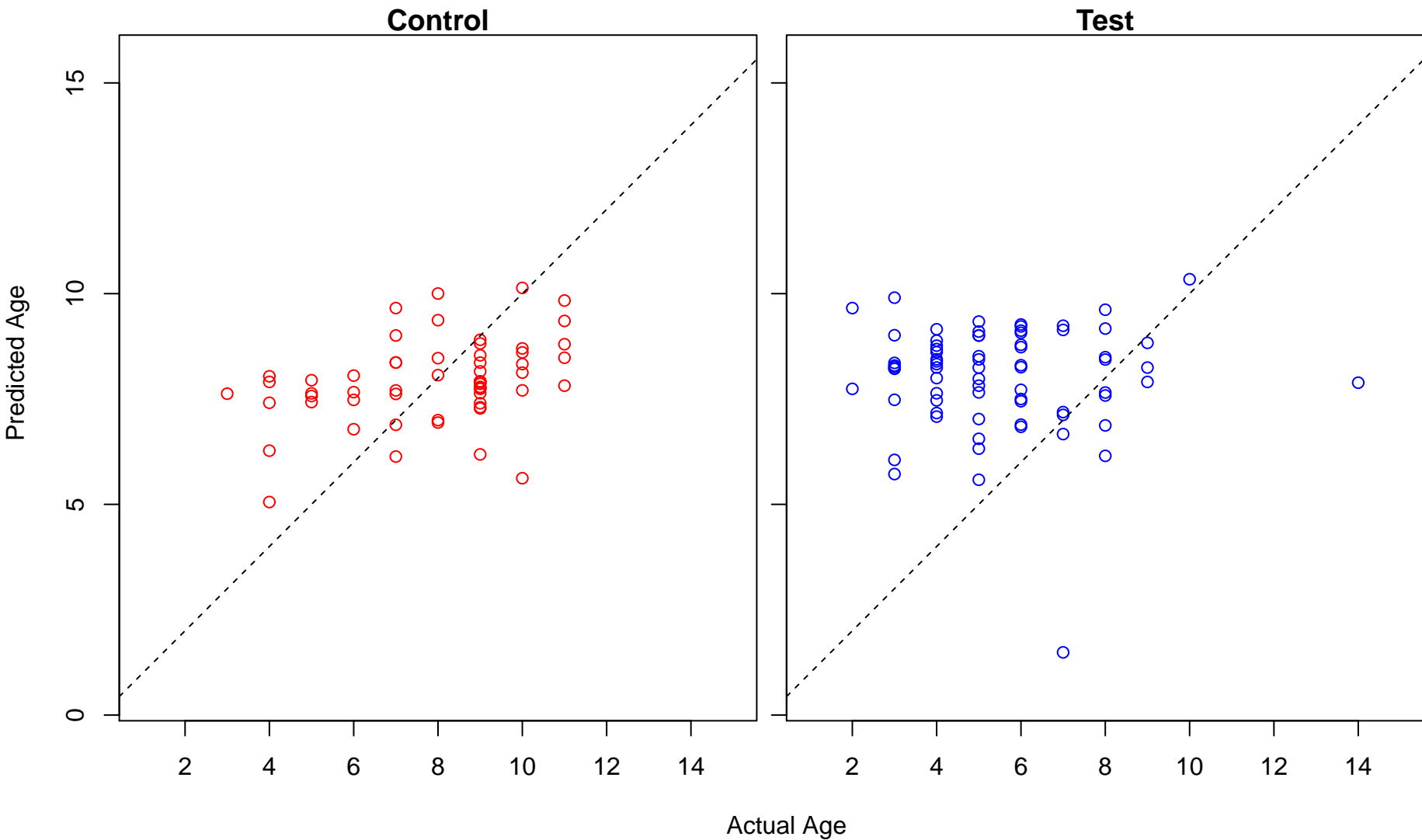
peptidyl-lysine hydroxylation to 5-hydroxy-L-lysine (Score: 0.604451)



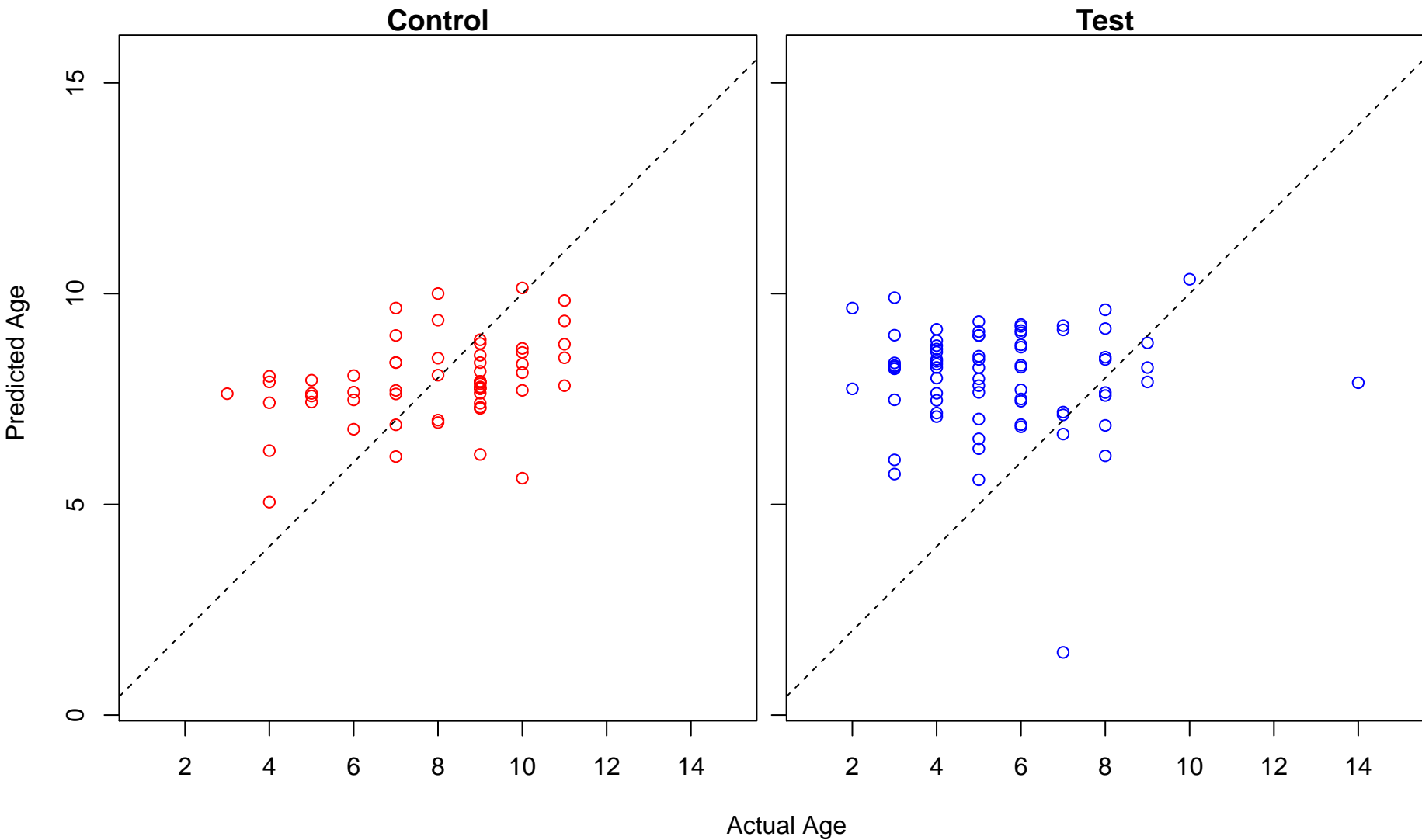
histone arginine demethylation (Score: 0.604451)



histone H3-R2 demethylation (Score: 0.604451)

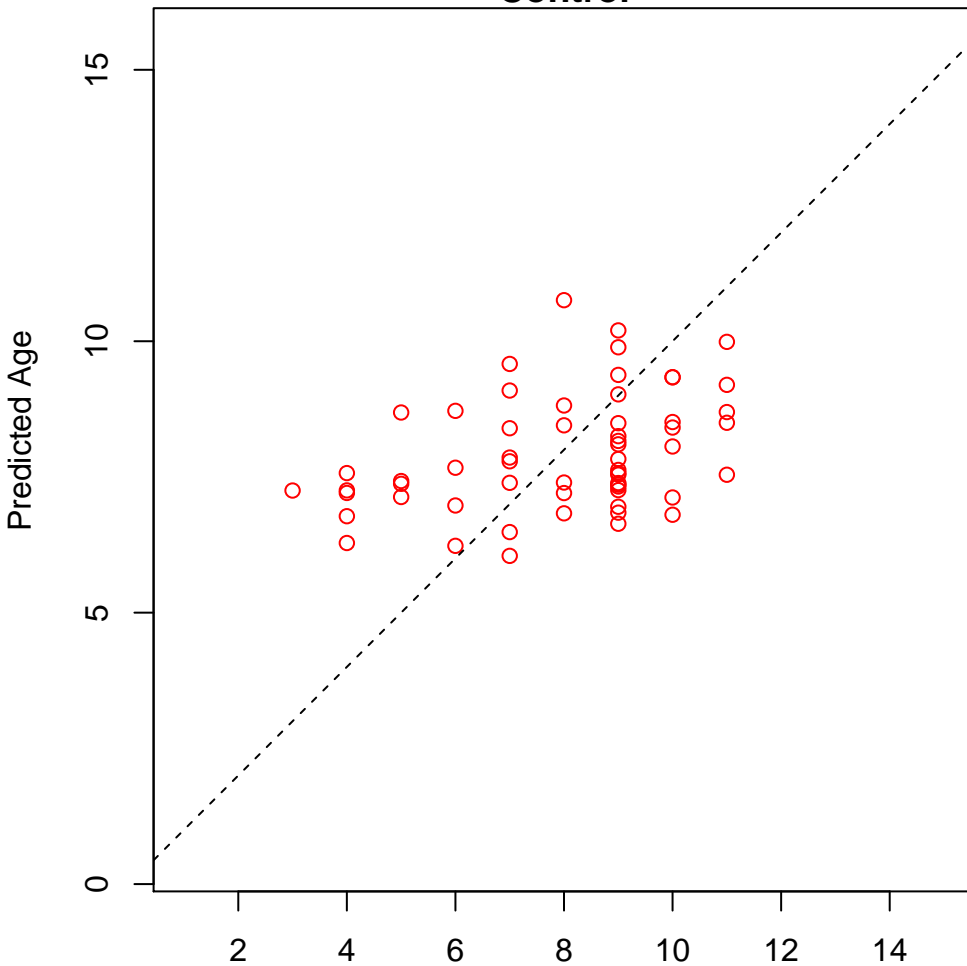


histone H4-R3 demethylation (Score: 0.604451)

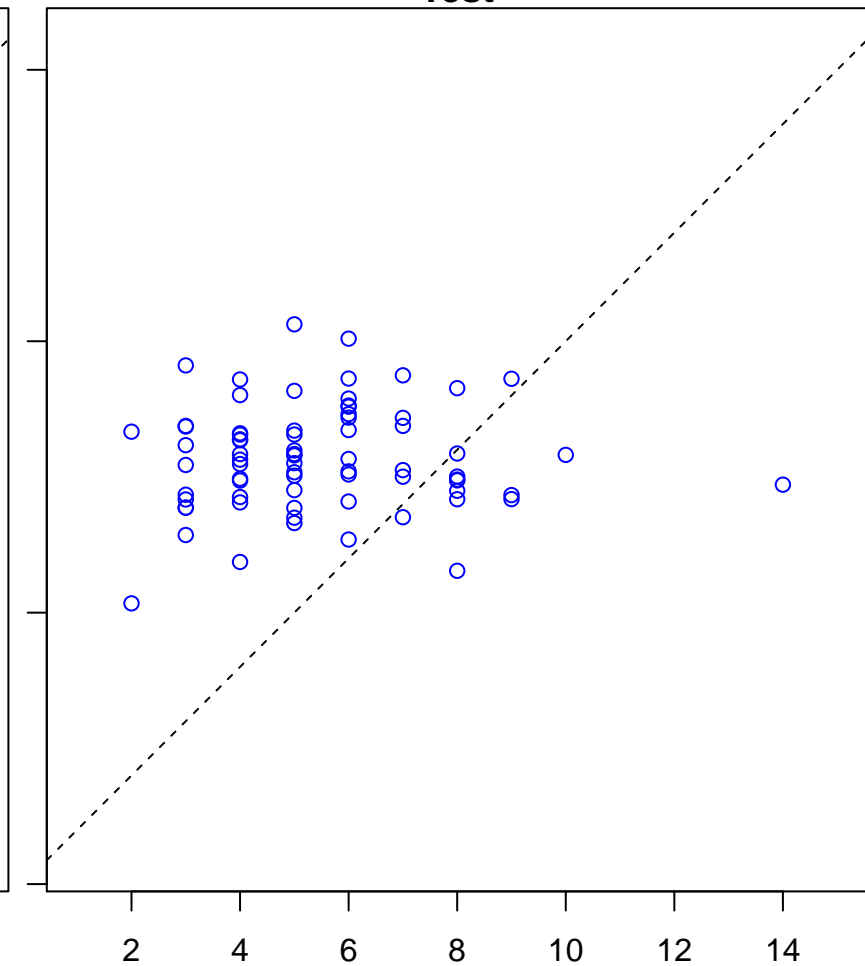


blood vessel endothelial cell migration (Score: 0.602977)

Control

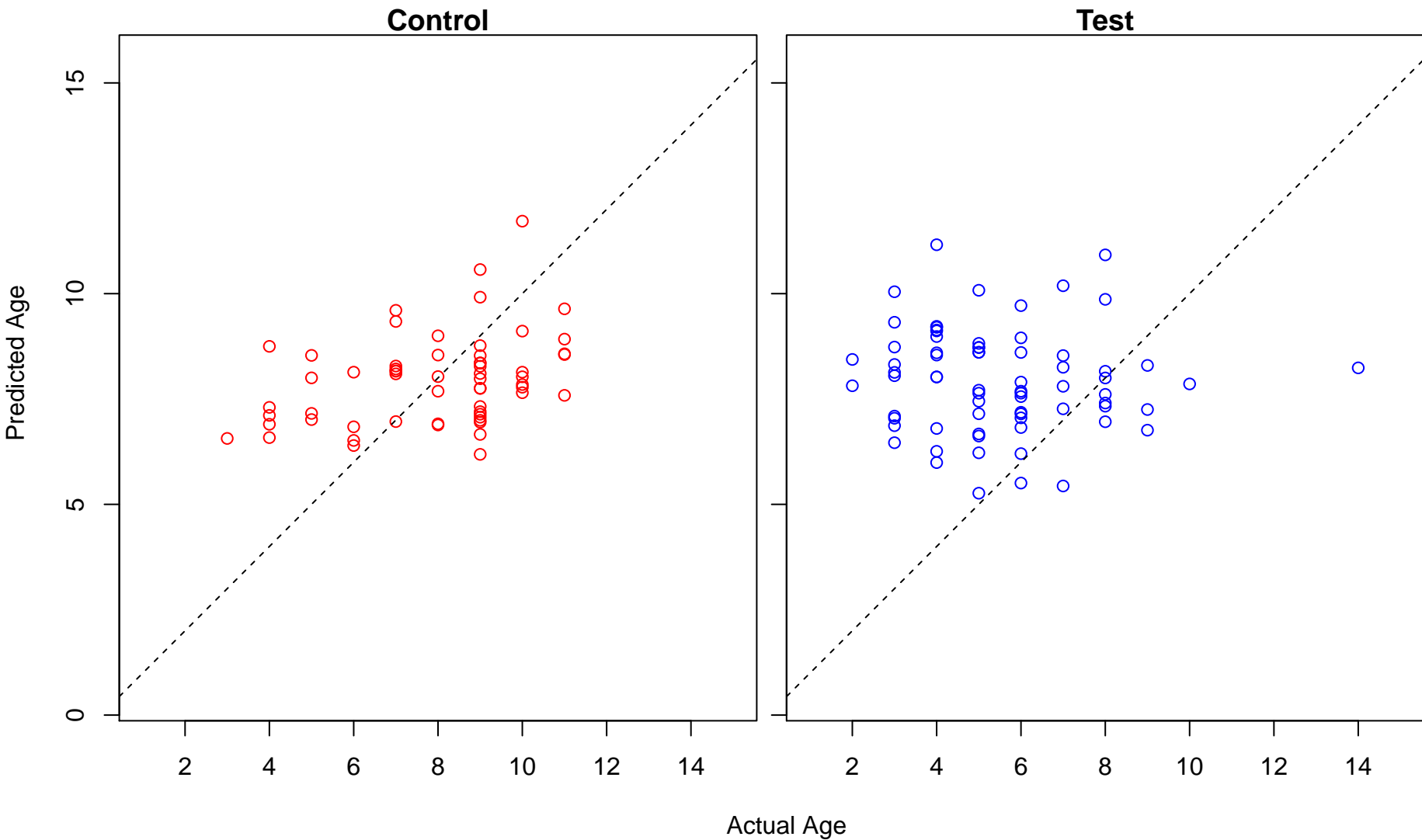


Test

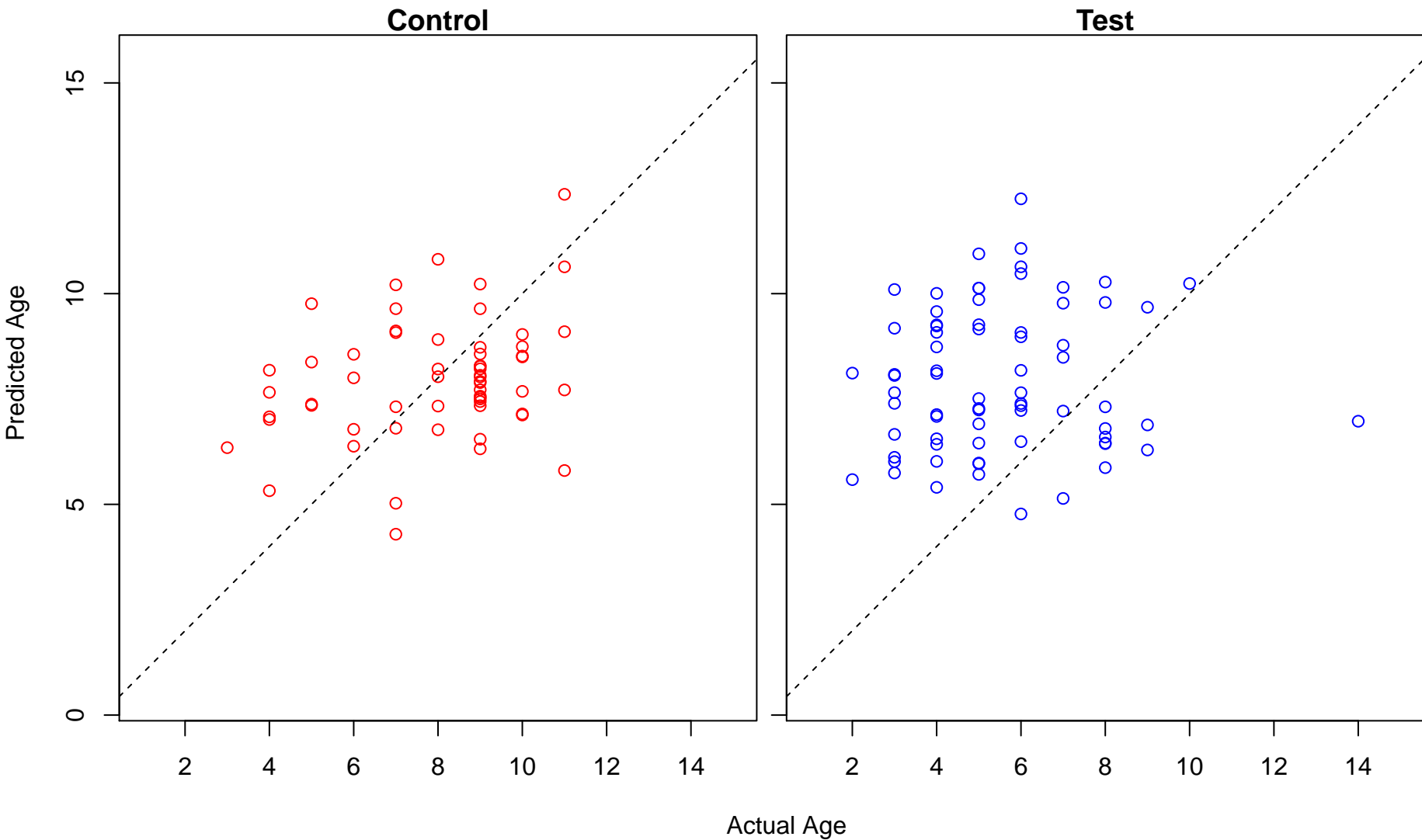


Actual Age

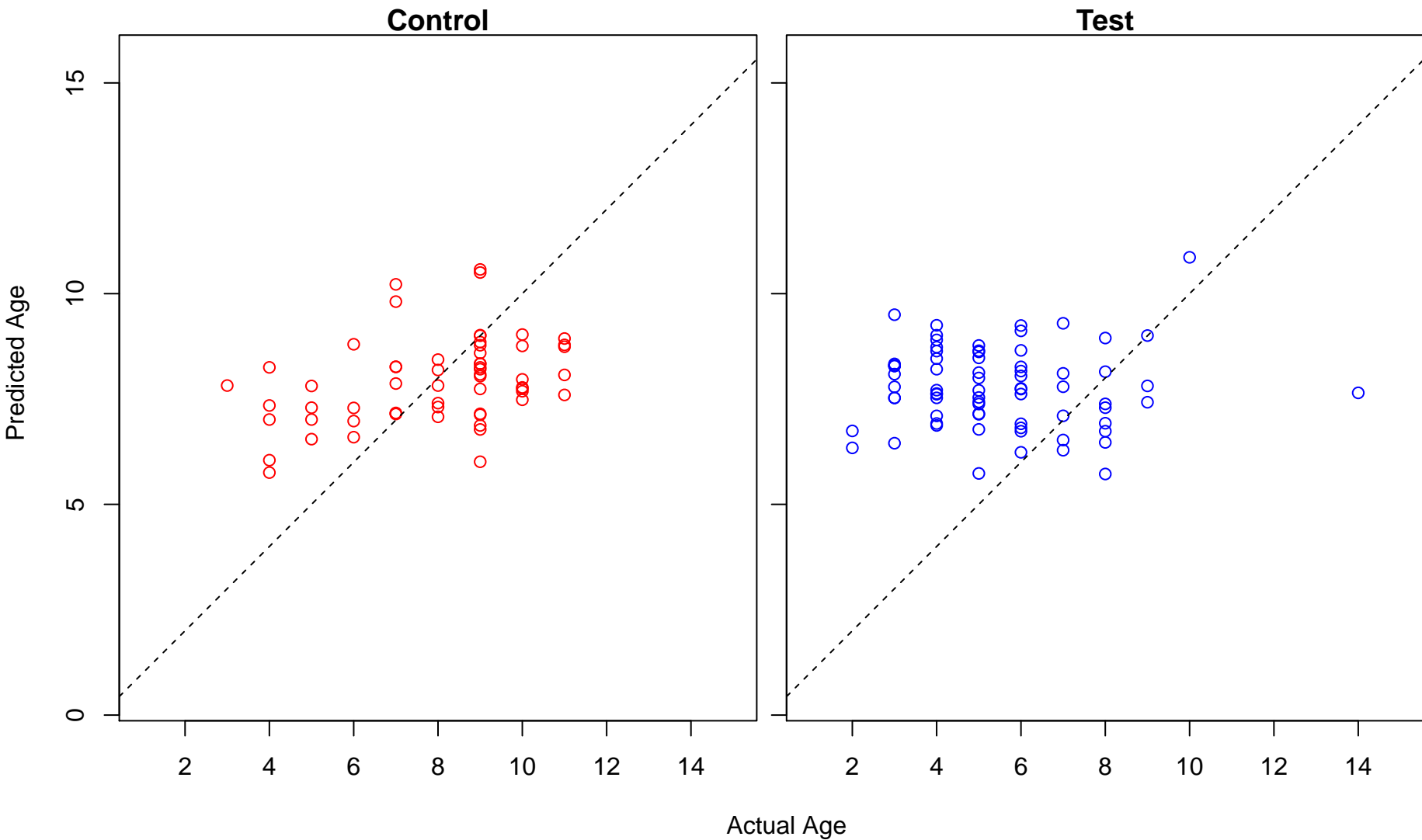
cell migration involved in heart formation (Score: 0.602786)



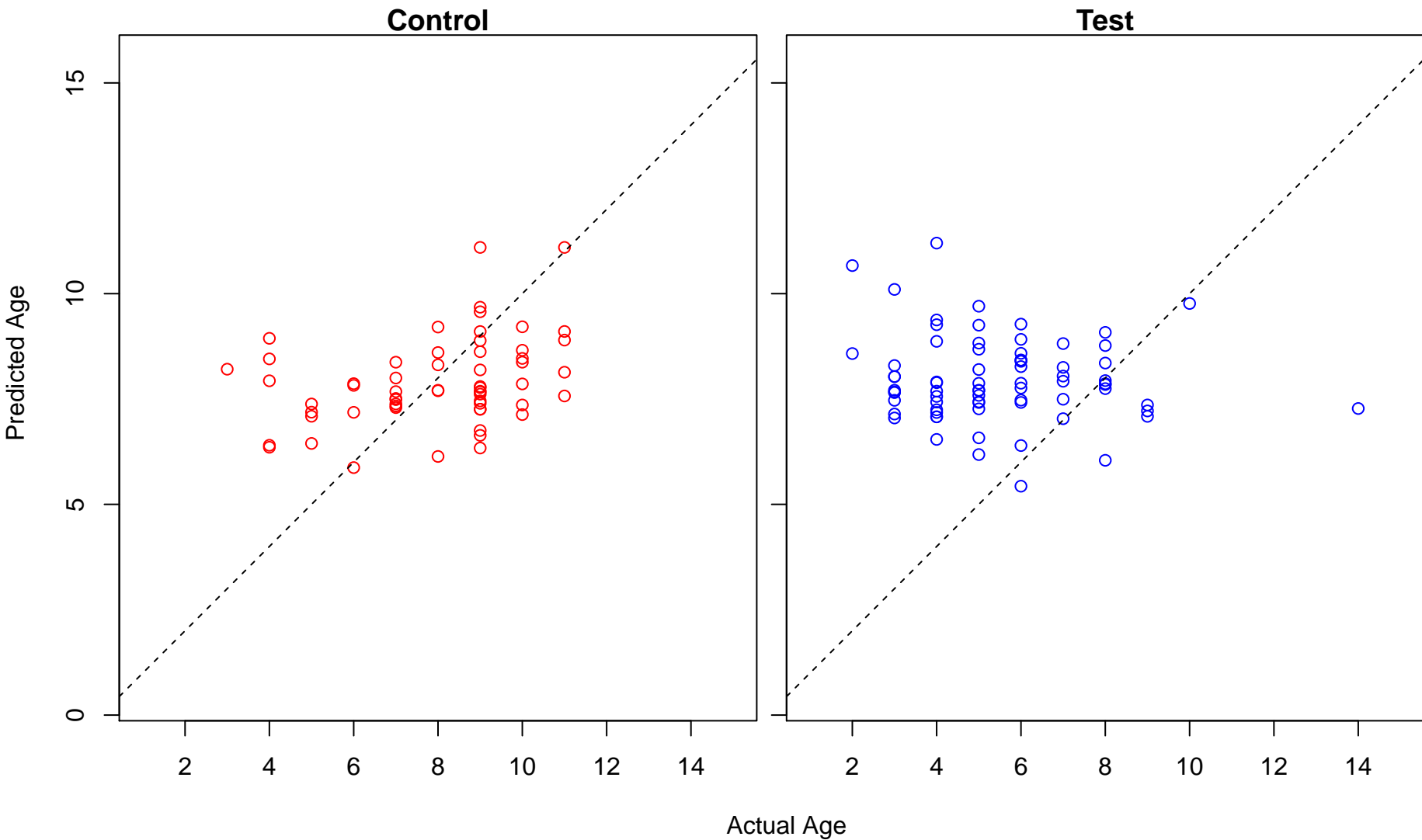
response to muramyl dipeptide (Score: 0.602302)



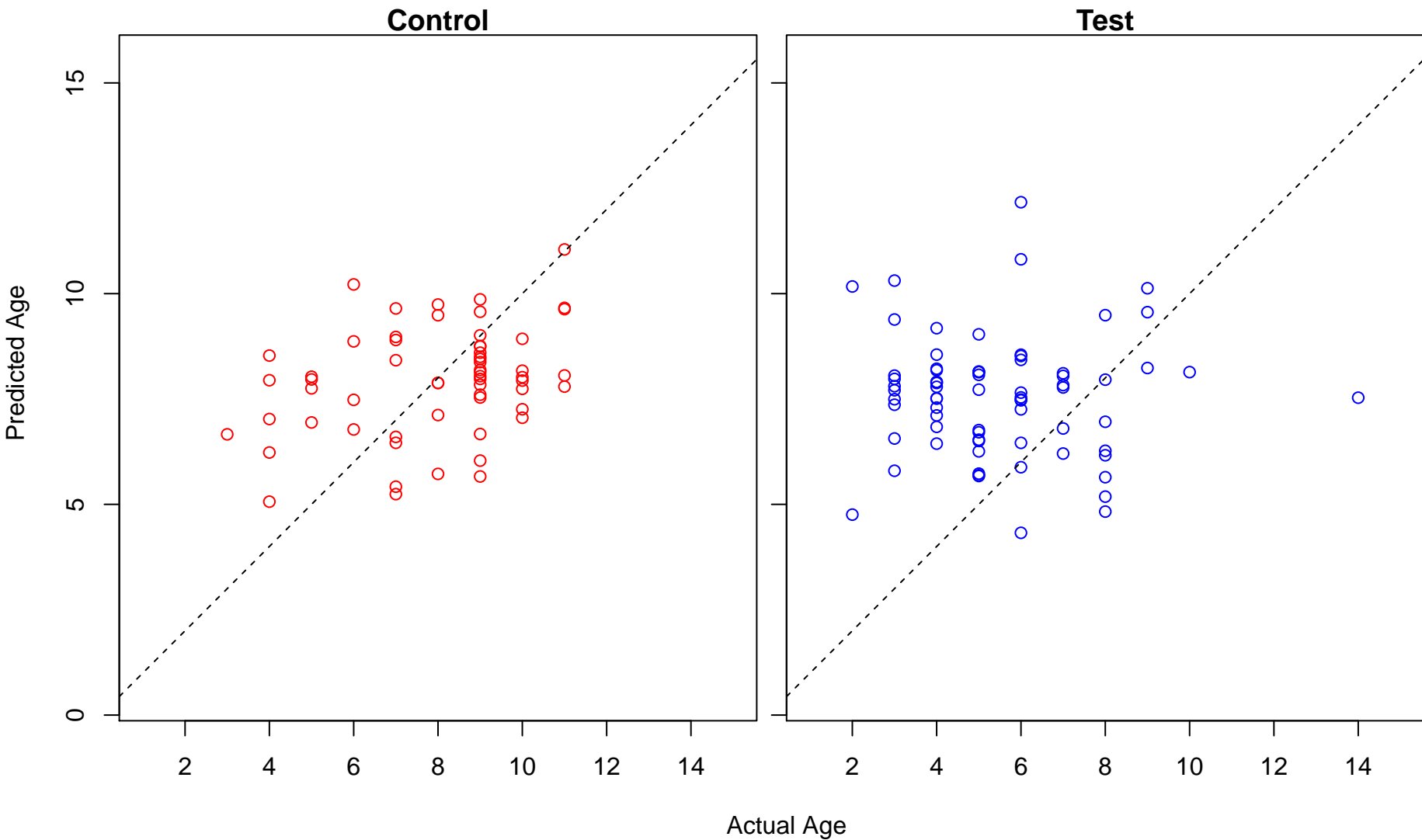
UDP-galactose transport (Score: 0.598877)



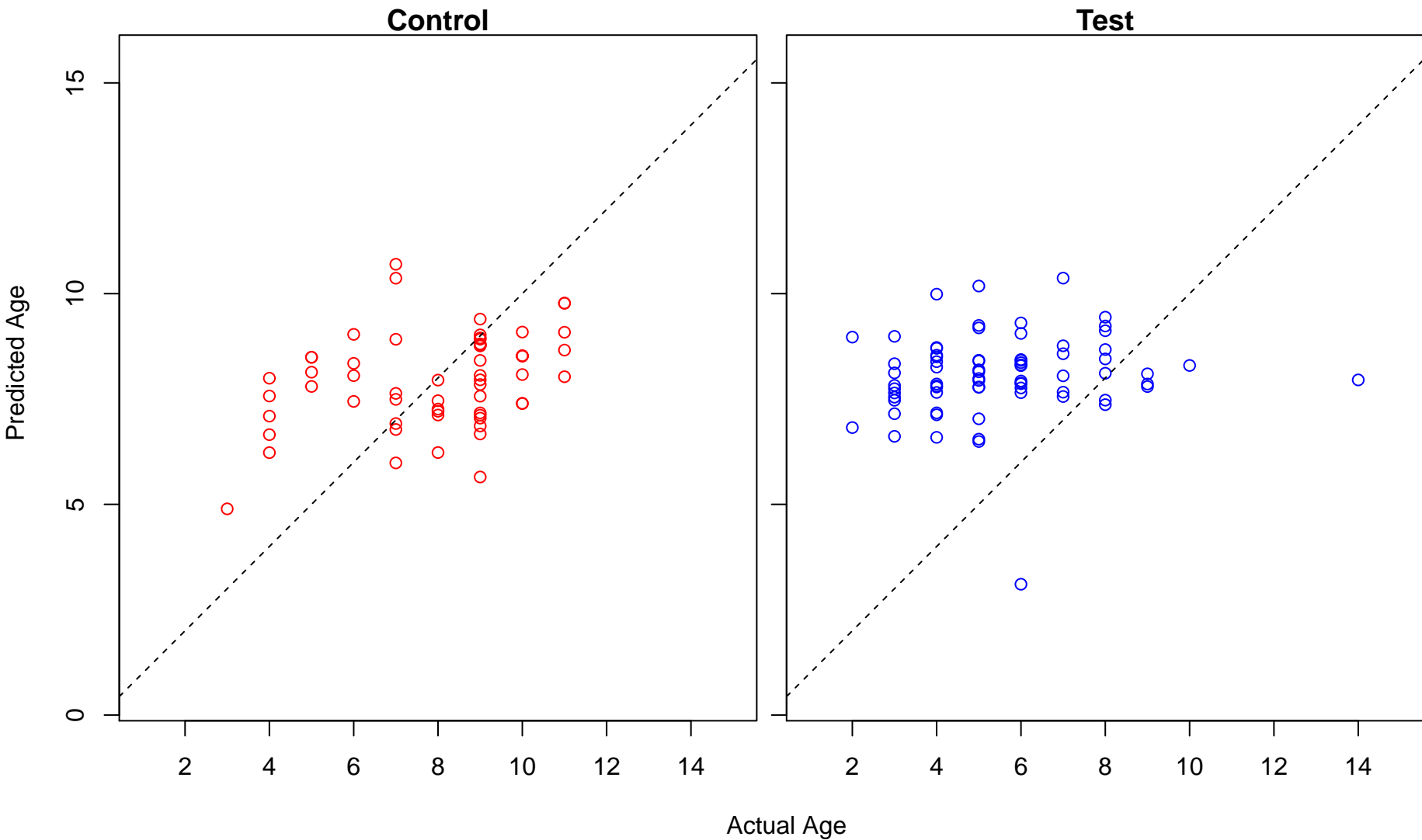
diencephalon morphogenesis (Score: 0.598169)



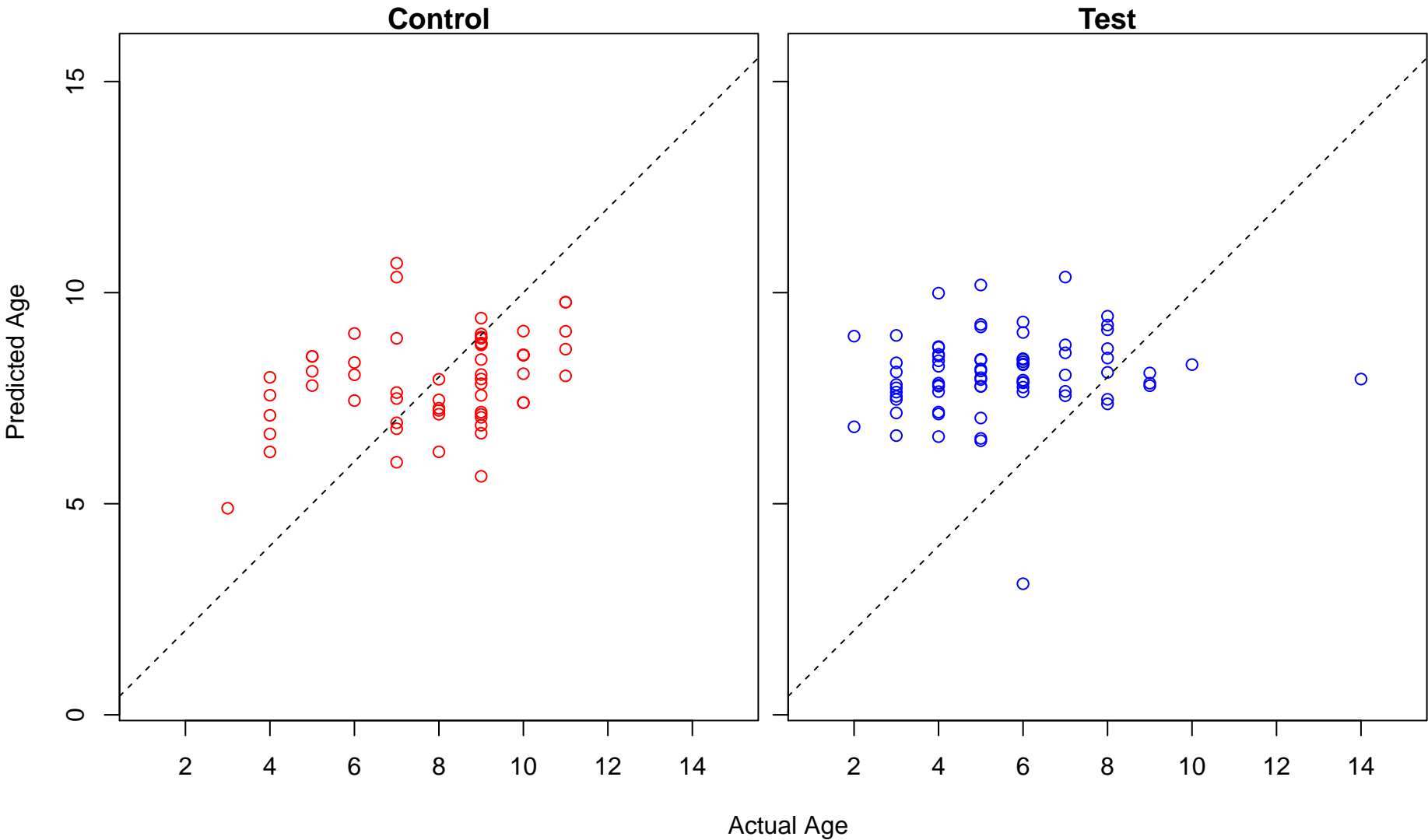
regulation of adaptive immune response (Score: 0.597911)



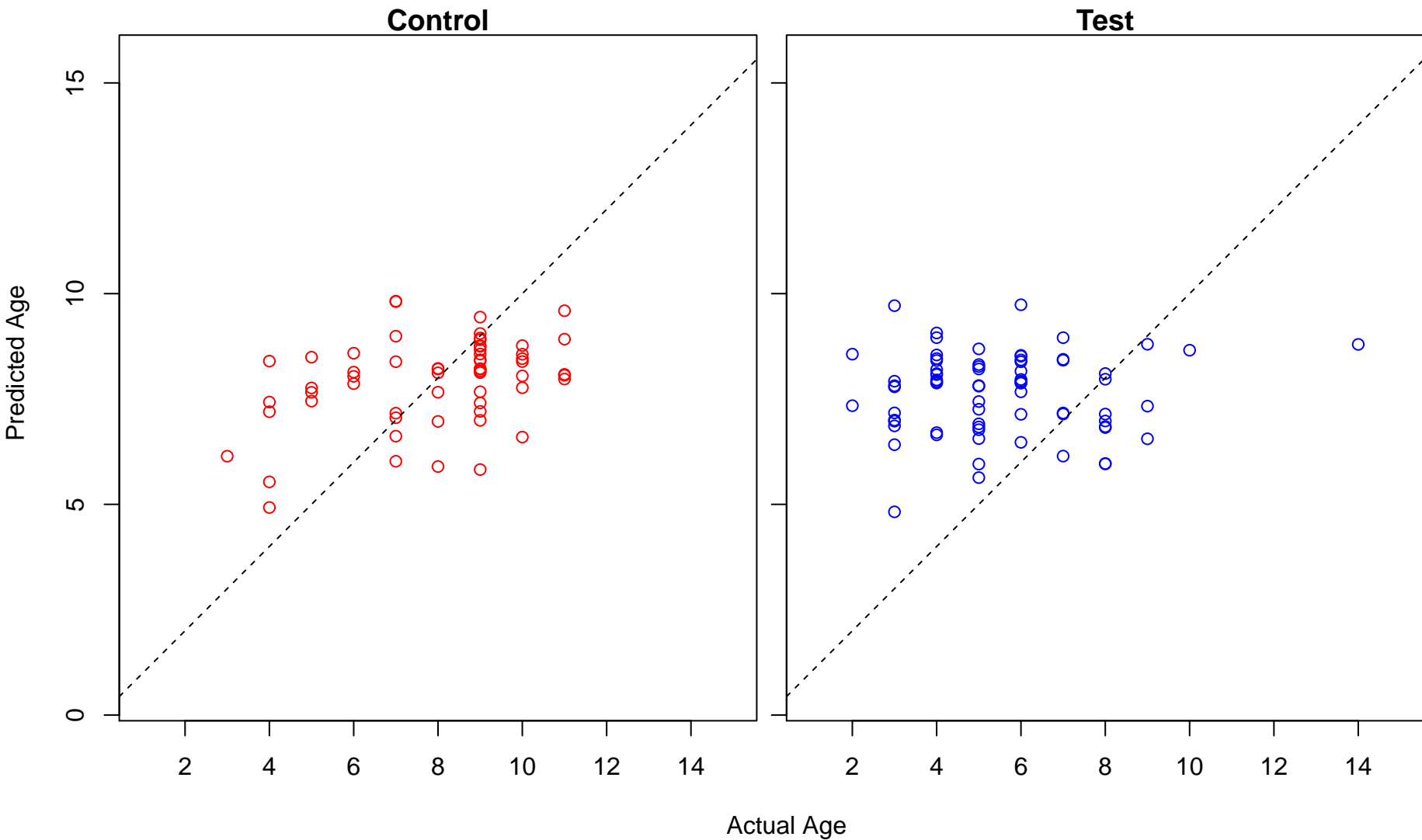
peptidyl-L-cysteine S-palmitoylation (Score: 0.597404)



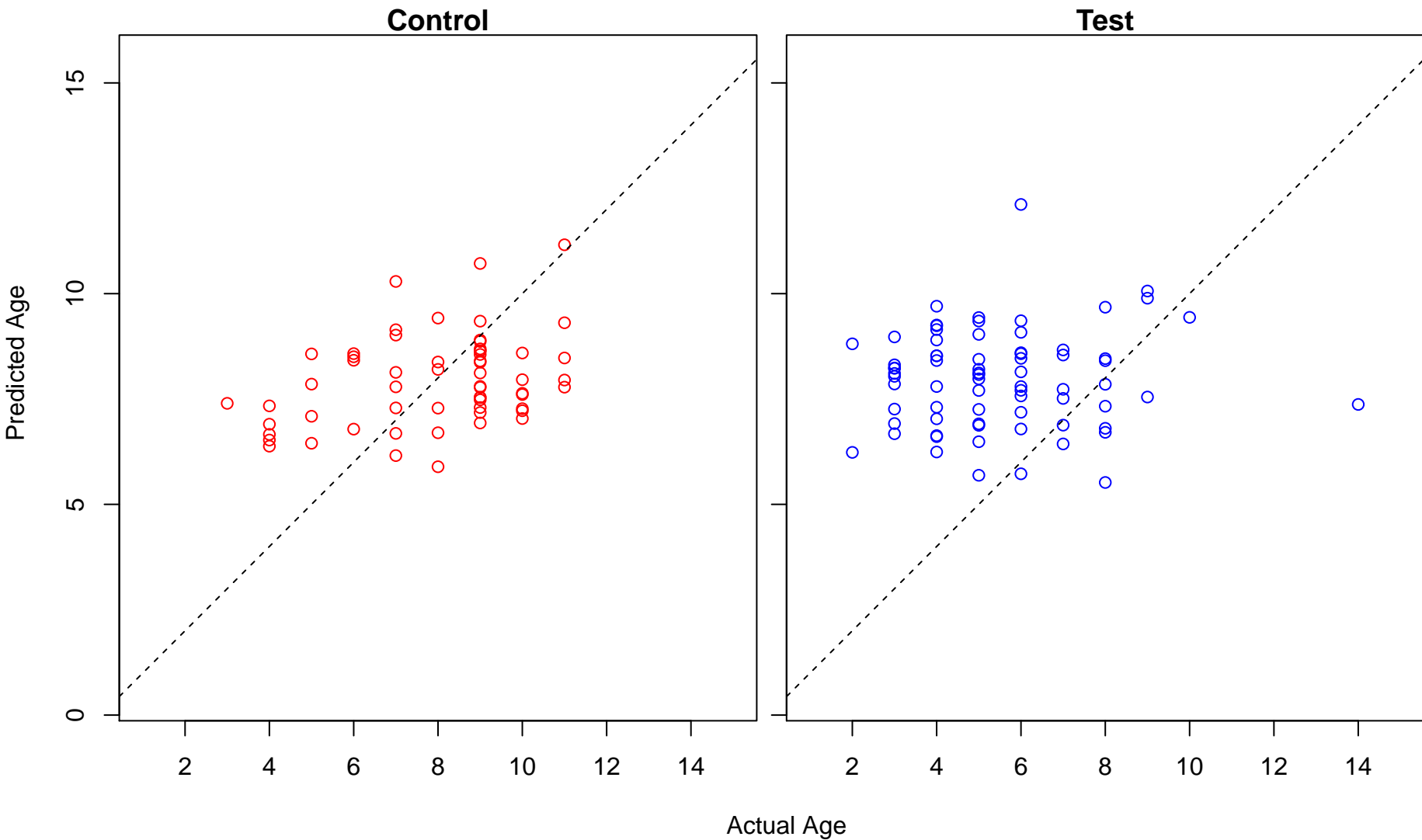
peptidyl-S-diacylglycerol-L-cysteine biosynthetic process from peptidyl-cysteine (Score: 0.59740)



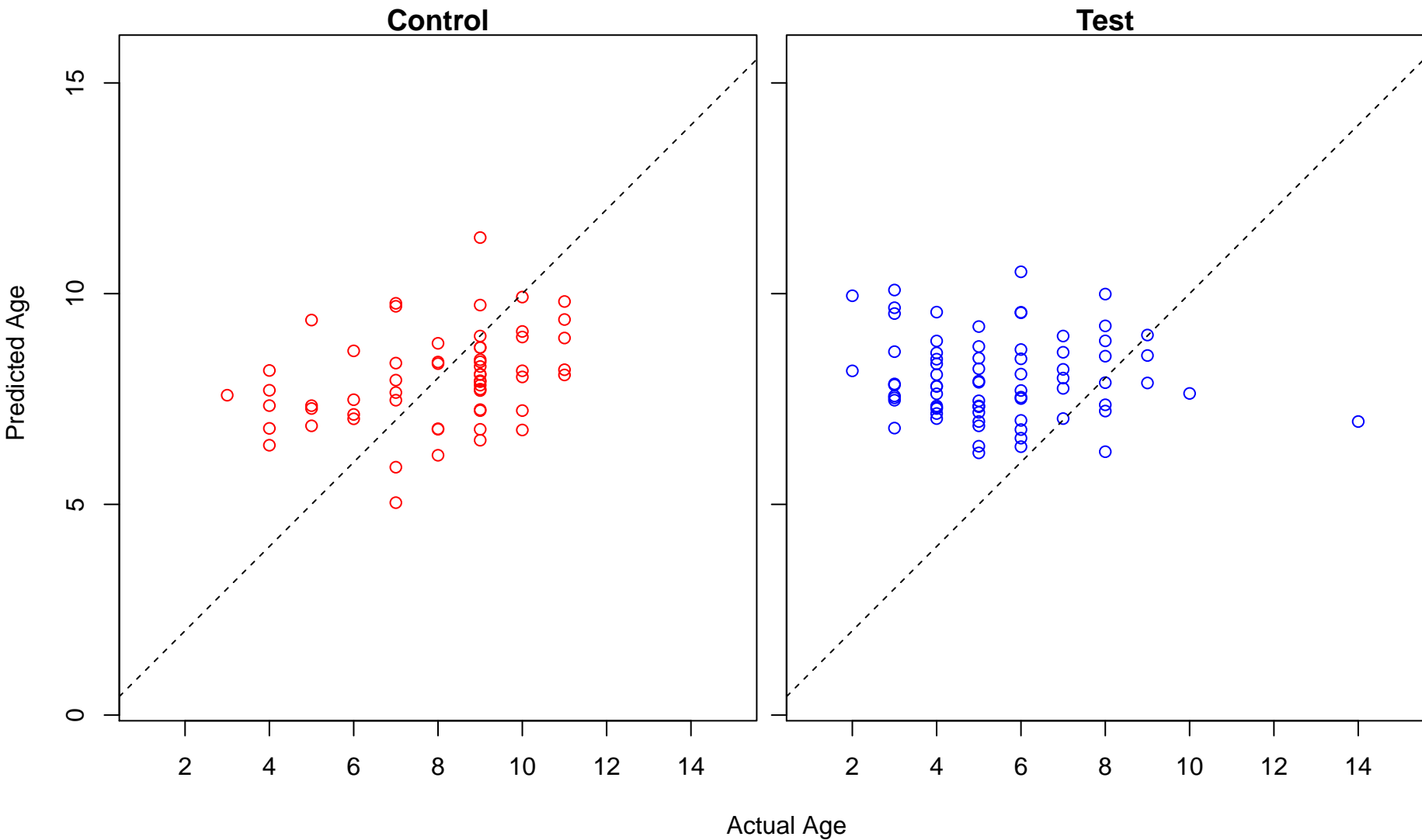
amino acid transmembrane transport (Score: 0.595514)



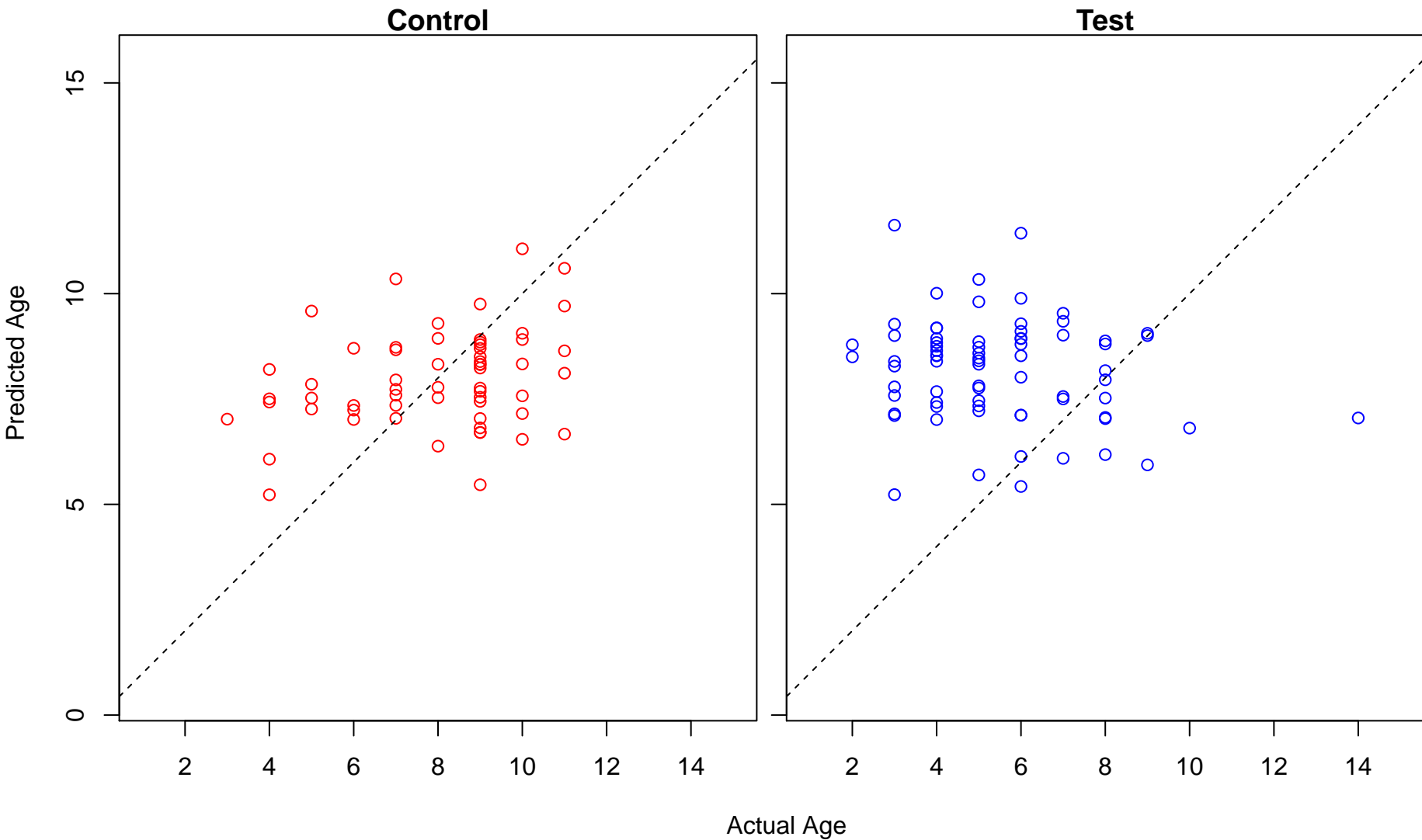
neutrophil homeostasis (Score: 0.593208)



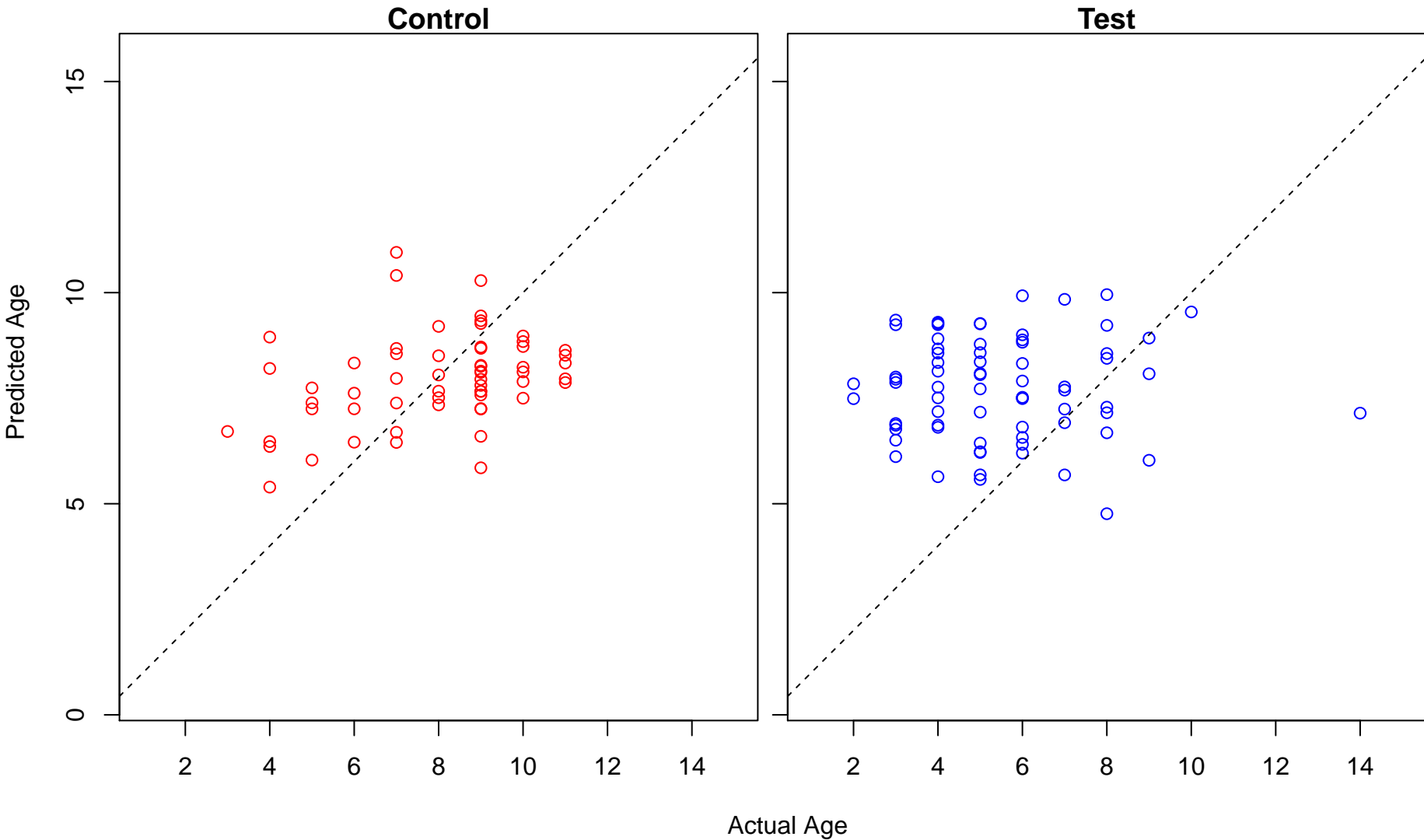
cell motility involved in cerebral cortex radial glia guided migration (Score: 0.591105)



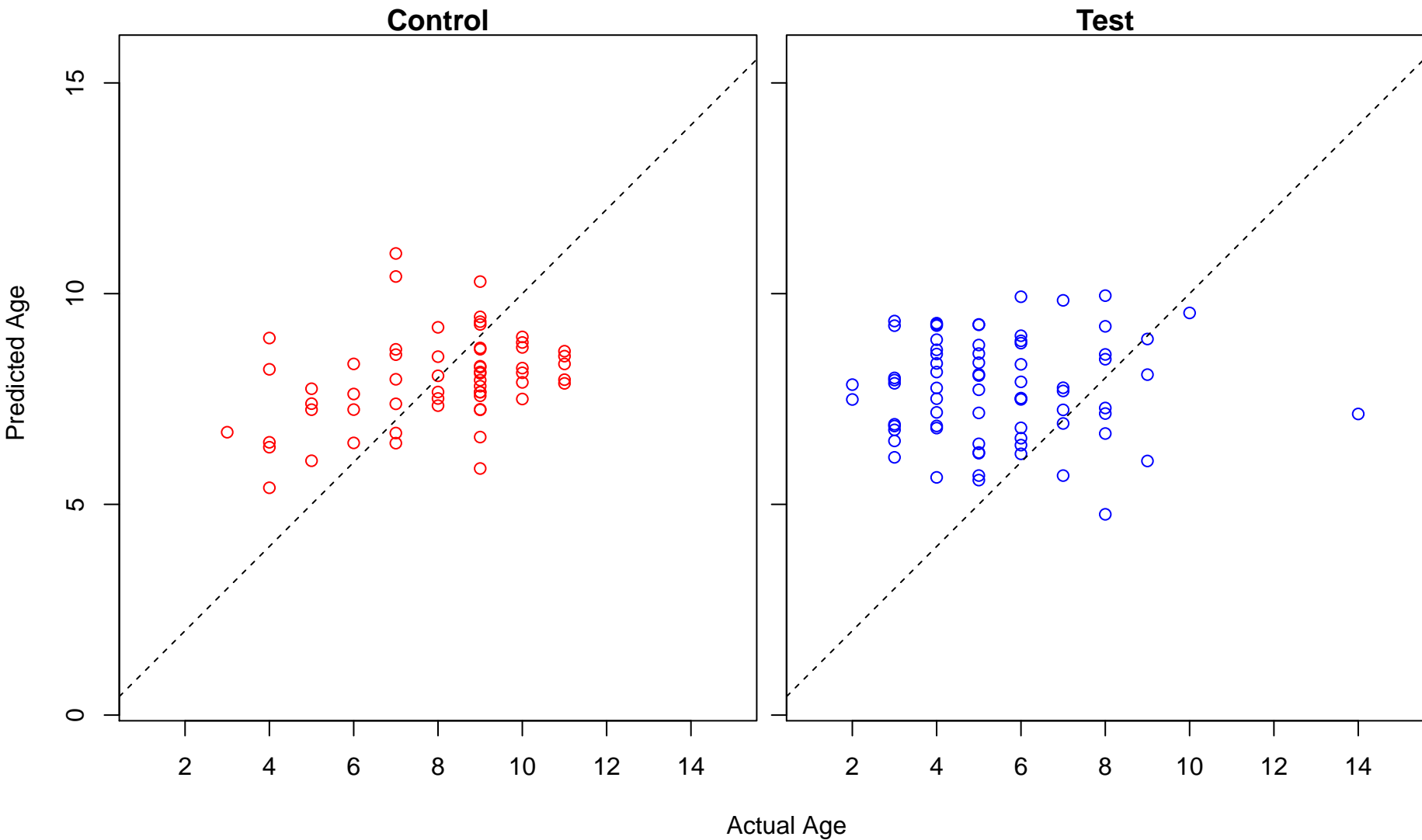
axonogenesis involved in innervation (Score: 0.590886)



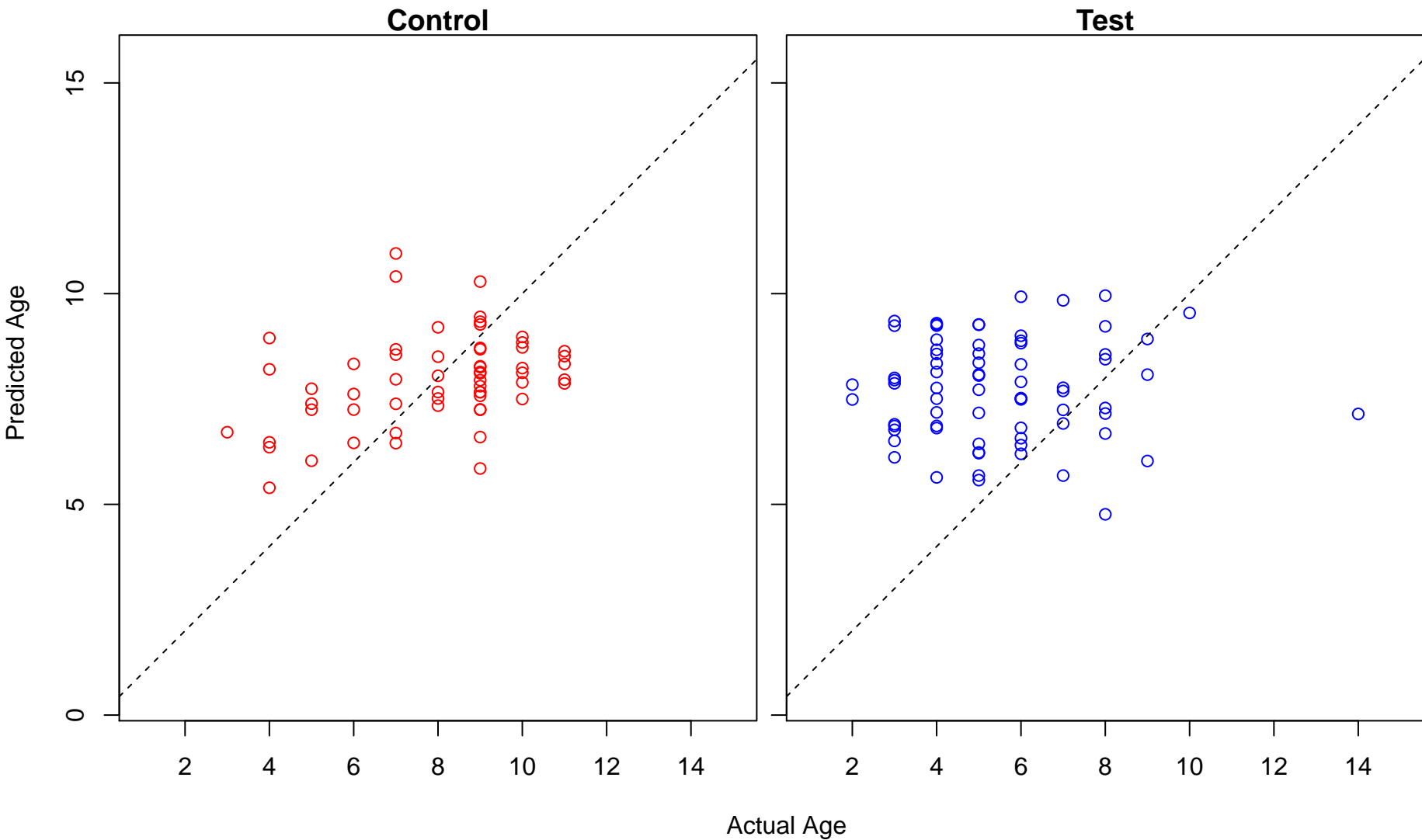
diadenosine polyphosphate catabolic process (Score: 0.590694)



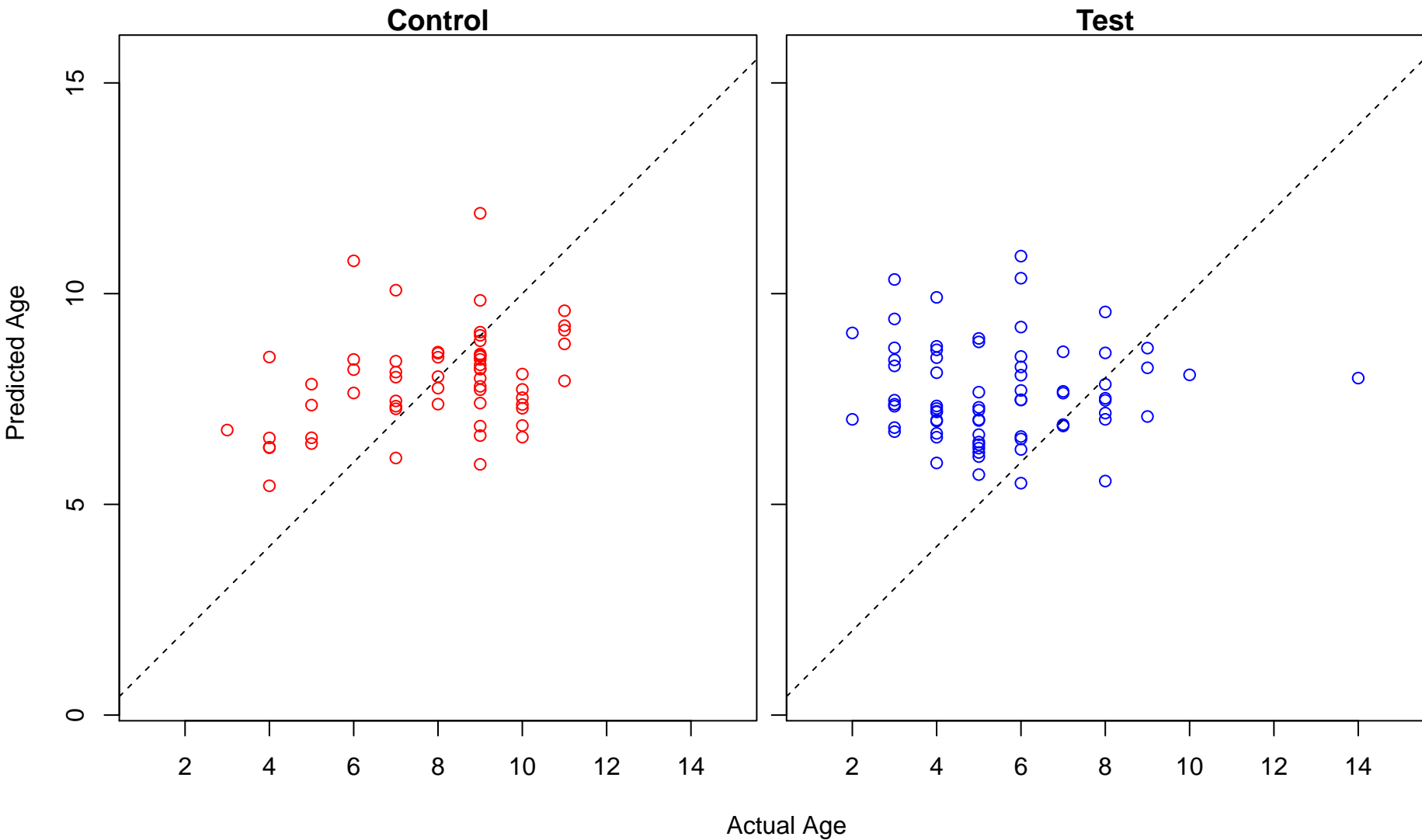
diphosphoinositol polyphosphate metabolic process (Score: 0.590694)



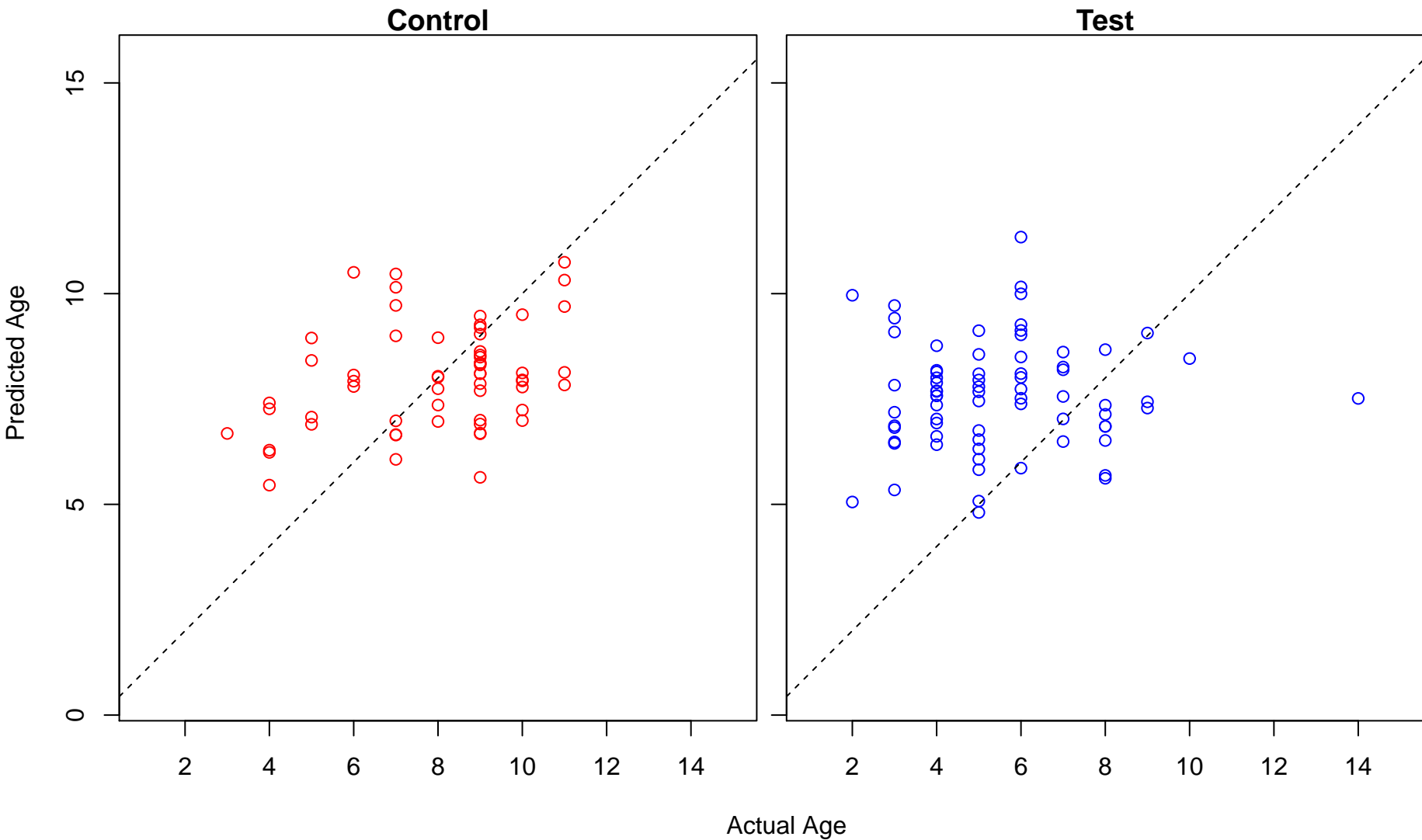
diphosphoinositol polyphosphate catabolic process (Score: 0.590694)



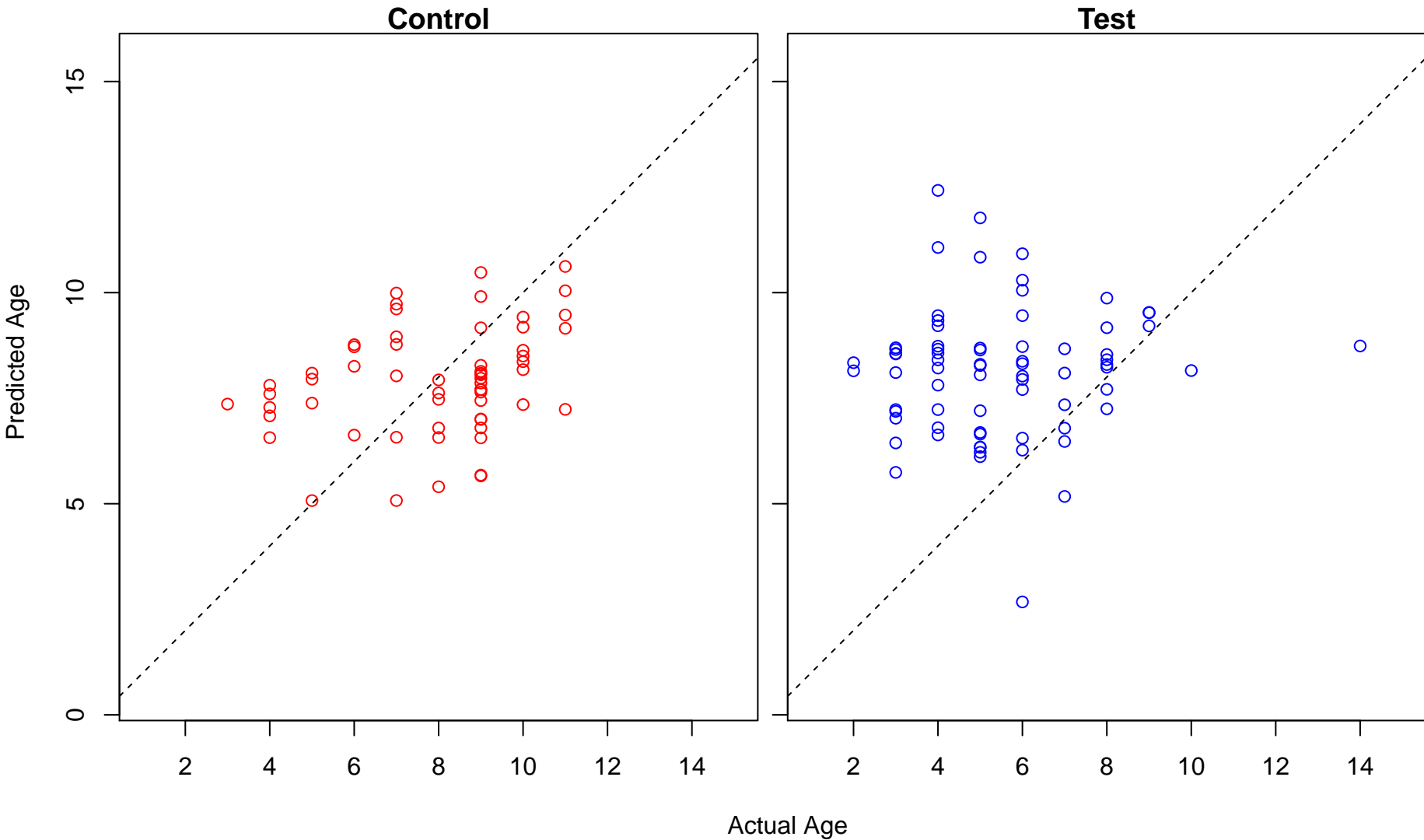
negative regulation of JAK-STAT cascade (Score: 0.590314)



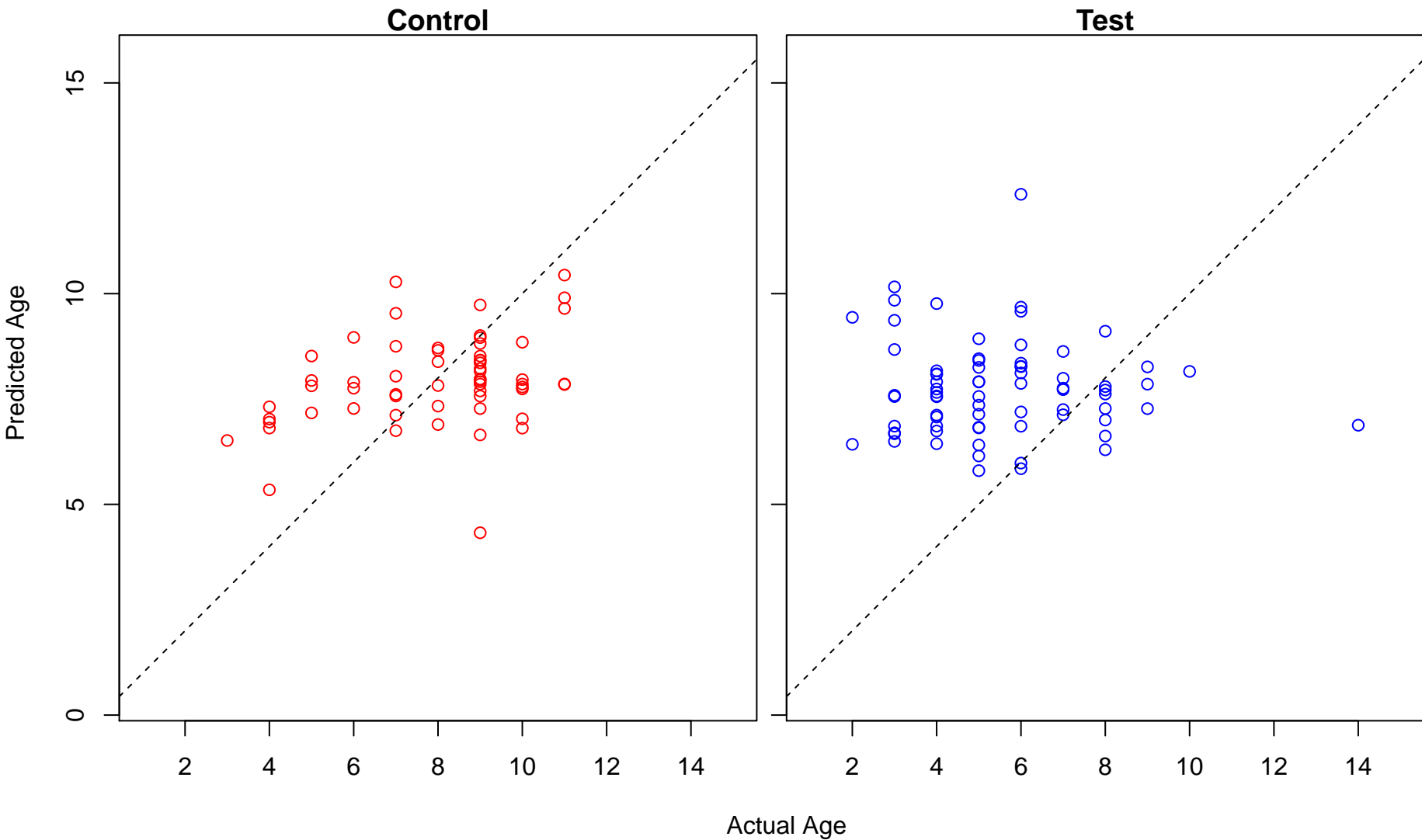
regulation of stem cell differentiation (Score: 0.589786)



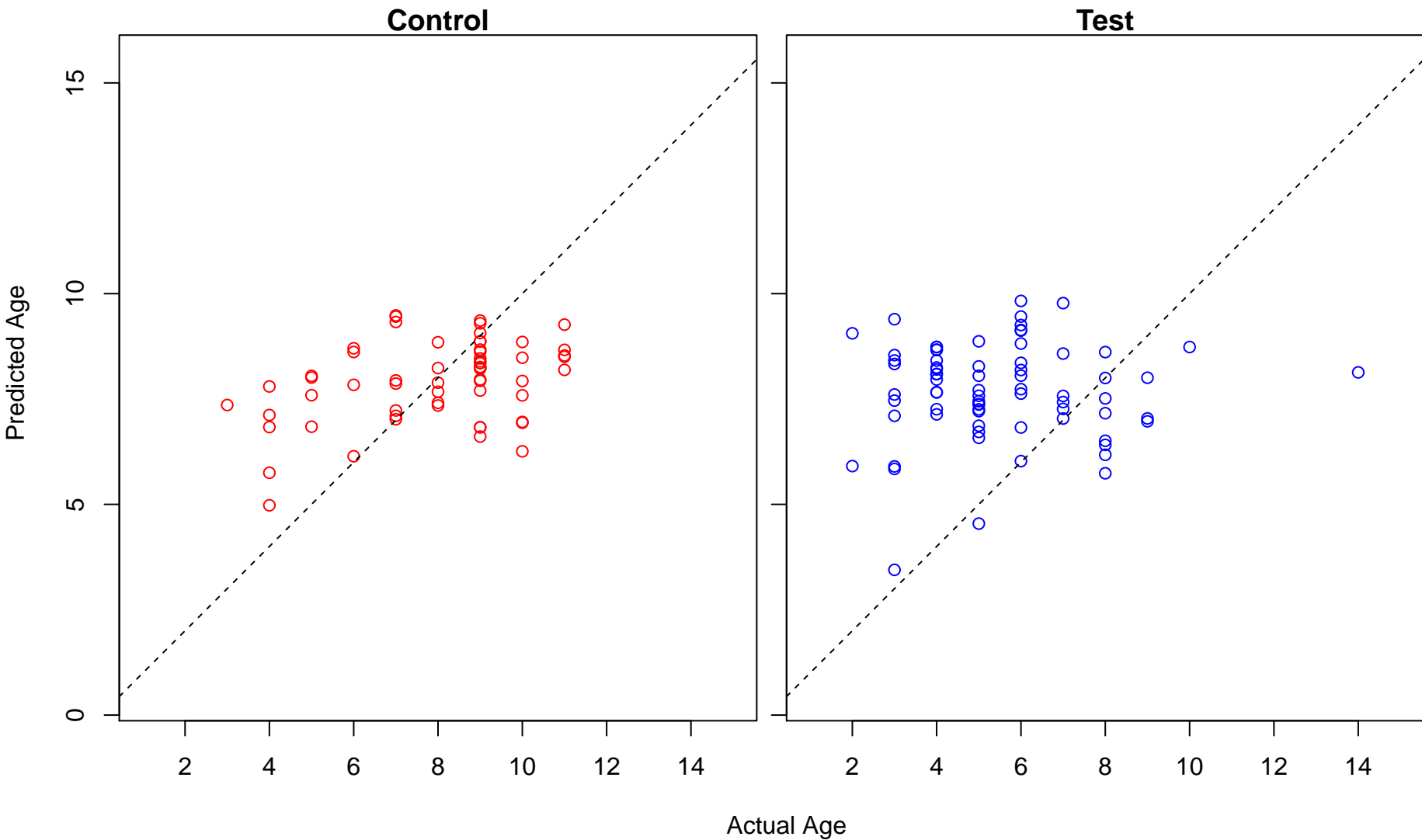
regulation of corticosteroid hormone secretion (Score: 0.589604)



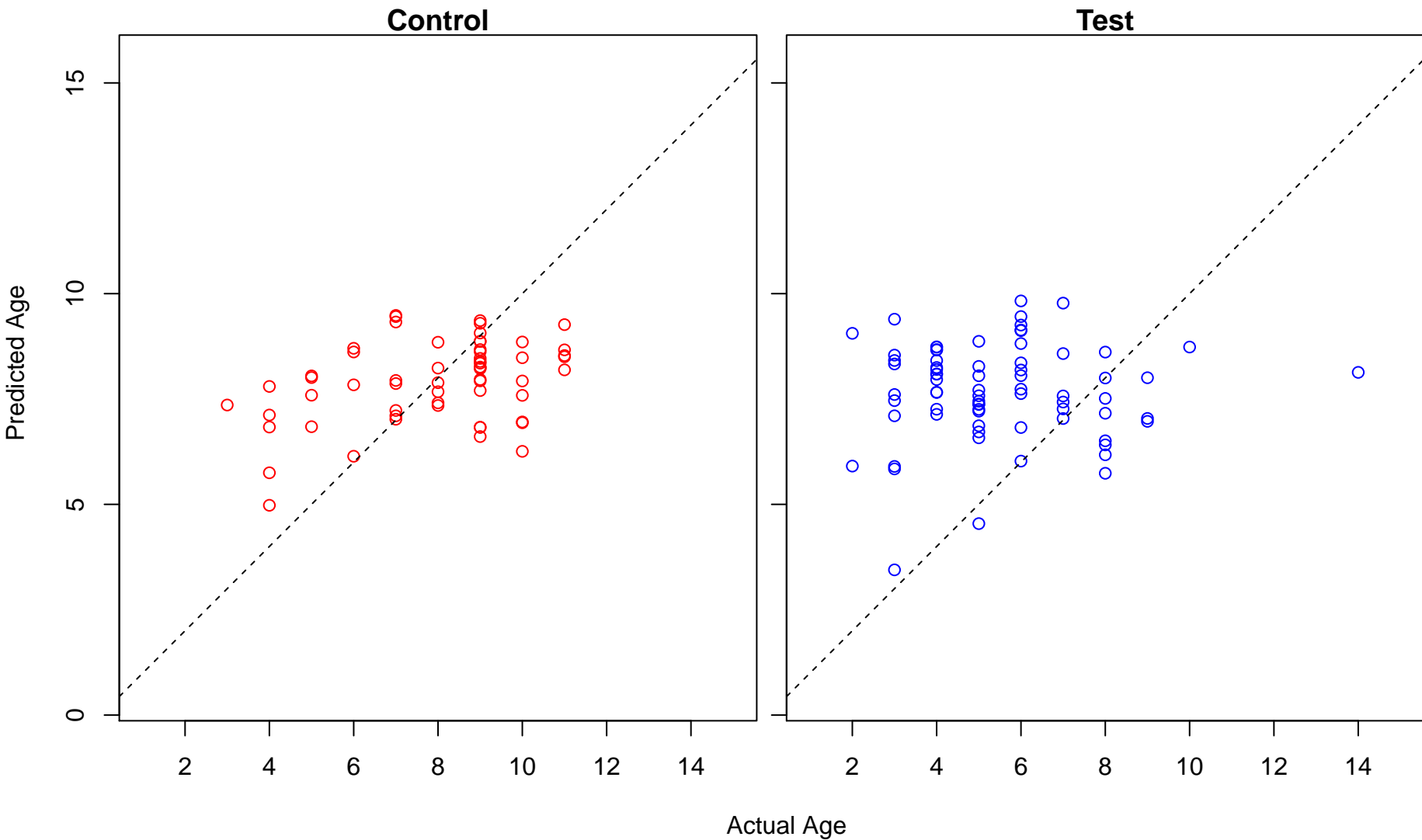
negative regulation of gene silencing (Score: 0.584862)



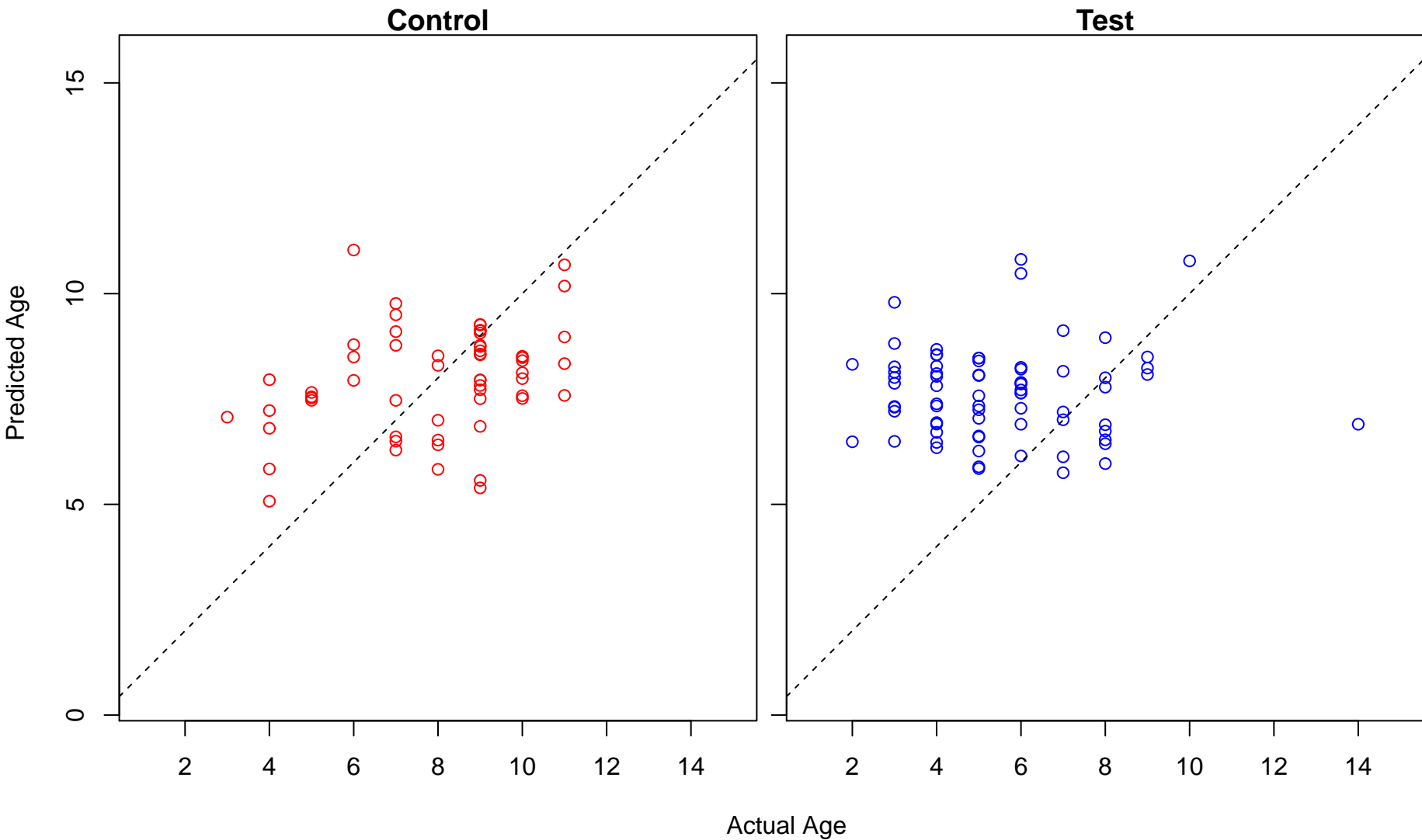
negative regulation of Ras protein signal transduction (Score: 0.583268)



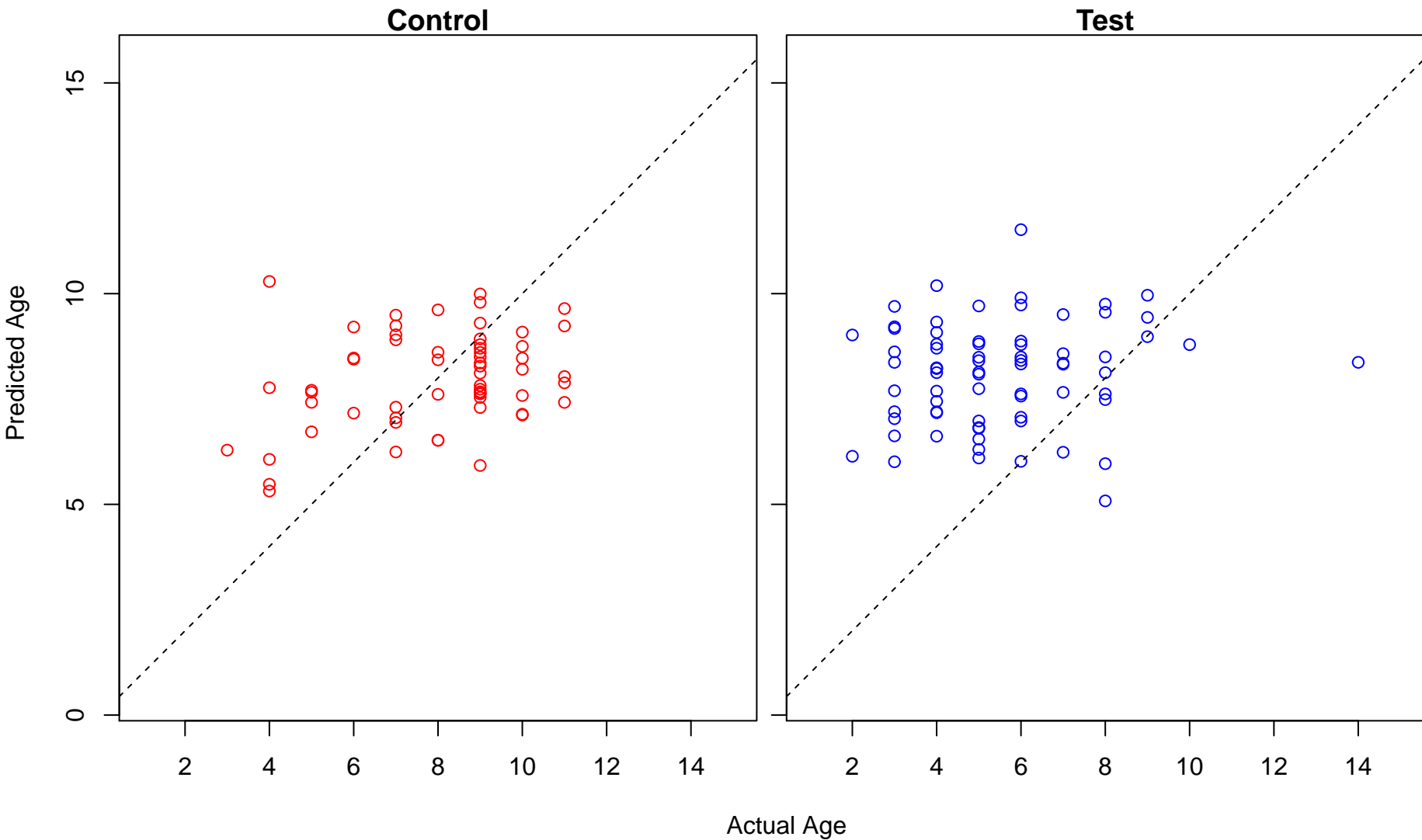
negative regulation of small GTPase mediated signal transduction (Score: 0.583265)



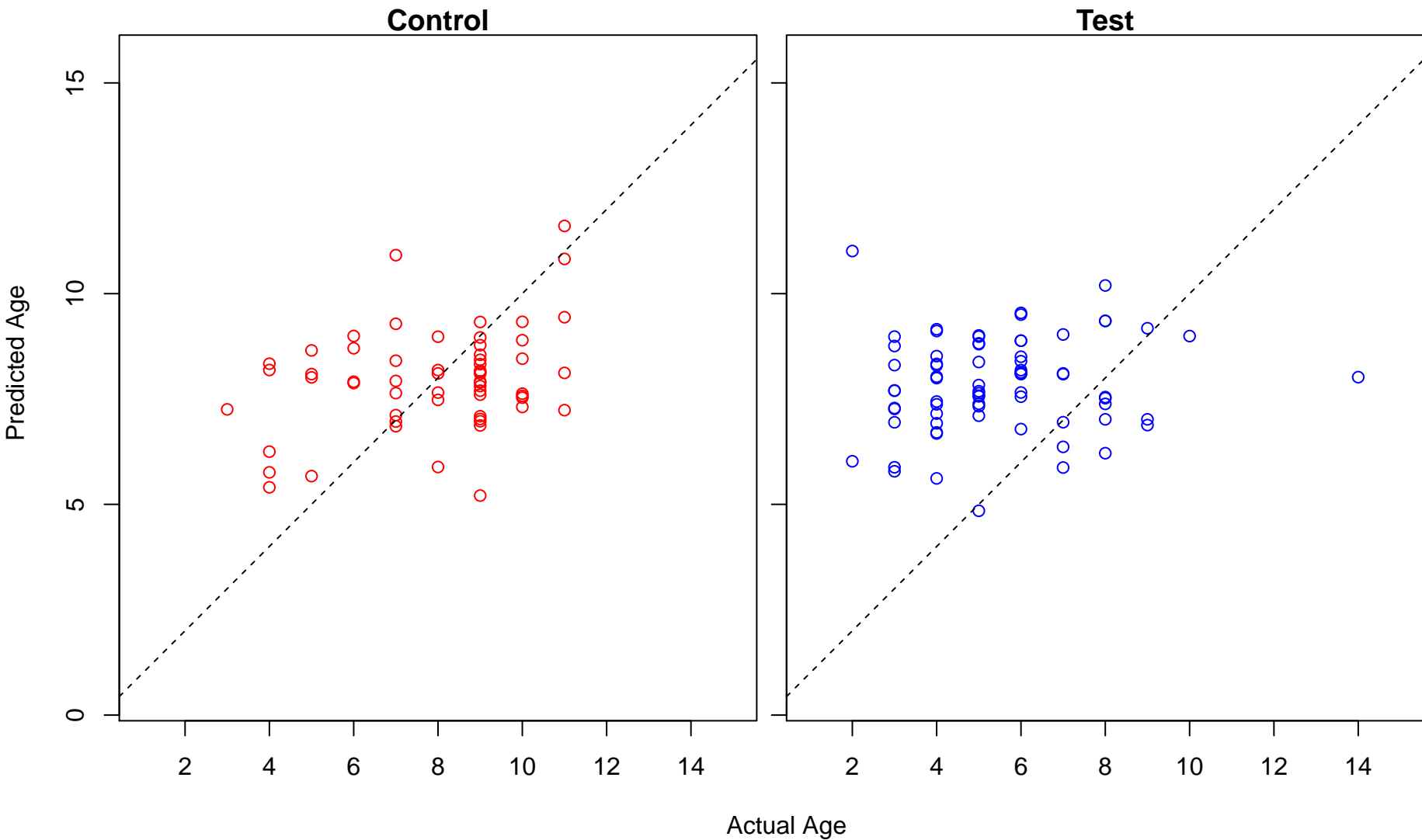
regulation of interleukin-8 production (Score: 0.582934)



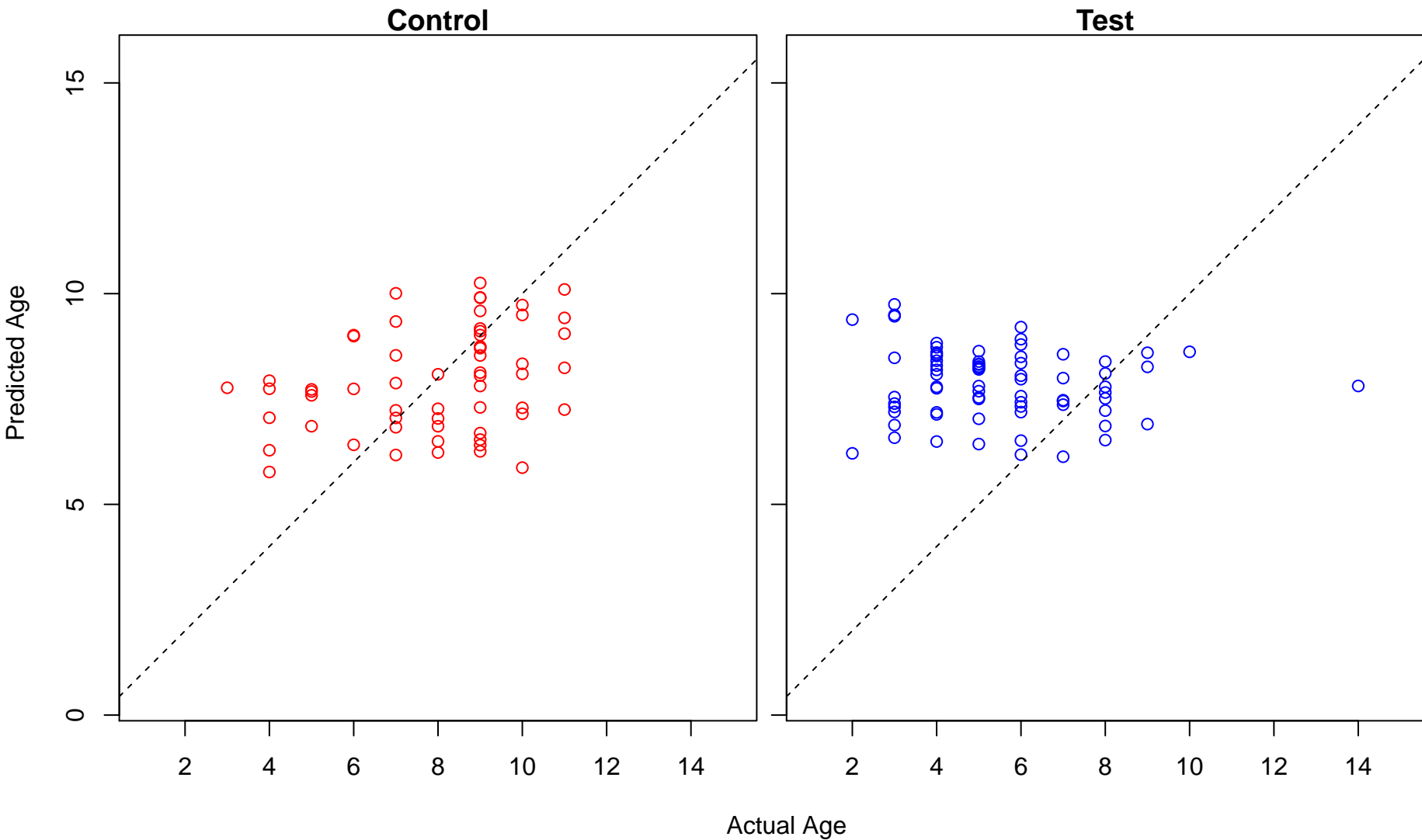
regulation of T-helper 1 type immune response (Score: 0.582766)



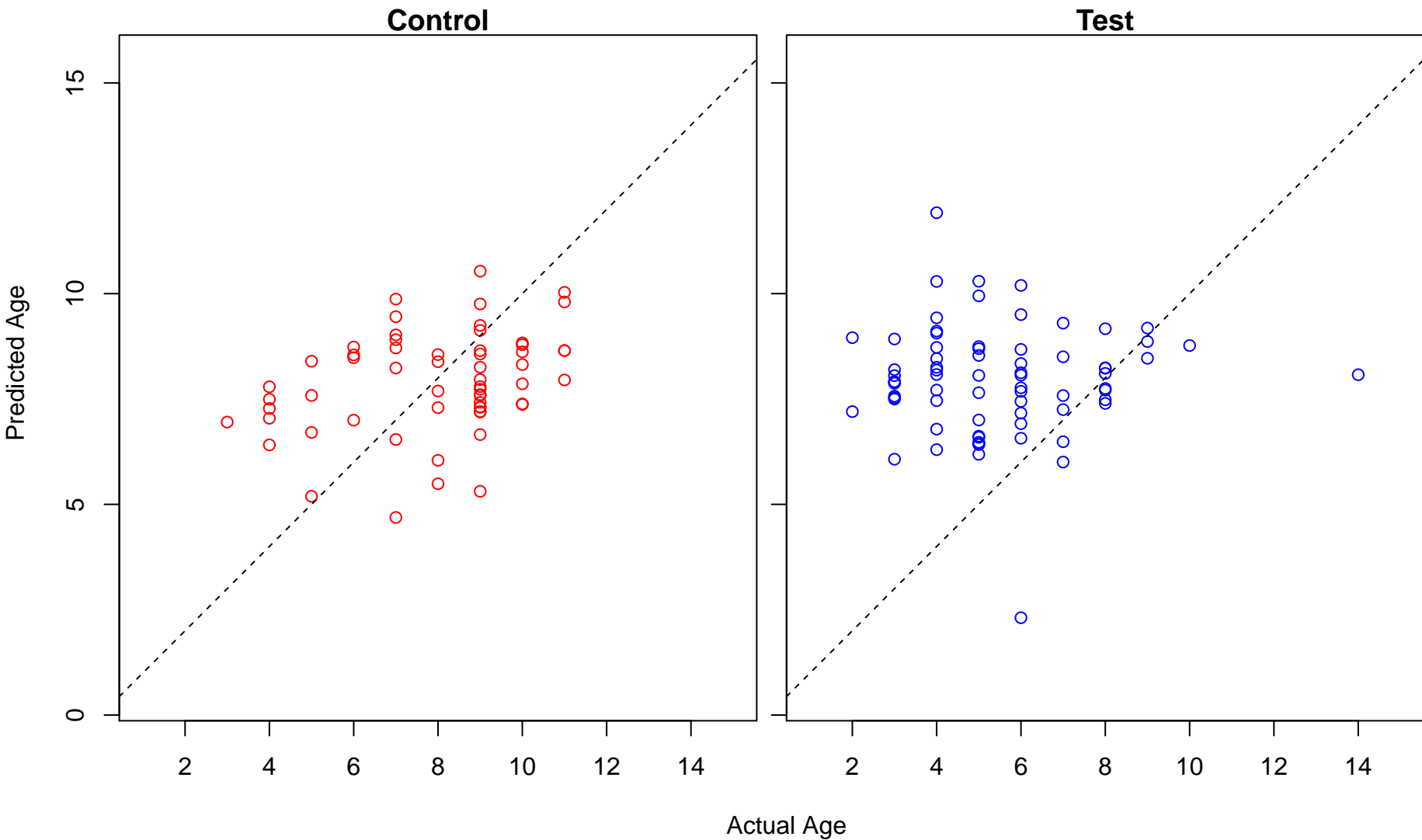
lipoprotein transport (Score: 0.581376)



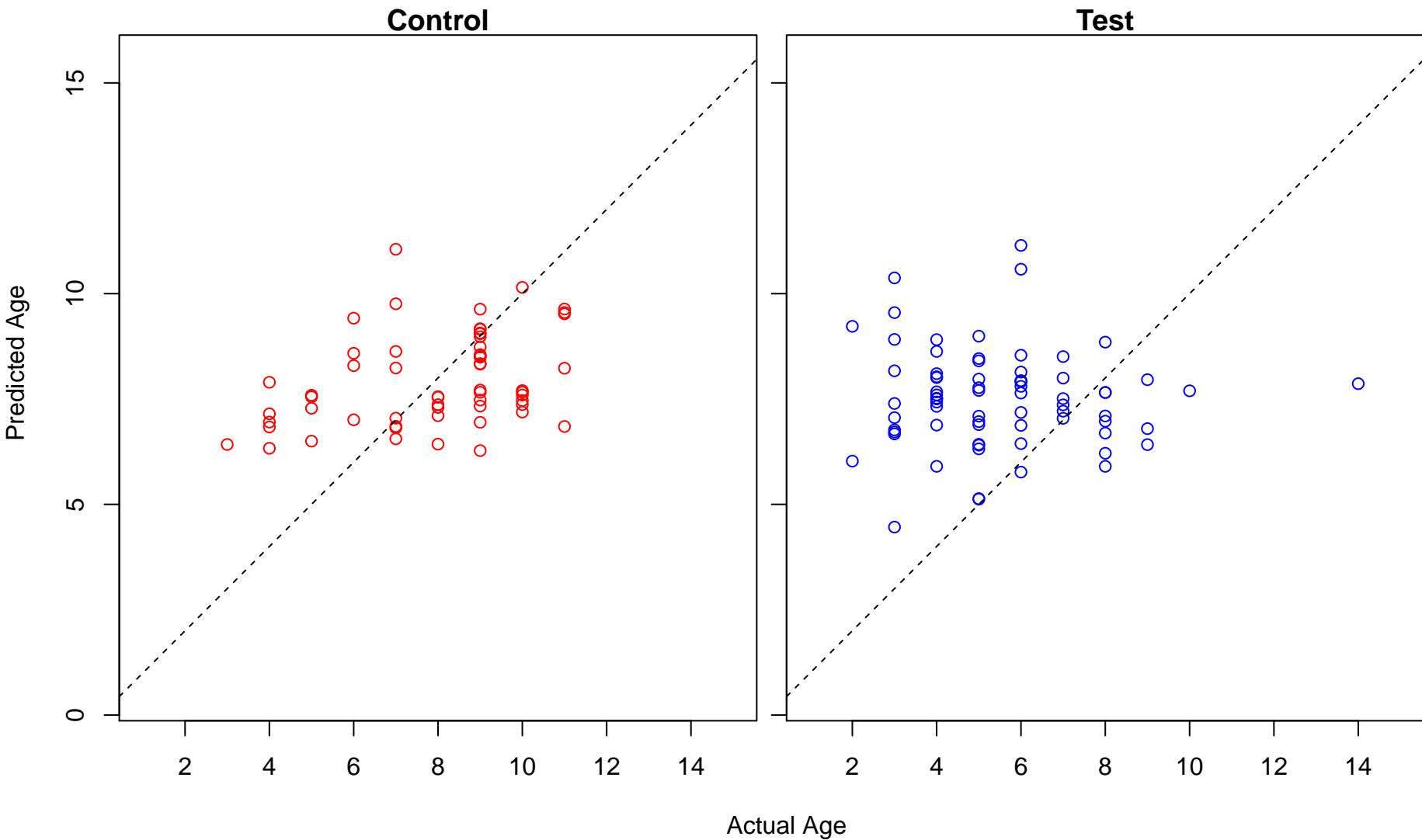
PML body organization (Score: 0.580466)



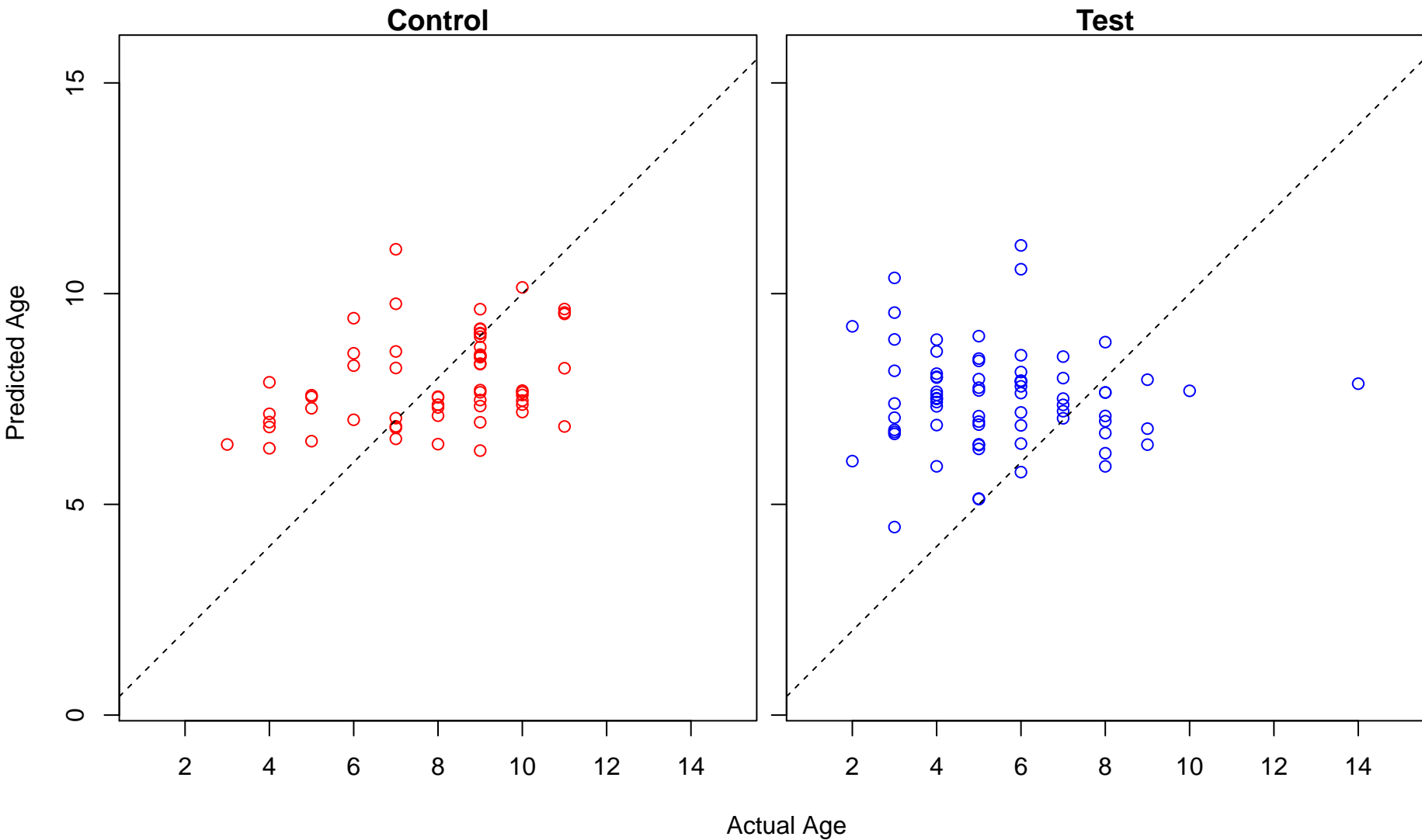
positive regulation of corticosteroid hormone secretion (Score: 0.580412)



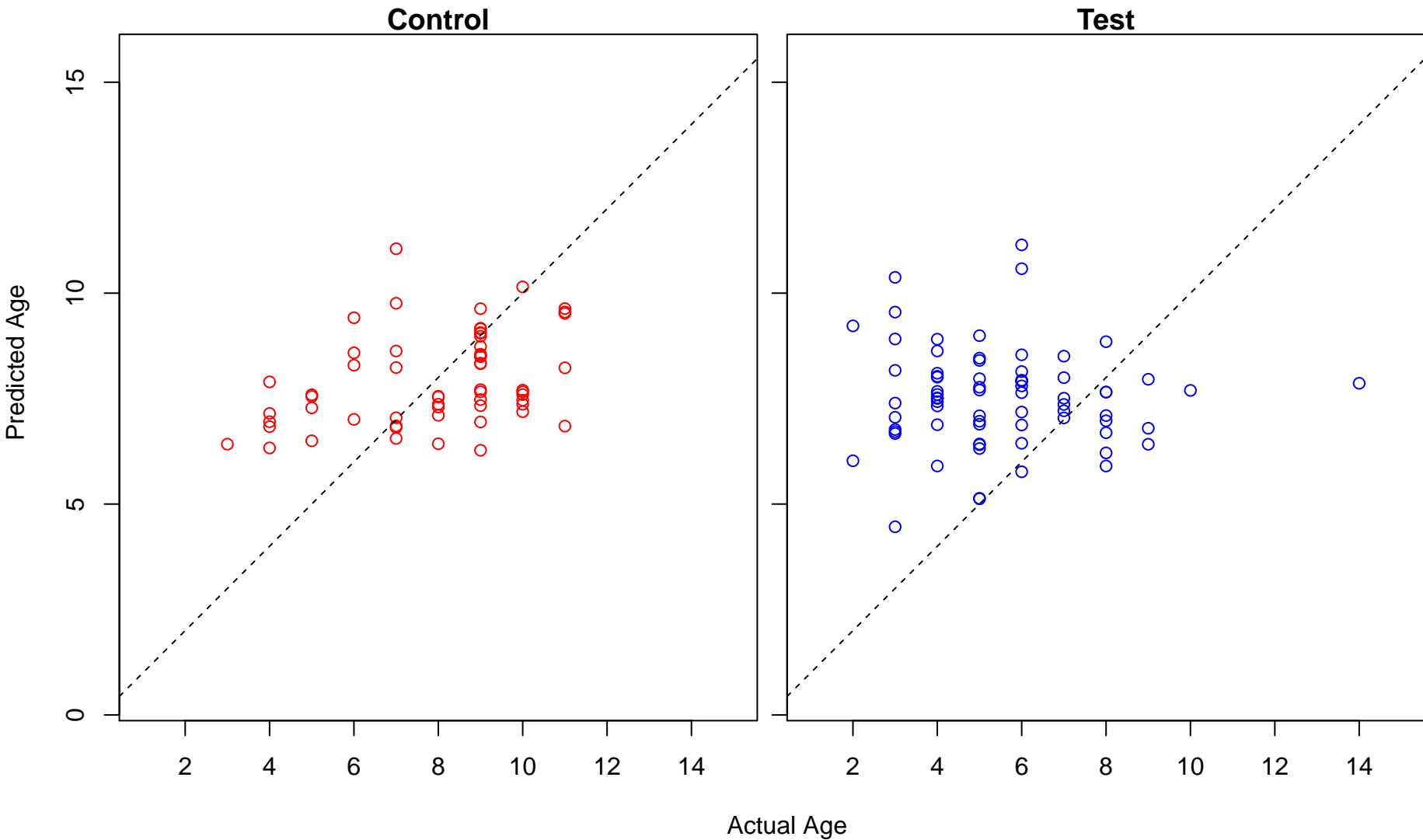
positive regulation of collagen metabolic process (Score: 0.579989)



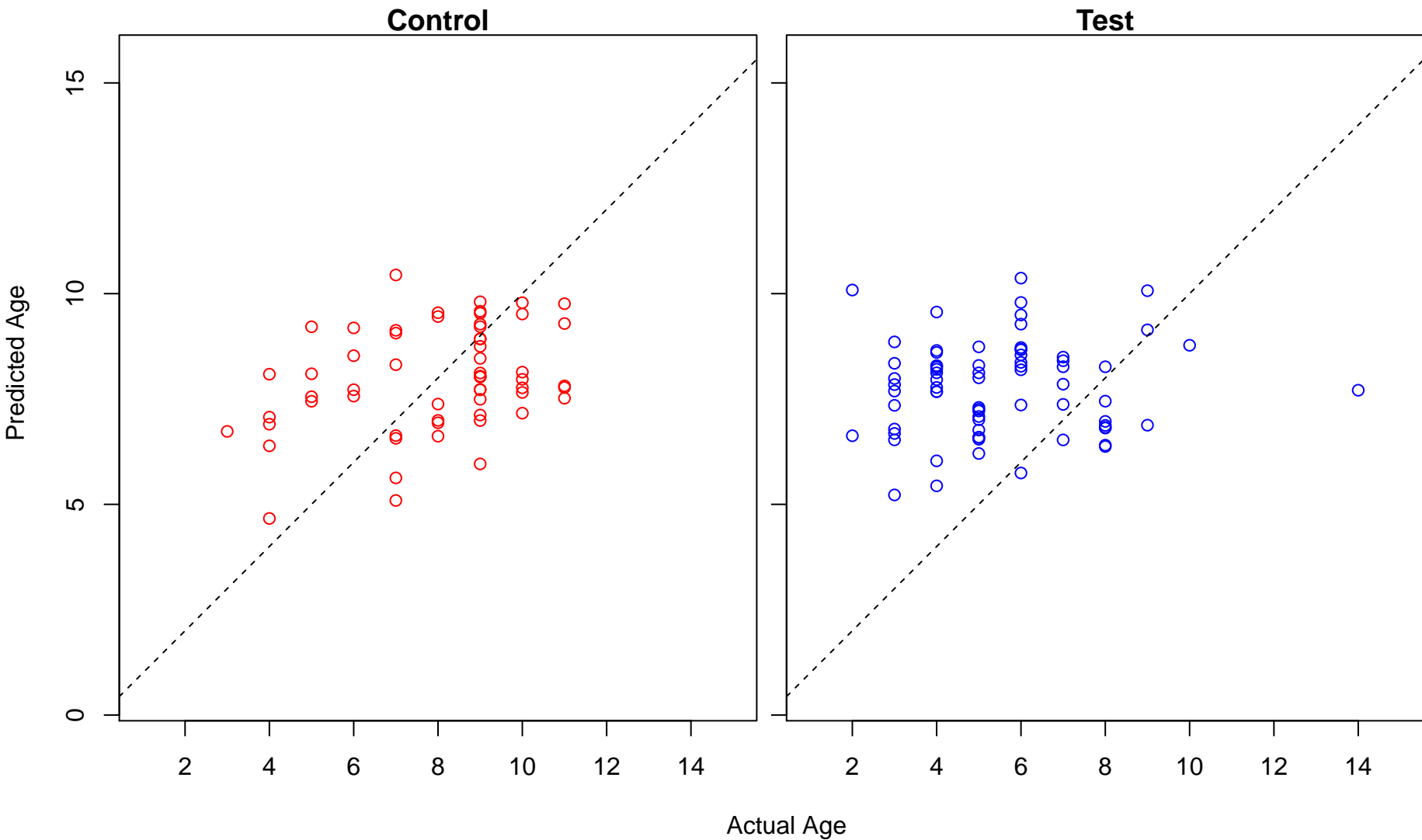
positive regulation of collagen biosynthetic process (Score: 0.579989)



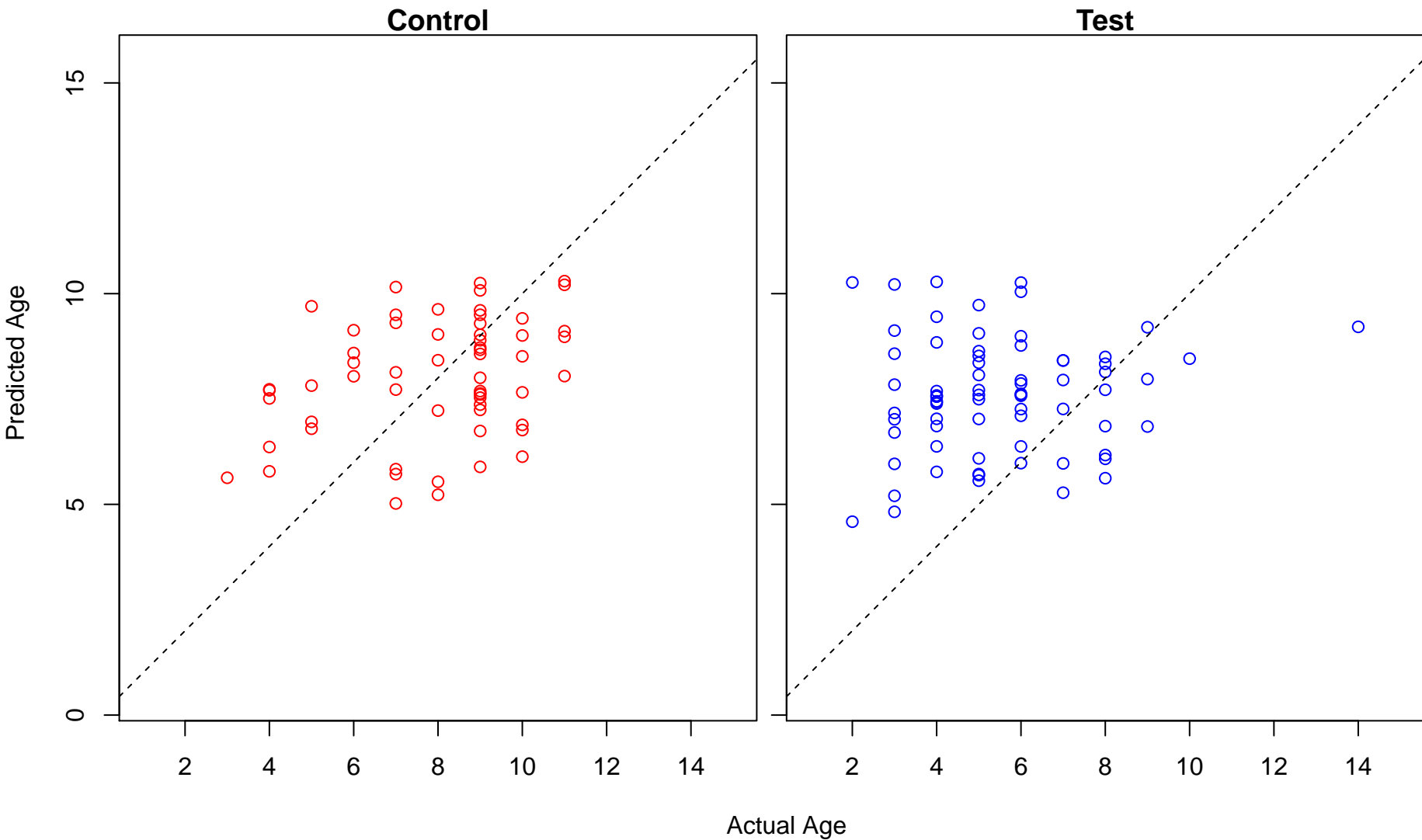
positive regulation of multicellular organismal metabolic process (Score: 0.579989)



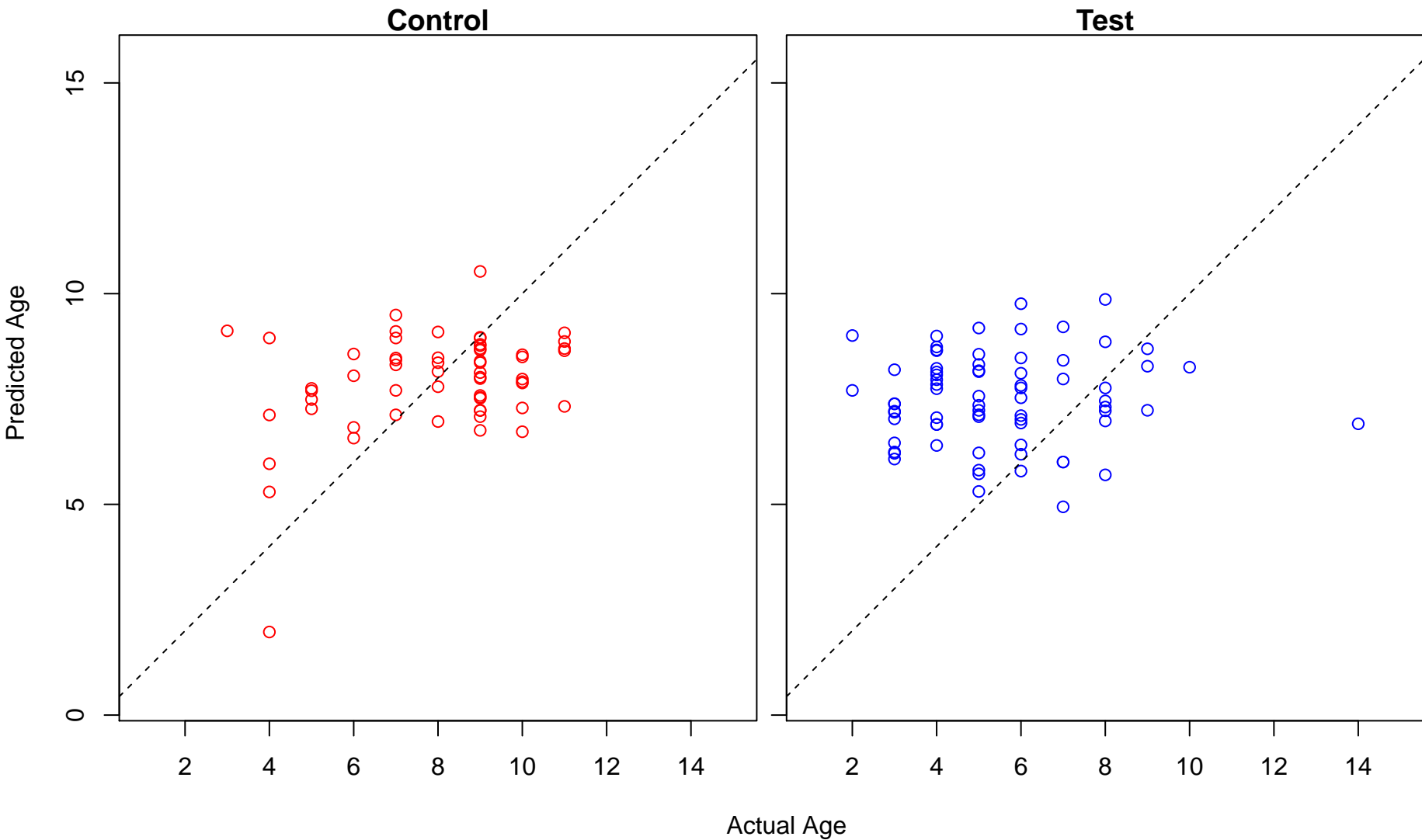
regulation of epidermis development (Score: 0.579815)



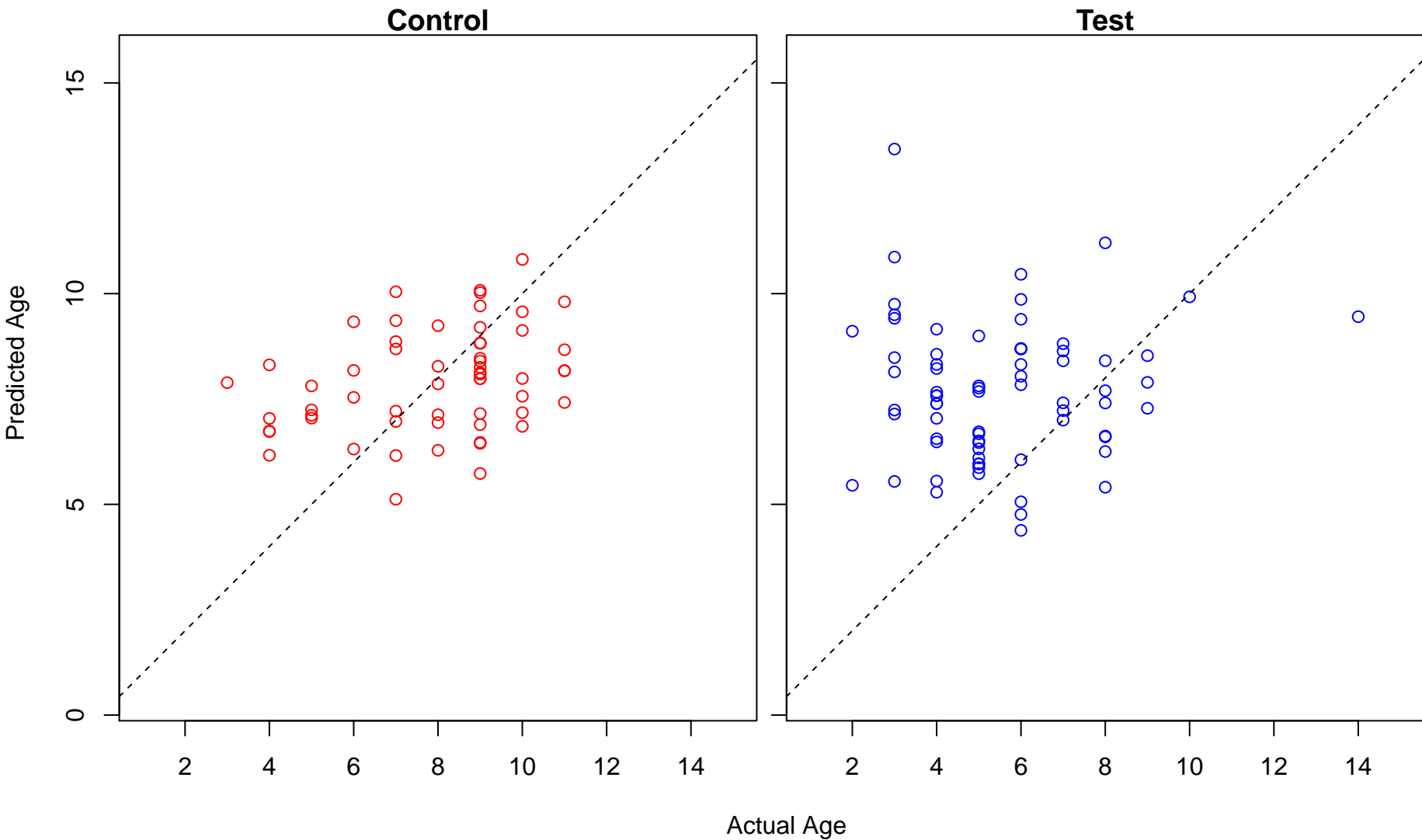
intrinsic apoptotic signaling pathway in response to oxidative stress (Score: 0.578972)



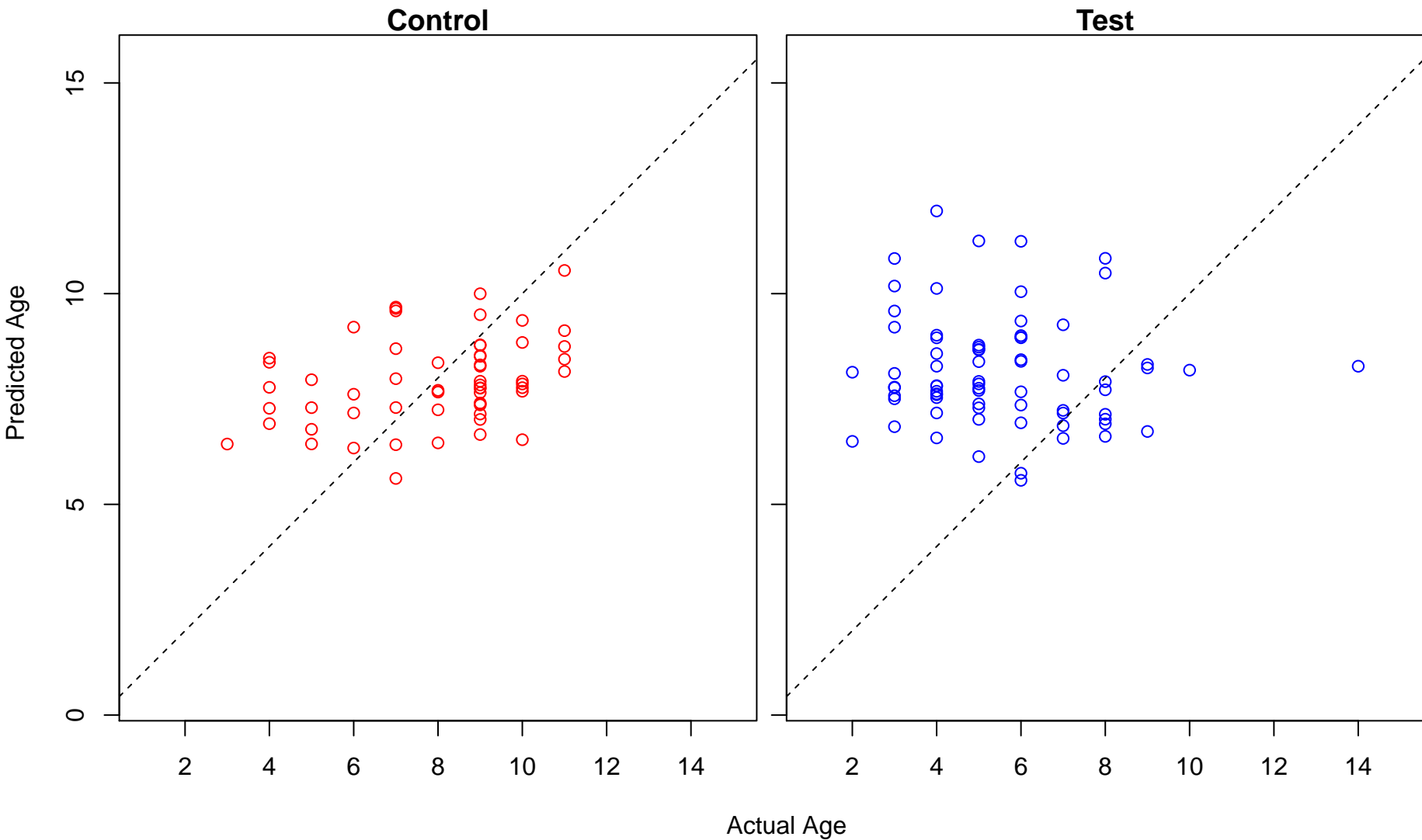
negative regulation of oxidative phosphorylation (Score: 0.577726)



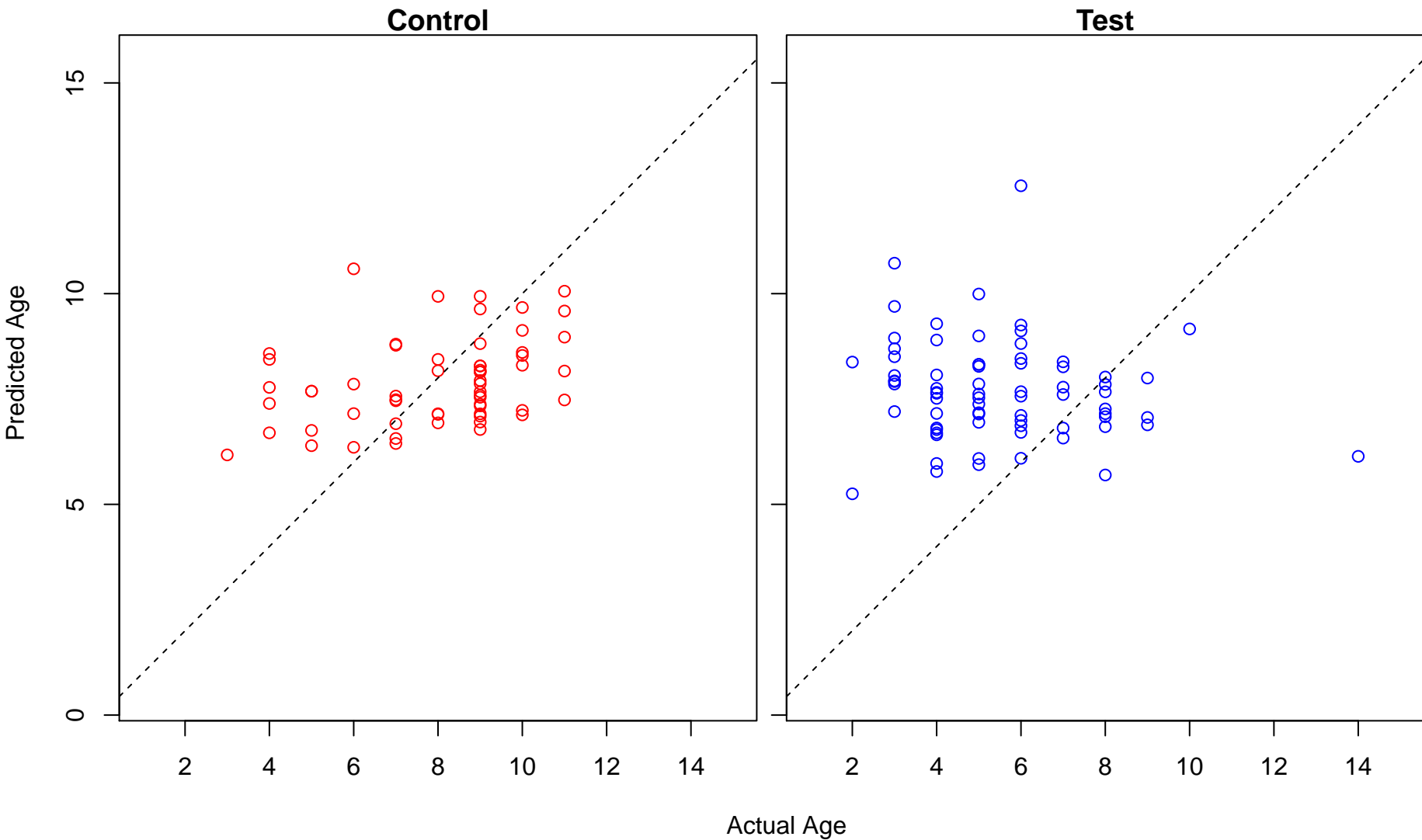
membrane tubulation (Score: 0.577666)



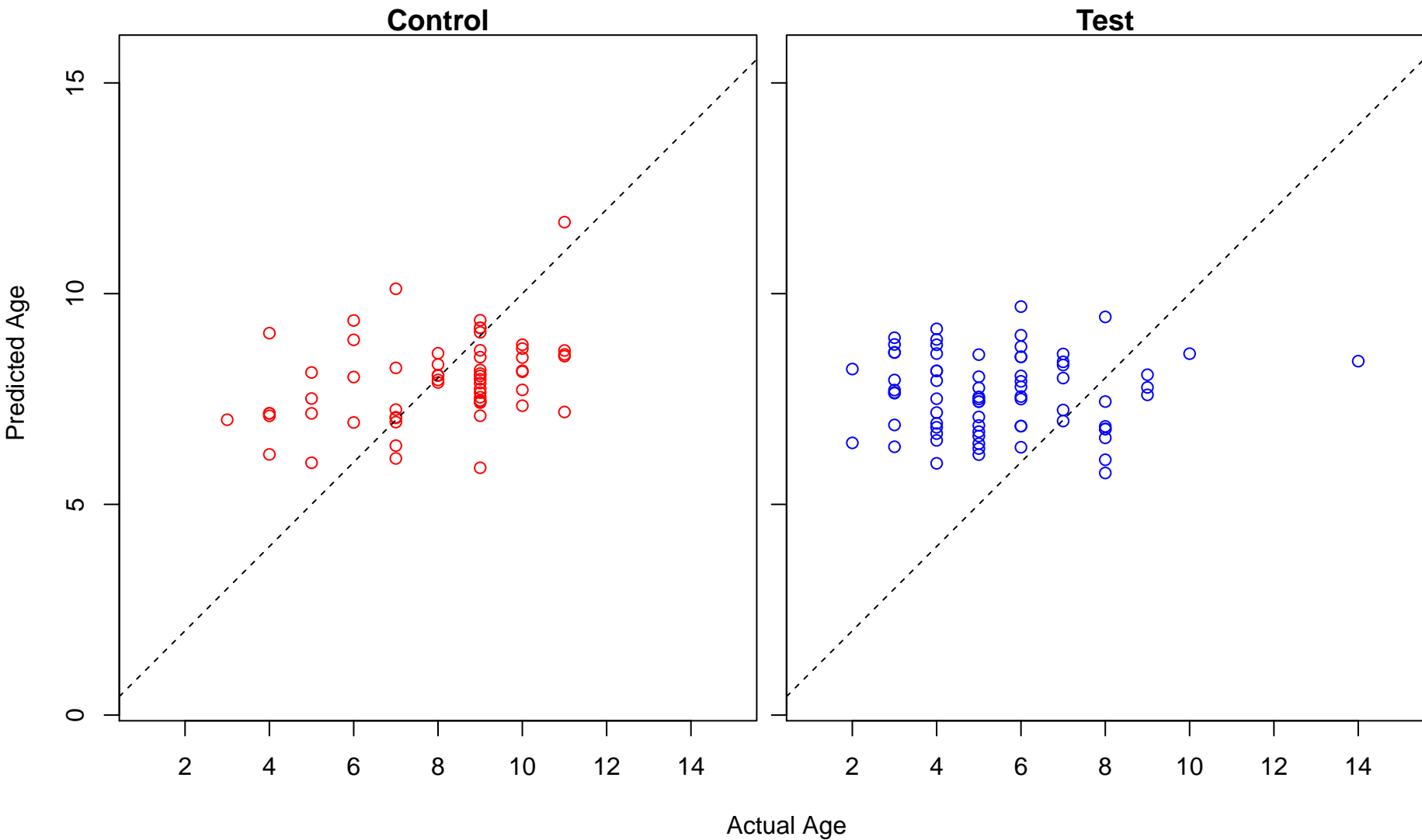
meiosis I (Score: 0.577190)



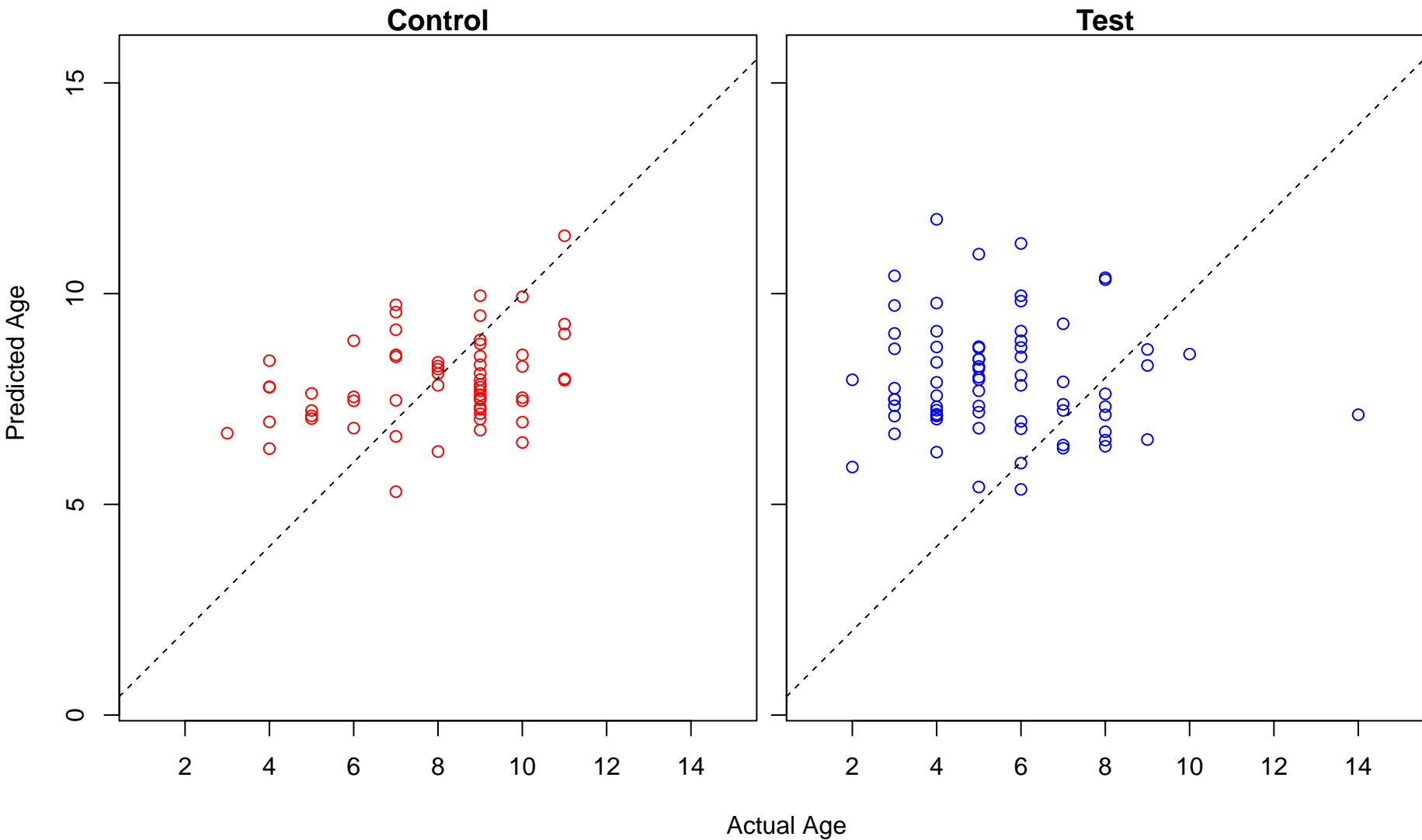
positive regulation of interleukin-13 secretion (Score: 0.576020)



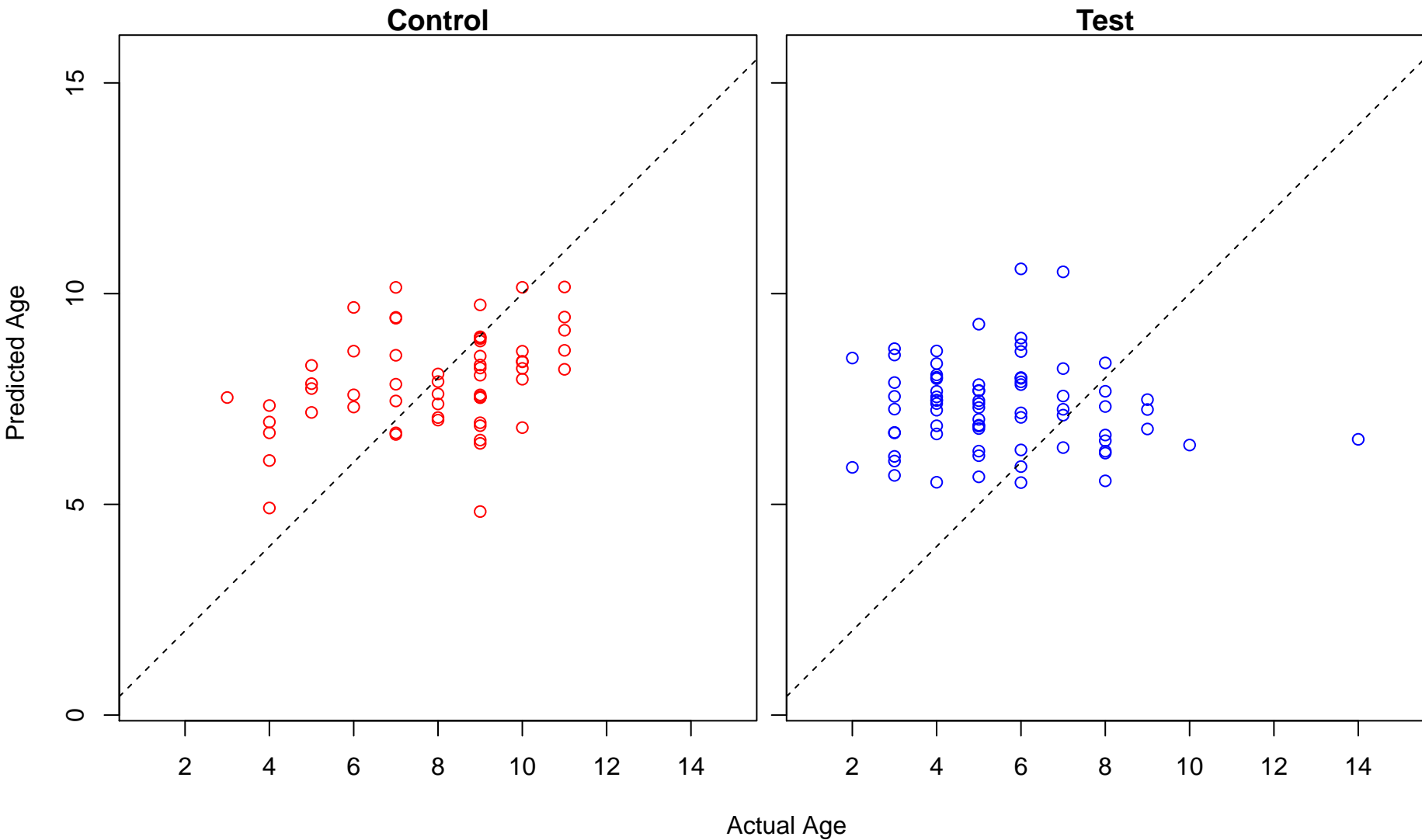
establishment of nucleus localization (Score: 0.573401)



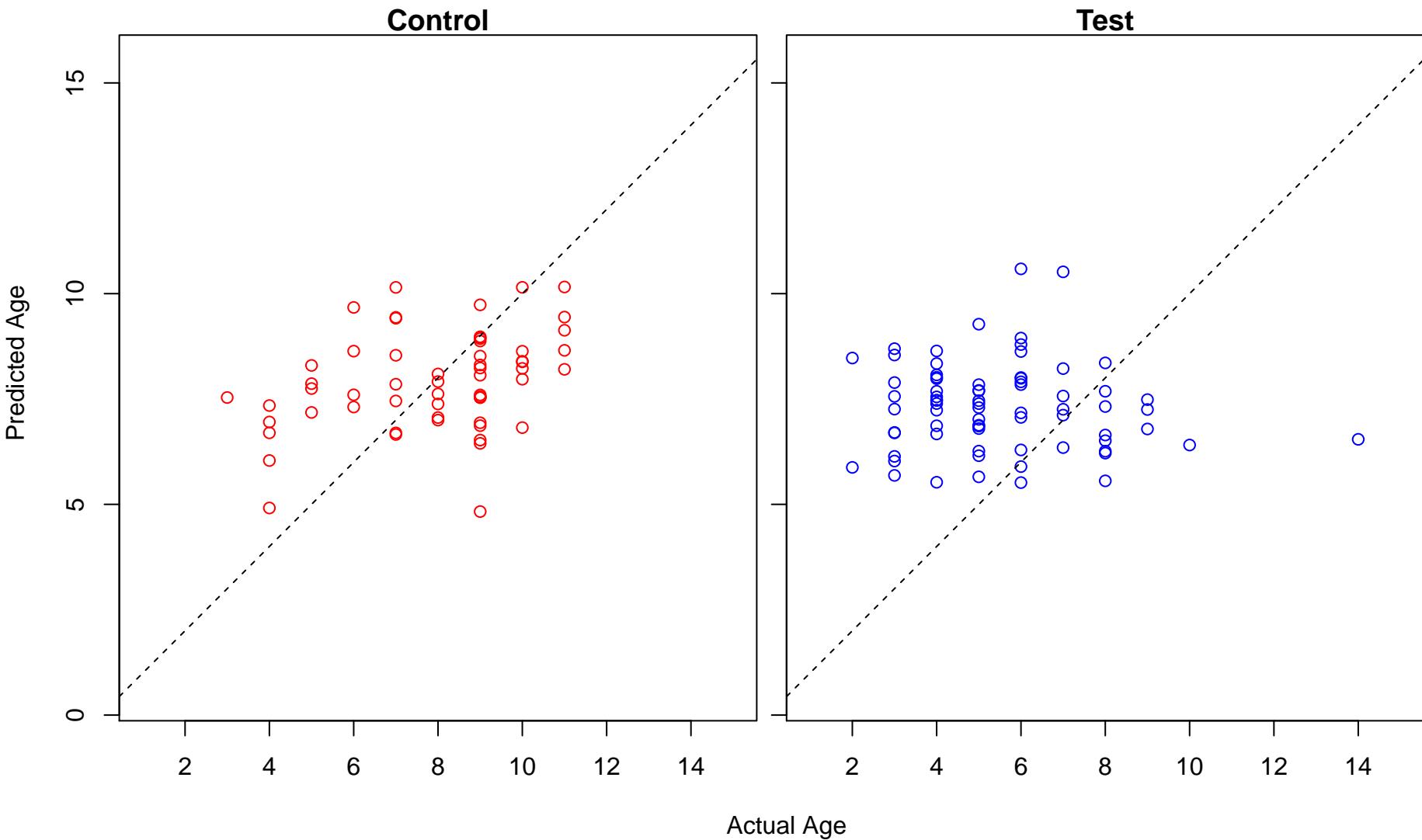
meiotic cell cycle (Score: 0.569026)



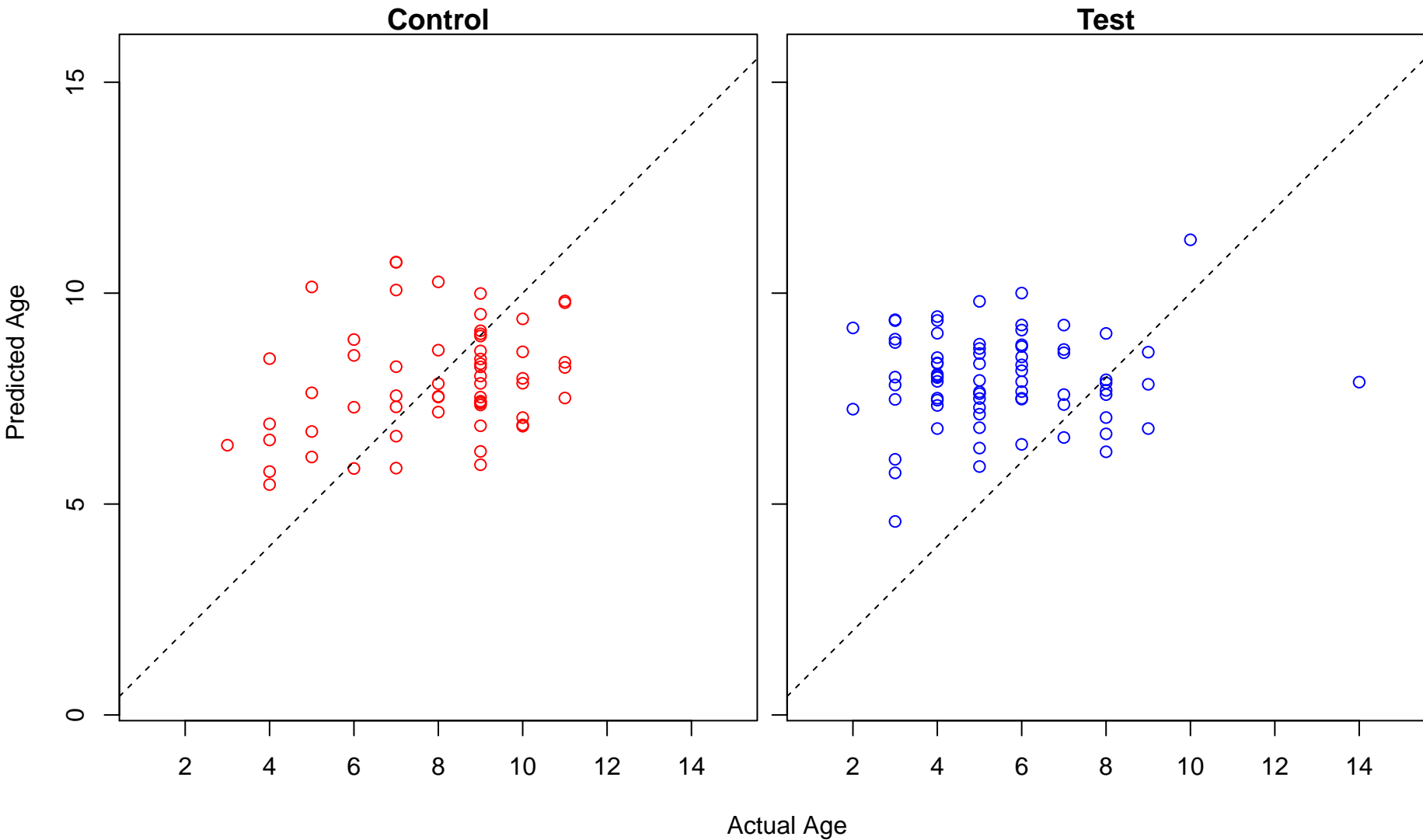
regulation of plasma membrane long-chain fatty acid transport (Score: 0.568792)



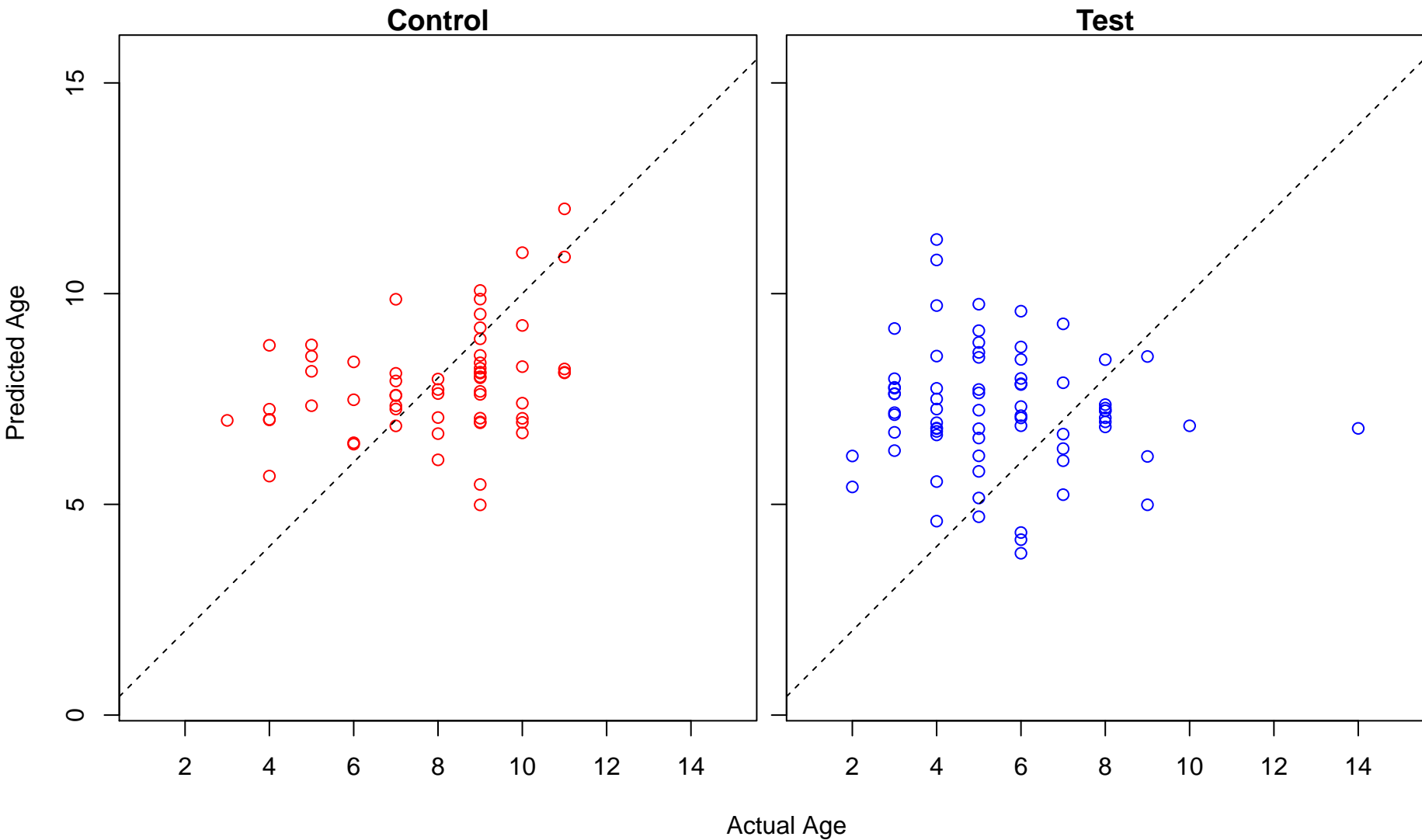
negative regulation of plasma membrane long-chain fatty acid transport (Score: 0.568792)



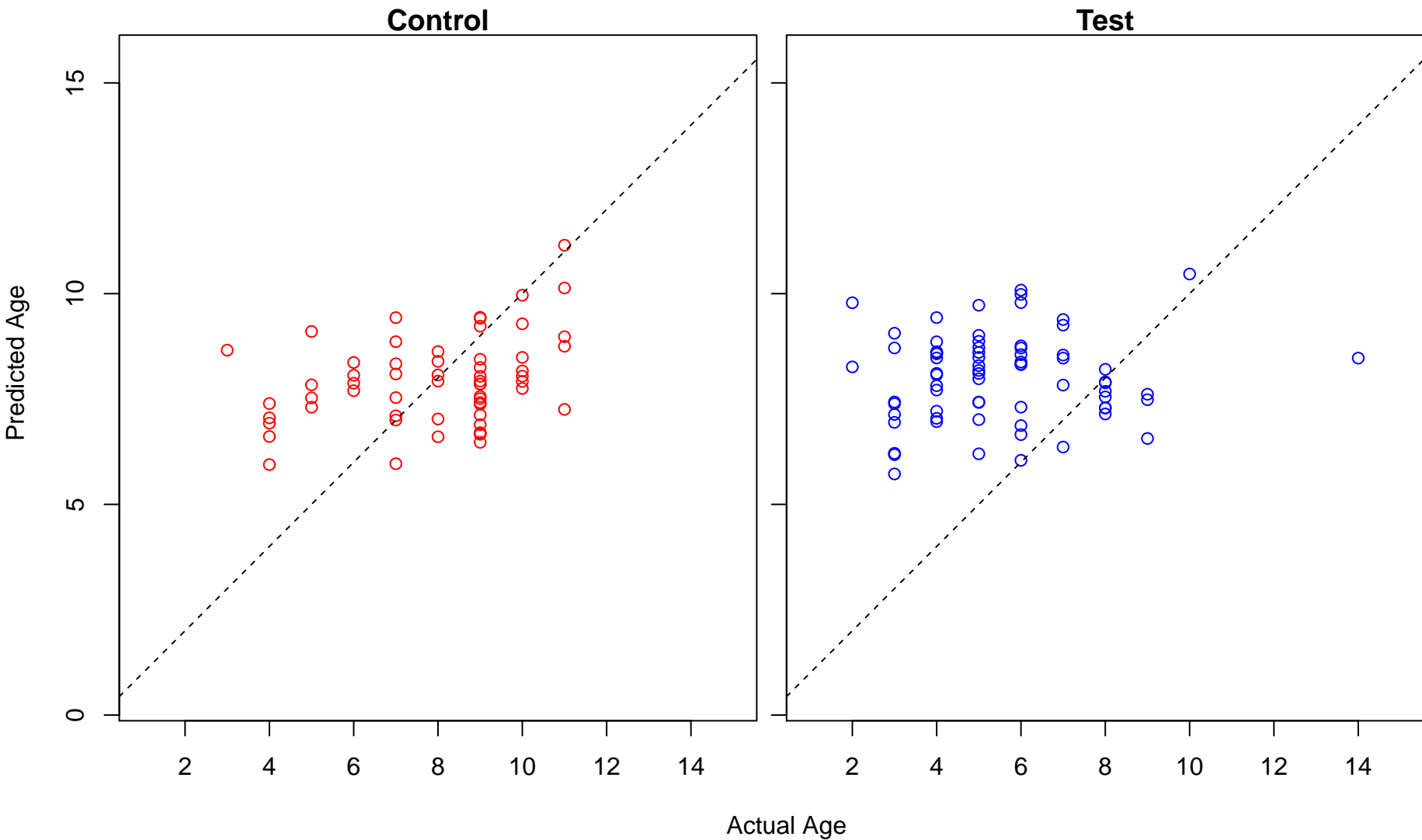
nuclear-transcribed mRNA catabolic process, exonucleolytic (Score: 0.568519)



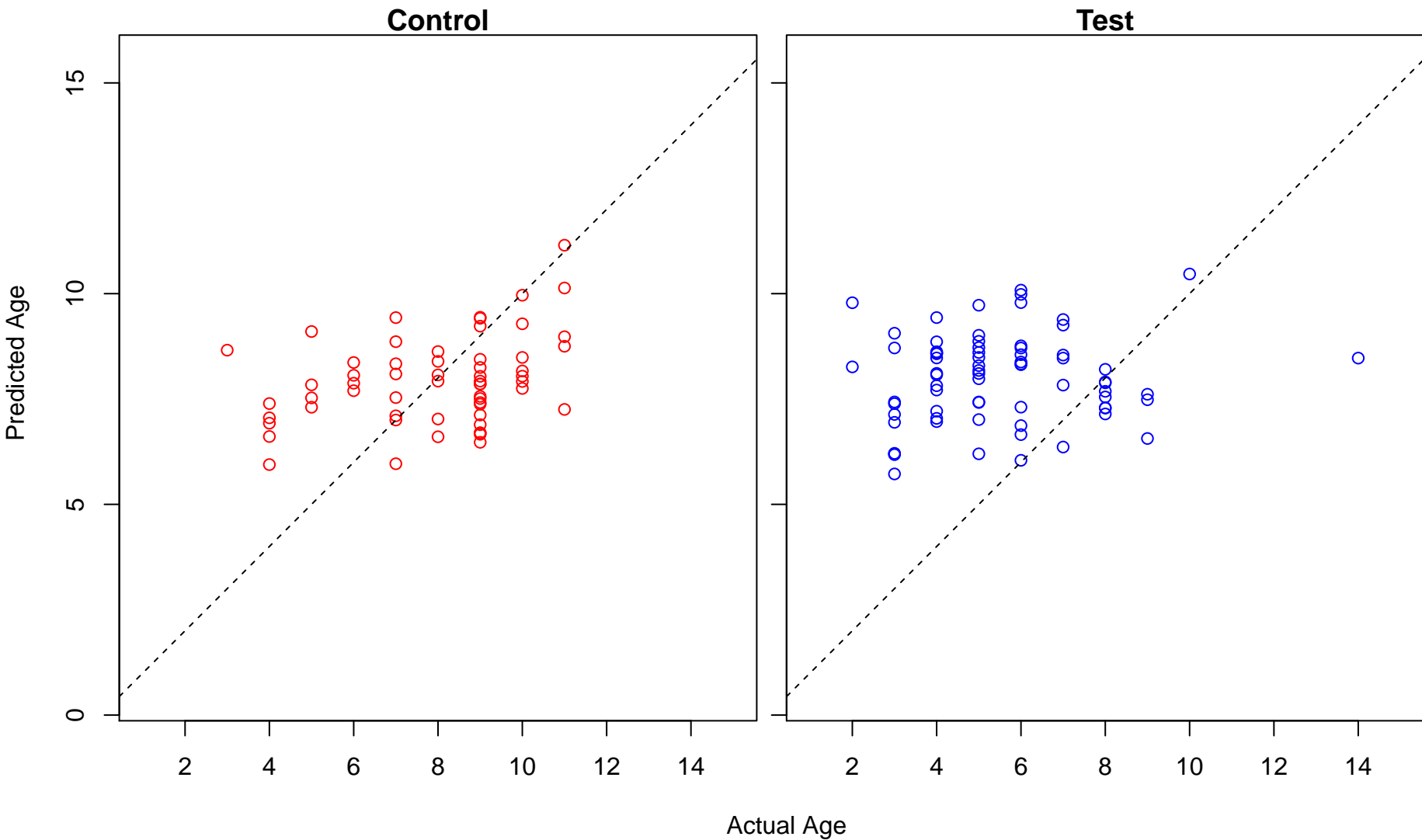
chondrocyte development involved in endochondral bone morphogenesis (Score: 0.568408)



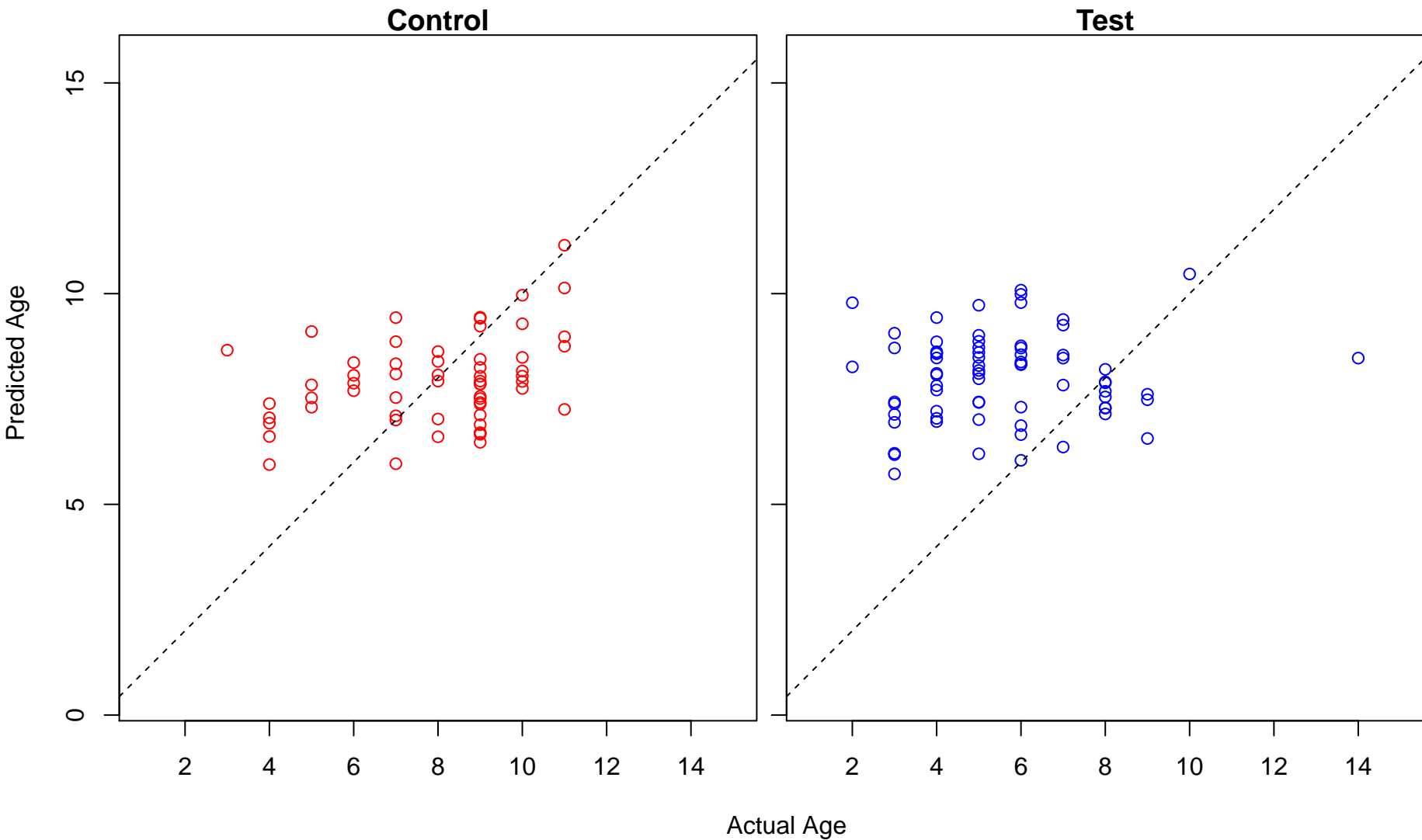
nickel cation transport (Score: 0.567185)



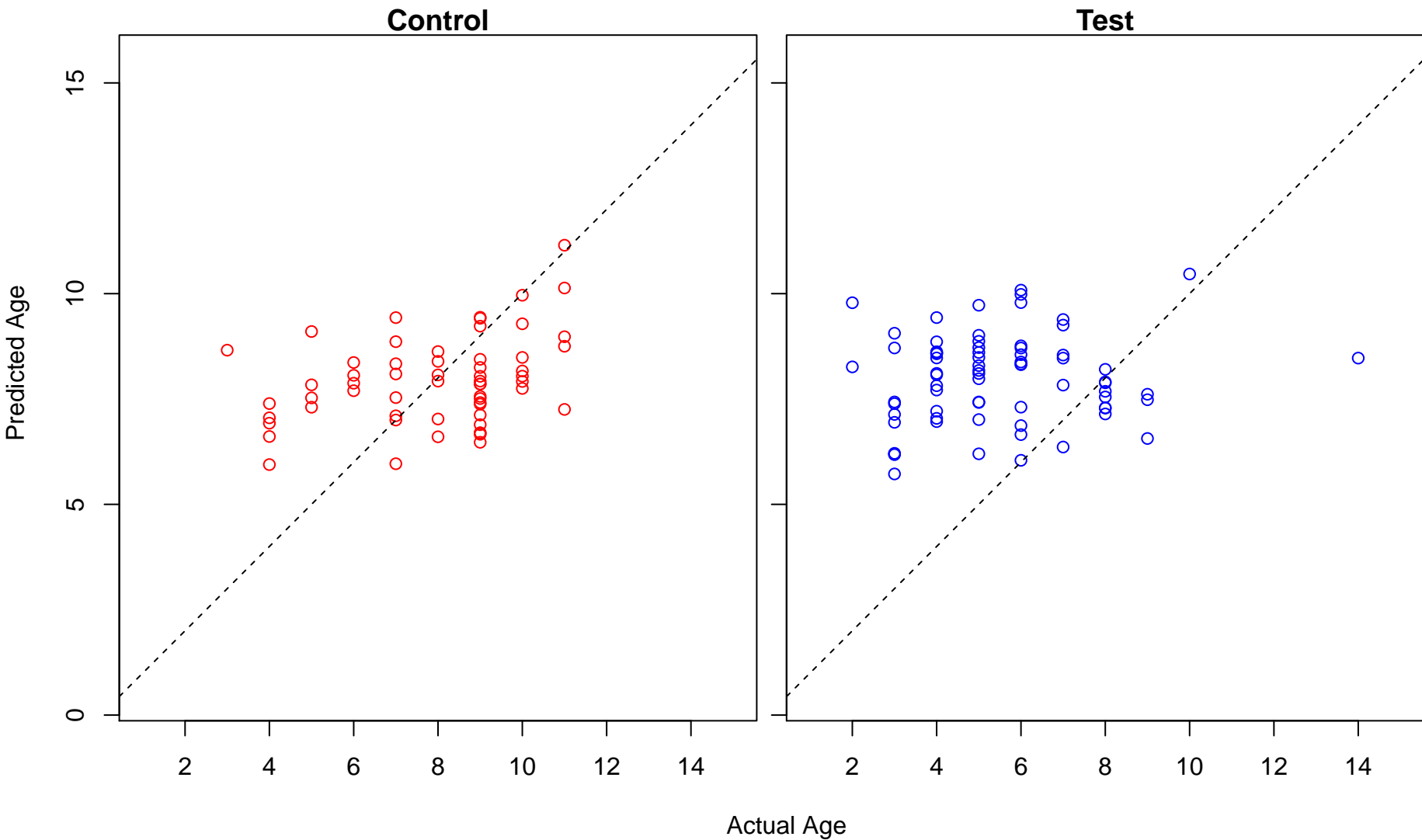
vanadium ion transport (Score: 0.567185)



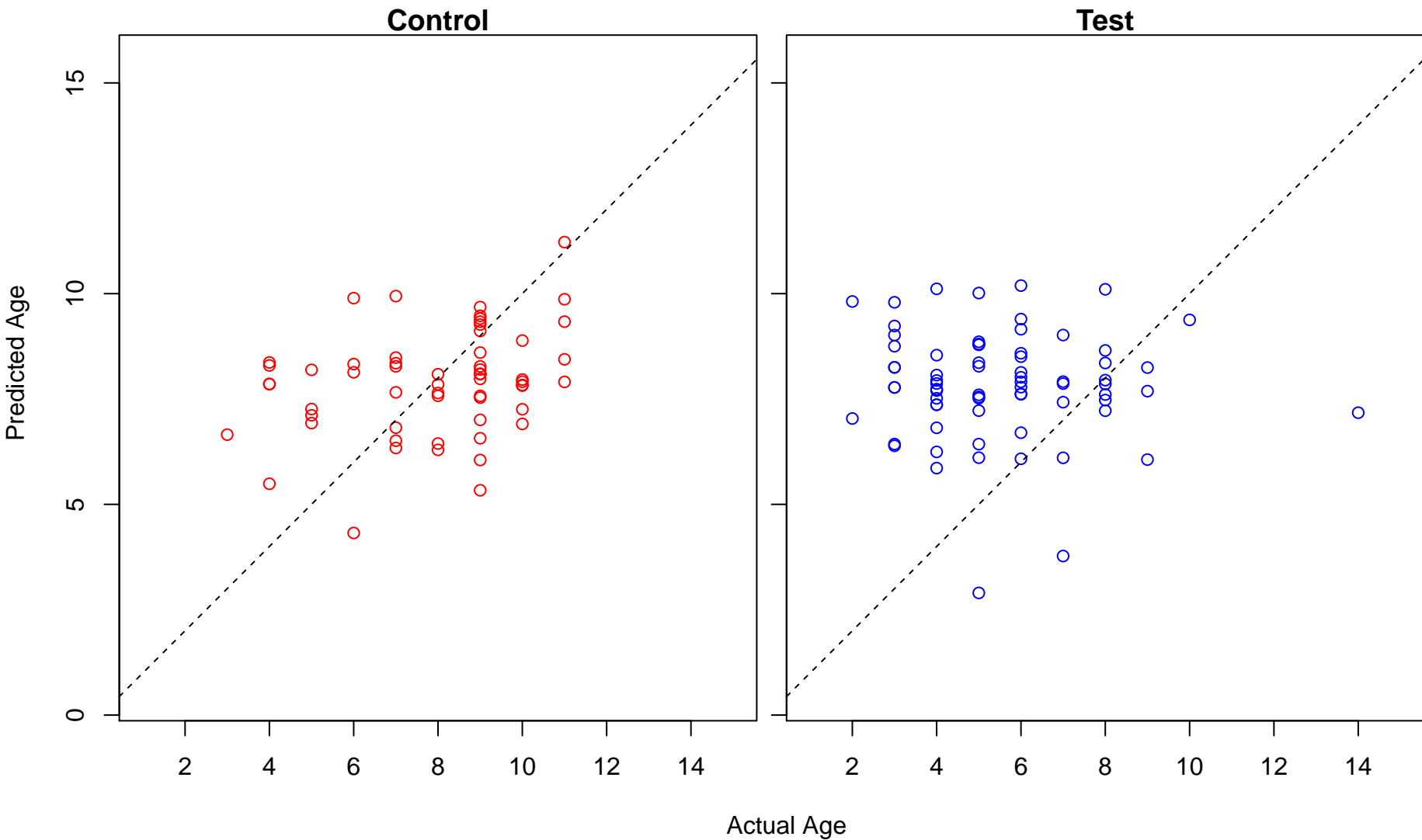
lead ion transport (Score: 0.567185)



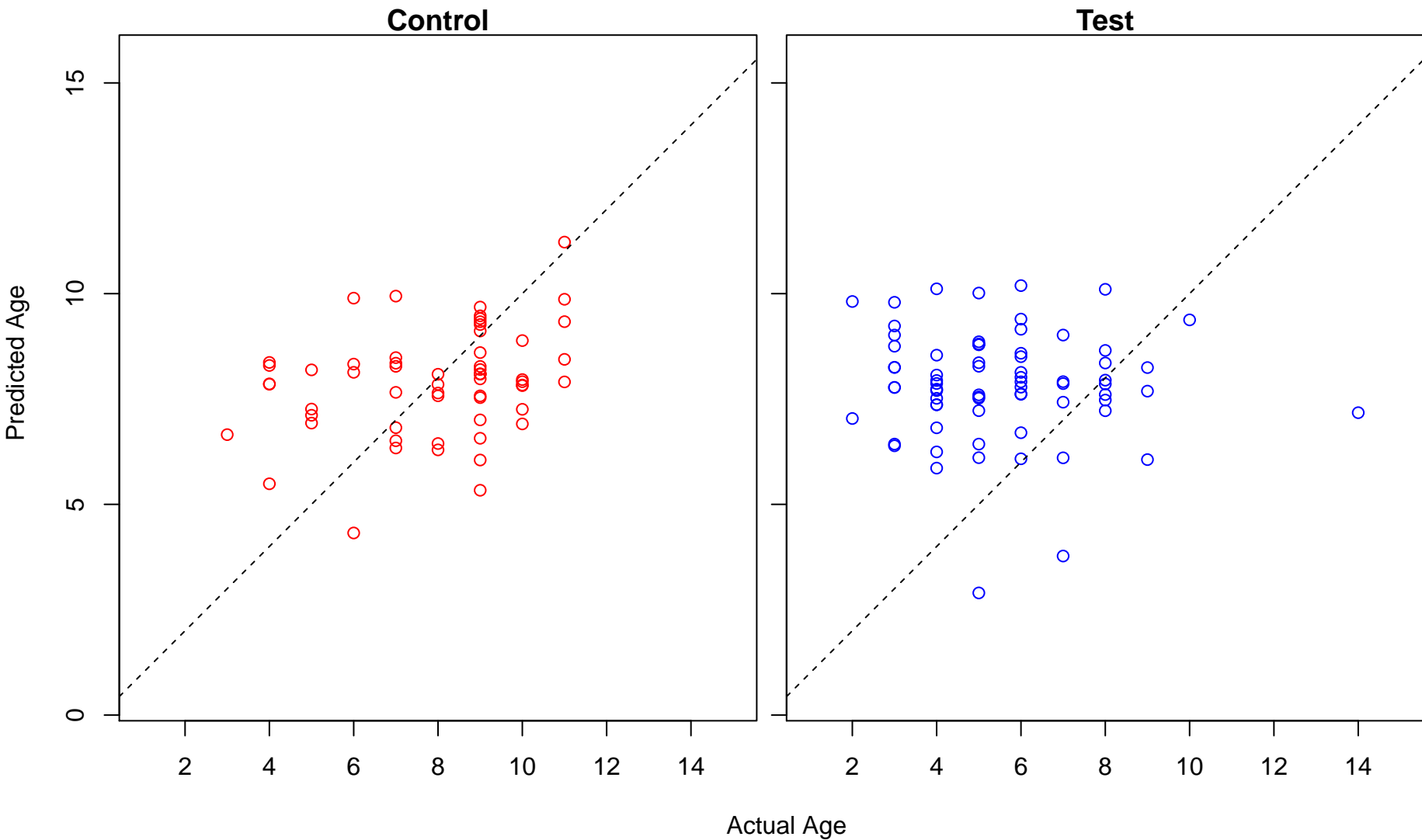
nickel cation transmembrane transport (Score: 0.567185)



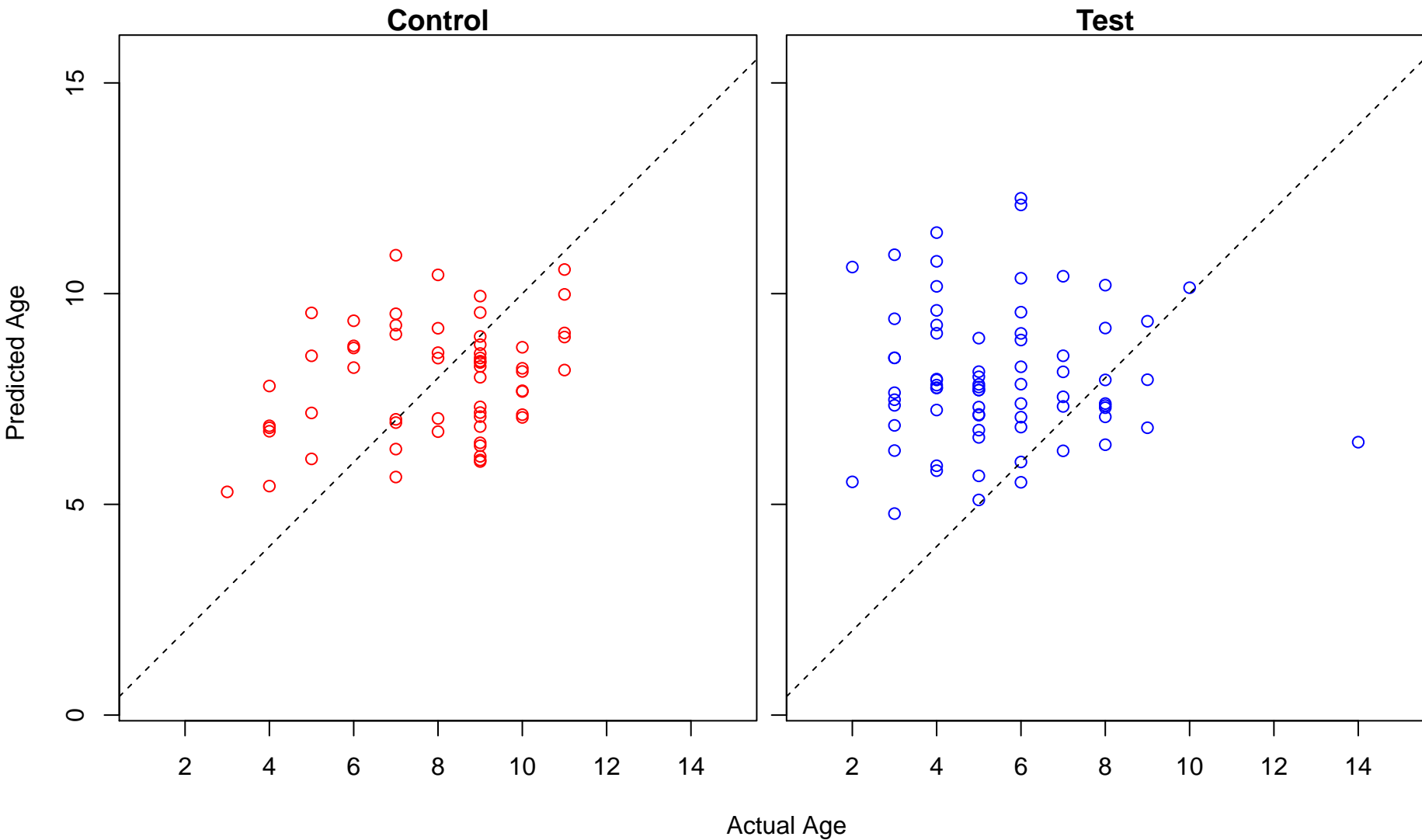
tube closure (Score: 0.567147)



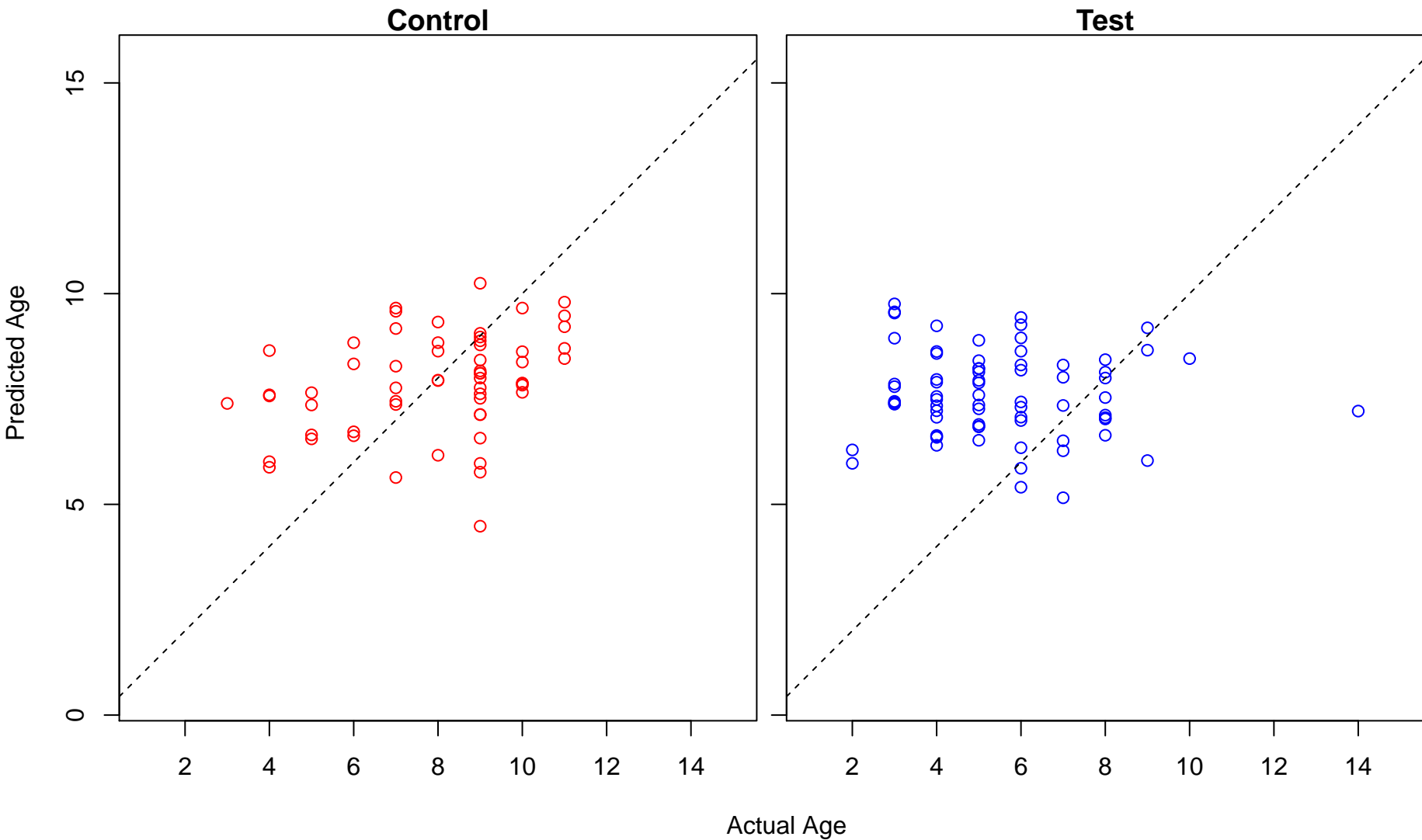
neural tube closure (Score: 0.567143)



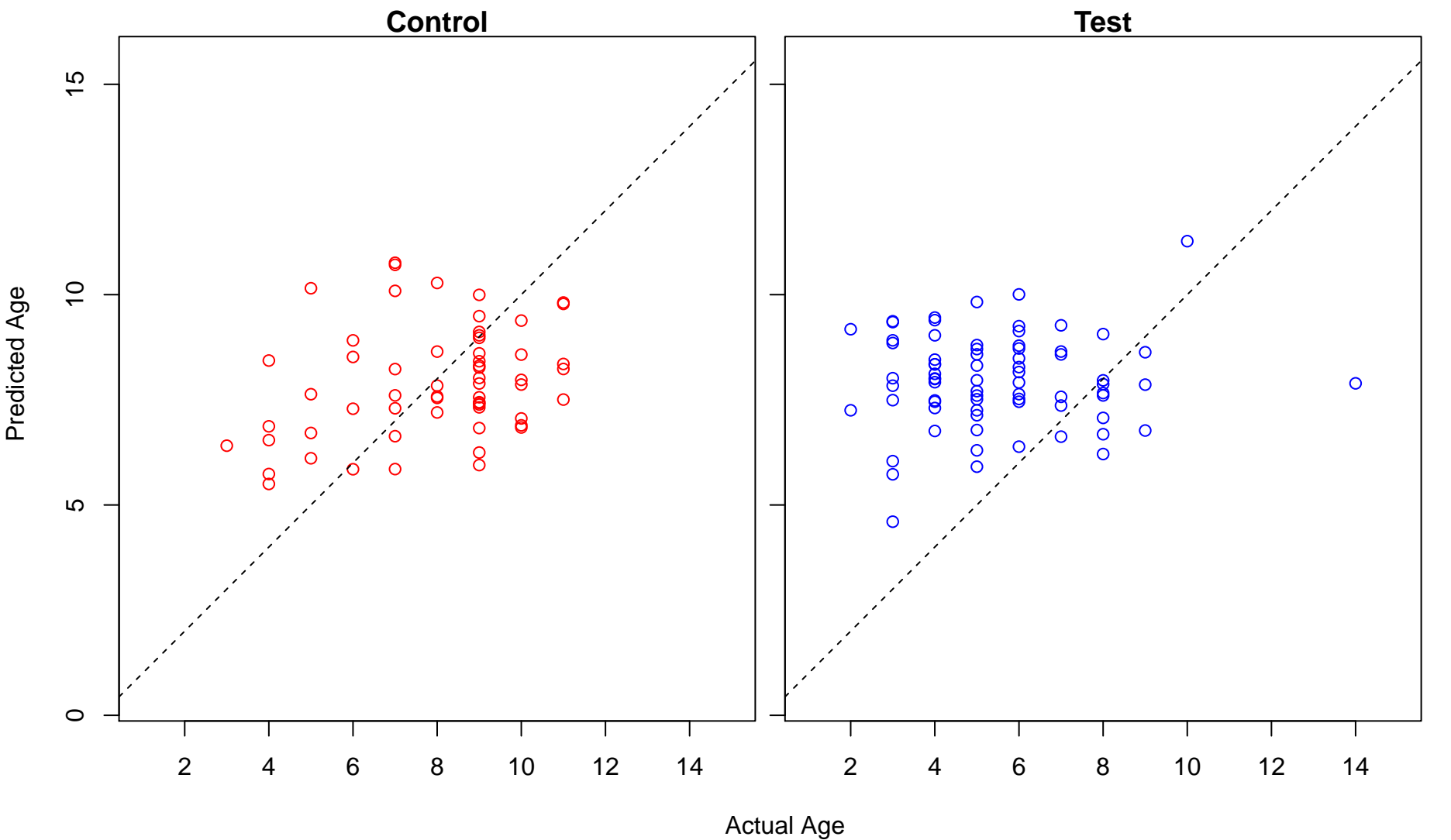
cardioblast differentiation (Score: 0.567034)



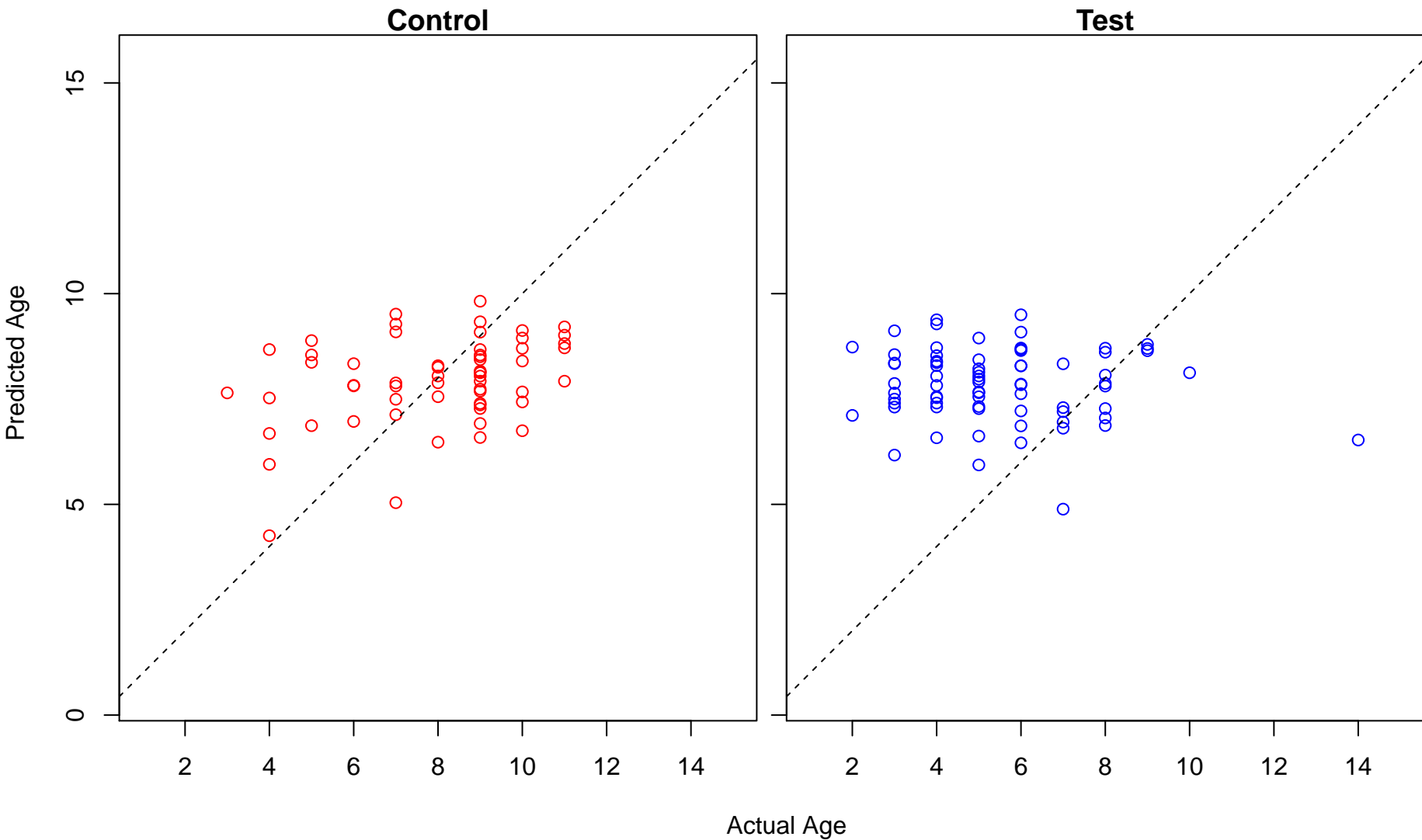
regulation of sequestering of zinc ion (Score: 0.566988)



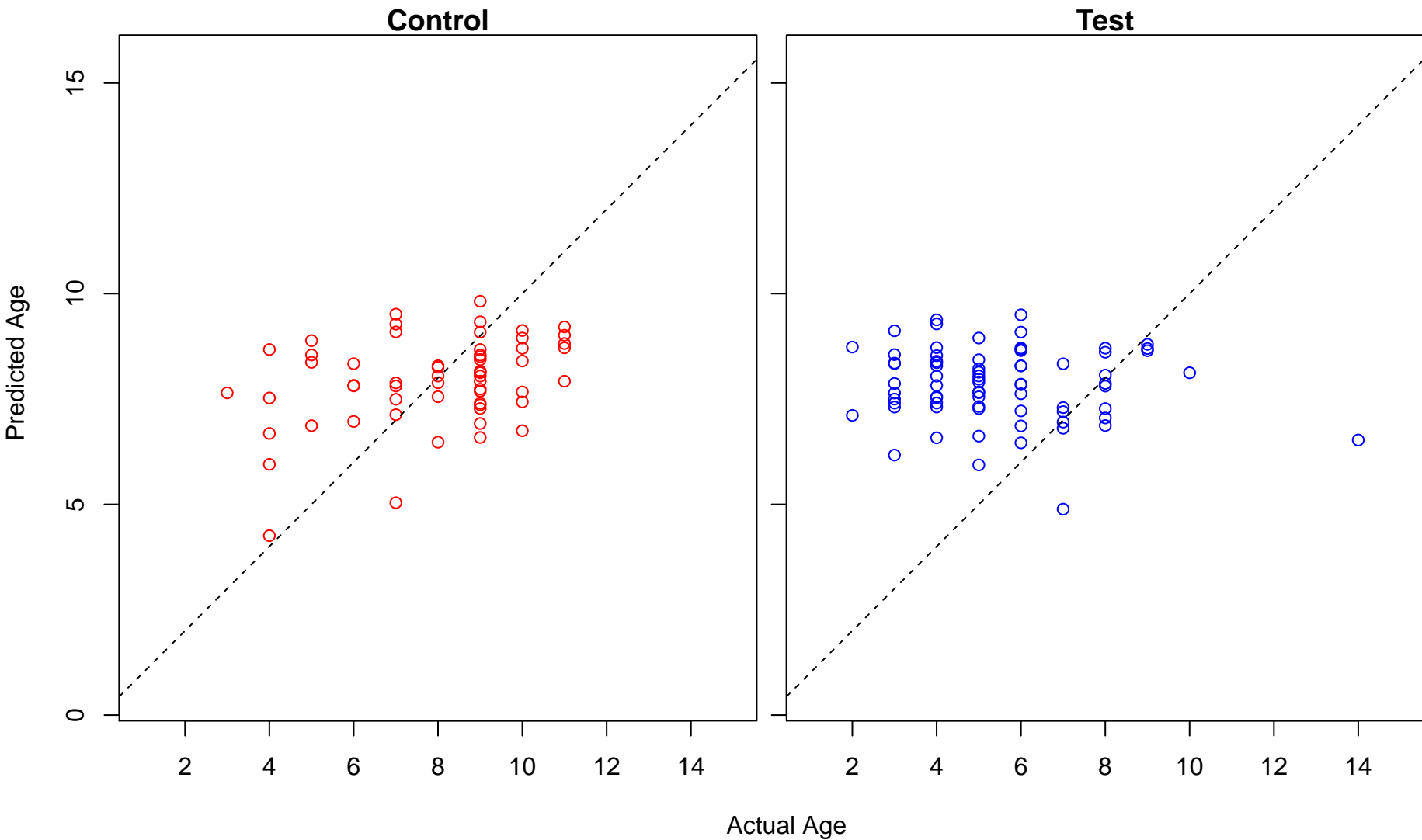
nucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay (Score)



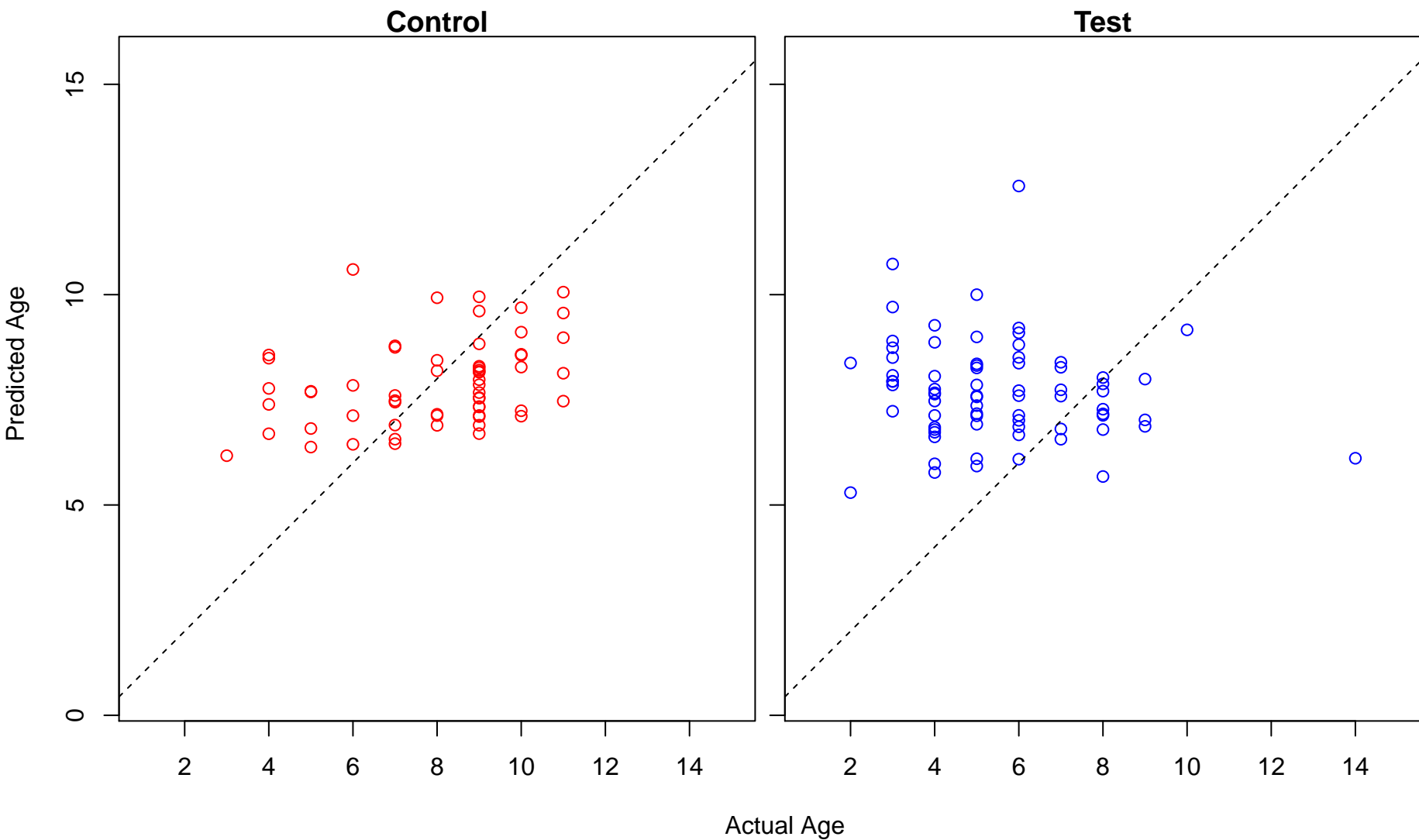
monoubiquitinated histone deubiquitination (Score: 0.566284)



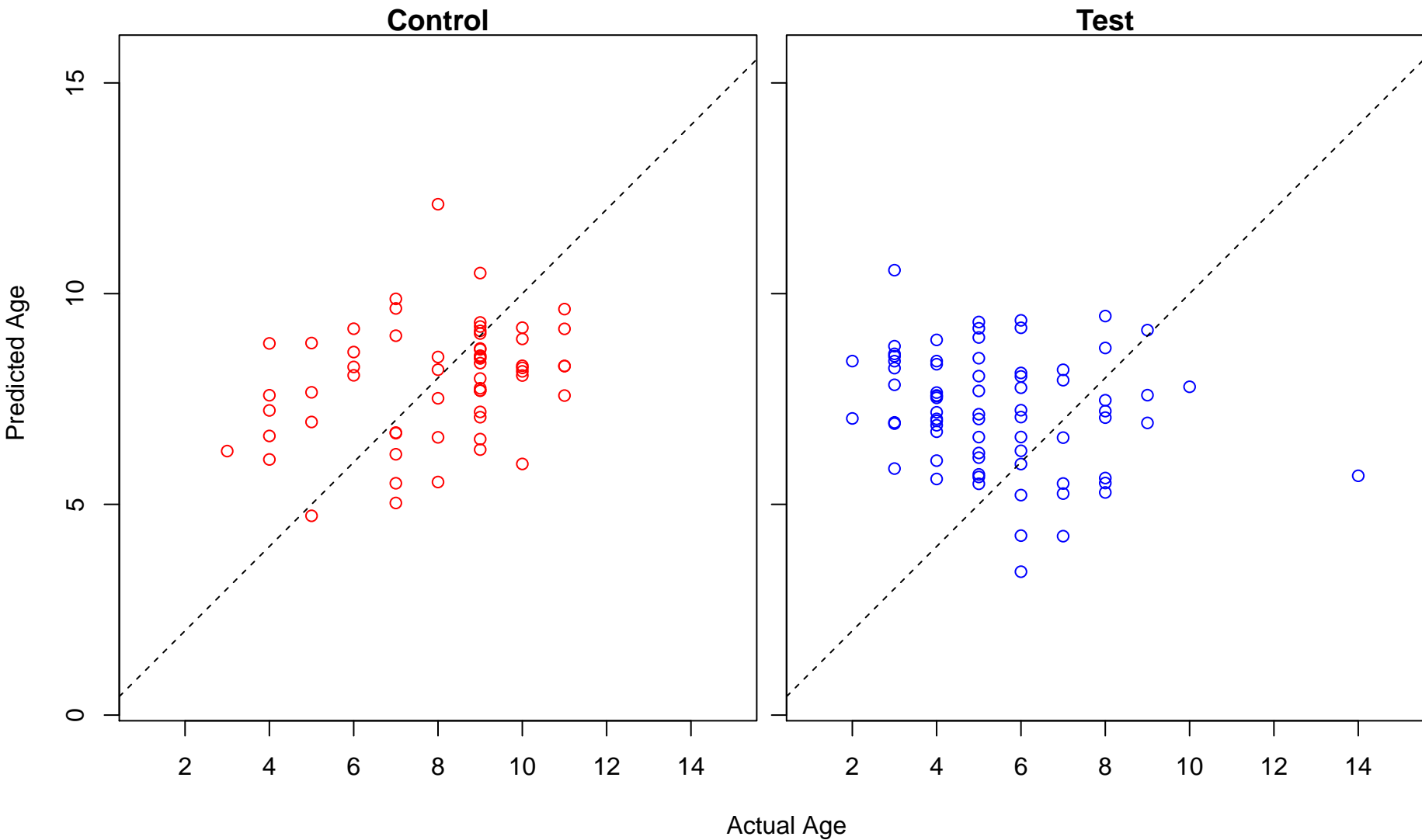
monoubiquitinated histone H2A deubiquitination (Score: 0.566284)



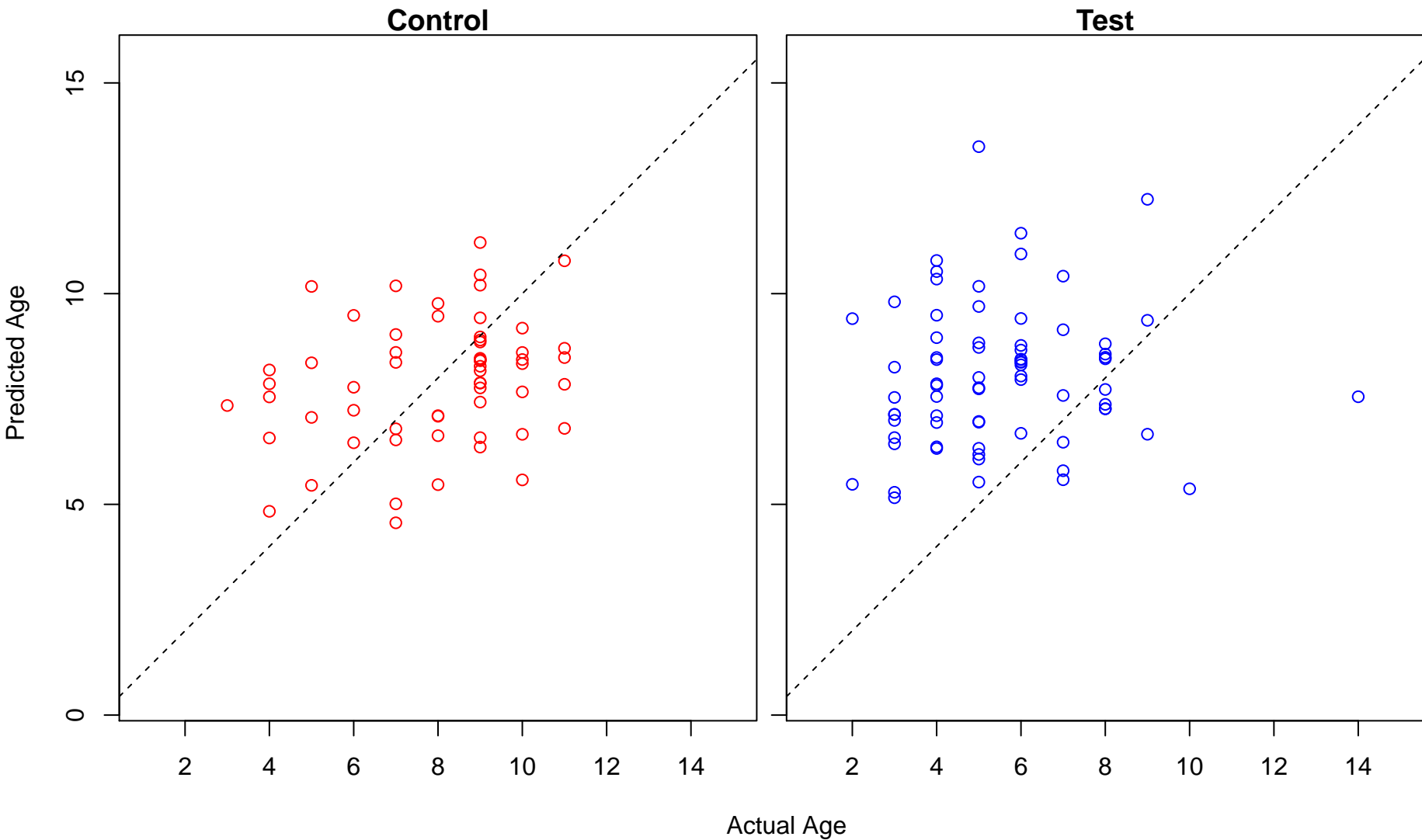
regulation of interleukin-13 secretion (Score: 0.565152)



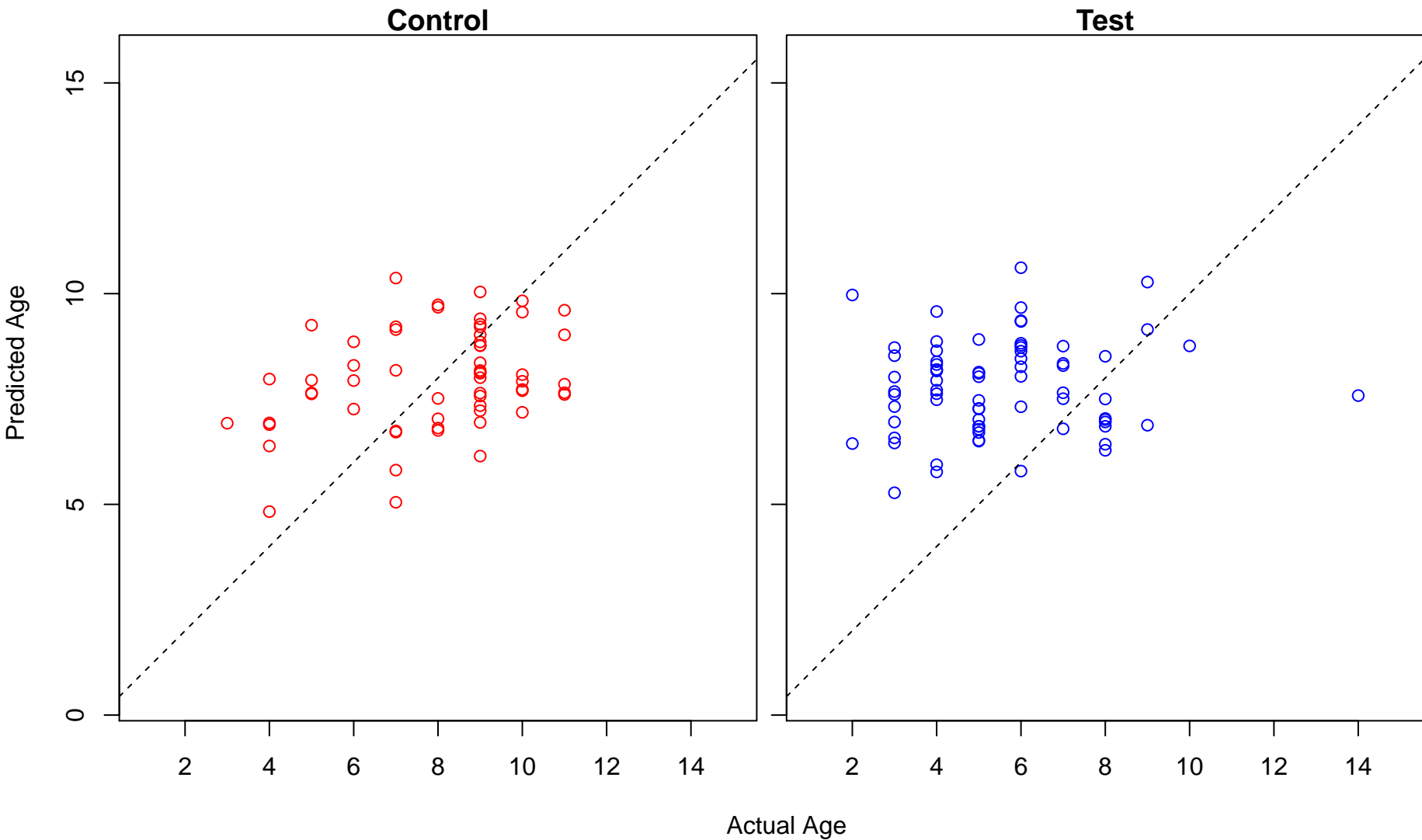
protein myristoylation (Score: 0.562533)



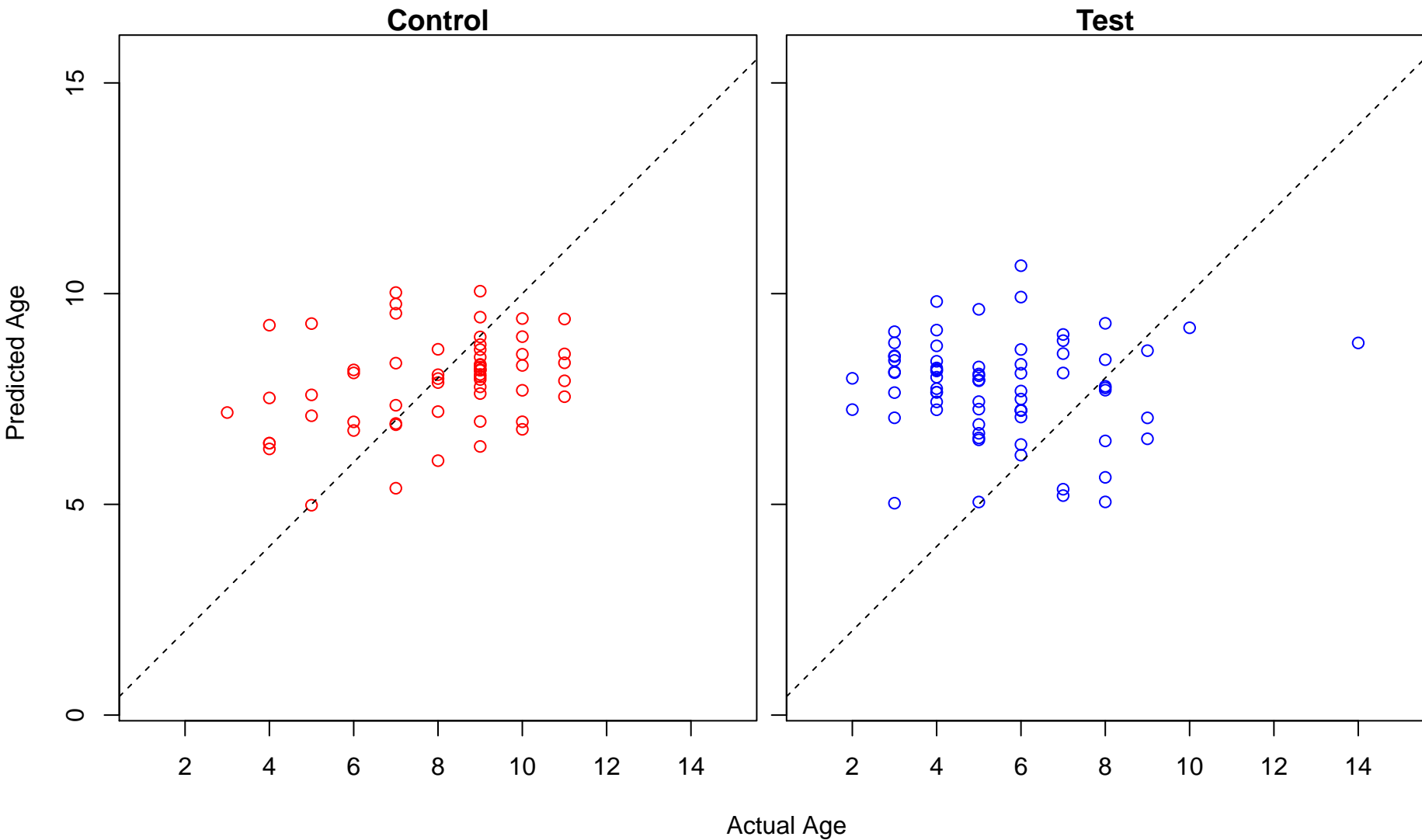
negative regulation of translational initiation (Score: 0.561939)



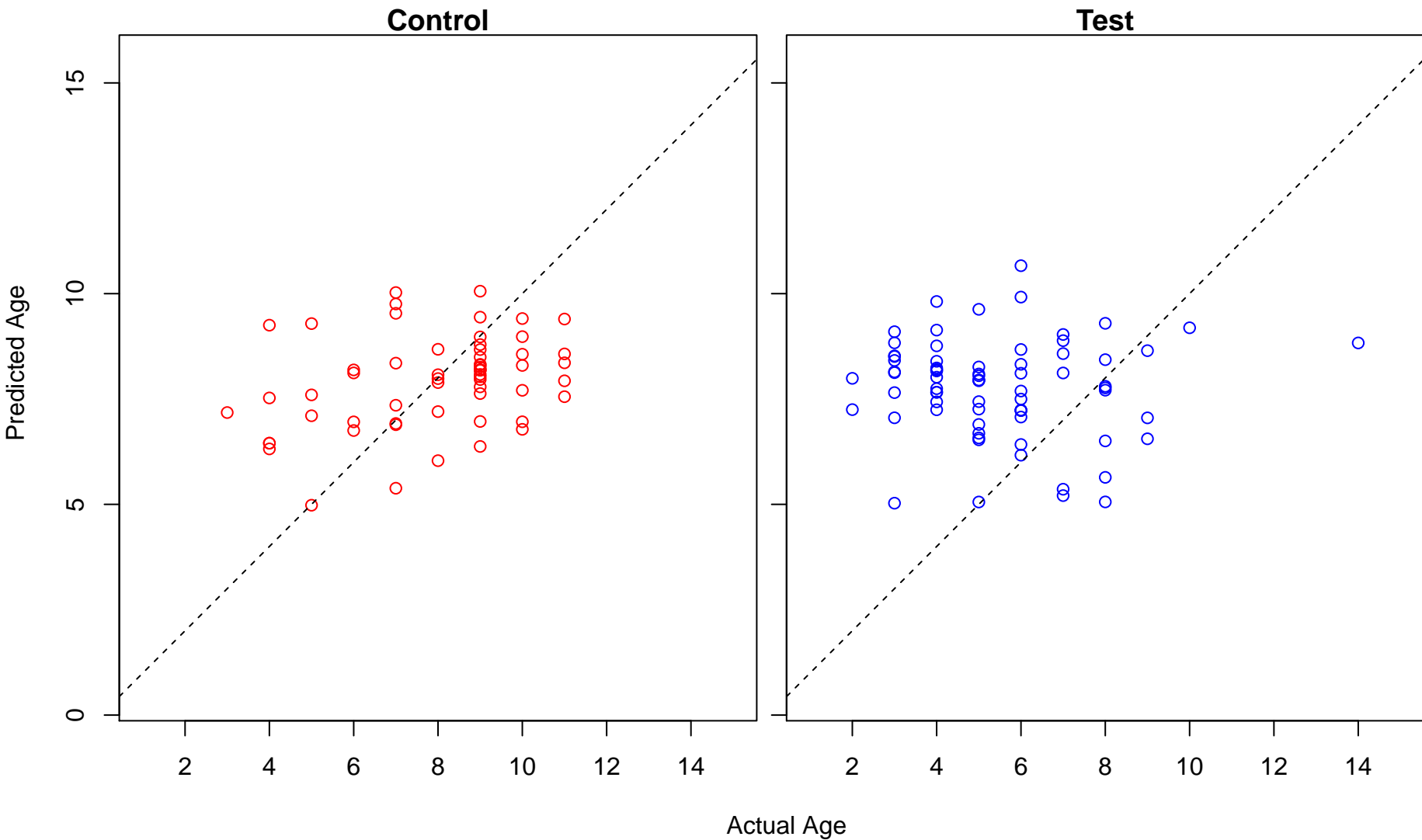
regulation of epidermal cell differentiation (Score: 0.561844)



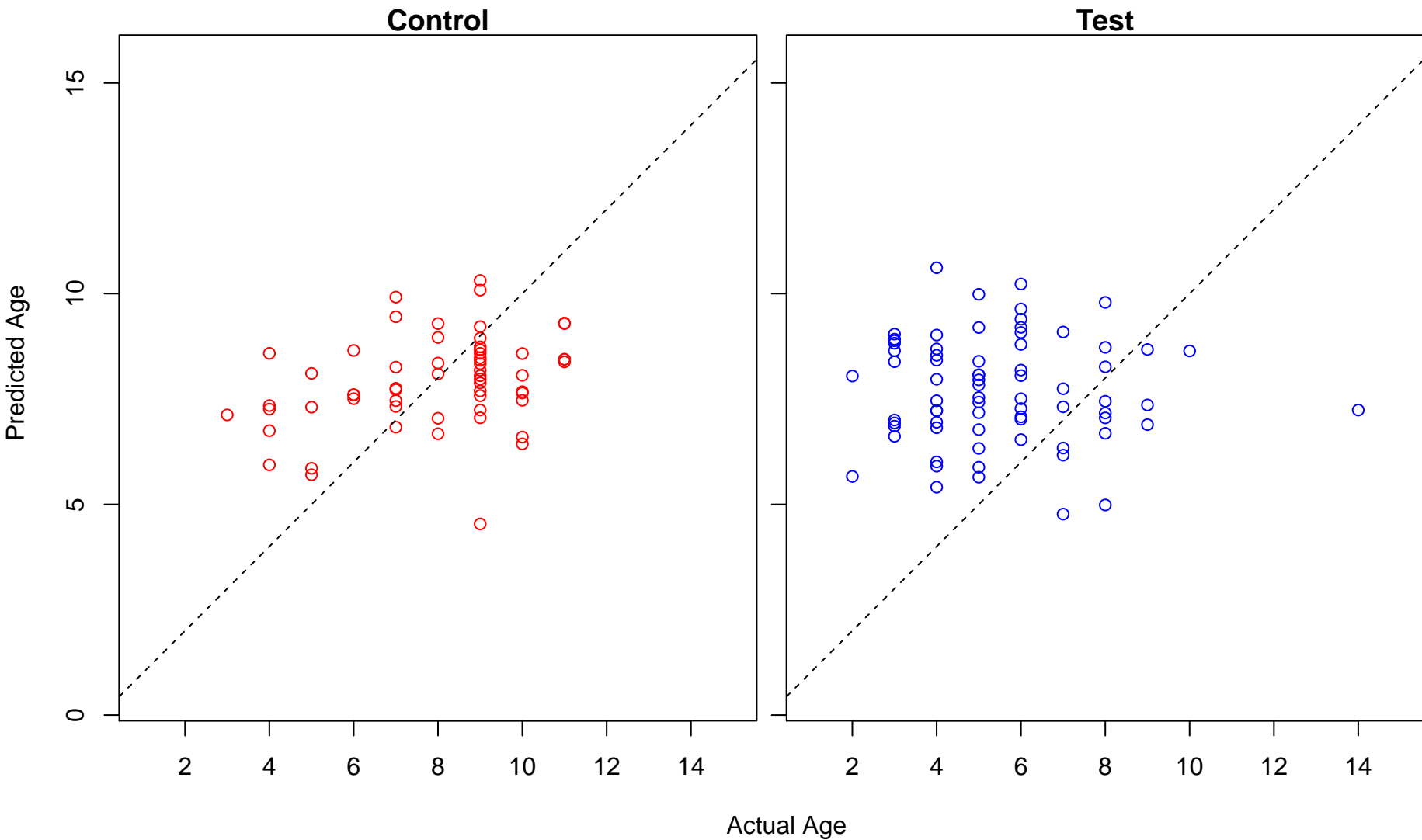
negative regulation of response to interferon-gamma (Score: 0.560994)



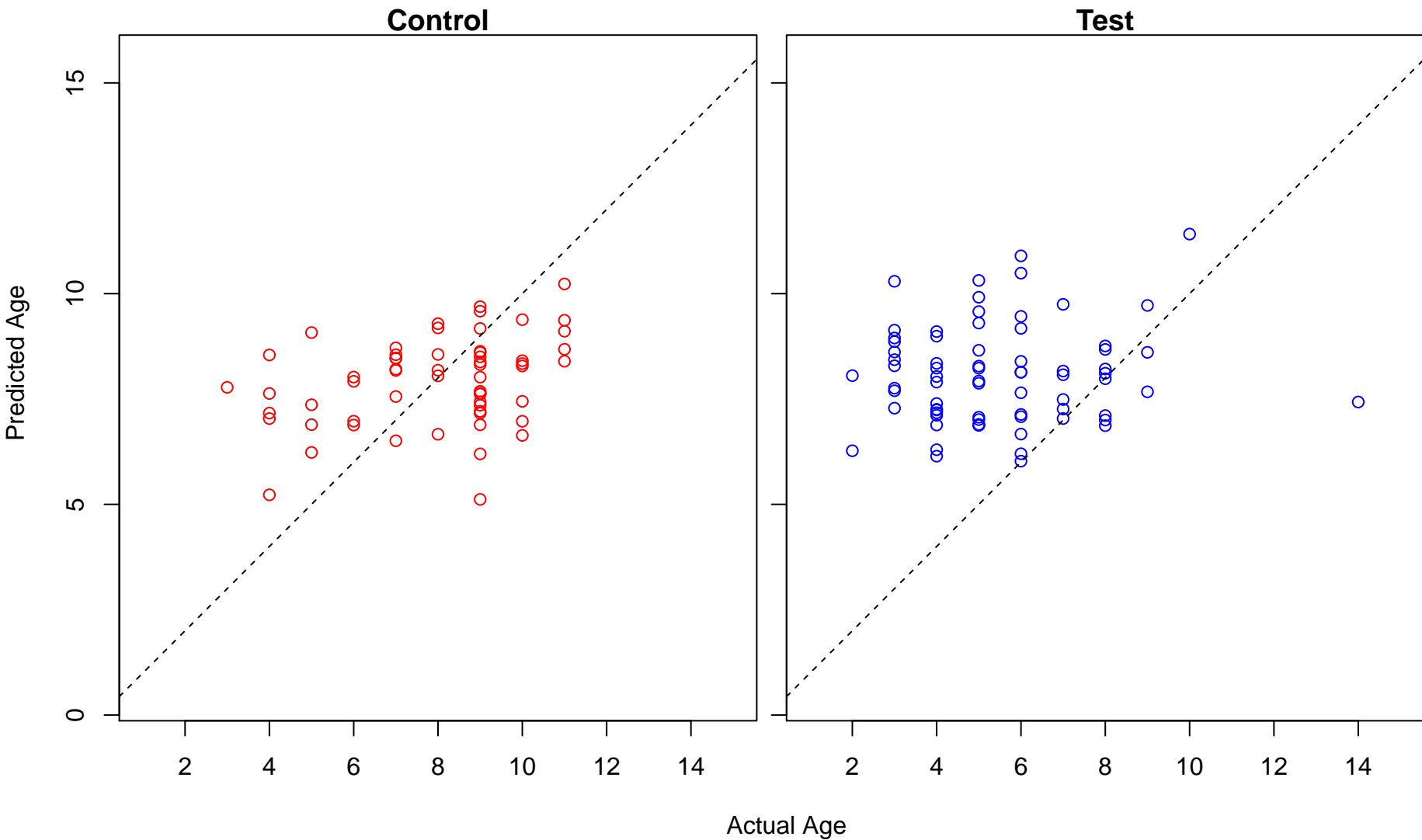
negative regulation of interferon-gamma-mediated signaling pathway (Score: 0.560994)



response to ammonium ion (Score: 0.558557)

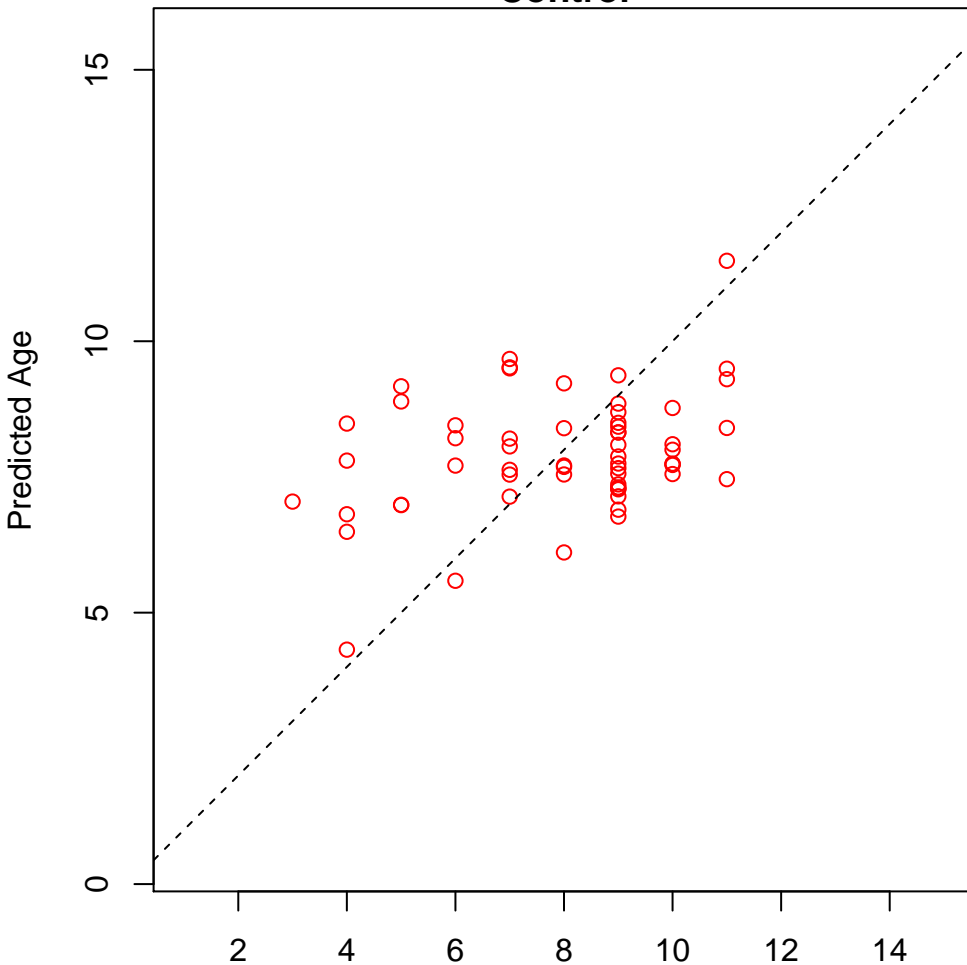


protein linear polyubiquitination (Score: 0.558275)

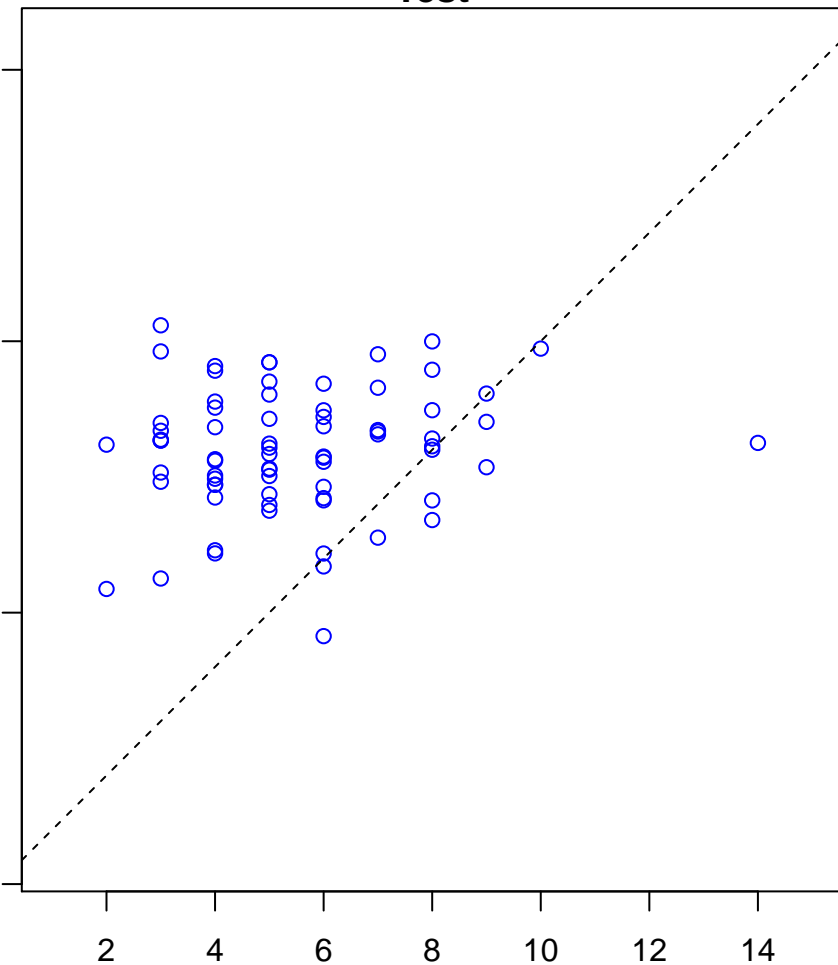


metanephric renal vesicle formation (Score: 0.557810)

Control

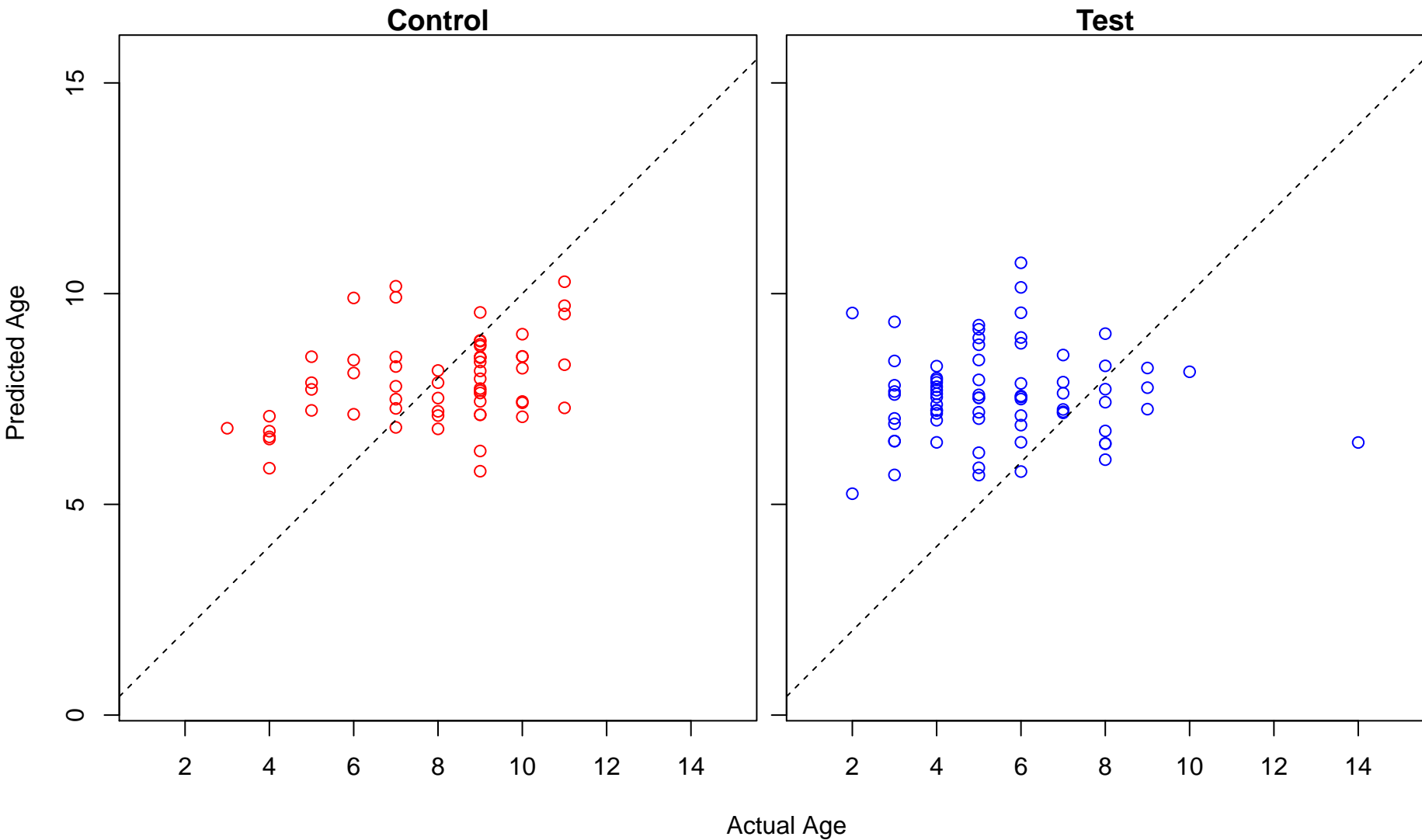


Test

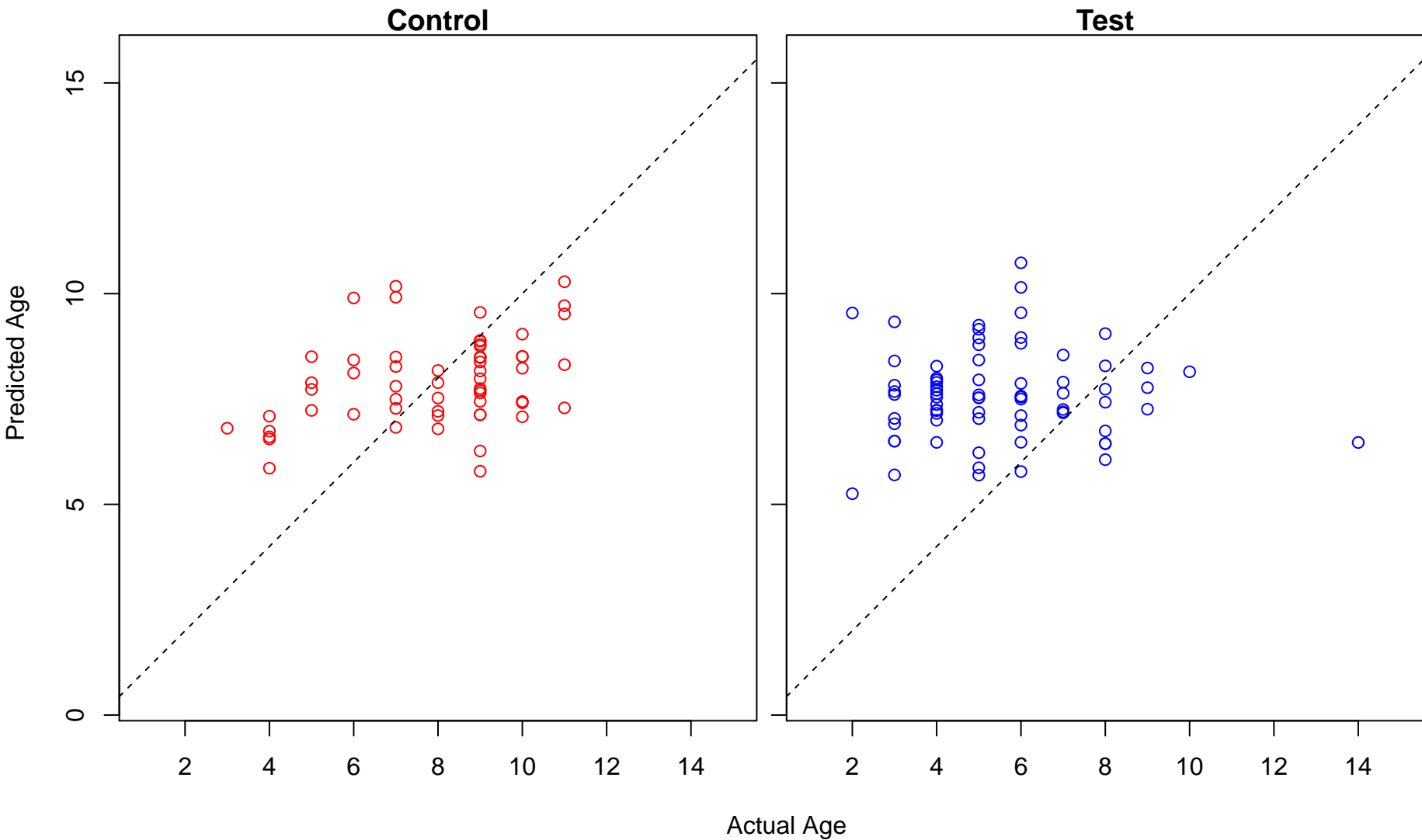


Actual Age

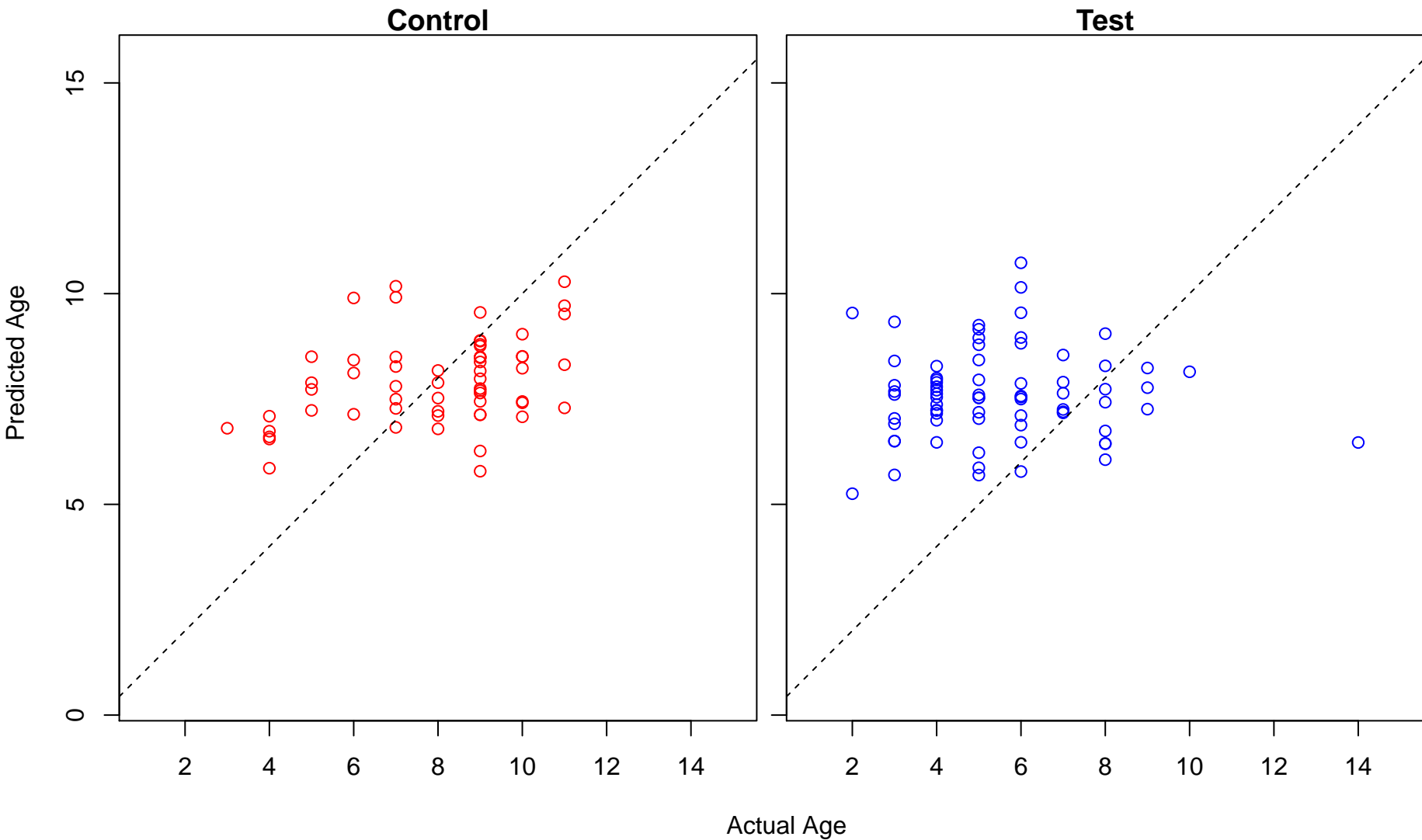
ferric iron transport (Score: 0.557700)



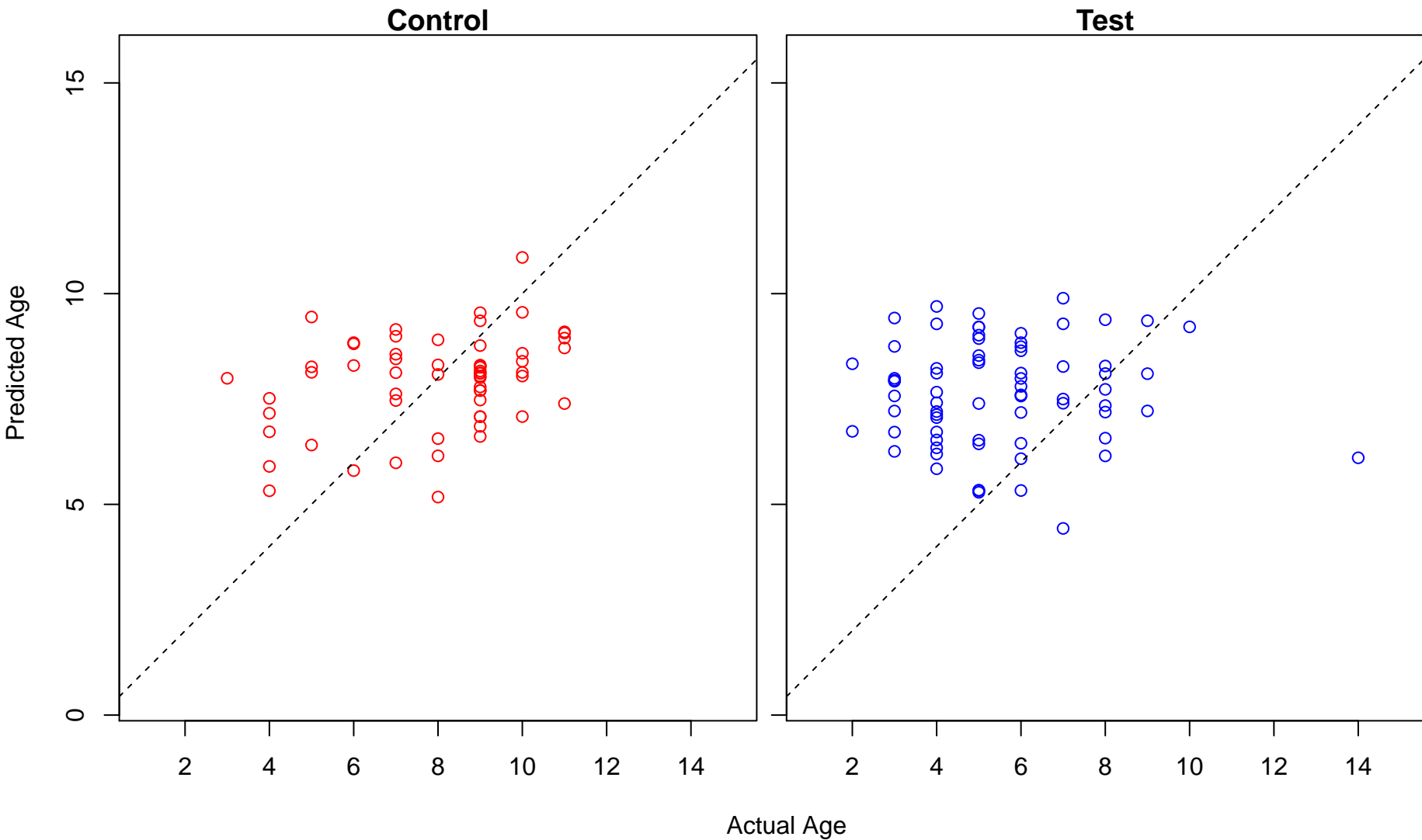
transferrin transport (Score: 0.557700)



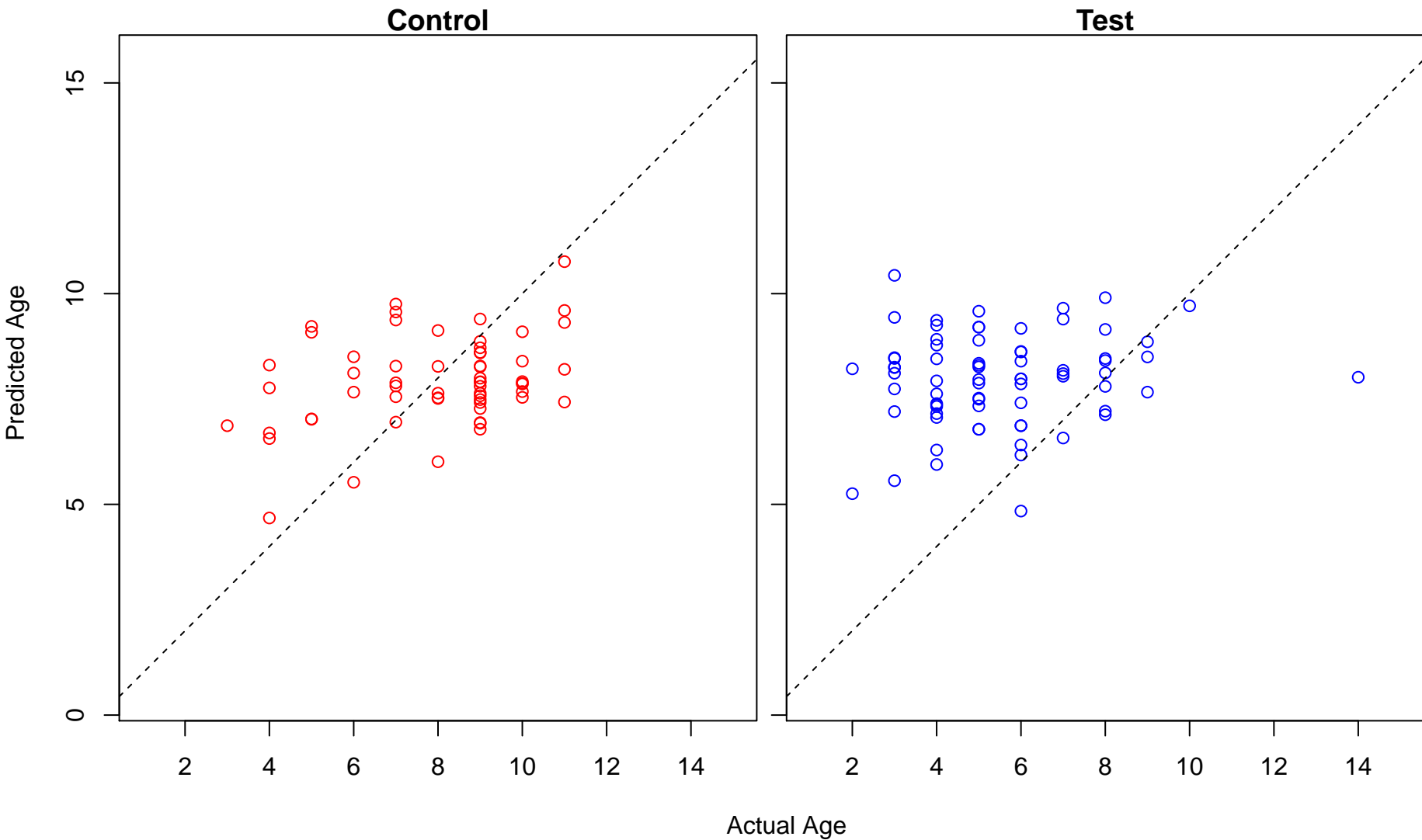
trivalent inorganic cation transport (Score: 0.557700)



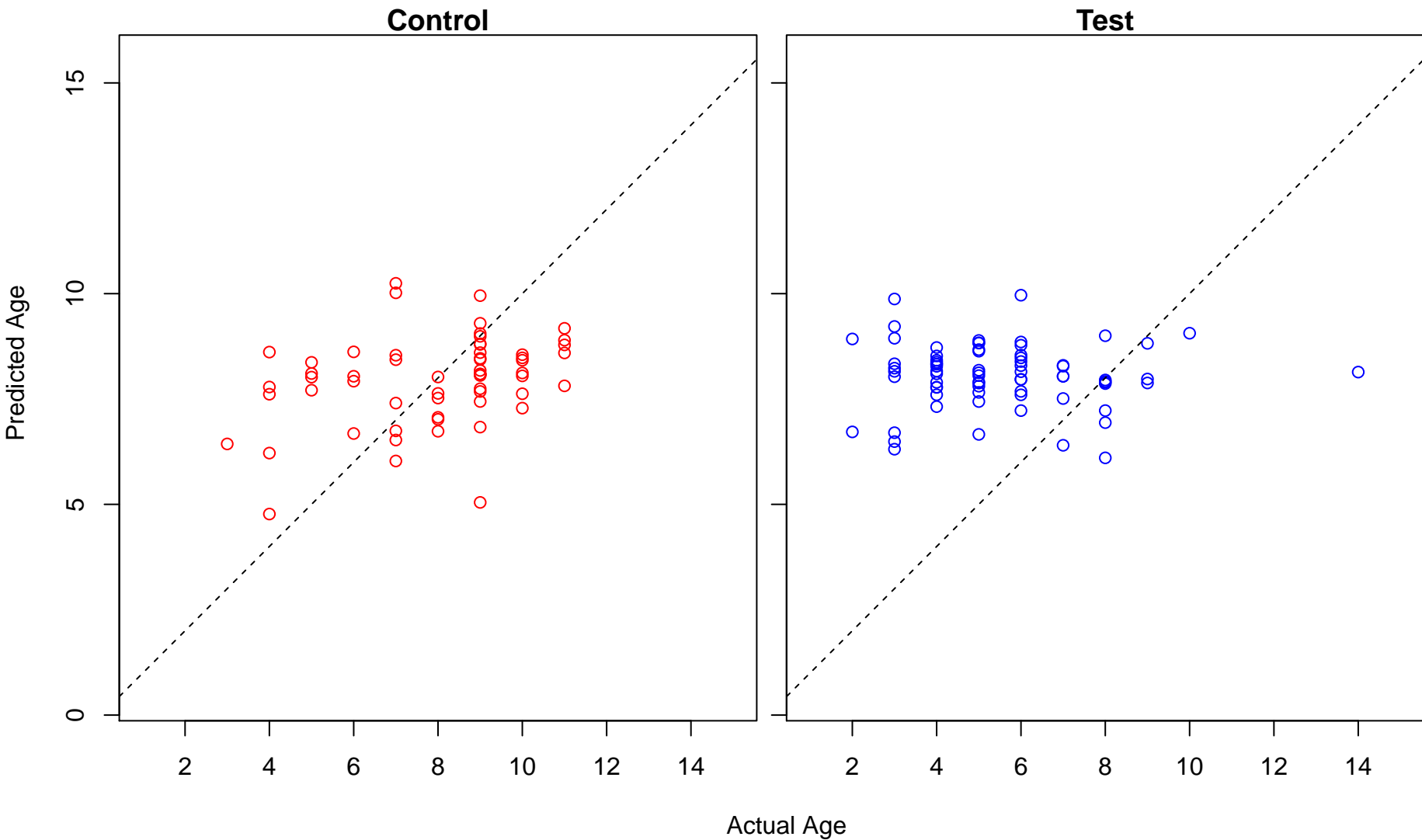
asymmetric neuroblast division (Score: 0.556378)



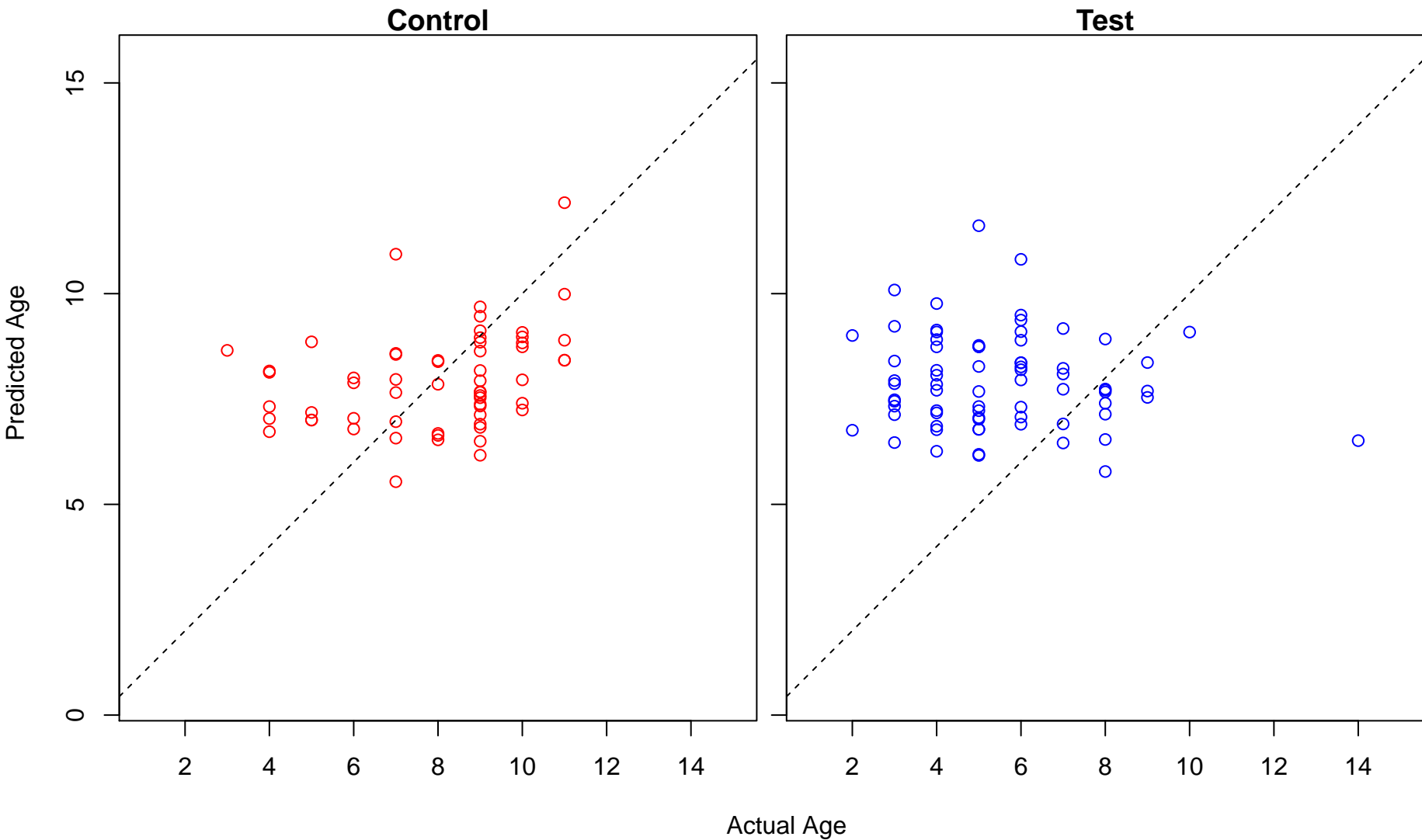
ureteric bud invasion (Score: 0.556348)



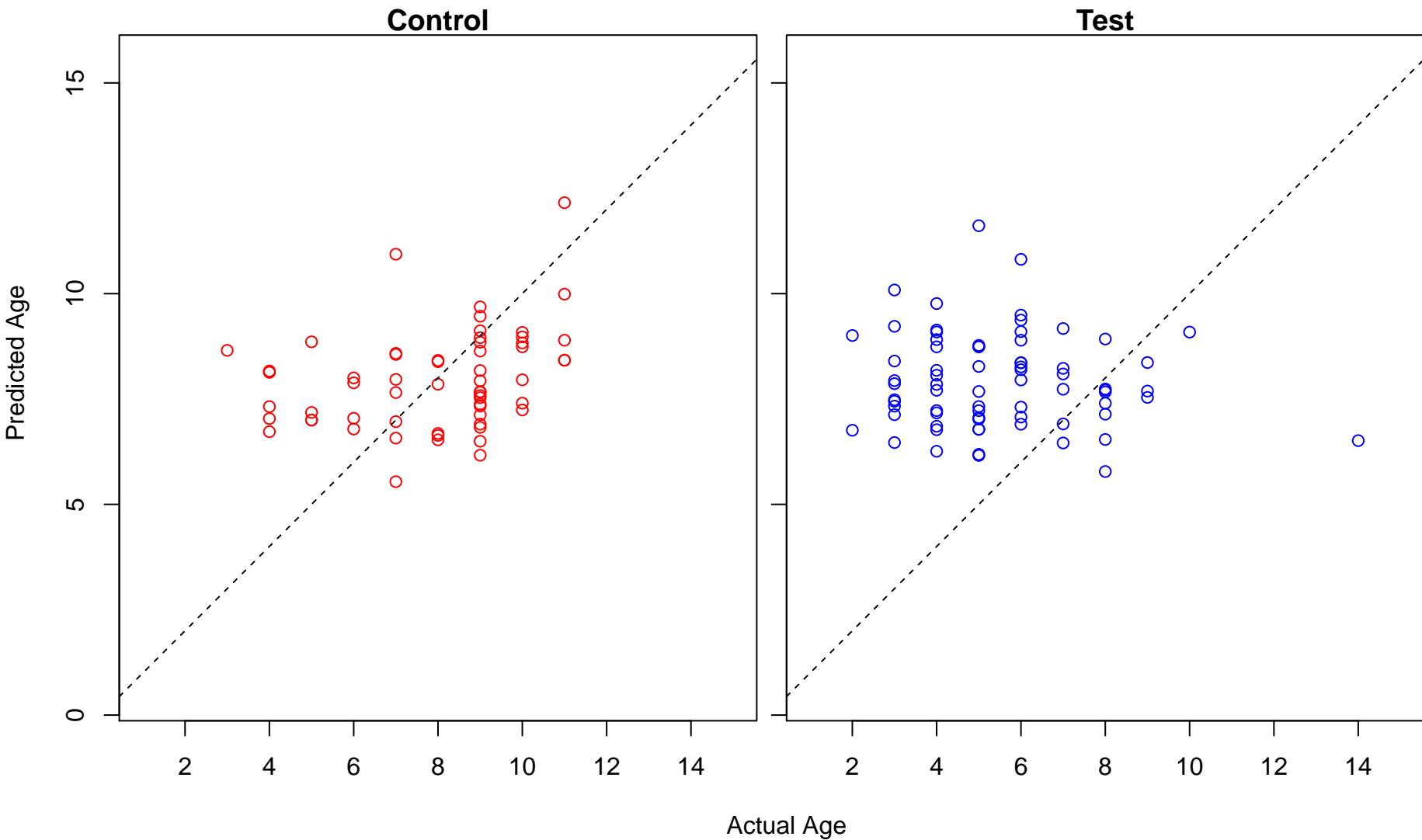
post-embryonic organ development (Score: 0.556325)



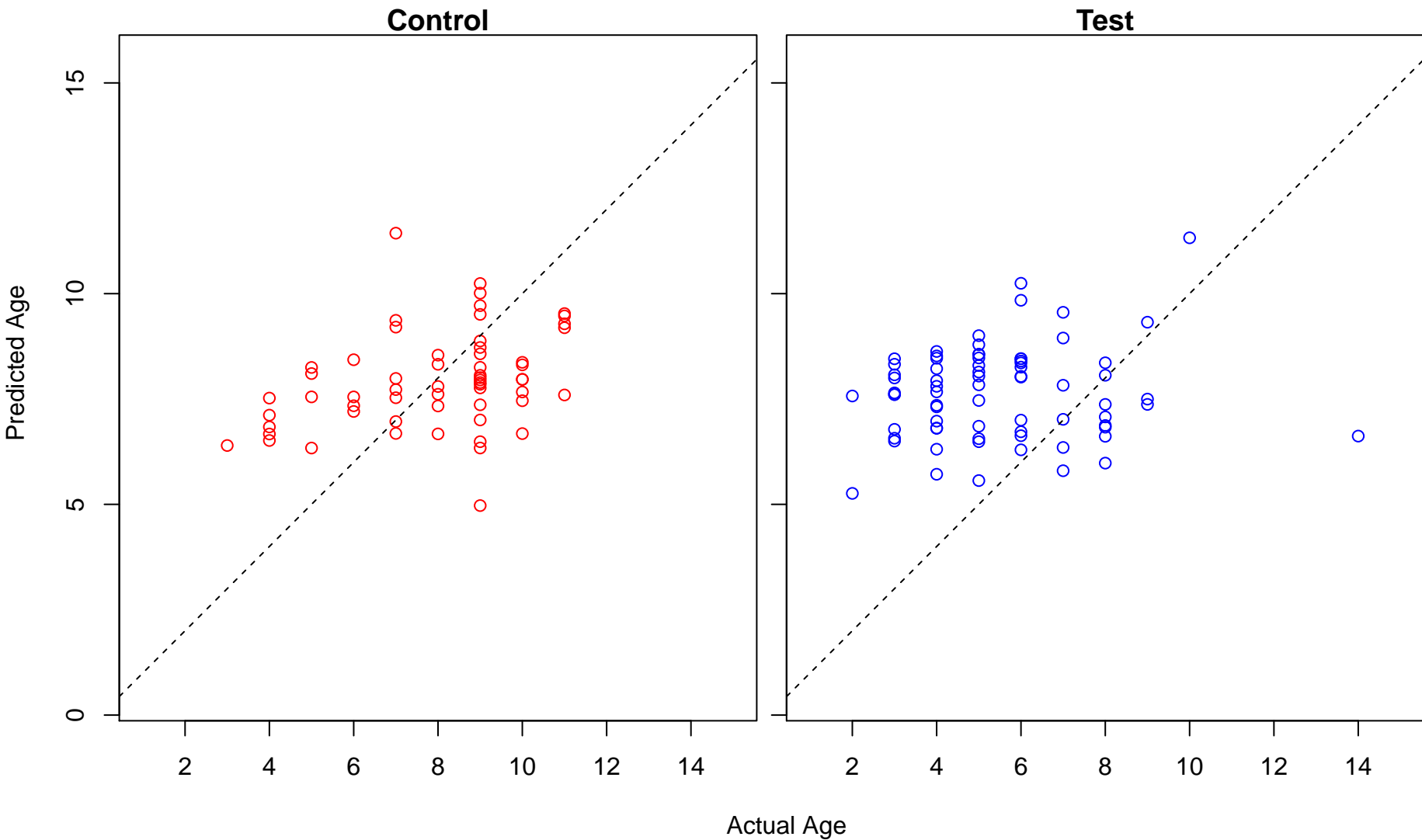
loop of Henle development (Score: 0.555748)



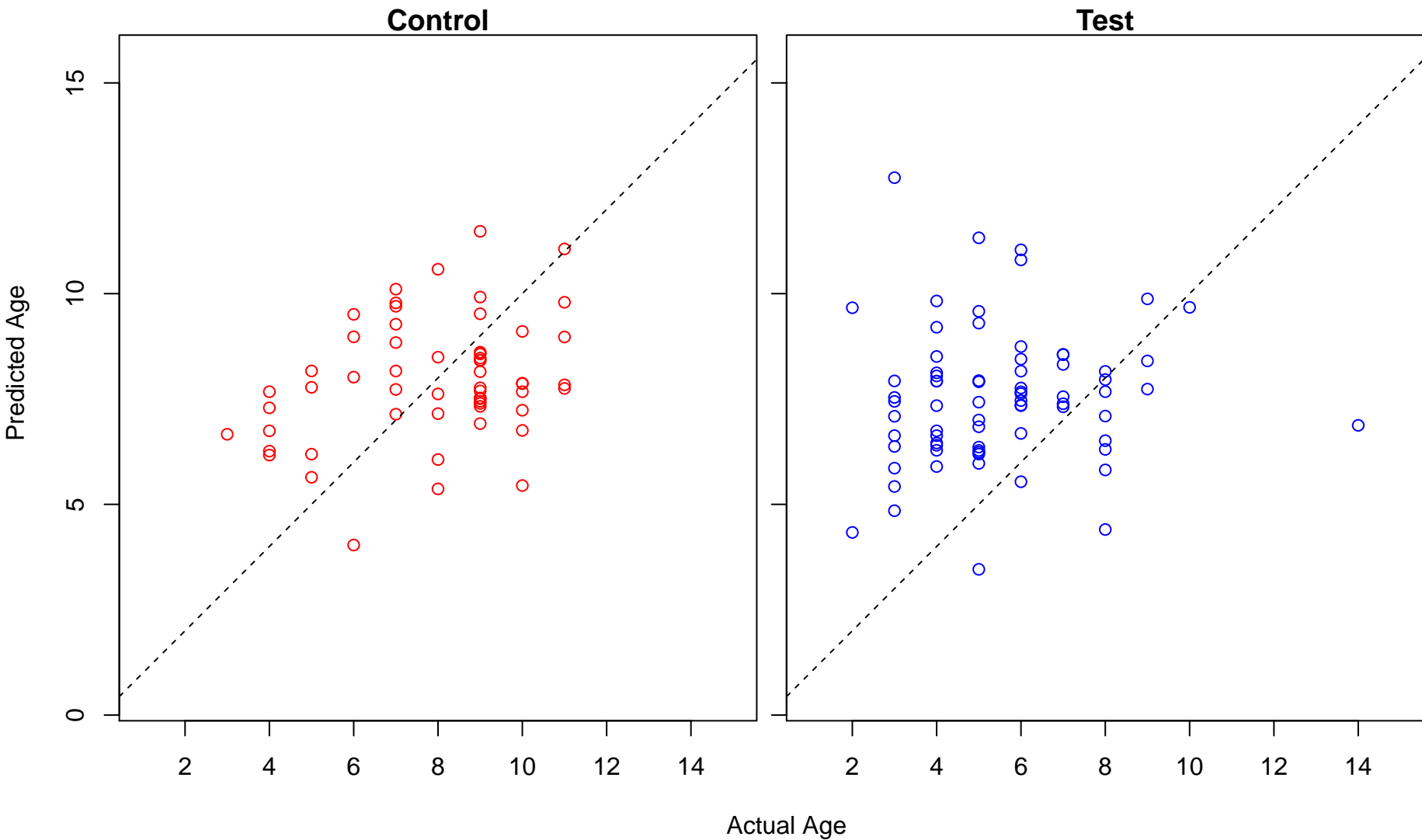
metanephric loop of Henle development (Score: 0.555748)



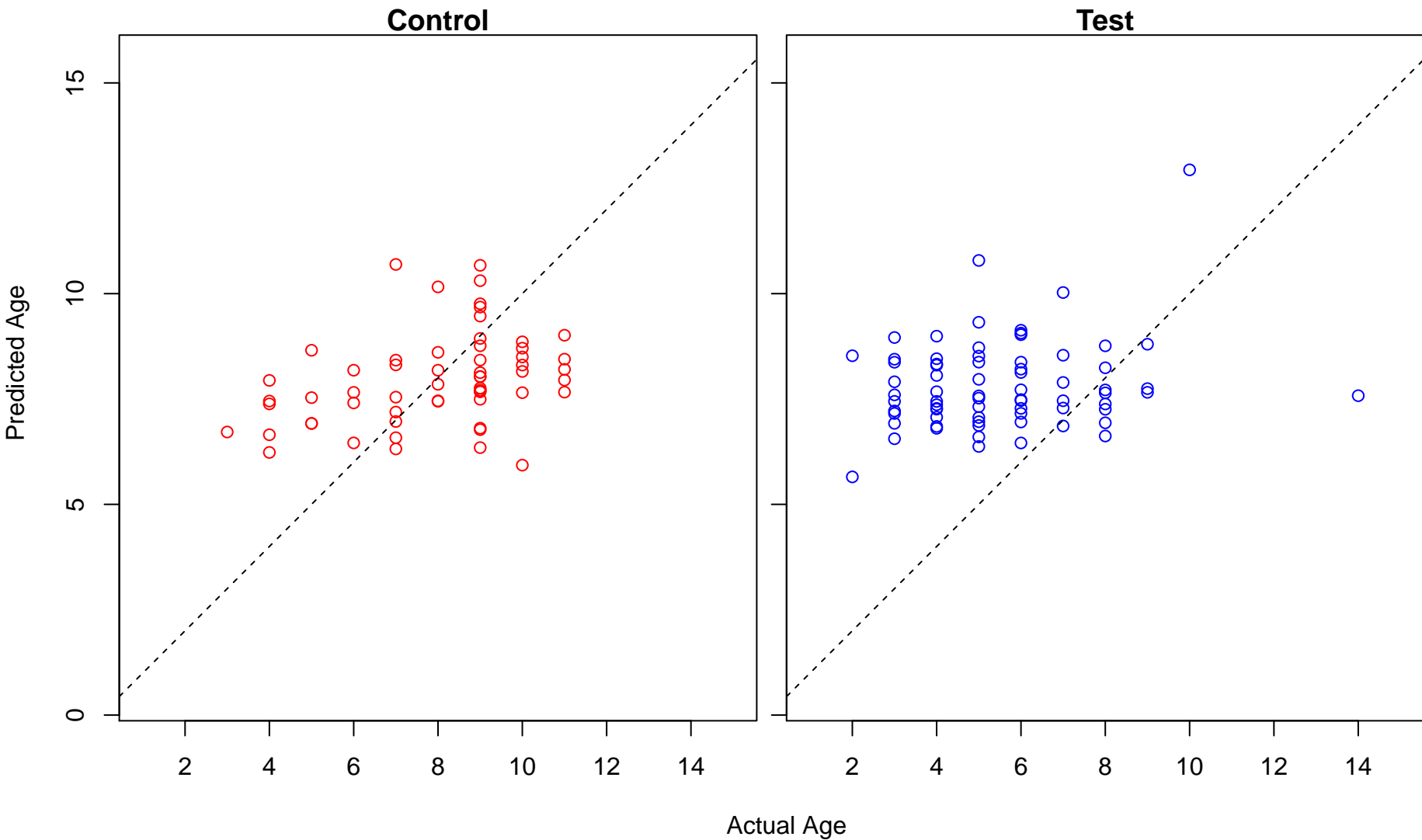
pinocytosis (Score: 0.554936)



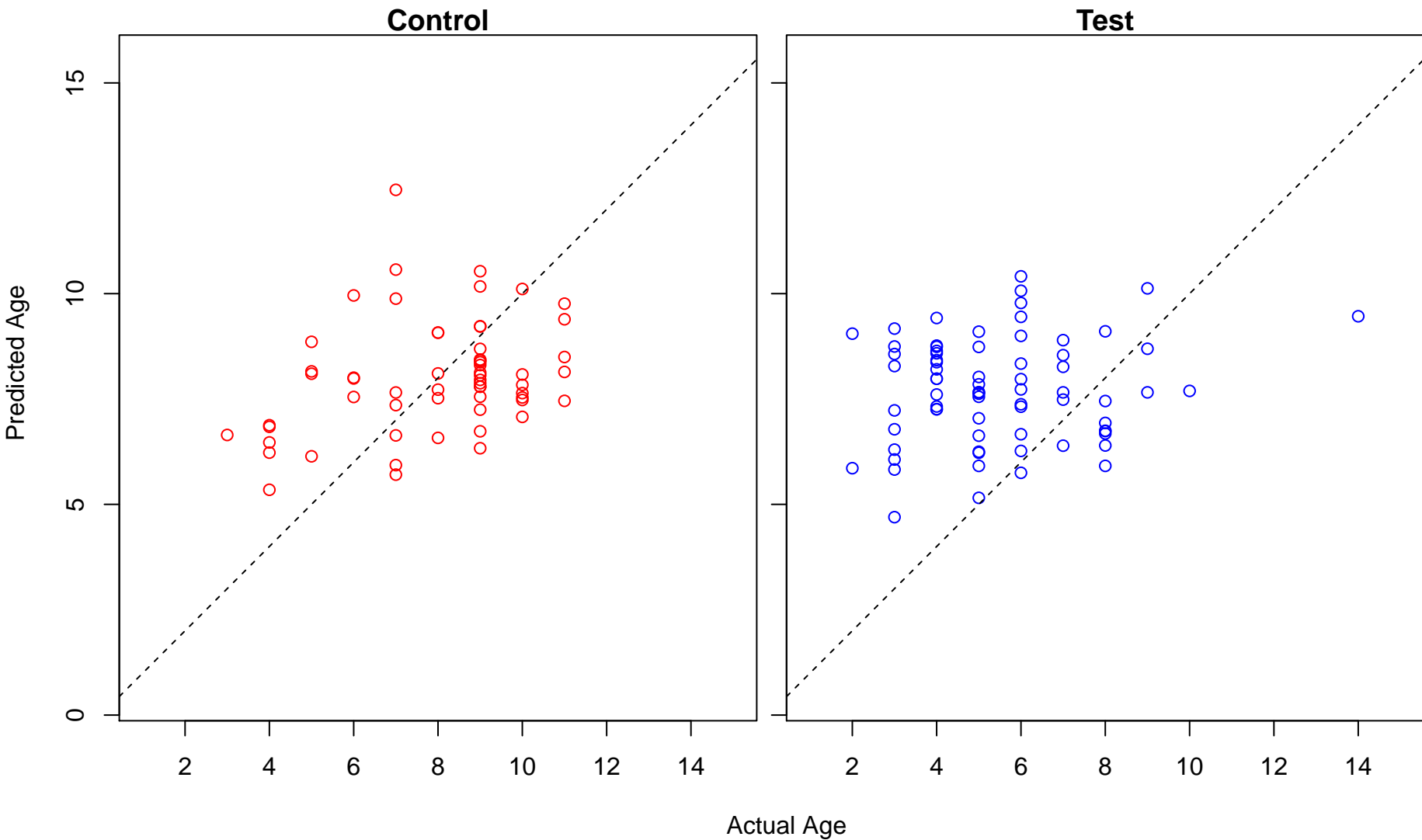
positive regulation of toll-like receptor signaling pathway (Score: 0.554113)



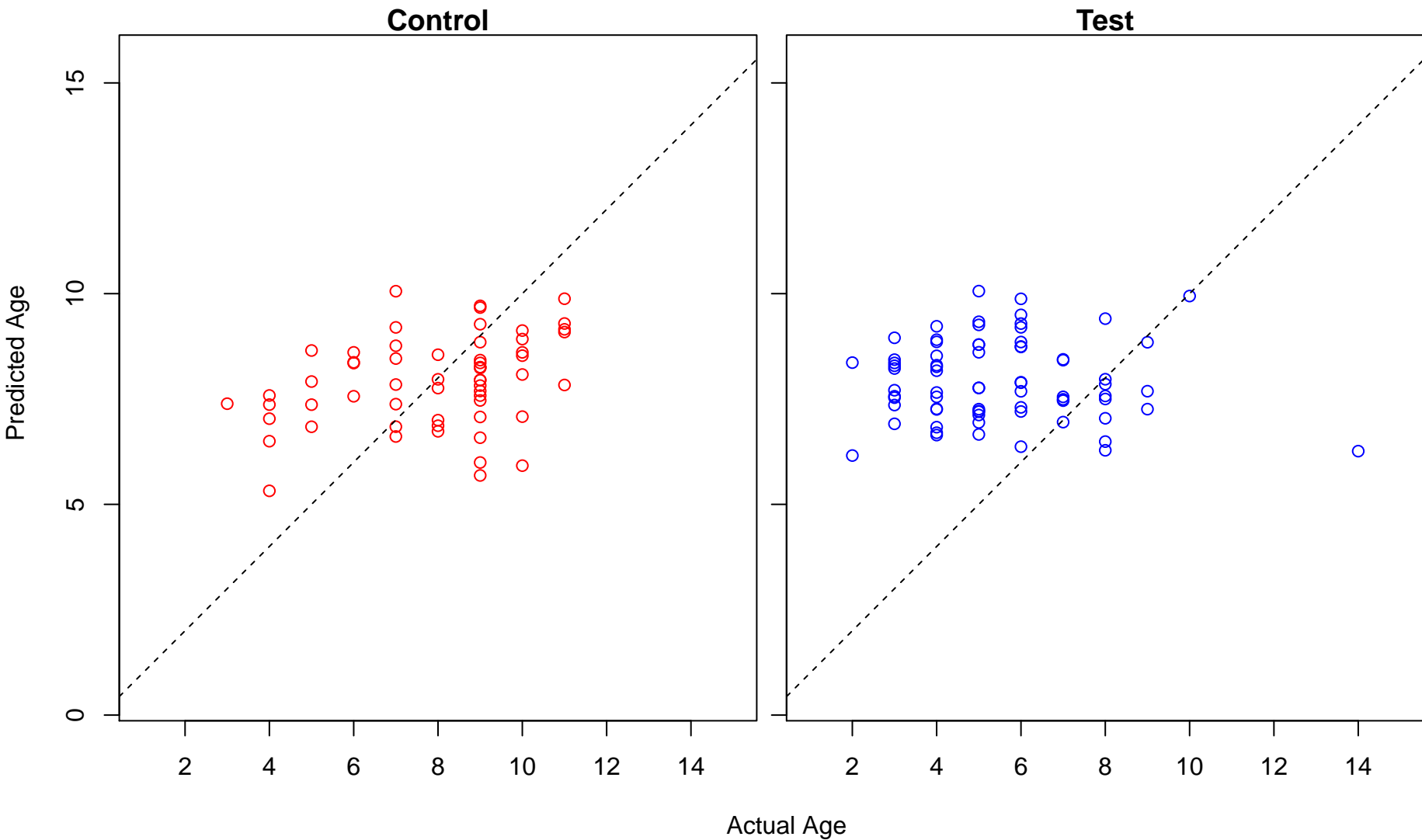
thiamine-containing compound metabolic process (Score: 0.554066)



