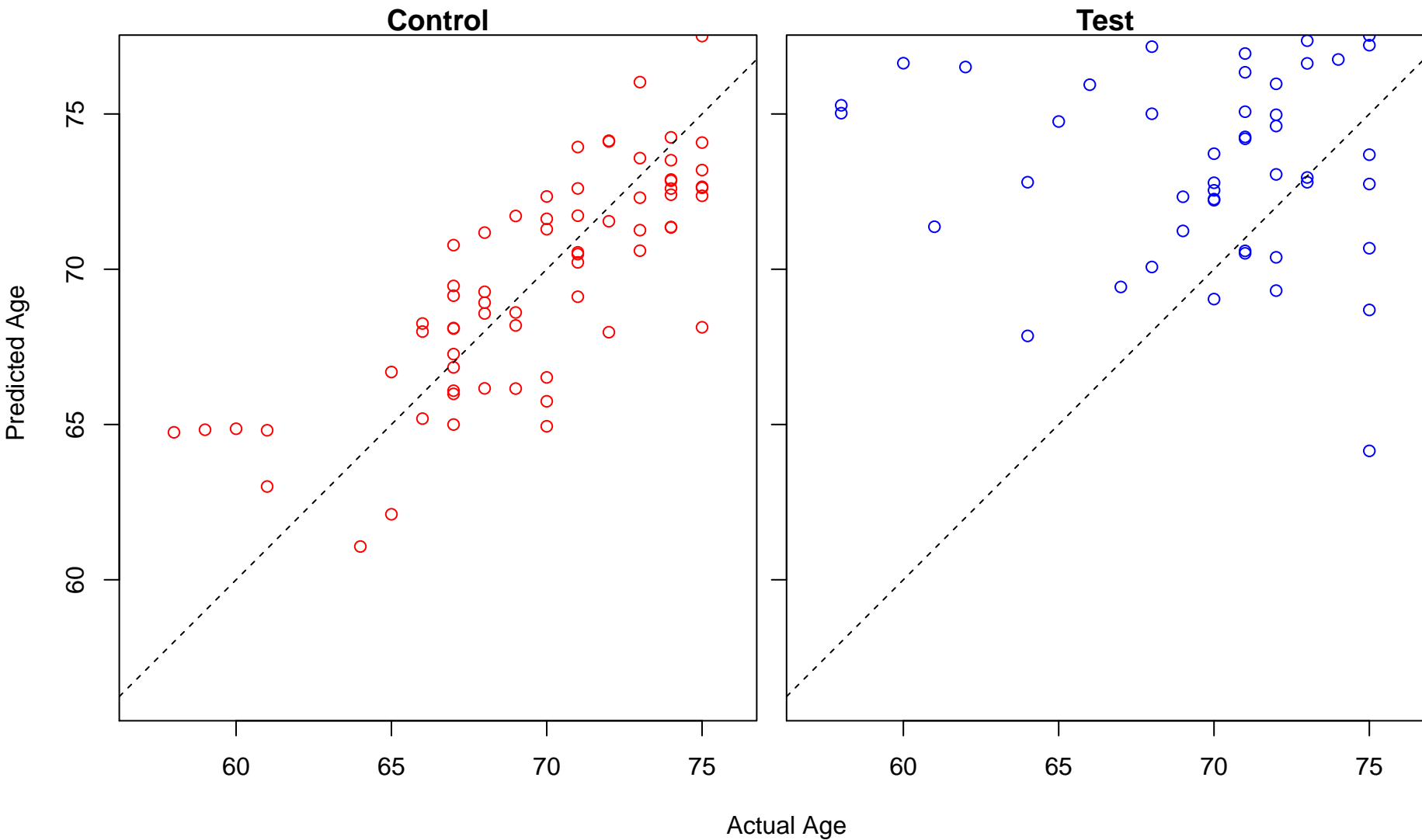
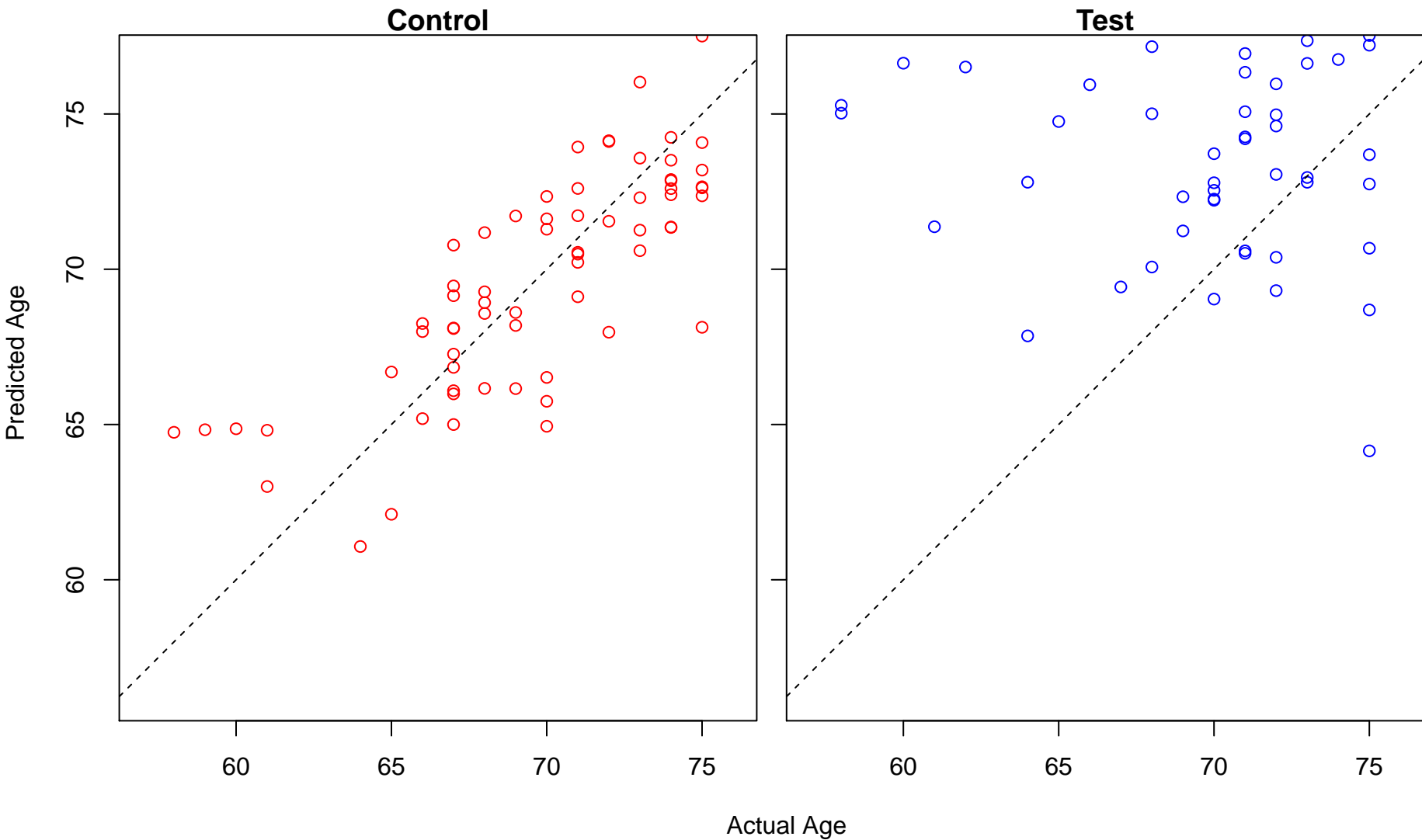


peptidyl-tyrosine phosphorylation (Score: 2.739437)

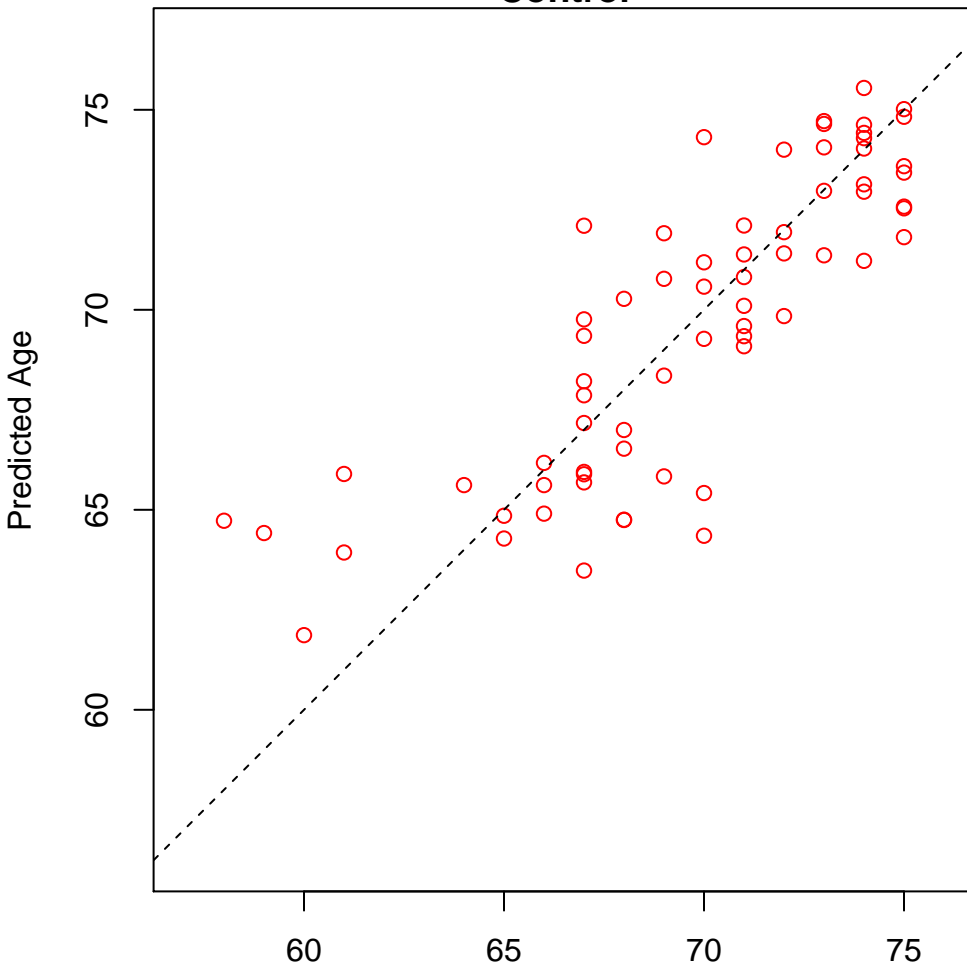


peptidyl-tyrosine modification (Score: 2.739437)

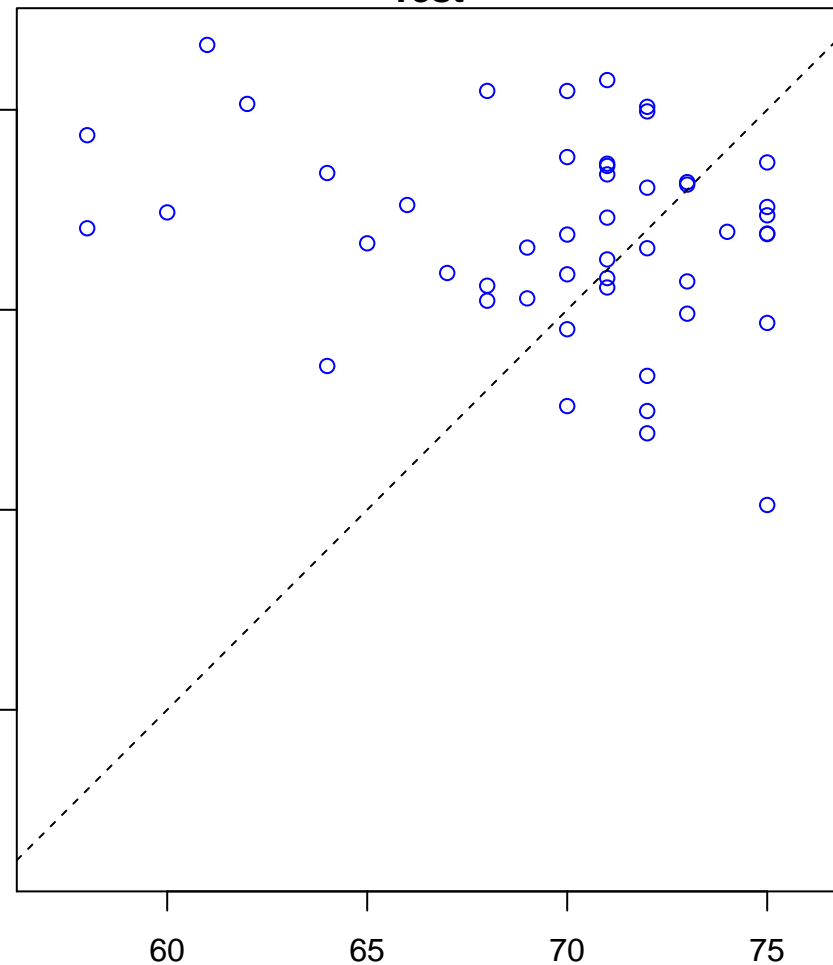


phosphatidylcholine metabolic process (Score: 2.727776)

Control

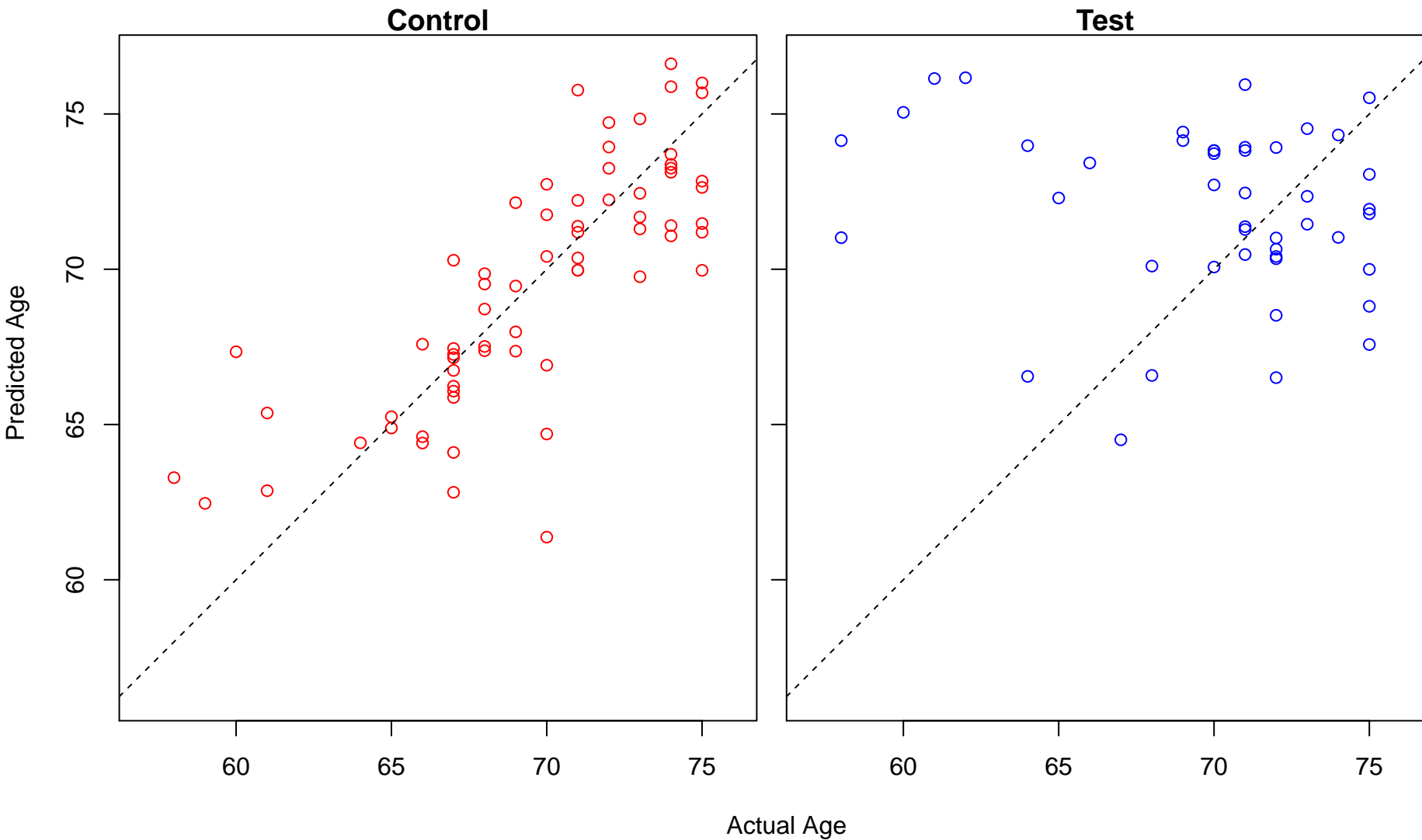


Test

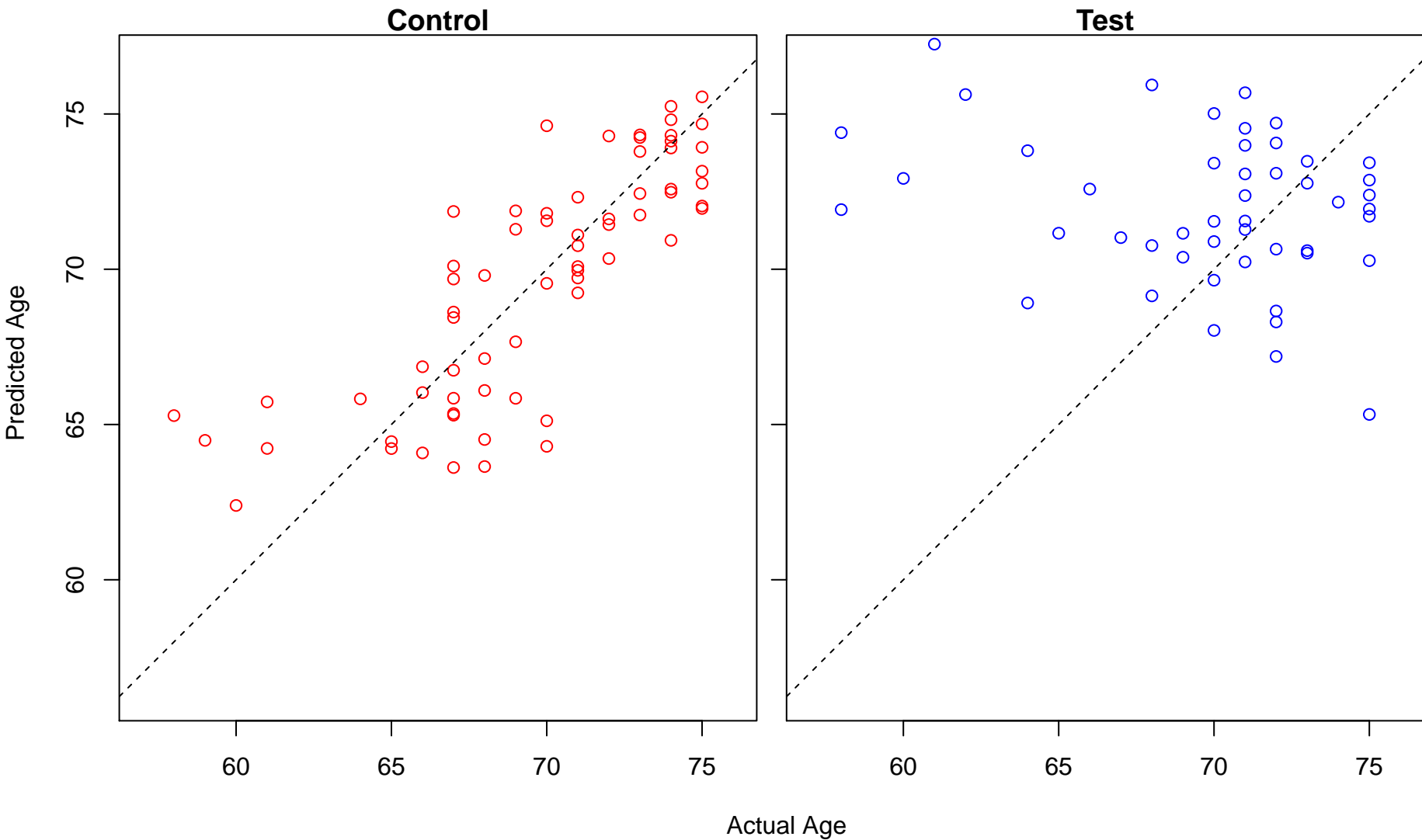


Actual Age

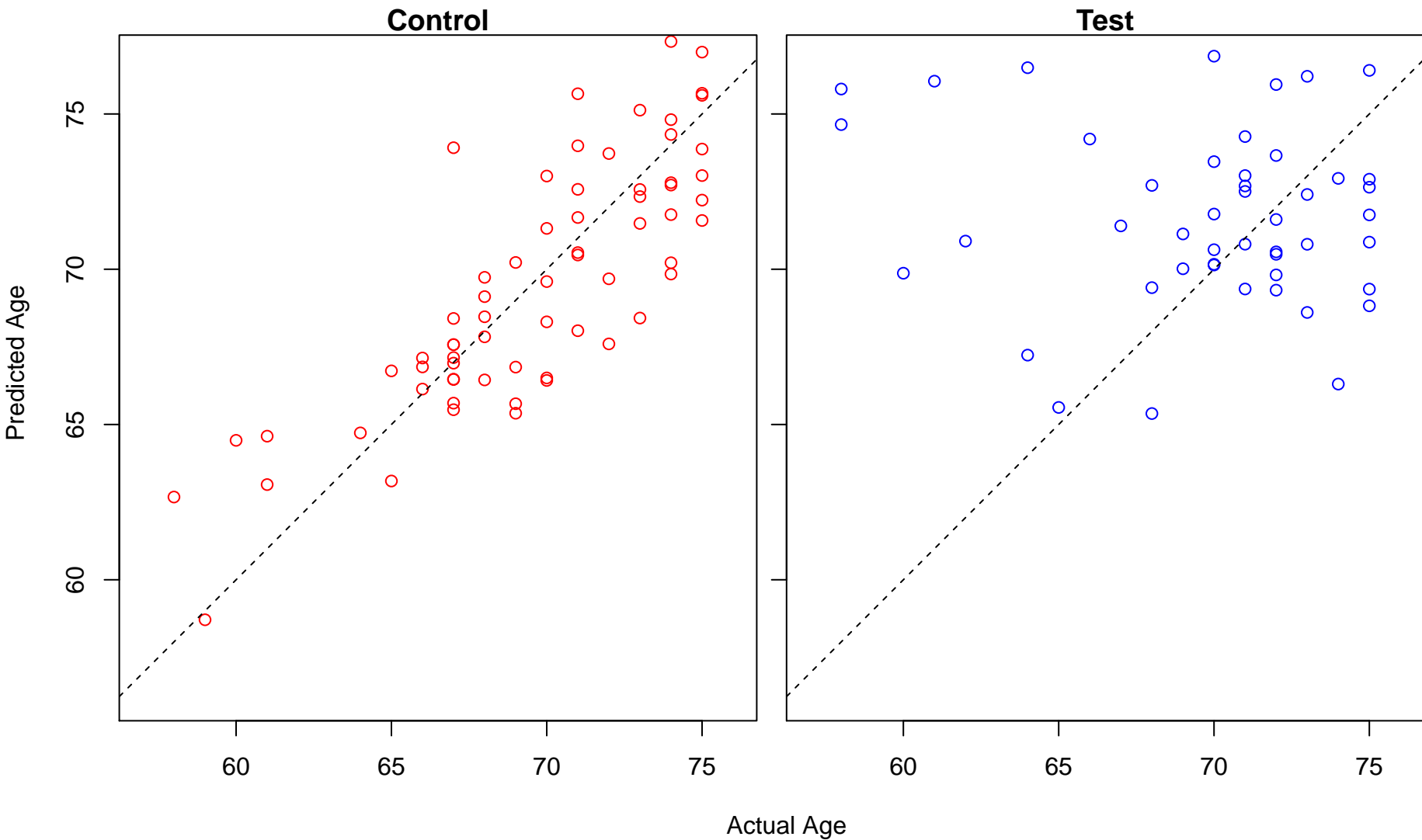
transcription elongation from RNA polymerase II promoter (Score: 2.596537)



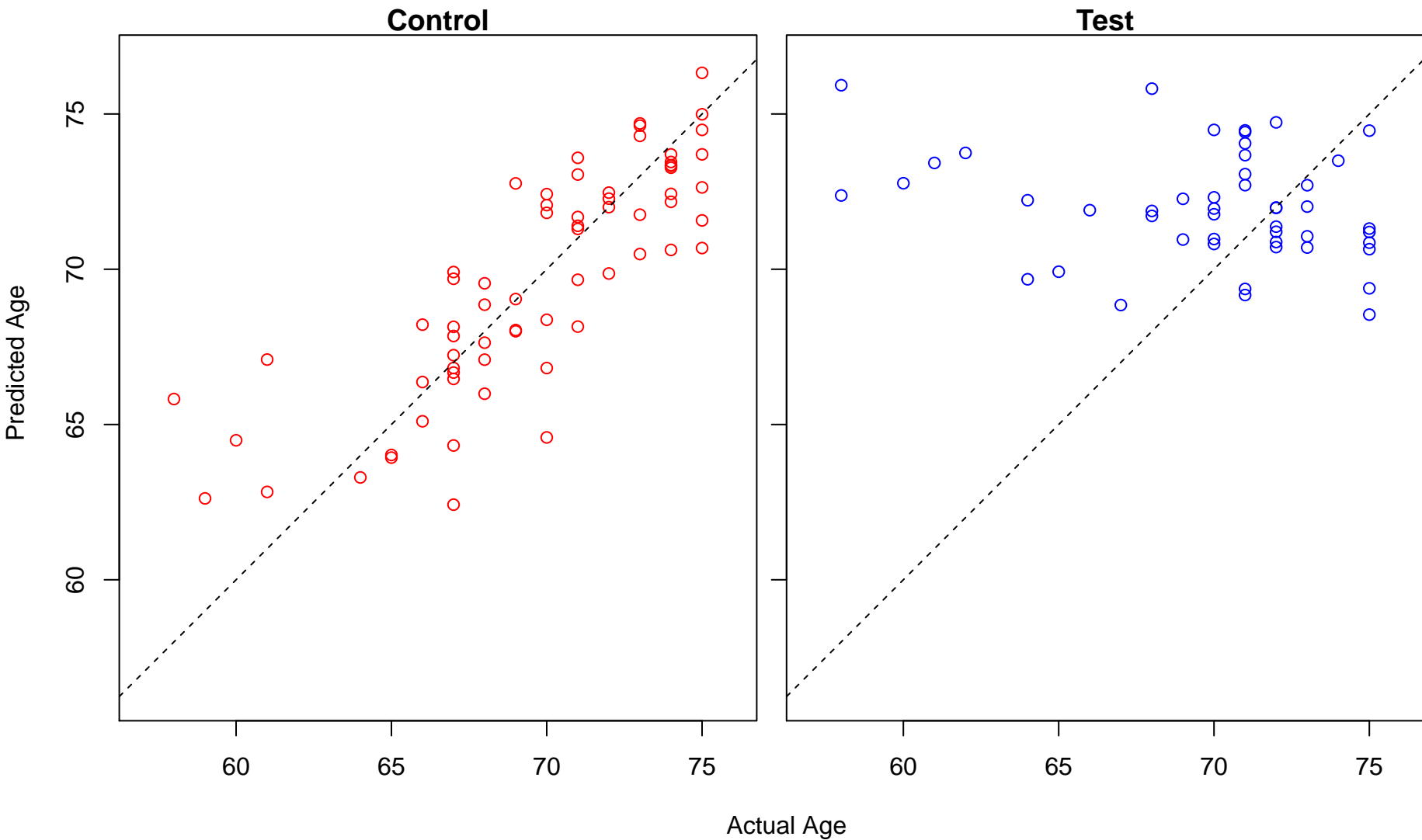
ethanolamine-containing compound metabolic process (Score: 2.491804)



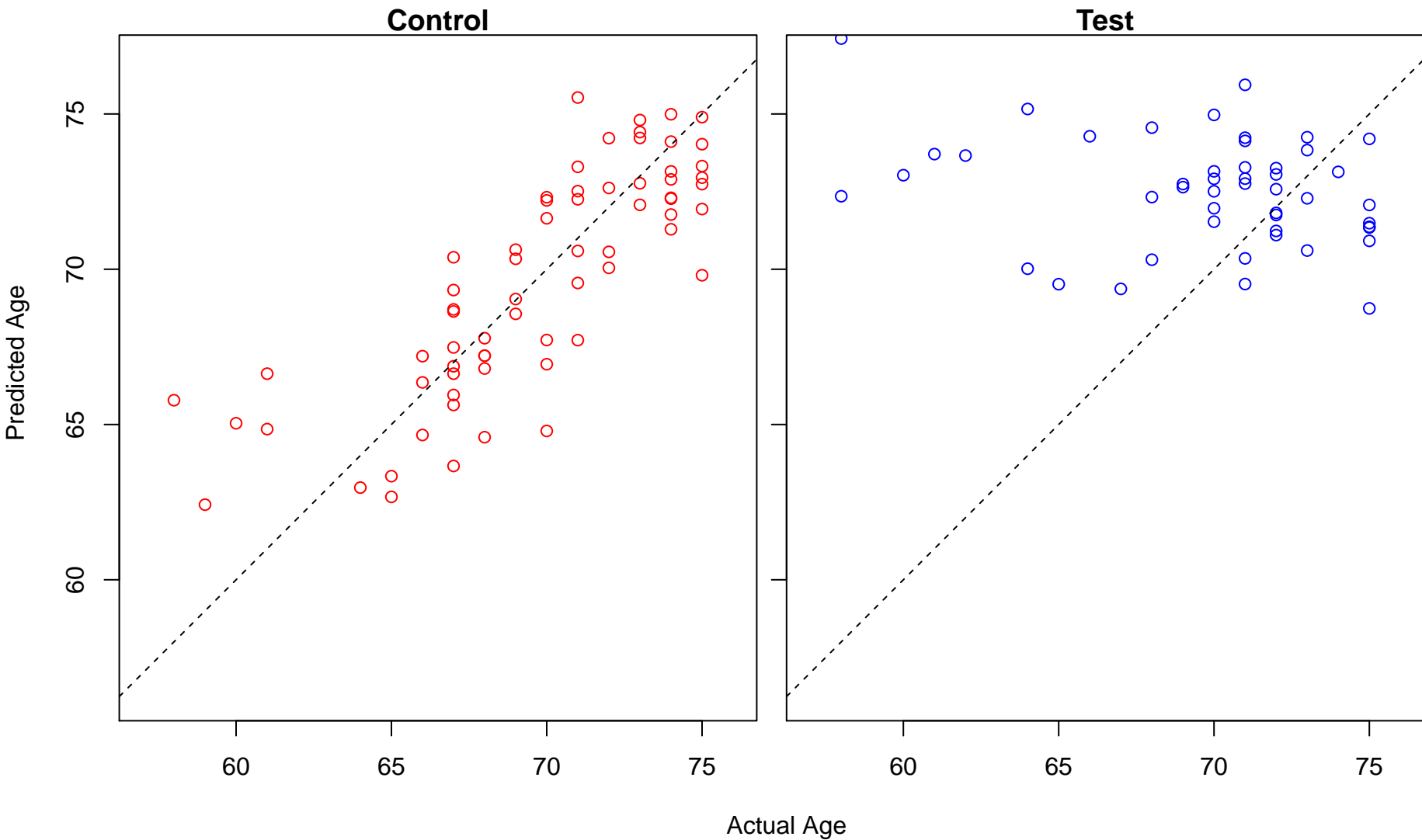
protein monoubiquitination (Score: 2.483265)



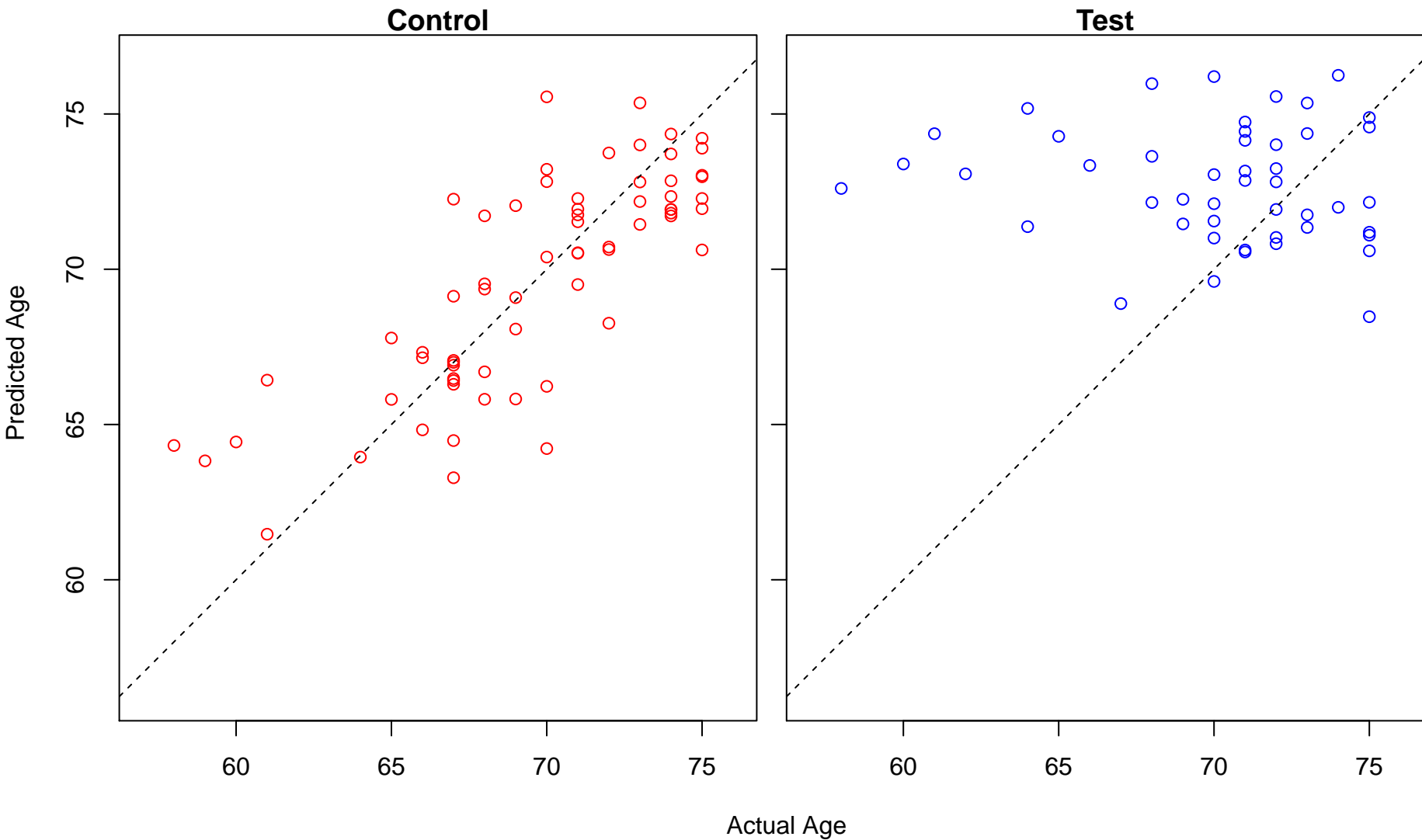
regulation of apoptotic signaling pathway (Score: 2.448310)



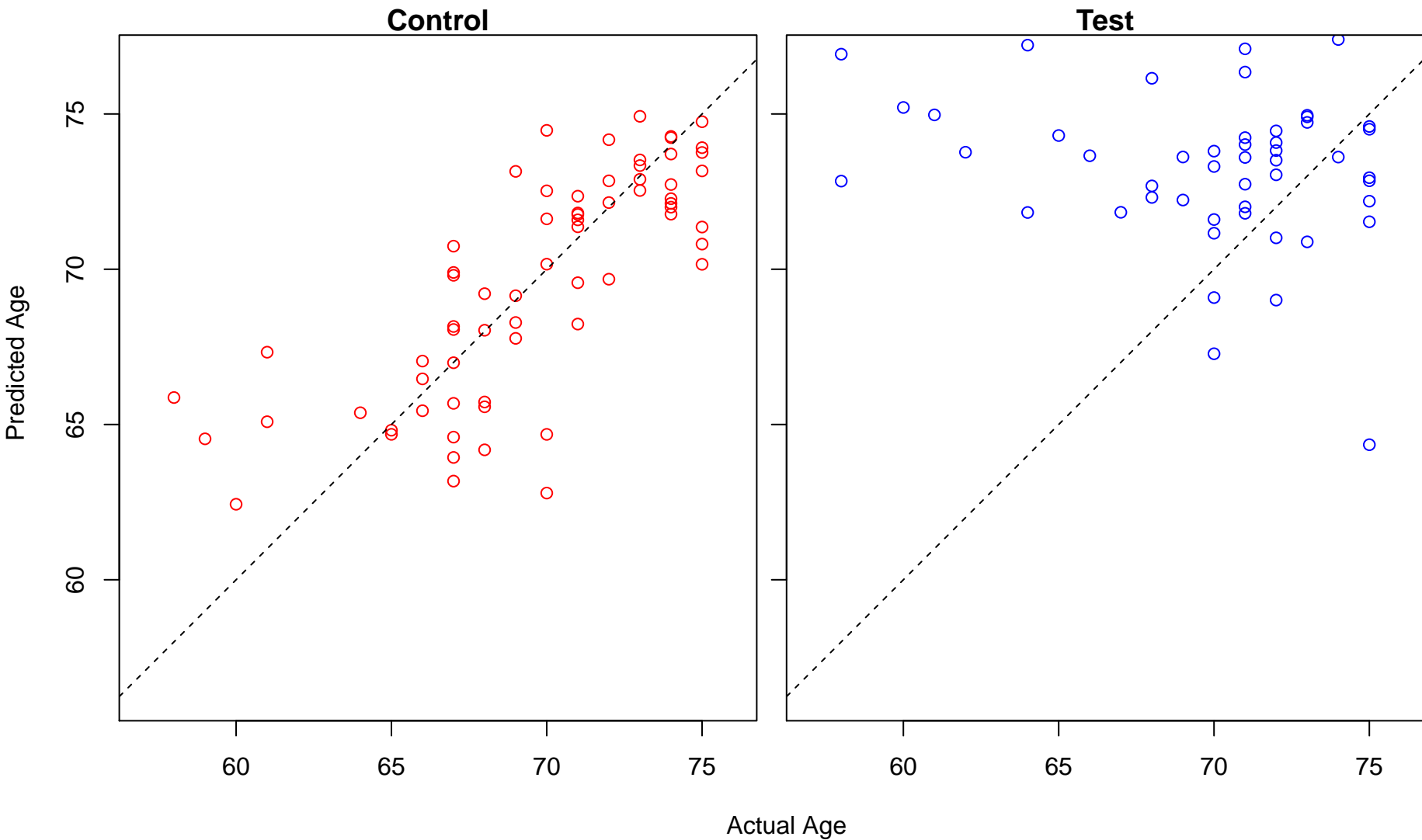
positive regulation of apoptotic signaling pathway (Score: 2.442829)



double-strand break repair via nonhomologous end joining (Score: 2.436547)

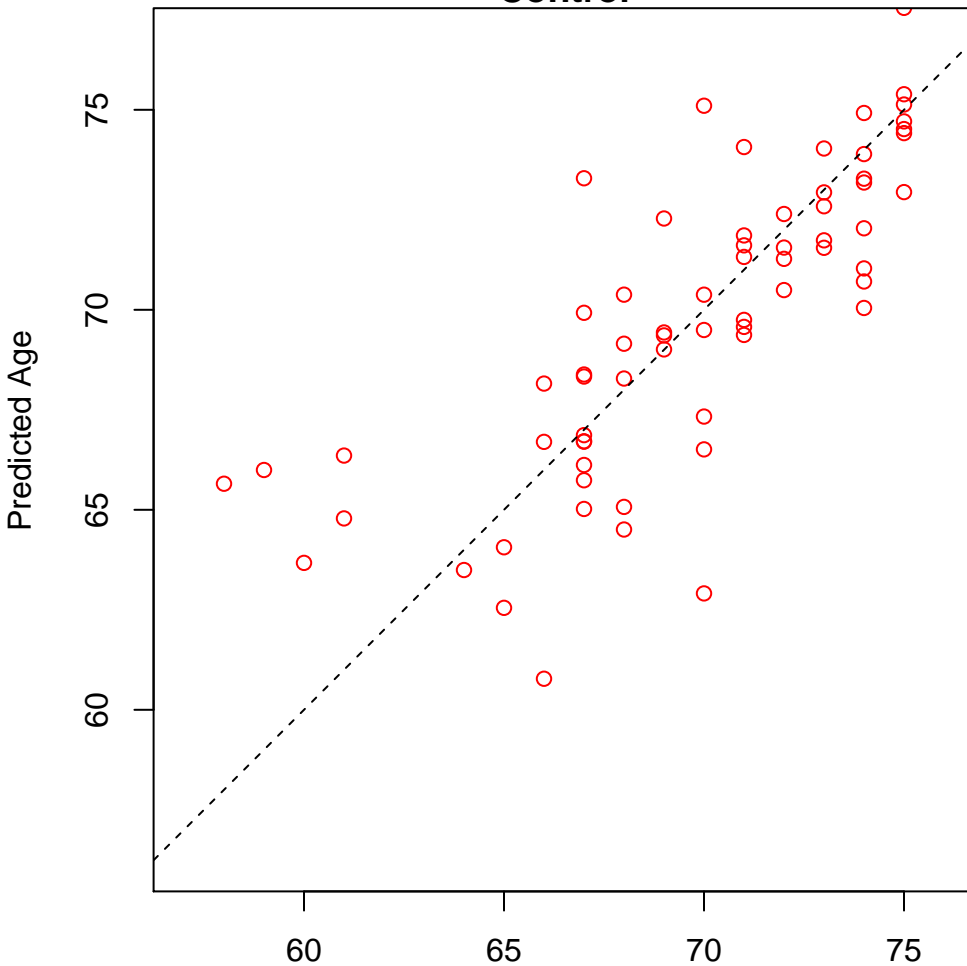


ammonium ion metabolic process (Score: 2.433502)

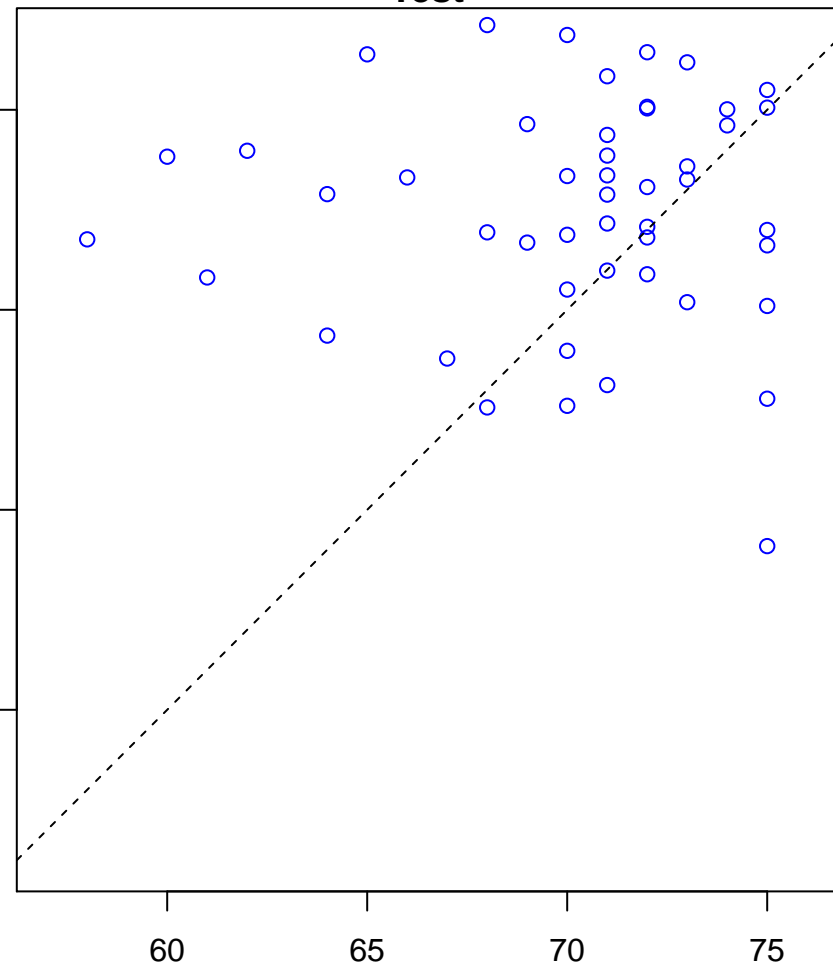


regulation of myeloid cell differentiation (Score: 2.430318)

Control

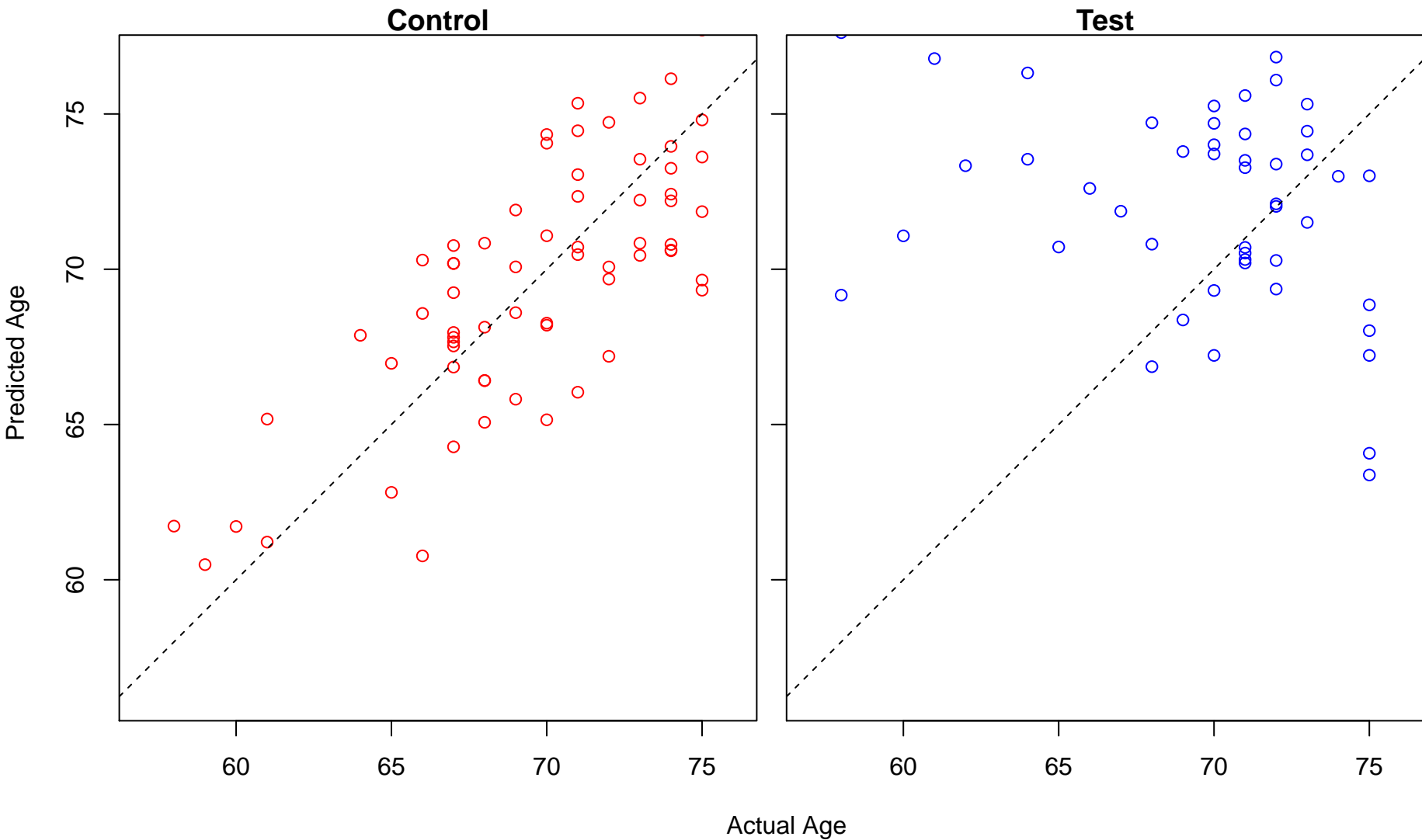


Test



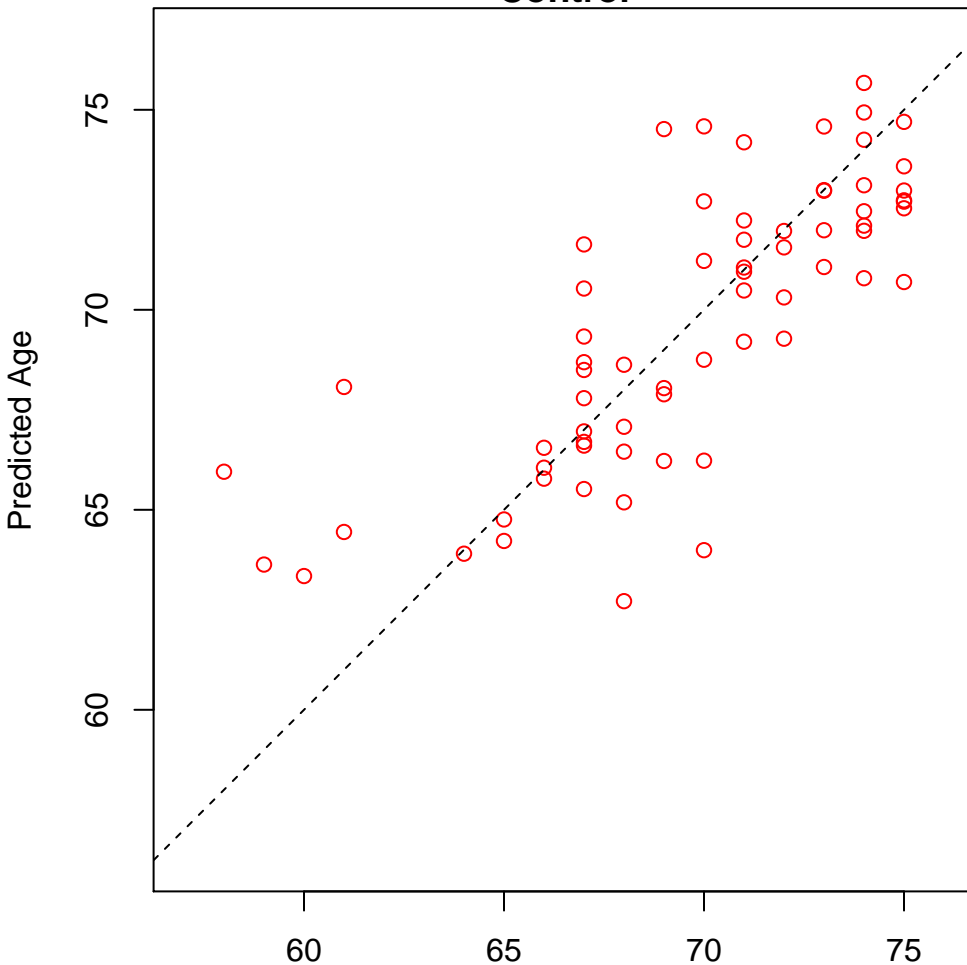
Actual Age

positive regulation of transporter activity (Score: 2.426809)

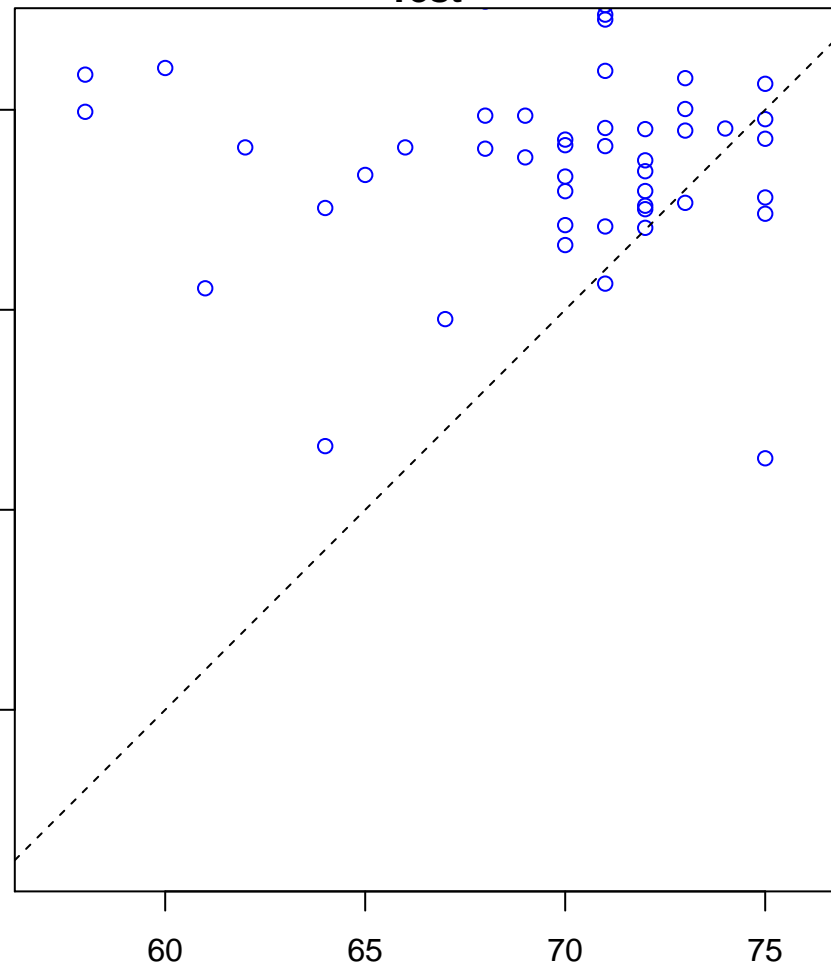


central nervous system development (Score: 2.416129)

Control

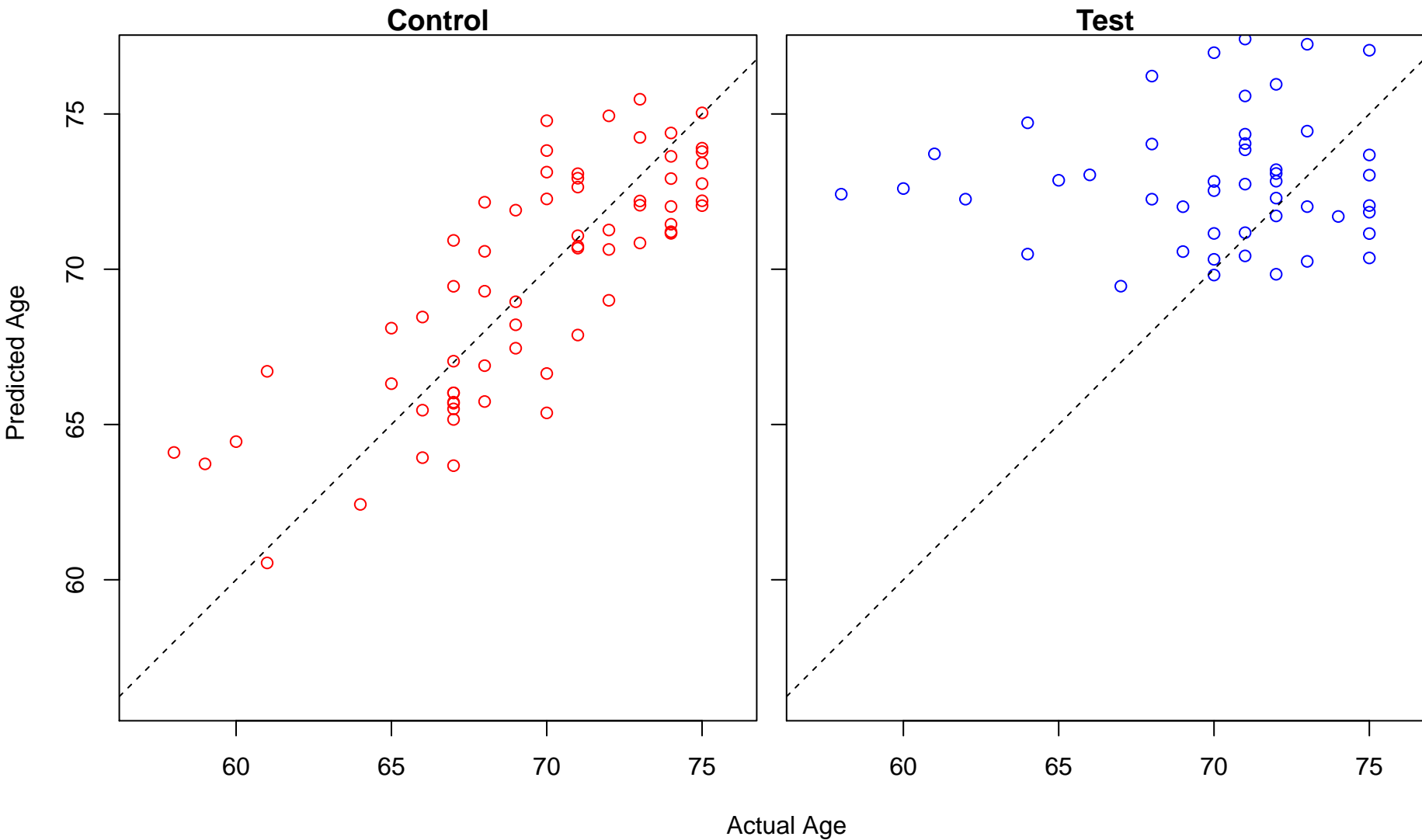


Test

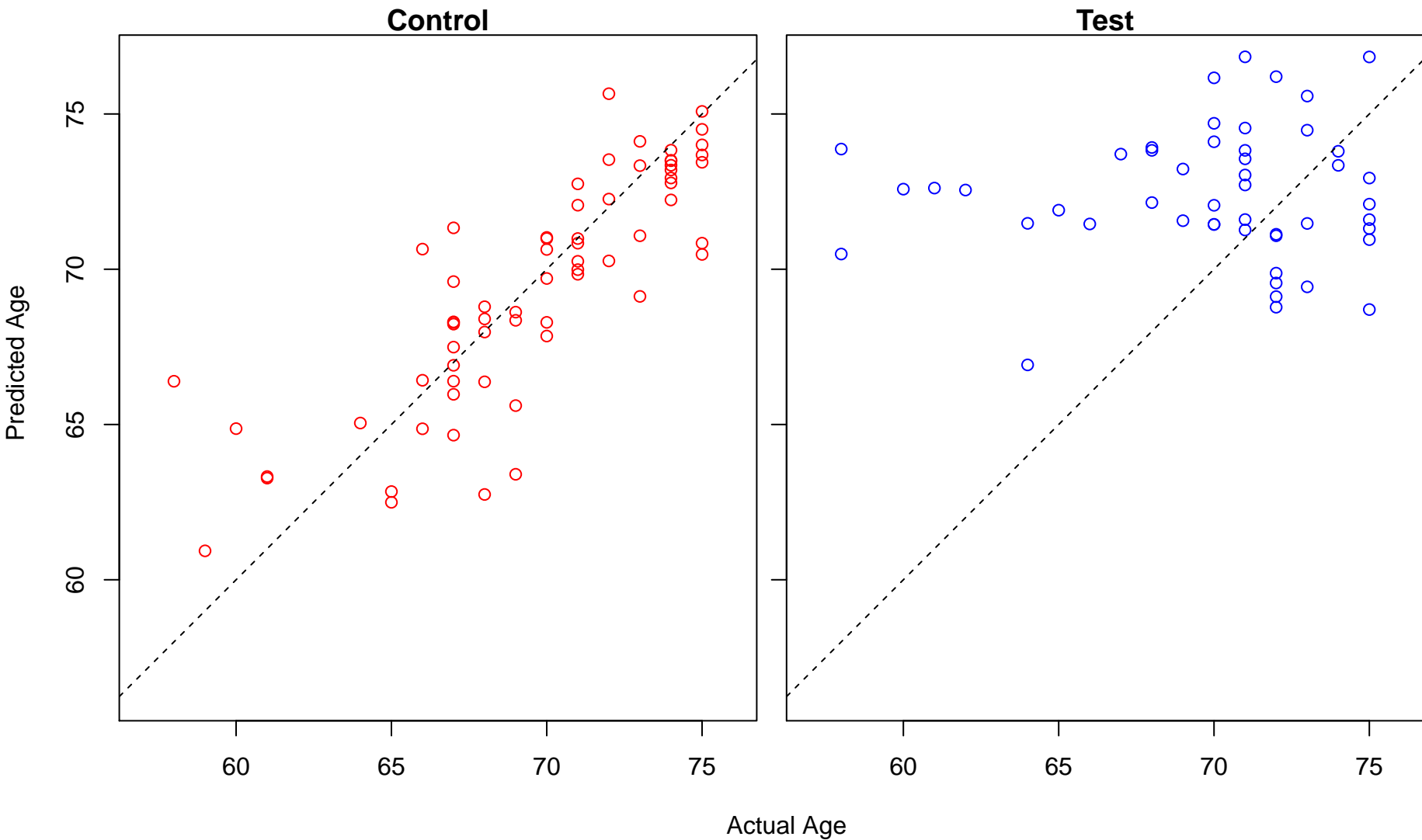


Actual Age

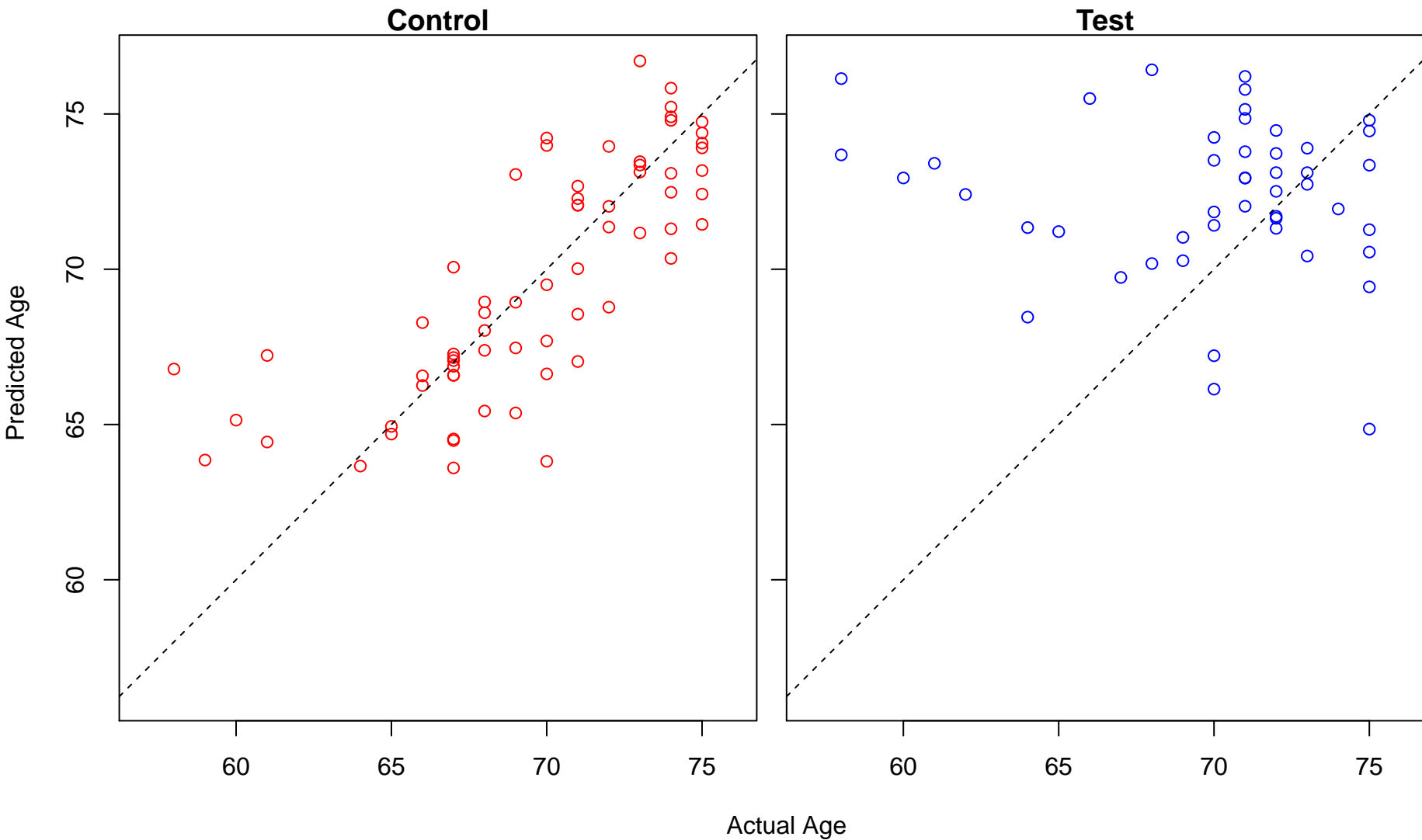
non-recombinational repair (Score: 2.405918)



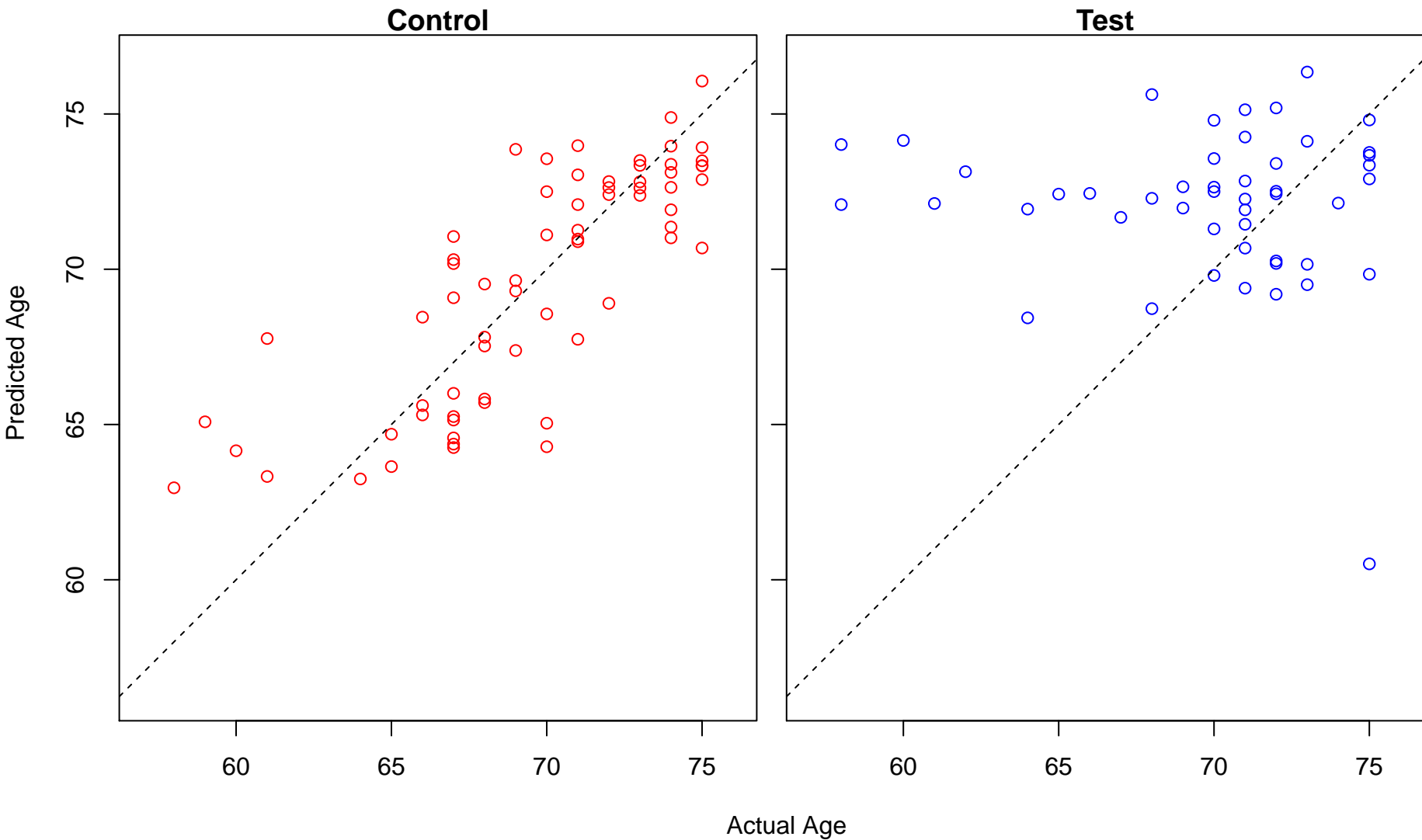
cell cycle arrest (Score: 2.377020)



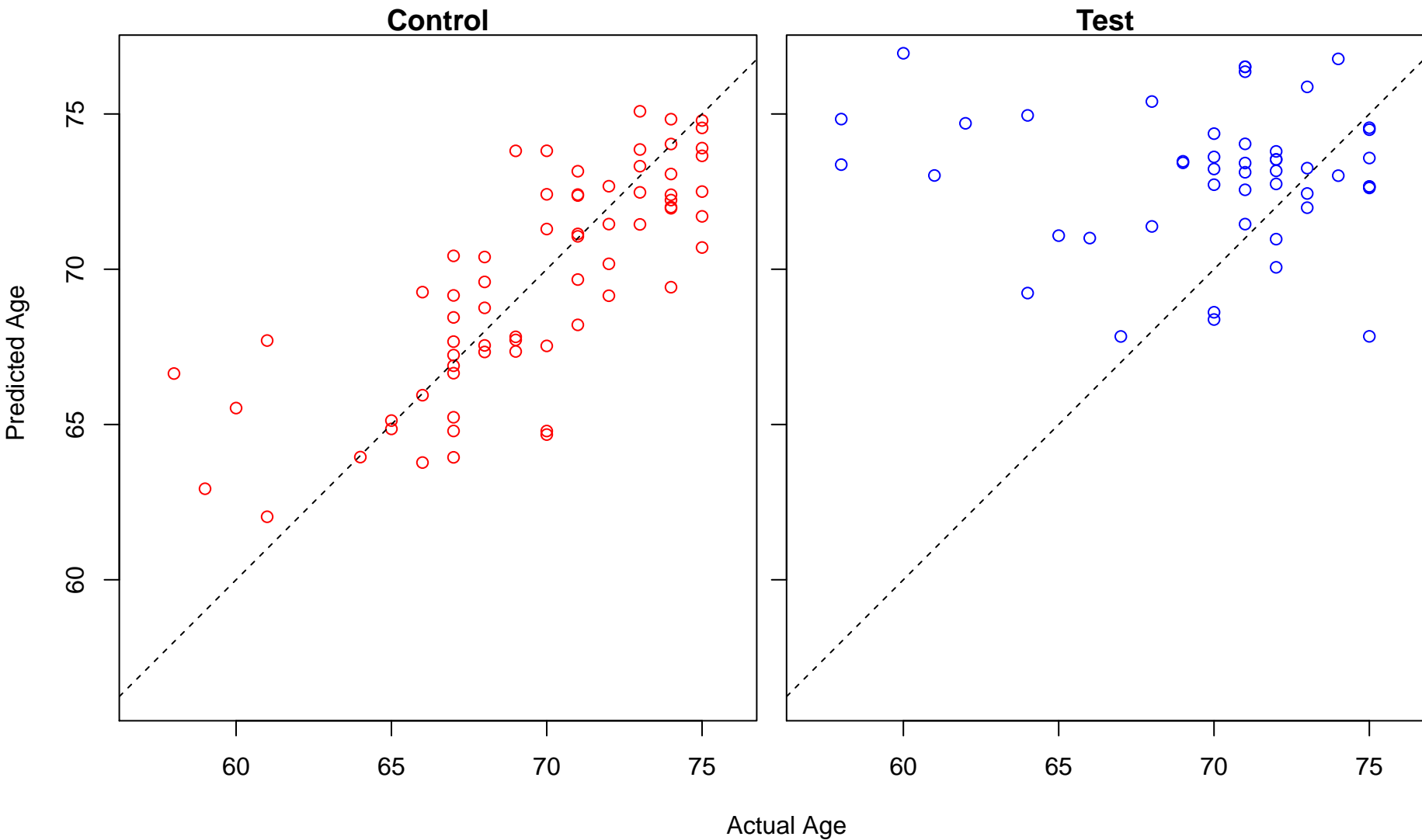
leukocyte cell-cell adhesion (Score: 2.373078)



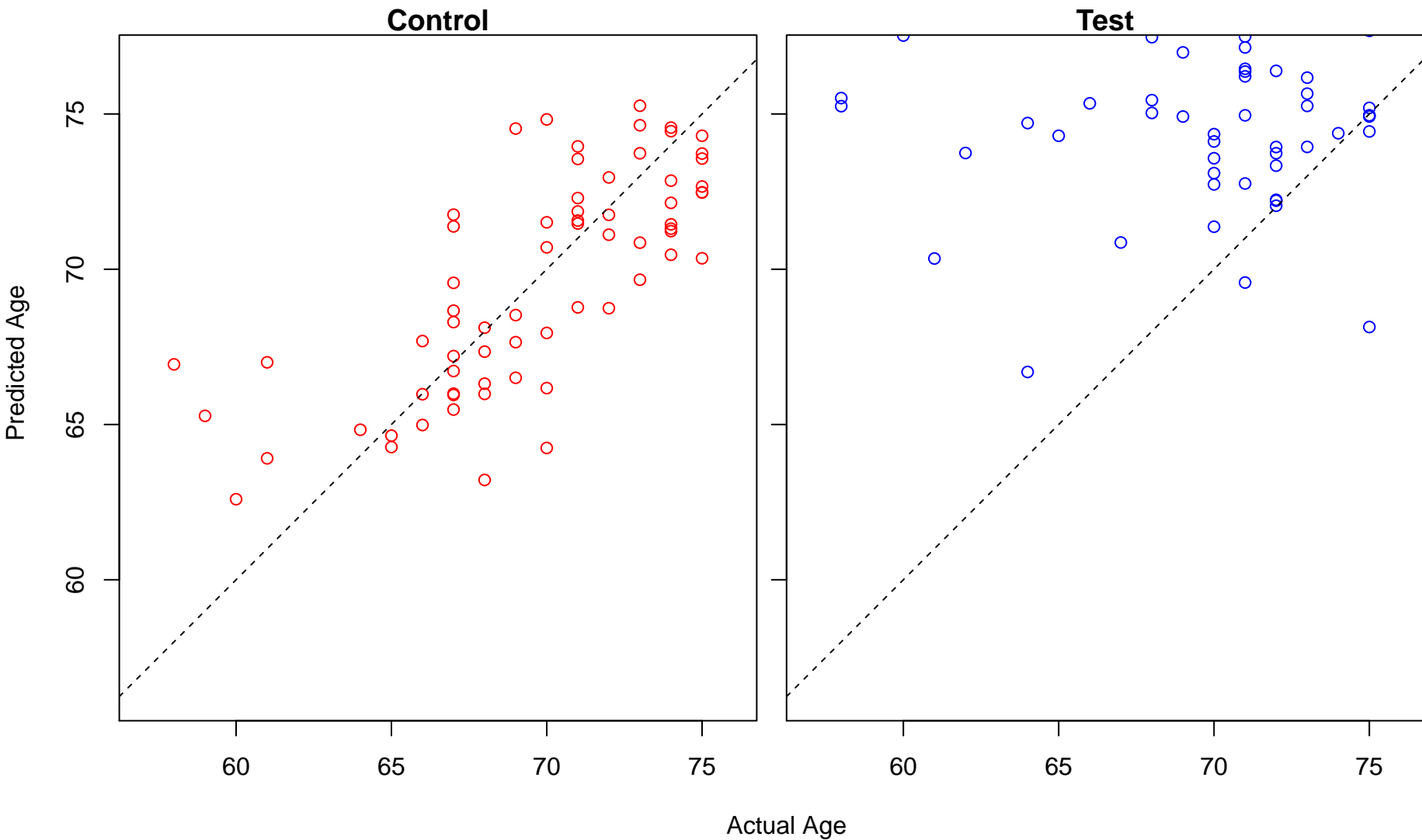
alcohol metabolic process (Score: 2.368053)



cell proliferation (Score: 2.306797)

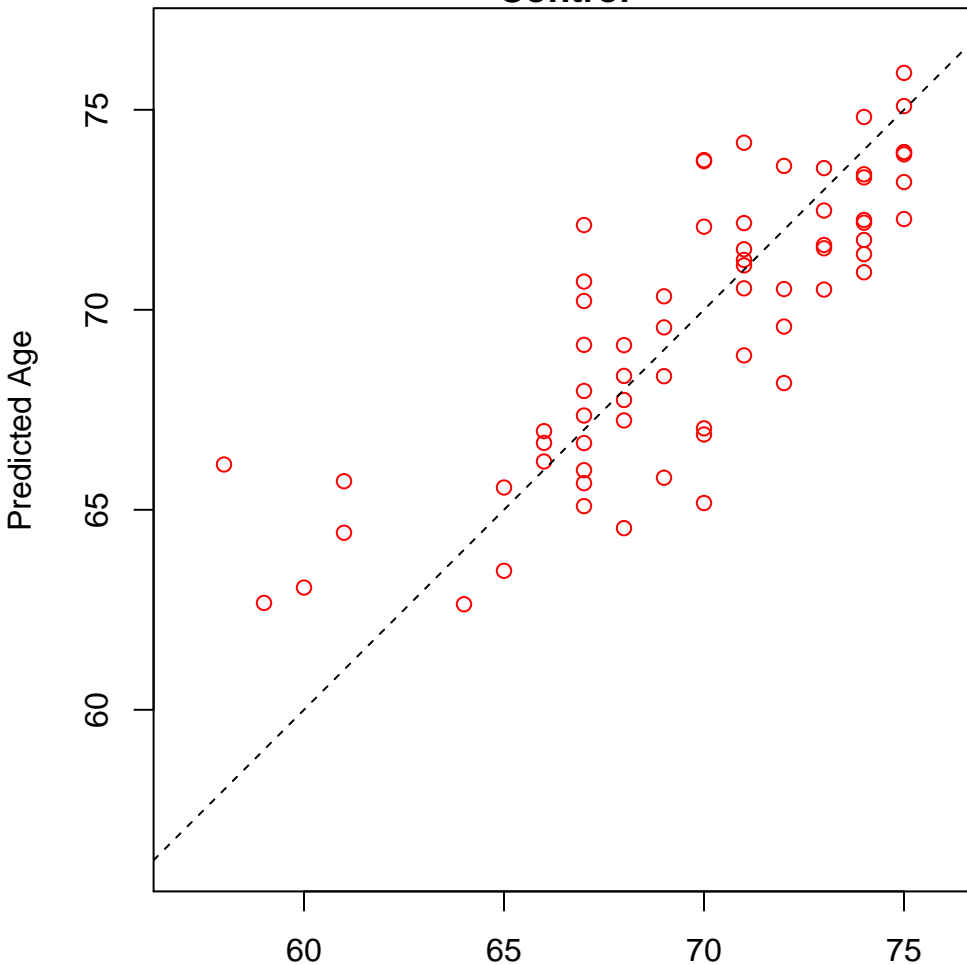


brain development (Score: 2.306564)

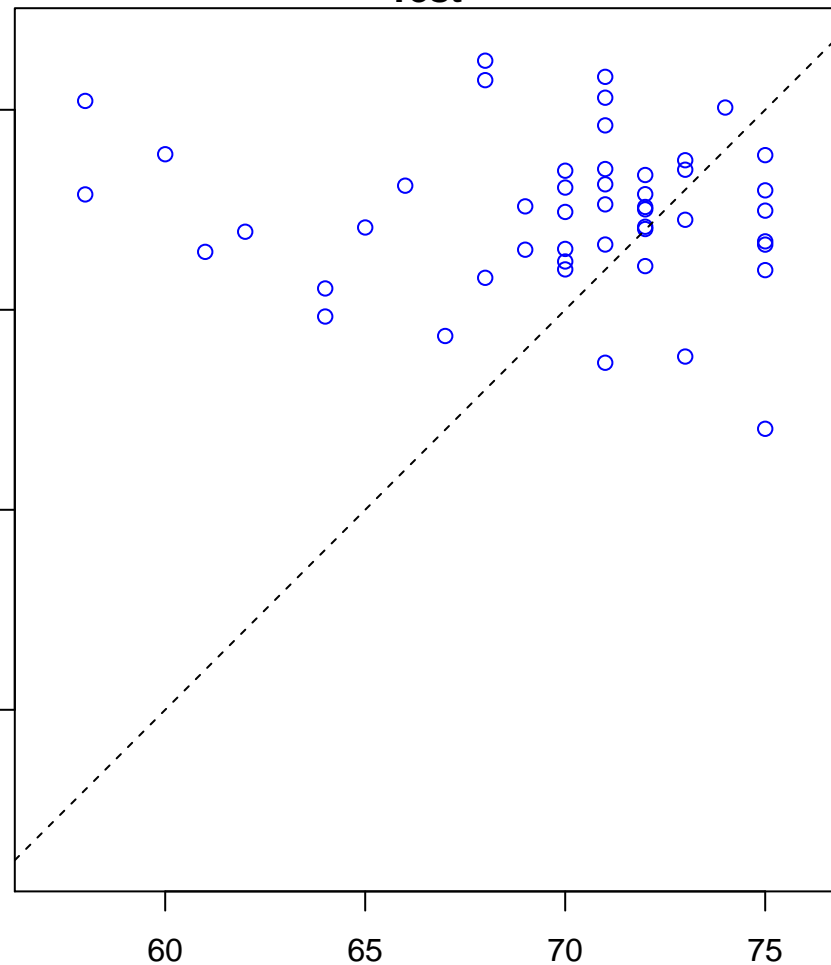


intrinsic apoptotic signaling pathway (Score: 2.298789)

Control

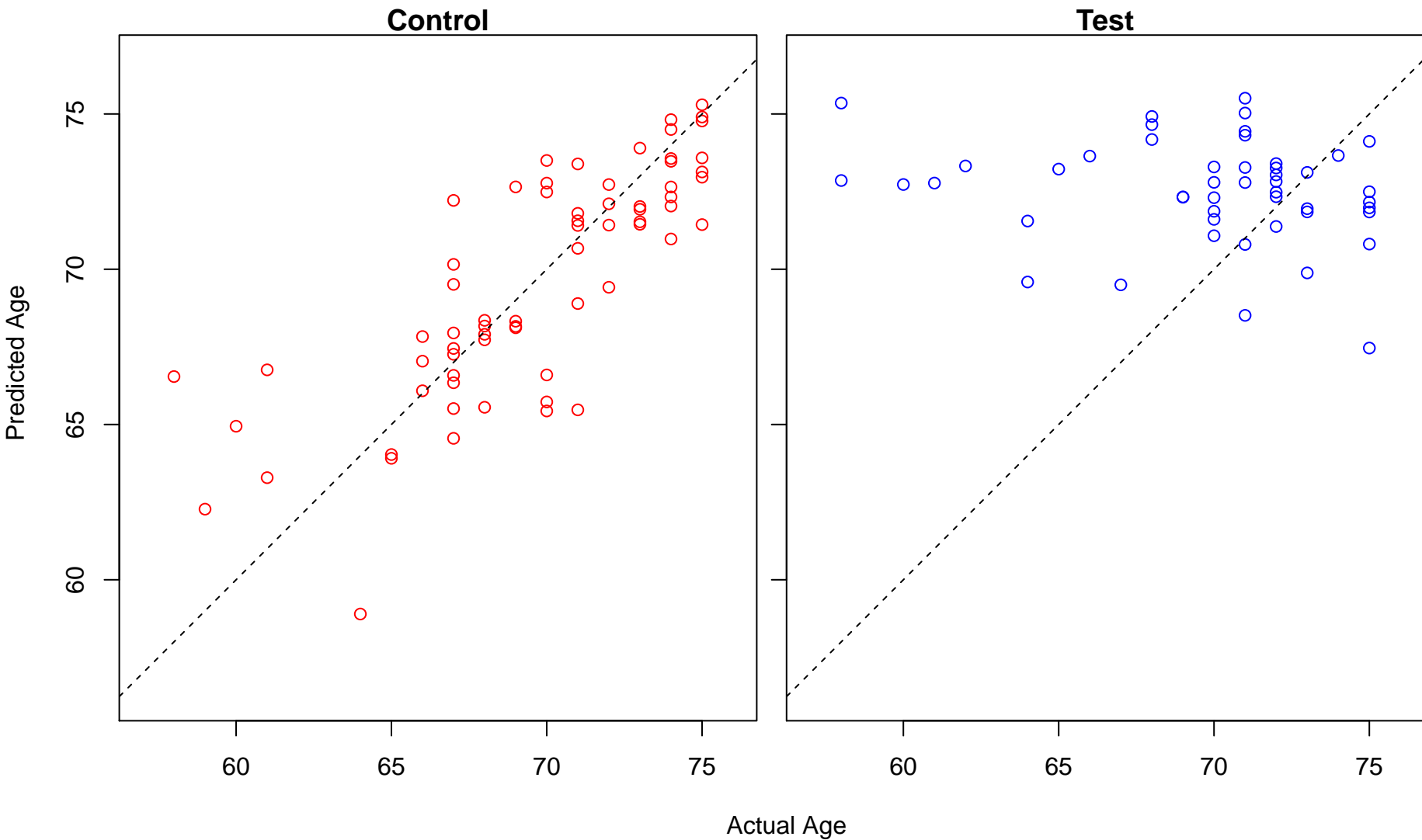


Test

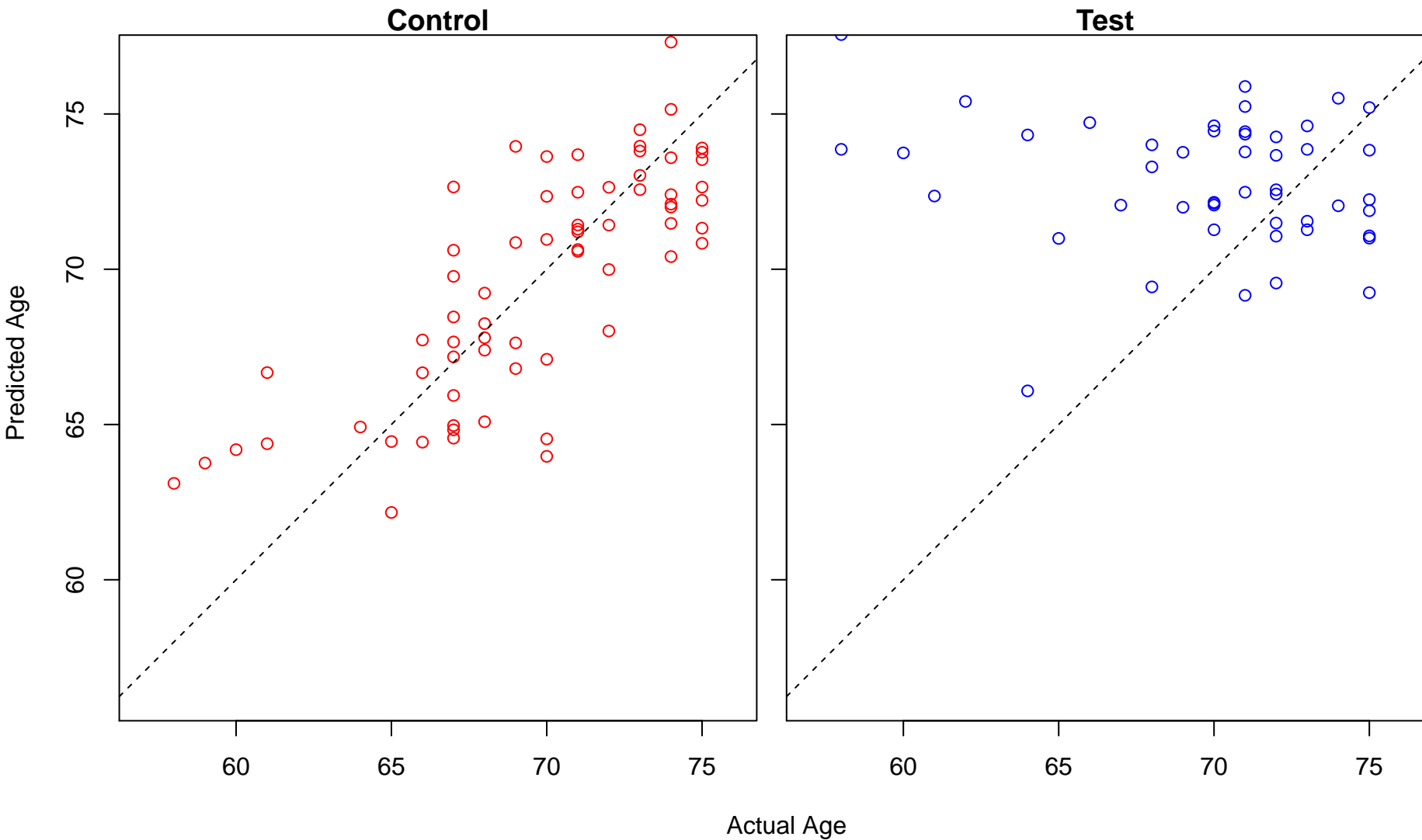


Actual Age

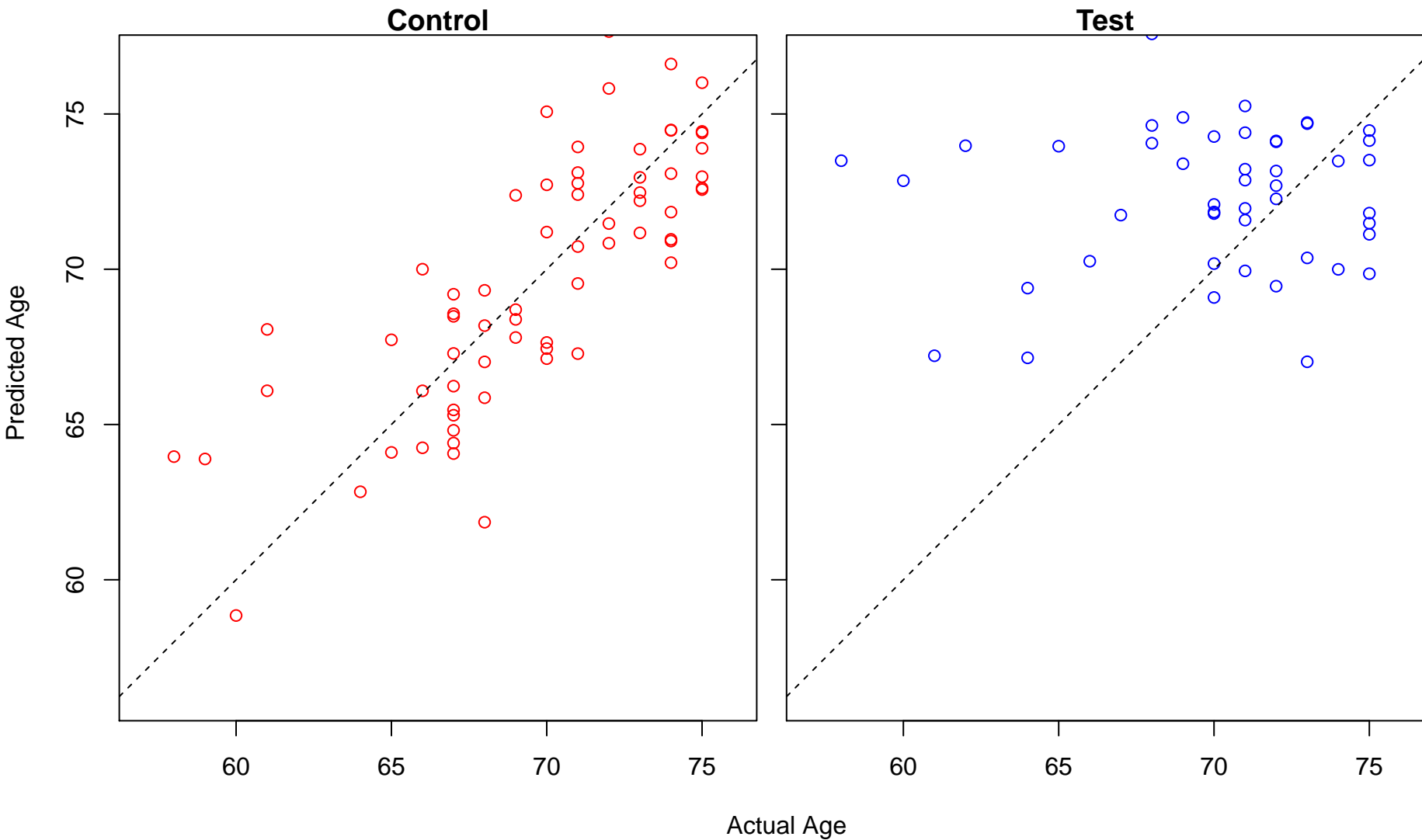
apoptotic signaling pathway (Score: 2.290620)



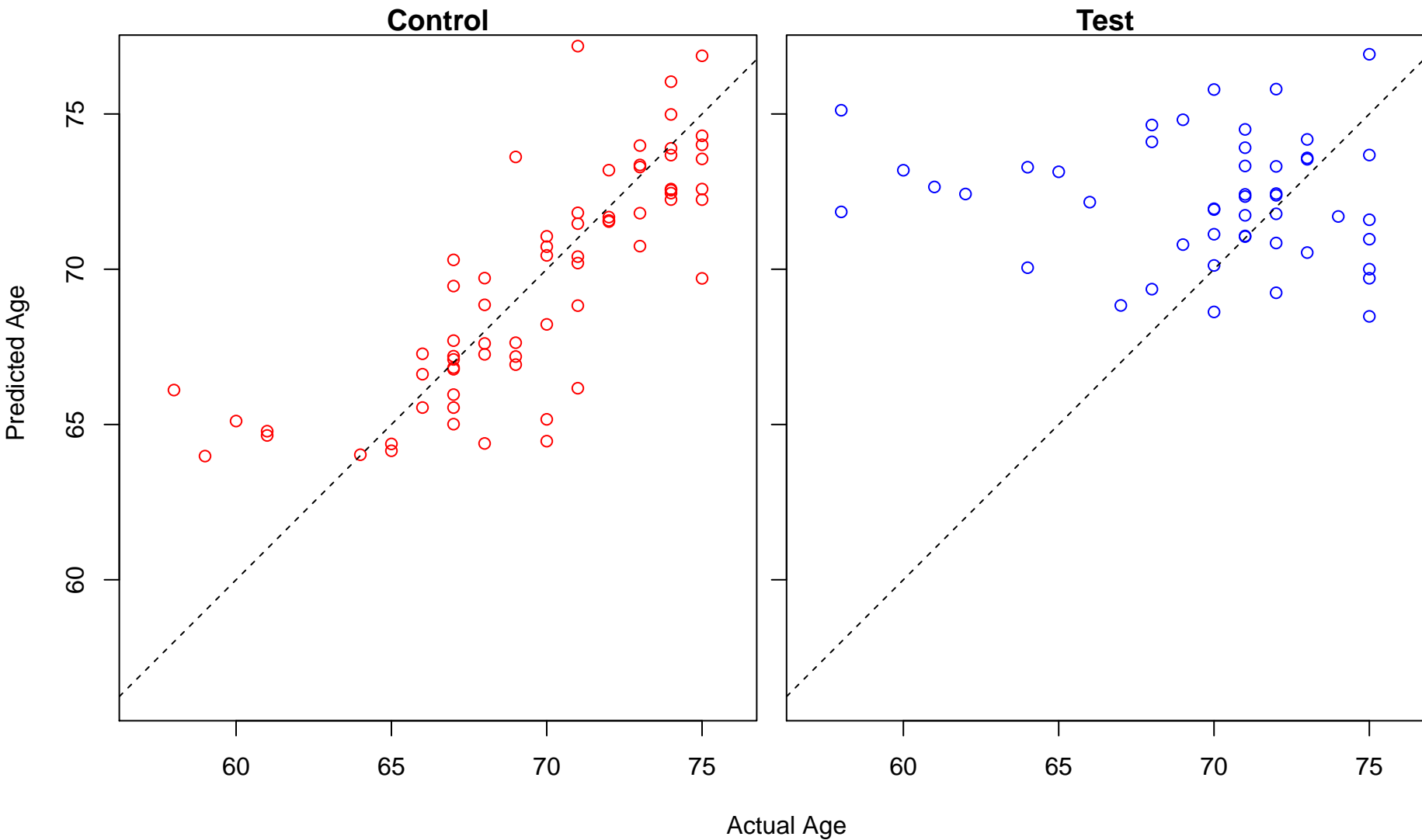
peptidyl-lysine modification (Score: 2.271012)



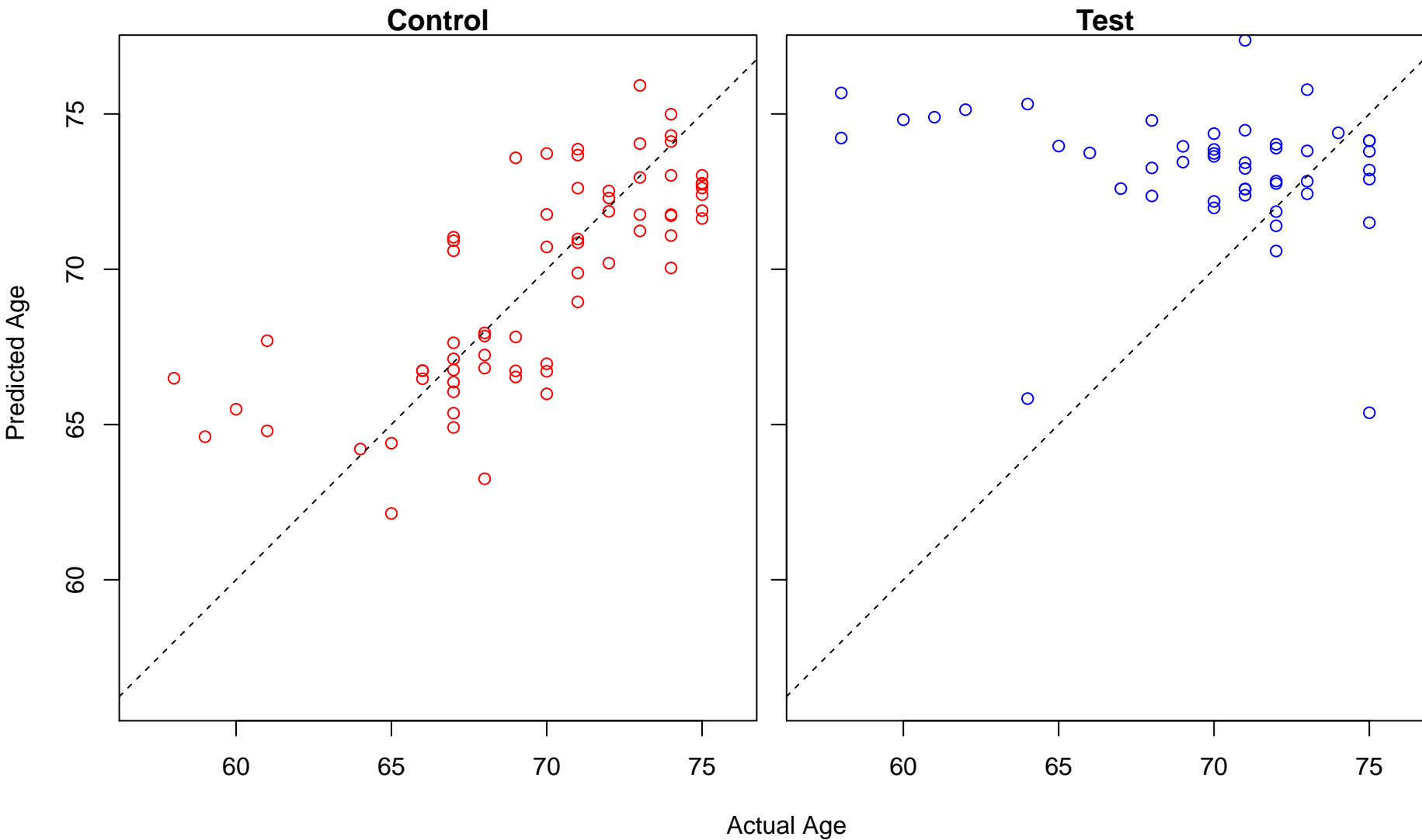
nuclear import (Score: 2.270506)



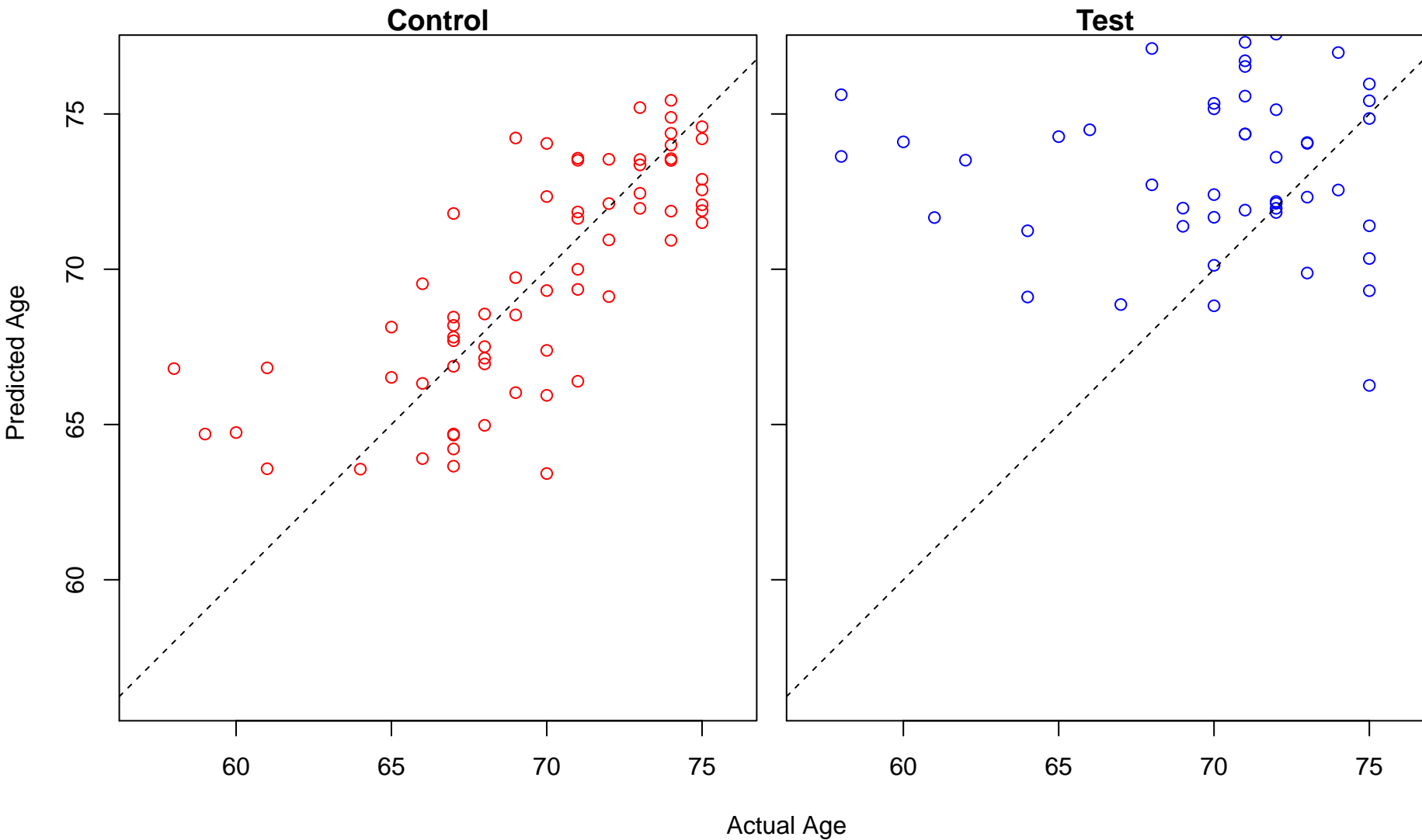
negative regulation of cell proliferation (Score: 2.264186)



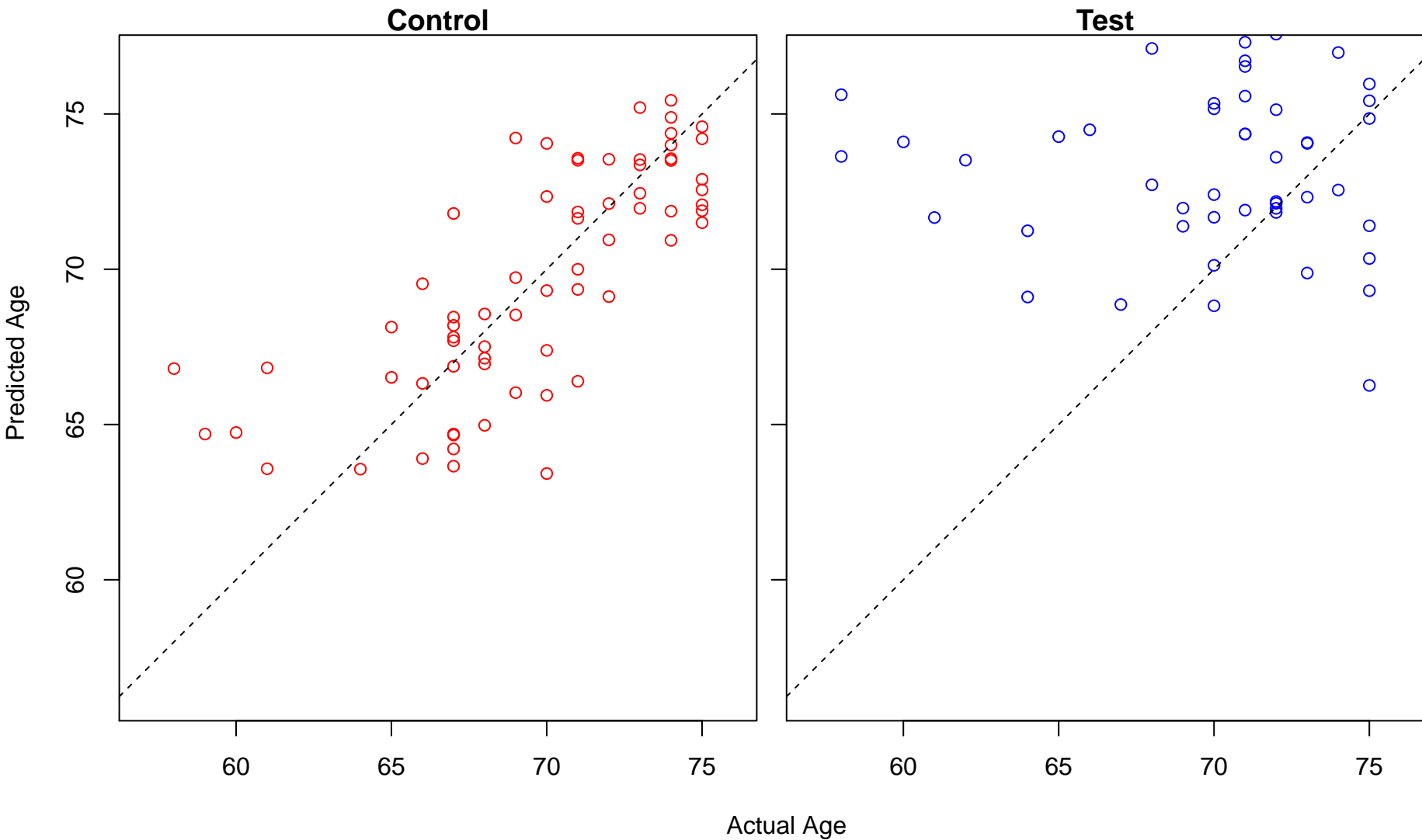
positive regulation of cell proliferation (Score: 2.259110)



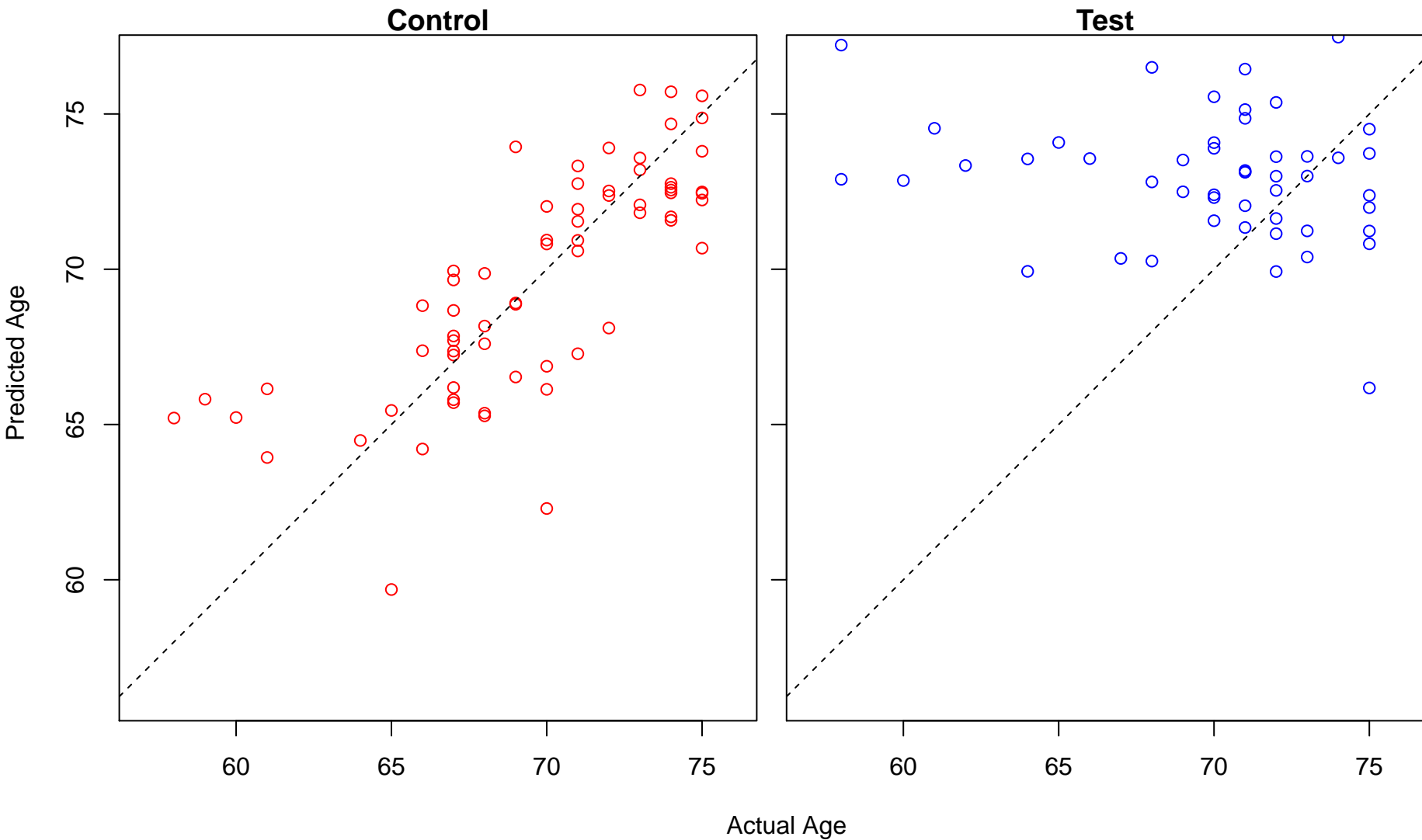
T cell activation (Score: 2.258242)



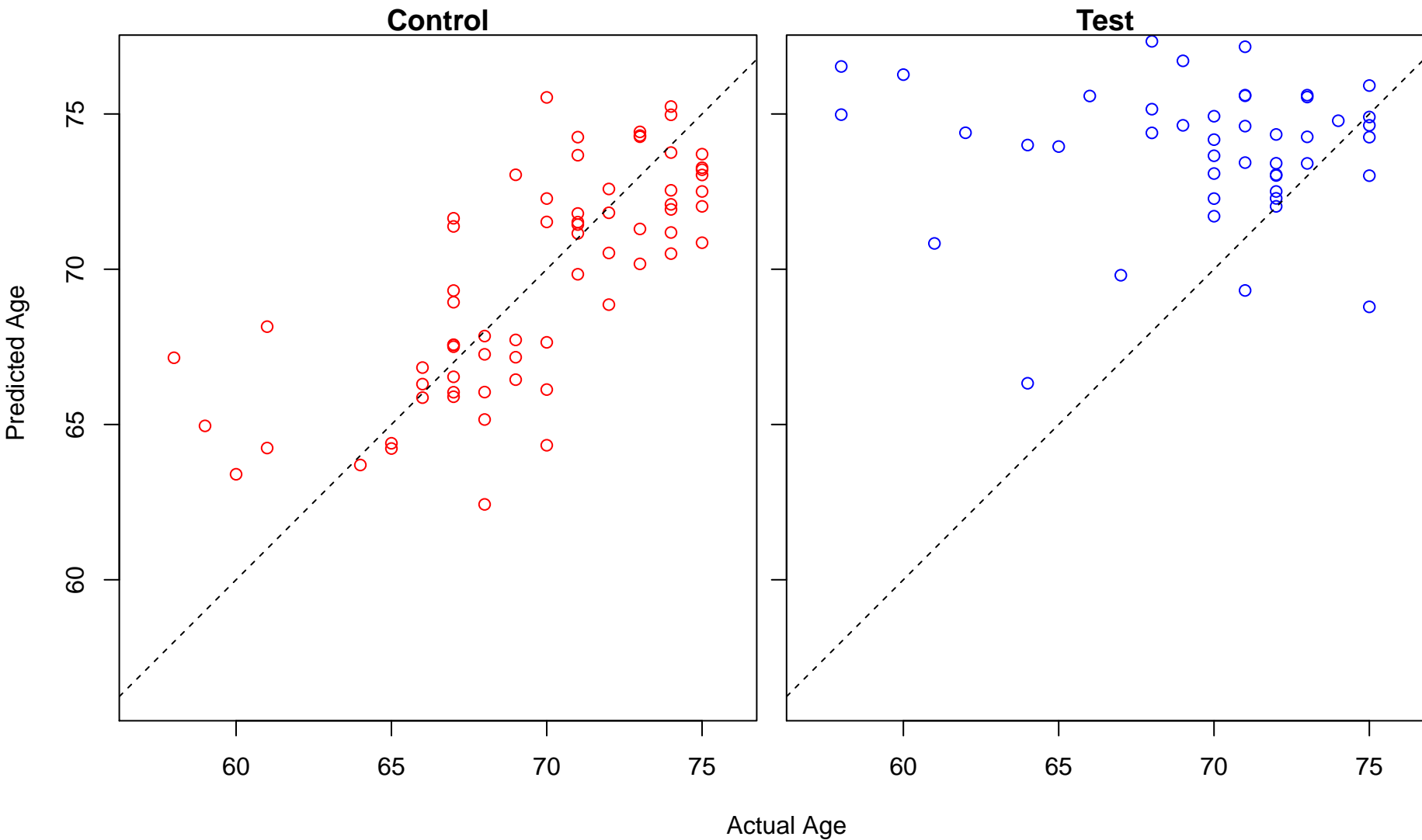
T cell aggregation (Score: 2.258242)



regulation of leukocyte differentiation (Score: 2.248699)

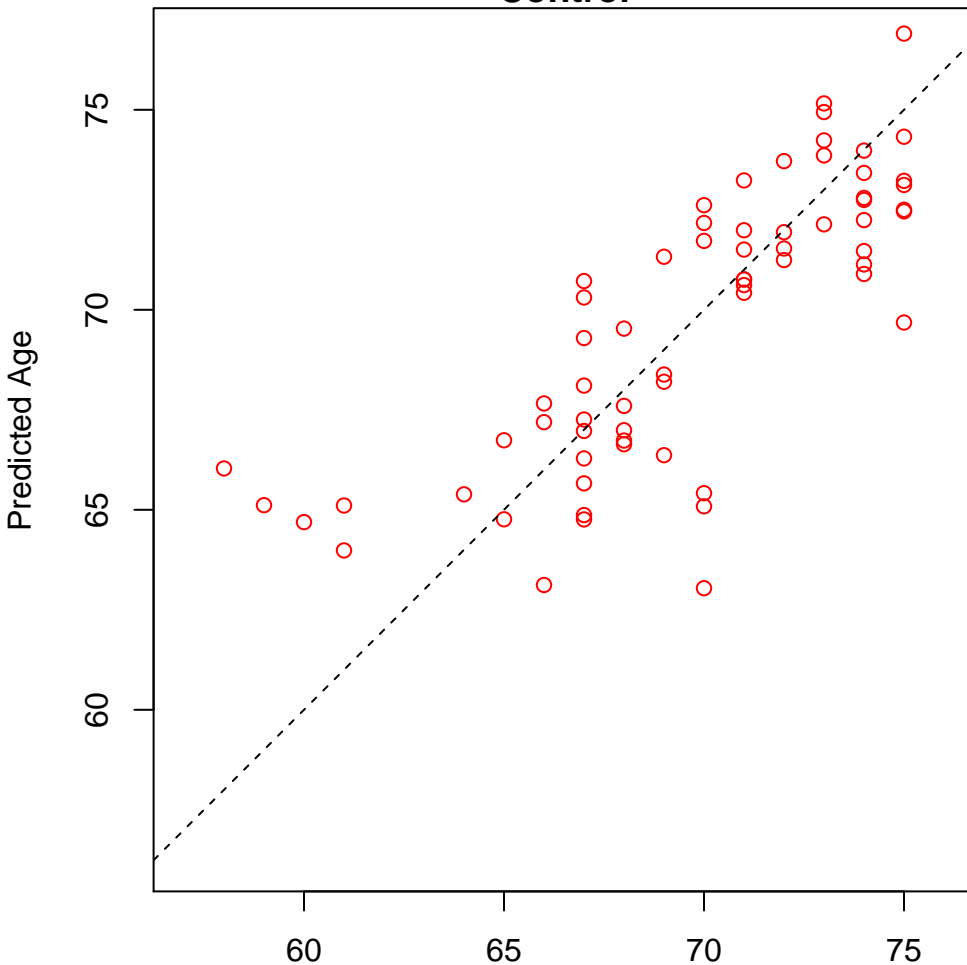


head development (Score: 2.242204)

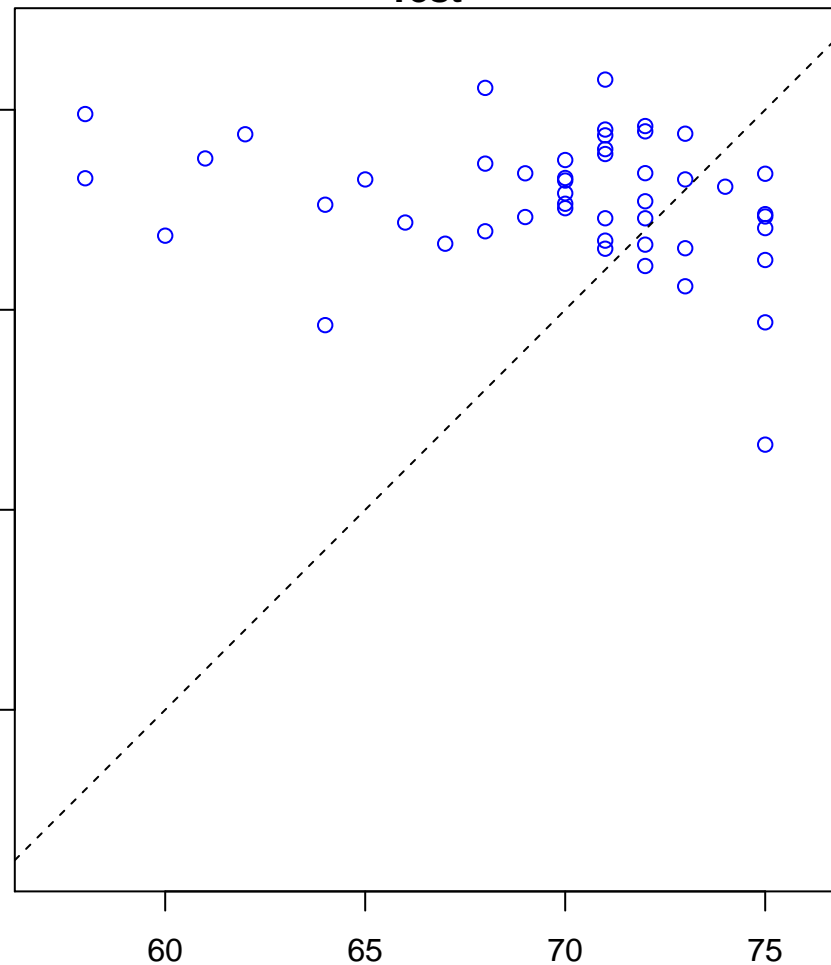


glycerophospholipid metabolic process (Score: 2.241240)

Control

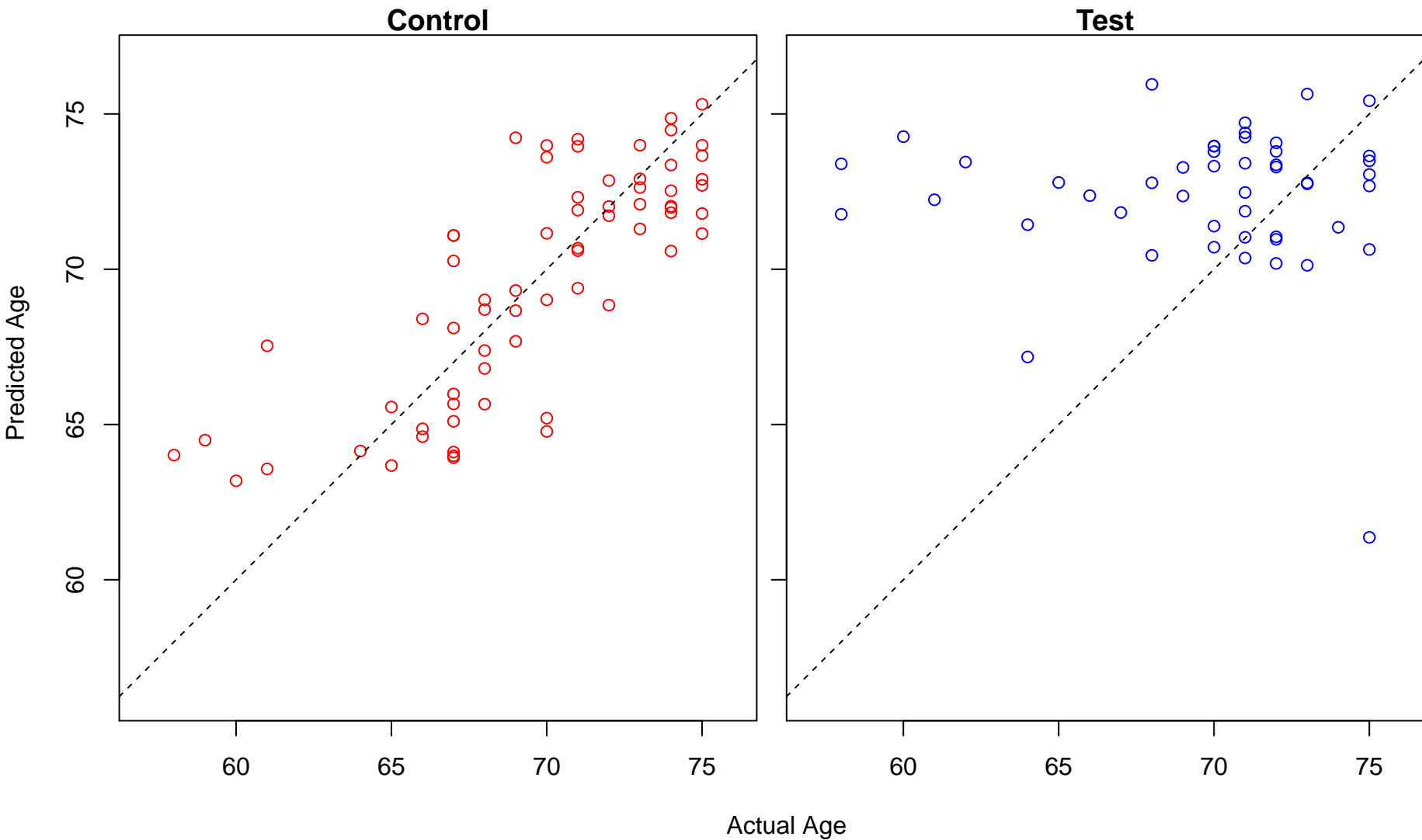


Test

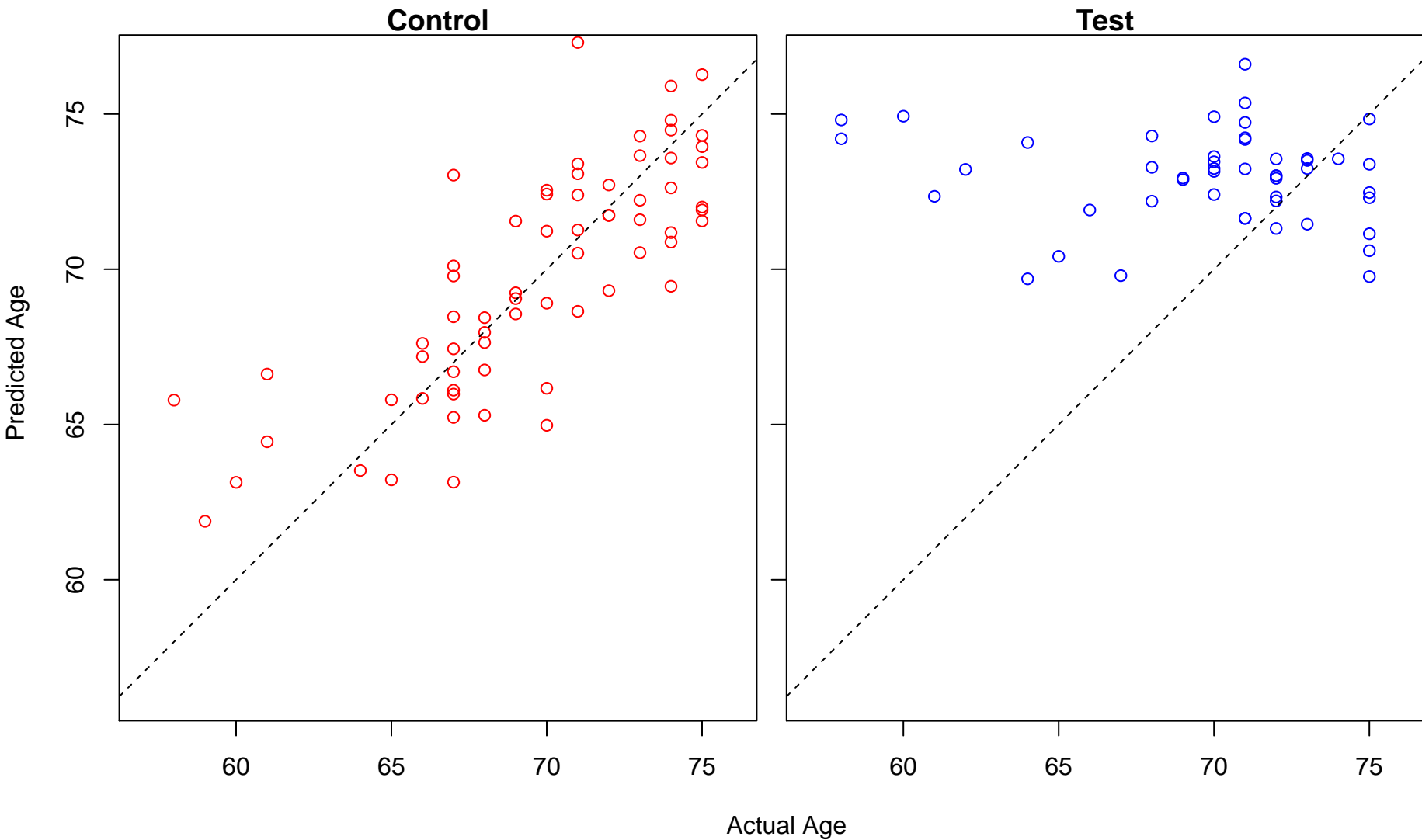


Actual Age

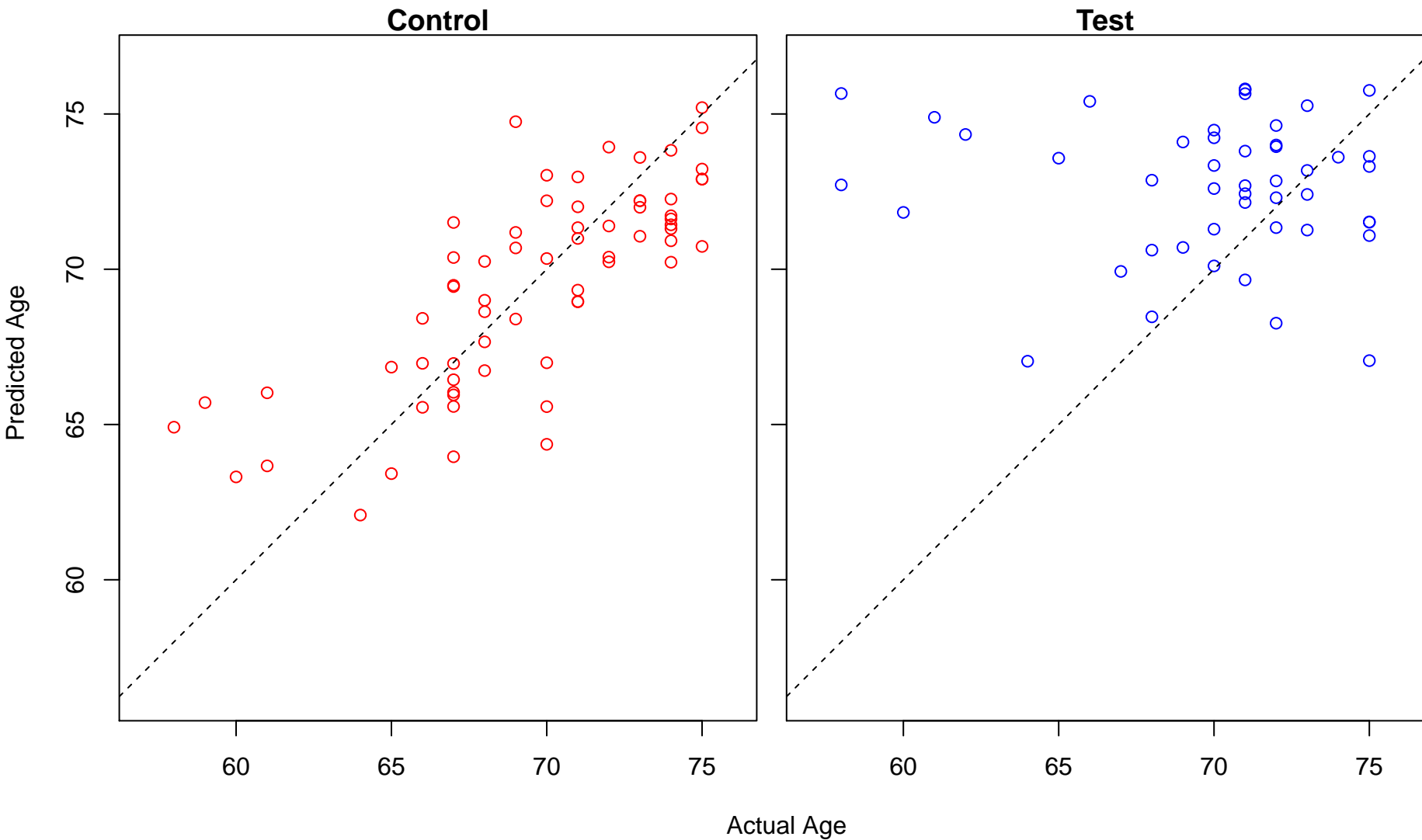
organic hydroxy compound metabolic process (Score: 2.234638)



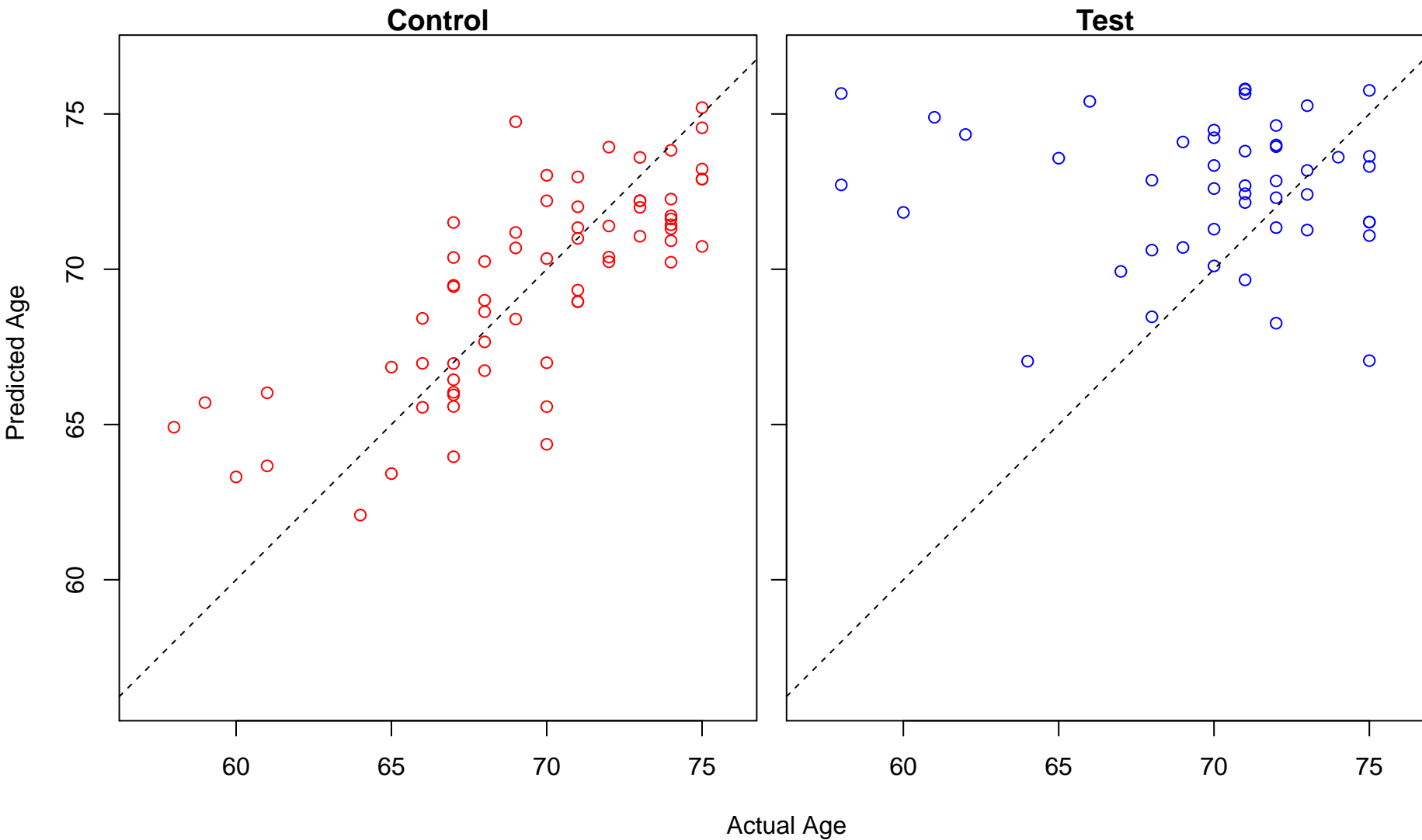
positive regulation of mitochondrion organization (Score: 2.229484)



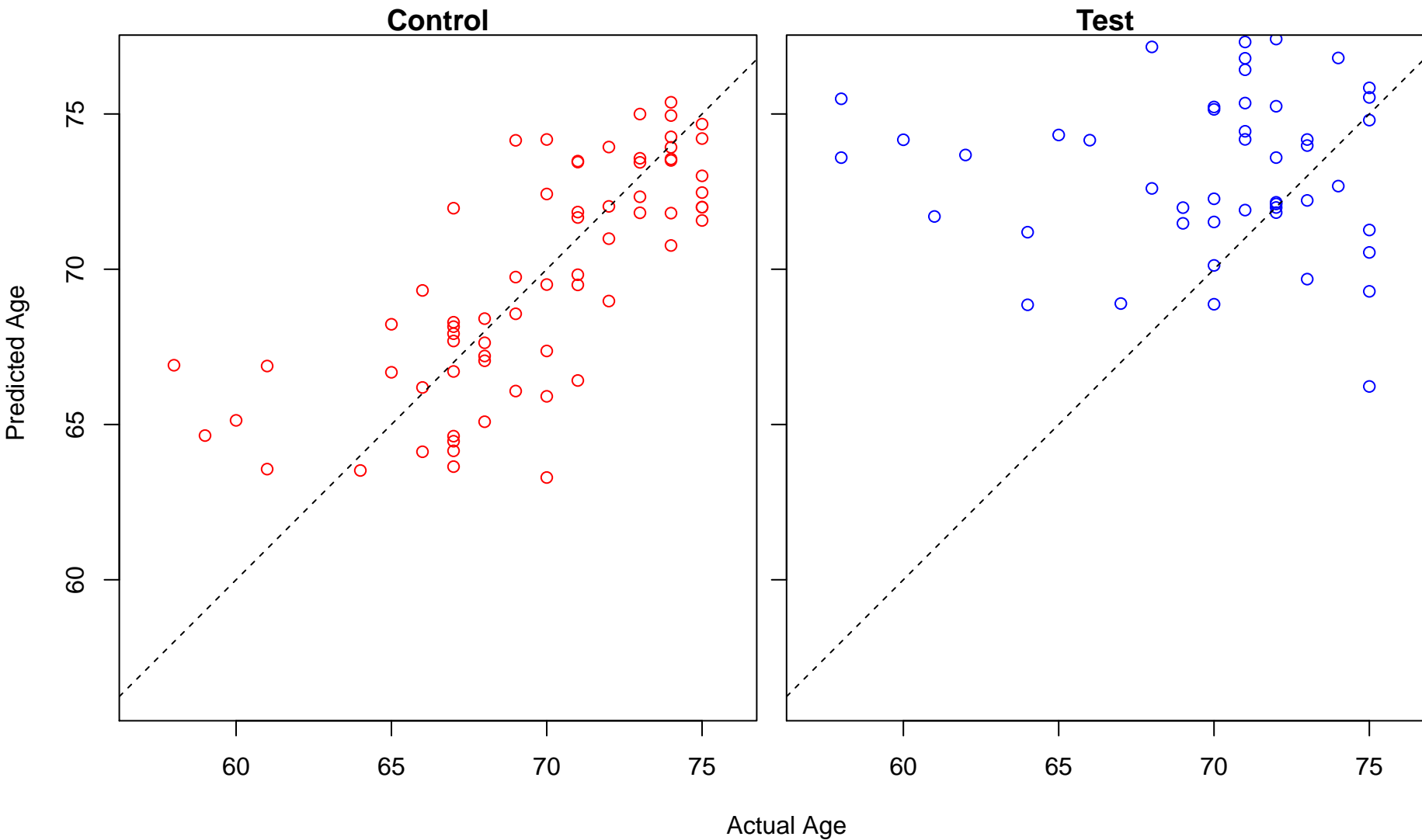
stress-activated protein kinase signaling cascade (Score: 2.214636)



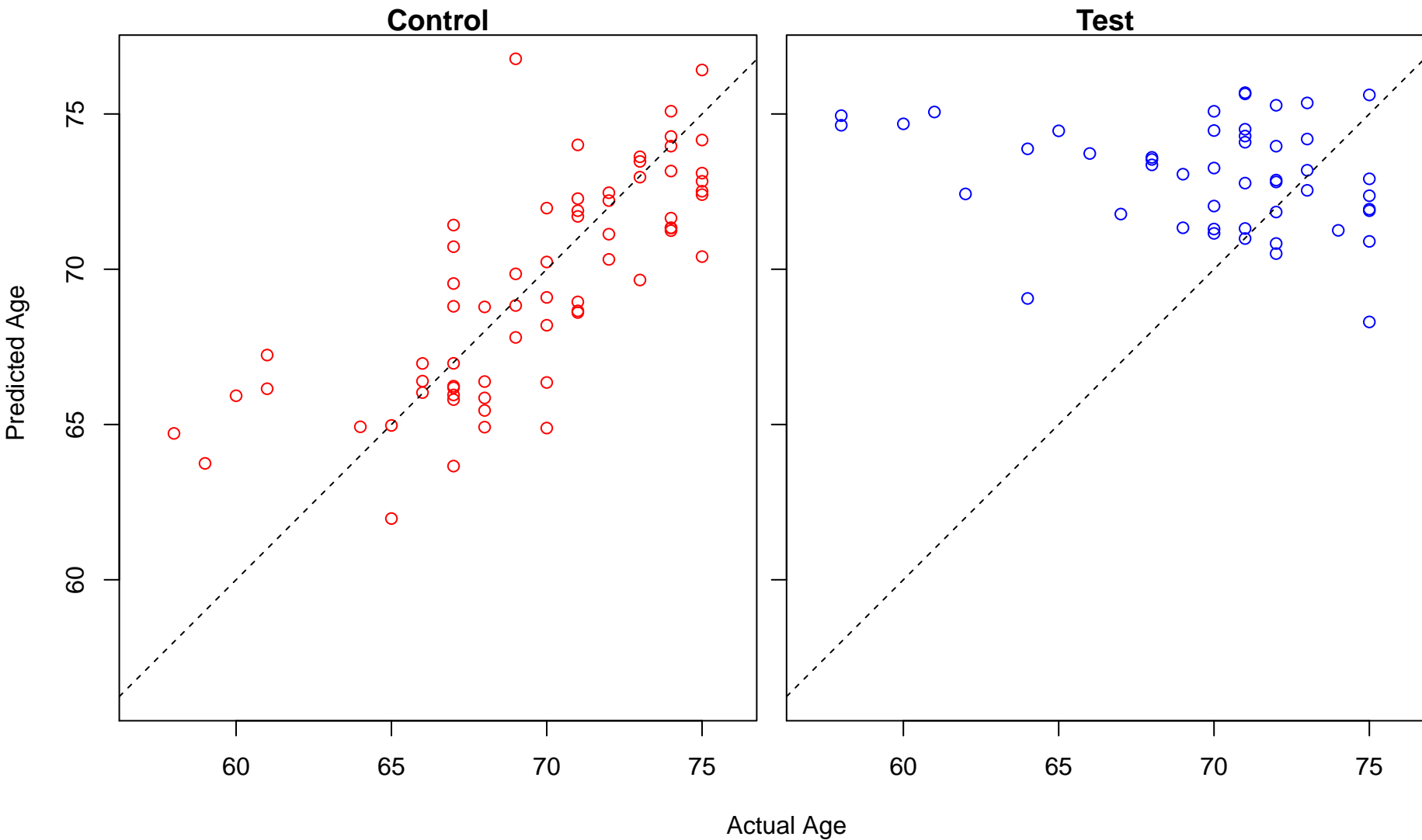
stress-activated MAPK cascade (Score: 2.214636)



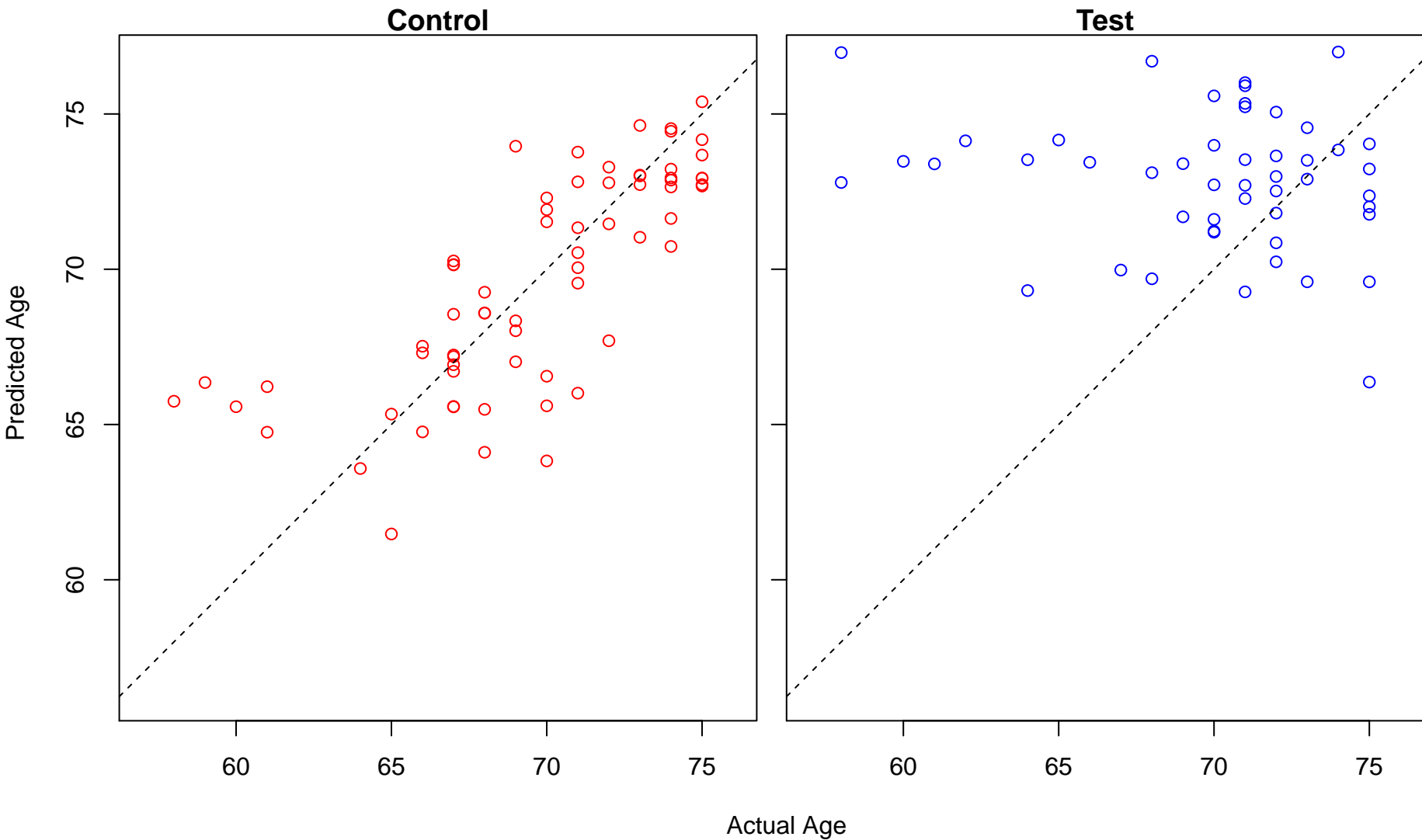
lymphocyte aggregation (Score: 2.212913)



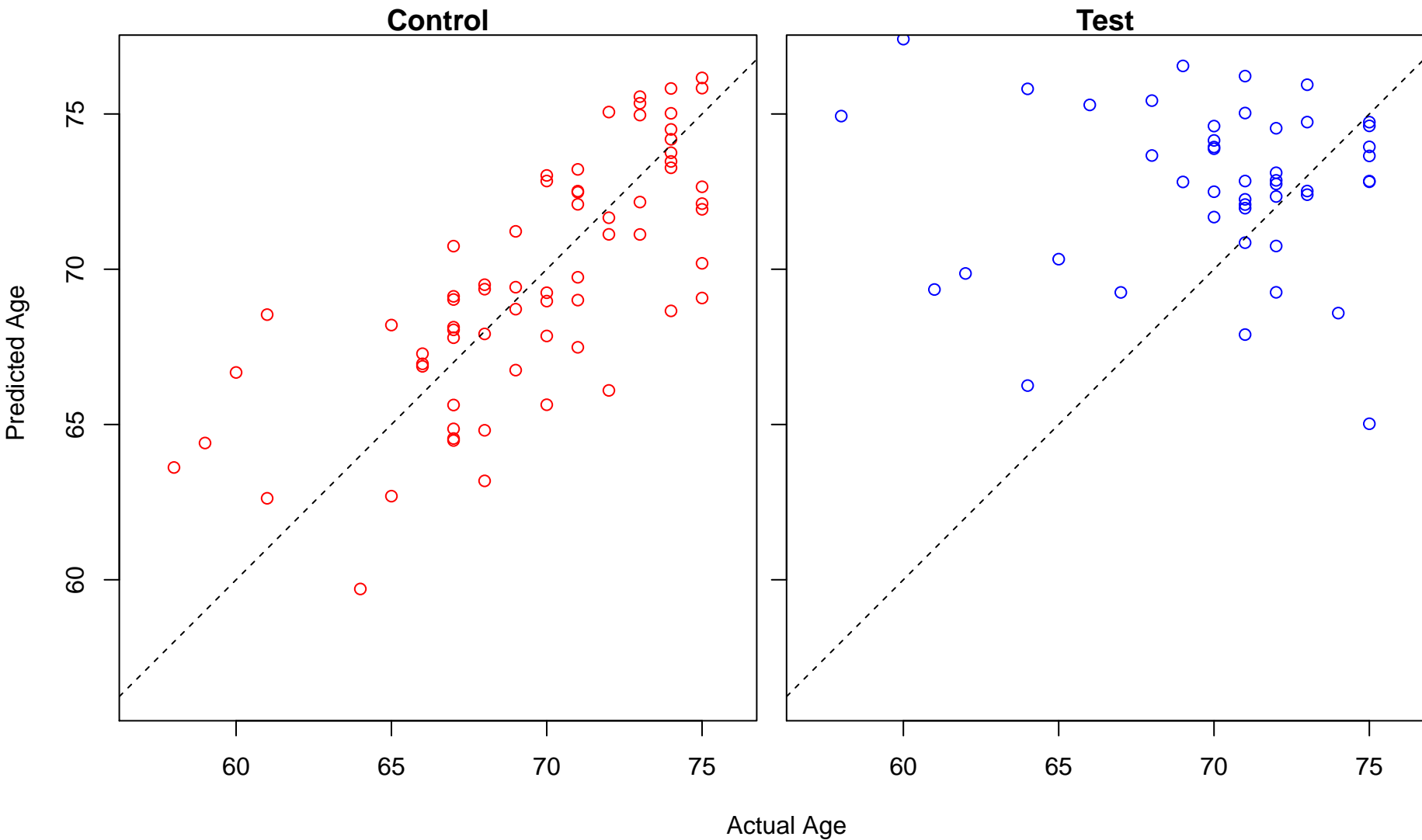
immune response–activating cell surface receptor signaling pathway (Score: 2.196705)



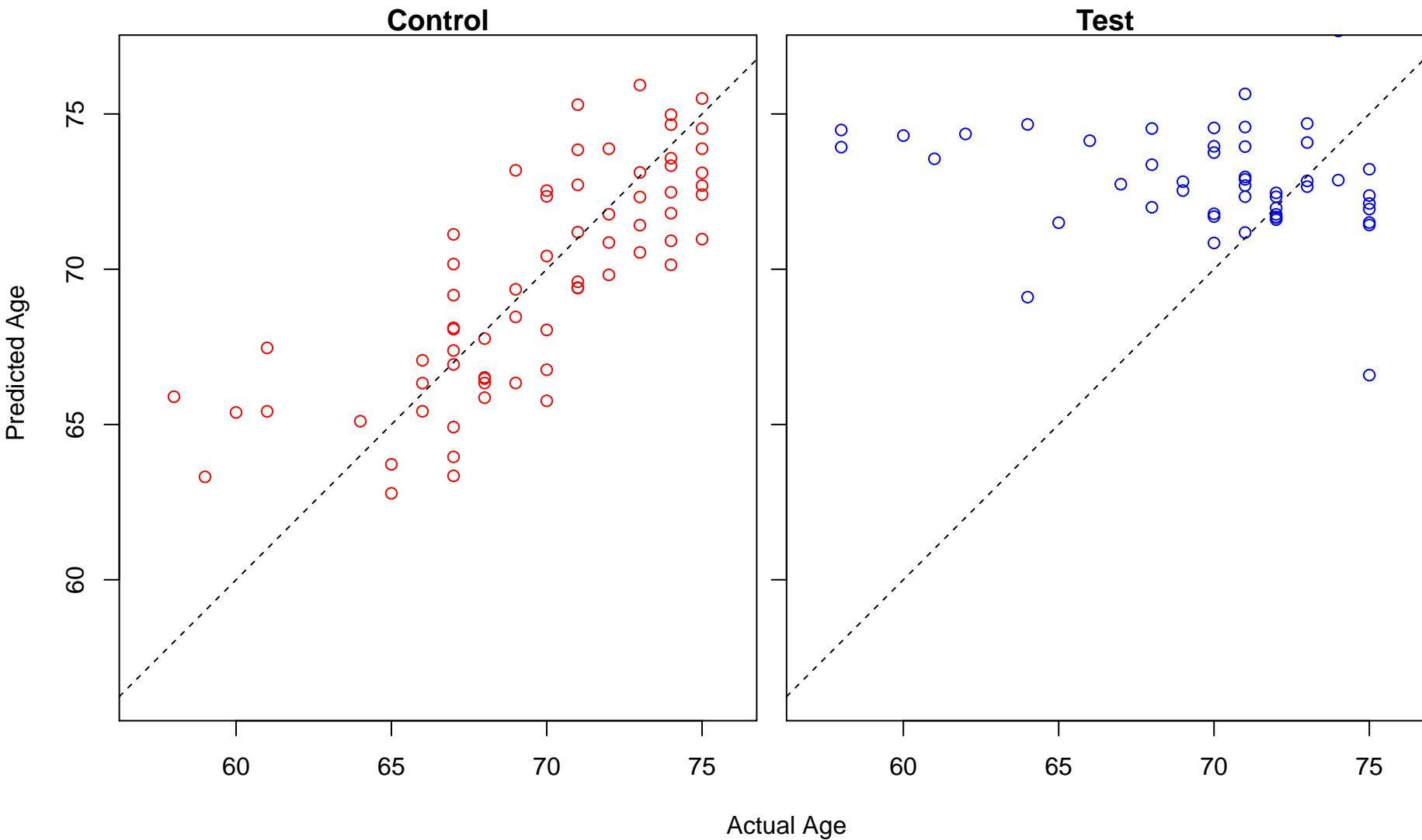
regulation of hemopoiesis (Score: 2.187653)



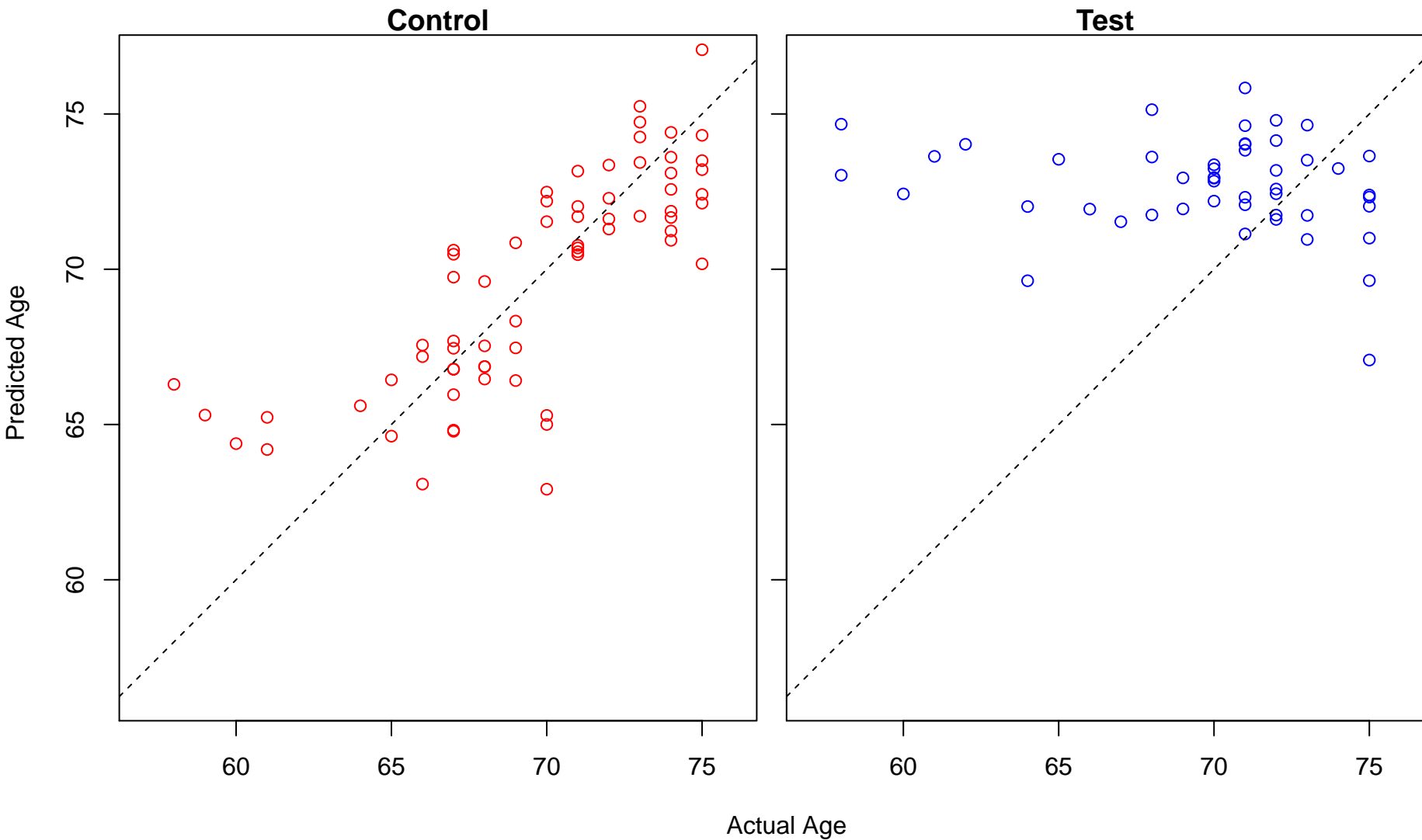
cytokine production (Score: 2.179345)



regulation of intrinsic apoptotic signaling pathway (Score: 2.176272)

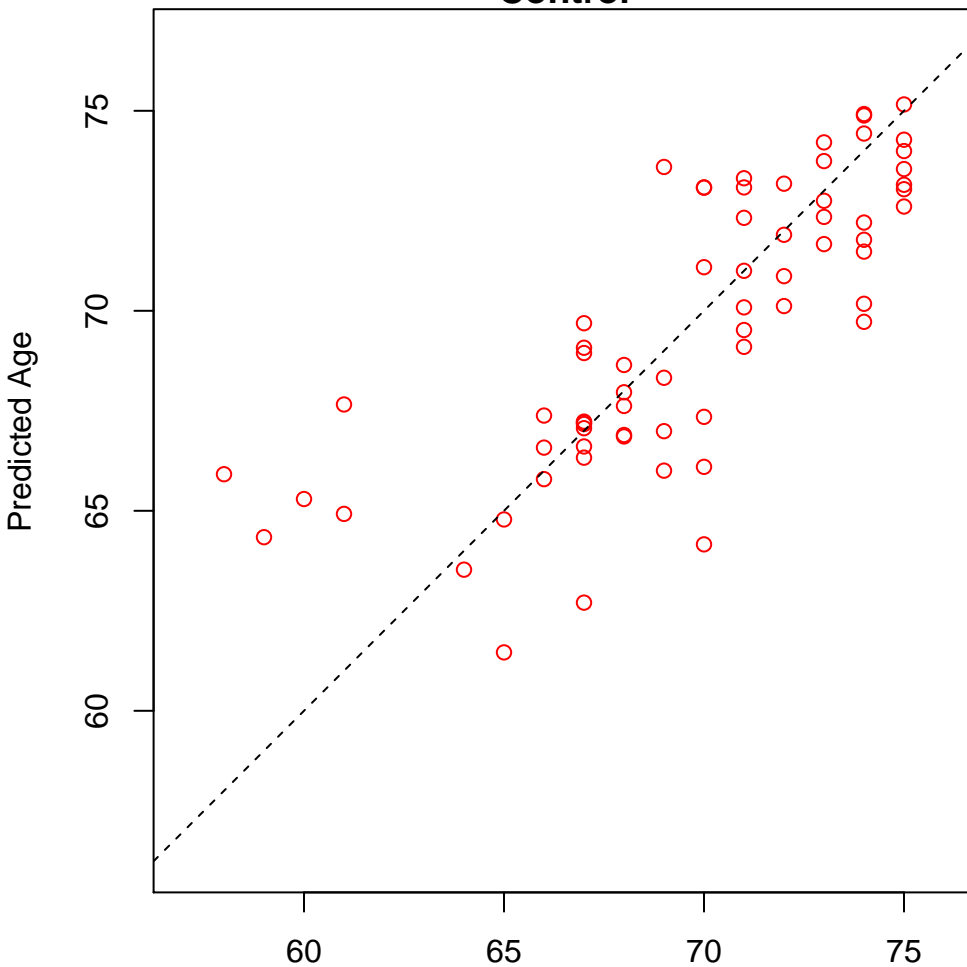


phospholipid metabolic process (Score: 2.167286)

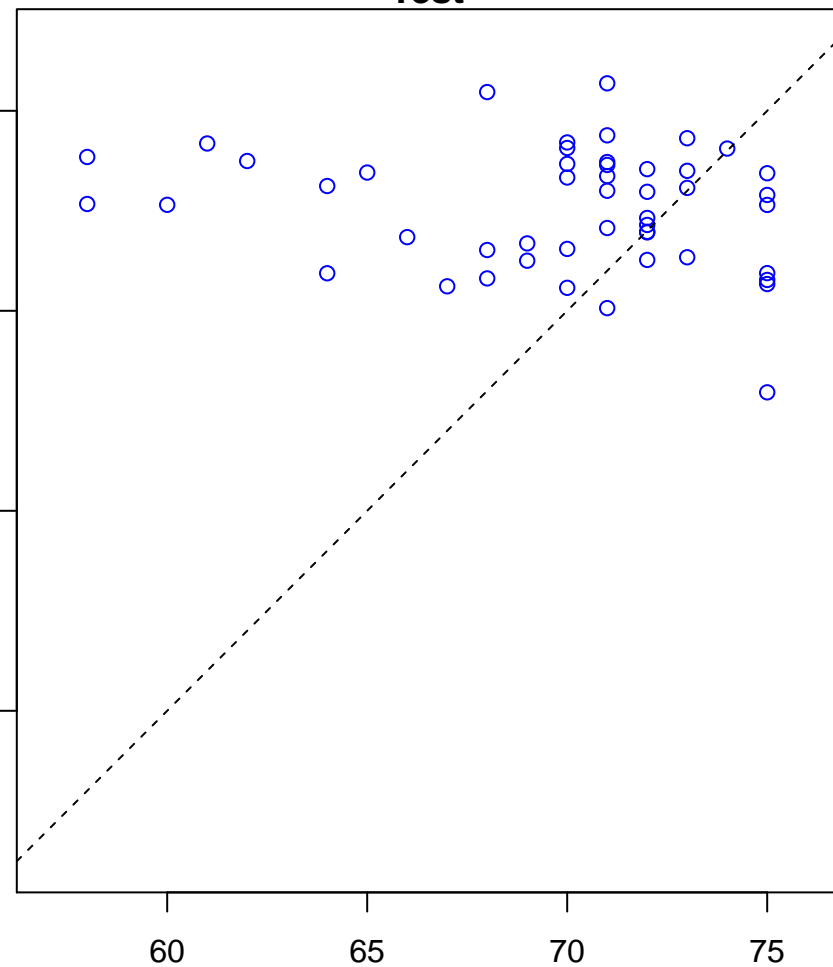


positive regulation of catabolic process (Score: 2.161517)

Control

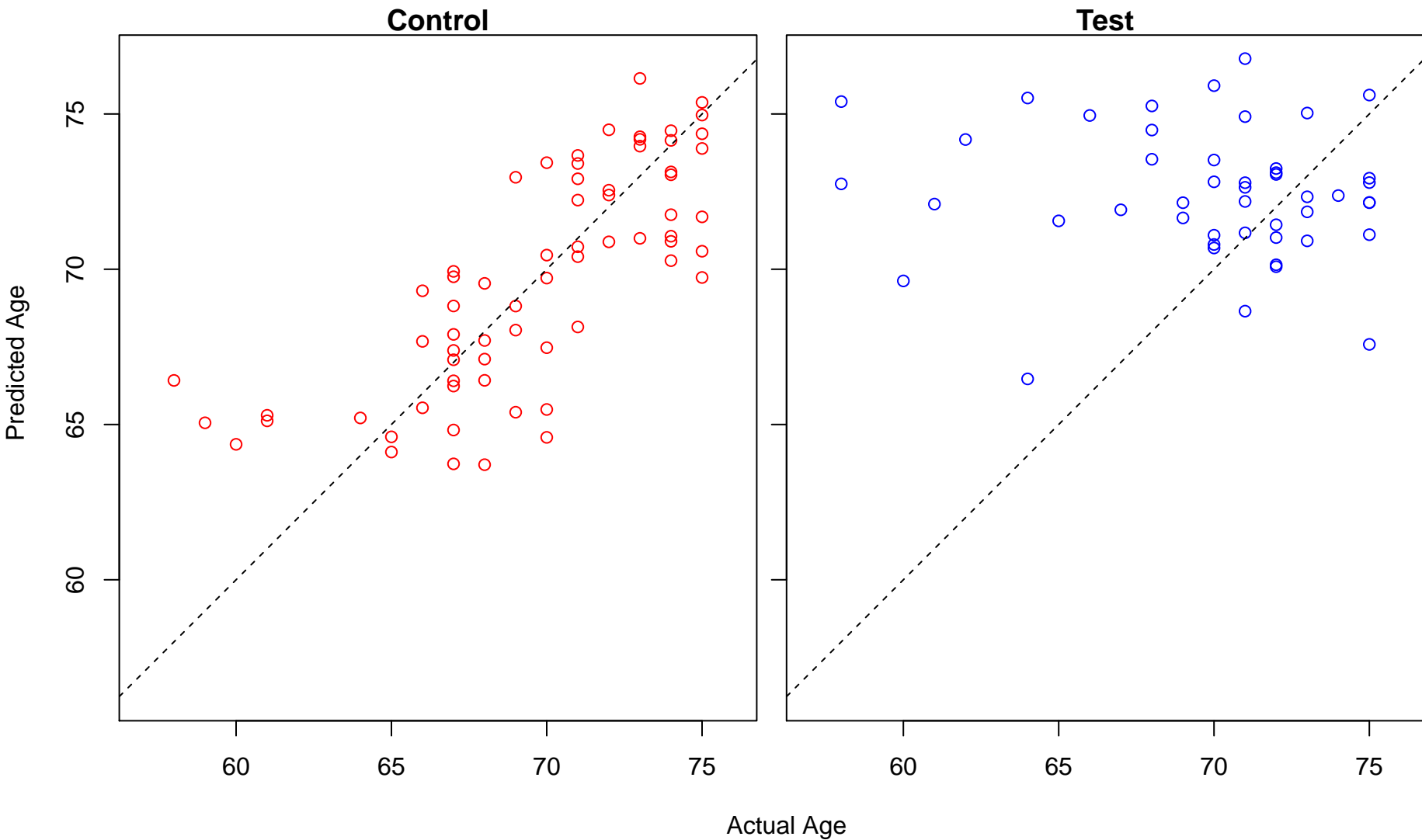


Test

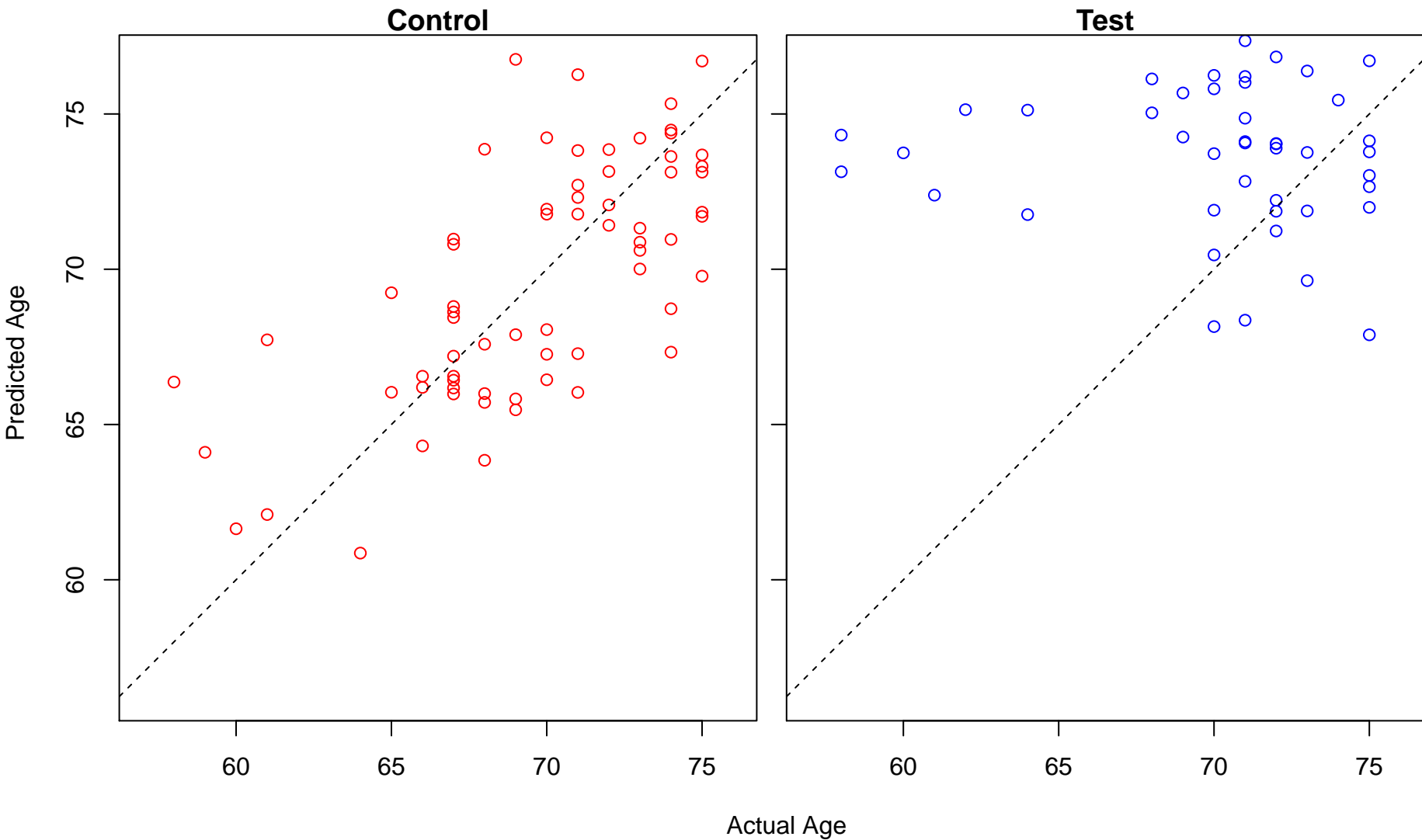


Actual Age

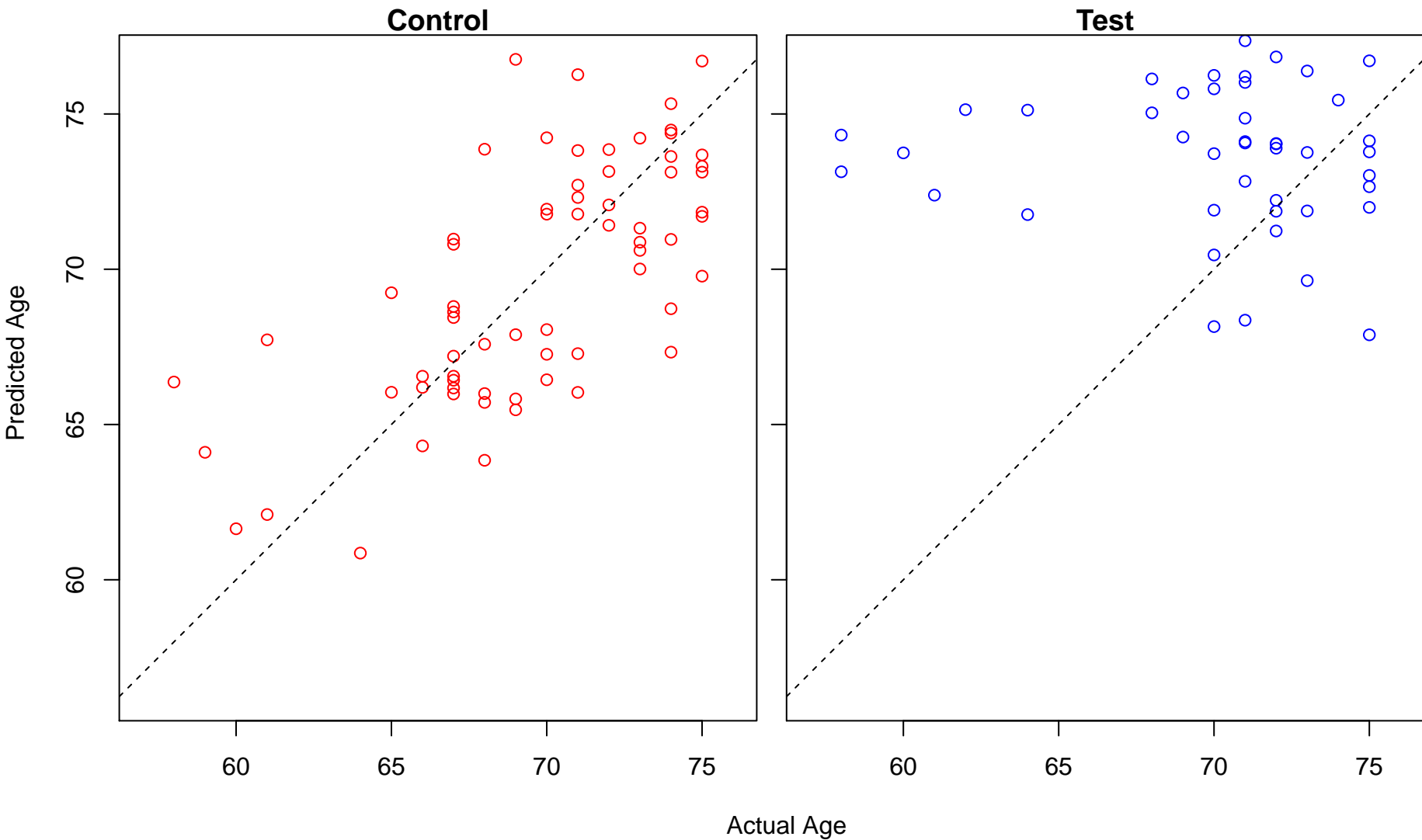
inflammatory response (Score: 2.160483)



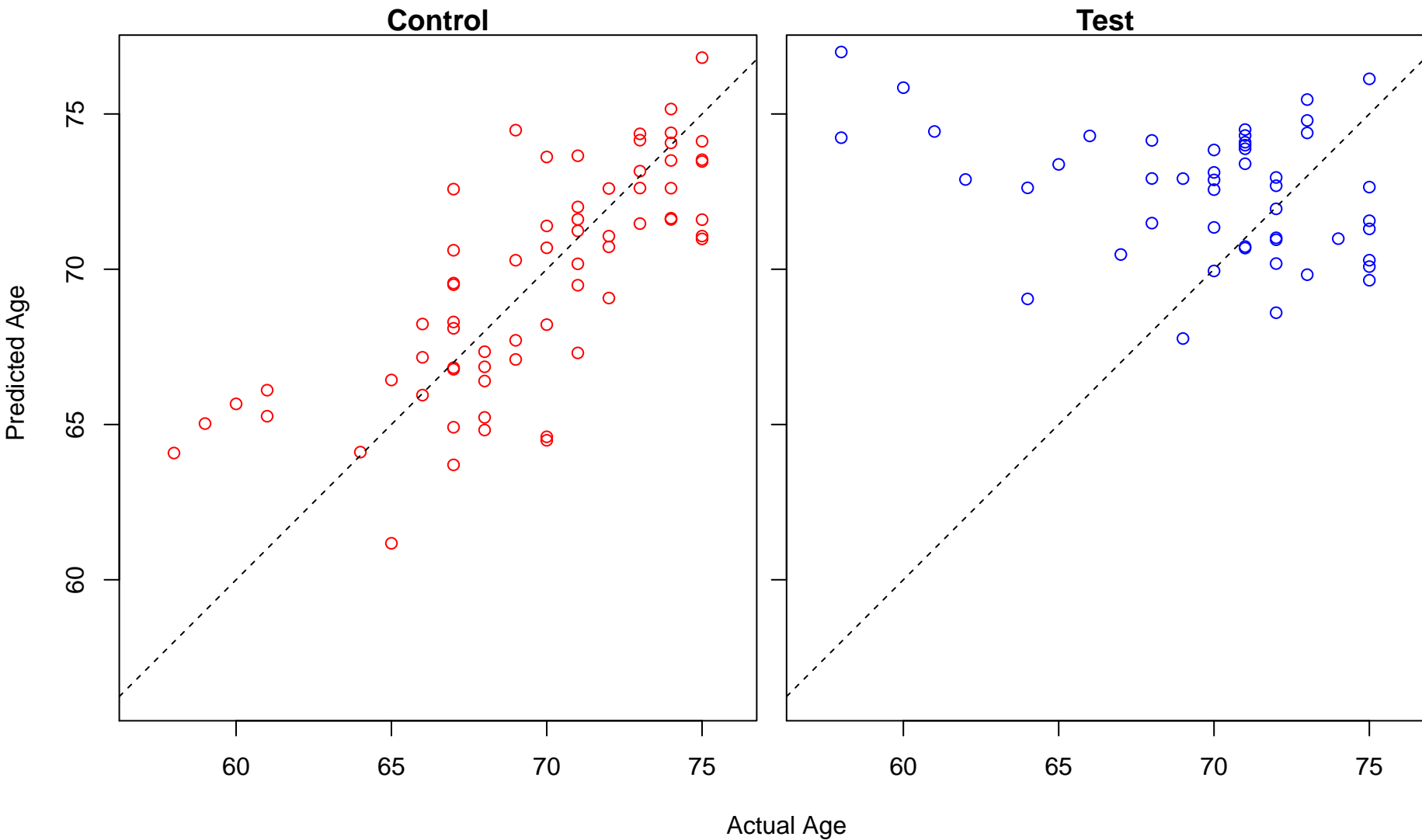
carbohydrate homeostasis (Score: 2.154508)



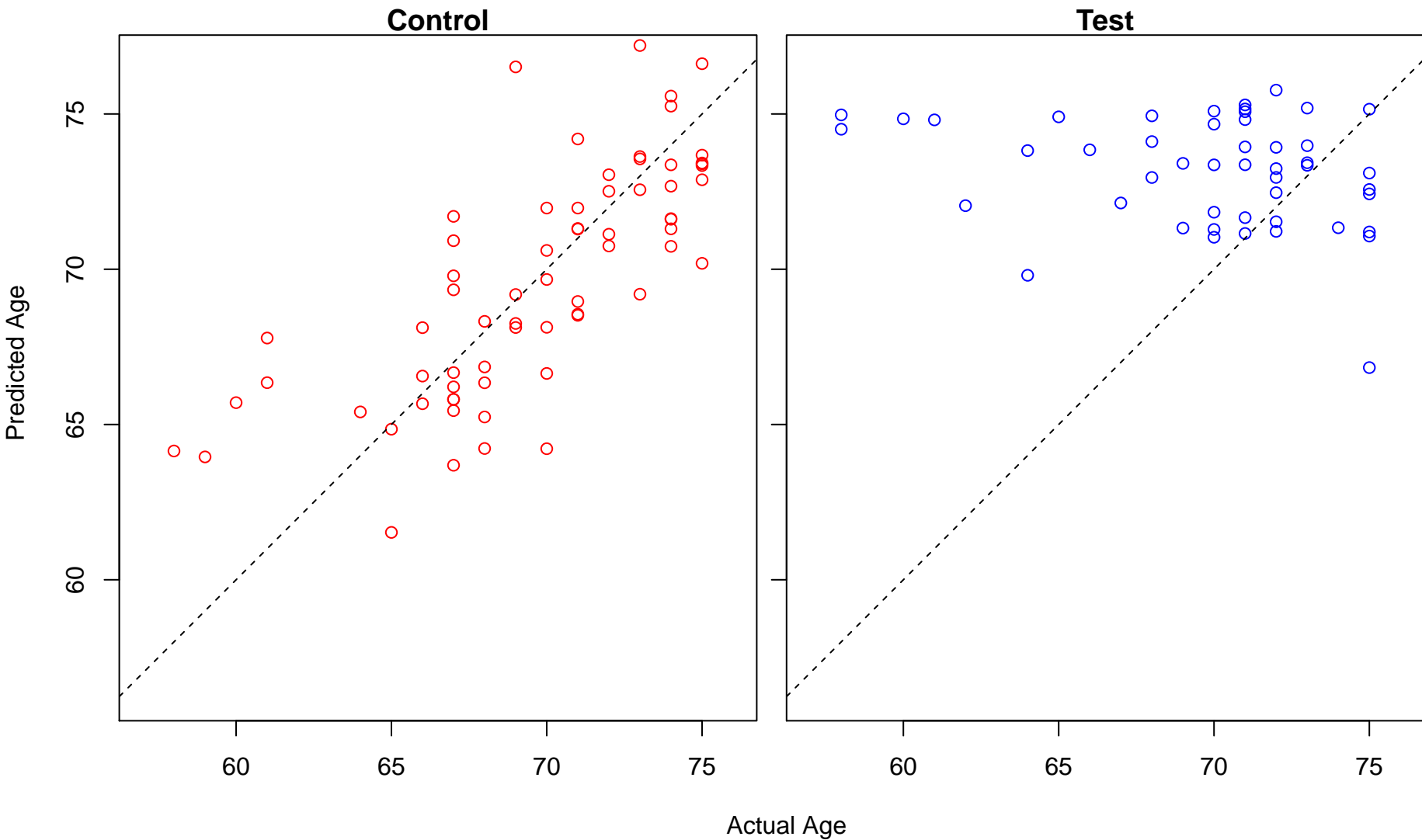
glucose homeostasis (Score: 2.154508)



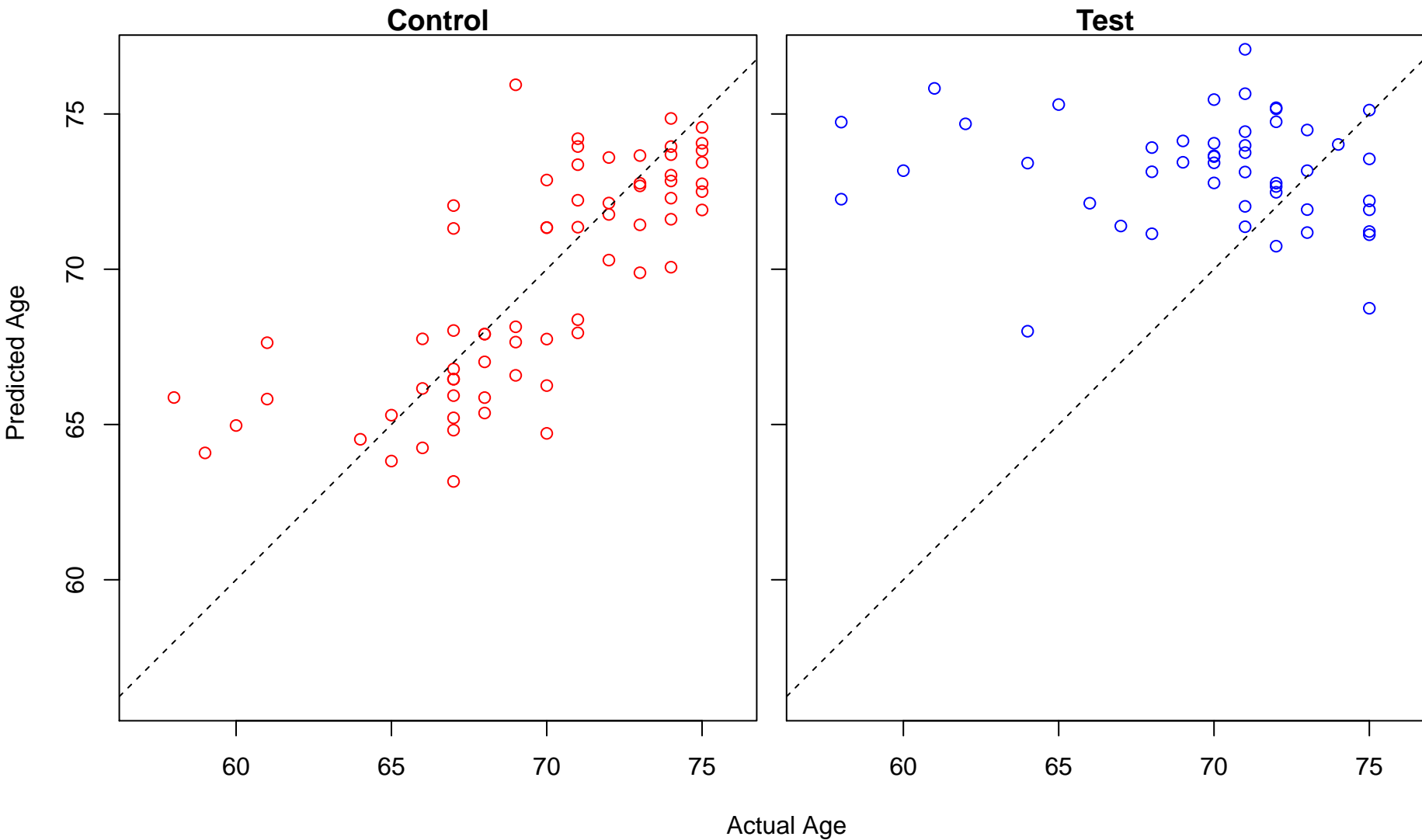
antigen processing and presentation of exogenous peptide antigen via MHC class II (Score: 2.15332)



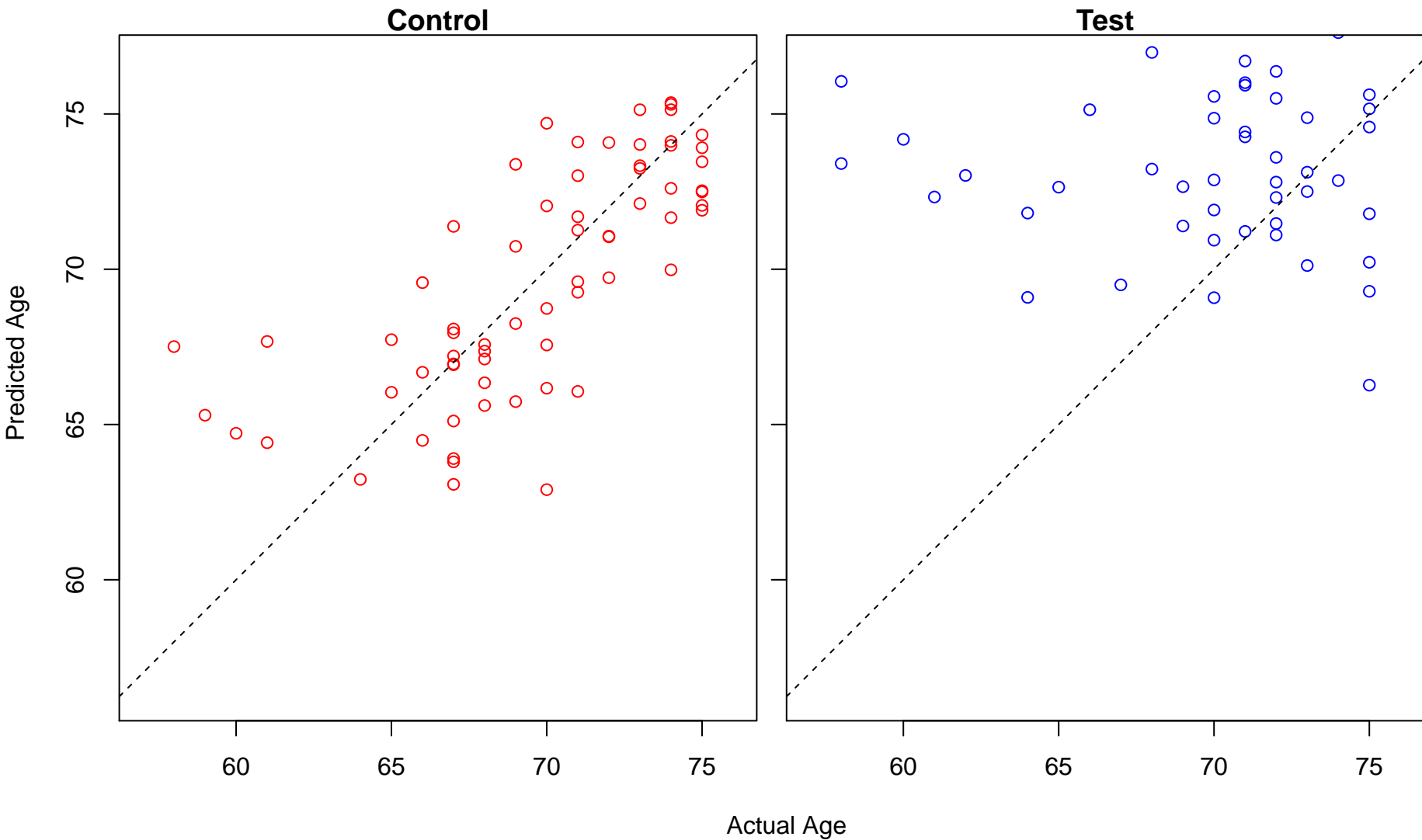
antigen receptor-mediated signaling pathway (Score: 2.151869)



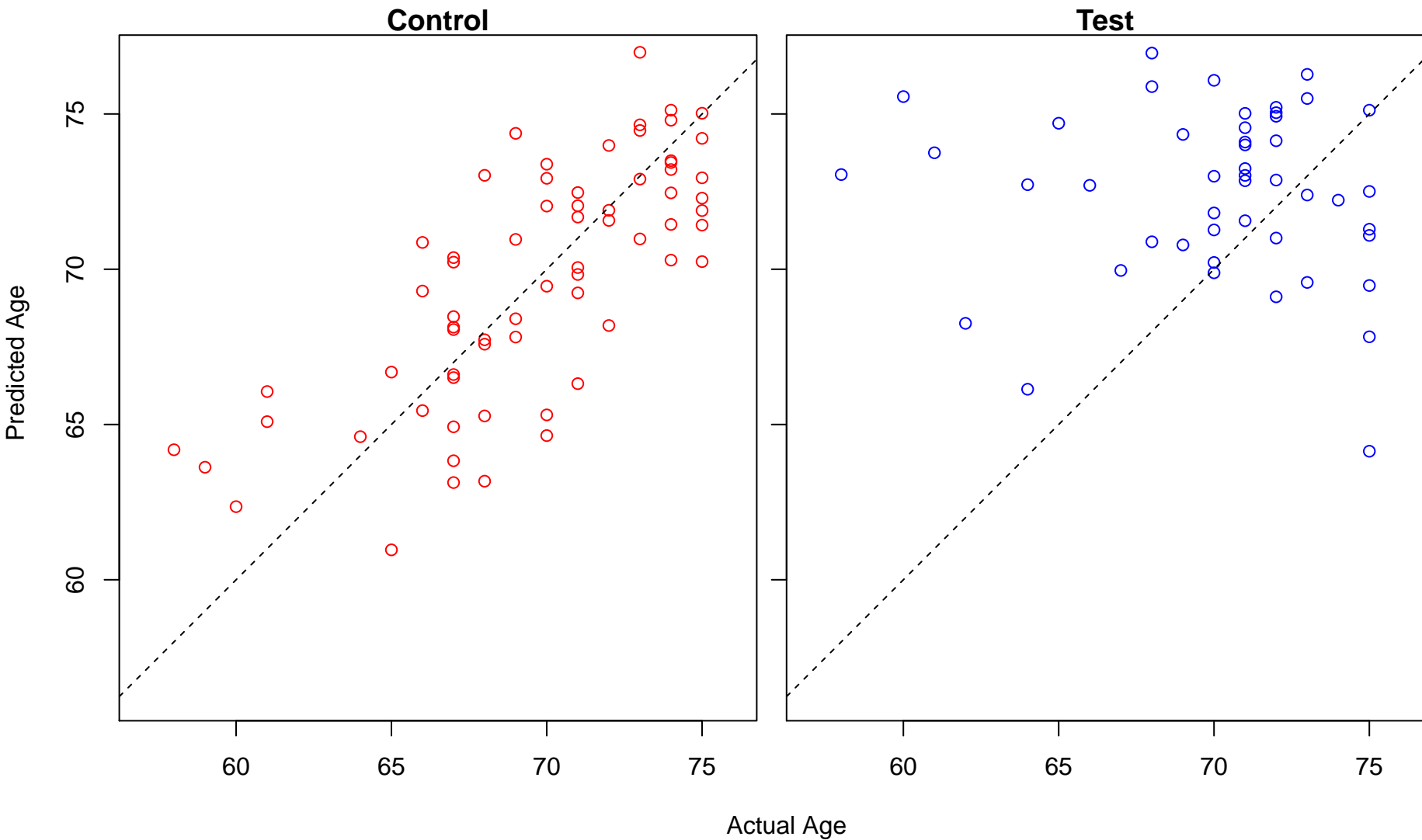
intracellular protein transport (Score: 2.151866)



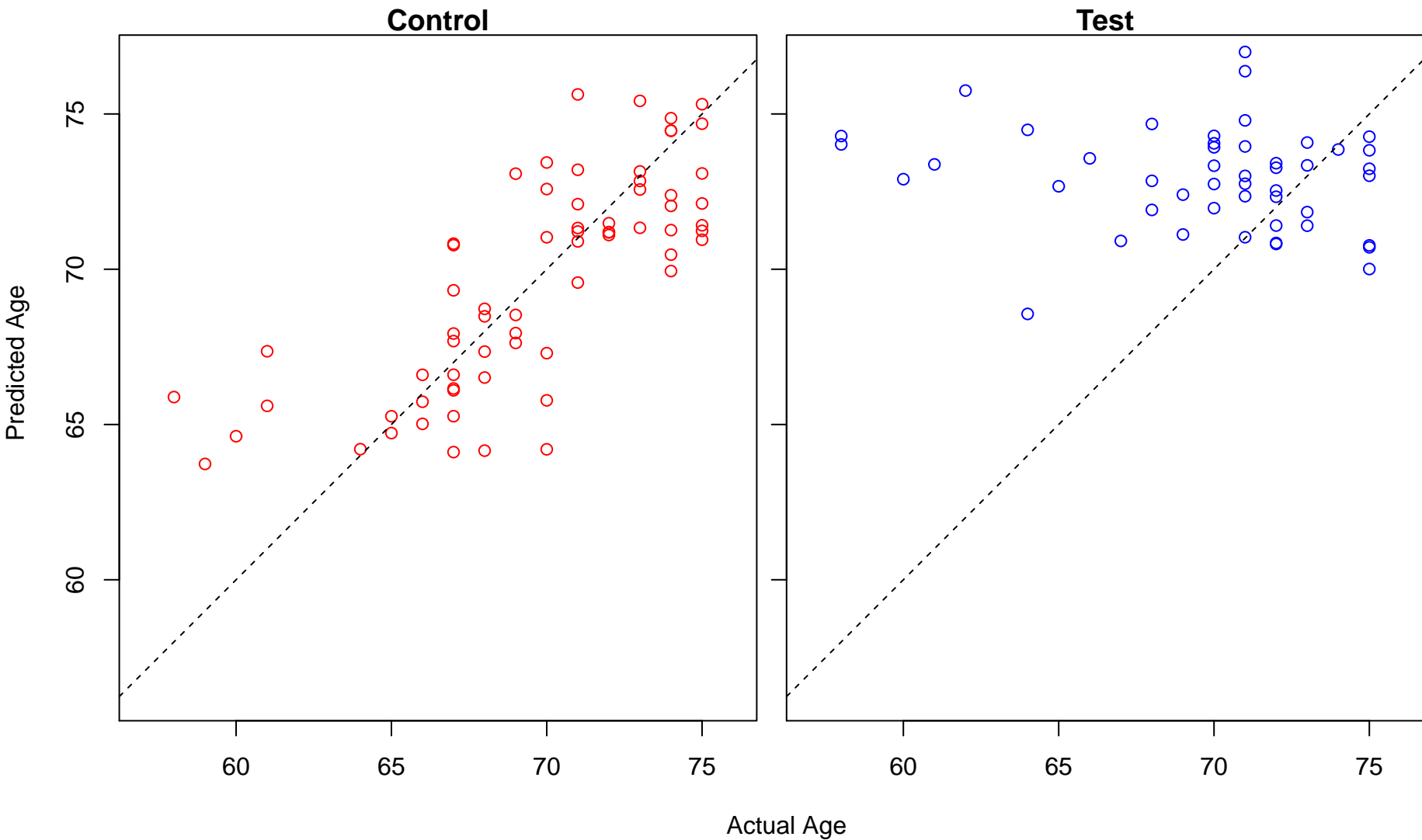
leukocyte aggregation (Score: 2.147981)



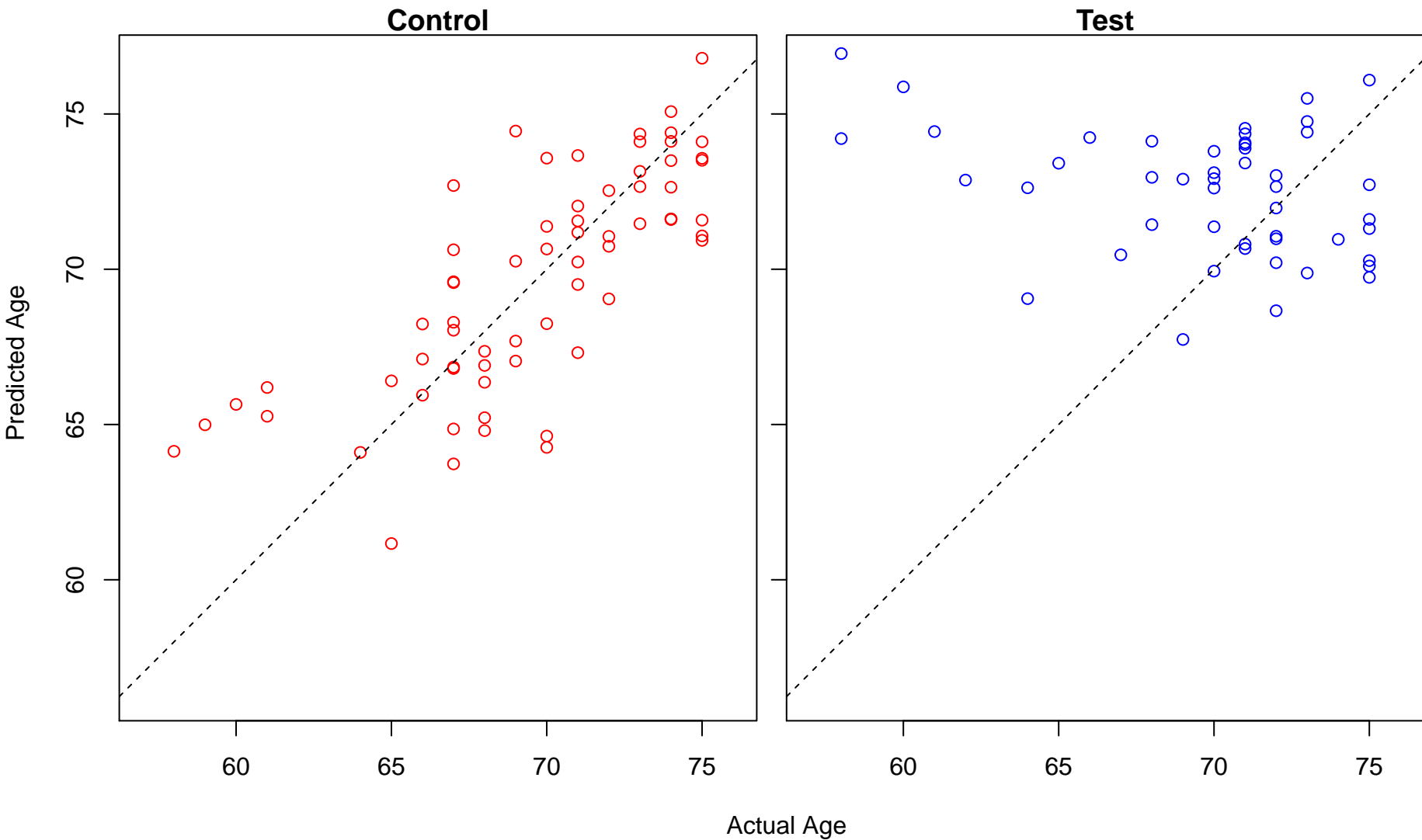
adaptive immune response (Score: 2.147514)



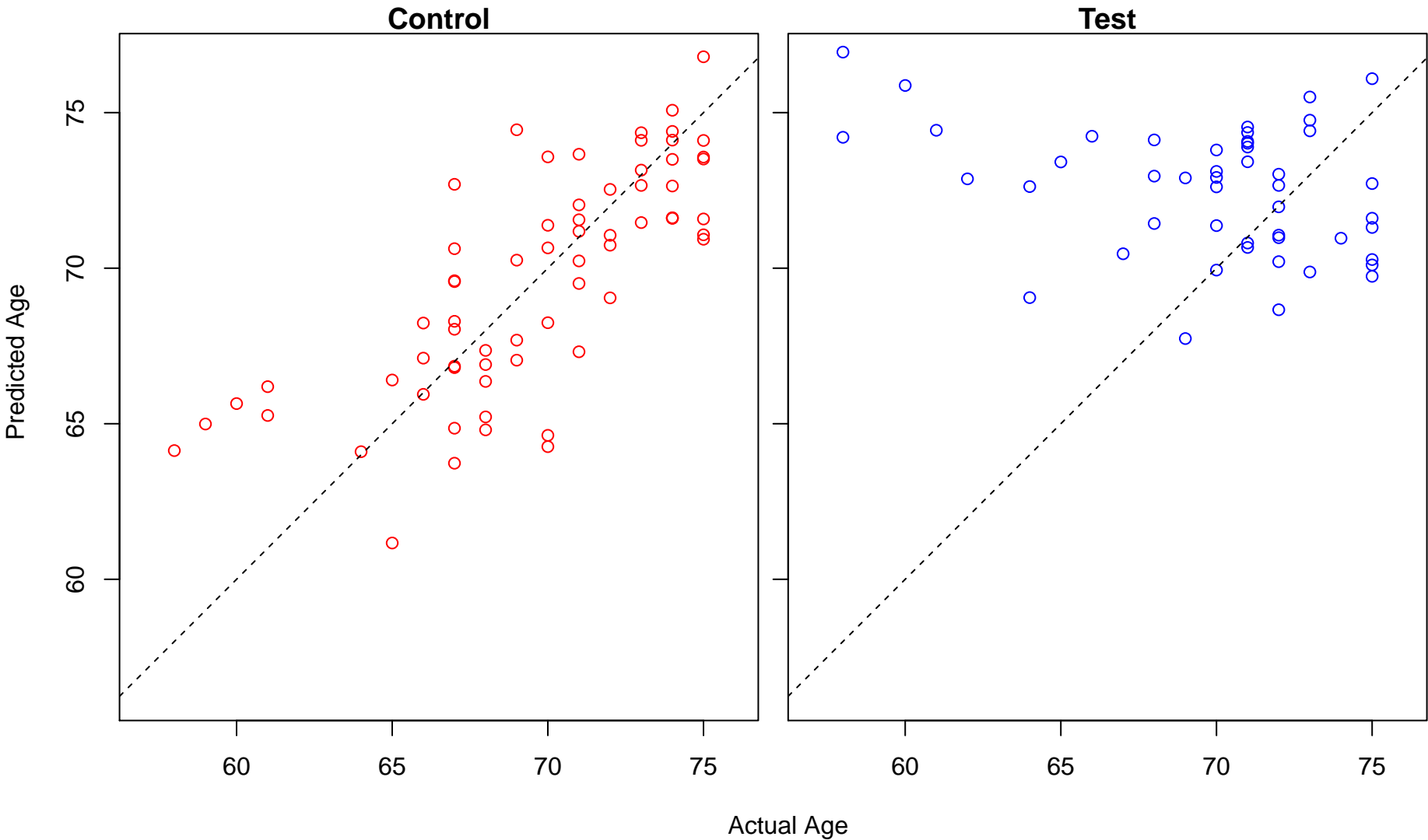
positive regulation of organelle organization (Score: 2.146433)



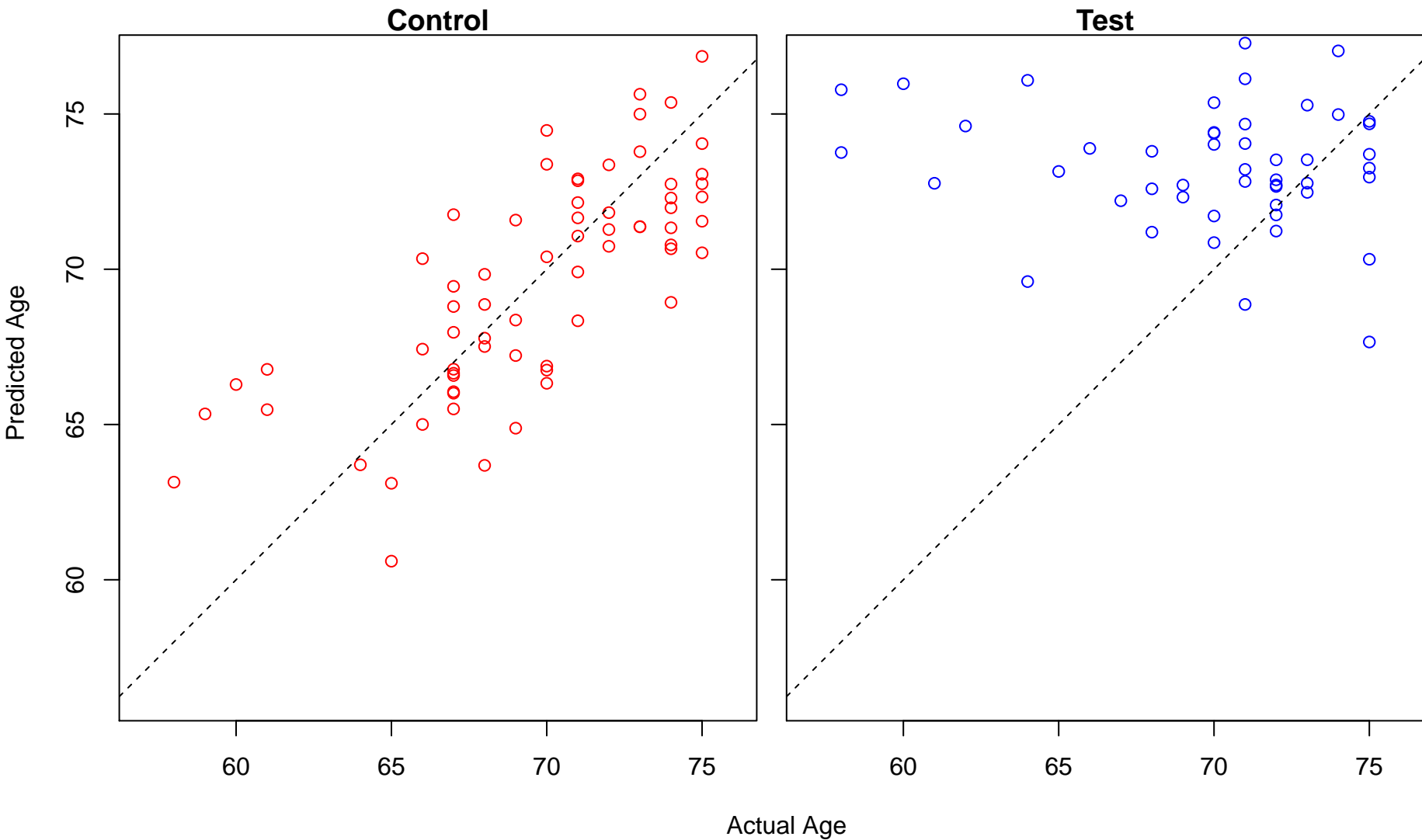
antigen processing and presentation of peptide antigen via MHC class II (Score: 2.139064)



antigen processing and presentation of peptide or polysaccharide antigen via MHC class II (Score: 2.13)

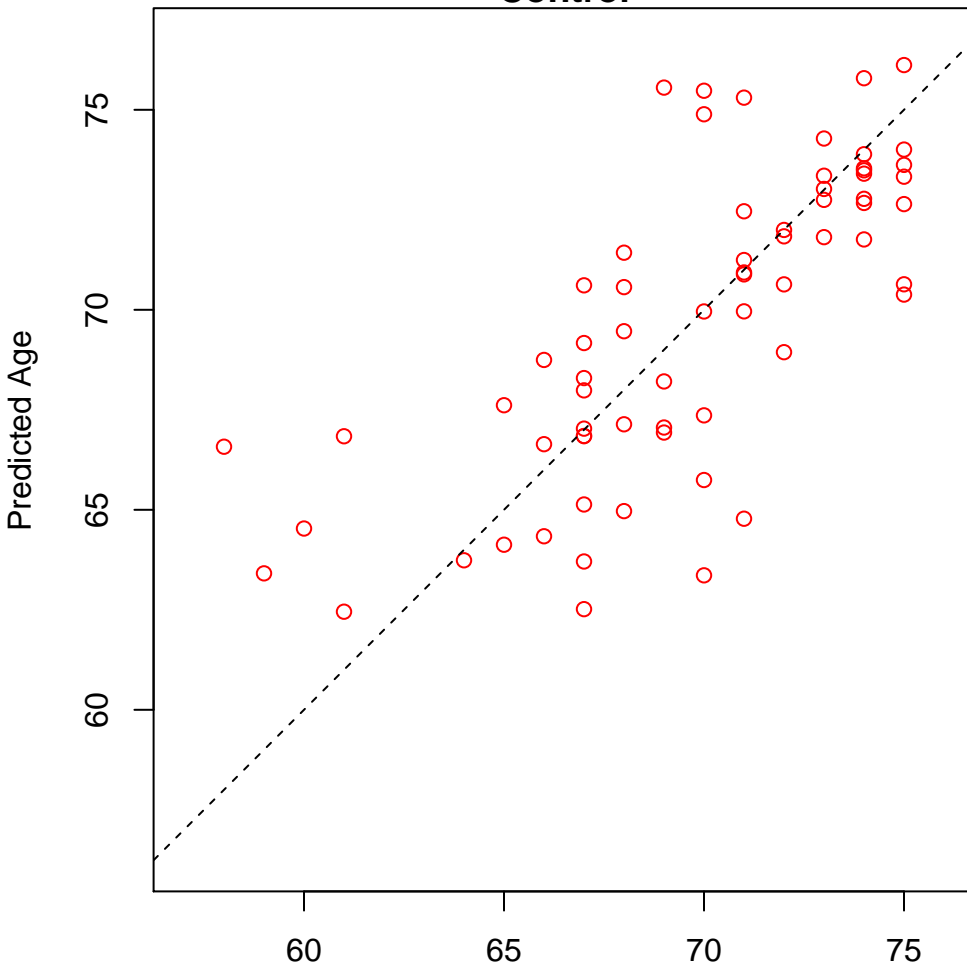


peptidyl-serine phosphorylation (Score: 2.135021)

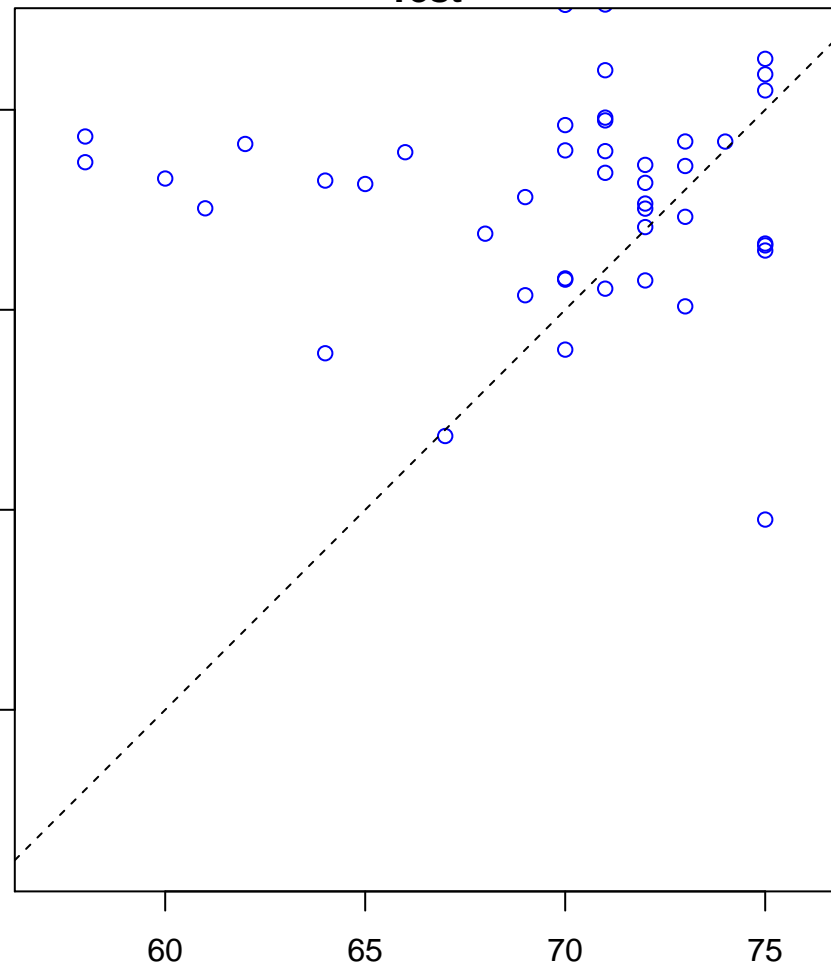


lymphocyte activation (Score: 2.134628)

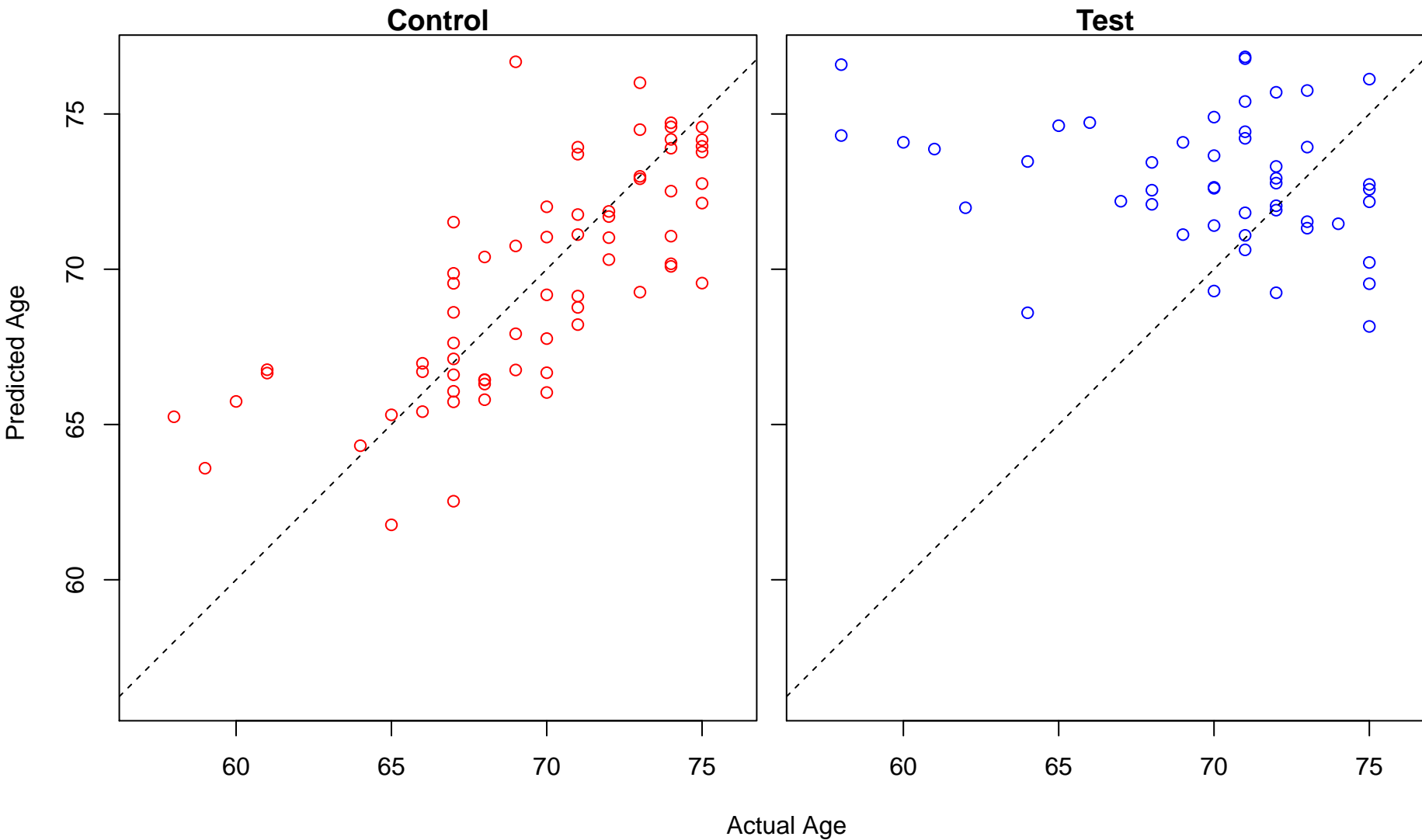
Control



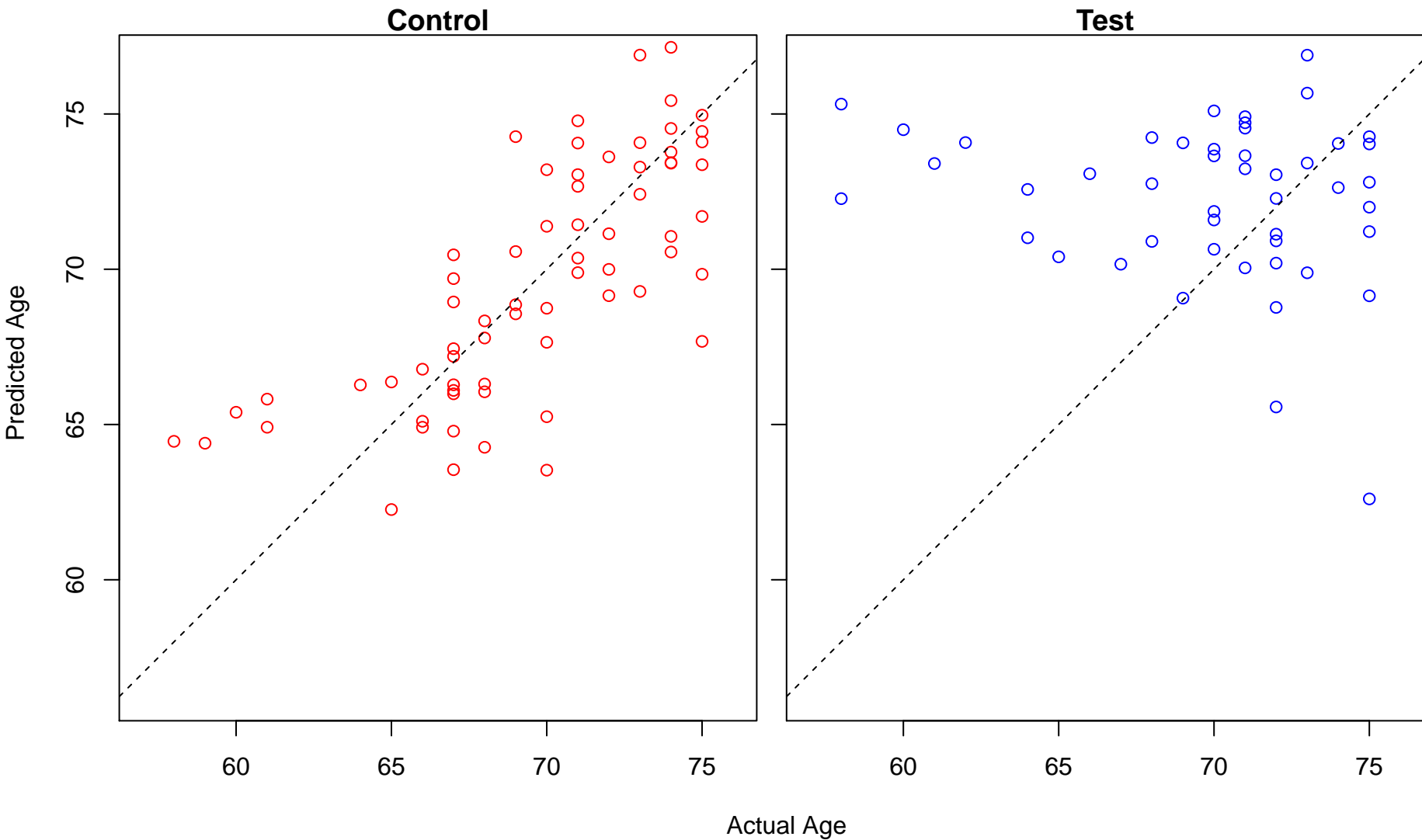
Test



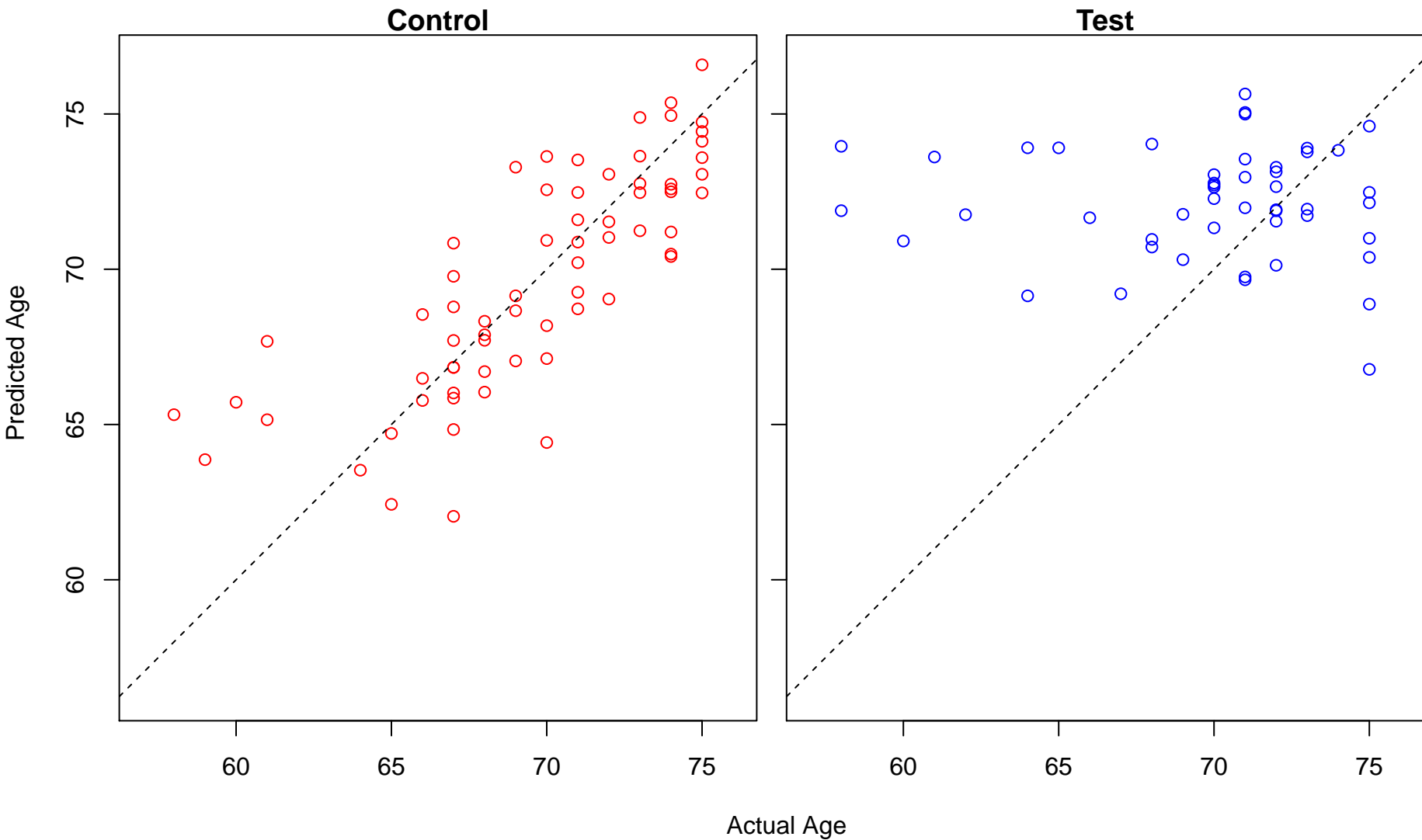
regulation of cell adhesion (Score: 2.134210)



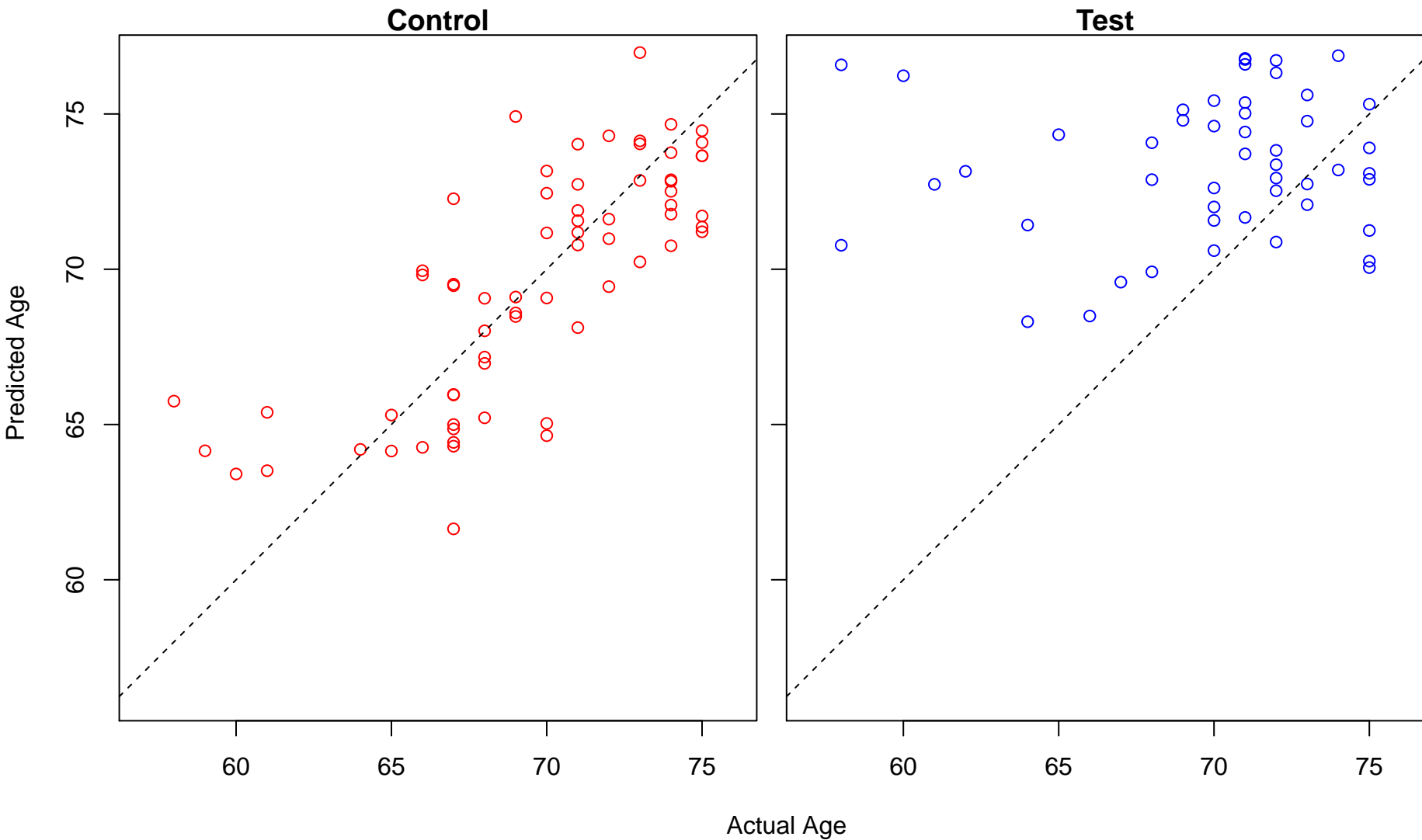
cellular response to decreased oxygen levels (Score: 2.130378)



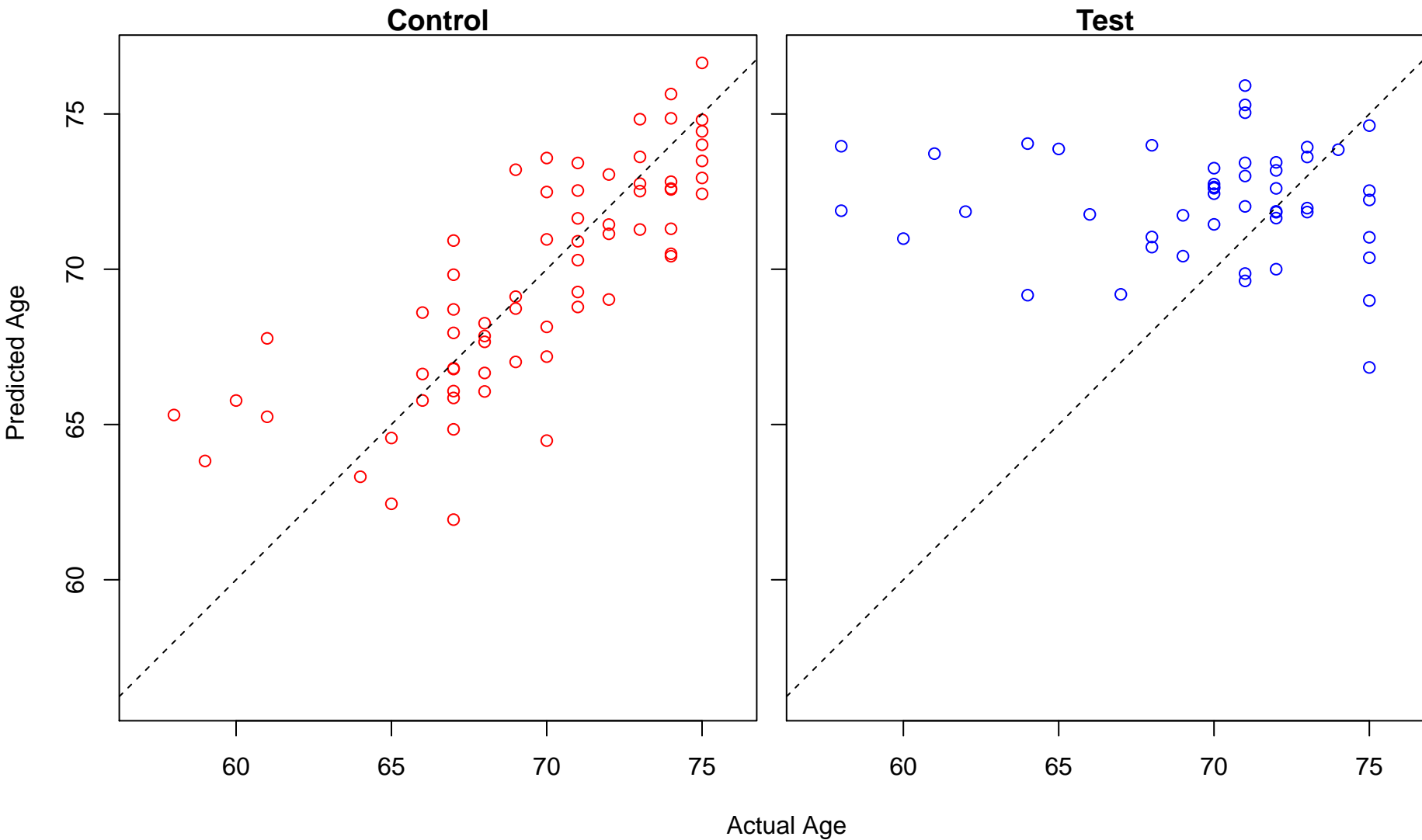
signal transduction by protein phosphorylation (Score: 2.129063)



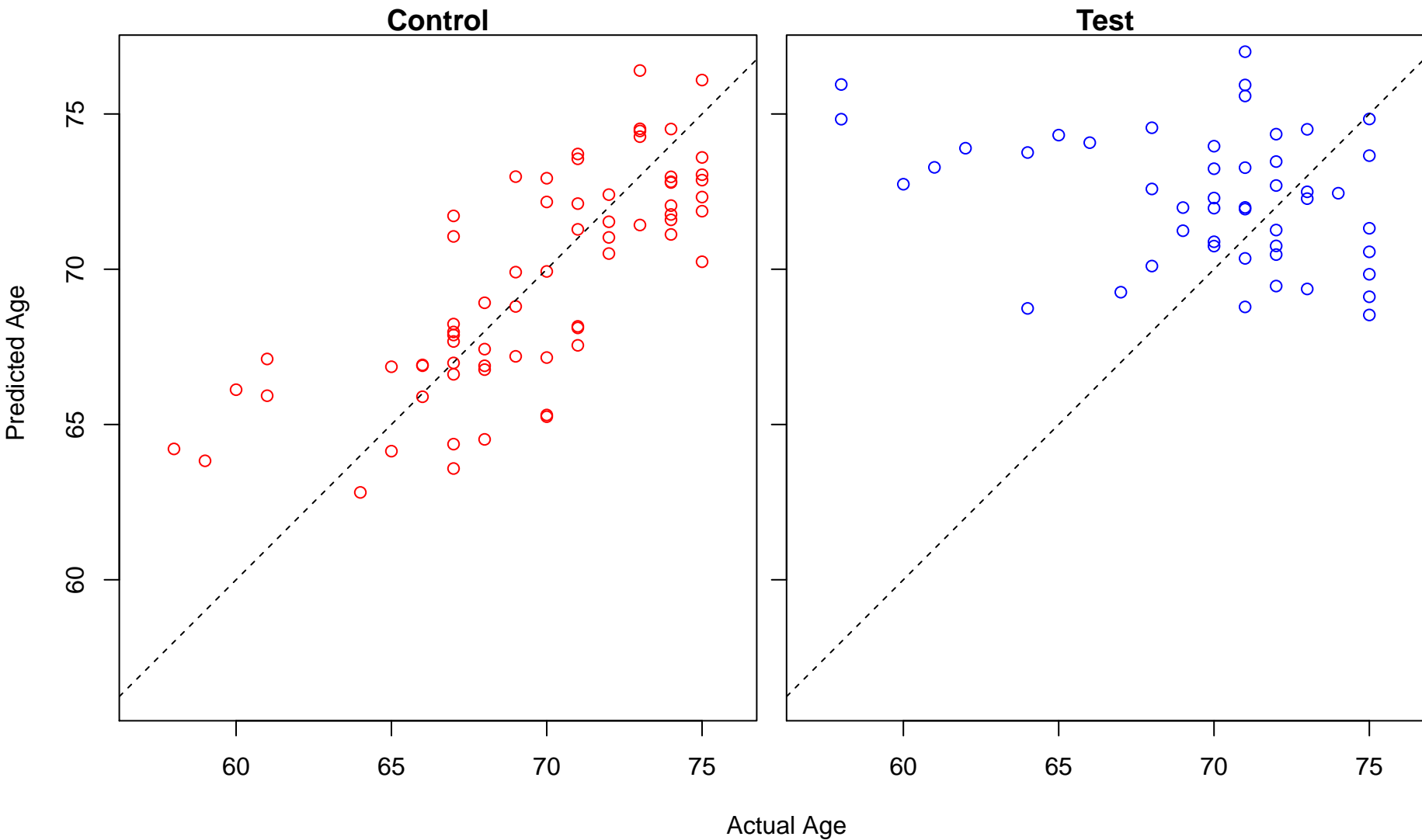
protein targeting (Score: 2.128659)



MAPK cascade (Score: 2.128302)

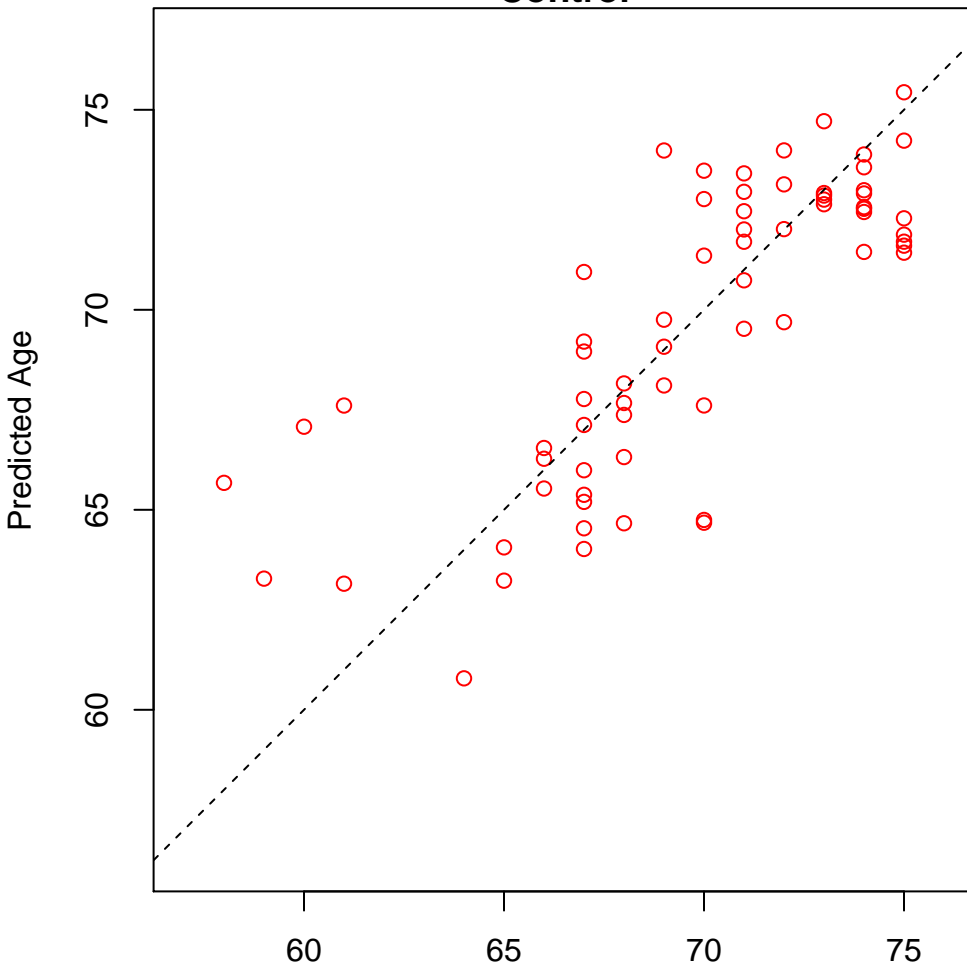


positive regulation of establishment of protein localization (Score: 2.127177)

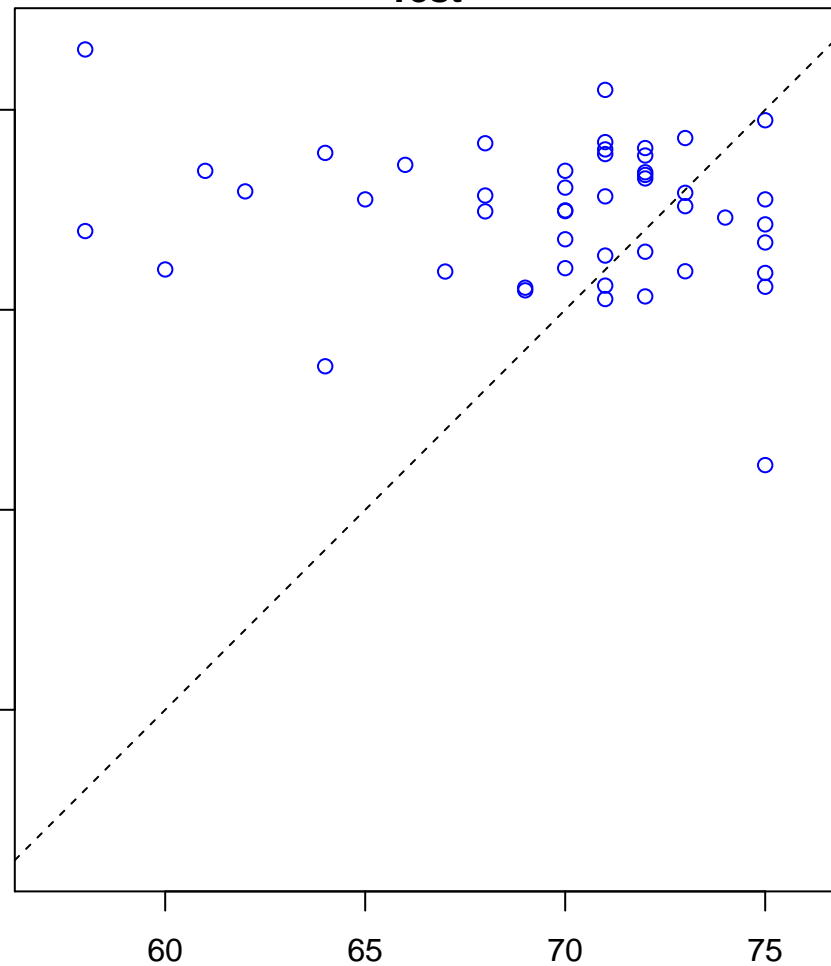


positive regulation of peptidase activity (Score: 2.126839)

Control

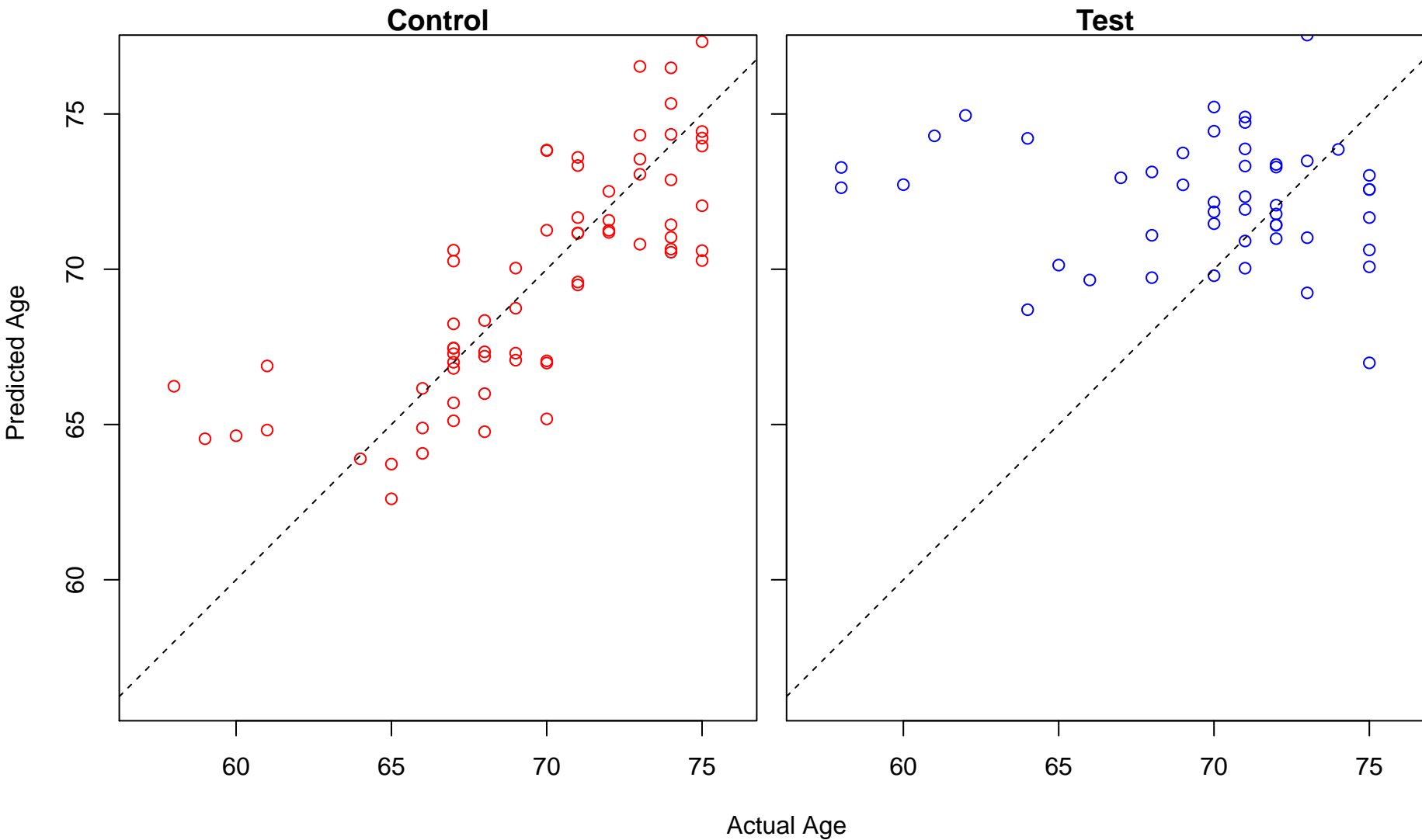


Test

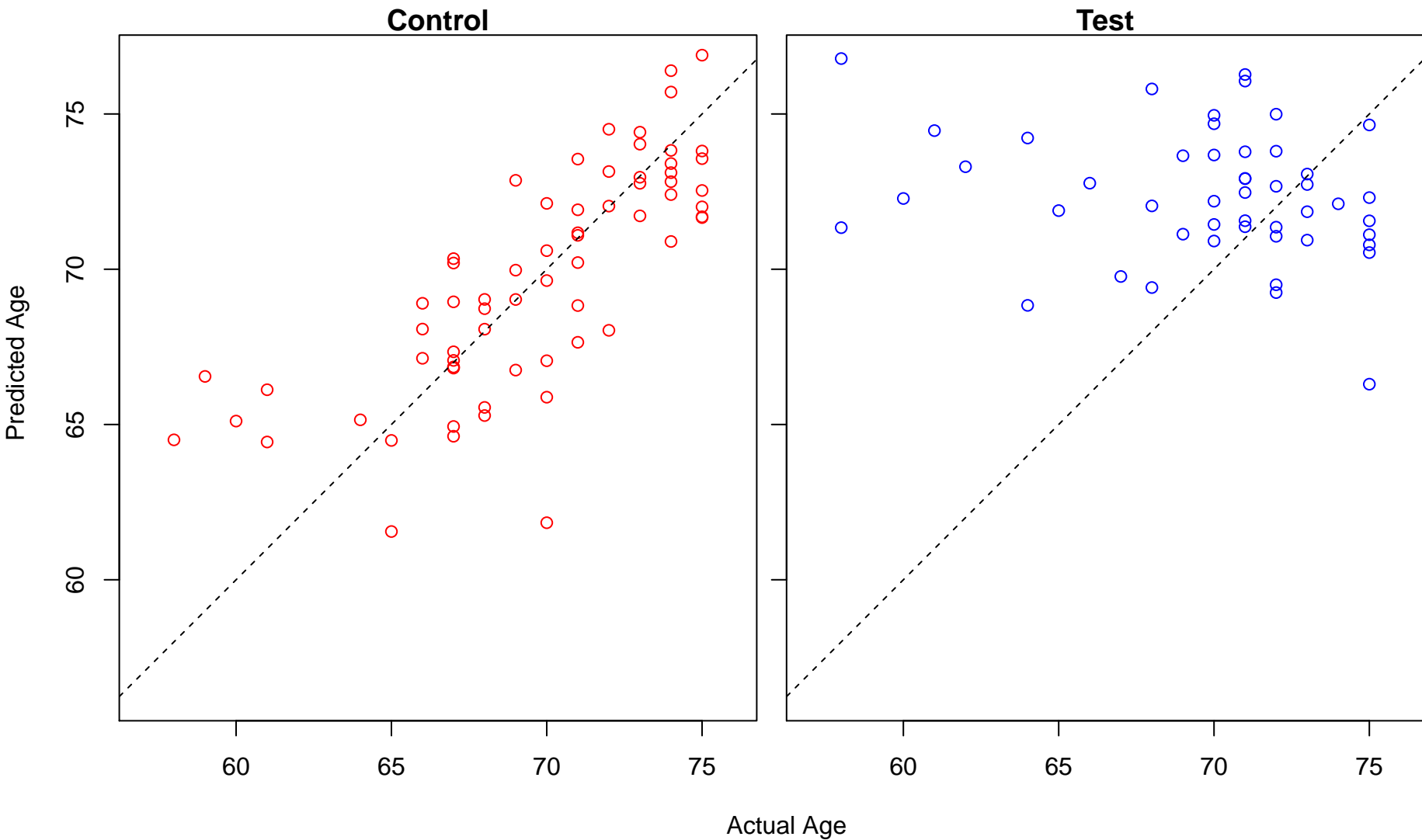


Actual Age

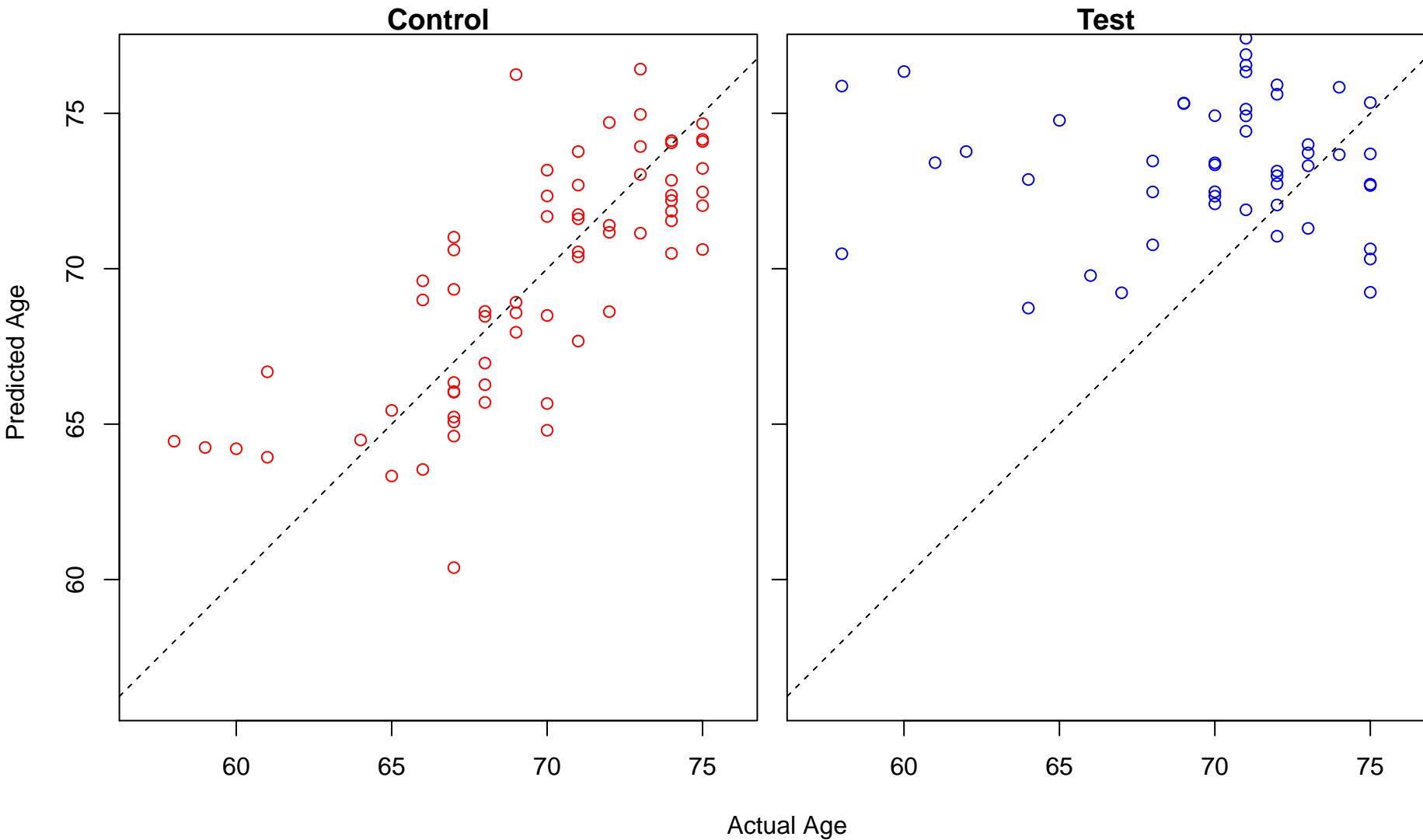
regulation of organelle assembly (Score: 2.125304)



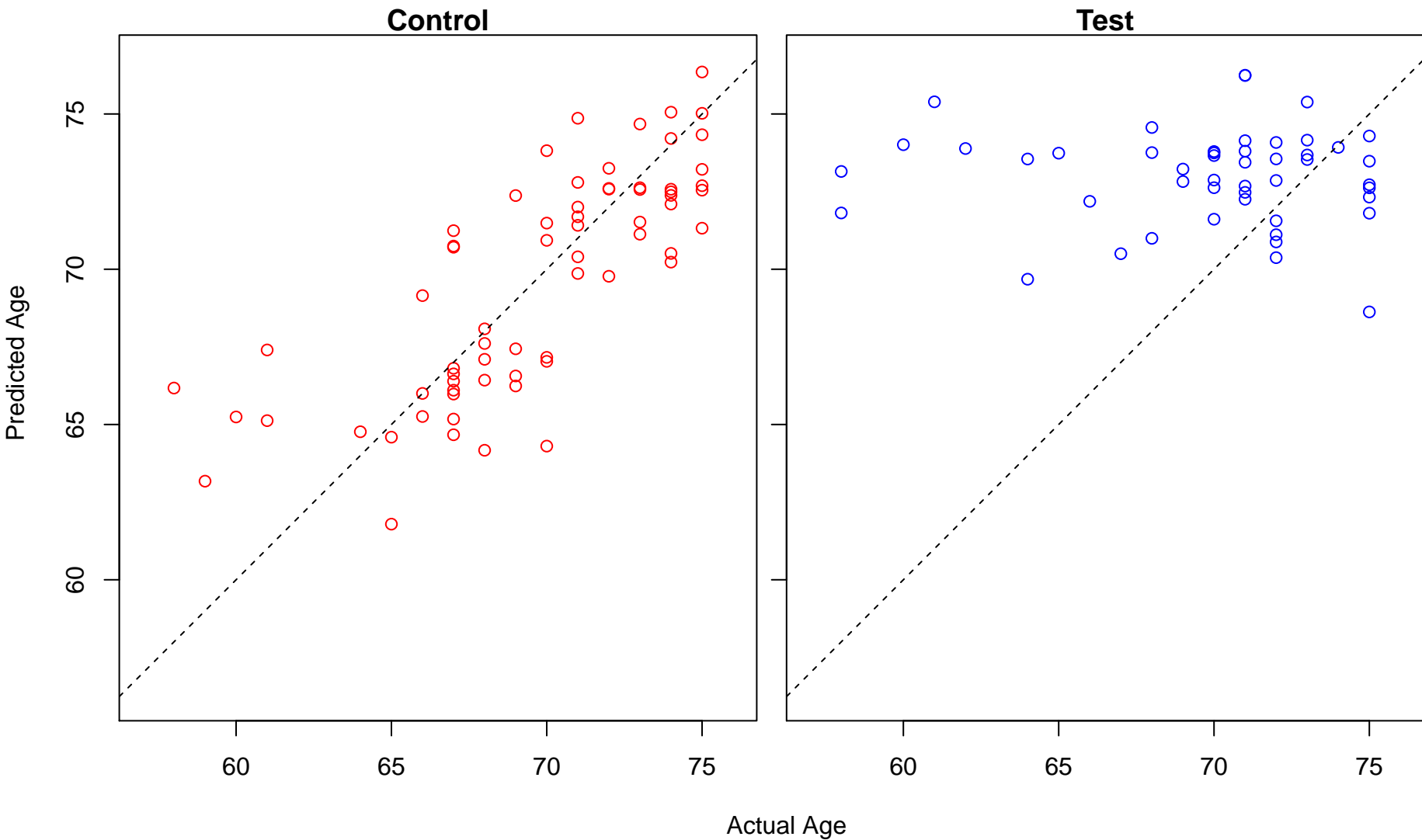
positive regulation of leukocyte differentiation (Score: 2.123266)



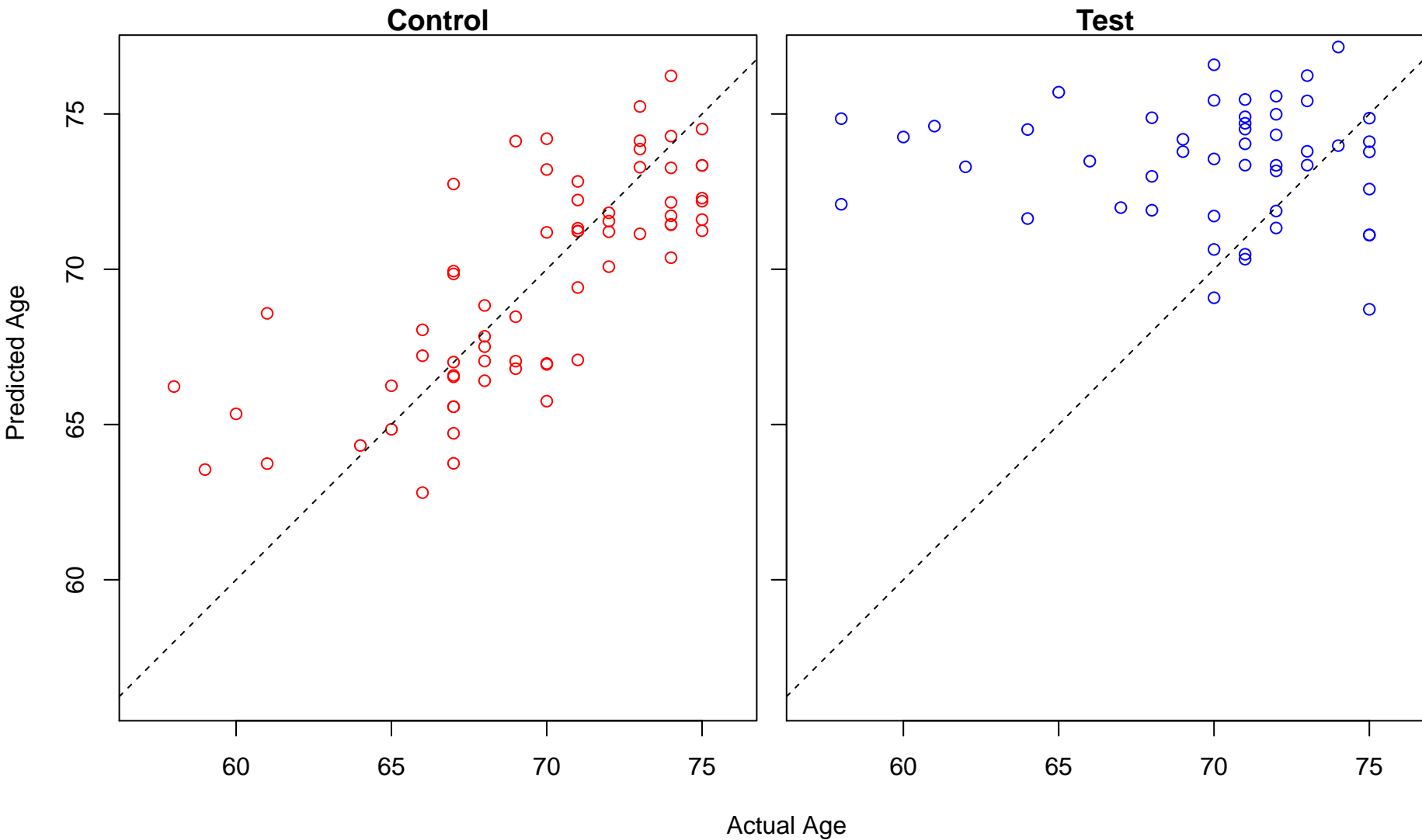
establishment of protein localization to organelle (Score: 2.123134)



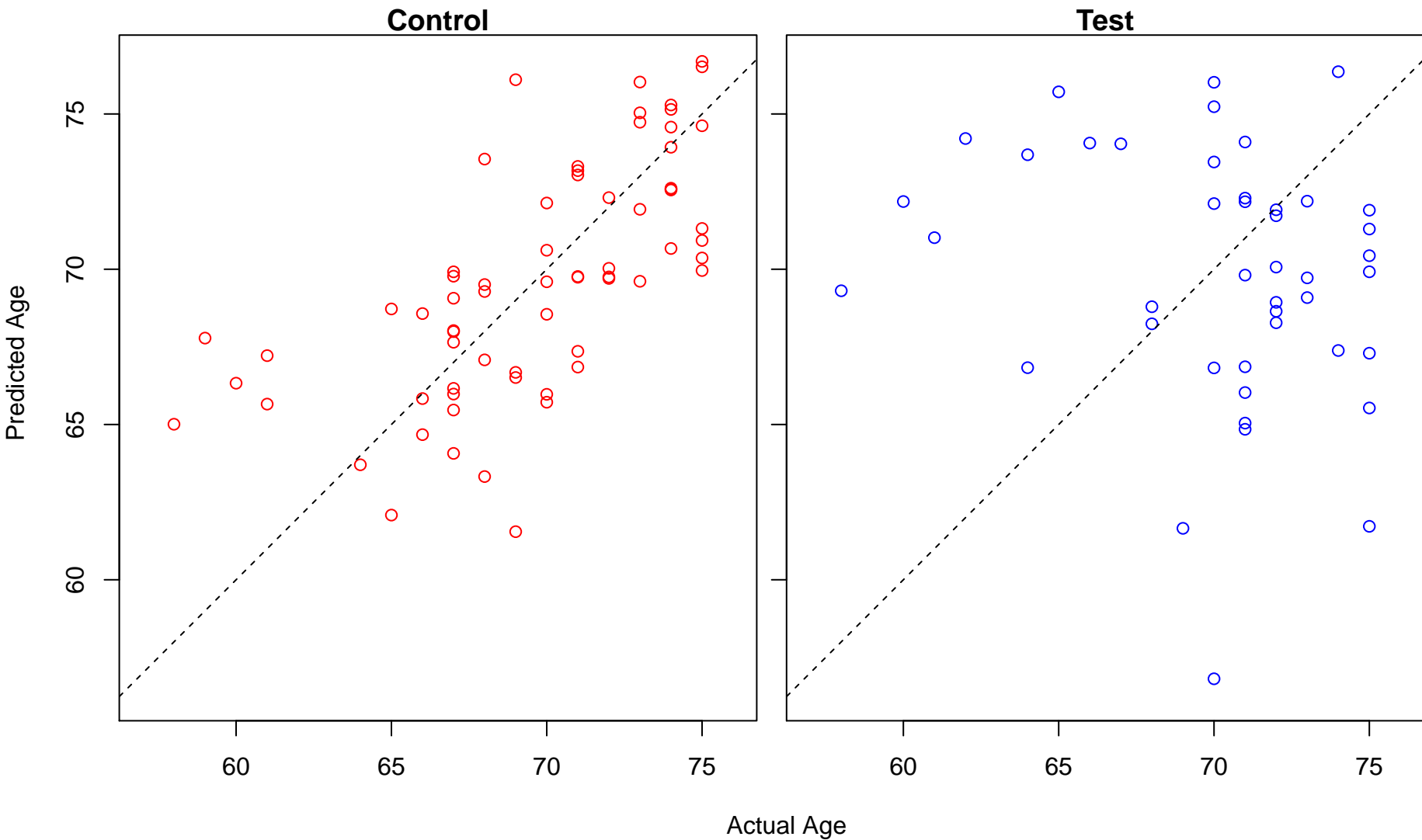
positive regulation of cell cycle (Score: 2.121809)



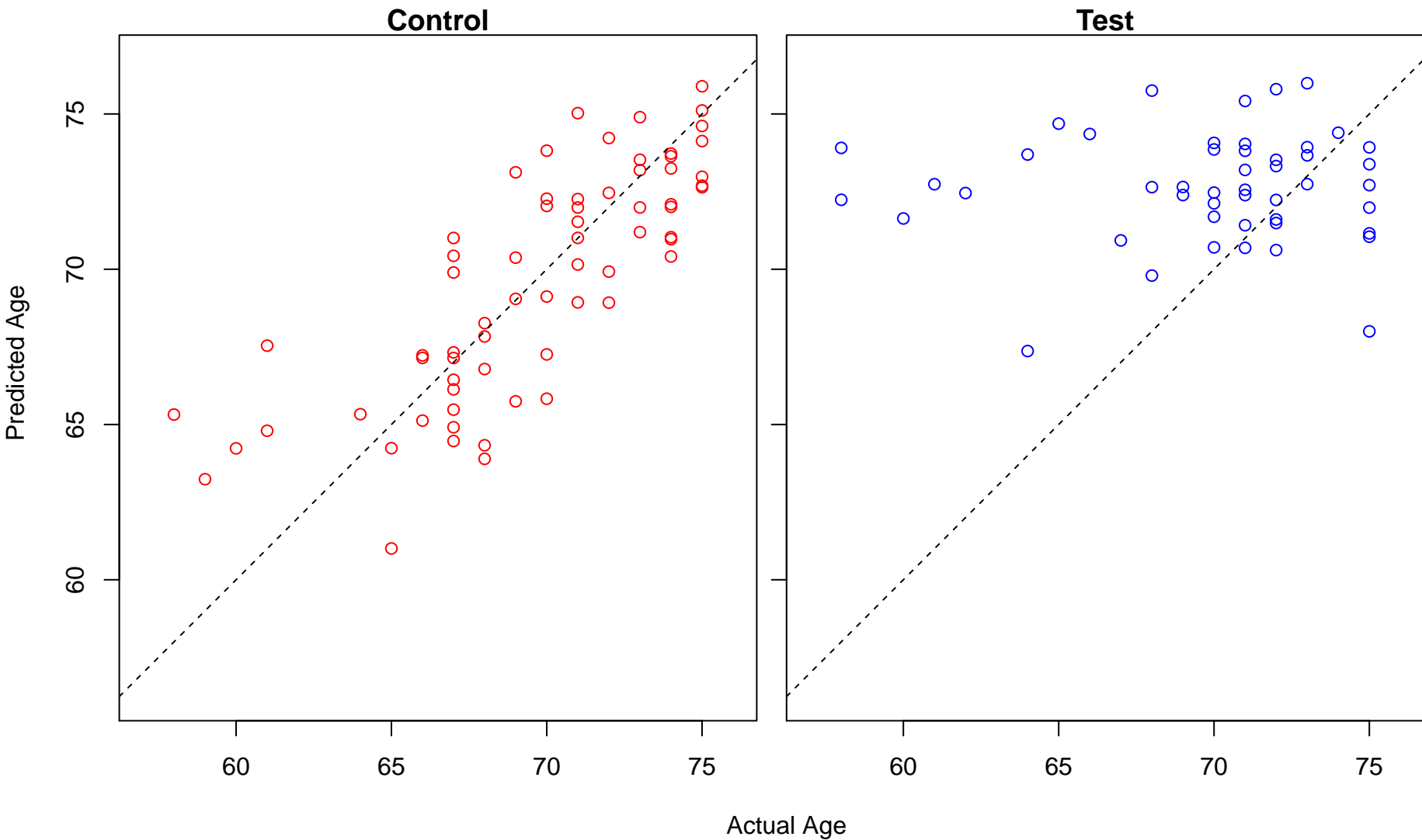
double-strand break repair (Score: 2.118550)



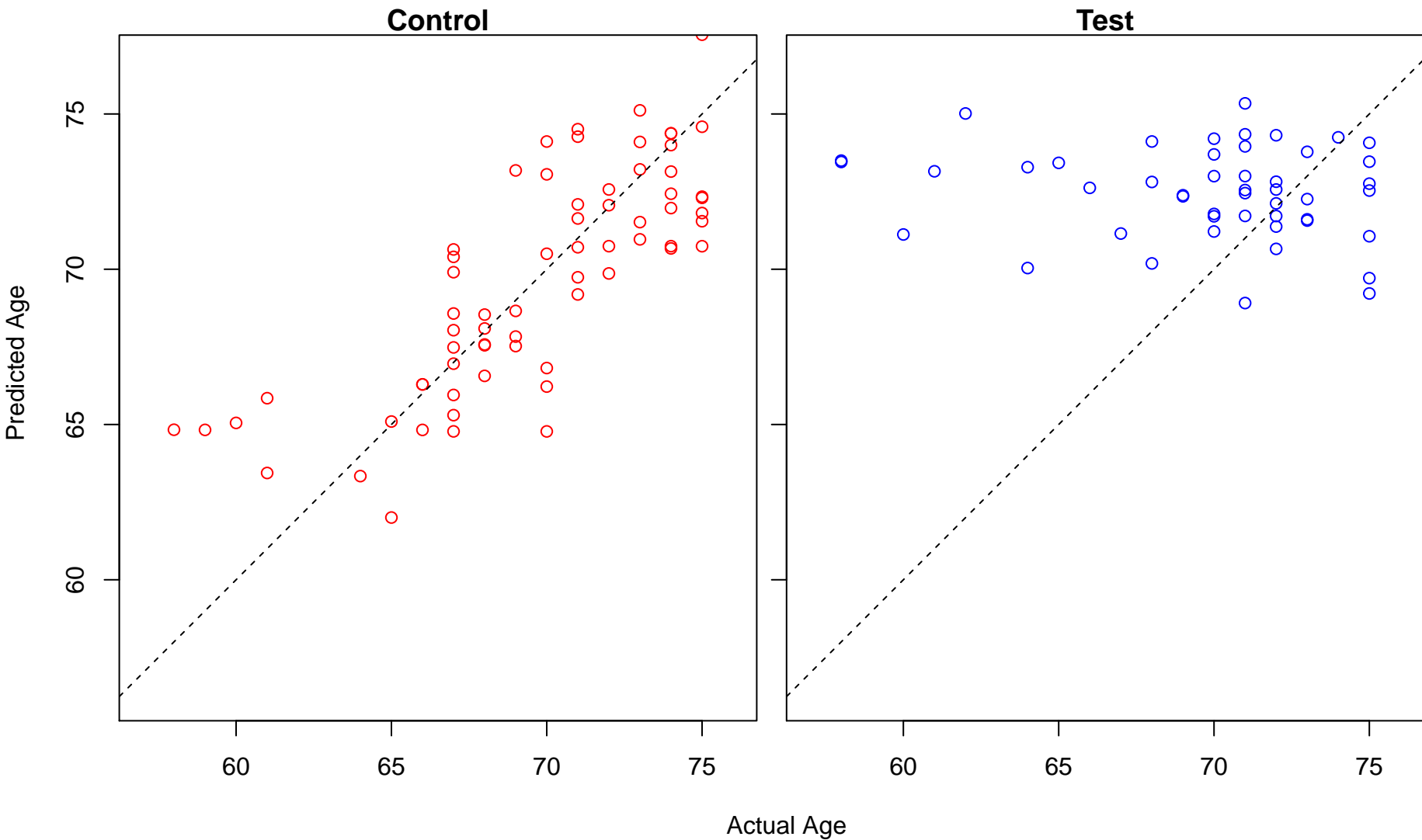
regulation of extracellular matrix organization (Score: 2.117117)



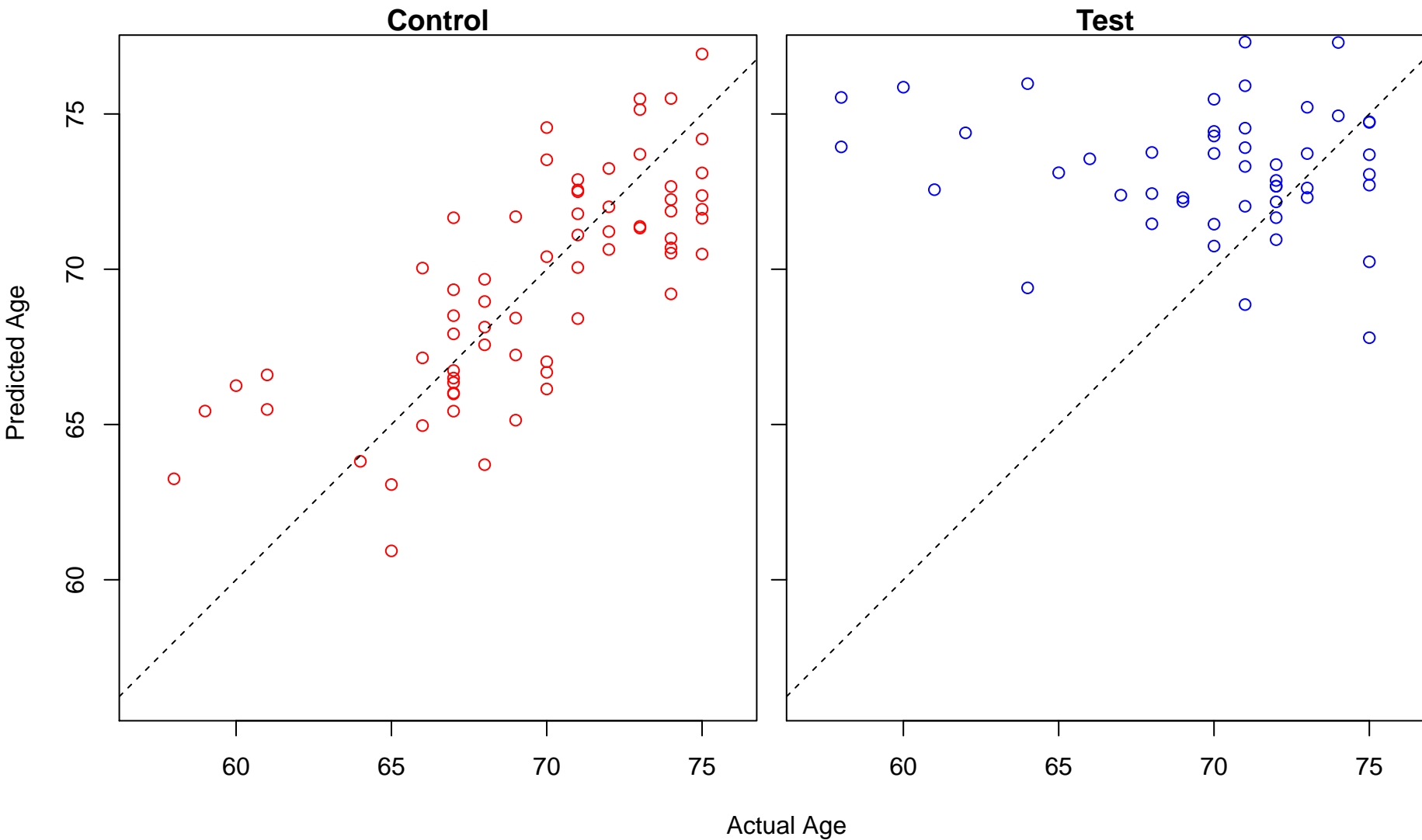
regulation of cellular ketone metabolic process (Score: 2.116660)



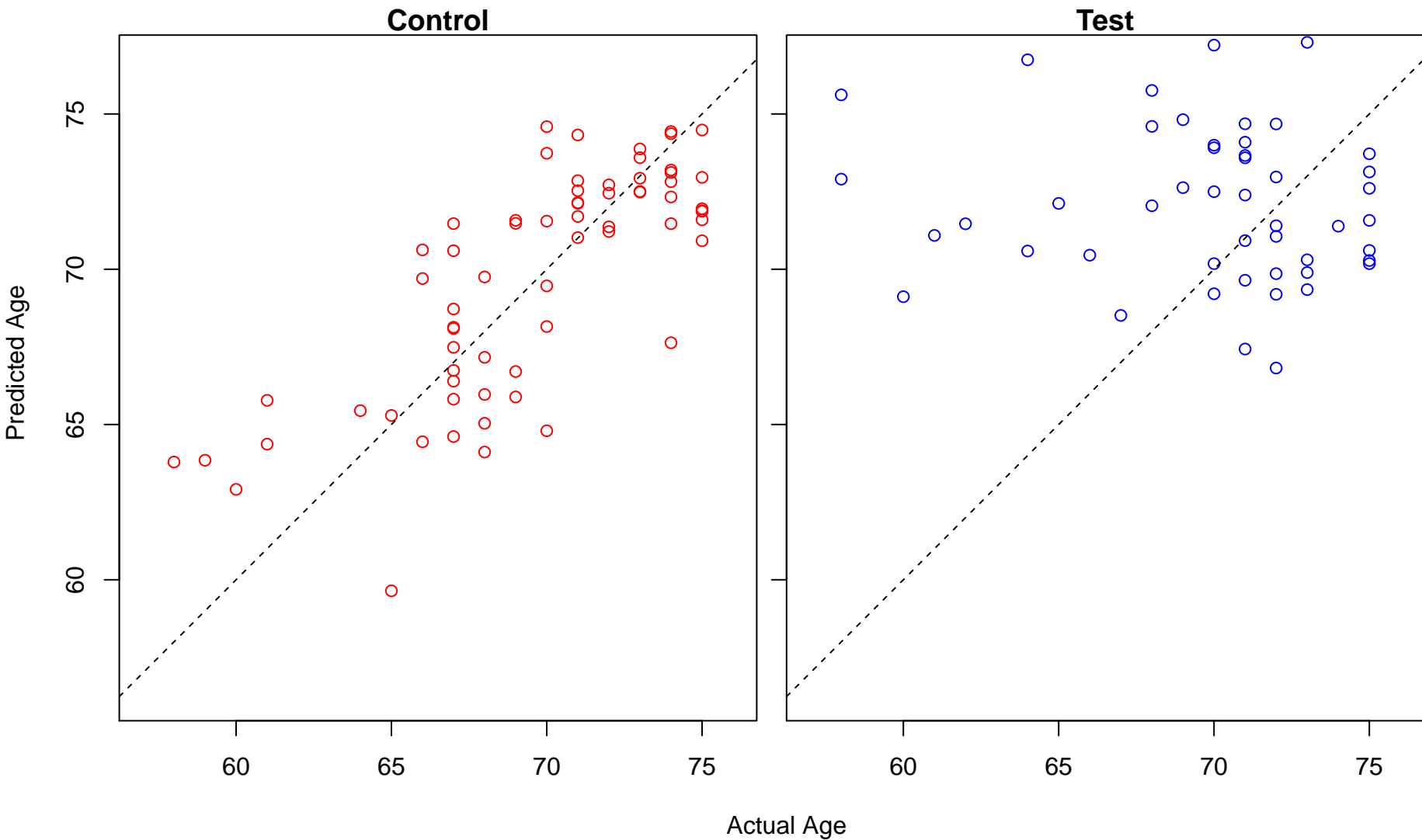
regulation of protein complex assembly (Score: 2.115716)



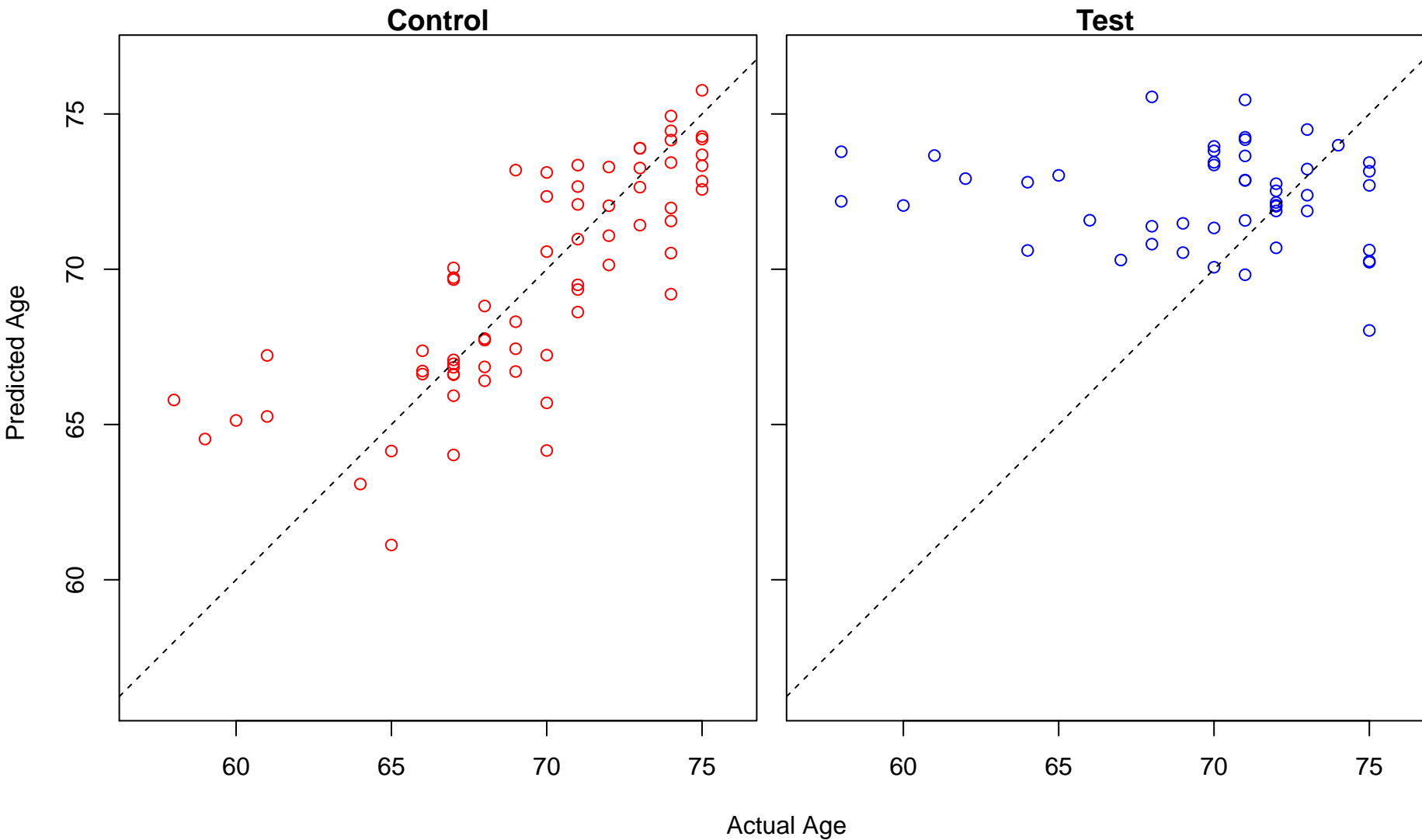
peptidyl-serine modification (Score: 2.114461)



mitotic nuclear division (Score: 2.113143)

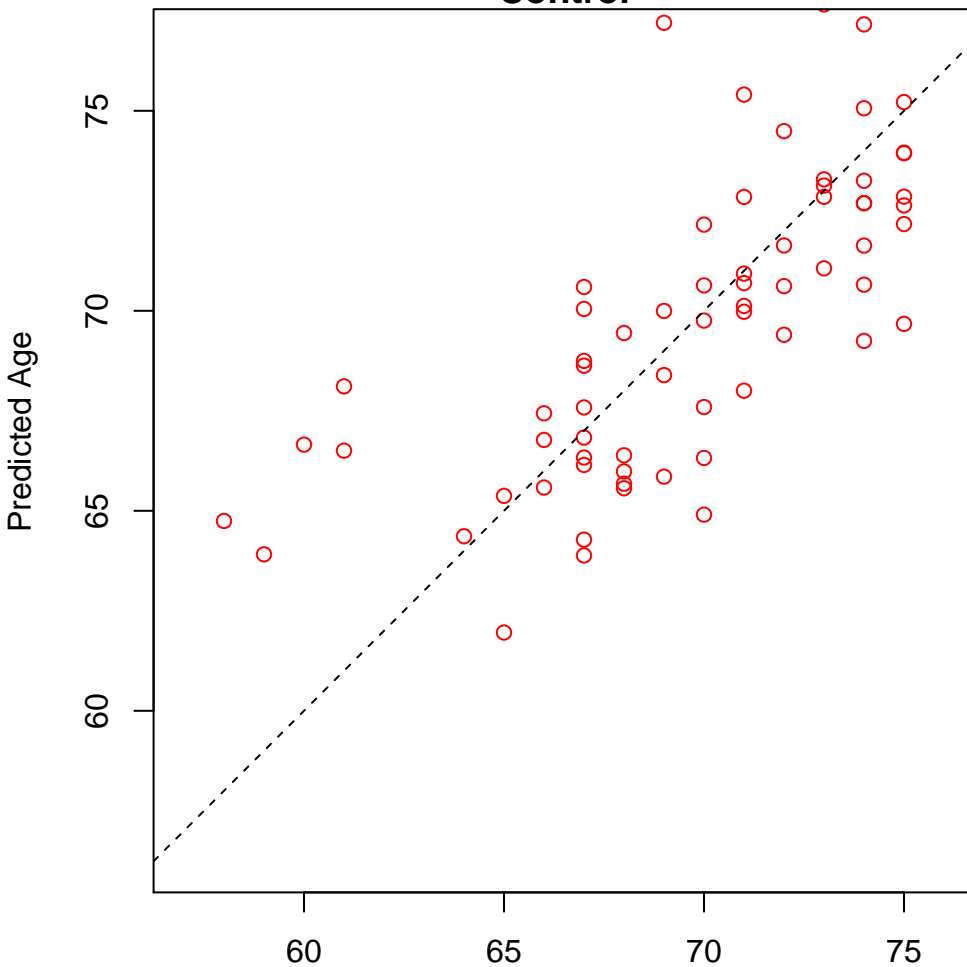


positive regulation of cellular catabolic process (Score: 2.112685)

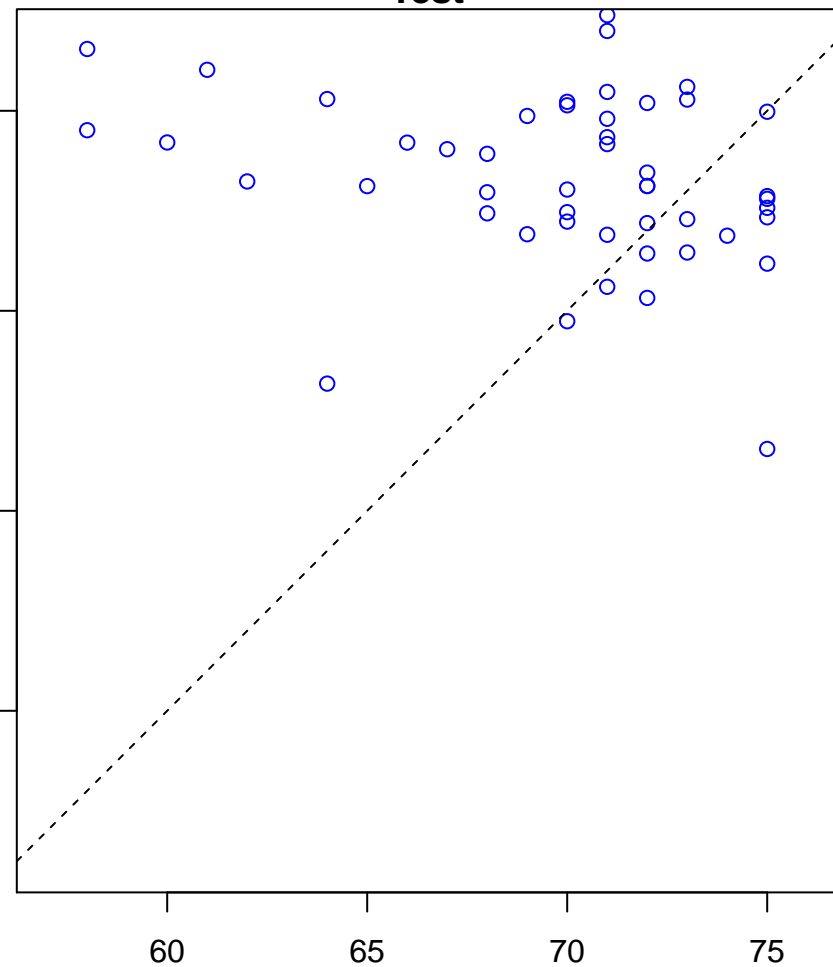


positive regulation of cell-cell adhesion (Score: 2.110653)

Control

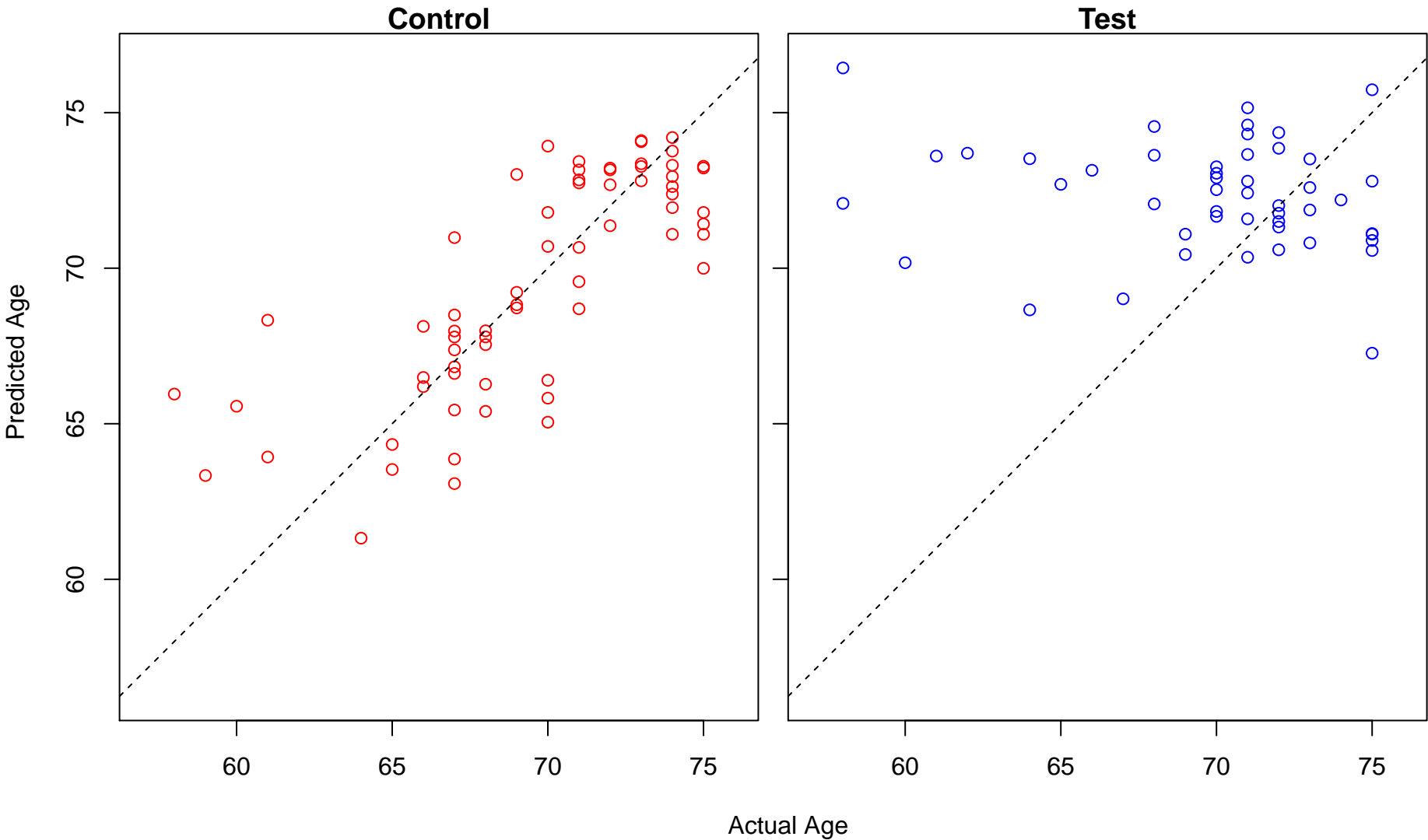


Test

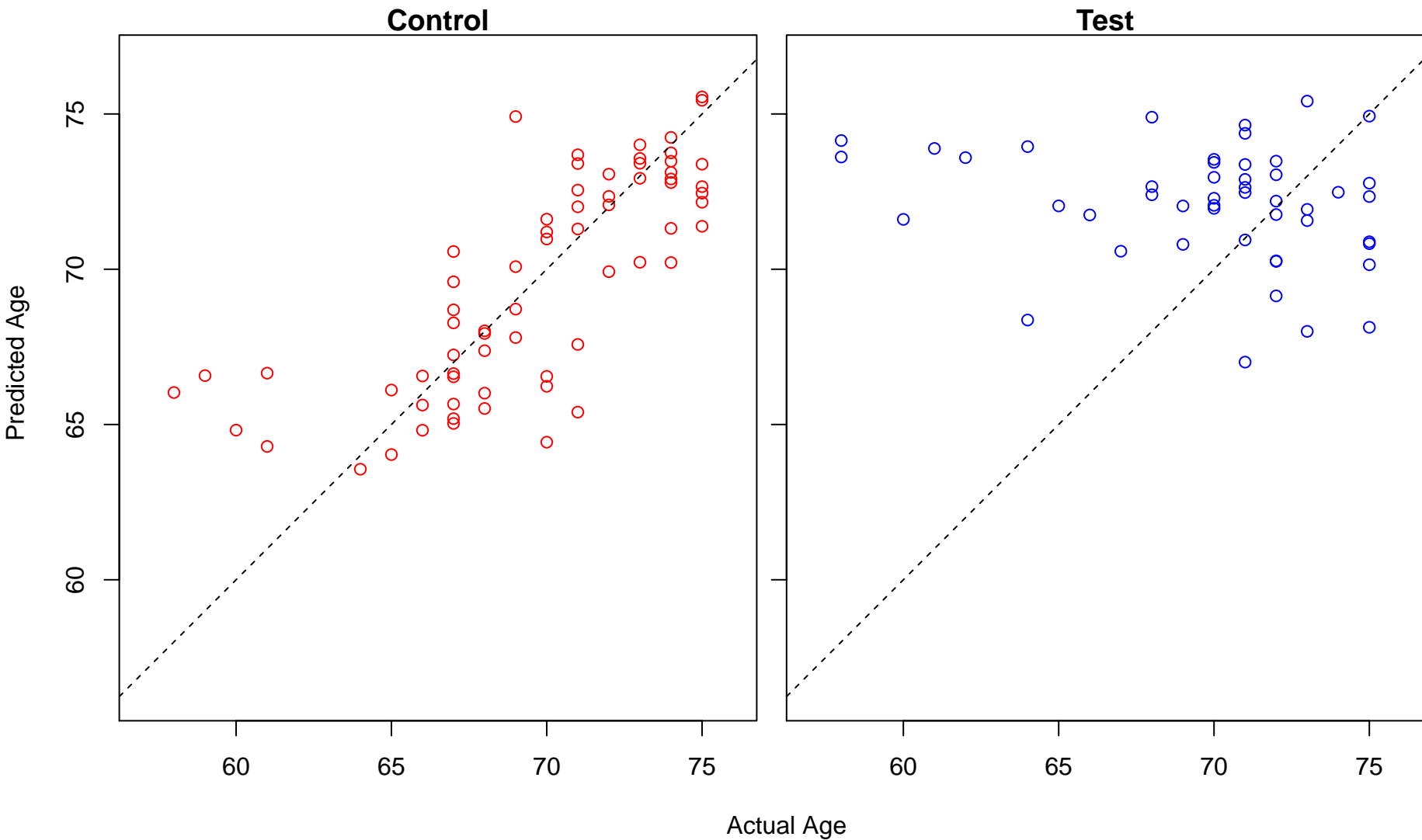


Actual Age

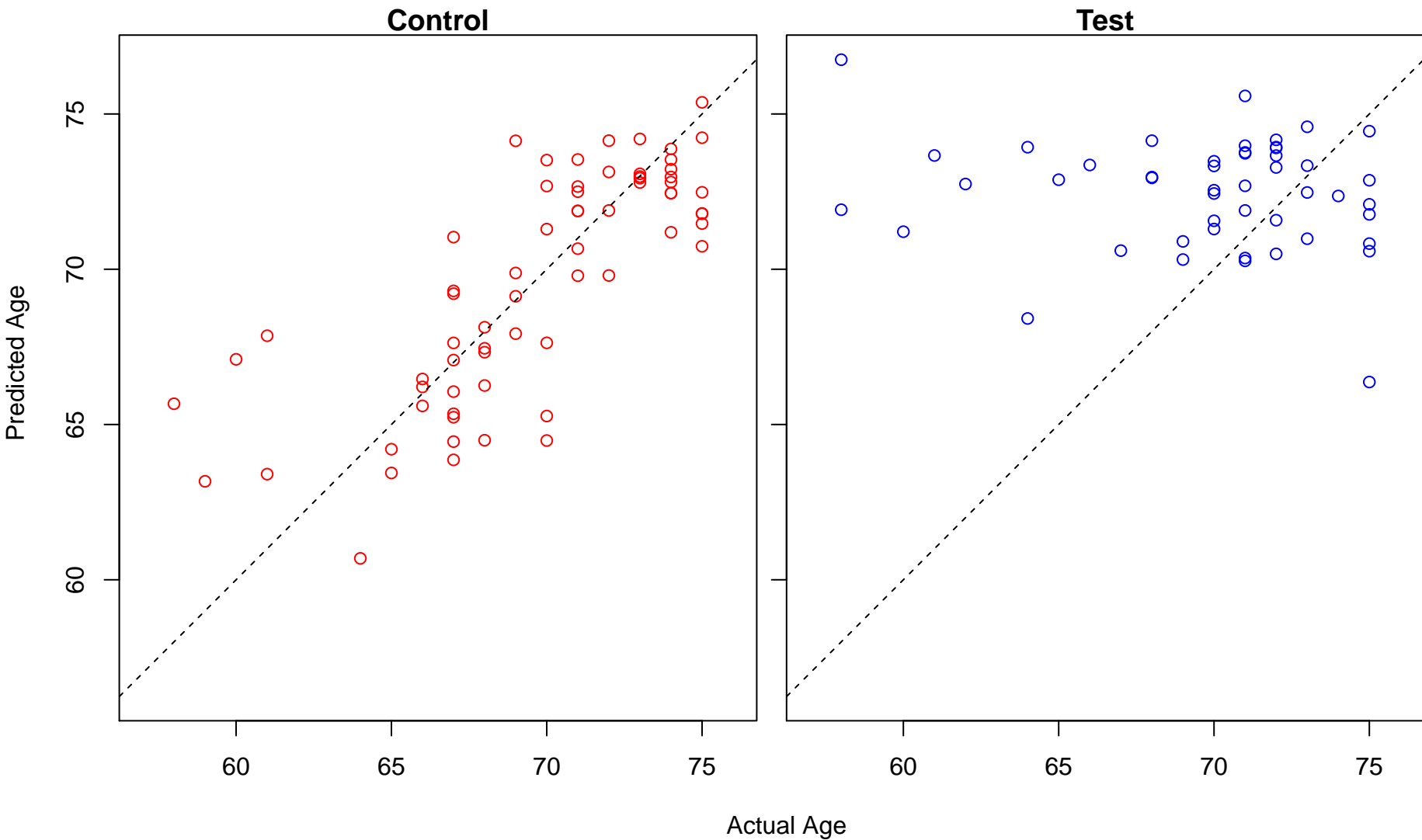
regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 2.110192)



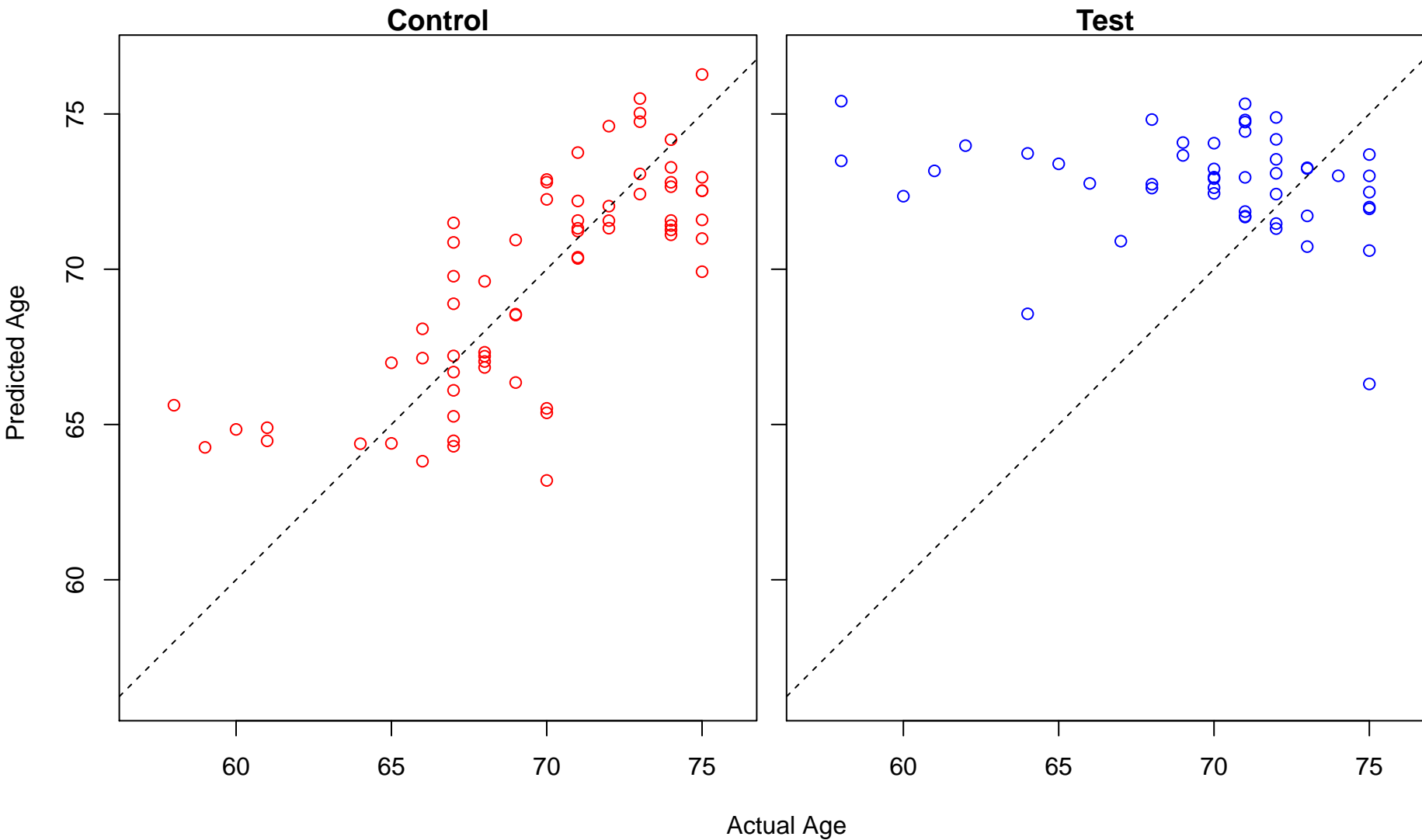
purine-containing compound metabolic process (Score: 2.110121)



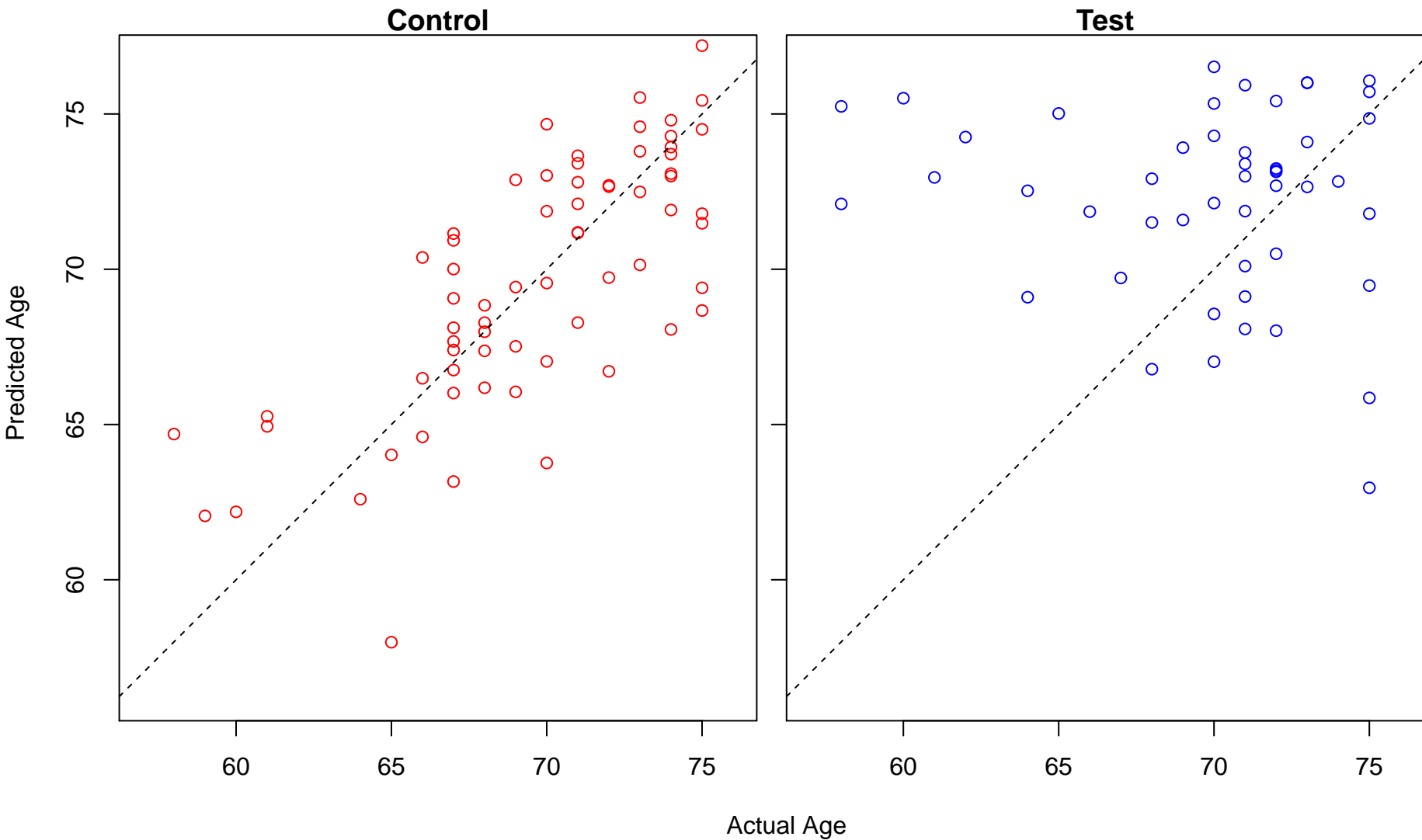
positive regulation of endopeptidase activity (Score: 2.108965)



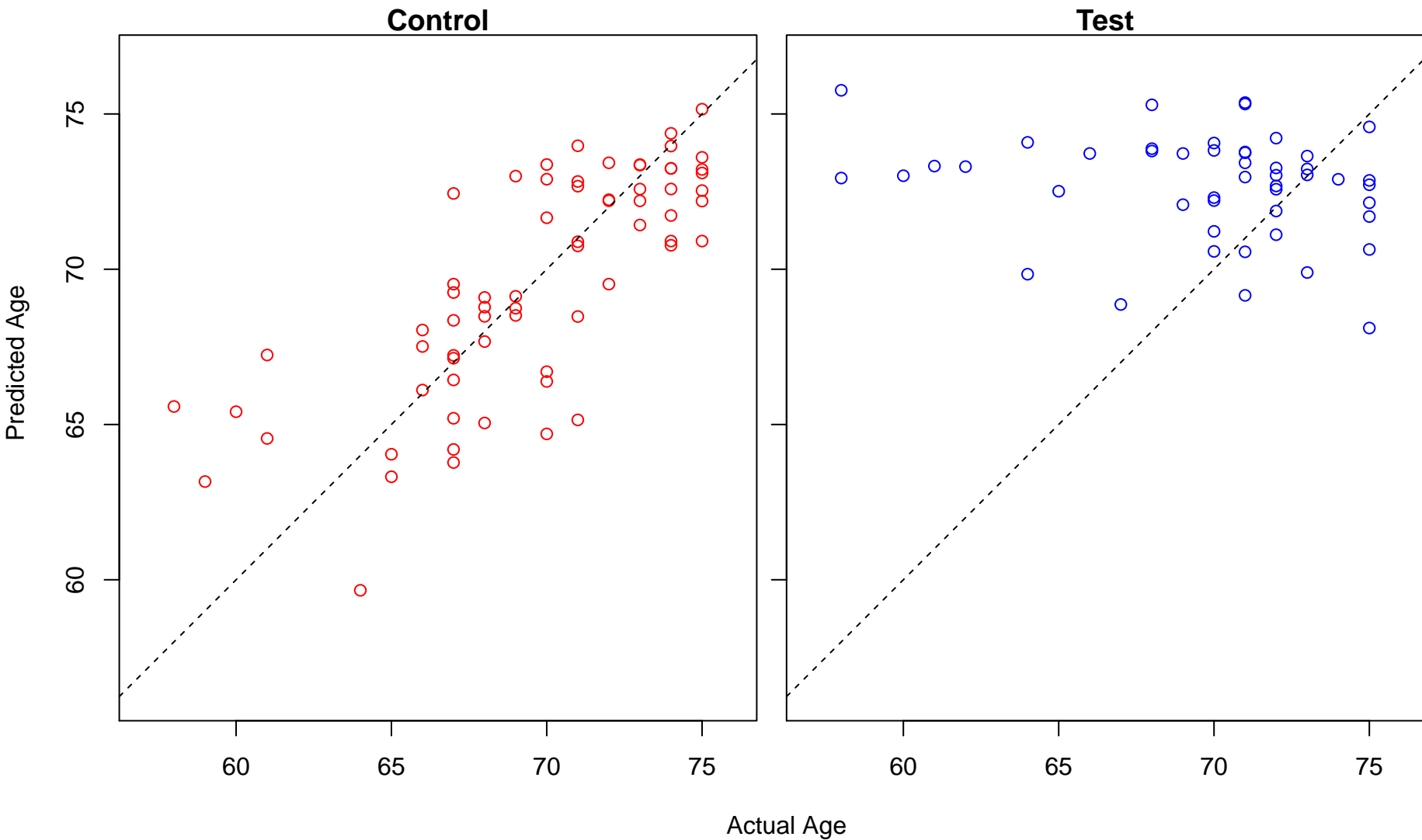
glycerolipid metabolic process (Score: 2.107849)



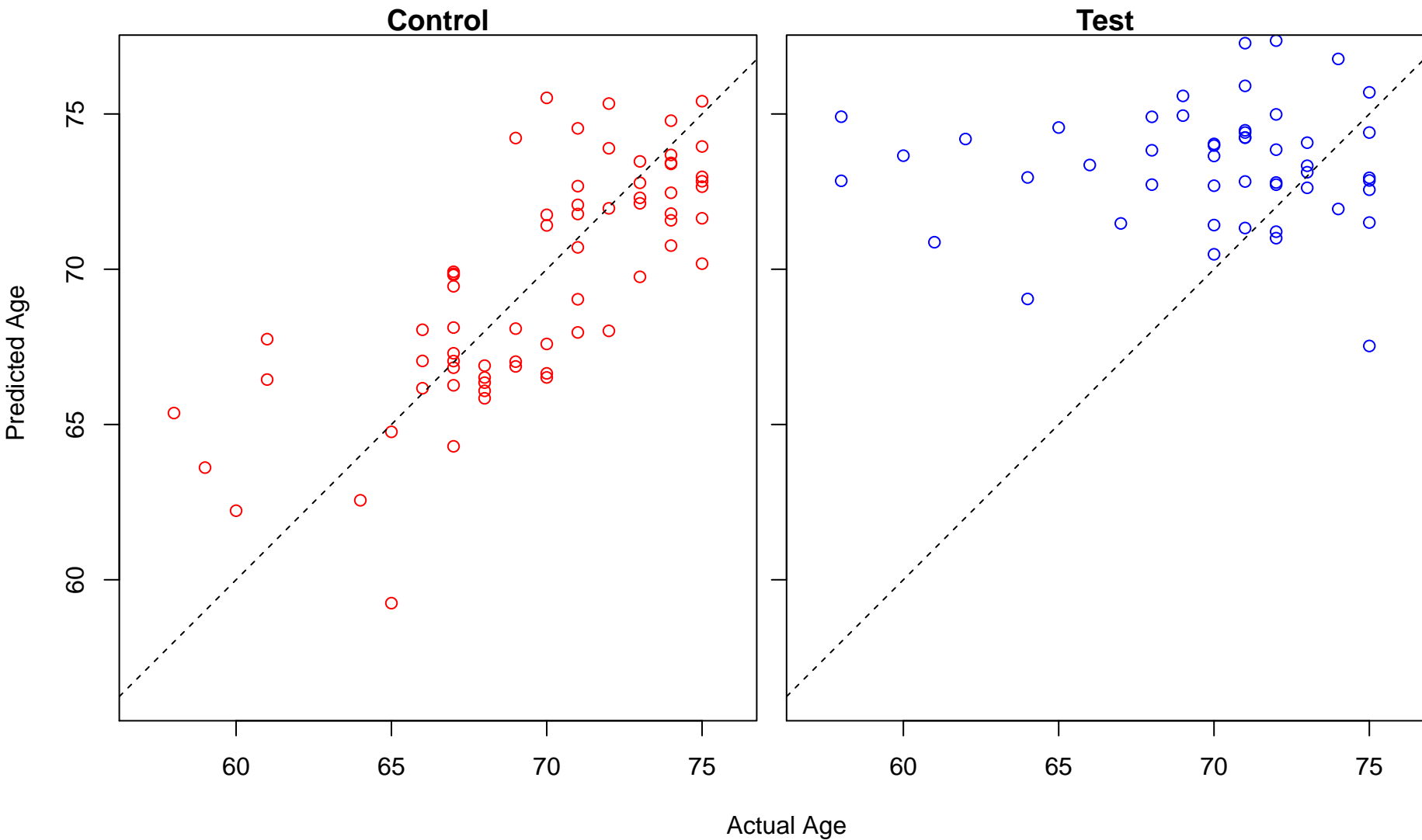
positive regulation of ion transmembrane transport (Score: 2.106556)



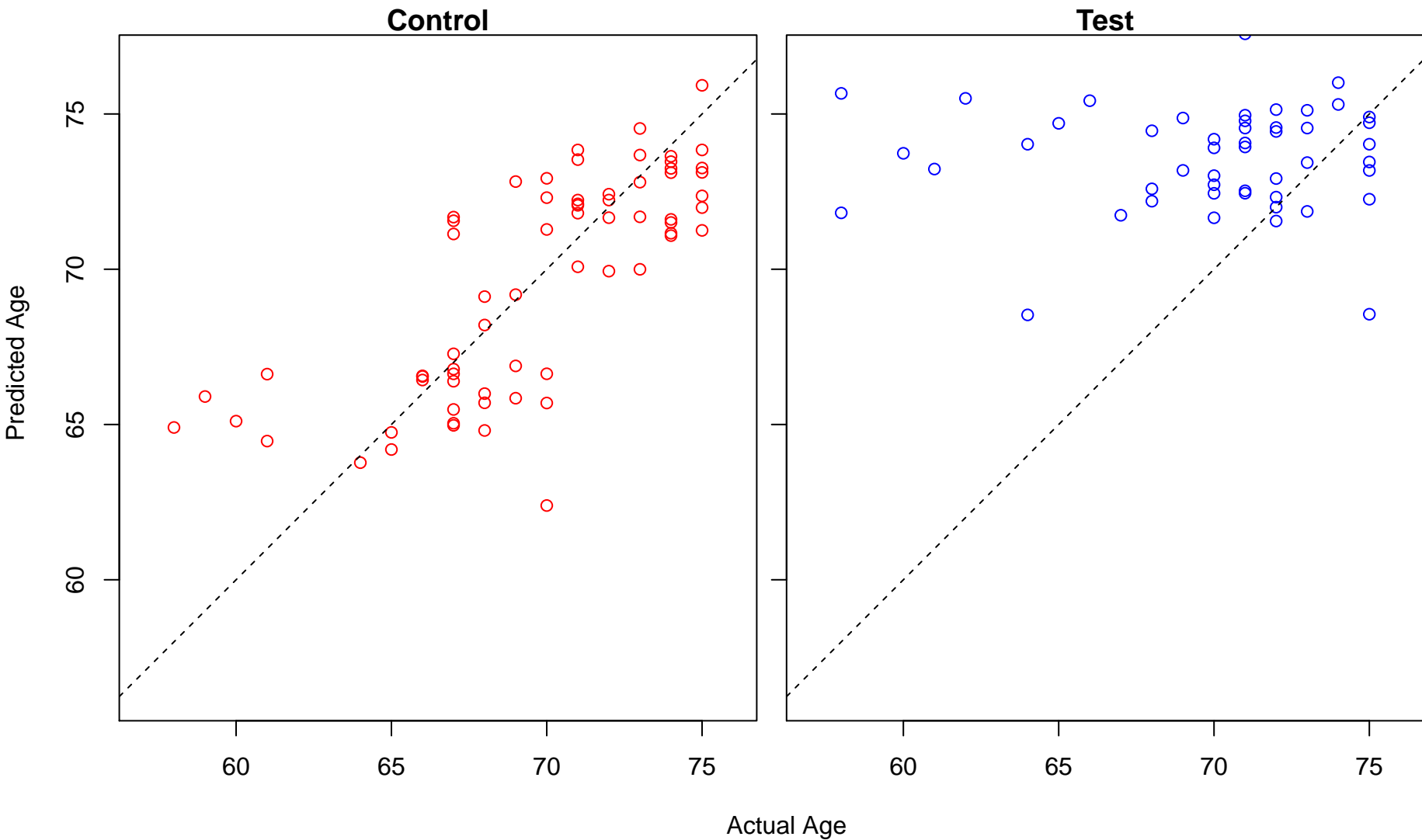
positive regulation of cell death (Score: 2.105606)



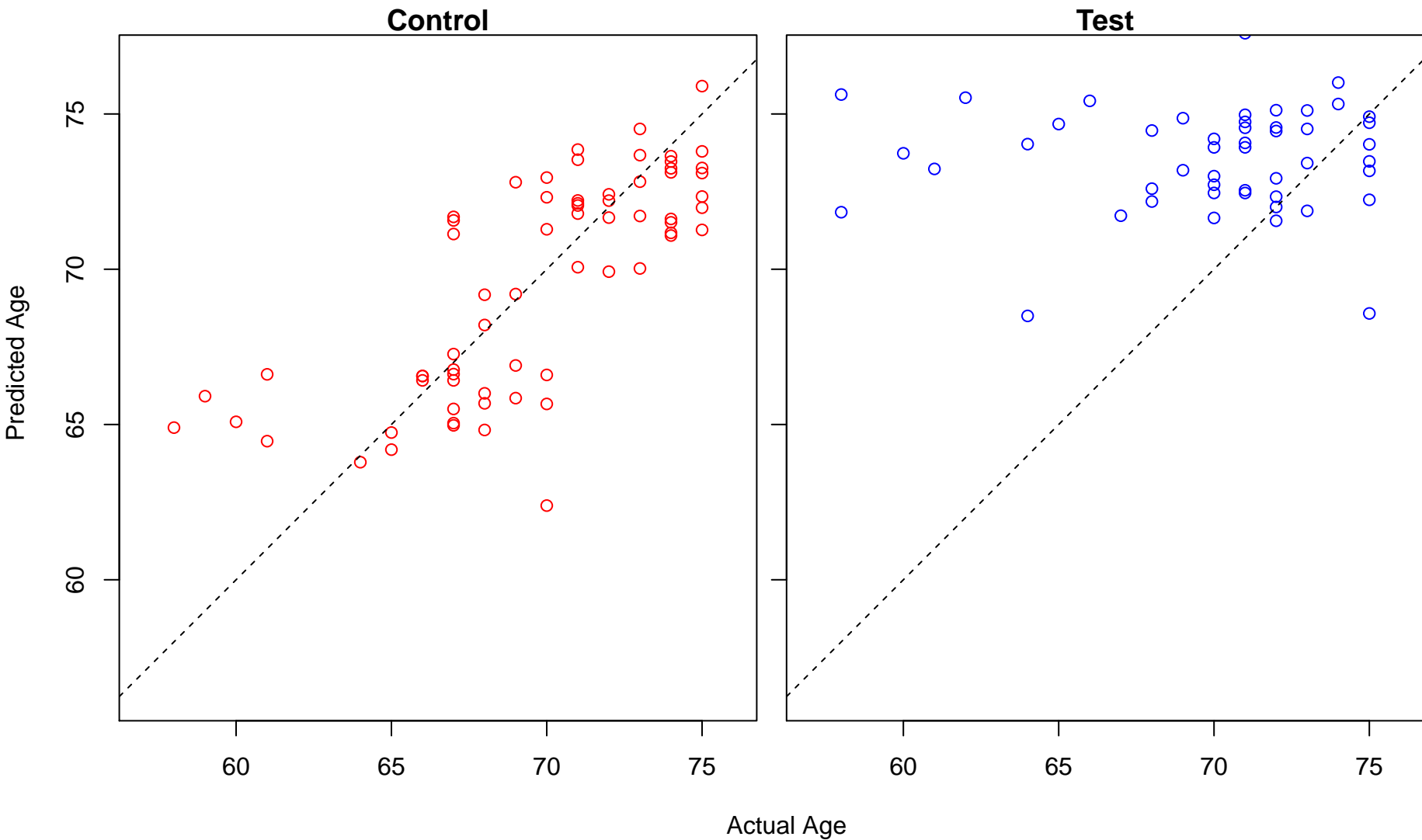
protein import (Score: 2.105602)



histone modification (Score: 2.104846)