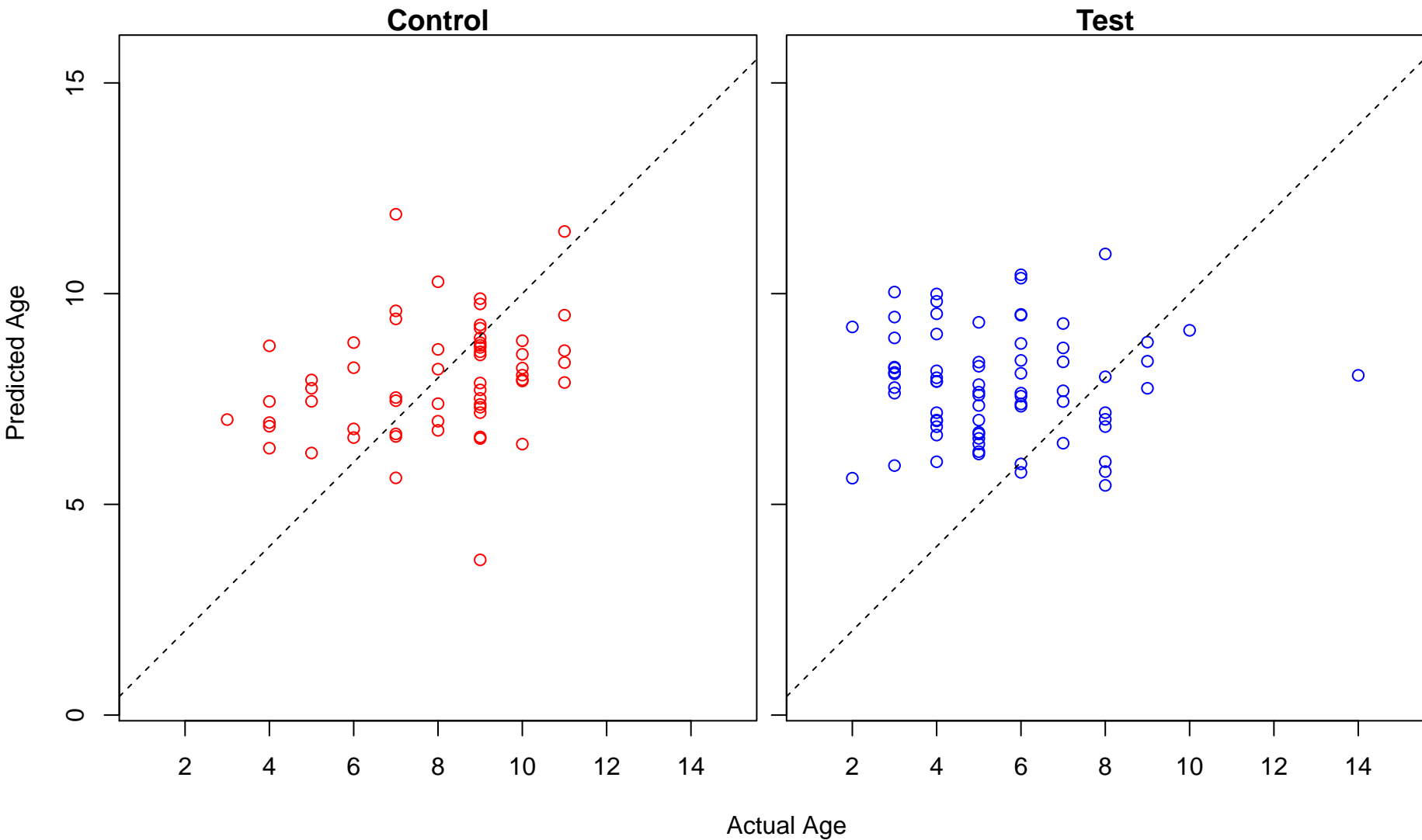
negative regulation of binding (Score: 0.554018)



beta-amyloid metabolic process (Score: 0.552424)

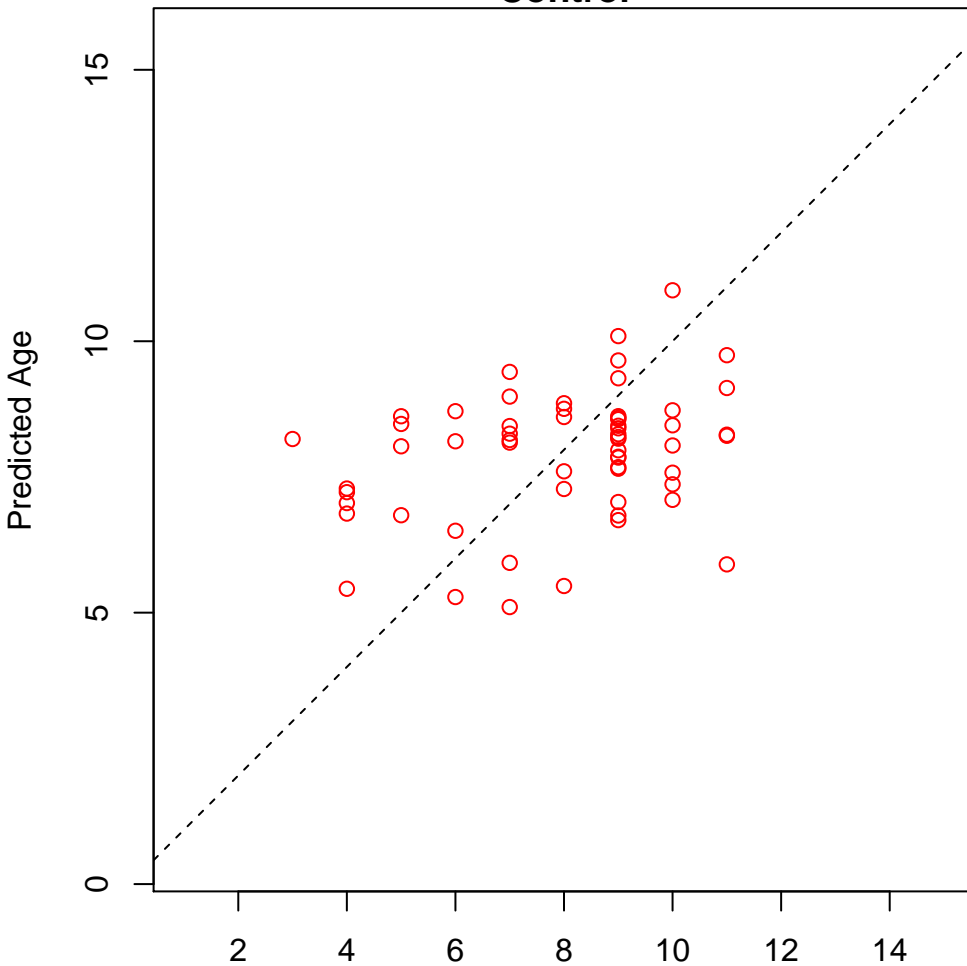


establishment or maintenance of cell polarity (Score: 0.552187)

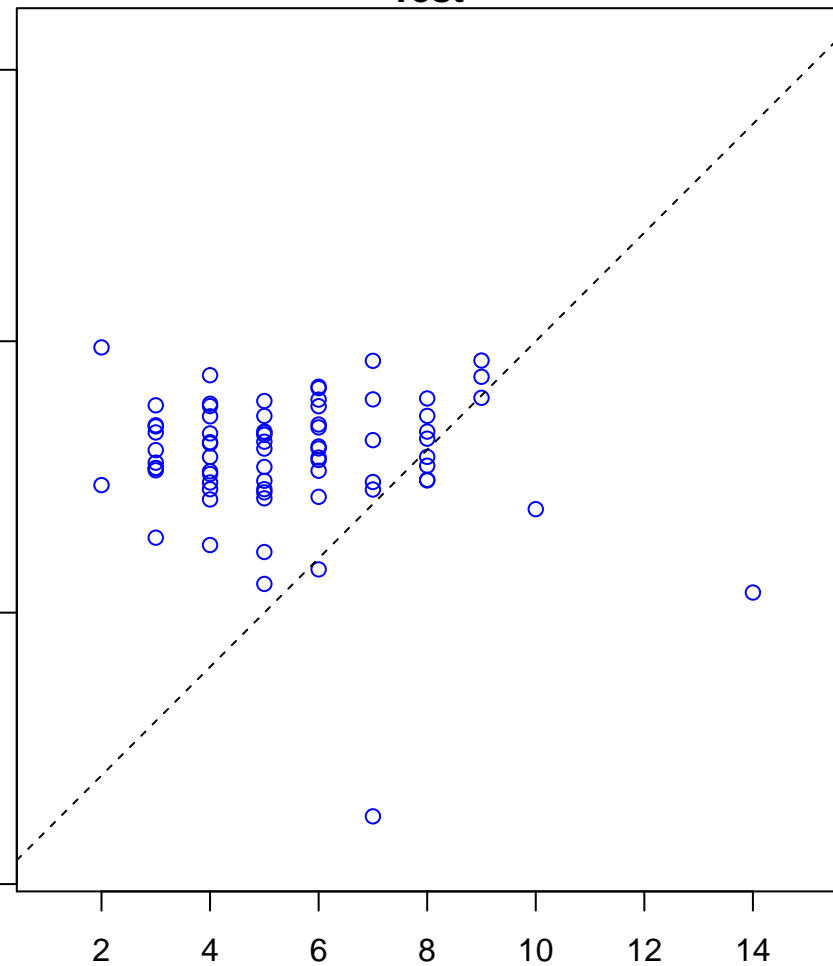


eyelid development in camera-type eye (Score: 0.551787)

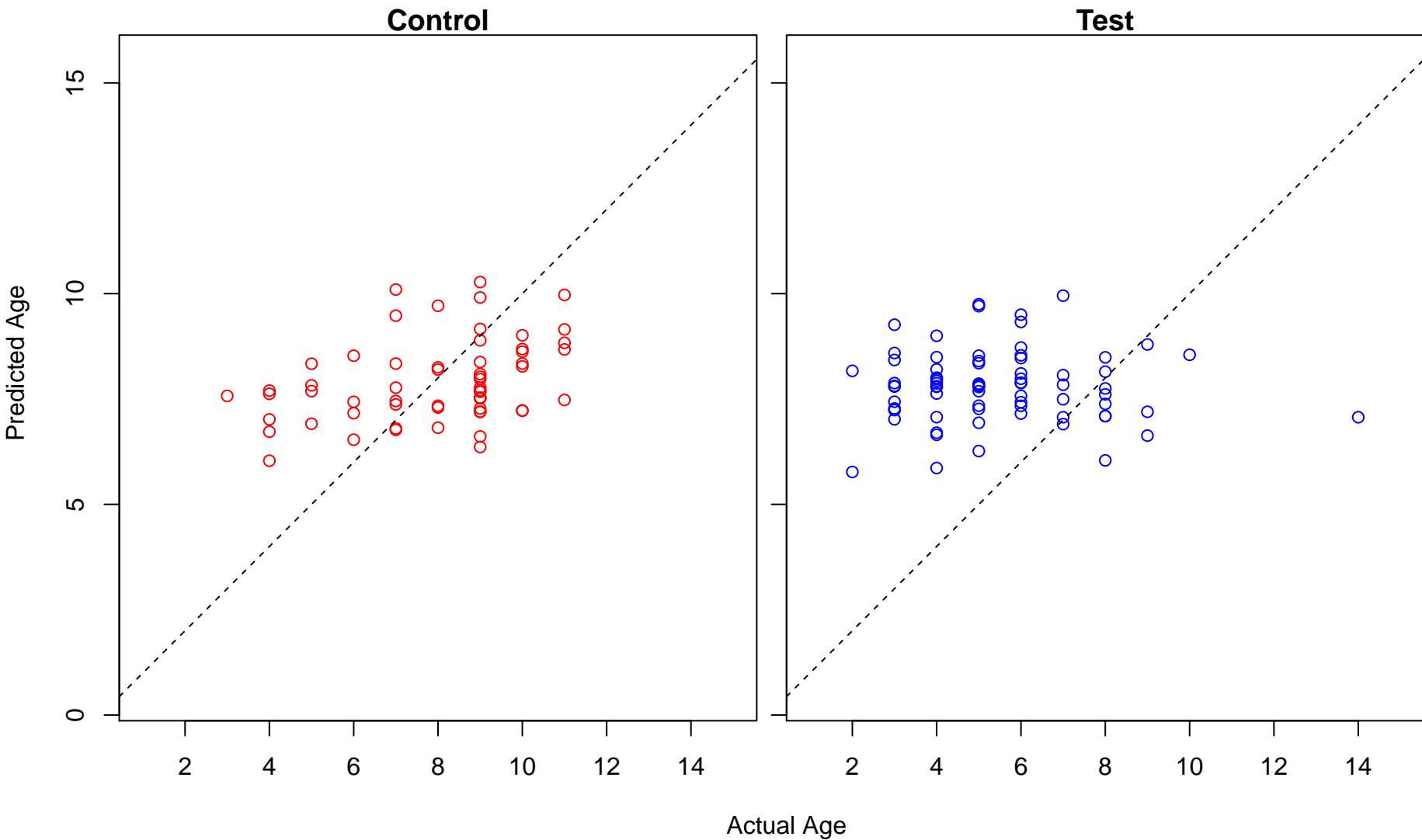
Control



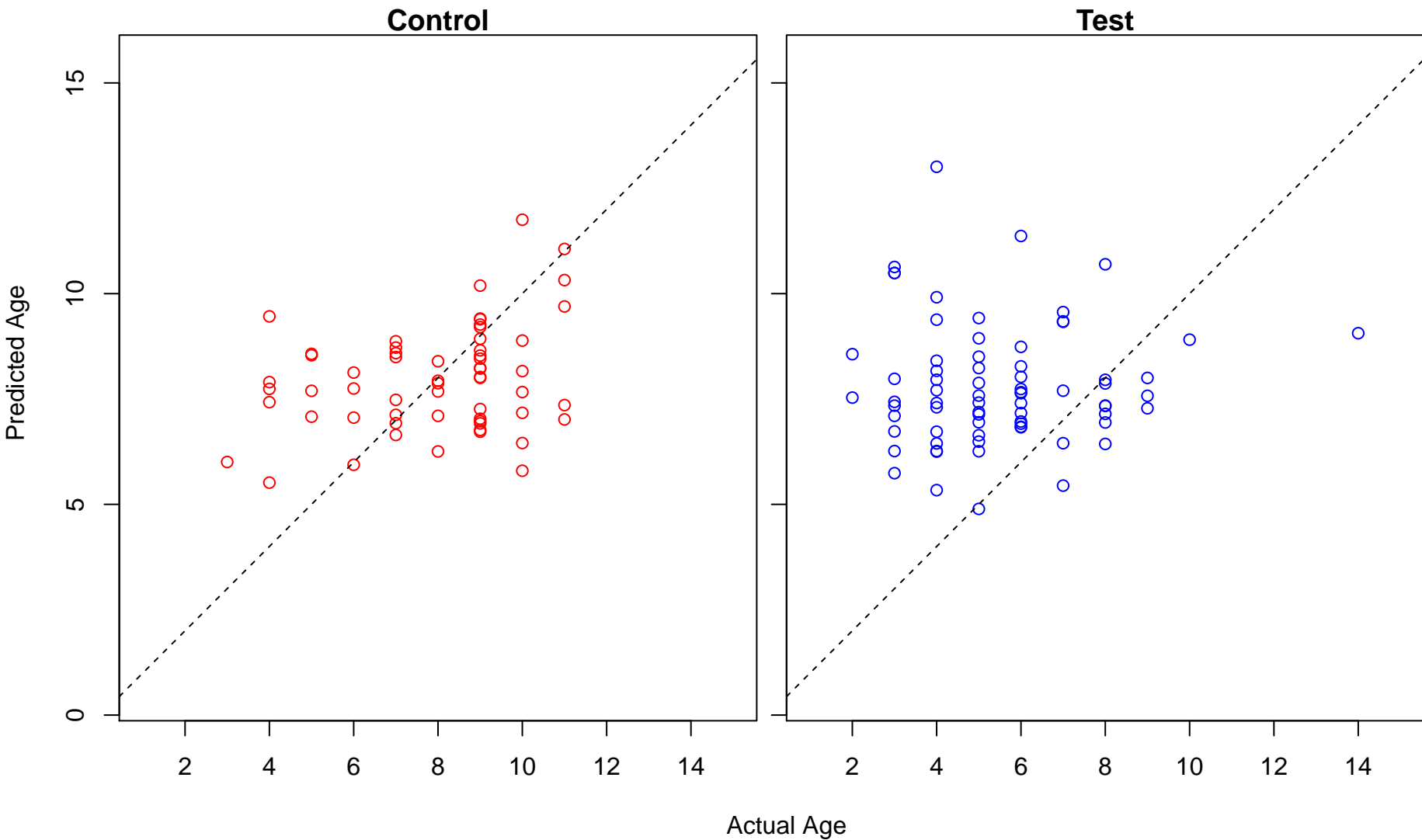
Test



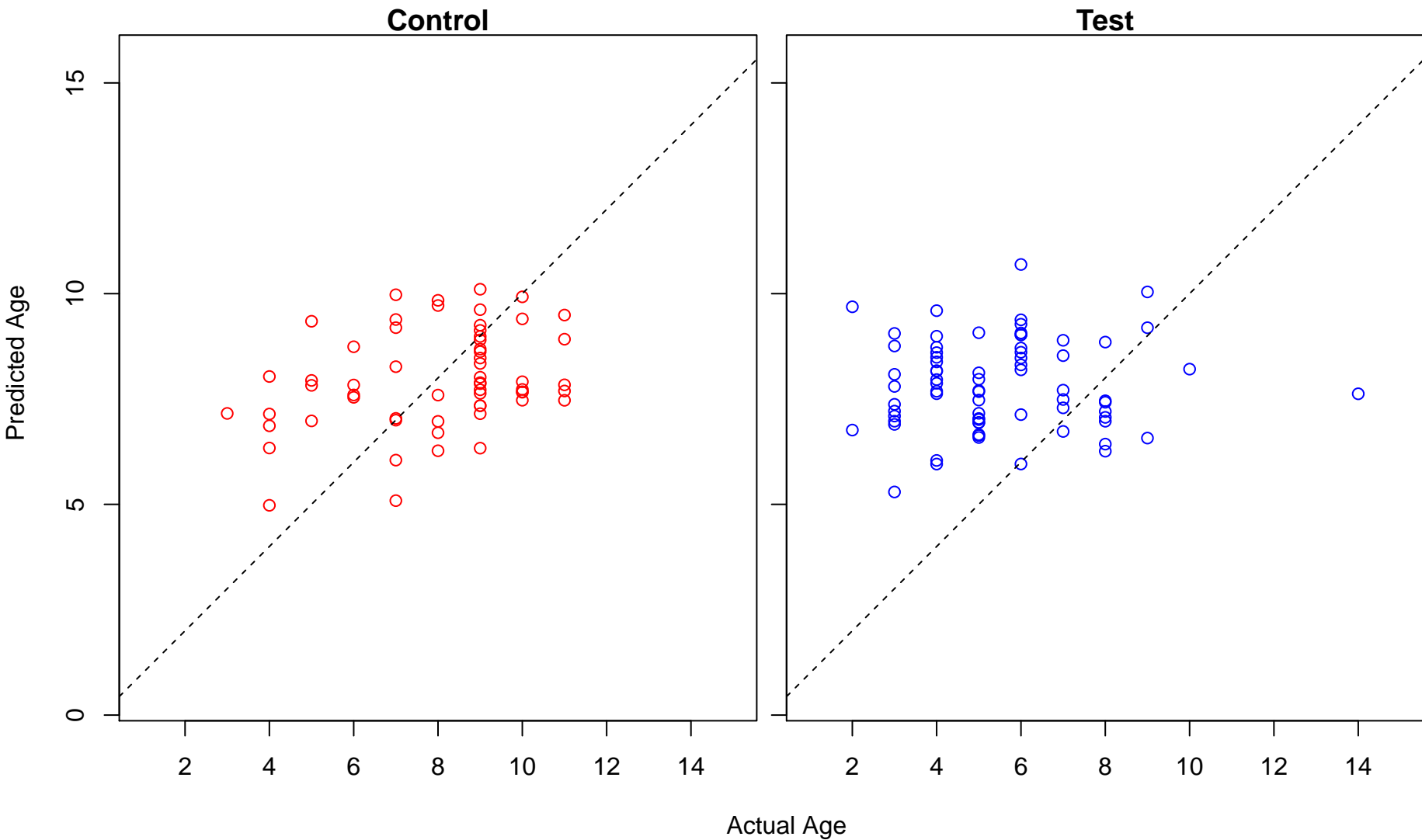
positive regulation of protein processing (Score: 0.550988)



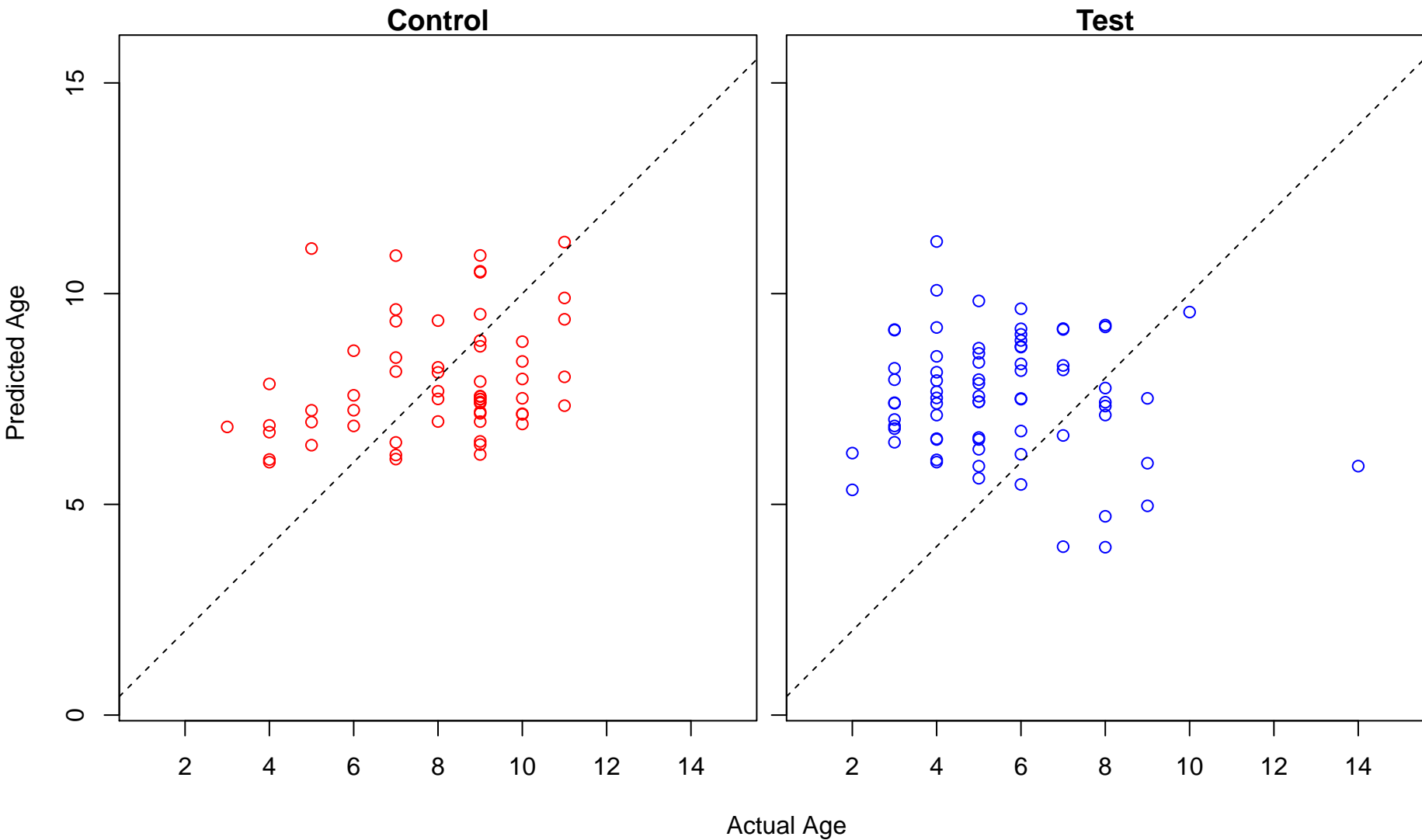
positive regulation of T-helper 17 type immune response (Score: 0.550533)



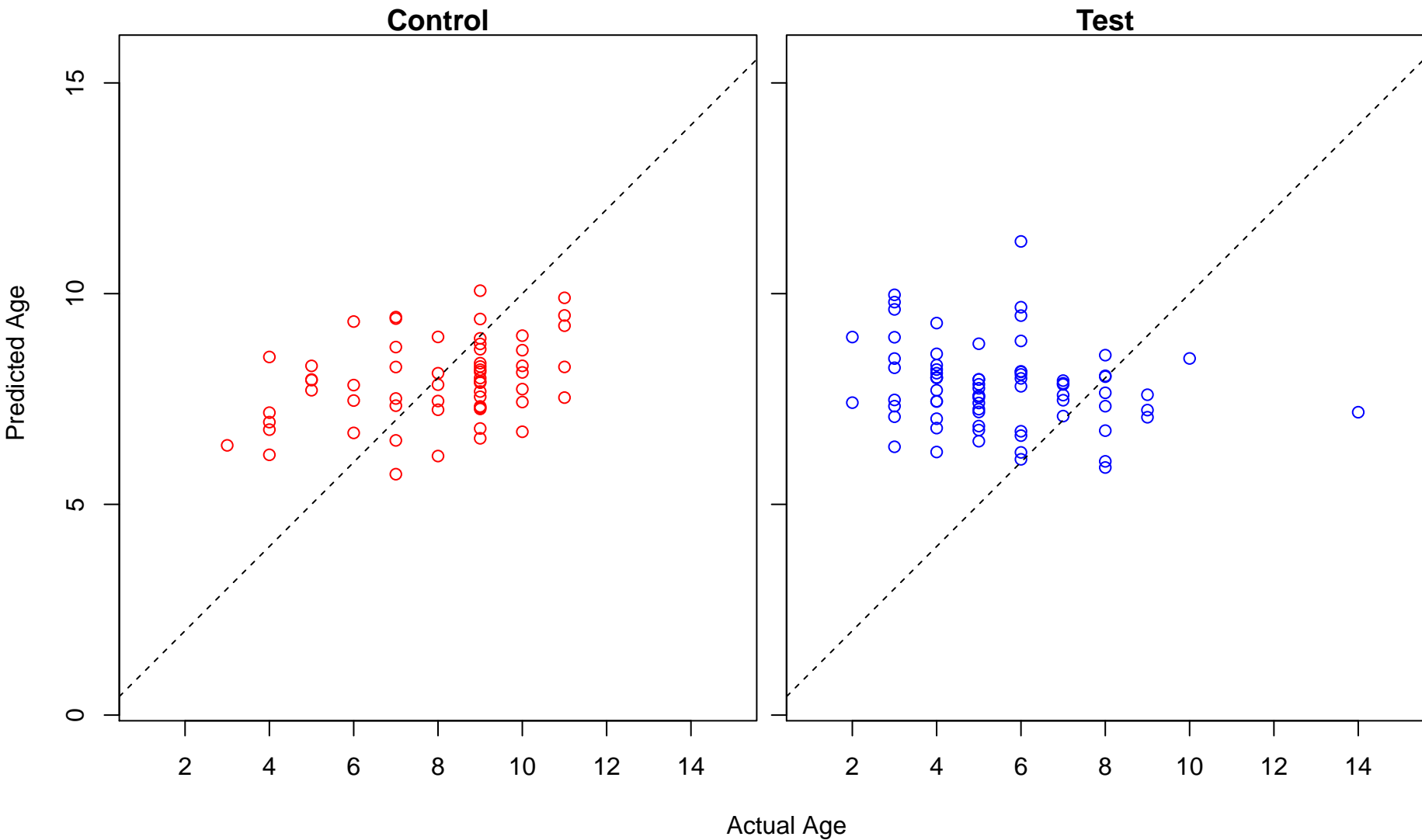
regulation of keratinocyte differentiation (Score: 0.549730)



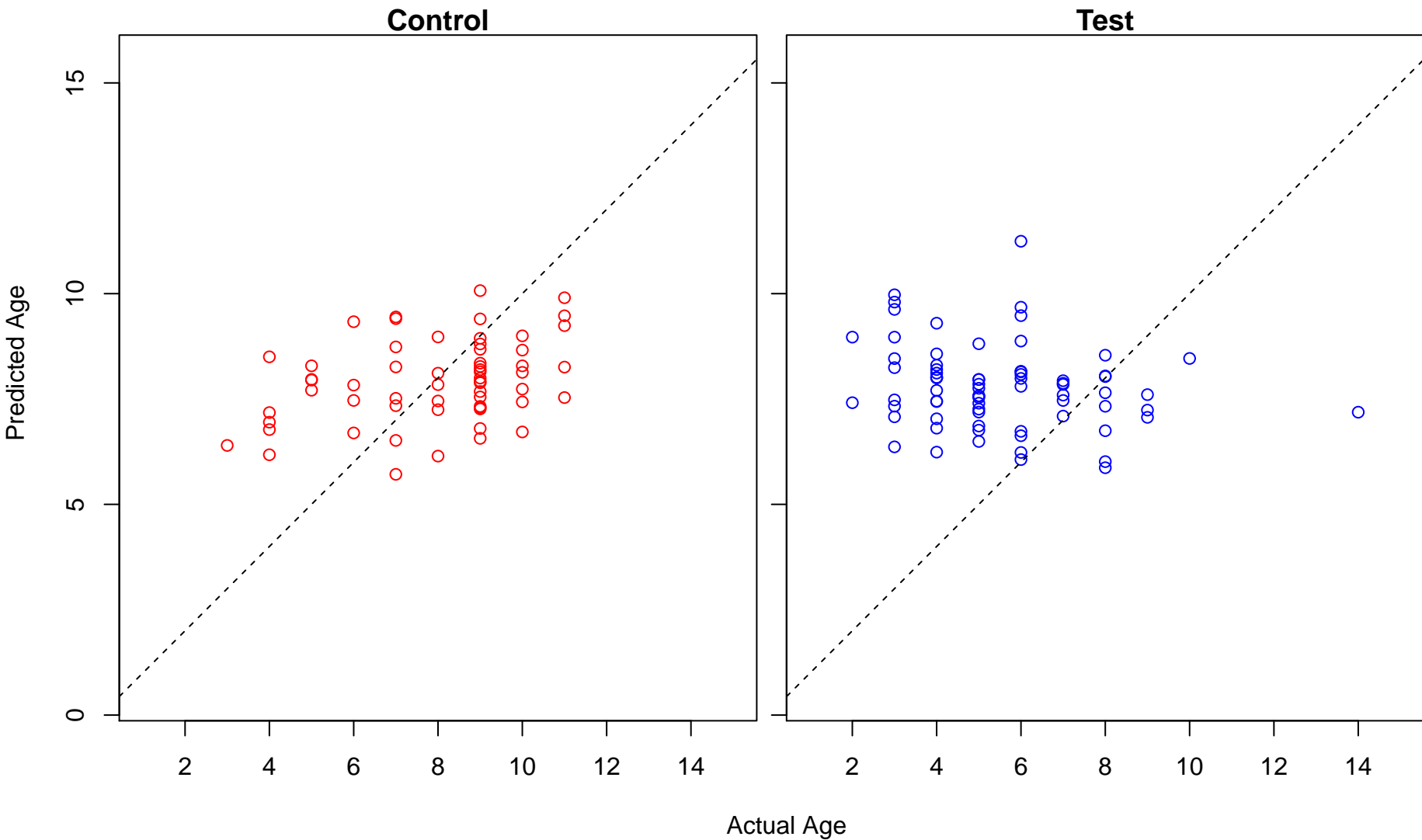
cellular anion homeostasis (Score: 0.548988)



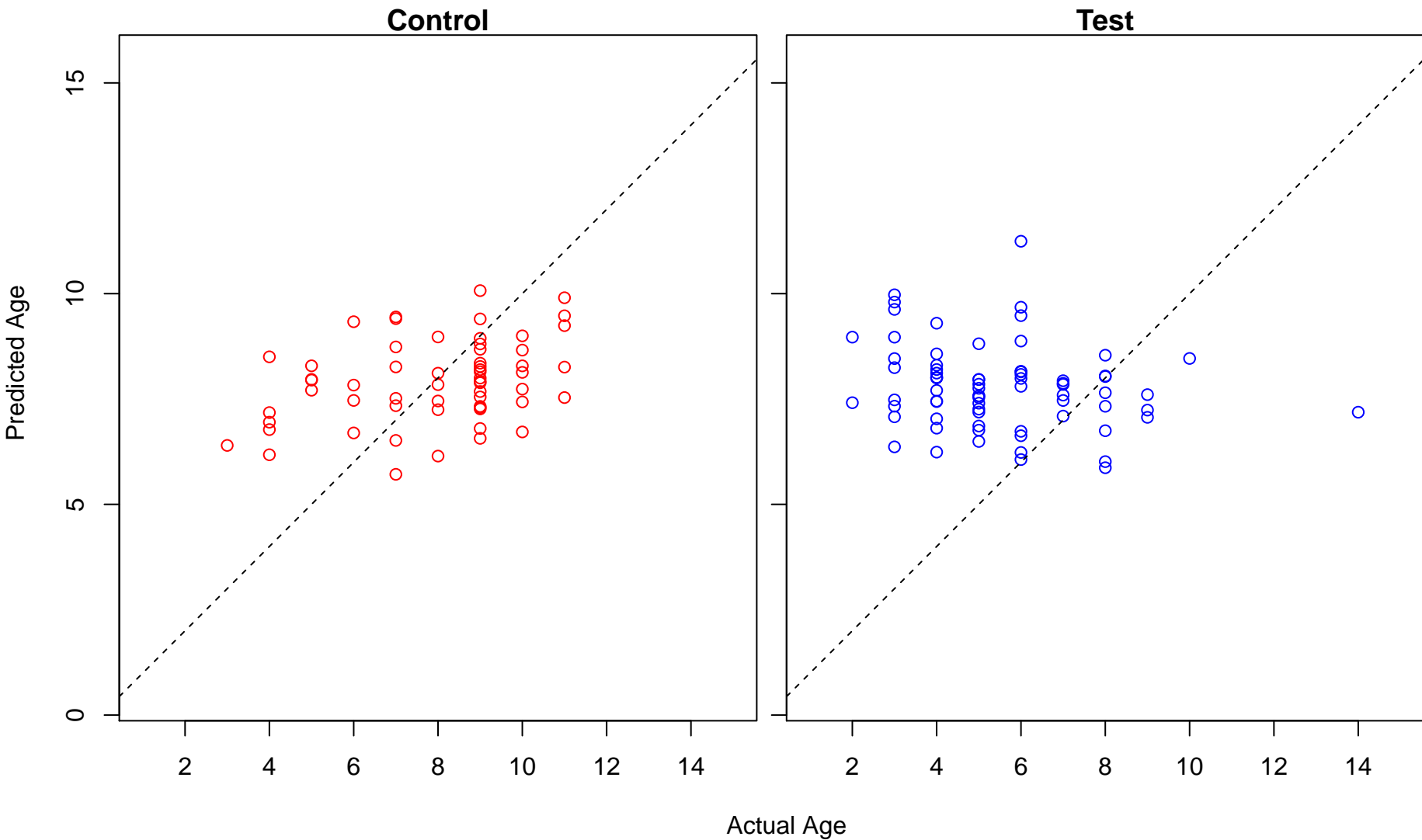
negative regulation of gene silencing by miRNA (Score: 0.548832)



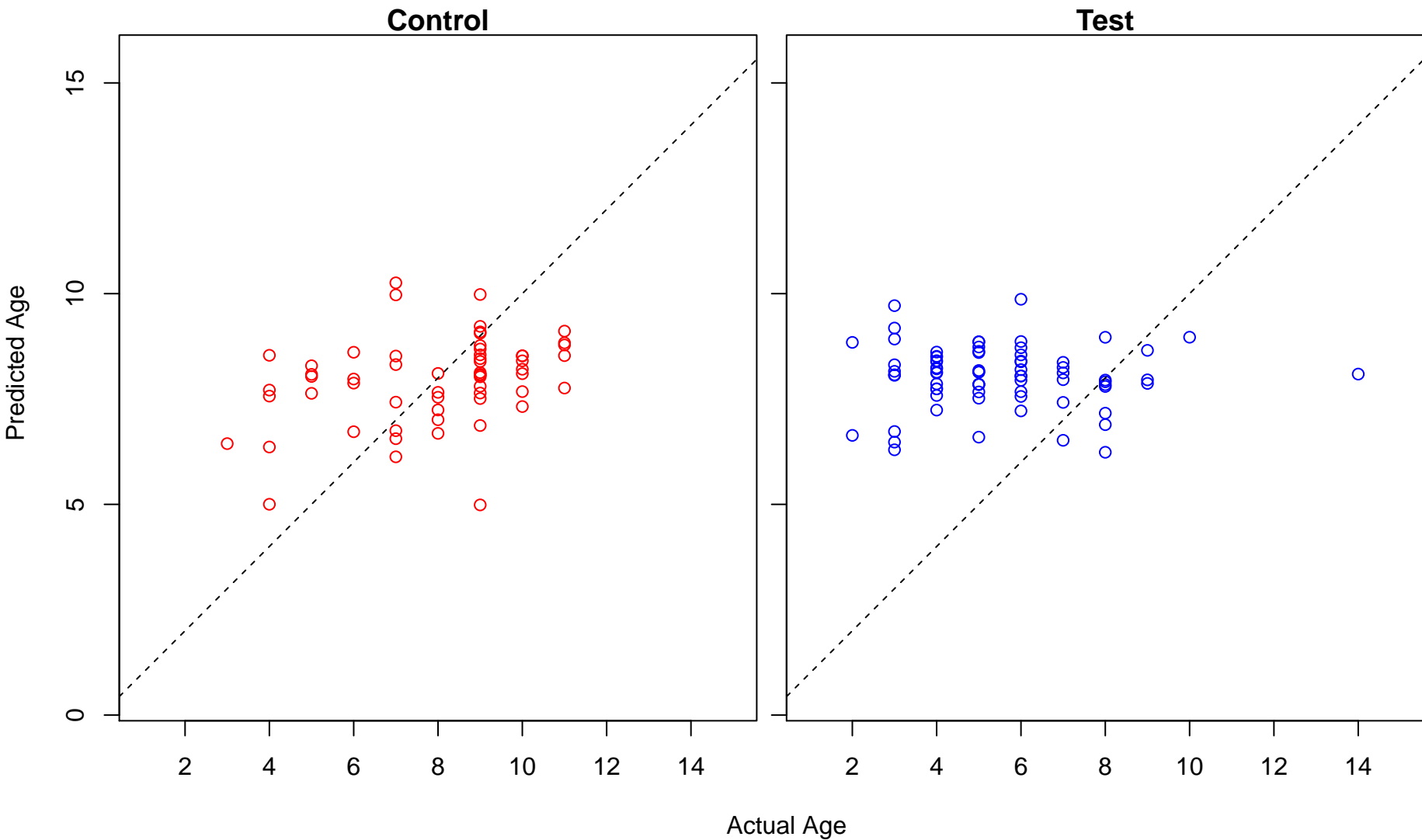
negative regulation of posttranscriptional gene silencing (Score: 0.547705)



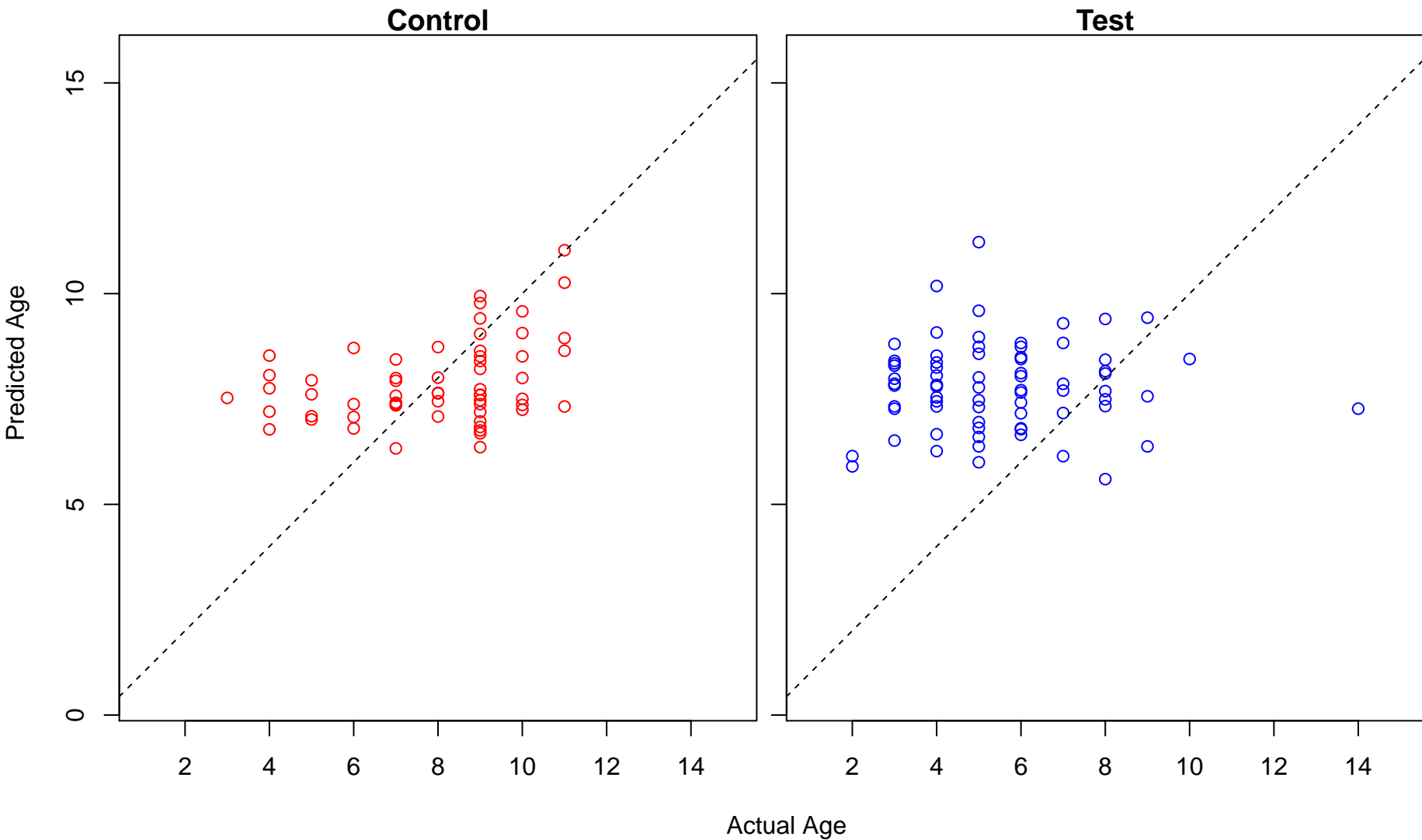
negative regulation of gene silencing by RNA (Score: 0.547705)



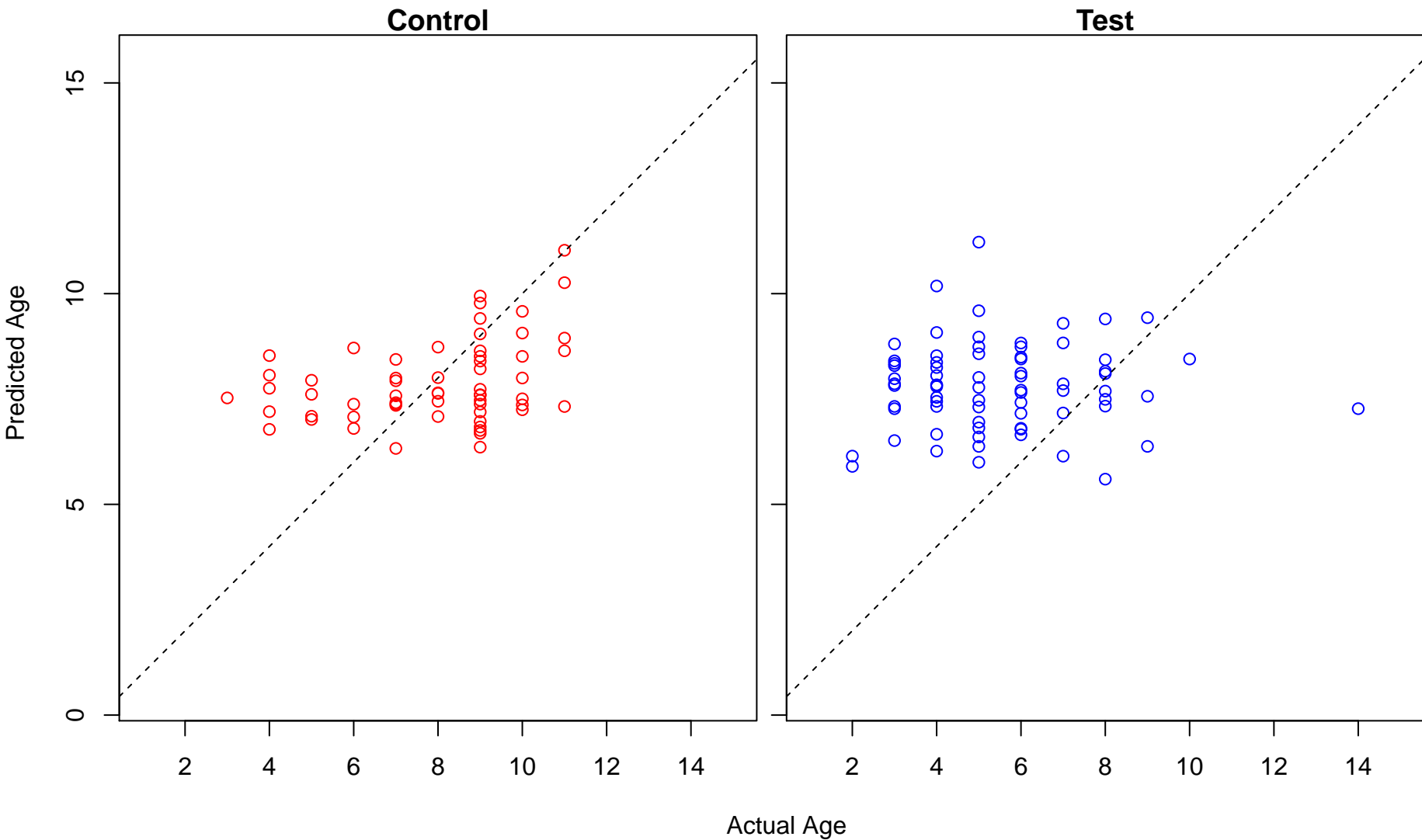
post-embryonic camera-type eye development (Score: 0.547566)



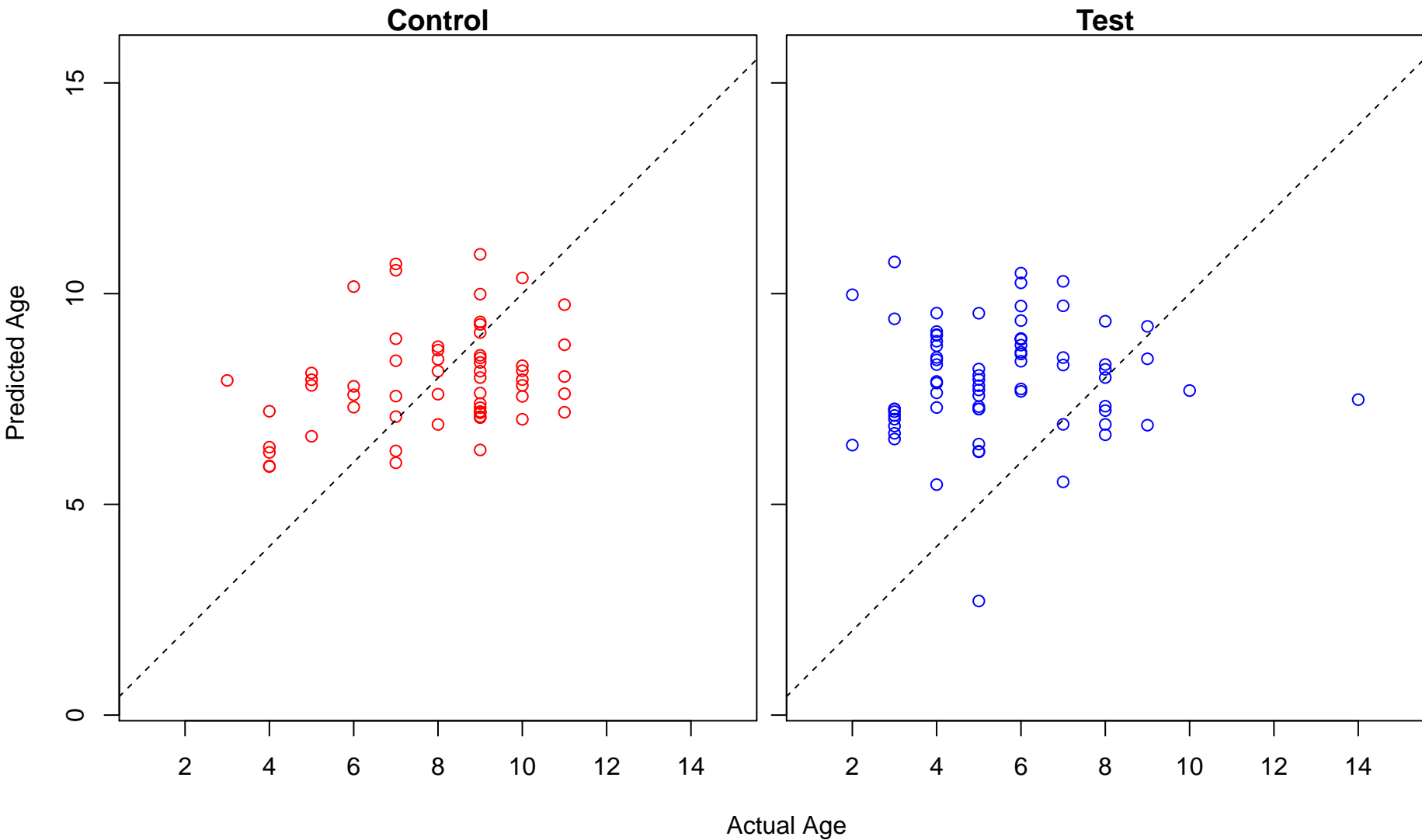
regulation of calcium ion binding (Score: 0.547112)



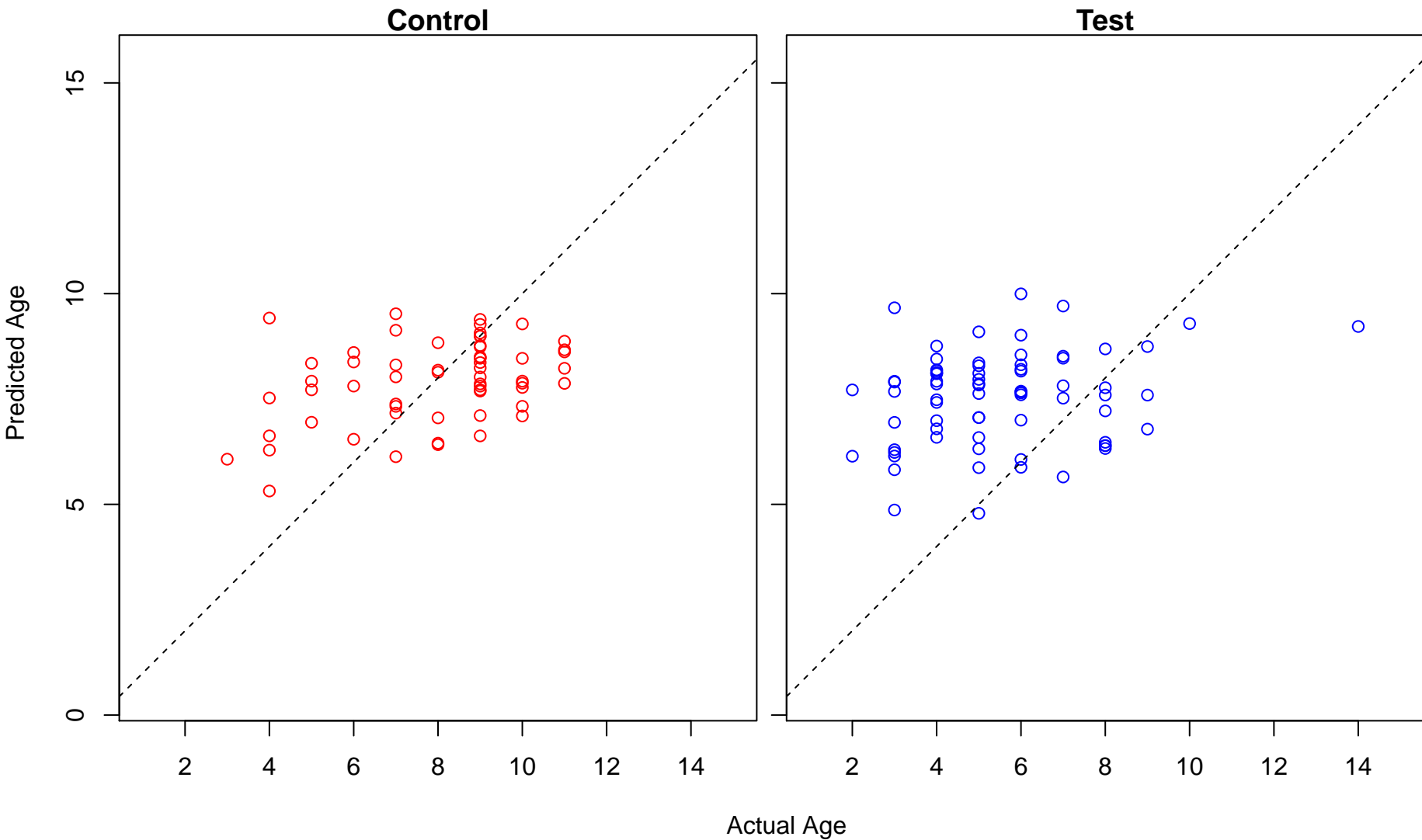
negative regulation of calcium ion binding (Score: 0.547112)



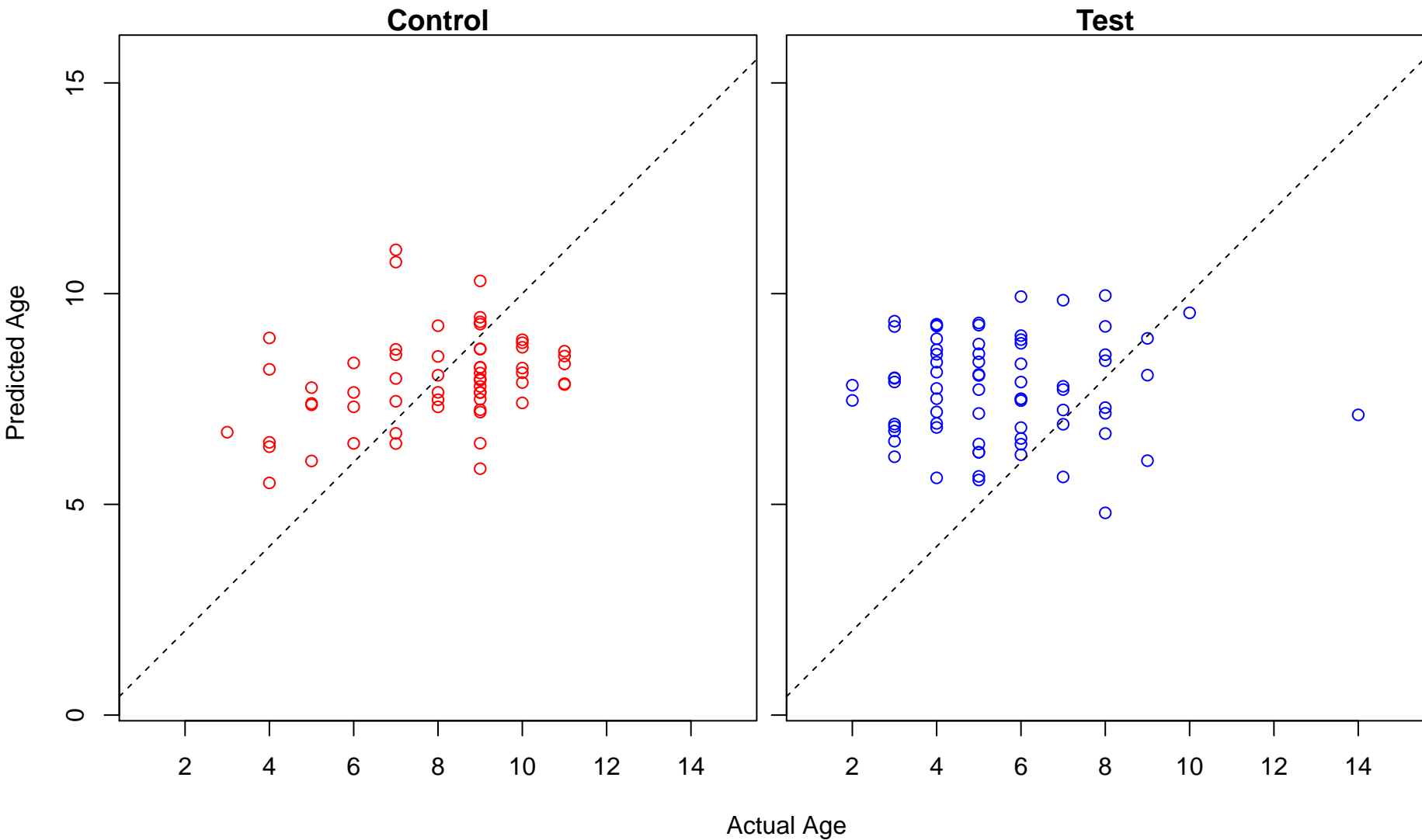
thrombin receptor signaling pathway (Score: 0.545053)



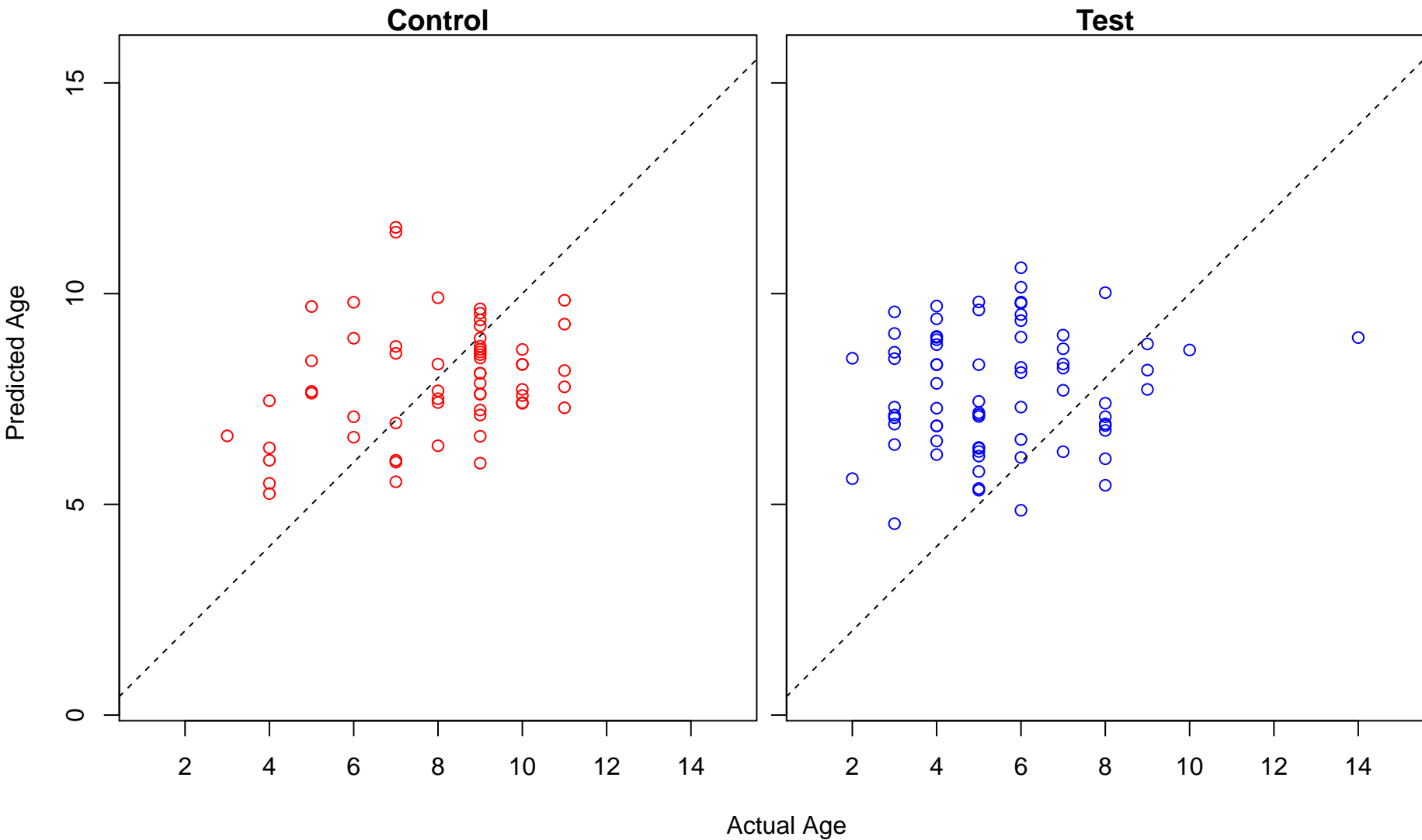
regulation of acute inflammatory response to antigenic stimulus (Score: 0.544801)



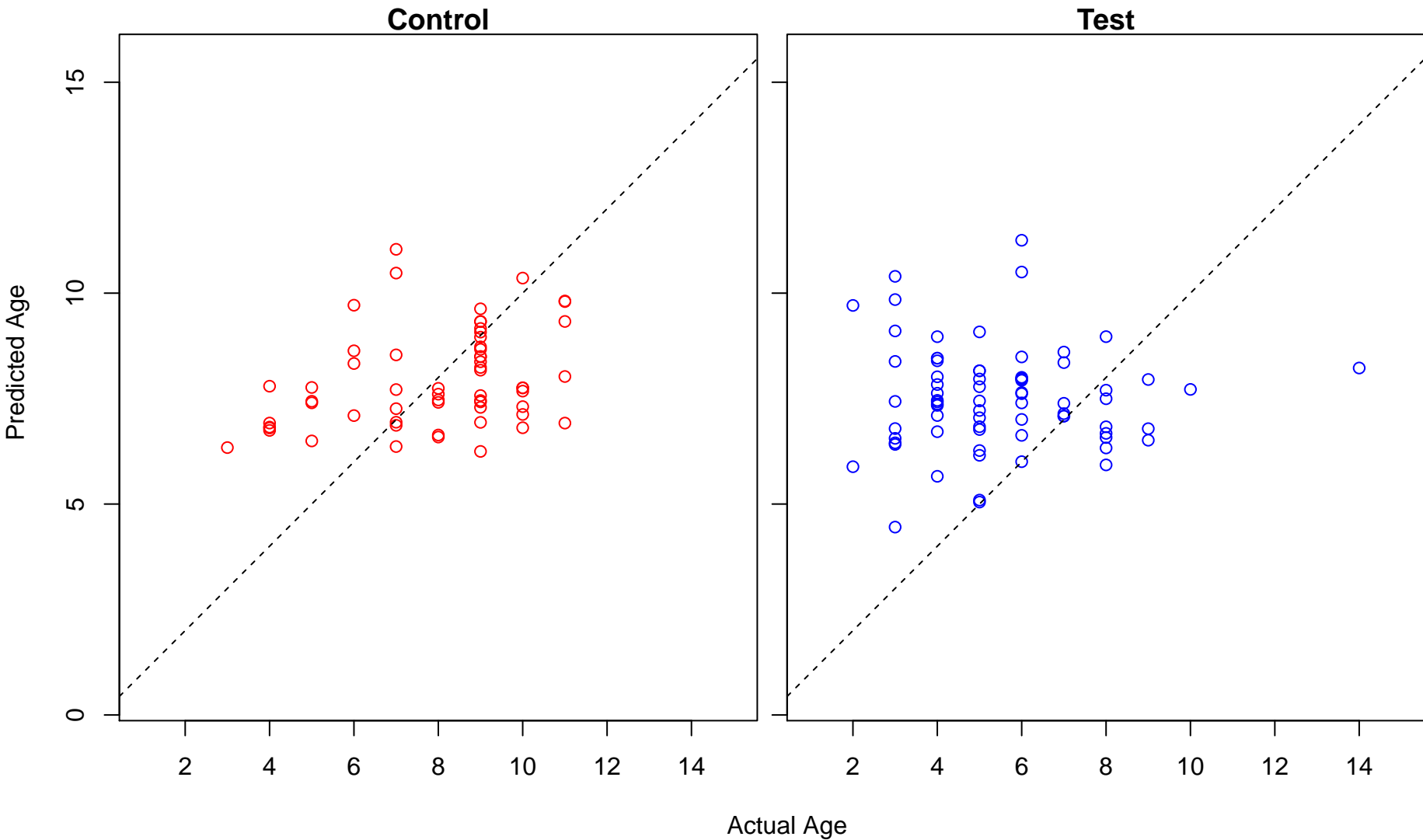
diadenosine polyphosphate metabolic process (Score: 0.544037)



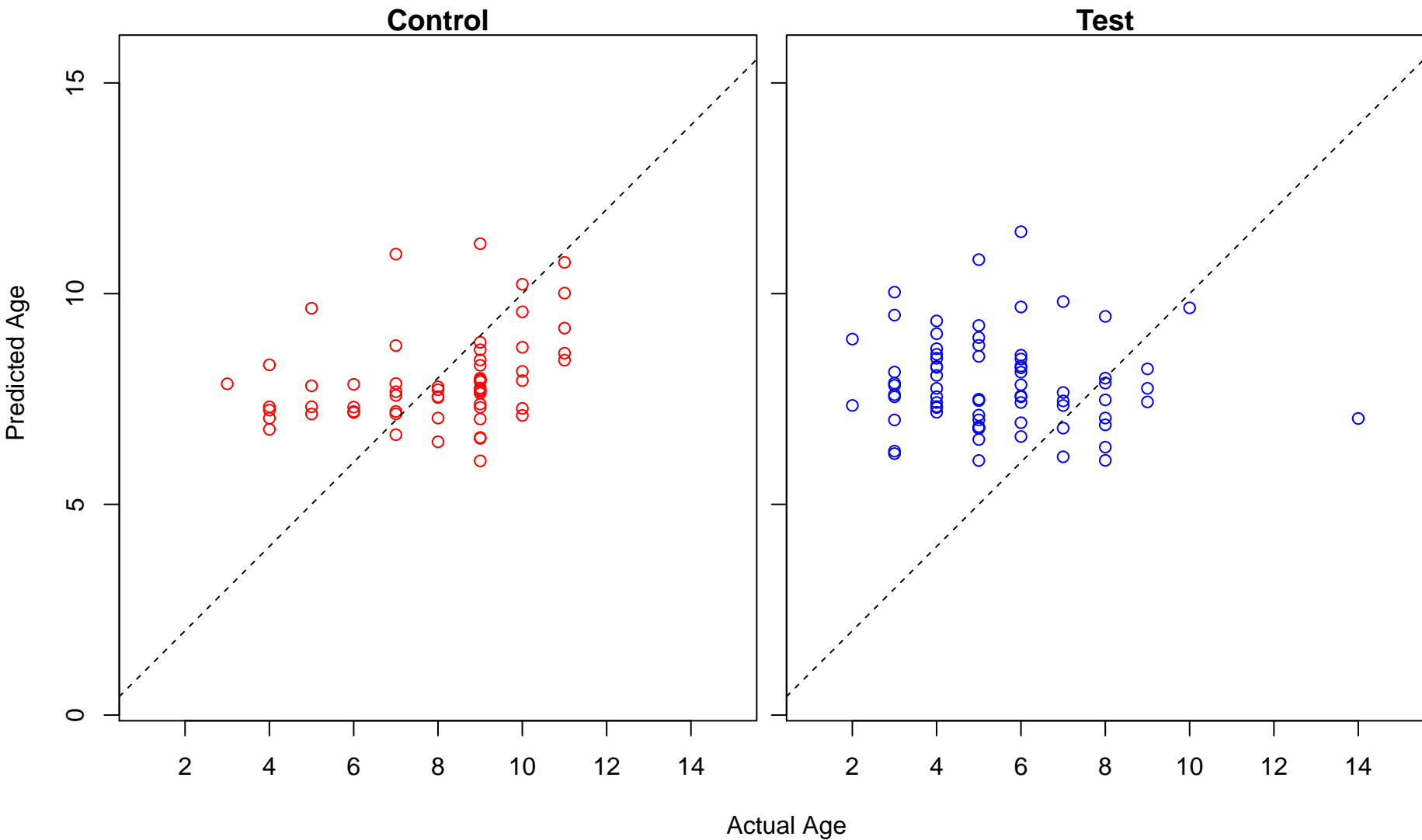
negative regulation of cell development (Score: 0.543531)



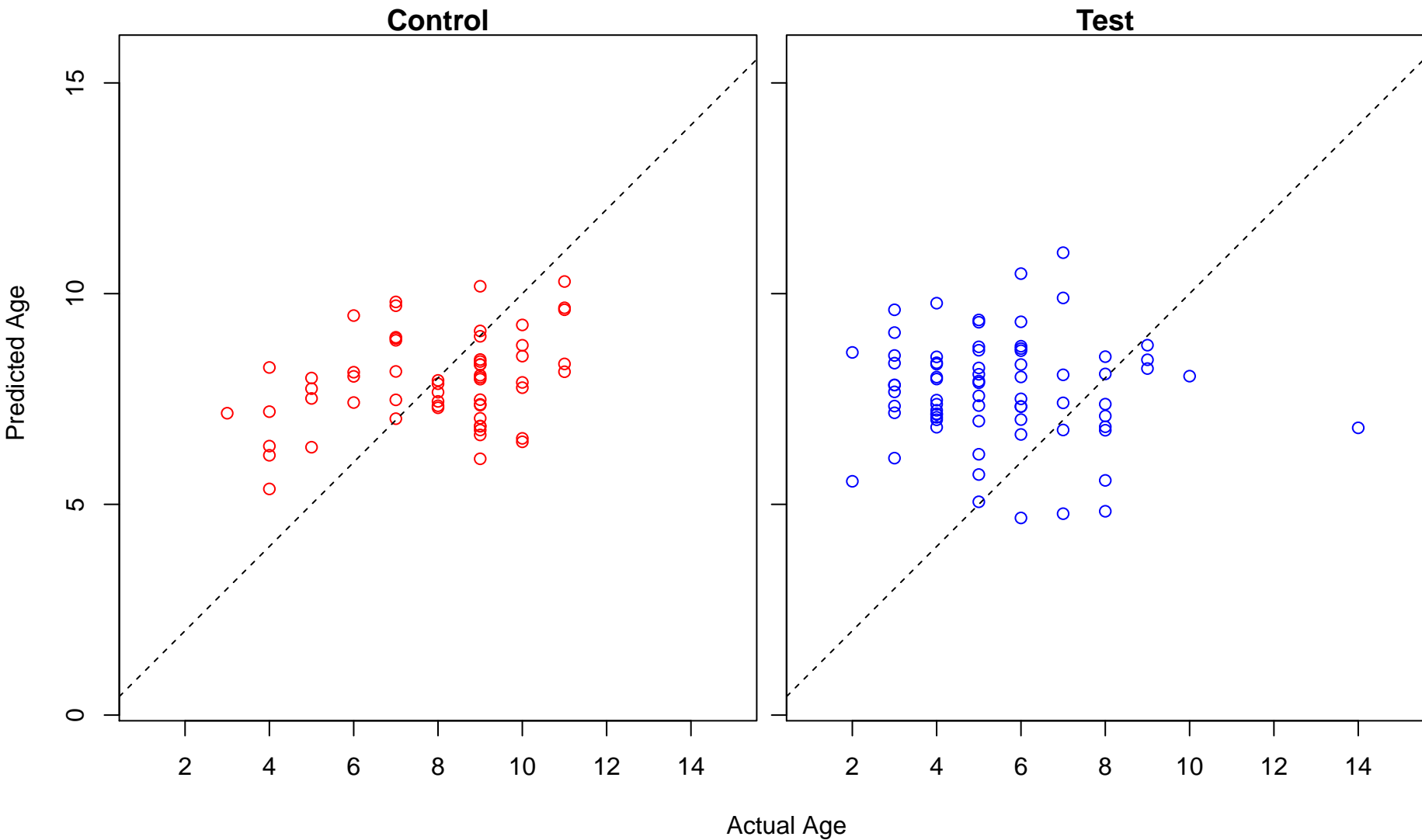
regulation of collagen biosynthetic process (Score: 0.542135)



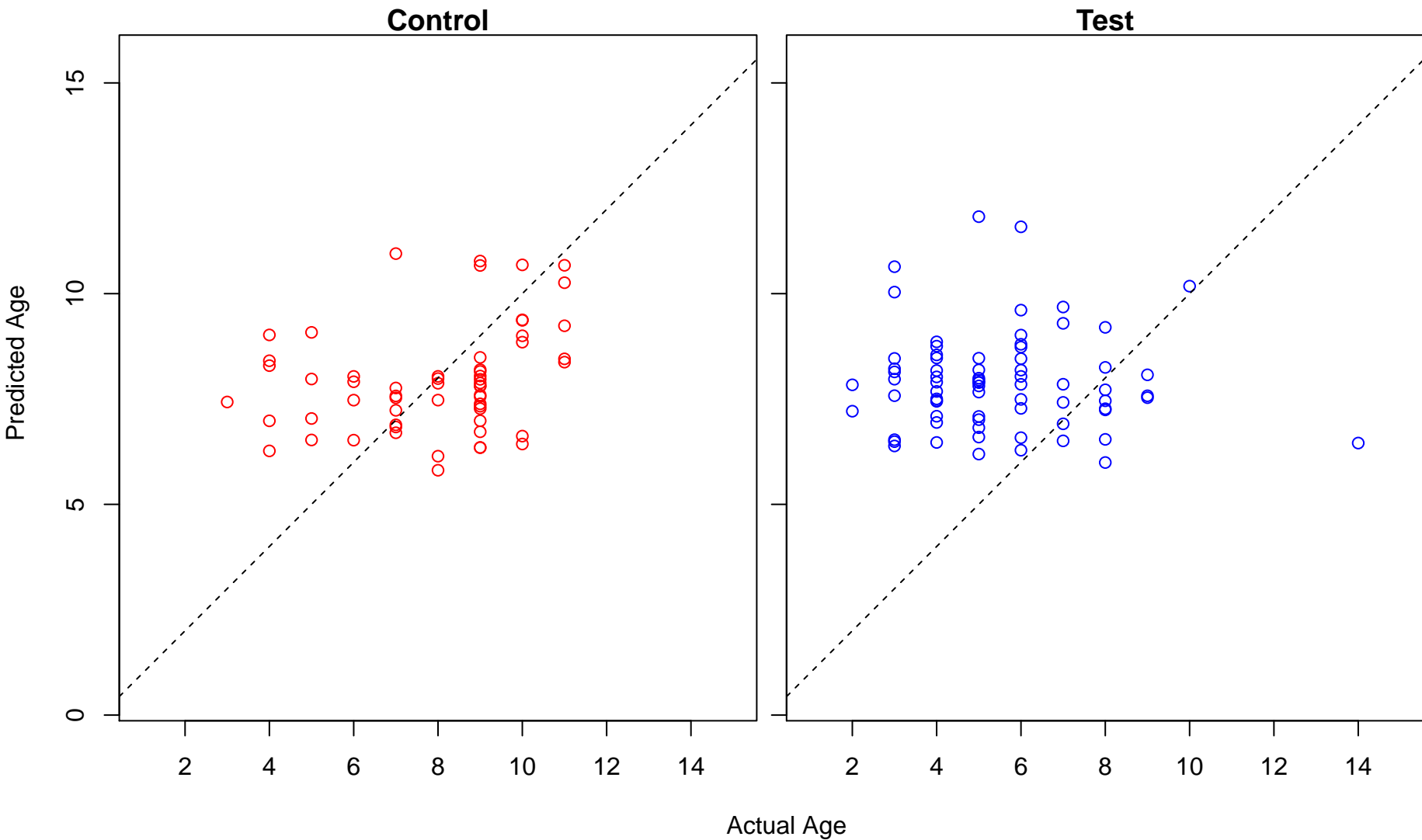
renal outer medulla development (Score: 0.541520)



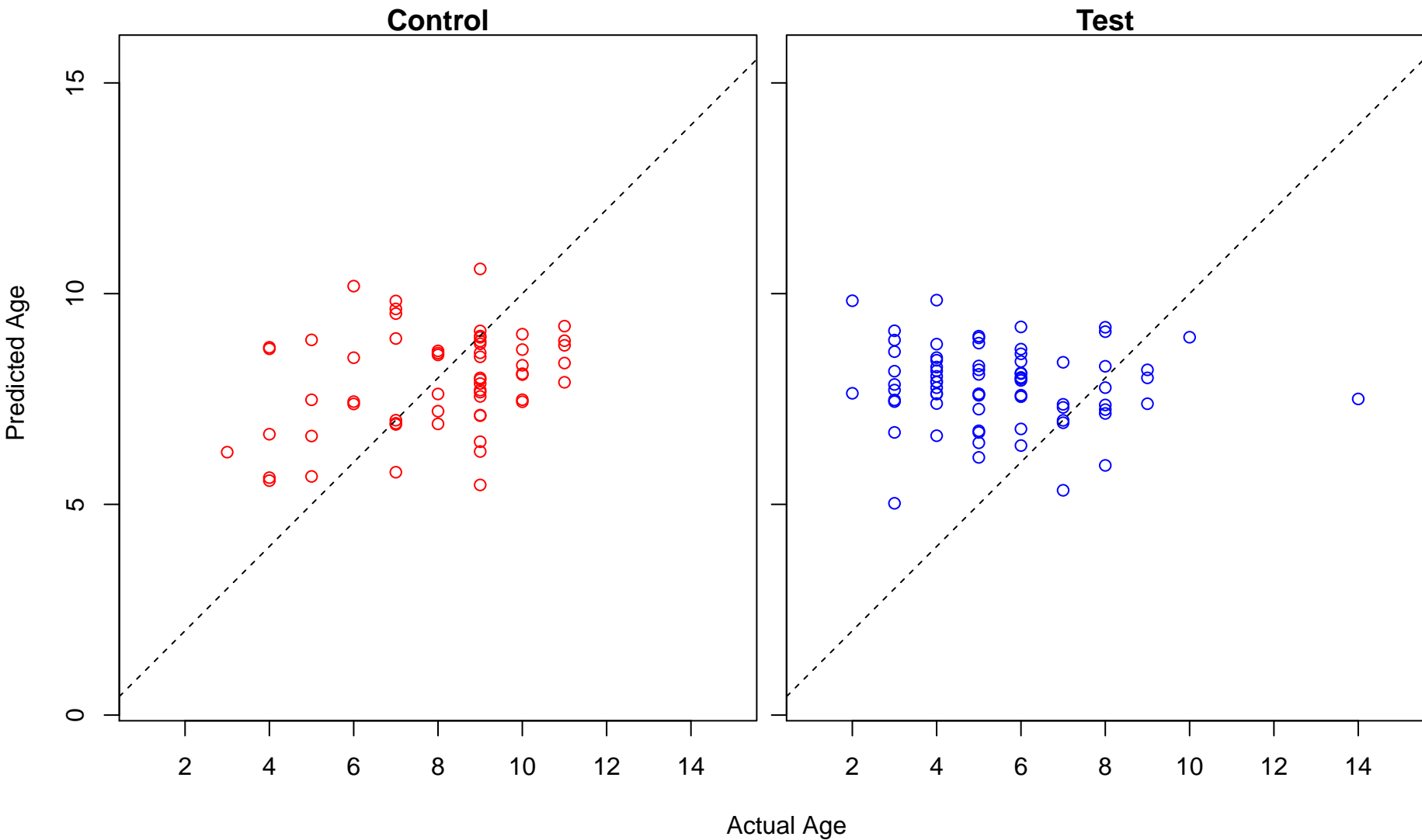
response to UV-A (Score: 0.541258)



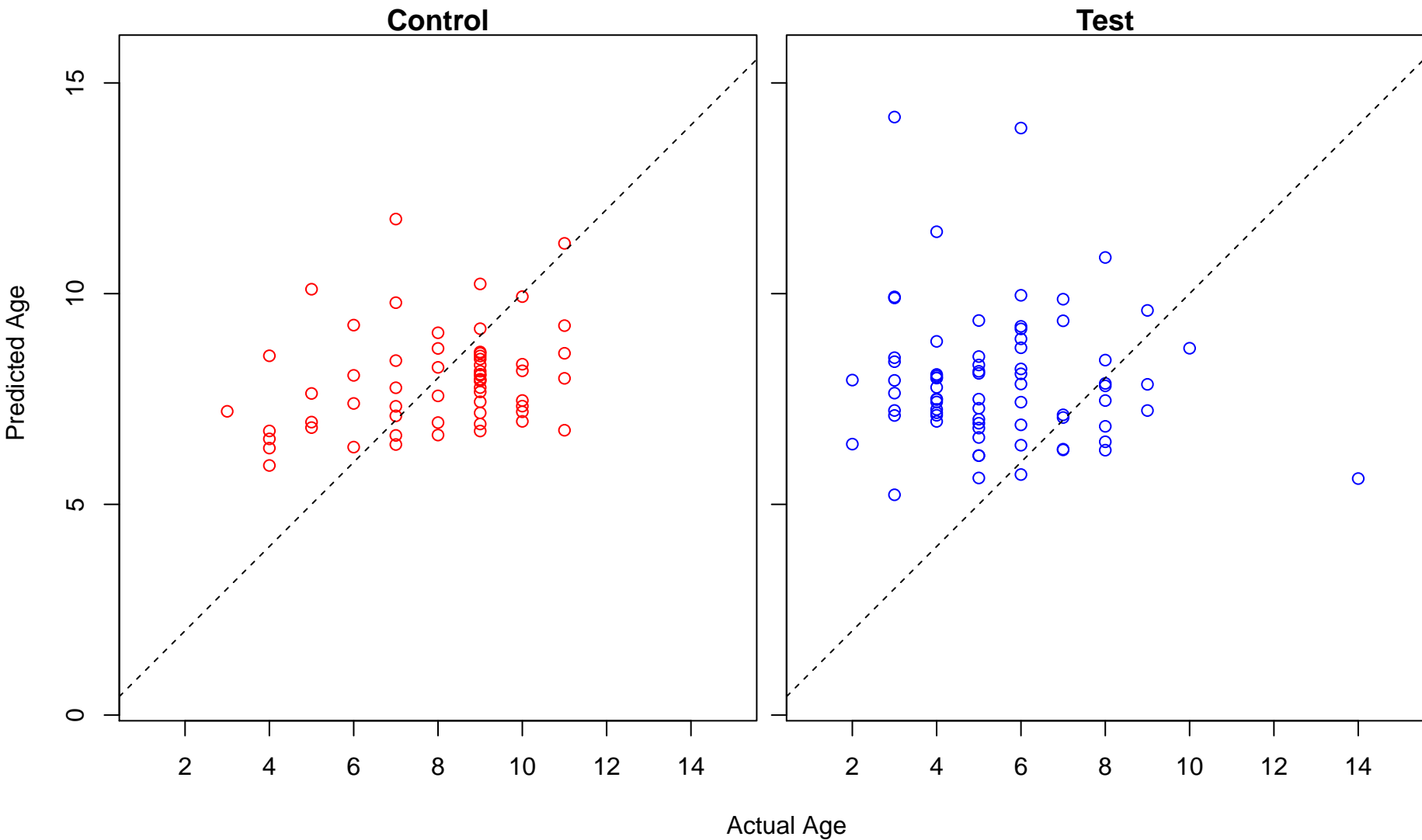
lobar bronchus development (Score: 0.540917)



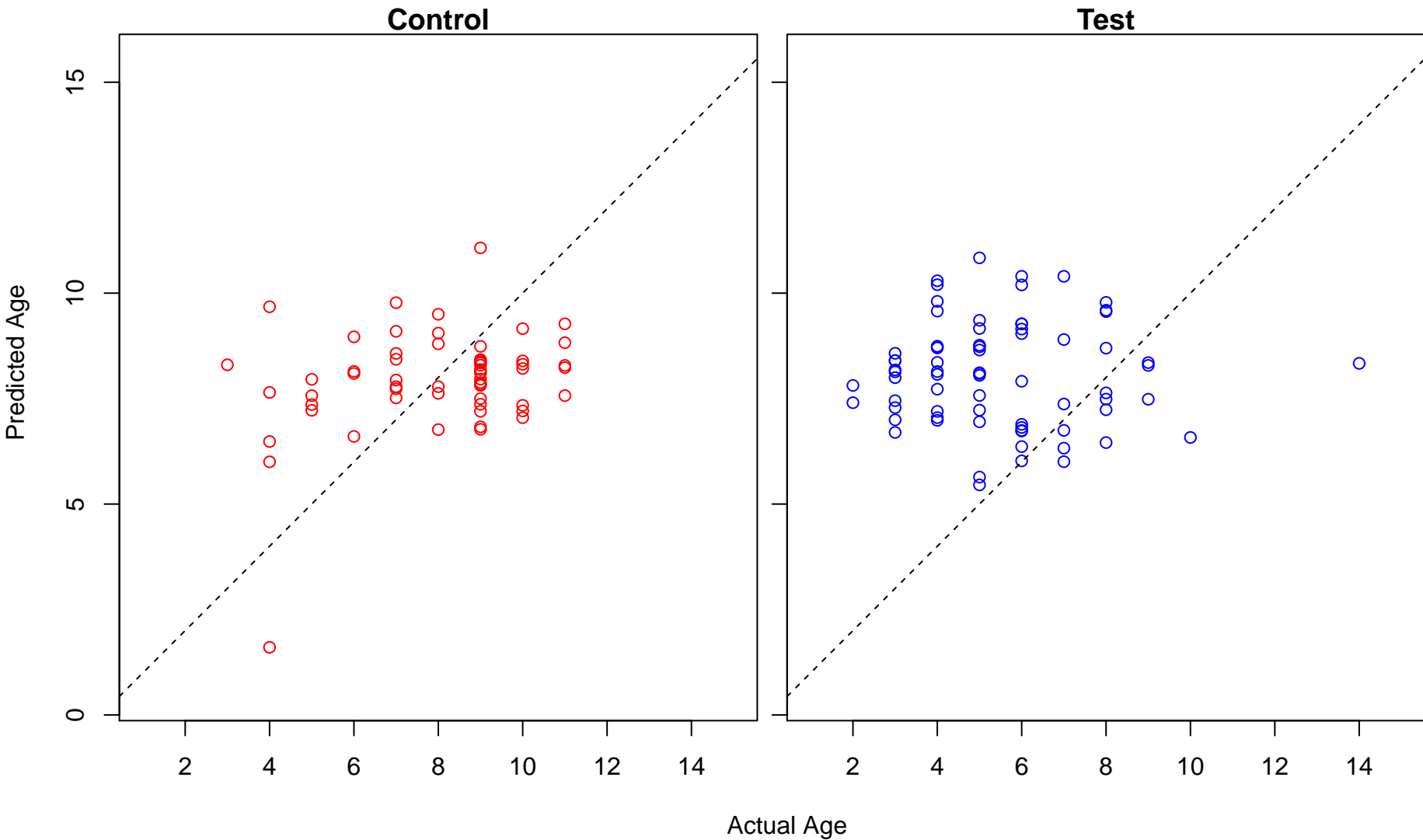
histone mRNA catabolic process (Score: 0.539541)



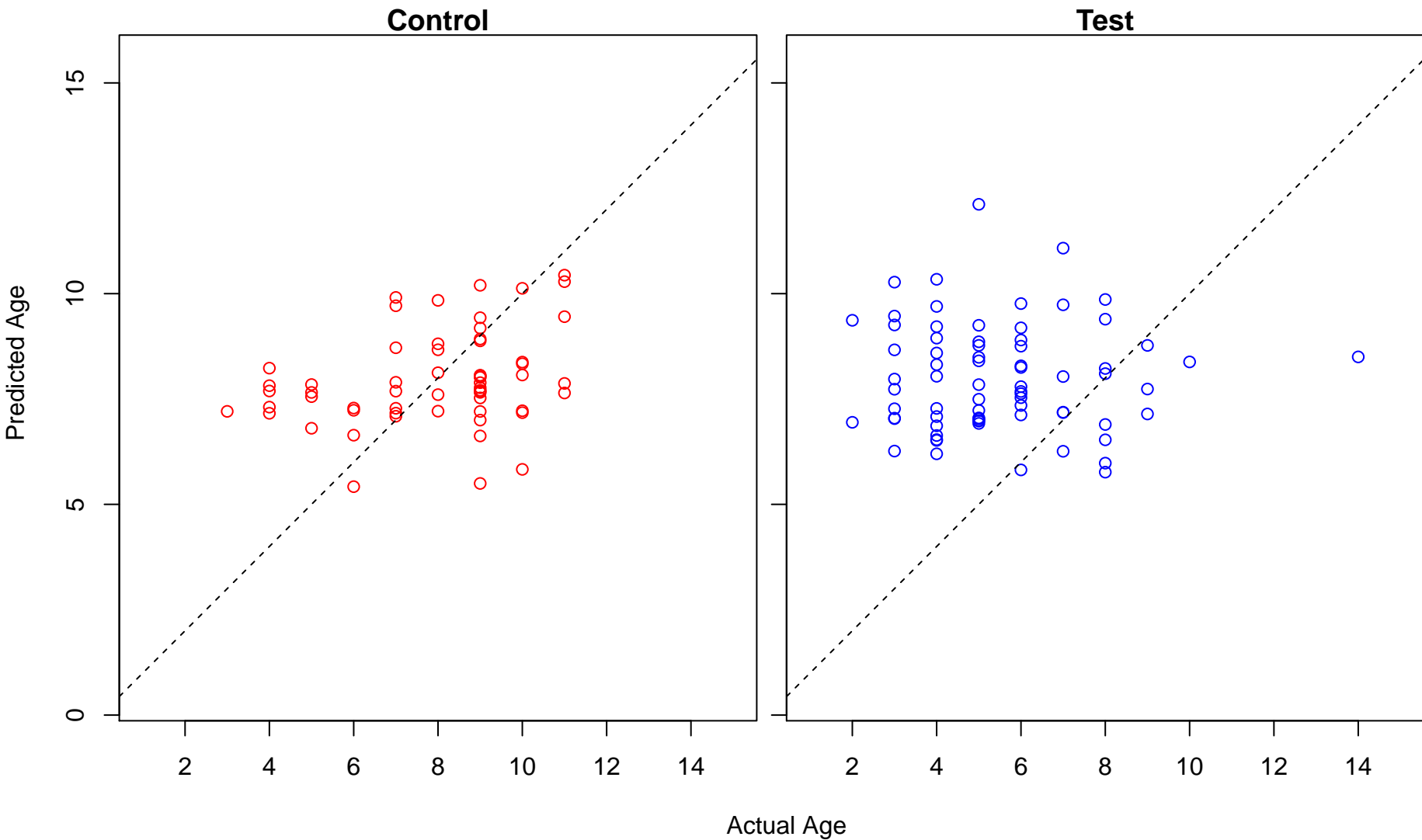
detection of calcium ion (Score: 0.539396)



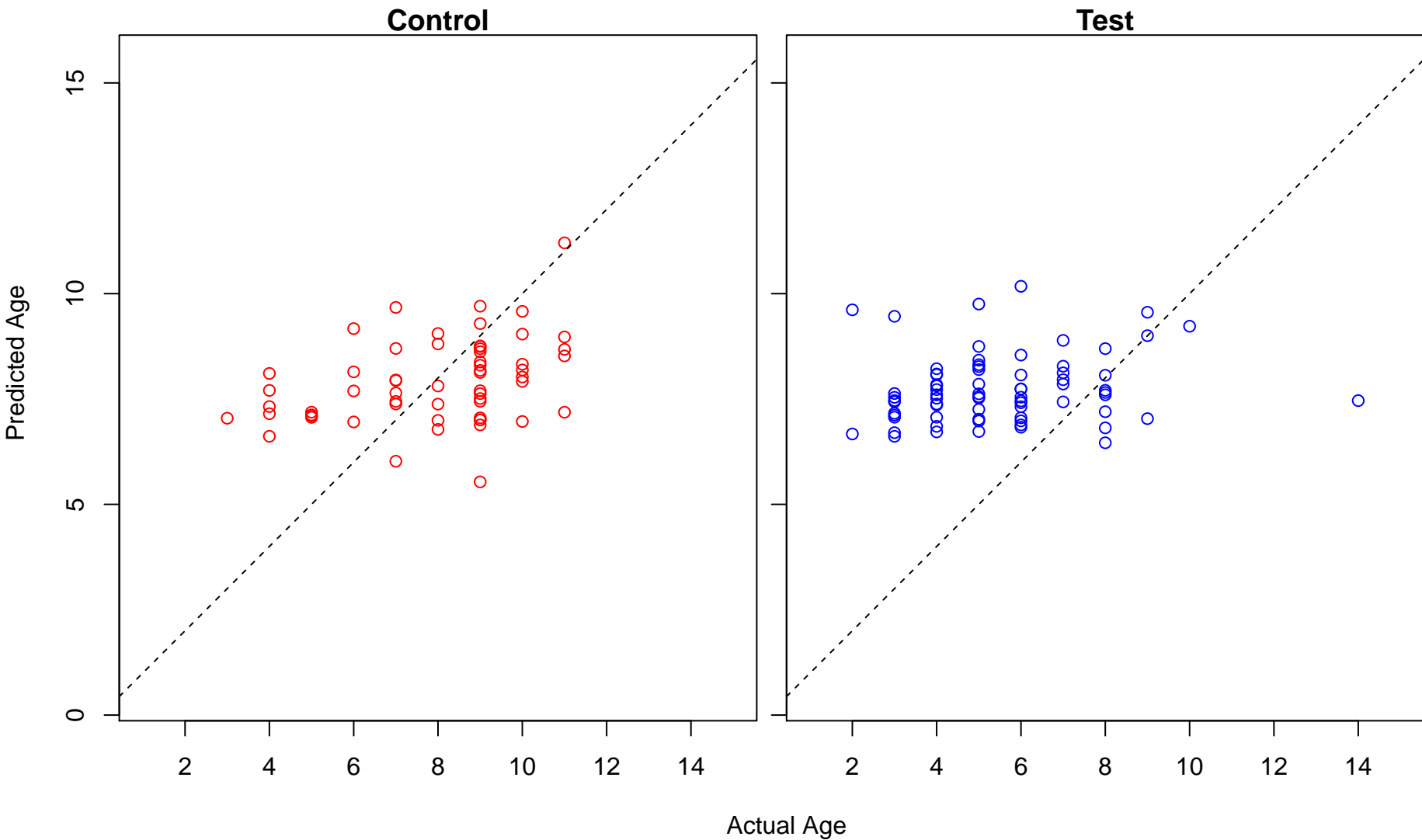
positive regulation of inositol phosphate biosynthetic process (Score: 0.537307)



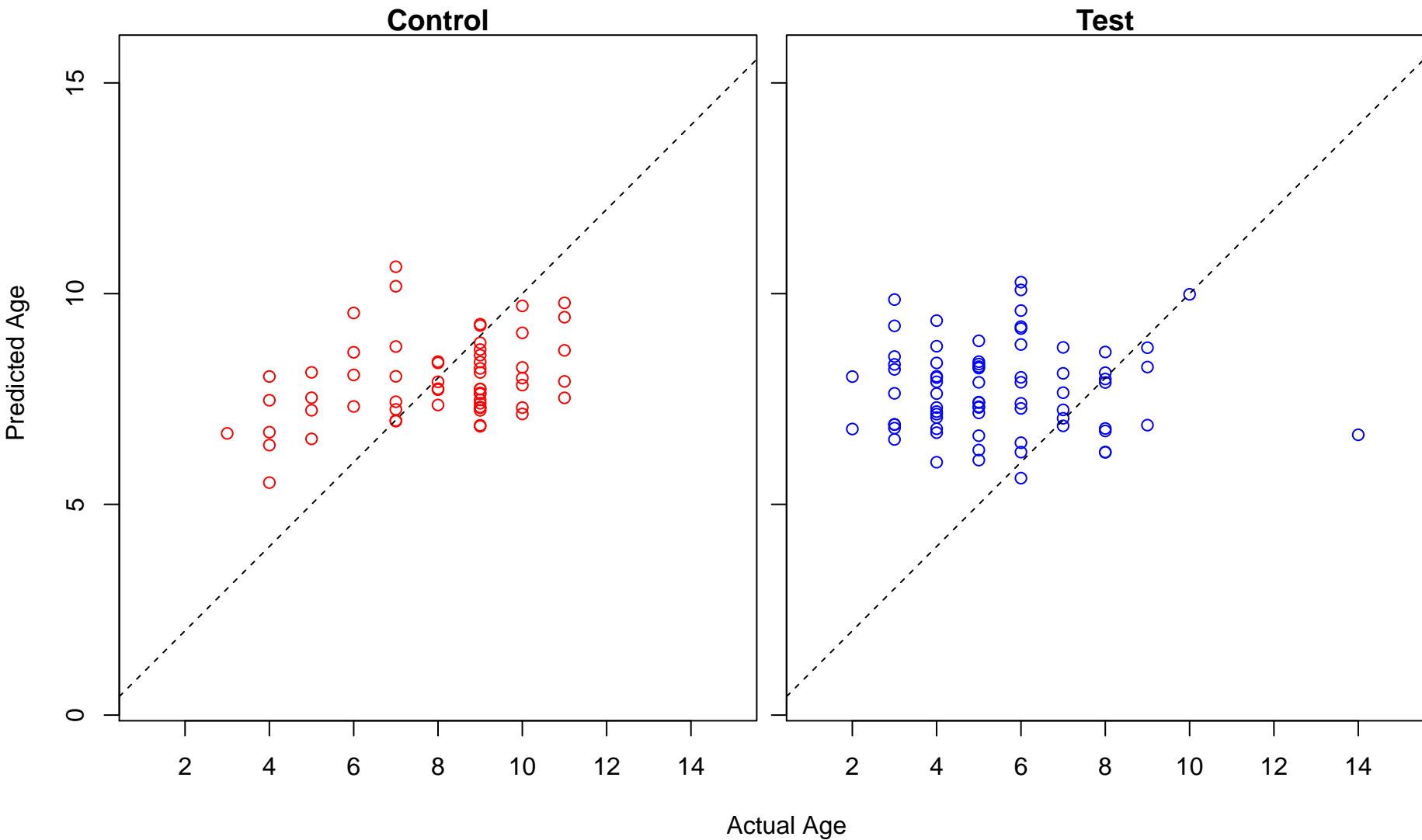
midgut development (Score: 0.536054)



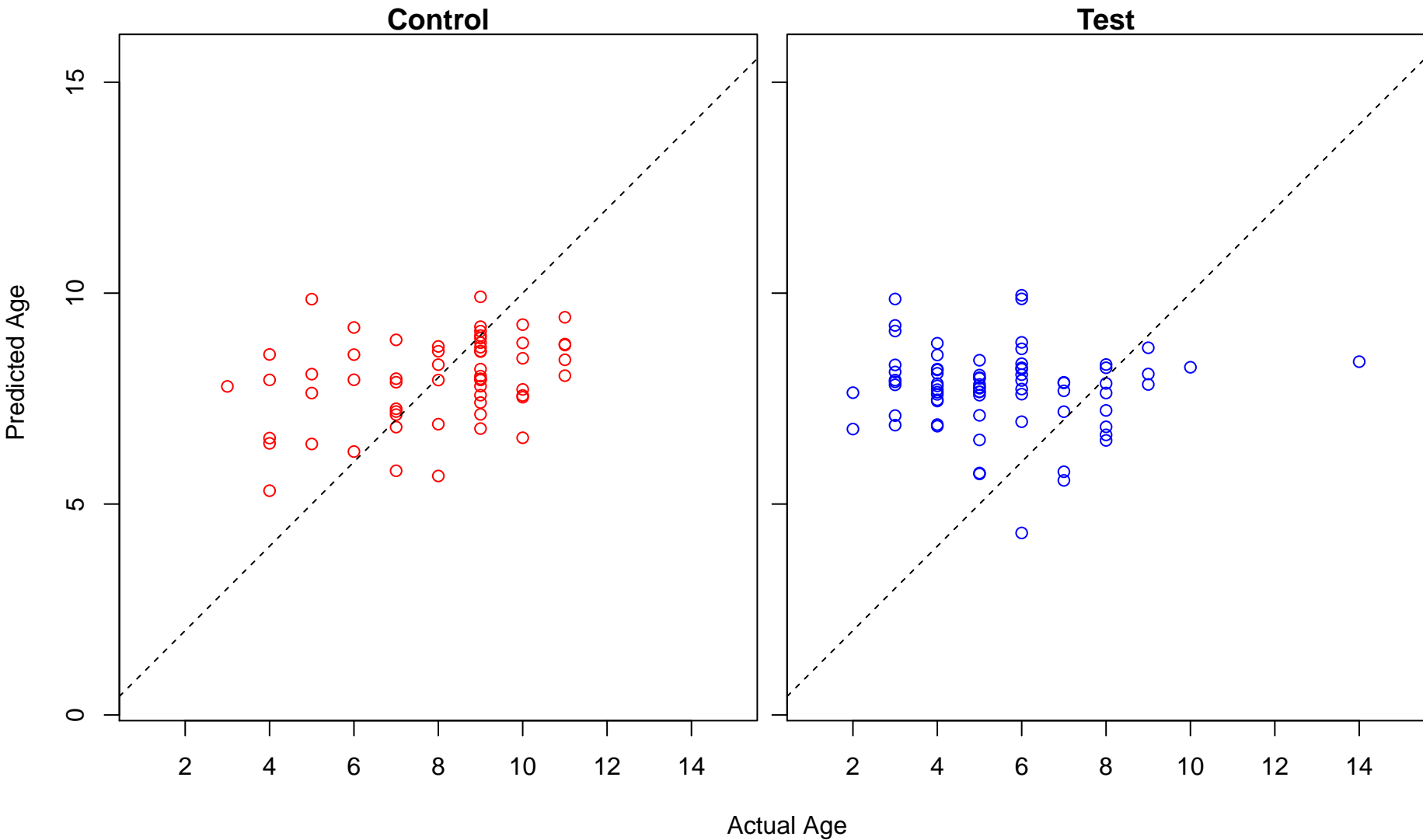
protein hexamerization (Score: 0.534766)



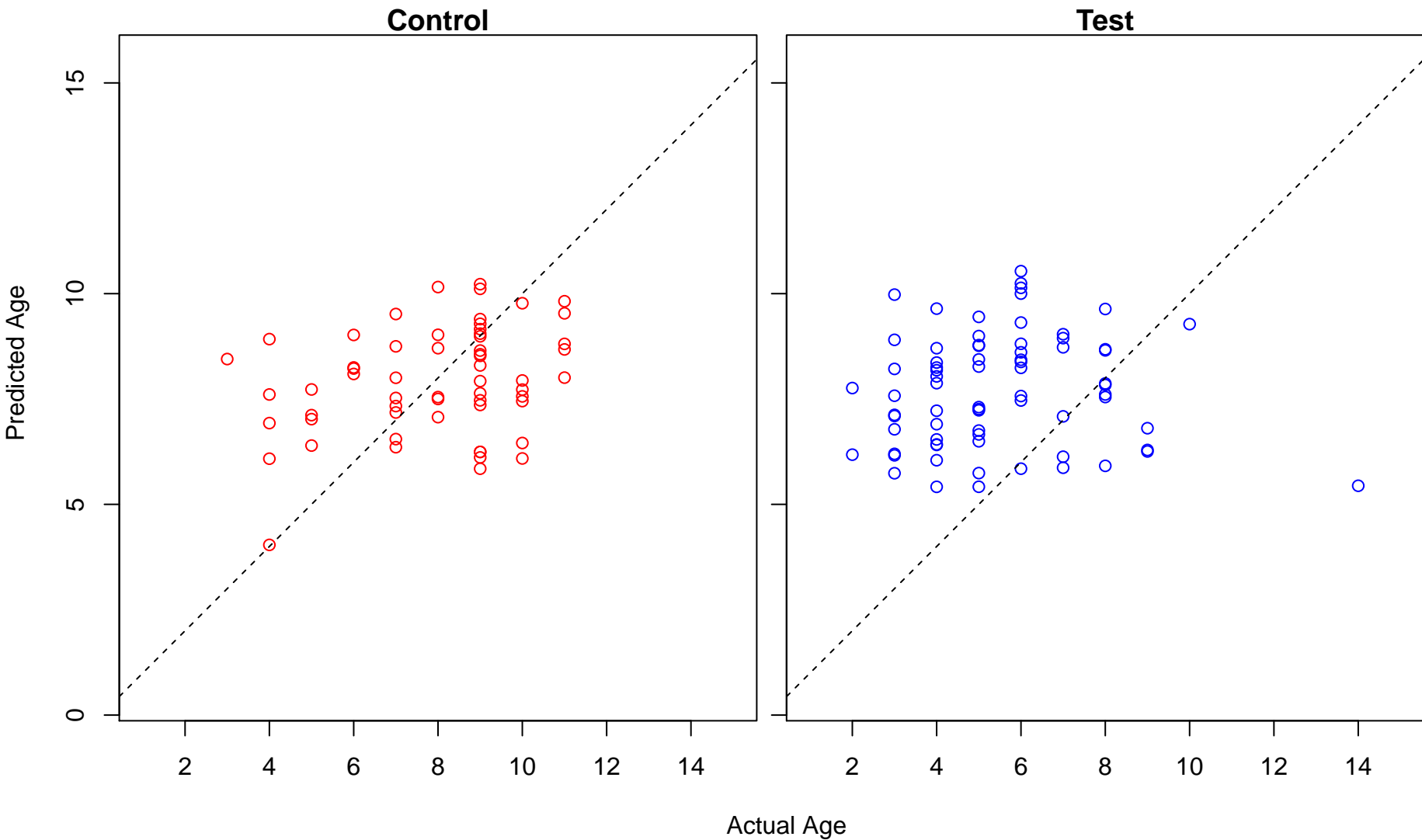
positive regulation of microtubule depolymerization (Score: 0.534711)



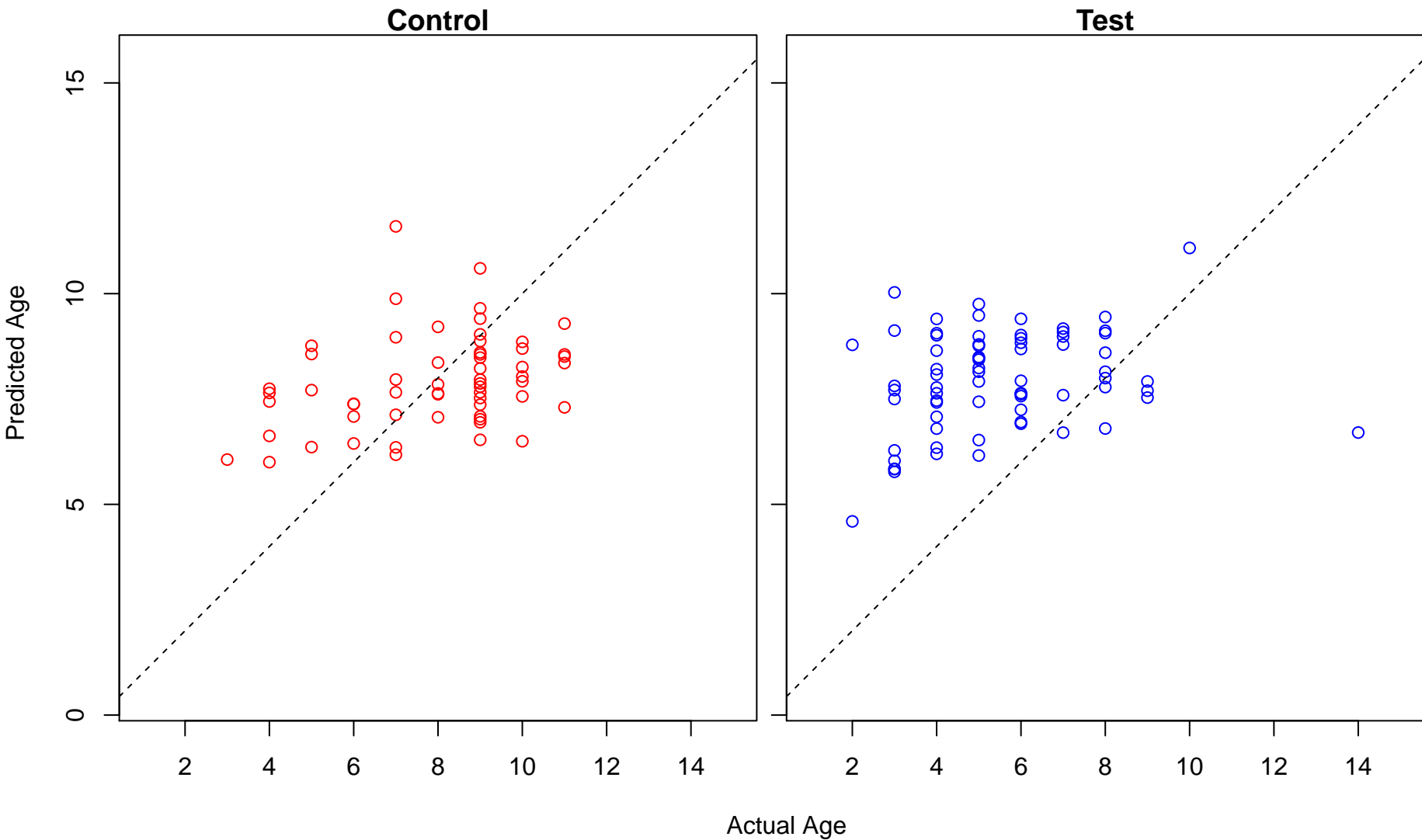
immunoglobulin biosynthetic process (Score: 0.533874)



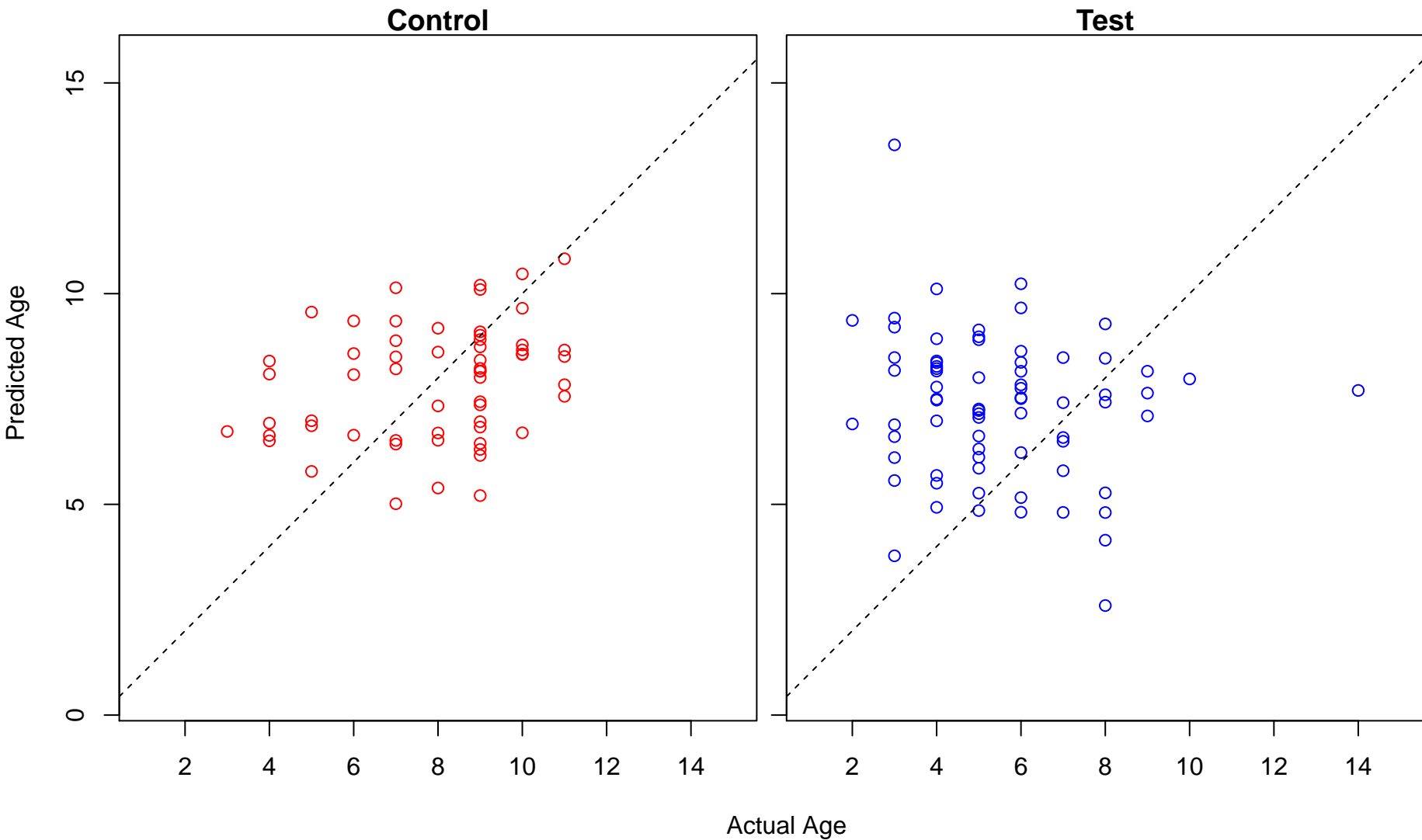
negative regulation of receptor-mediated endocytosis (Score: 0.532839)



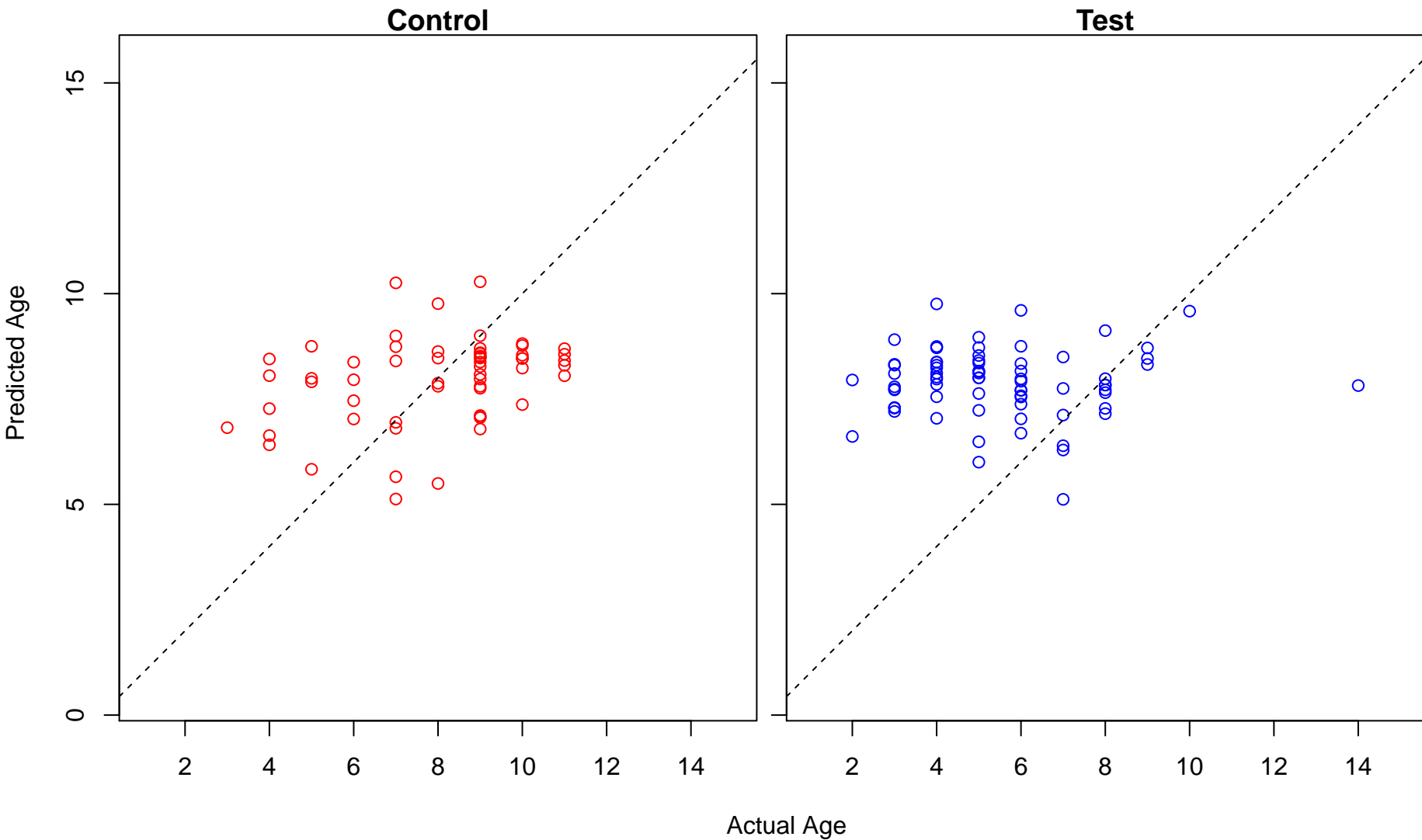
urate metabolic process (Score: 0.531962)



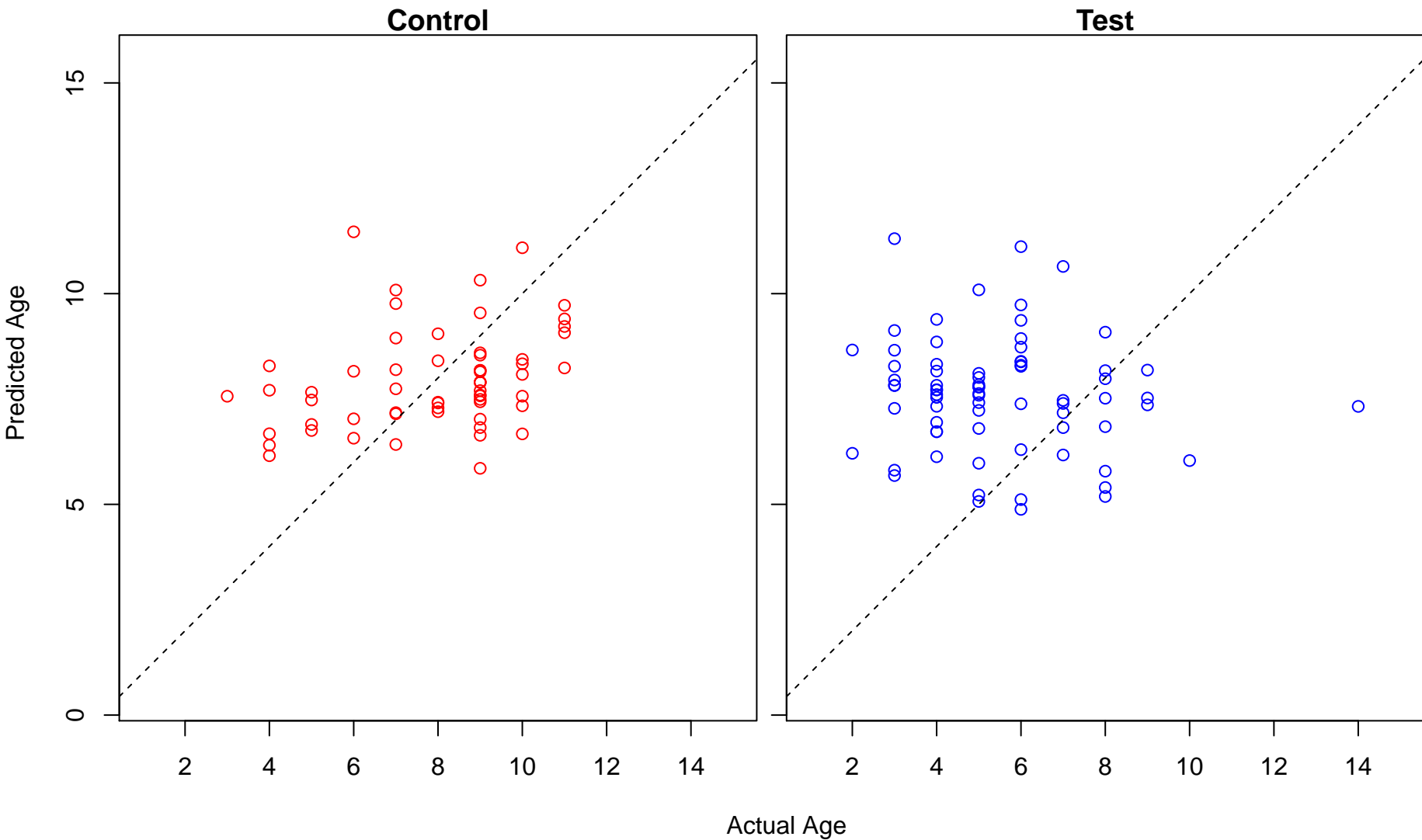
circadian regulation of translation (Score: 0.531303)



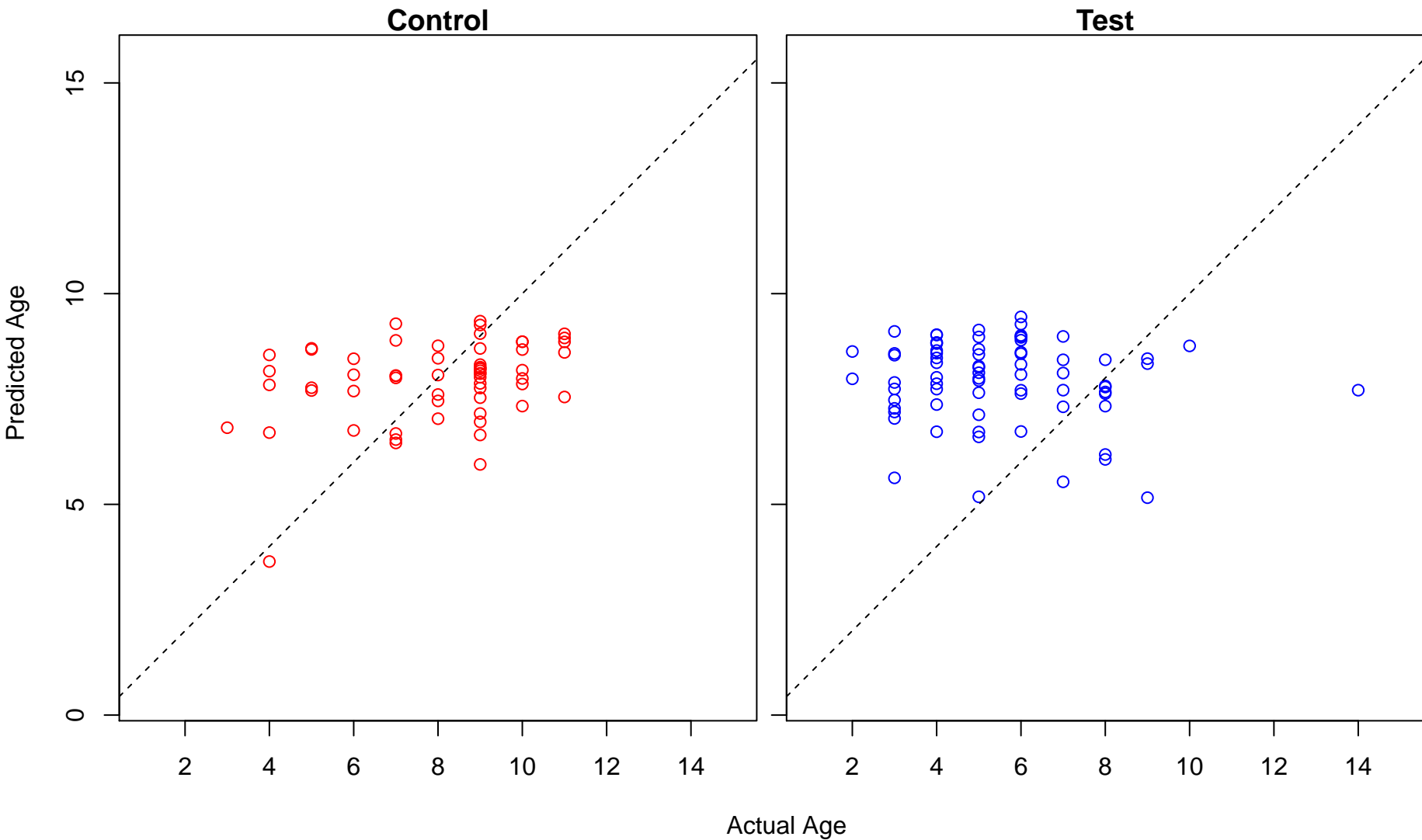
G0 to G1 transition (Score: 0.530913)



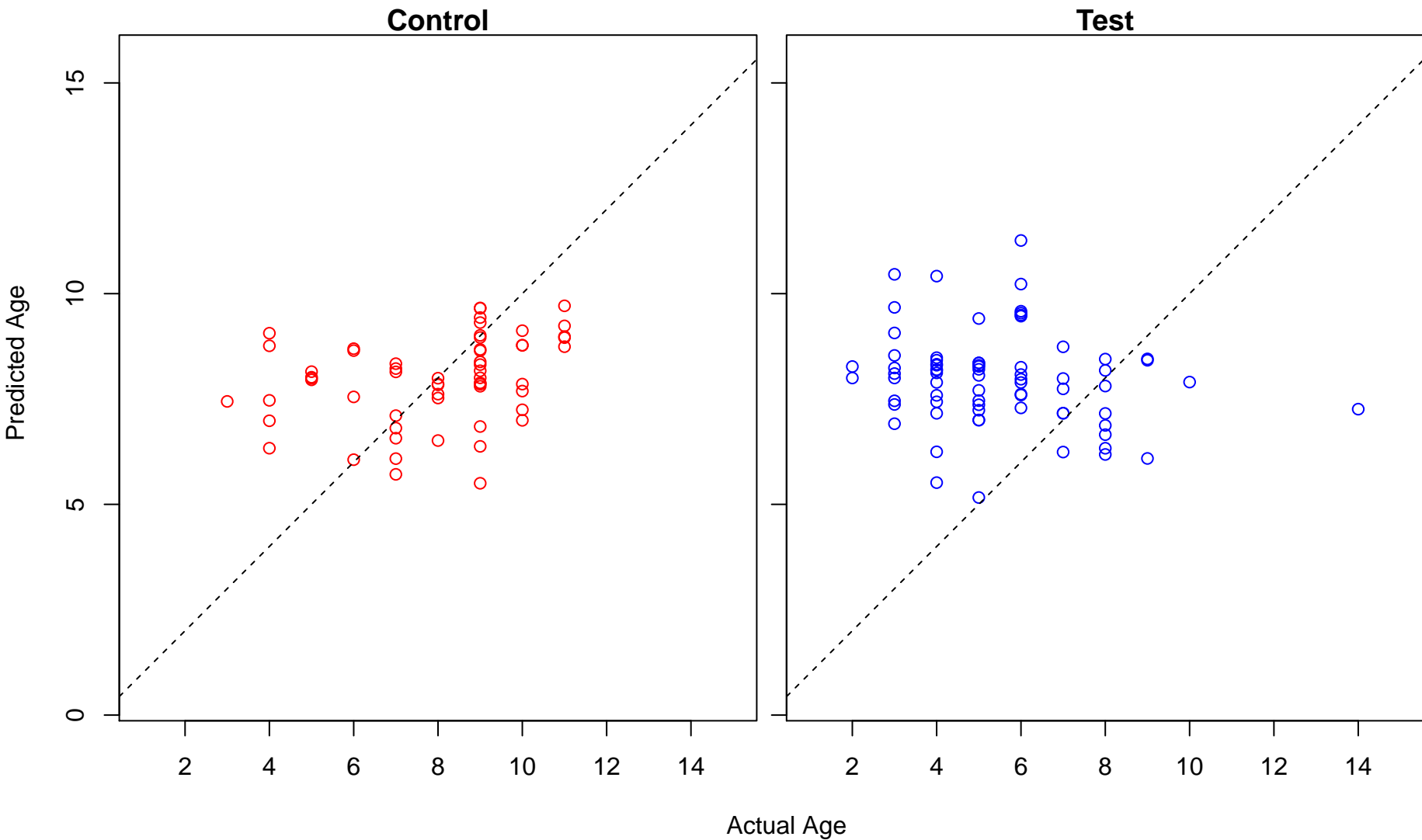
positive regulation of monooxygenase activity (Score: 0.530369)



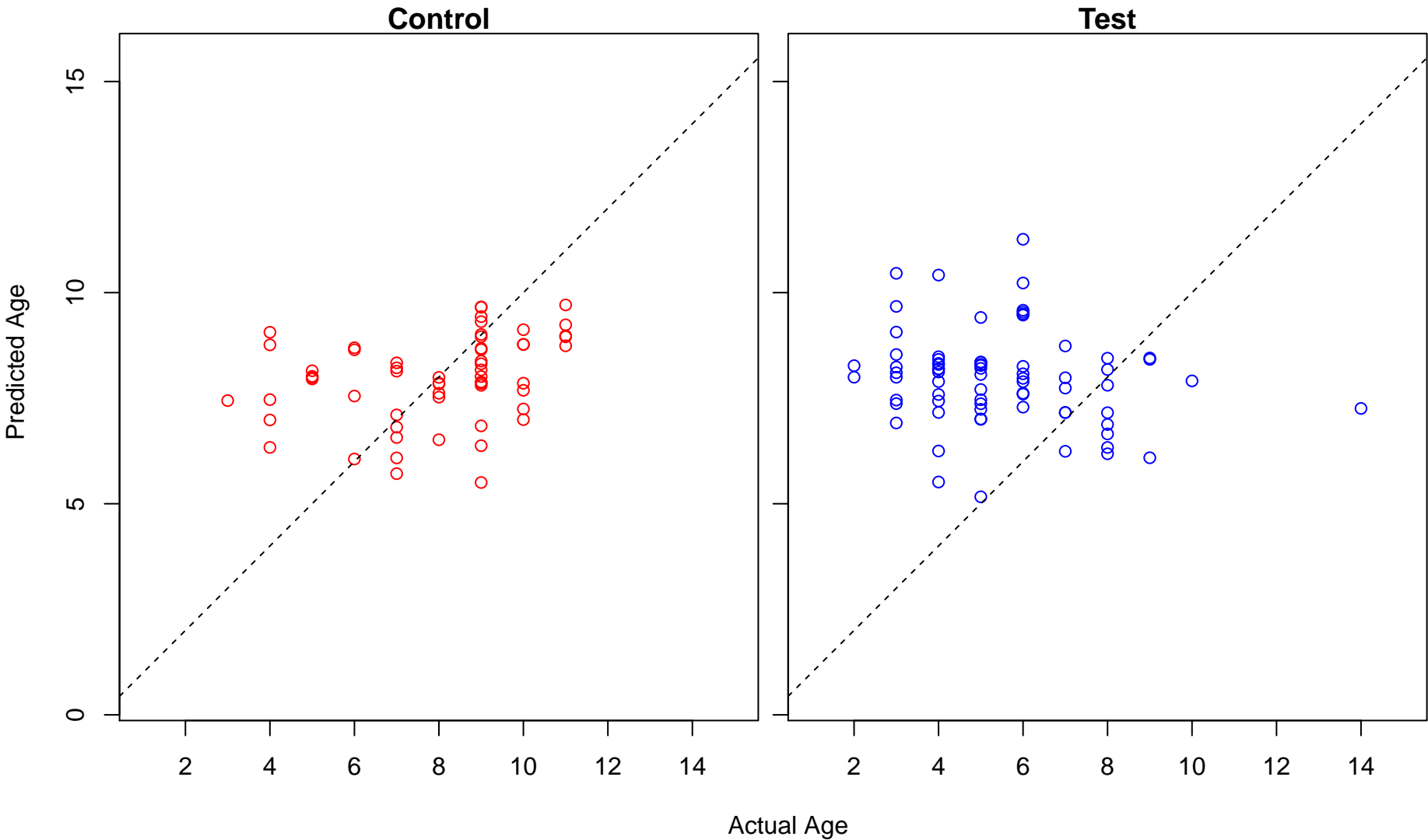
miRNA metabolic process (Score: 0.529701)



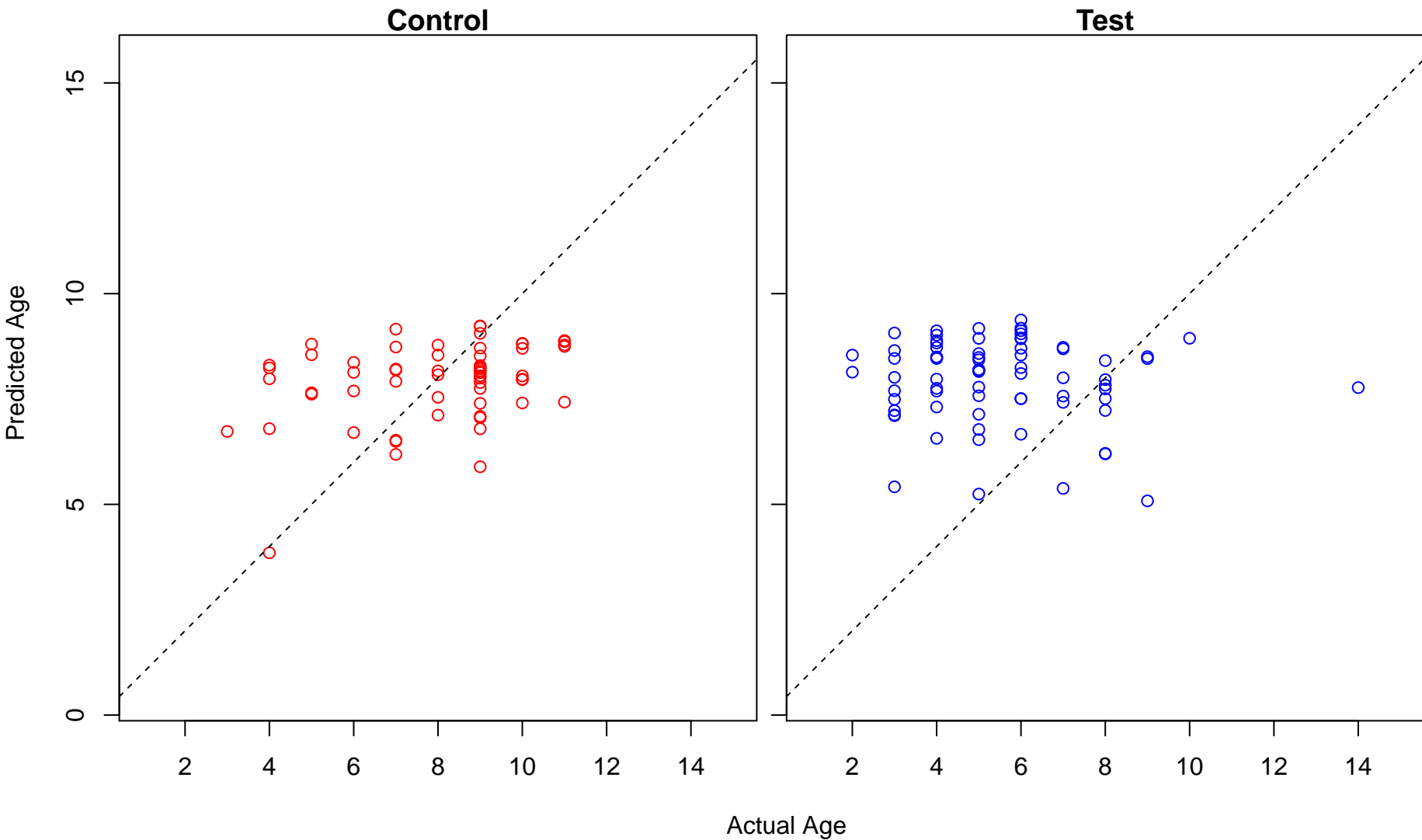
epithelial structure maintenance (Score: 0.528380)



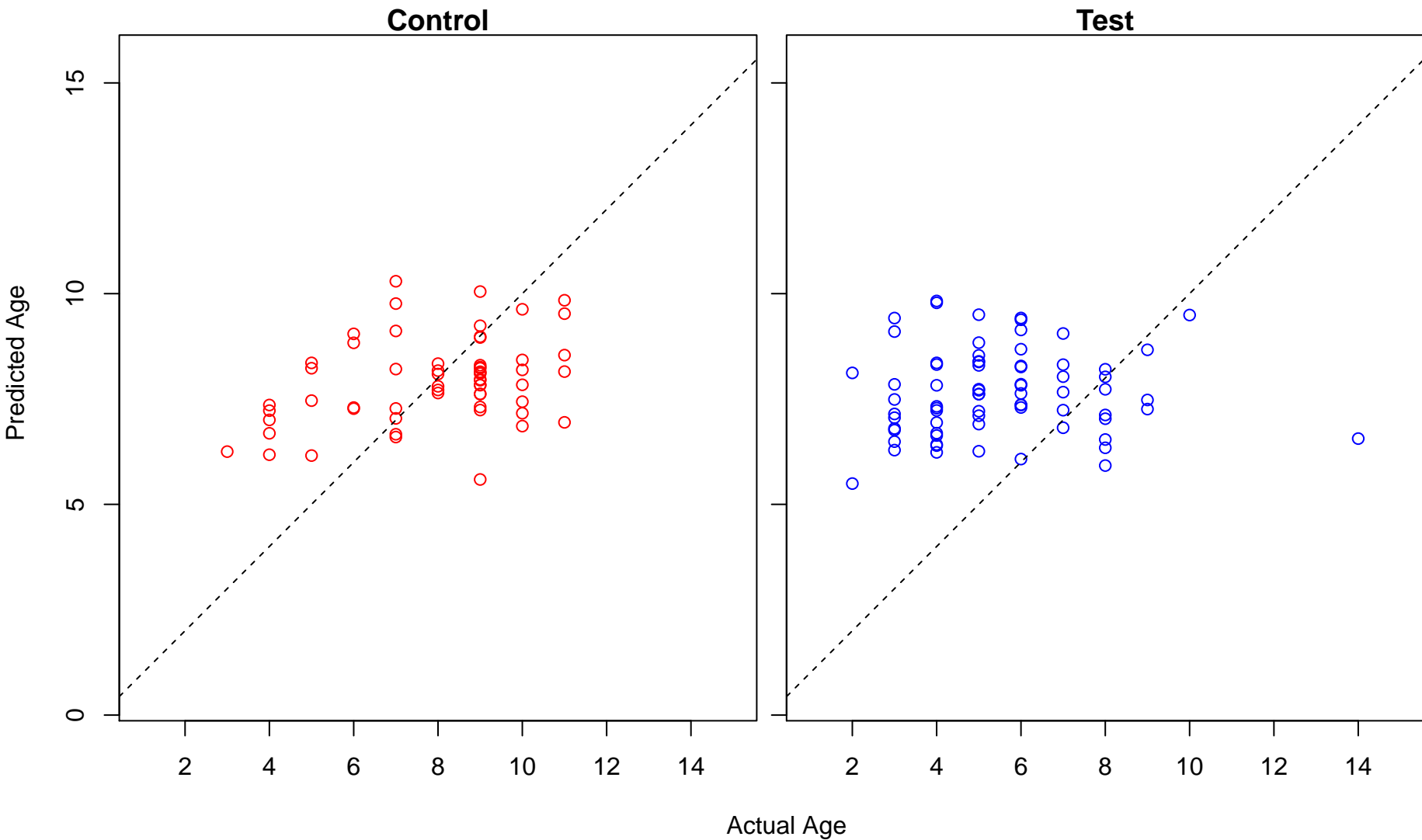
maintenance of gastrointestinal epithelium (Score: 0.528294)



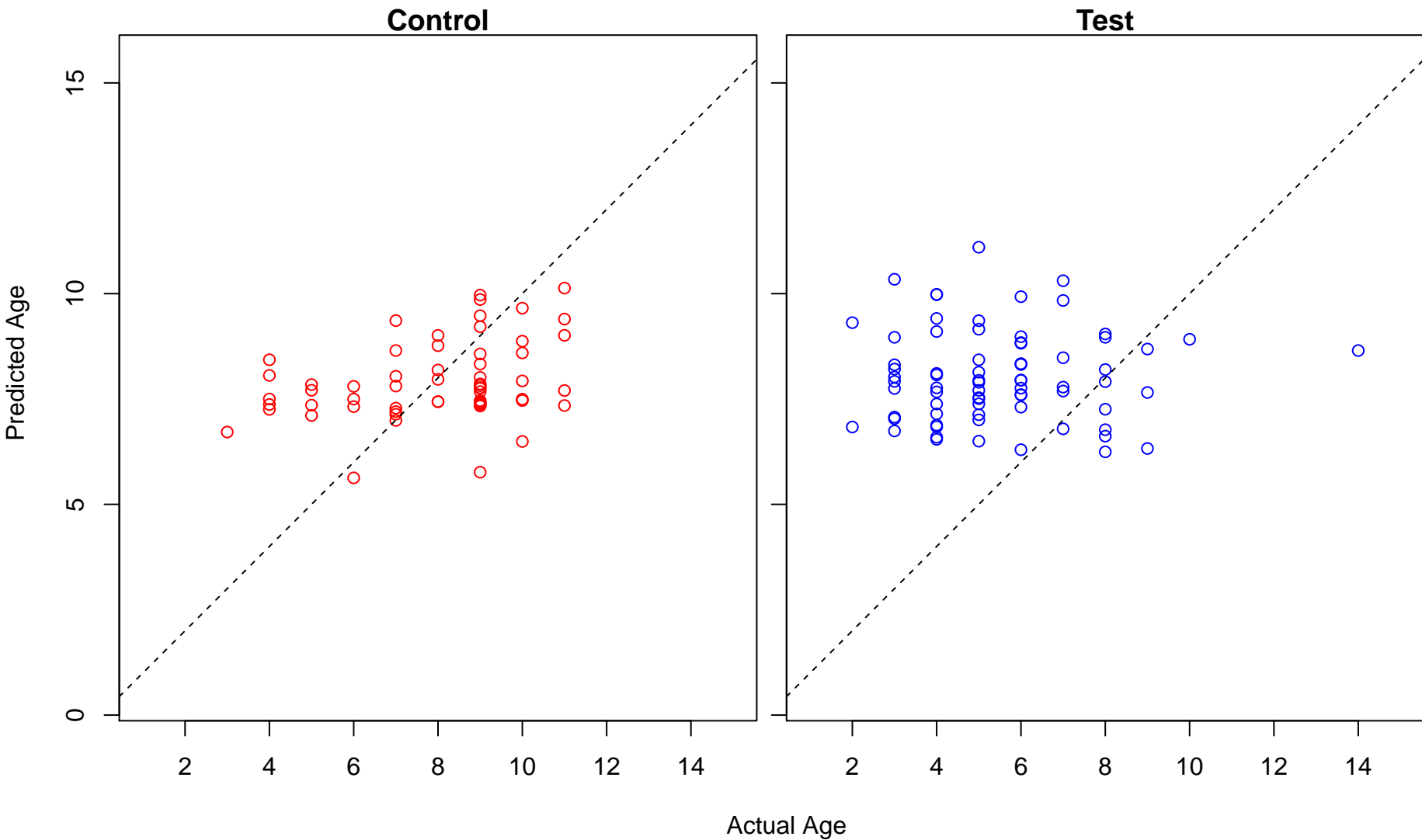
miRNA catabolic process (Score: 0.527720)



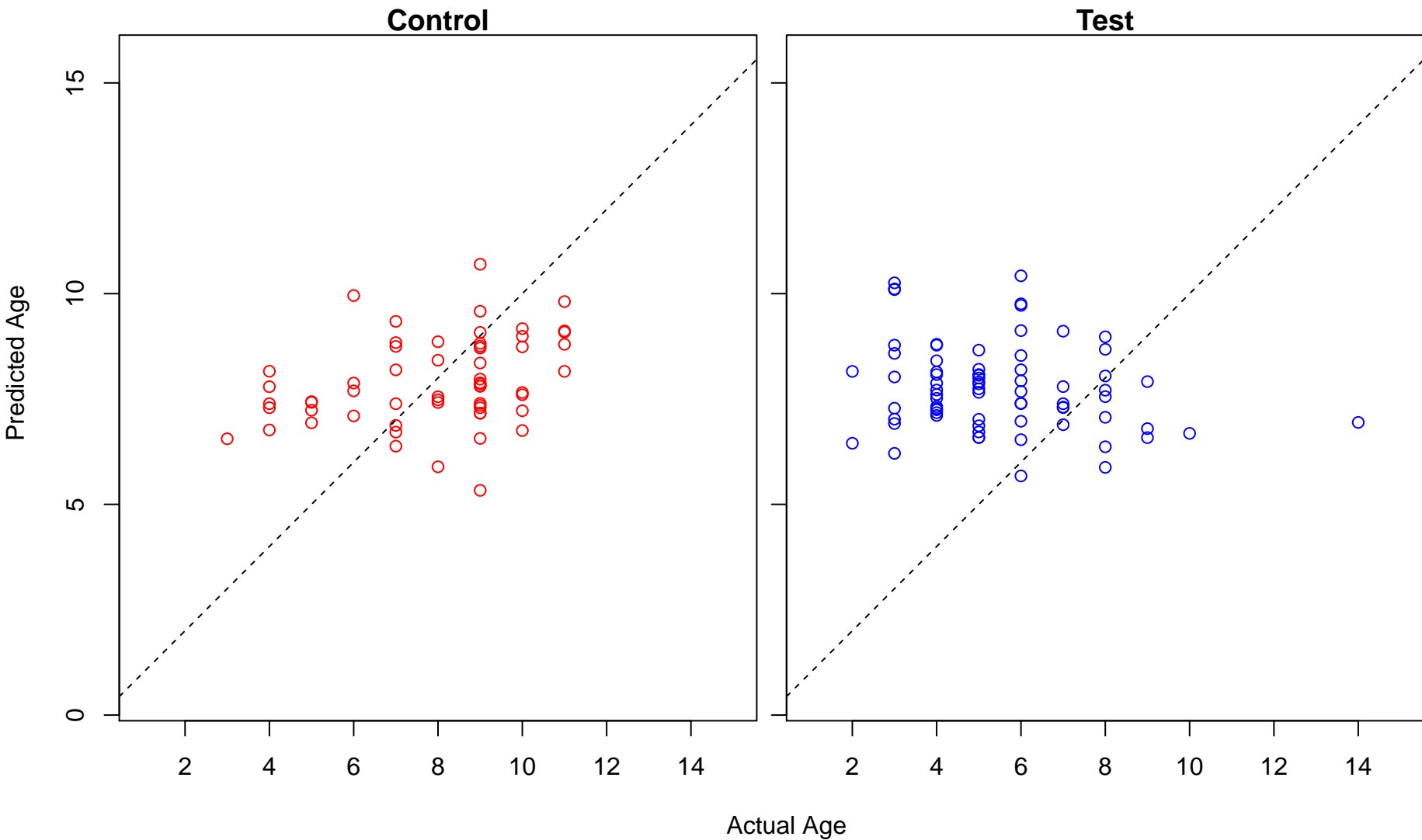
regulation of glycogen (starch) synthase activity (Score: 0.526029)



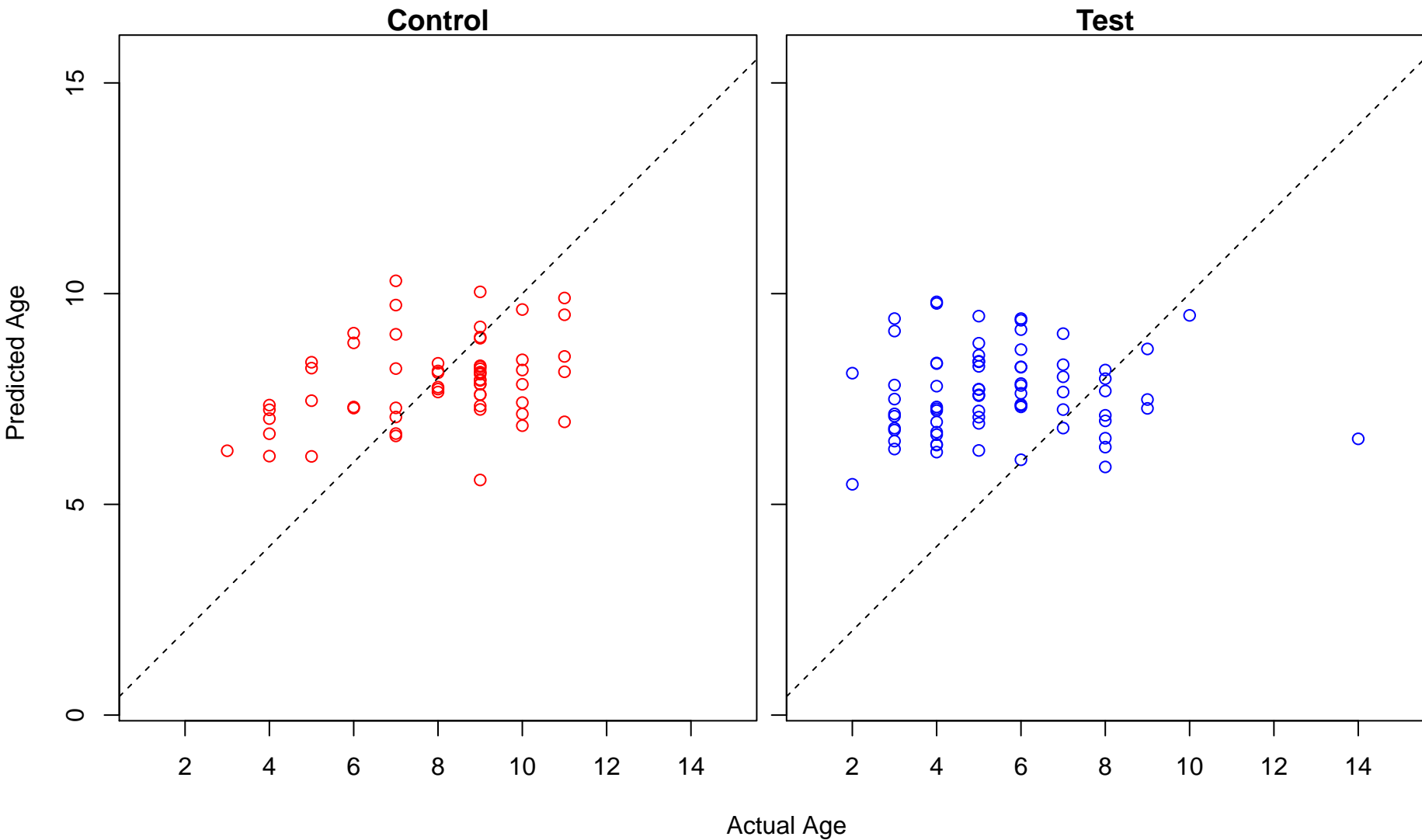
posterior midgut development (Score: 0.524321)



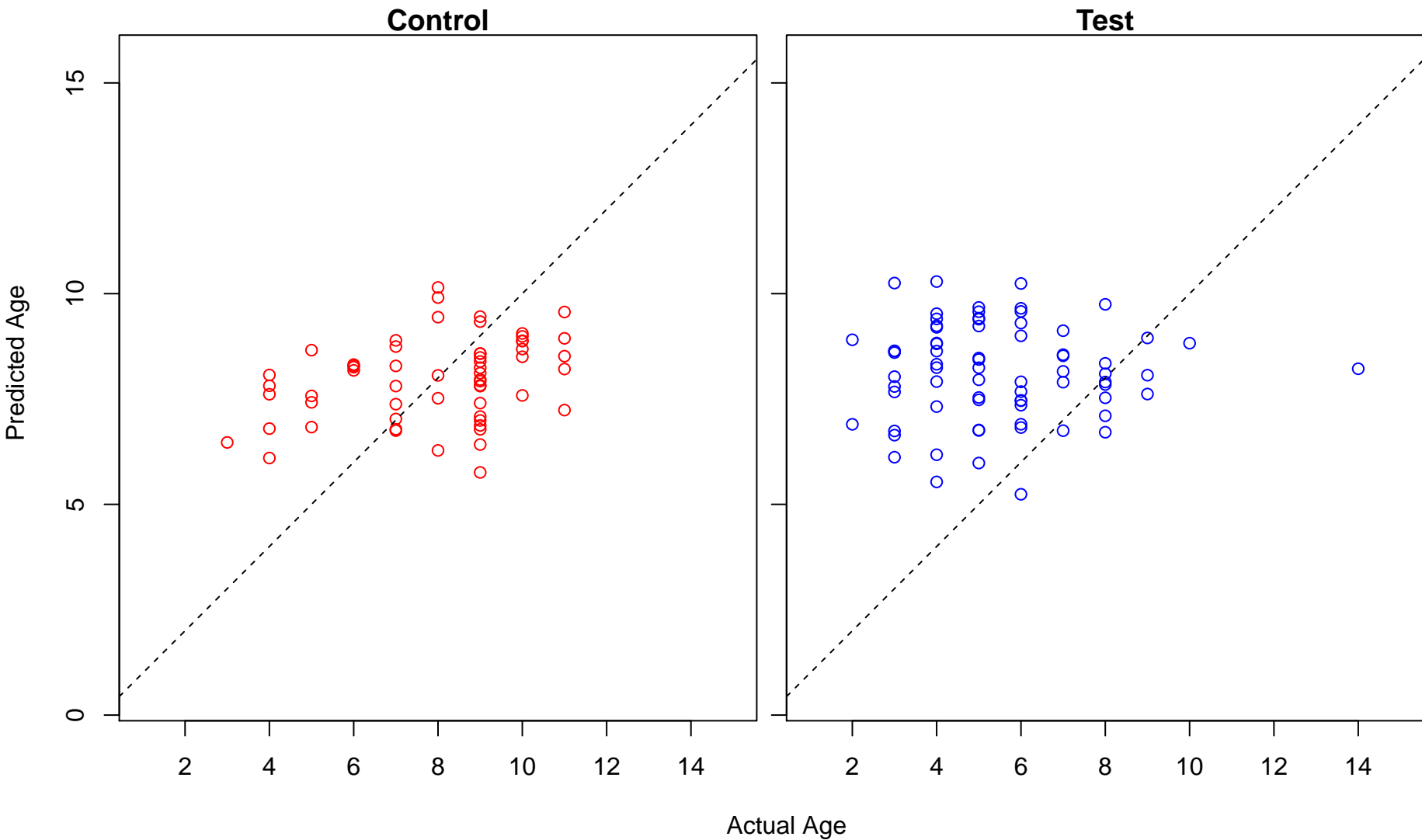
response to manganese ion (Score: 0.523340)



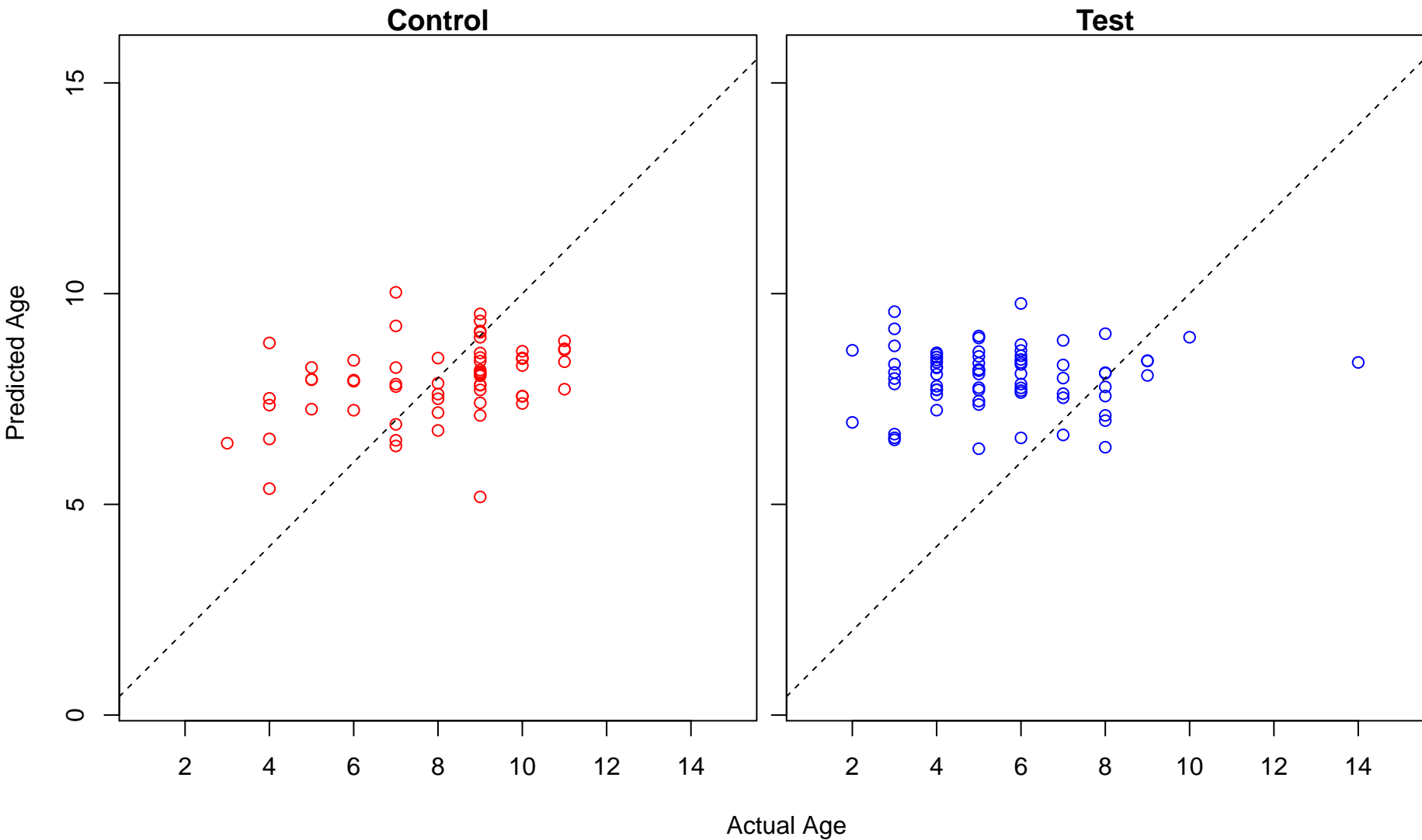
negative regulation of glycogen (starch) synthase activity (Score: 0.522131)



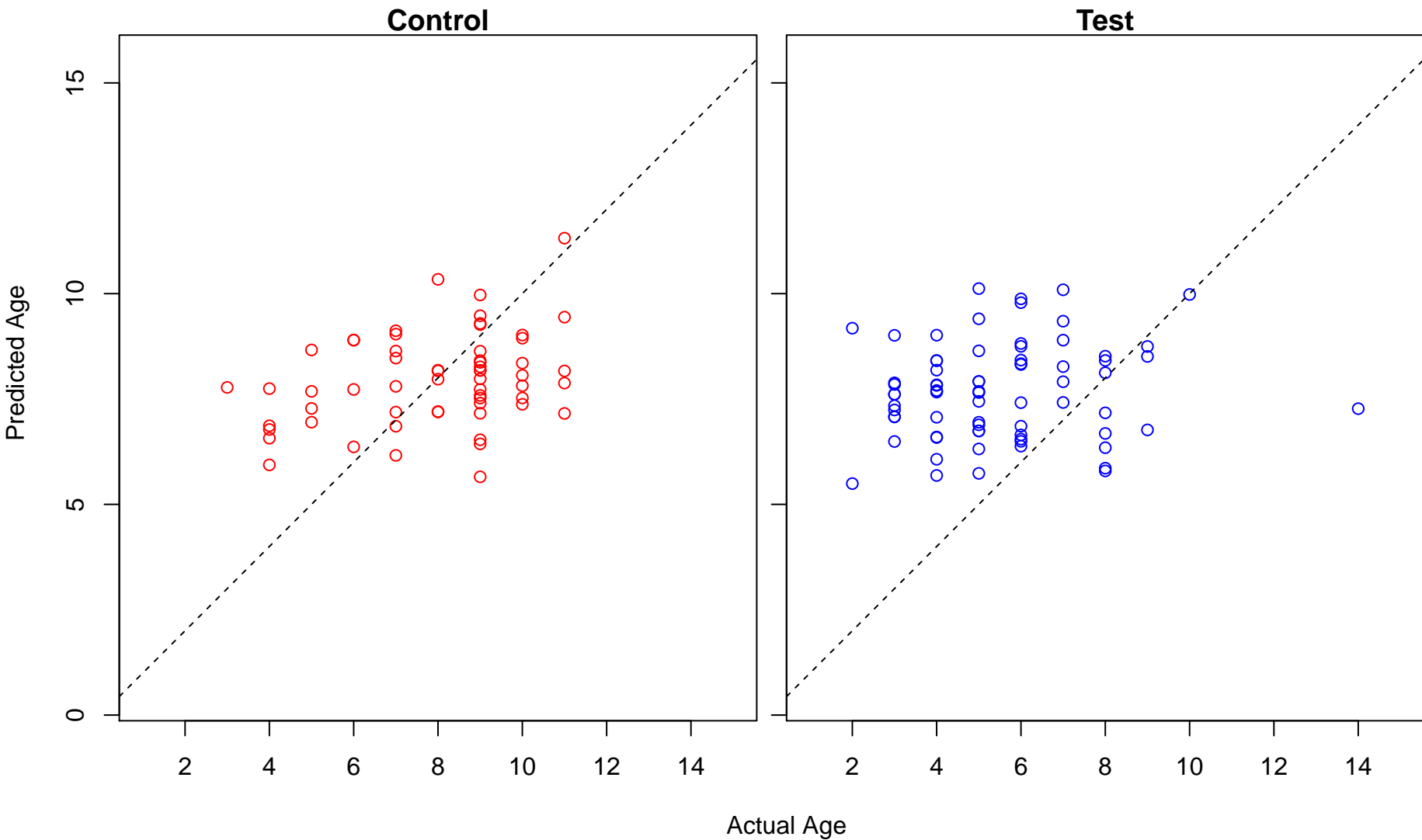
resolution of meiotic recombination intermediates (Score: 0.522055)



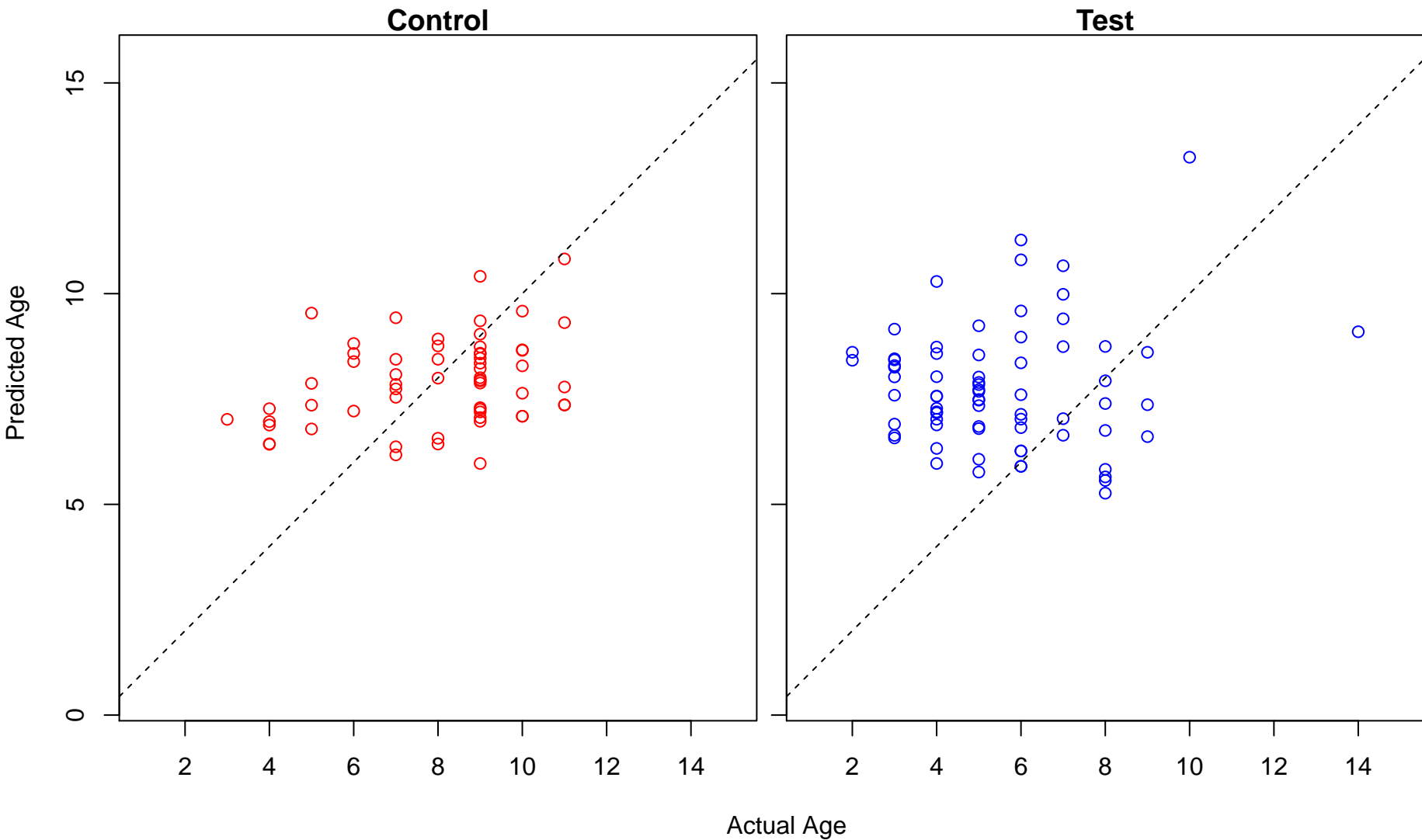
keratinocyte development (Score: 0.520788)



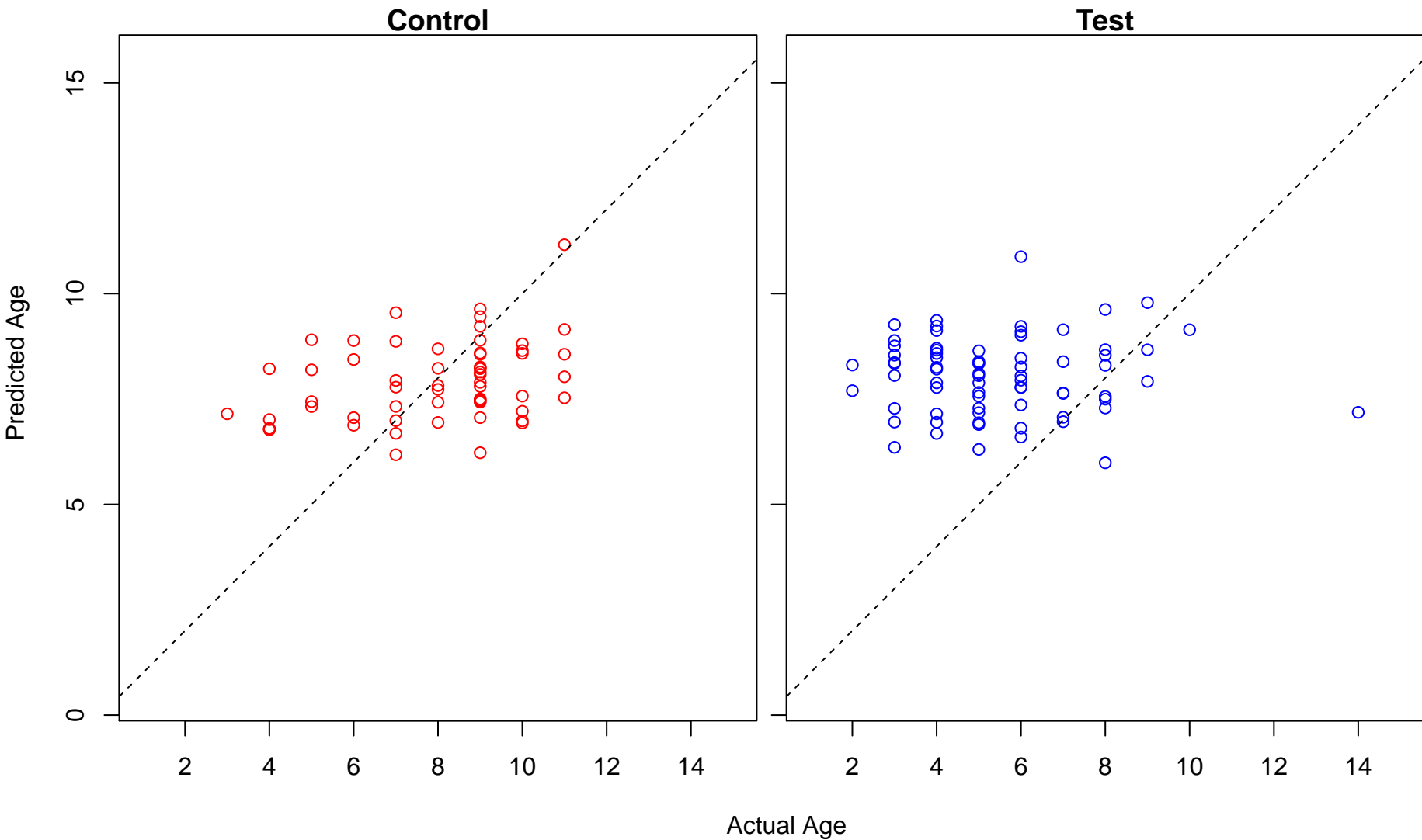
regulation of extent of cell growth (Score: 0.519330)



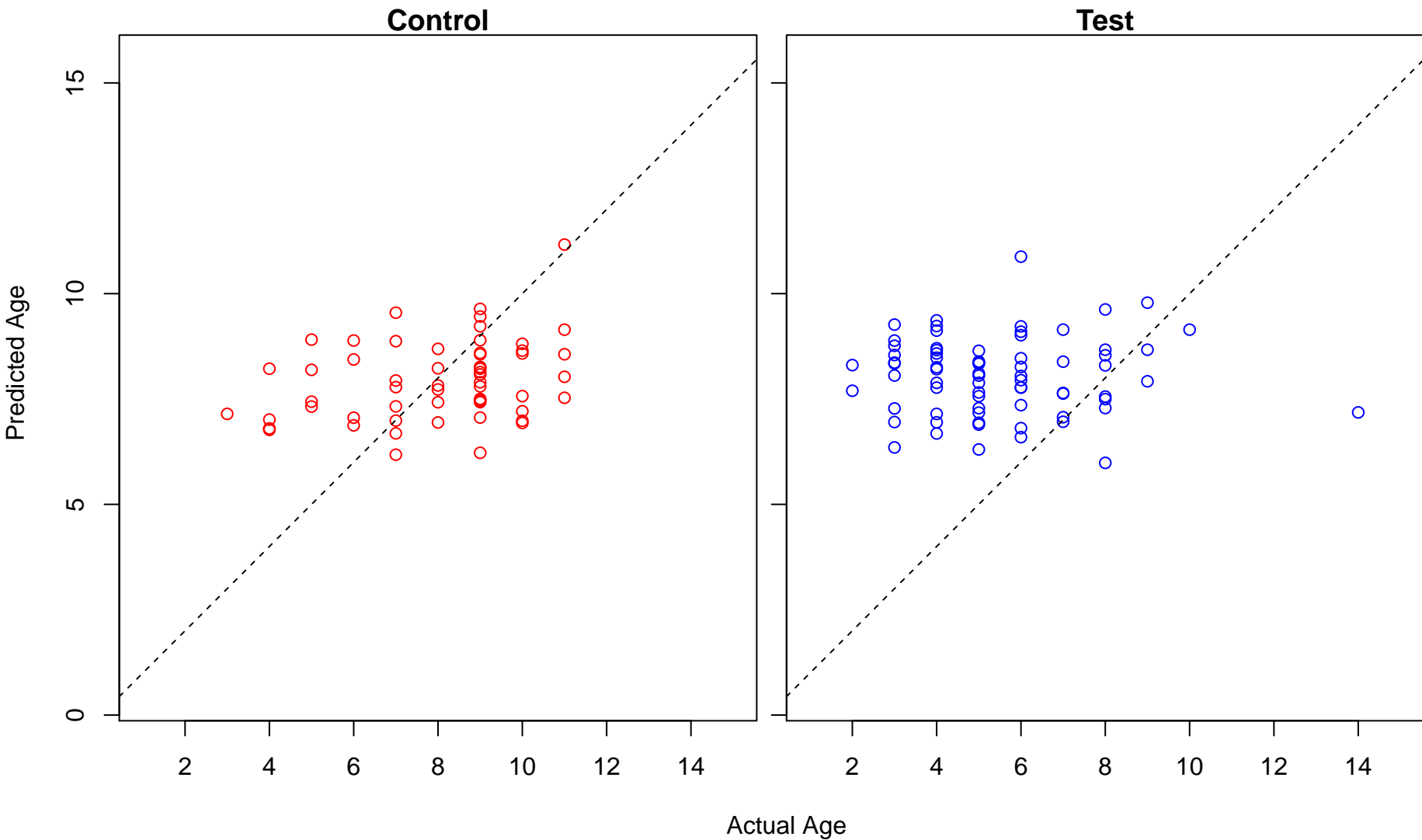
protein repair (Score: 0.519097)



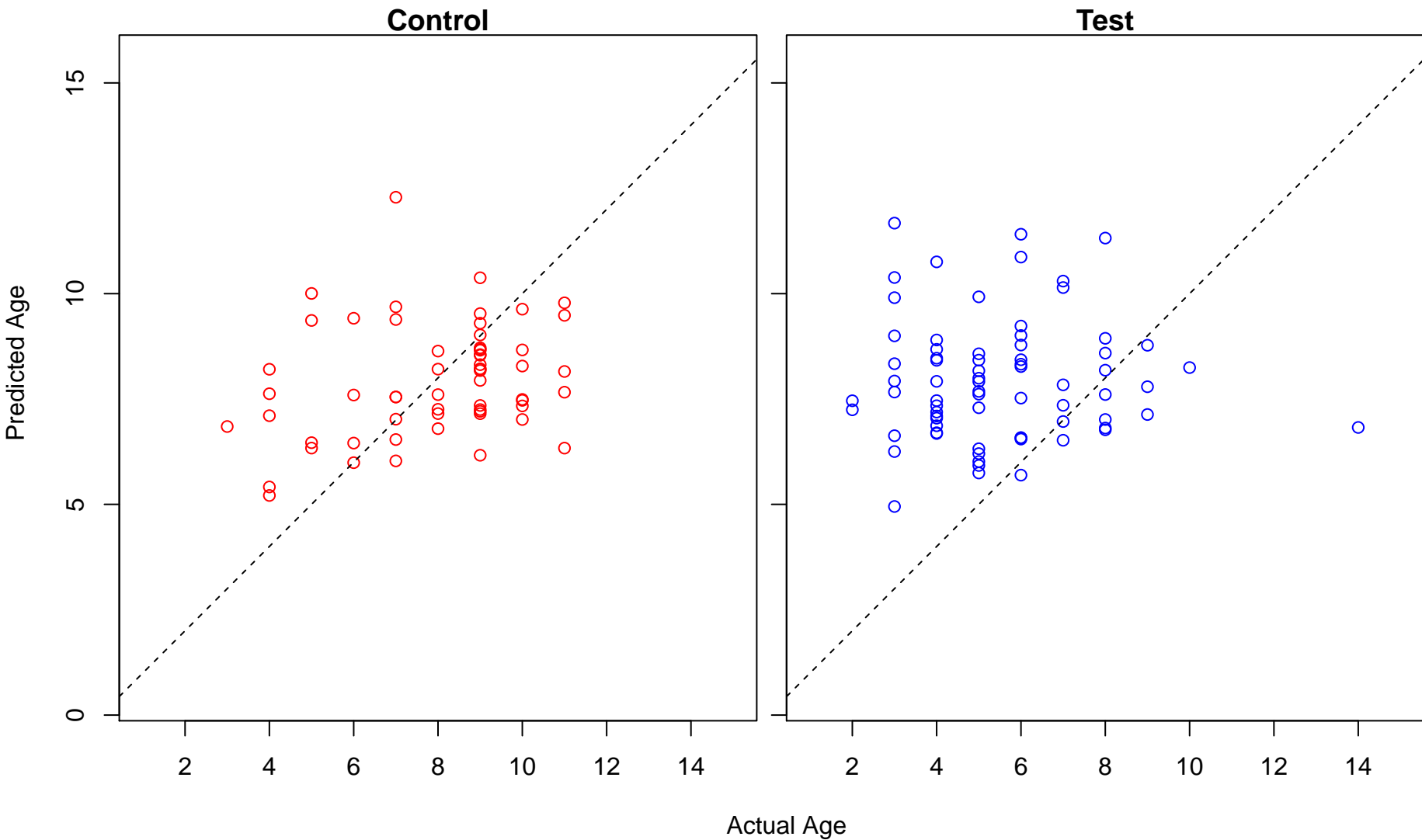
negative regulation of T-helper 2 cell differentiation (Score: 0.518732)



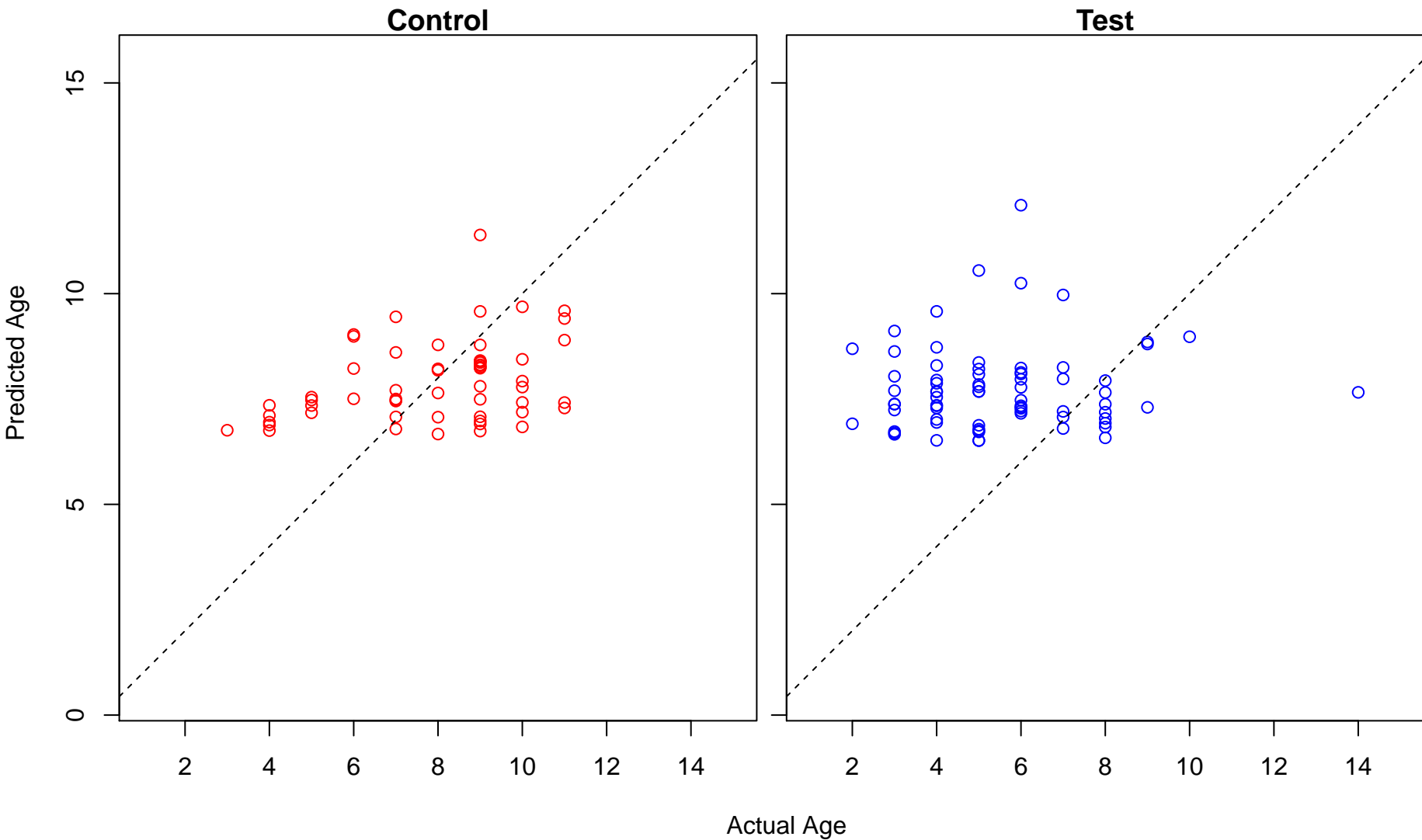
positive regulation of T-helper 1 cell differentiation (Score: 0.518635)



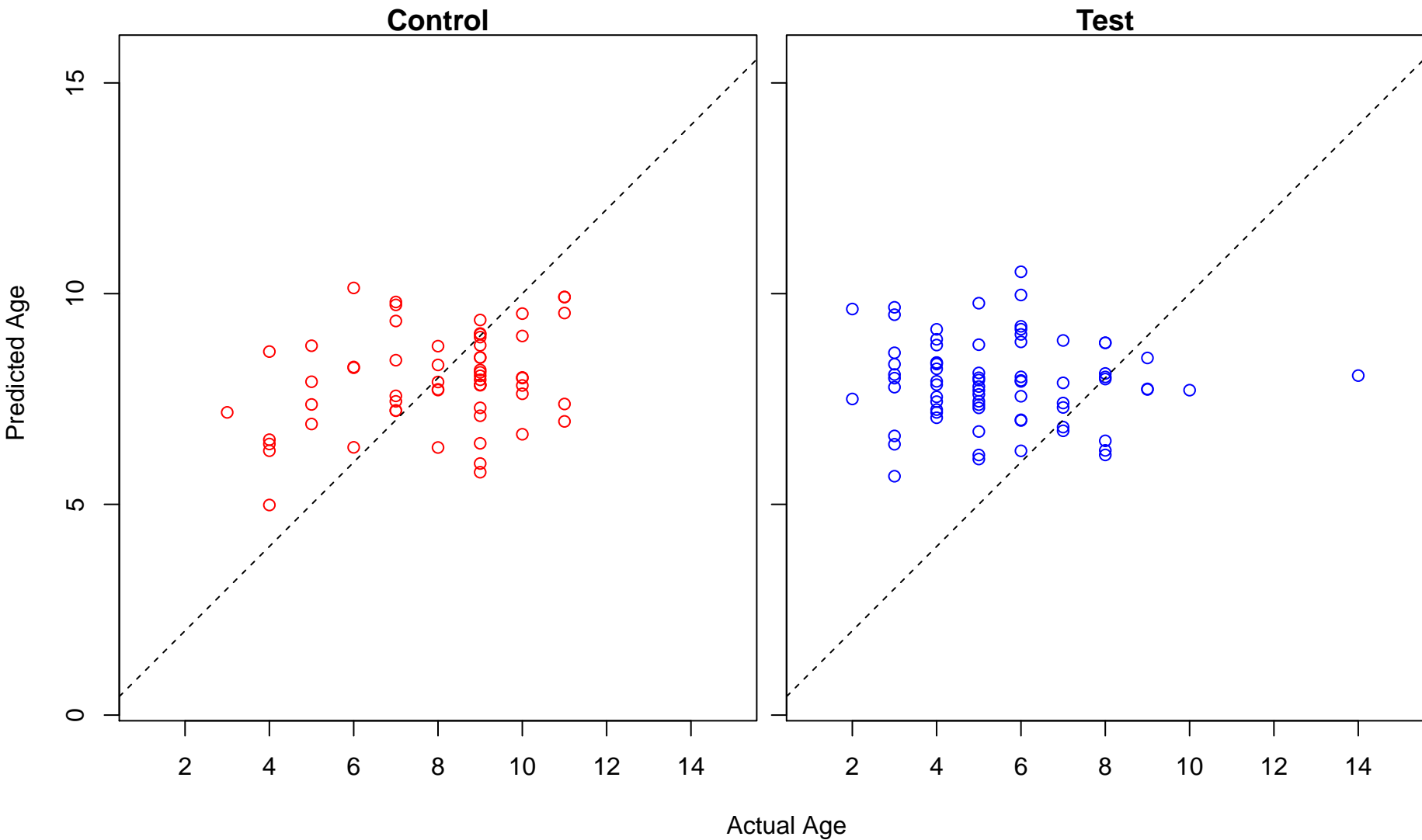
positive regulation of phosphoprotein phosphatase activity (Score: 0.518477)



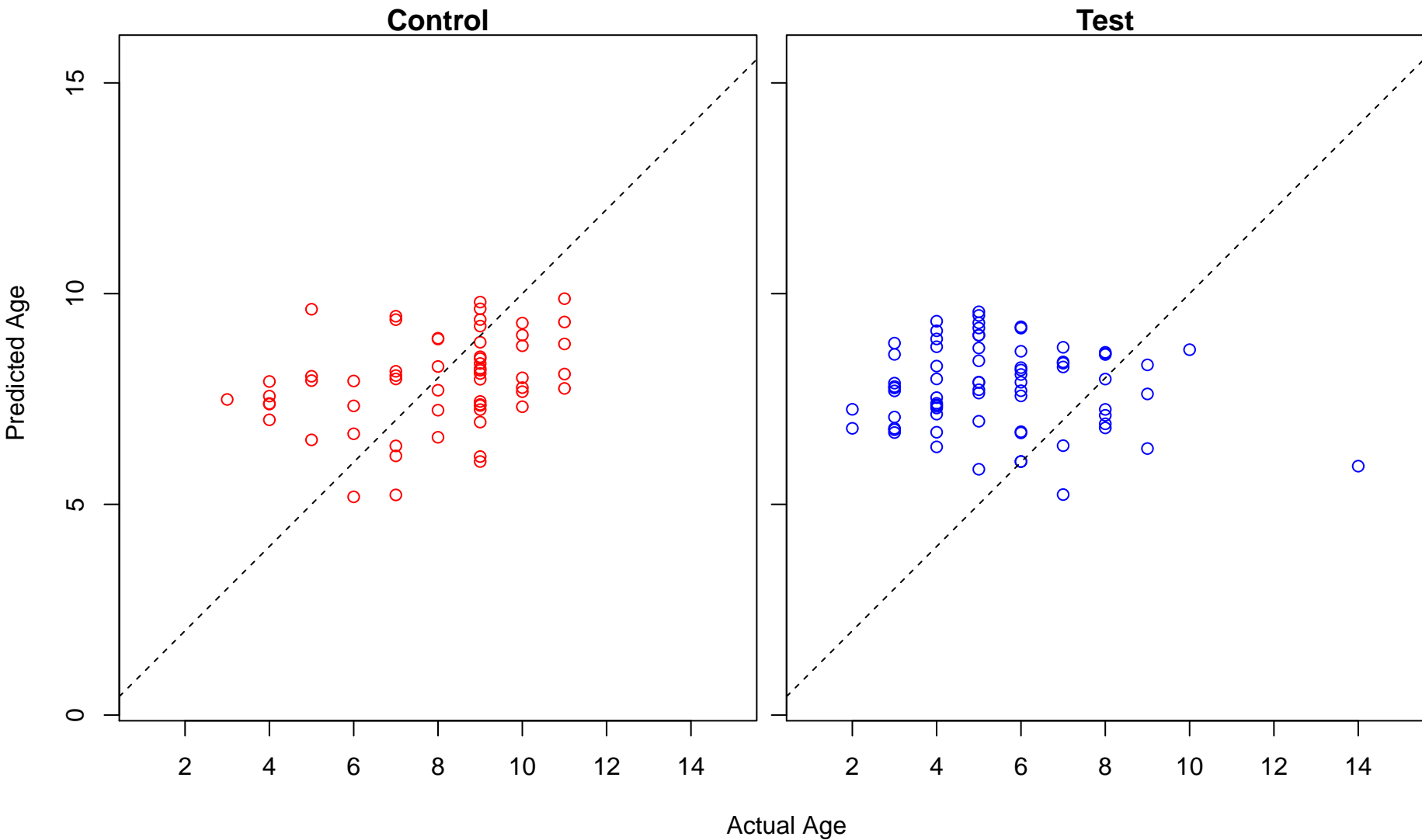
macrophage differentiation (Score: 0.516806)



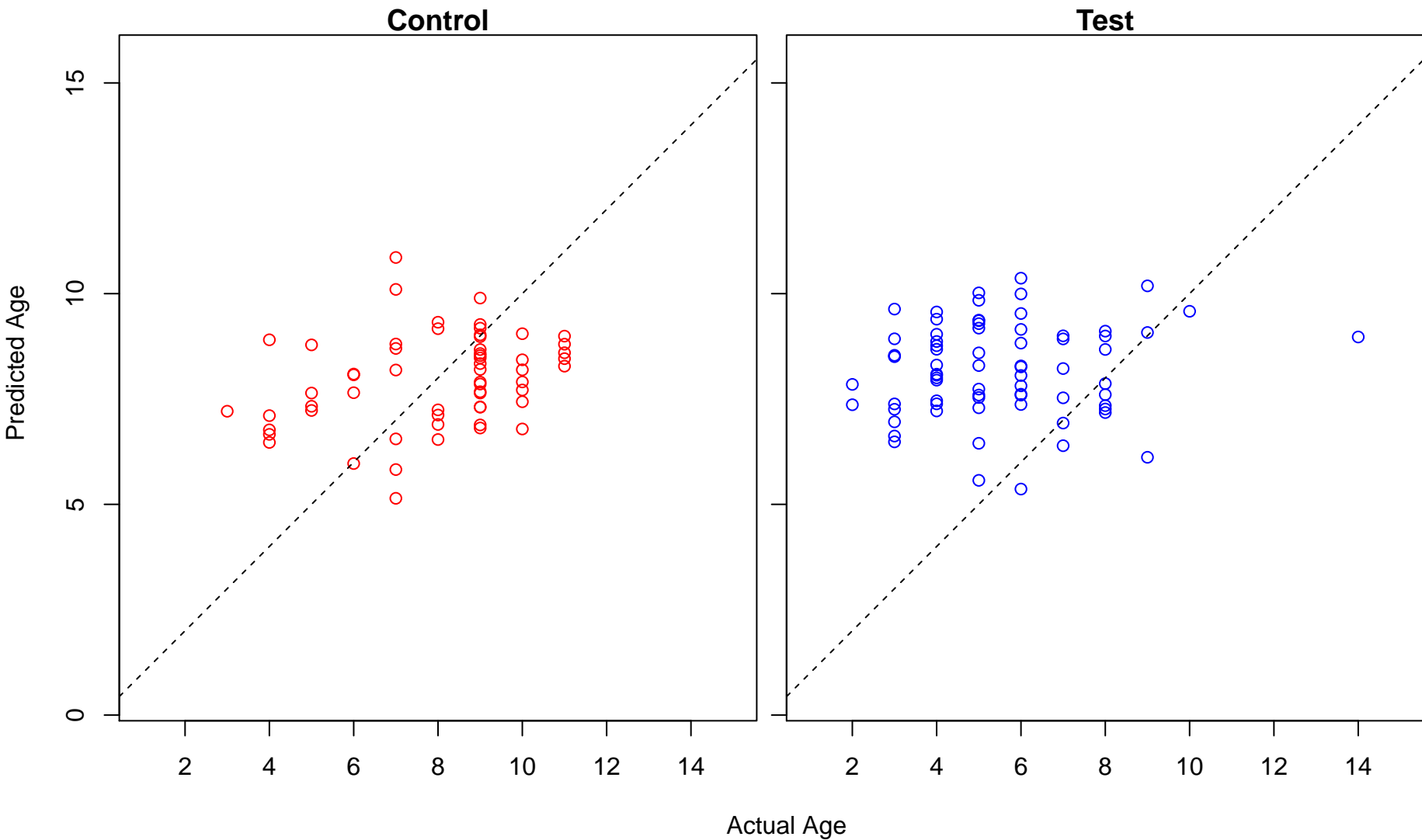
regulation of peptidyl-serine phosphorylation (Score: 0.516802)



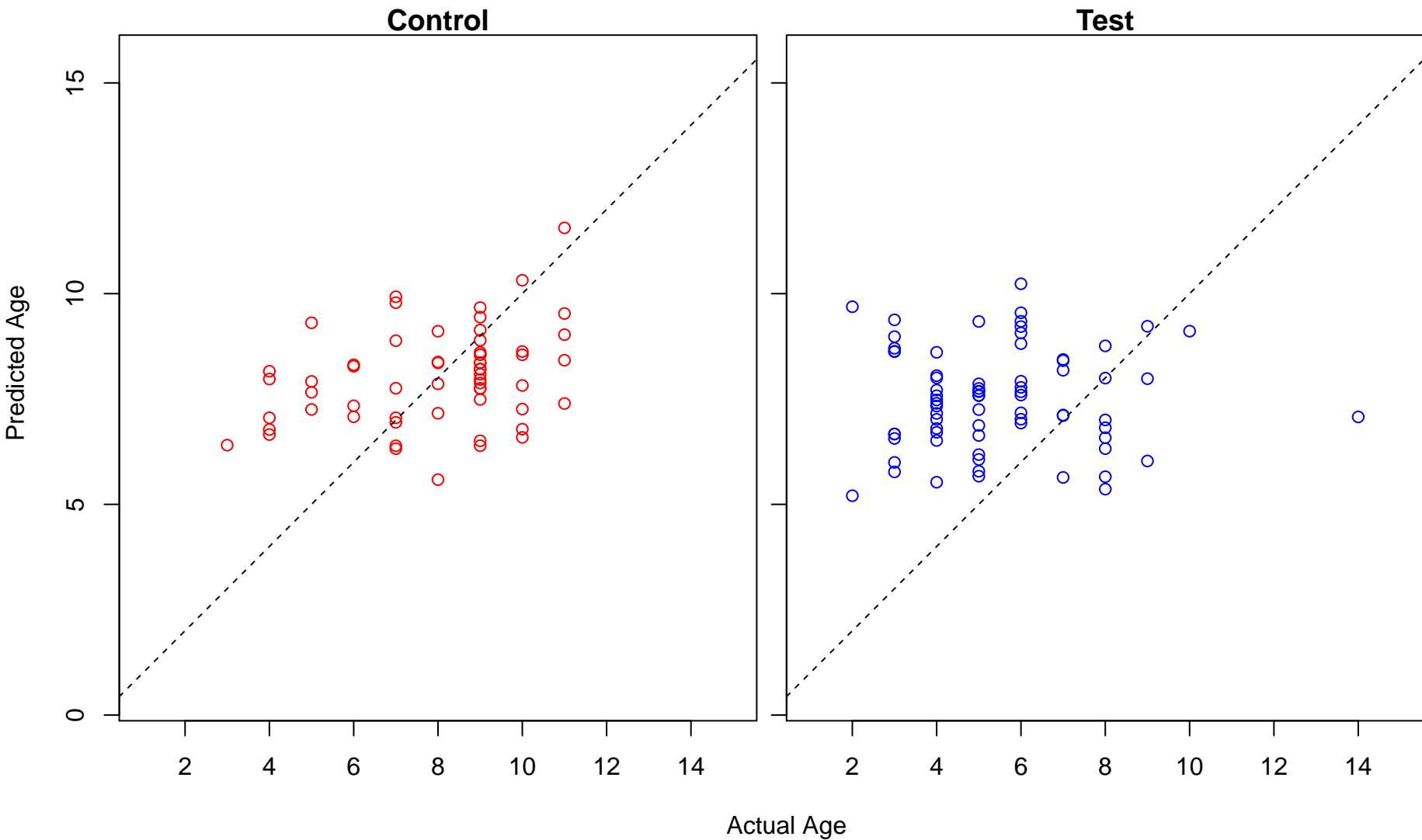
positive regulation of protein sumoylation (Score: 0.516580)



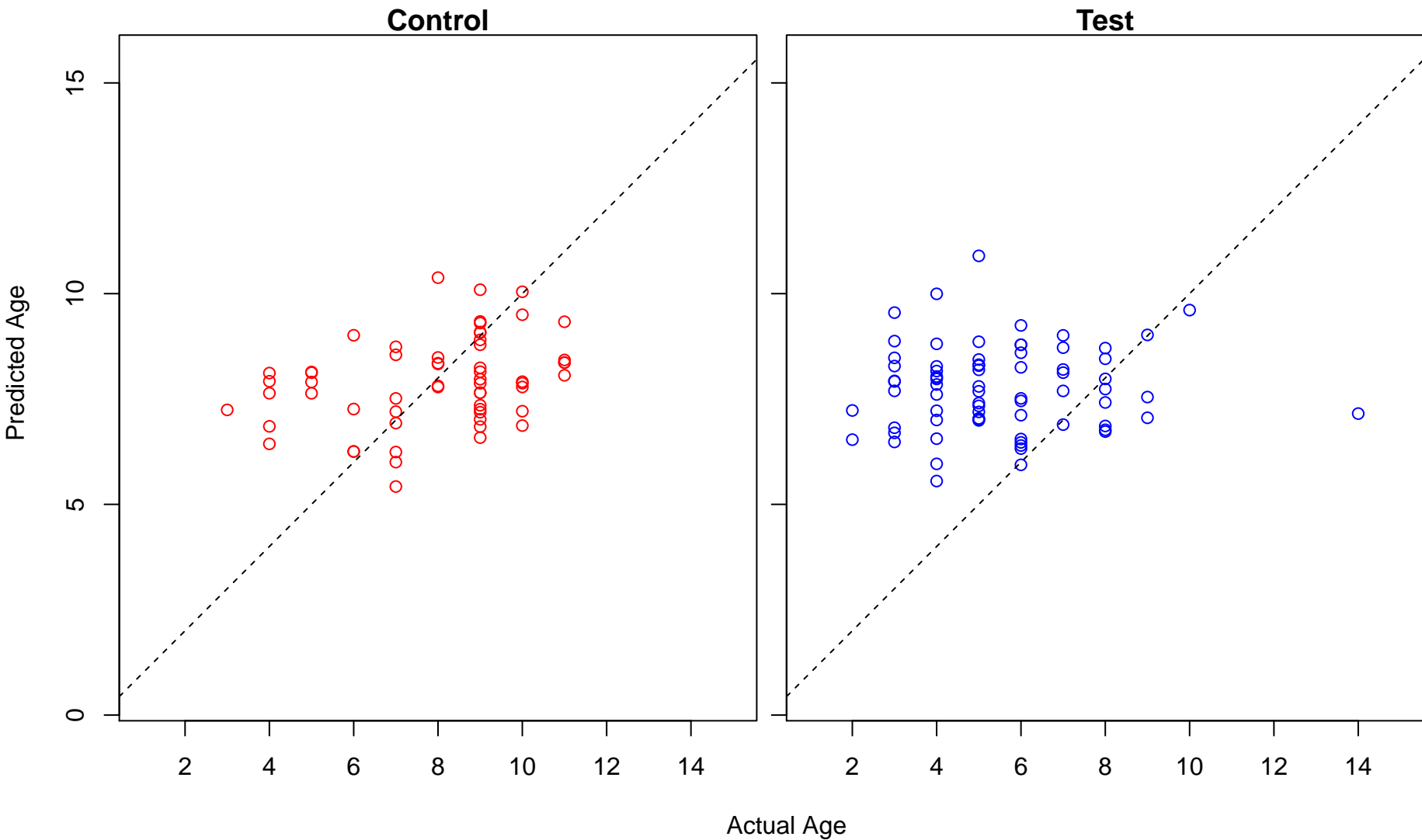
paraxial mesoderm morphogenesis (Score: 0.515980)



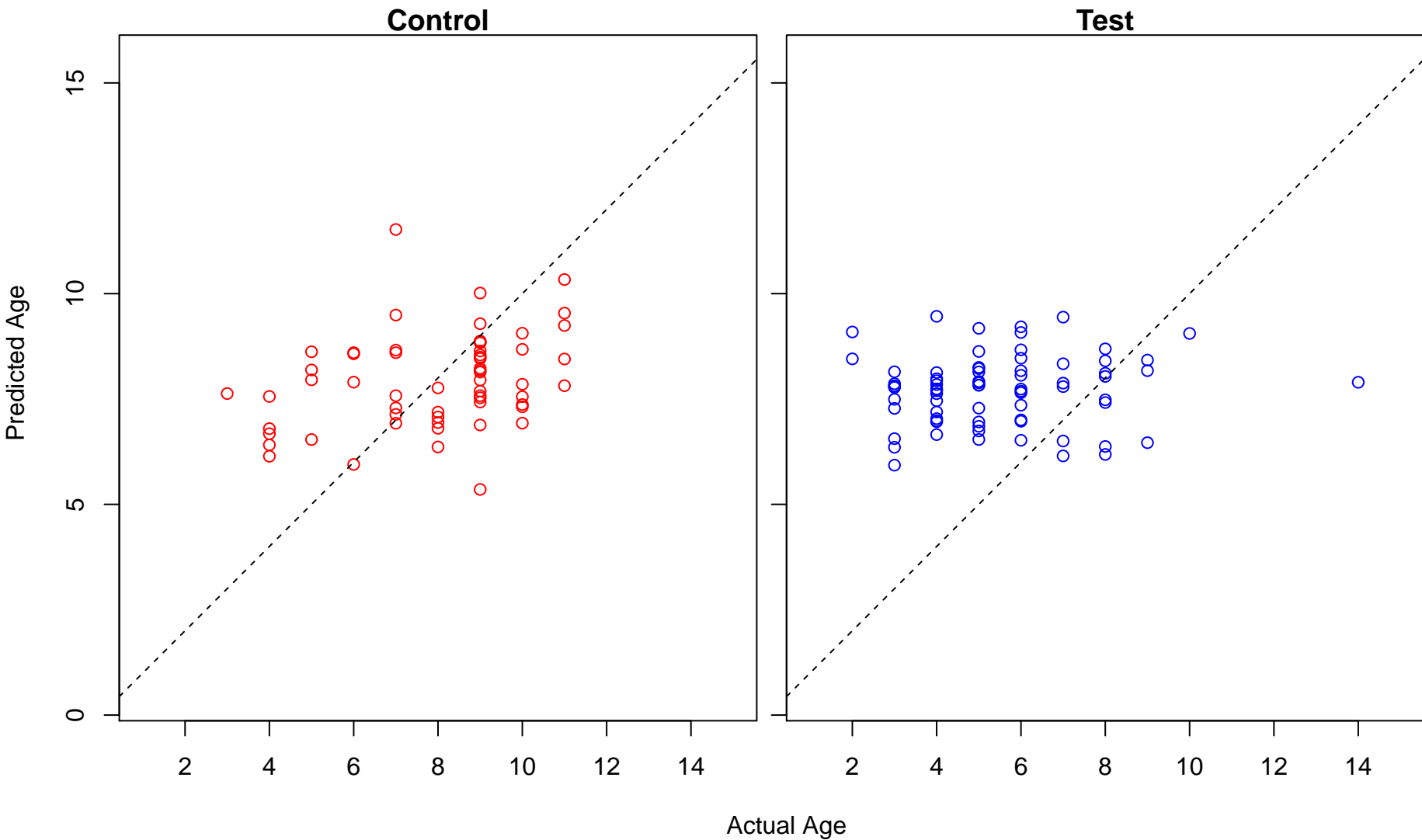
establishment of protein localization to chromosome (Score: 0.515348)



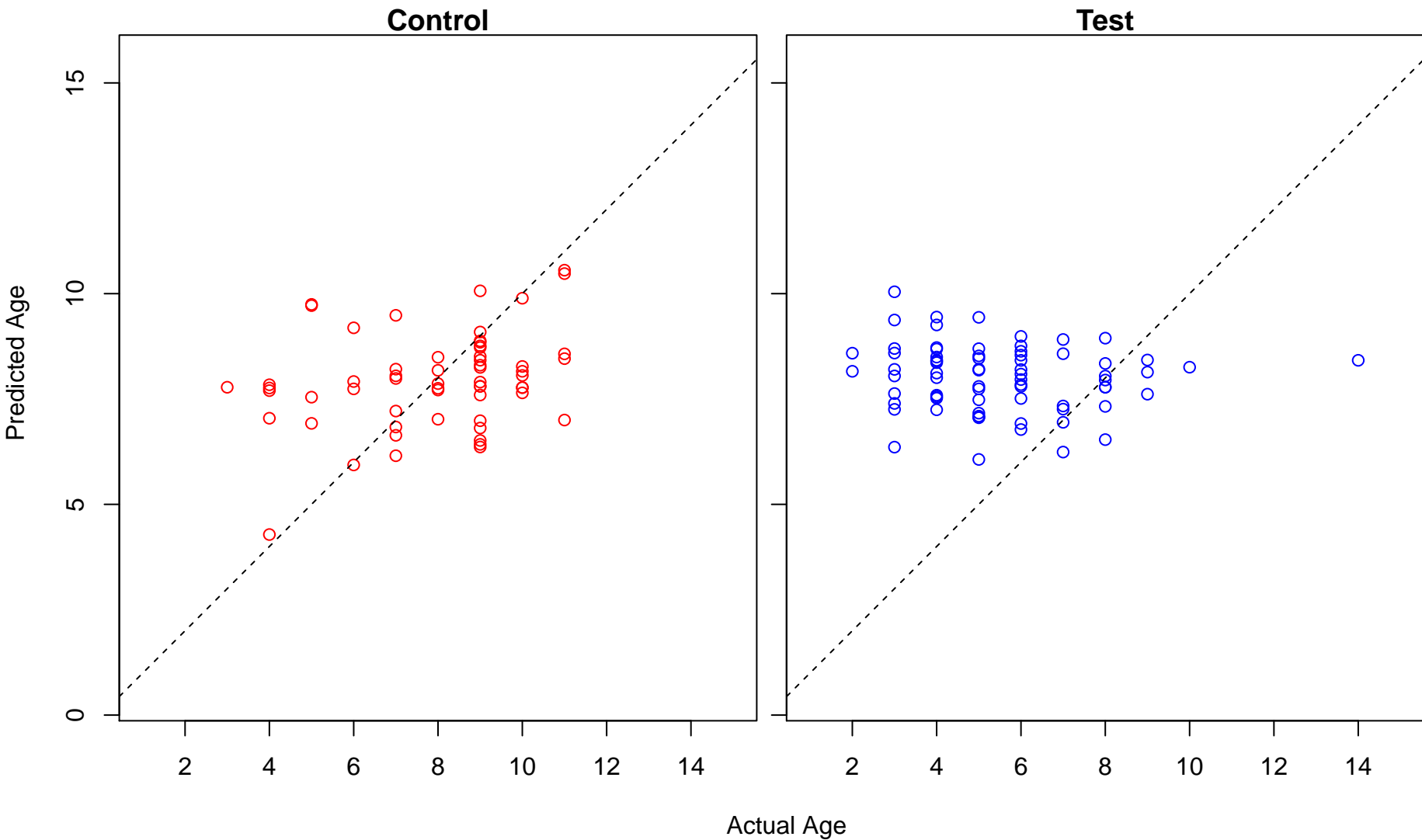
UDP-glucose metabolic process (Score: 0.514493)



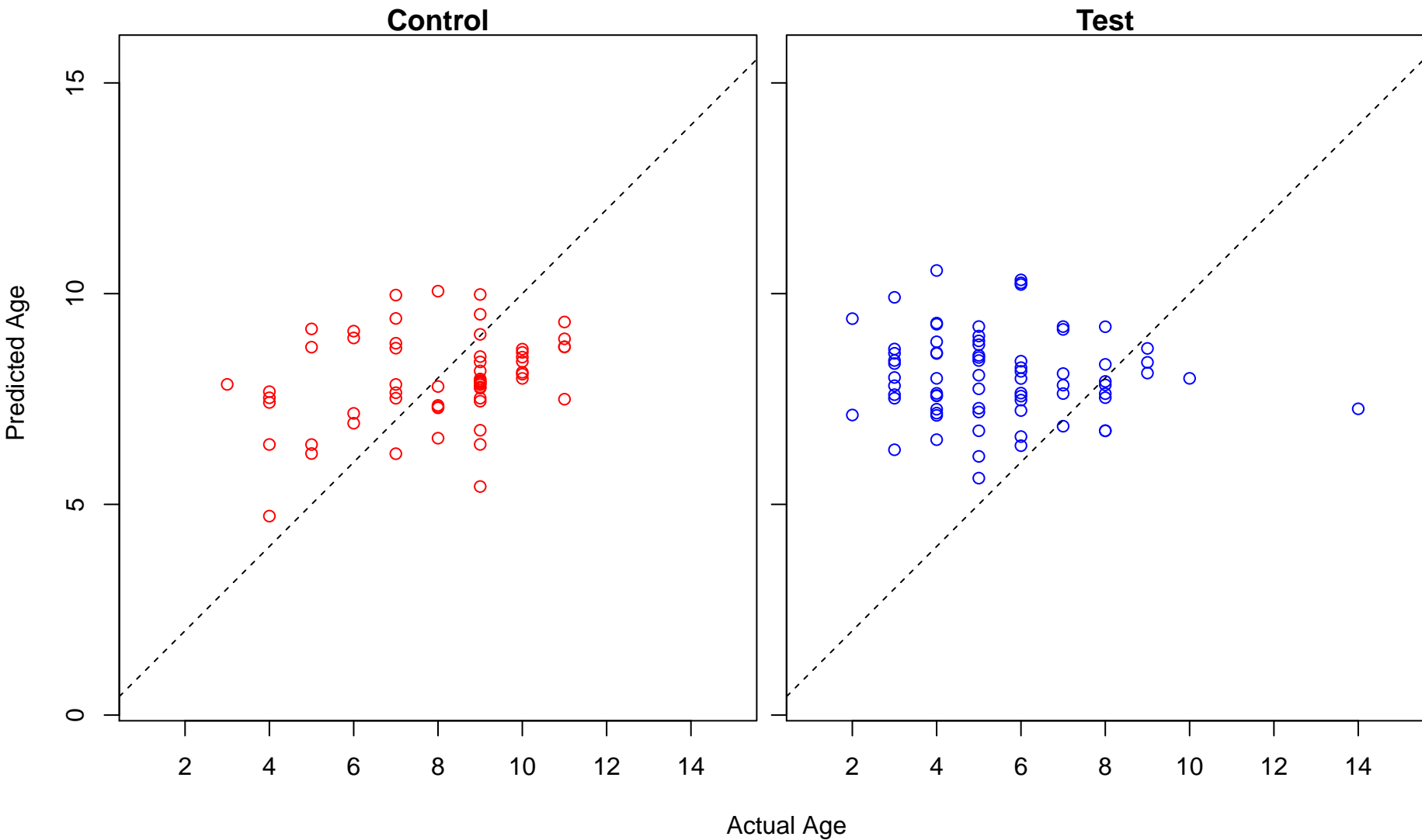
replicative cell aging (Score: 0.514301)



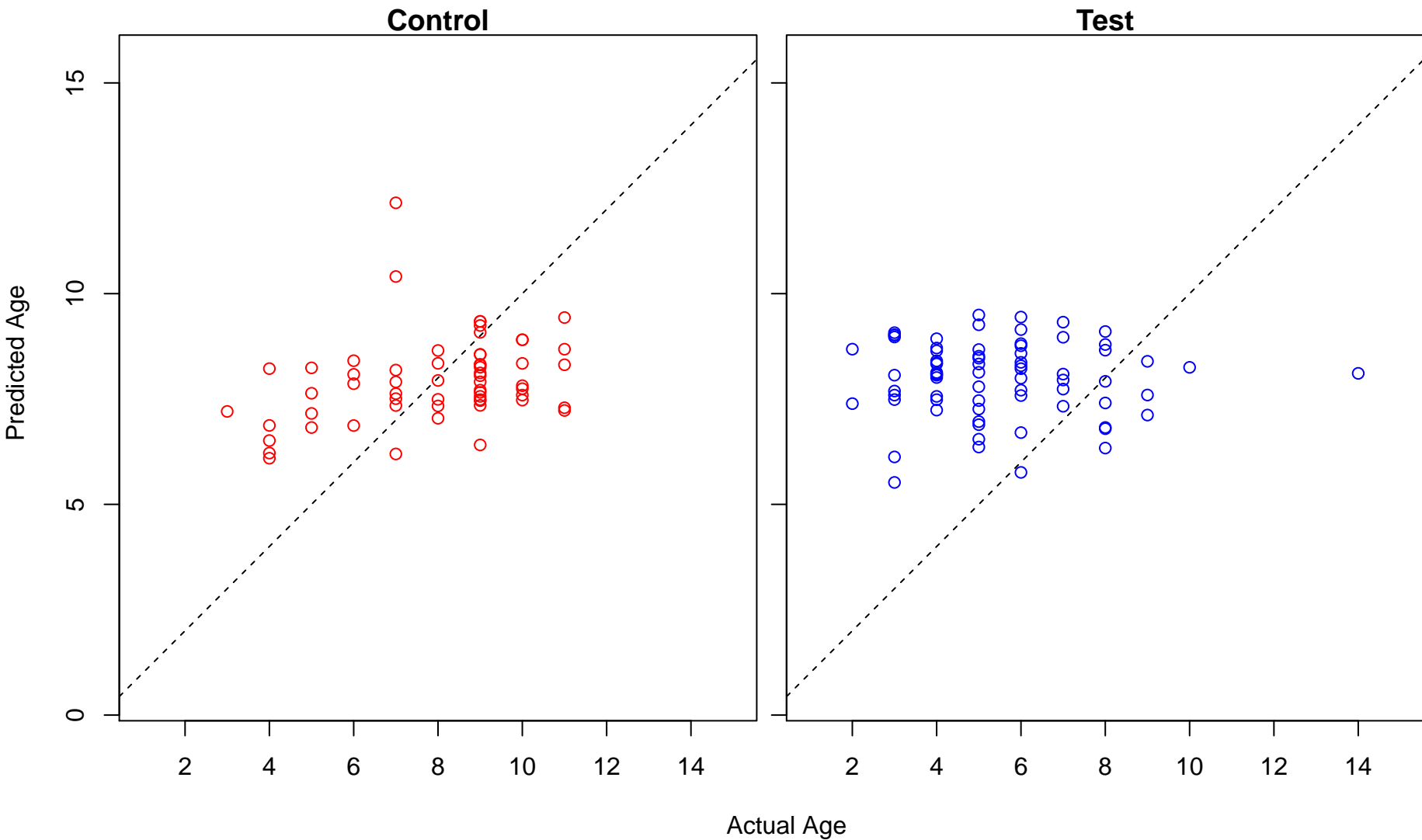
negative regulation of RIG-I signaling pathway (Score: 0.510142)



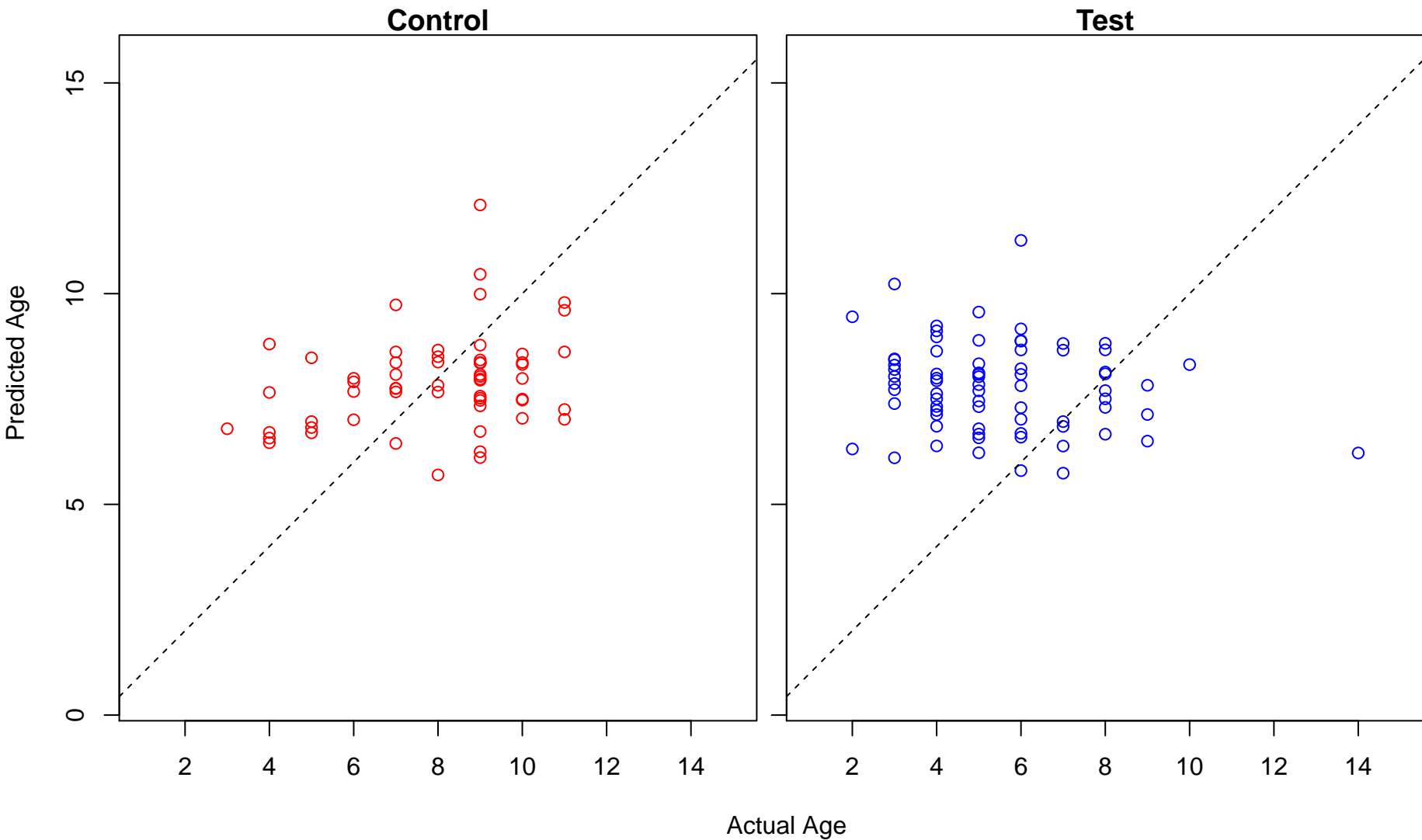
endoplasmic reticulum tubular network organization (Score: 0.509133)



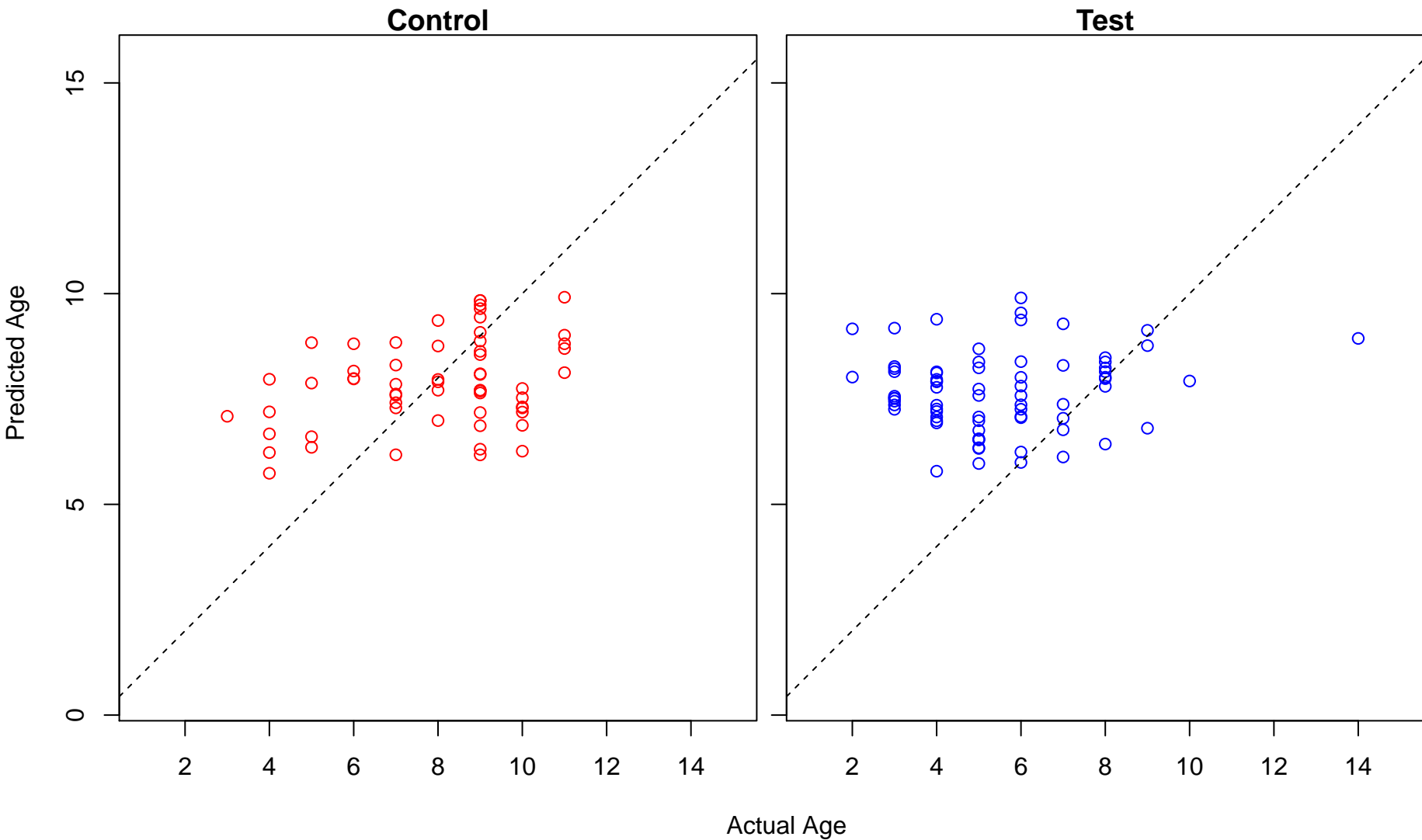
positive regulation of receptor internalization (Score: 0.509043)



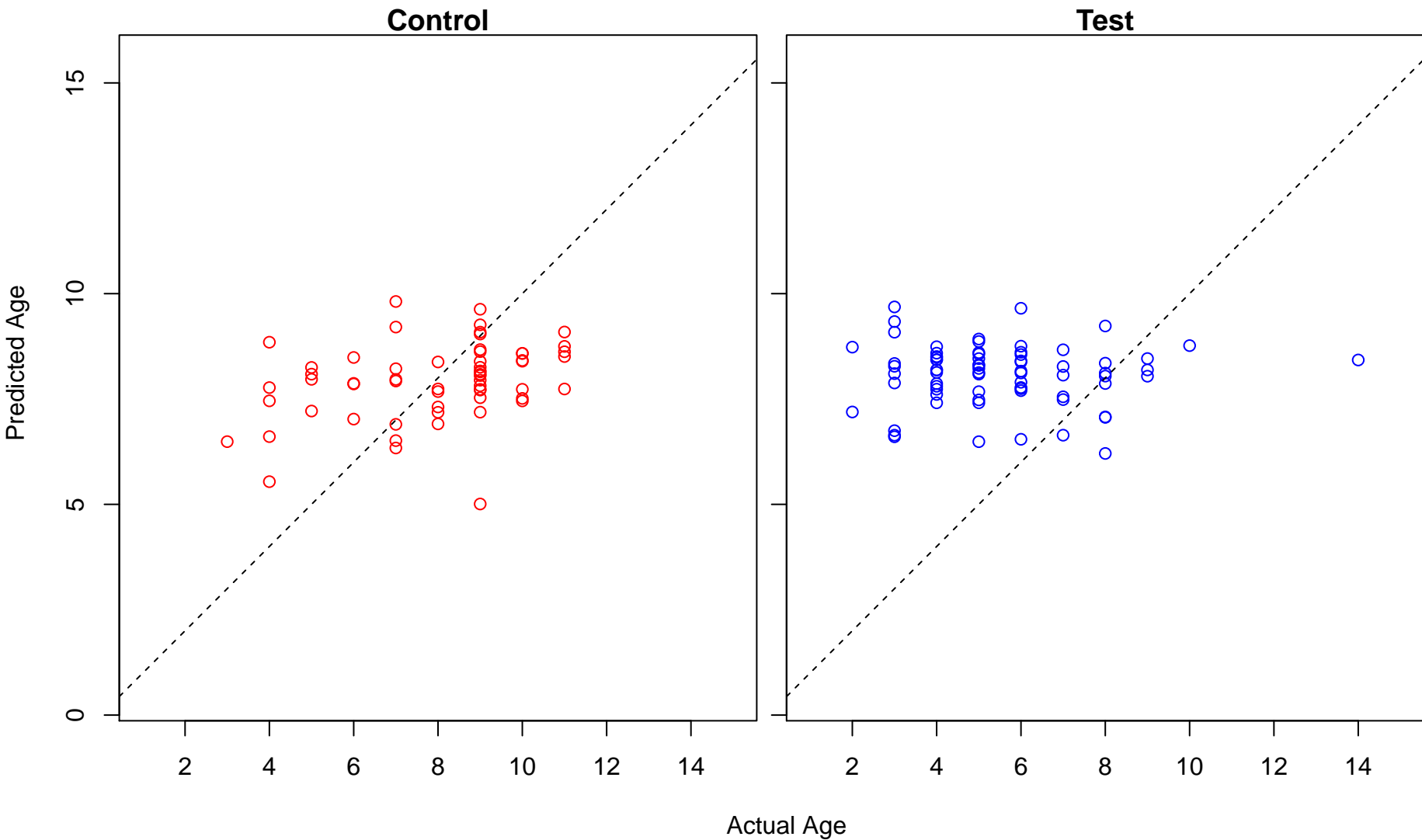
cellular response to progesterone stimulus (Score: 0.508852)



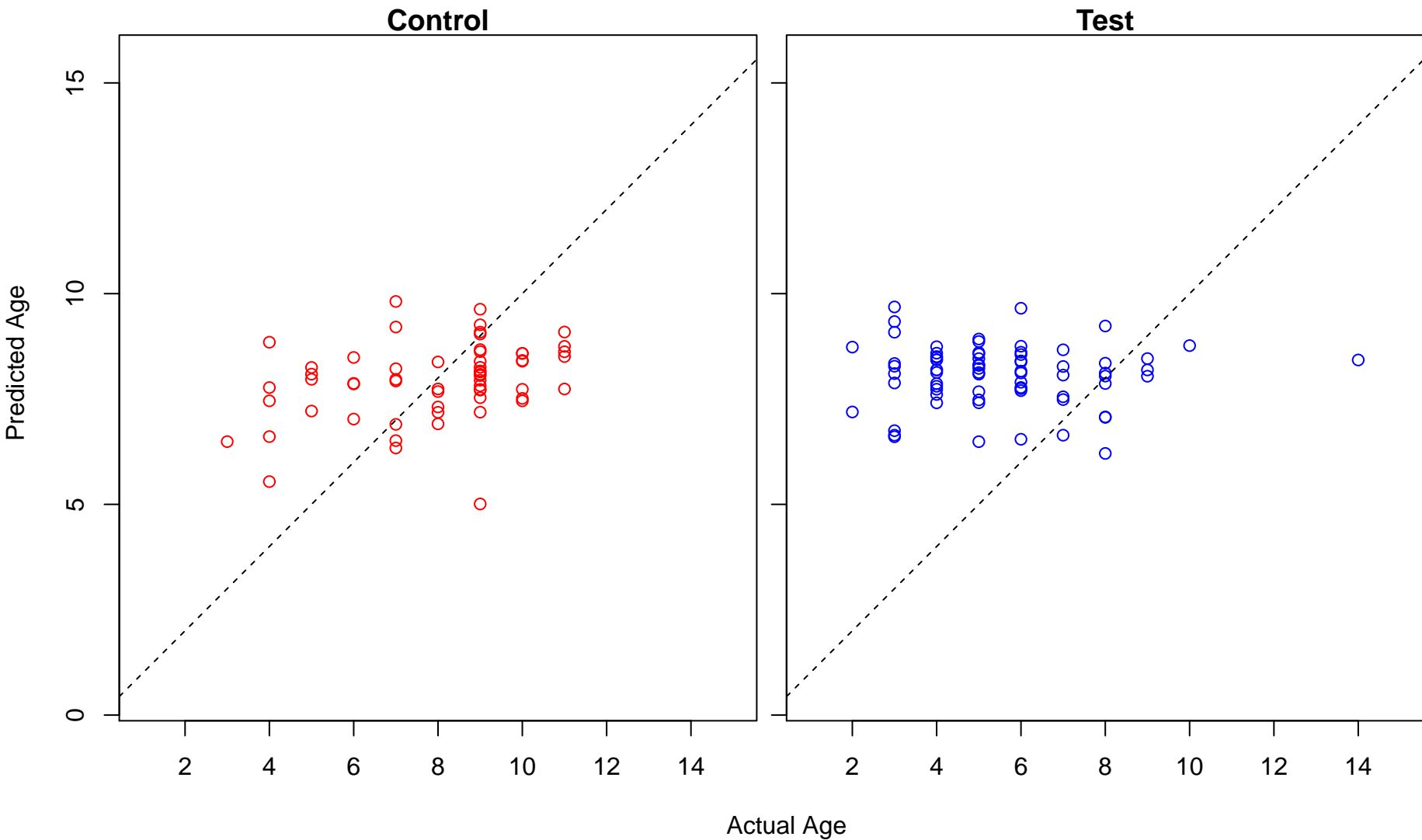
regulation of growth hormone receptor signaling pathway (Score: 0.508666)



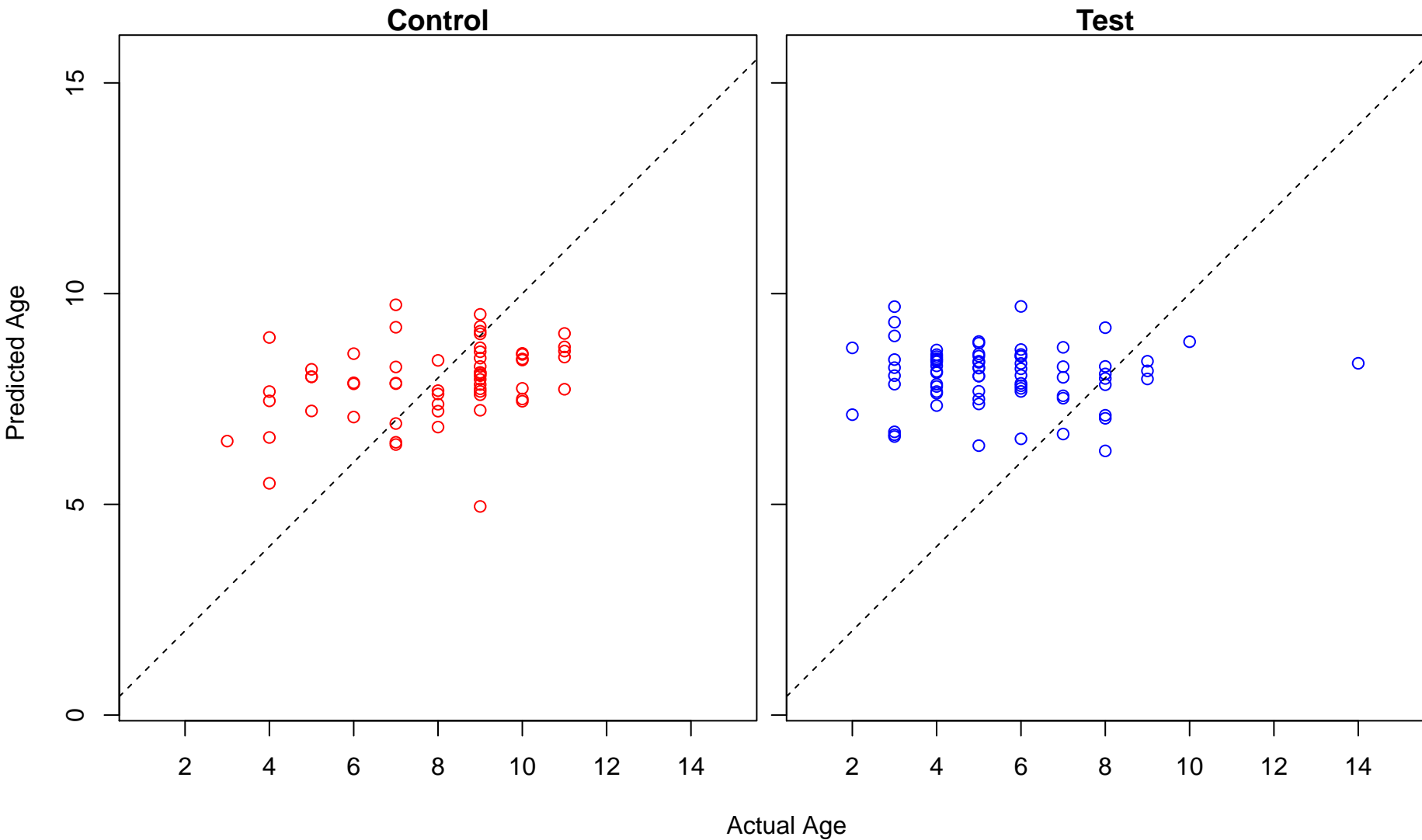
striatum development (Score: 0.508553)



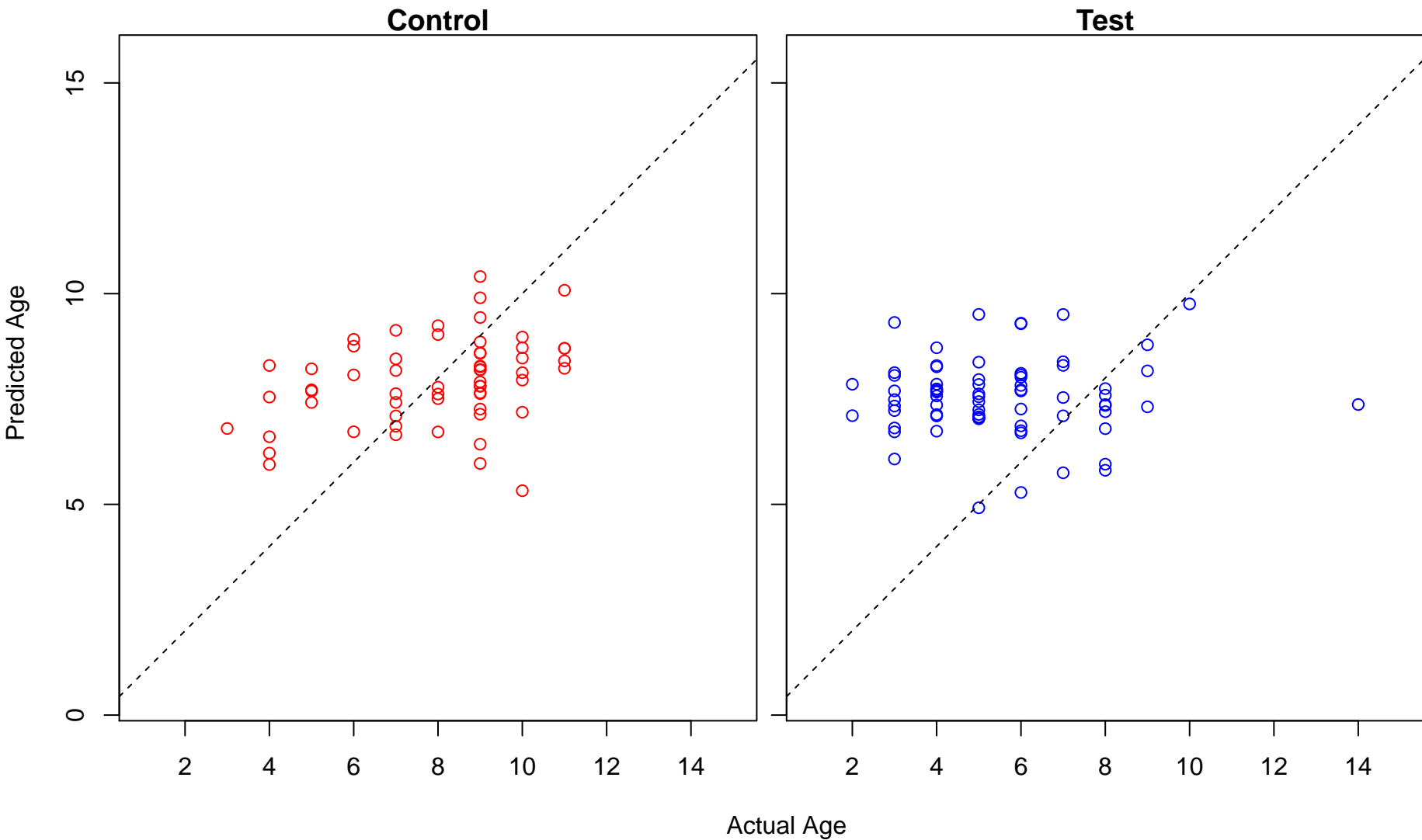
subpallium development (Score: 0.508426)



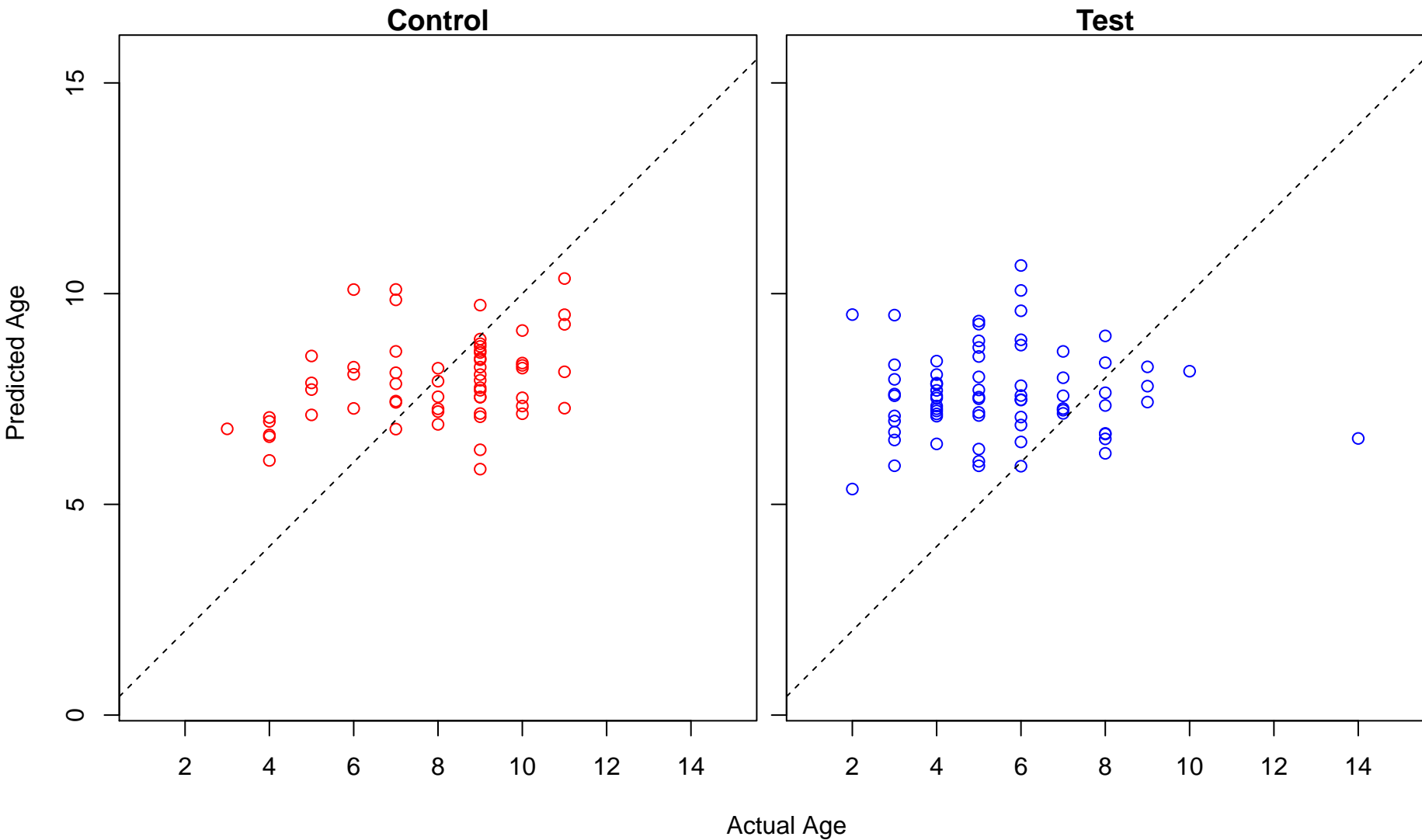
forebrain neuron fate commitment (Score: 0.507106)



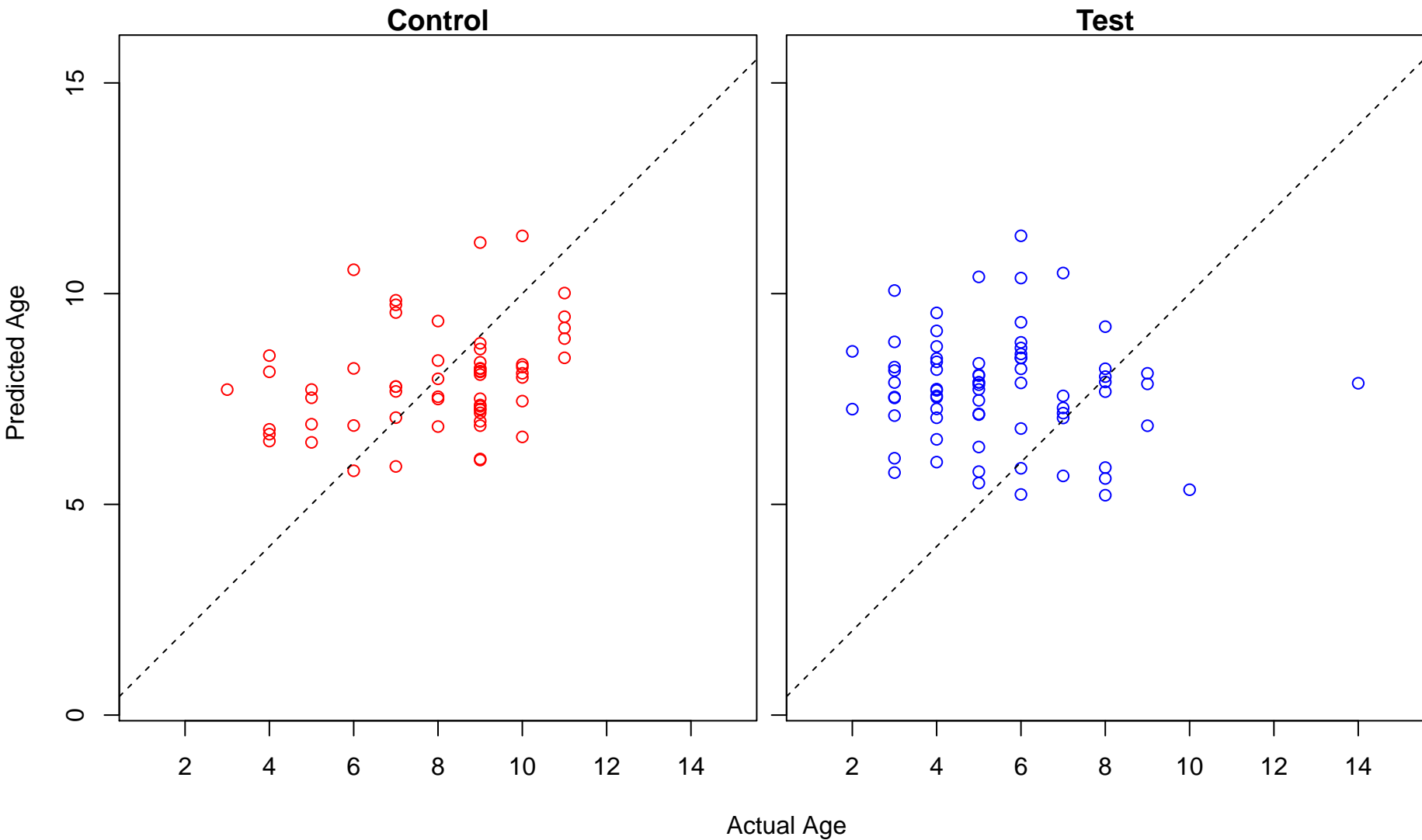
negative regulation of interleukin-6 biosynthetic process (Score: 0.506397)



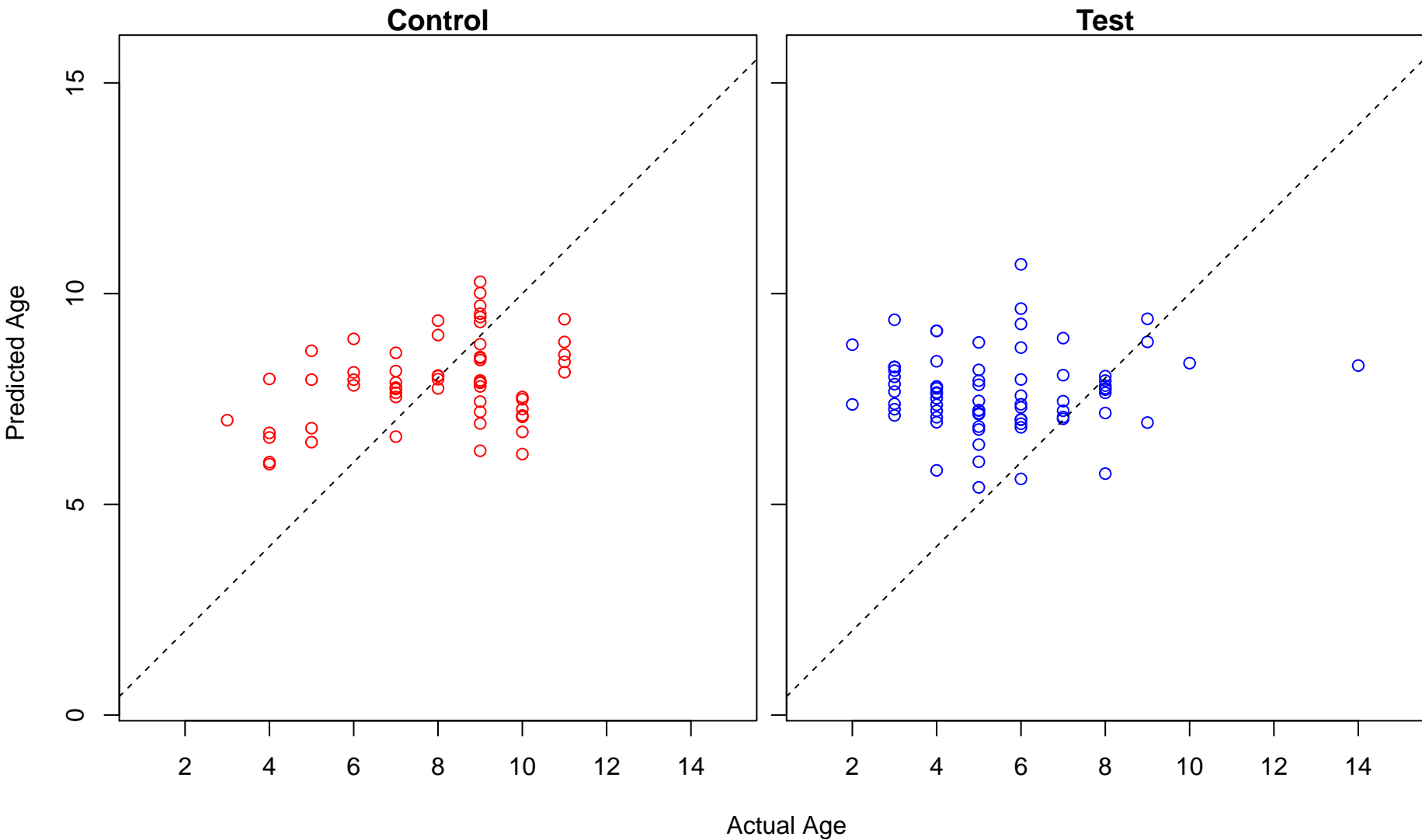
transition metal ion transport (Score: 0.505645)



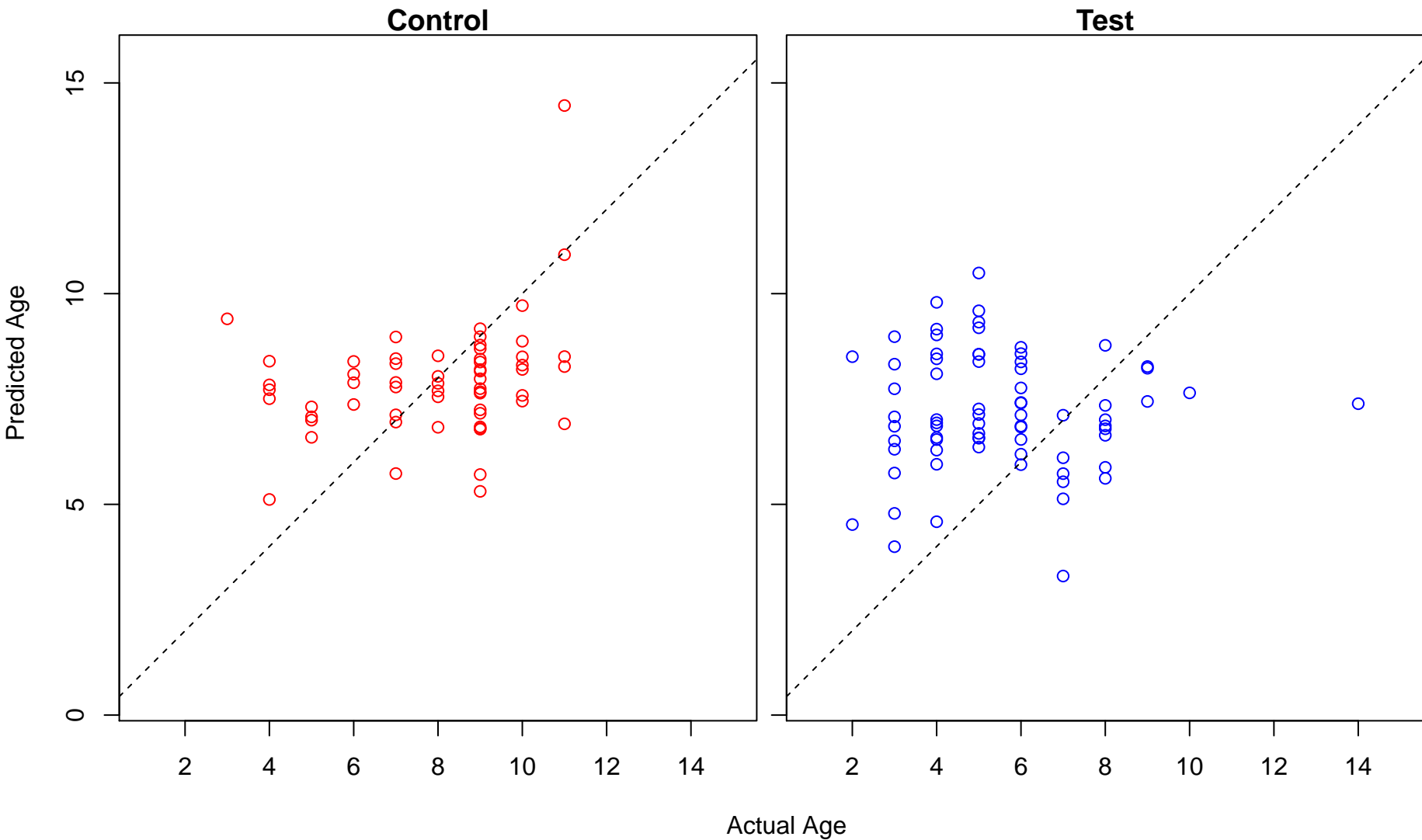
positive regulation of oxidoreductase activity (Score: 0.504697)



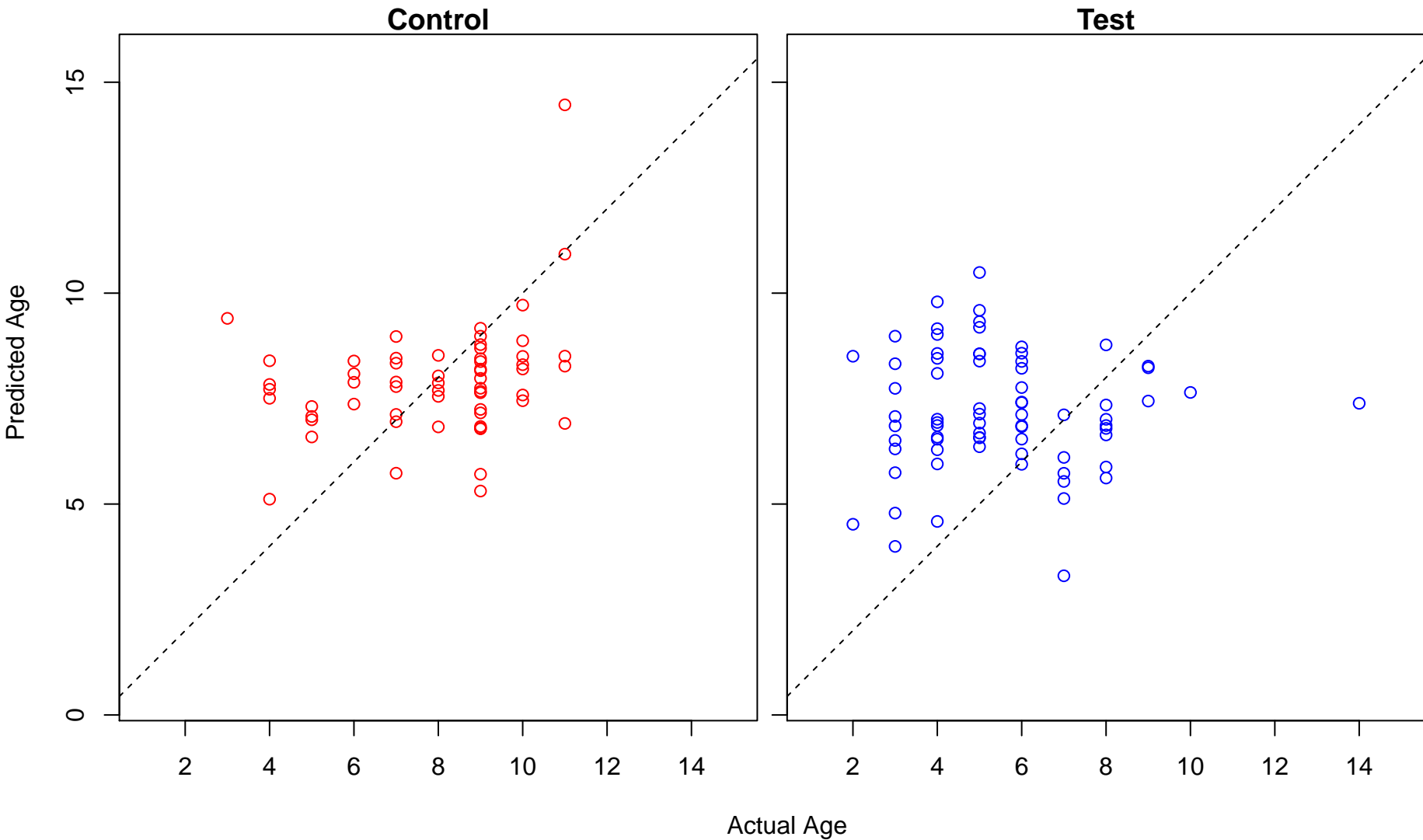
negative regulation of growth hormone receptor signaling pathway (Score: 0.504668)



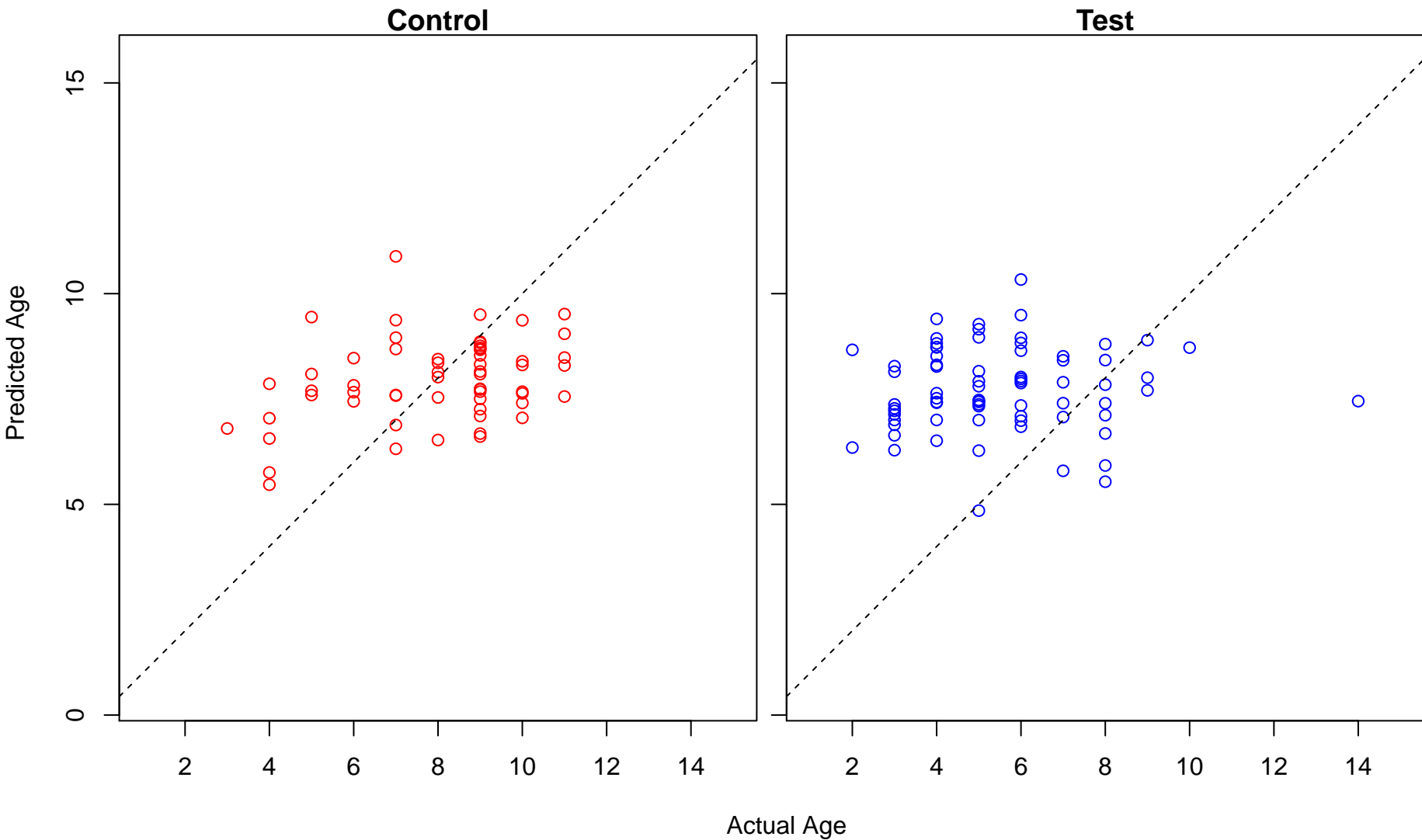
mesenchymal cell differentiation involved in kidney development (Score: 0.503773)



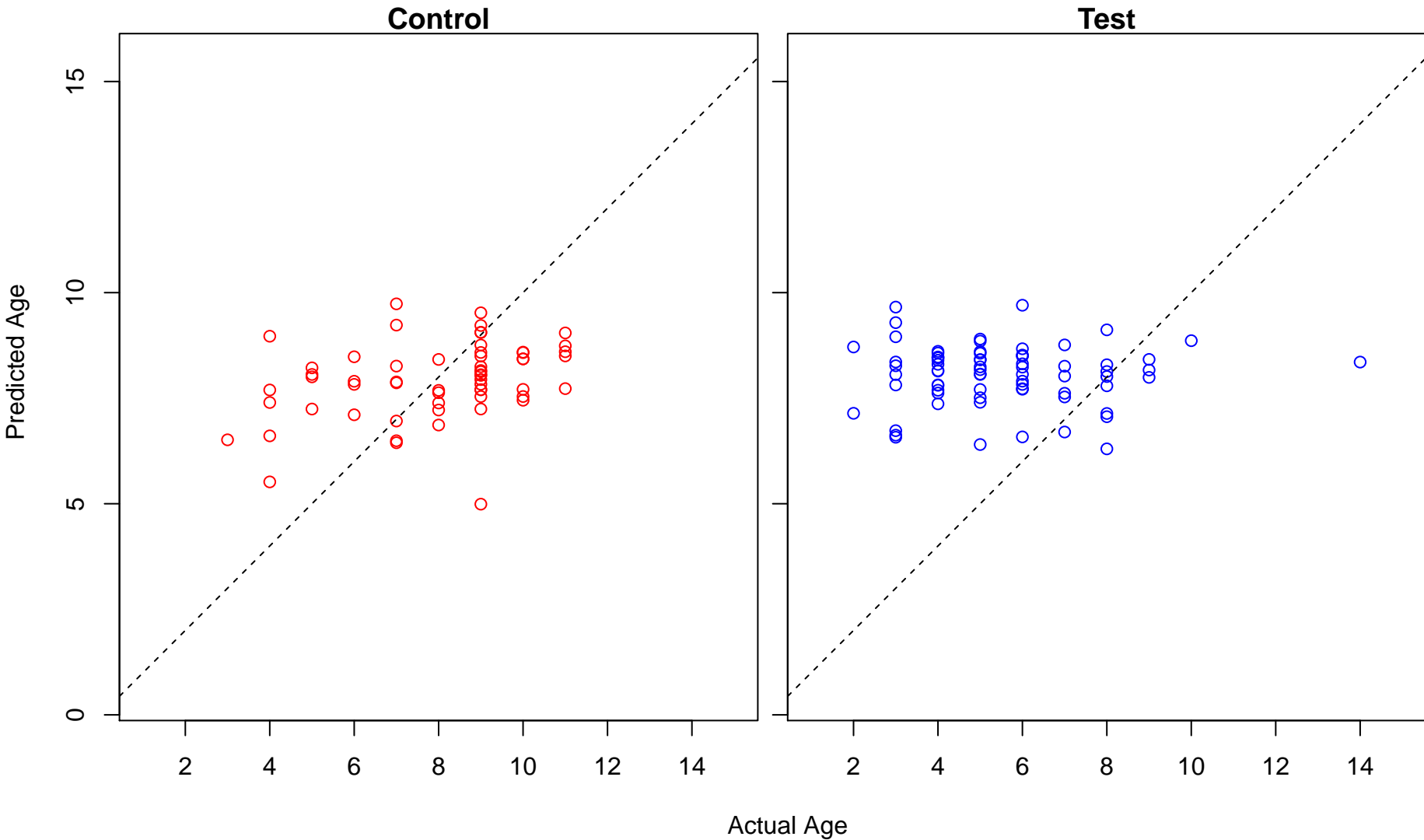
mesenchymal cell differentiation involved in renal system development (Score: 0.503773)



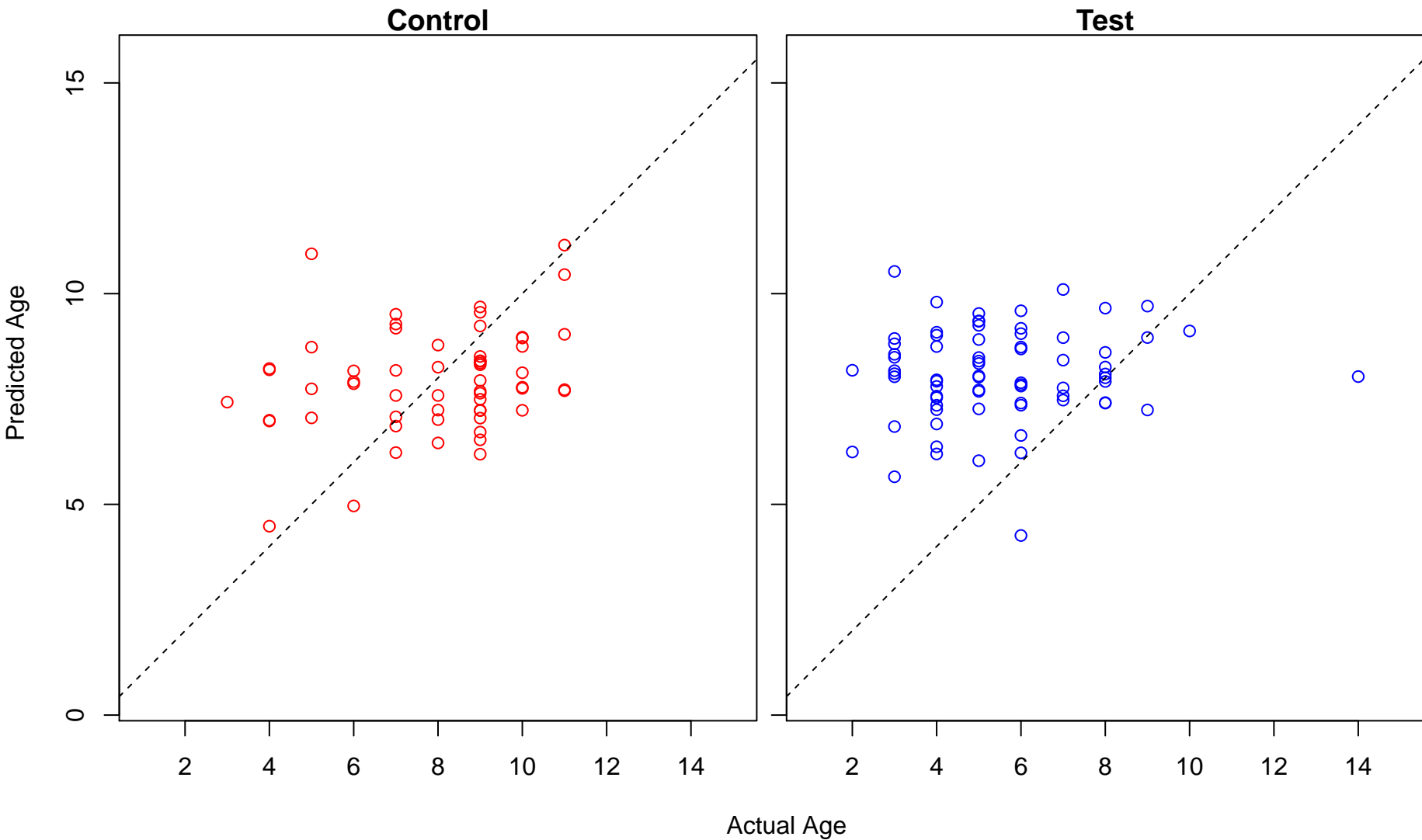
vascular endothelial growth factor receptor-2 signaling pathway (Score: 0.502301)



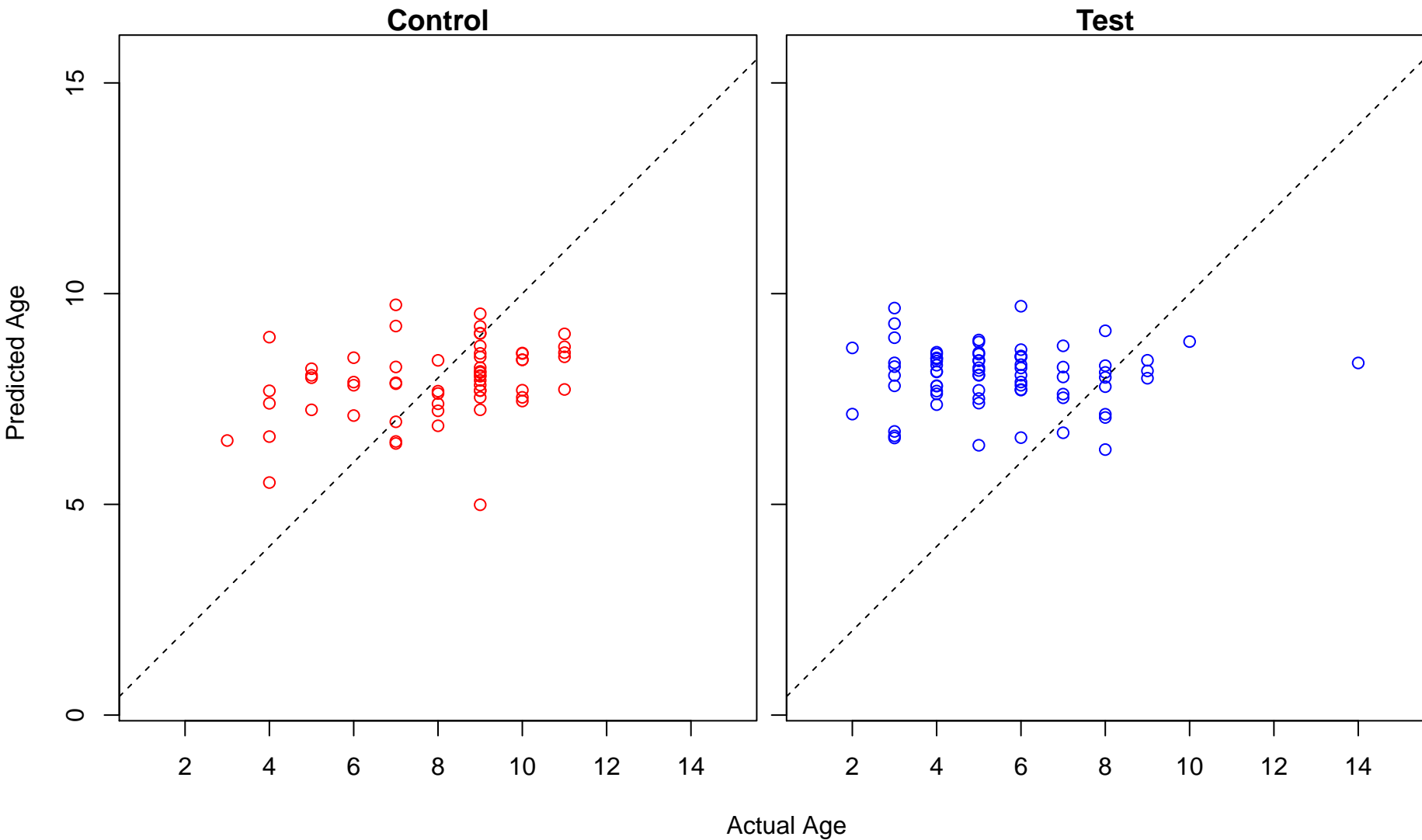
striatal medium spiny neuron differentiation (Score: 0.501326)



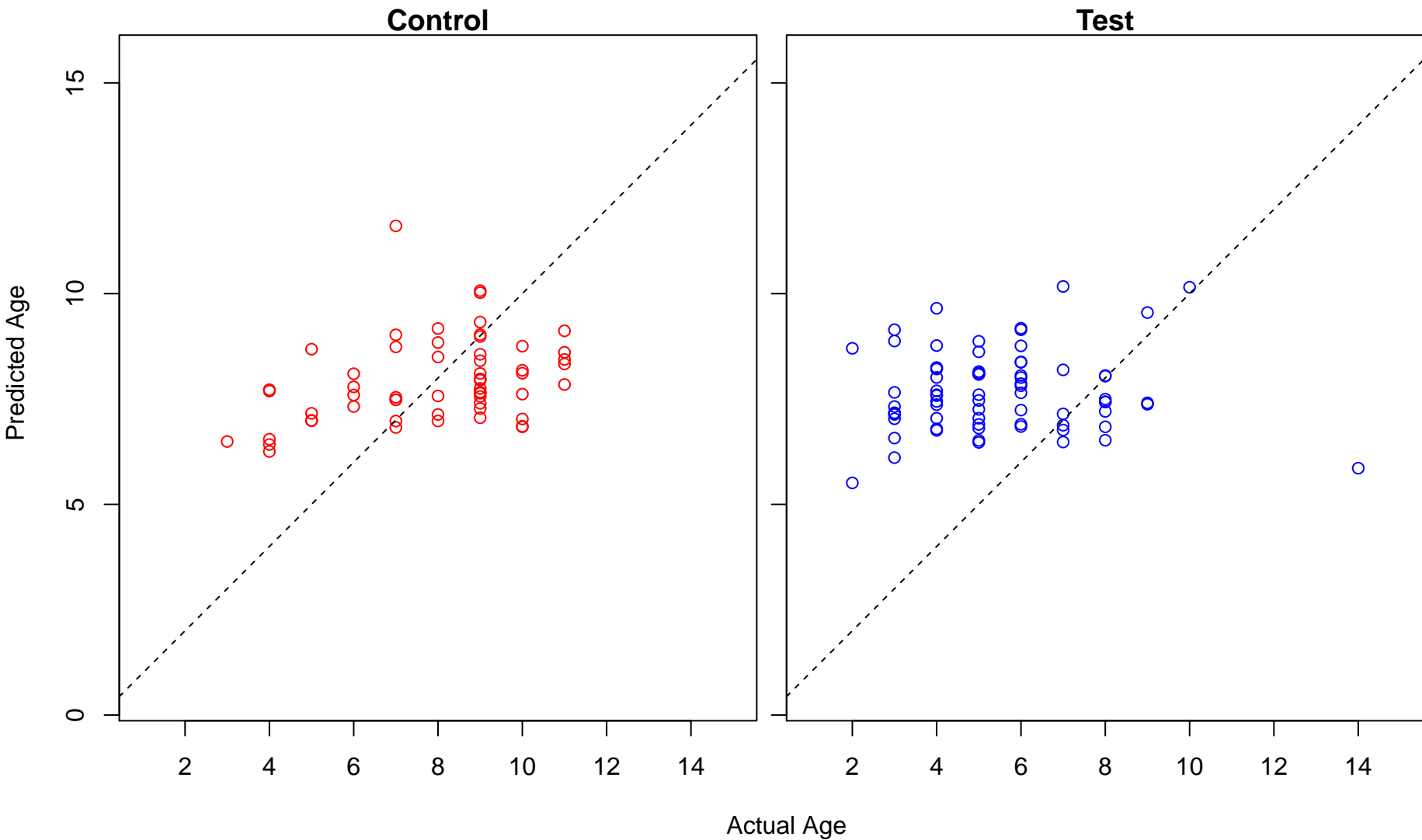
ureteric bud elongation (Score: 0.501202)



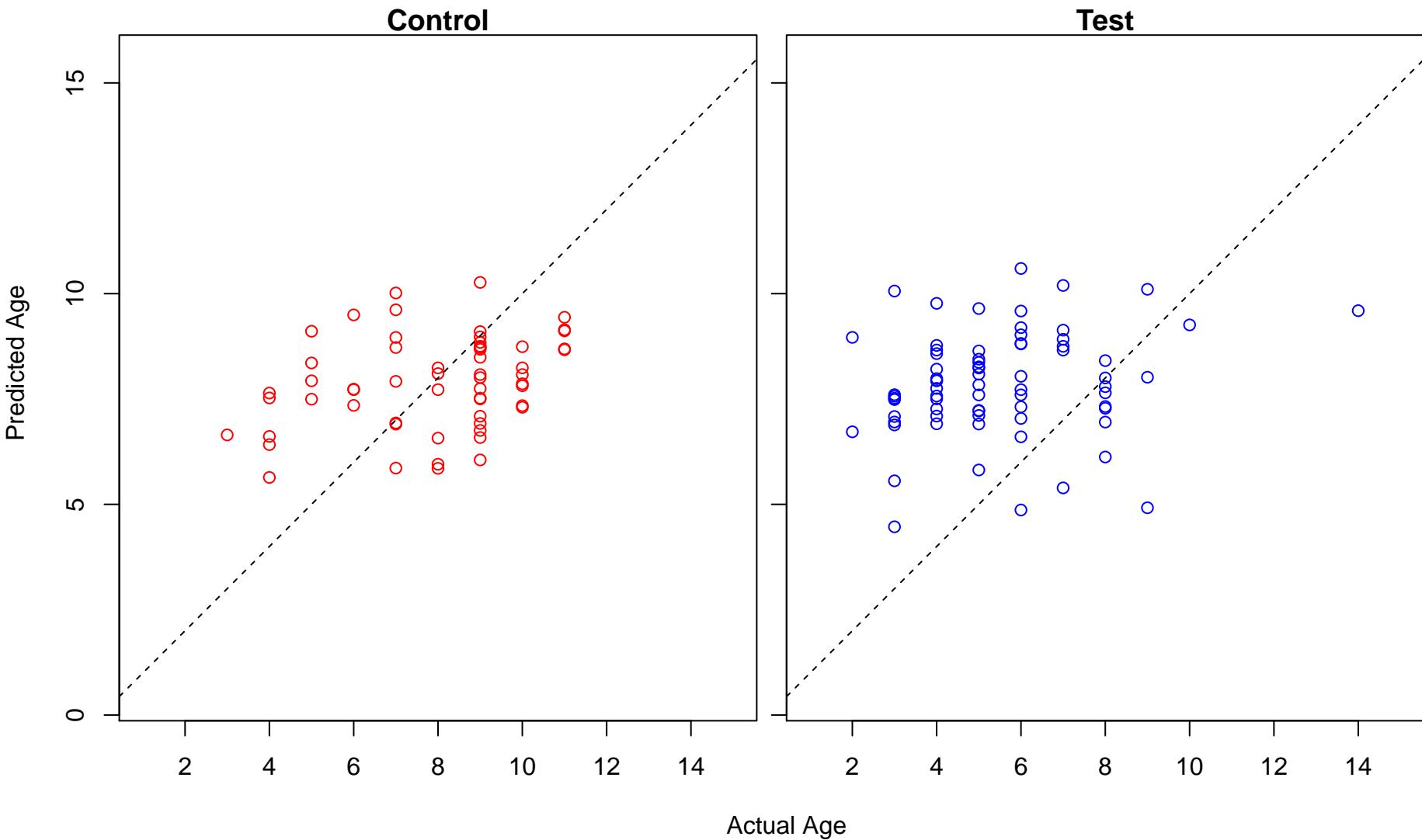
olfactory bulb axon guidance (Score: 0.501200)



phagosome-lysosome fusion (Score: 0.500888)

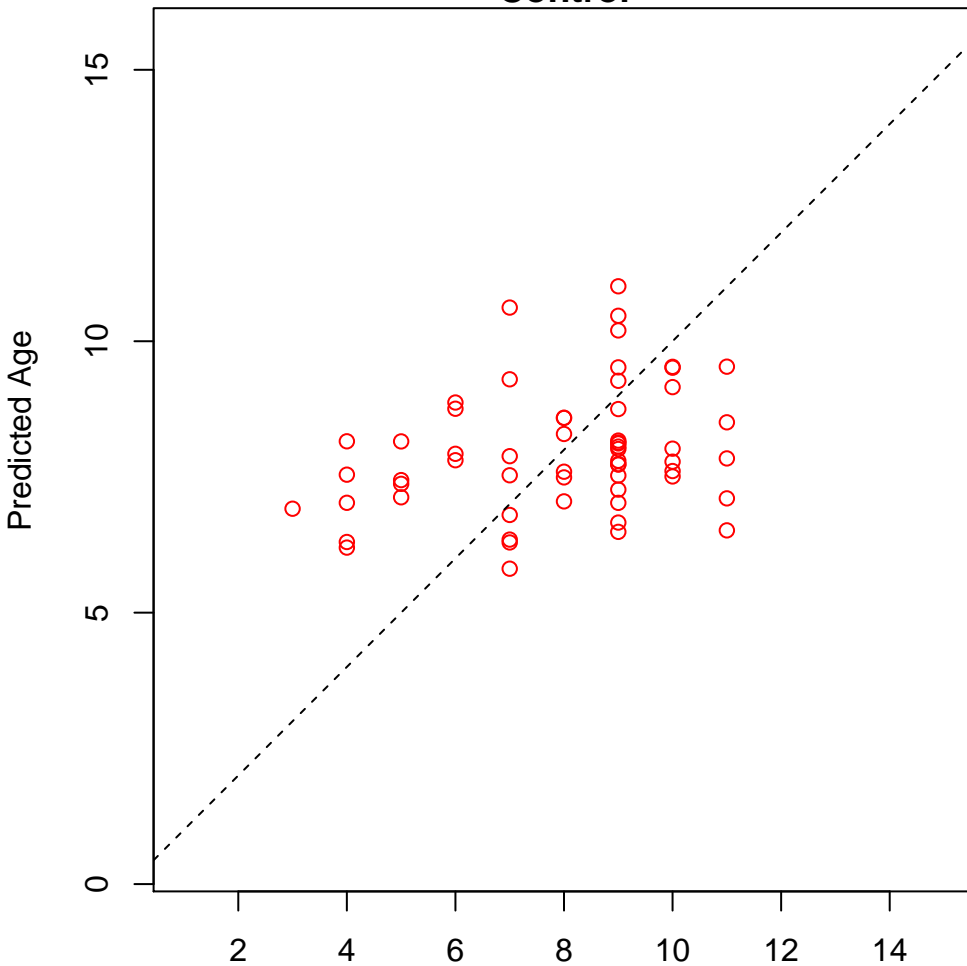


forebrain radial glial cell differentiation (Score: 0.500135)

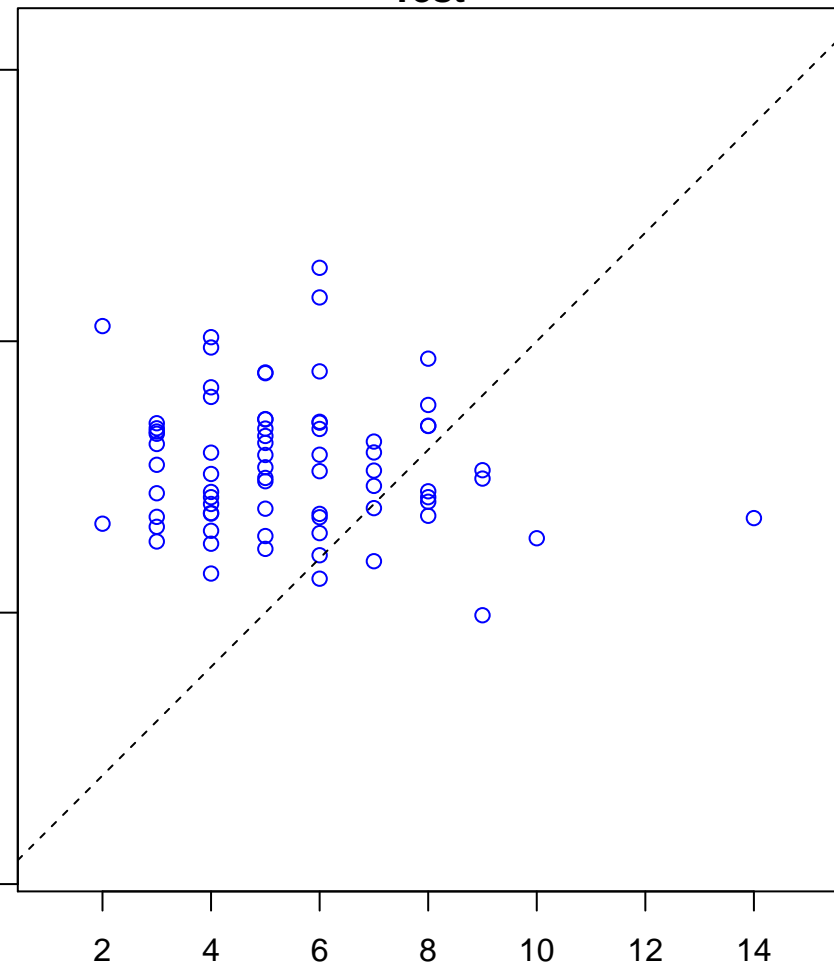


regulation of receptor catabolic process (Score: 0.499244)

Control

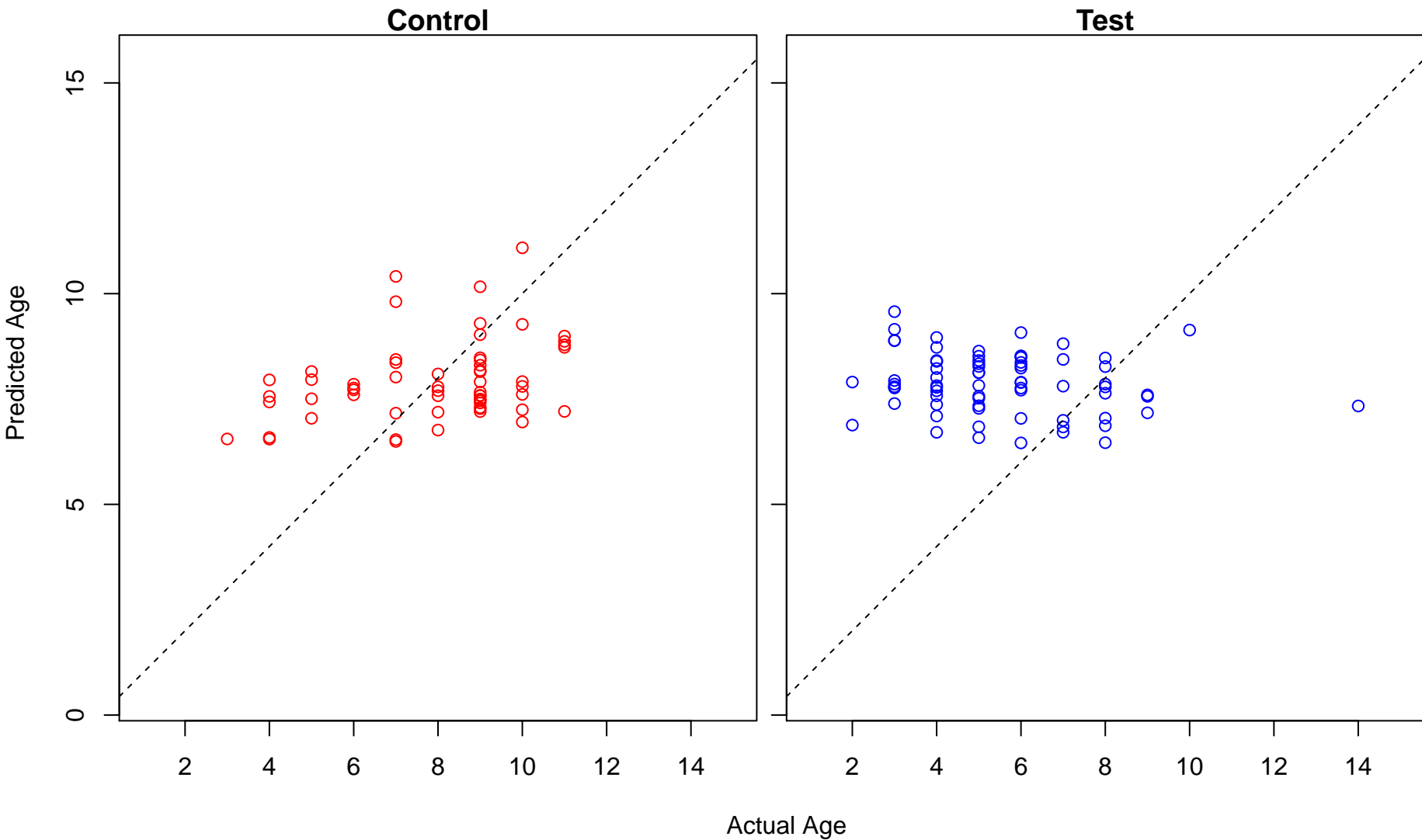


Test

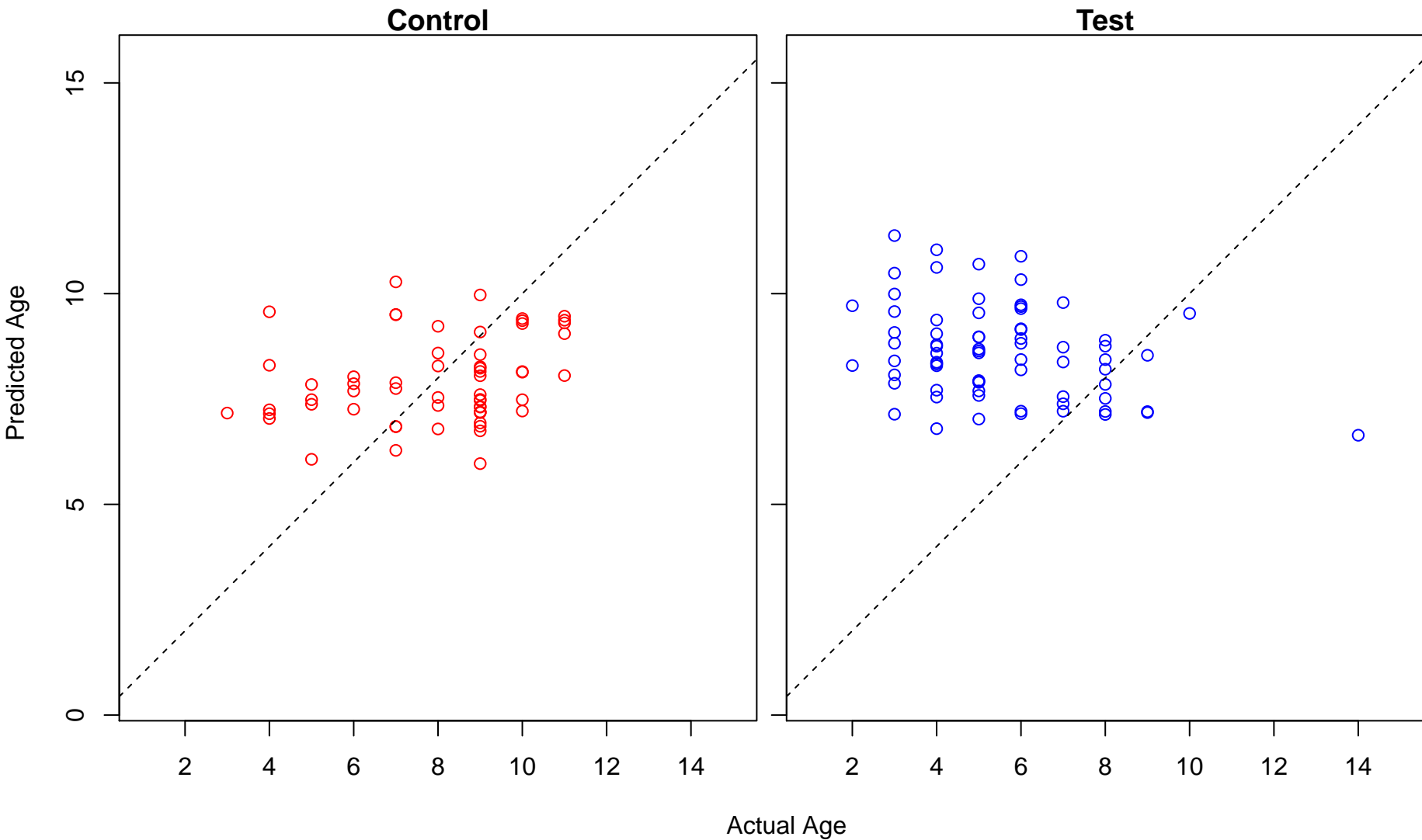


Actual Age

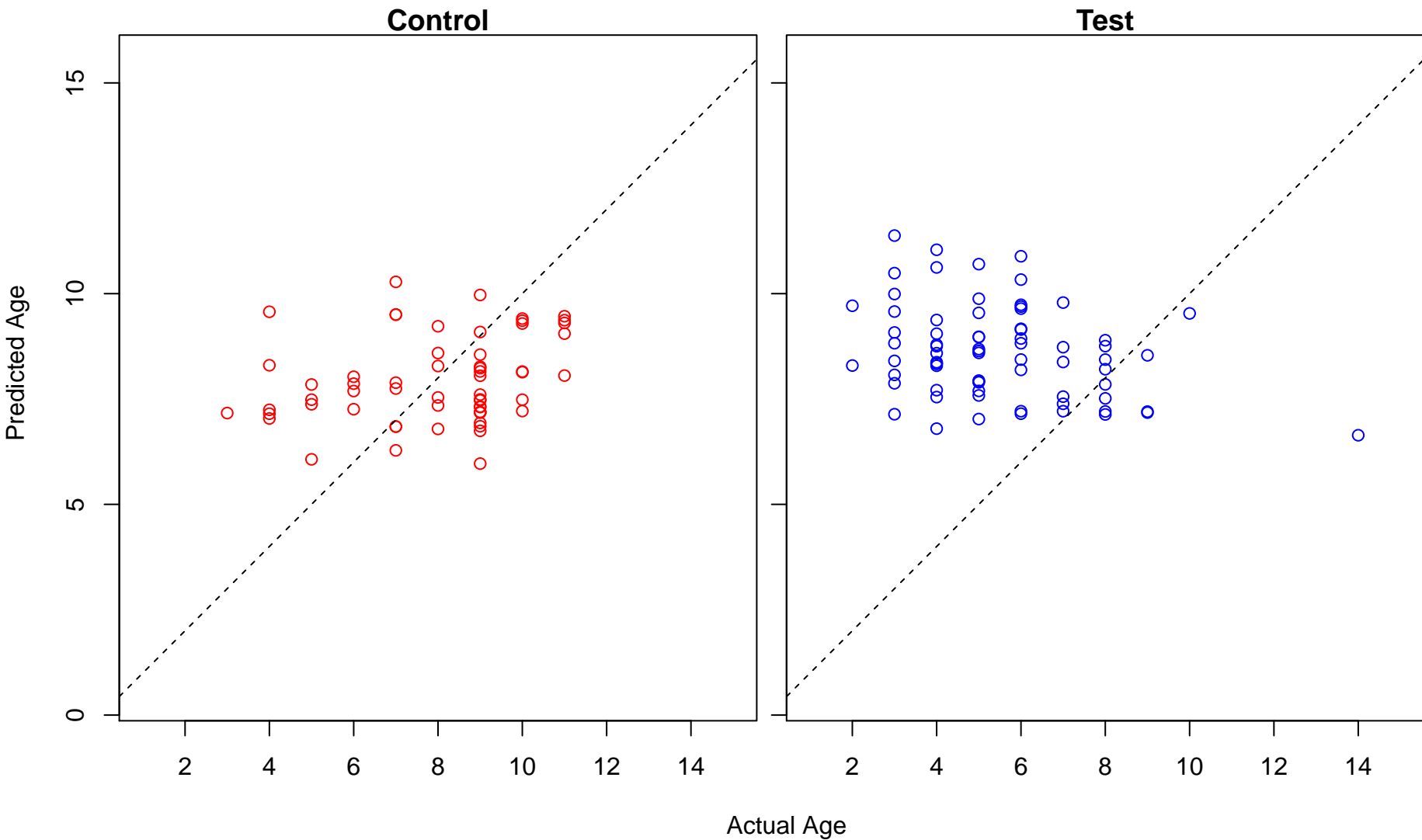
enamel mineralization (Score: 0.499213)



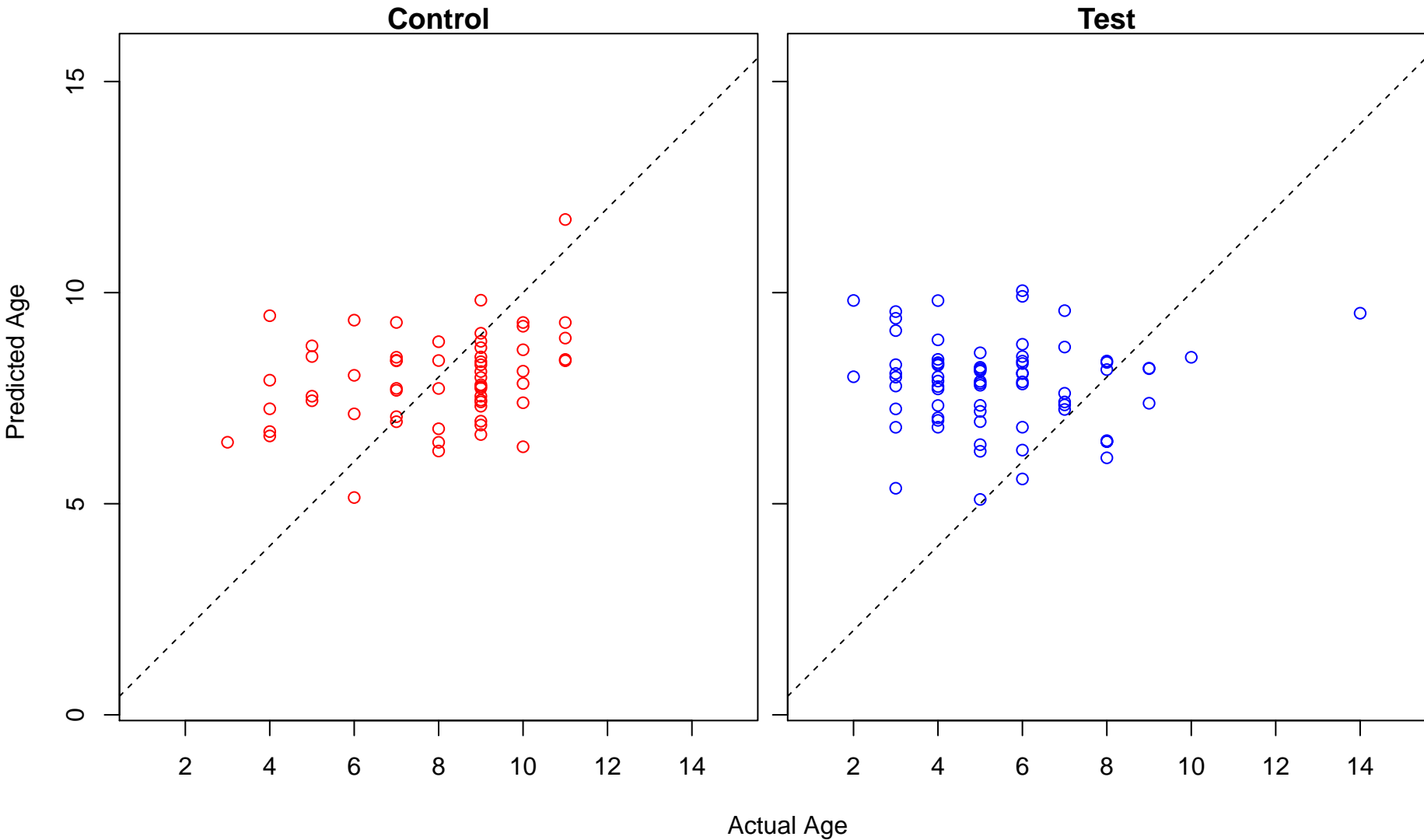
ureter smooth muscle development (Score: 0.498760)



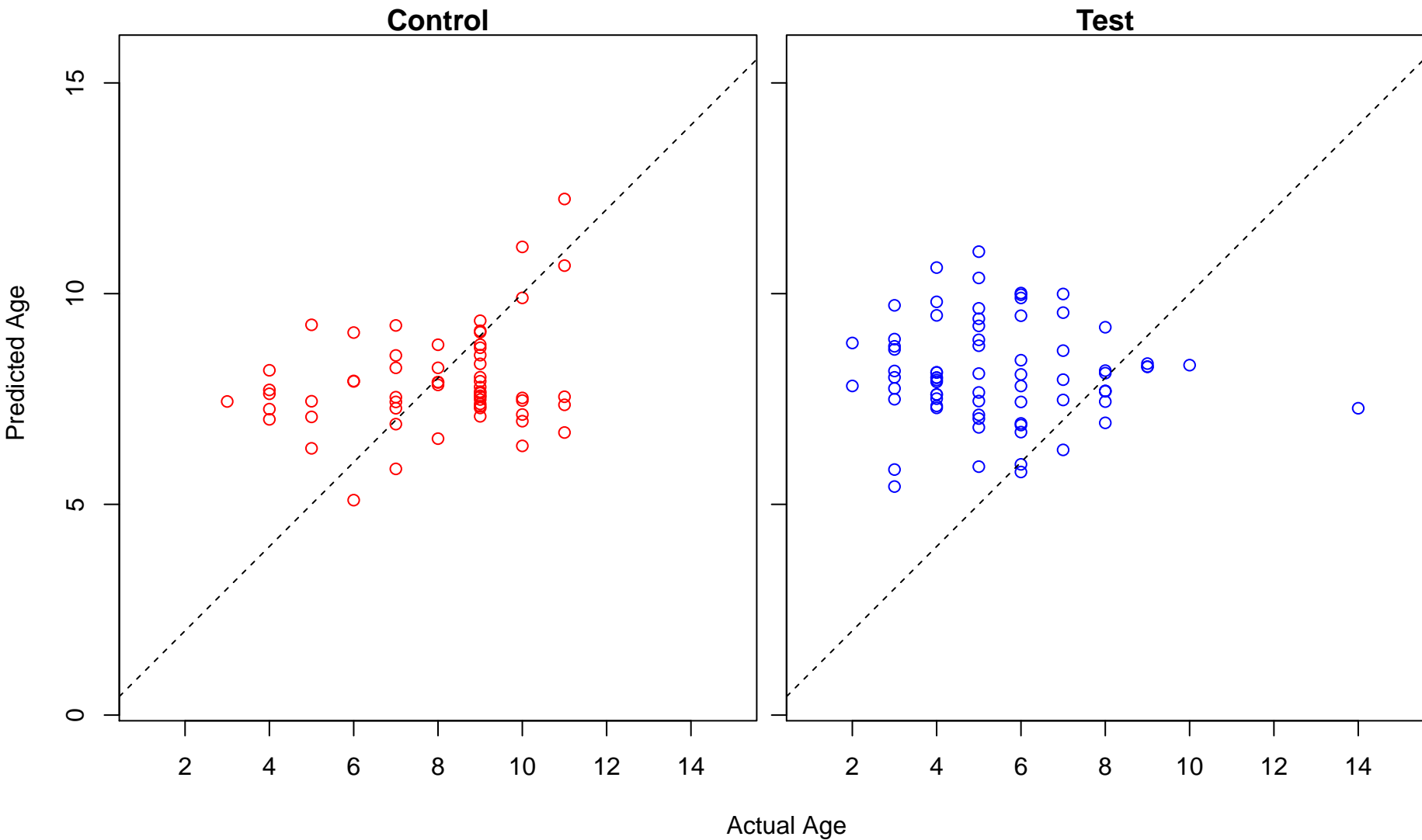
ureter smooth muscle cell differentiation (Score: 0.498760)



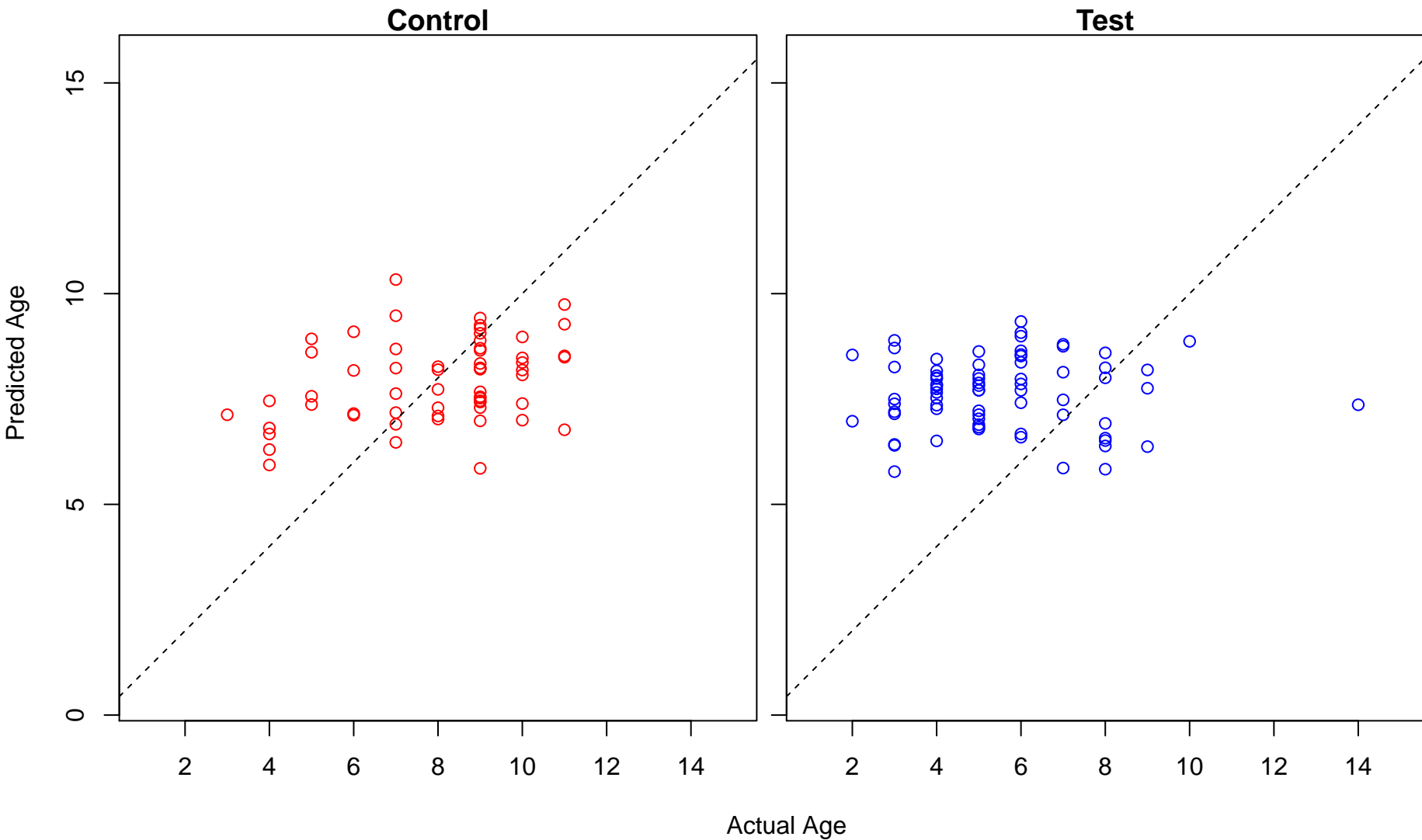
negative regulation of positive chemotaxis (Score: 0.498384)



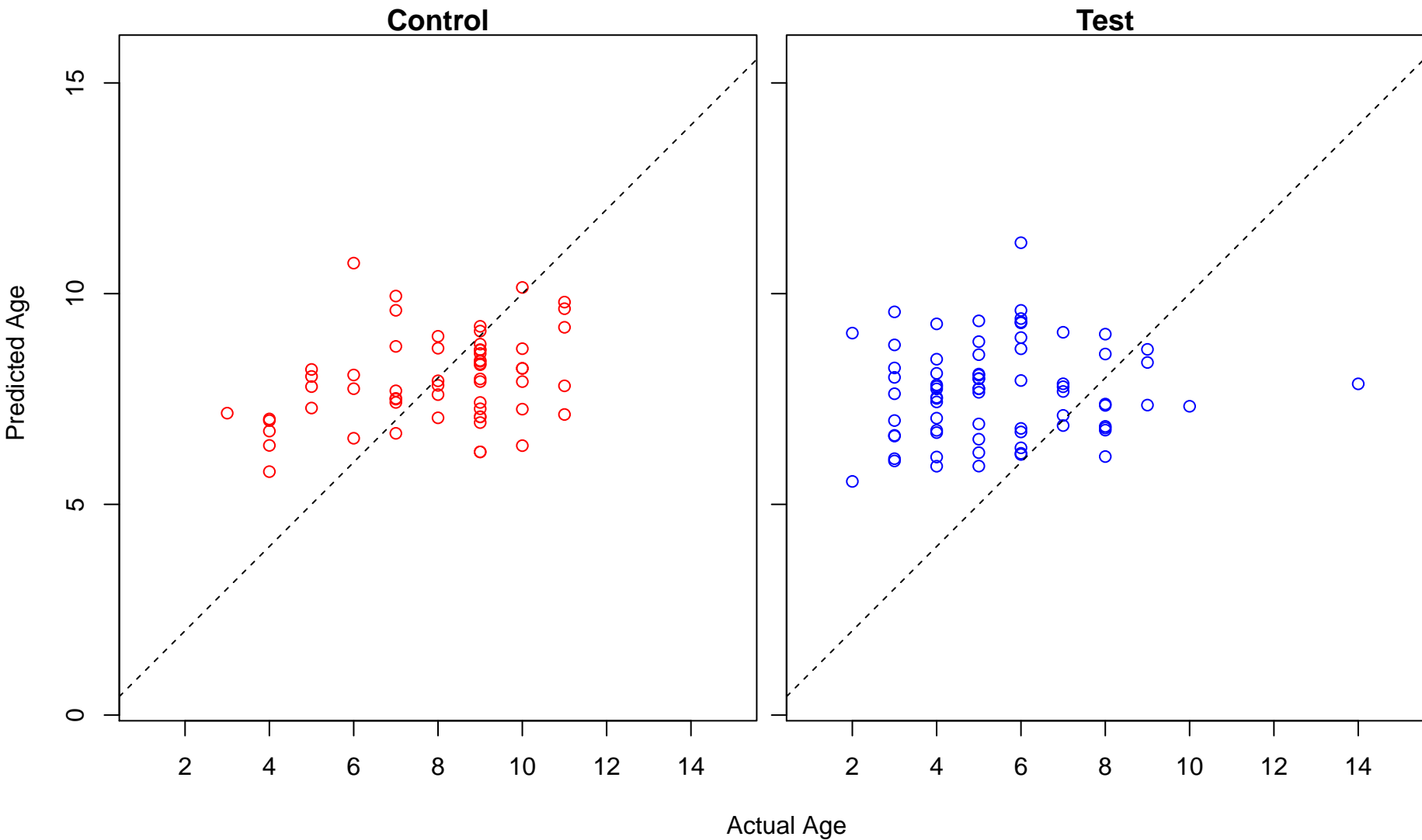
regulation of response to alcohol (Score: 0.497334)



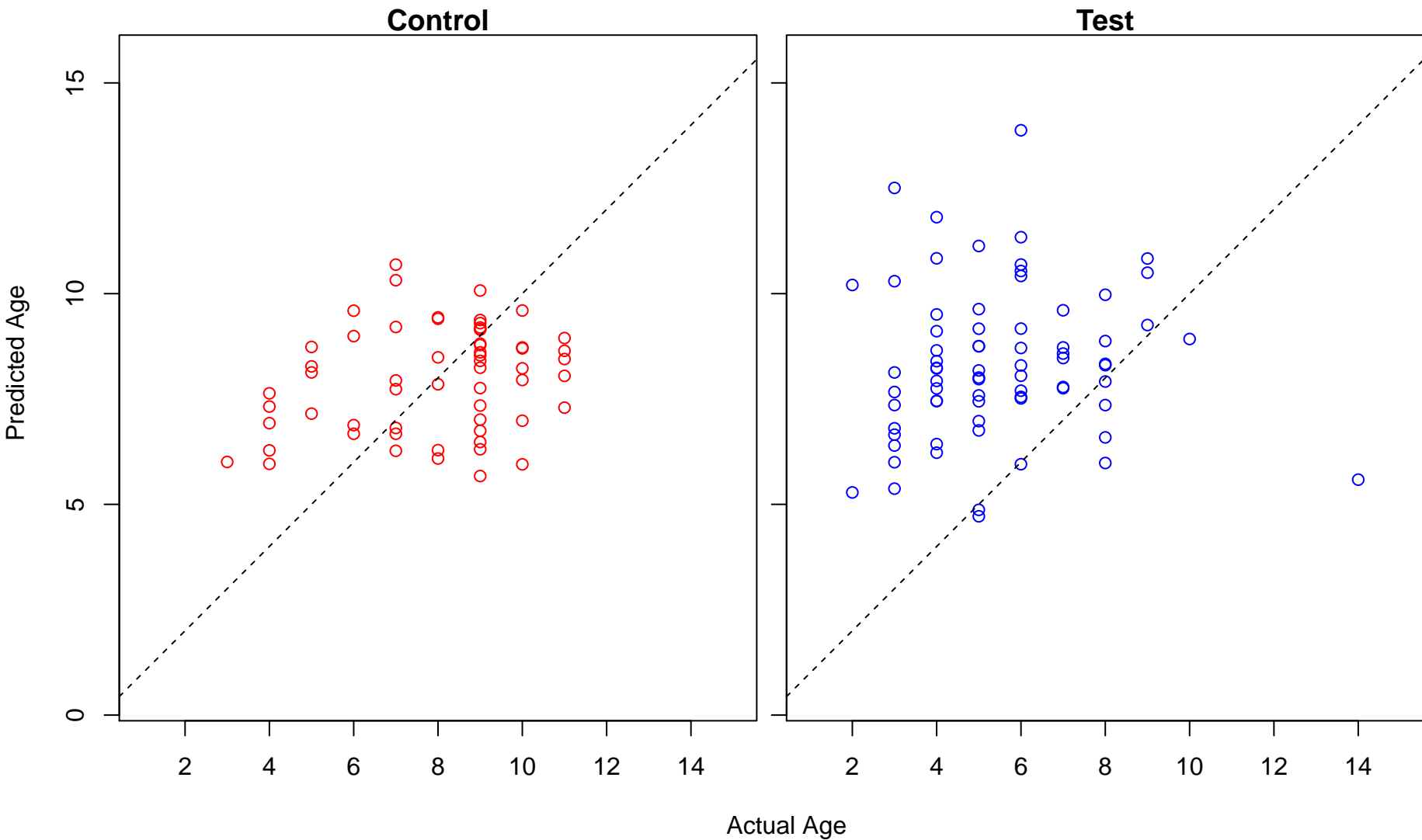
regulation of histone H3-K27 methylation (Score: 0.496960)



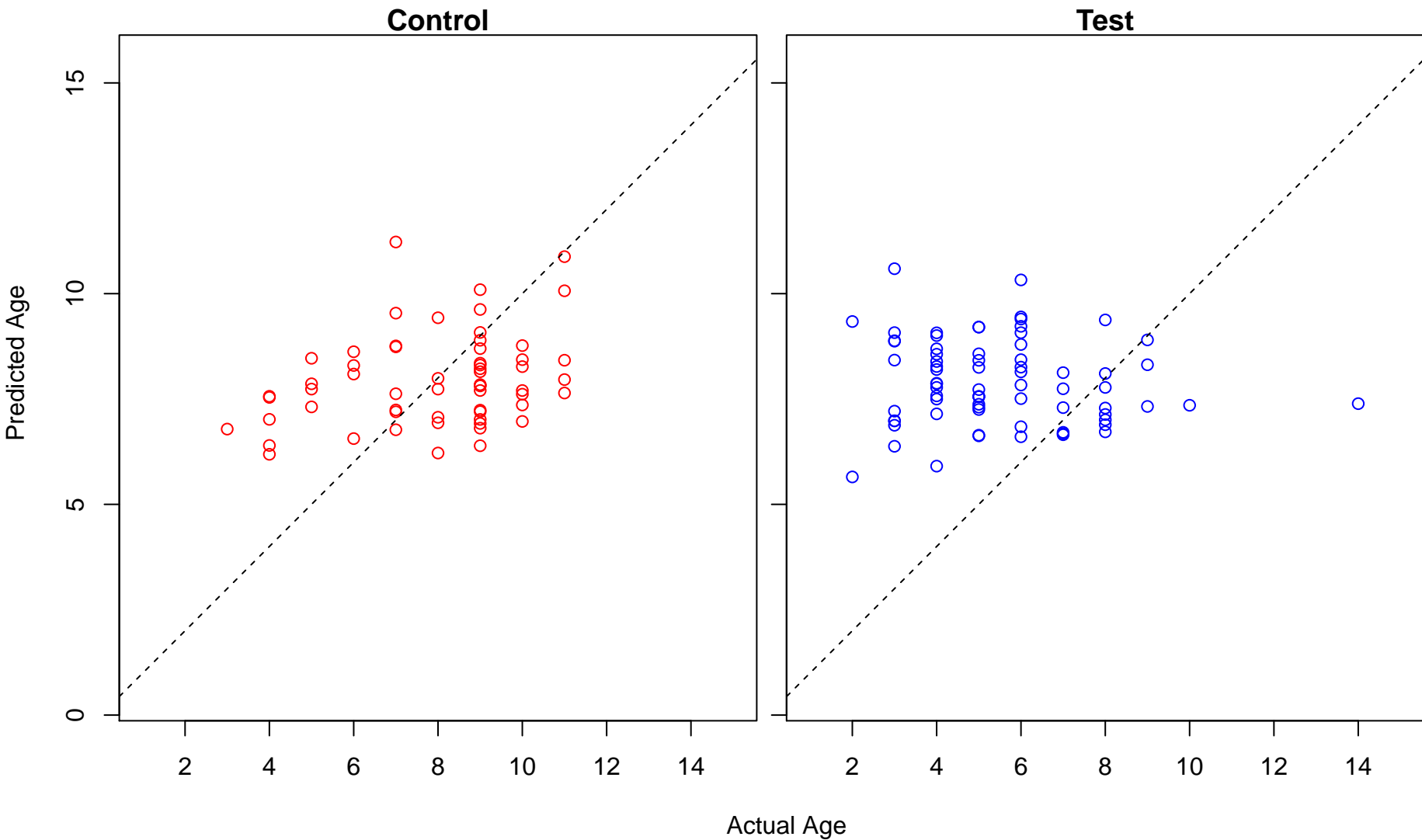
insulin-like growth factor receptor signaling pathway (Score: 0.494634)



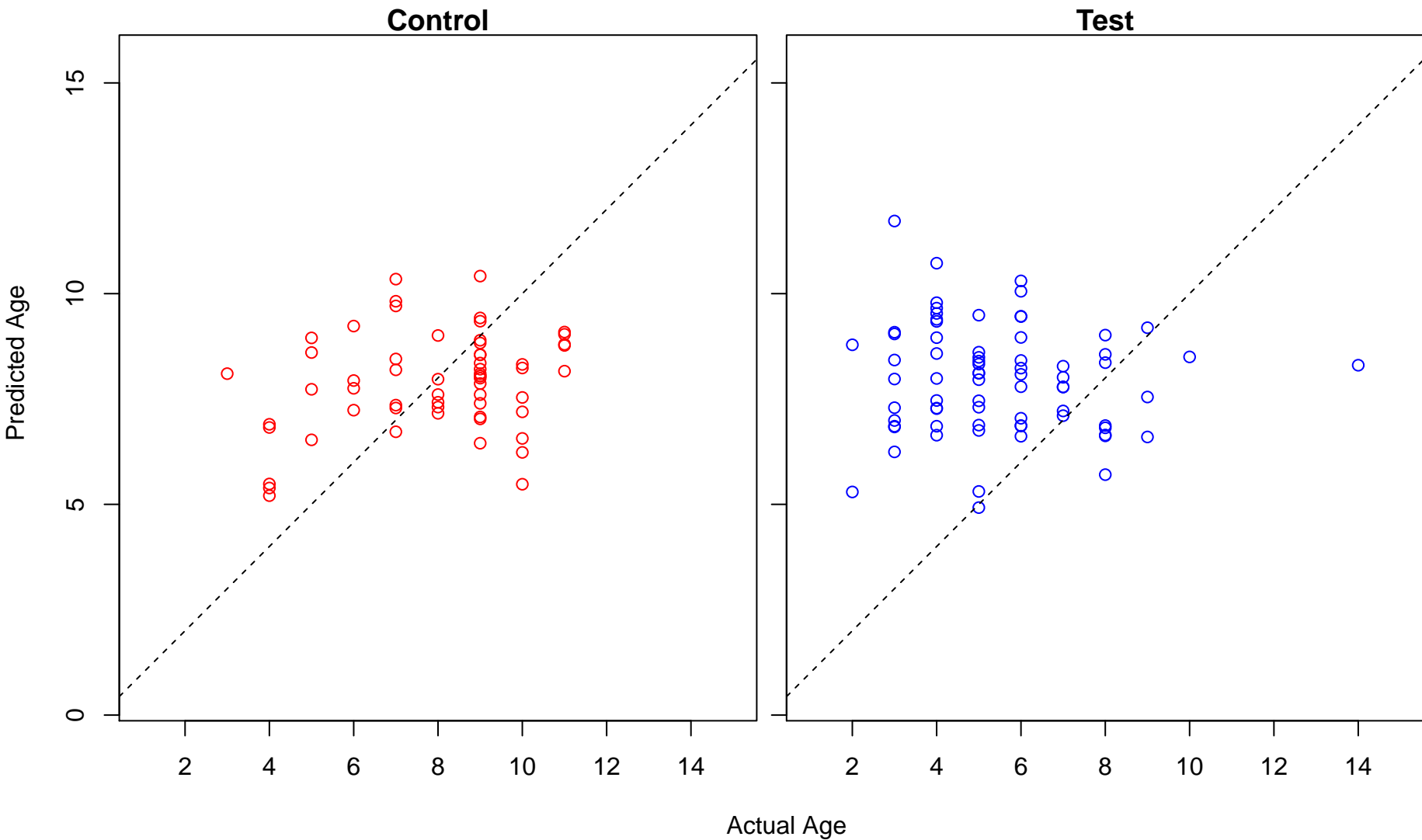
primary alcohol metabolic process (Score: 0.494077)



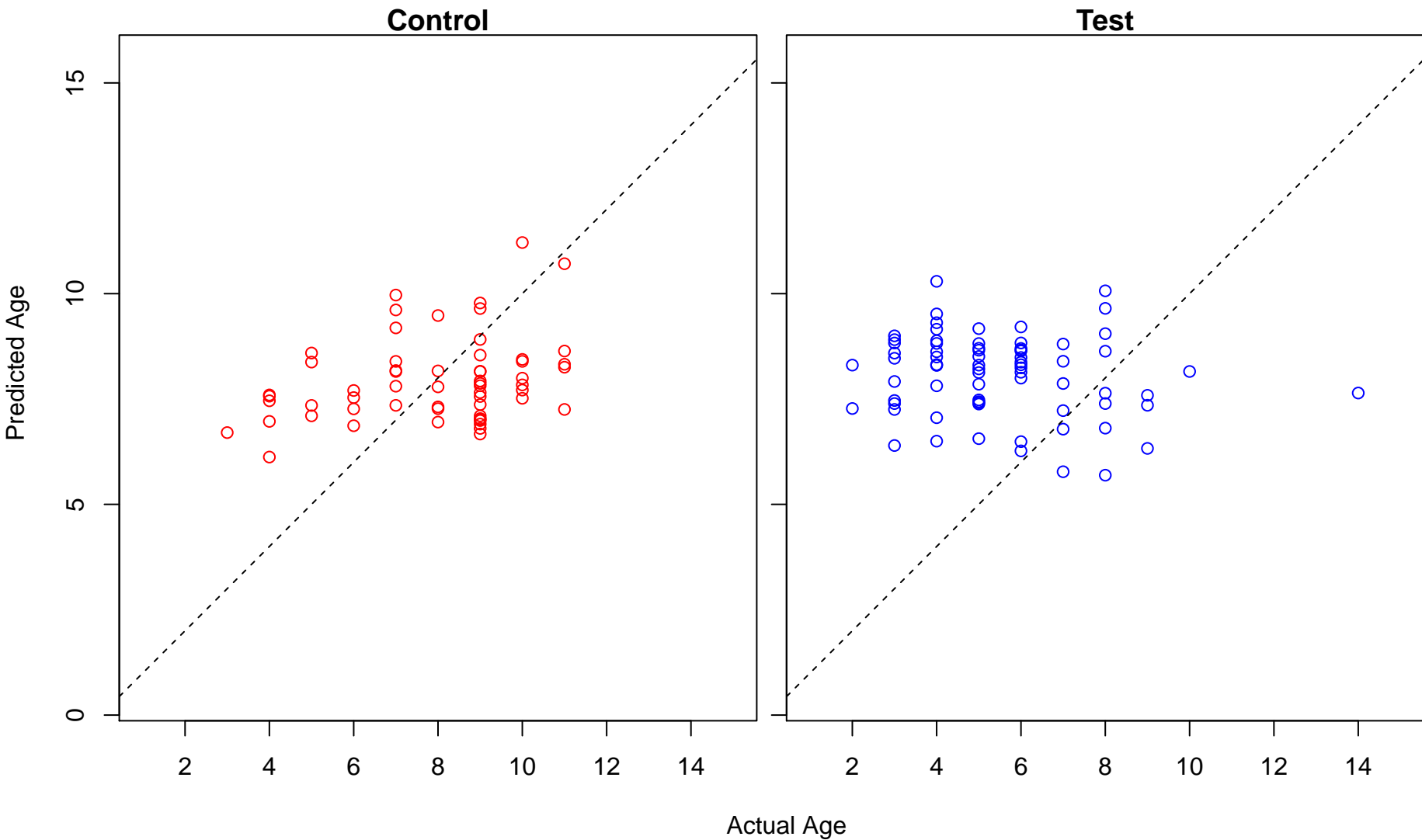
negative regulation of histone H3–K27 methylation (Score: 0.492700)



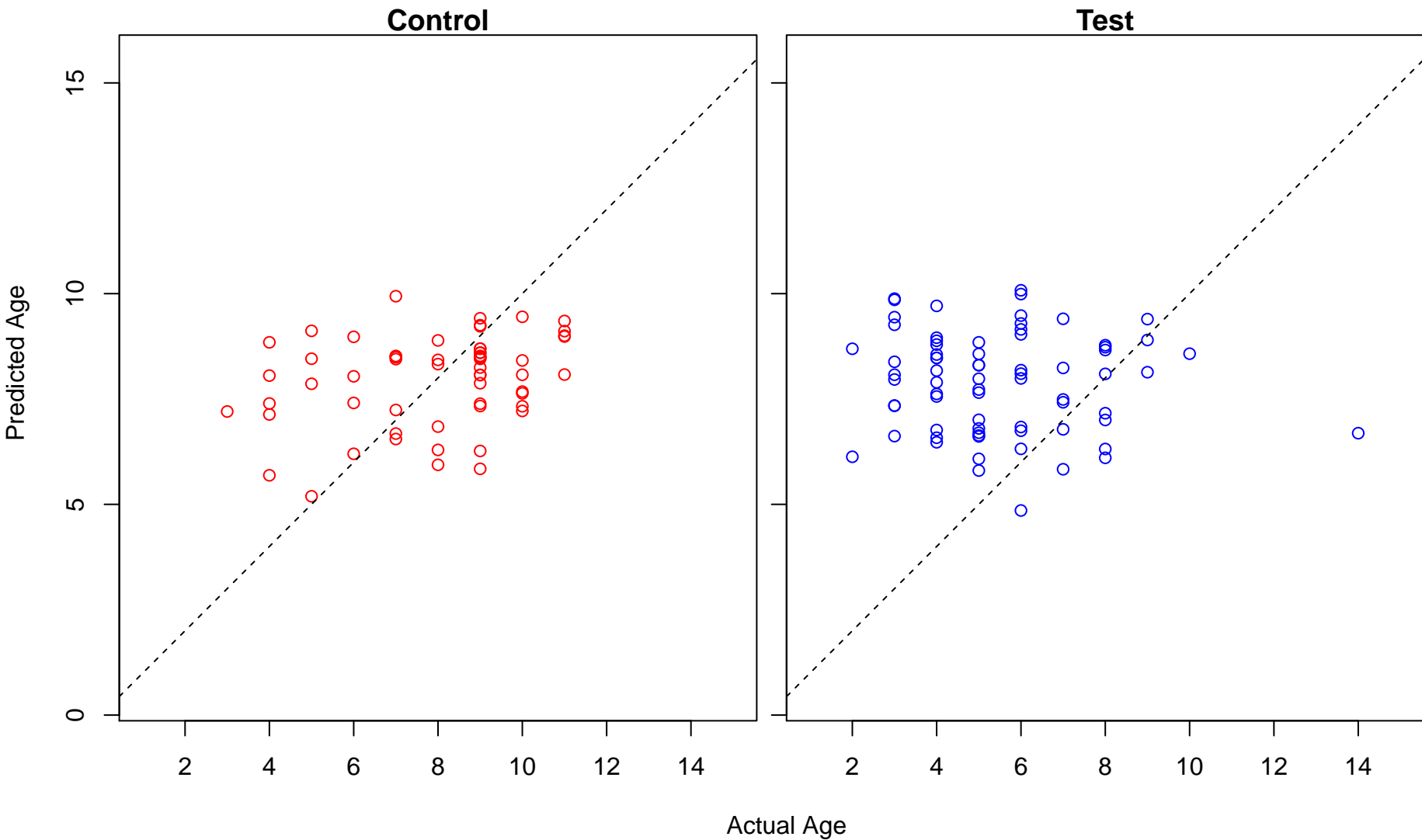
negative regulation of interleukin-12 production (Score: 0.491759)



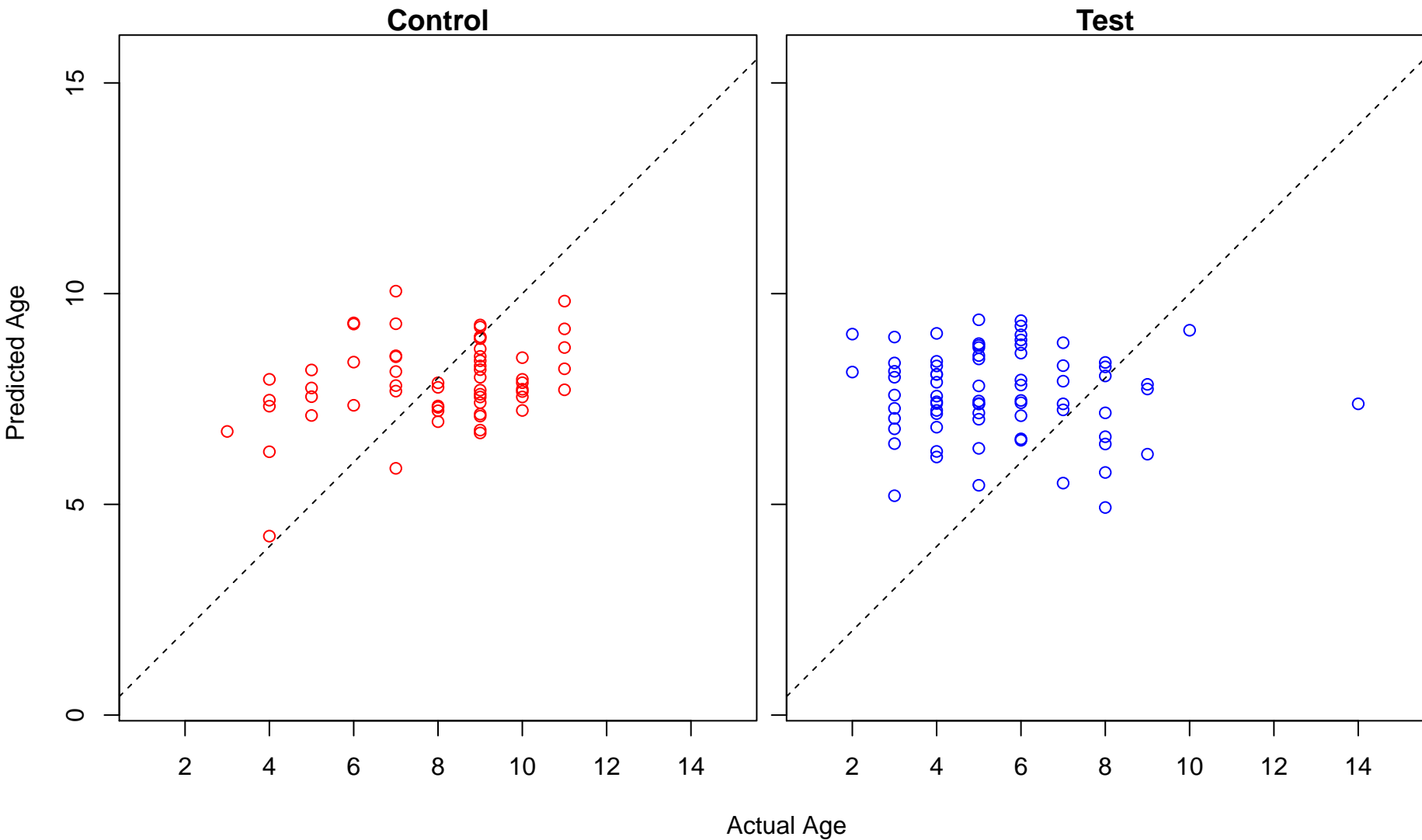
cardiac cell fate determination (Score: 0.490878)



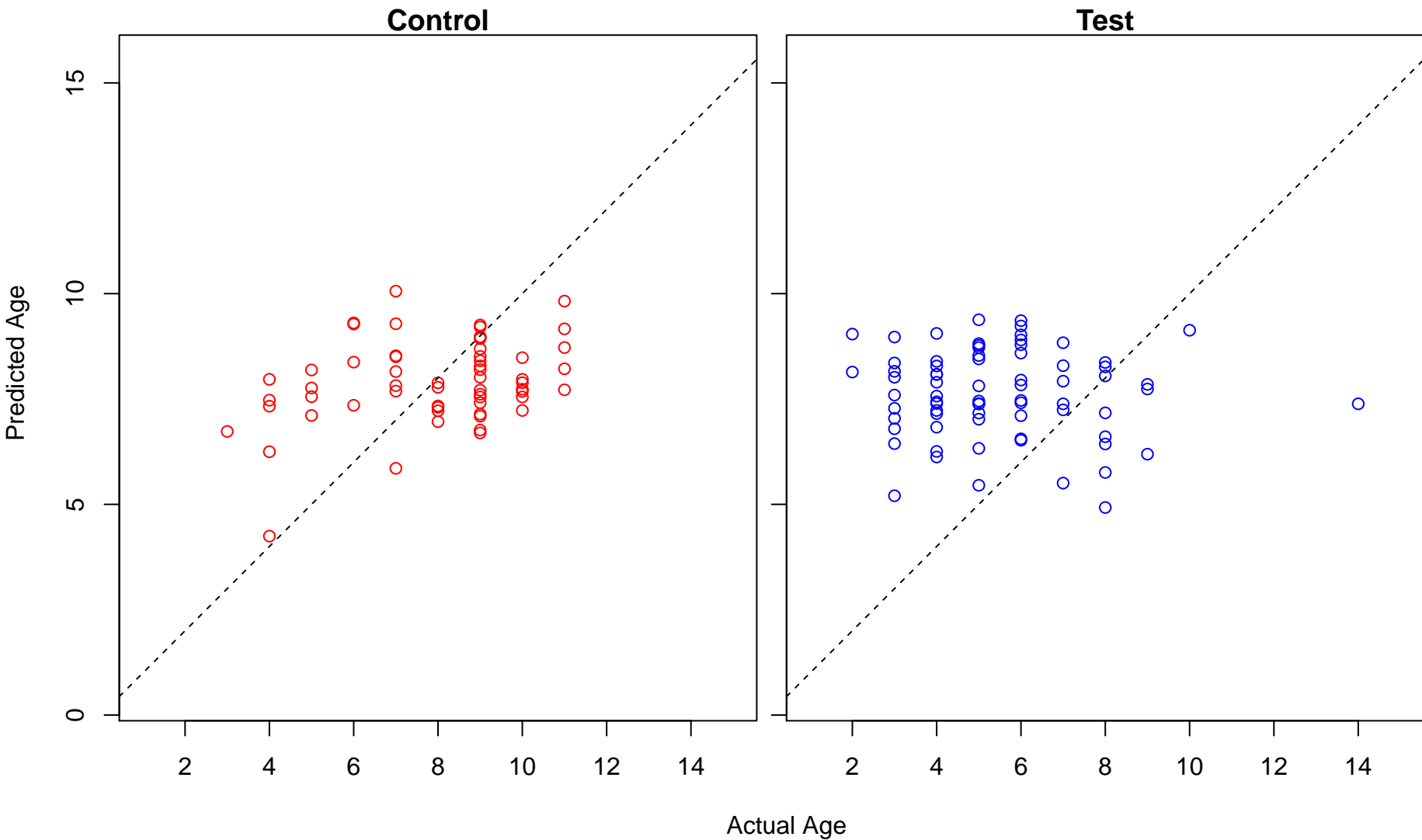
neural retina development (Score: 0.486737)



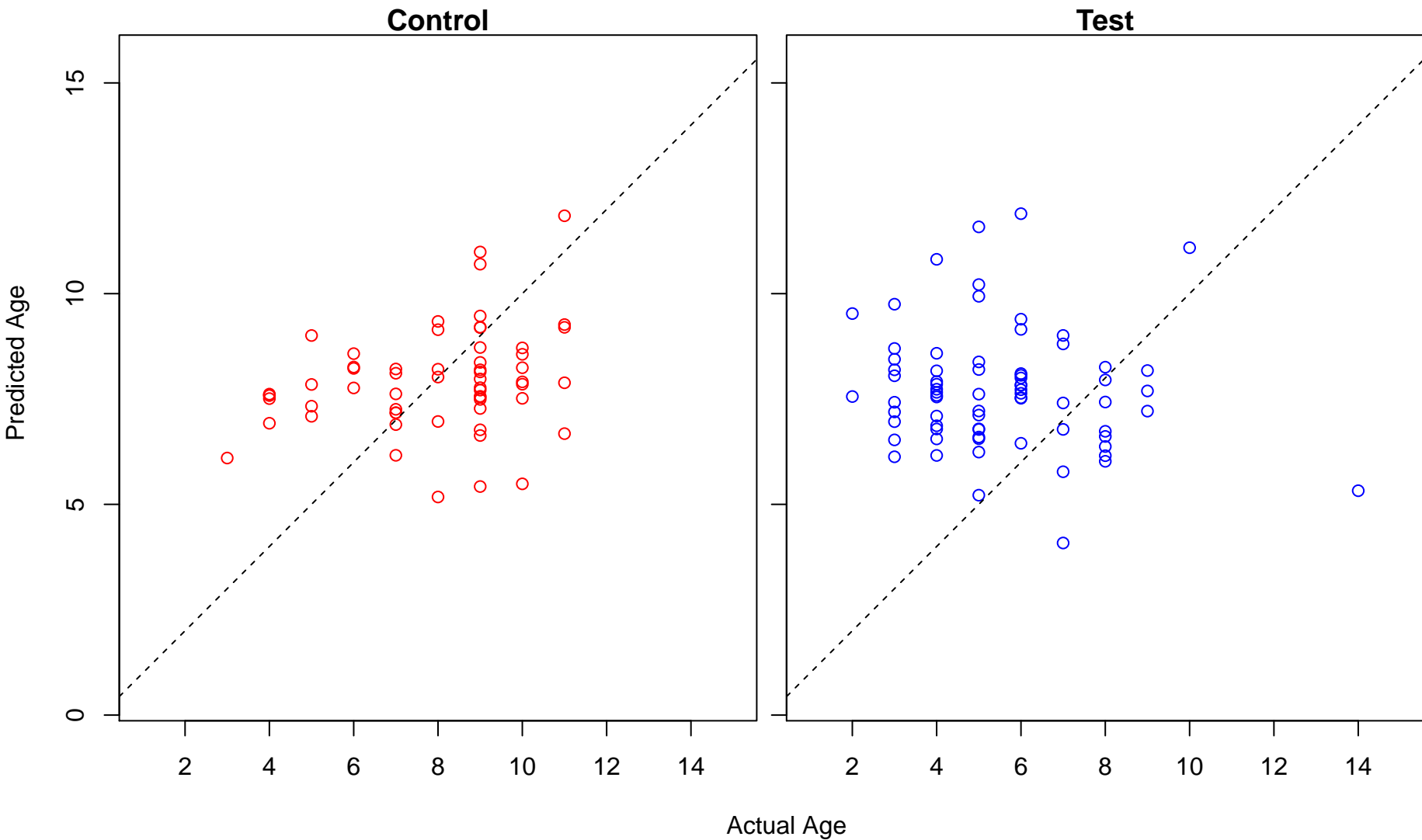
interferon-gamma secretion (Score: 0.486551)



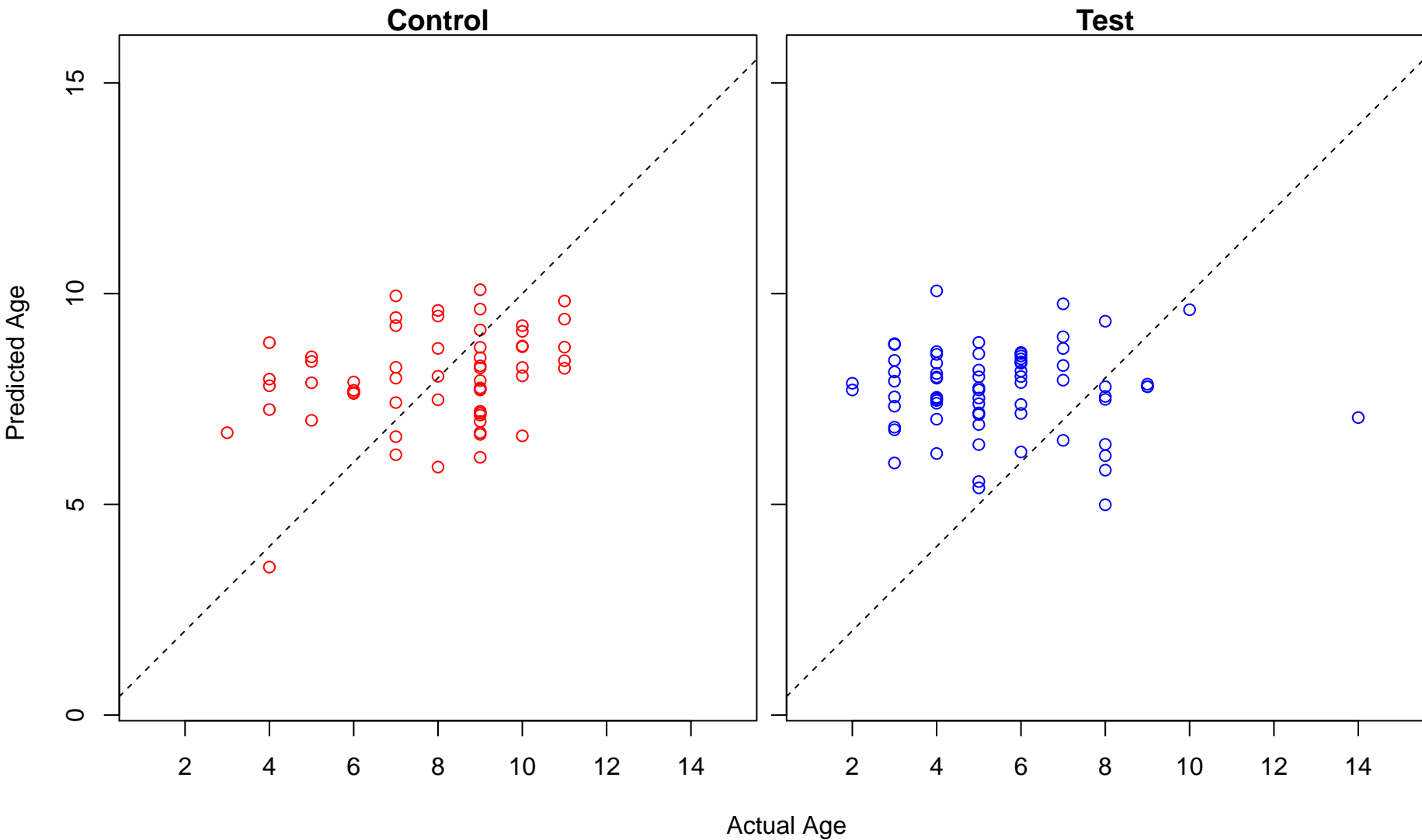
interferon- γ production (Score: 0.486537)



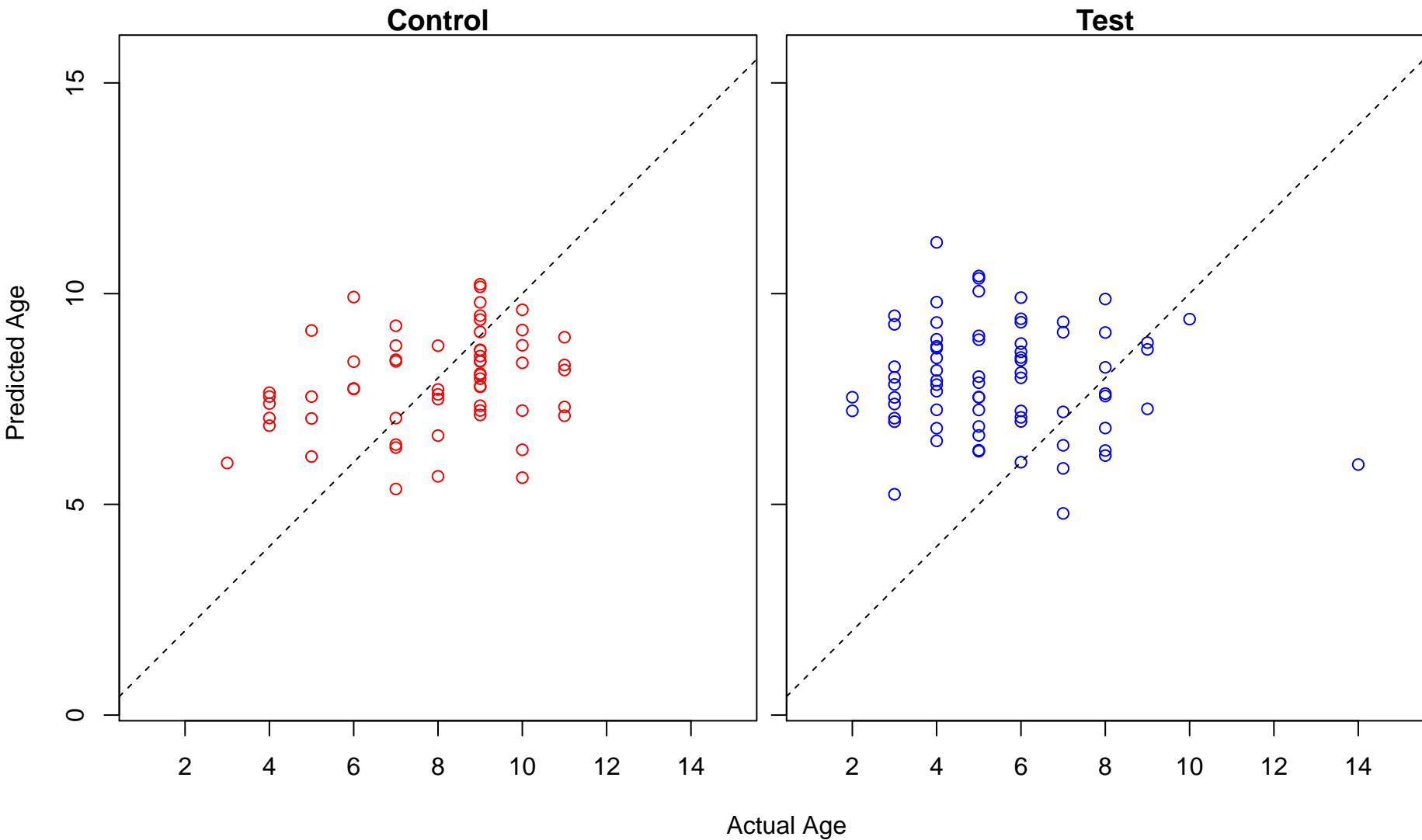
sequestering of actin monomers (Score: 0.485558)



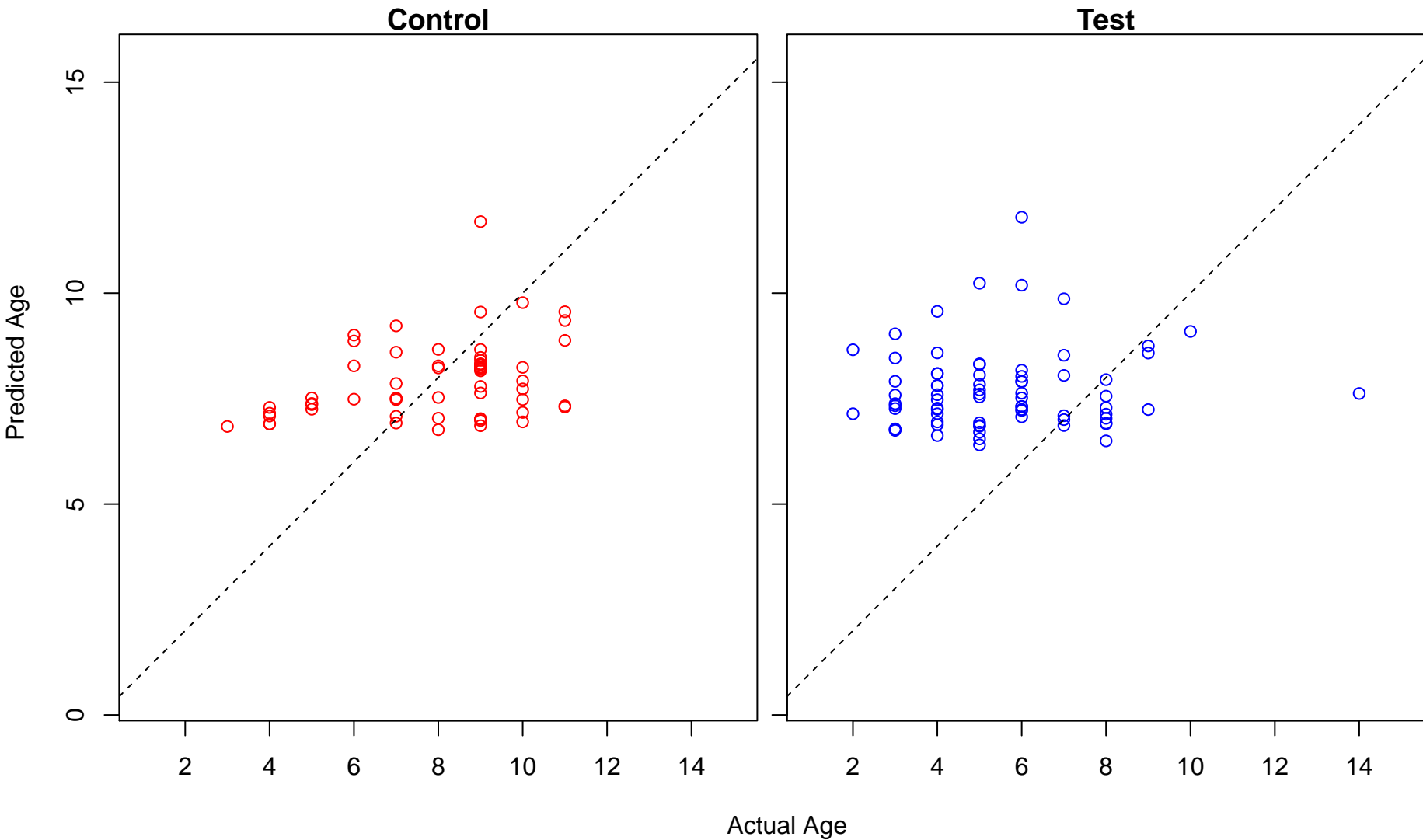
protein deglutamylation (Score: 0.484428)



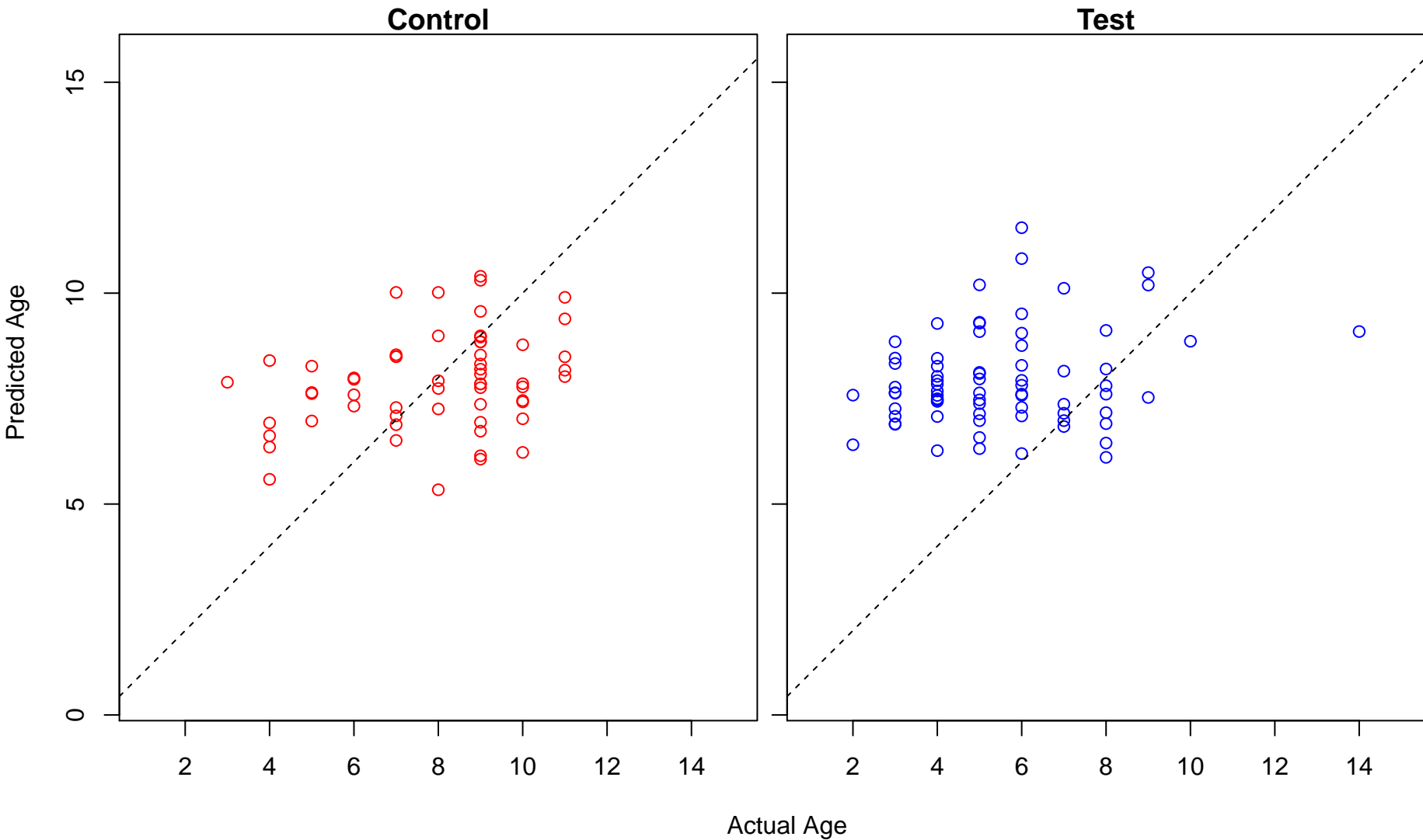
membrane hyperpolarization (Score: 0.484118)



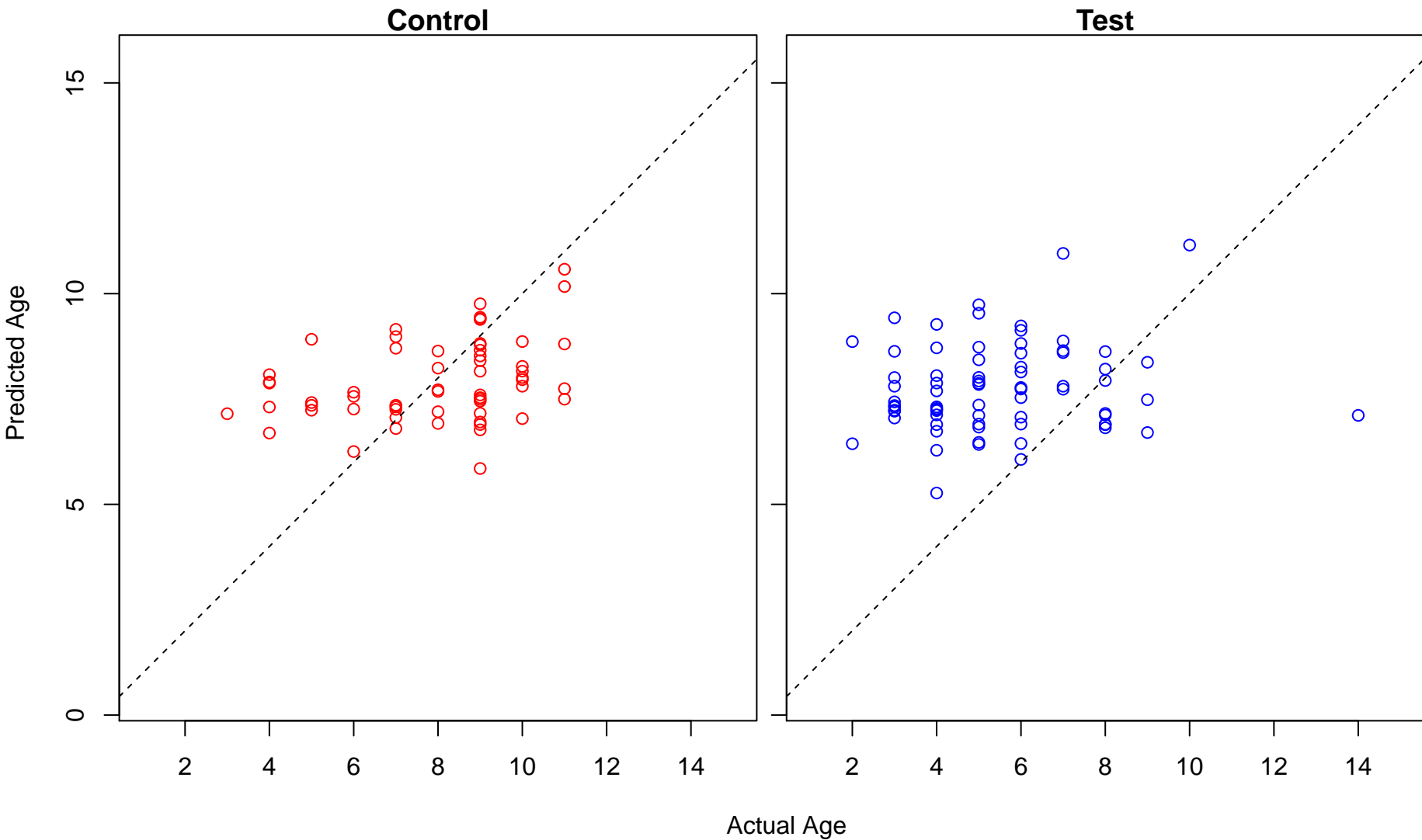
positive regulation of epidermal growth factor receptor signaling pathway (Score: 0.483852)



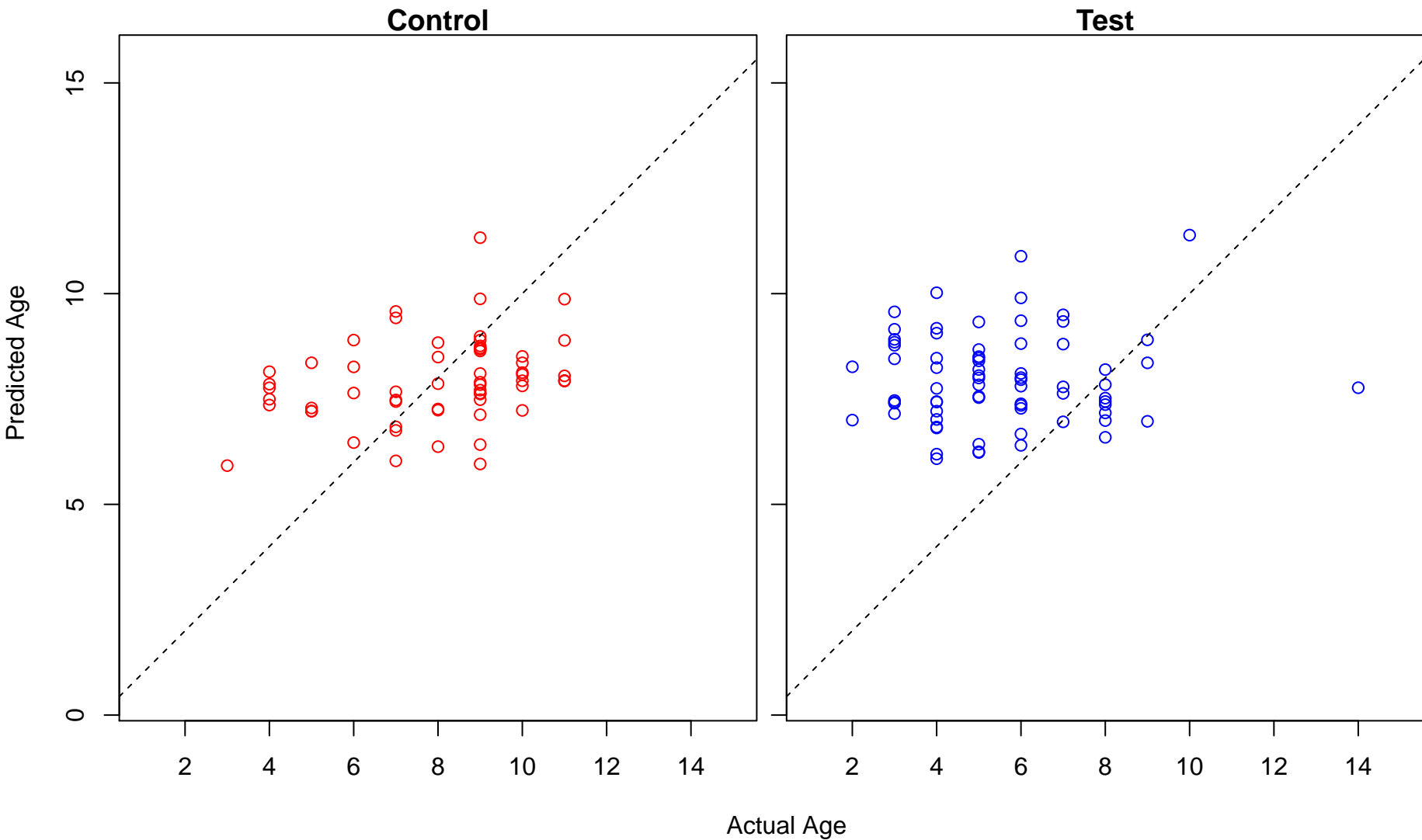
negative regulation of establishment of protein localization to plasma membrane (Score: 0.482362)



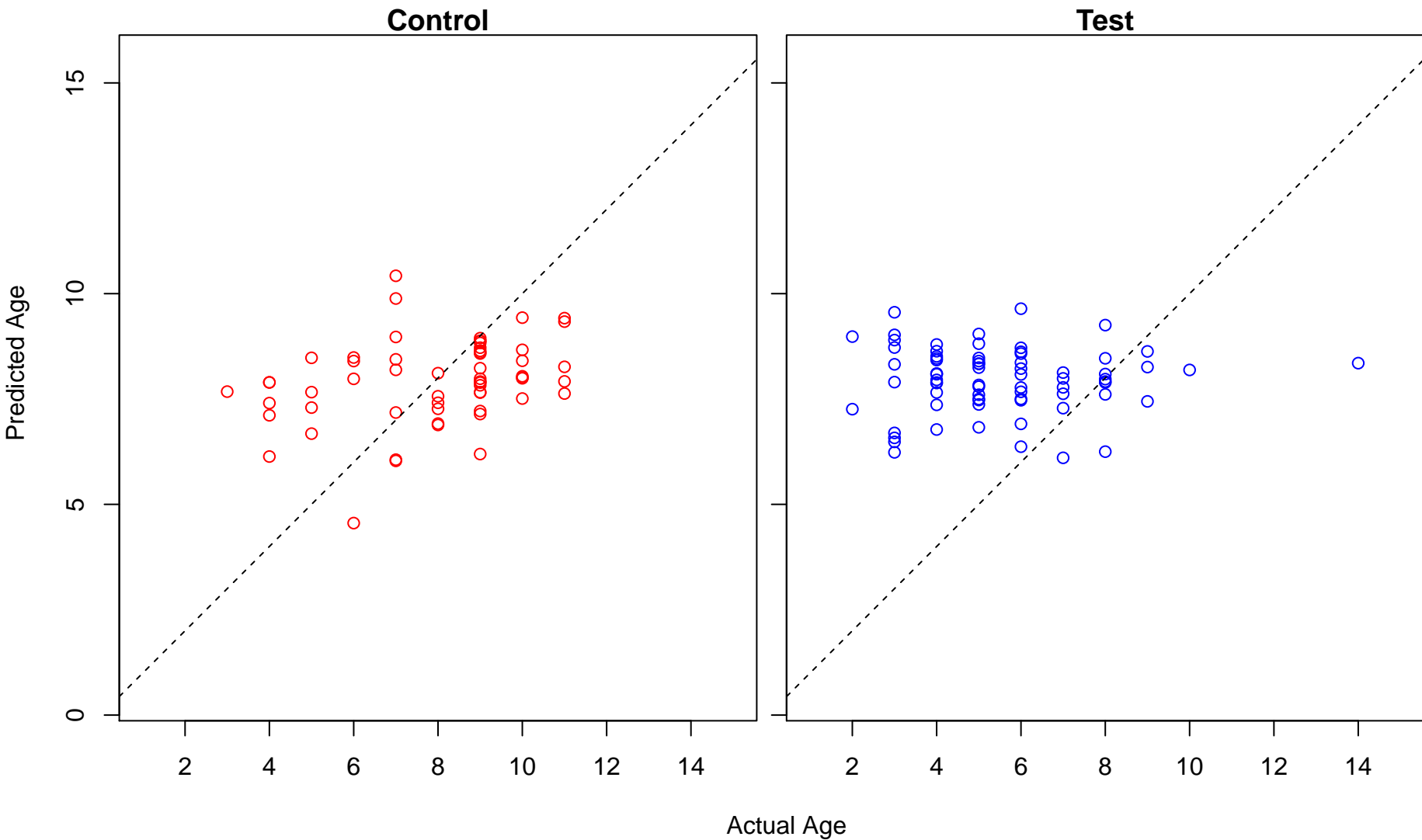
negative regulation of alkaline phosphatase activity (Score: 0.481846)



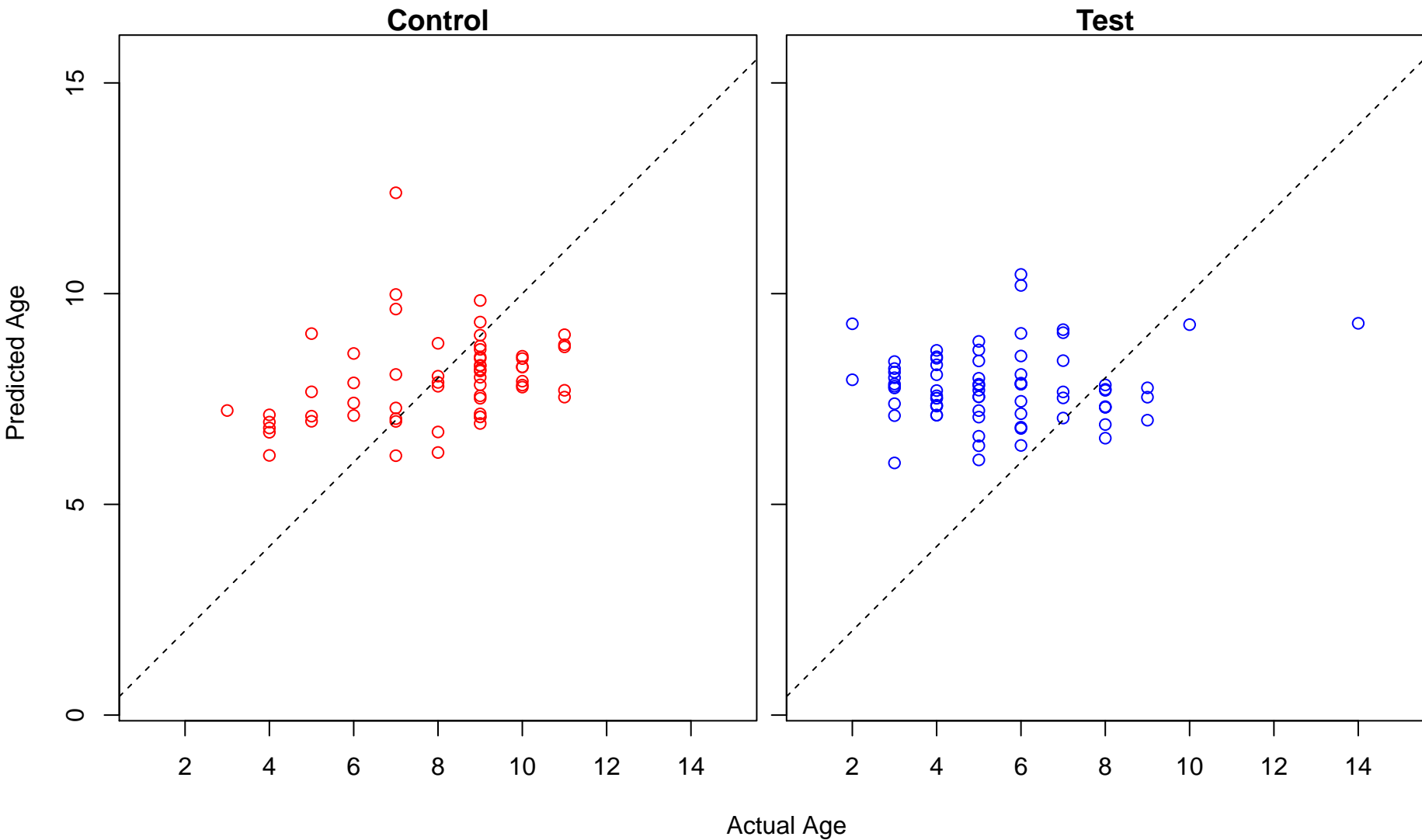
receptor recycling (Score: 0.480446)



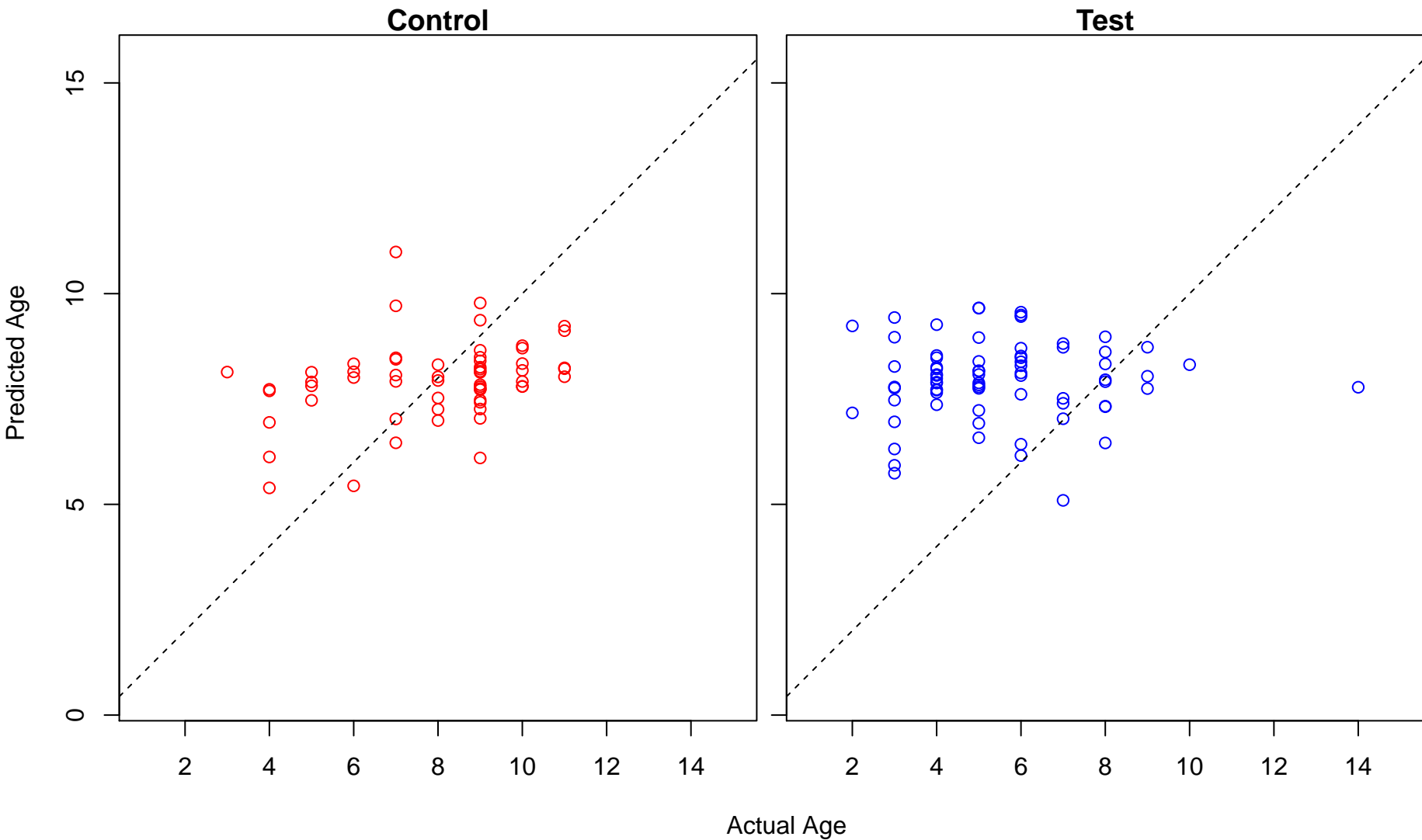
nucleotide transport (Score: 0.480044)



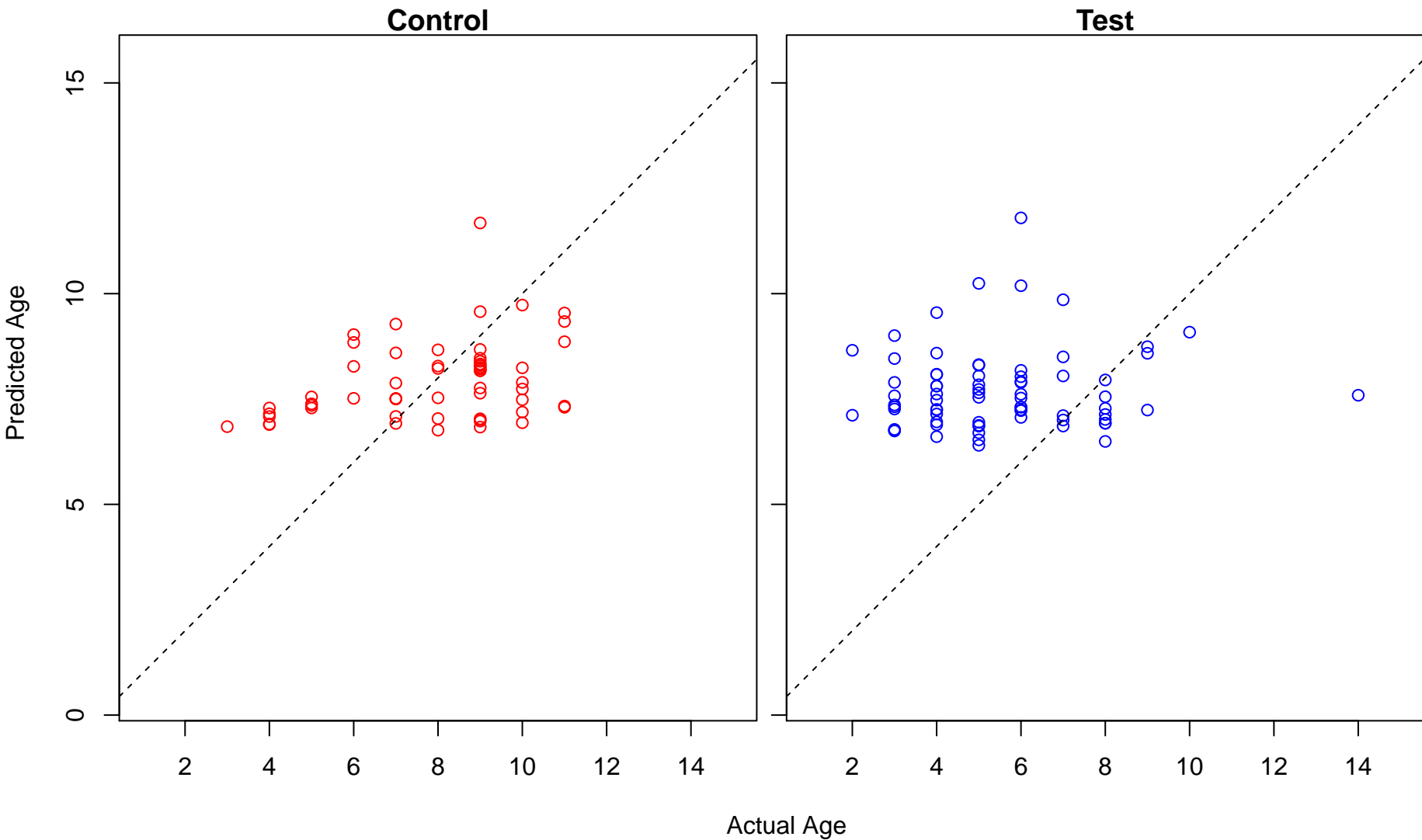
ventricular system development (Score: 0.477957)



UDP-glucuronate biosynthetic process (Score: 0.476768)

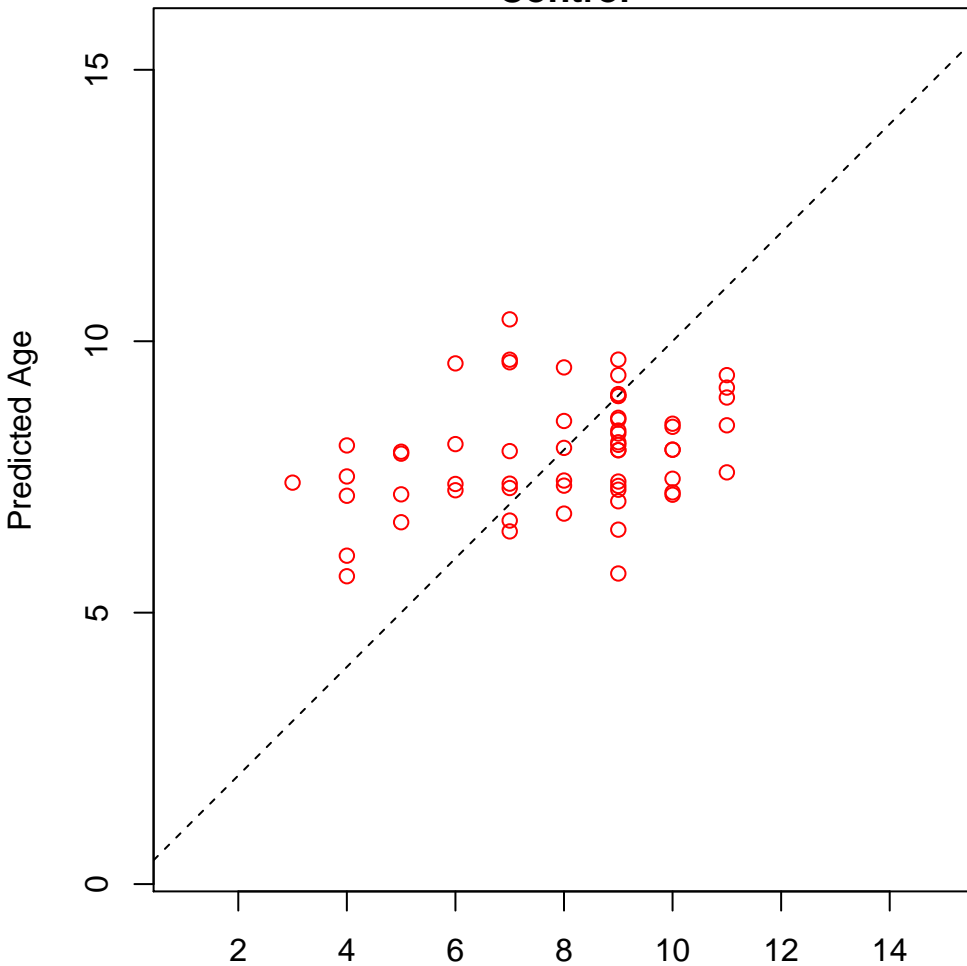


positive regulation of ERBB signaling pathway (Score: 0.474533)

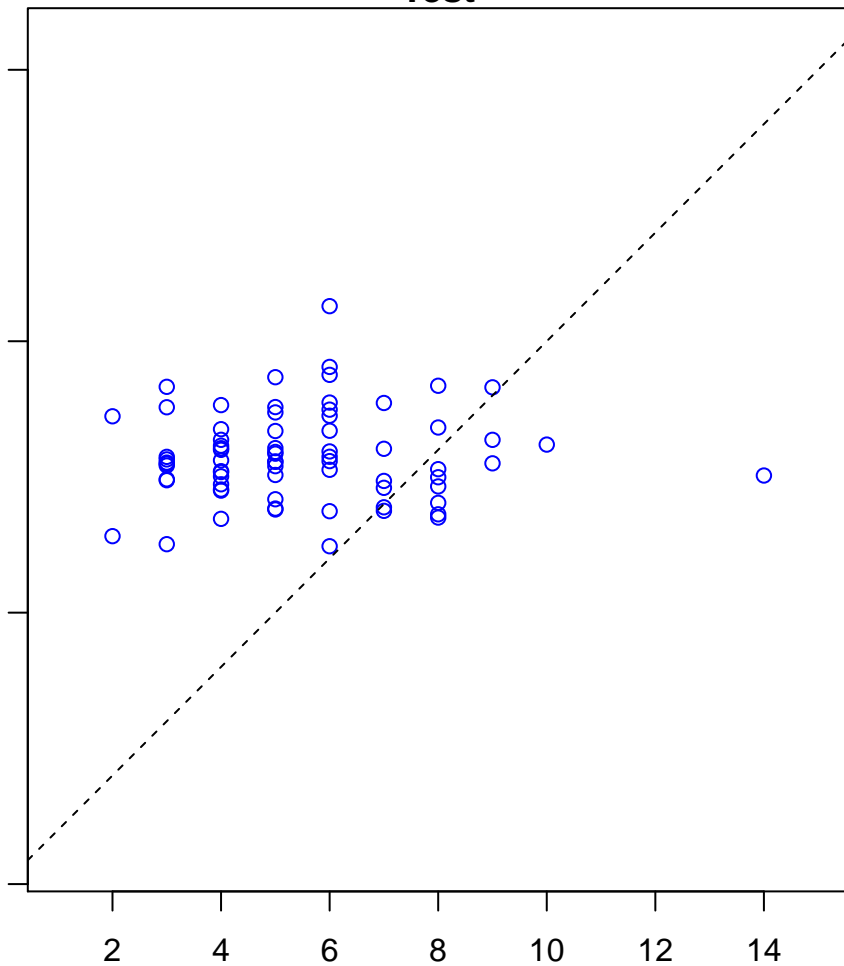


positive regulation of tissue remodeling (Score: 0.471200)

Control

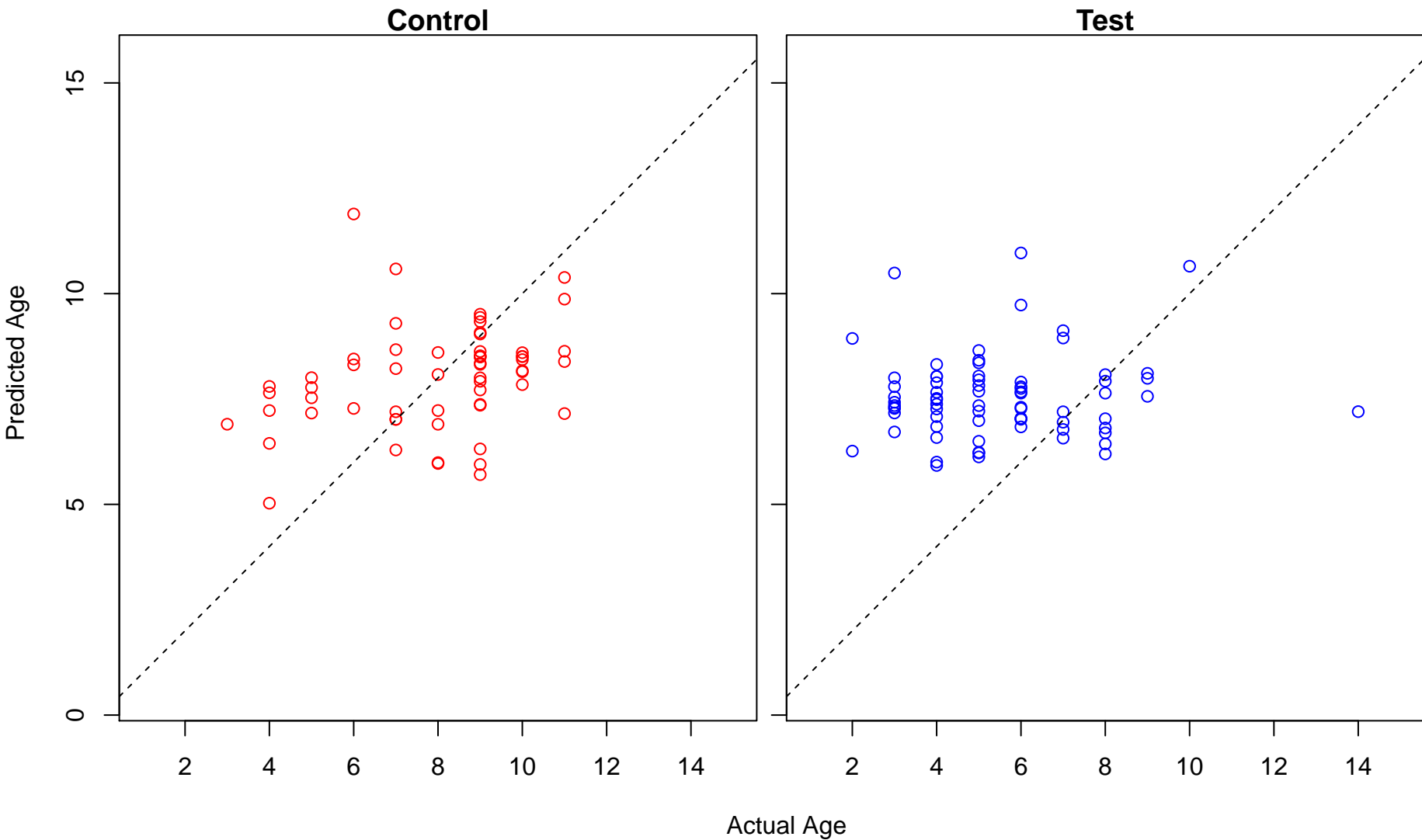


Test

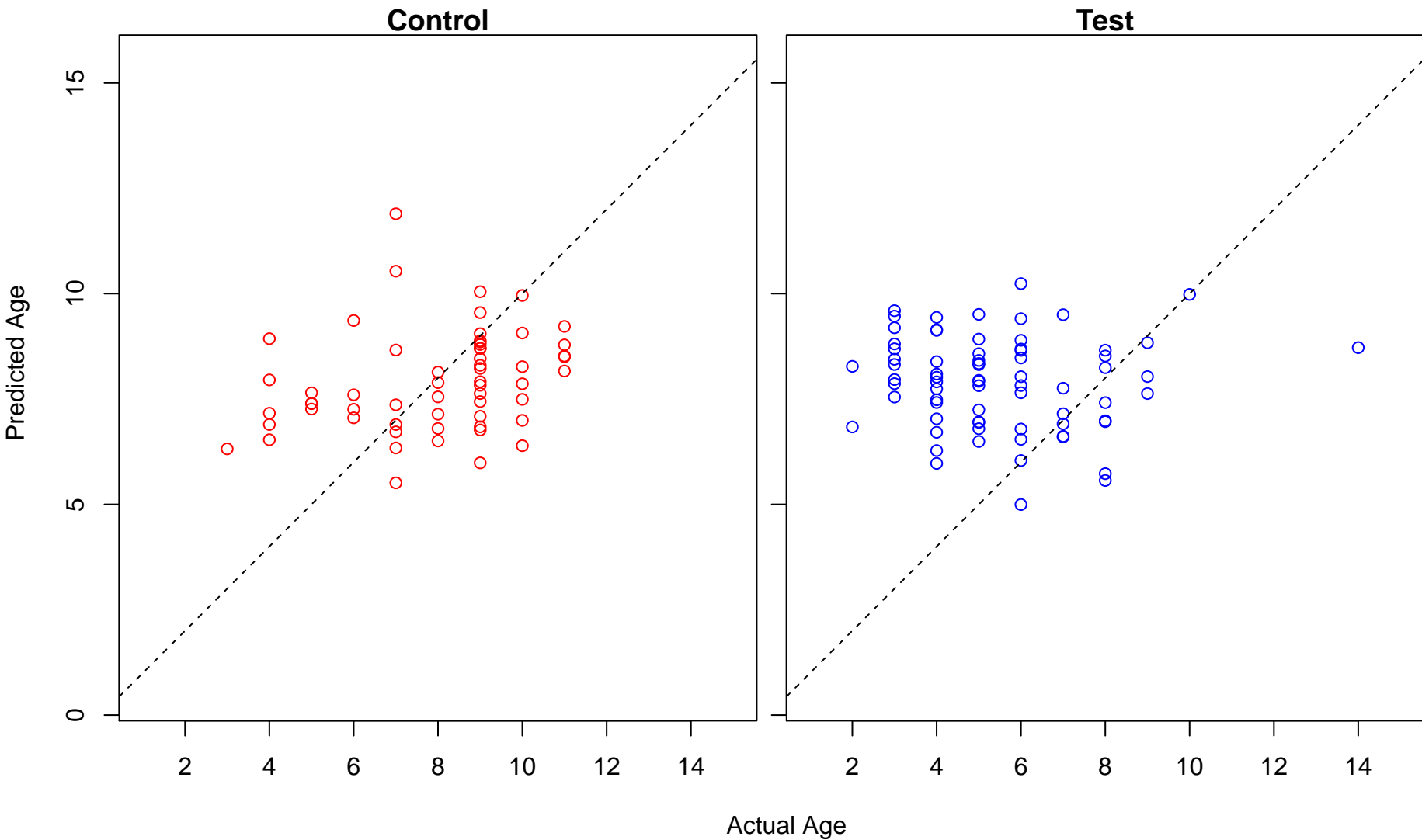


Actual Age

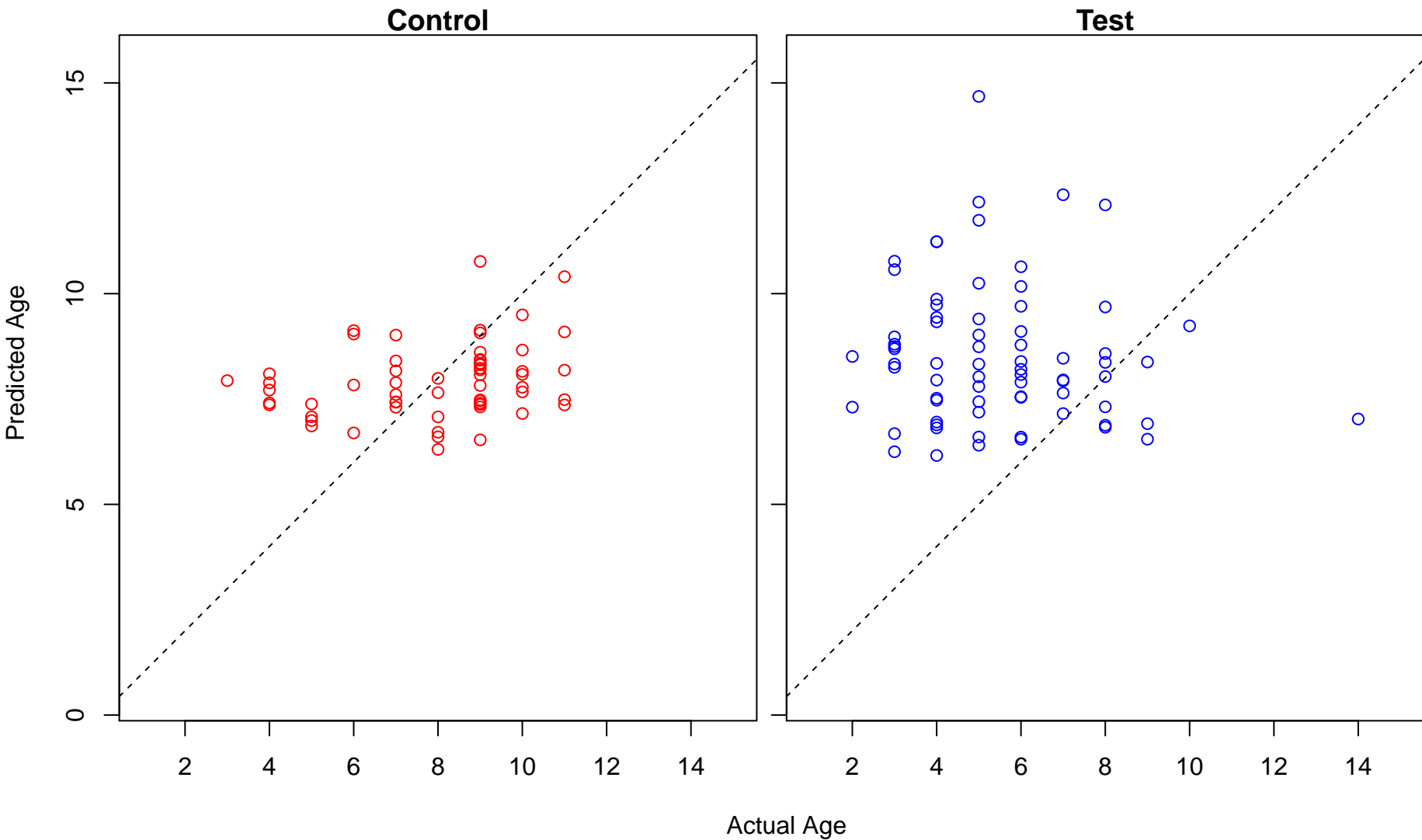
positive regulation of interleukin-8 production (Score: 0.471077)



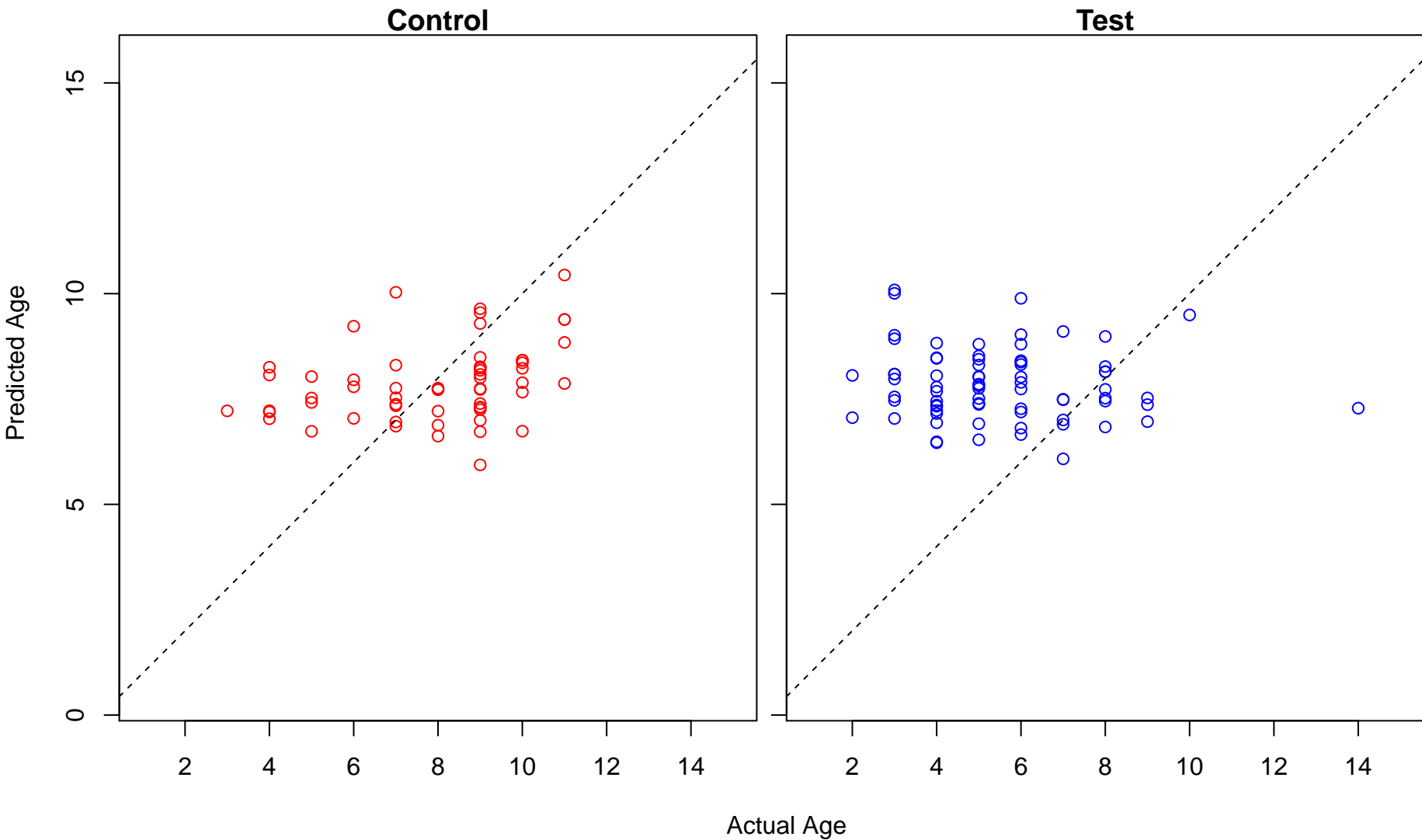
carbohydrate phosphorylation (Score: 0.469244)



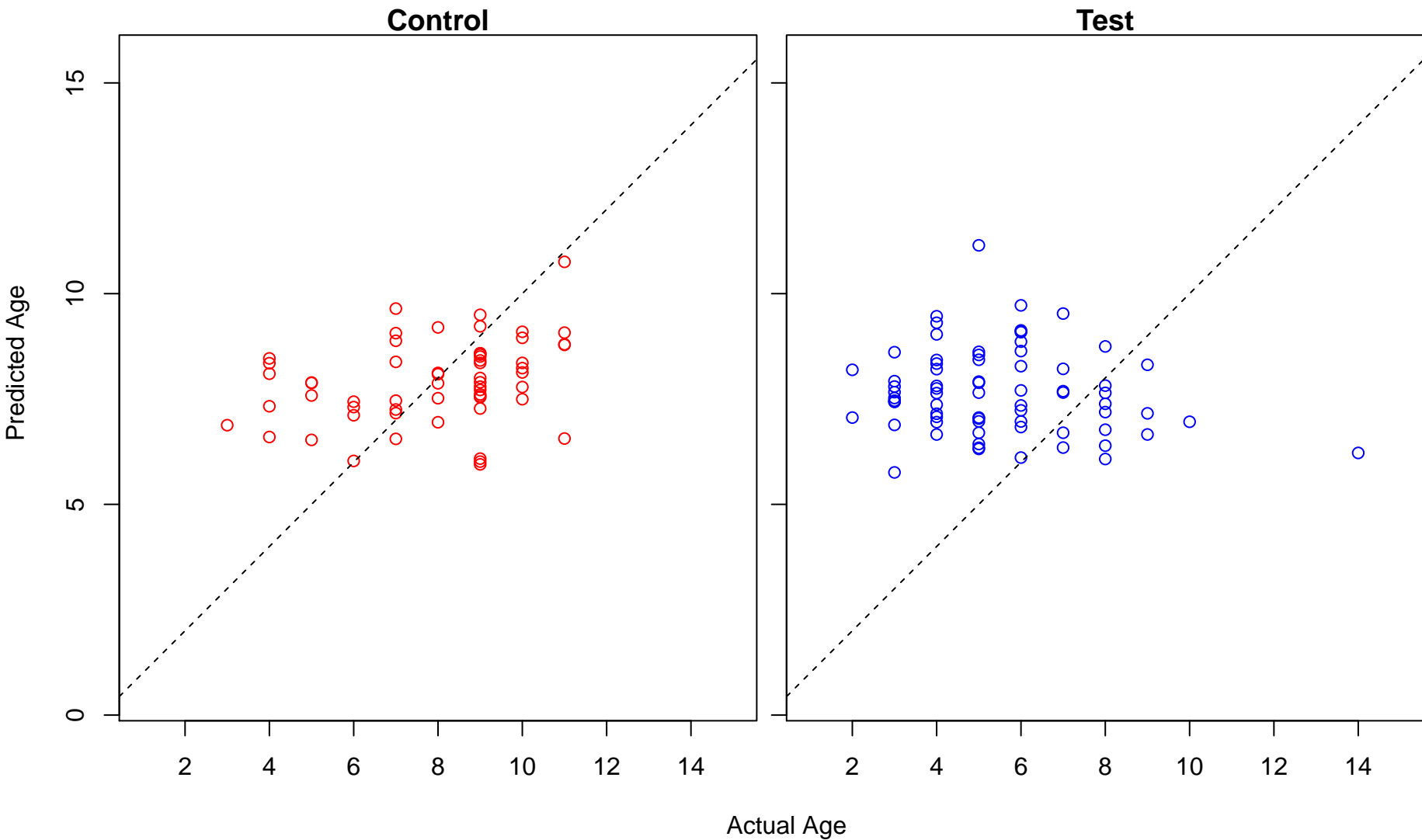
sphingomyelin catabolic process (Score: 0.468222)



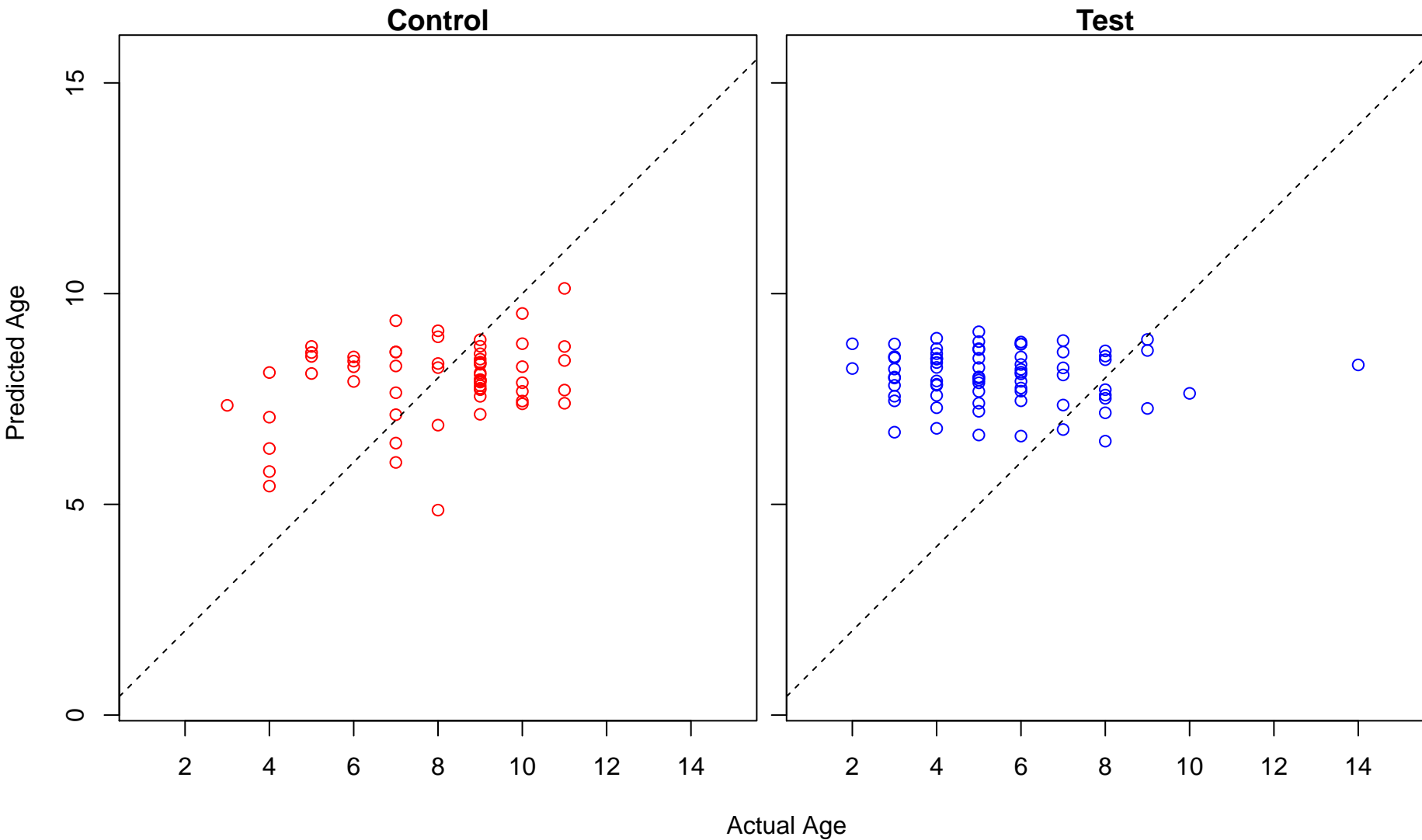
cardiolipin biosynthetic process (Score: 0.466875)



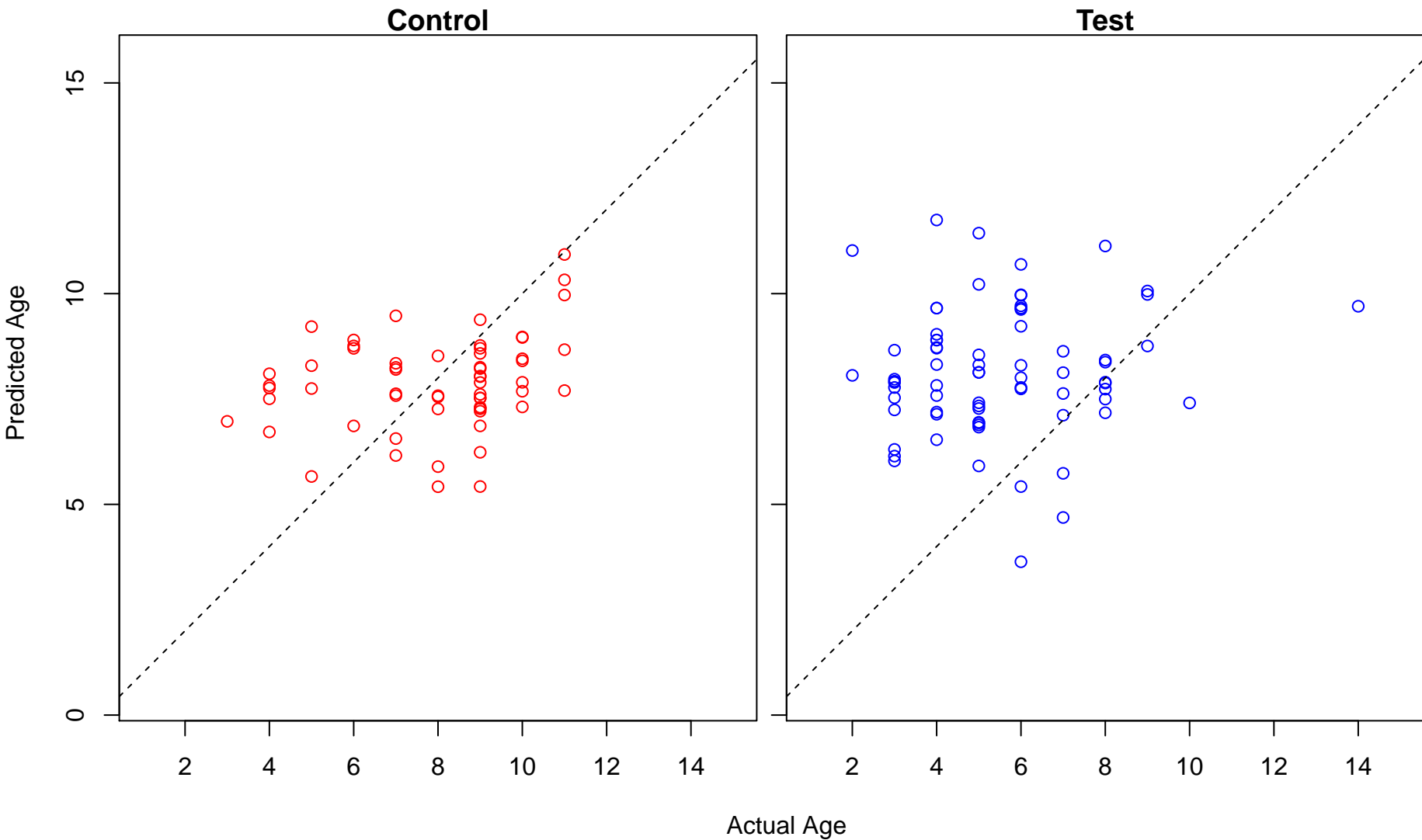
tyrosine catabolic process (Score: 0.465608)



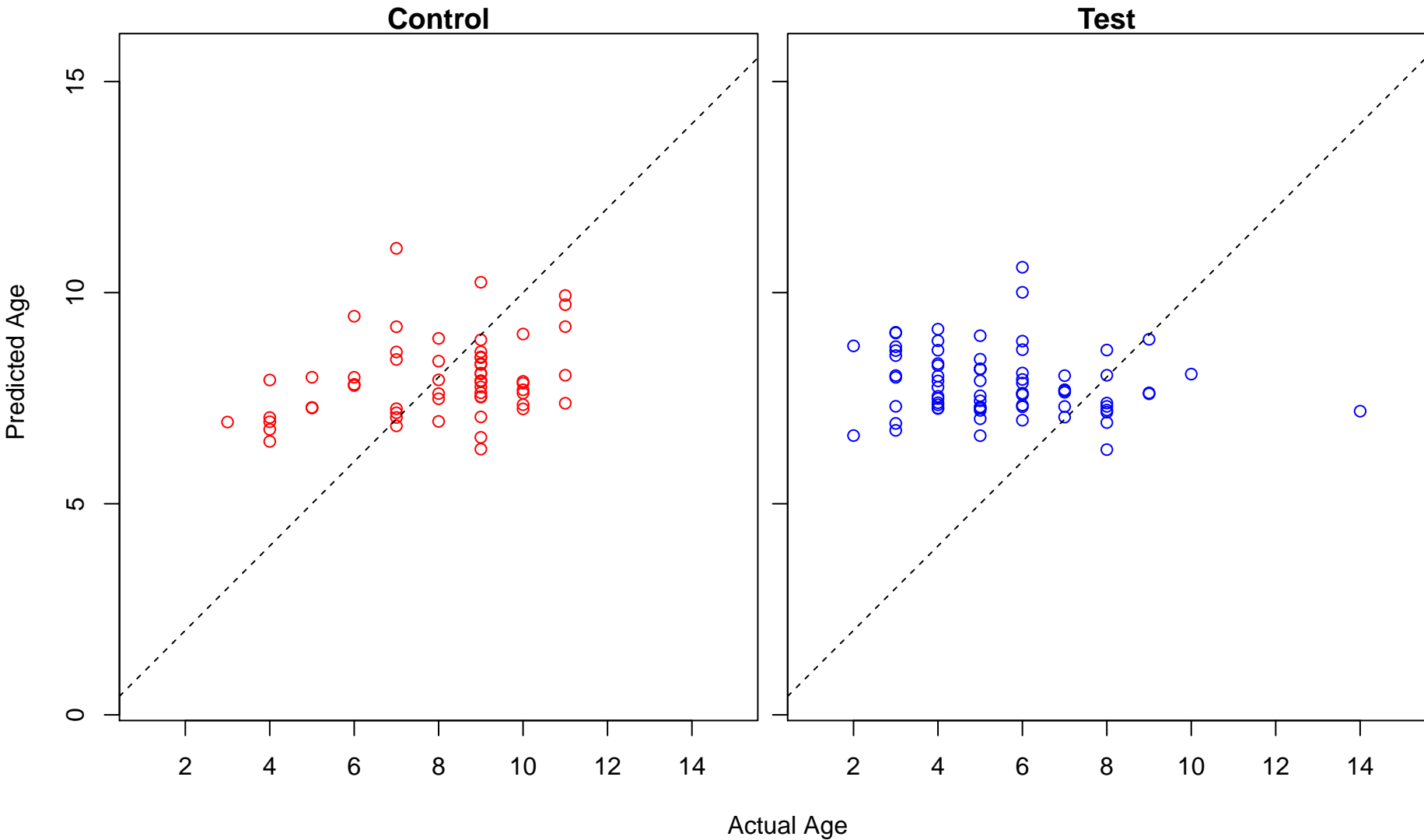
RNA polymerase II transcriptional preinitiation complex assembly (Score: 0.465502)



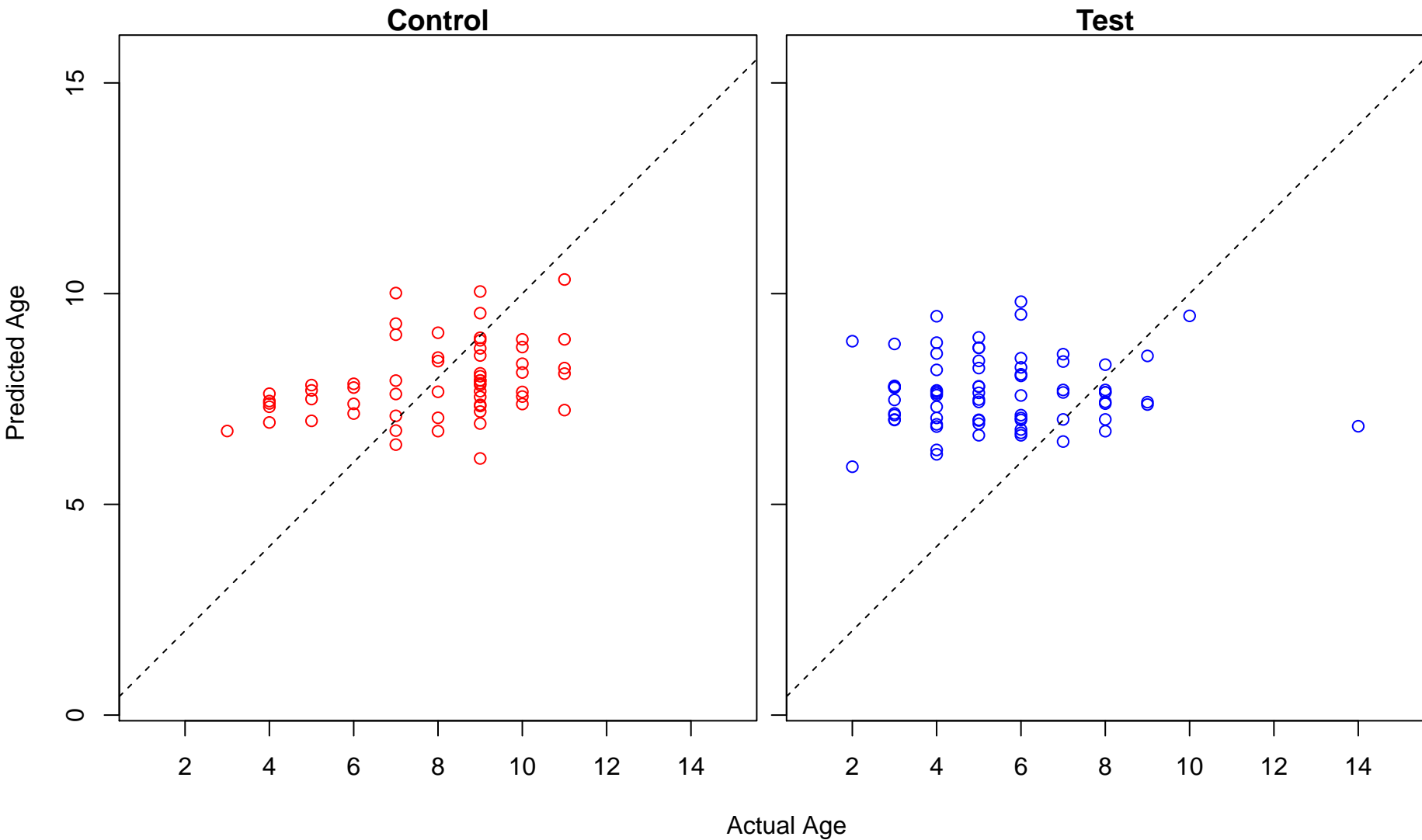
regulation of glucocorticoid secretion (Score: 0.464245)



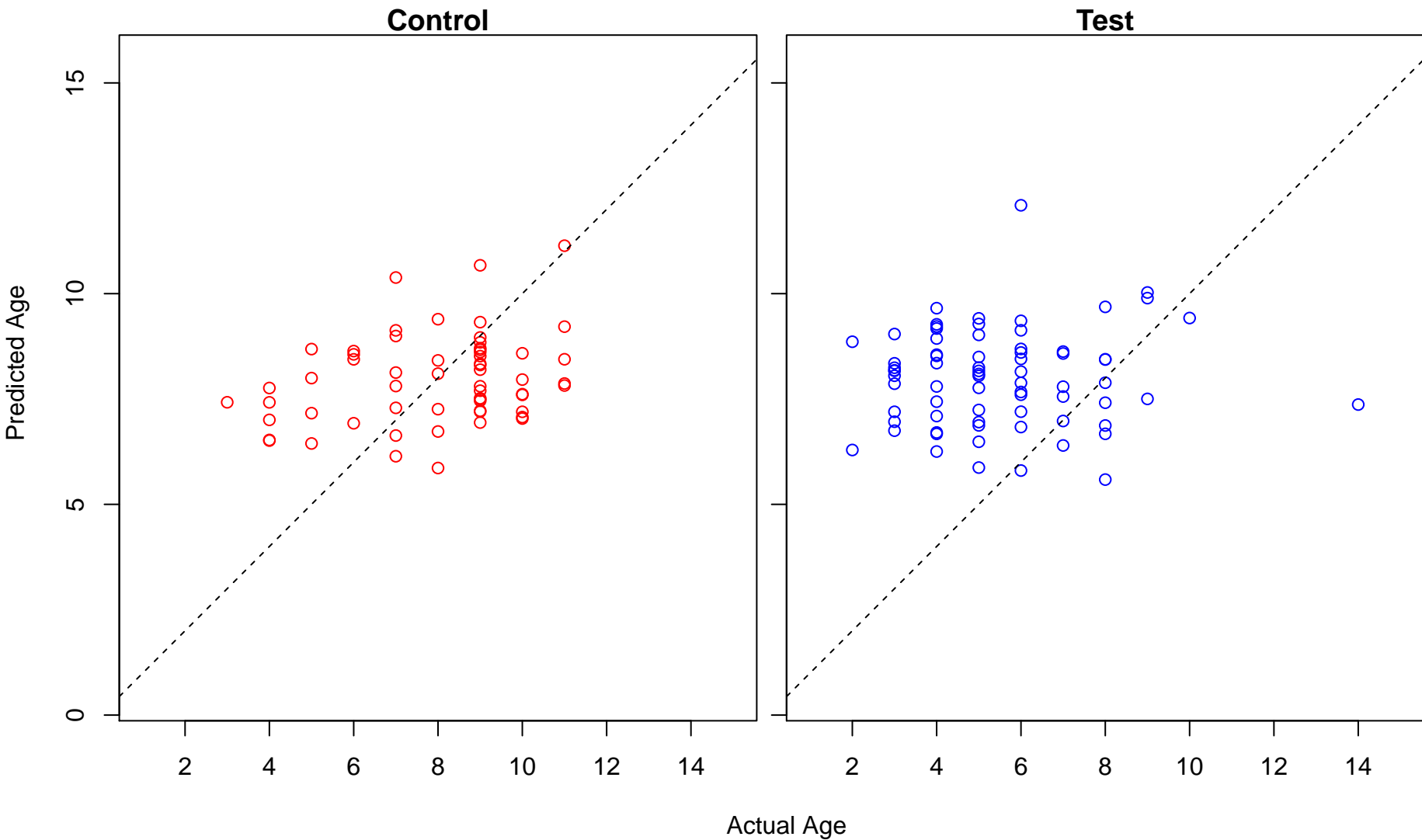
pentose-phosphate shunt, oxidative branch (Score: 0.462308)



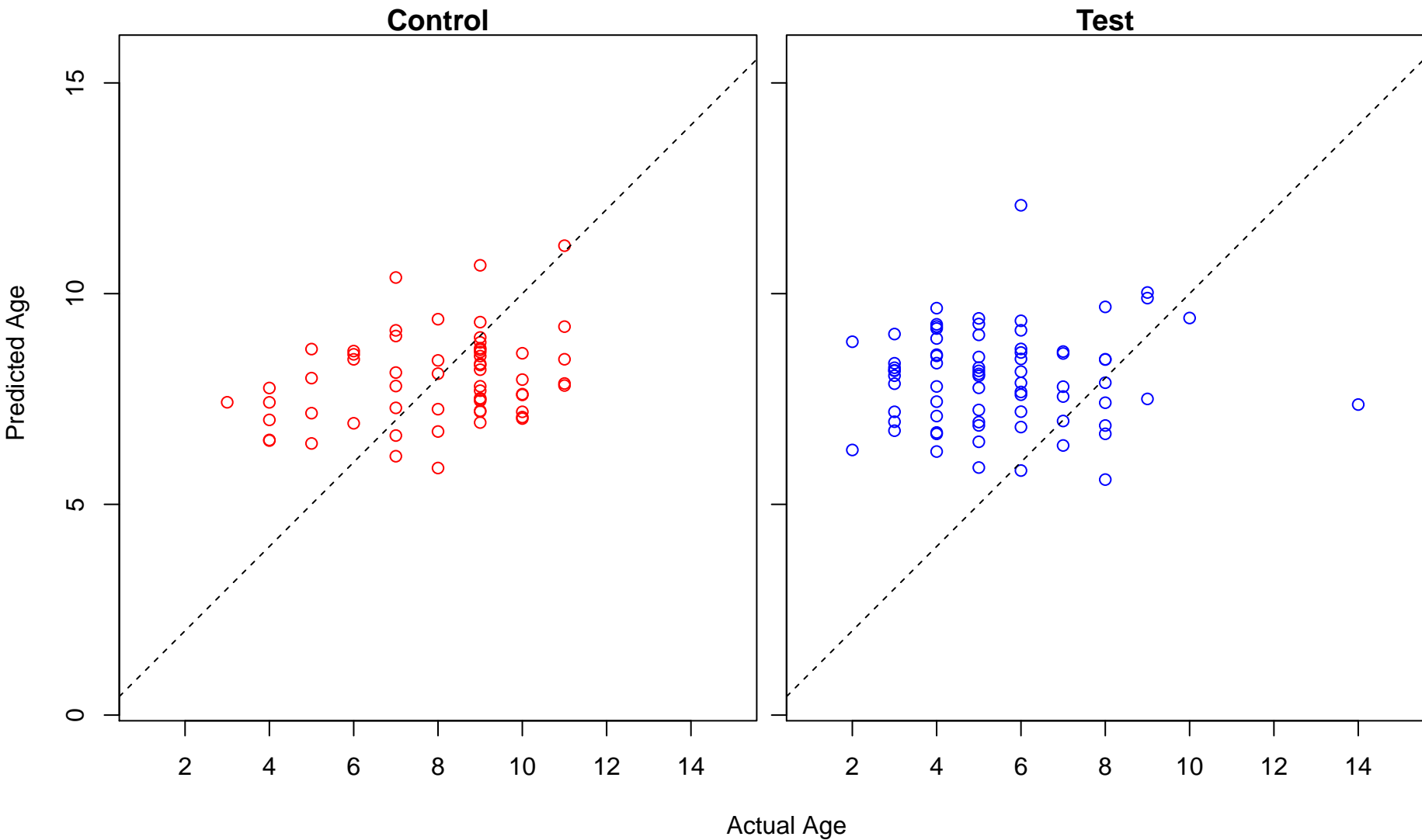
leukocyte adhesive activation (Score: 0.461735)



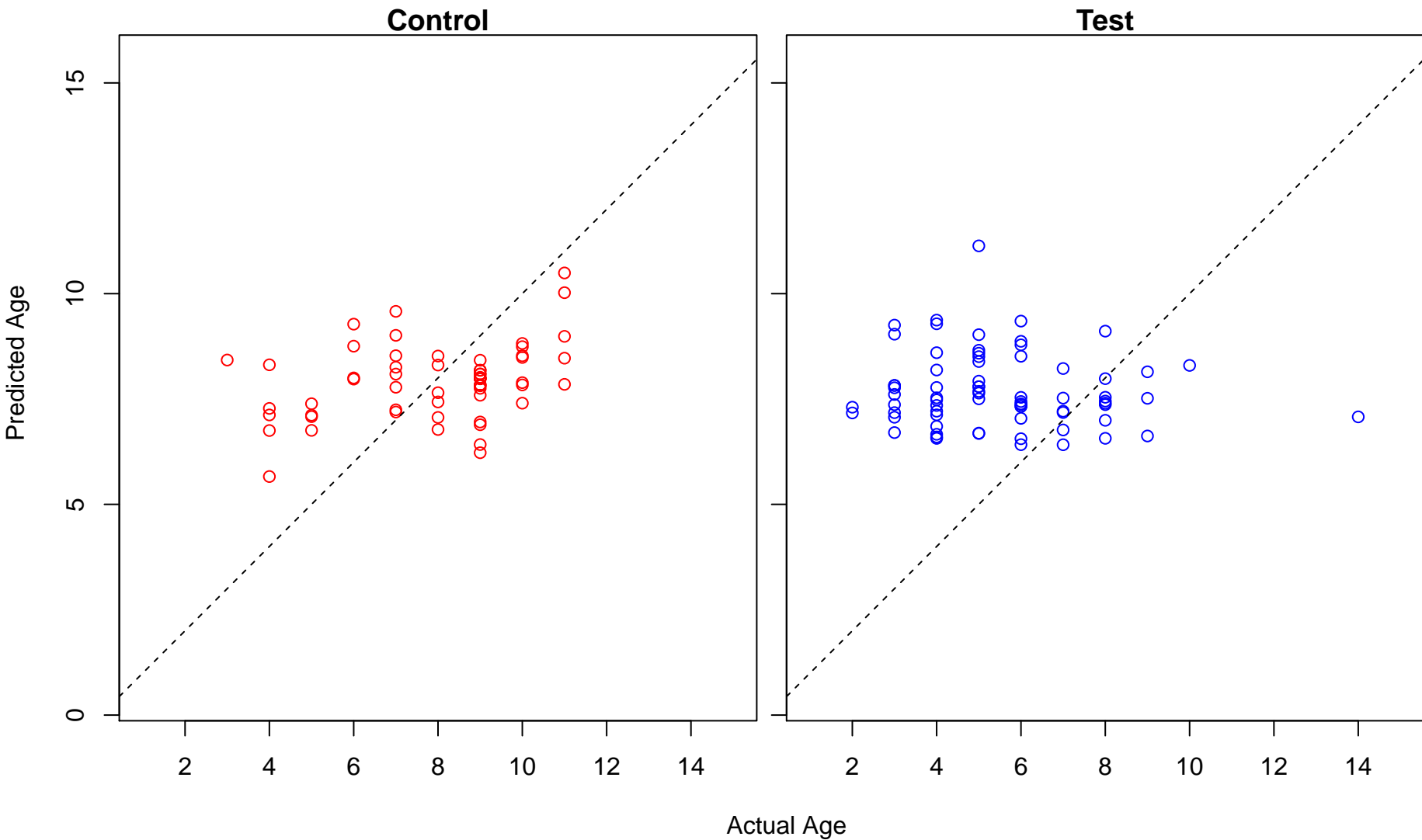
negative regulation of CD4-positive, alpha-beta T cell differentiation (Score: 0.460560)



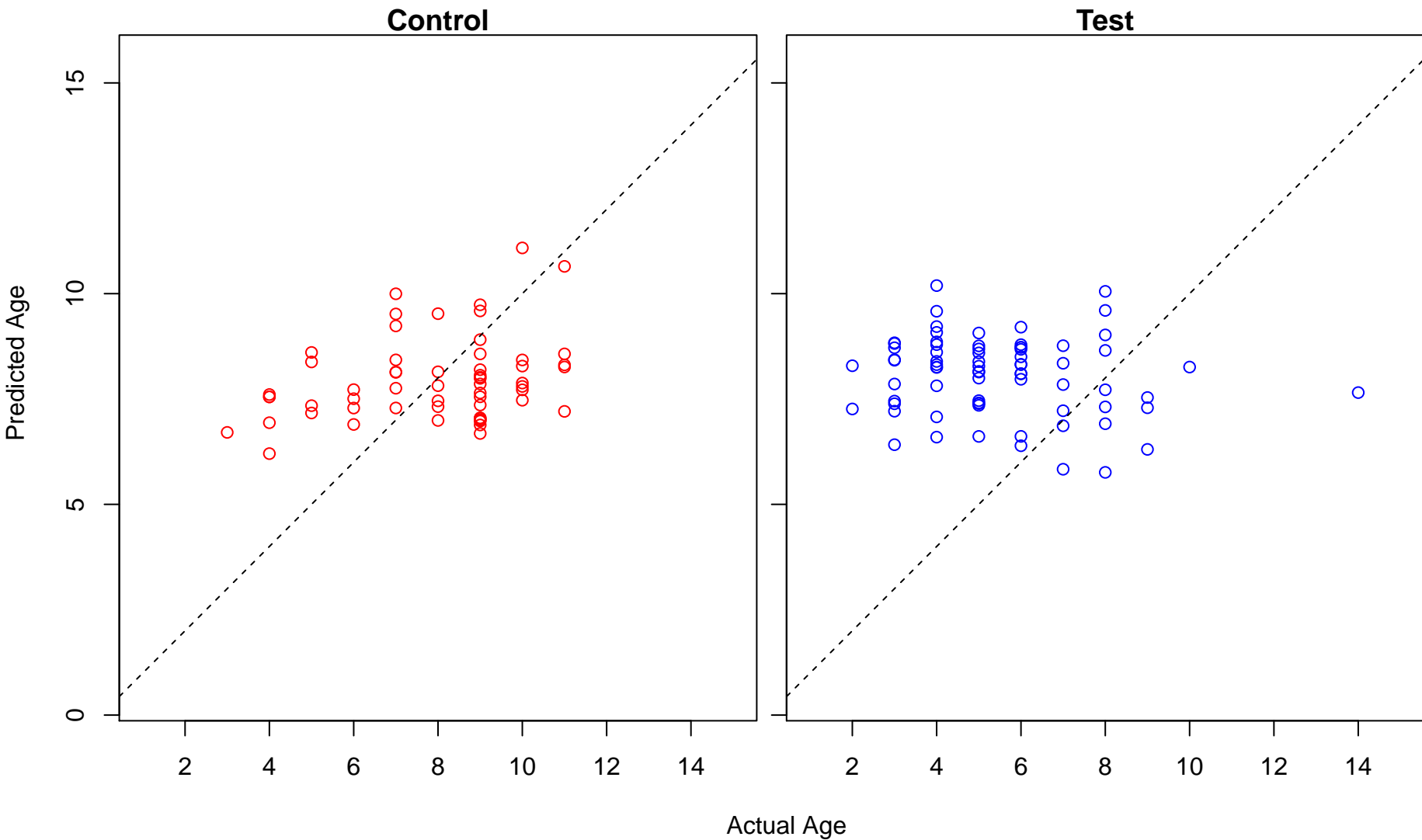
negative regulation of alpha-beta T cell differentiation (Score: 0.460553)



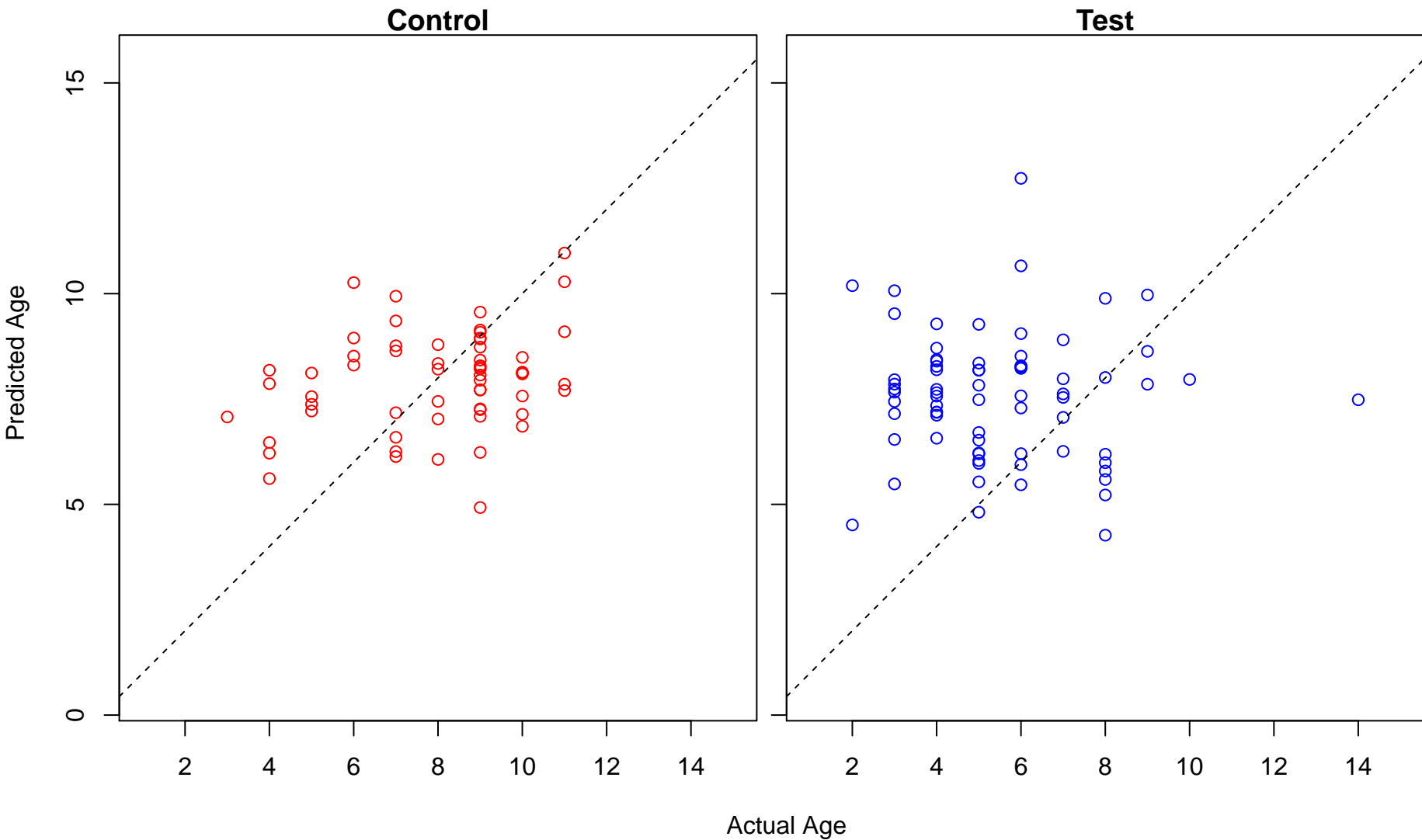
posterior mesonephric tubule development (Score: 0.460254)



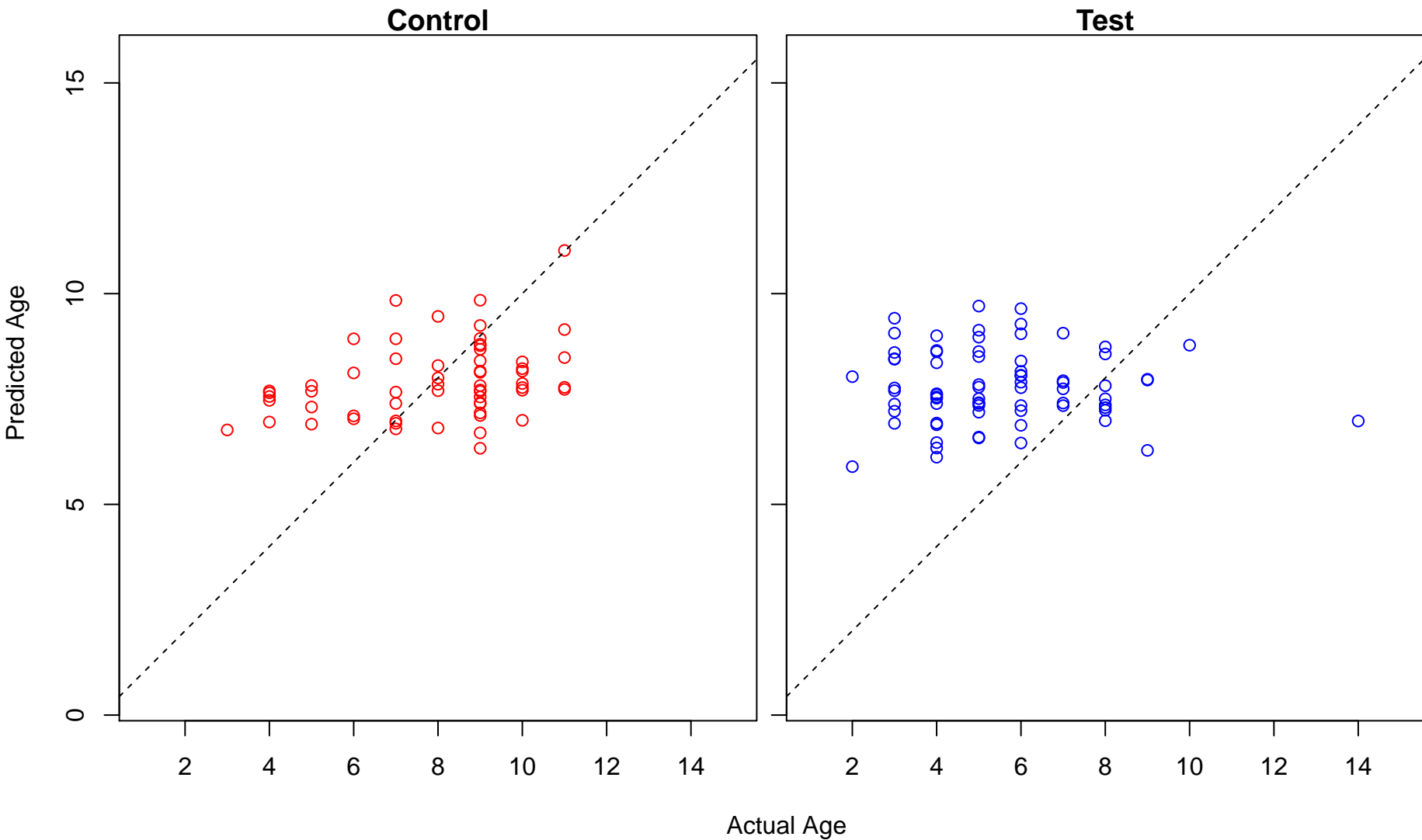
regulation of heart induction (Score: 0.458566)



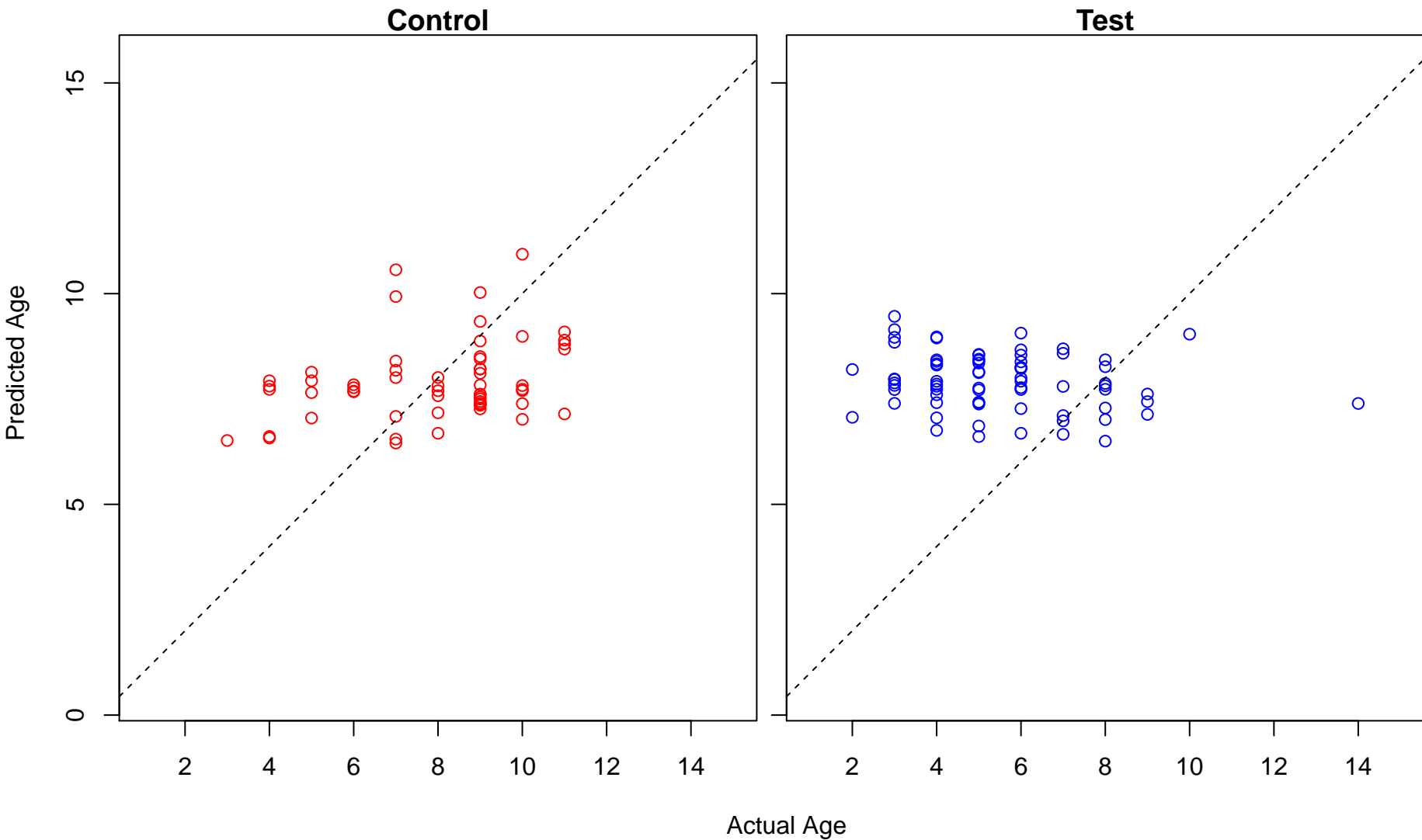
positive regulation of adaptive immune response (Score: 0.457969)



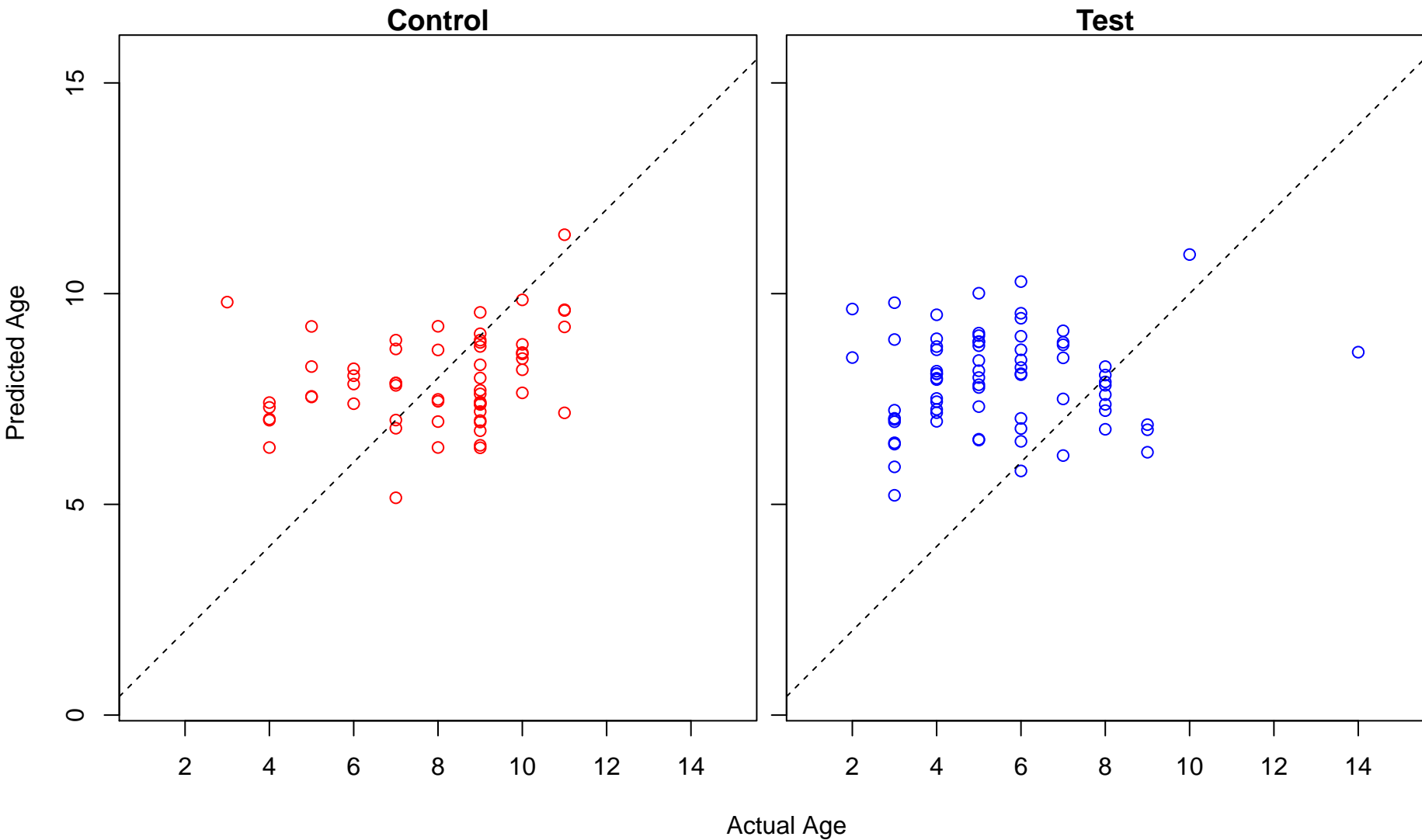
embryonic neurocranium morphogenesis (Score: 0.457468)



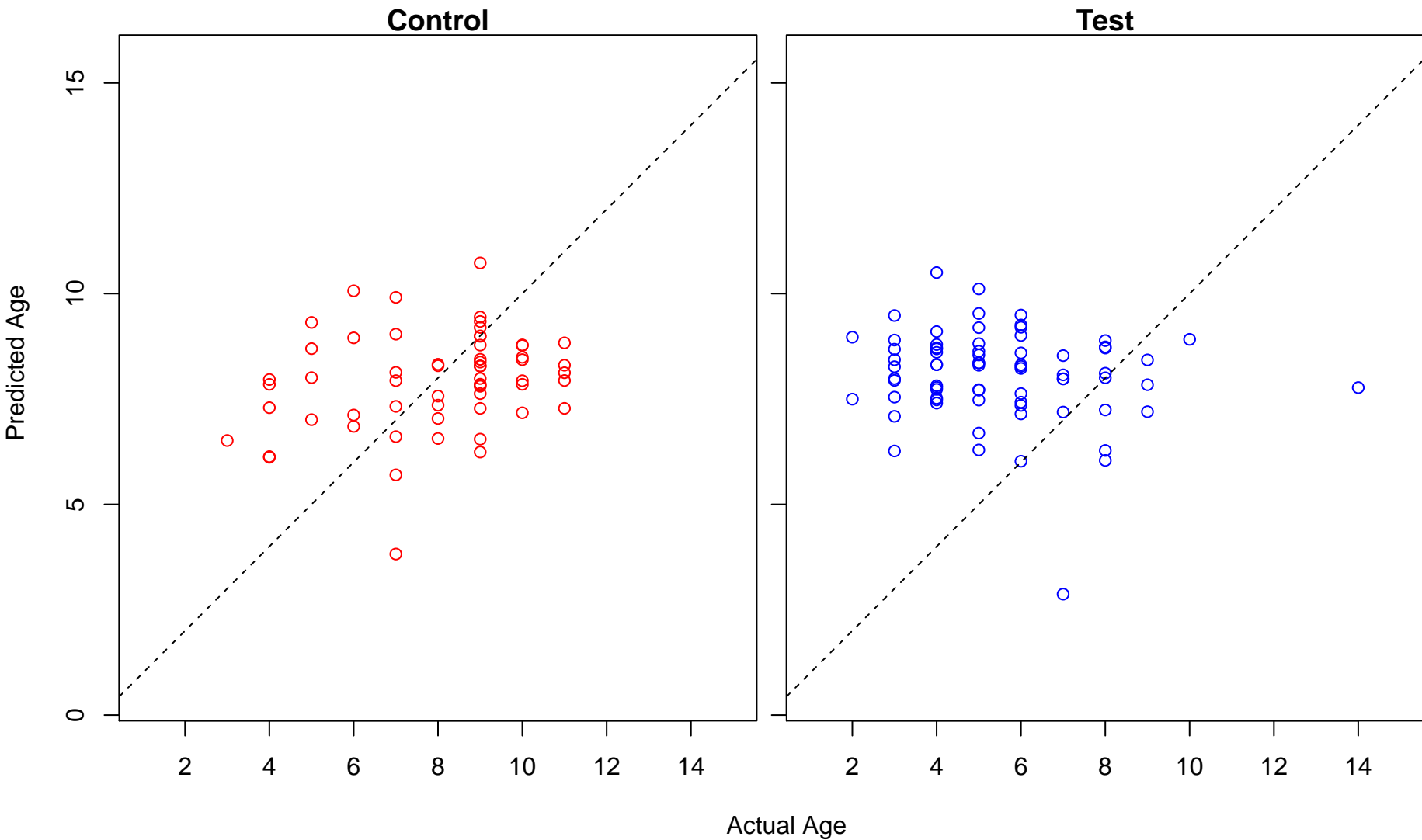
tooth mineralization (Score: 0.455633)



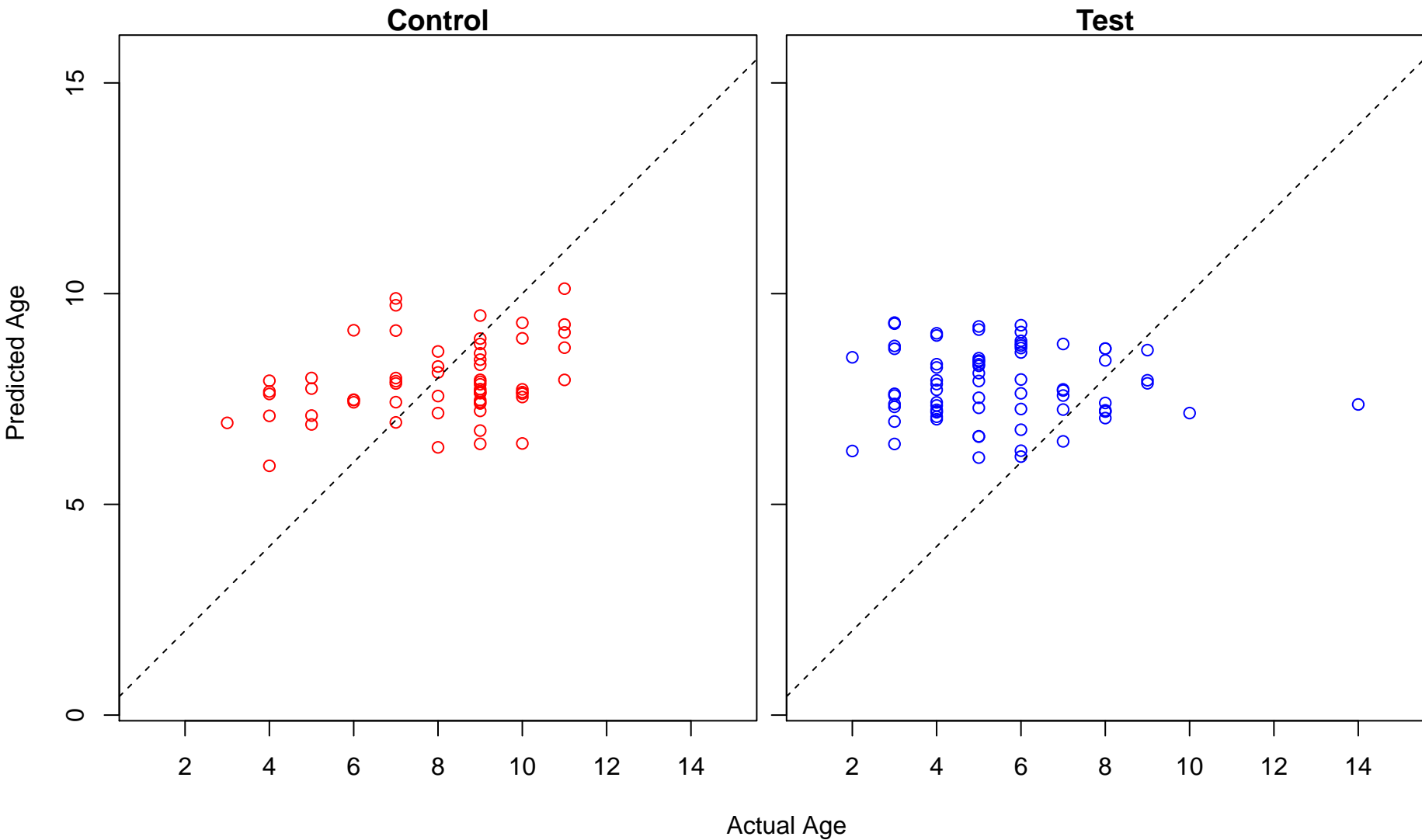
cobalt ion transport (Score: 0.454064)



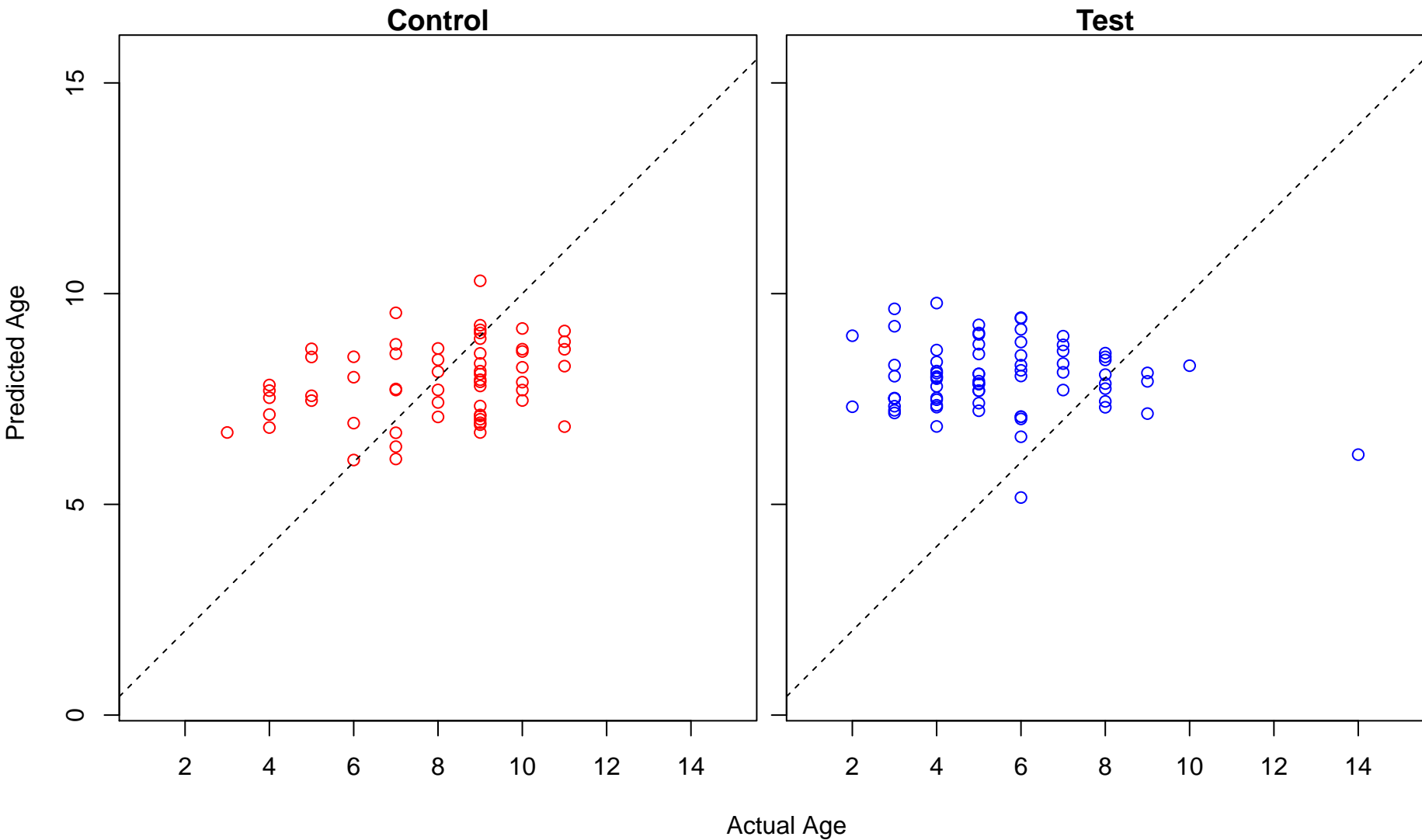
mRNA 5'-splice site recognition (Score: 0.454031)



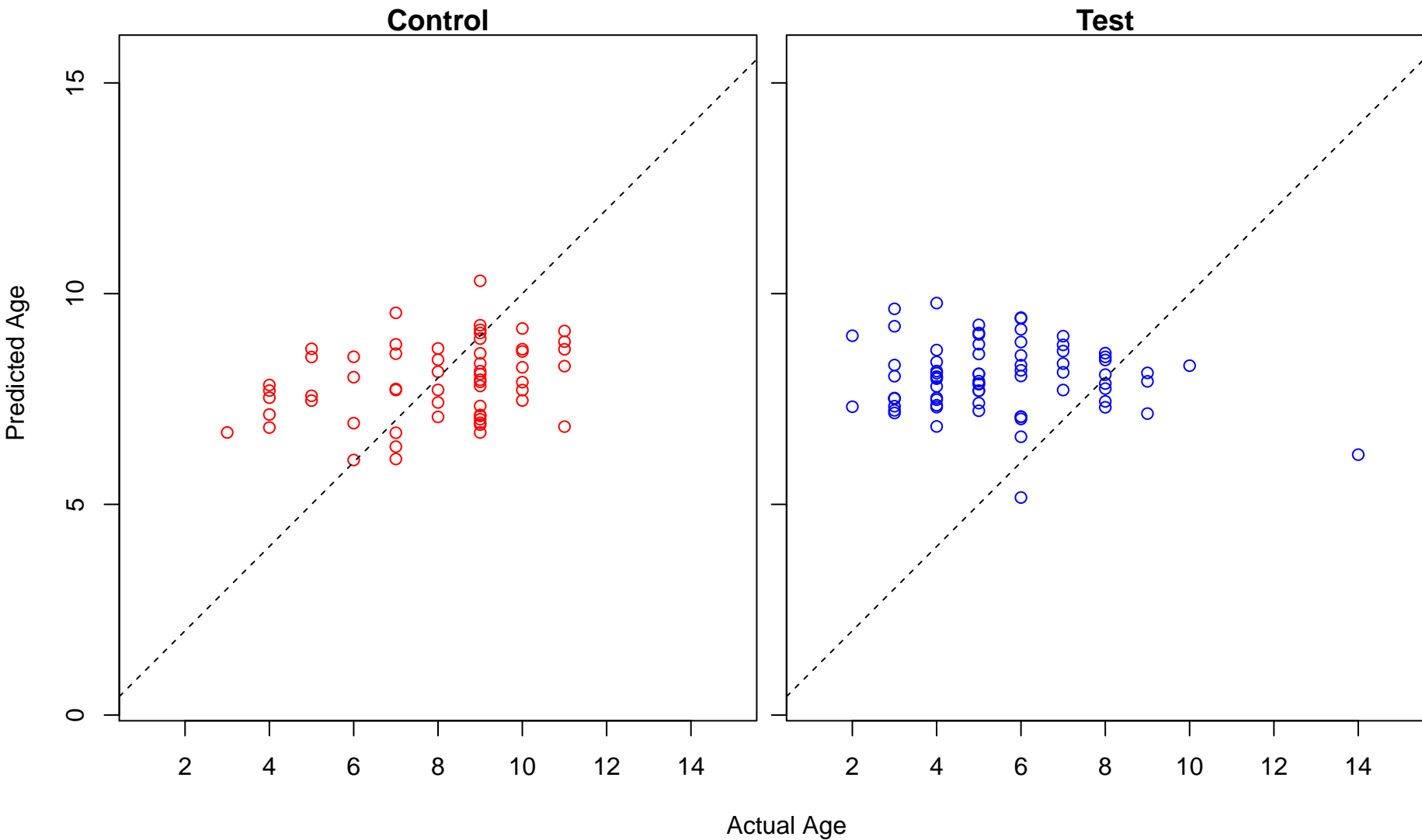
megakaryocyte development (Score: 0.451775)



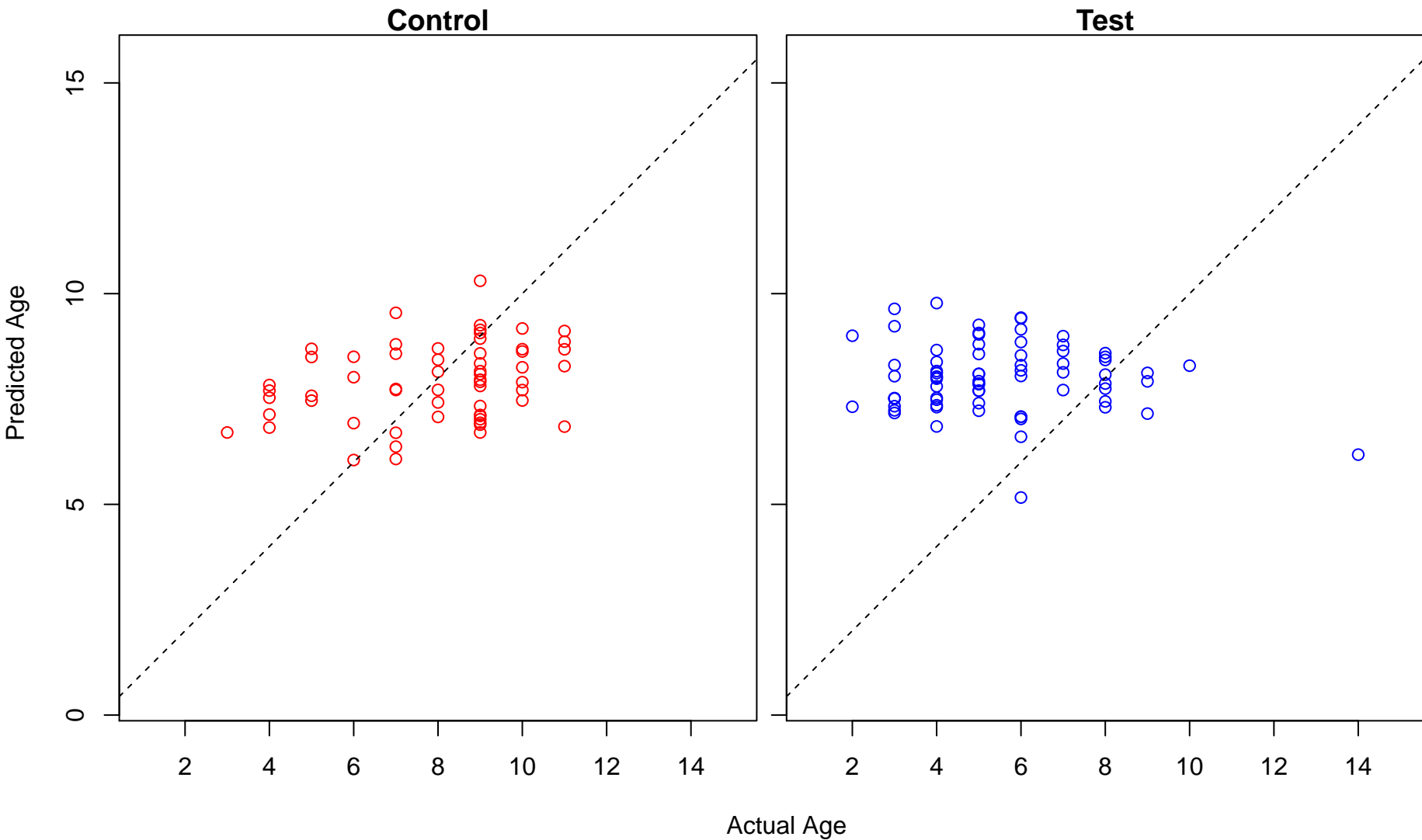
cellular manganese ion homeostasis (Score: 0.451768)



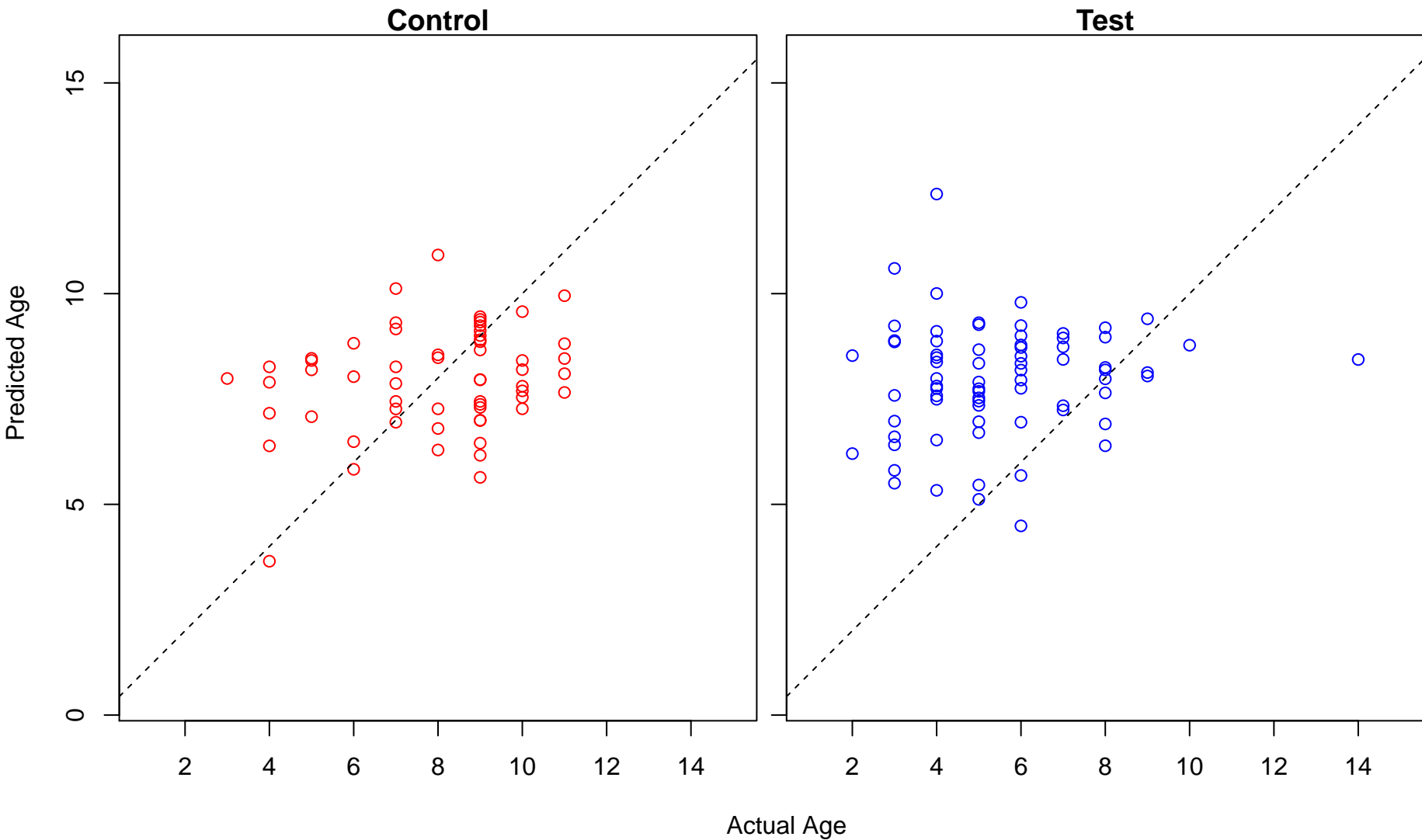
Golgi calcium ion homeostasis (Score: 0.451768)



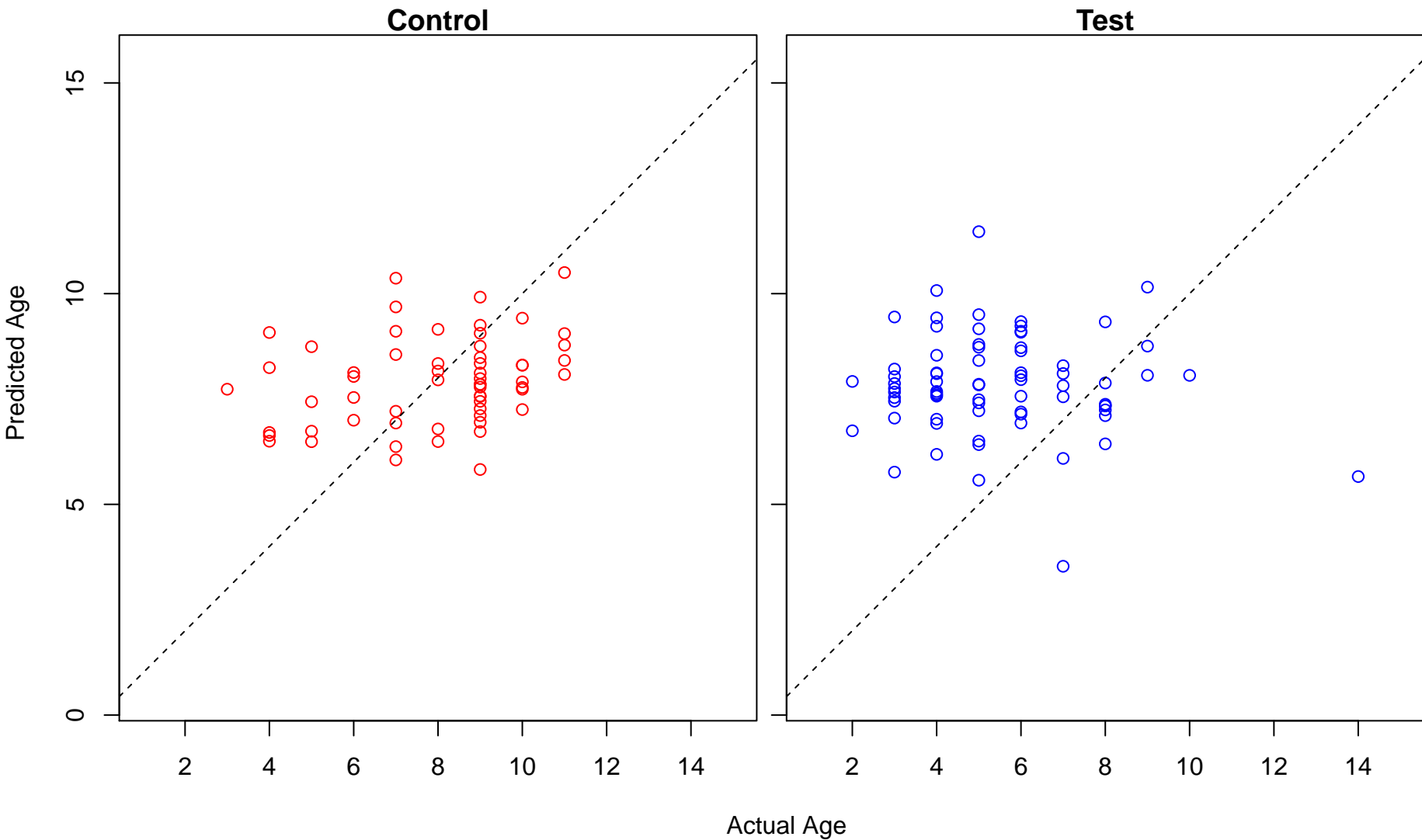
manganese ion homeostasis (Score: 0.451768)



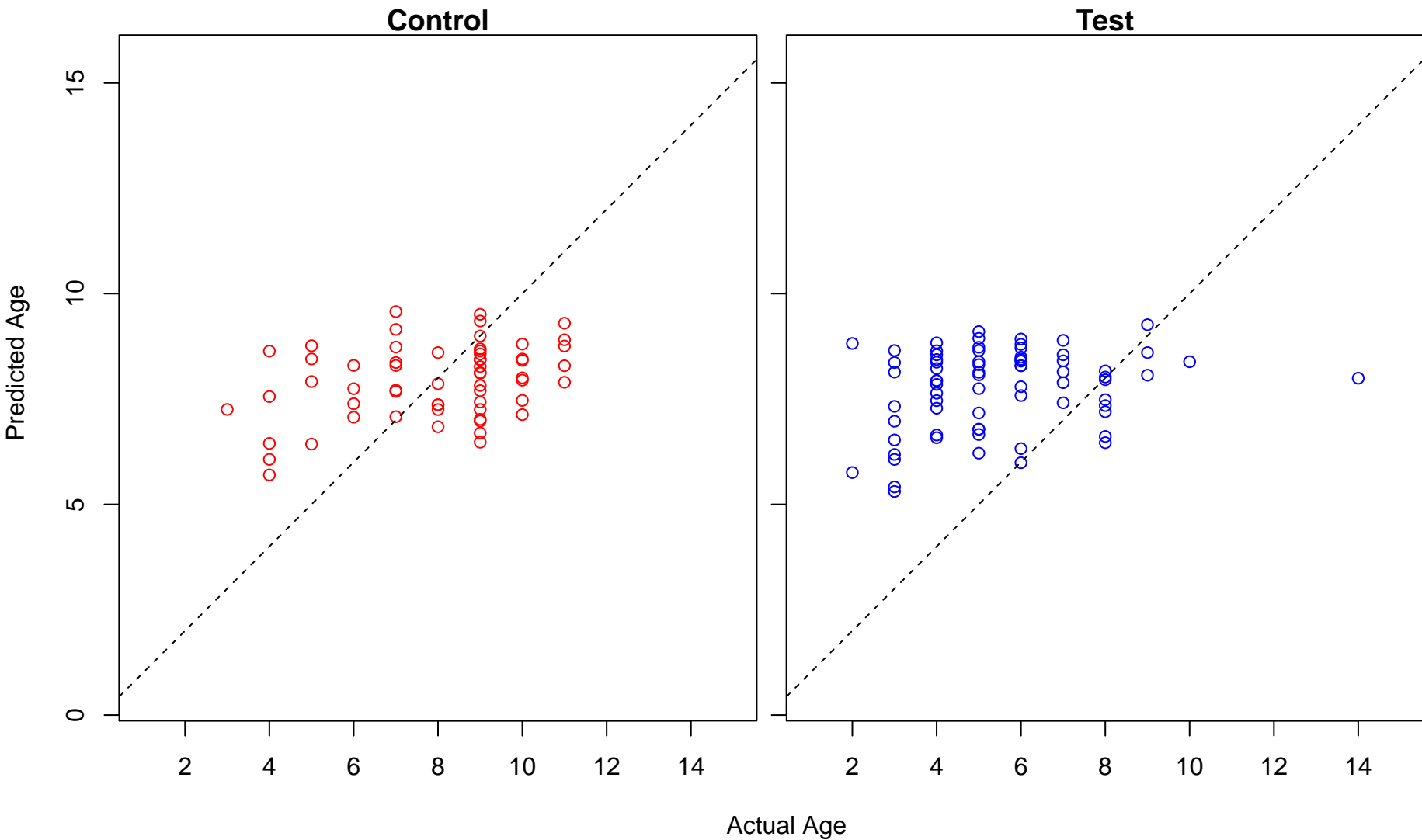
UV-damage excision repair (Score: 0.451615)



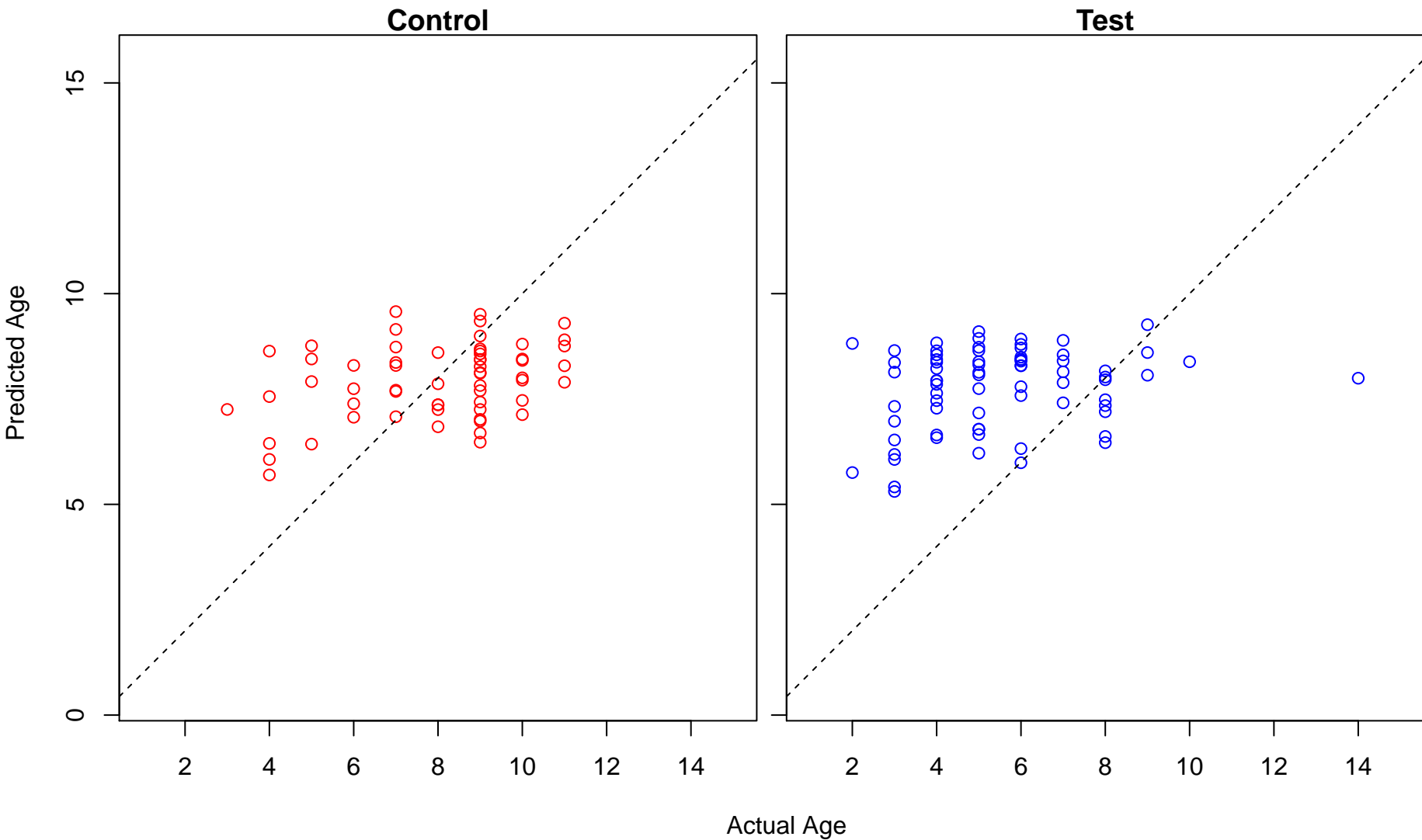
positive regulation of chromatin silencing (Score: 0.449662)



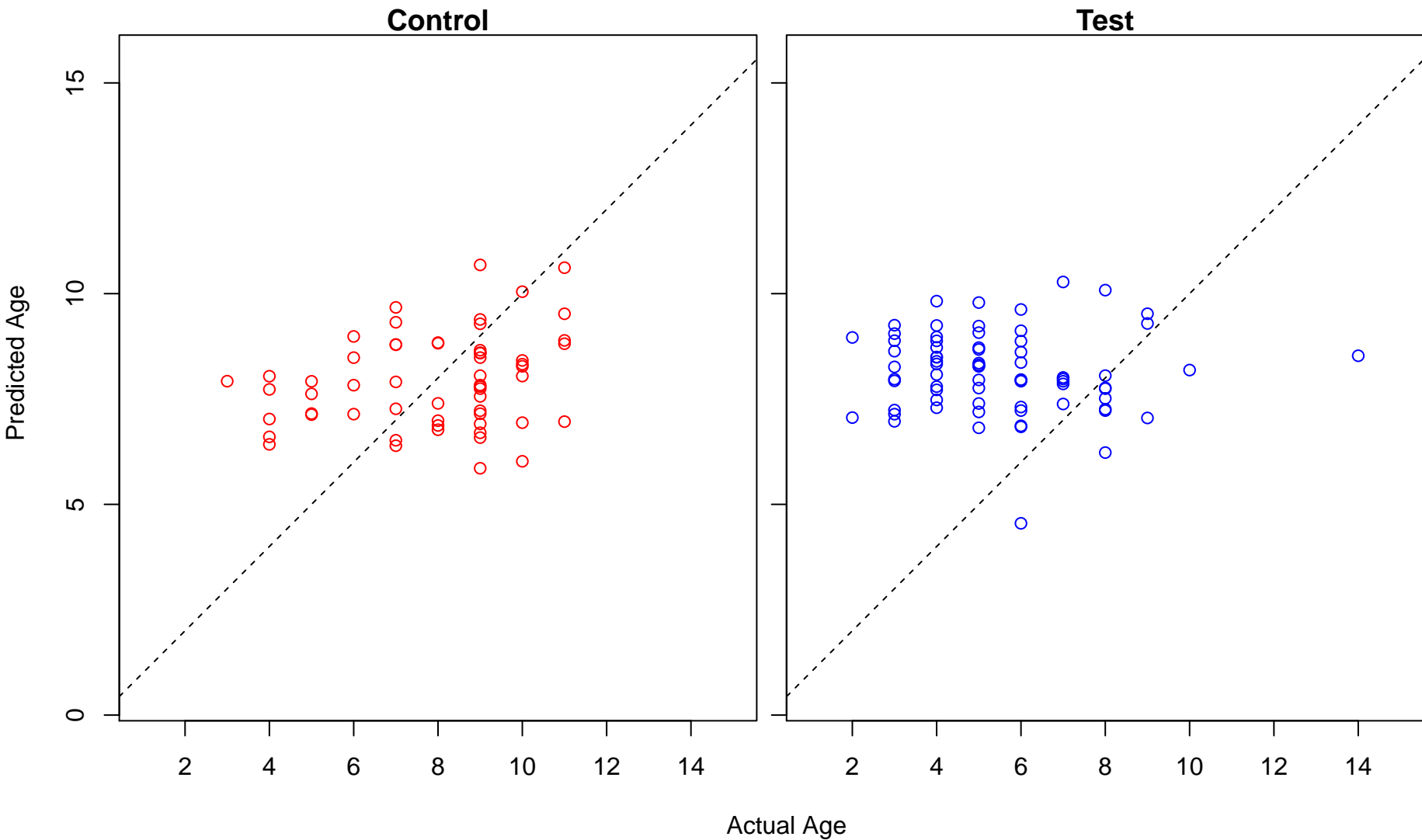
agmatine biosynthetic process (Score: 0.449266)



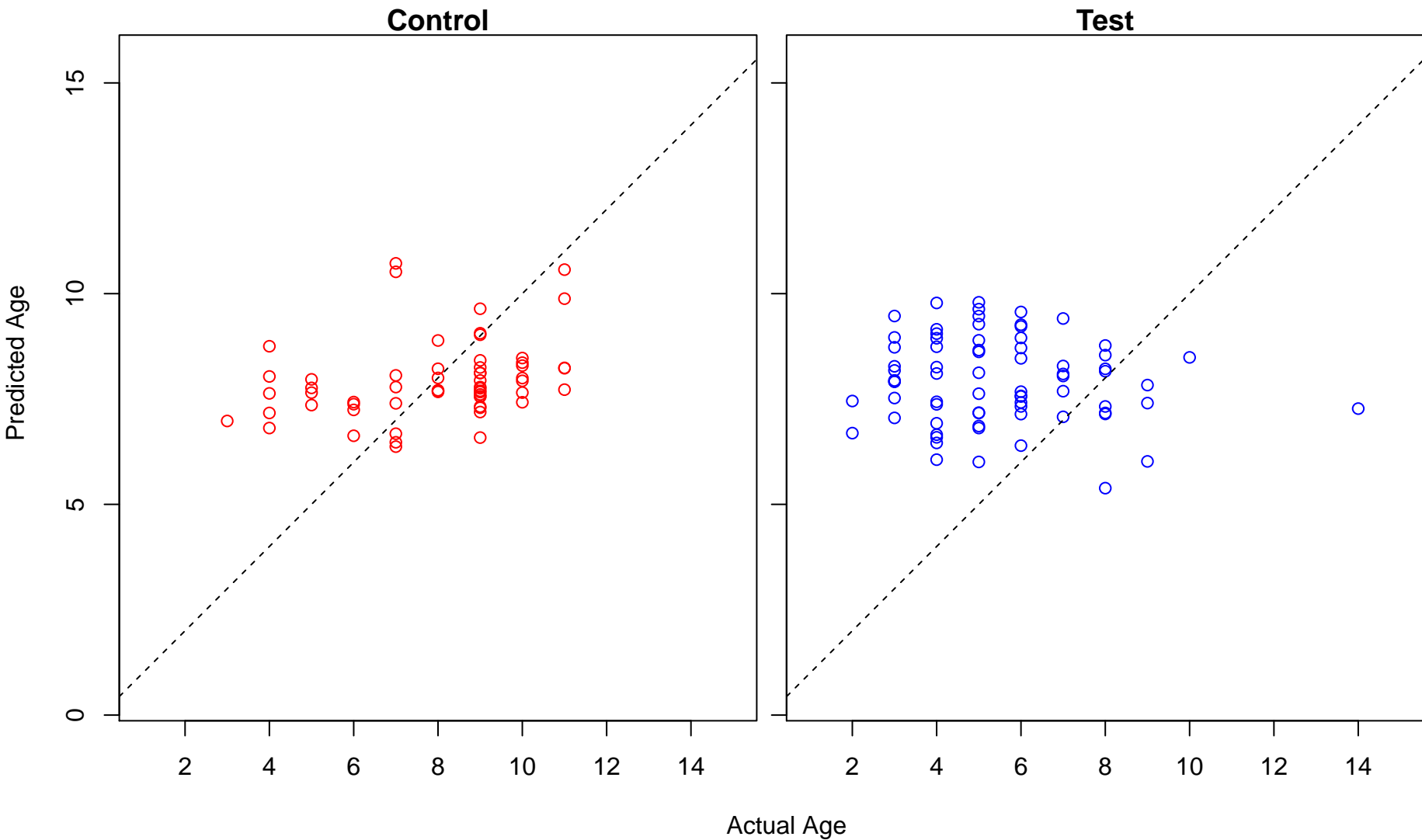
primary amino compound biosynthetic process (Score: 0.449266)



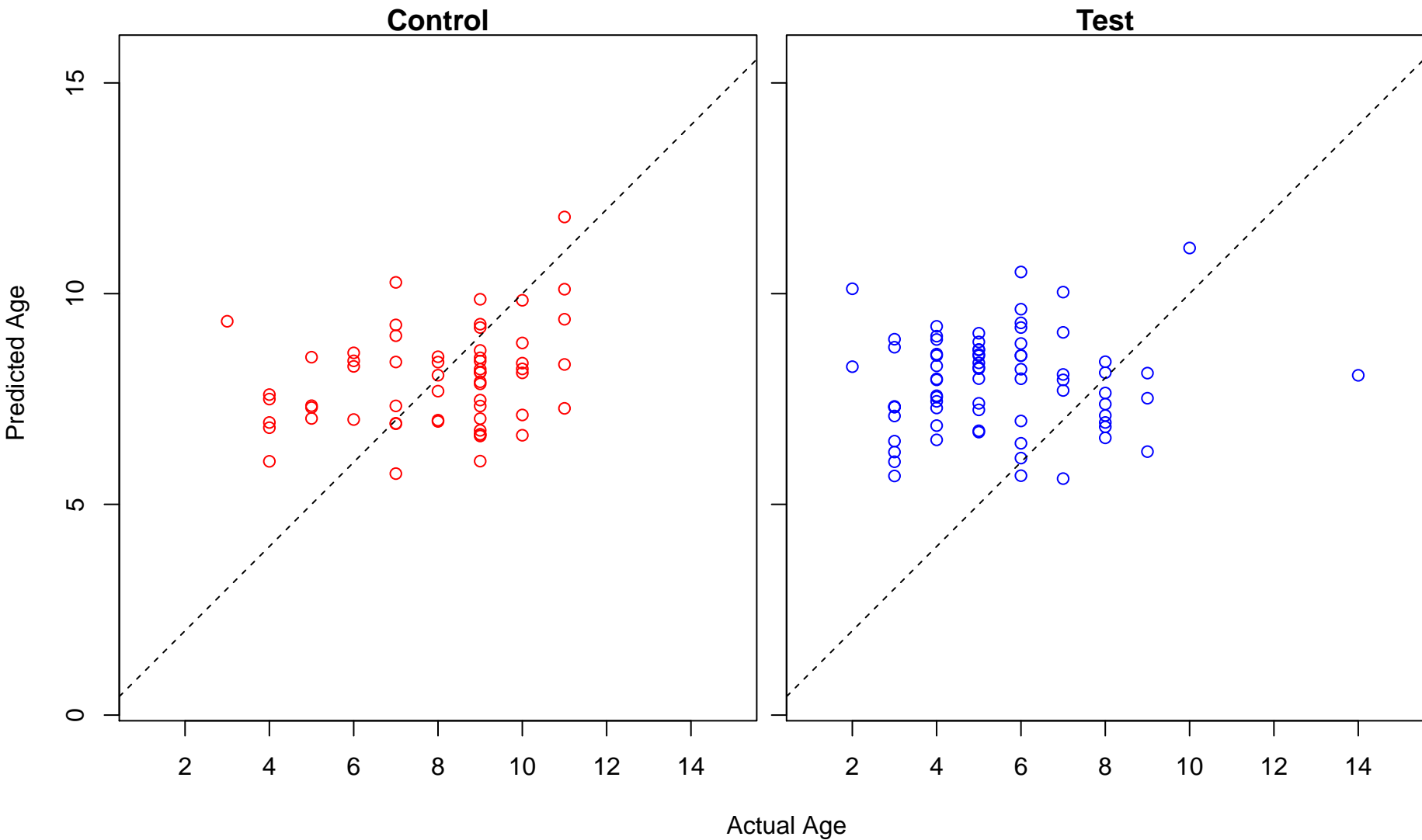
Golgi to endosome transport (Score: 0.448618)



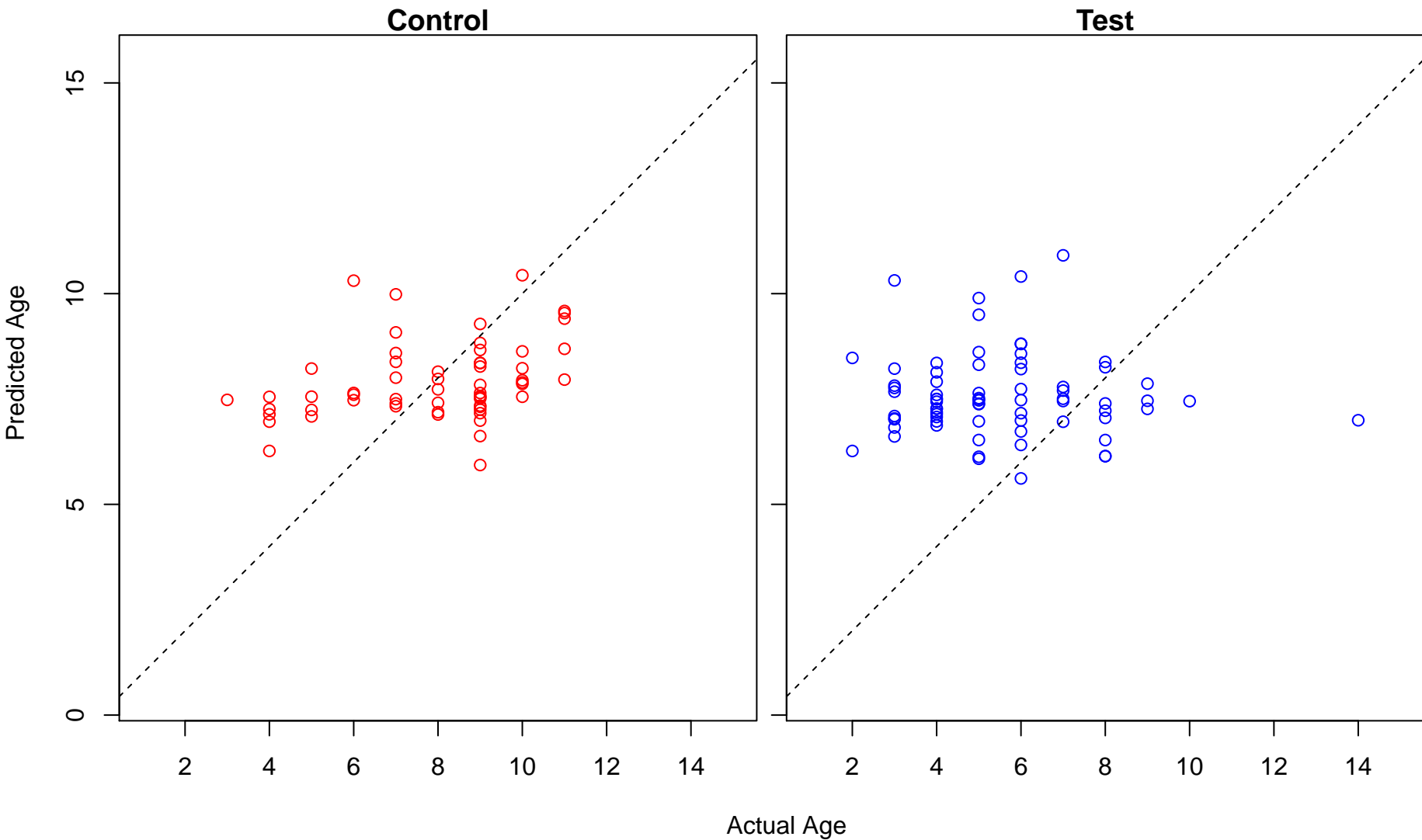
nucleotide-binding oligomerization domain containing 2 signaling pathway (Score: 0.447869)



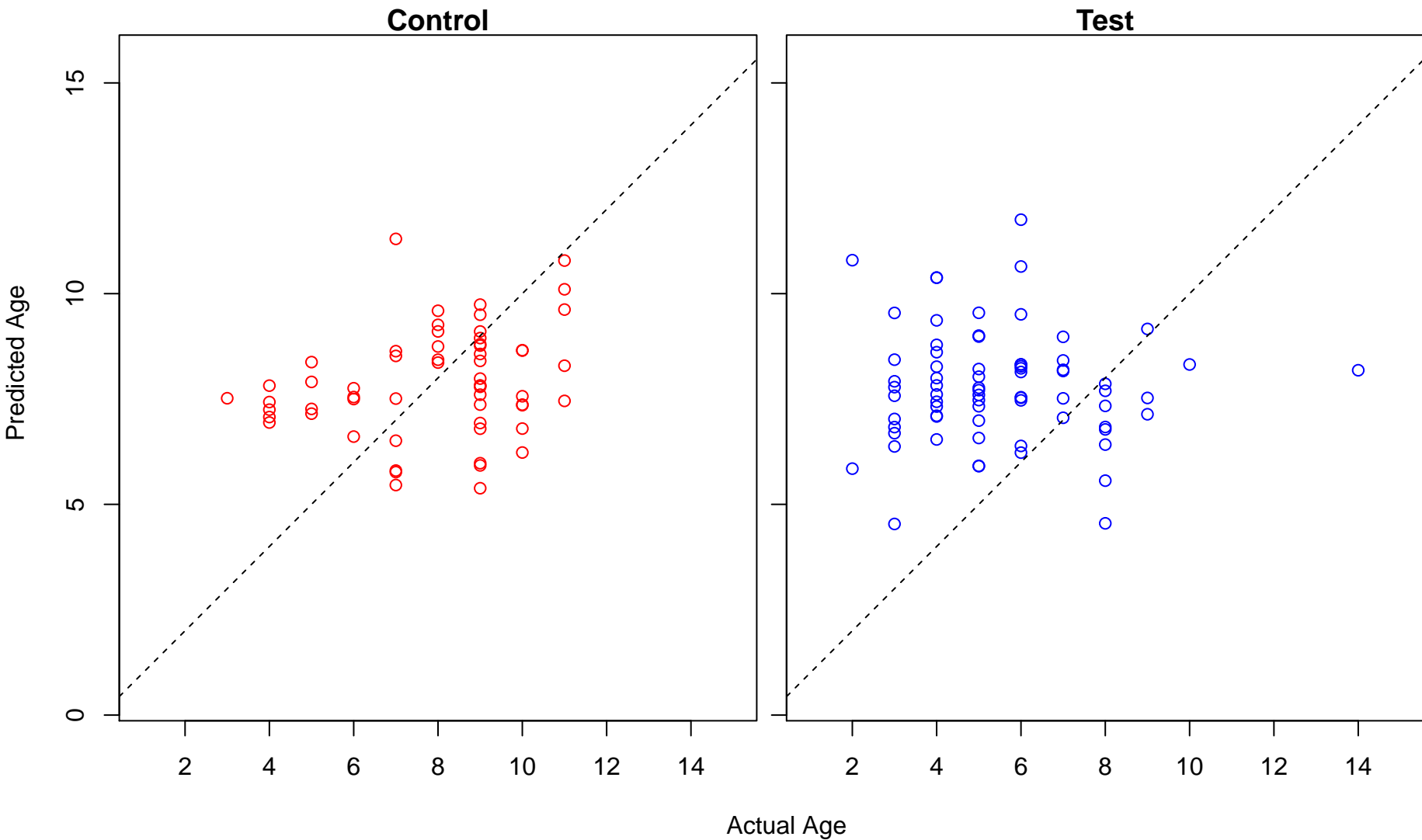
copper ion transmembrane transport (Score: 0.447822)



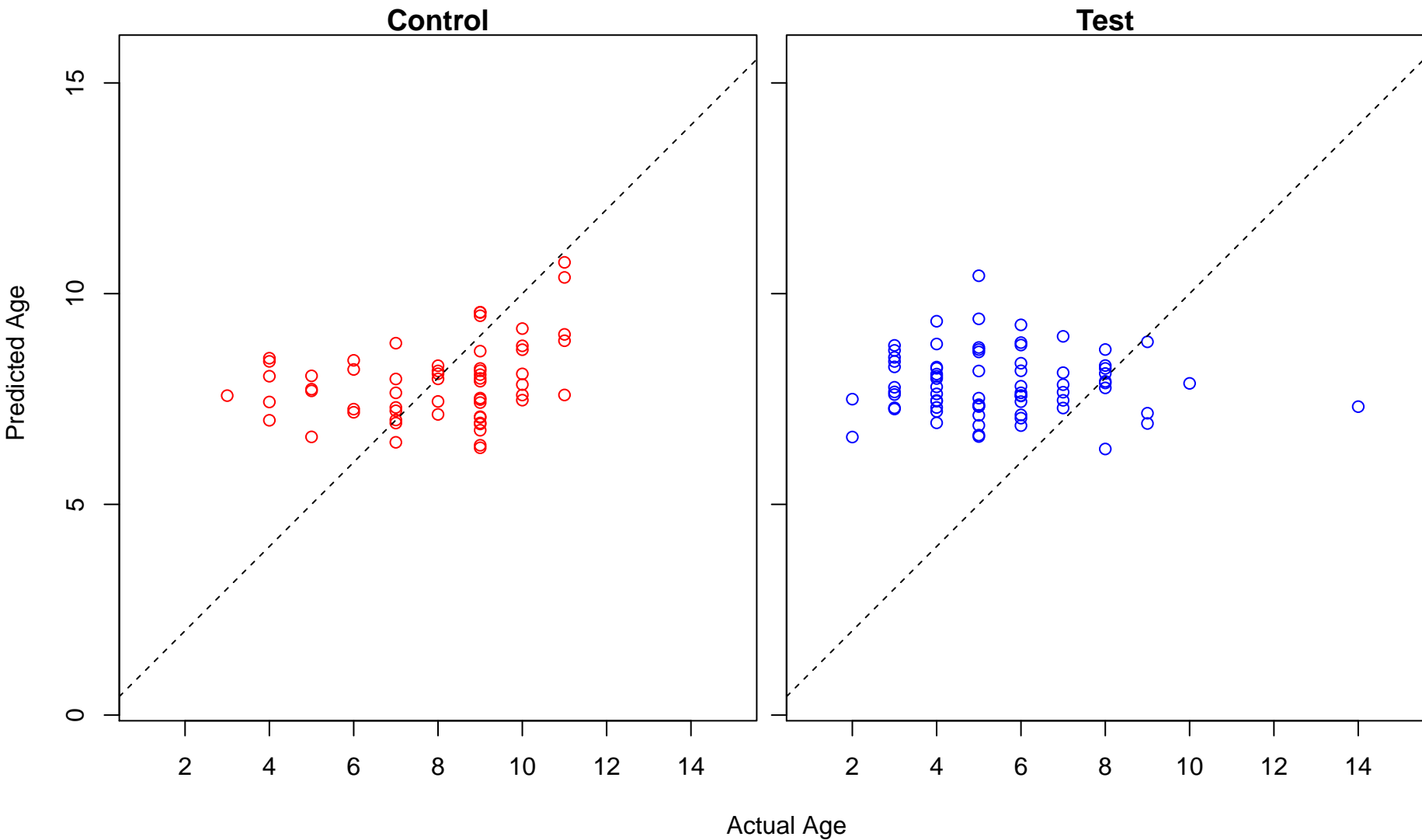
activation-induced cell death of T cells (Score: 0.447505)



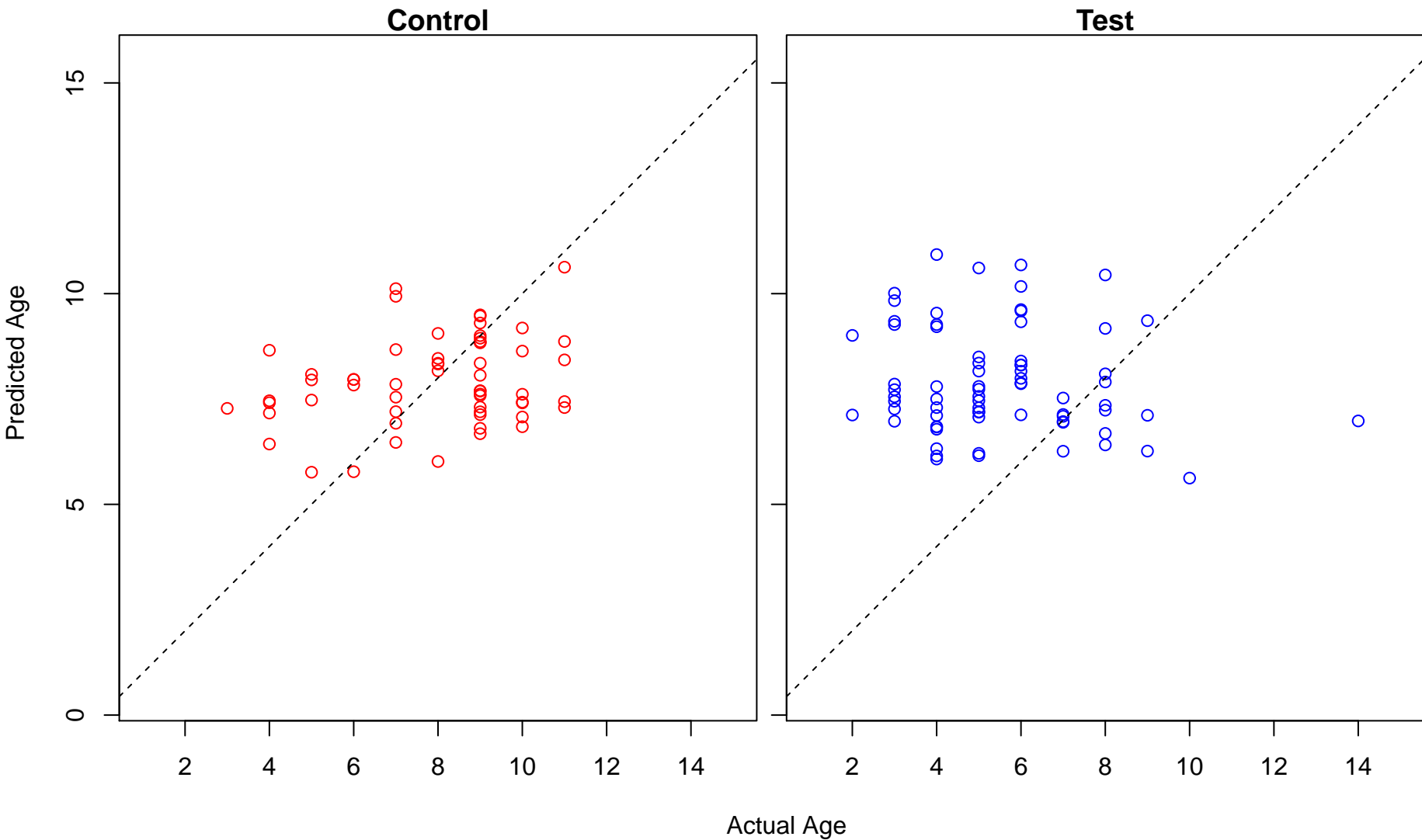
maintenance of DNA repeat elements (Score: 0.444882)



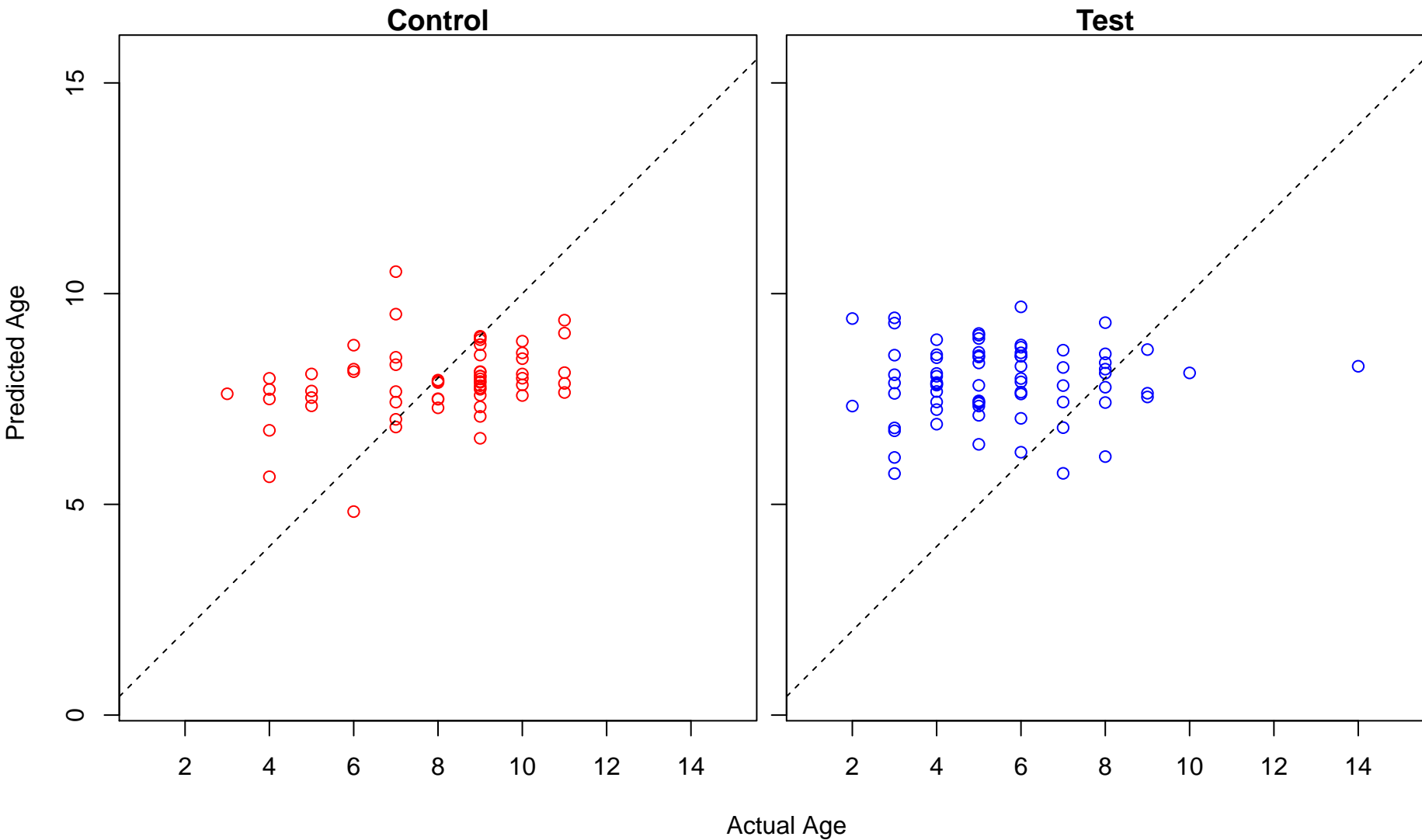
negative regulation of calcium-transporting ATPase activity (Score: 0.442262)



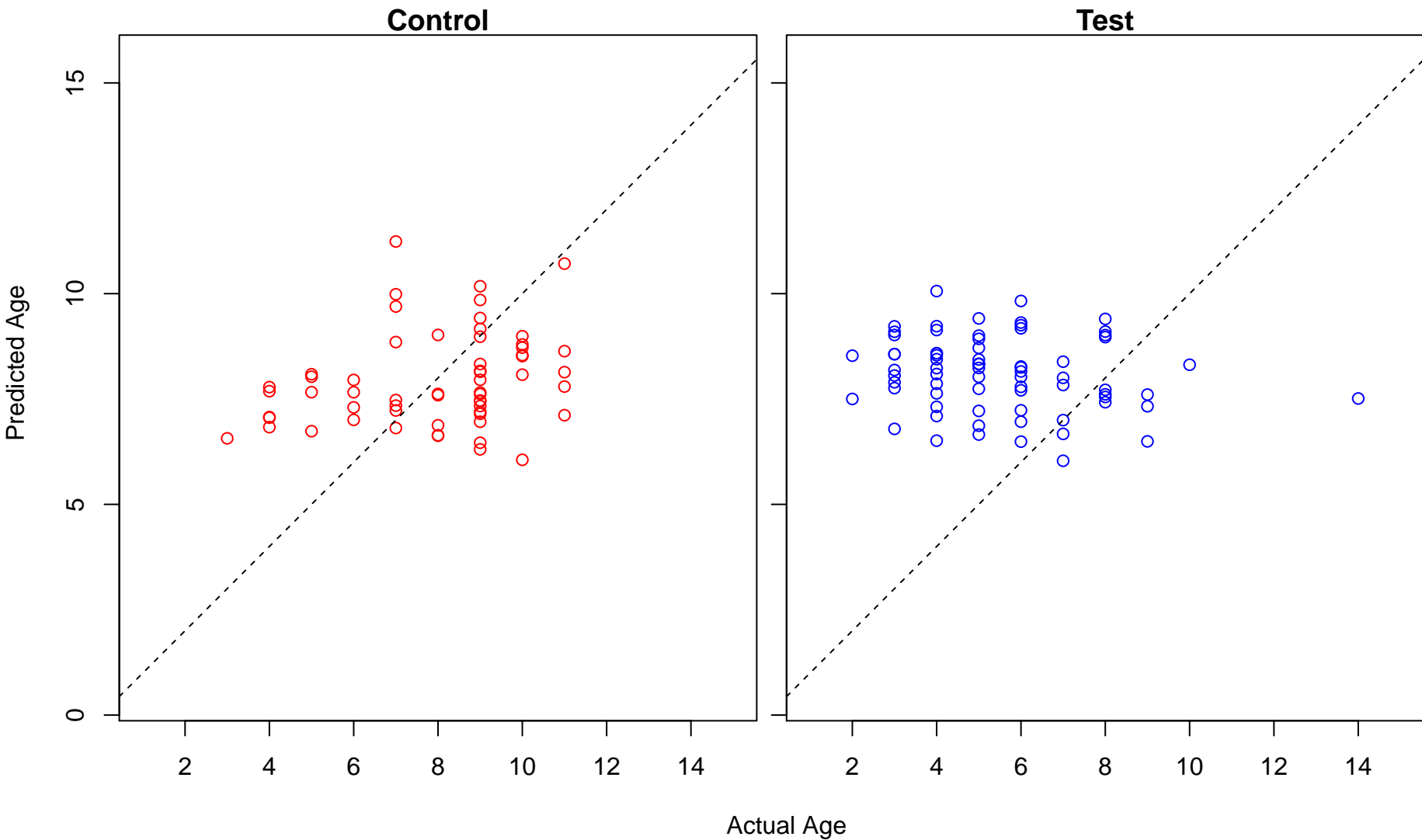
positive regulation of lipid kinase activity (Score: 0.441994)



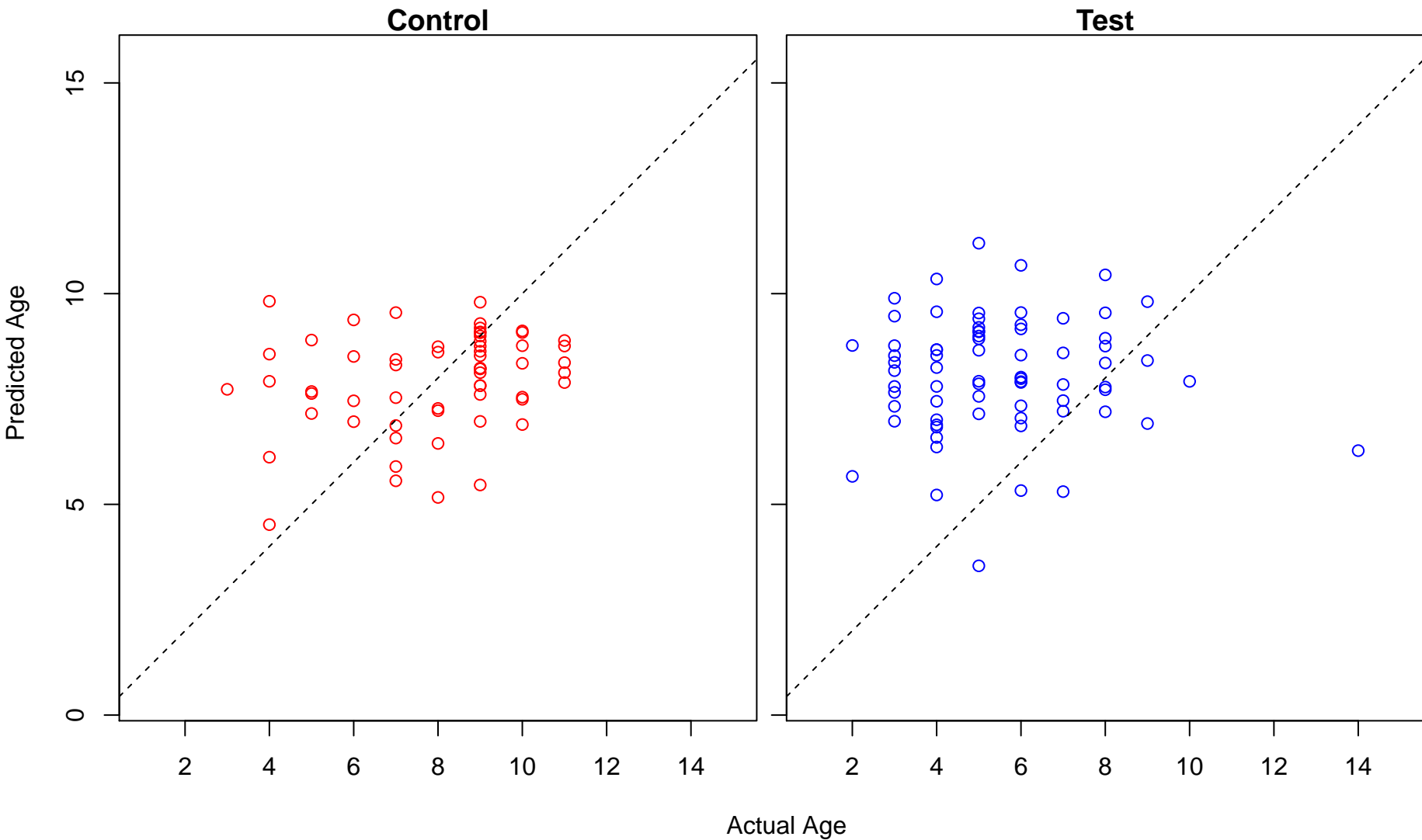
UDP-glucuronic acid transport (Score: 0.441013)



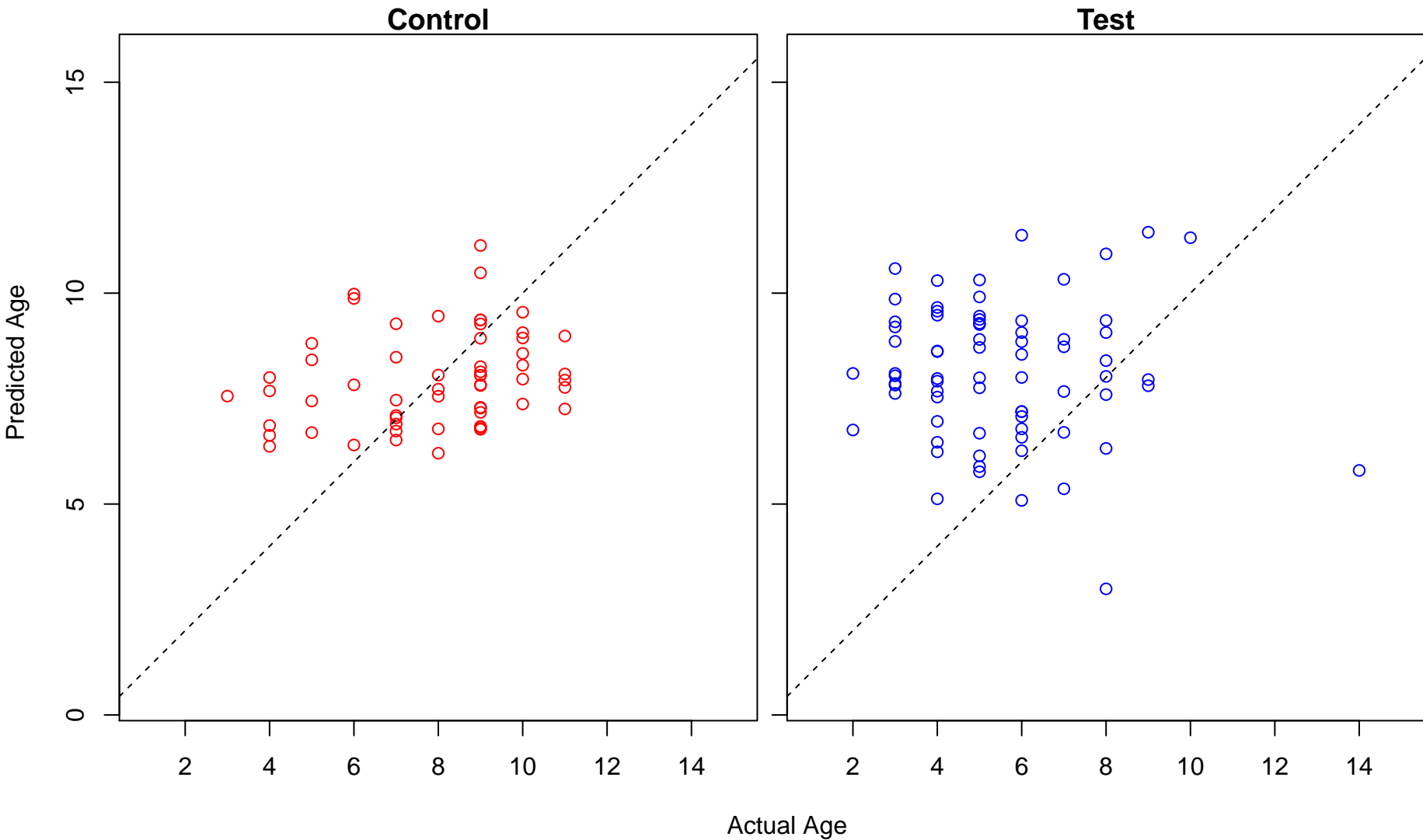
convergent extension involved in organogenesis (Score: 0.439563)



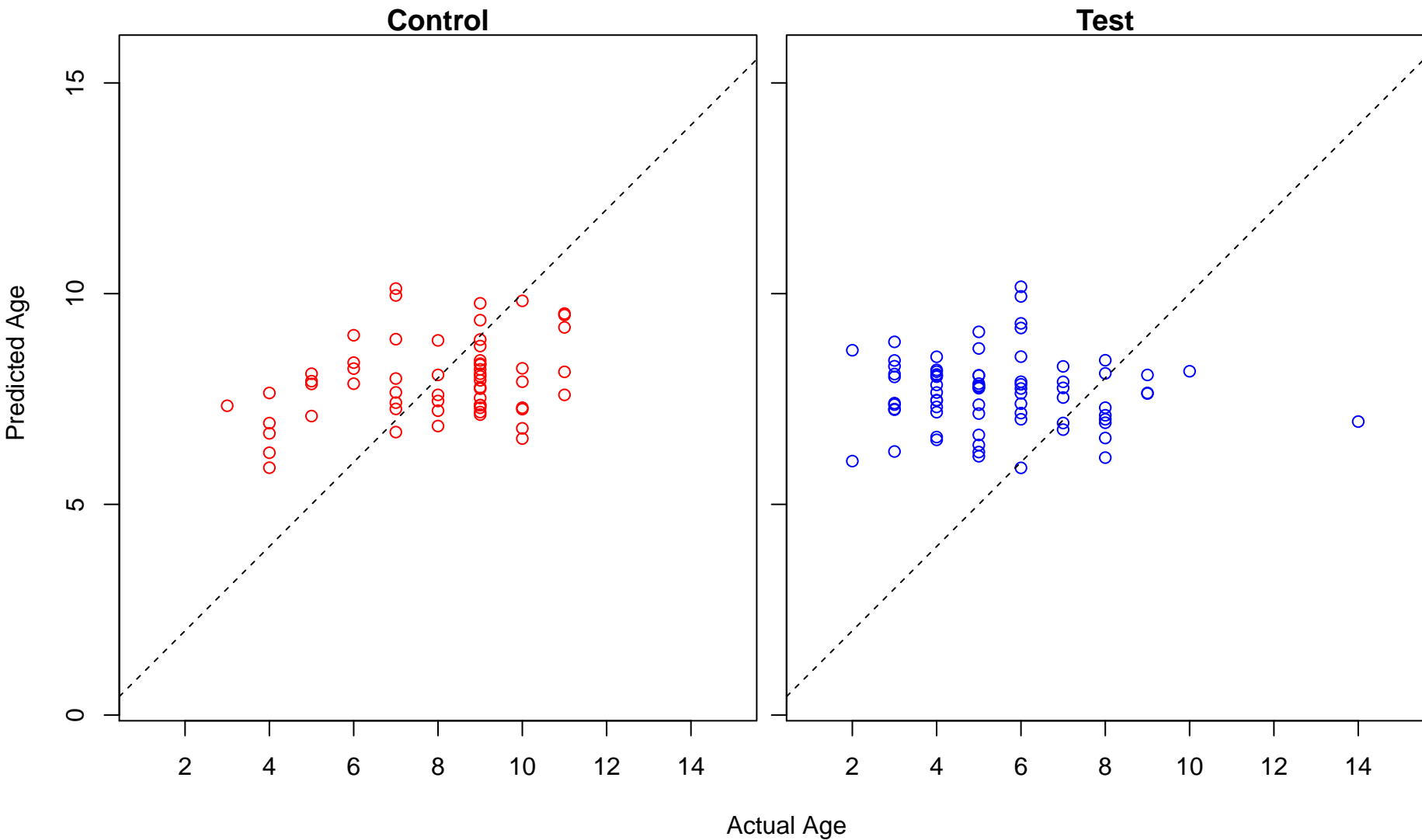
dermatan sulfate proteoglycan metabolic process (Score: 0.438977)



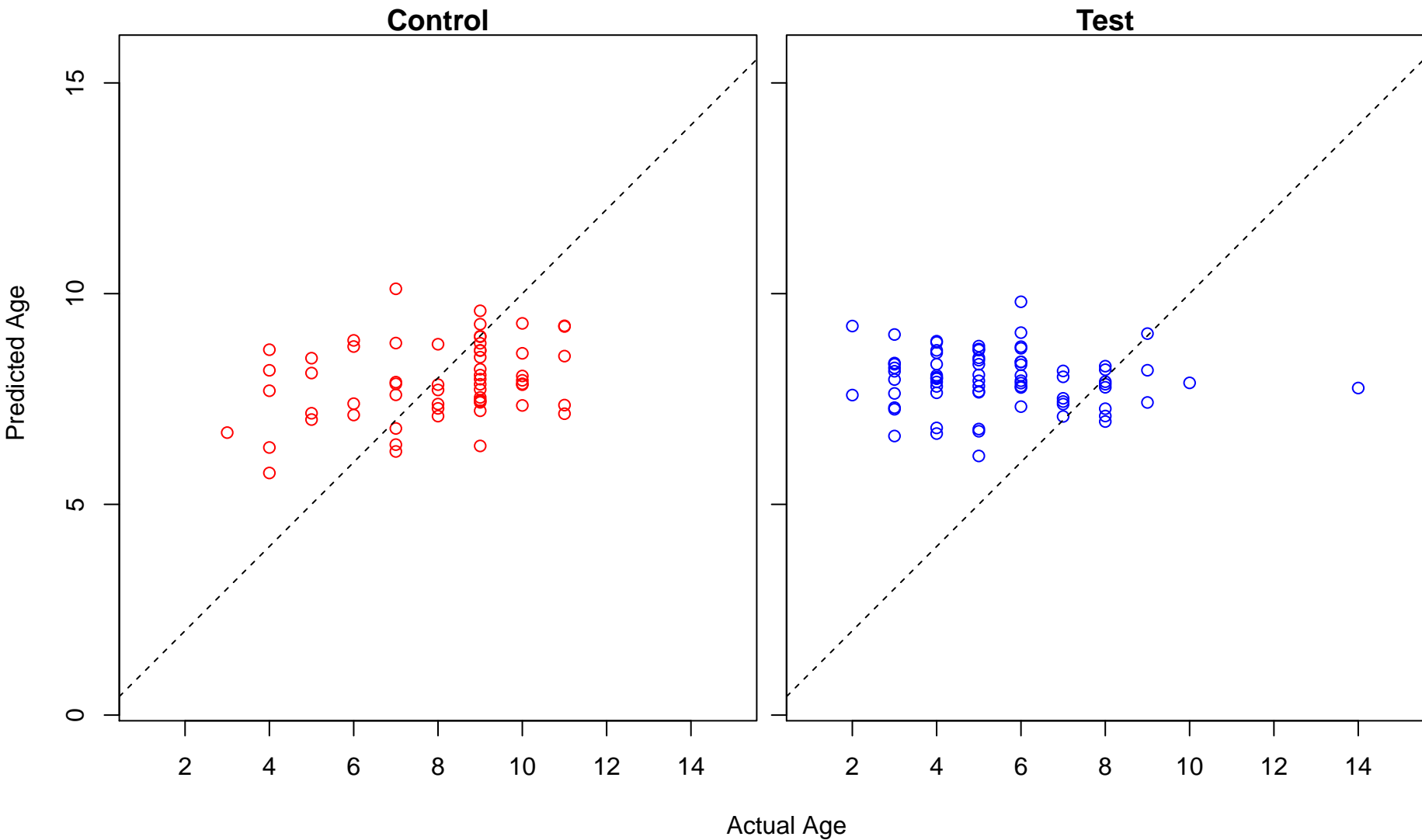
cell differentiation involved in salivary gland development (Score: 0.436624)



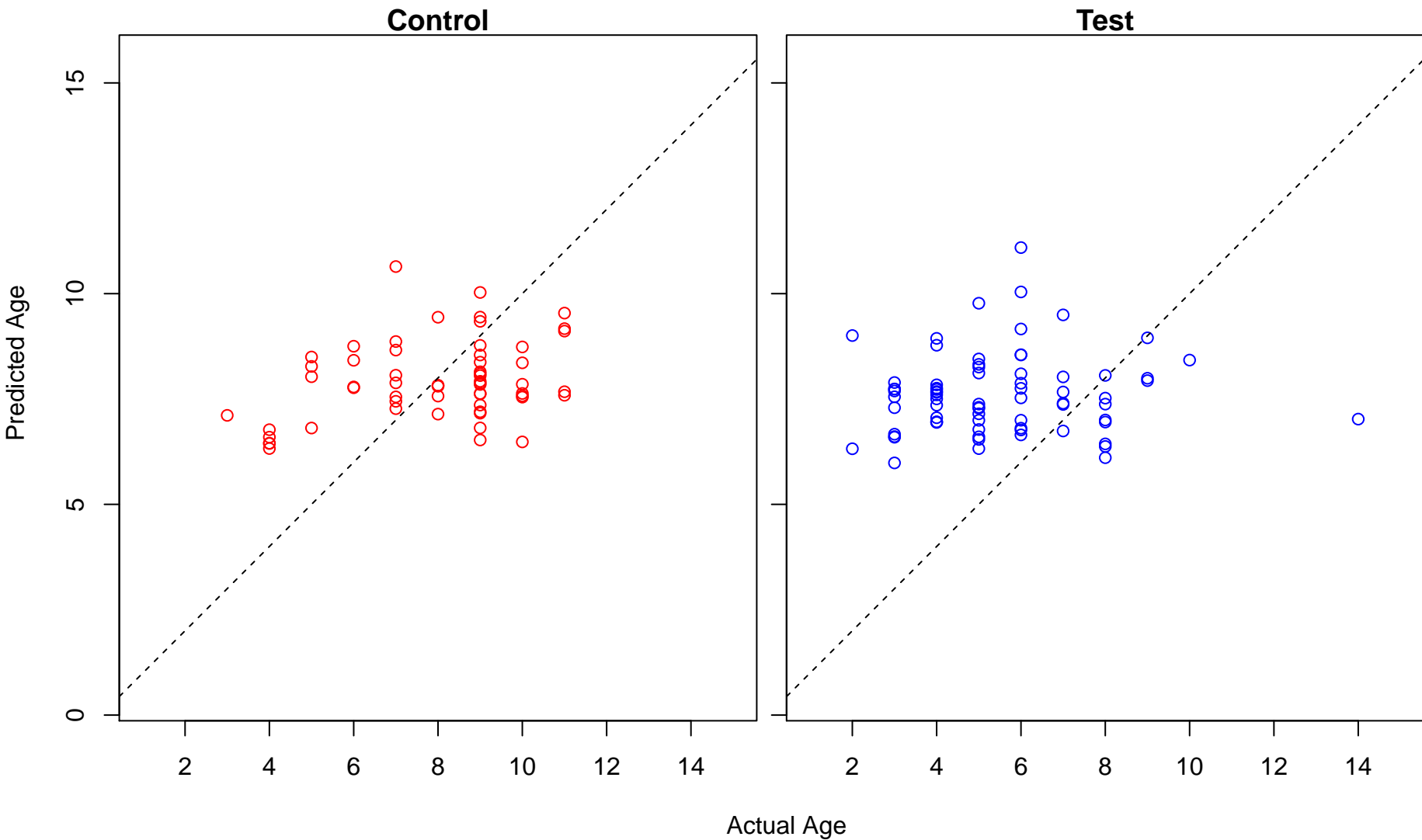
embryonic morphogenesis (Score: 0.435076)



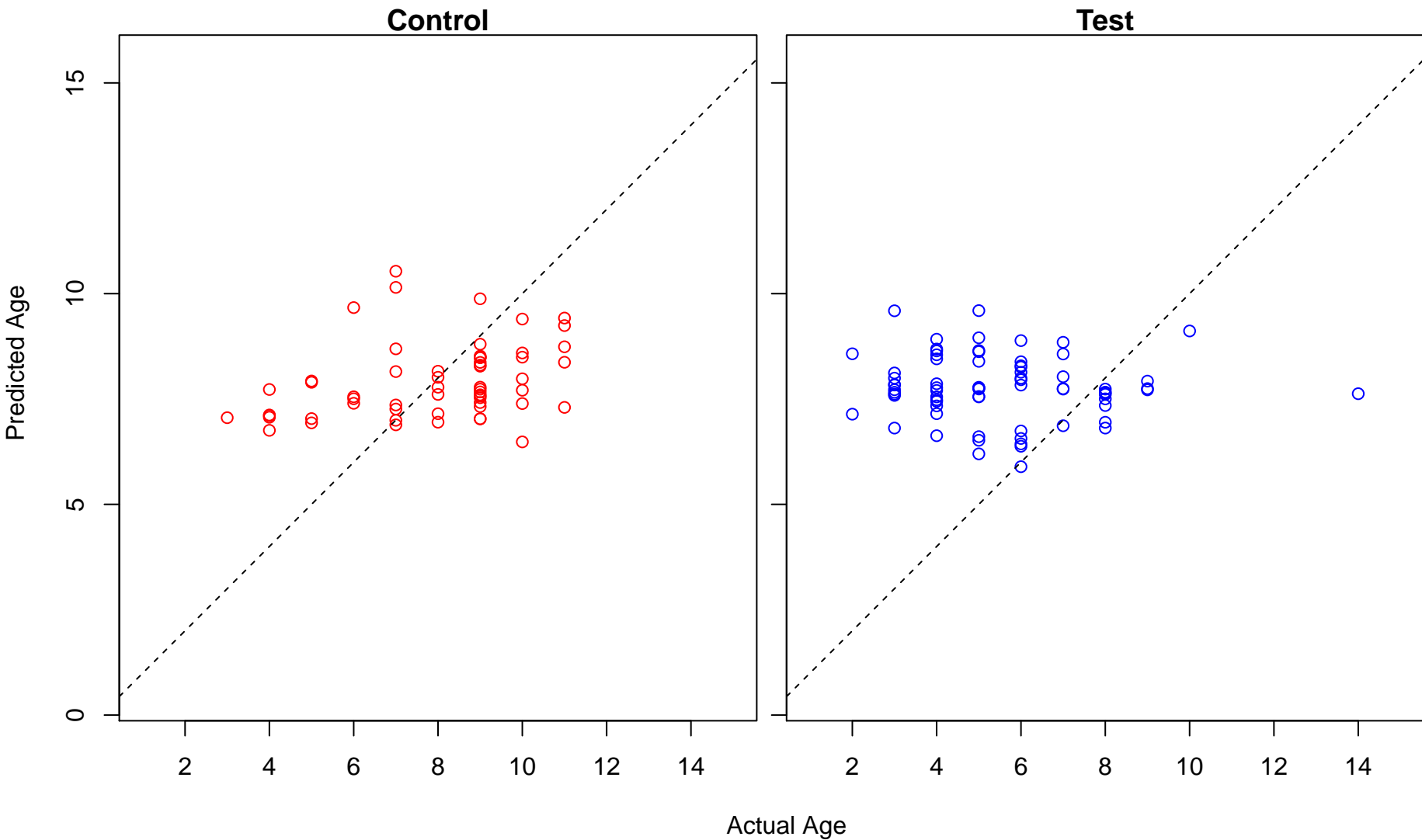
regulation of keratinocyte proliferation (Score: 0.434813)



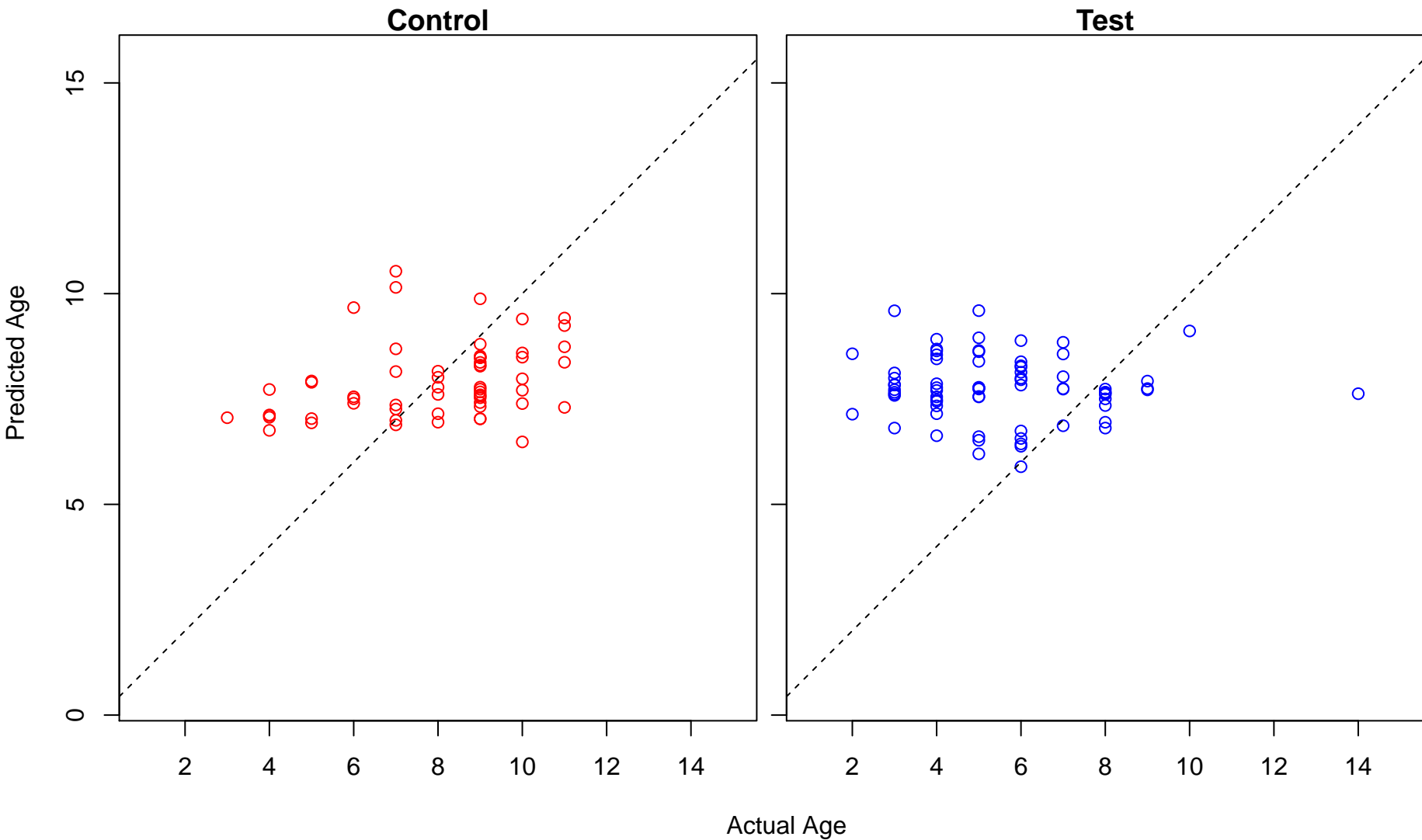
extracellular matrix disassembly (Score: 0.432626)



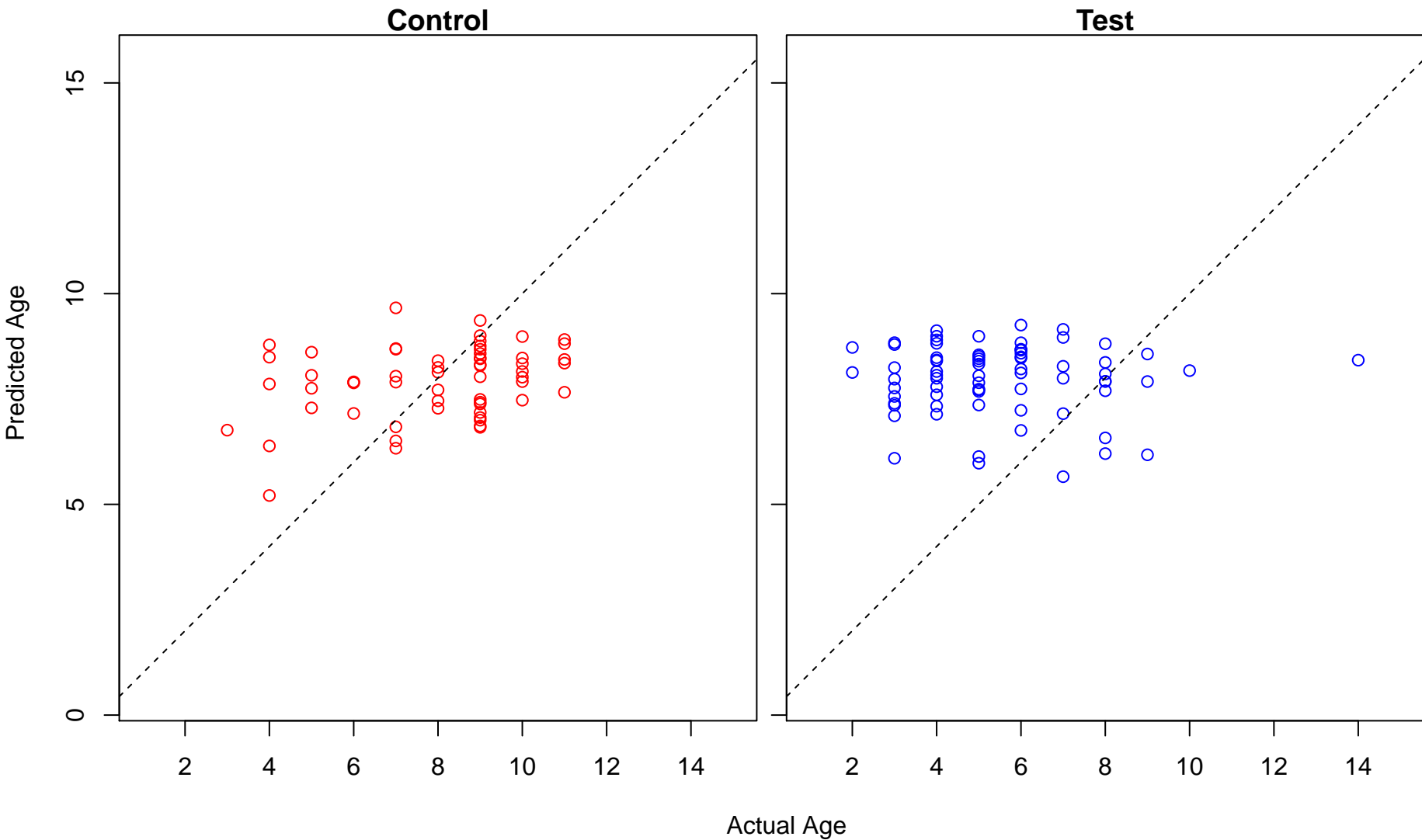
carbon catabolite repression of transcription (Score: 0.429261)



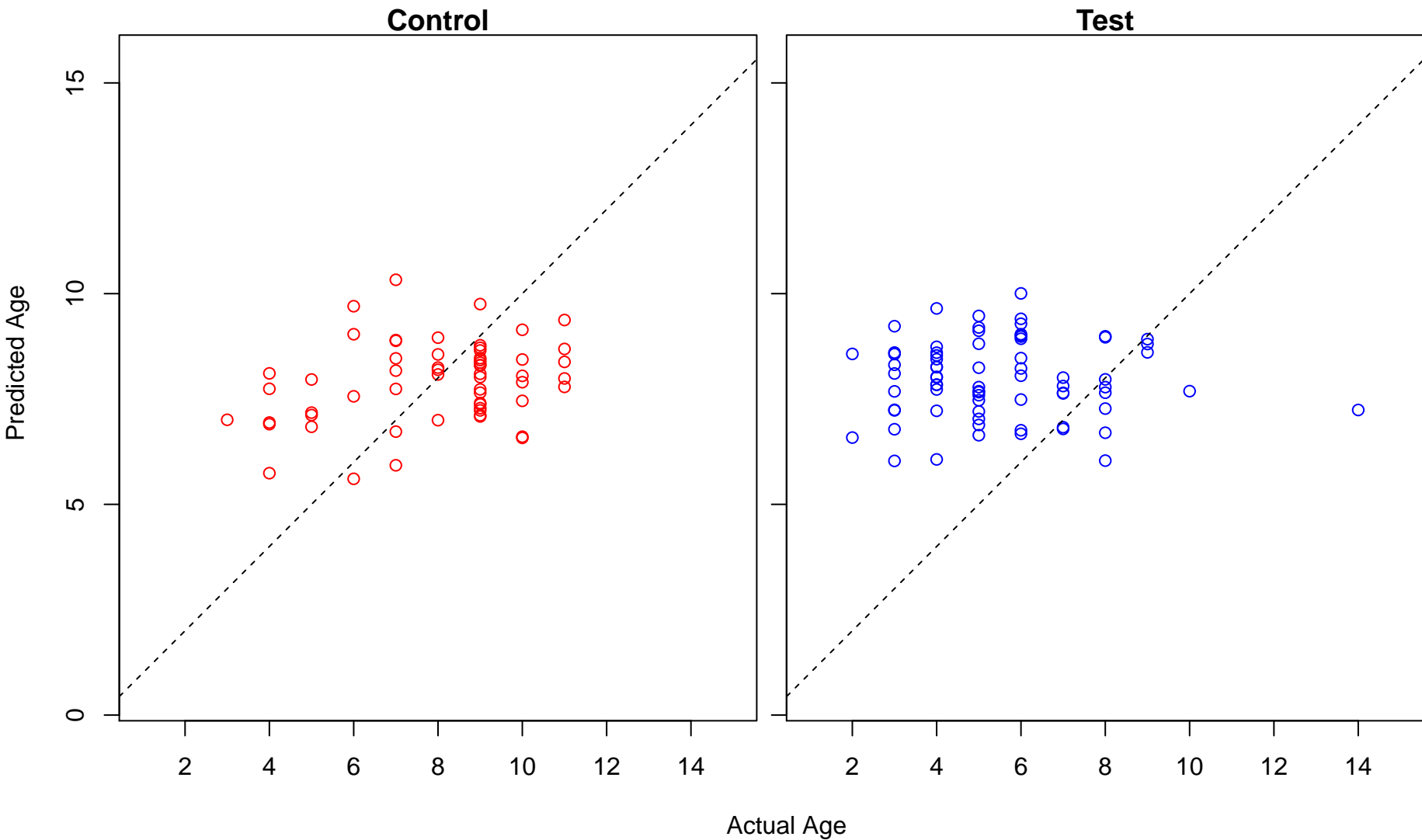
negative regulation of transcription by glucose (Score: 0.429261)



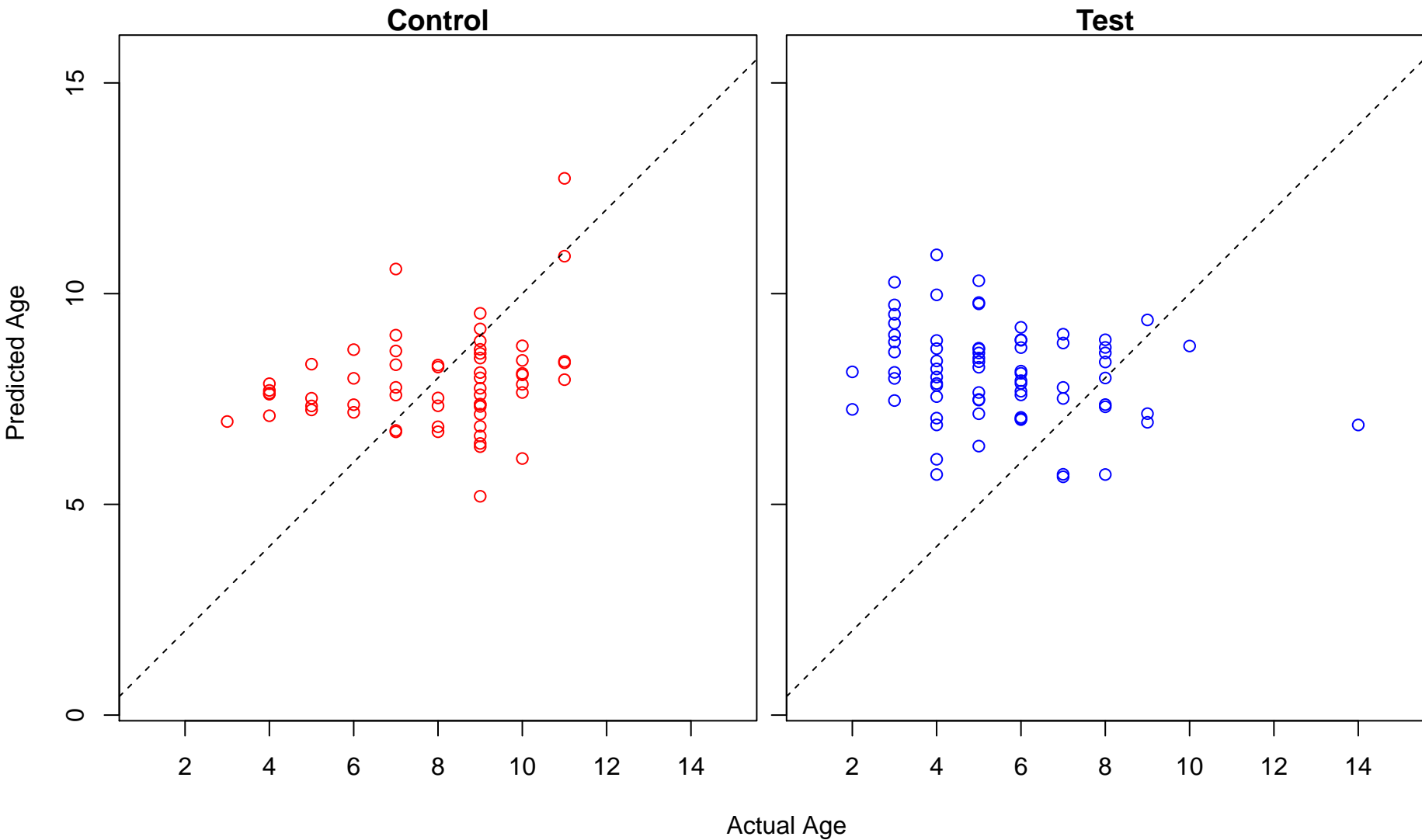
mitotic sister chromatid separation (Score: 0.429007)



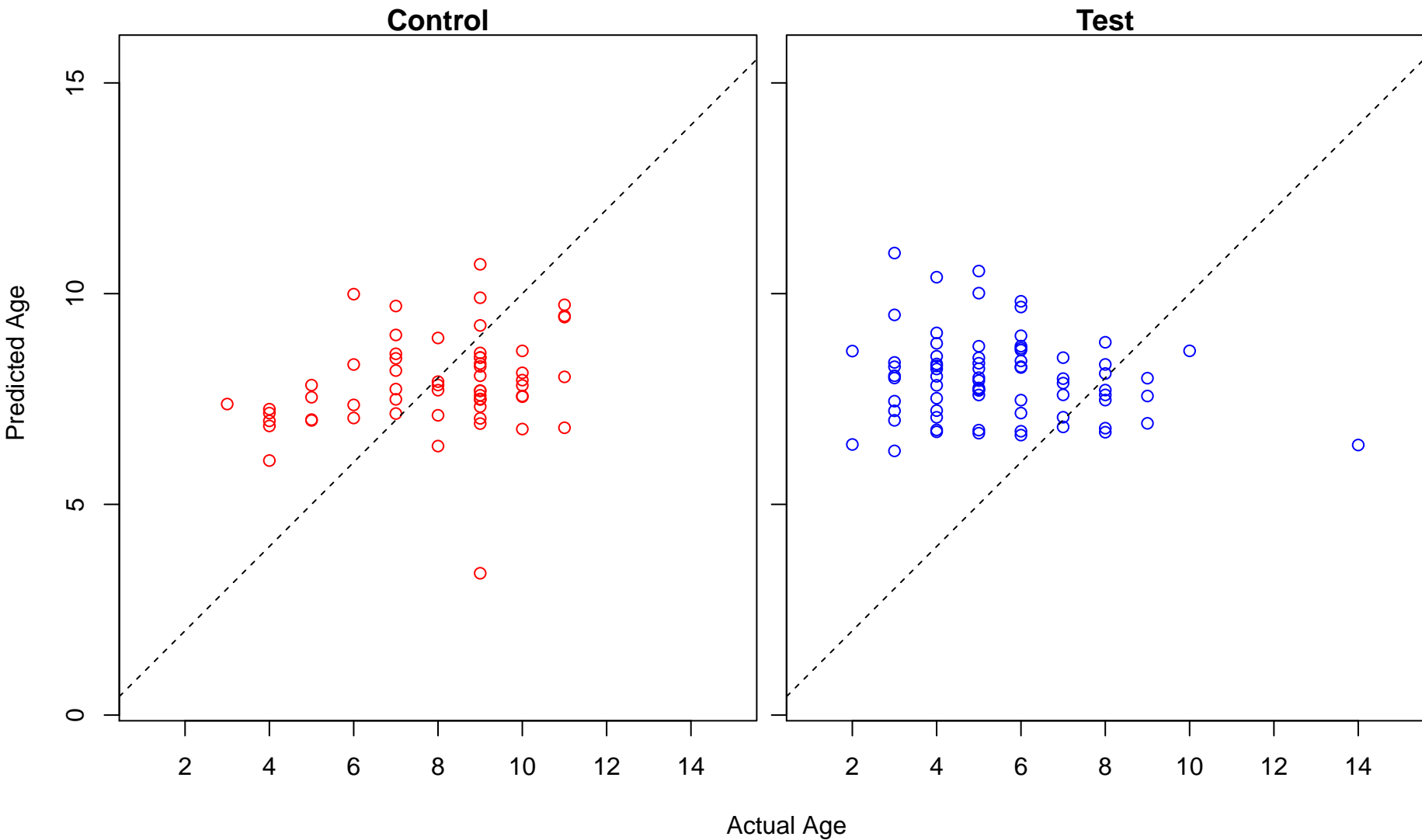
regulation of protein glycosylation (Score: 0.428789)



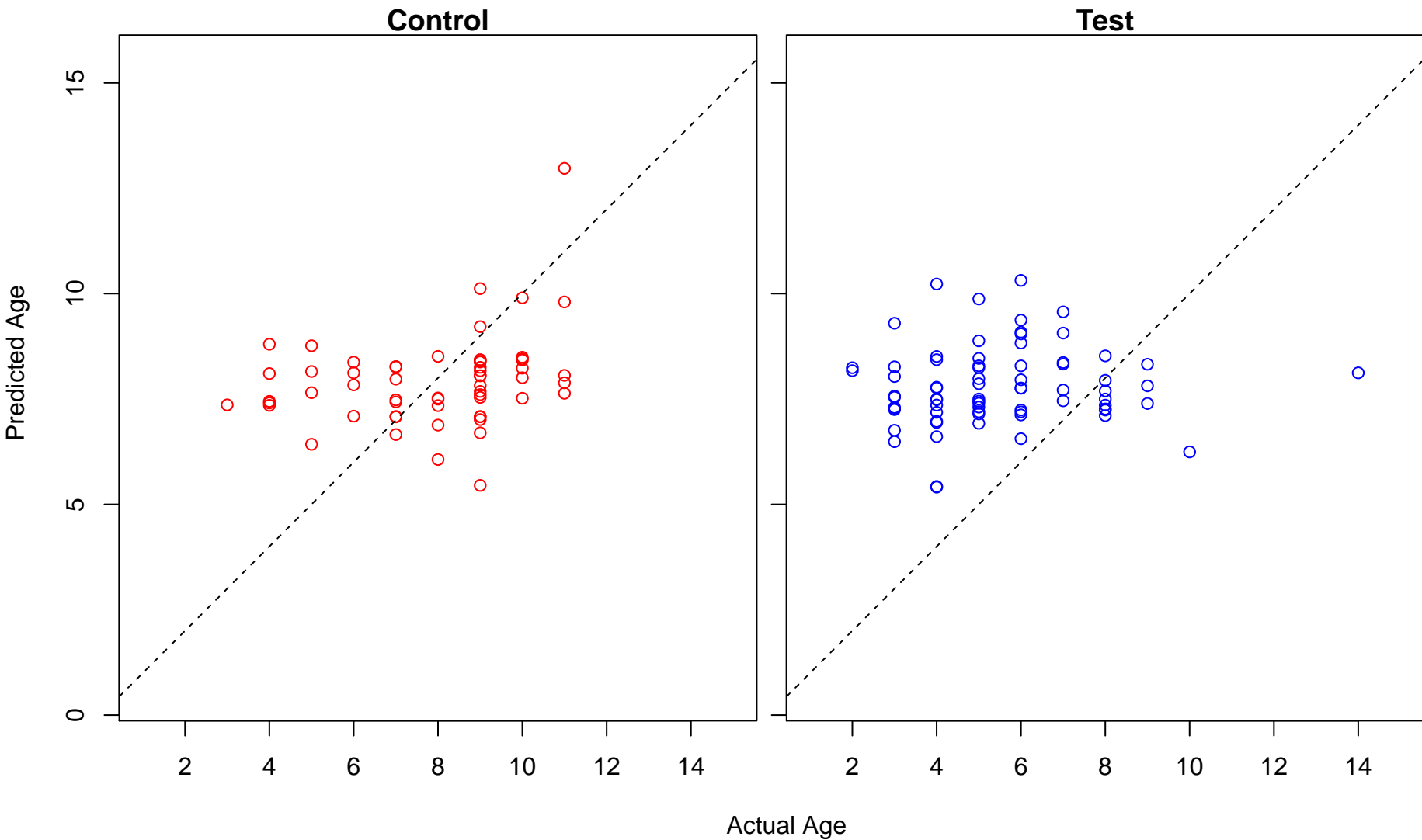
inner dynein arm assembly (Score: 0.428268)



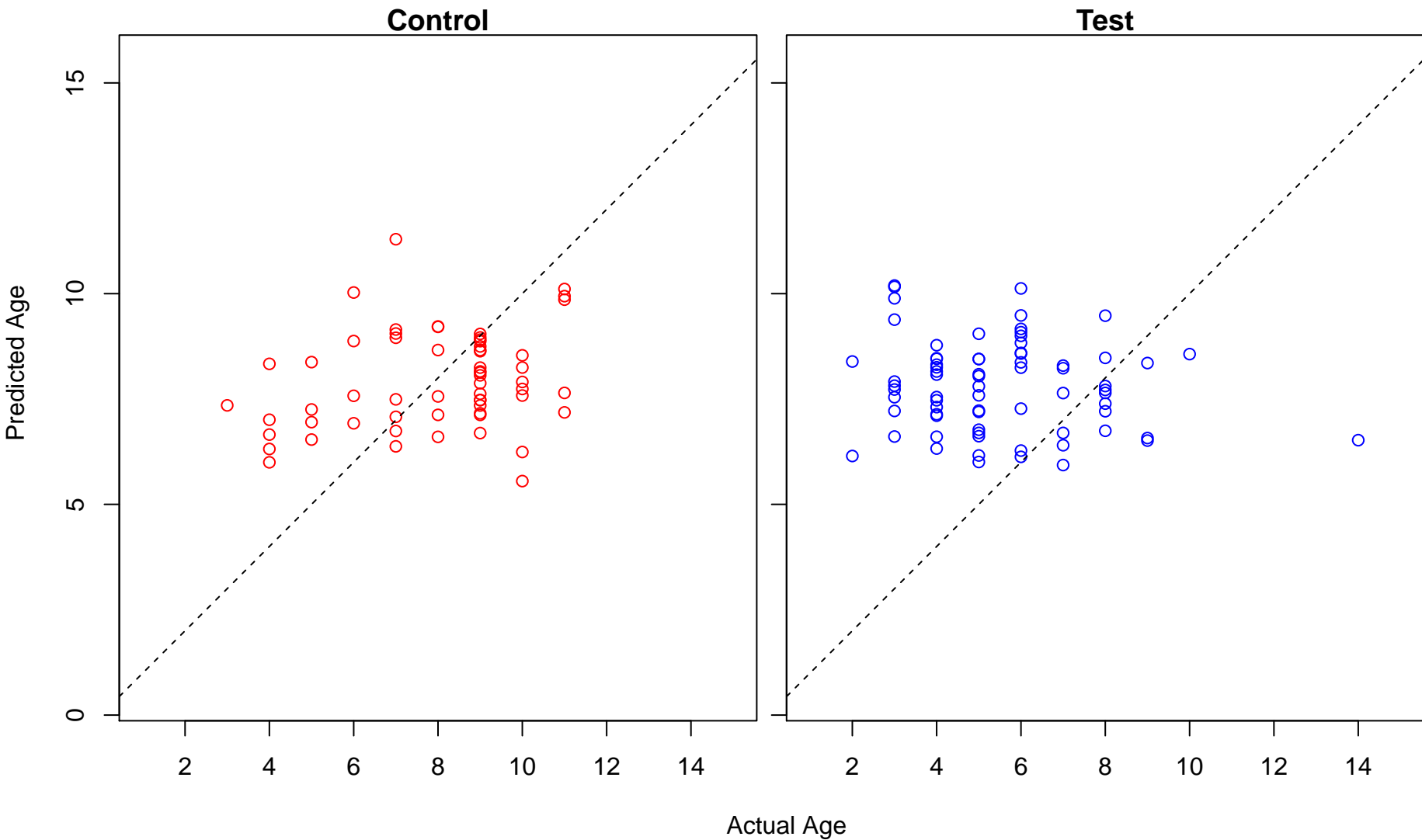
medium-chain fatty-acyl-CoA metabolic process (Score: 0.428067)



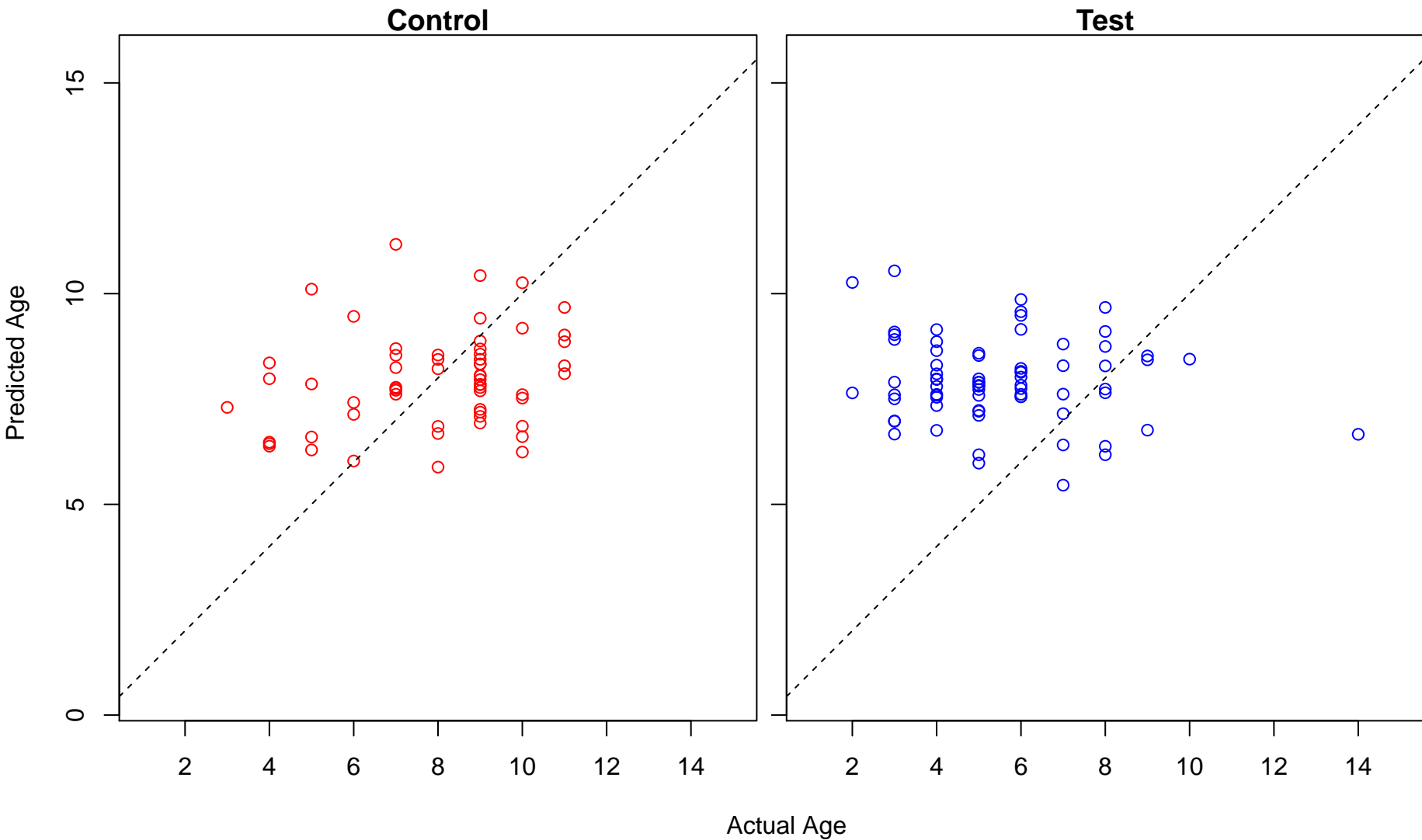
Spemann organizer formation (Score: 0.427840)



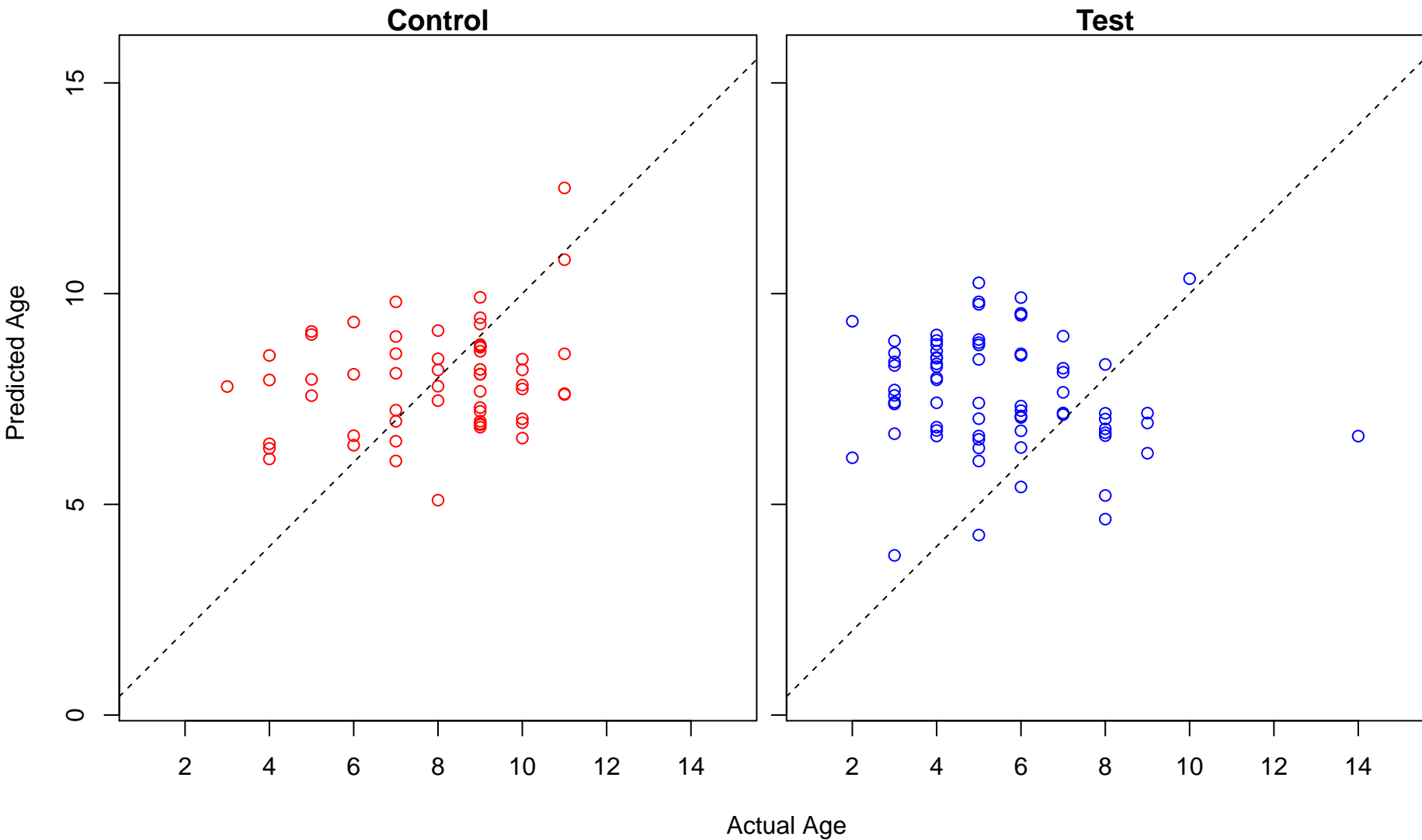
synaptic vesicle endocytosis (Score: 0.427277)



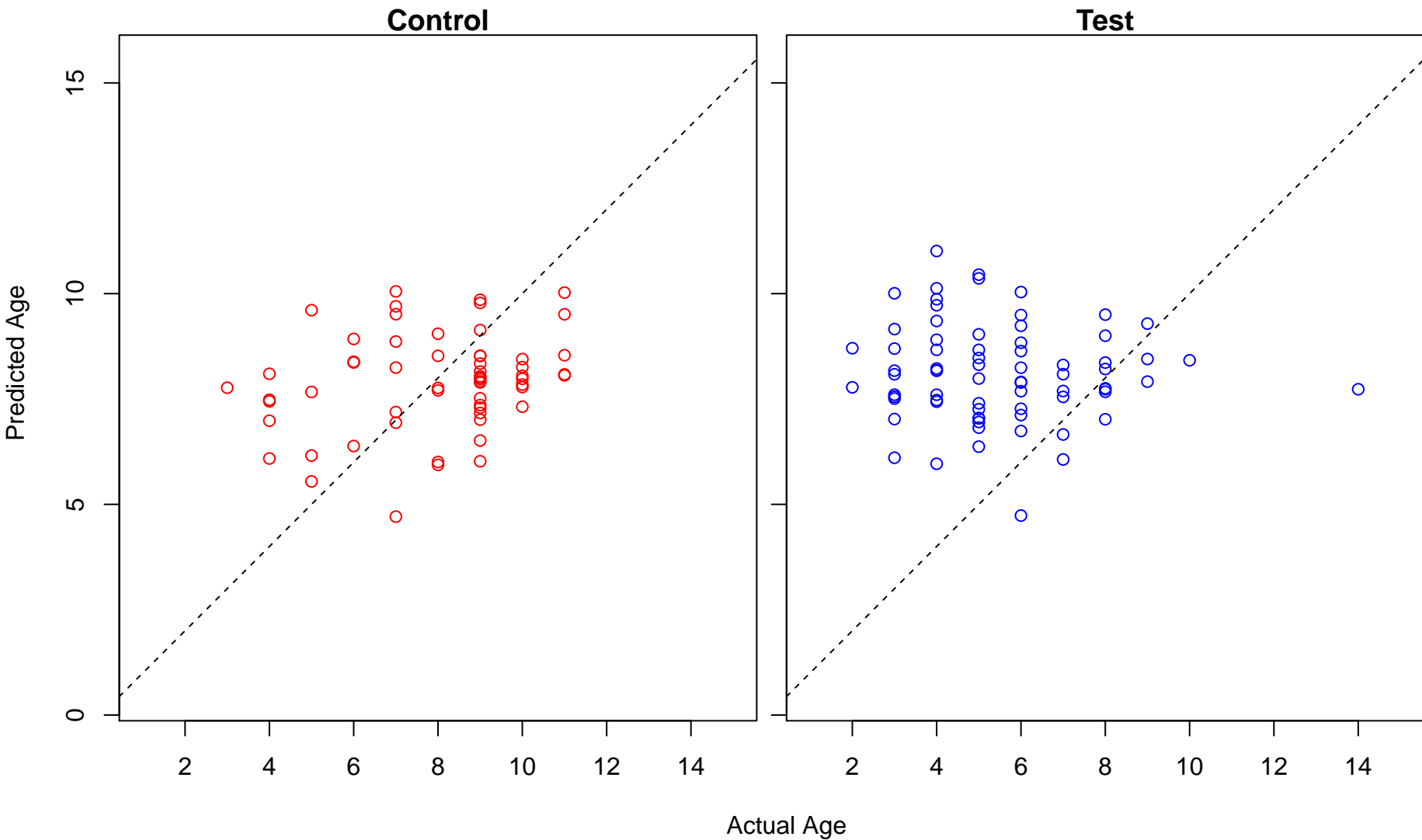
xenobiotic catabolic process (Score: 0.427227)