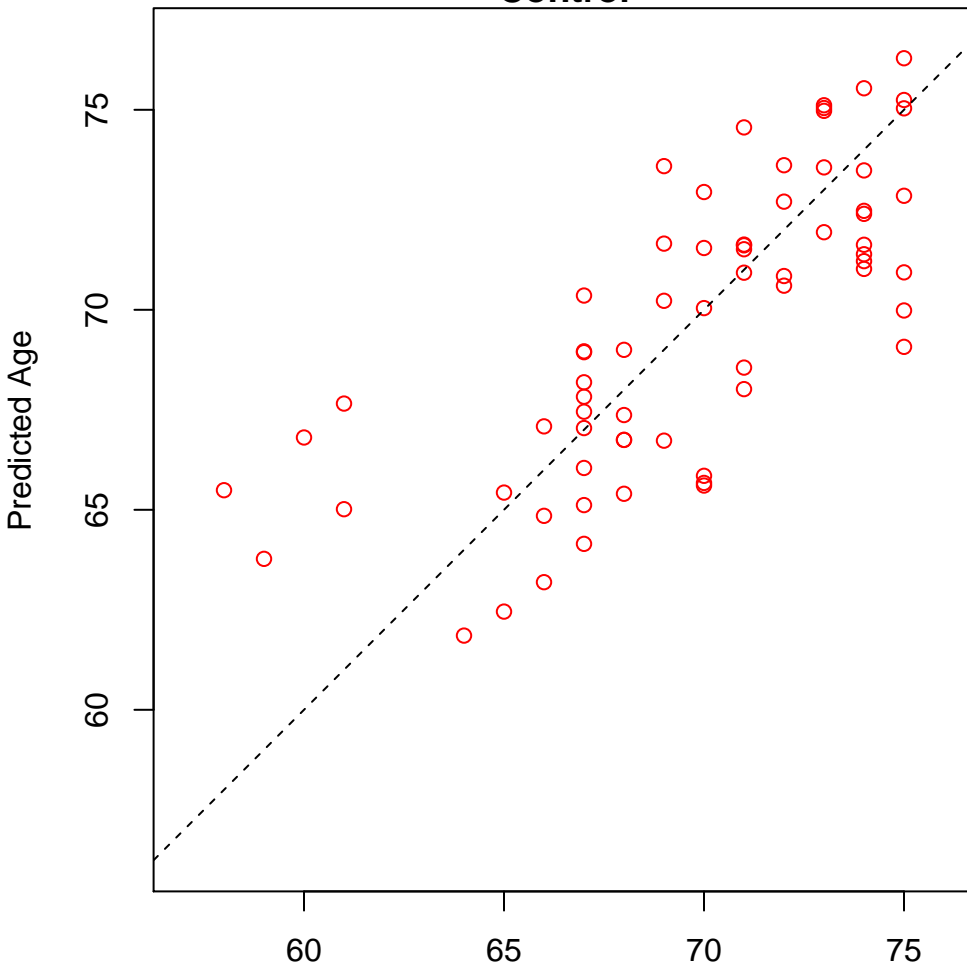


covalent chromatin modification (Score: 2.103285)

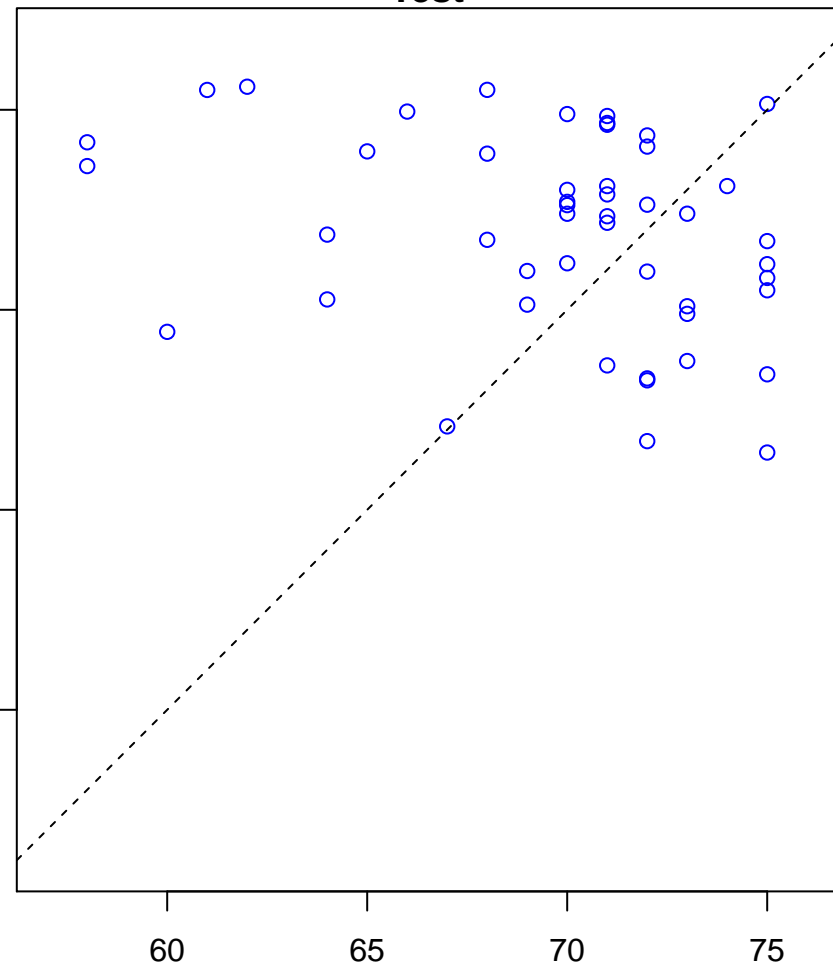


negative regulation of hydrolase activity (Score: 2.101792)

Control

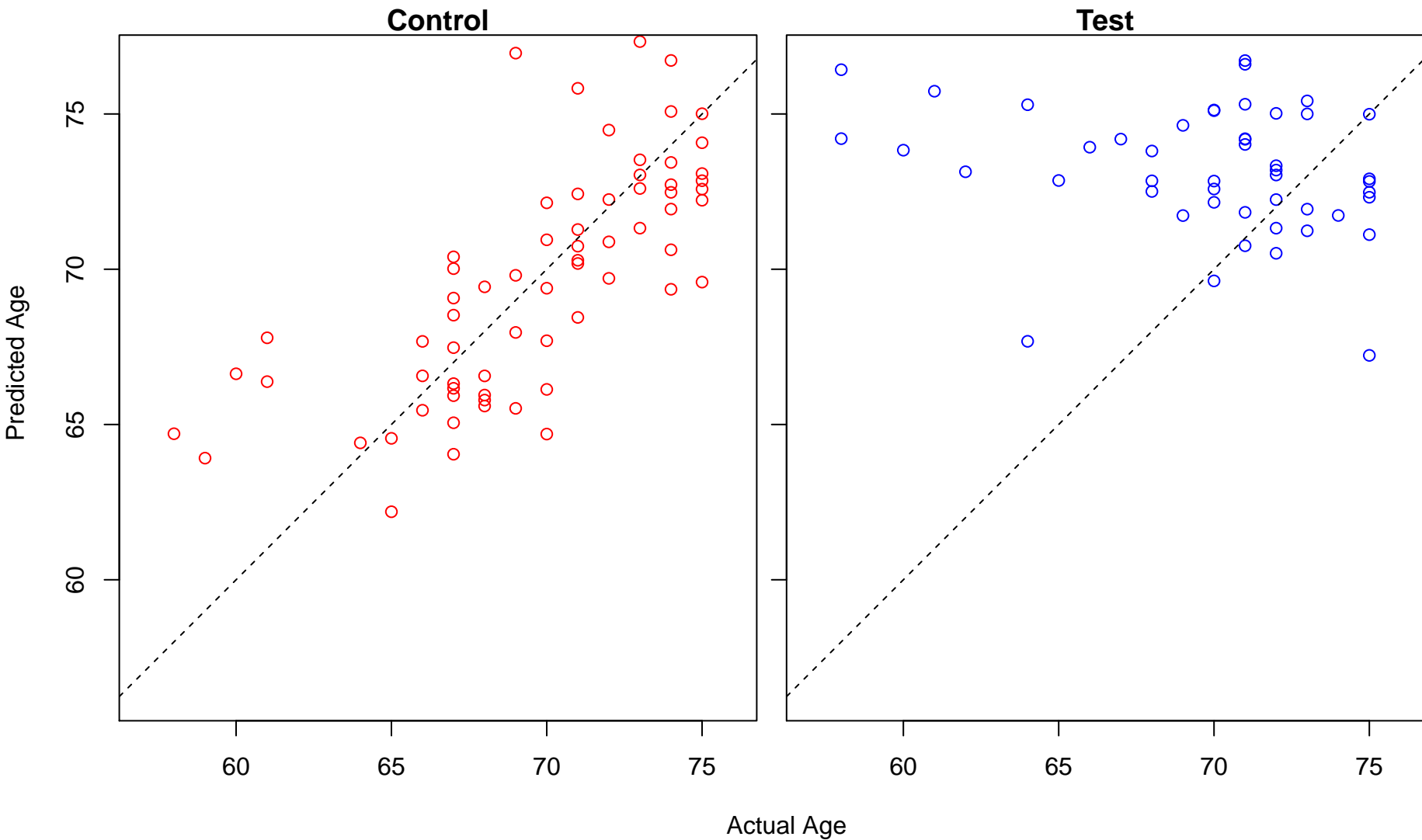


Test

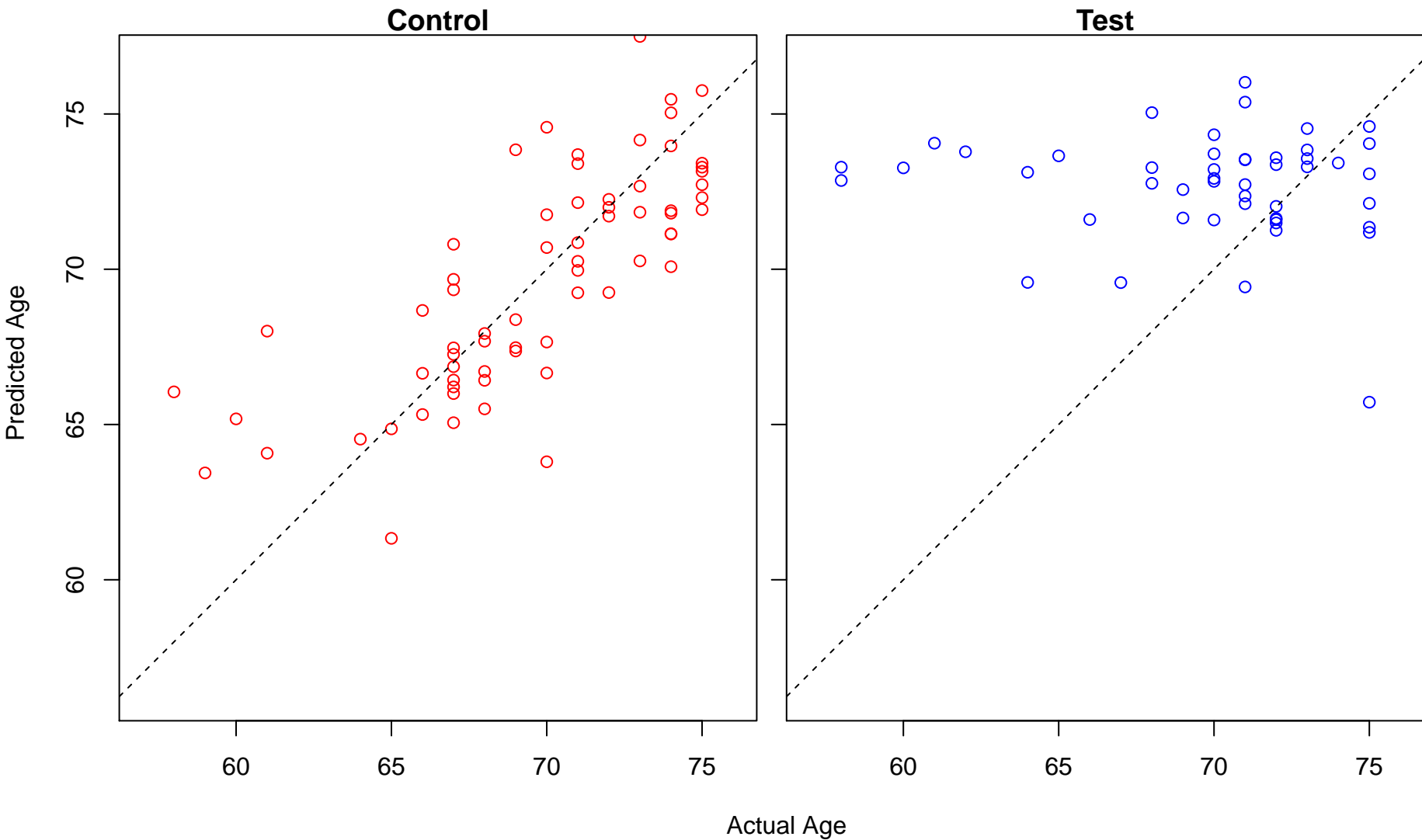


Actual Age

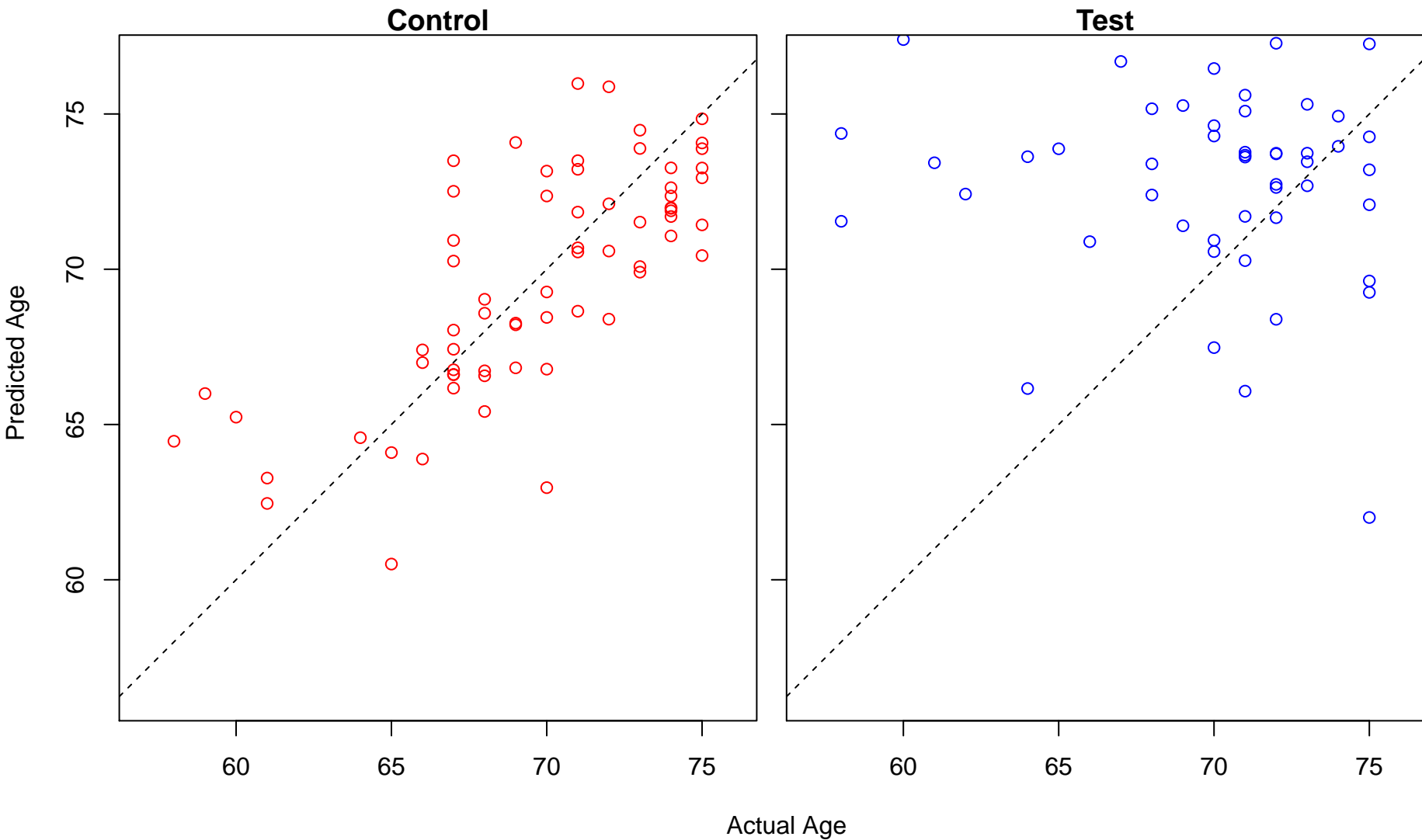
positive regulation of T cell activation (Score: 2.098367)



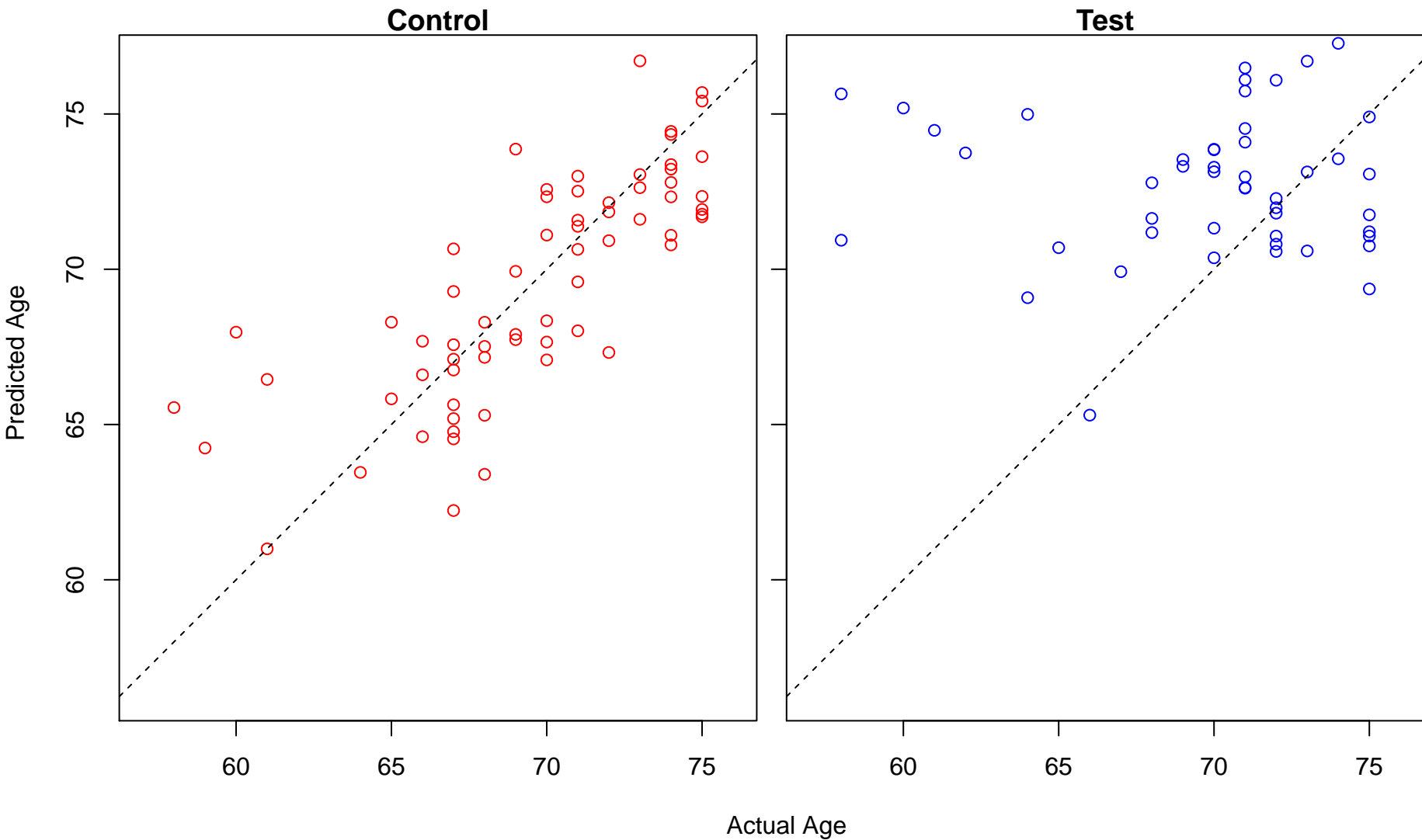
Fc receptor signaling pathway (Score: 2.096970)



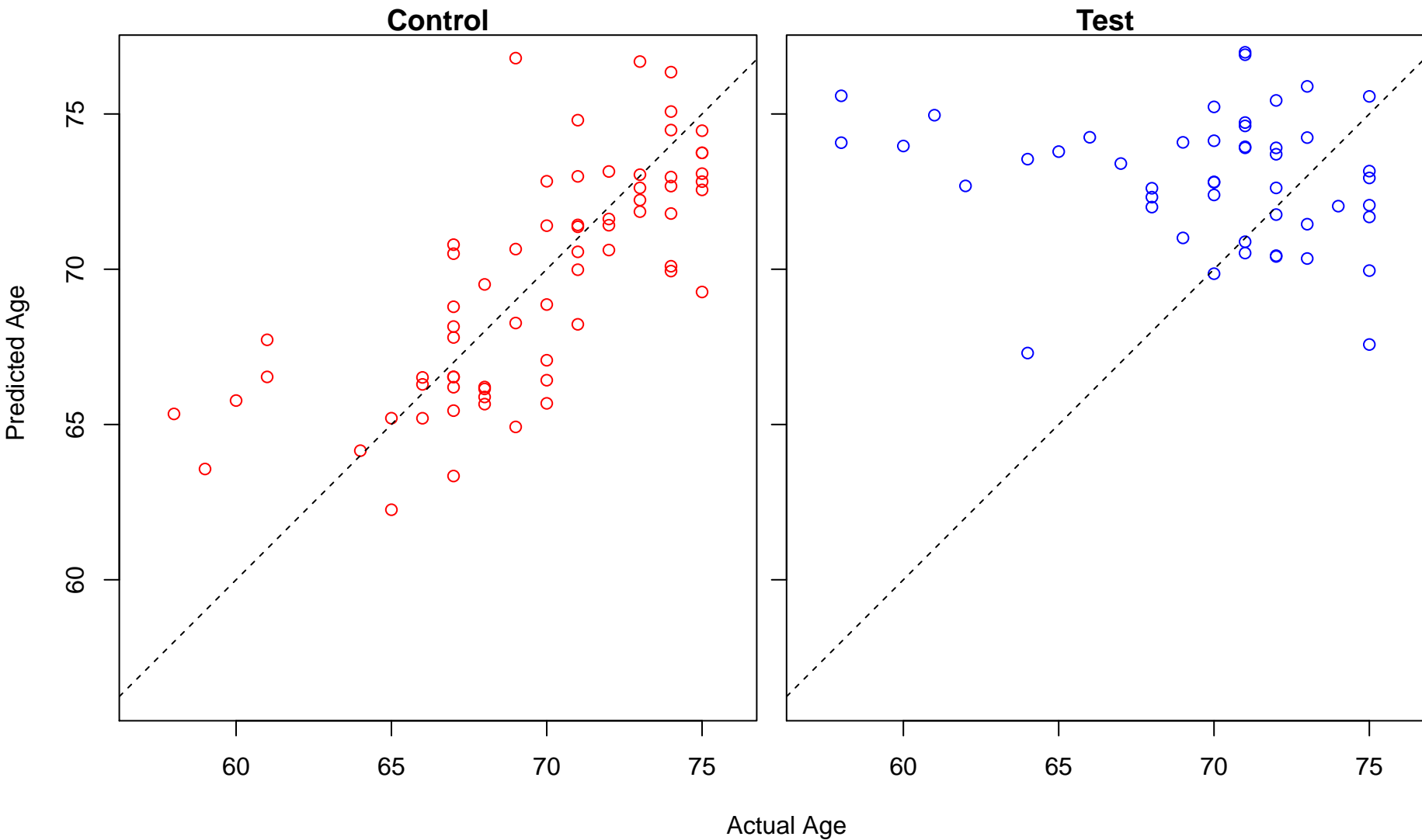
response to organophosphorus (Score: 2.096042)



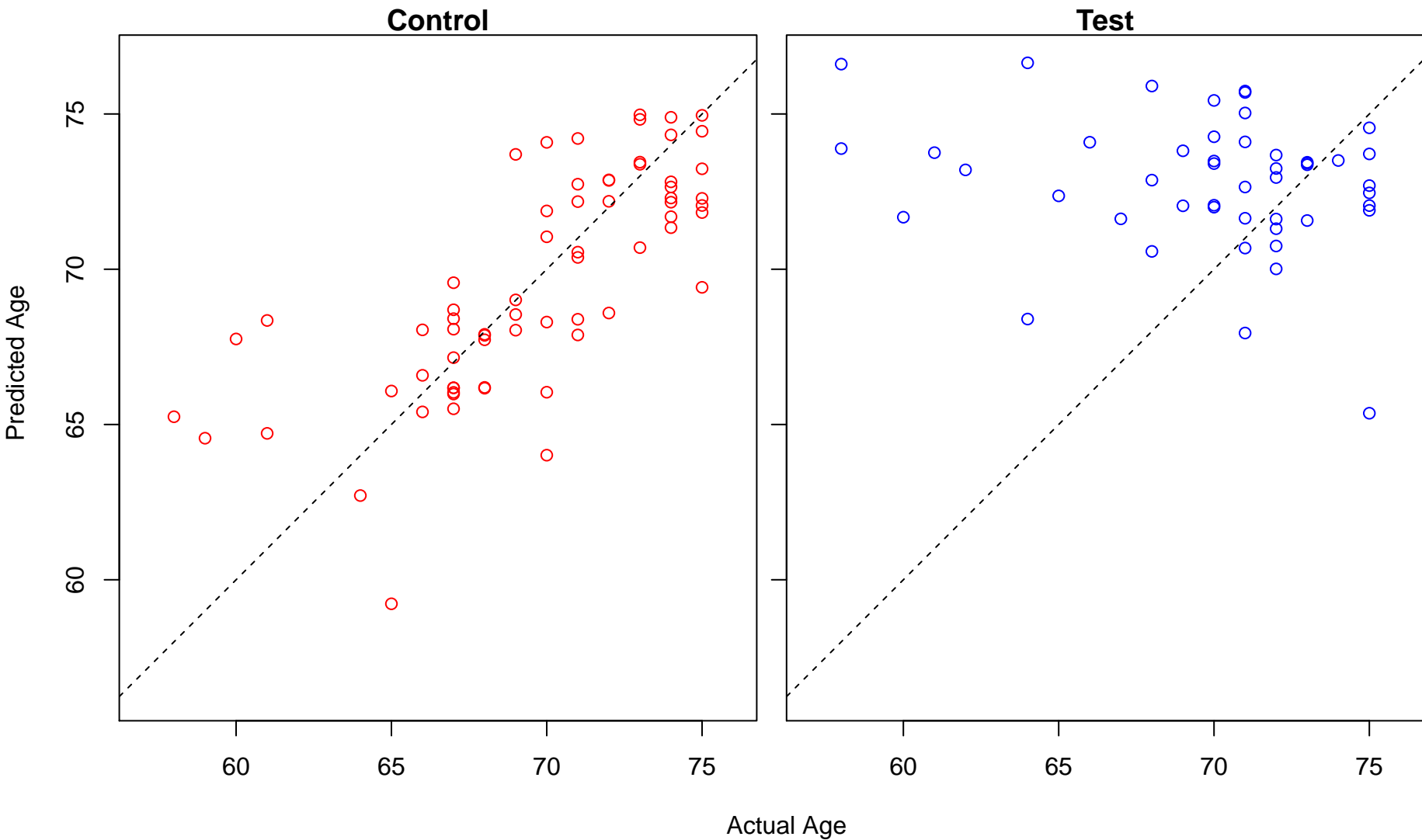
protein targeting to mitochondrion (Score: 2.095658)



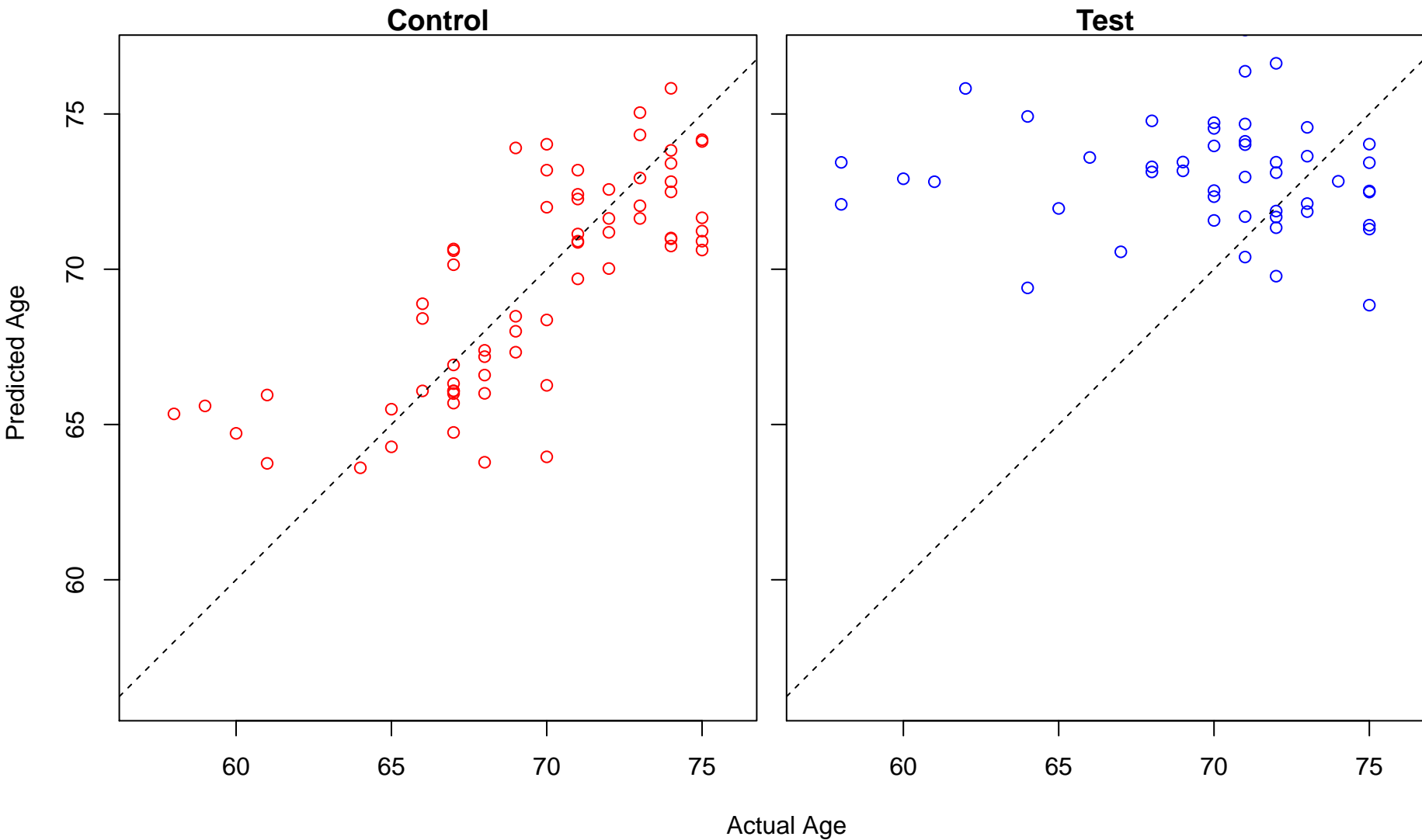
positive regulation of cell adhesion (Score: 2.095298)



positive regulation of NF-kappaB transcription factor activity (Score: 2.095005)

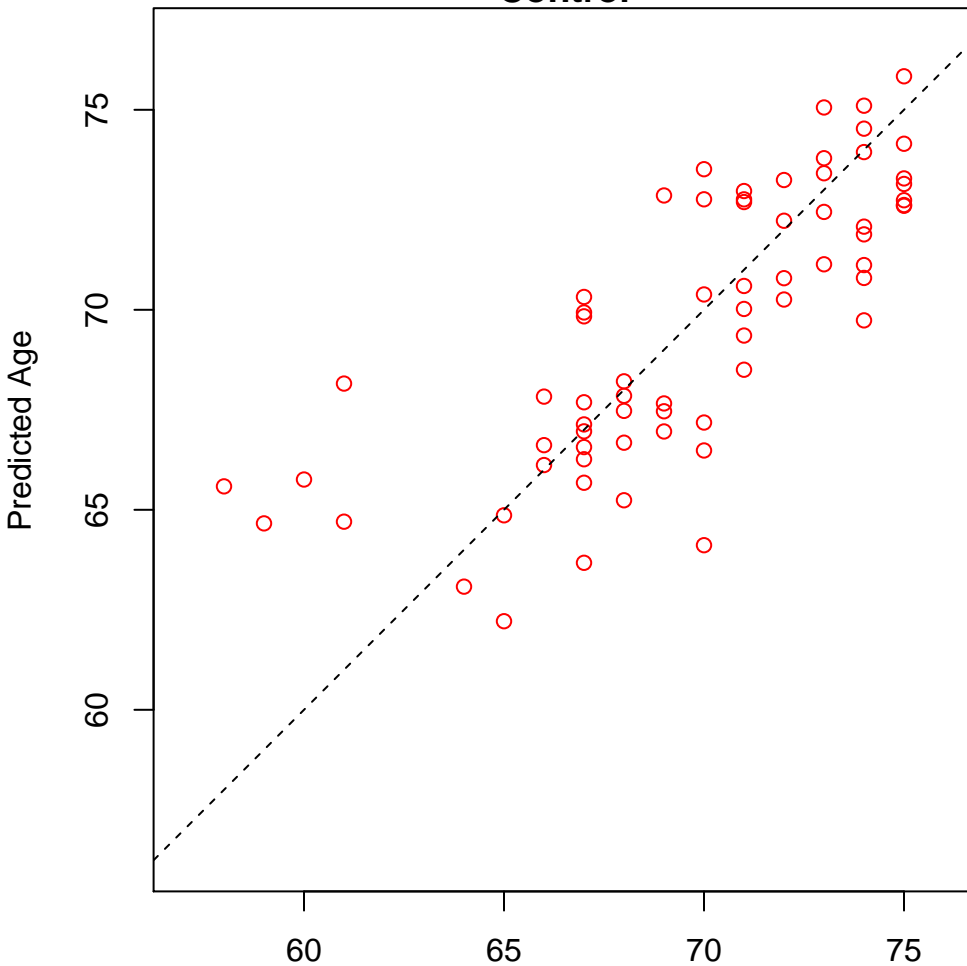


membrane budding (Score: 2.094753)

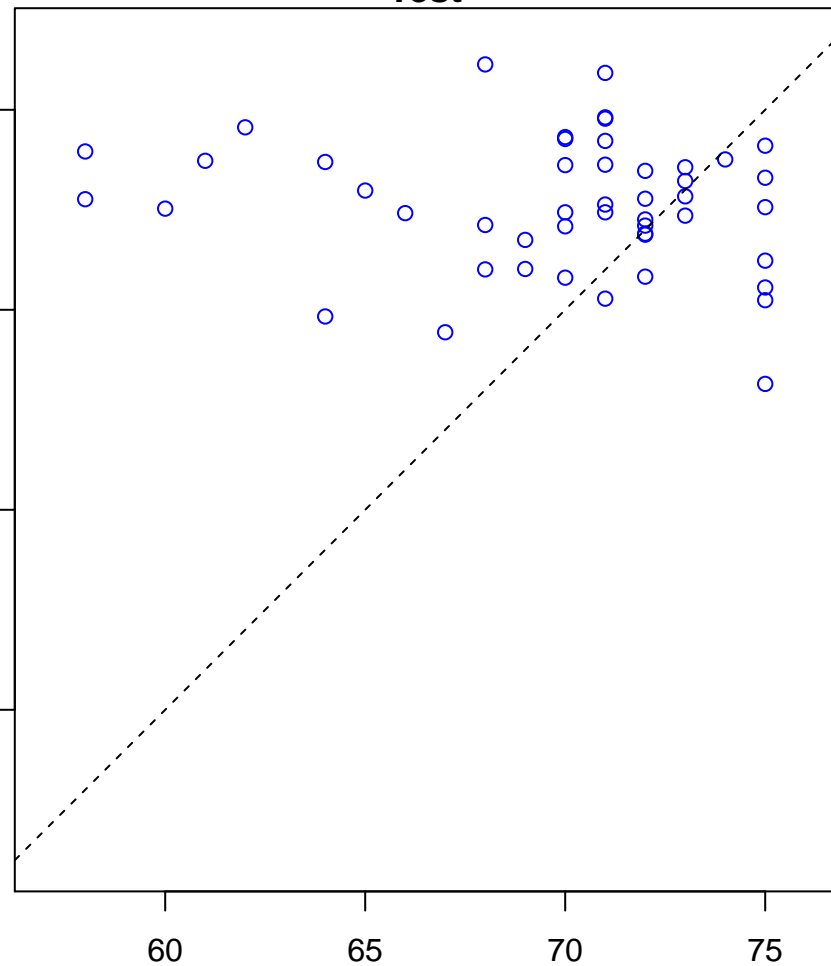


regulation of cellular catabolic process (Score: 2.092974)

Control

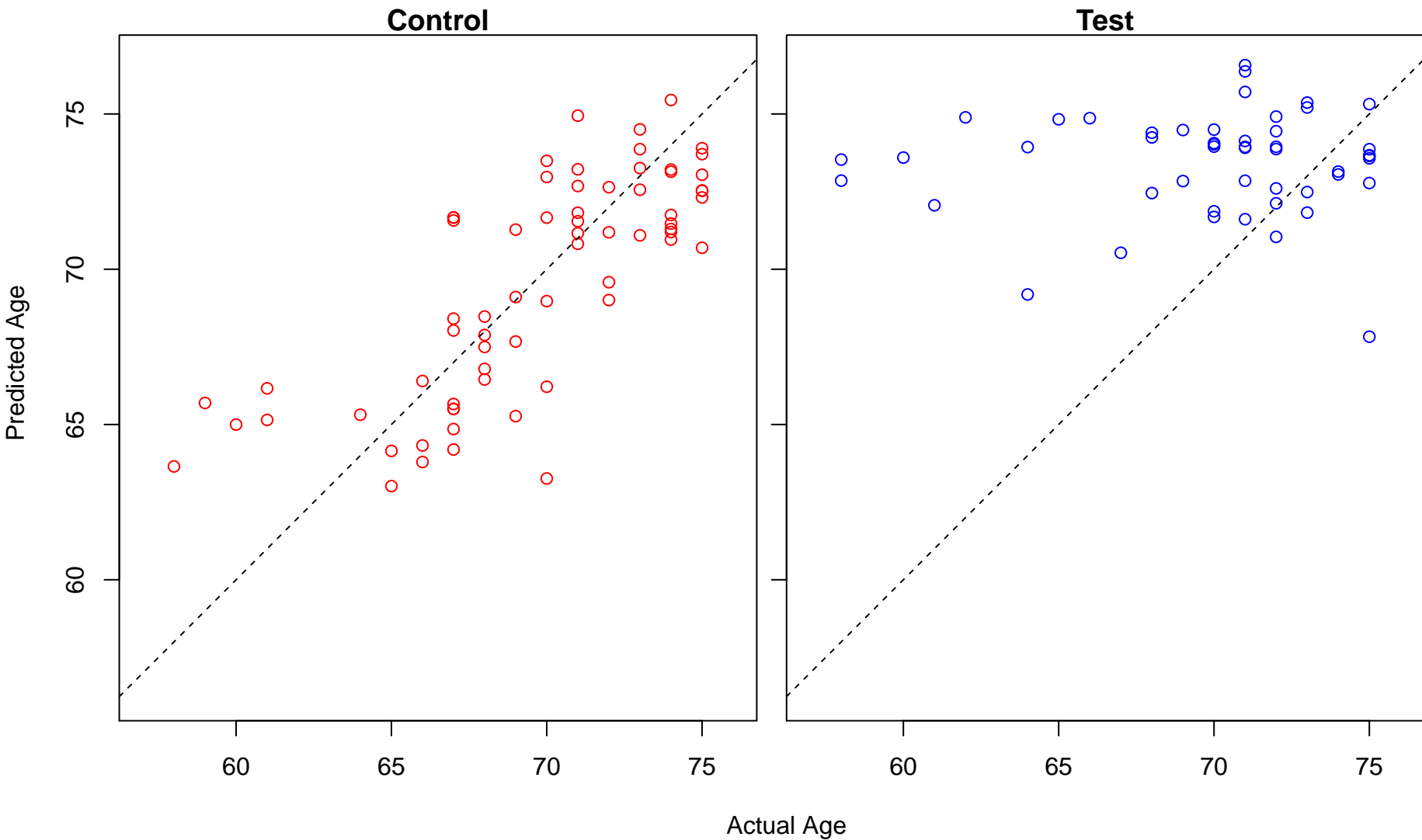


Test

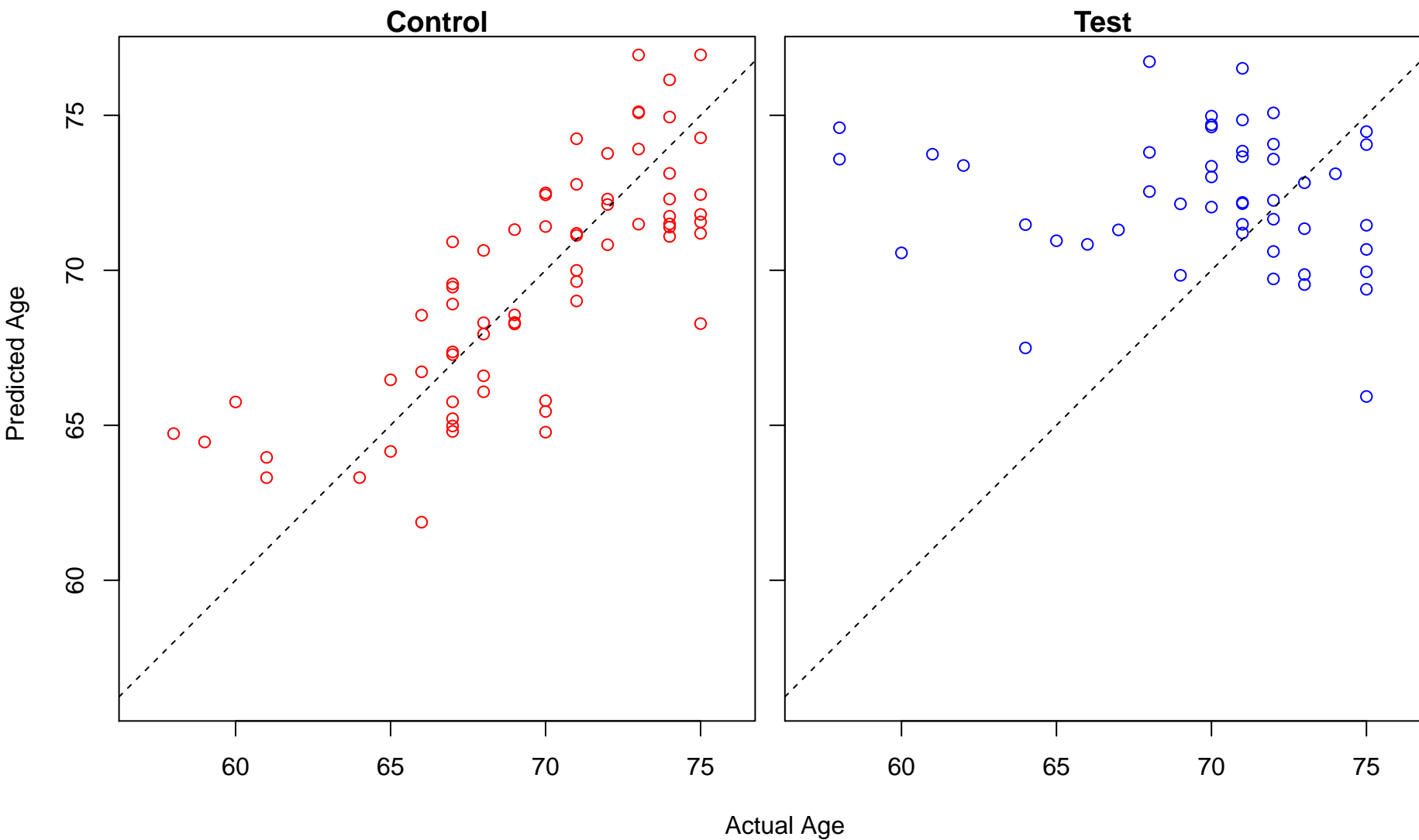


Actual Age

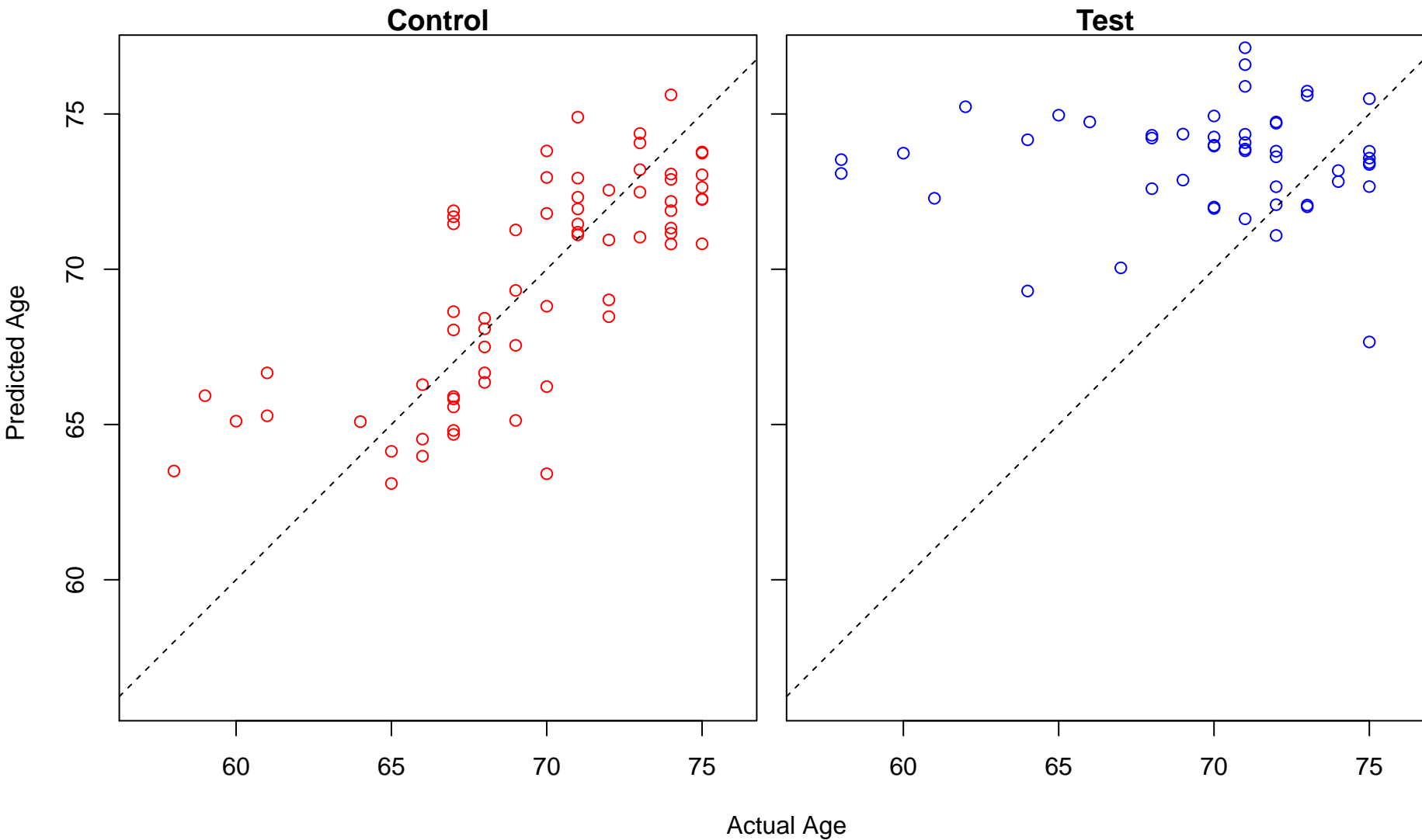
peptidyl-lysine acetylation (Score: 2.092695)



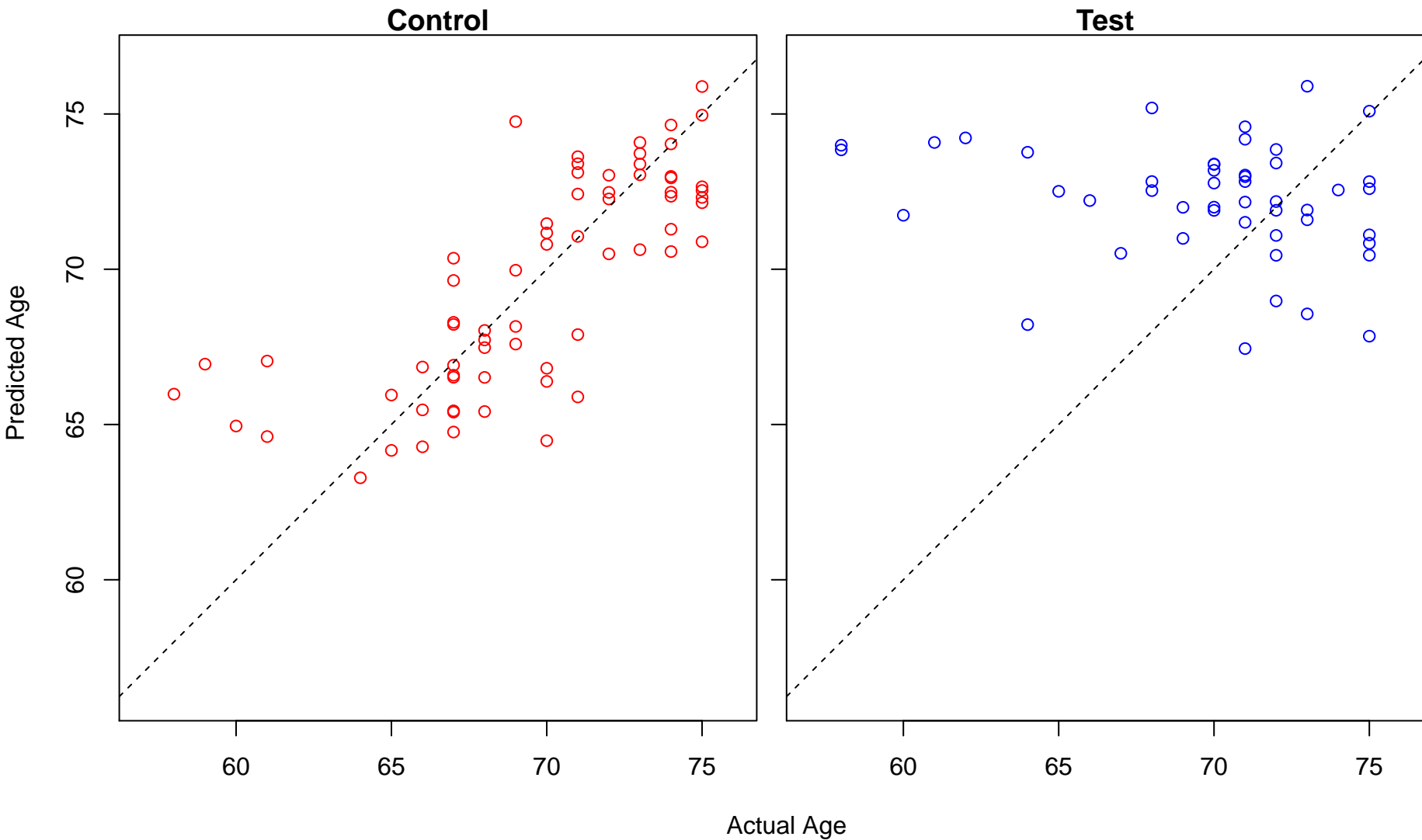
glycerophospholipid biosynthetic process (Score: 2.092272)



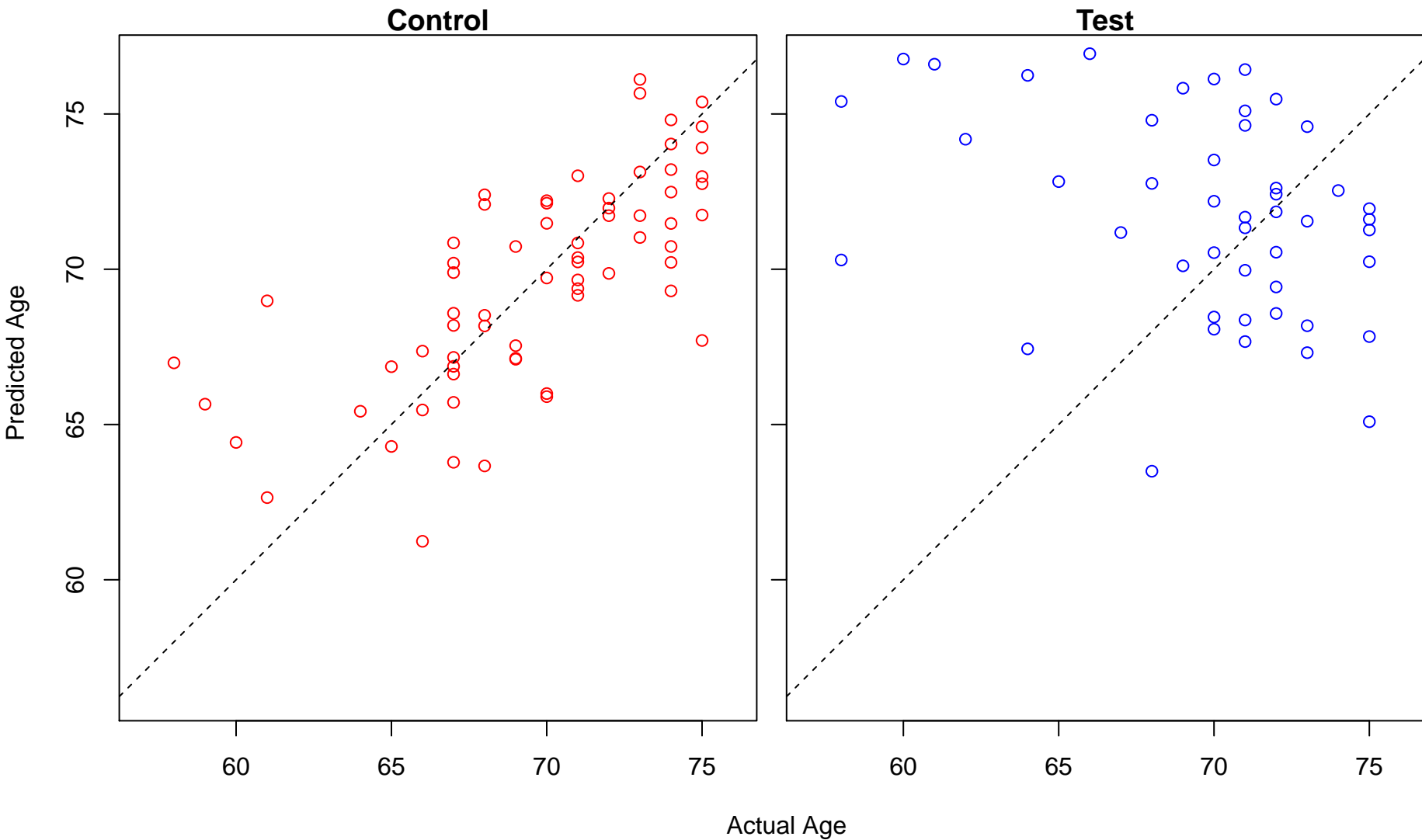
protein acetylation (Score: 2.092119)



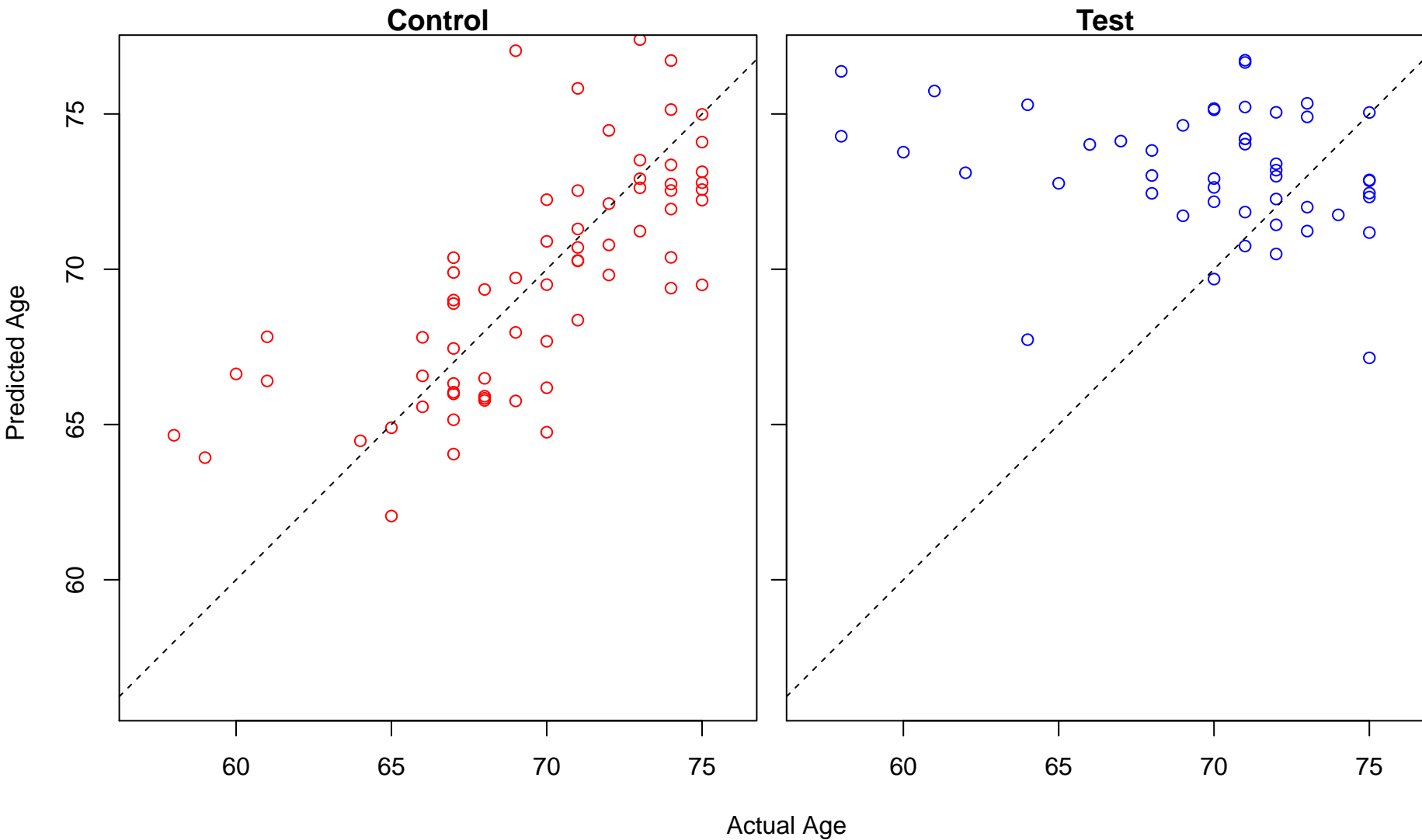
nucleotide metabolic process (Score: 2.091836)



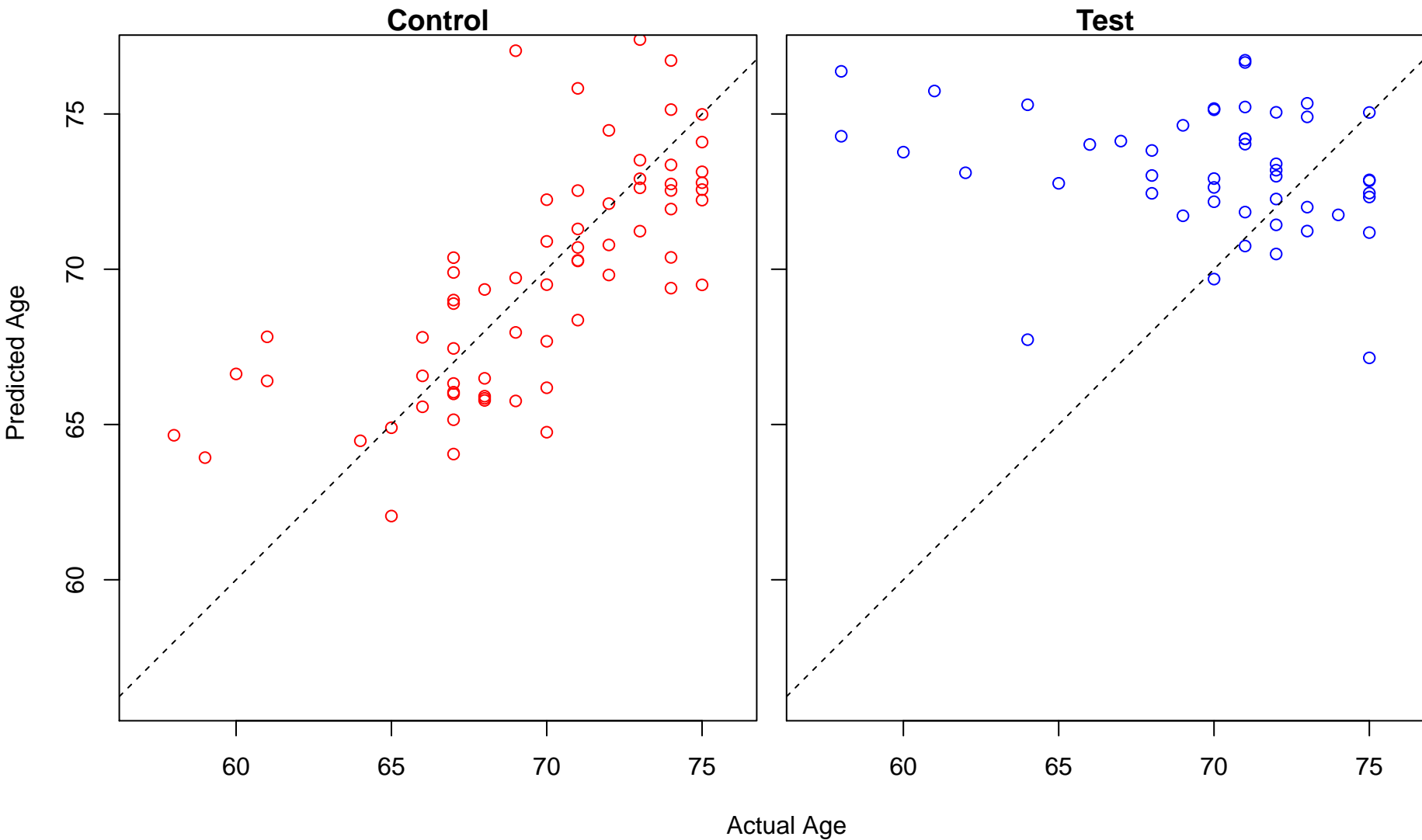
phosphatidylserine acyl-chain remodeling (Score: 2.090236)



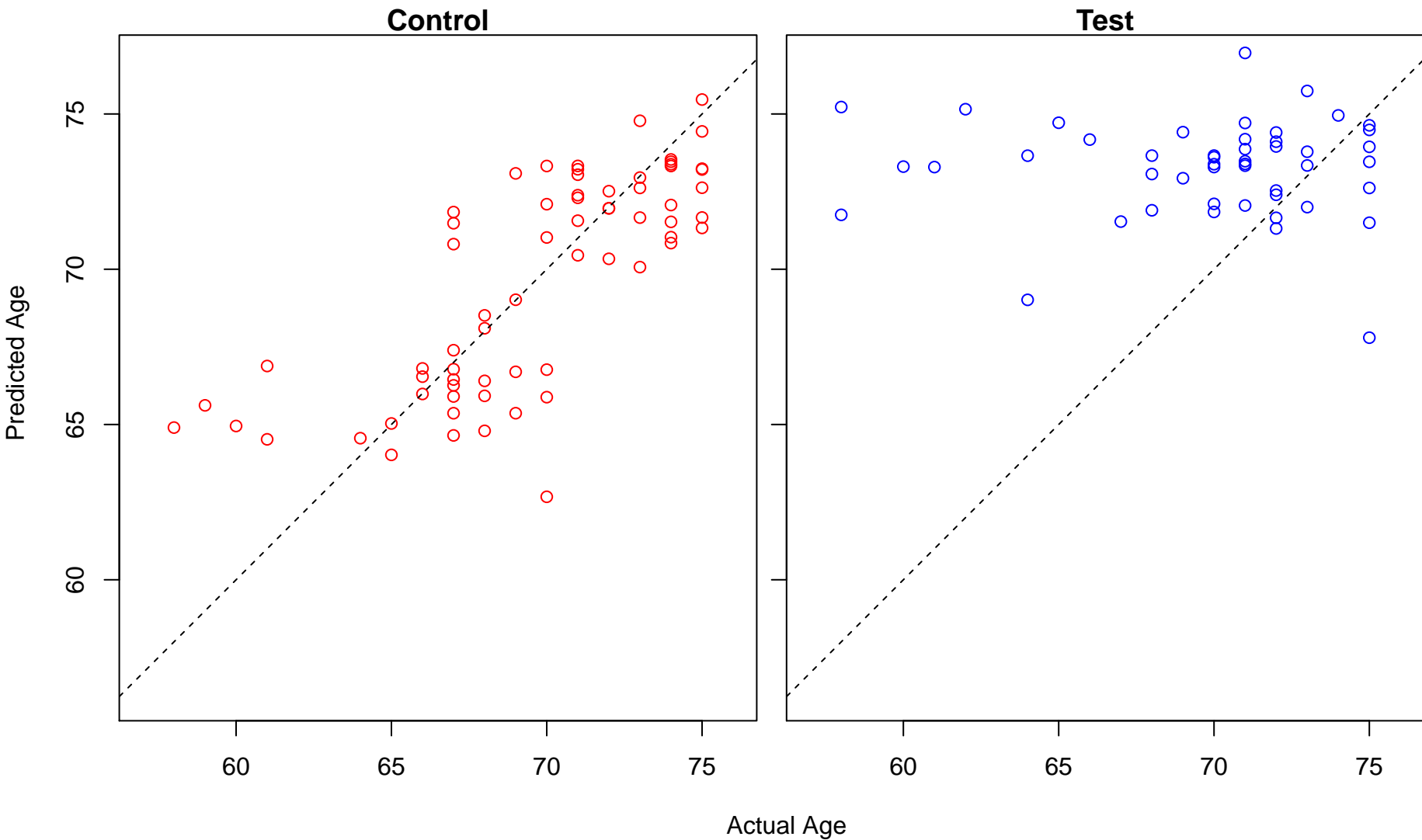
positive regulation of homotypic cell-cell adhesion (Score: 2.088646)



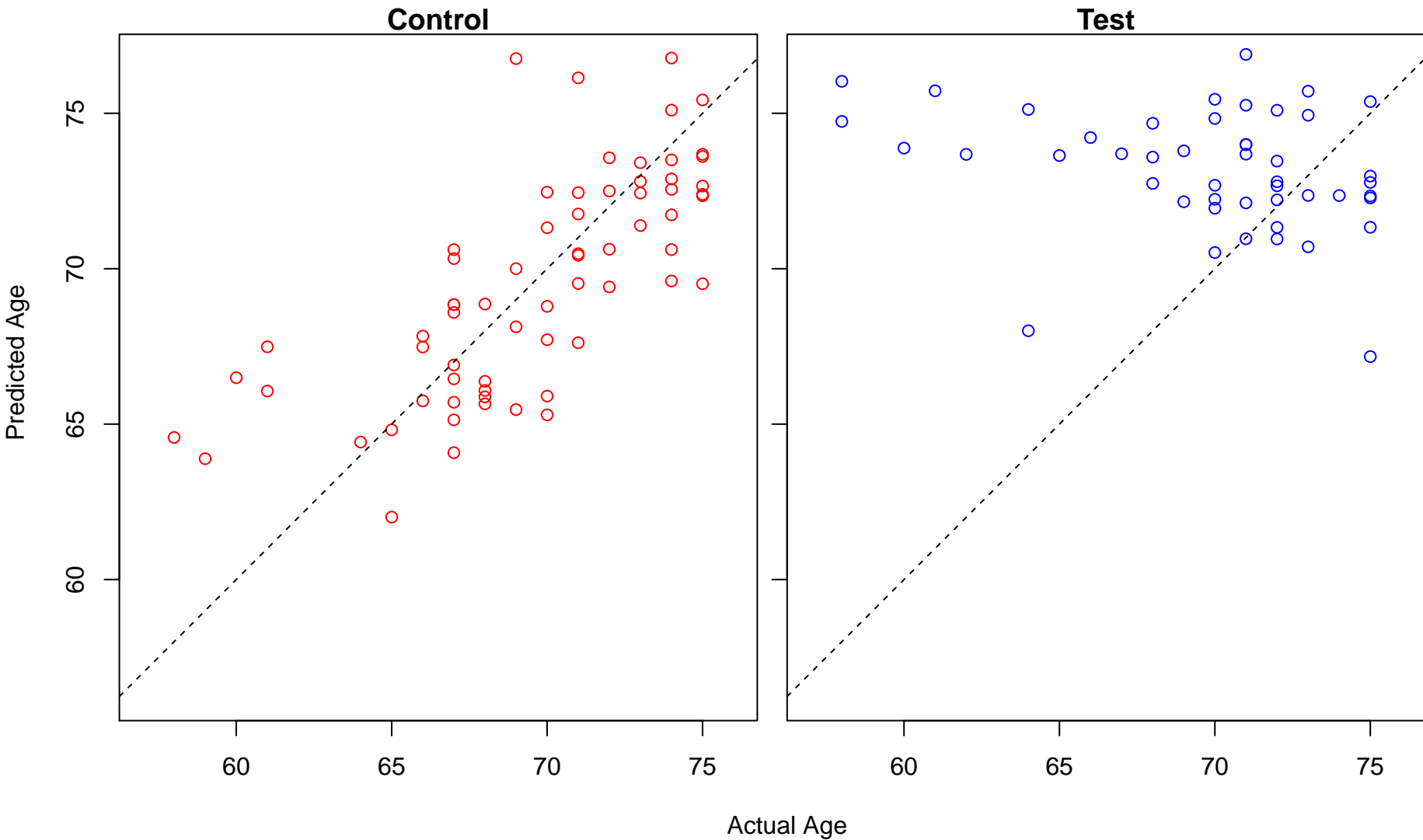
positive regulation of leukocyte cell-cell adhesion (Score: 2.088646)



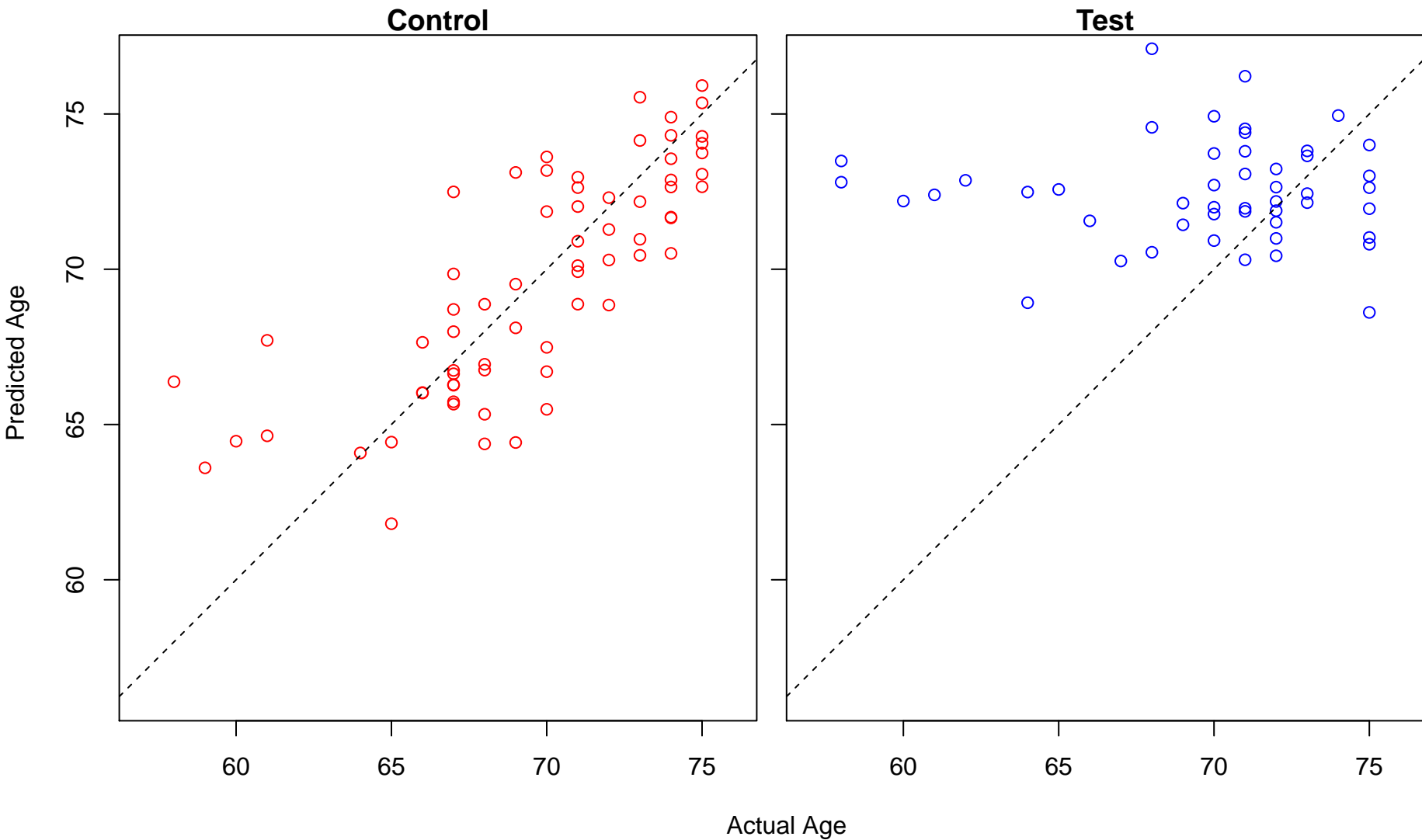
chromatin modification (Score: 2.087844)



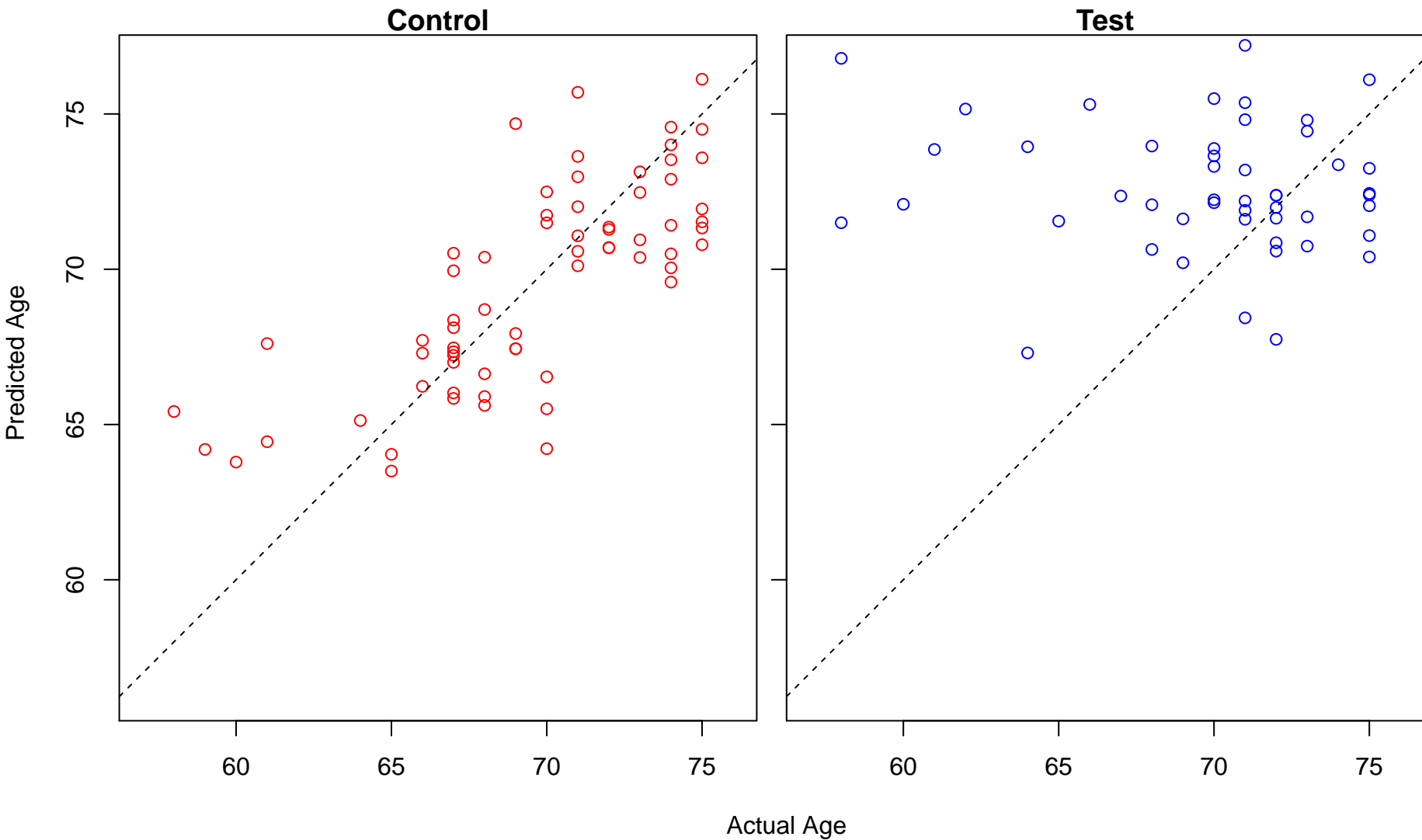
positive regulation of lymphocyte activation (Score: 2.084330)



signal transduction by p53 class mediator (Score: 2.083606)

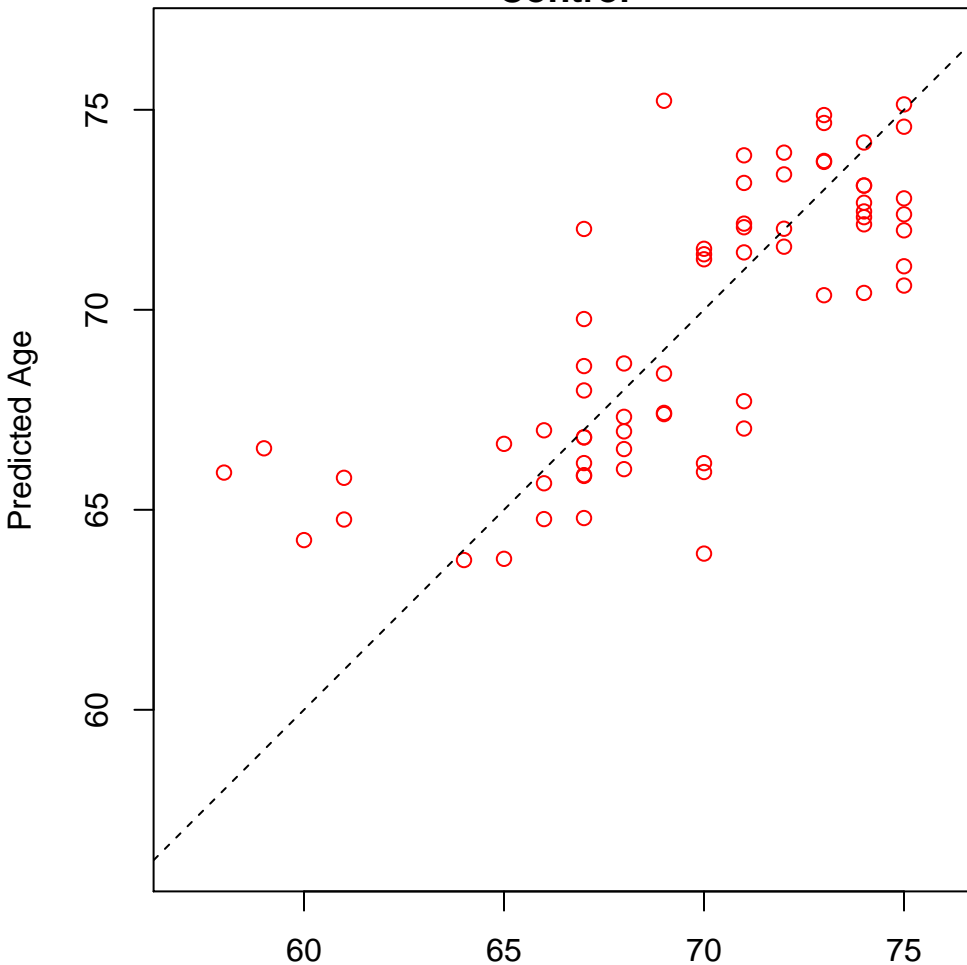


ephrin receptor signaling pathway (Score: 2.082678)

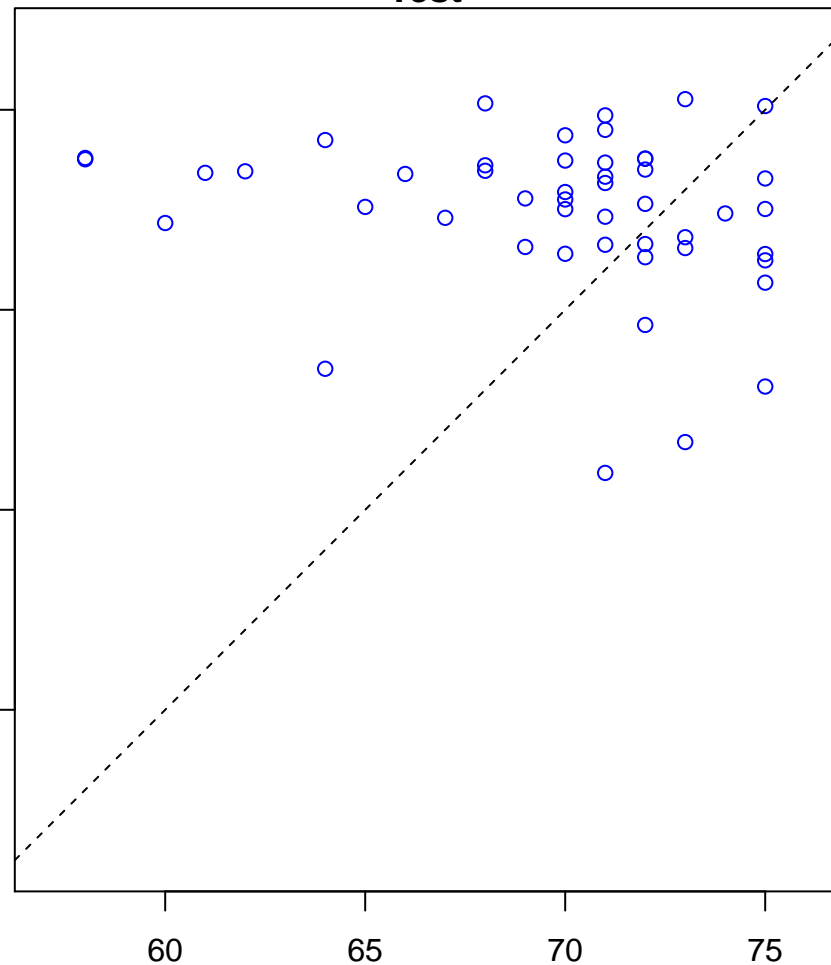


organophosphate biosynthetic process (Score: 2.080358)

Control

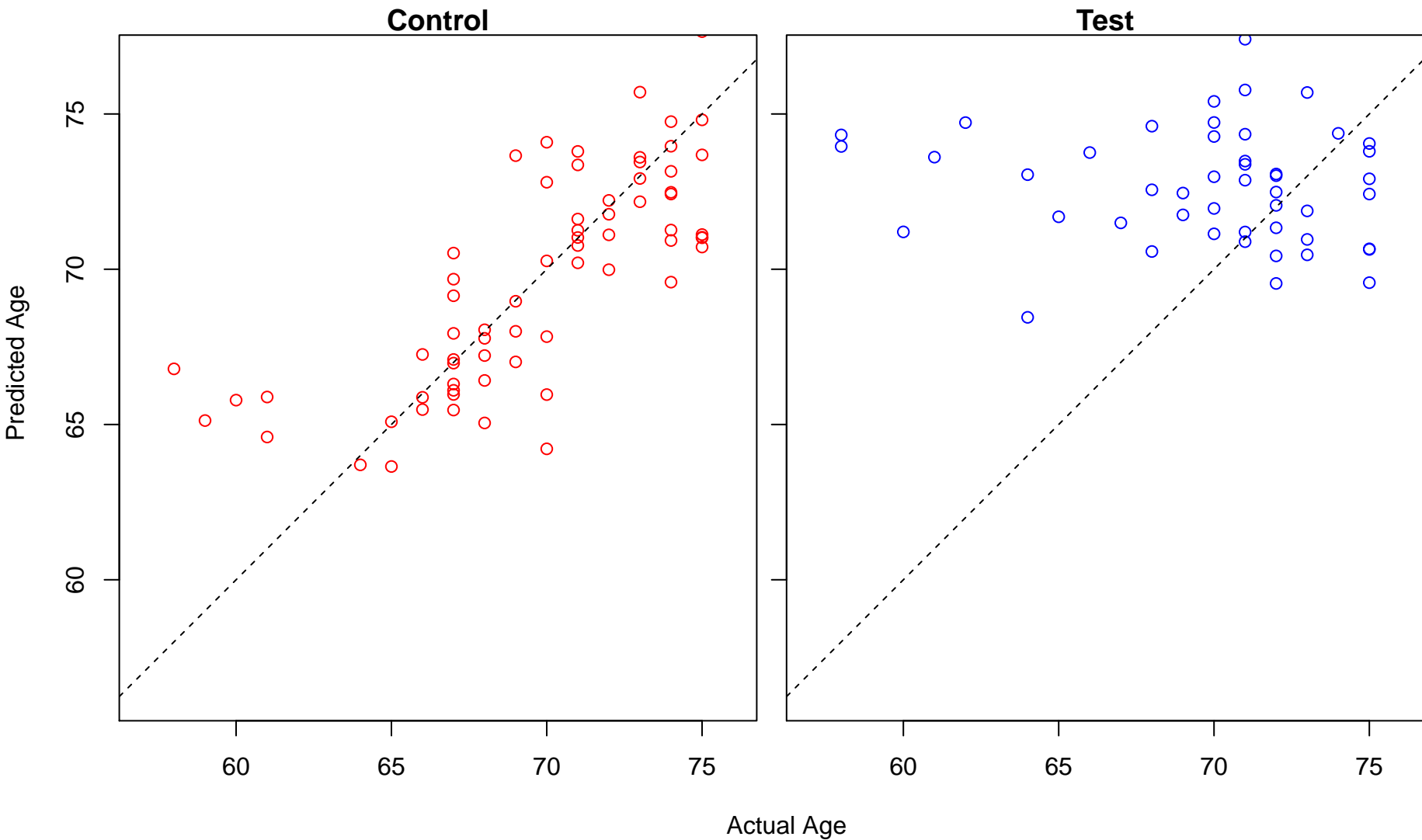


Test

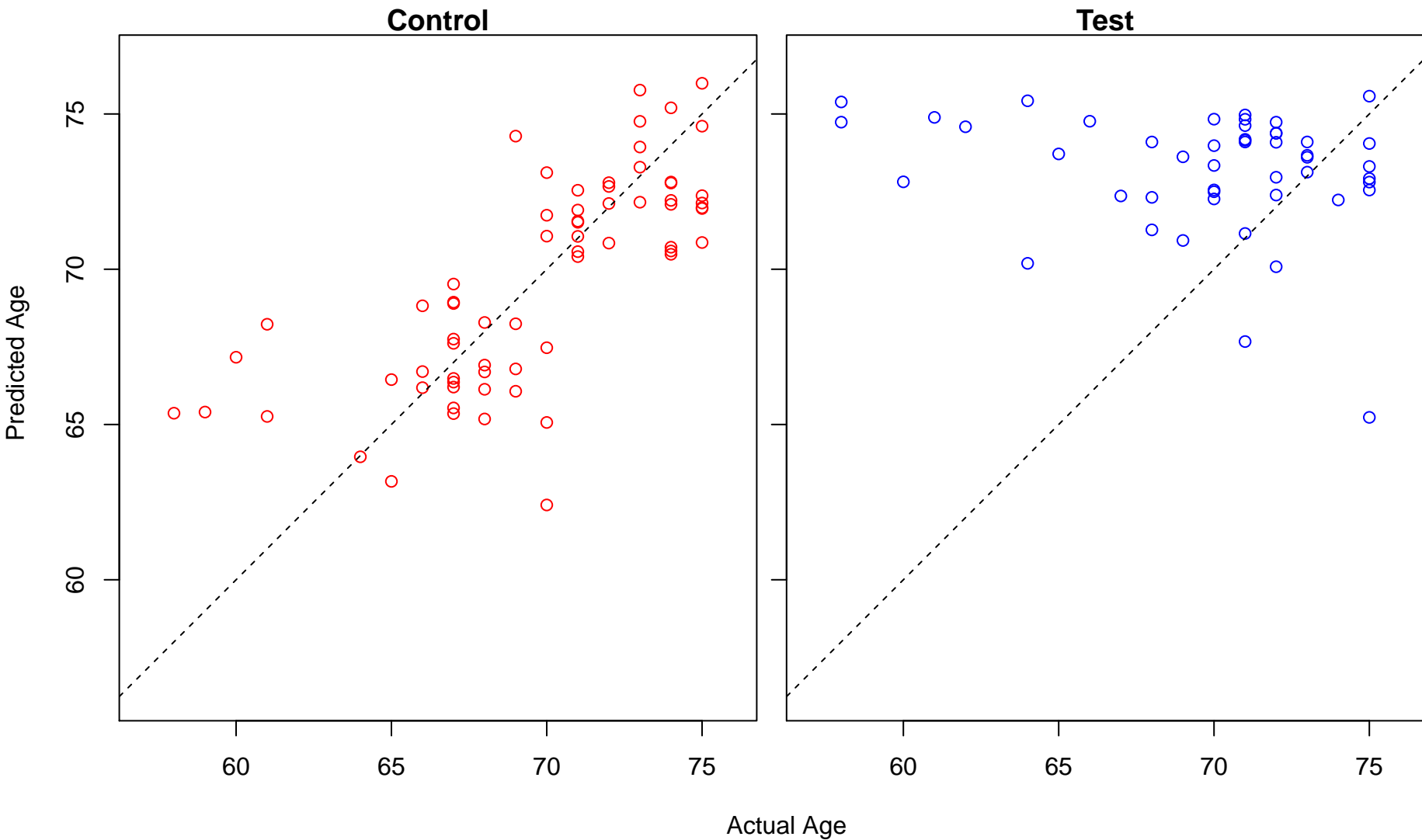


Actual Age

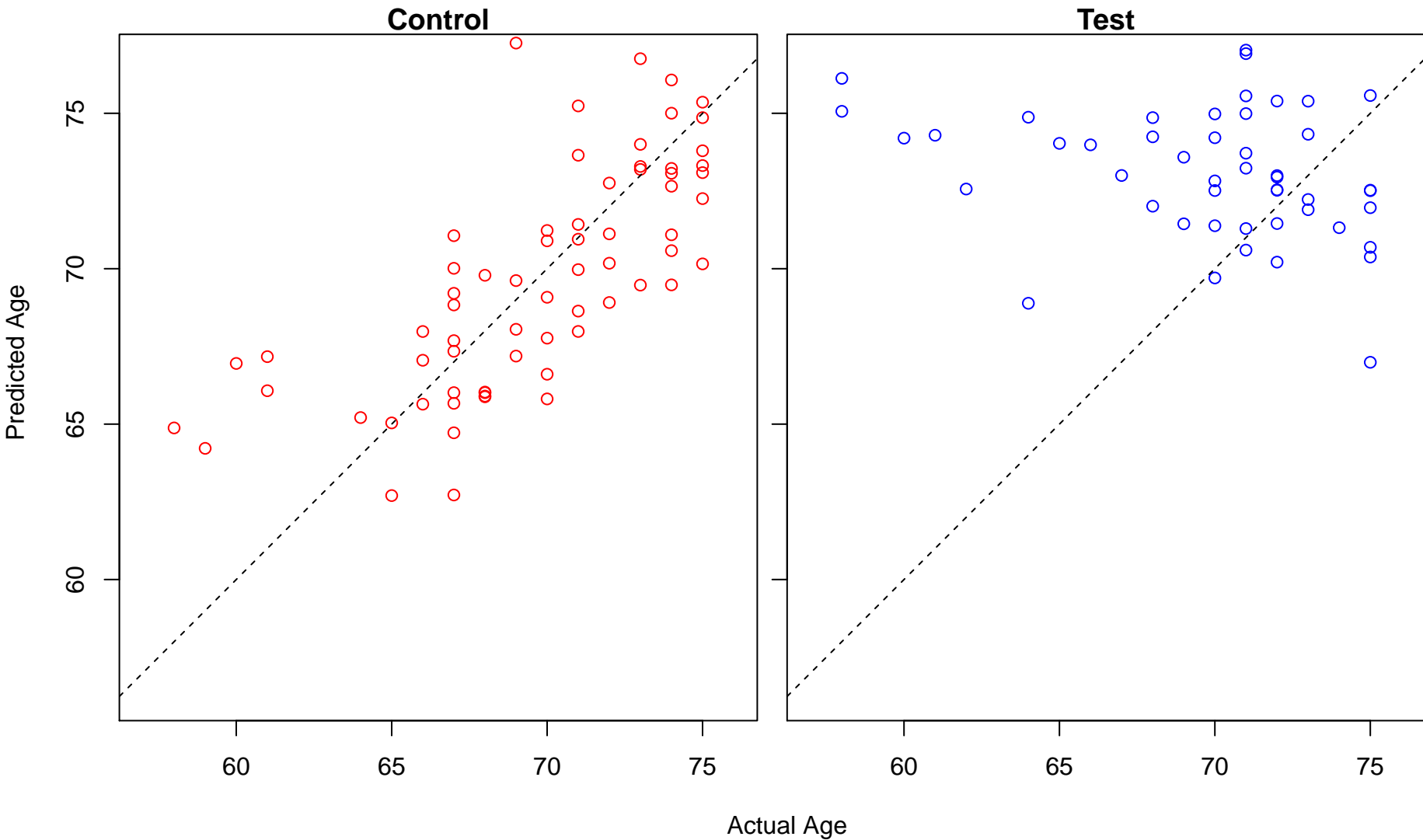
regulation of cytoskeleton organization (Score: 2.078924)



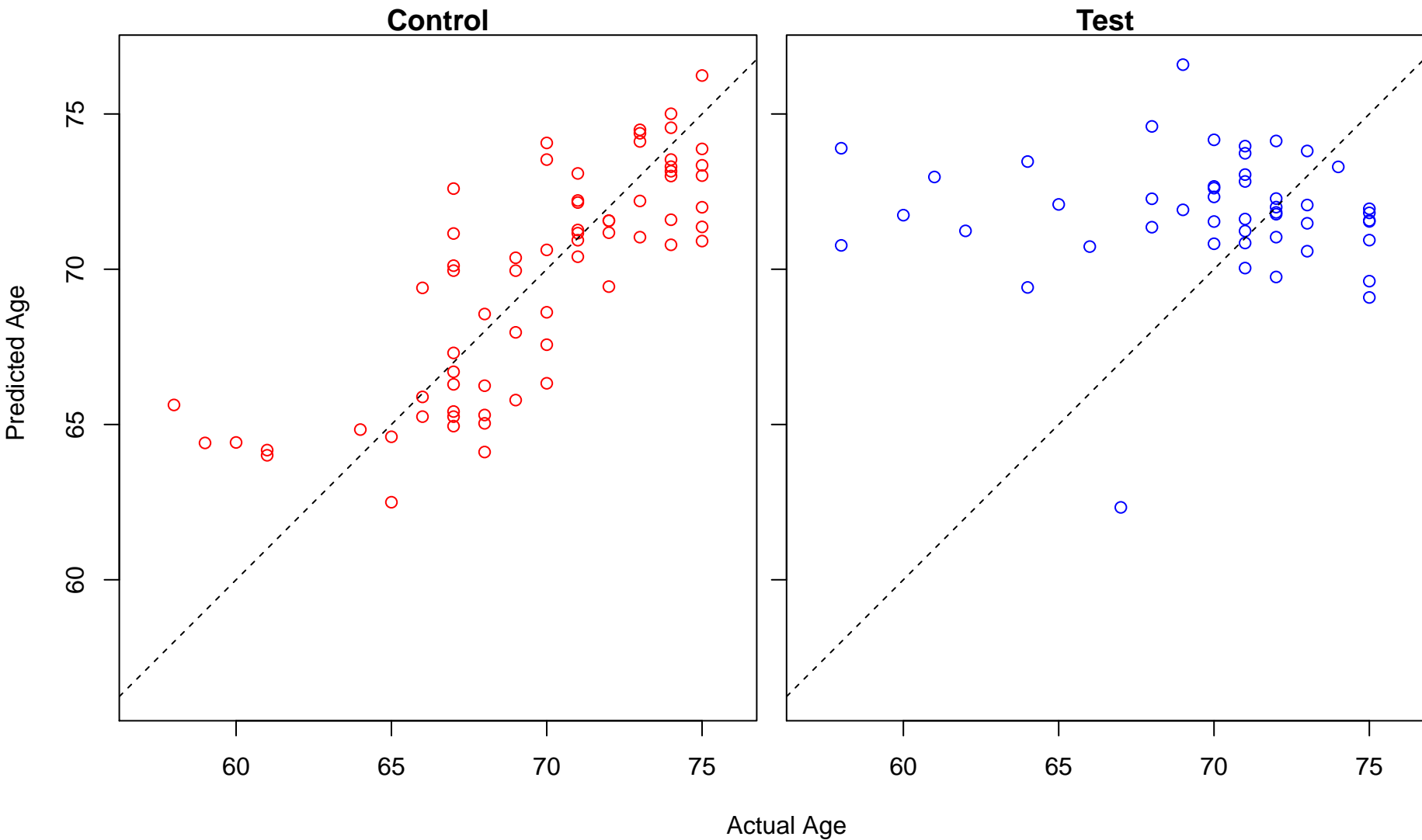
positive regulation of I-kappaB kinase/NF-kappaB signaling (Score: 2.078632)



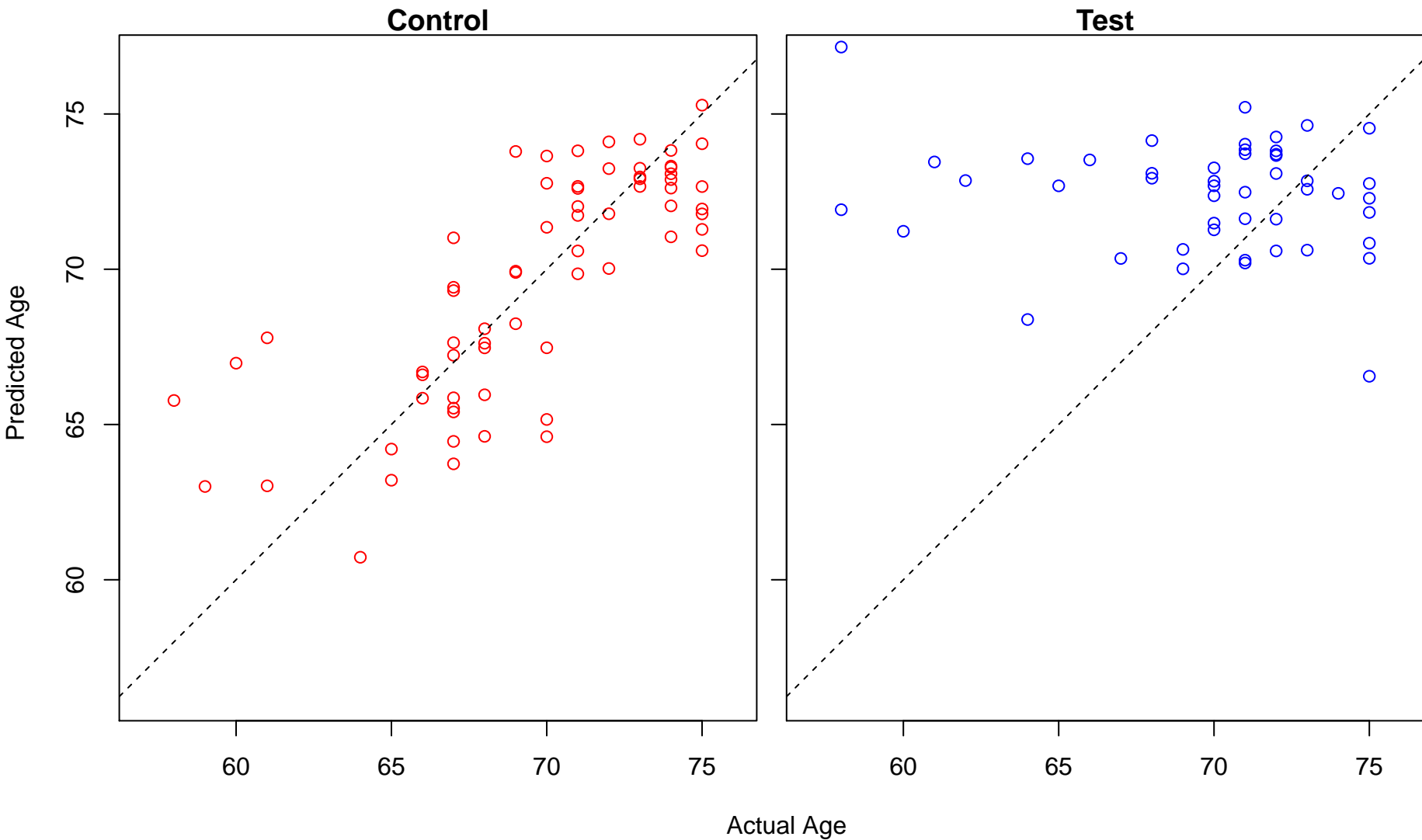
regulation of lymphocyte activation (Score: 2.078135)



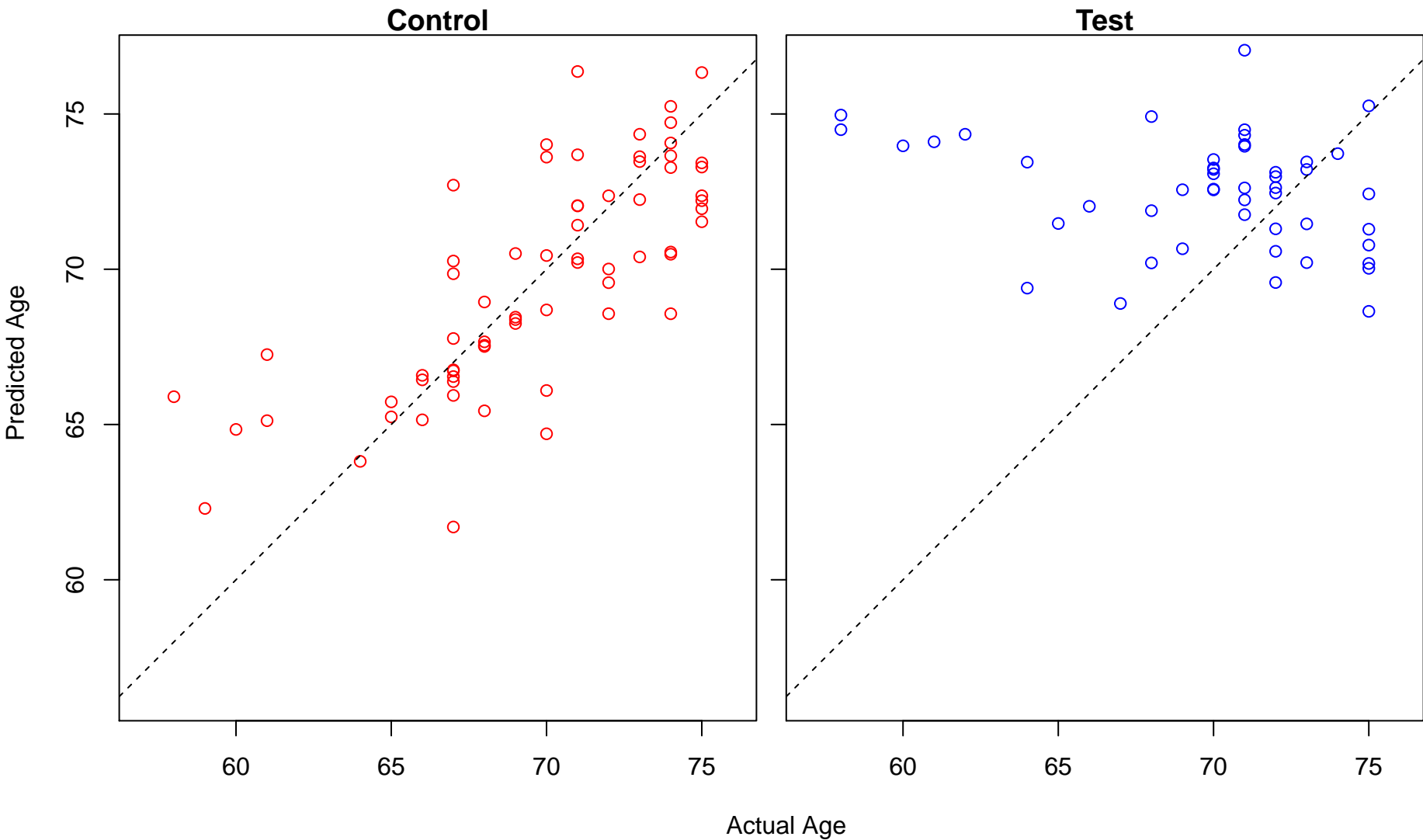
cell division (Score: 2.078014)



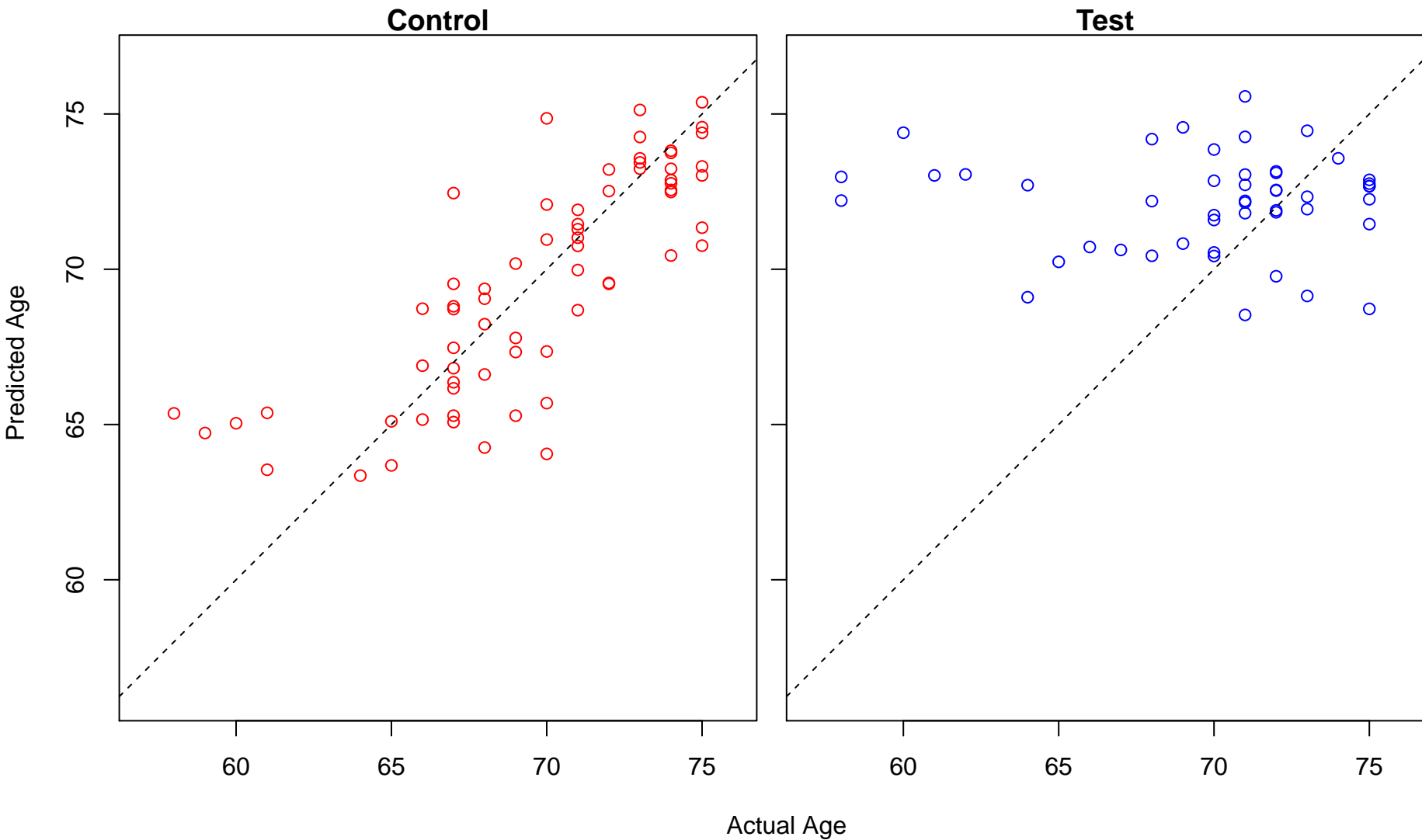
positive regulation of cysteine-type endopeptidase activity (Score: 2.076970)



positive regulation of establishment of protein localization to mitochondrion (Score: 2.071865)

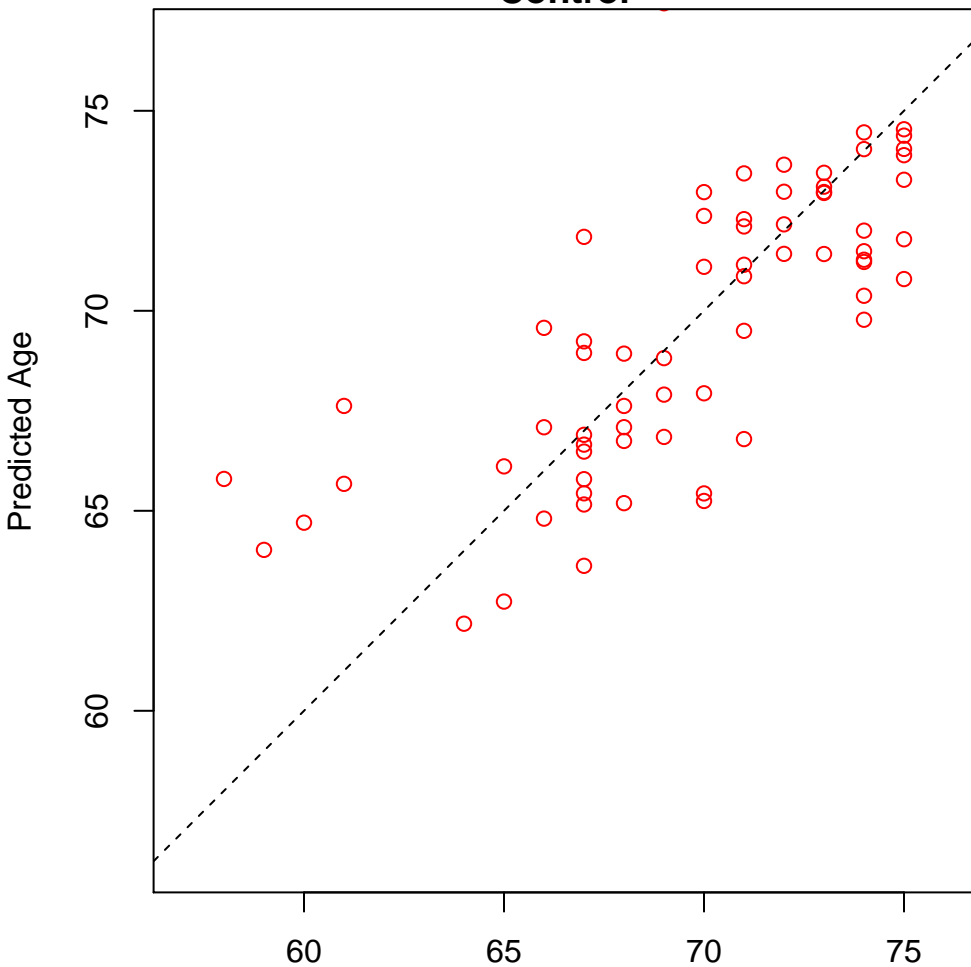


regulation of cell division (Score: 2.070039)

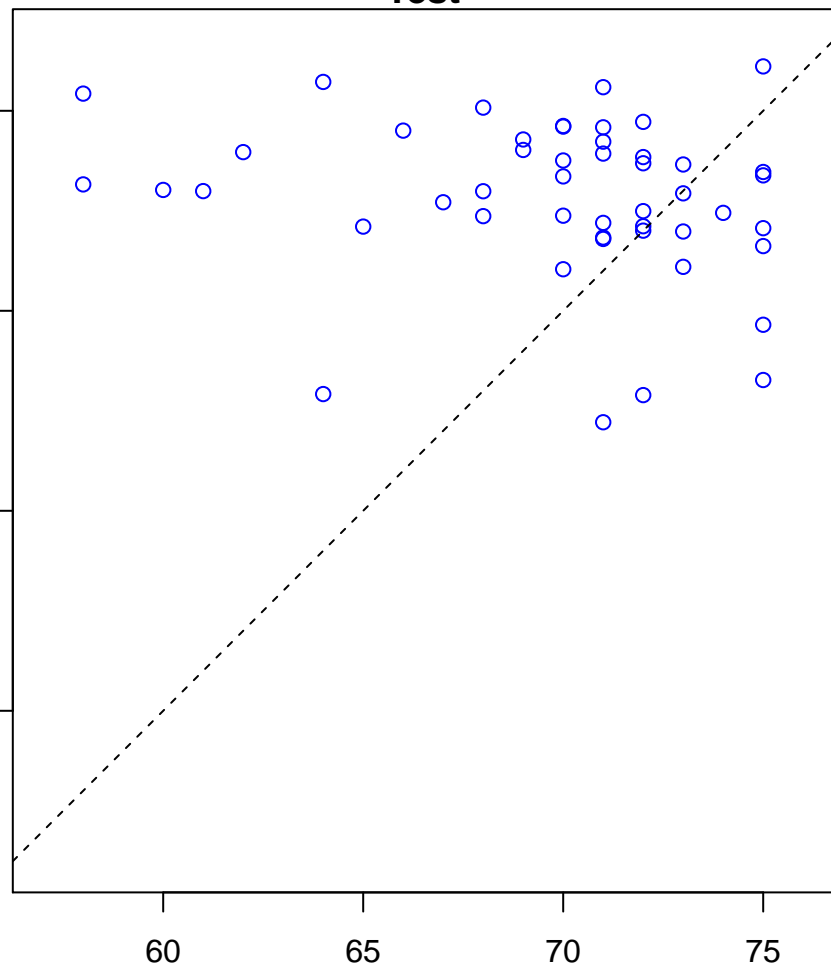


regulation of immune effector process (Score: 2.067993)

Control

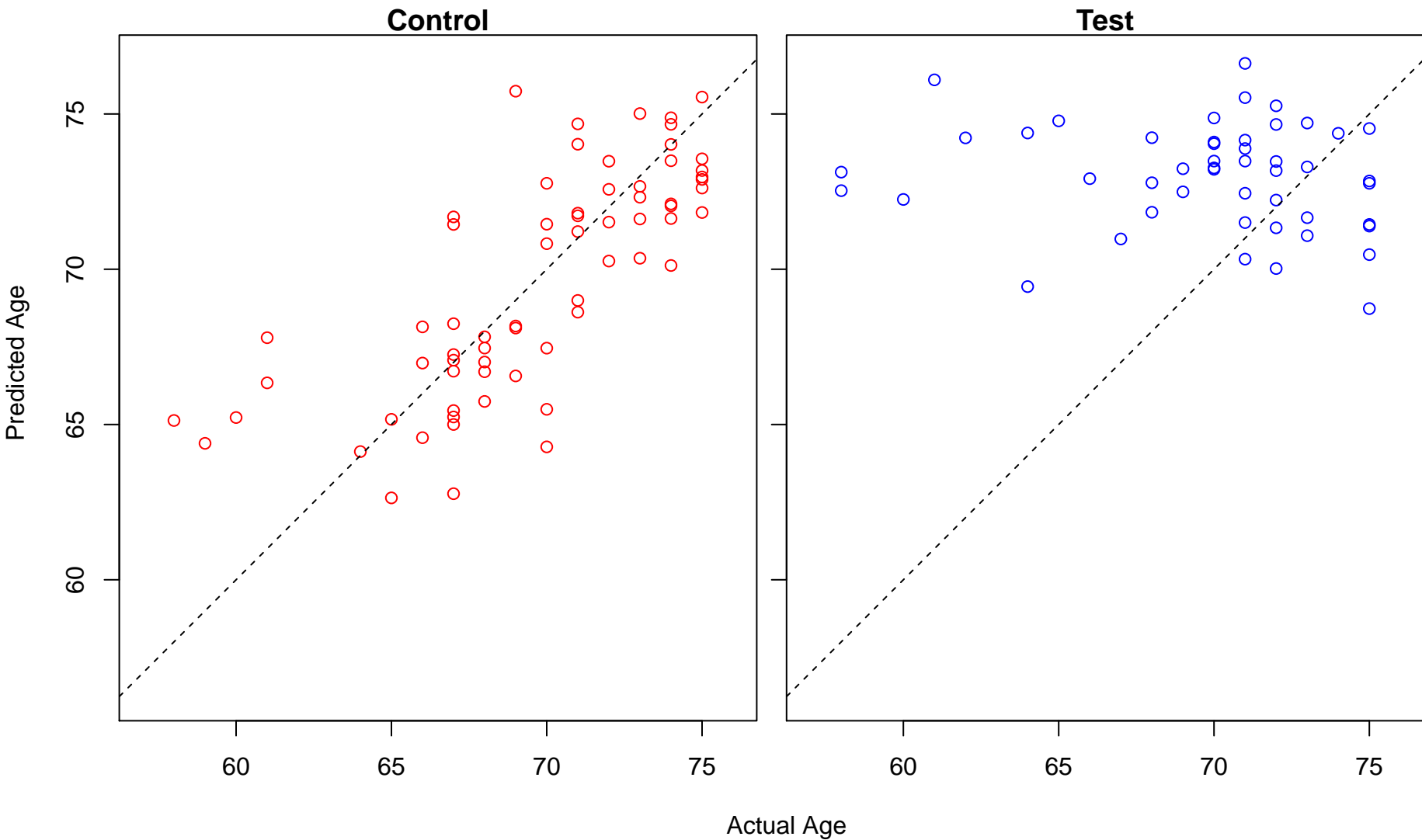


Test

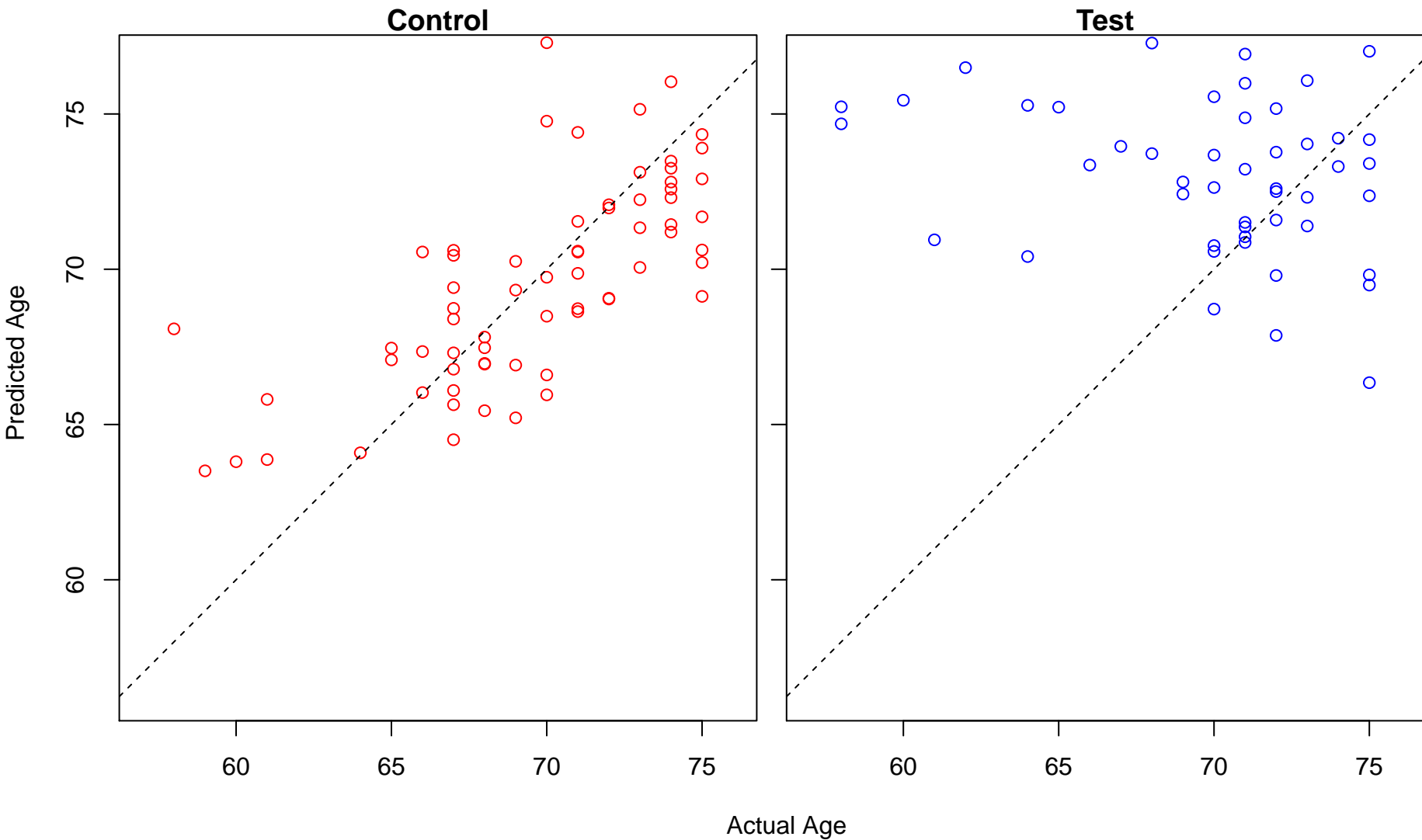


Actual Age

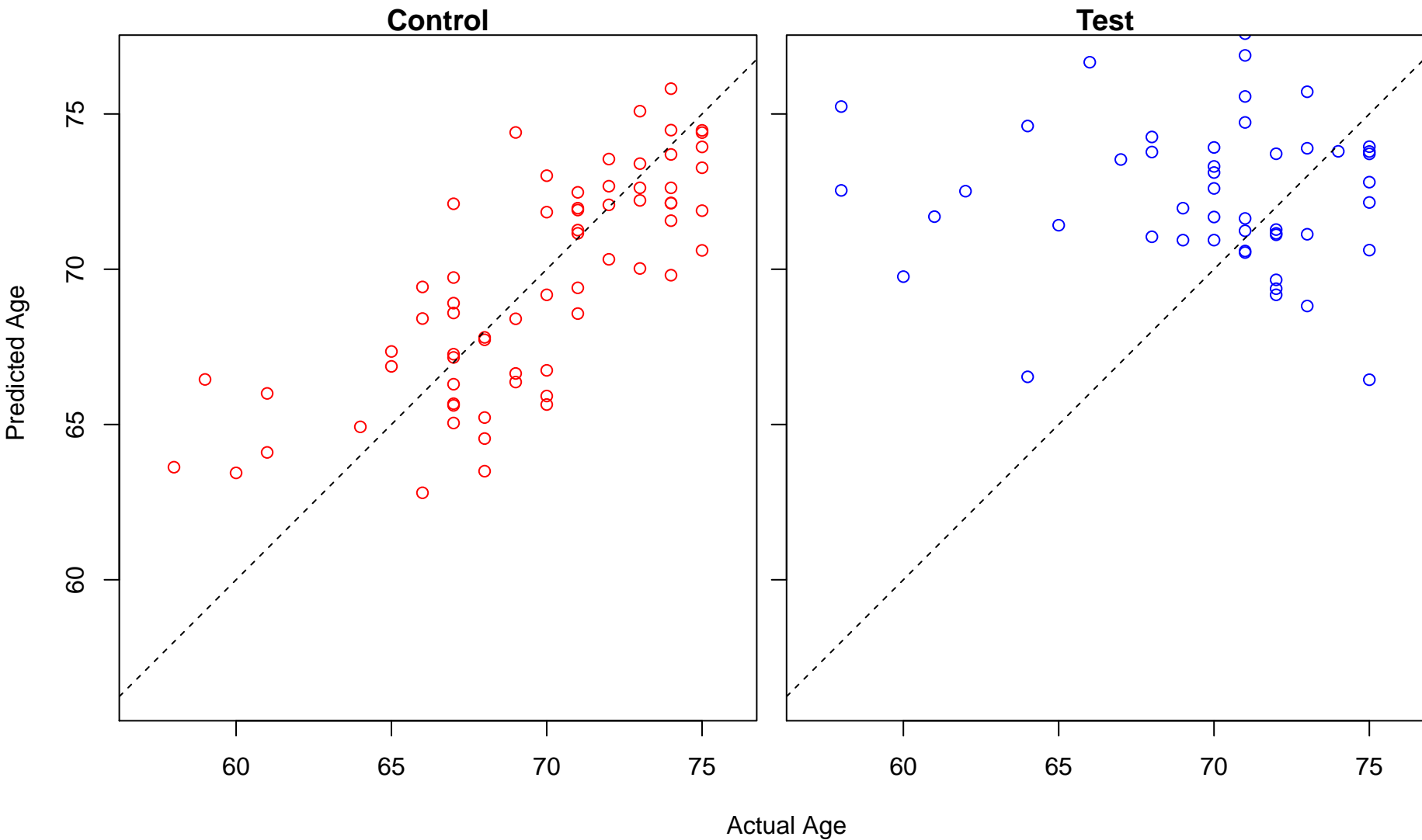
multi-organism cellular process (Score: 2.065319)



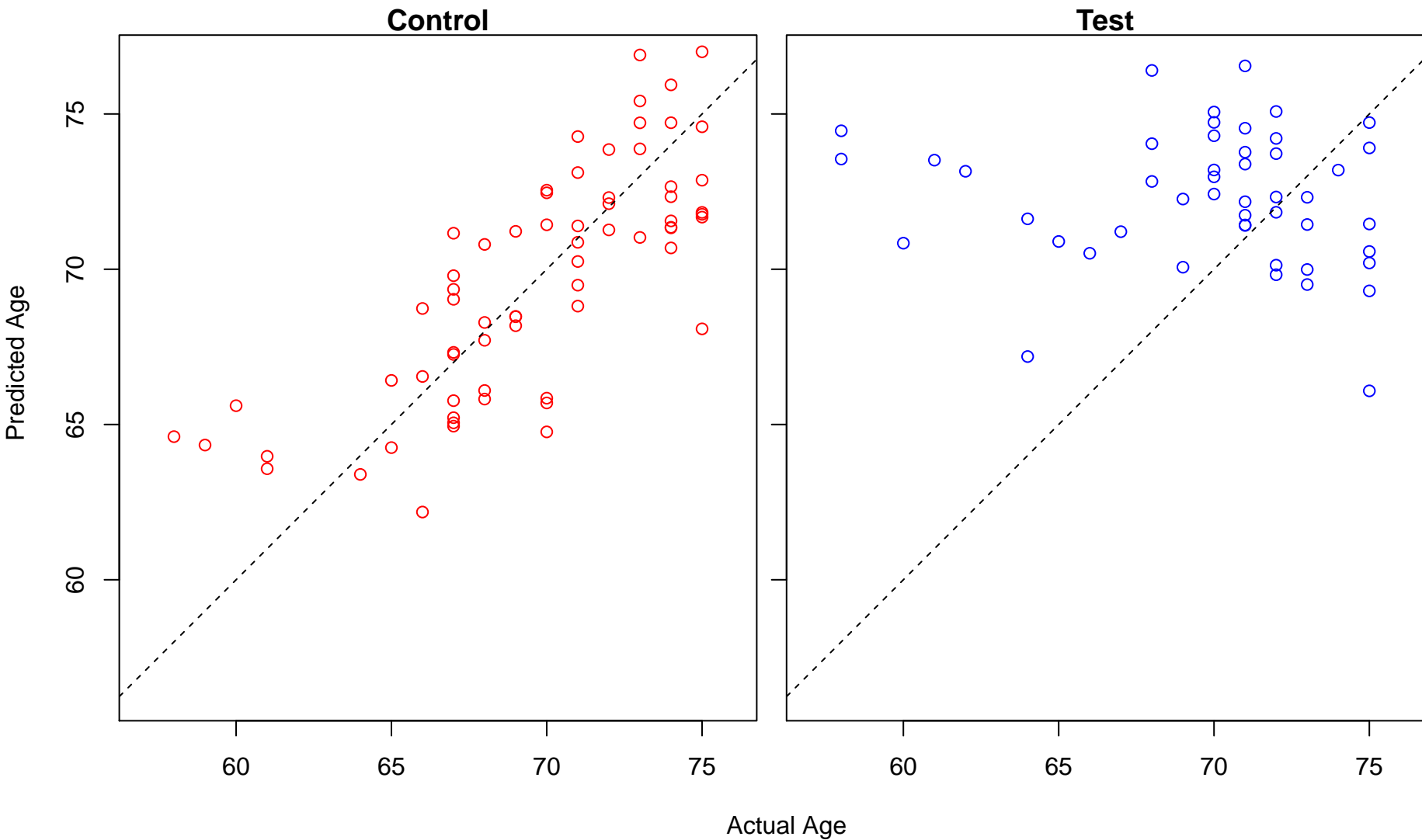
regulation of TOR signaling (Score: 2.064435)



negative regulation of response to external stimulus (Score: 2.064112)

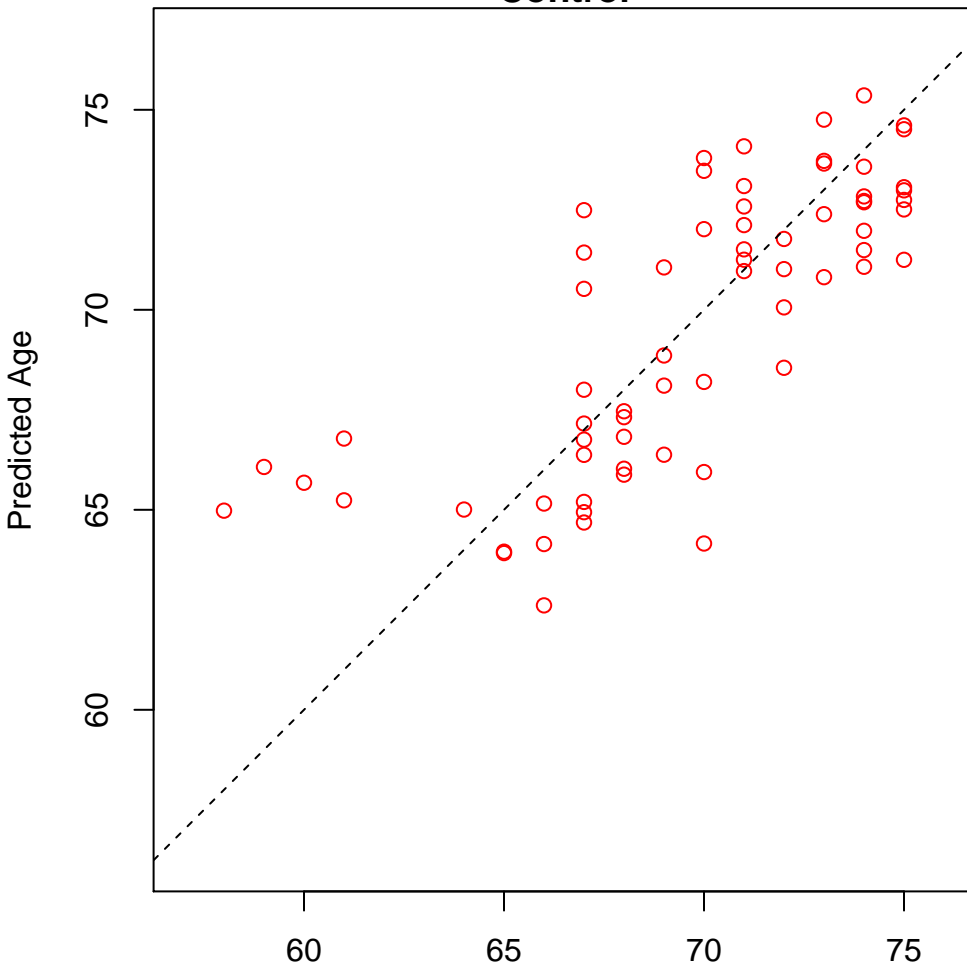


phospholipid biosynthetic process (Score: 2.063376)

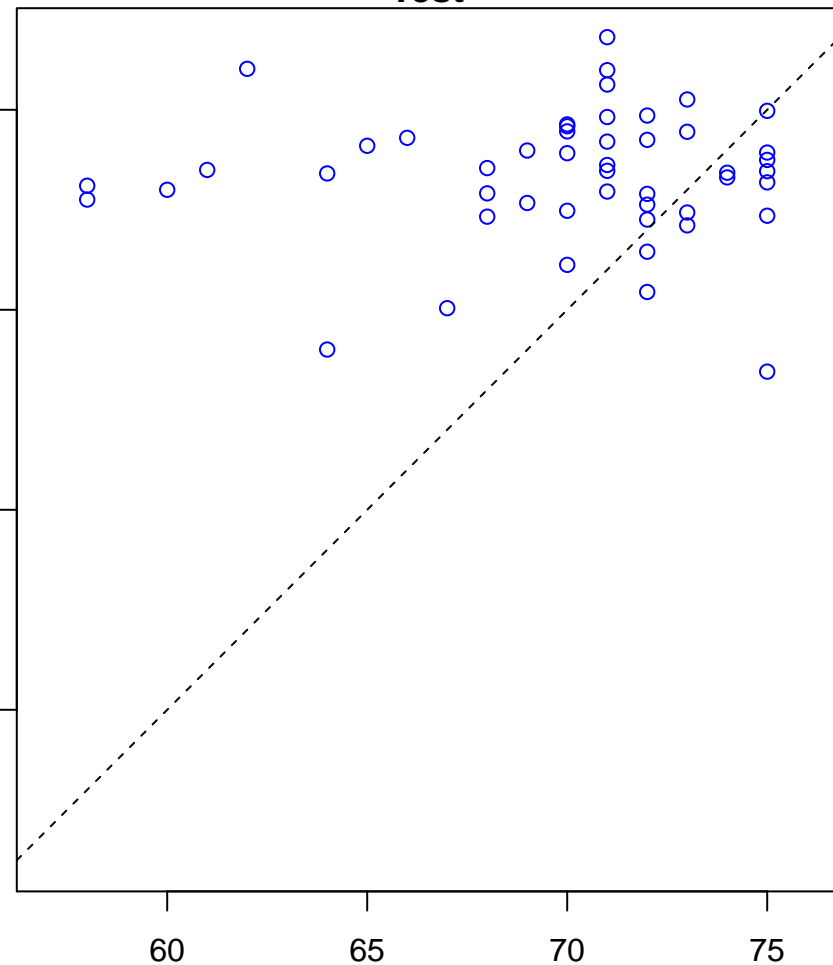


internal protein amino acid acetylation (Score: 2.063303)

Control

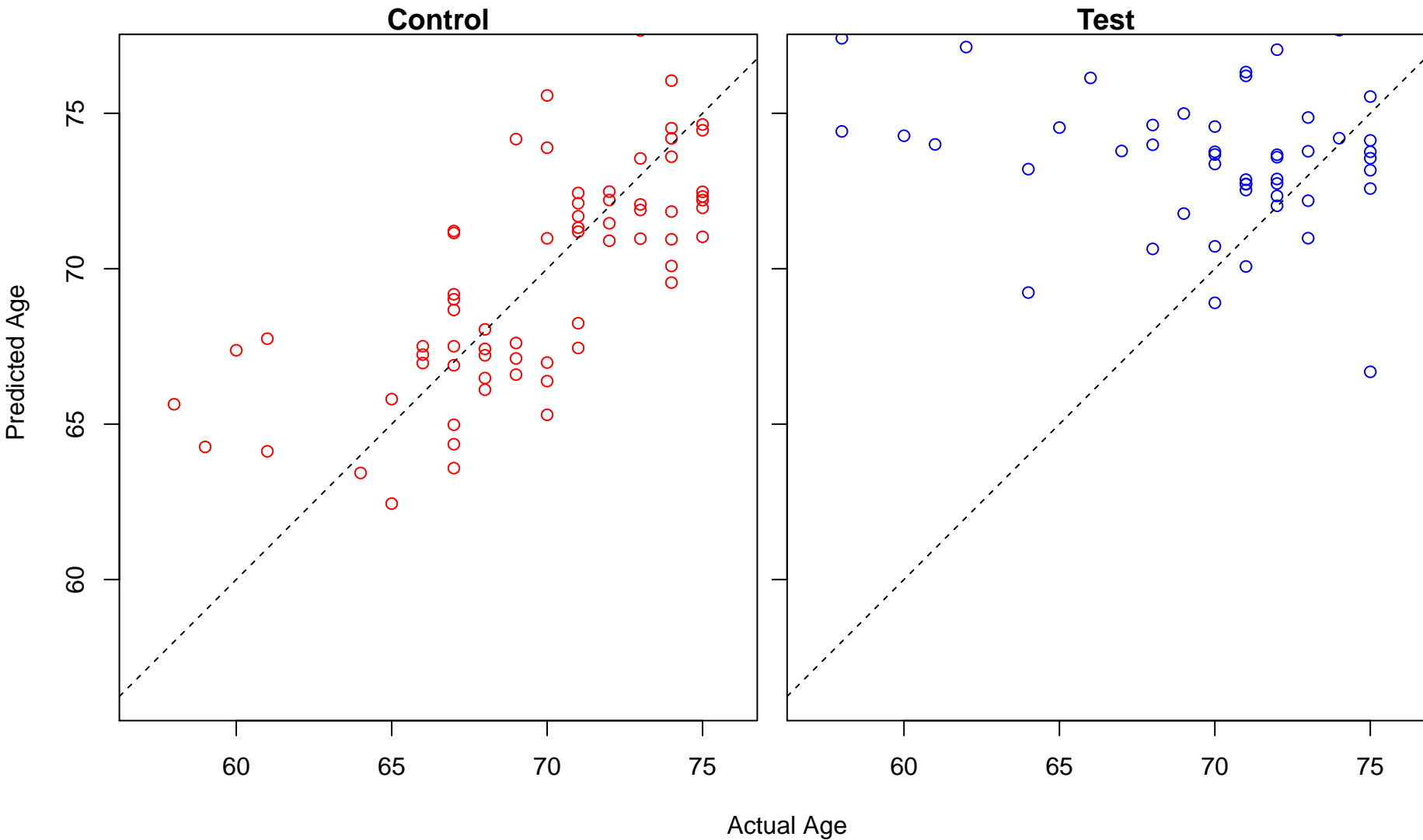


Test

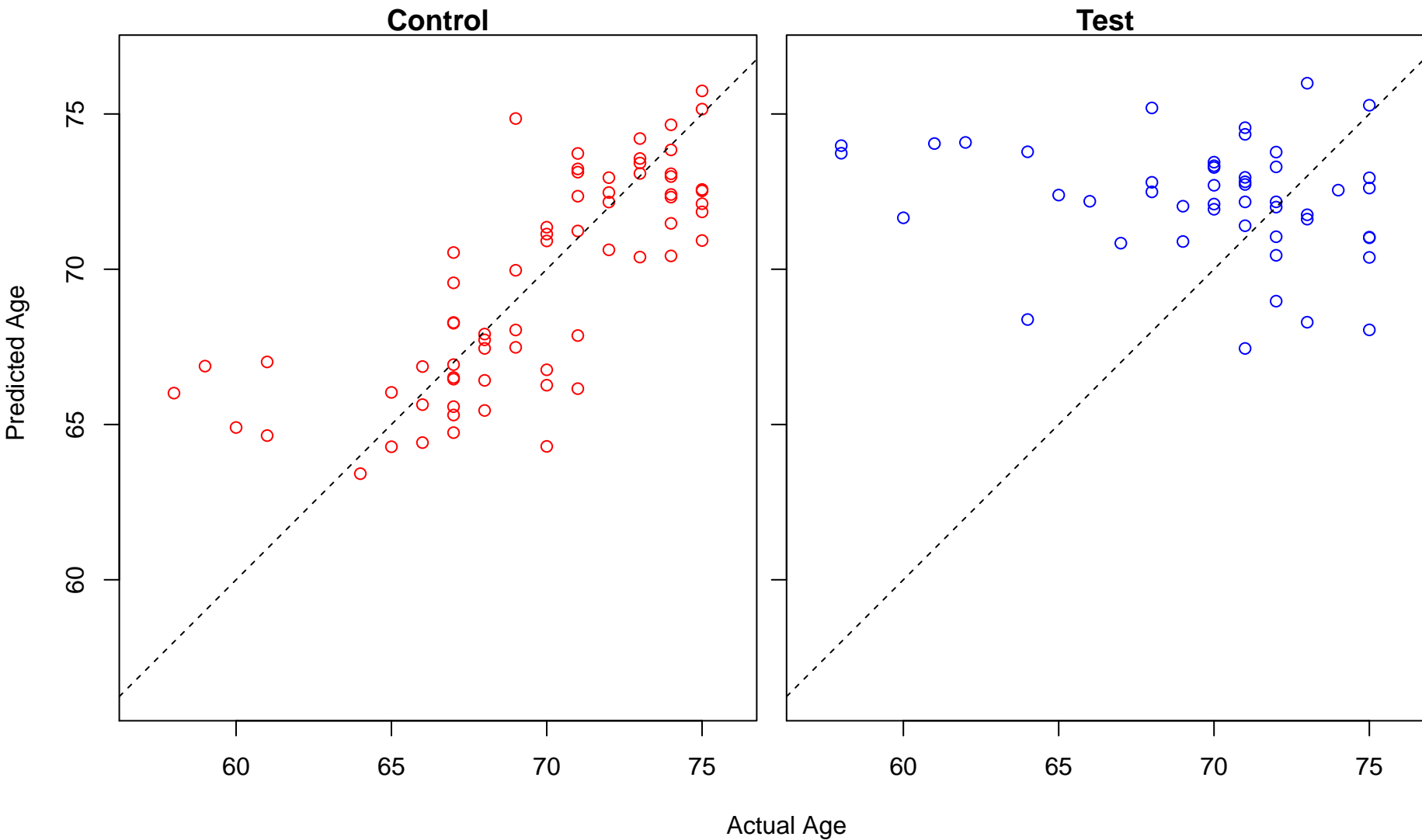


Actual Age

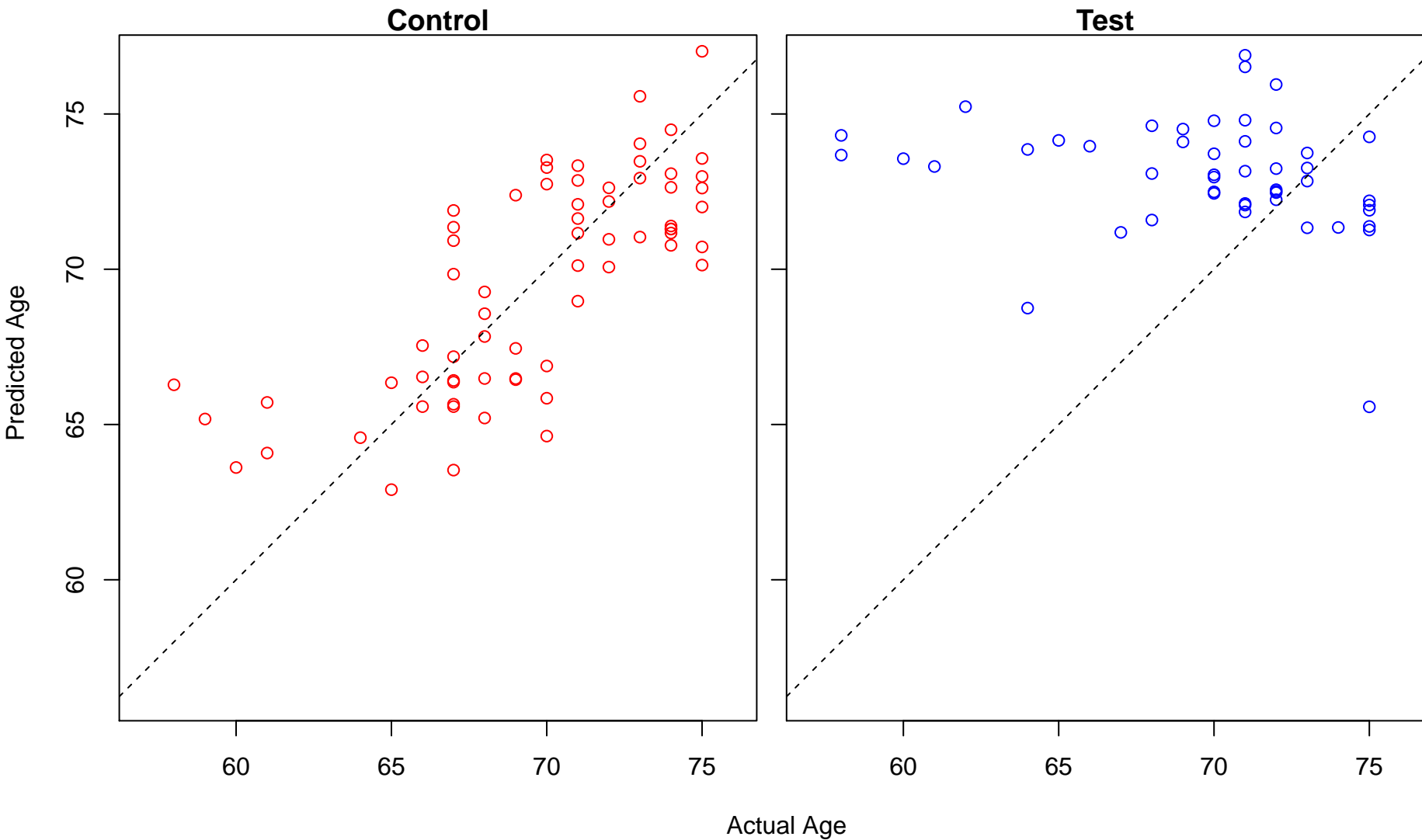
regulation of response to cytokine stimulus (Score: 2.063054)



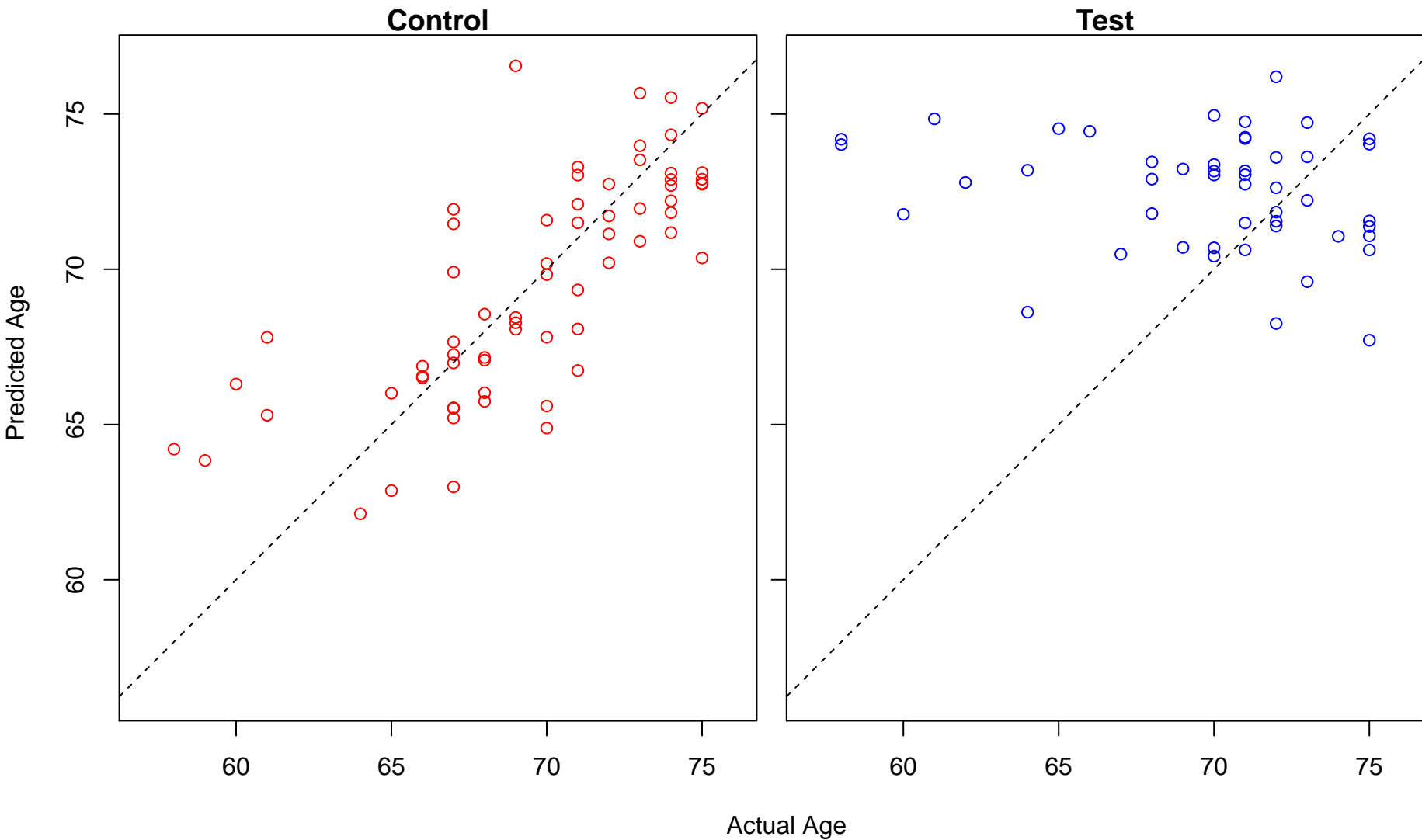
nucleoside phosphate metabolic process (Score: 2.062794)



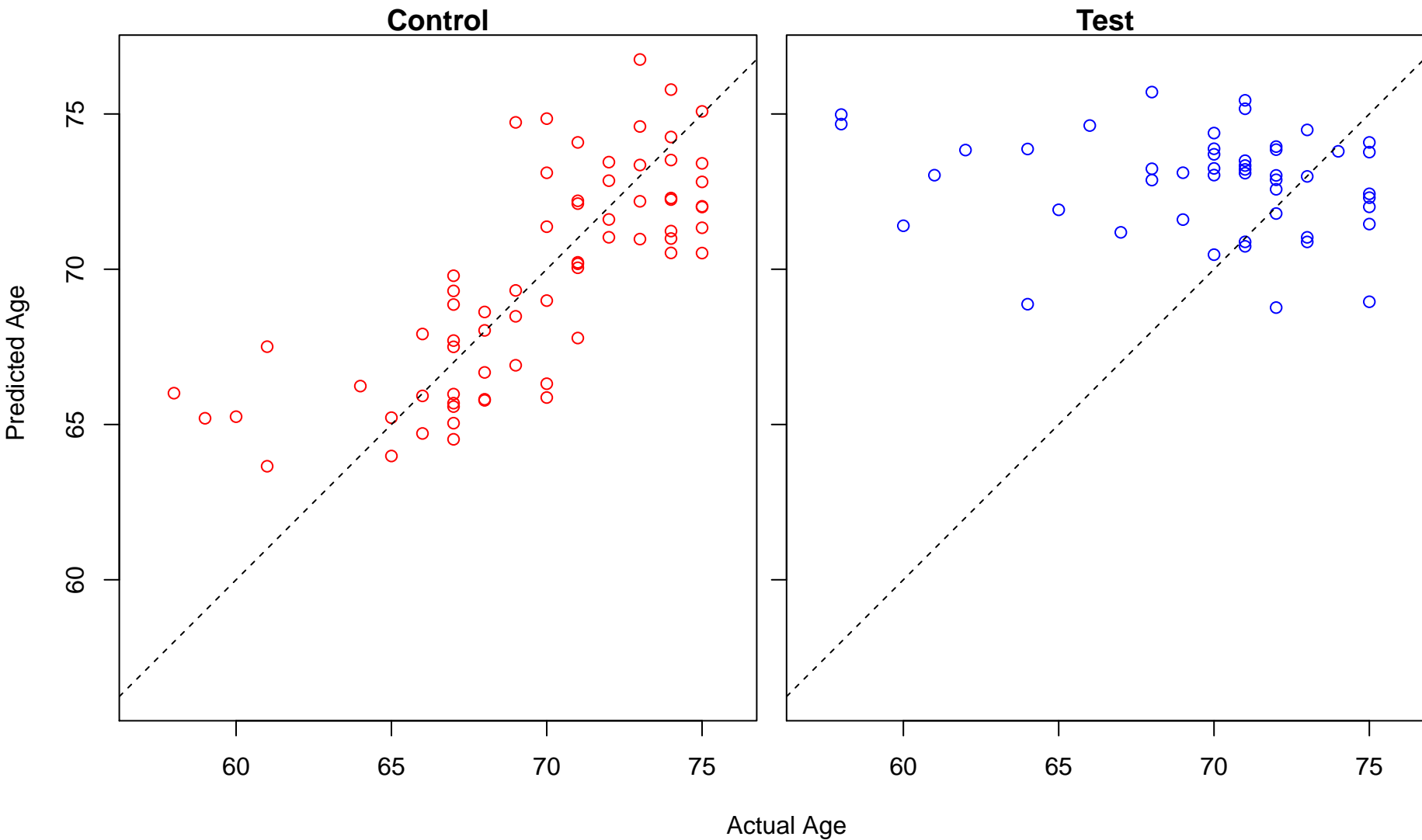
lipid biosynthetic process (Score: 2.061172)



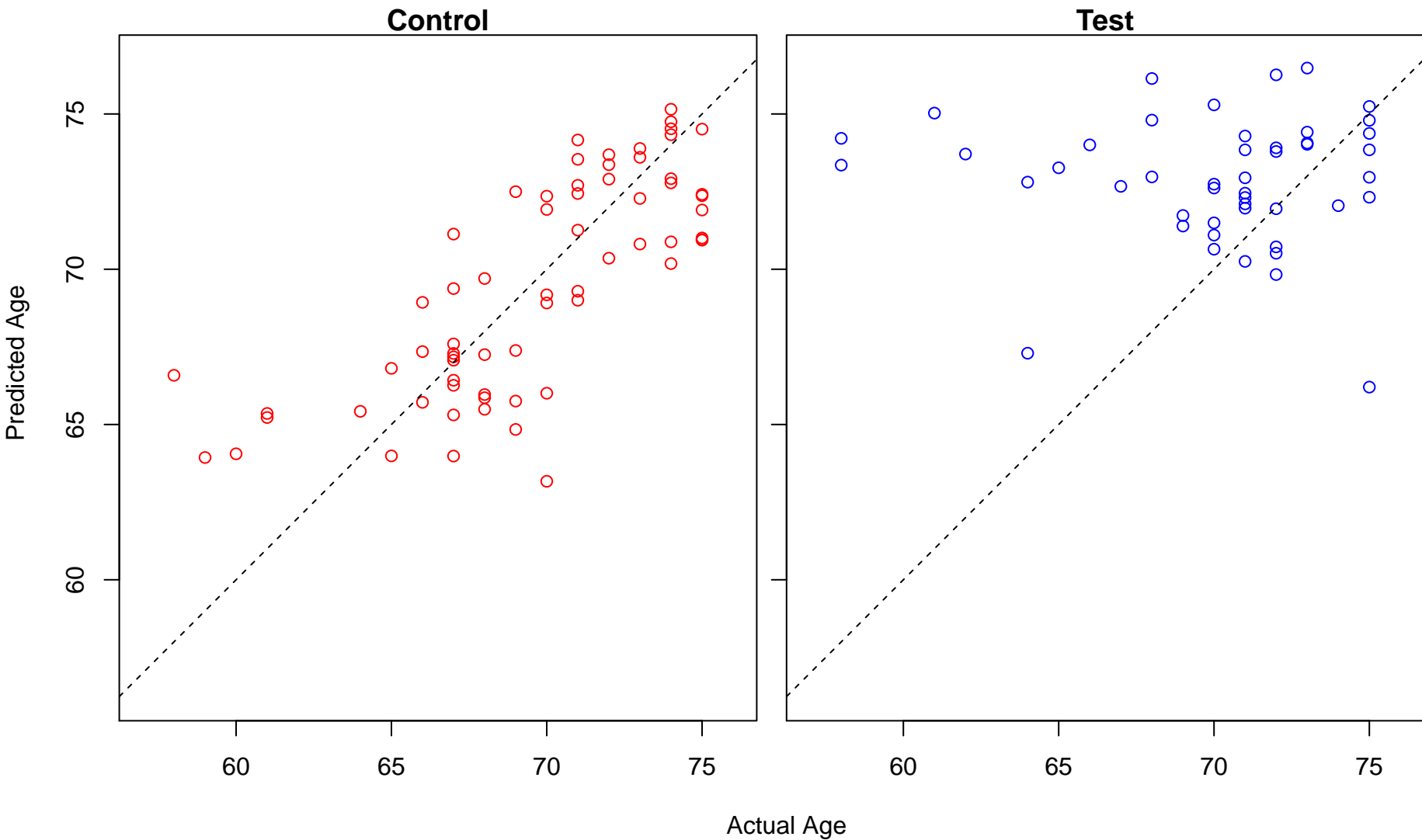
cytokine-mediated signaling pathway (Score: 2.060516)



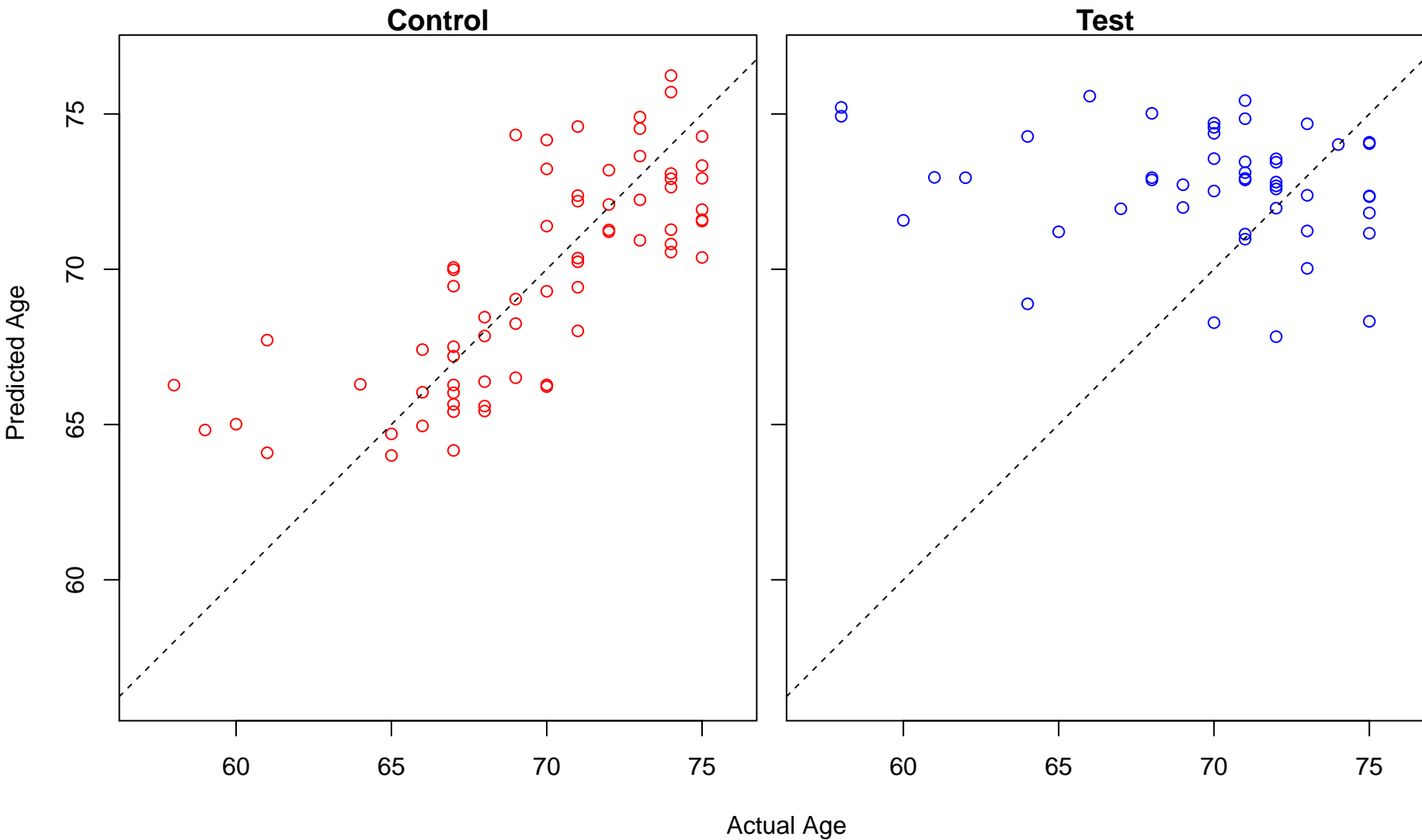
cellular homeostasis (Score: 2.060304)