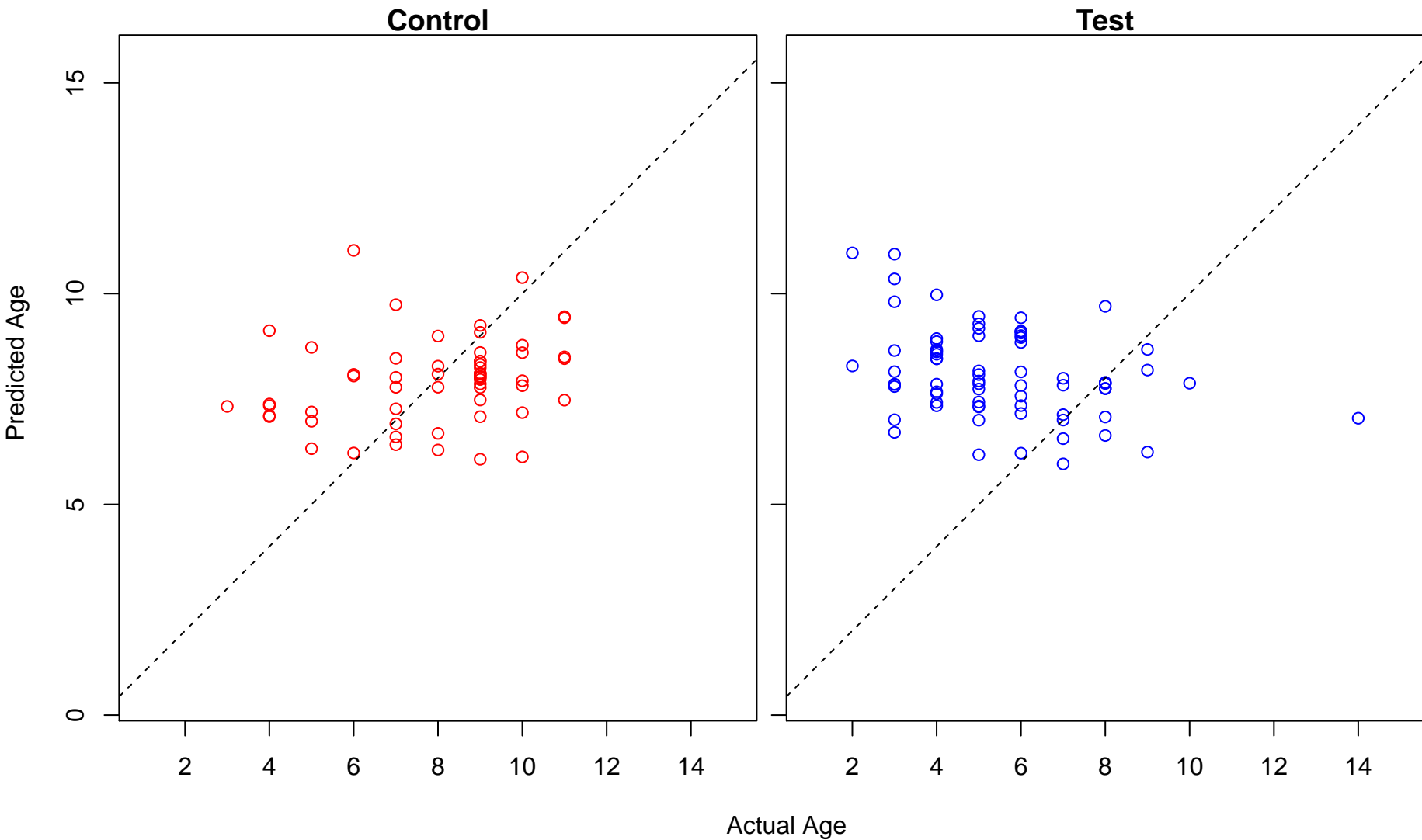
mitochondrion distribution (Score: 0.426946)



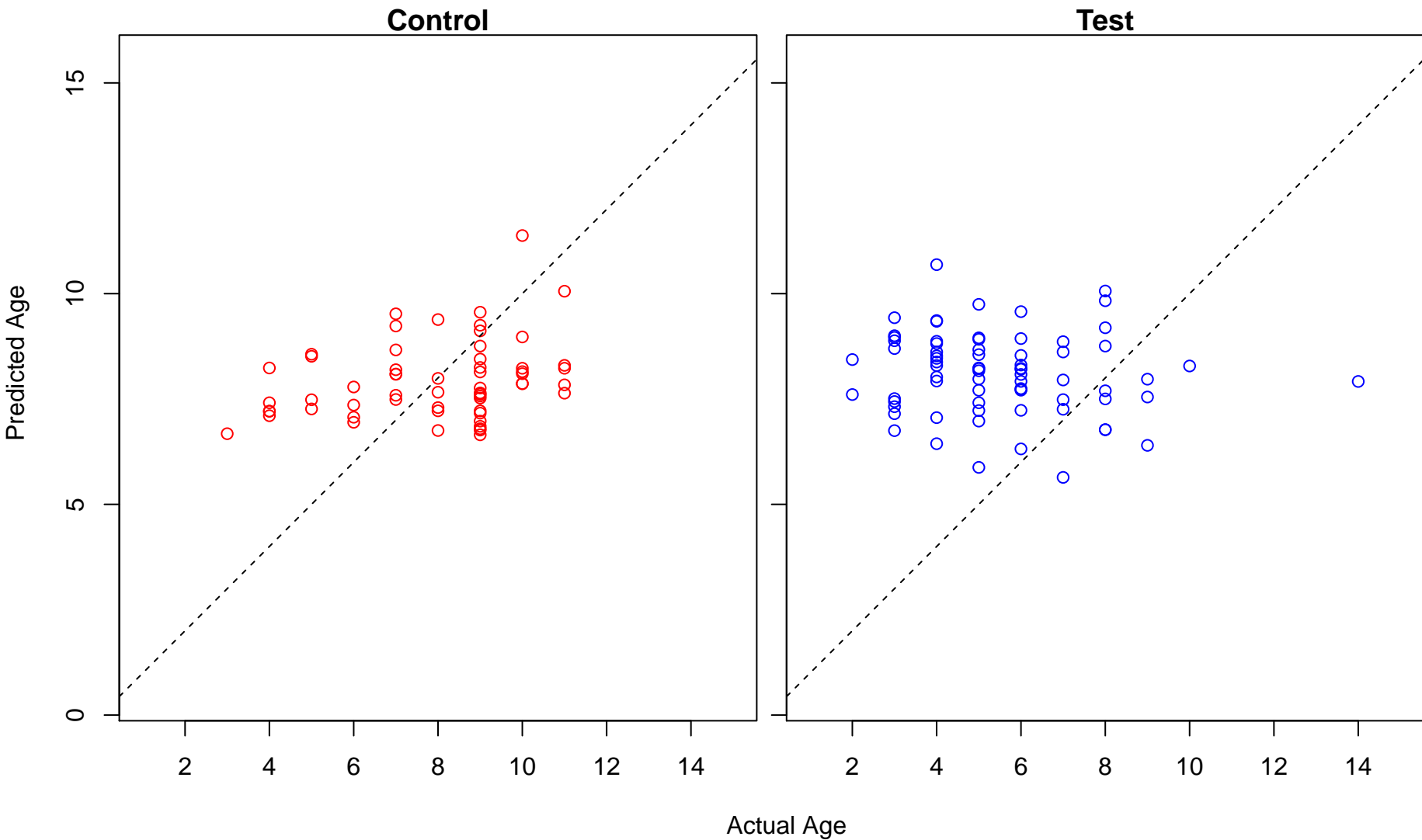
positive regulation of steroid hormone secretion (Score: 0.426812)



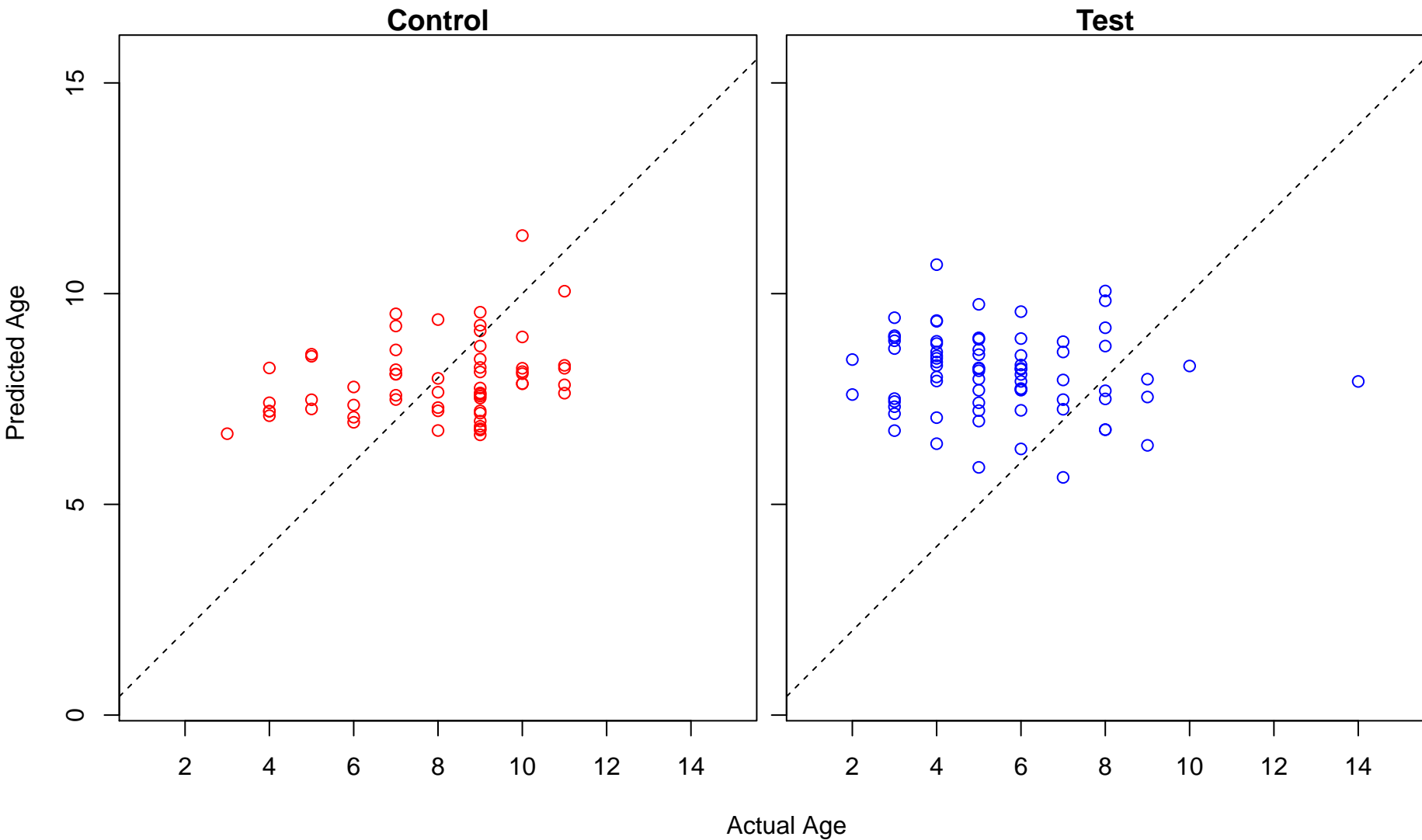
negative regulation of protein acetylation (Score: 0.424963)



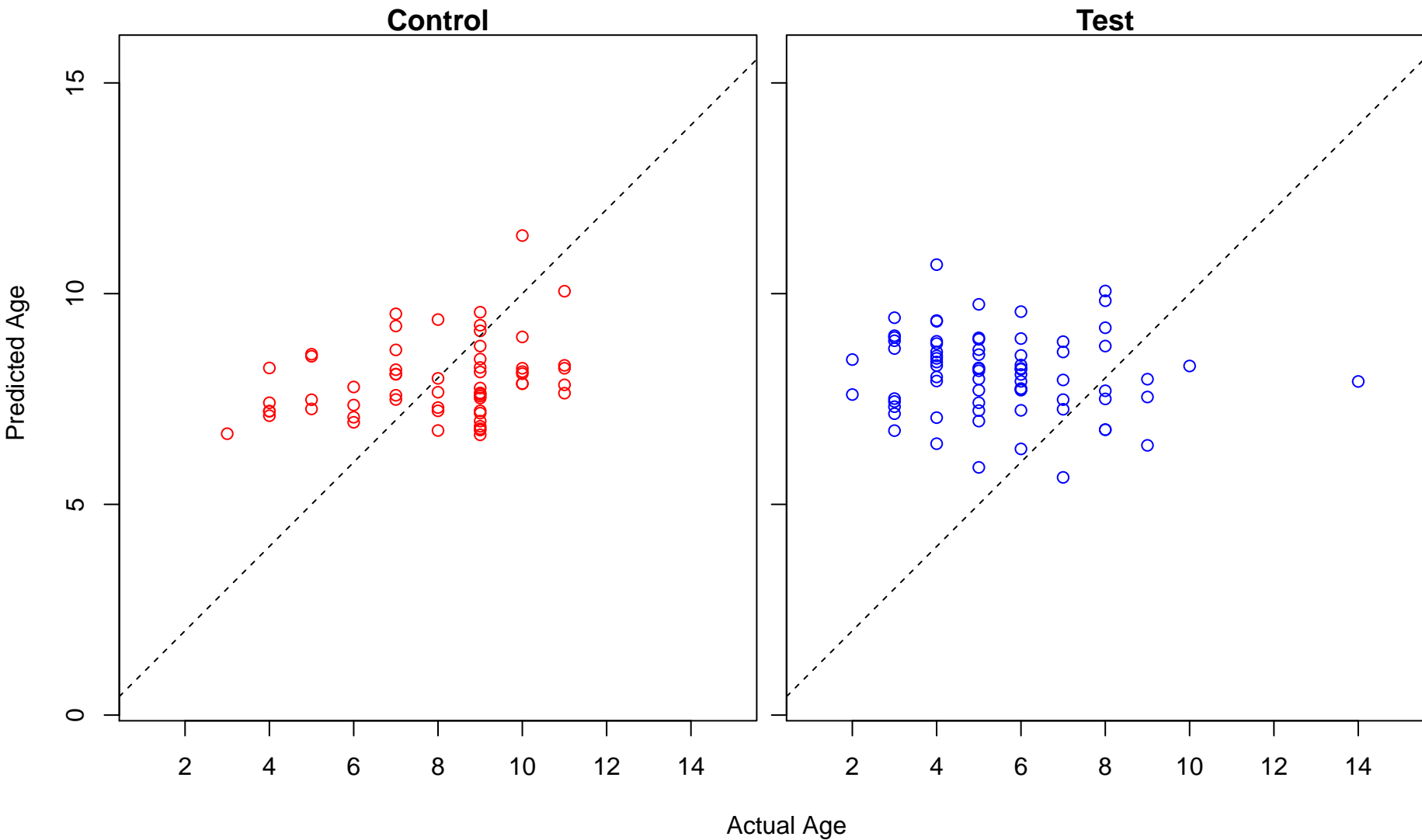
cardiac atrium formation (Score: 0.423798)



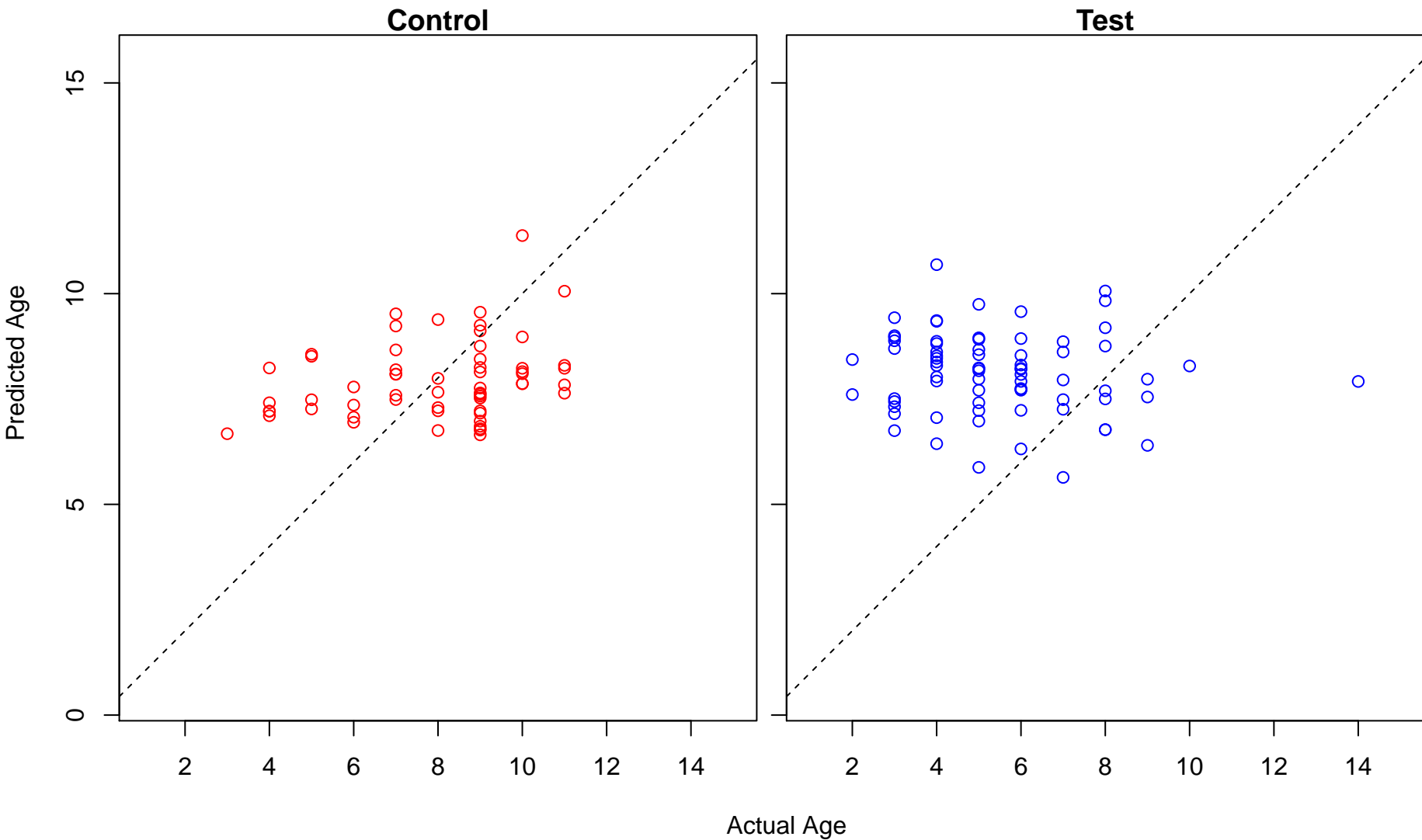
sinus venosus development (Score: 0.423798)



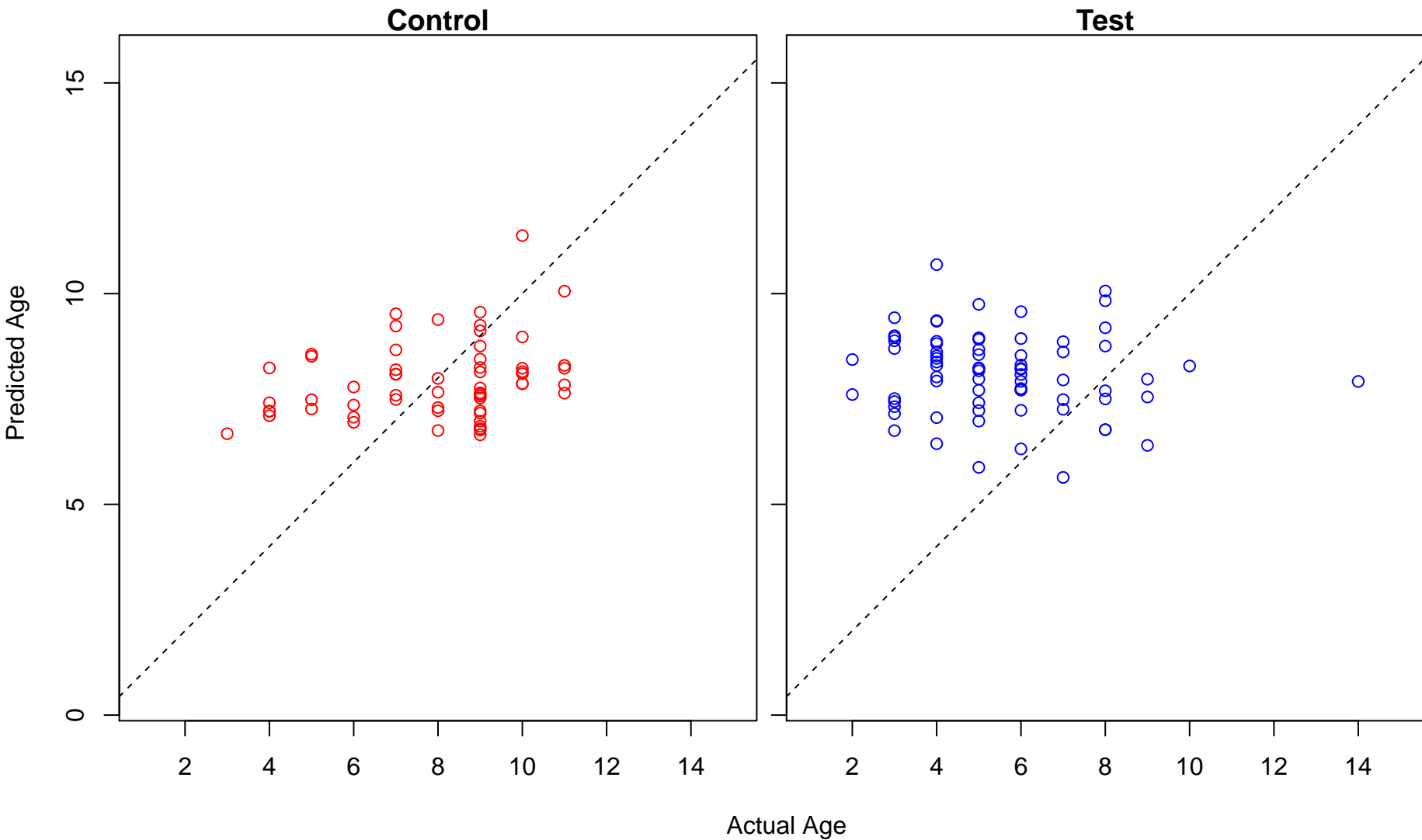
sinus venosus morphogenesis (Score: 0.423798)



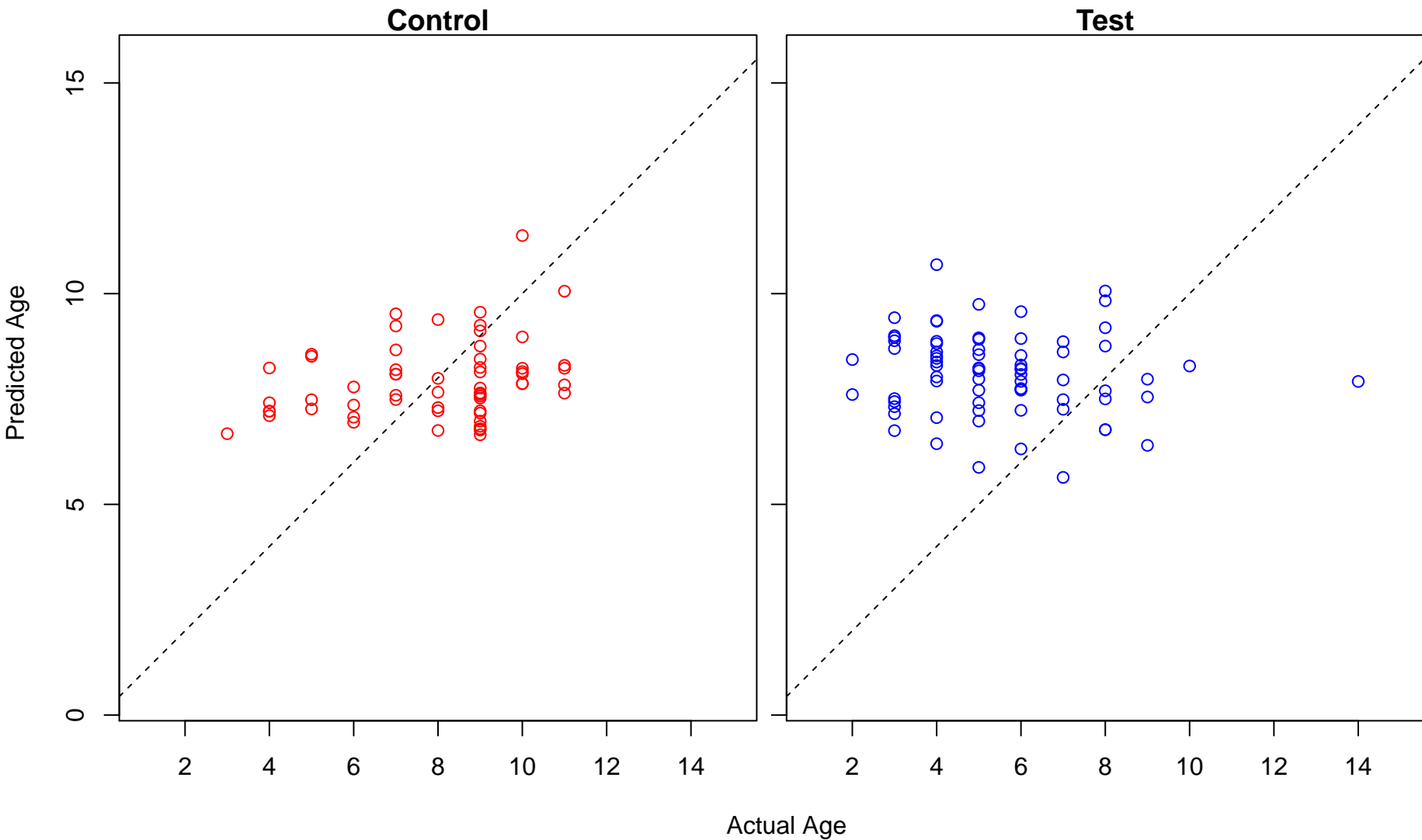
cardioblast anterior-lateral migration (Score: 0.423798)



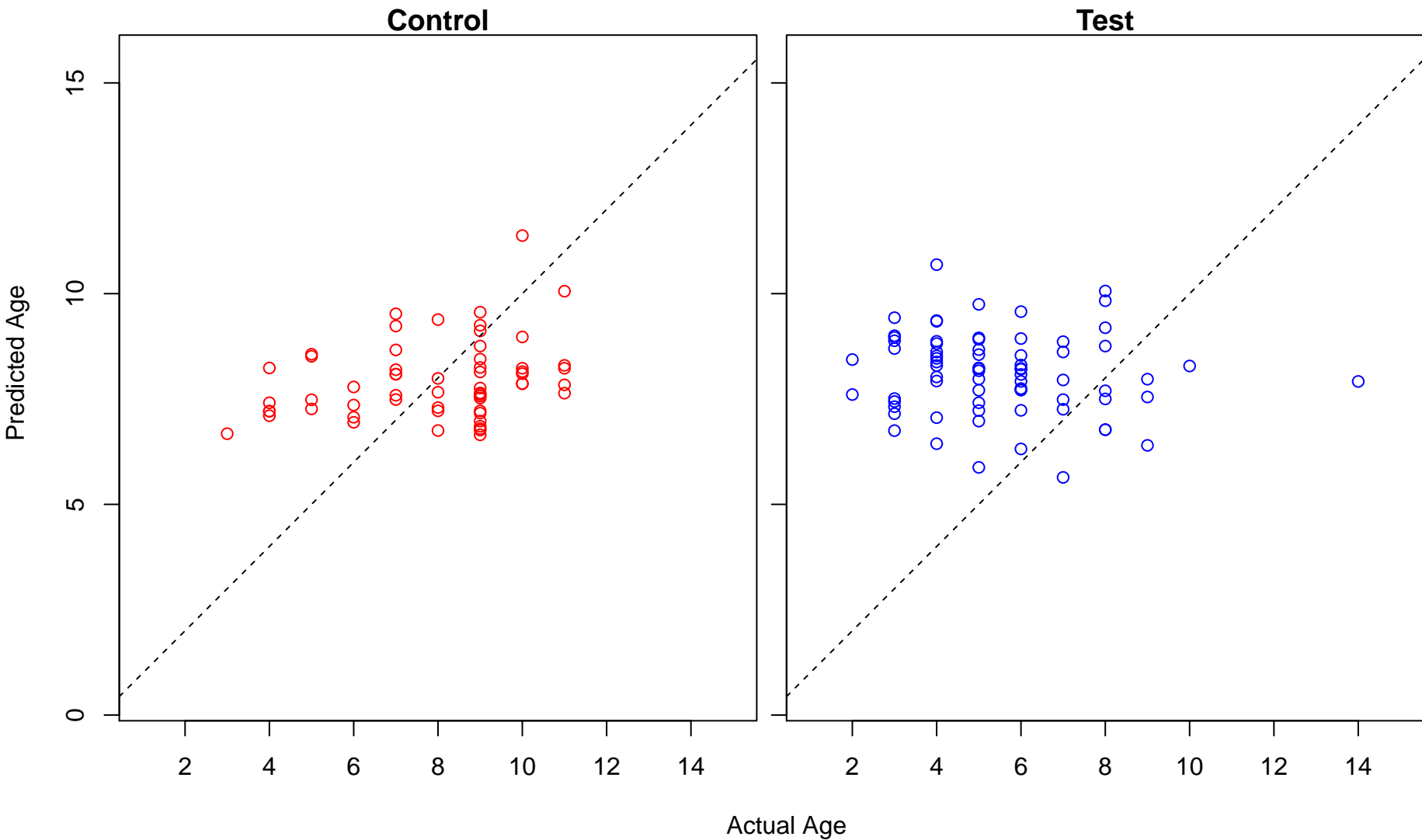
cardioblast migration (Score: 0.423798)



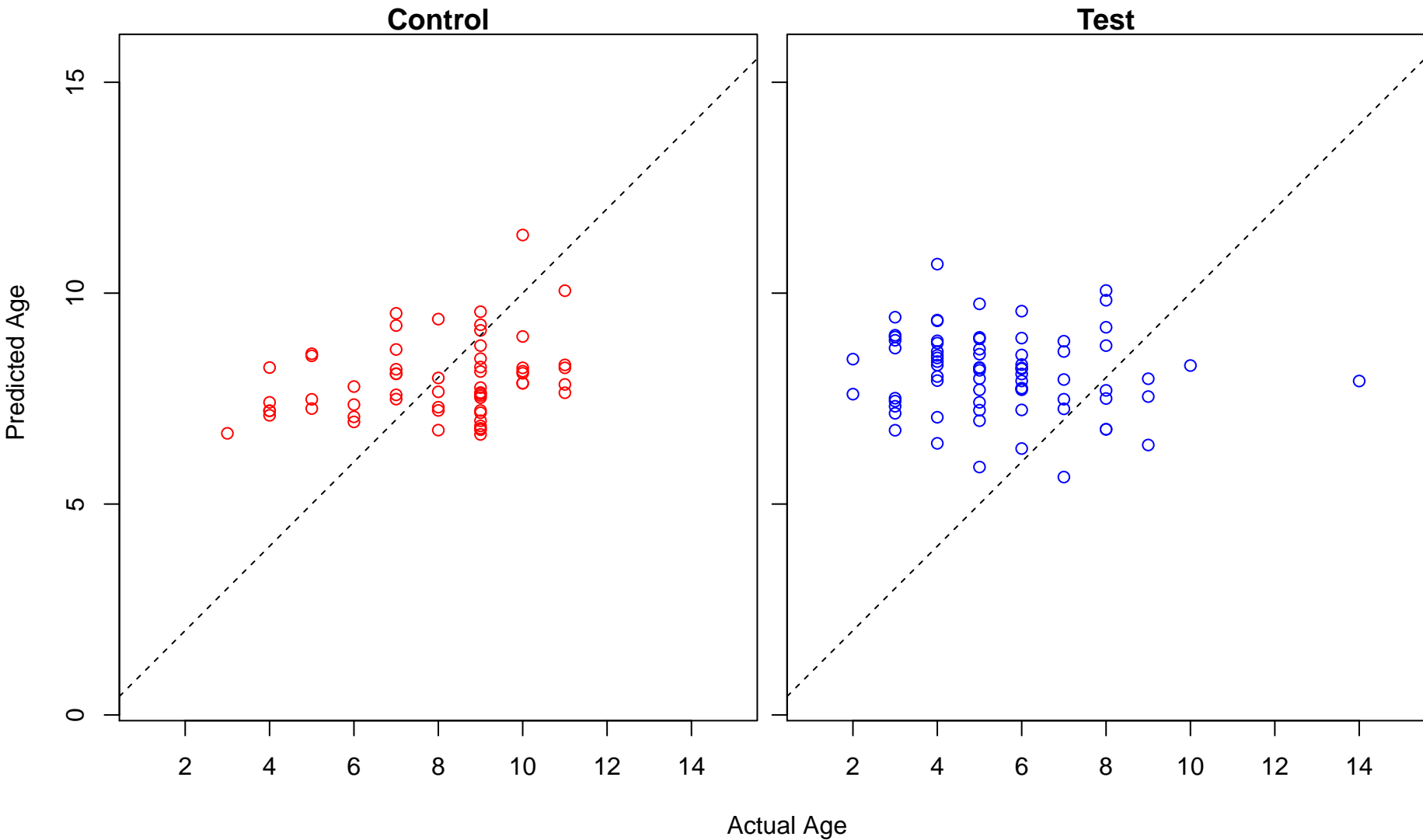
cell migration to the midline involved in heart development (Score: 0.423798)



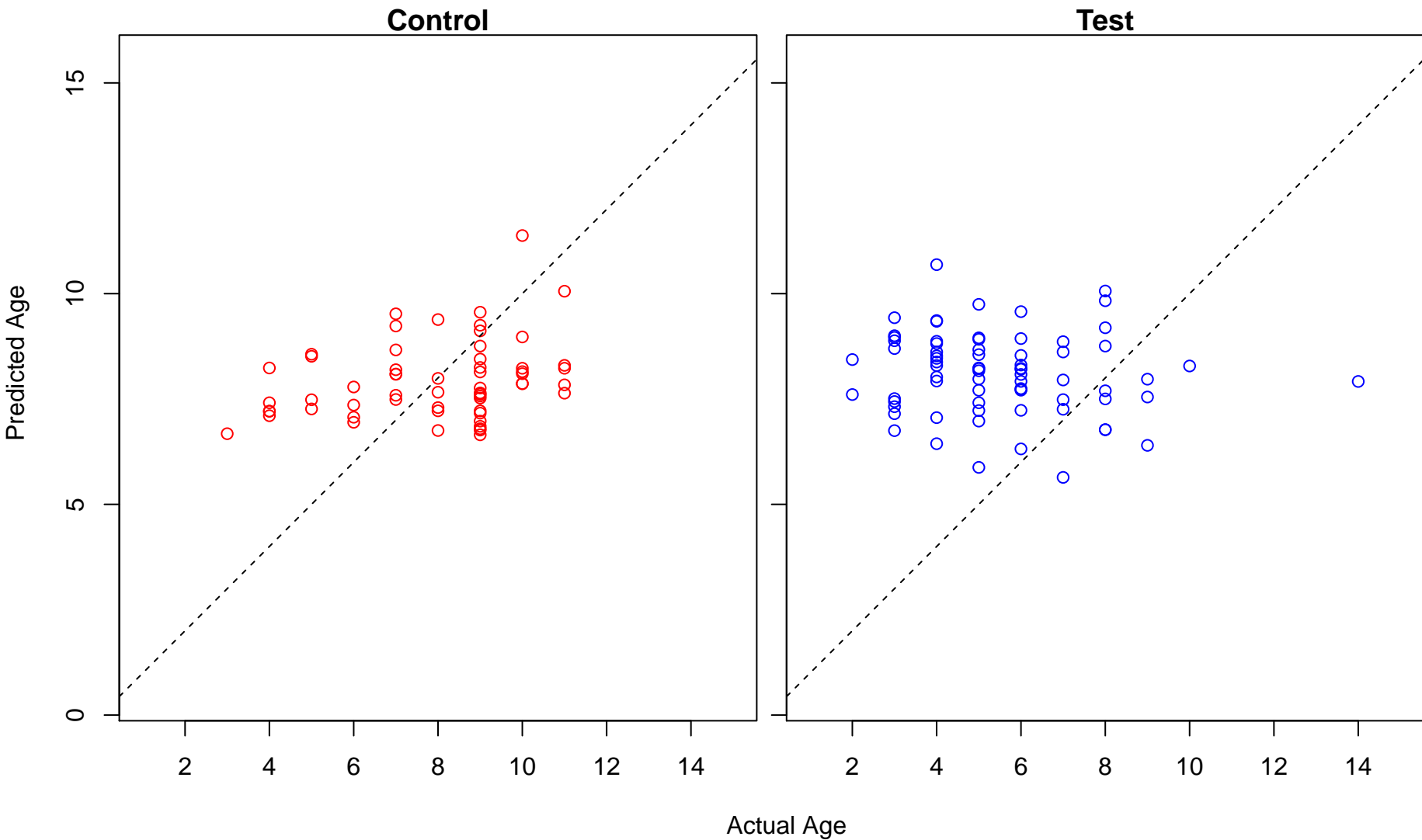
negative regulation of endodermal cell fate specification (Score: 0.423798)



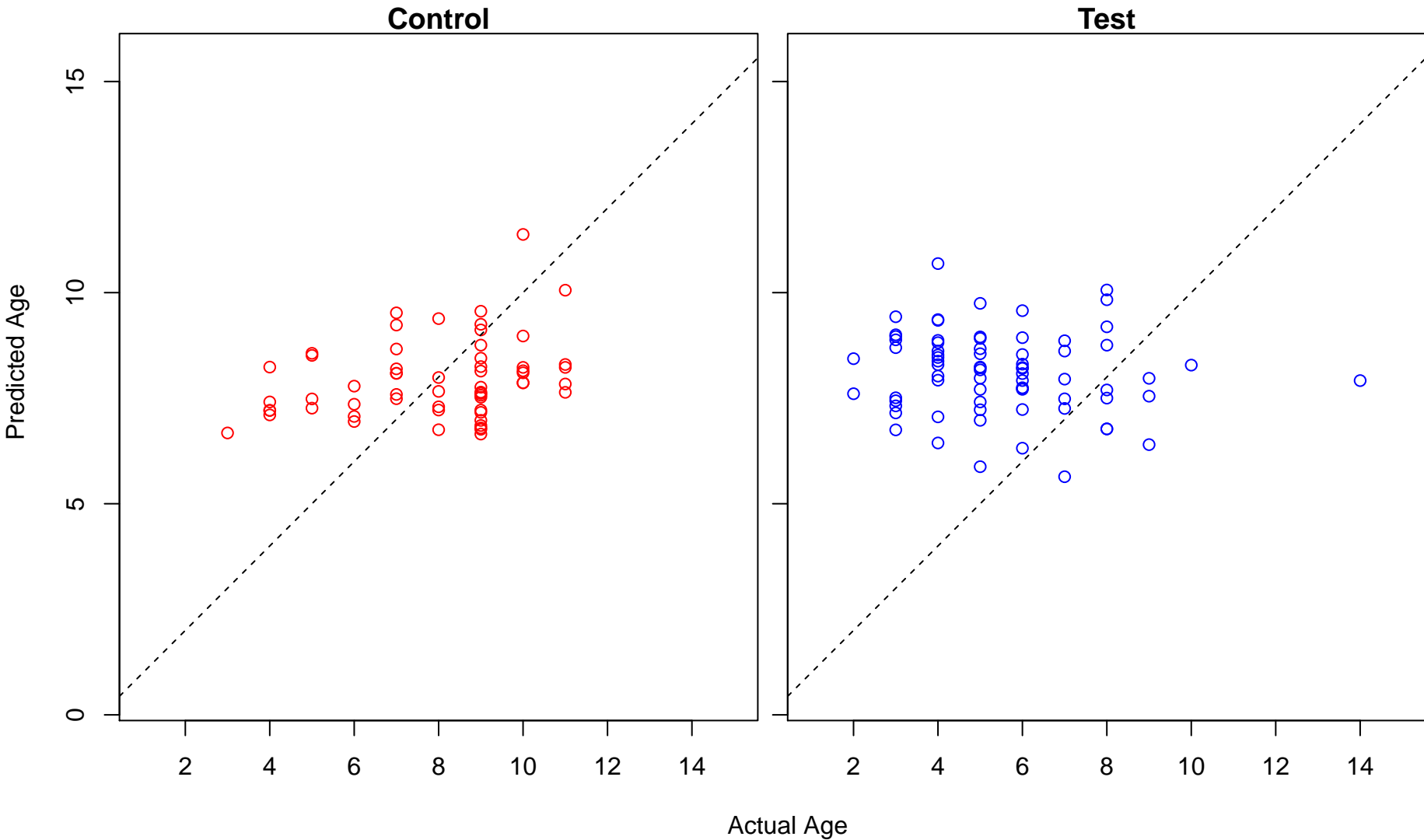
cardioblast migration to the midline involved in heart field formation (Score: 0.423798)



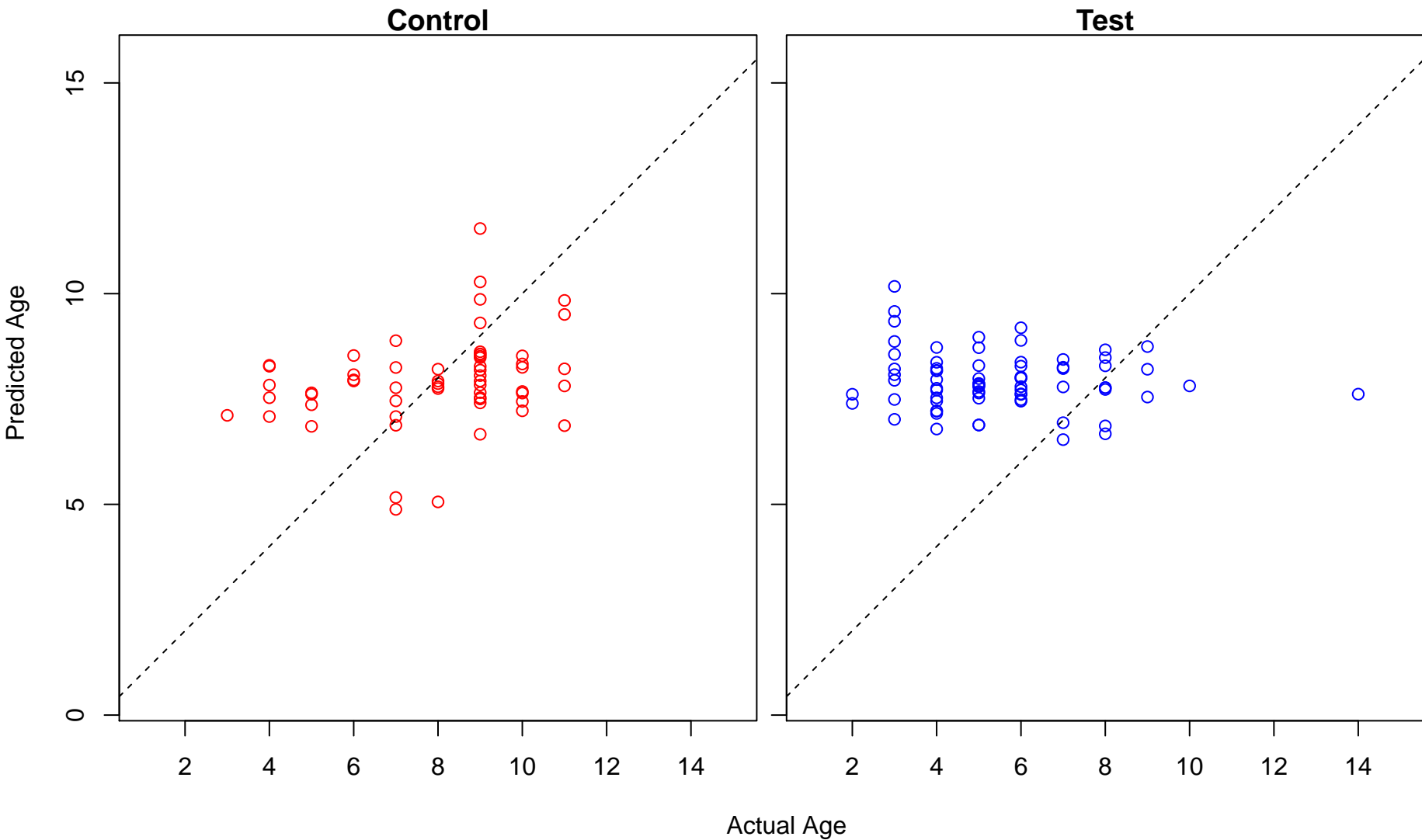
regulation of hepatocyte differentiation (Score: 0.423798)



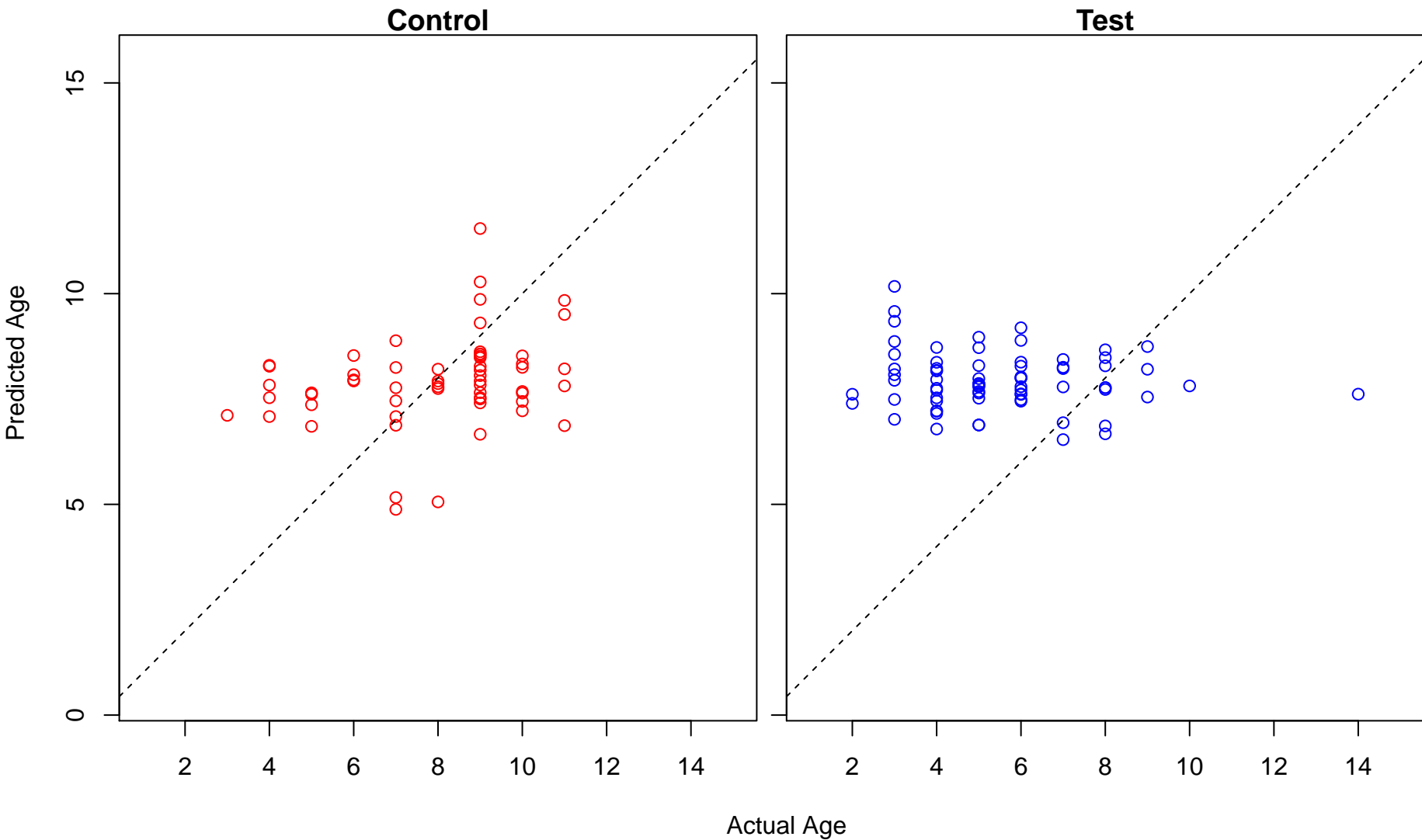
positive regulation of hepatocyte differentiation (Score: 0.423798)



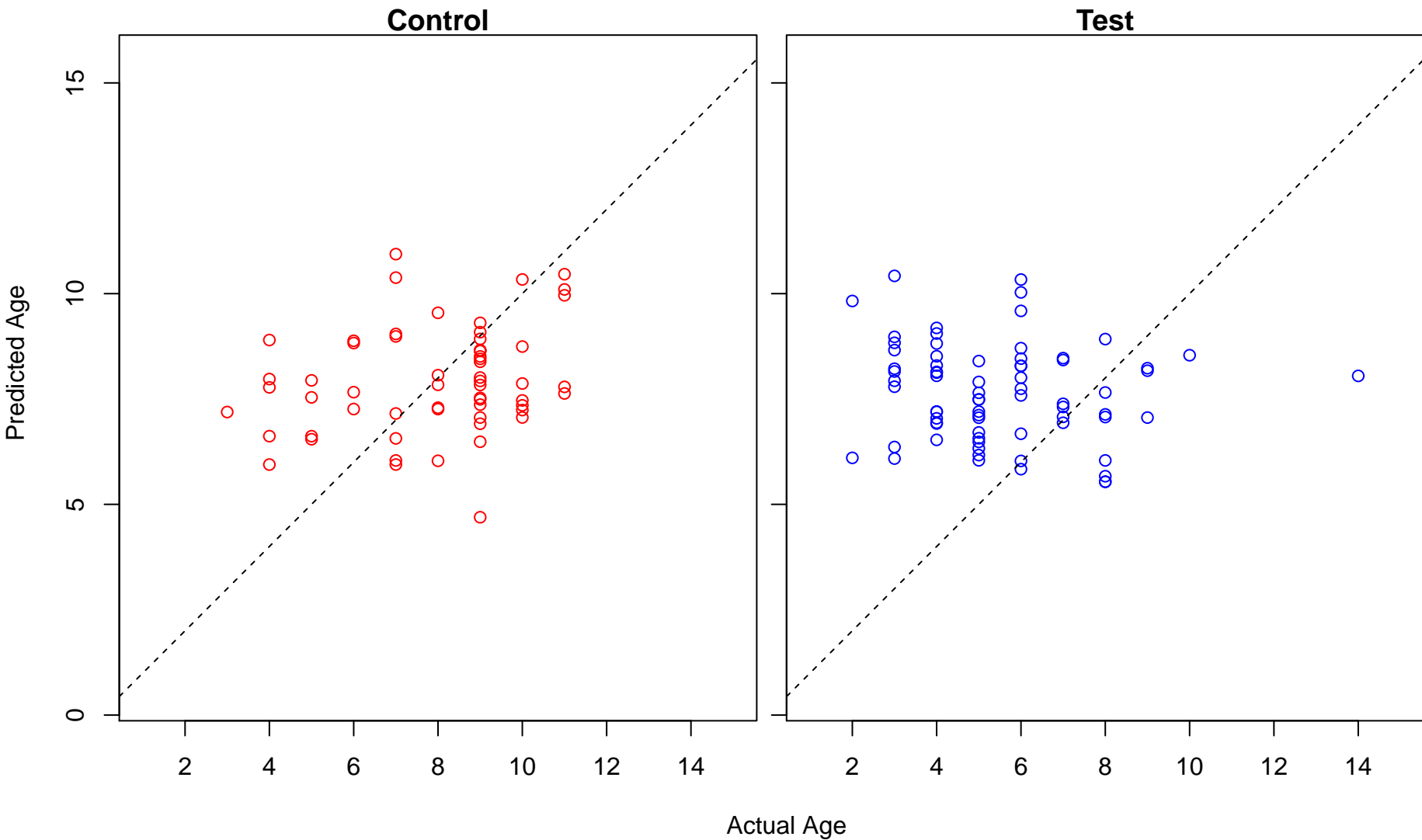
regulation of lymphangiogenesis (Score: 0.423622)



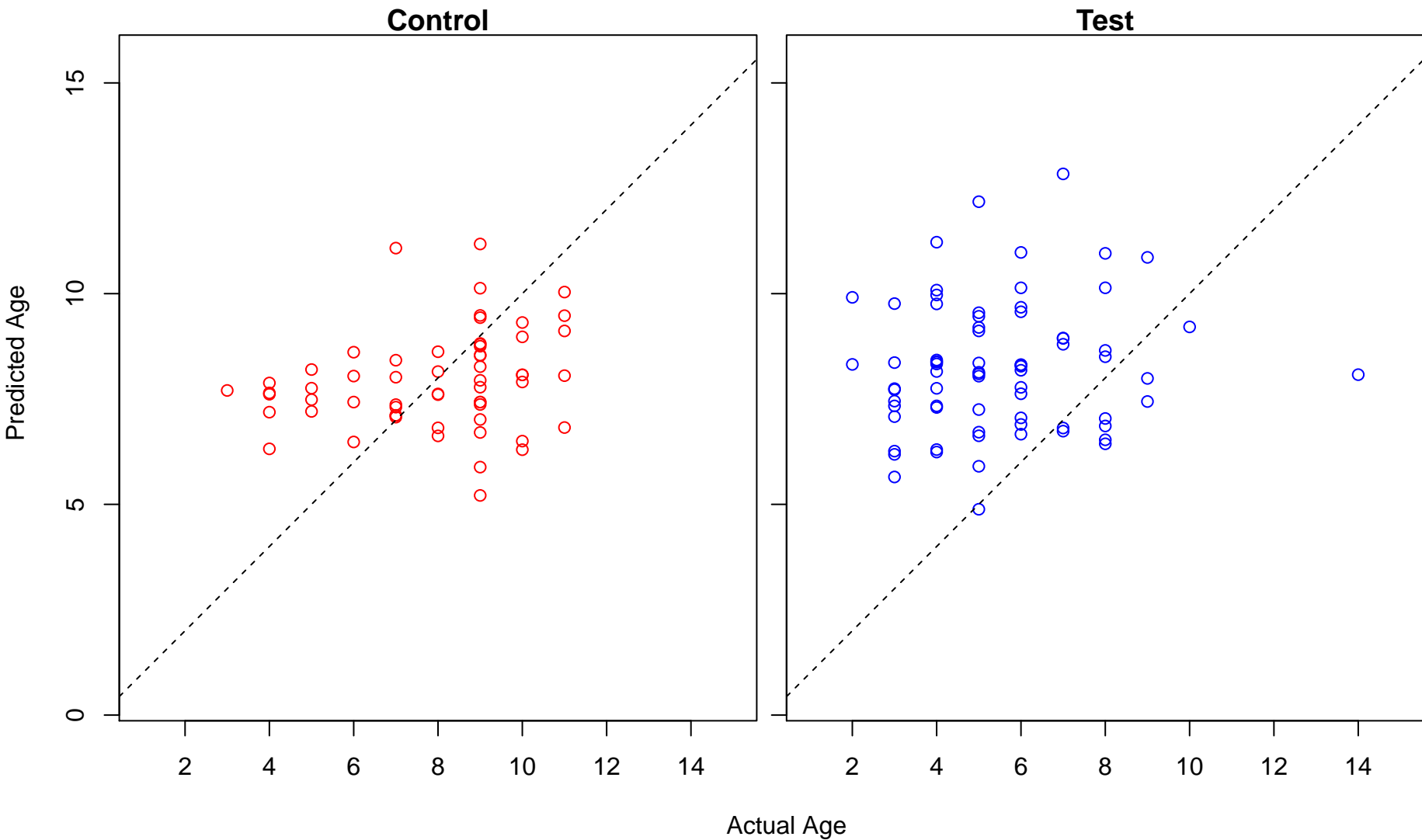
negative regulation of lymphangiogenesis (Score: 0.423622)



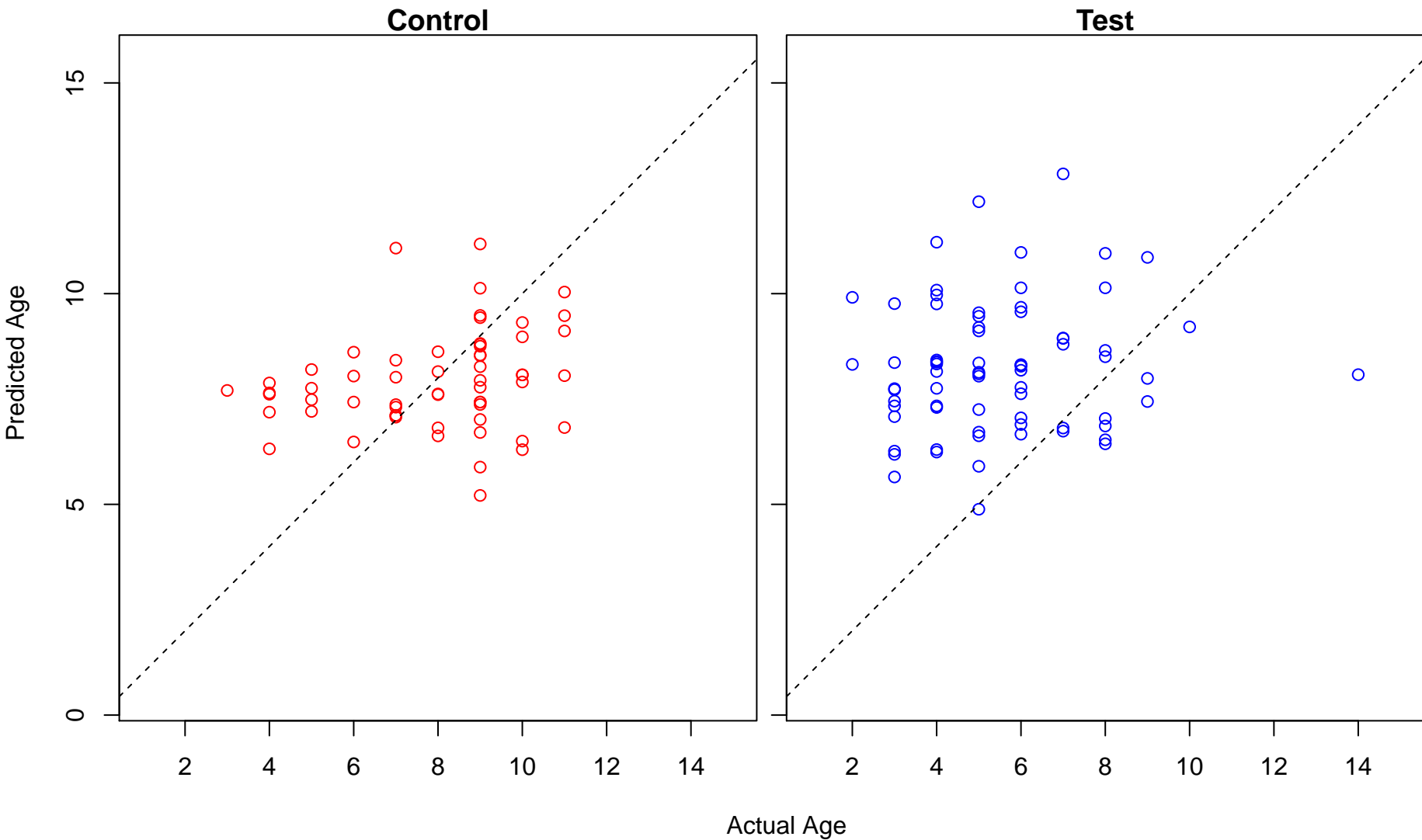
negative regulation of ERK1 and ERK2 cascade (Score: 0.422611)



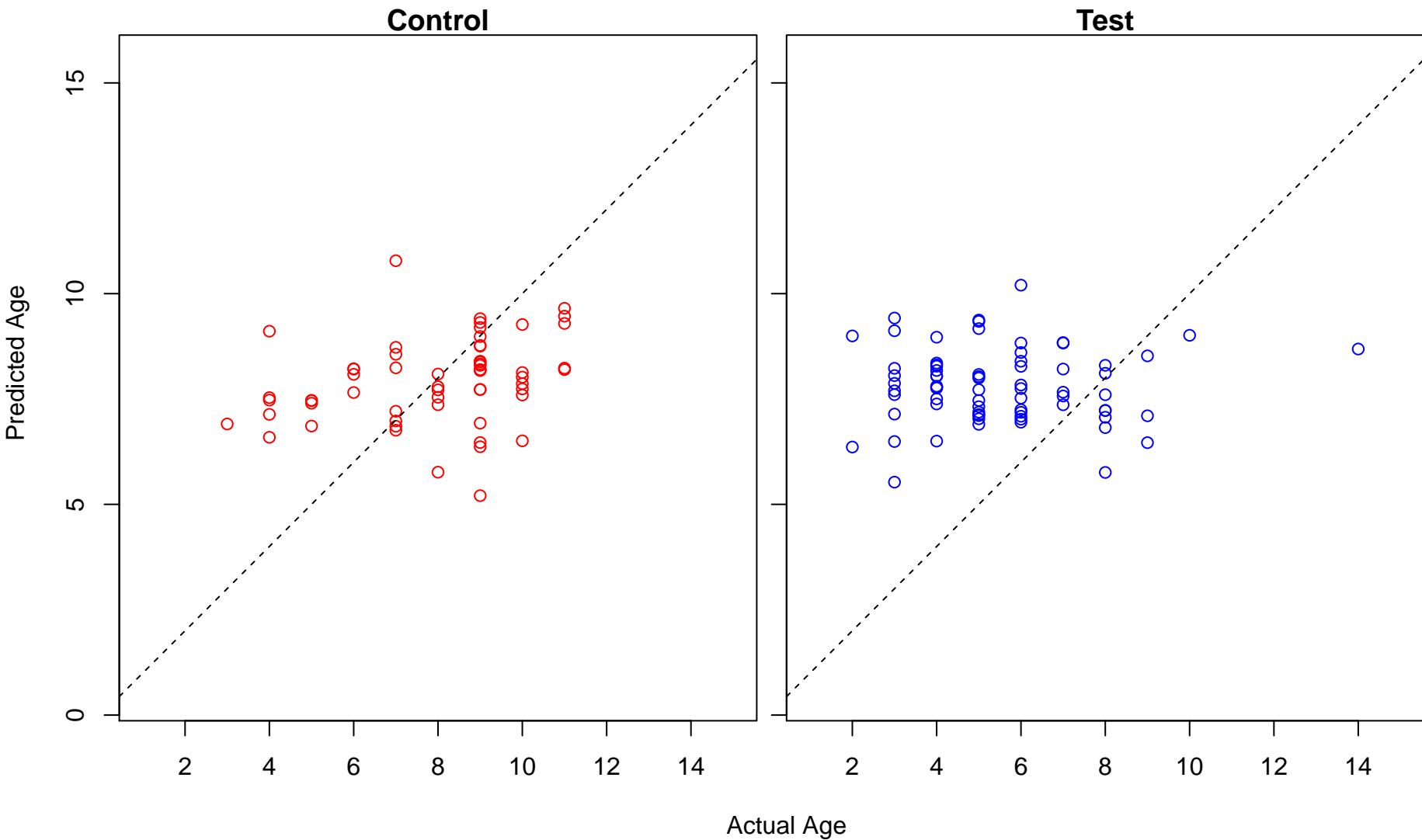
acetylcholine metabolic process (Score: 0.421991)



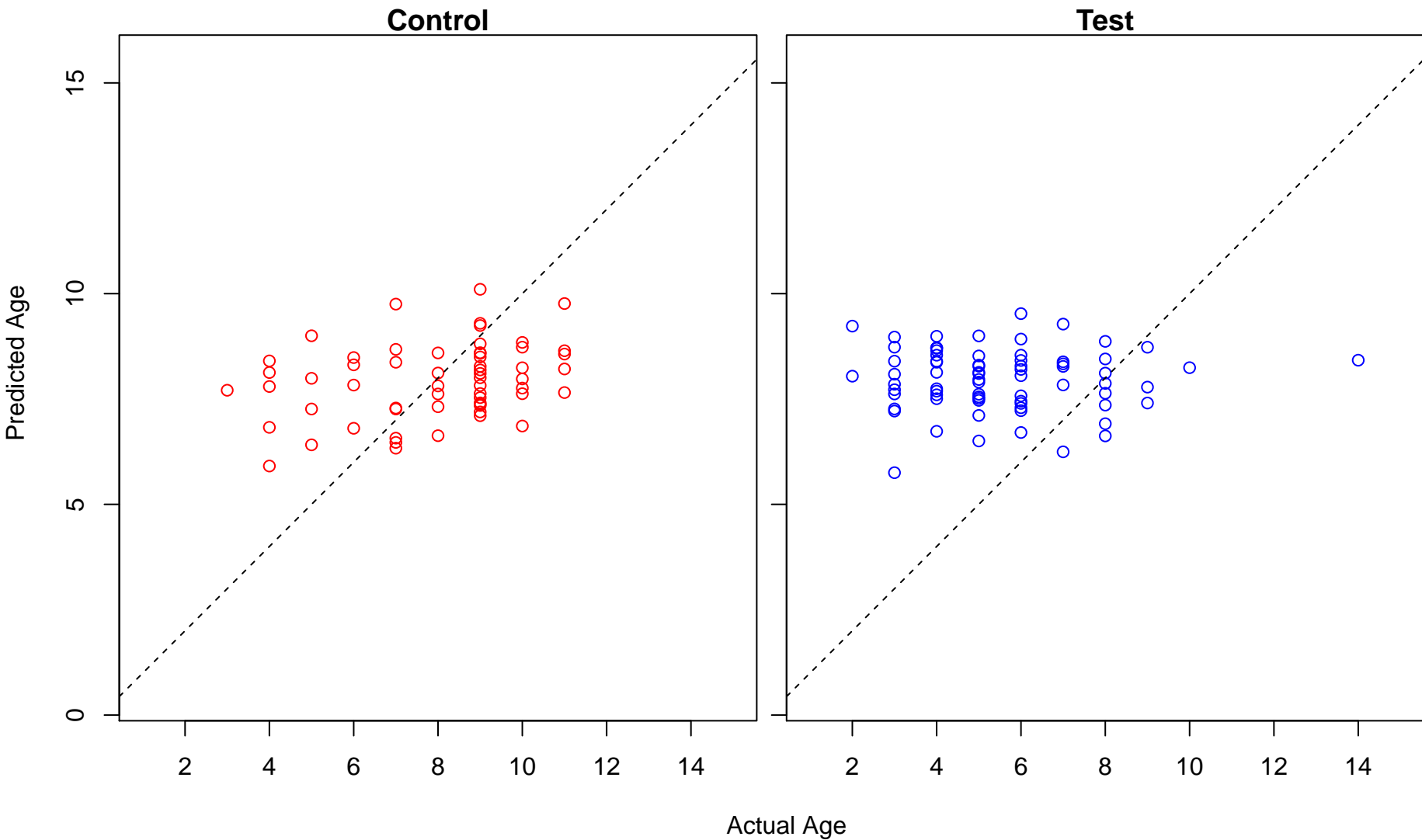
acetate ester metabolic process (Score: 0.421991)



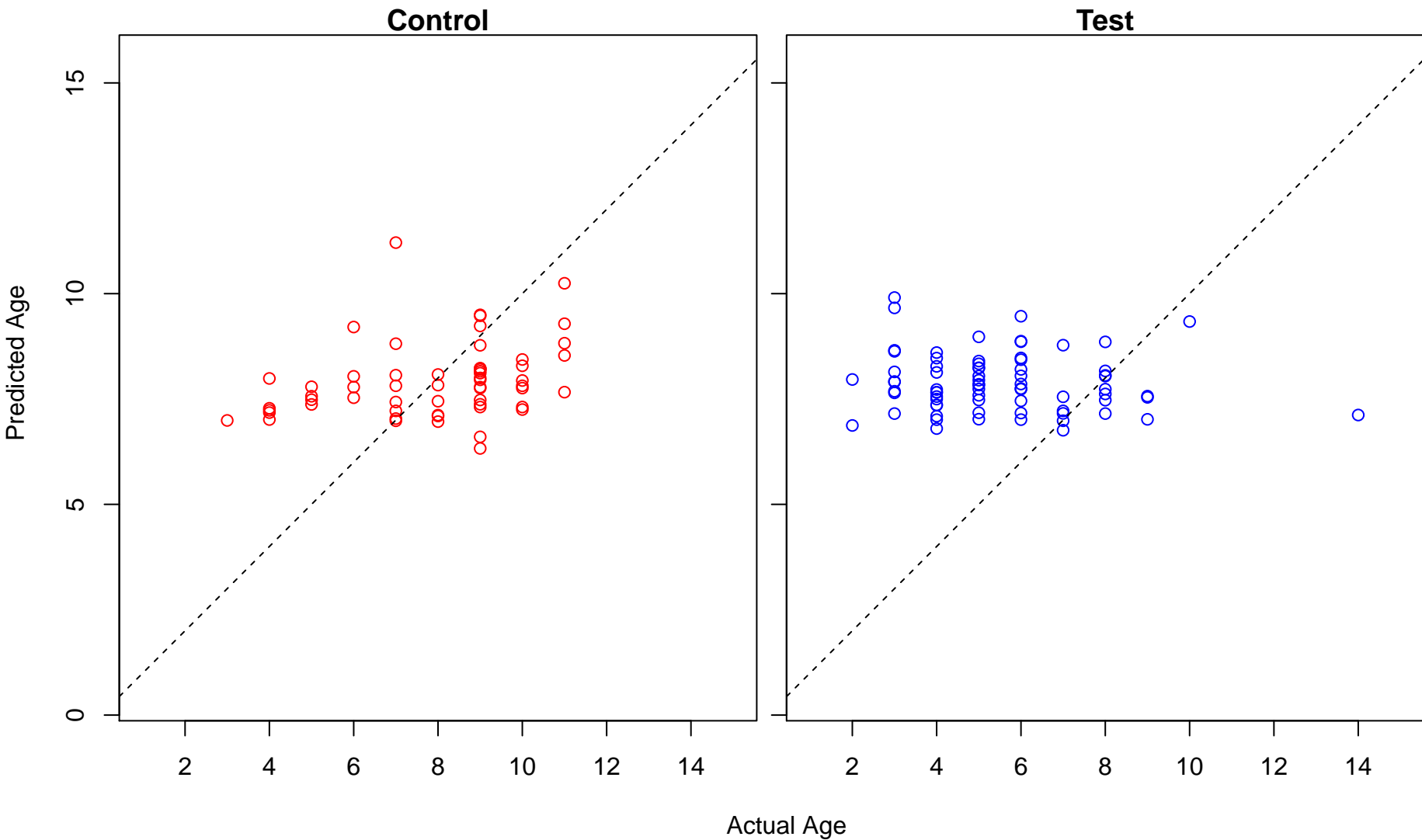
aromatic amino acid transport (Score: 0.421908)



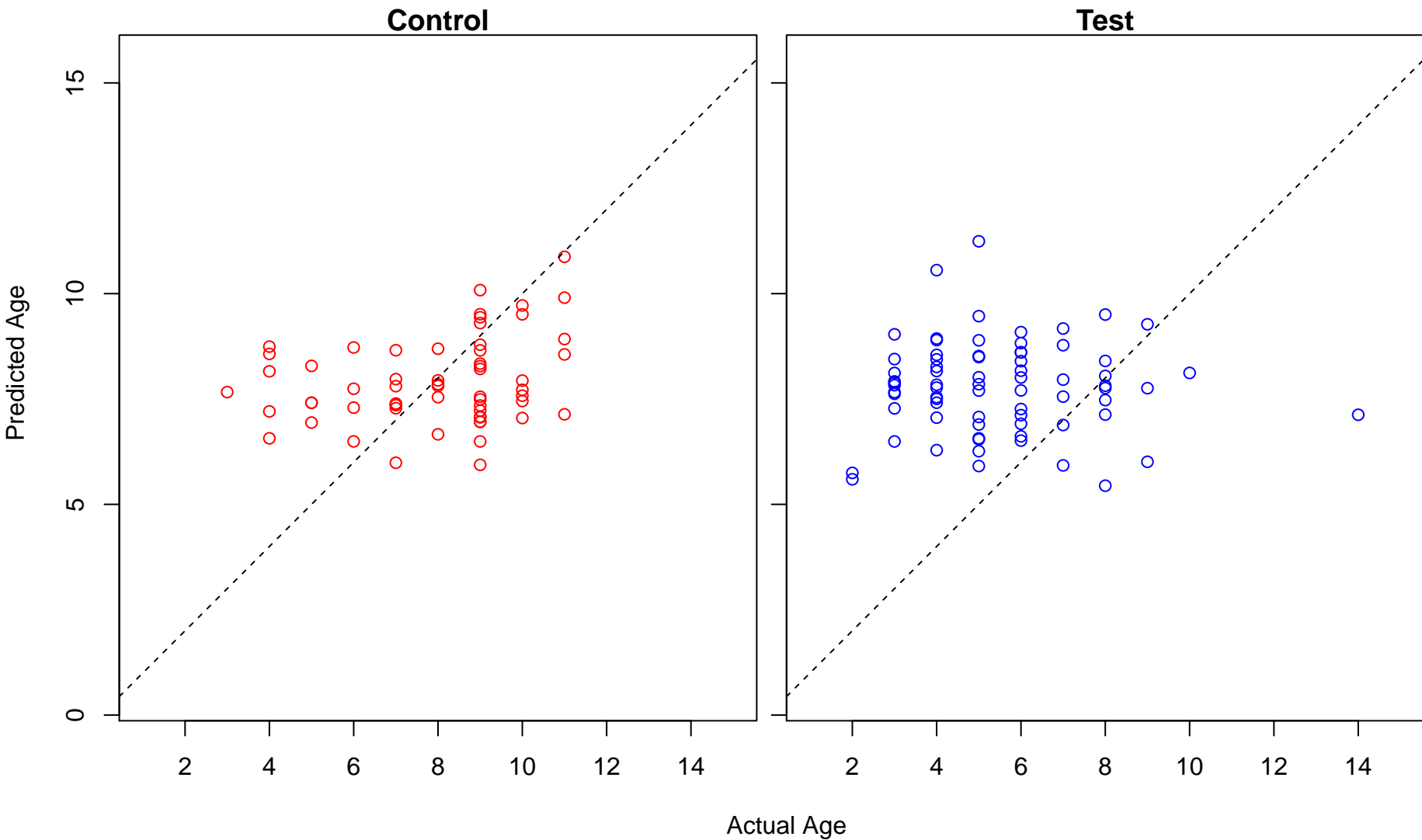
poly(A)+ mRNA export from nucleus (Score: 0.418243)



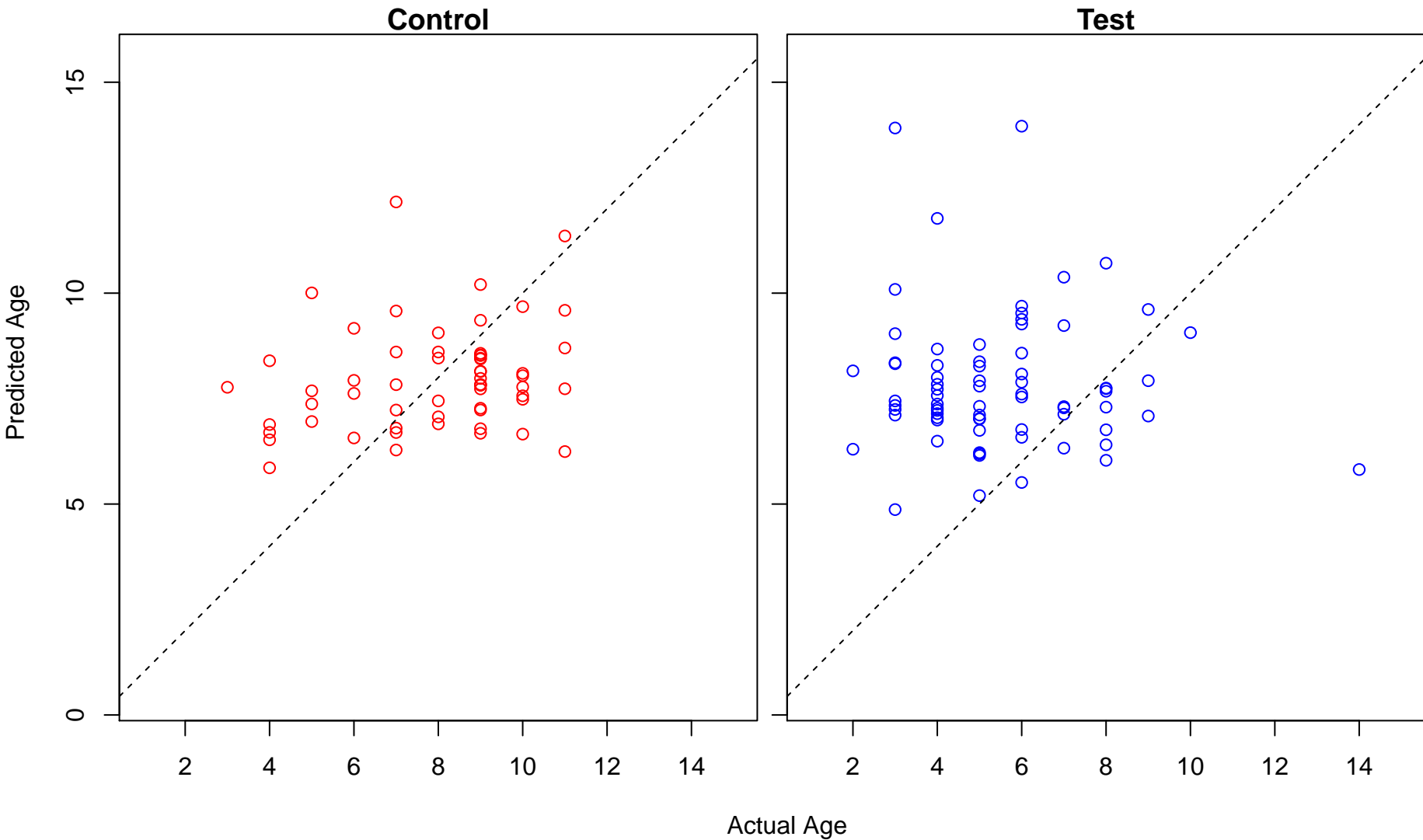
negative regulation of phospholipid biosynthetic process (Score: 0.418219)



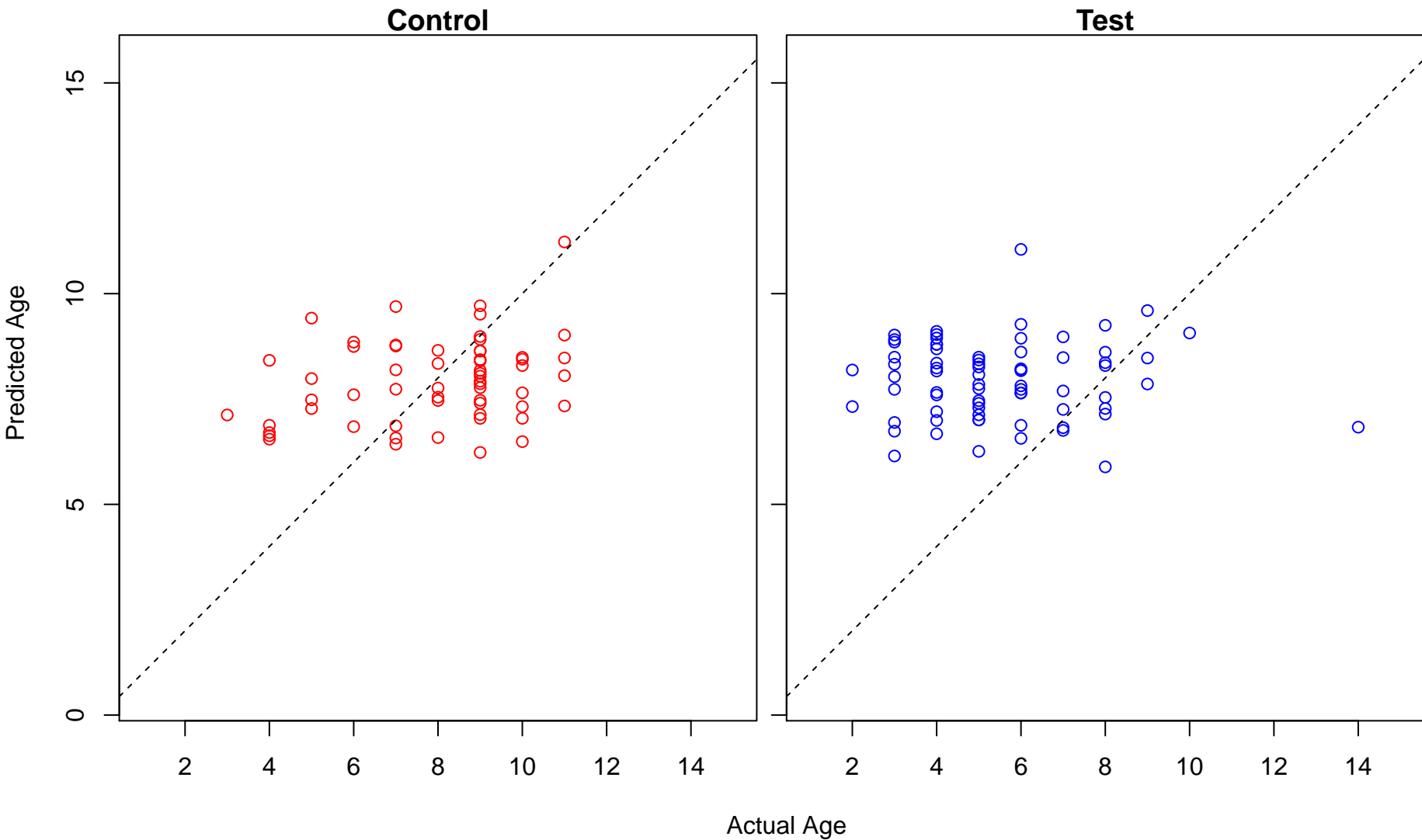
regulation of calcium-transporting ATPase activity (Score: 0.416591)



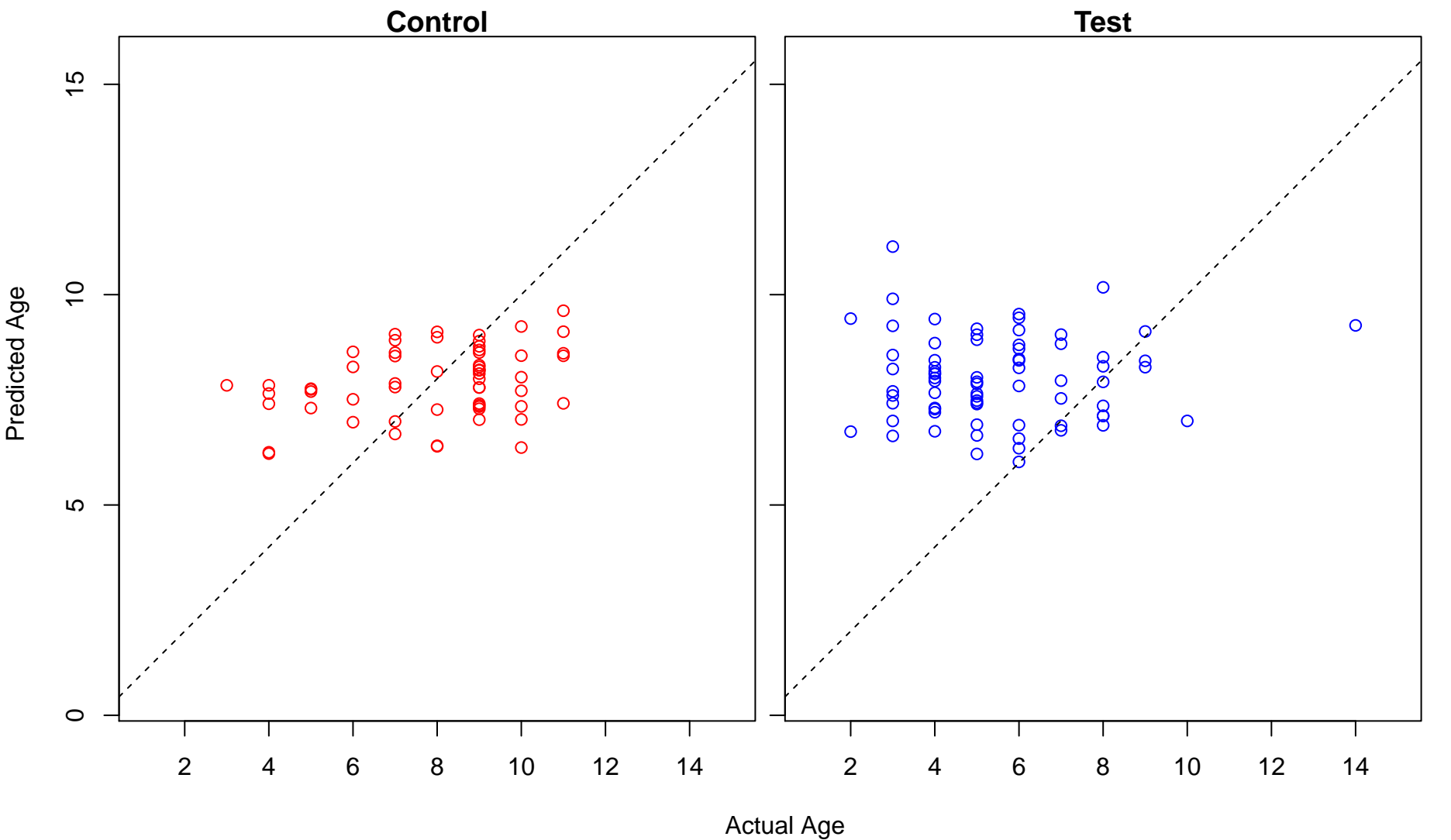
positive regulation of cyclic-nucleotide phosphodiesterase activity (Score: 0.416231)



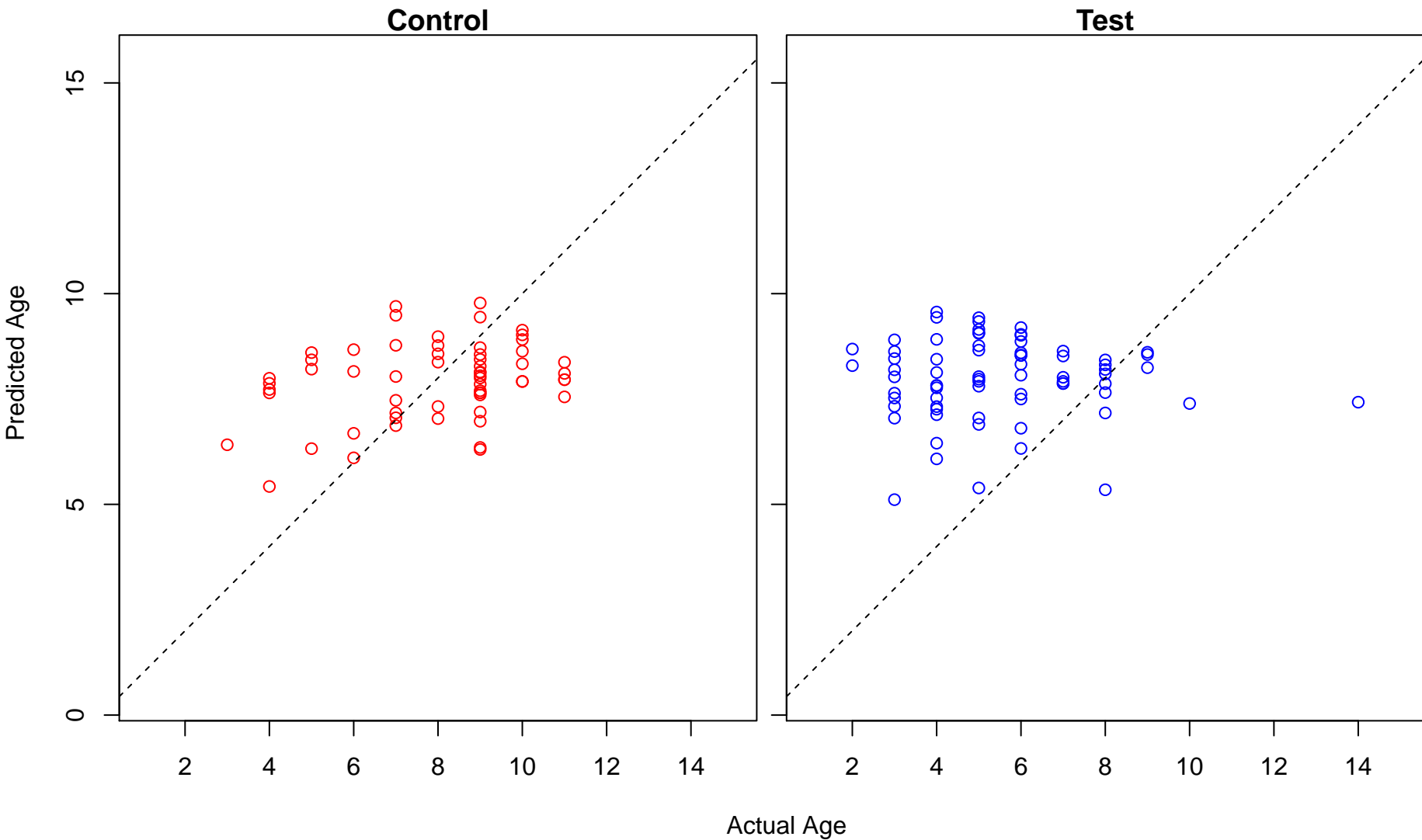
negative regulation of type 2 immune response (Score: 0.416073)



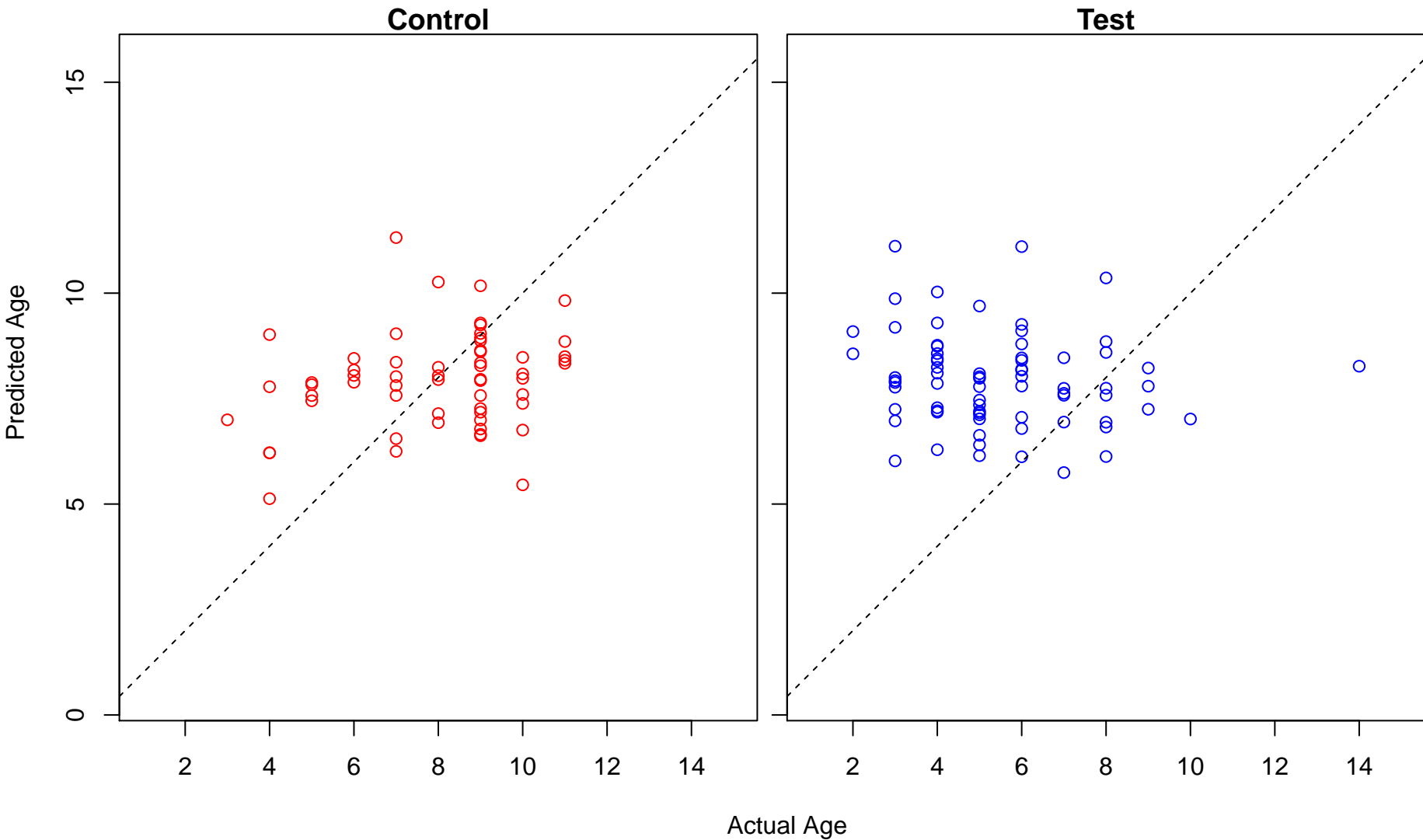
activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell (Sc



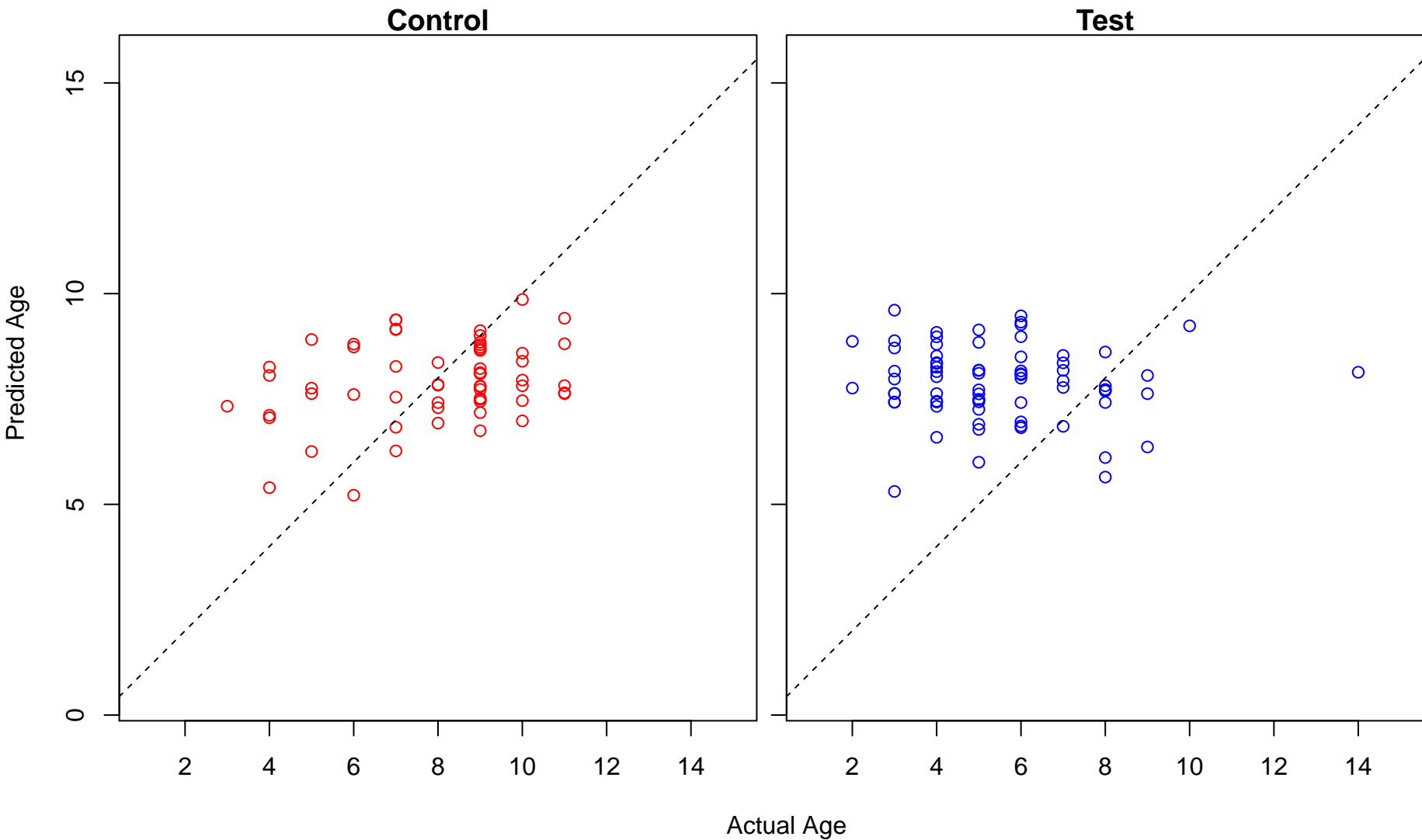
synaptic vesicle to endosome fusion (Score: 0.414883)



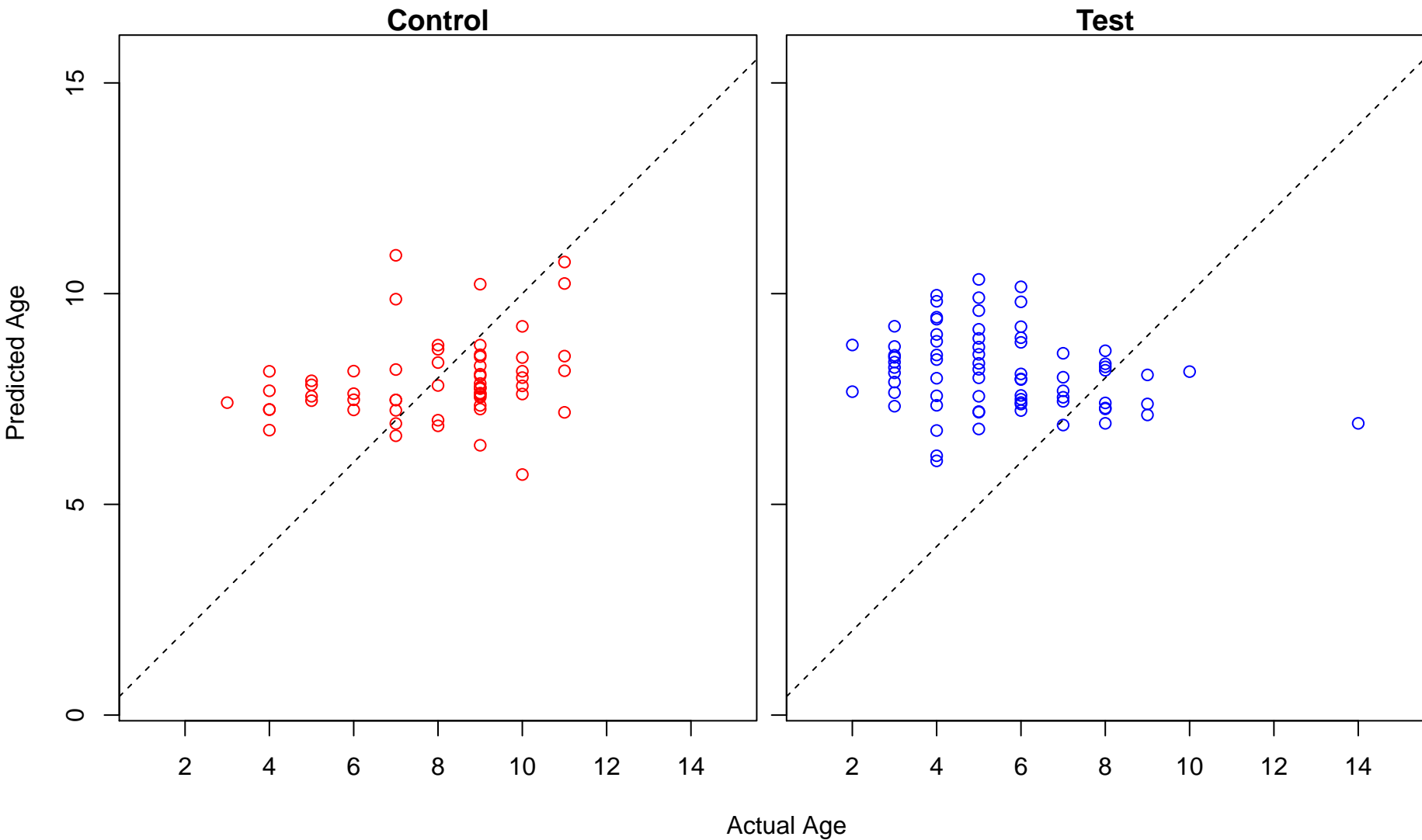
regulation of lamellipodium morphogenesis (Score: 0.414052)



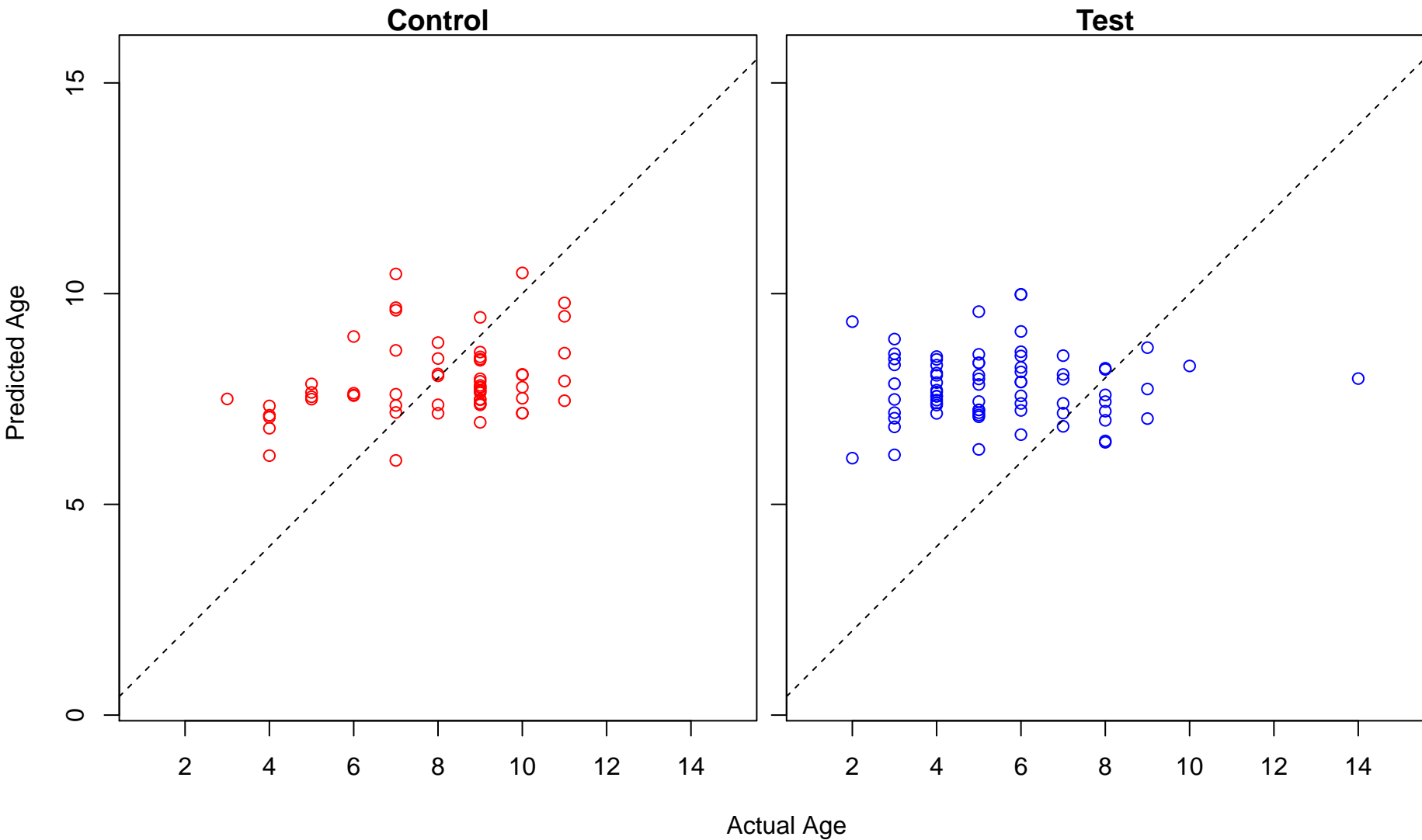
self proteolysis (Score: 0.413394)



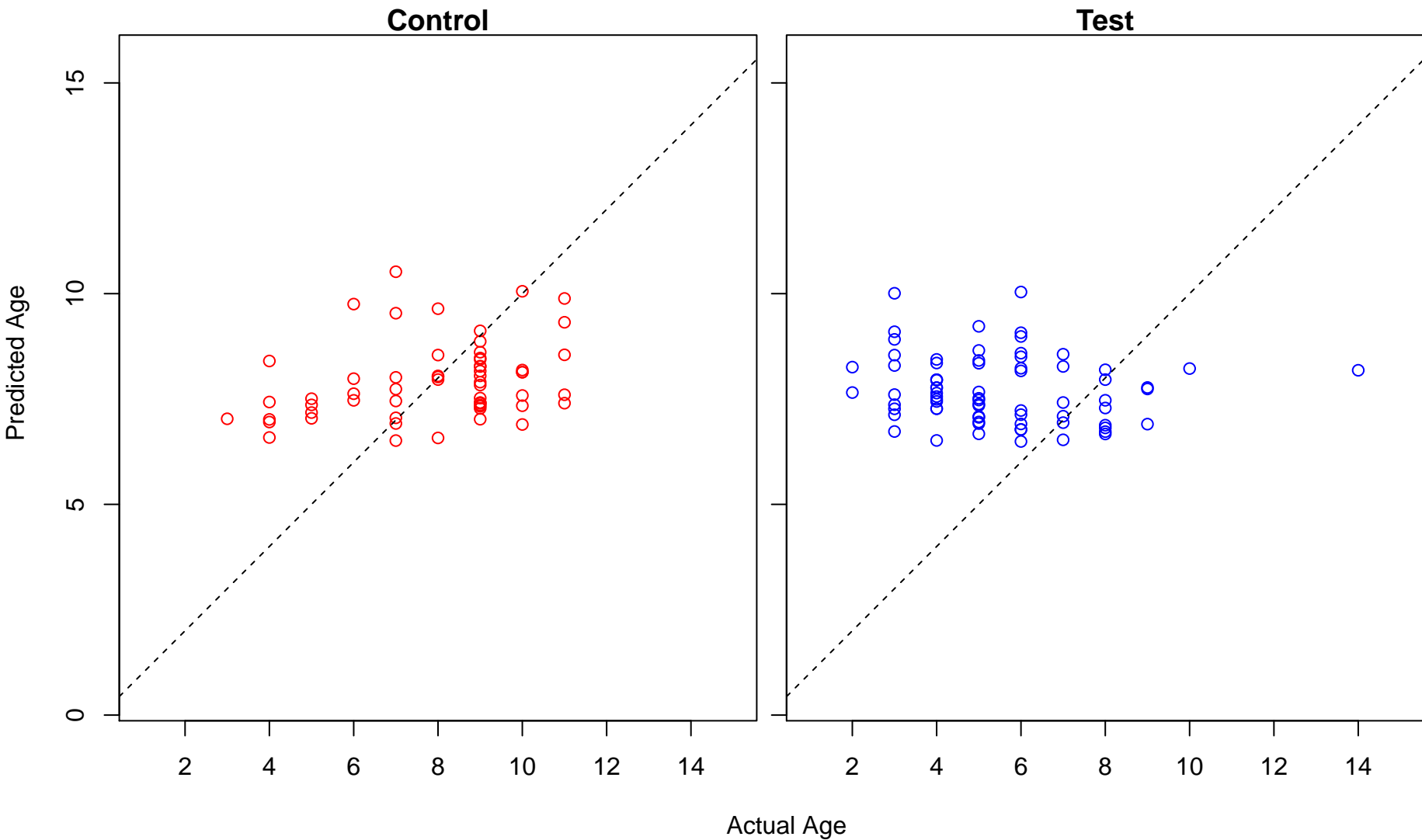
regulation of cilium beat frequency (Score: 0.411994)



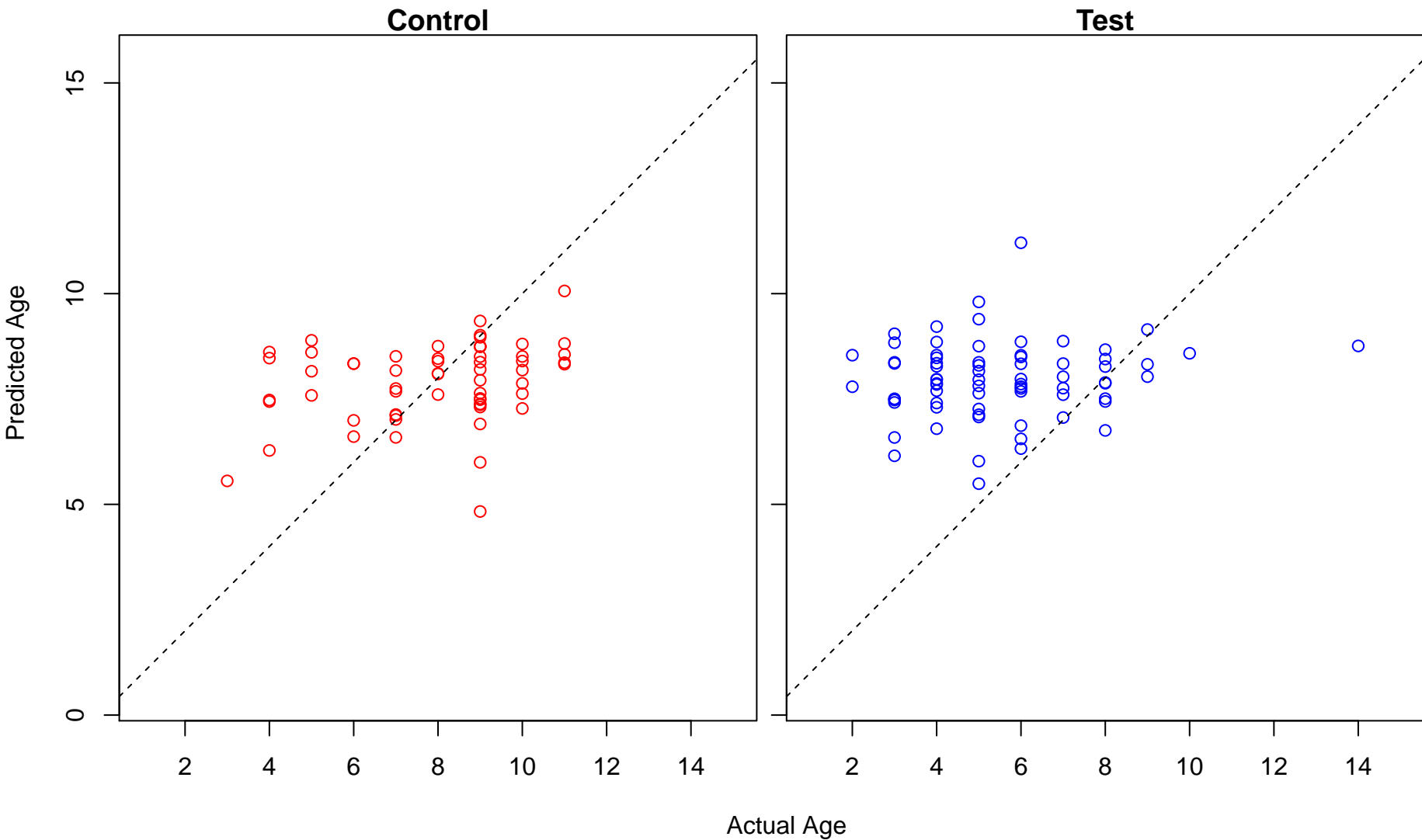
regulation of amine transport (Score: 0.411549)



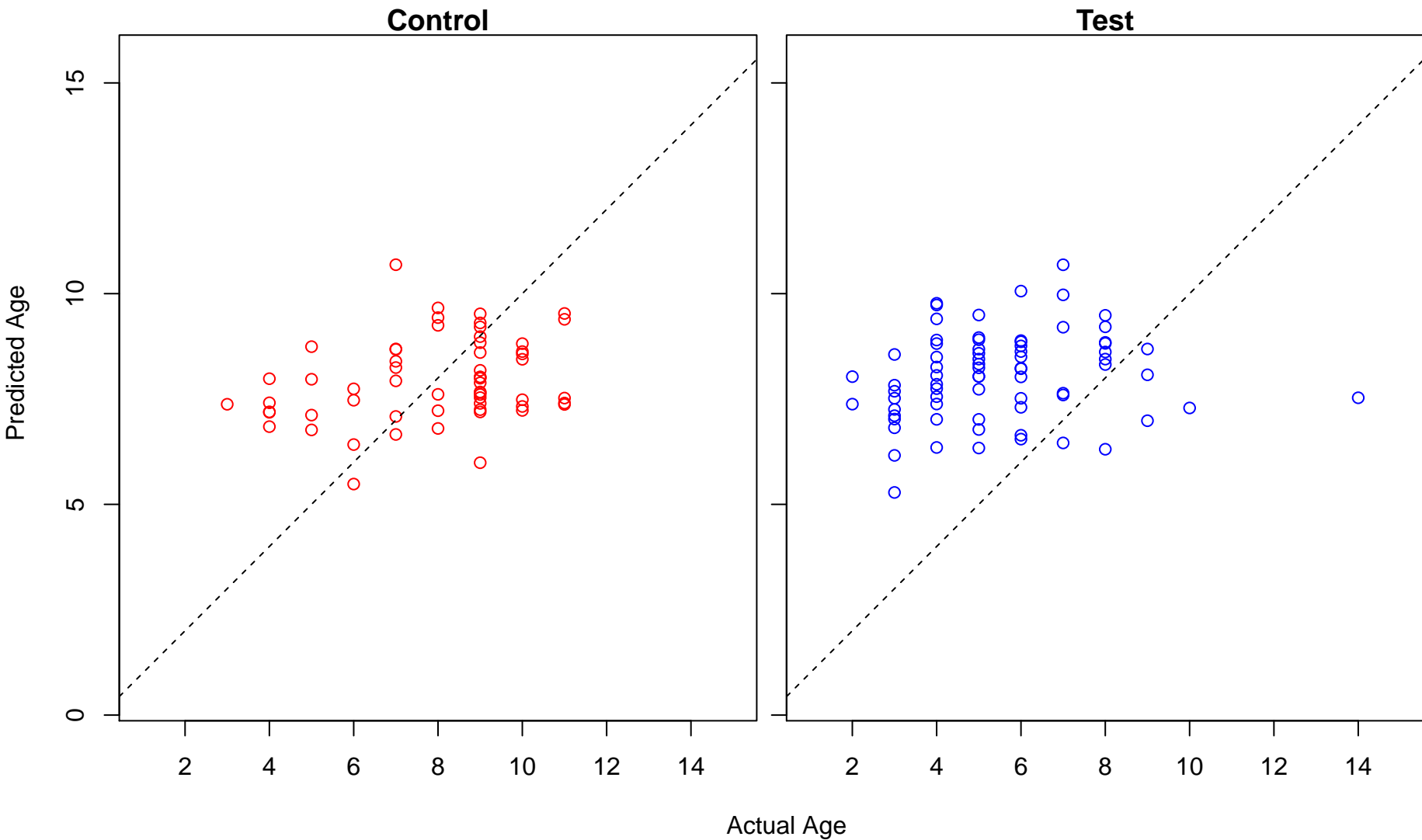
negative regulation of heart contraction (Score: 0.410925)



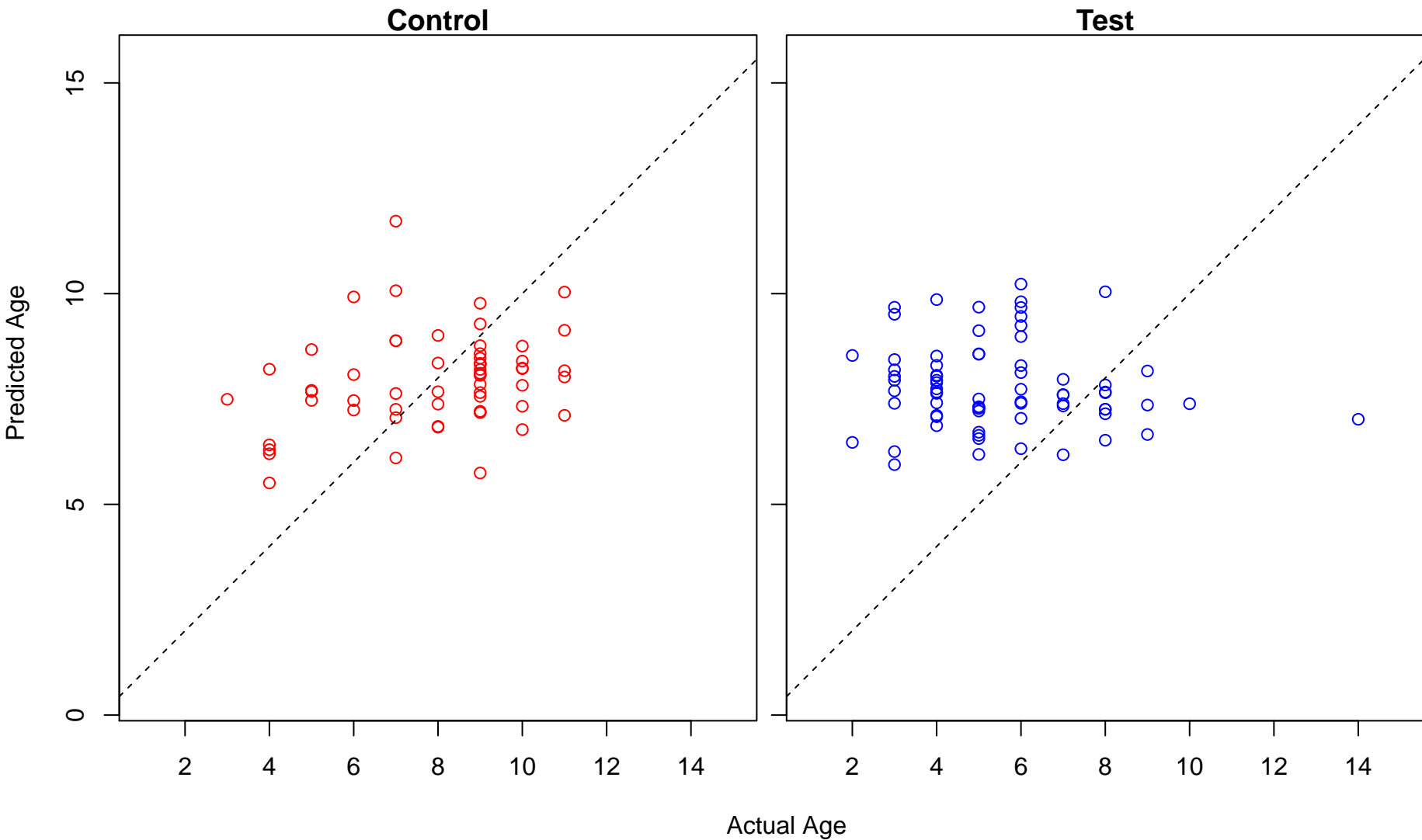
phosphatidylethanolamine catabolic process (Score: 0.409184)



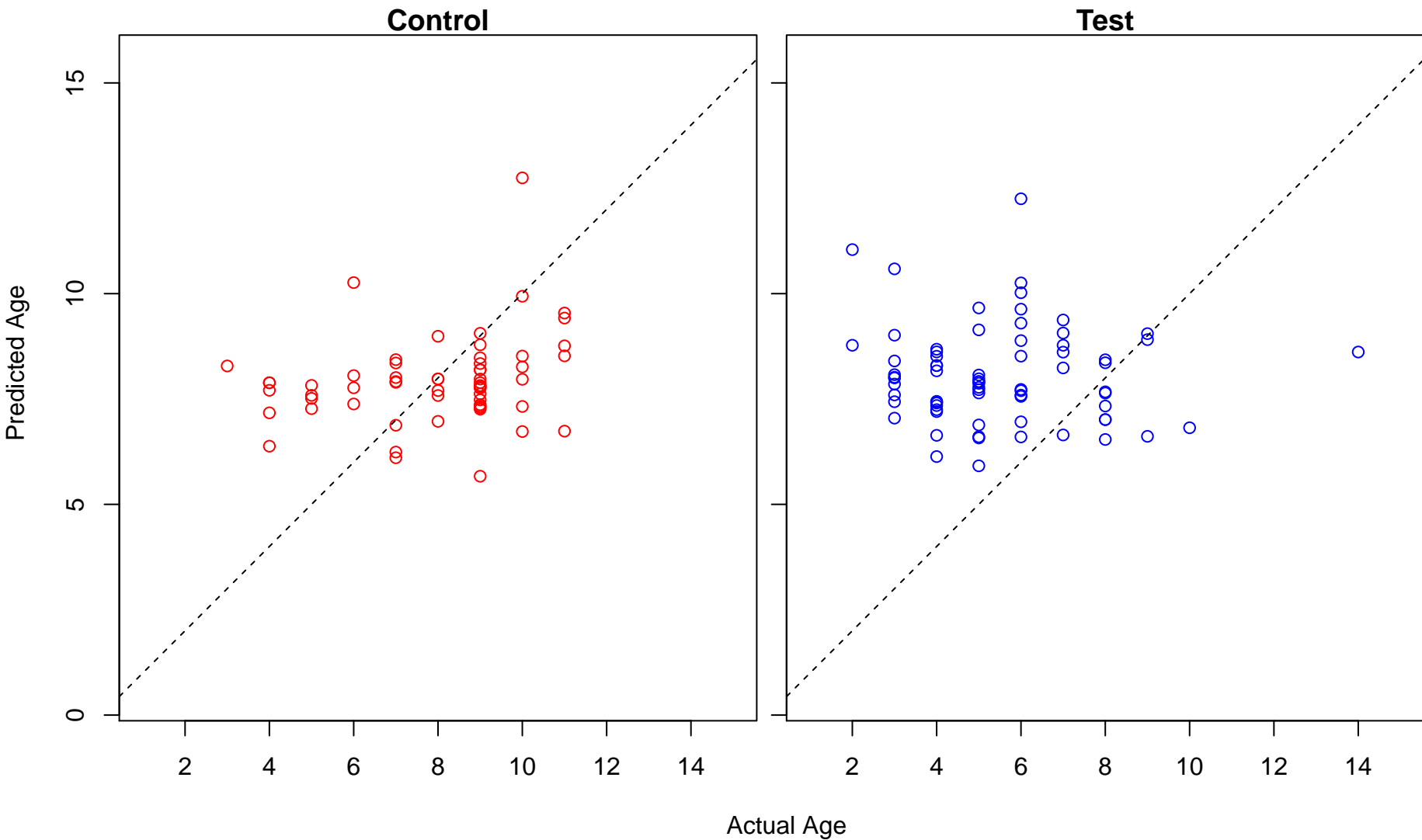
positive regulation of lipopolysaccharide-mediated signaling pathway (Score: 0.409173)



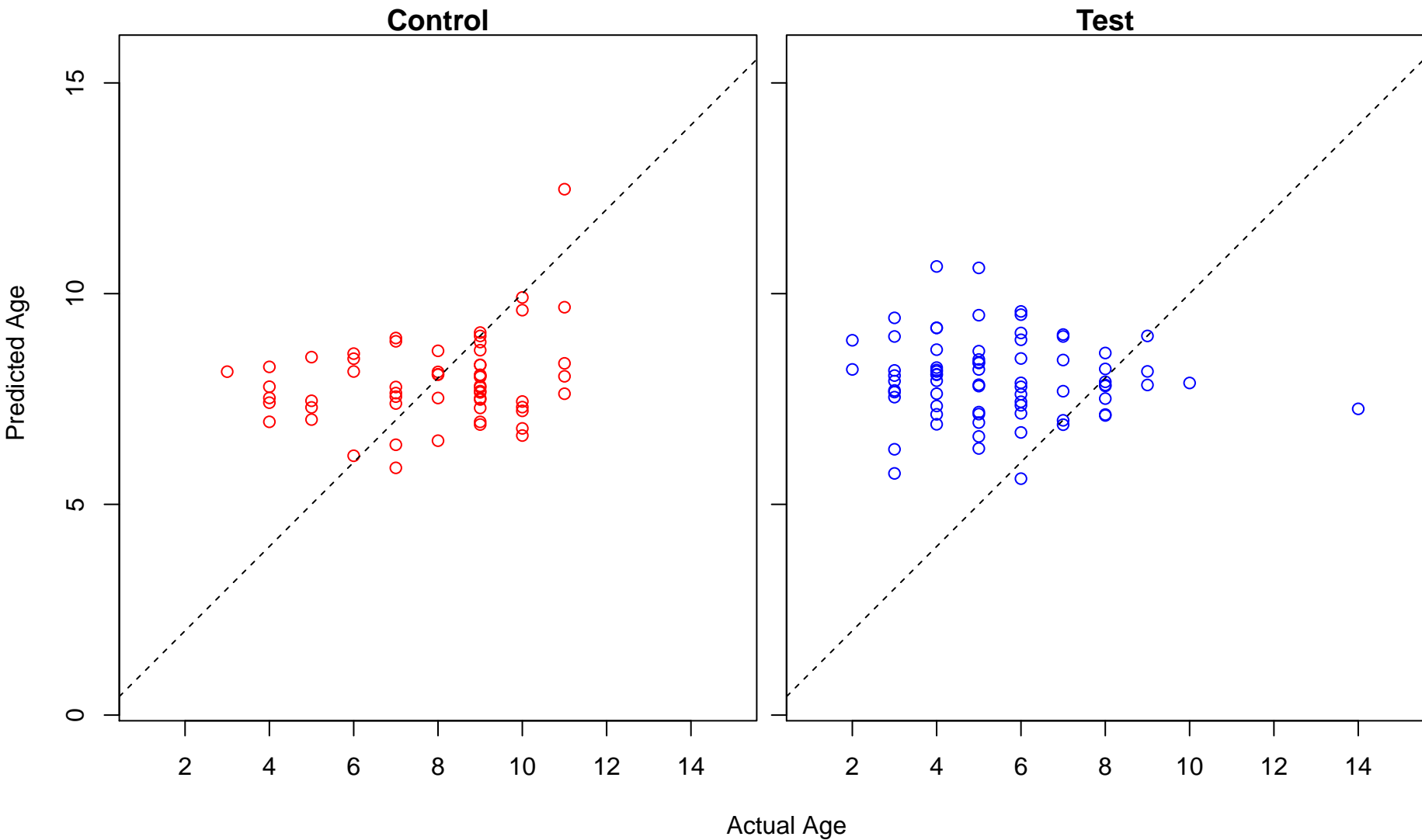
negative regulation of axonogenesis (Score: 0.408753)



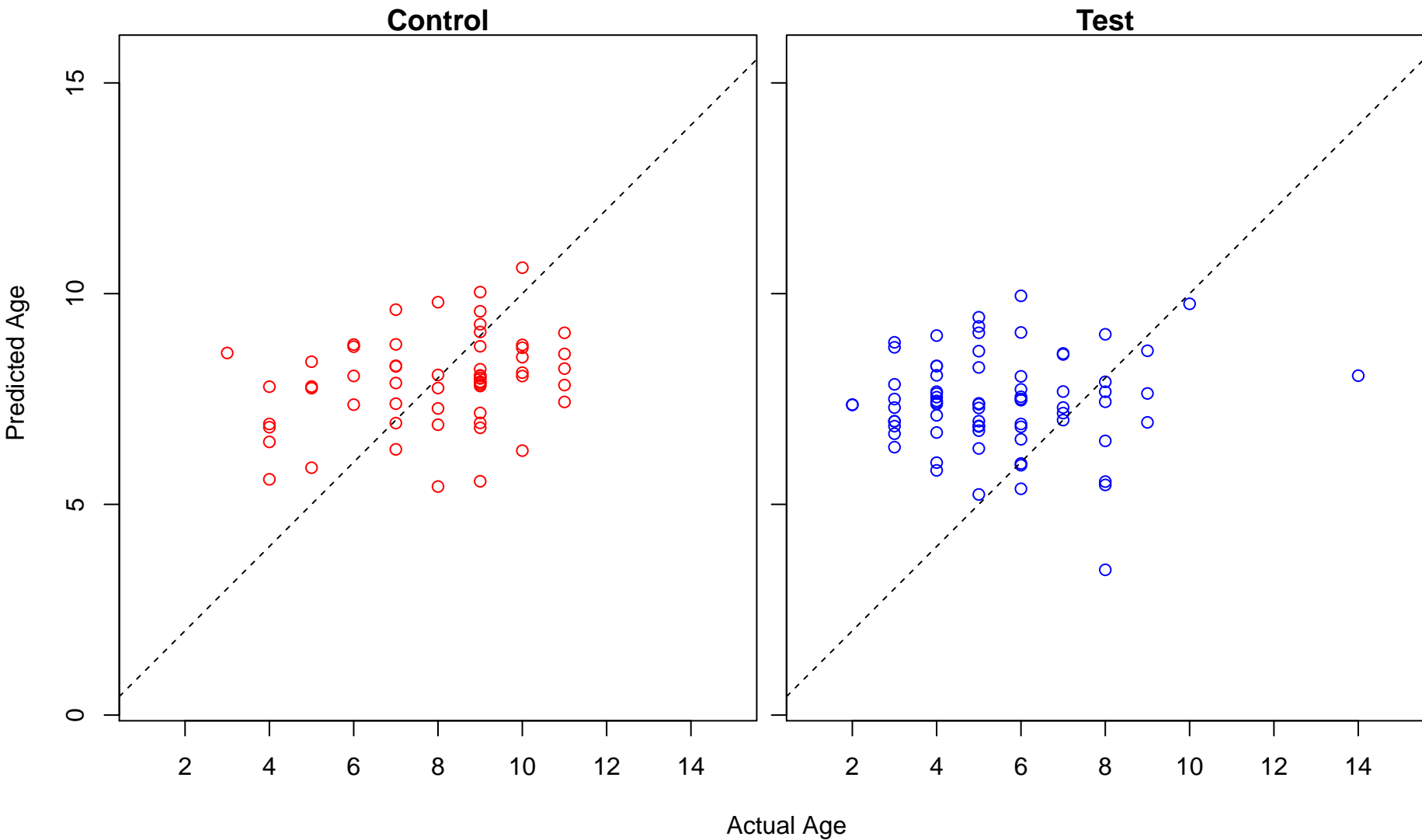
toxin transport (Score: 0.406301)



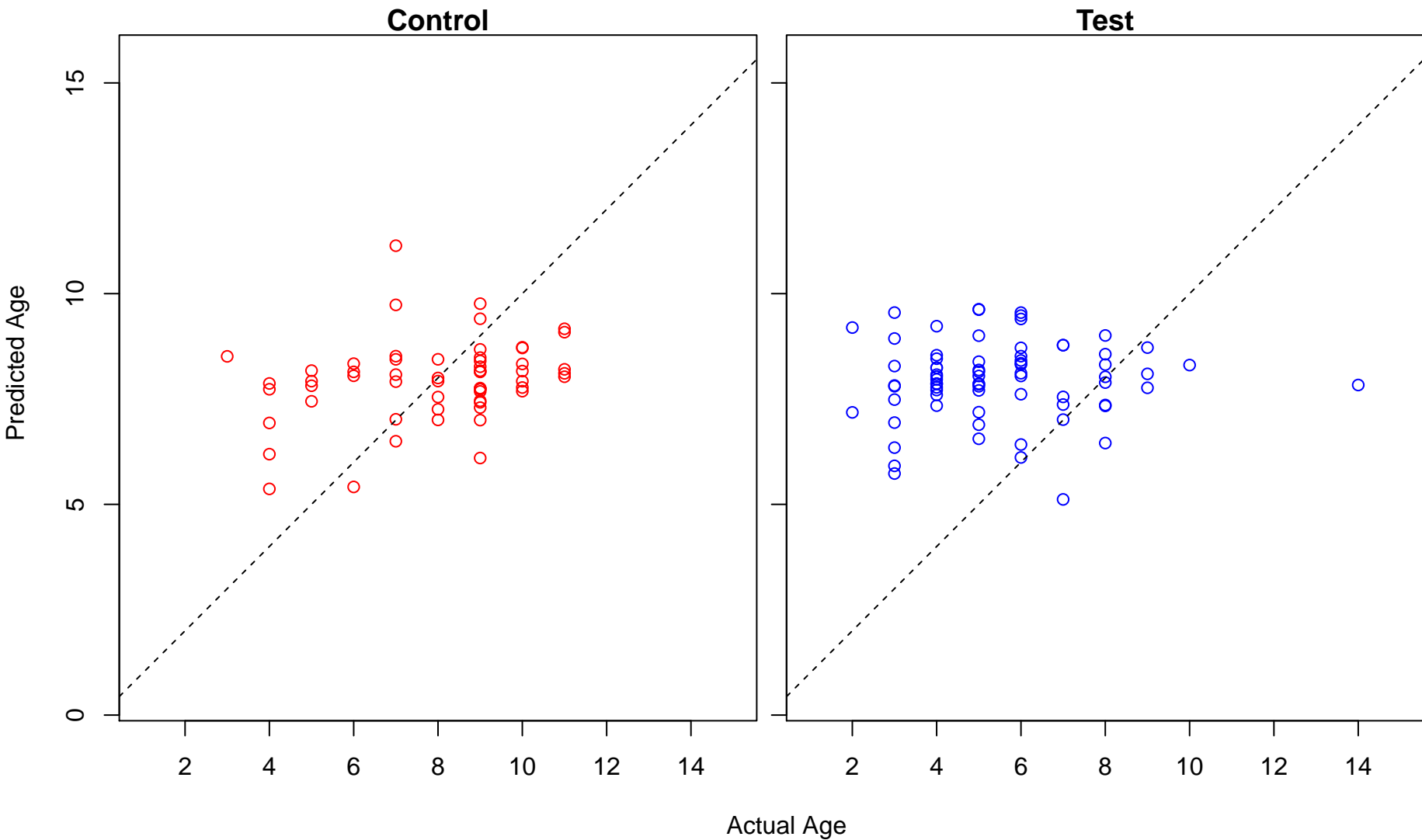
regulation of vitamin D receptor signaling pathway (Score: 0.405815)



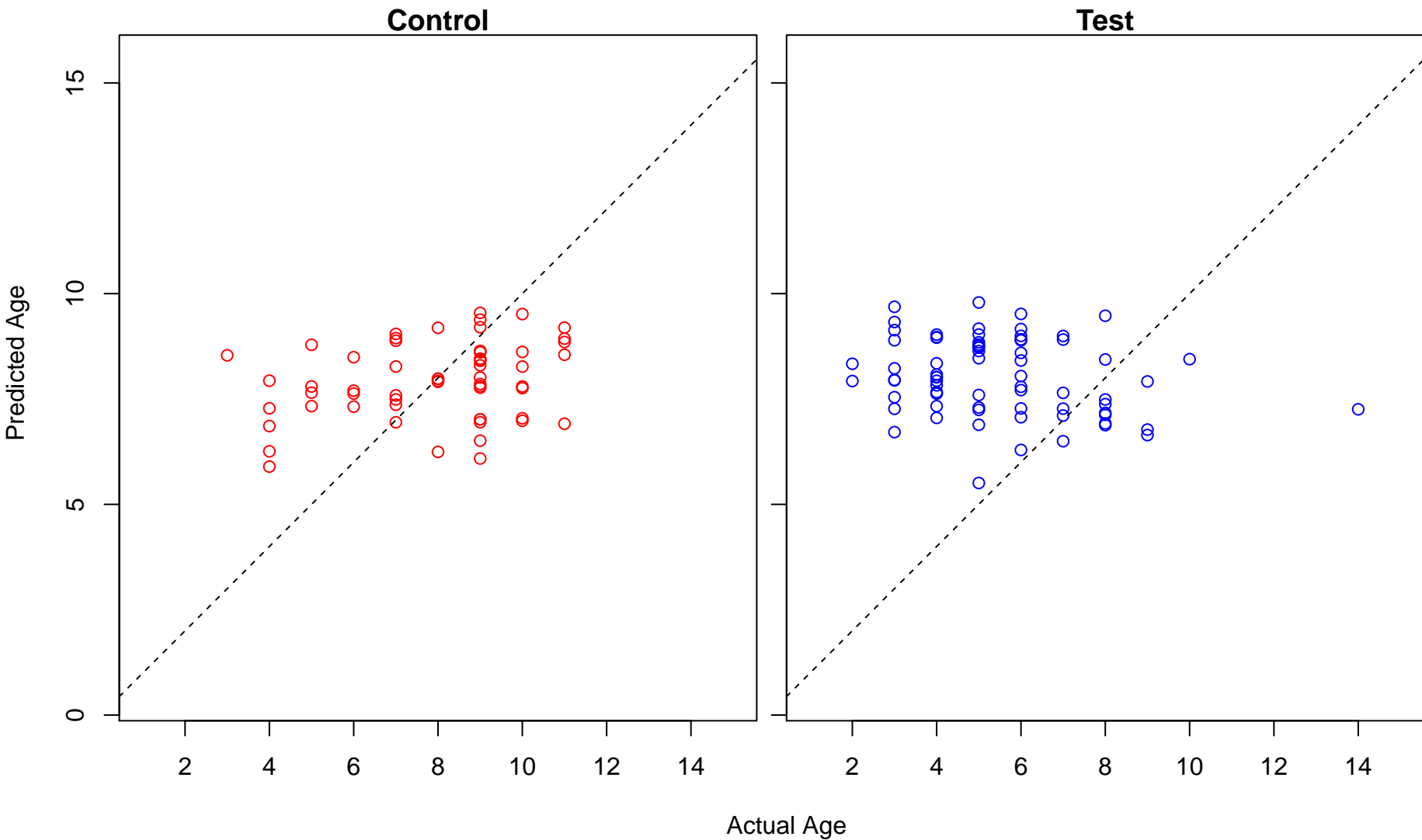
positive regulation of vascular endothelial growth factor signaling pathway (Score: 0.405490)



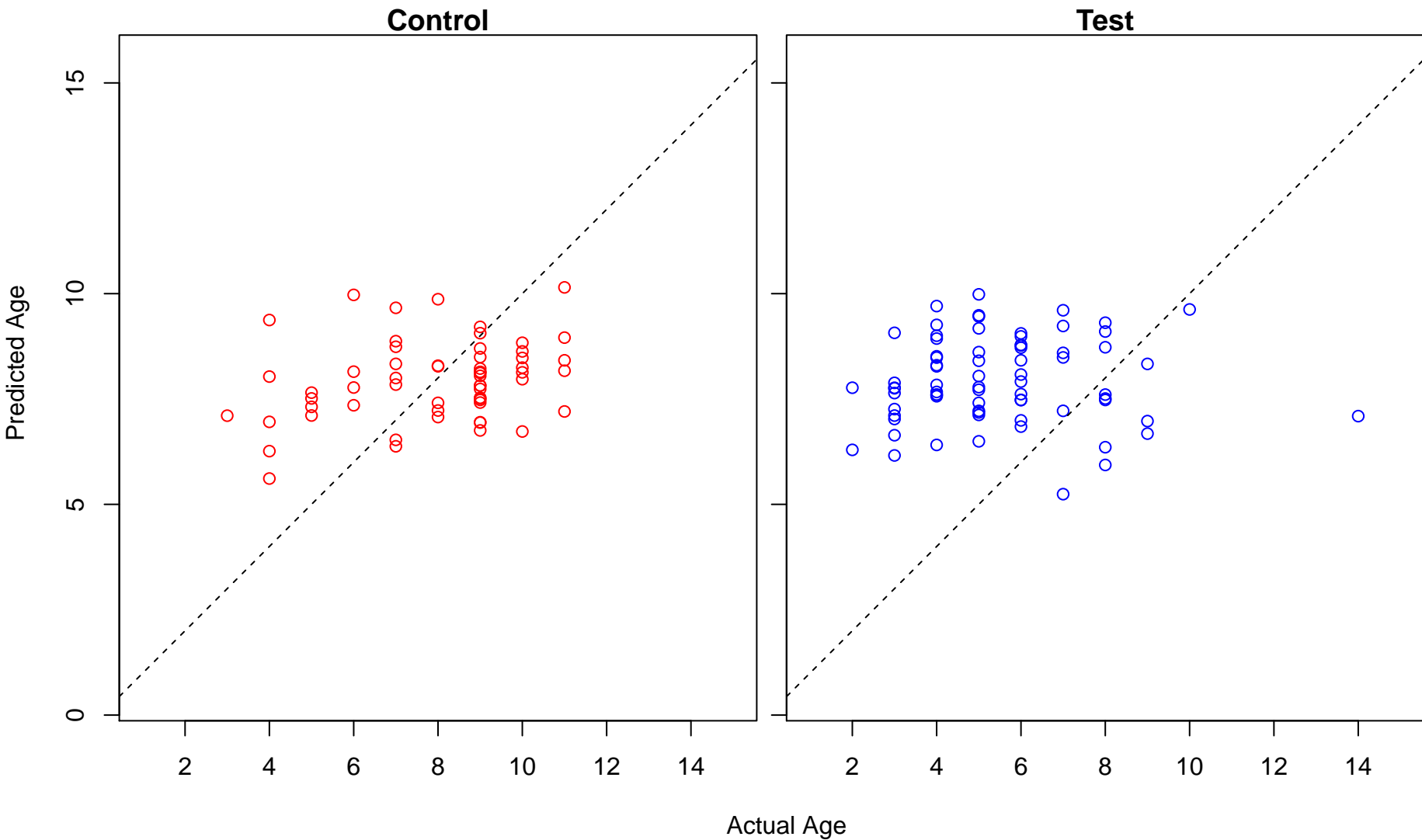
UDP-glucuronate metabolic process (Score: 0.405118)



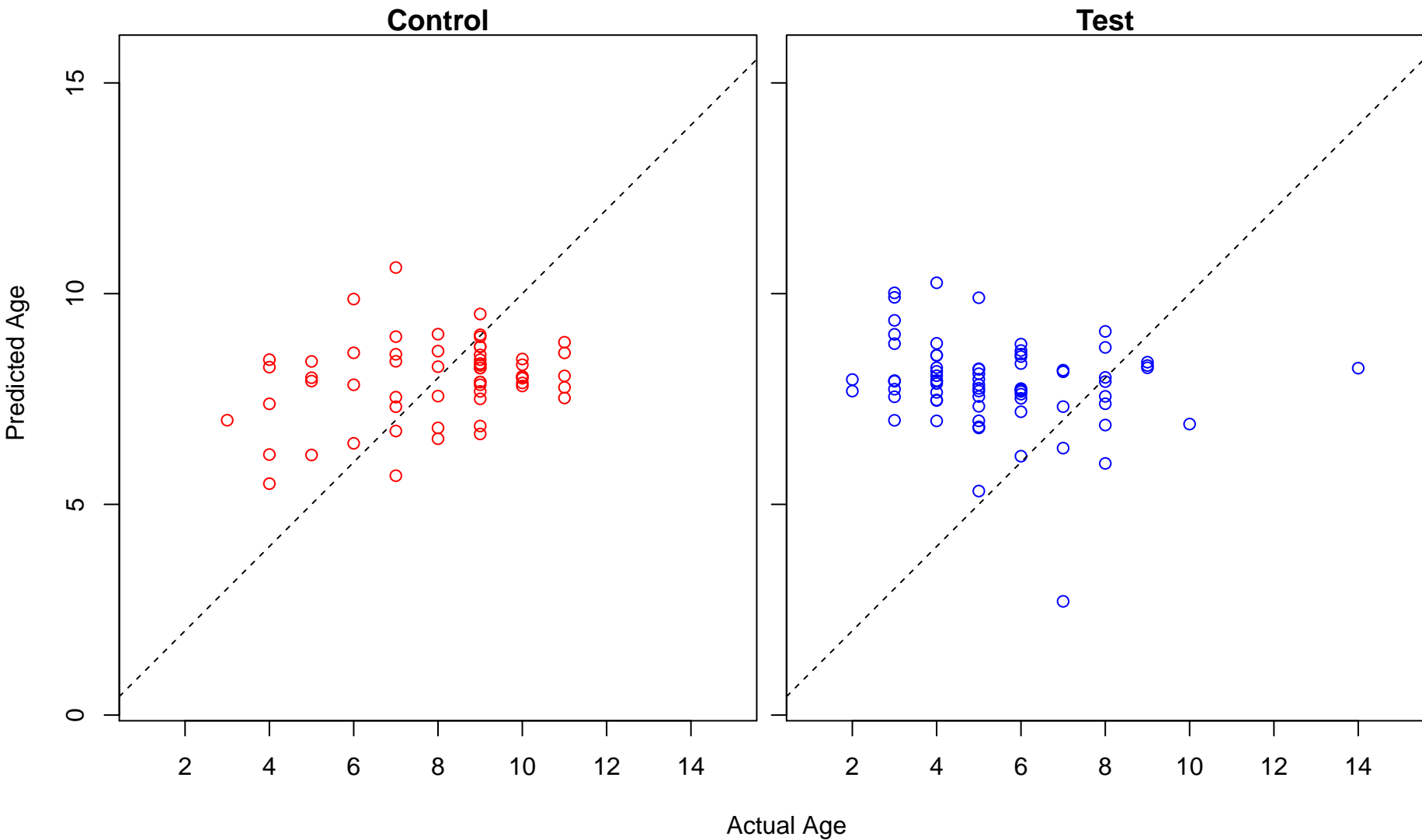
positive regulation of trophoblast cell migration (Score: 0.403298)



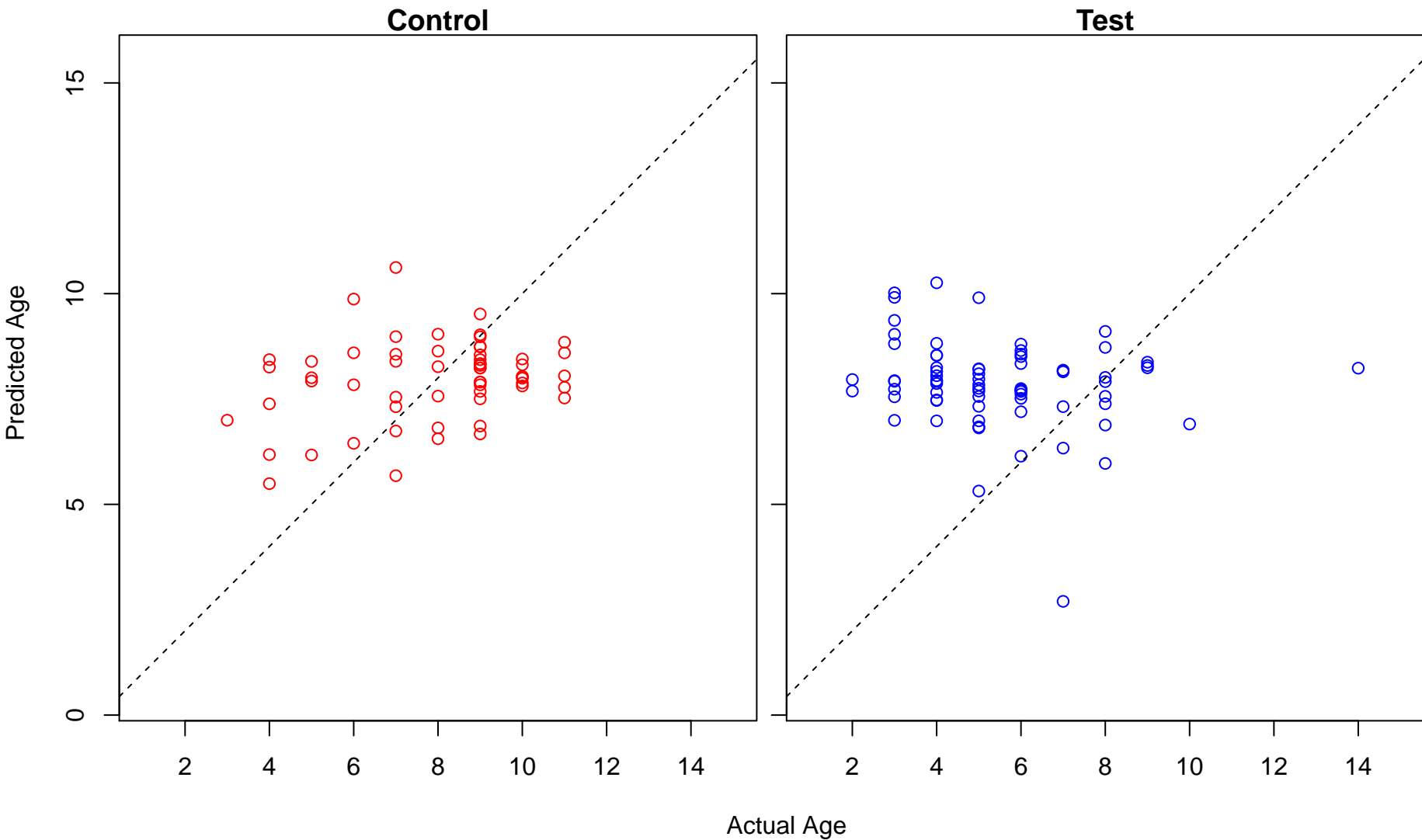
positive regulation of cell size (Score: 0.402698)



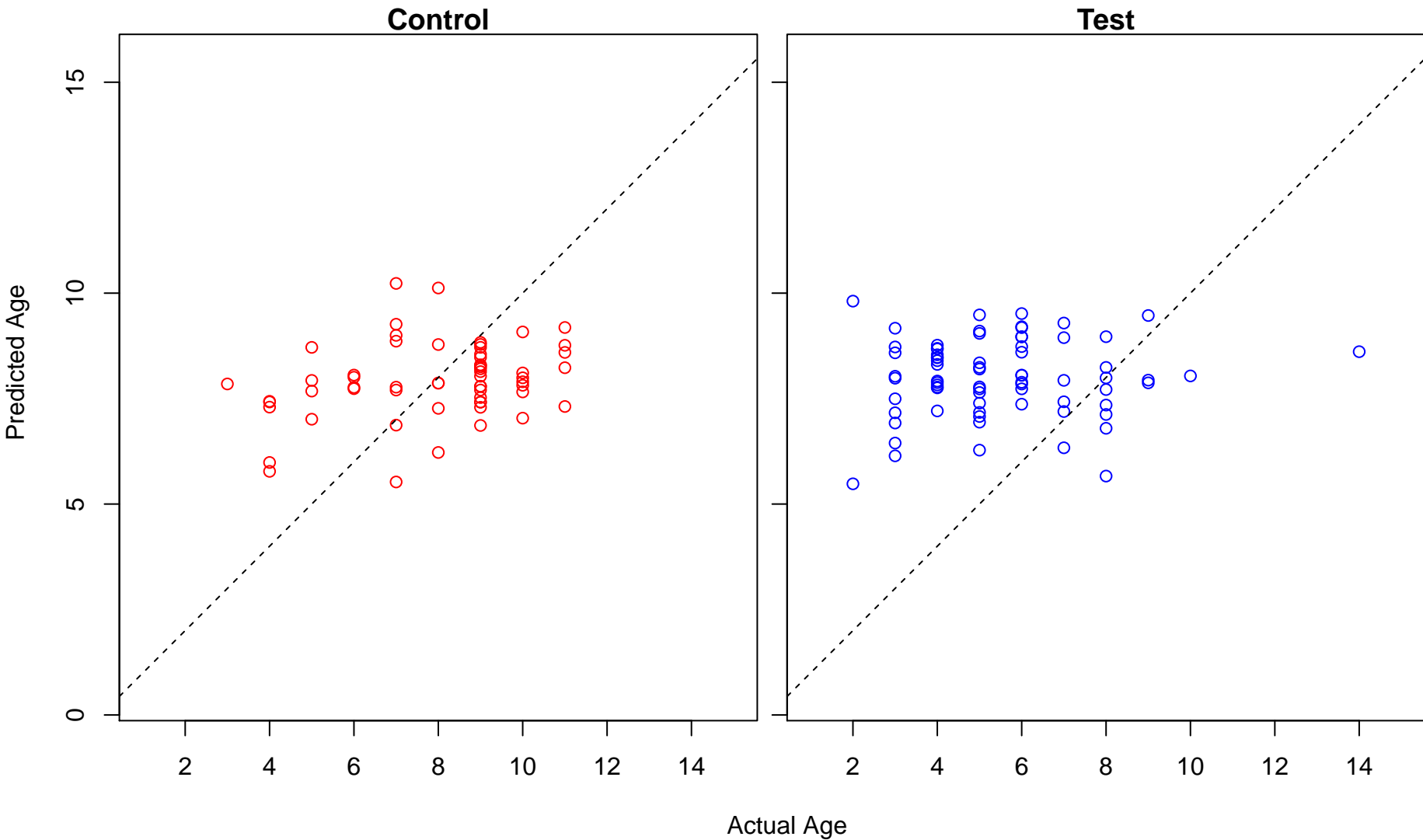
lysine metabolic process (Score: 0.402063)



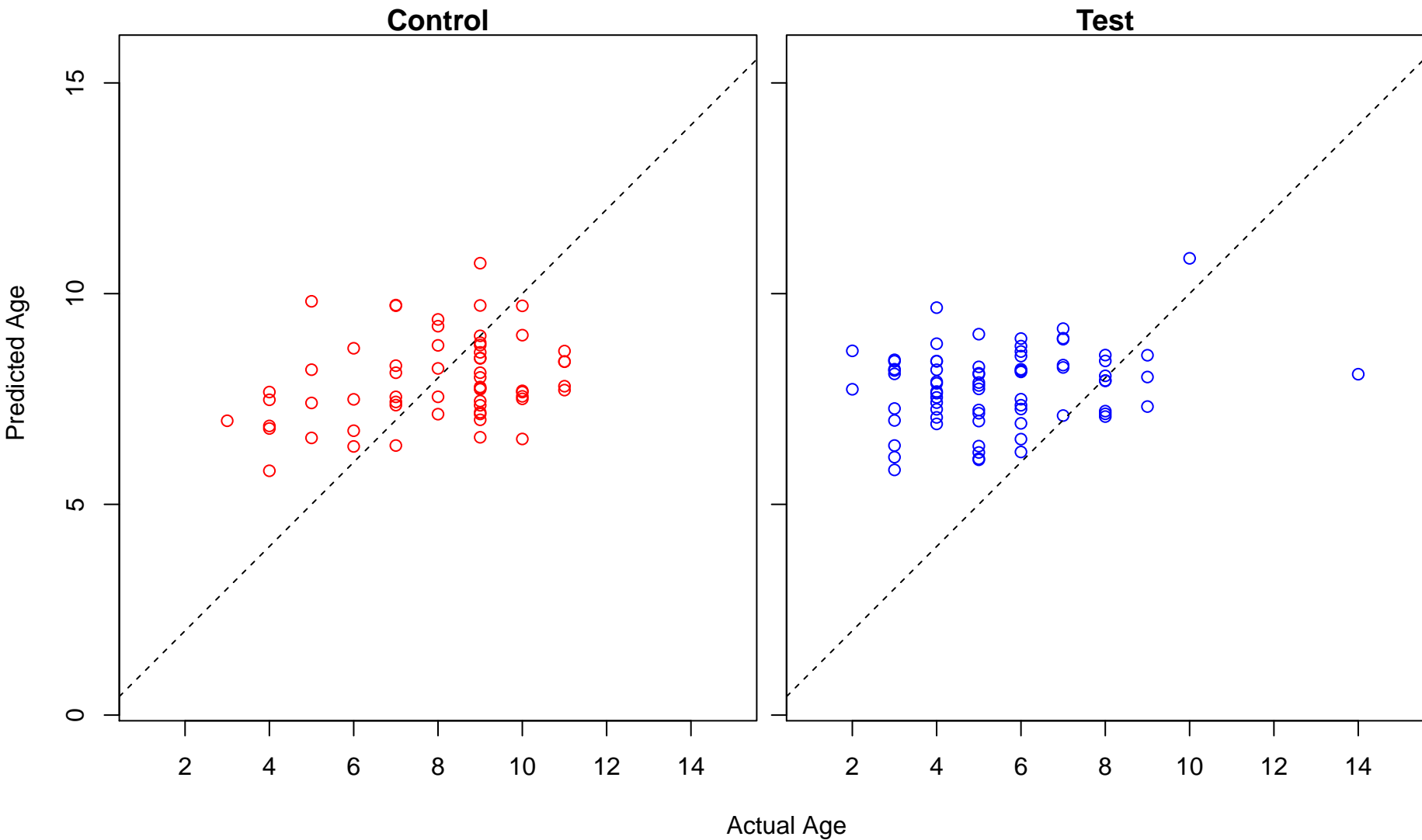
lysine catabolic process (Score: 0.402063)



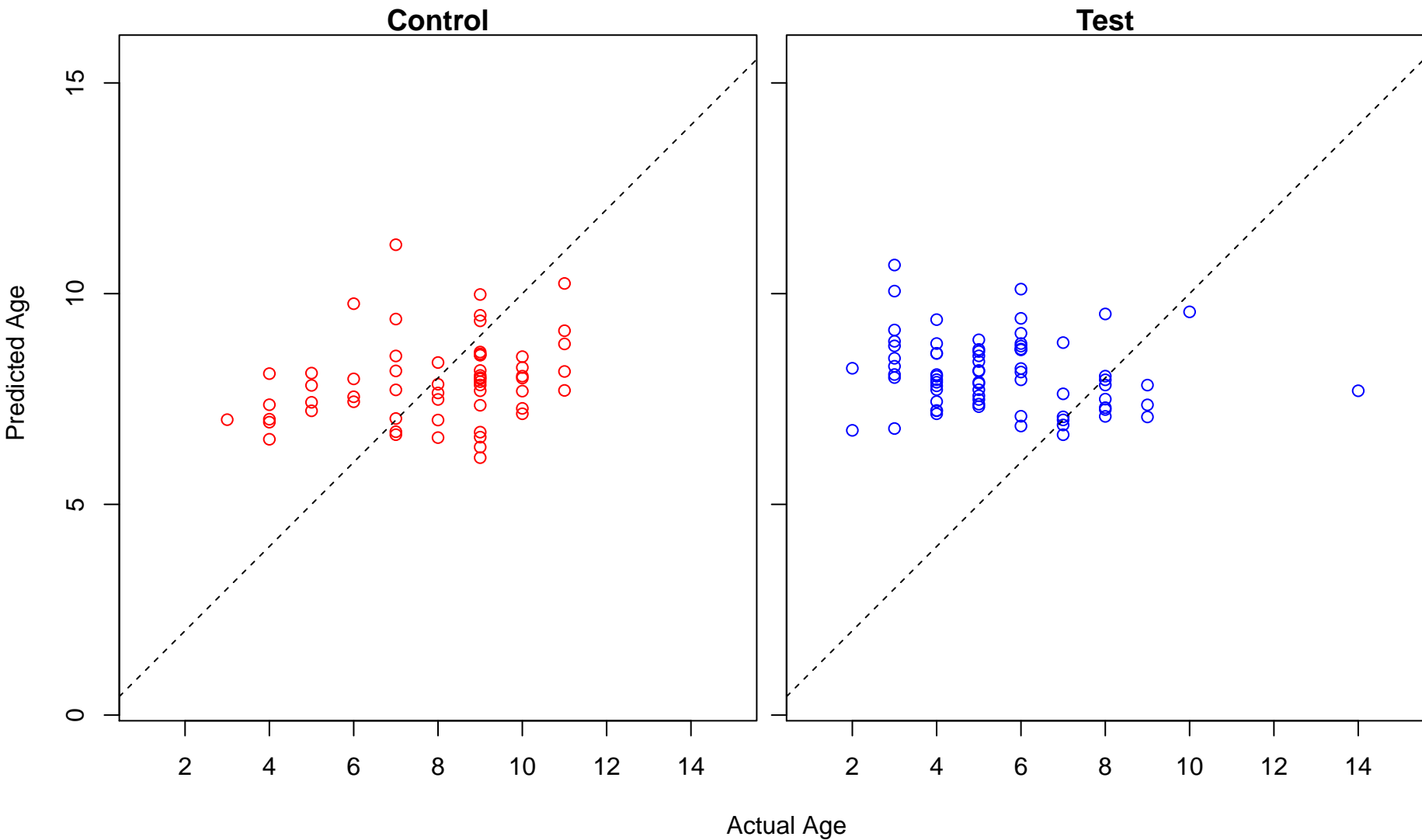
regulation of lipoprotein metabolic process (Score: 0.401866)



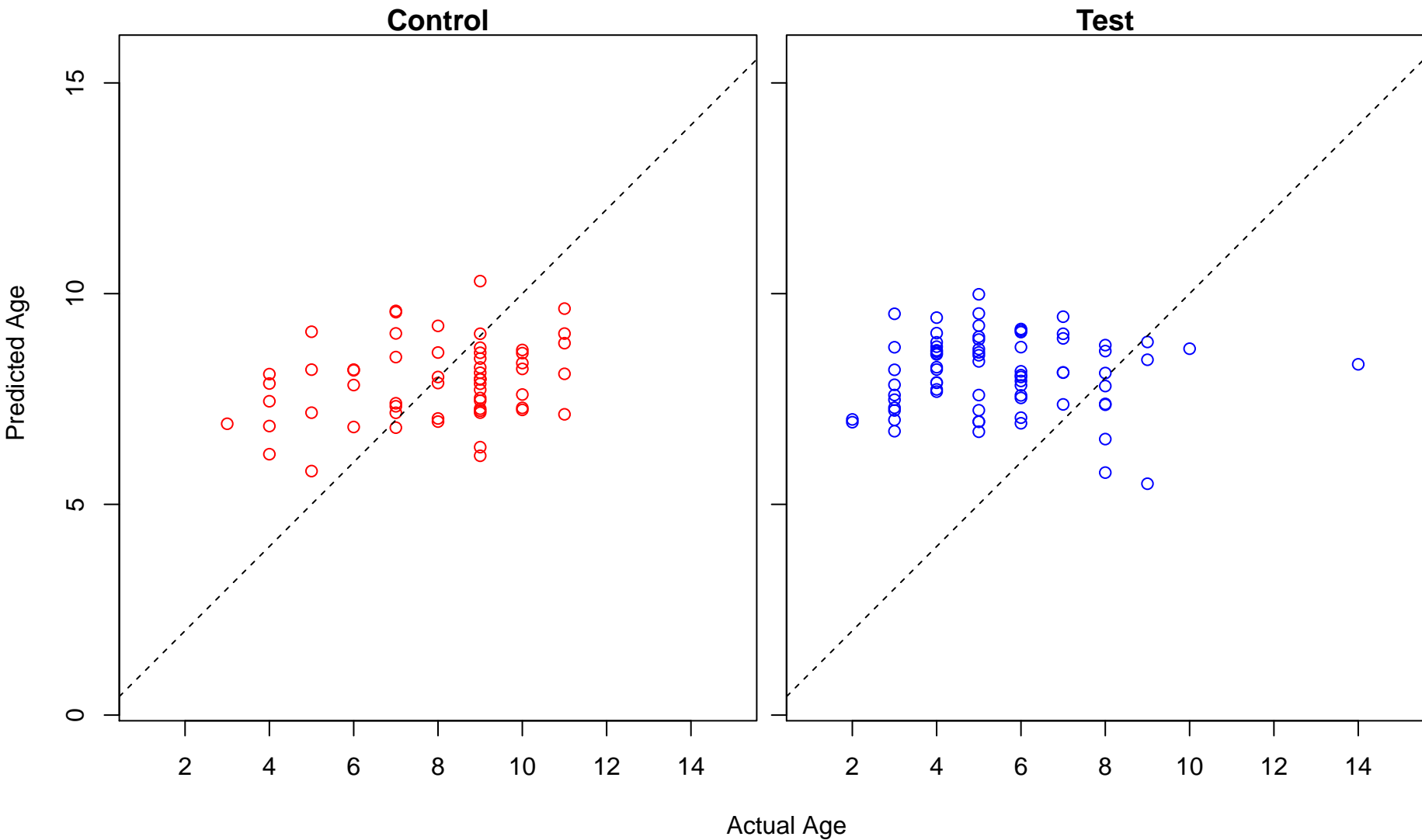
protein mannosylation (Score: 0.401689)



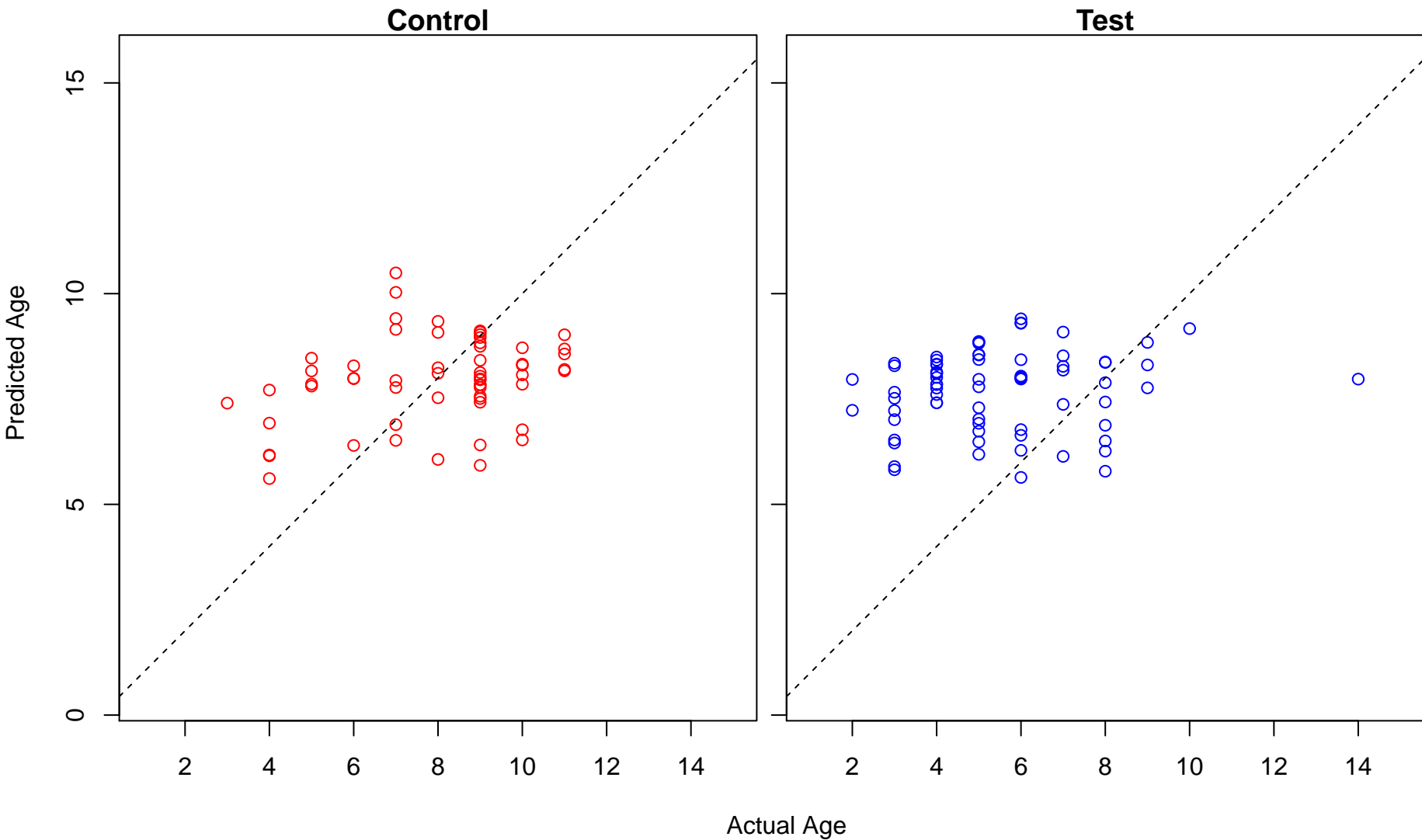
regulation of phospholipid biosynthetic process (Score: 0.401087)



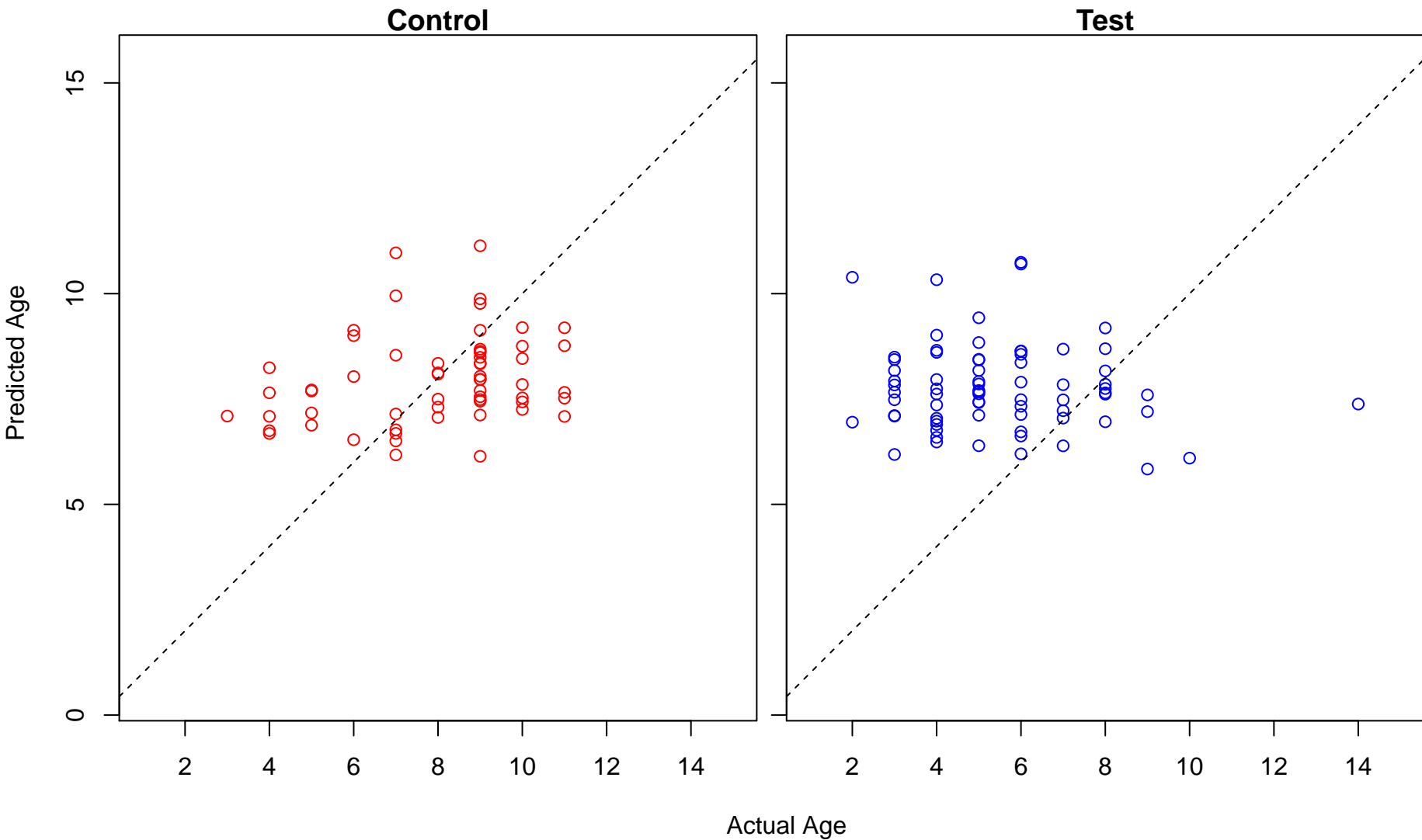
inorganic diphosphate transport (Score: 0.399081)



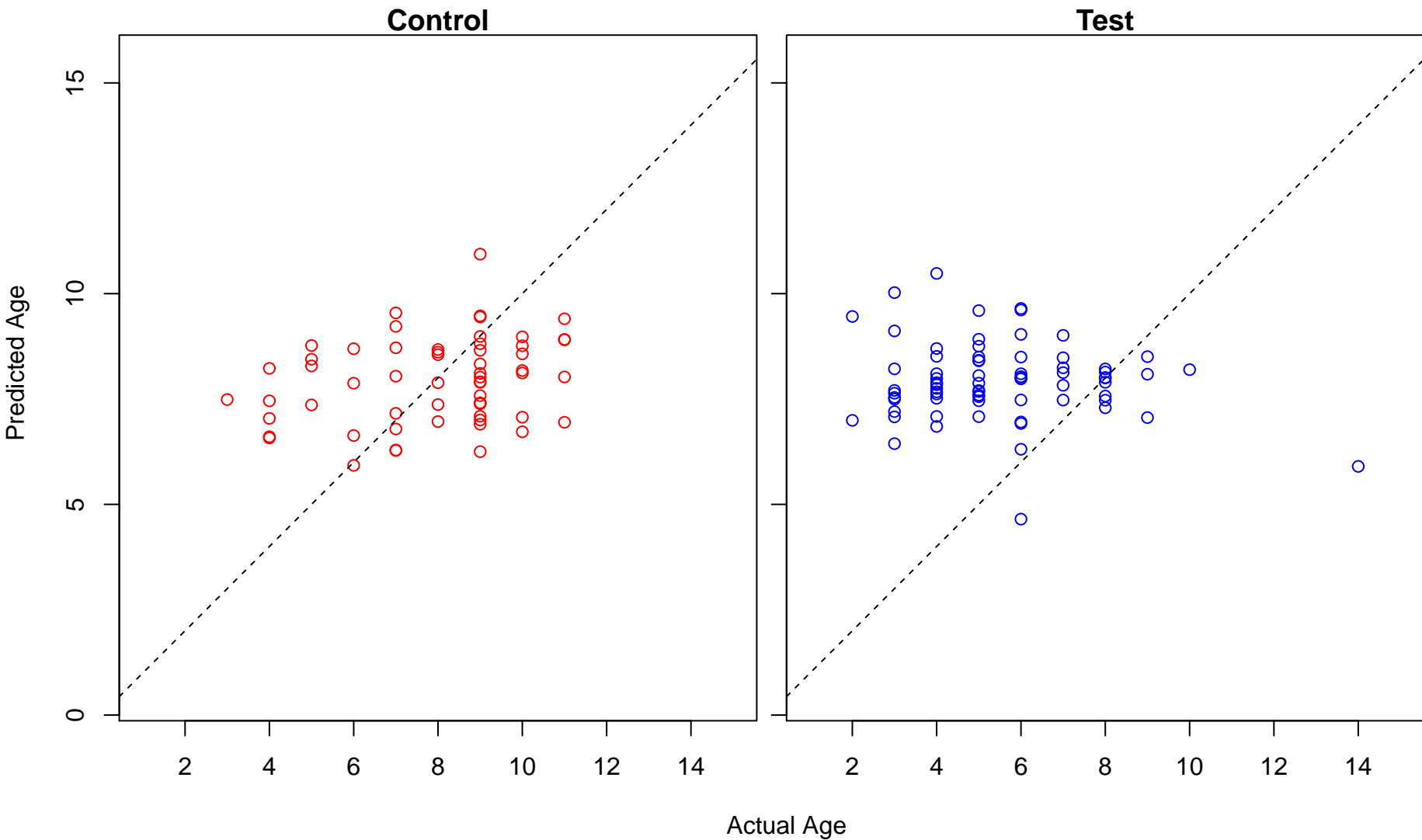
protein deacylation (Score: 0.398216)



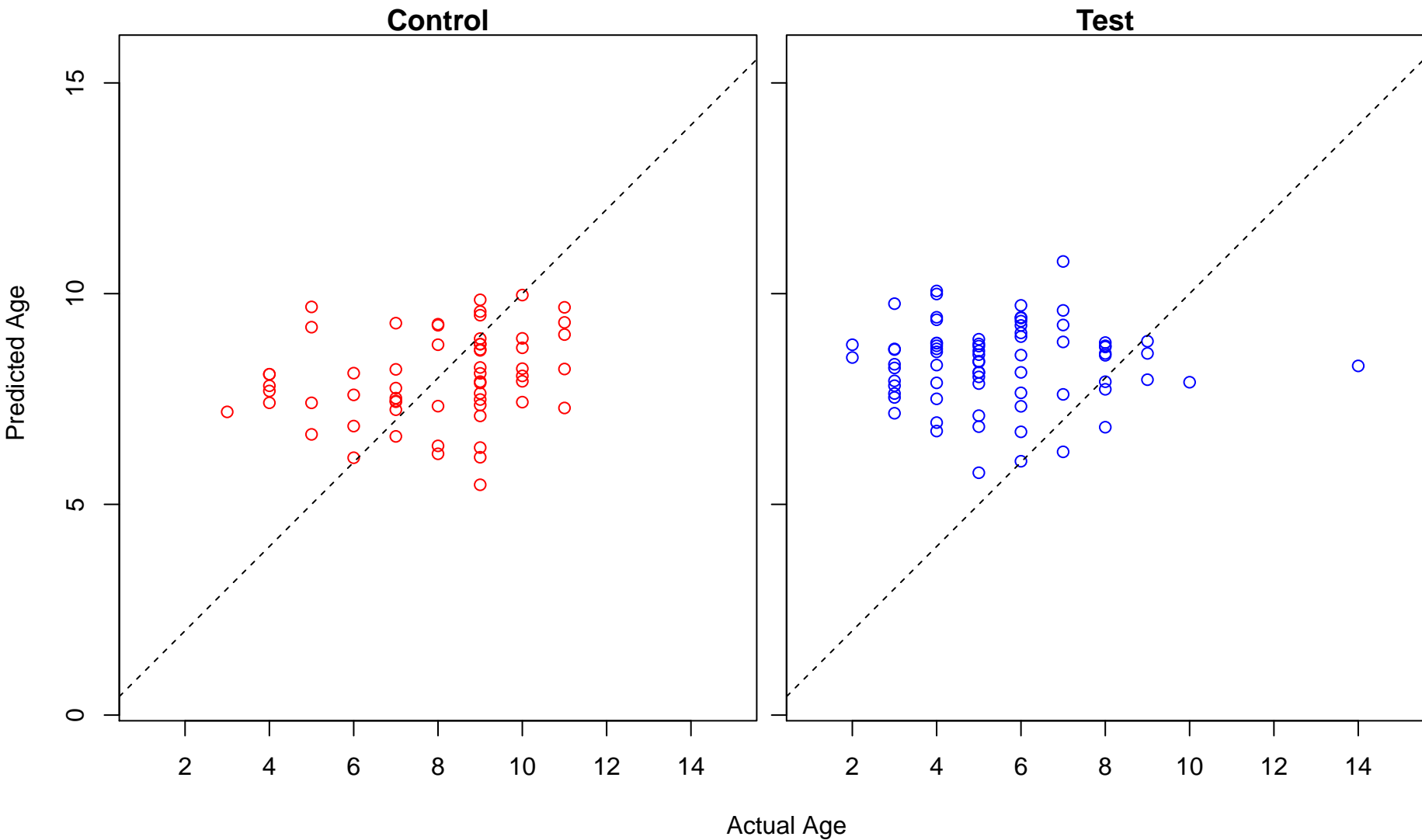
negative regulation of receptor catabolic process (Score: 0.398087)



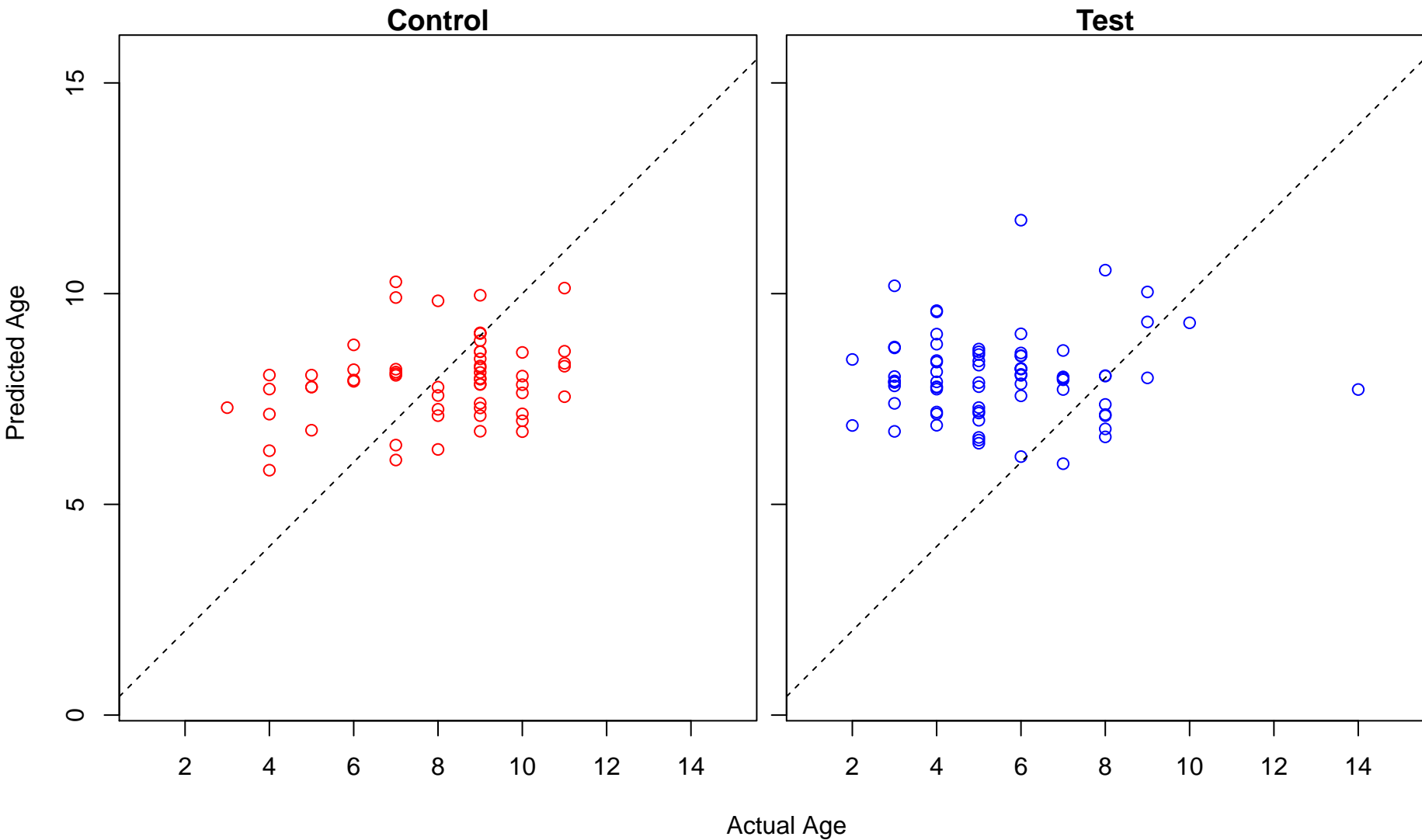
Golgi calcium ion transport (Score: 0.397536)



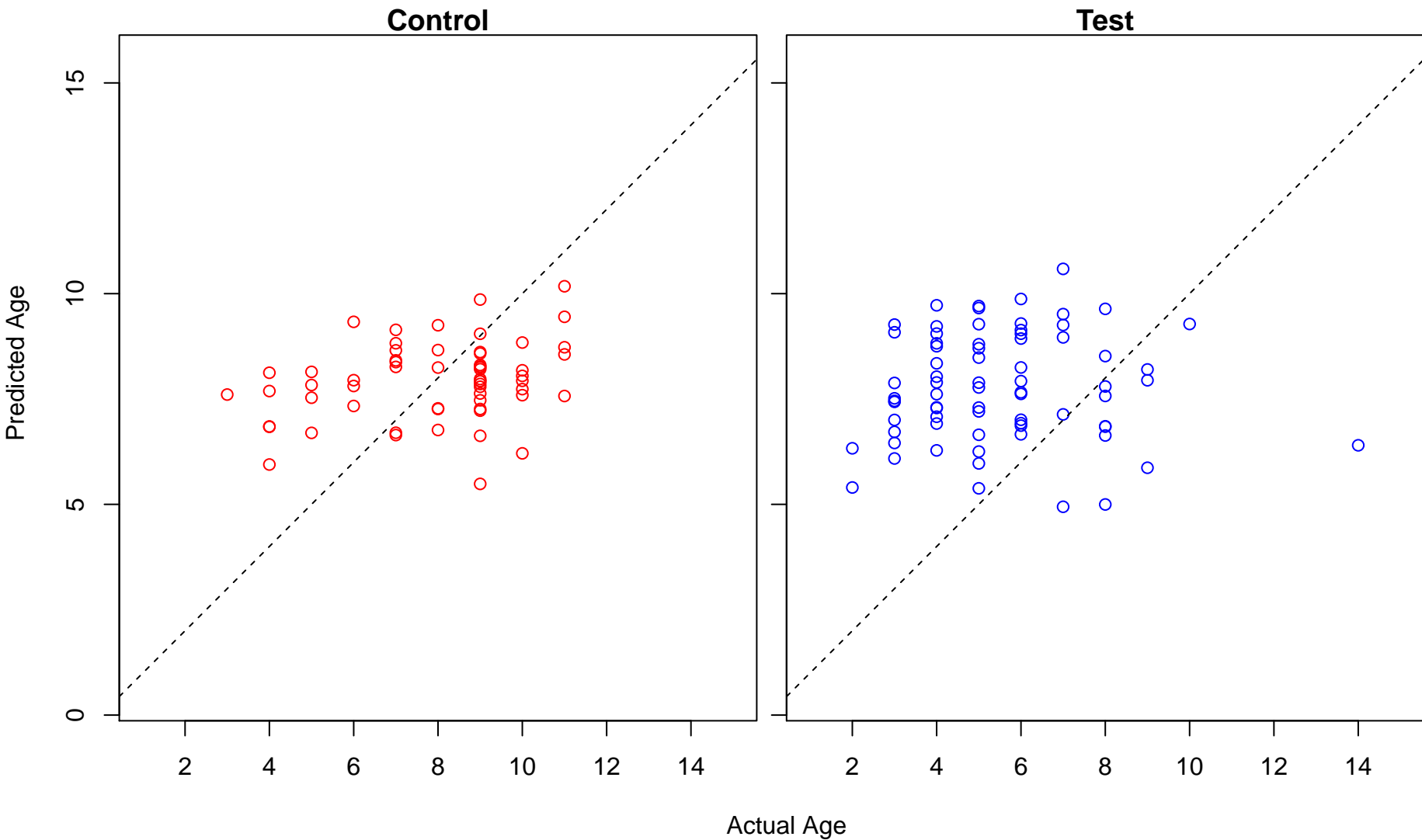
retina morphogenesis in camera-type eye (Score: 0.397235)



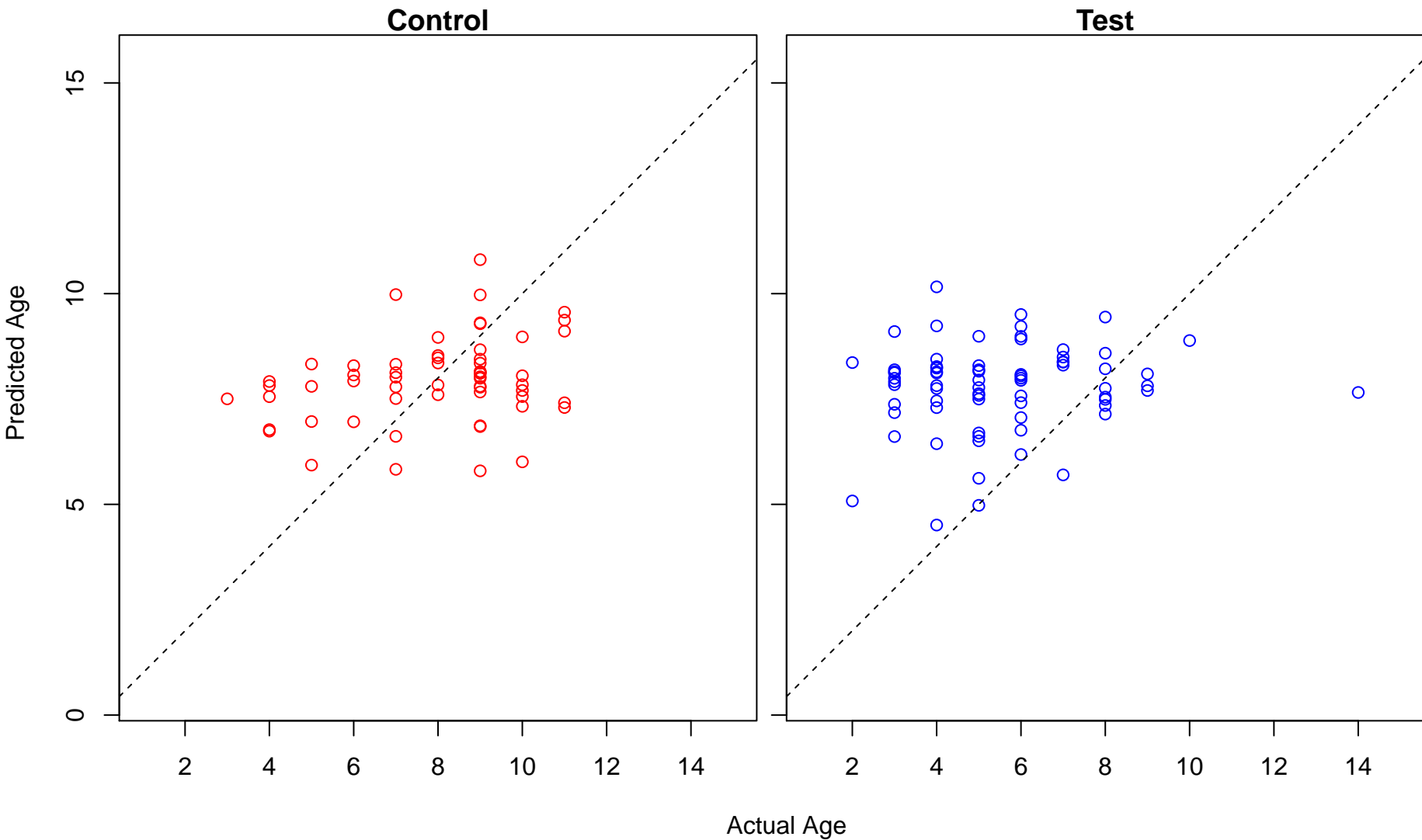
negative regulation of alpha-beta T cell activation (Score: 0.396587)



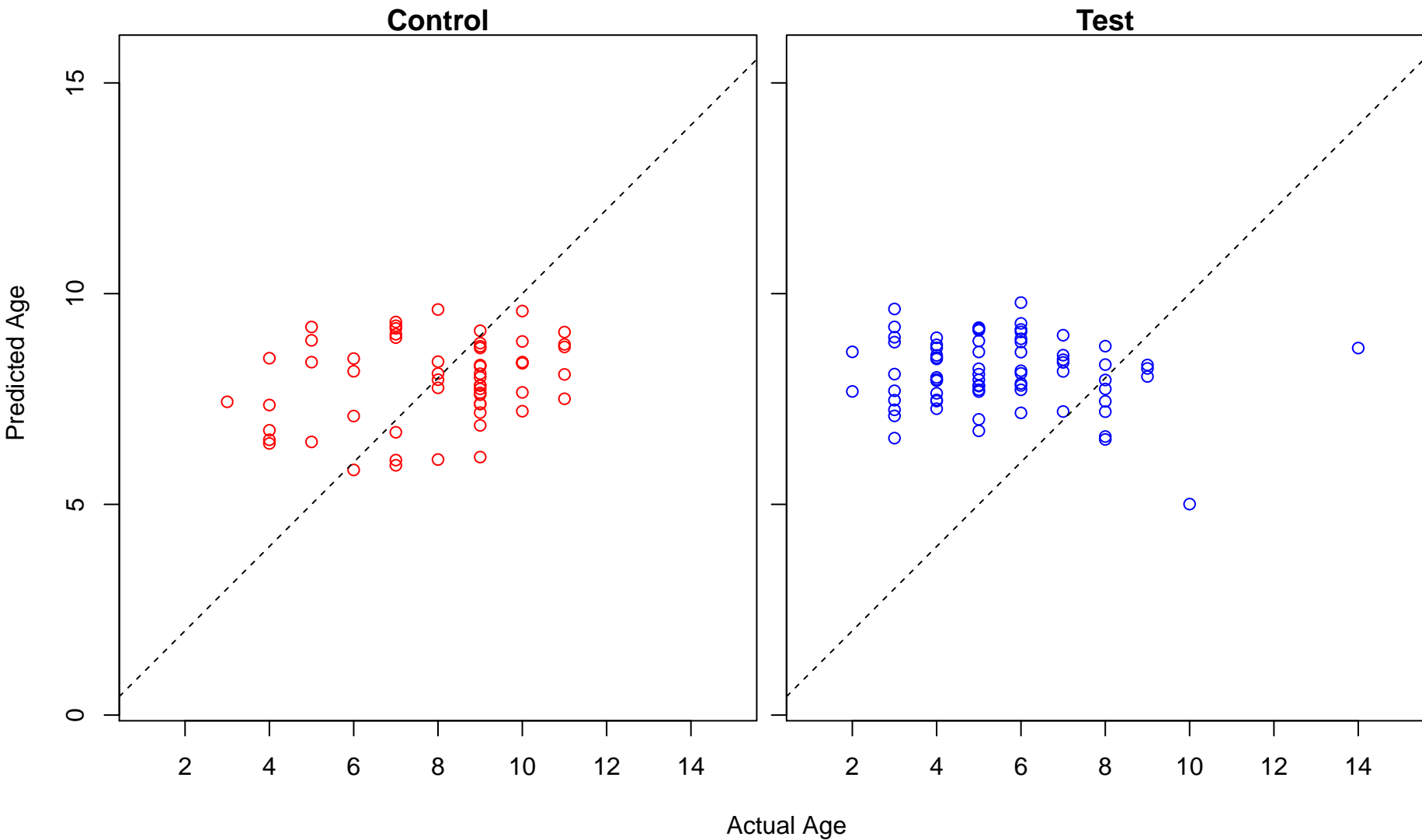
vein smooth muscle contraction (Score: 0.394543)



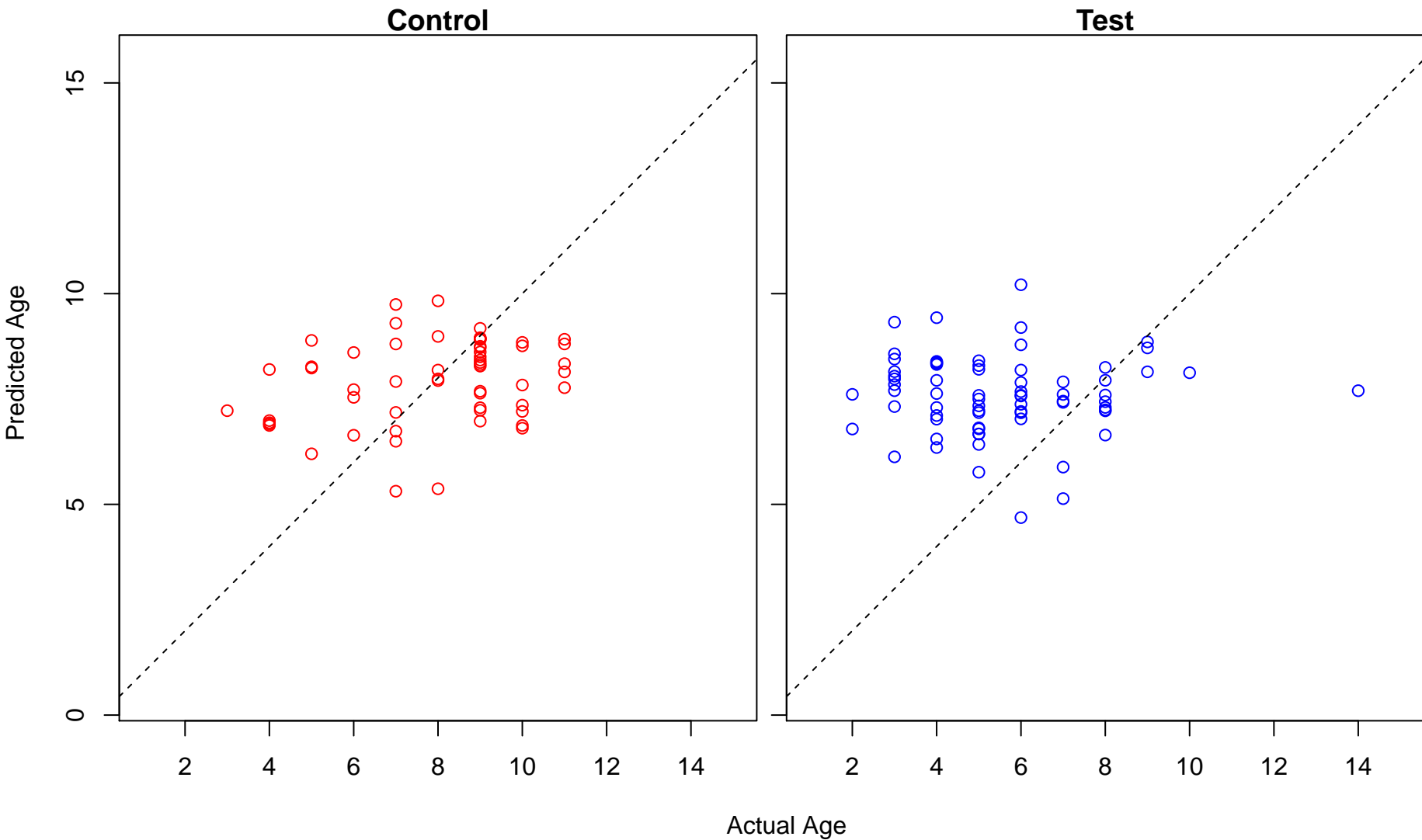
mammary placode formation (Score: 0.394400)



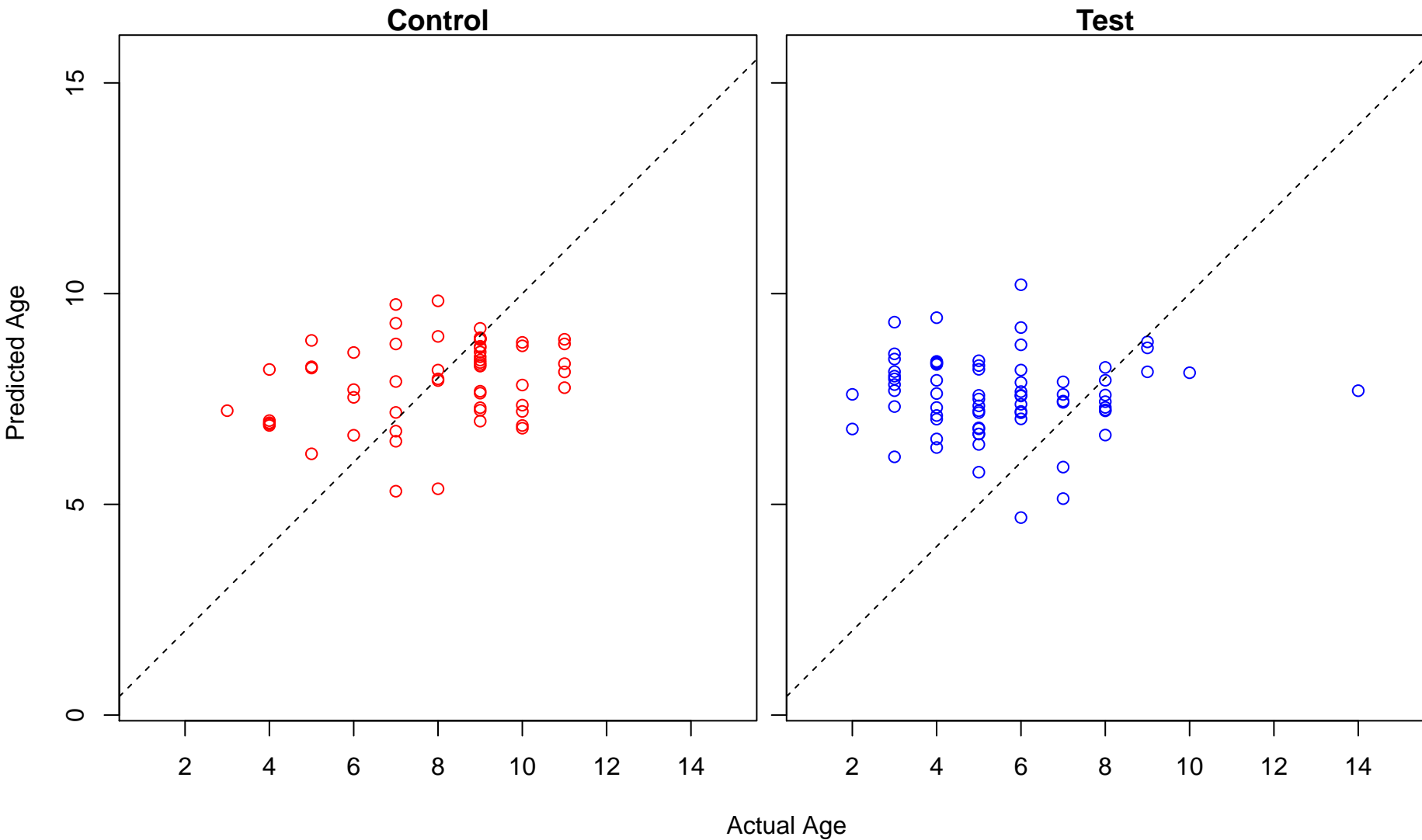
glutamyl-tRNA^{Gln} biosynthesis via transamidation (Score: 0.393550)



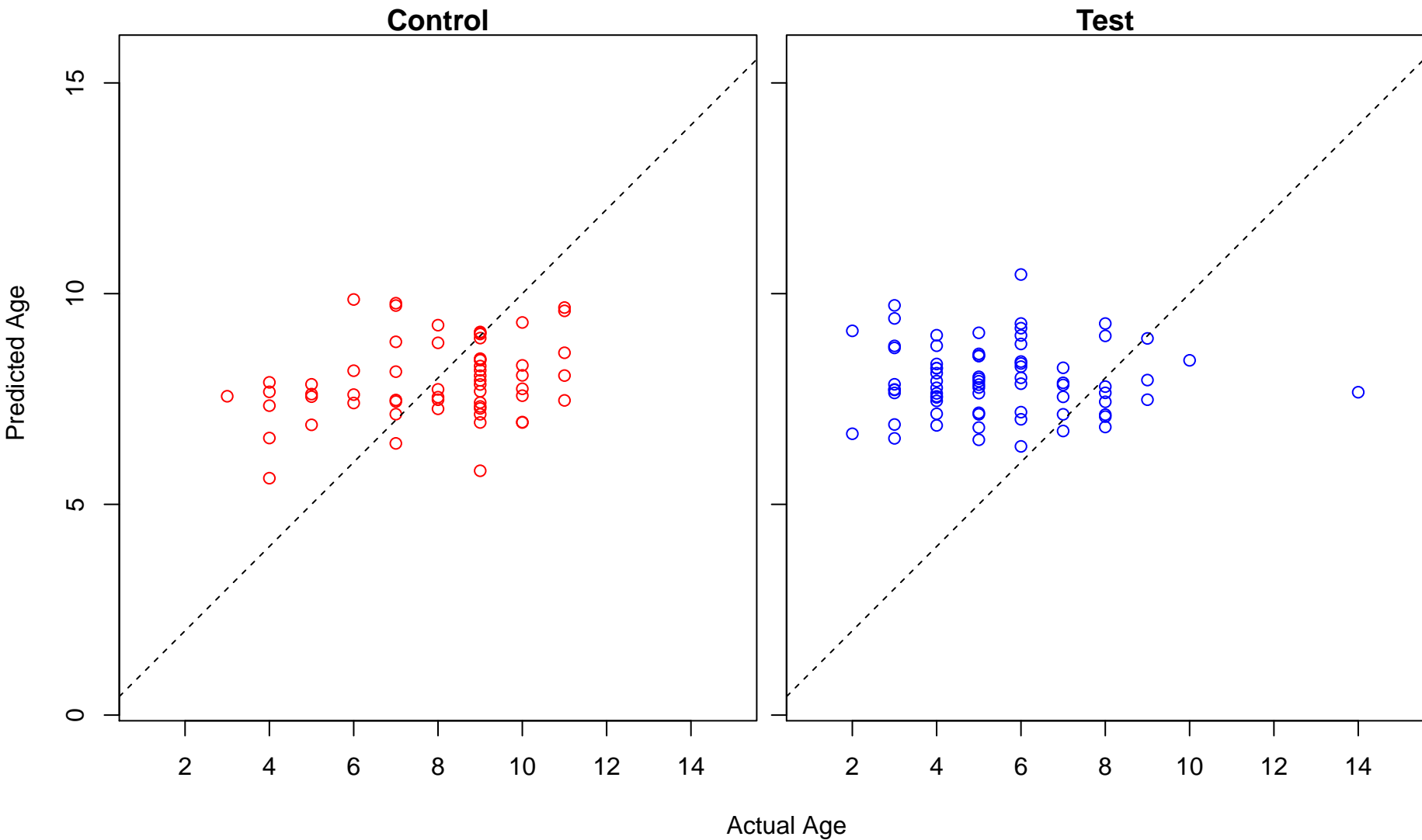
regulation of hematopoietic stem cell migration (Score: 0.392757)



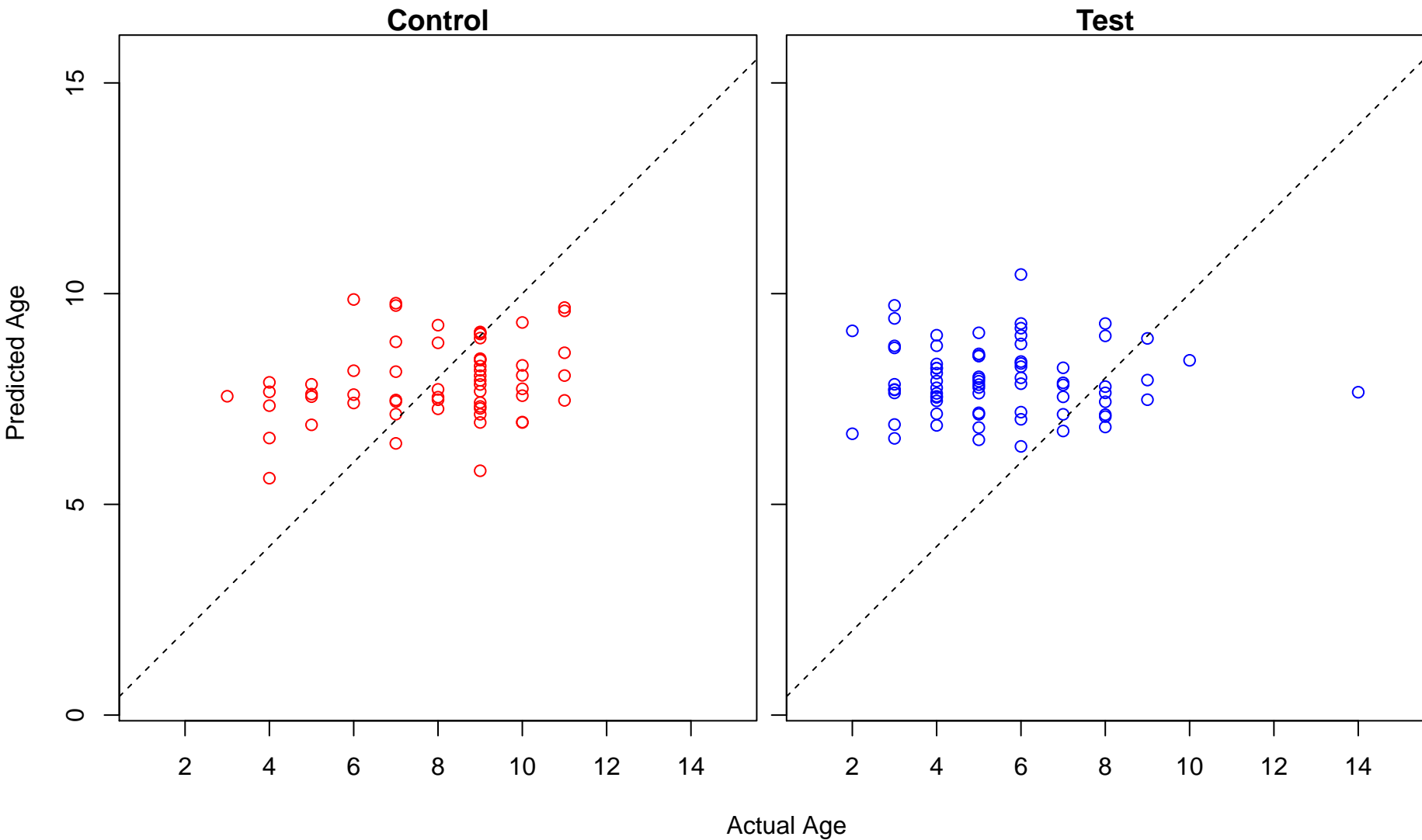
positive regulation of hematopoietic stem cell migration (Score: 0.392757)



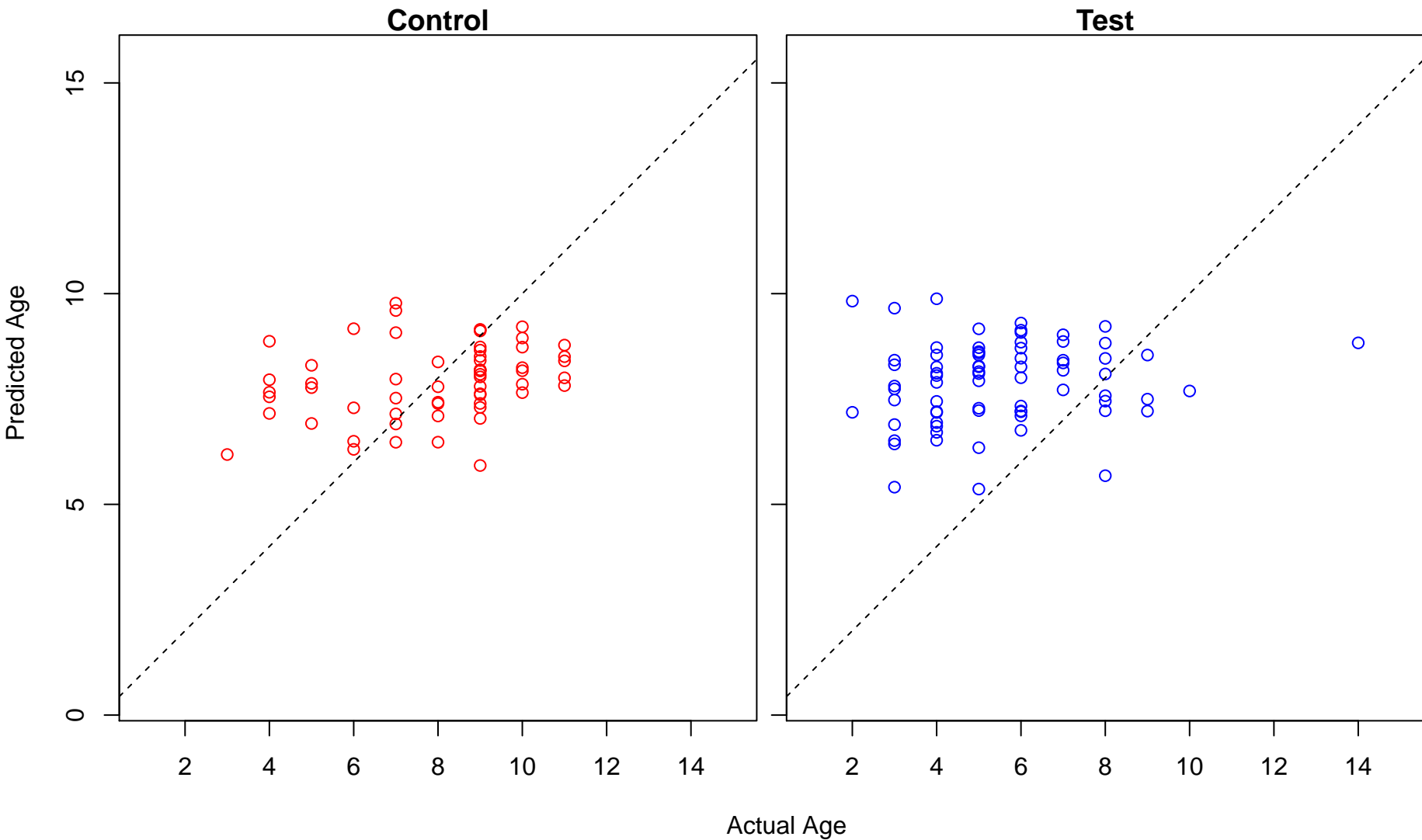
positive regulation of bone resorption (Score: 0.391629)



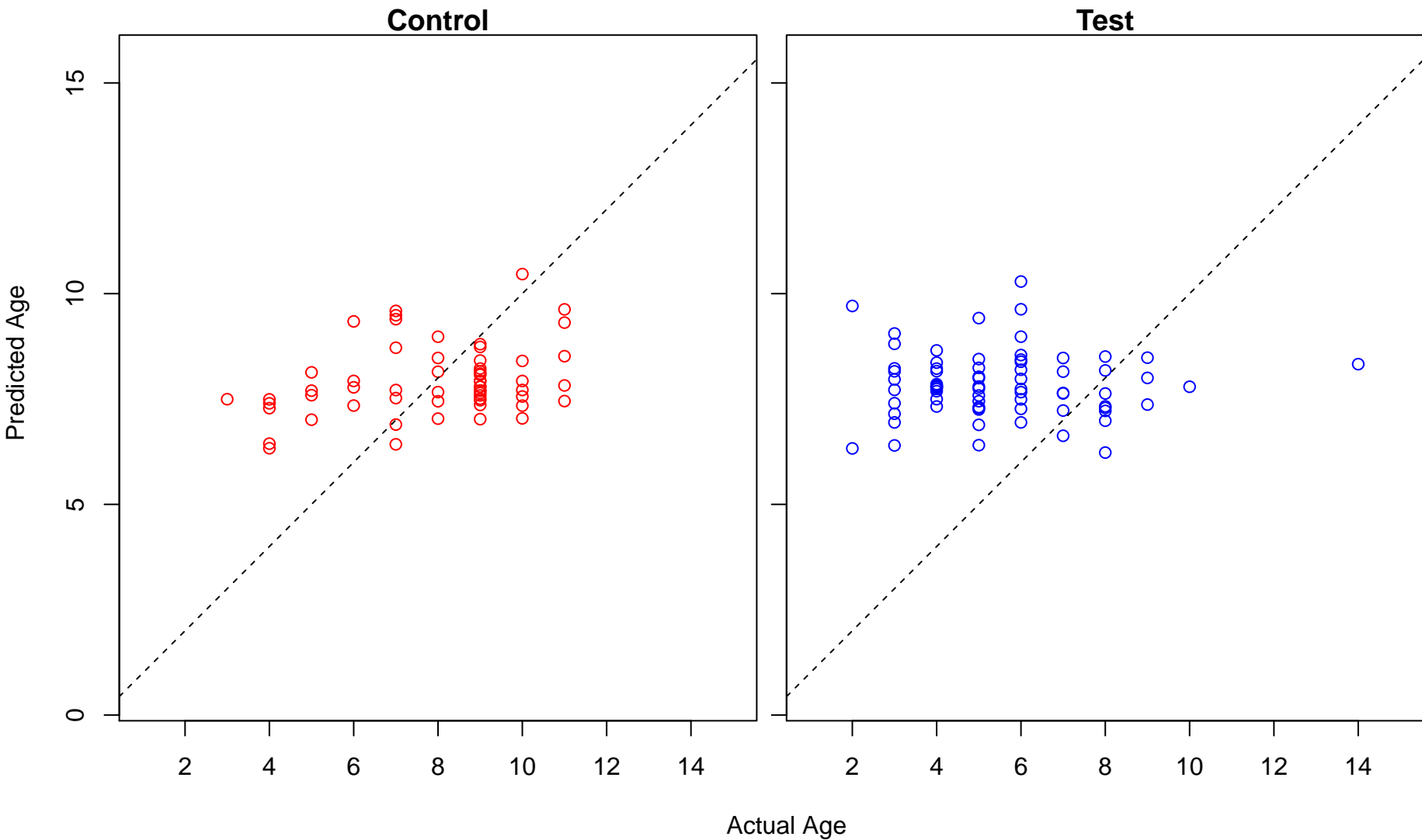
positive regulation of bone remodeling (Score: 0.391629)



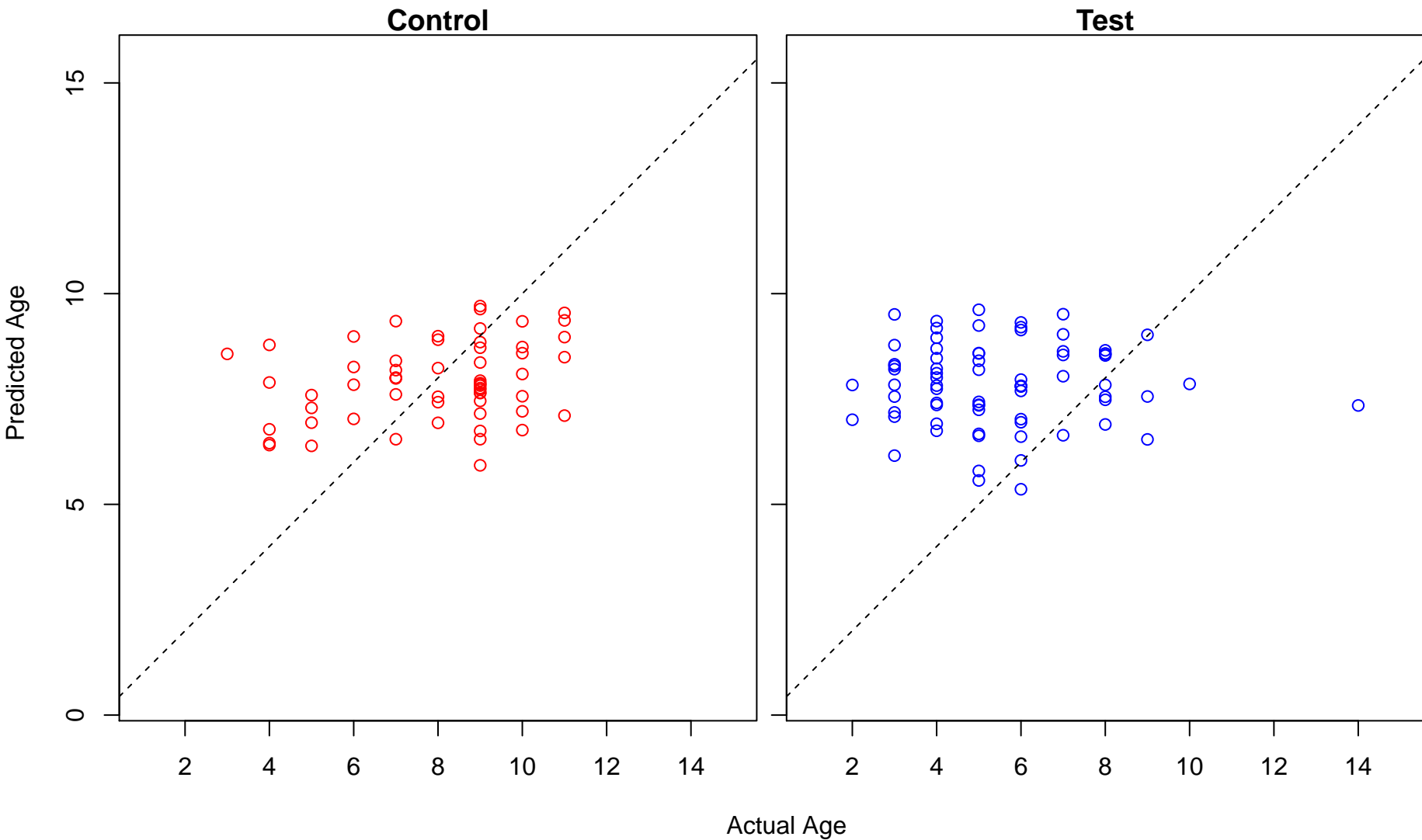
serine phosphorylation of STAT3 protein (Score: 0.389276)



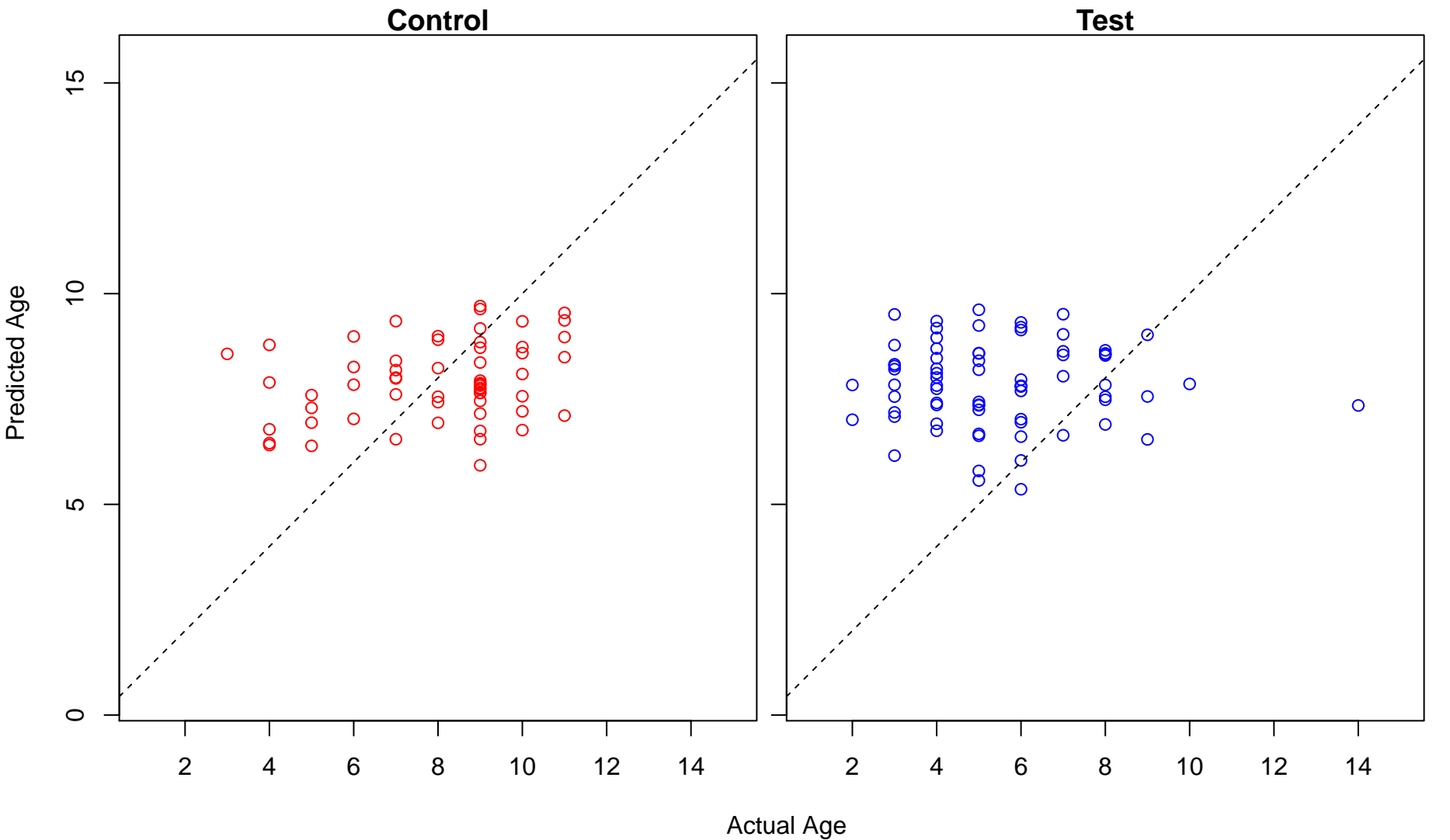
positive regulation of amine transport (Score: 0.386678)



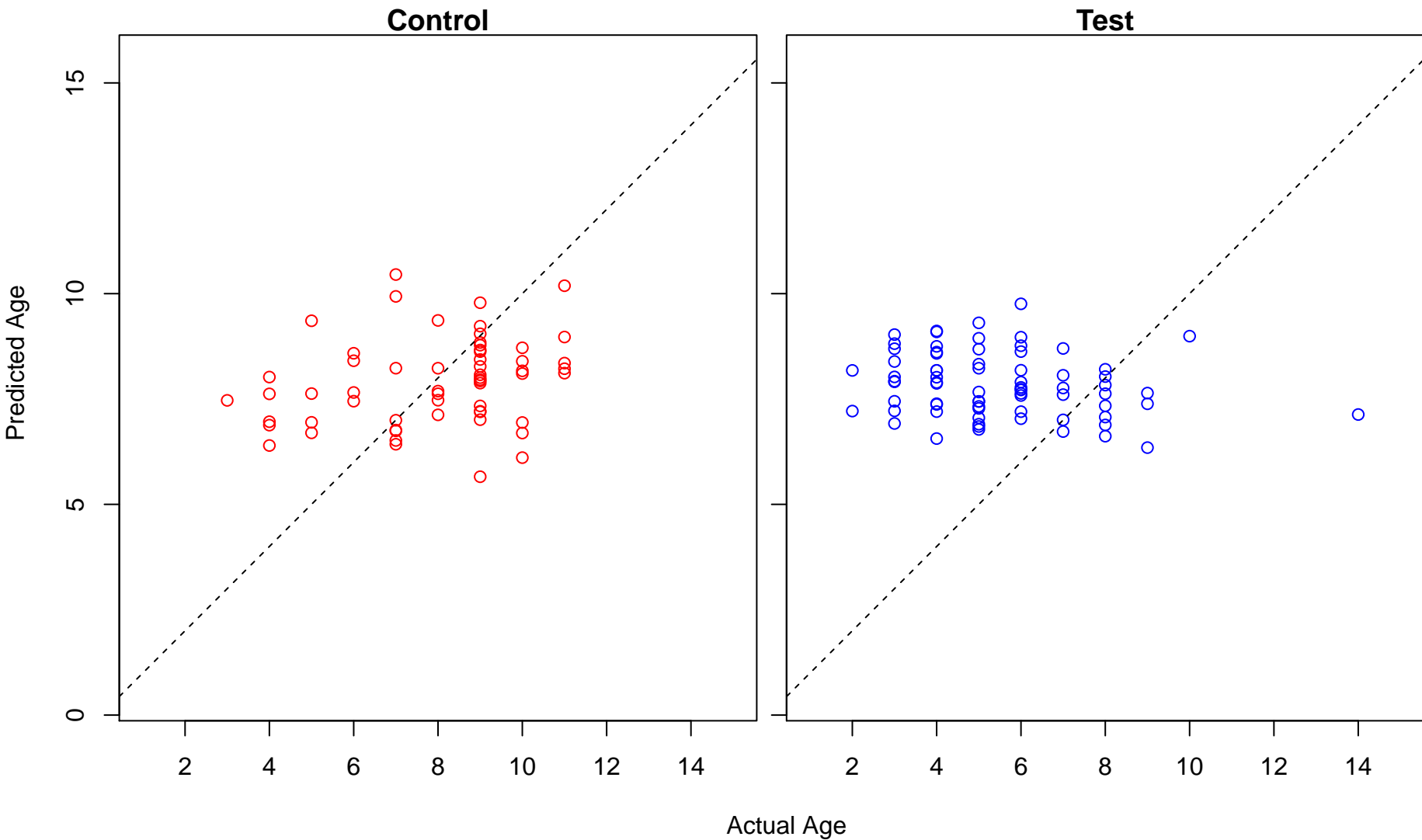
regulation of proteinase activated receptor activity (Score: 0.386260)



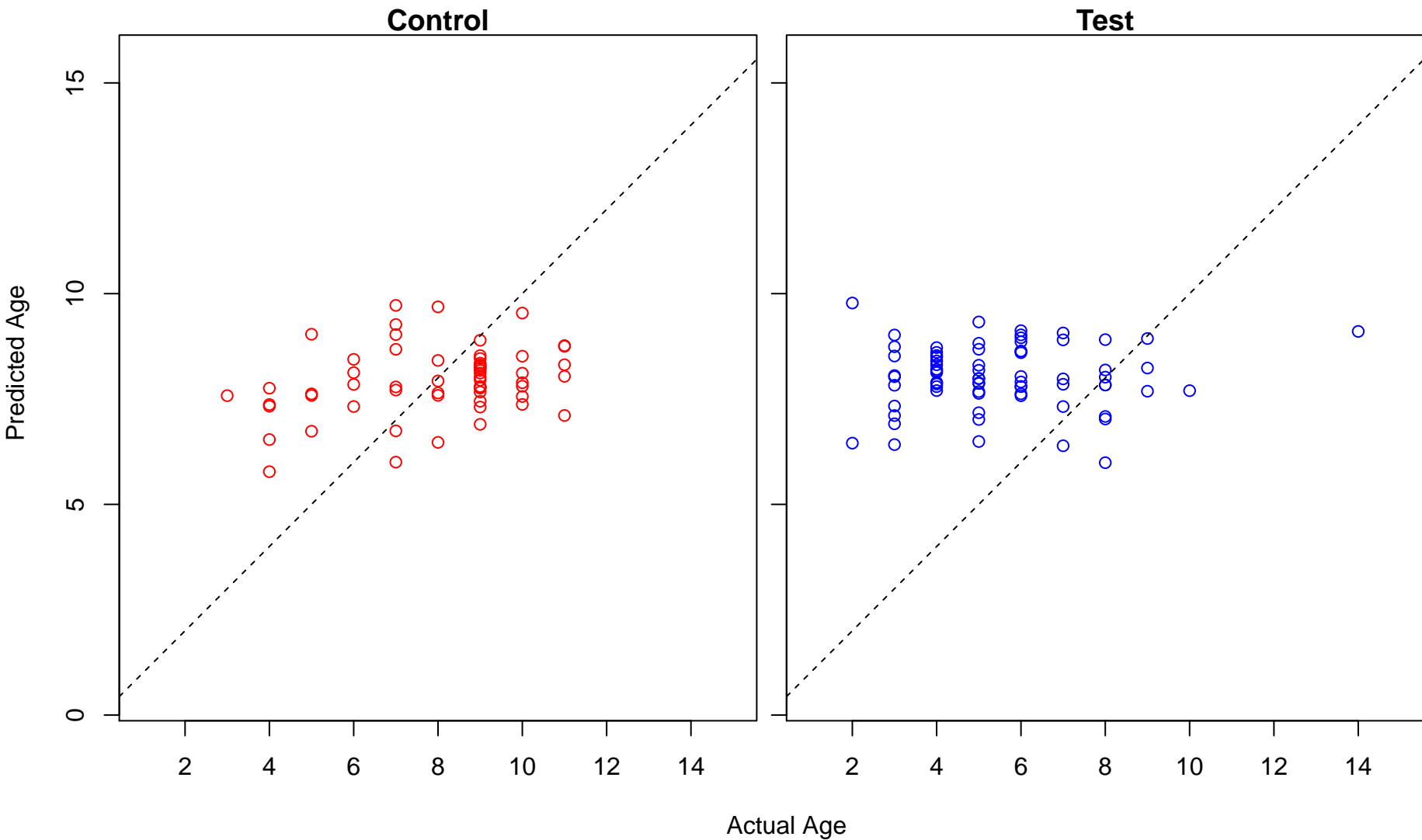
negative regulation of phospholipase C-activating G-protein coupled receptor signaling pathway (Score: 0)



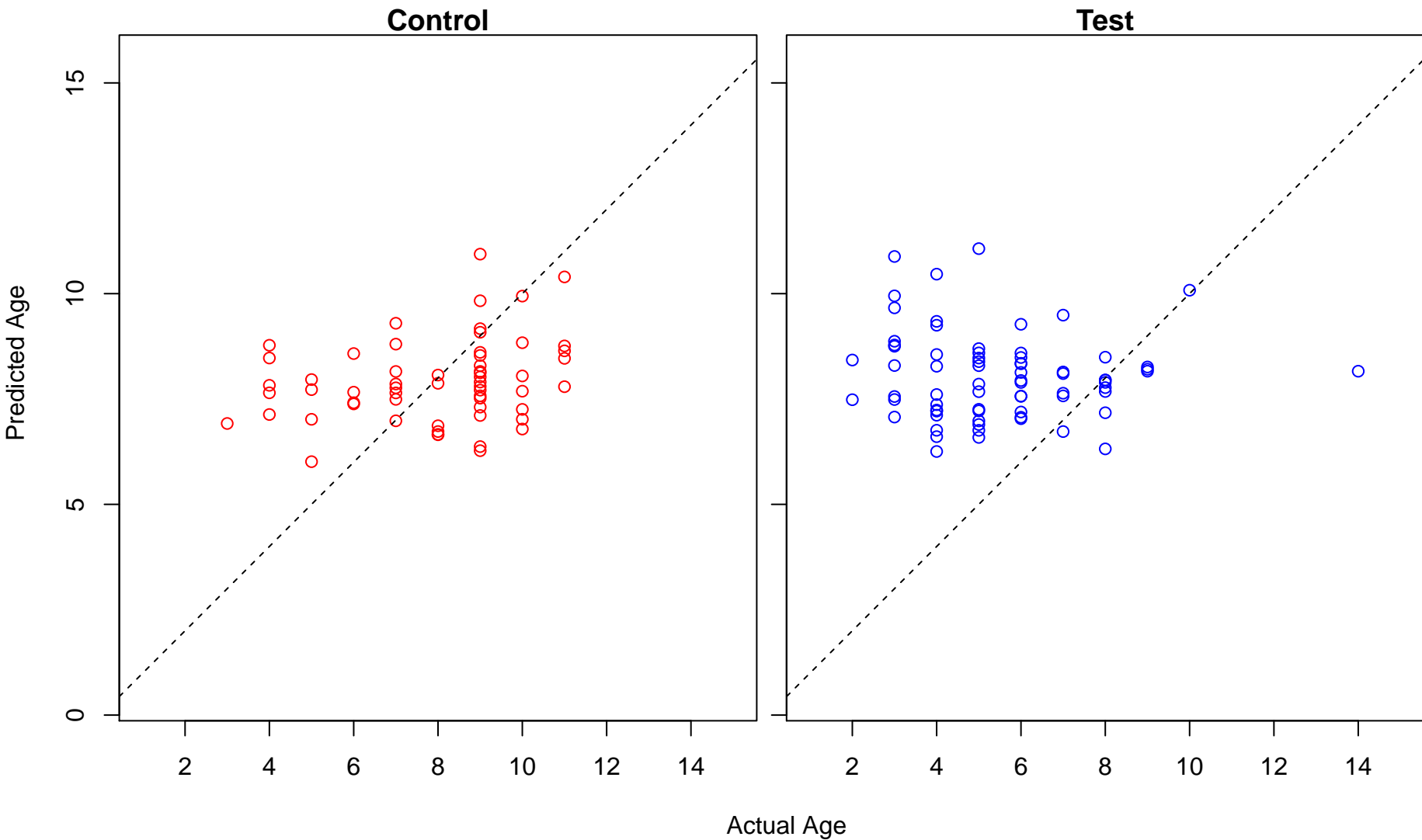
regulation of cilium movement (Score: 0.383121)



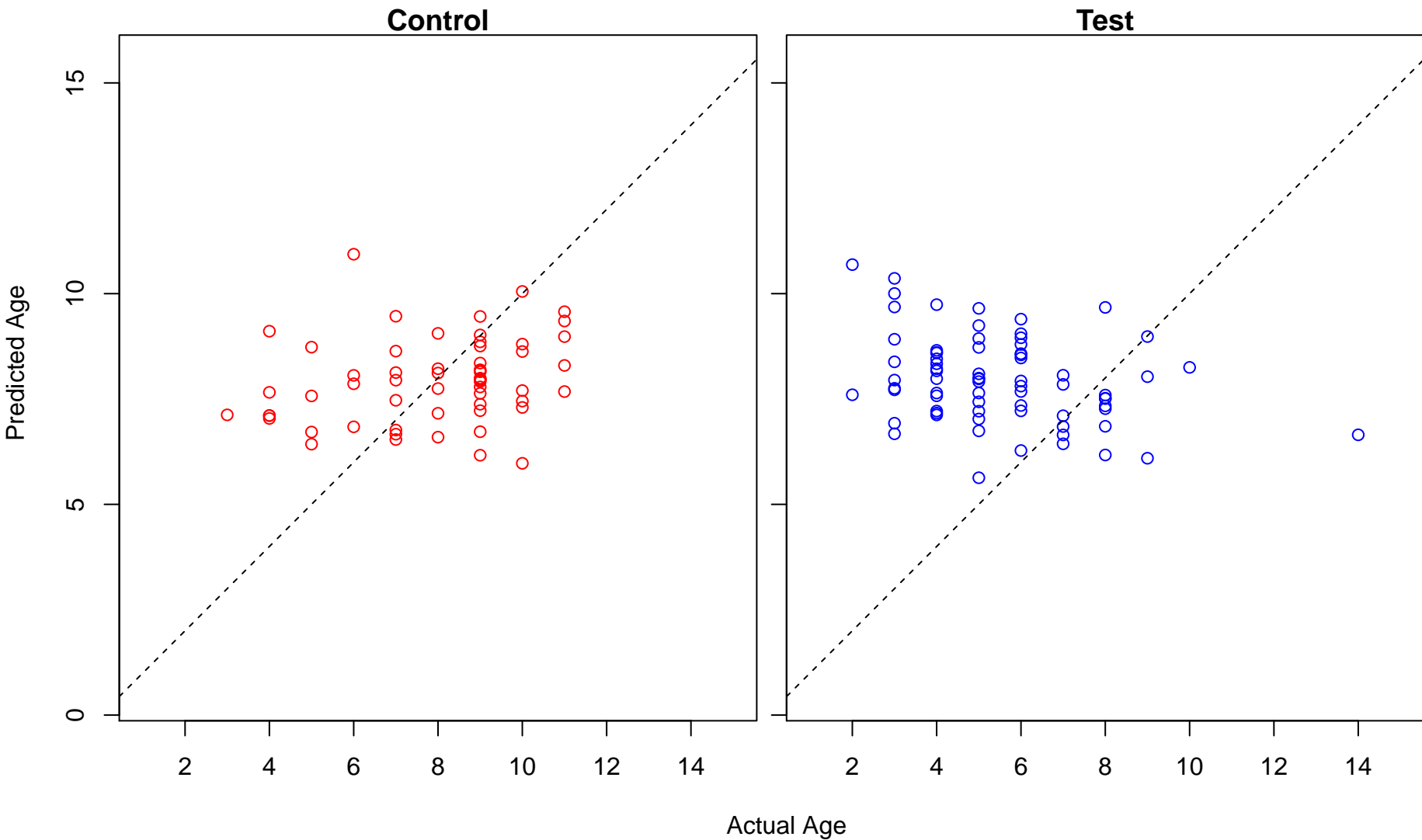
regulation of short-term neuronal synaptic plasticity (Score: 0.382520)



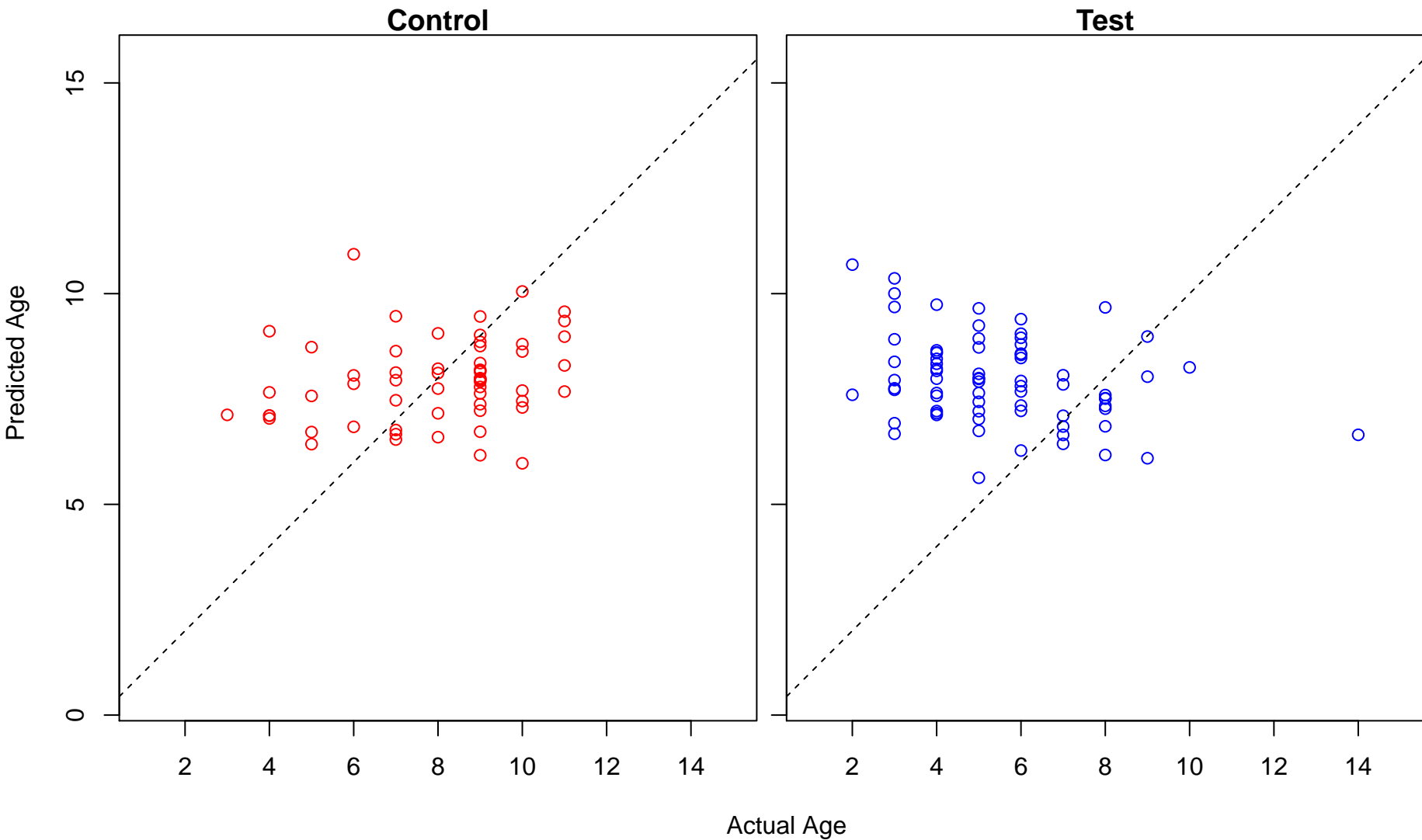
mevalonate transport (Score: 0.380486)



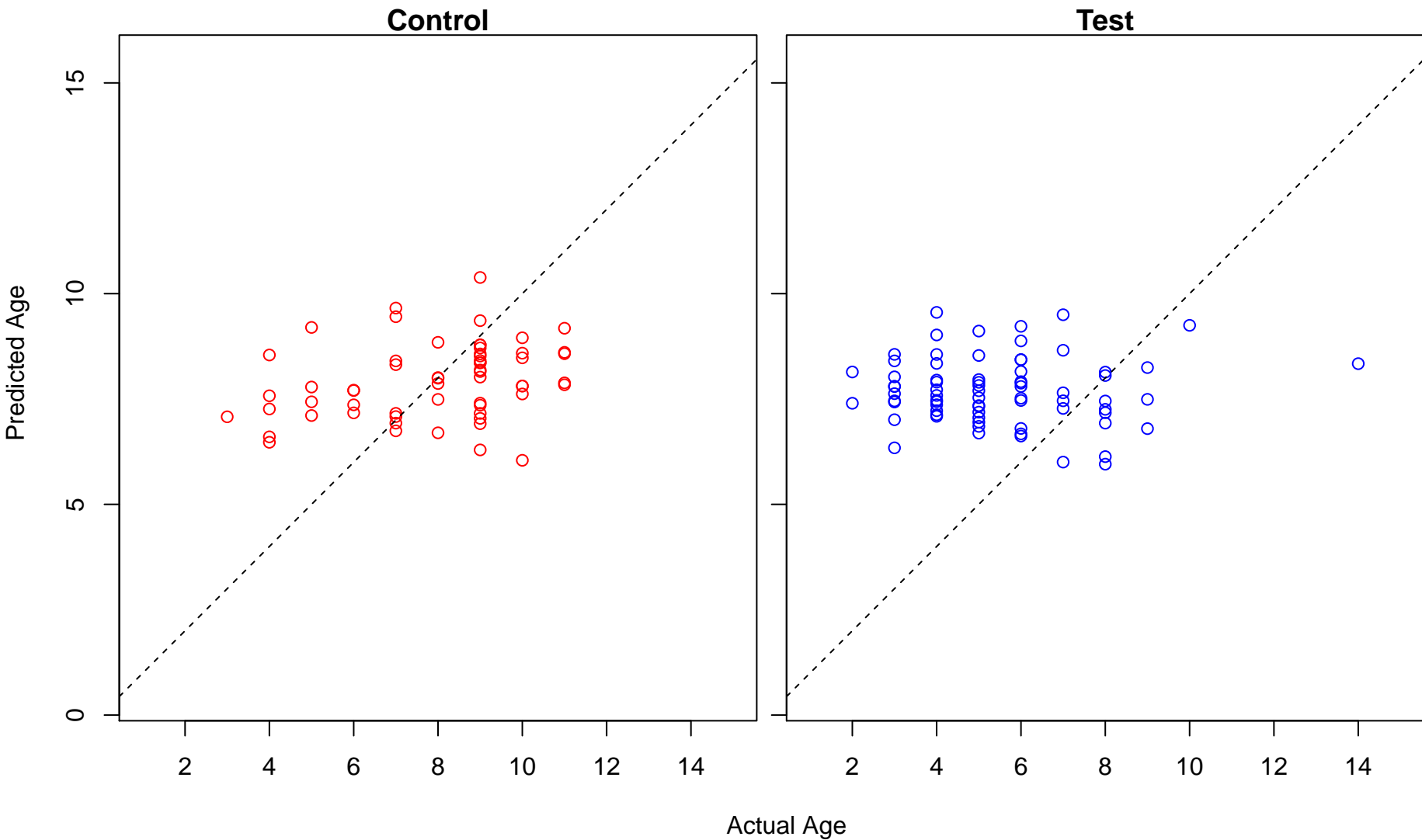
negative regulation of histone acetylation (Score: 0.375736)



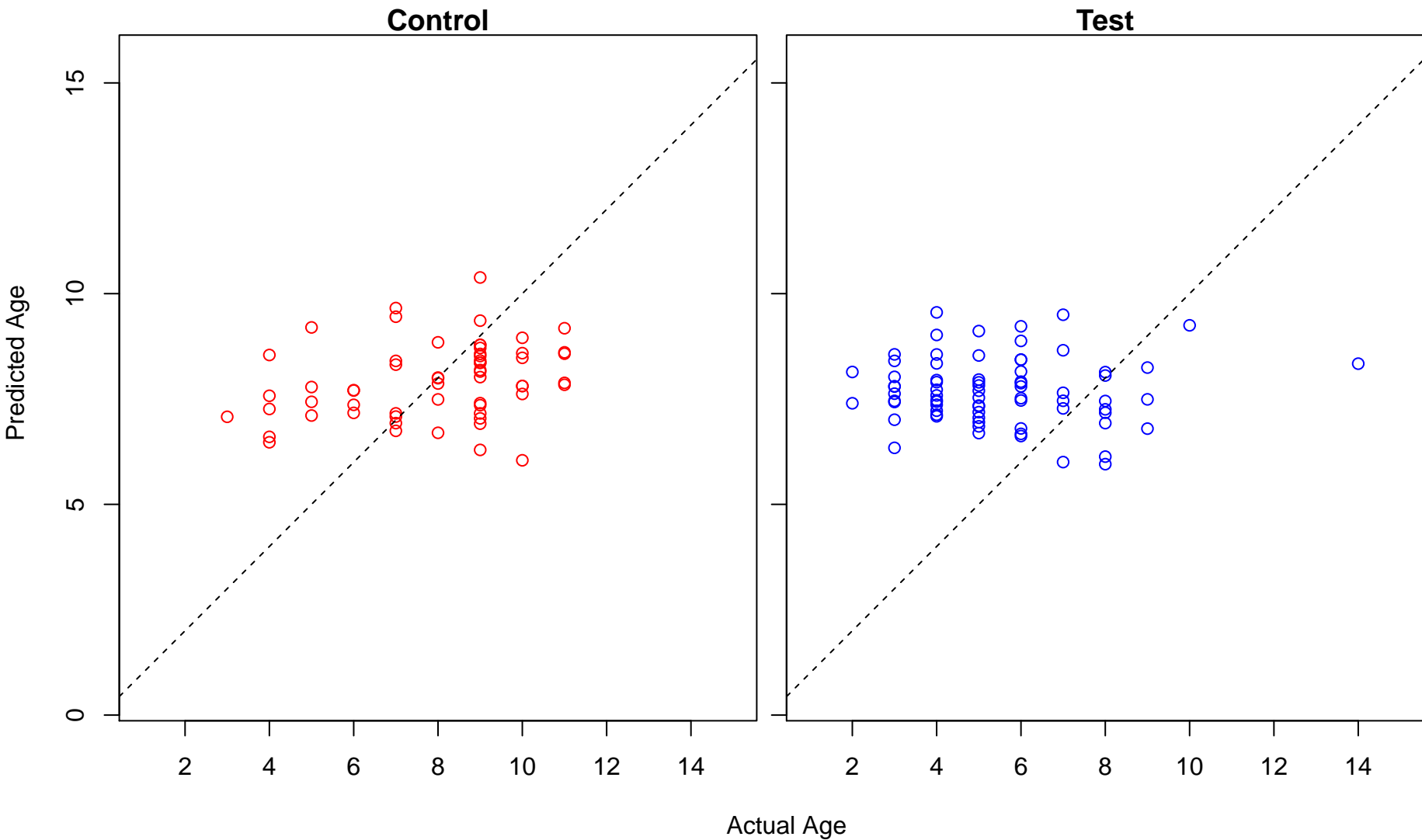
negative regulation of peptidyl-lysine acetylation (Score: 0.375698)



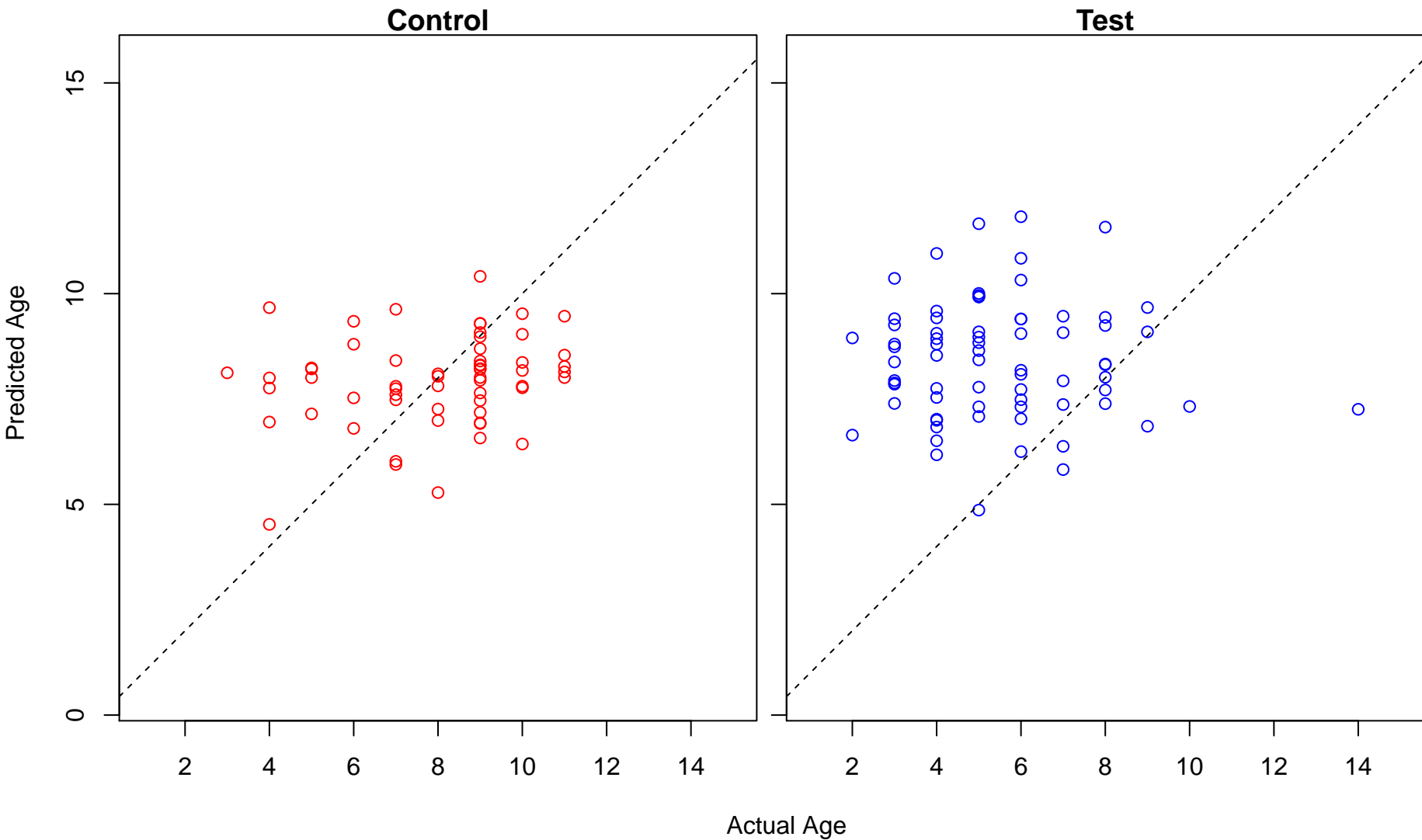
selenocysteine incorporation (Score: 0.374320)



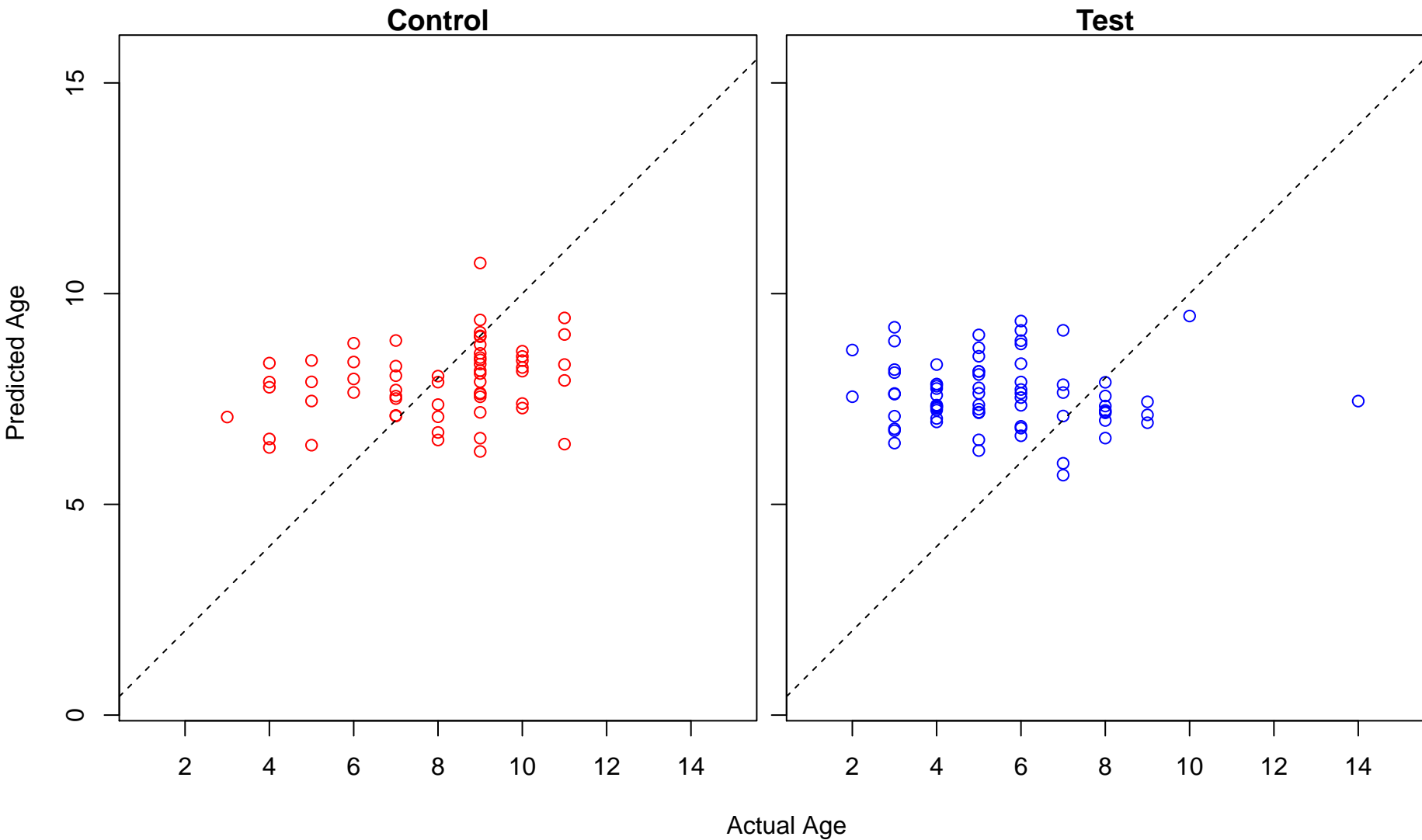
translational readthrough (Score: 0.374320)



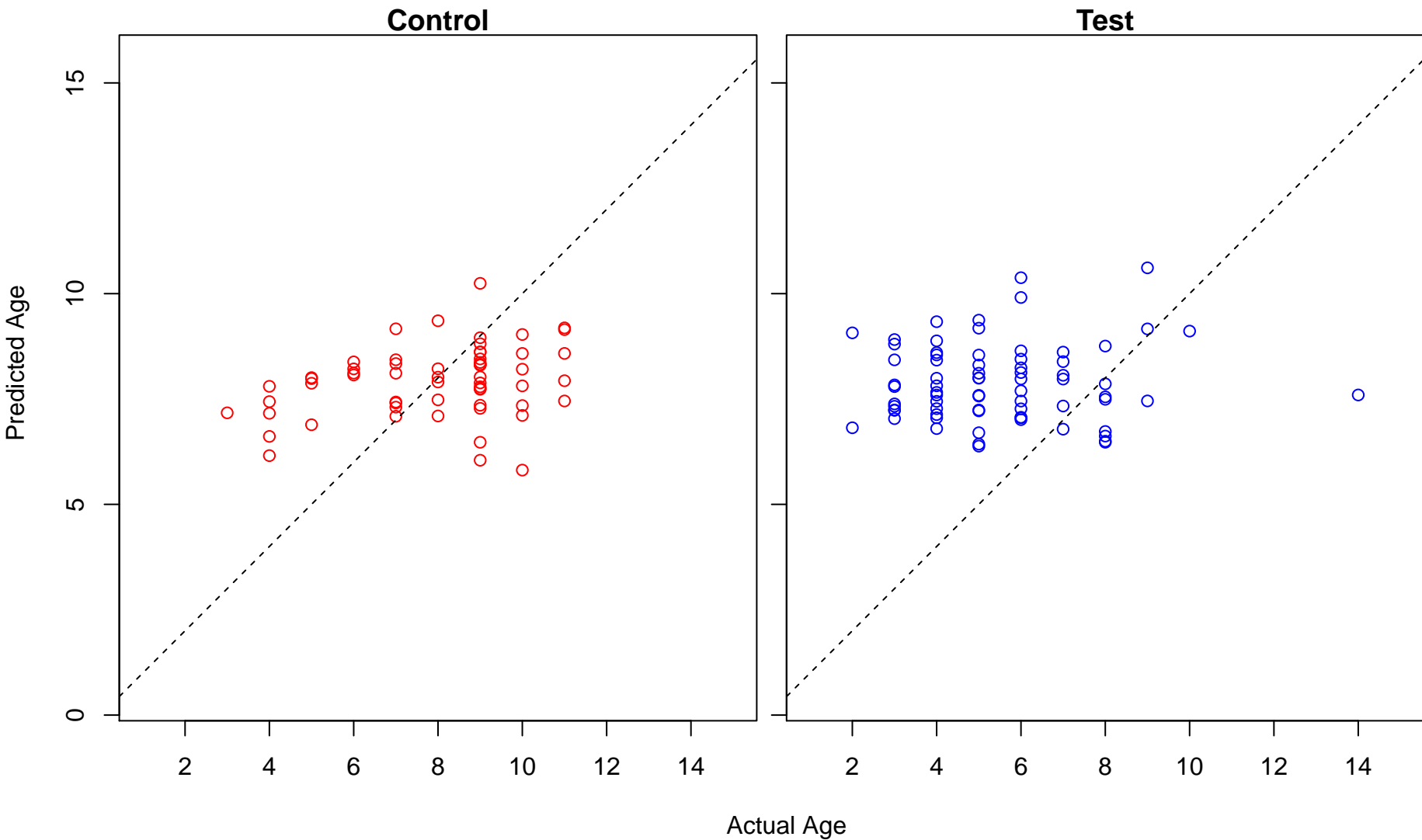
dermatan sulfate metabolic process (Score: 0.372098)



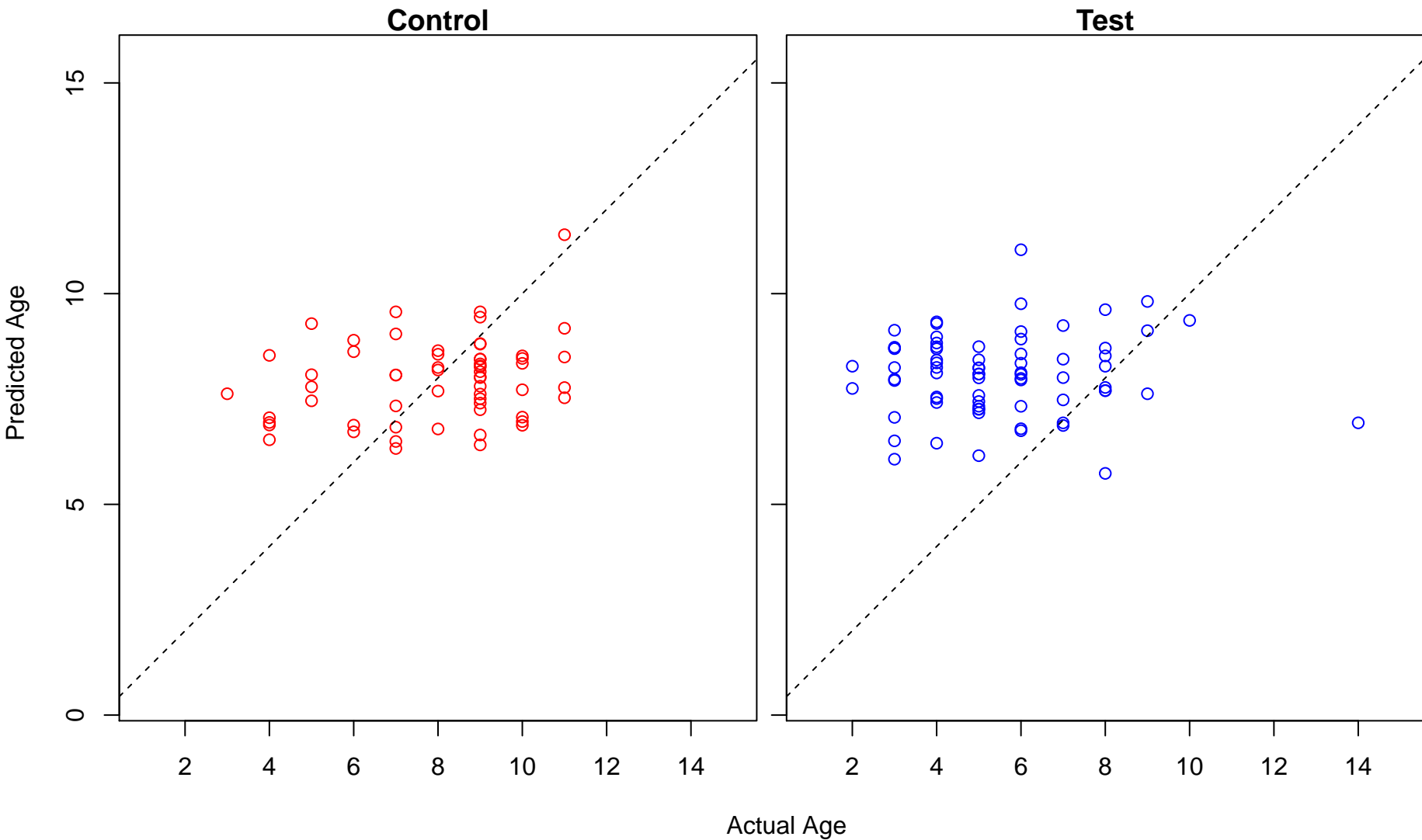
hepatocyte differentiation (Score: 0.371257)



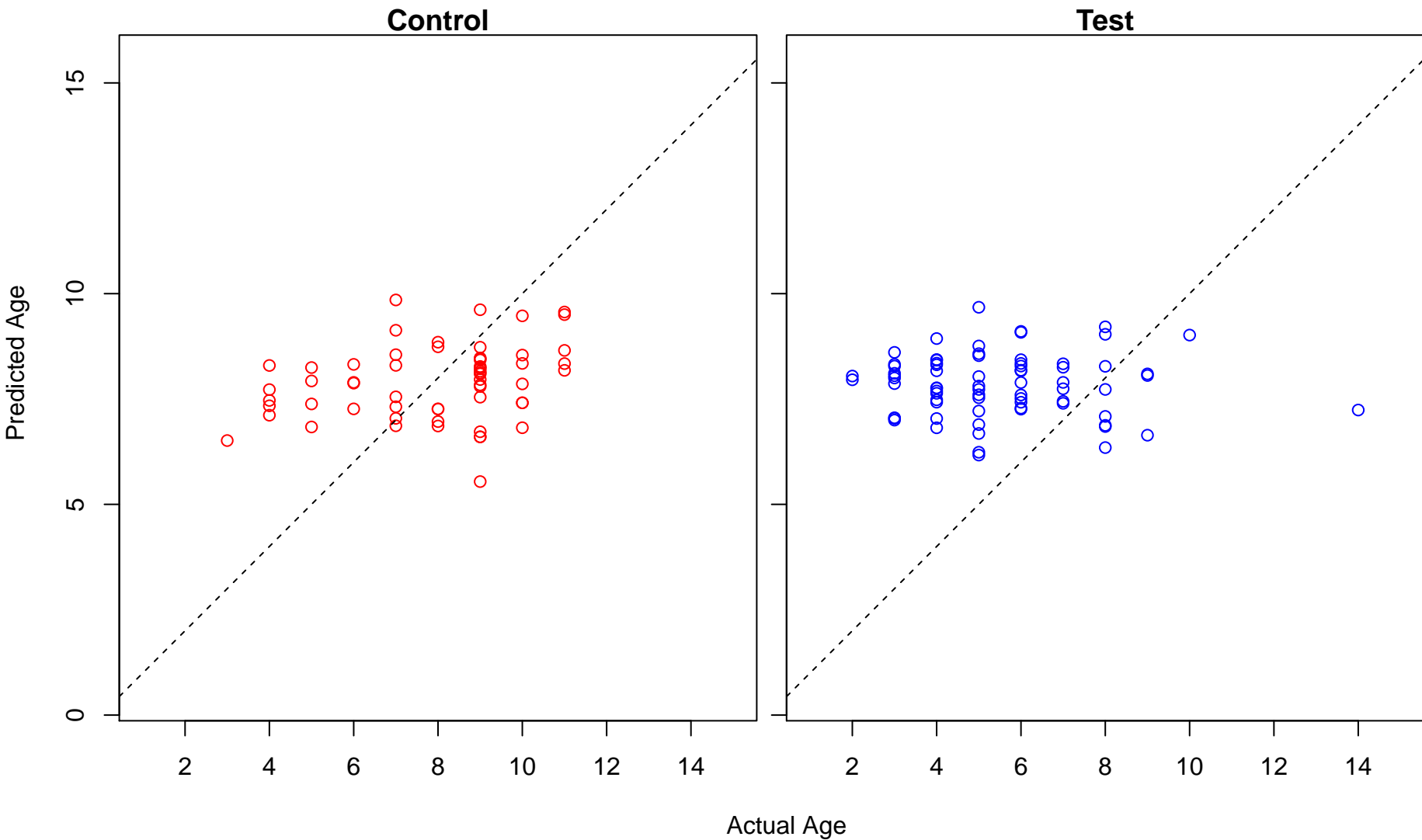
citrulline metabolic process (Score: 0.370124)



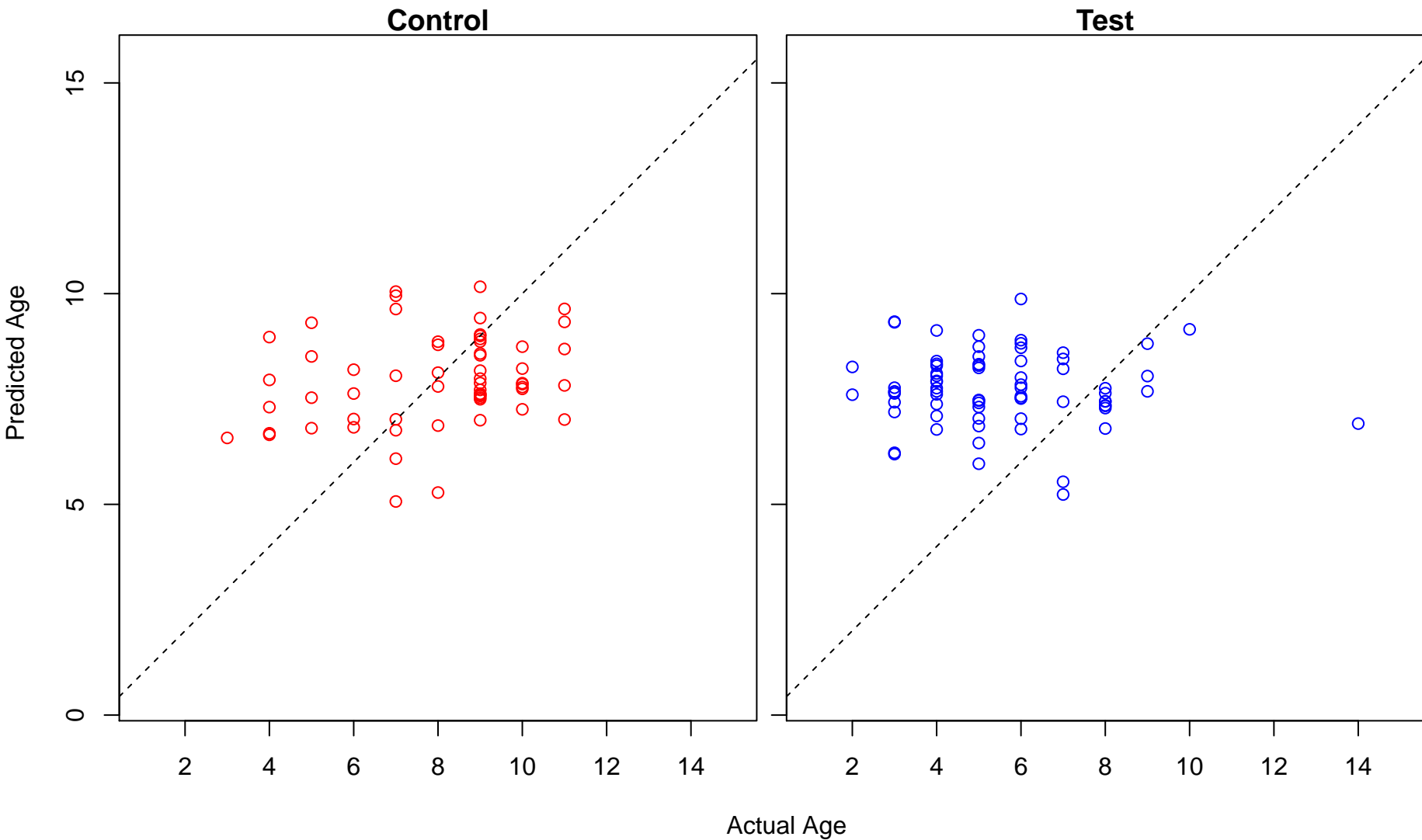
regulation of T-helper 1 cell differentiation (Score: 0.369982)



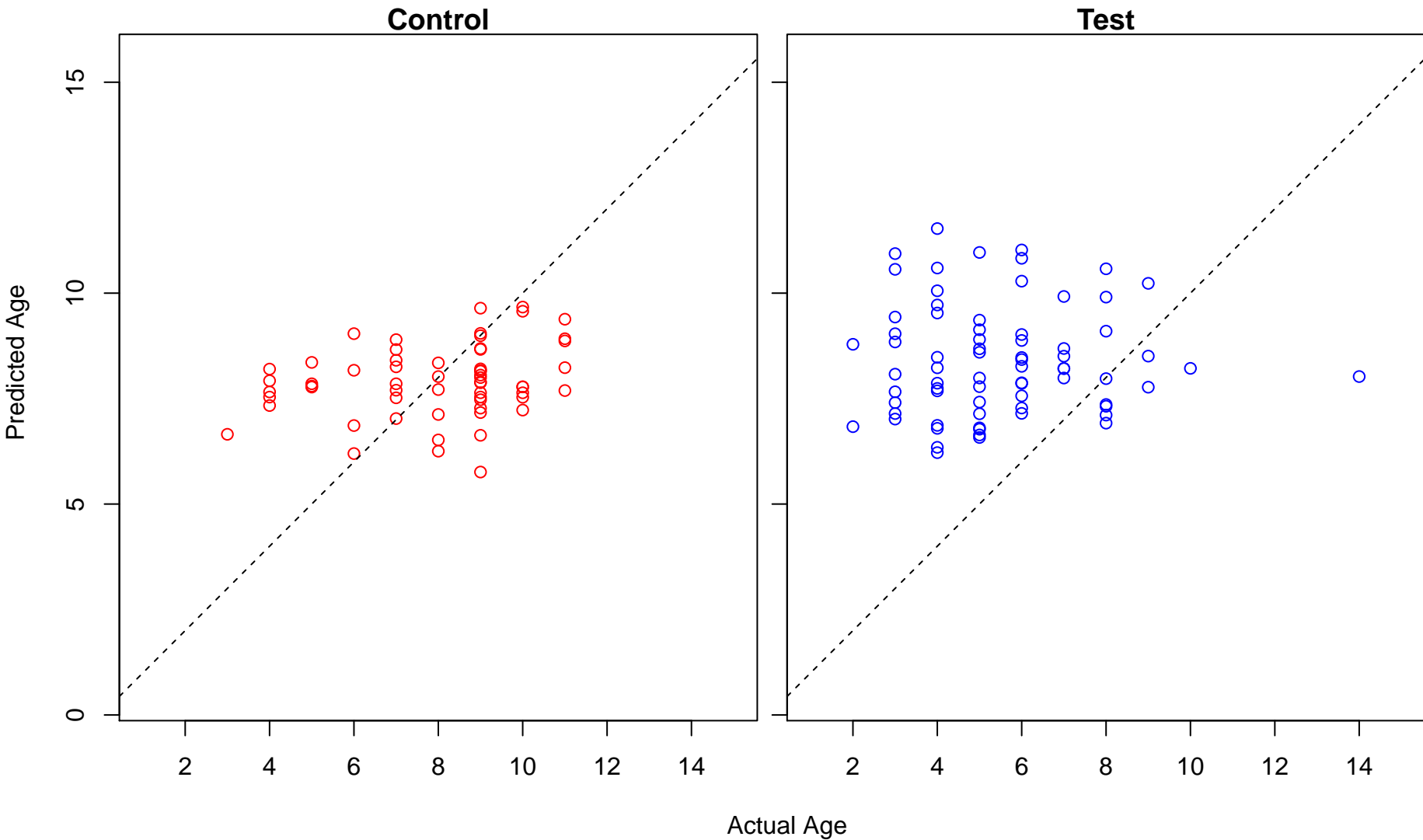
compound eye development (Score: 0.368218)



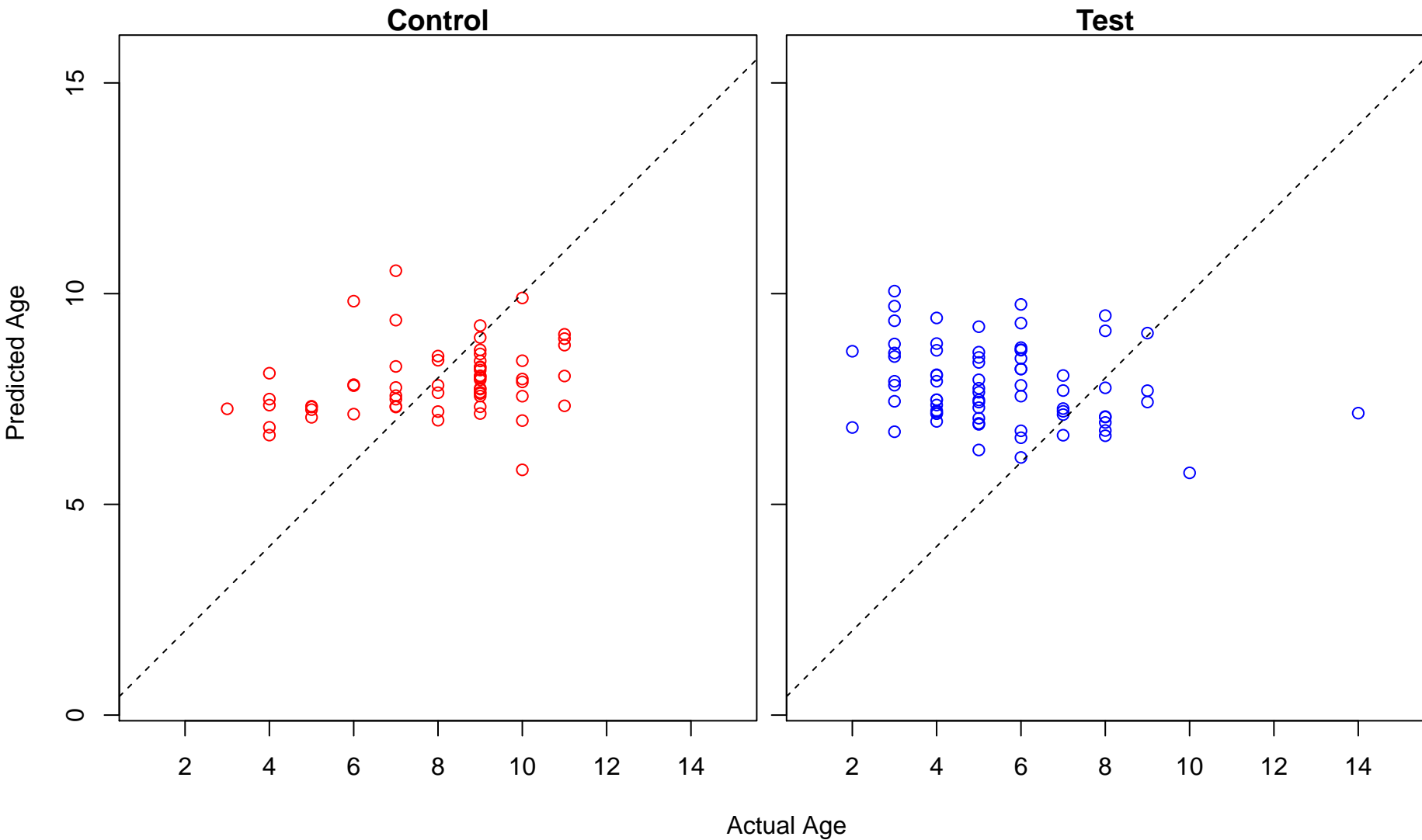
positive regulation of maintenance of mitotic sister chromatid cohesion (Score: 0.366812)



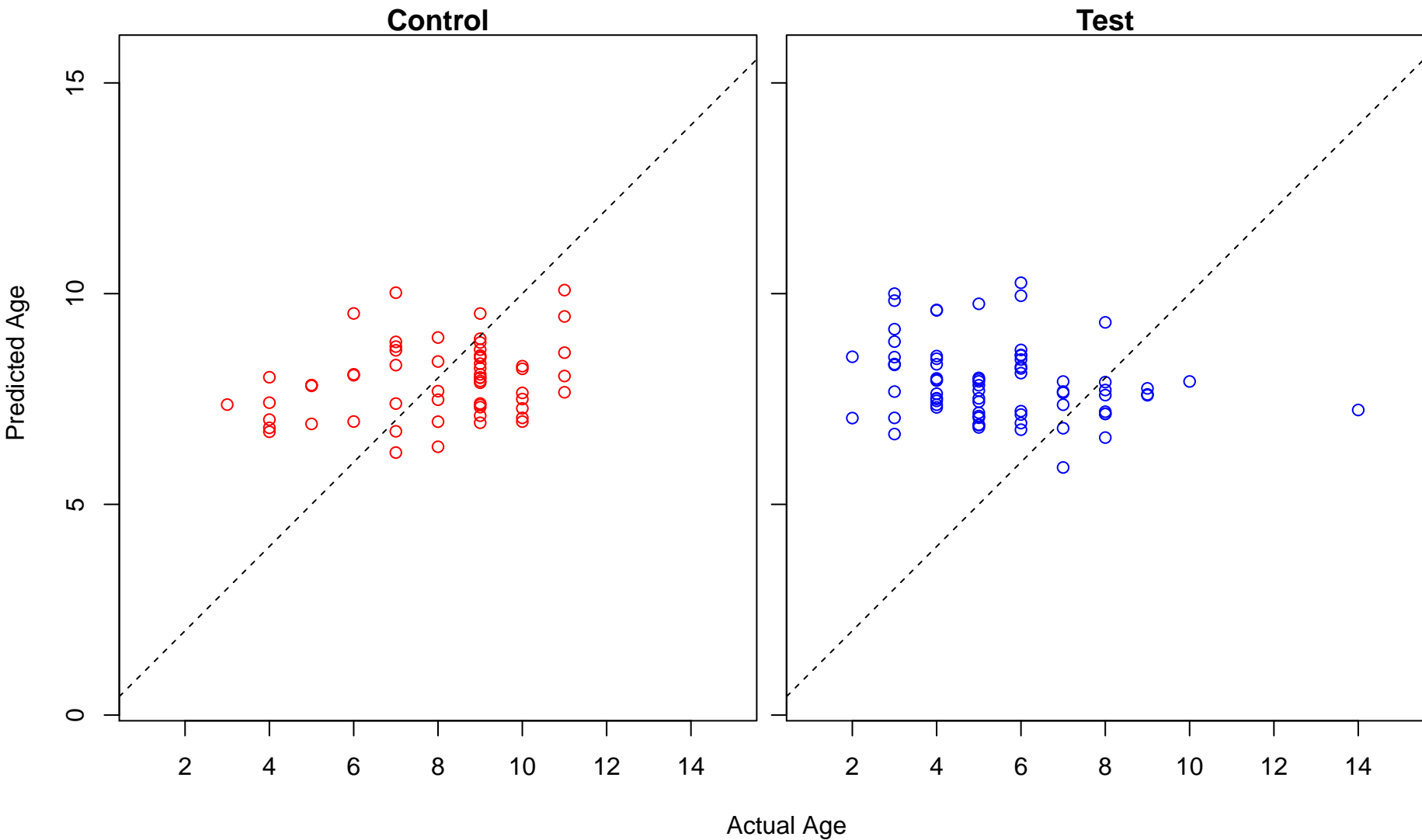
positive regulation of cartilage development (Score: 0.366003)