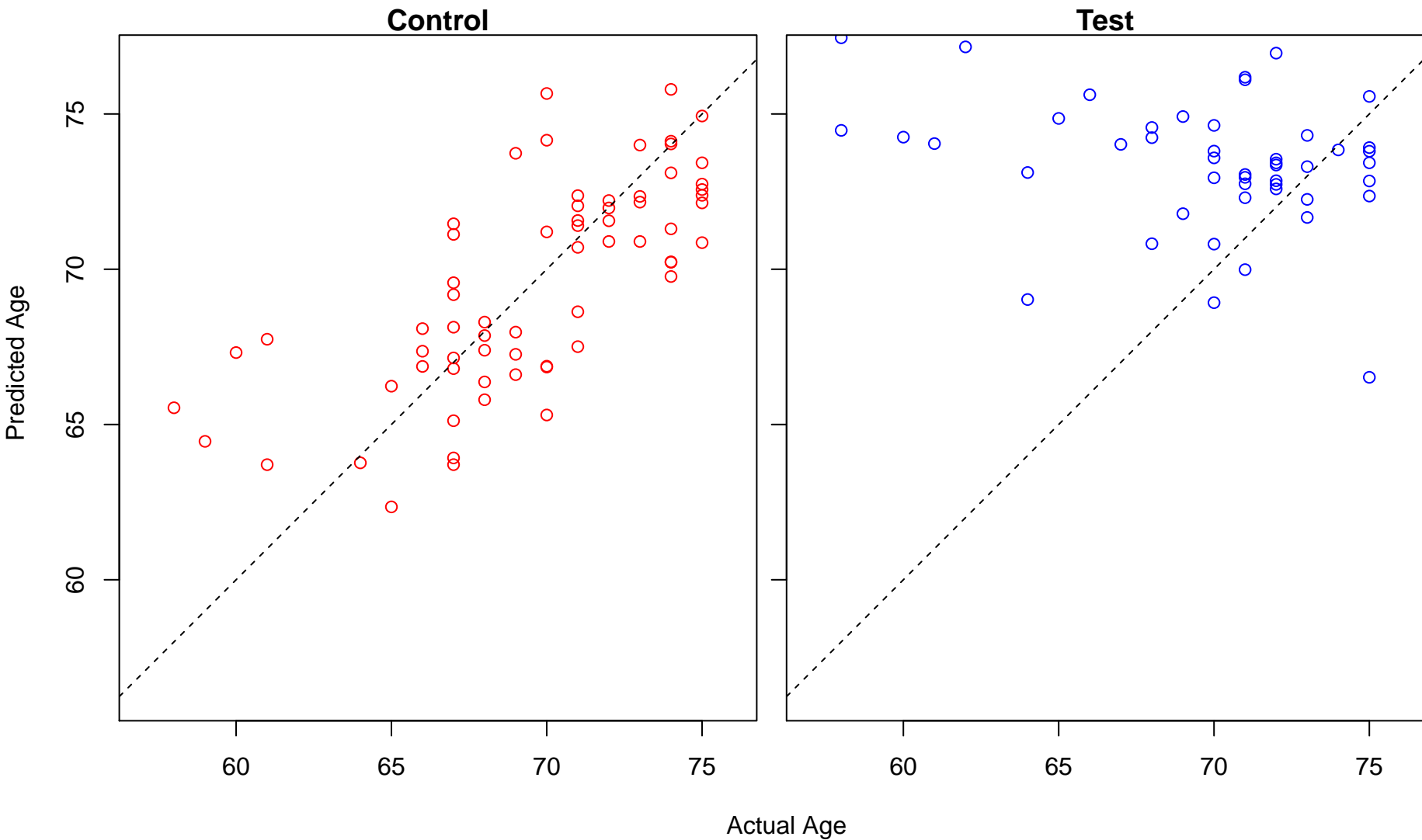
regulation of cell growth (Score: 2.060165)



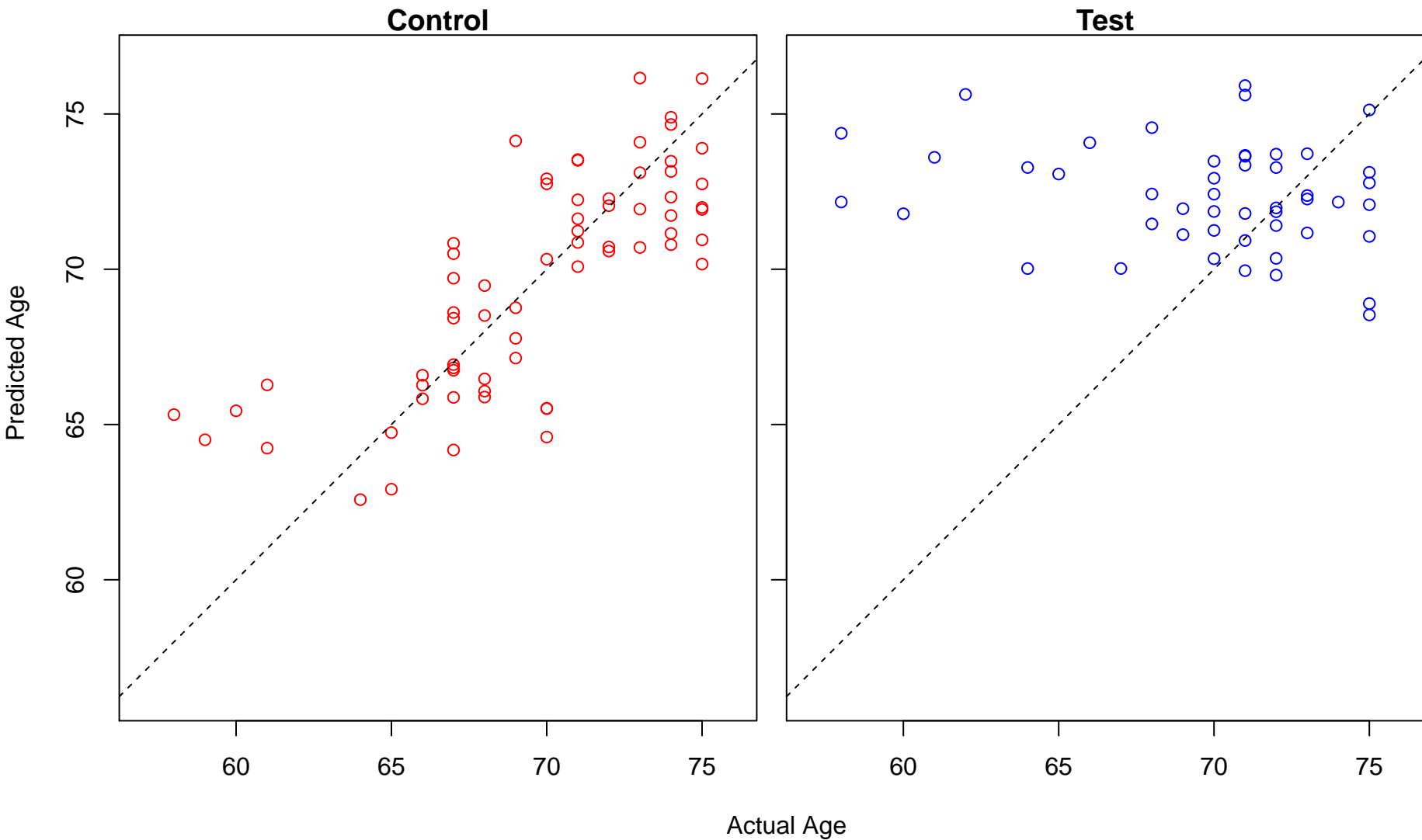
cellular chemical homeostasis (Score: 2.055517)



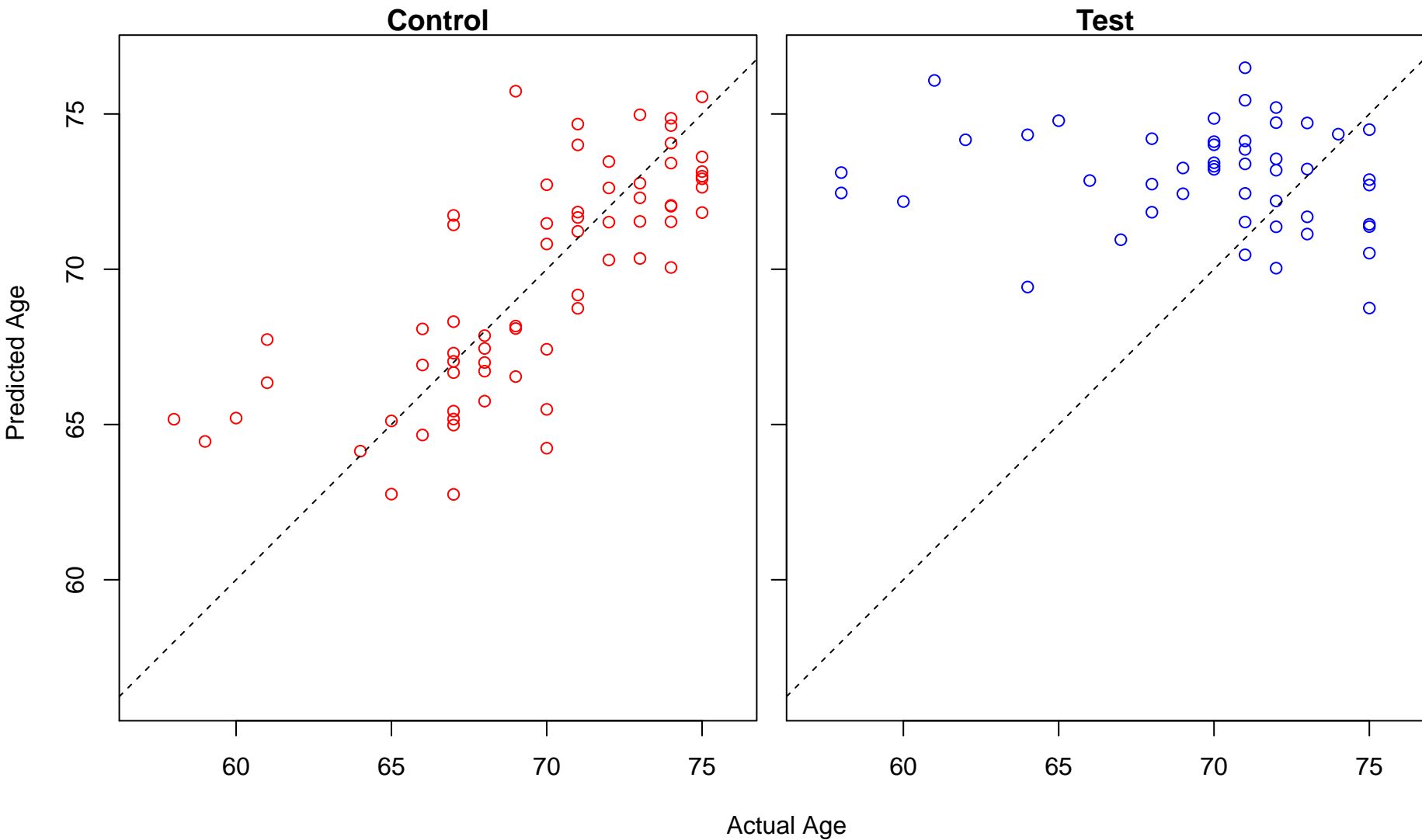
regulation of cytokine-mediated signaling pathway (Score: 2.053969)



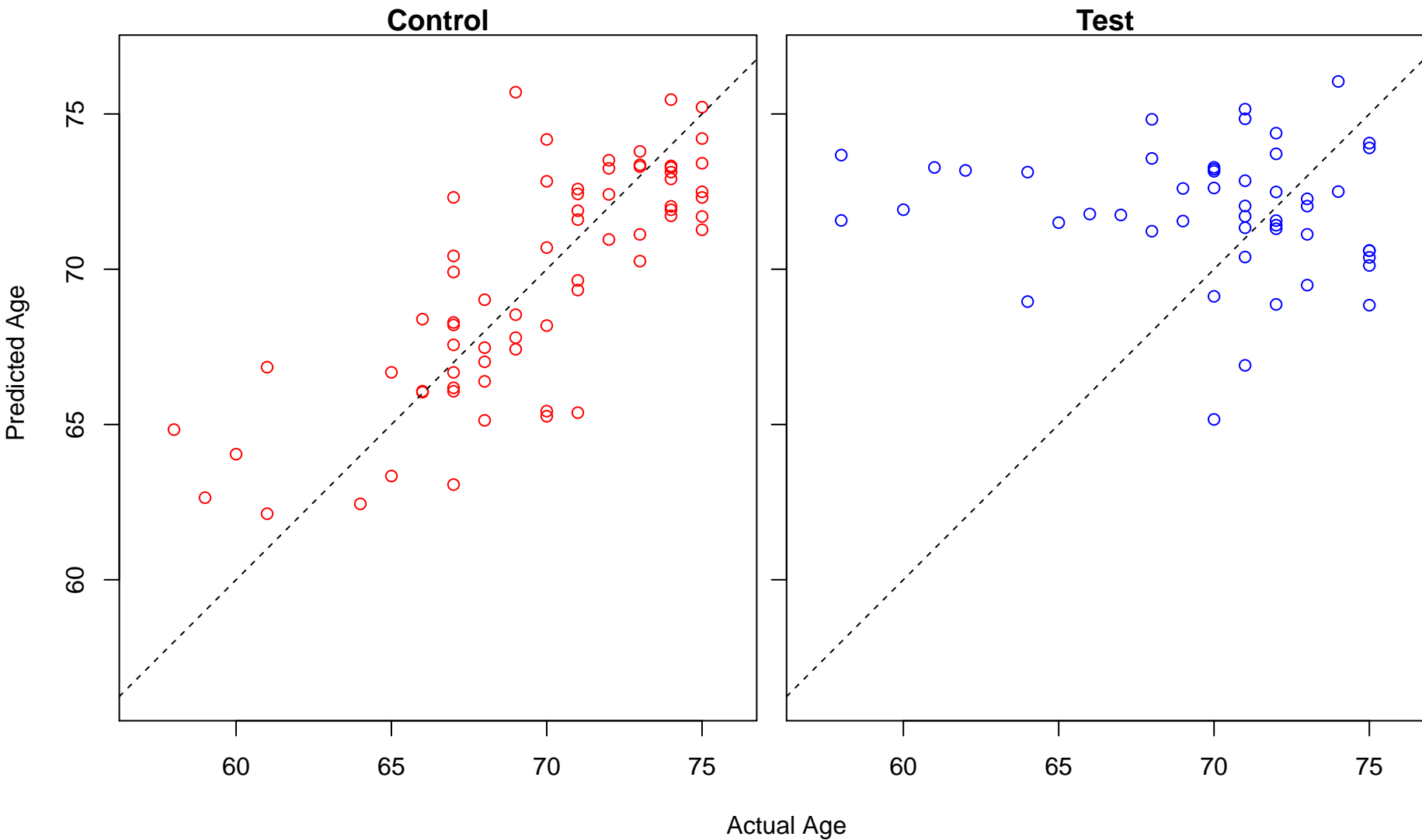
positive regulation of cellular component biogenesis (Score: 2.052675)



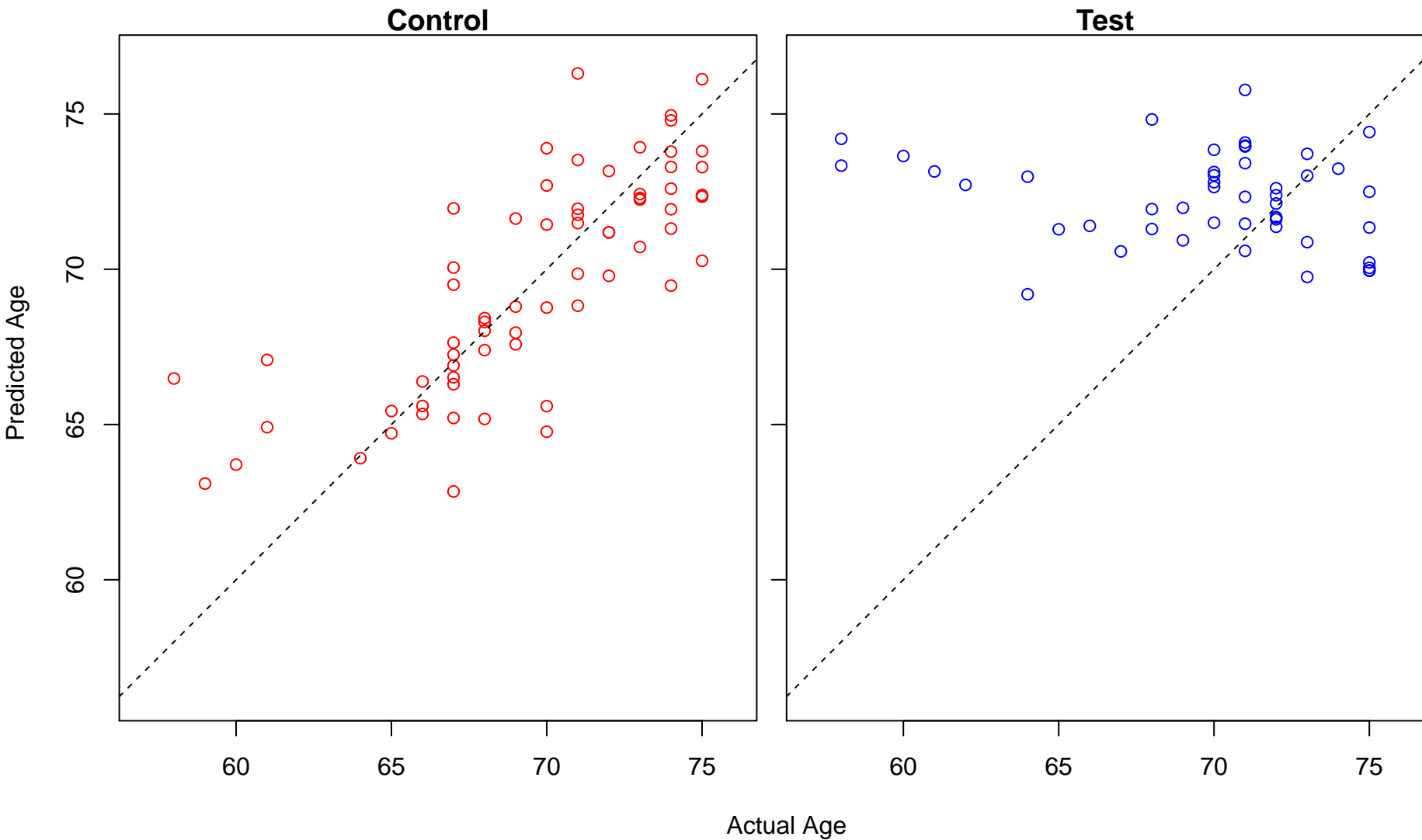
viral process (Score: 2.052556)



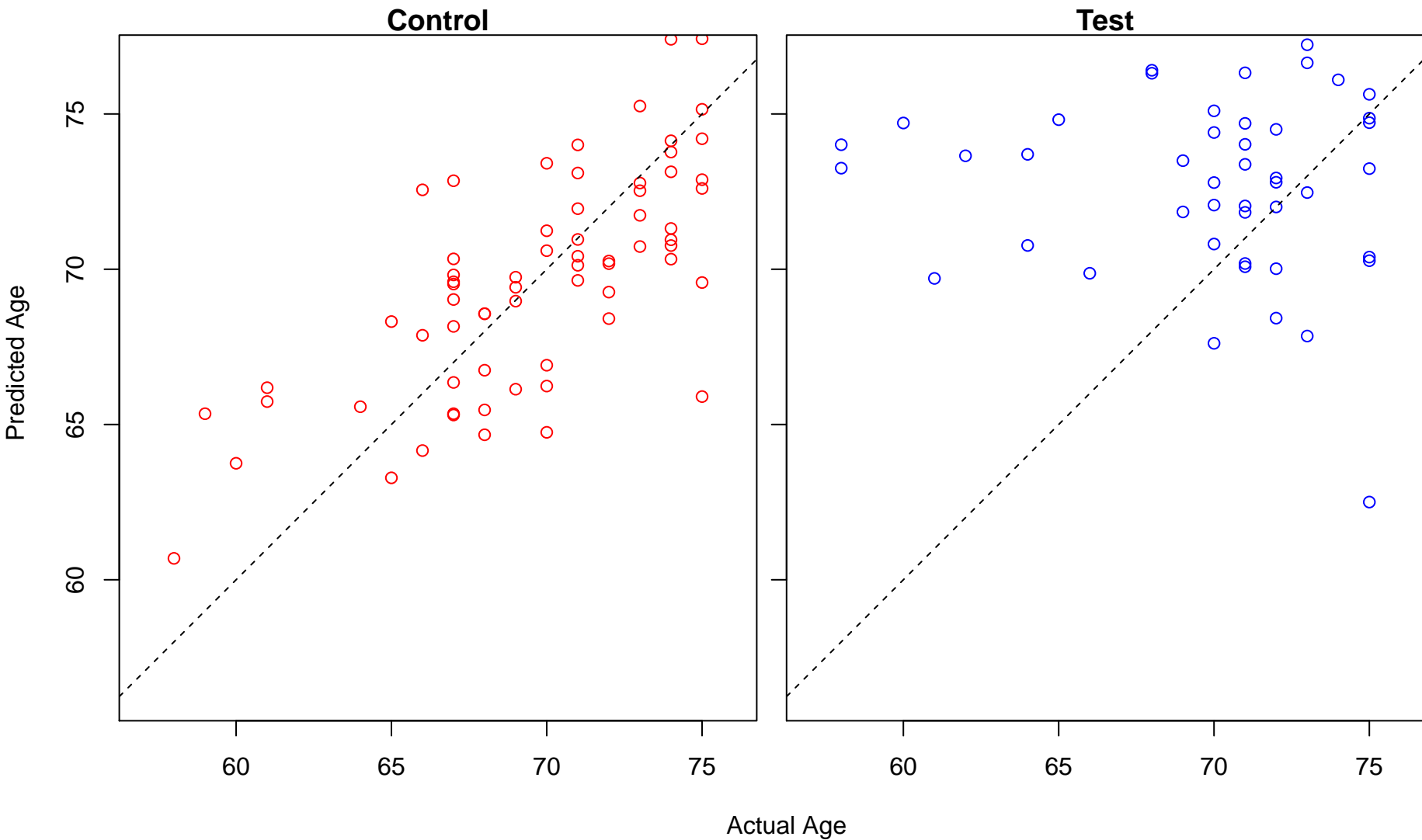
apoptotic mitochondrial changes (Score: 2.048833)



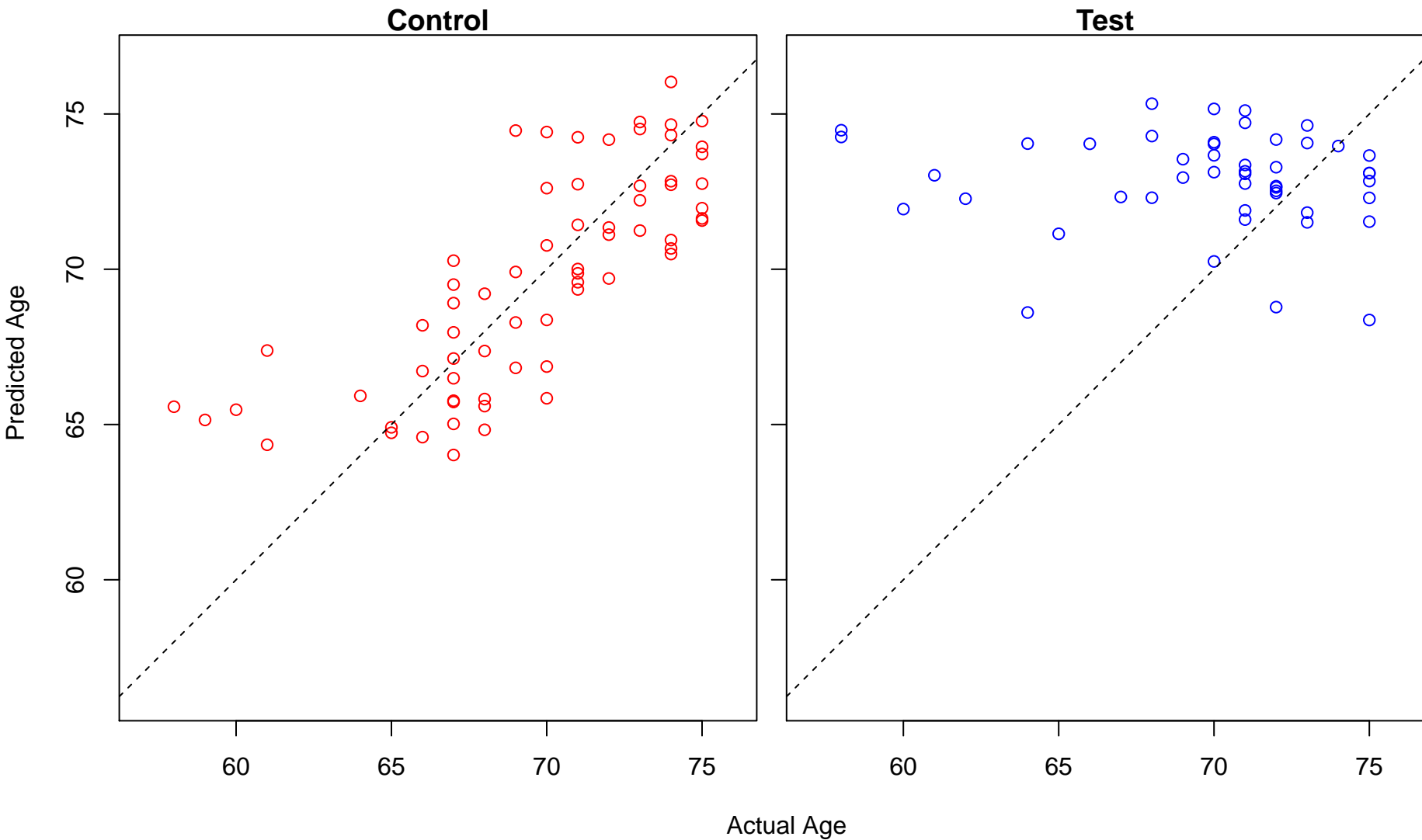
regulation of mitochondrion organization (Score: 2.047647)



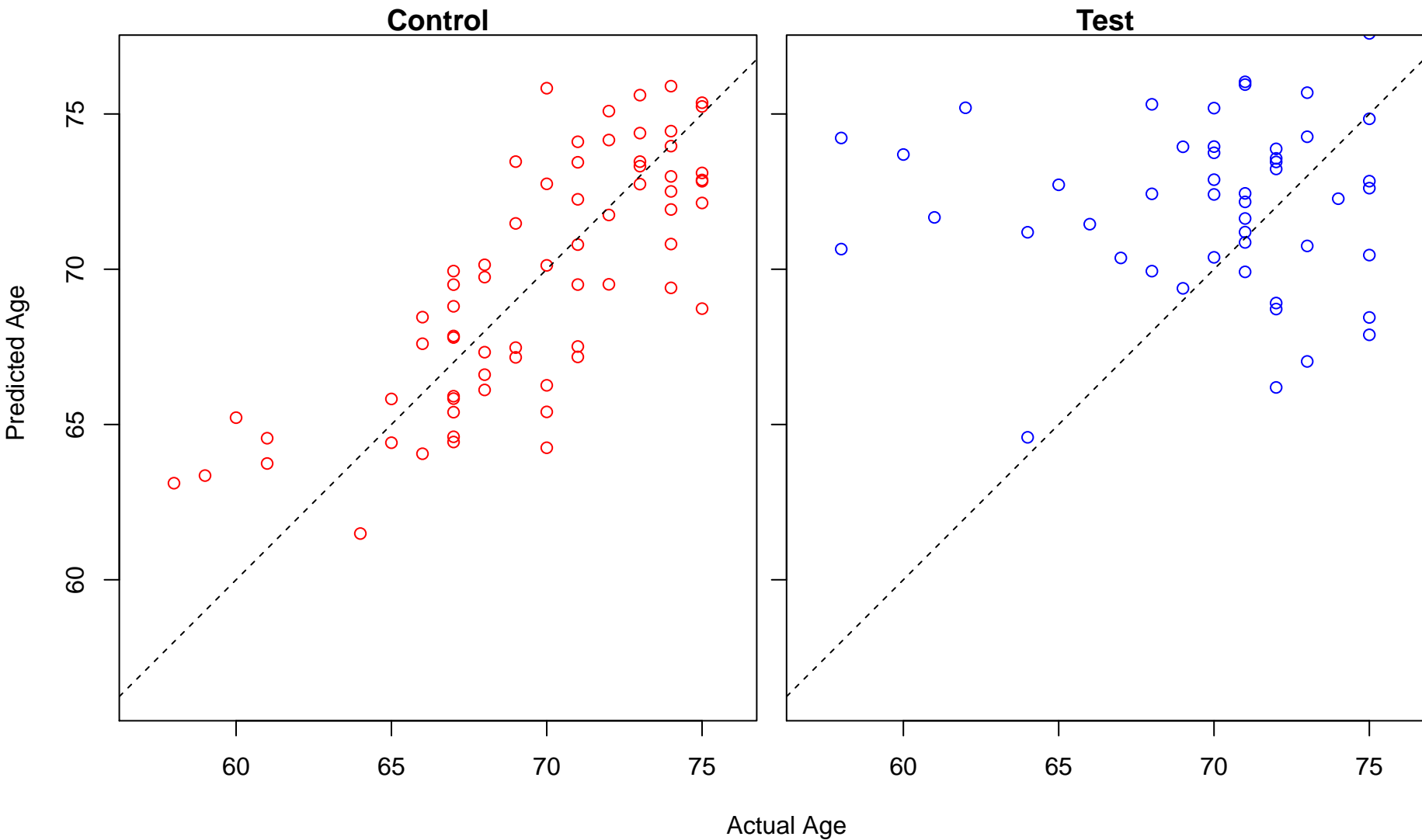
lipid homeostasis (Score: 2.046693)



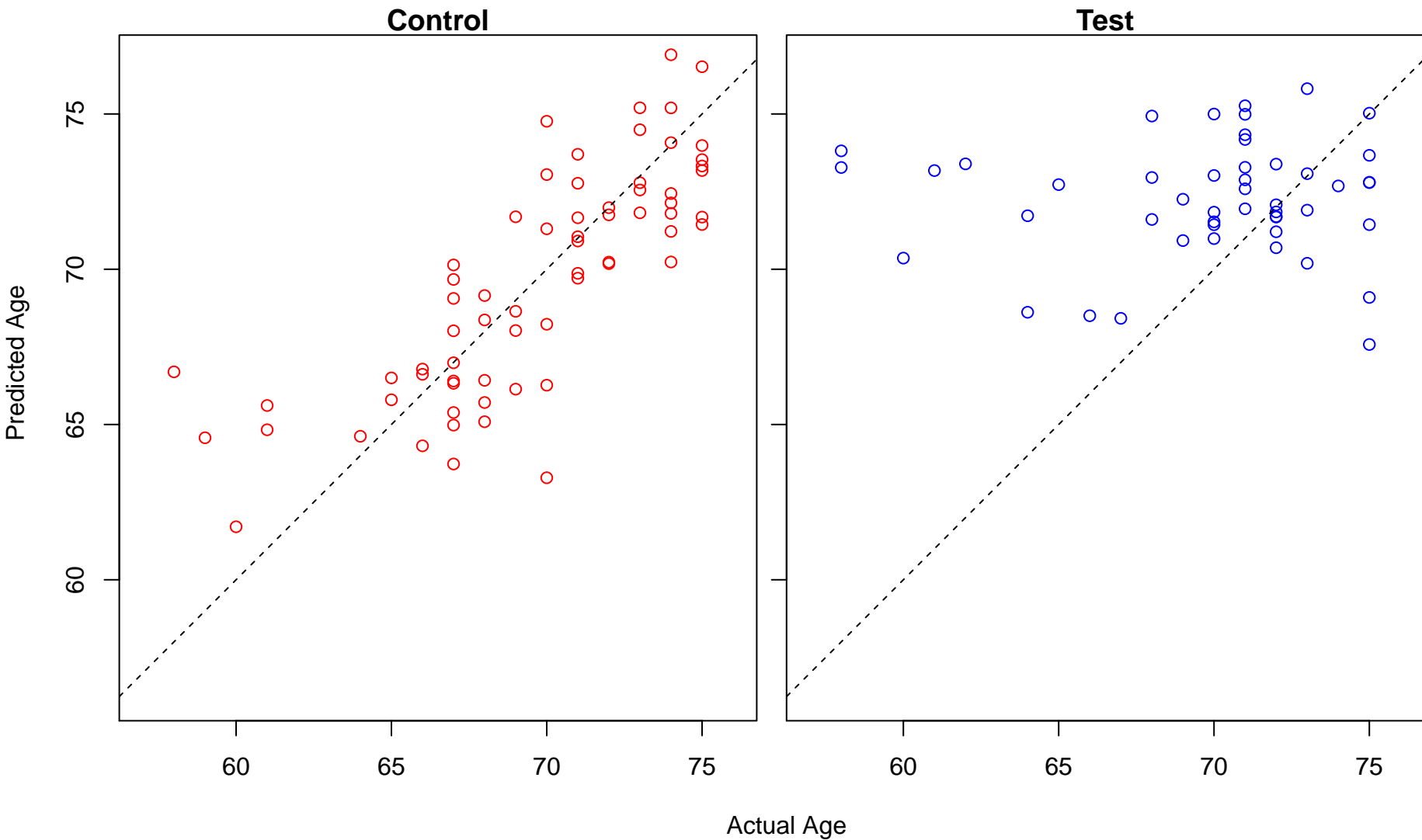
ion homeostasis (Score: 2.045816)



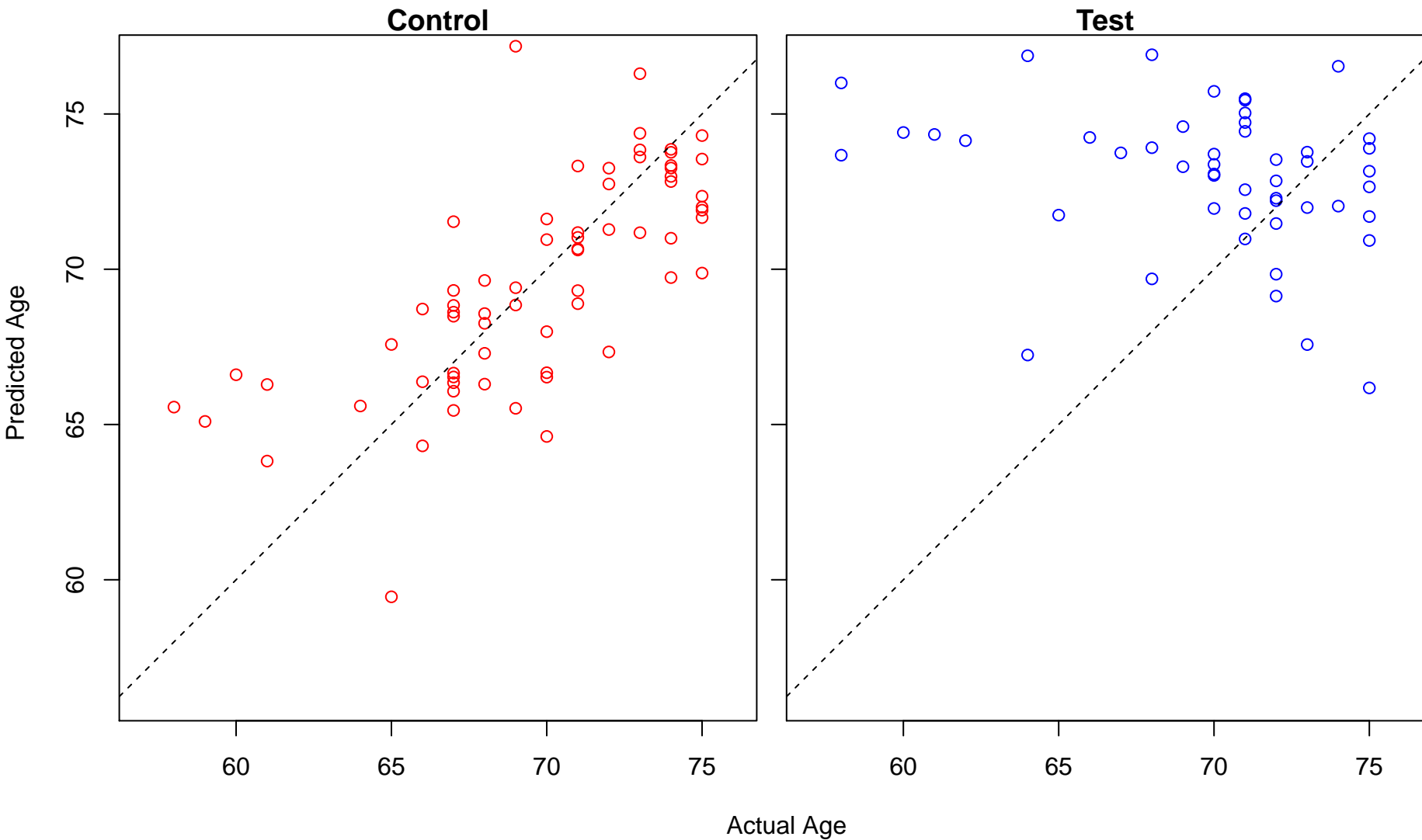
positive regulation of viral life cycle (Score: 2.045499)



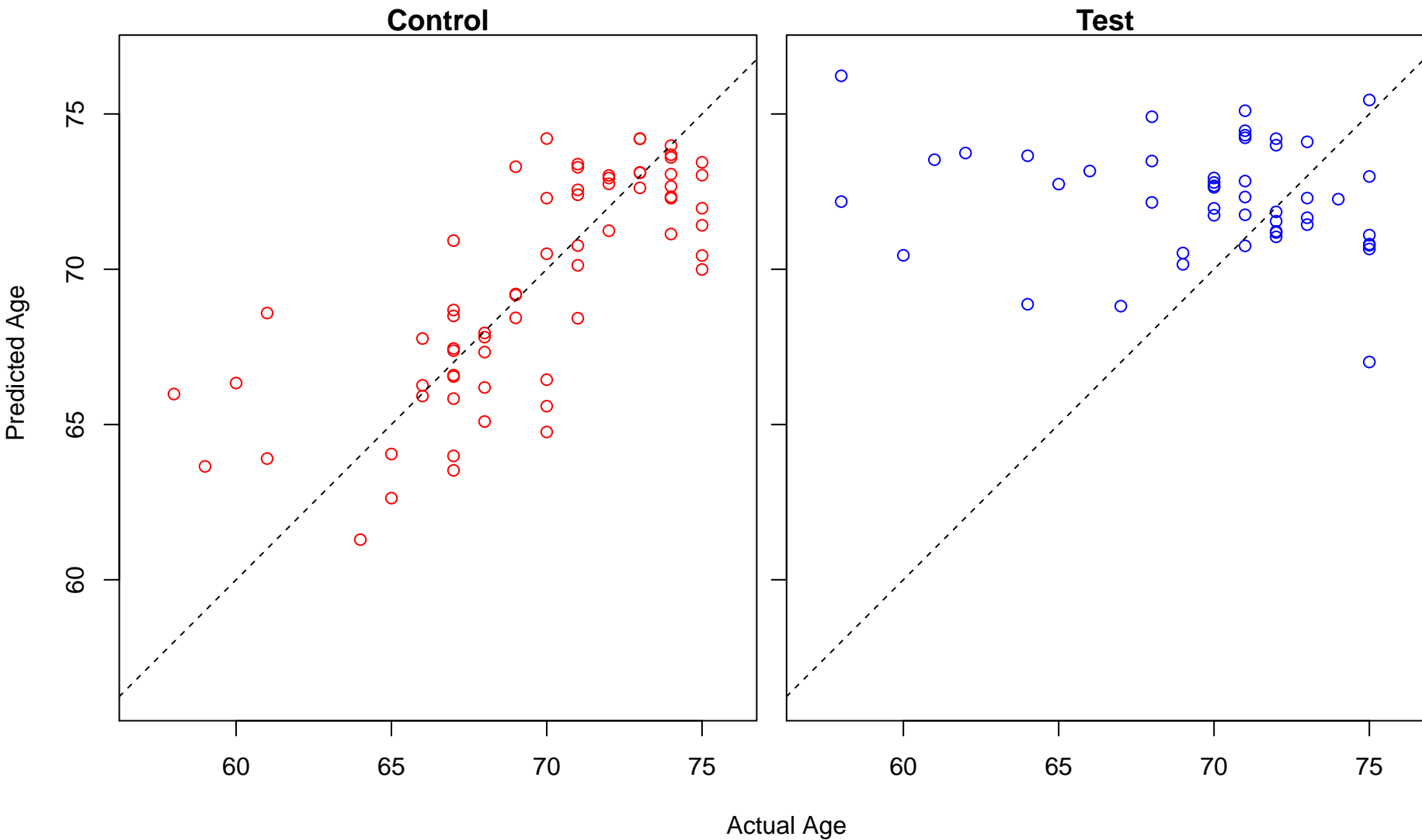
hydrogen transport (Score: 2.044031)



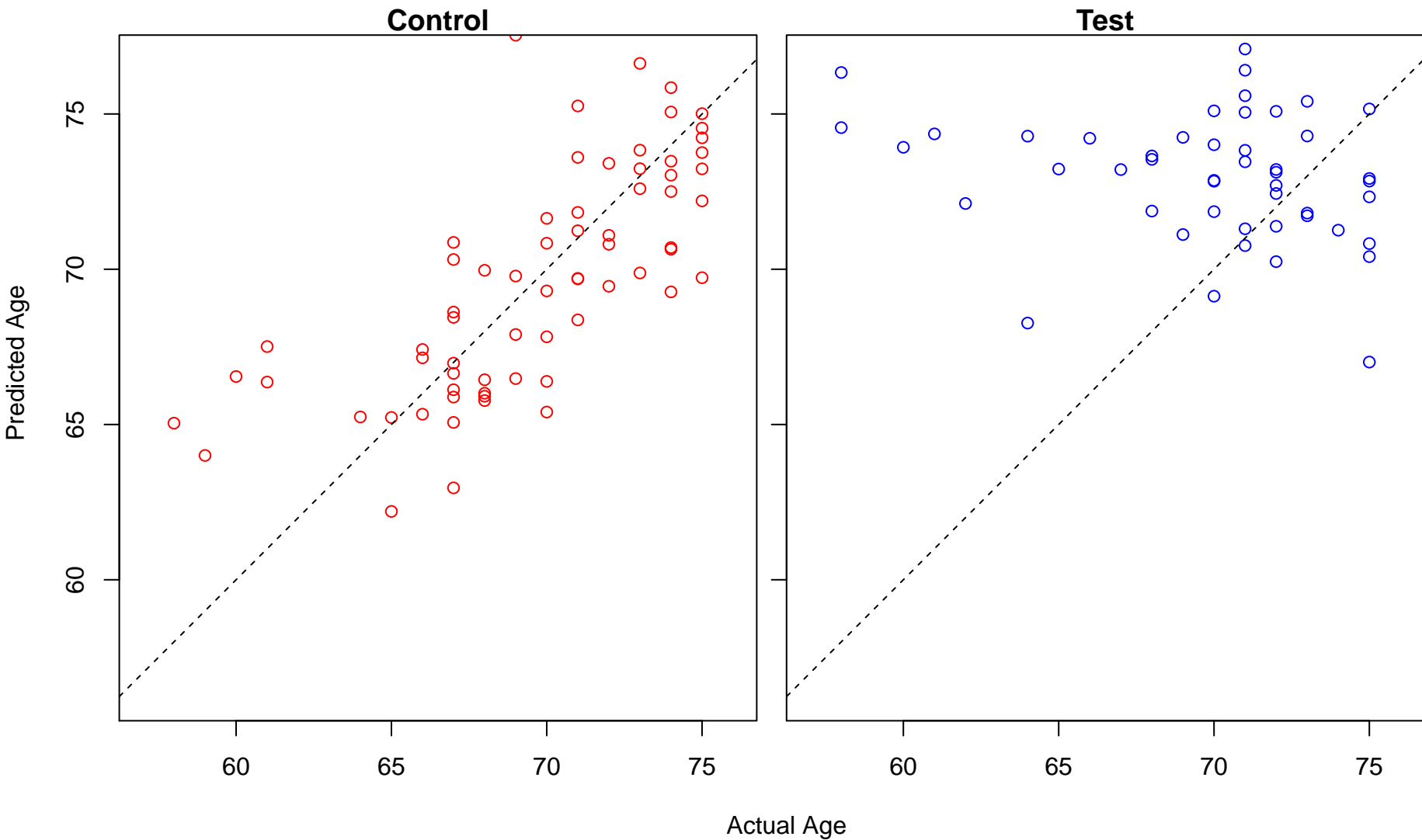
regulation of T cell differentiation (Score: 2.041364)



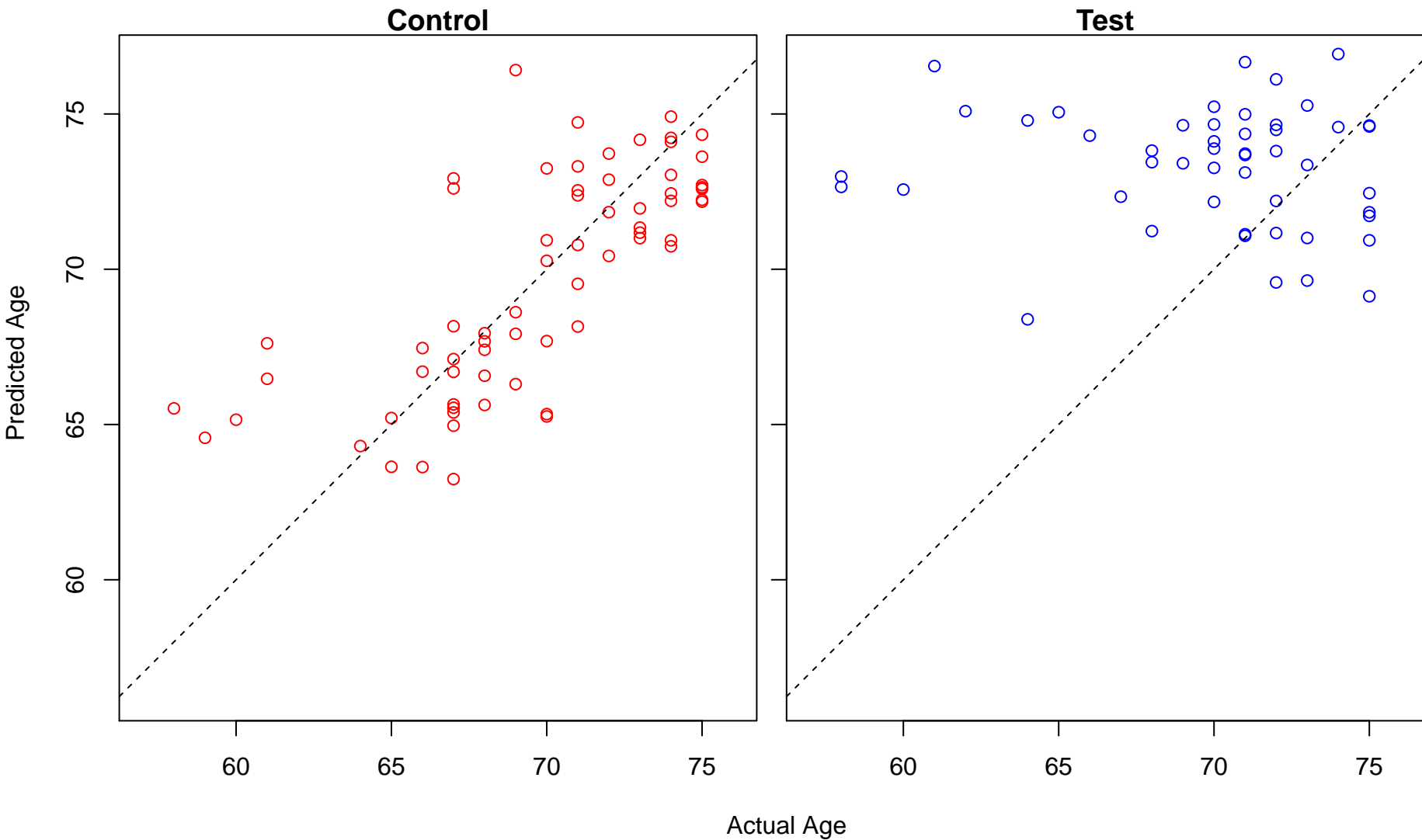
regulation of cysteine-type endopeptidase activity (Score: 2.041134)



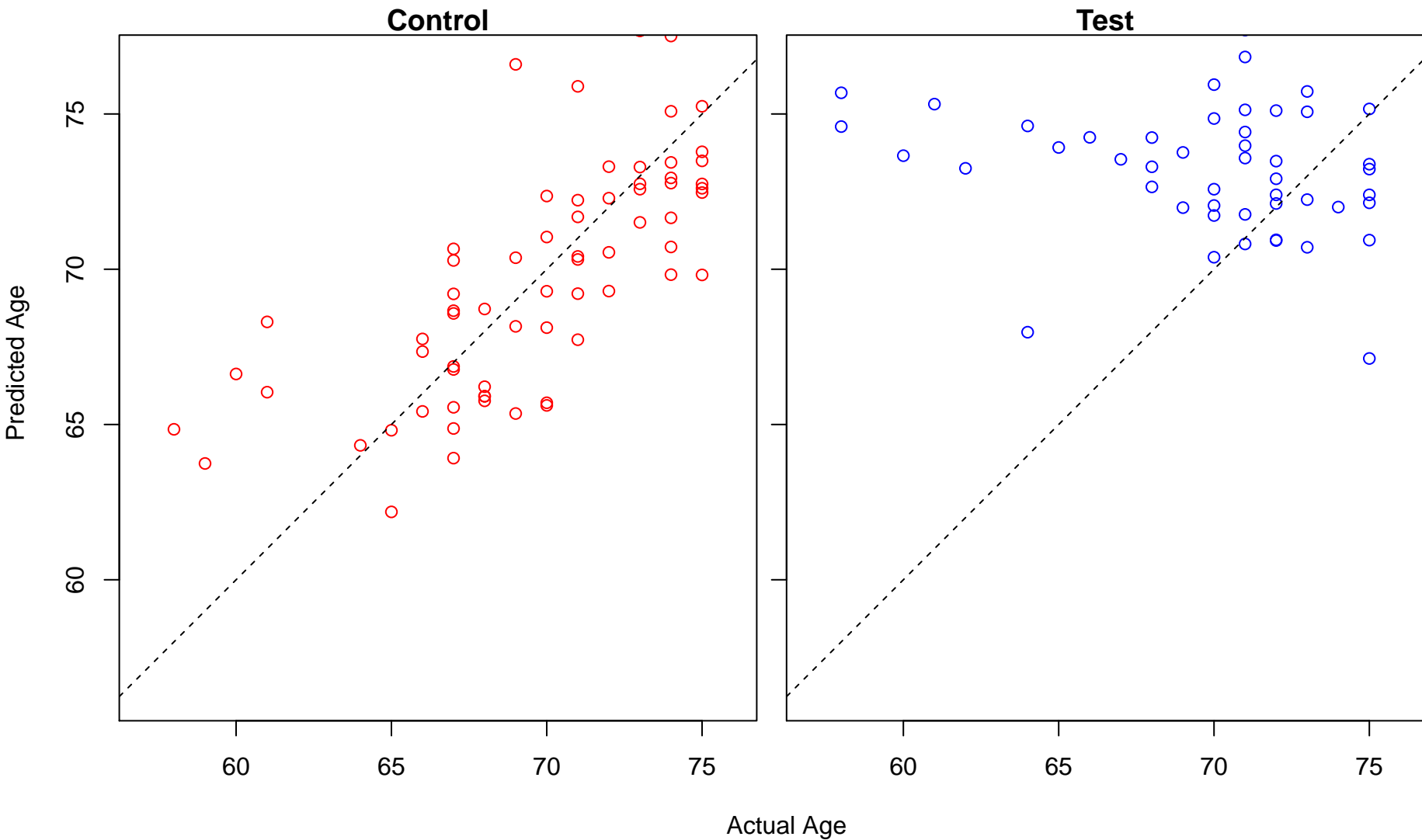
regulation of homotypic cell-cell adhesion (Score: 2.040760)



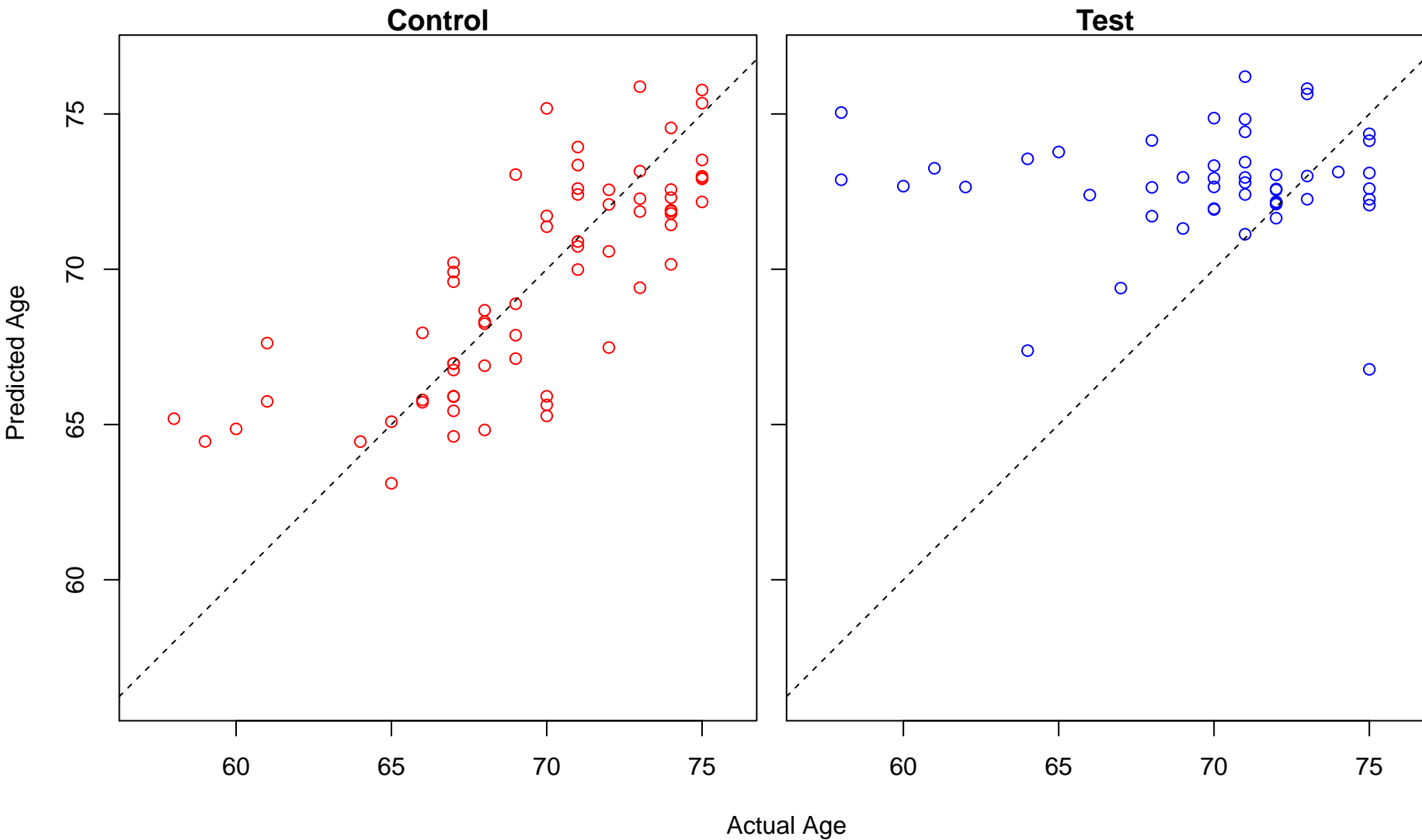
viral life cycle (Score: 2.040230)



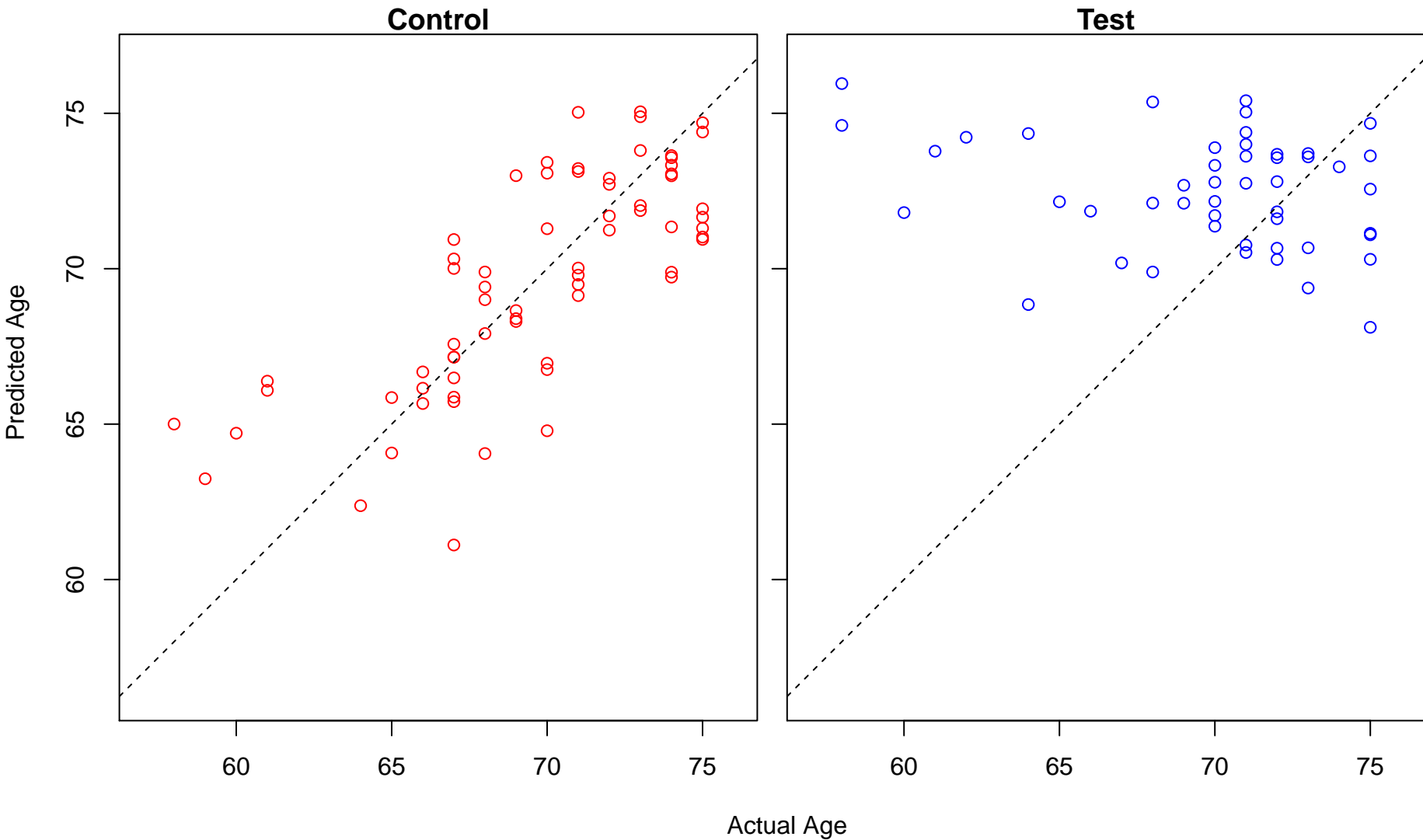
positive regulation of leukocyte activation (Score: 2.039209)



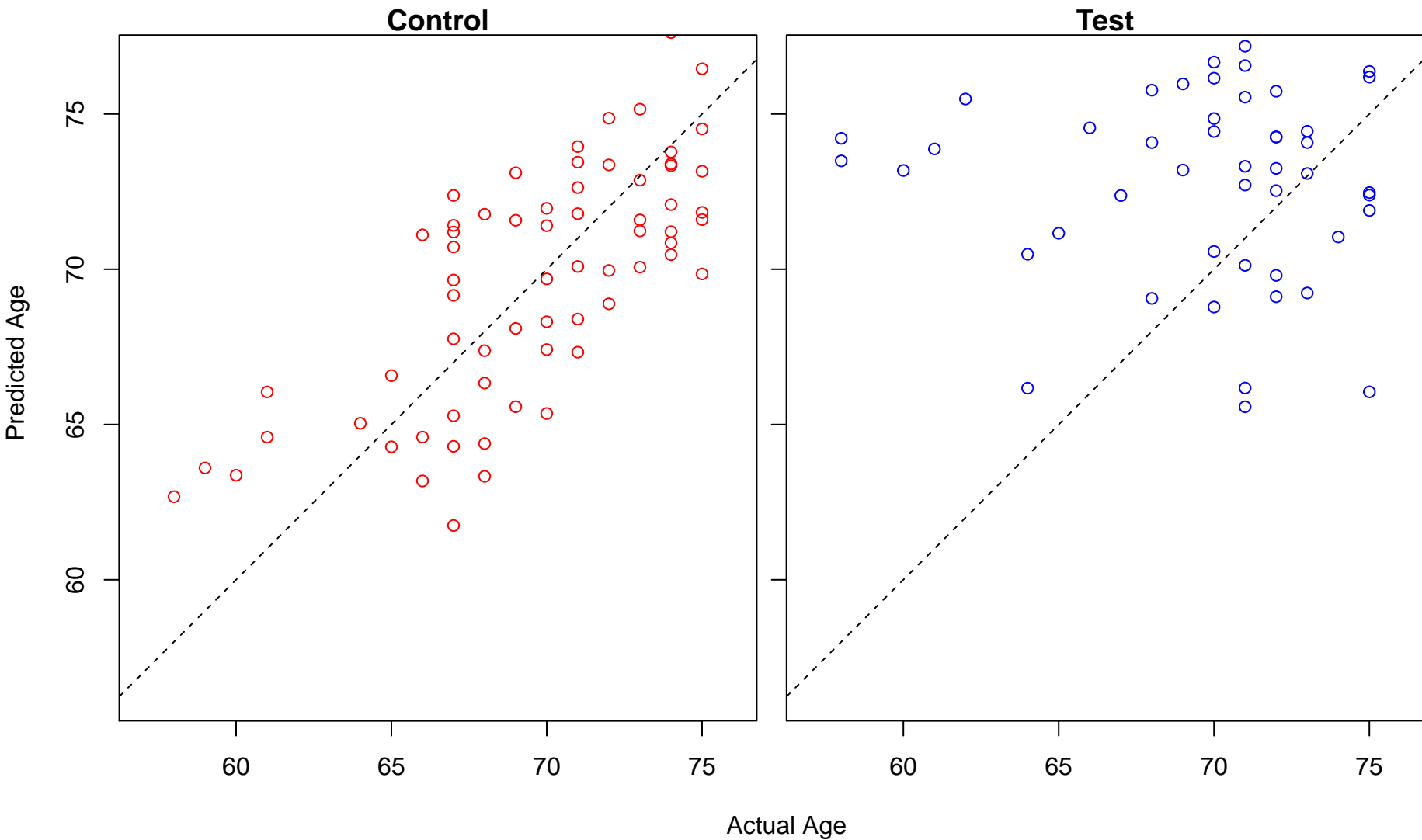
response to radiation (Score: 2.038815)



positive regulation of intracellular transport (Score: 2.035930)

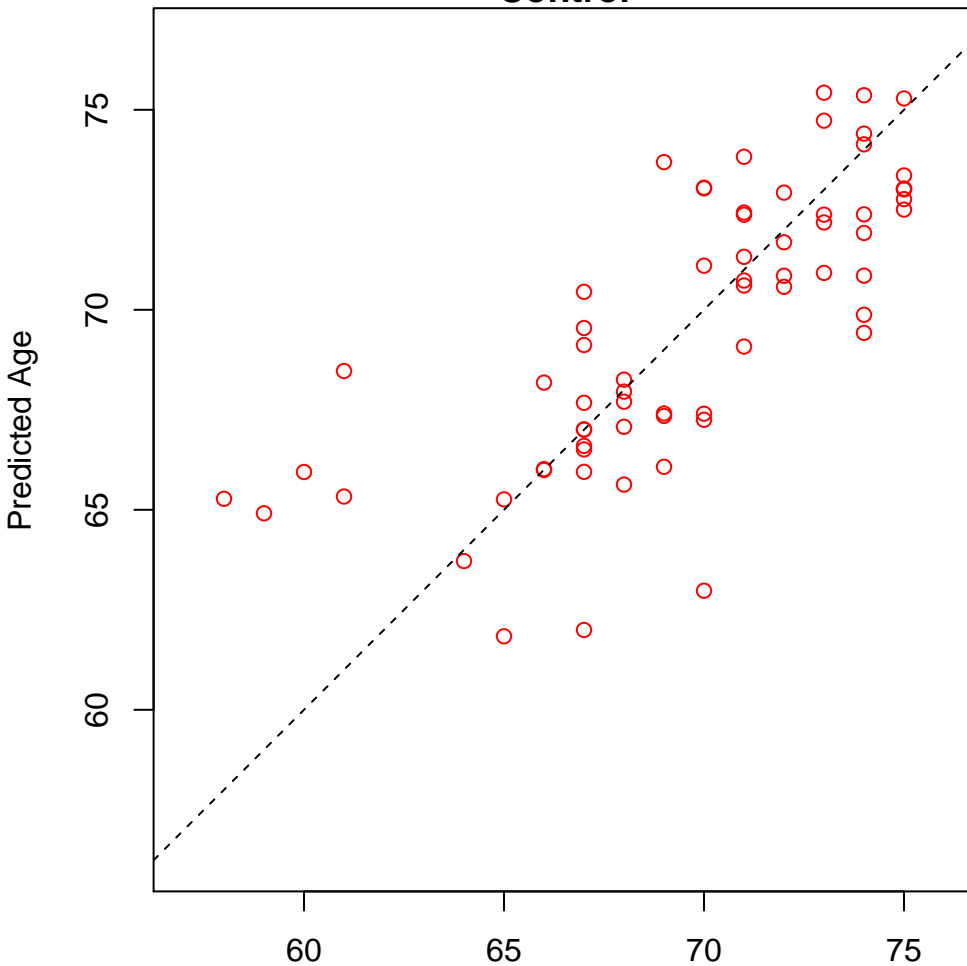


sterol metabolic process (Score: 2.035700)

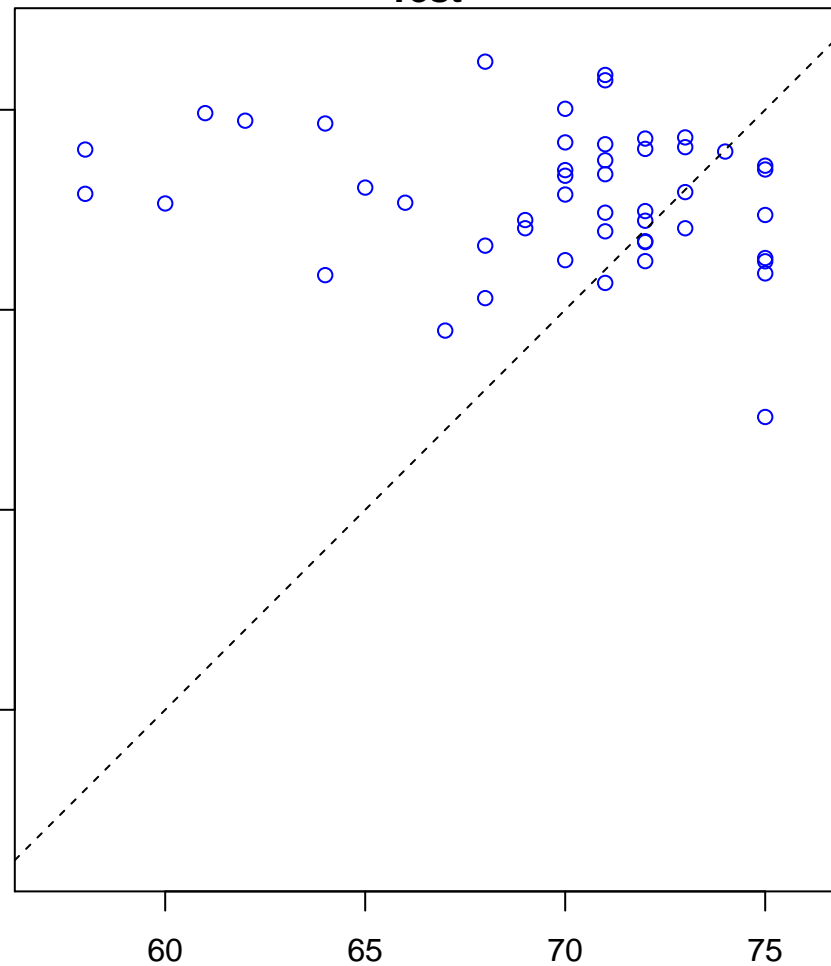


regulation of protein catabolic process (Score: 2.033984)

Control

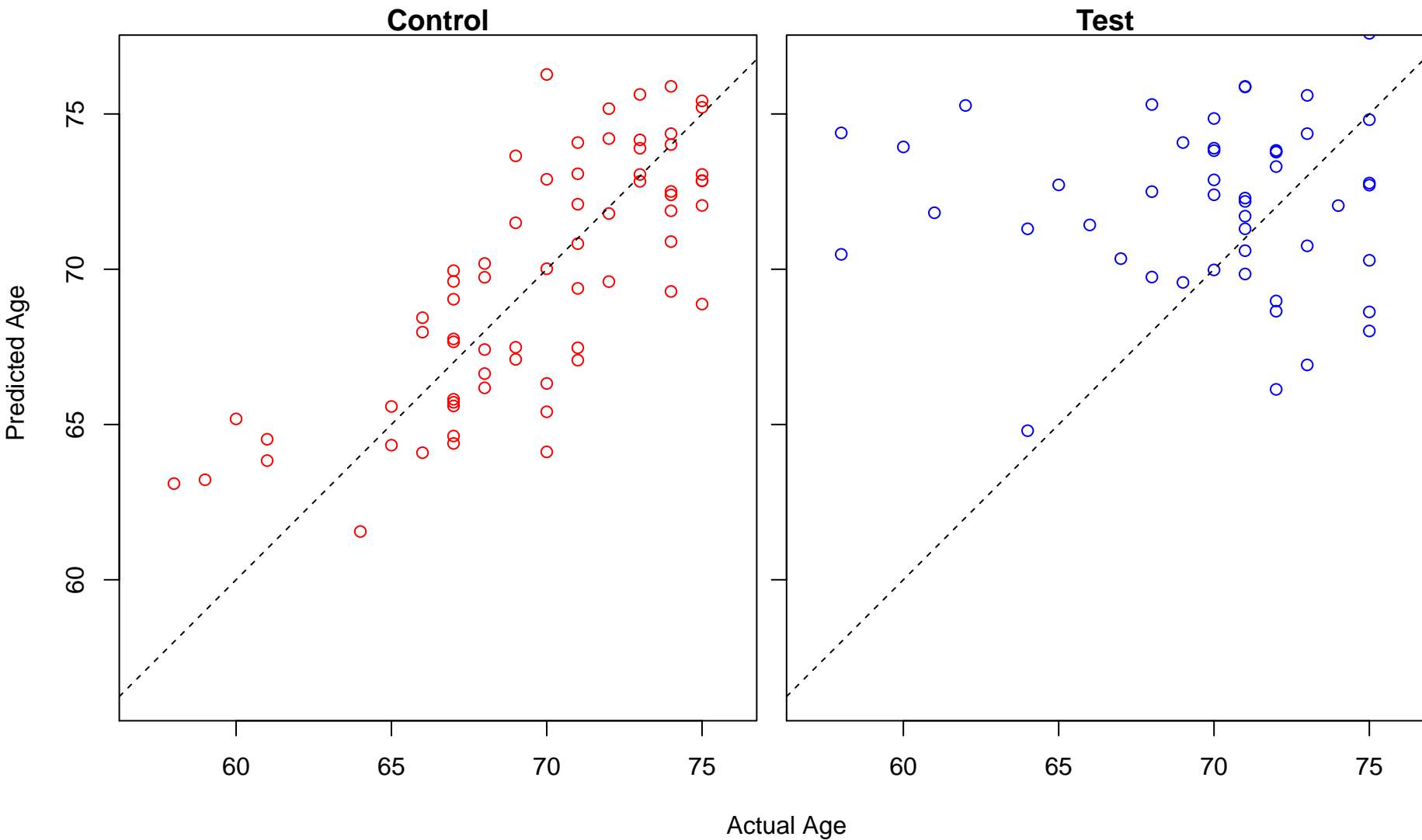


Test

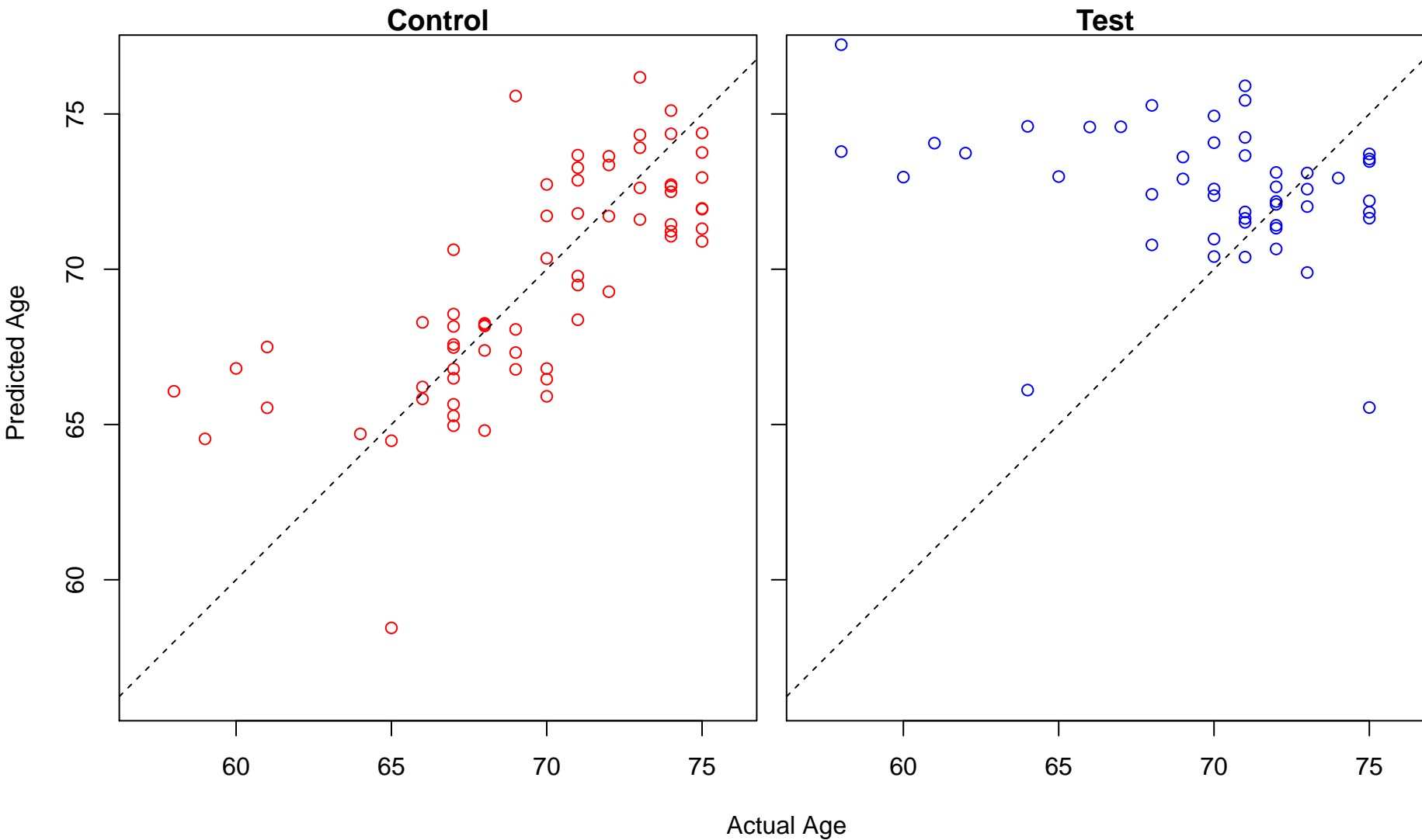


Actual Age

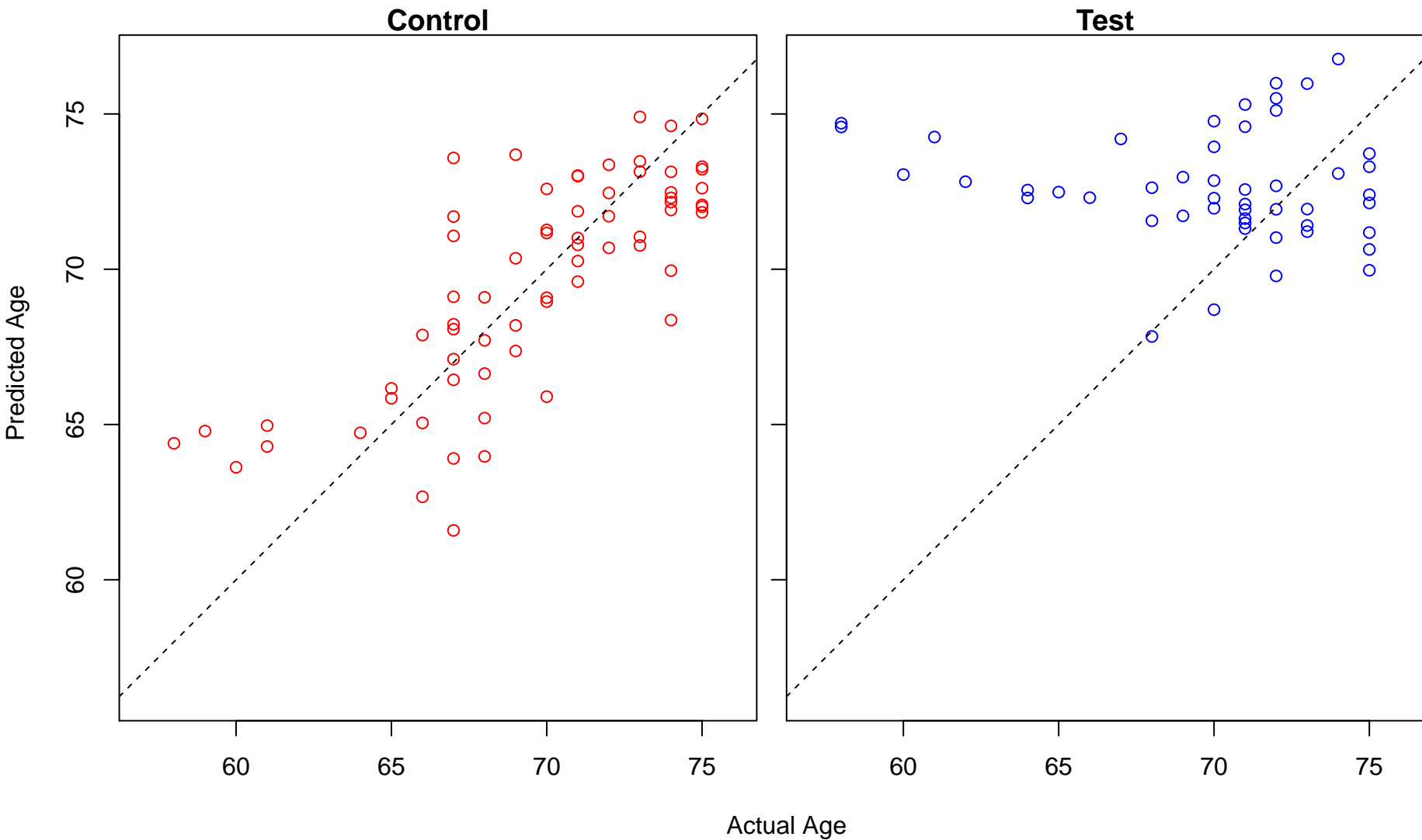
positive regulation of viral process (Score: 2.033078)



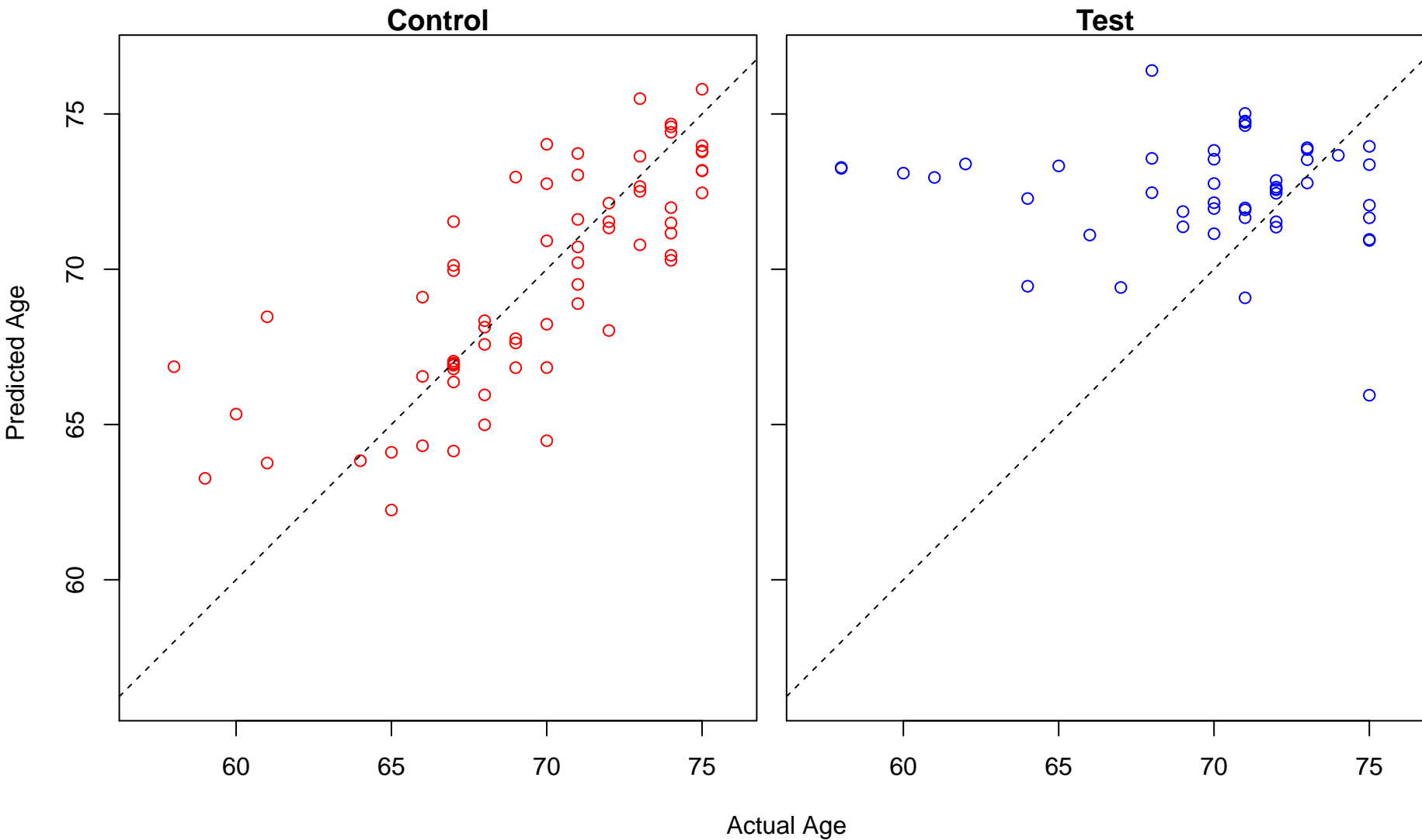
positive regulation of response to external stimulus (Score: 2.033062)



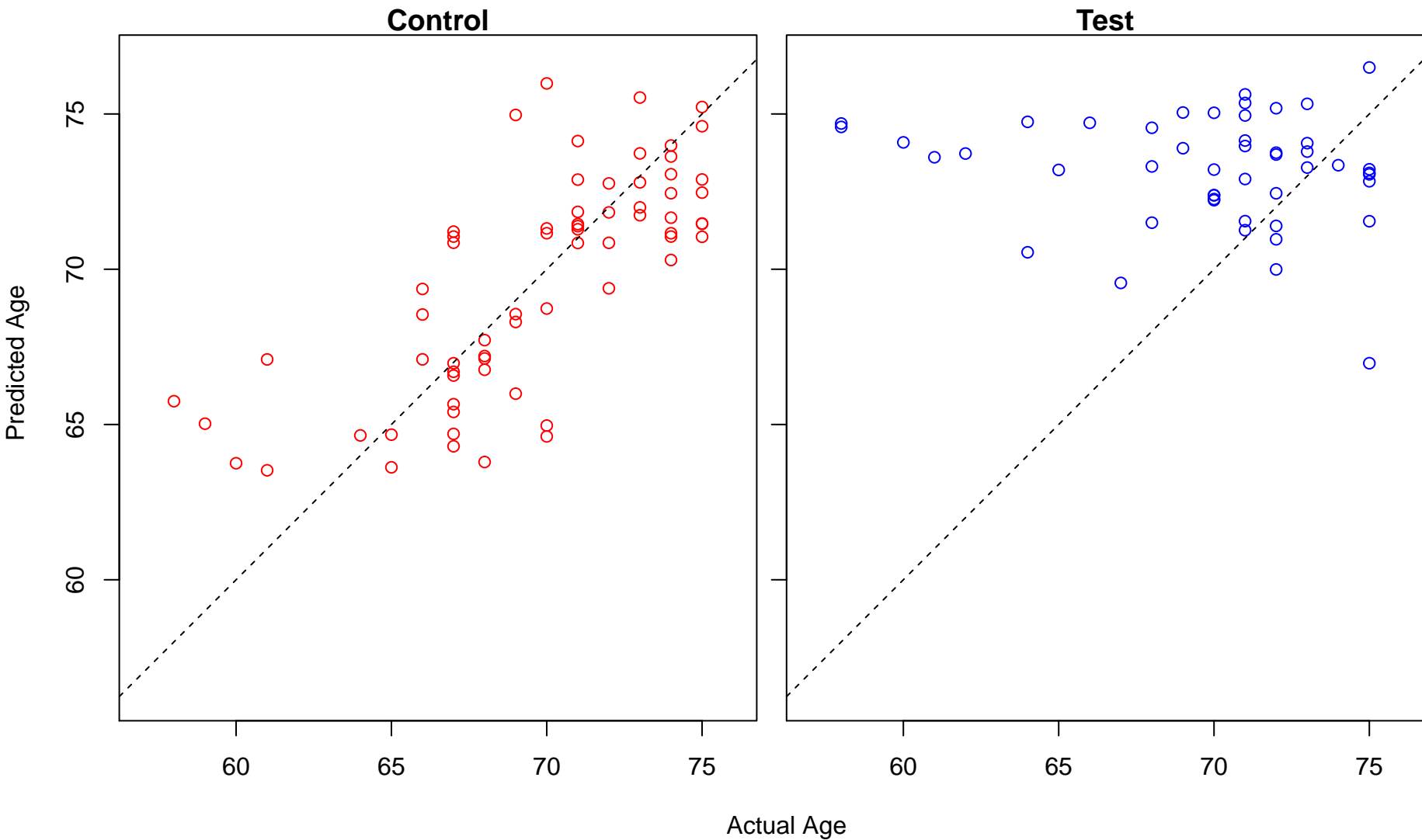
mitochondrial fusion (Score: 2.031616)



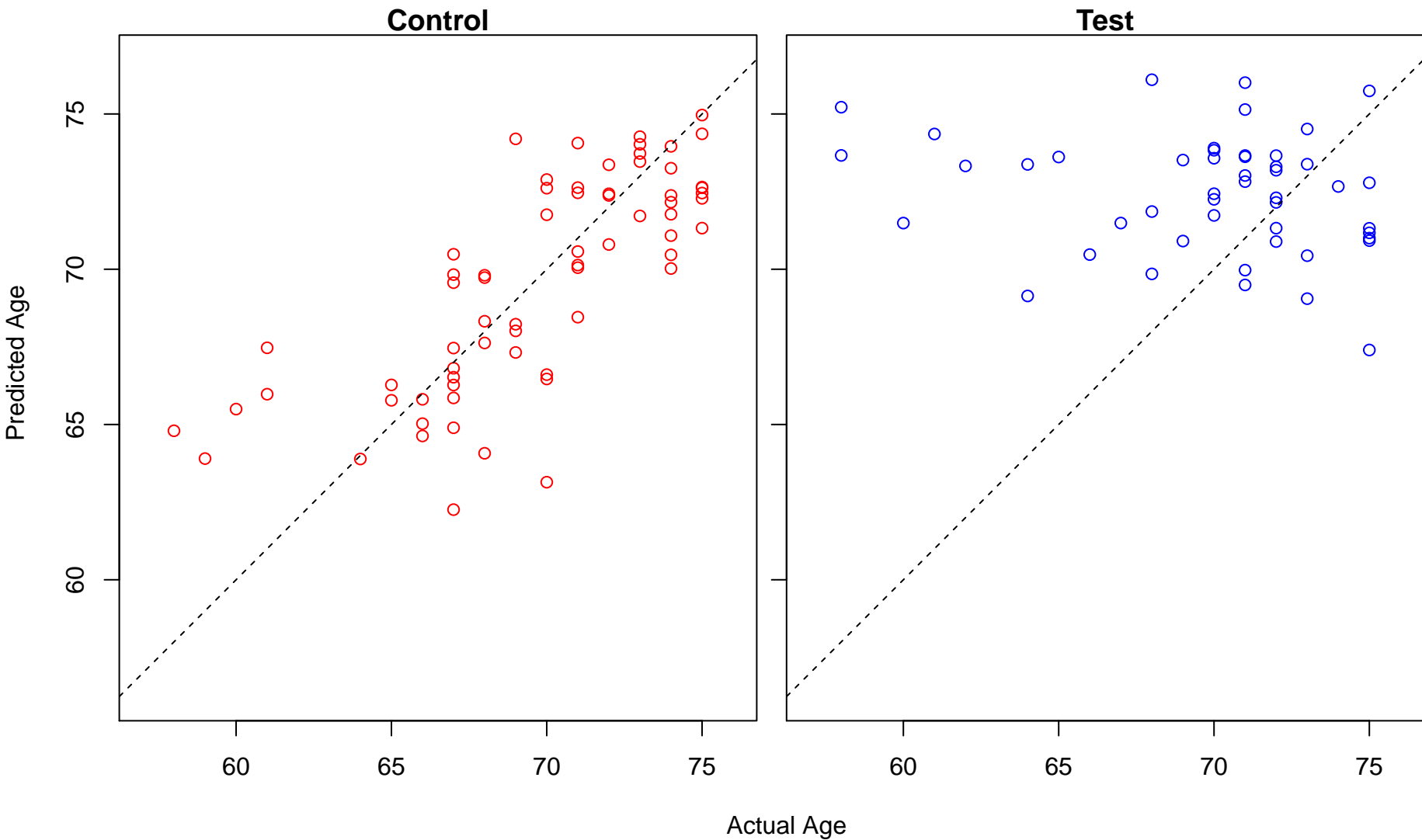
neurotrophin TRK receptor signaling pathway (Score: 2.030503)



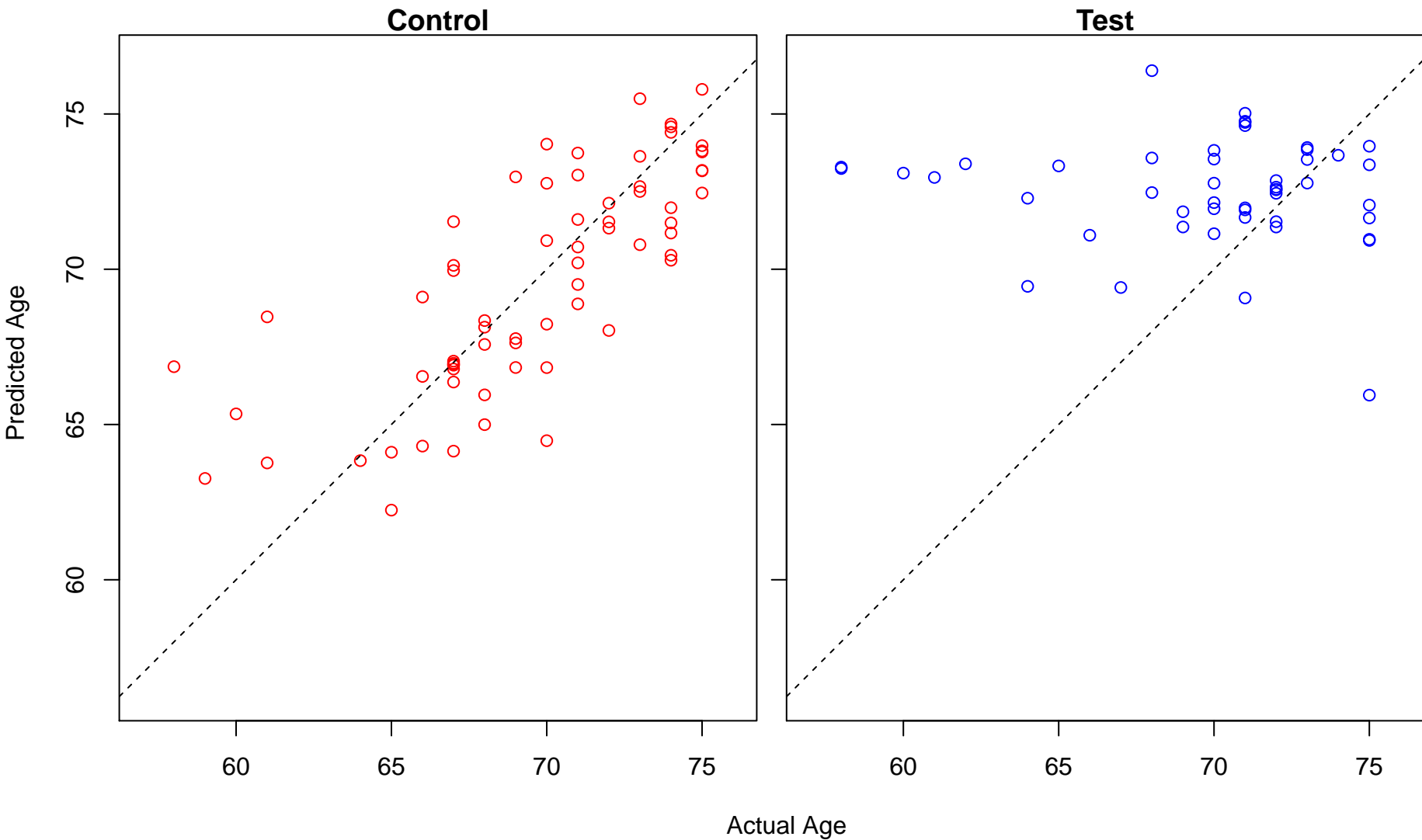
peptidyl-asparagine modification (Score: 2.030444)



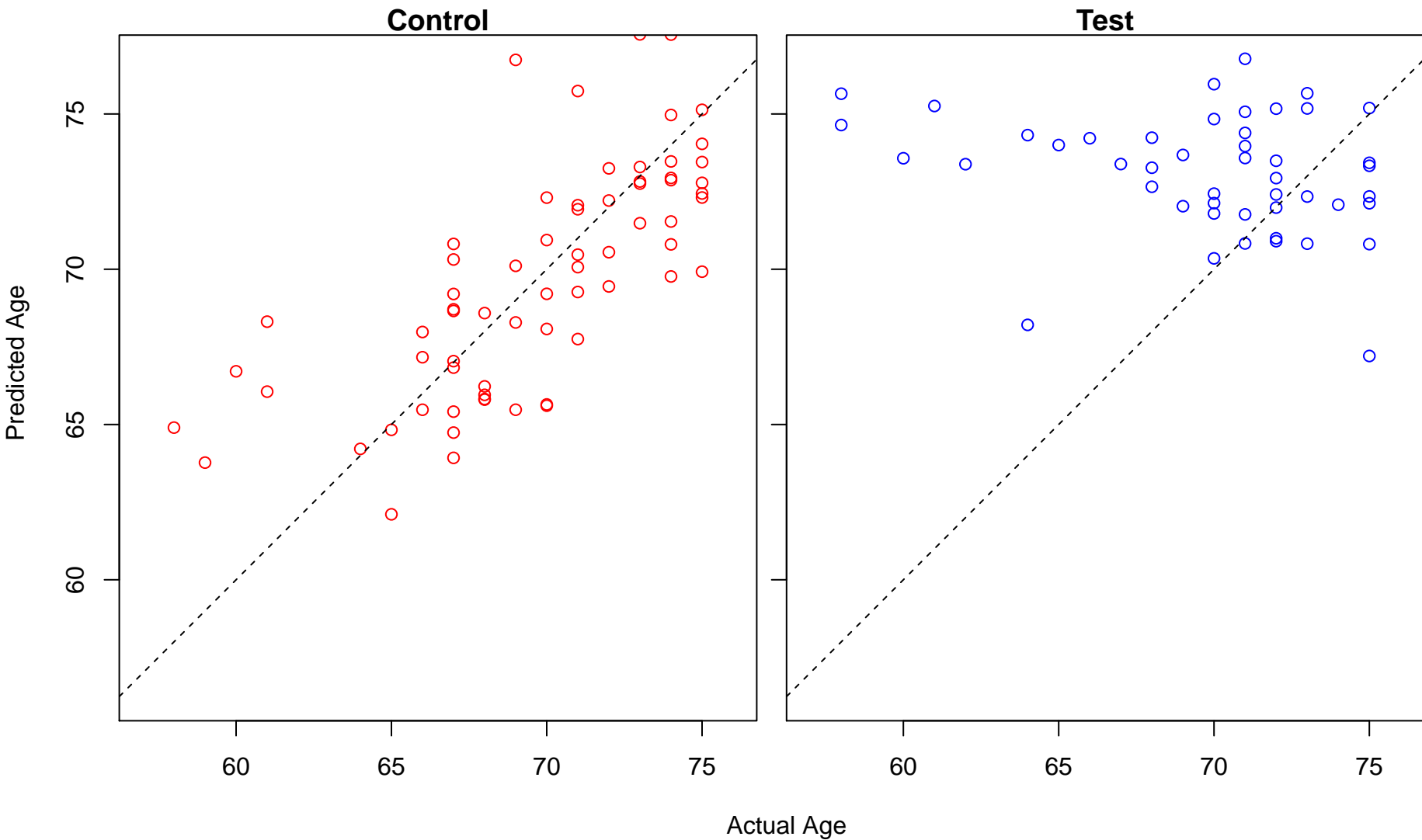
regulation of protein targeting (Score: 2.030101)



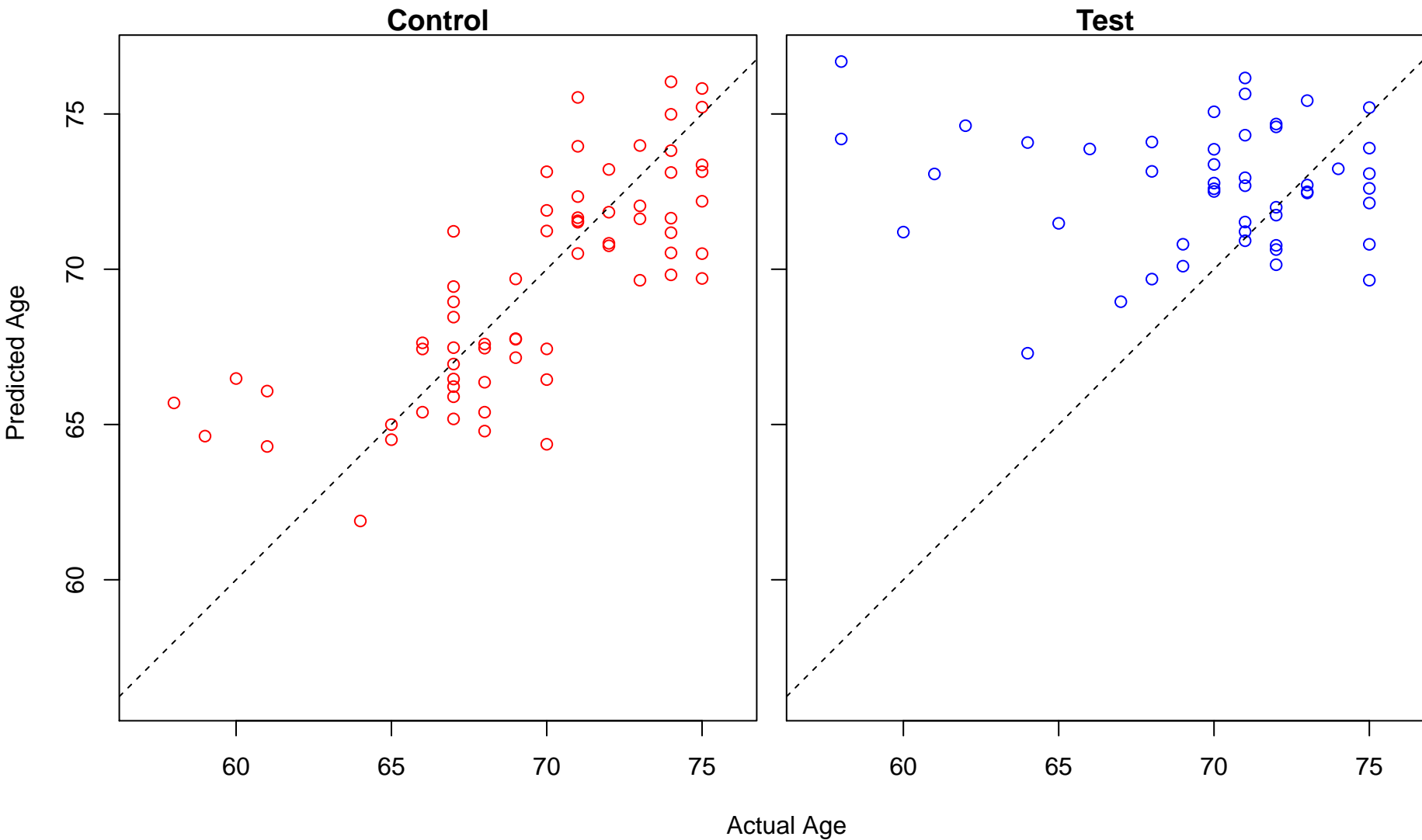
neurotrophin signaling pathway (Score: 2.029686)



positive regulation of cell activation (Score: 2.025177)

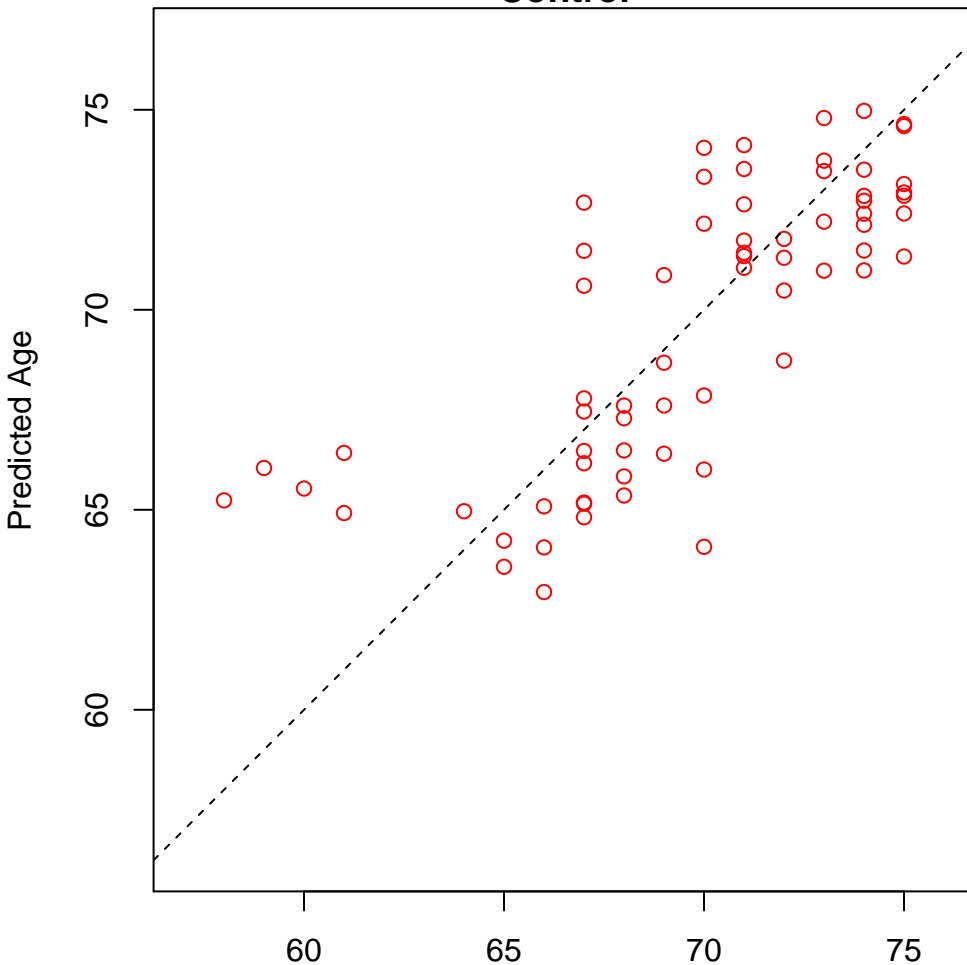


actin filament-based process (Score: 2.024331)

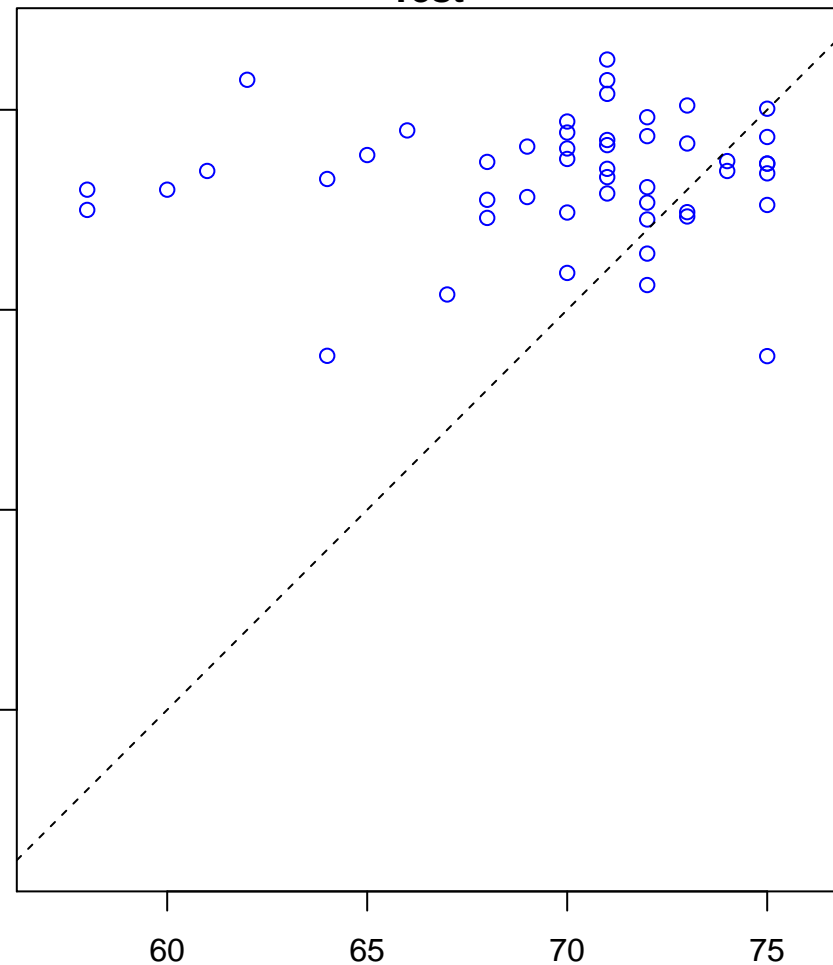


internal peptidyl-lysine acetylation (Score: 2.023663)

Control

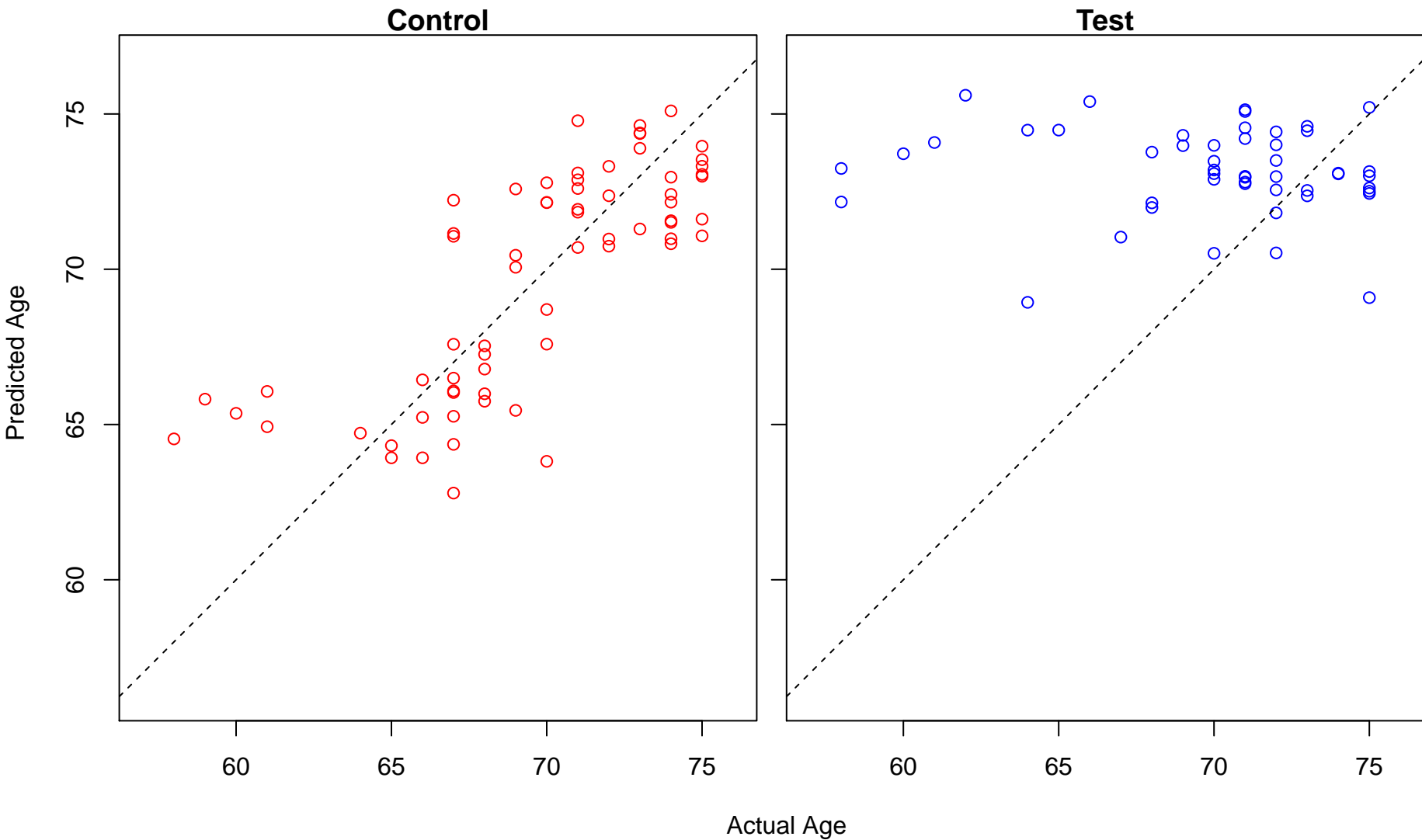


Test

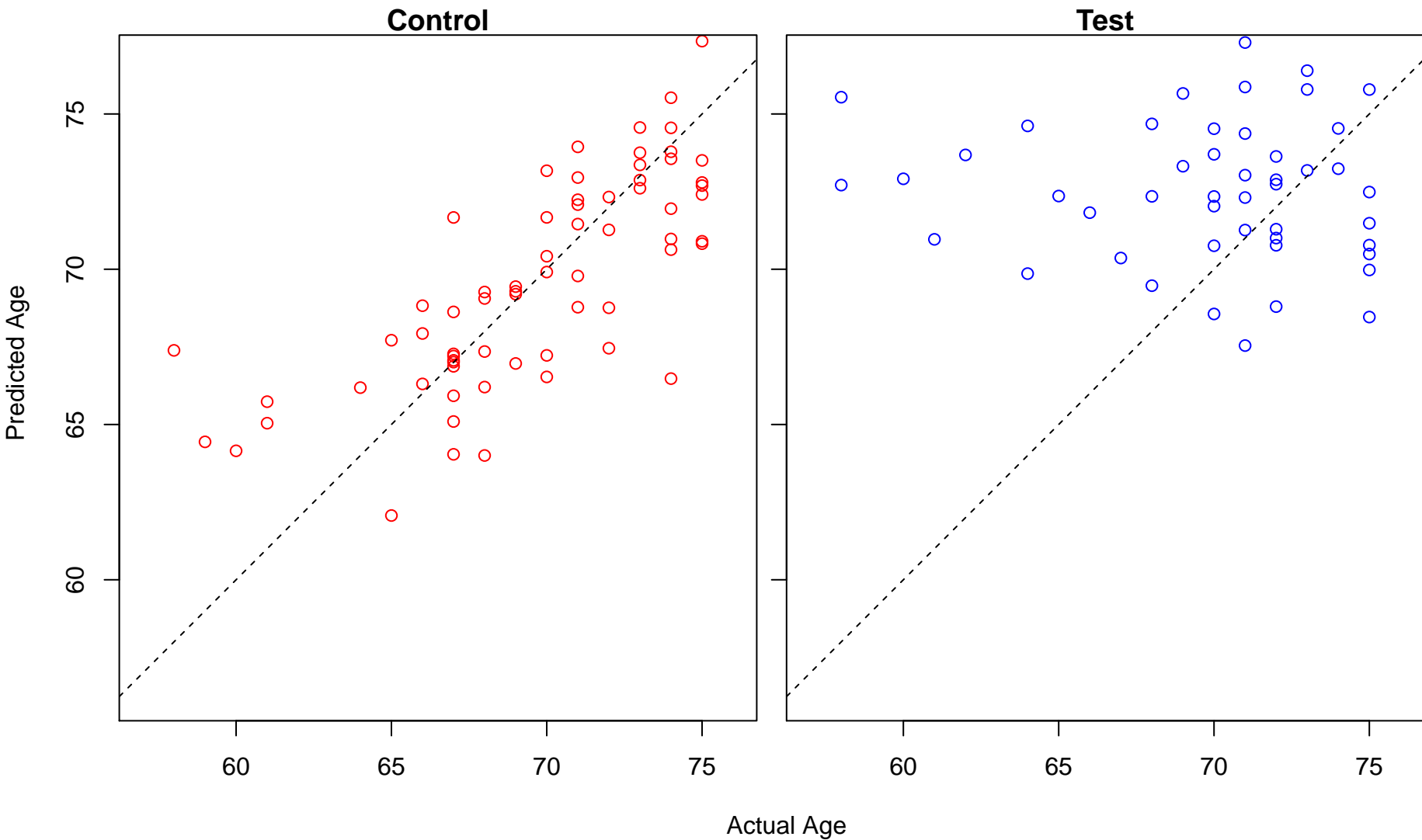


Actual Age

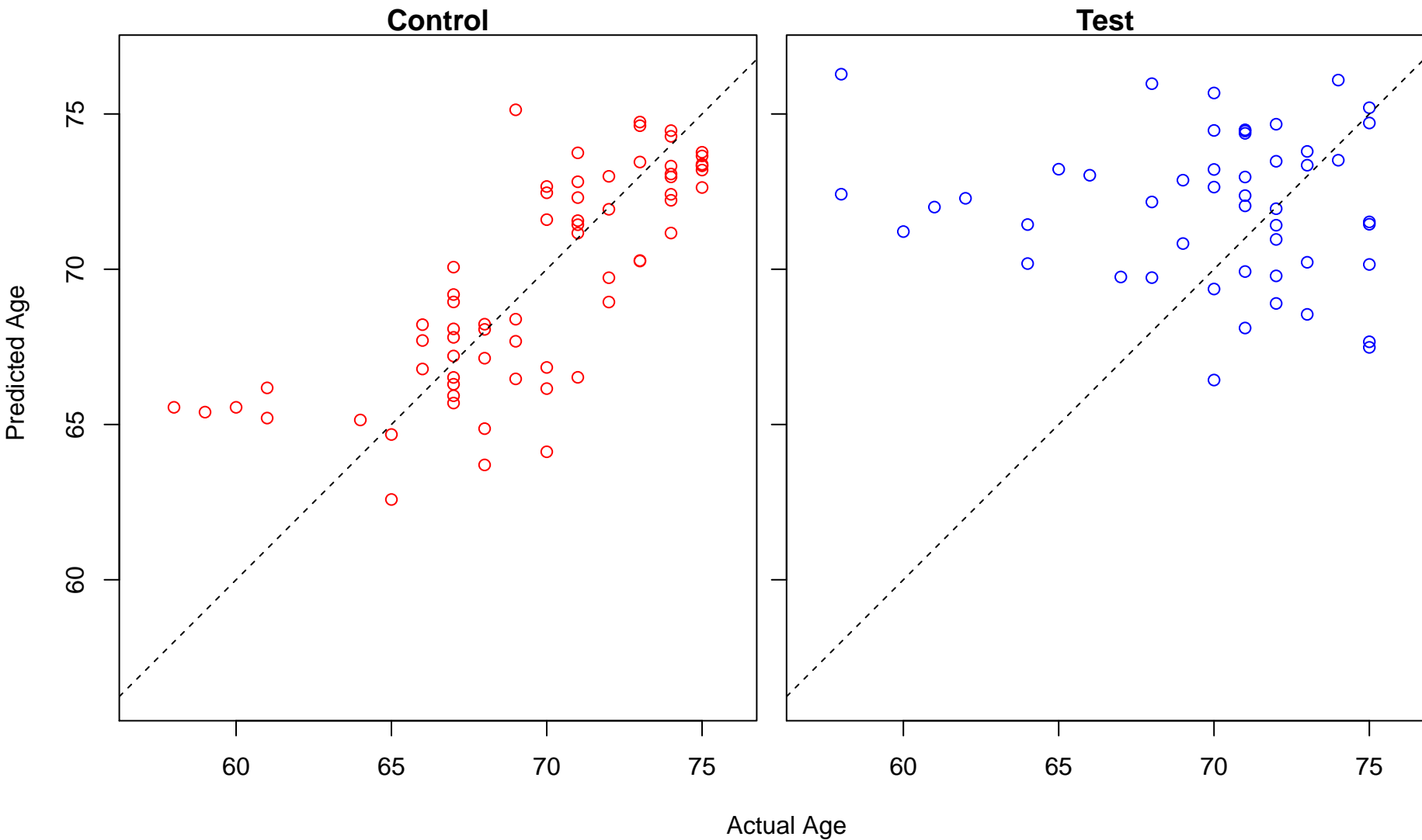
histone H4 acetylation (Score: 2.022482)



regulation of Ras protein signal transduction (Score: 2.022236)

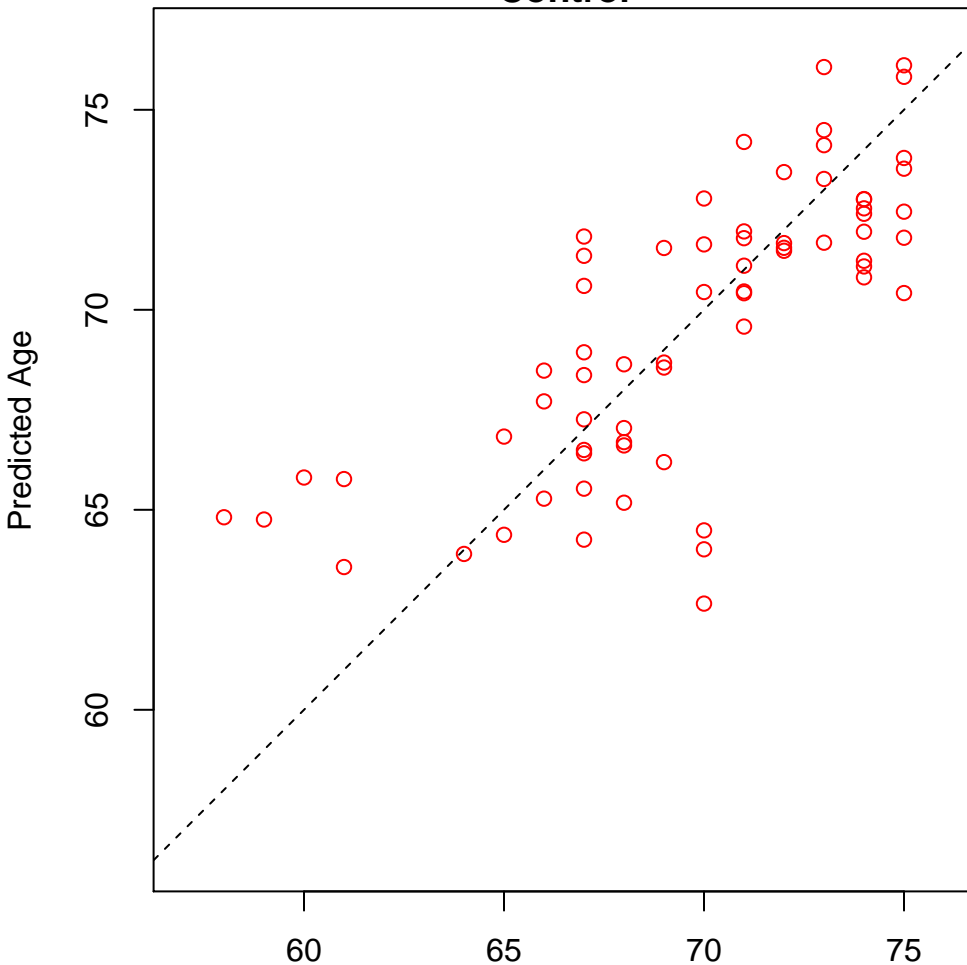


regulation of myeloid leukocyte differentiation (Score: 2.021680)

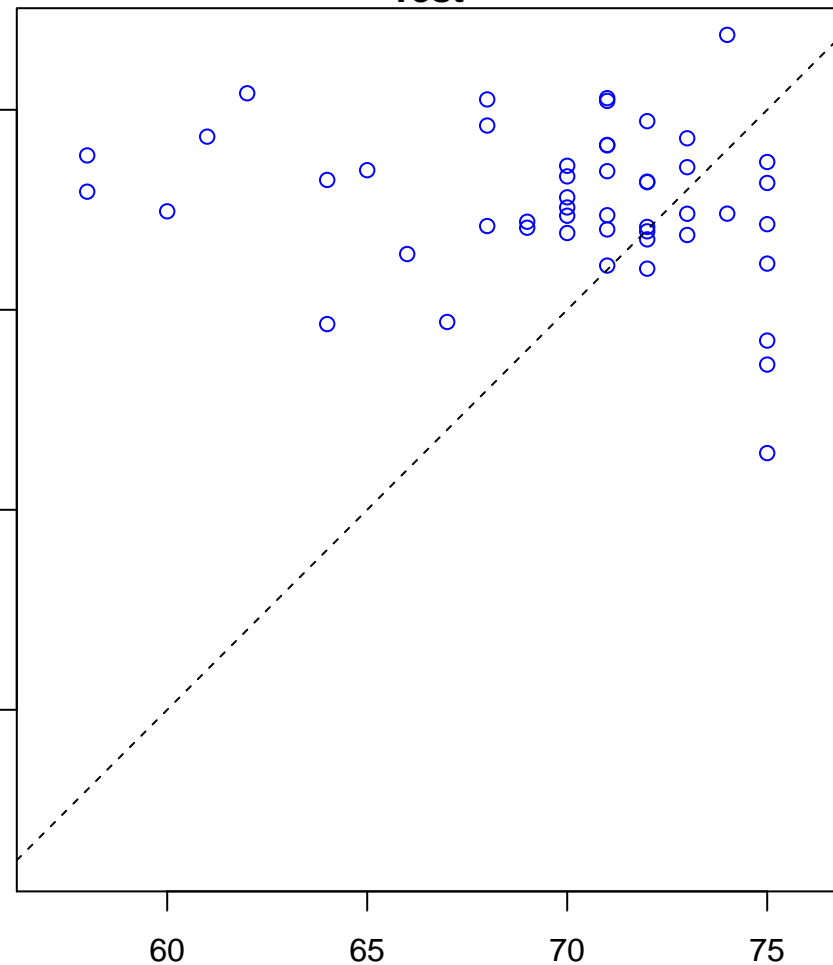


phosphatidylinositol metabolic process (Score: 2.021388)

Control

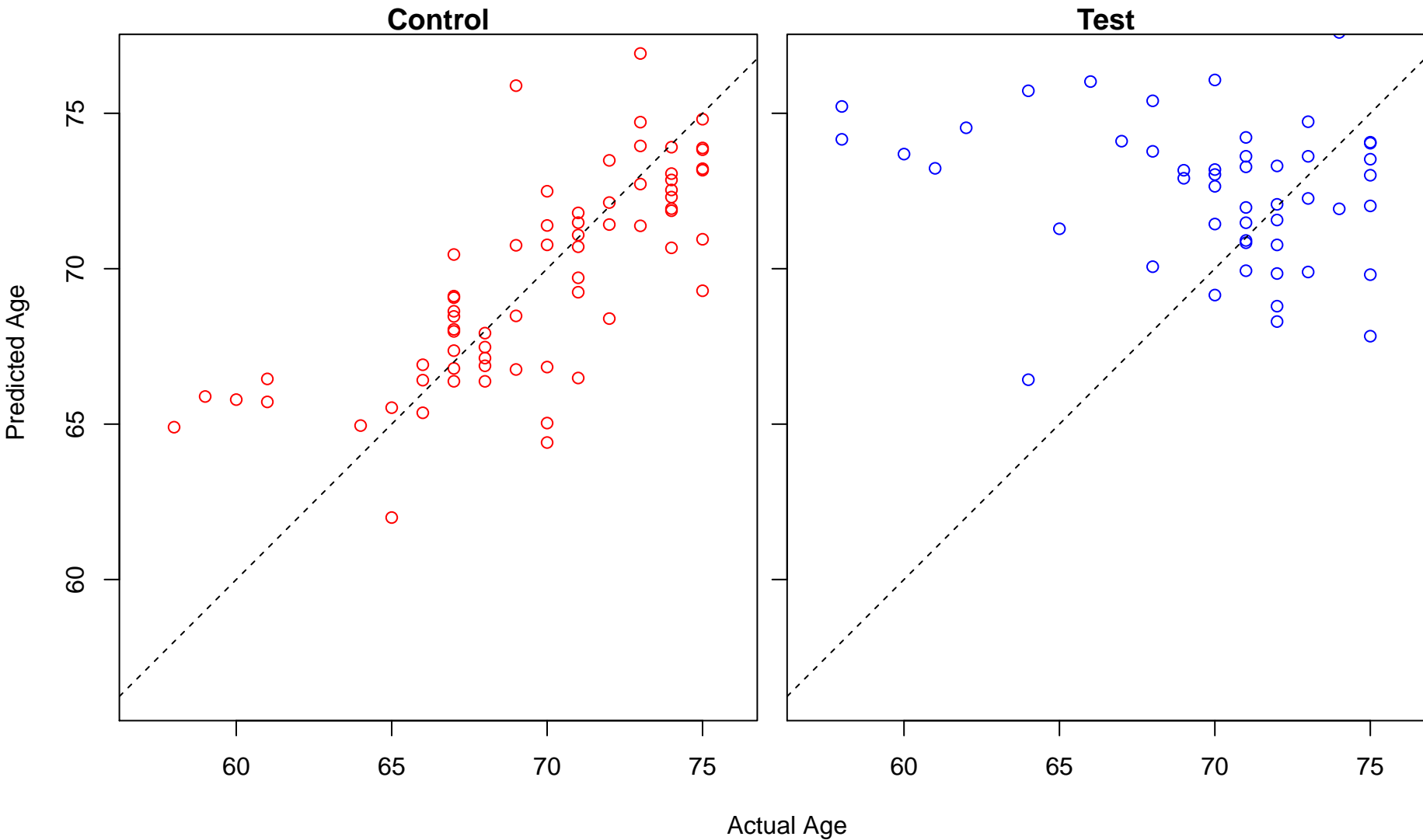


Test

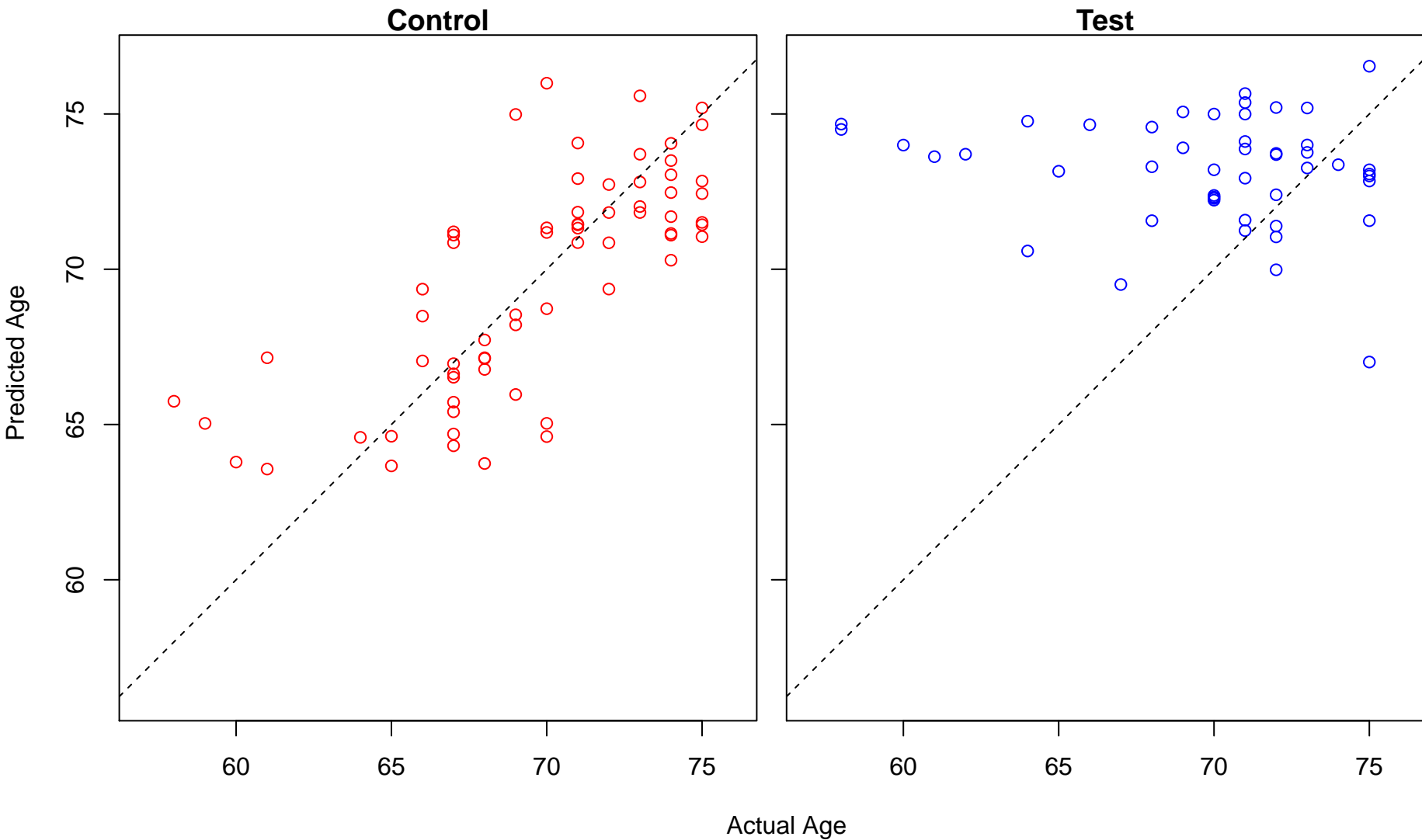


Actual Age

leukocyte migration involved in inflammatory response (Score: 2.020814)

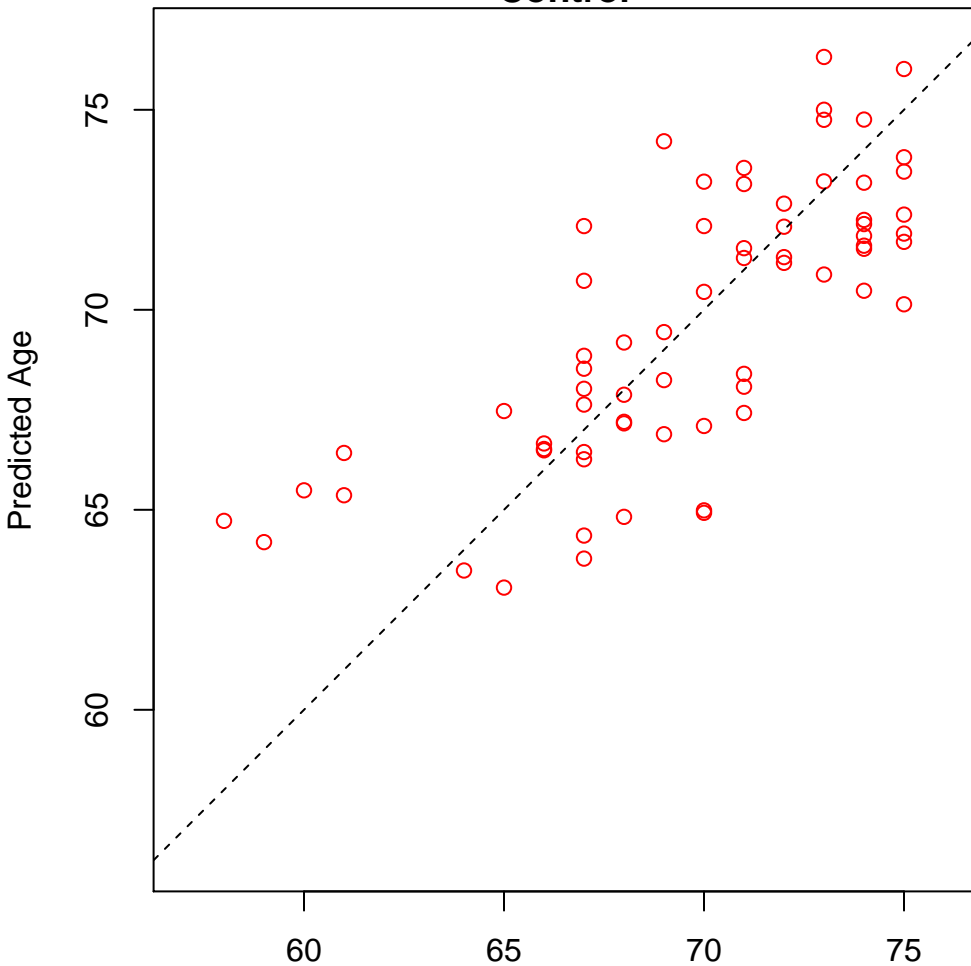


protein N-linked glycosylation via asparagine (Score: 2.020257)

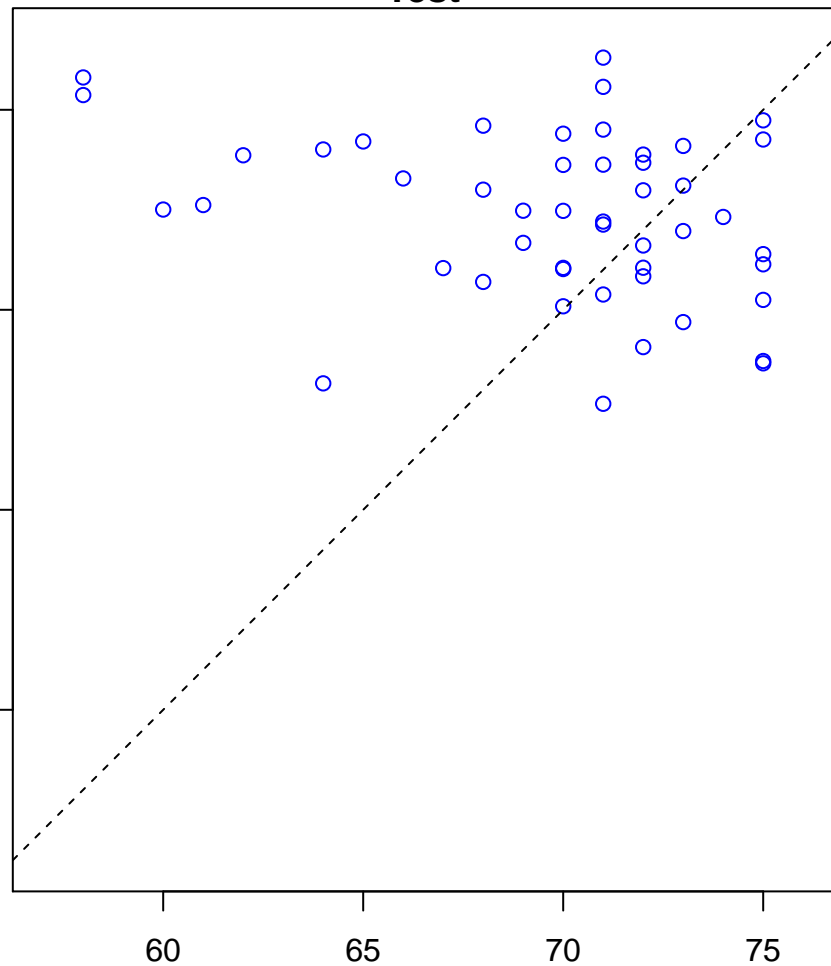


positive regulation of protein transport (Score: 2.020177)

Control

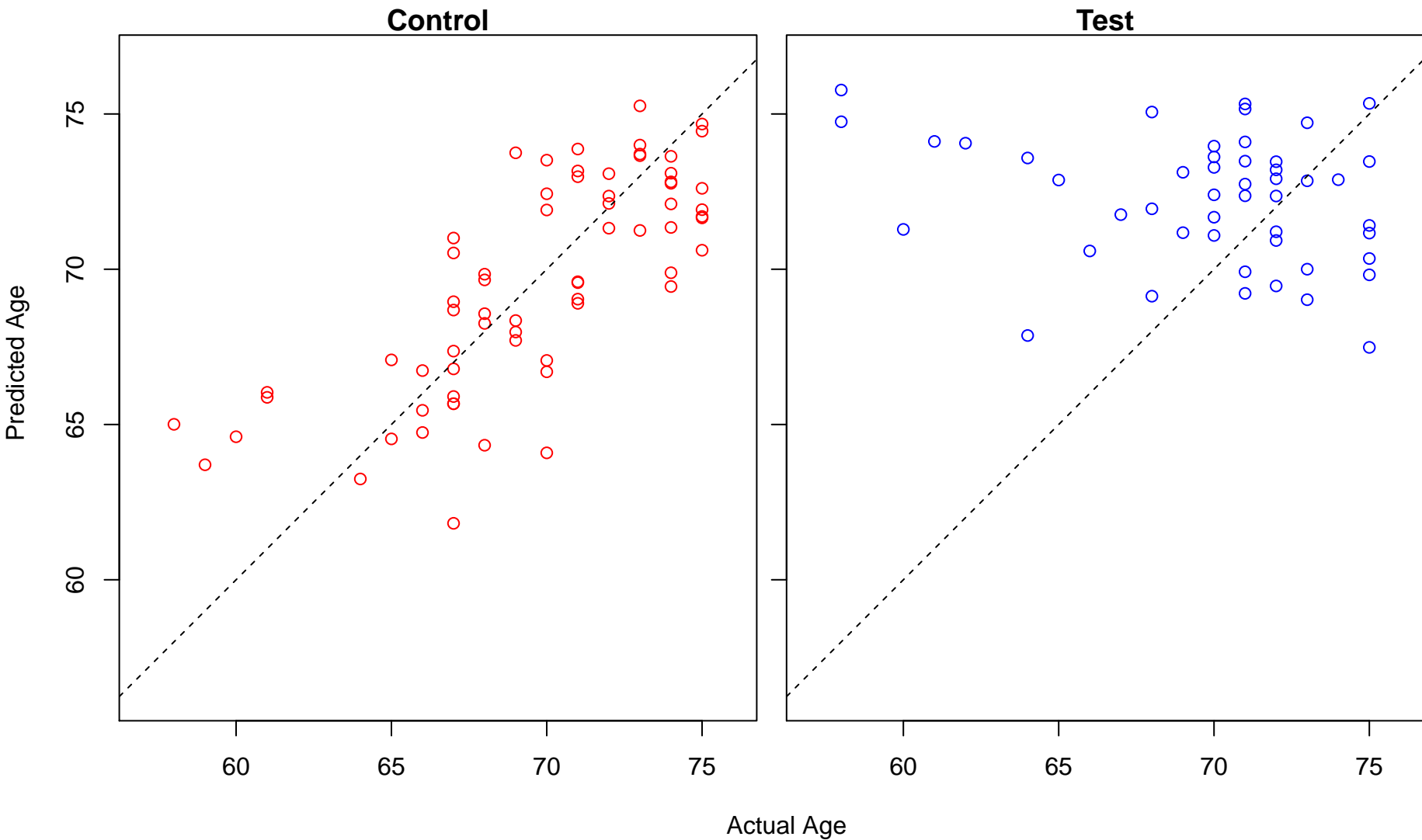


Test

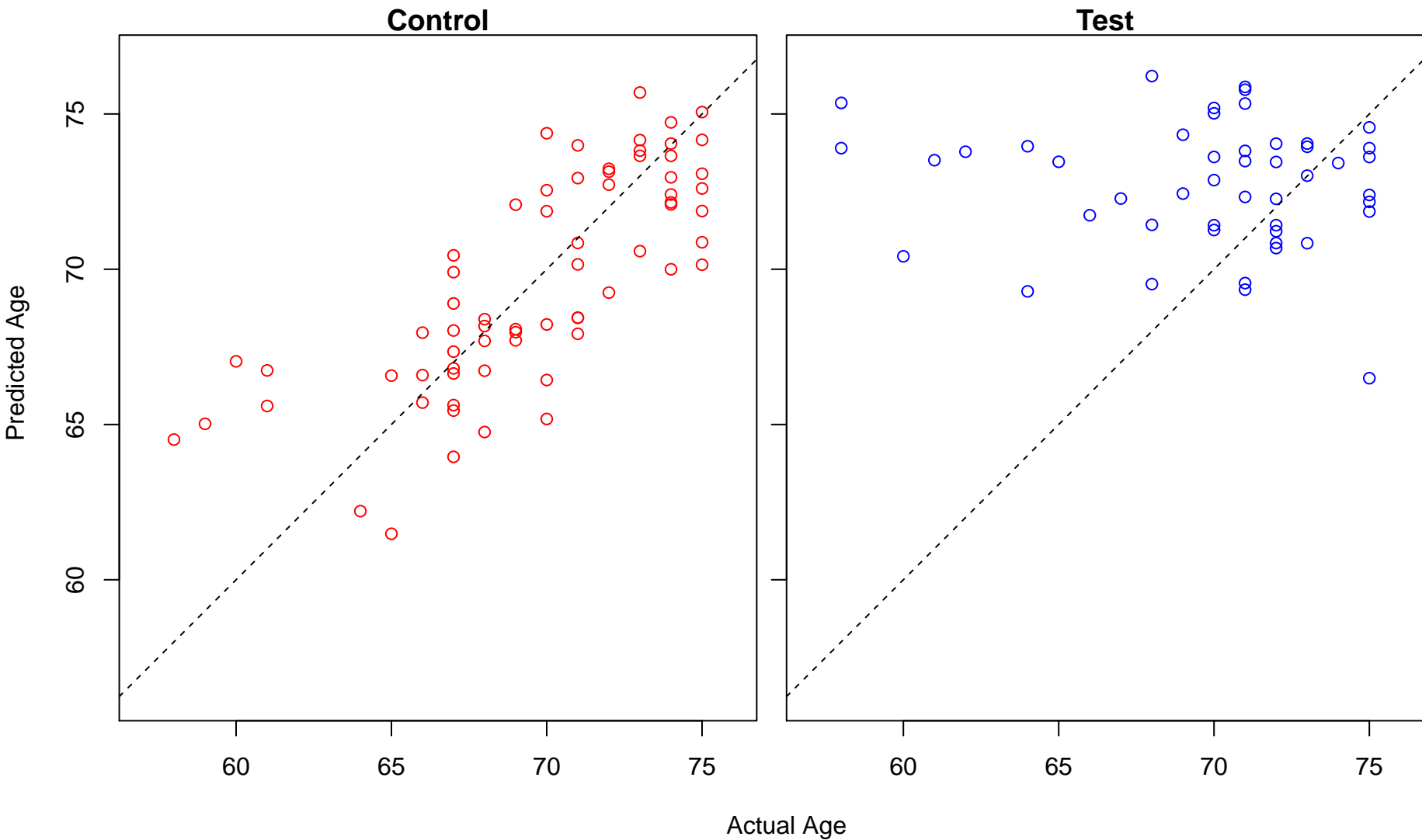


Actual Age

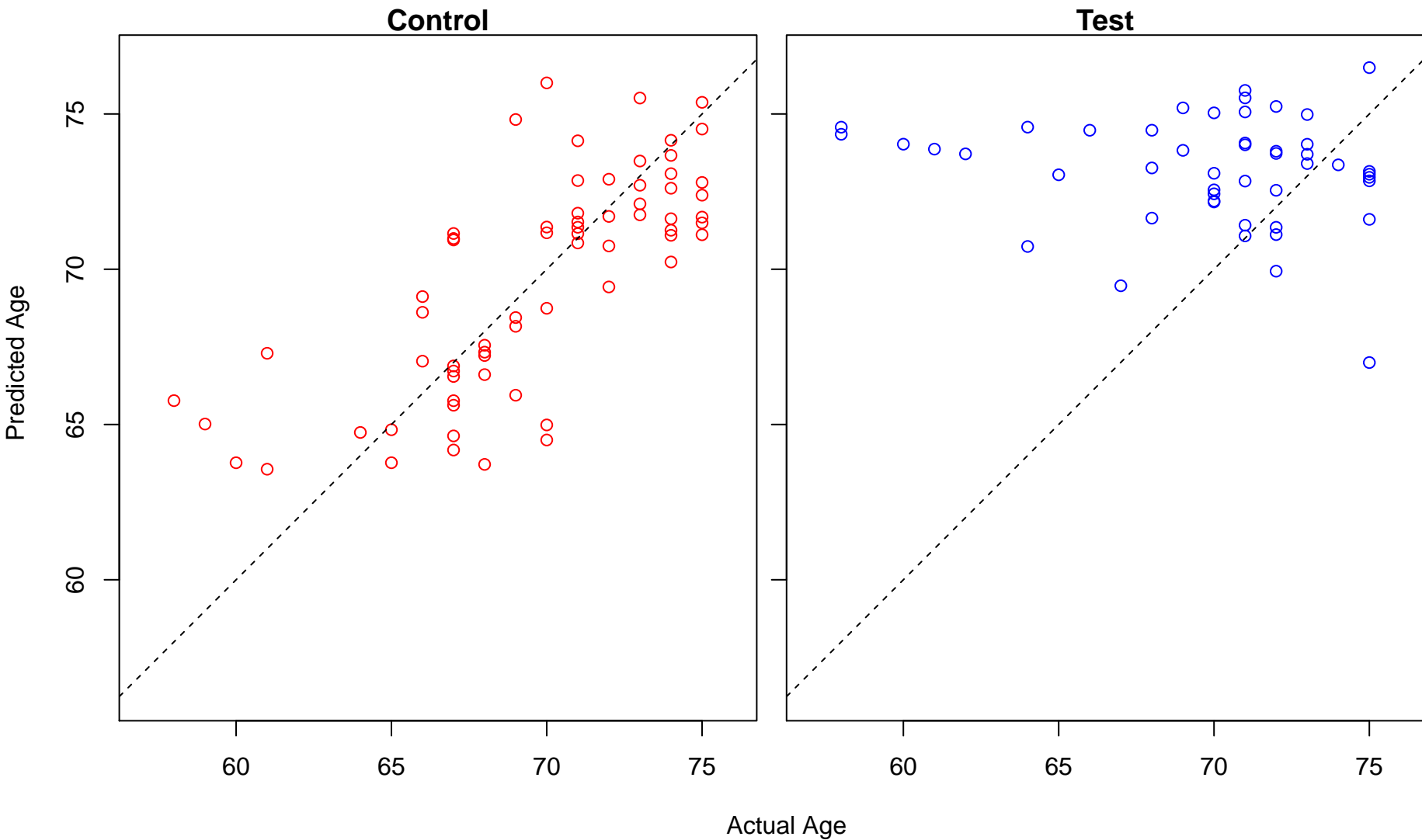
positive regulation of intracellular protein transport (Score: 2.019806)



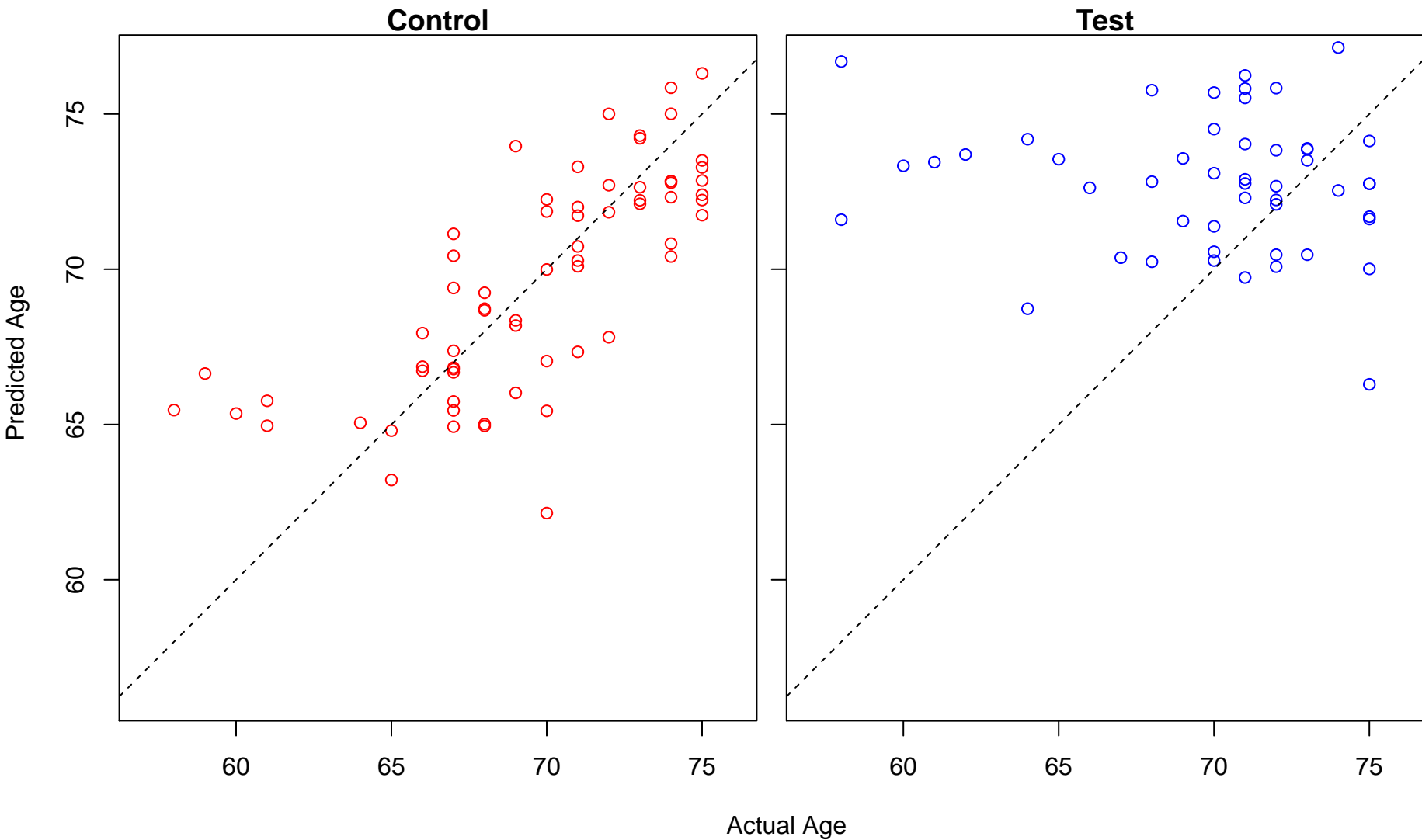
positive regulation of sequence-specific DNA binding transcription factor activity (Score: 2.018570)



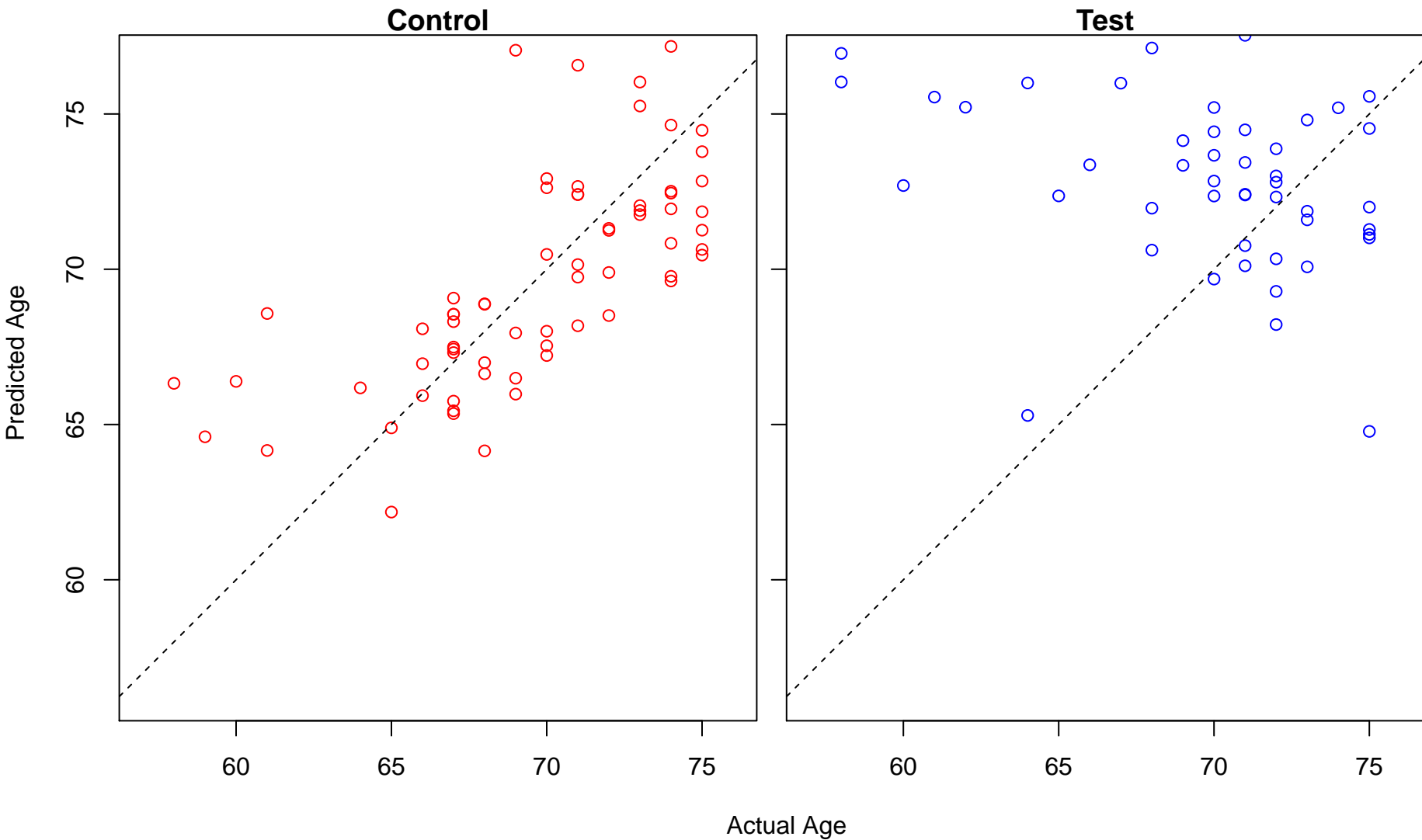
protein N-linked glycosylation (Score: 2.018182)



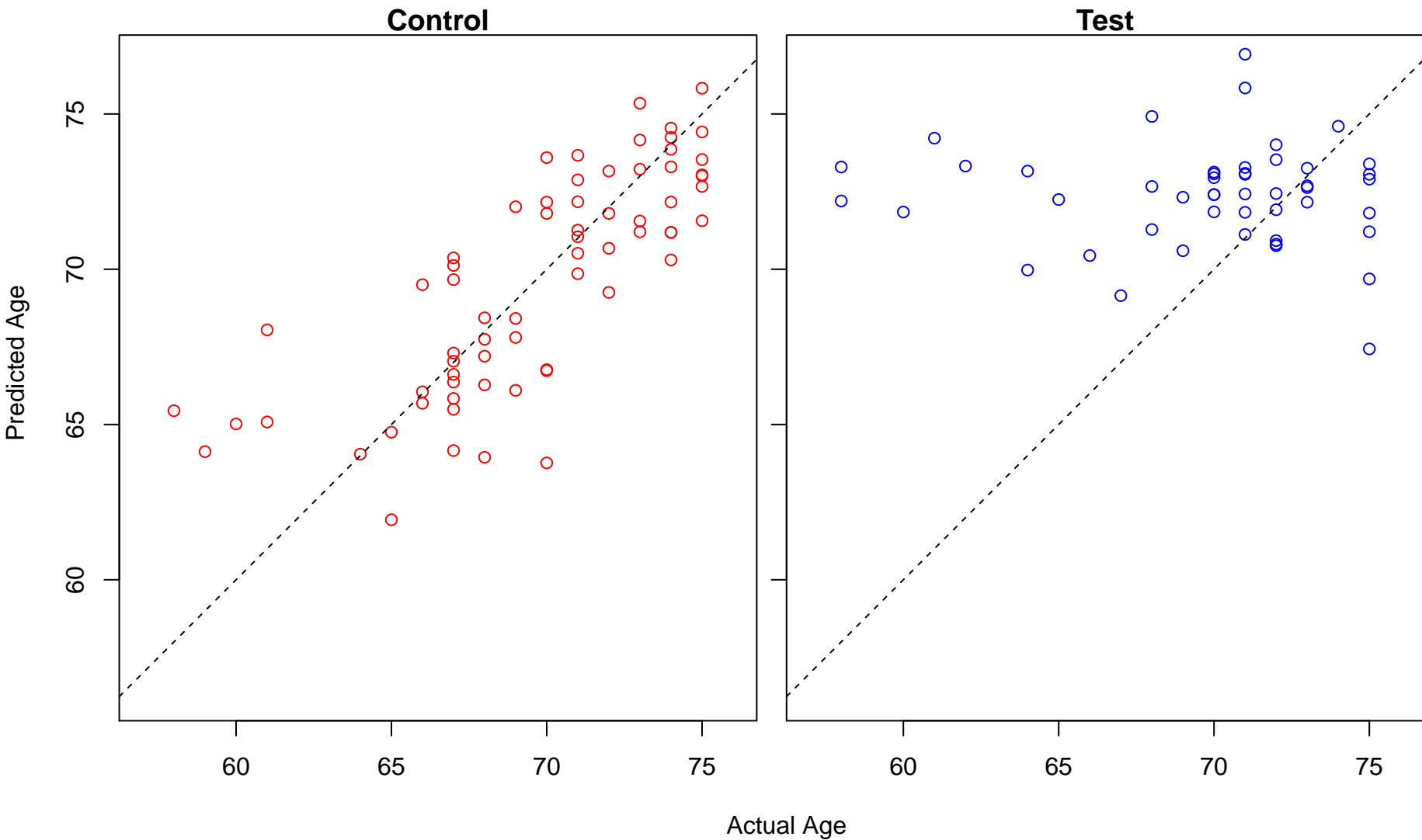
positive regulation of hemopoiesis (Score: 2.017076)



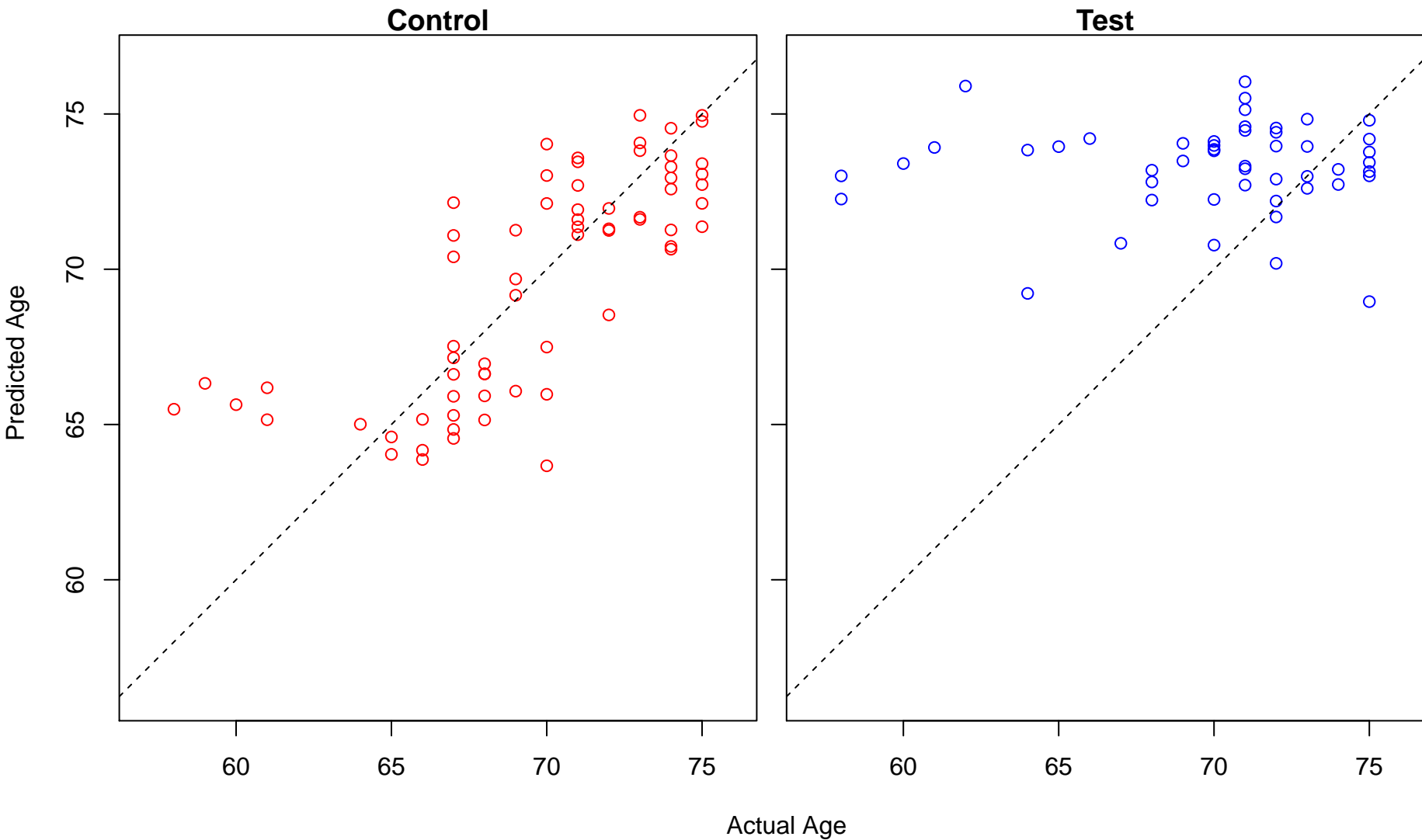
positive regulation of mononuclear cell proliferation (Score: 2.015137)



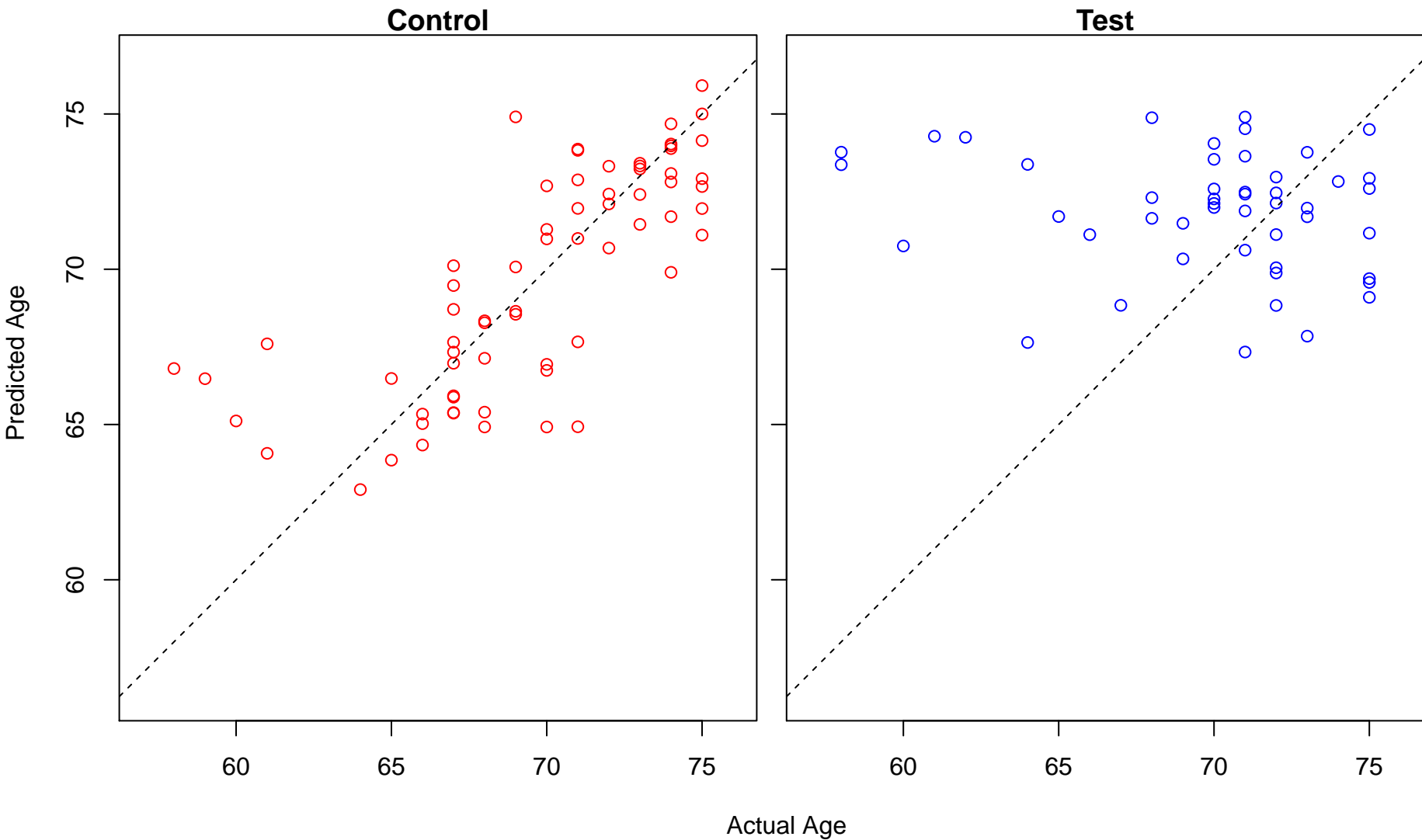
regulation of mitotic cell cycle (Score: 2.014453)



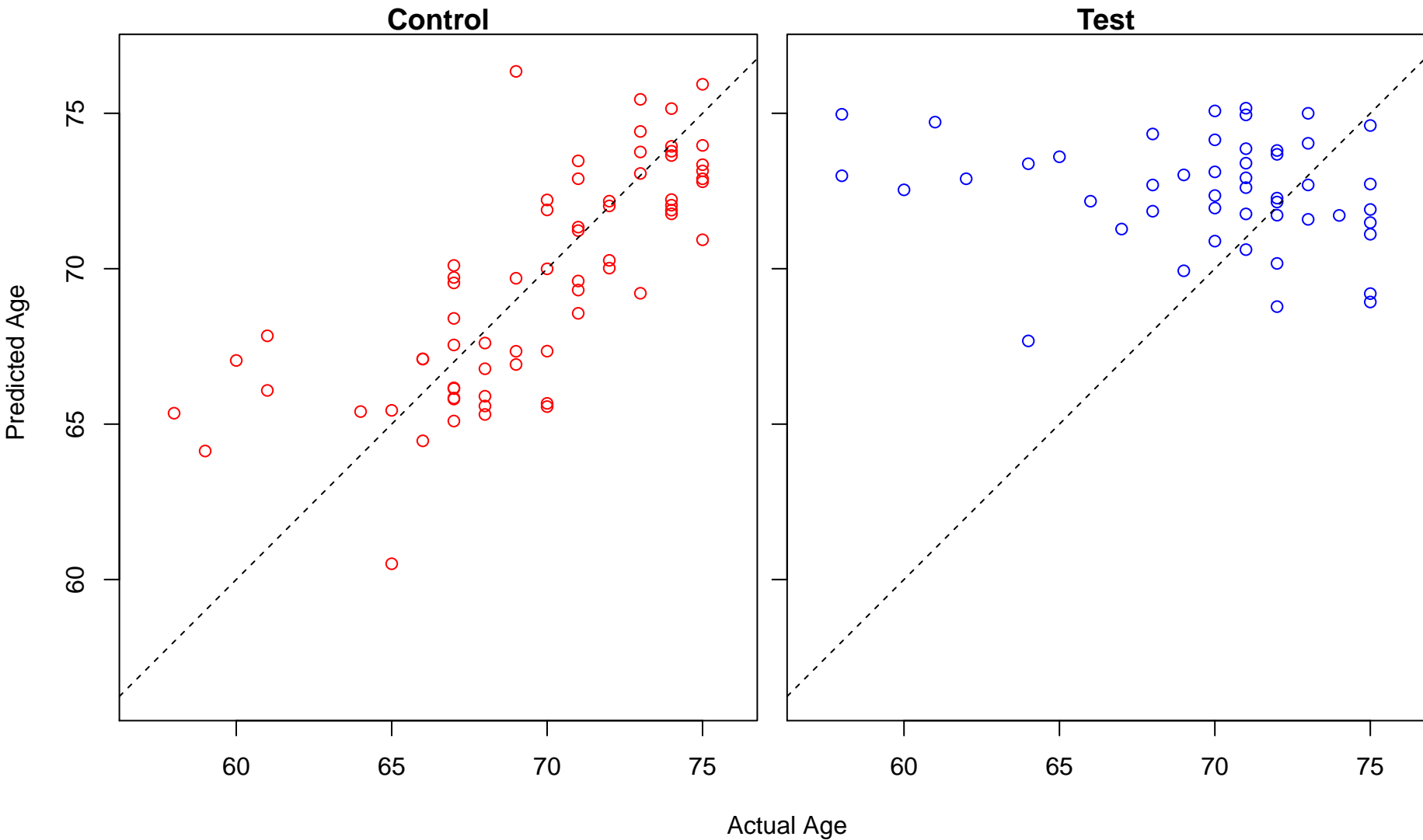
histone acetylation (Score: 2.013208)



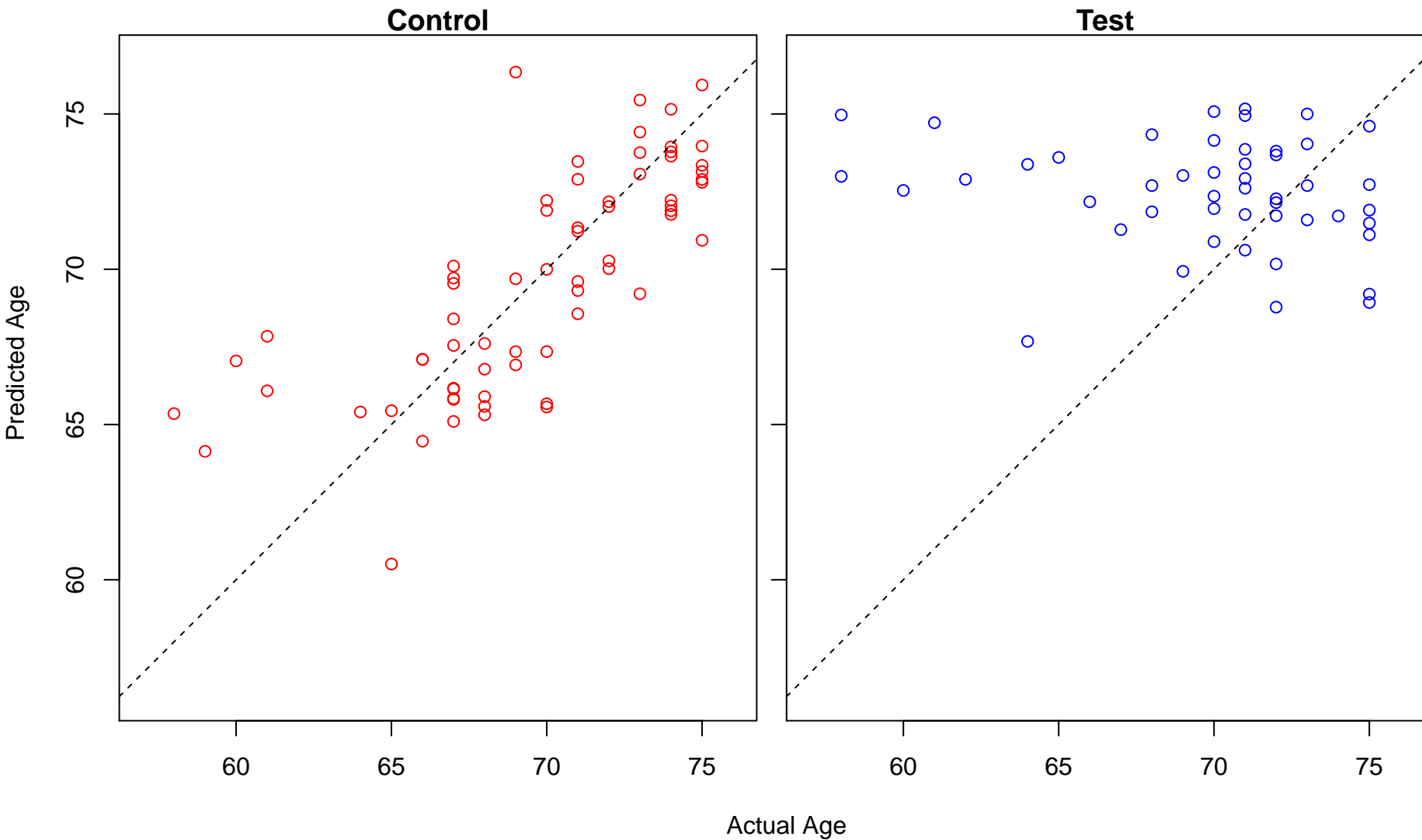
purine nucleotide metabolic process (Score: 2.012674)



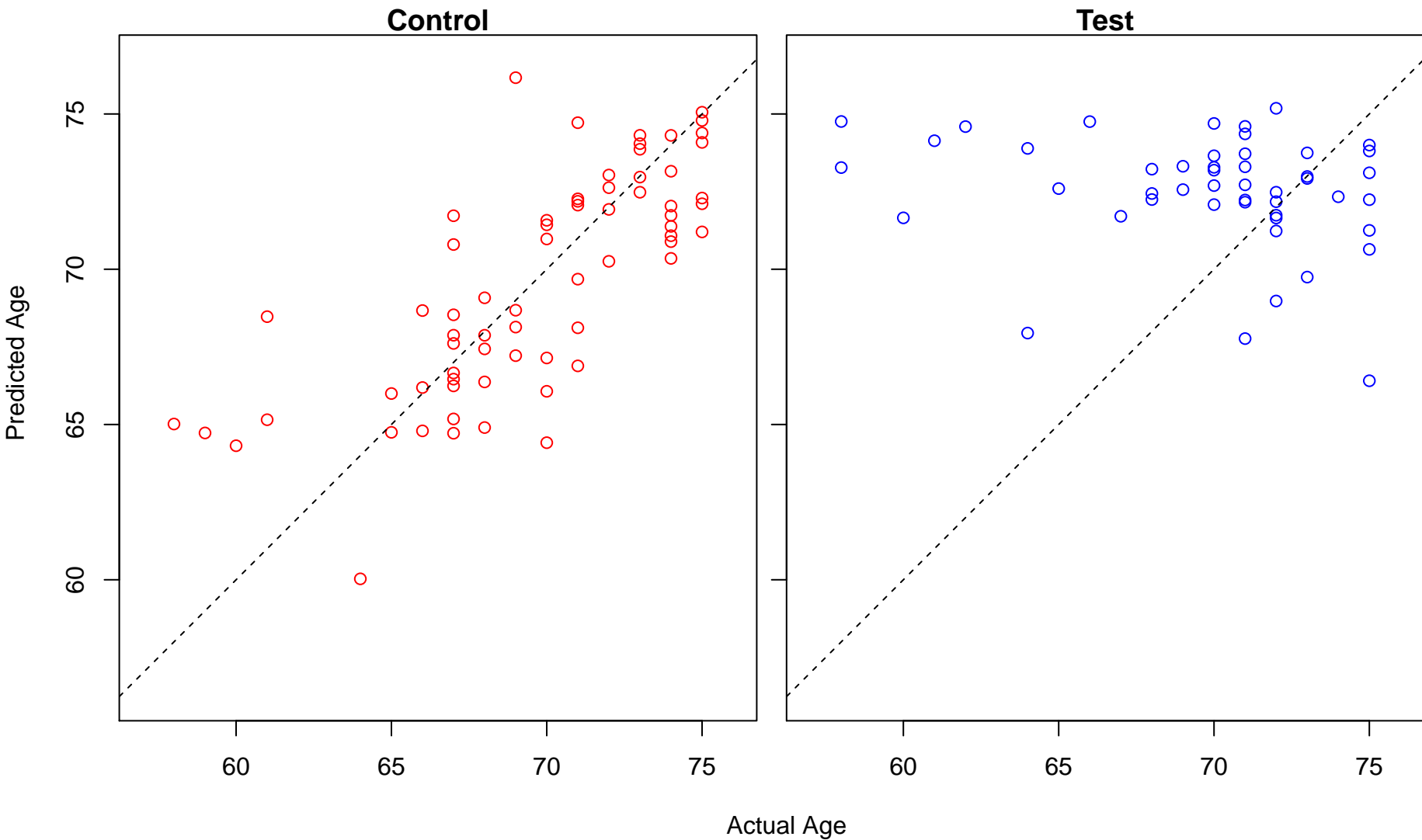
antigen processing and presentation of exogenous peptide antigen (Score: 2.012068)



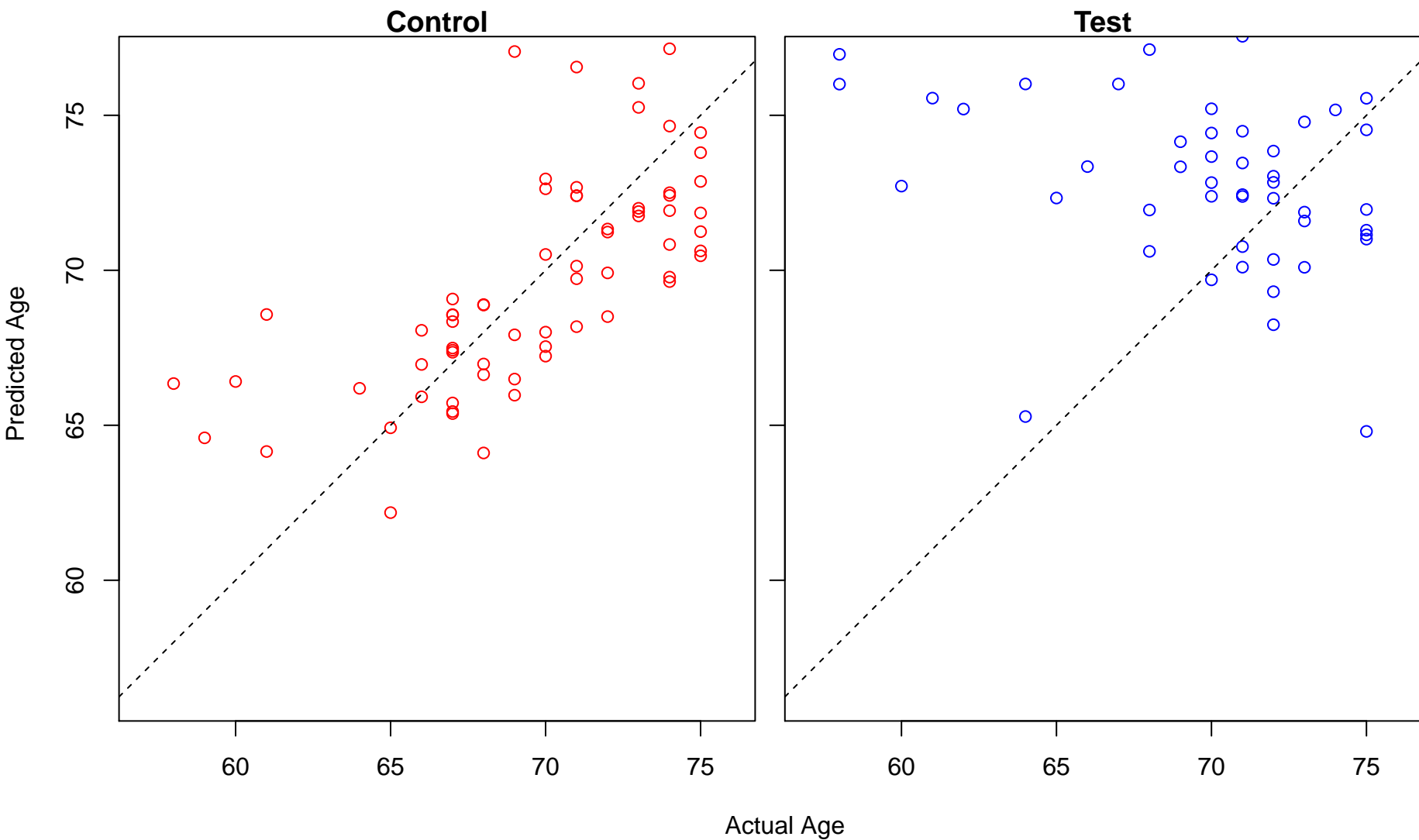
antigen processing and presentation of exogenous antigen (Score: 2.012068)



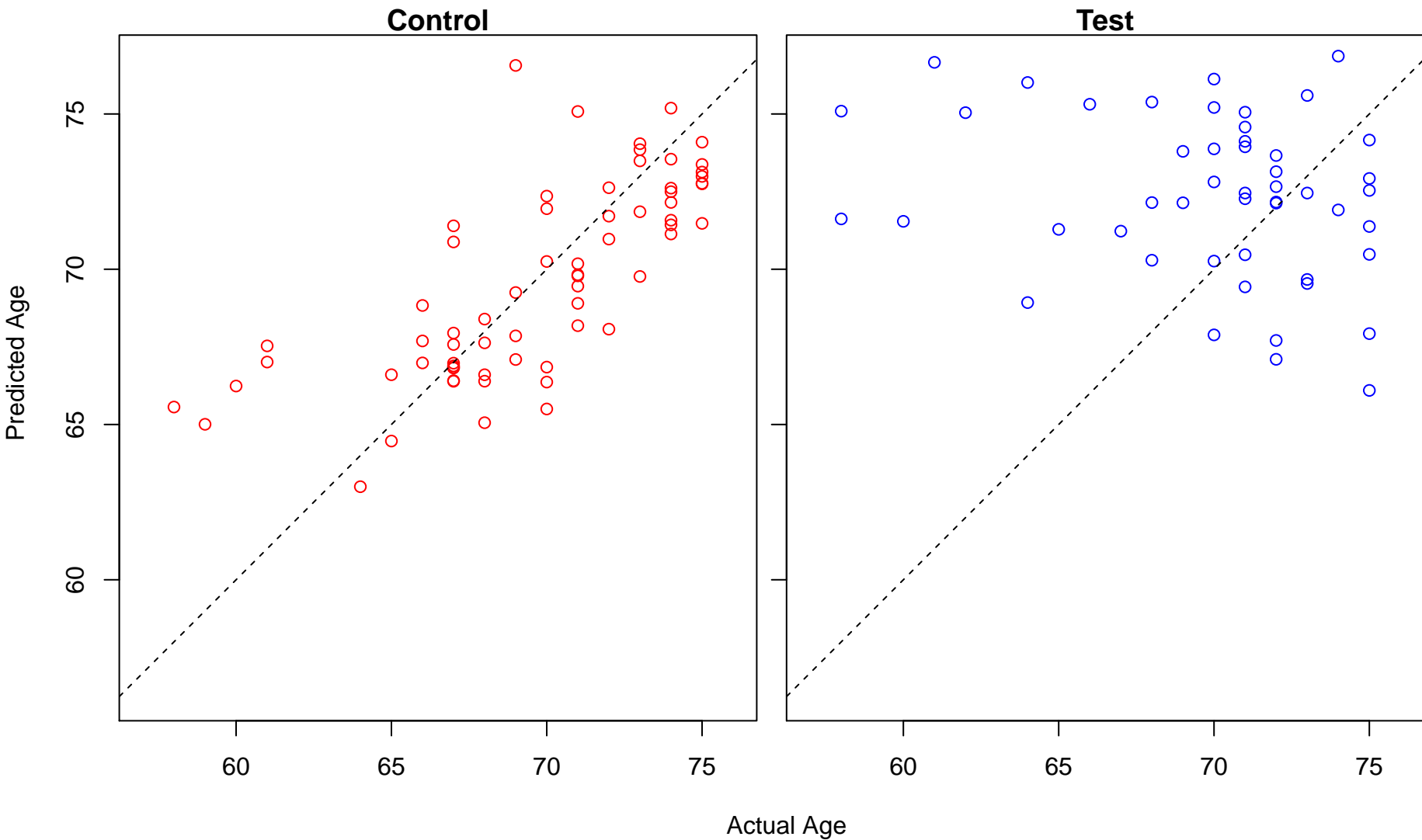
regulation of multi-organism process (Score: 2.010693)



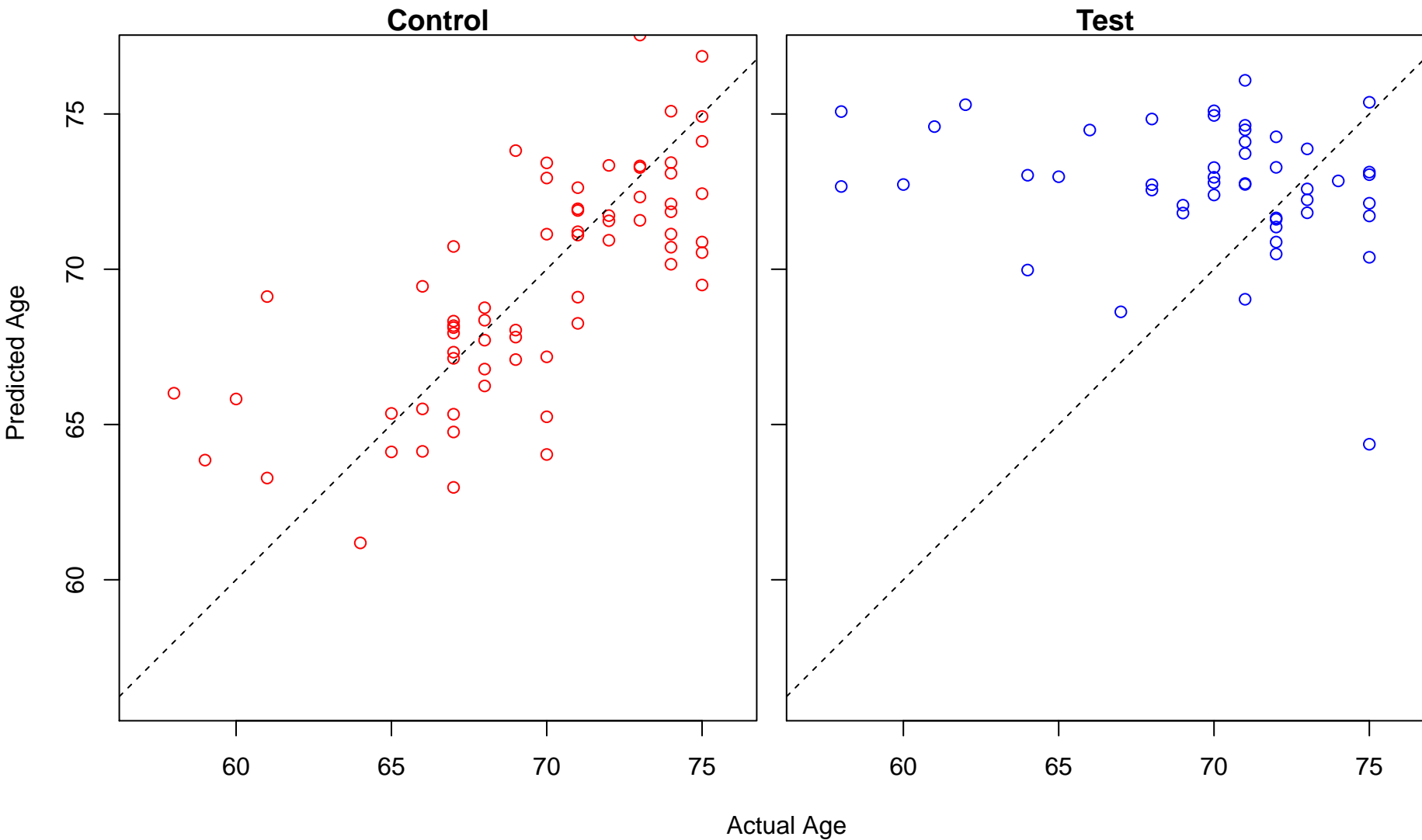
positive regulation of lymphocyte proliferation (Score: 2.008754)



regulation of defense response to virus by host (Score: 2.008189)

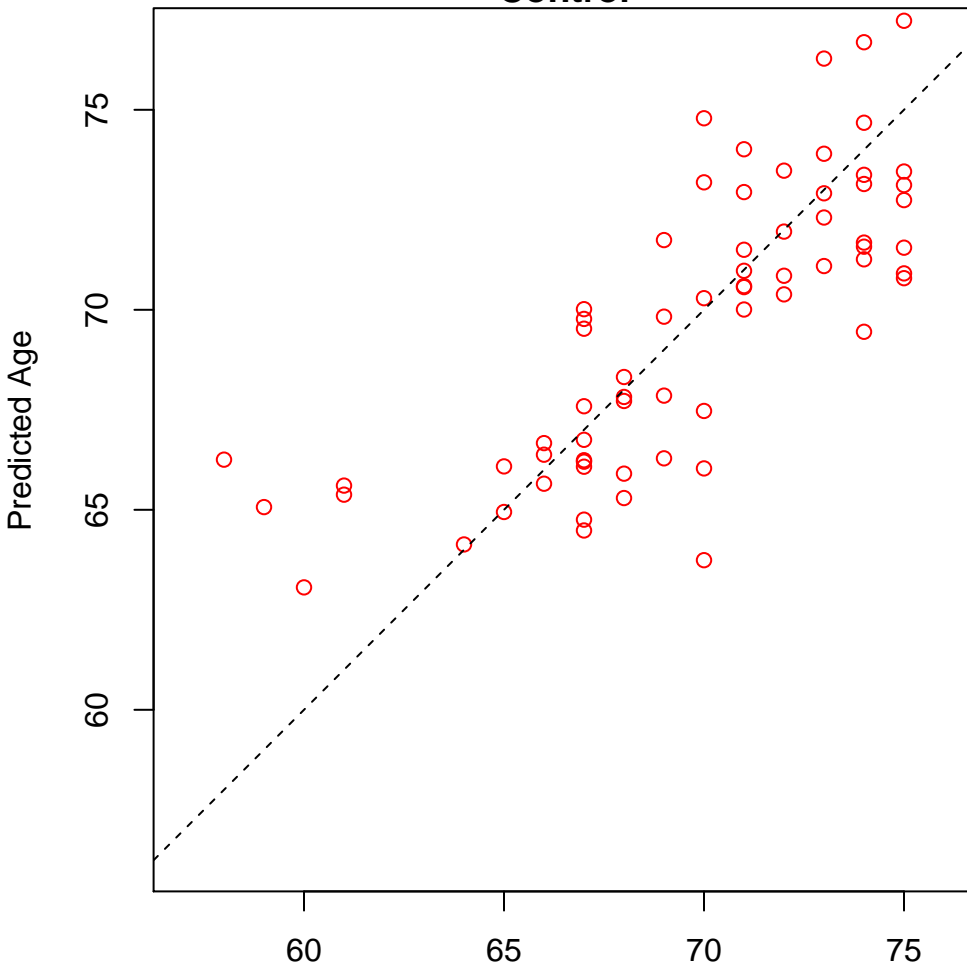


negative regulation of proteolysis (Score: 2.007794)

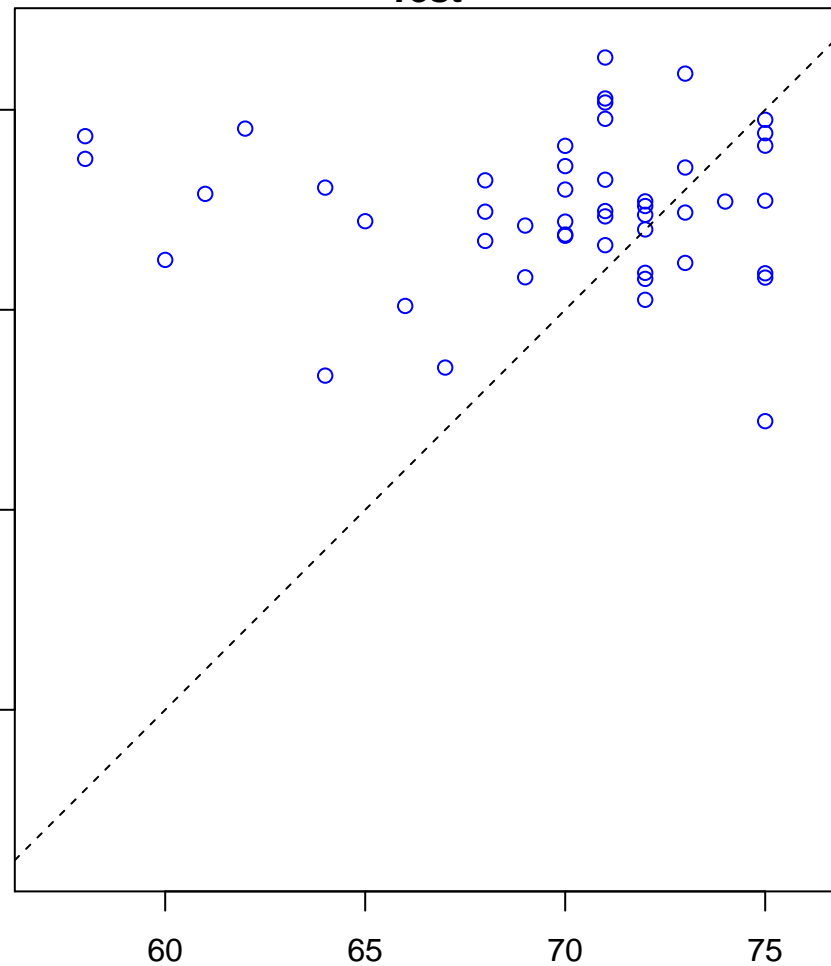


monovalent inorganic cation transport (Score: 2.006787)

Control

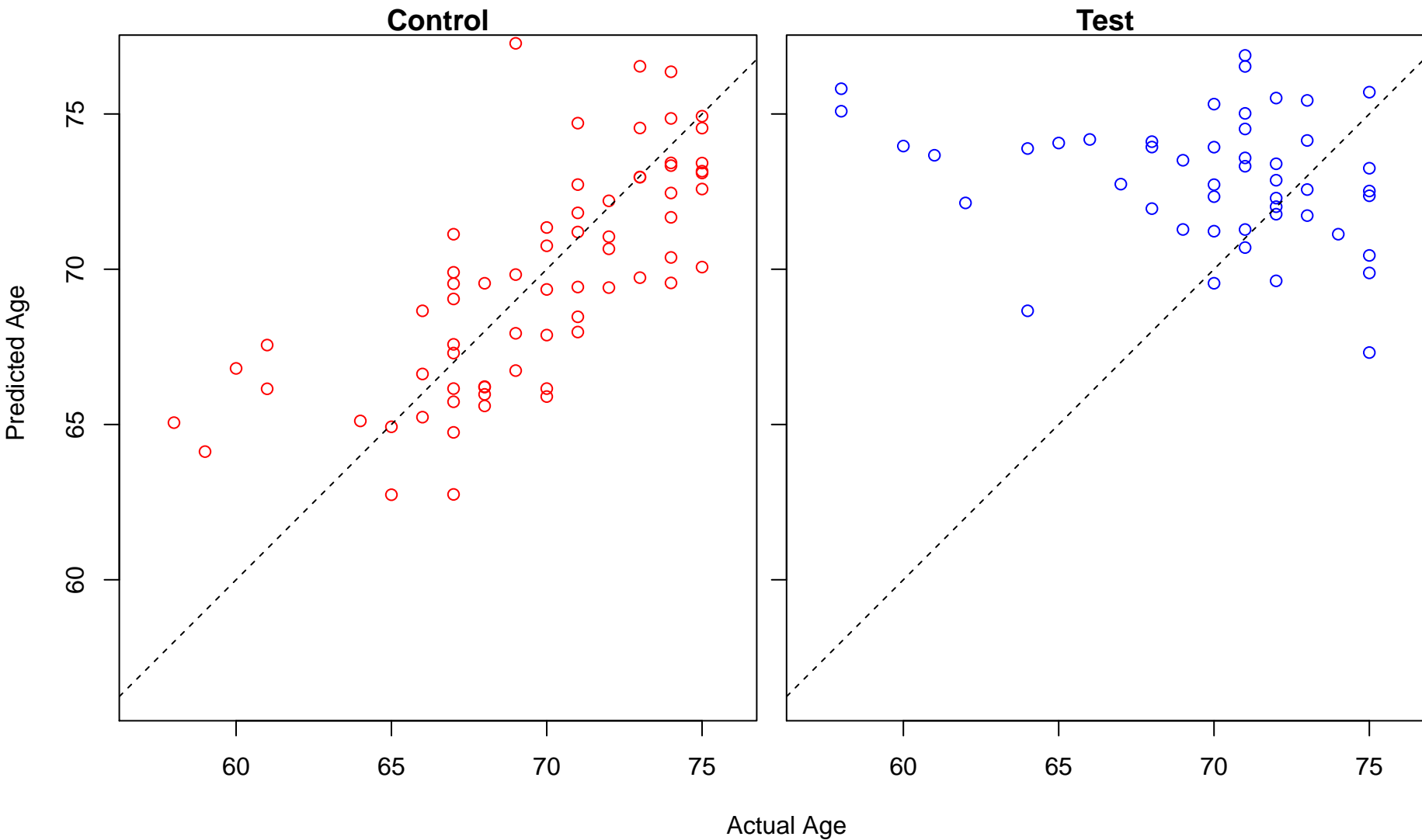


Test

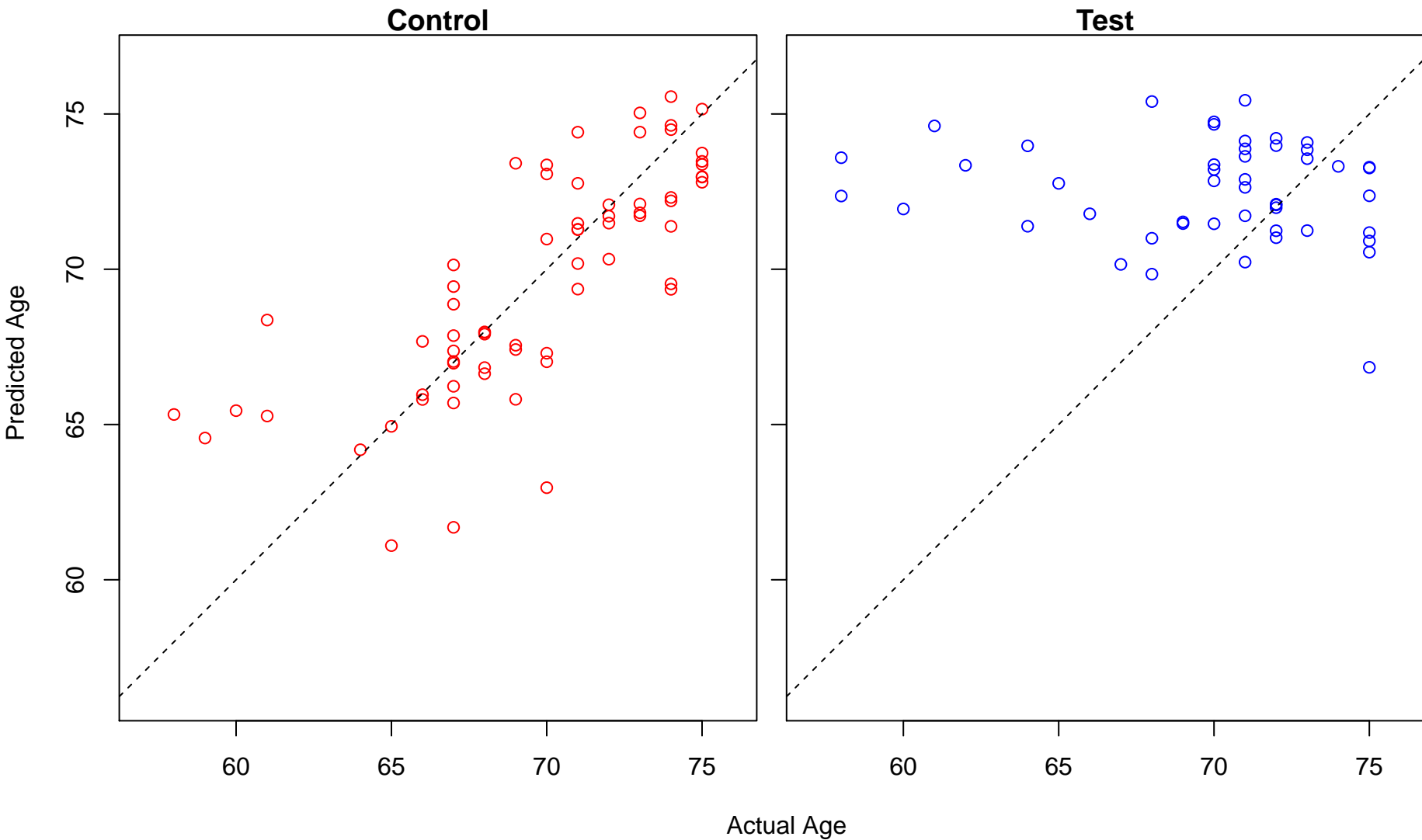


Actual Age

regulation of cell activation (Score: 2.006732)

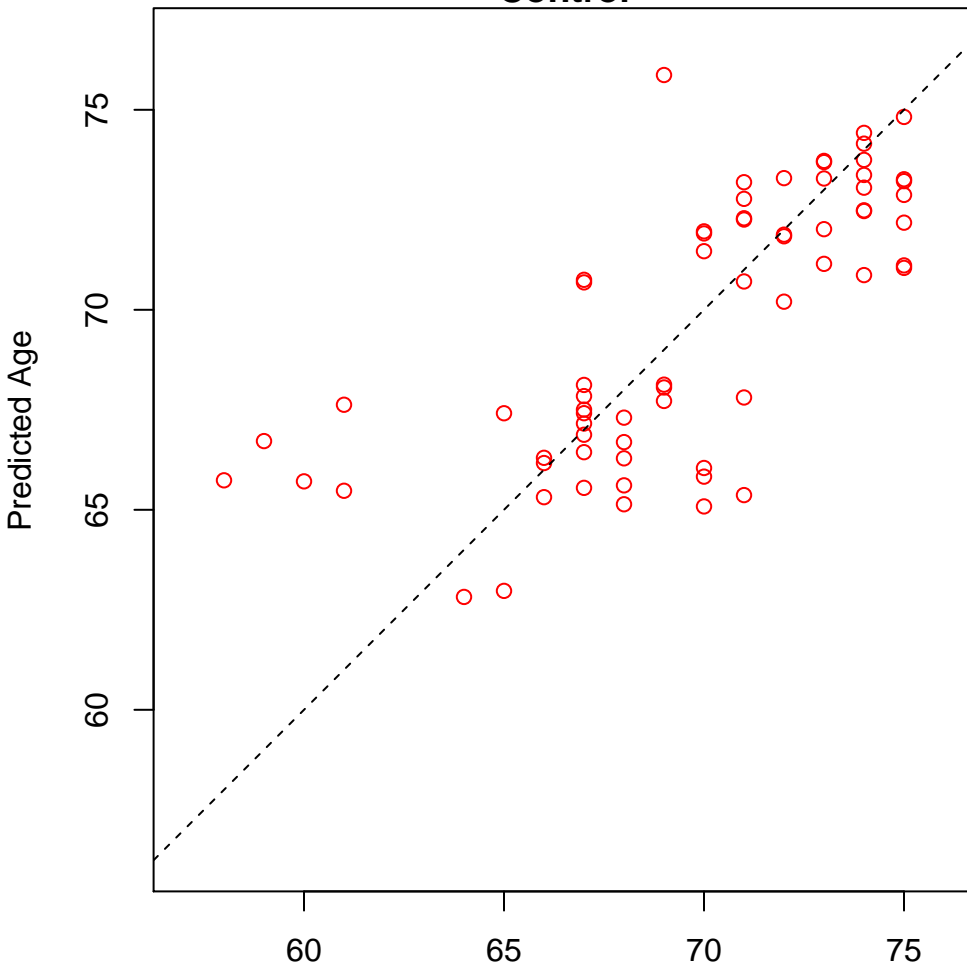


positive regulation of protein catabolic process (Score: 2.006320)

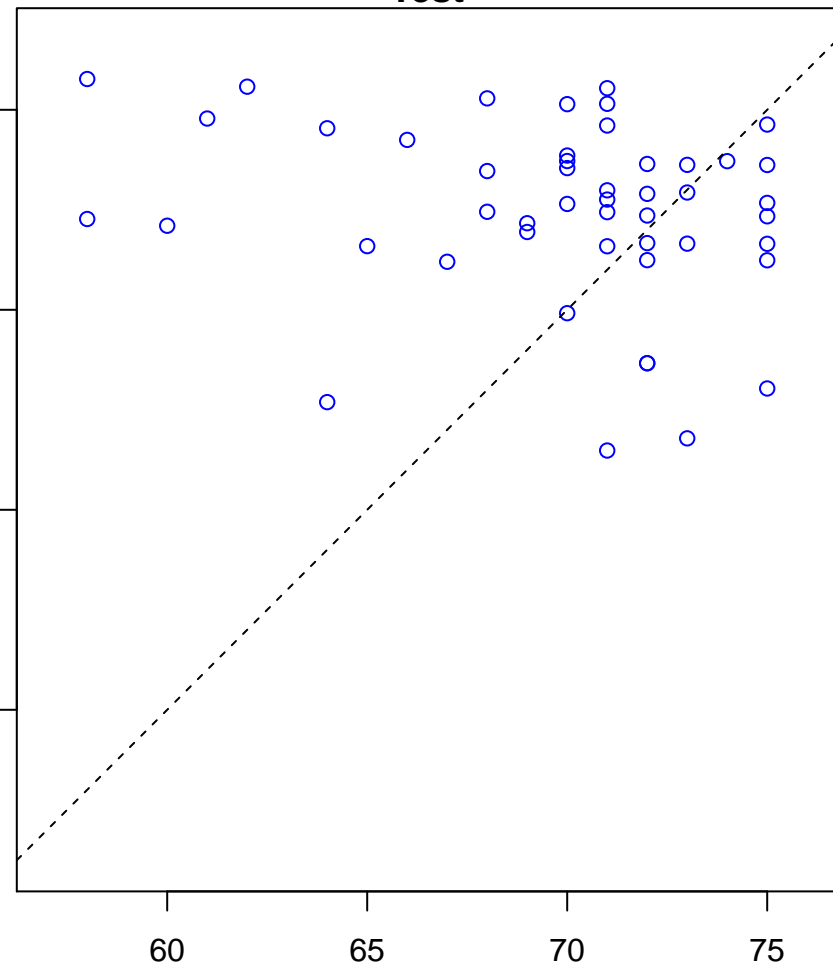


purine nucleotide biosynthetic process (Score: 2.005501)

Control

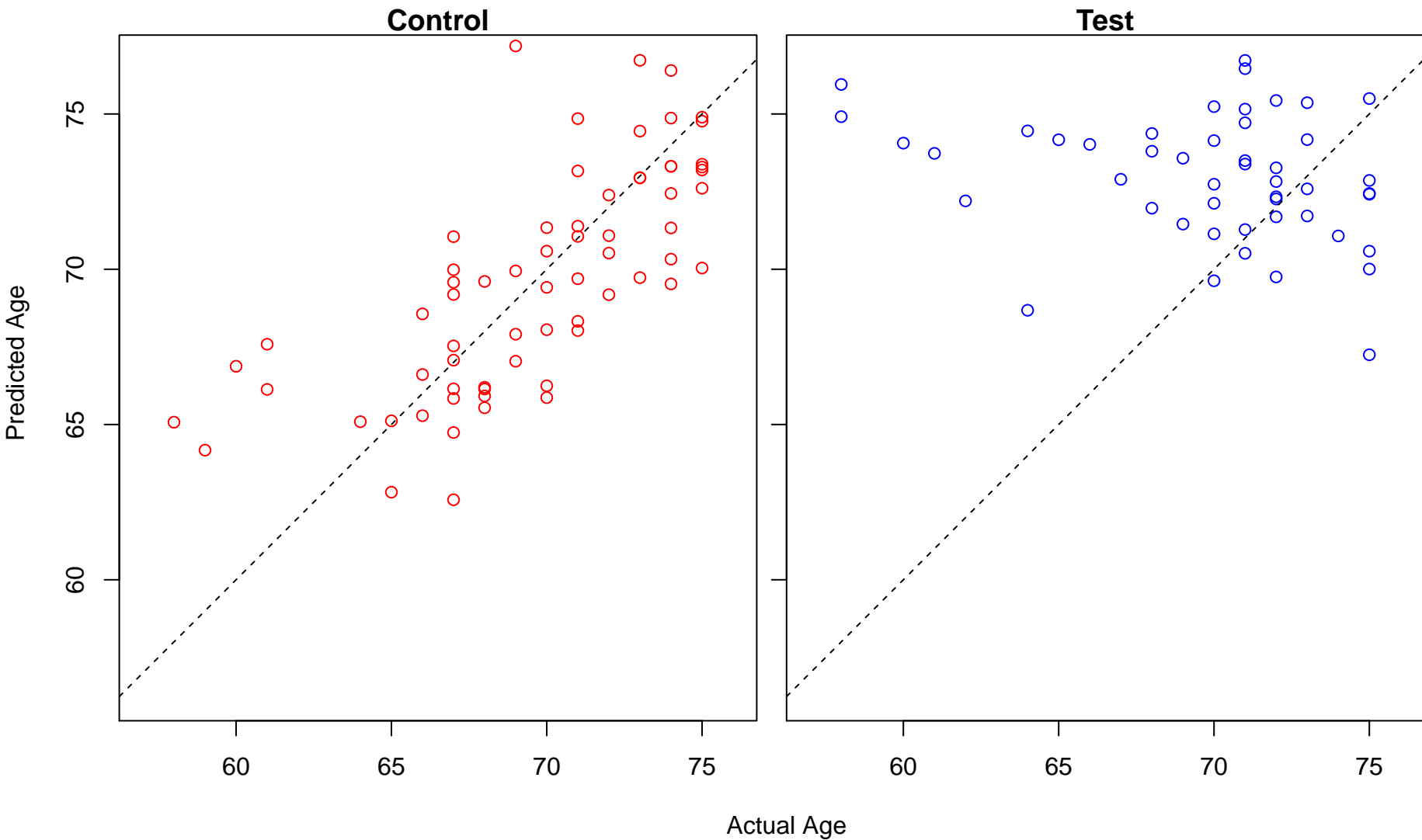


Test

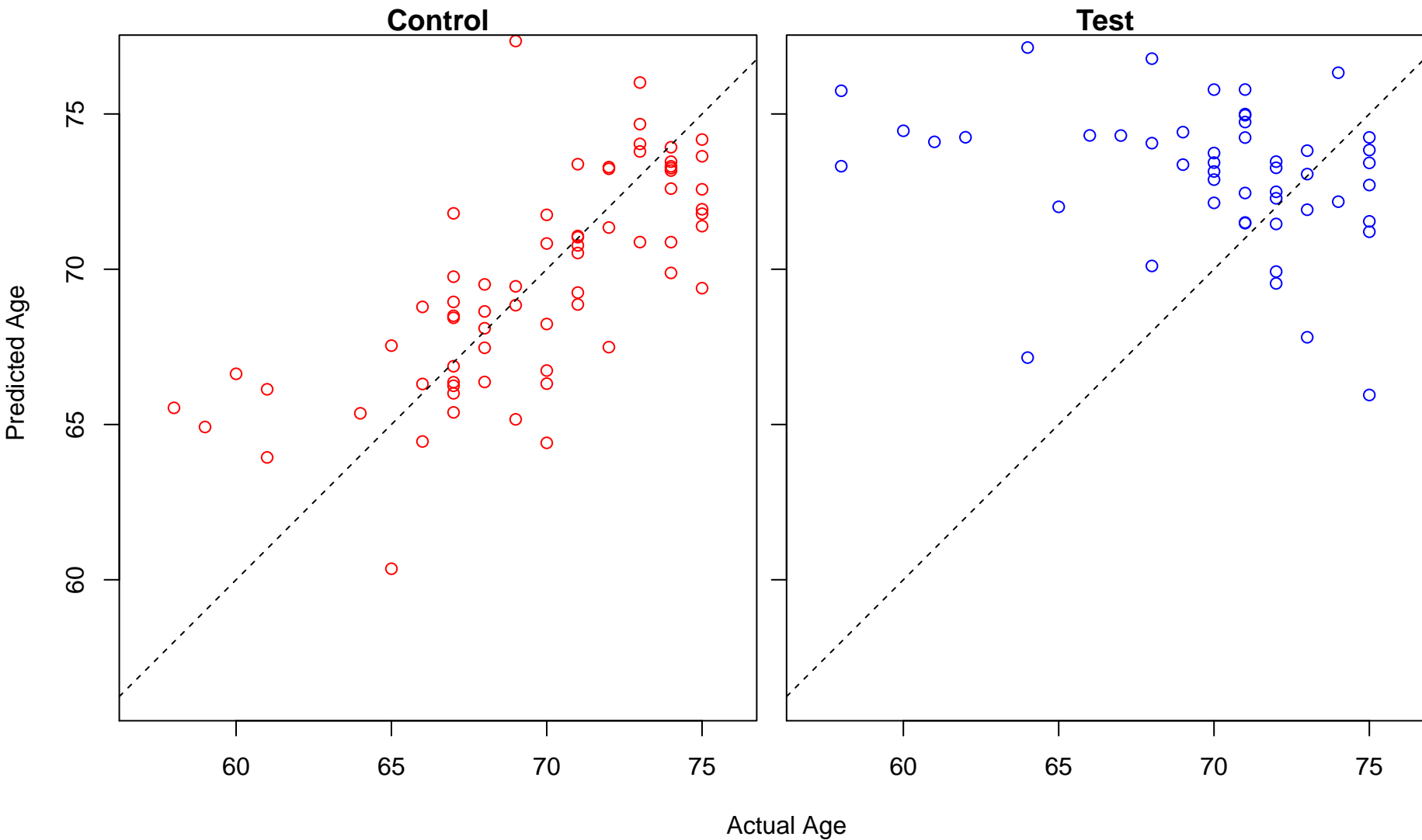


Actual Age

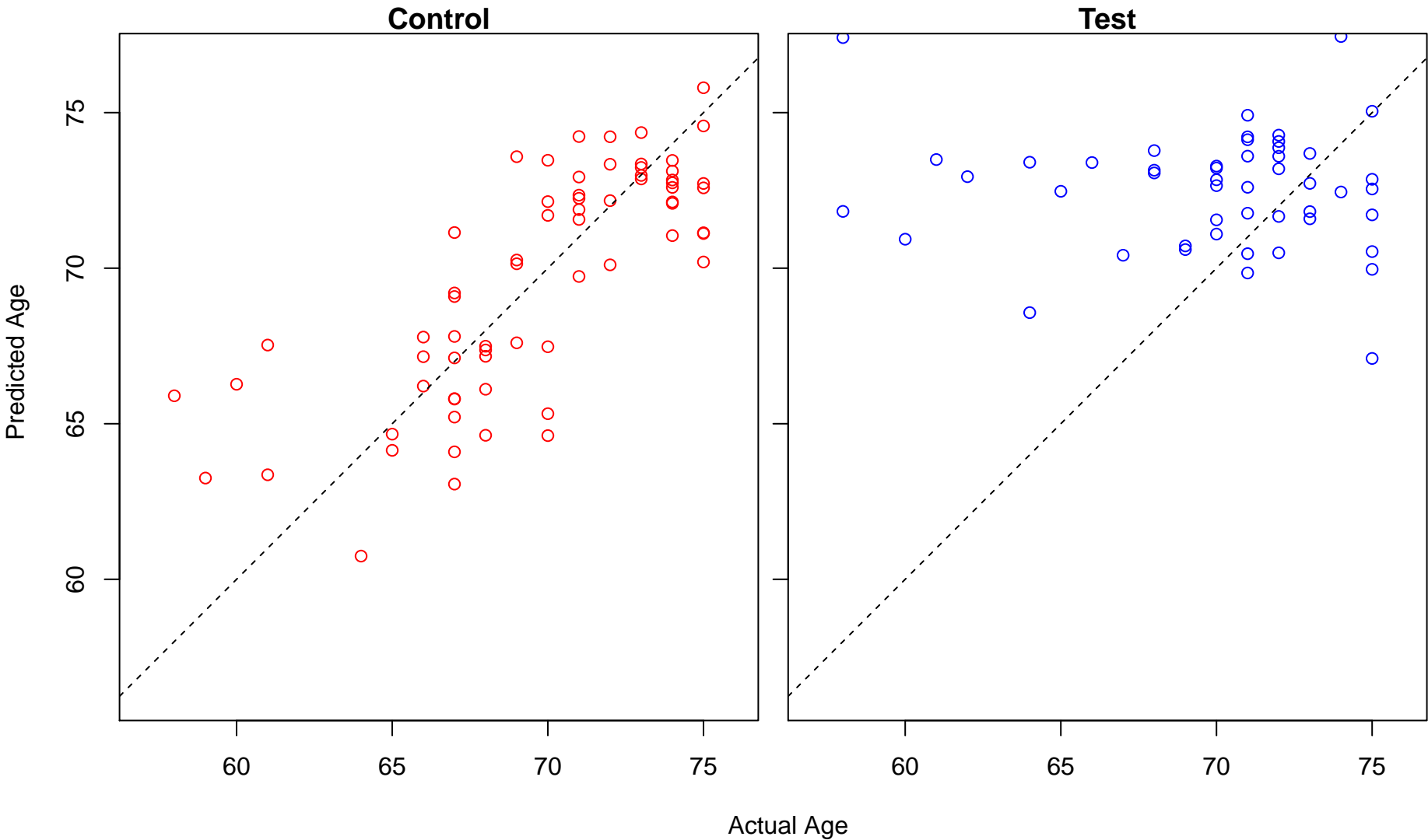
regulation of leukocyte activation (Score: 2.005240)



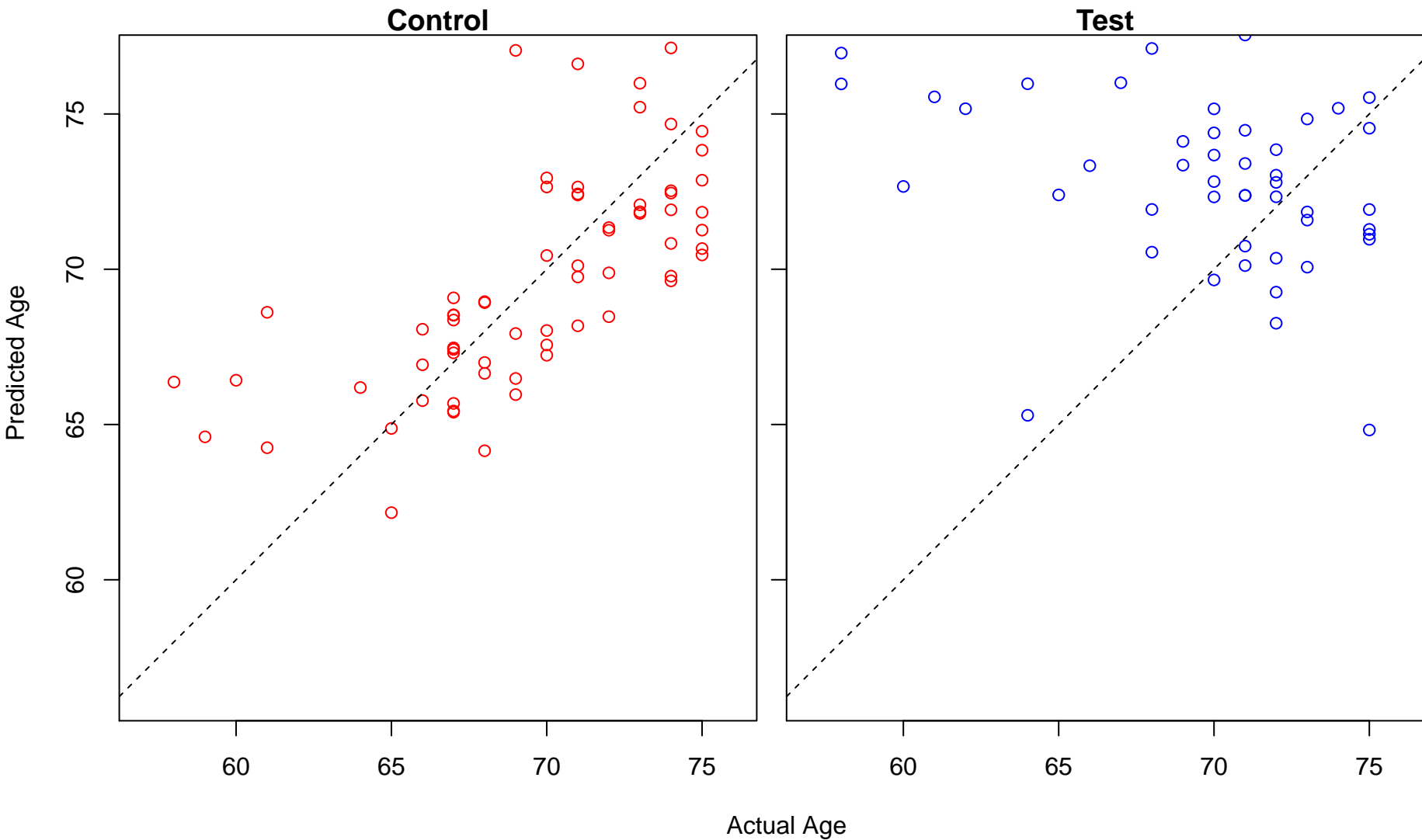
regulation of lymphocyte differentiation (Score: 2.004815)



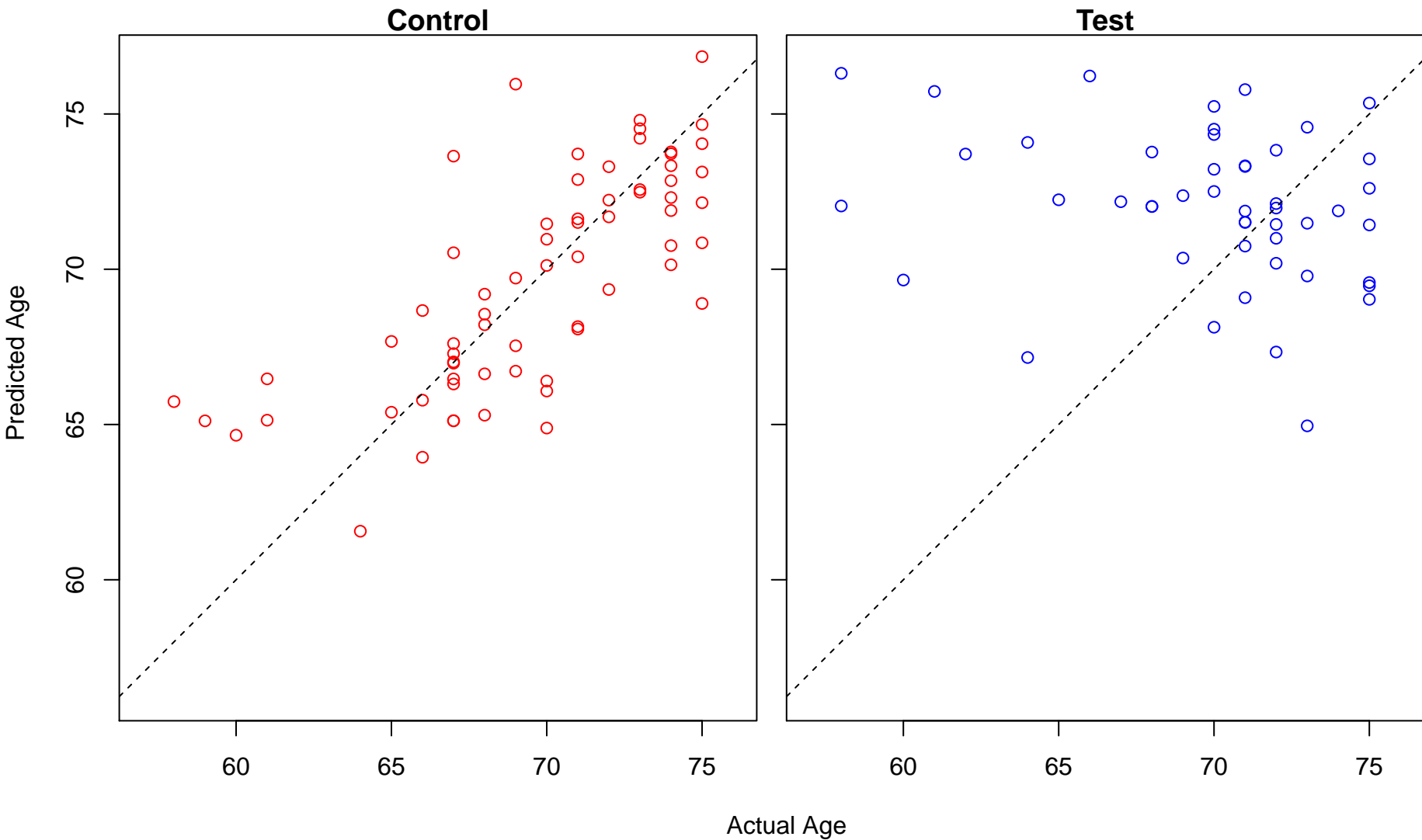
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 2.00)



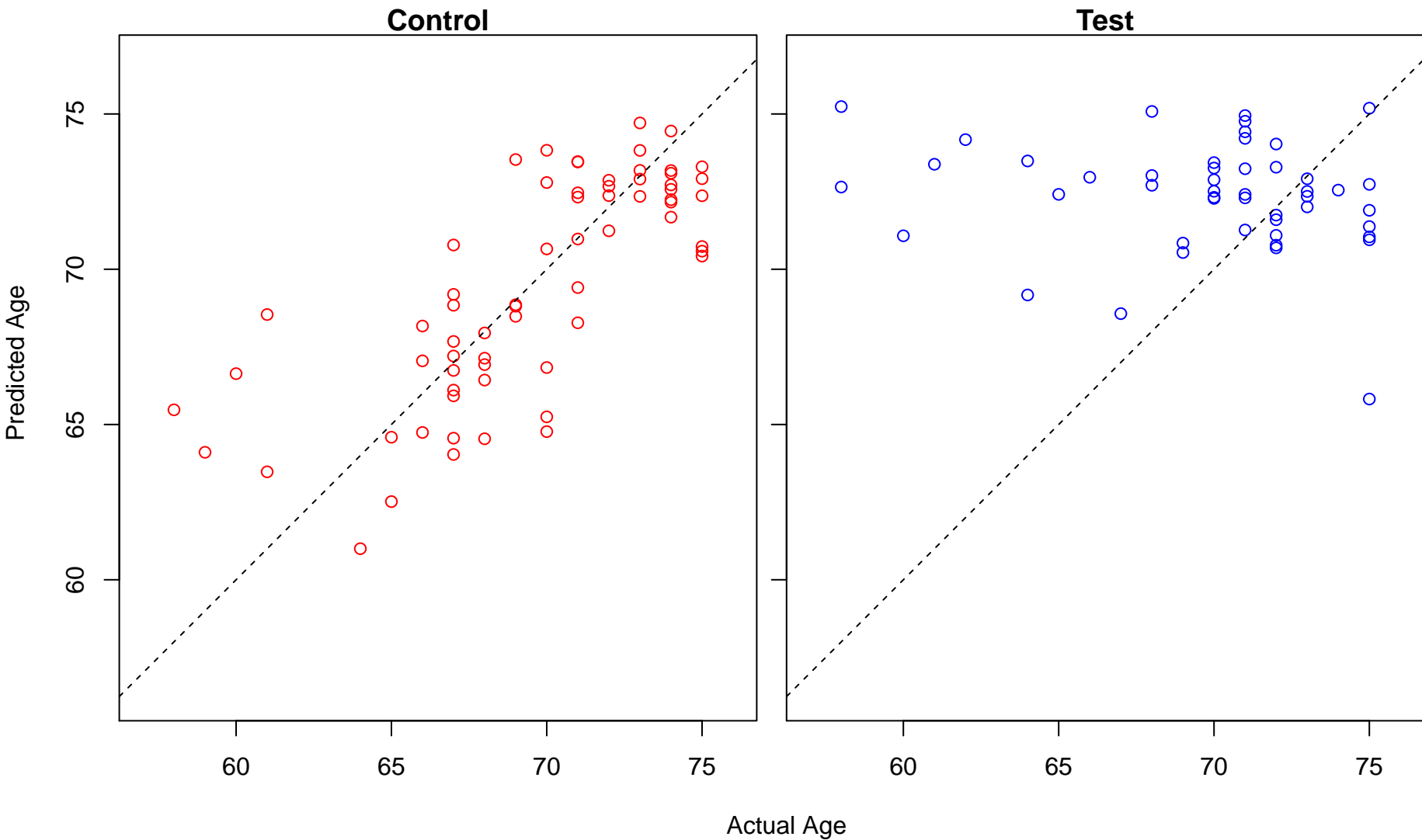
positive regulation of leukocyte proliferation (Score: 2.003000)



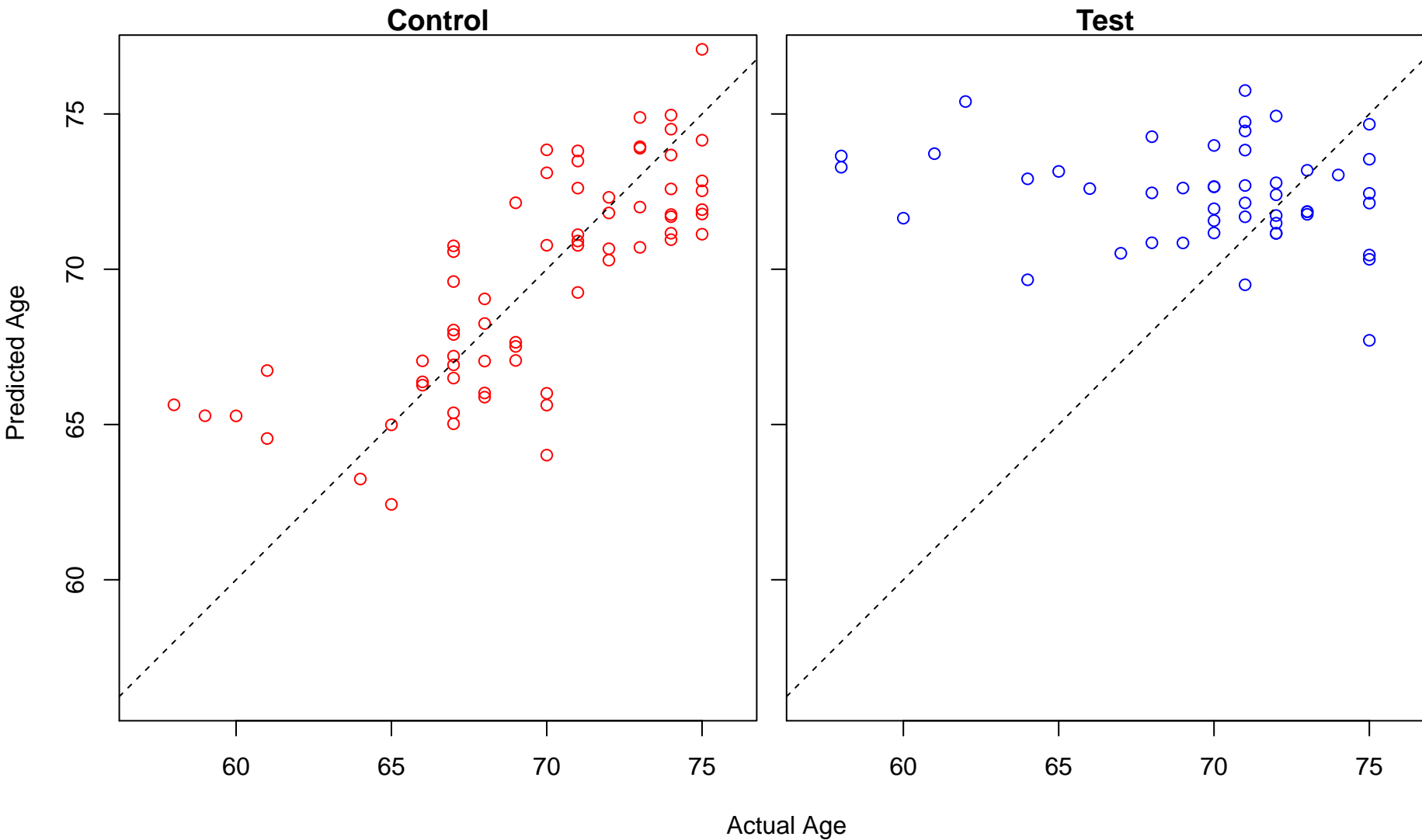
negative regulation of viral life cycle (Score: 2.002246)



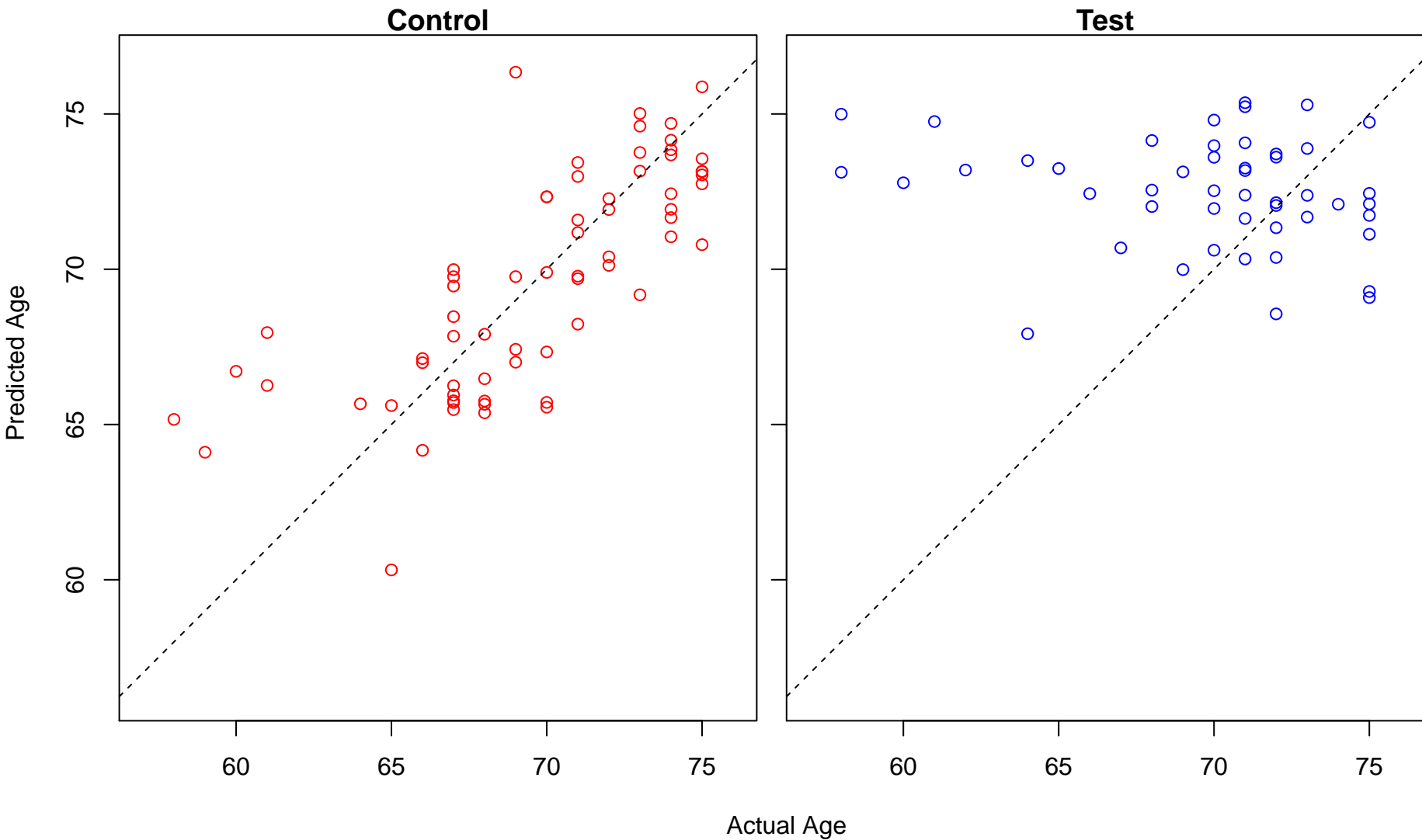
regulation of peptidase activity (Score: 2.001045)



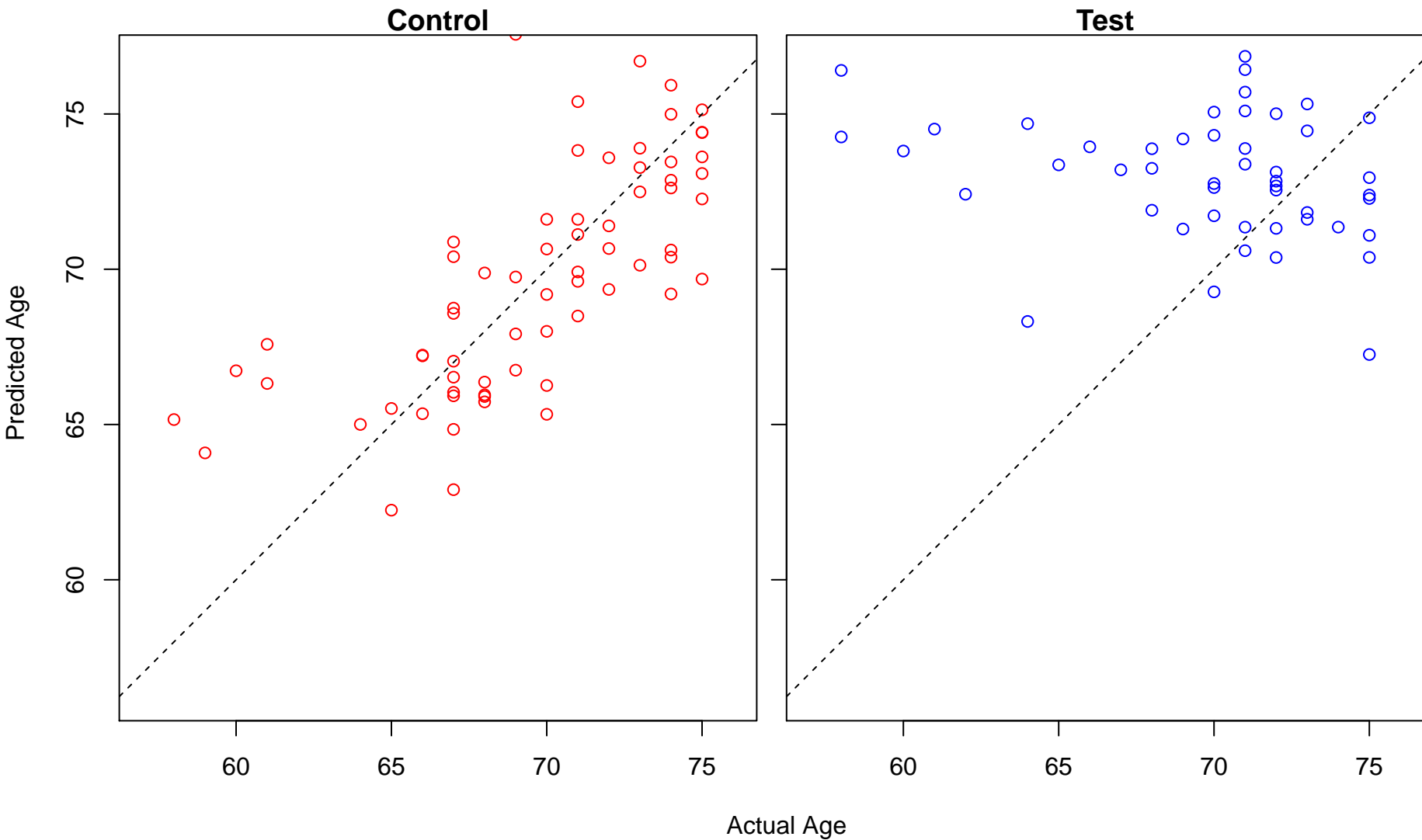
regulation of cellular component biogenesis (Score: 2.000877)



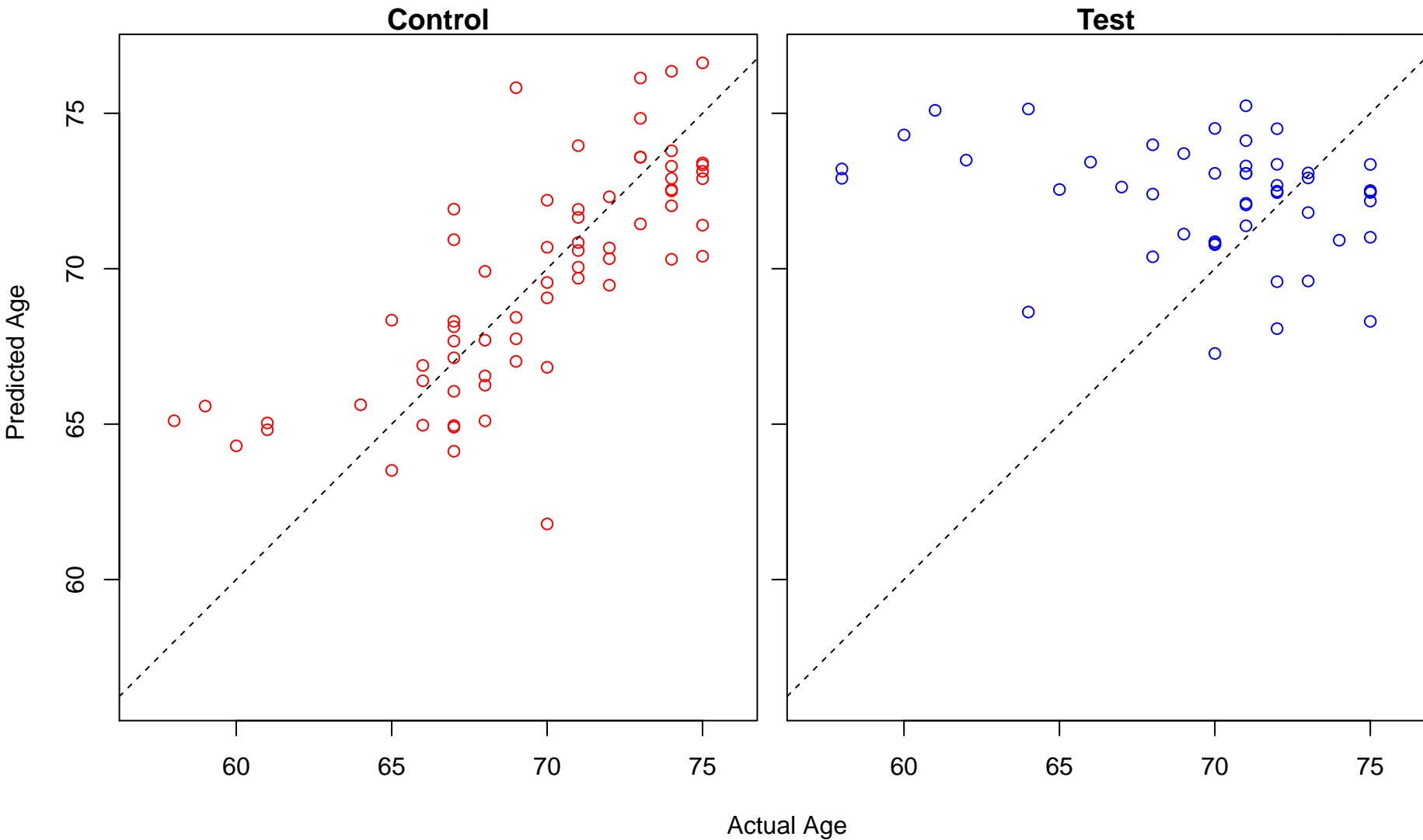
antigen processing and presentation of peptide antigen (Score: 2.000135)



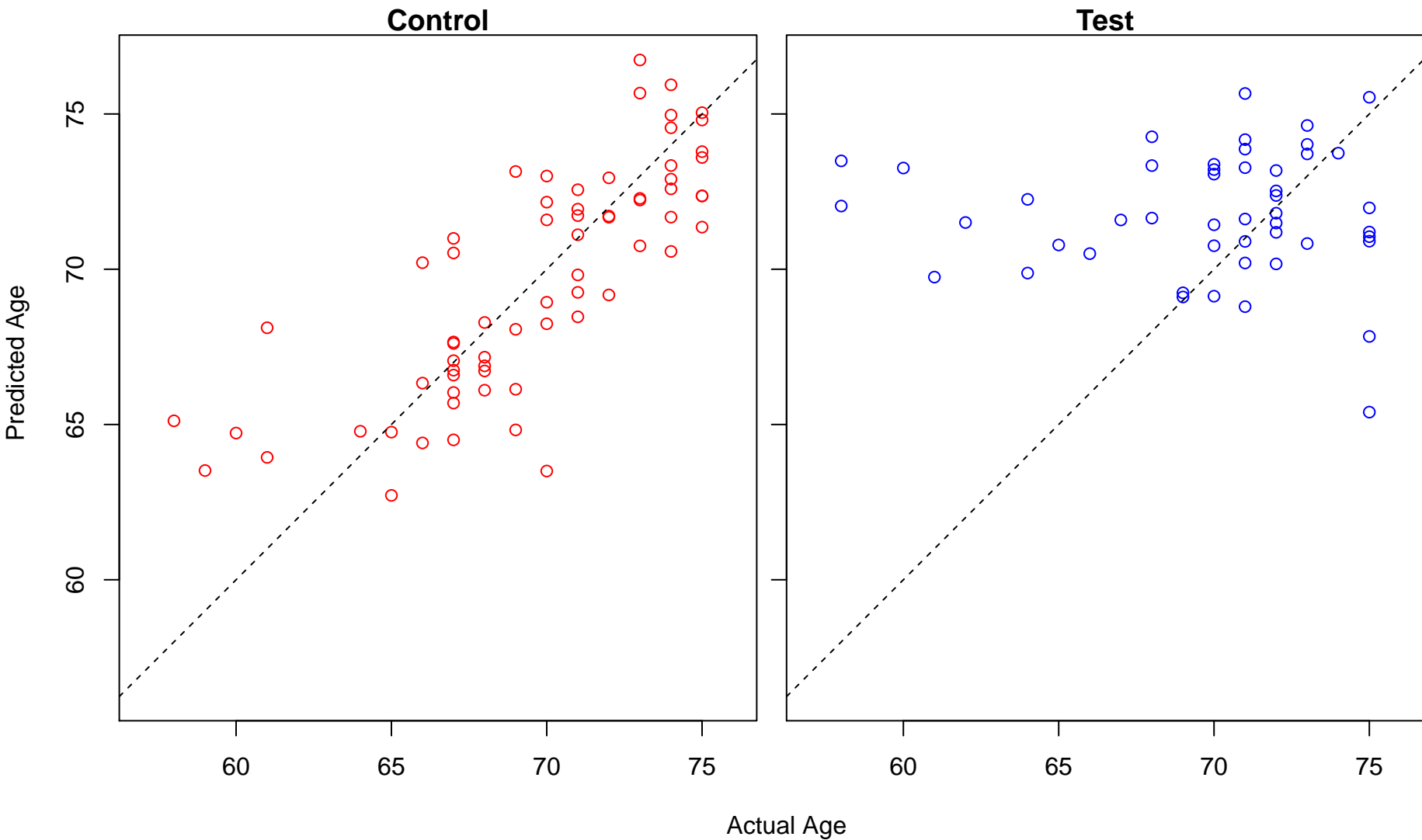
regulation of T cell activation (Score: 1.998738)



phosphatidylcholine acyl-chain remodeling (Score: 1.998215)

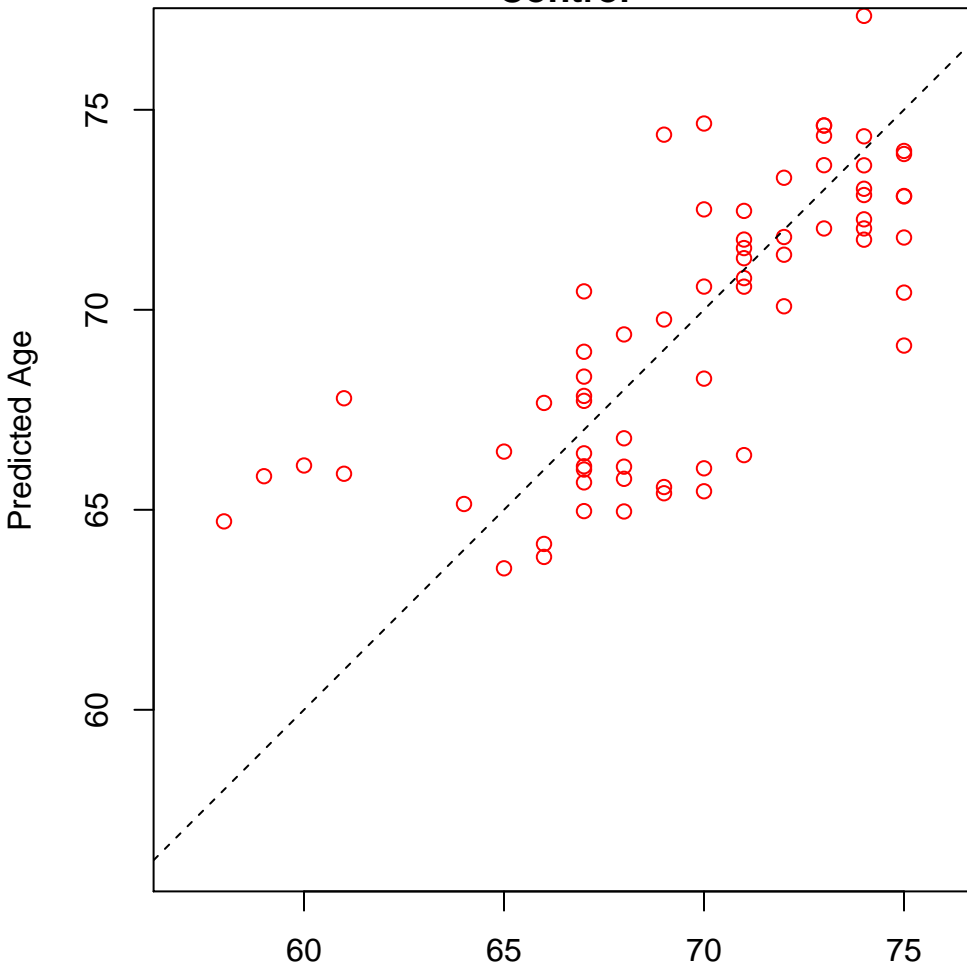


Ras protein signal transduction (Score: 1.997651)

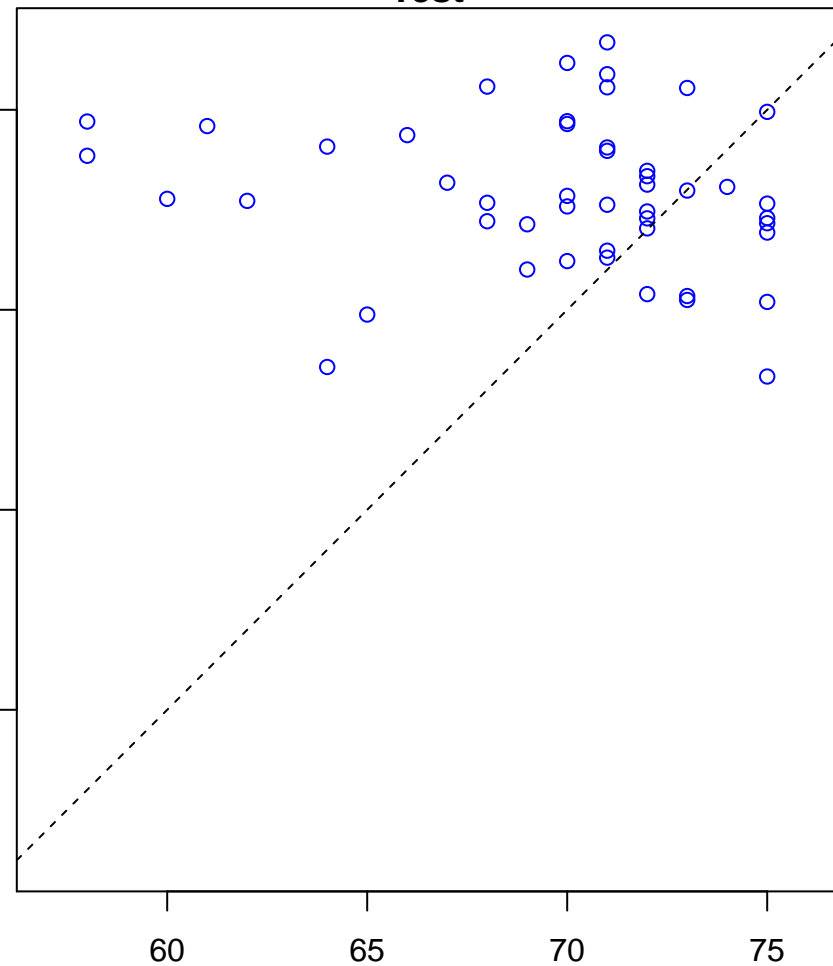


cellular transition metal ion homeostasis (Score: 1.997255)

Control

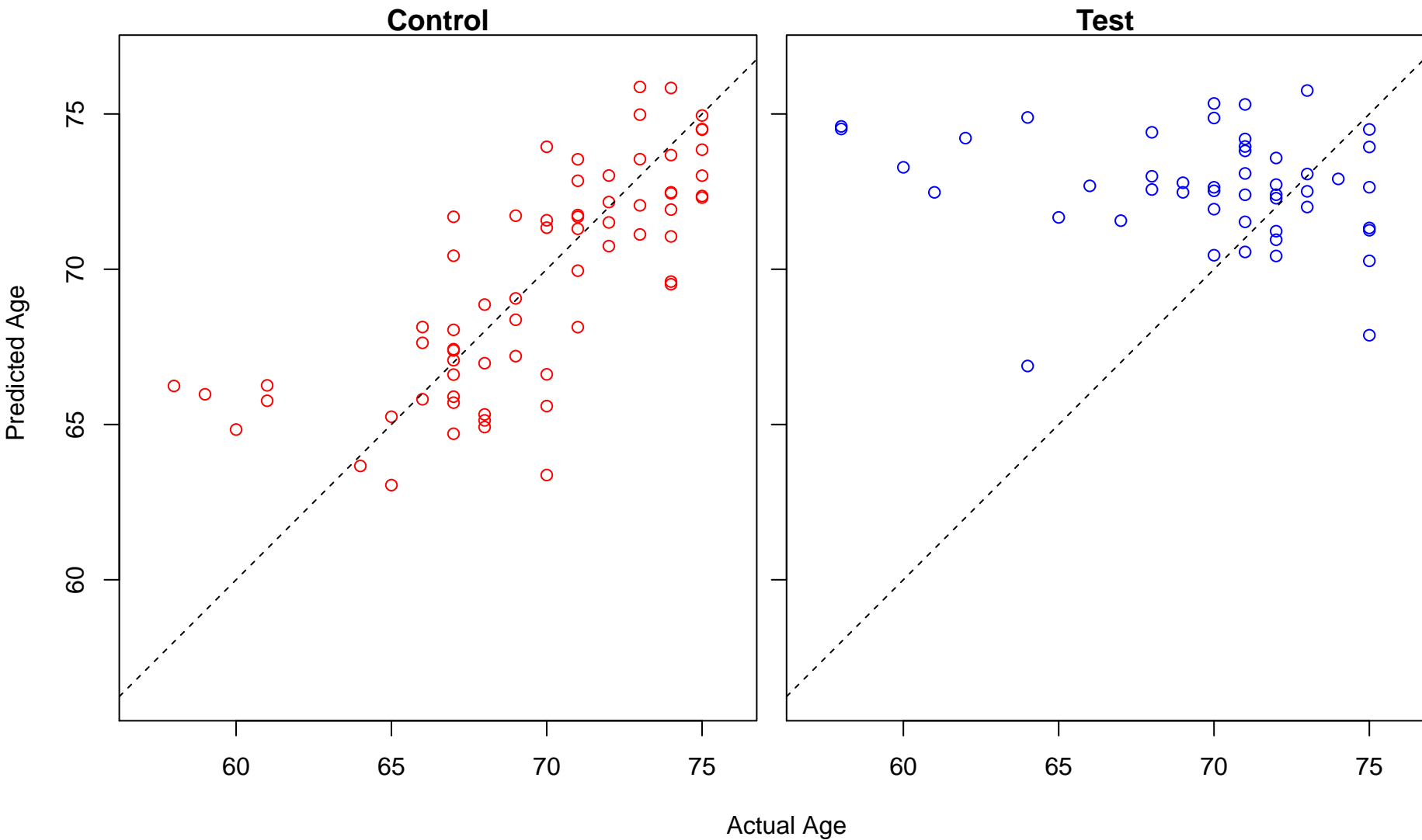


Test



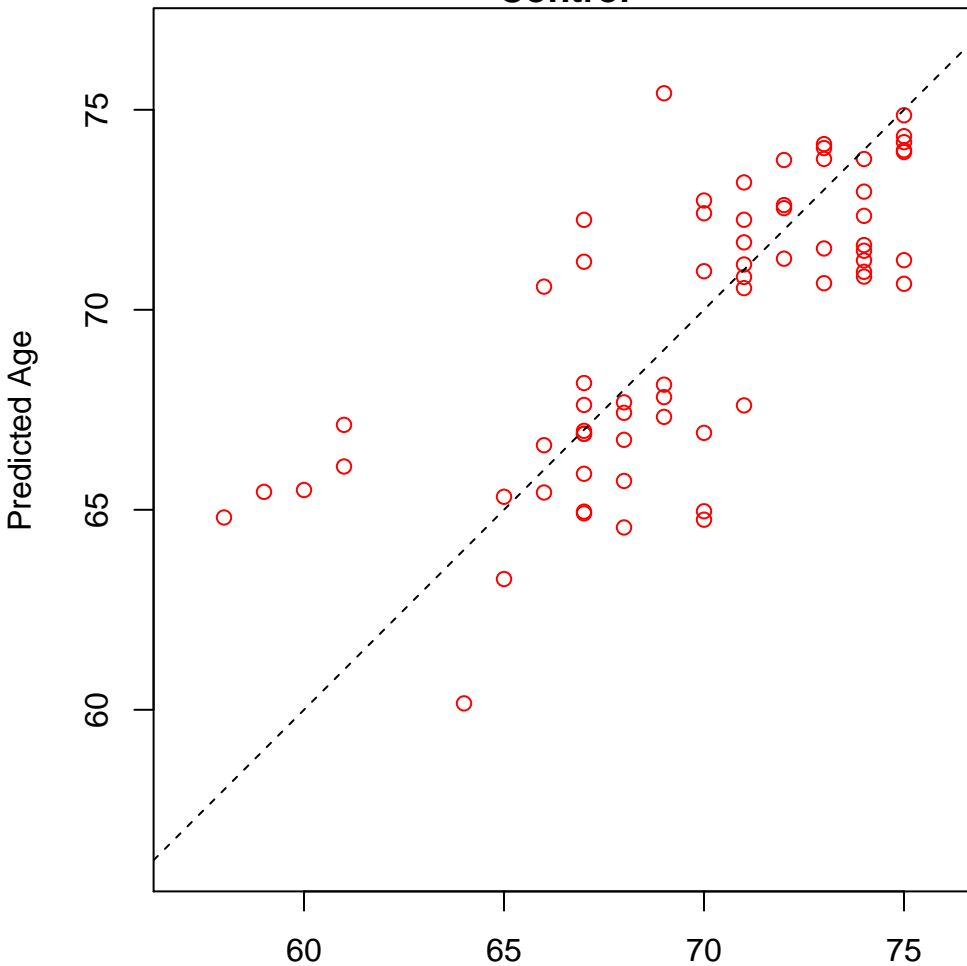
Actual Age

autophagy (Score: 1.995338)

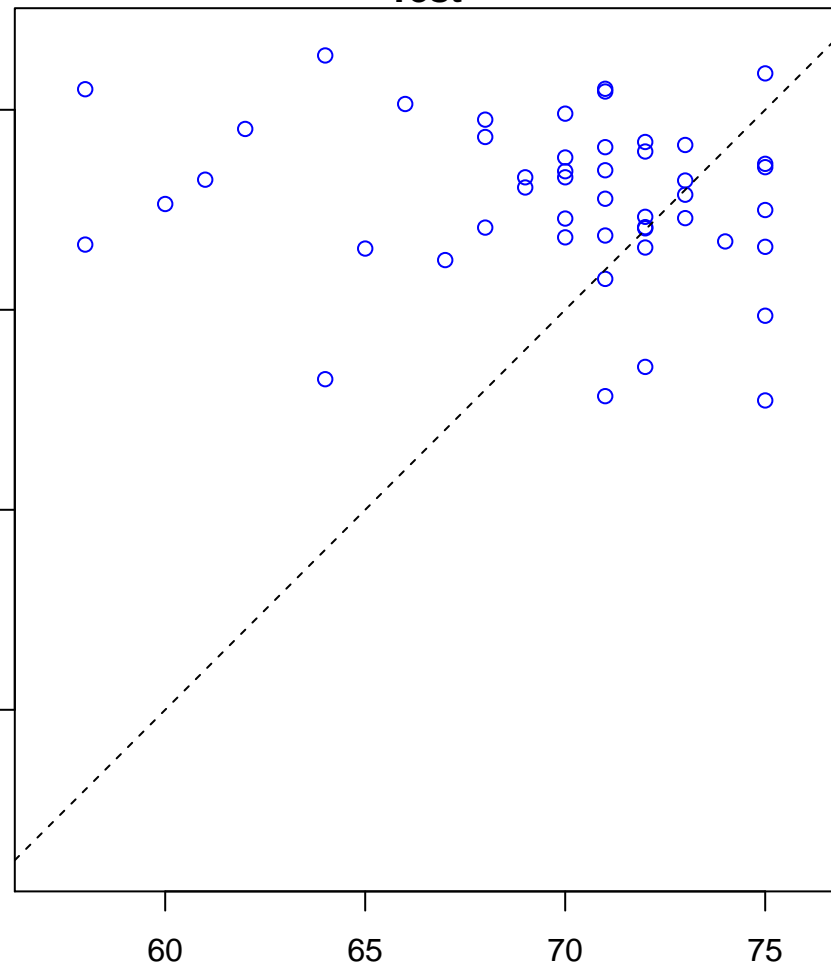


regulation of response to biotic stimulus (Score: 1.993692)

Control

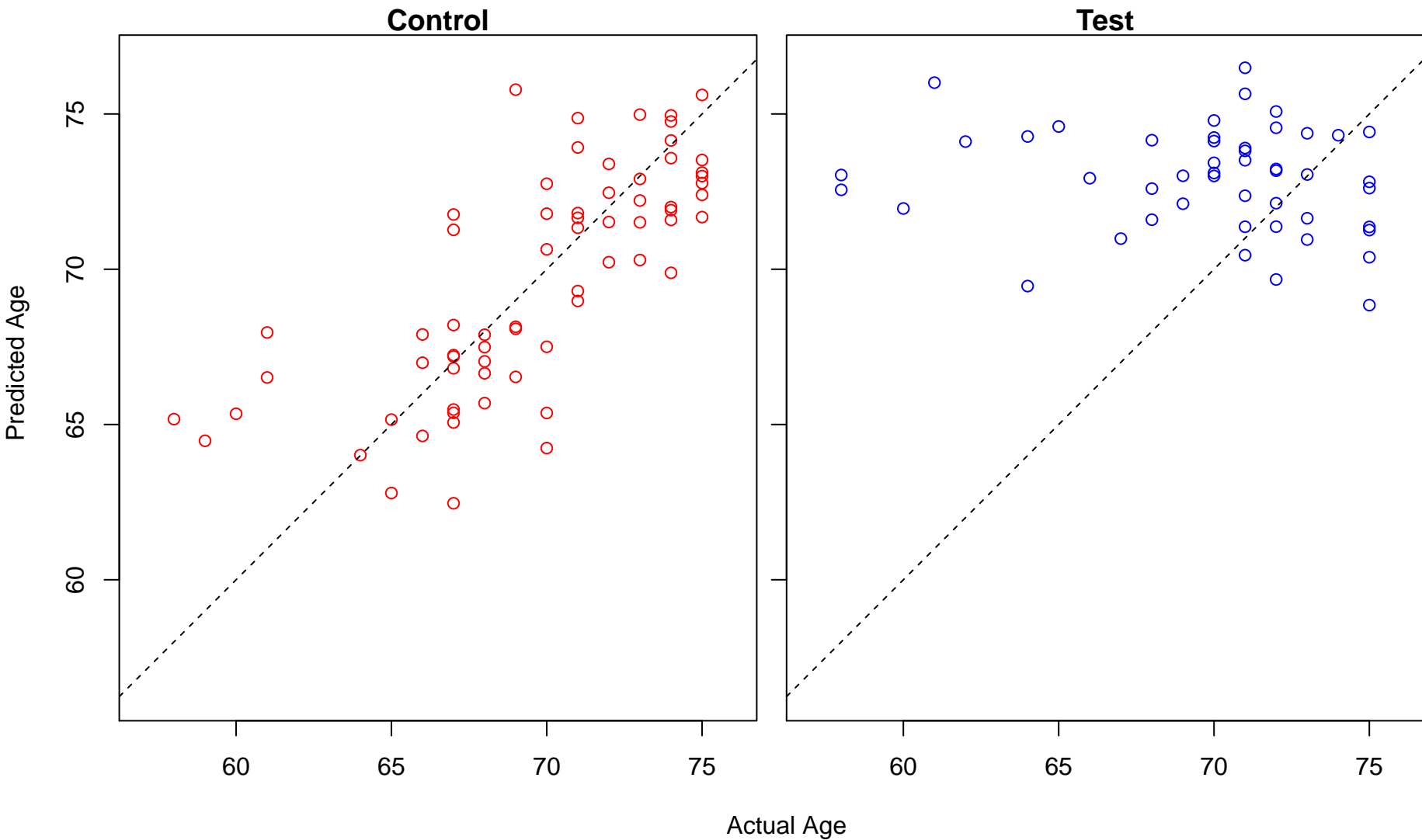


Test

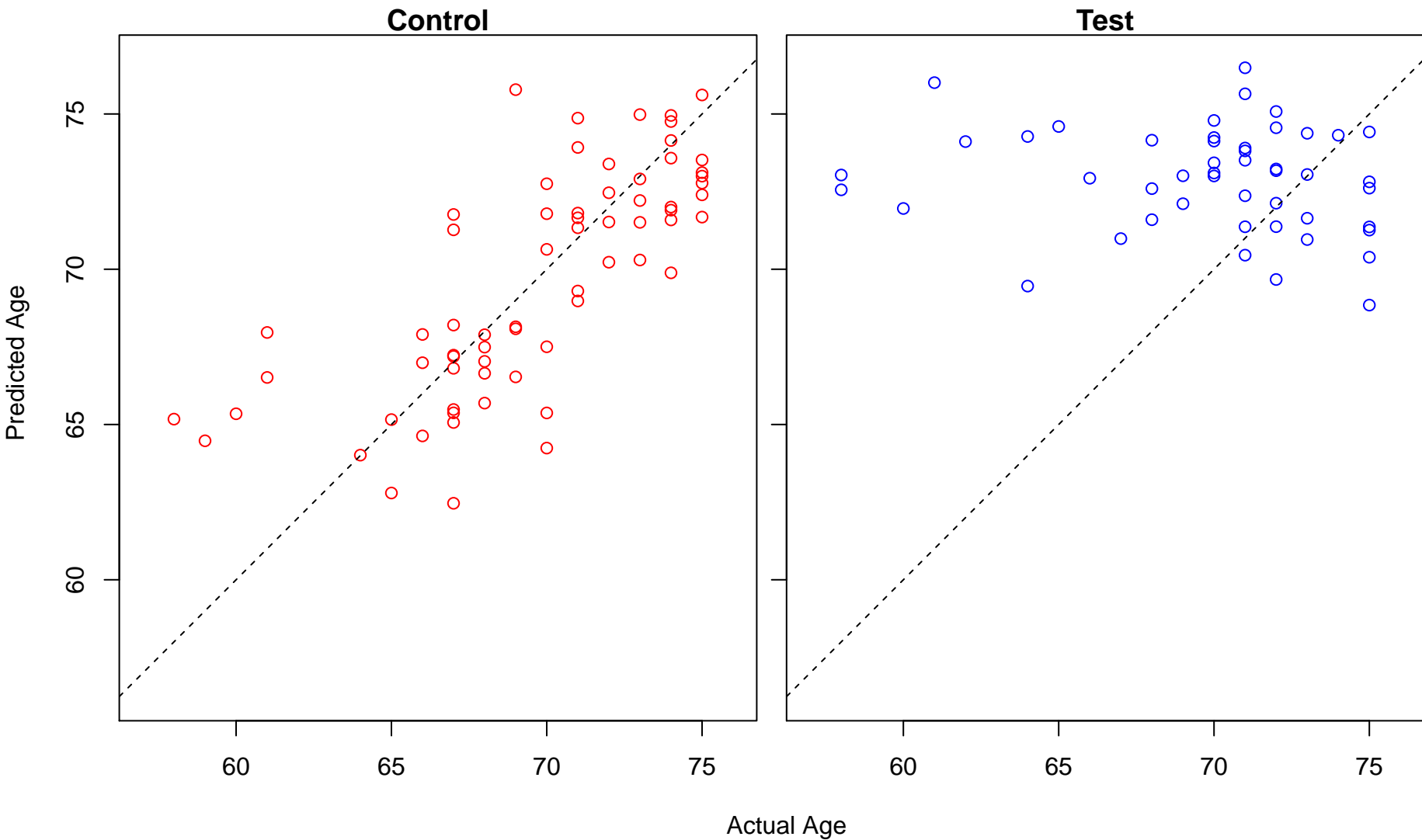


Actual Age

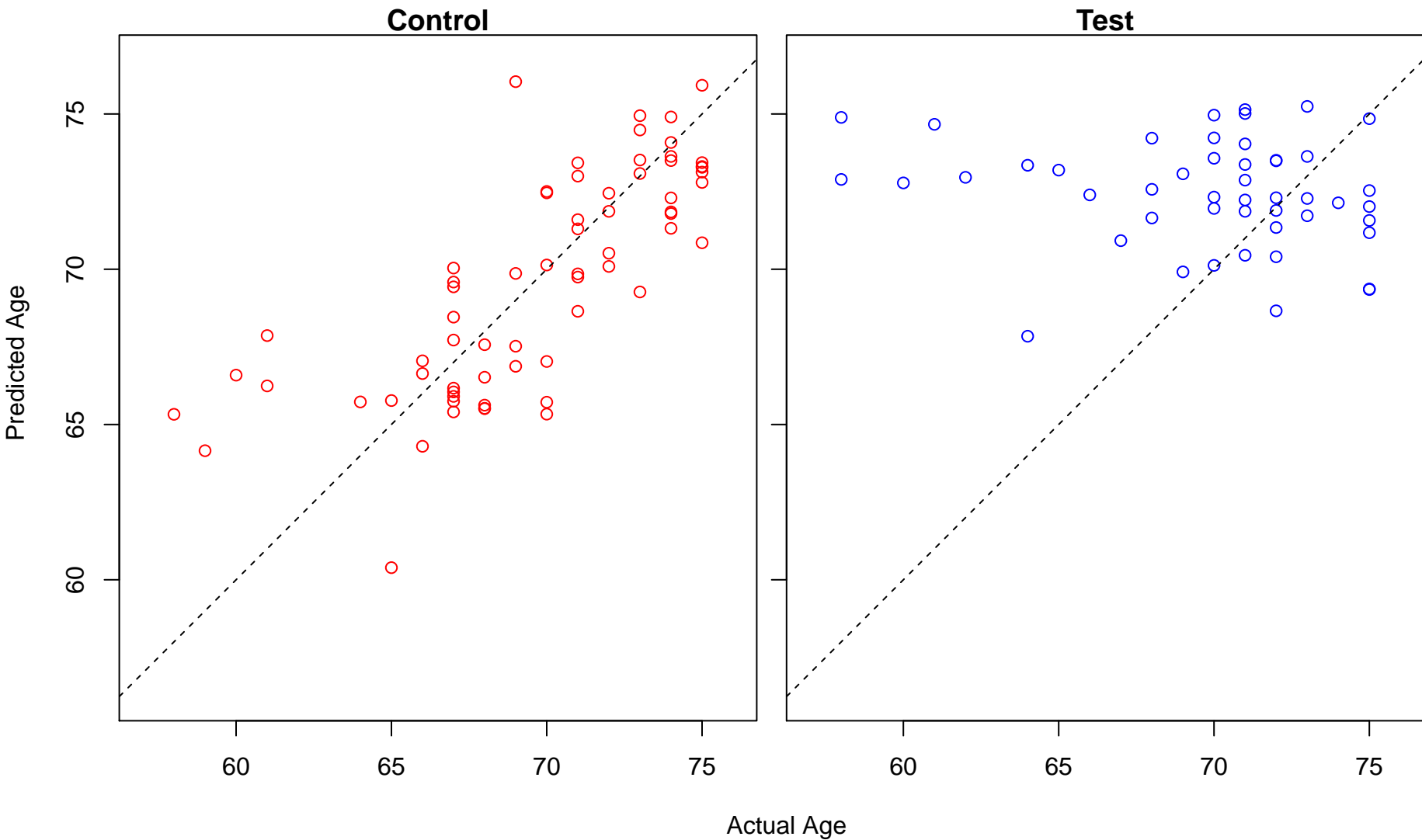
symbiosis, encompassing mutualism through parasitism (Score: 1.992693)



interspecies interaction between organisms (Score: 1.992693)

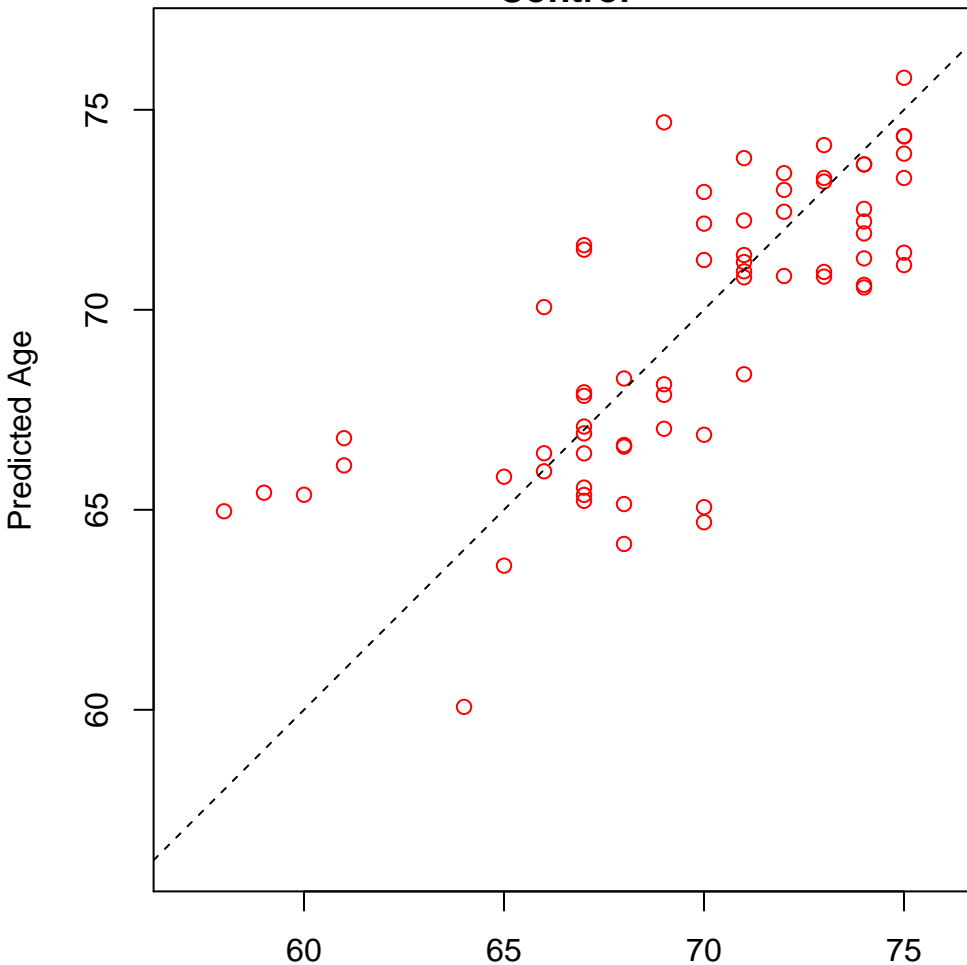


antigen processing and presentation (Score: 1.992541)

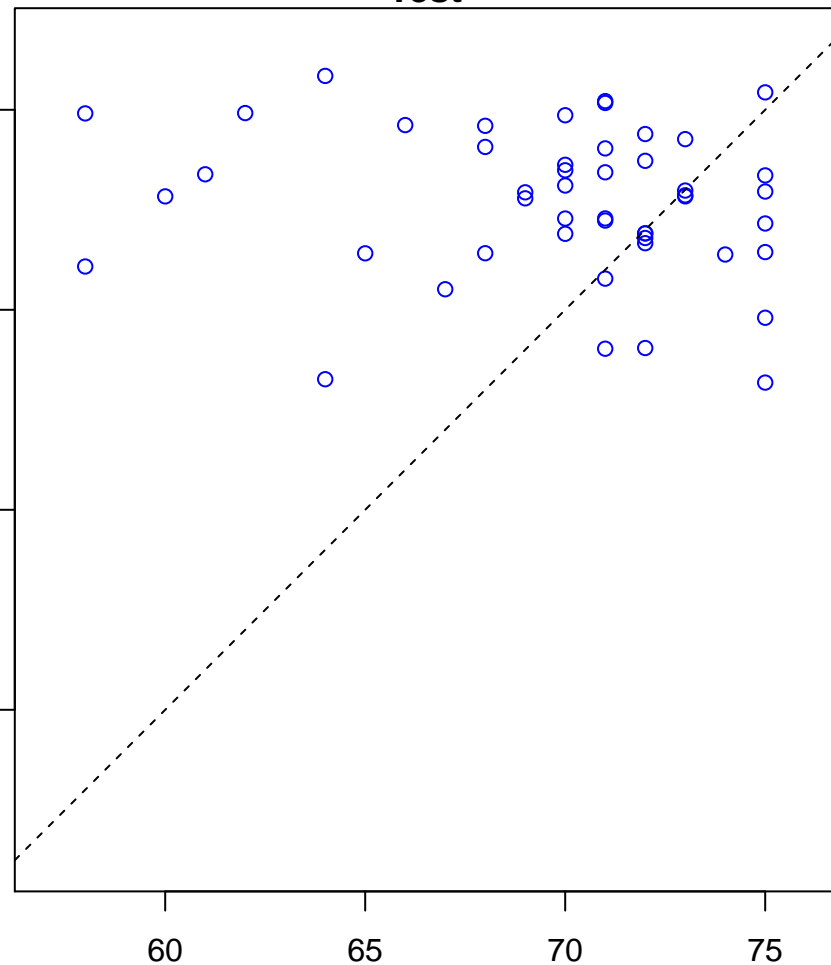


regulation of defense response to virus (Score: 1.991956)

Control

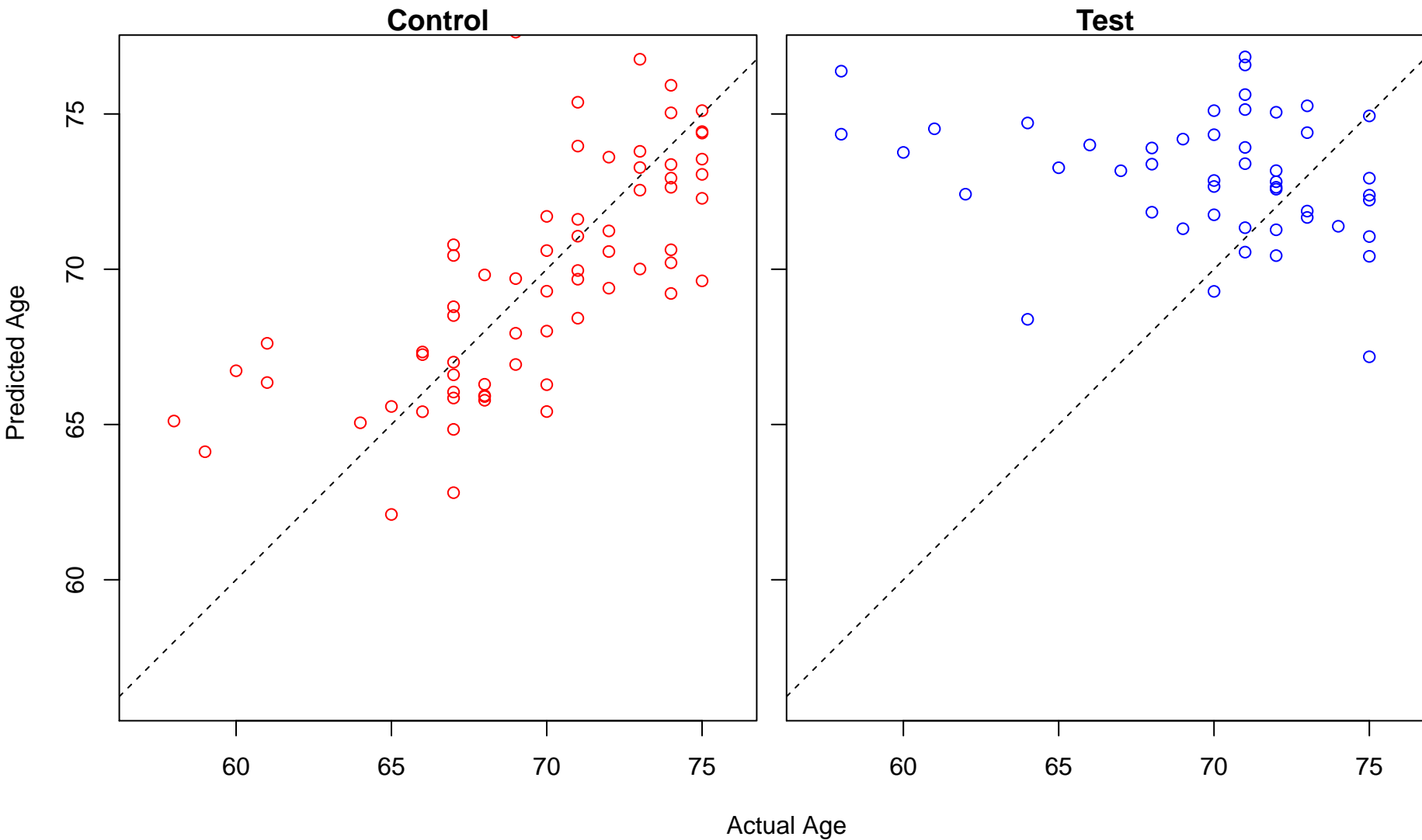


Test

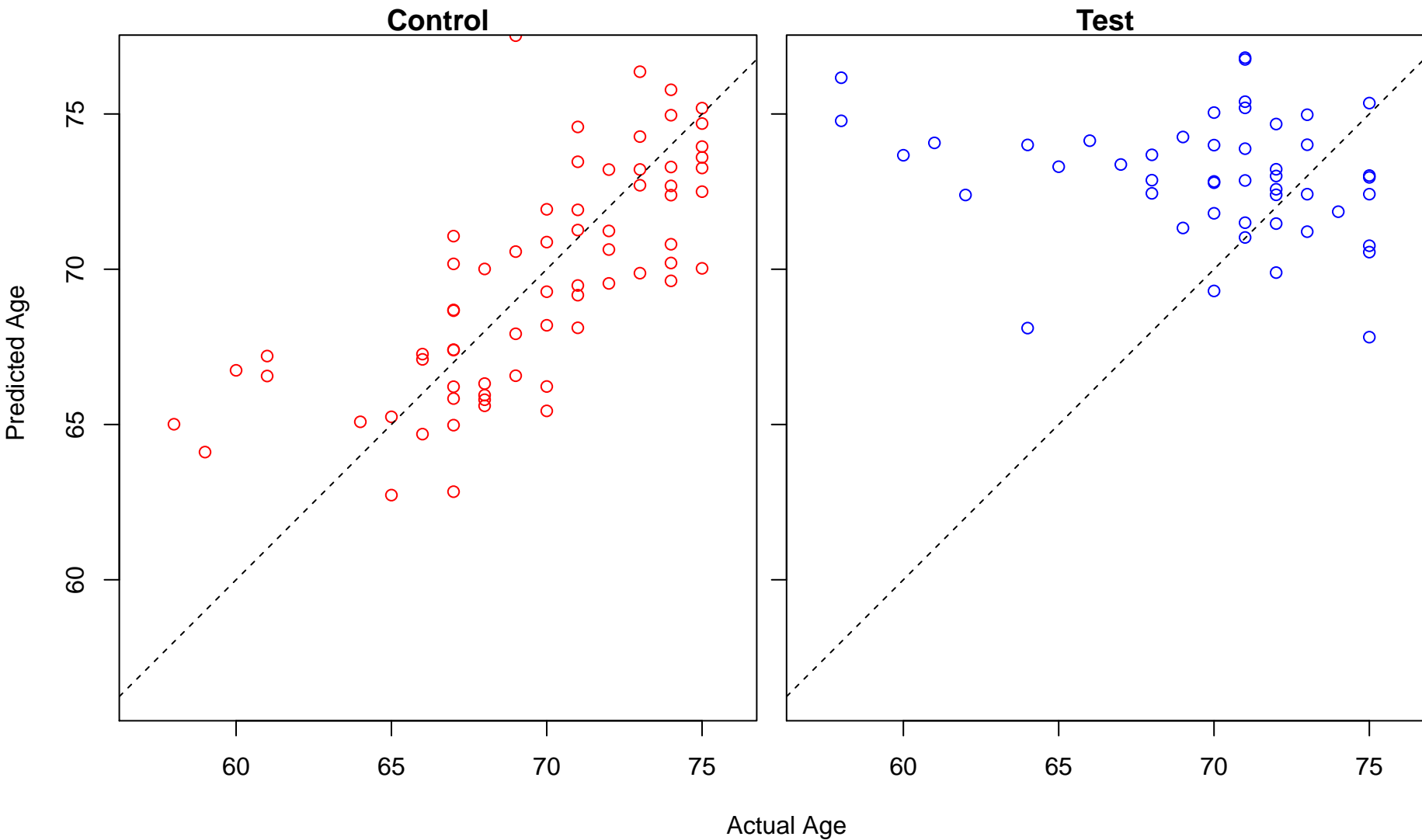


Actual Age

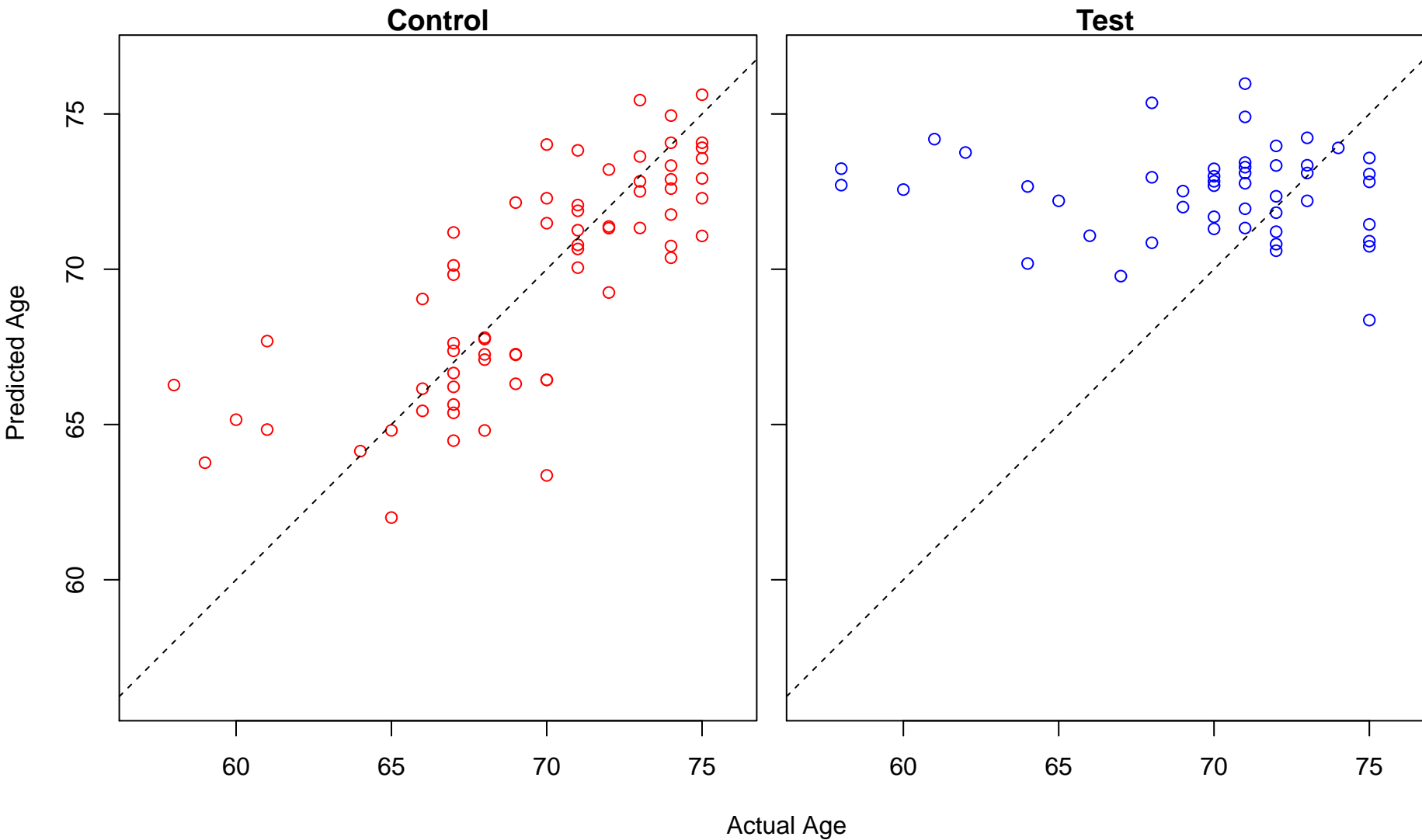
regulation of leukocyte cell-cell adhesion (Score: 1.990700)



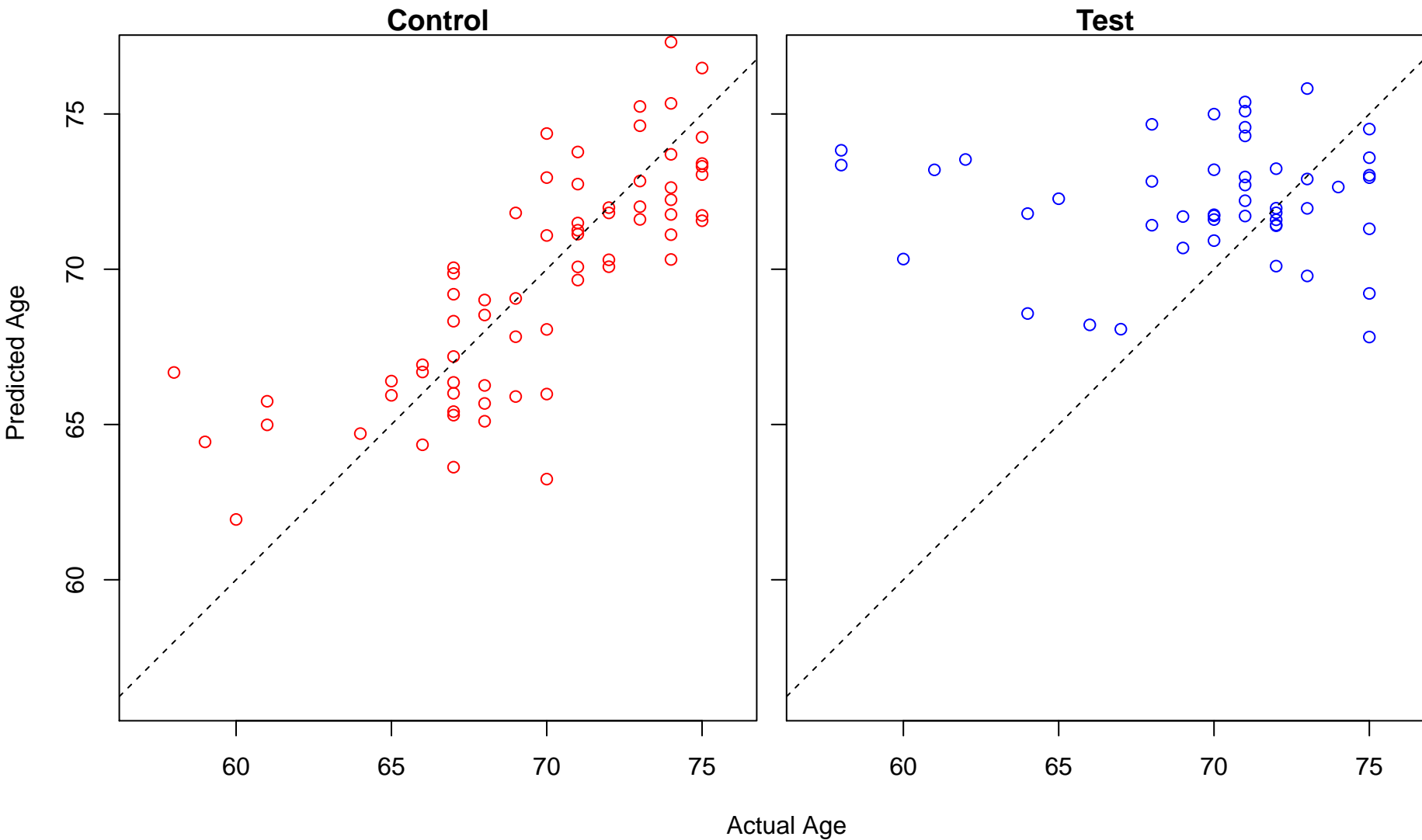
regulation of cell-cell adhesion (Score: 1.989643)



regulation of cell cycle process (Score: 1.989641)

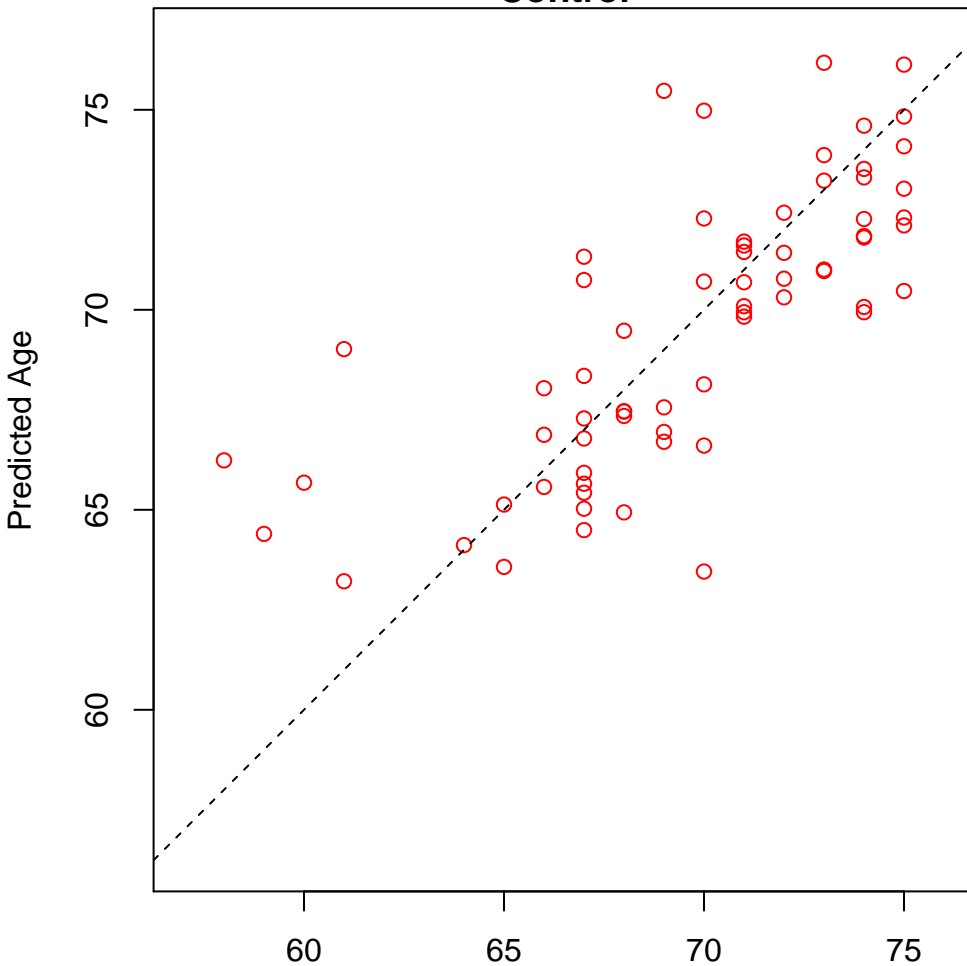


proton transport (Score: 1.988940)

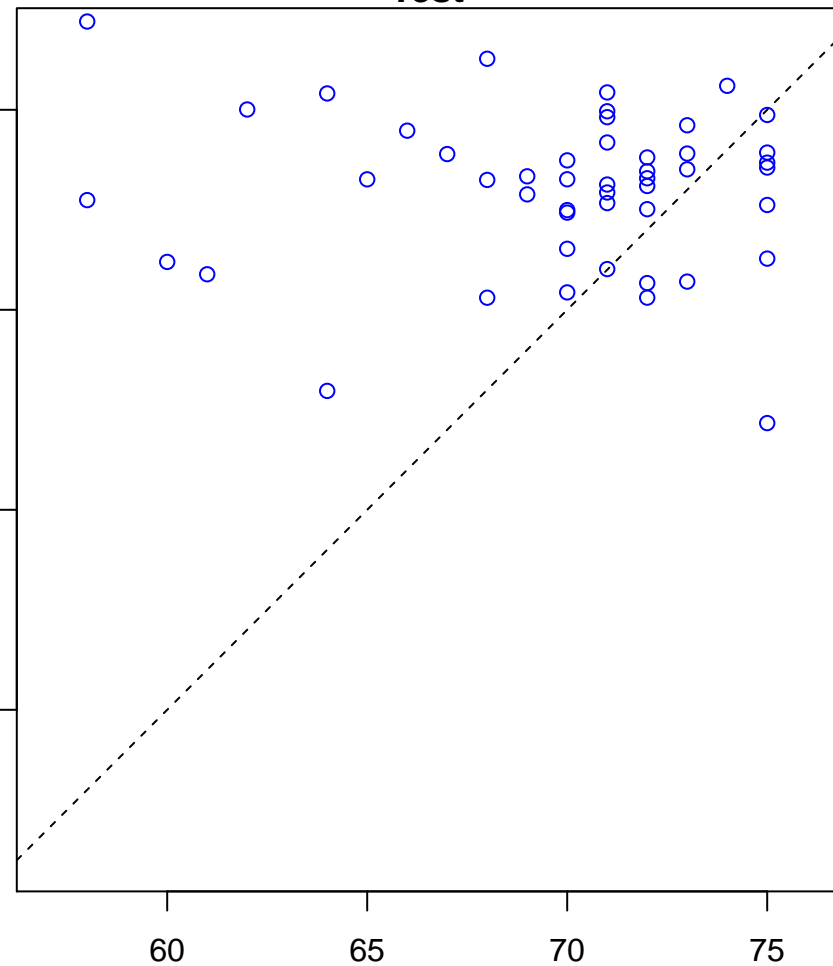


regulation of chromosome organization (Score: 1.988161)

Control

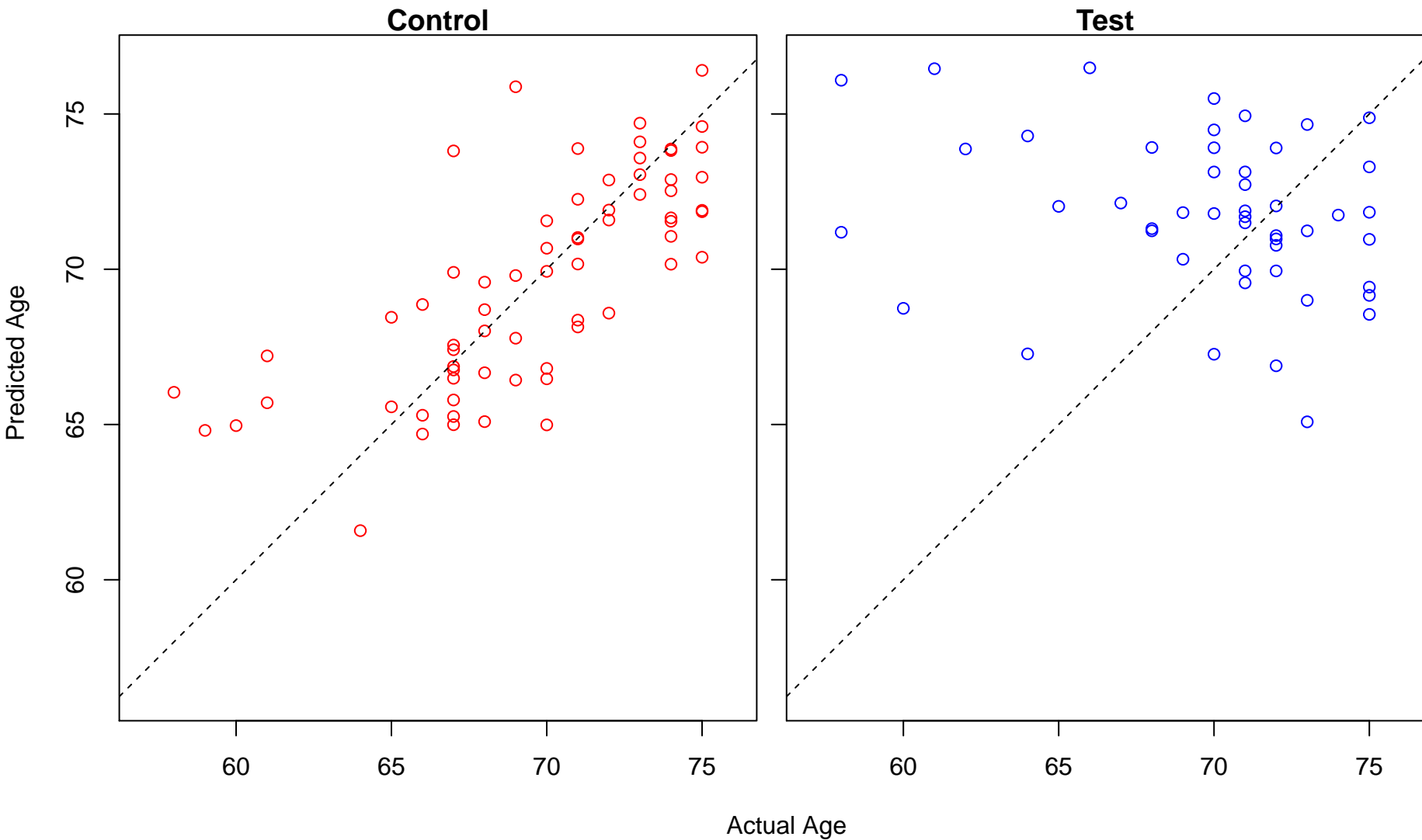


Test

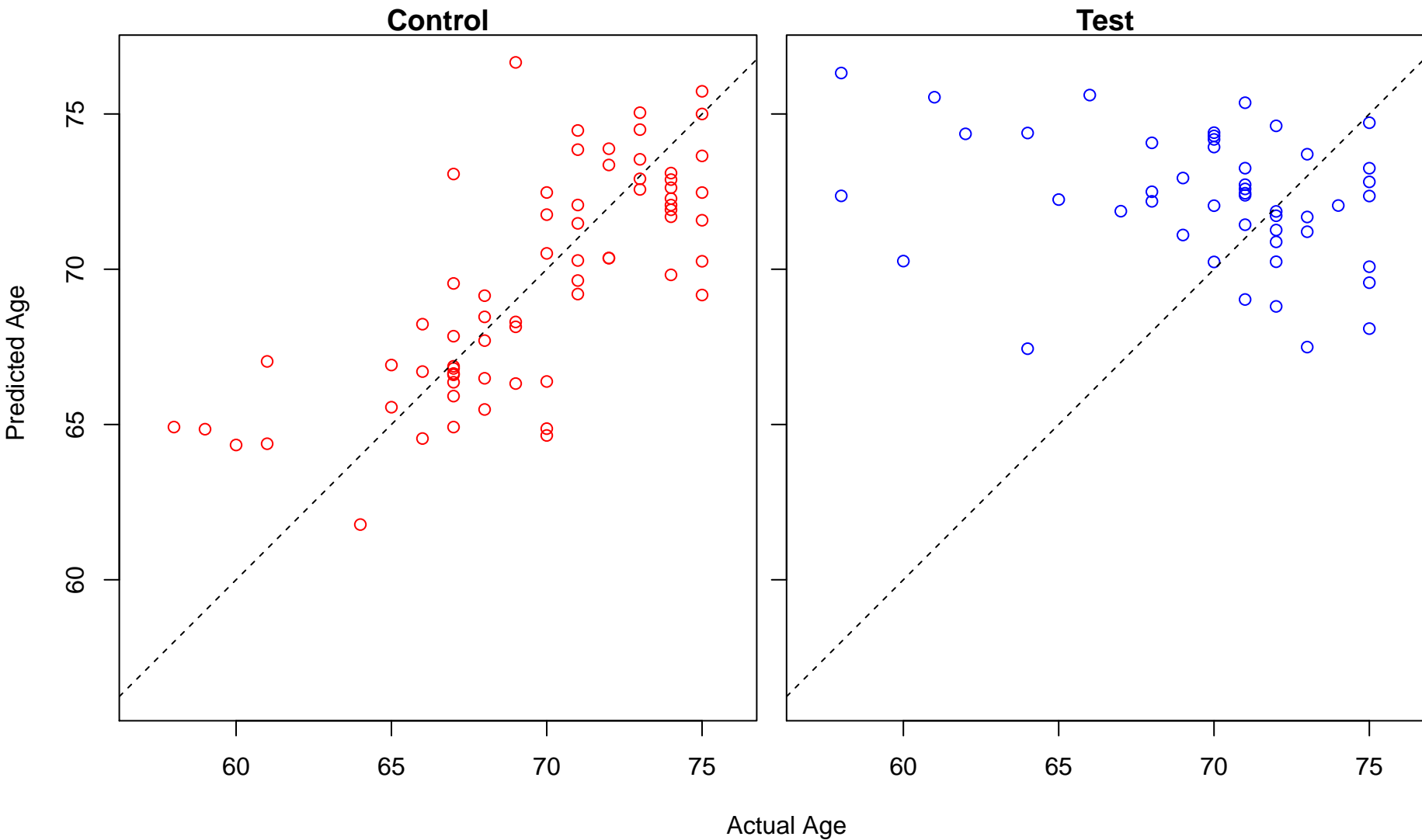


Actual Age

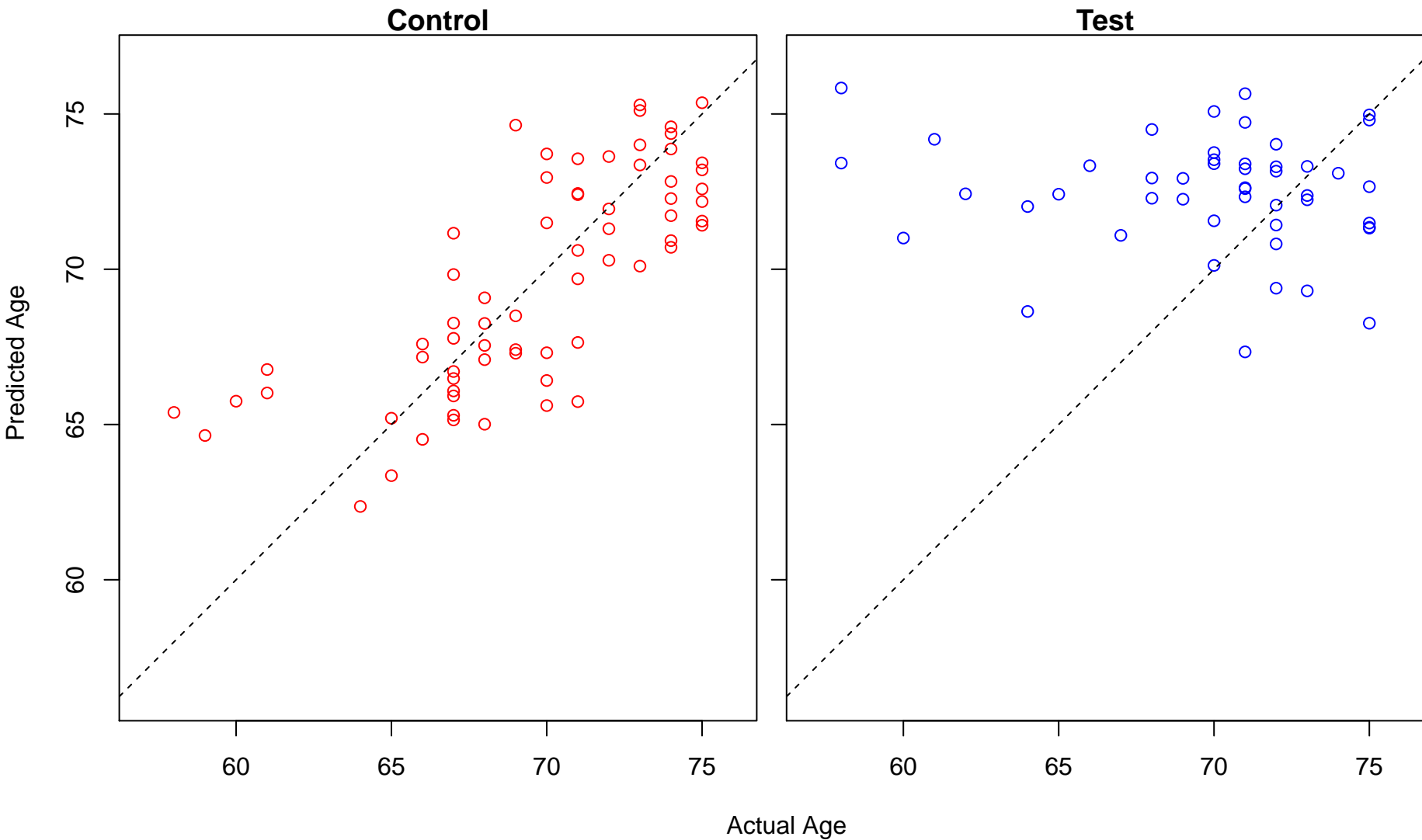
negative regulation of viral genome replication (Score: 1.987353)



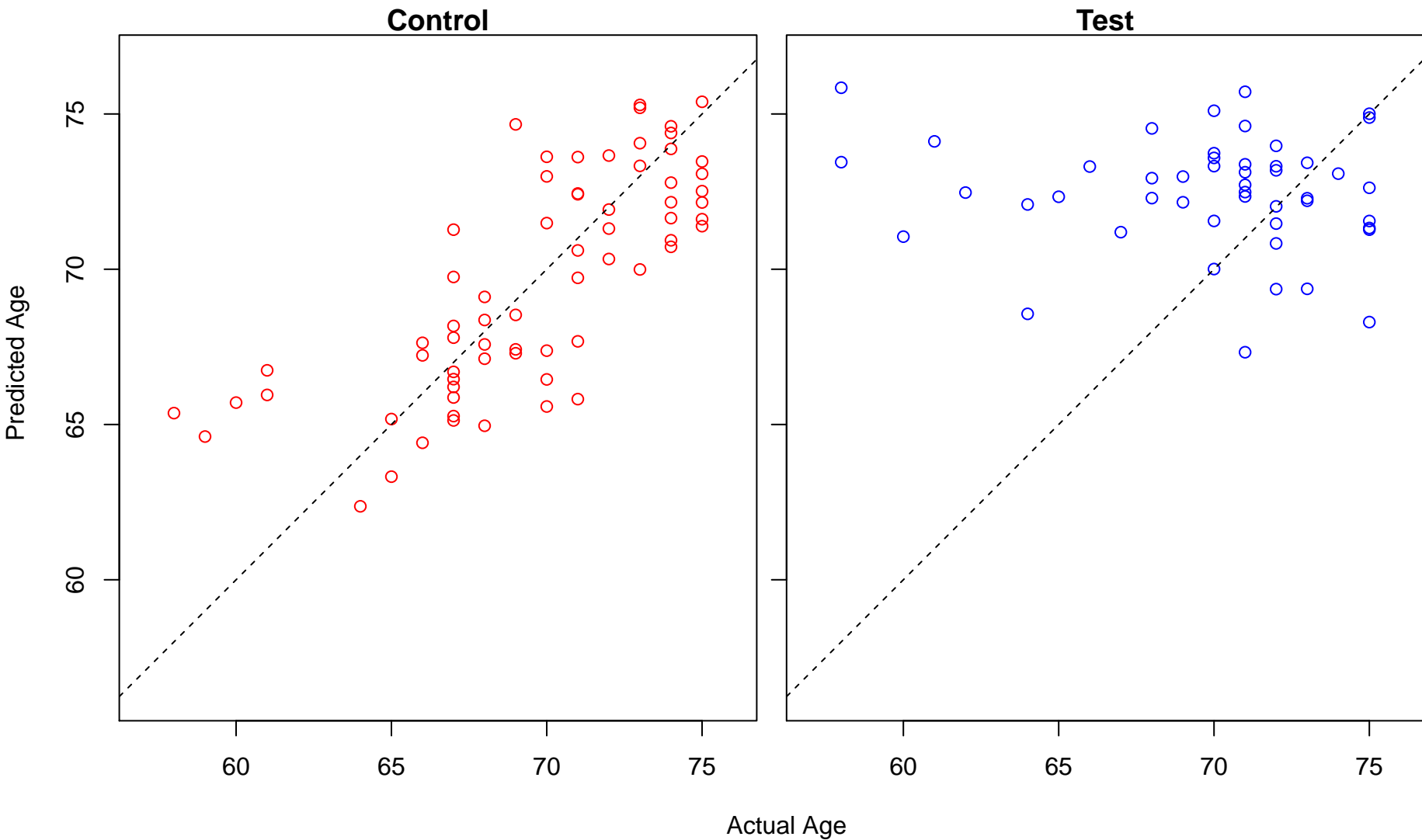
regulation of viral life cycle (Score: 1.983192)



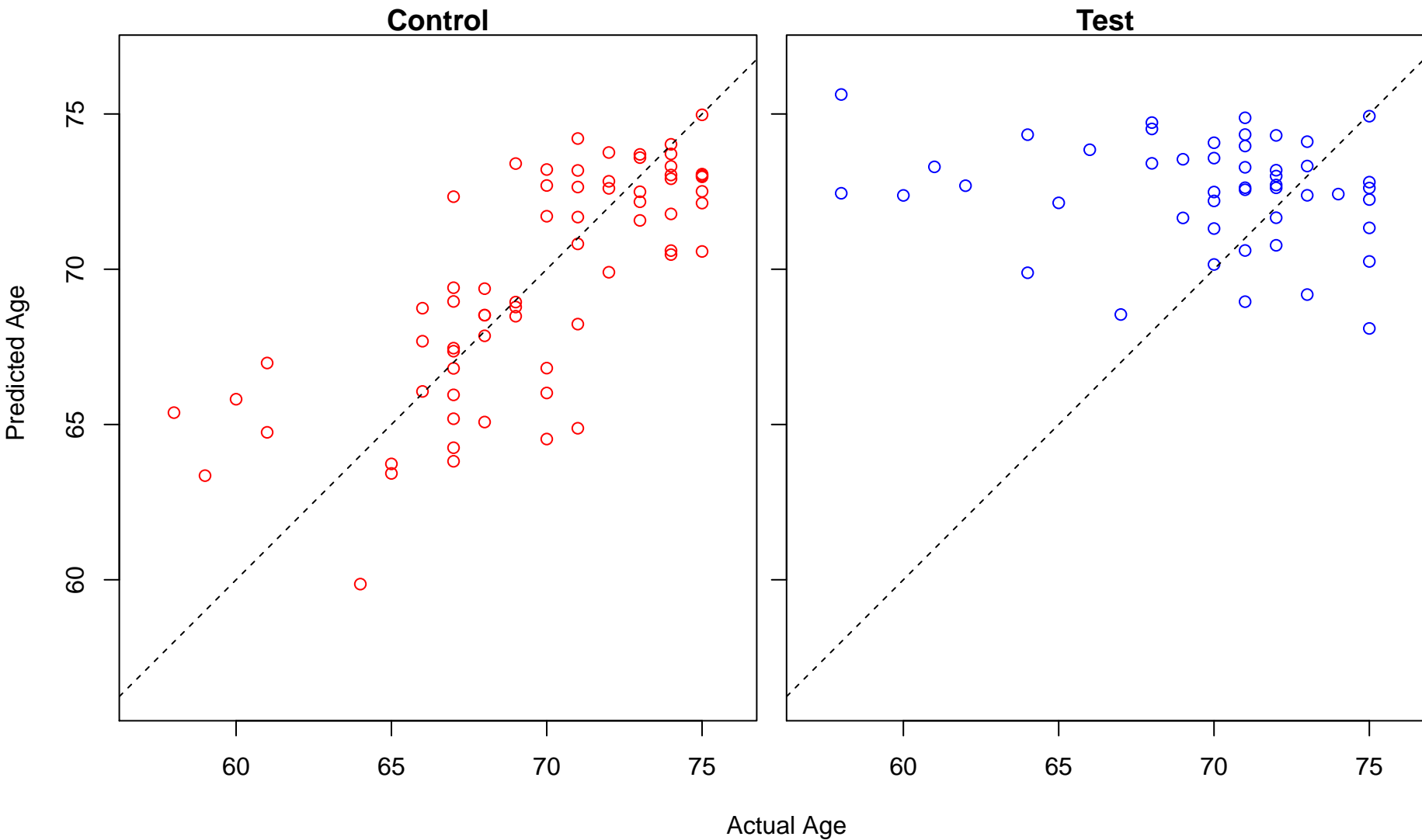
single organism cell adhesion (Score: 1.982498)