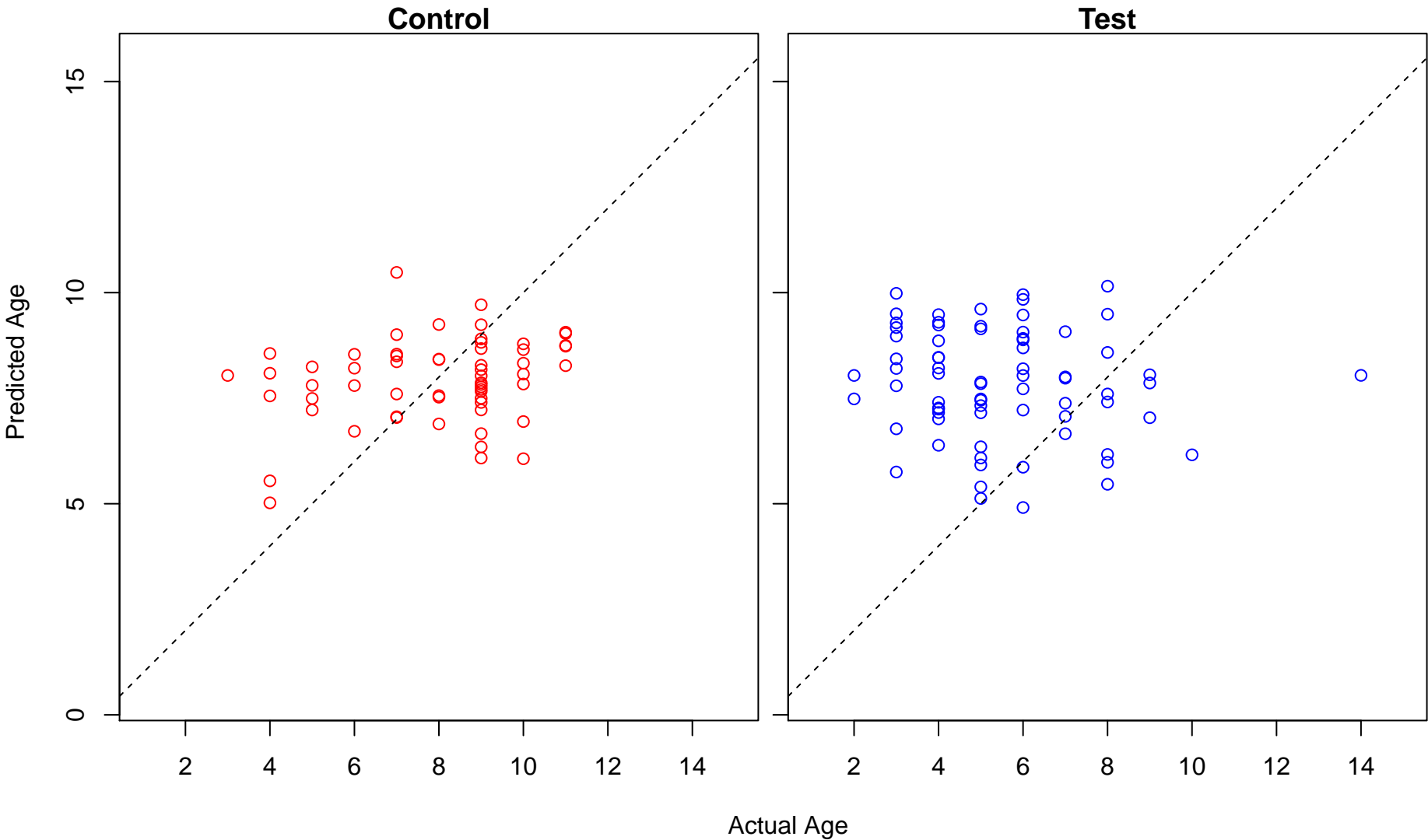


histone H3-T11 phosphorylation (Score: 0.364838)

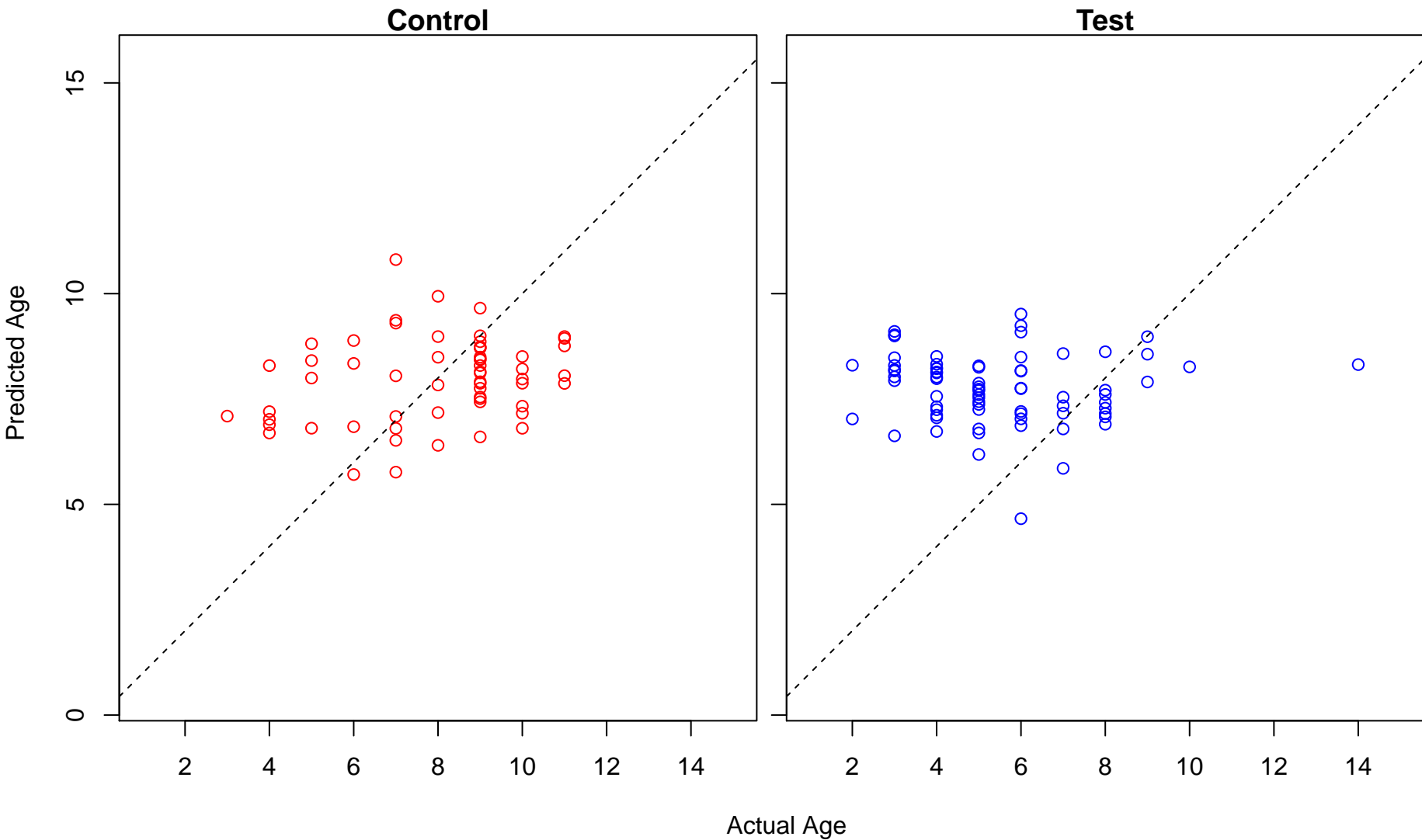


erythrocyte maturation (Score: 0.364147)

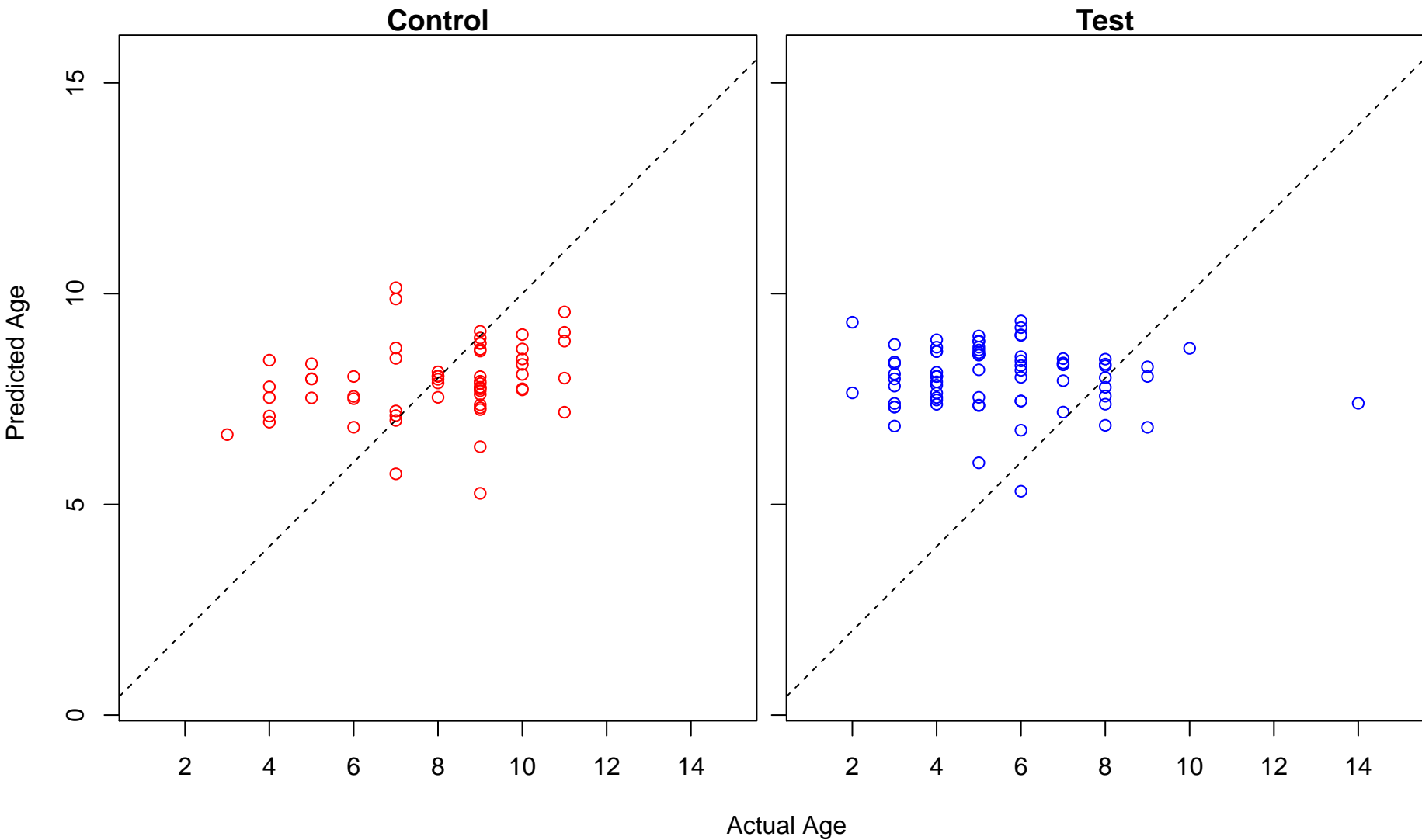




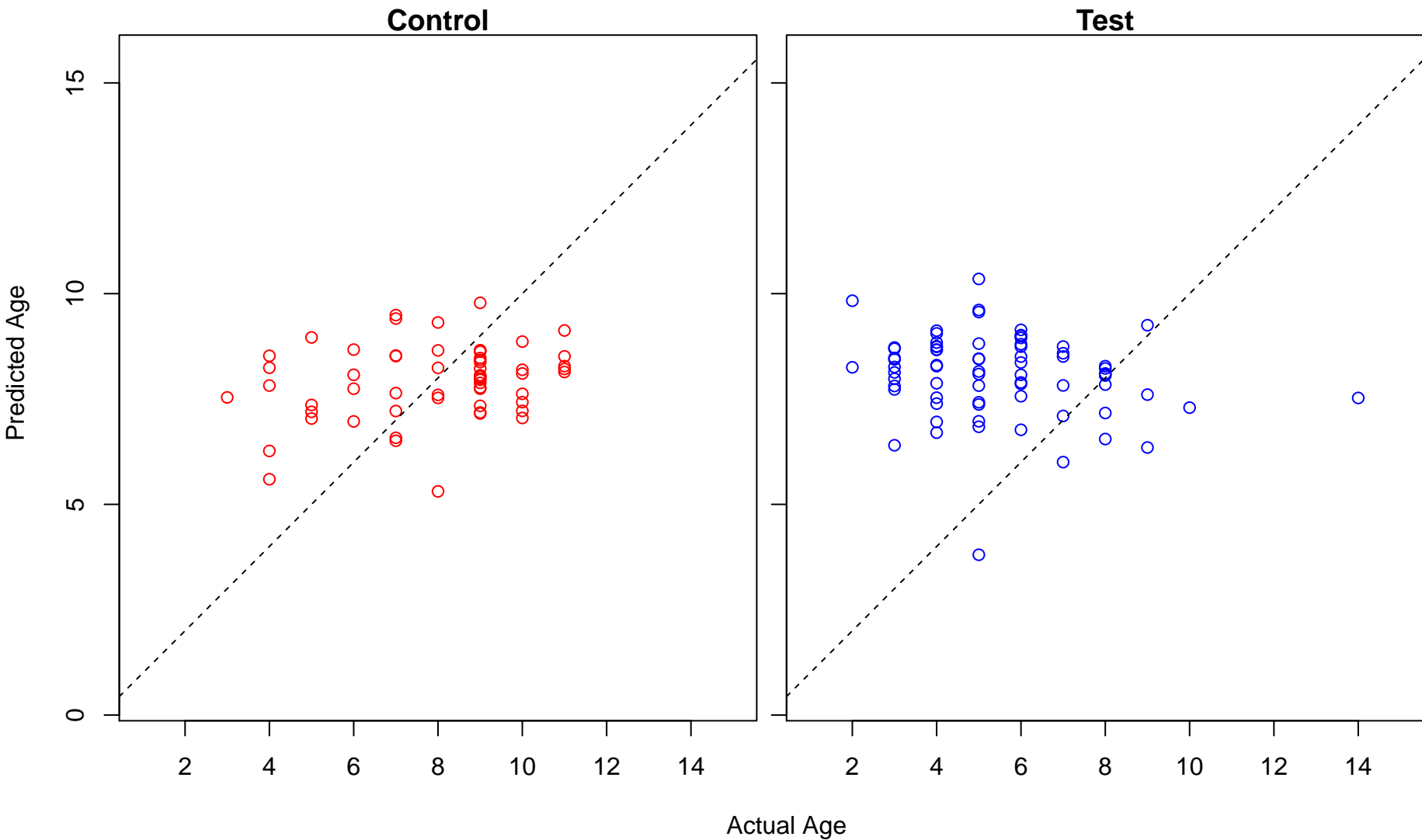
negative regulation of T cell mediated cytotoxicity (Score: 0.362207)



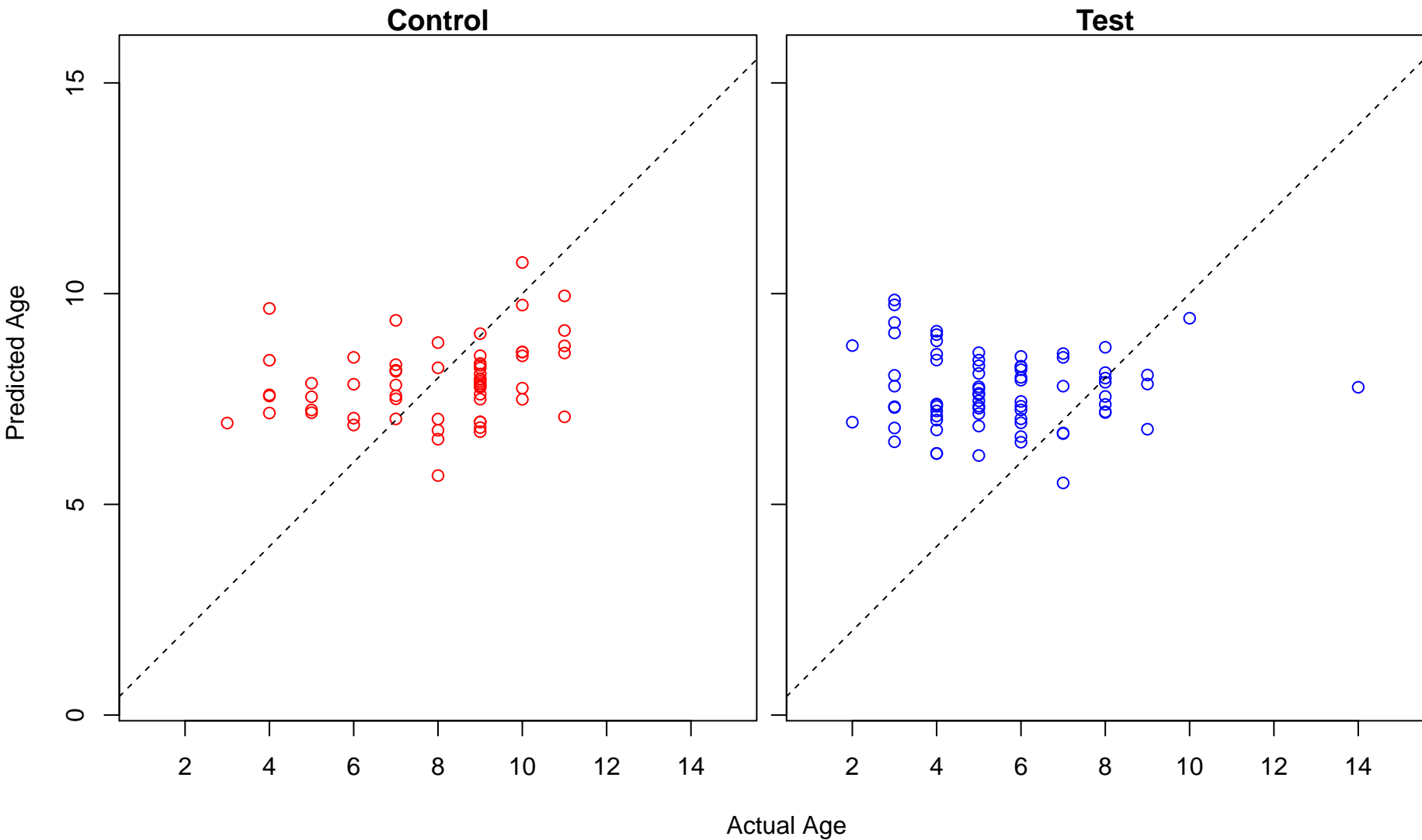
actin polymerization-dependent cell motility (Score: 0.360801)



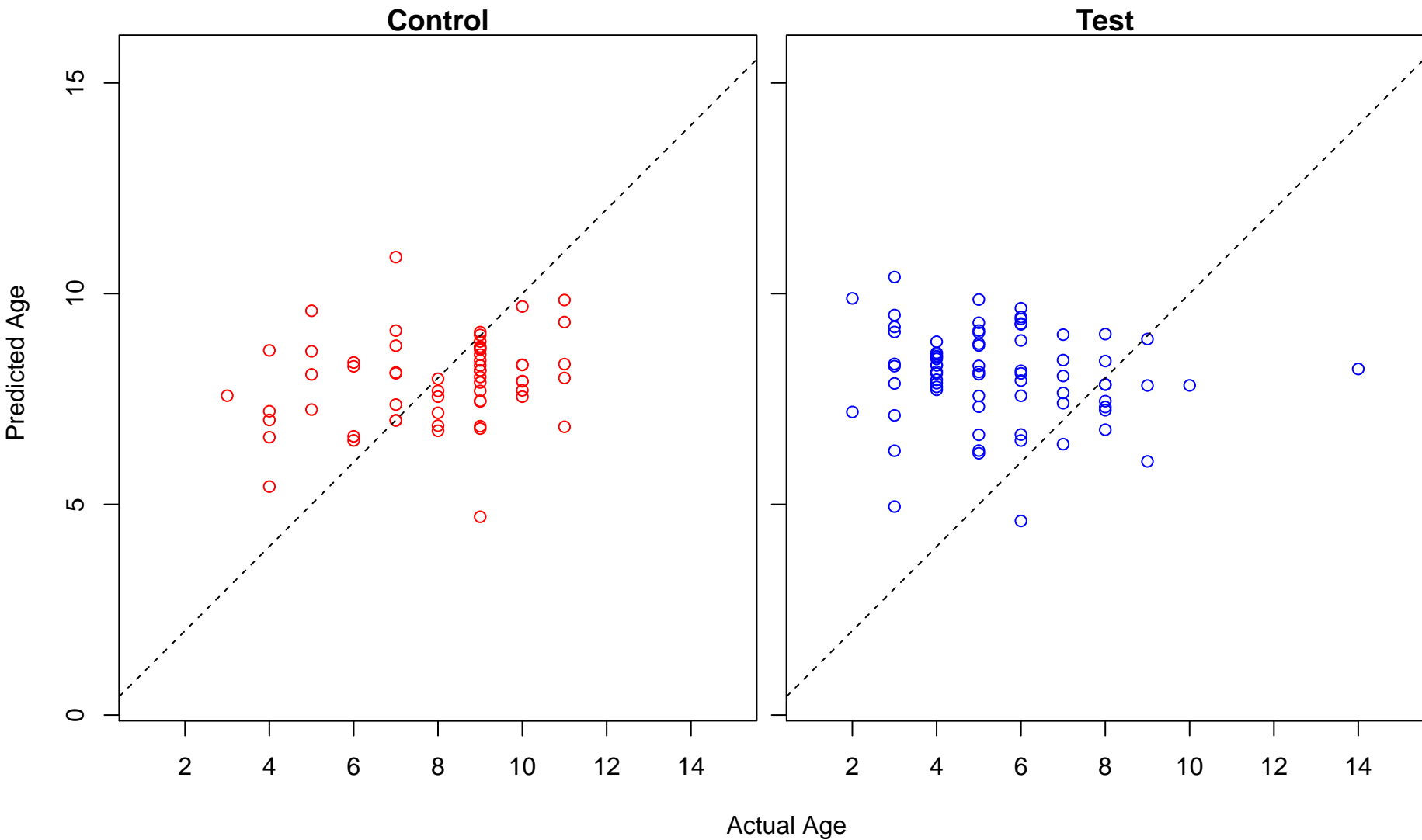
ERK5 cascade (Score: 0.360359)



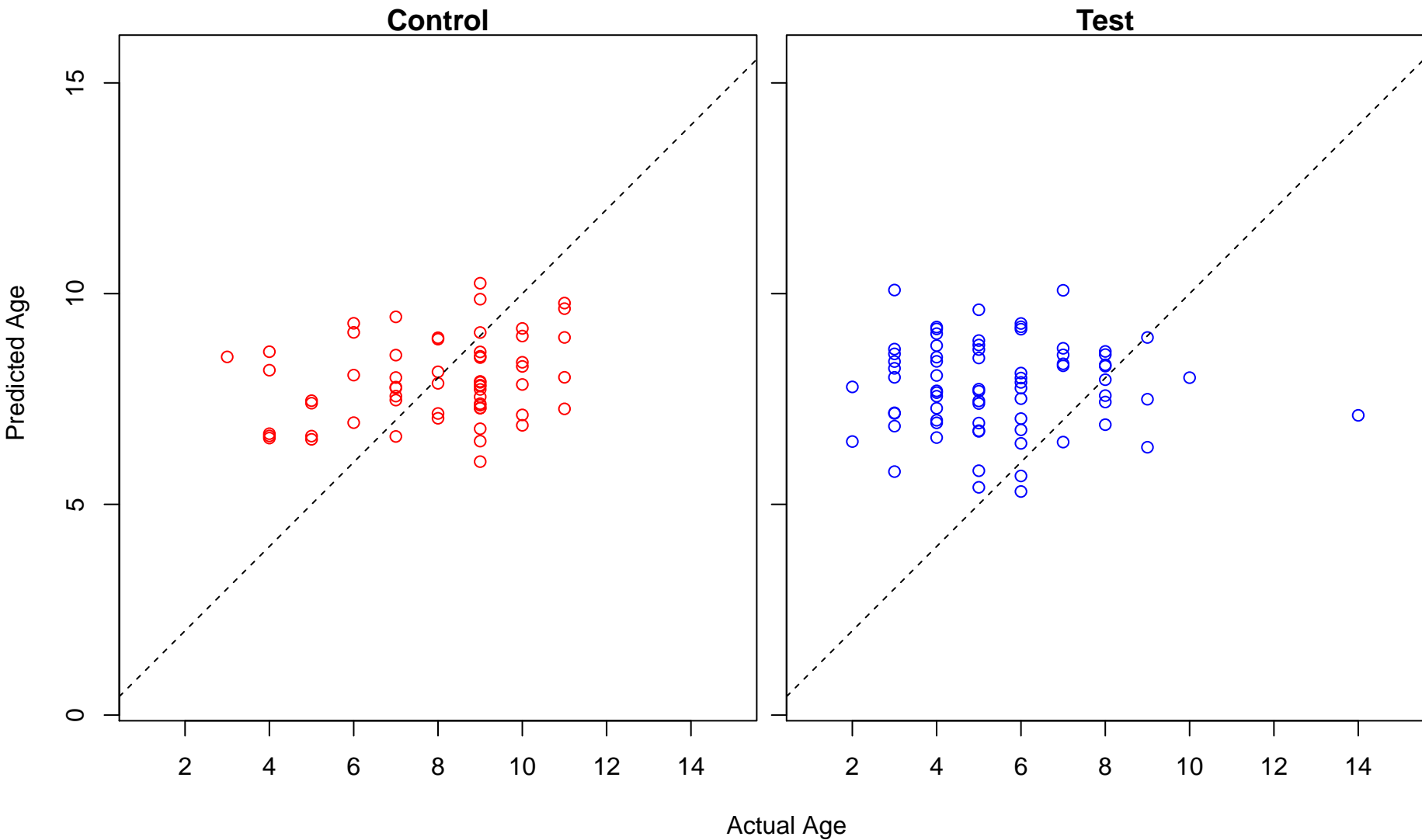
4-hydroxyproline catabolic process (Score: 0.357330)



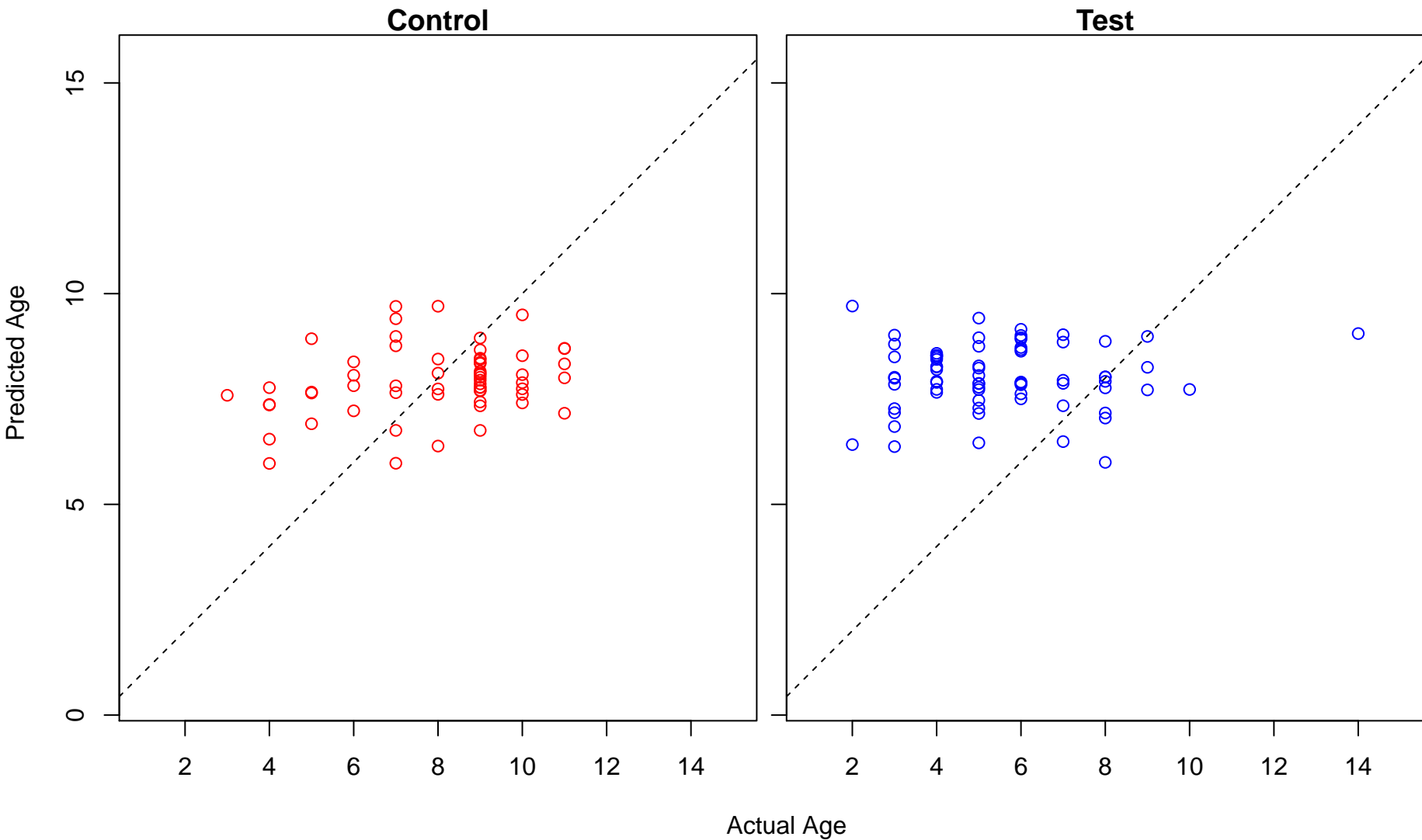
mature ribosome assembly (Score: 0.356562)



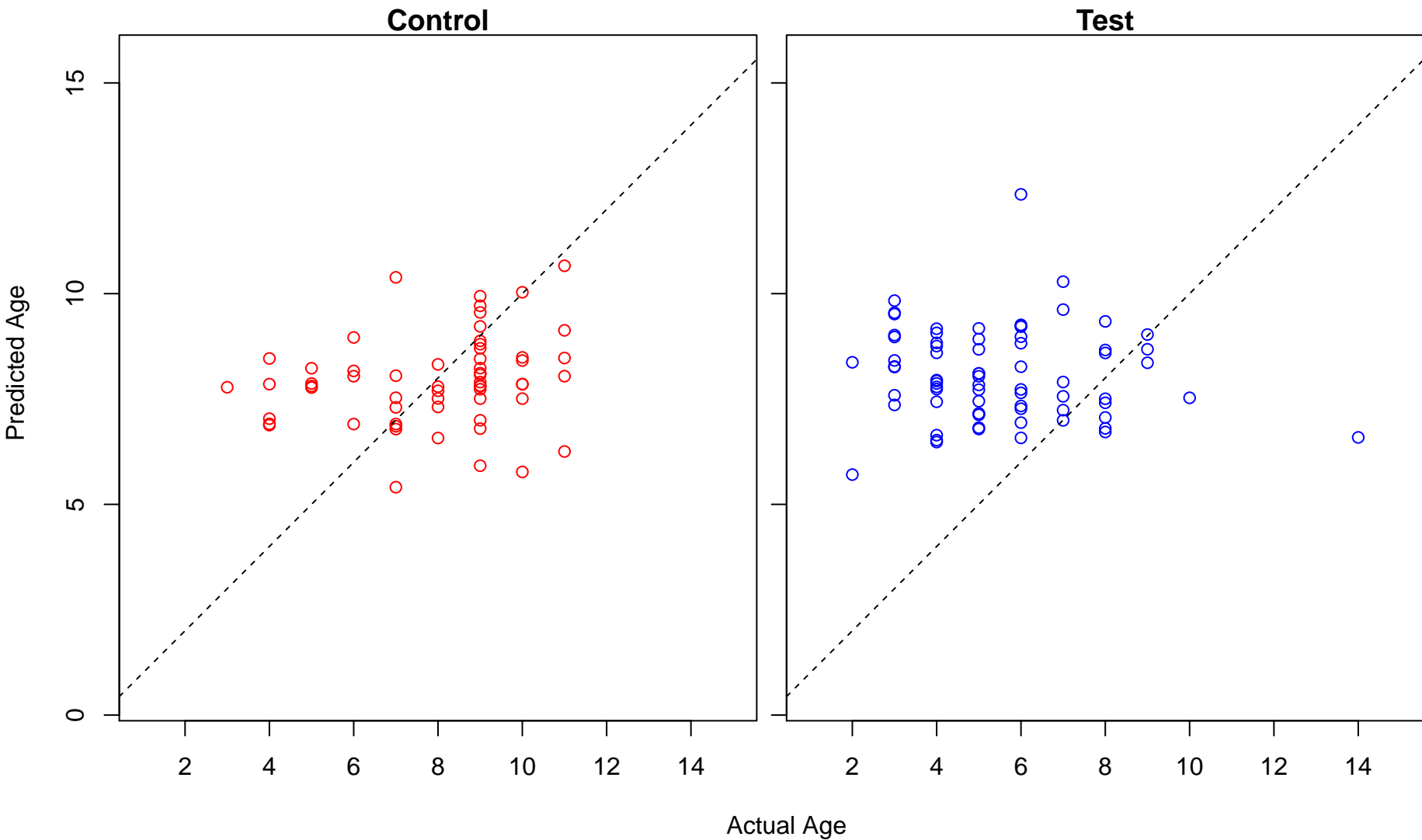
negative regulation of phospholipase C activity (Score: 0.356436)



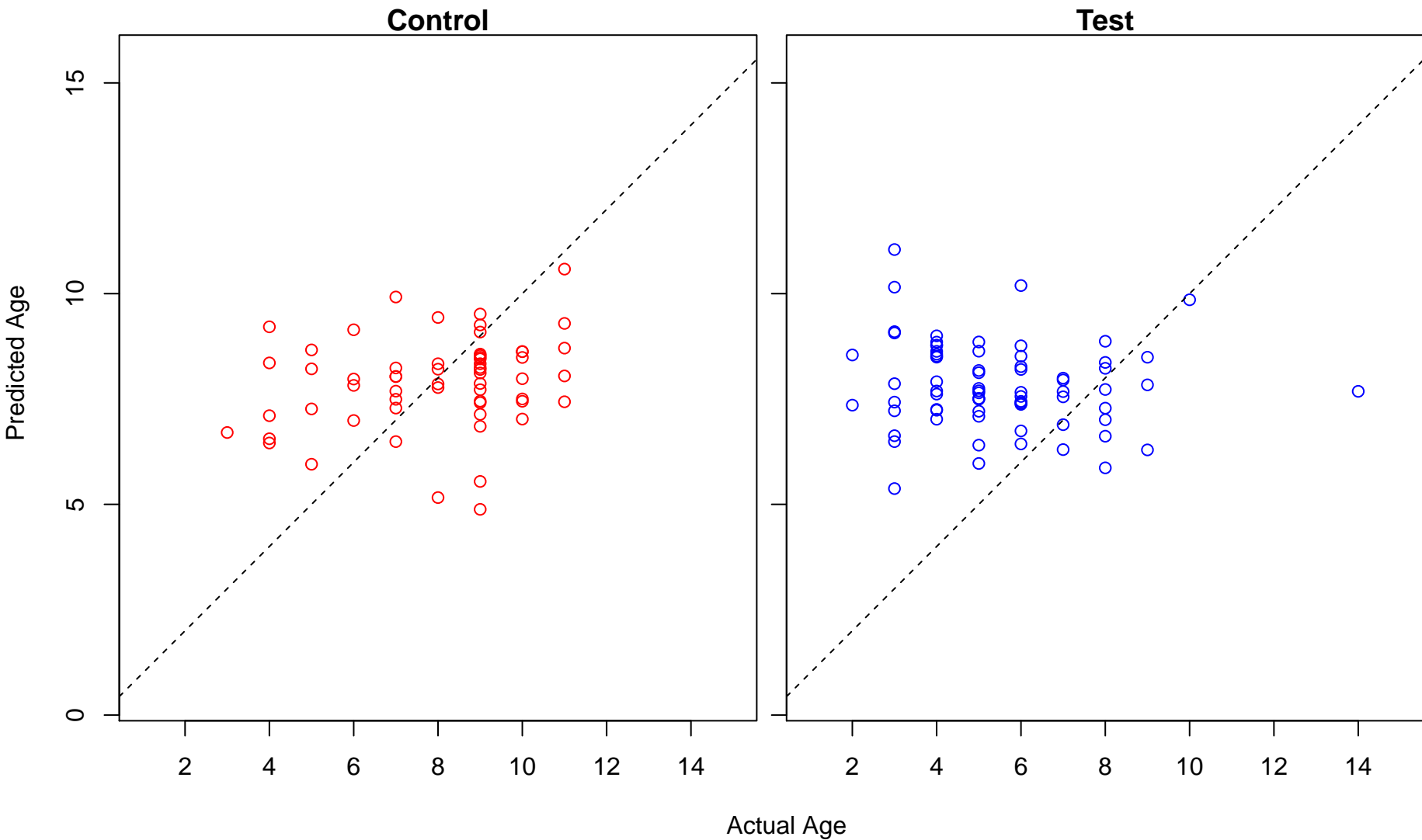
positive regulation of neurotransmitter transport (Score: 0.354292)



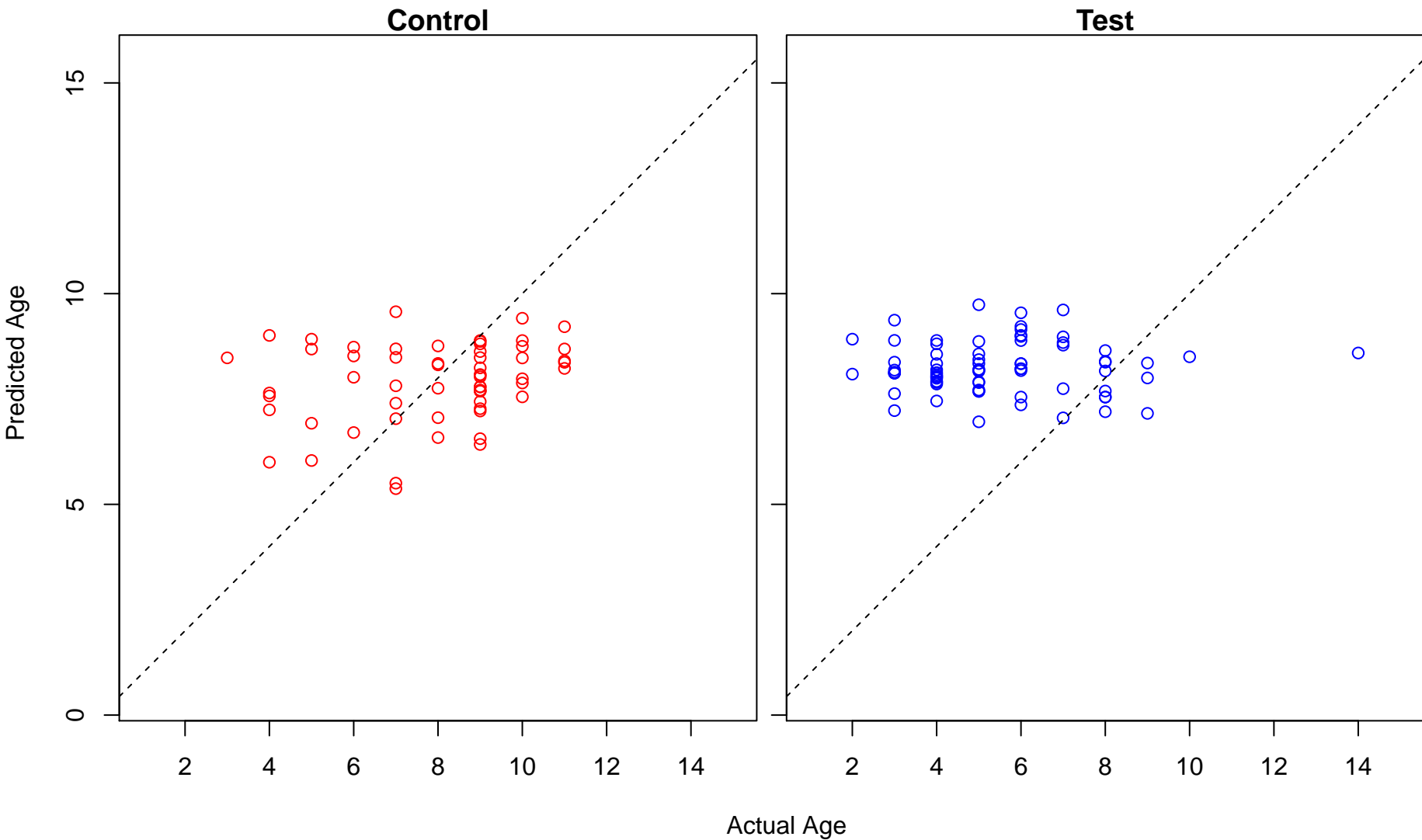
retina layer formation (Score: 0.354036)



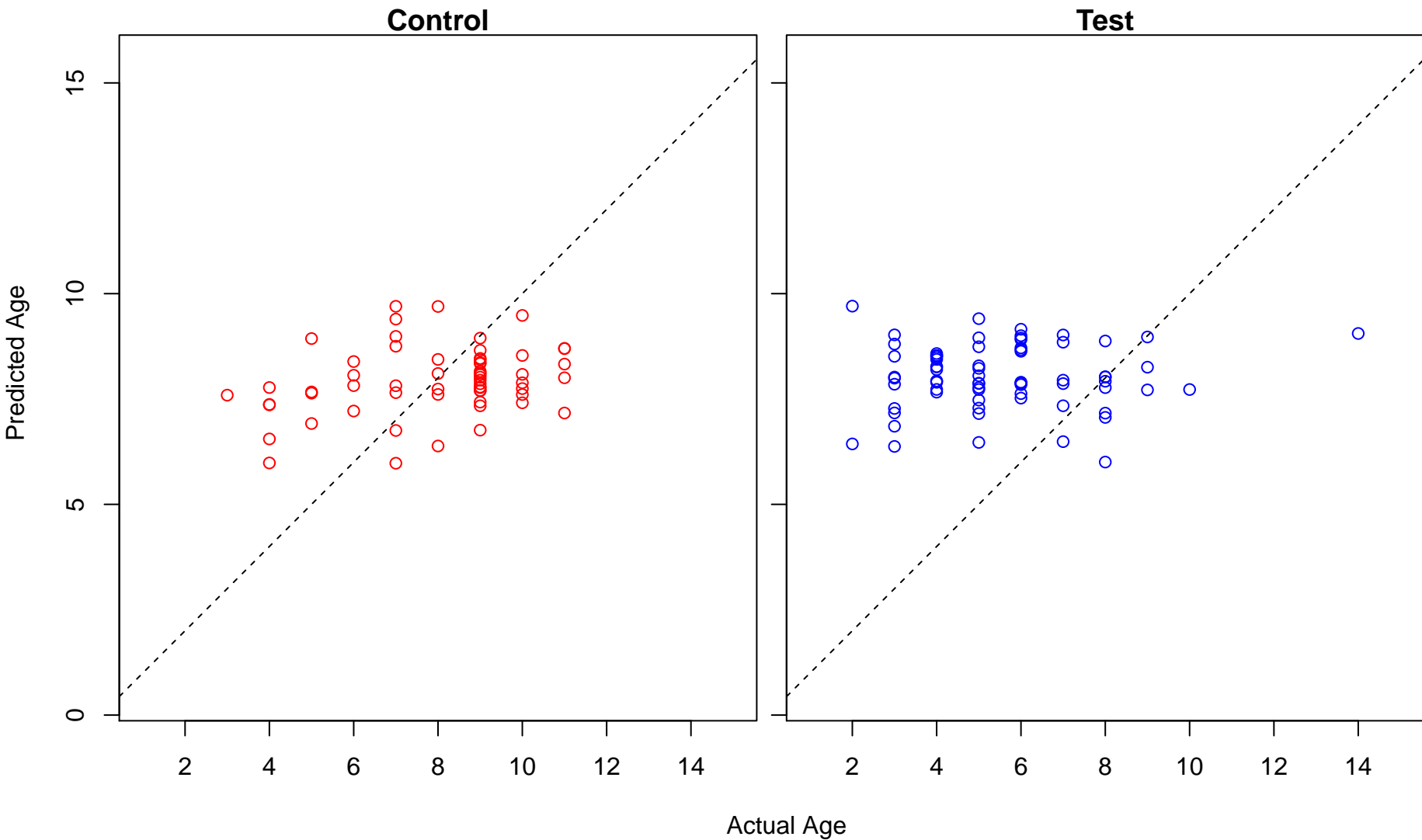
negative regulation of histone H3–K9 methylation (Score: 0.353660)



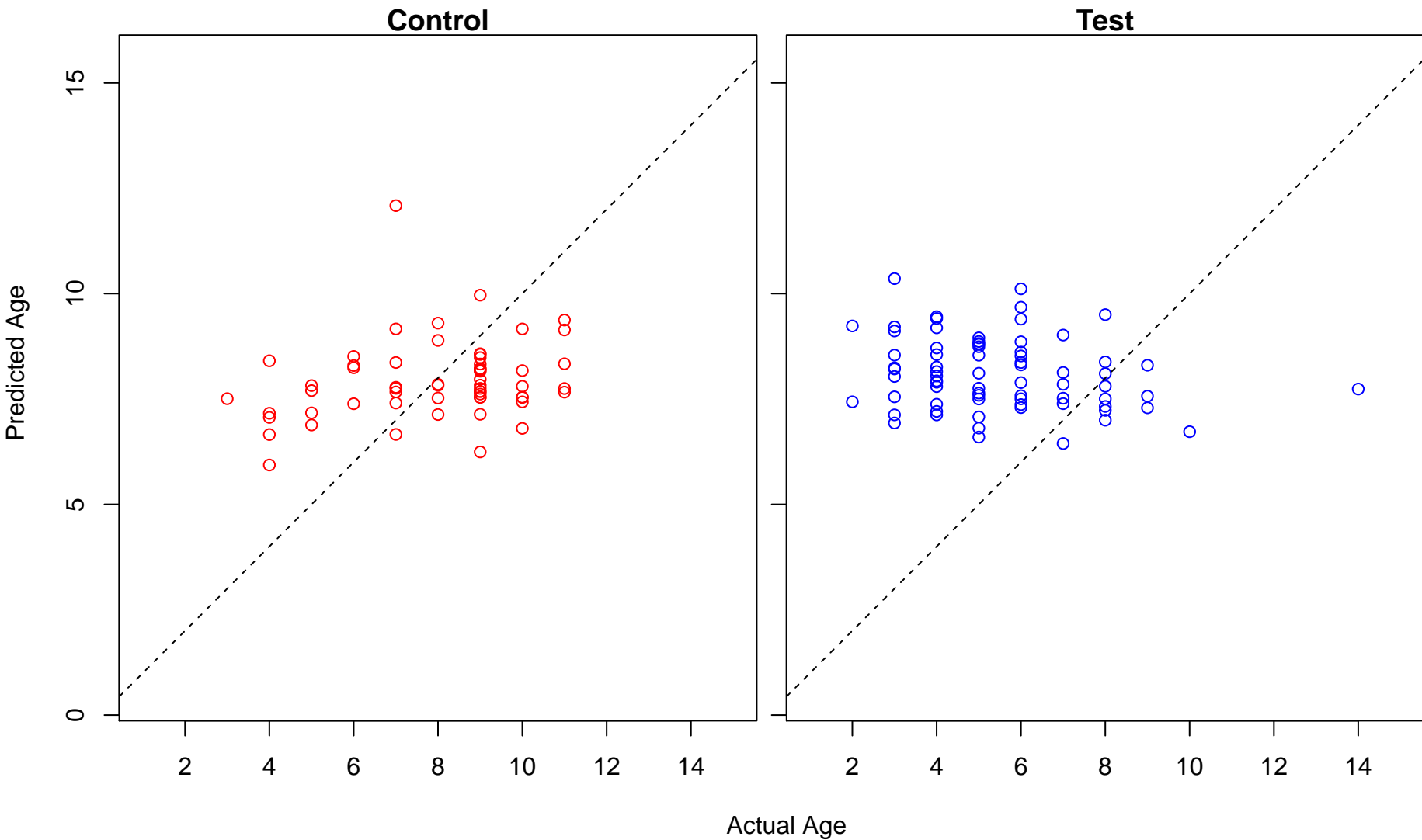
malate-aspartate shuttle (Score: 0.353185)



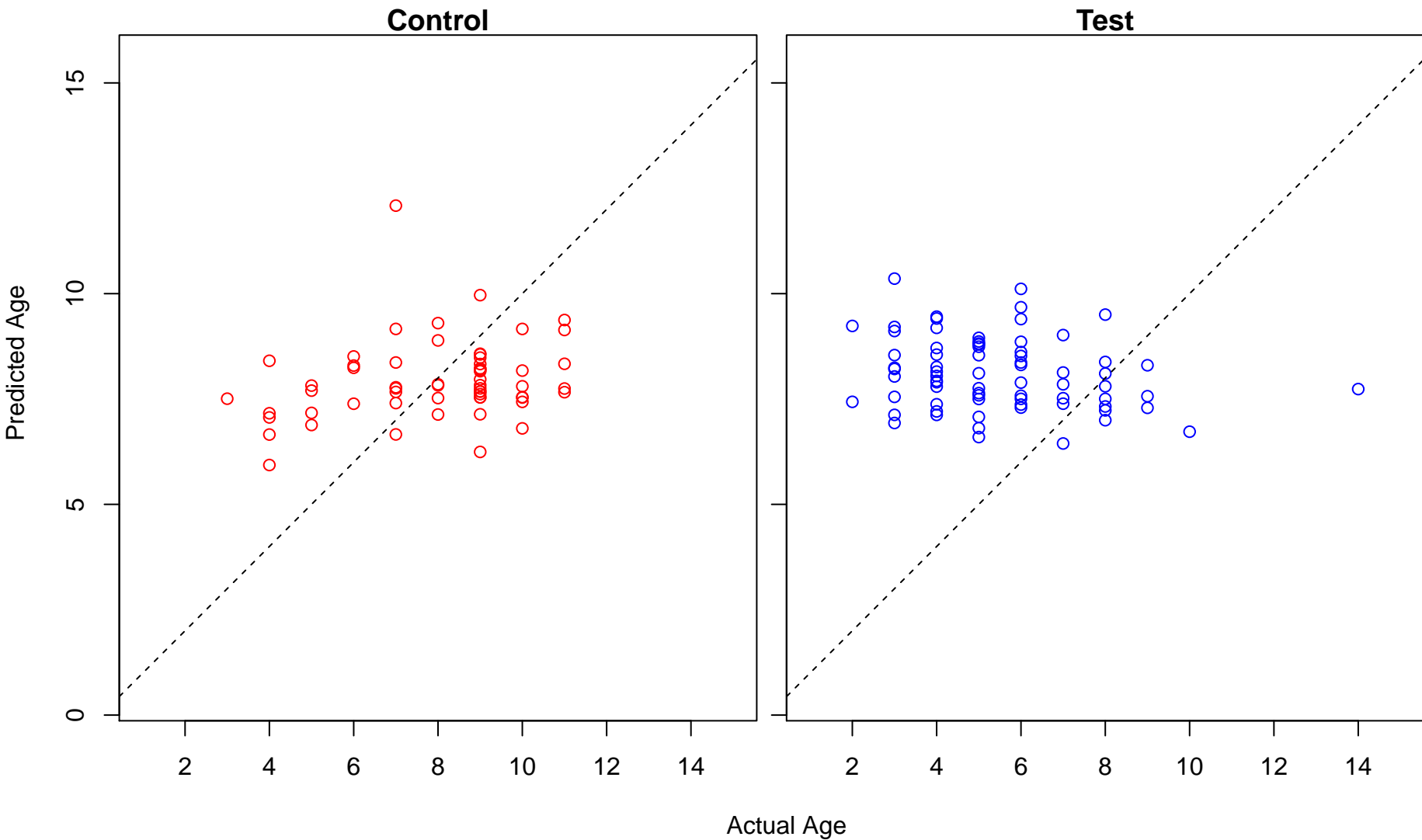
positive regulation of neurotransmitter secretion (Score: 0.352428)



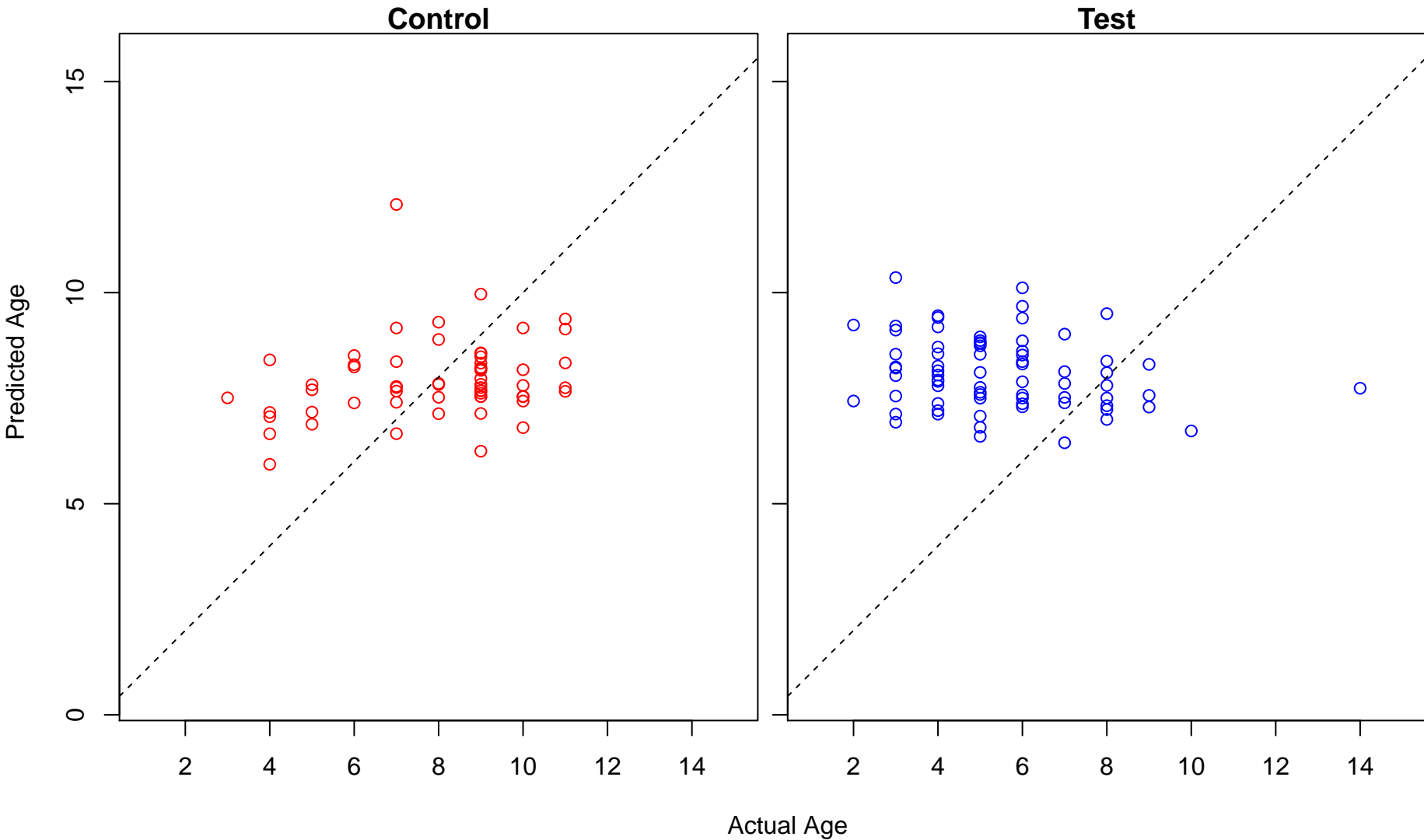
positive regulation of muscle tissue development (Score: 0.352192)



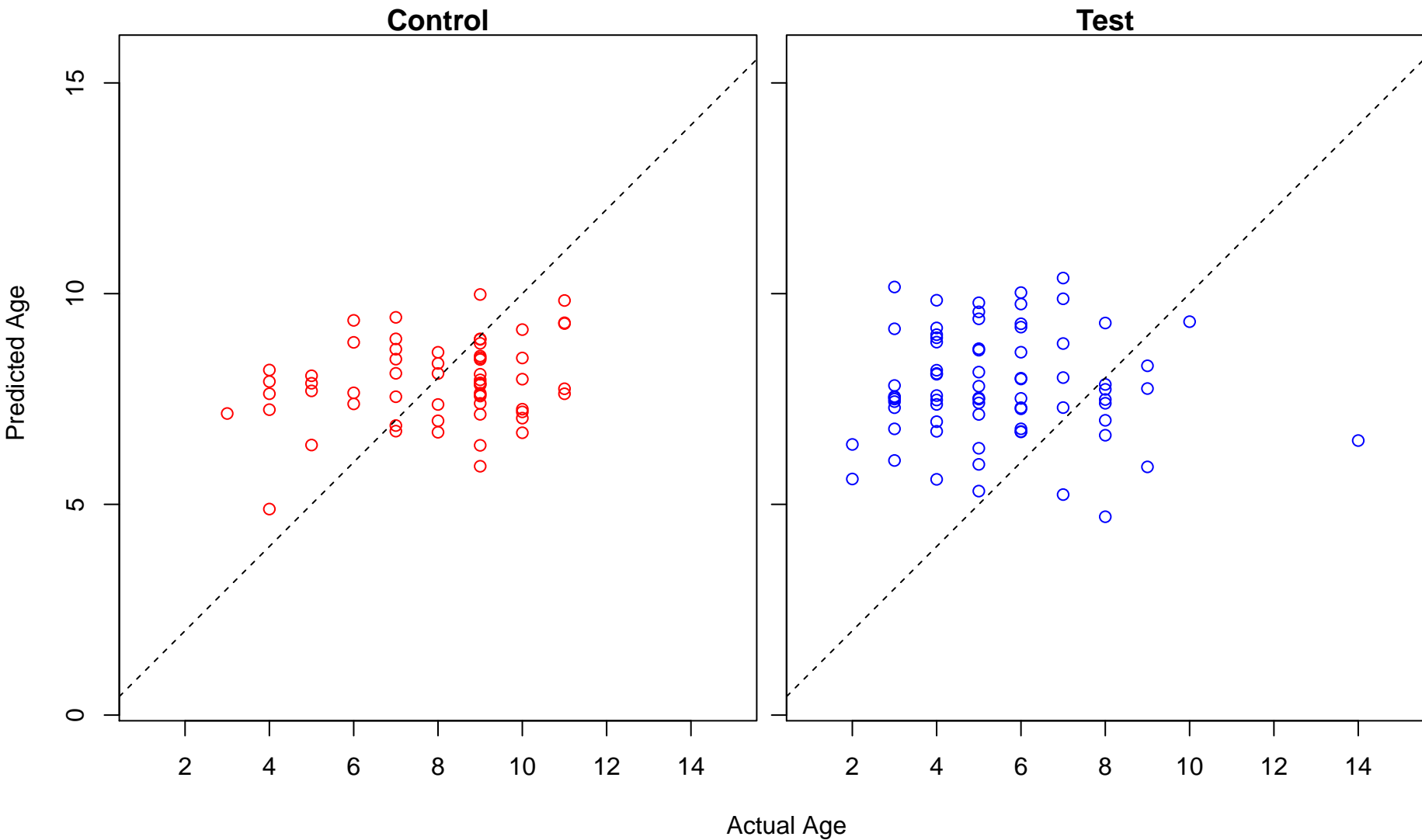
positive regulation of striated muscle tissue development (Score: 0.352183)



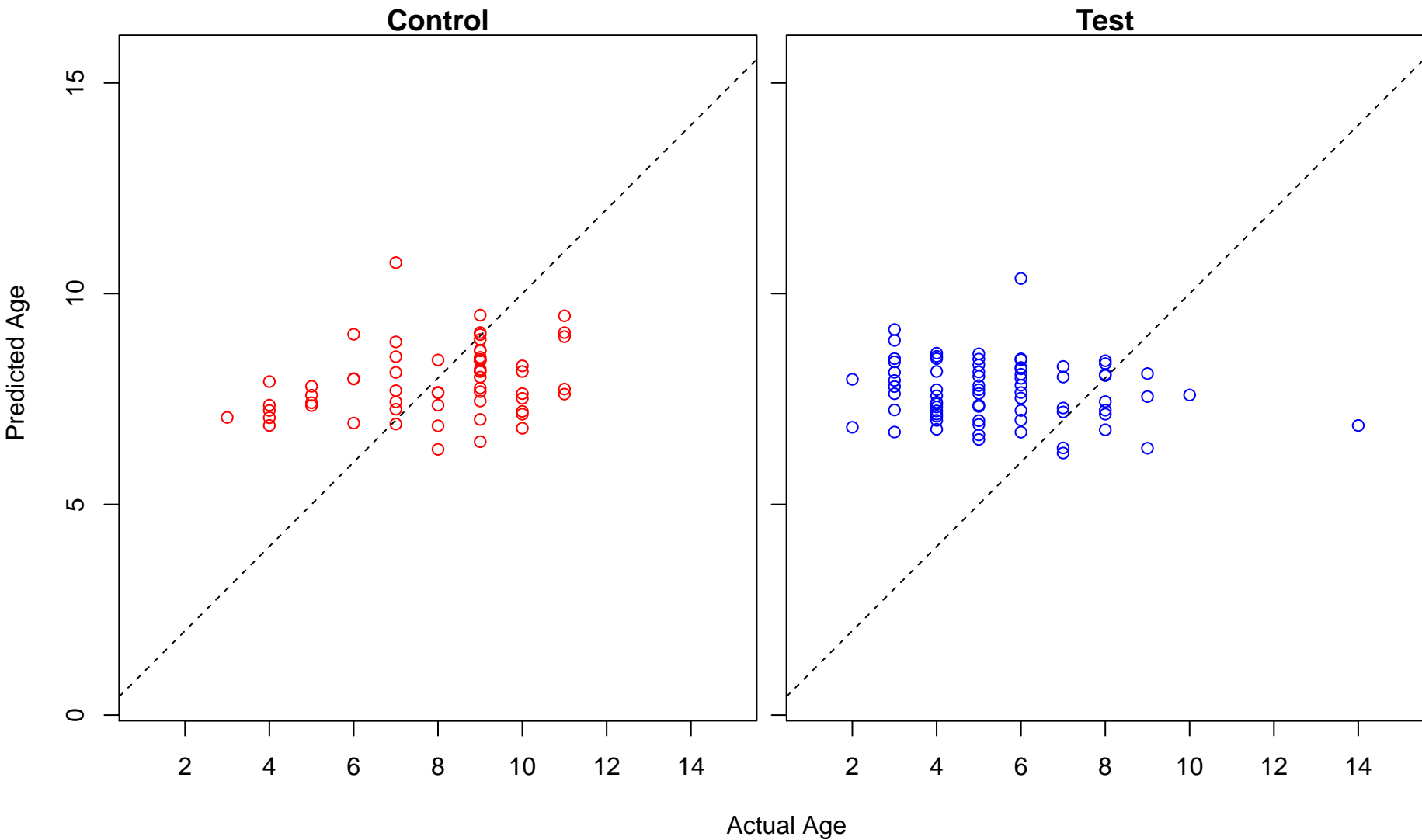
positive regulation of muscle organ development (Score: 0.352183)



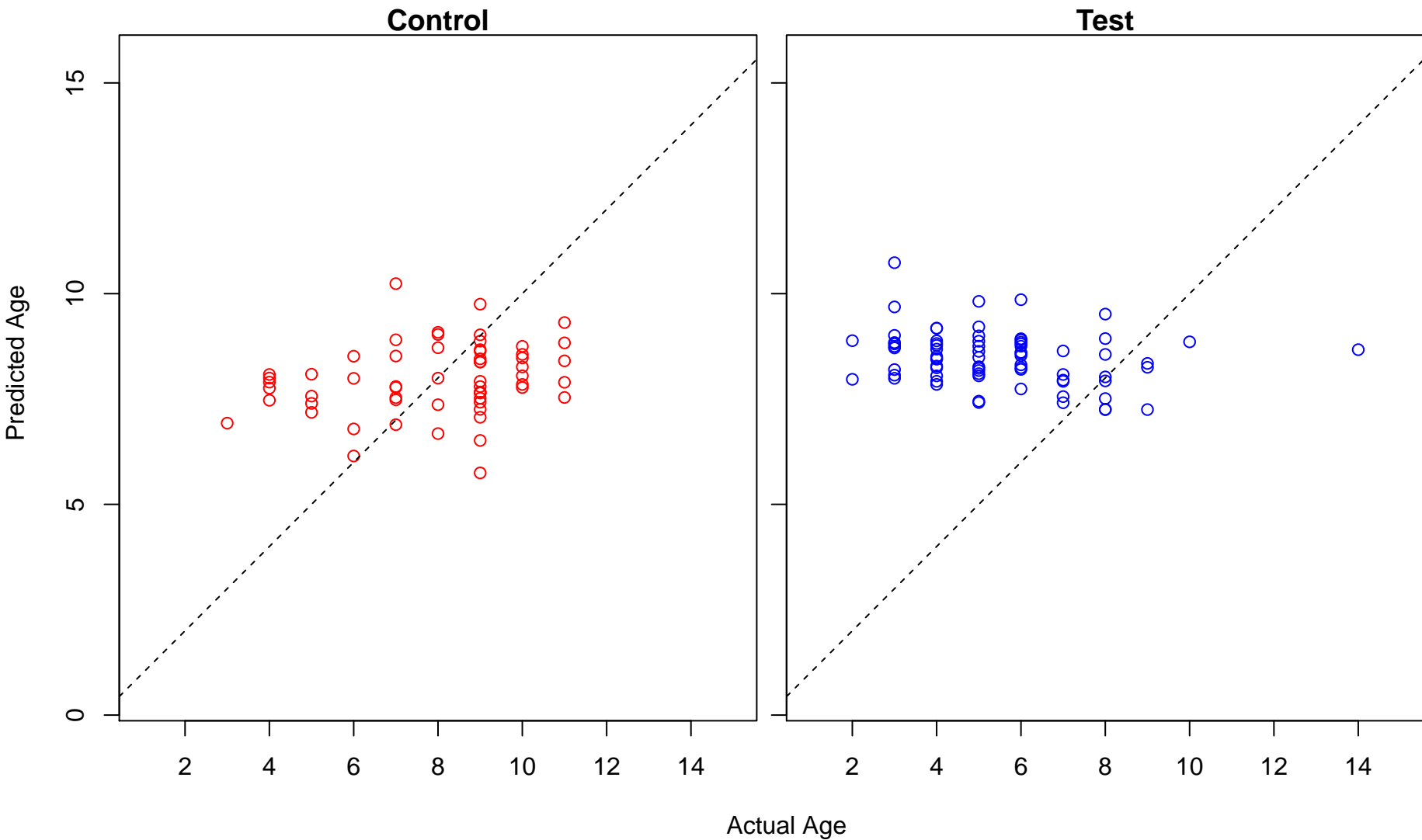
regulation of systemic arterial blood pressure by endothelin (Score: 0.349780)



fibril organization (Score: 0.349129)

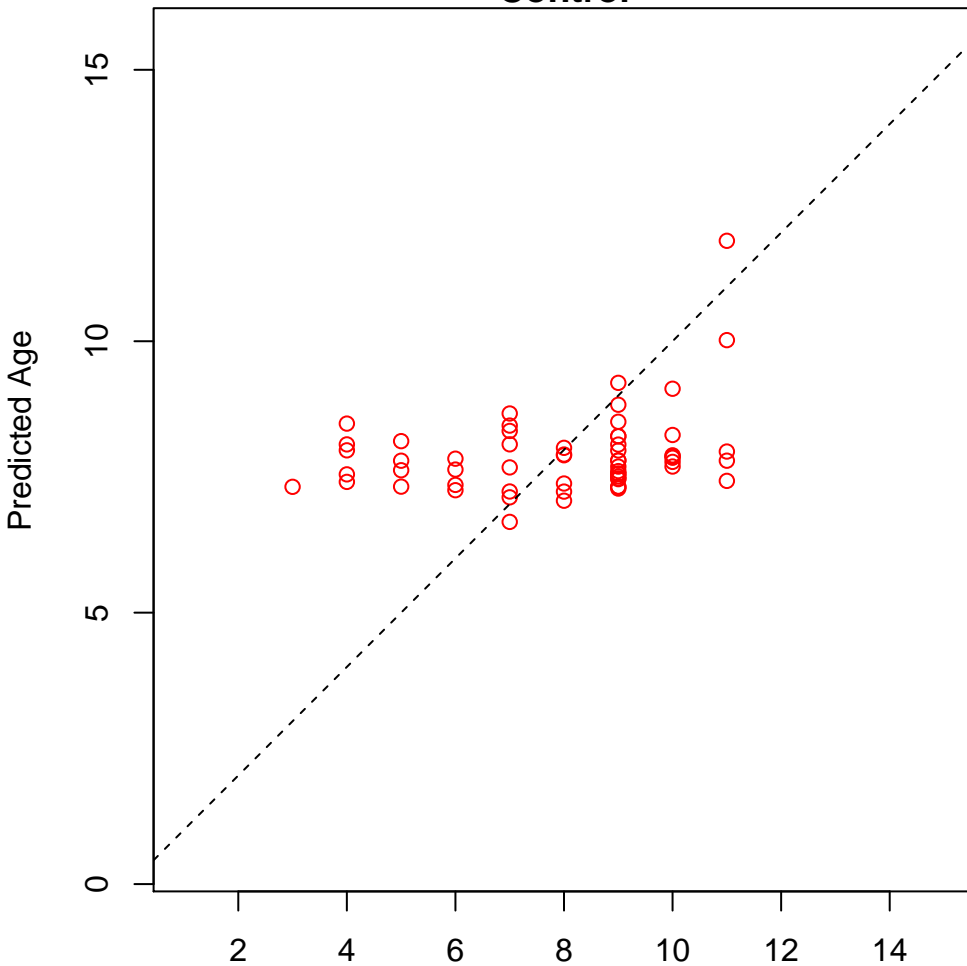


positive regulation of phospholipid biosynthetic process (Score: 0.347528)

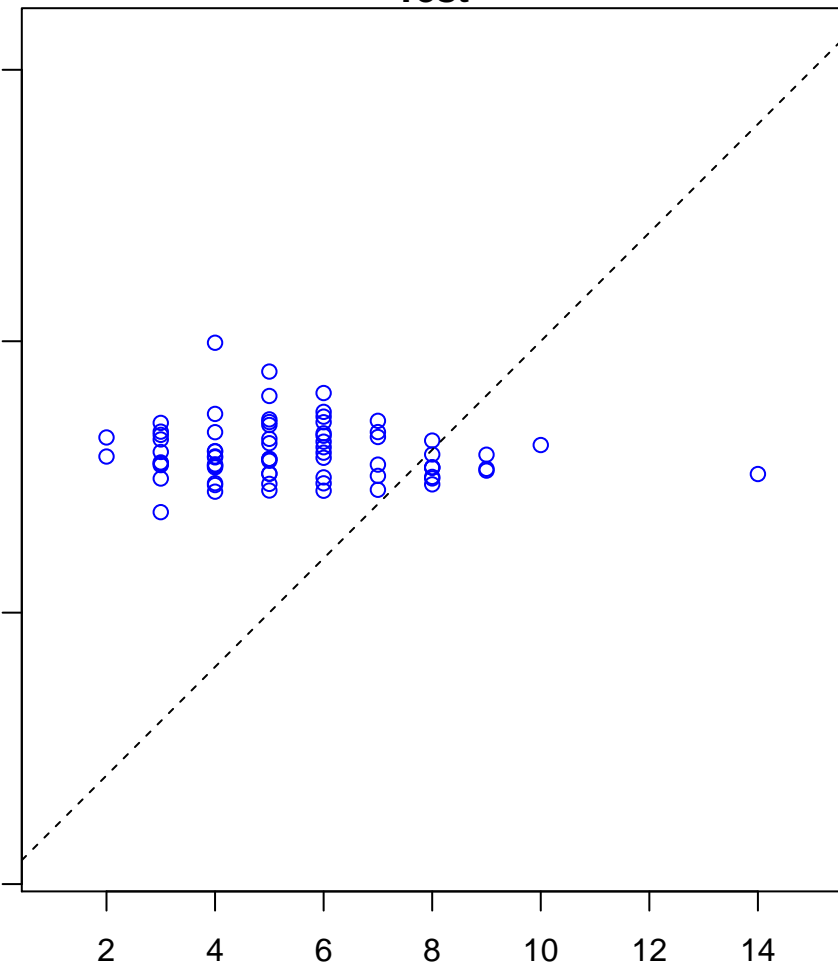


central nervous system morphogenesis (Score: 0.346979)

Control

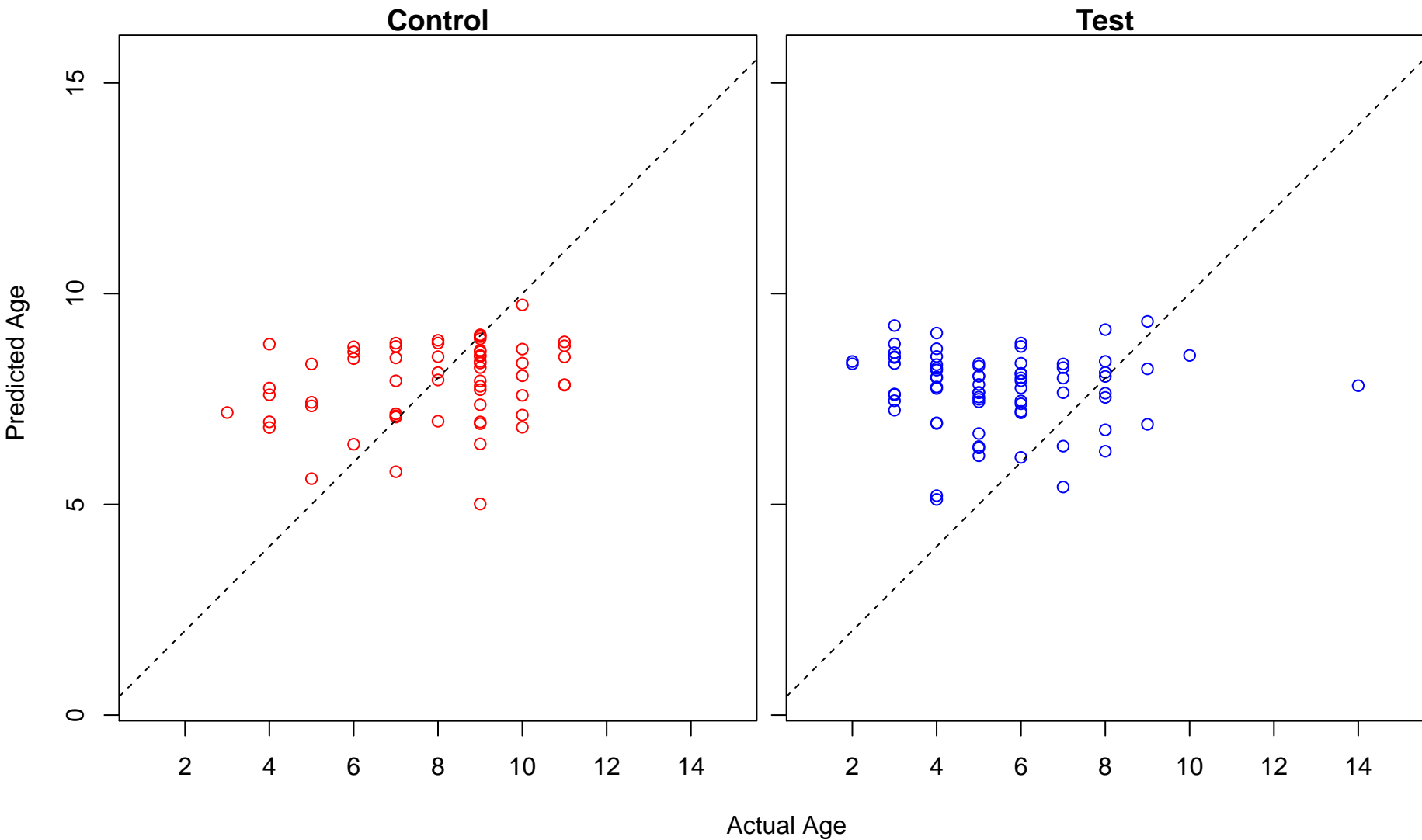


Test

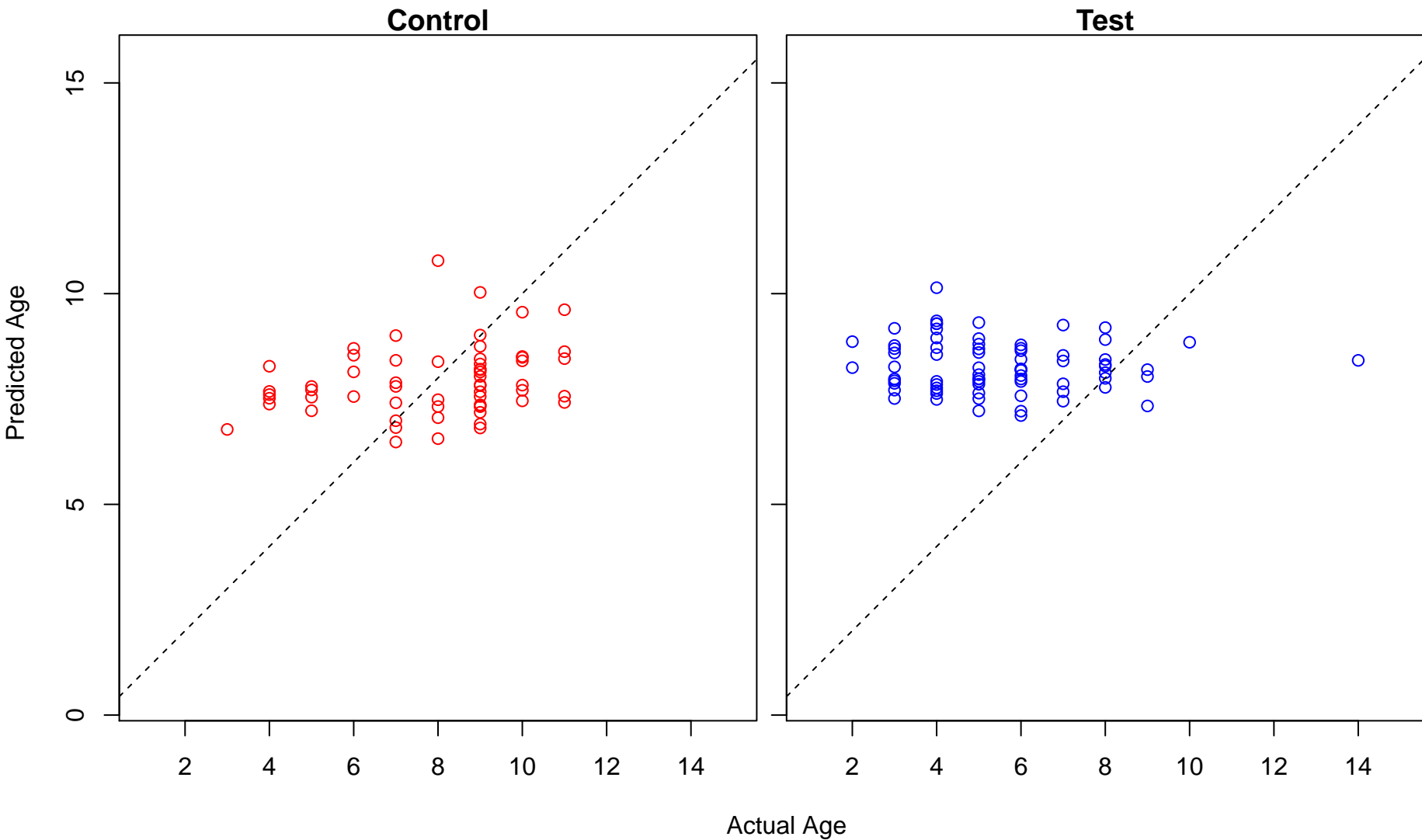


Actual Age

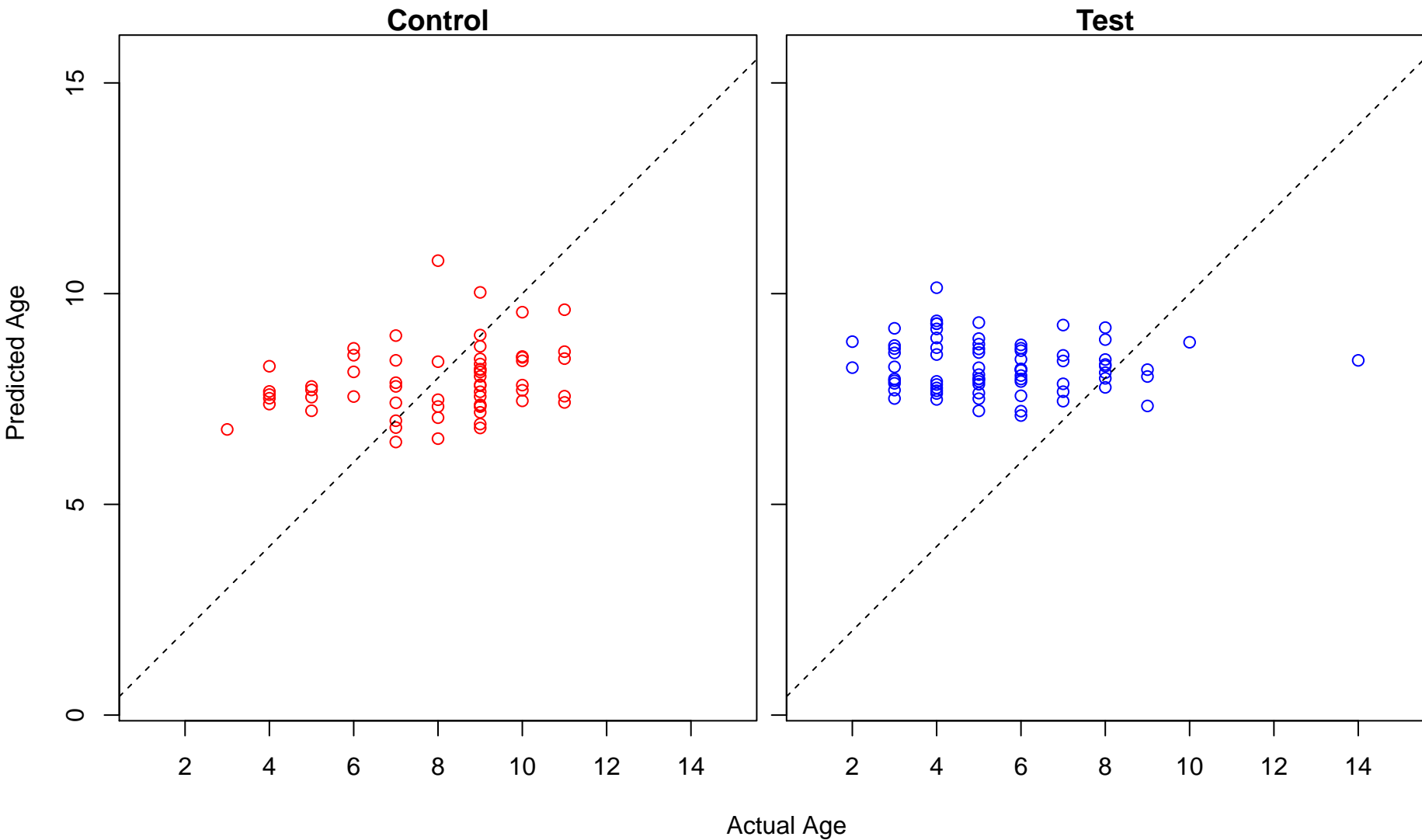
DNA replication, synthesis of RNA primer (Score: 0.343212)



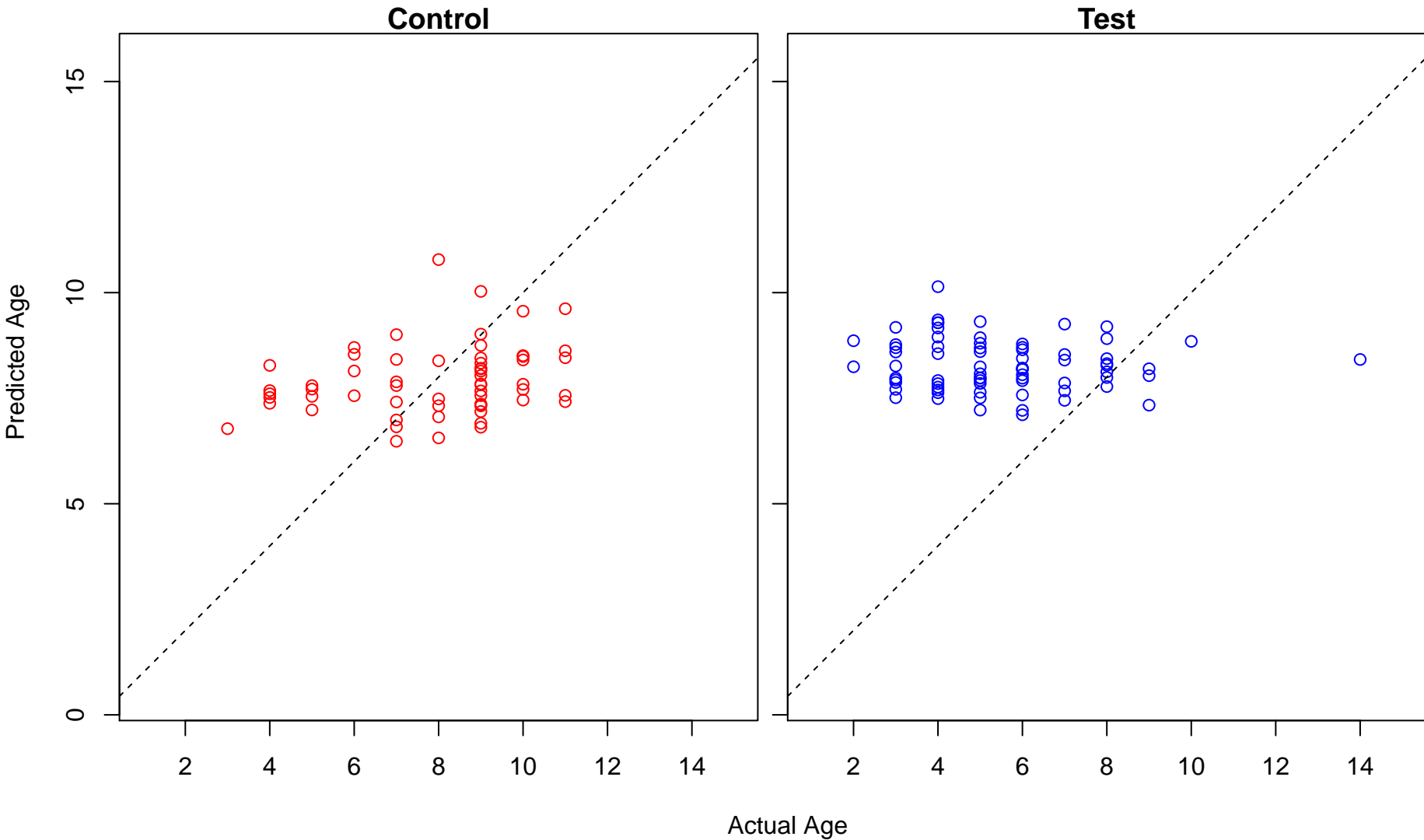
positive regulation of gonadotropin secretion (Score: 0.341399)



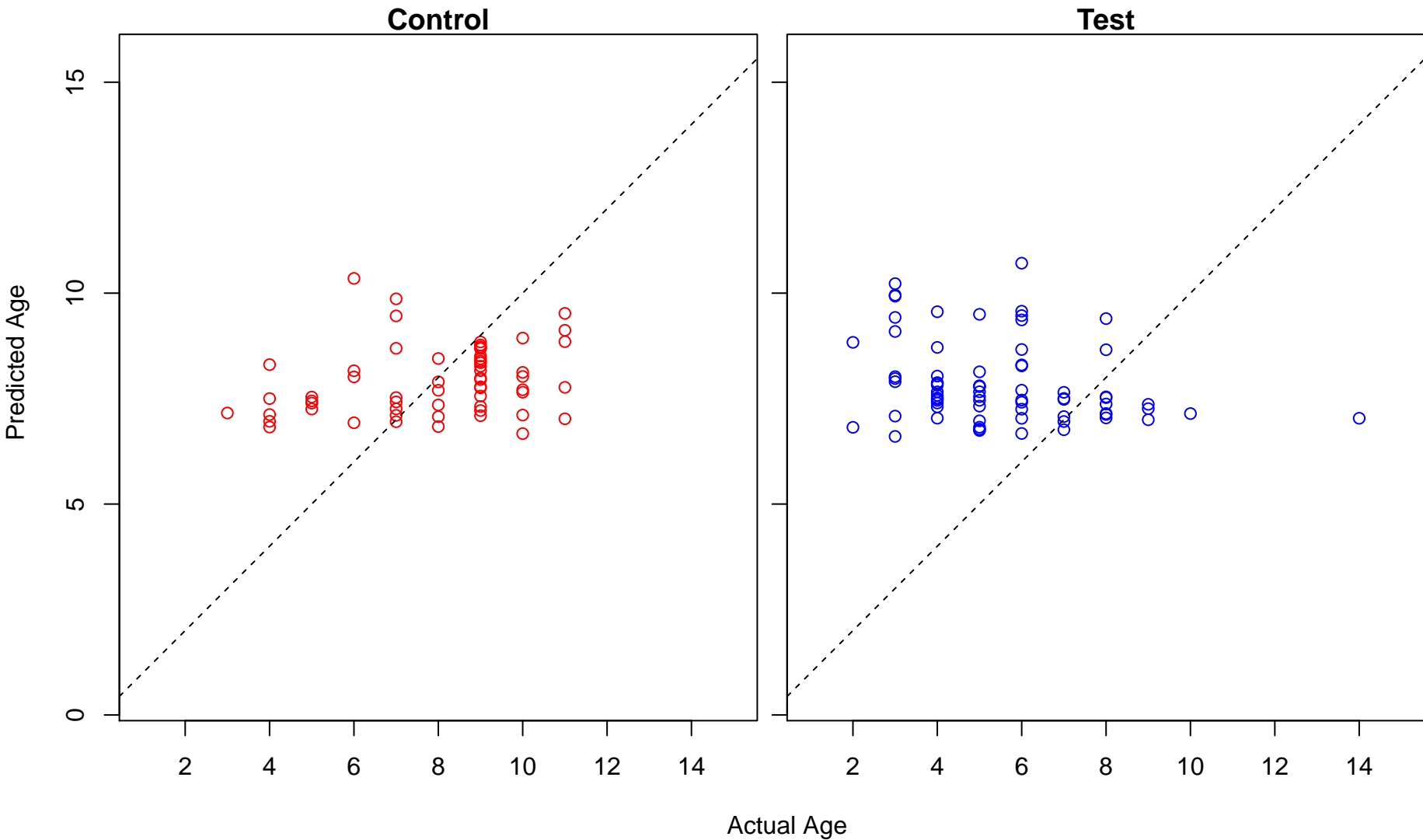
regulation of follicle-stimulating hormone secretion (Score: 0.341399)



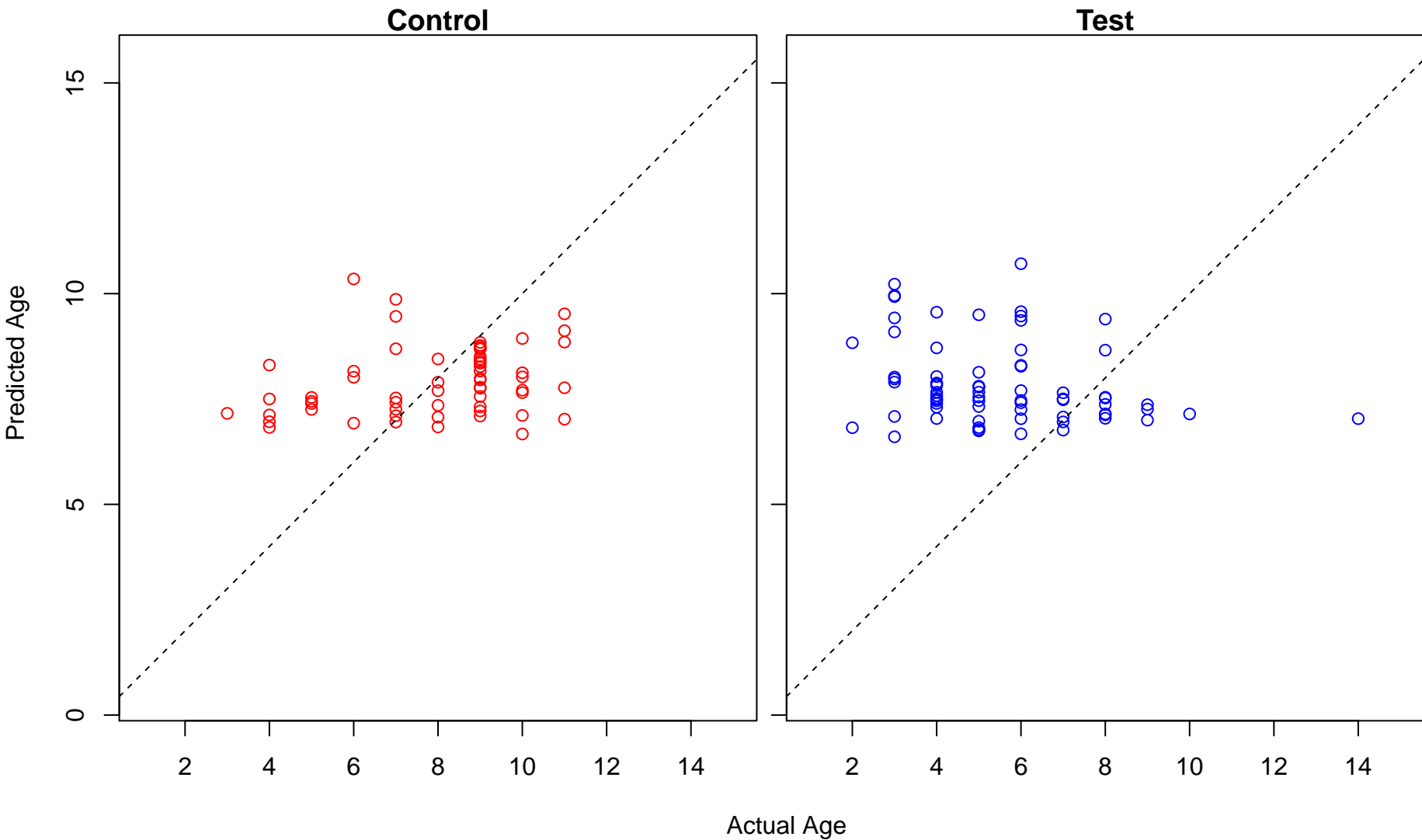
positive regulation of follicle-stimulating hormone secretion (Score: 0.341399)



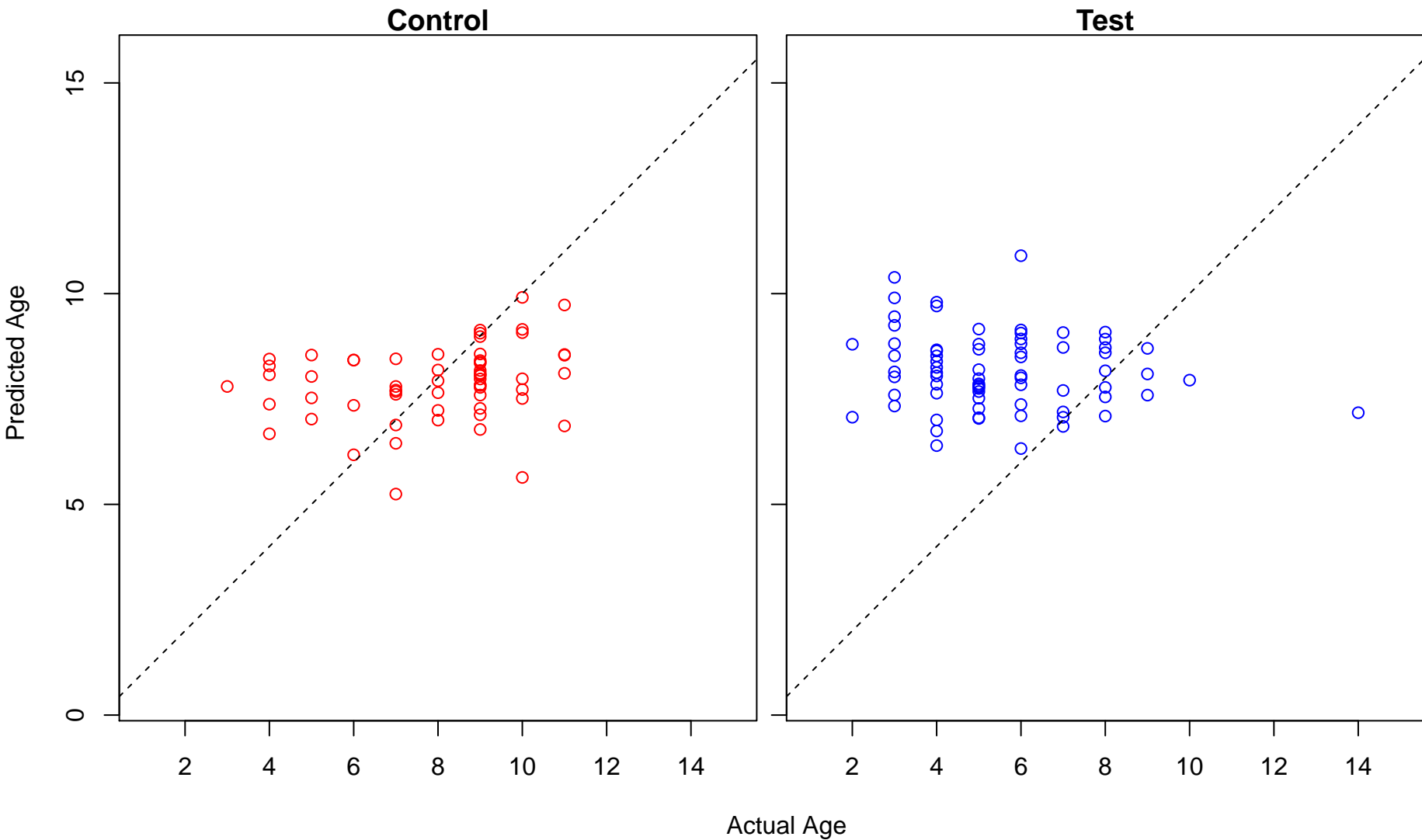
positive regulation of B cell mediated immunity (Score: 0.340213)



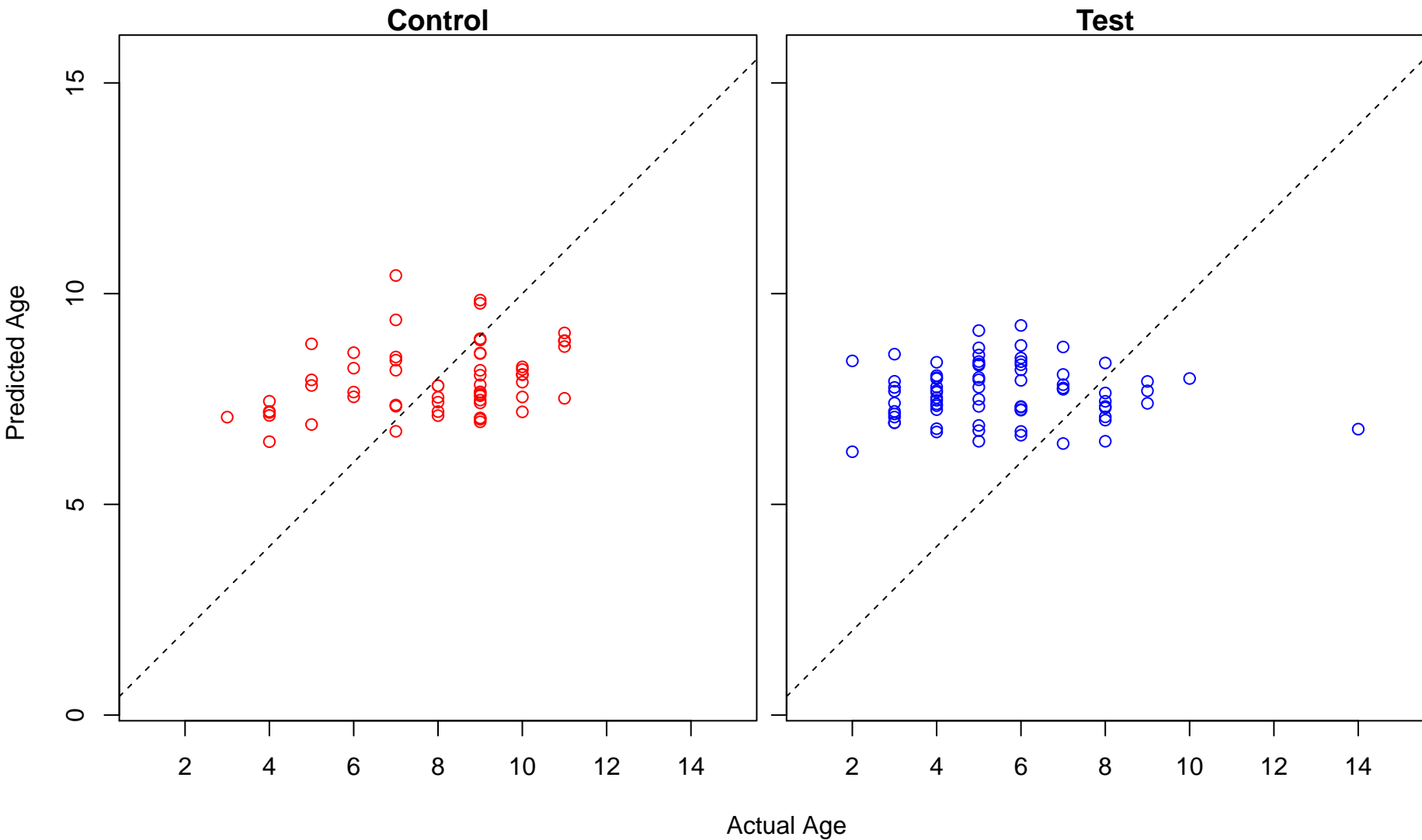
positive regulation of immunoglobulin mediated immune response (Score: 0.340213)



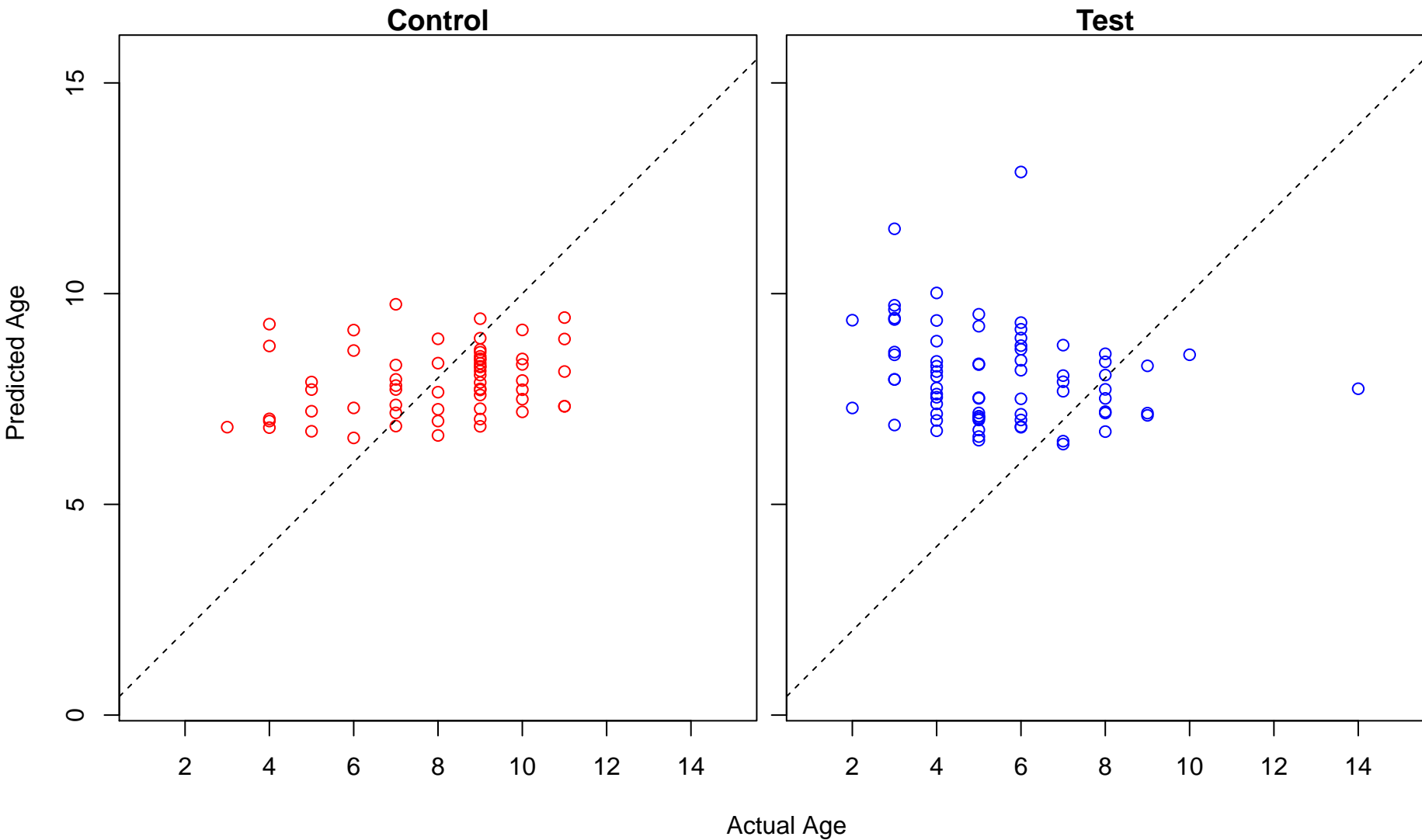
embryonic retina morphogenesis in camera-type eye (Score: 0.339879)



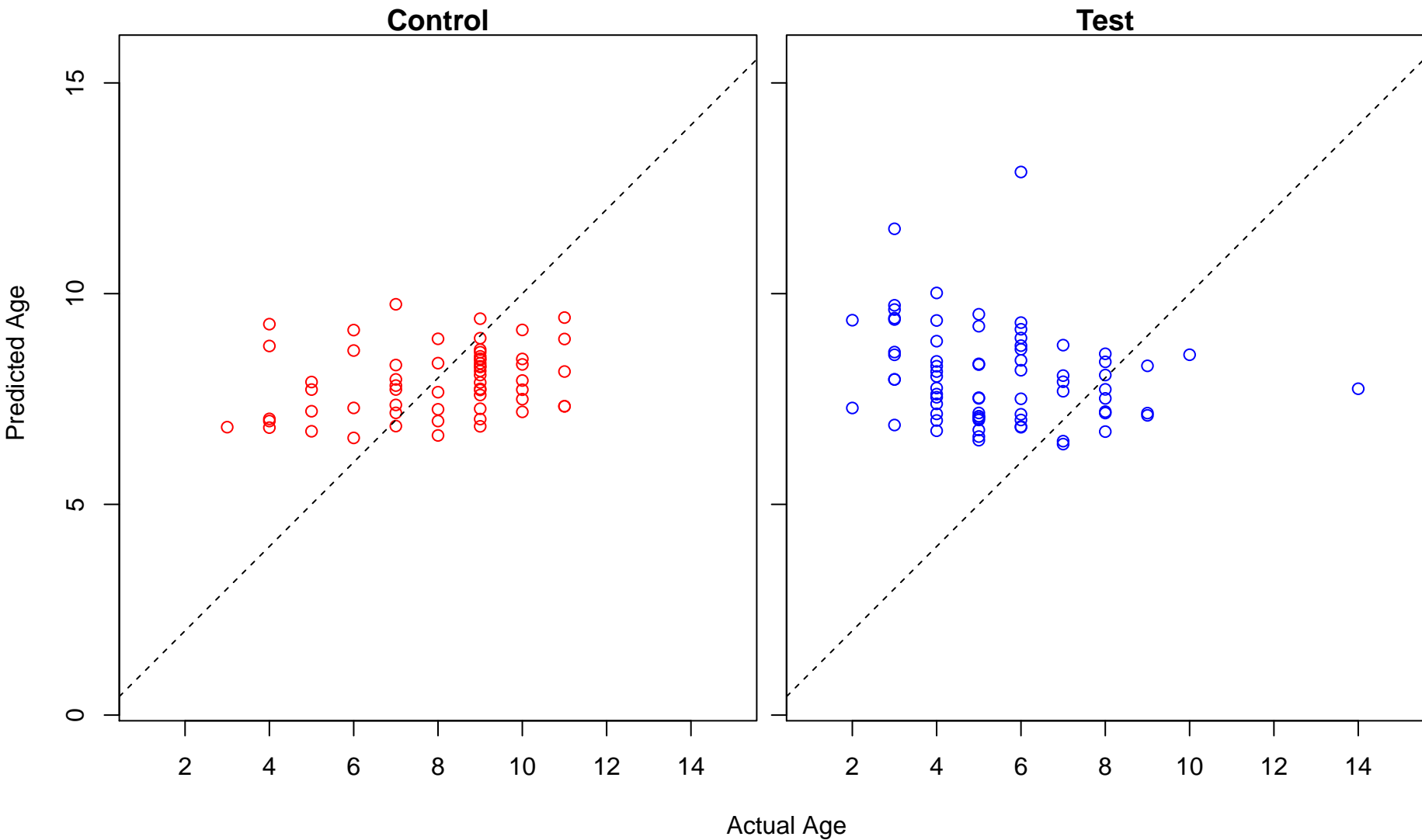
fructose metabolic process (Score: 0.339630)



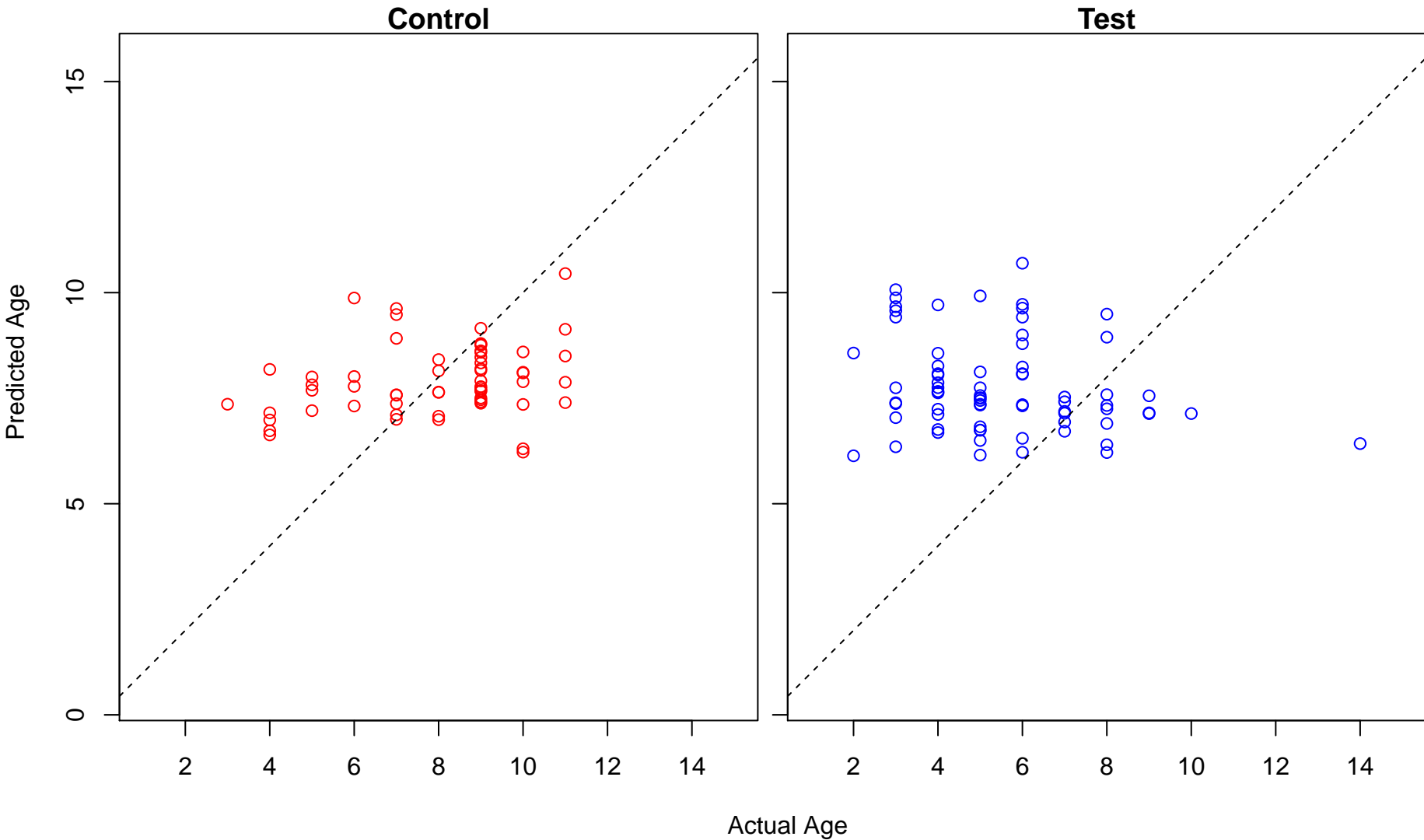
negative regulation of alpha-beta T cell proliferation (Score: 0.338702)



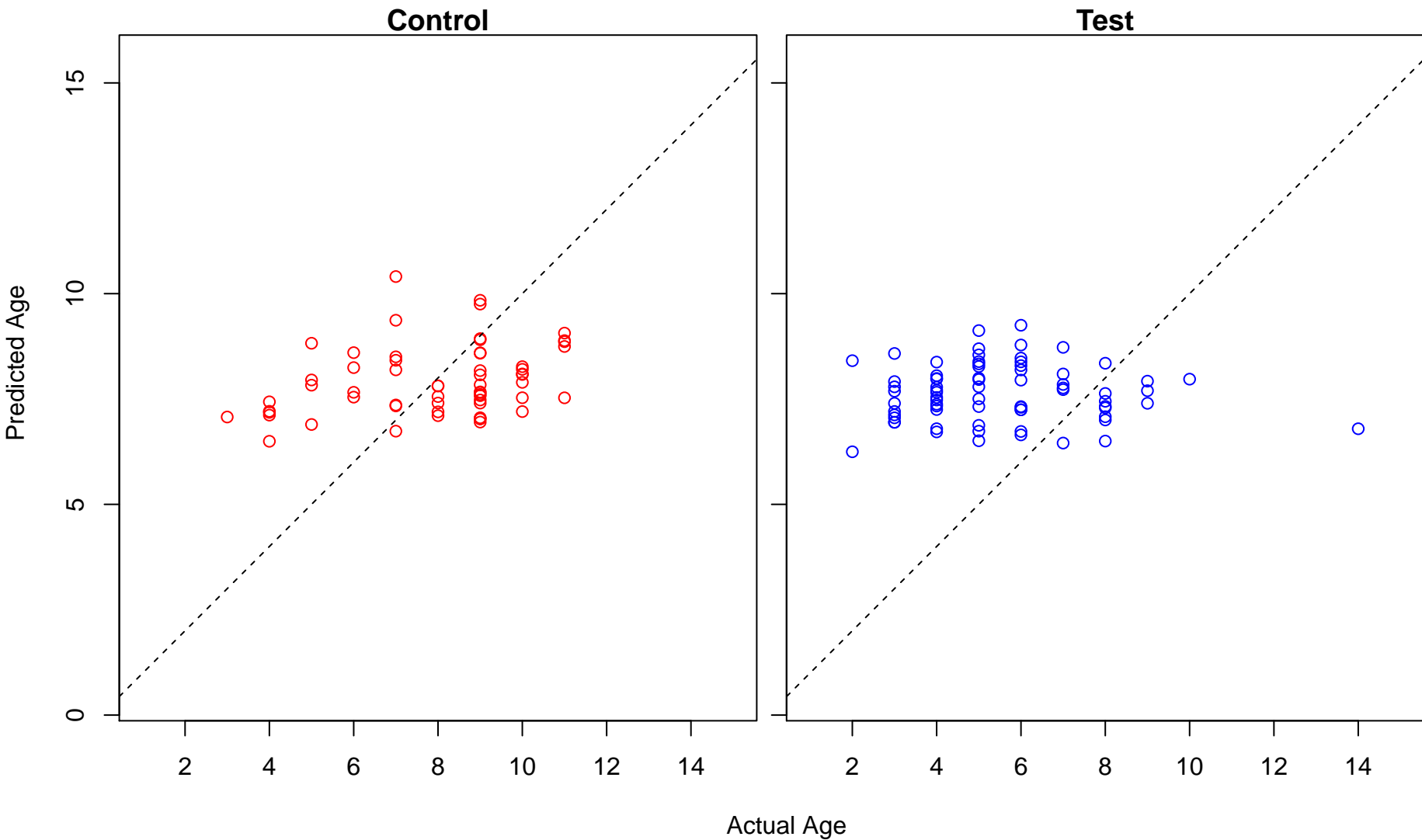
negative regulation of CD4-positive, alpha-beta T cell proliferation (Score: 0.338702)



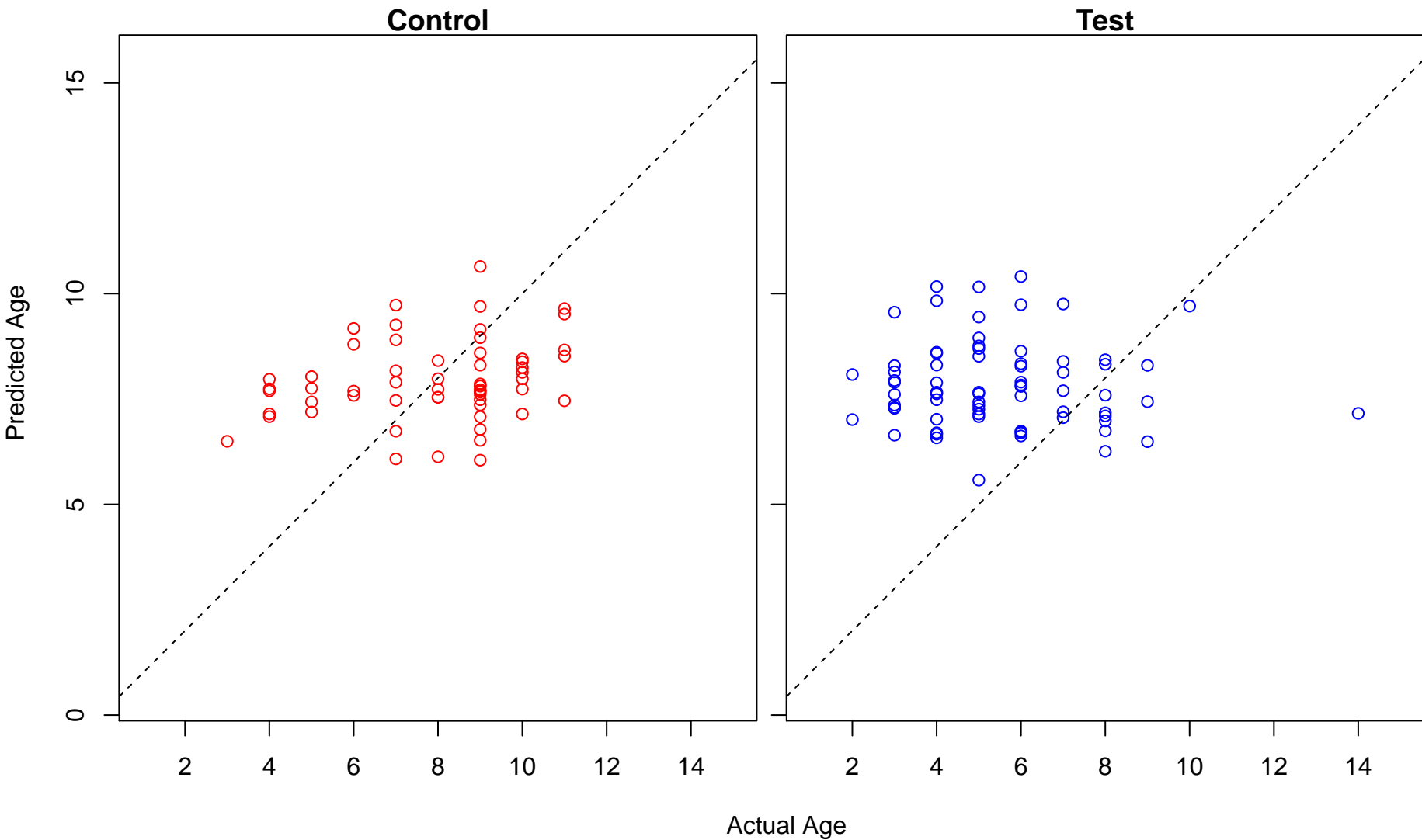
regulation of hyaluronan biosynthetic process (Score: 0.338589)



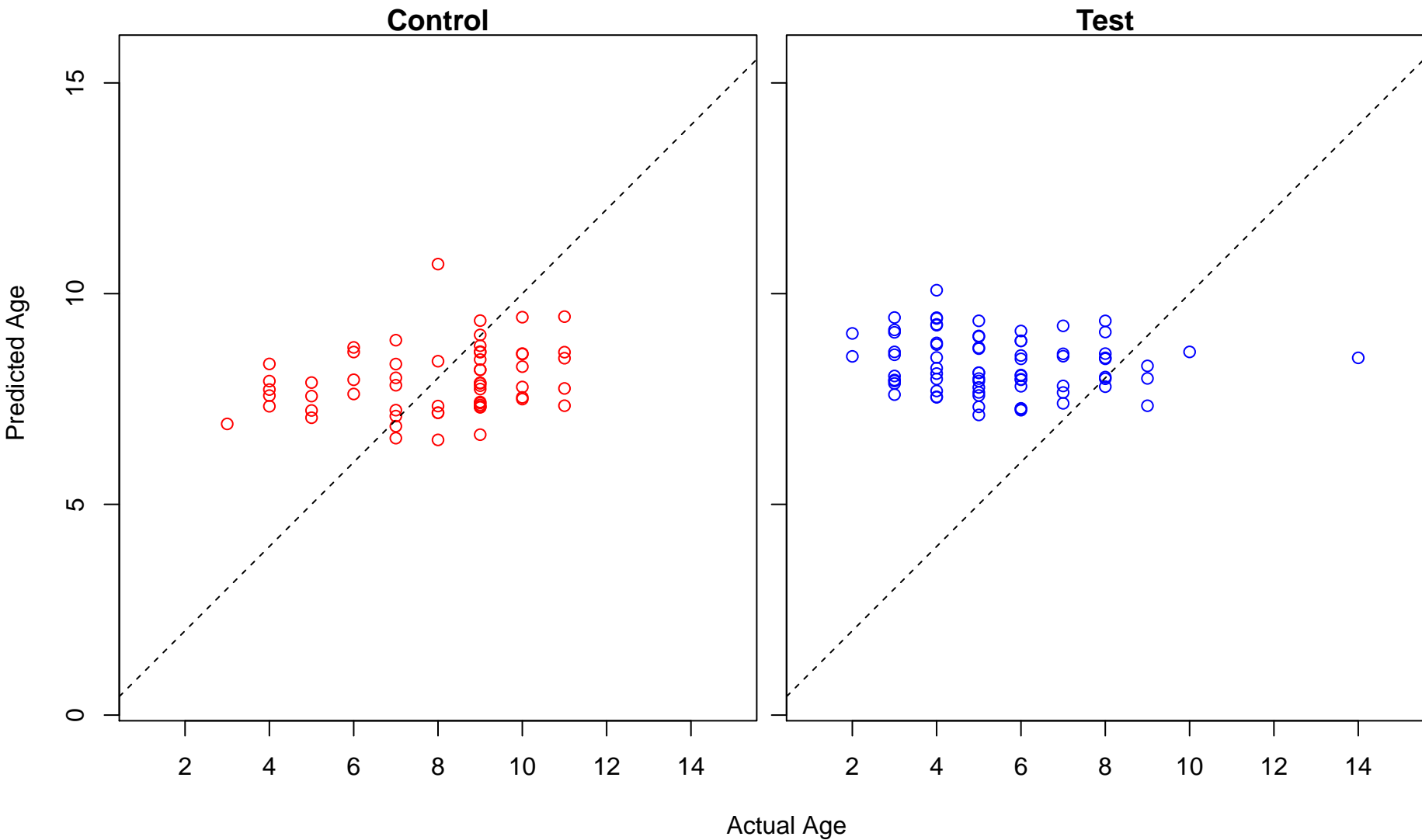
fructose 1,6-bisphosphate metabolic process (Score: 0.338044)



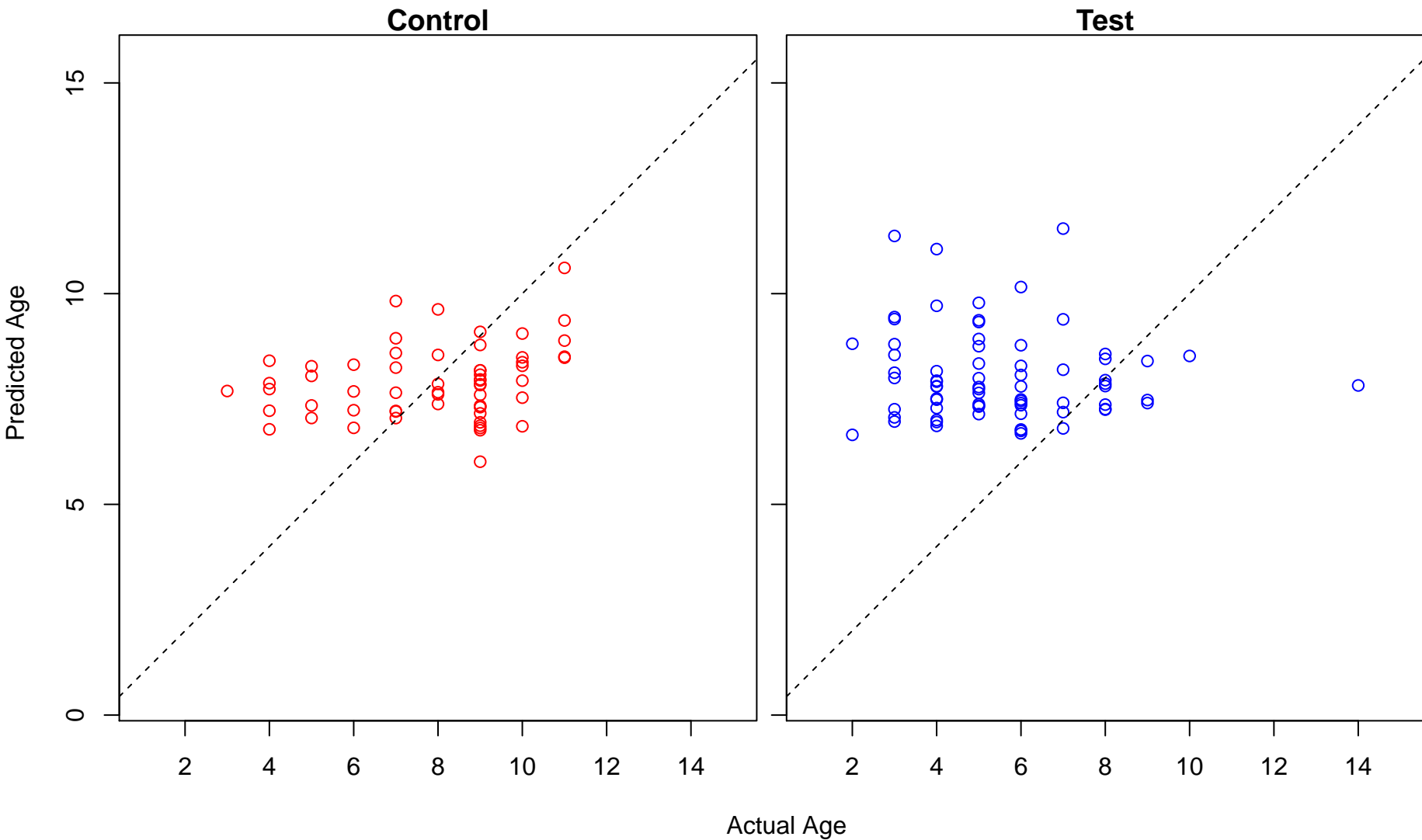
cellular response to UV-B (Score: 0.337215)



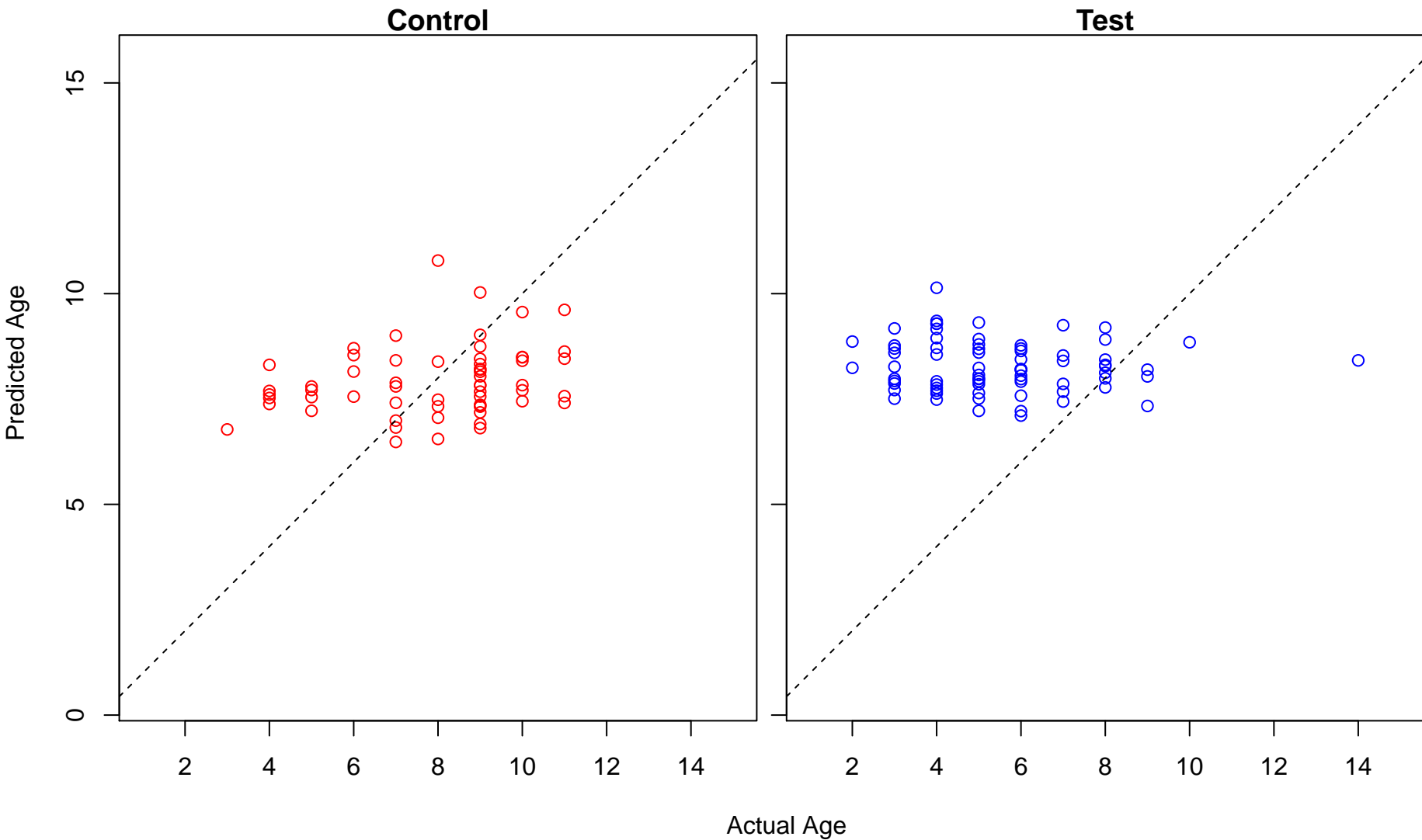
negative regulation of B cell differentiation (Score: 0.336595)



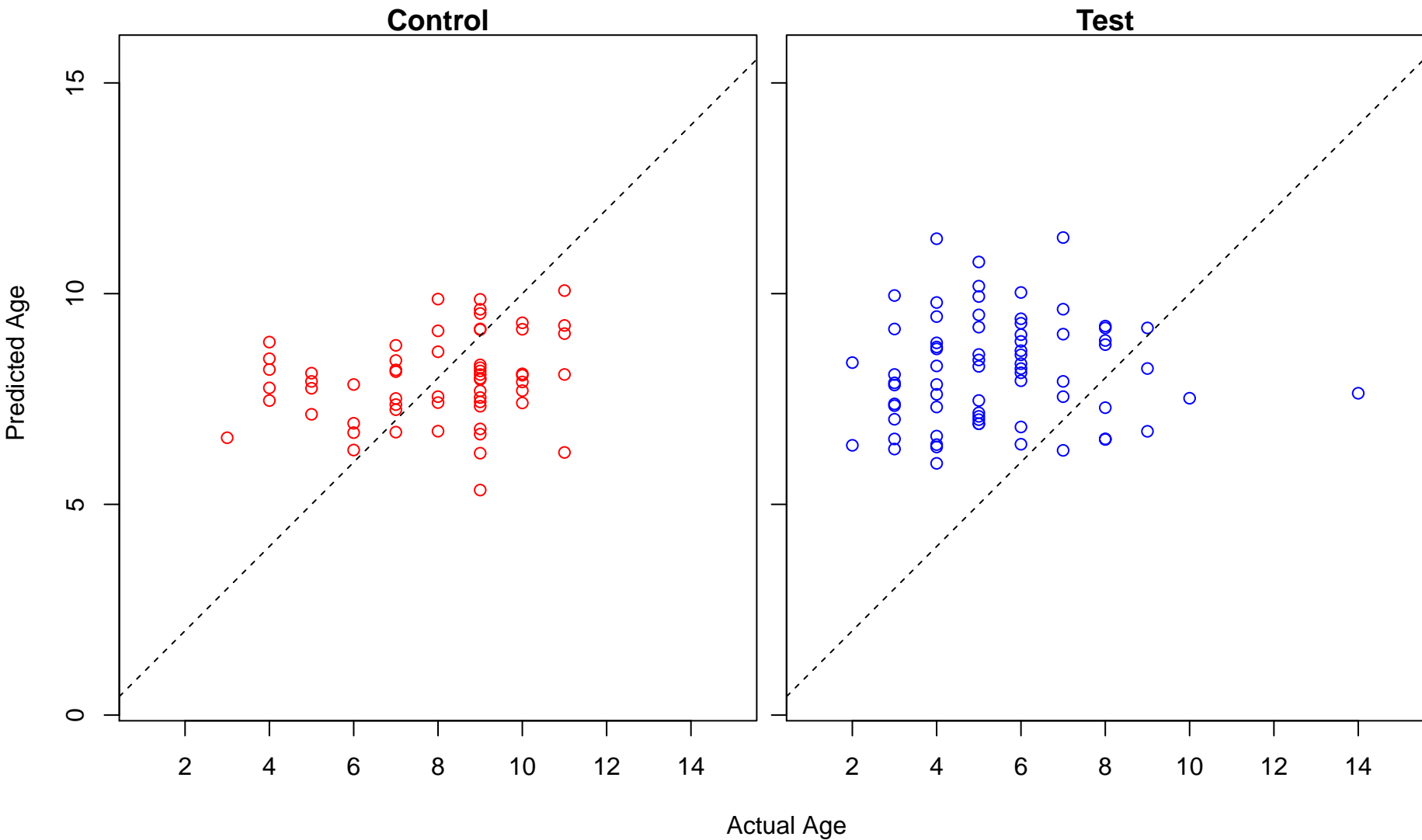
T-helper 1 cell lineage commitment (Score: 0.336219)



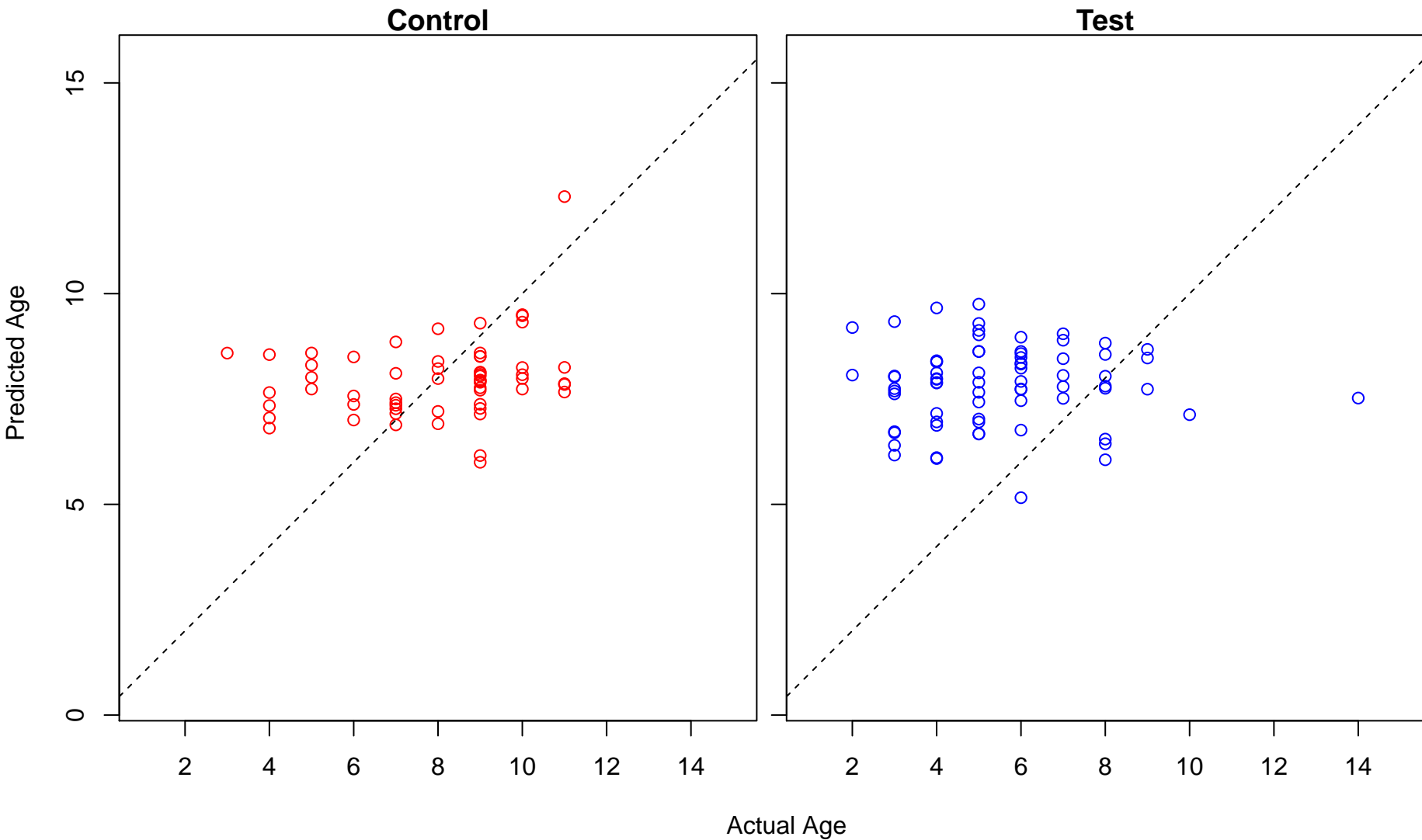
regulation of gonadotropin secretion (Score: 0.335813)



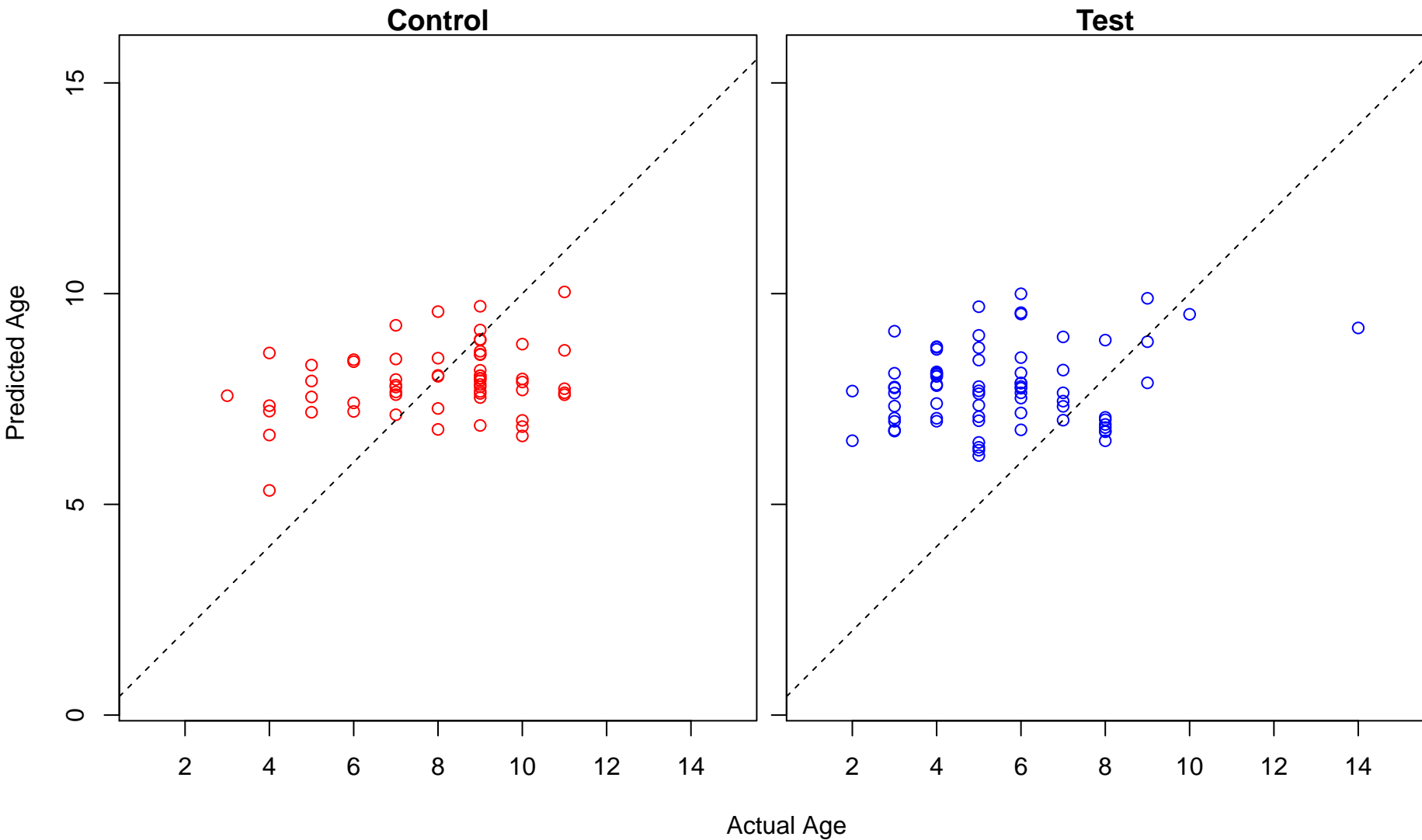
ureter maturation (Score: 0.335585)



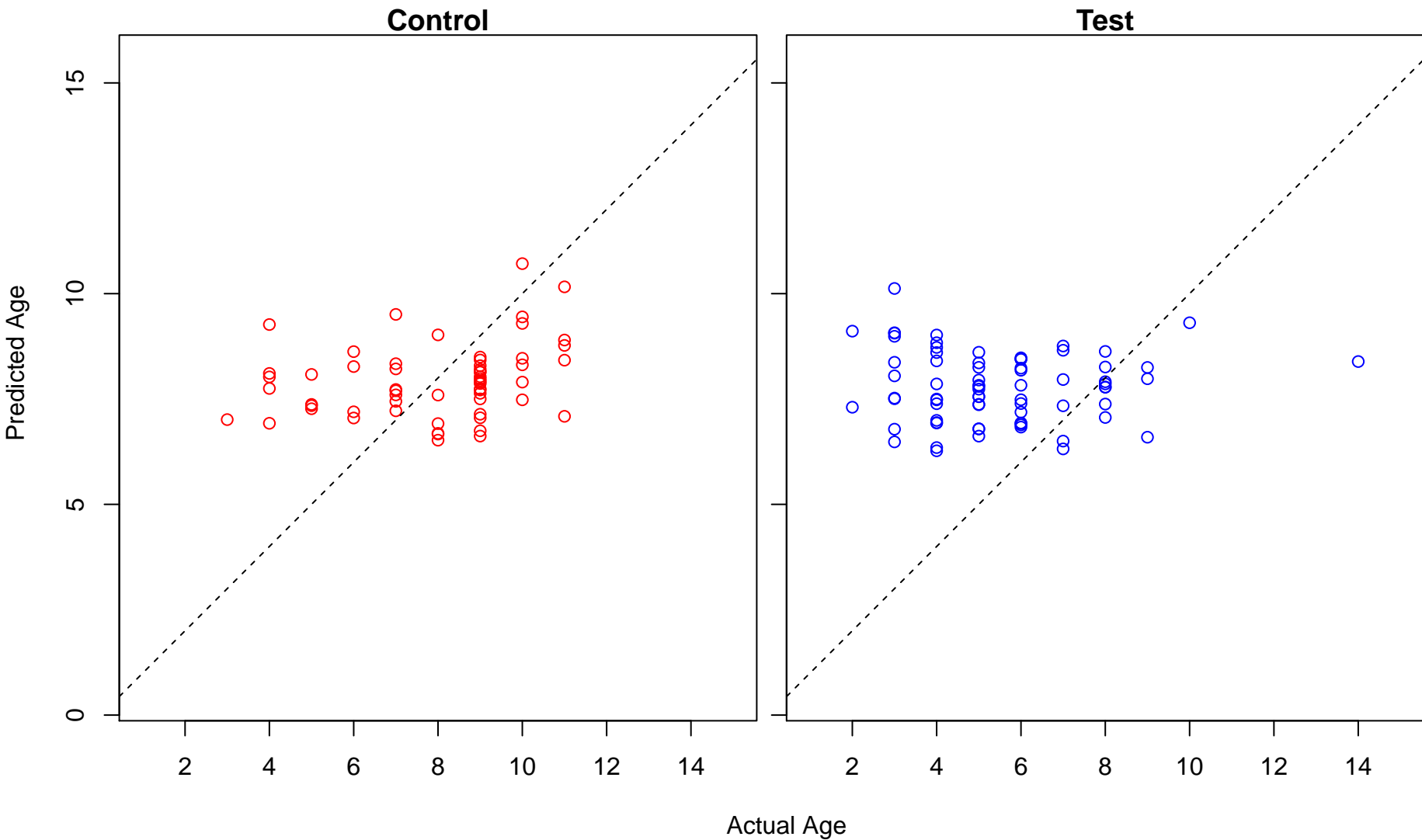
positive regulation of synaptic transmission, GABAergic (Score: 0.335220)



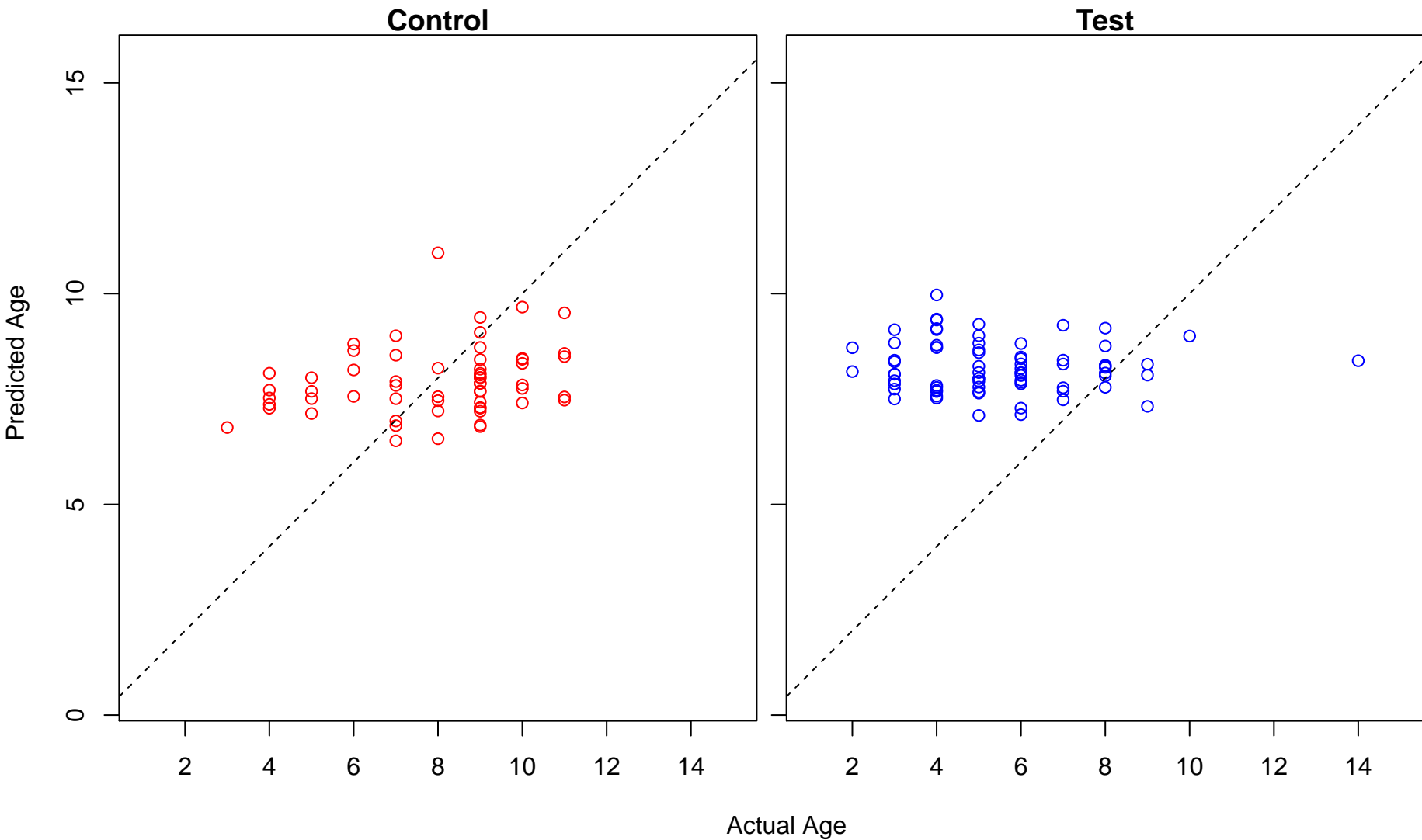
negative regulation of lipid kinase activity (Score: 0.334252)



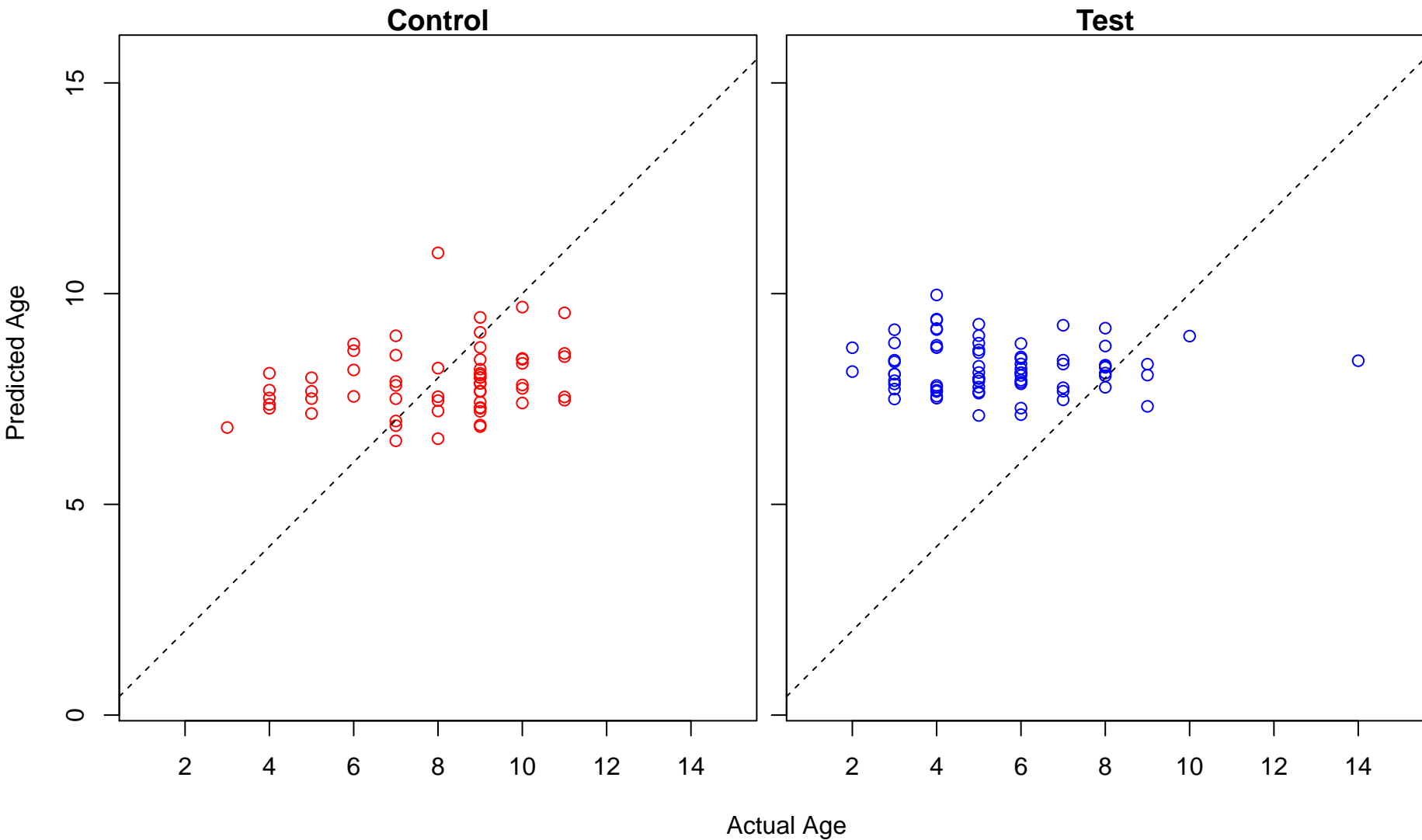
proline catabolic process (Score: 0.333591)



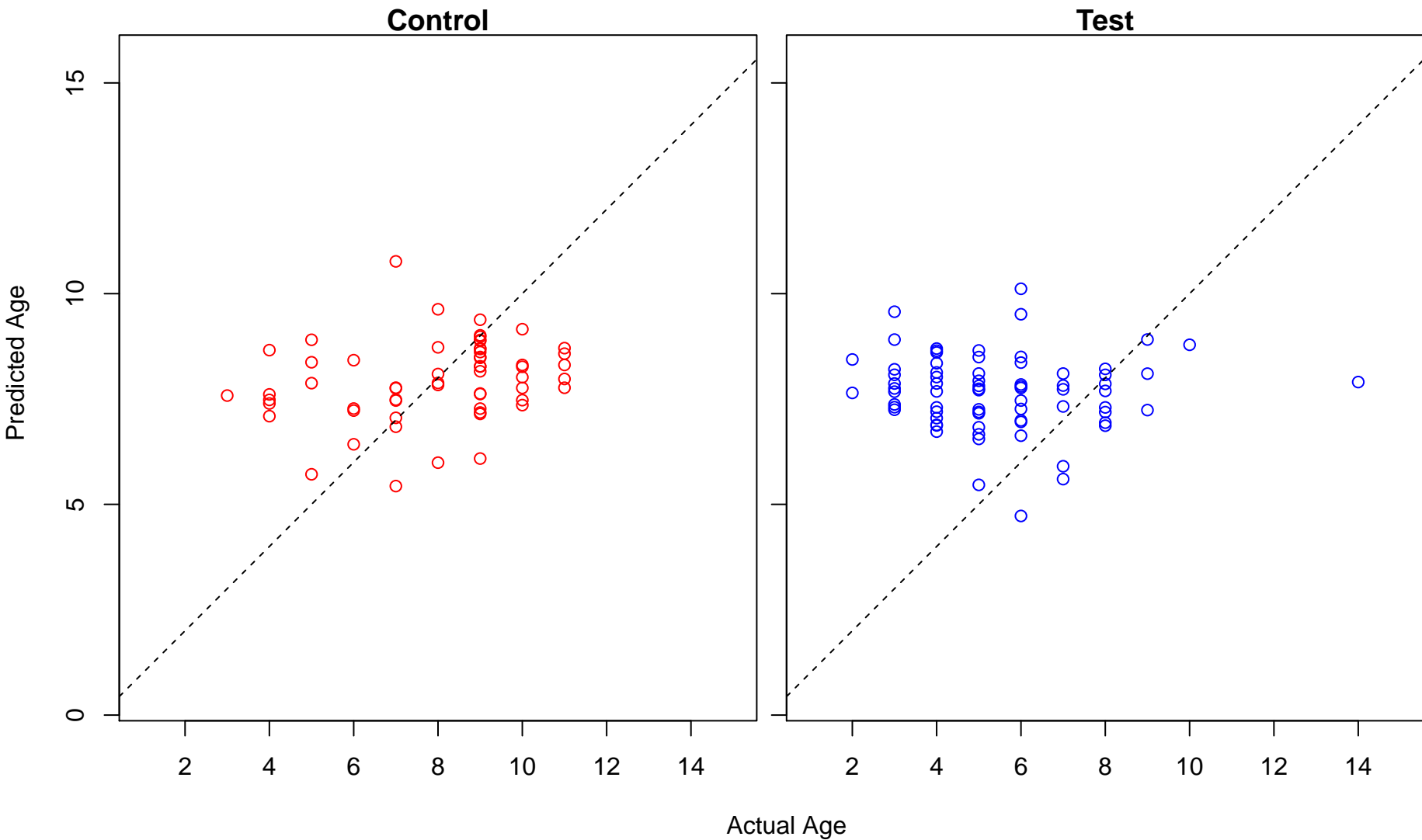
regulation of ovulation (Score: 0.332643)



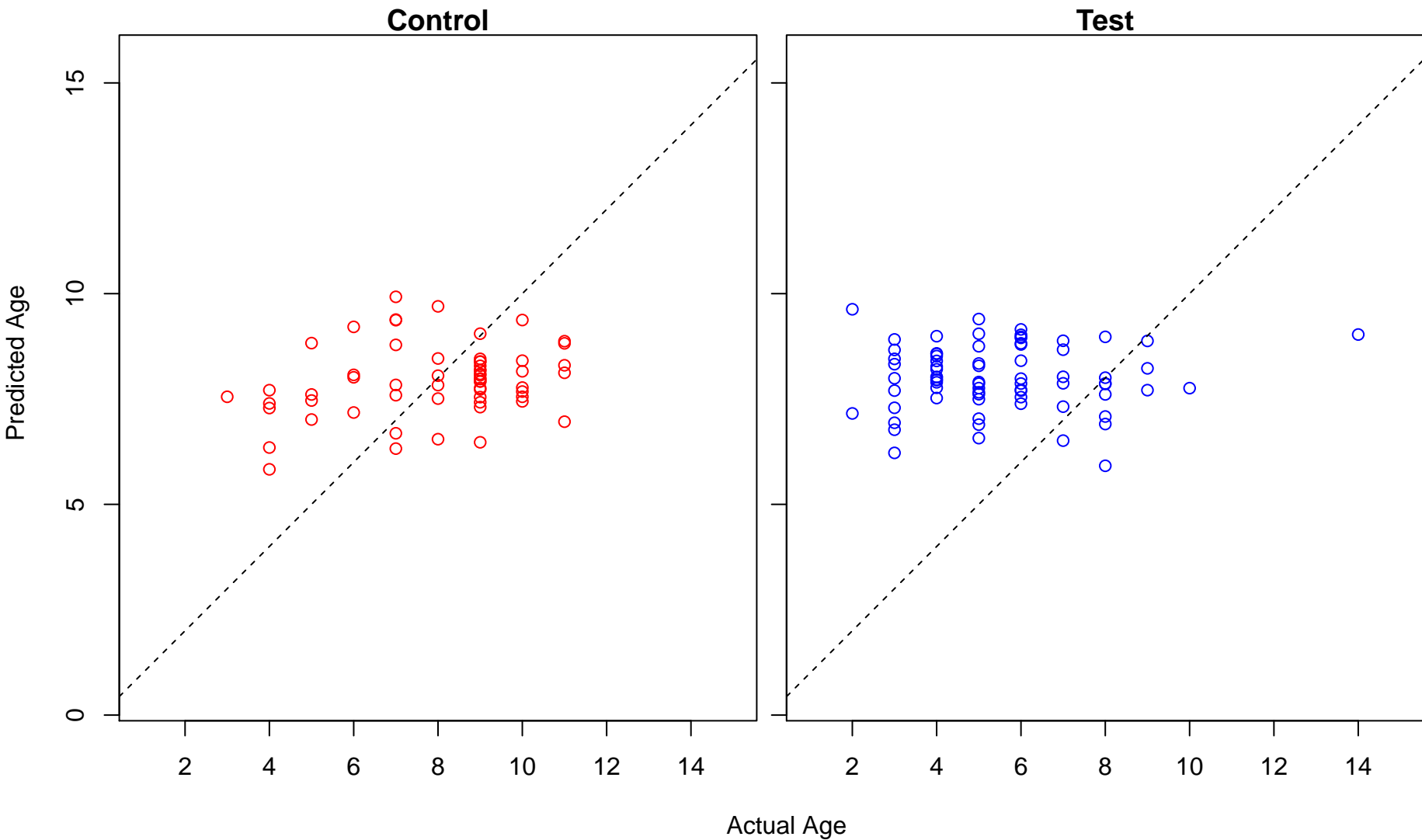
positive regulation of ovulation (Score: 0.332643)



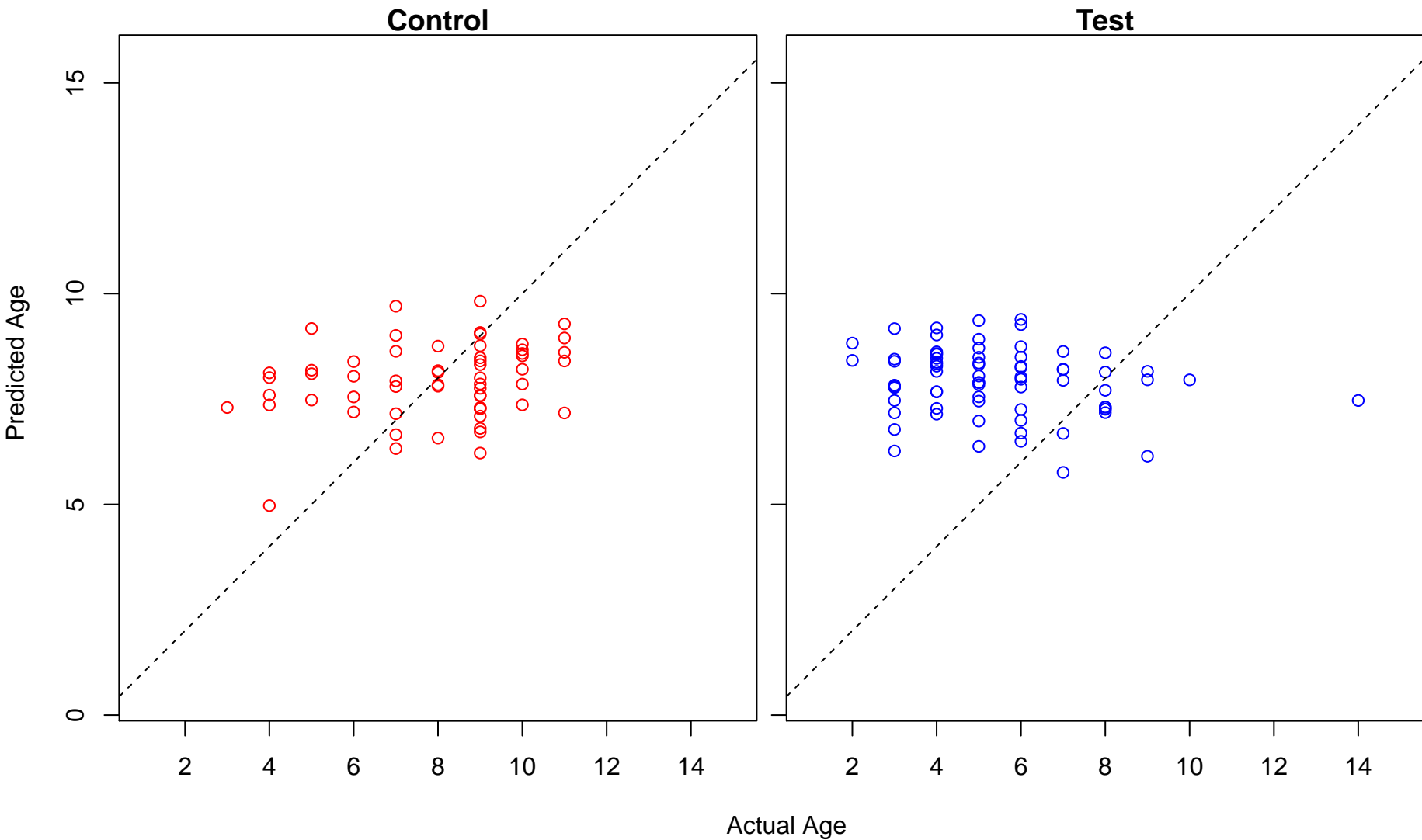
negative regulation of cell adhesion involved in substrate-bound cell migration (Score: 0.331291)



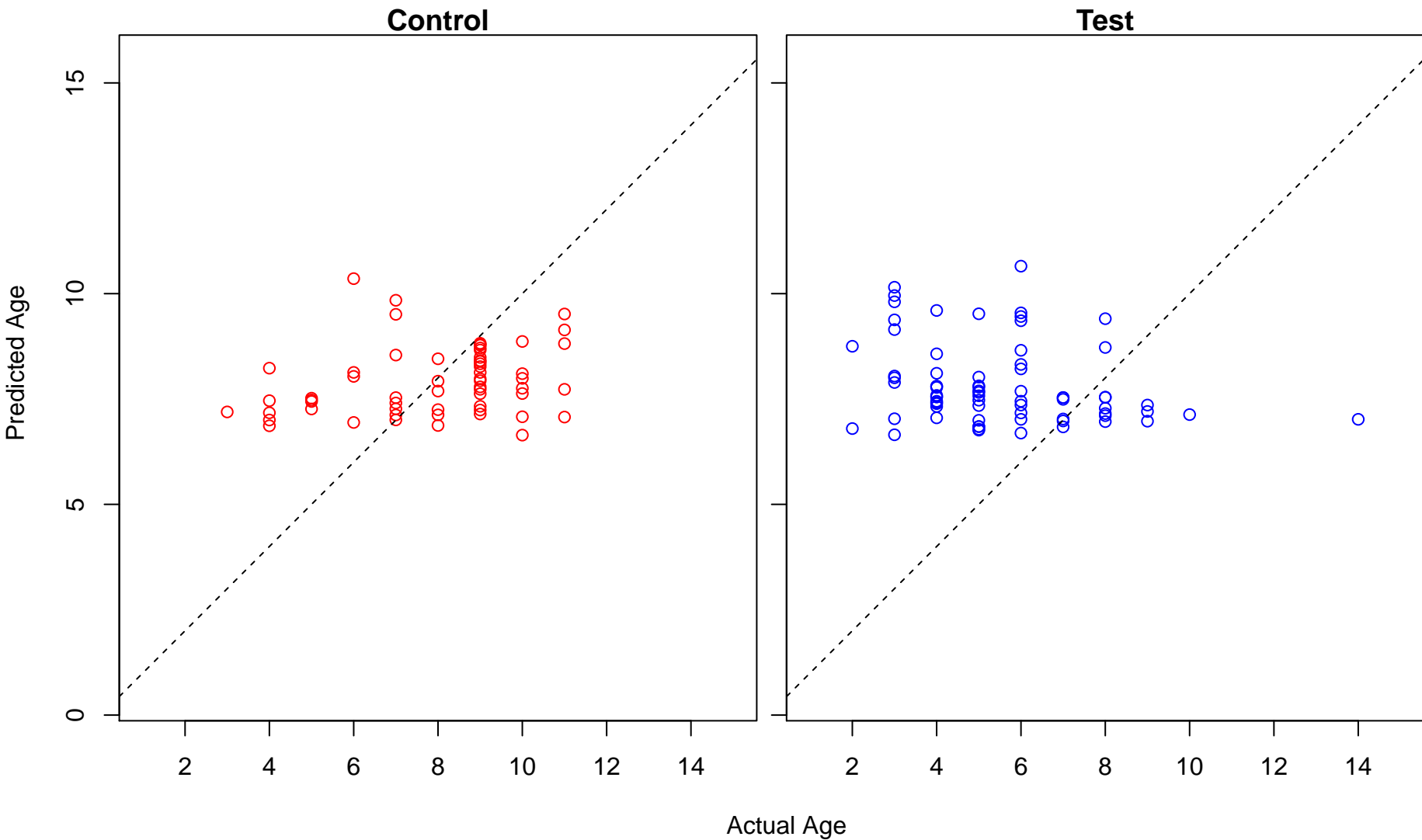
hypothalamus development (Score: 0.328797)



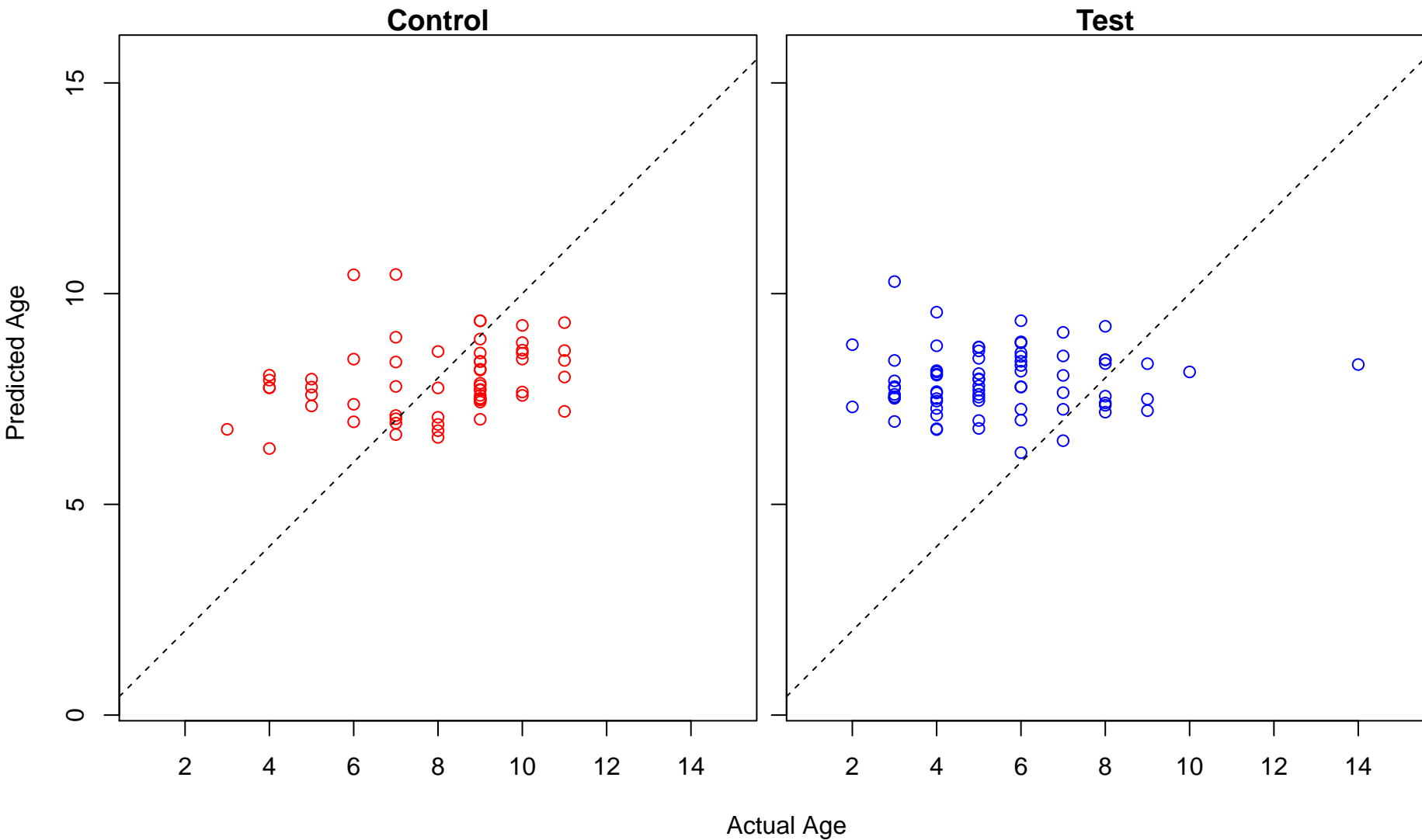
organic cation transport (Score: 0.328525)



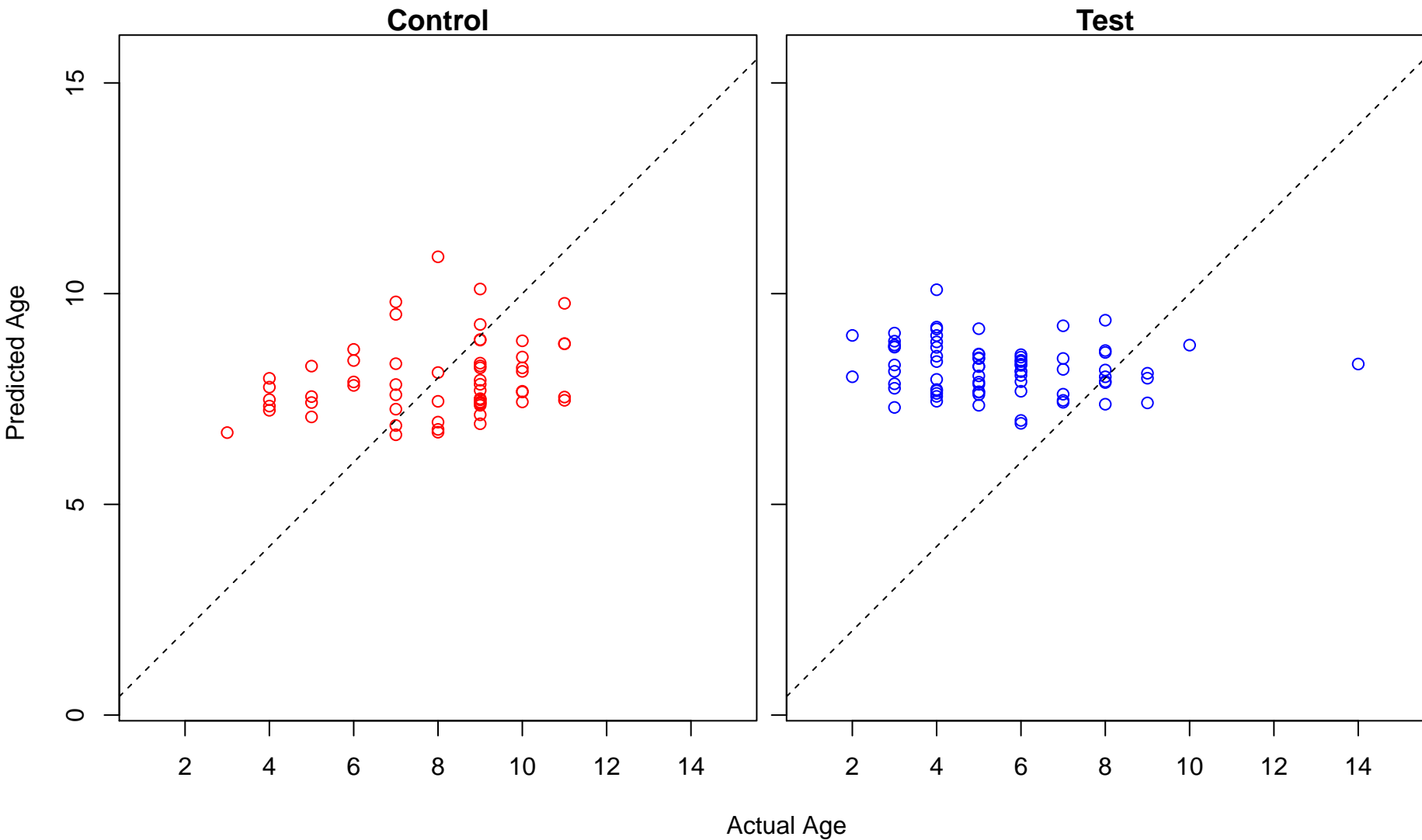
regulation of isotype switching (Score: 0.328309)



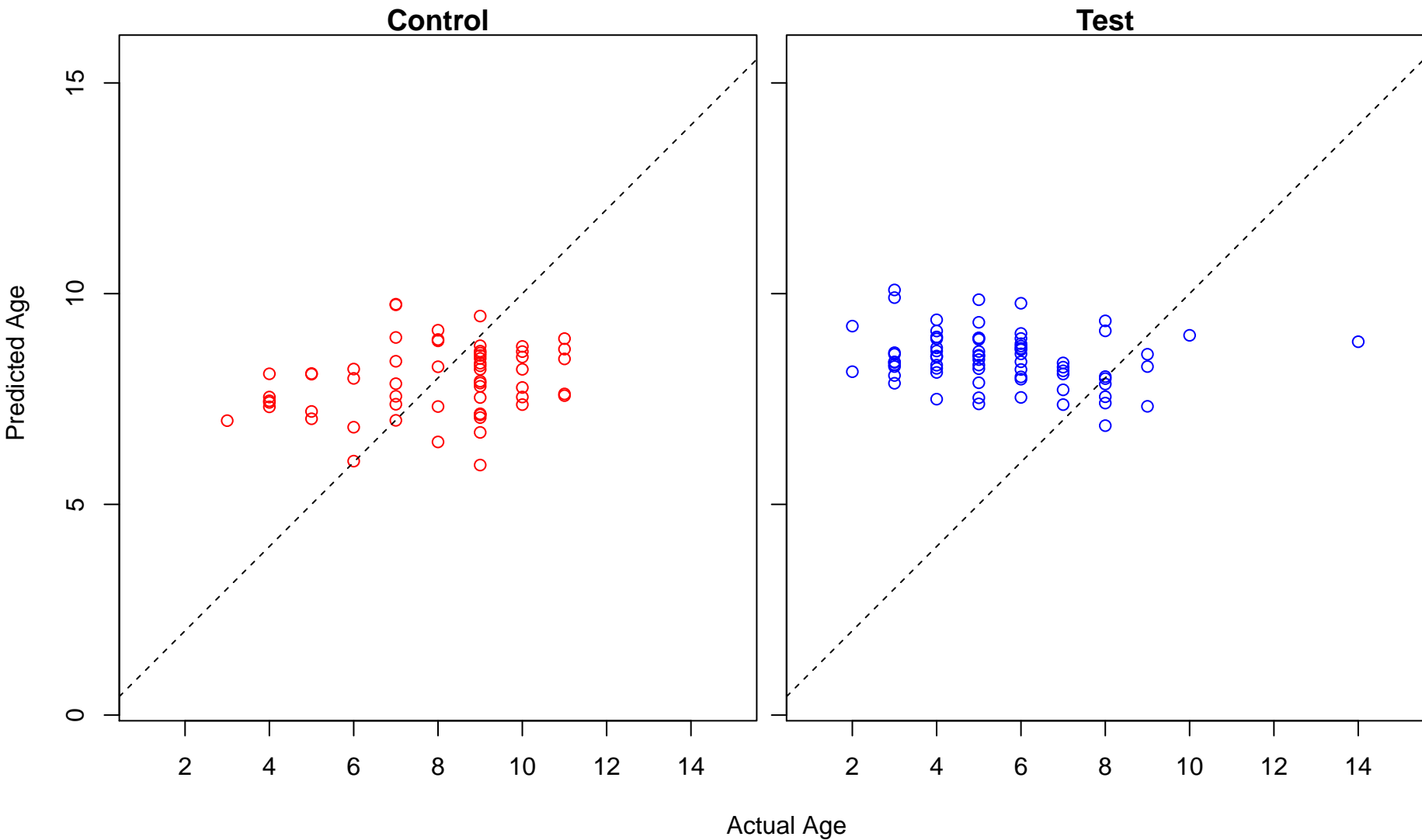
NADPH oxidation (Score: 0.327817)



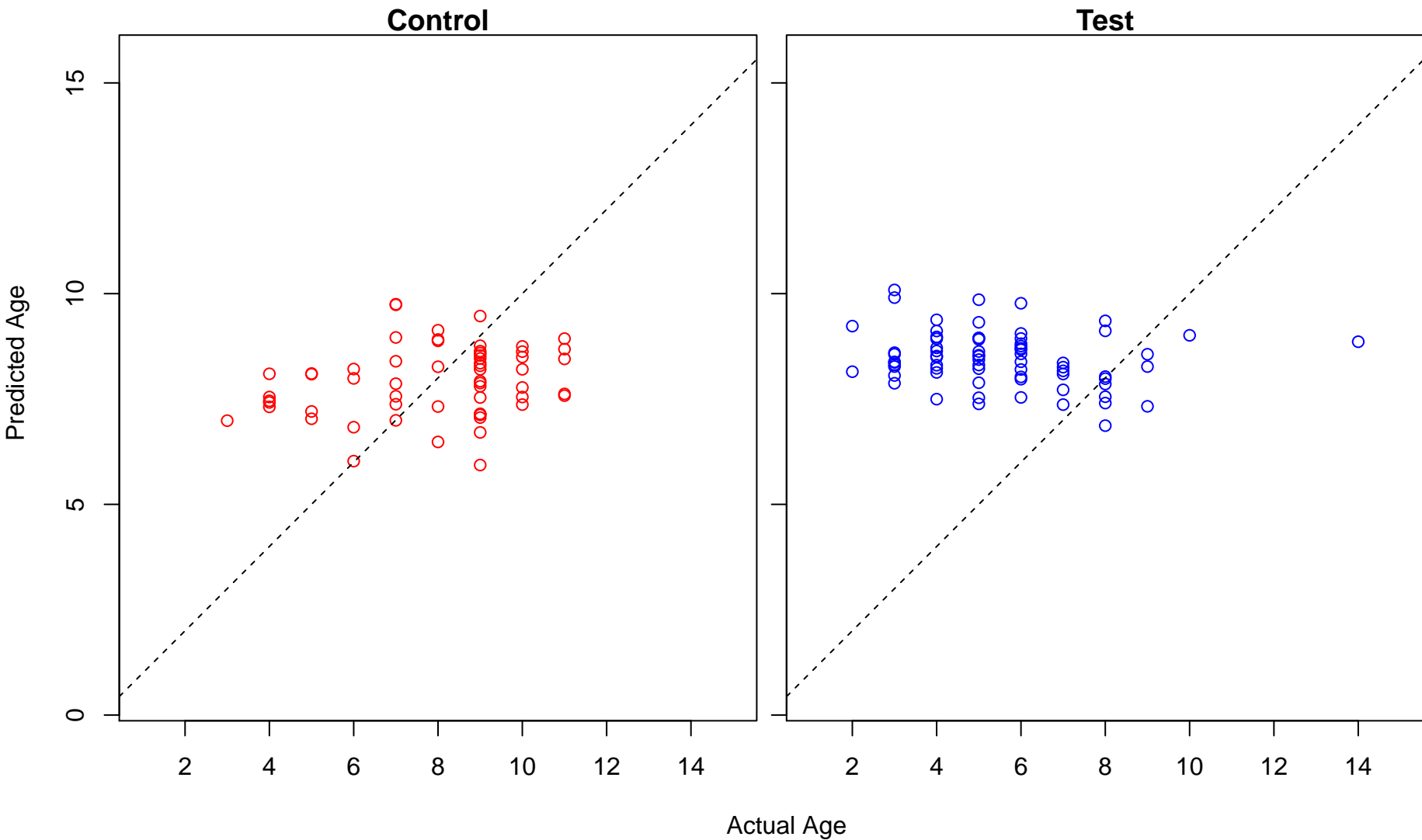
negative regulation of interferon-gamma biosynthetic process (Score: 0.324641)



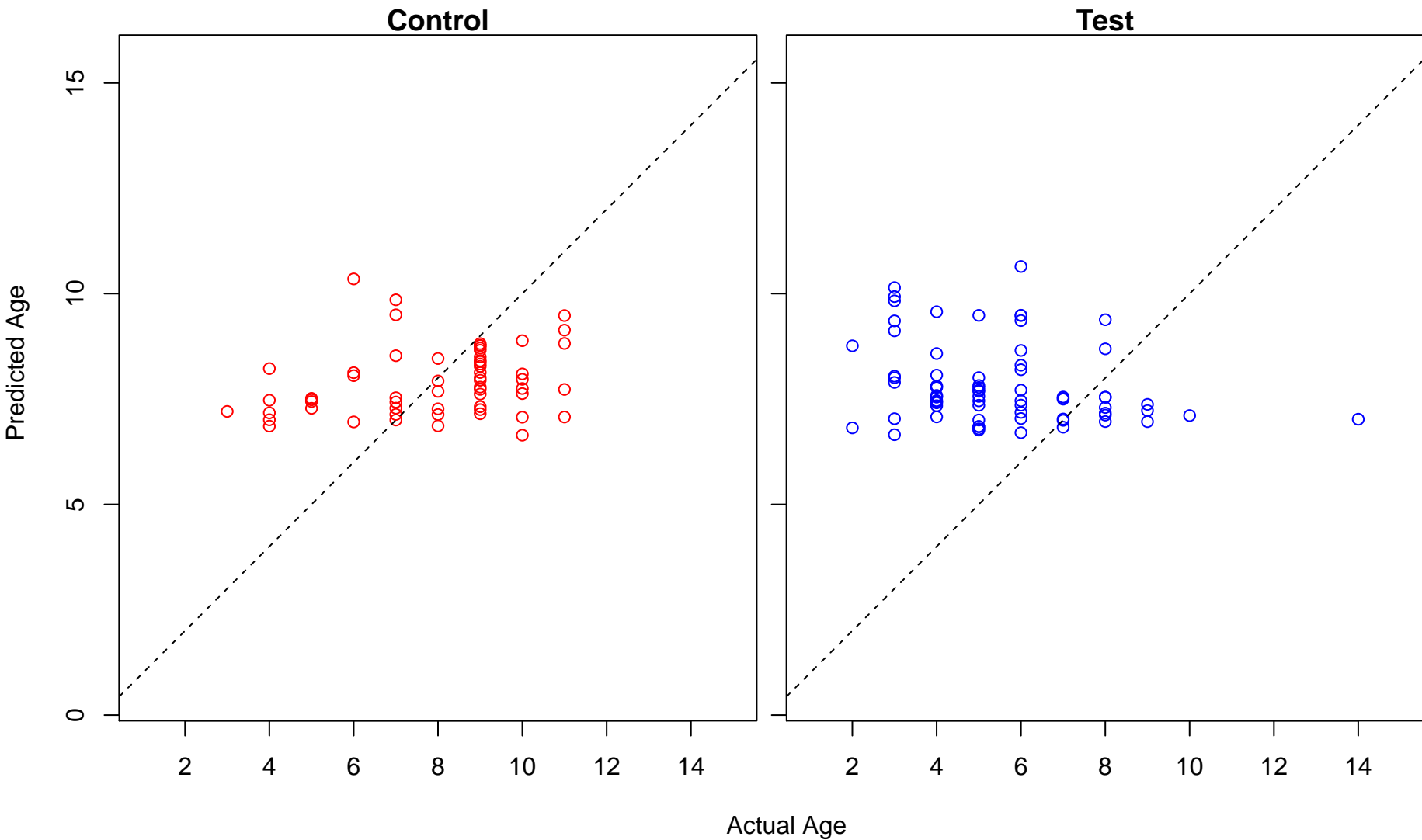
regulation of phosphatidylcholine biosynthetic process (Score: 0.324249)



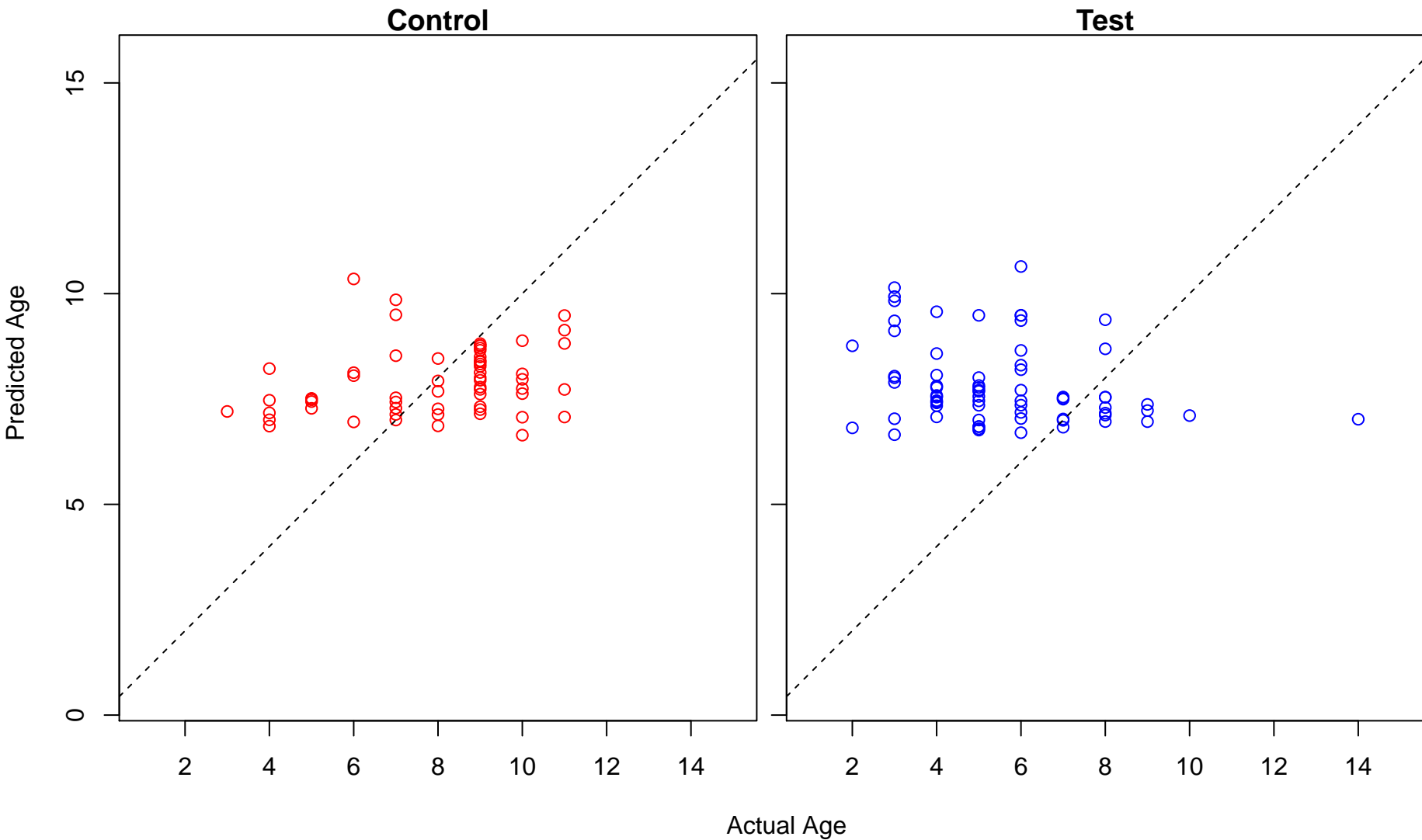
positive regulation of phosphatidylcholine biosynthetic process (Score: 0.324249)



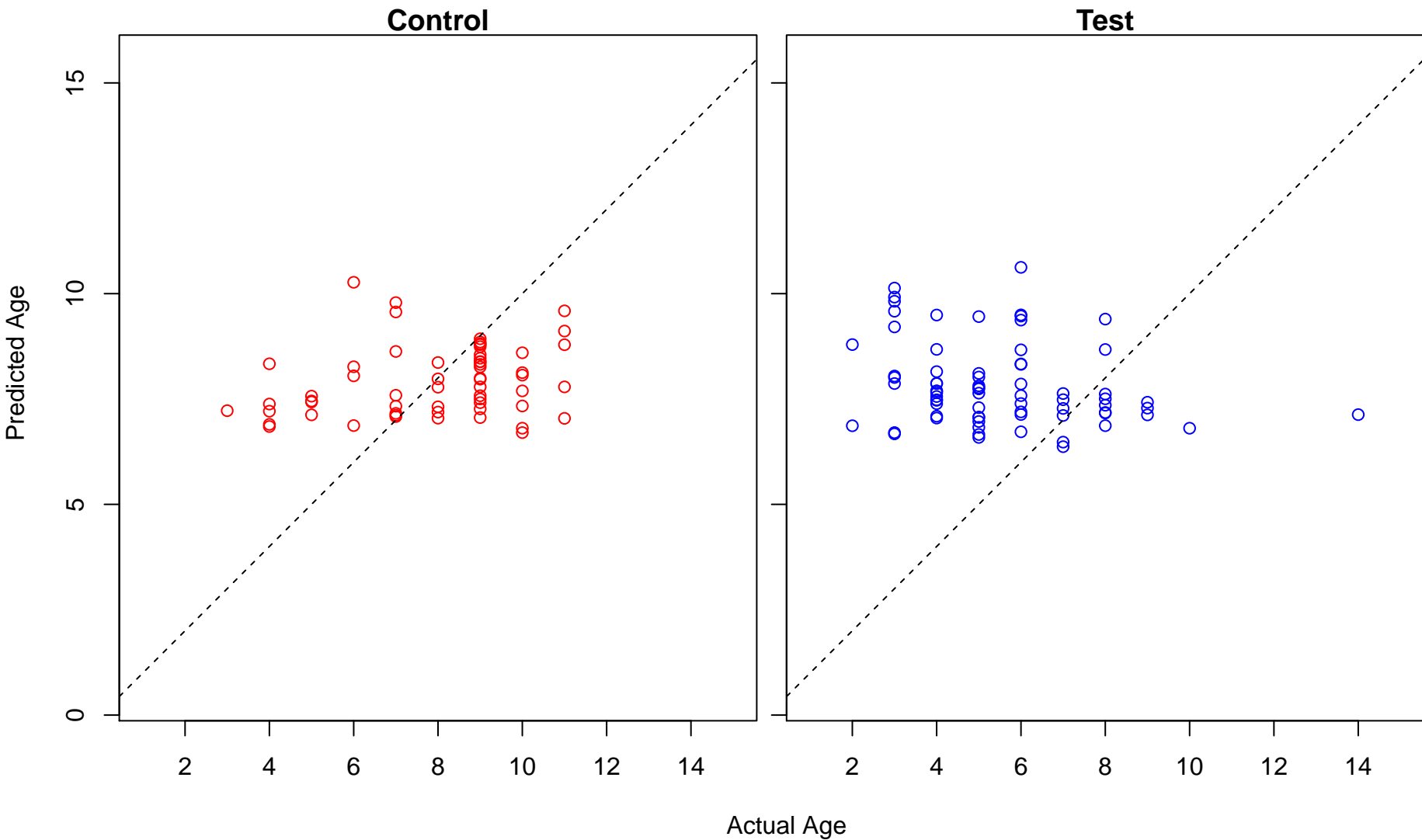
positive regulation of DNA recombination (Score: 0.322795)



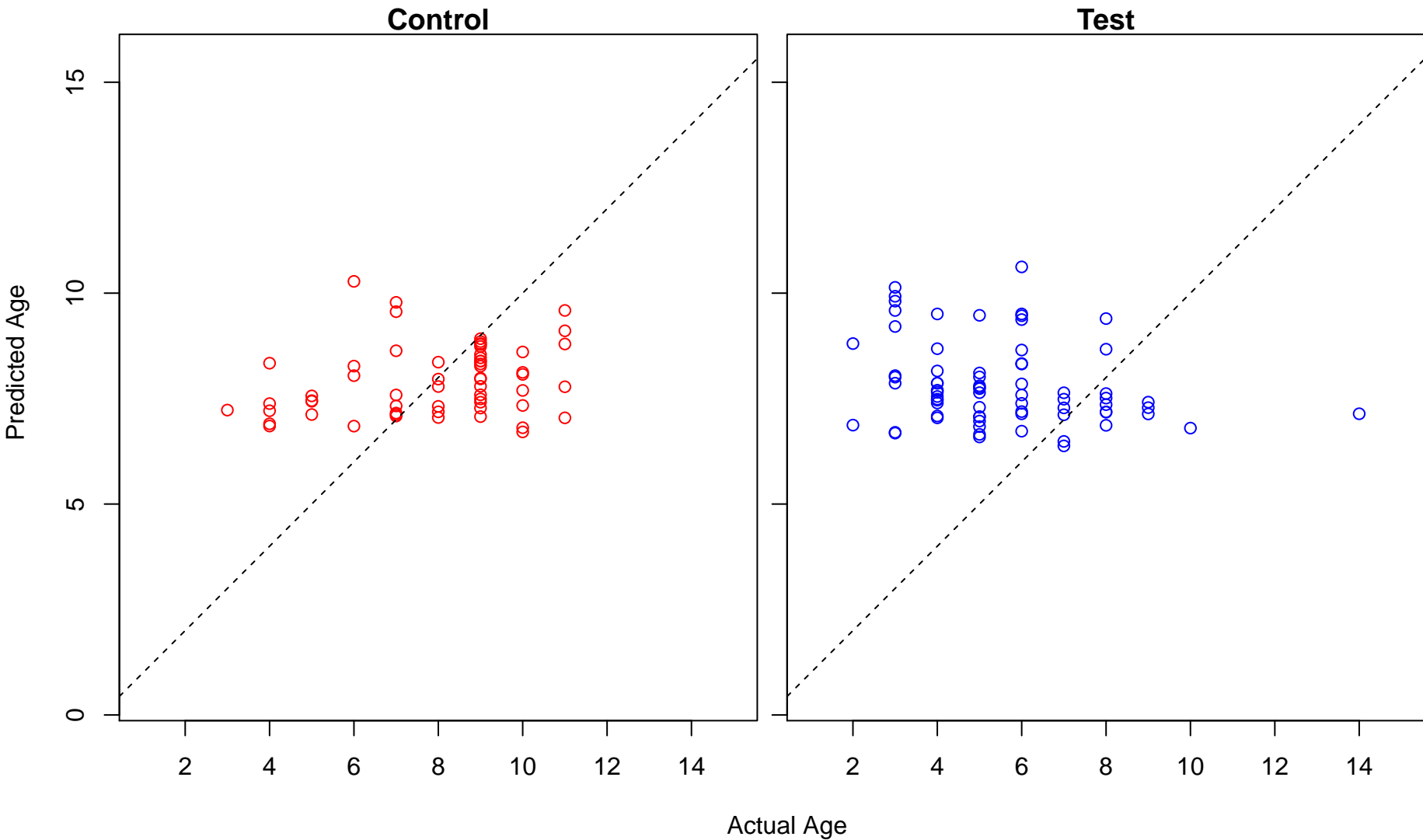
positive regulation of isotype switching (Score: 0.322791)



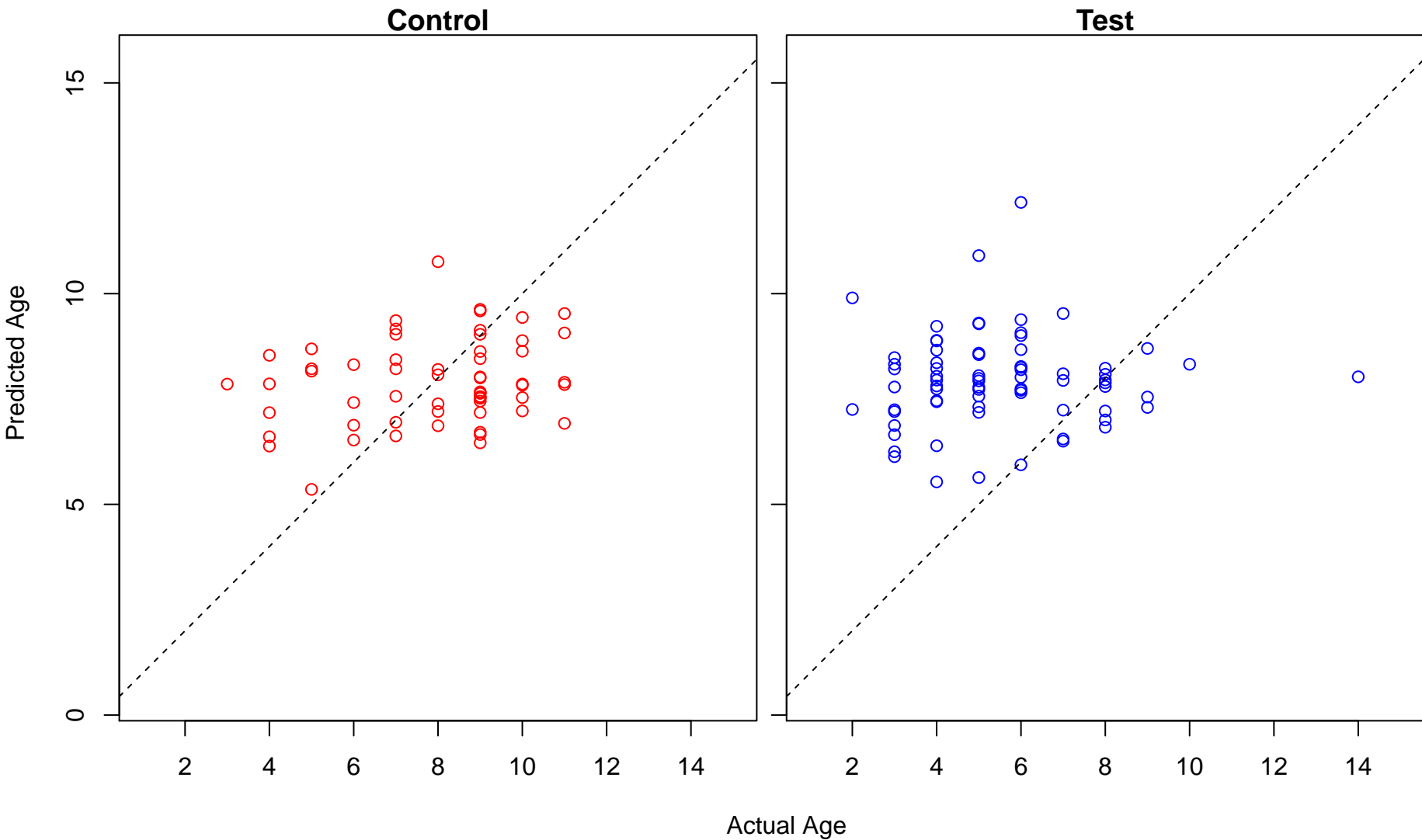
regulation of B cell mediated immunity (Score: 0.322394)



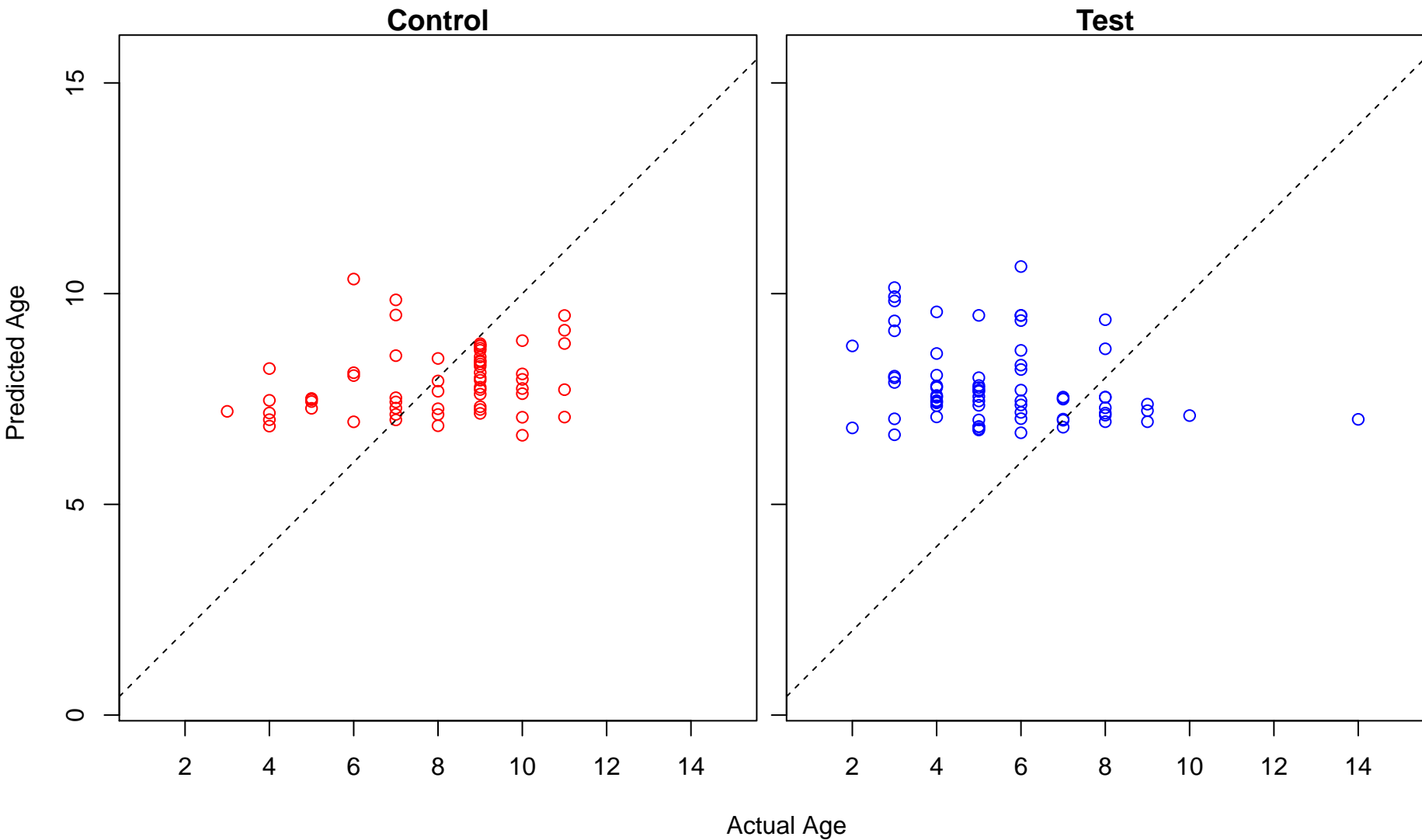
regulation of immunoglobulin mediated immune response (Score: 0.322273)



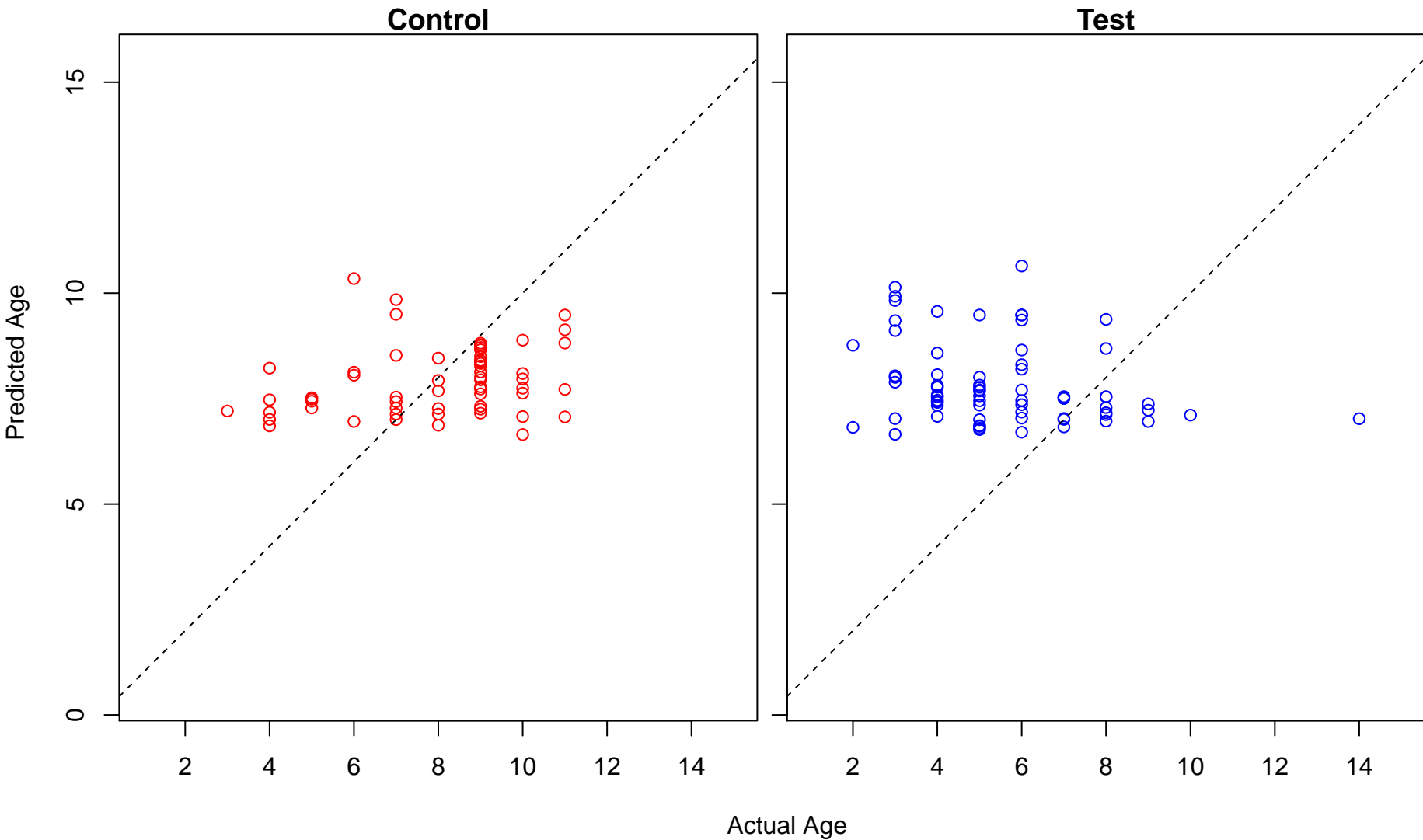
gastro-intestinal system smooth muscle contraction (Score: 0.322172)



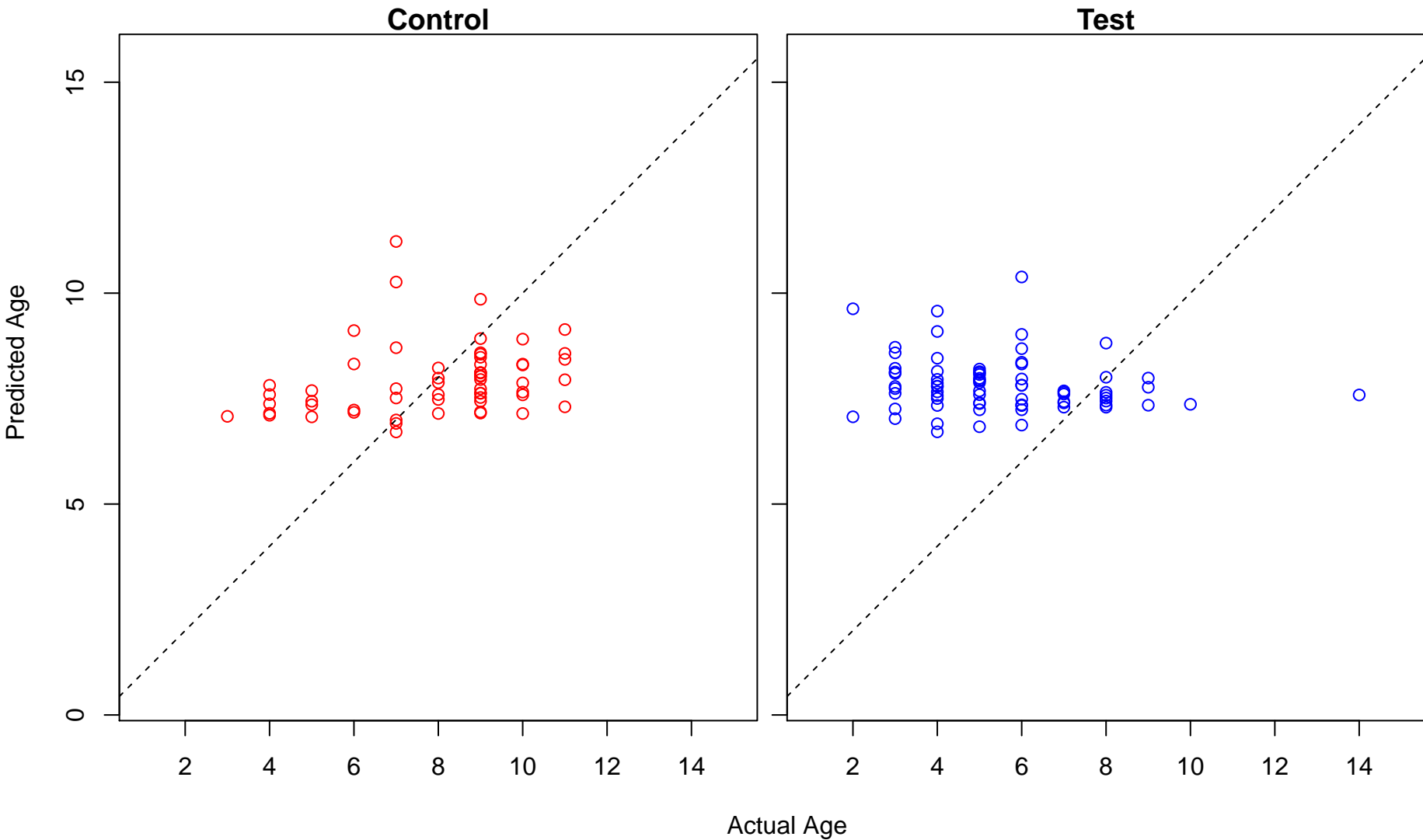
positive regulation of isotype switching to IgA isotypes (Score: 0.322006)



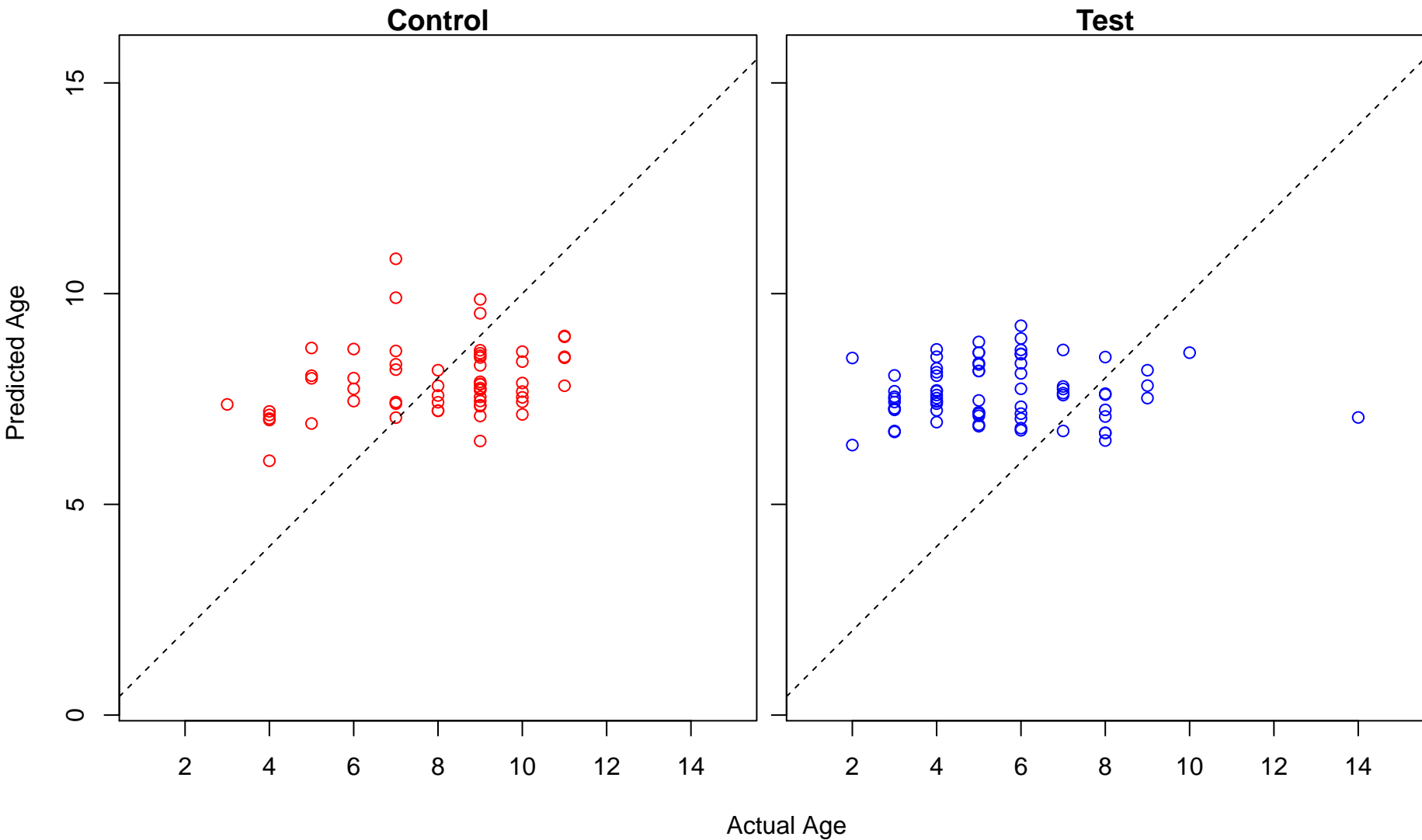
regulation of isotype switching to IgA isotypes (Score: 0.321497)



negative regulation of transforming growth factor beta1 production (Score: 0.318014)

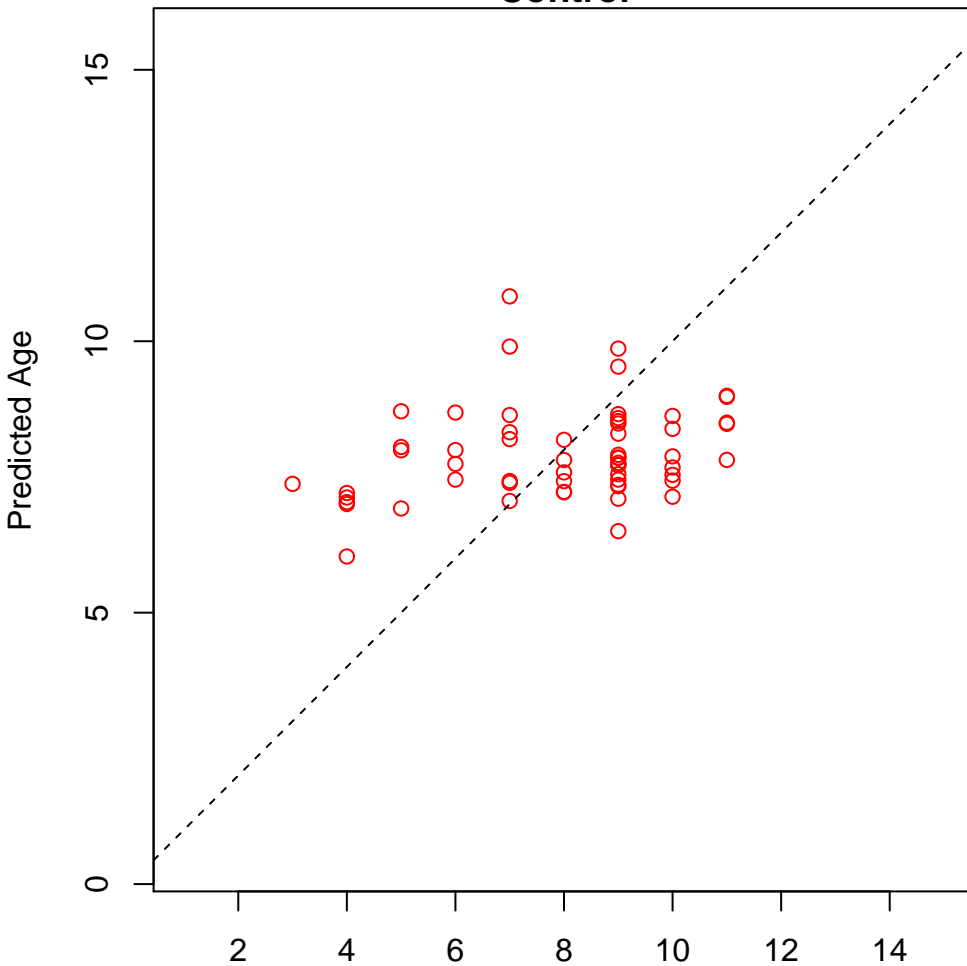


oxidoreduction coenzyme metabolic process (Score: 0.317464)

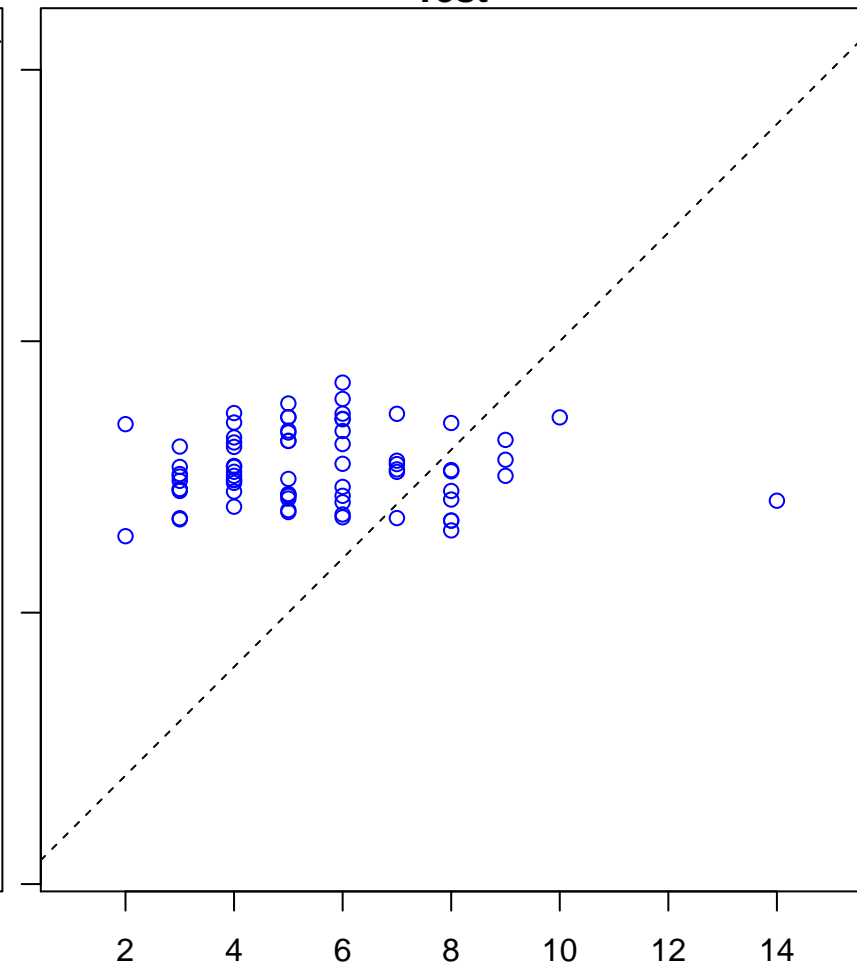


pyridine nucleotide metabolic process (Score: 0.317359)

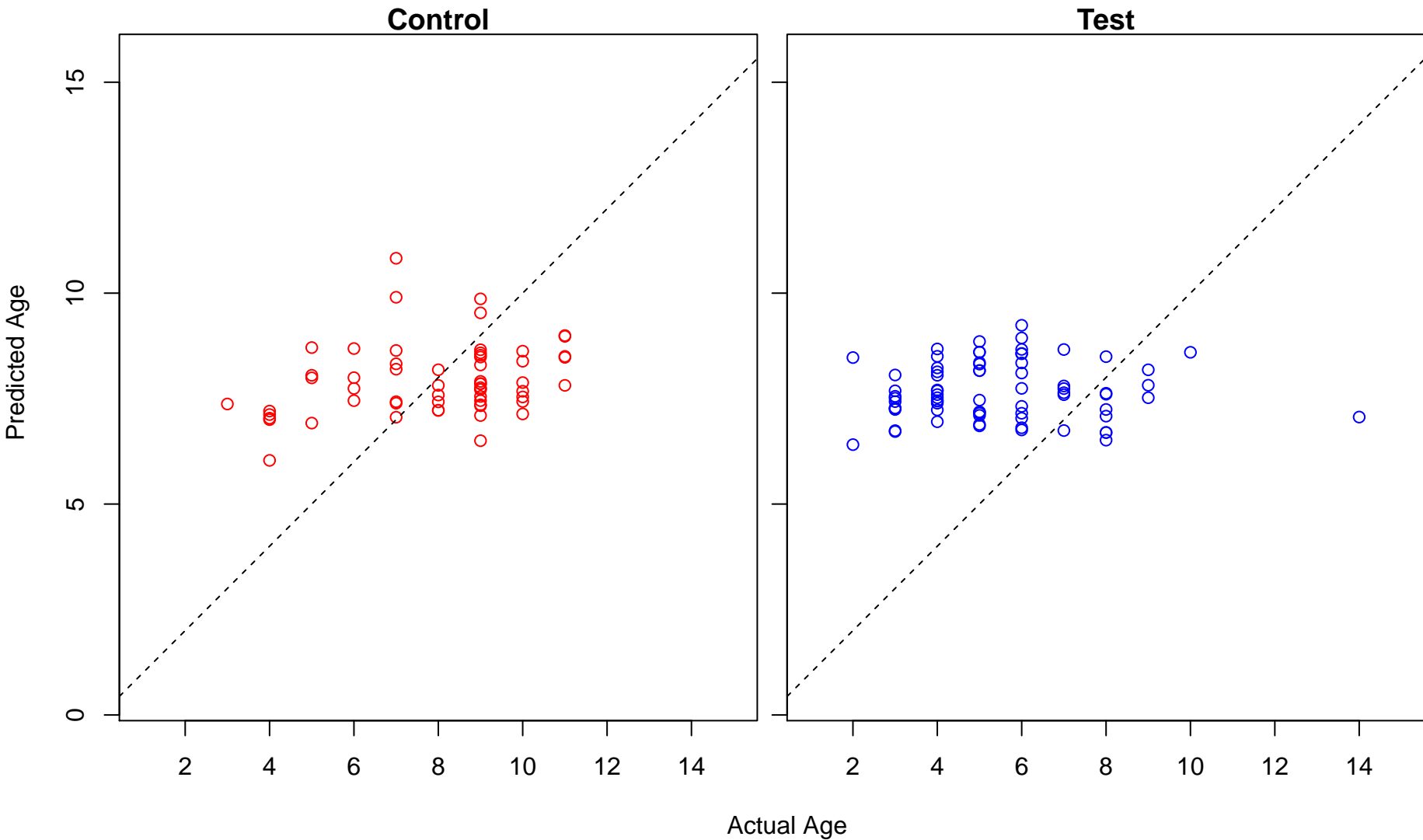
Control



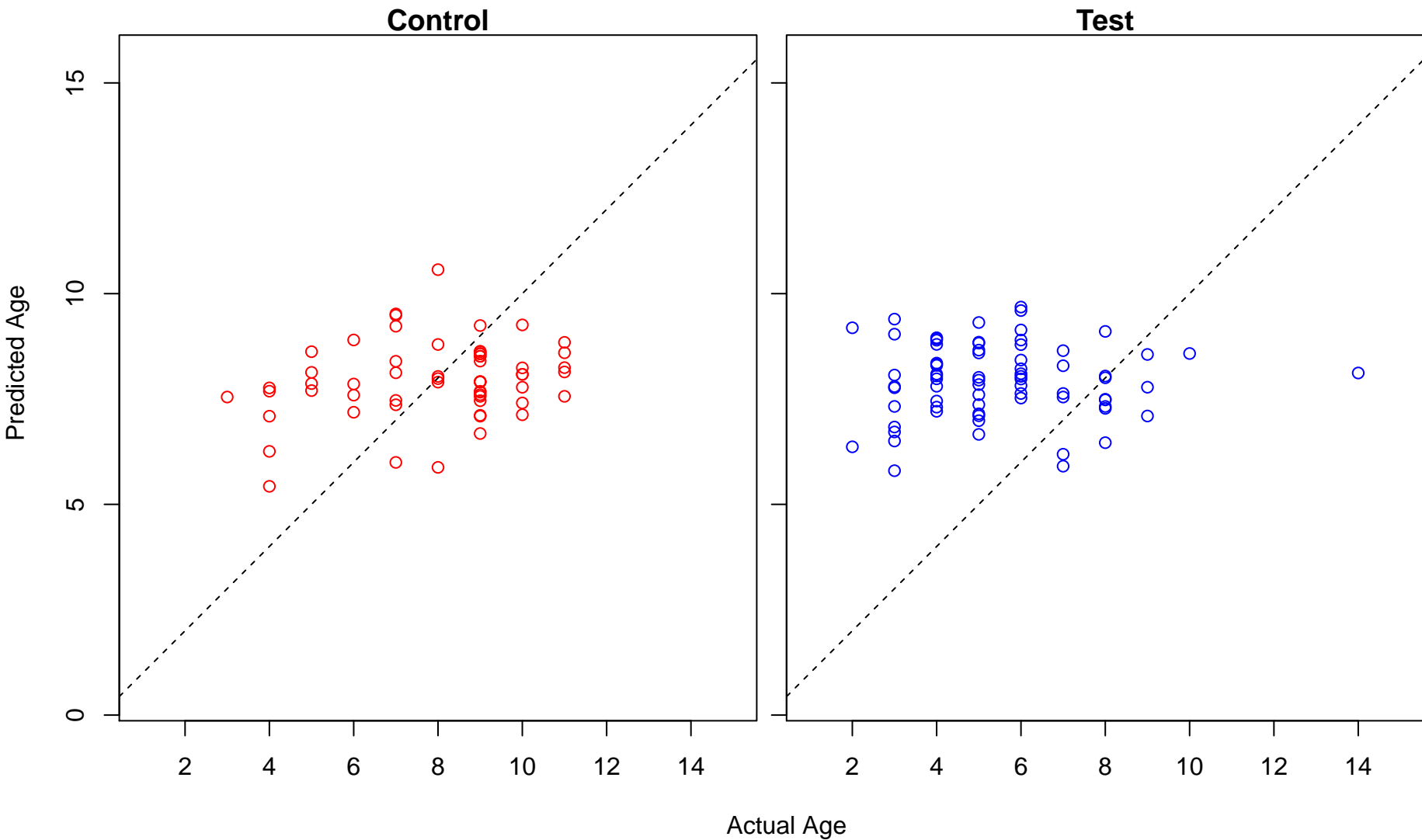
Test



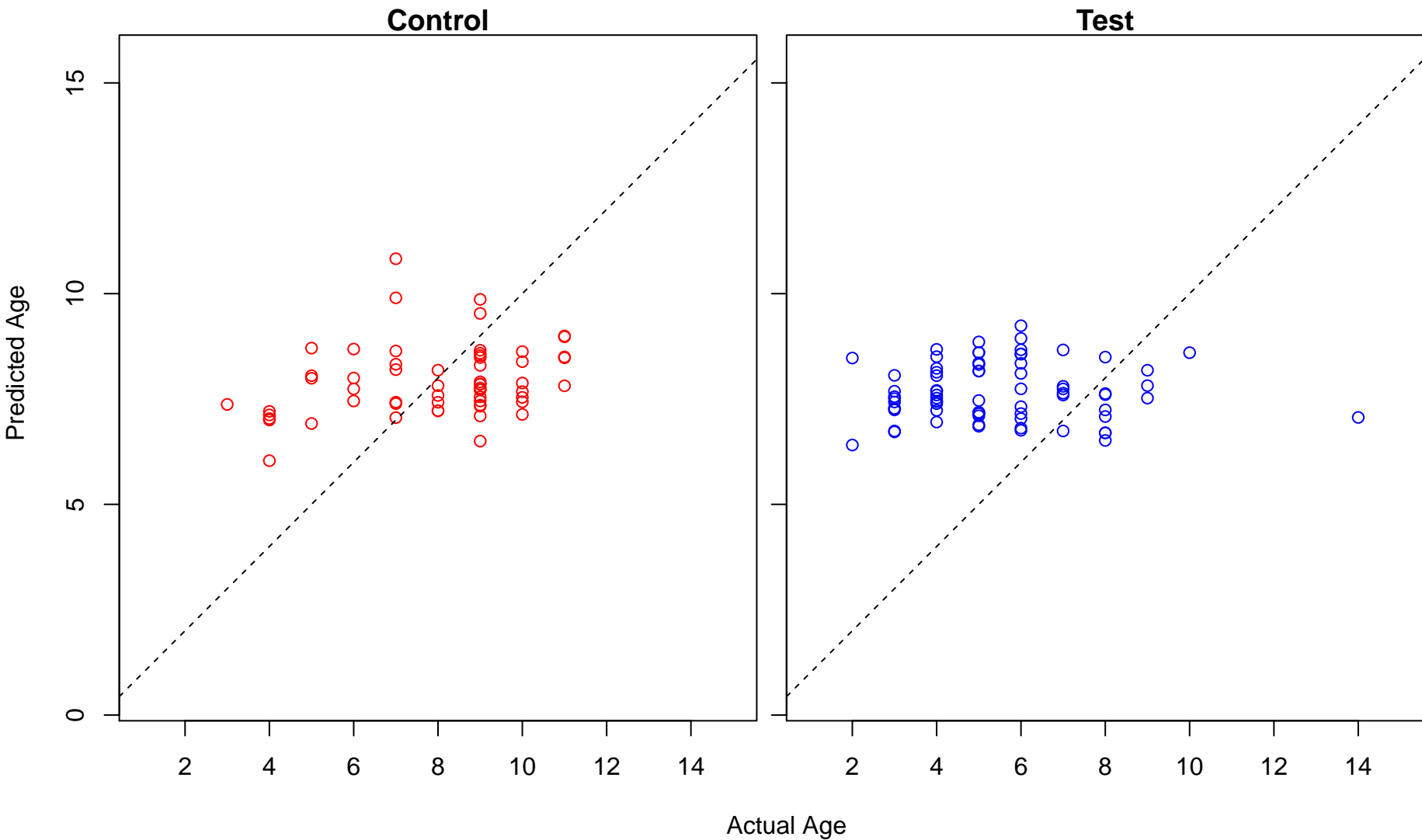
nicotinamide nucleotide metabolic process (Score: 0.317359)



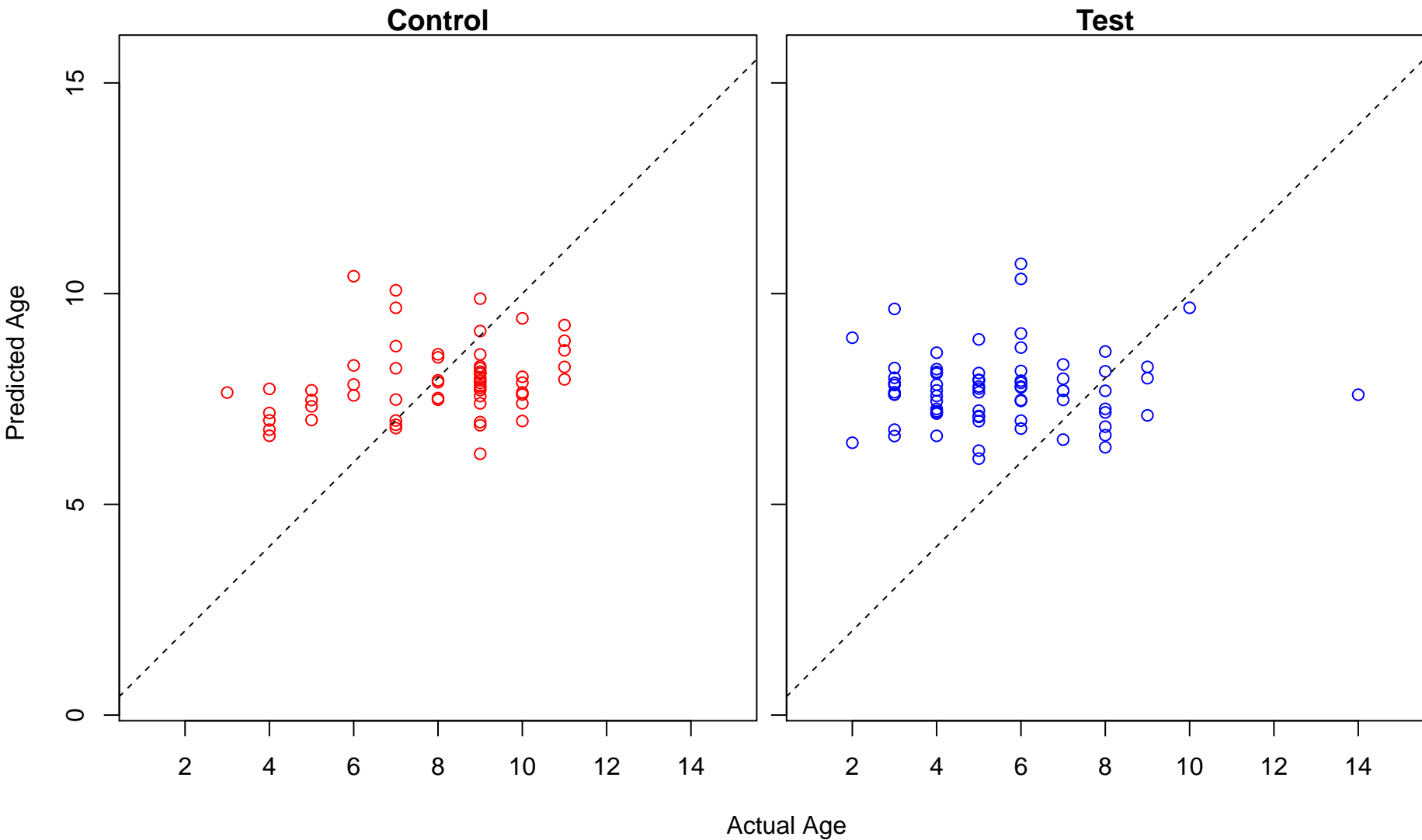
regulation of postsynaptic membrane potential (Score: 0.317218)



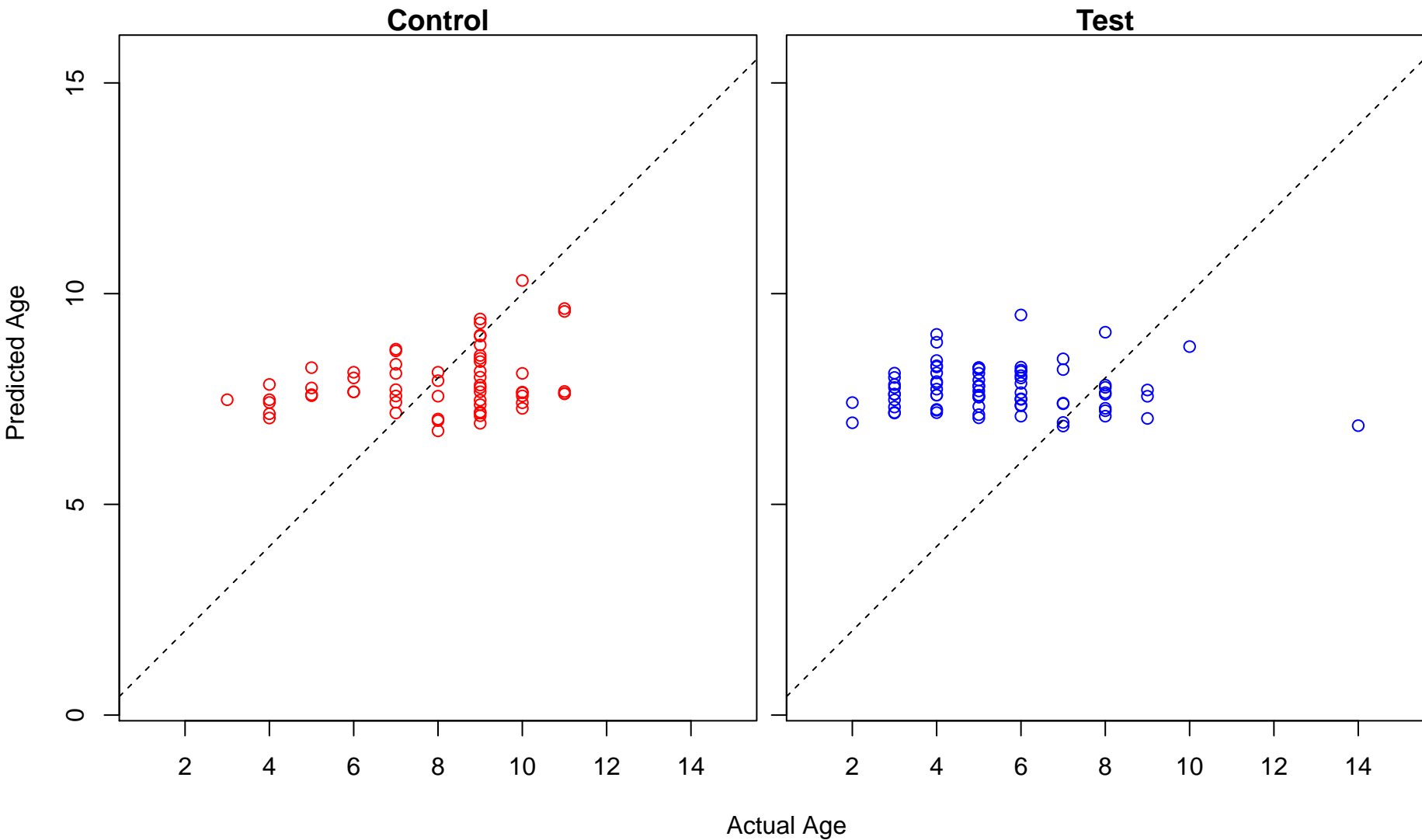
pyridine-containing compound metabolic process (Score: 0.317019)



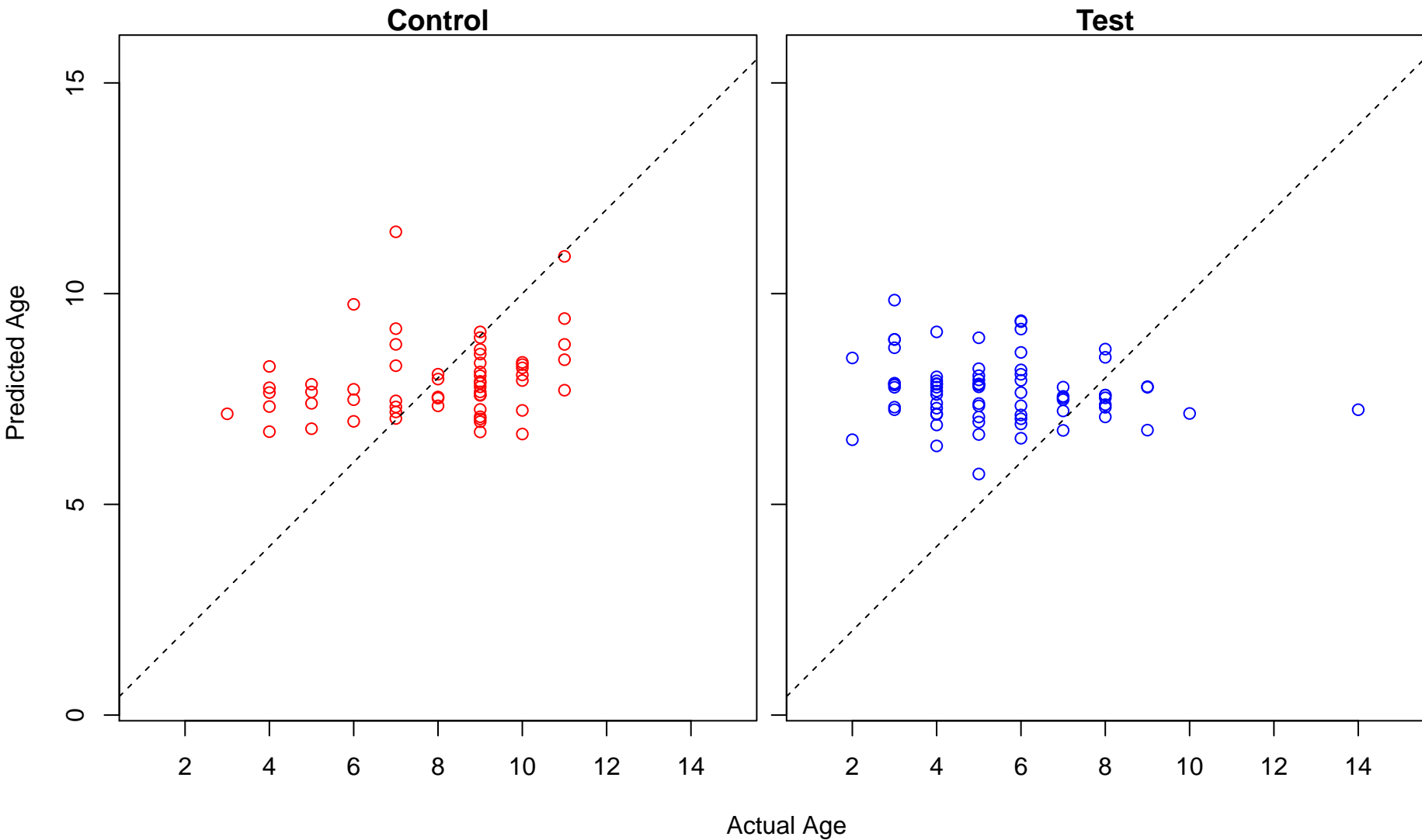
regulation of hydrogen peroxide metabolic process (Score: 0.316557)



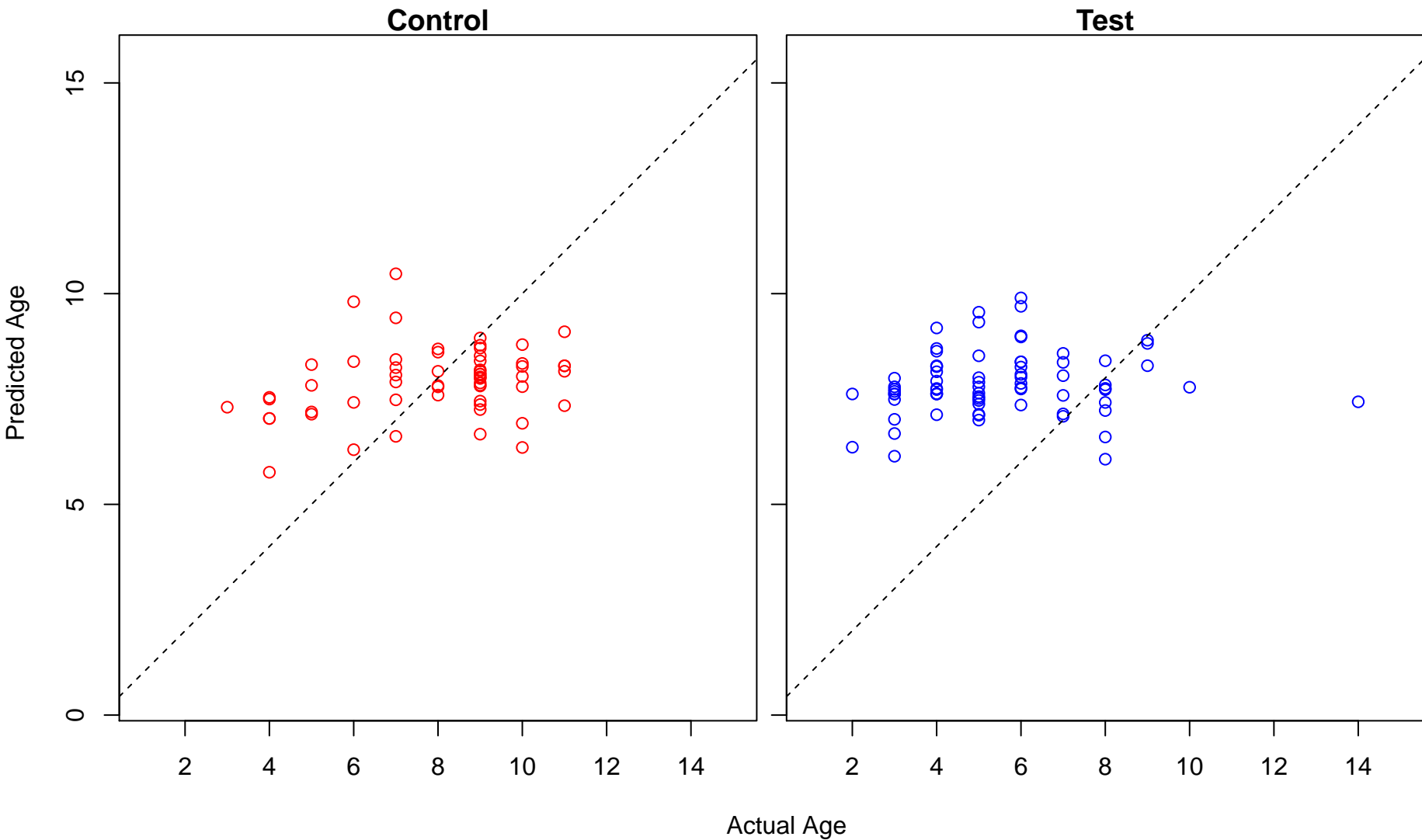
diacylglycerol biosynthetic process (Score: 0.310178)



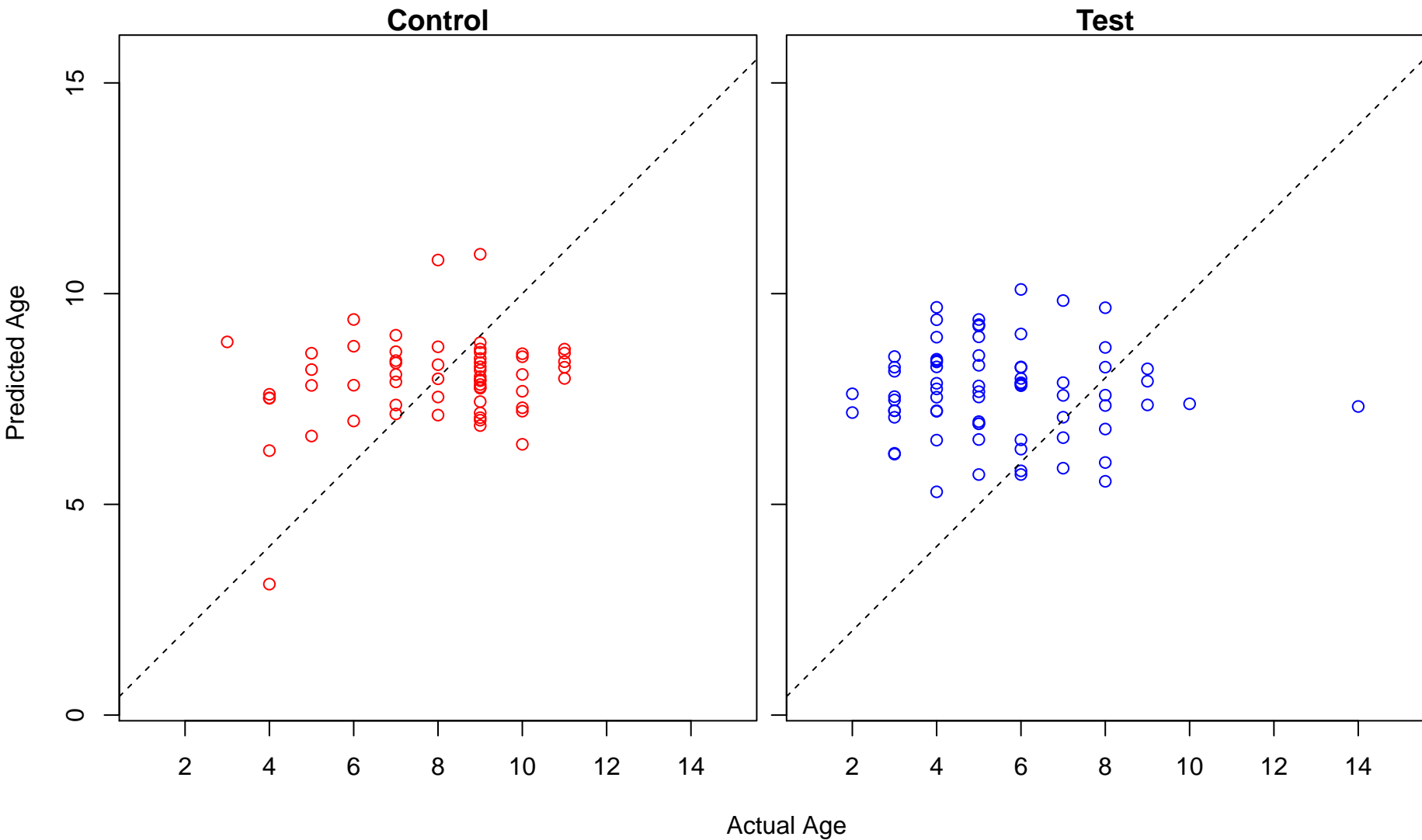
neutrophil degranulation (Score: 0.308680)



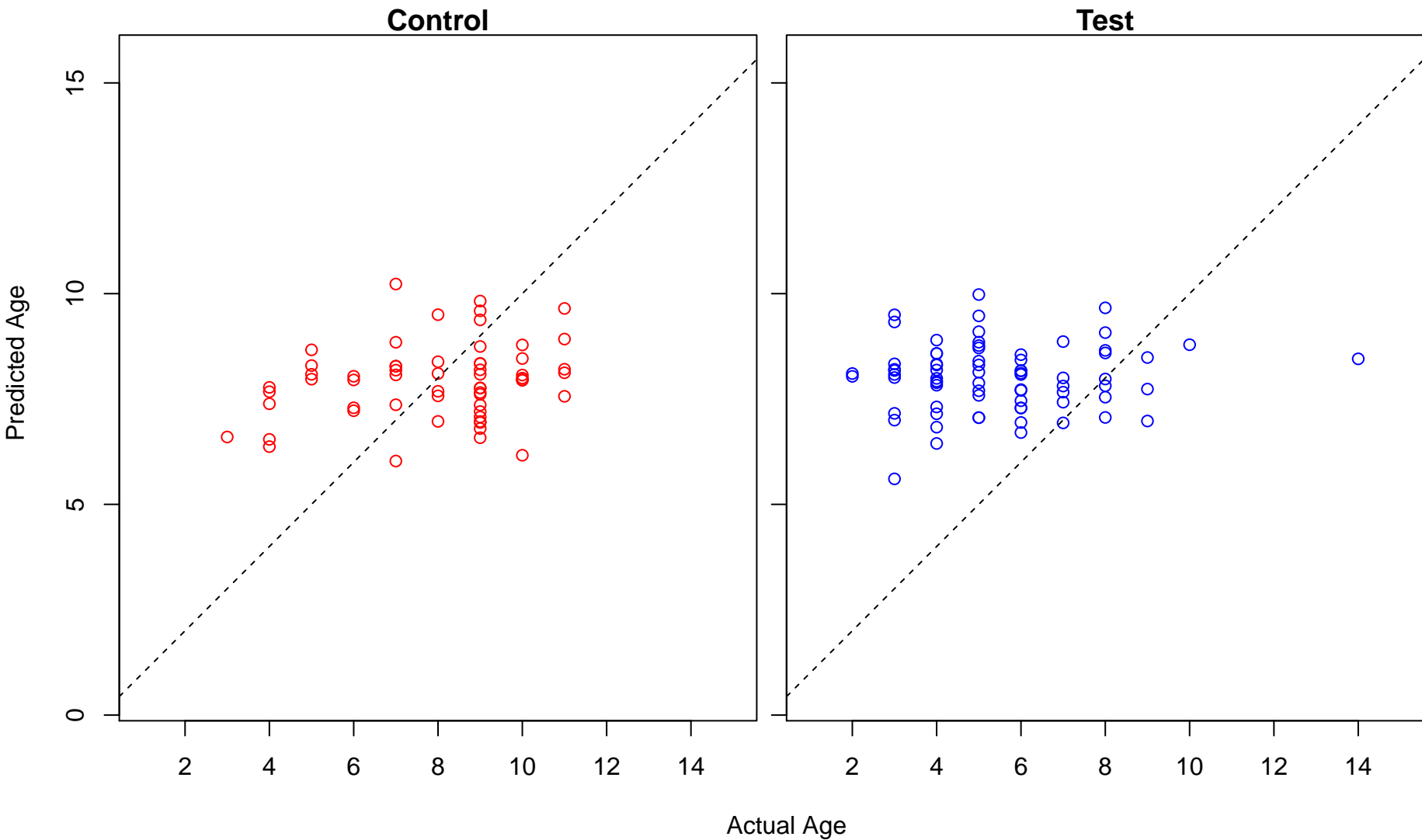
negative regulation of calcineurin–NFAT signaling cascade (Score: 0.308445)



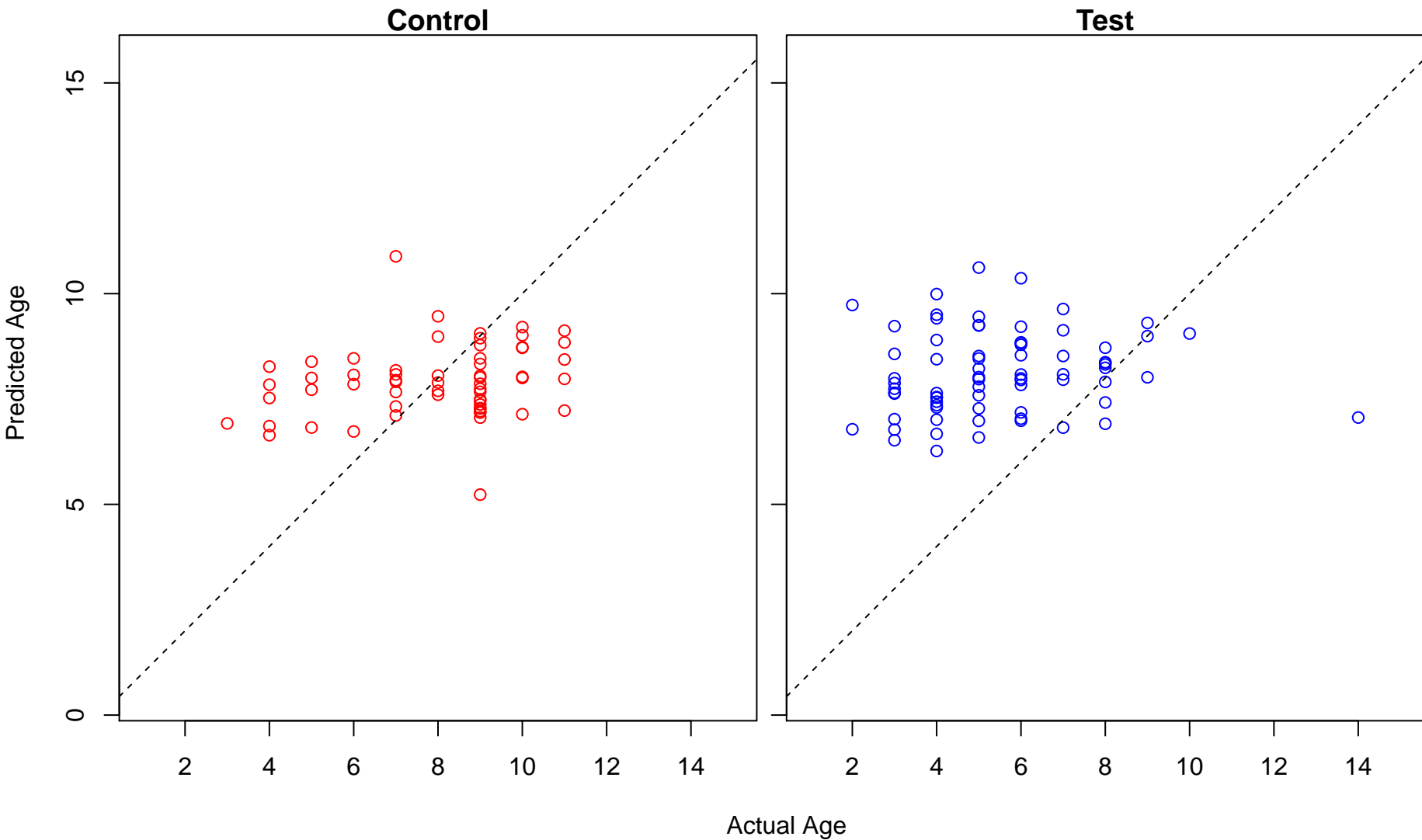
regulation of dopamine uptake involved in synaptic transmission (Score: 0.307978)



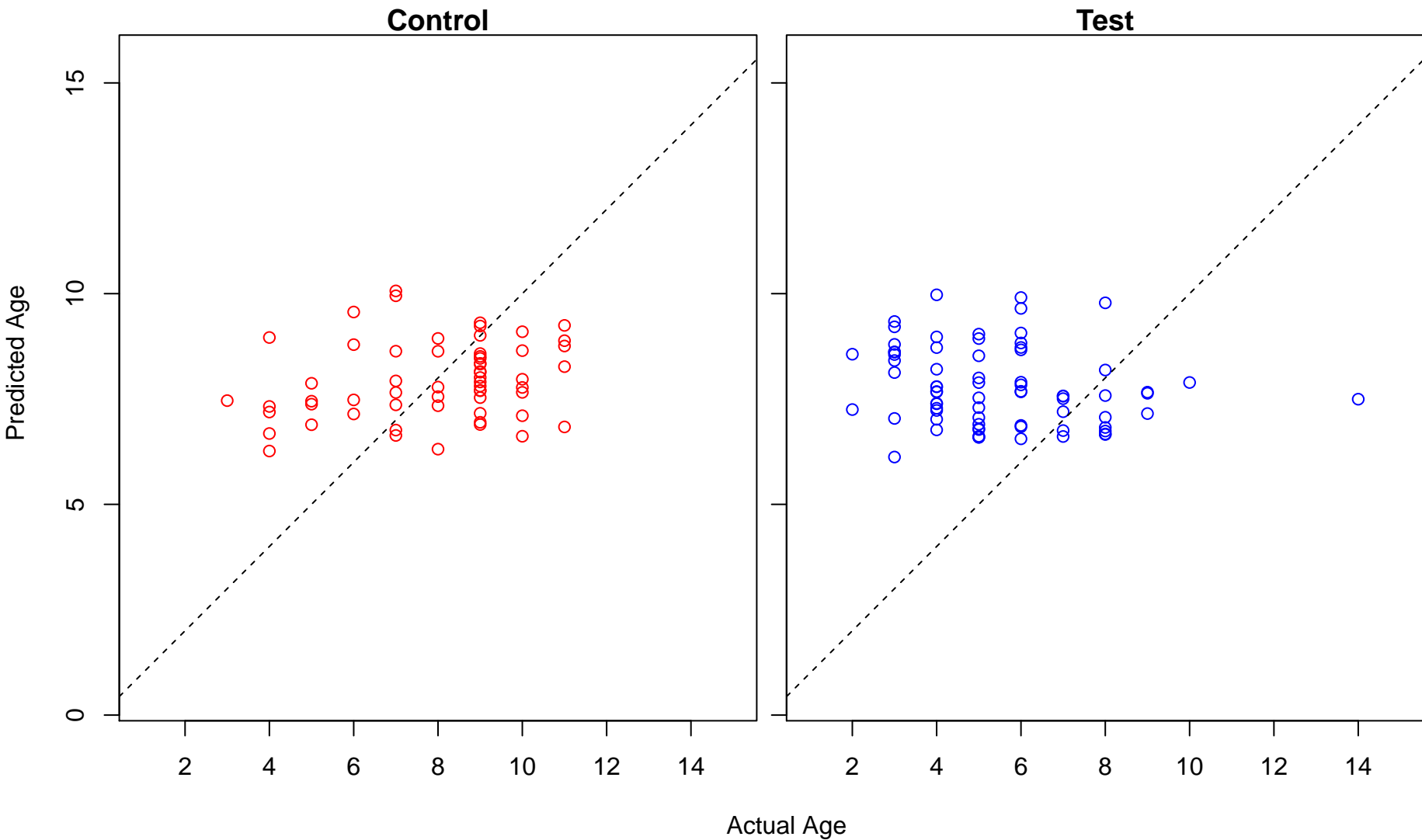
negative regulation of negative chemotaxis (Score: 0.306624)



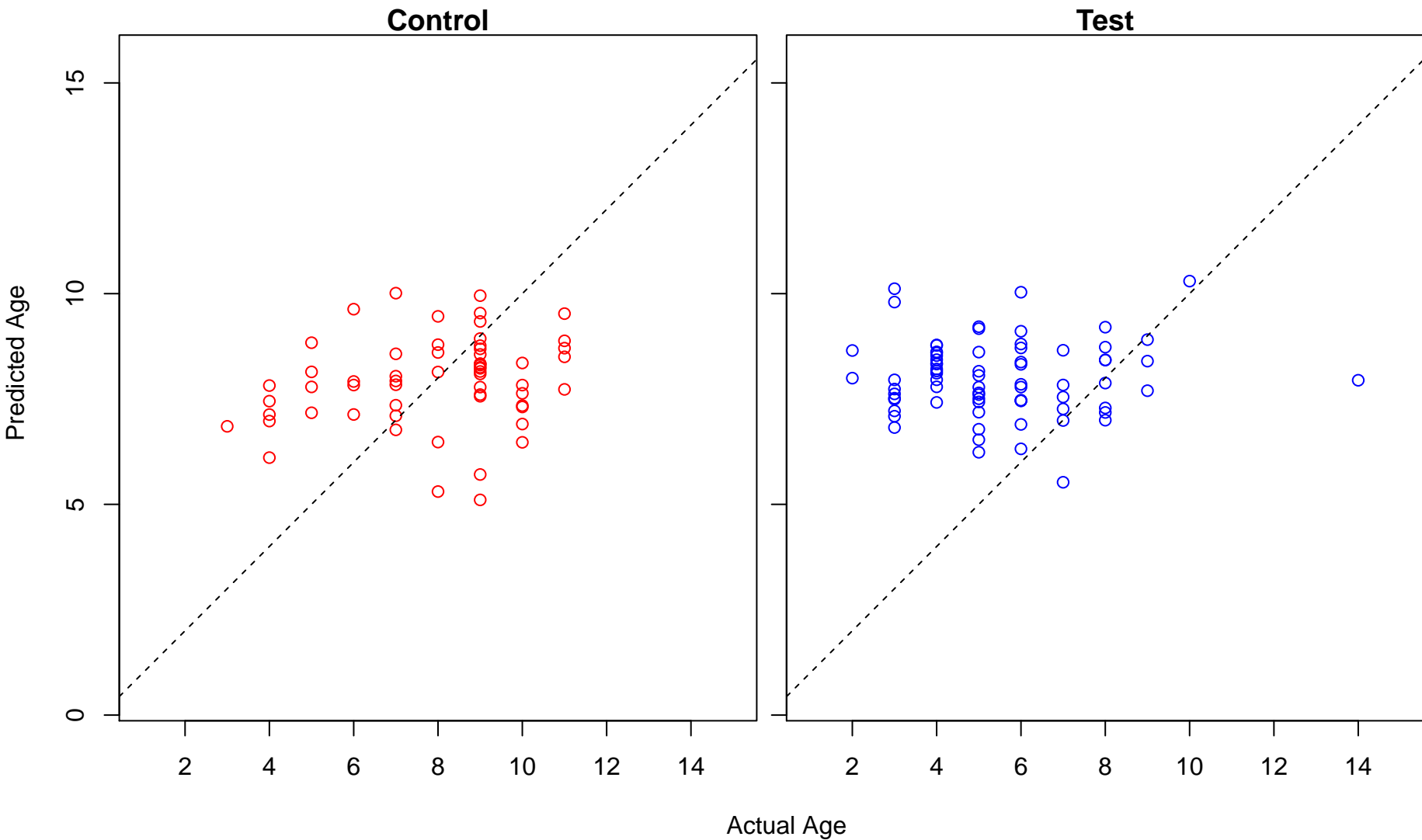
natural killer cell chemotaxis (Score: 0.306545)



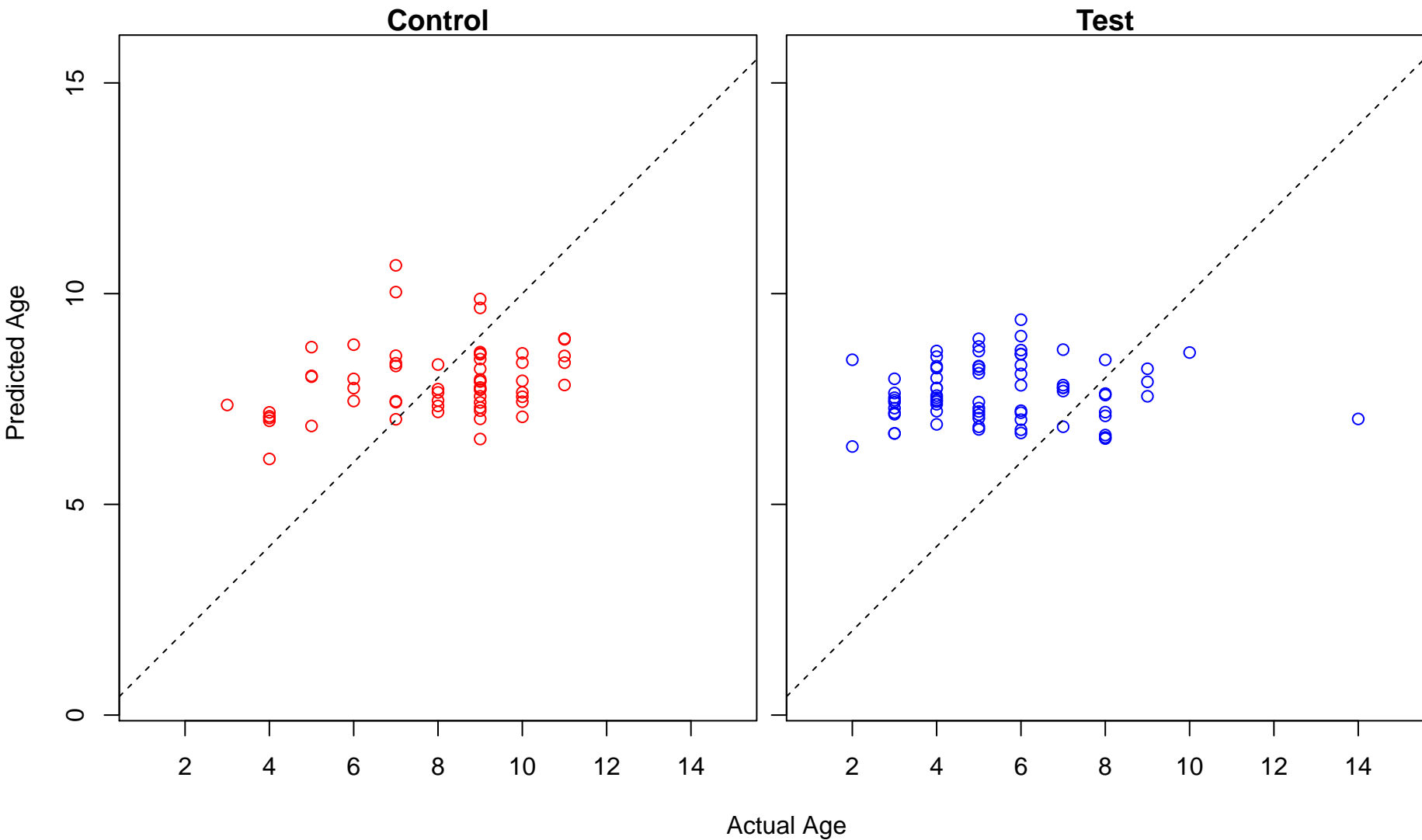
acidic amino acid transport (Score: 0.306398)



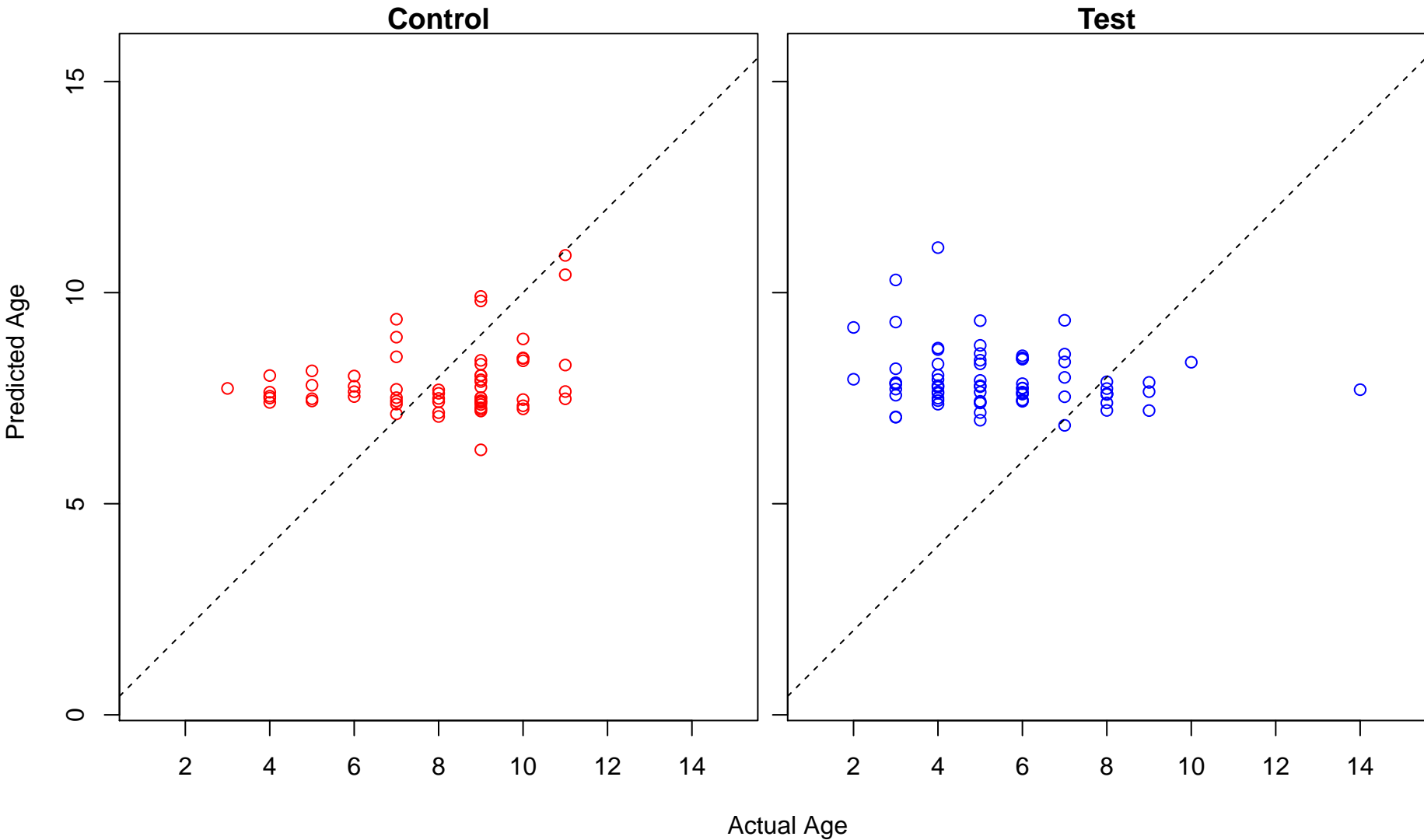
antigen processing and presentation via MHC class Ib (Score: 0.305542)



coenzyme metabolic process (Score: 0.305302)

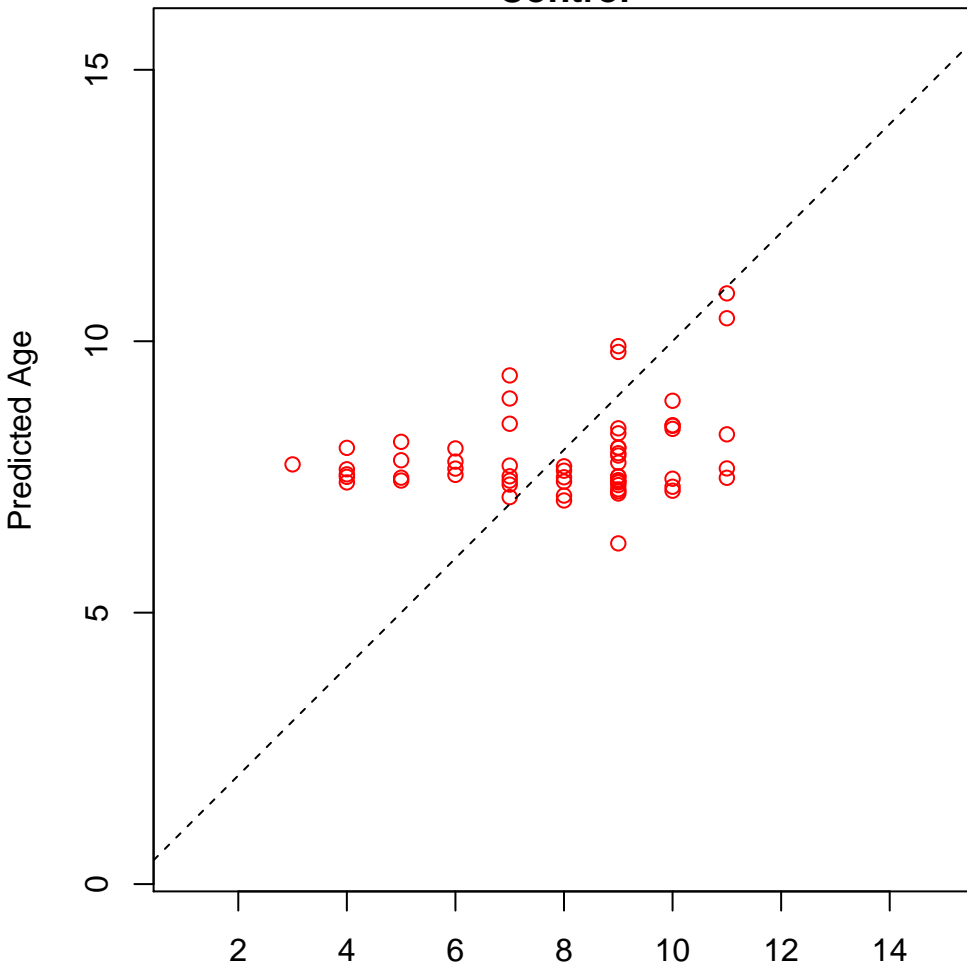


urinary bladder smooth muscle contraction (Score: 0.304545)

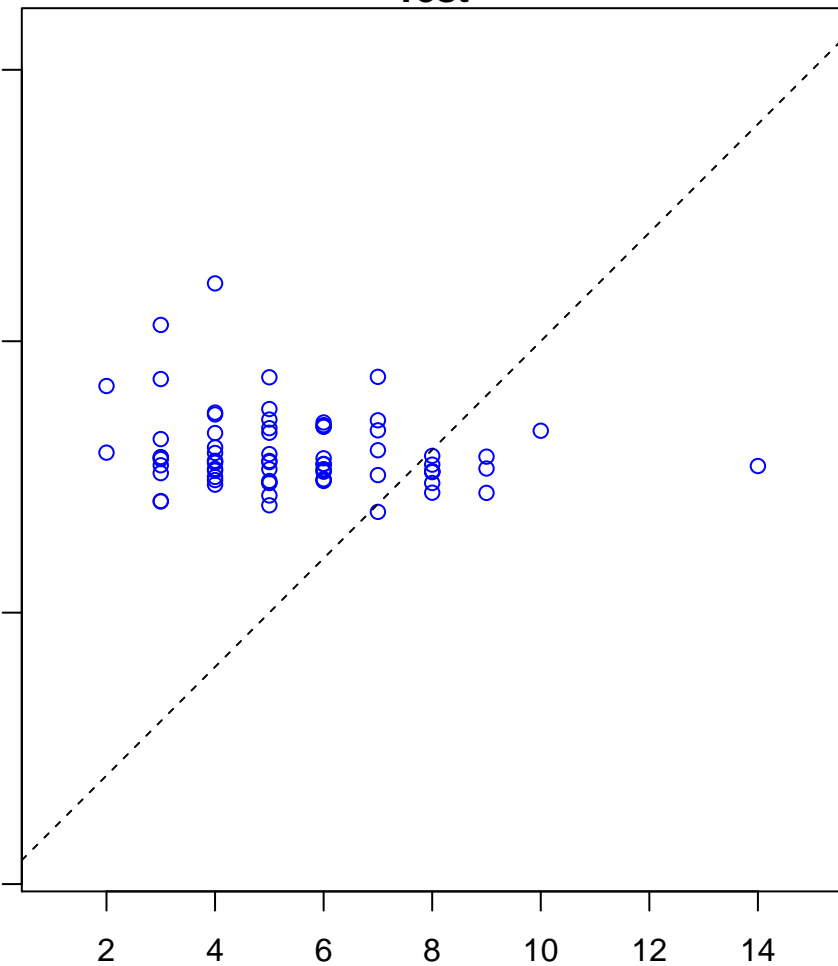


urinary tract smooth muscle contraction (Score: 0.304545)