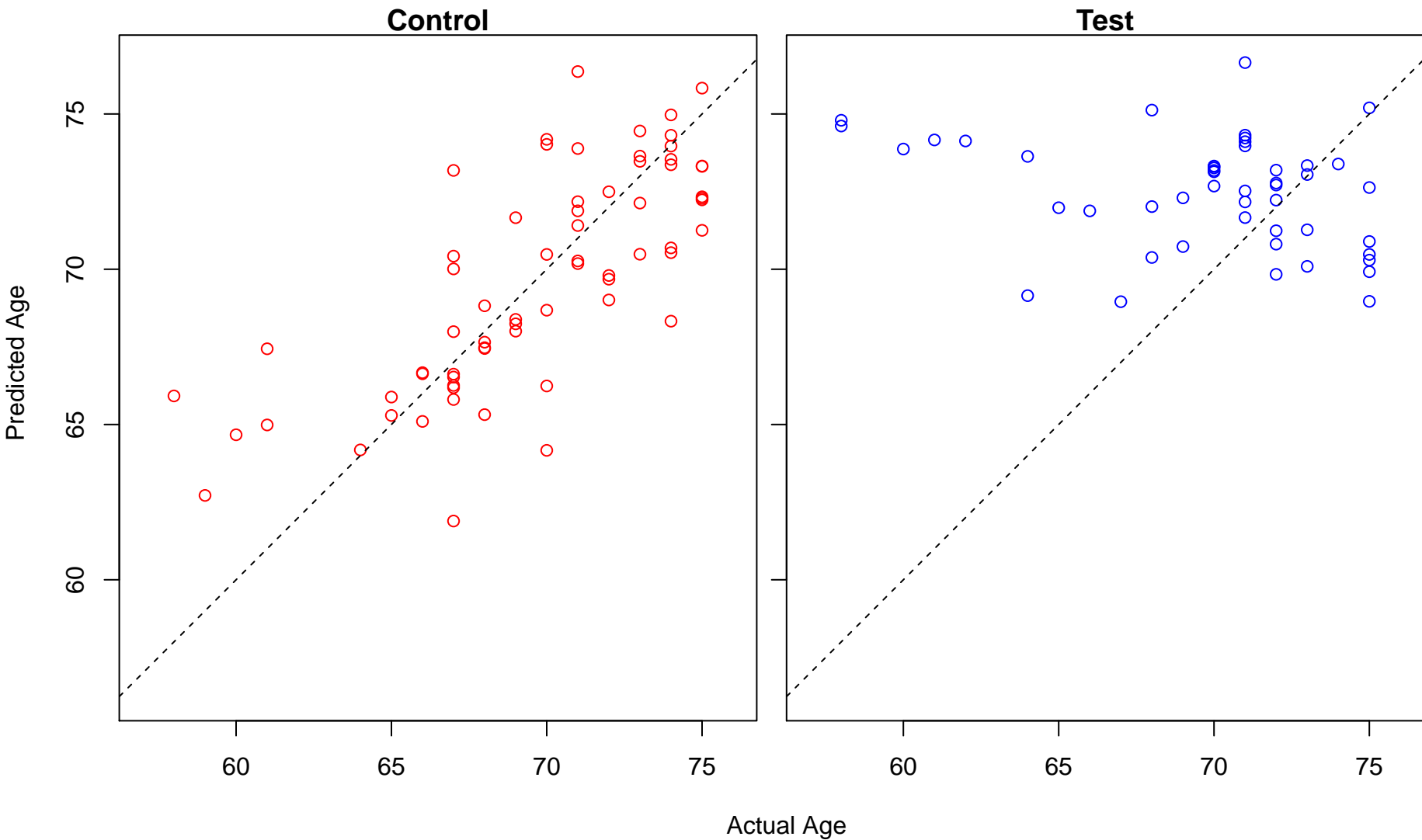
single organismal cell-cell adhesion (Score: 1.981366)



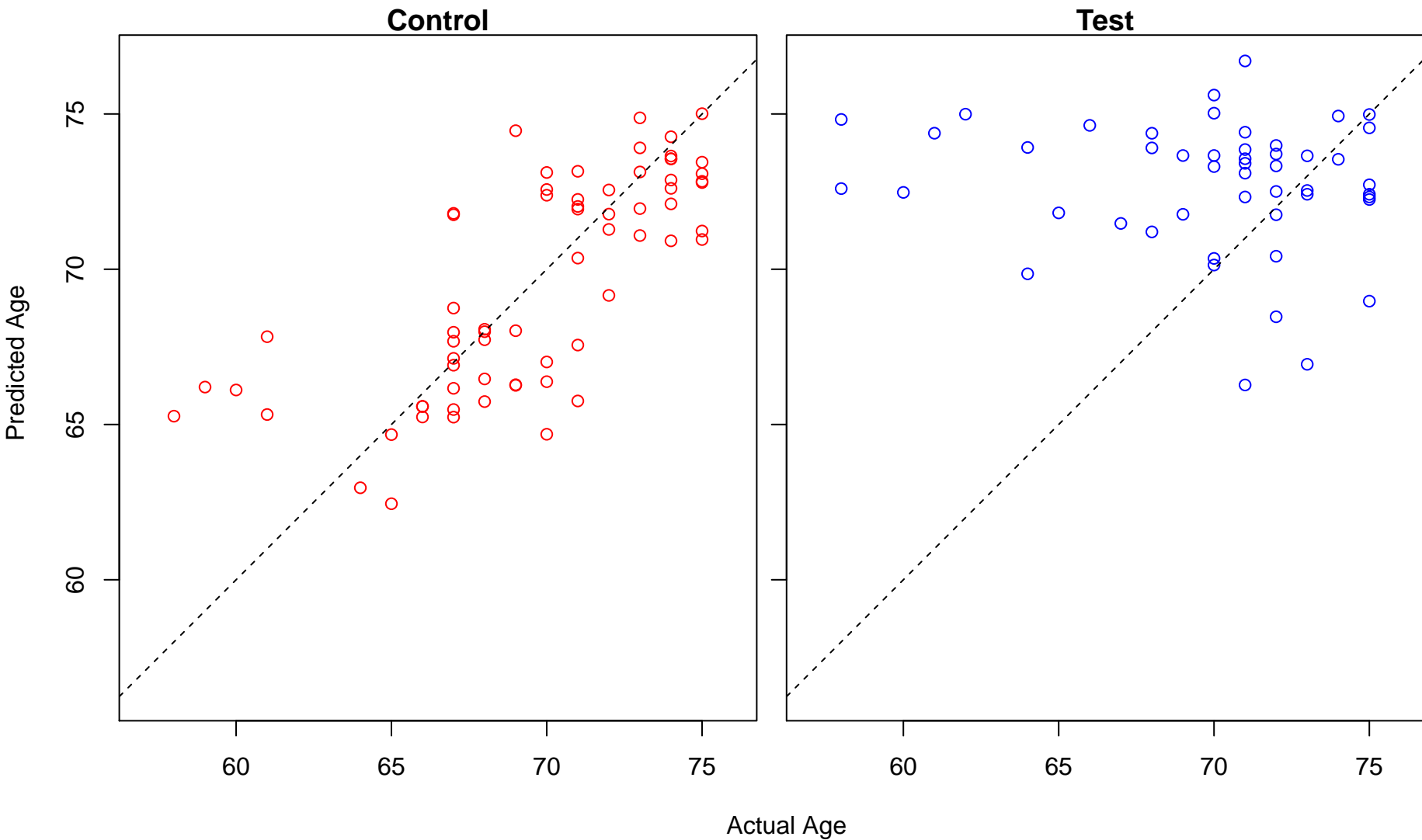
positive regulation of programmed cell death (Score: 1.981310)



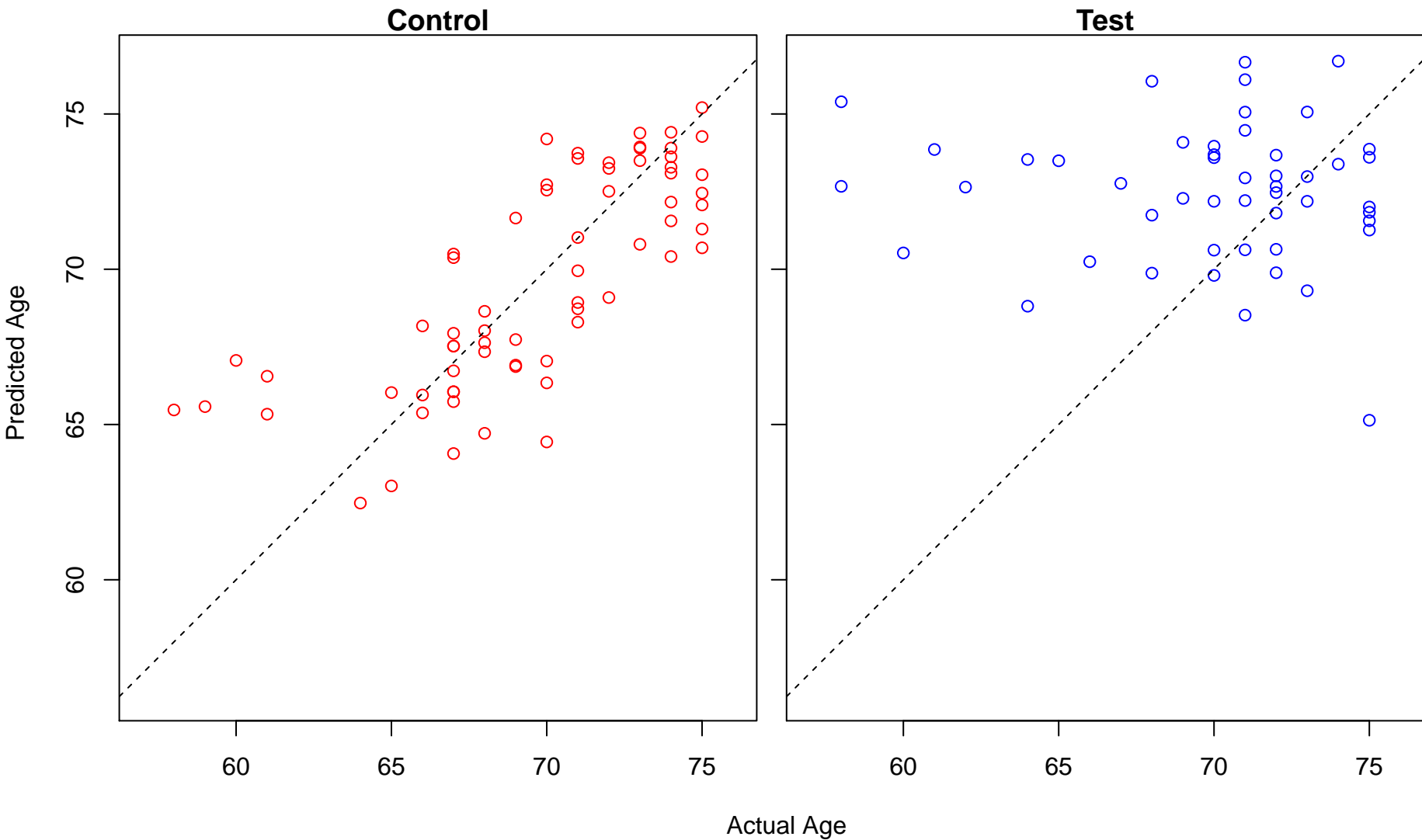
regulation of establishment of protein localization to mitochondrion (Score: 1.981094)



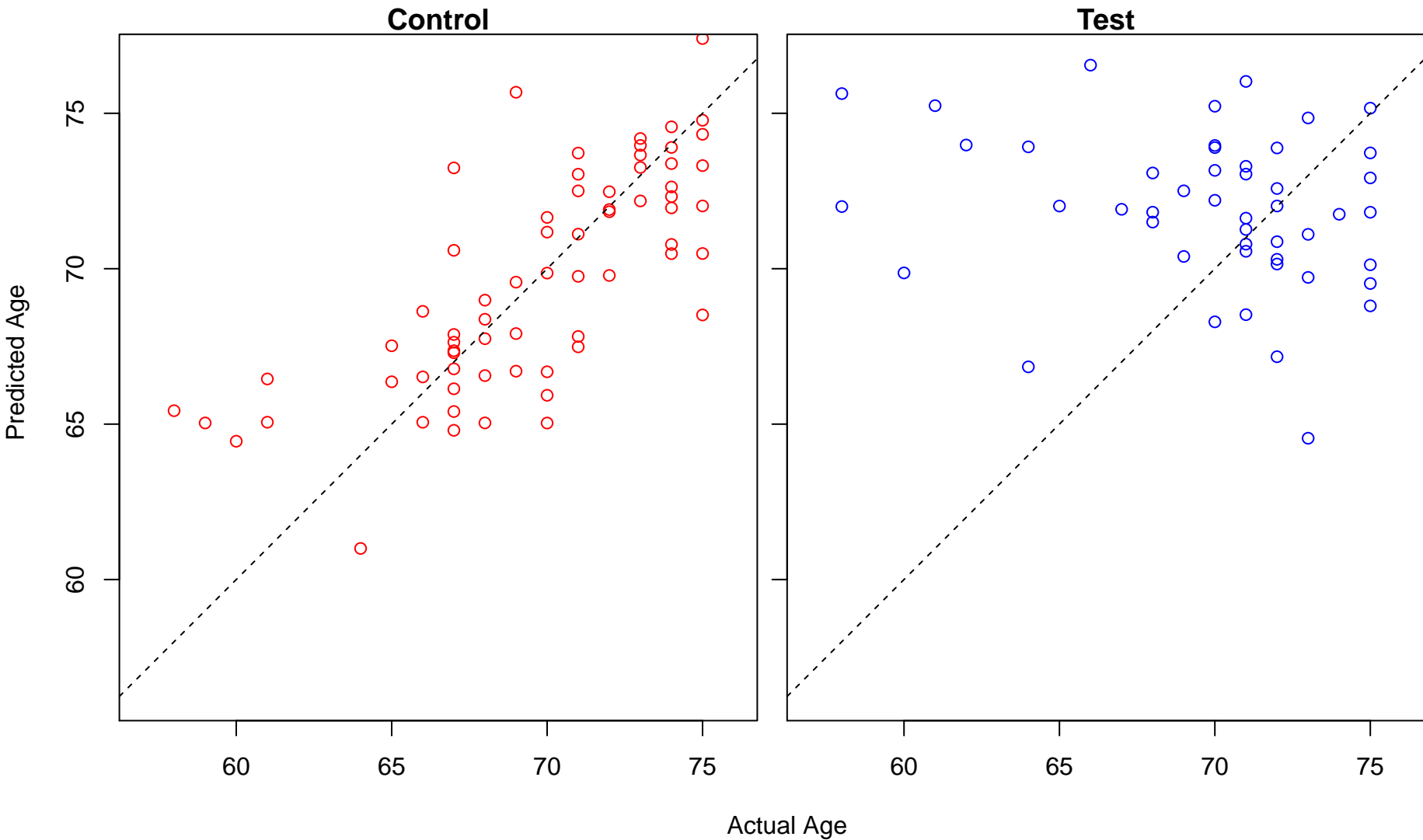
protein acylation (Score: 1.979429)



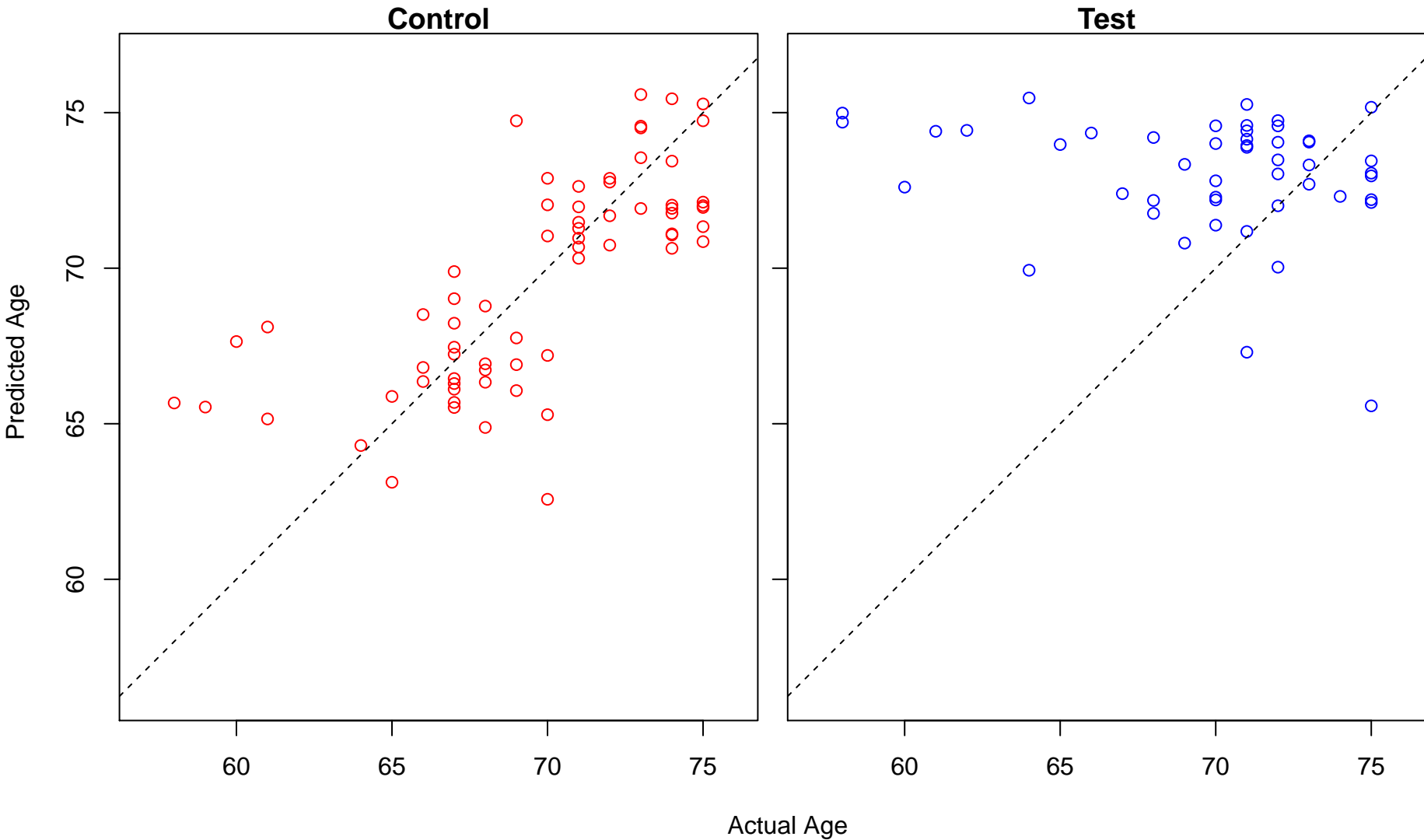
regulation of sequence-specific DNA binding transcription factor activity (Score: 1.978730)



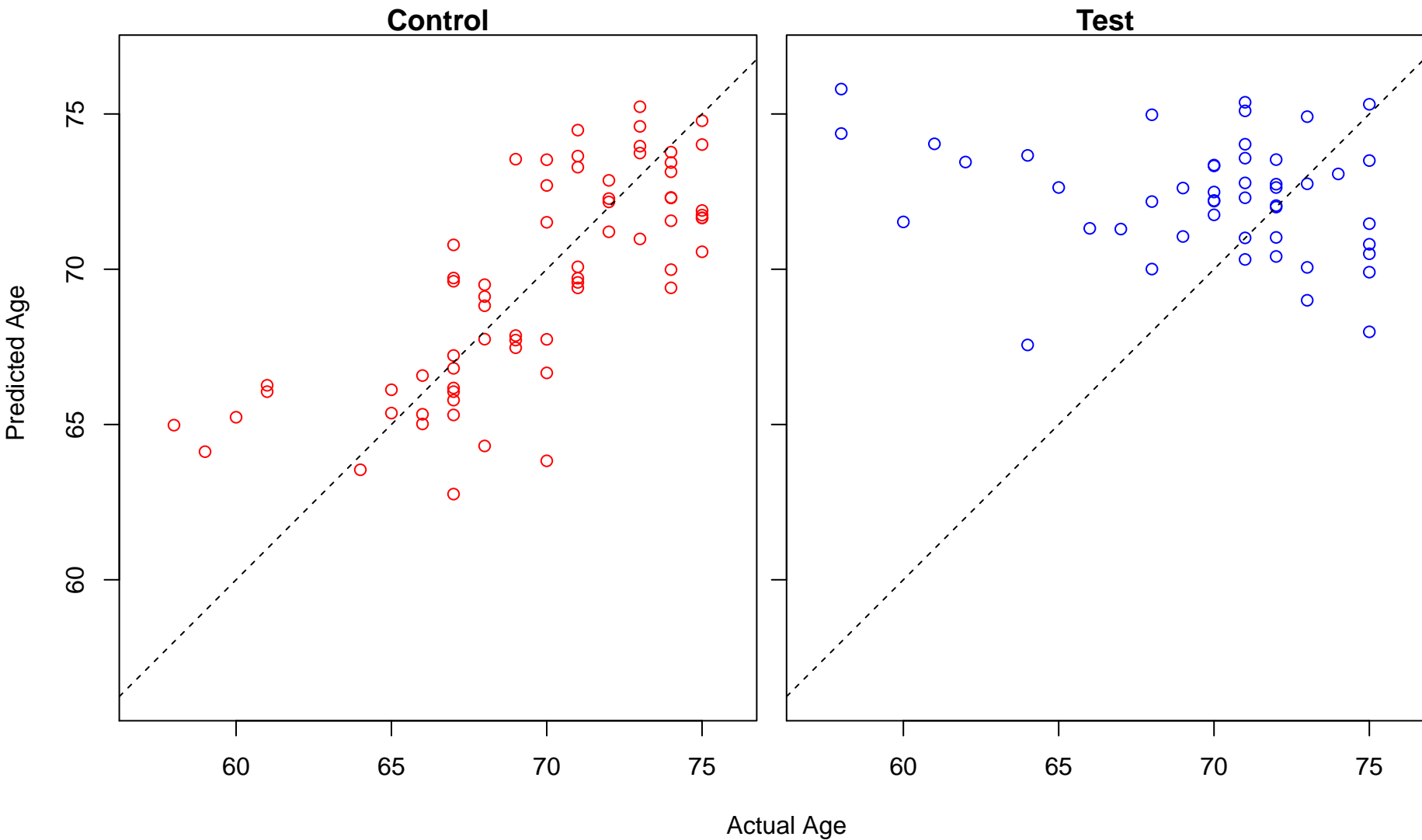
negative regulation of viral process (Score: 1.977890)



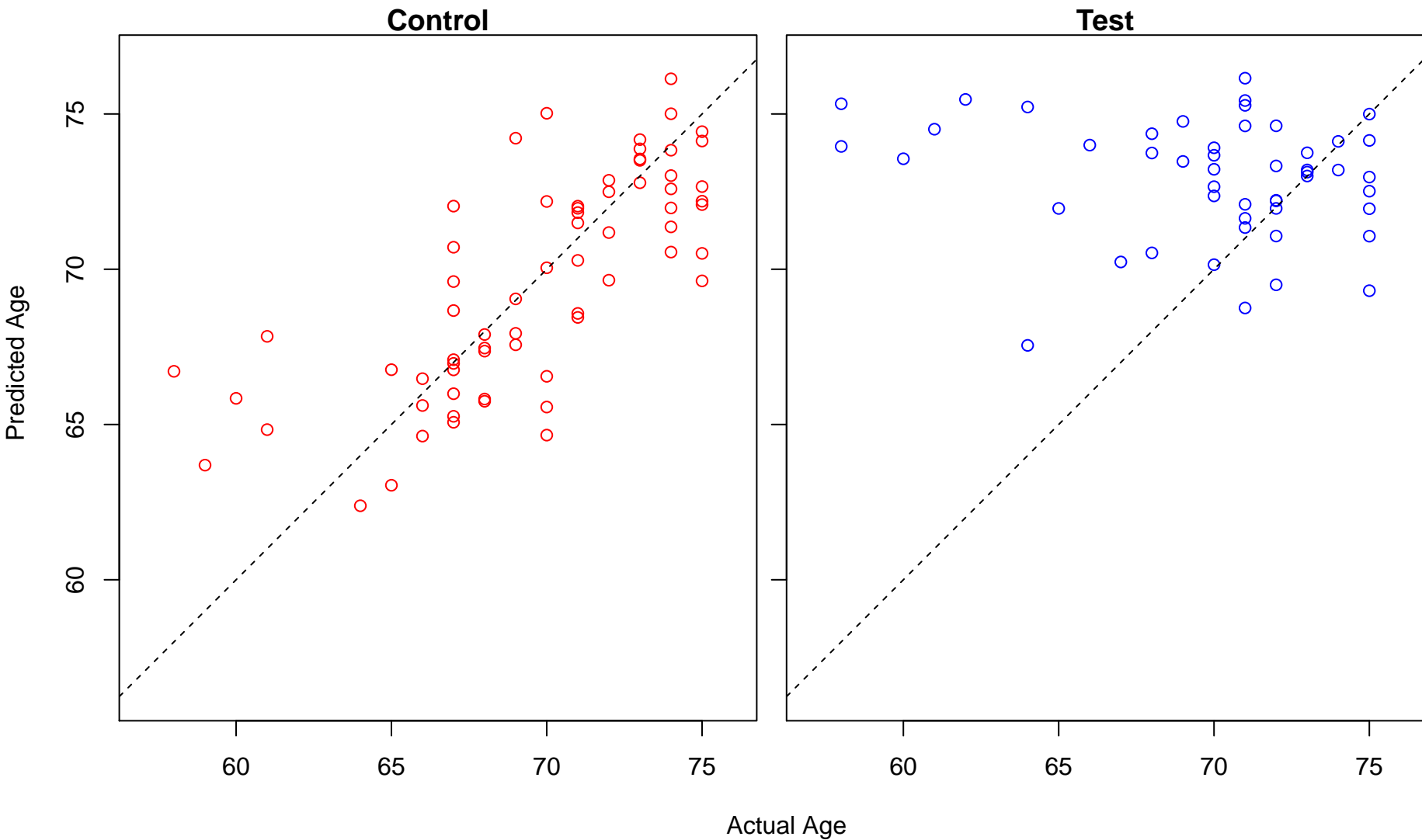
regulation of I-kappaB kinase/NF-kappaB signaling (Score: 1.977300)



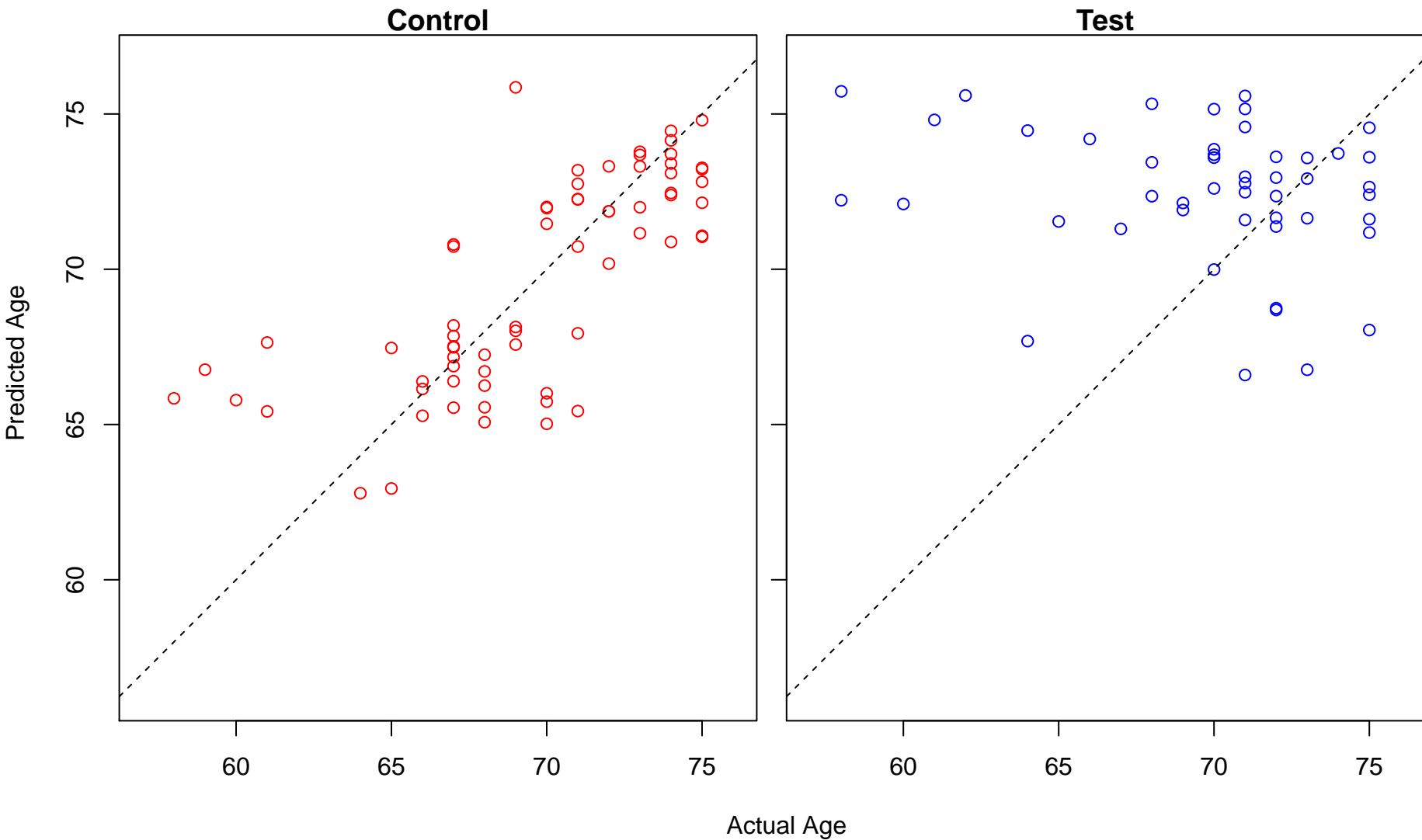
positive regulation of cellular protein localization (Score: 1.977190)



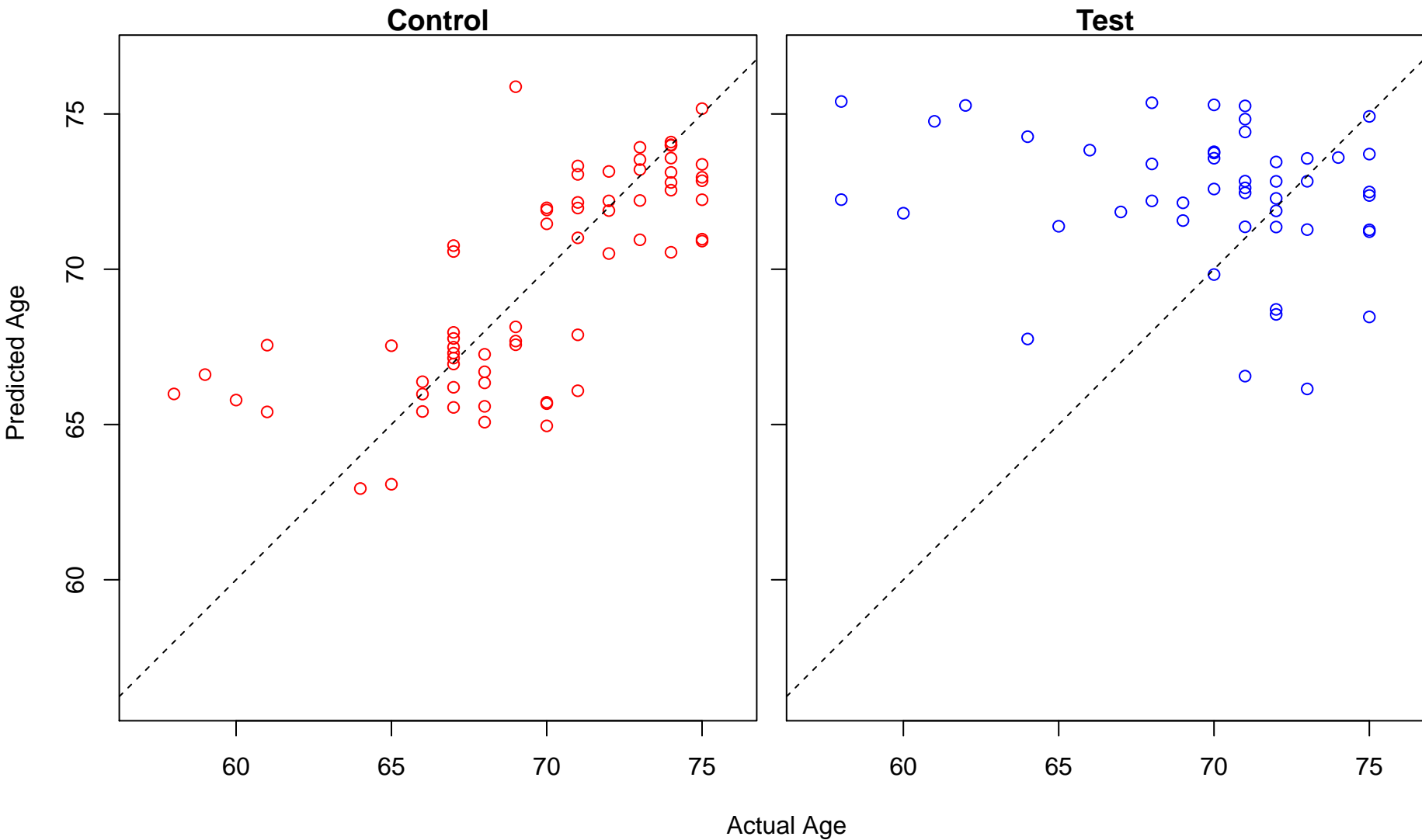
protein sumoylation (Score: 1.976939)



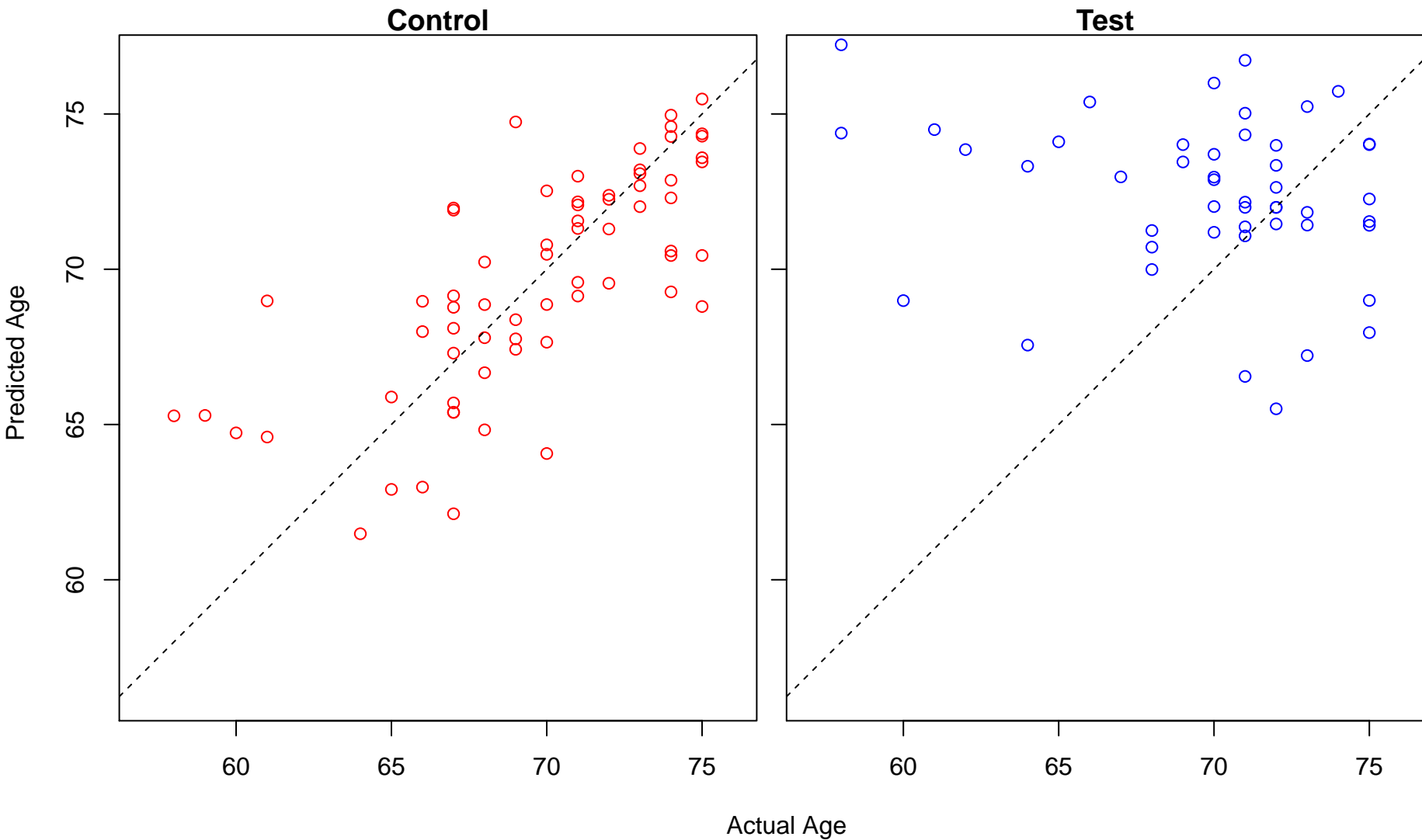
nucleotide biosynthetic process (Score: 1.976137)



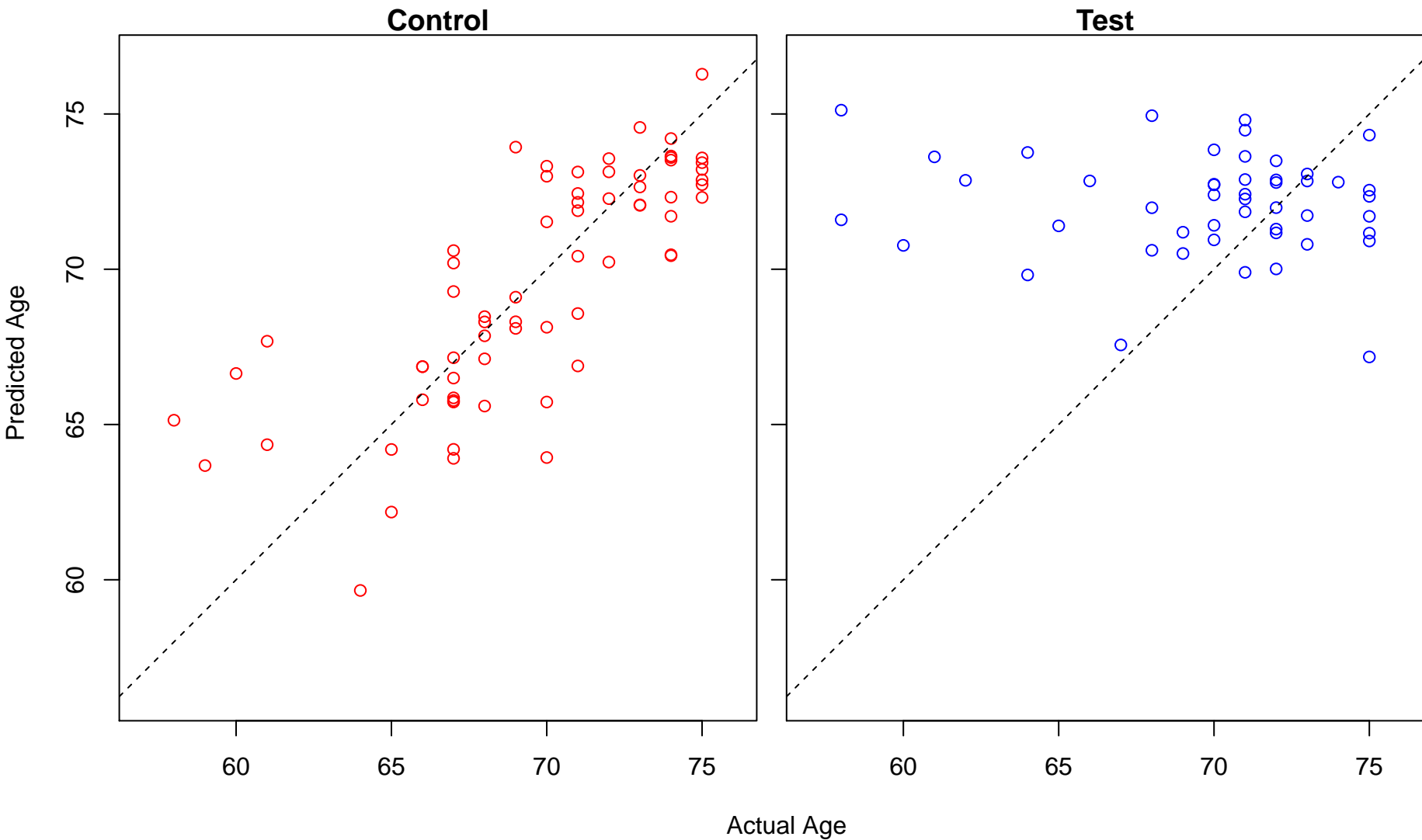
nucleoside phosphate biosynthetic process (Score: 1.976027)



interaction with host (Score: 1.975896)

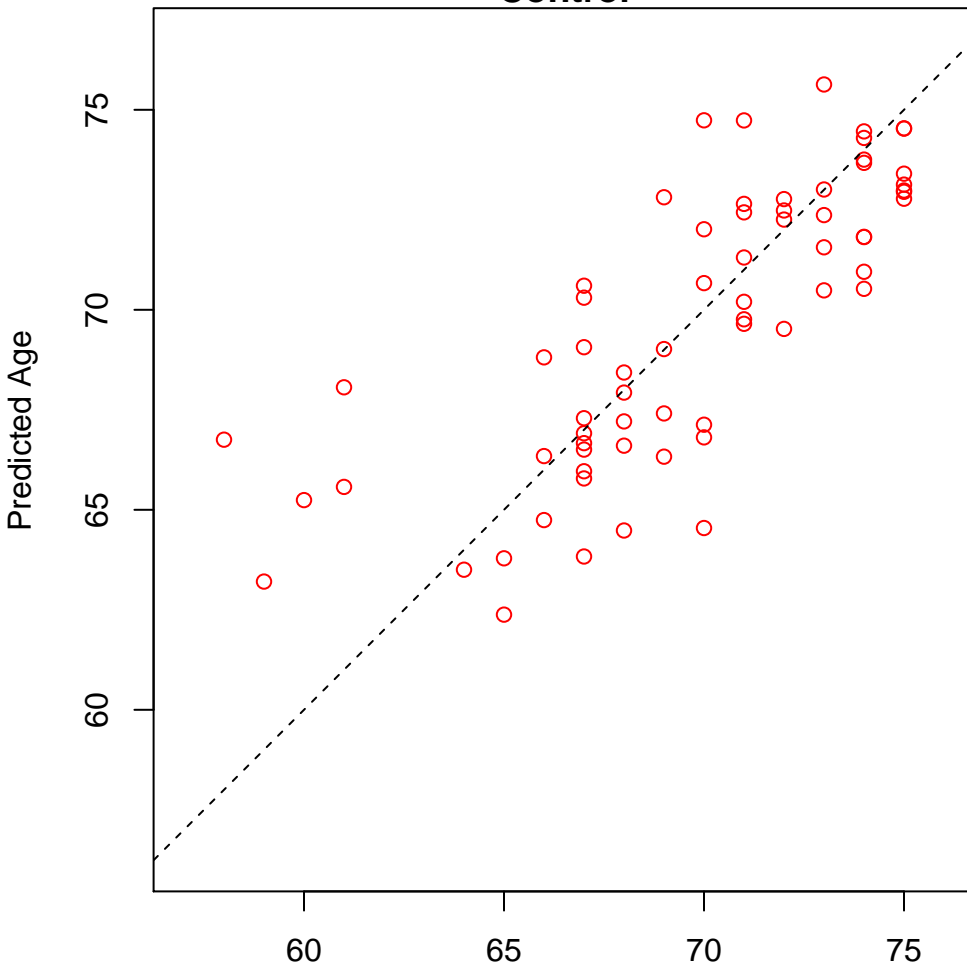


positive regulation of proteolysis (Score: 1.974307)

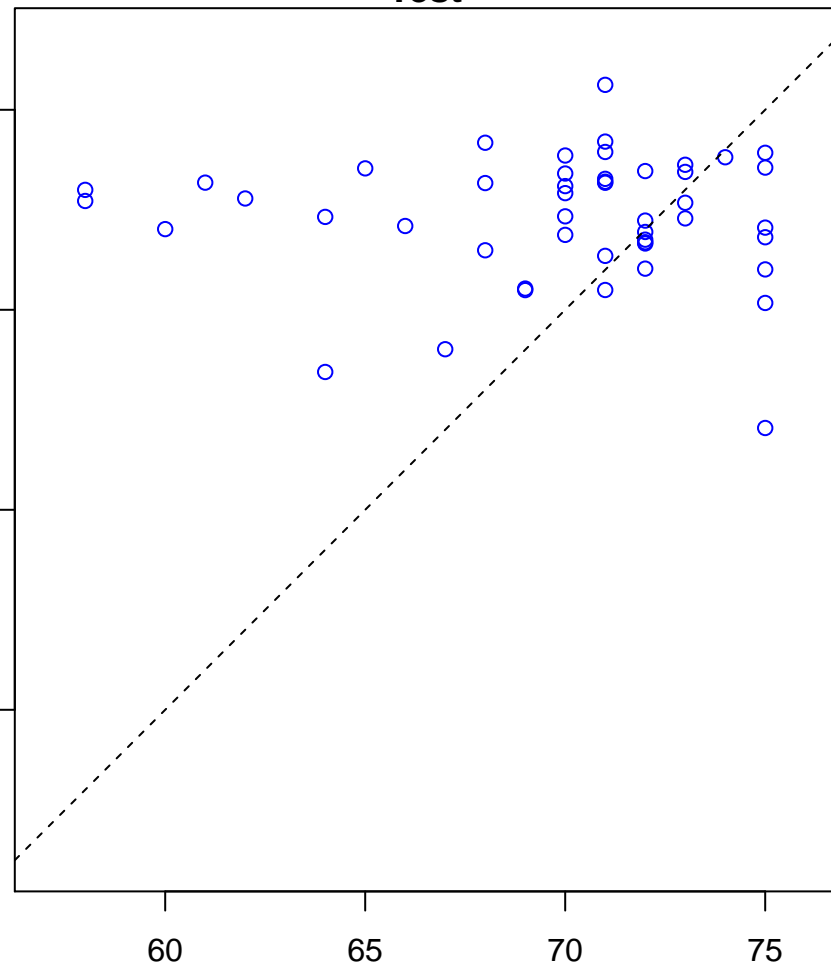


cellular response to hormone stimulus (Score: 1.973104)

Control

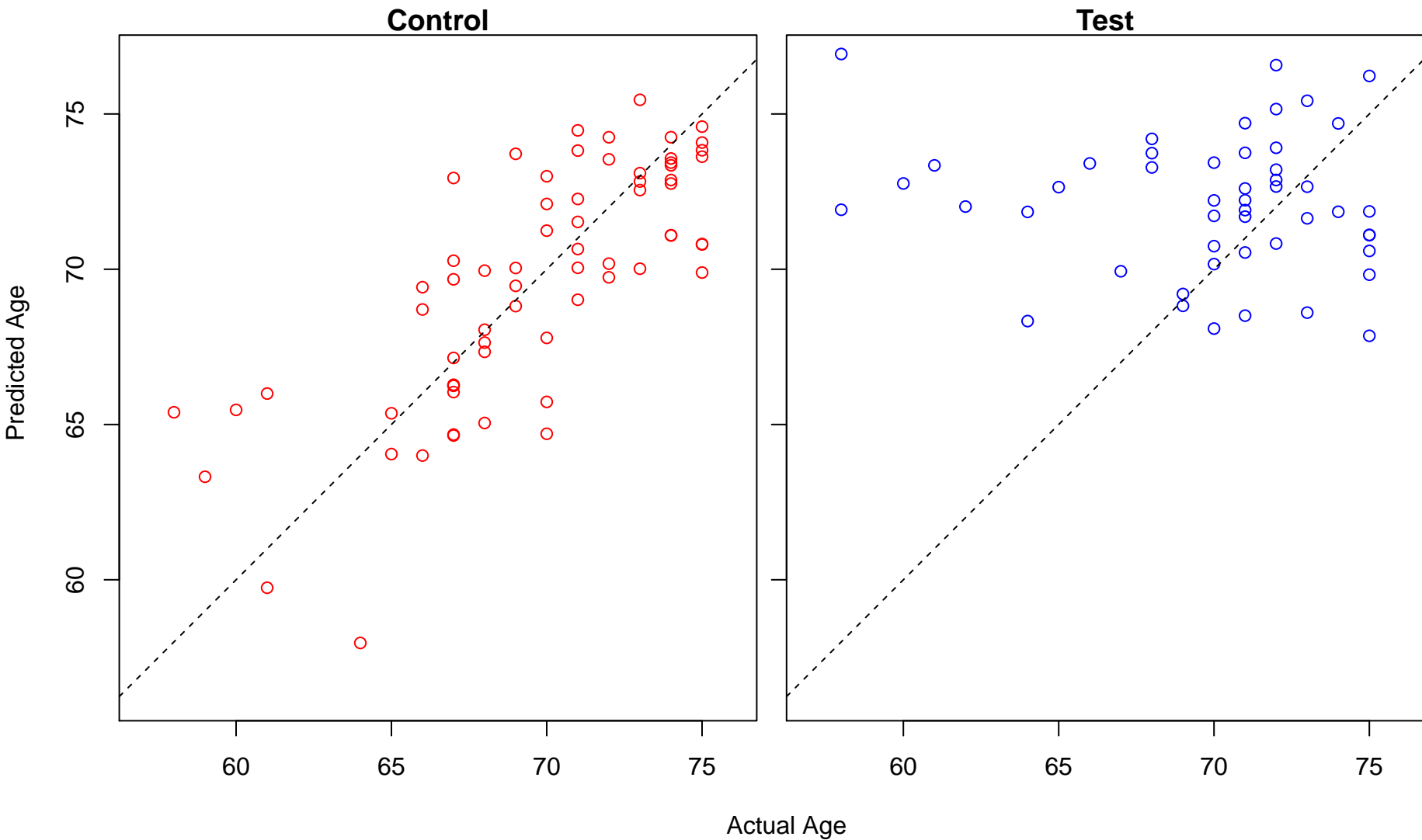


Test

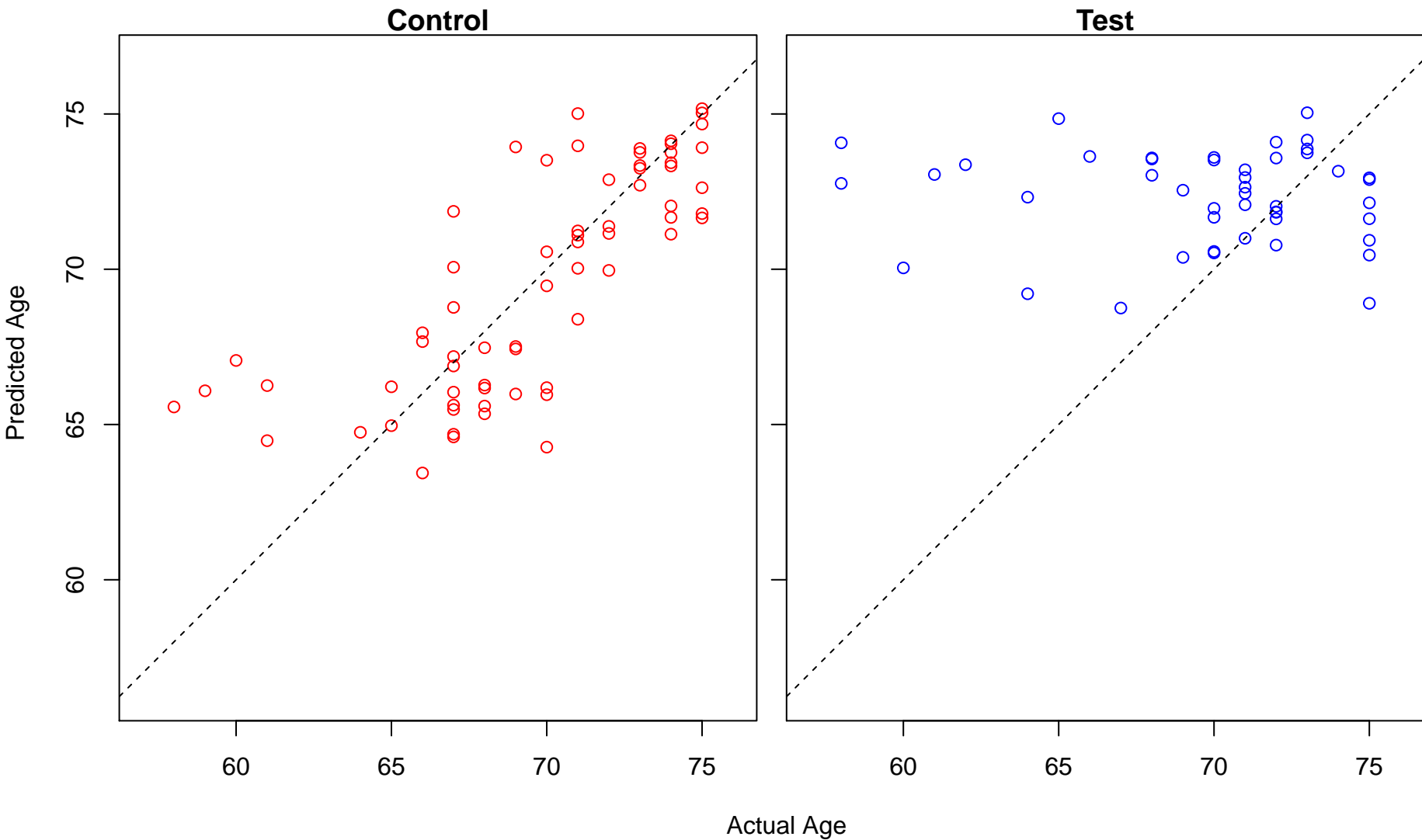


Actual Age

activation of cysteine-type endopeptidase activity (Score: 1.972475)

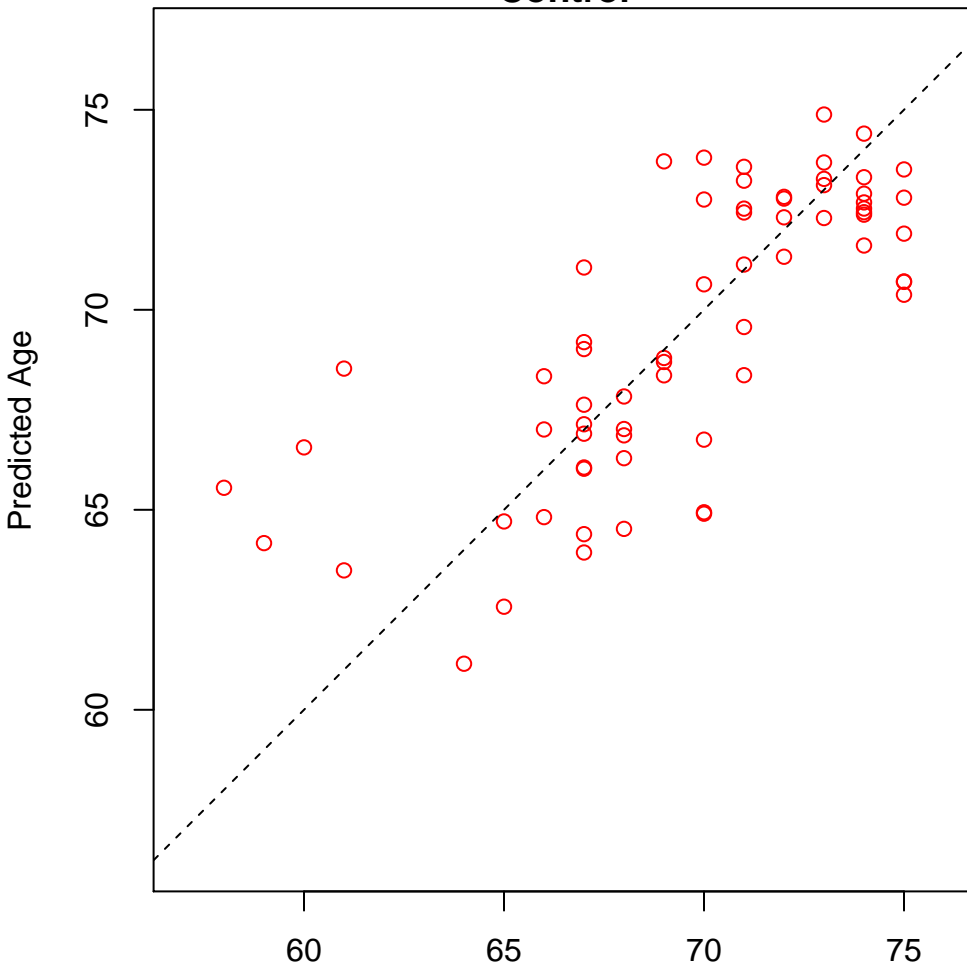


cellular macromolecular complex assembly (Score: 1.971295)

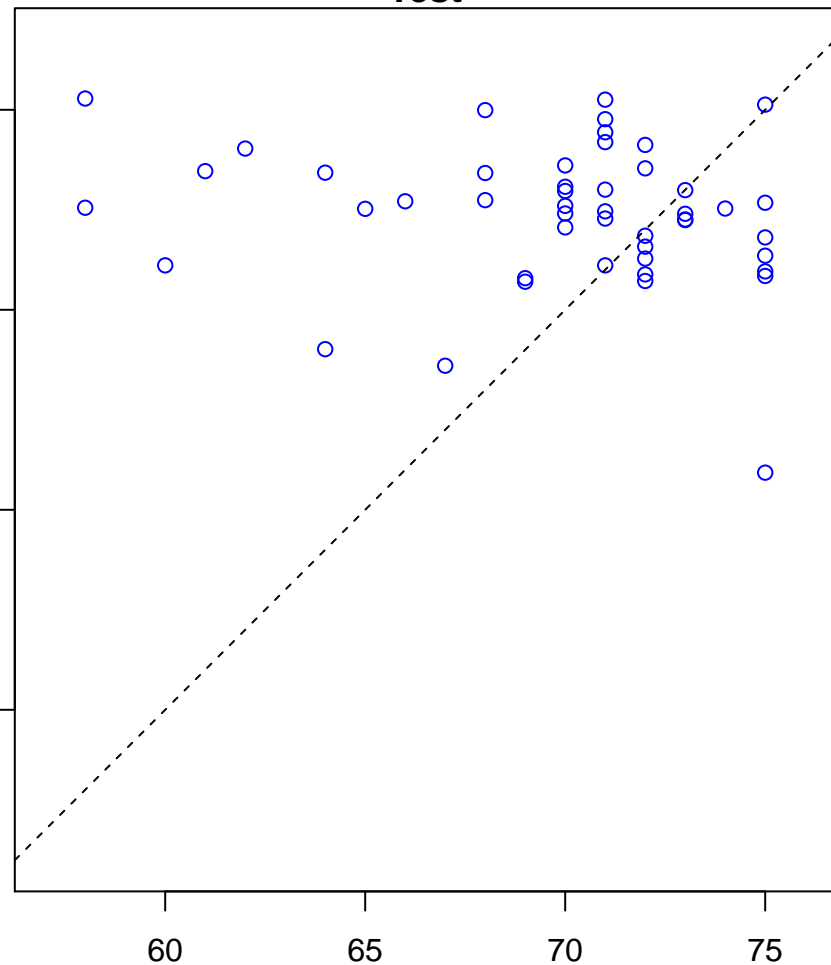


regulation of endopeptidase activity (Score: 1.968813)

Control



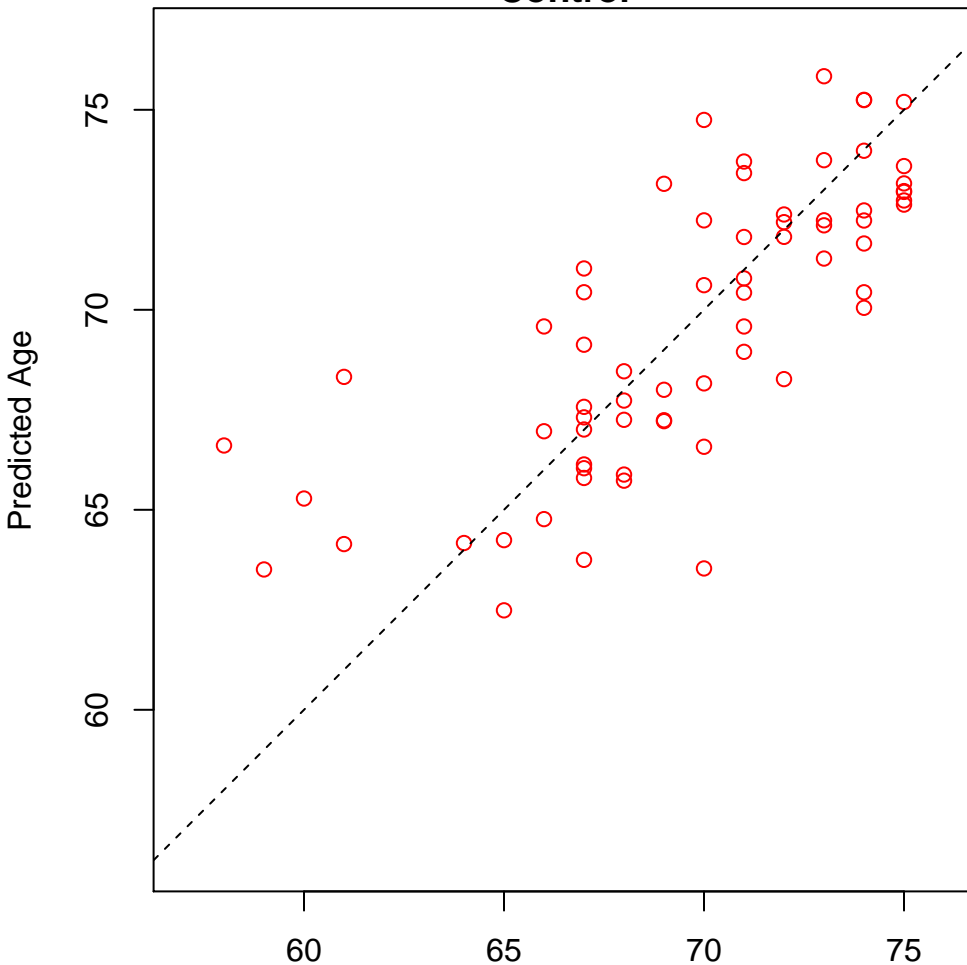
Test



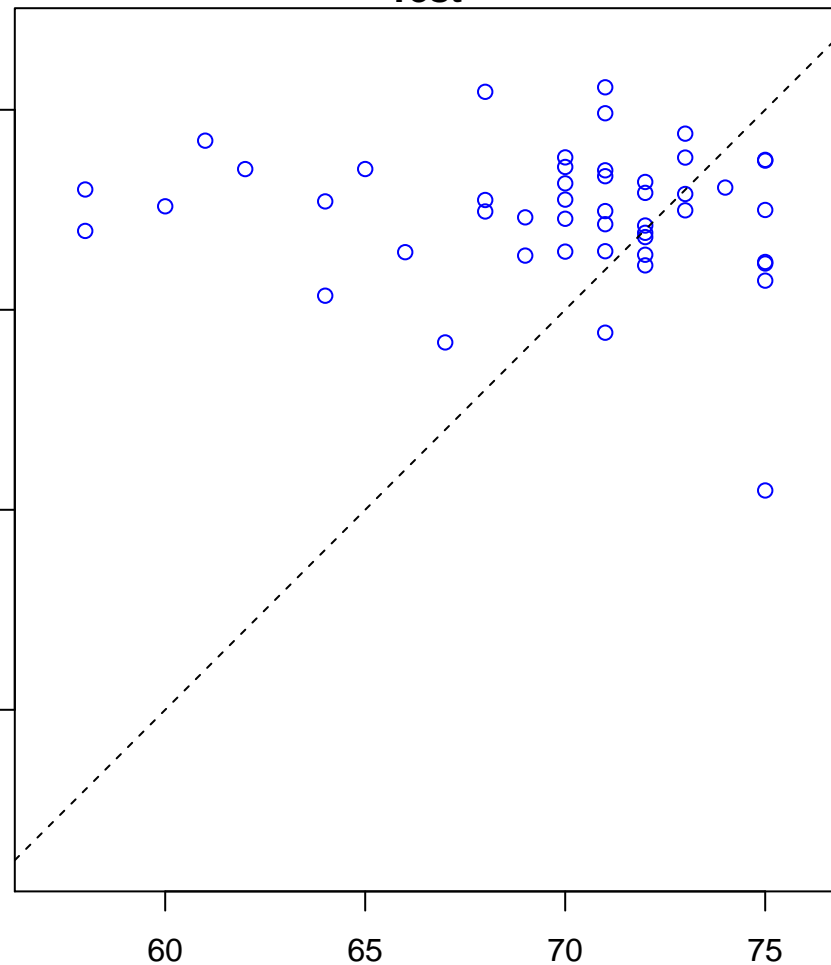
Actual Age

Fc-epsilon receptor signaling pathway (Score: 1.968696)

Control



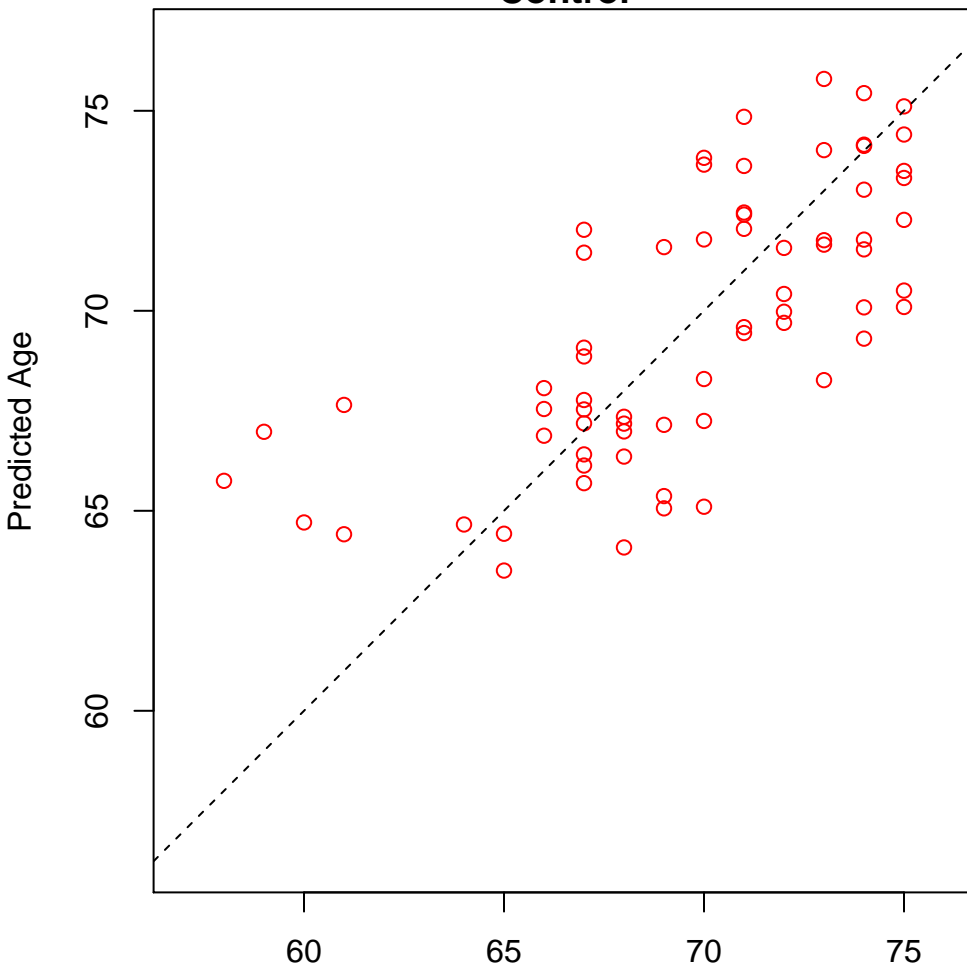
Test



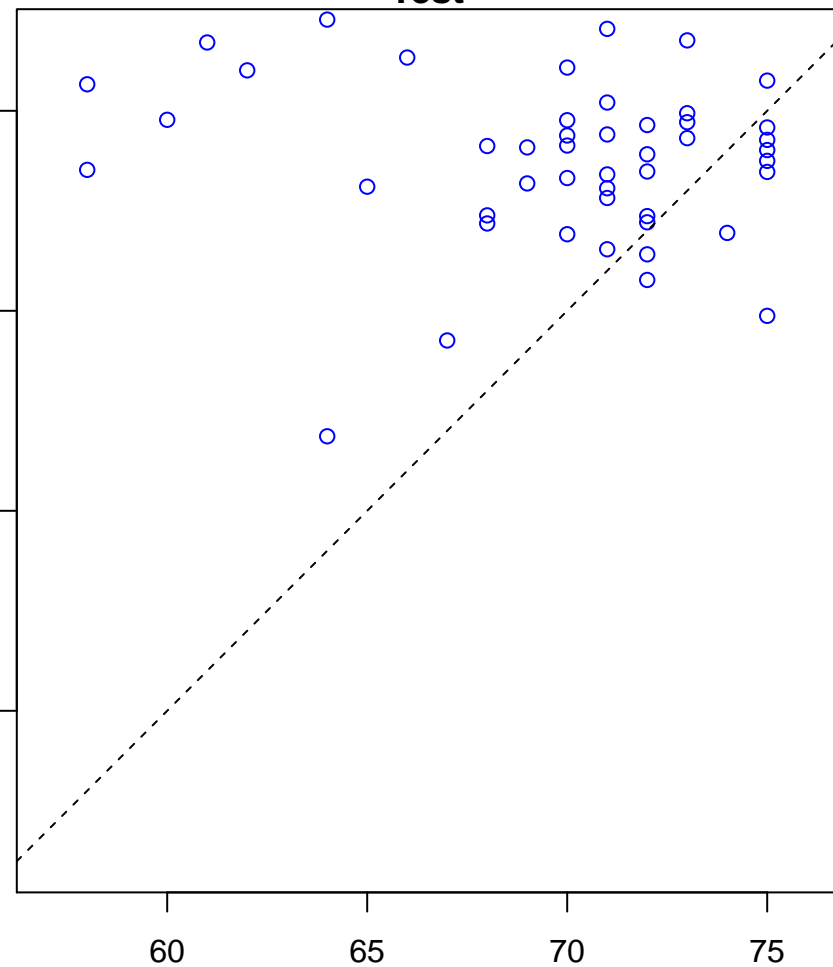
Actual Age

G2/M transition of mitotic cell cycle (Score: 1.968545)

Control

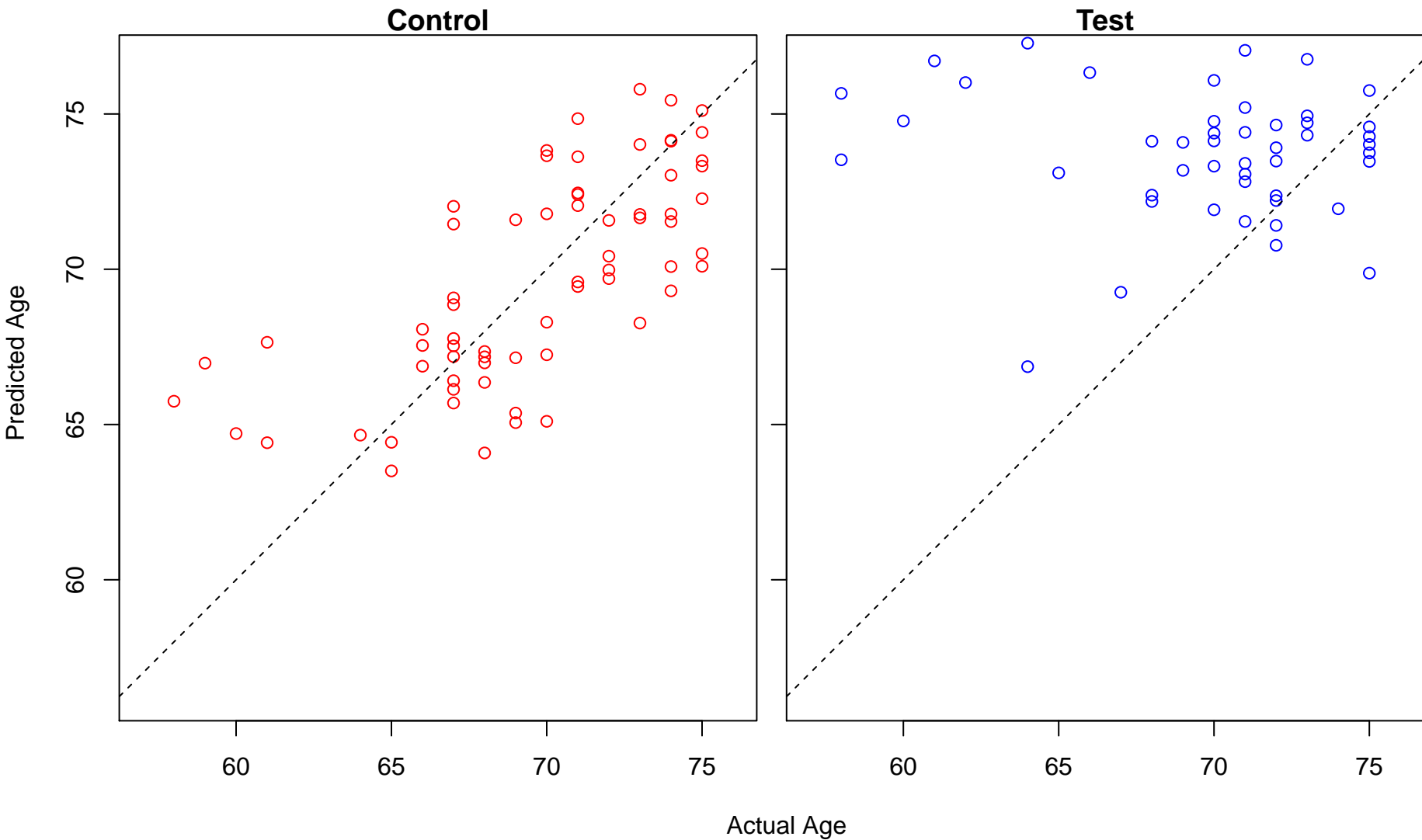


Test

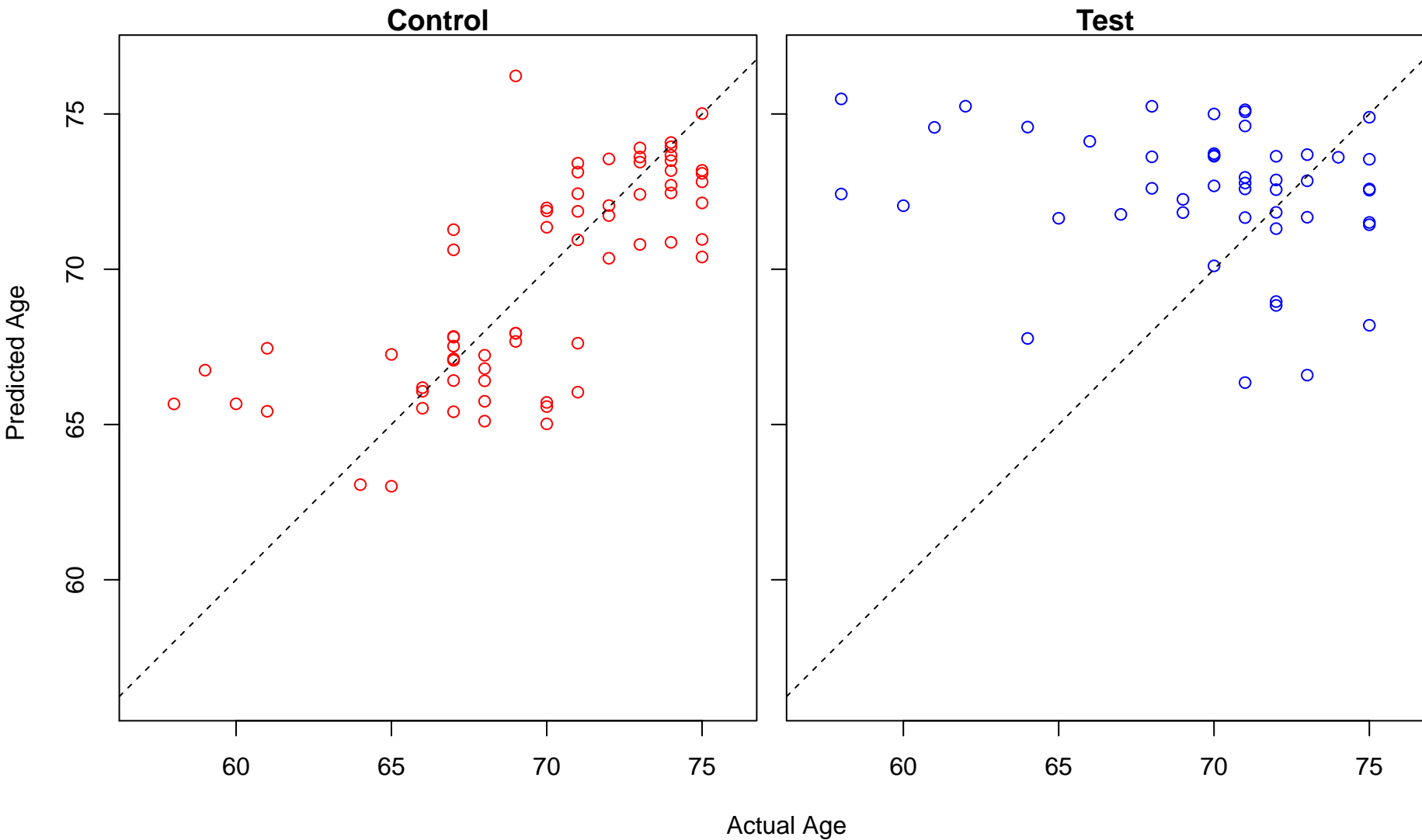


Actual Age

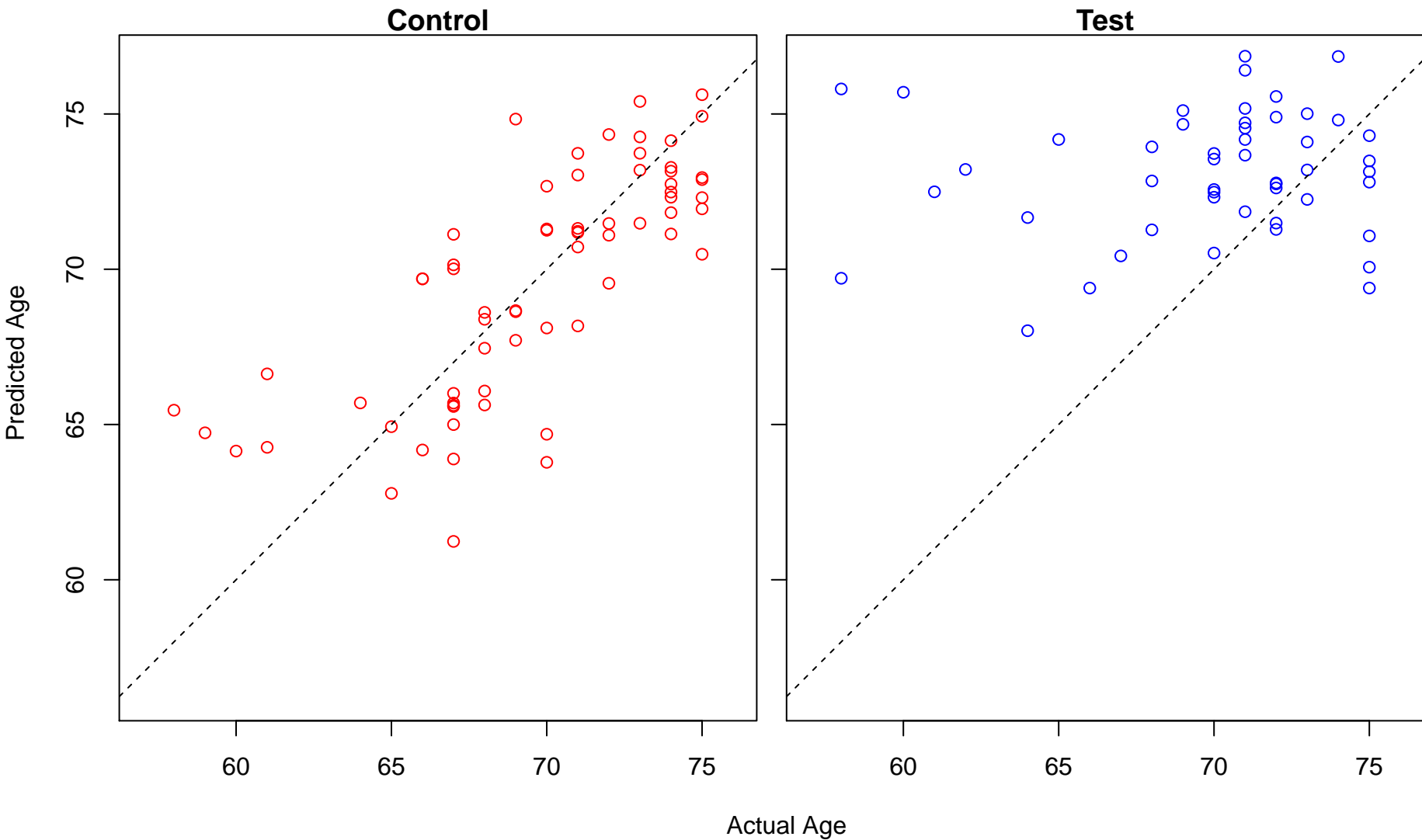
cell cycle G2/M phase transition (Score: 1.968545)



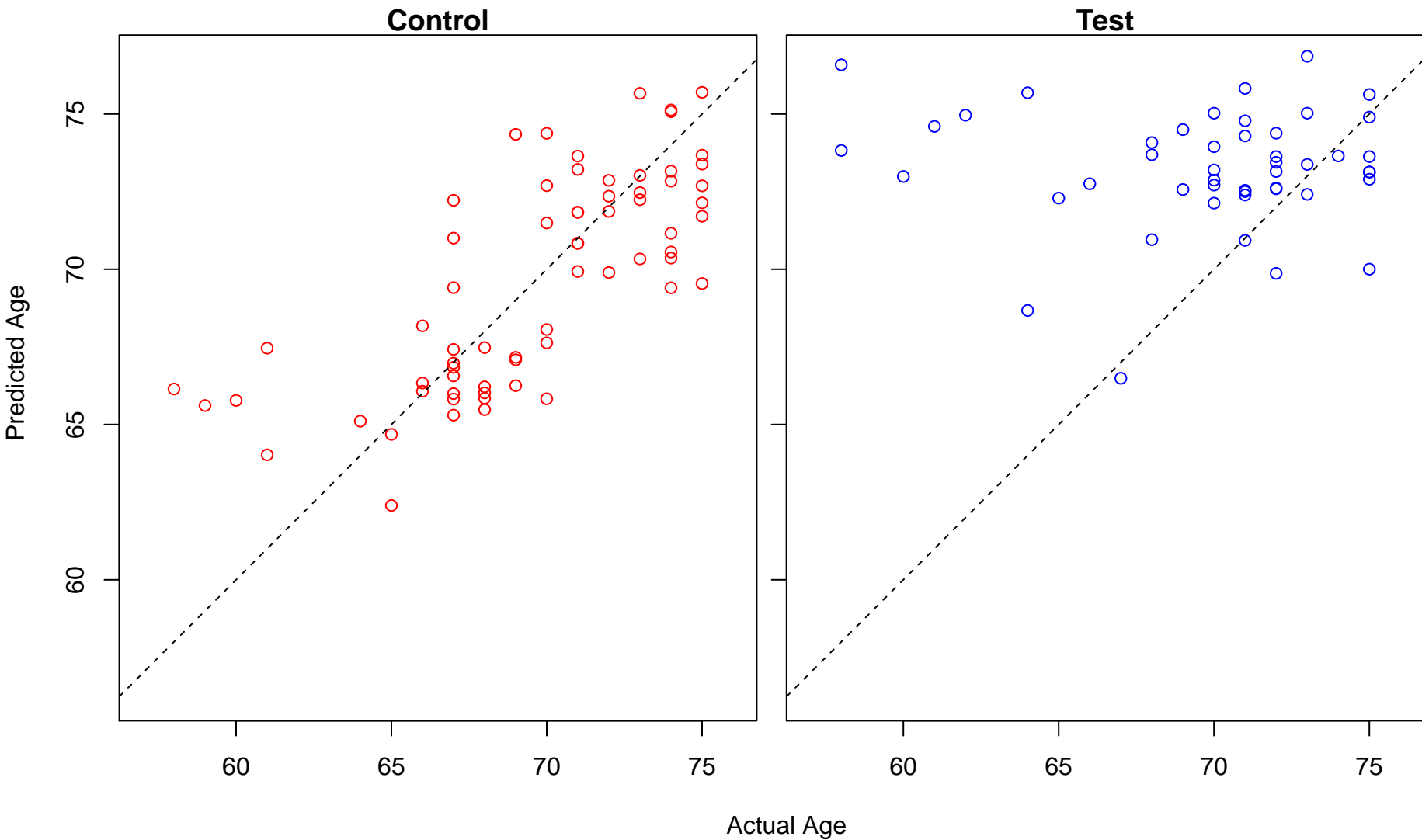
purine-containing compound biosynthetic process (Score: 1.968499)



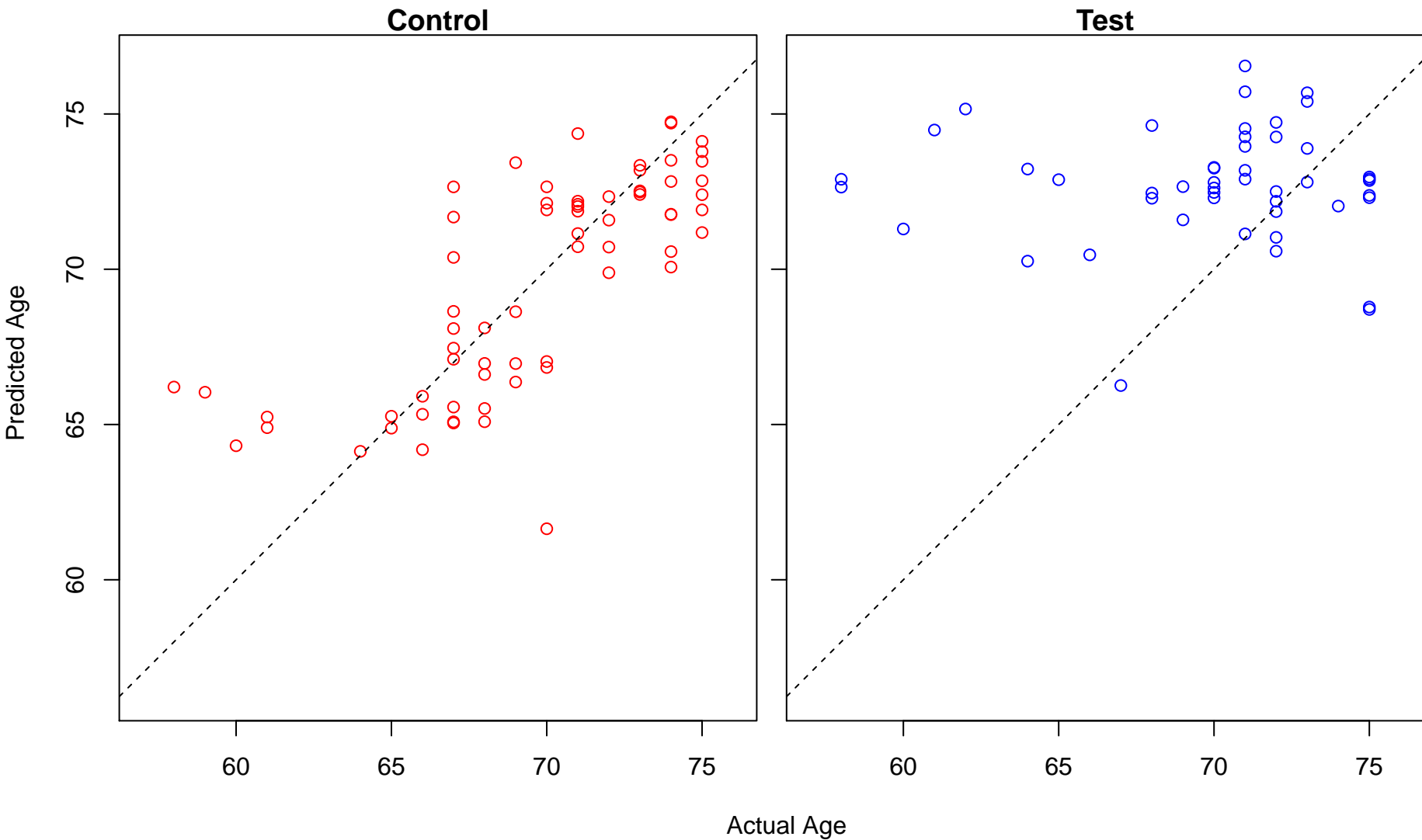
protein localization to organelle (Score: 1.966363)



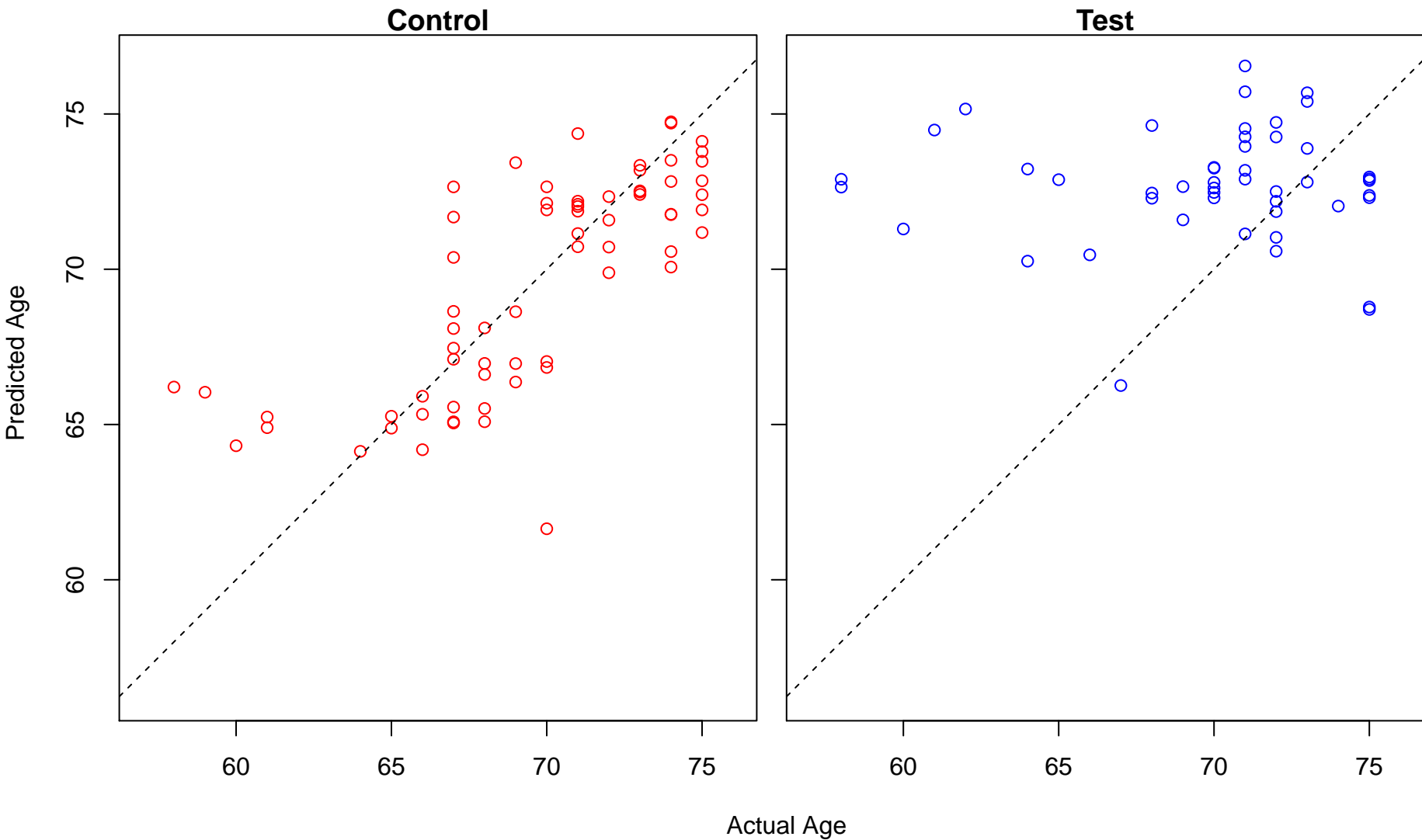
microtubule-based process (Score: 1.966034)



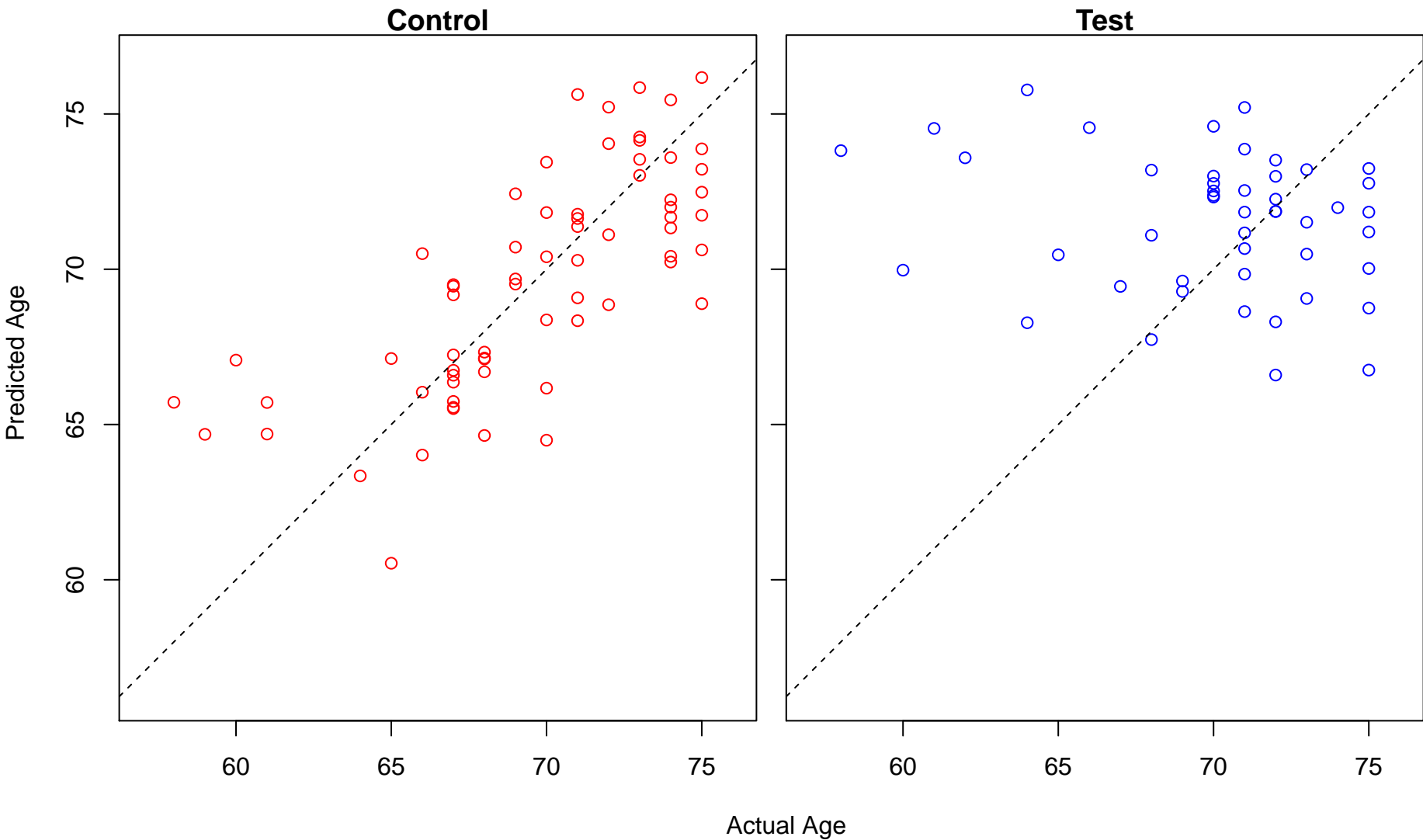
electron transport chain (Score: 1.965299)



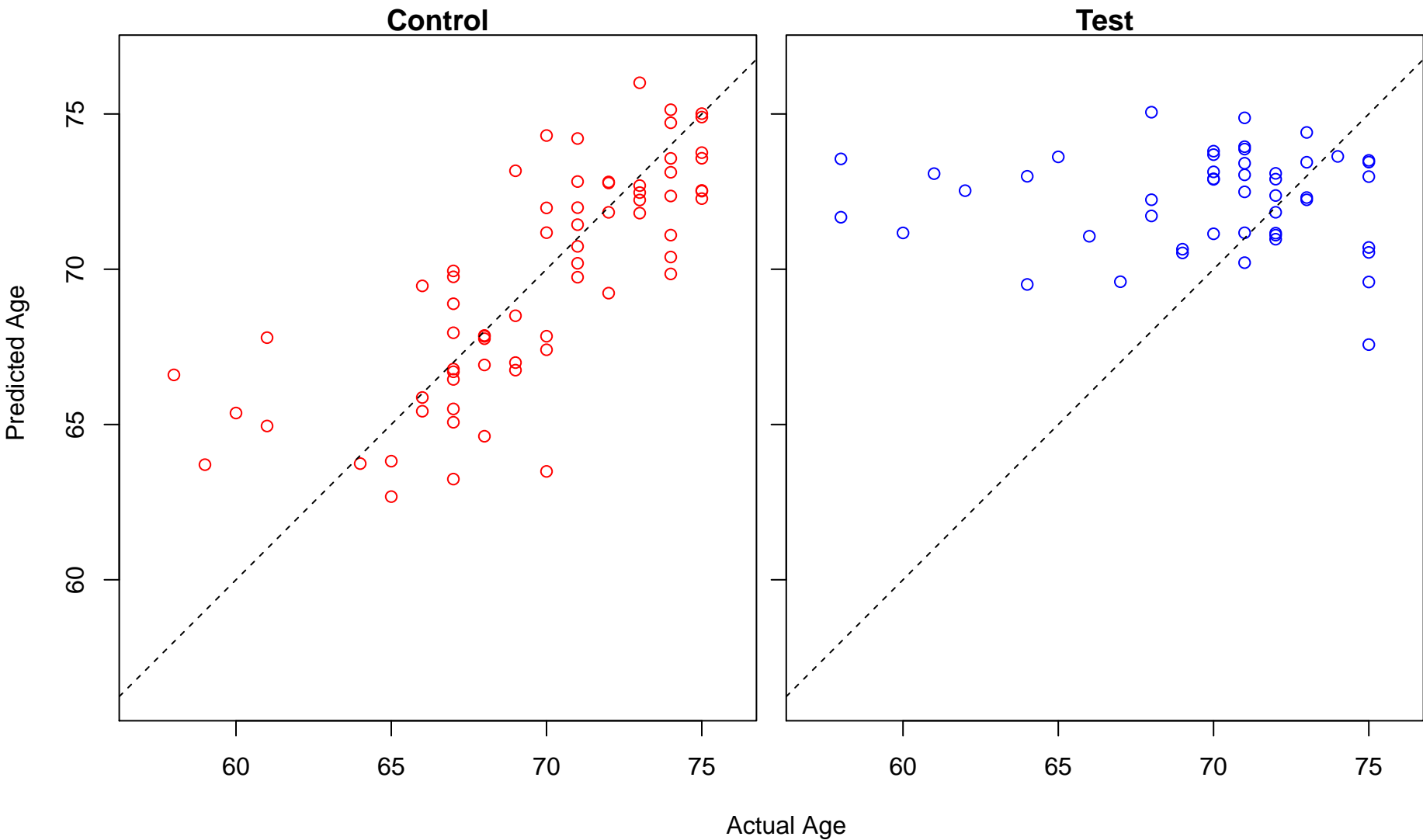
respiratory electron transport chain (Score: 1.965299)



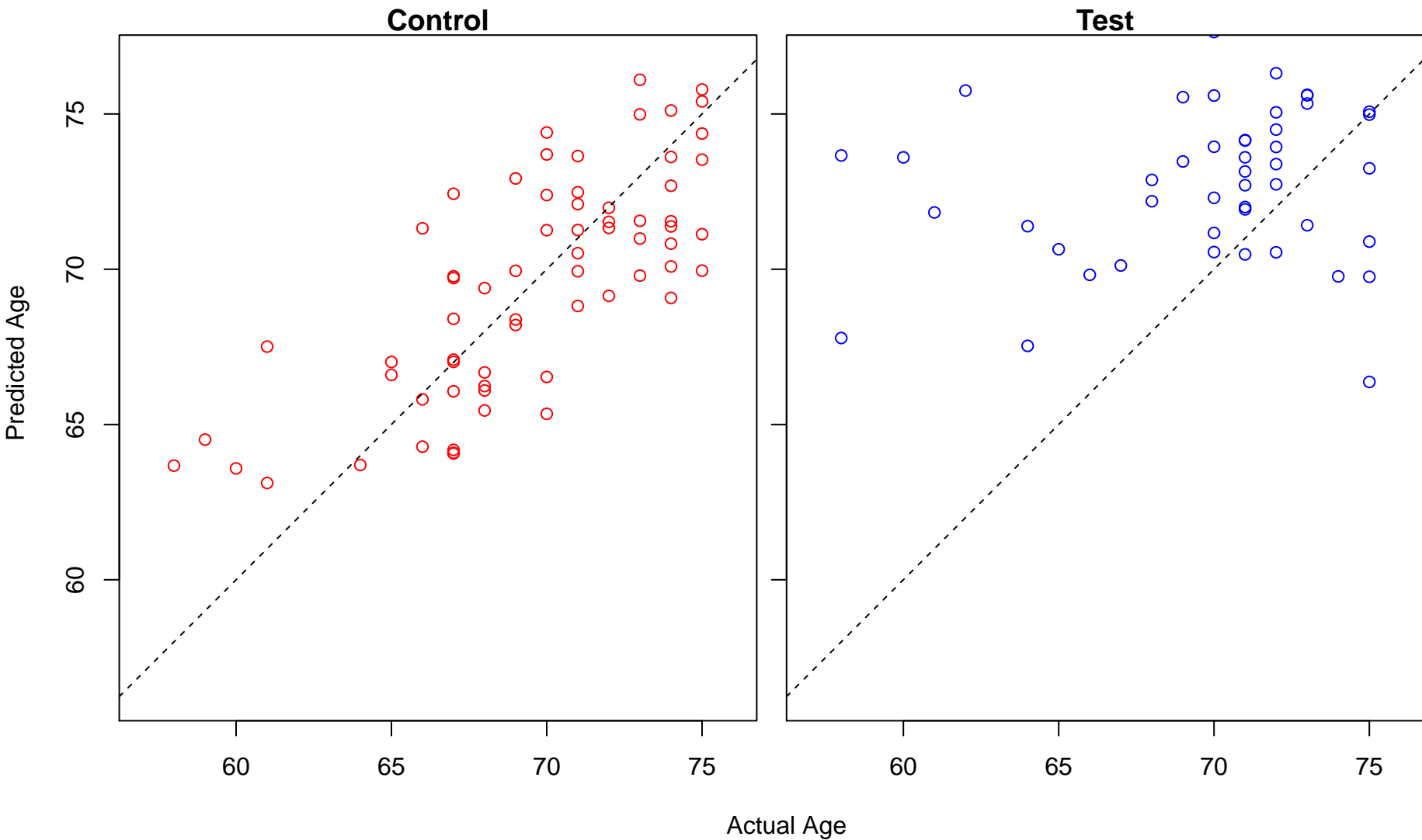
positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 1.0)



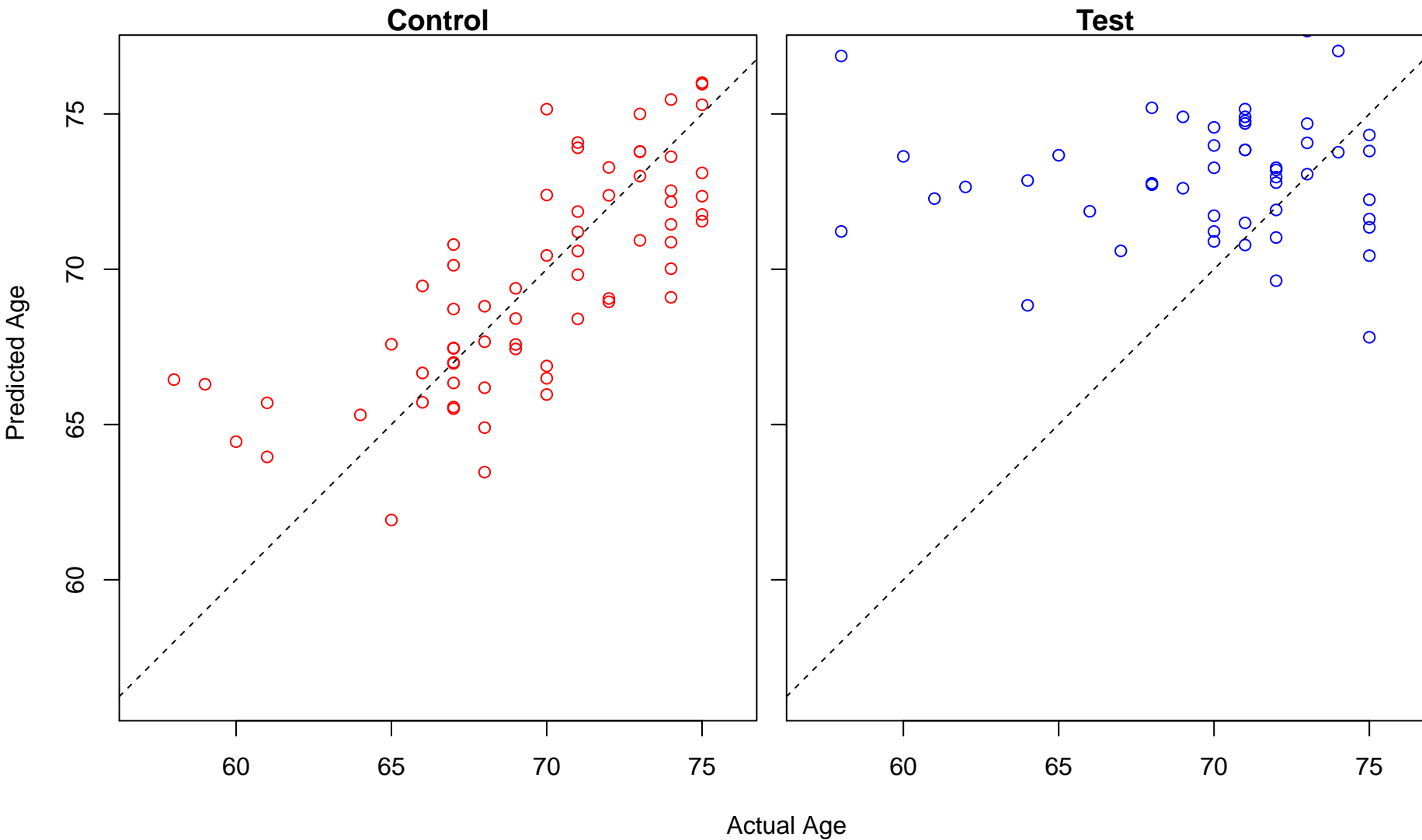
response to insulin (Score: 1.961818)



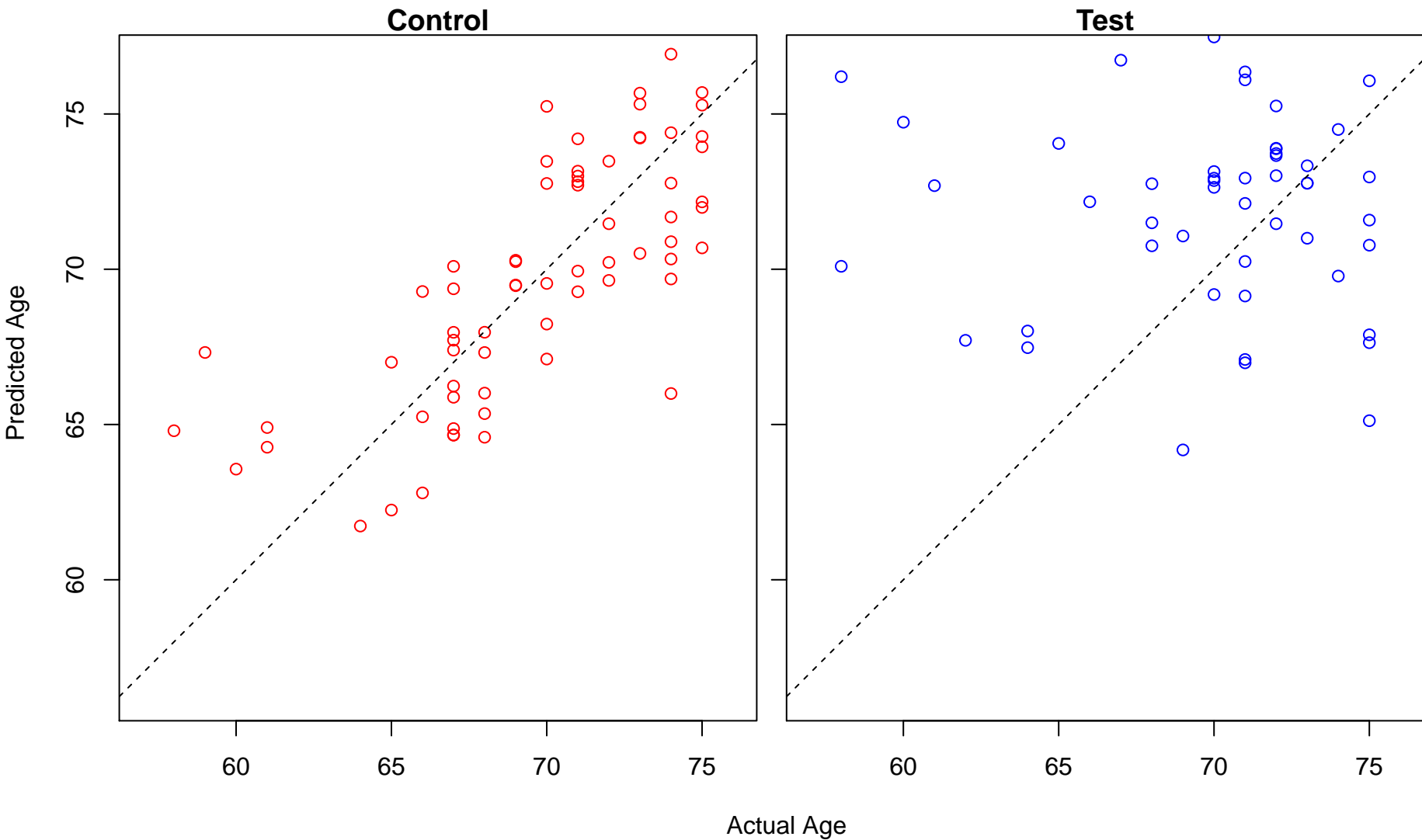
steroid metabolic process (Score: 1.960351)



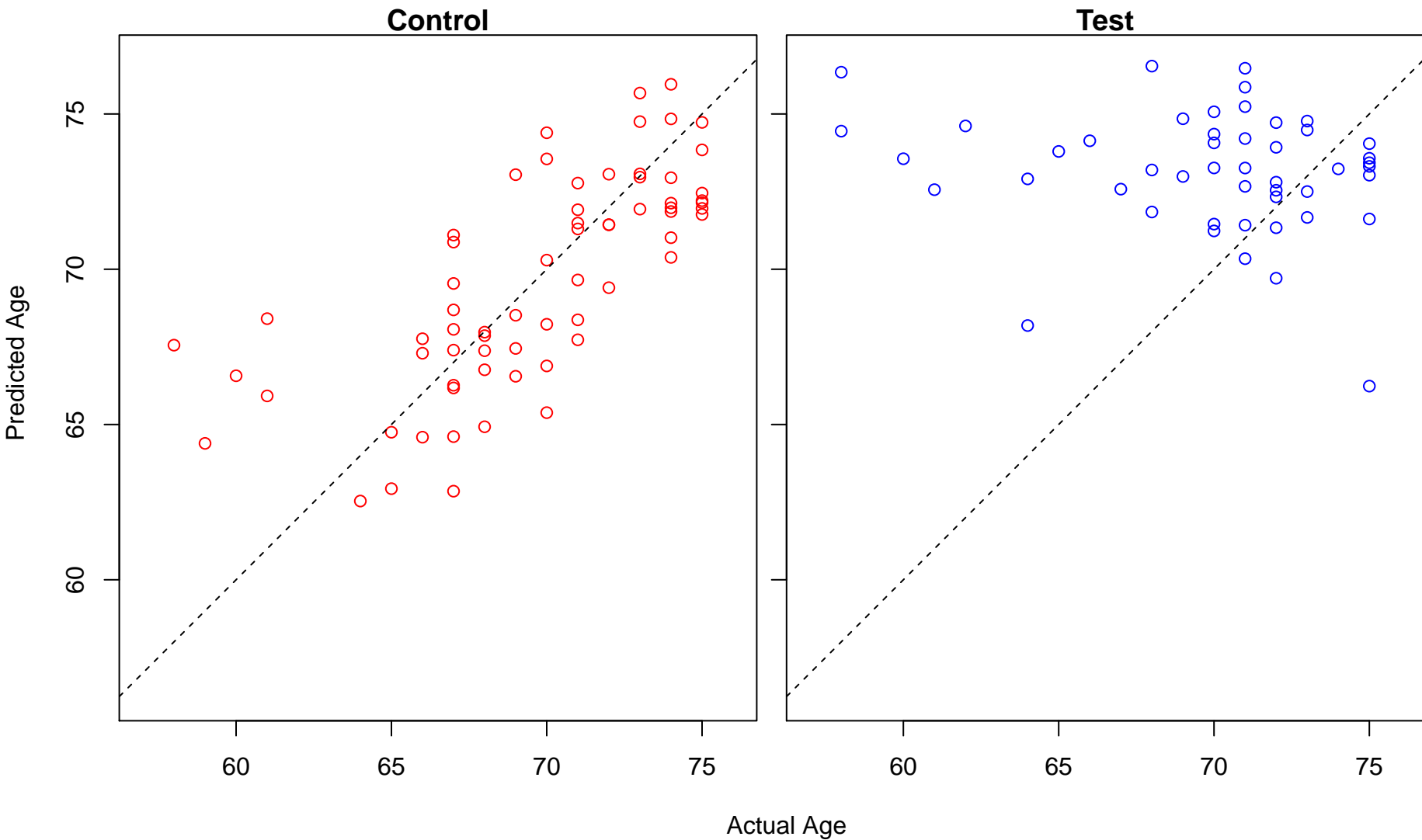
regulation of small GTPase mediated signal transduction (Score: 1.957576)



regulation of necrotic cell death (Score: 1.957497)

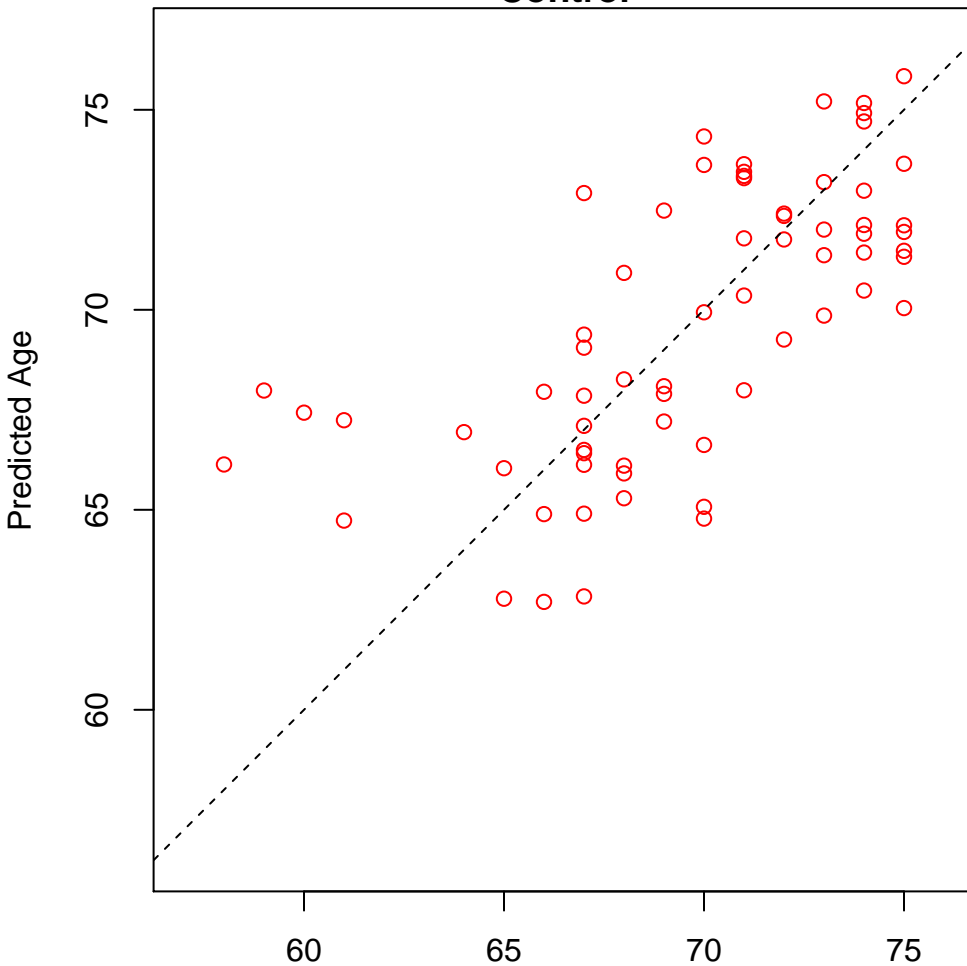


cell migration (Score: 1.956224)

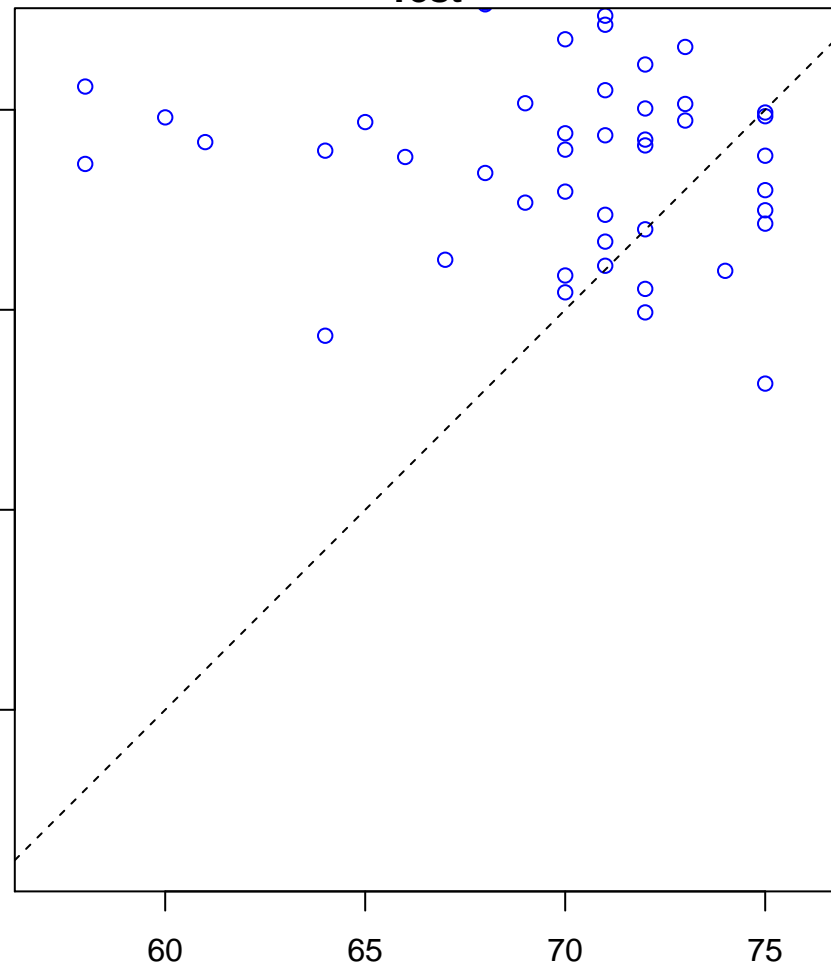


cellular response to oxidative stress (Score: 1.955309)

Control

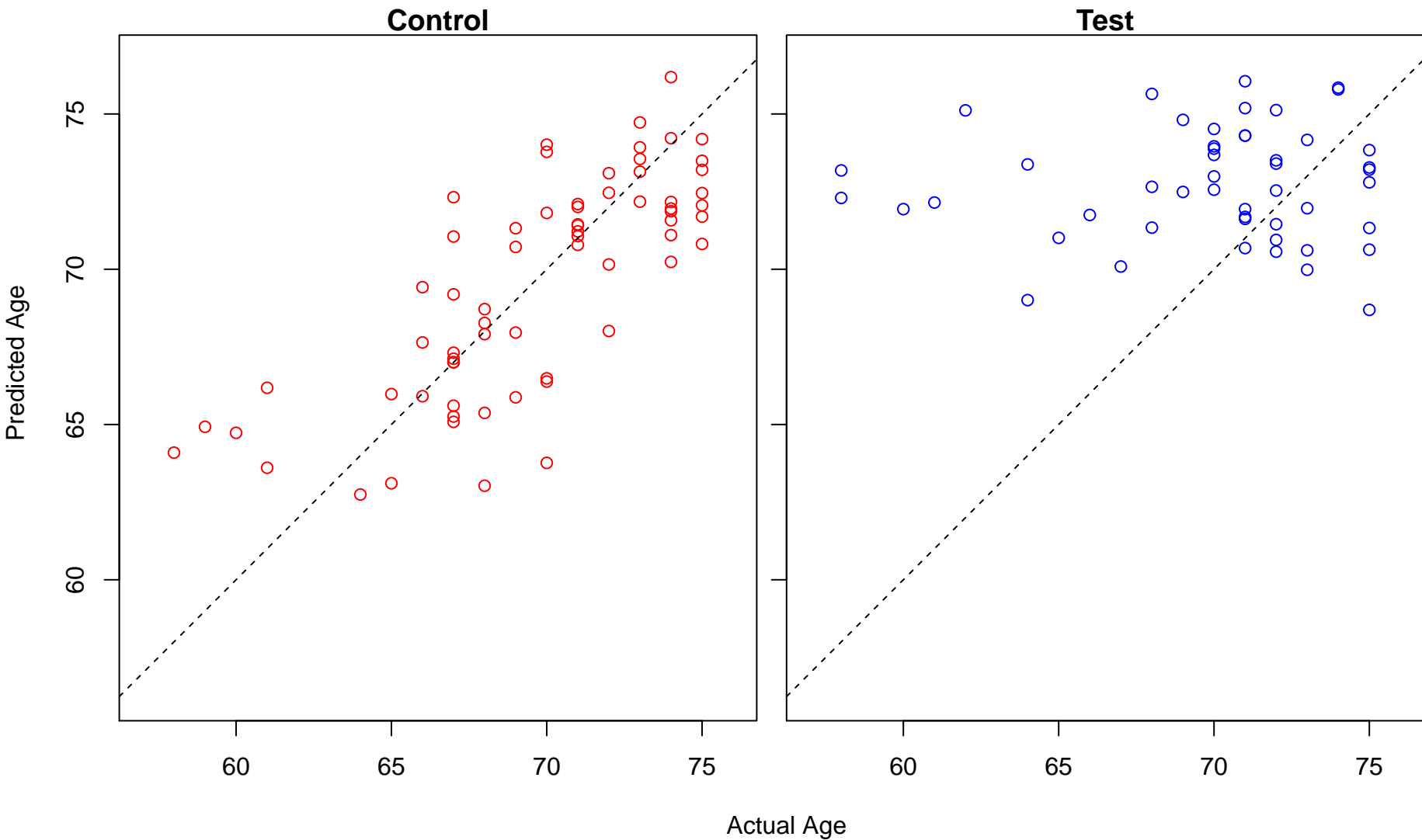


Test

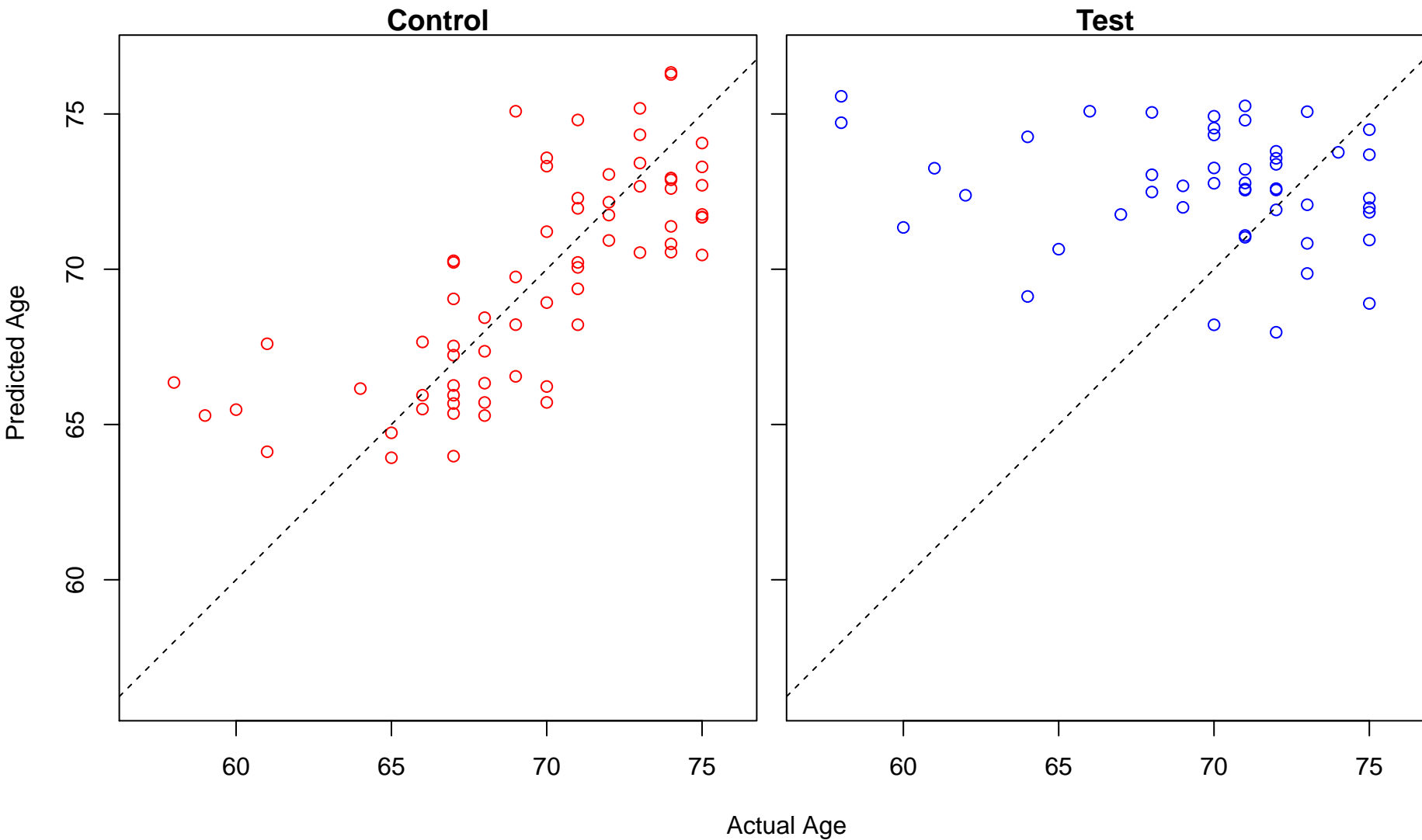


Actual Age

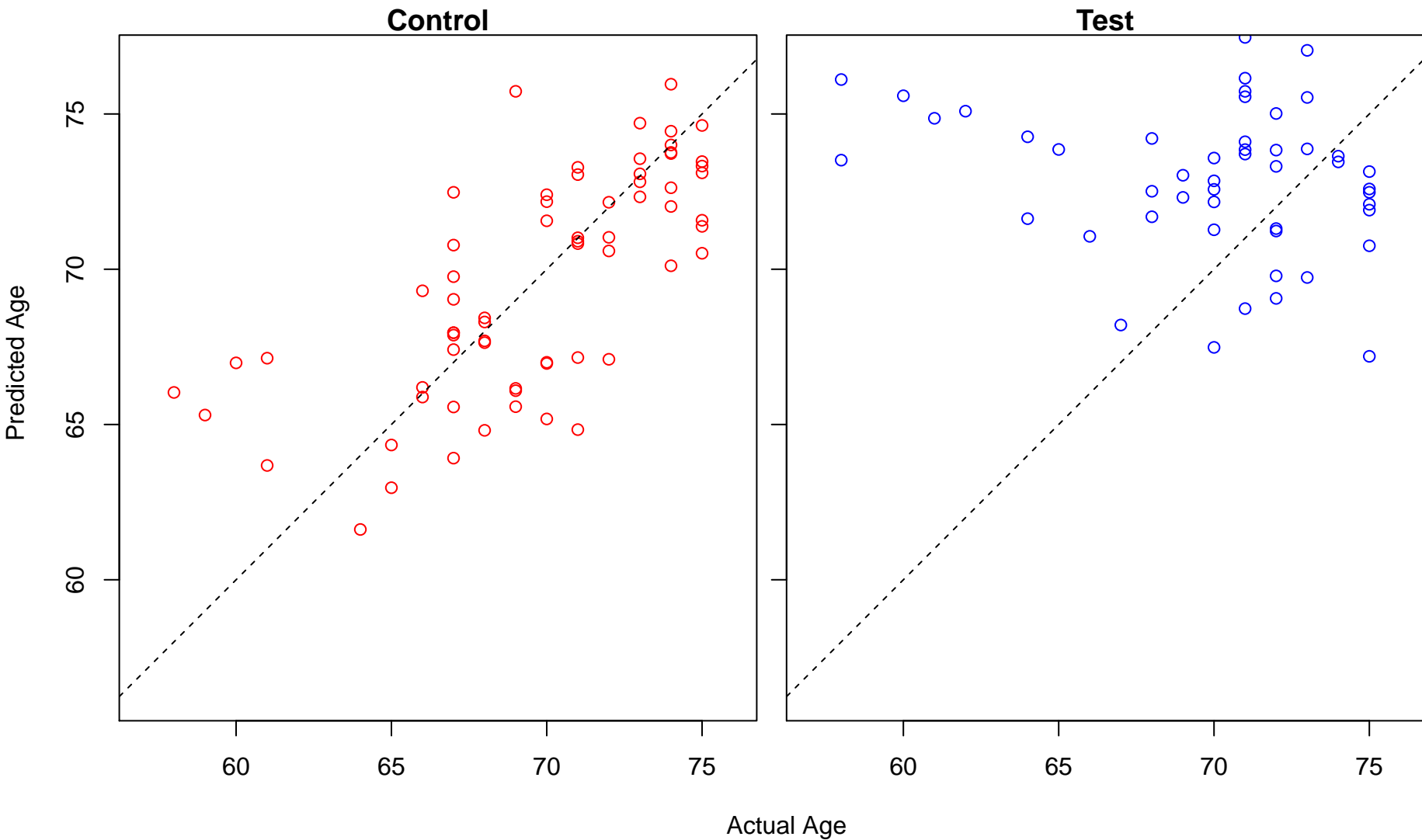
regulation of nuclear division (Score: 1.953292)



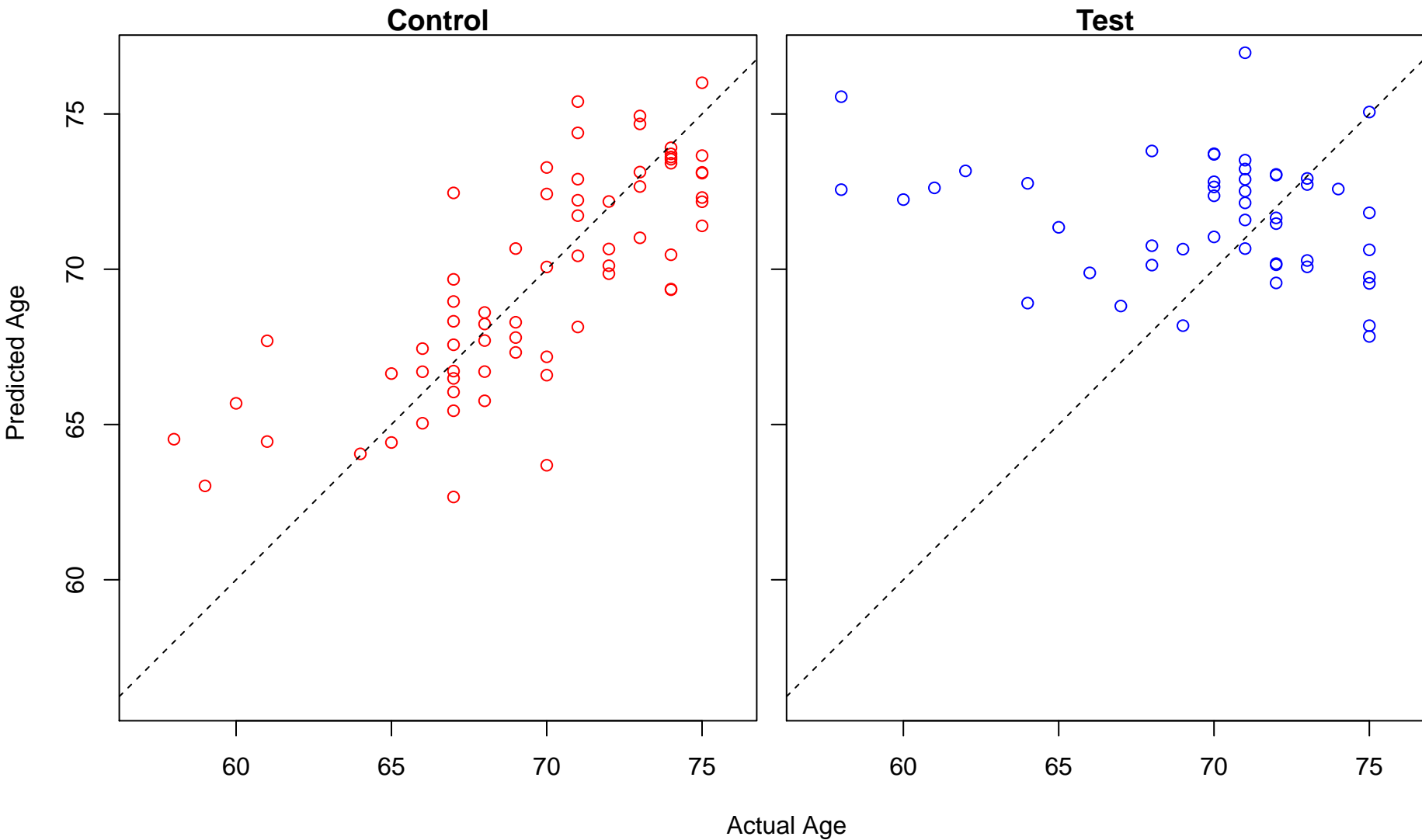
cellular ion homeostasis (Score: 1.953266)



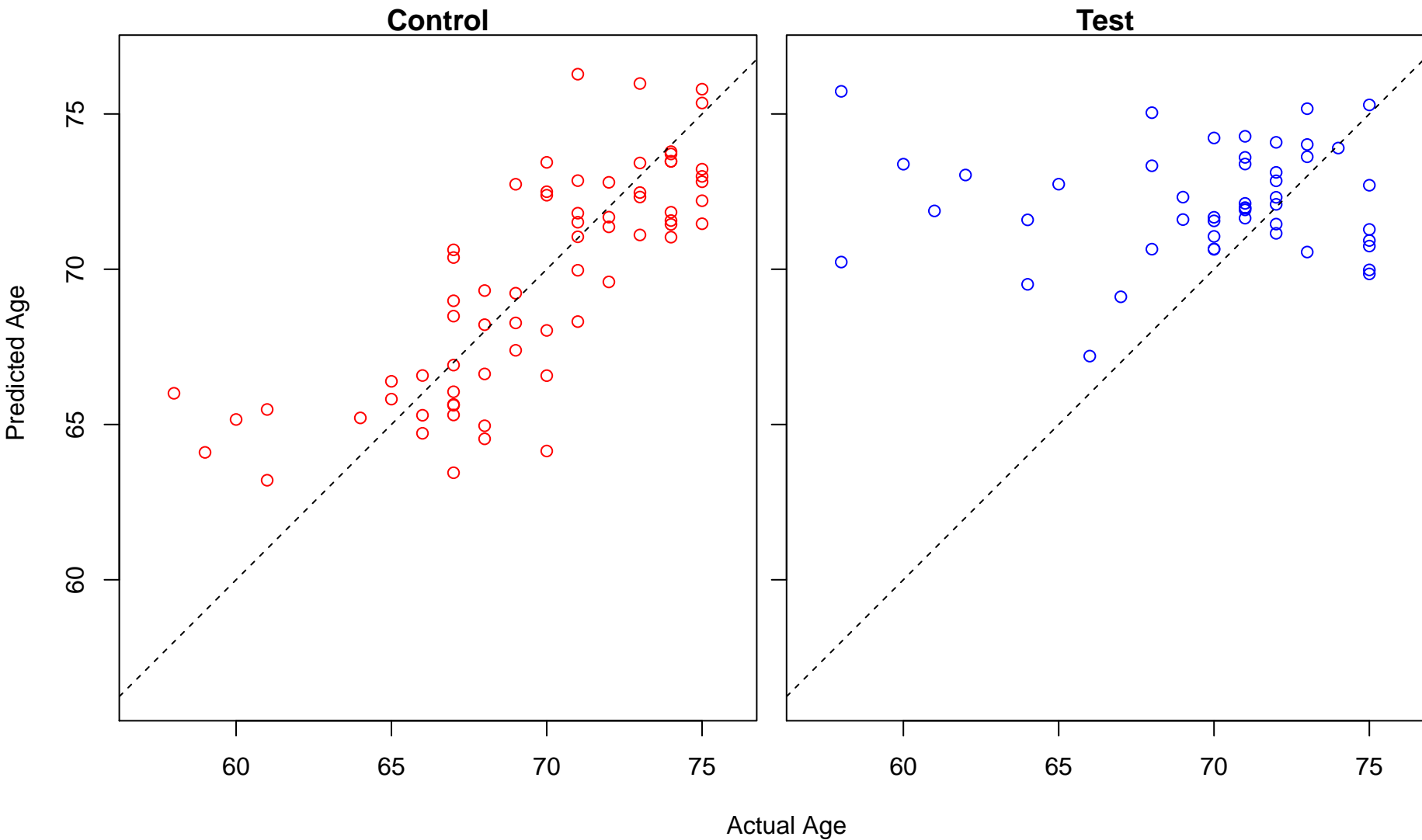
regulation of cyclin-dependent protein serine/threonine kinase activity (Score: 1.952981)



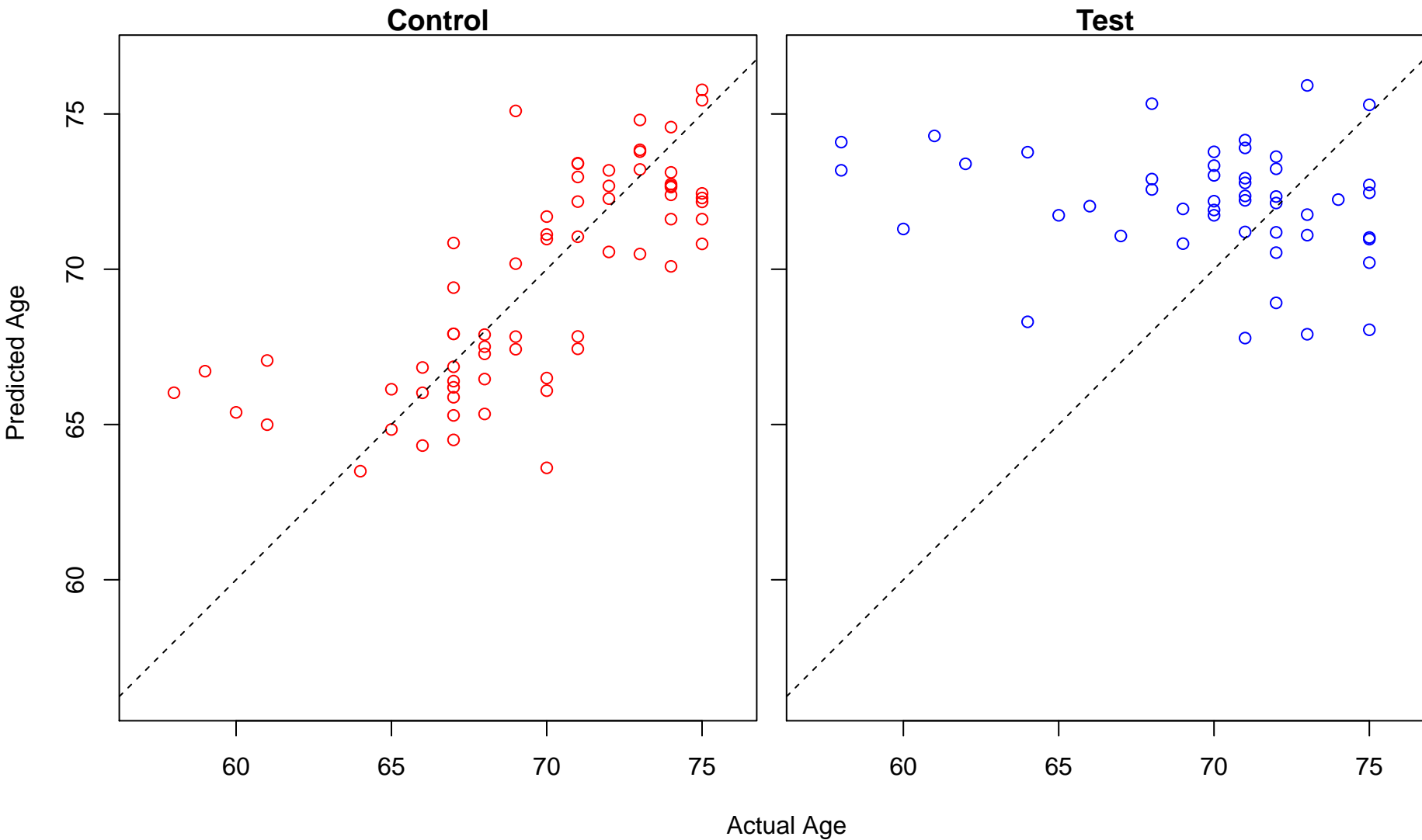
positive regulation of protein targeting to mitochondrion (Score: 1.952928)



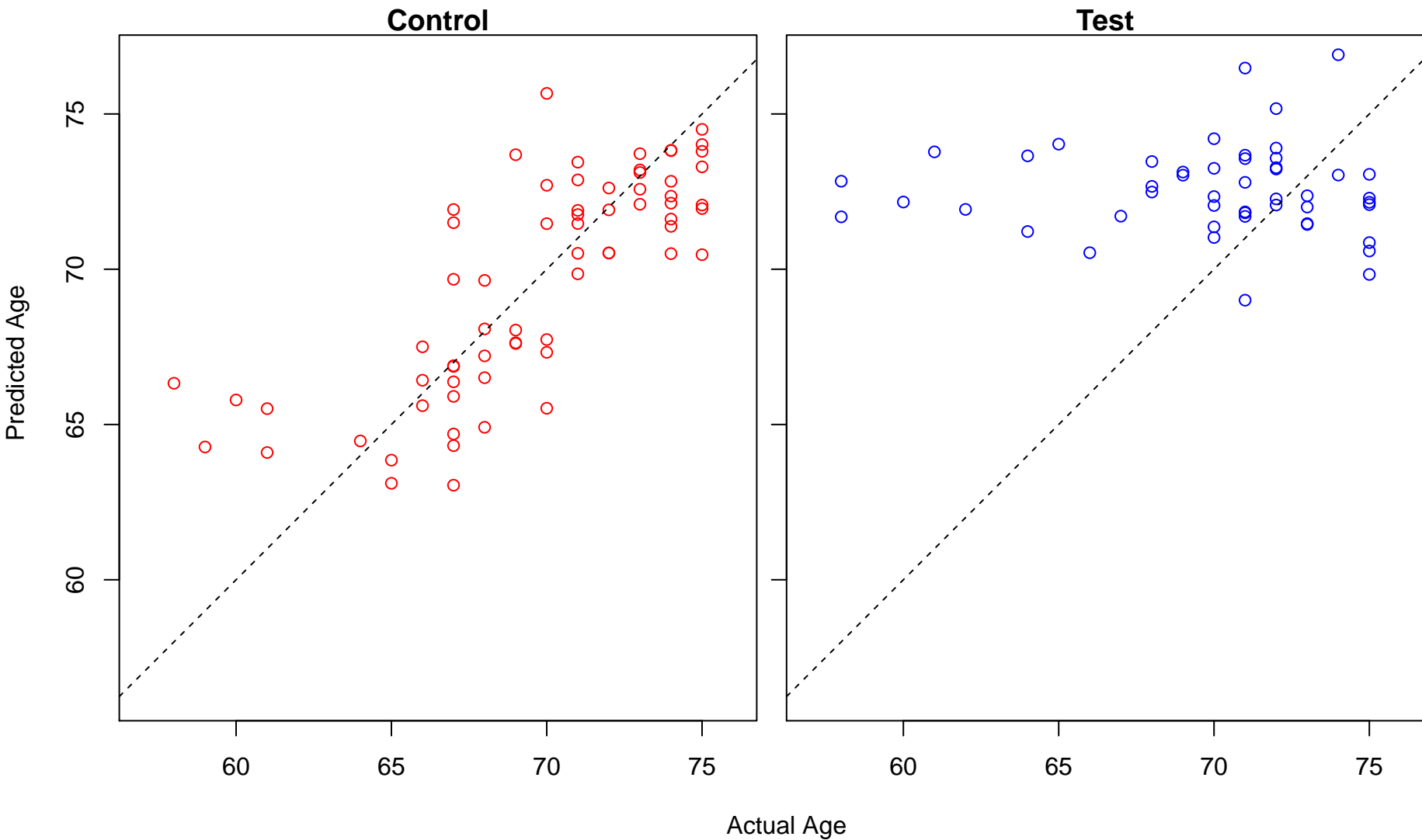
mitochondrial transport (Score: 1.952800)



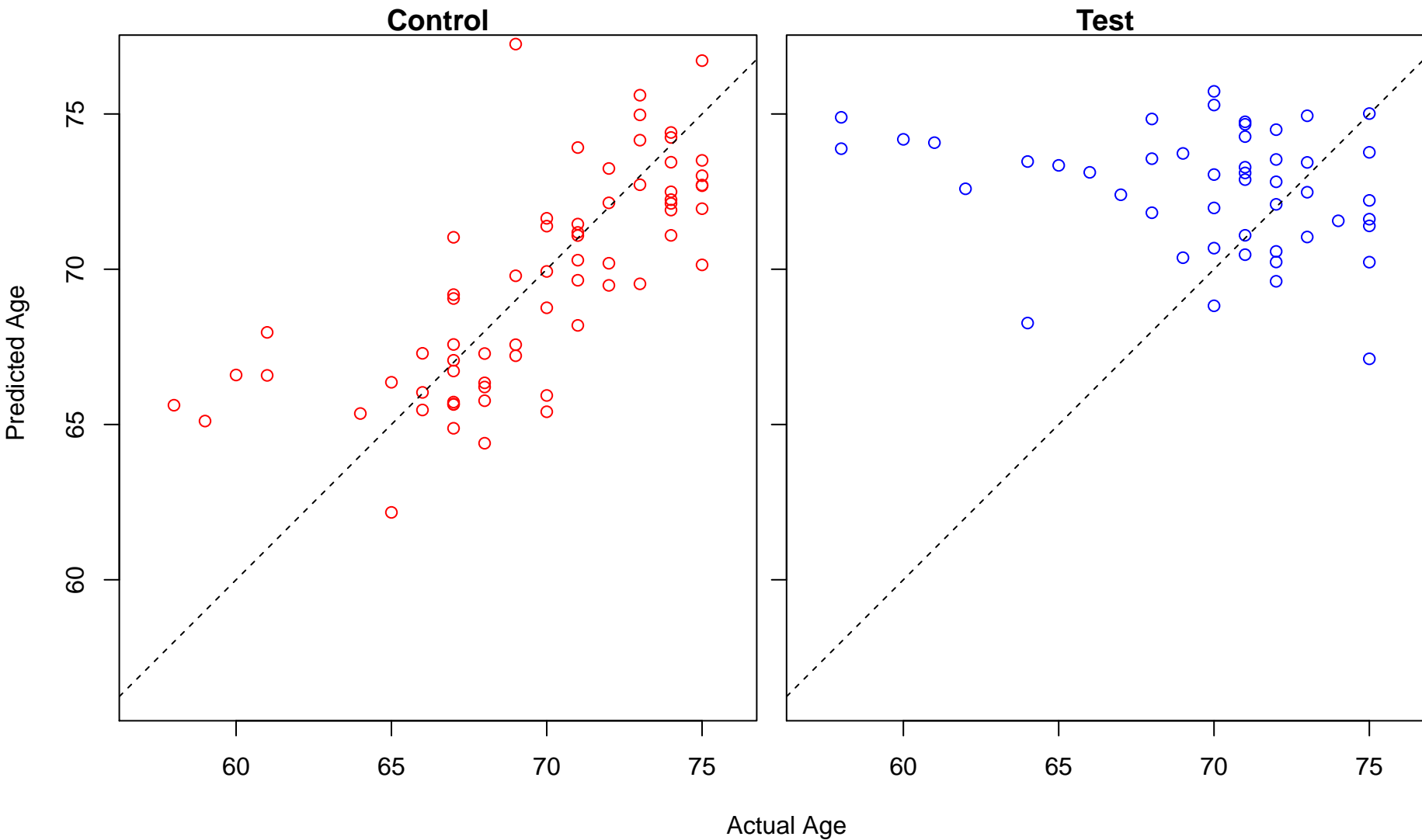
nucleobase-containing small molecule metabolic process (Score: 1.952639)



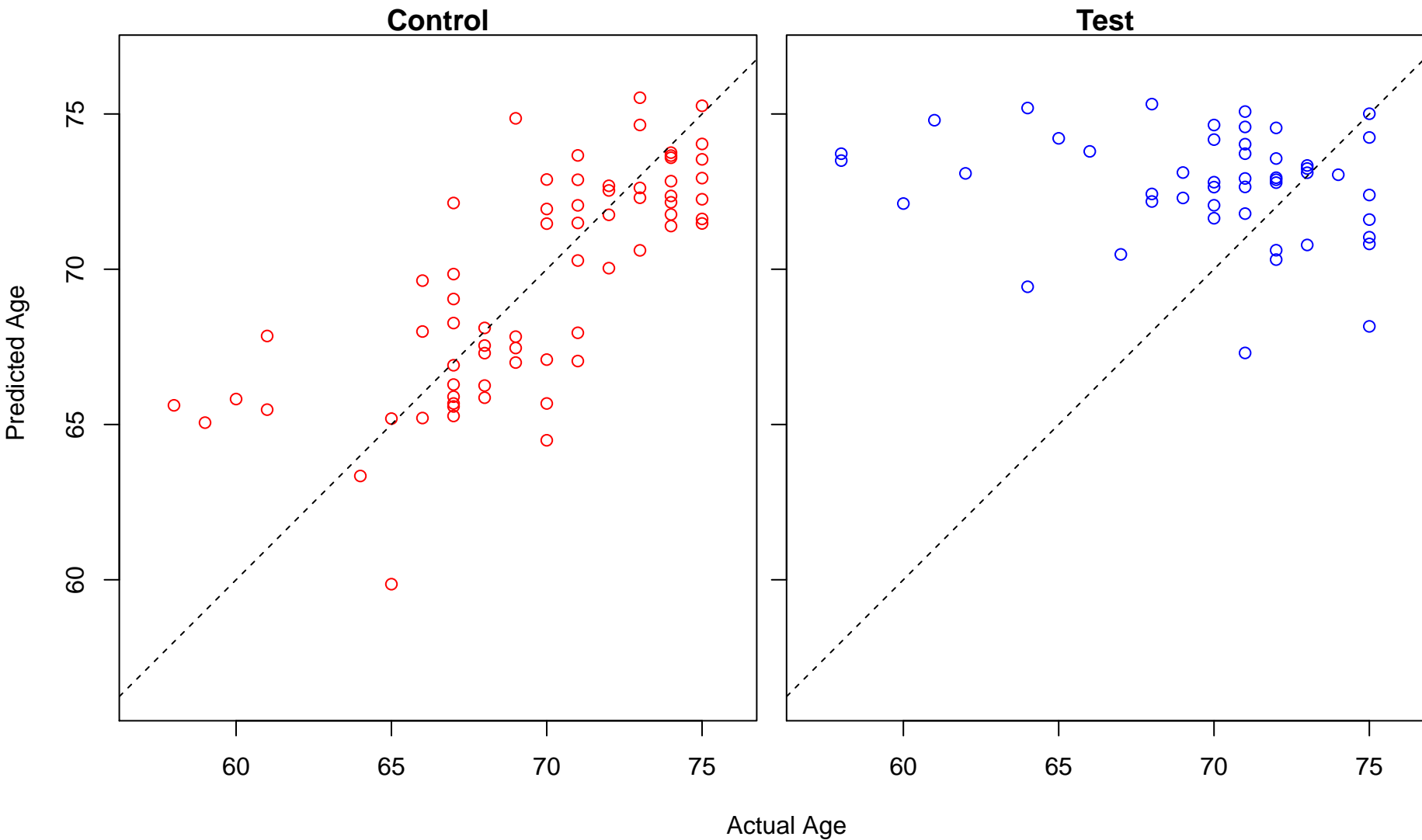
organelle fission (Score: 1.951574)



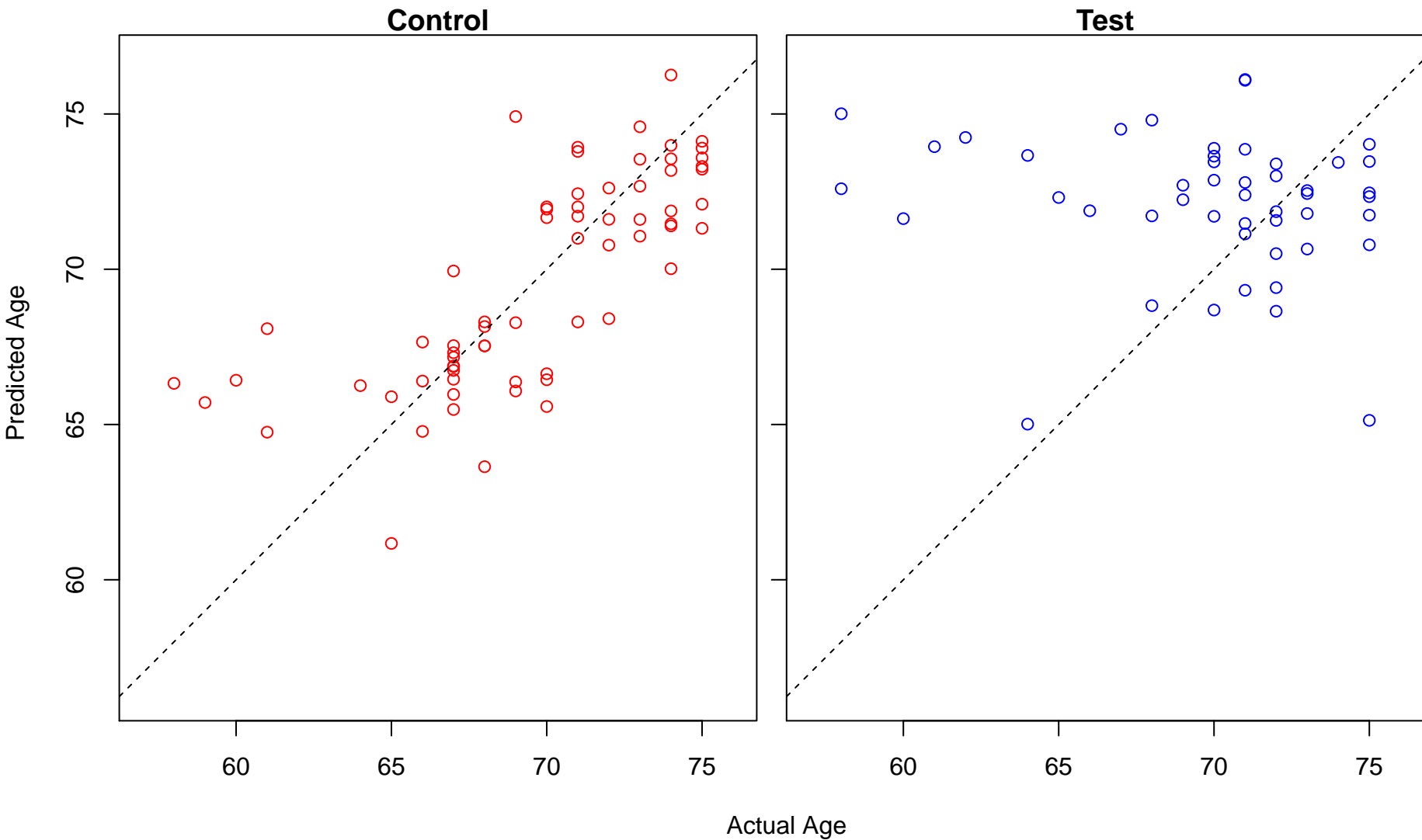
T cell receptor signaling pathway (Score: 1.951552)



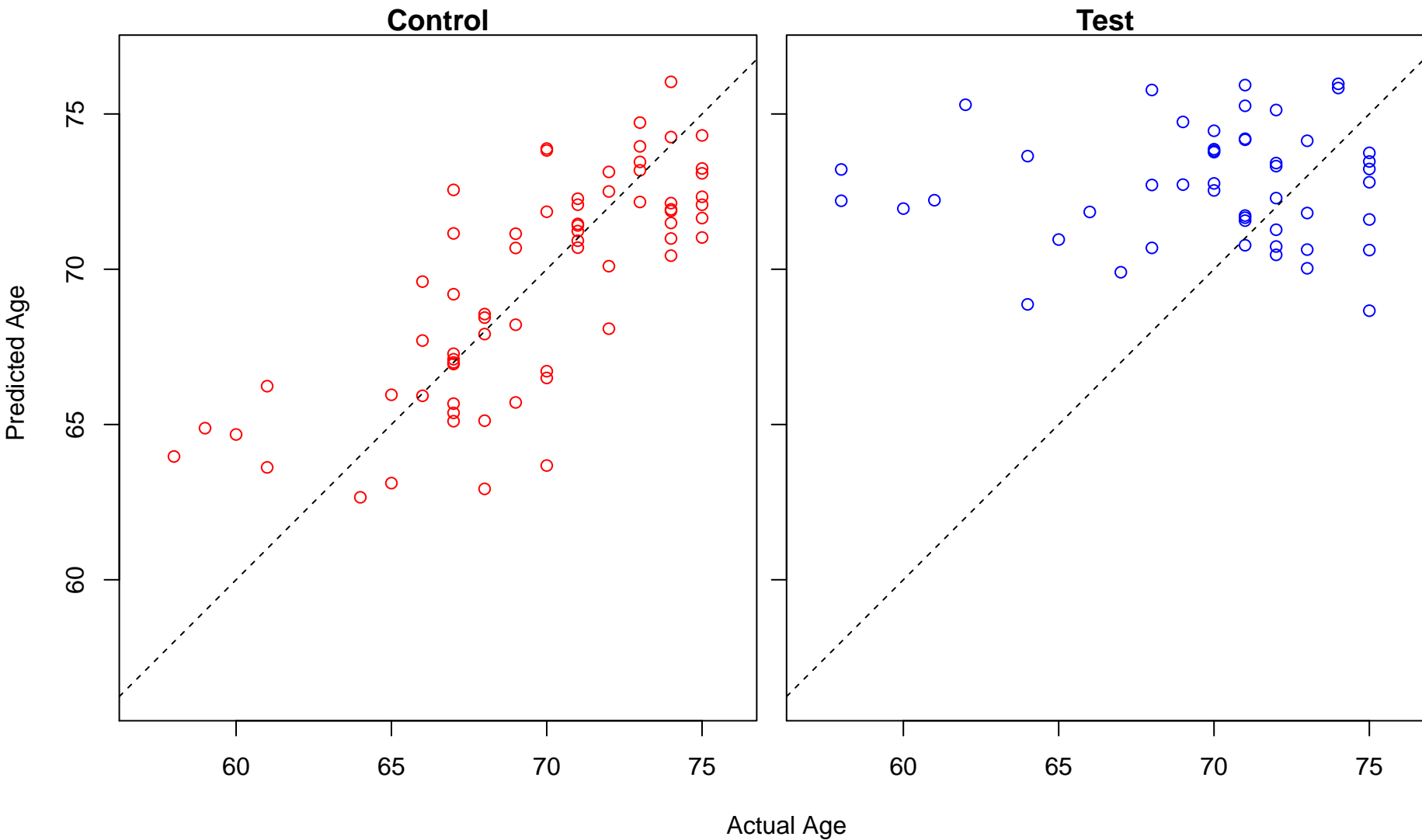
regulation of innate immune response (Score: 1.949312)