Control

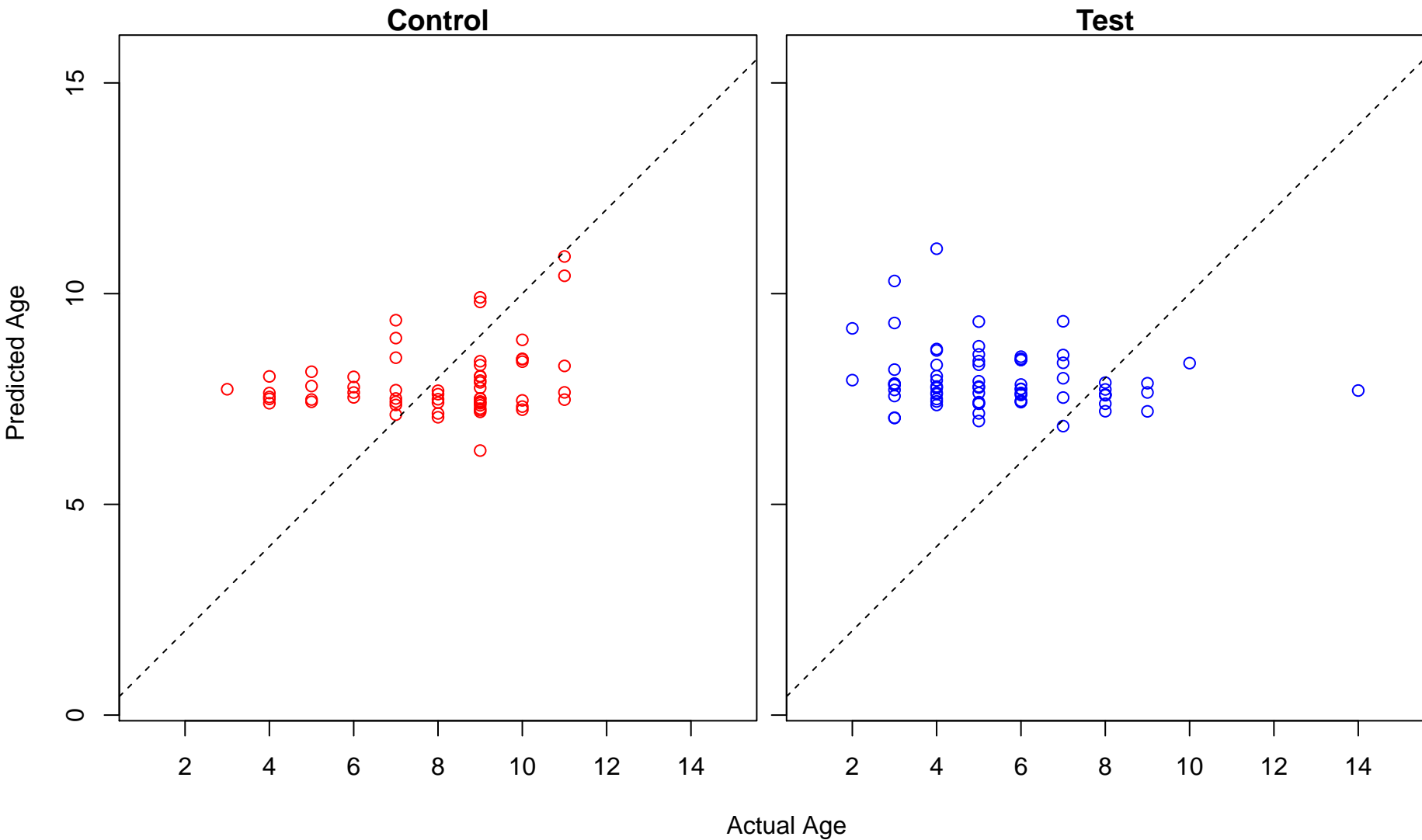


Test

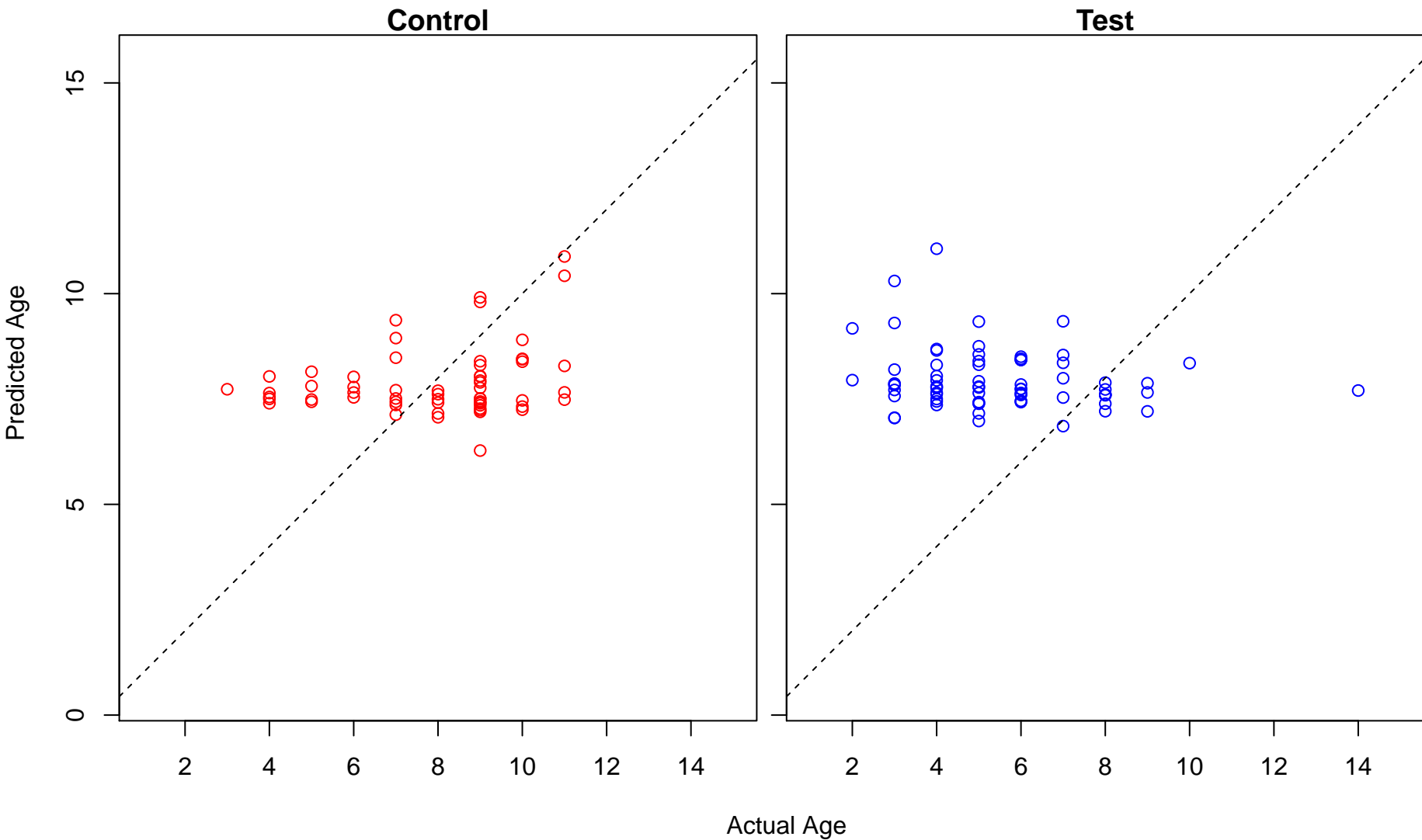


Actual Age

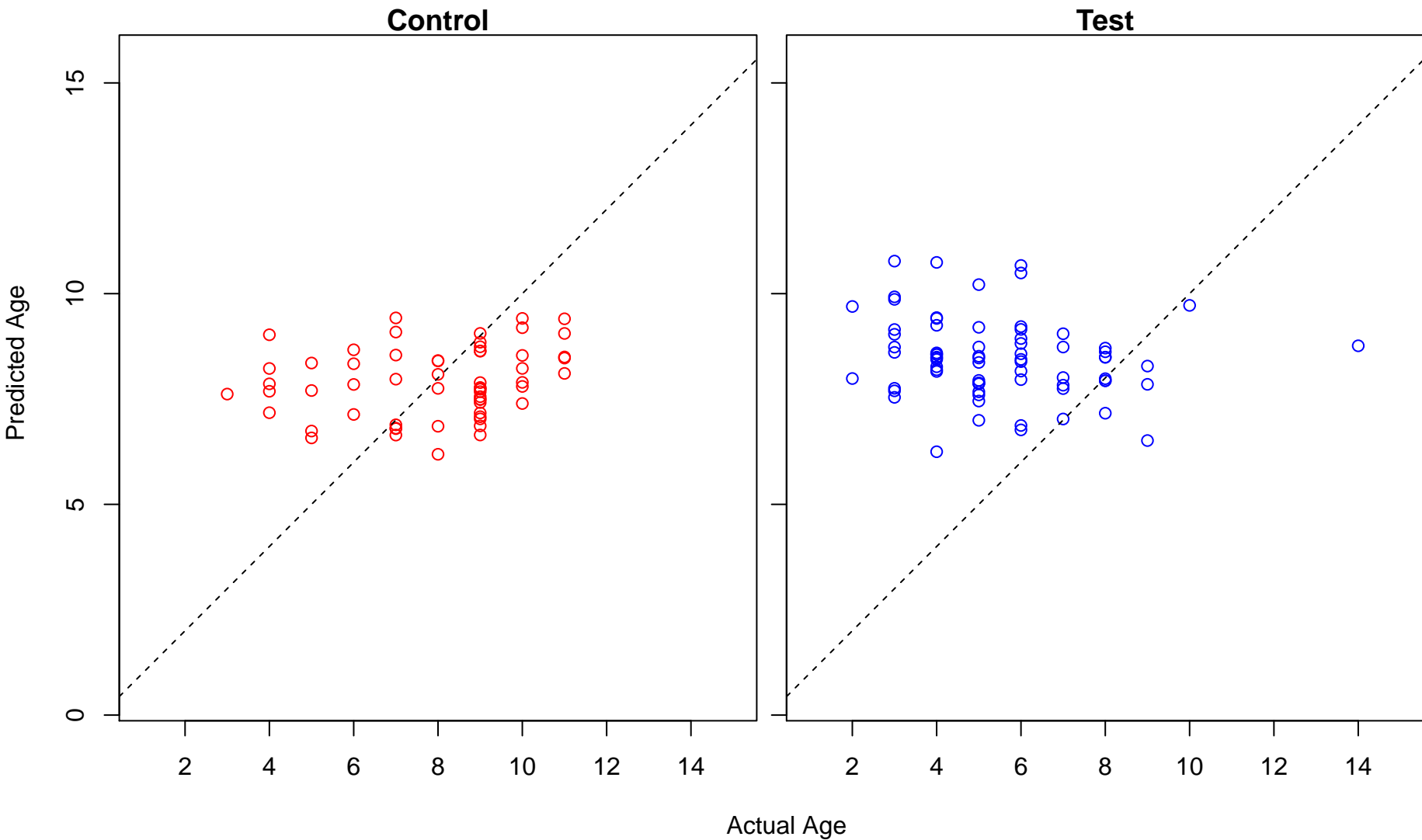
response to carbon monoxide (Score: 0.304545)



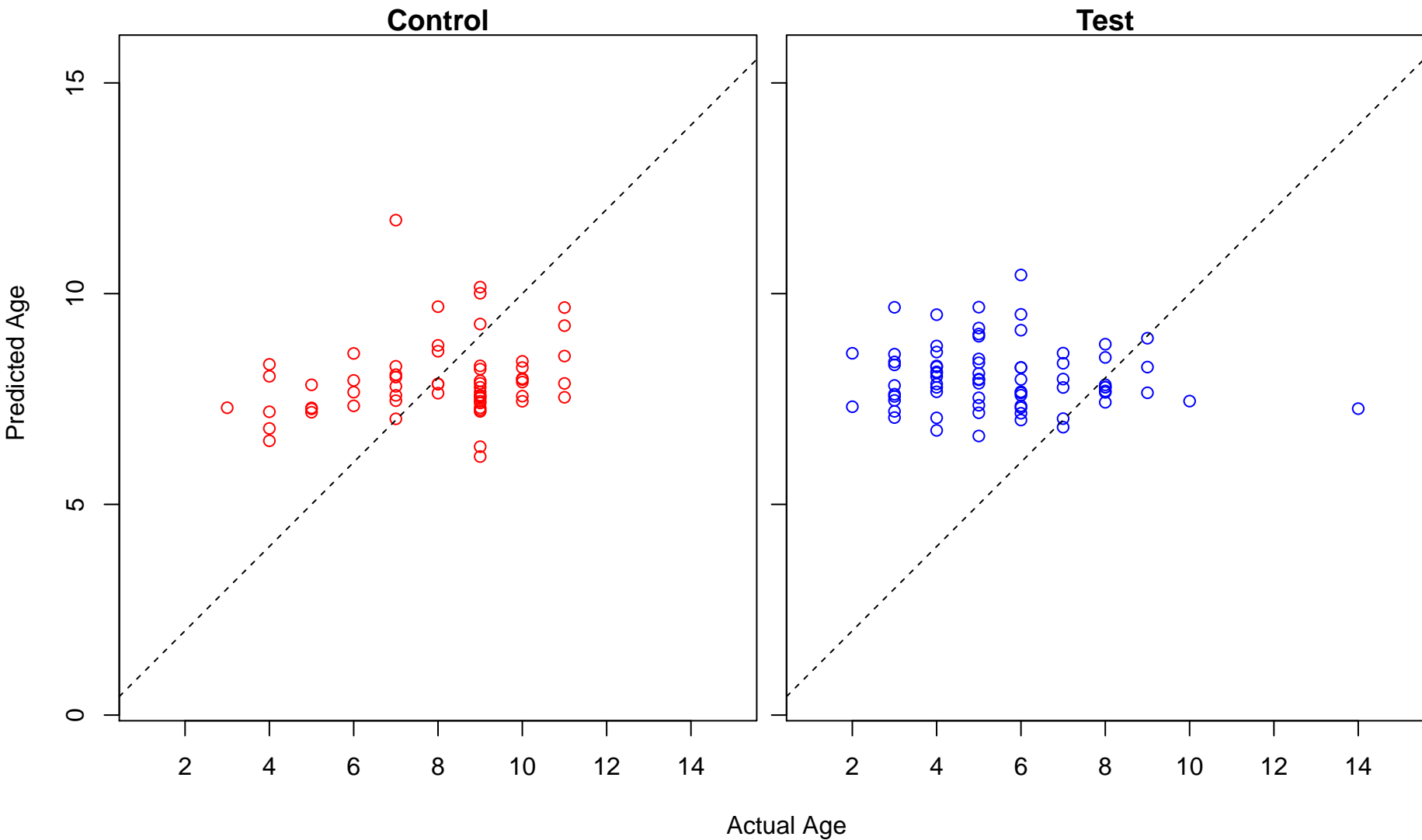
smooth muscle contraction involved in micturition (Score: 0.304545)



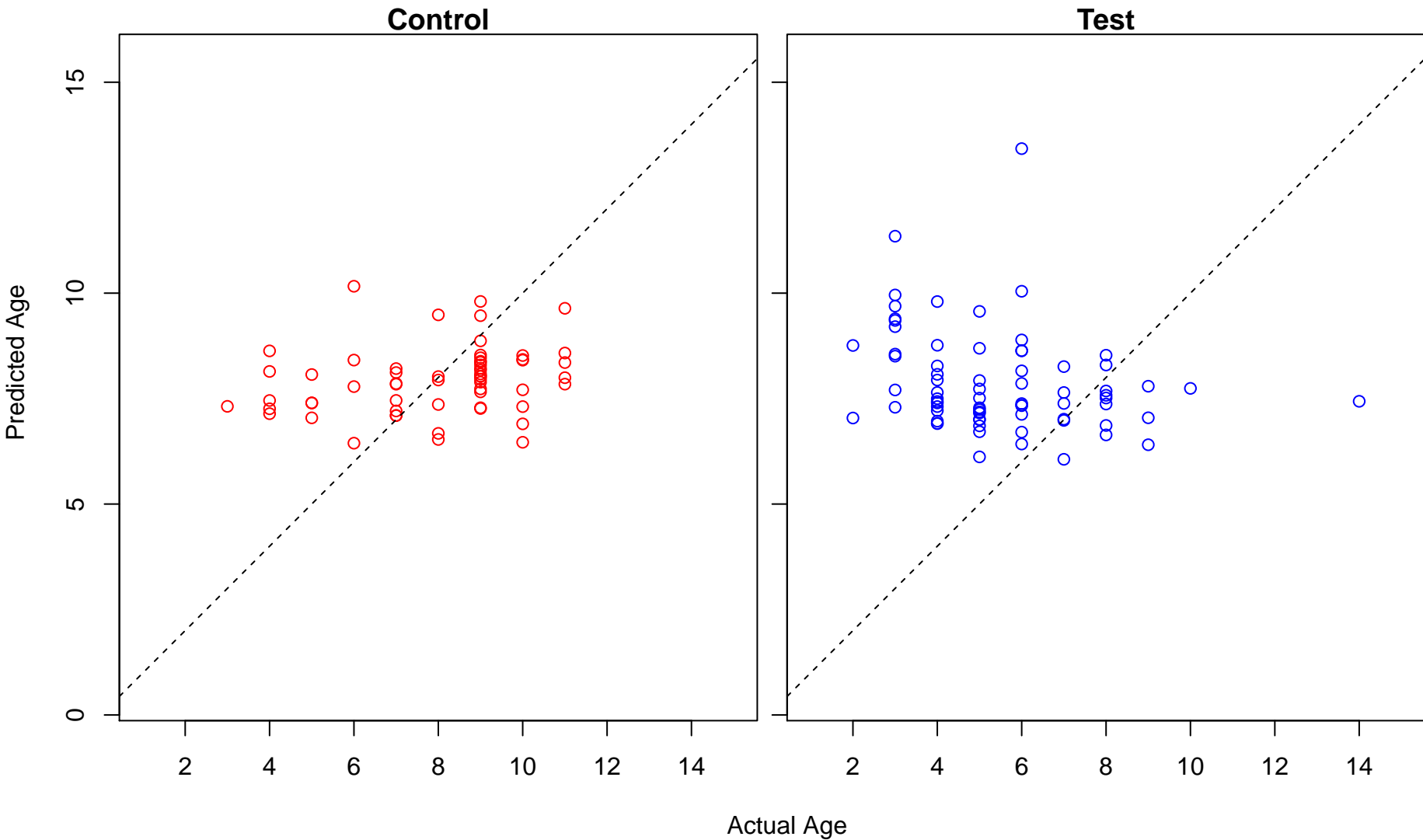
regulation of branch elongation involved in ureteric bud branching (Score: 0.302373)



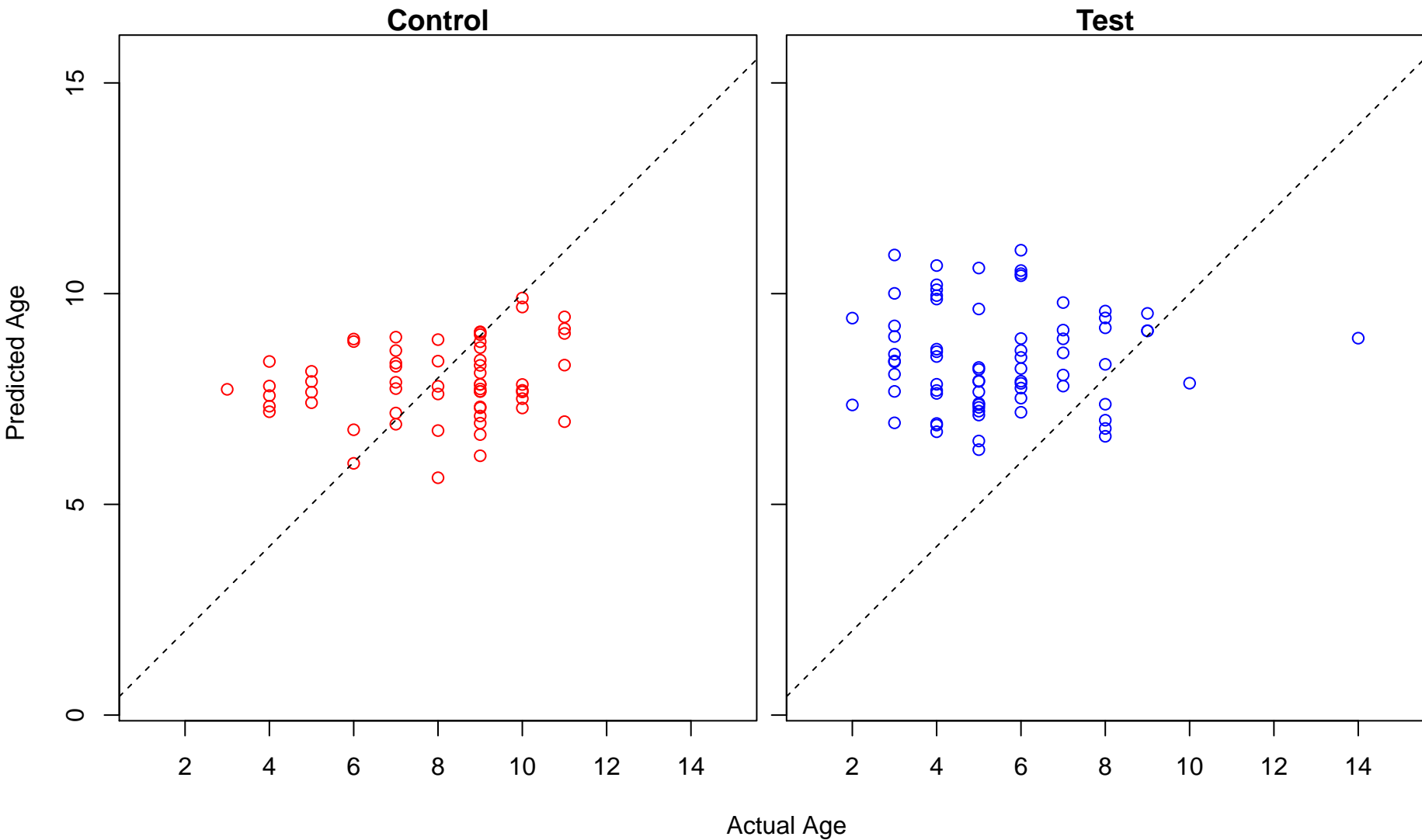
positive regulation of heterotypic cell–cell adhesion (Score: 0.302005)



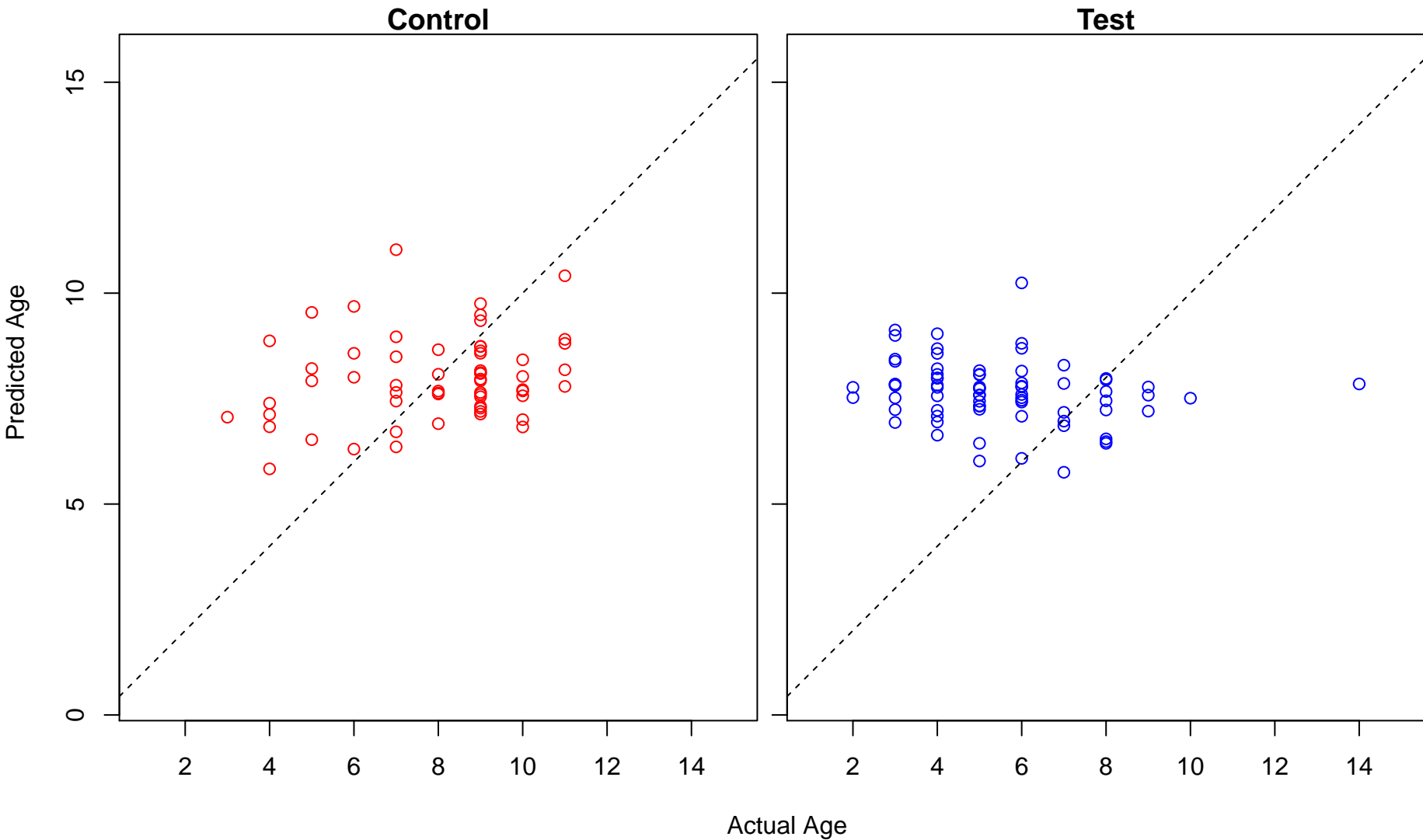
positive regulation of monocyte chemotactic protein-1 production (Score: 0.301107)



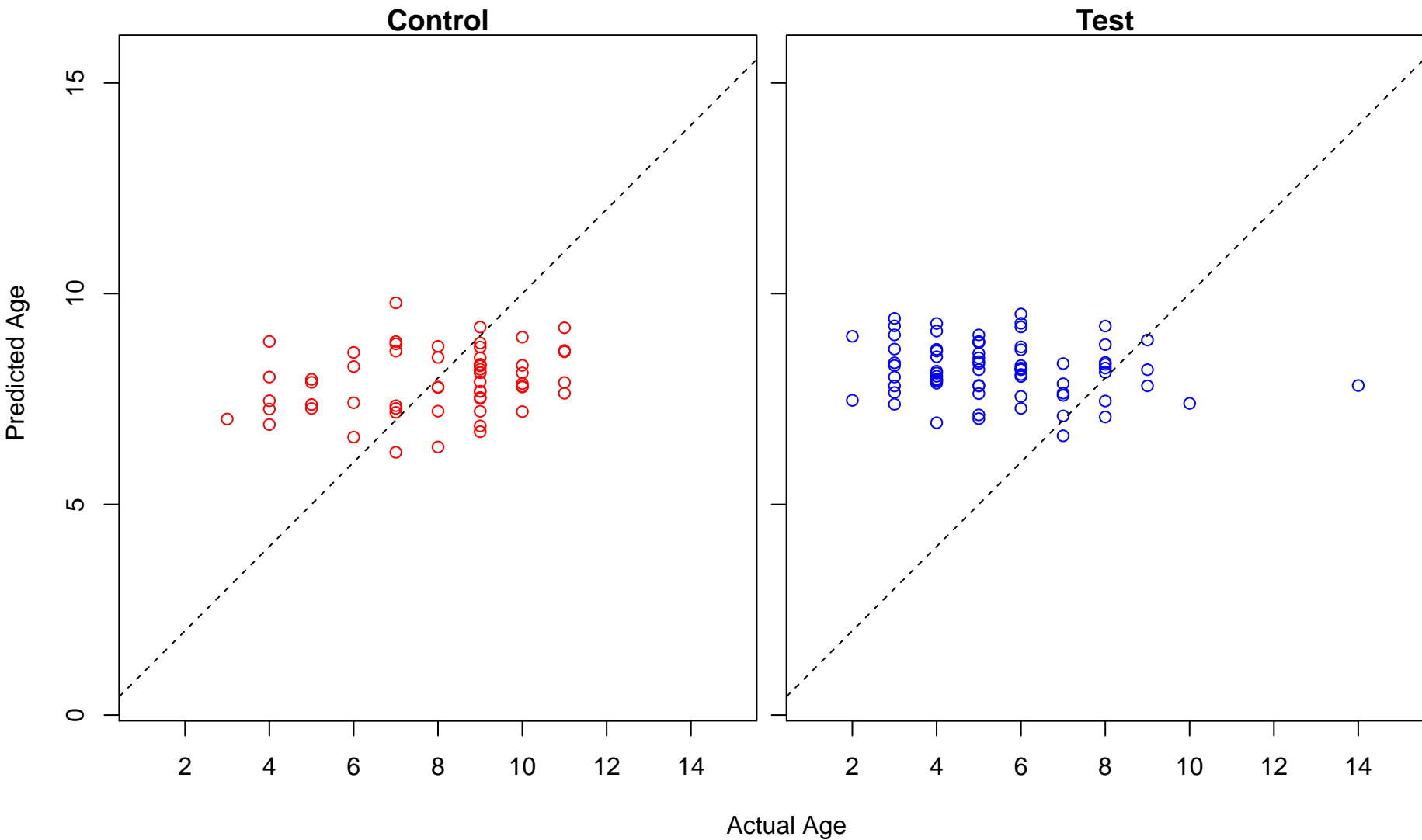
regulation of chondrocyte differentiation (Score: 0.300536)



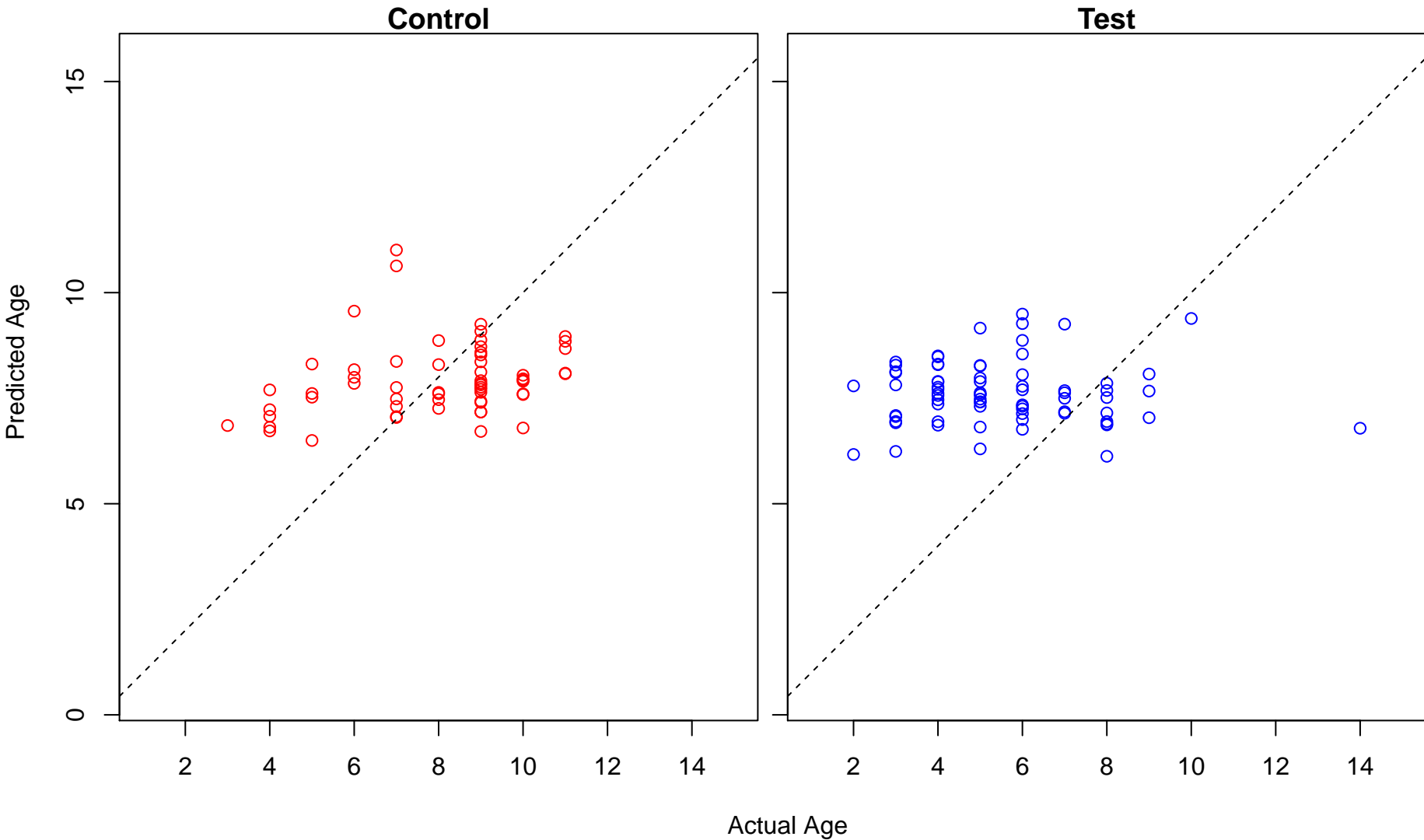
negative regulation of tumor necrosis factor biosynthetic process (Score: 0.300438)



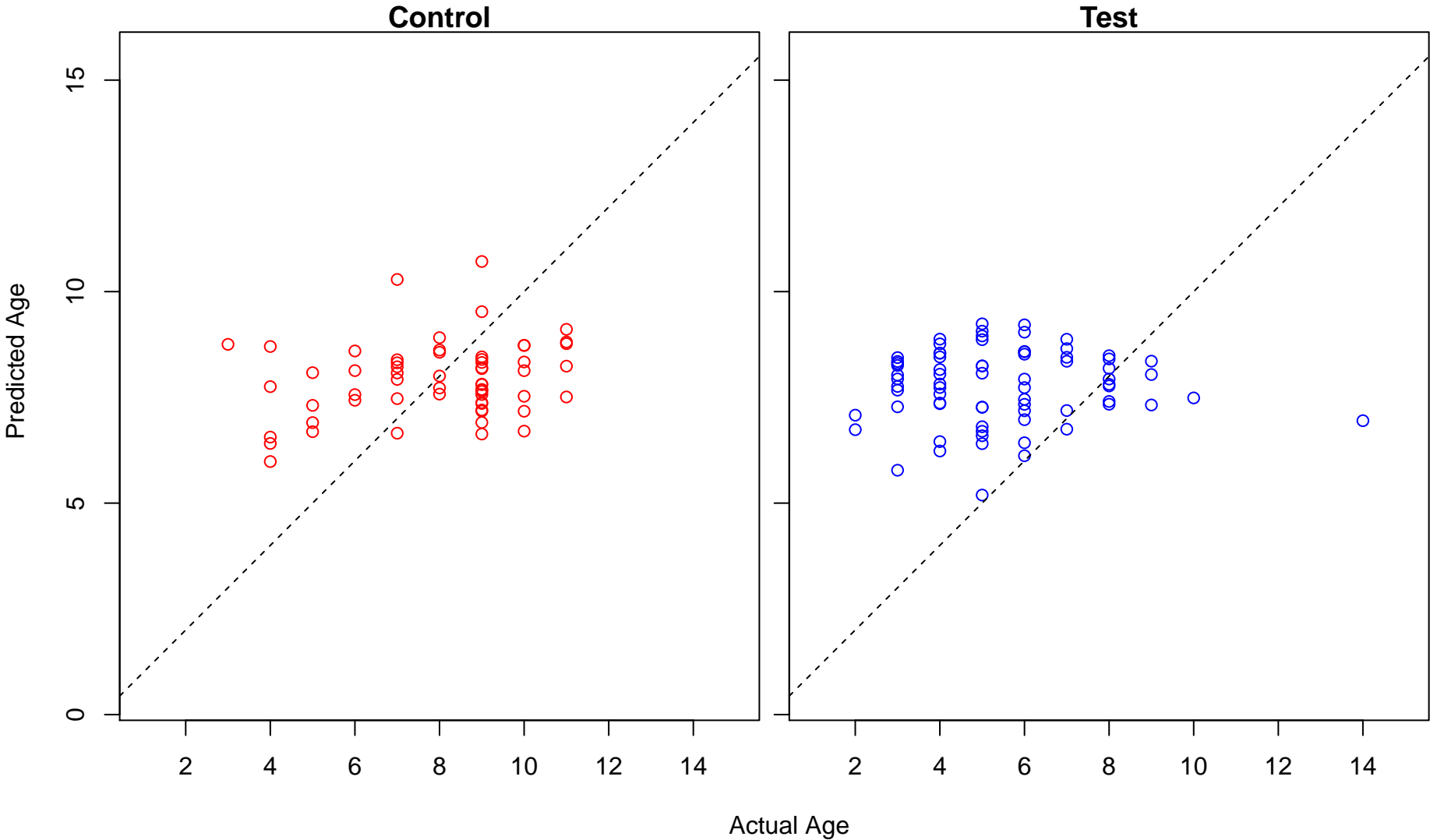
epithelial cell proliferation involved in mammary gland duct elongation (Score: 0.300396)



positive regulation of cellular extravasation (Score: 0.300030)

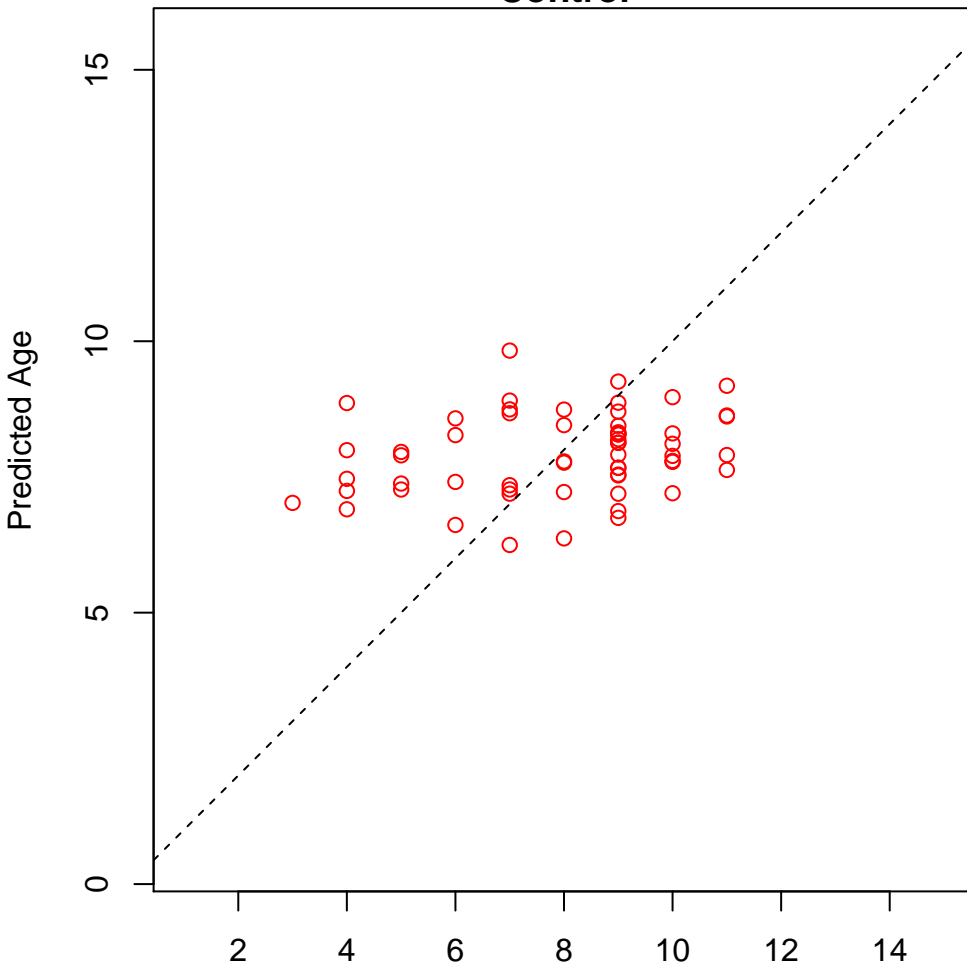


regulation of phospholipase C-activating G-protein coupled receptor signaling pathway (Score: 0.299)

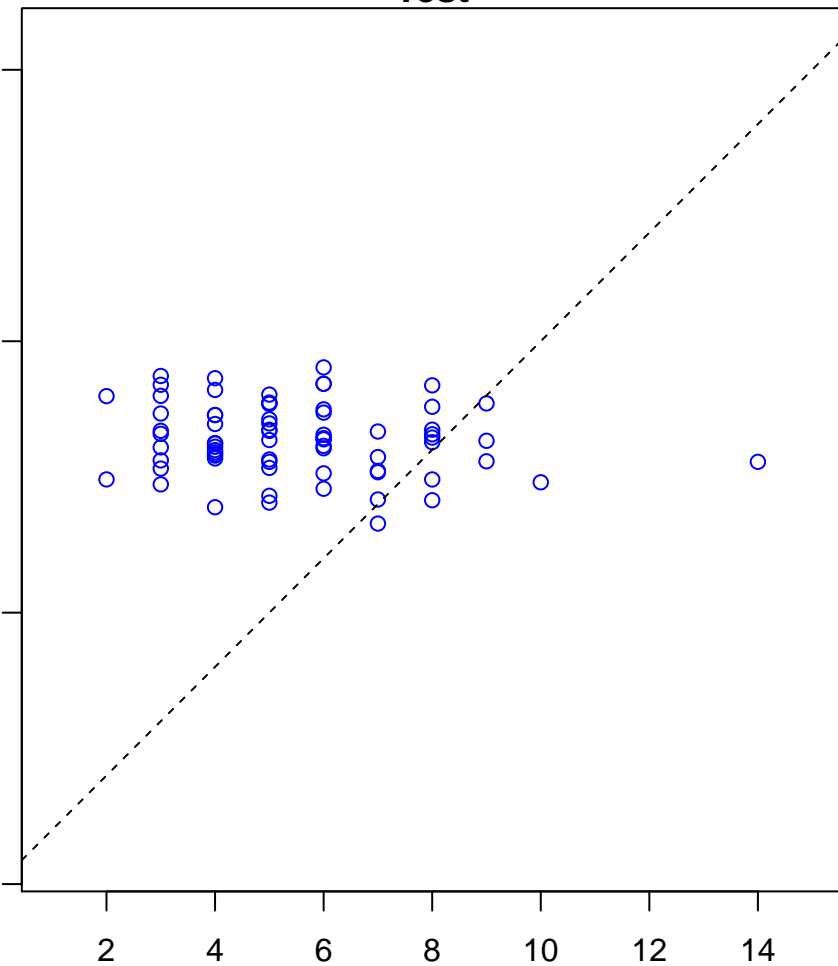


retinal pigment epithelium development (Score: 0.299873)

Control

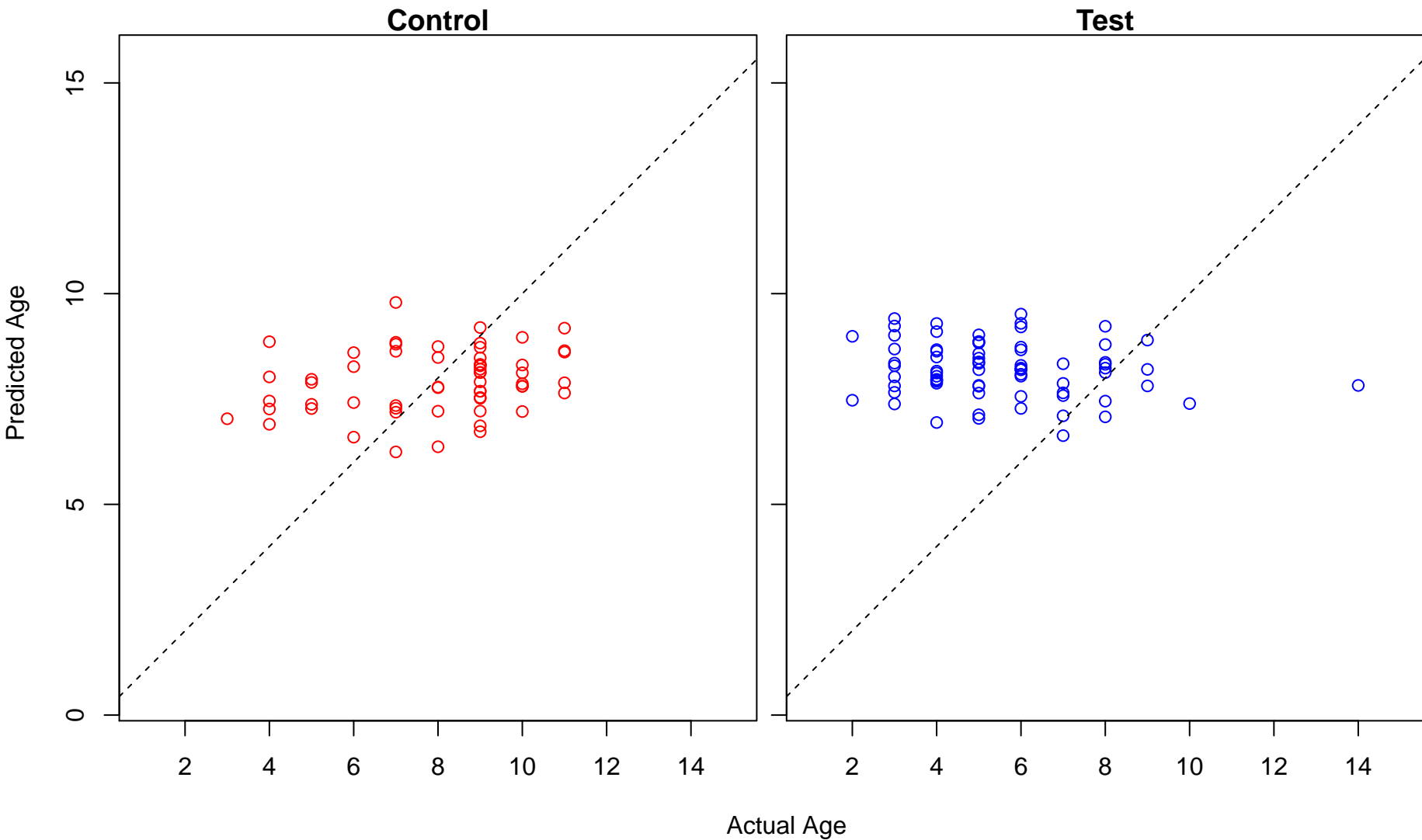


Test

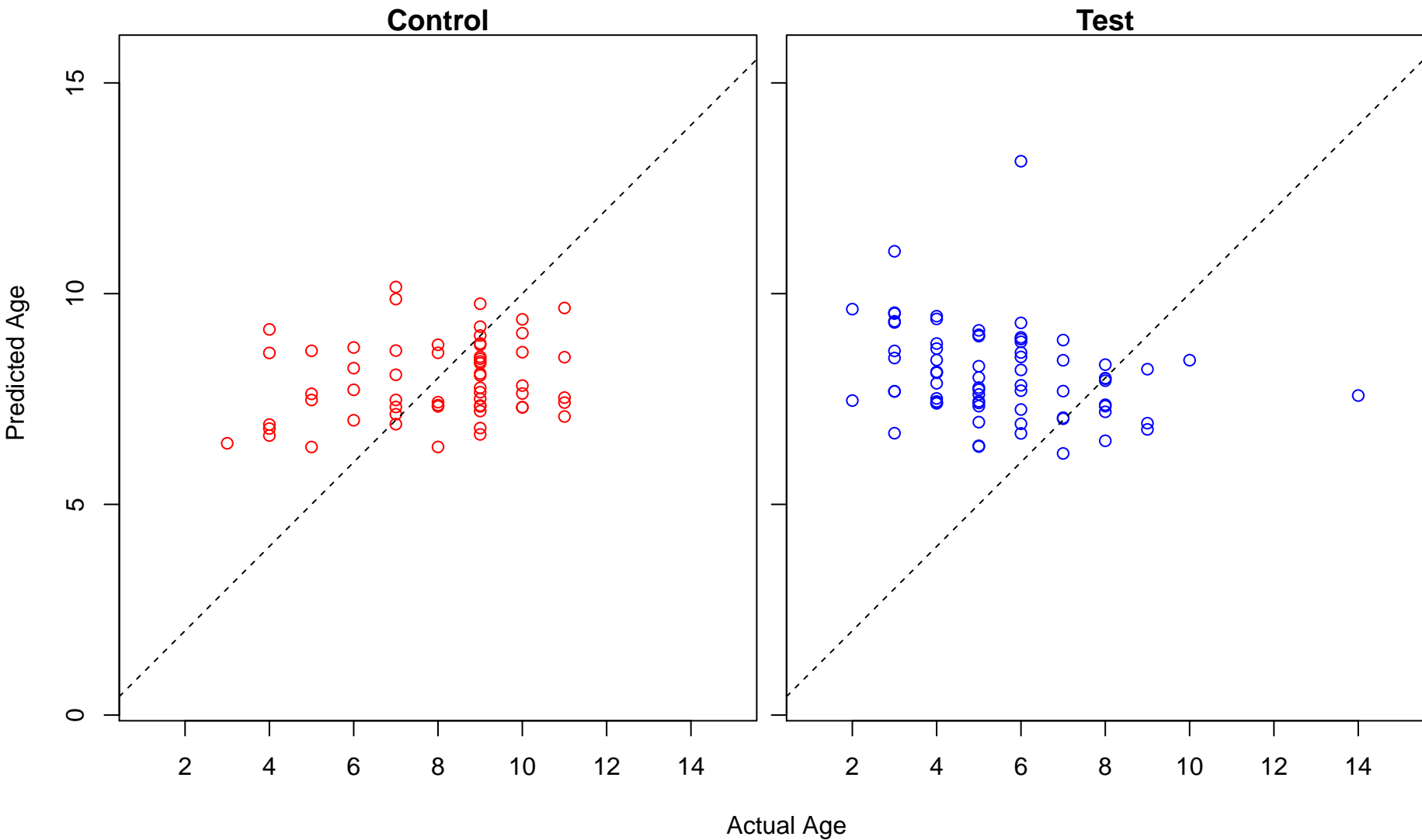


Actual Age

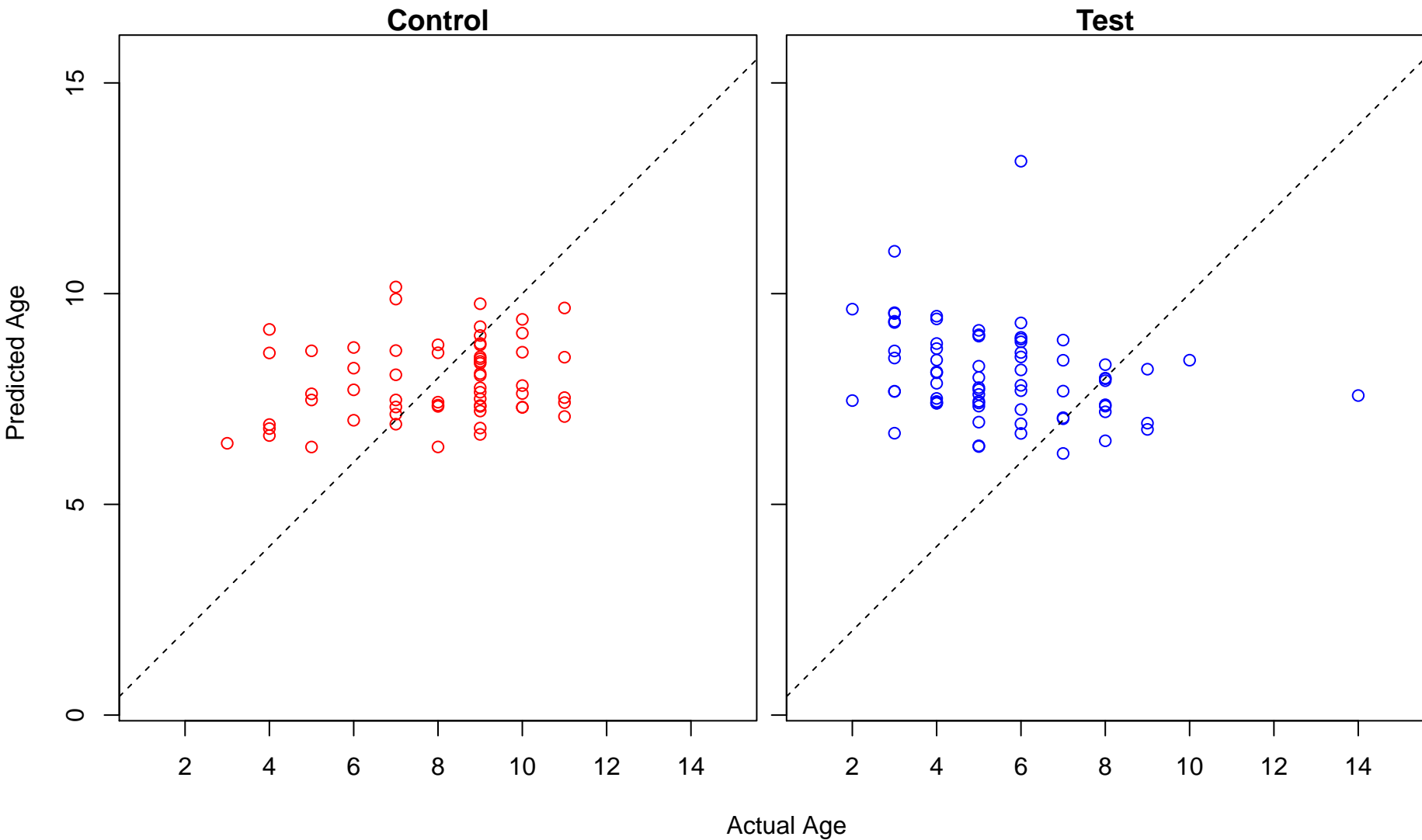
thyroid hormone mediated signaling pathway (Score: 0.299736)



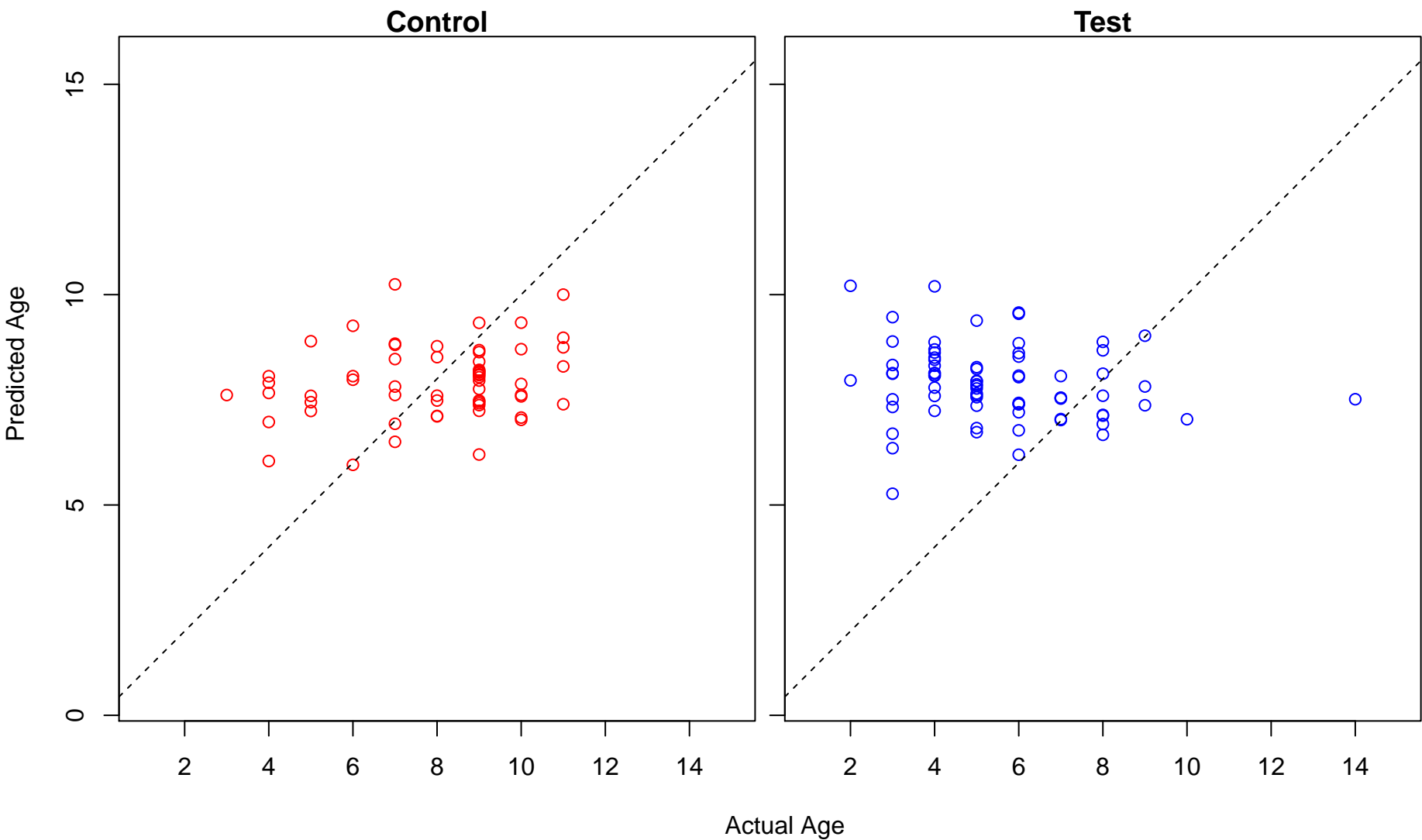
regulation of CD4-positive, alpha-beta T cell proliferation (Score: 0.299540)



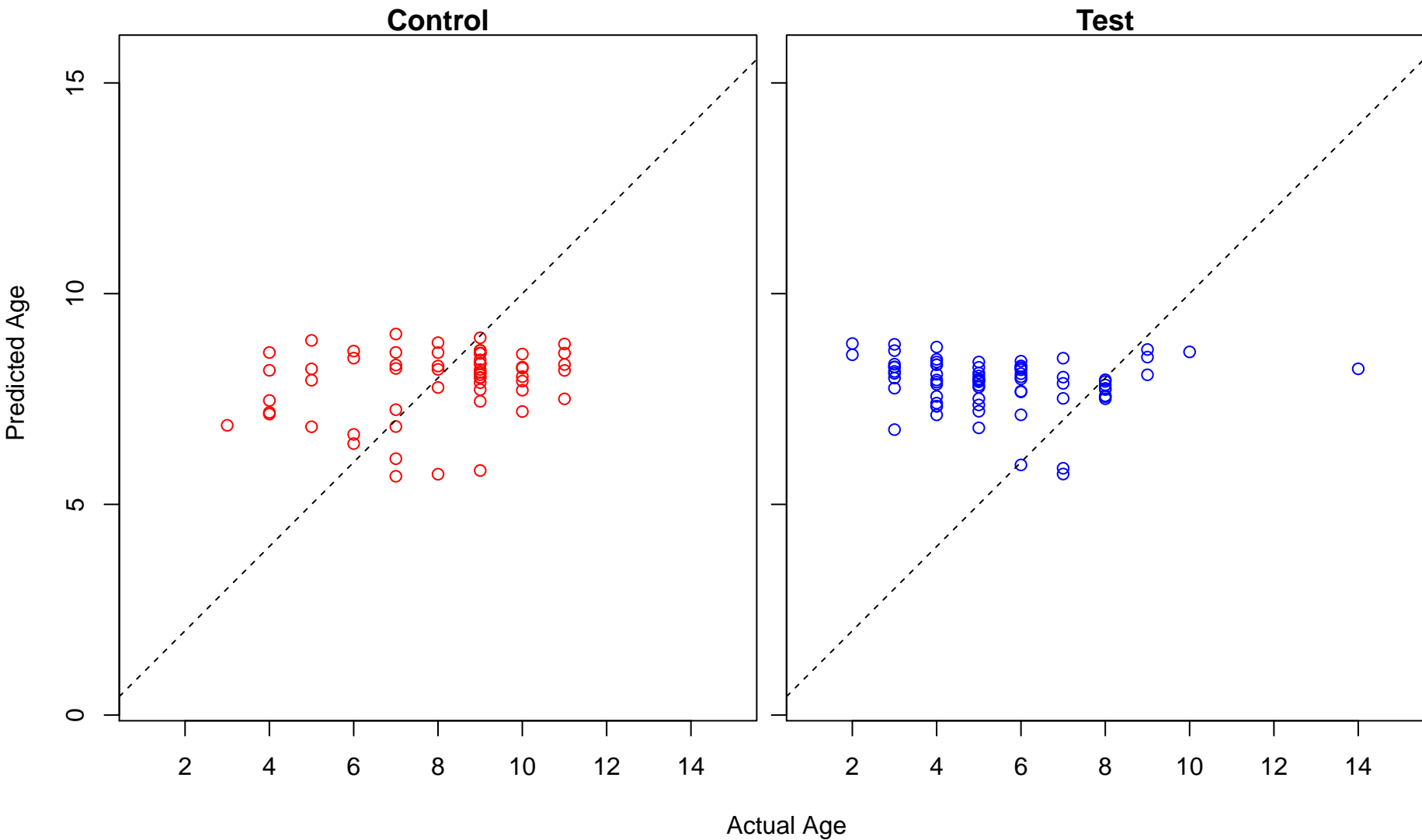
positive regulation of CD4-positive, alpha-beta T cell proliferation (Score: 0.299540)



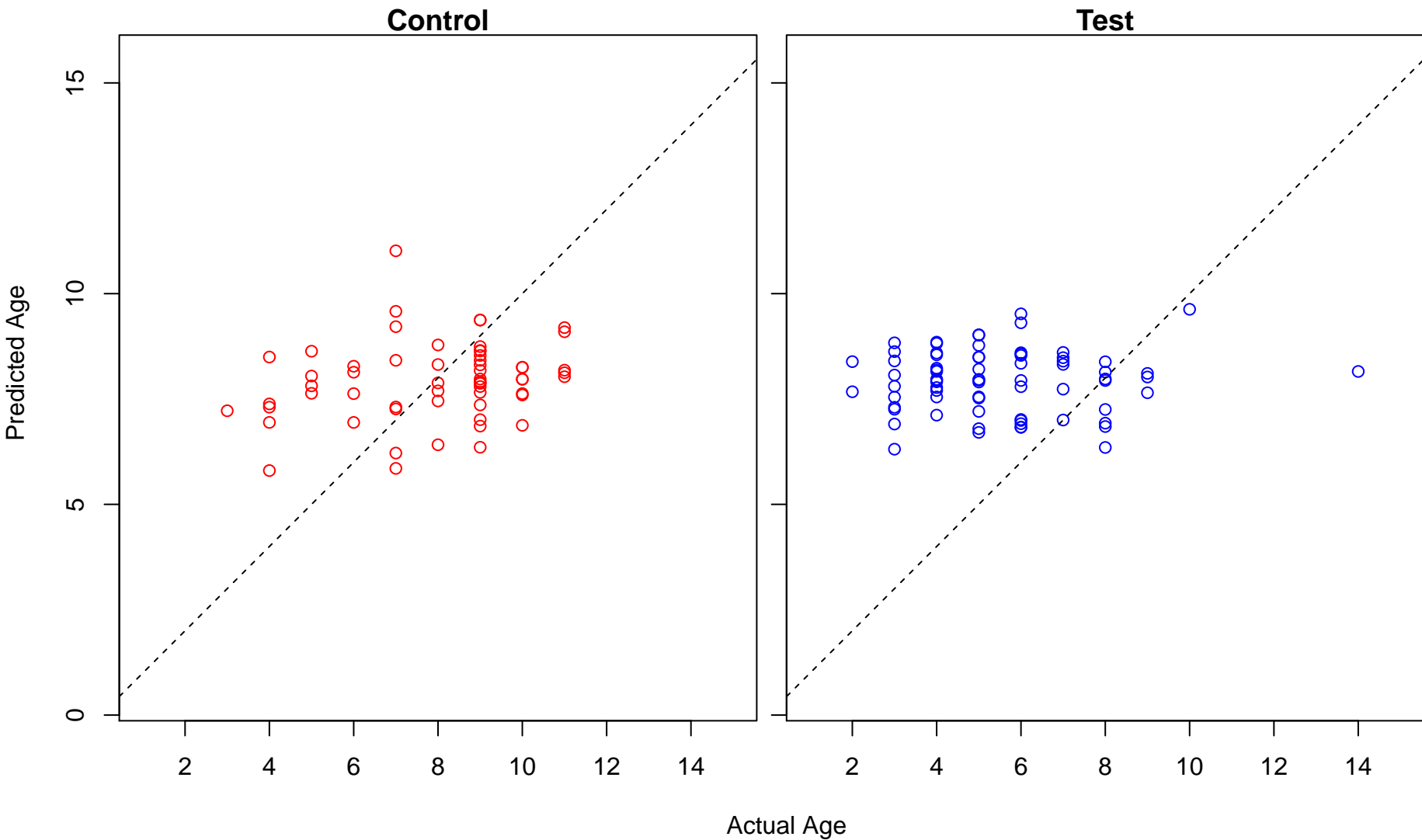
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (Score: 0.2



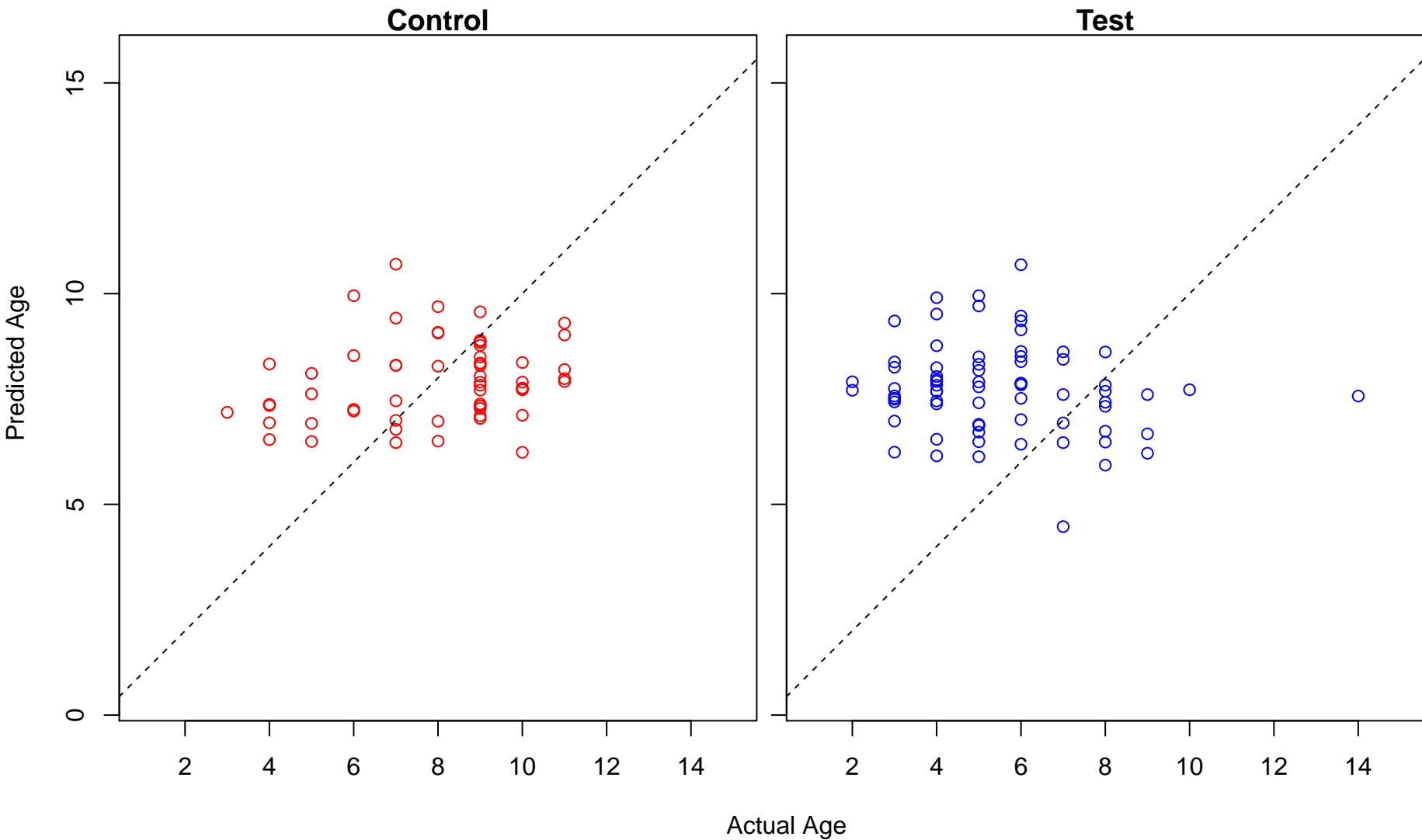
negative regulation of sister chromatid cohesion (Score: 0.297583)



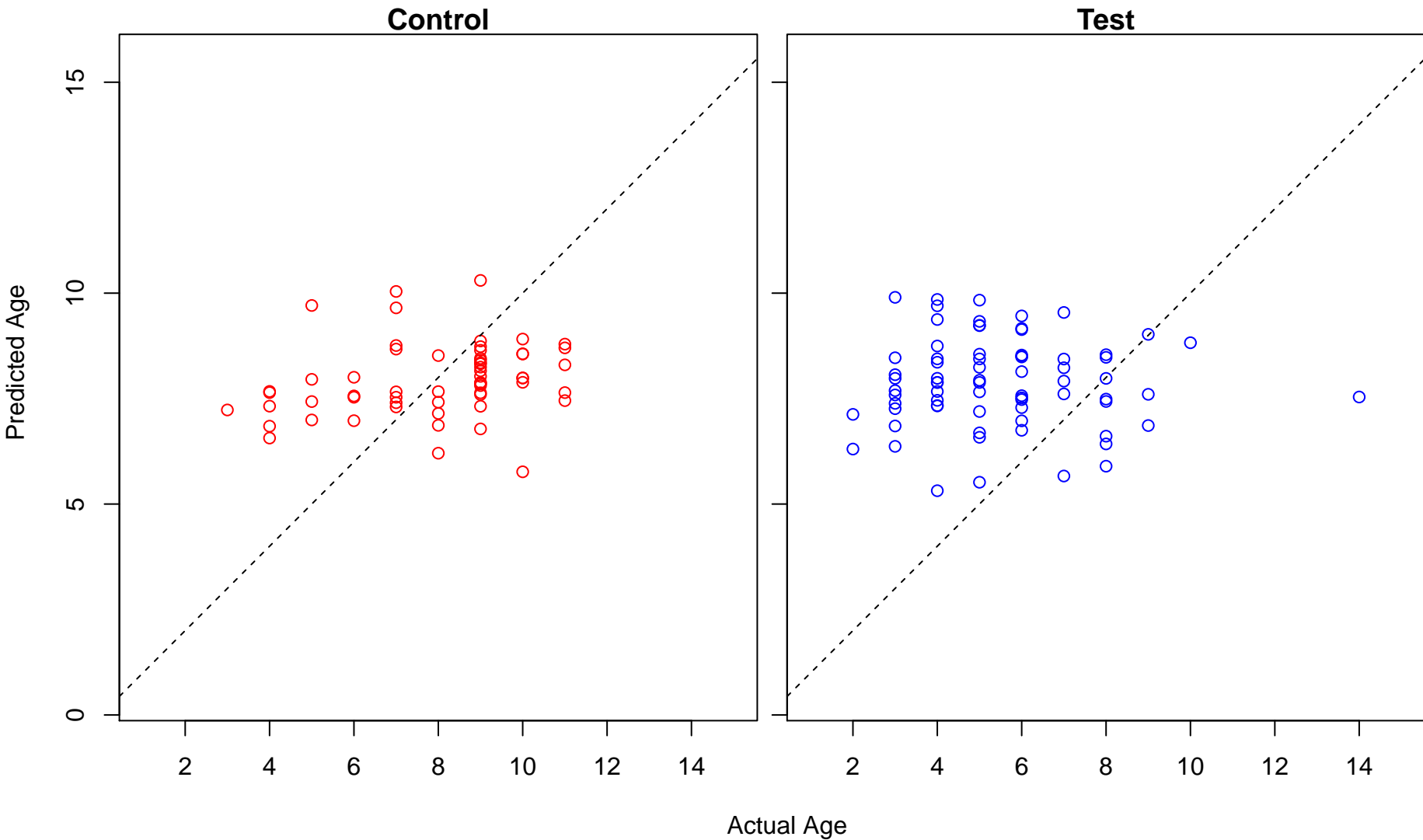
histone H3 deacetylation (Score: 0.295771)



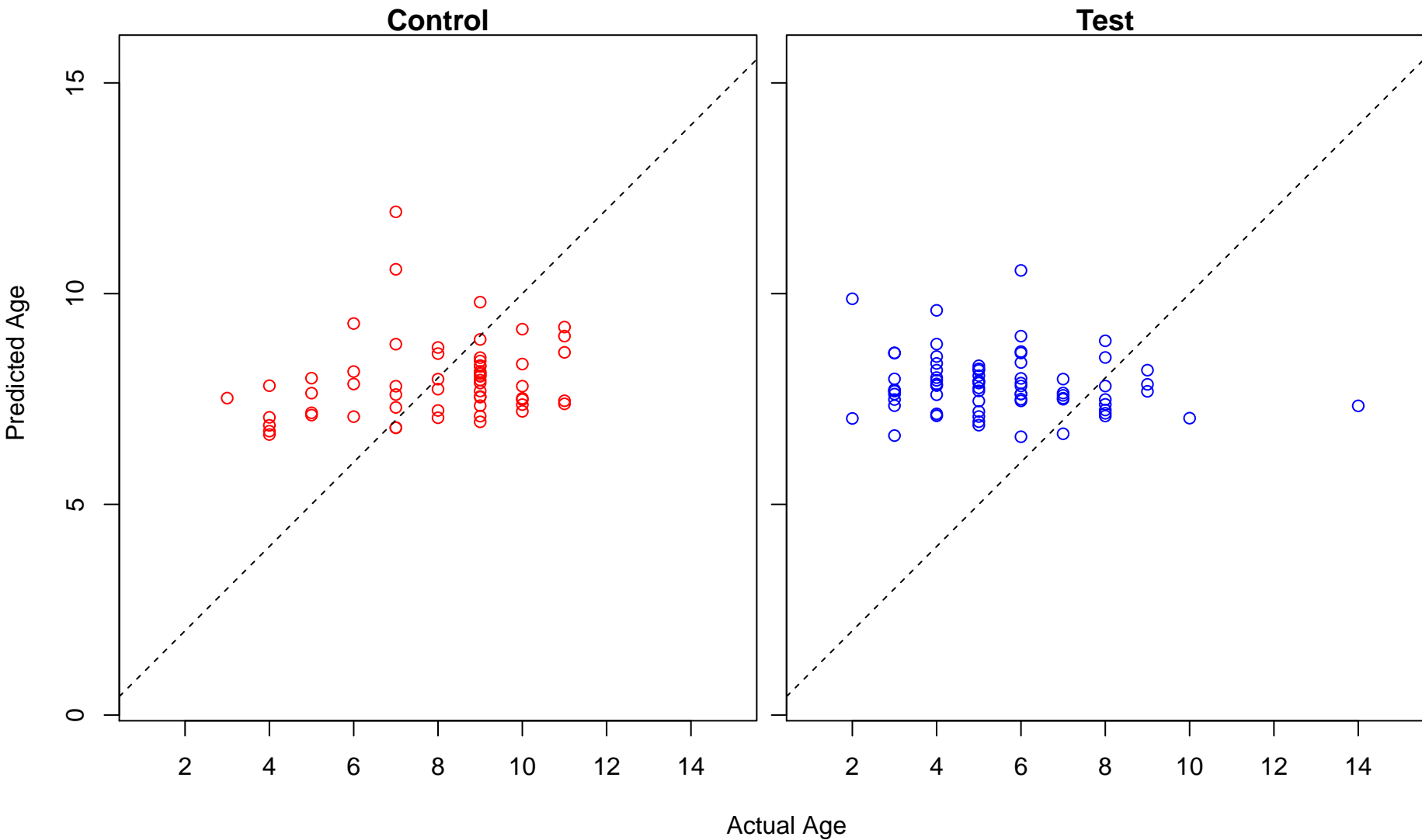
negative regulation of protein phosphatase type 2B activity (Score: 0.295533)



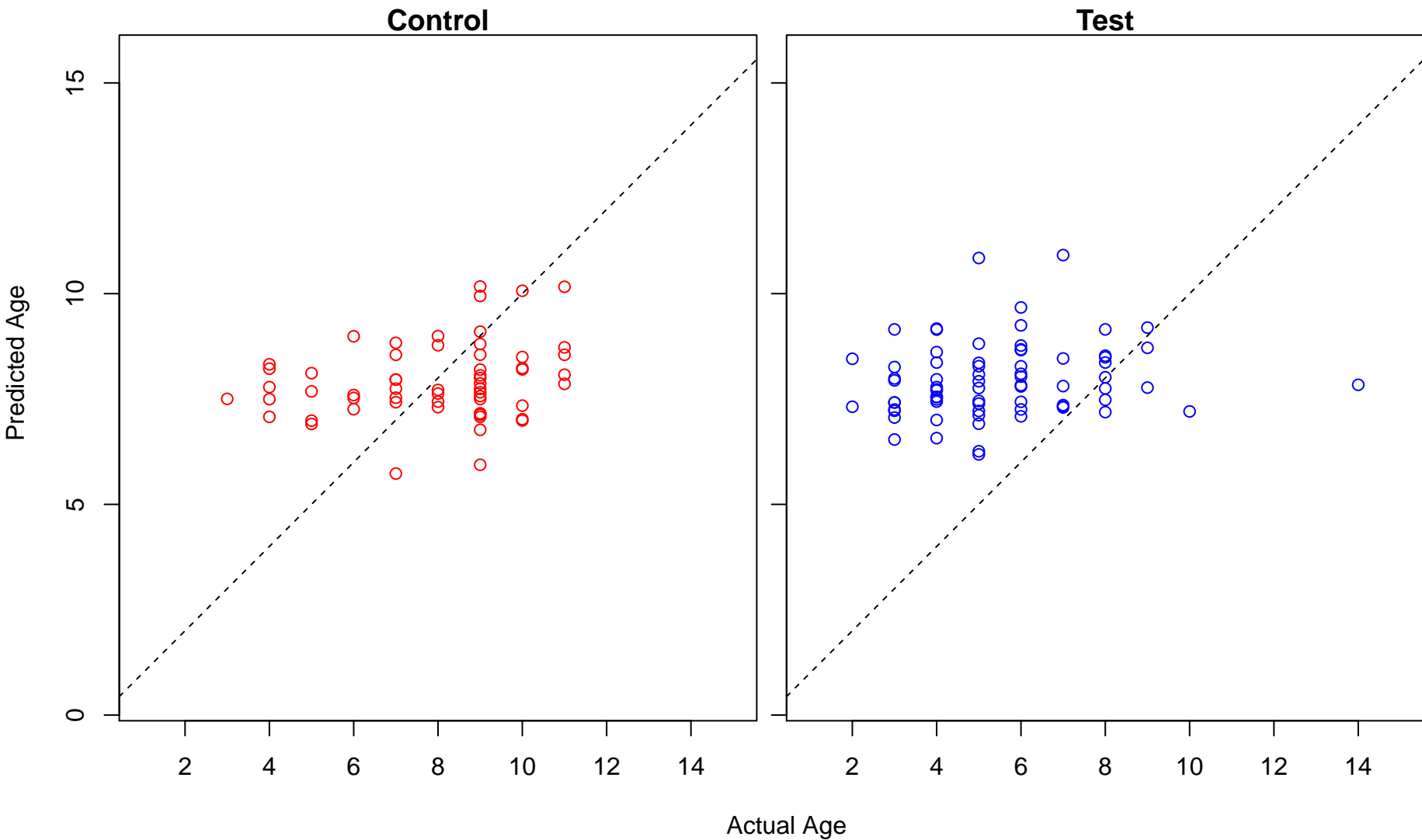
smooth muscle cell-matrix adhesion (Score: 0.294960)



regulation of transforming growth factor beta1 production (Score: 0.294581)

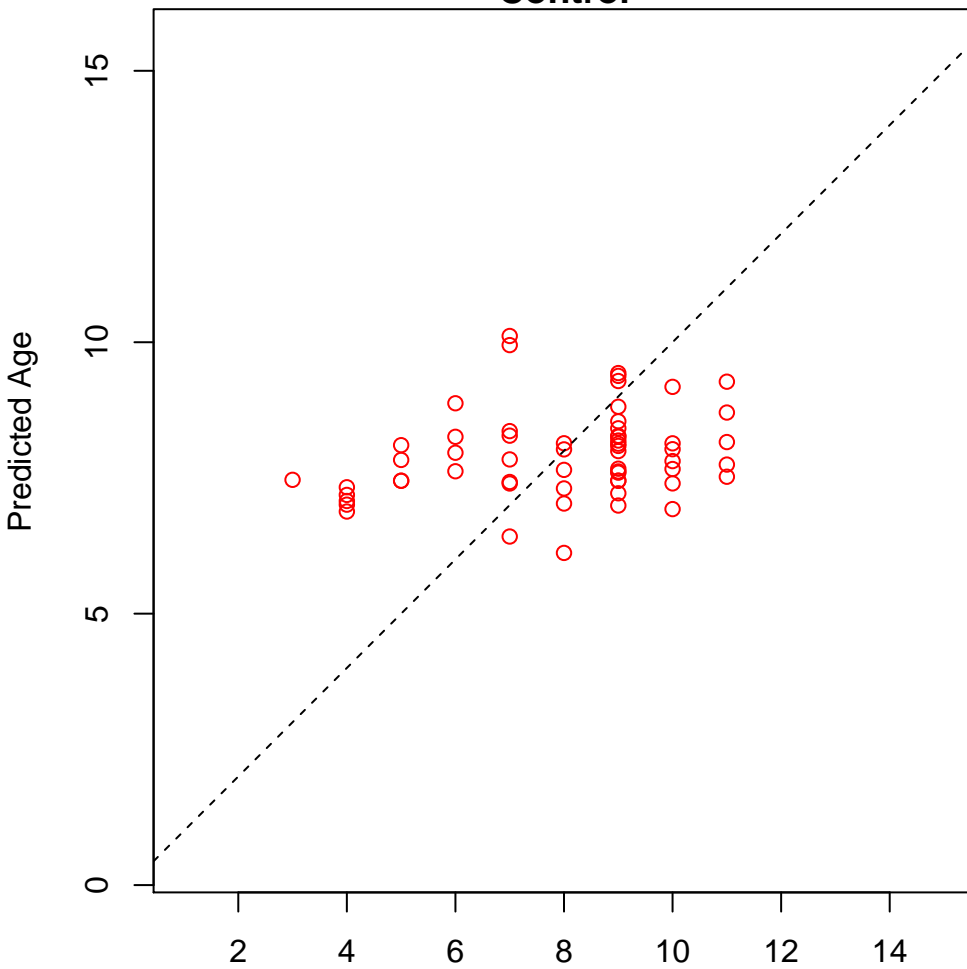


gamma-tubulin complex localization (Score: 0.293748)

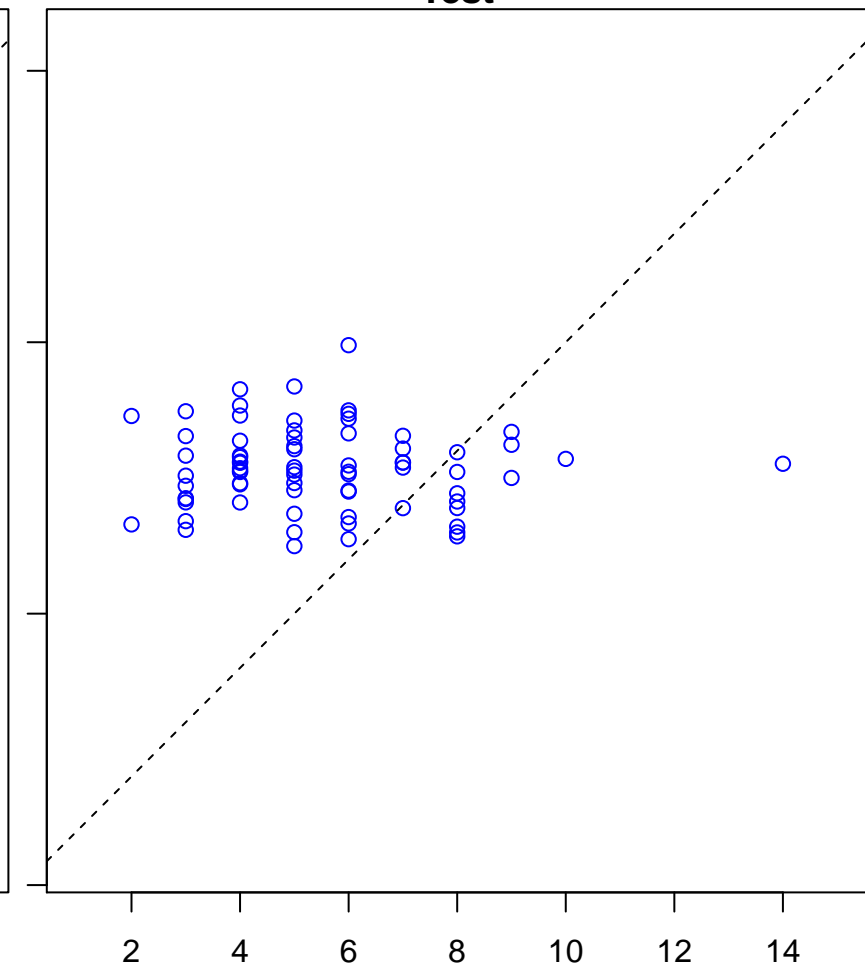


peptidyl-cysteine S-trans-nitrosylation (Score: 0.293611)

Control

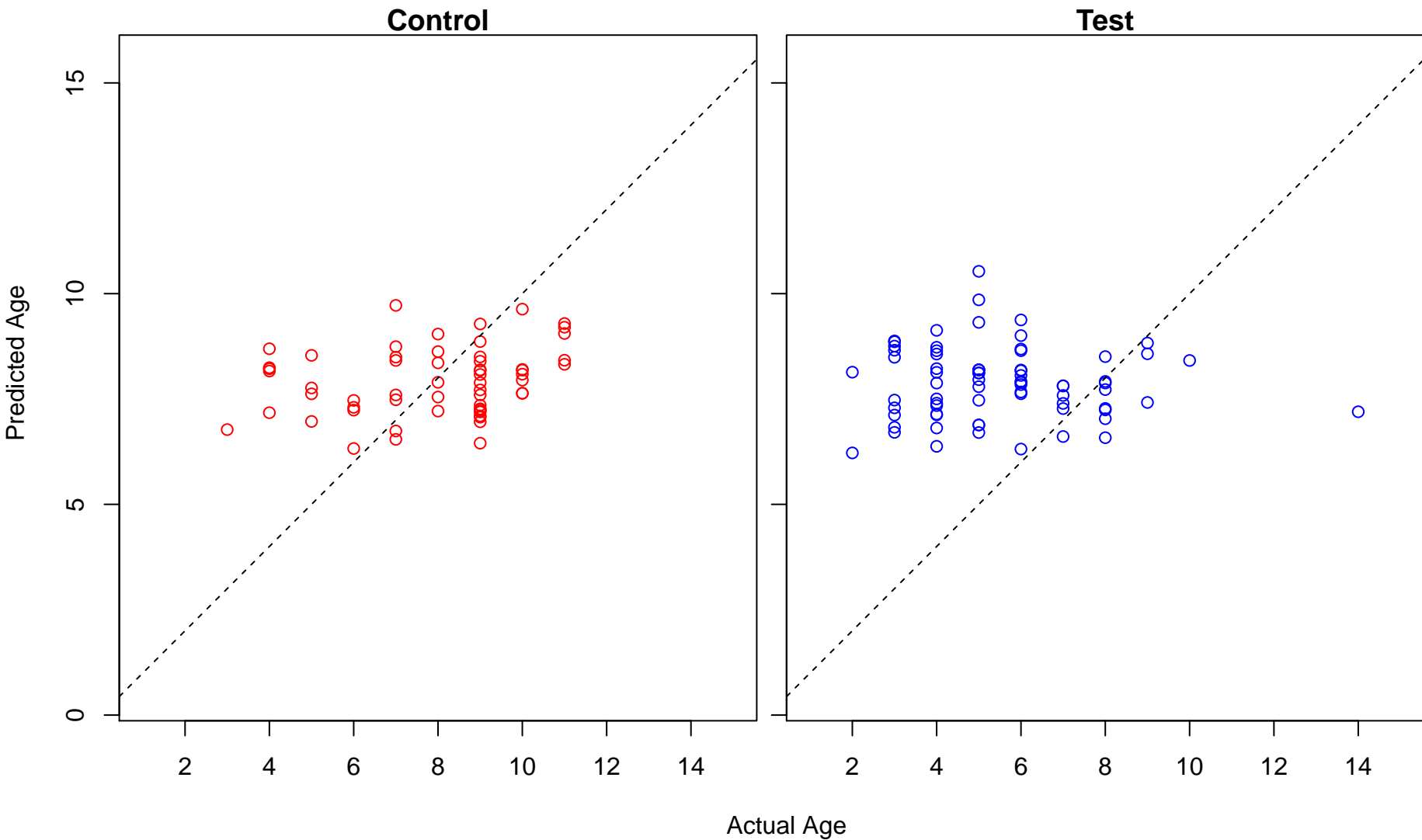


Test

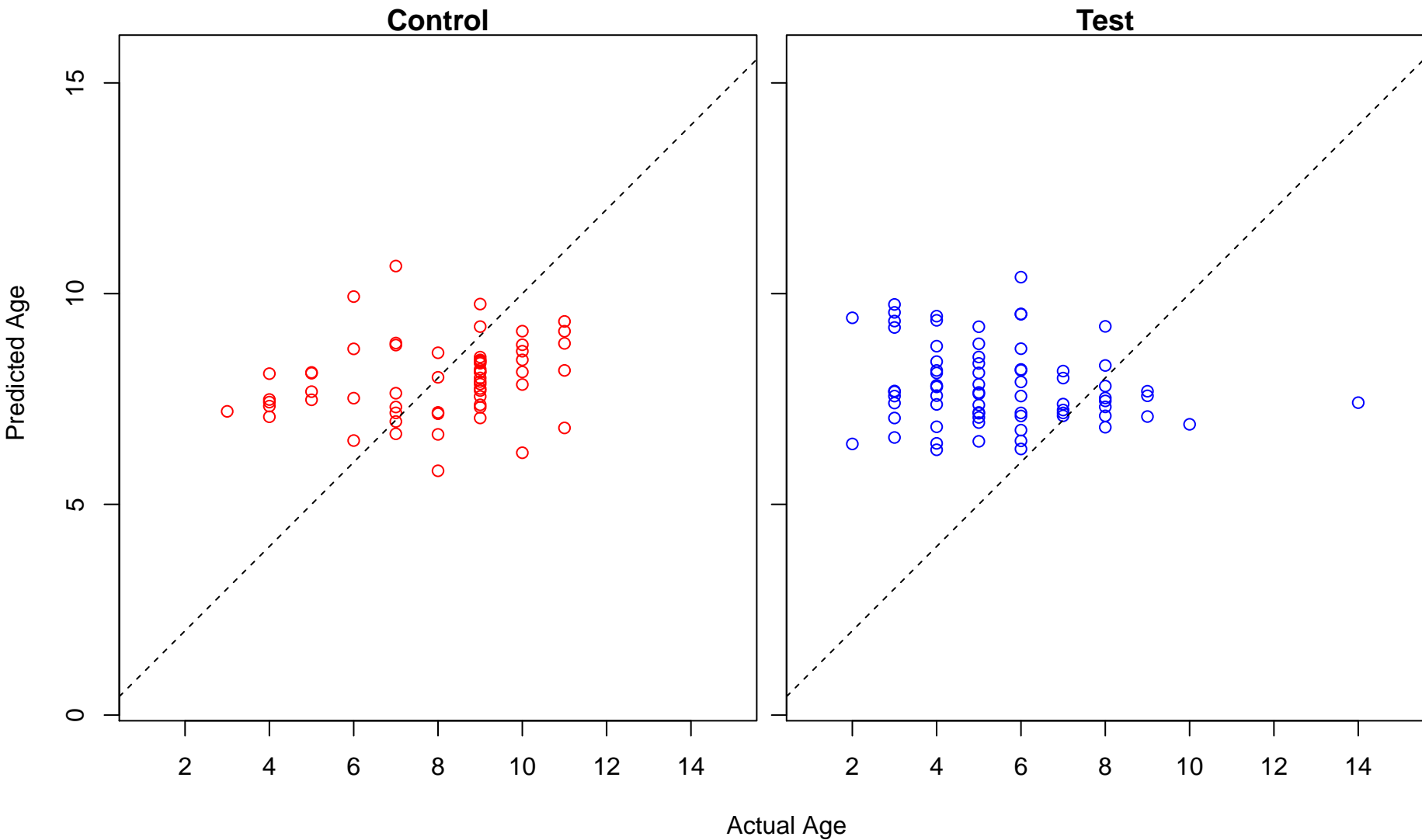


Actual Age

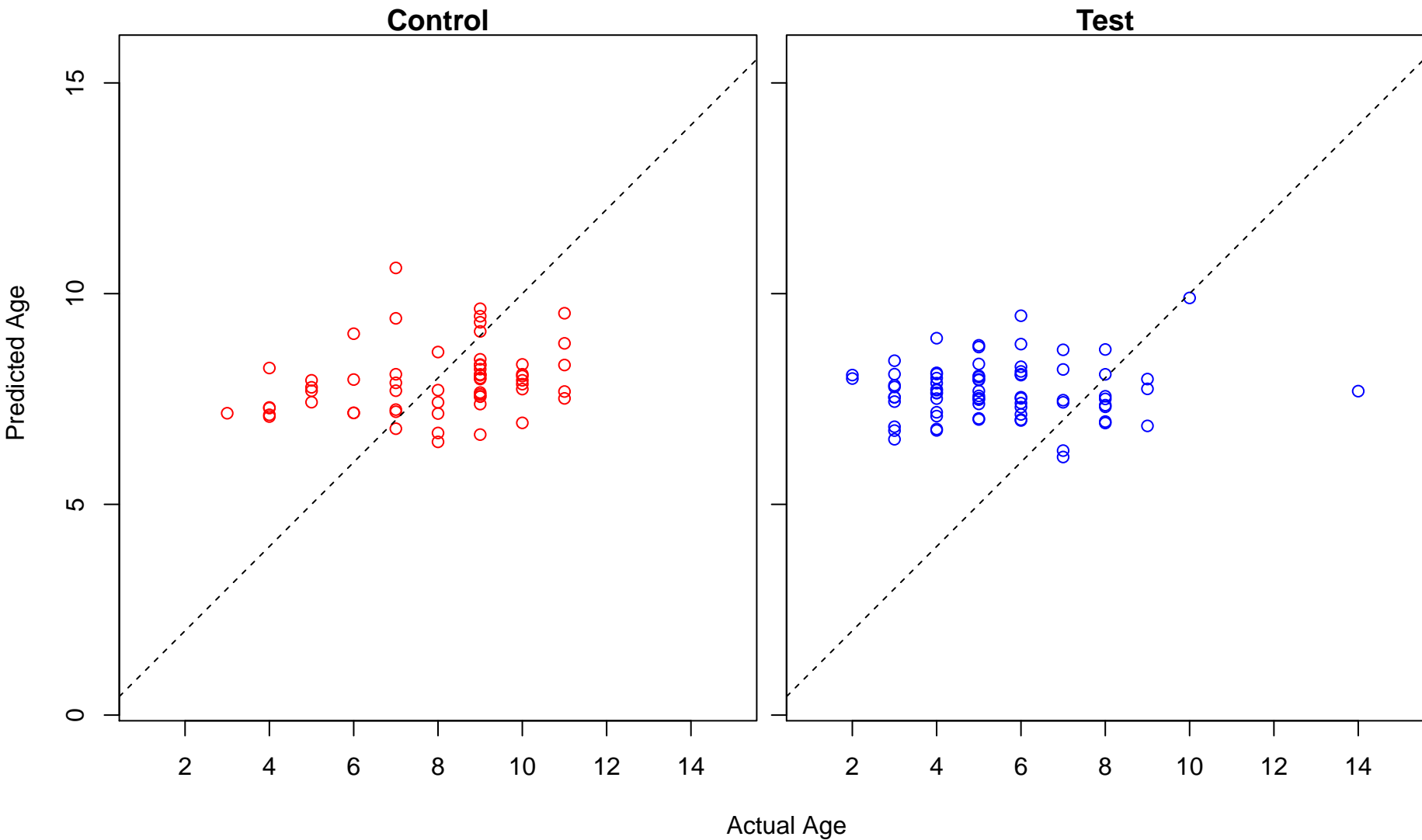
negative regulation of double-strand break repair via nonhomologous end joining (Score: 0.293423)



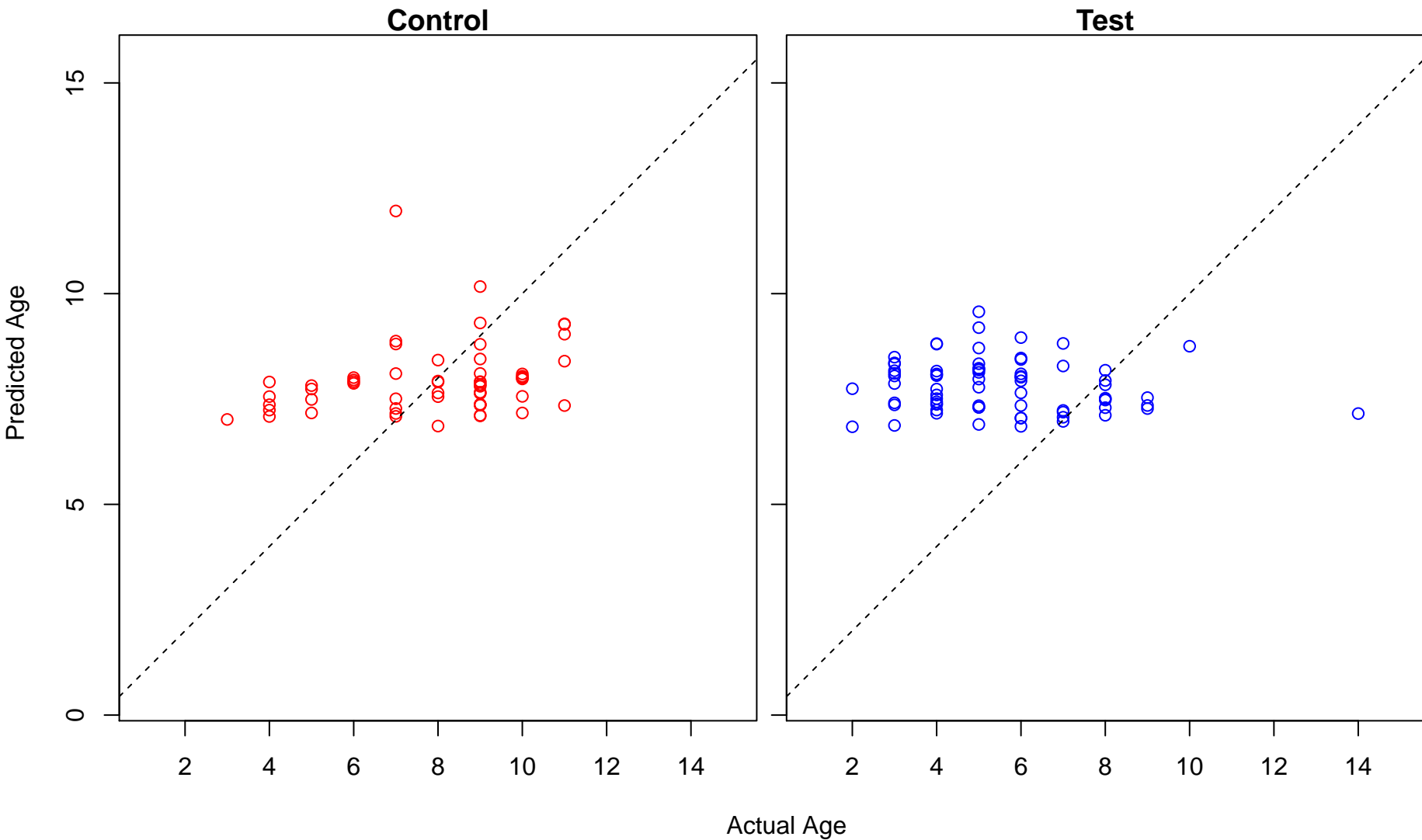
amide transport (Score: 0.293274)



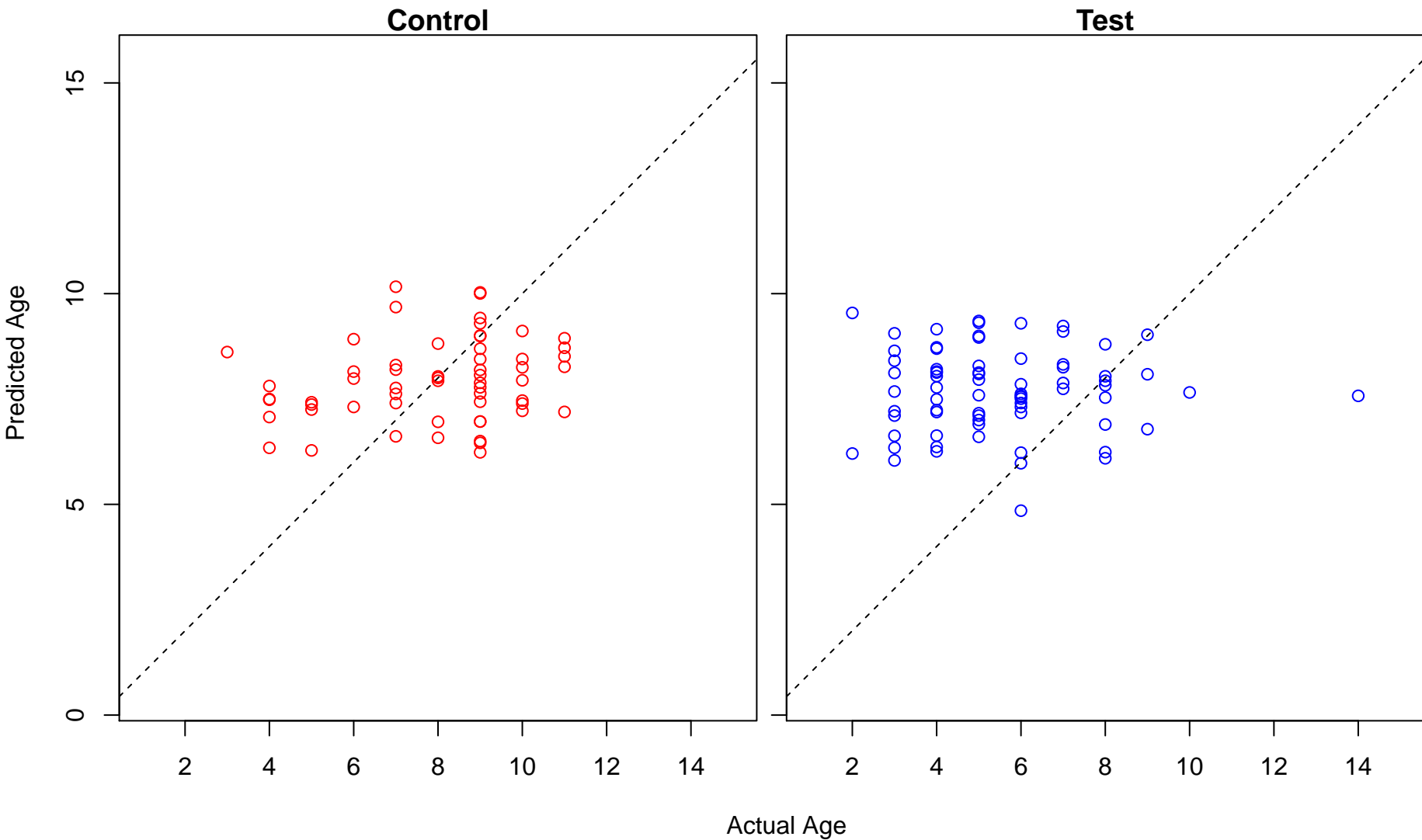
nucleotide-excision repair, DNA incision, 3'-to lesion (Score: 0.293115)



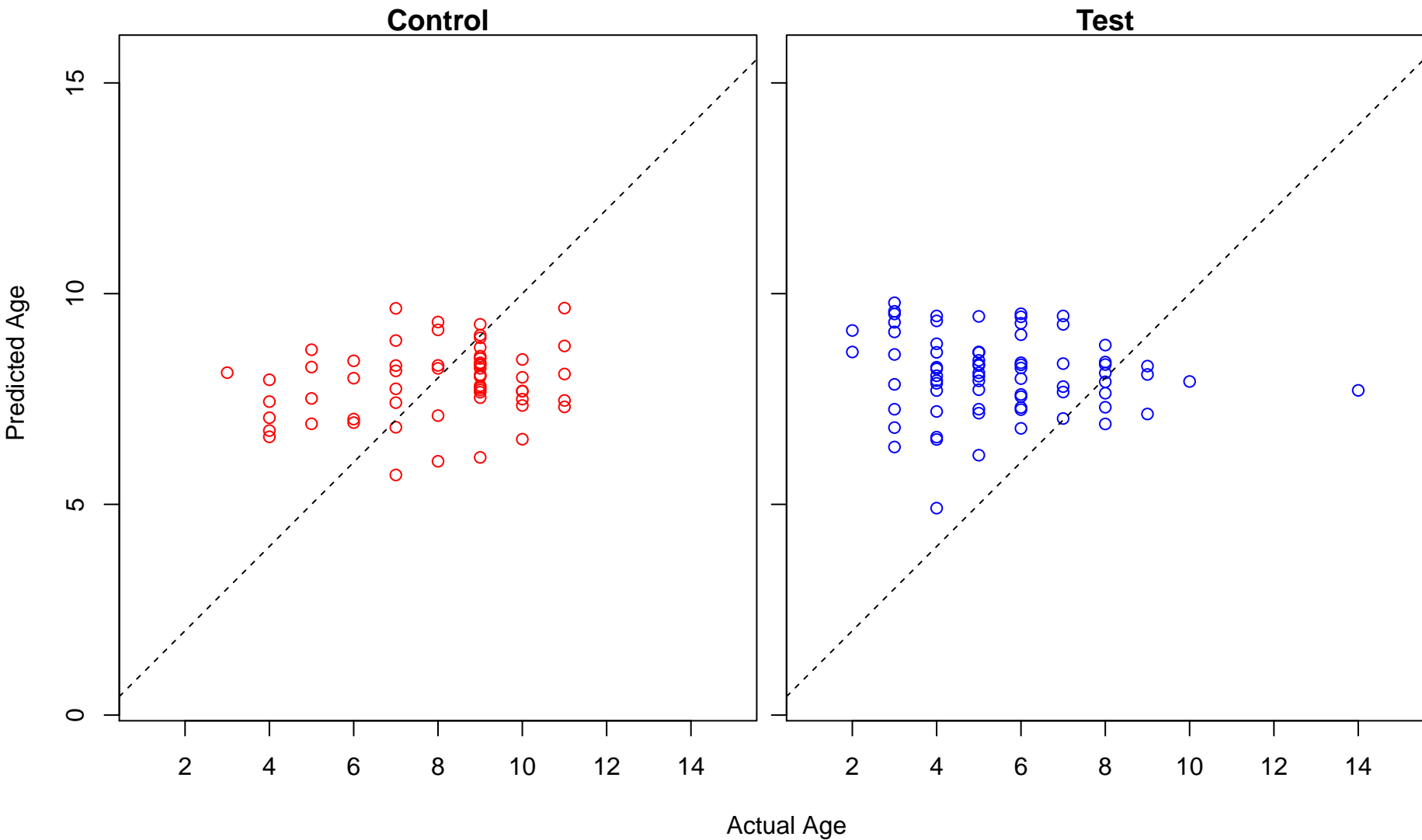
fructose 6-phosphate metabolic process (Score: 0.289367)



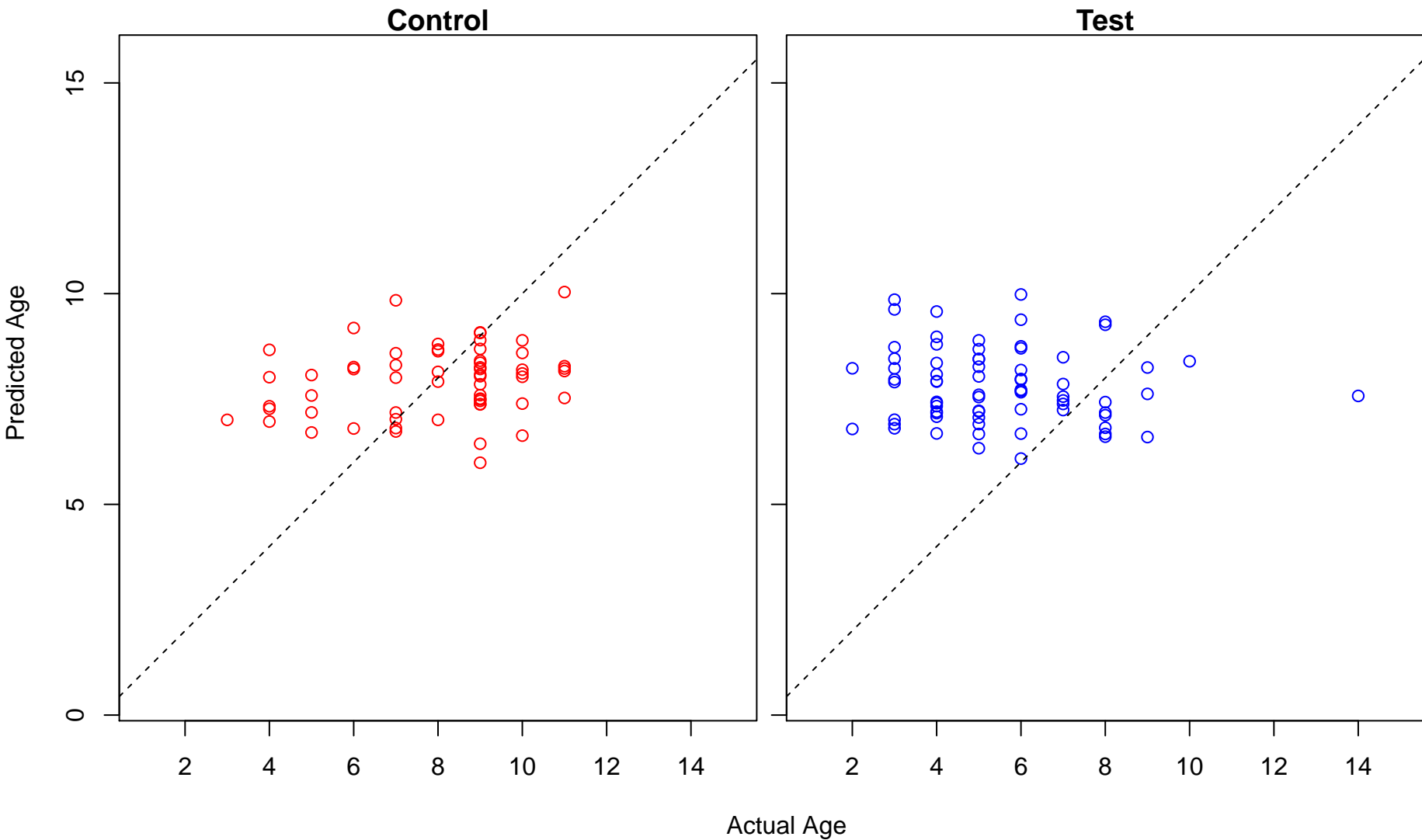
DNA ligation involved in DNA repair (Score: 0.288182)



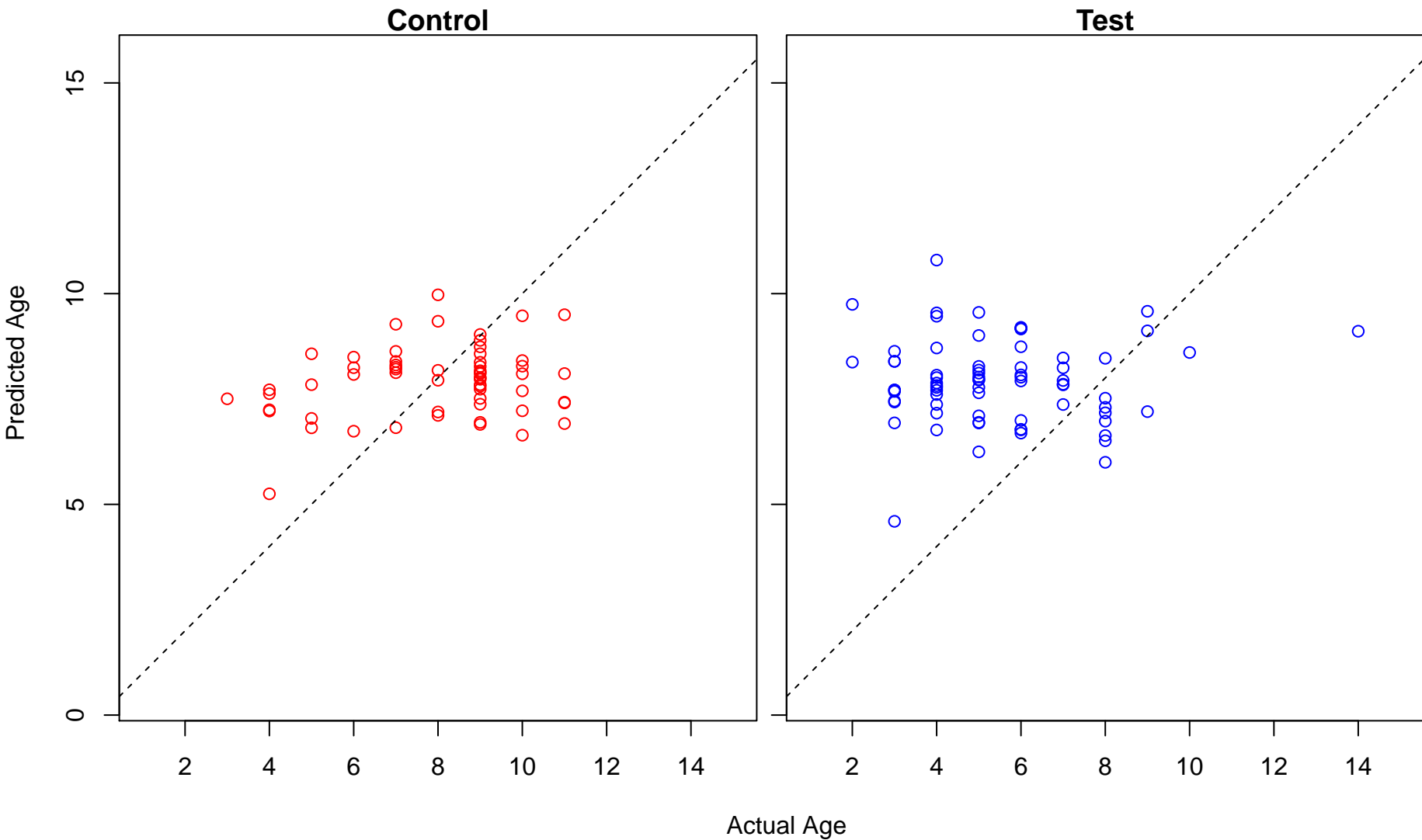
bronchus morphogenesis (Score: 0.284258)



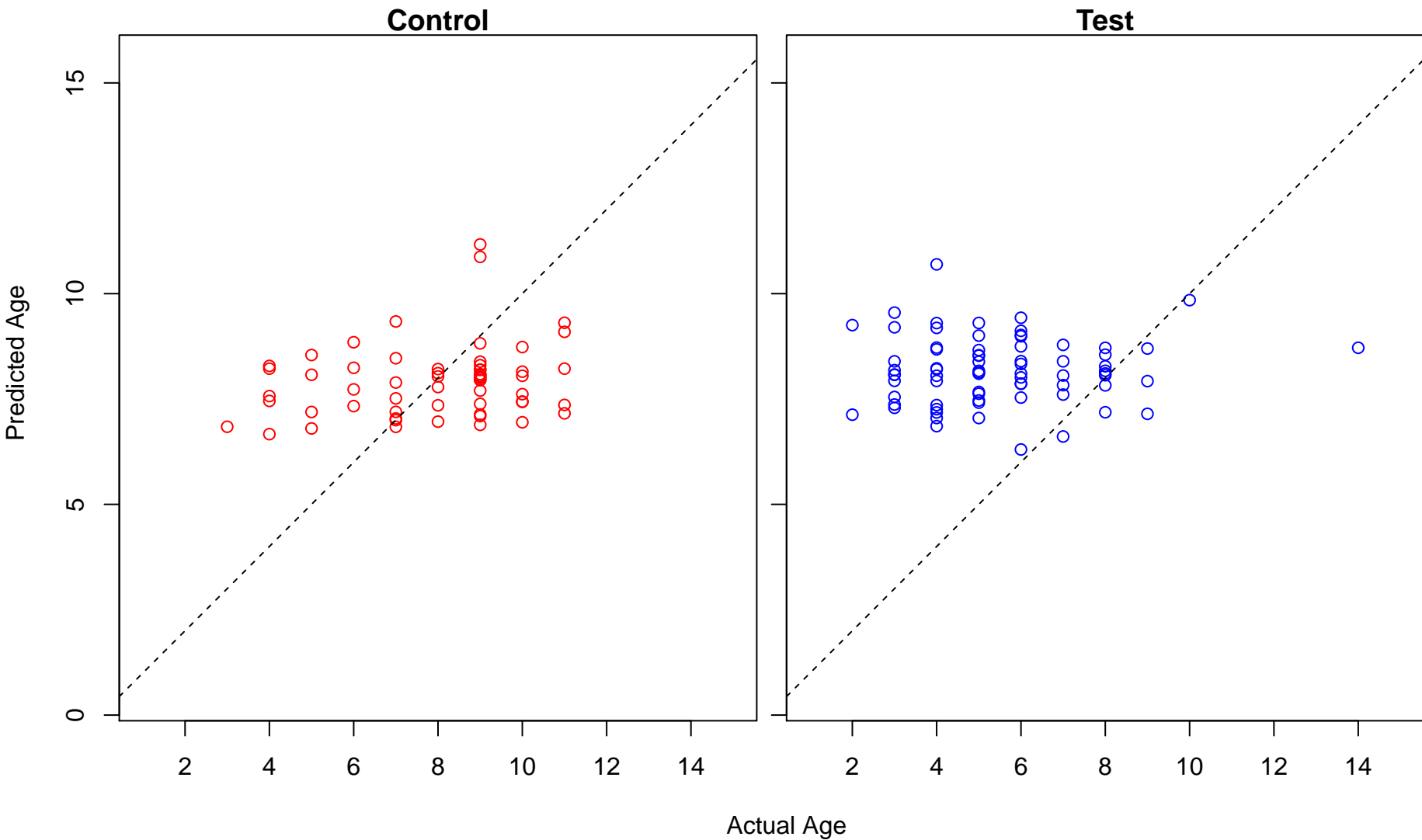
positive regulation of thymocyte apoptotic process (Score: 0.282058)



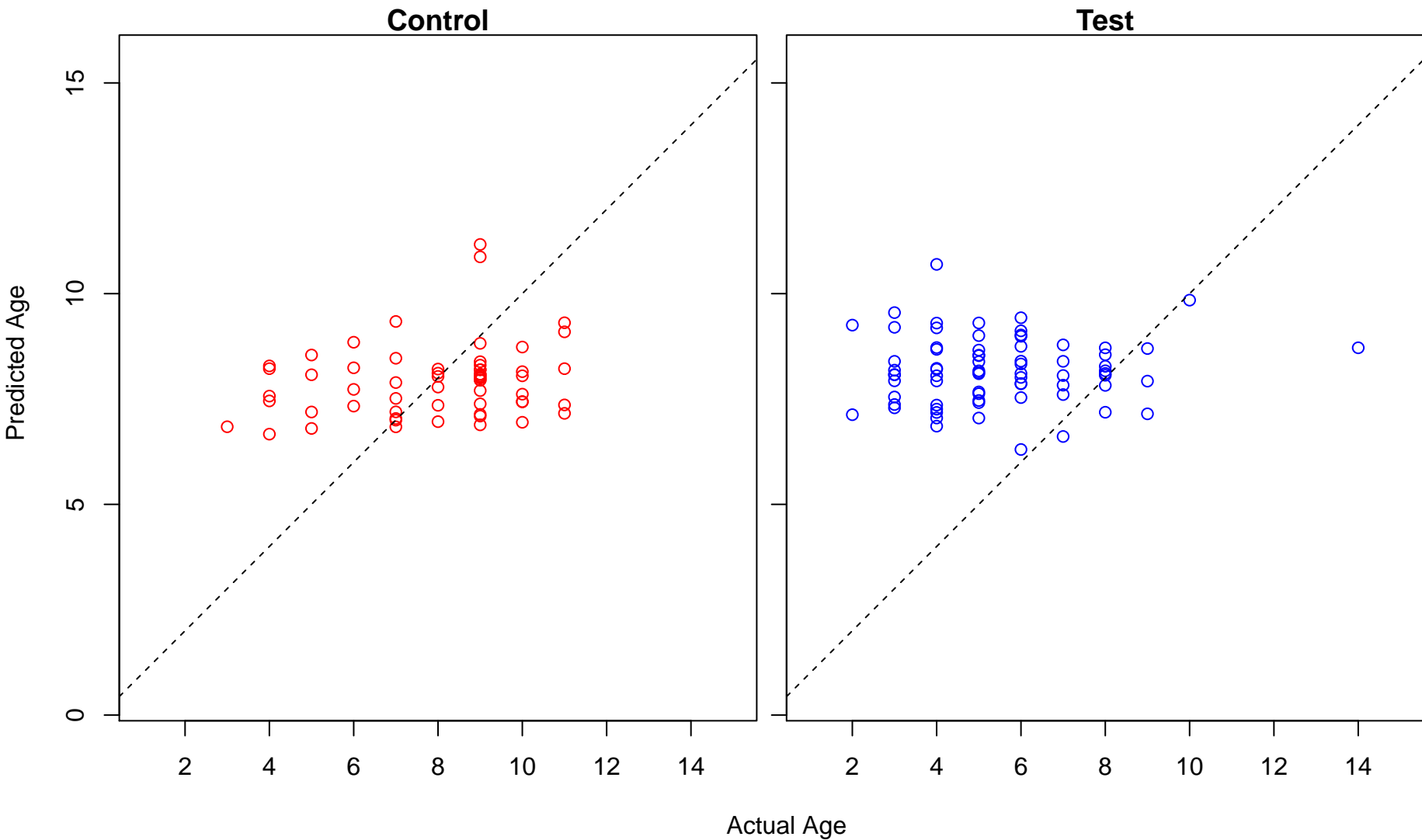
retinal cell programmed cell death (Score: 0.281480)



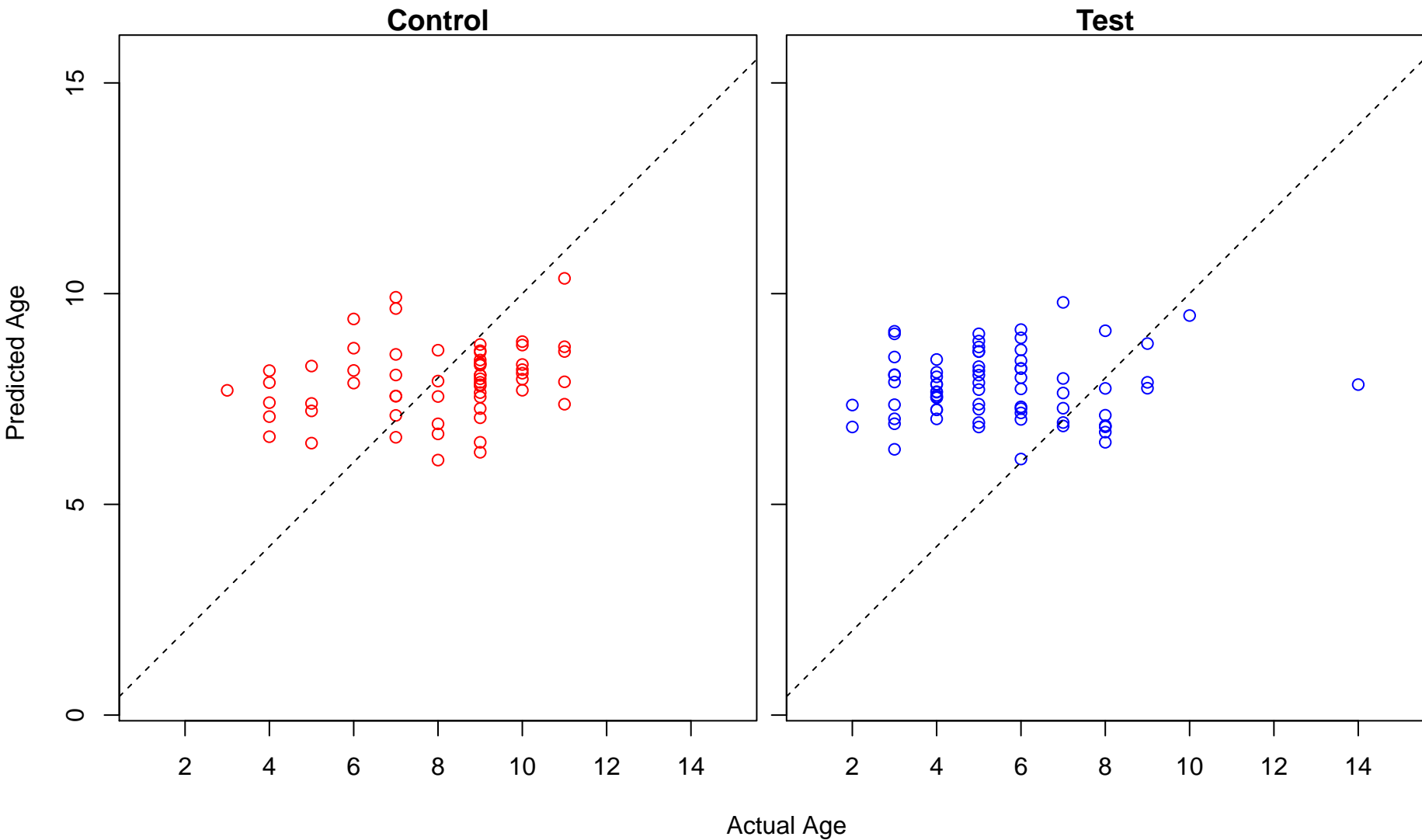
regulation of NK T cell proliferation (Score: 0.280378)



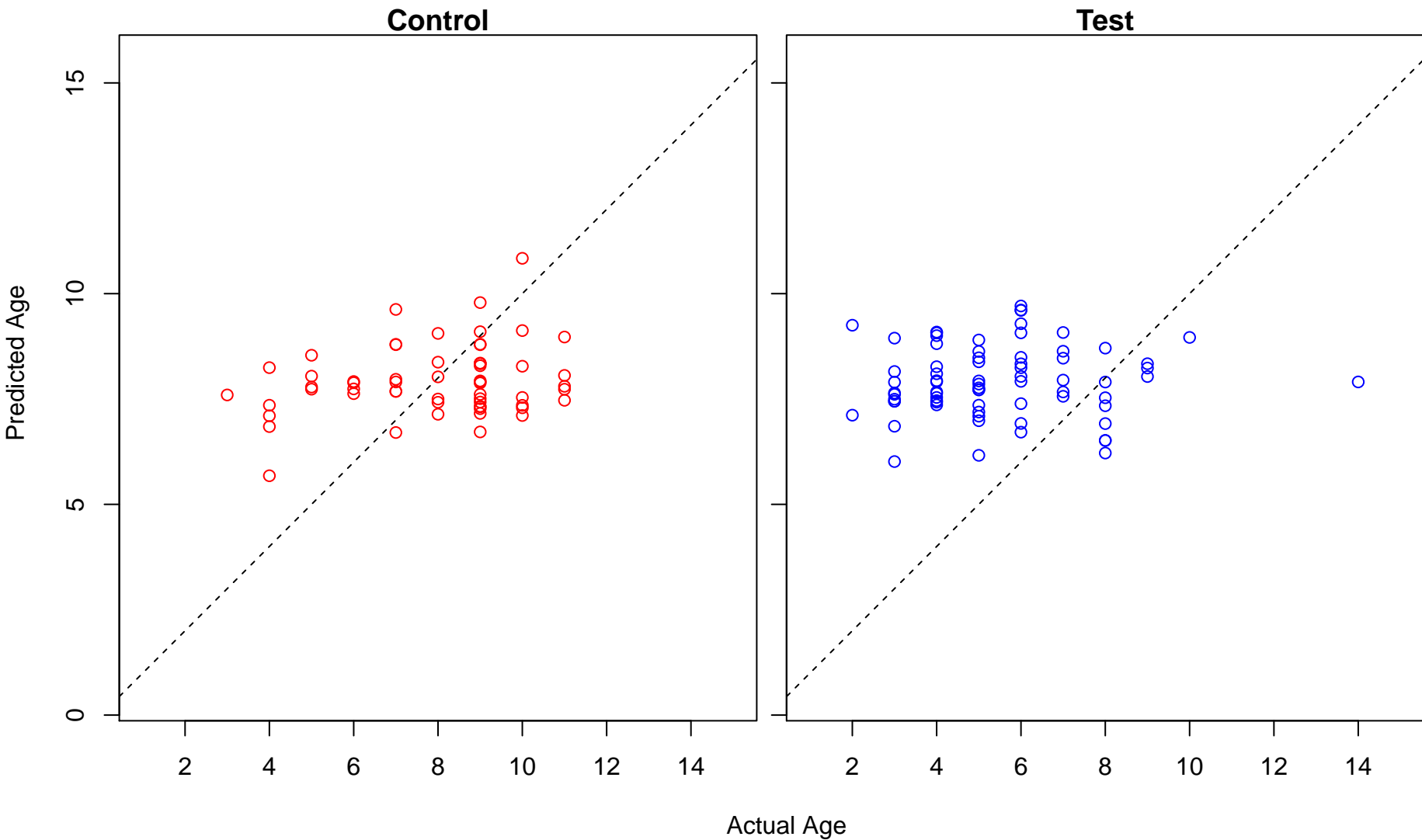
positive regulation of NK T cell proliferation (Score: 0.280378)



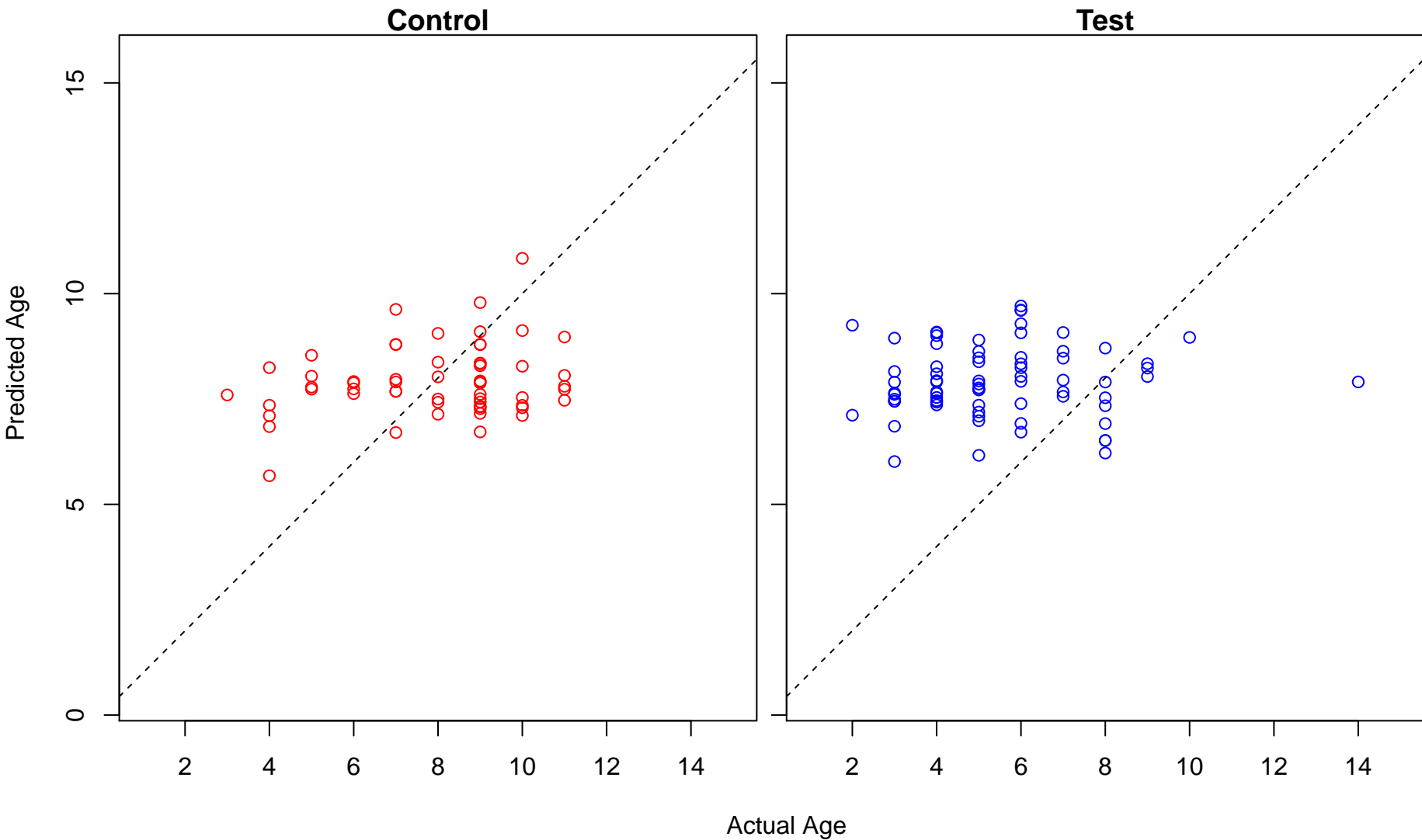
arginine metabolic process (Score: 0.279755)



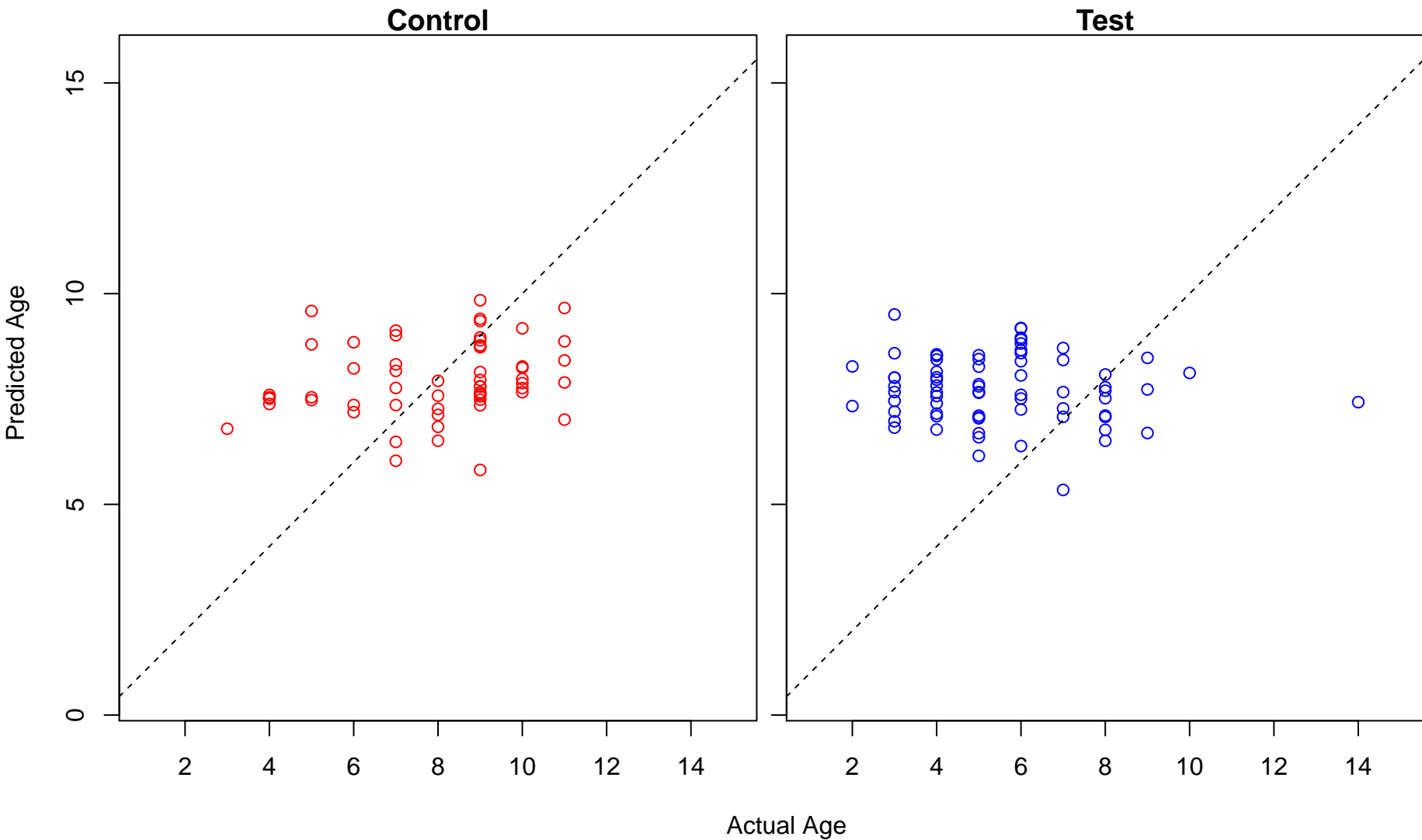
response to activity (Score: 0.277047)



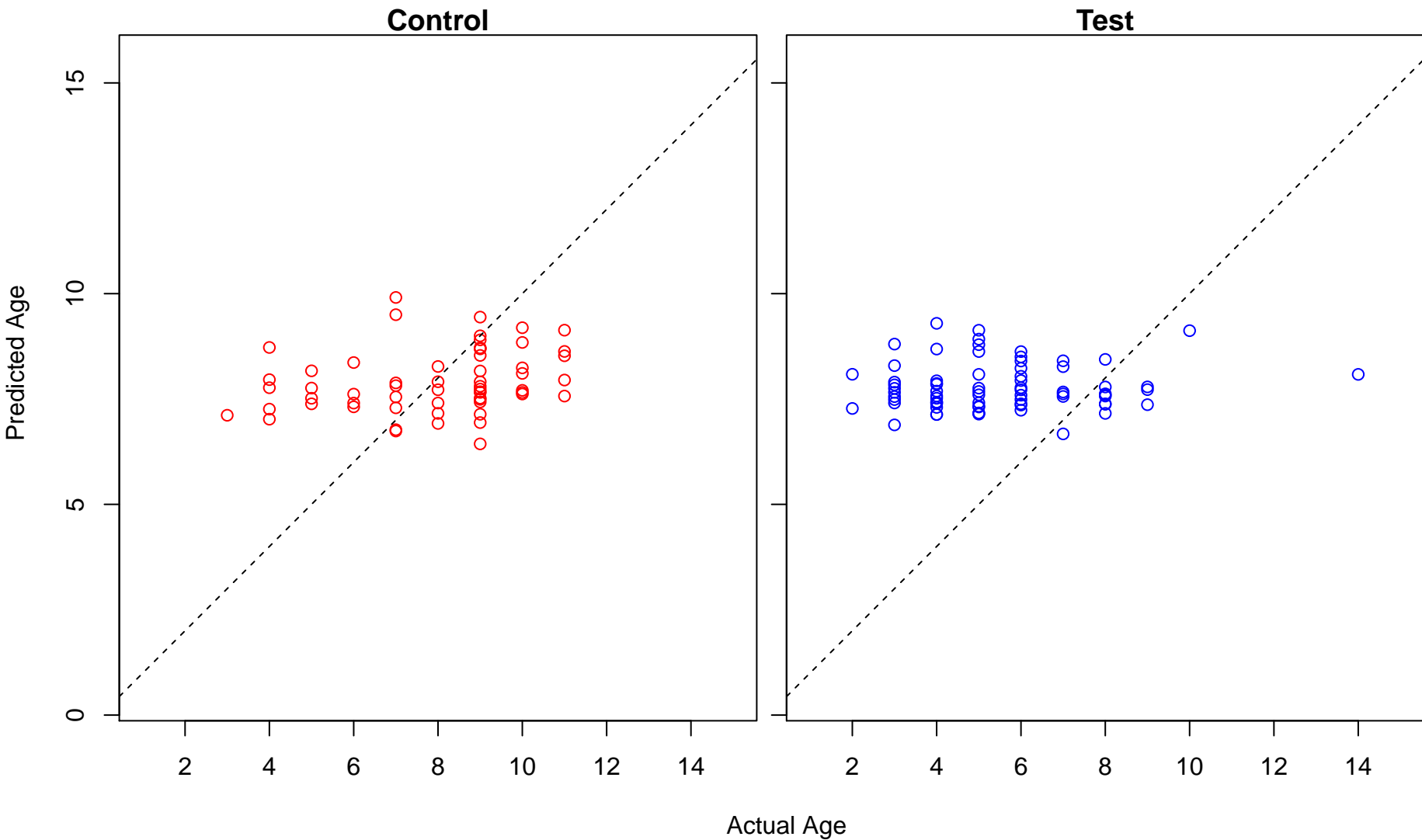
response to muscle activity (Score: 0.277047)



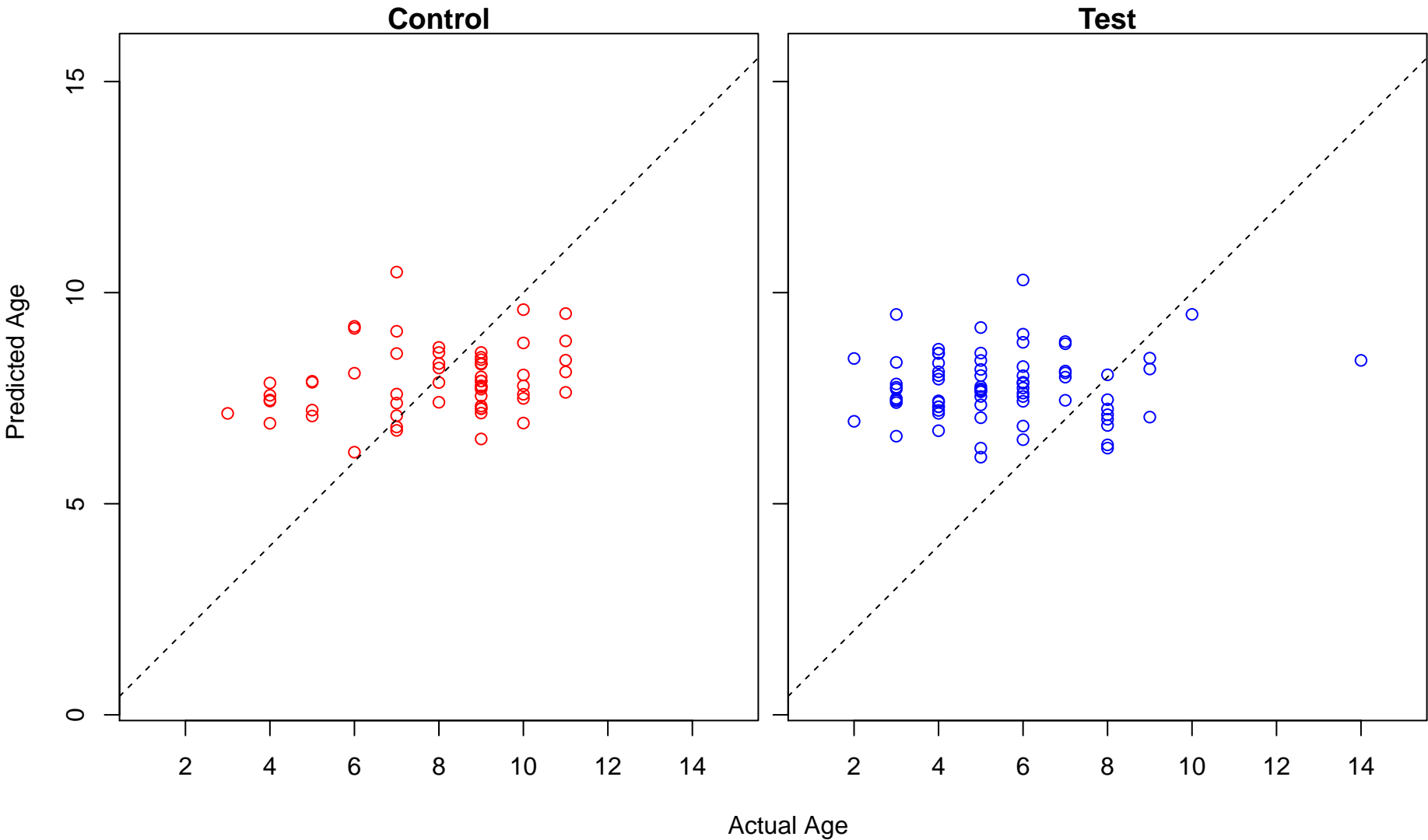
negative regulation of histone H3–K4 methylation (Score: 0.273029)



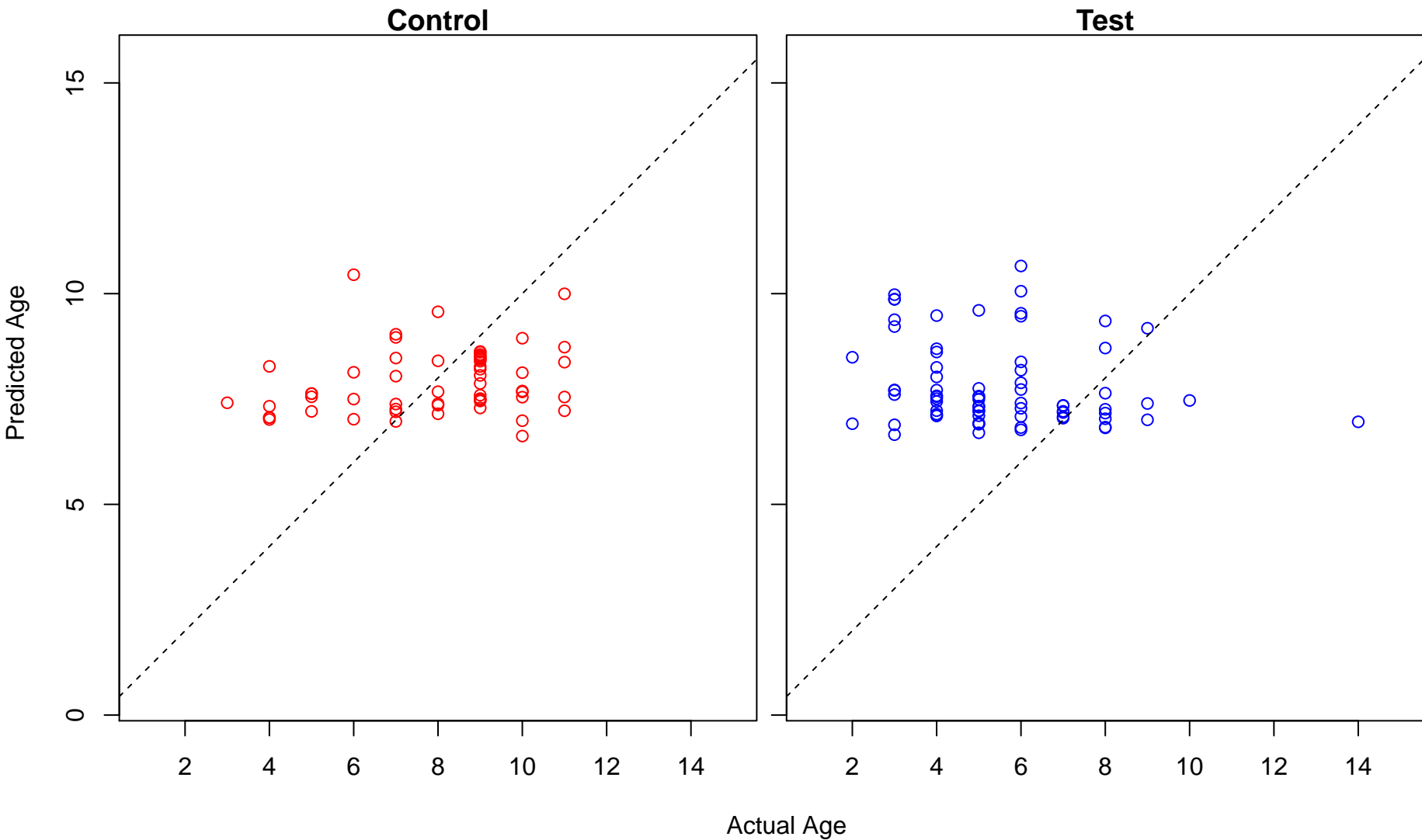
follicle-stimulating hormone signaling pathway (Score: 0.272757)



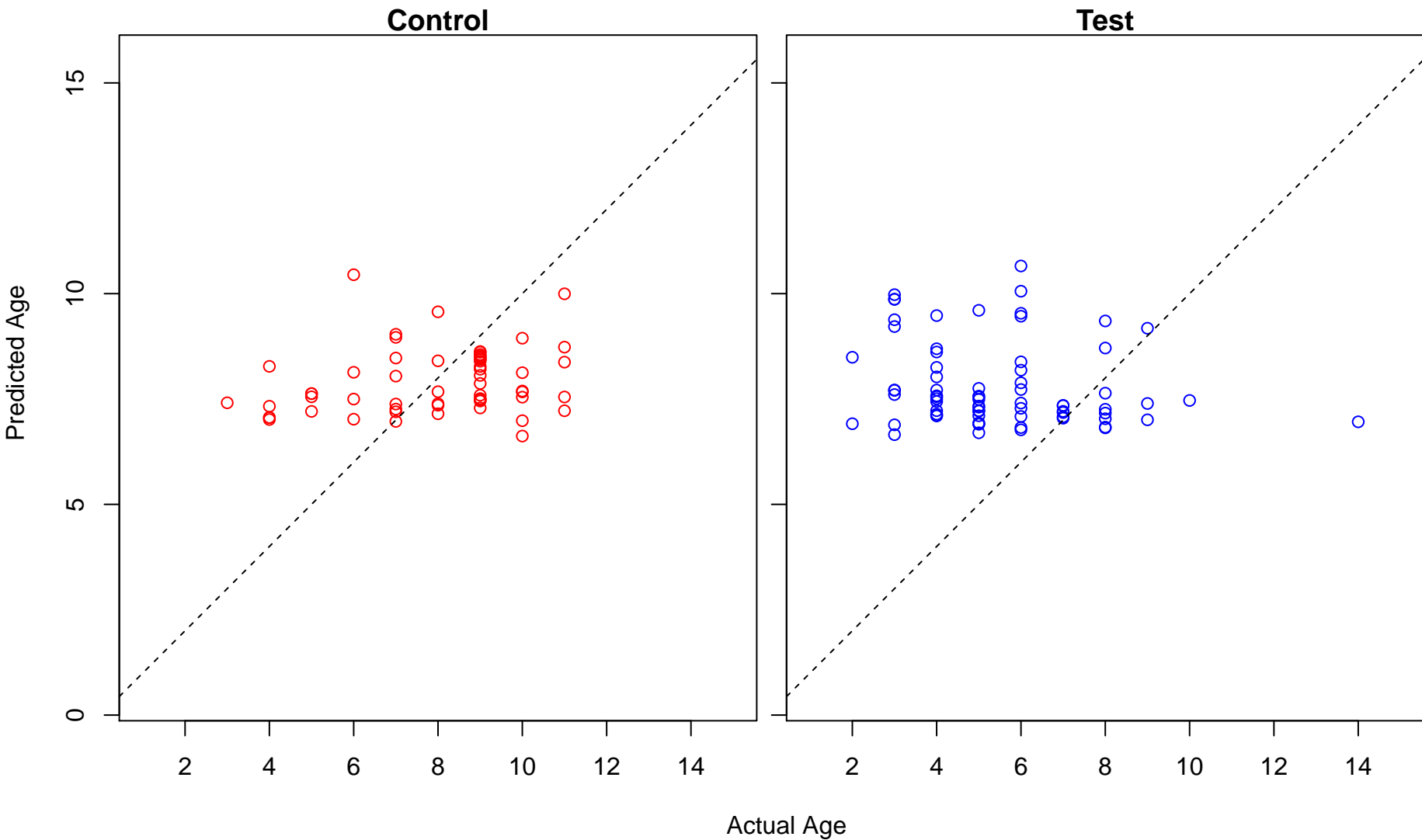
positive regulation of tumor necrosis factor (ligand) superfamily member 11 production (Score: 0.272



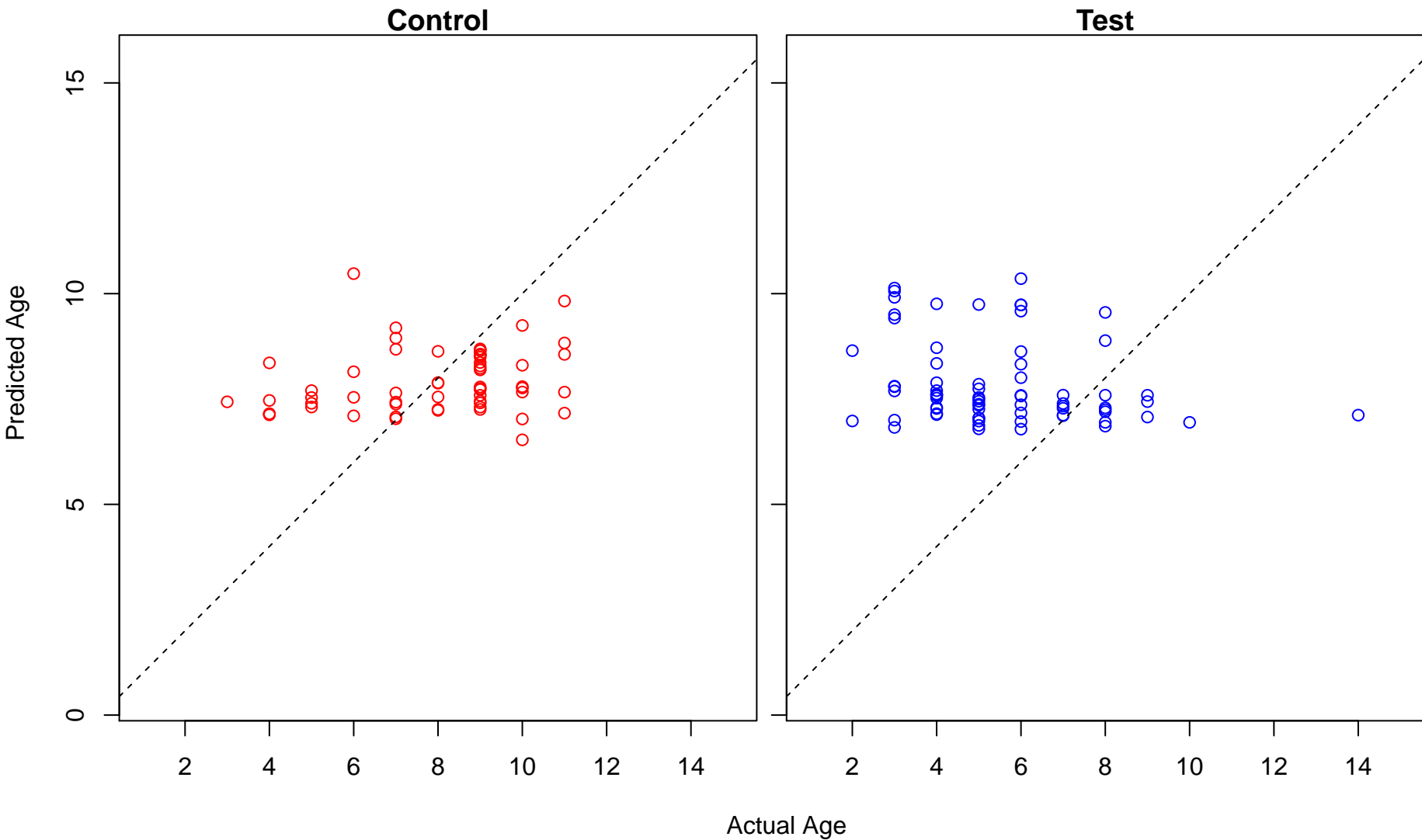
positive regulation of bone mineralization (Score: 0.271366)



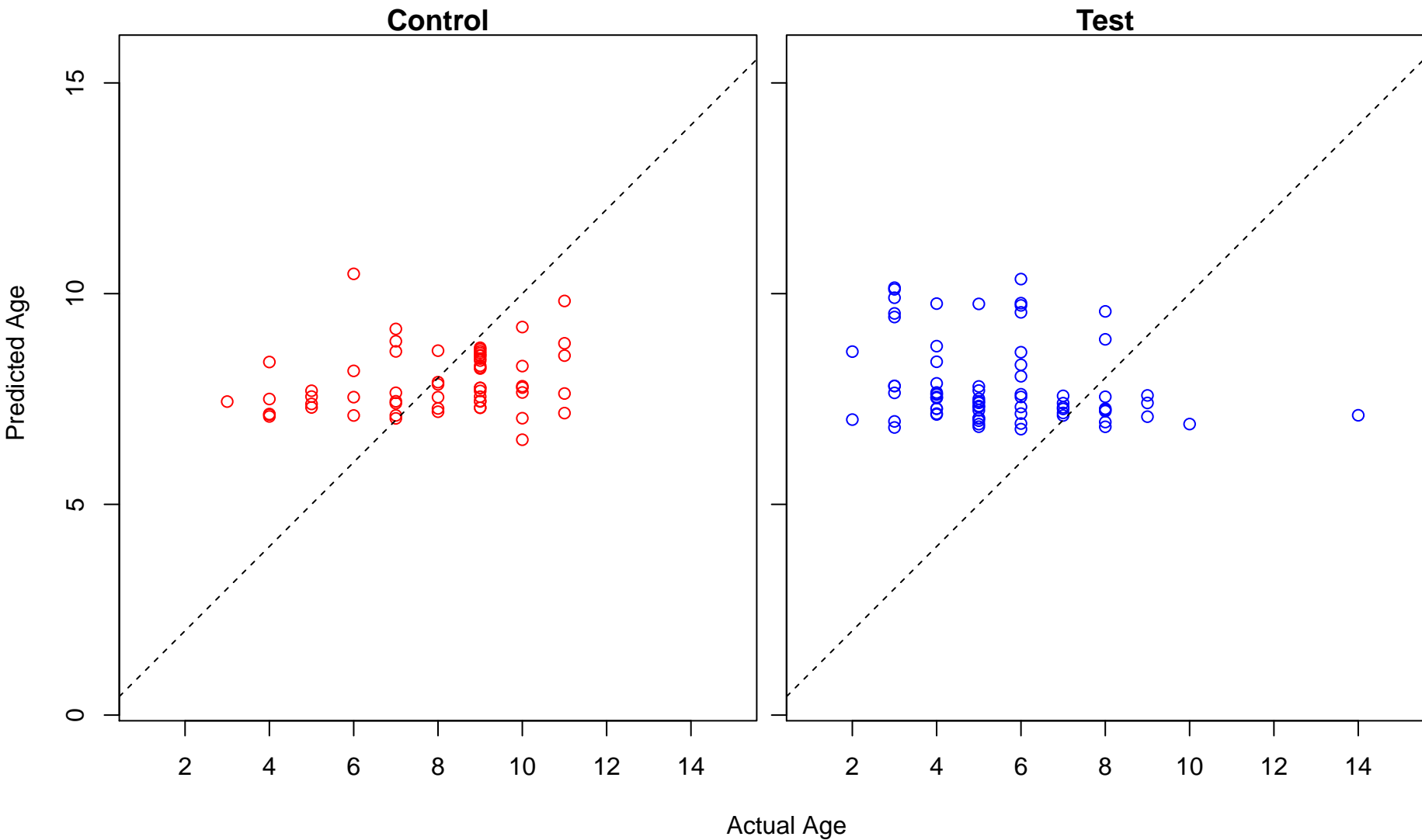
positive regulation of biomineral tissue development (Score: 0.271348)



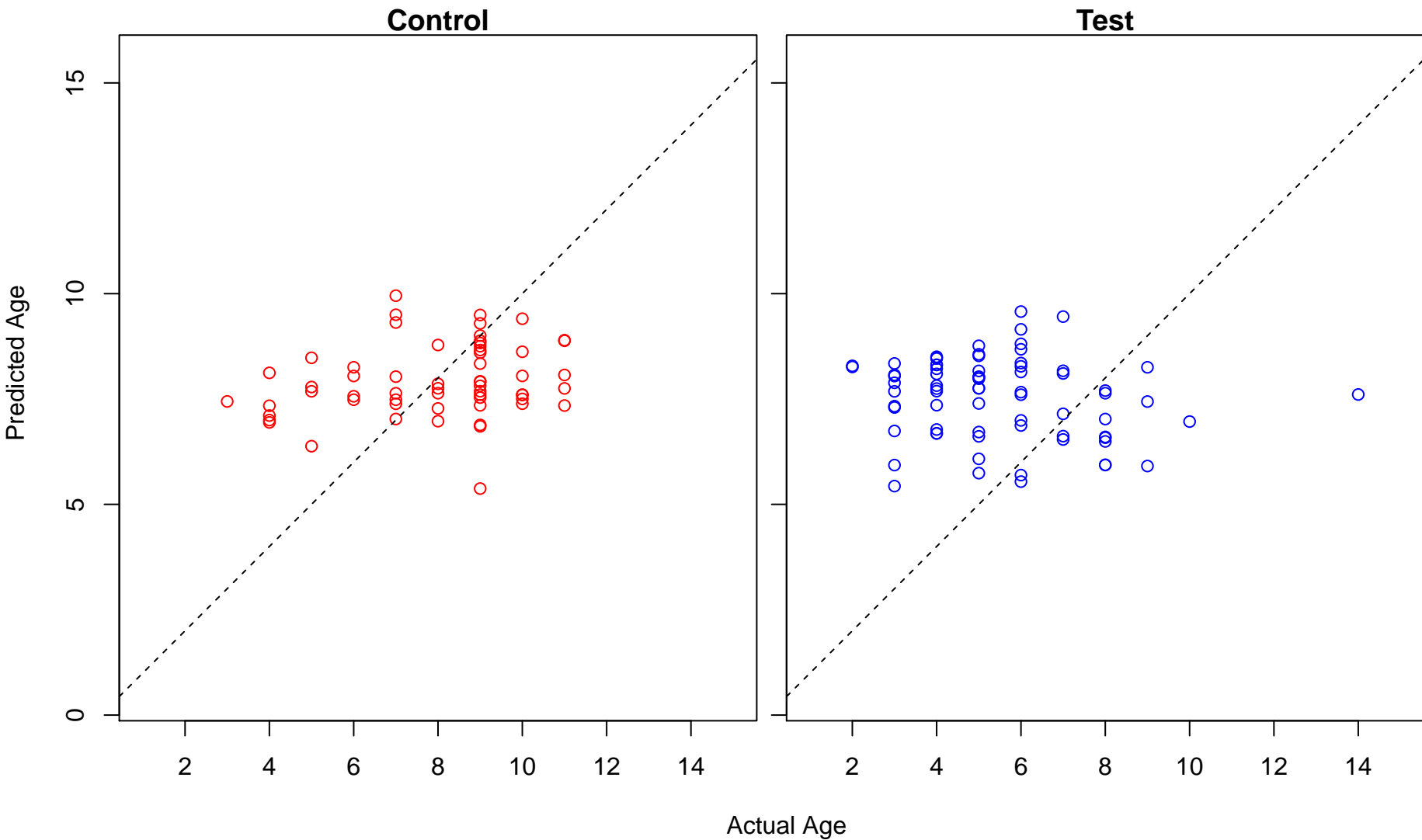
common-partner SMAD protein phosphorylation (Score: 0.271052)



positive regulation of fibroblast migration (Score: 0.269162)

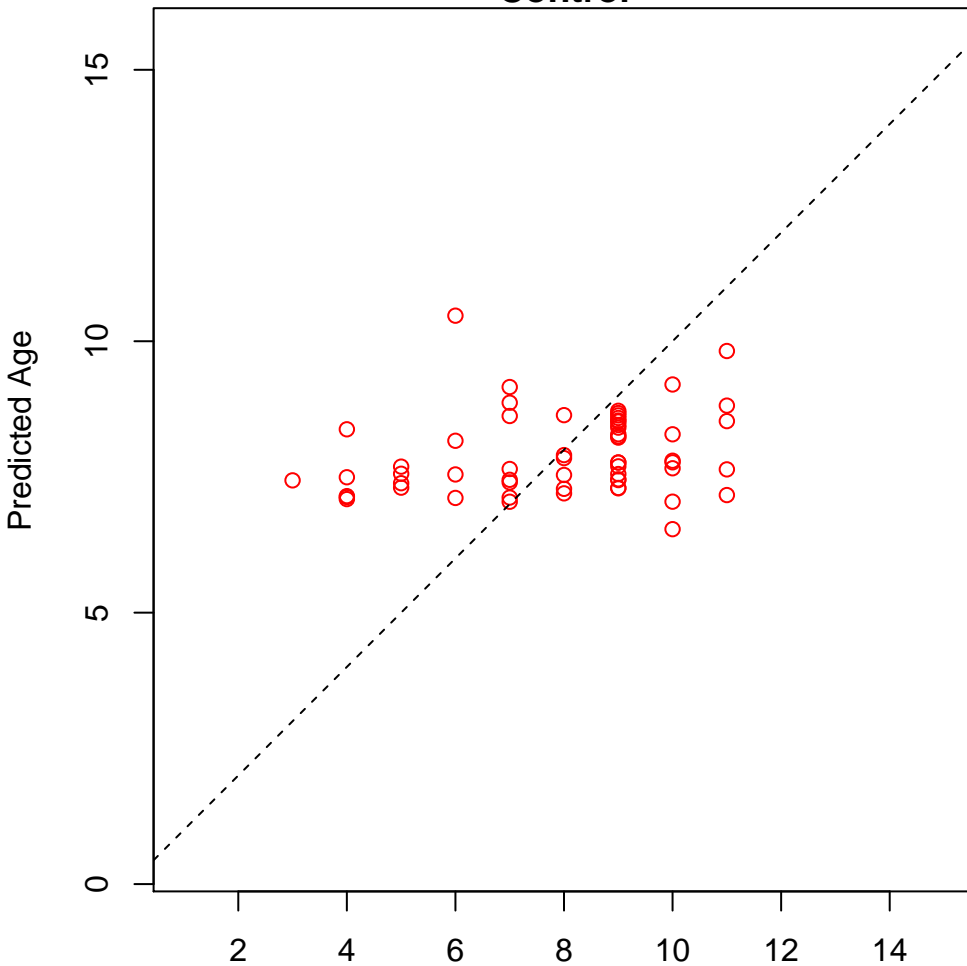


depurination (Score: 0.268945)

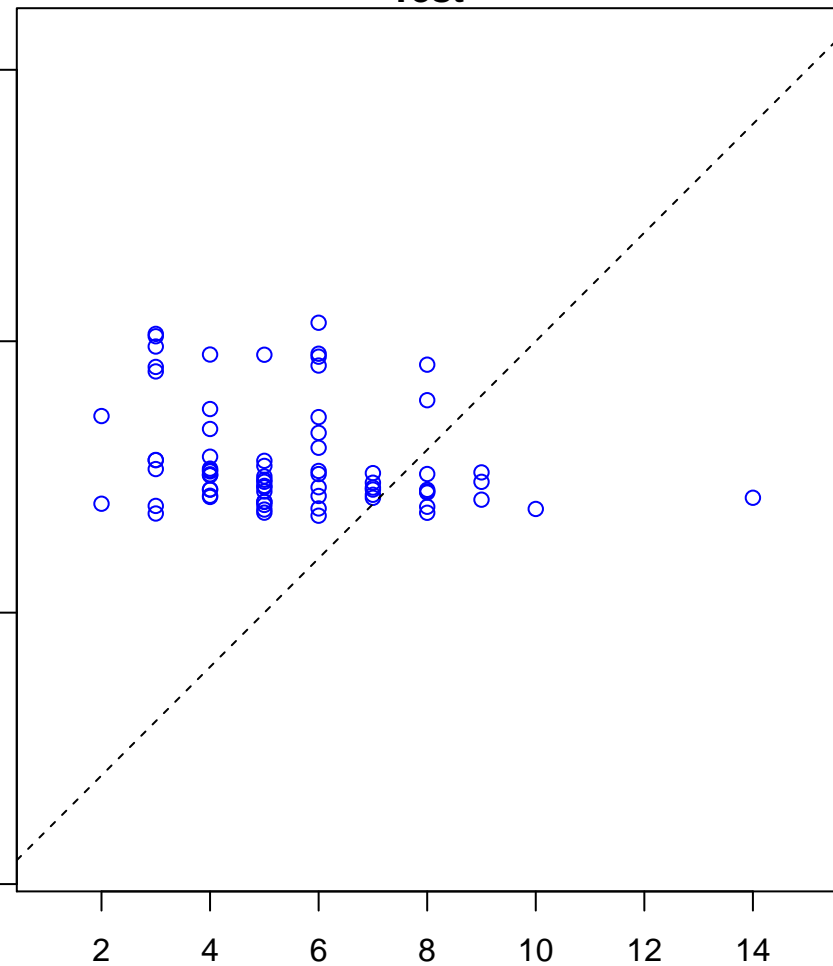


ossification involved in bone remodeling (Score: 0.268829)

Control

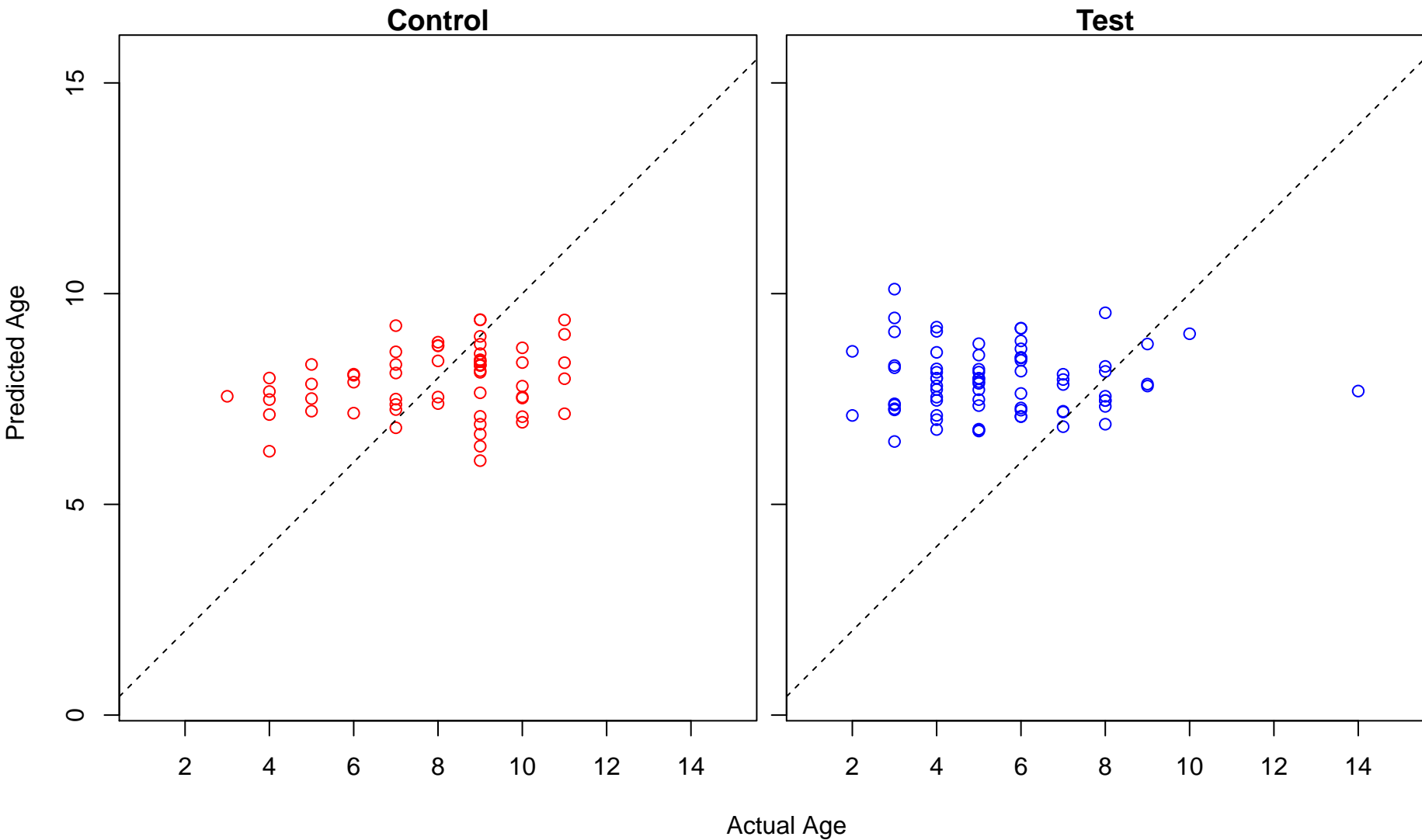


Test

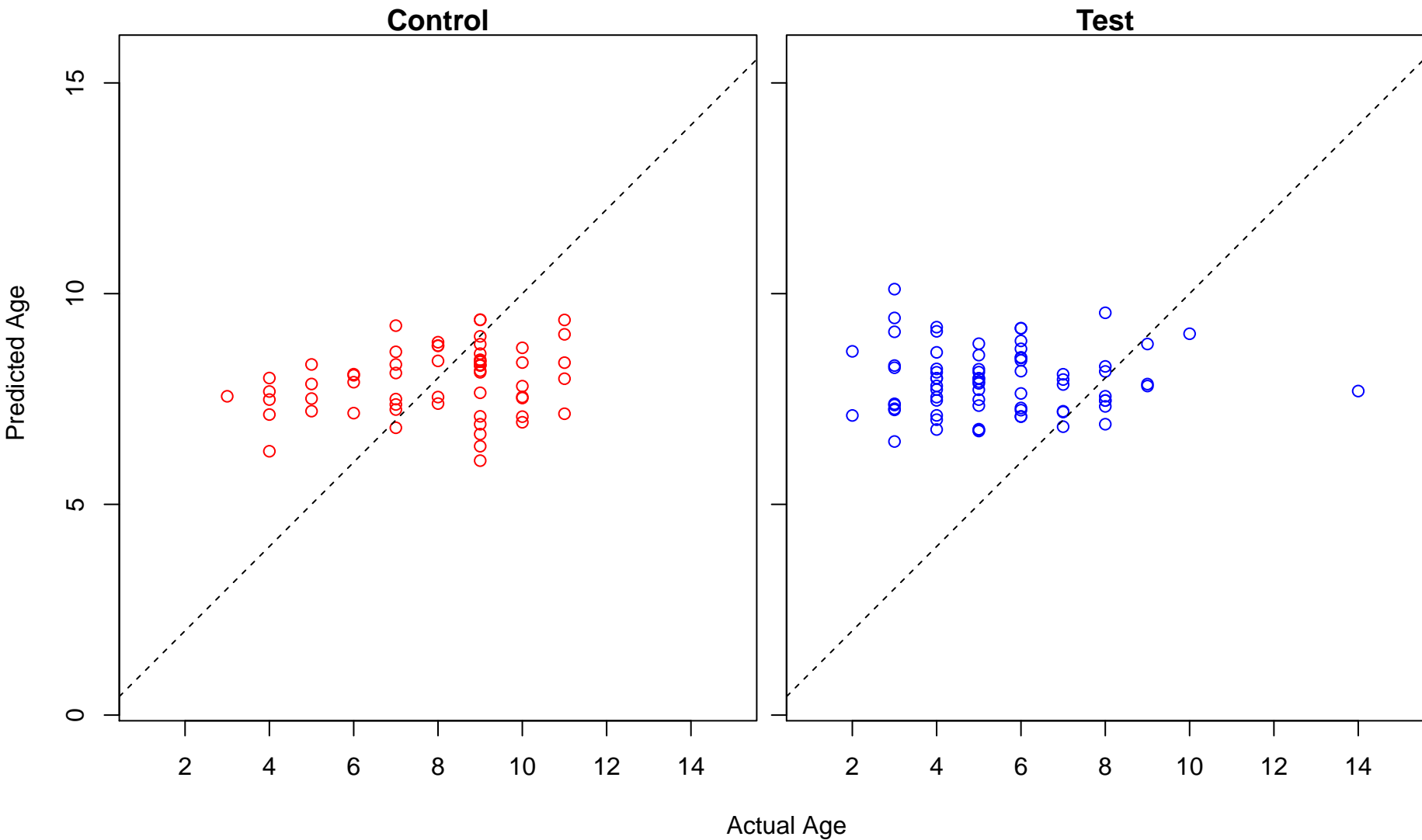


Actual Age

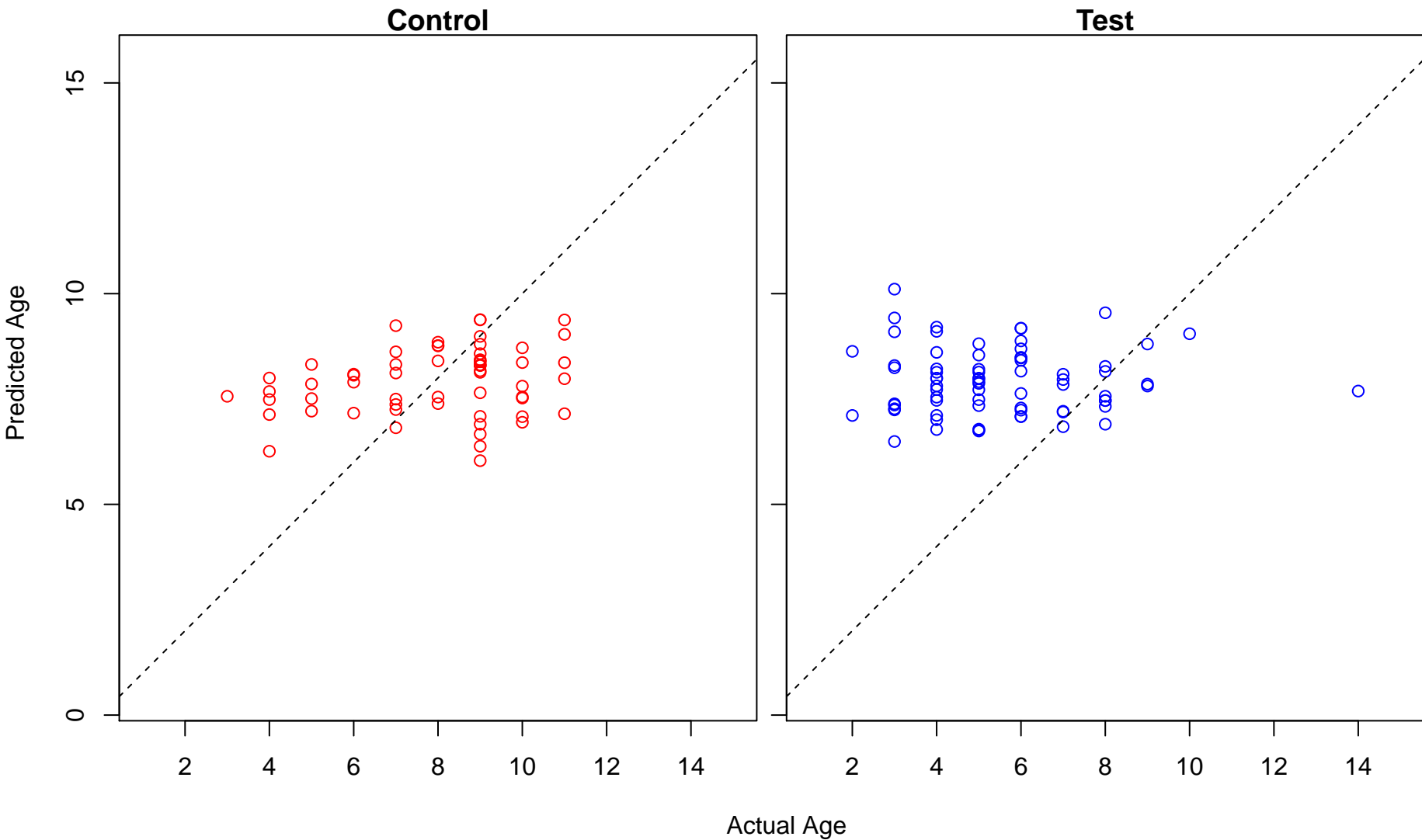
serotonin secretion (Score: 0.268631)



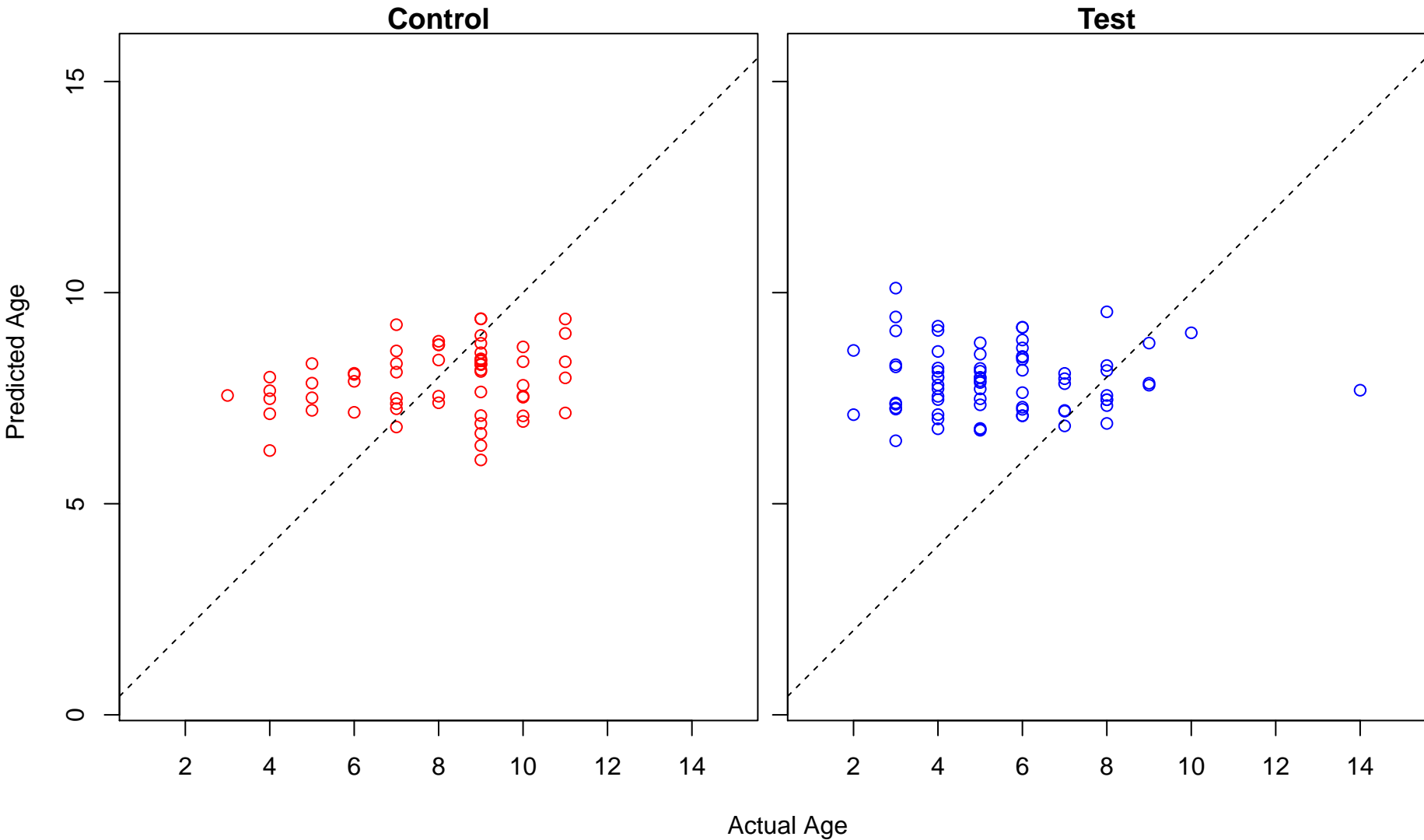
response to molecule of fungal origin (Score: 0.268631)



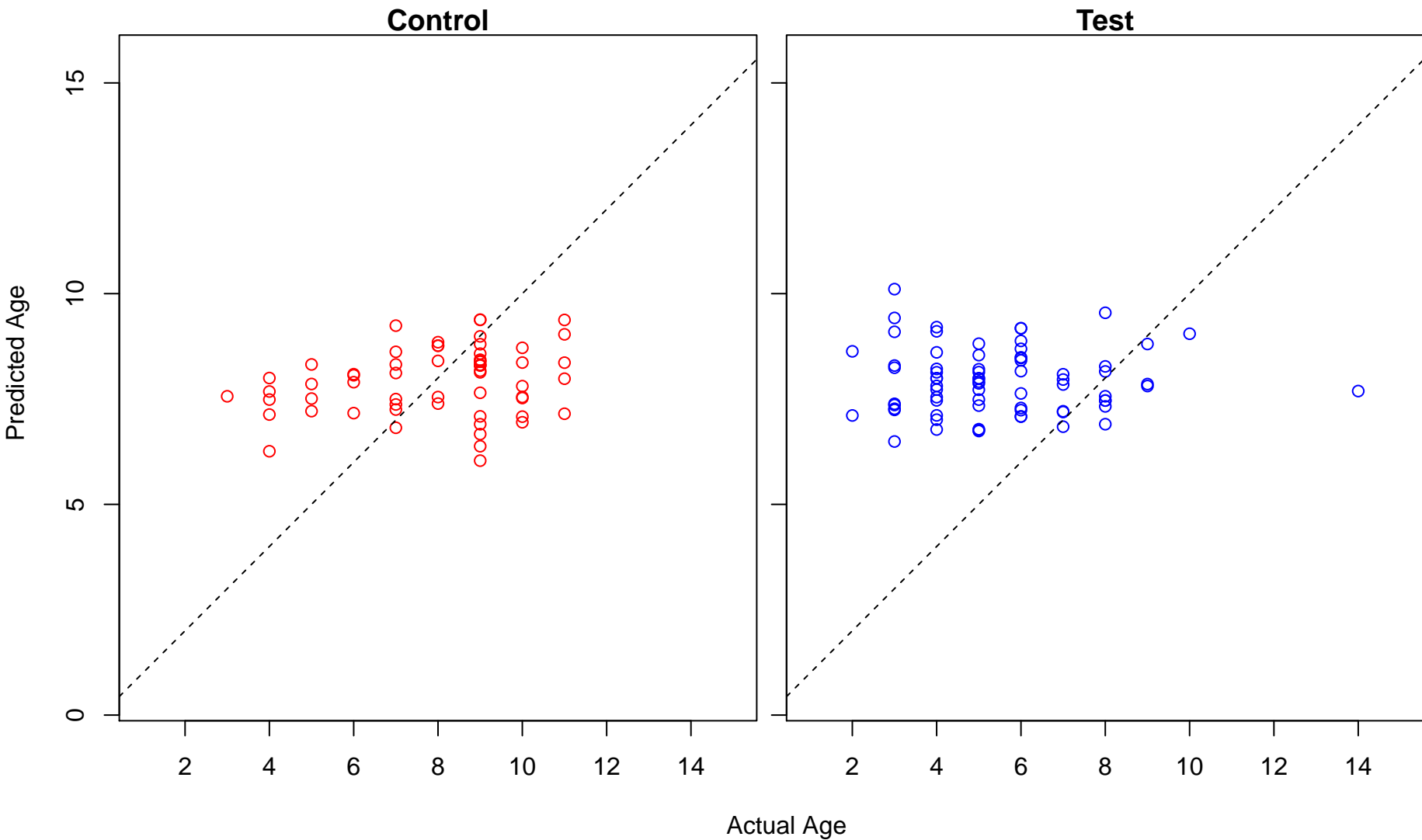
serotonin production involved in inflammatory response (Score: 0.268631)



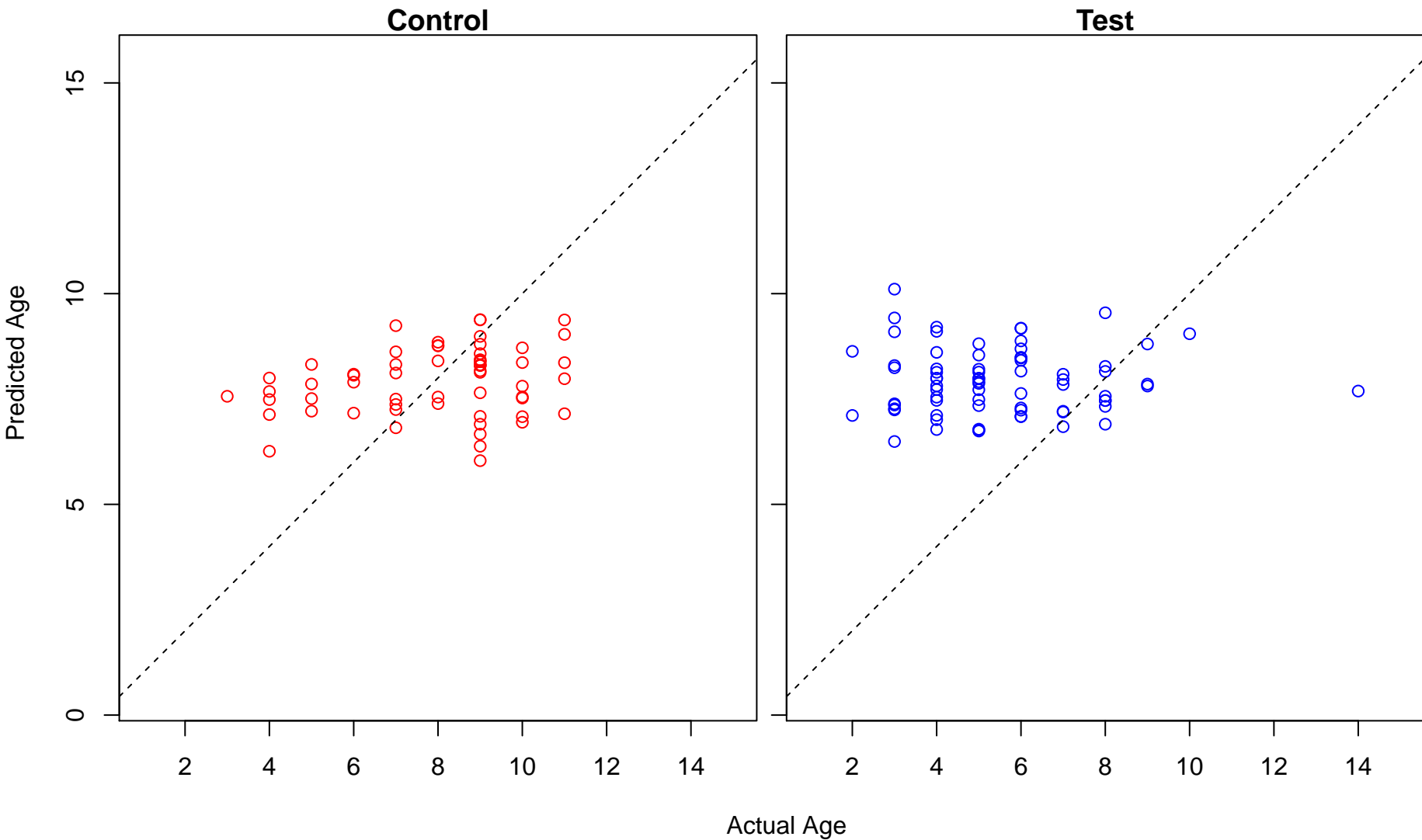
serotonin secretion involved in inflammatory response (Score: 0.268631)



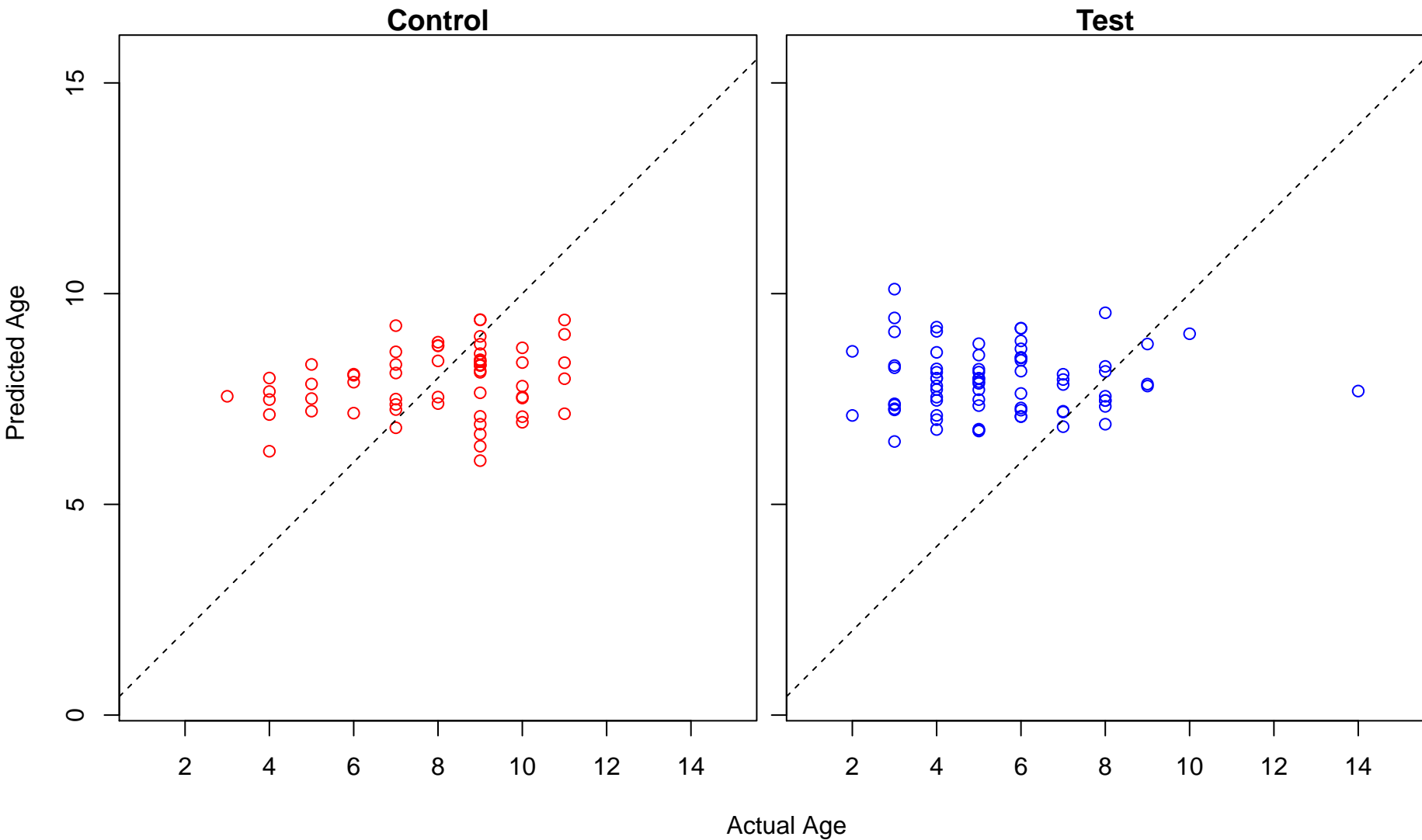
serotonin secretion by platelet (Score: 0.268631)



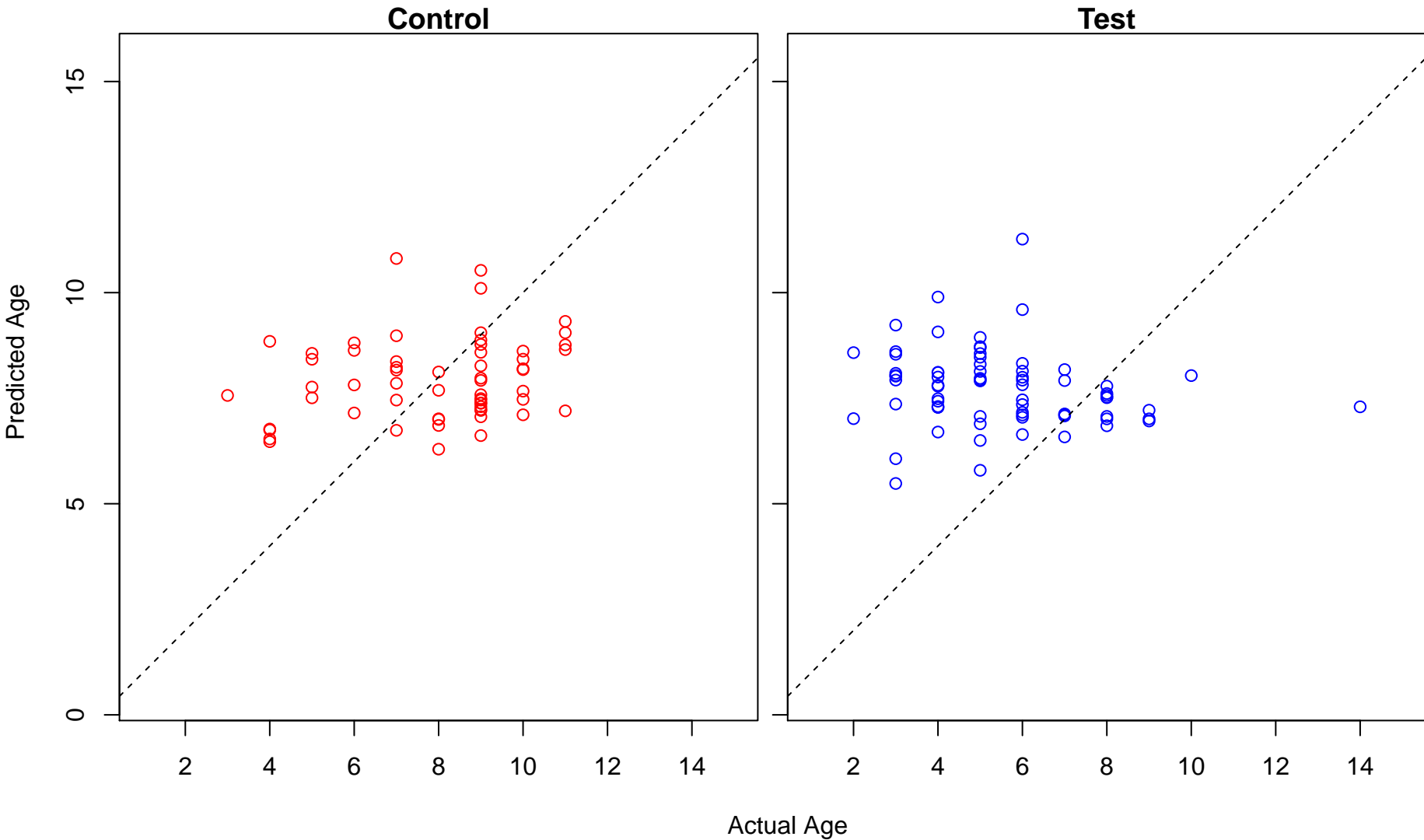
regulation of neutrophil degranulation (Score: 0.268631)



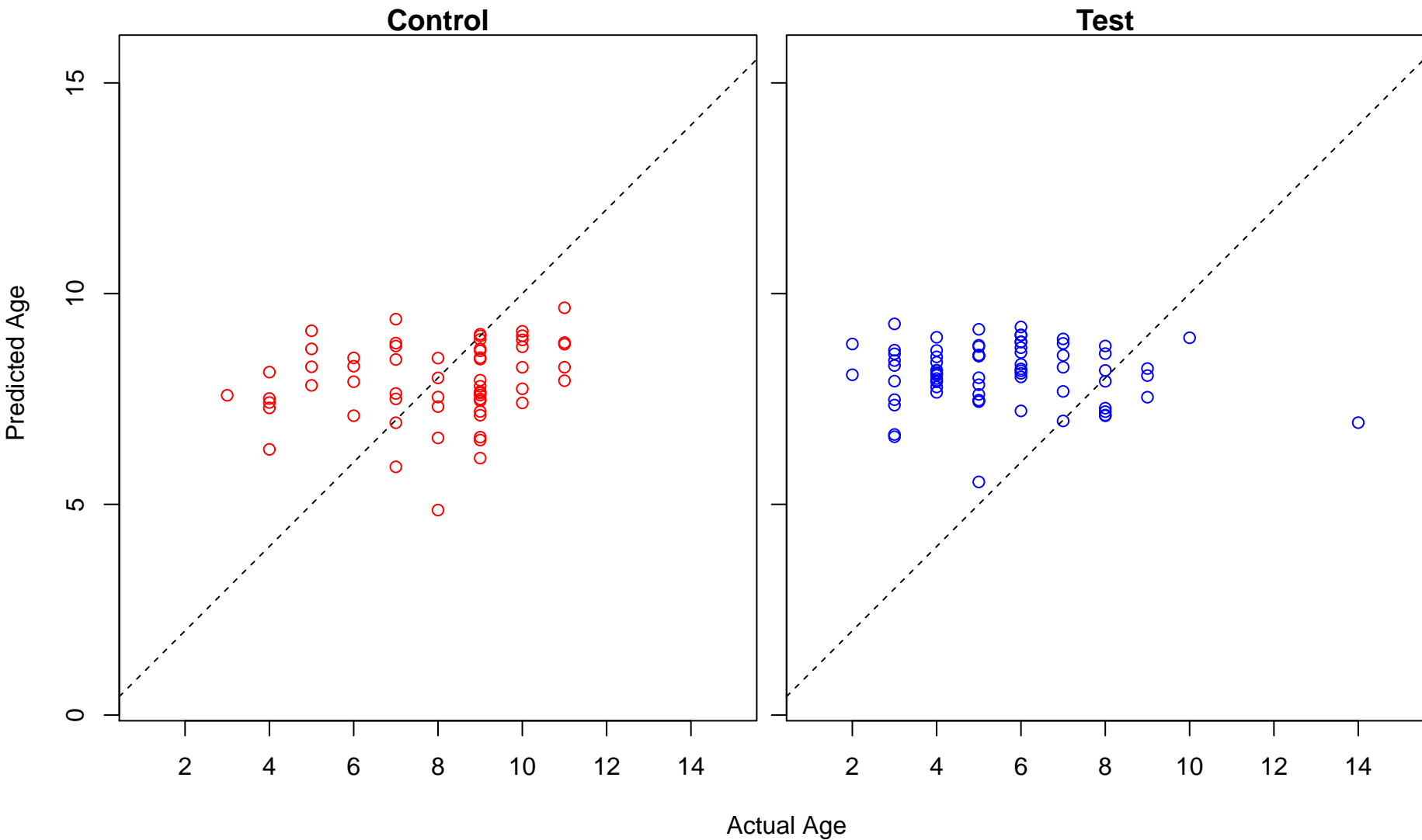
cellular response to molecule of fungal origin (Score: 0.268631)



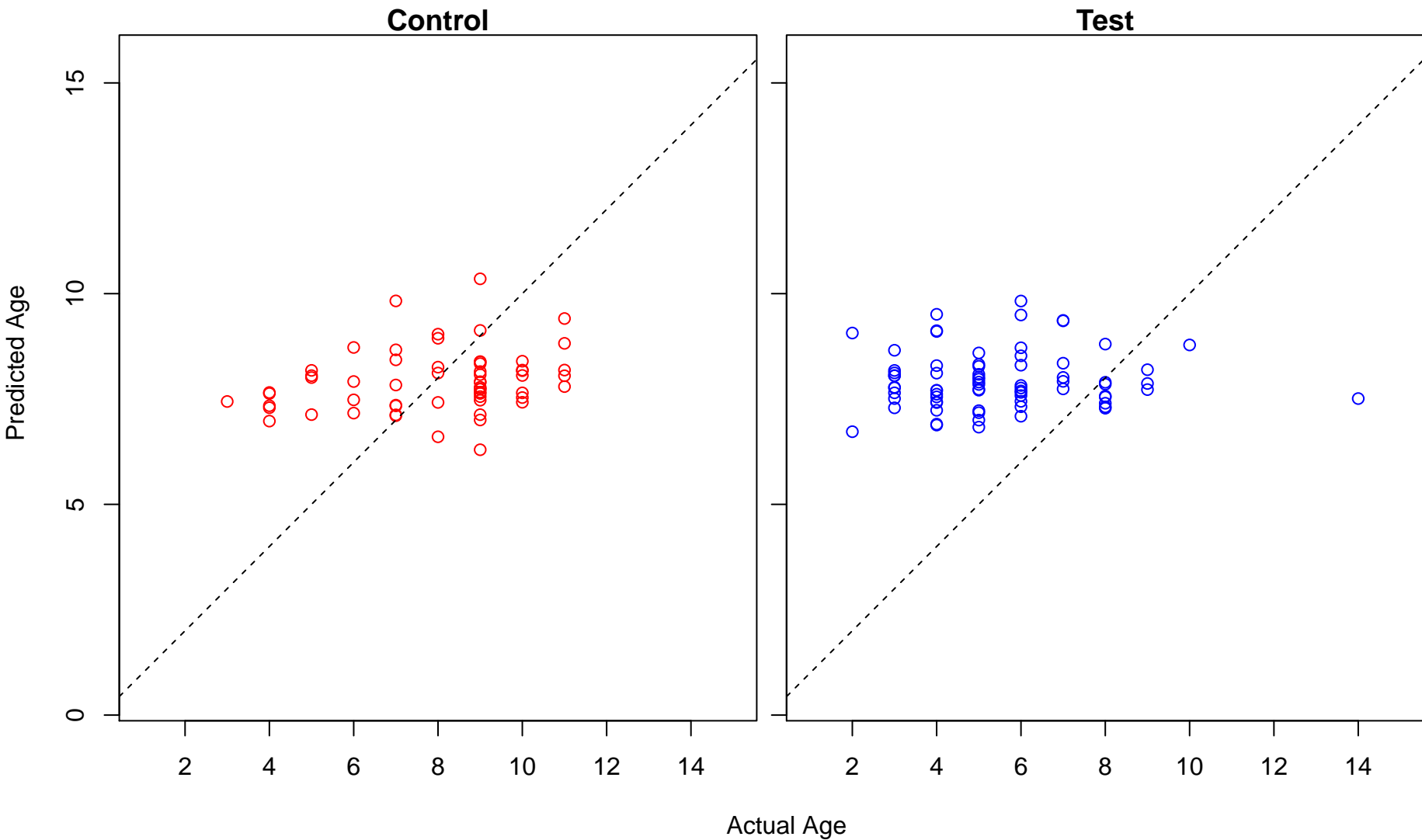
negative regulation of beta-amyloid clearance (Score: 0.267273)



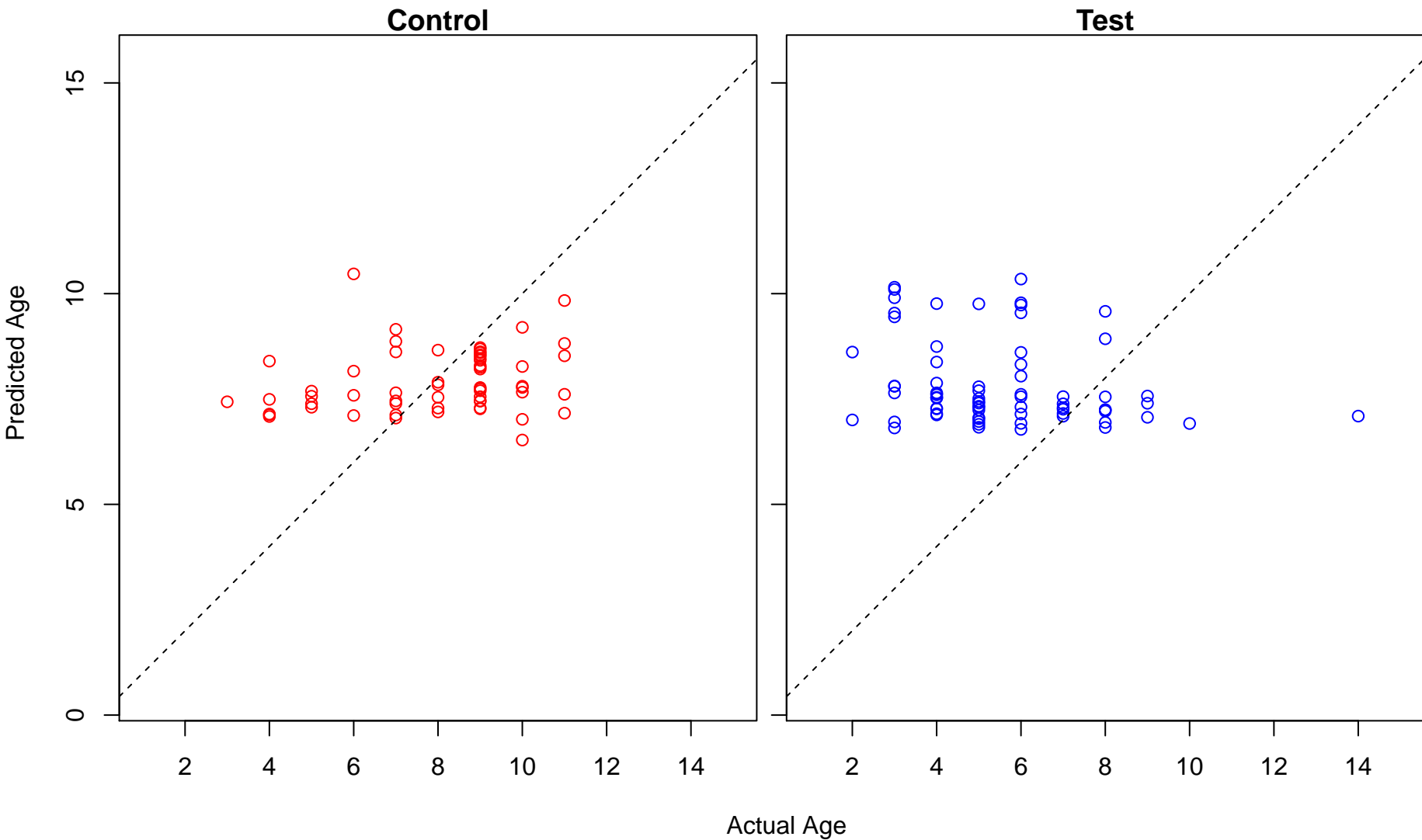
photoreceptor cell maintenance (Score: 0.266638)



engulfment of apoptotic cell (Score: 0.266443)

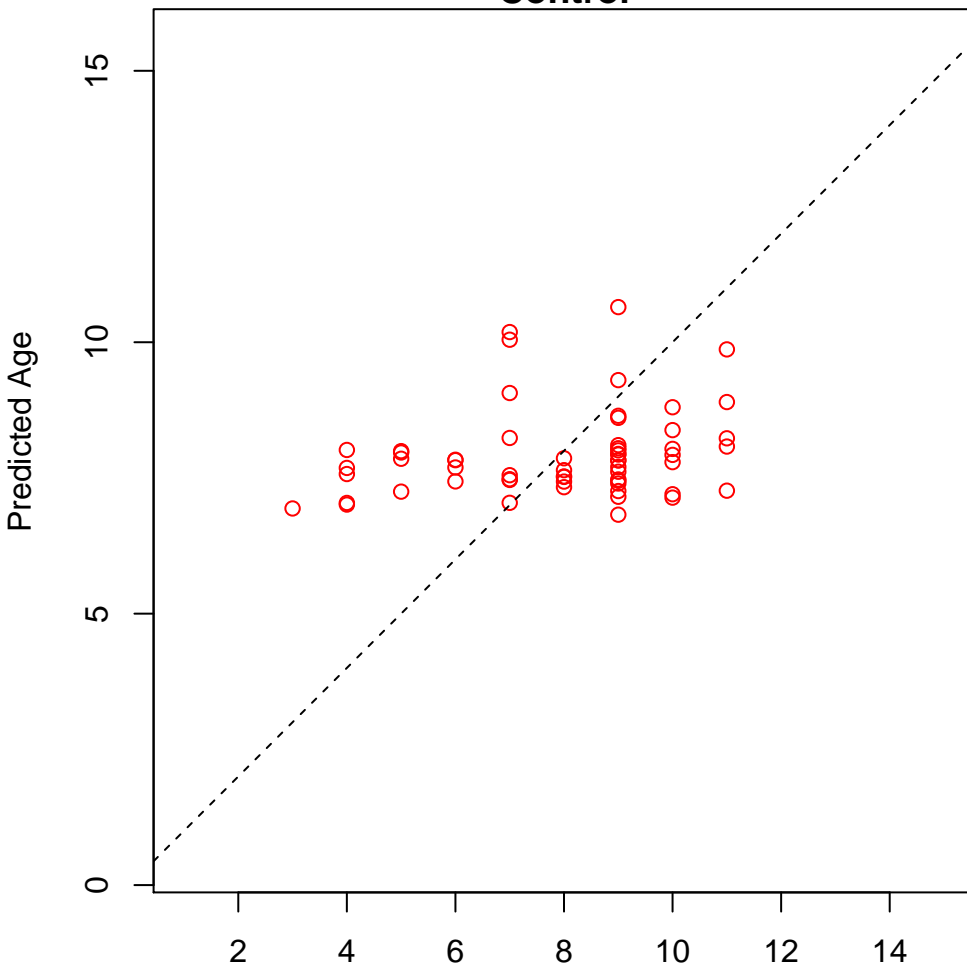


positive regulation of cardiac muscle cell differentiation (Score: 0.264614)

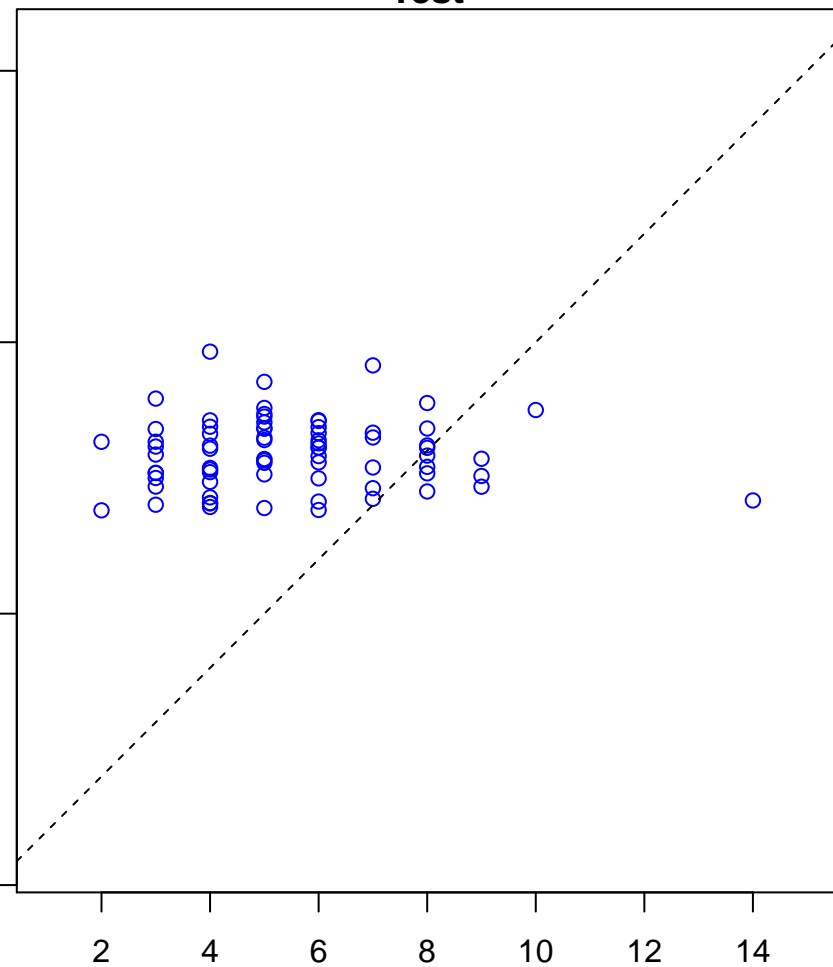


spinal cord dorsal/ventral patterning (Score: 0.263920)

Control

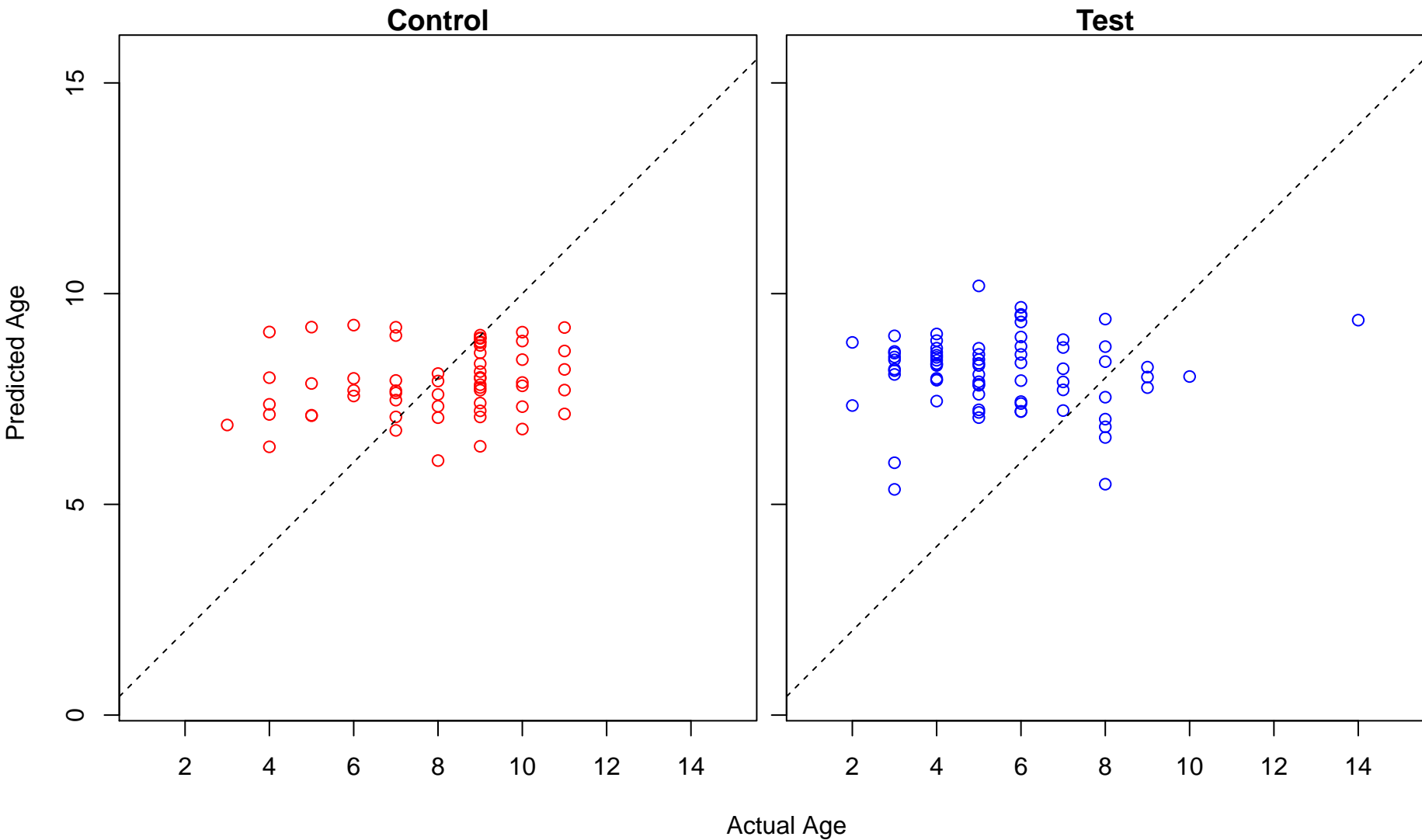


Test

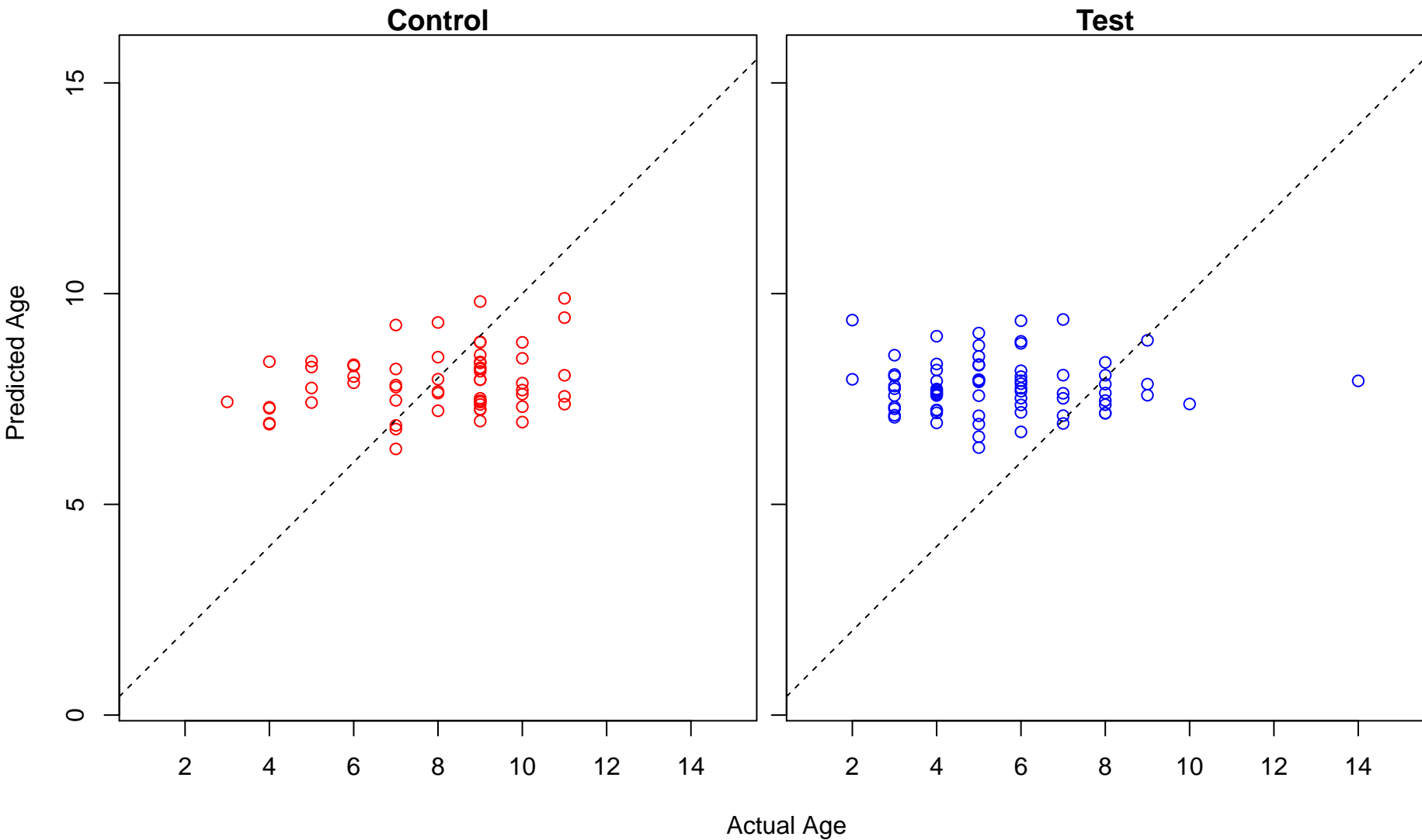


Actual Age

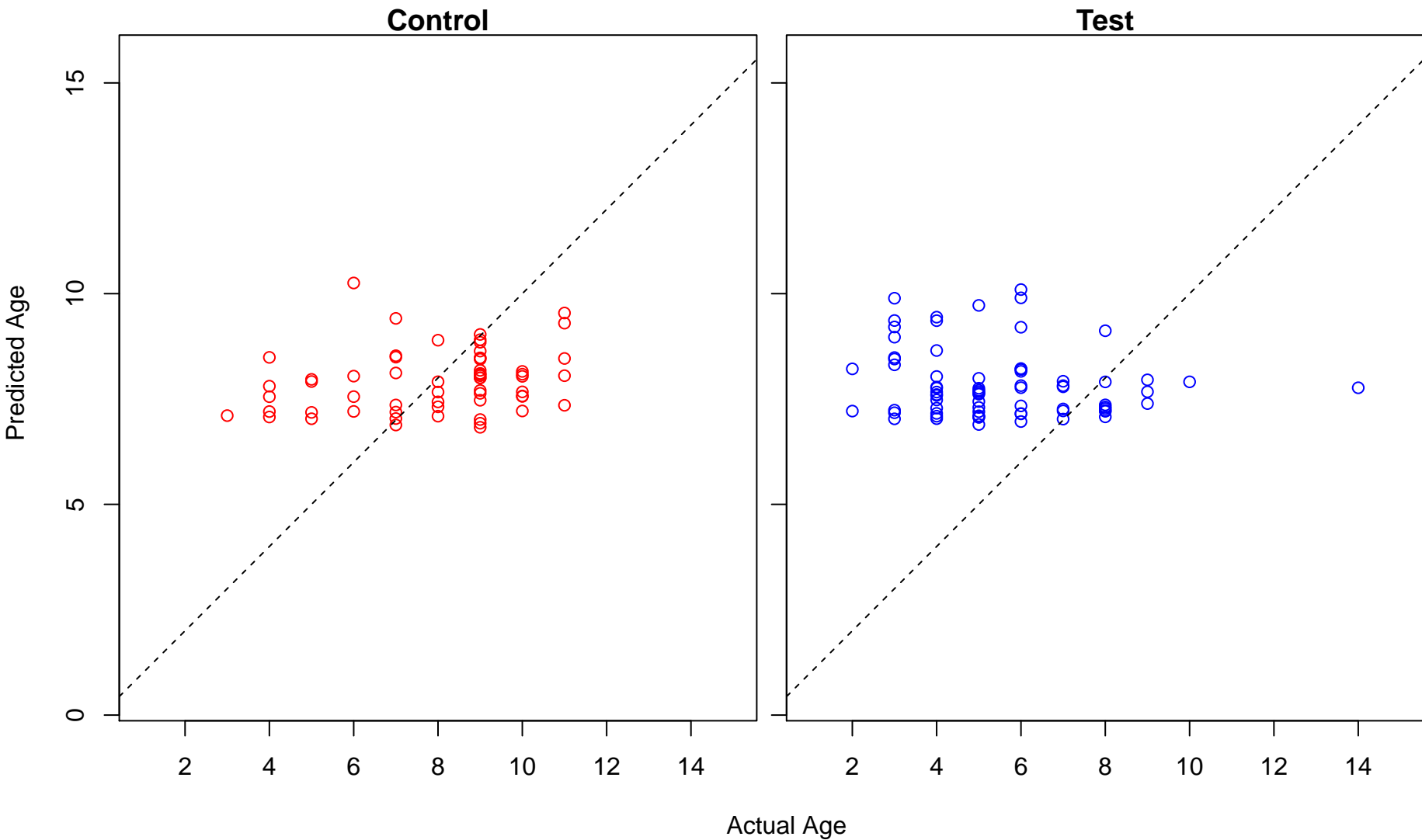
DNA rewinding (Score: 0.259856)



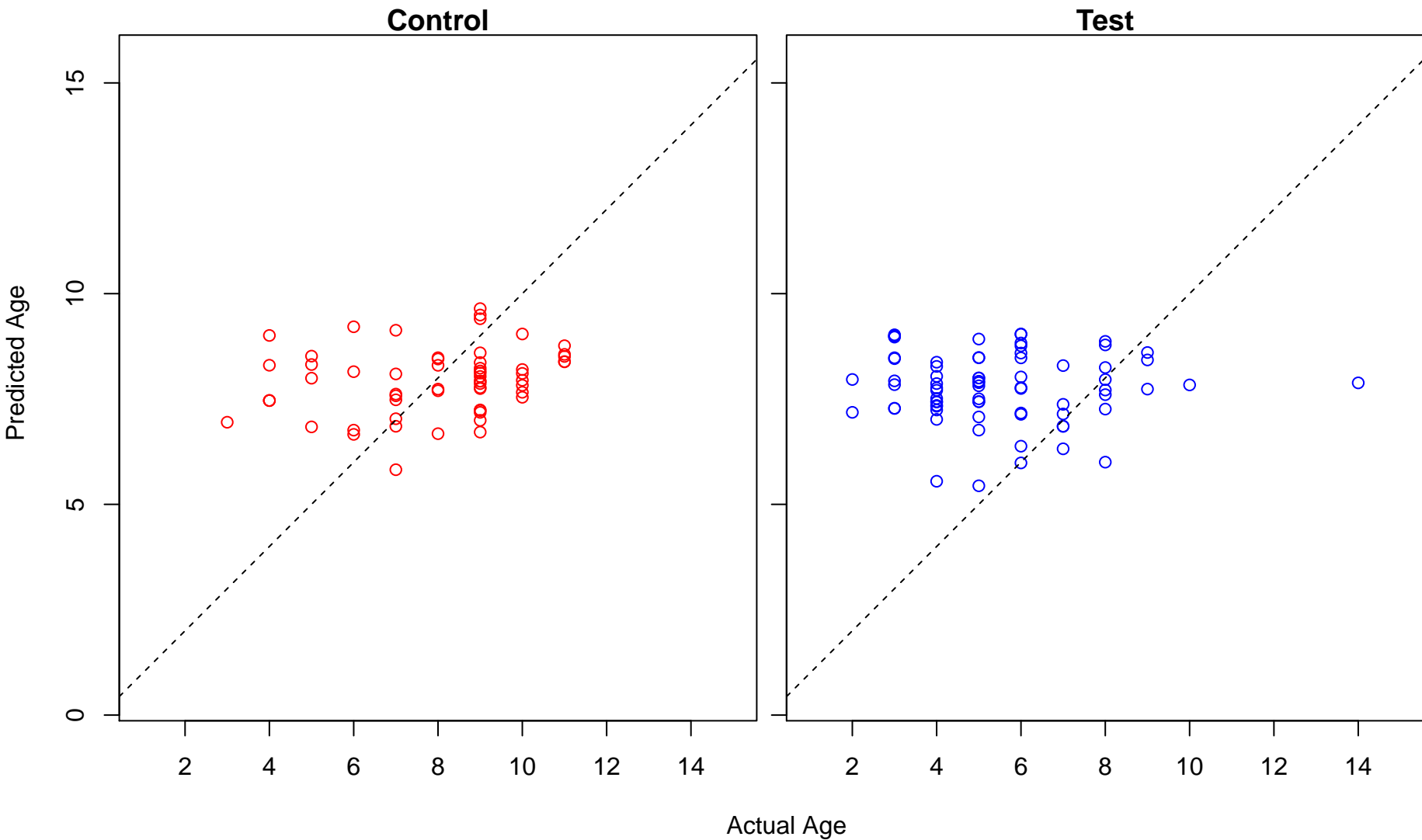
peptidyl-glutamine modification (Score: 0.259243)



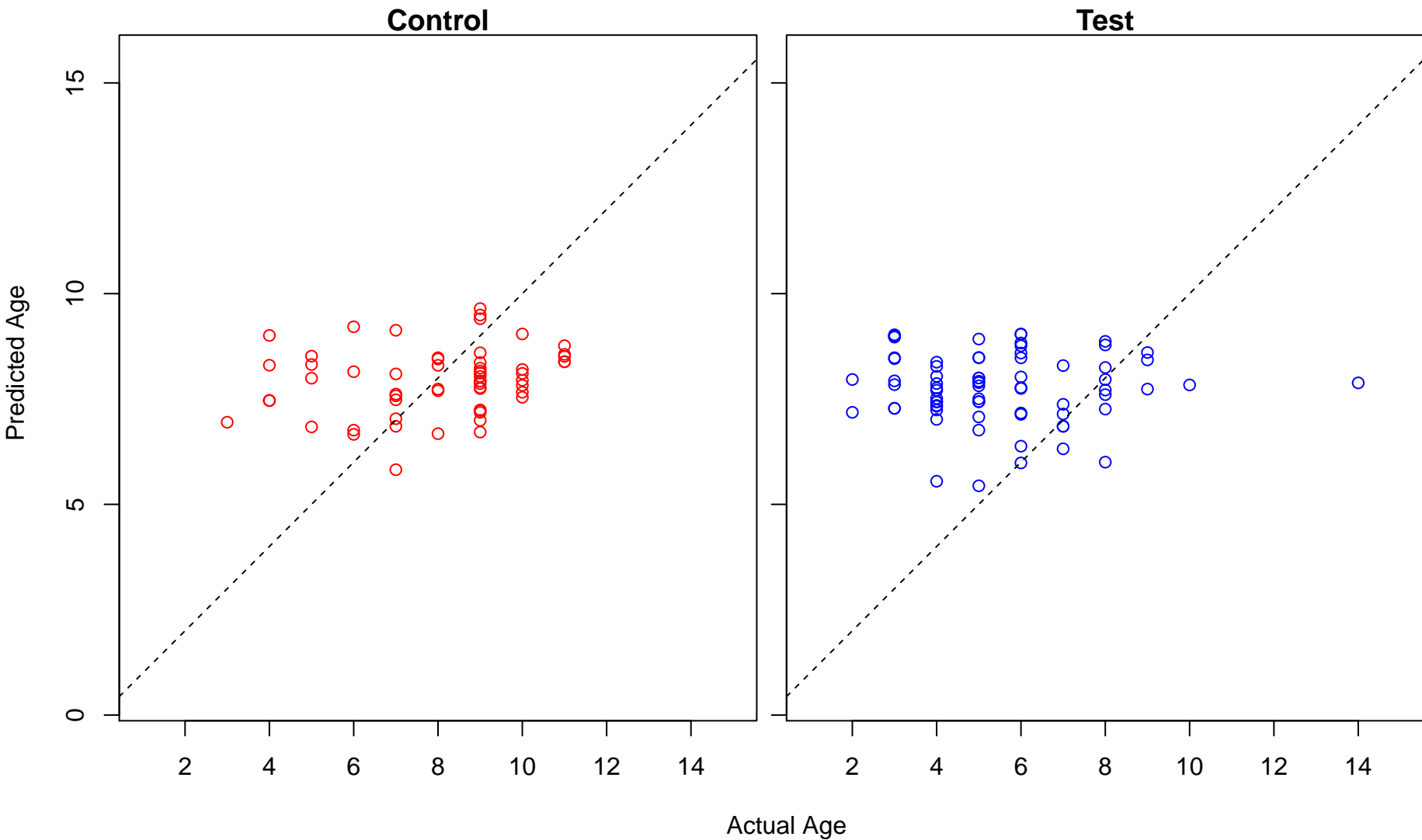
NADPH regeneration (Score: 0.259198)



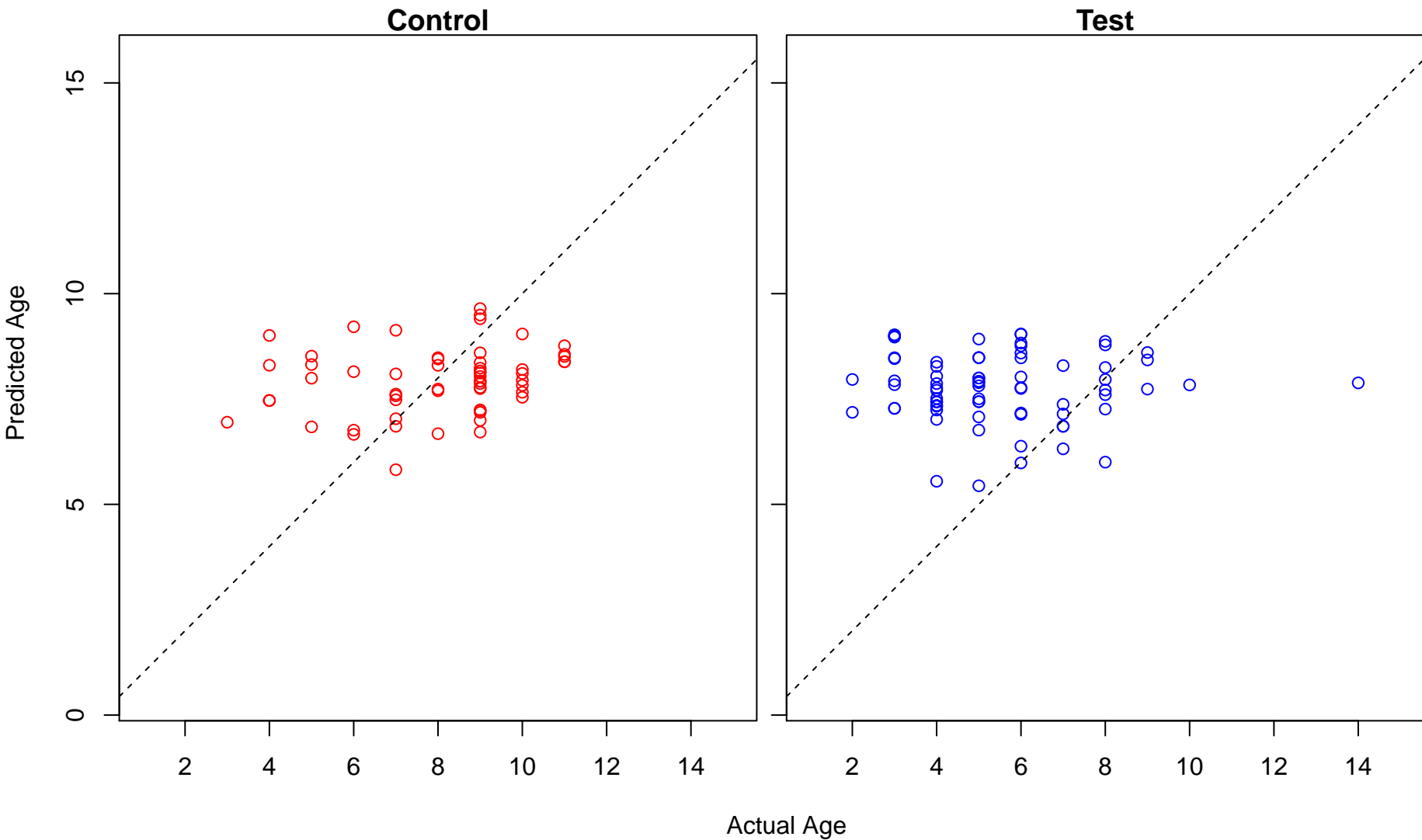
eye pigment biosynthetic process (Score: 0.258694)



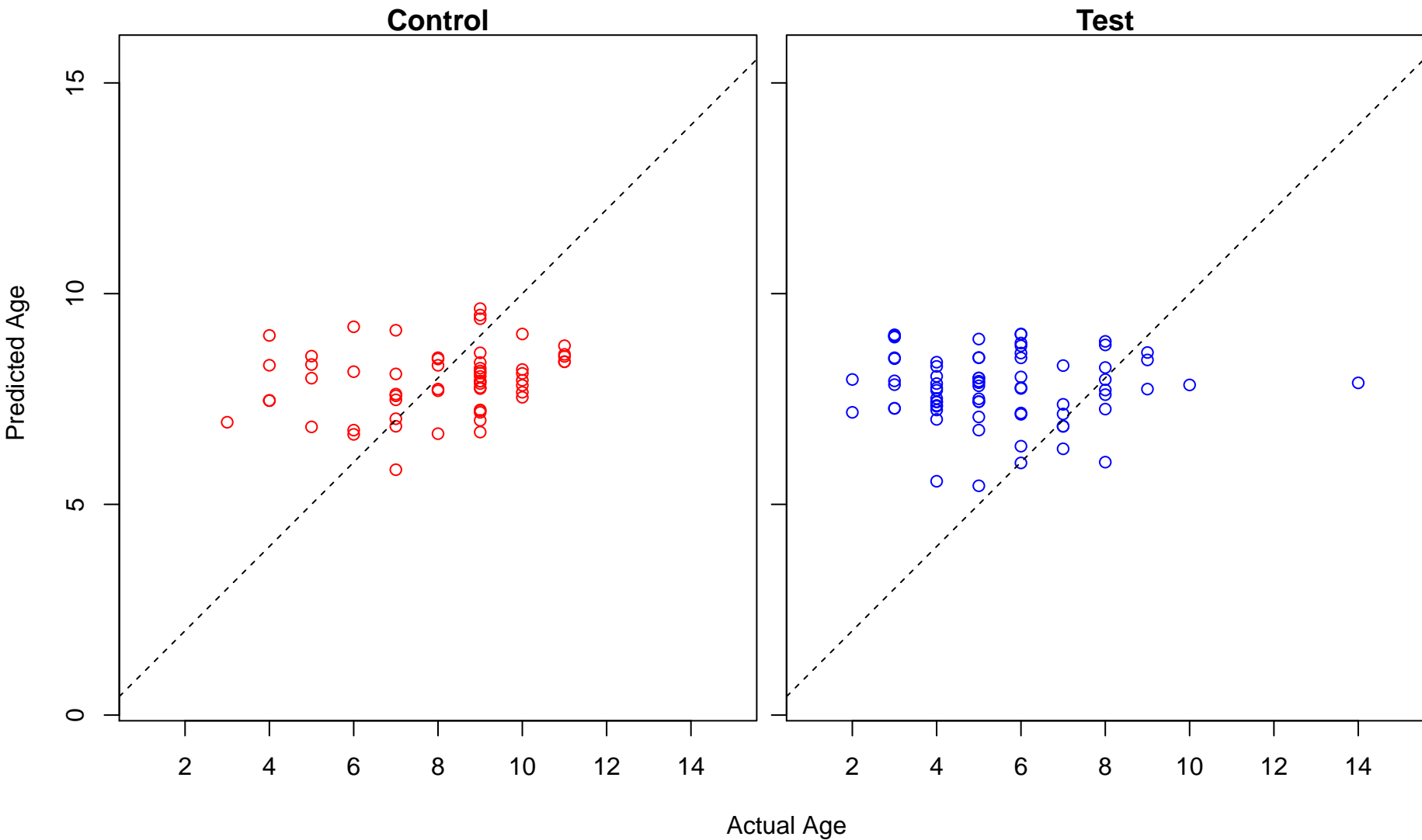
eye pigment metabolic process (Score: 0.258694)



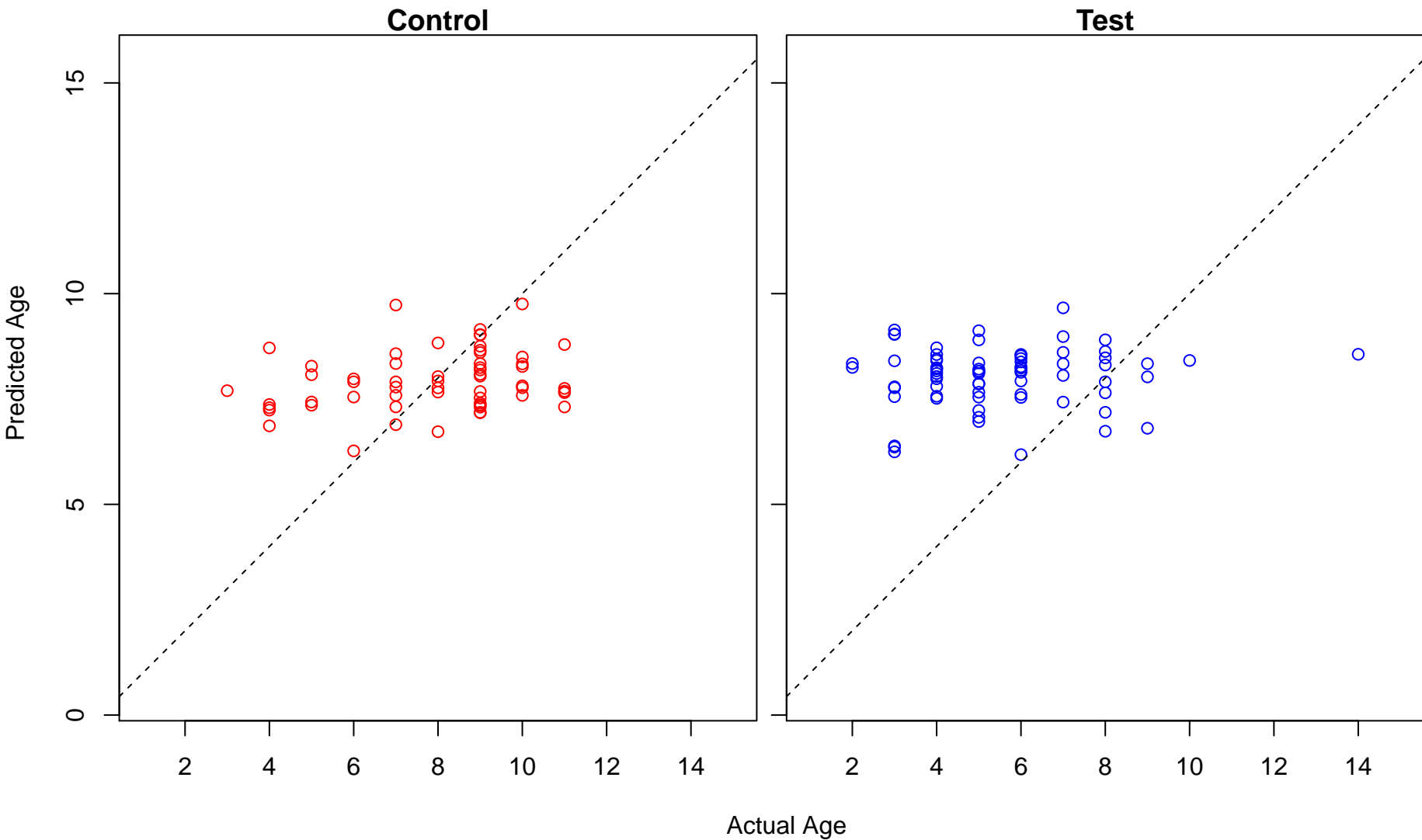
pigment metabolic process involved in developmental pigmentation (Score: 0.258694)



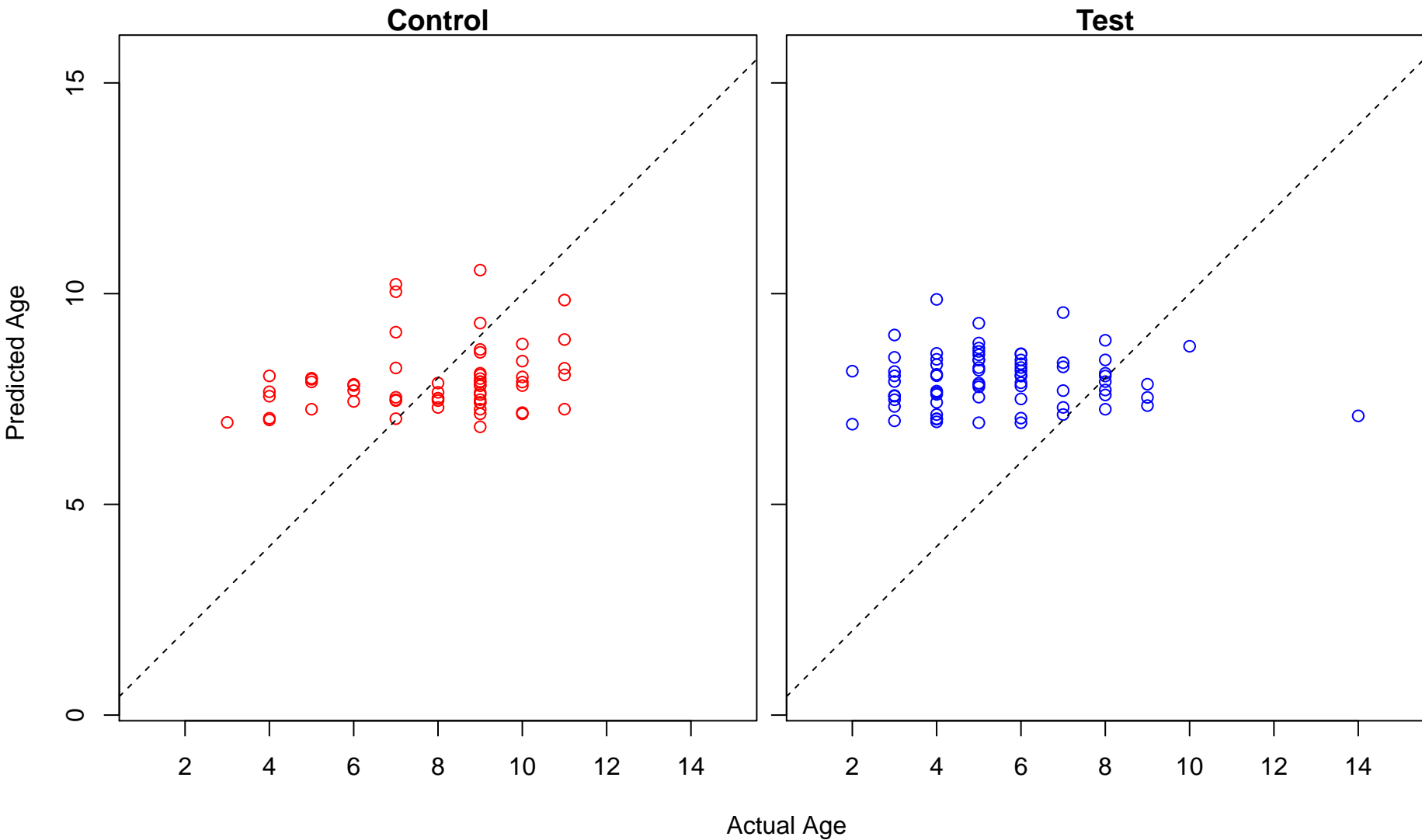
pigment metabolic process involved in pigmentation (Score: 0.258694)



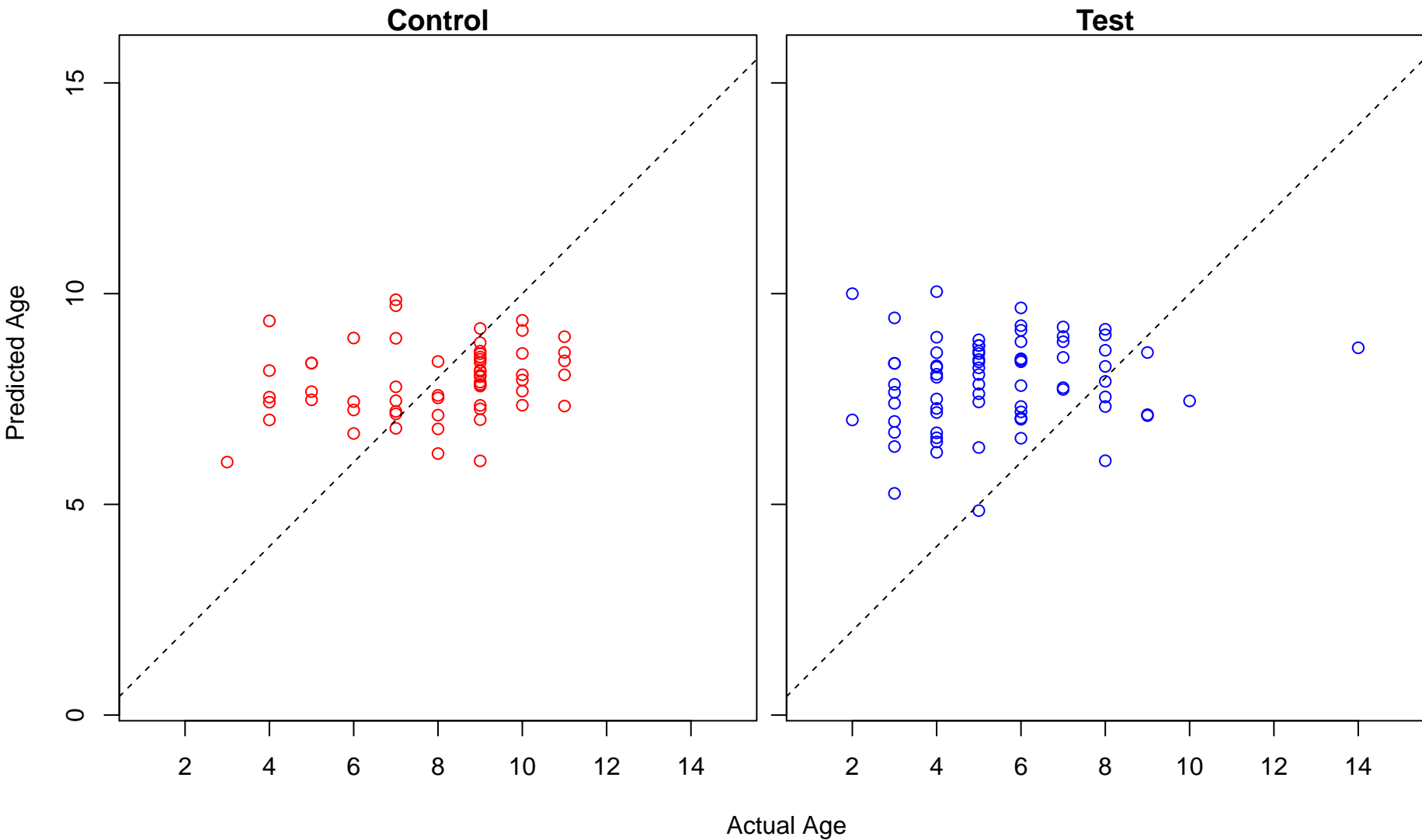
regulation of rubidium ion transport (Score: 0.256602)



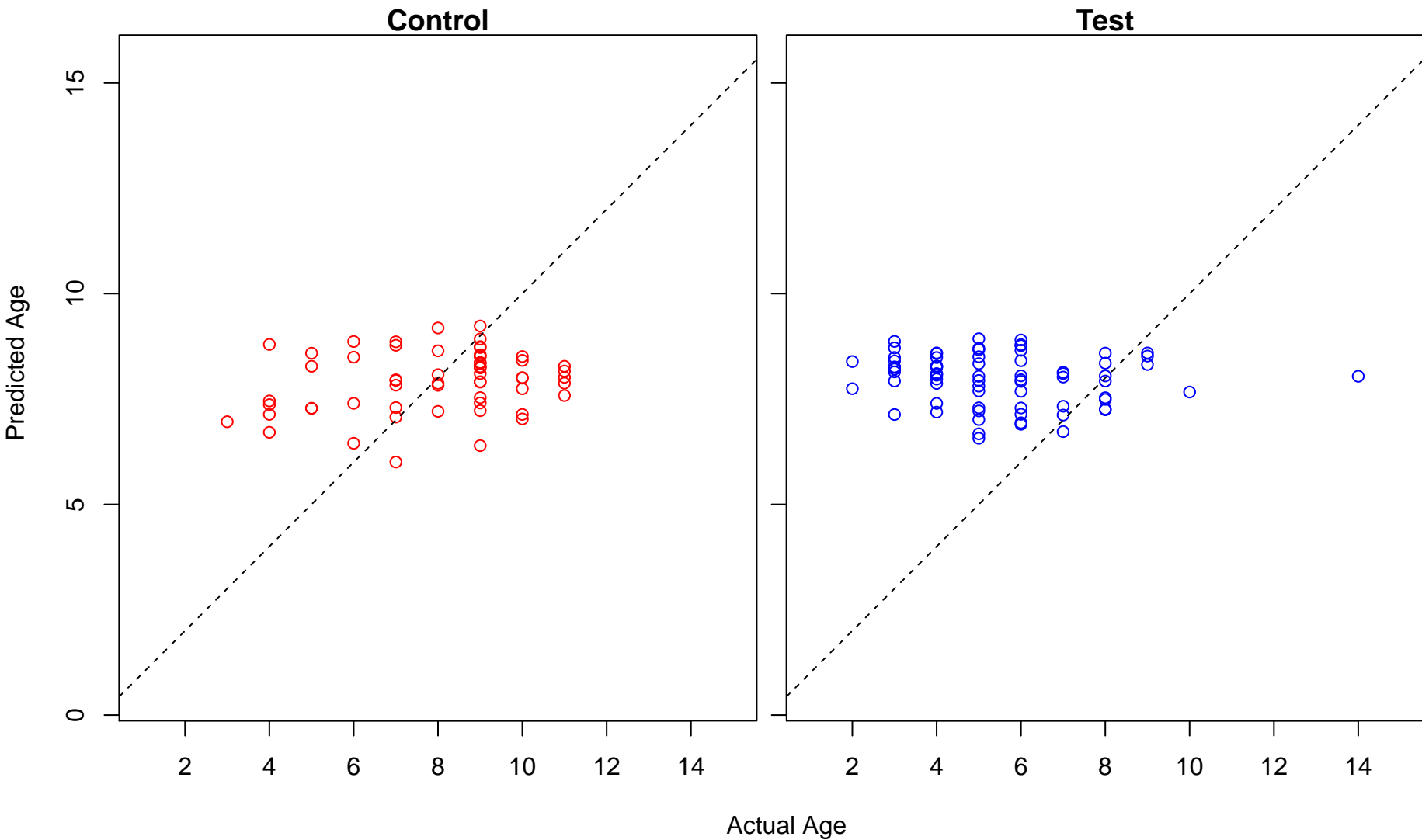
spinal cord patterning (Score: 0.256077)



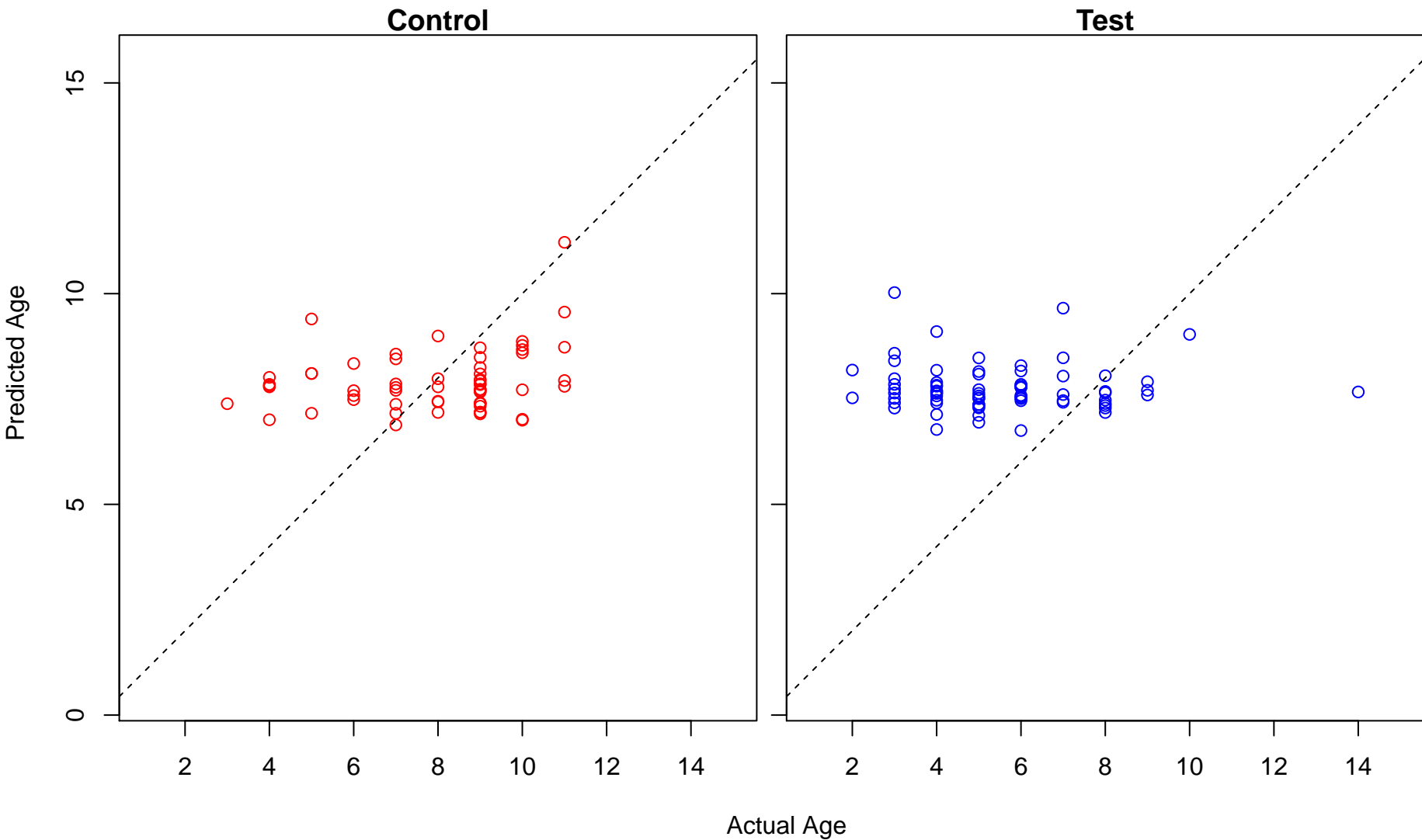
serine phosphorylation of STAT protein (Score: 0.255777)



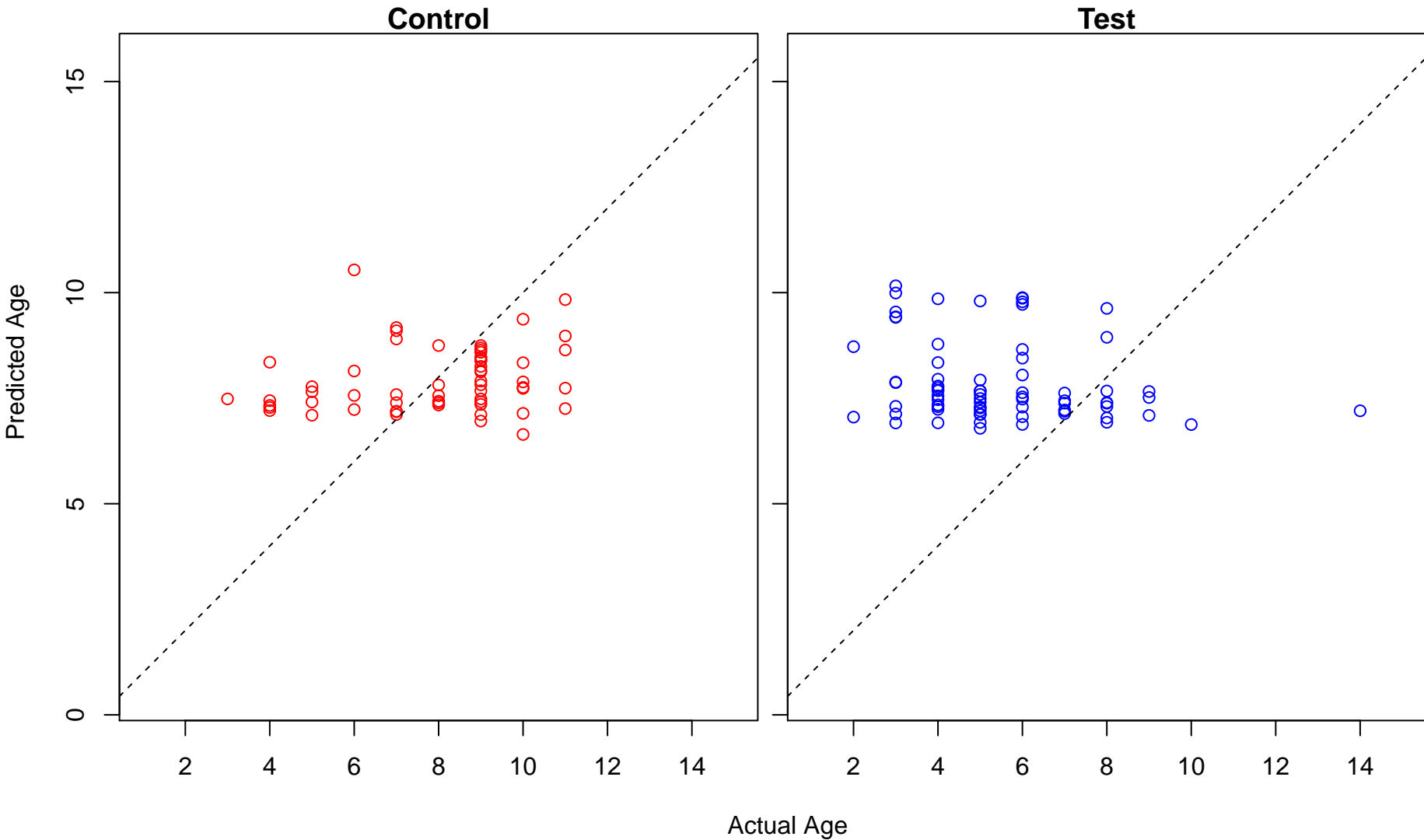
7-methylguanosine cap hypermethylation (Score: 0.252554)



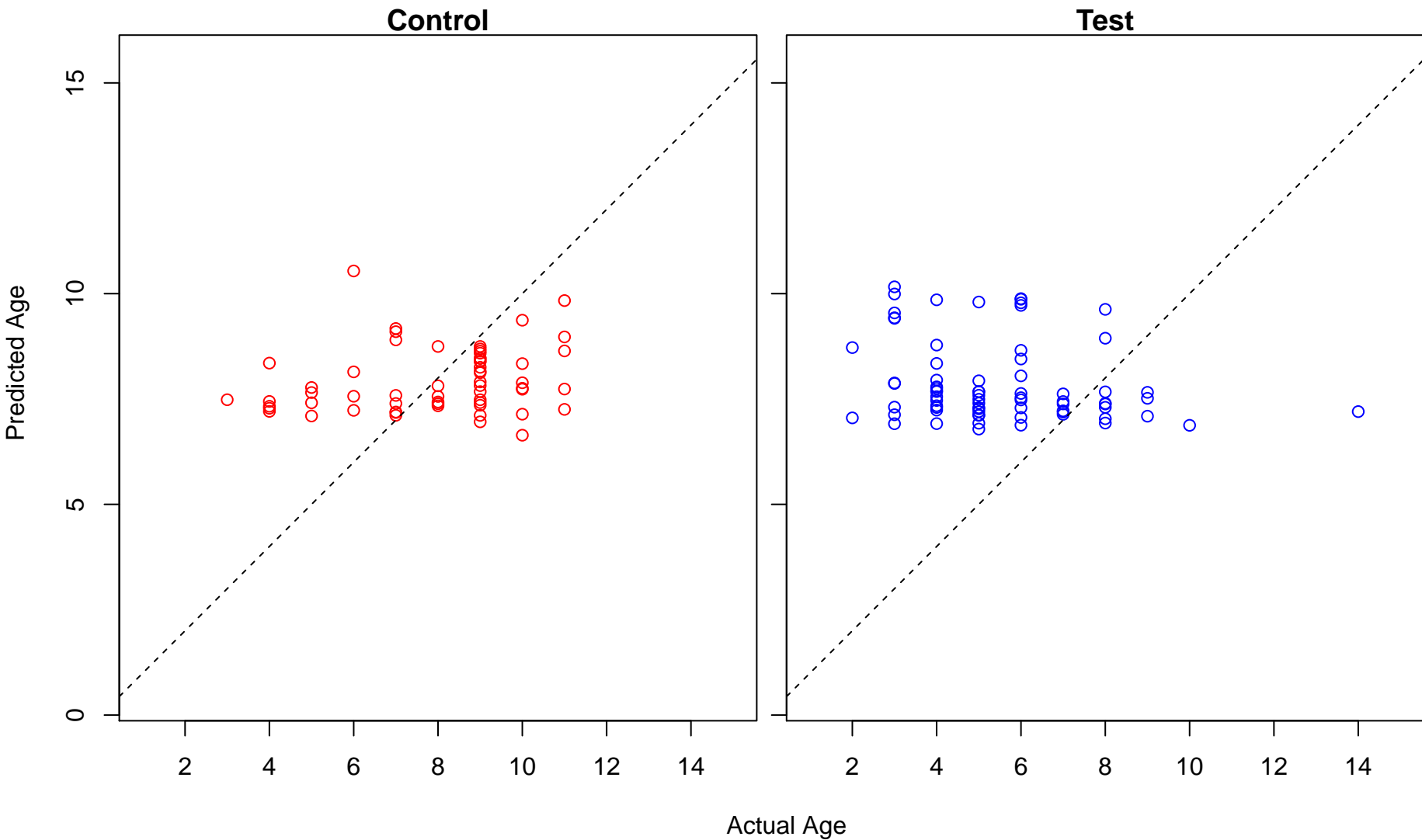
mesenchymal-epithelial cell signaling involved in prostate gland development (Score: 0.252438)



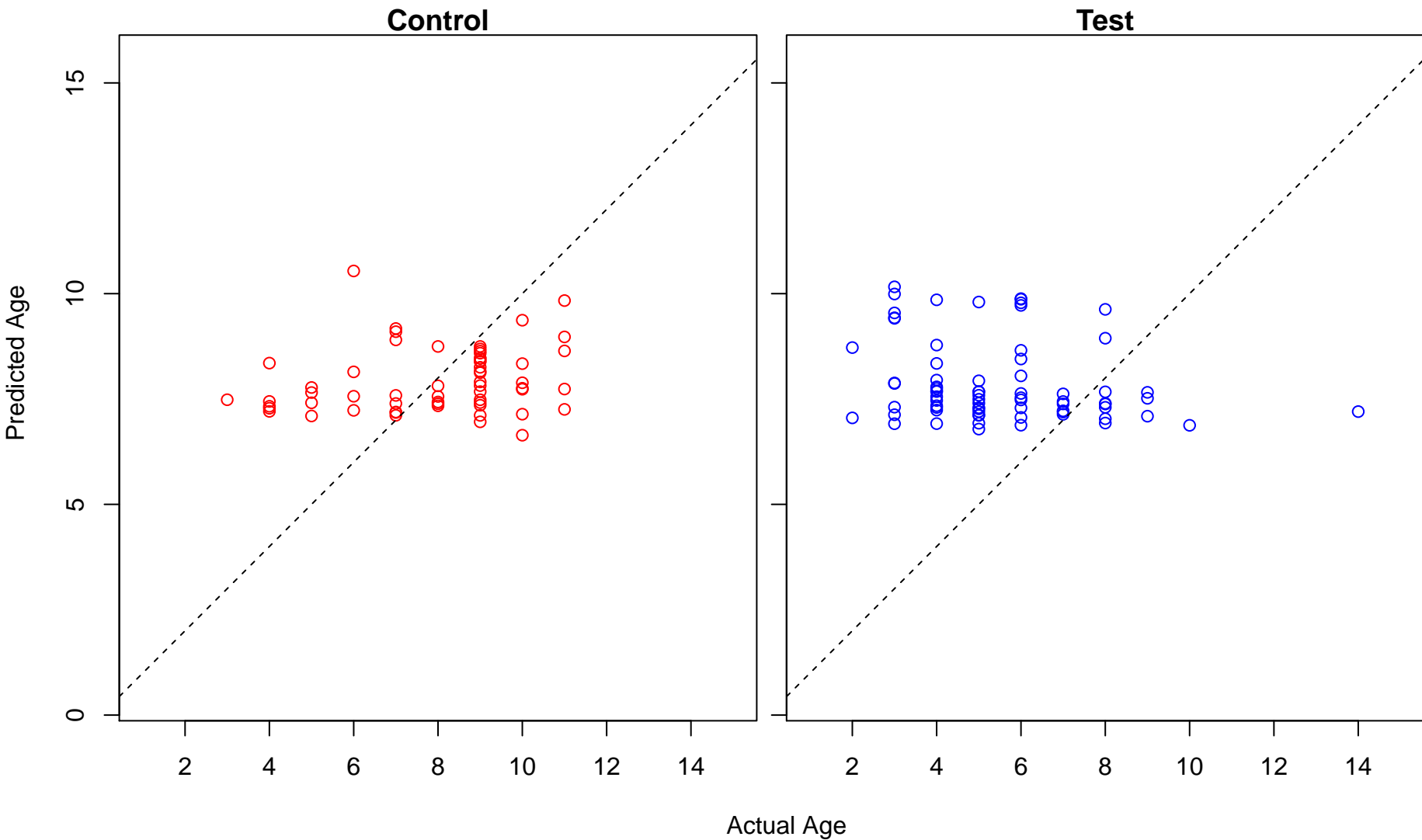
evasion or tolerance of host defenses by virus (Score: 0.252065)



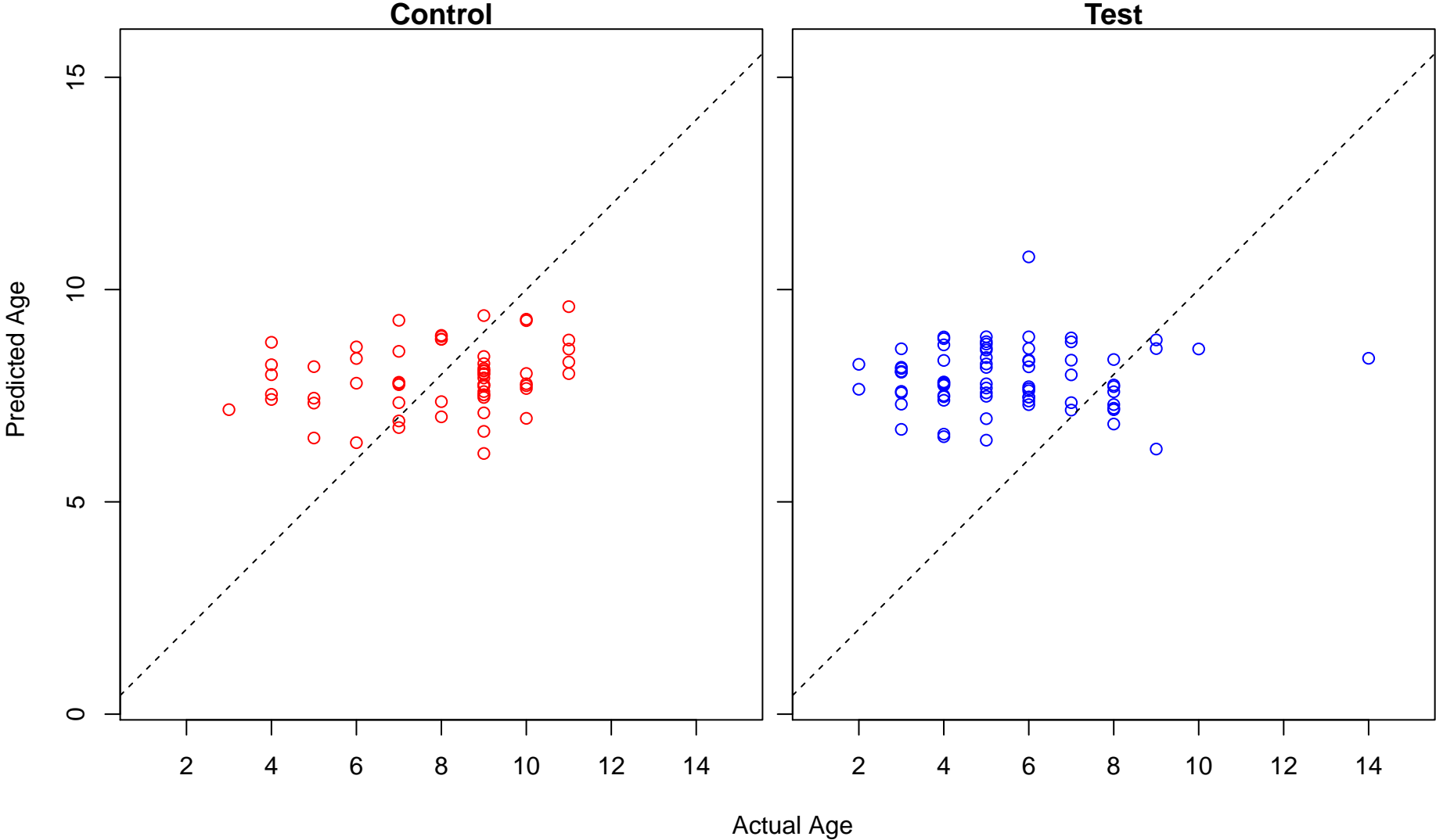
avoidance of host defenses (Score: 0.252065)



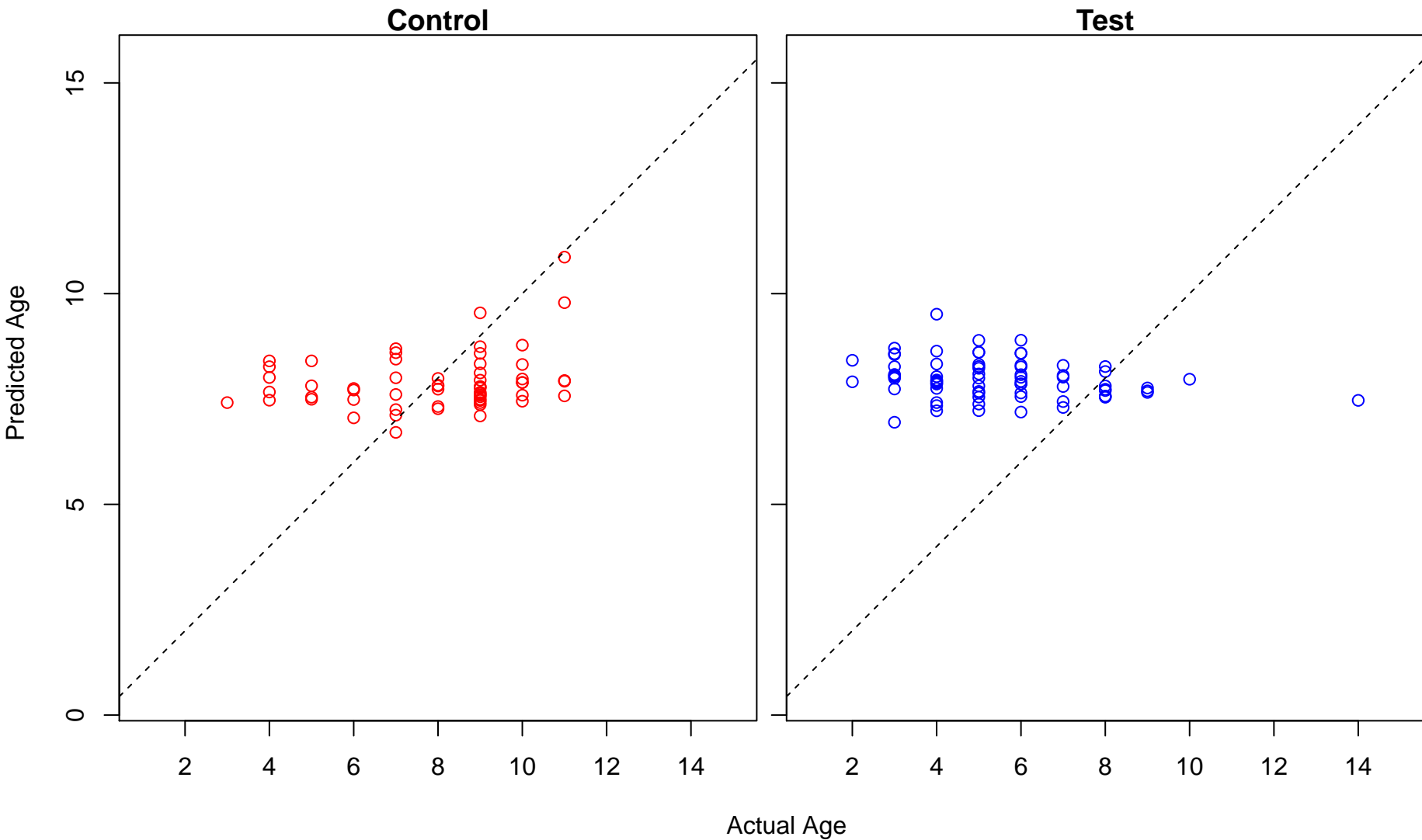
evasion or tolerance of host defenses (Score: 0.252065)



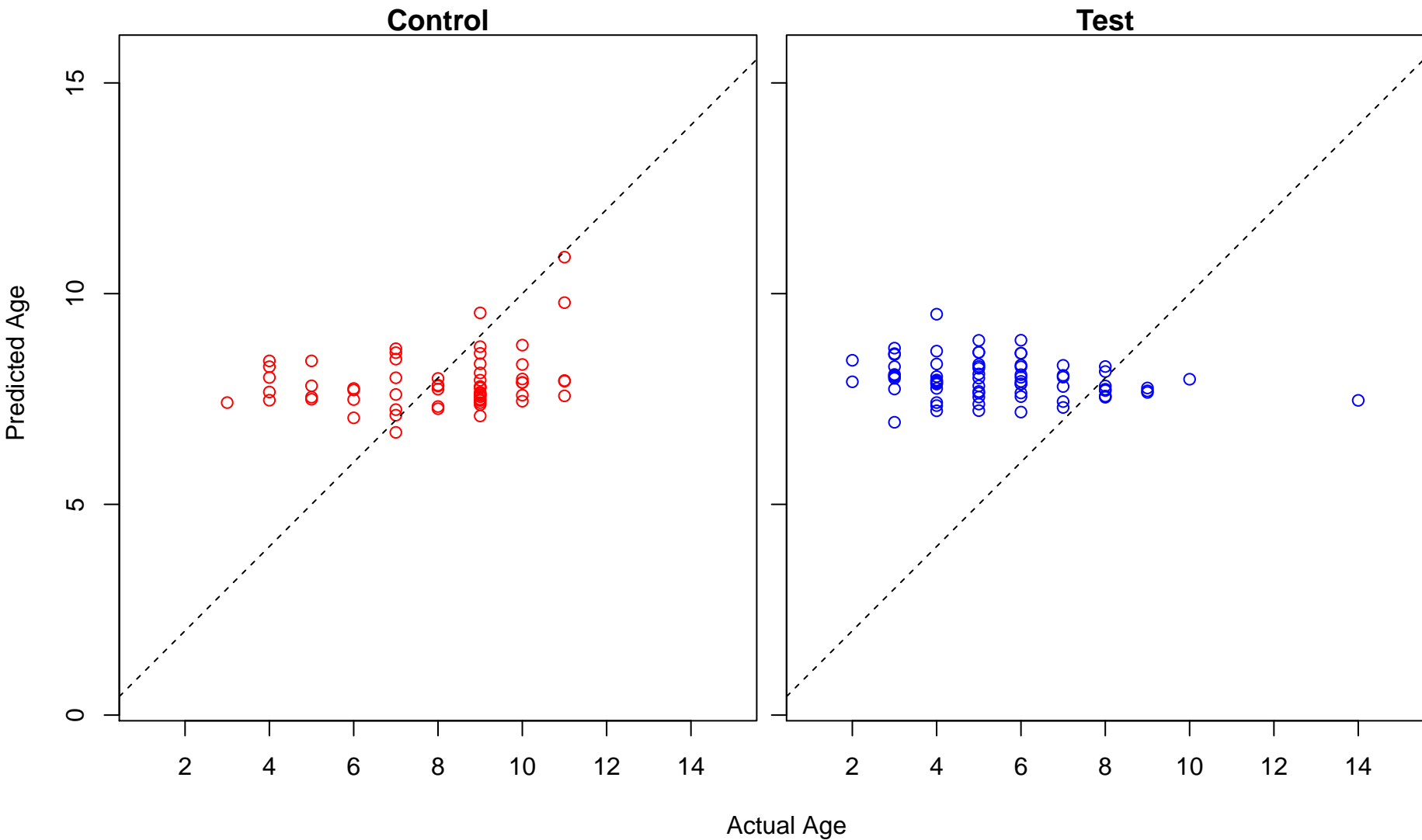
activation of MAPK activity involved in innate immune response (Score: 0.251502)



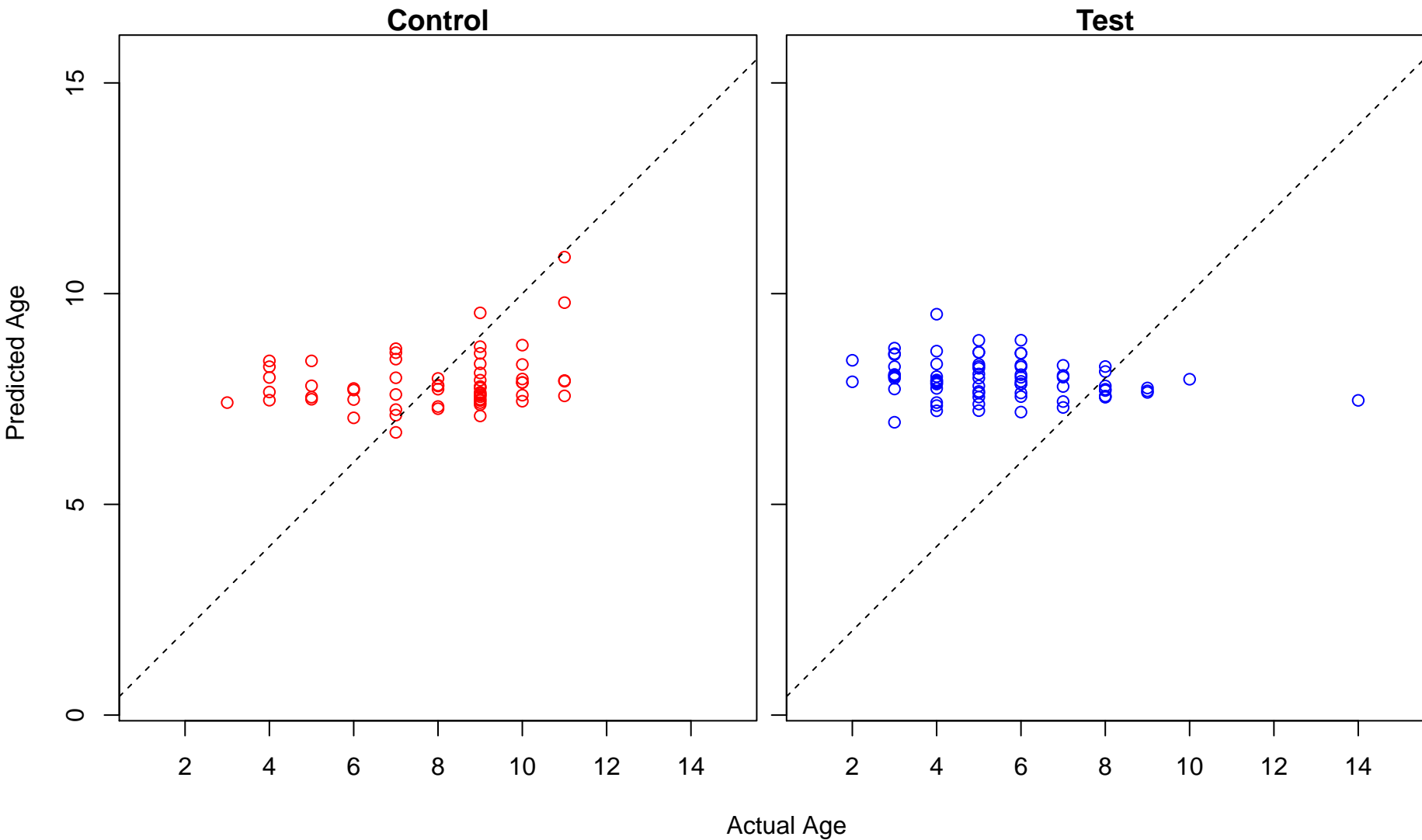
cardiac muscle tissue regeneration (Score: 0.249923)



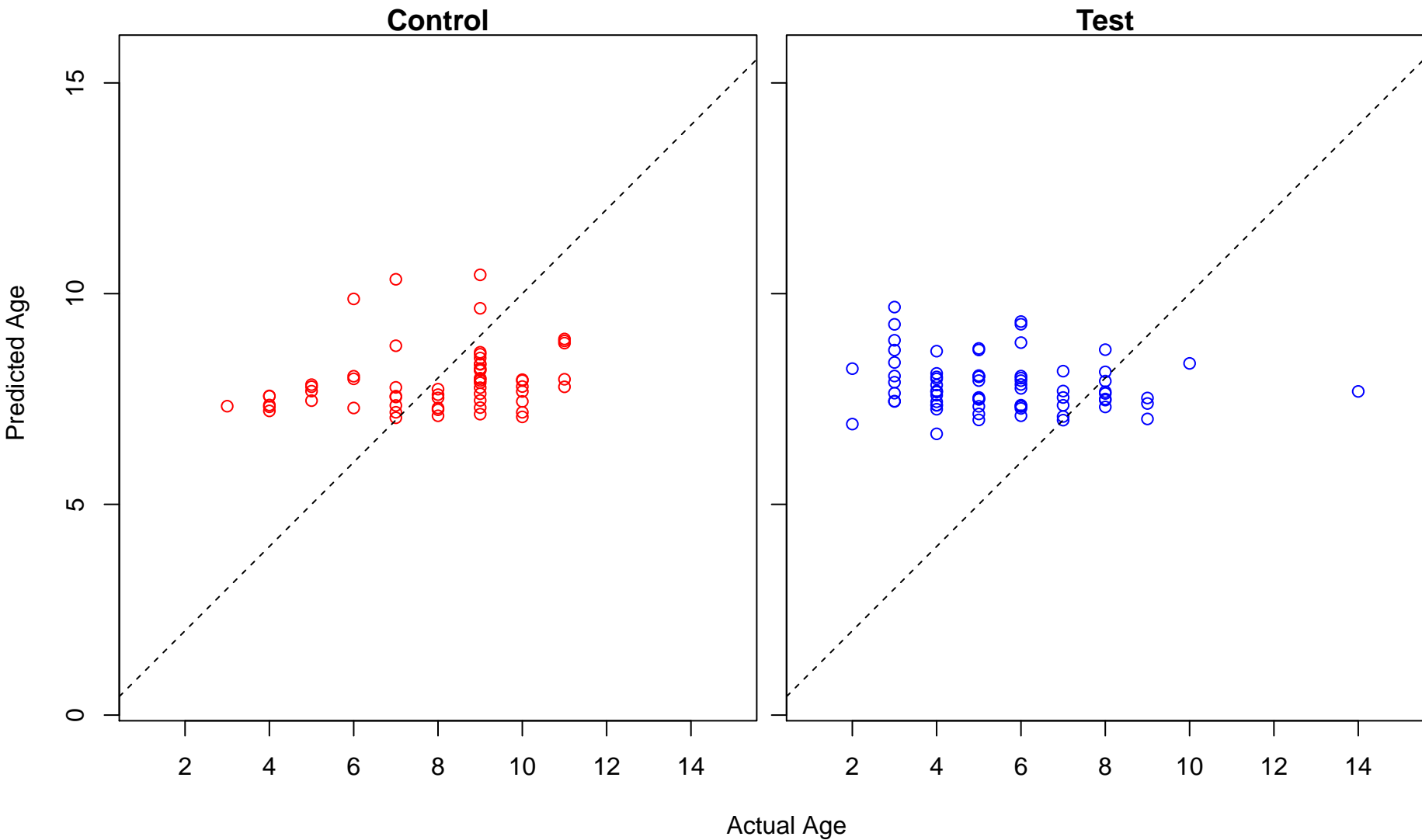
regulation of STAT protein import into nucleus (Score: 0.249923)



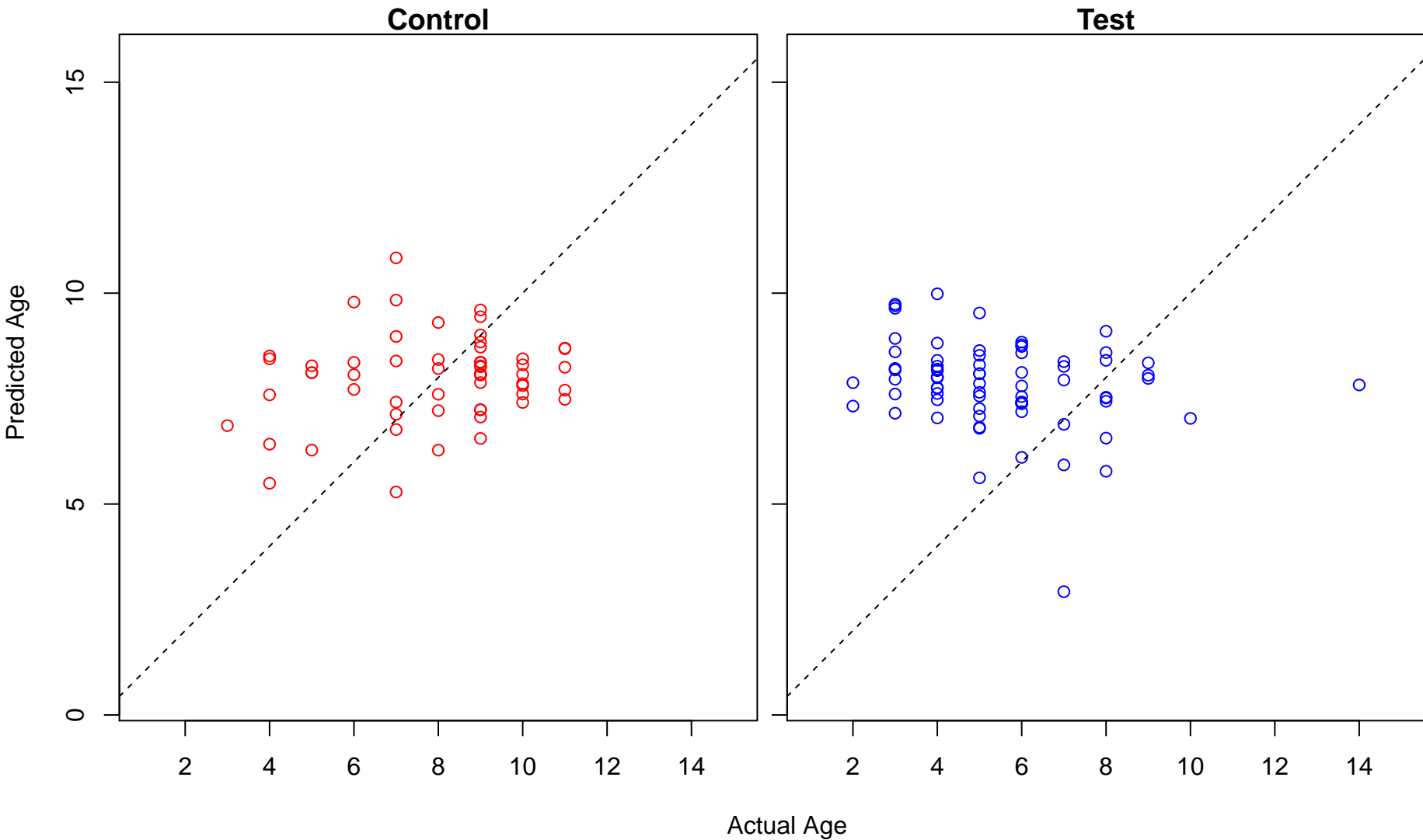
positive regulation of STAT protein import into nucleus (Score: 0.249923)



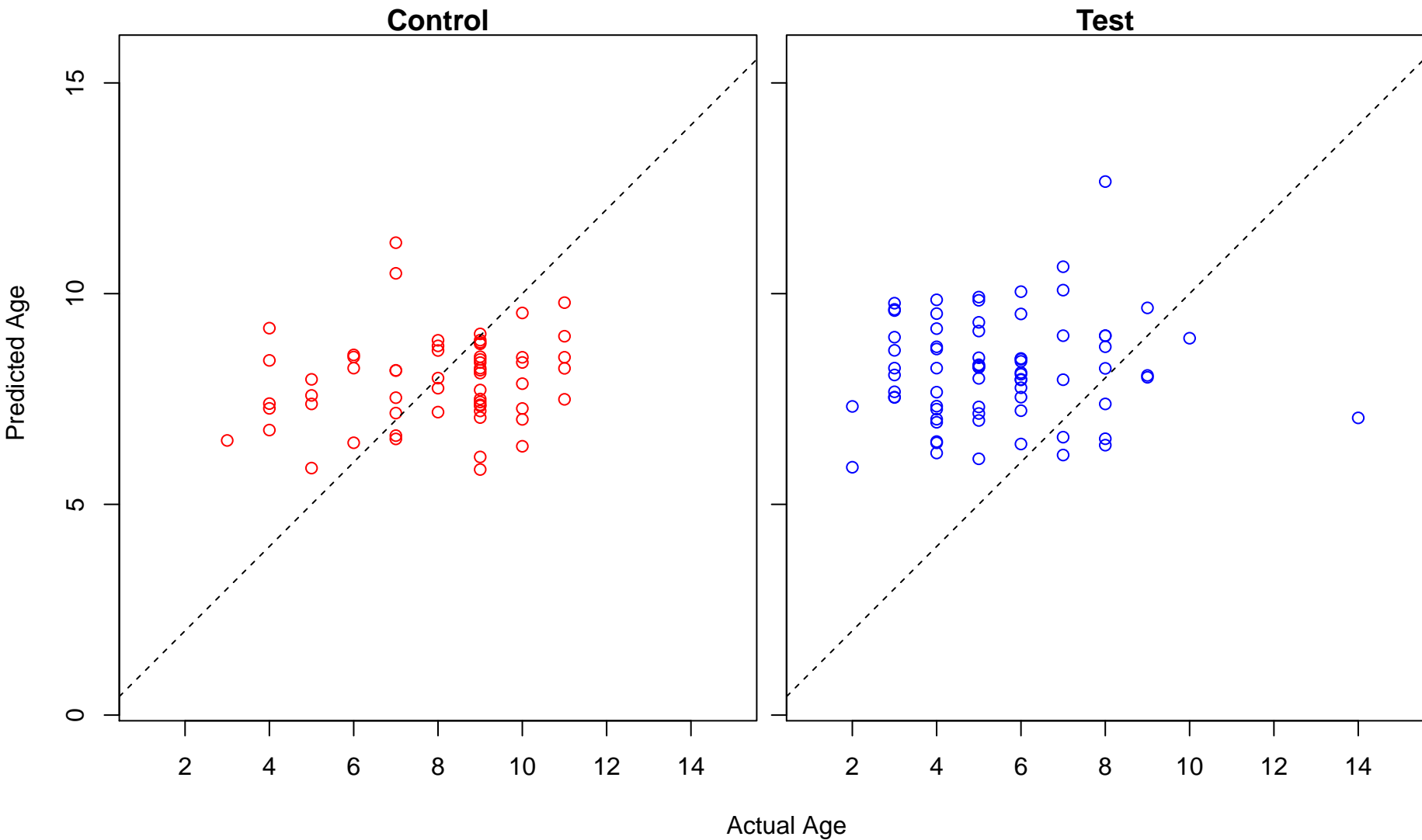
beta-amyloid clearance (Score: 0.249807)



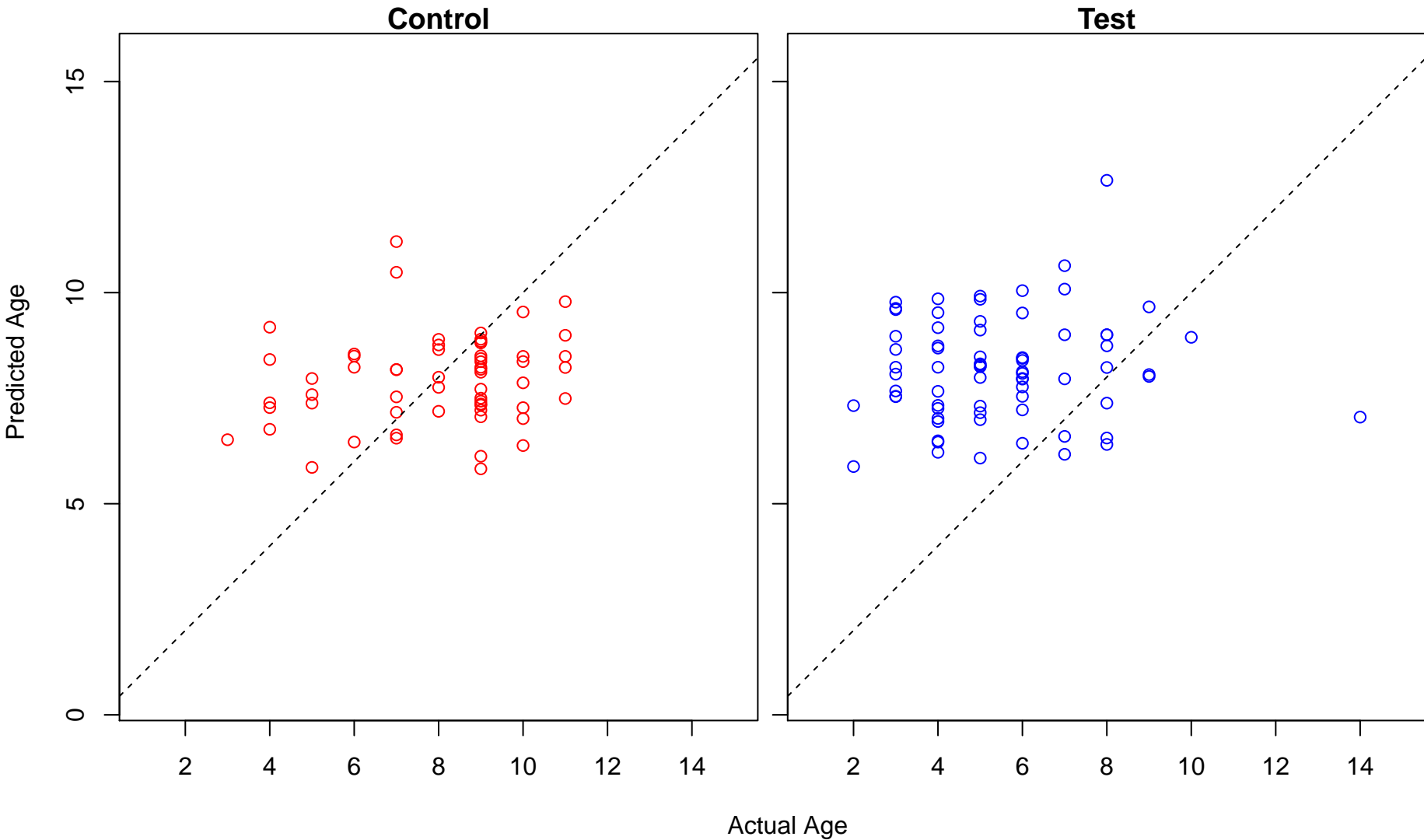
aspartate family amino acid catabolic process (Score: 0.247928)



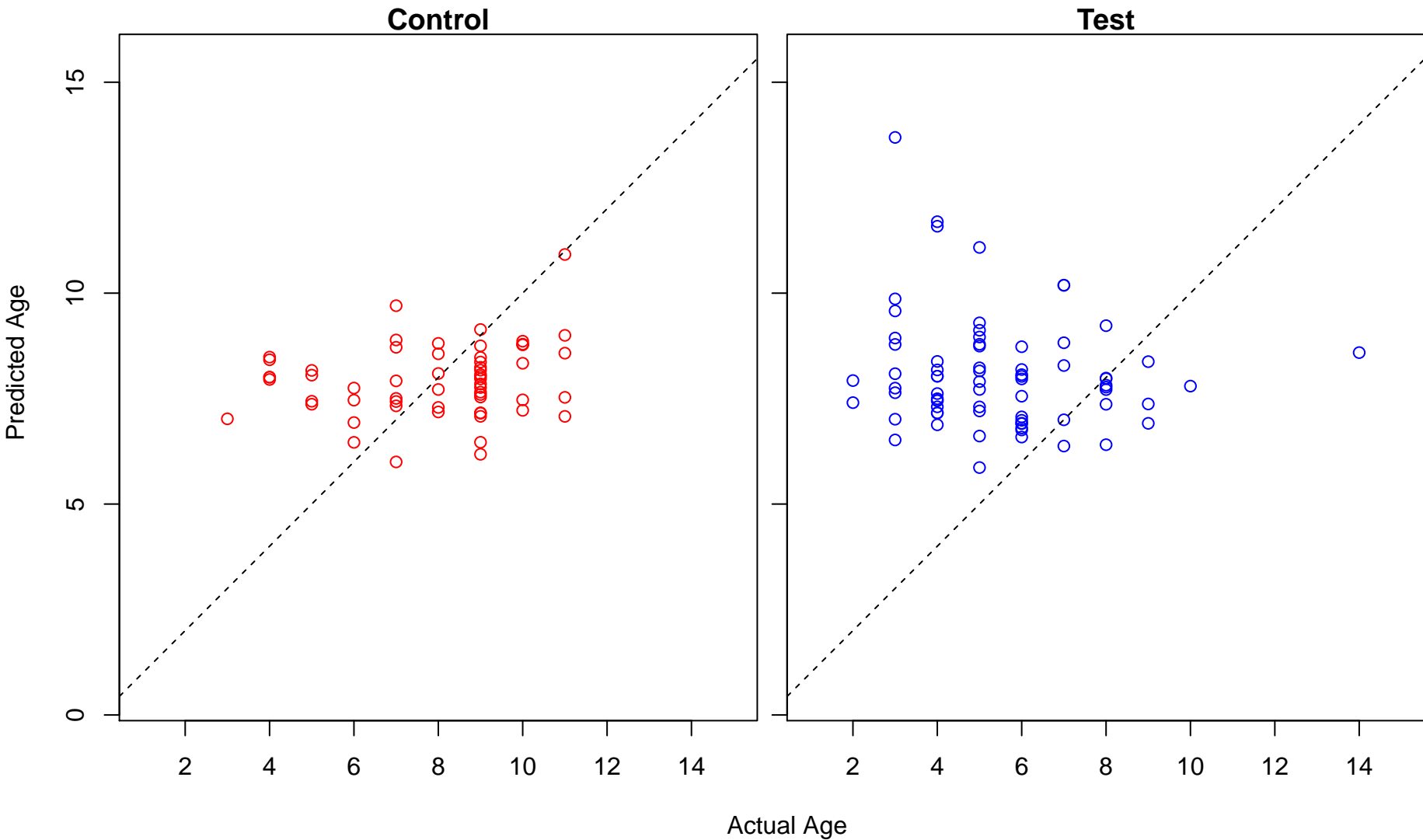
regulation of thyroid hormone generation (Score: 0.246676)



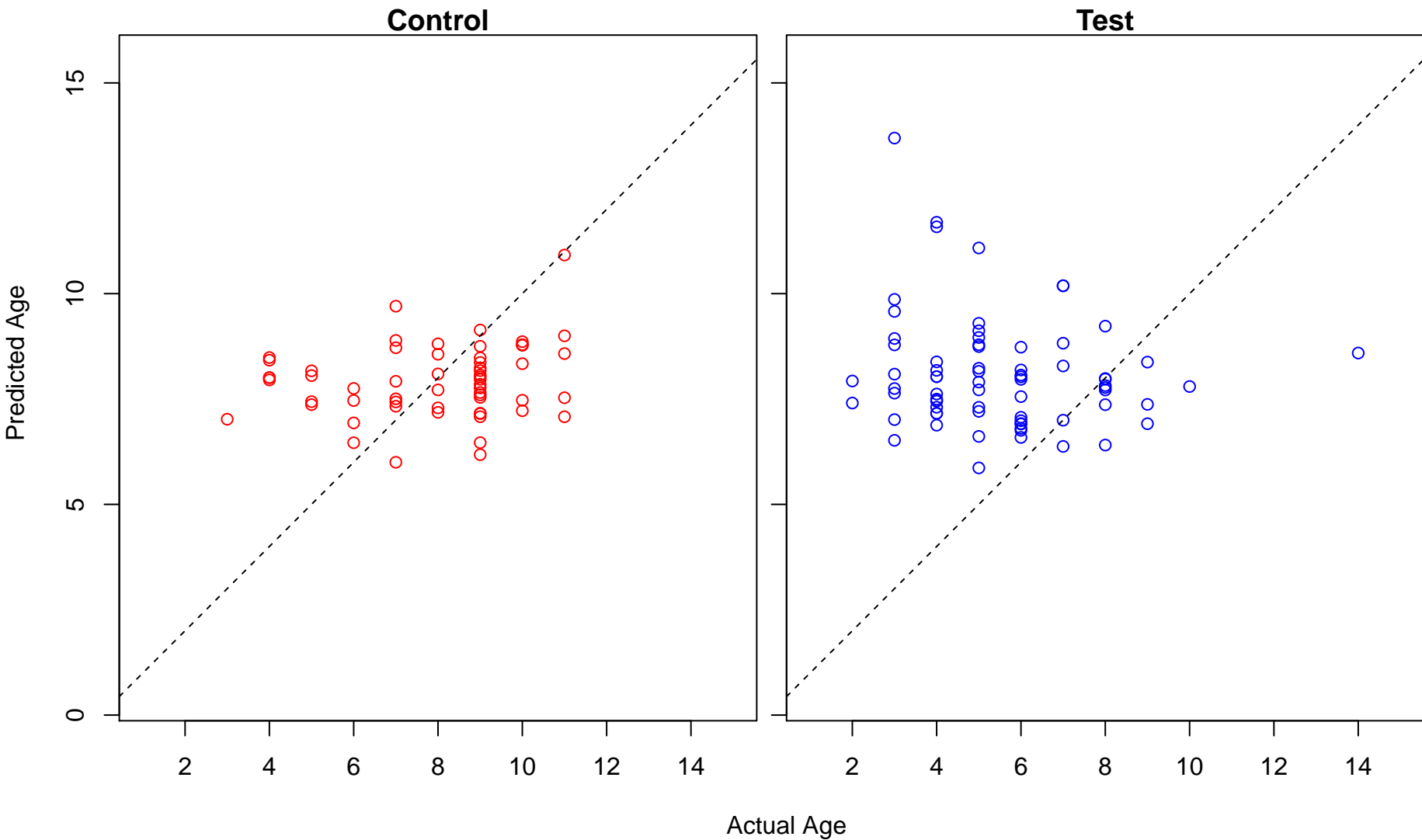
positive regulation of thyroid hormone generation (Score: 0.246676)



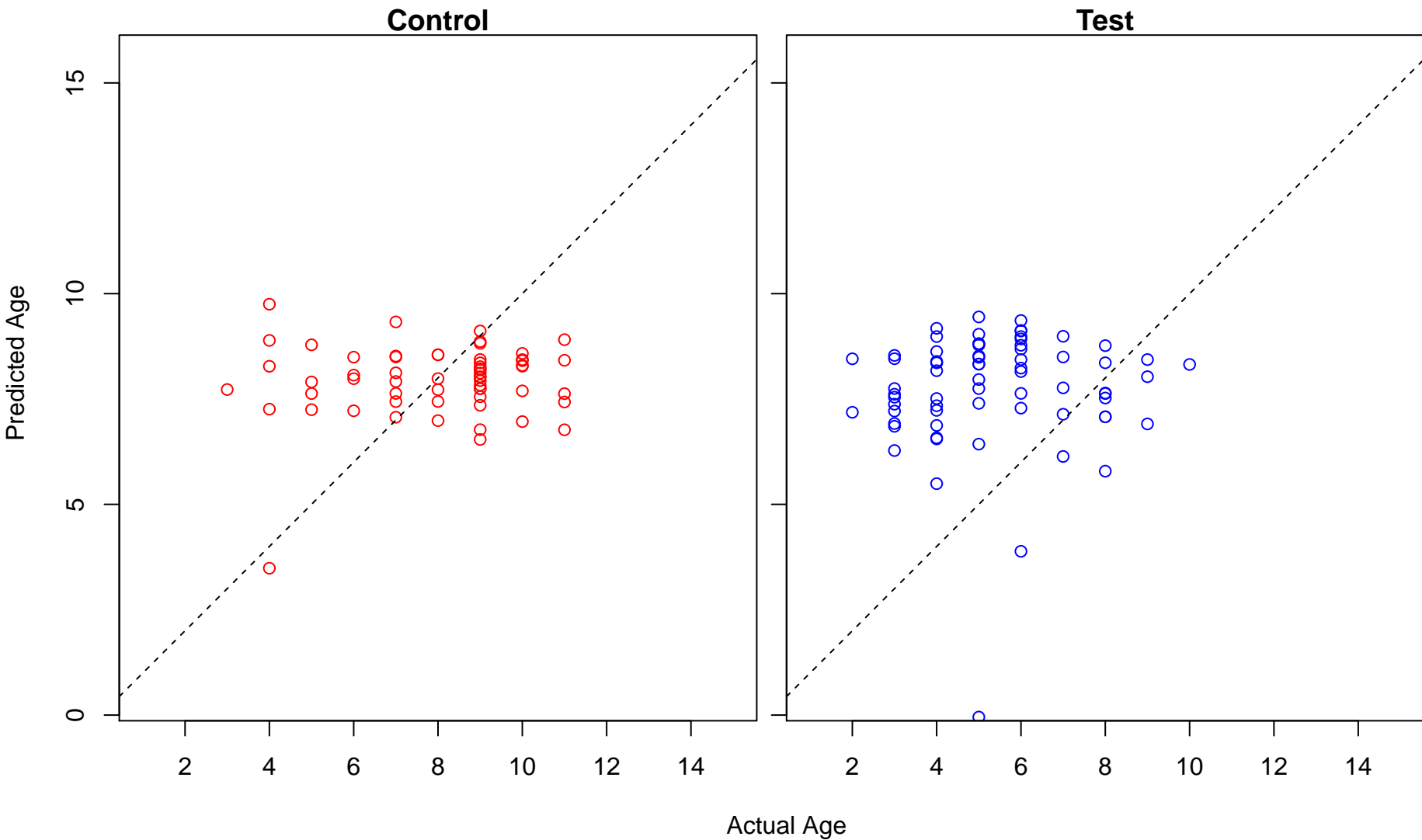
regulation of isotype switching to IgE isotypes (Score: 0.246309)



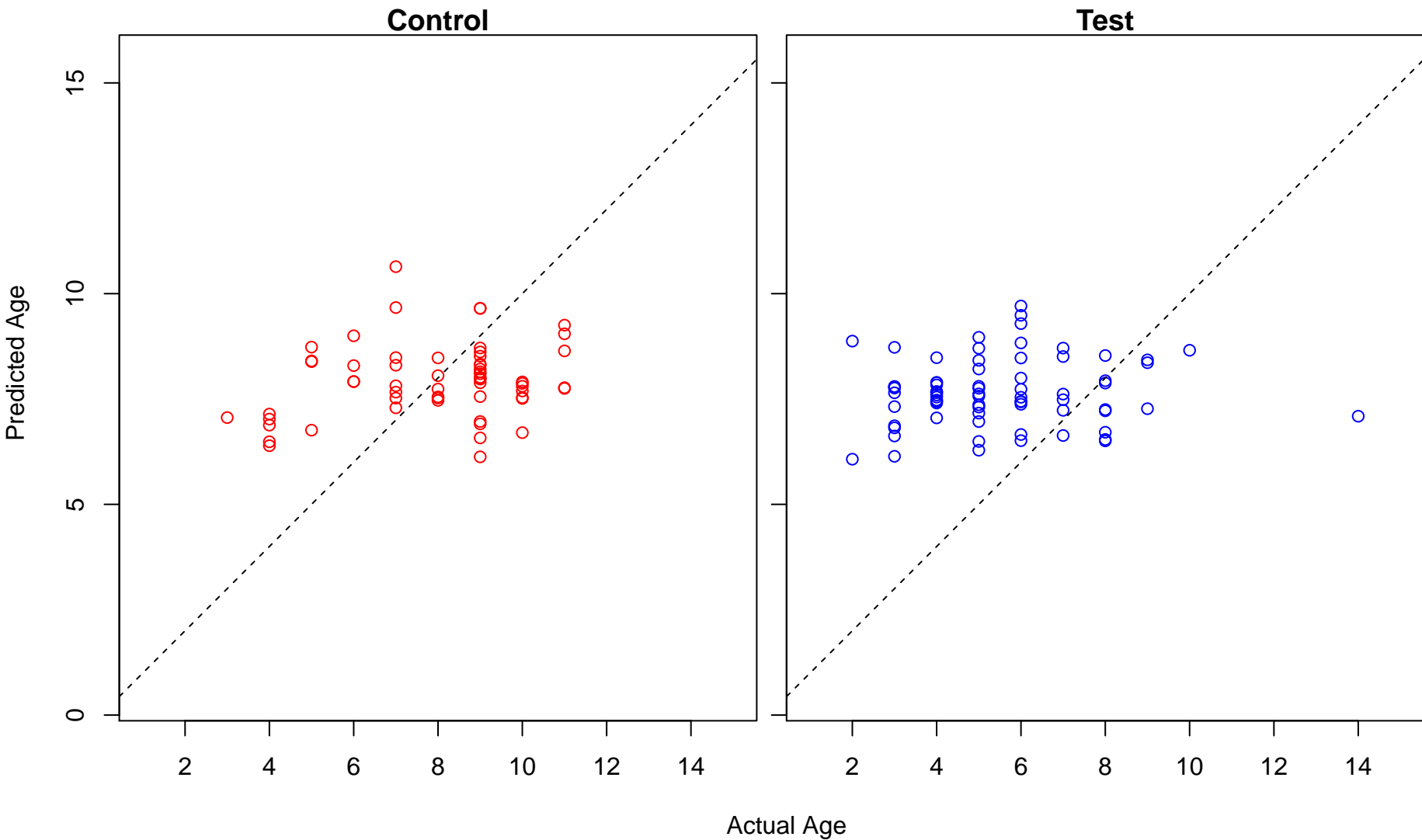
positive regulation of isotype switching to IgE isotypes (Score: 0.246309)



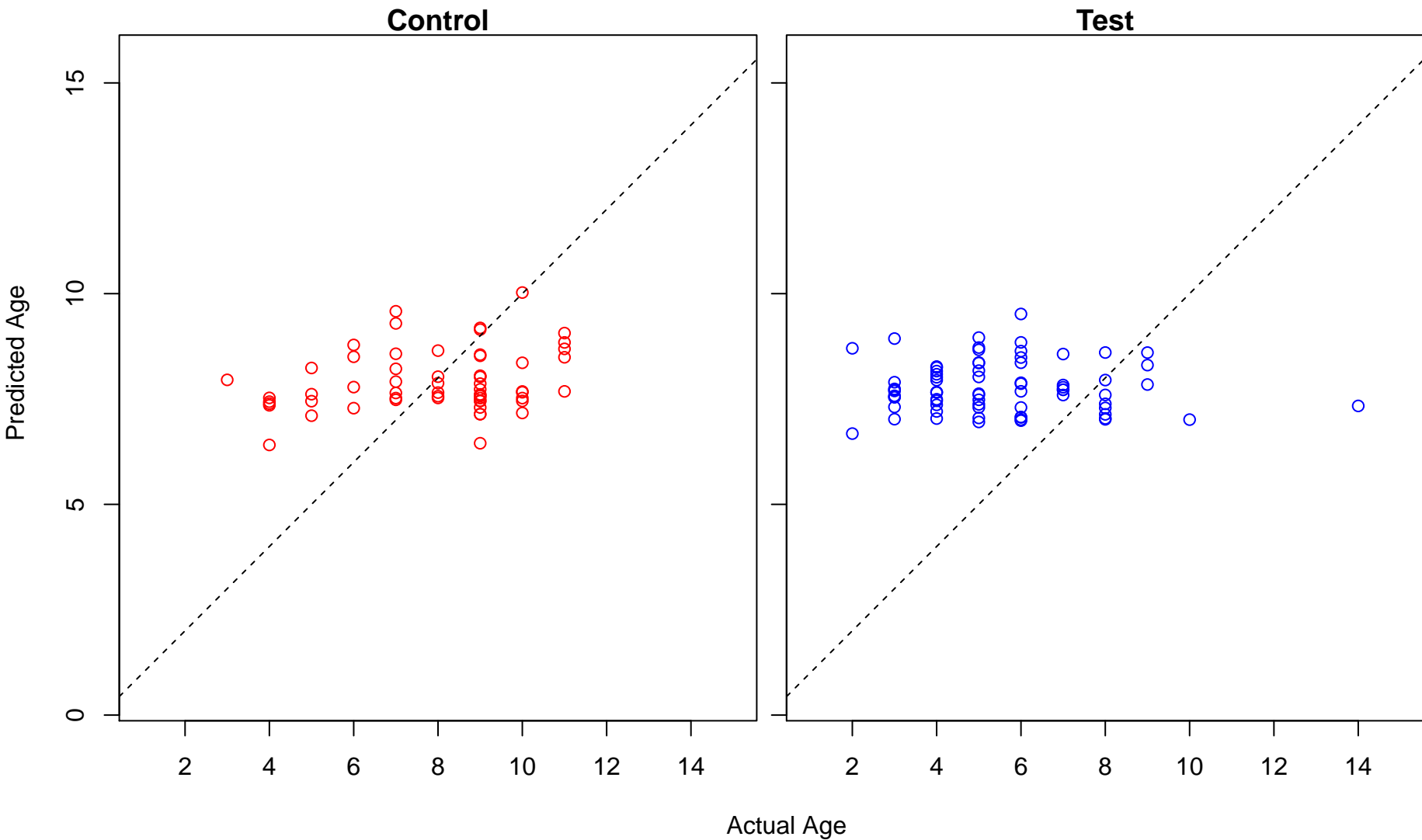
rhombomere 5 development (Score: 0.245321)



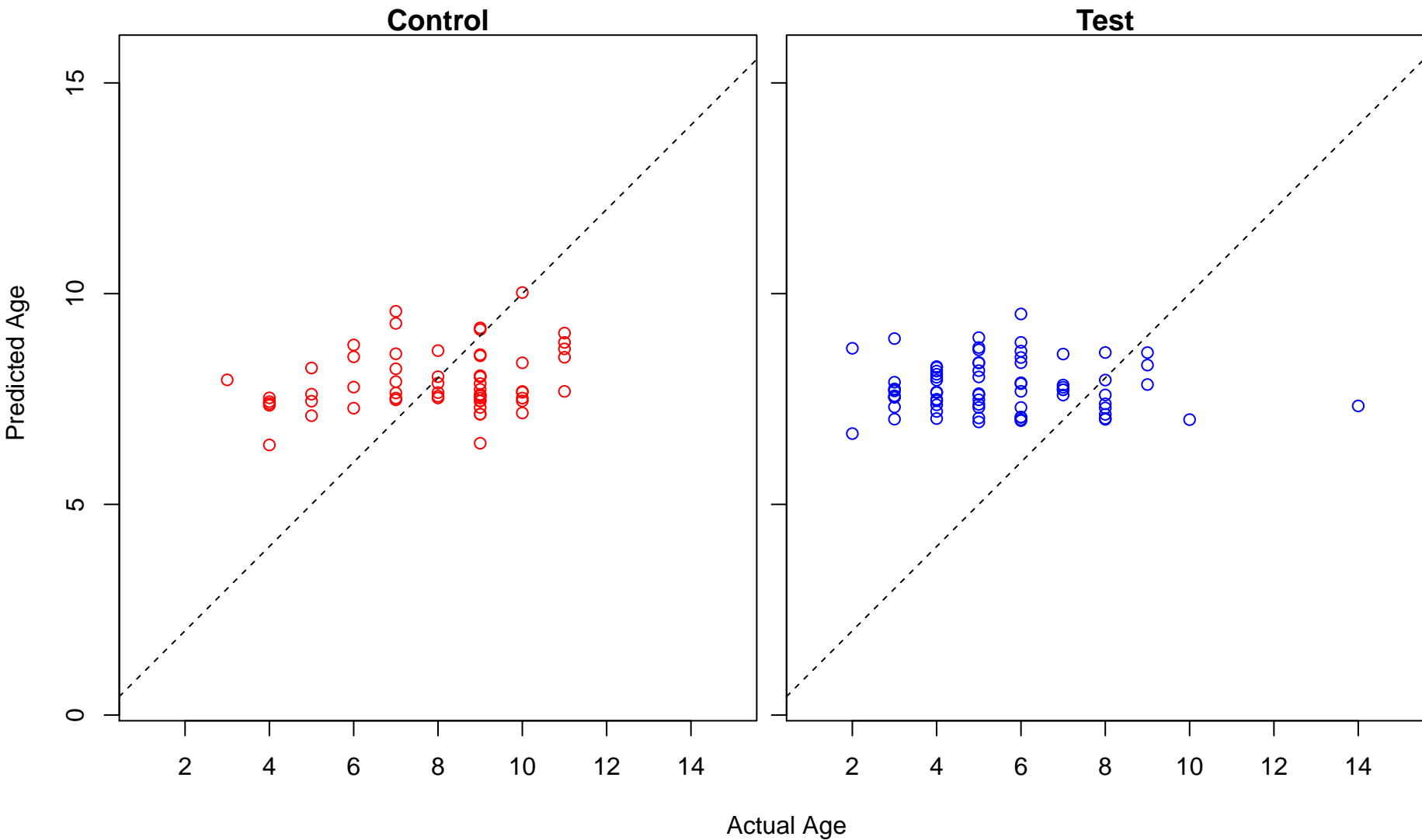
epithelial cell differentiation (Score: 0.244788)



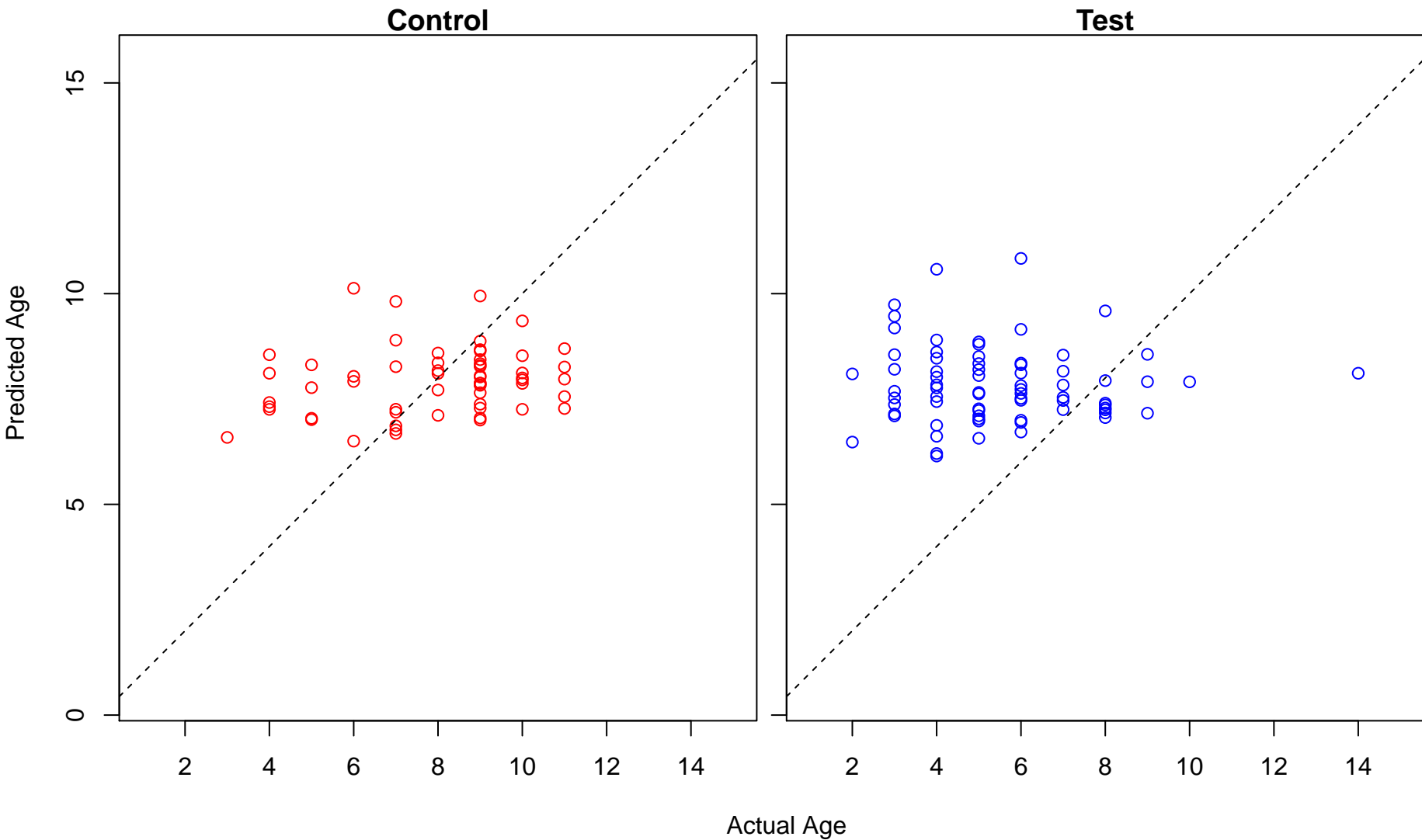
zygote asymmetric cell division (Score: 0.244435)



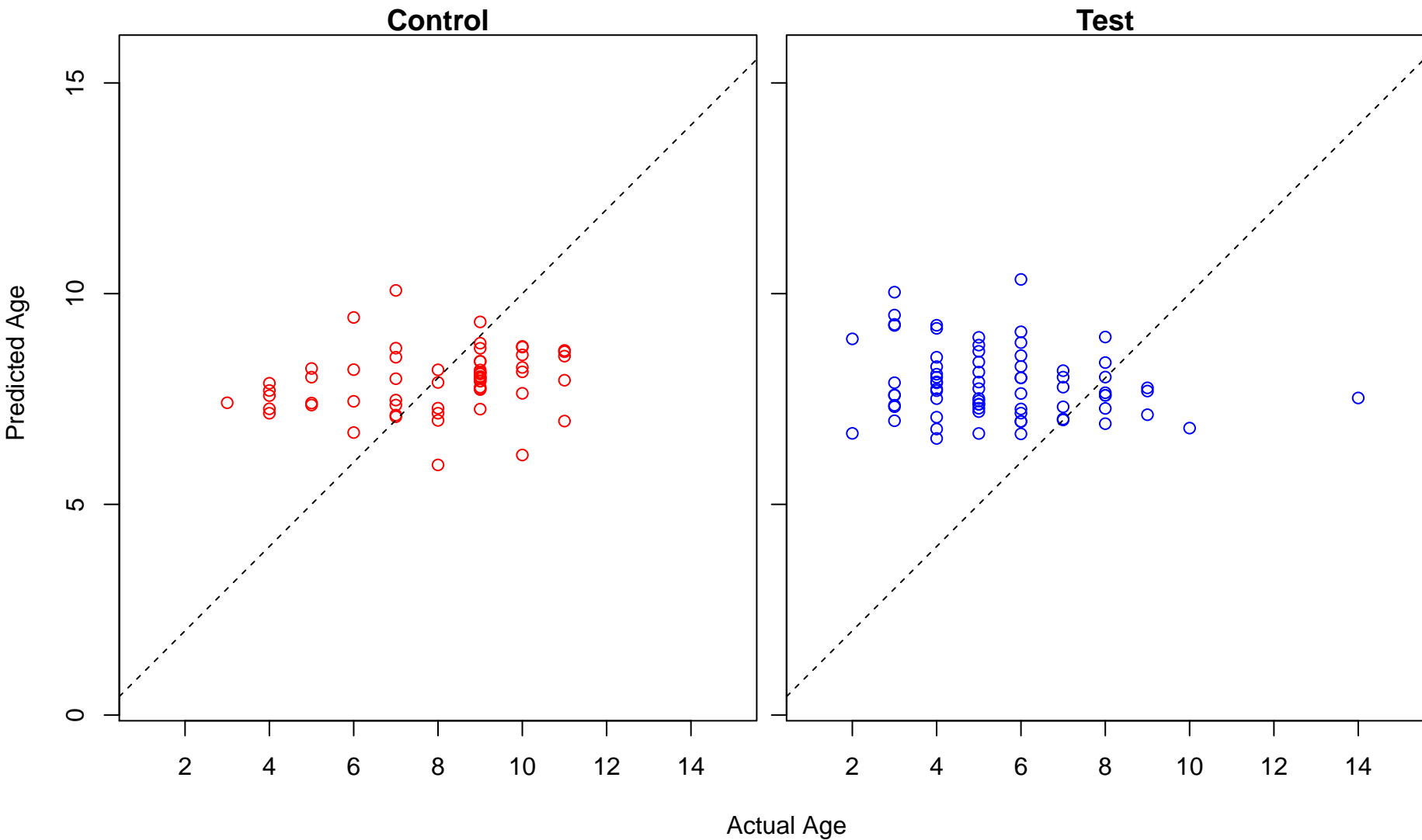
negative regulation of synaptic plasticity (Score: 0.244435)



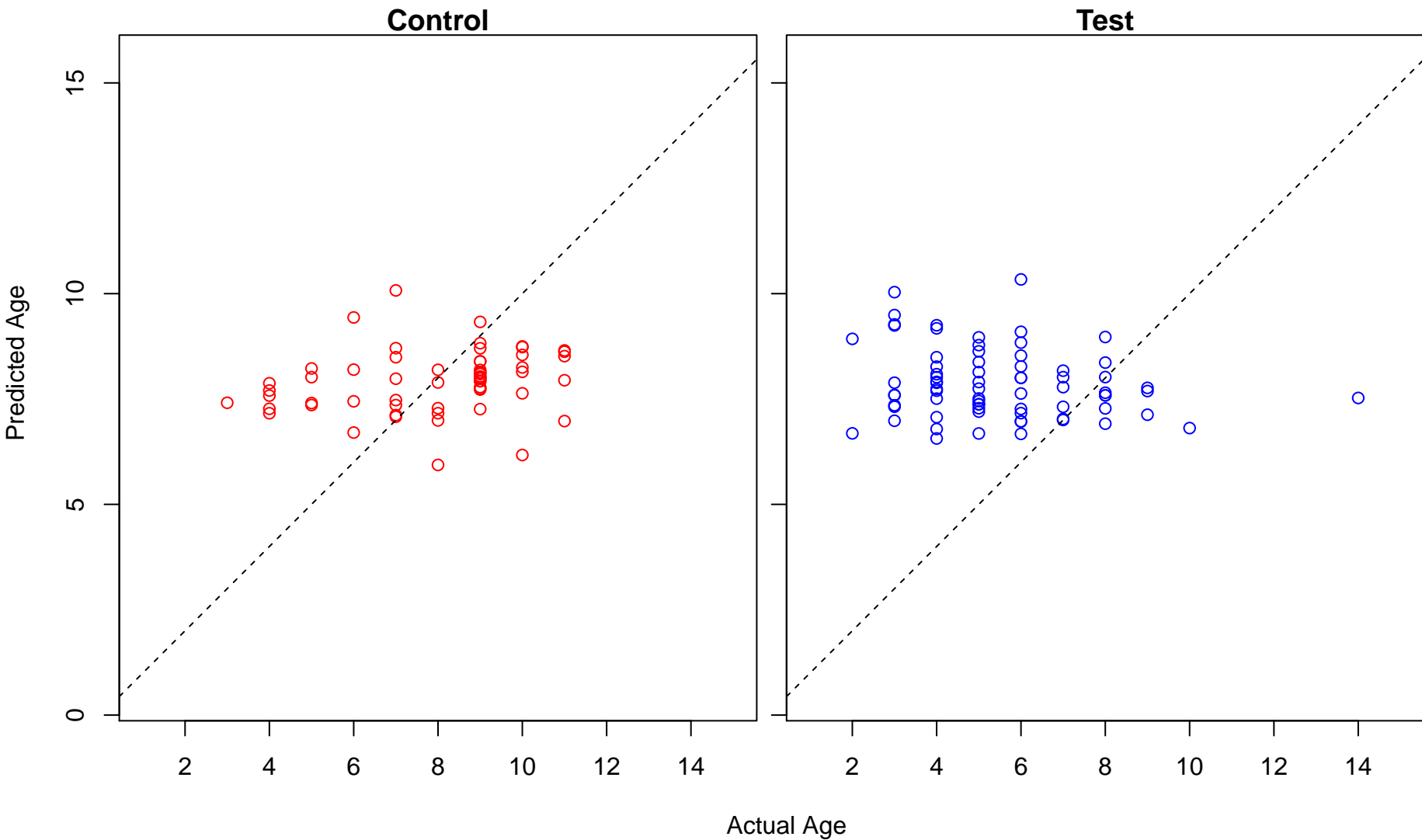
T-helper 2 cell differentiation (Score: 0.243934)



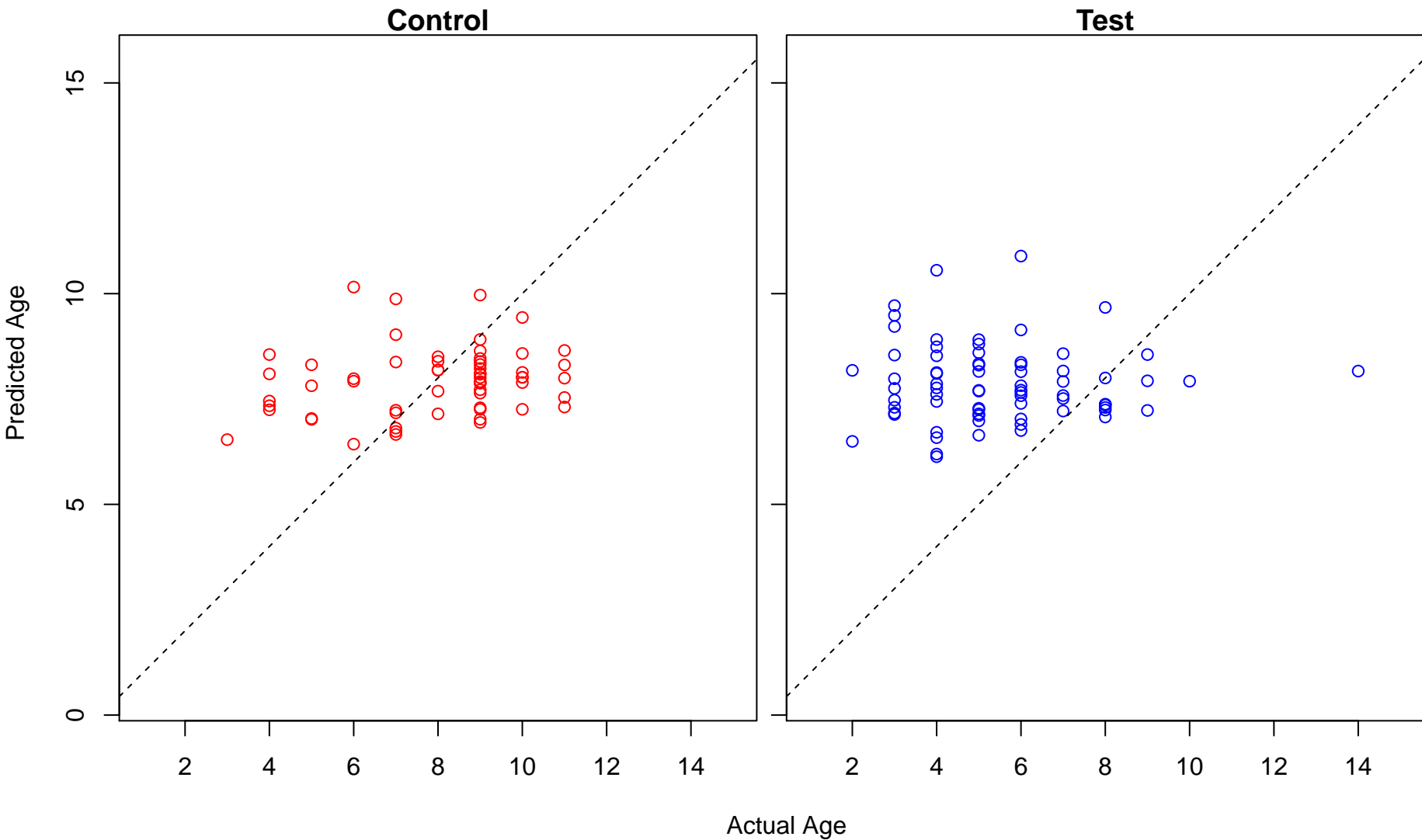
peptide stabilization (Score: 0.241698)



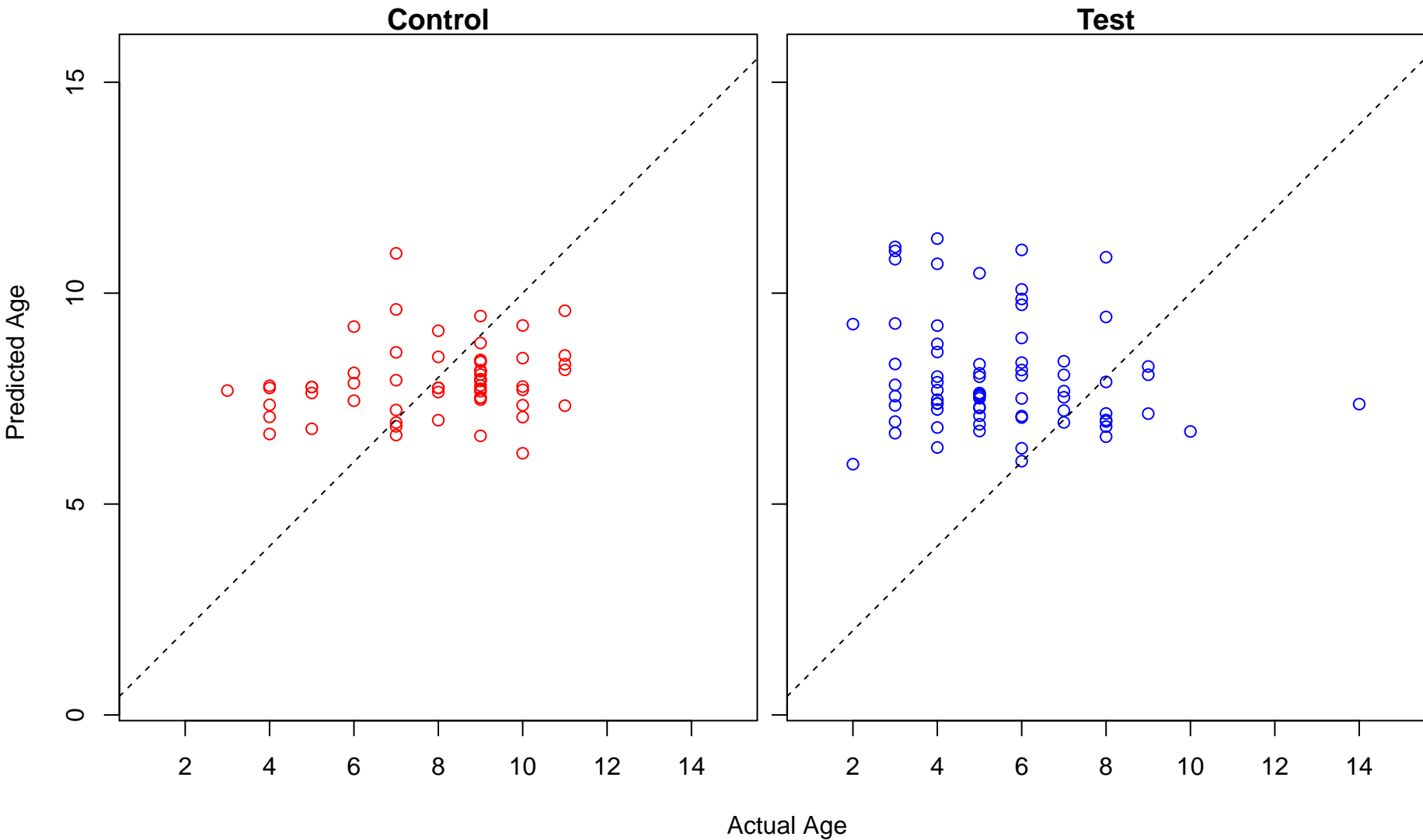
peptide antigen stabilization (Score: 0.241698)



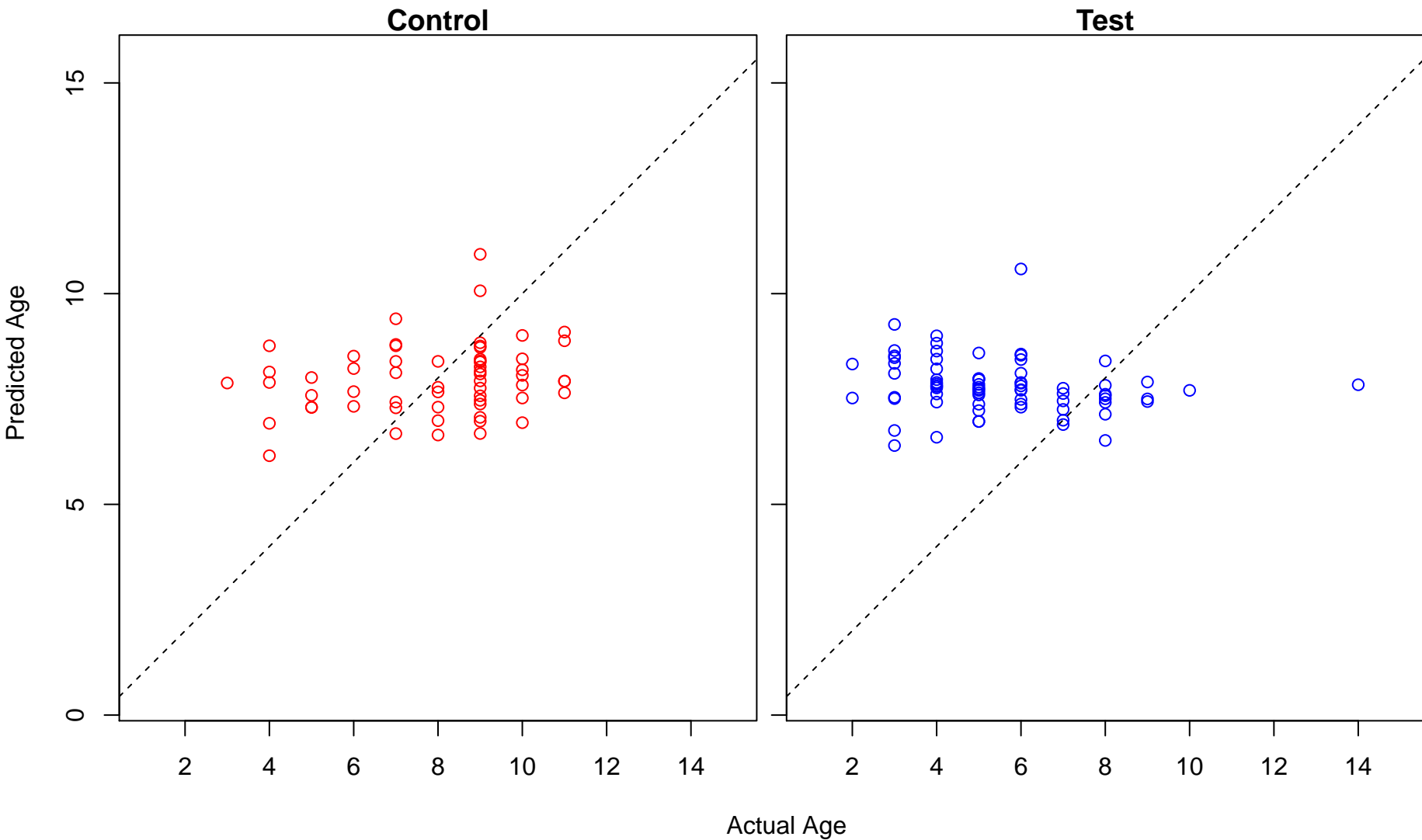
type 2 immune response (Score: 0.241335)



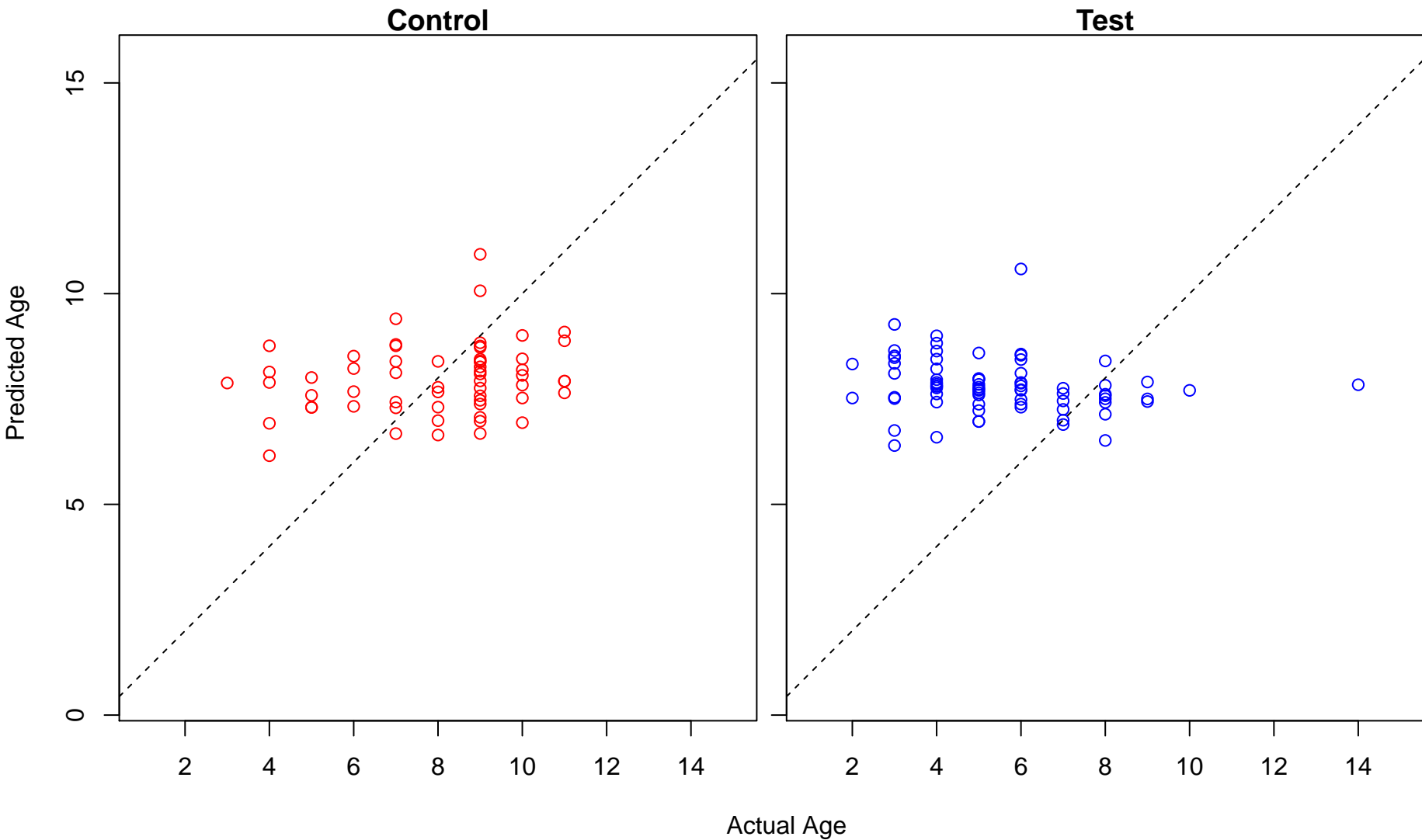
maintenance of protein localization in endoplasmic reticulum (Score: 0.241075)



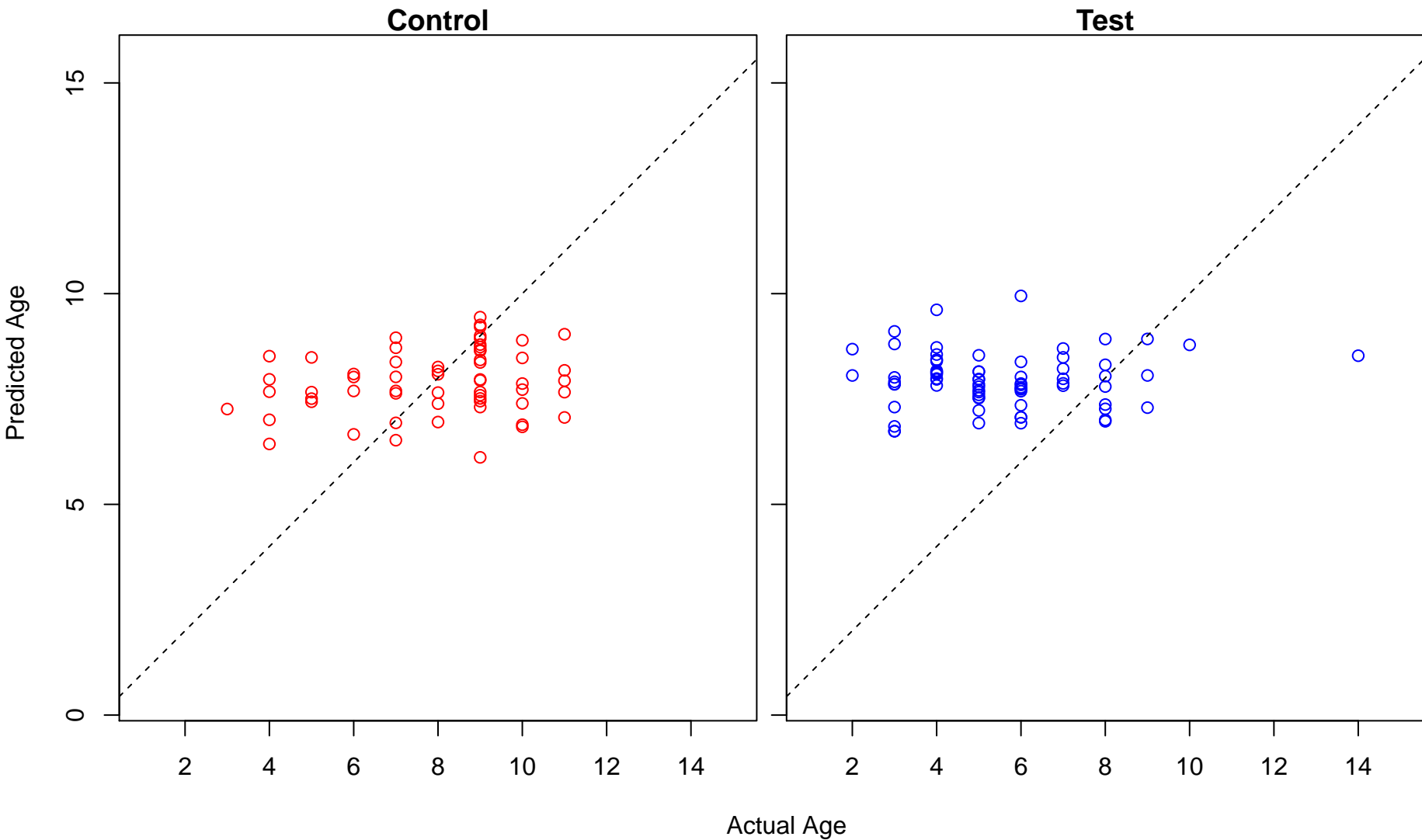
negative regulation of translation in response to oxidative stress (Score: 0.239900)



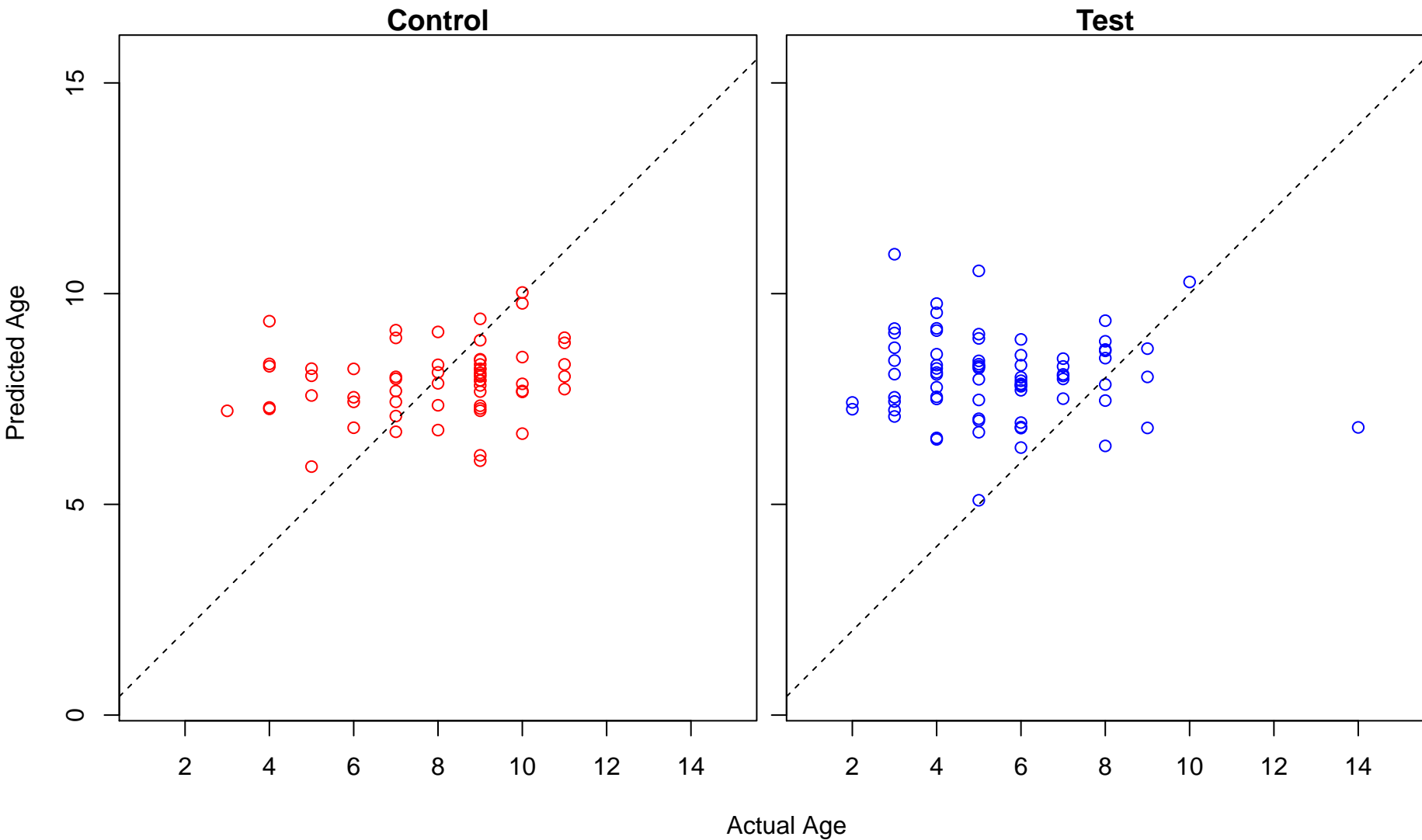
regulation of translation in response to oxidative stress (Score: 0.239900)



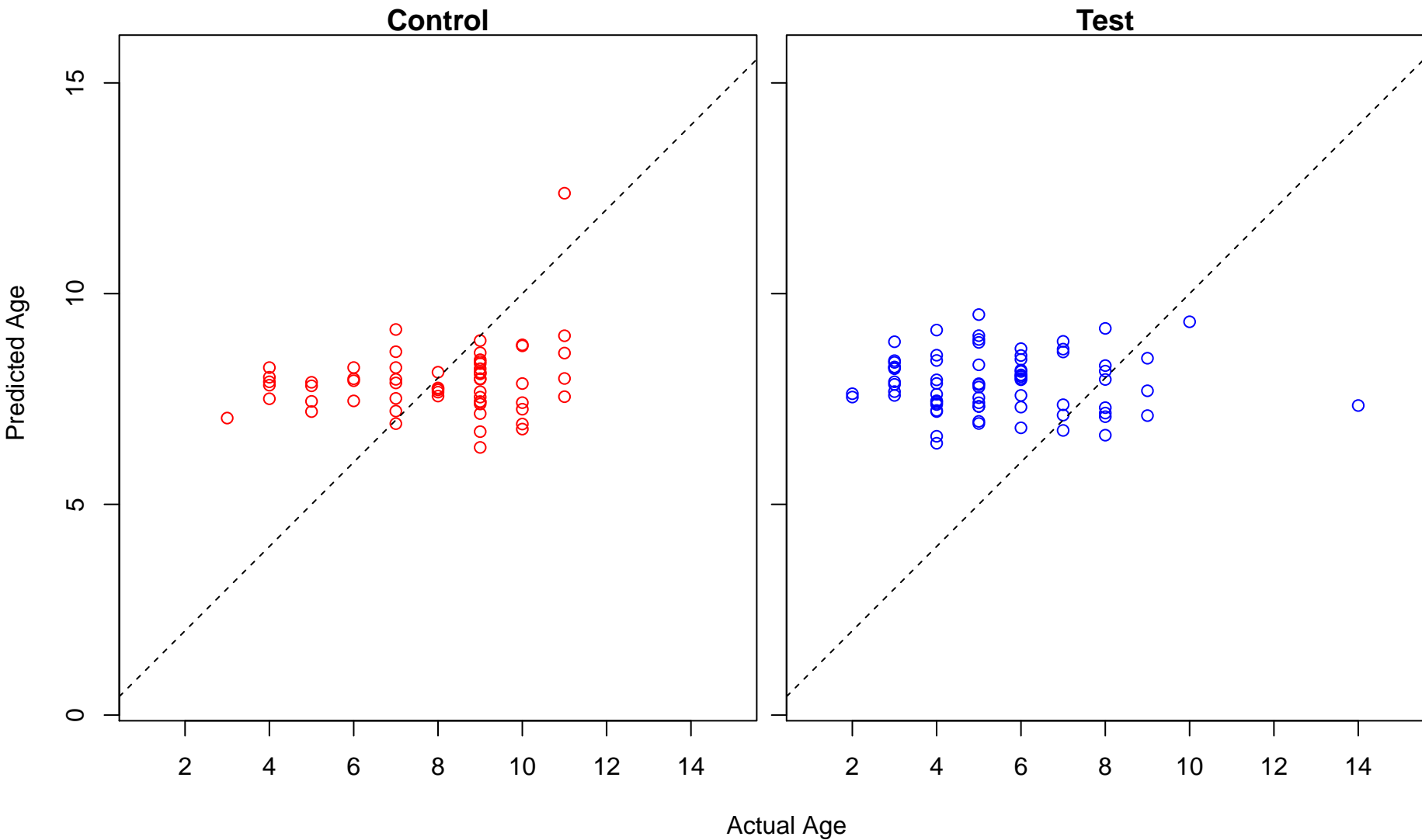
negative regulation of protein ADP-ribosylation (Score: 0.235551)



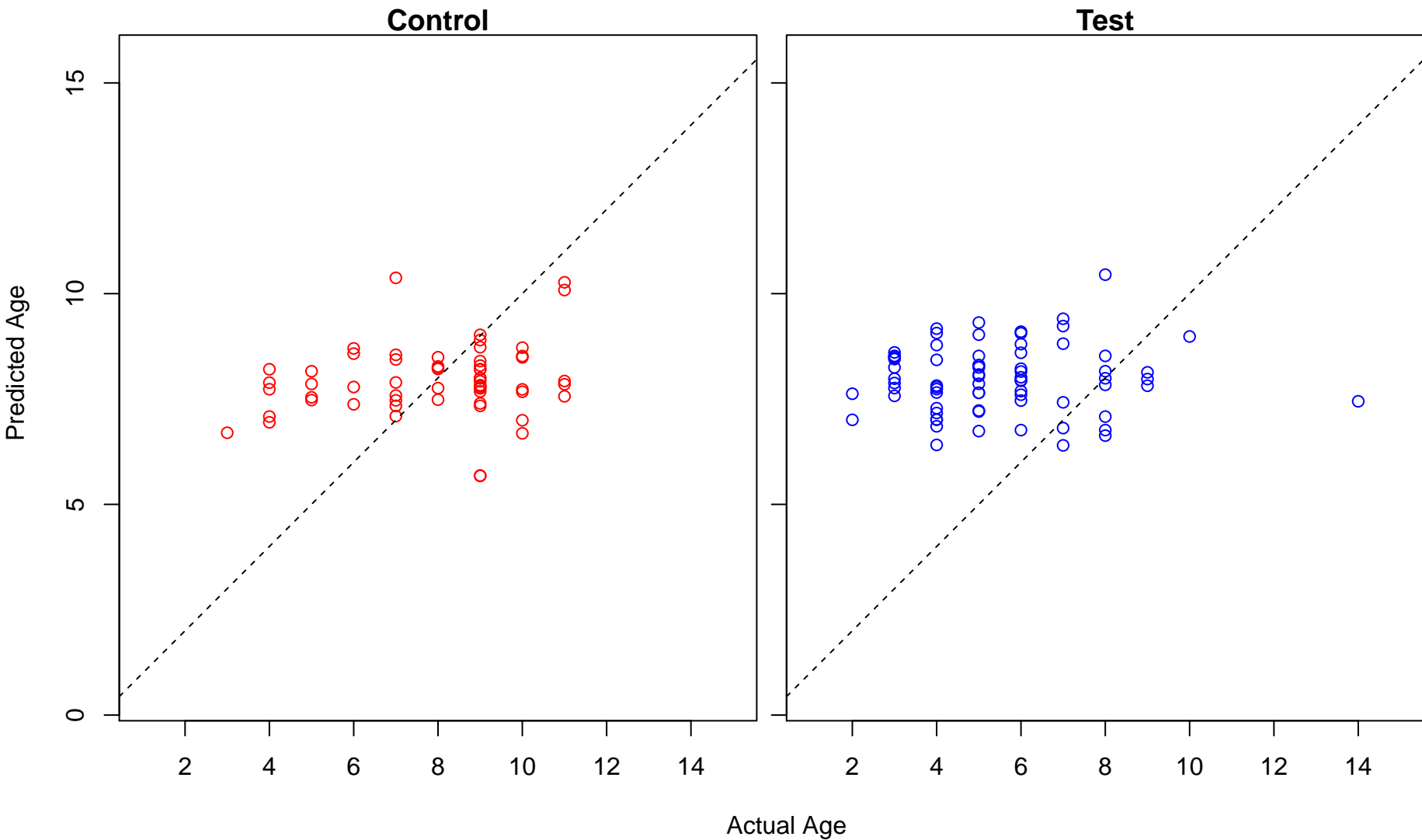
NADH oxidation (Score: 0.235025)



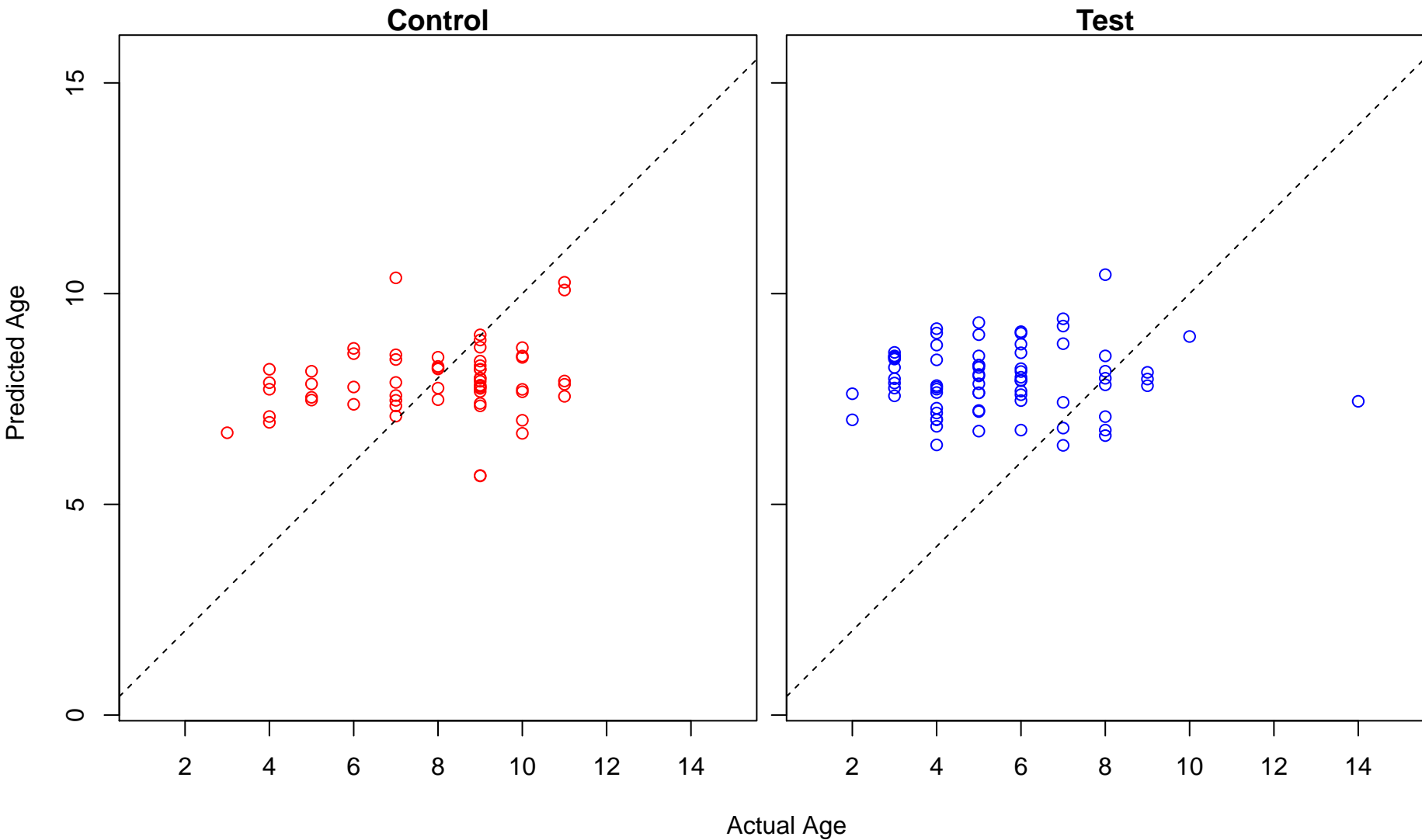
comma-shaped body morphogenesis (Score: 0.233864)



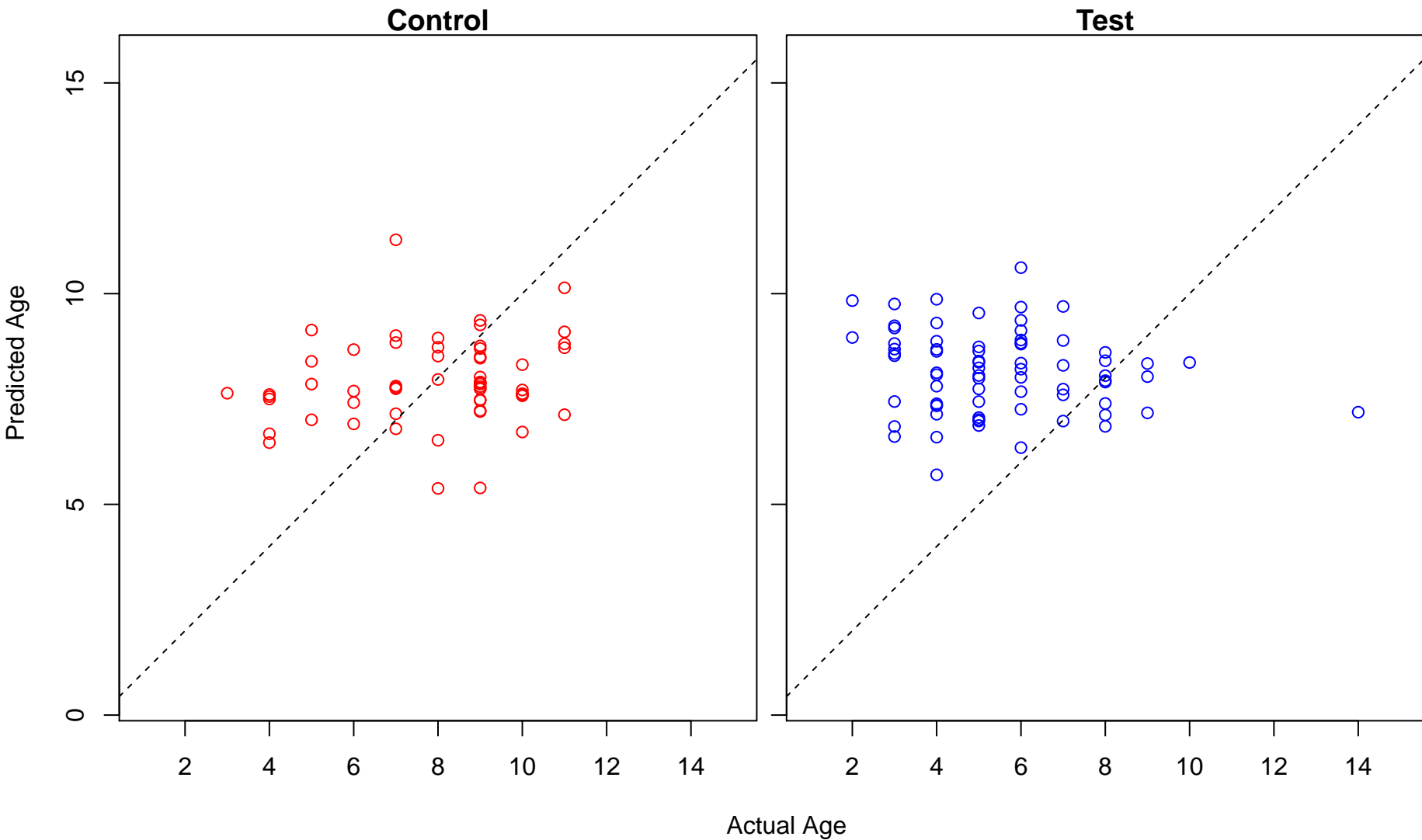
metanephric comma-shaped body morphogenesis (Score: 0.233743)



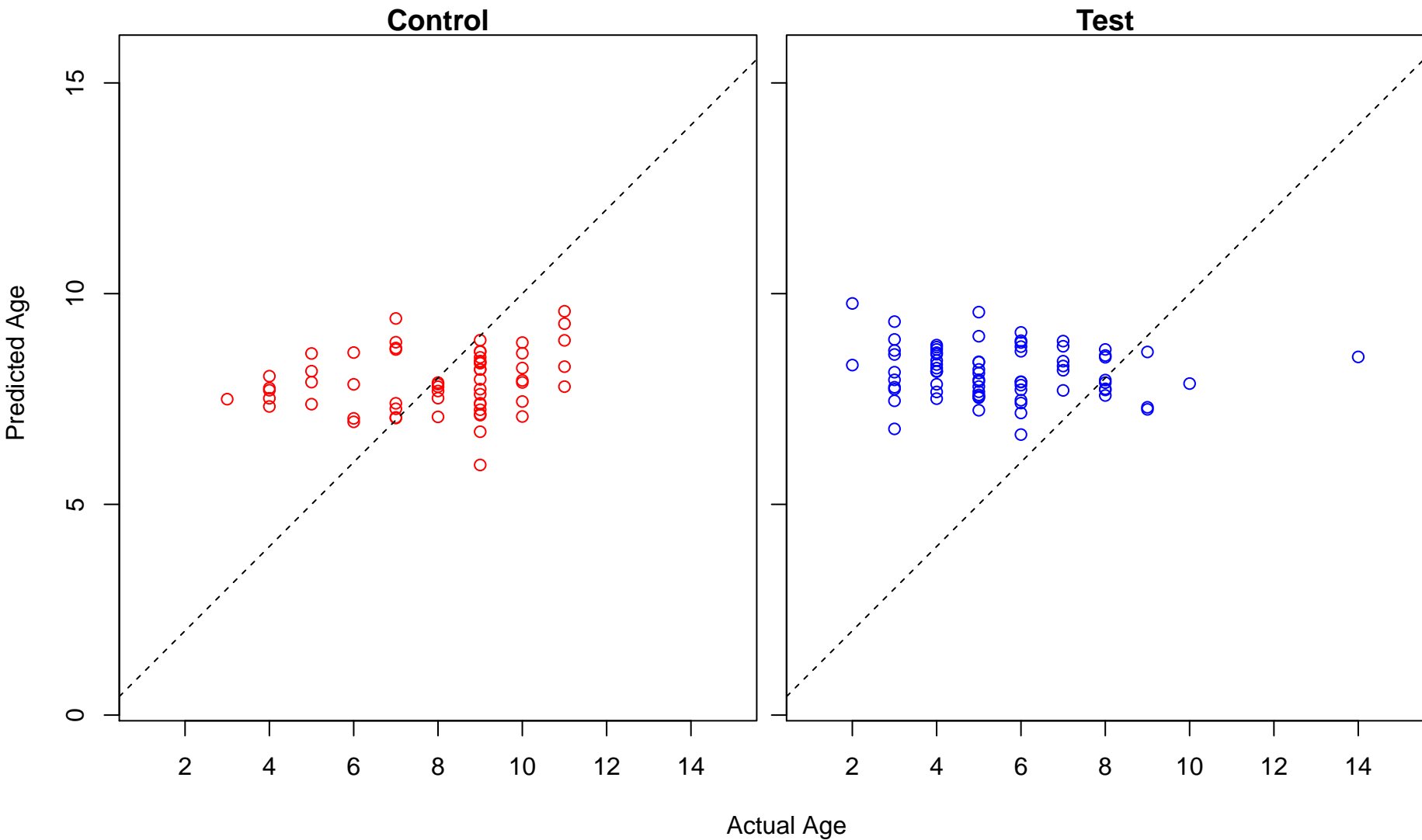
regulation of thyroid-stimulating hormone secretion (Score: 0.233743)



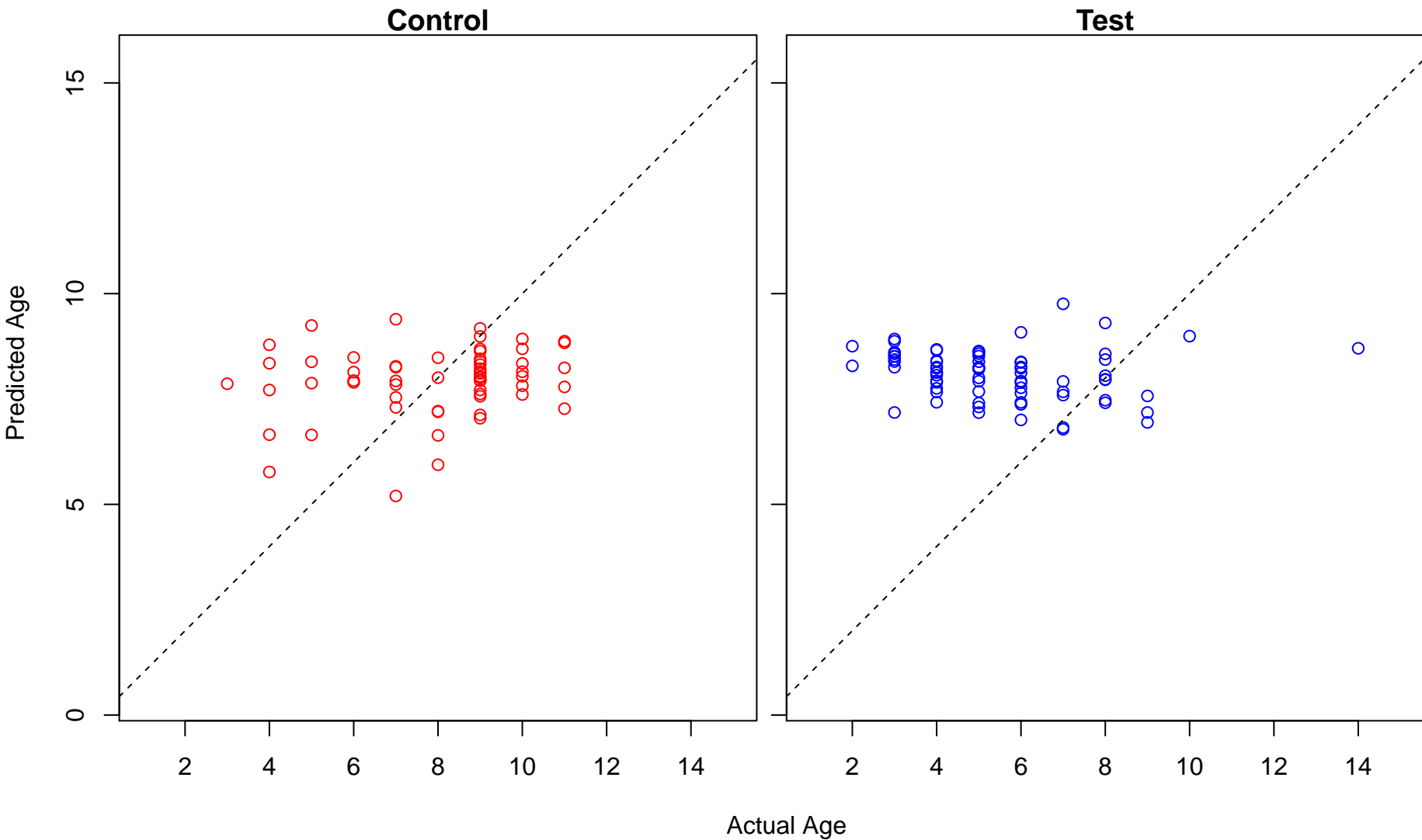
bronchus development (Score: 0.233706)



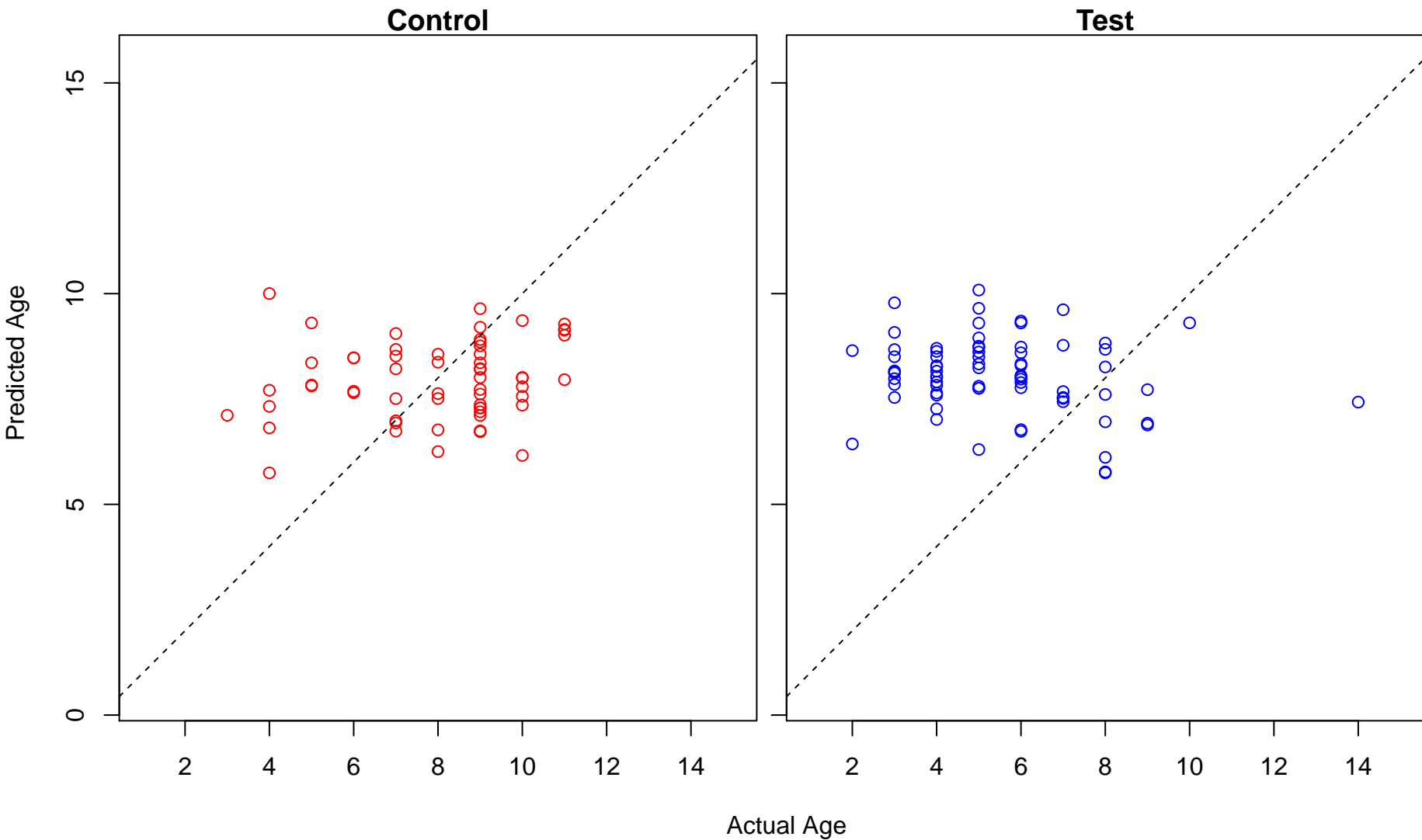
bud outgrowth involved in lung branching (Score: 0.232603)



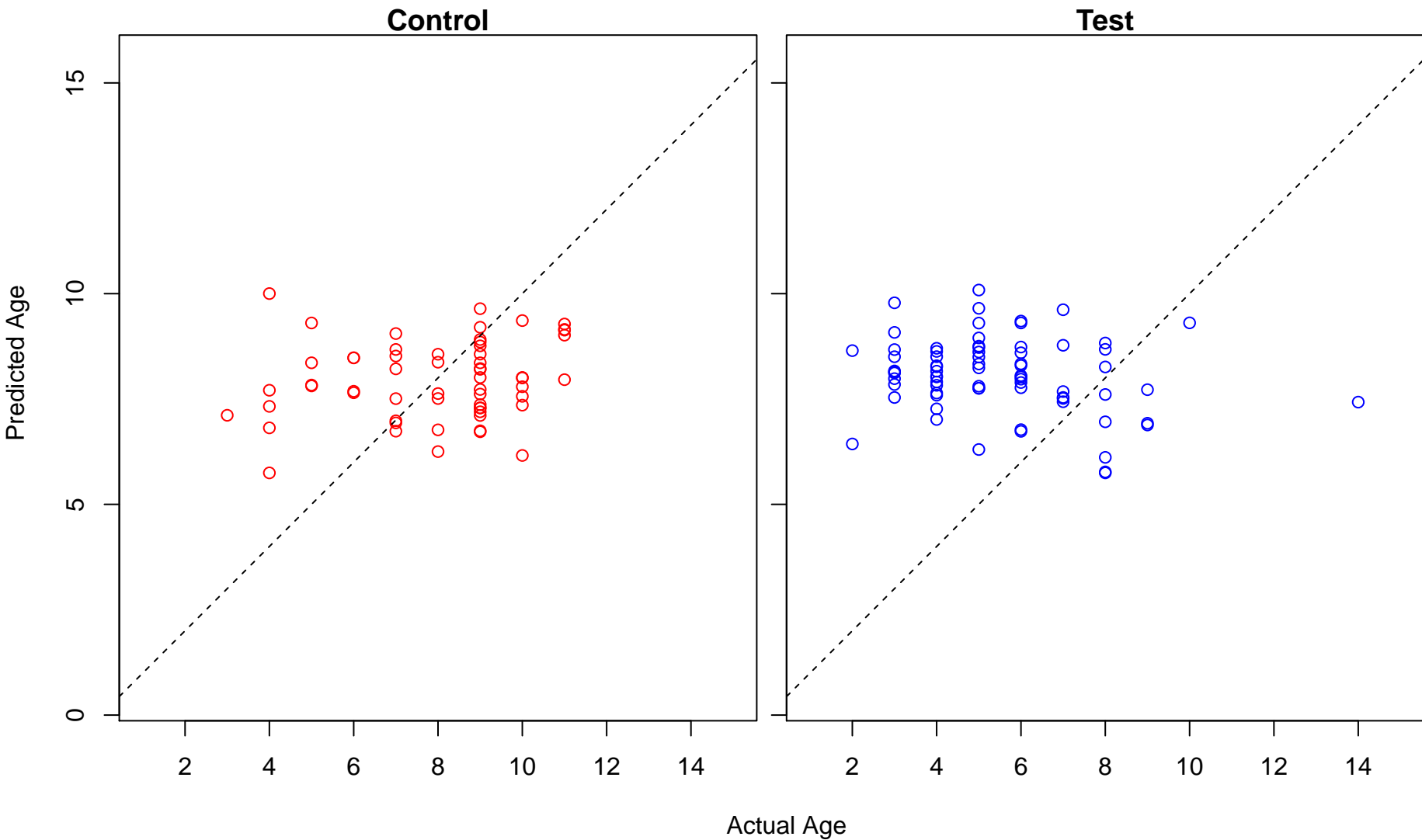
fatty acid elongation, polyunsaturated fatty acid (Score: 0.230964)



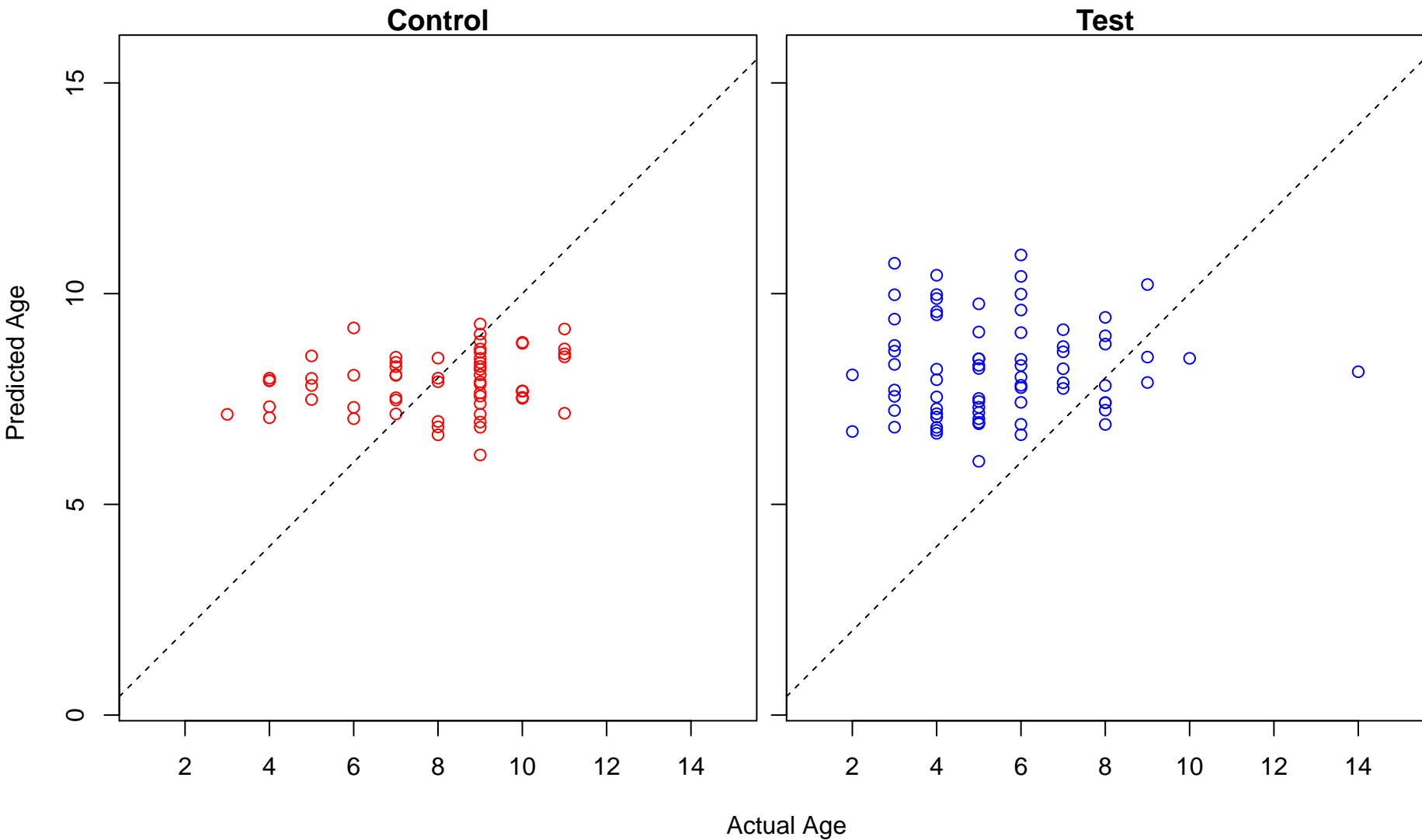
D-amino acid biosynthetic process (Score: 0.224816)



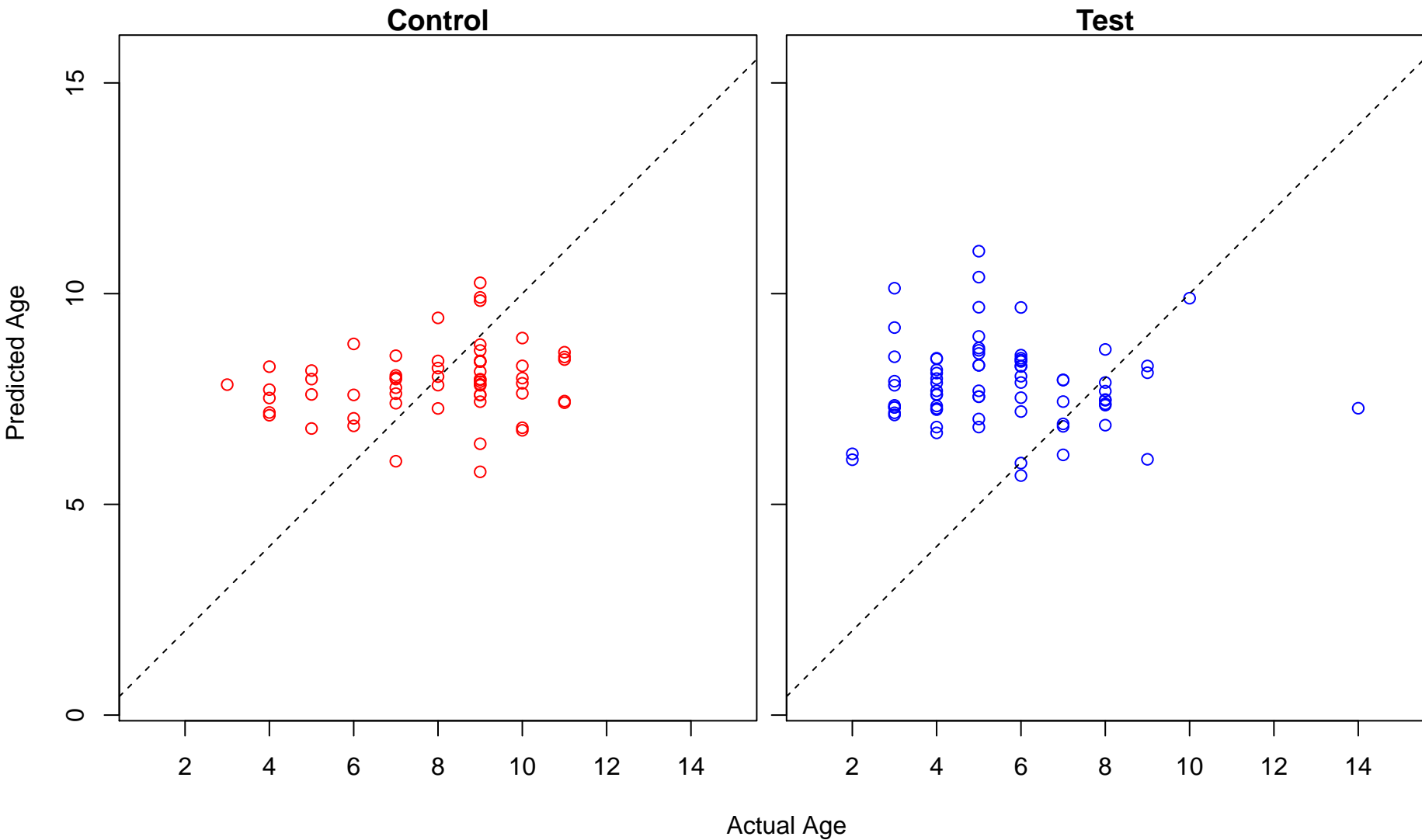
D-serine biosynthetic process (Score: 0.224816)



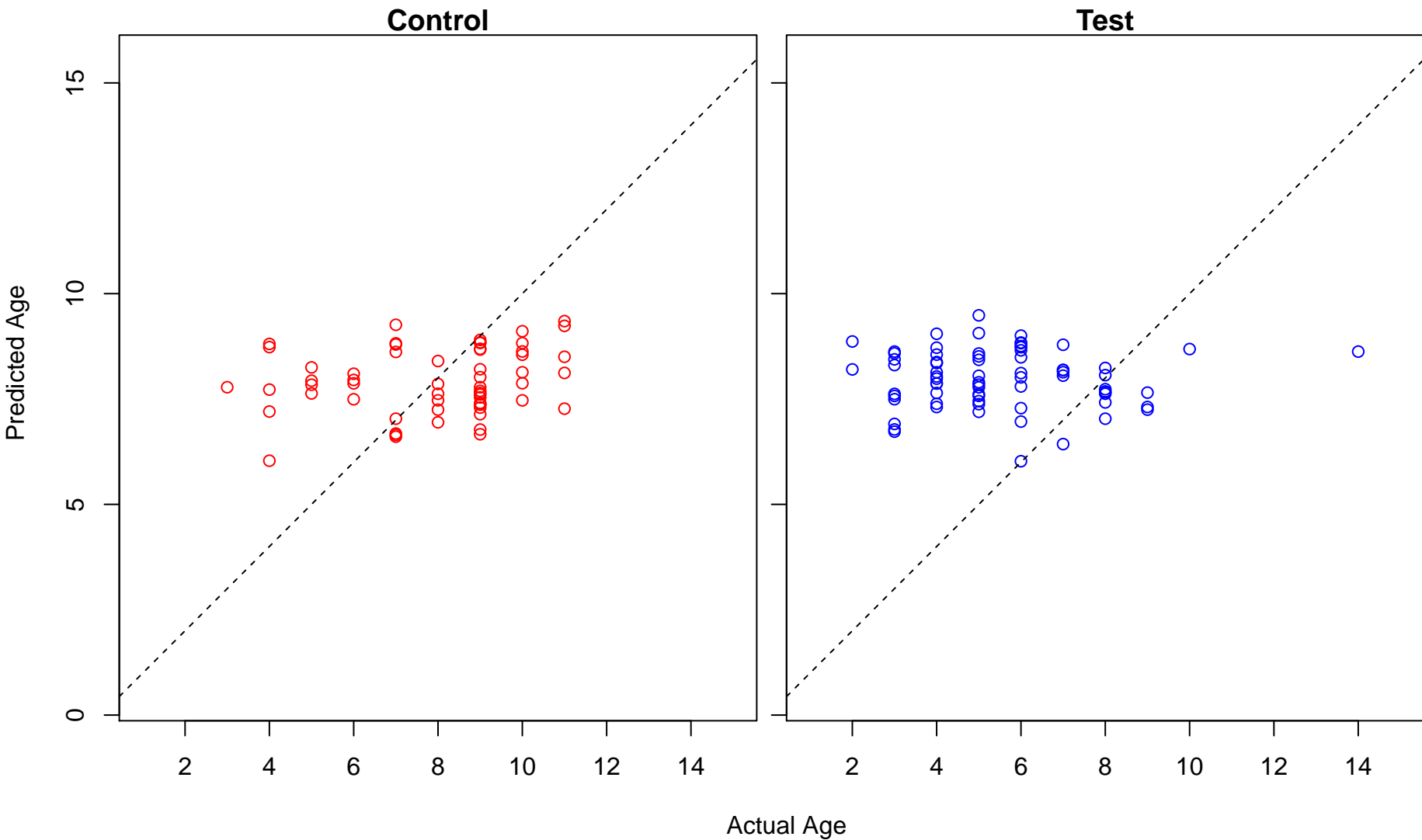
germ-line stem cell division (Score: 0.220742)



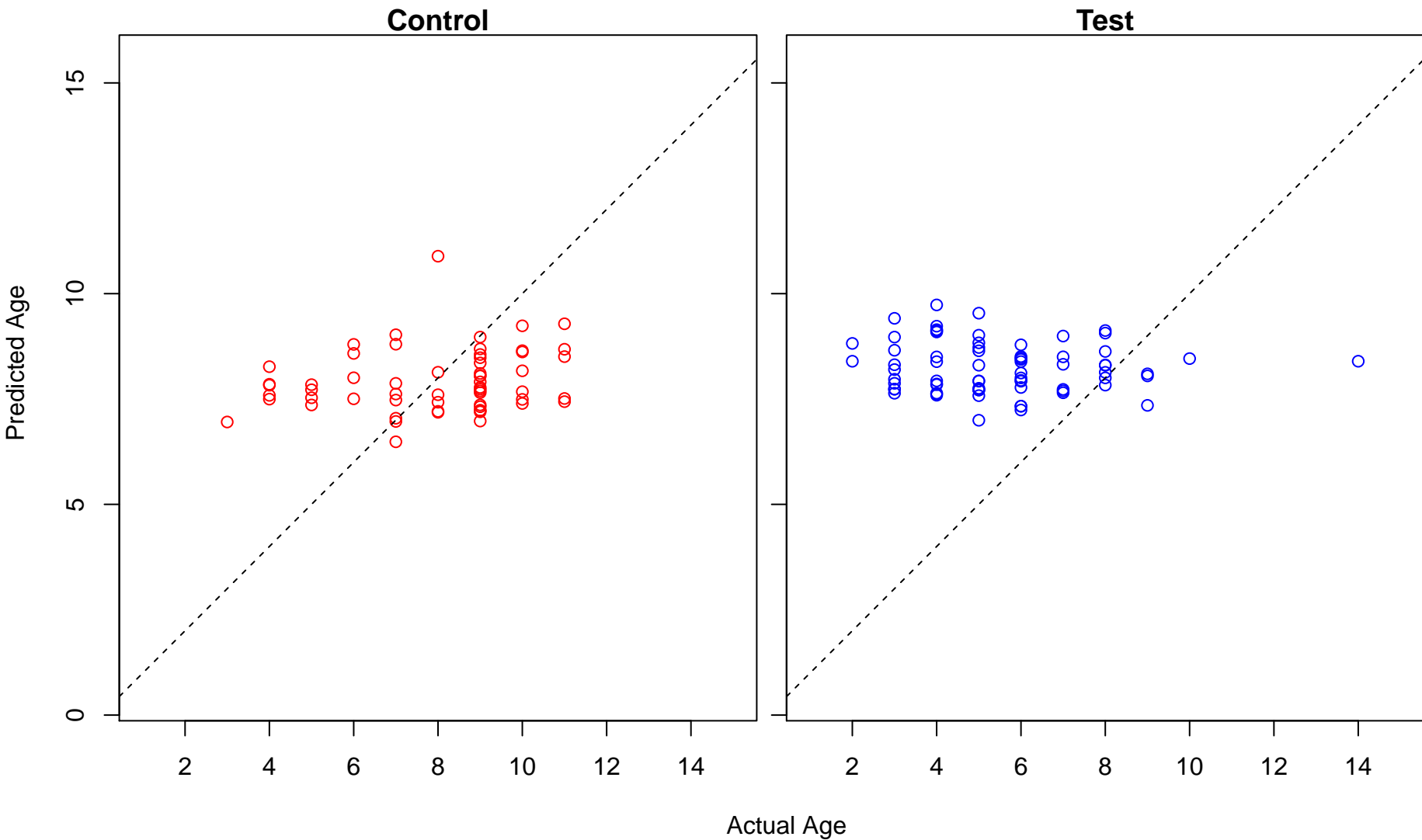
regulation of glutamate metabolic process (Score: 0.218617)



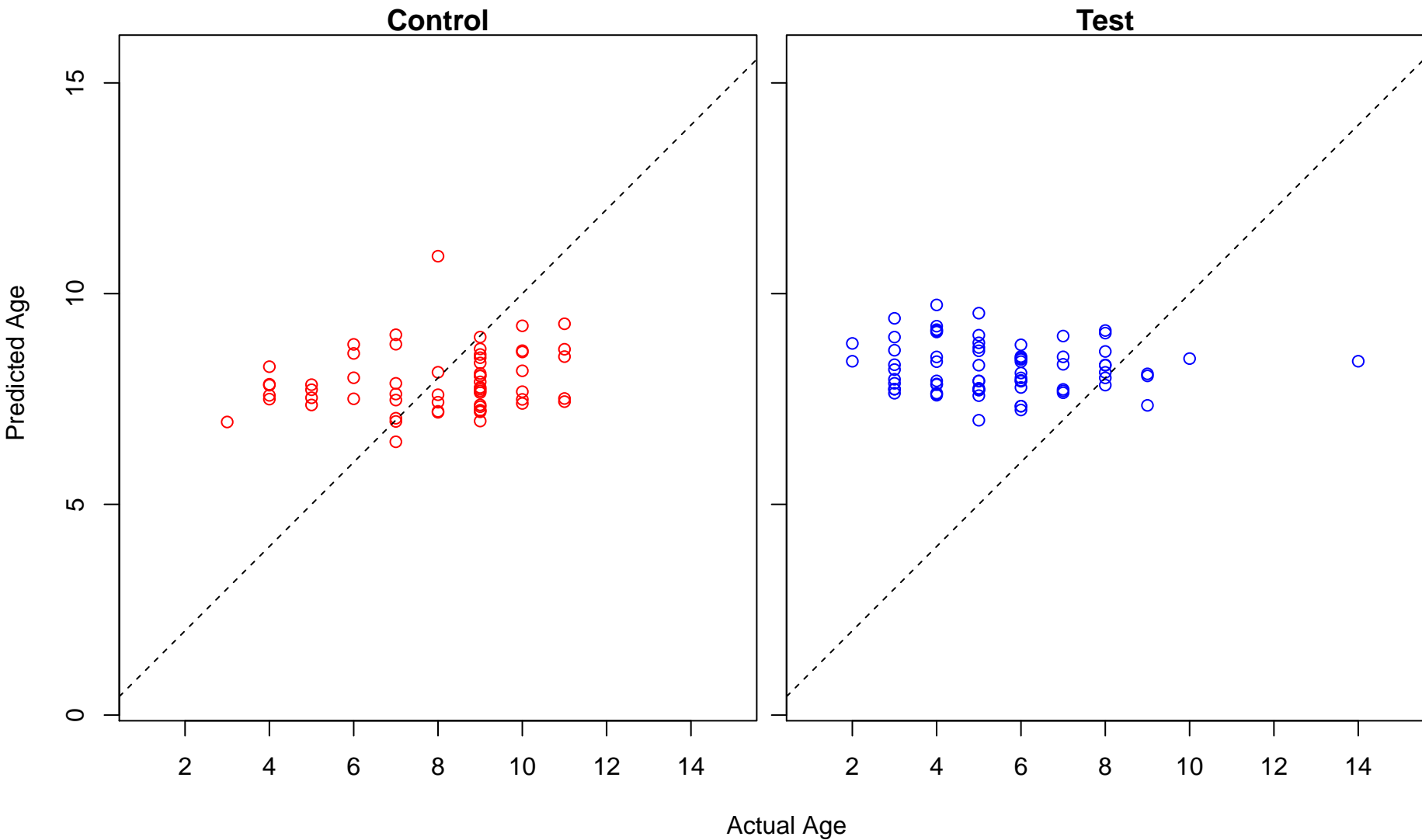
ferrous iron transport (Score: 0.217396)



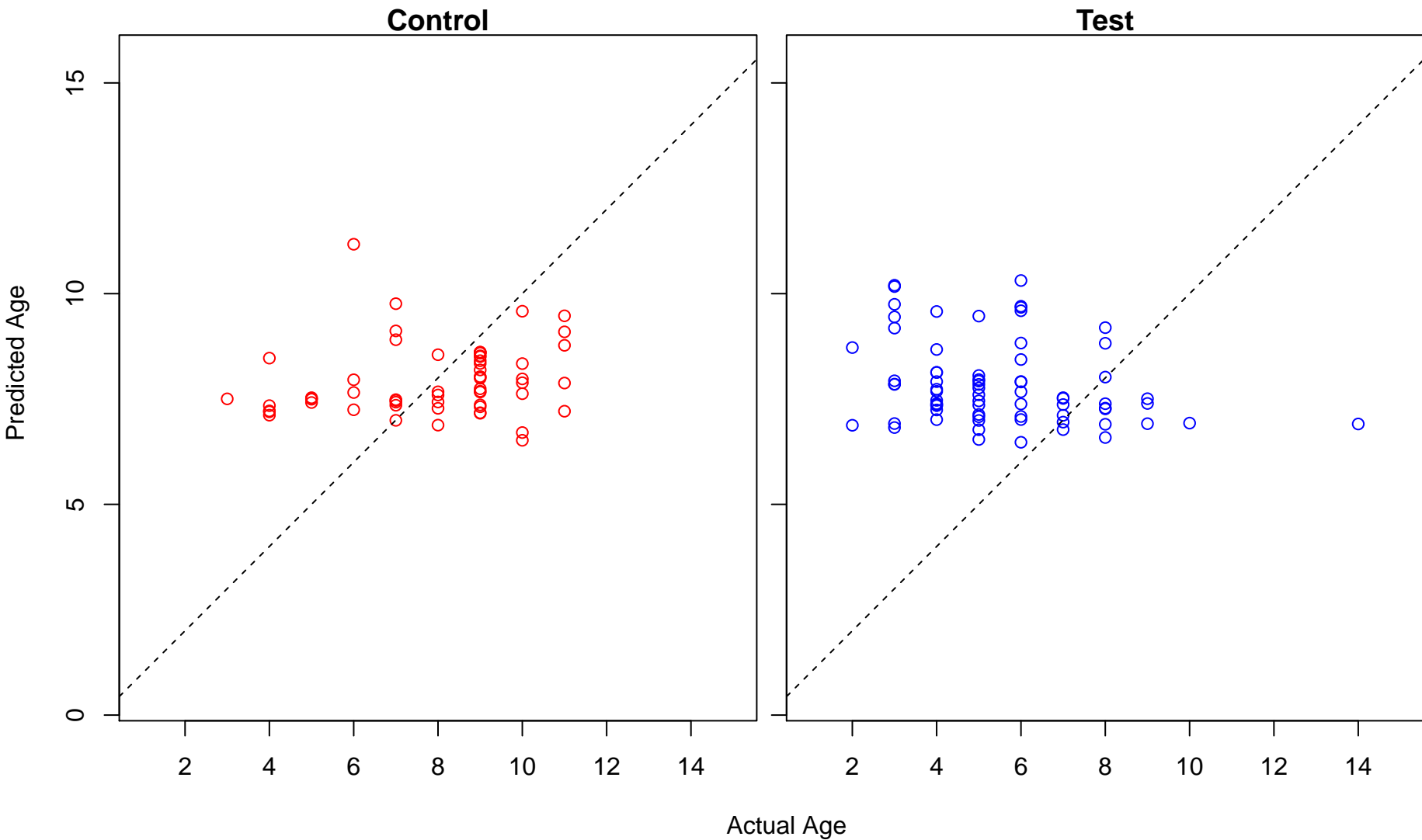
steroid hormone secretion (Score: 0.215653)



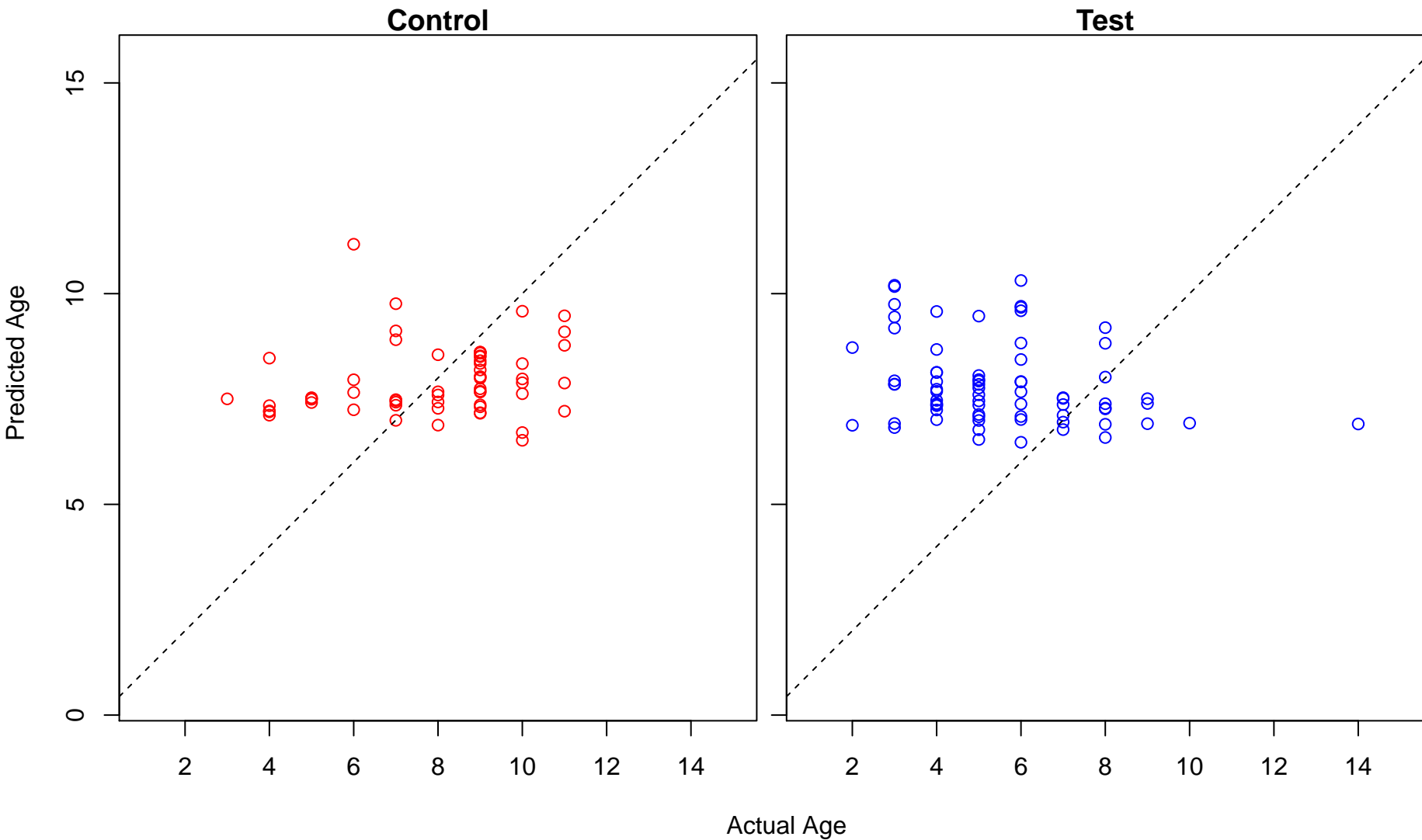
progesterone secretion (Score: 0.215653)



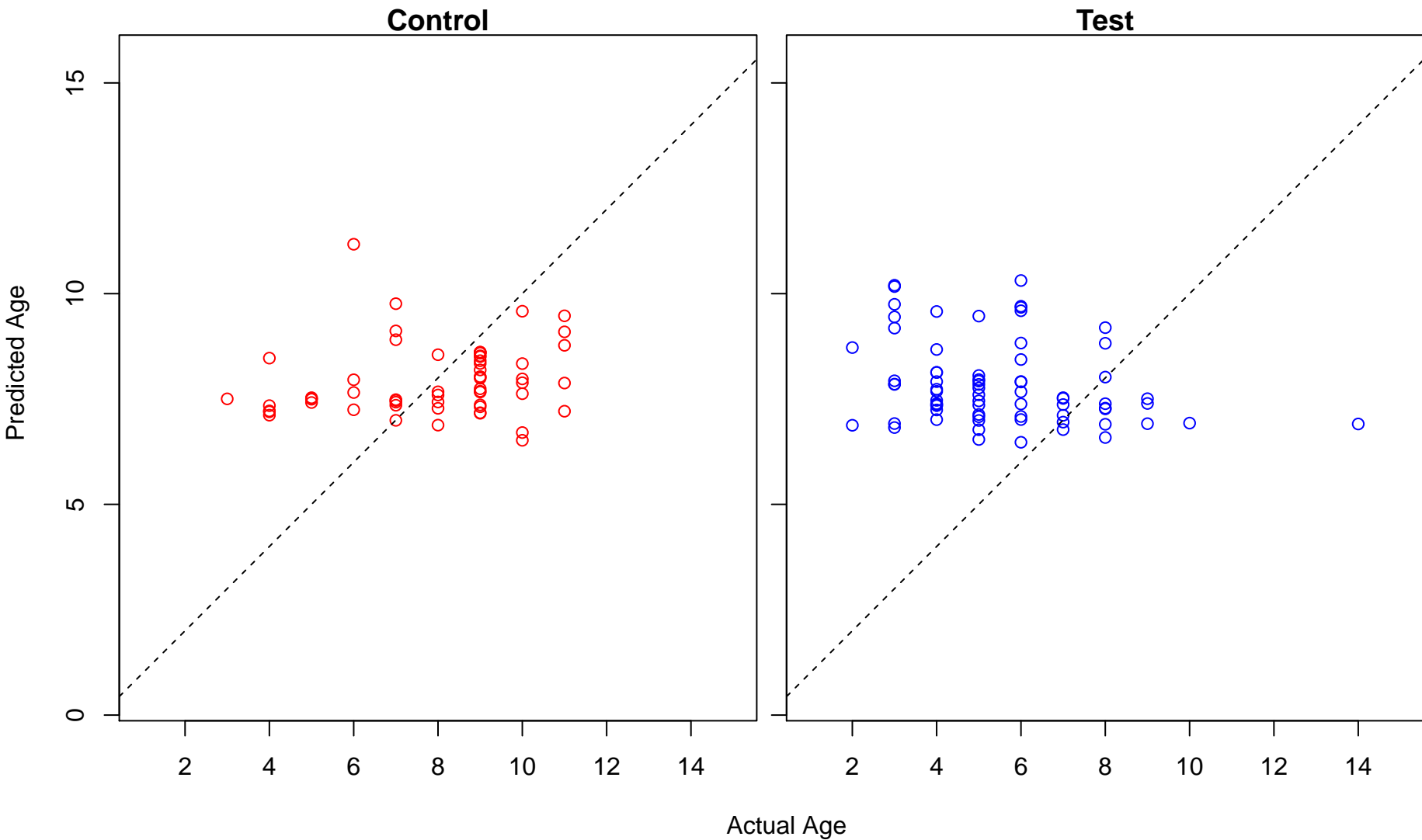
induction by symbiont of host defense response (Score: 0.213404)



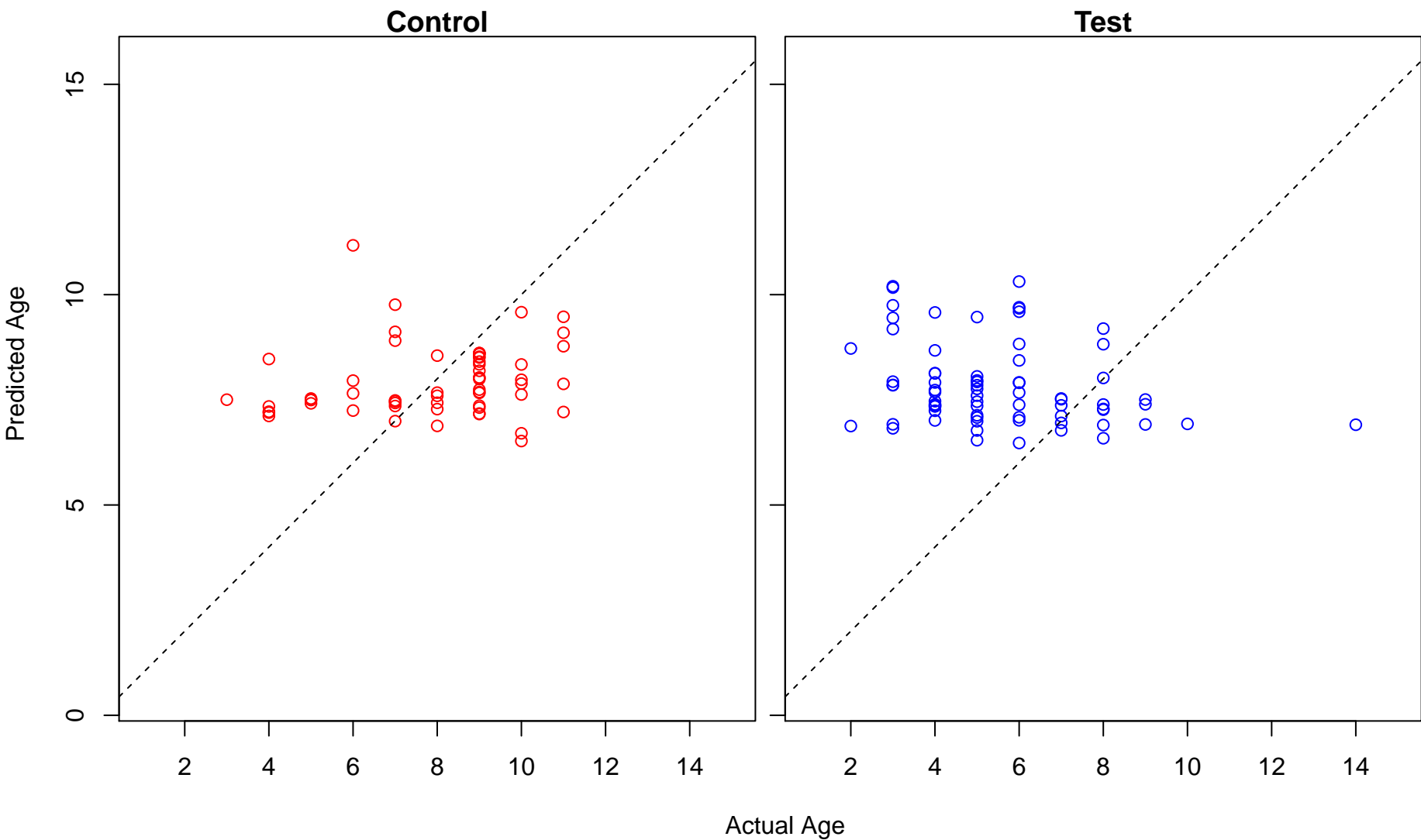
induction of host immune response by virus (Score: 0.213404)



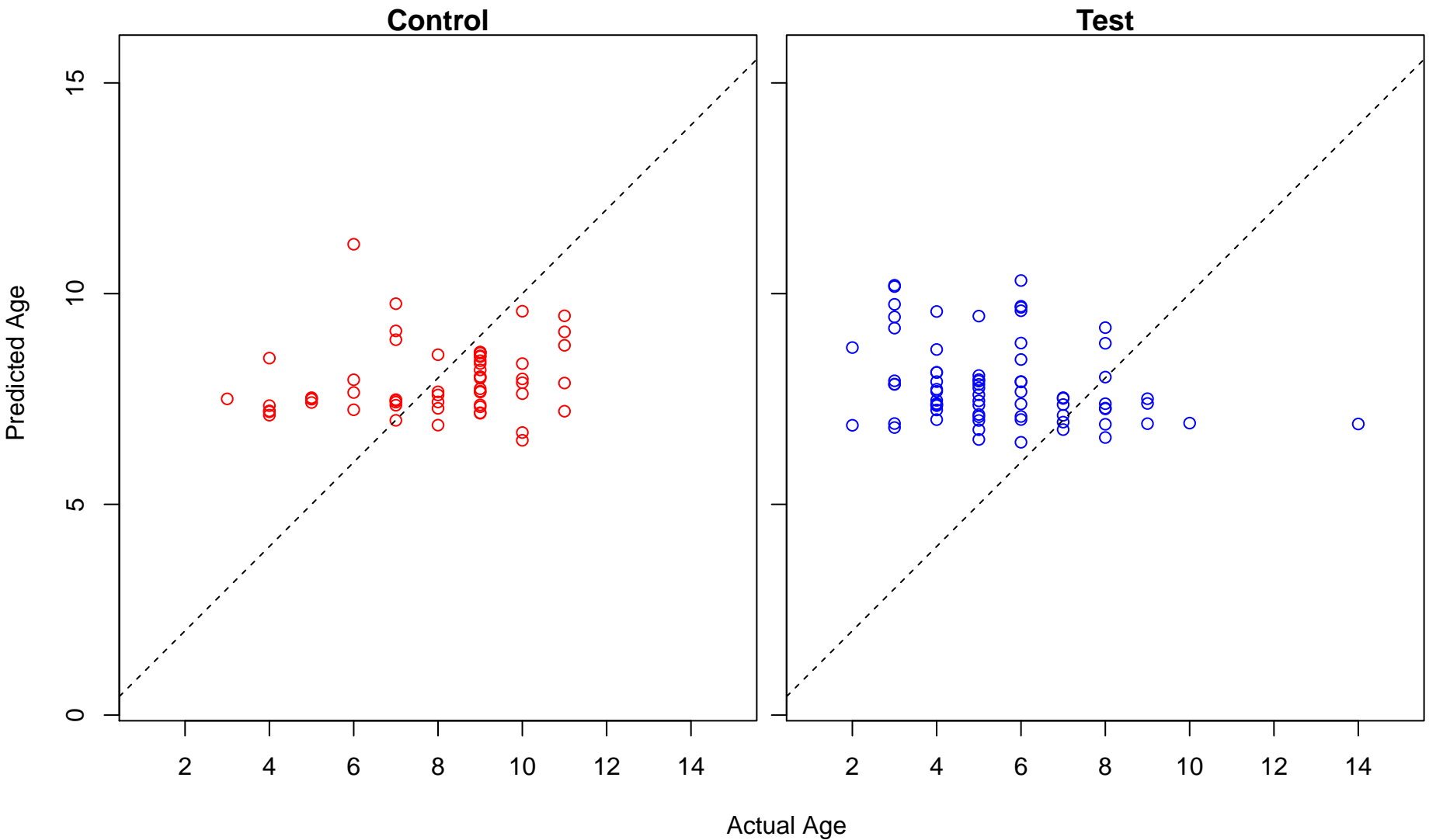
active induction of host immune response by virus (Score: 0.213404)



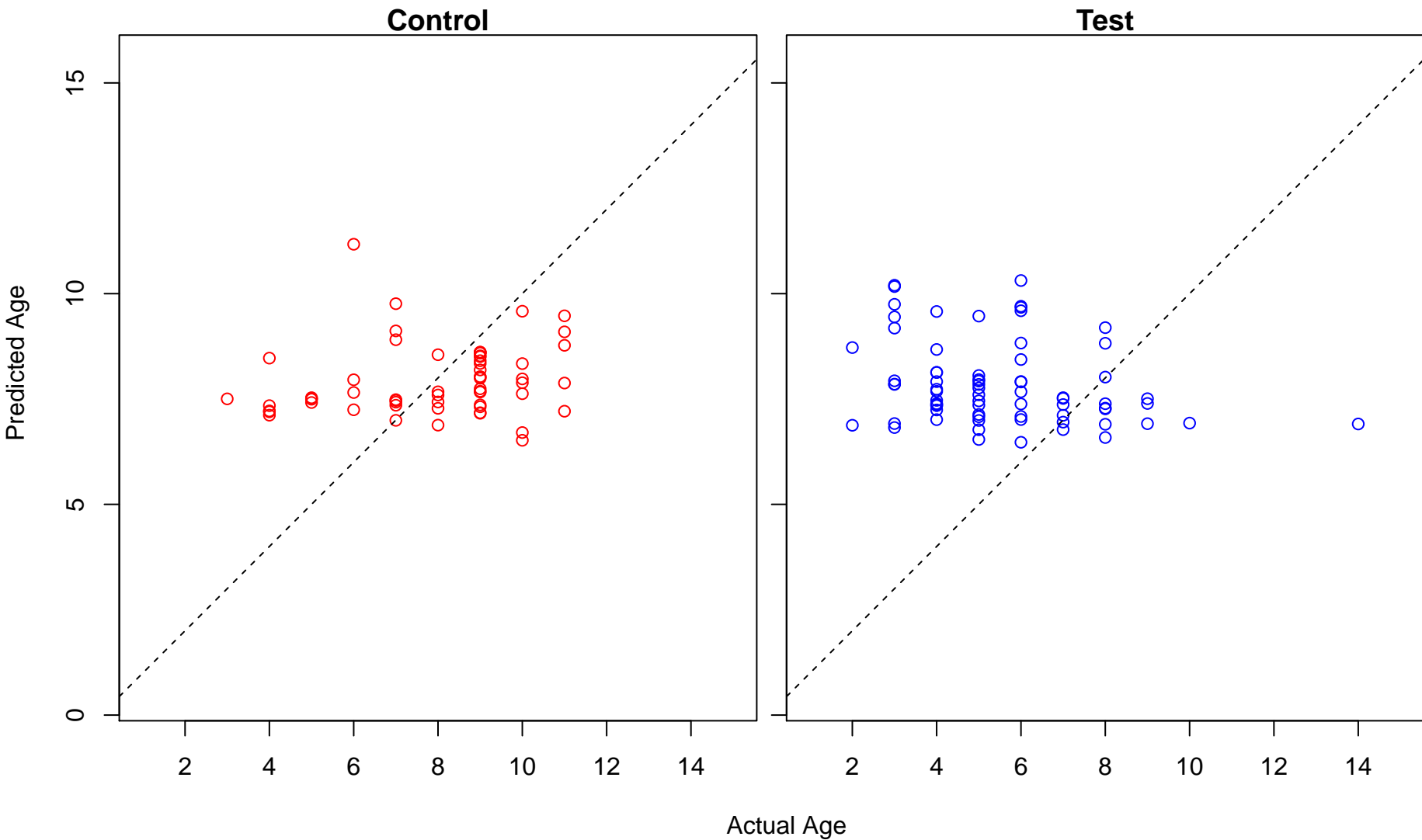
Induction by organism of defense response of other organism involved in symbiotic interaction (Score: 0.



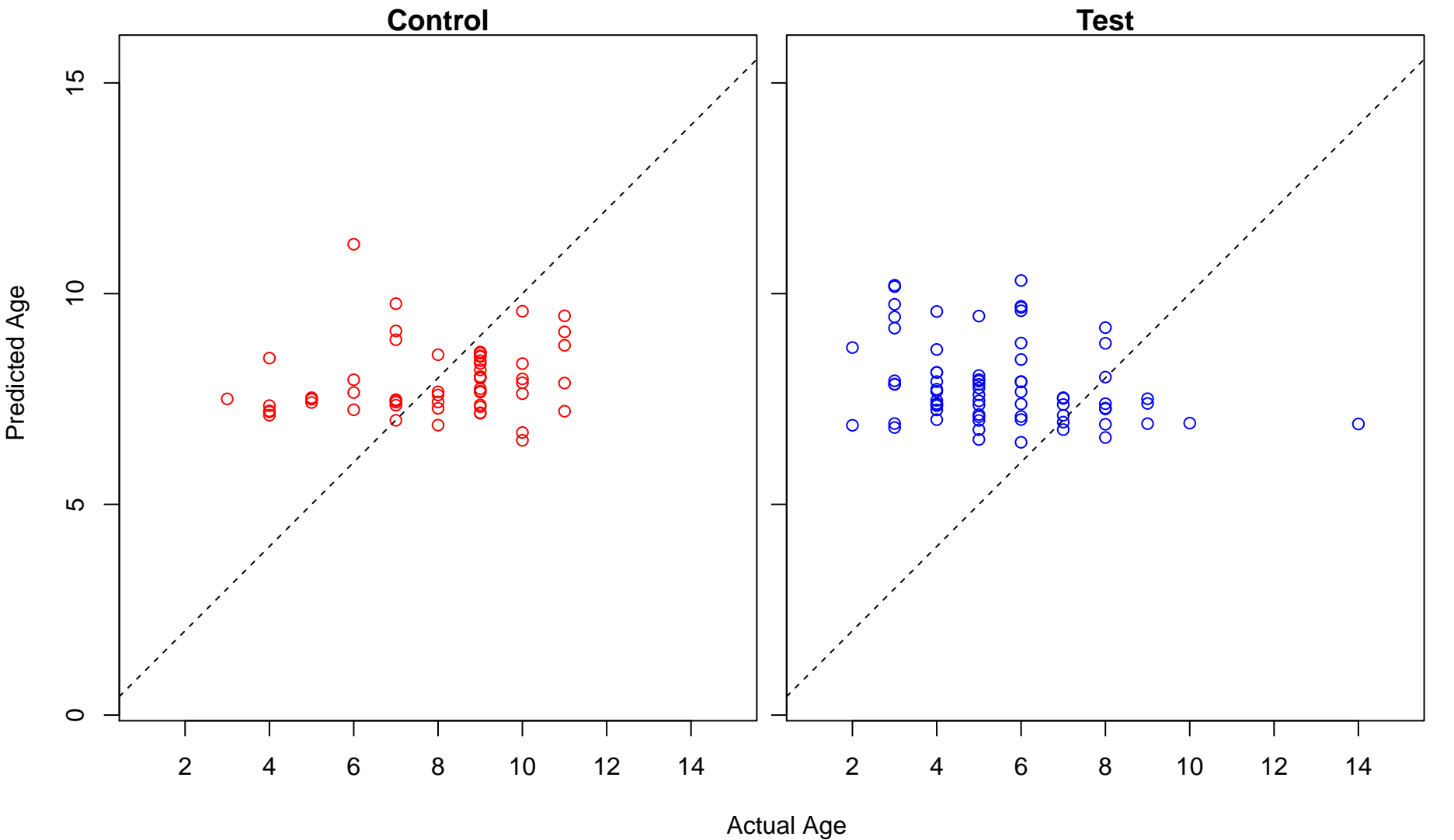
modulation by organism of defense response of other organism involved in symbiotic interaction (Score: 0)



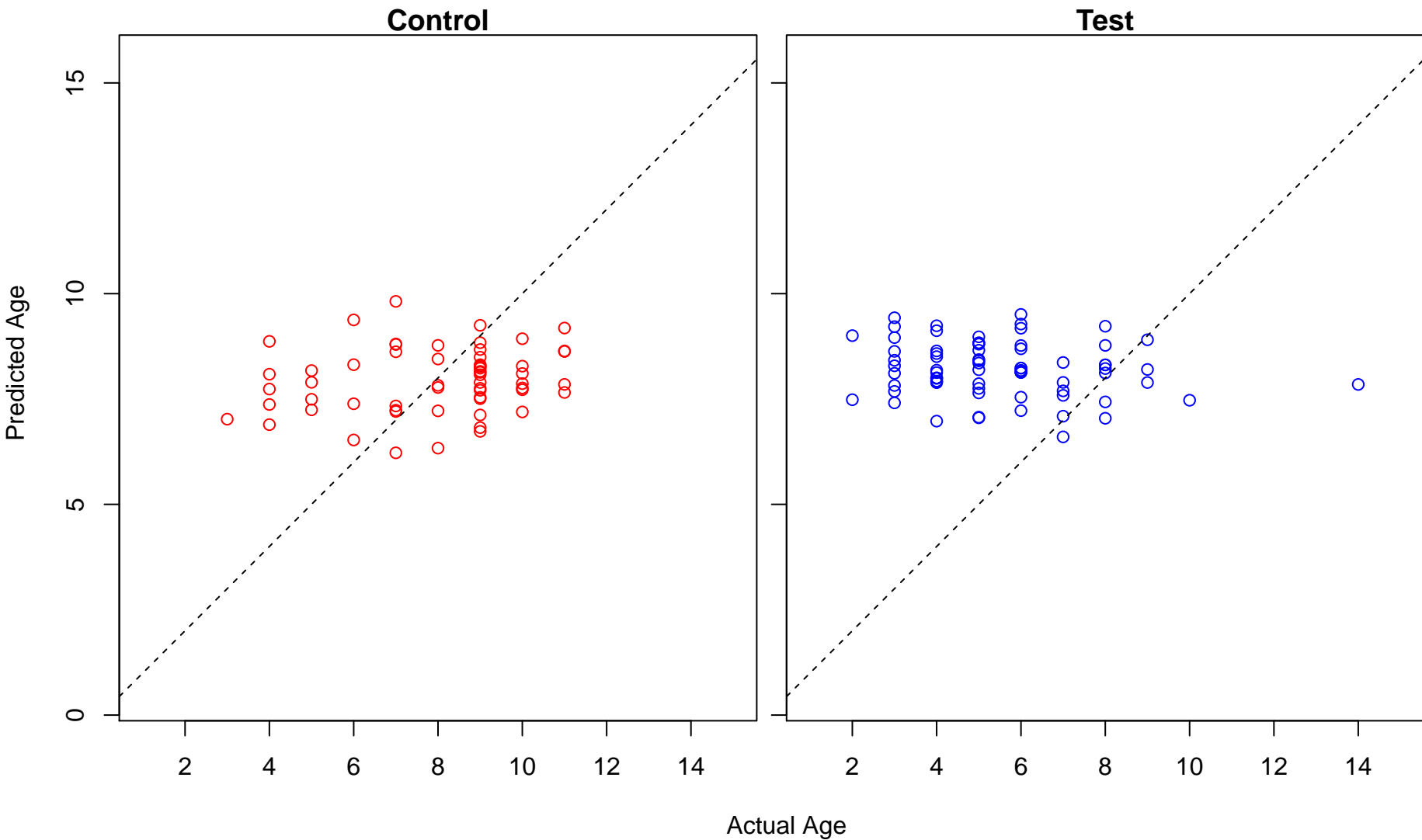
positive regulation by symbiont of host defense response (Score: 0.213404)



Positive regulation by organism of defense response of other organism involved in symbiotic interaction (Sco

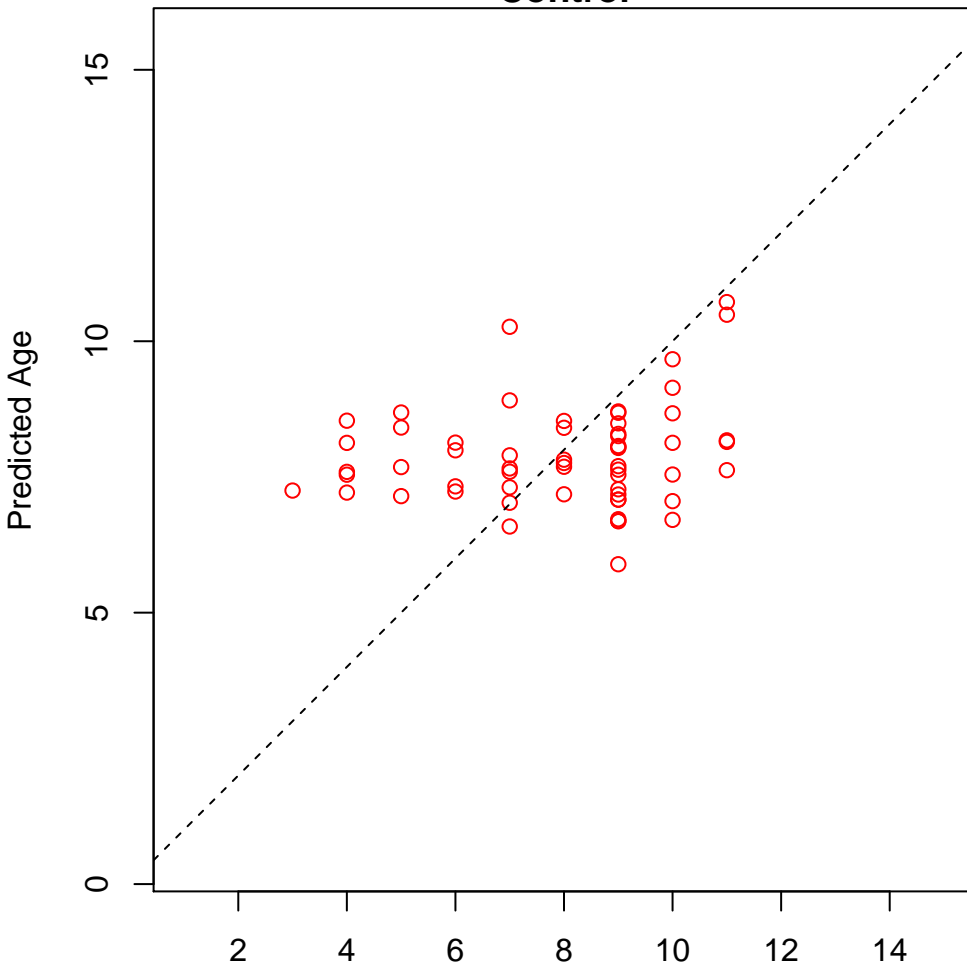


enucleate erythrocyte development (Score: 0.212407)

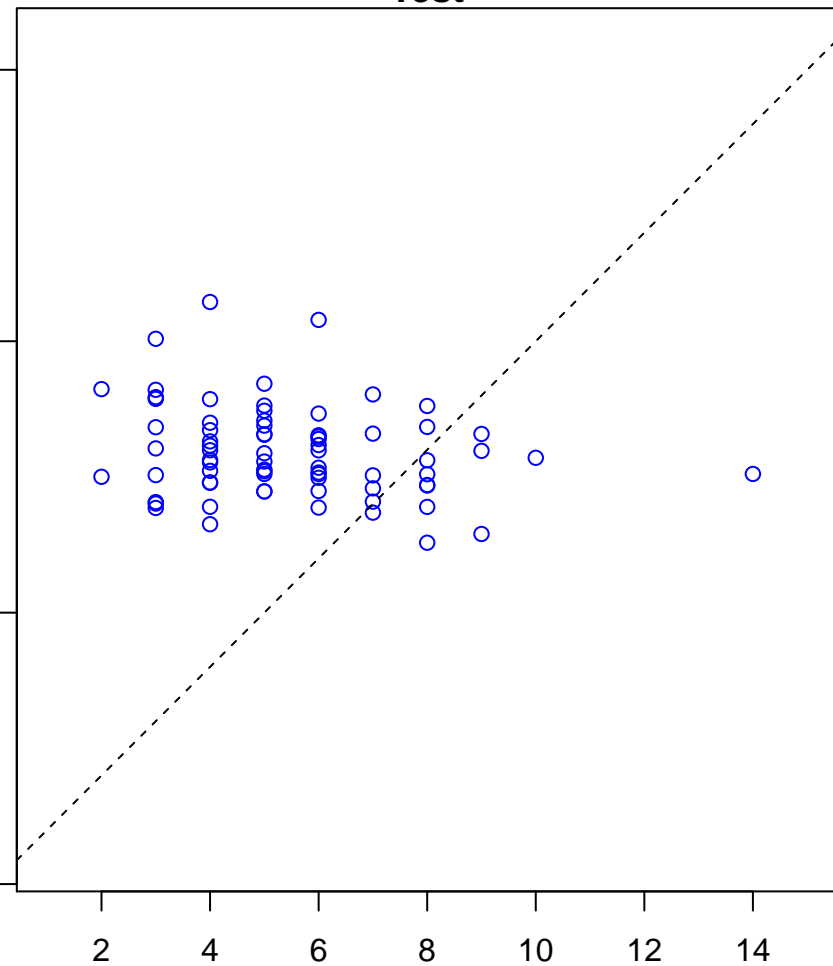


cornea development in camera-type eye (Score: 0.212356)

Control

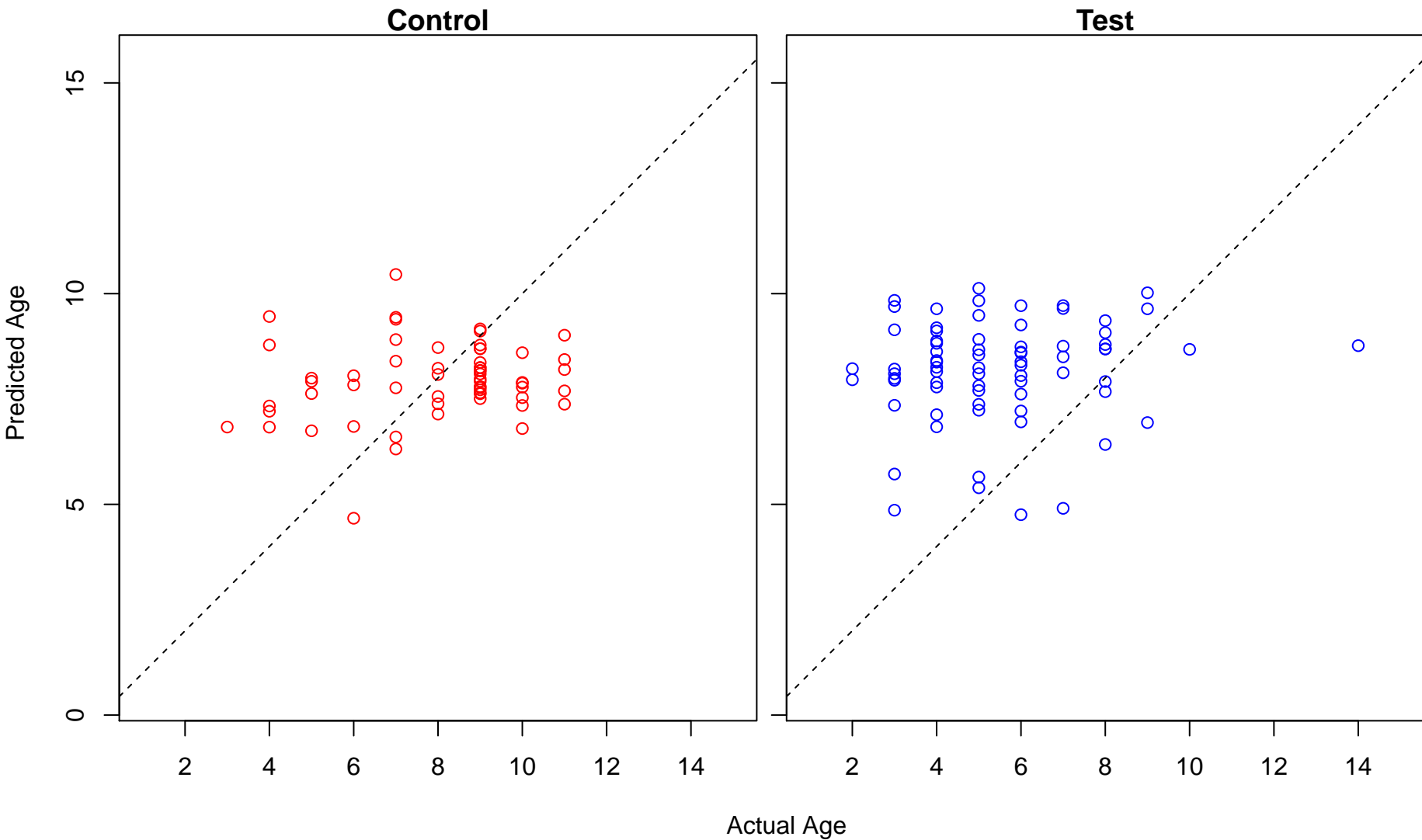


Test

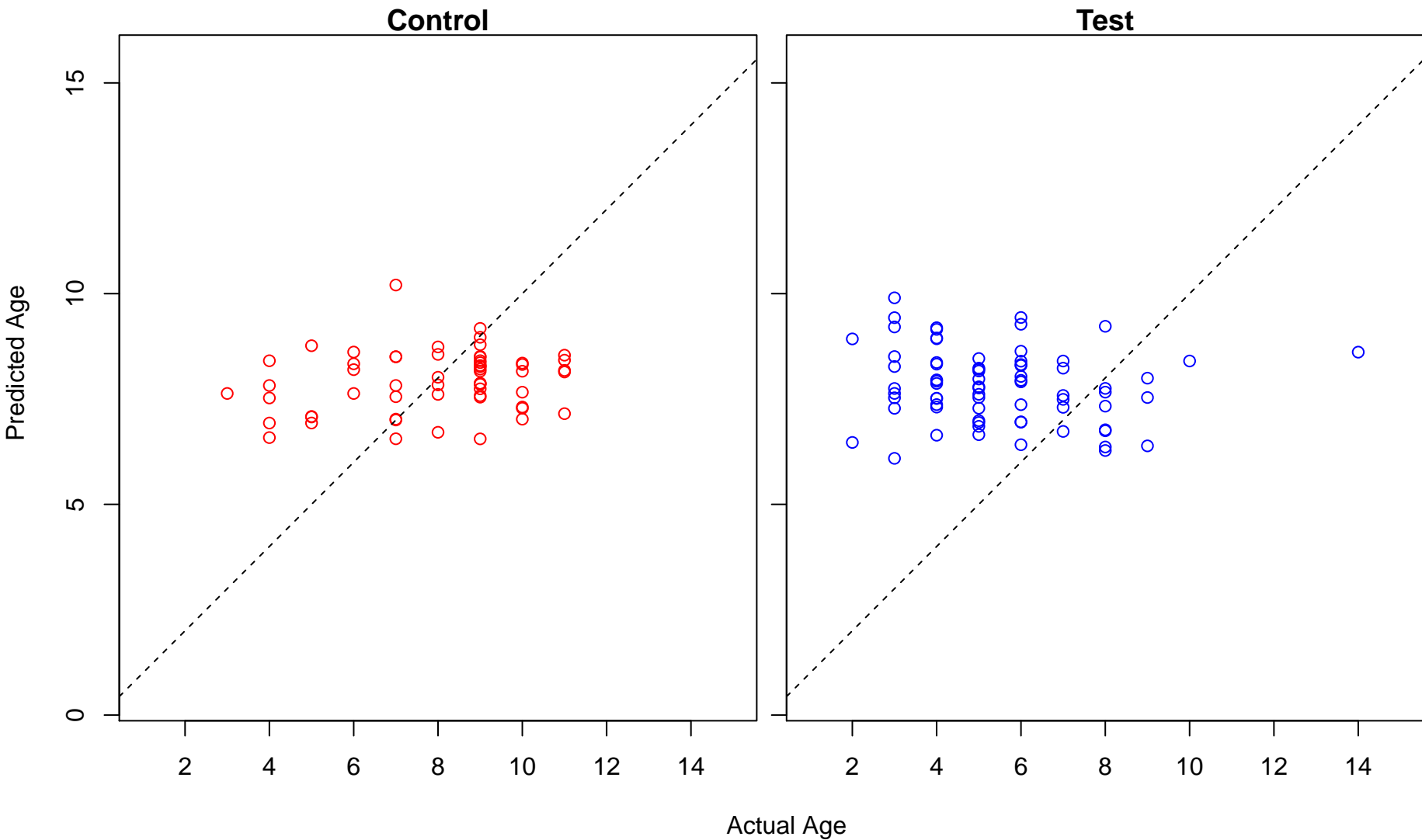


Actual Age

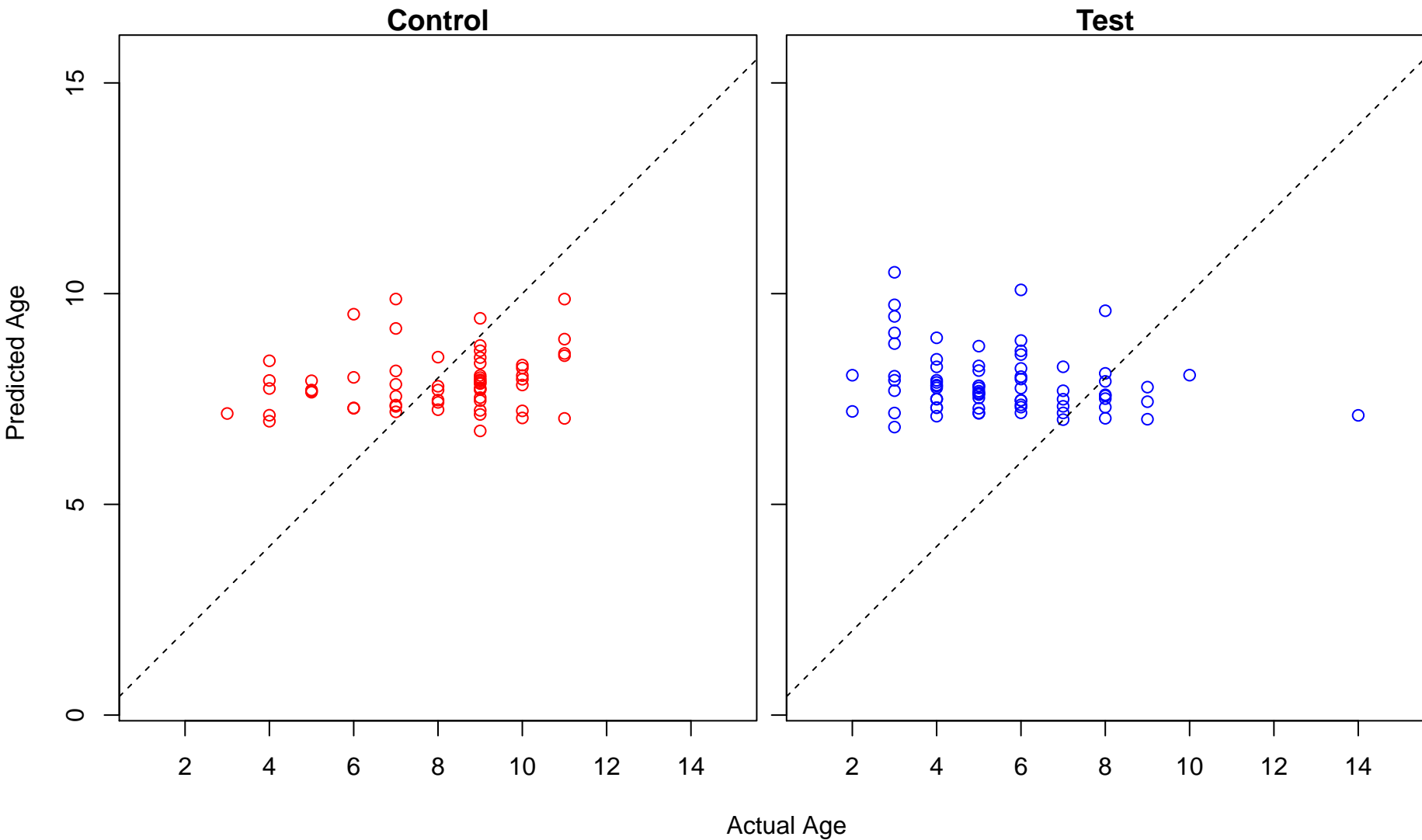
positive regulation of fibroblast apoptotic process (Score: 0.210884)



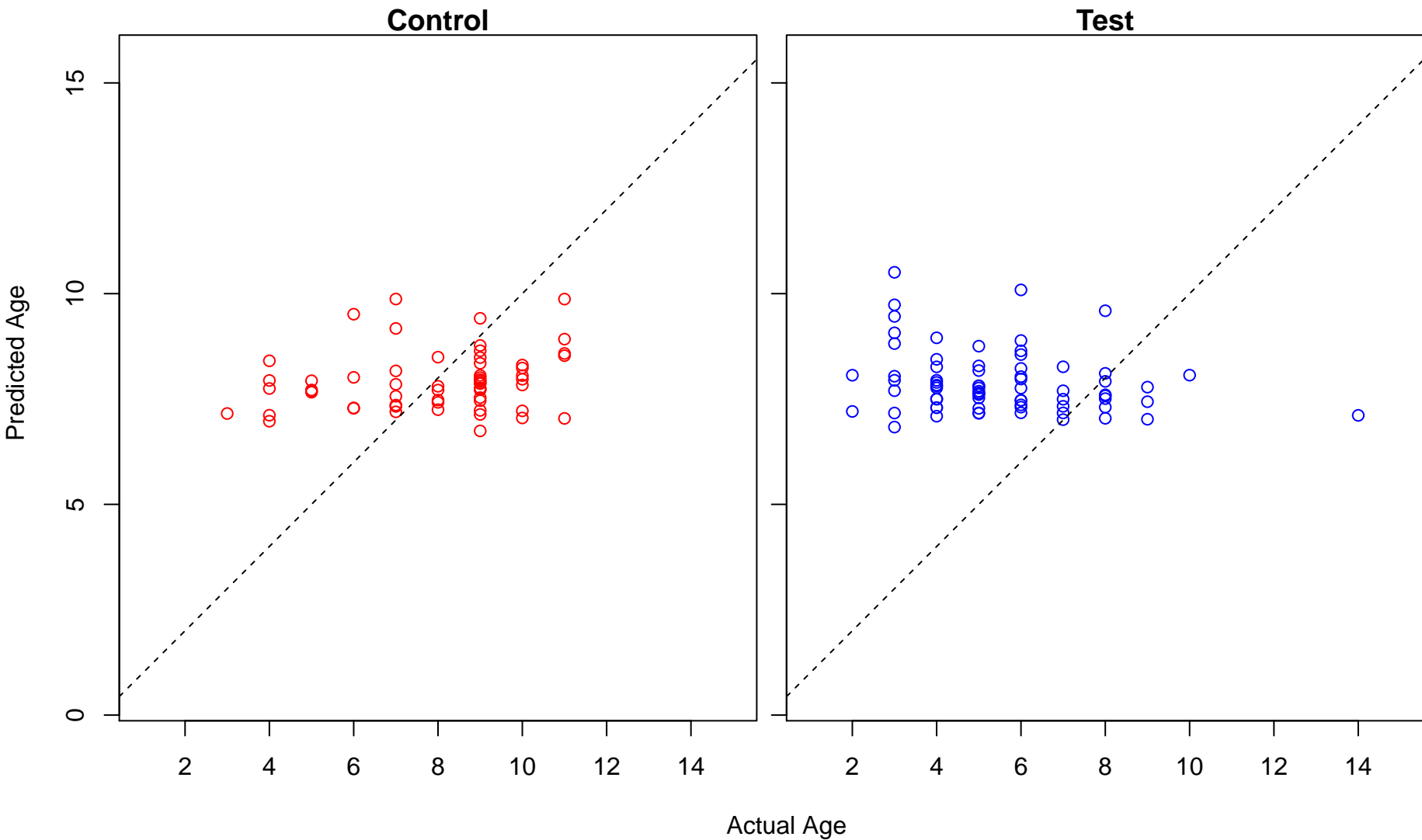
interleukin-7-mediated signaling pathway (Score: 0.210120)



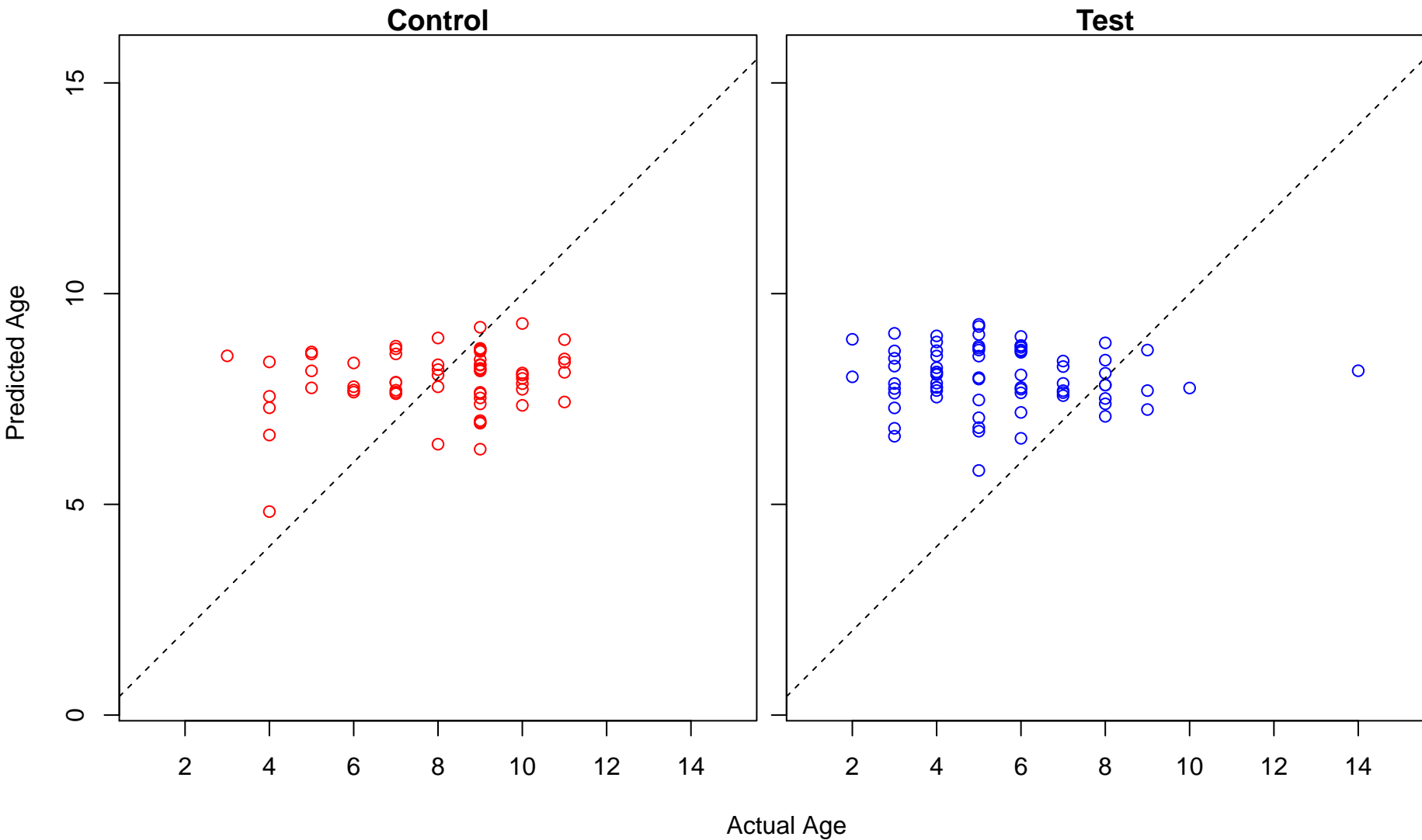
fatty-acyl-CoA transport (Score: 0.206775)



thioester transport (Score: 0.206775)

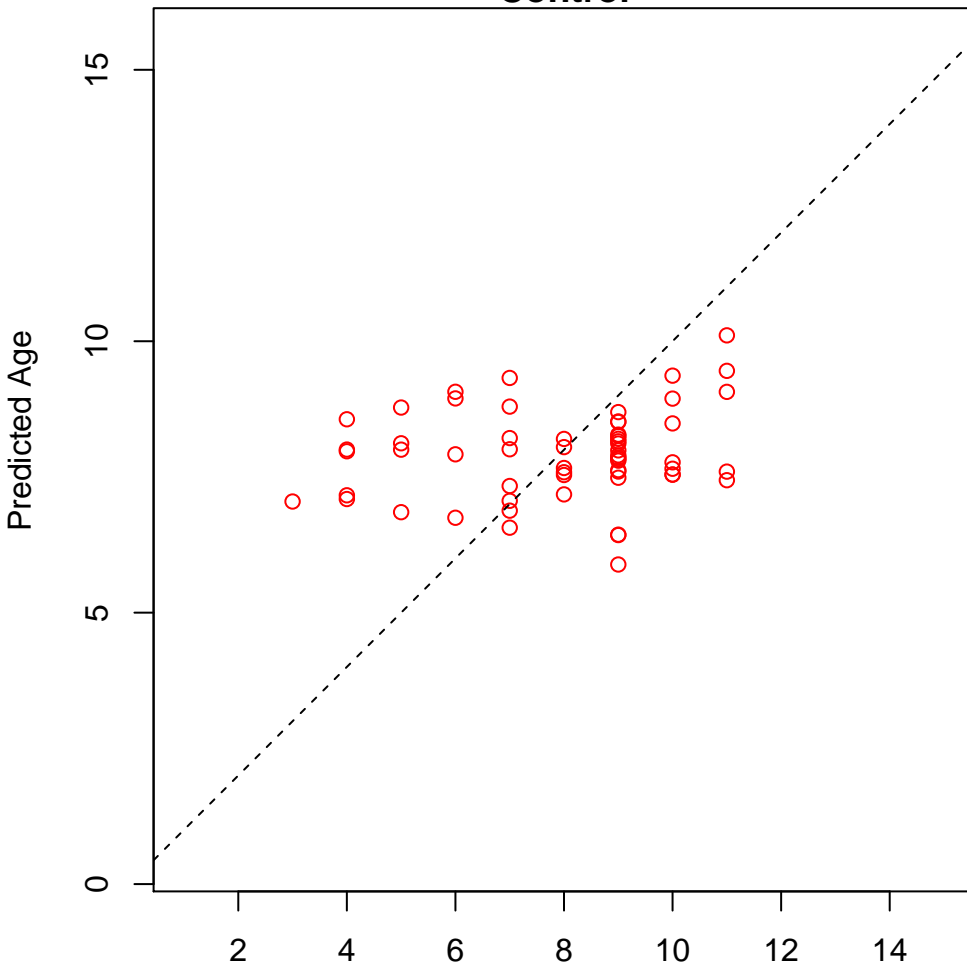


negative regulation of MDA-5 signaling pathway (Score: 0.206288)

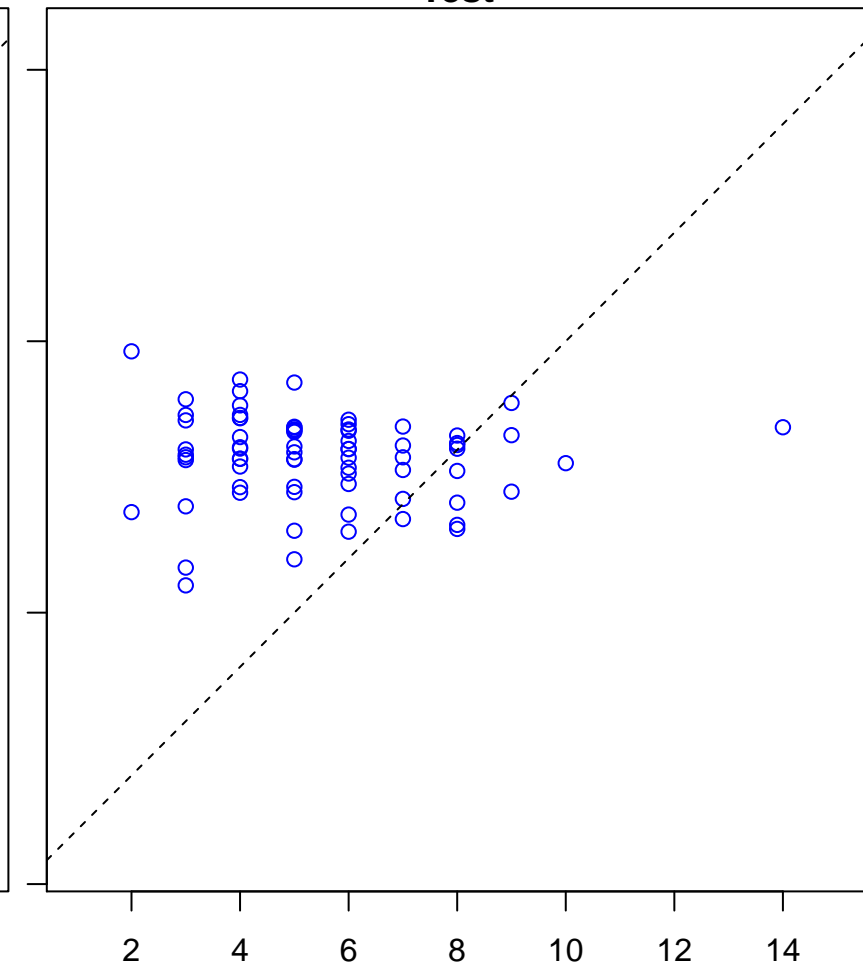


mitochondrial protein catabolic process (Score: 0.206020)

Control

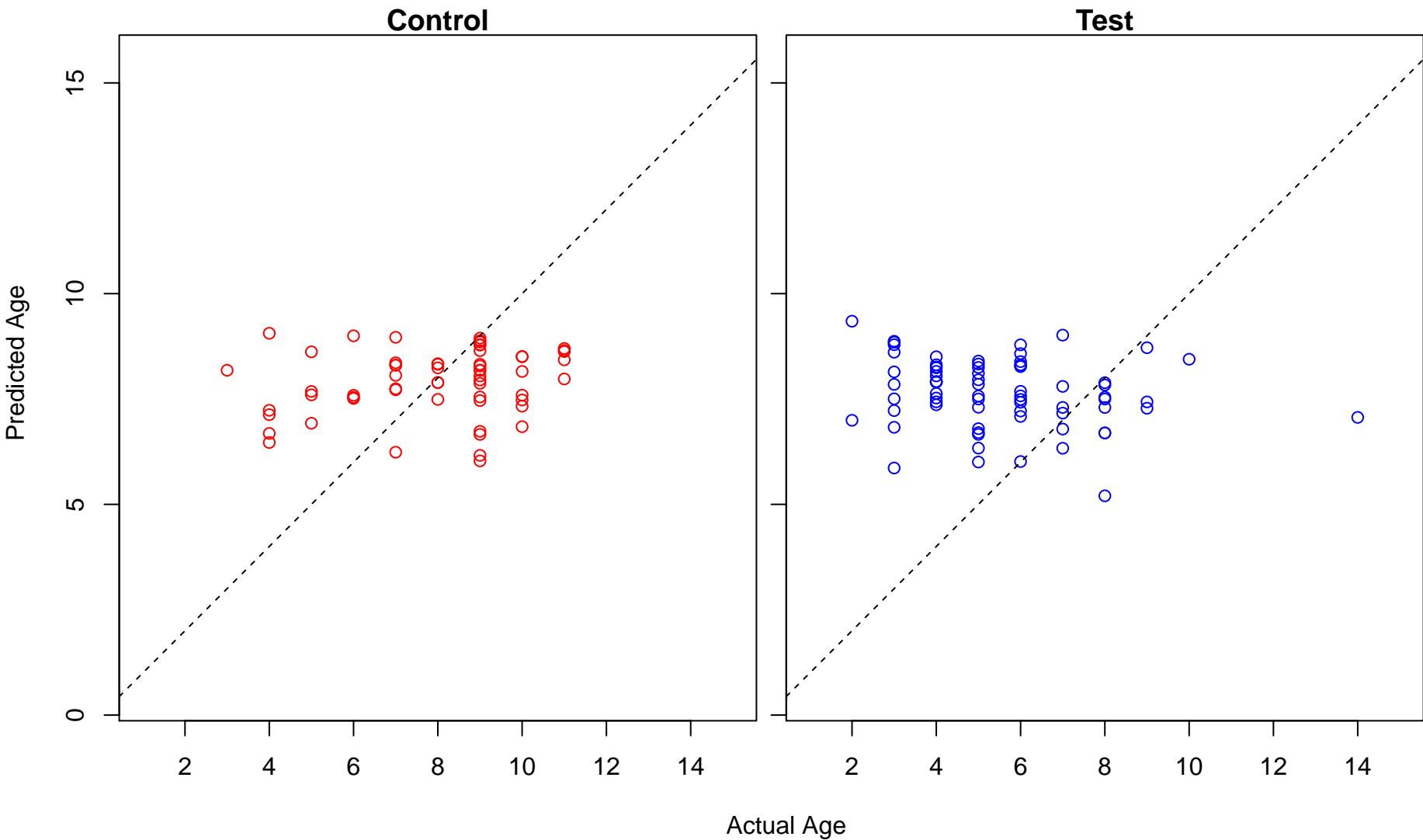


Test

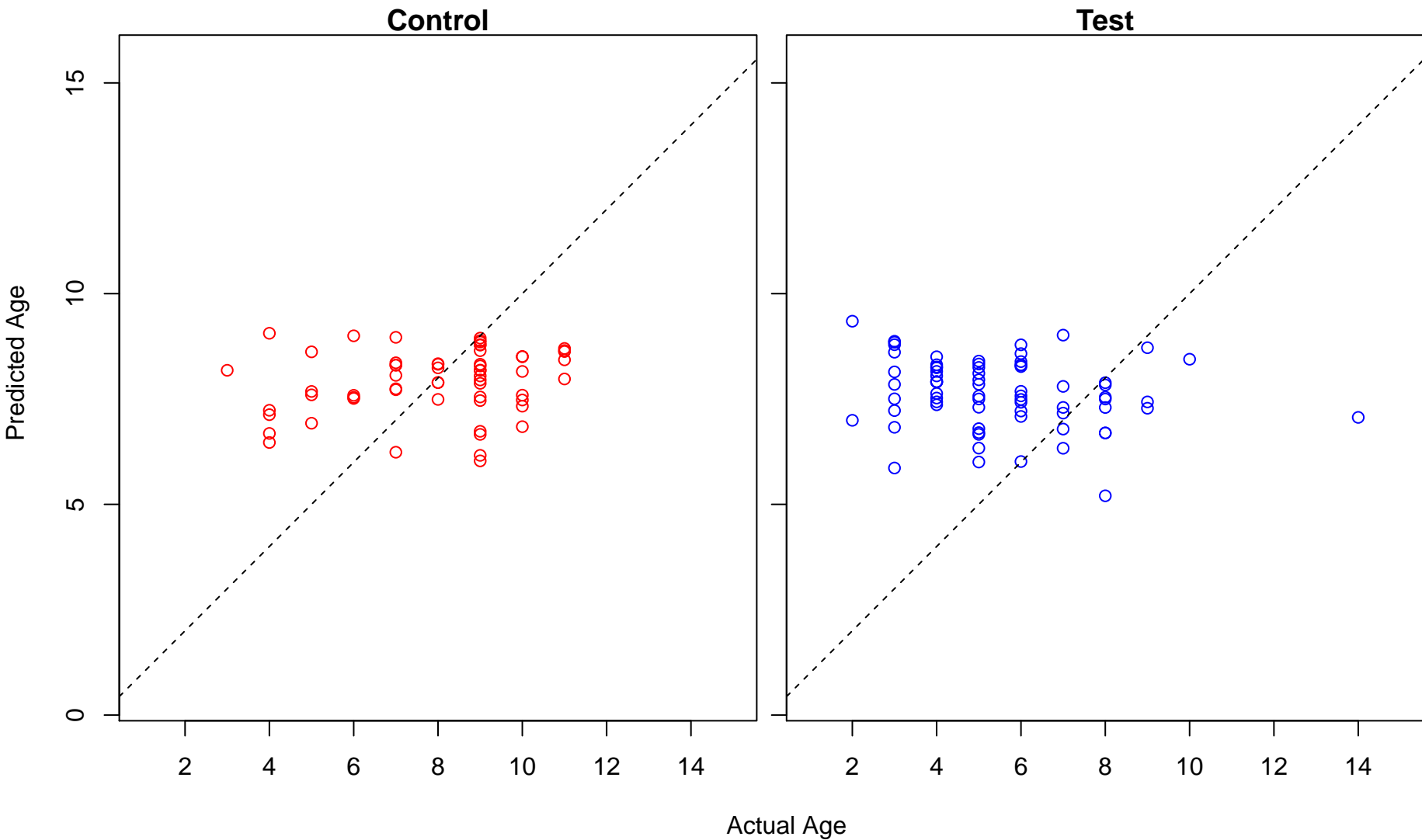


Actual Age

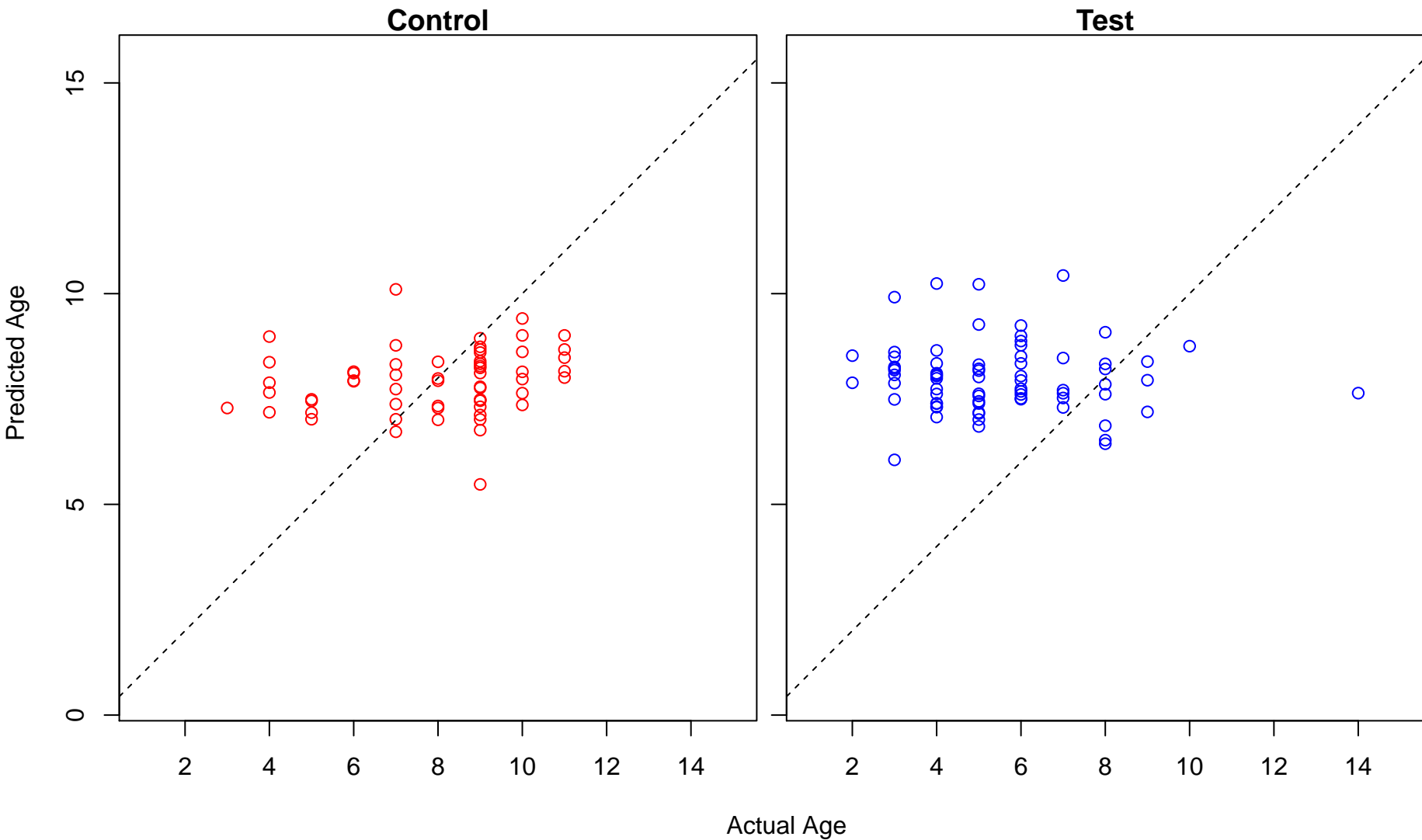
onse to blood flow involved in circulatory renin–angiotensin regulation of systemic arterial blood pressure



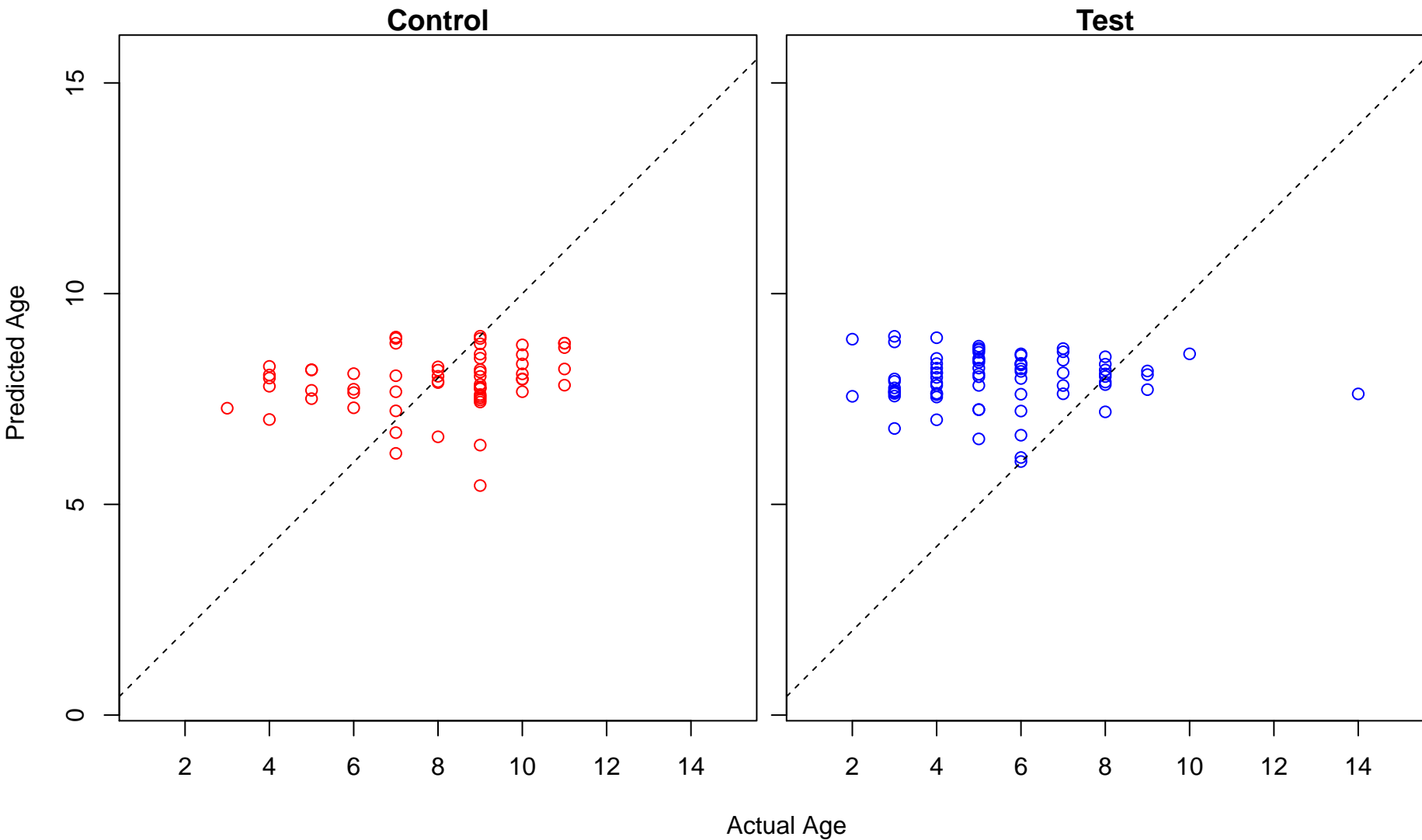
renin secretion into blood stream (Score: 0.204238)



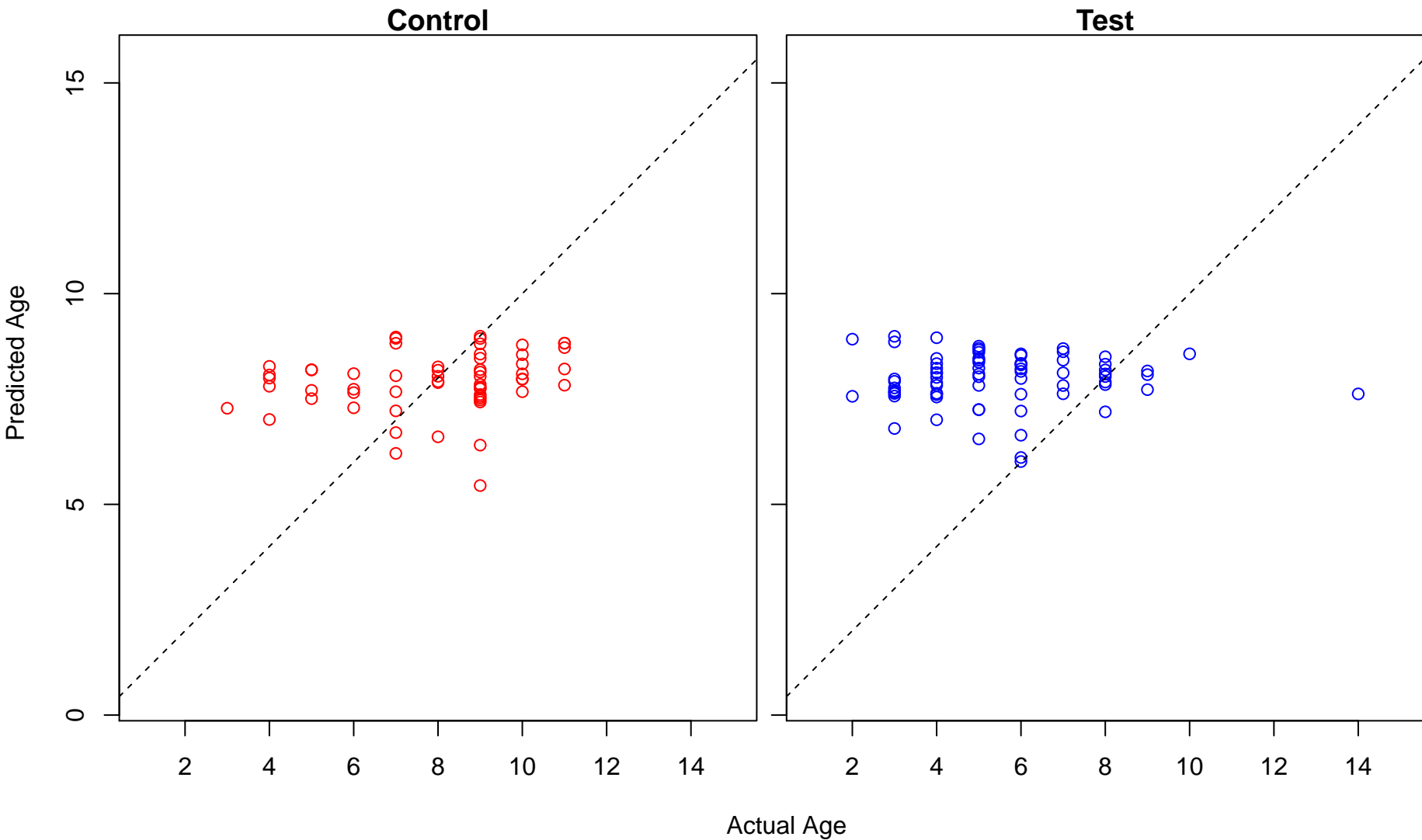
telomere formation via telomerase (Score: 0.203977)



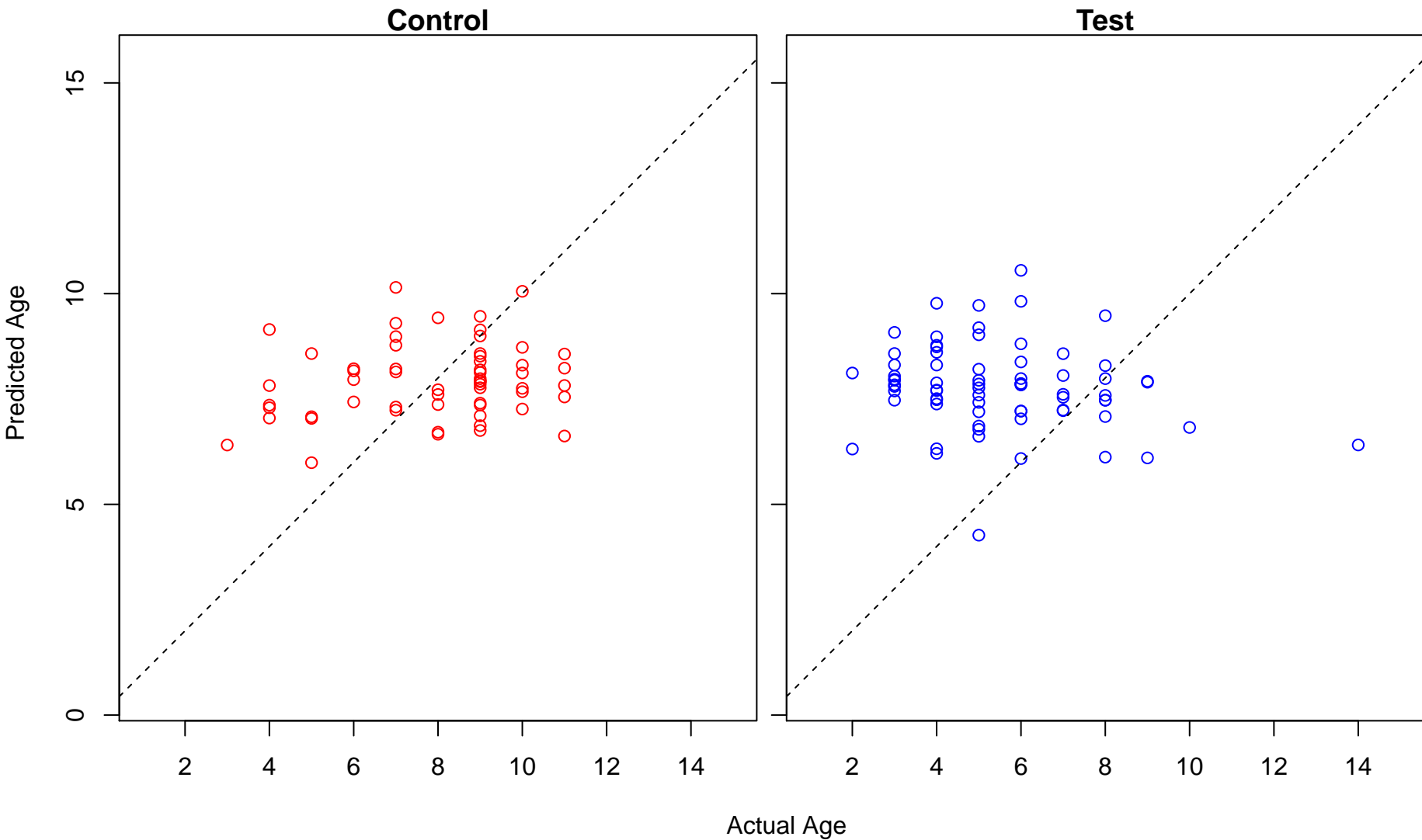
pyruvate transport (Score: 0.203641)



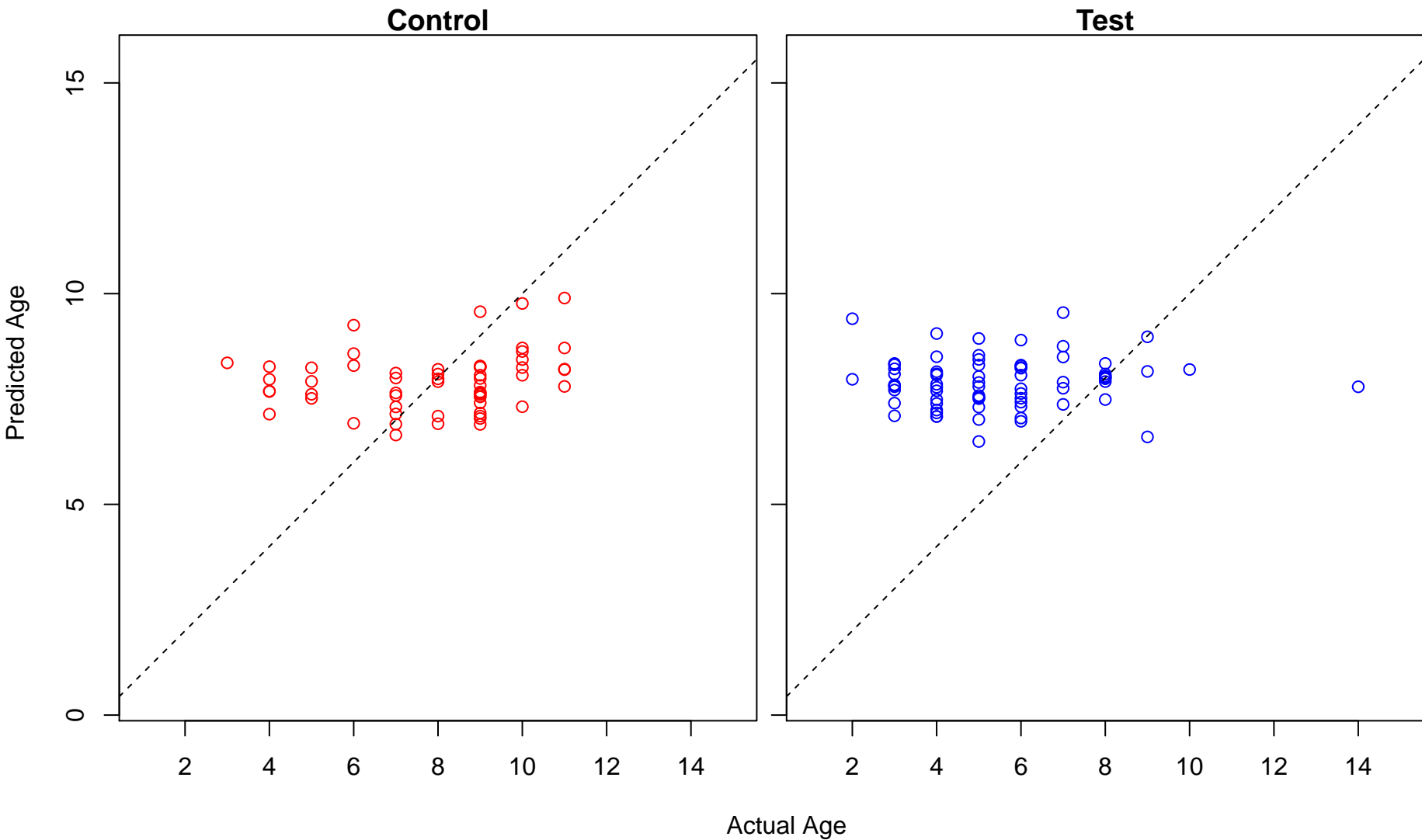
pyruvate transmembrane transport (Score: 0.203641)



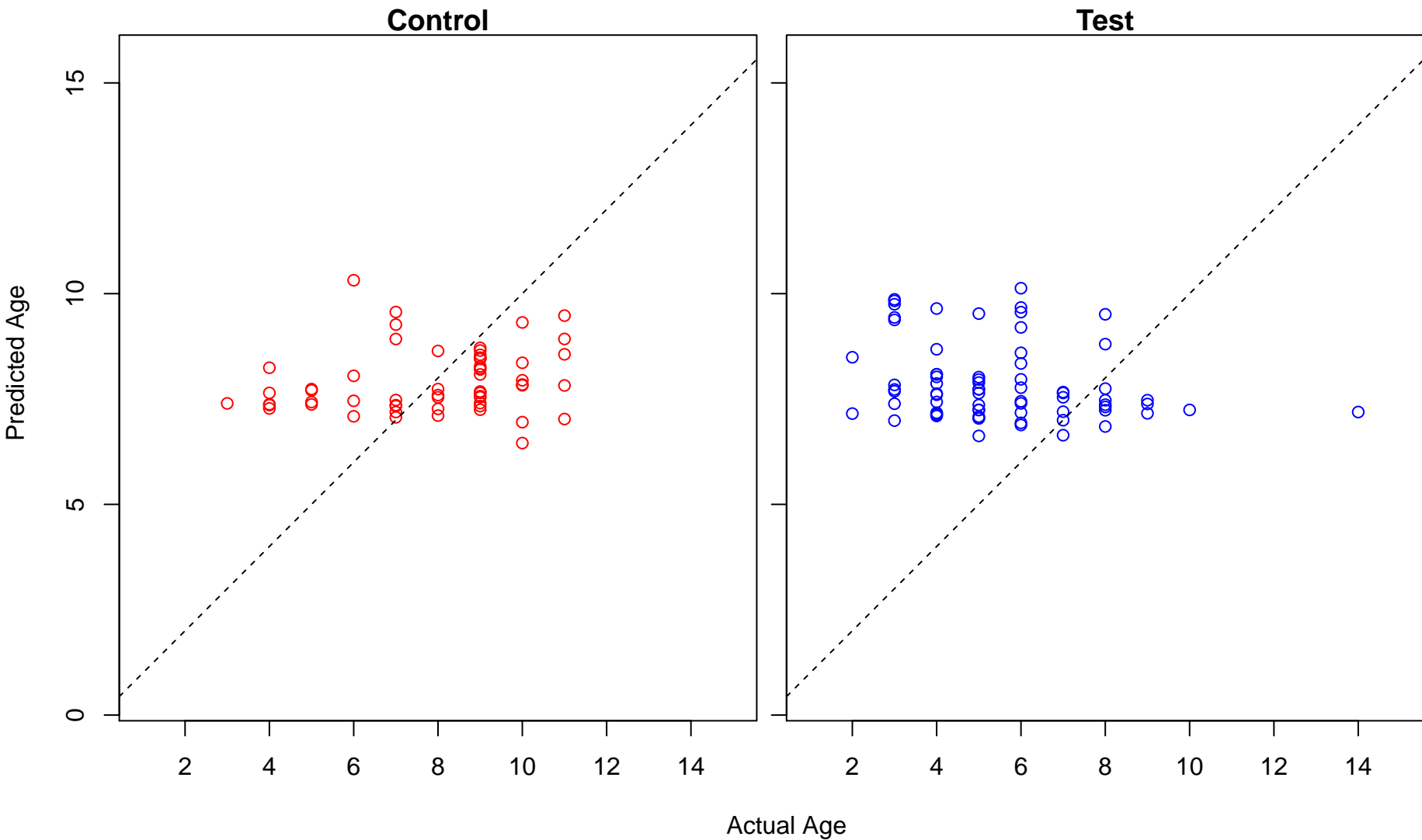
protein deamination (Score: 0.201706)



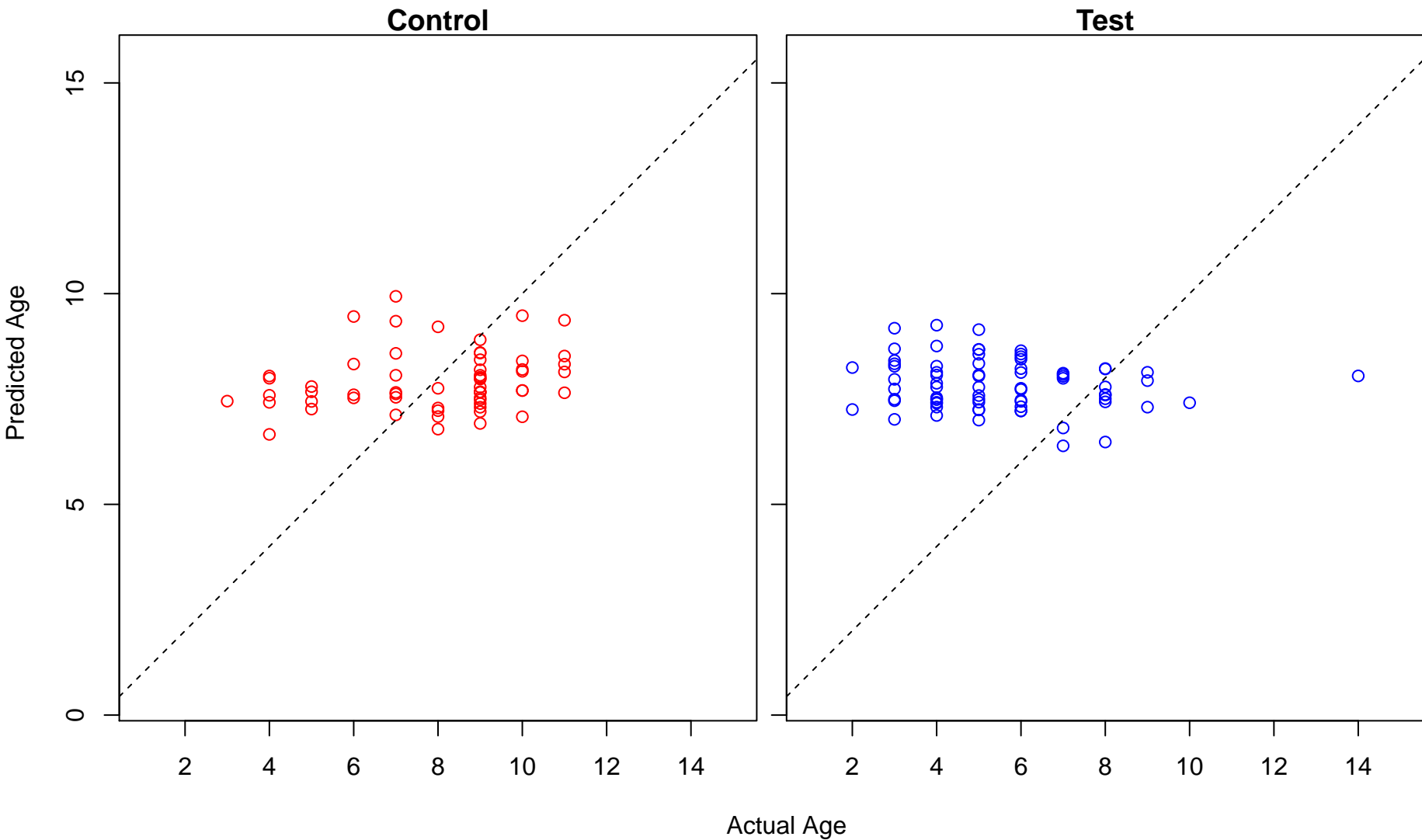
vitamin A metabolic process (Score: 0.198585)



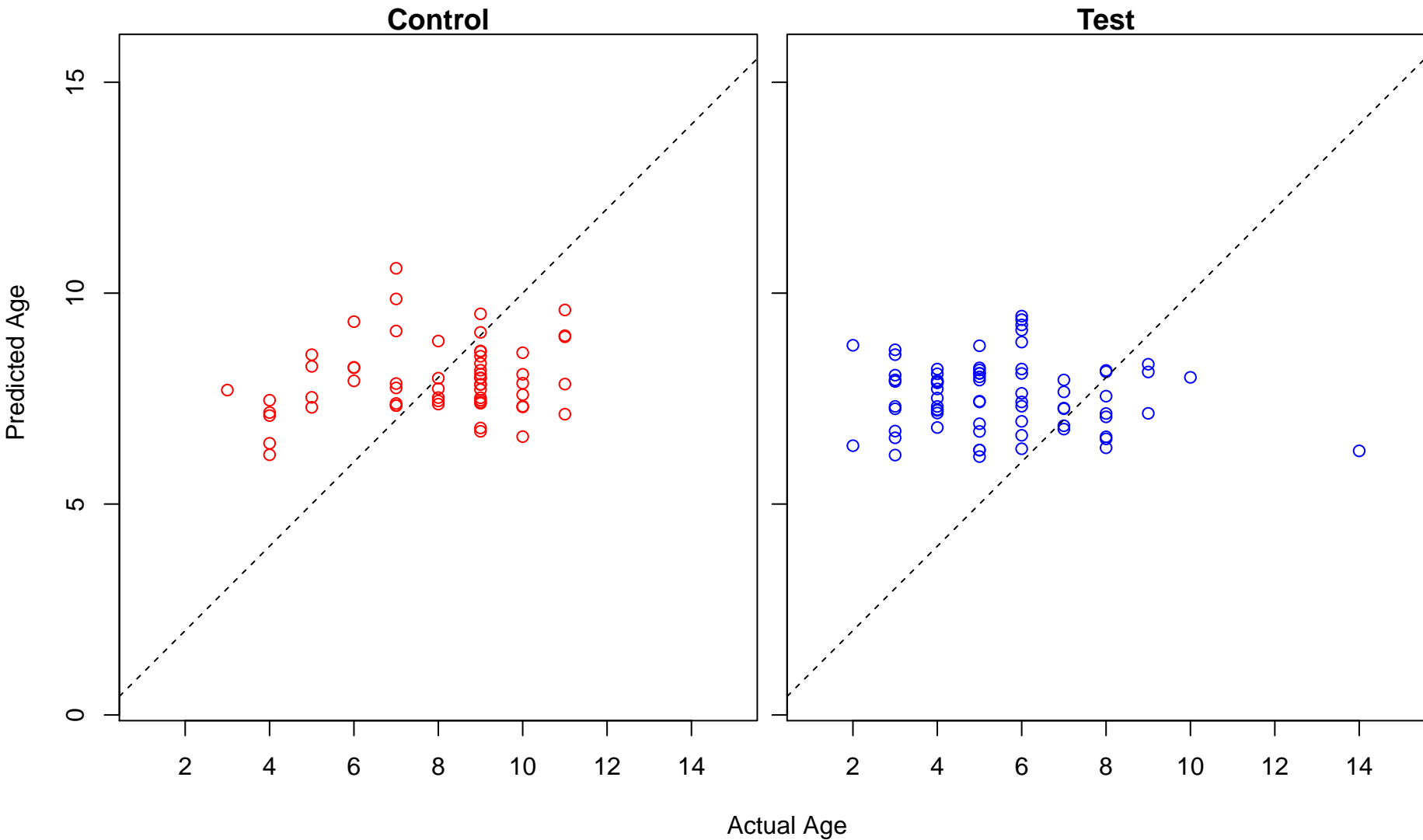
connective tissue replacement involved in inflammatory response wound healing (Score: 0.196772)



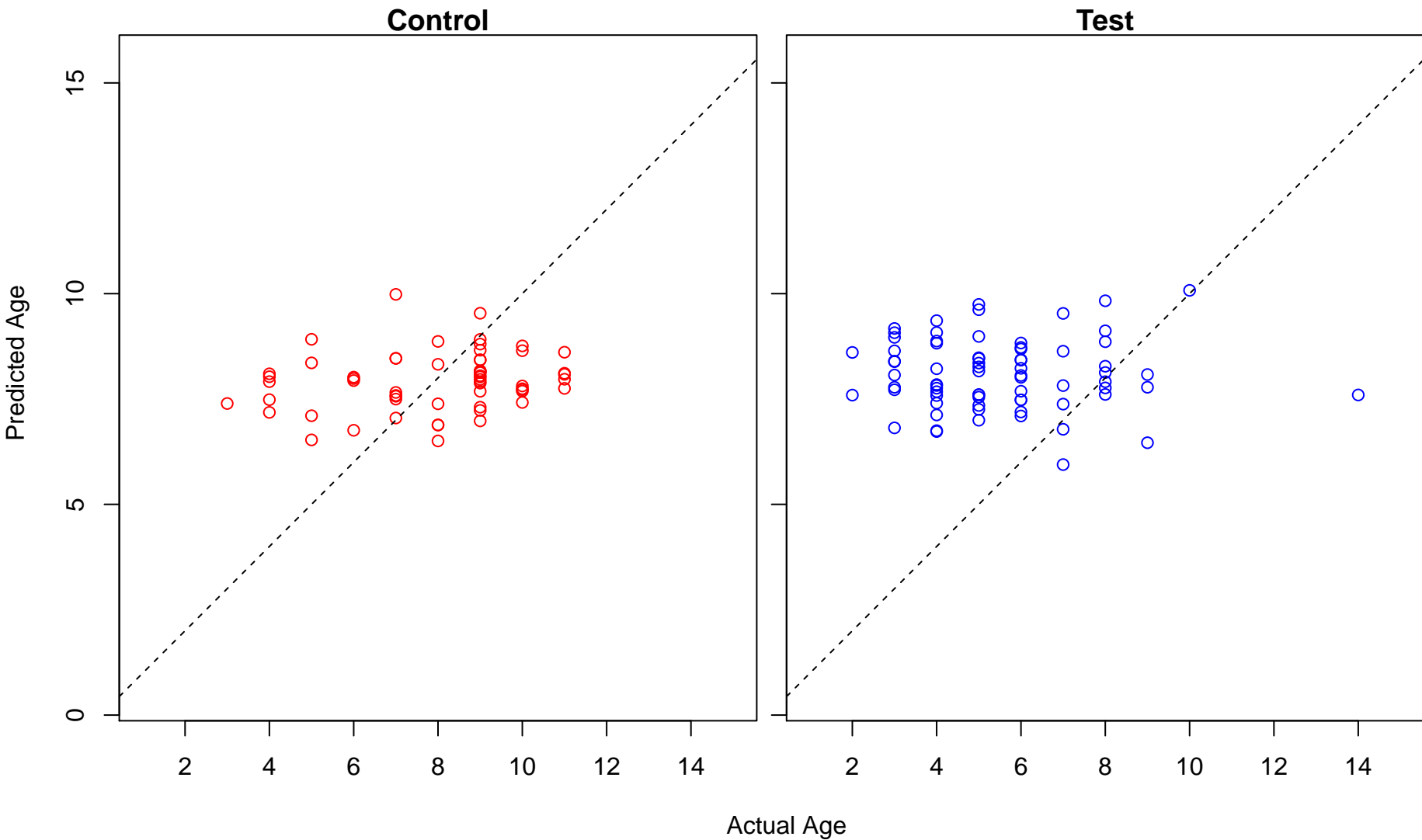
isocitrate metabolic process (Score: 0.196524)



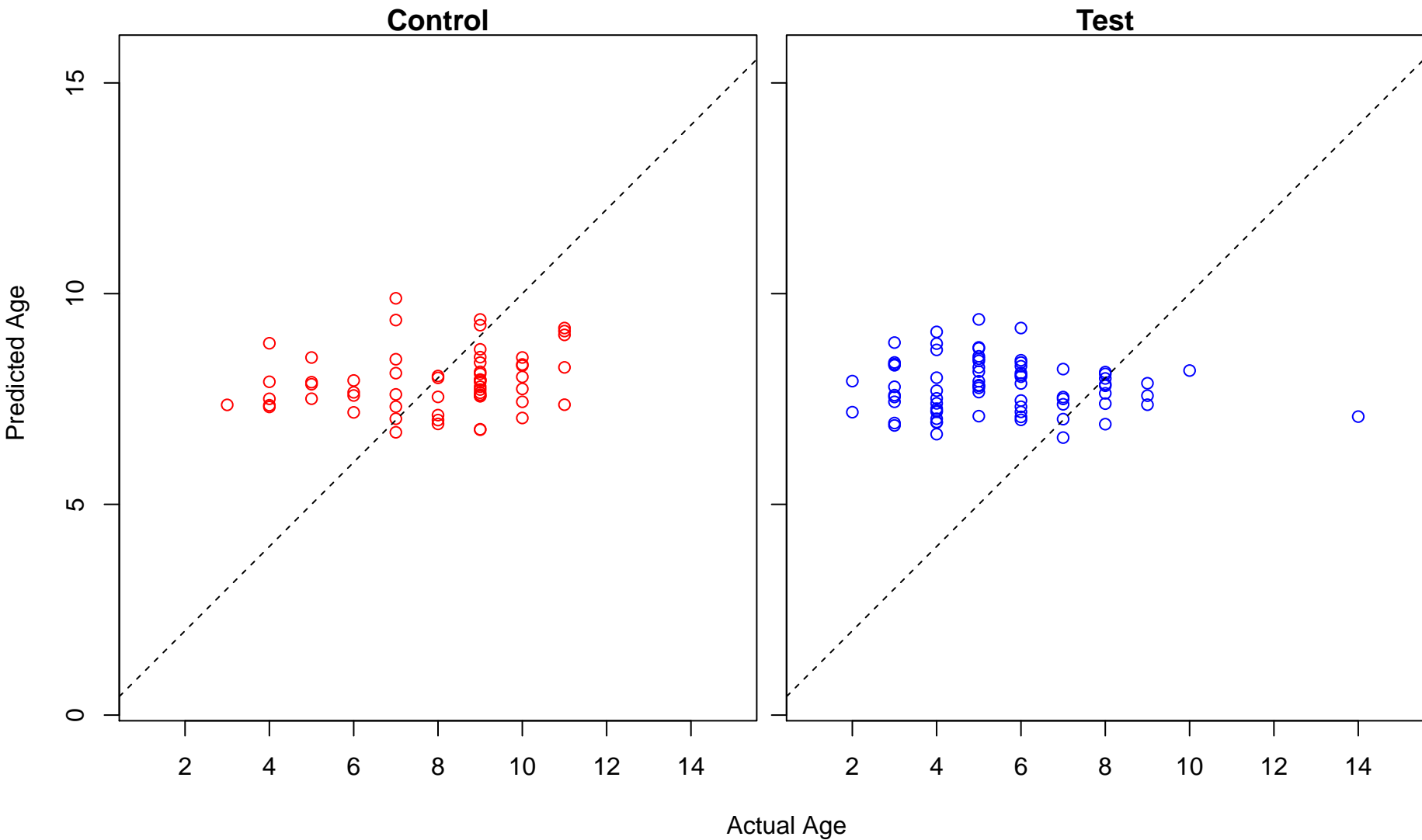
transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 0.194914)



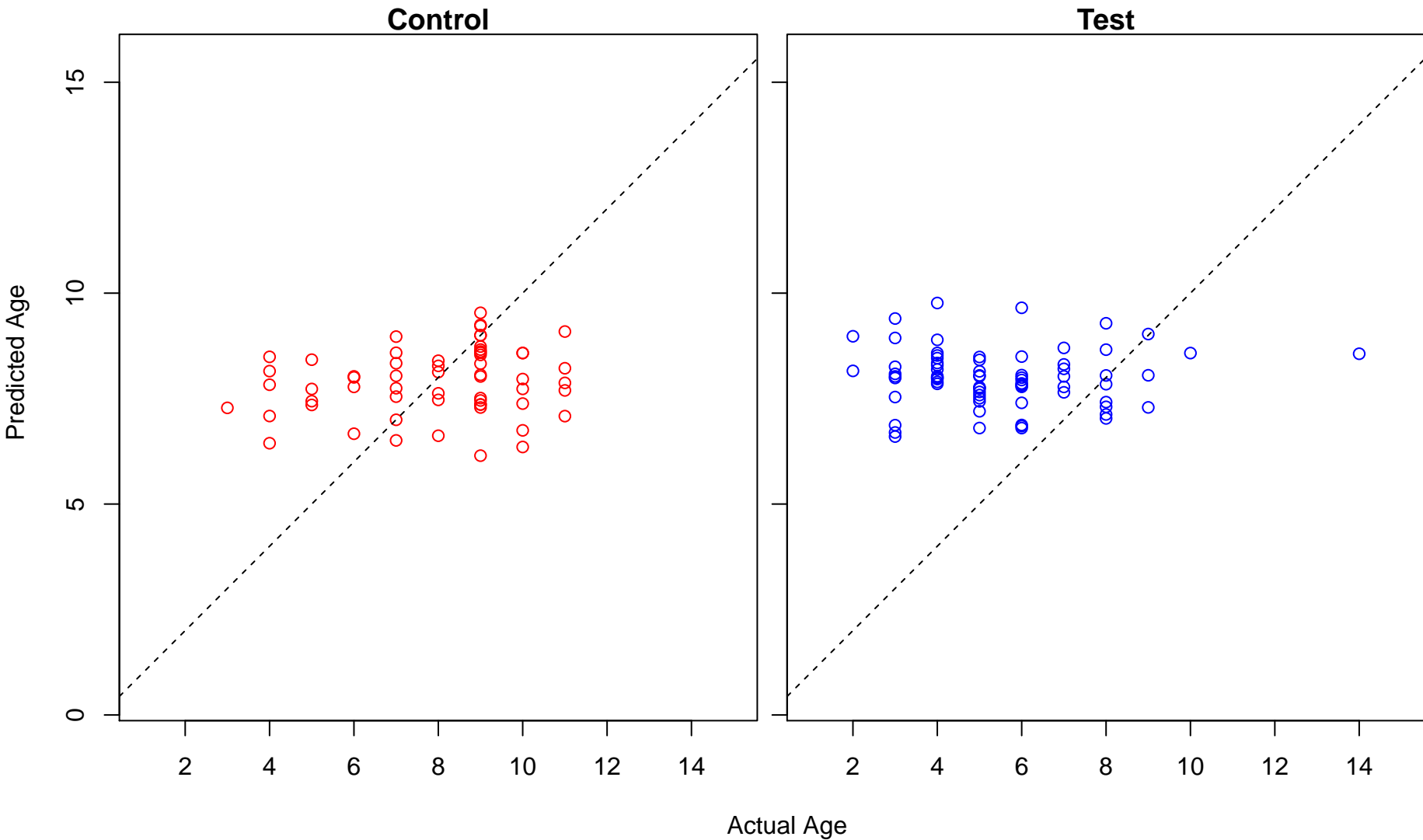
spermine metabolic process (Score: 0.194725)



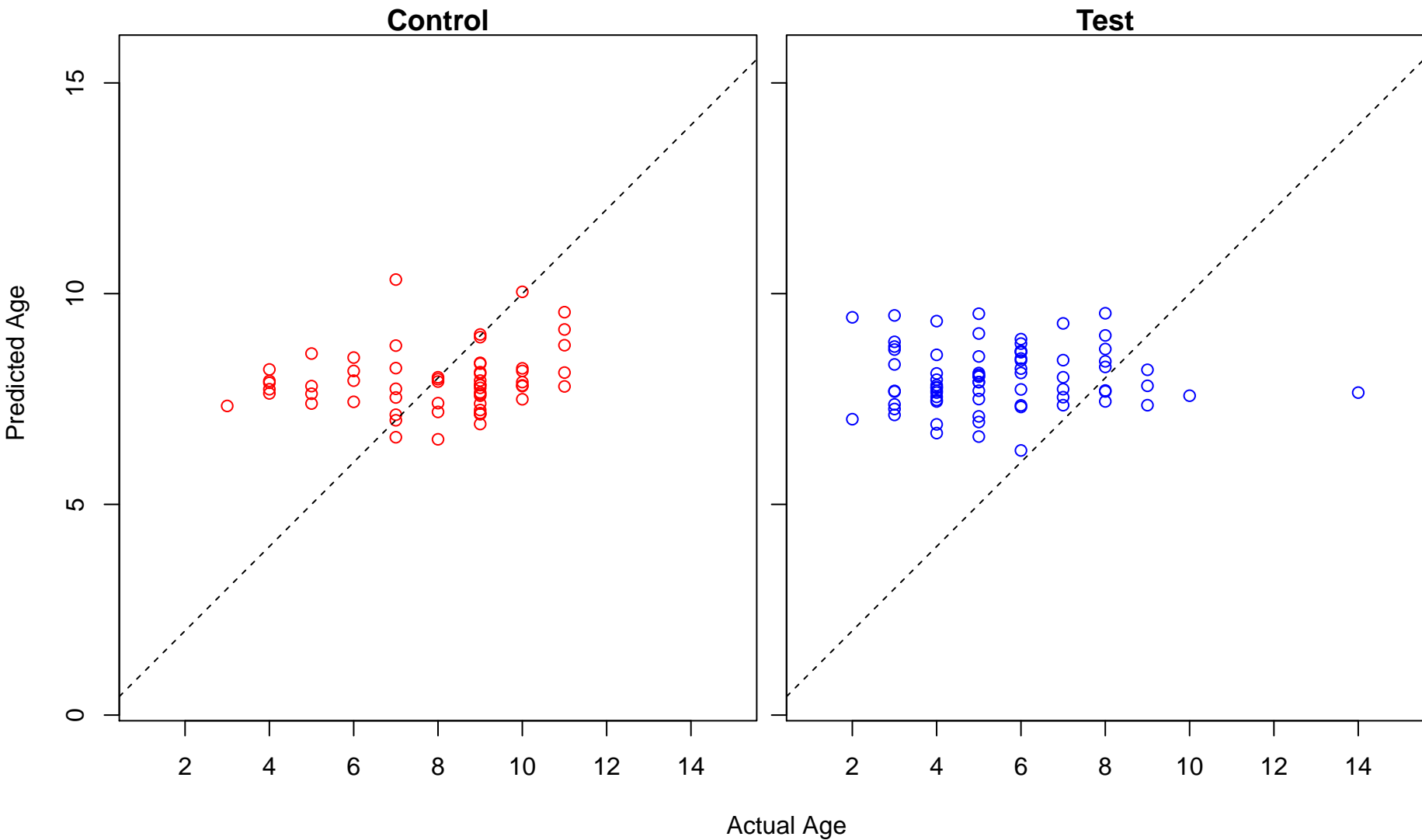
central nervous system myelin formation (Score: 0.189164)



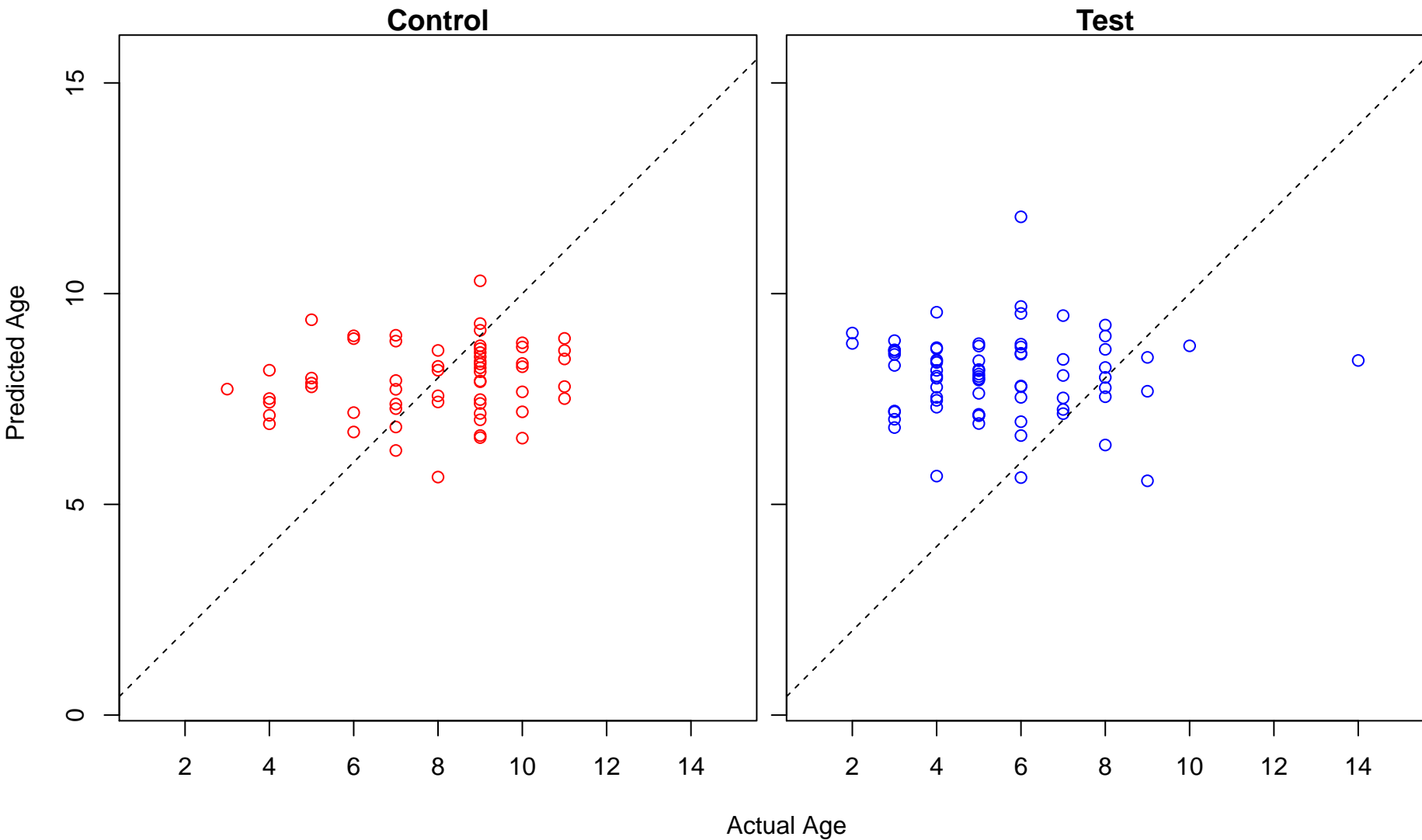
negative regulation of protein glycosylation (Score: 0.188523)



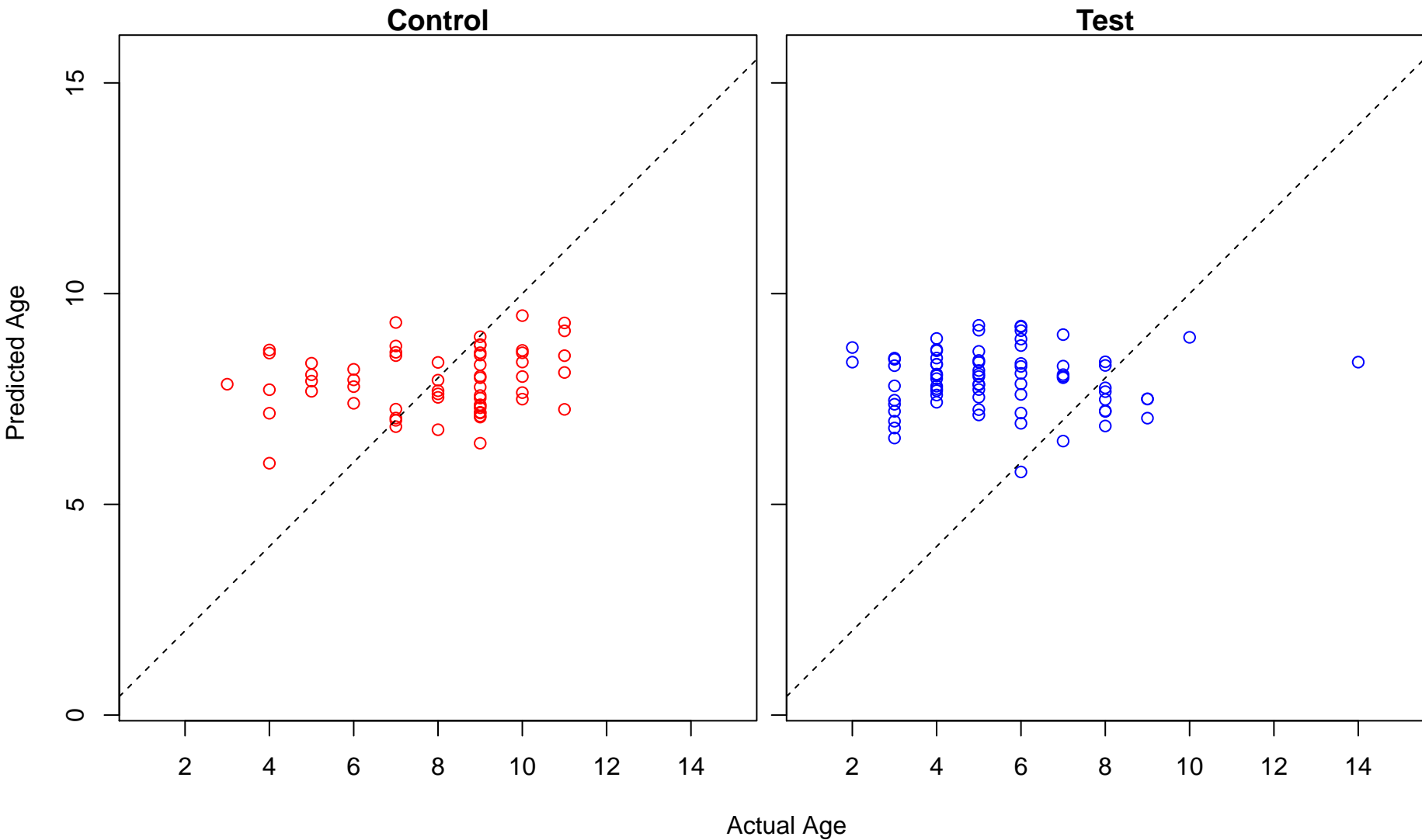
carnitine metabolic process, CoA-linked (Score: 0.184205)



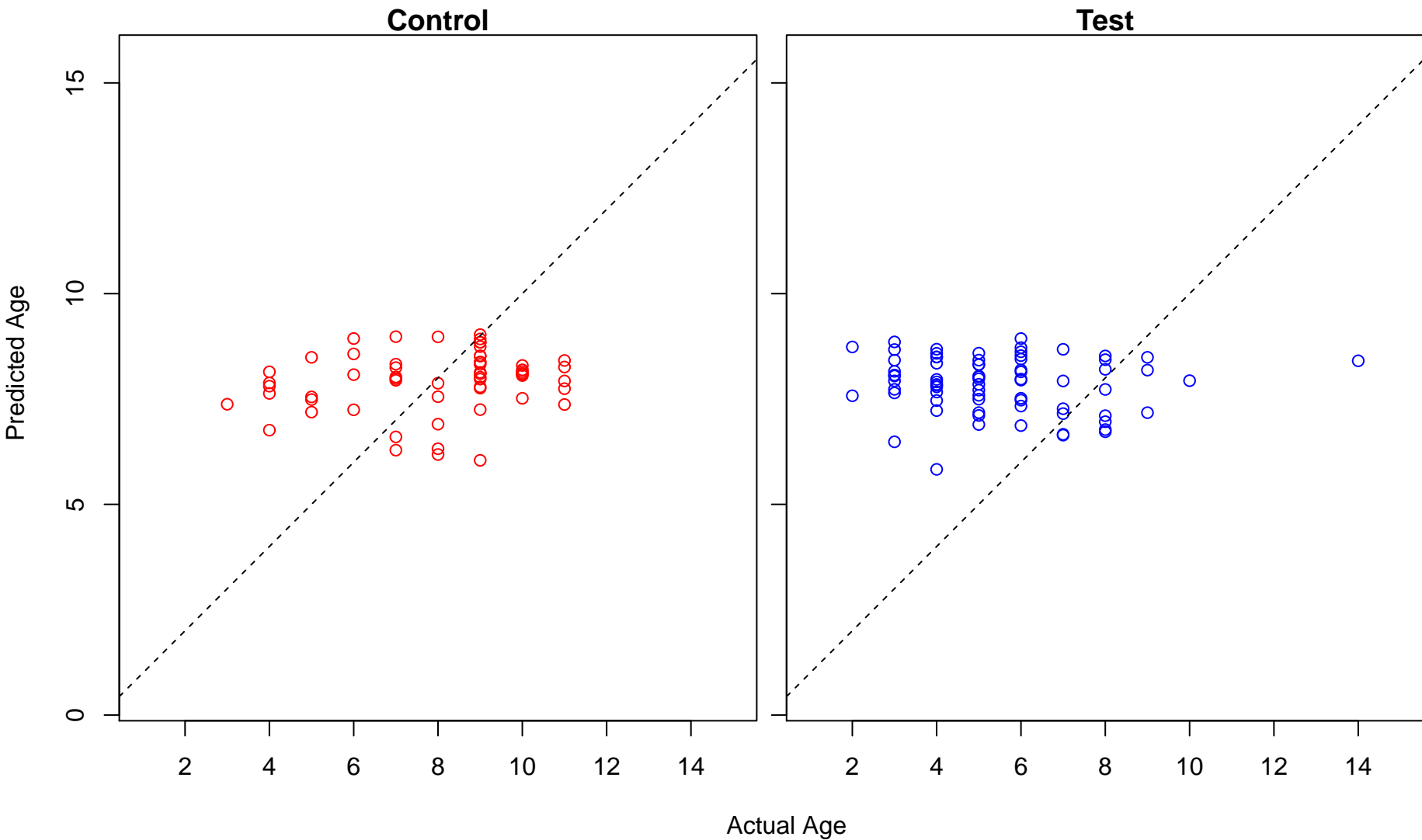
actin rod assembly (Score: 0.183996)



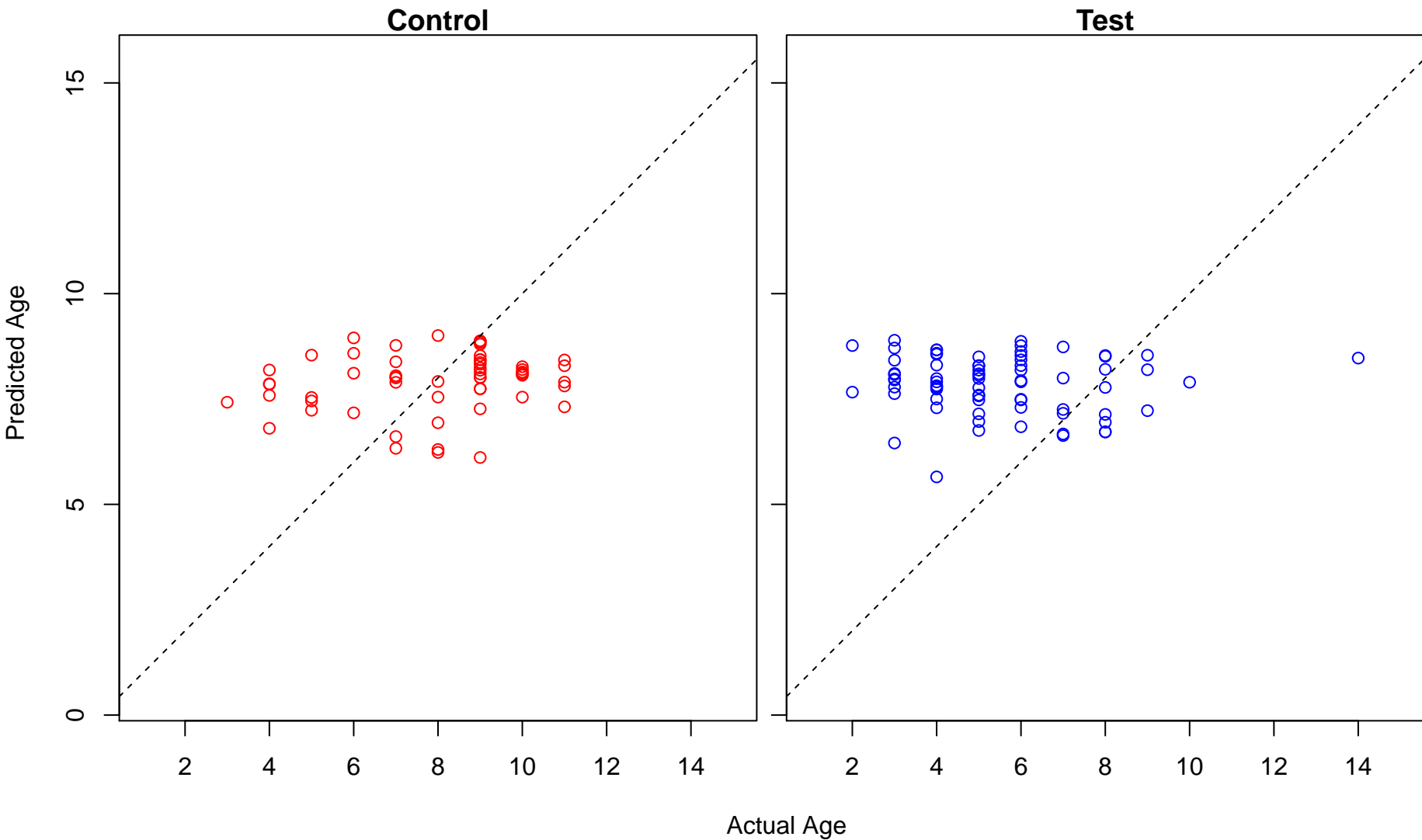
iron ion transmembrane transport (Score: 0.183805)



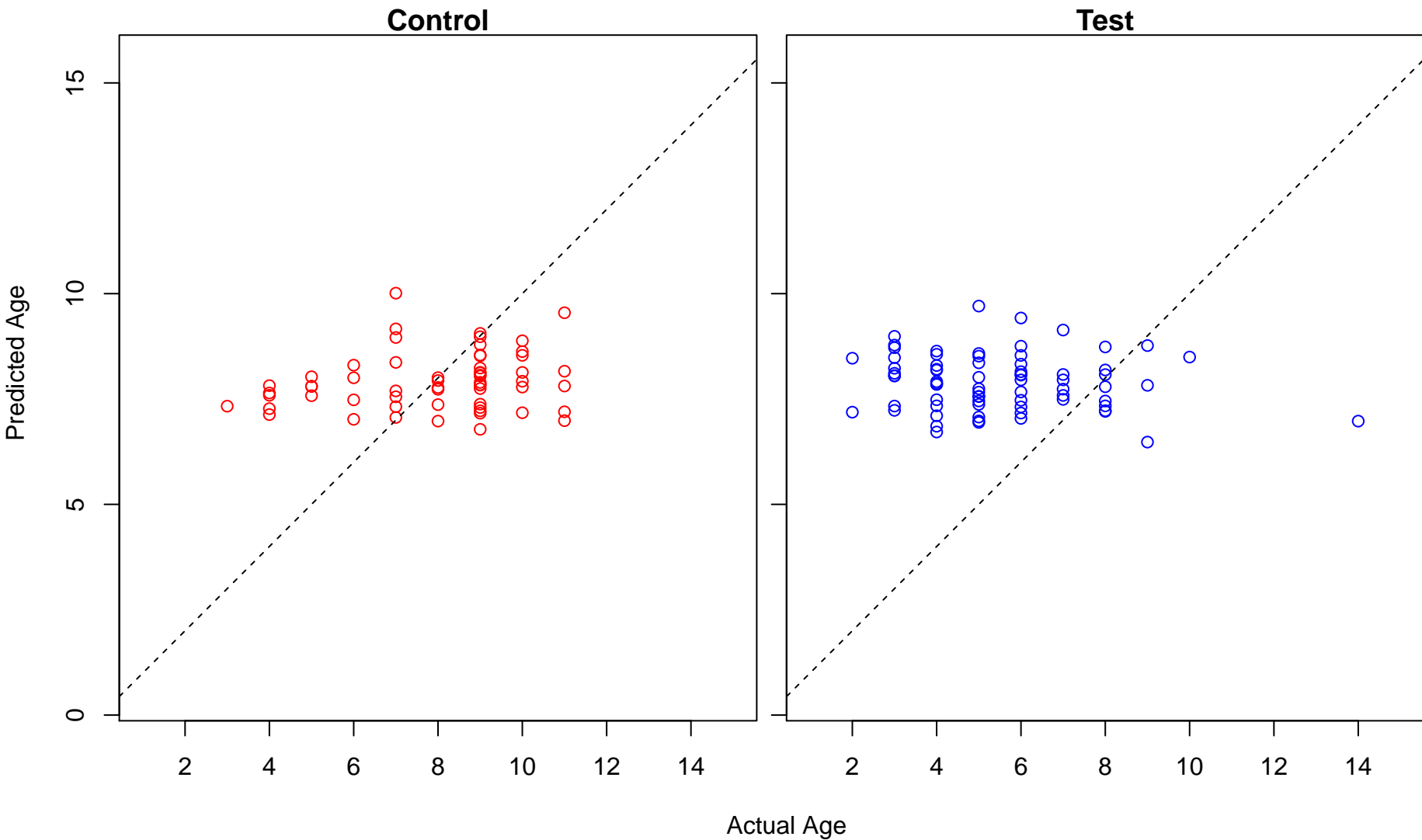
fasciculation of sensory neuron axon (Score: 0.183308)



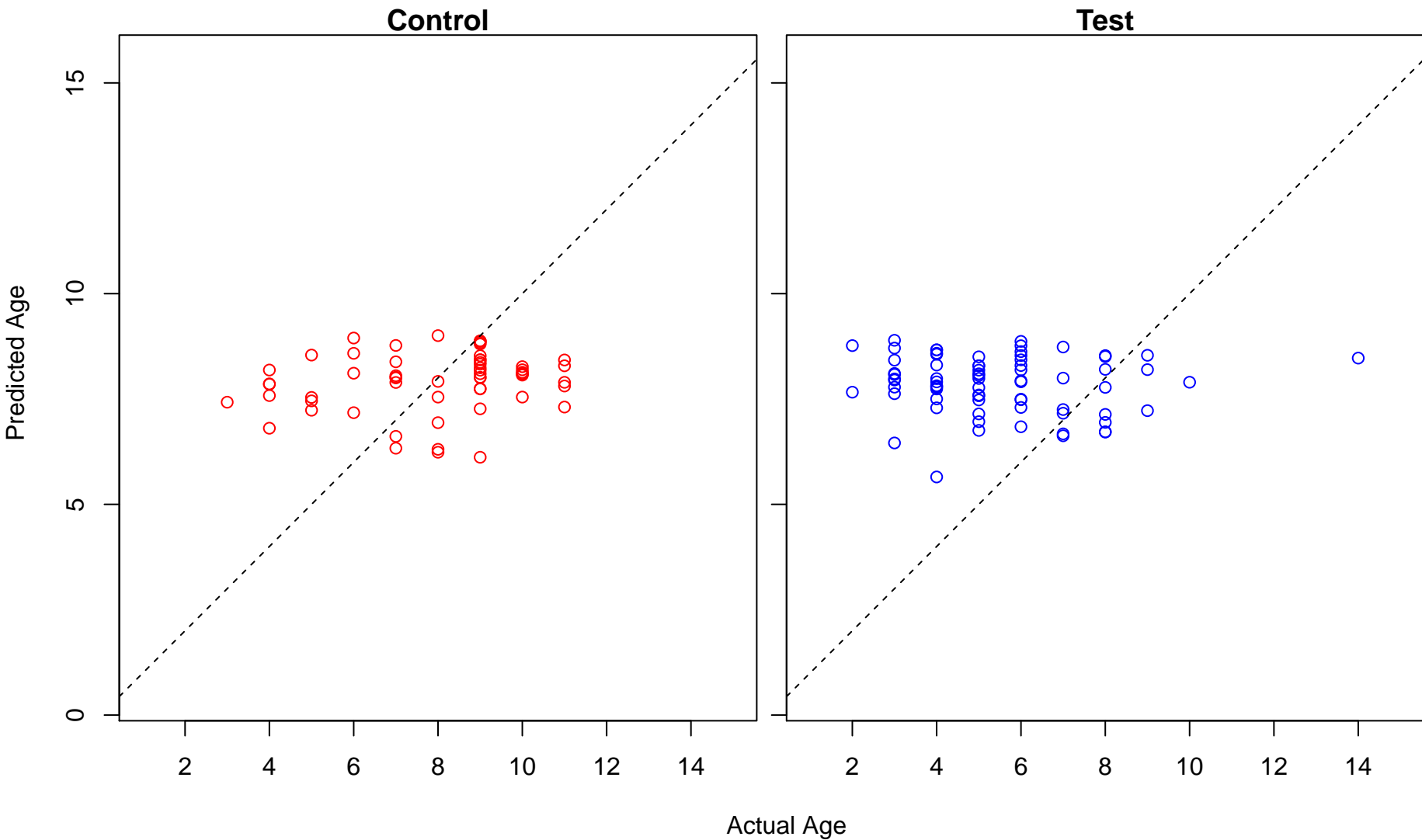
fasciculation of motor neuron axon (Score: 0.182675)



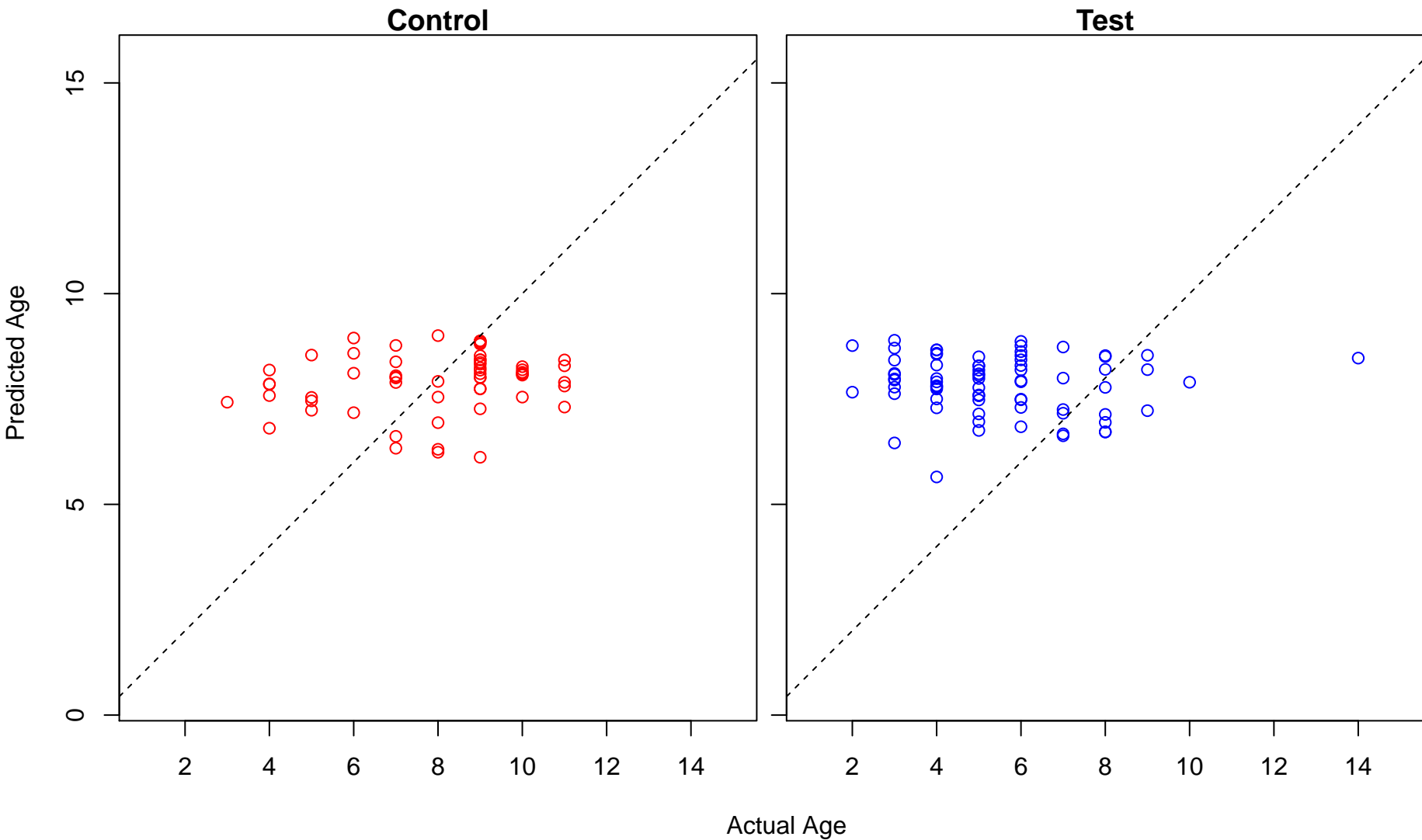
microspike assembly (Score: 0.182308)



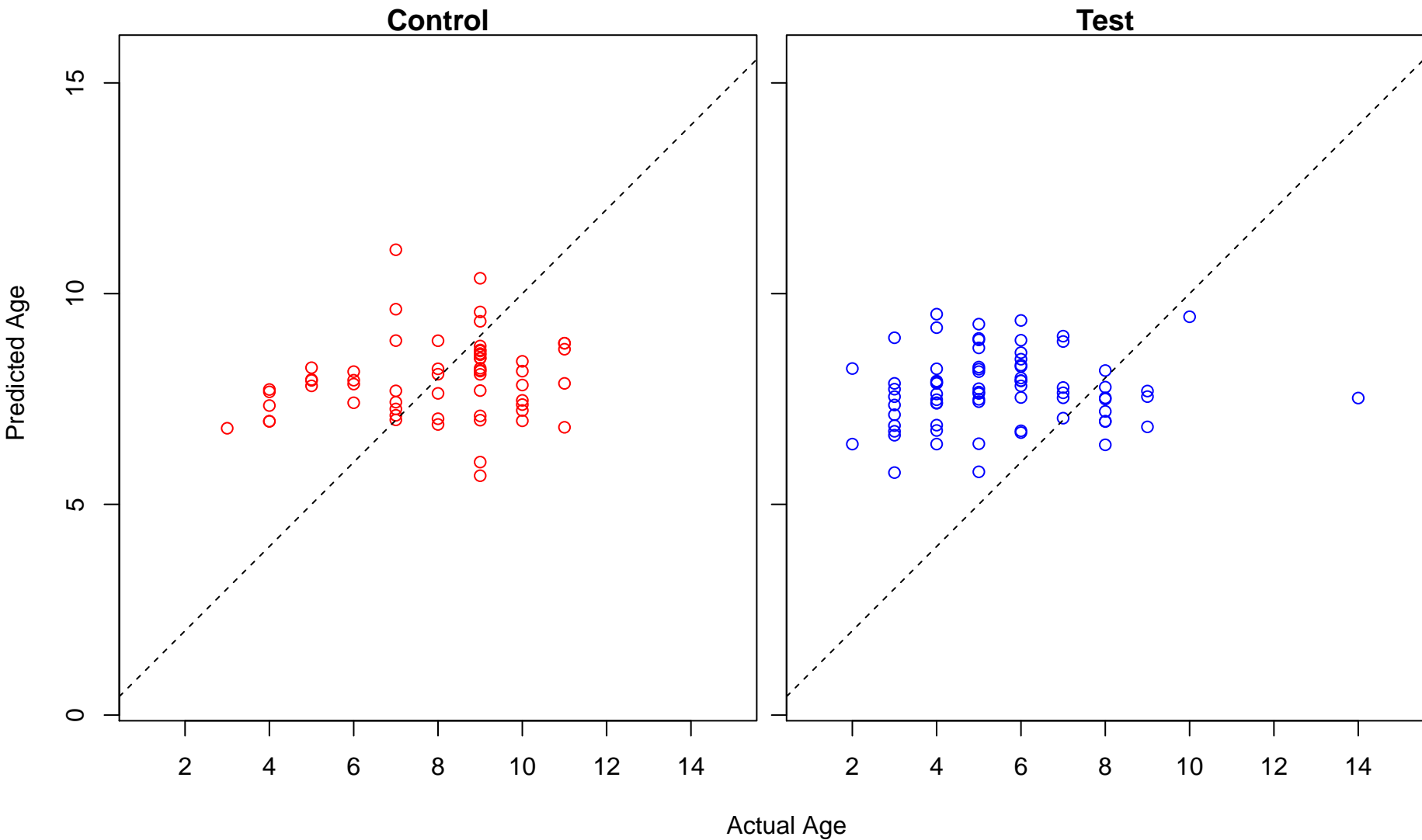
regulation of Rho guanyl–nucleotide exchange factor activity (Score: 0.182164)



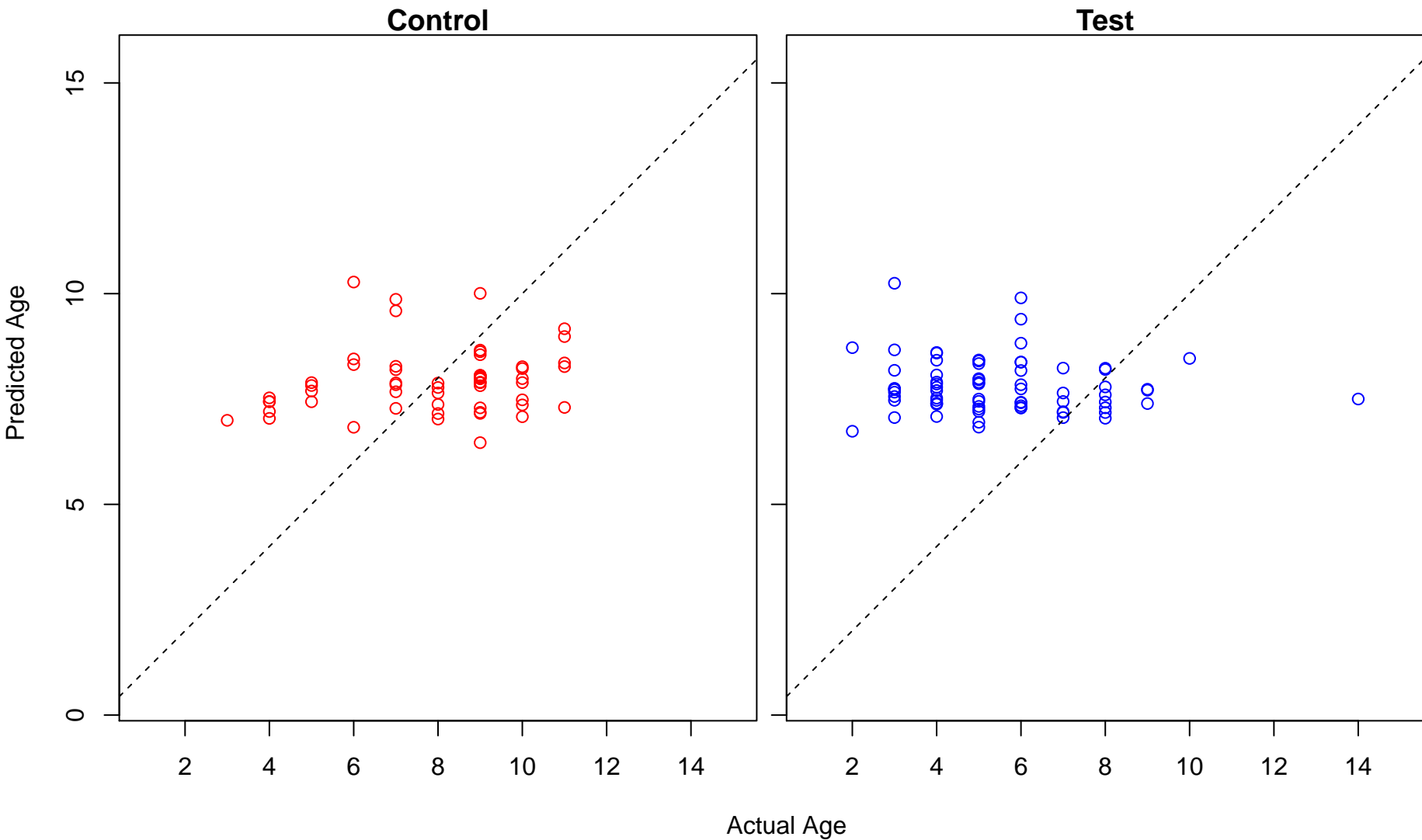
positive regulation of Rho guanyl-nucleotide exchange factor activity (Score: 0.182164)



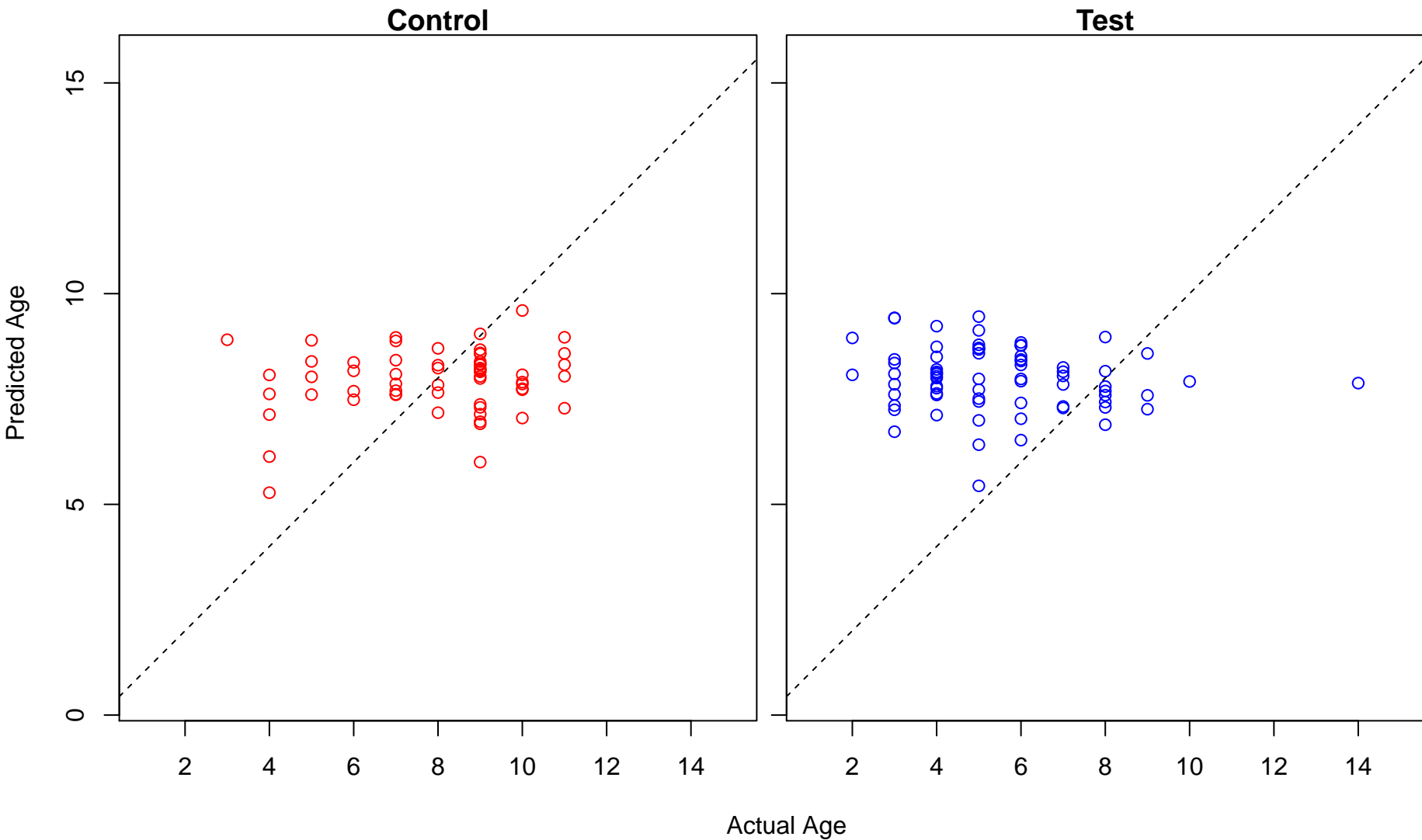
regulation of NFAT protein import into nucleus (Score: 0.179474)



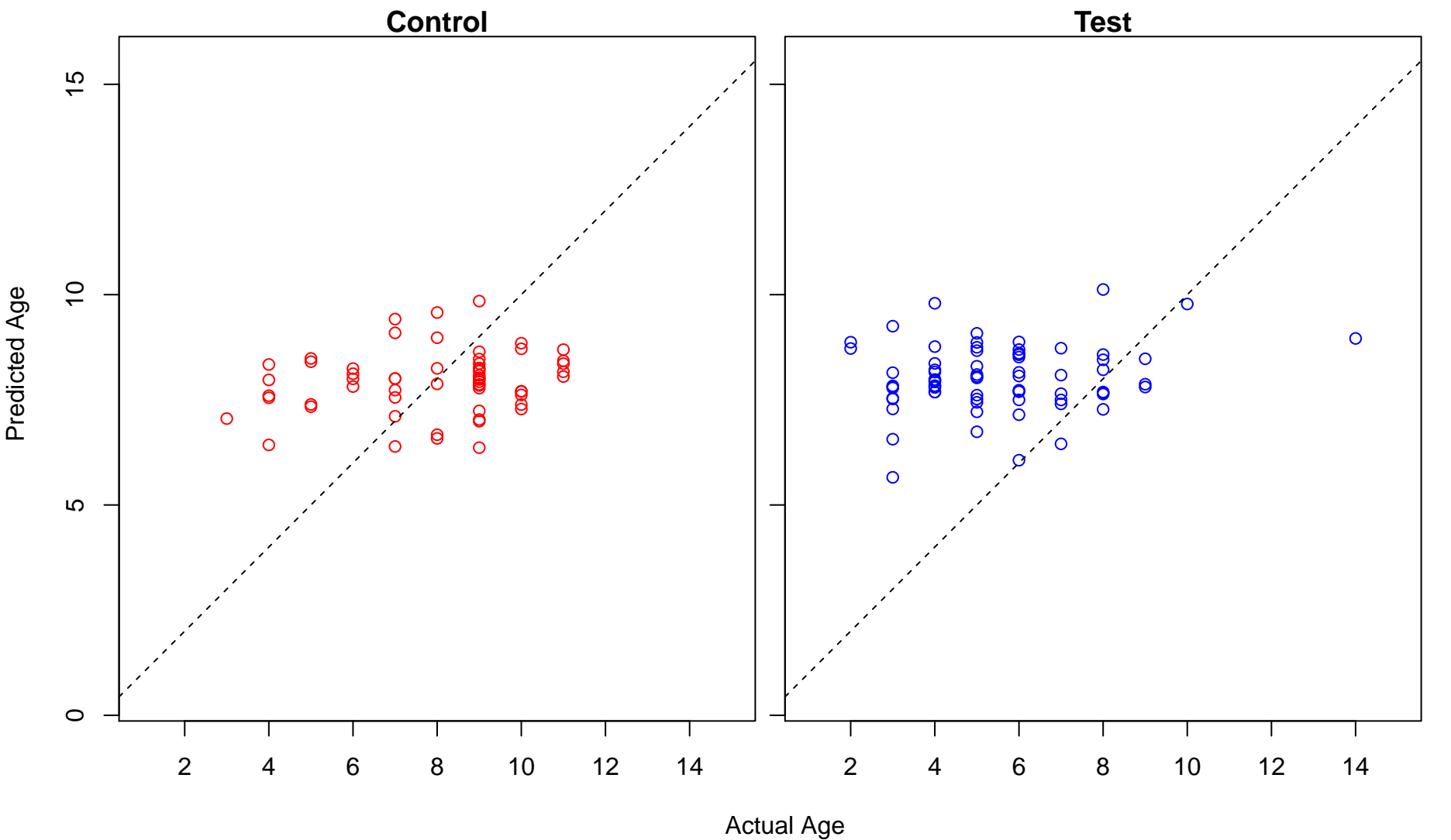
complement activation, alternative pathway (Score: 0.177221)



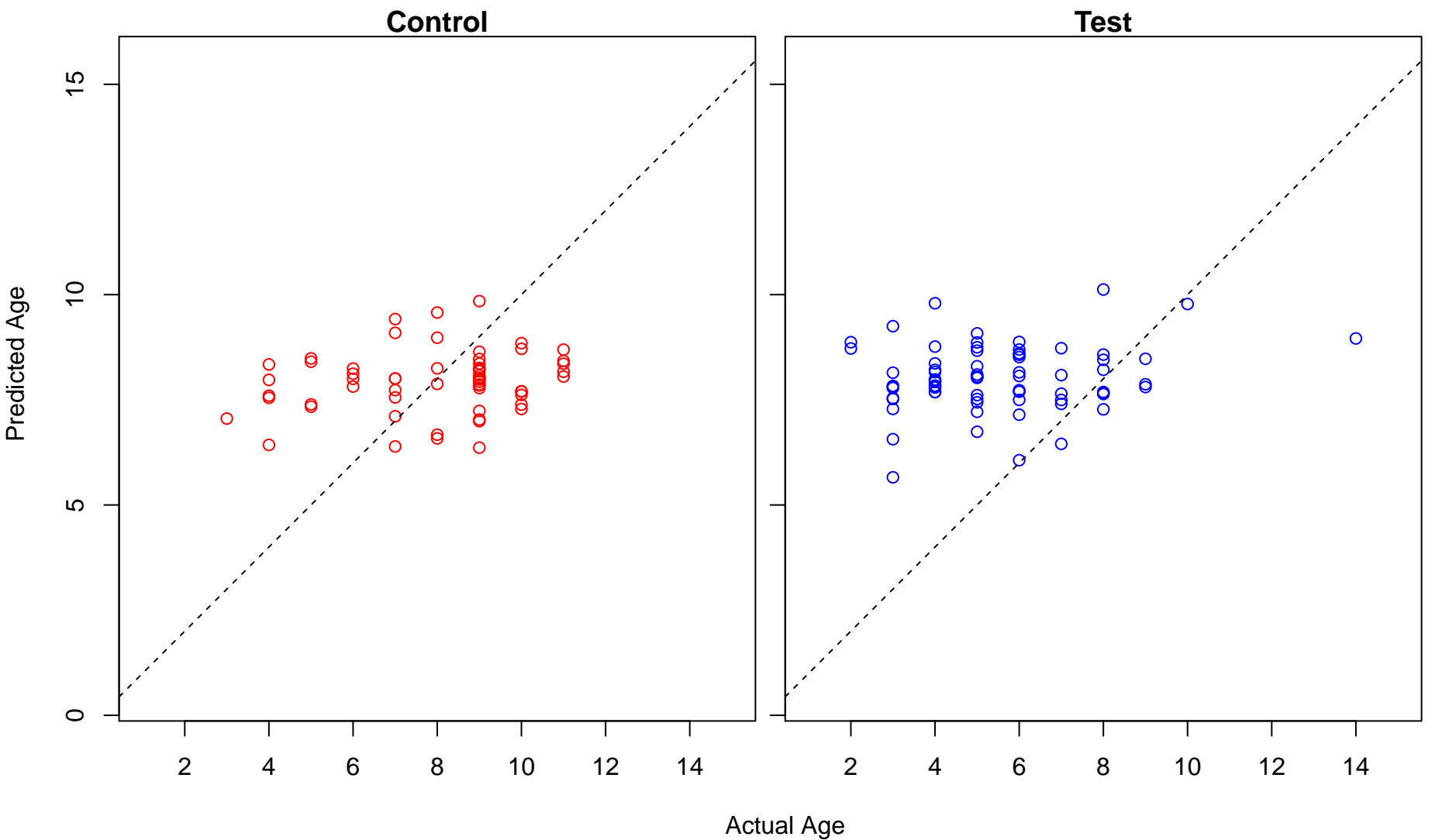
positive regulation of mitochondrial translation (Score: 0.176316)



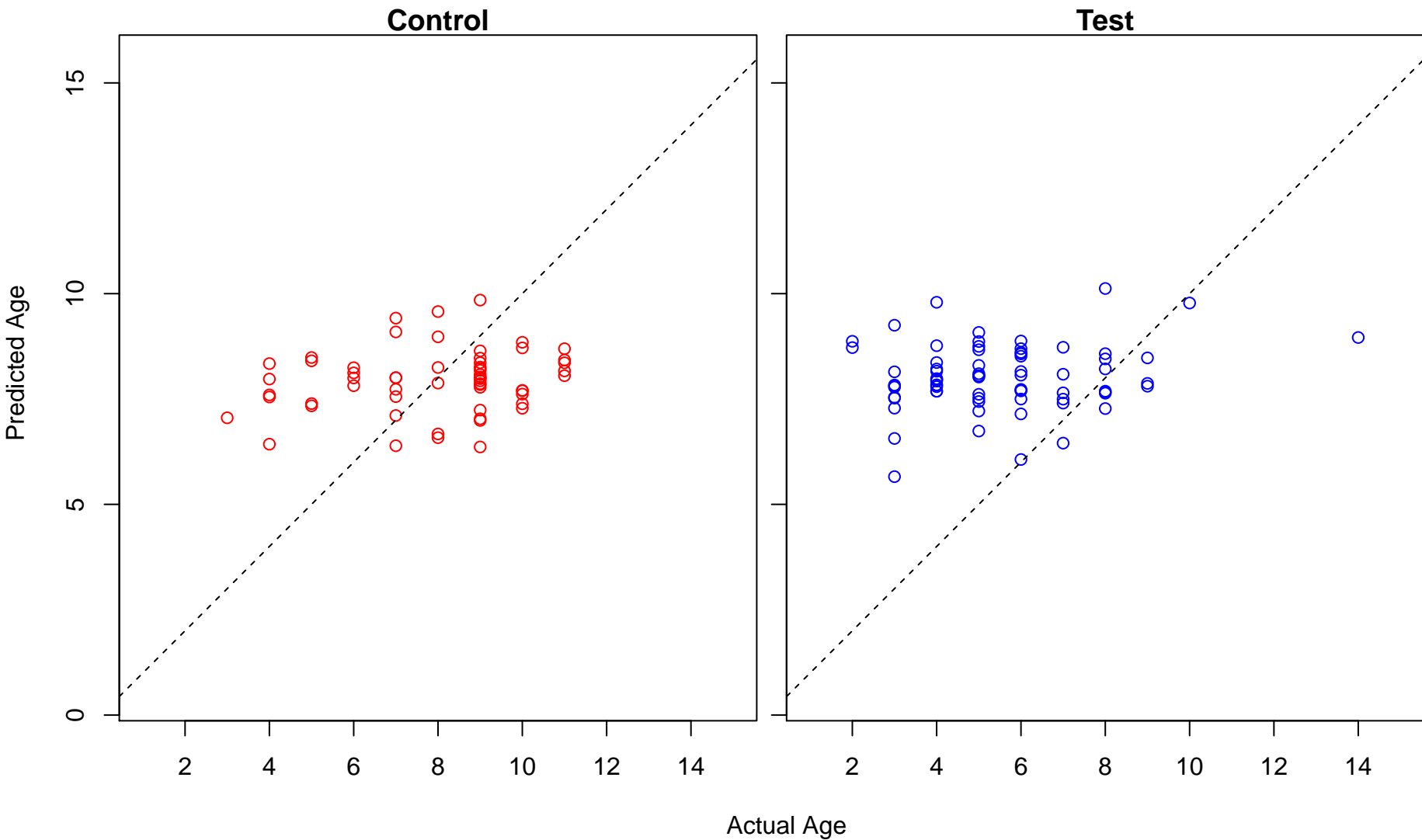
Antigen processing and presentation of endogenous peptide antigen via MHC class Ib via ER pathway (Score



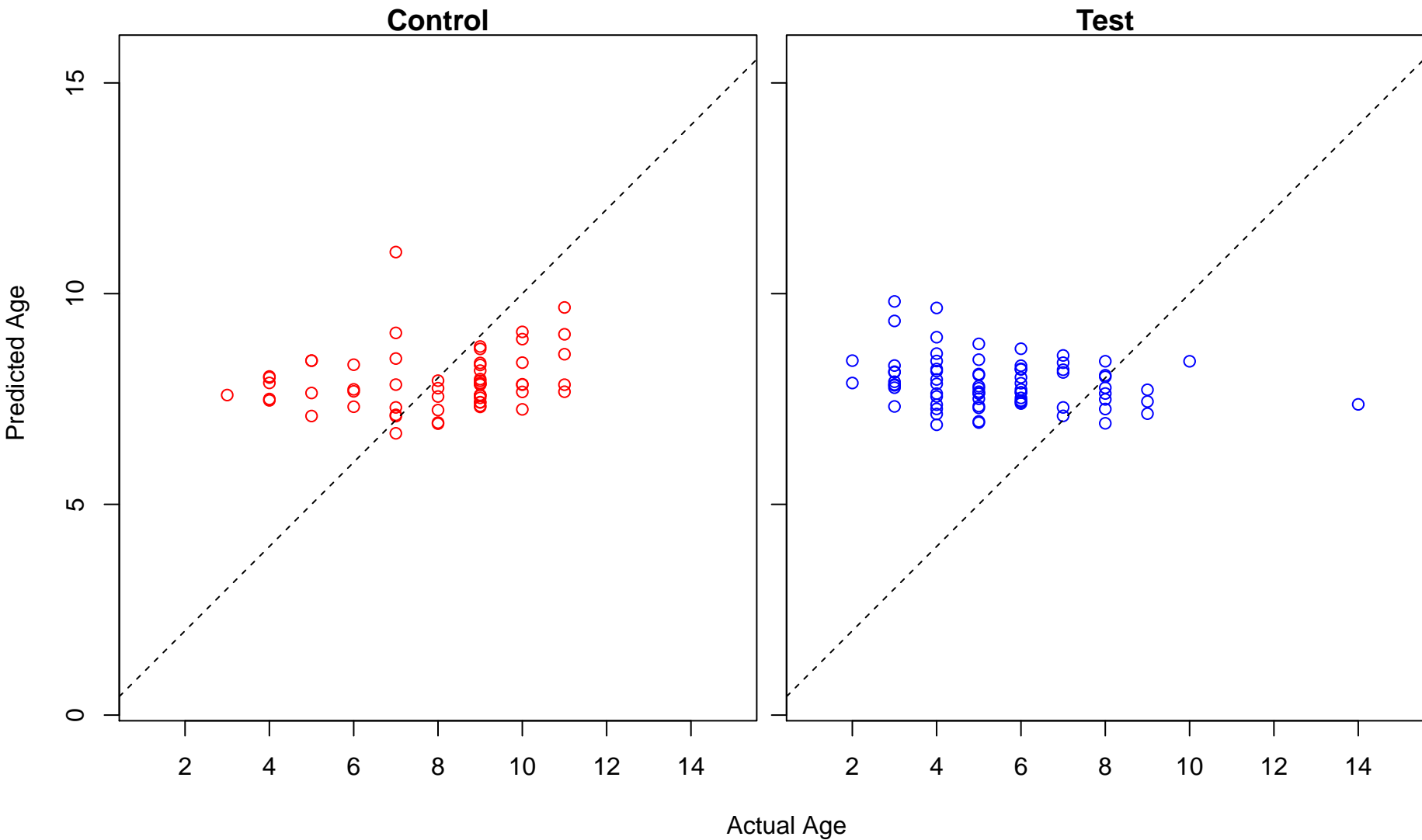
Processing and presentation of endogenous peptide antigen via MHC class Ib via ER pathway, TAP-depende



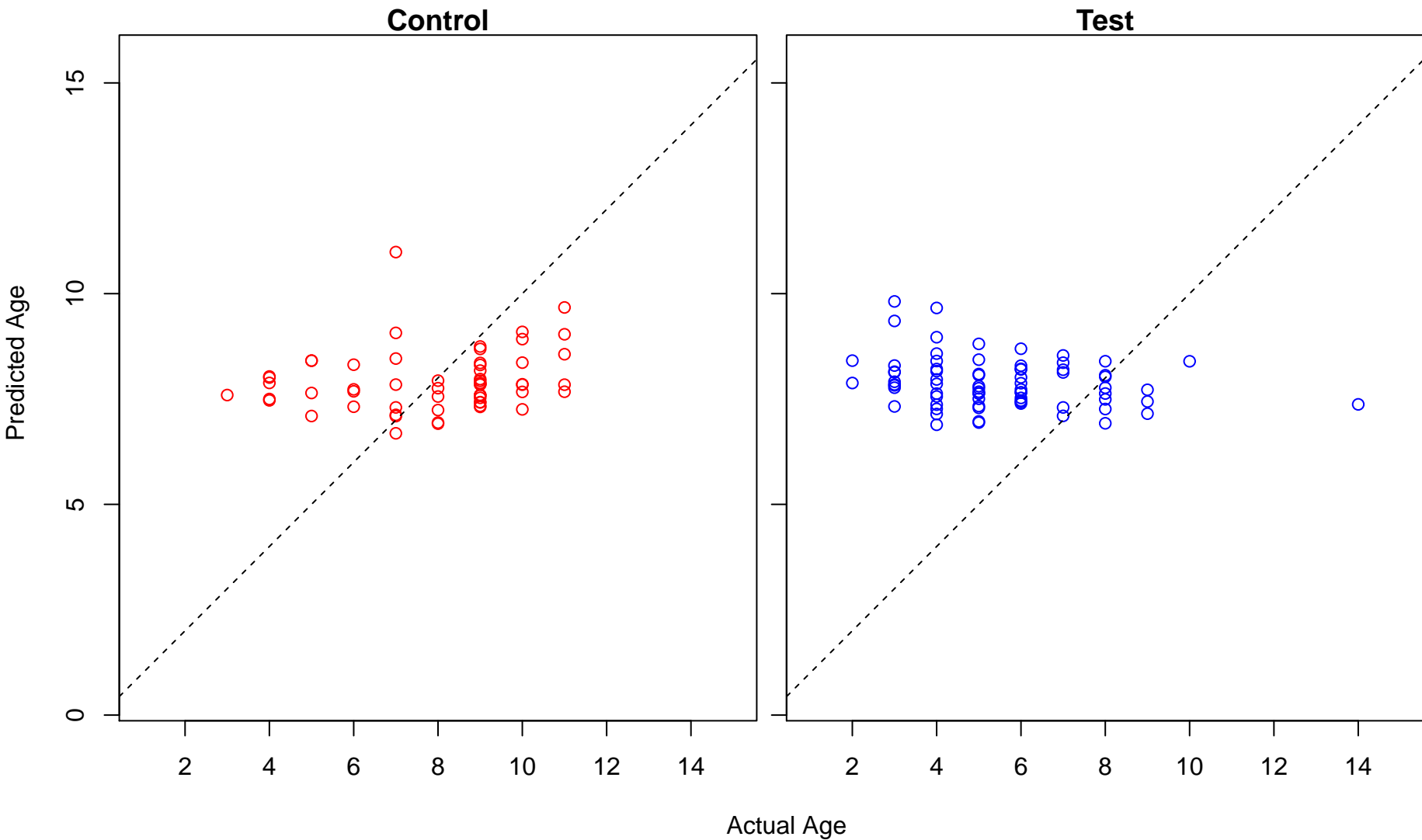
peptide antigen transport (Score: 0.173158)



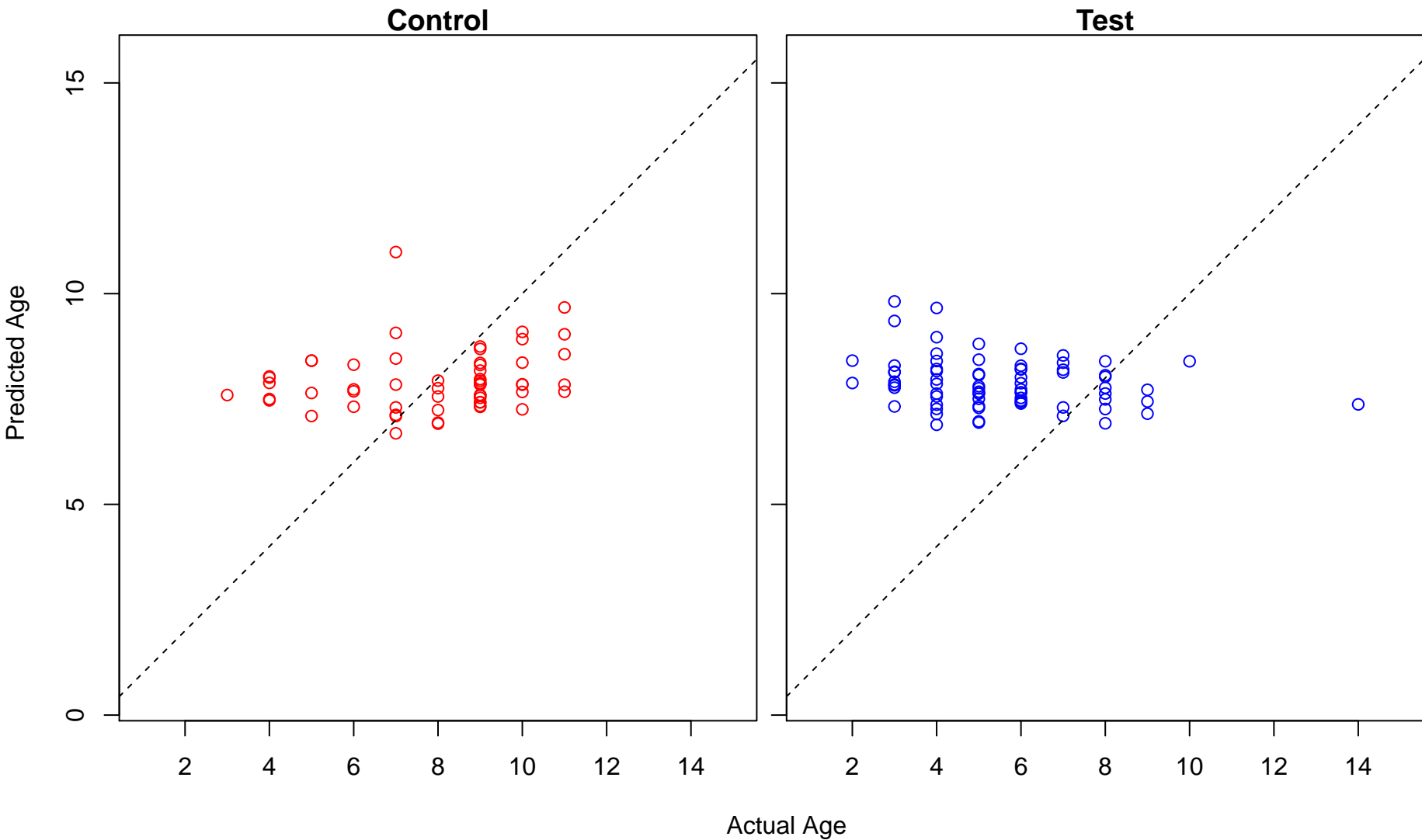
creatinine homeostasis (Score: 0.172076)