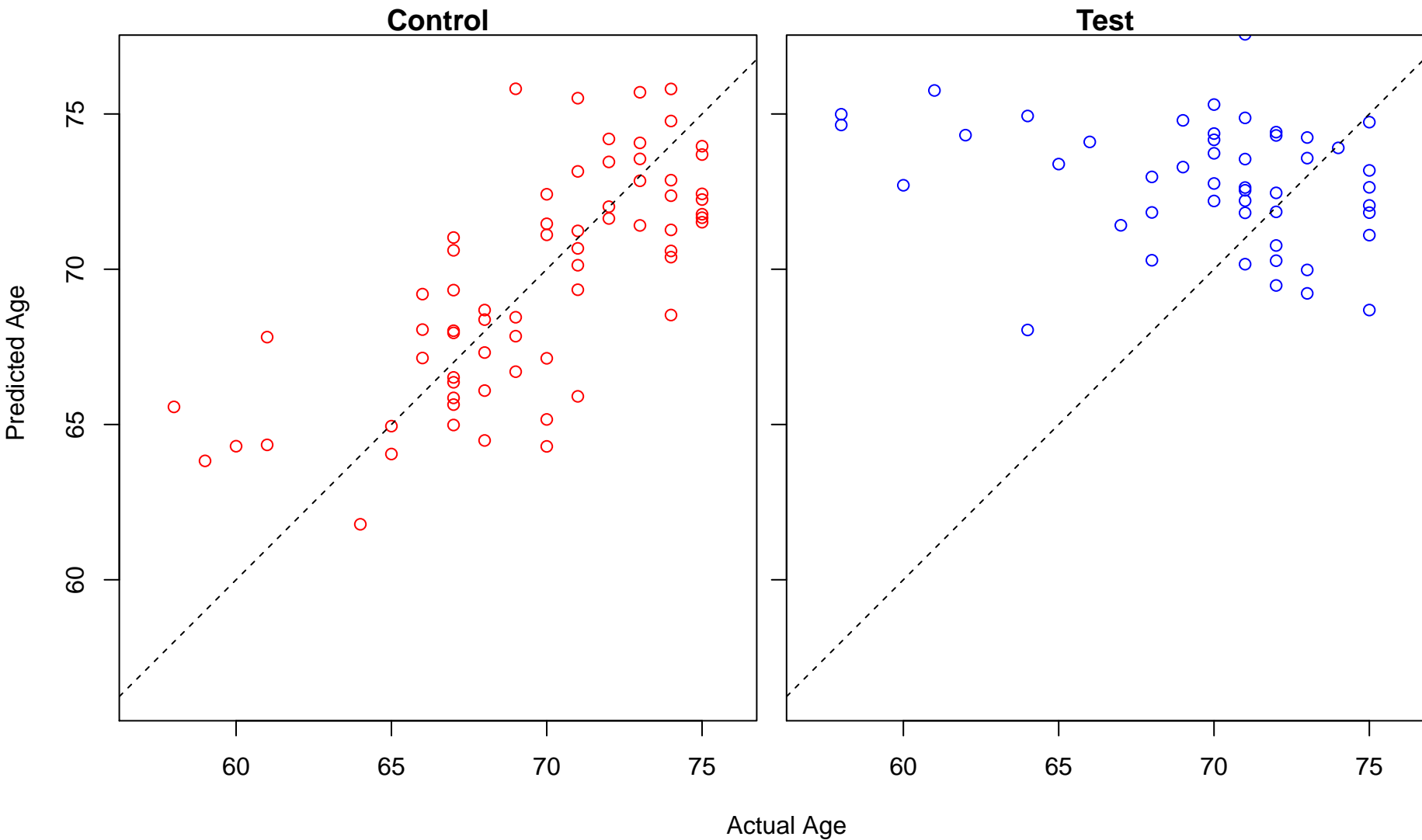
positive regulation of leukocyte migration (Score: 1.945538)



regulation of mitotic nuclear division (Score: 1.944952)

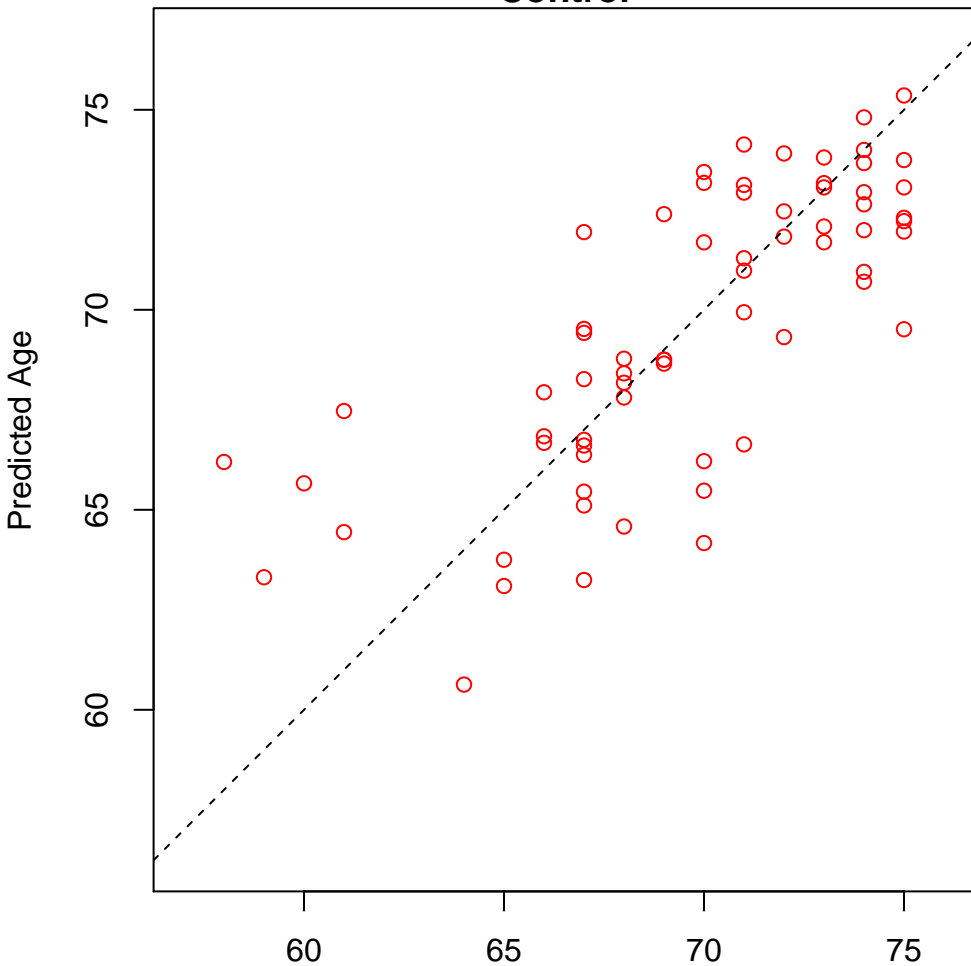


positive regulation of multi-organism process (Score: 1.943432)

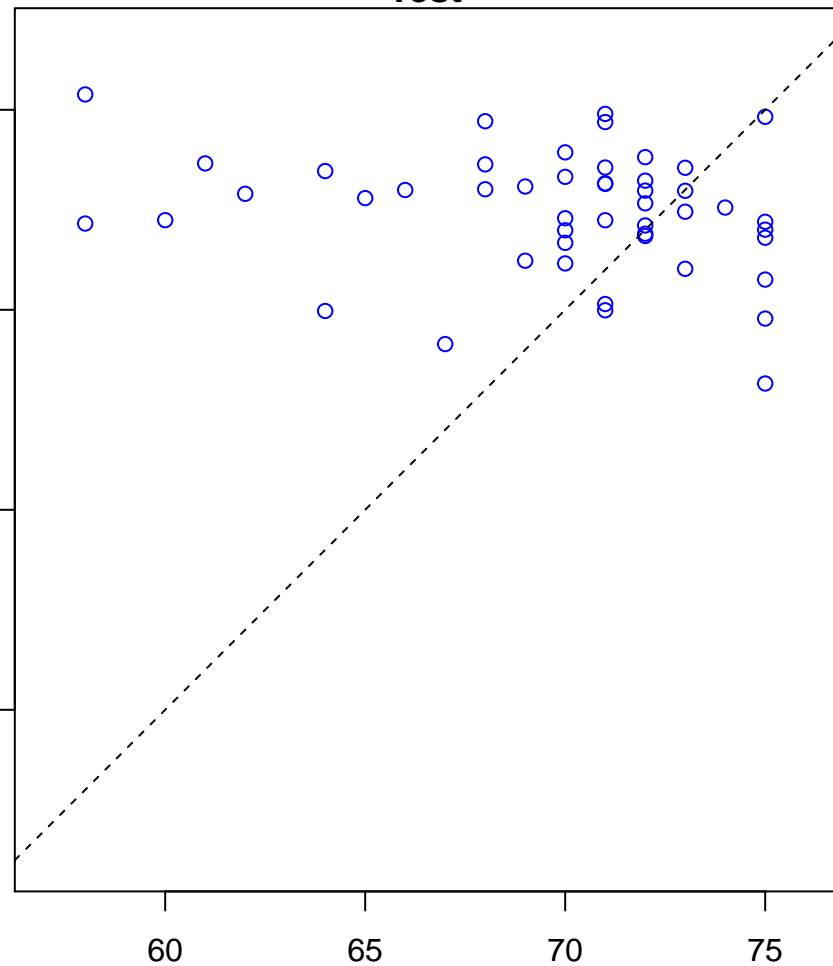


positive regulation of apoptotic process (Score: 1.941675)

Control

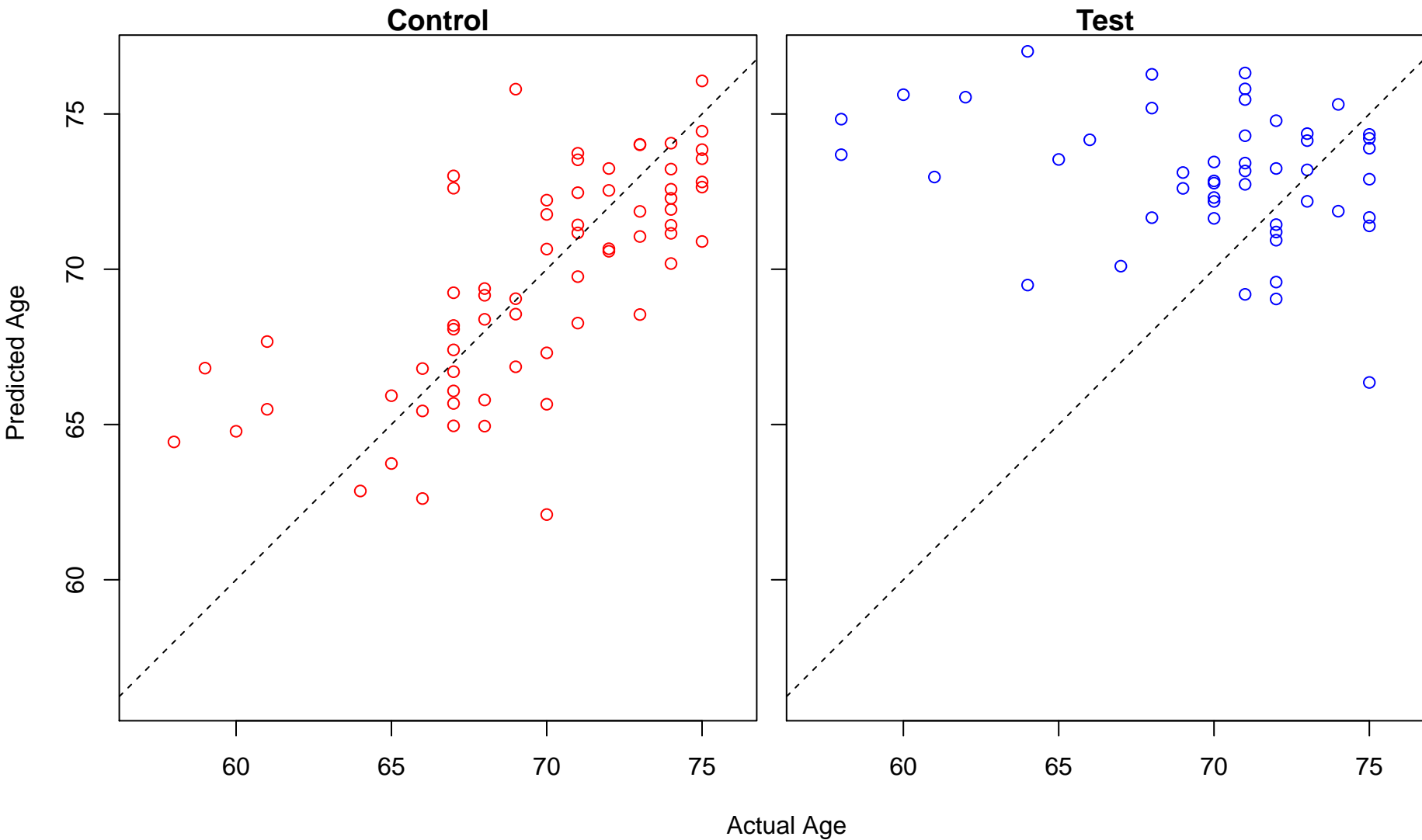


Test

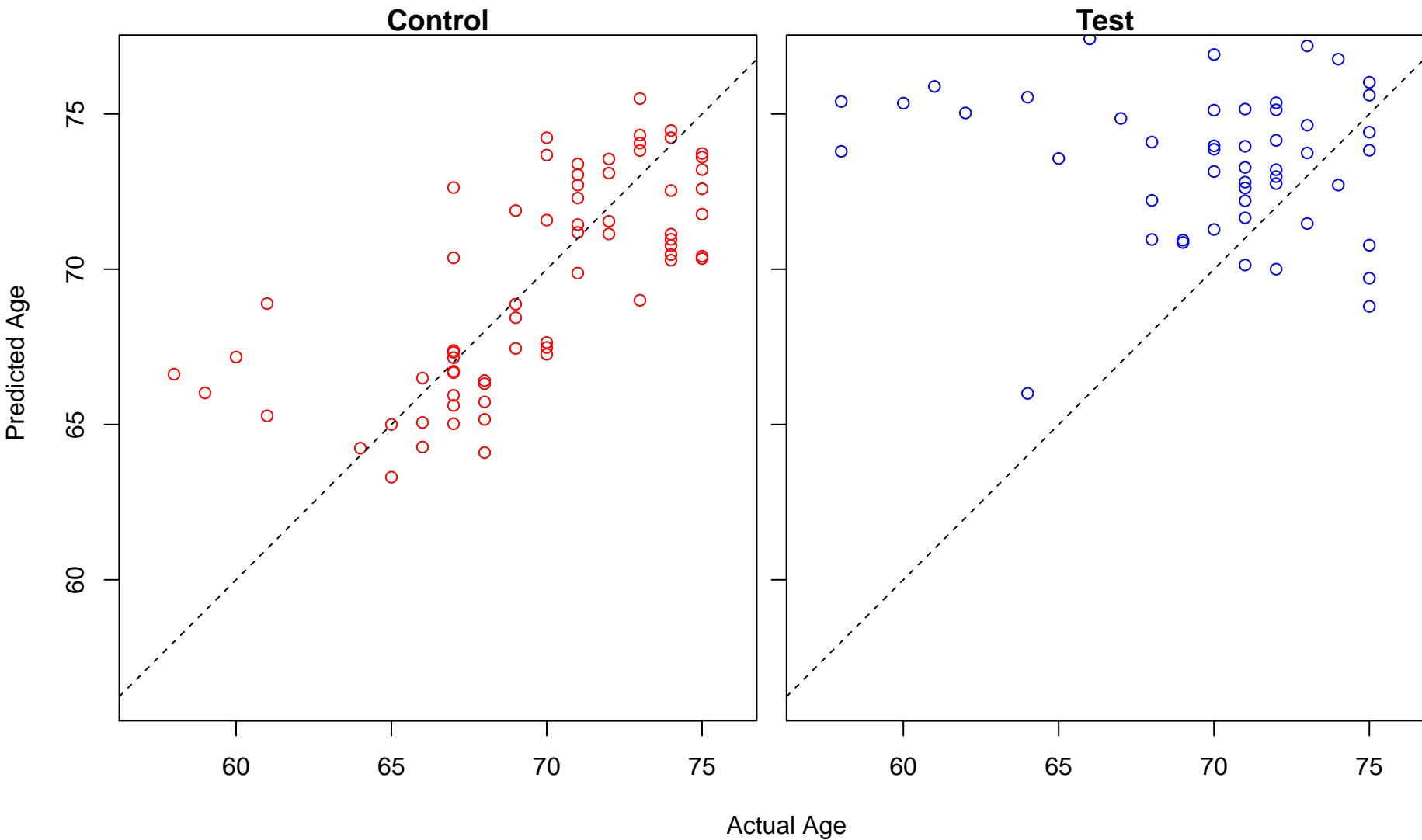


Actual Age

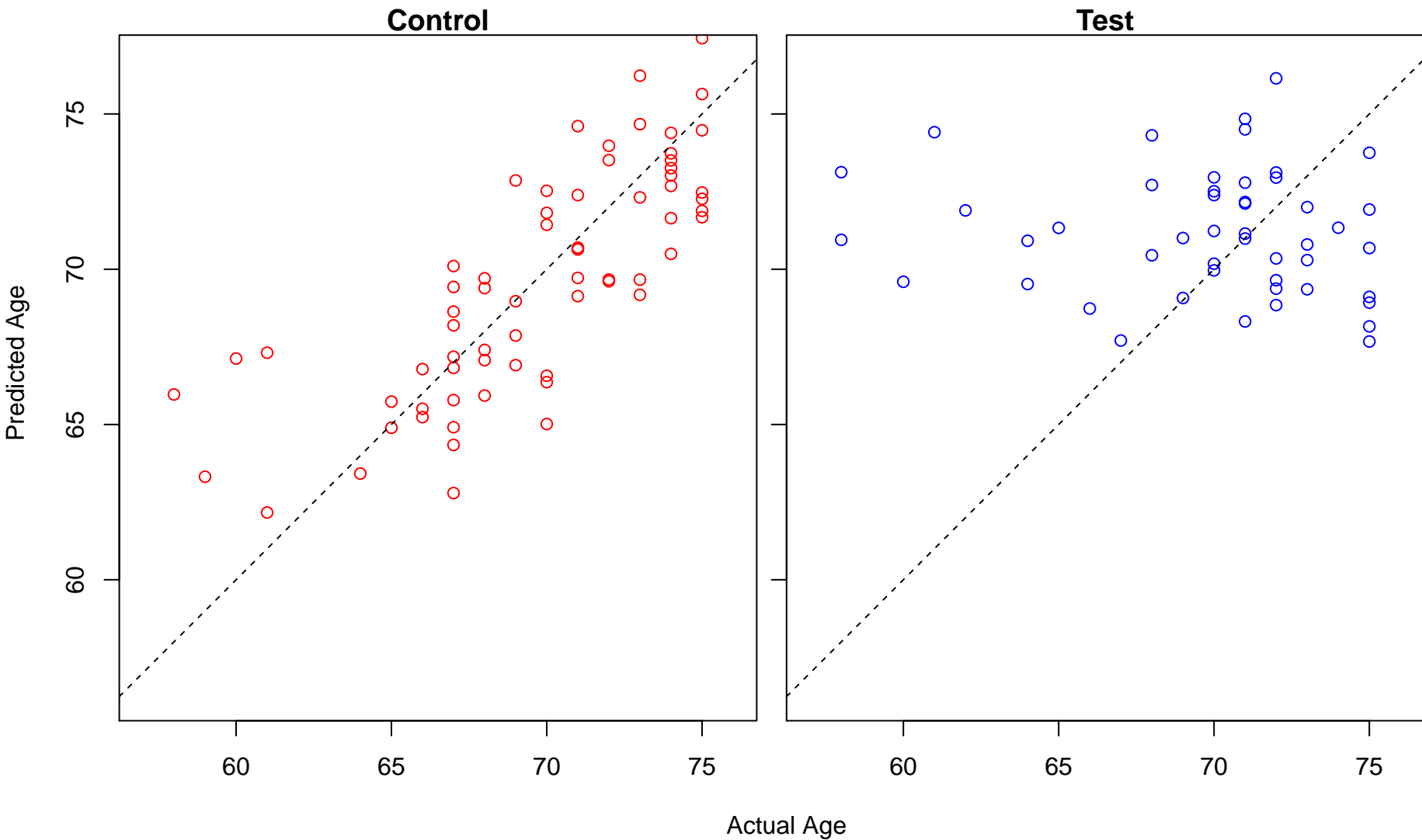
xenophagy (Score: 1.941465)



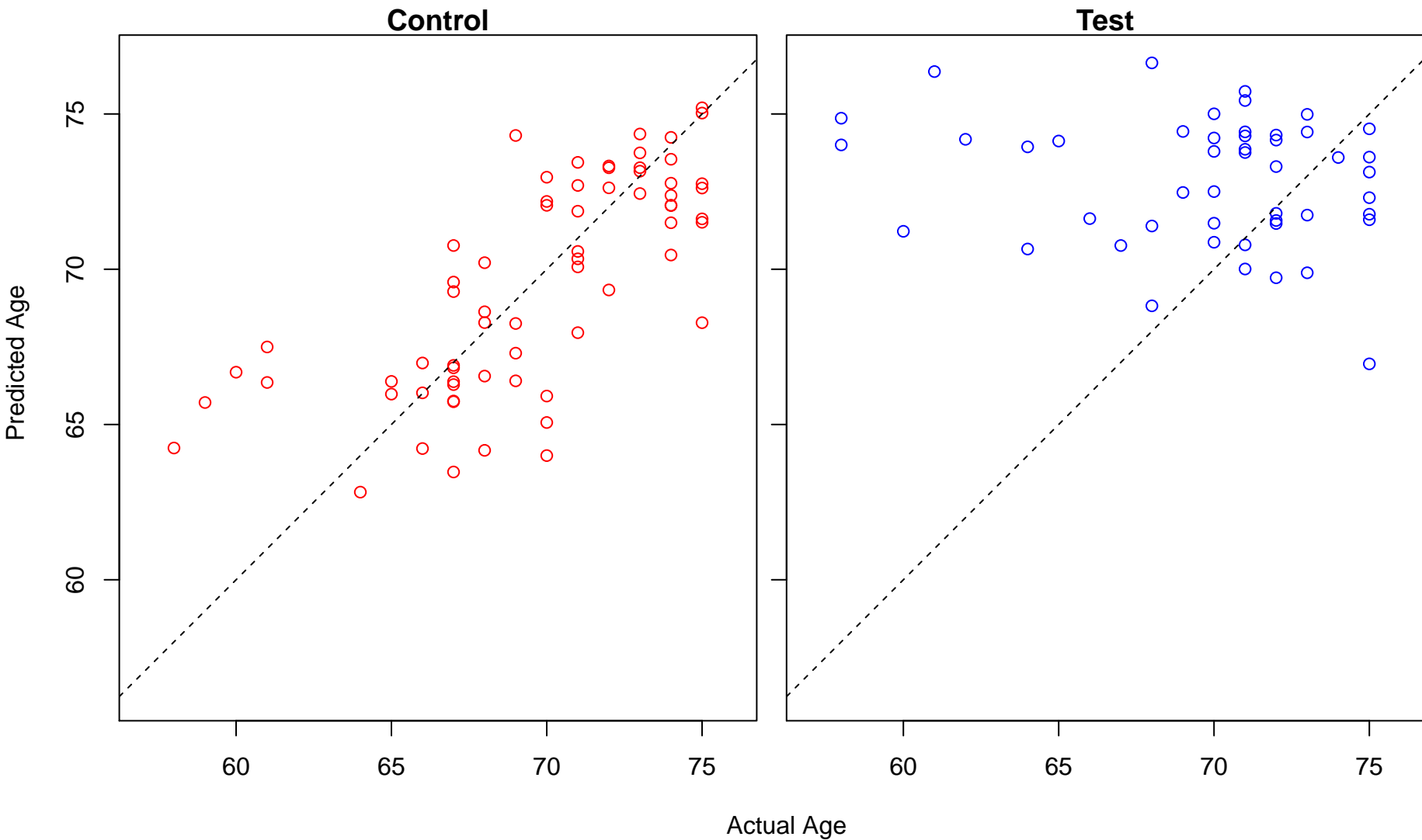
necrotic cell death (Score: 1.940091)



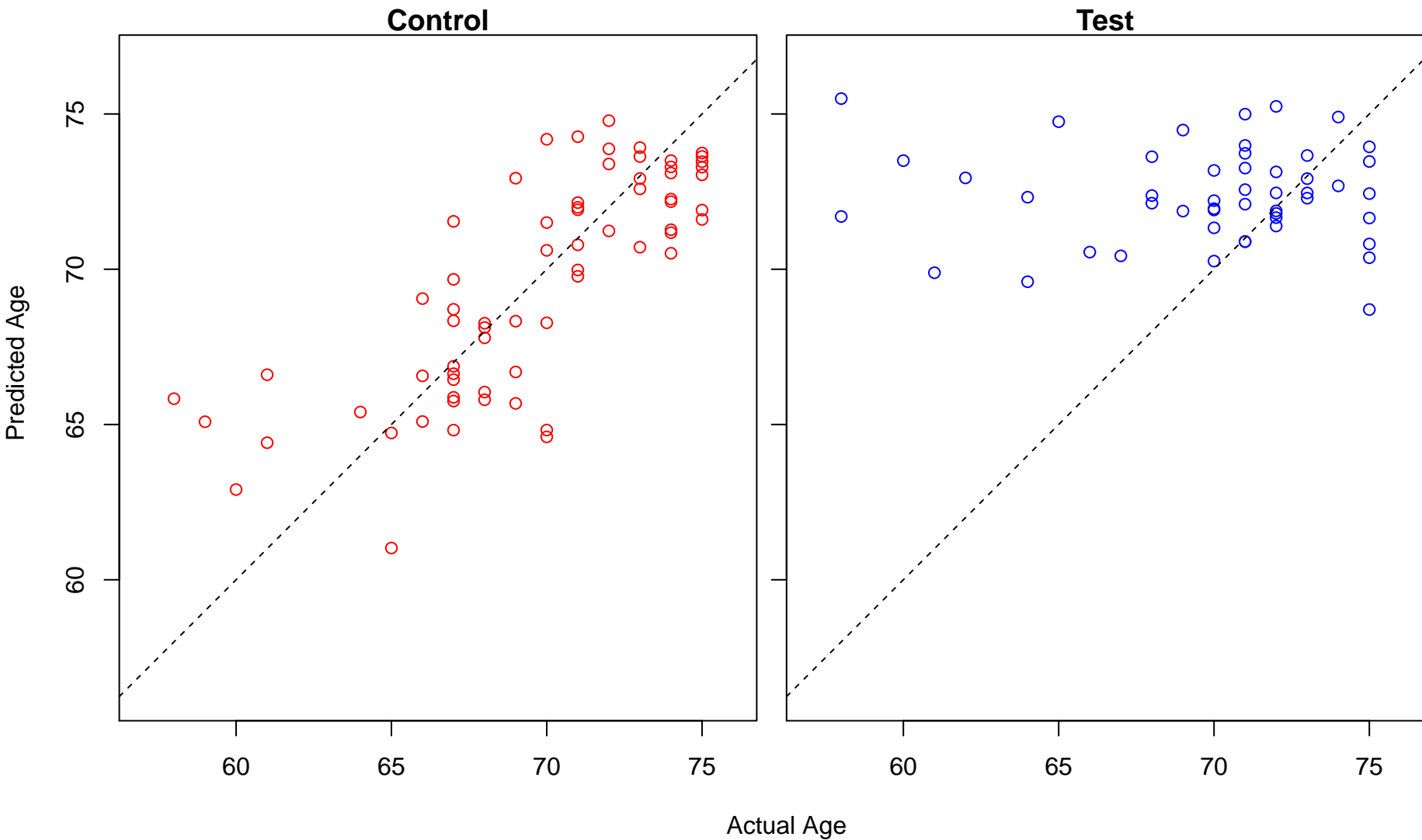
negative regulation of apoptotic signaling pathway (Score: 1.938958)



regulation of protein localization to nucleus (Score: 1.938677)

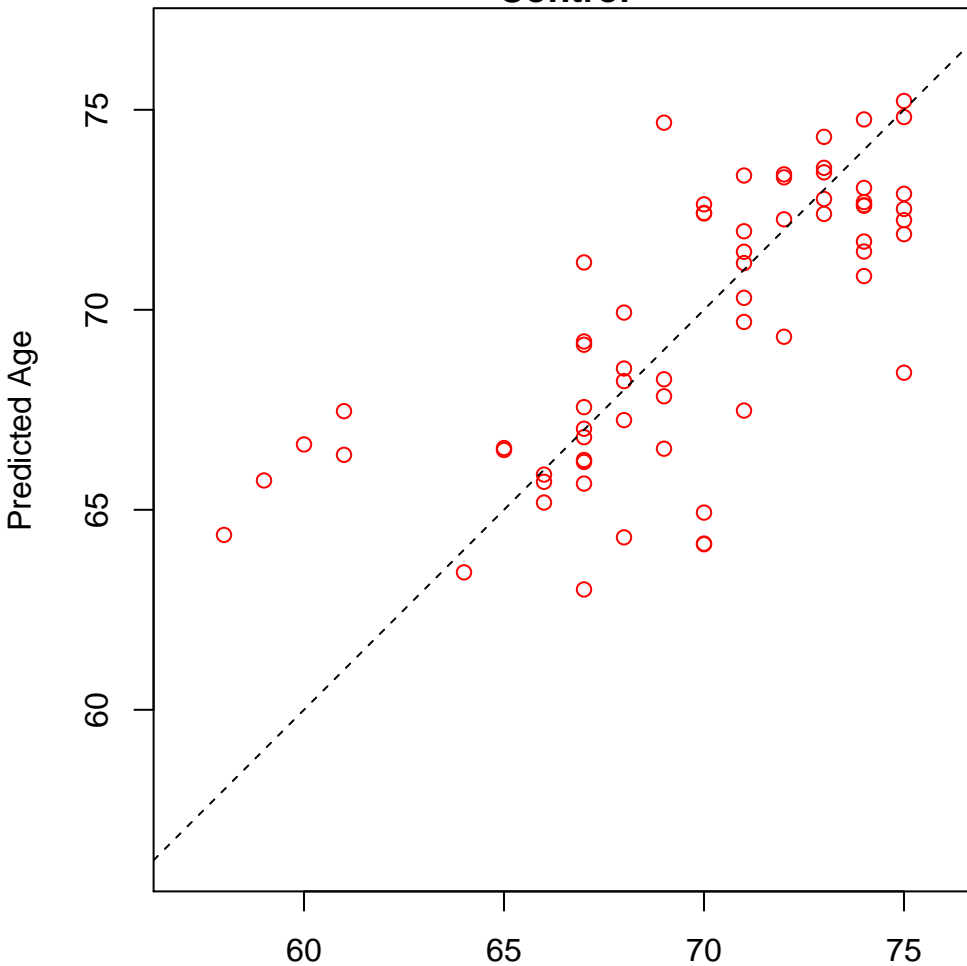


nucleocytoplasmic transport (Score: 1.937149)

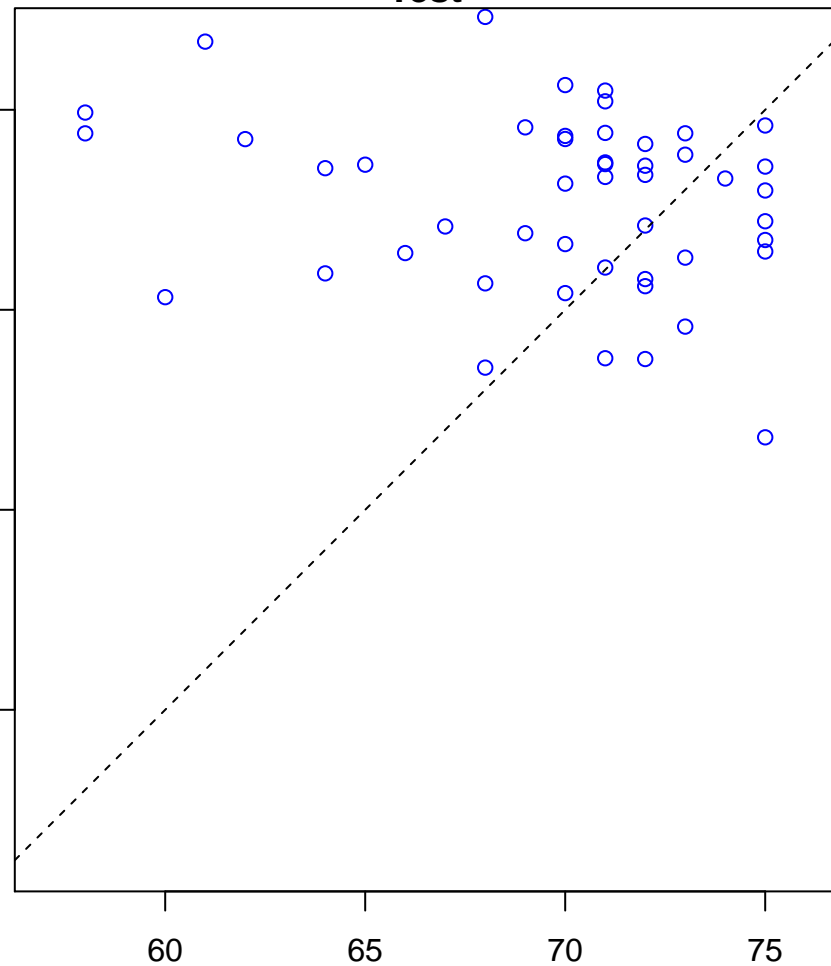


regulation of protein import into nucleus (Score: 1.936980)

Control

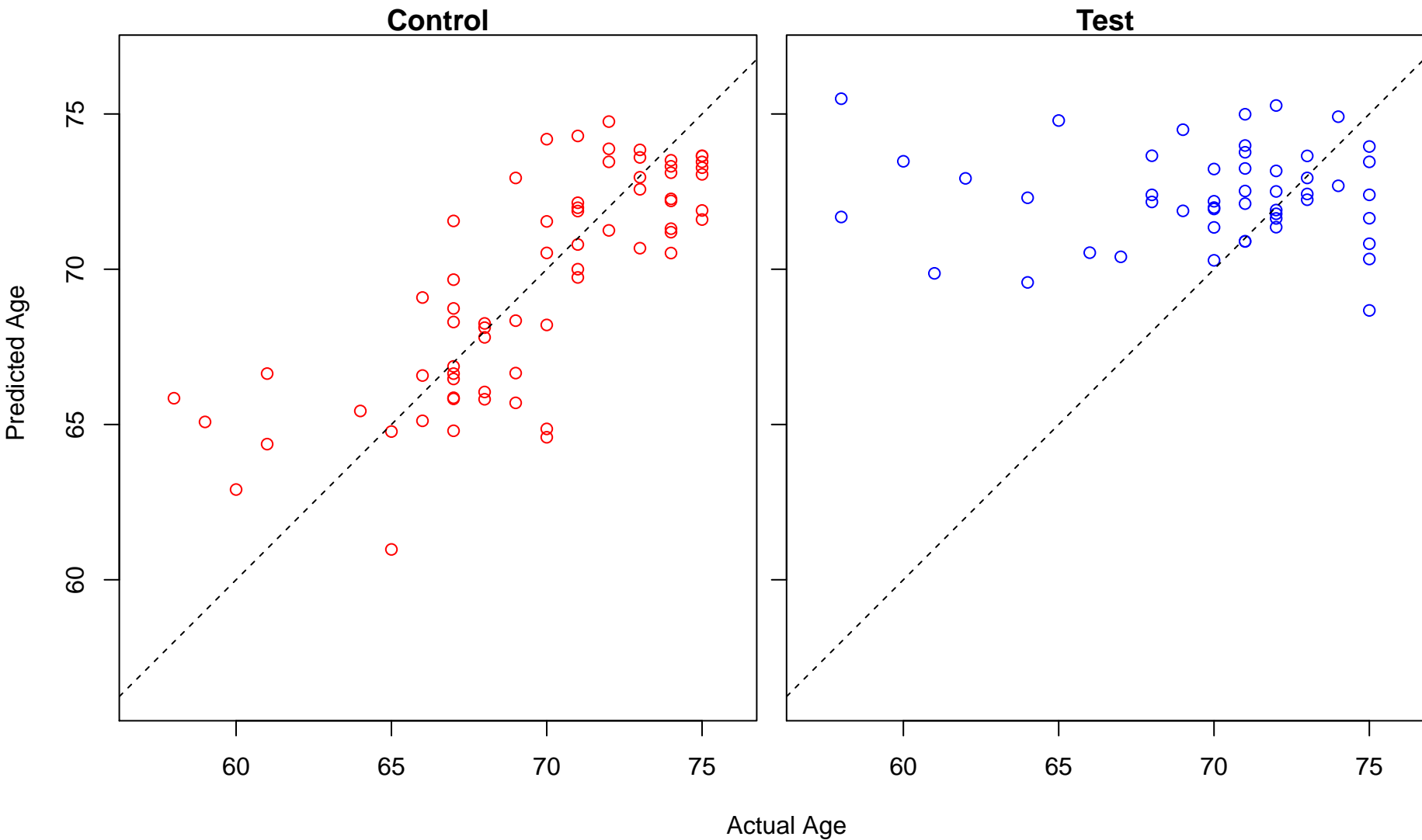


Test

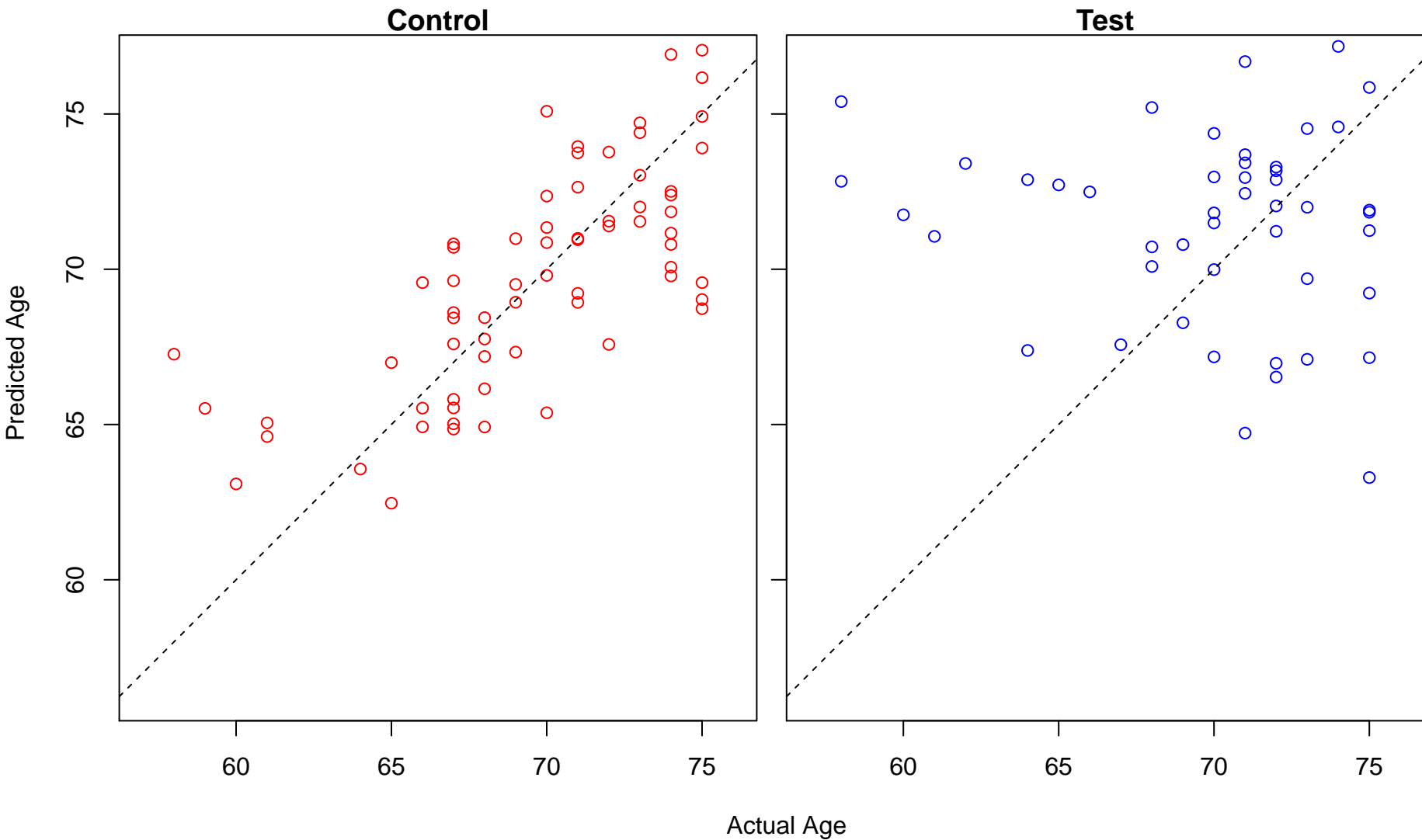


Actual Age

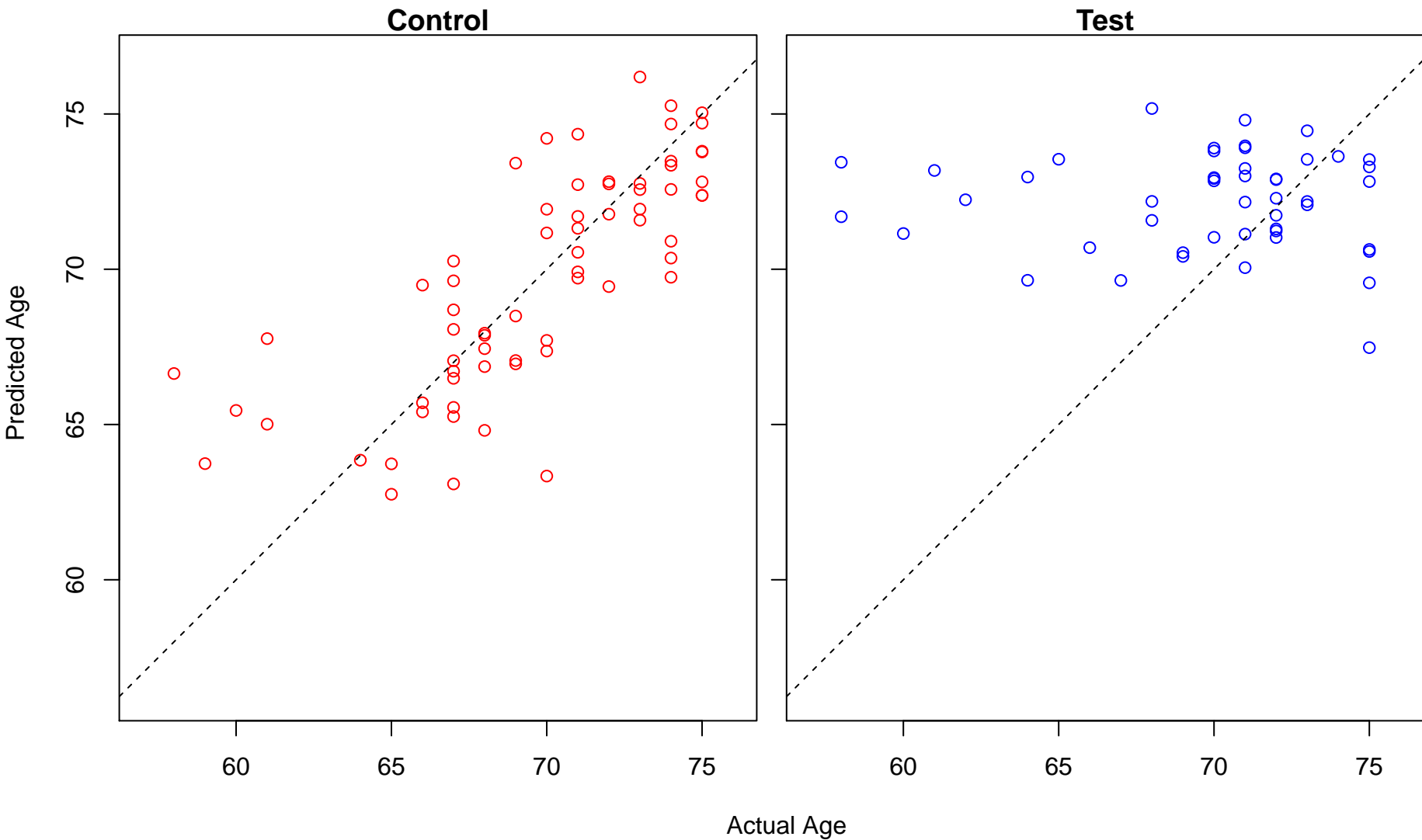
nuclear transport (Score: 1.936697)



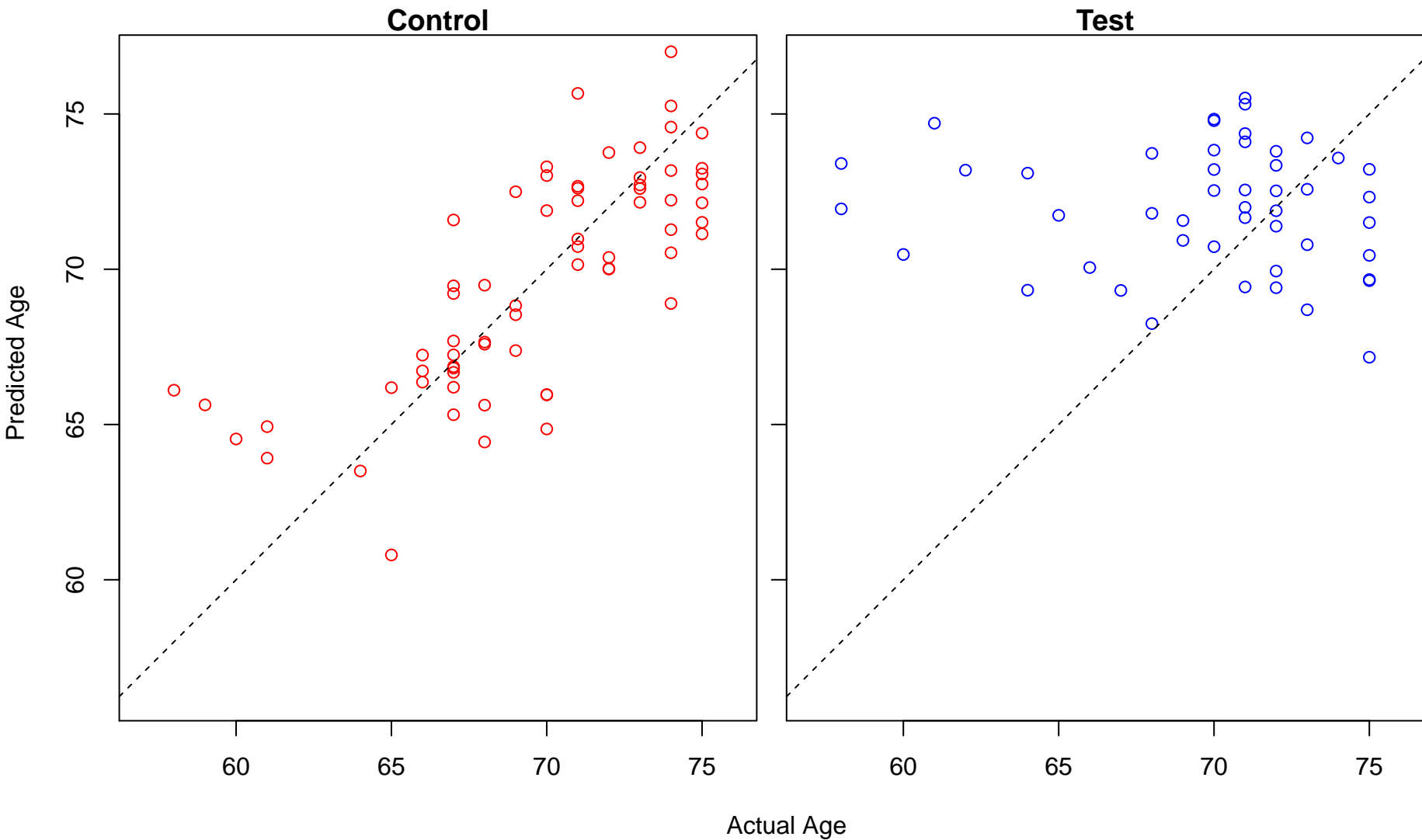
positive regulation of cell-substrate adhesion (Score: 1.936155)



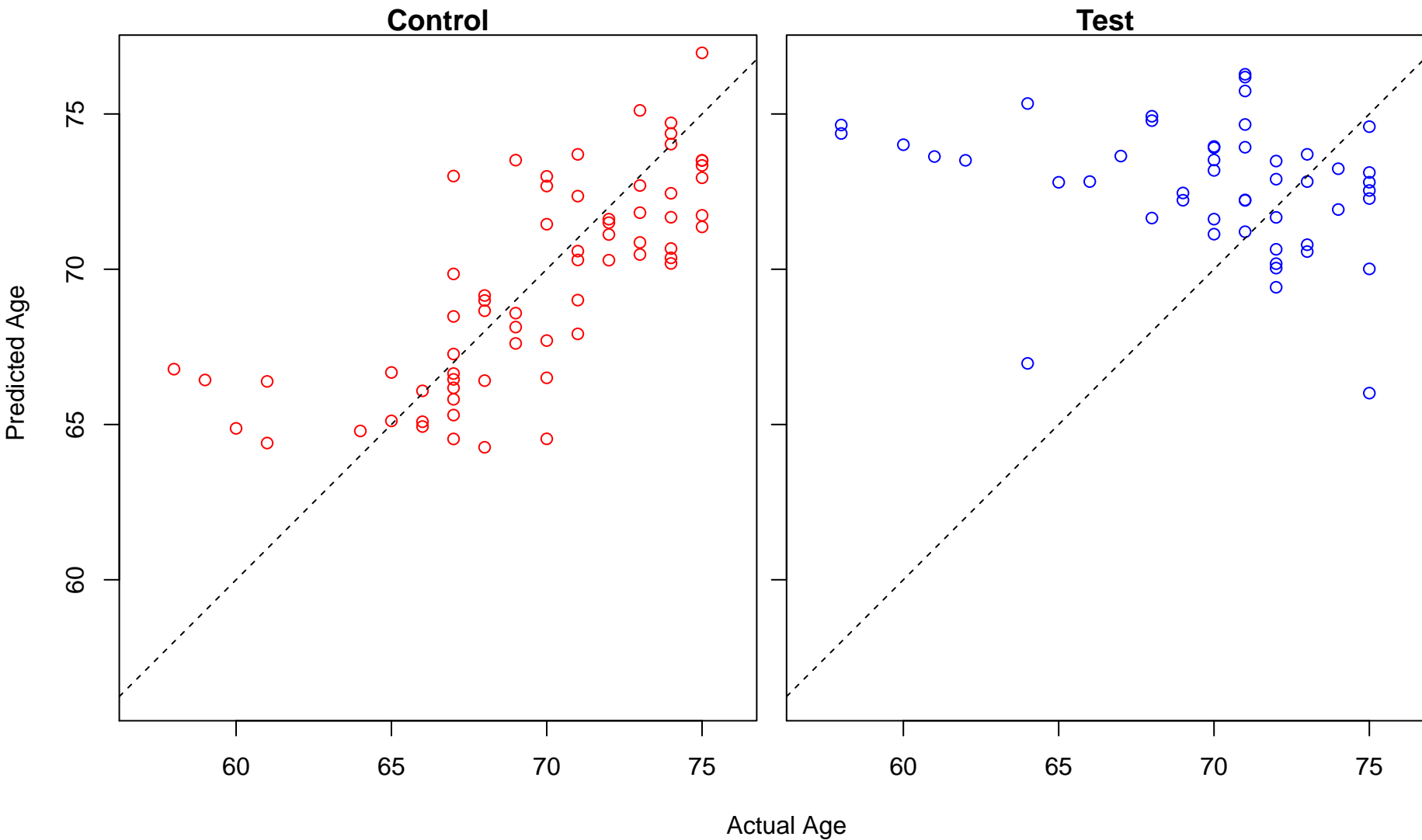
cellular response to insulin stimulus (Score: 1.934837)



nucleus organization (Score: 1.934050)

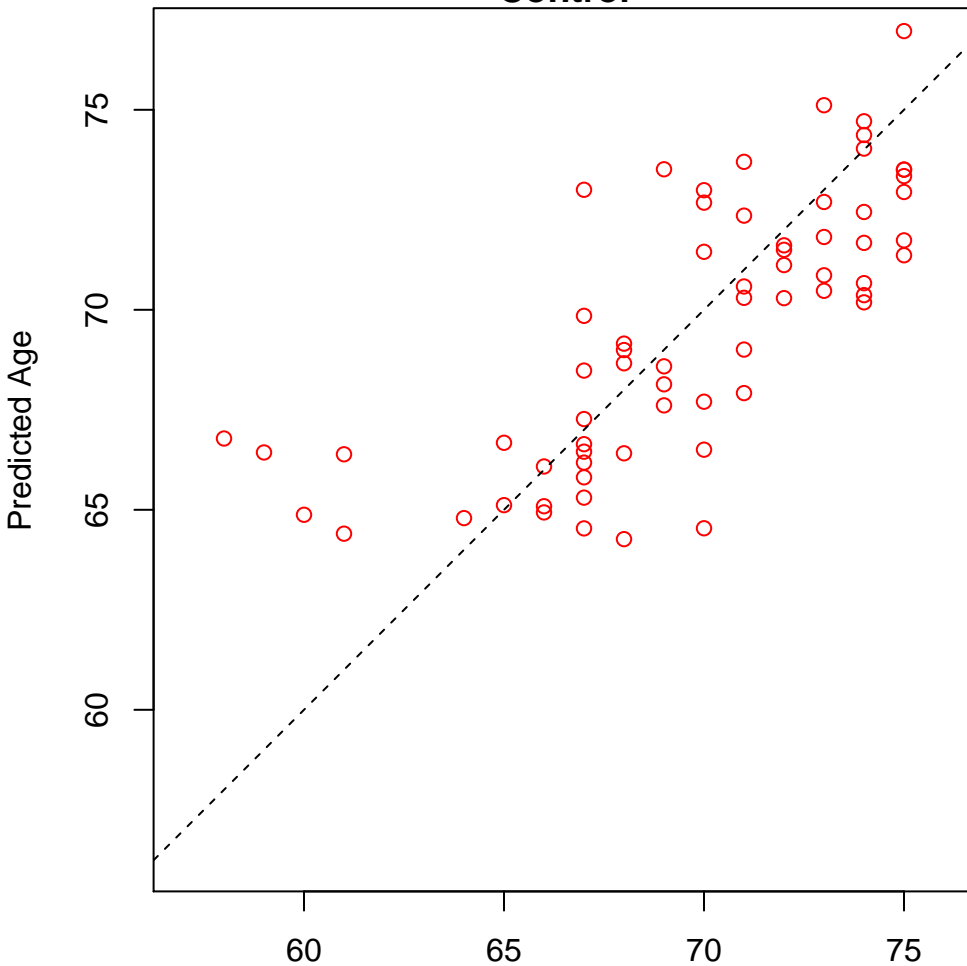


mitophagy in response to mitochondrial depolarization (Score: 1.933326)

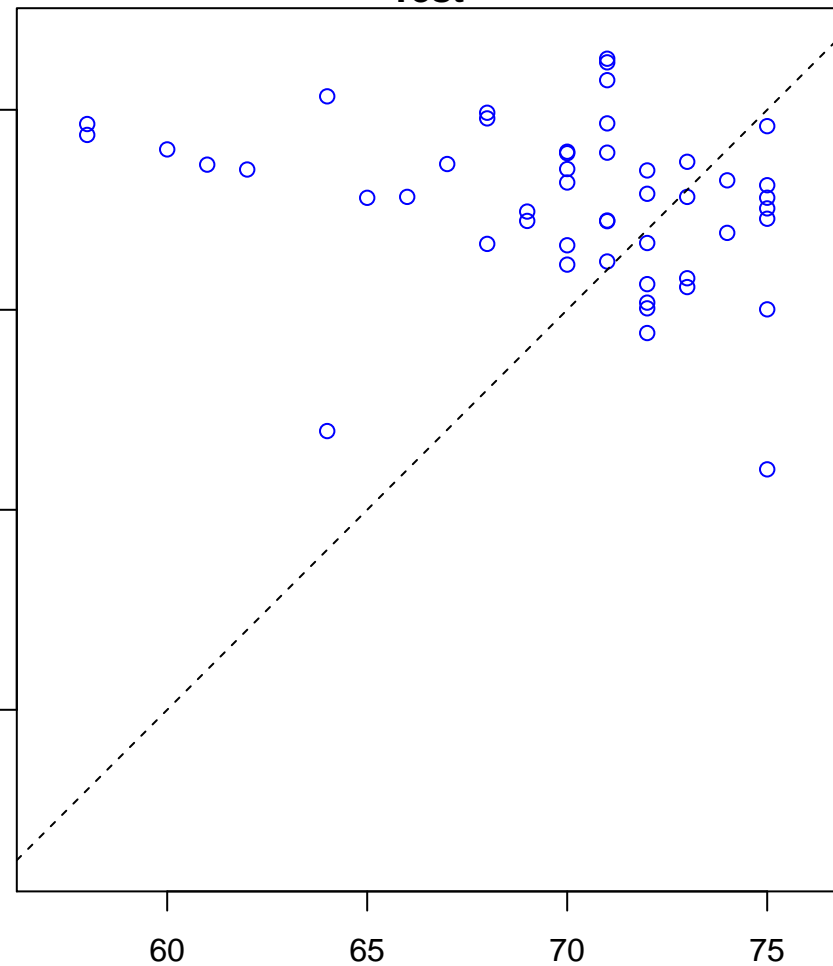


response to mitochondrial depolarisation (Score: 1.93326)

Control

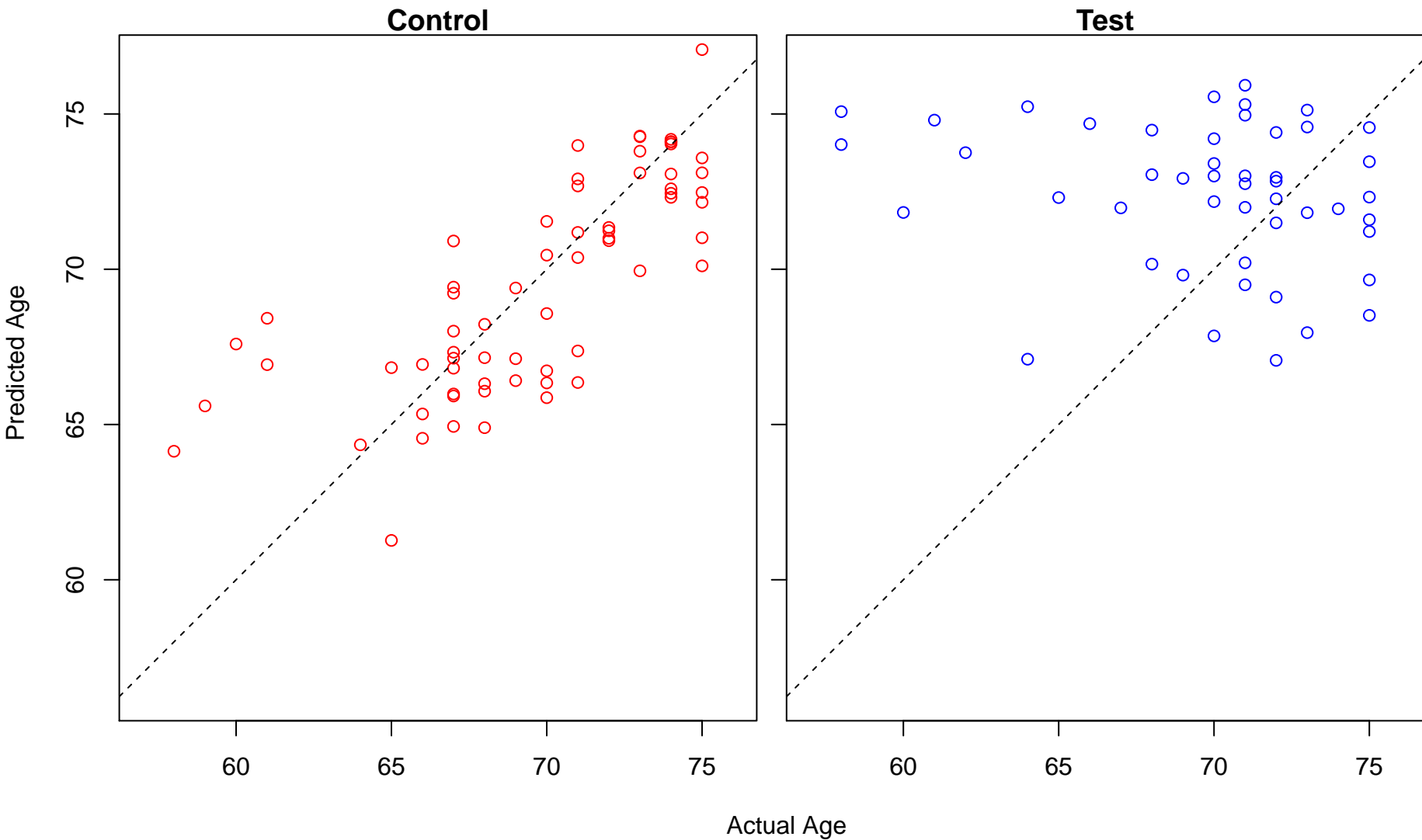


Test

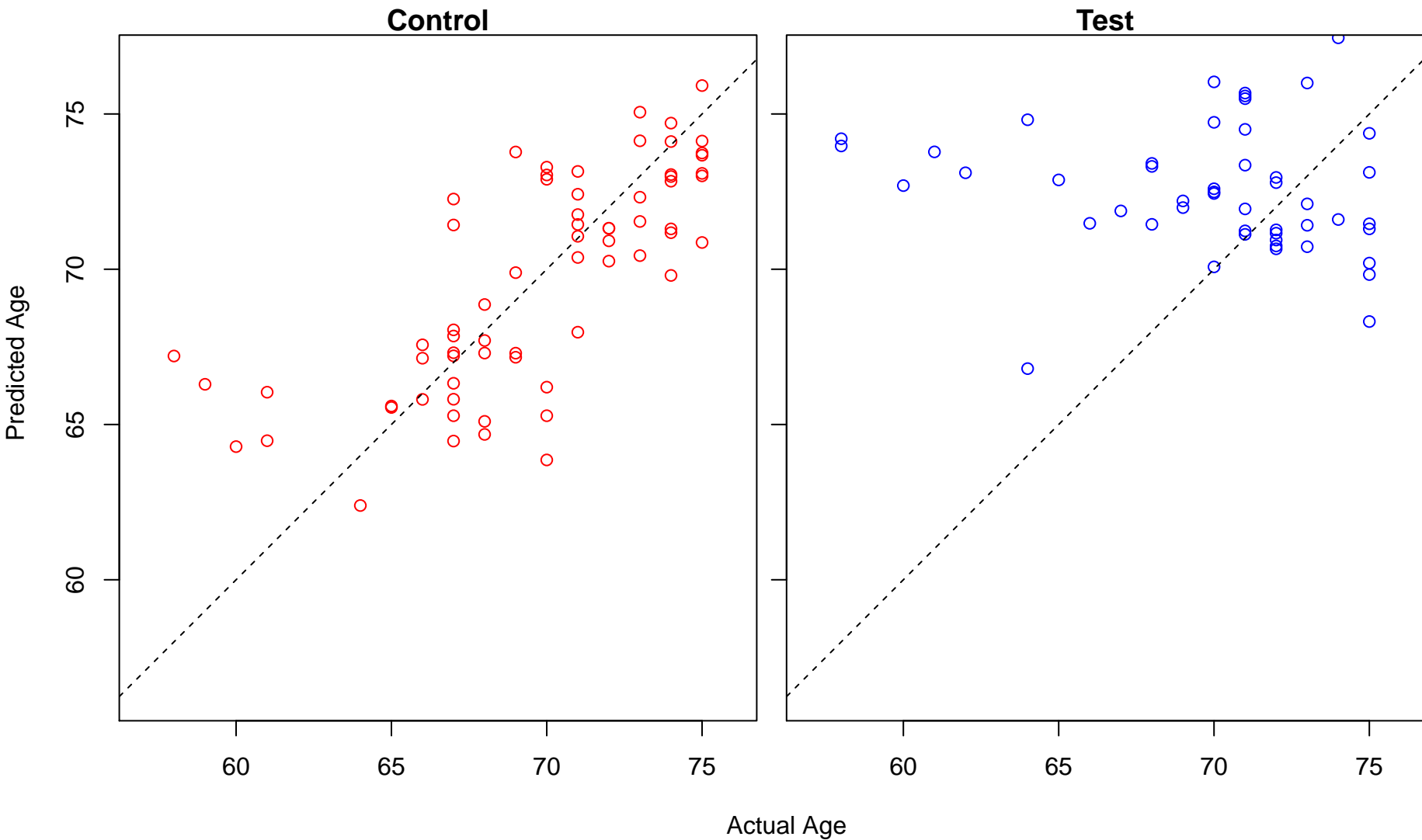


Actual Age

response to interferon-gamma (Score: 1.930980)

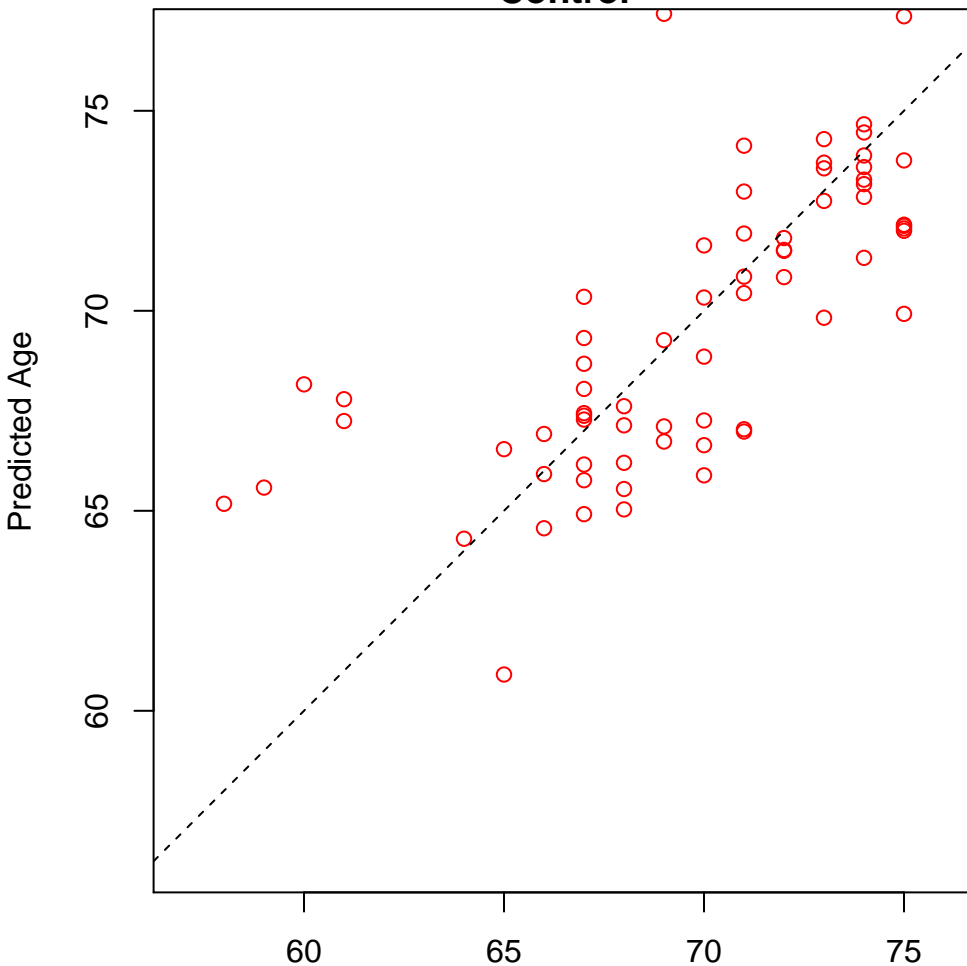


organelle disassembly (Score: 1.930100)

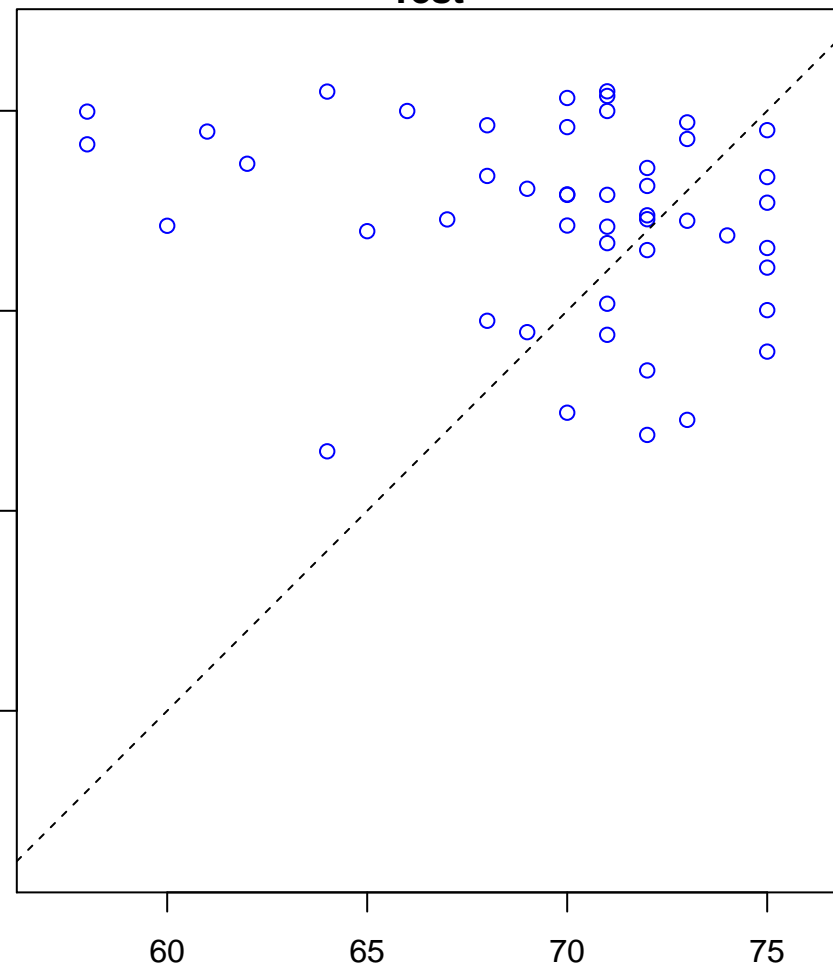


cellular response to interferon-gamma (Score: 1.929388)

Control

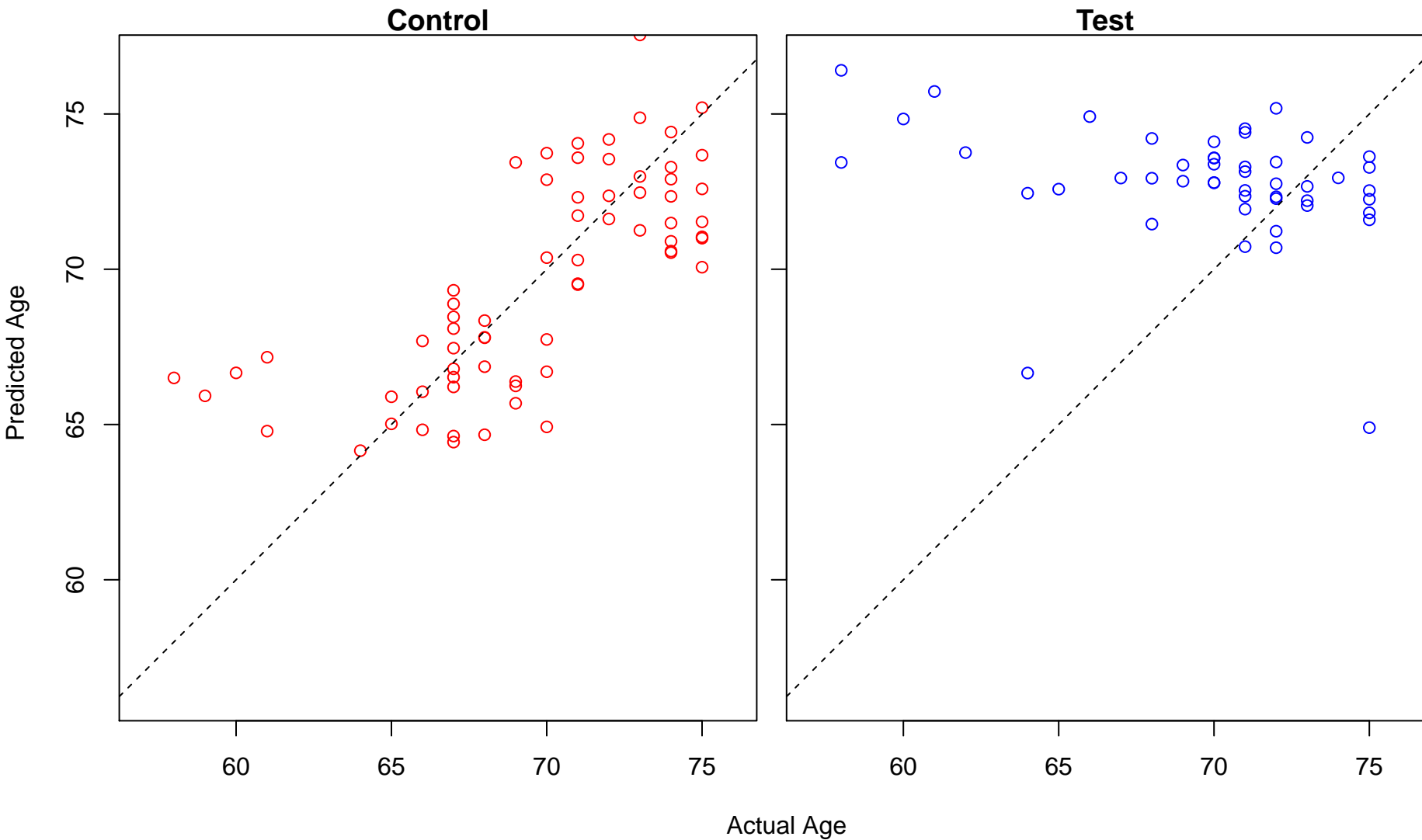


Test

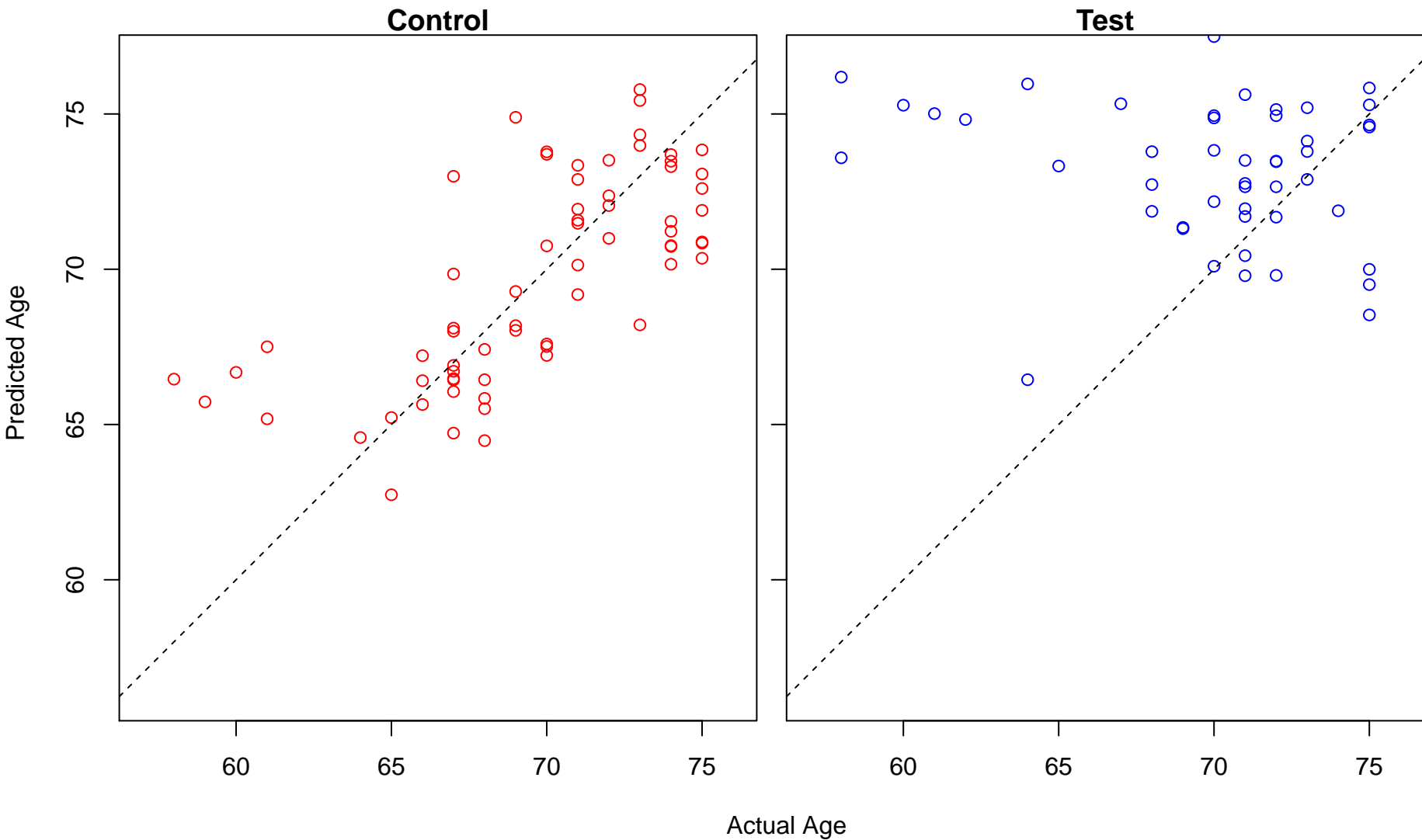


Actual Age

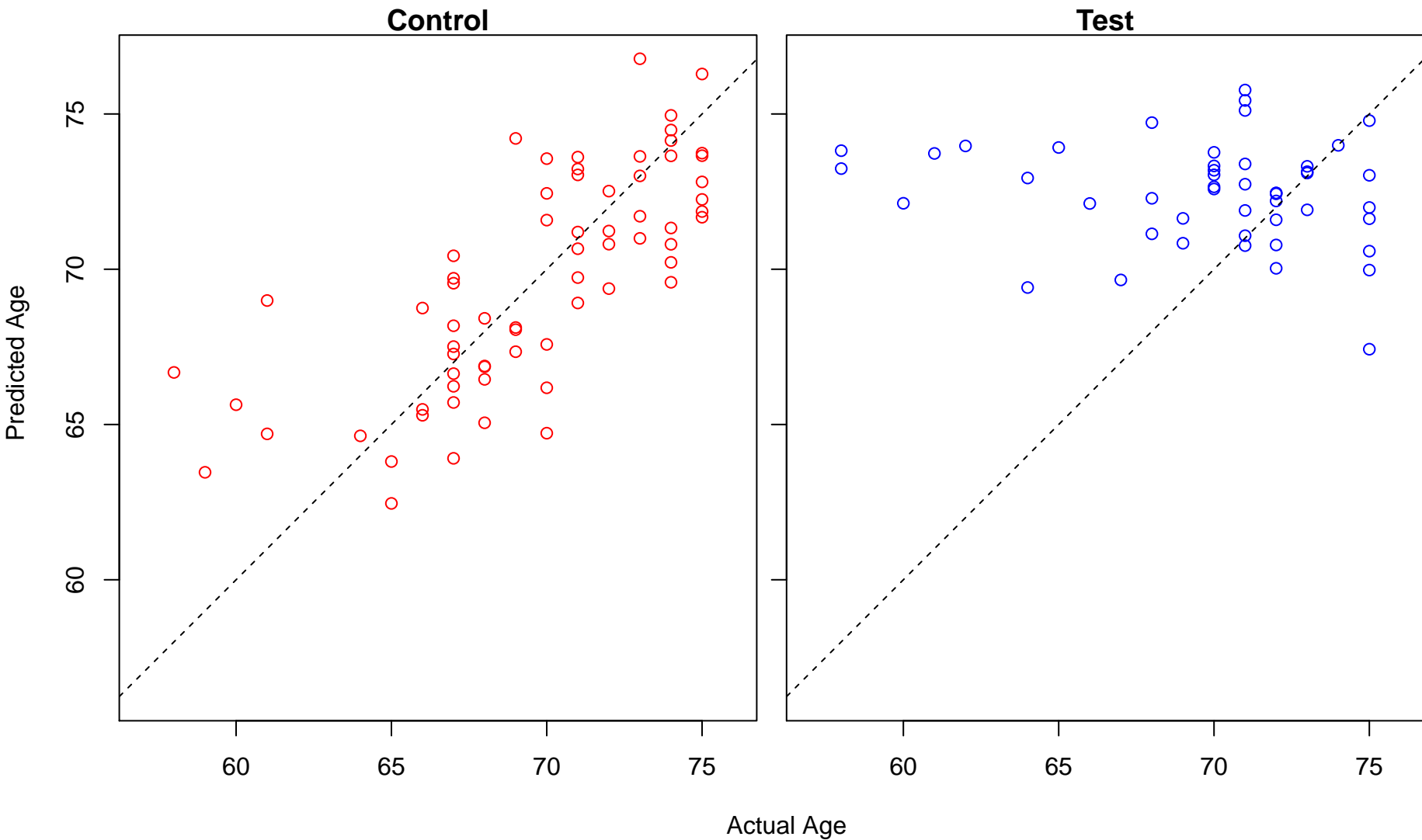
regulation of growth (Score: 1.927561)



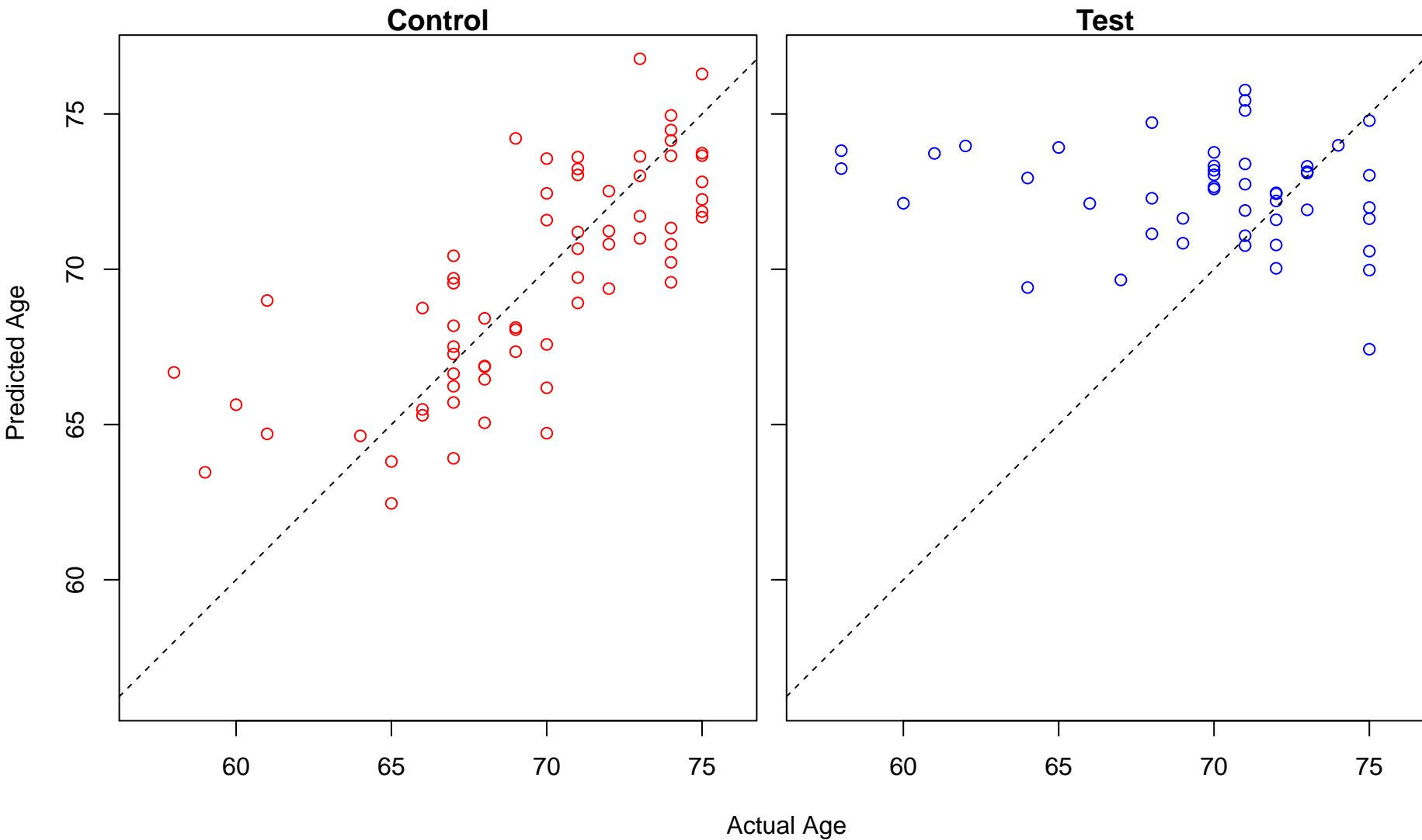
necroptotic process (Score: 1.925420)



axon guidance (Score: 1.923764)

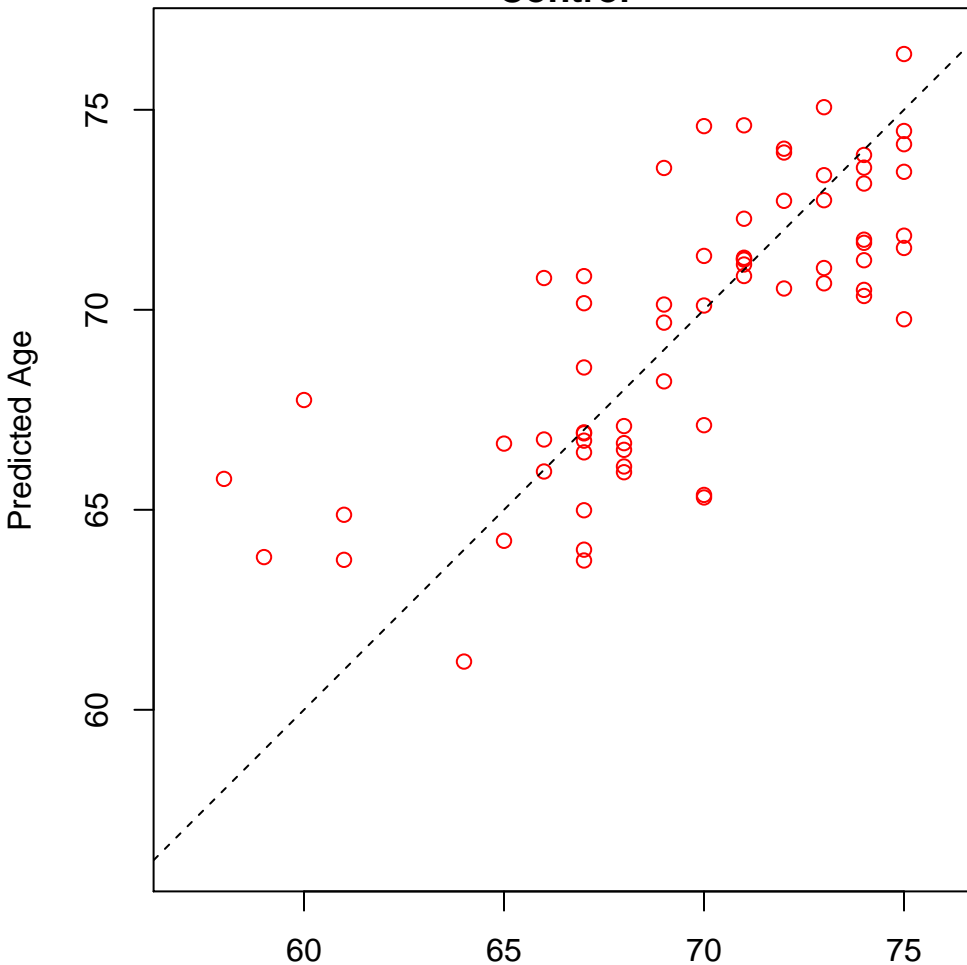


neuron projection guidance (Score: 1.923764)

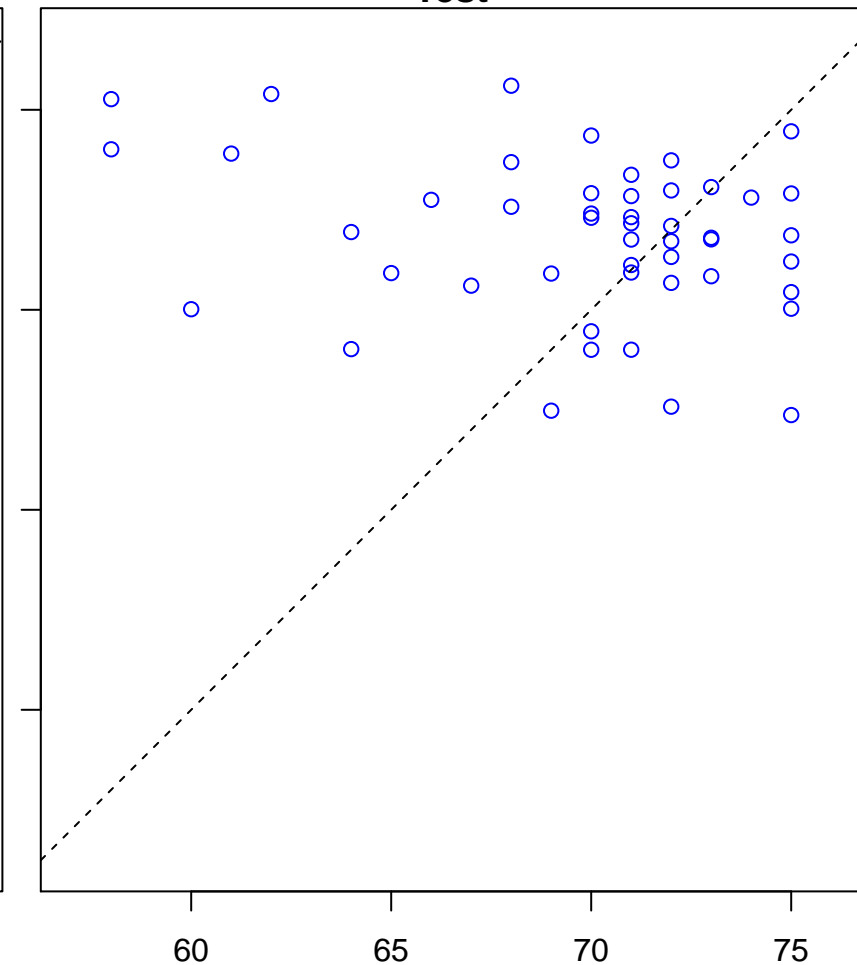


extrinsic apoptotic signaling pathway (Score: 1.923500)

Control

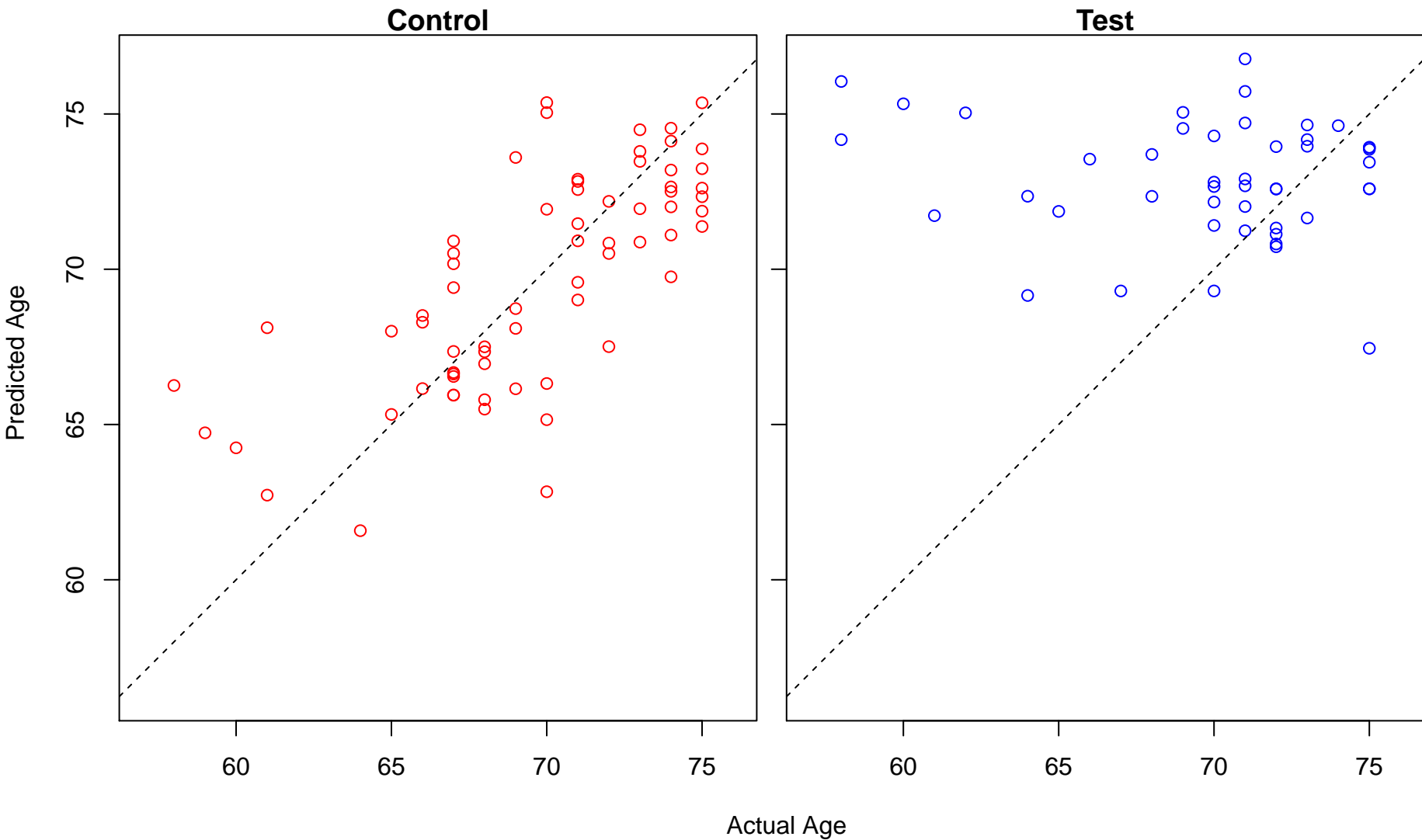


Test

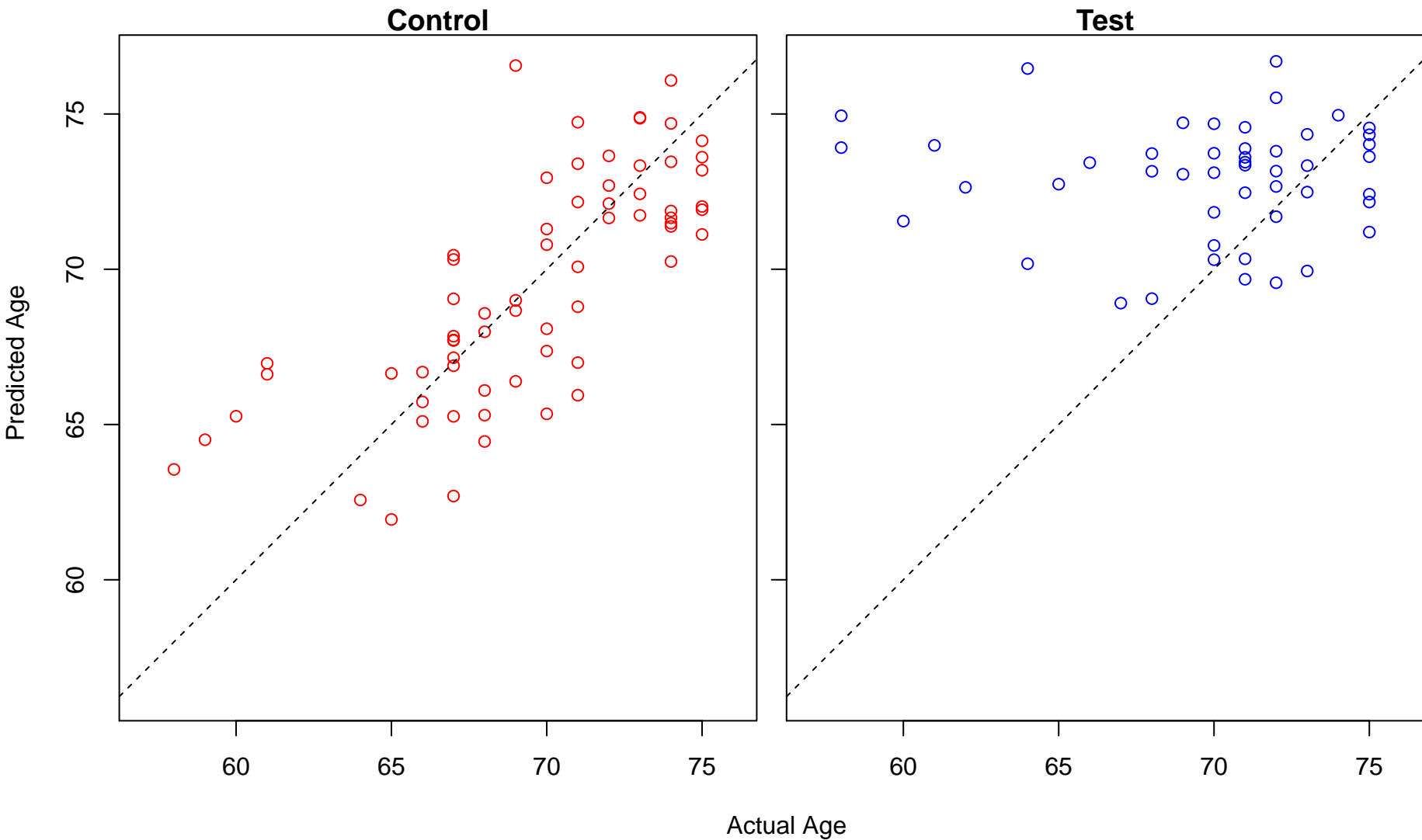


Actual Age

transcription initiation from RNA polymerase II promoter (Score: 1.921544)

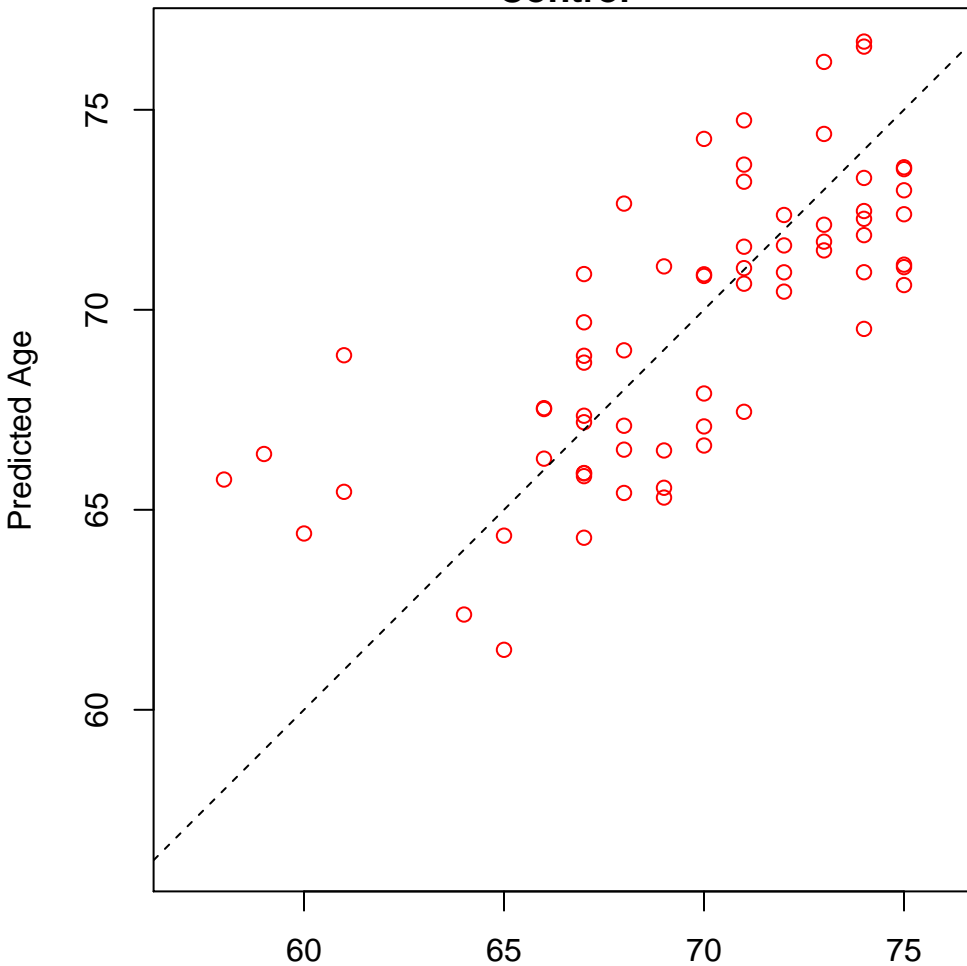


negative regulation of protein binding (Score: 1.919028)

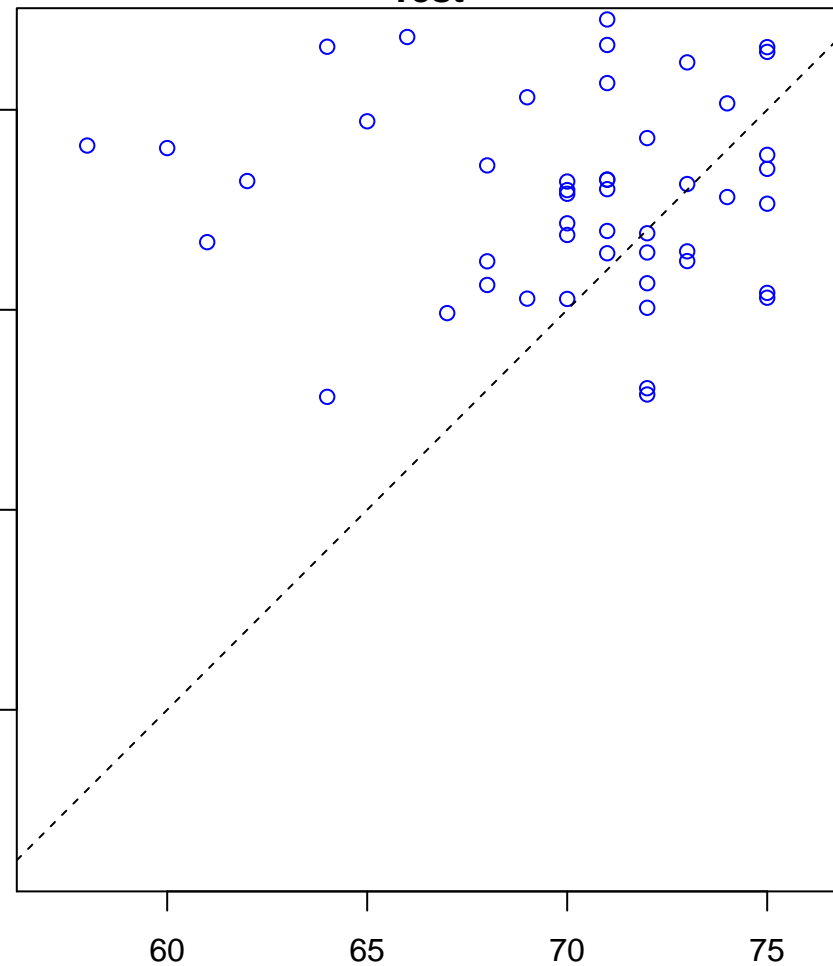


regulation of dendrite morphogenesis (Score: 1.918931)

Control

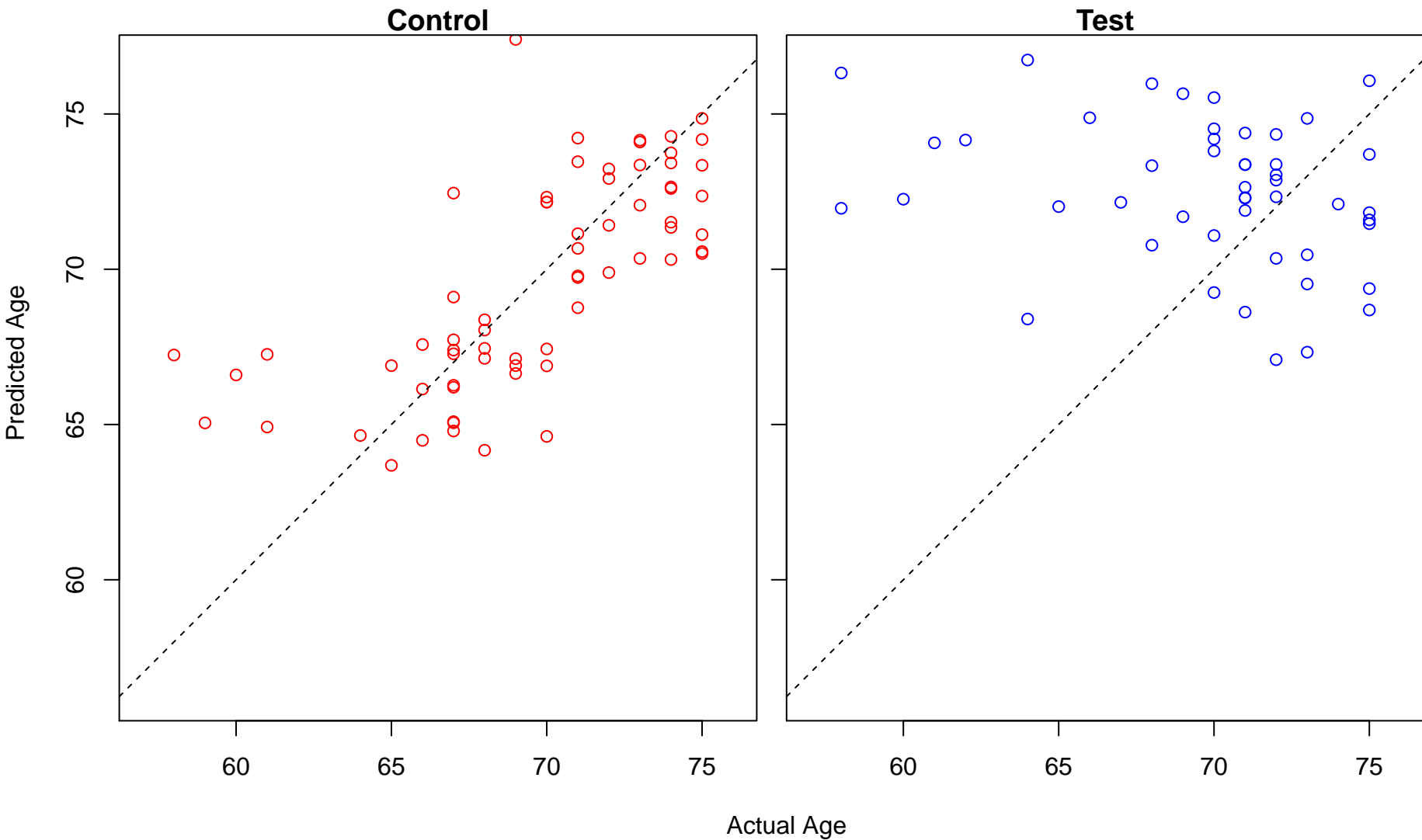


Test

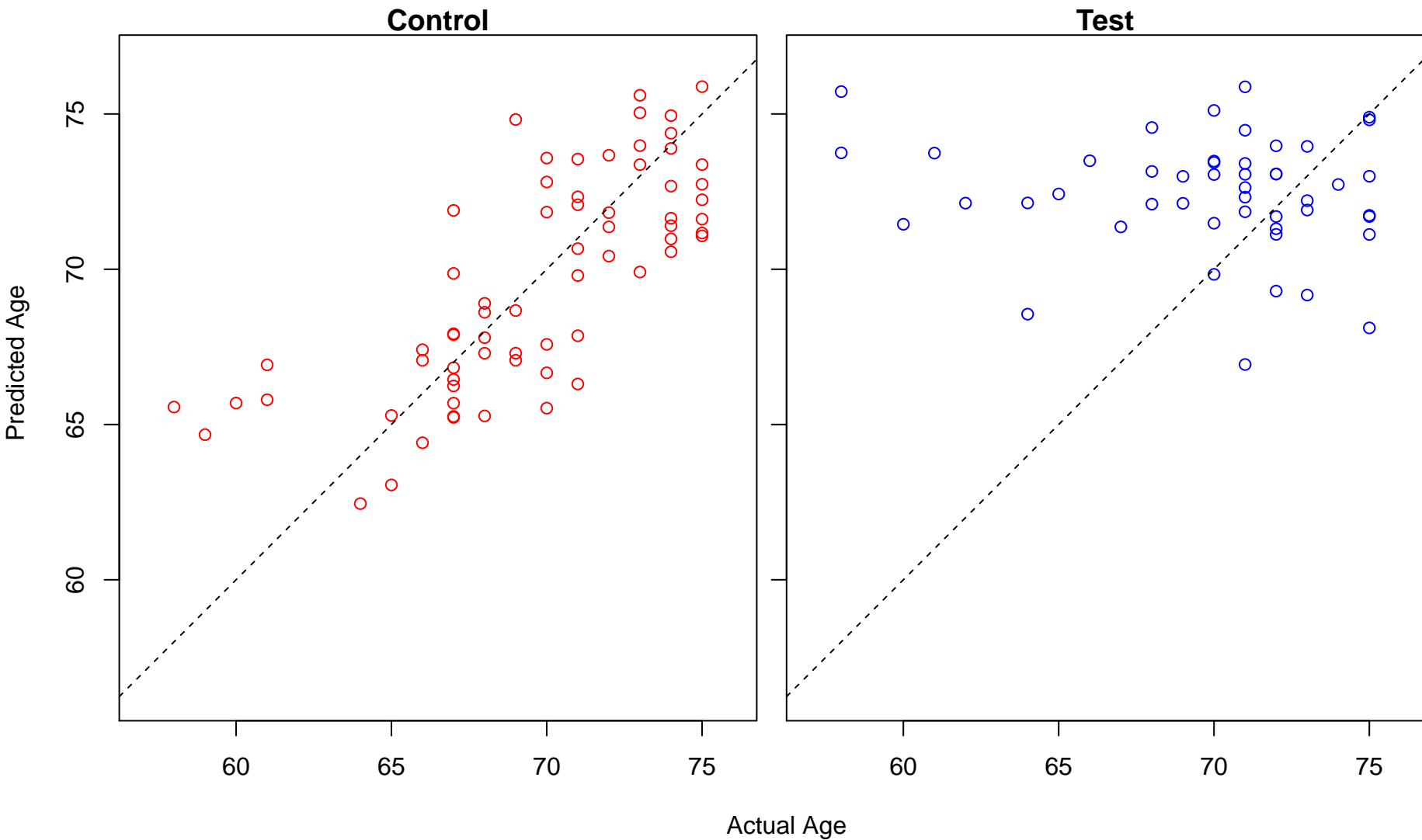


Actual Age

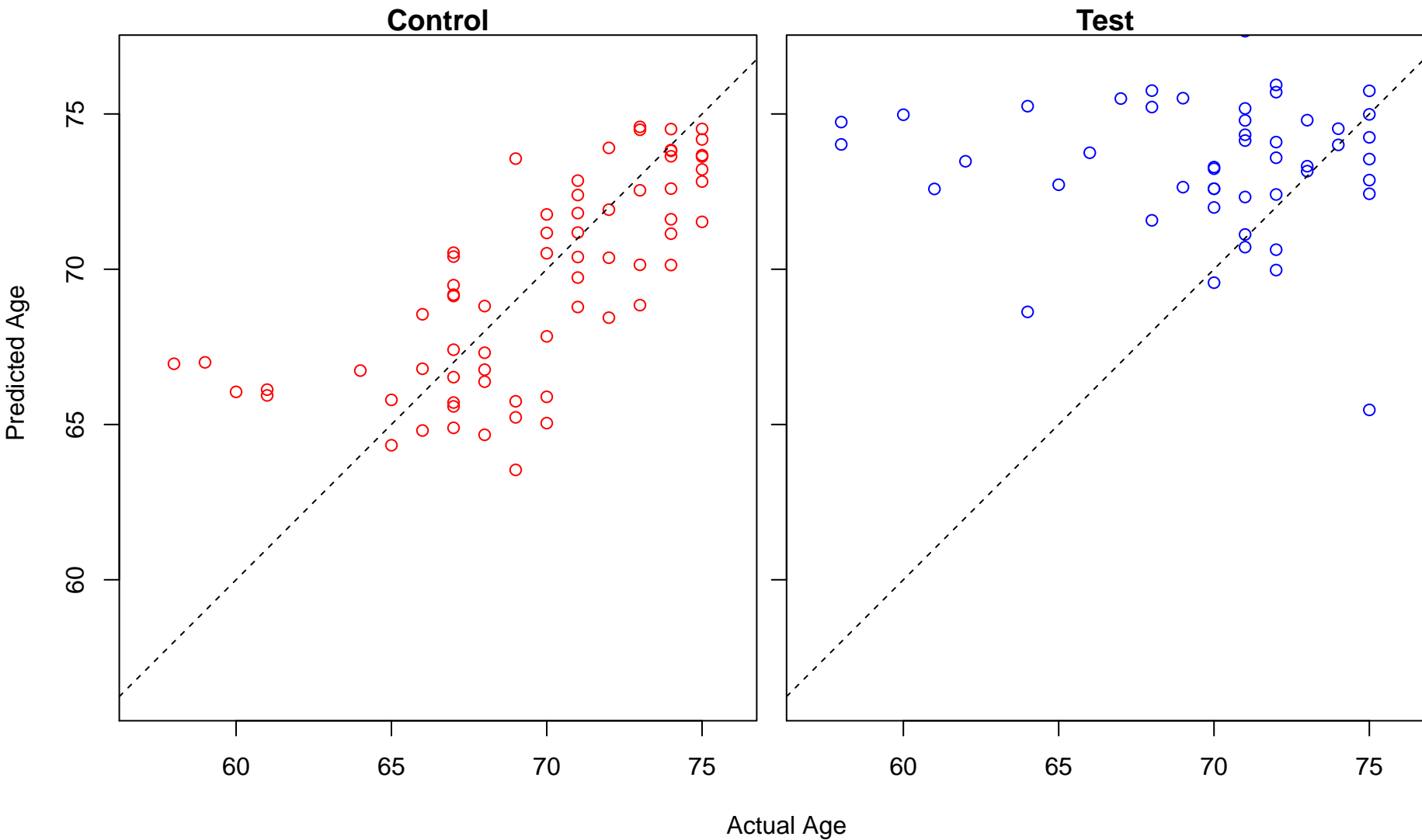
negative regulation of immune system process (Score: 1.918850)



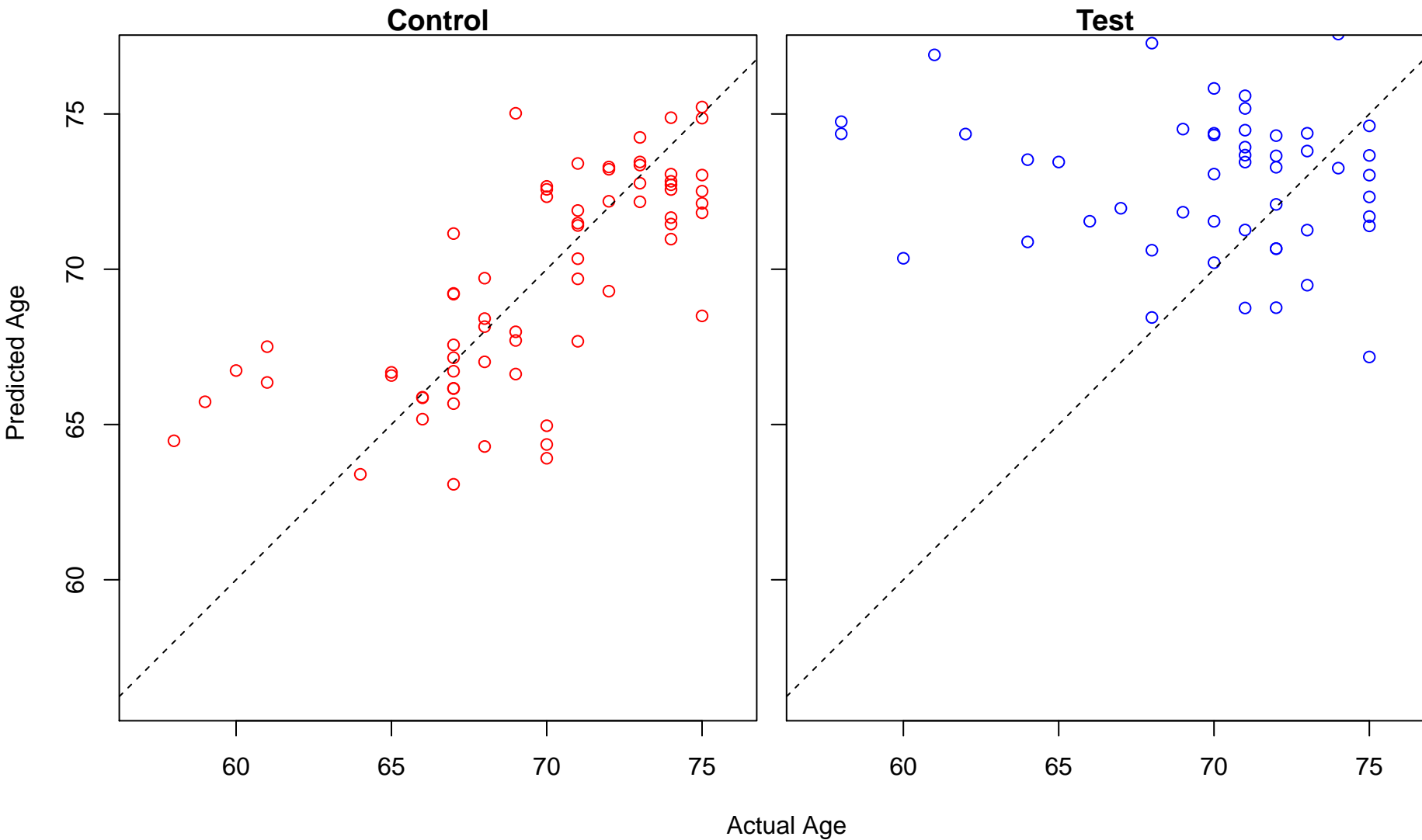
cell-cell adhesion (Score: 1.917629)



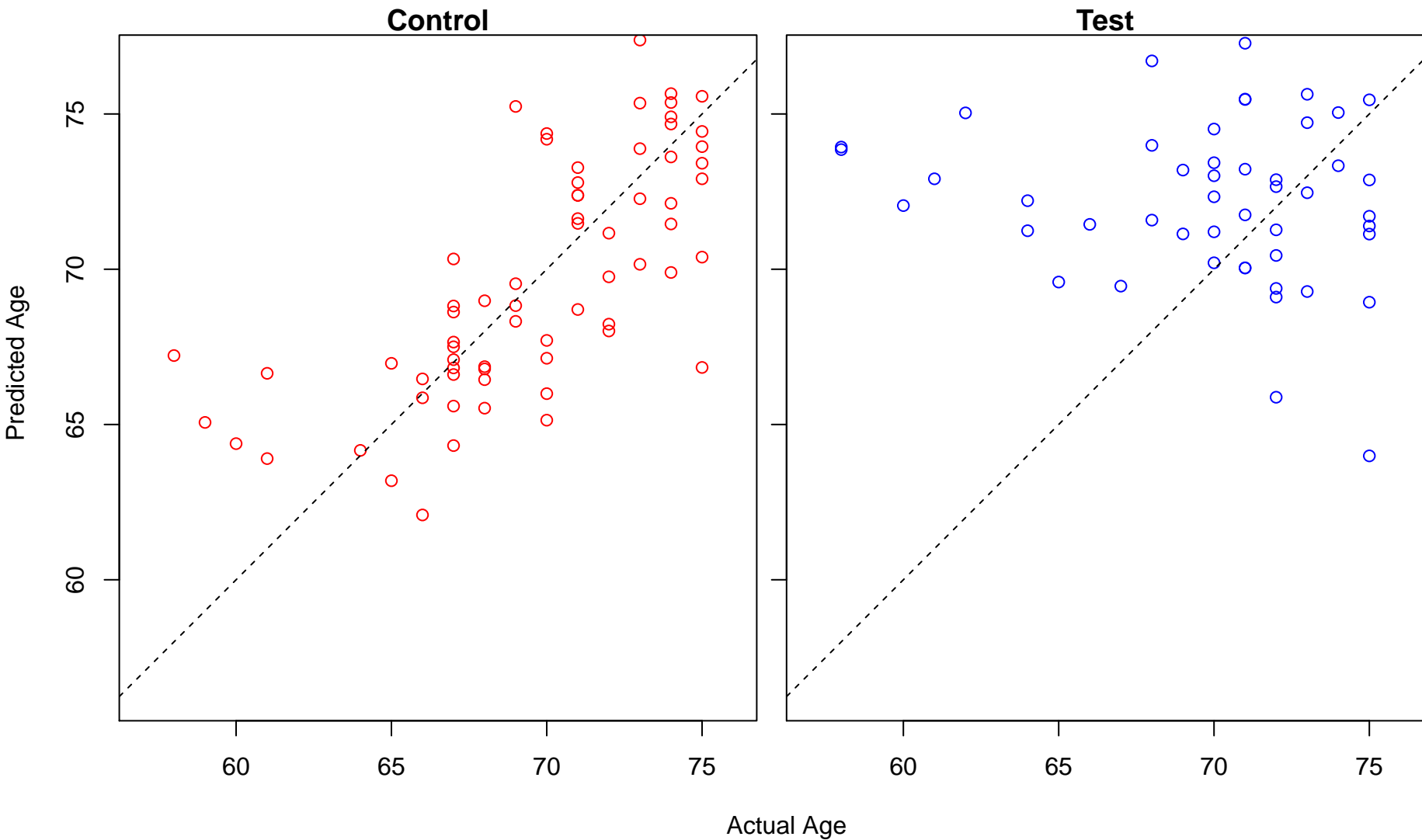
negative regulation of cell migration (Score: 1.917001)



regulation of protein import (Score: 1.916662)

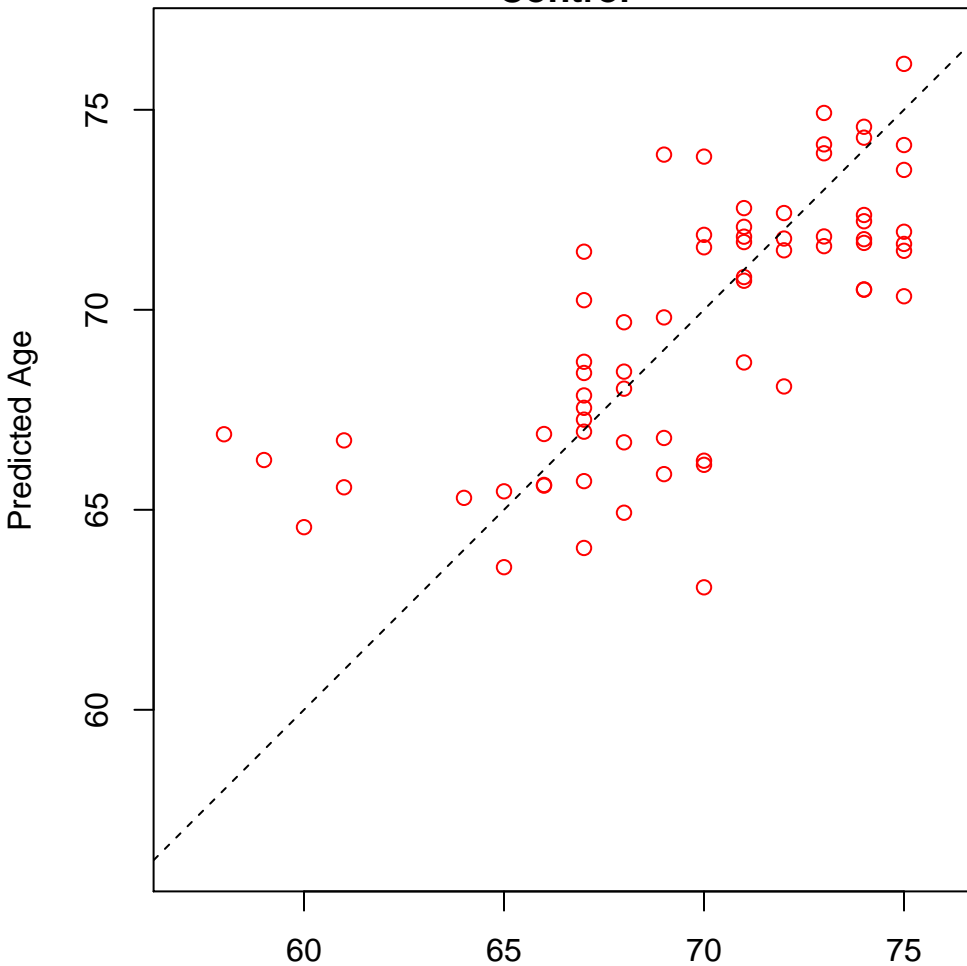


response to decreased oxygen levels (Score: 1.914650)

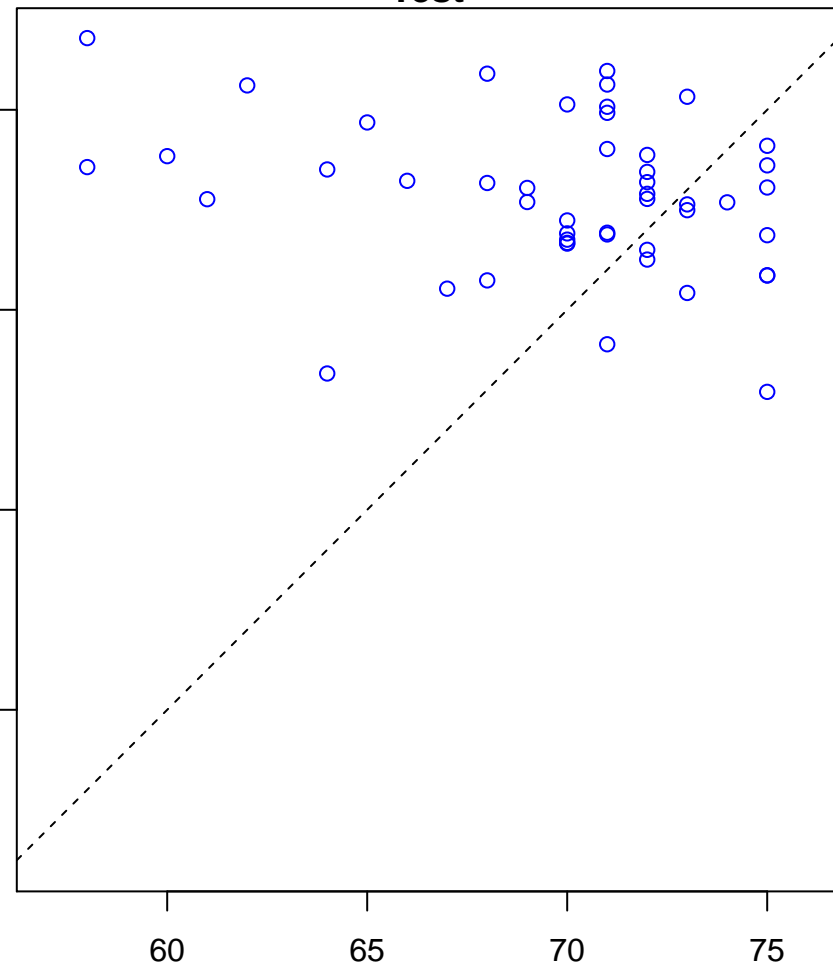


positive regulation of cell differentiation (Score: 1.912914)

Control

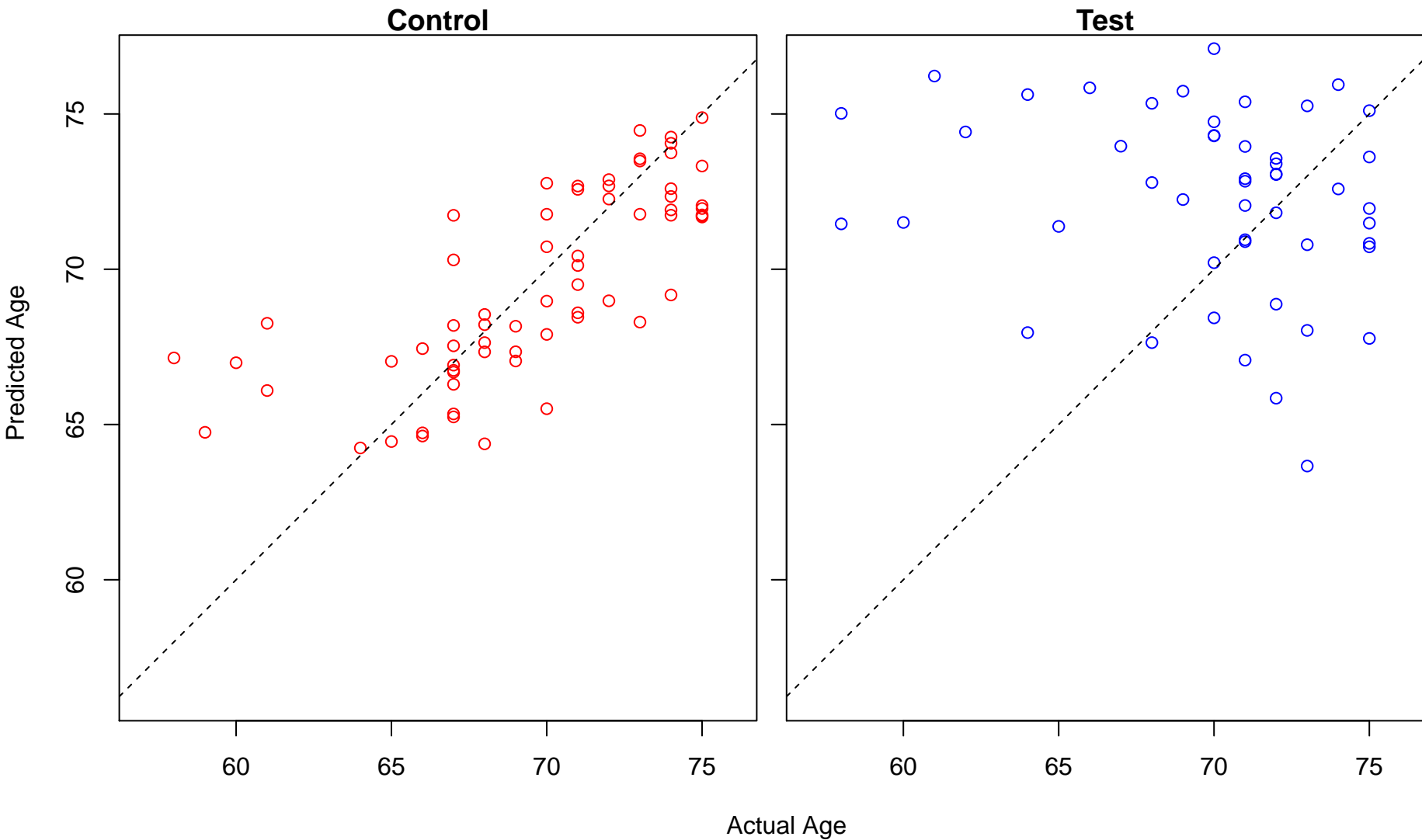


Test

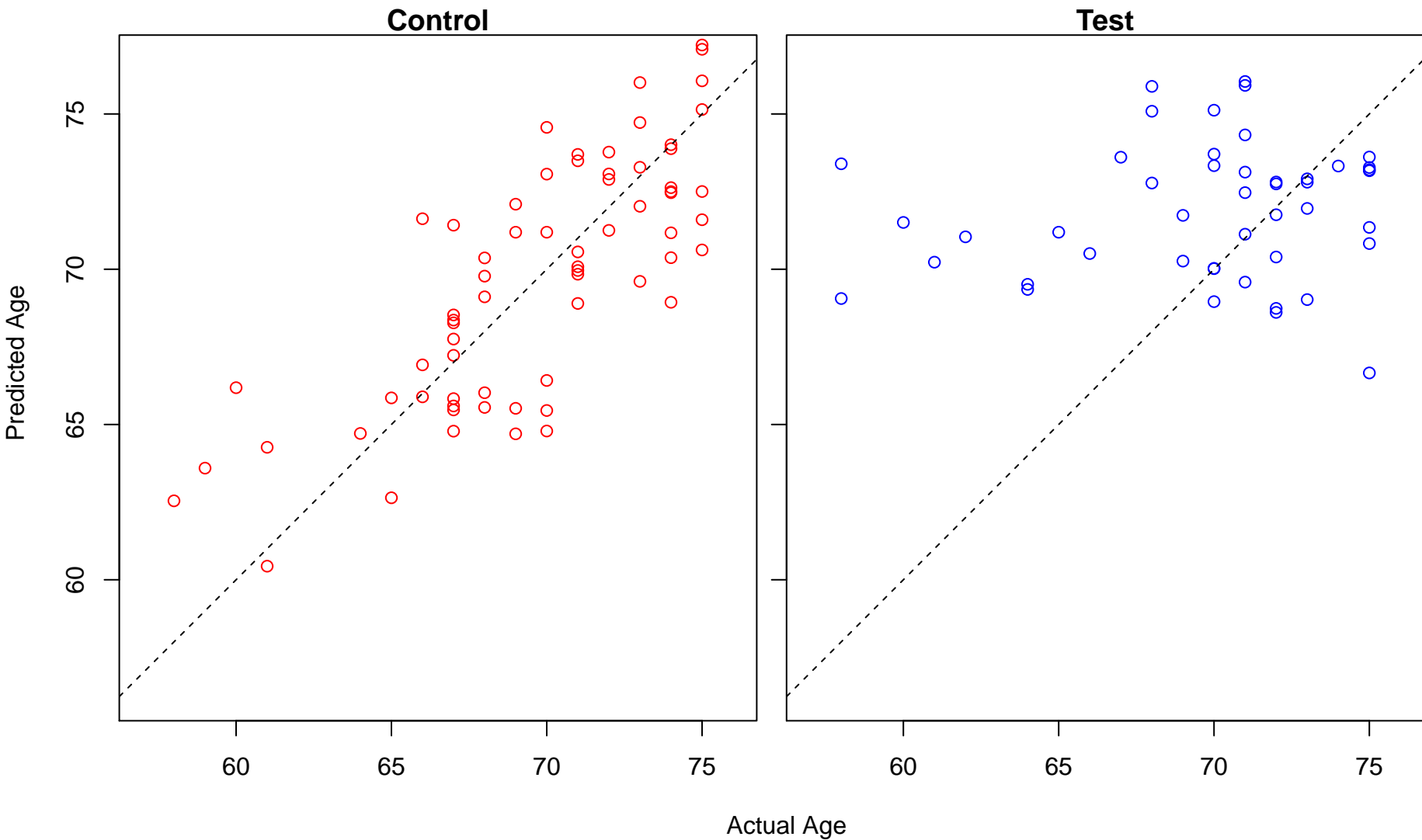


Actual Age

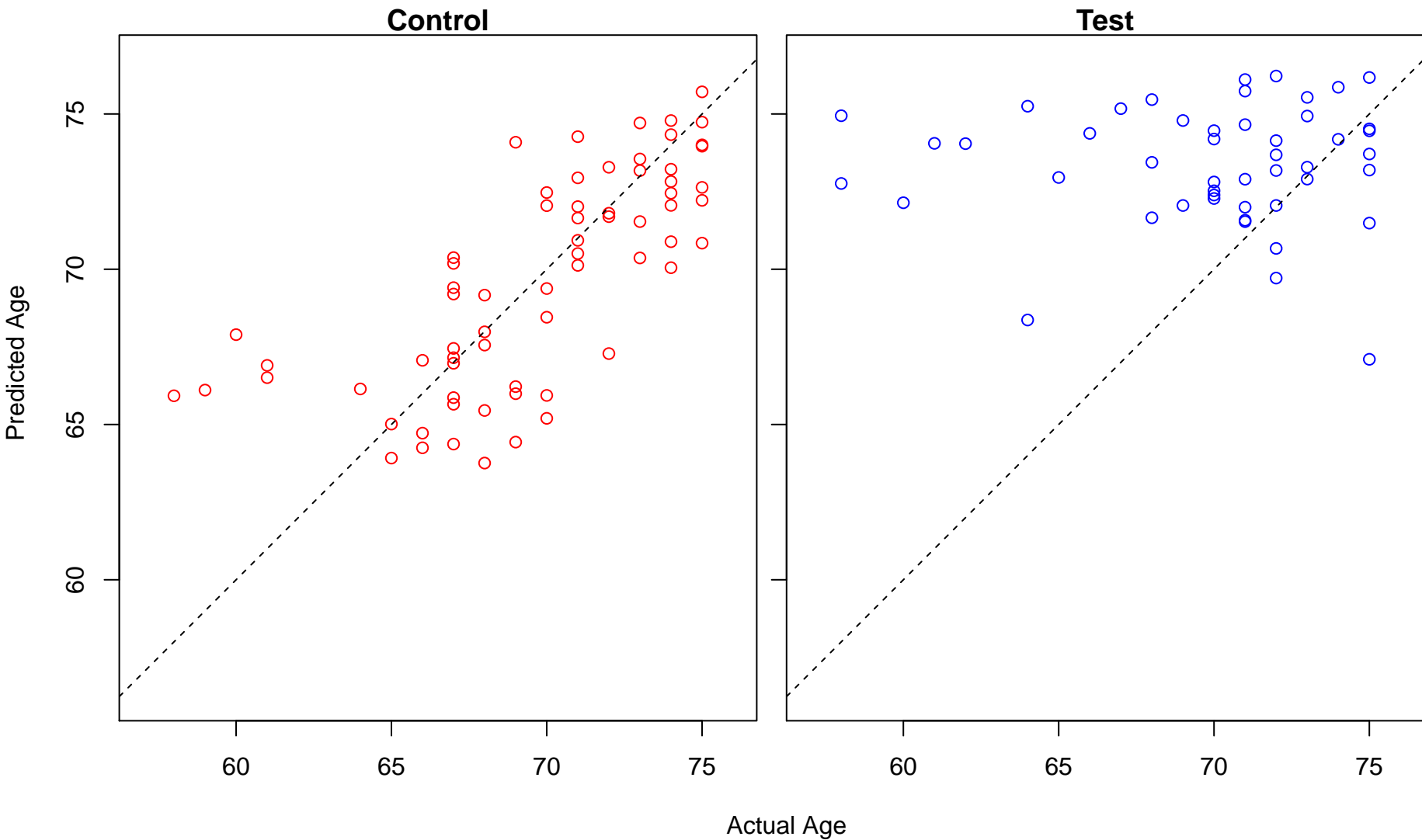
negative regulation of immune effector process (Score: 1.912896)



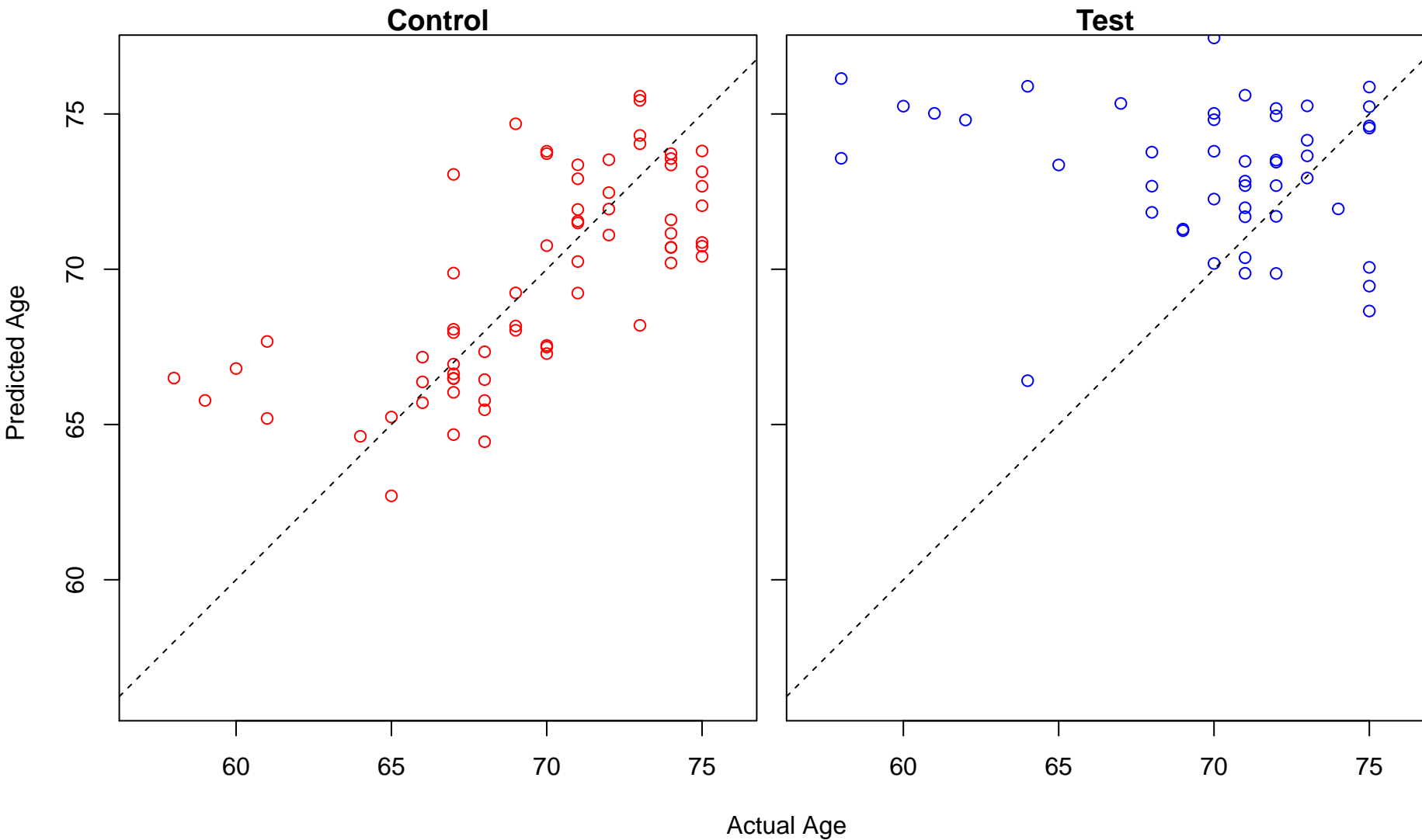
glycolipid metabolic process (Score: 1.912810)



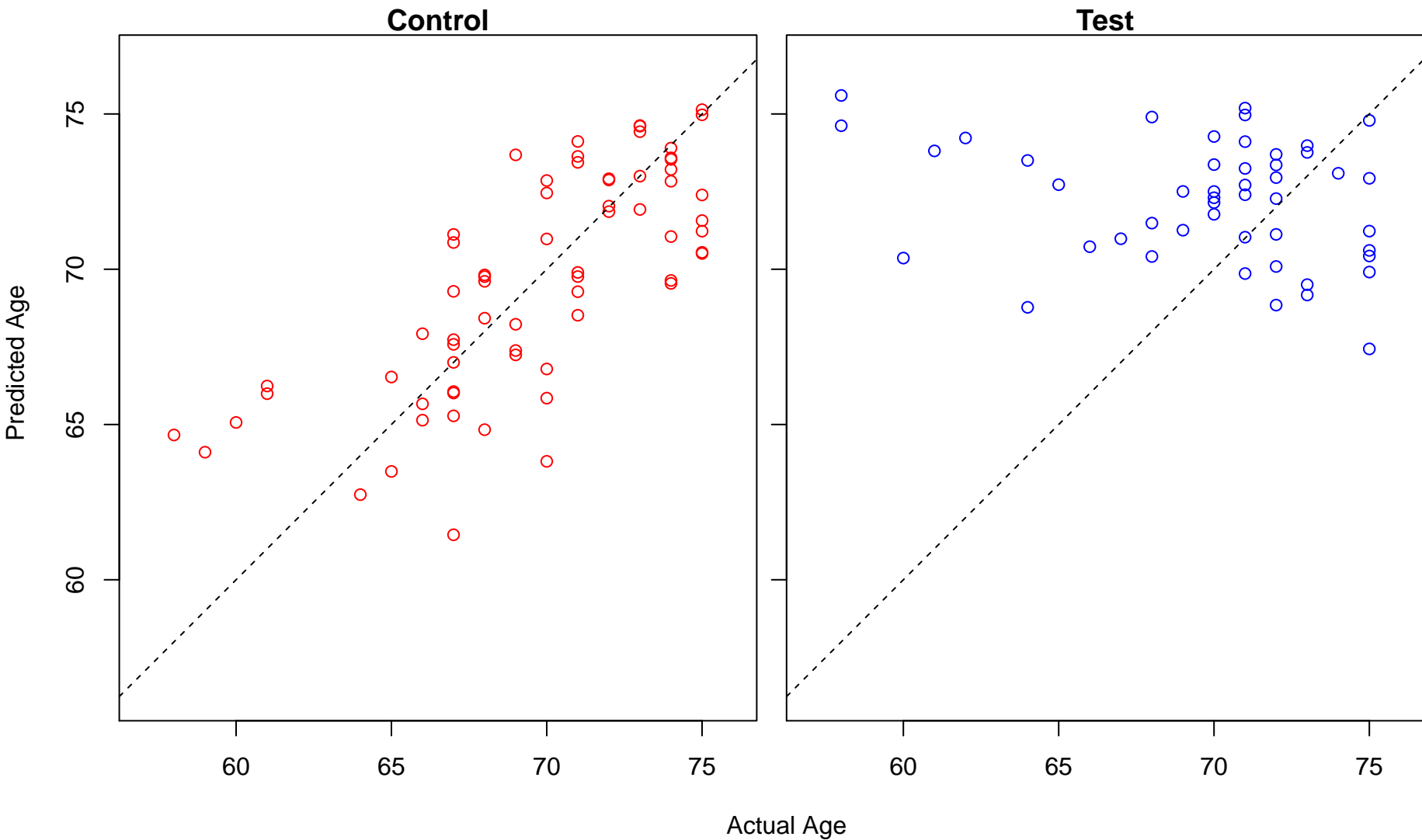
negative regulation of locomotion (Score: 1.910799)



programmed necrotic cell death (Score: 1.910371)

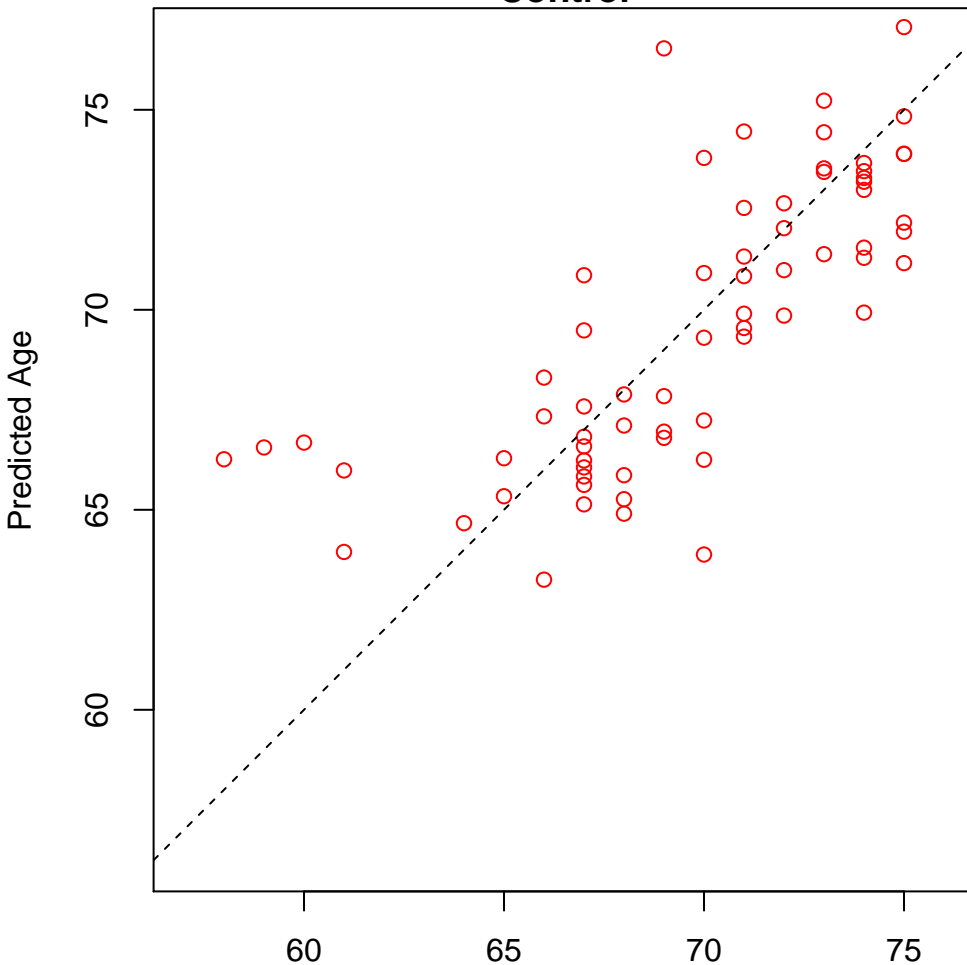


positive regulation of cytoplasmic transport (Score: 1.910188)

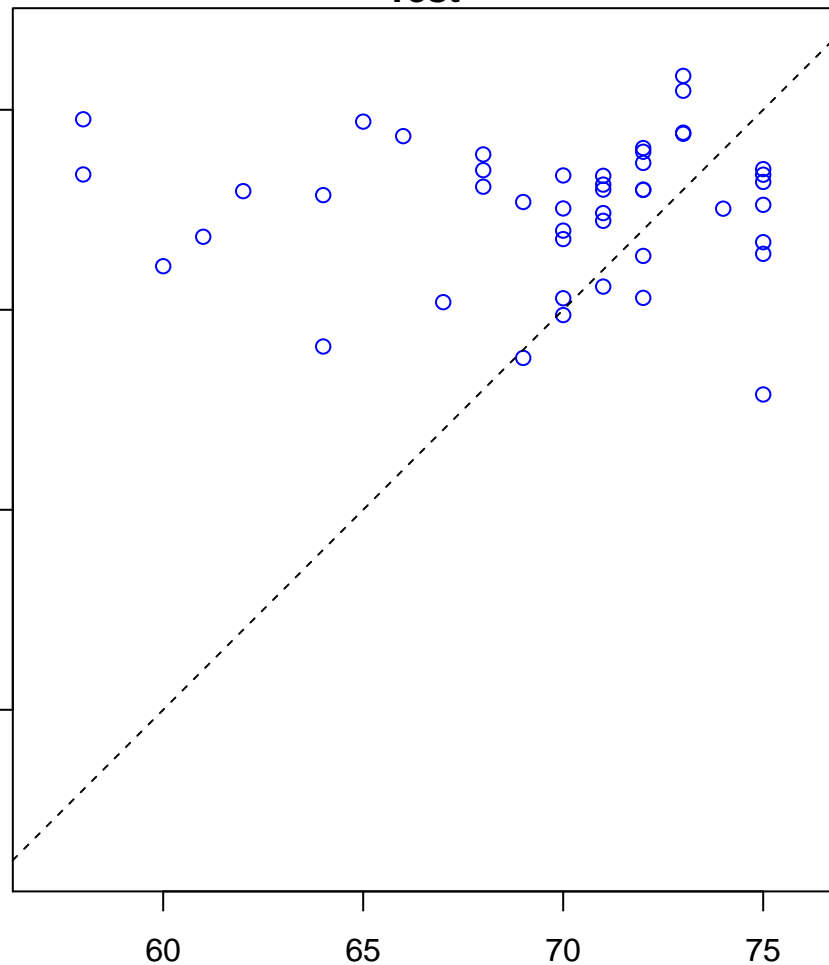


cellular protein complex assembly (Score: 1.910094)

Control

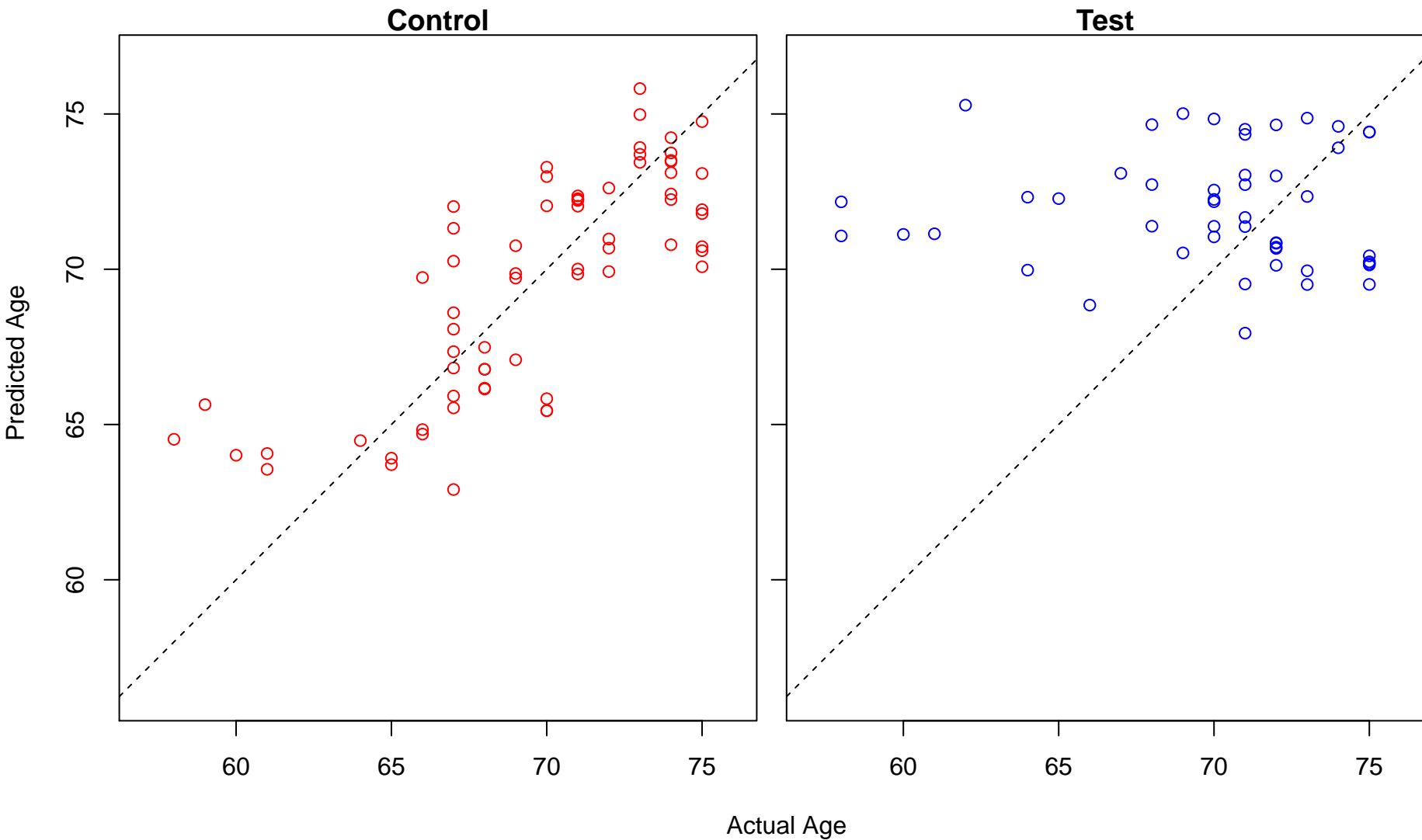


Test



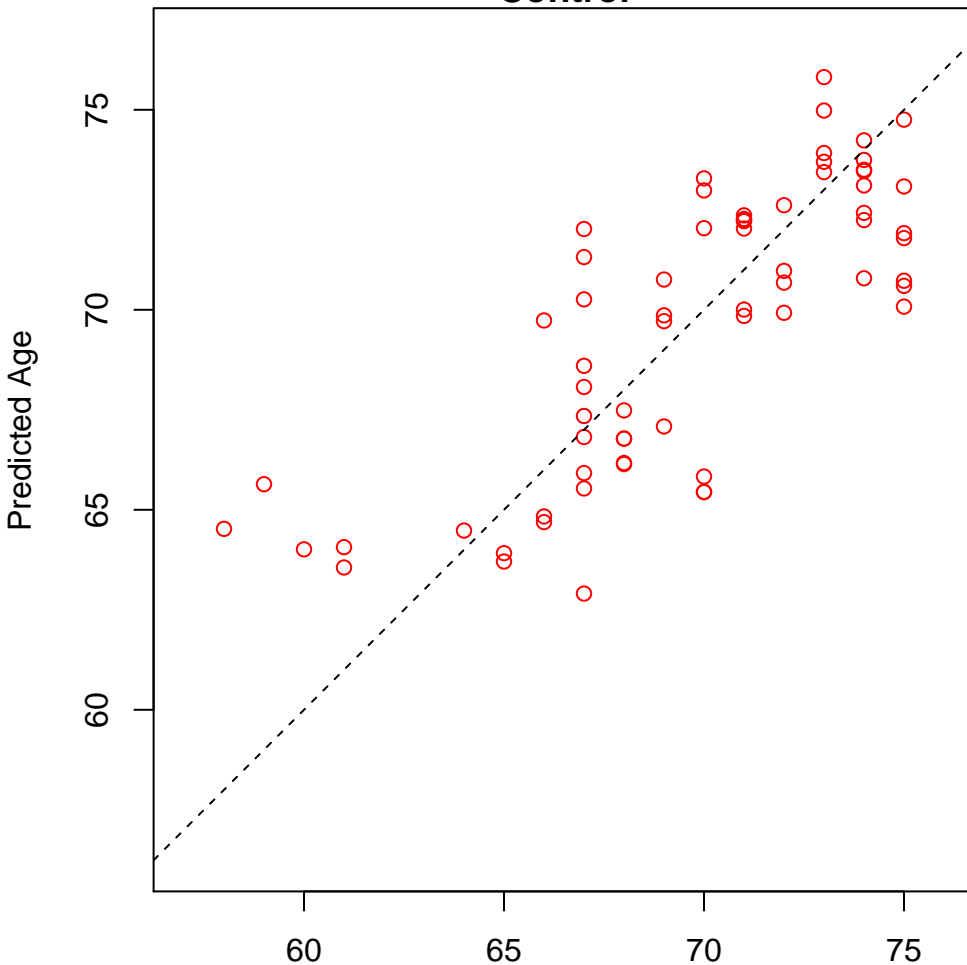
Actual Age

viral budding (Score: 1.910025)

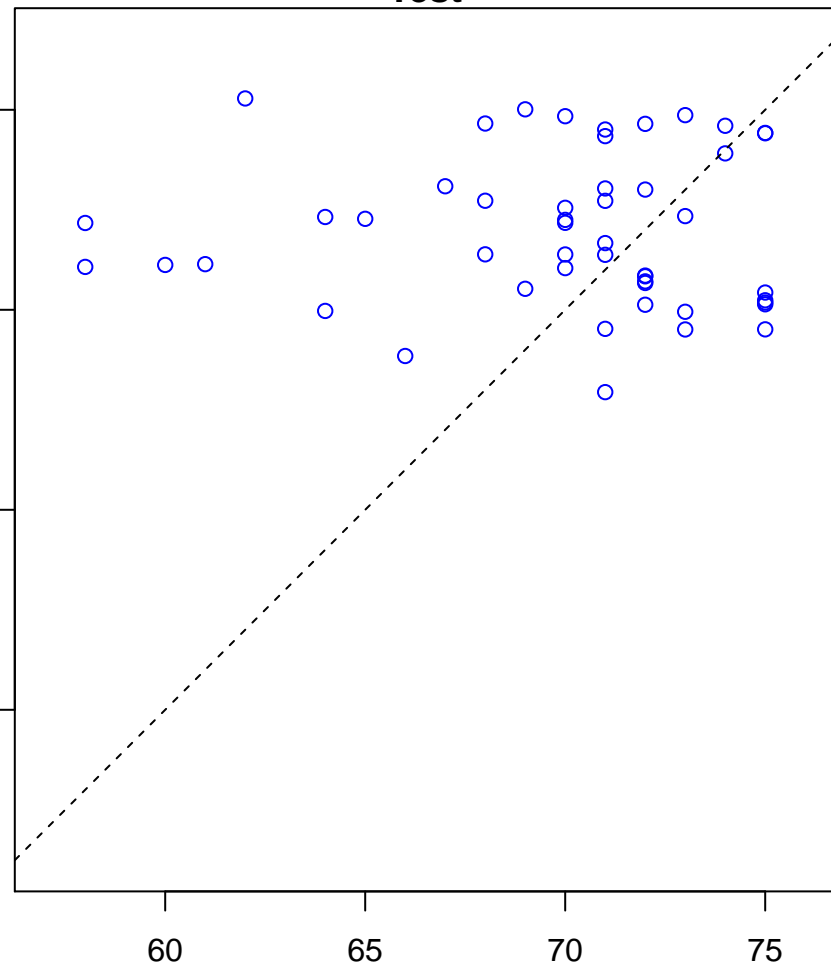


multi-organism organelle organization (Score: 1.910025)