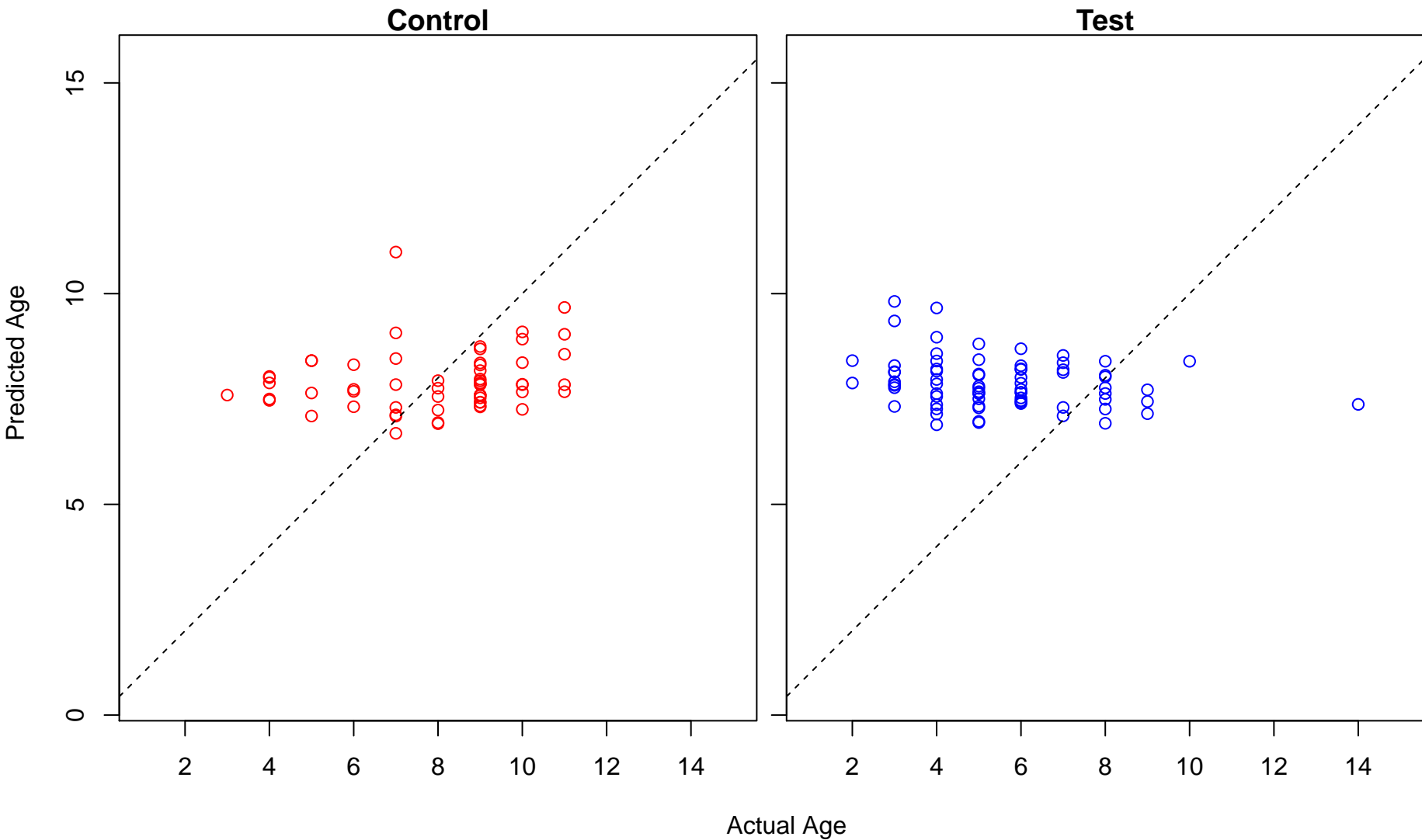
urea homeostasis (Score: 0.172076)



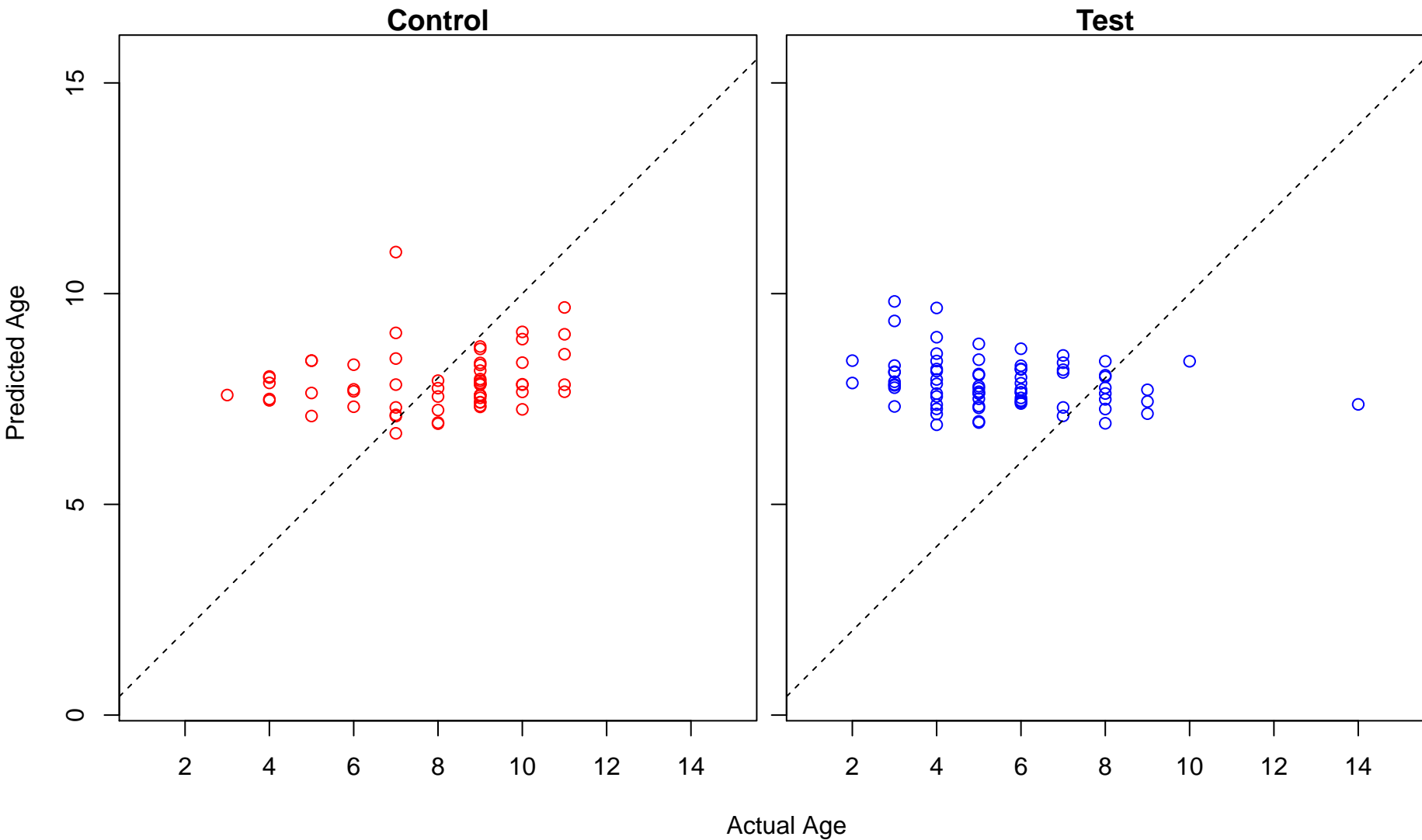
cellular ammonia homeostasis (Score: 0.172076)



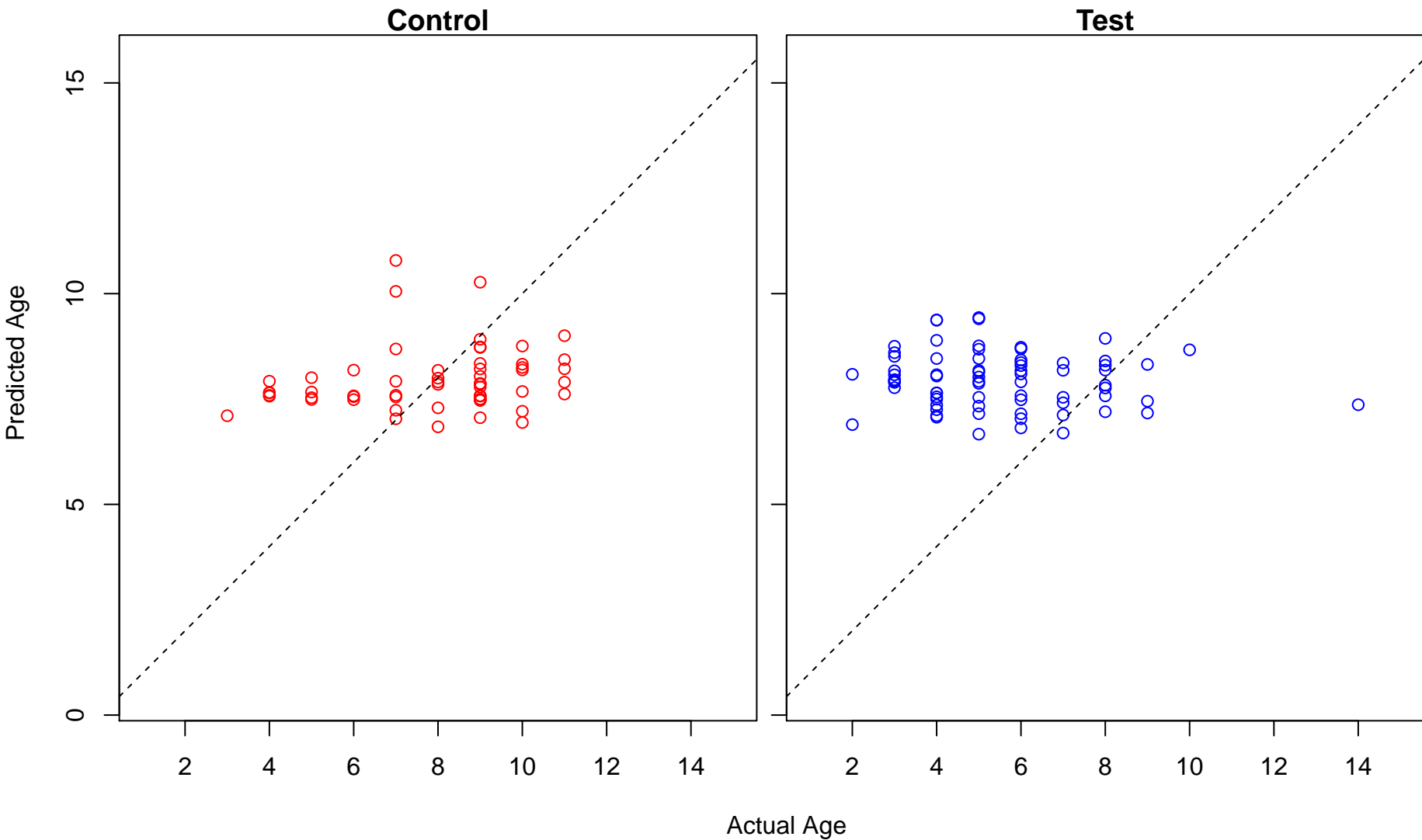
cellular creatinine homeostasis (Score: 0.172076)



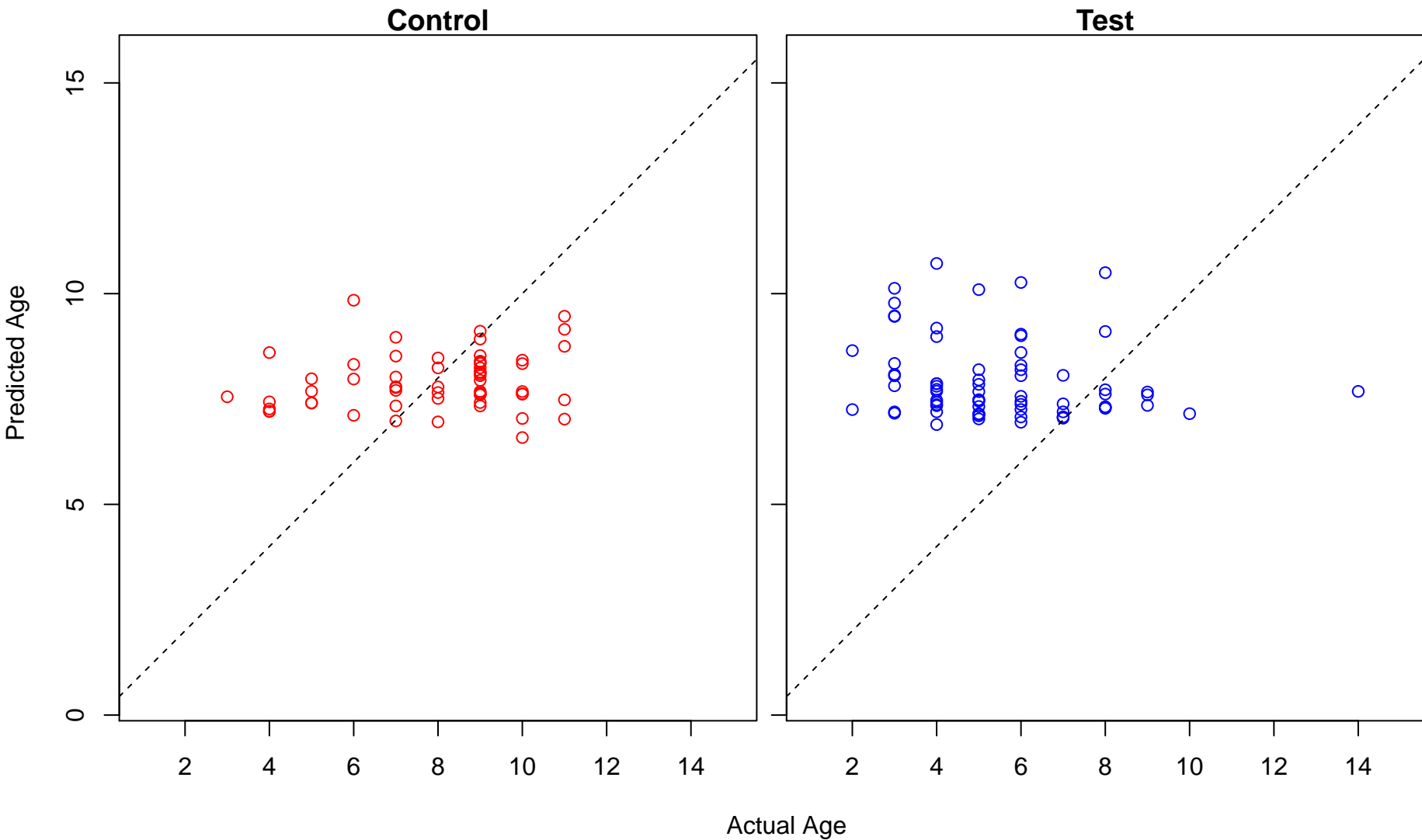
cellular urea homeostasis (Score: 0.172076)



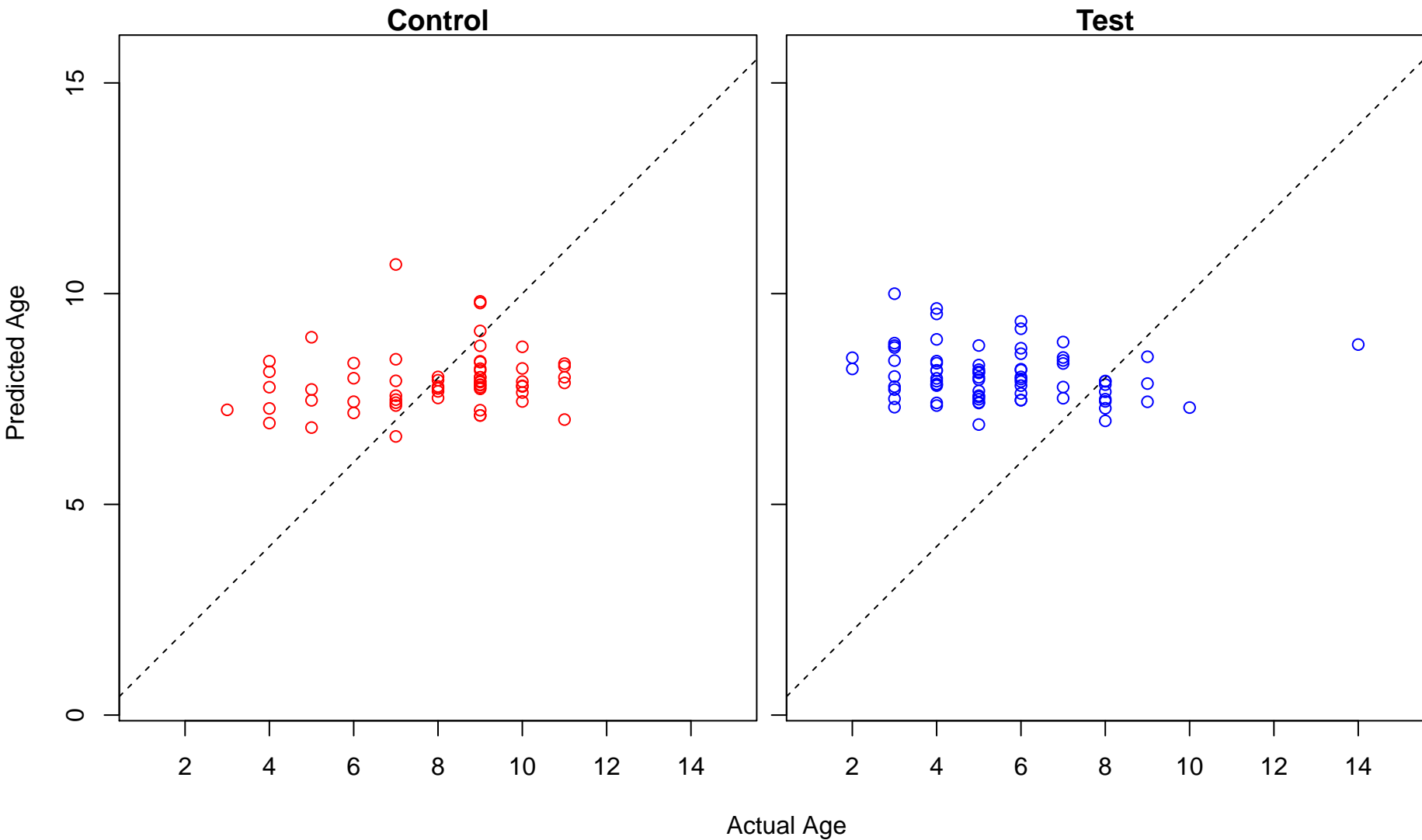
tubulin deacetylation (Score: 0.171653)



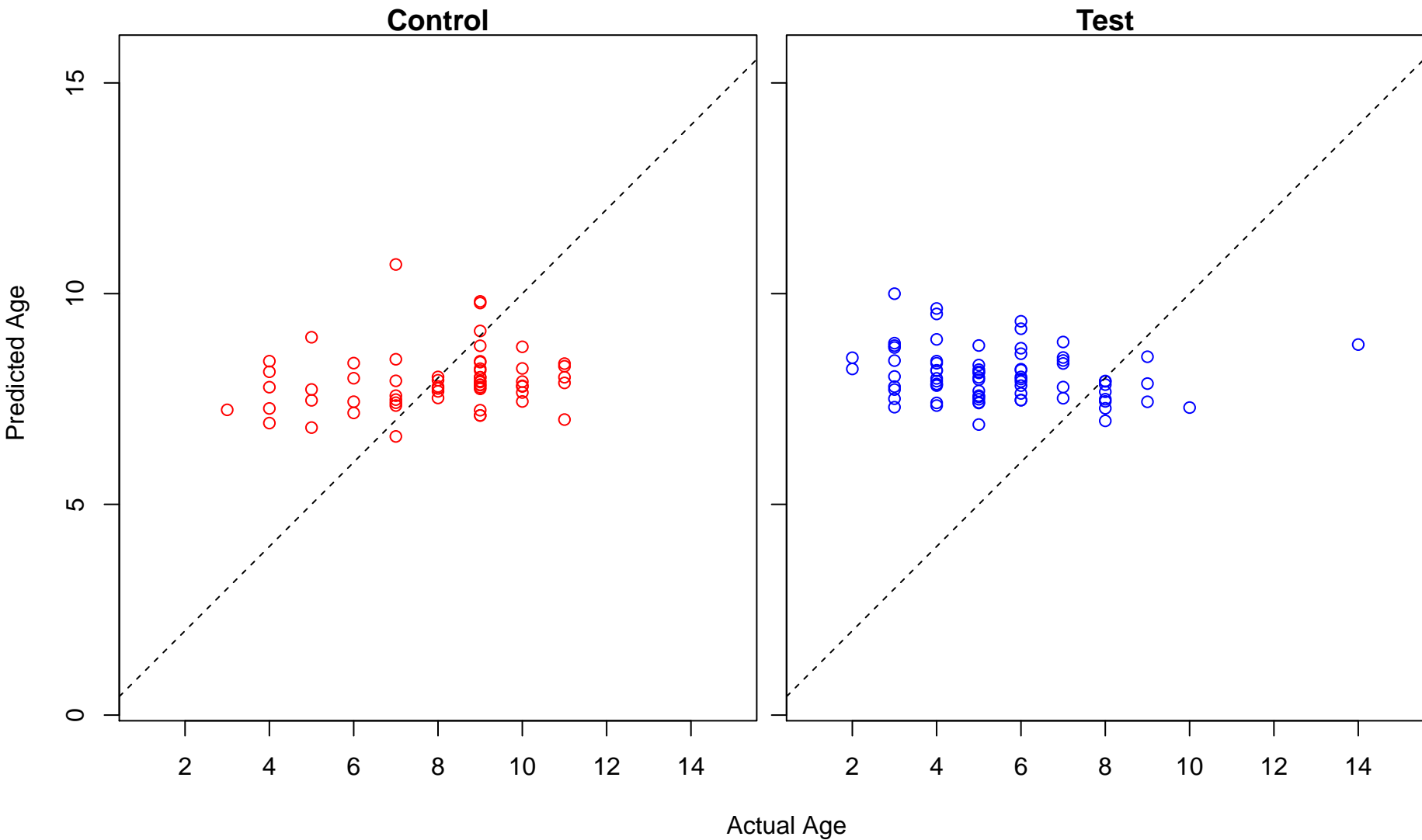
regulation of opioid receptor signaling pathway (Score: 0.171067)



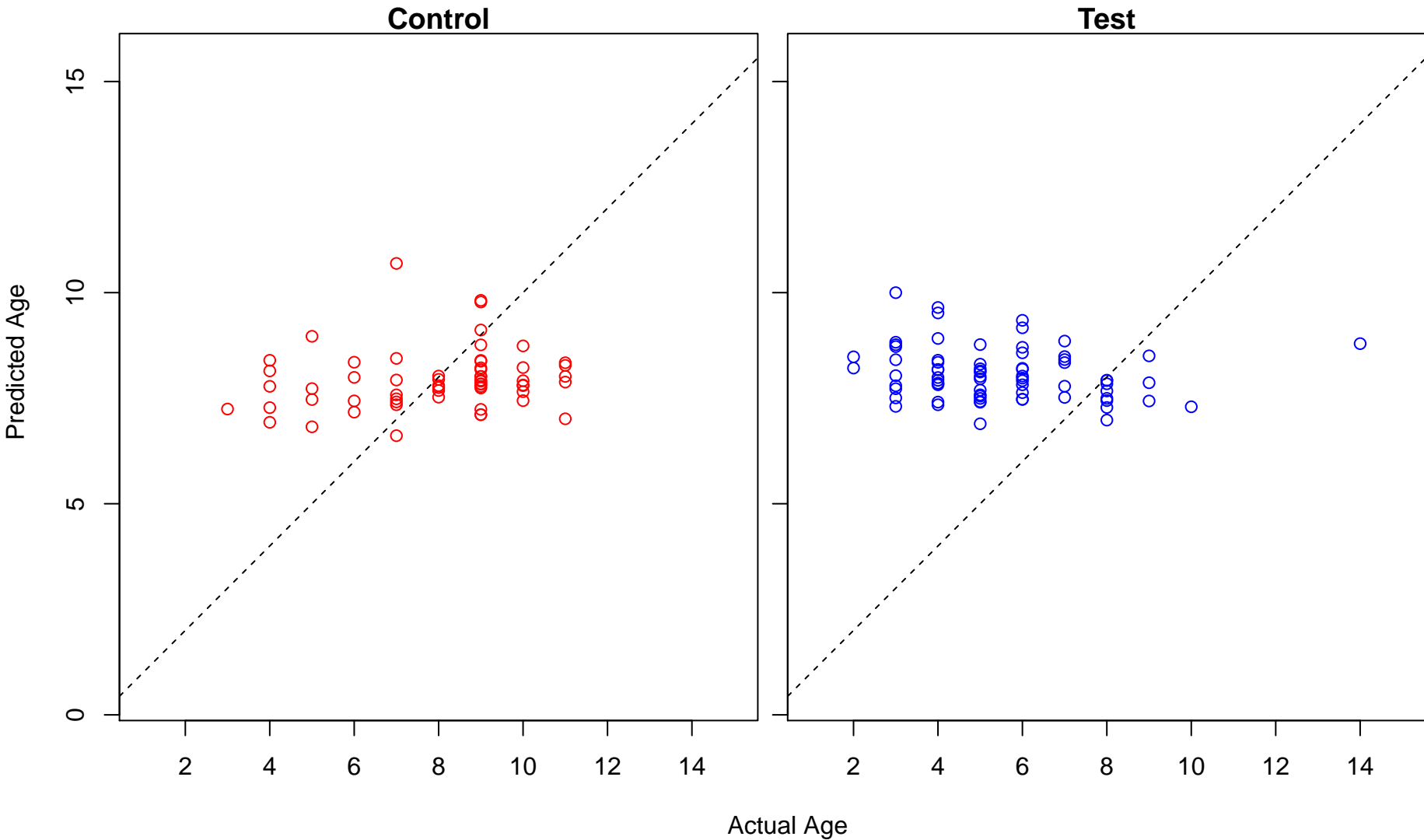
metanephric glomerulus morphogenesis (Score: 0.171010)



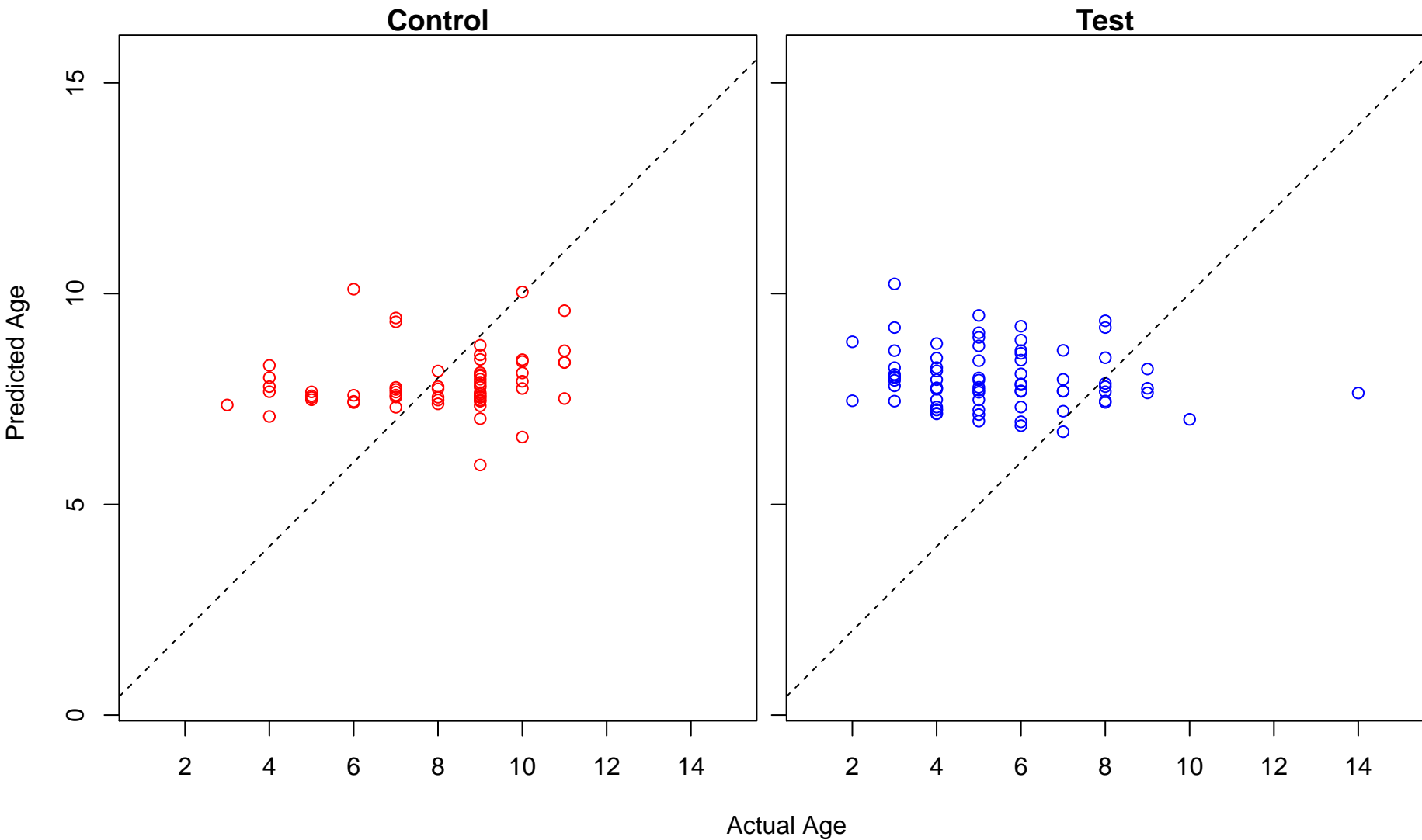
metanephric glomerulus vasculature morphogenesis (Score: 0.171010)



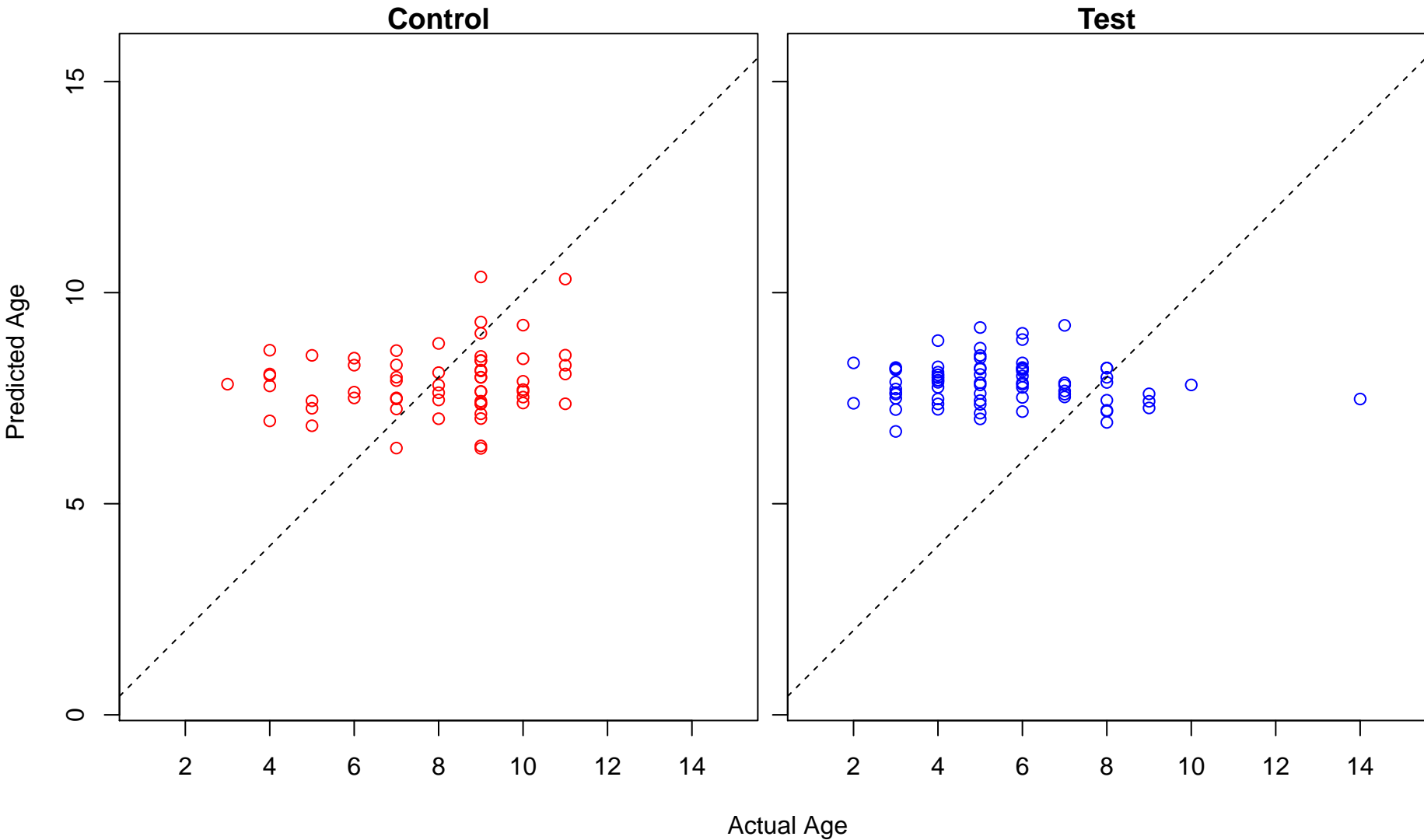
metanephric glomerular capillary formation (Score: 0.171010)



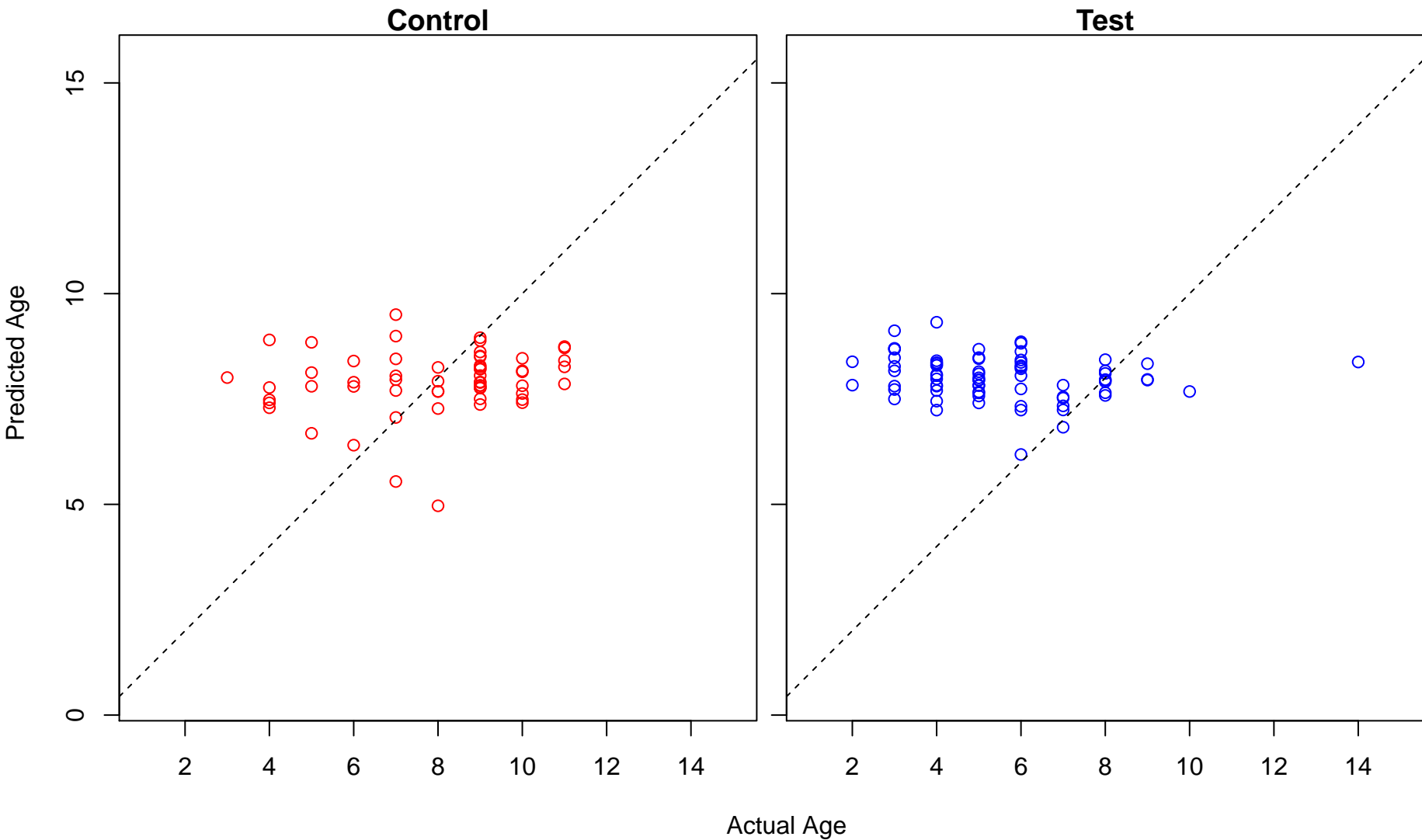
positive regulation of synaptic plasticity (Score: 0.169465)



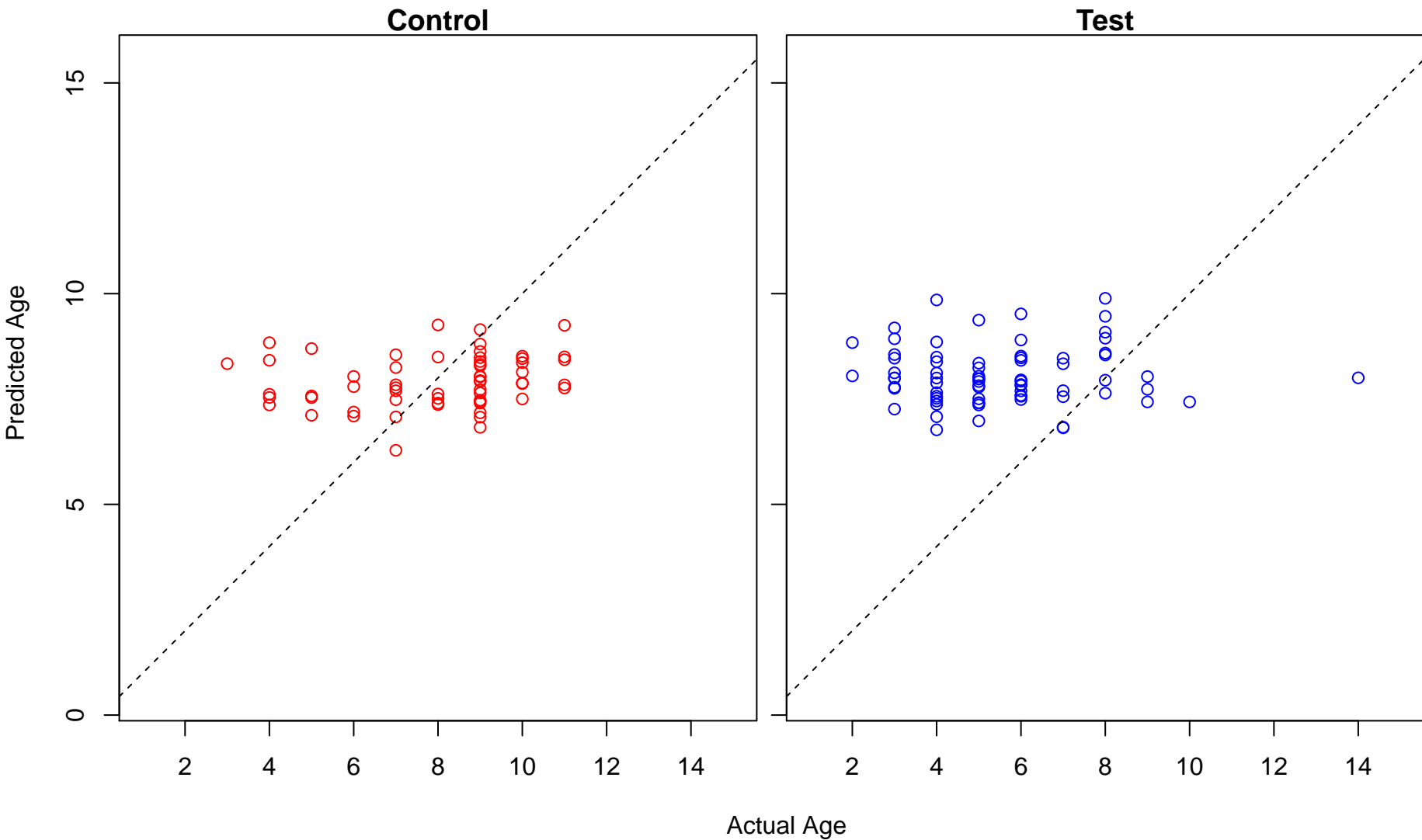
regulation of methylation-dependent chromatin silencing (Score: 0.167716)



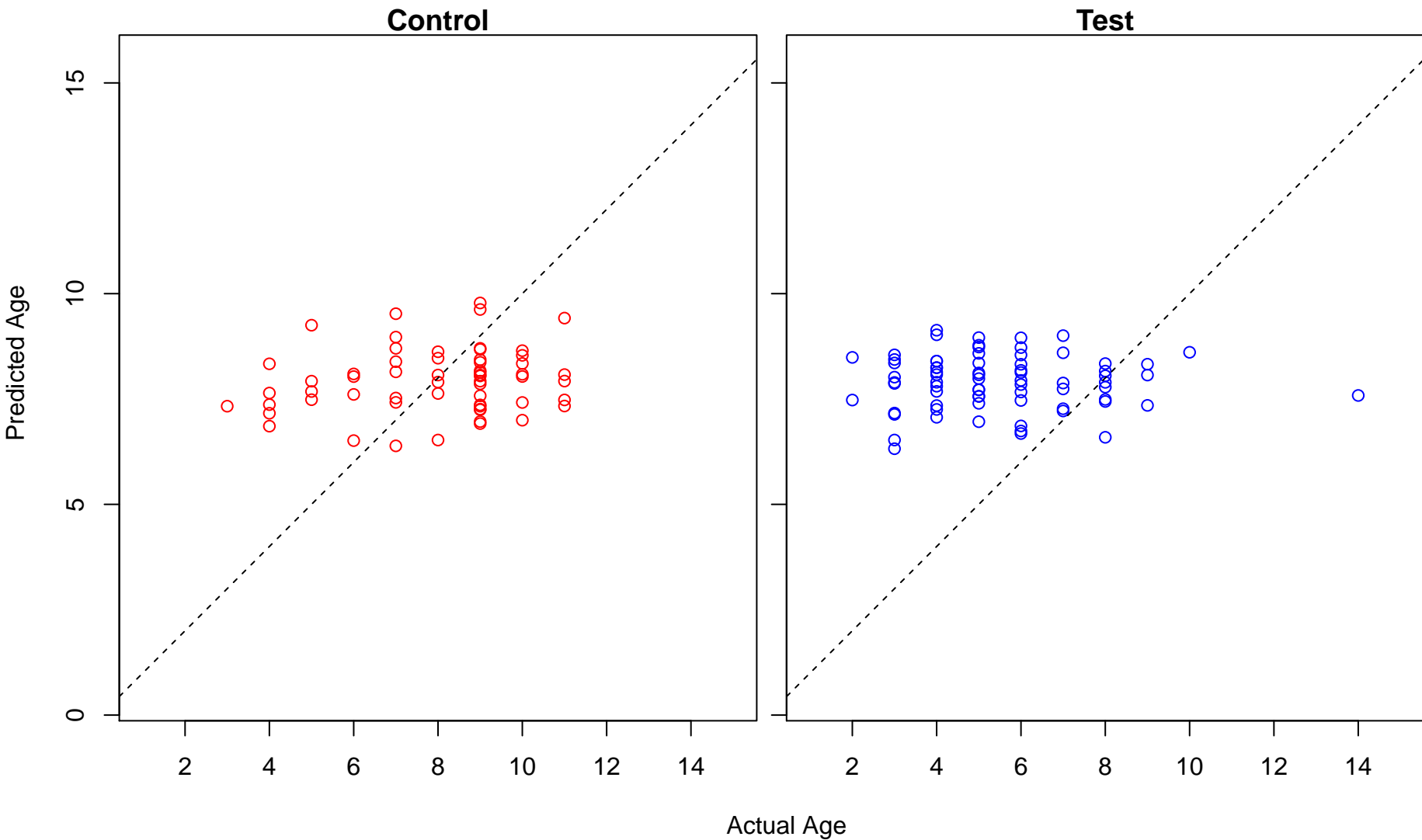
histone H3-K36 demethylation (Score: 0.159282)



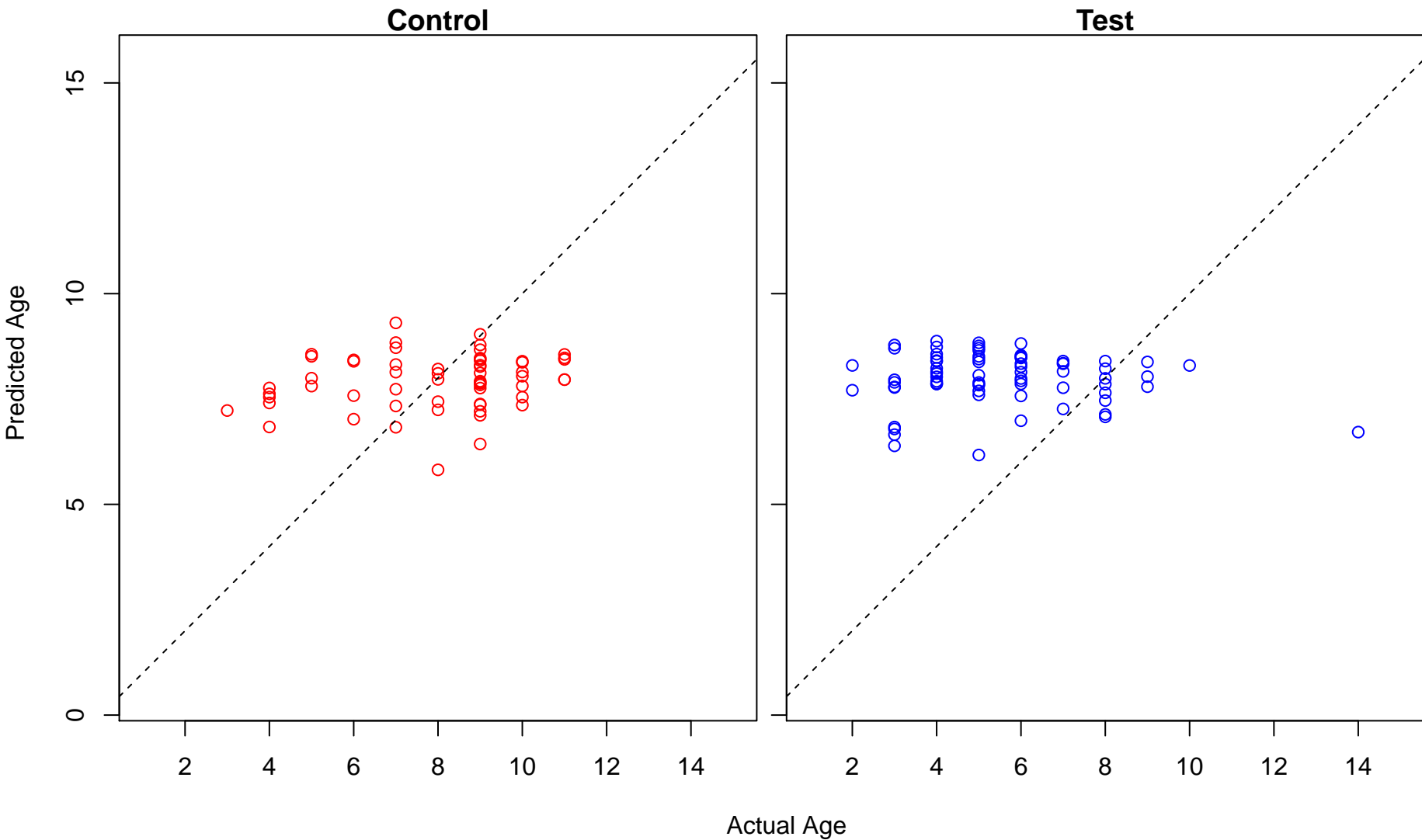
calcium-mediated signaling using extracellular calcium source (Score: 0.159274)



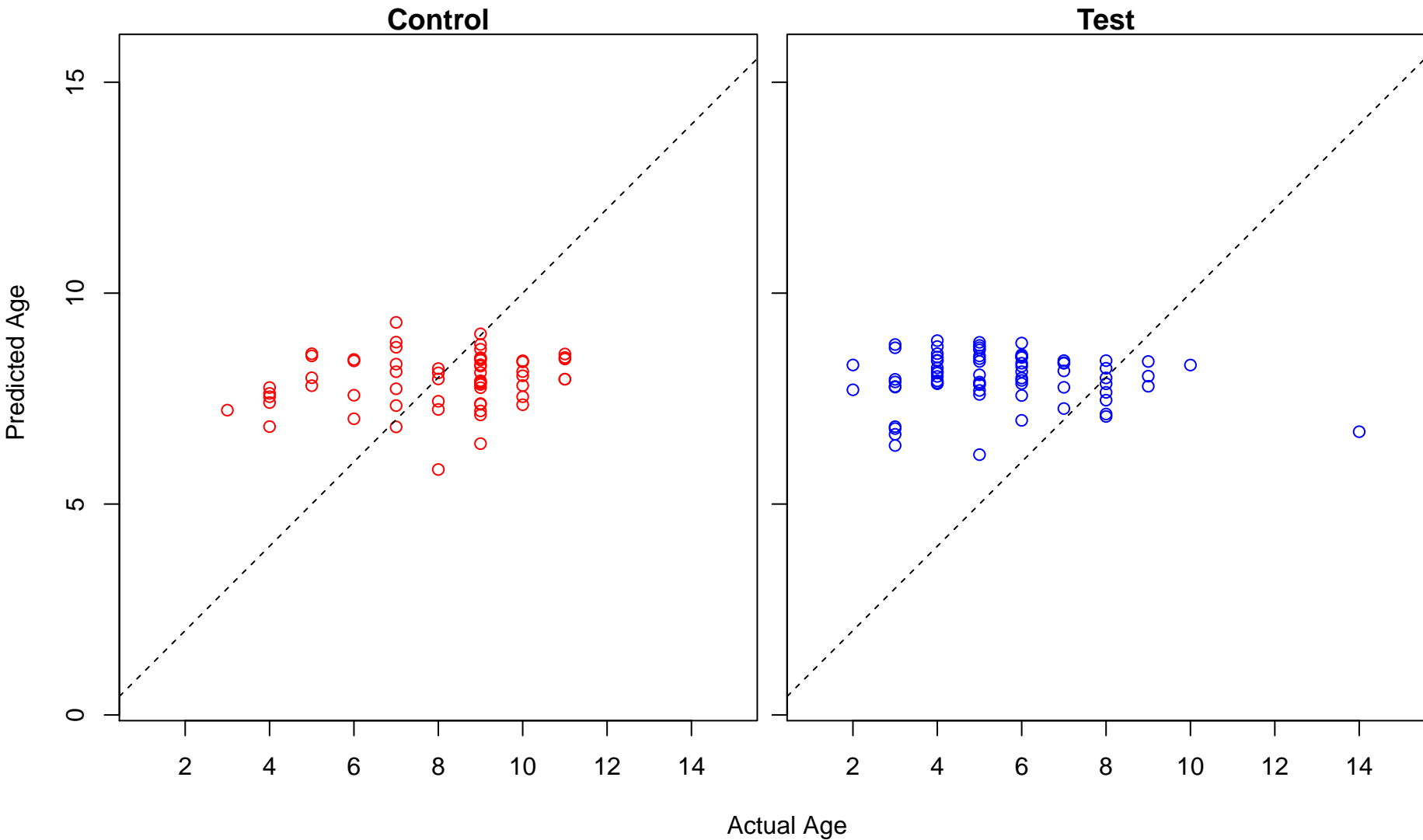
negative regulation of telomerase activity (Score: 0.158817)



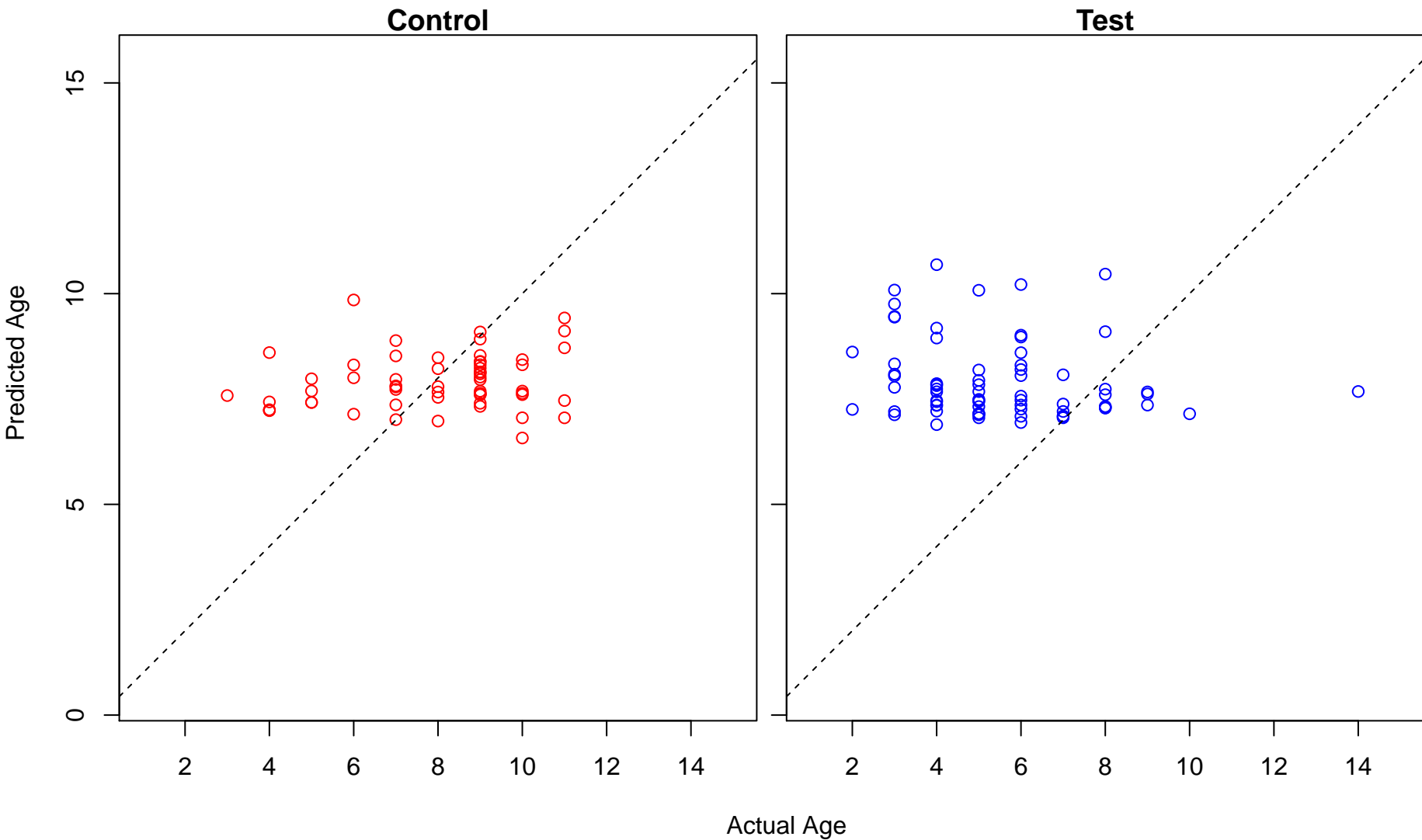
determination of intestine left/right asymmetry (Score: 0.158806)



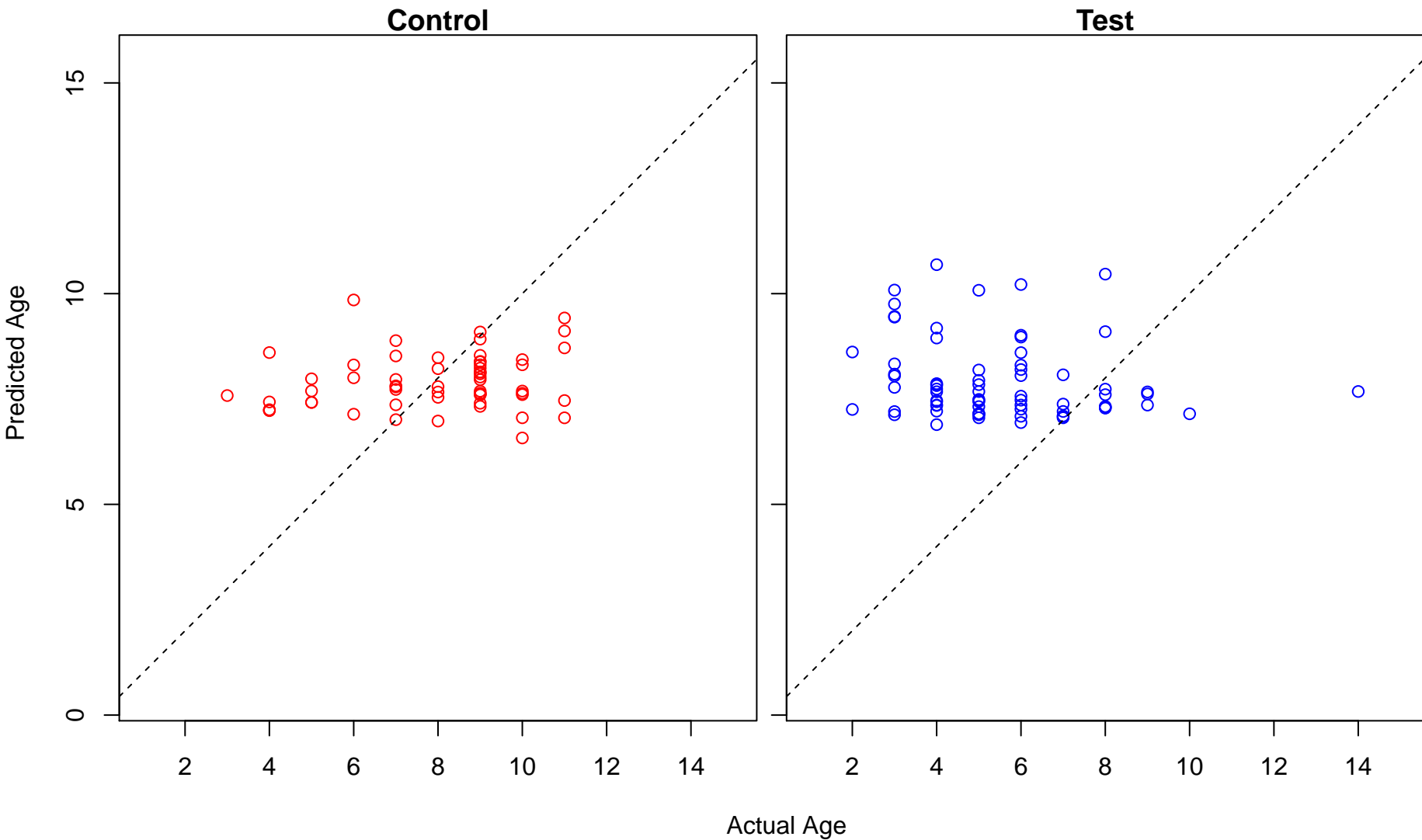
determination of stomach left/right asymmetry (Score: 0.158806)



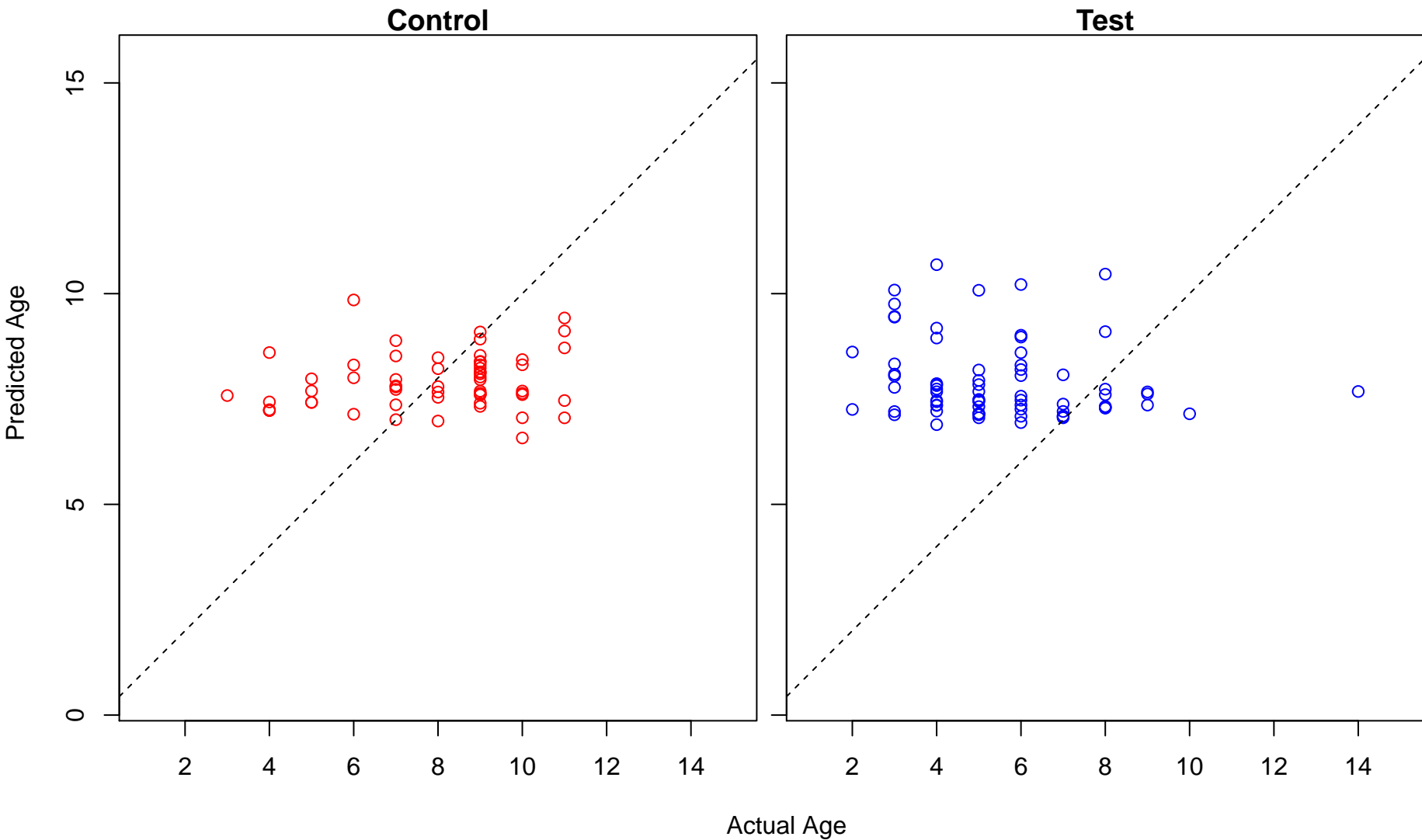
regulation of cell growth by extracellular stimulus (Score: 0.158597)



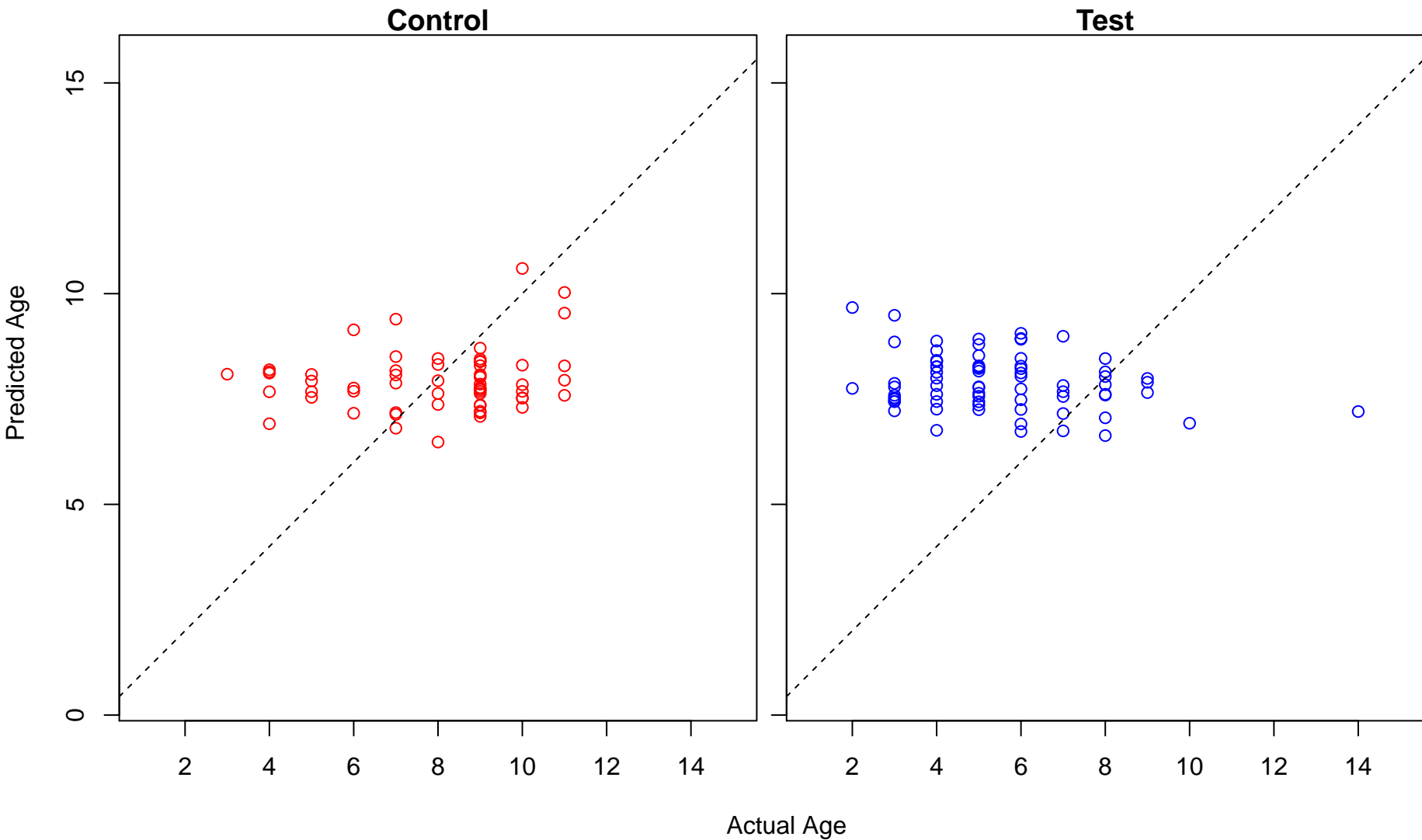
cellular response to morphine (Score: 0.158498)



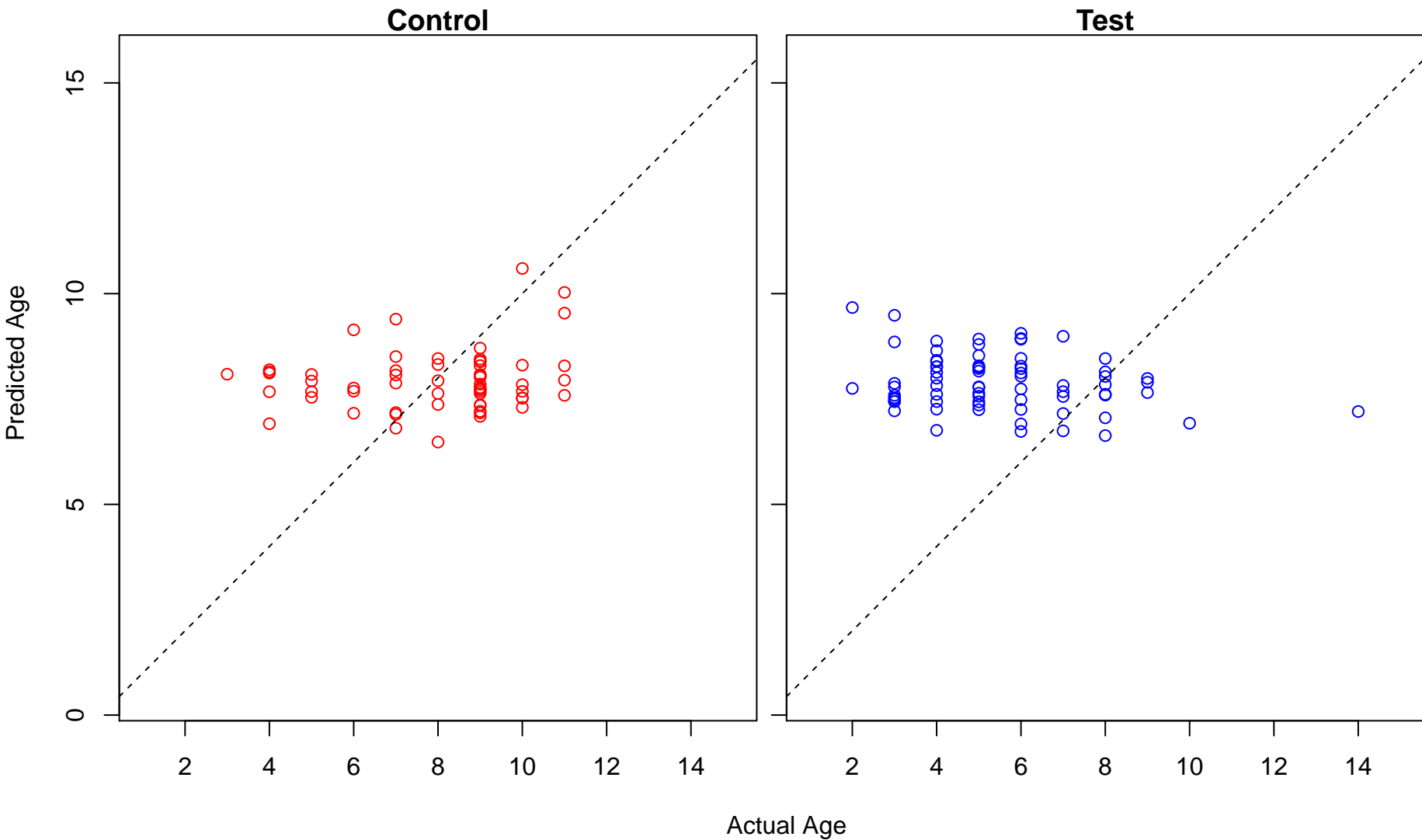
cellular response to isoquinoline alkaloid (Score: 0.158498)



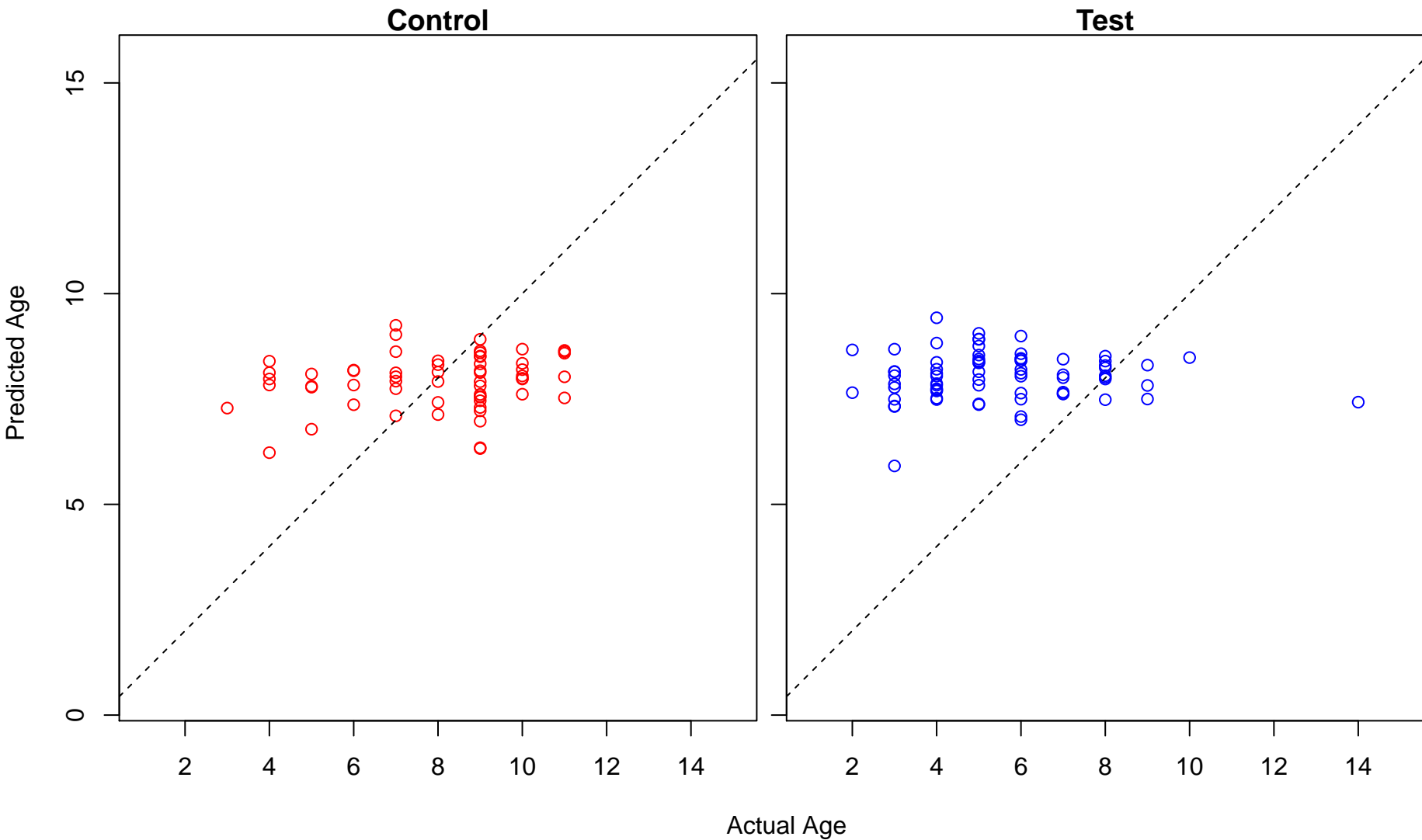
metanephric proximal tubule development (Score: 0.156136)



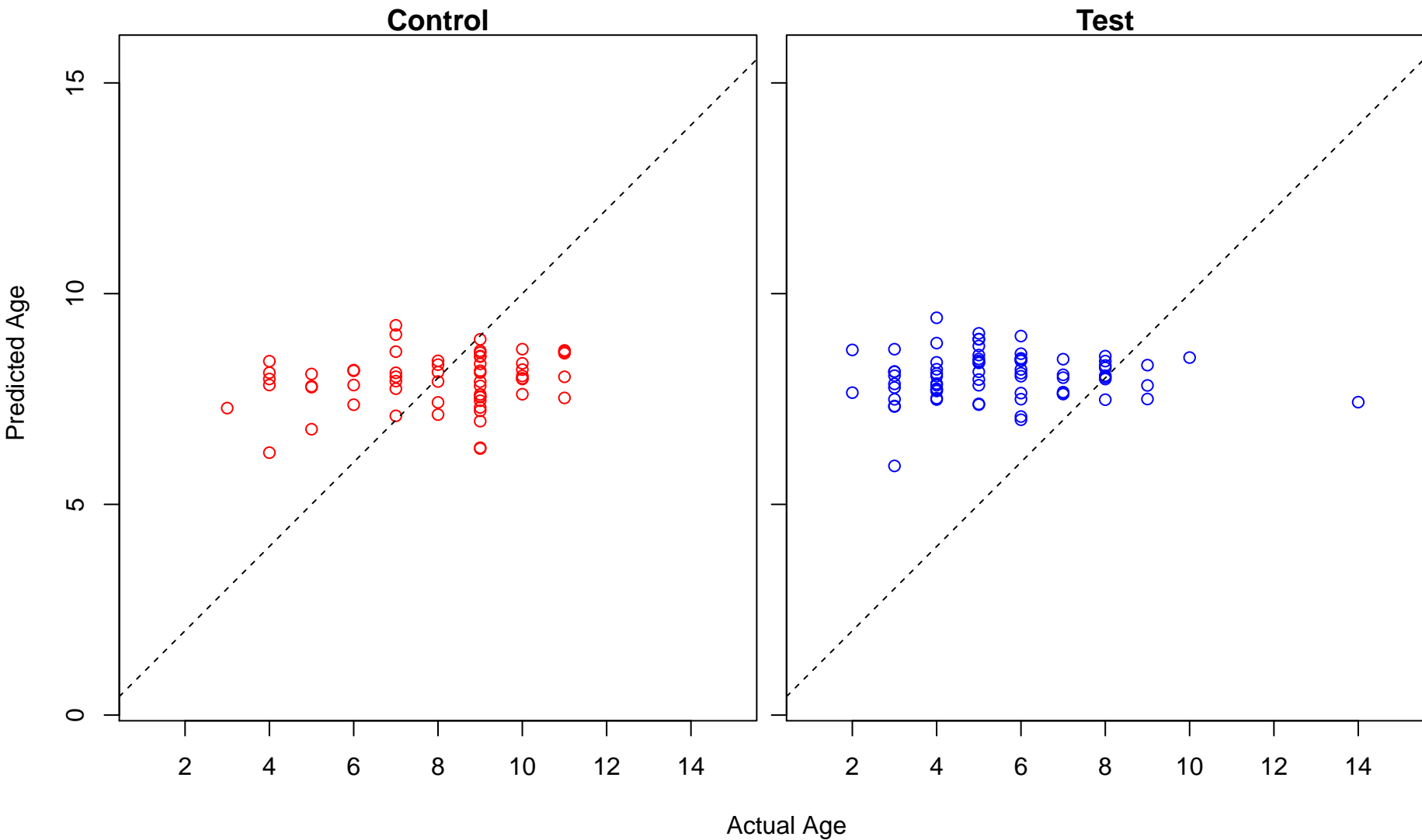
metanephric distal tubule morphogenesis (Score: 0.156136)



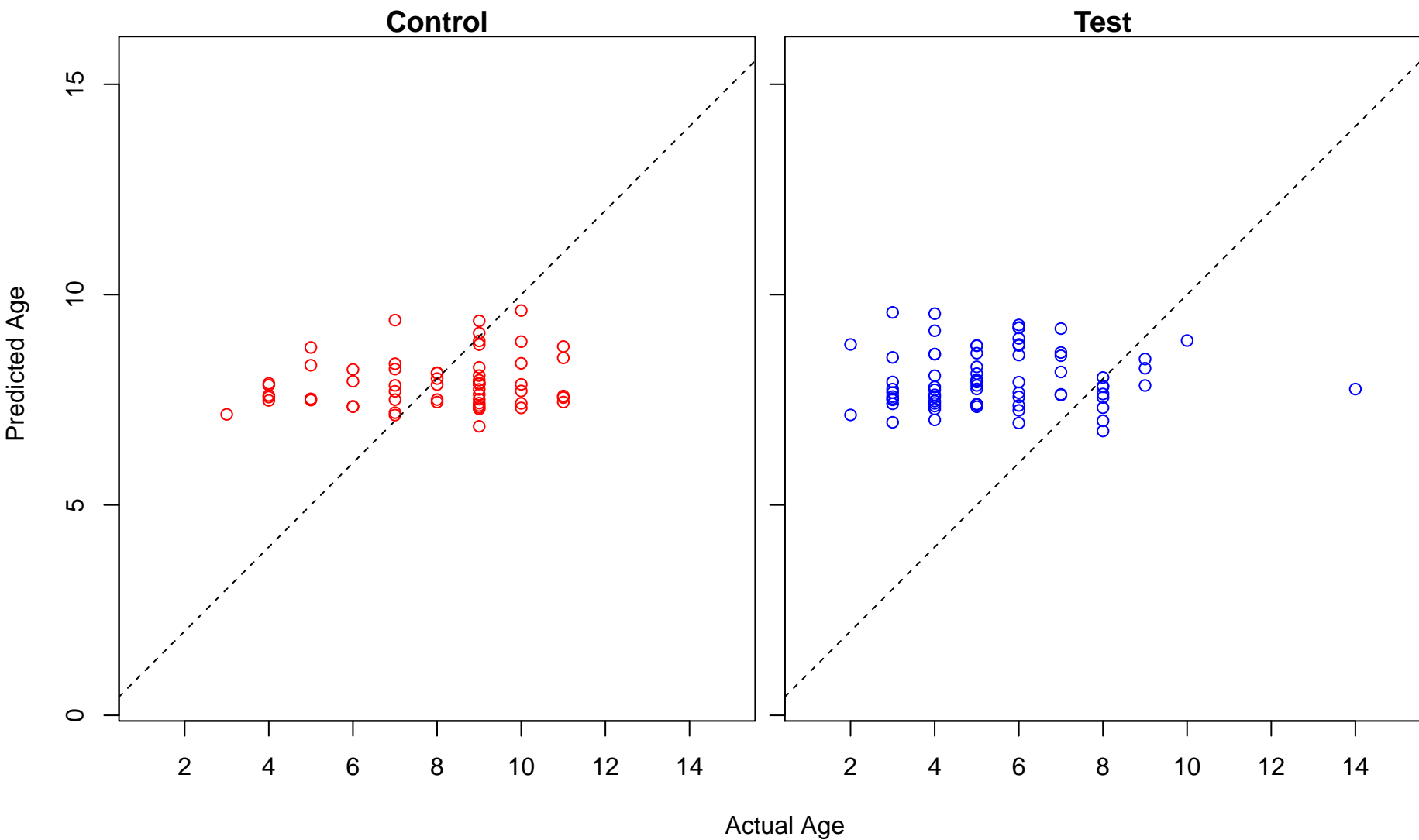
nuclear RNA surveillance (Score: 0.152035)



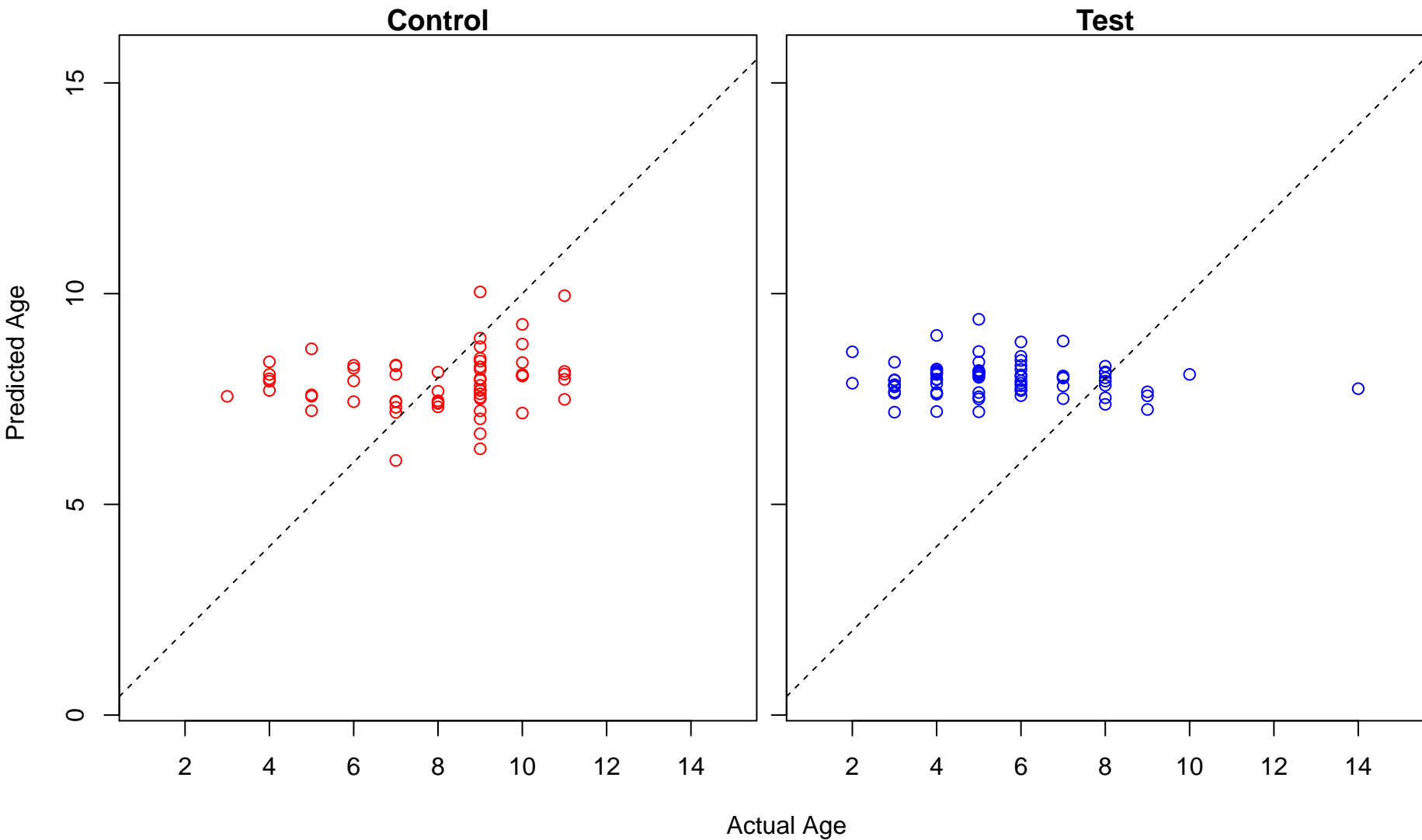
nuclear mRNA surveillance (Score: 0.152035)



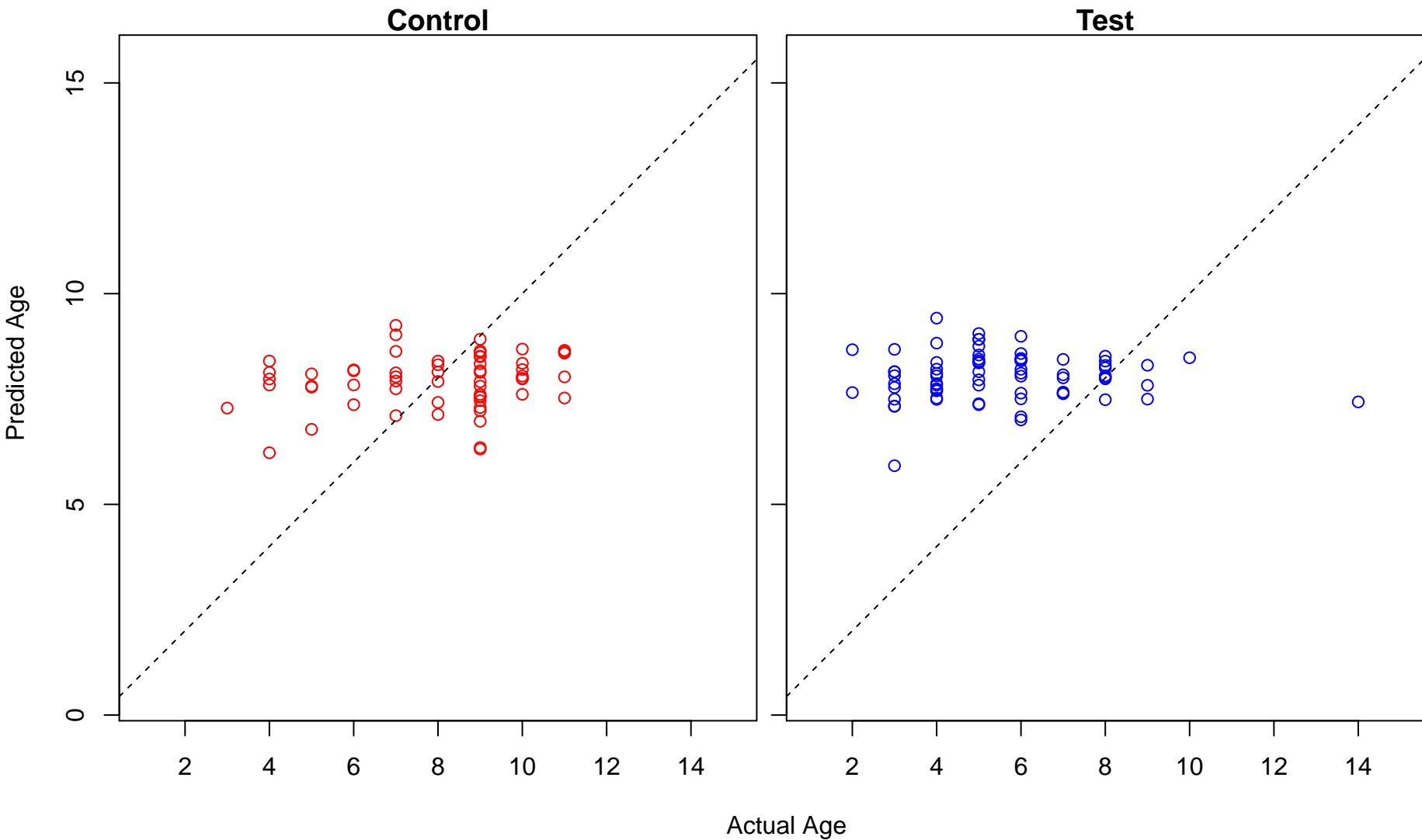
positive regulation of energy homeostasis (Score: 0.151117)



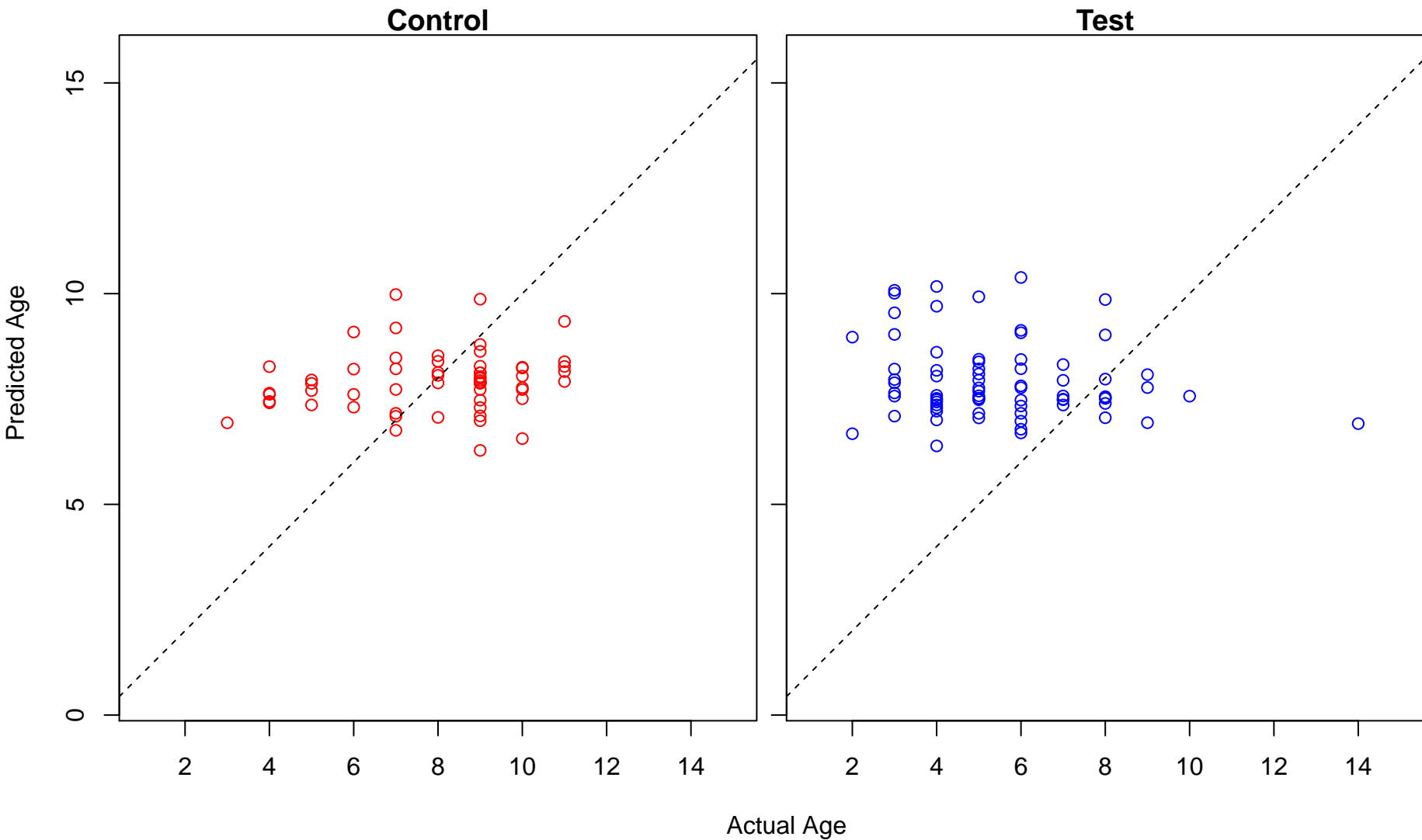
negative regulation of methylation-dependent chromatin silencing (Score: 0.150632)



RNA surveillance (Score: 0.150455)

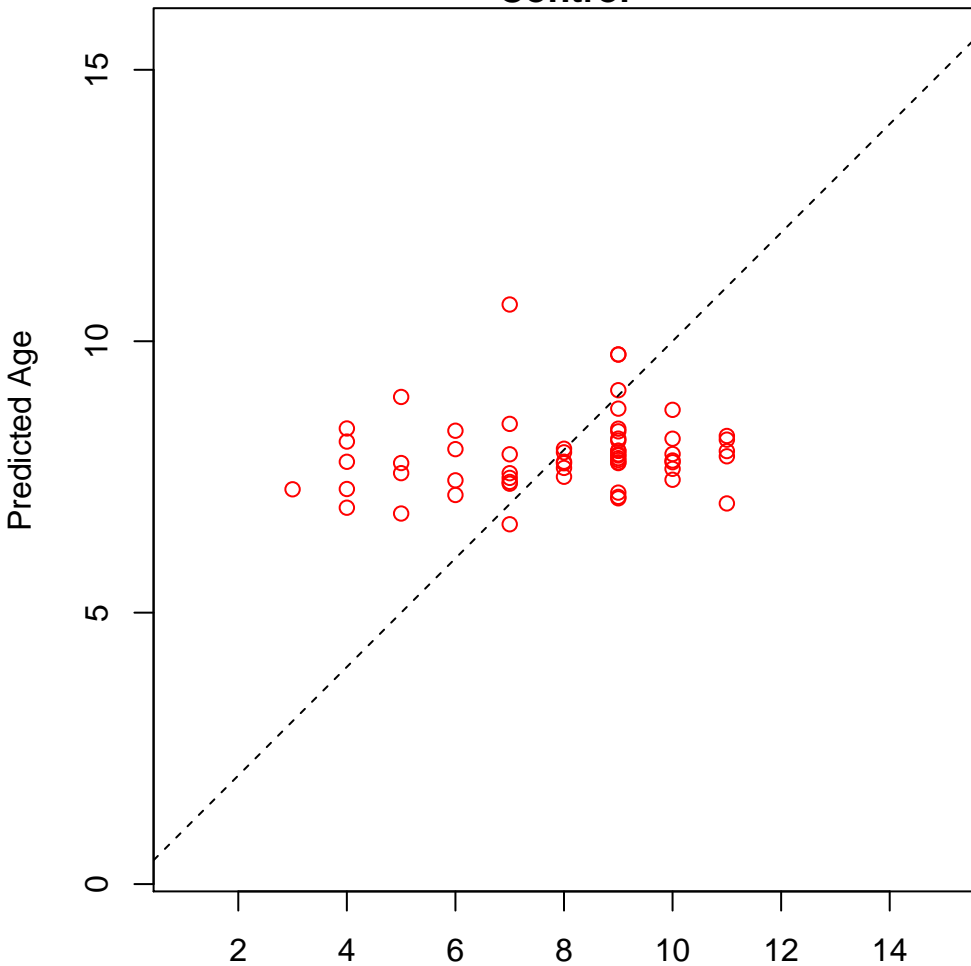


protein retention in ER lumen (Score: 0.145245)

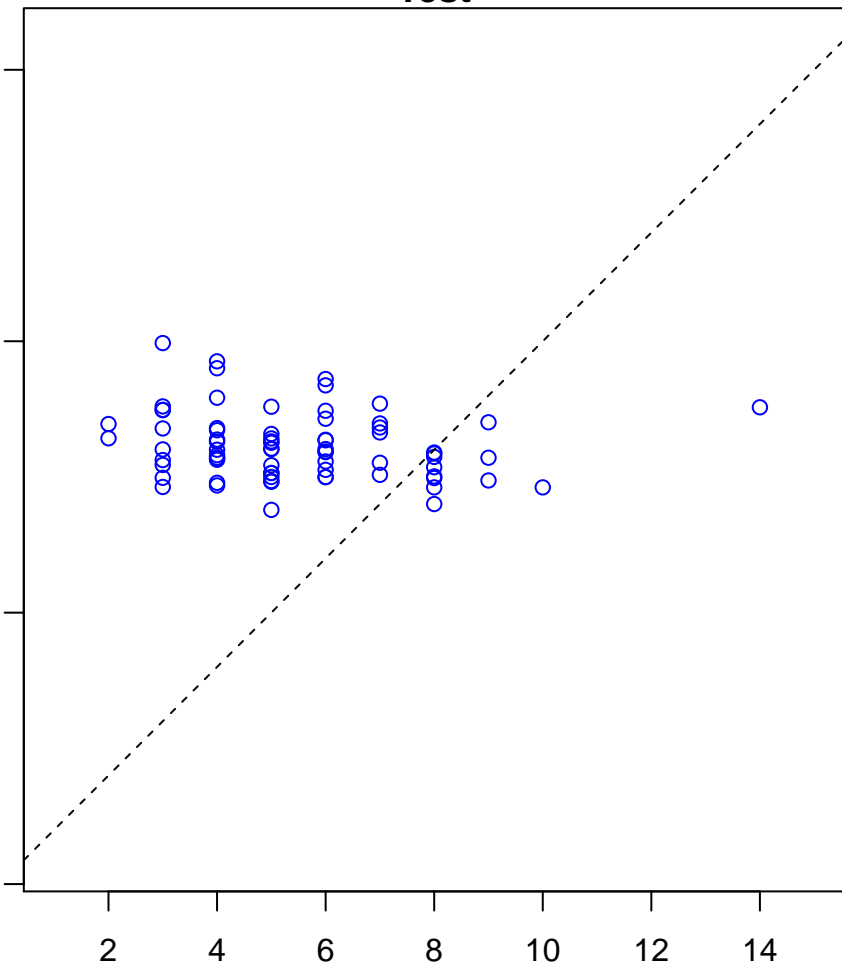


glomerulus vasculature morphogenesis (Score: 0.143606)

Control

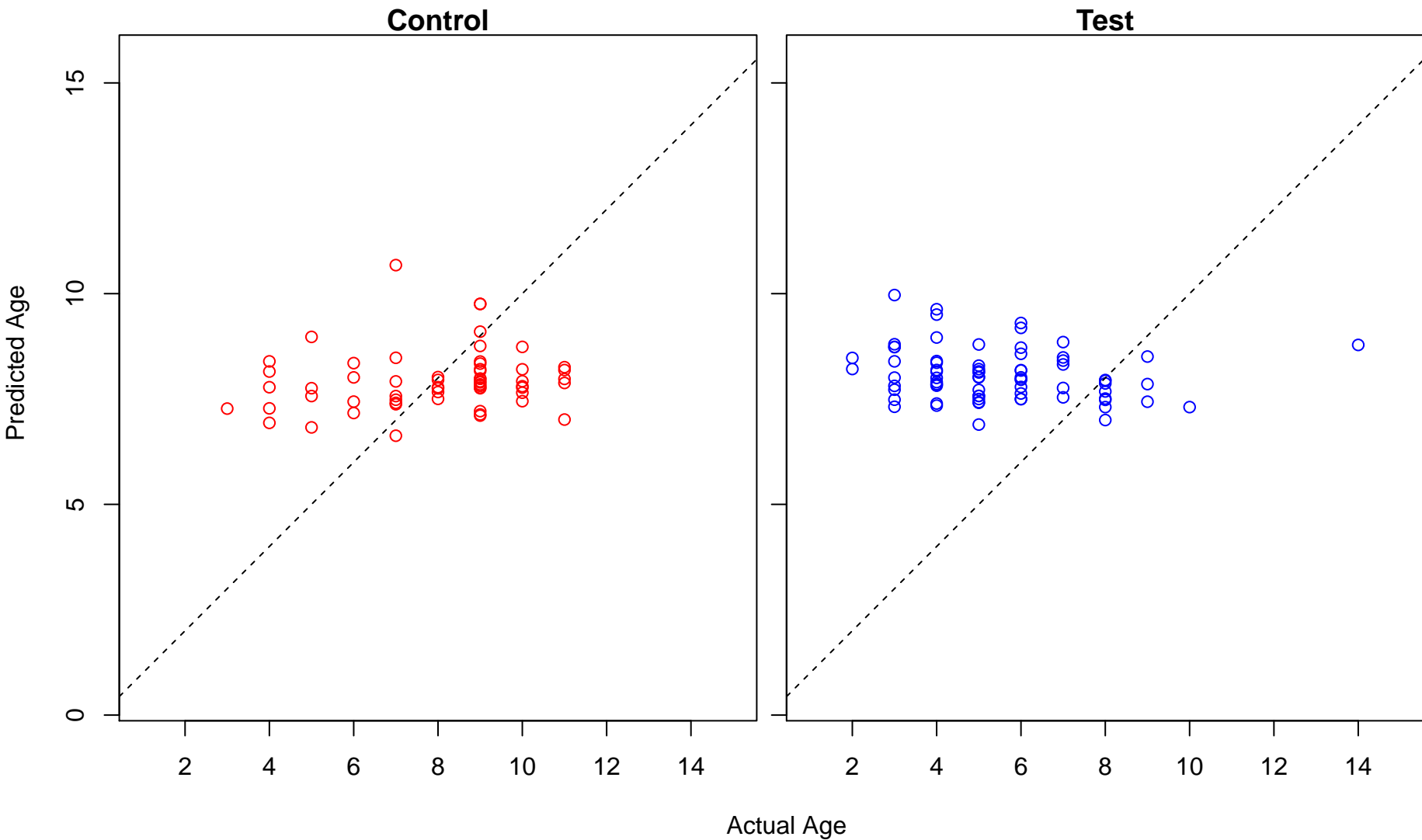


Test



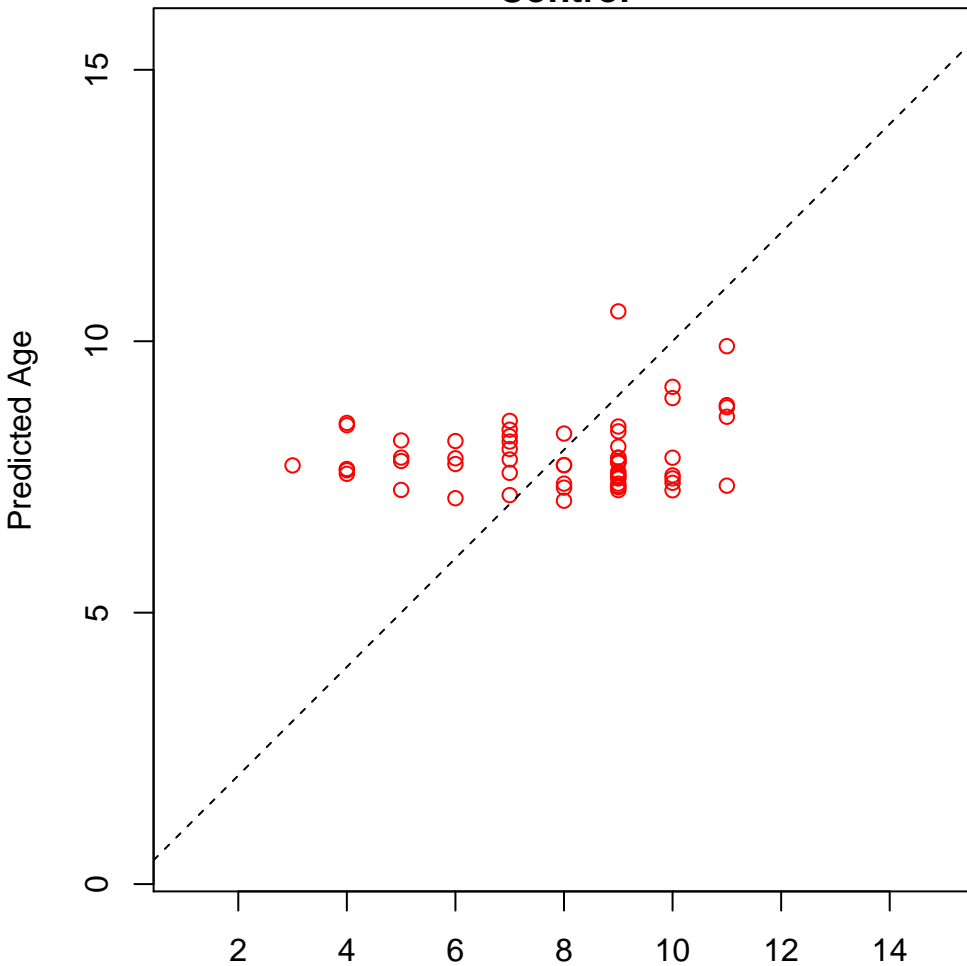
Actual Age

glomerular capillary formation (Score: 0.143606)

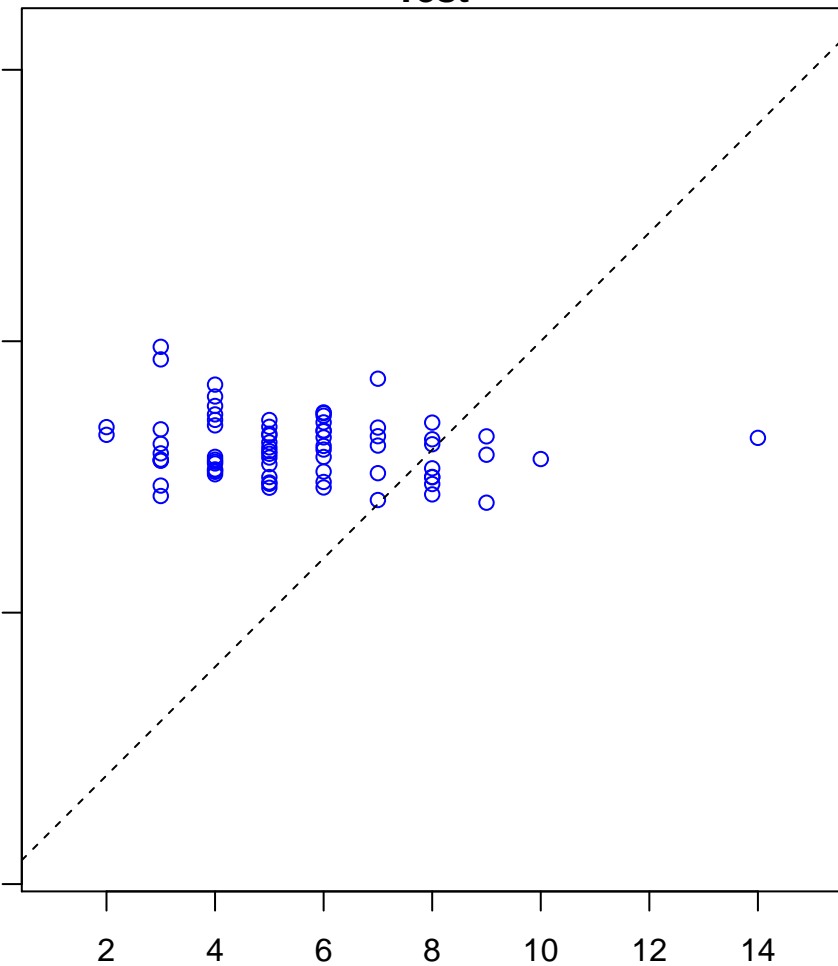


subpallium cell proliferation in forebrain (Score: 0.142850)

Control

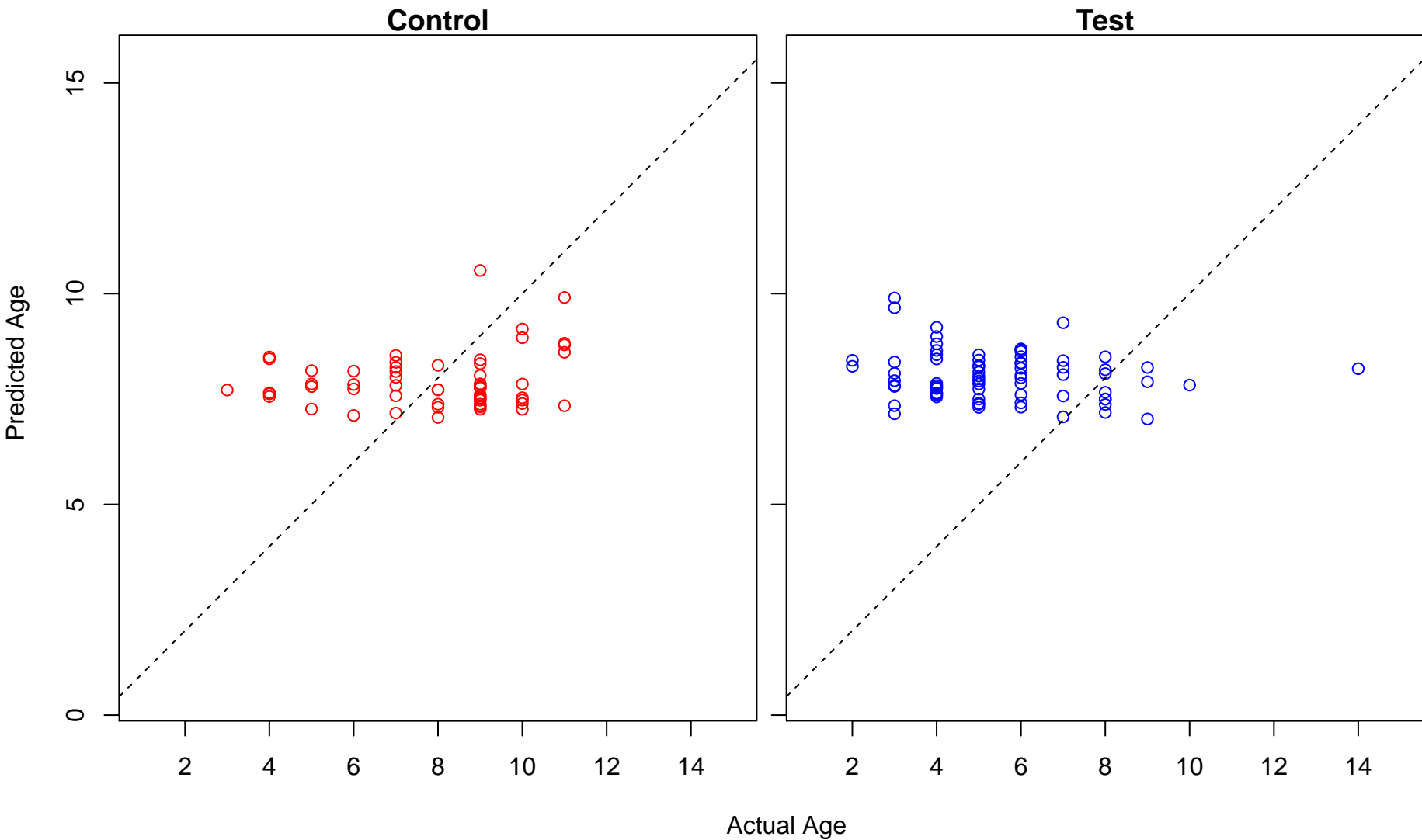


Test

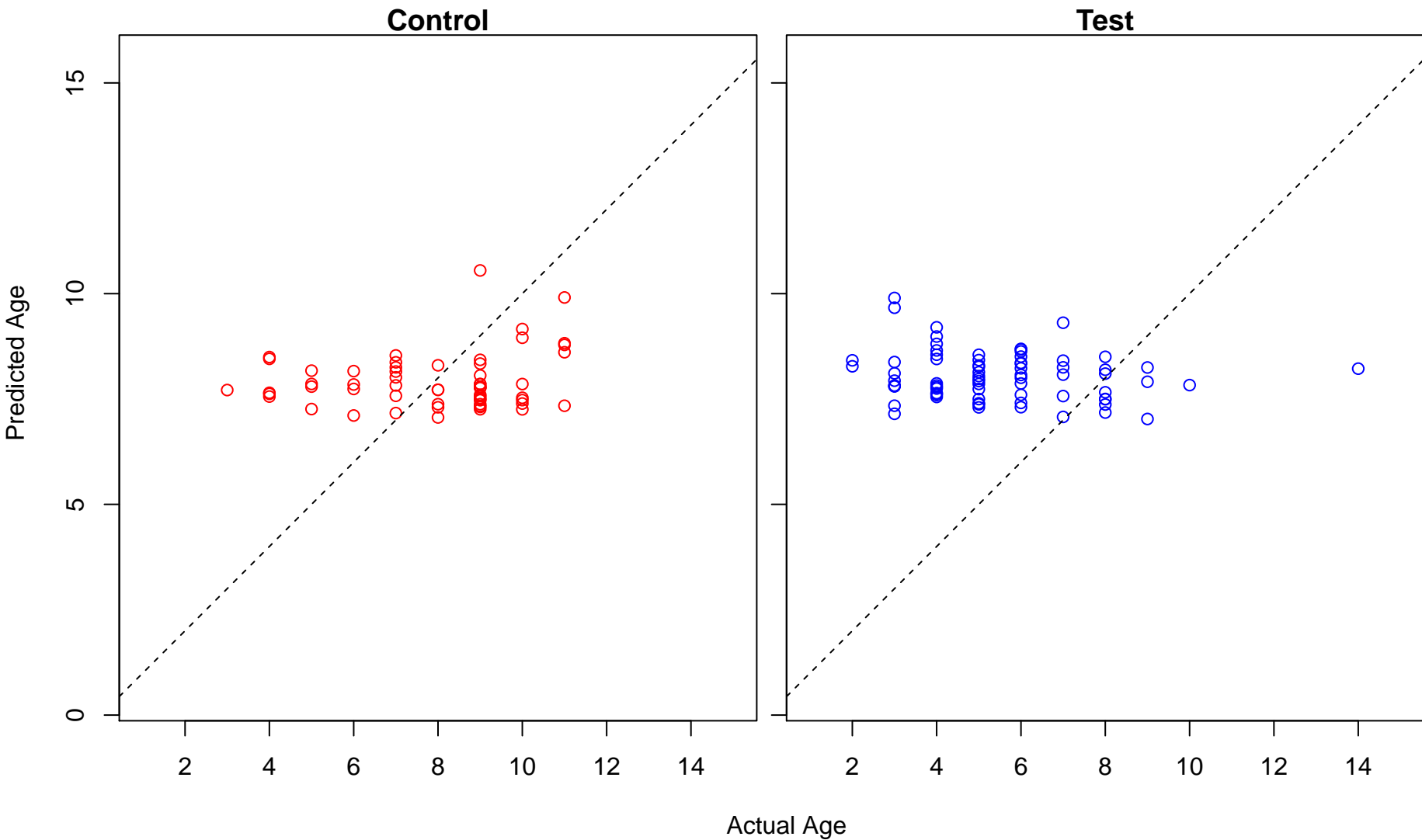


Actual Age

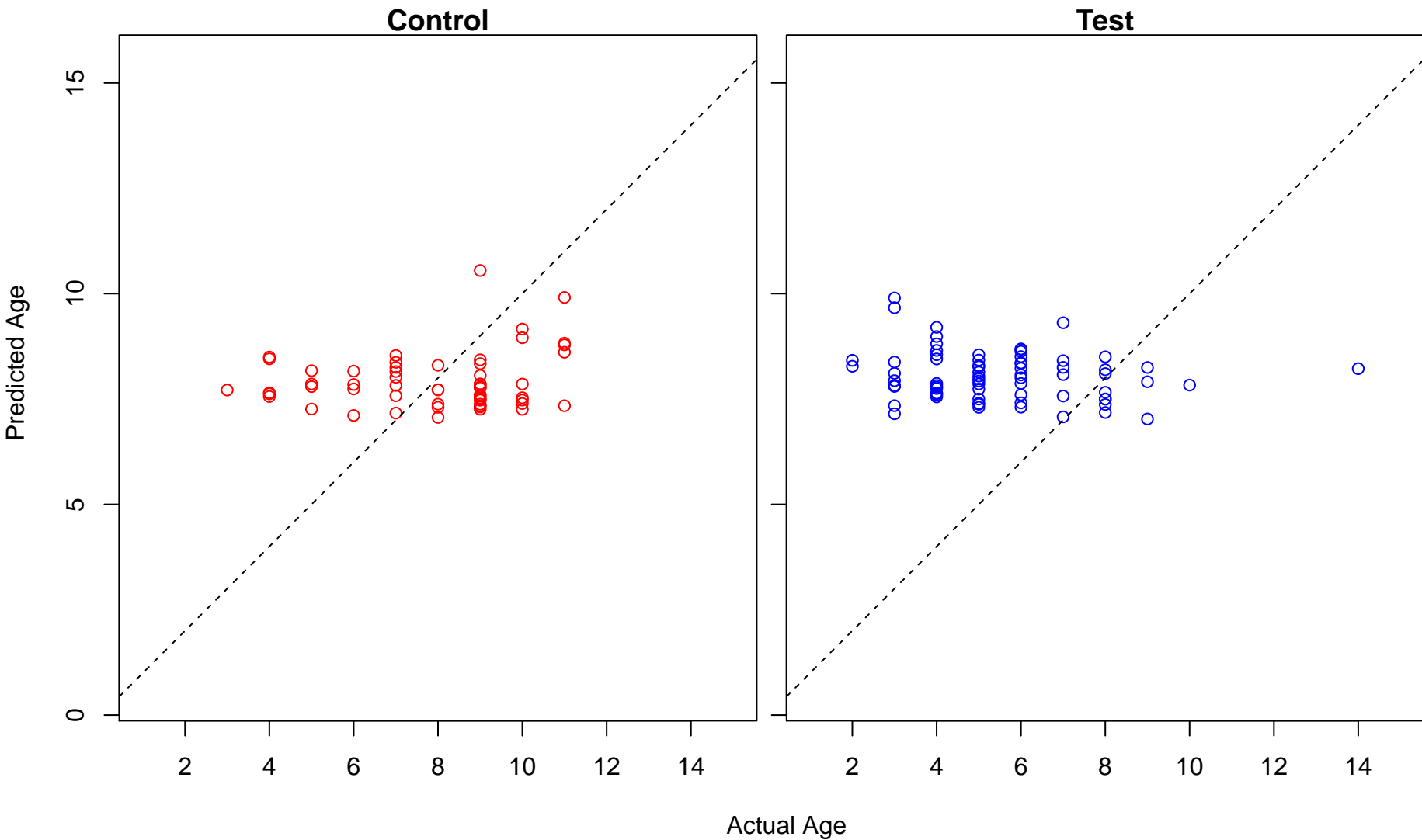
lateral ganglionic eminence cell proliferation (Score: 0.142850)



lambdoid suture morphogenesis (Score: 0.142850)

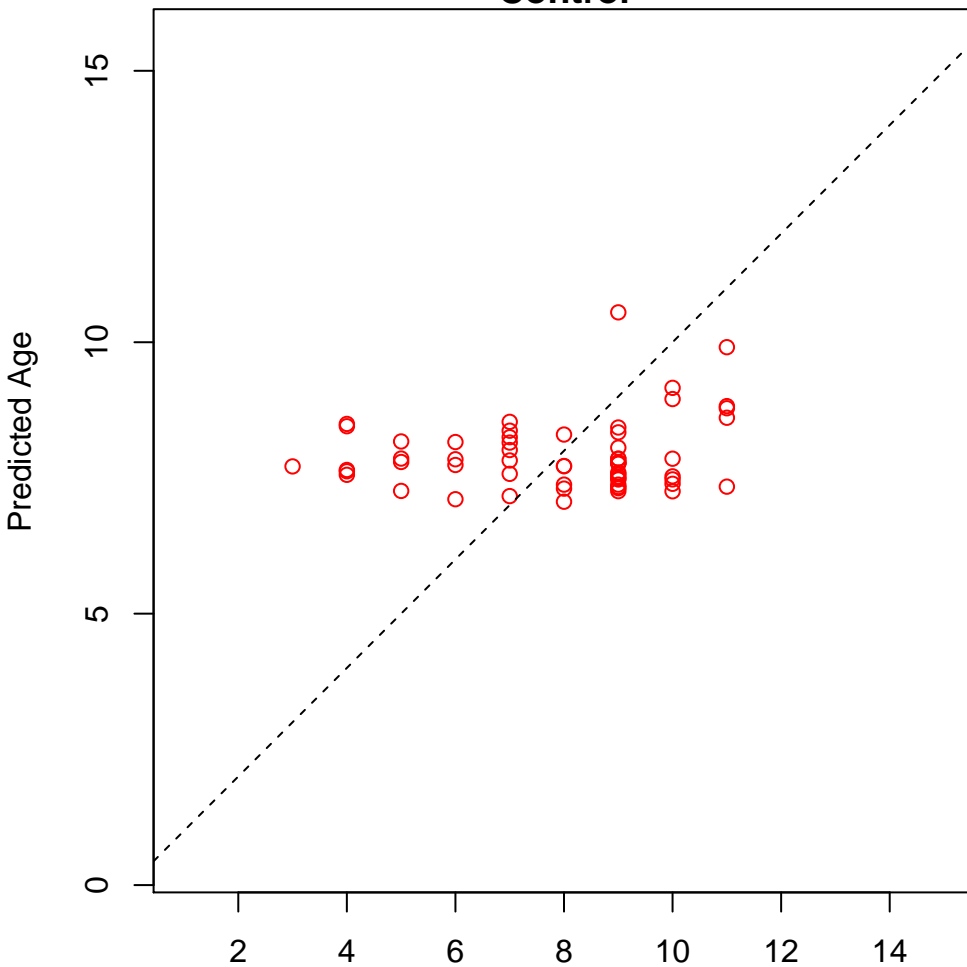


sagittal suture morphogenesis (Score: 0.142850)

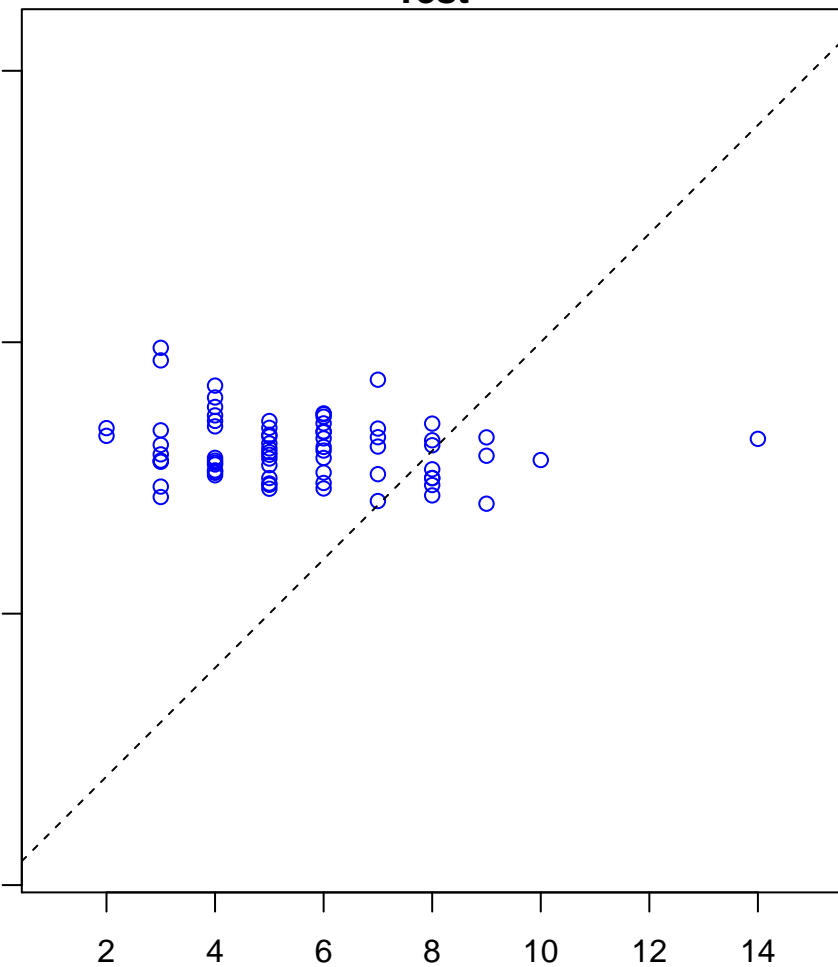


anterior semicircular canal development (Score: 0.142850)

Control



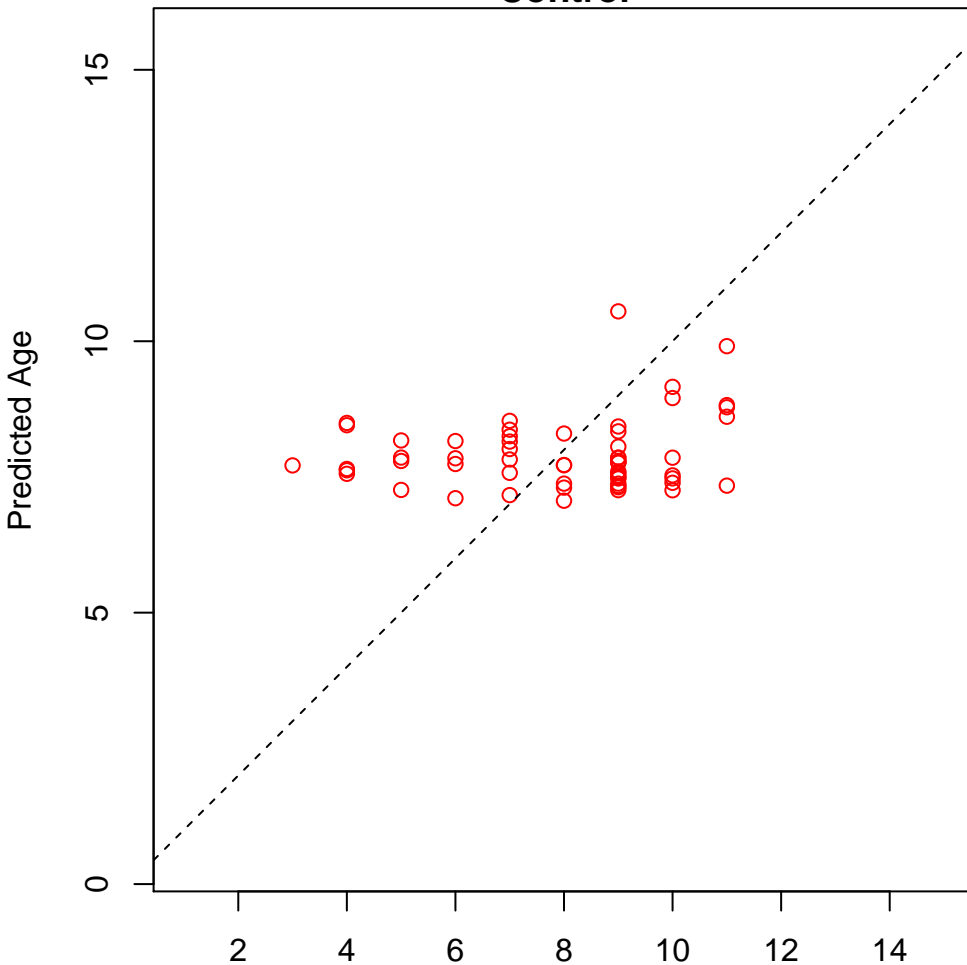
Test



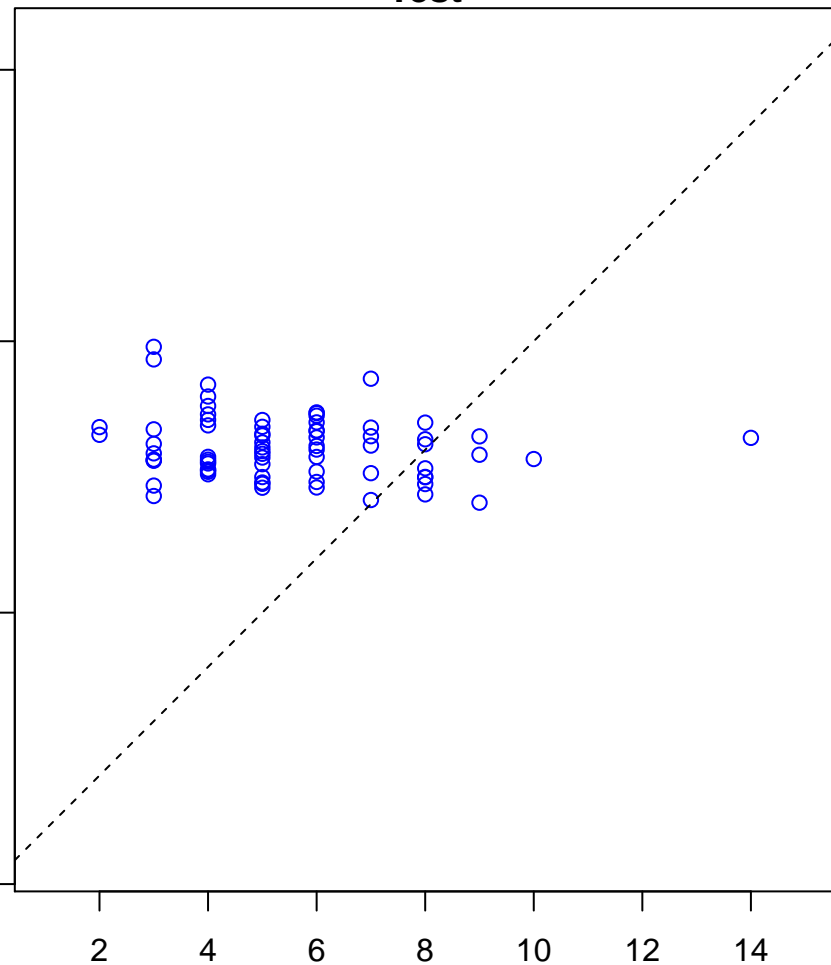
Actual Age

lateral semicircular canal development (Score: 0.142850)

Control

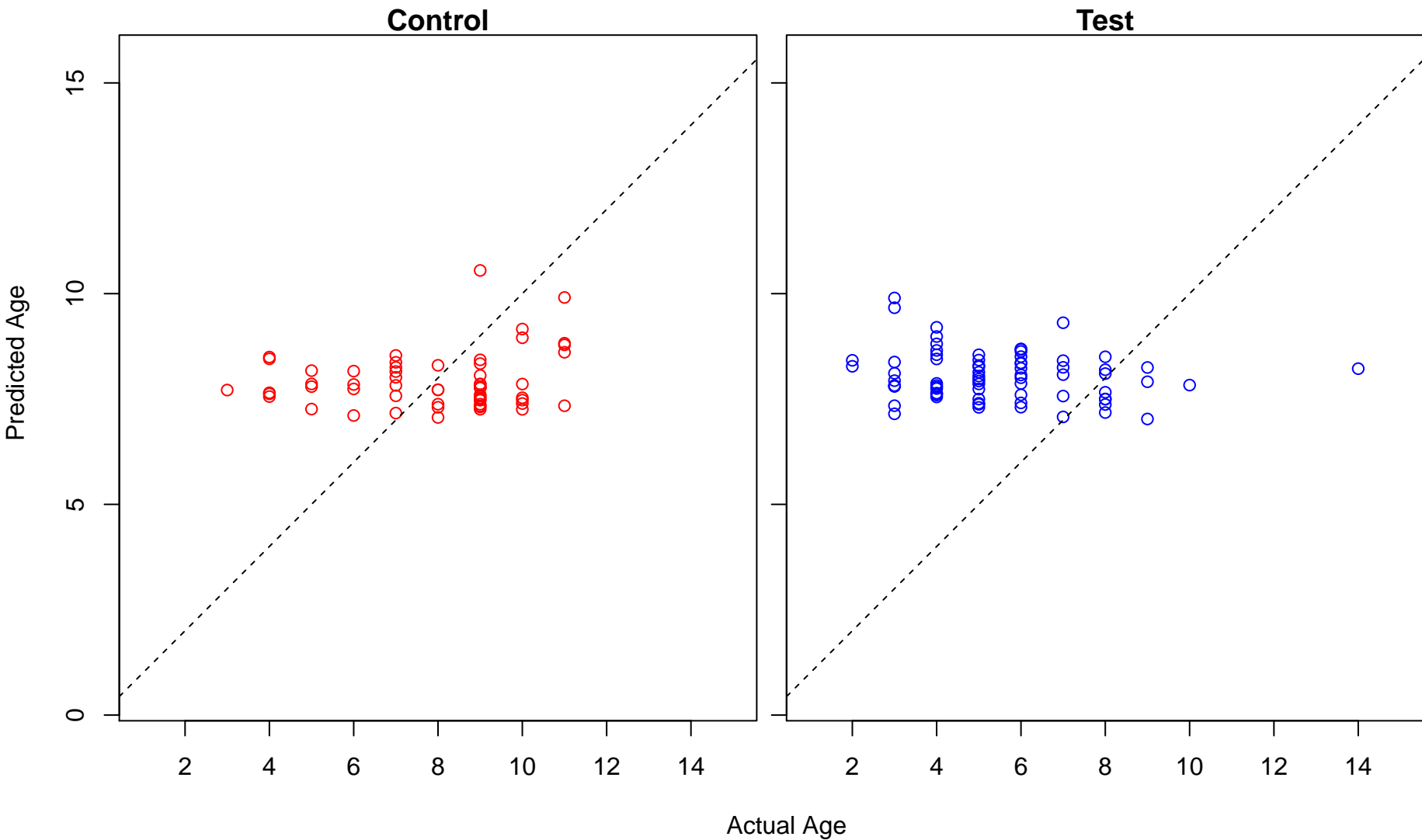


Test

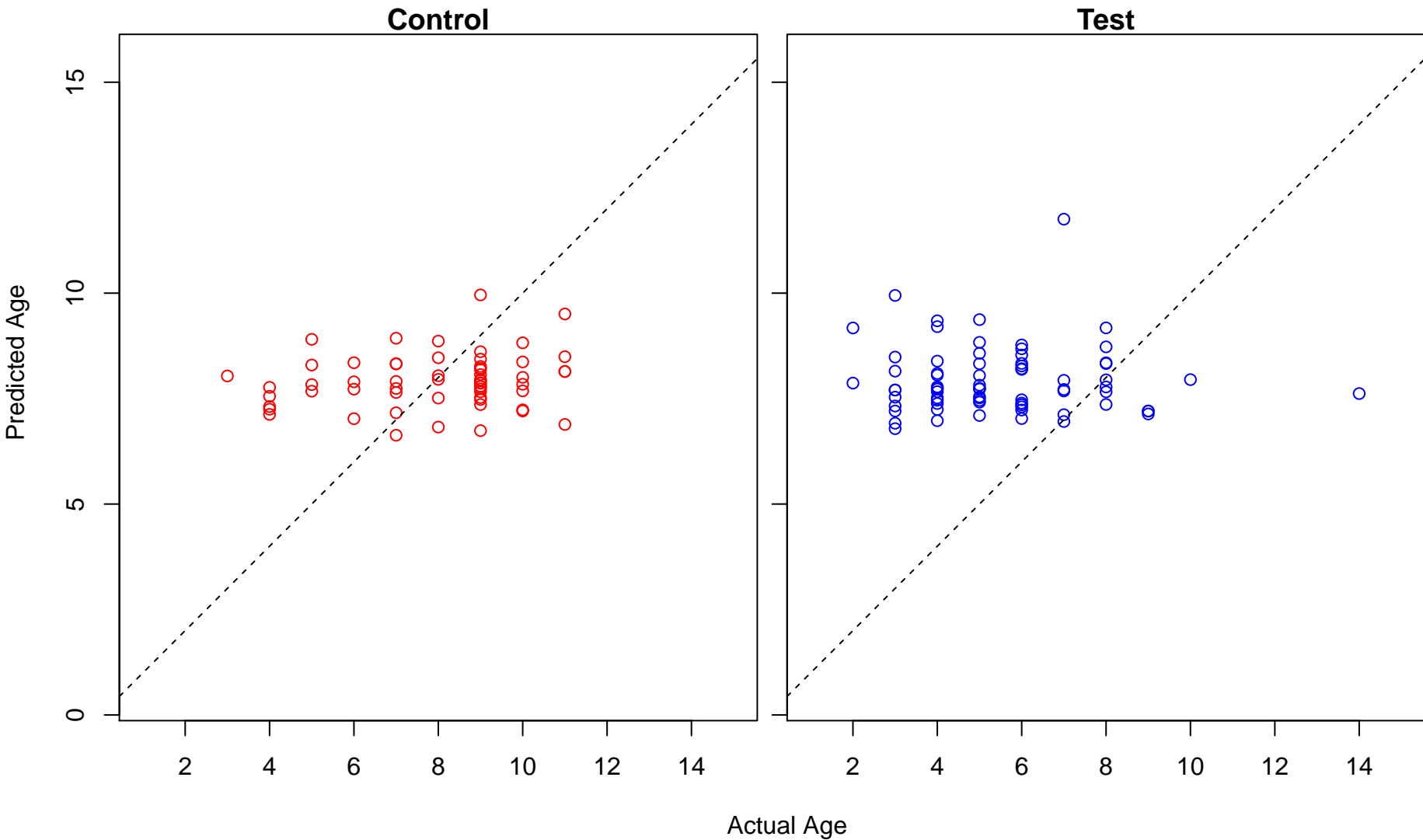


Actual Age

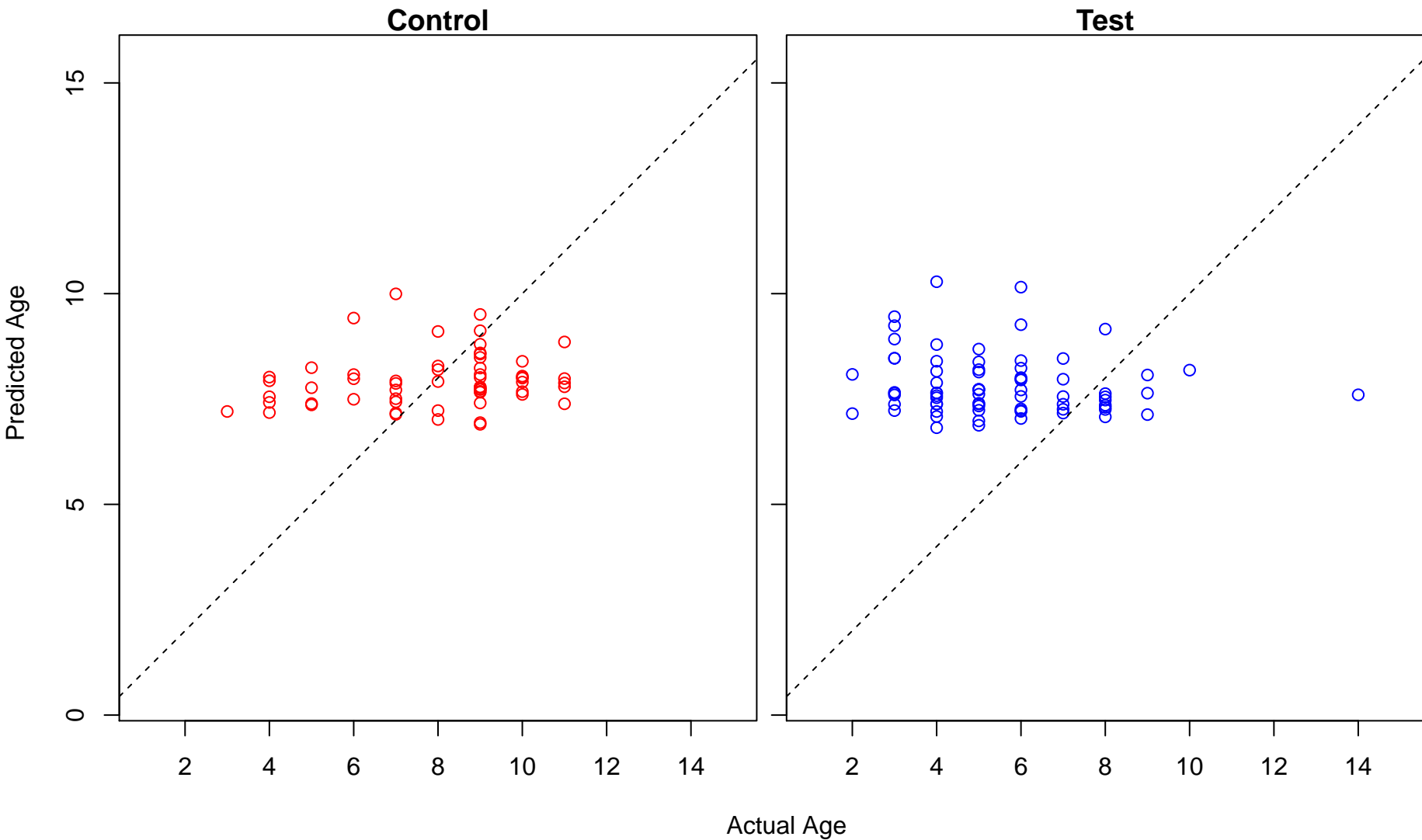
thymocyte apoptotic process (Score: 0.142850)



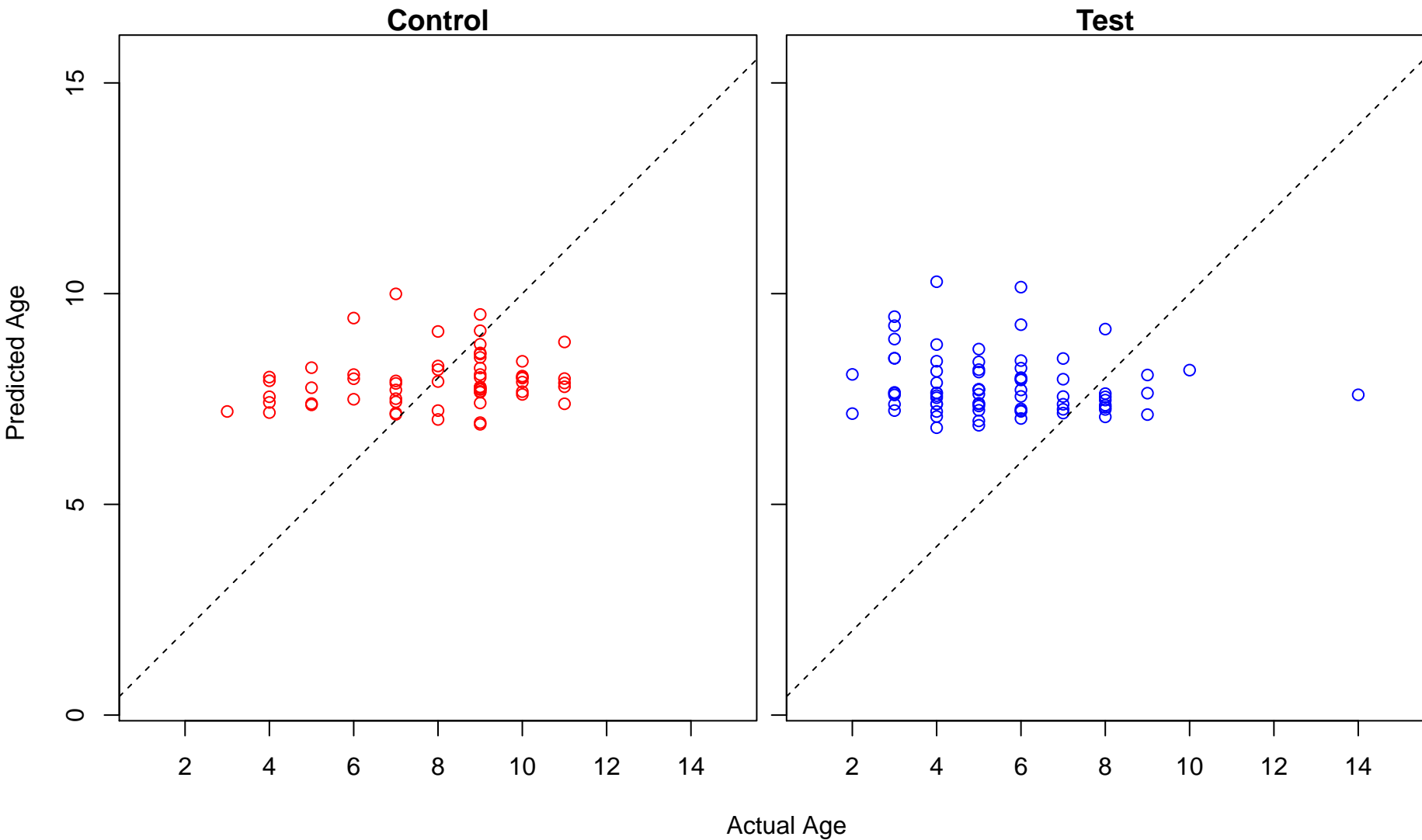
cytoplasmic actin-based contraction involved in cell motility (Score: 0.142288)



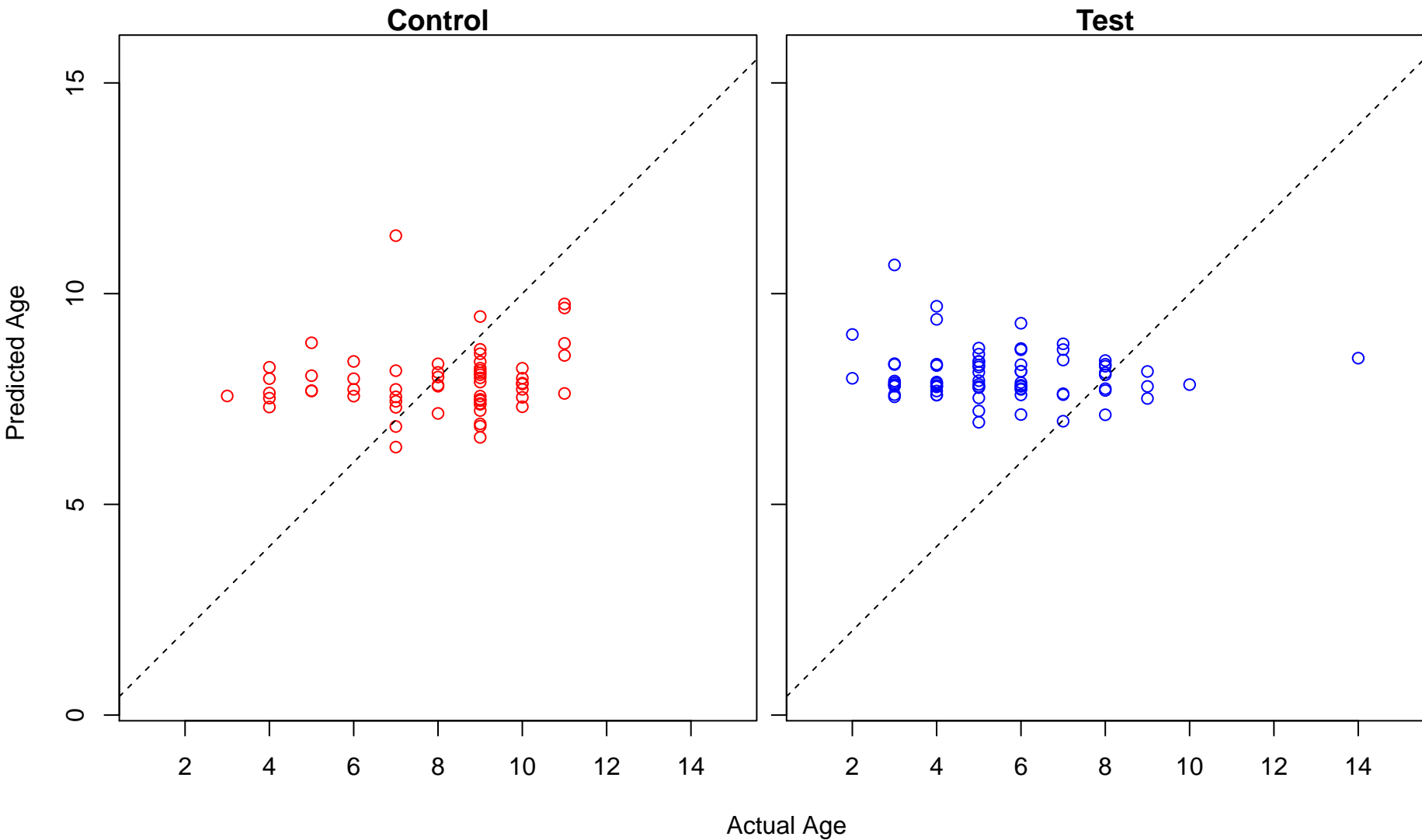
follicular dendritic cell activation (Score: 0.141118)



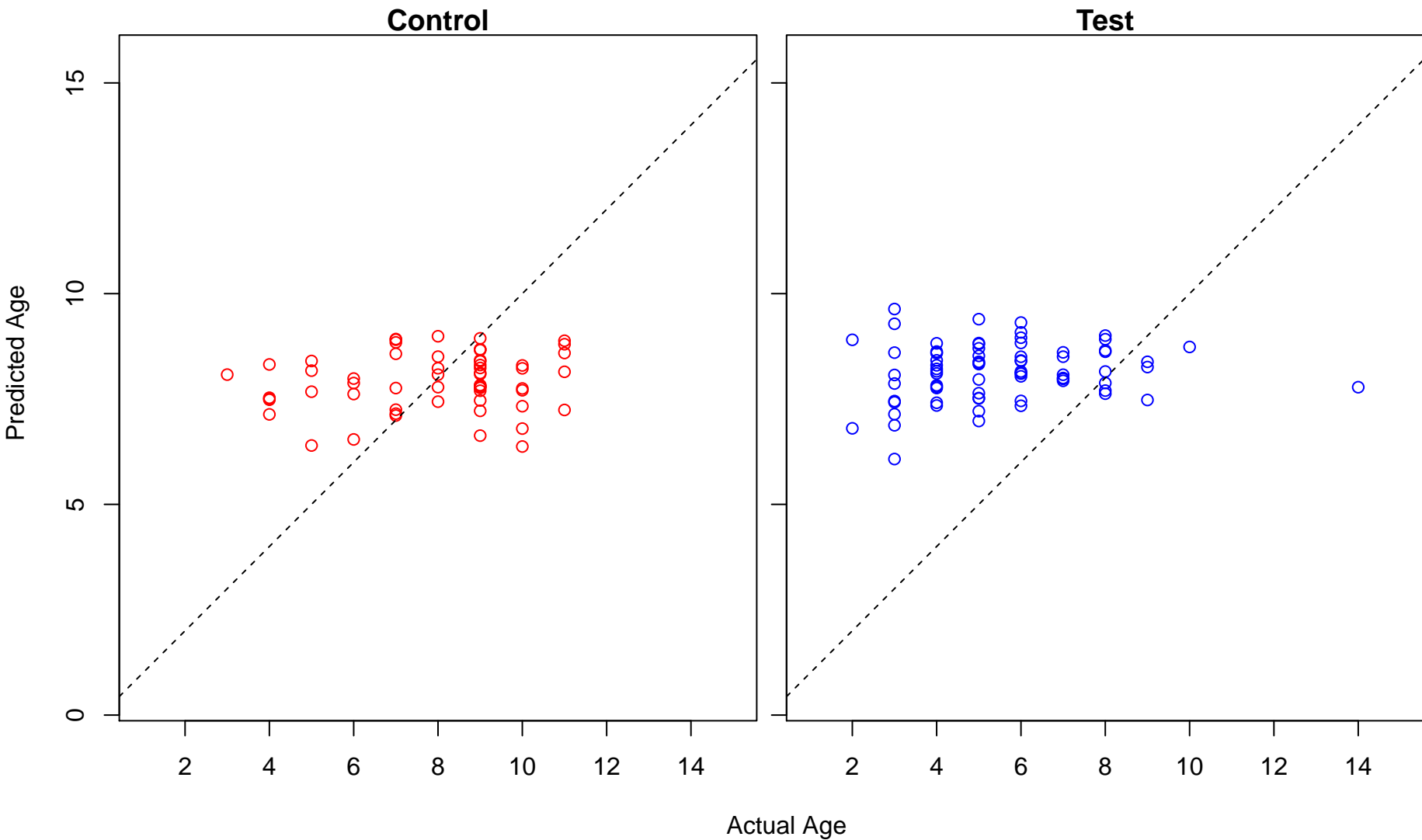
follicular dendritic cell differentiation (Score: 0.141118)



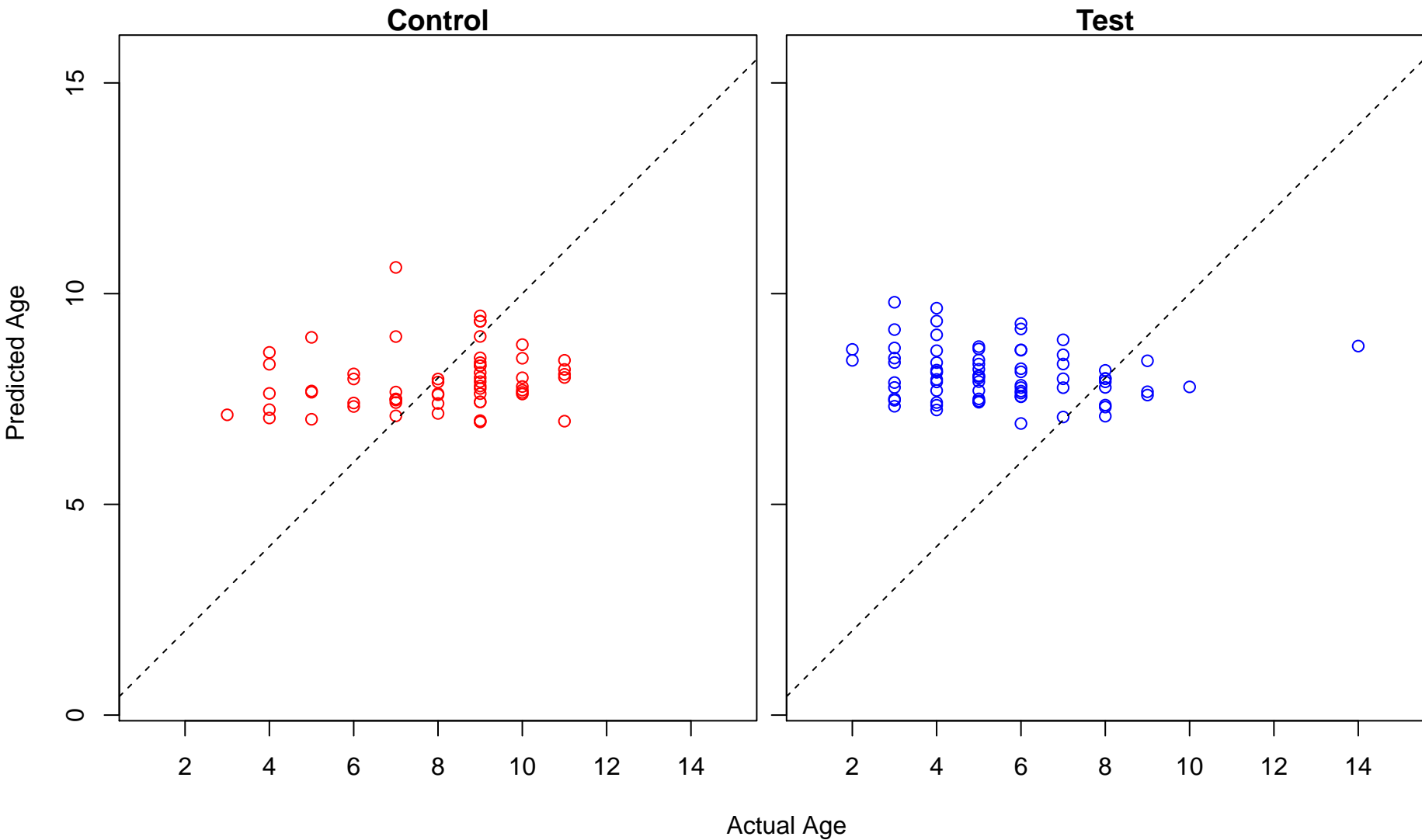
positive regulation of prostaglandin secretion (Score: 0.138301)



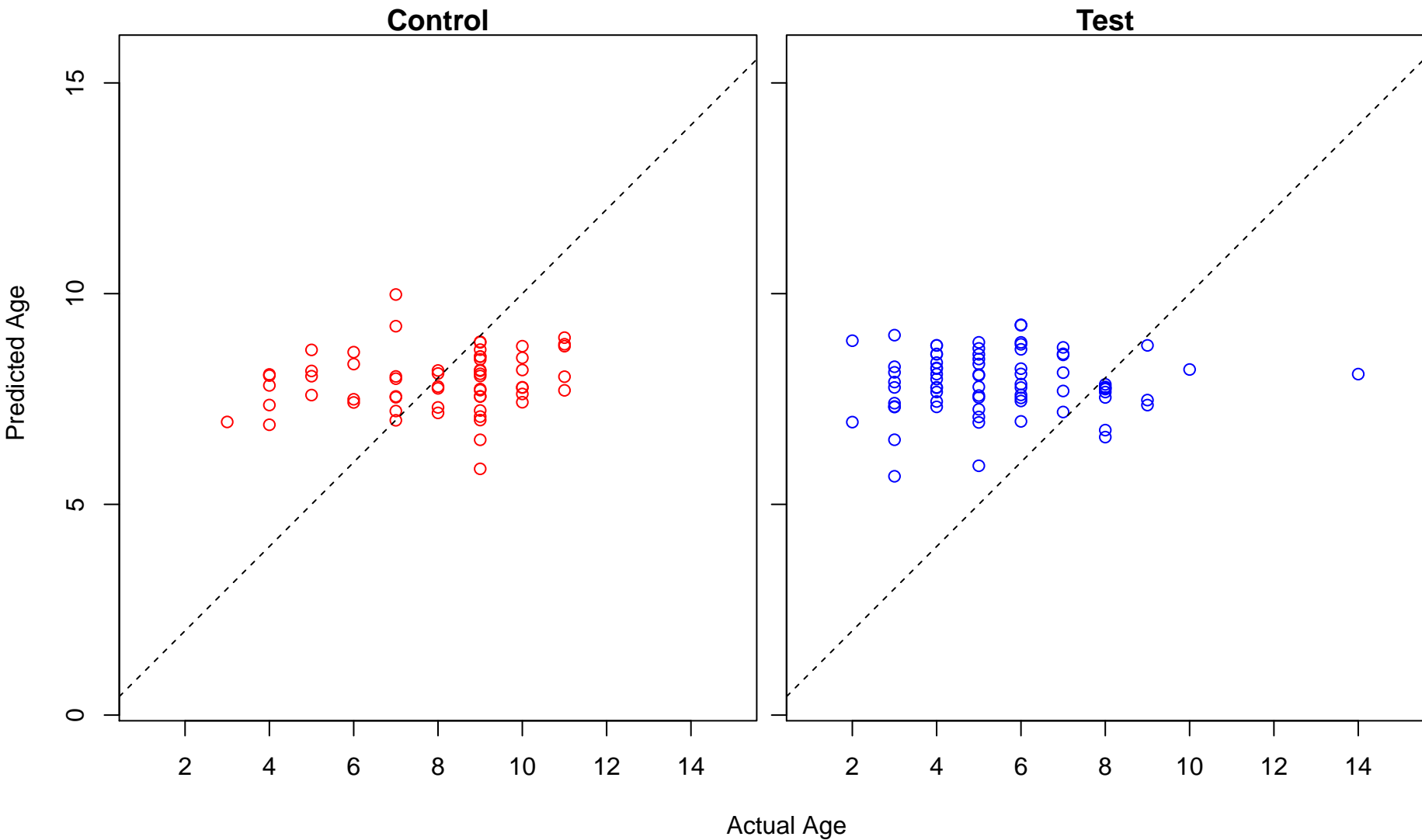
urate biosynthetic process (Score: 0.133608)



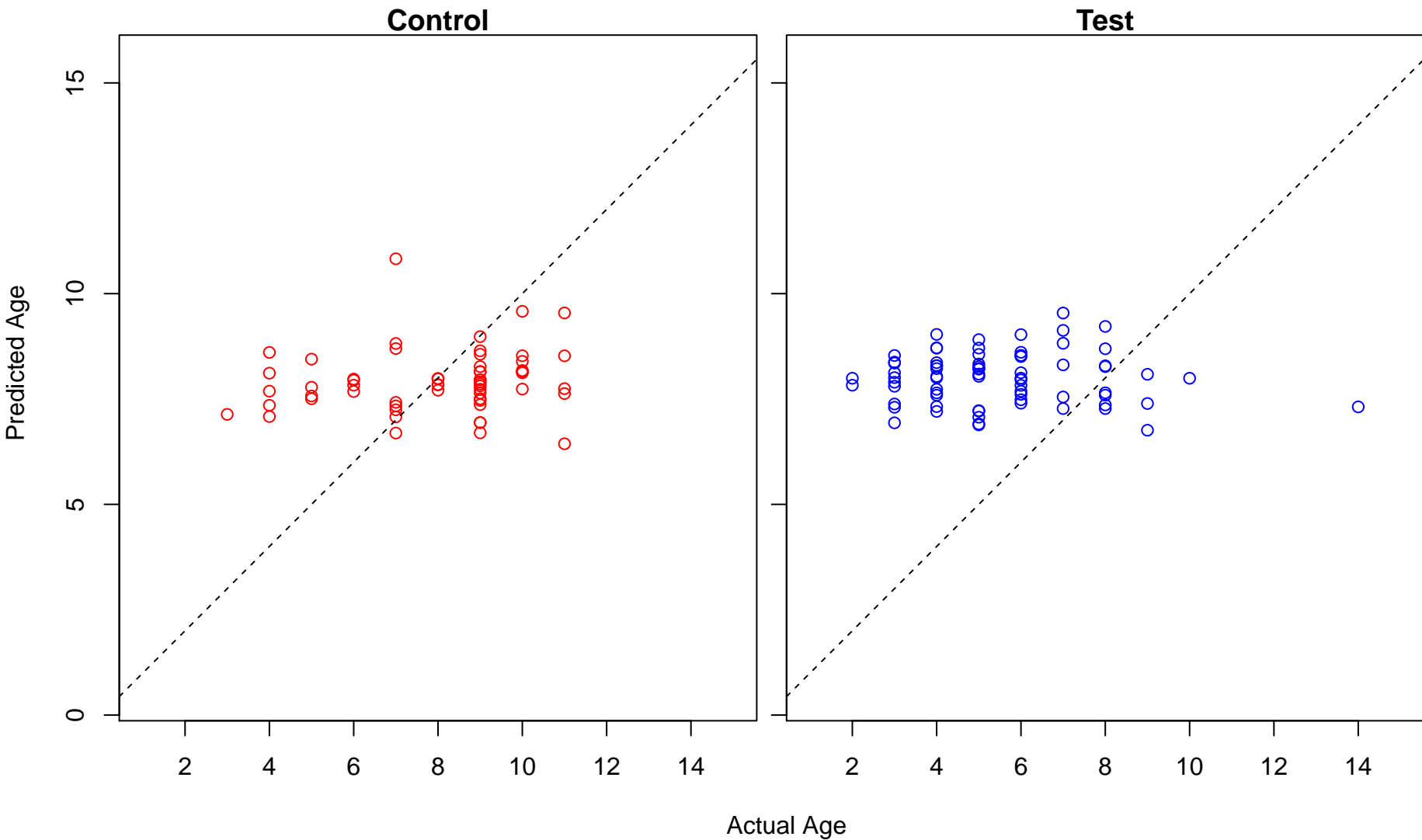
kidney vasculature morphogenesis (Score: 0.129474)



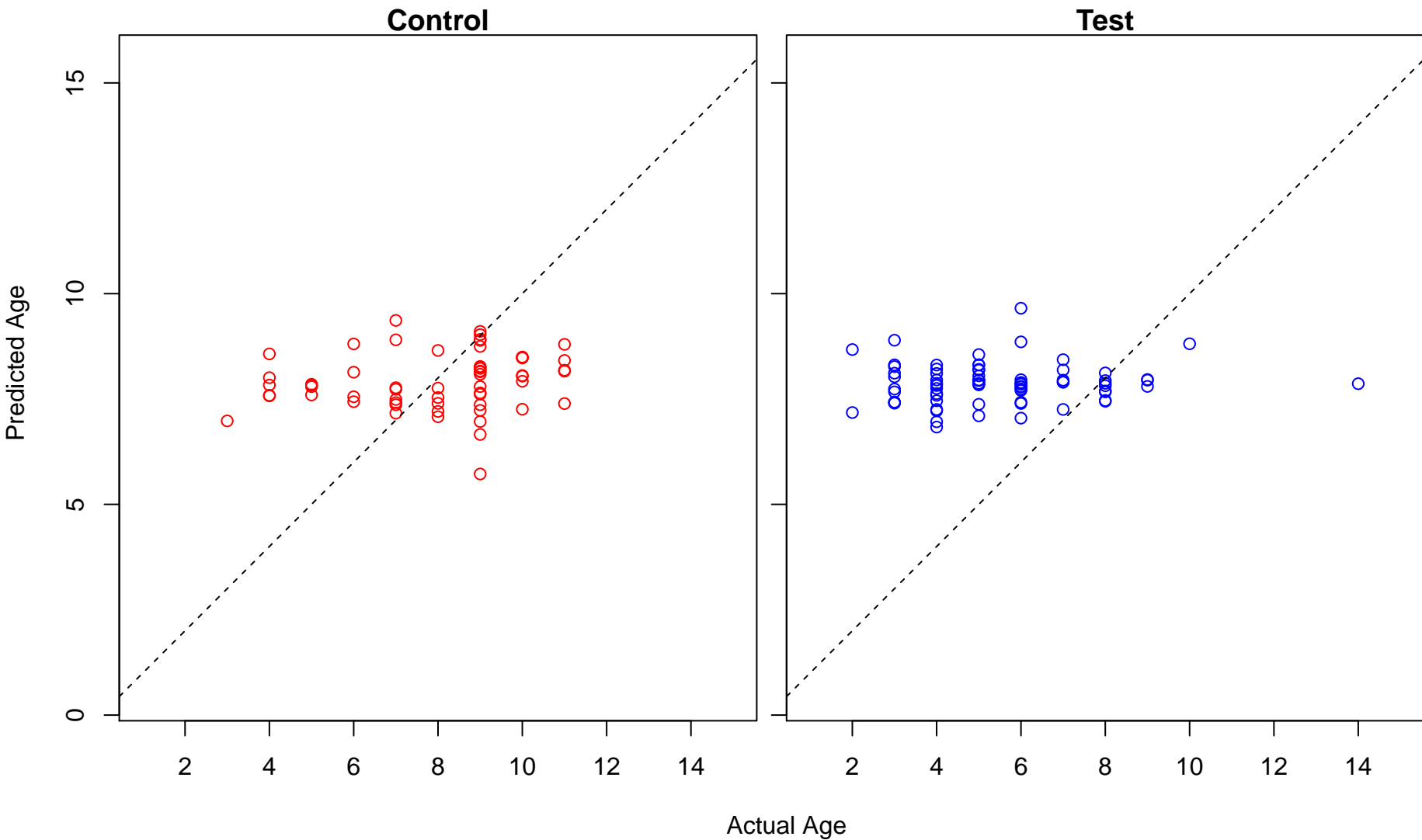
response to cobalt ion (Score: 0.127669)



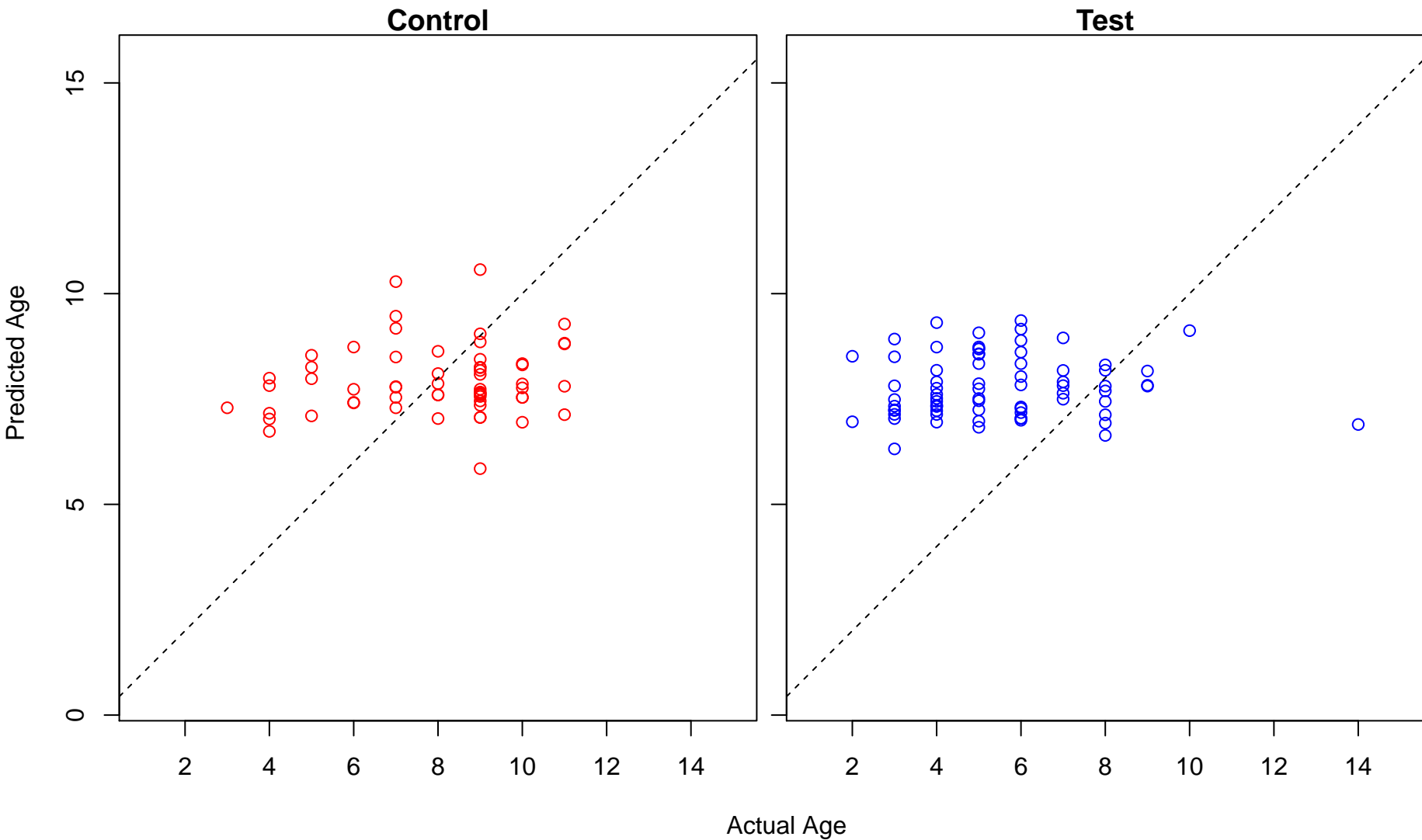
integrin biosynthetic process (Score: 0.122510)



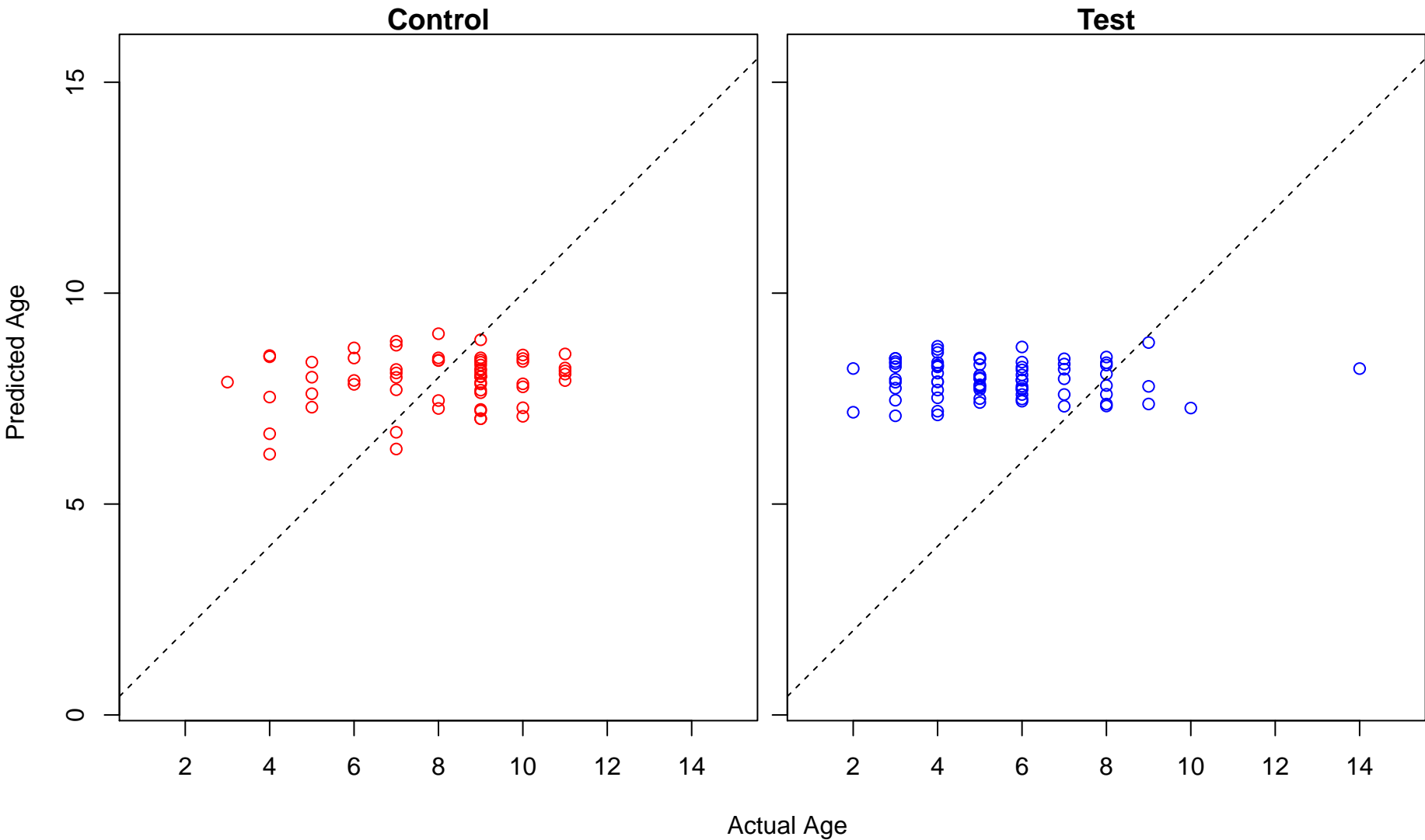
positive regulation of interleukin-10 production (Score: 0.122340)



cerebellar cortex morphogenesis (Score: 0.120813)

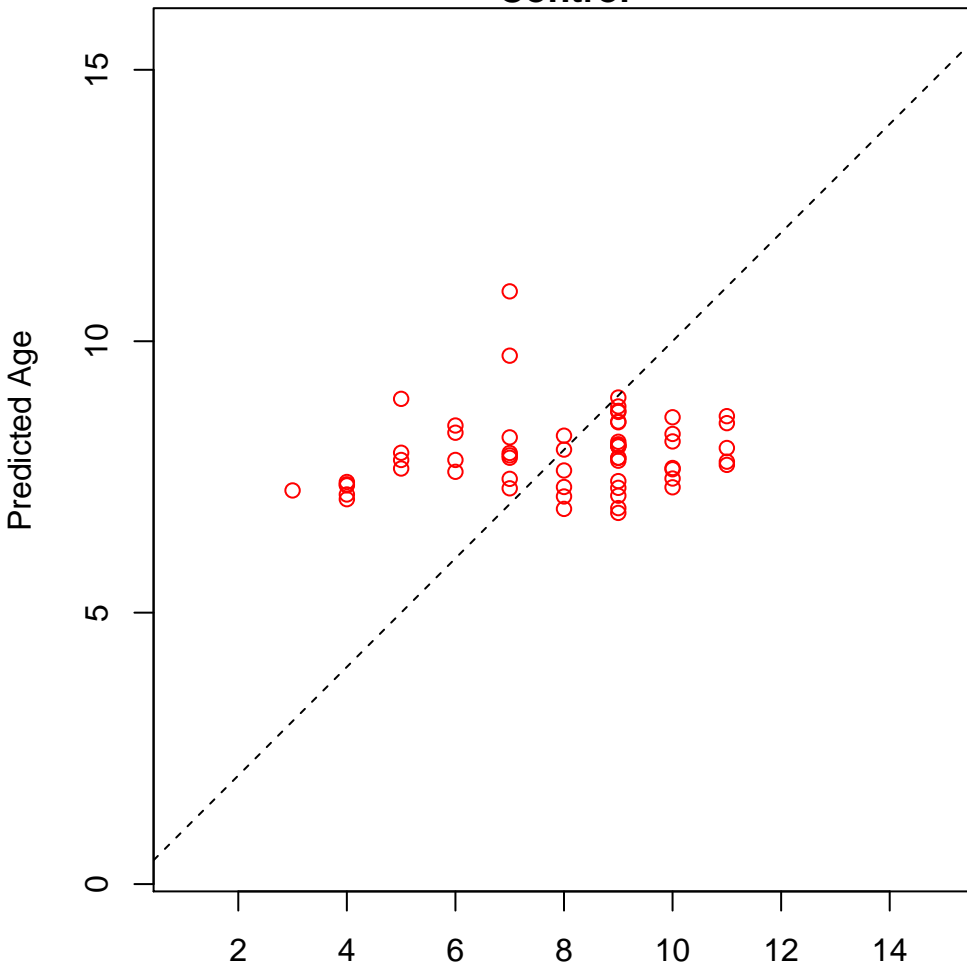


lung connective tissue development (Score: 0.116640)

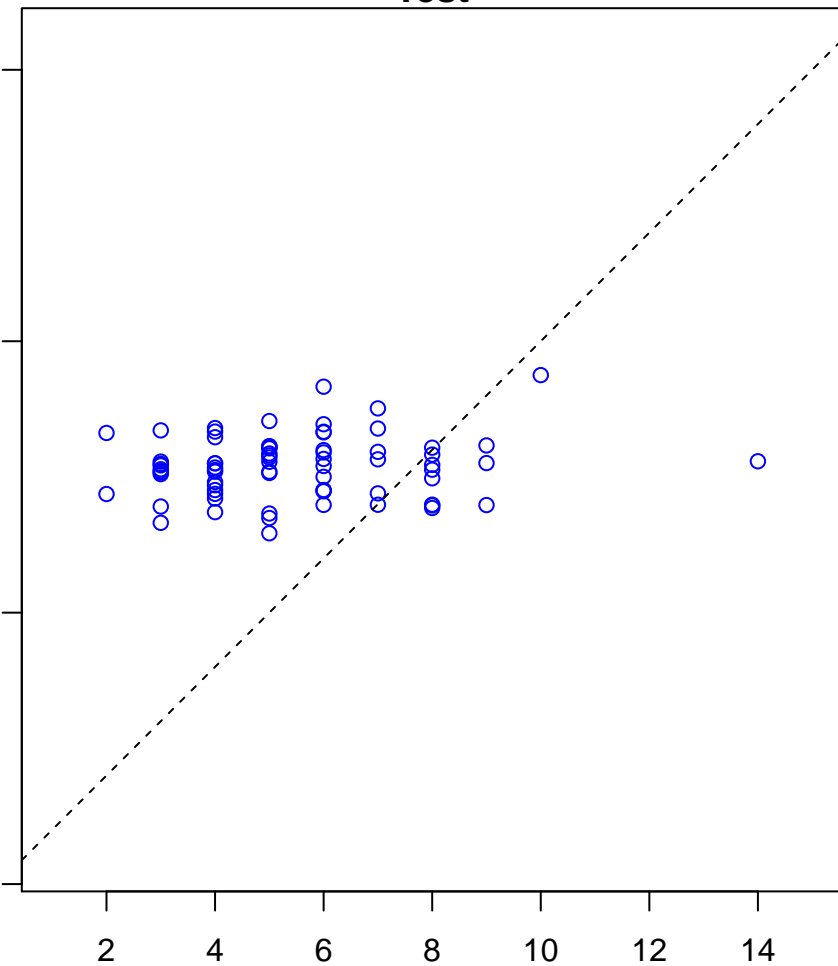


actin polymerization or depolymerization (Score: 0.109965)

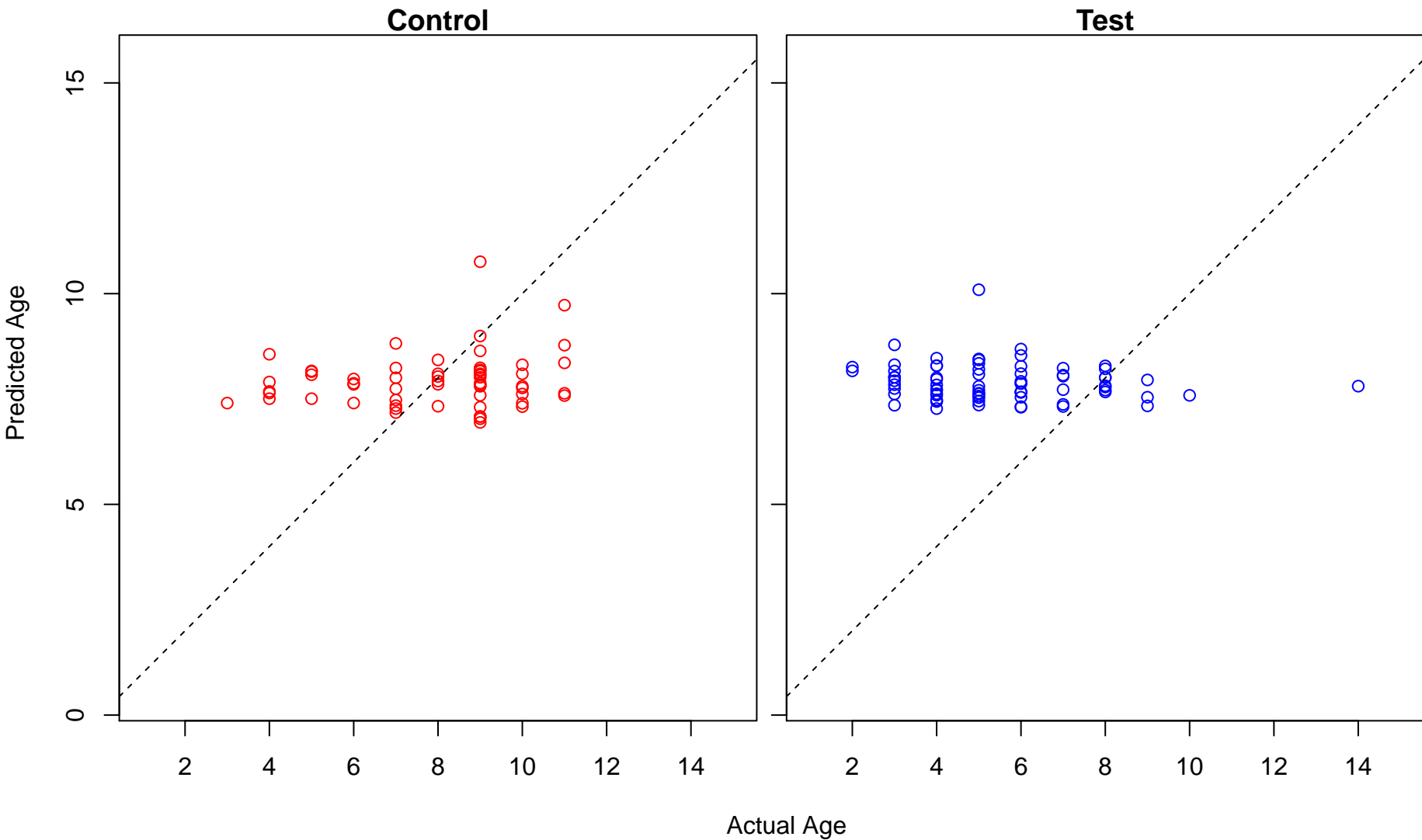
Control



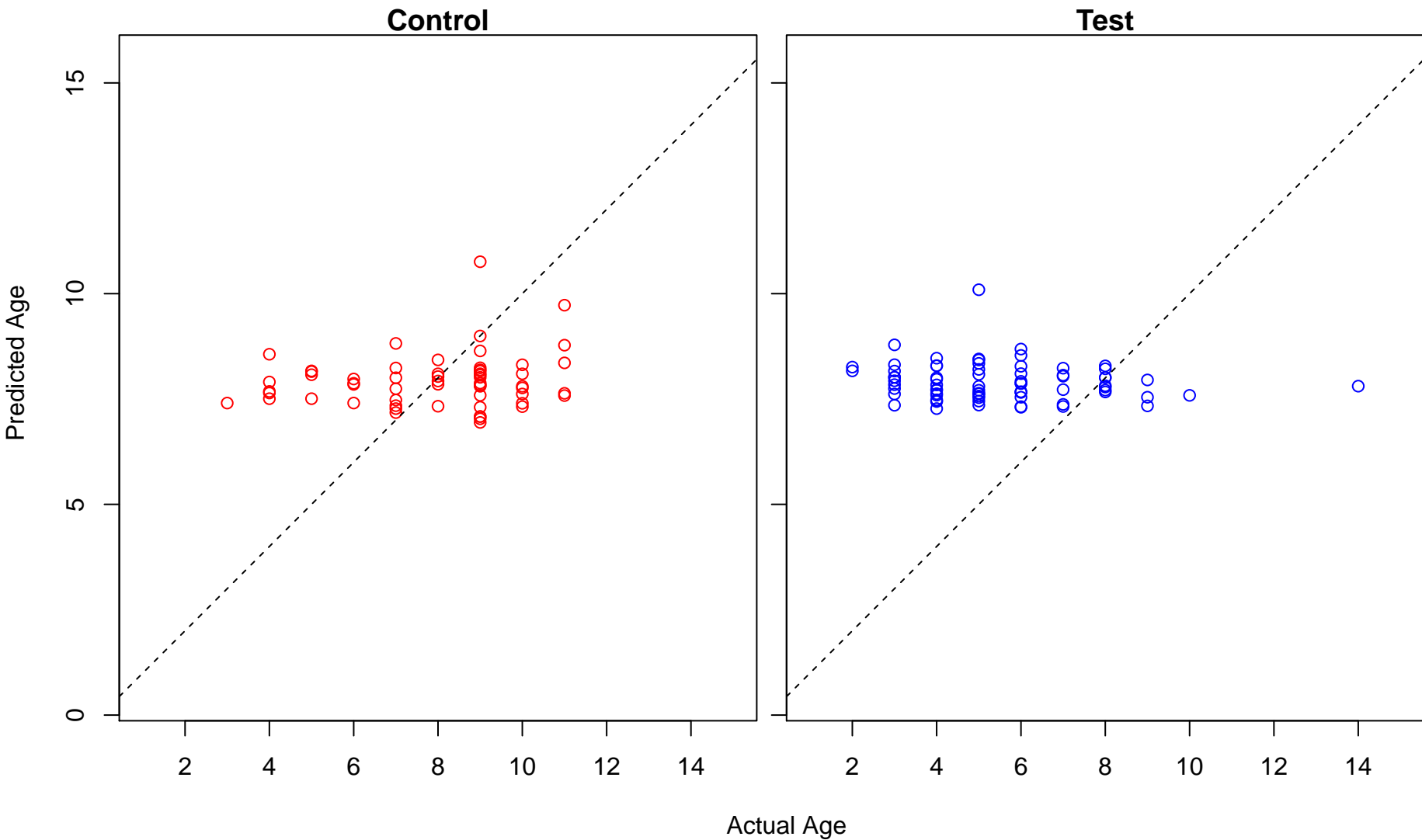
Test



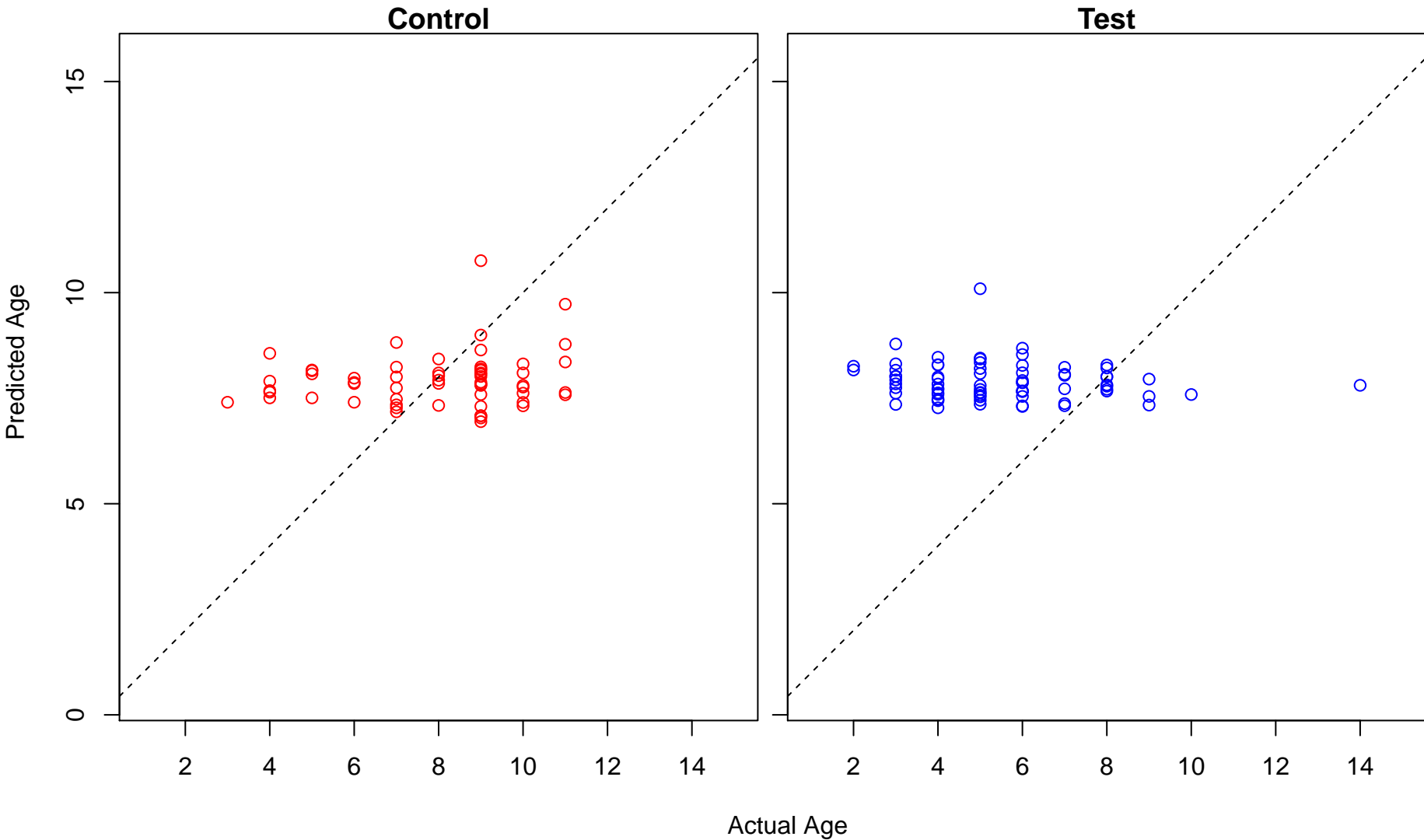
cytolysis by symbiont of host cells (Score: 0.107134)



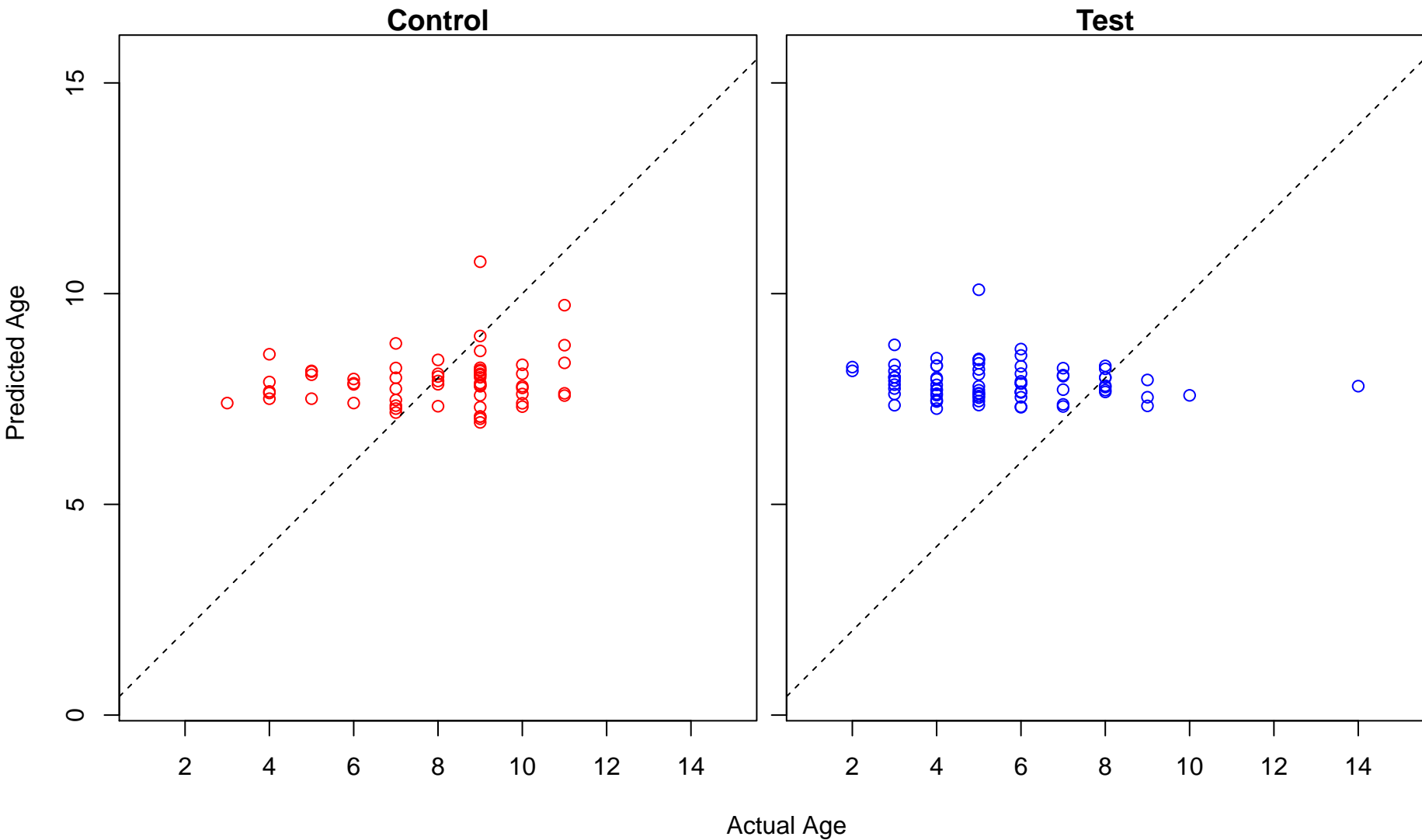
killing by symbiont of host cells (Score: 0.107134)



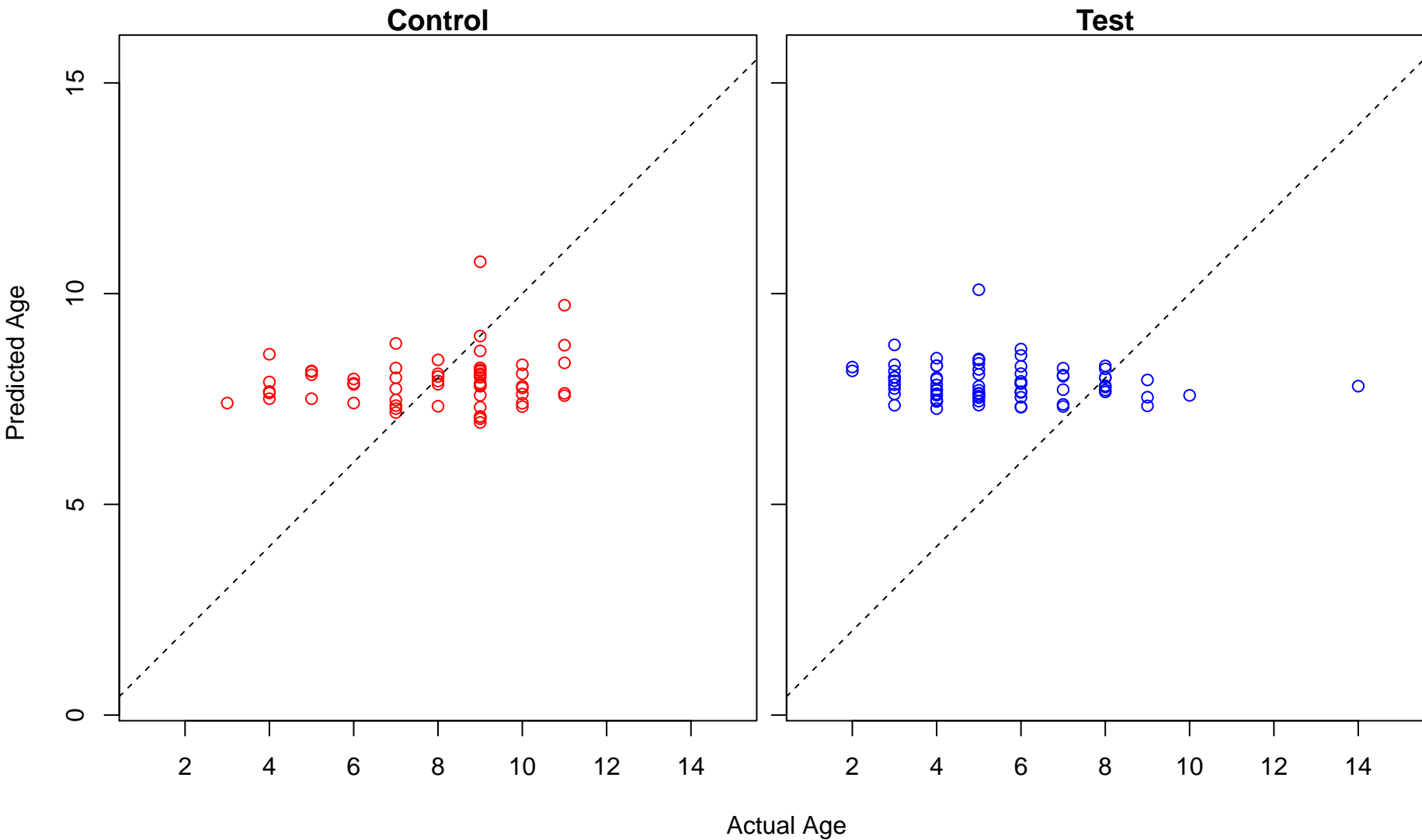
hemolysis by symbiont of host erythrocytes (Score: 0.107134)



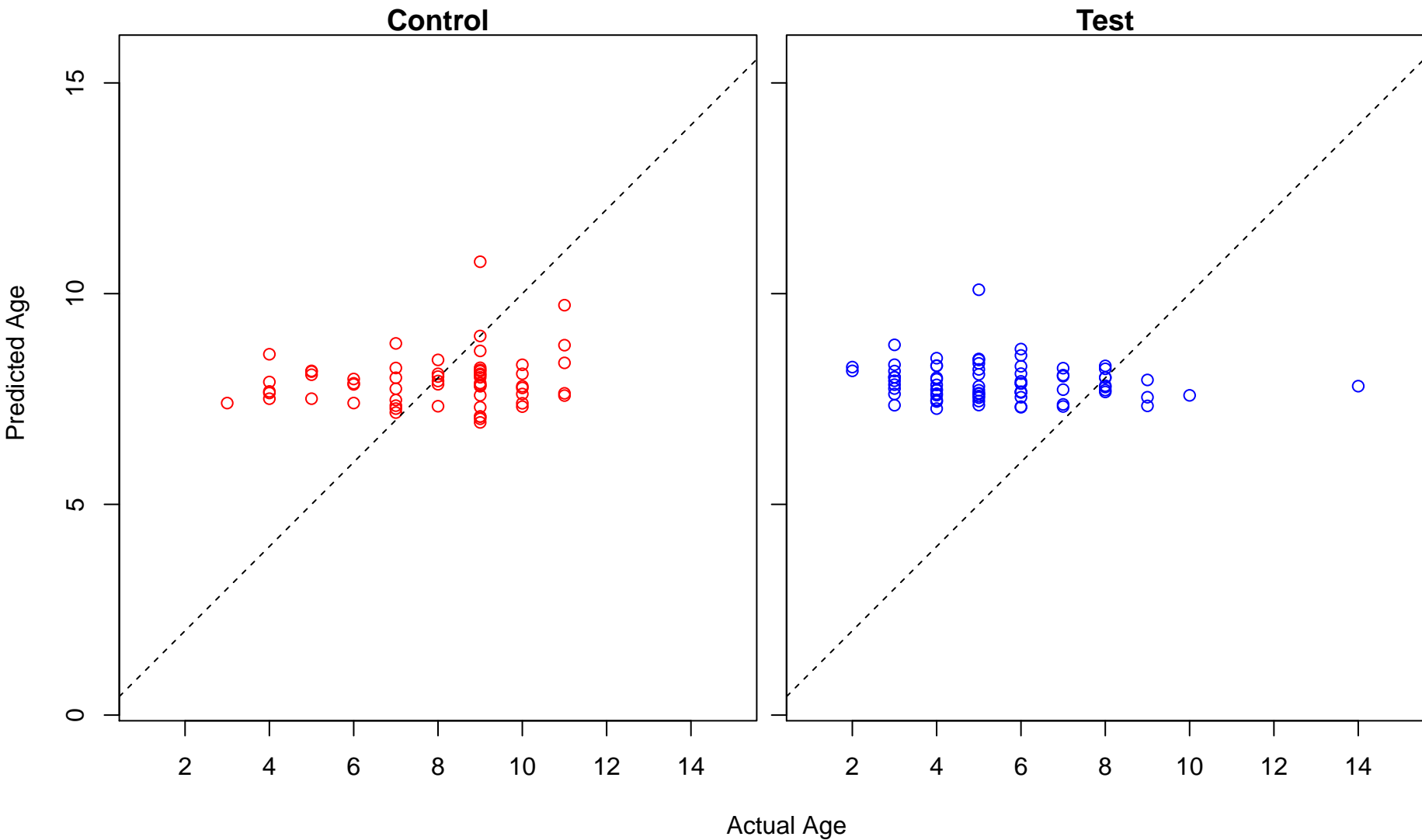
disruption by symbiont of host cell (Score: 0.107134)



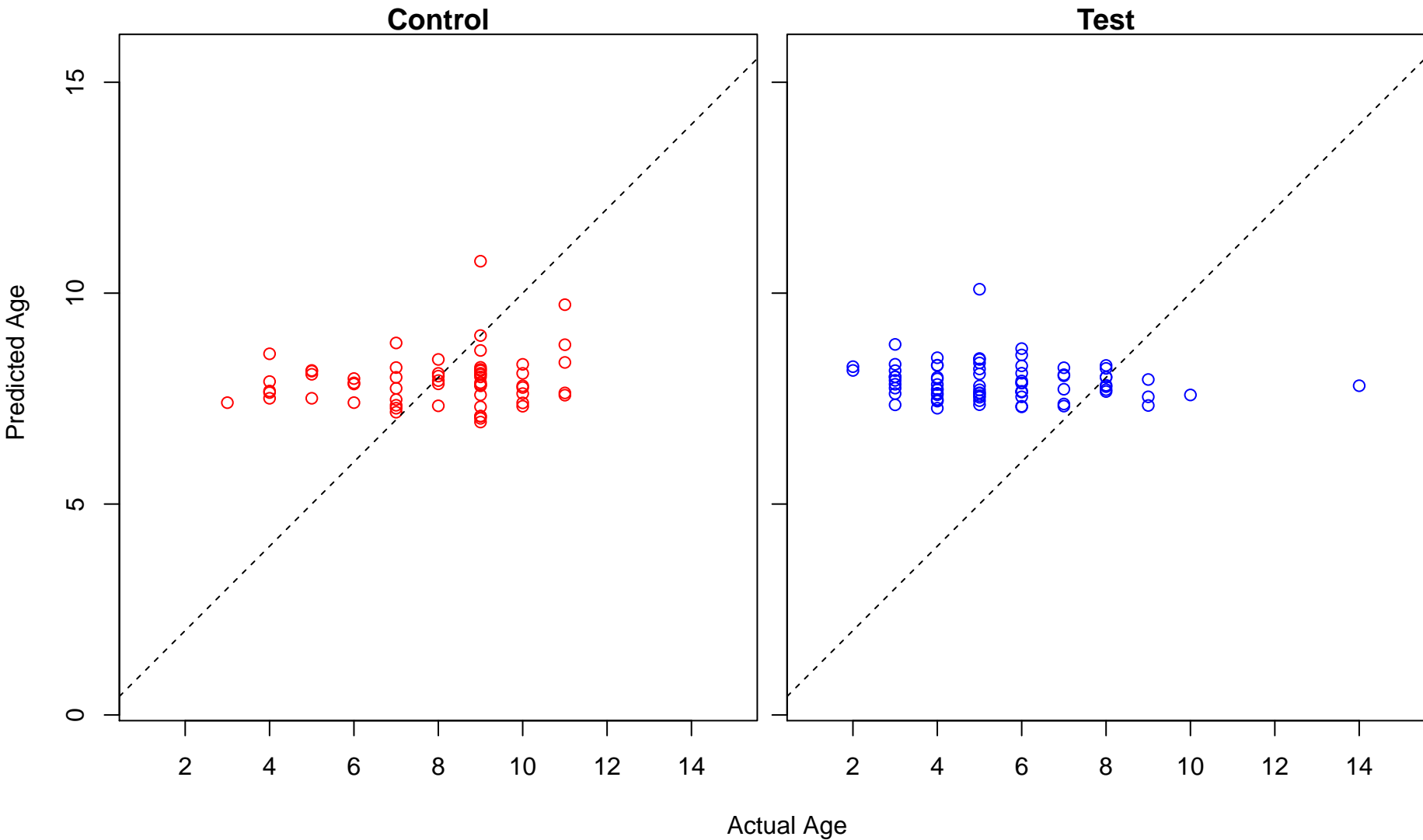
hemolysis in other organism (Score: 0.107134)



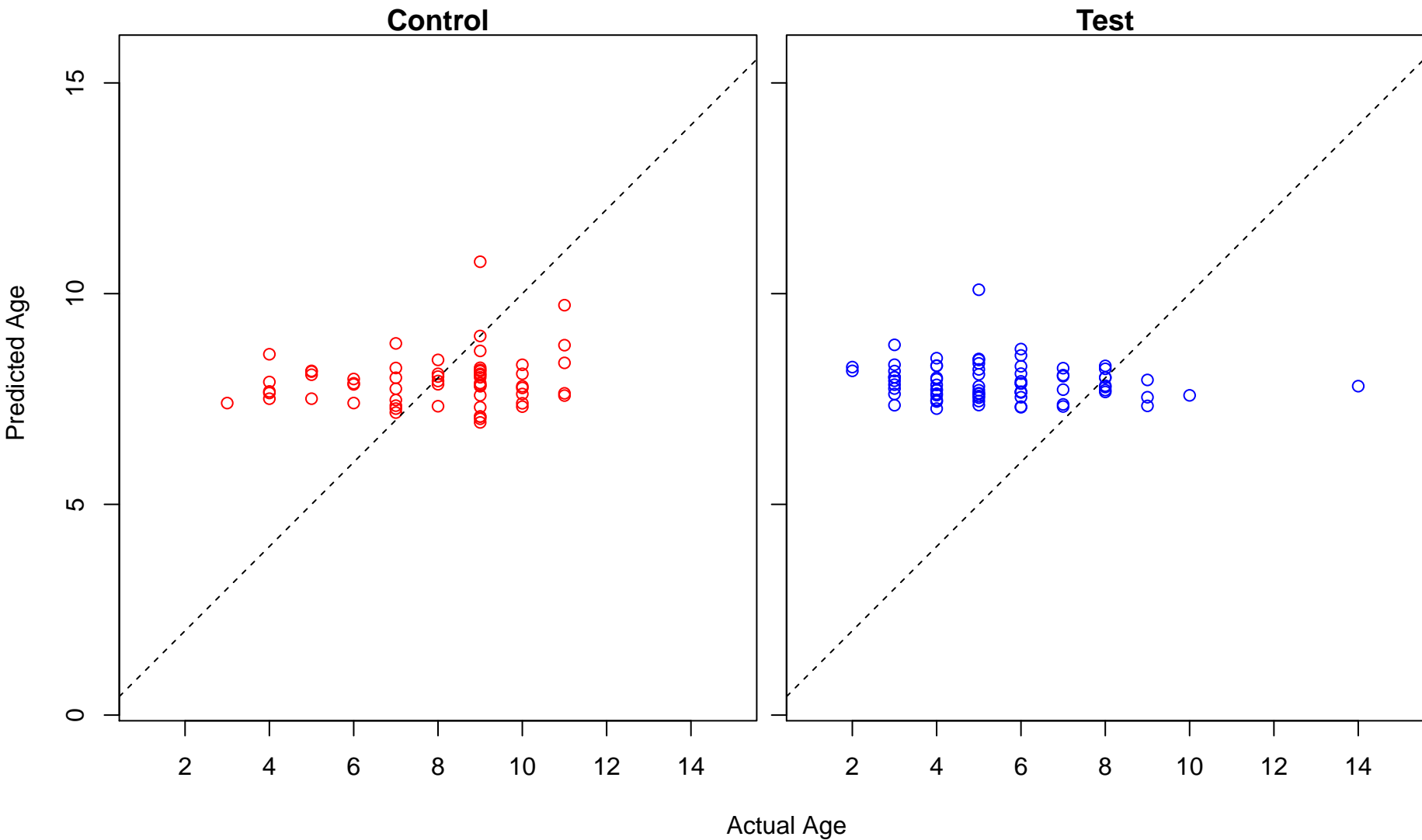
cytolysis in other organism (Score: 0.107134)



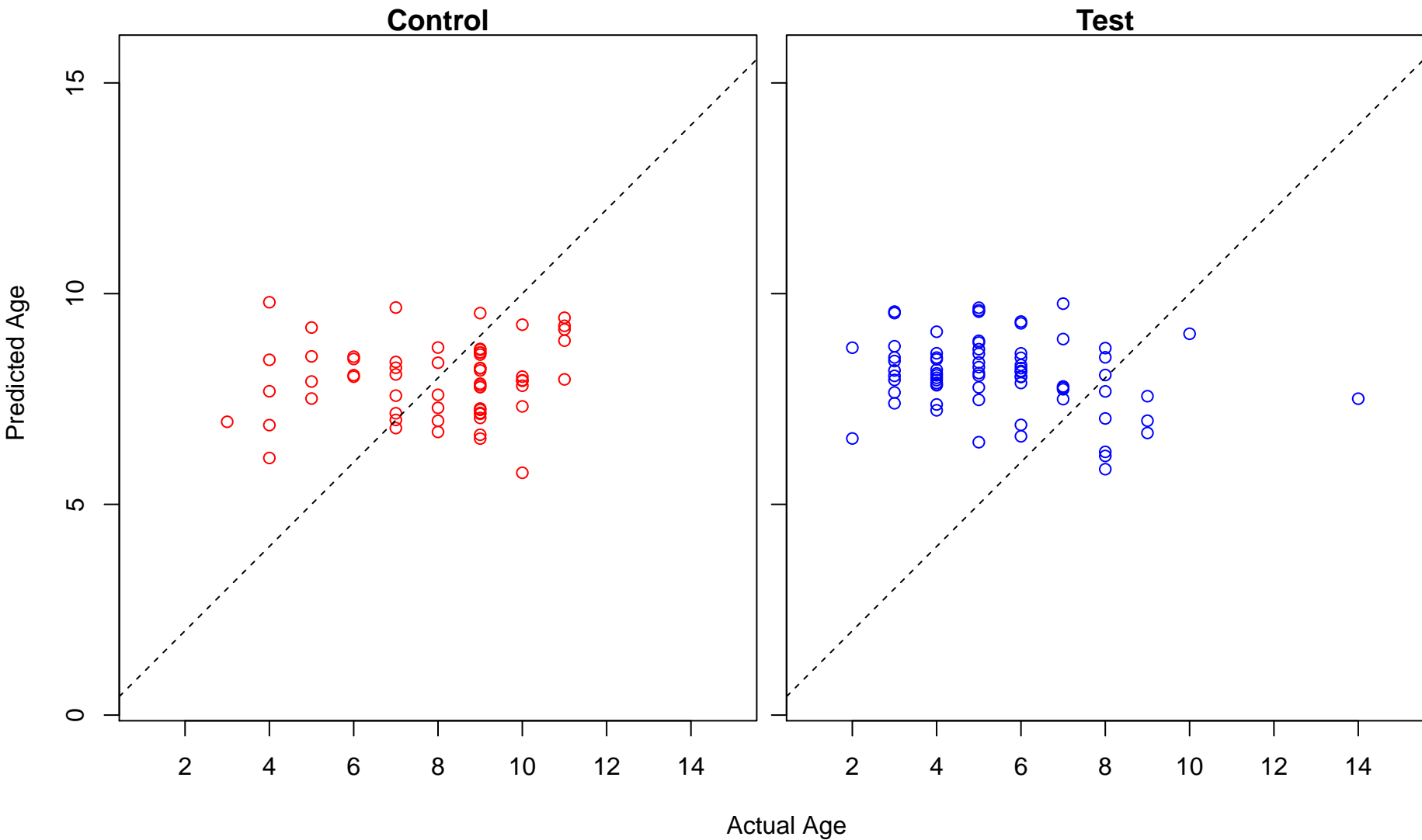
cytolysis in other organism involved in symbiotic interaction (Score: 0.107134)



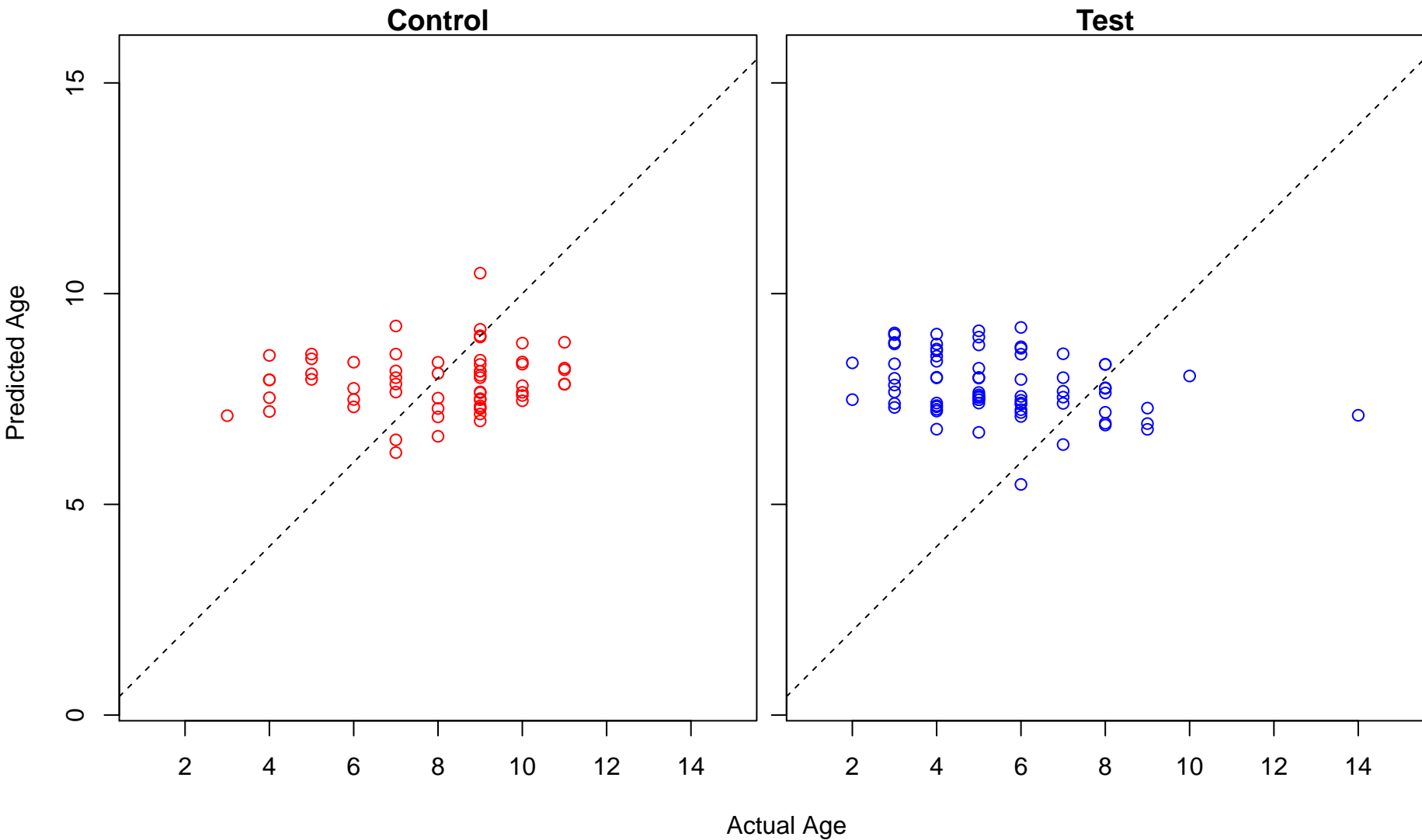
hemolysis in other organism involved in symbiotic interaction (Score: 0.107134)



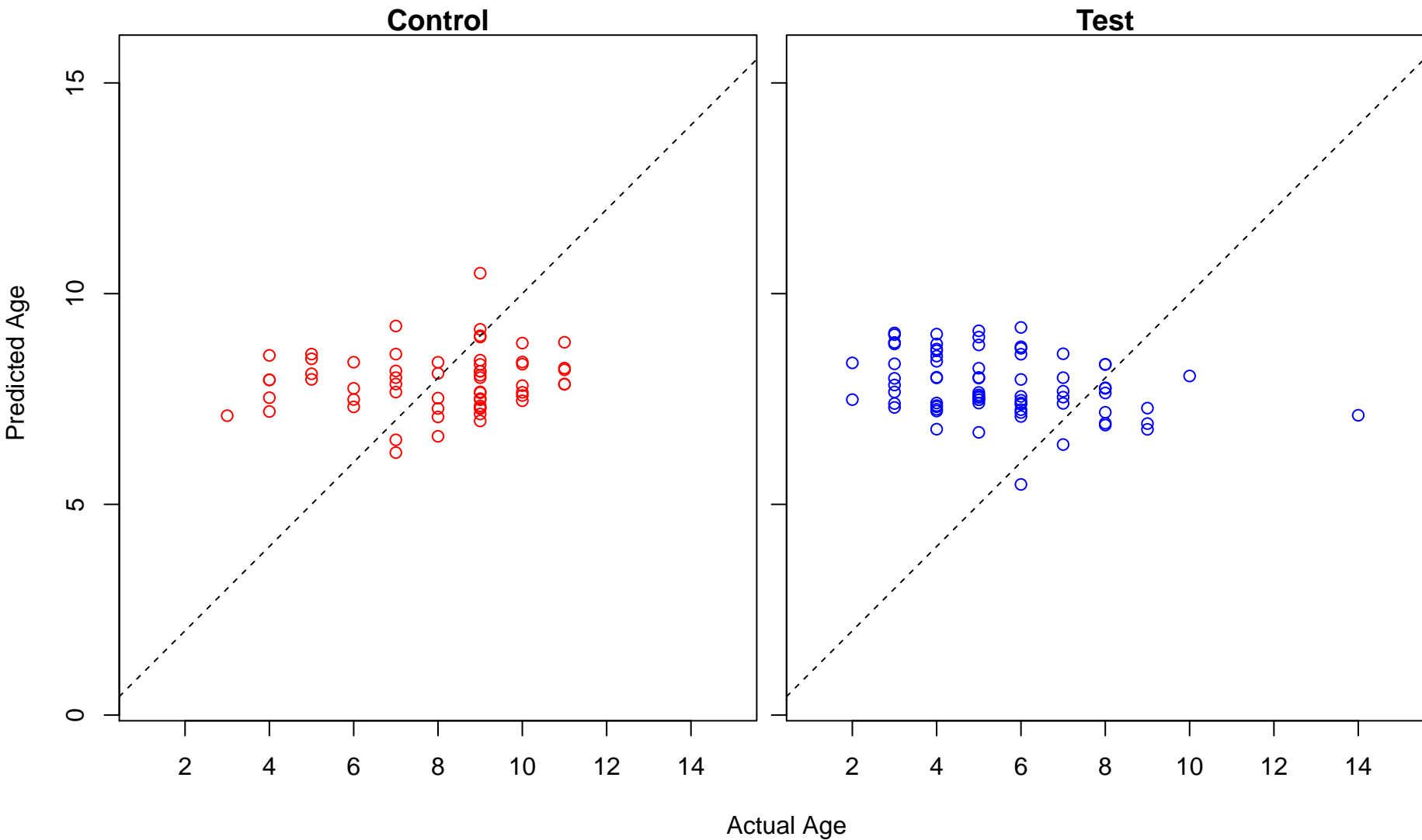
D-serine metabolic process (Score: 0.104808)



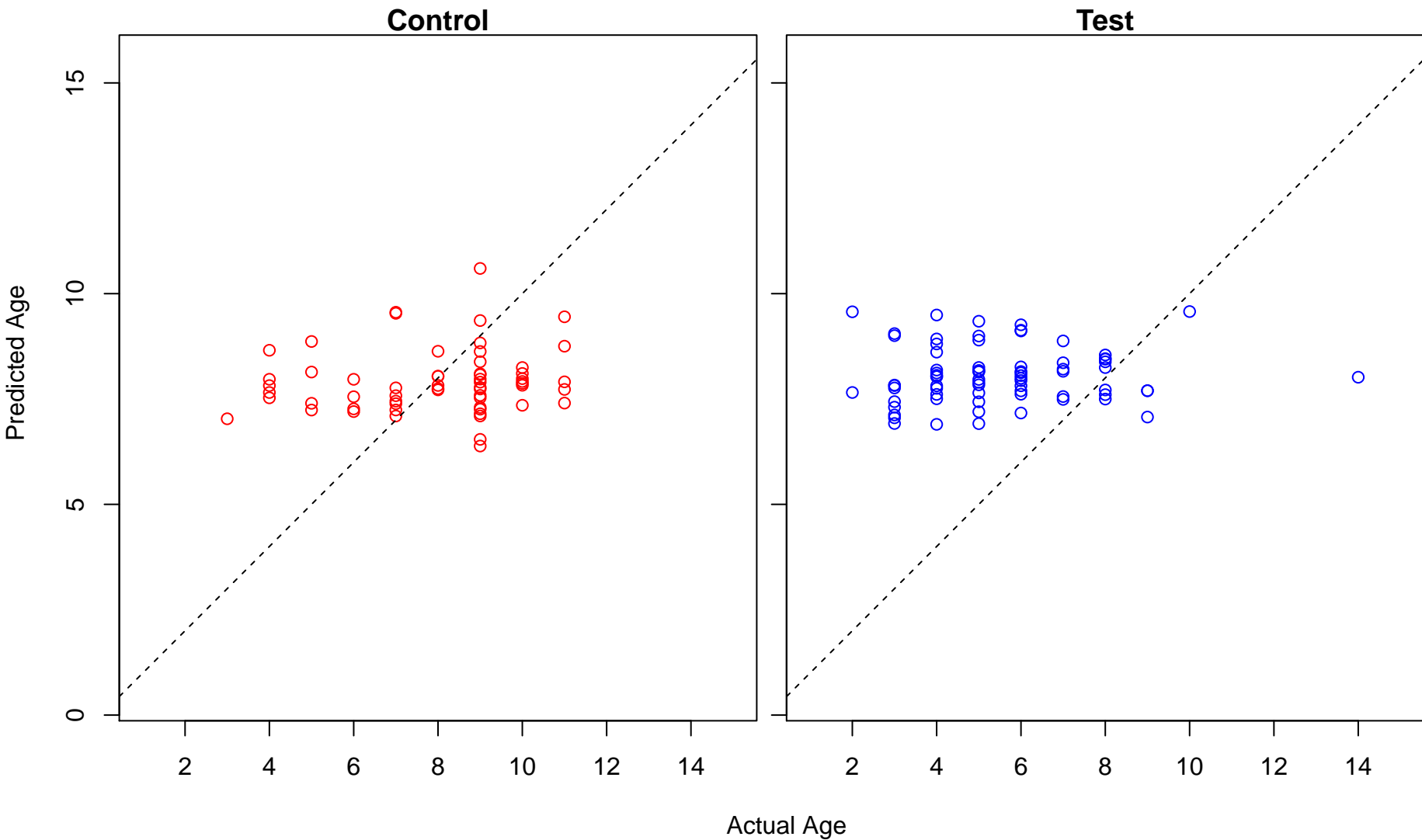
regulation of immature T cell proliferation (Score: 0.104538)



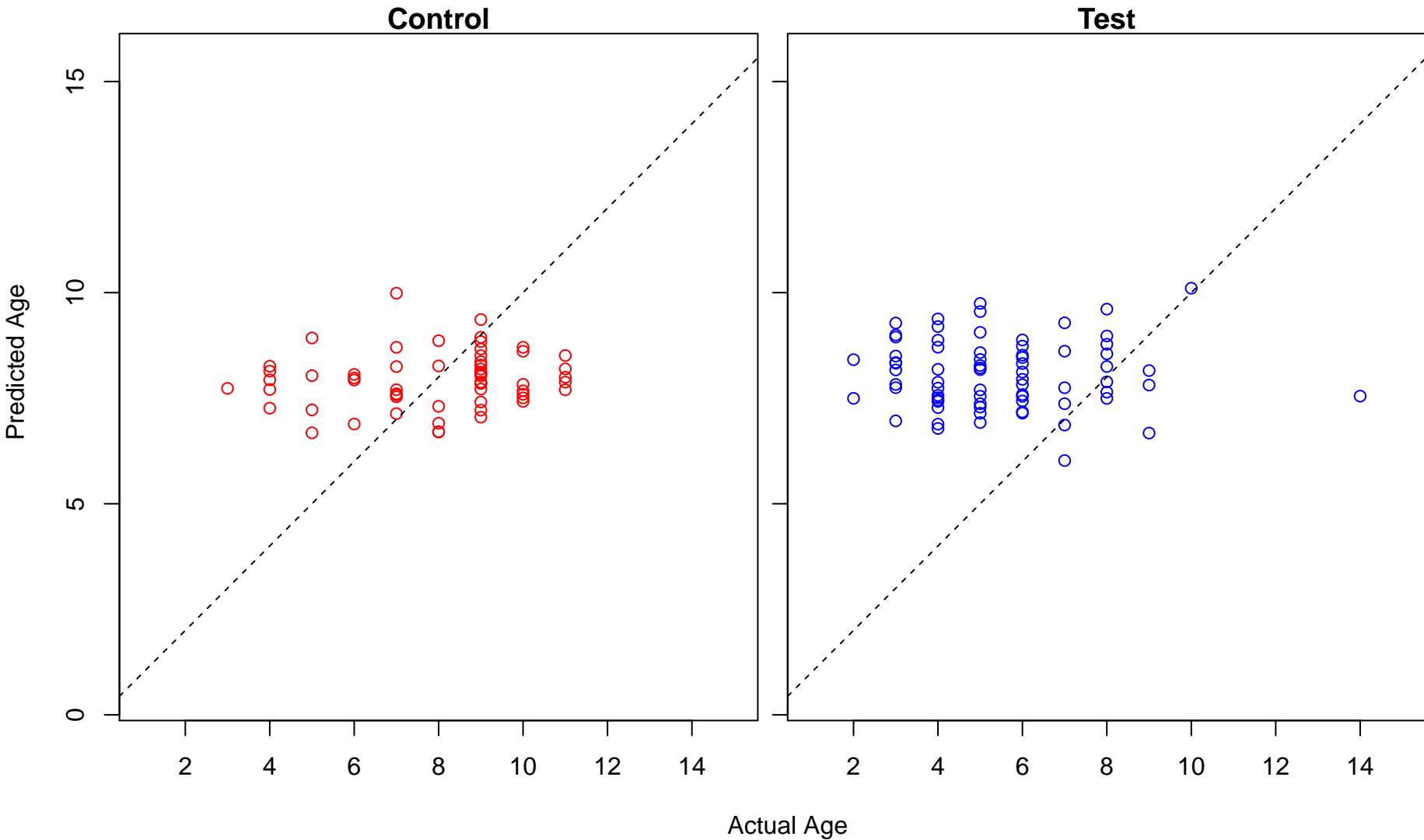
regulation of immature T cell proliferation in thymus (Score: 0.104538)



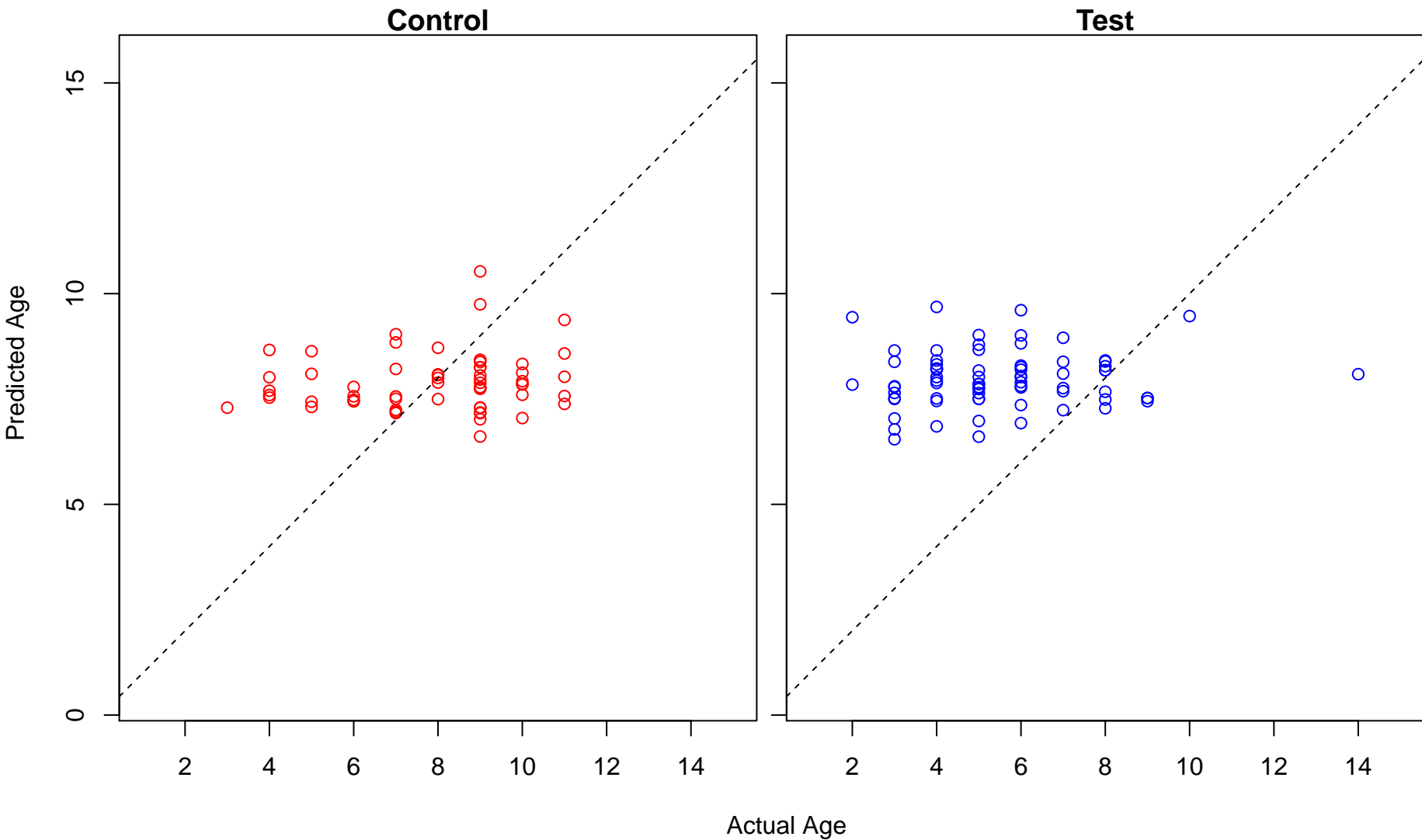
regulation of tyrosine phosphorylation of Stat4 protein (Score: 0.098944)

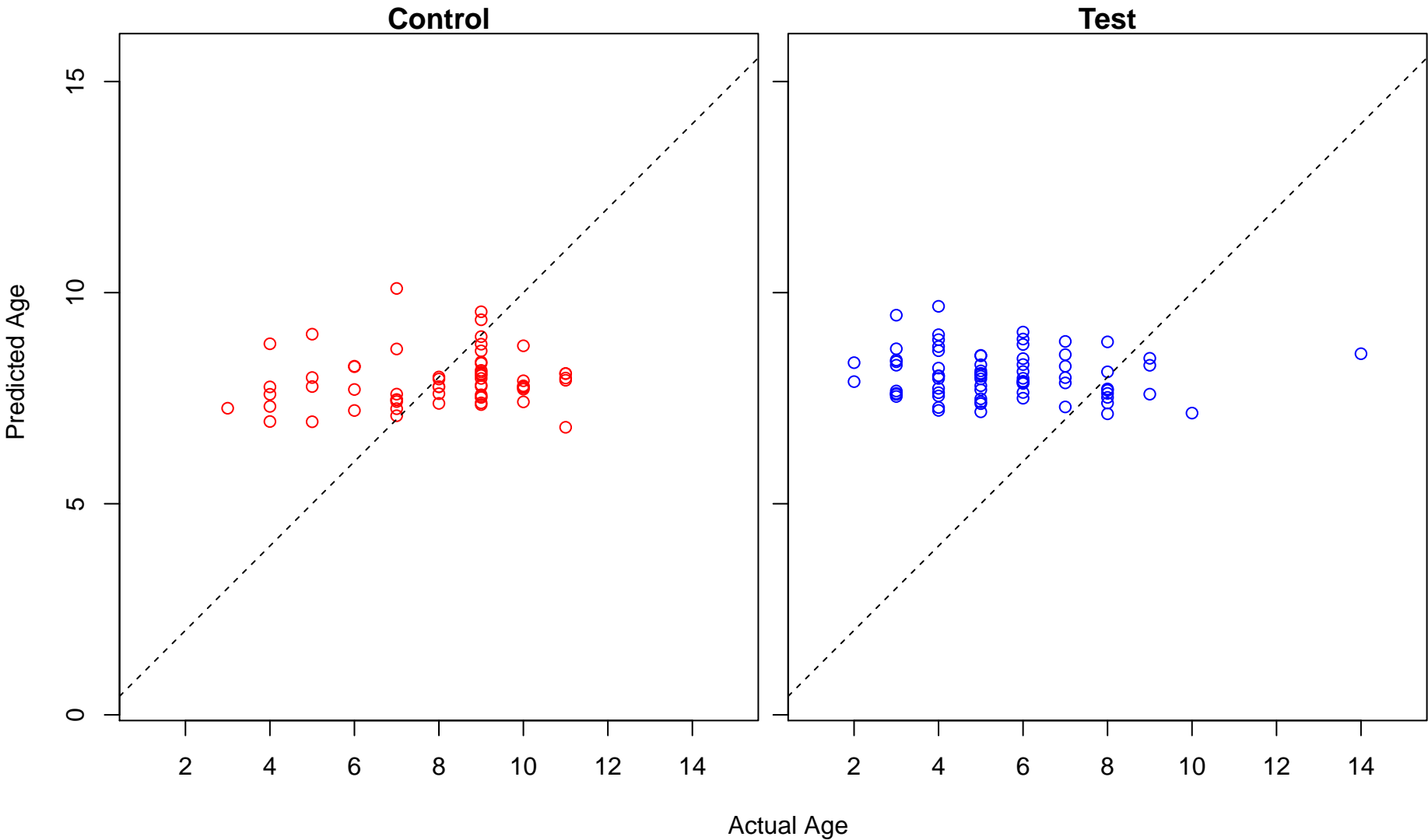


putrescine metabolic process (Score: 0.096873)

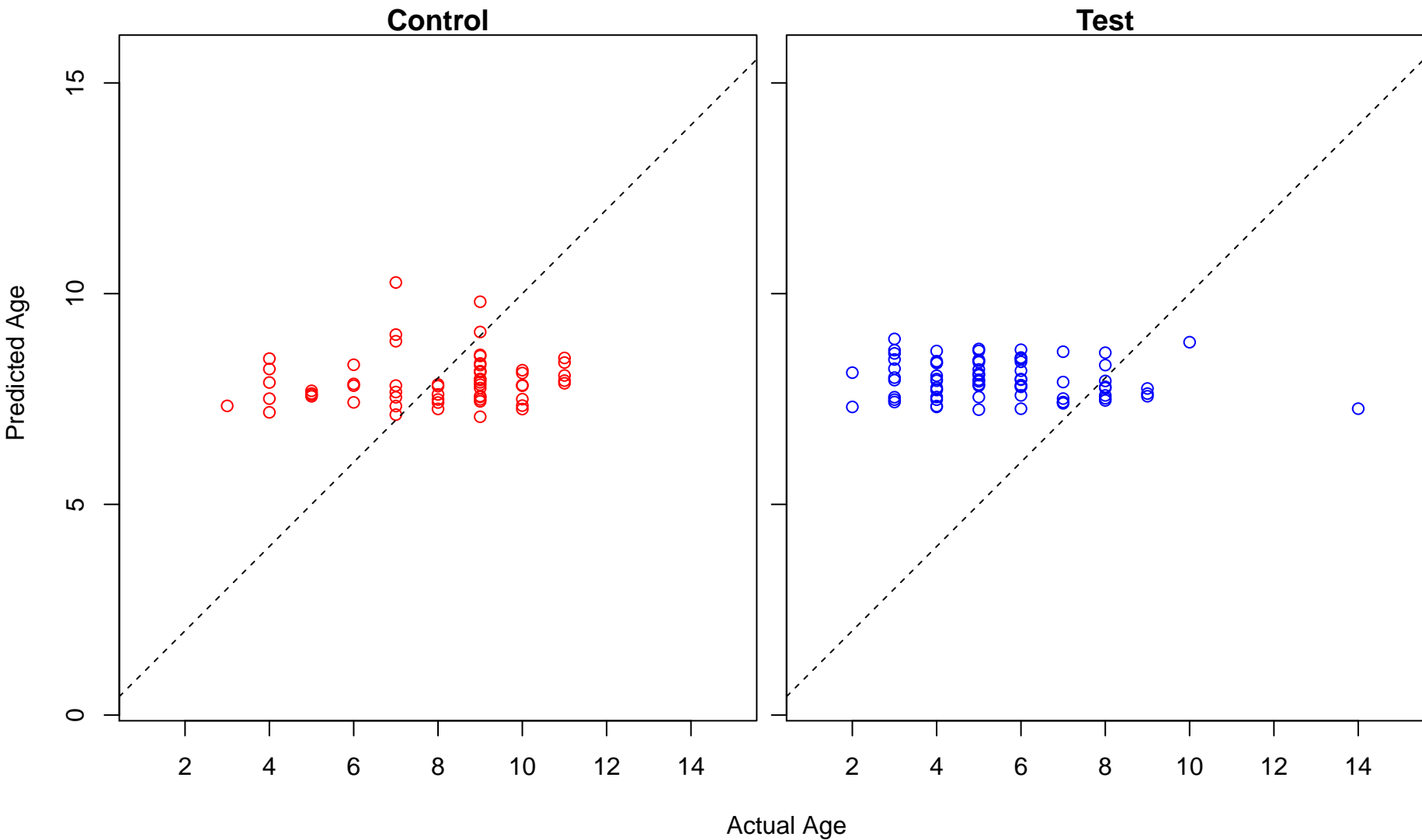


positive regulation of tyrosine phosphorylation of Stat4 protein (Score: 0.095937)

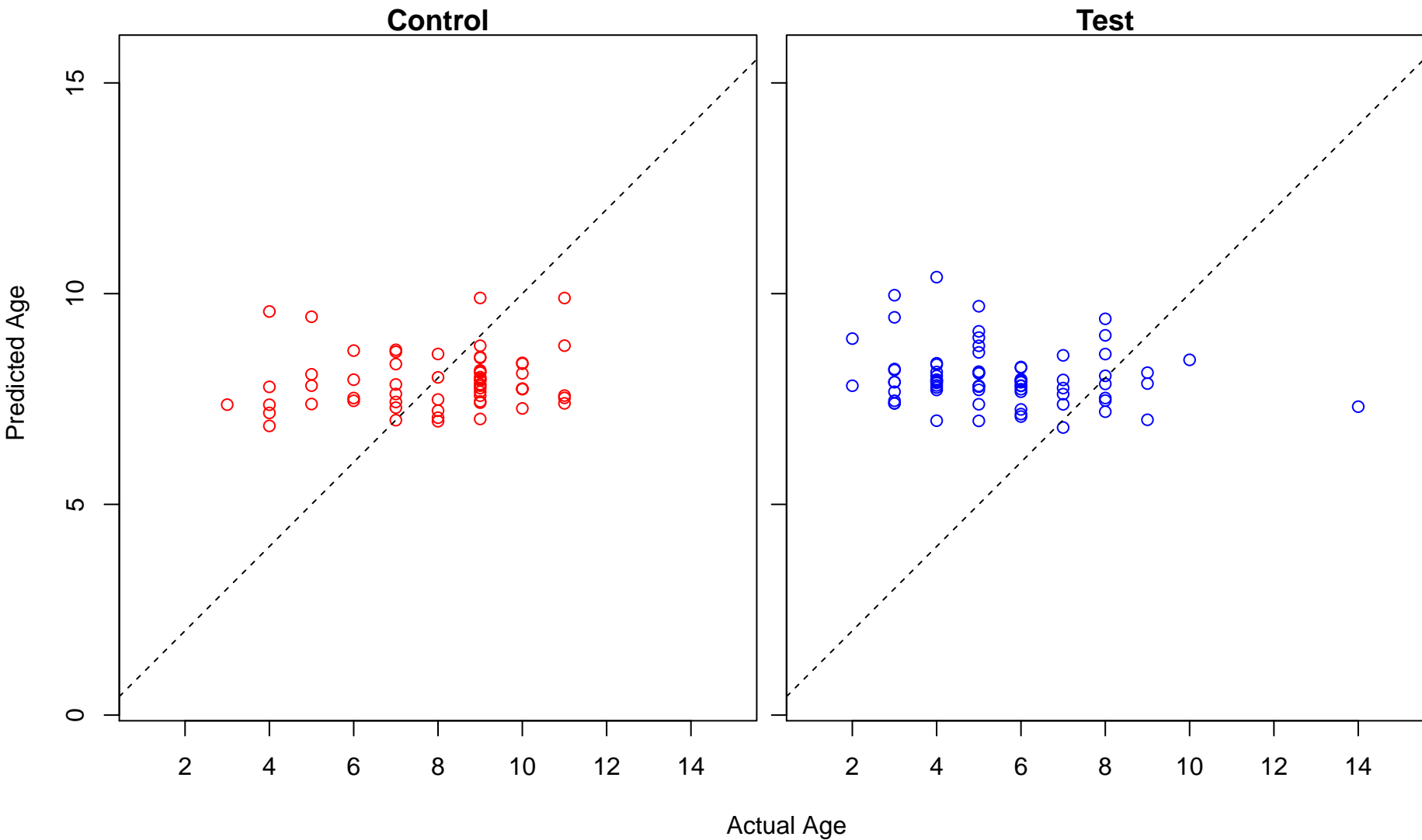




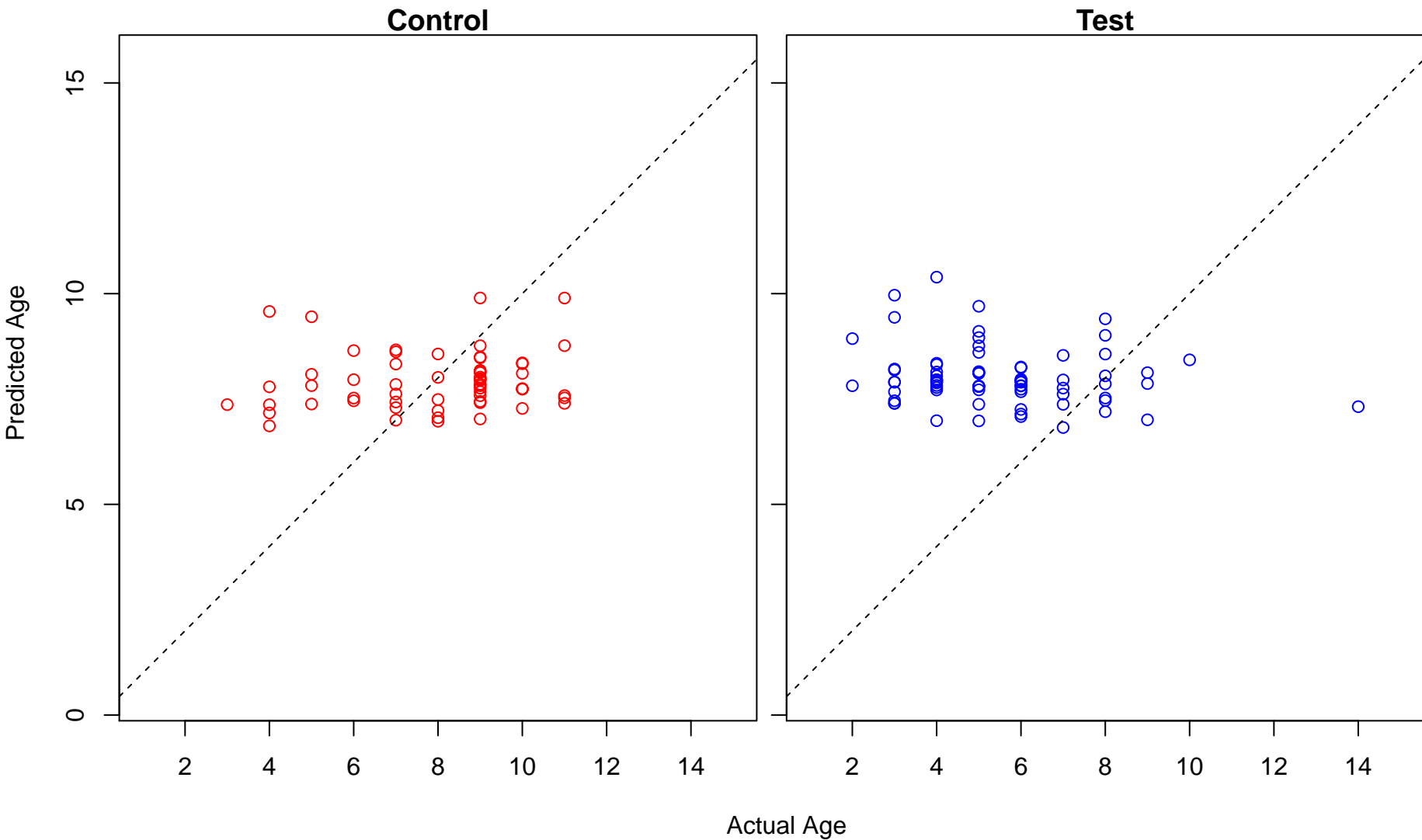
positive regulation of systemic arterial blood pressure (Score: 0.083127)



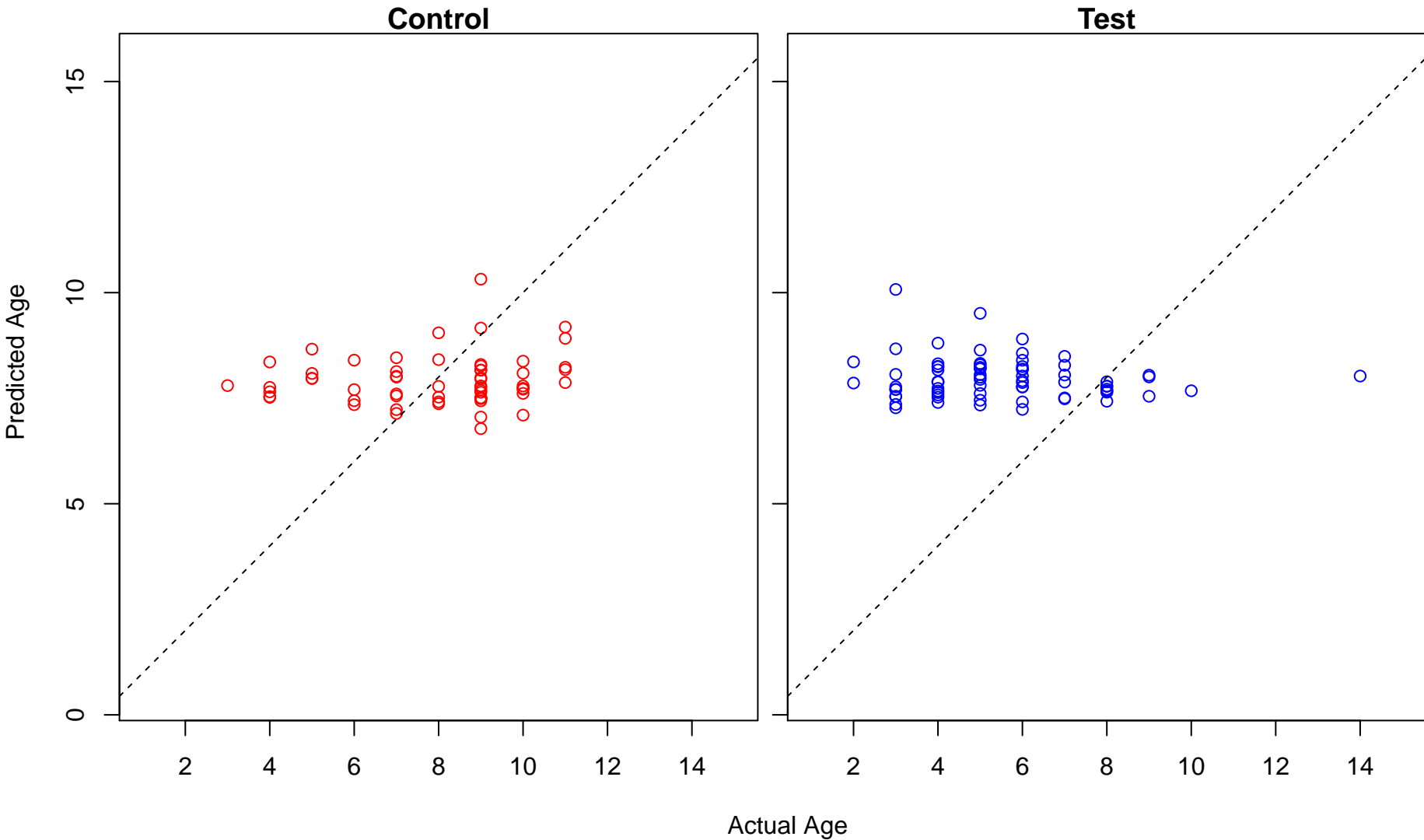
pulmonary valve formation (Score: 0.083033)



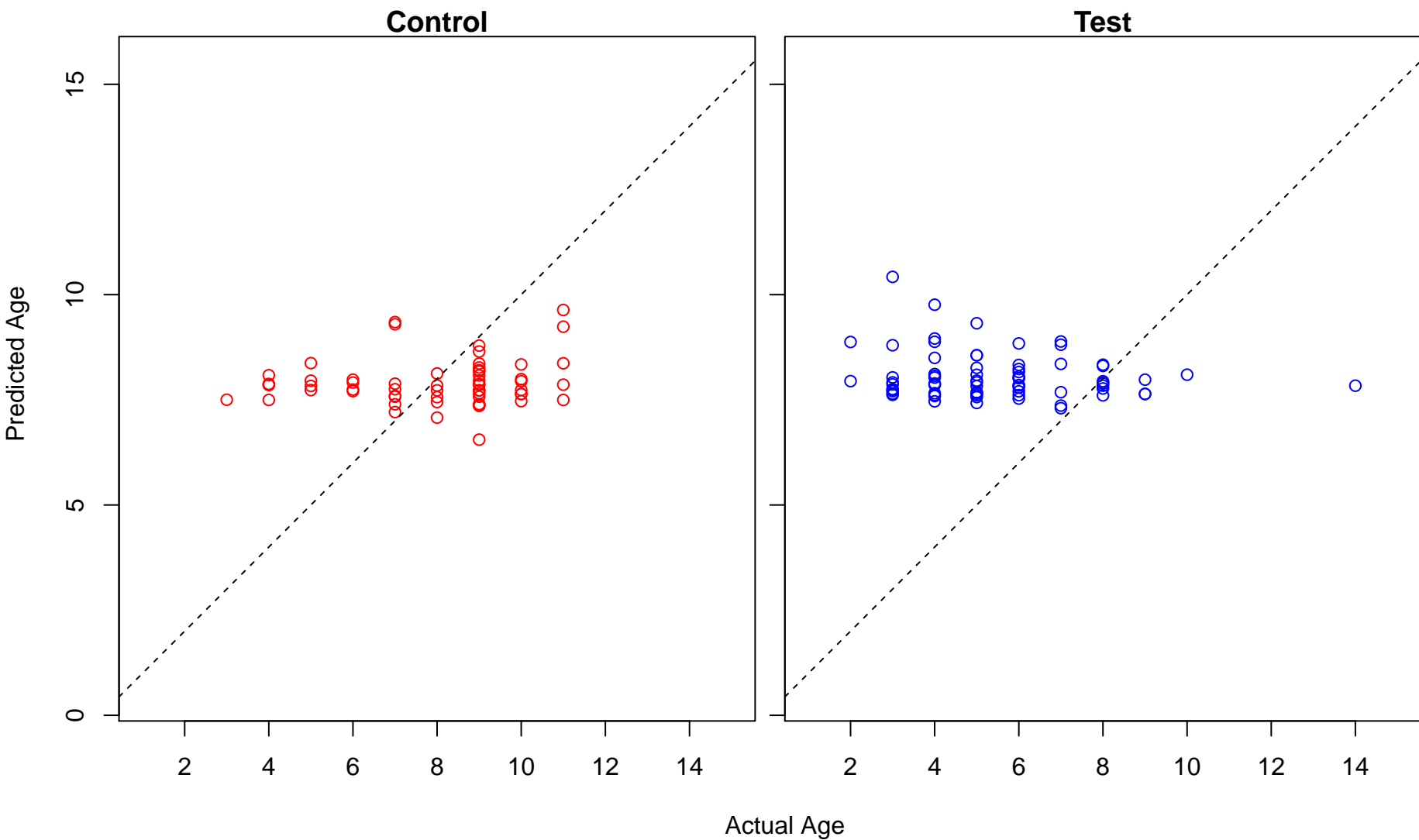
foramen ovale closure (Score: 0.083033)



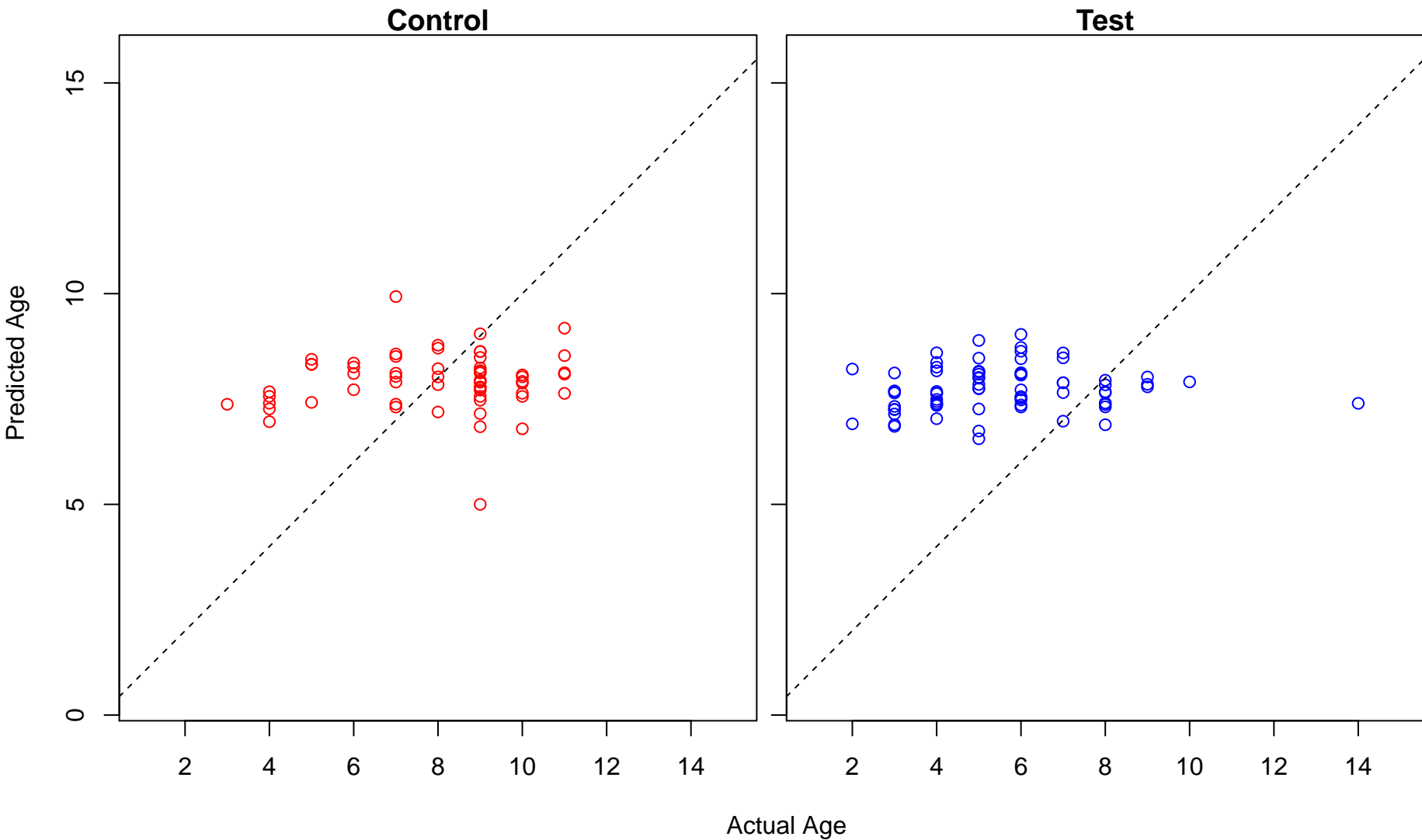
sensory system development (Score: 0.082263)



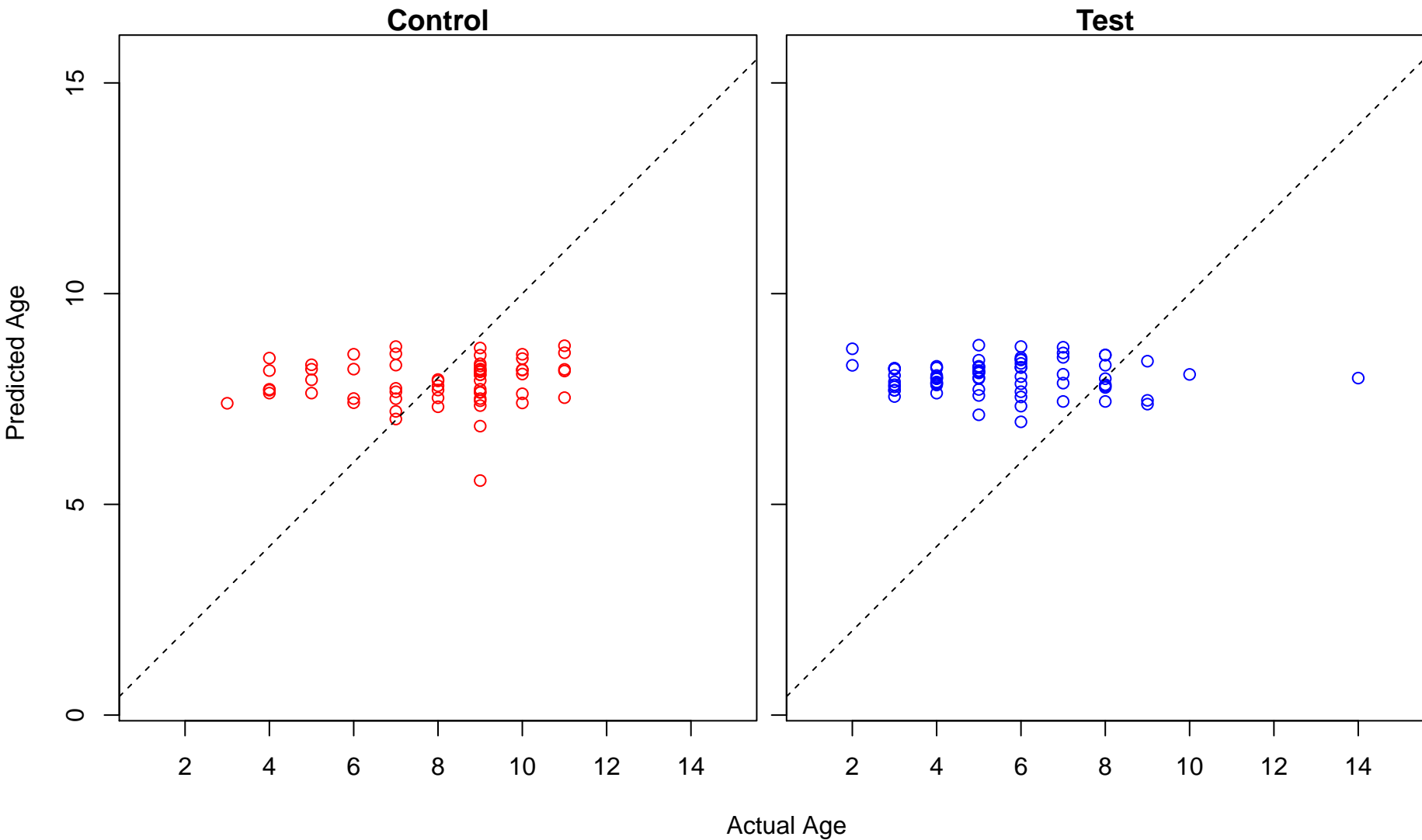
positive regulation of arachidonic acid secretion (Score: 0.081607)



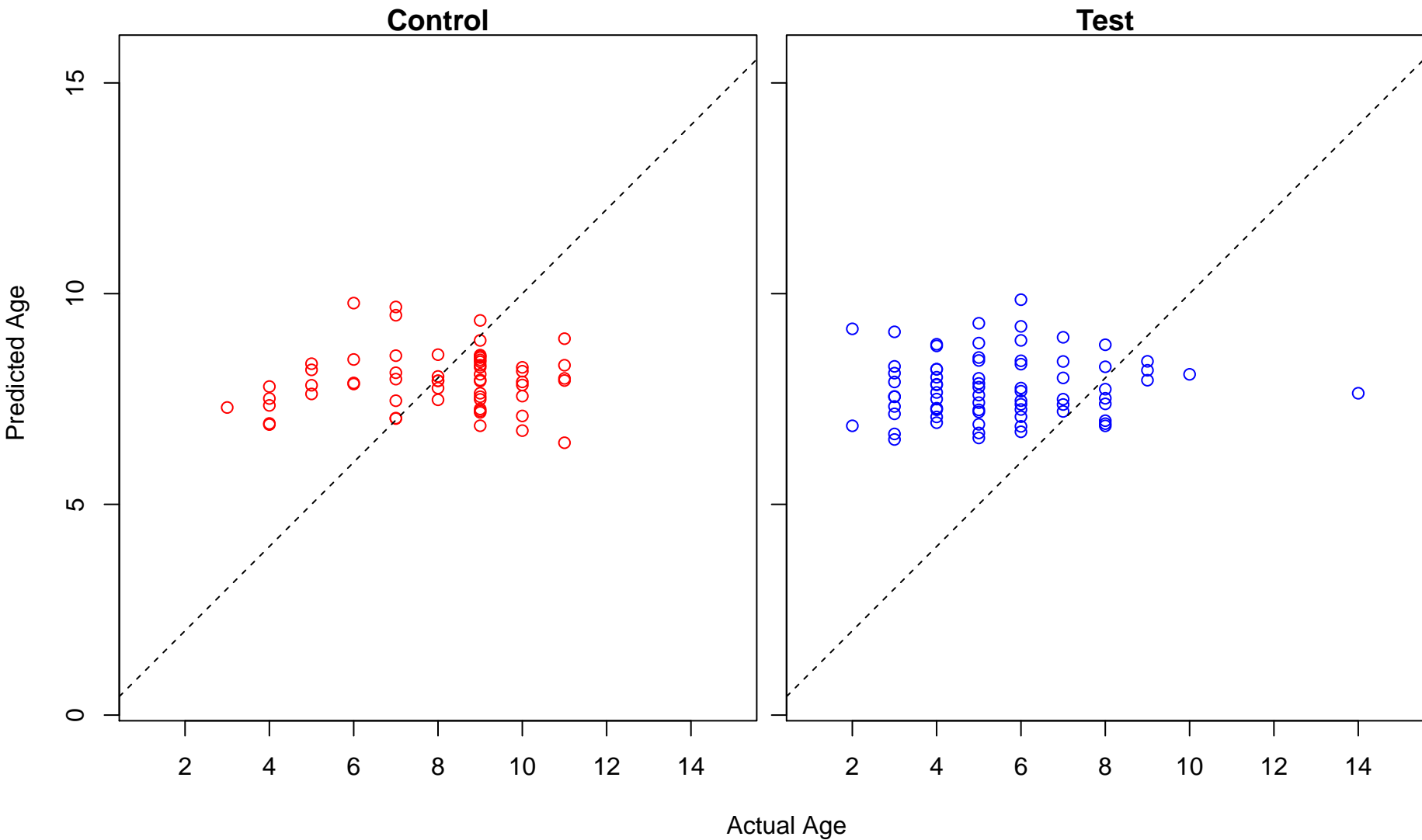
kidney development (Score: 0.047881)



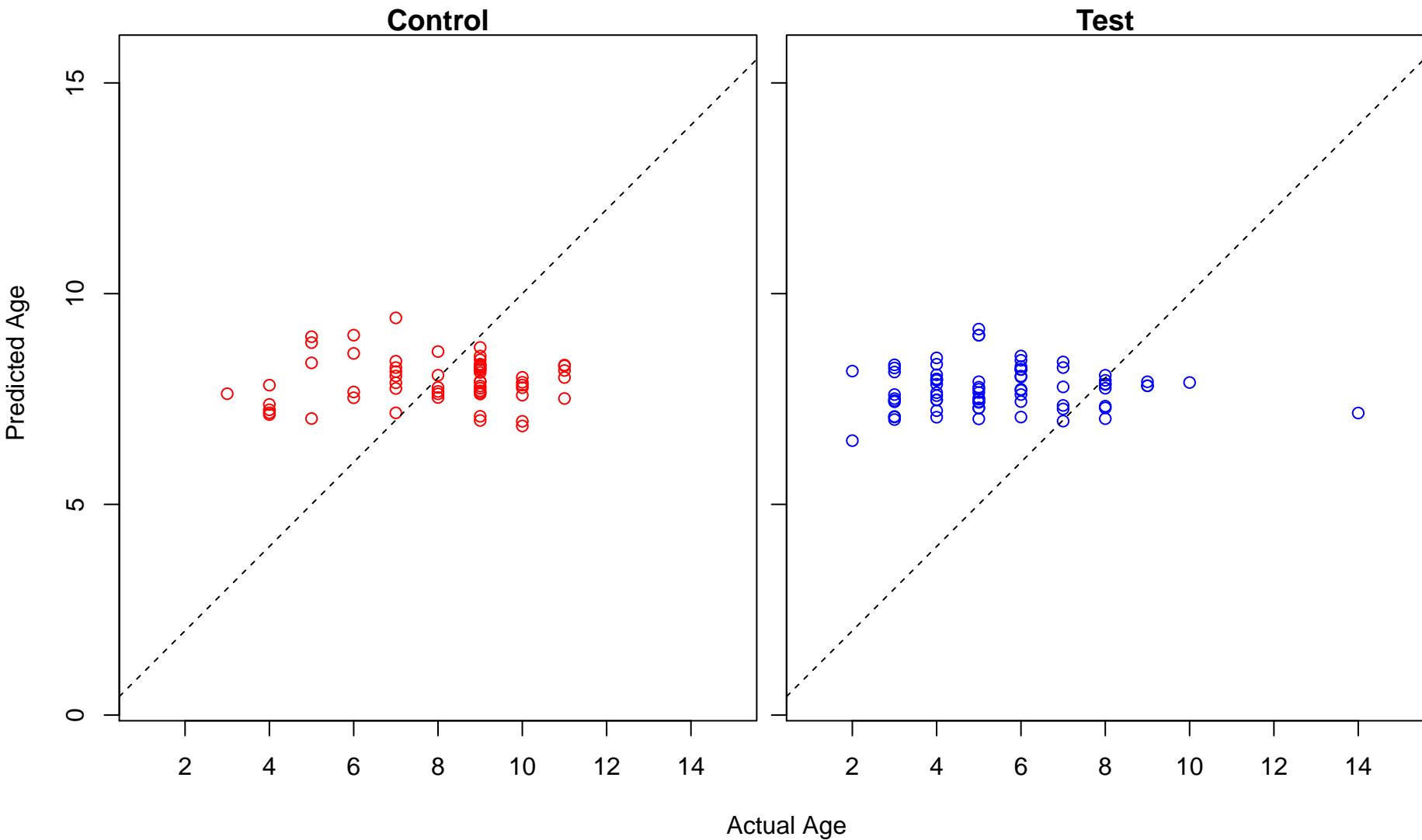
osteoblast proliferation (Score: 0.042065)



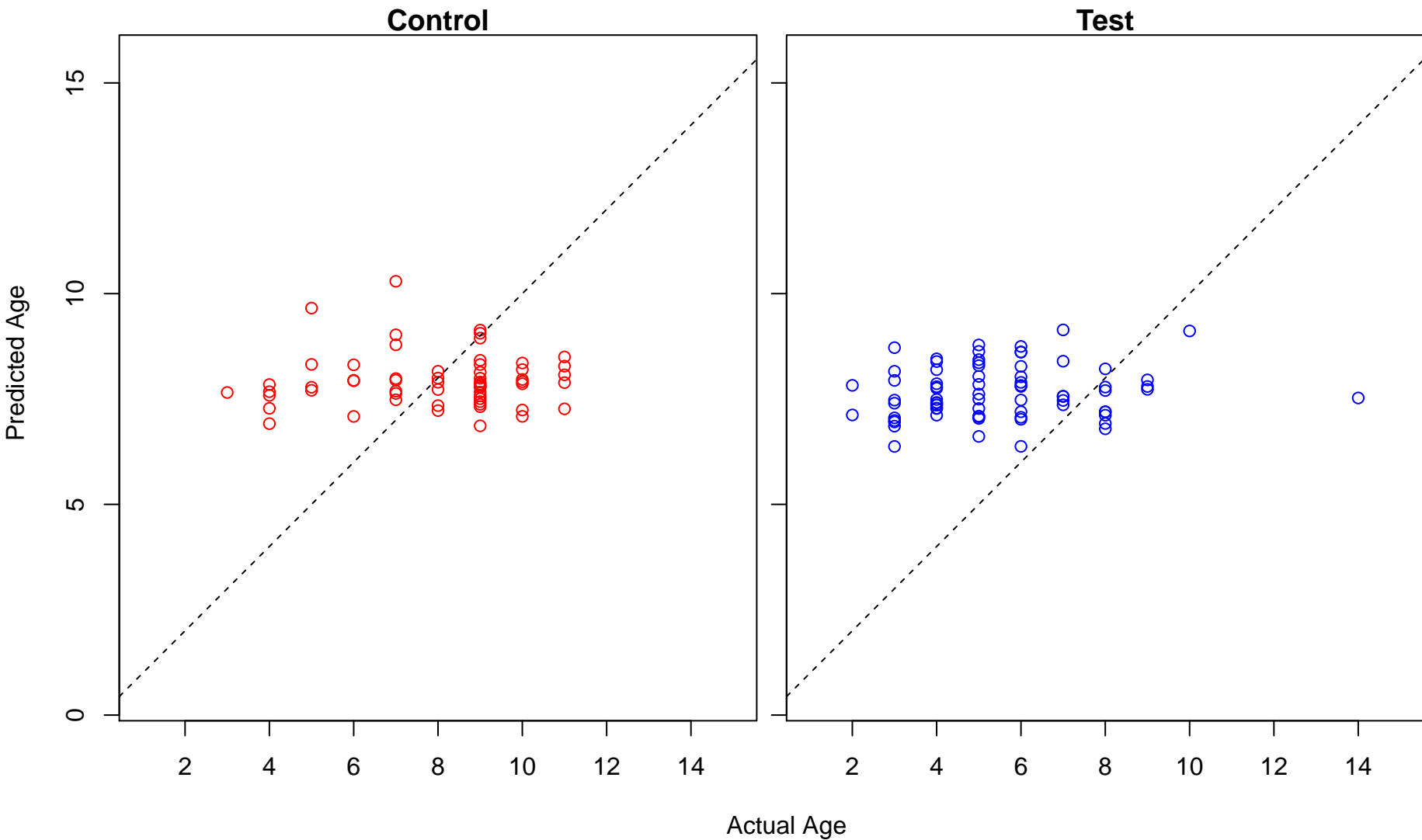
intracellular pH reduction (Score: 0.031566)



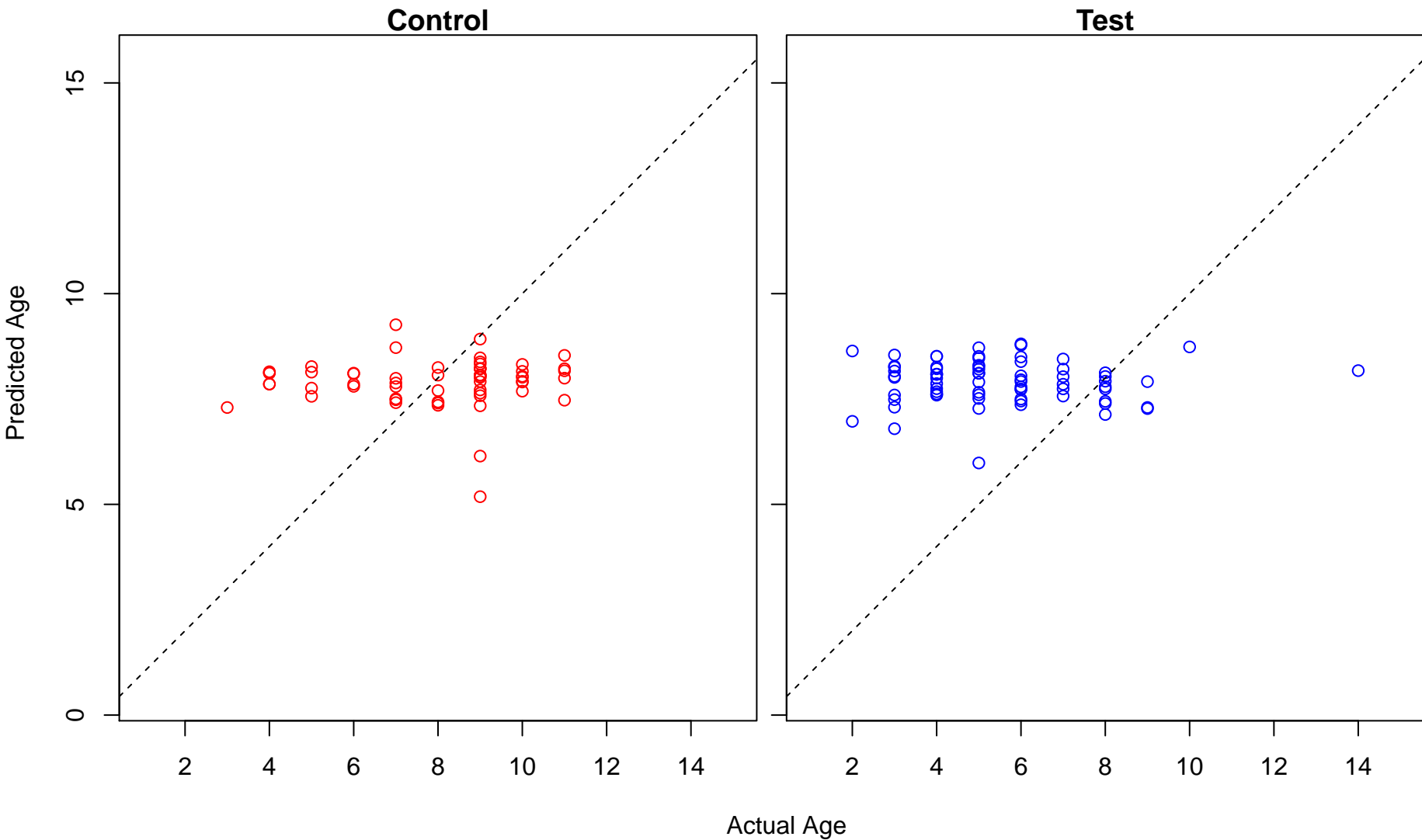
glycosaminoglycan biosynthetic process (Score: 0.007477)



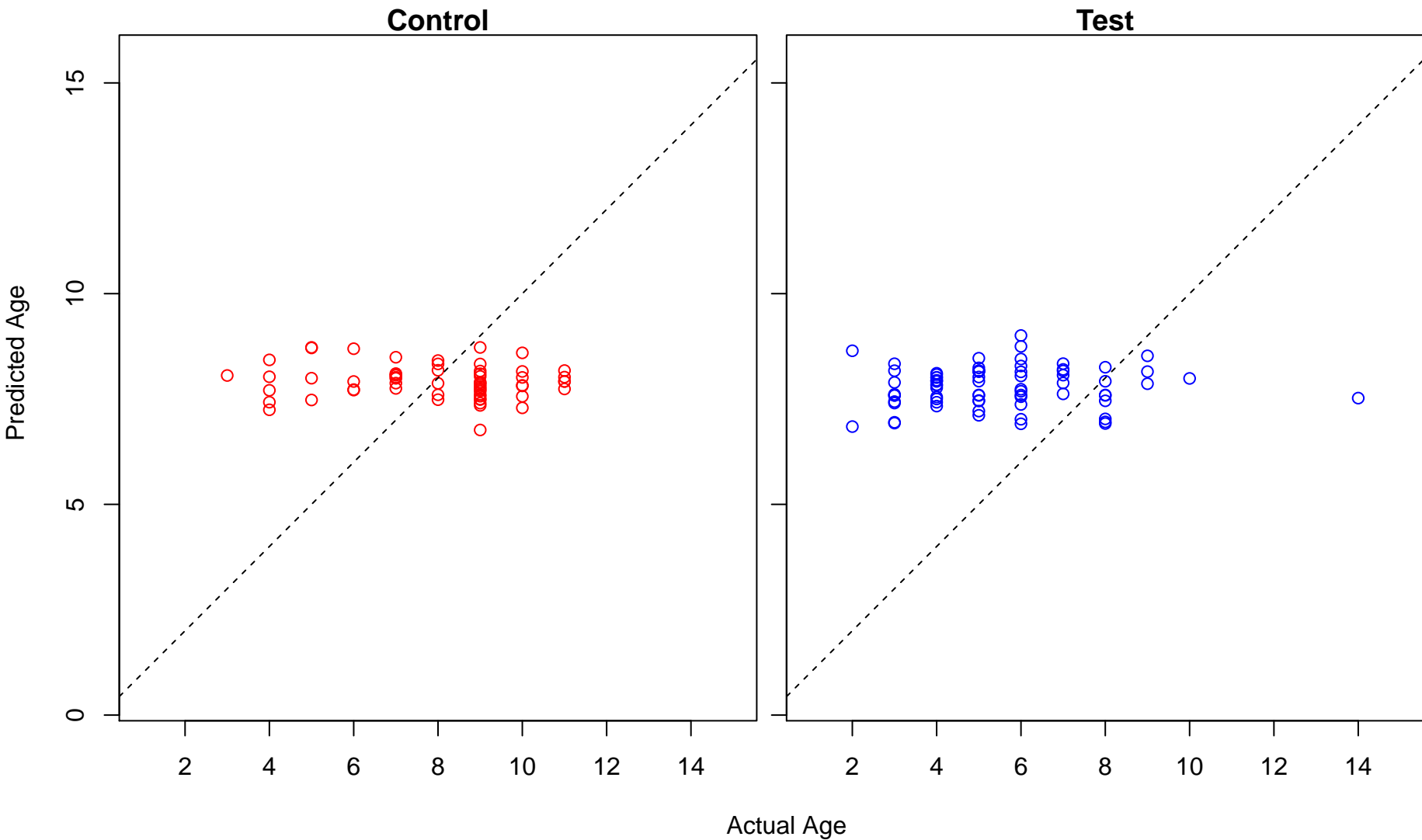
negative regulation of G1/S transition of mitotic cell cycle (Score: 0.005540)



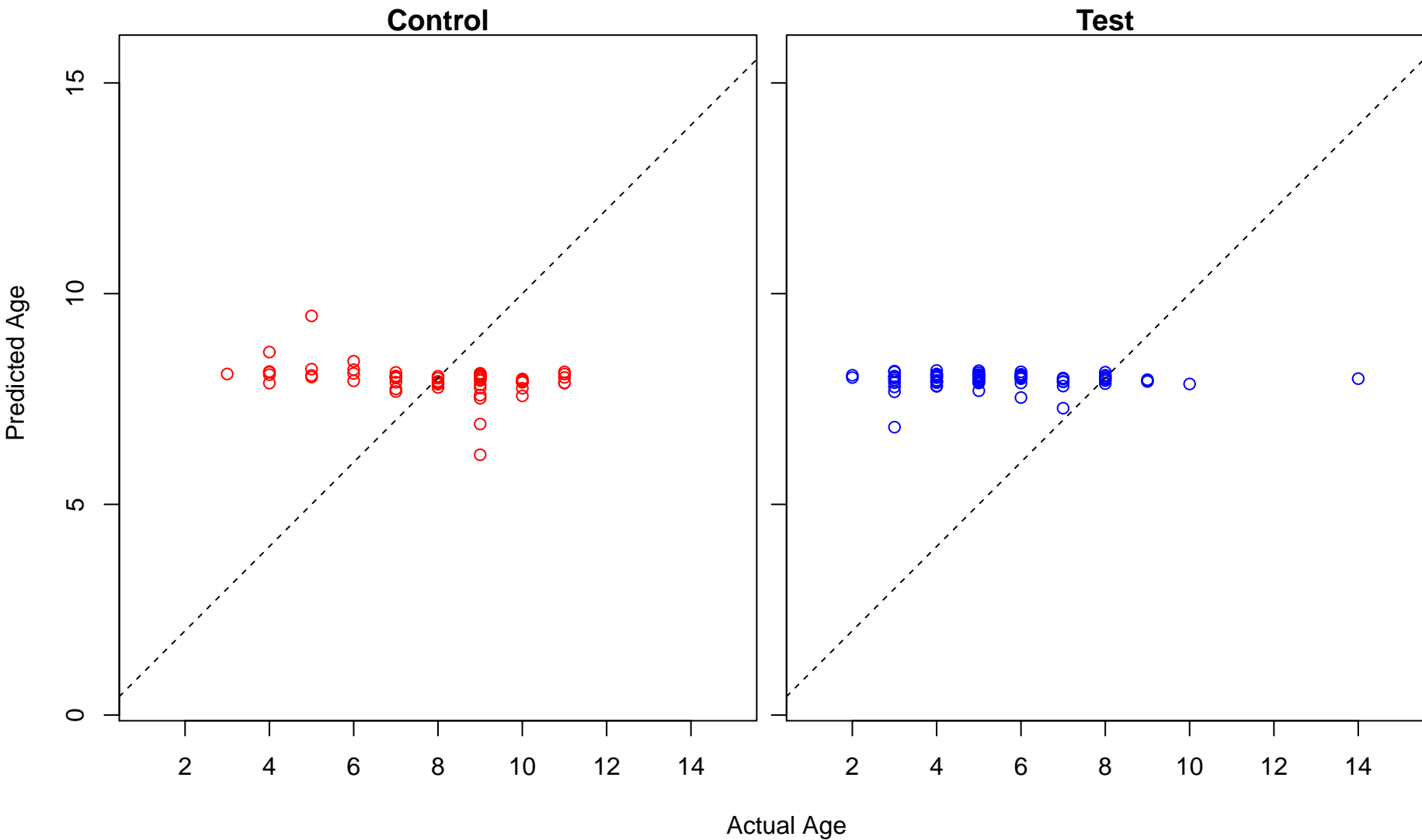
cytokine biosynthetic process (Score: 0.002097)



detection of bacterium (Score: -0.041549)



interleukin-1 beta secretion (Score: -0.174868)



interleukin-1 beta production (Score: -0.174868)