Control

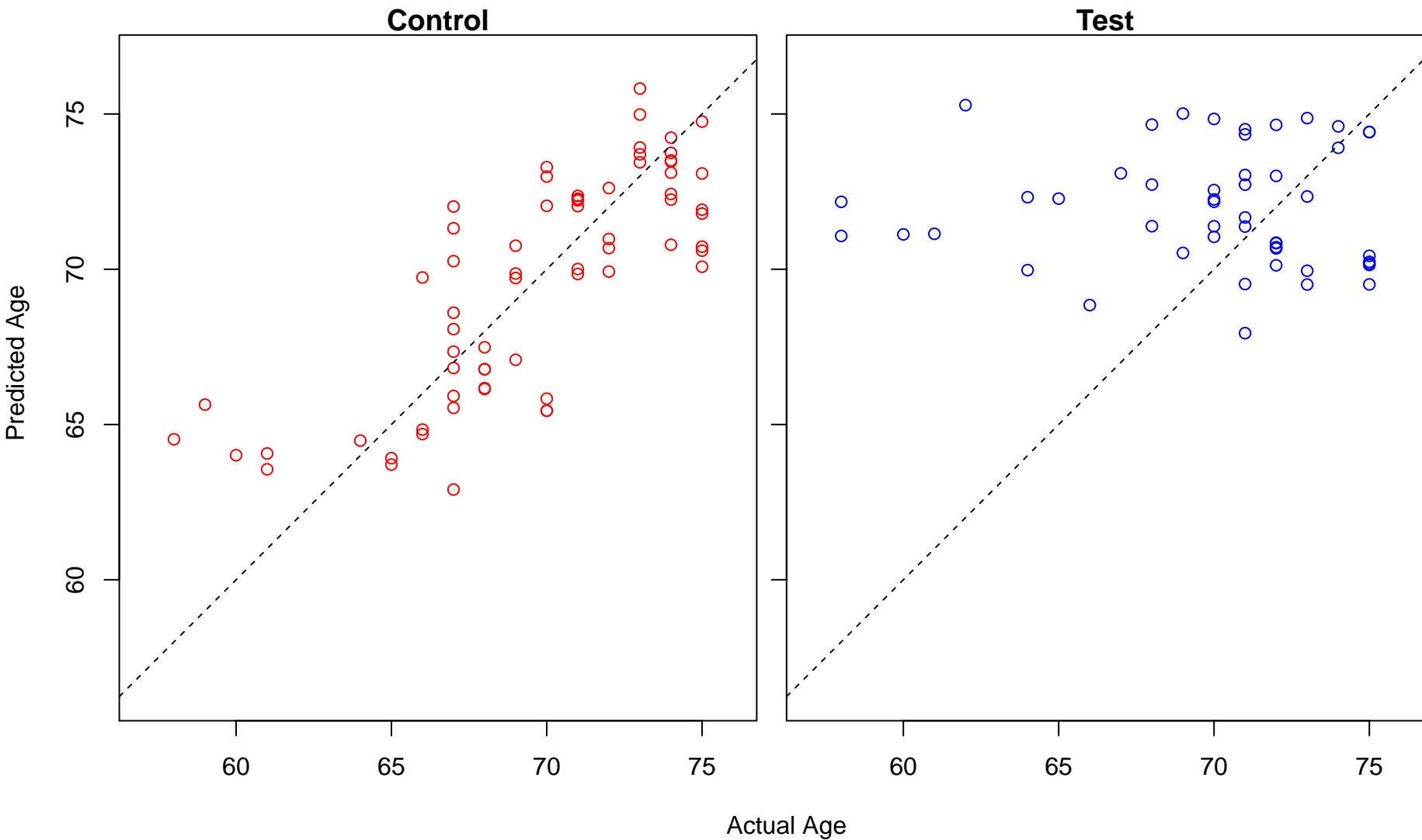


Test

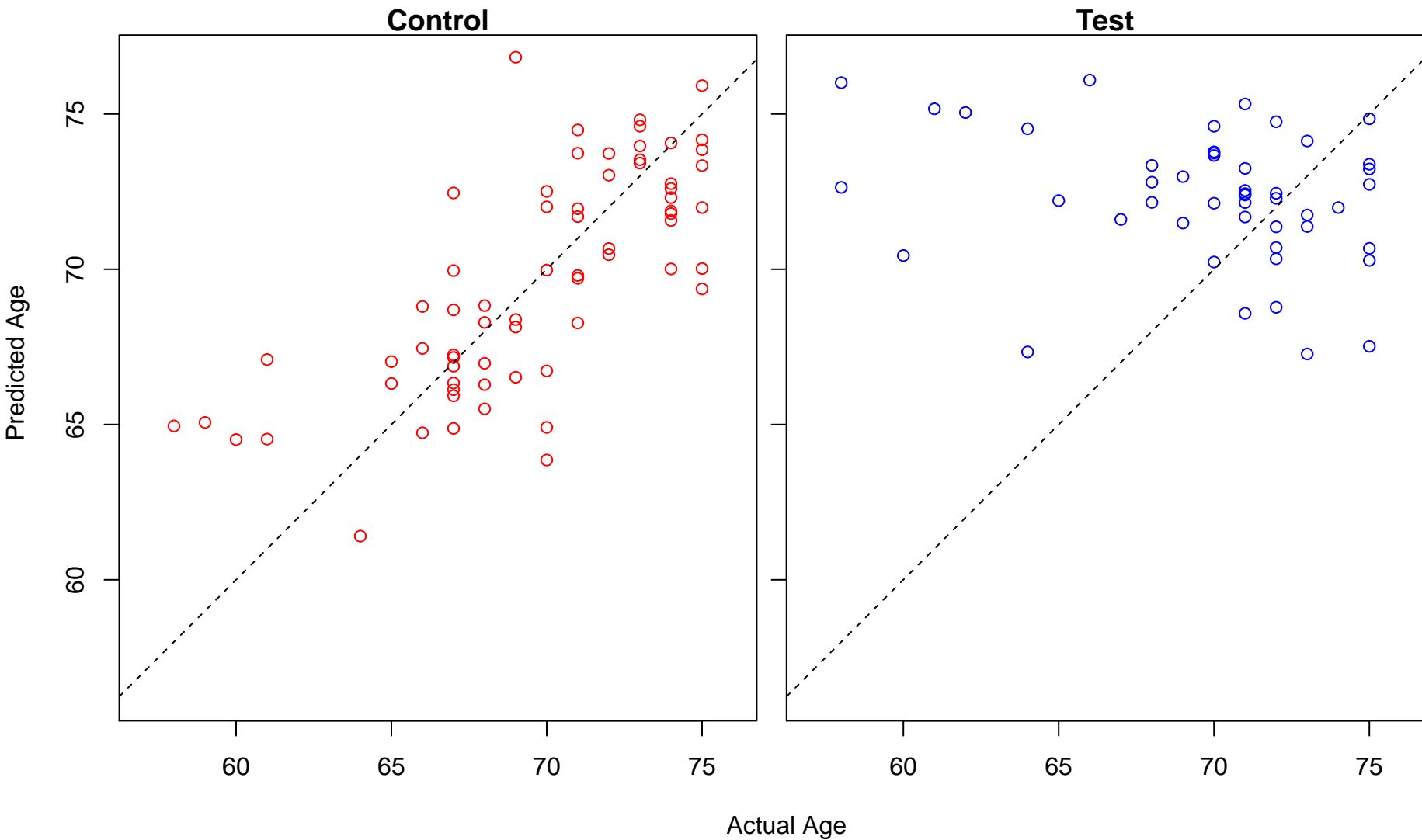


Actual Age

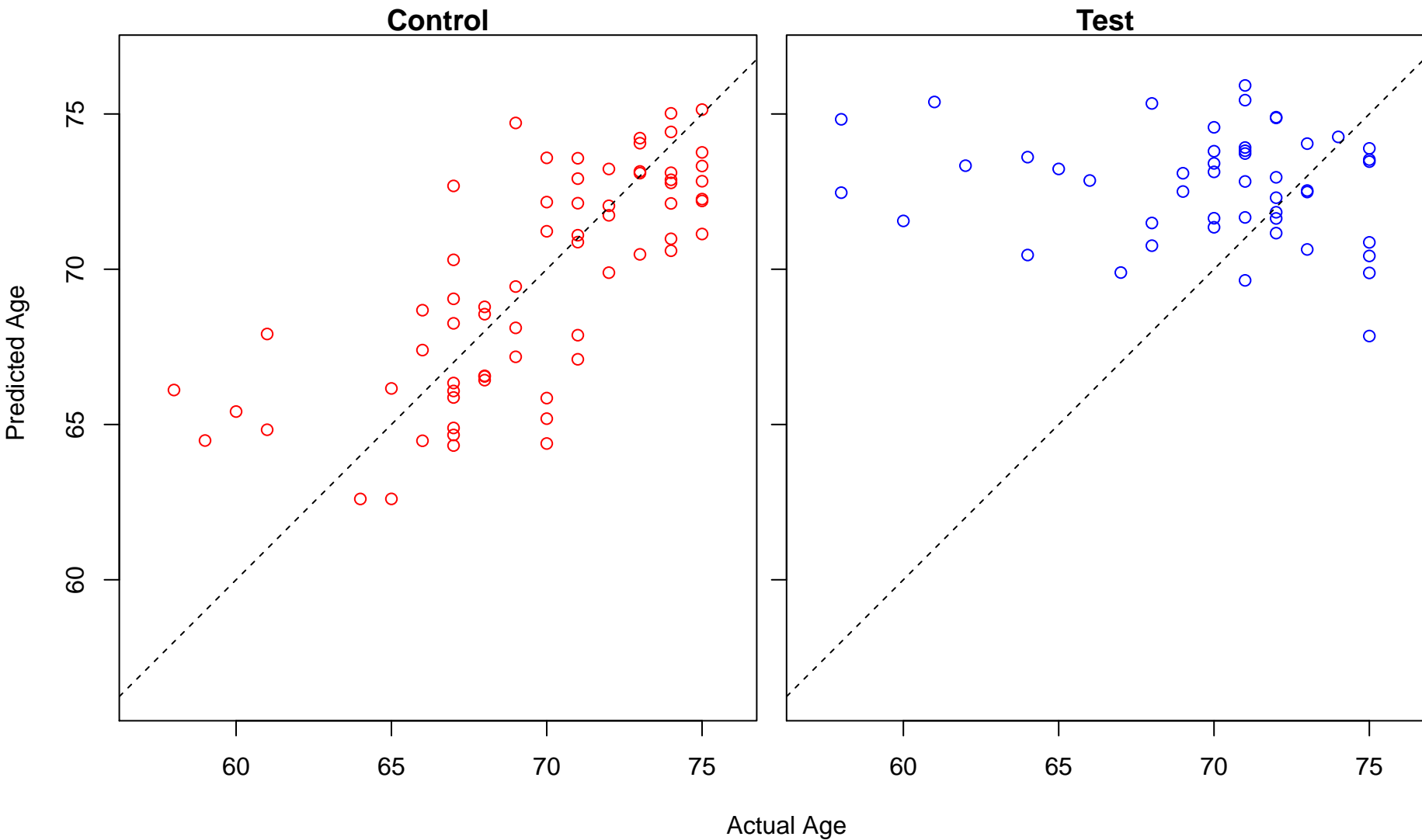
multi-organism membrane budding (Score: 1.910025)



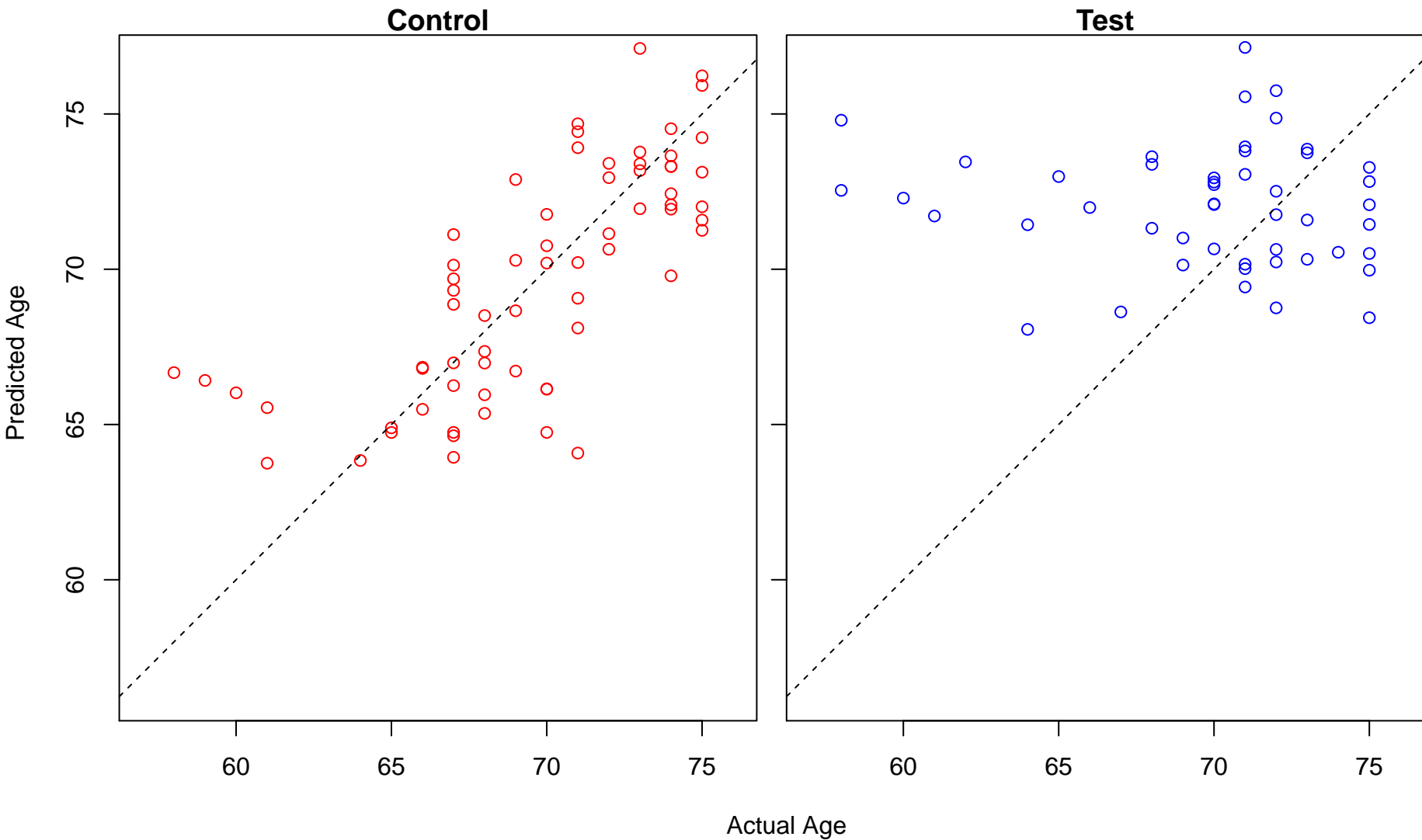
regulation of symbiosis, encompassing mutualism through parasitism (Score: 1.906923)



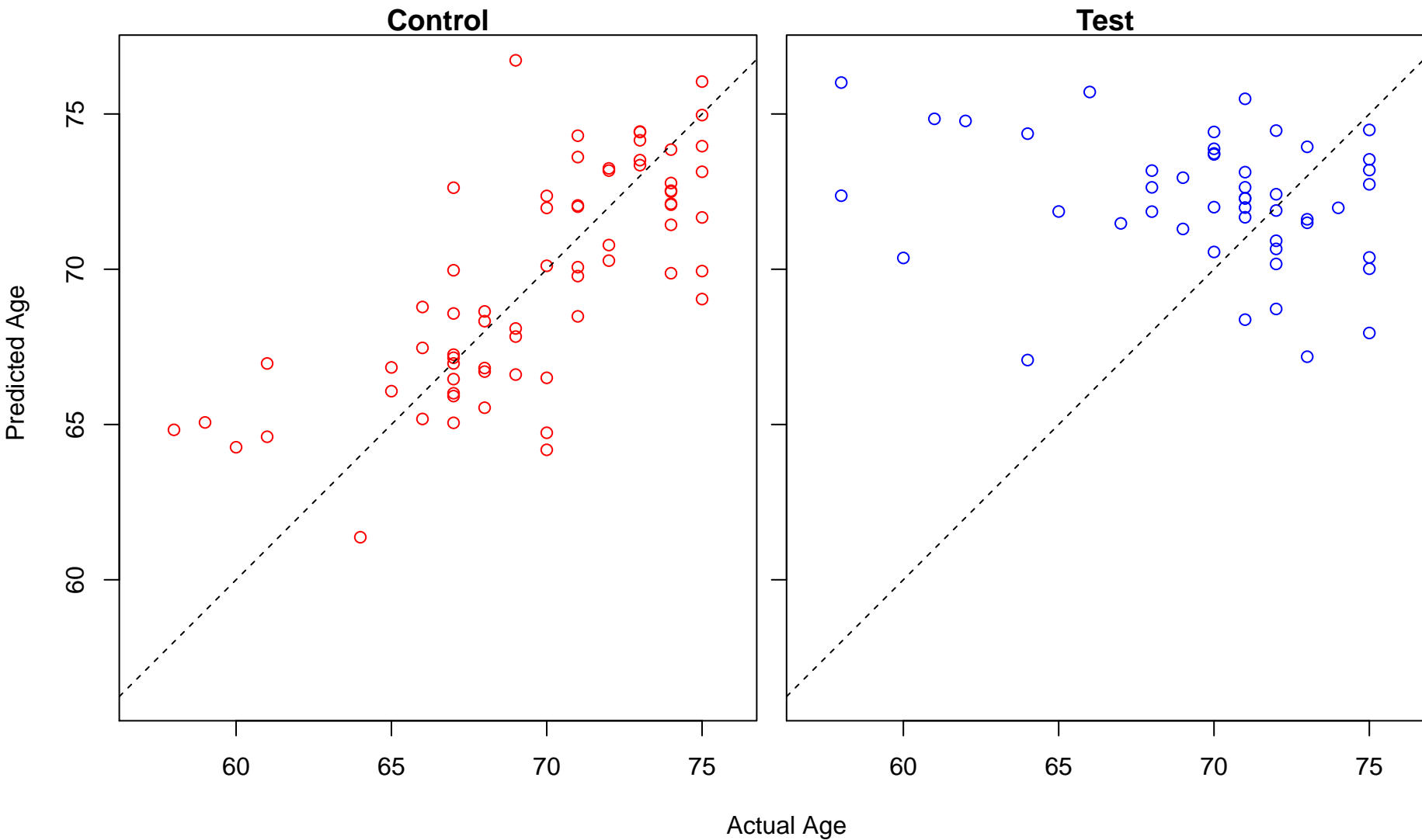
DNA repair (Score: 1.906277)



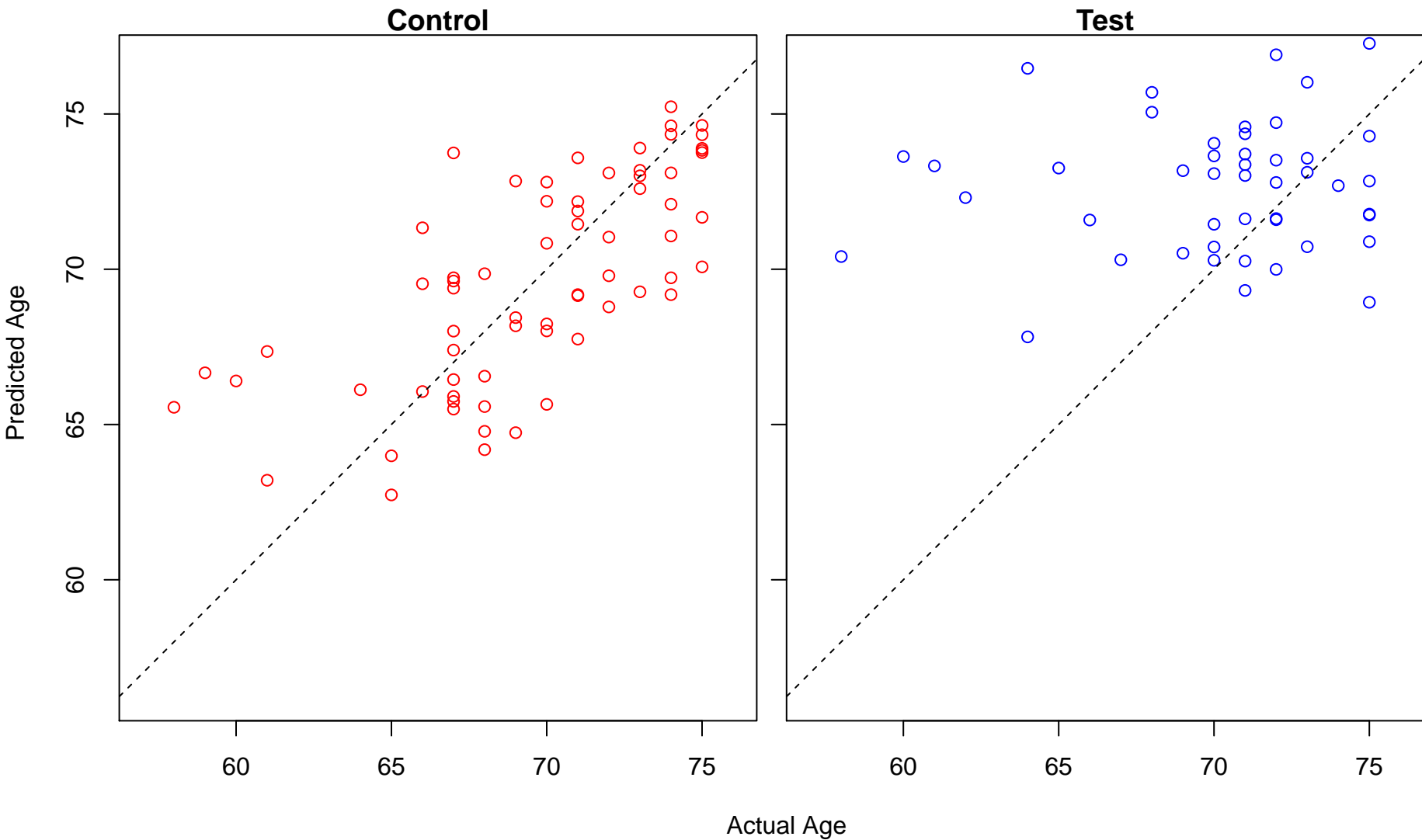
protein oligomerization (Score: 1.905715)



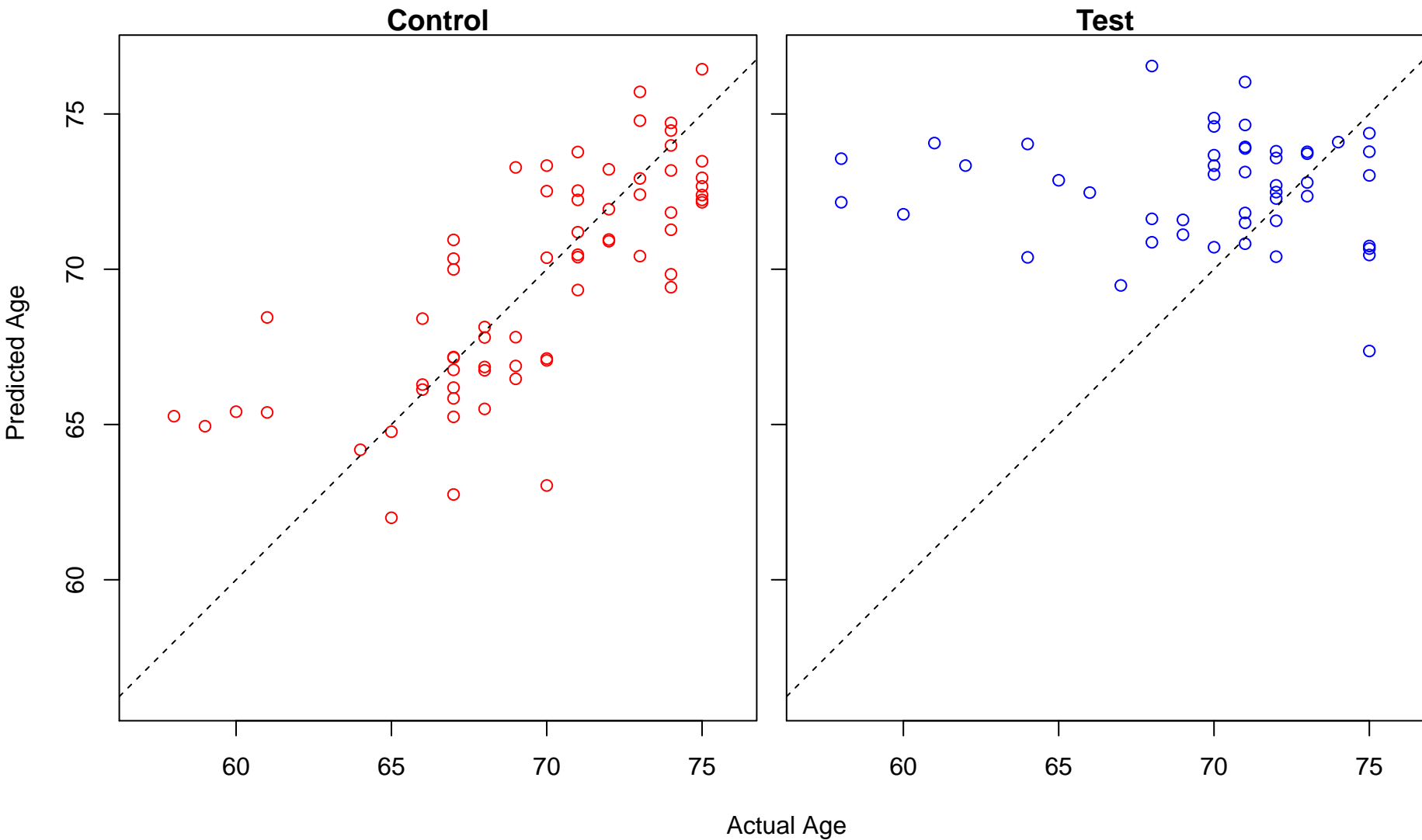
regulation of viral process (Score: 1.905655)



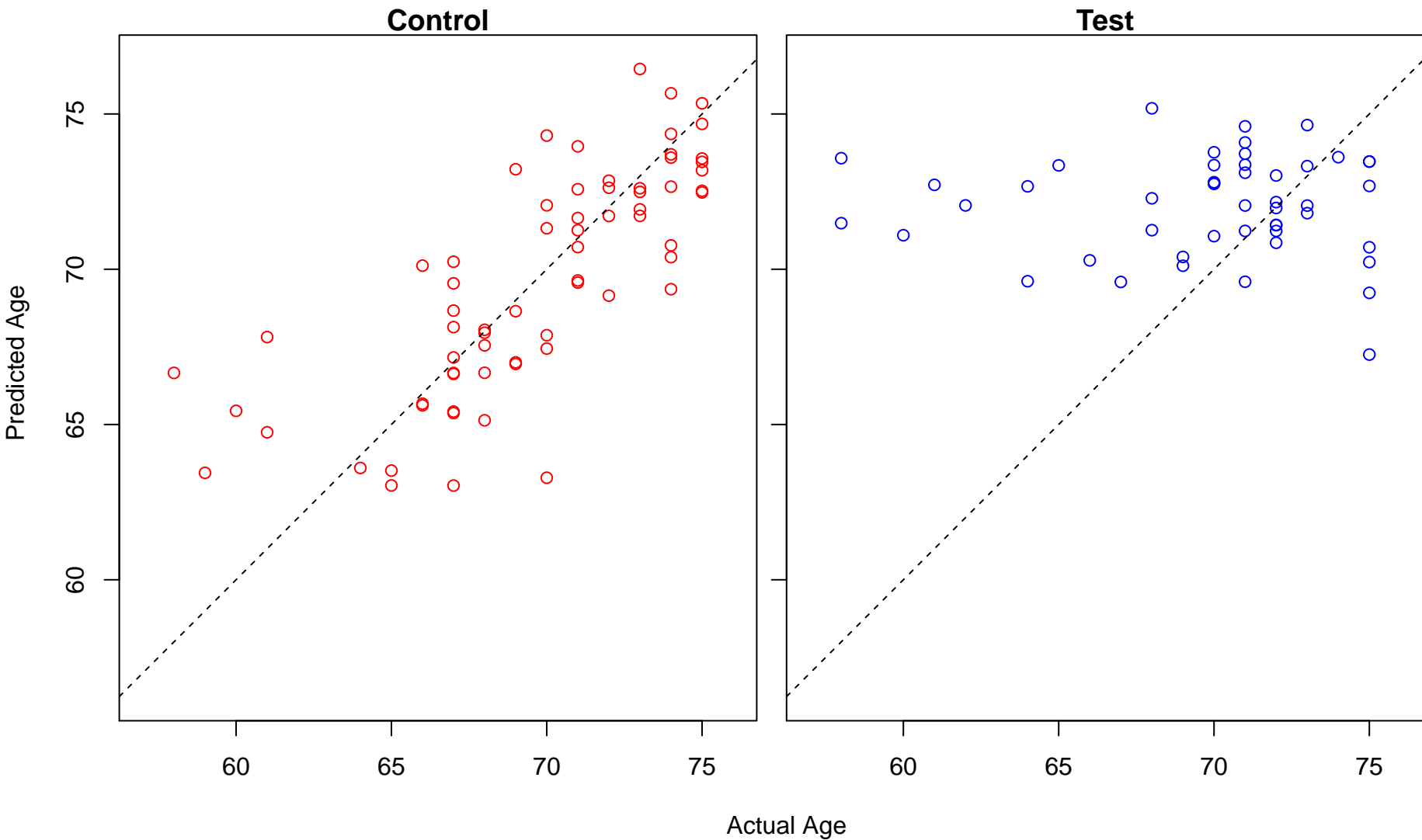
regulation of B cell activation (Score: 1.905546)



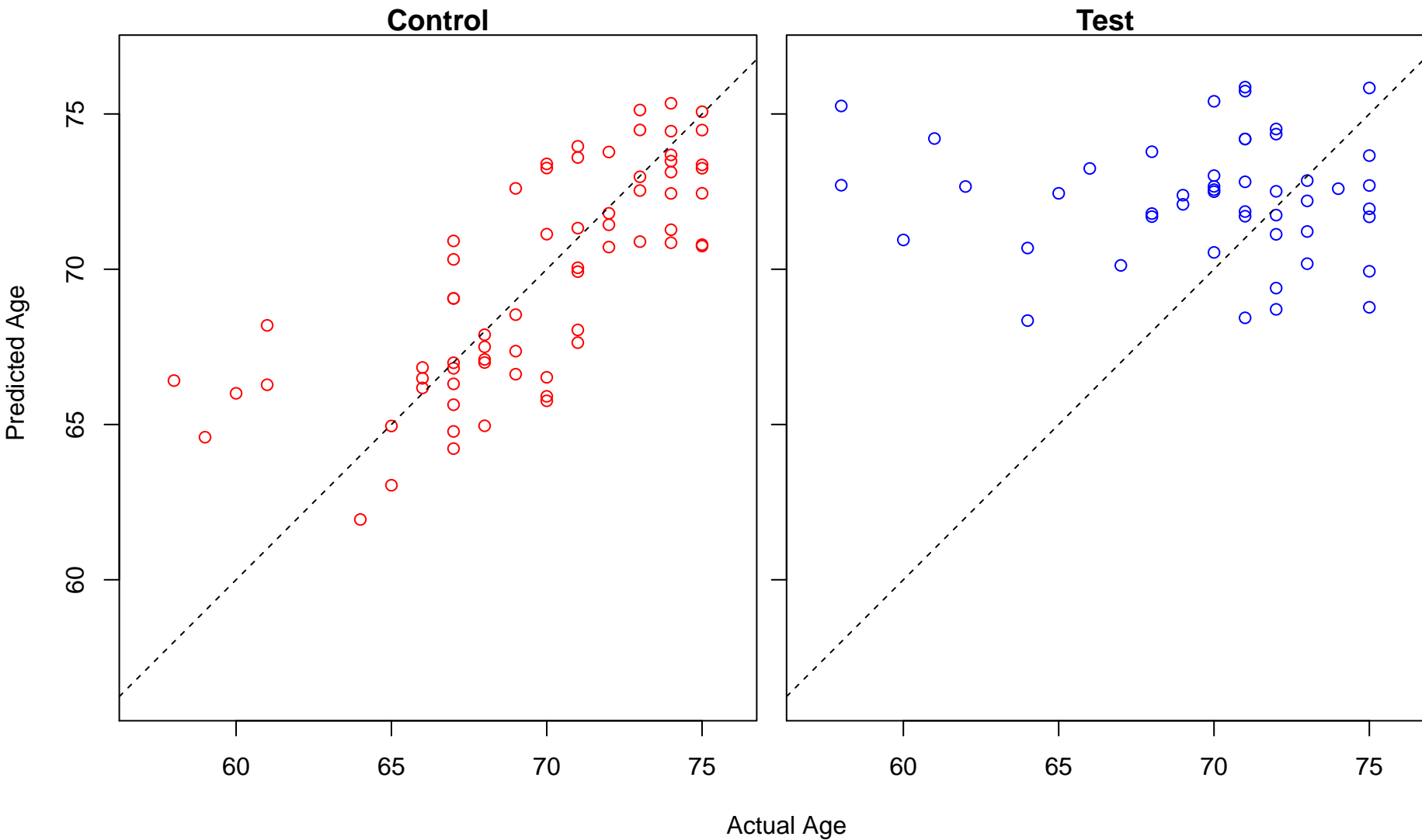
regulation of cellular protein catabolic process (Score: 1.905401)



insulin receptor signaling pathway (Score: 1.904557)

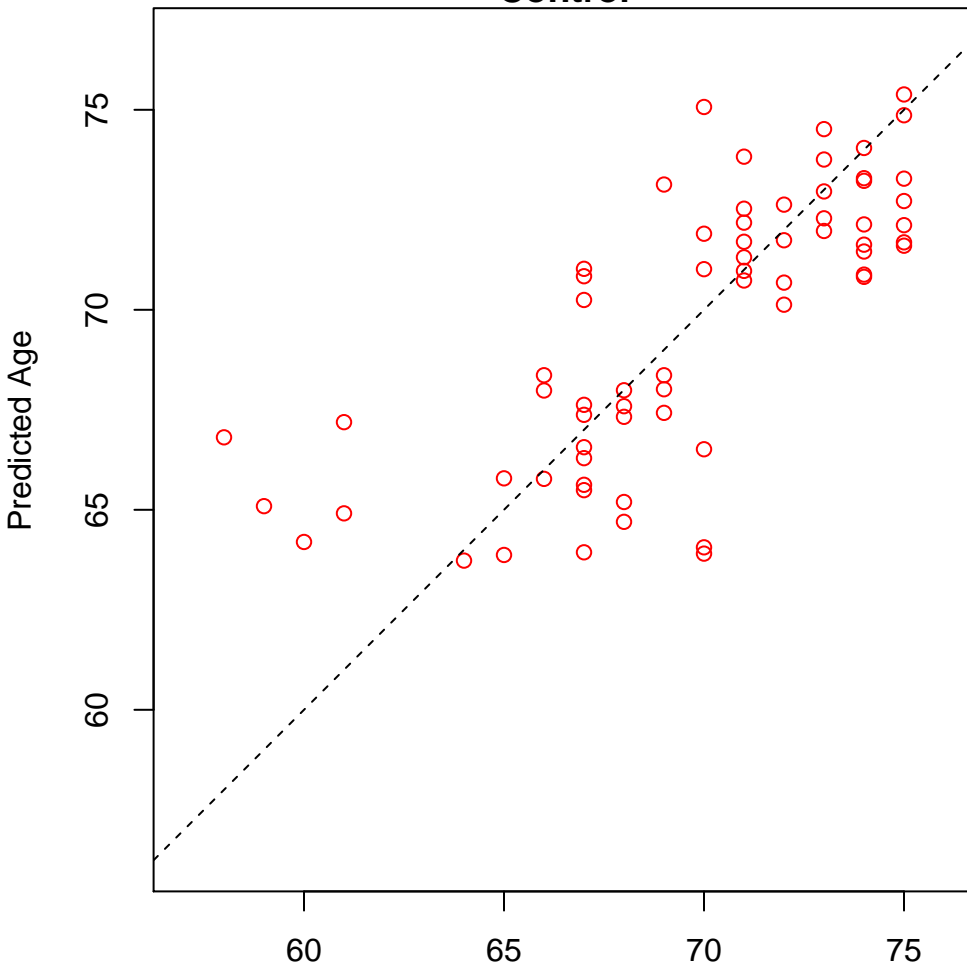


biological adhesion (Score: 1.904381)

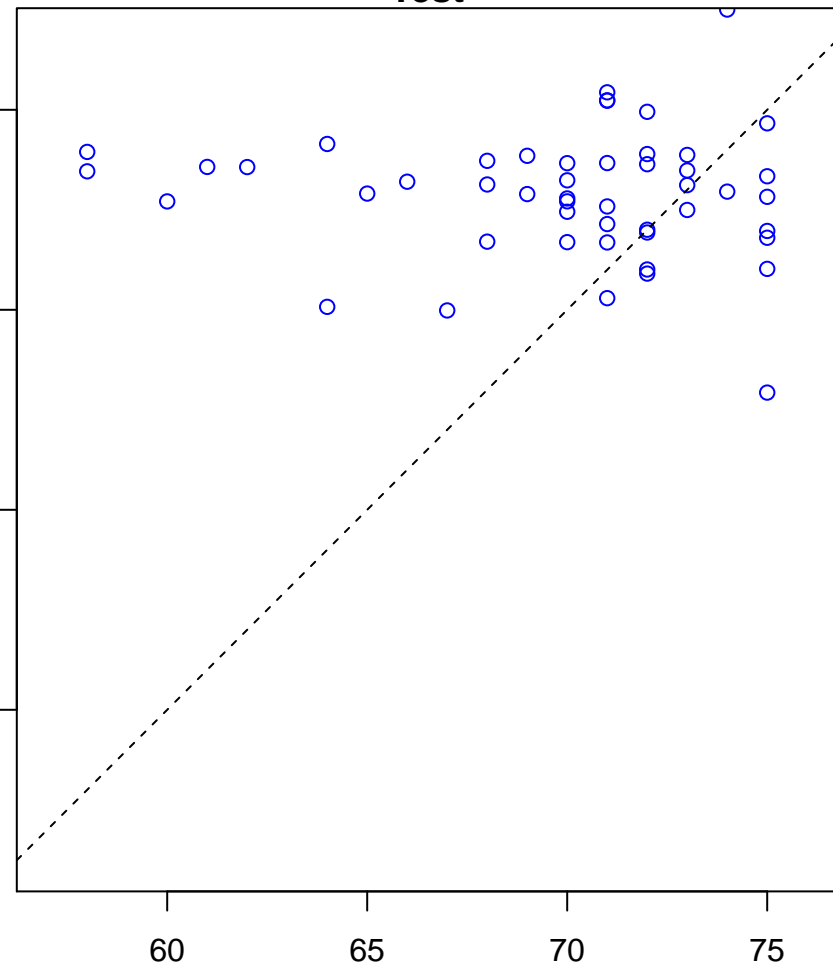


post-translational protein modification (Score: 1.903331)

Control

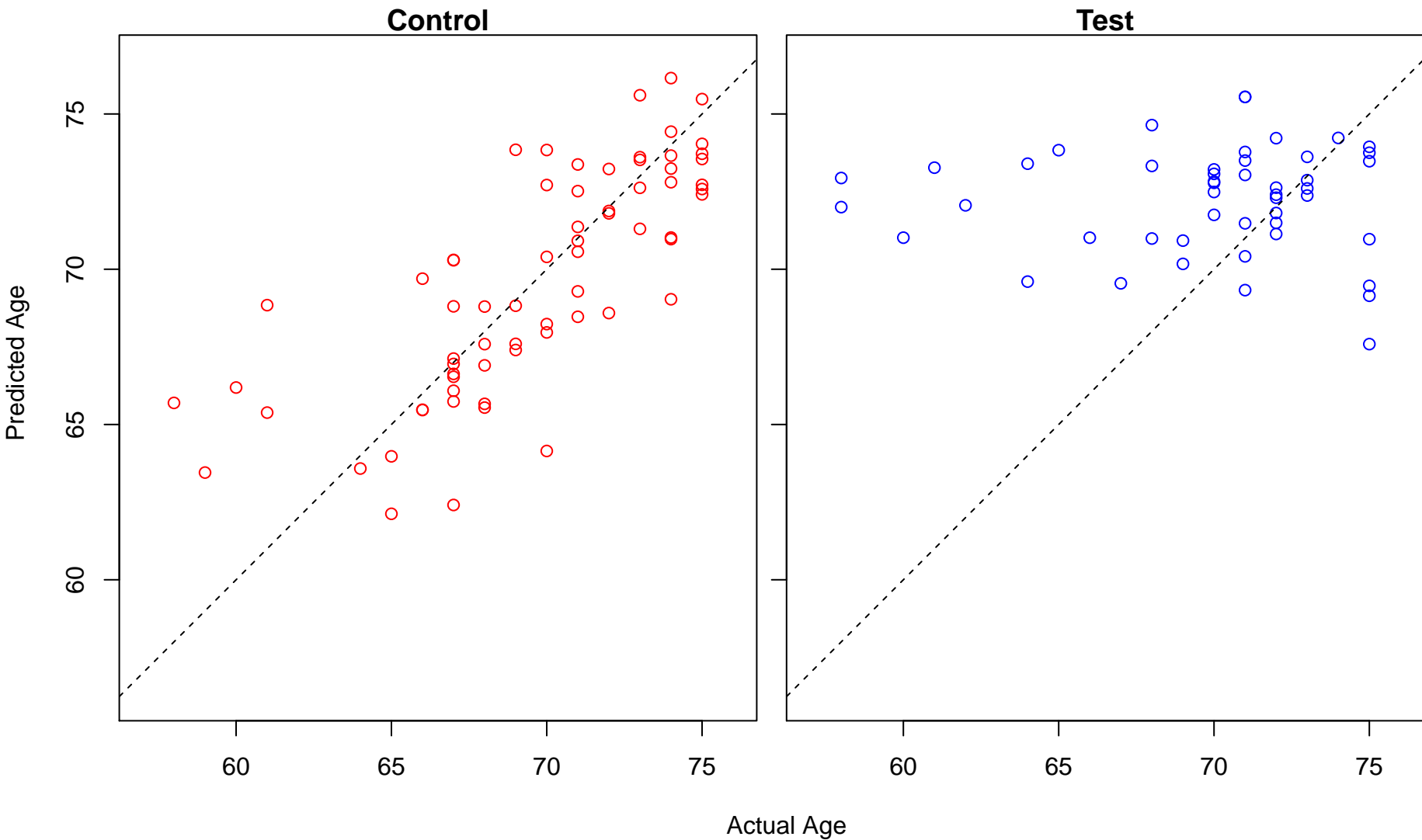


Test

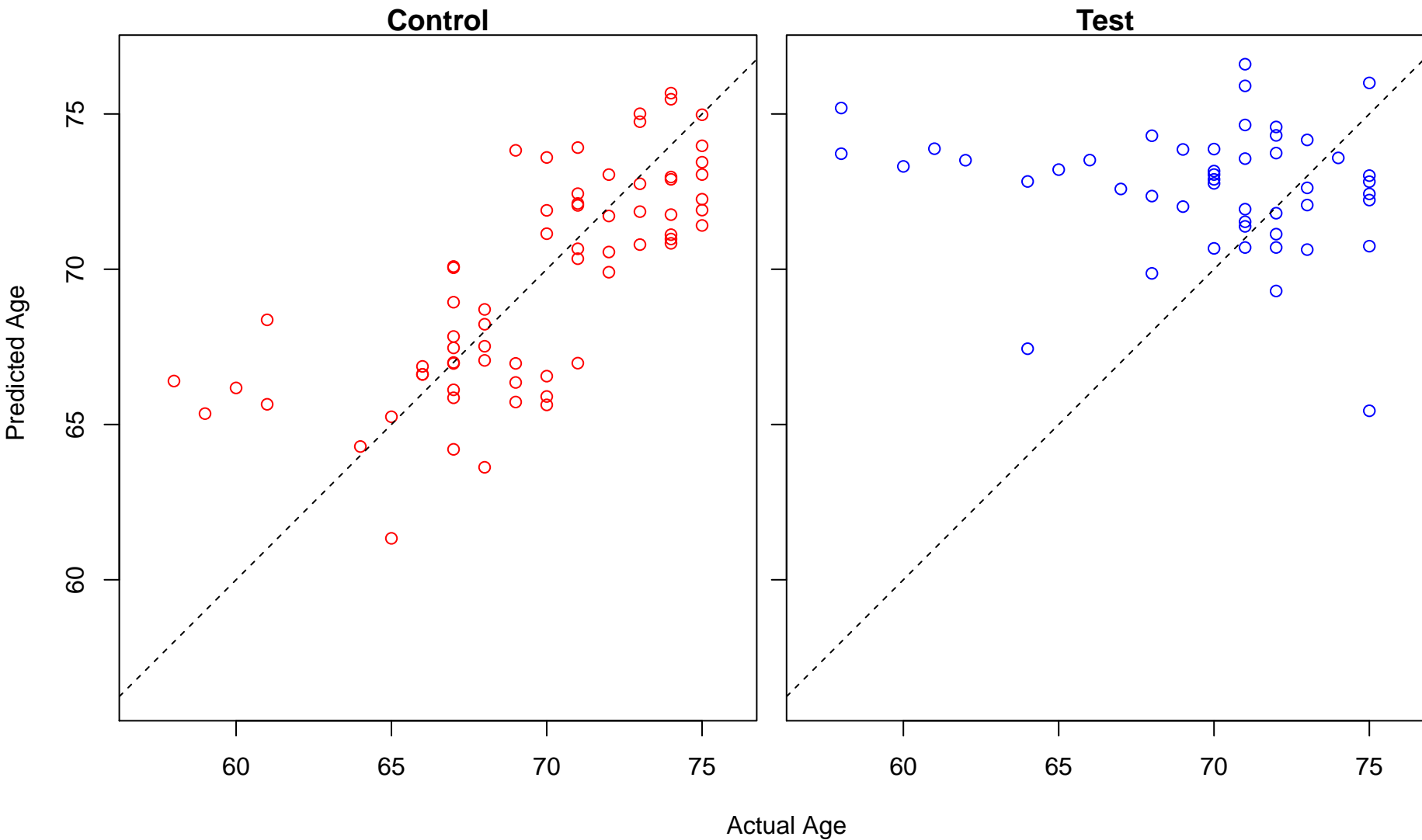


Actual Age

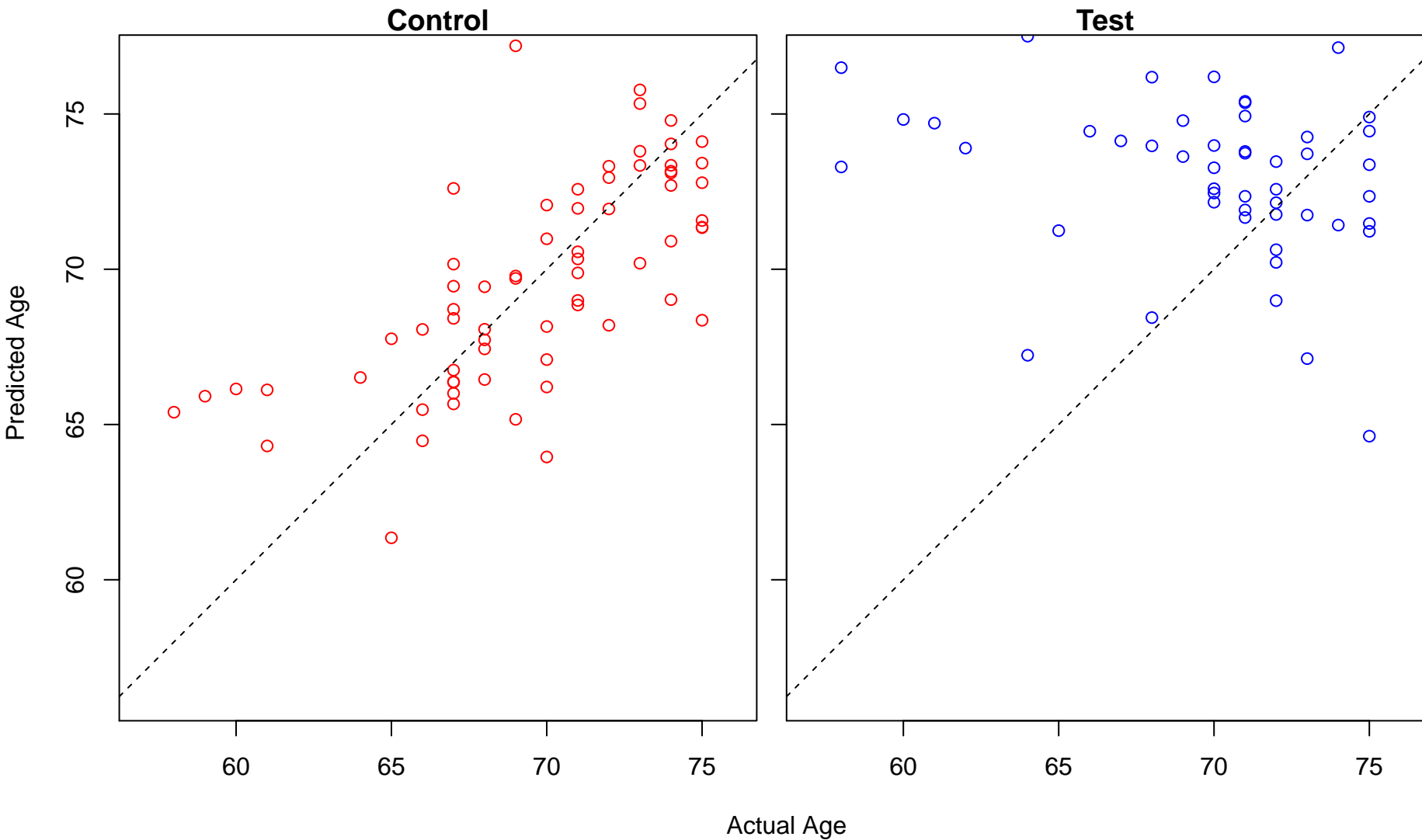
activation of MAPKK activity (Score: 1.901966)



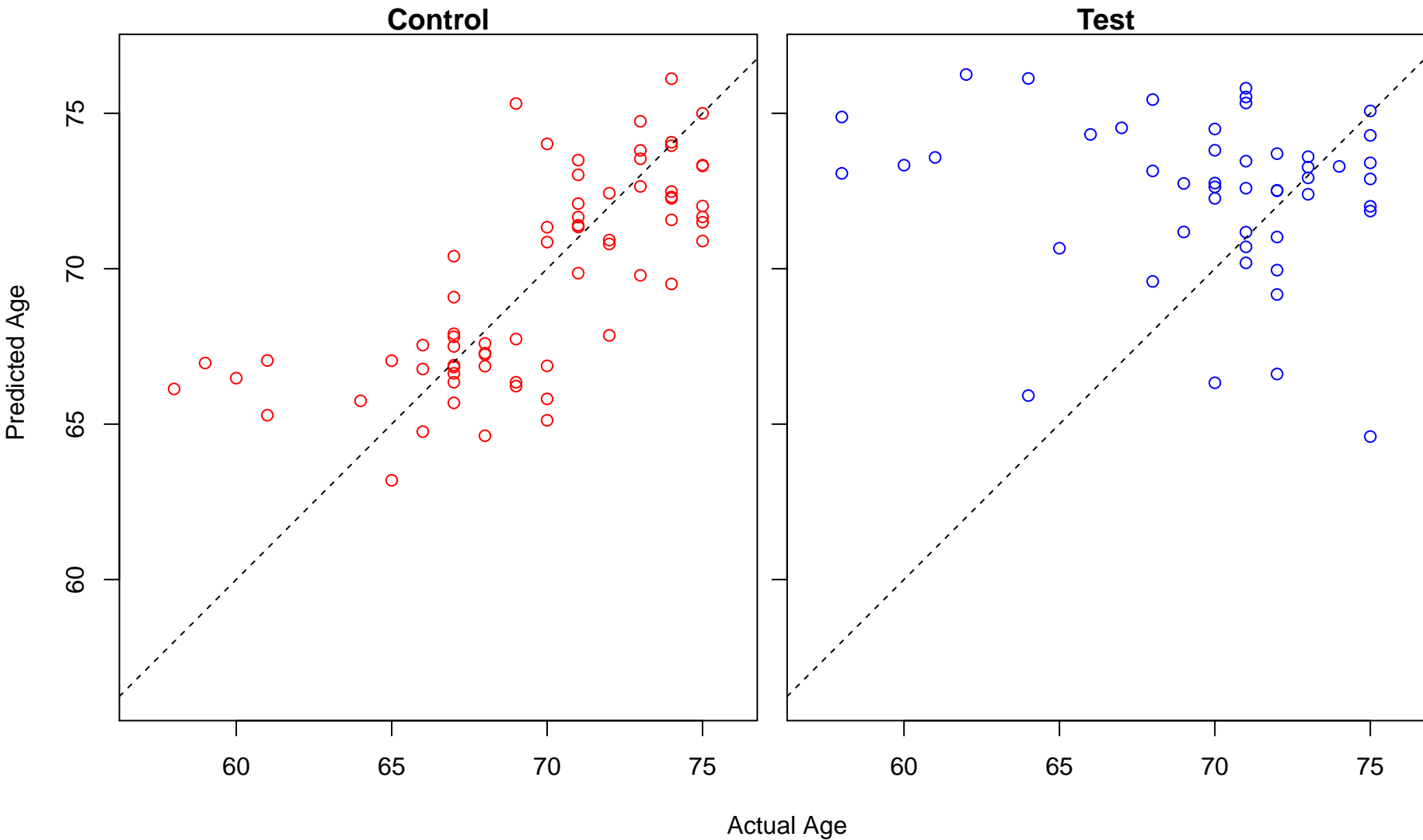
regulation of cell motility (Score: 1.901909)



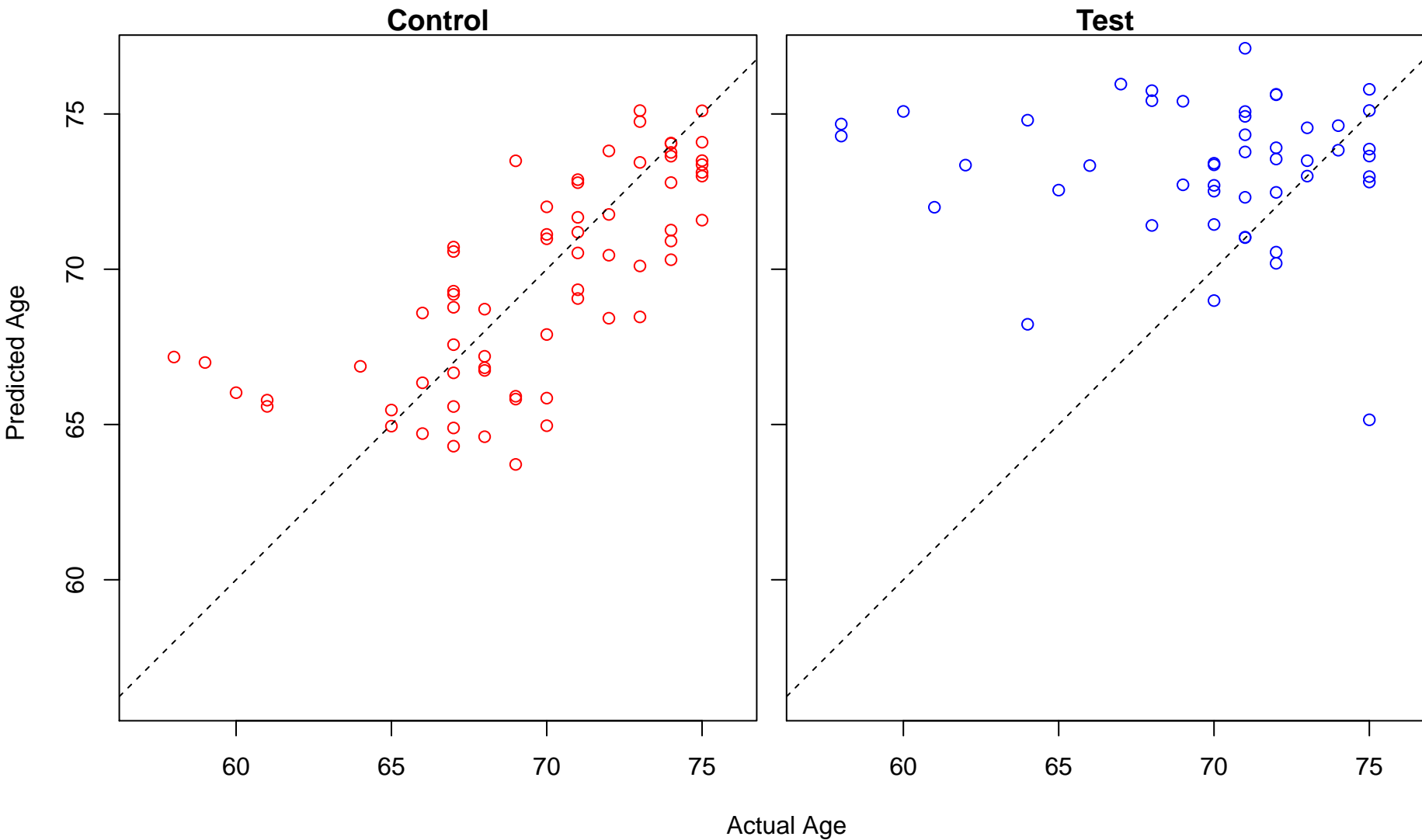
positive regulation of T cell differentiation (Score: 1.901734)



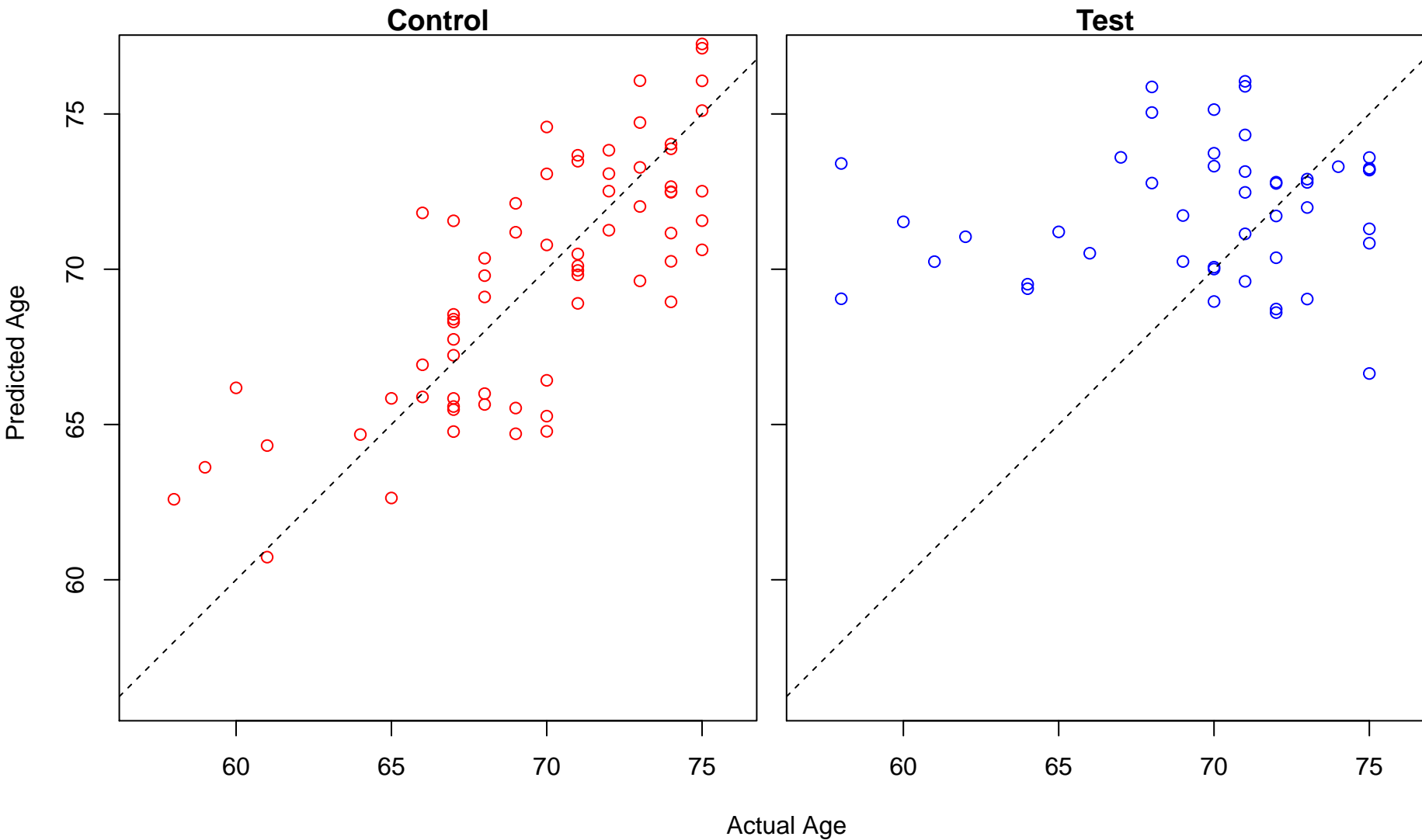
positive regulation of lymphocyte migration (Score: 1.901295)



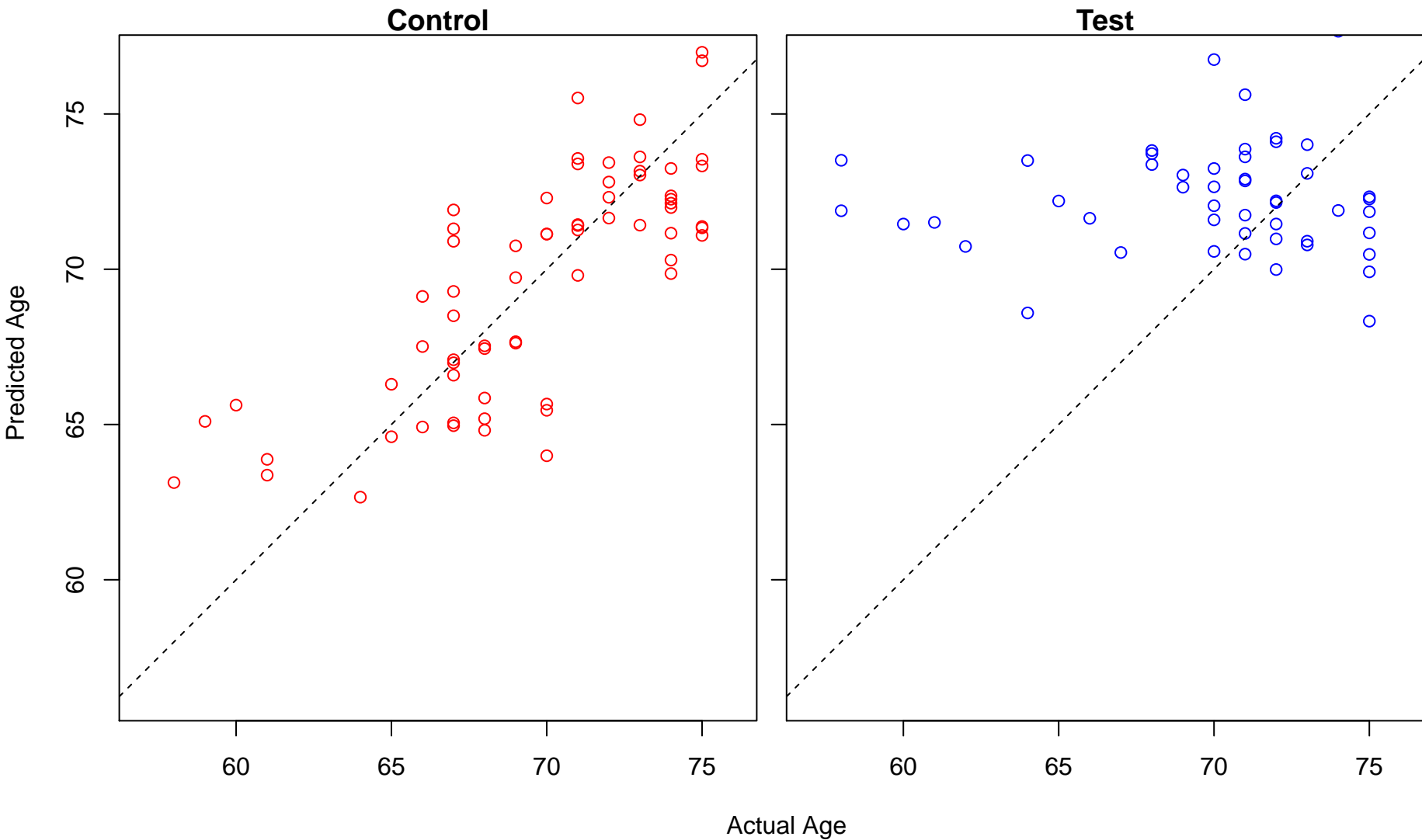
negative regulation of cell motility (Score: 1.901153)



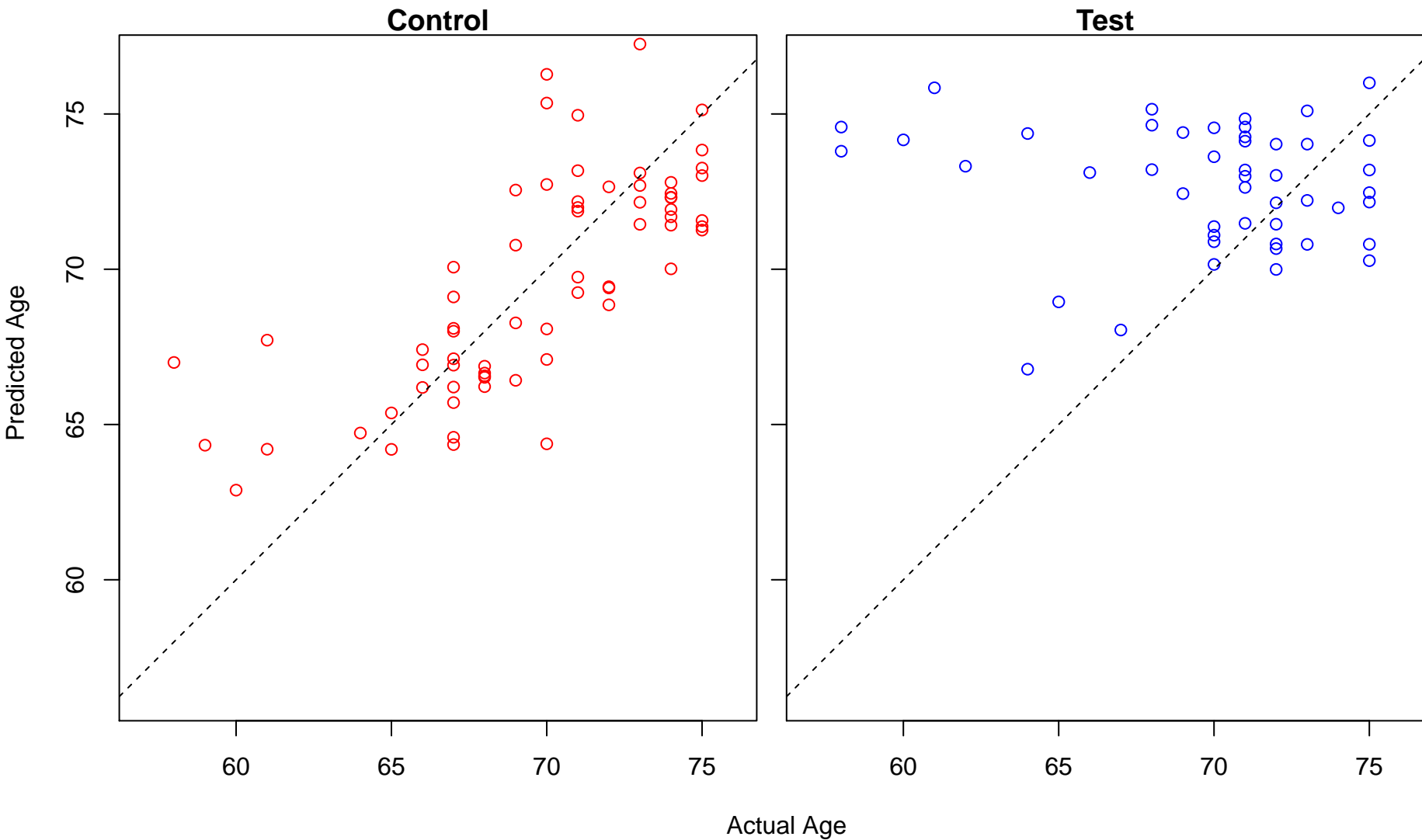
liposaccharide metabolic process (Score: 1.900689)



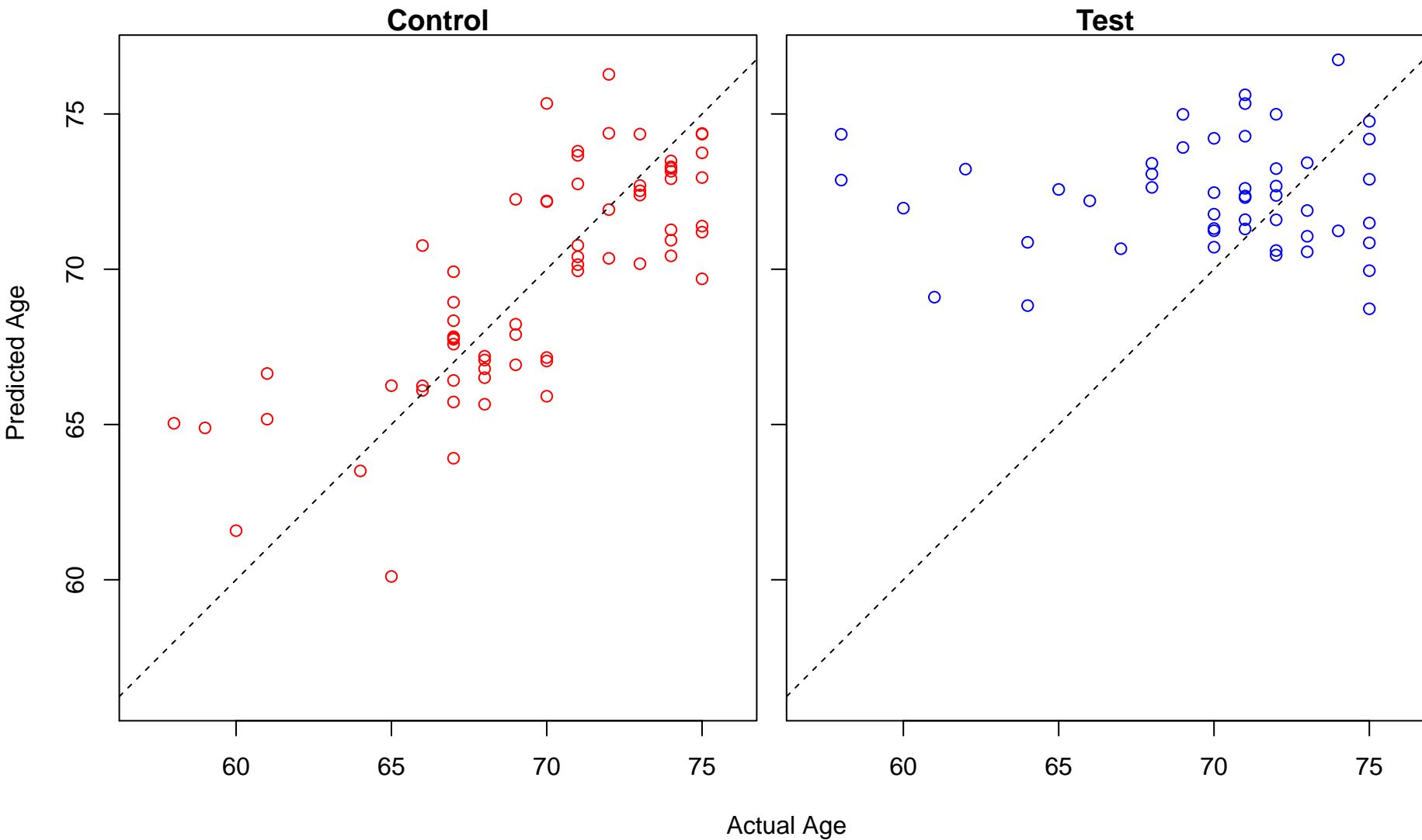
C-terminal protein amino acid modification (Score: 1.900653)



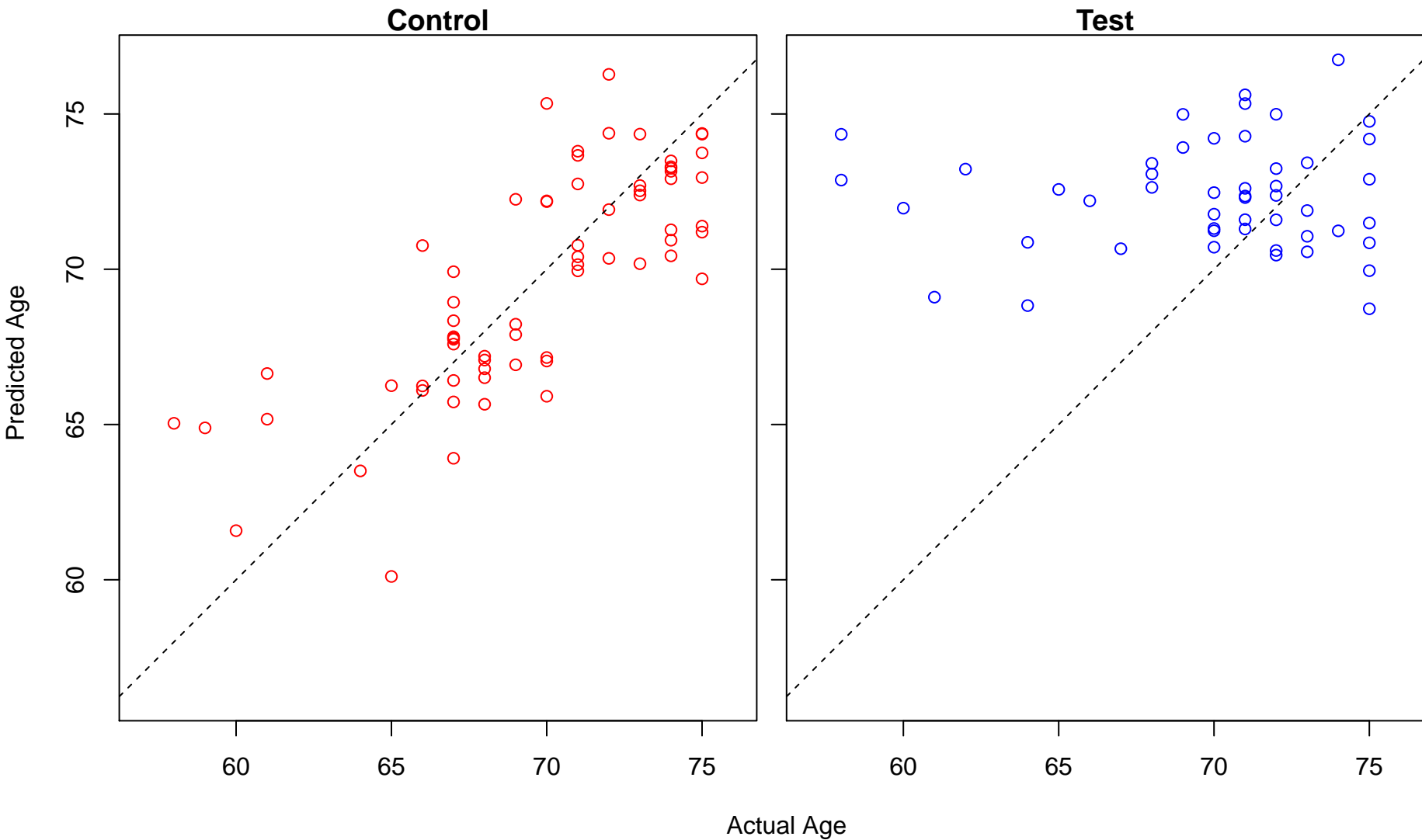
epithelium development (Score: 1.900141)



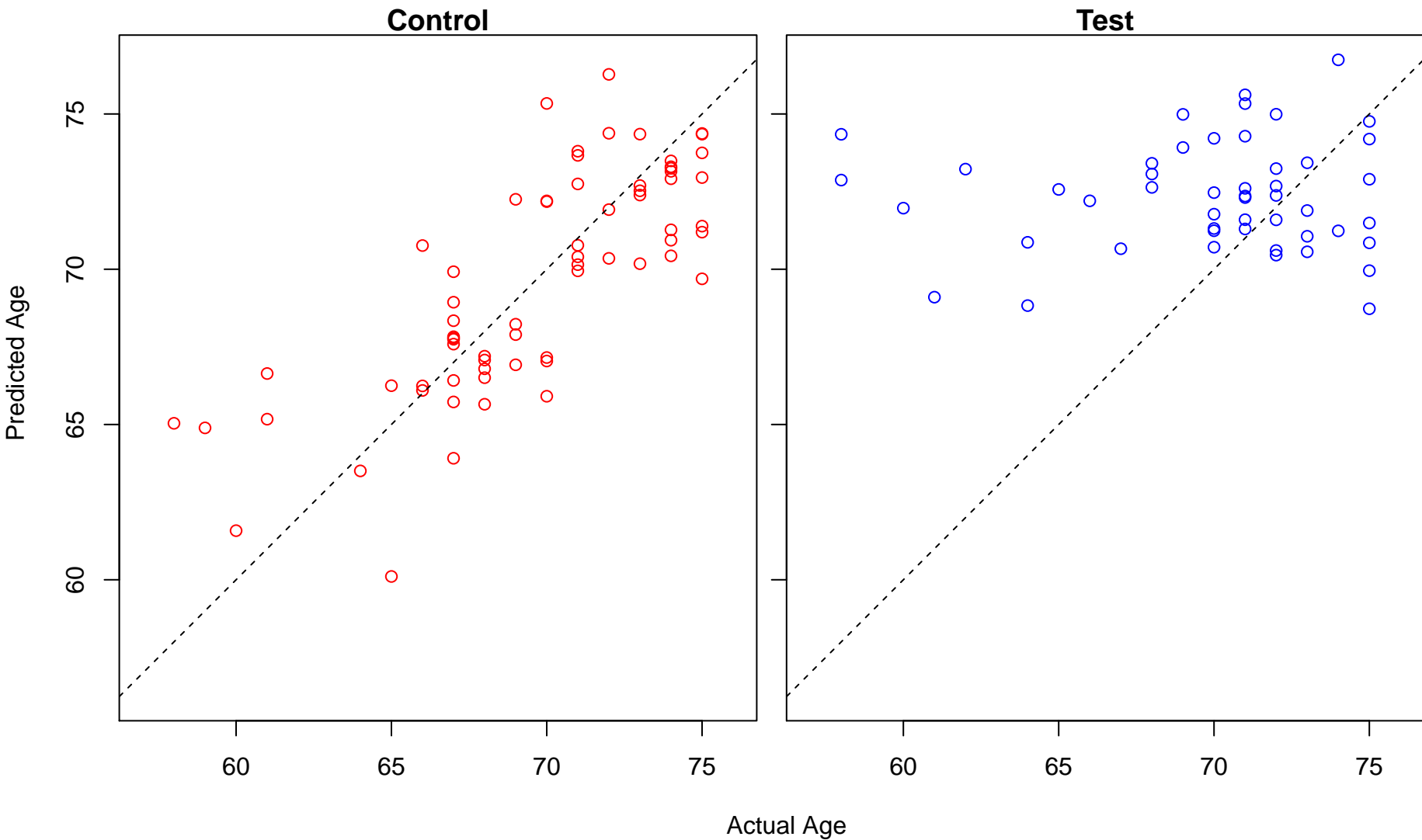
protein import into nucleus (Score: 1.899883)



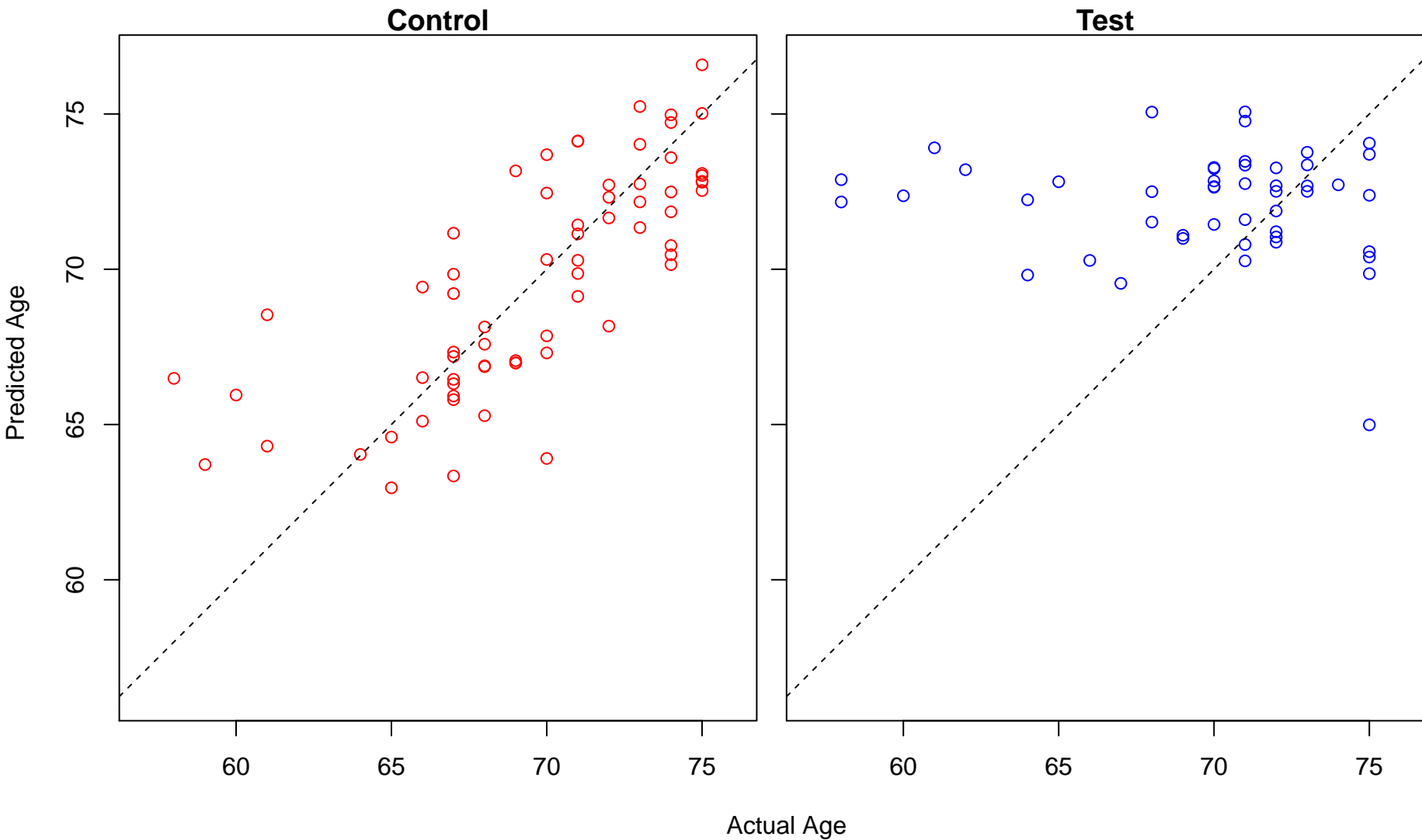
protein targeting to nucleus (Score: 1.899883)



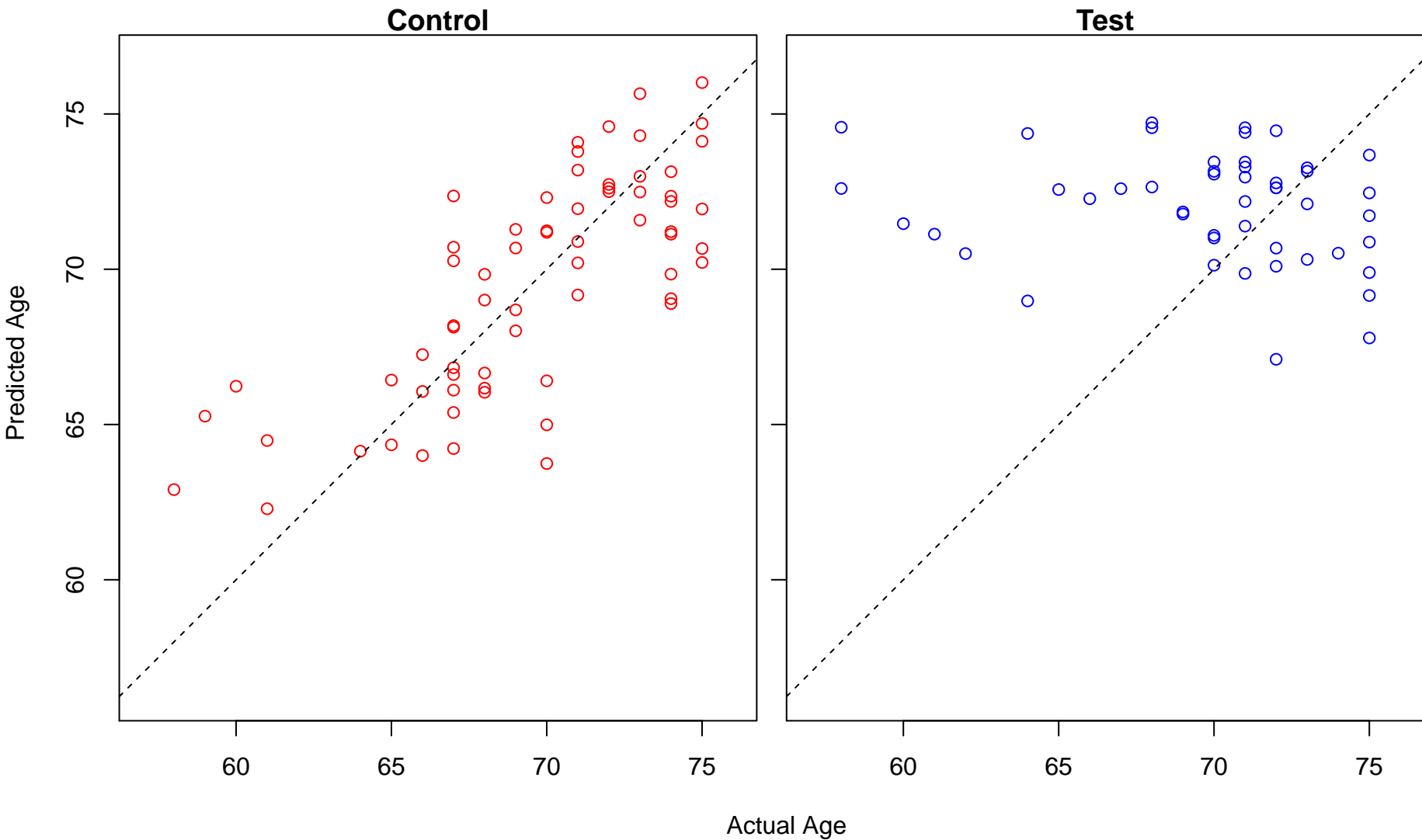
single-organism nuclear import (Score: 1.899883)



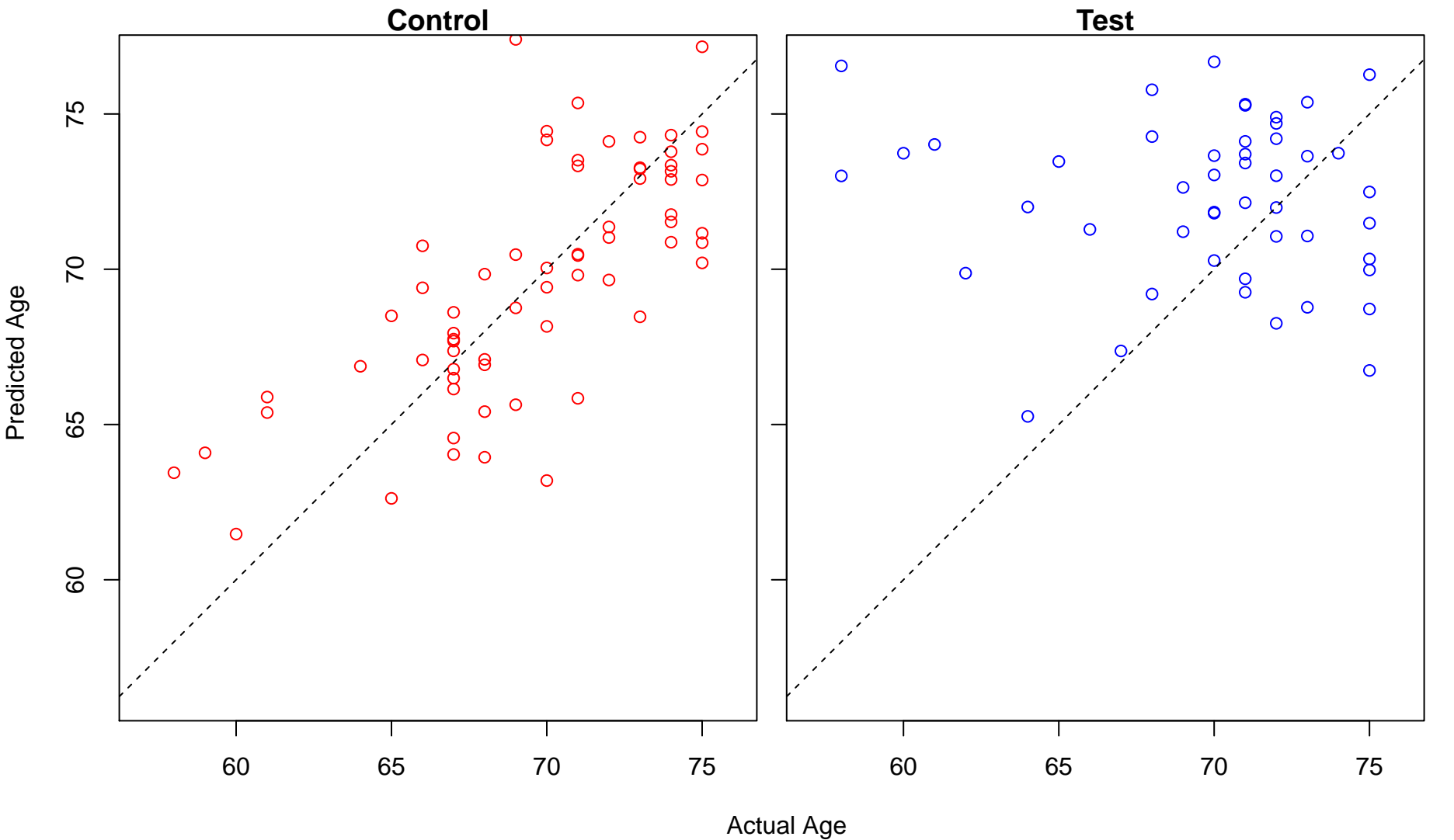
ERBB signaling pathway (Score: 1.898732)



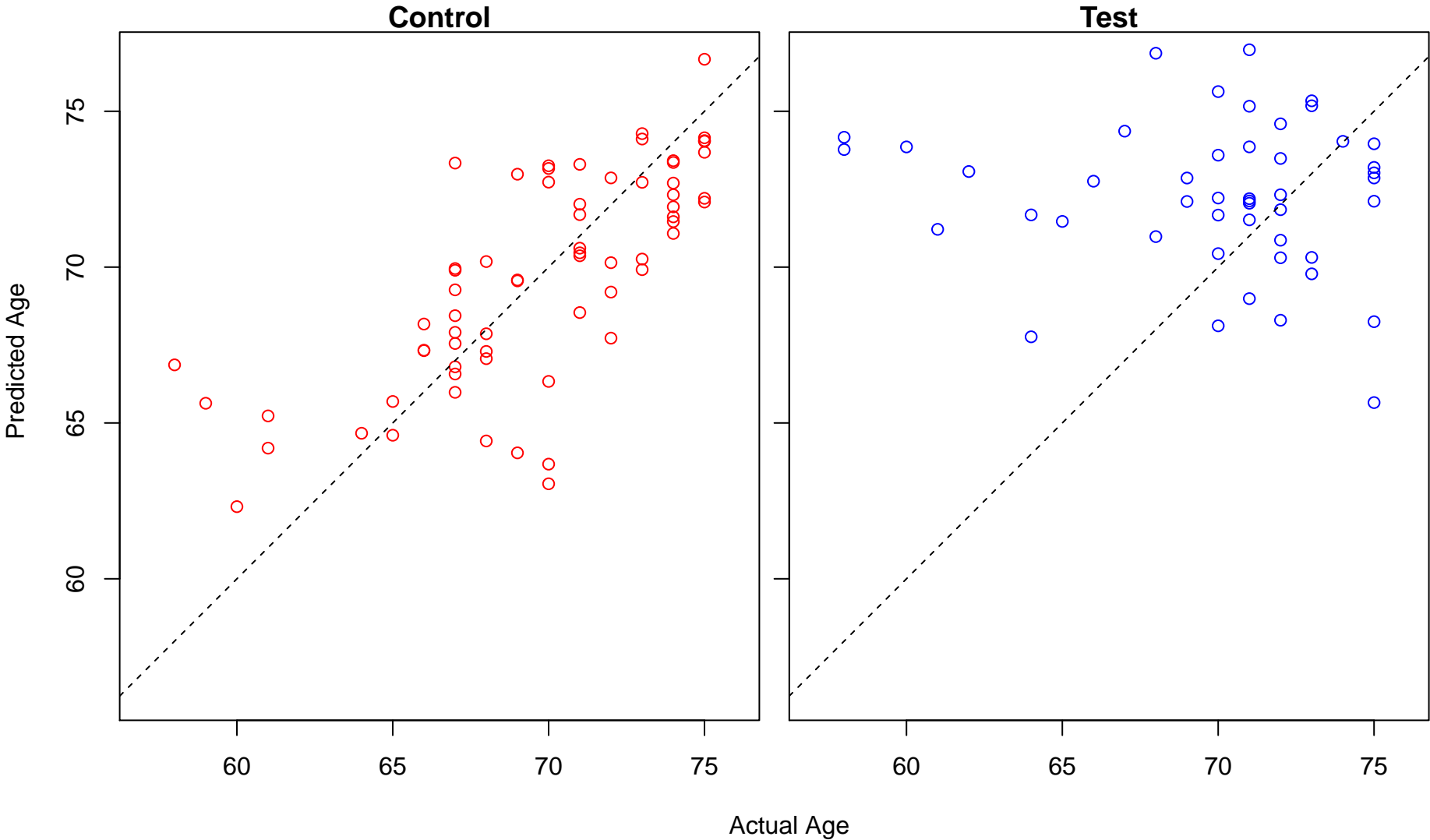
C-terminal protein lipidation (Score: 1.897171)



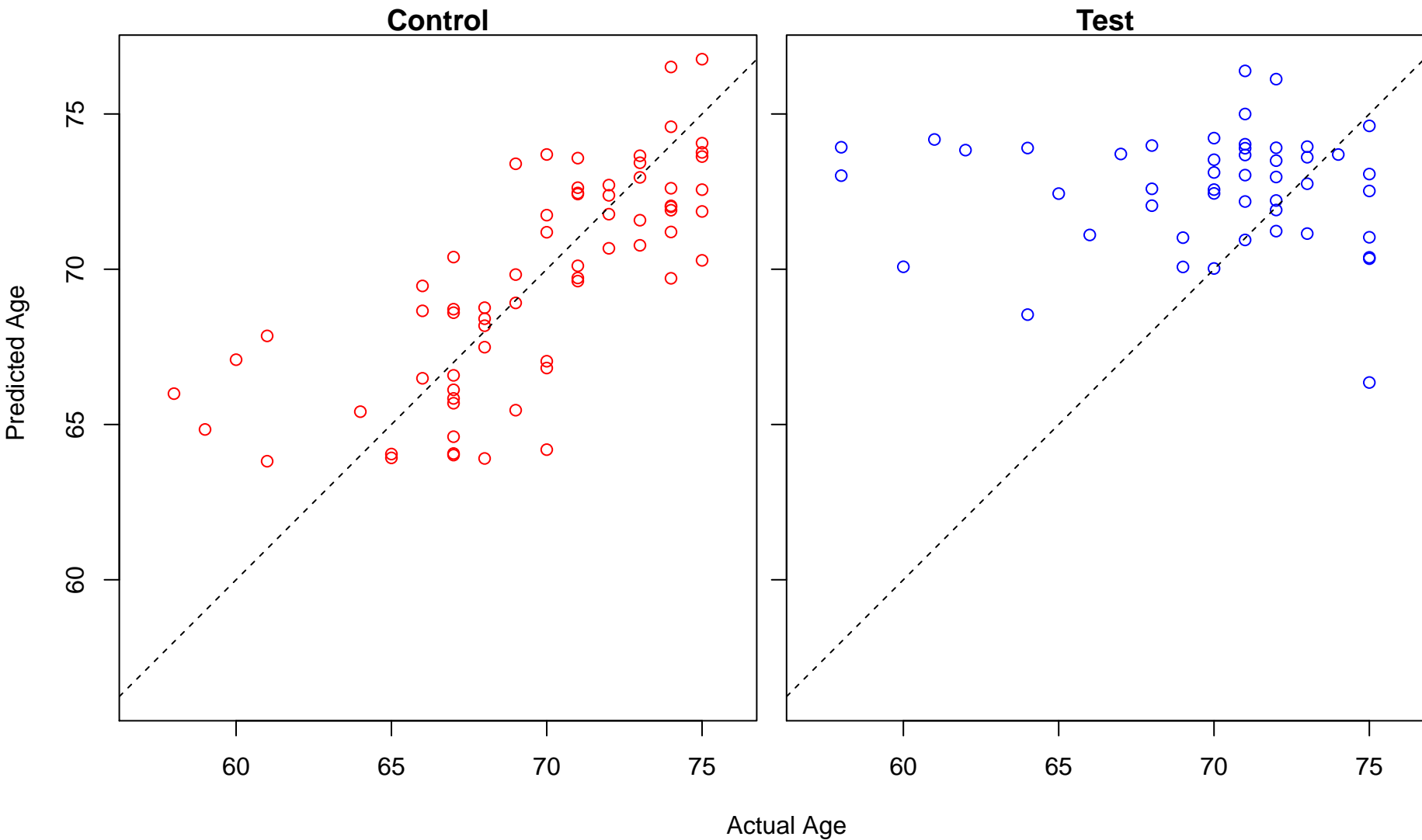
response based on somatic recombination of immune receptors built from immunoglobulin superfamily c



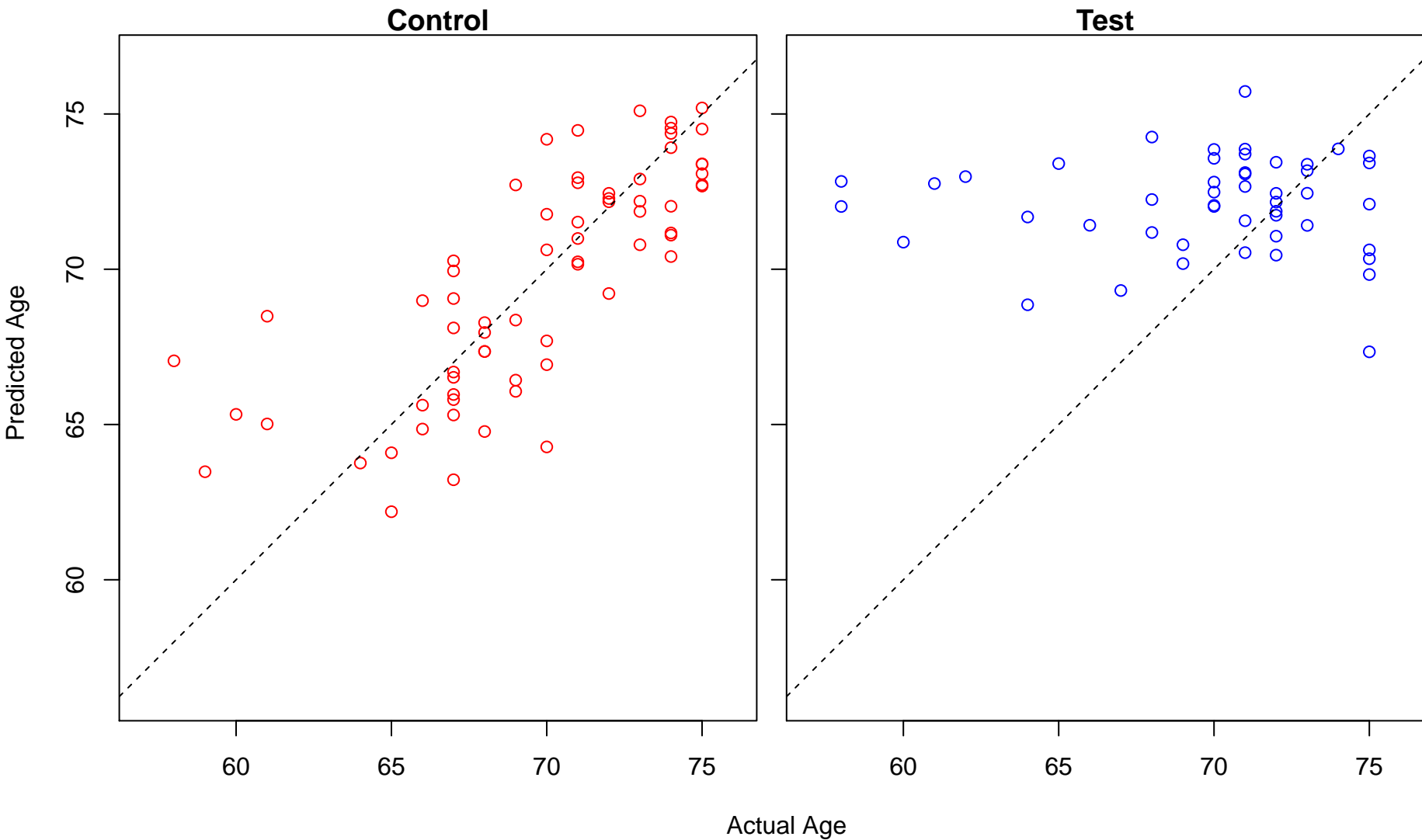
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (Score: 1.896)



DNA conformation change (Score: 1.895955)

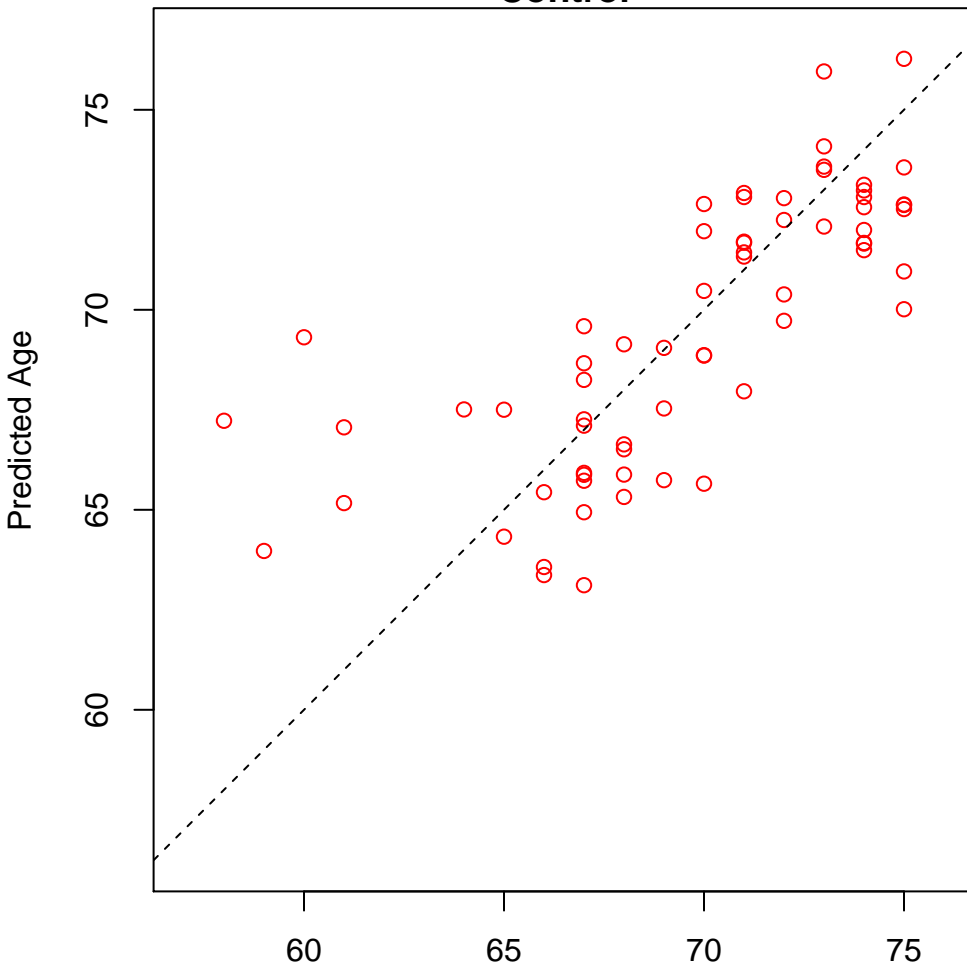


response to peptide hormone (Score: 1.895766)

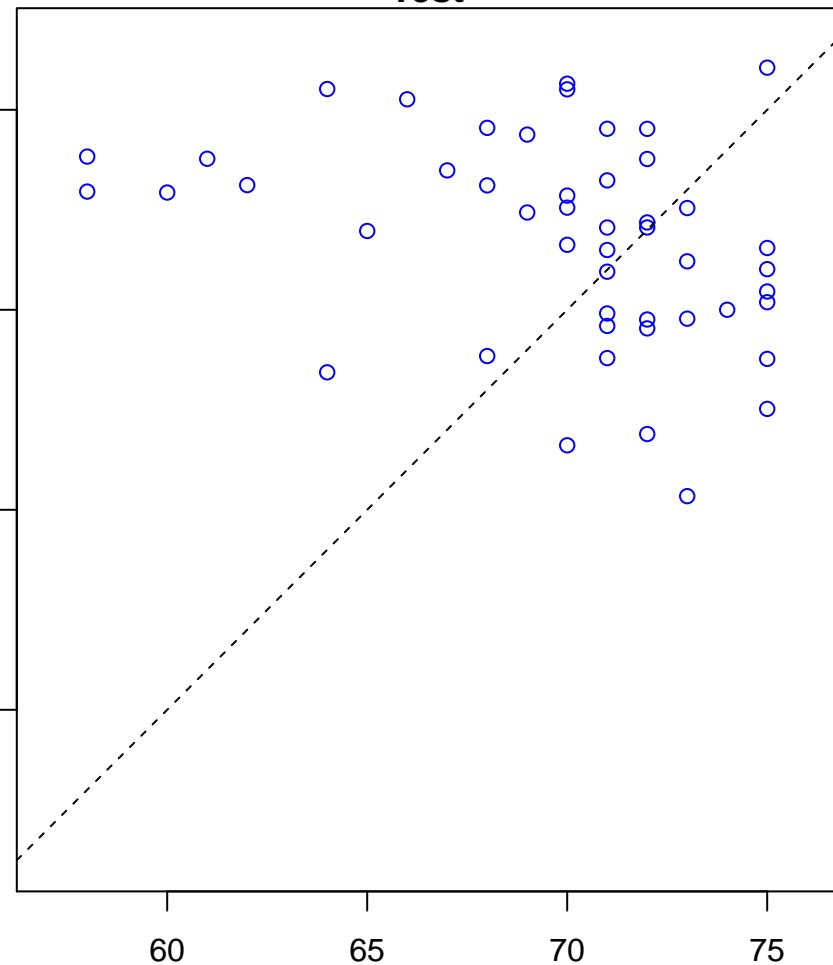


negative regulation of immune response (Score: 1.895503)

Control

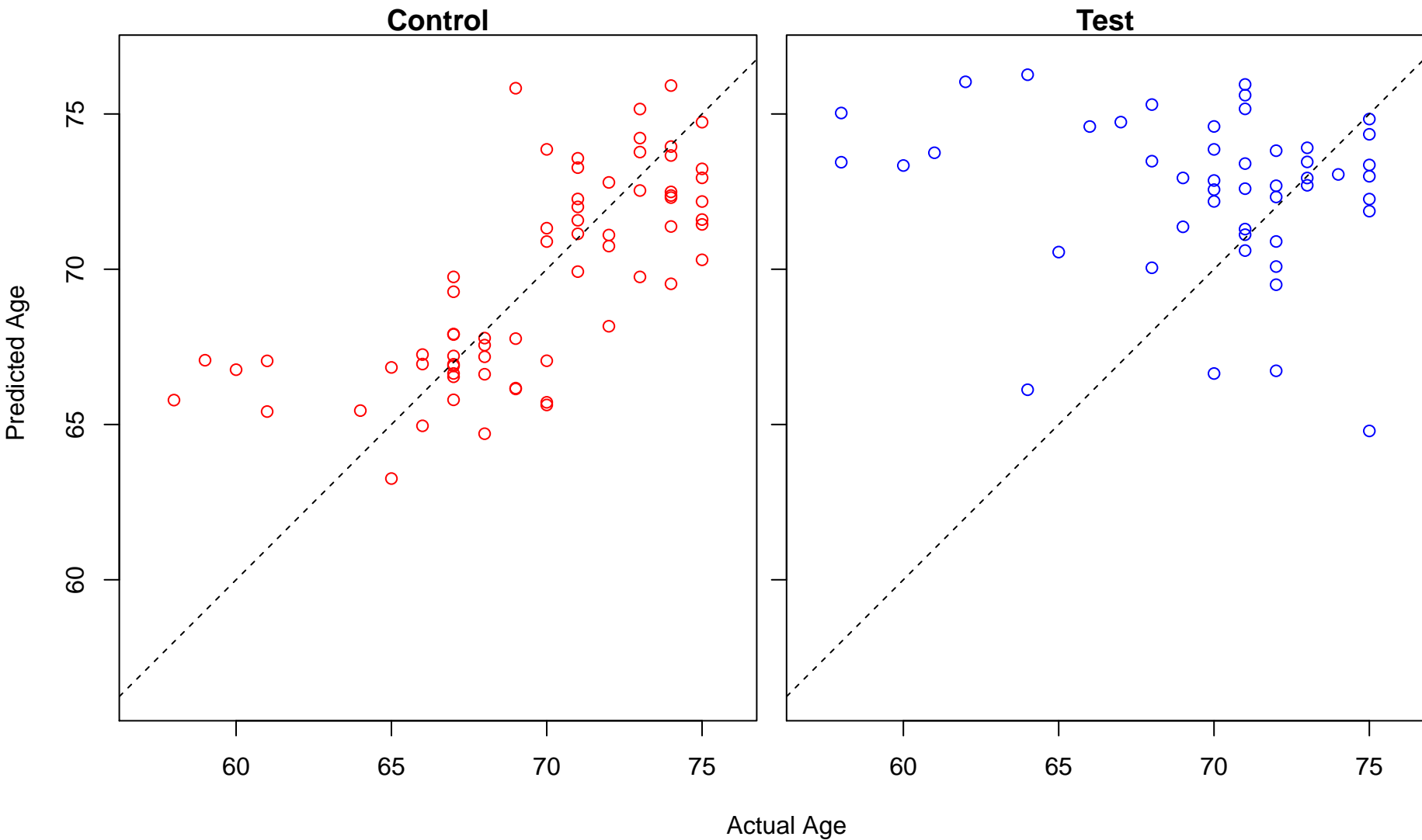


Test

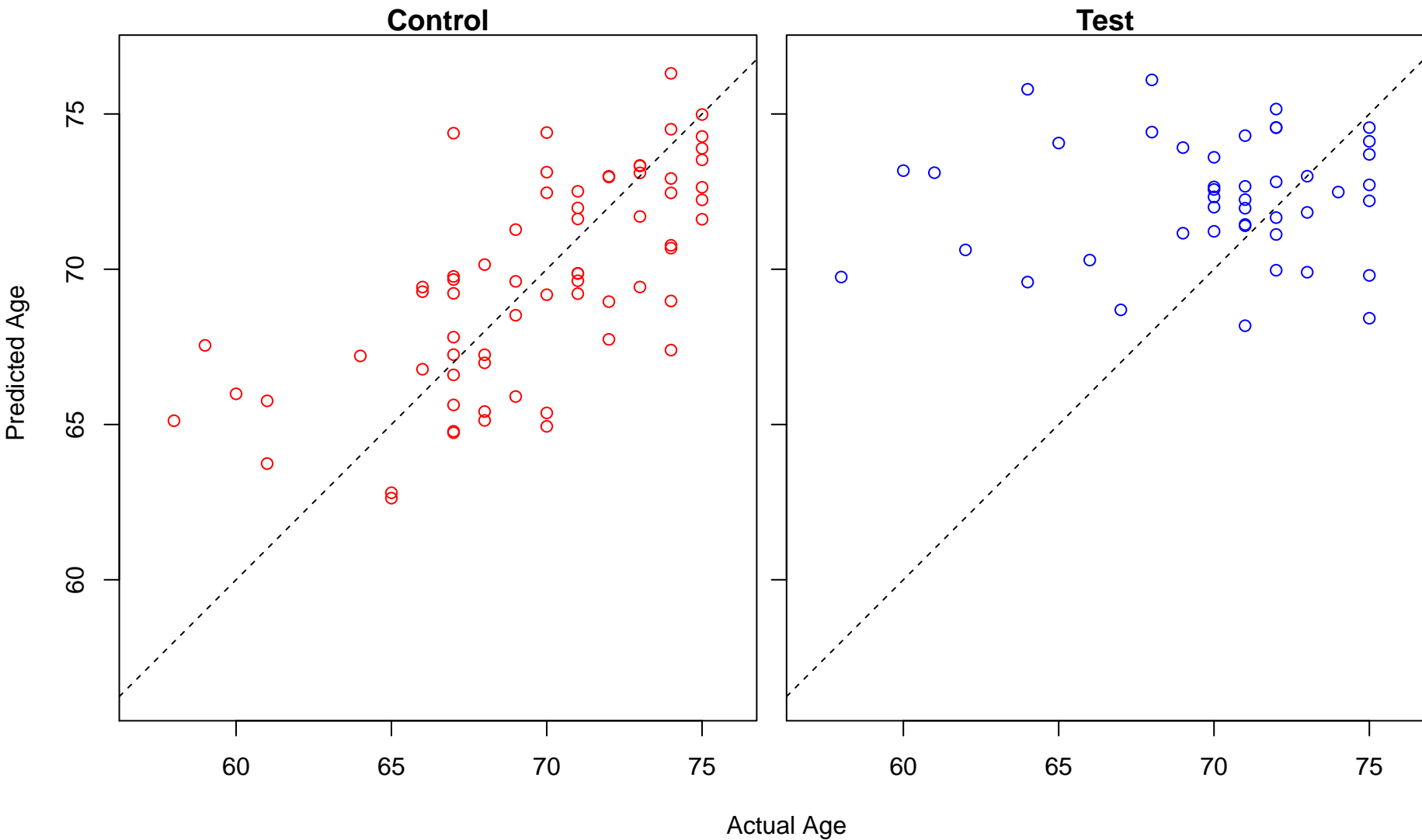


Actual Age

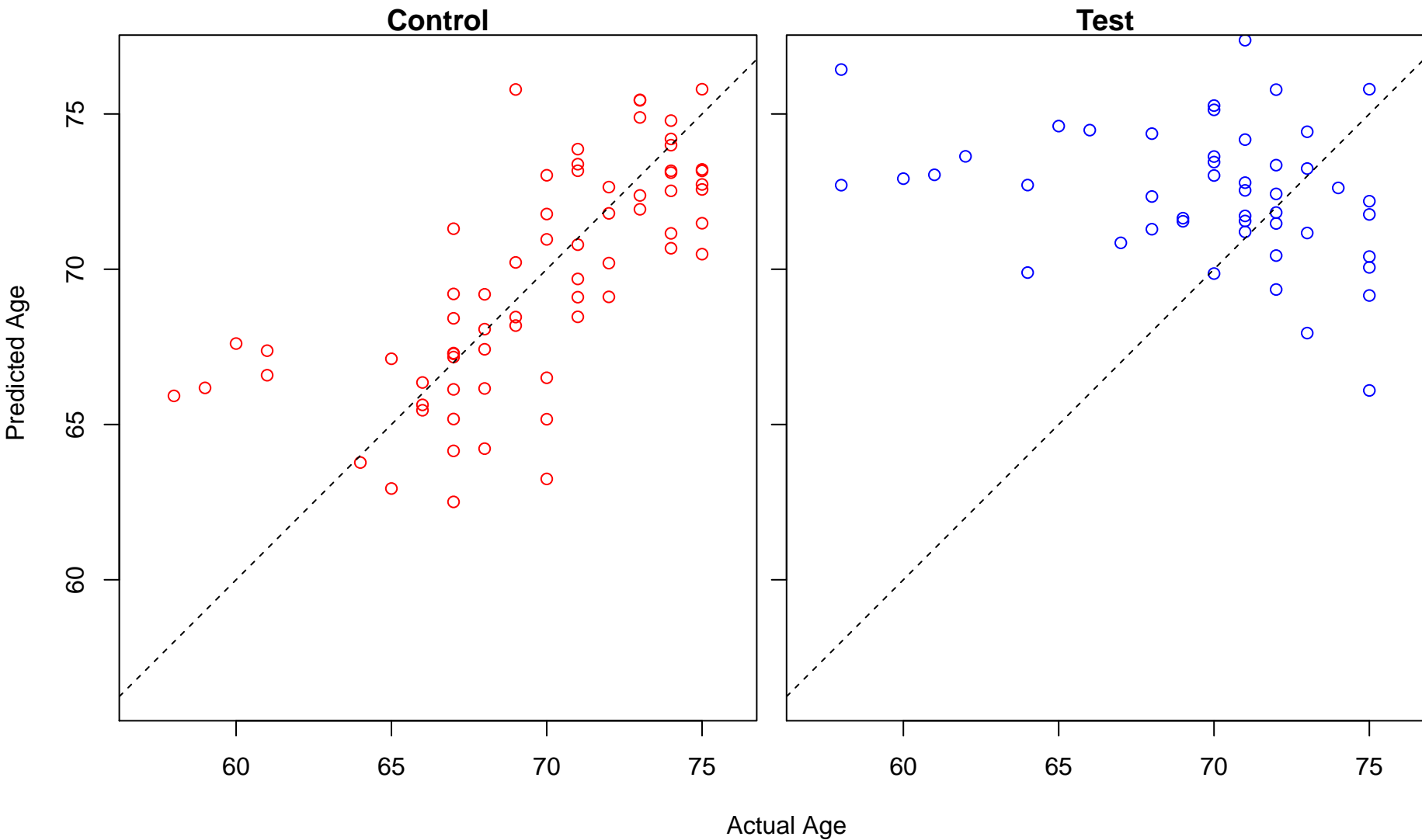
regulation of T cell migration (Score: 1.894666)



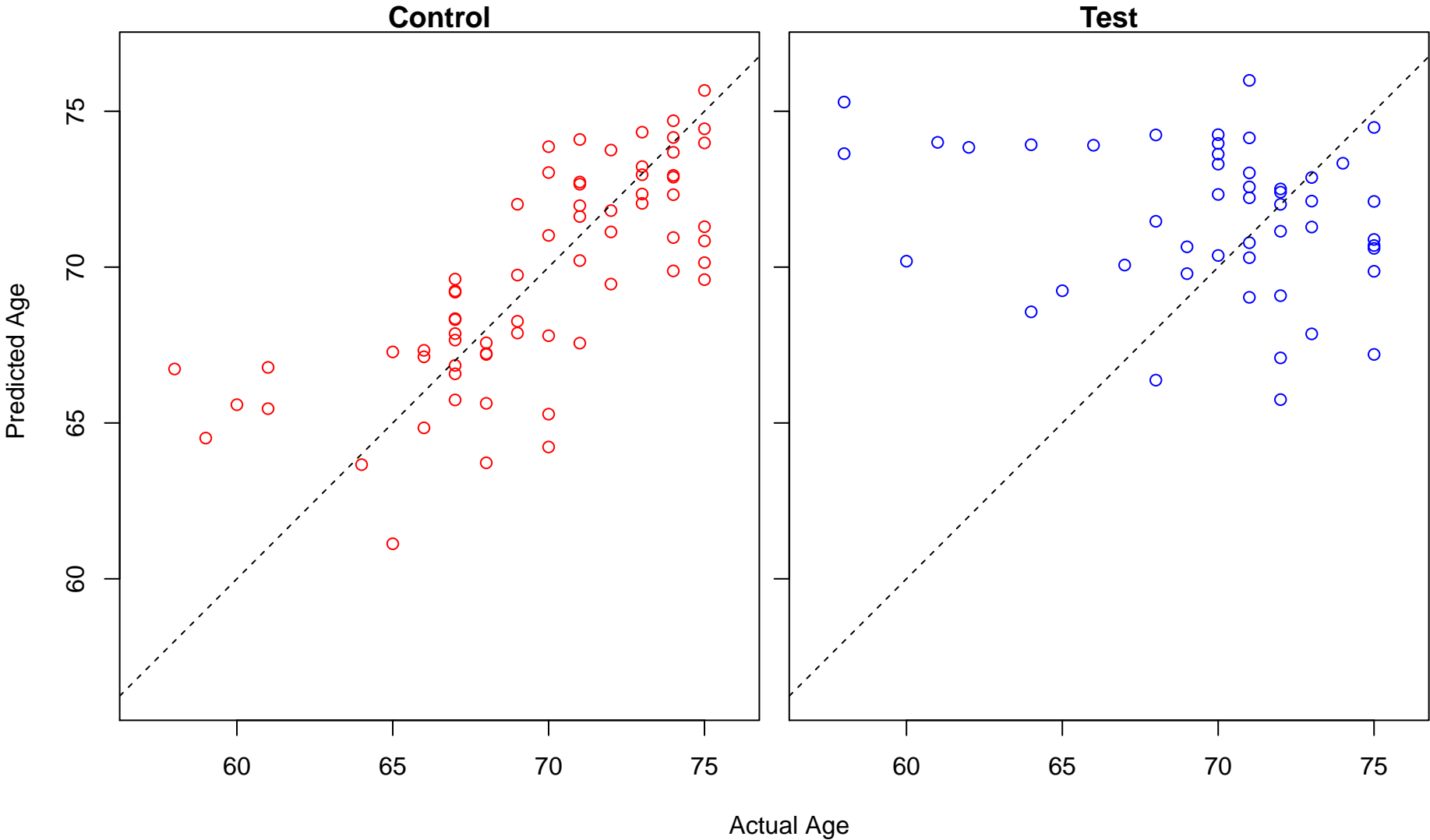
regulation of B cell proliferation (Score: 1.893980)



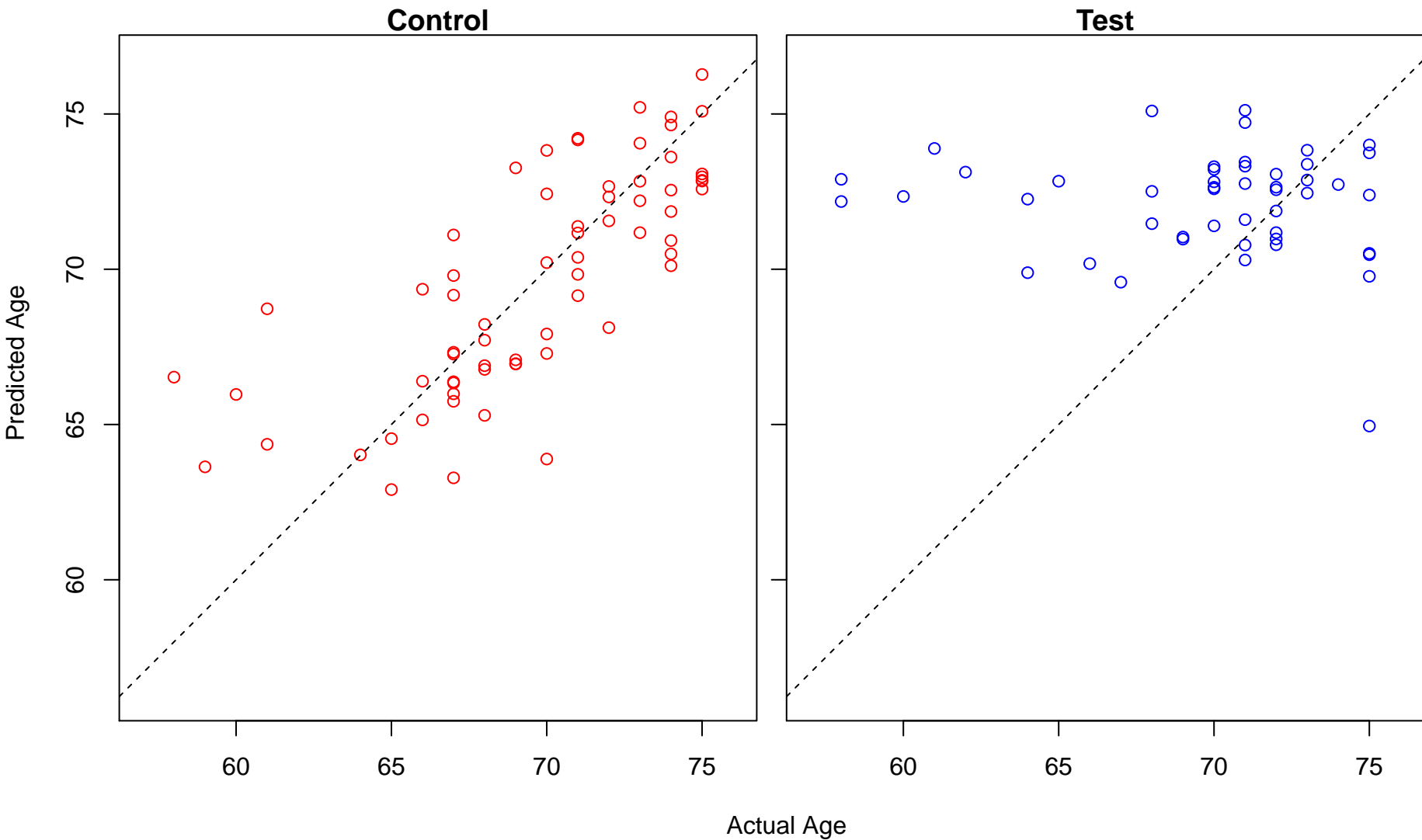
regulation of cytokine production (Score: 1.892751)



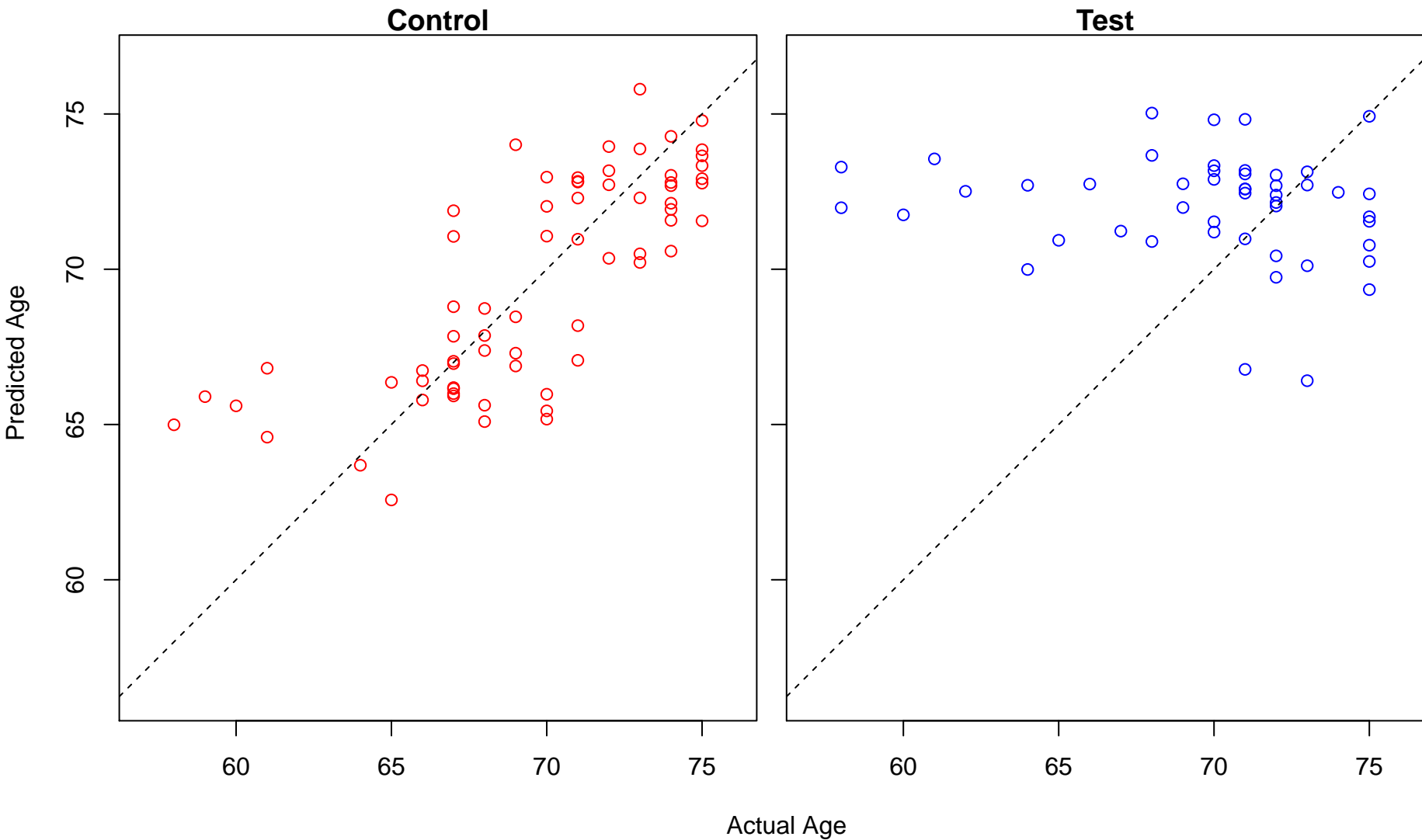
regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 1.89)



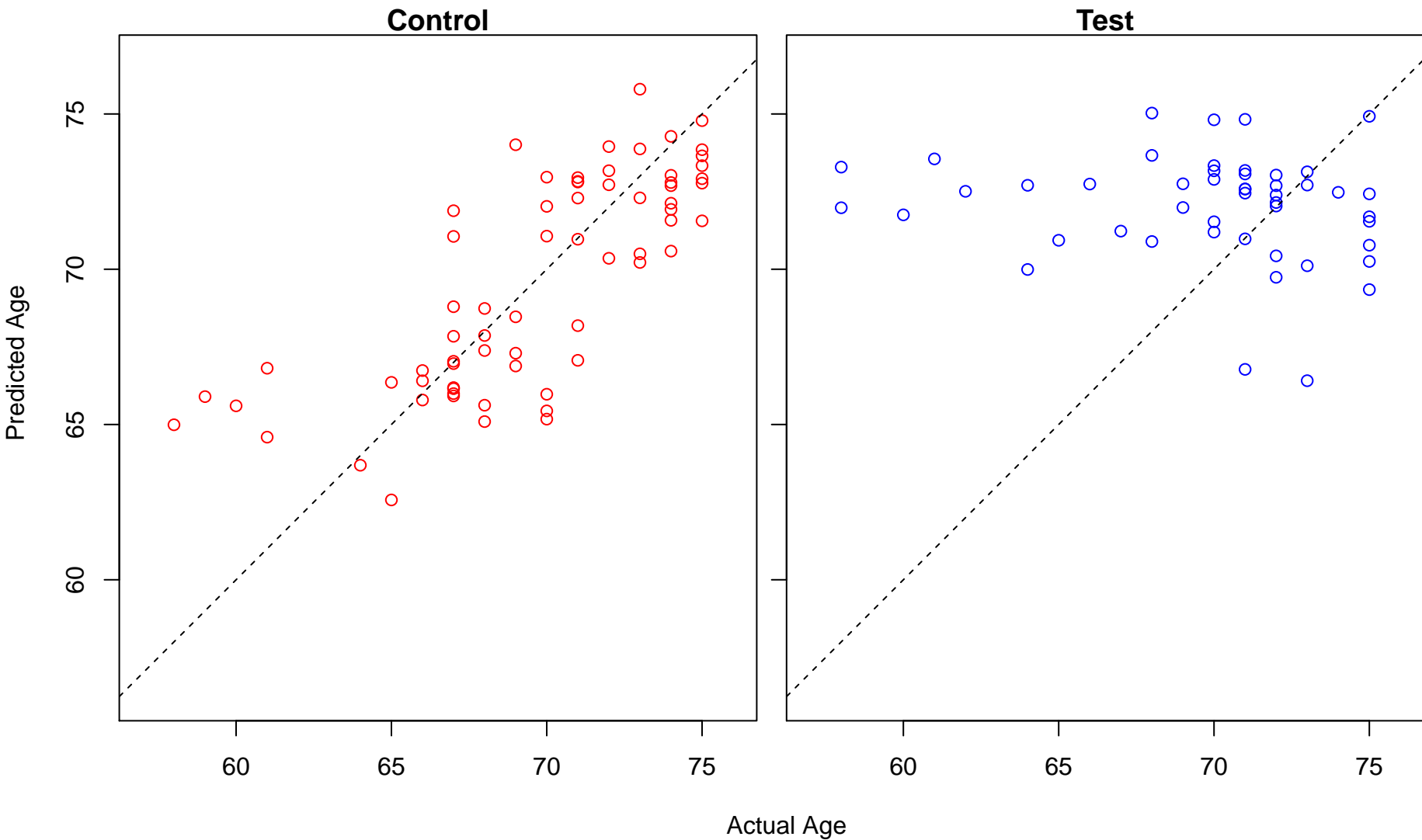
epidermal growth factor receptor signaling pathway (Score: 1.891383)



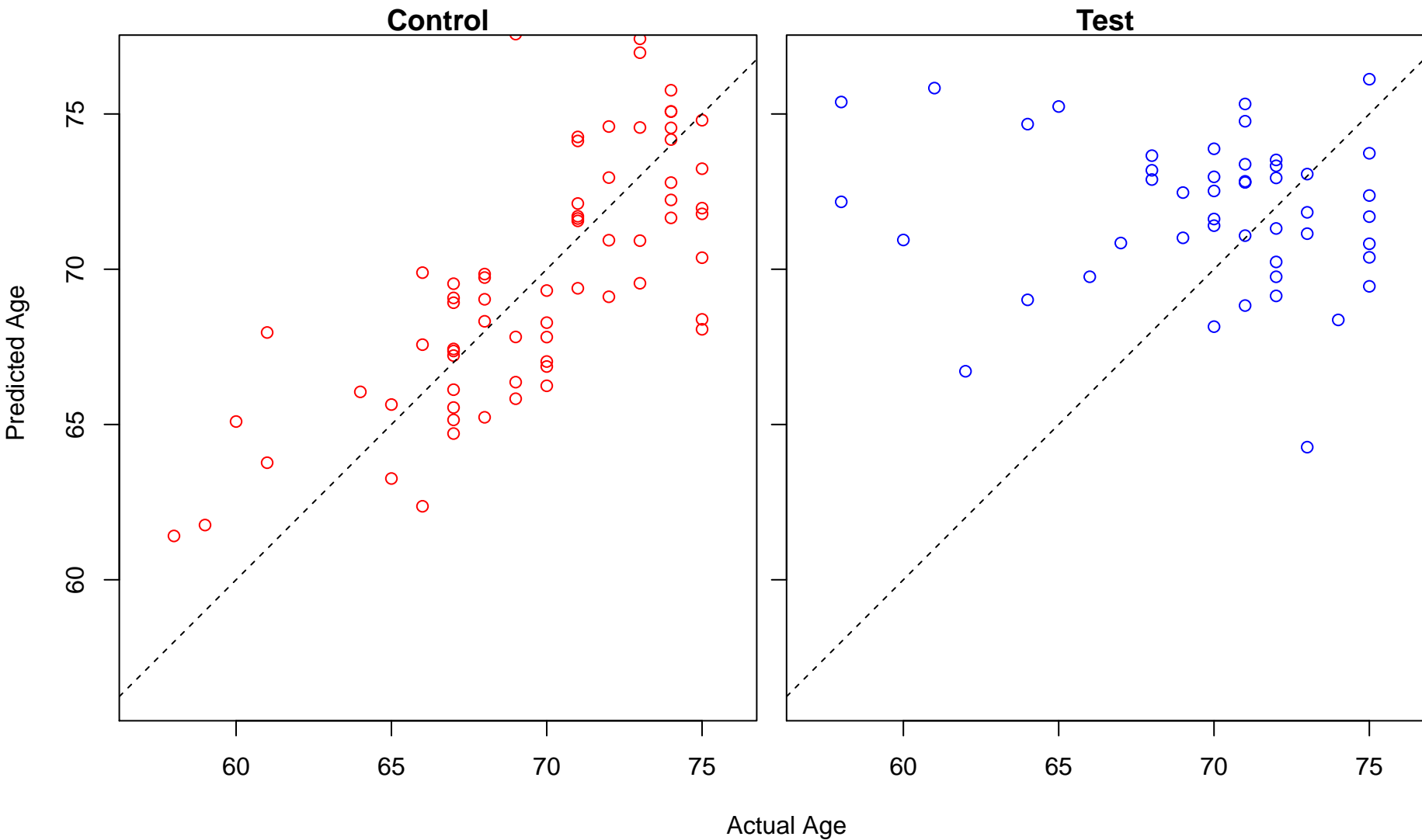
protein lipidation (Score: 1.891280)



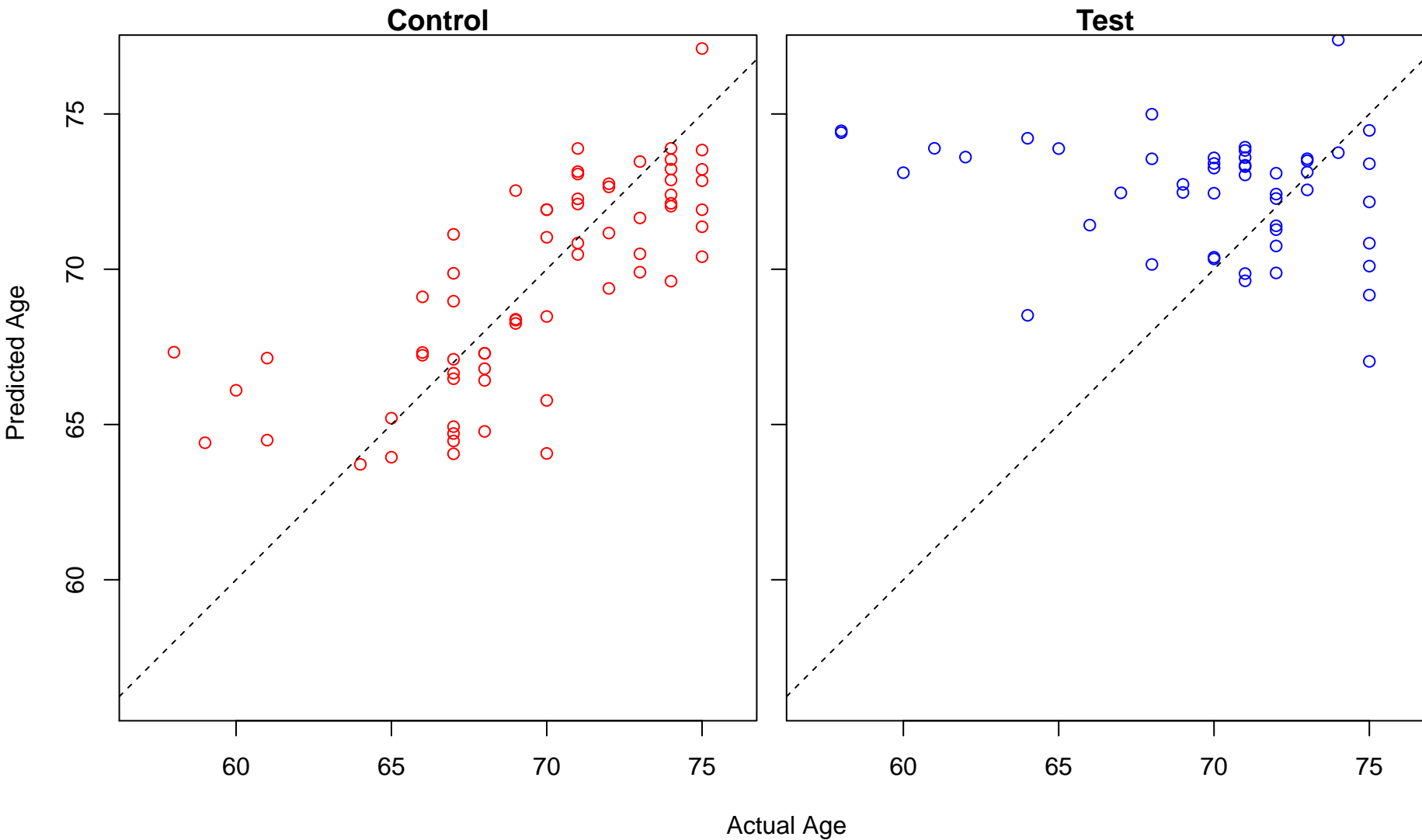
lipoprotein biosynthetic process (Score: 1.891280)



branched-chain amino acid catabolic process (Score: 1.891064)

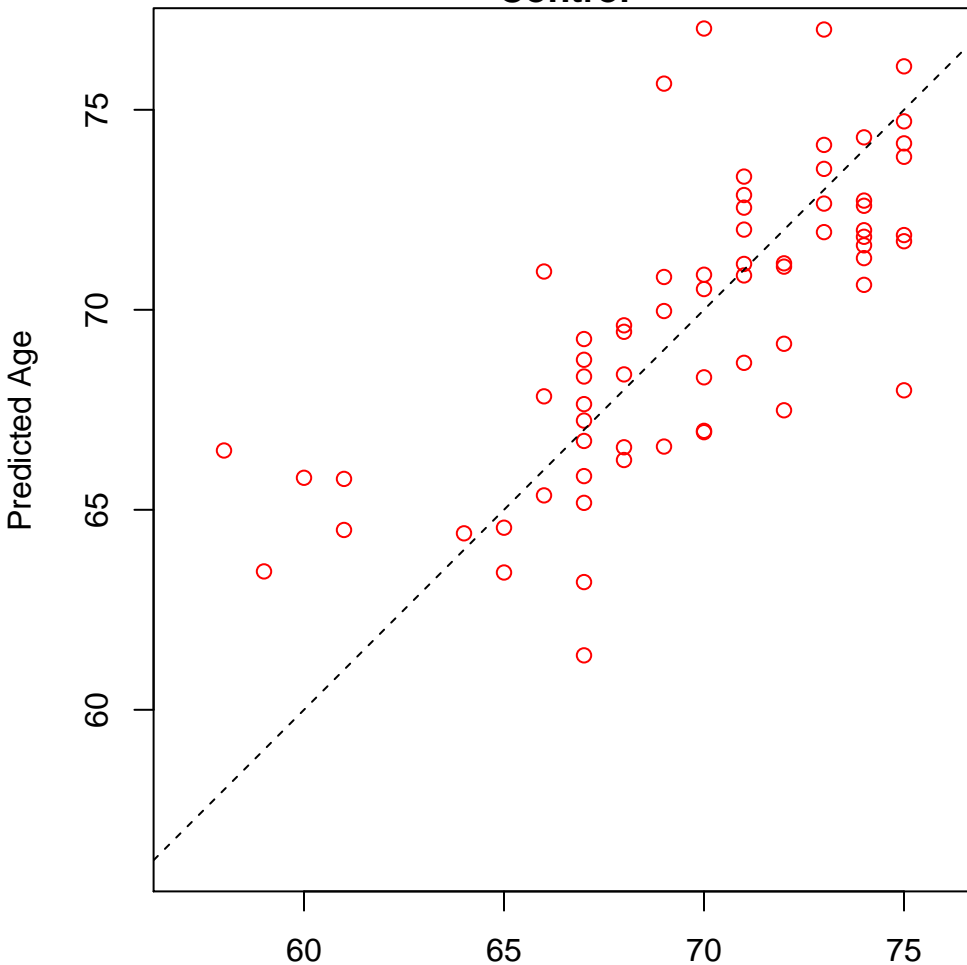


regulation of protein stability (Score: 1.890700)

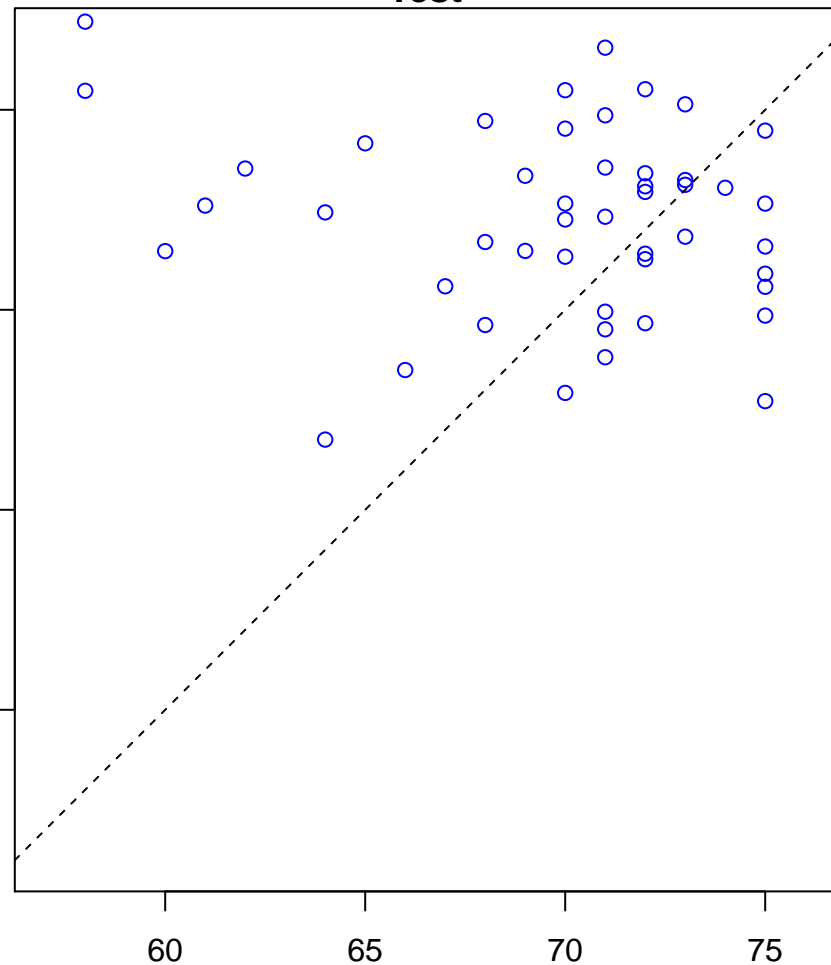


response to temperature stimulus (Score: 1.889632)

Control

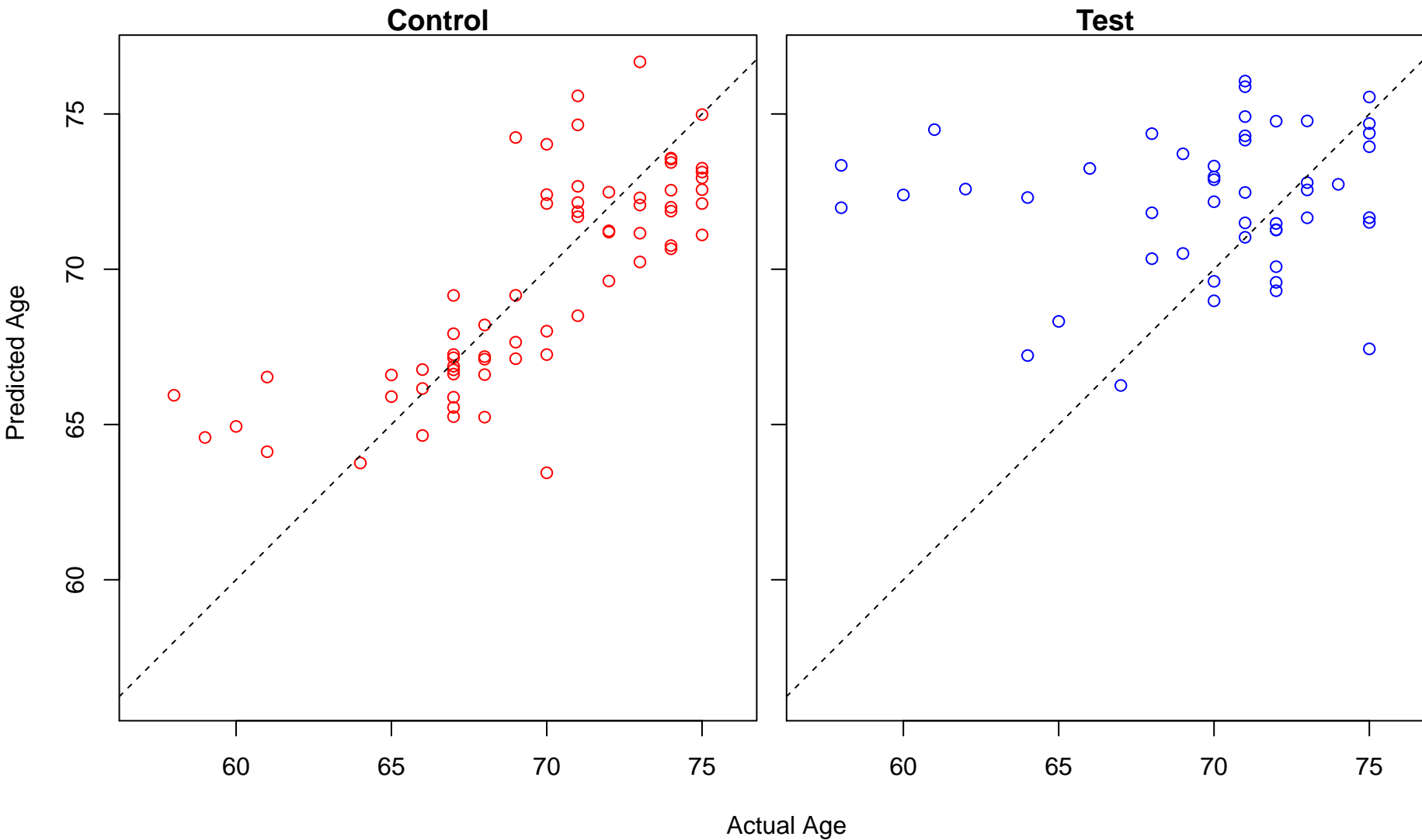


Test

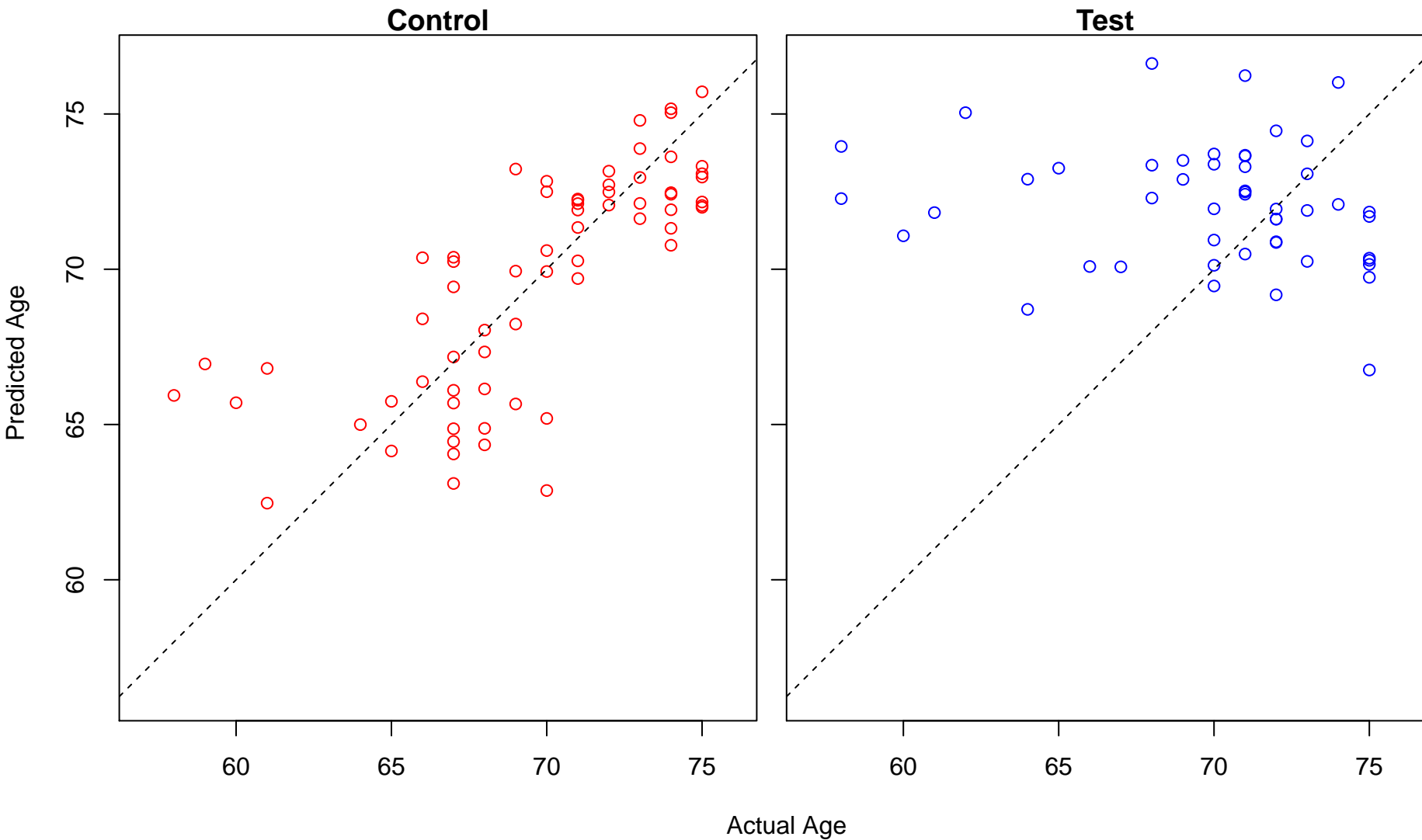


Actual Age

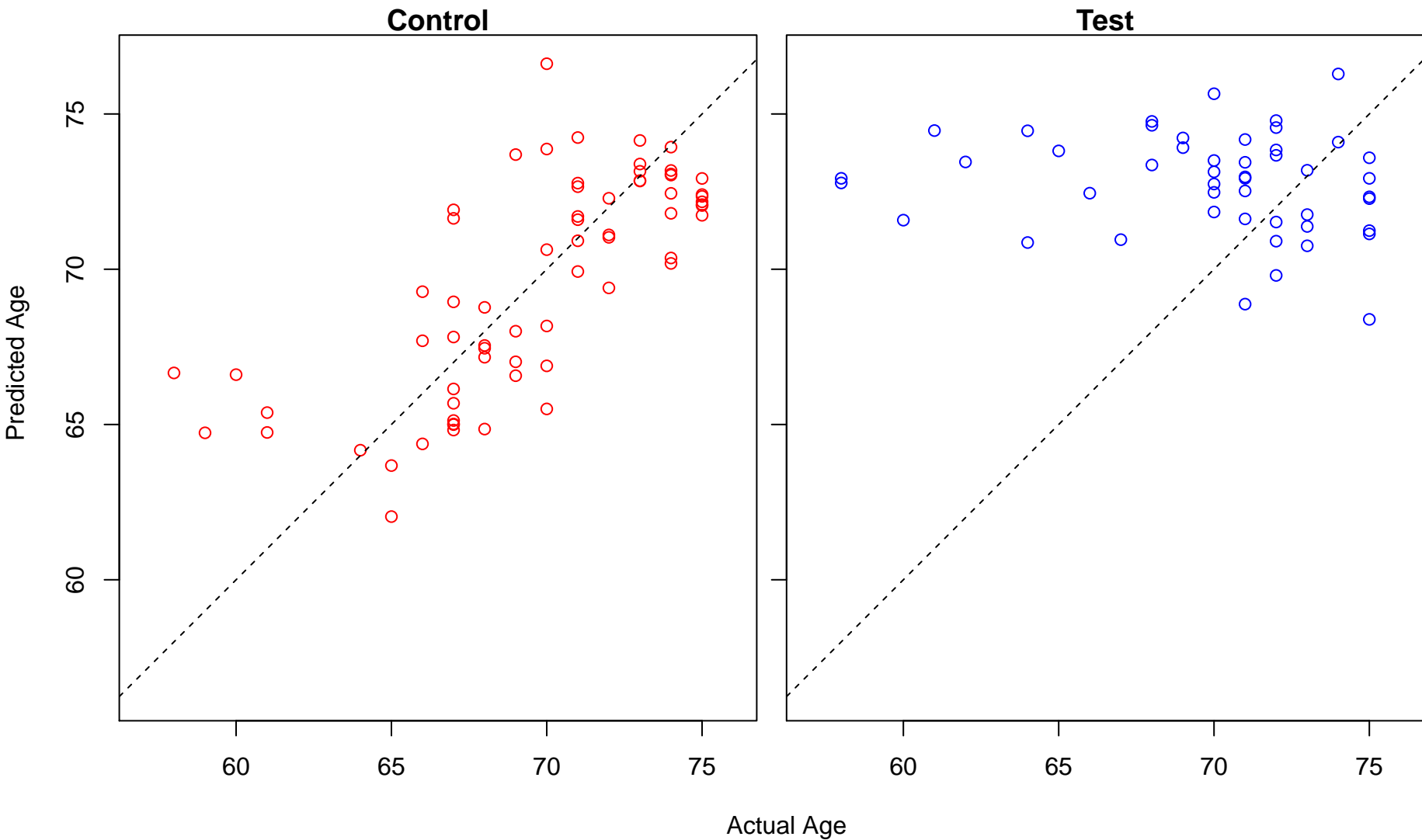
tissue morphogenesis (Score: 1.889044)



RNA splicing (Score: 1.888913)

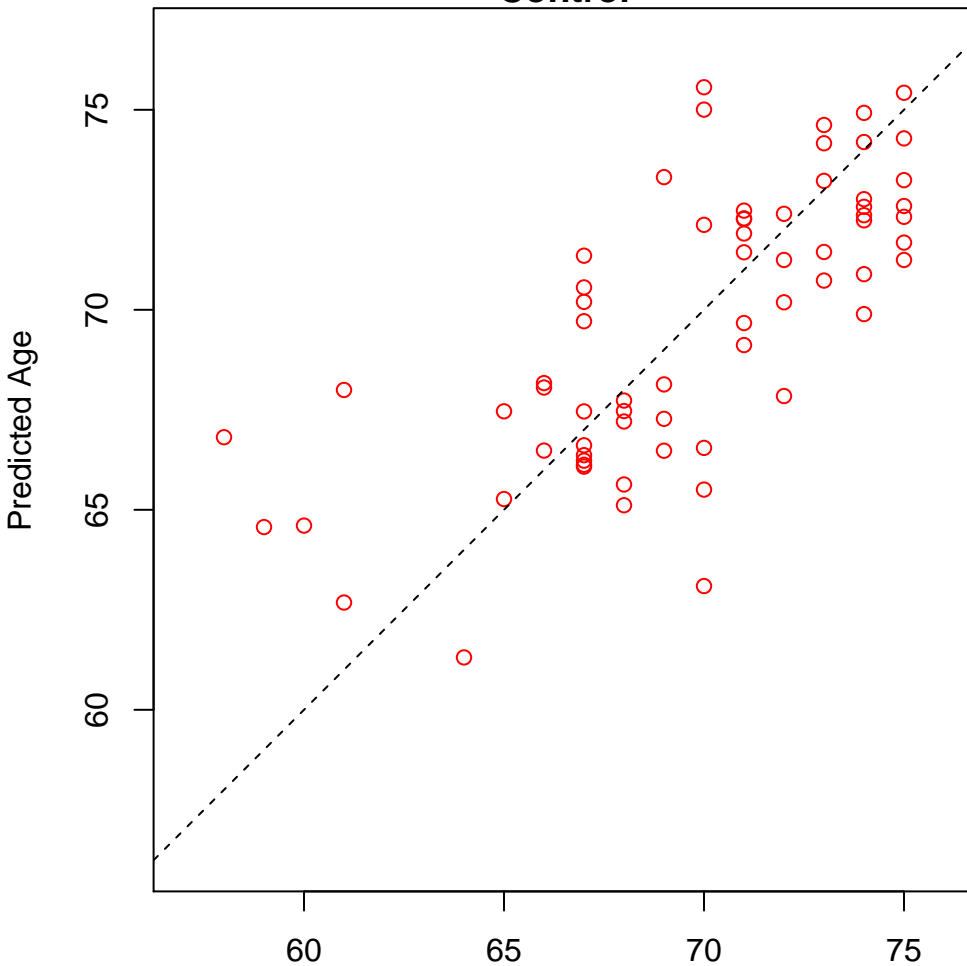


nuclear division (Score: 1.888518)

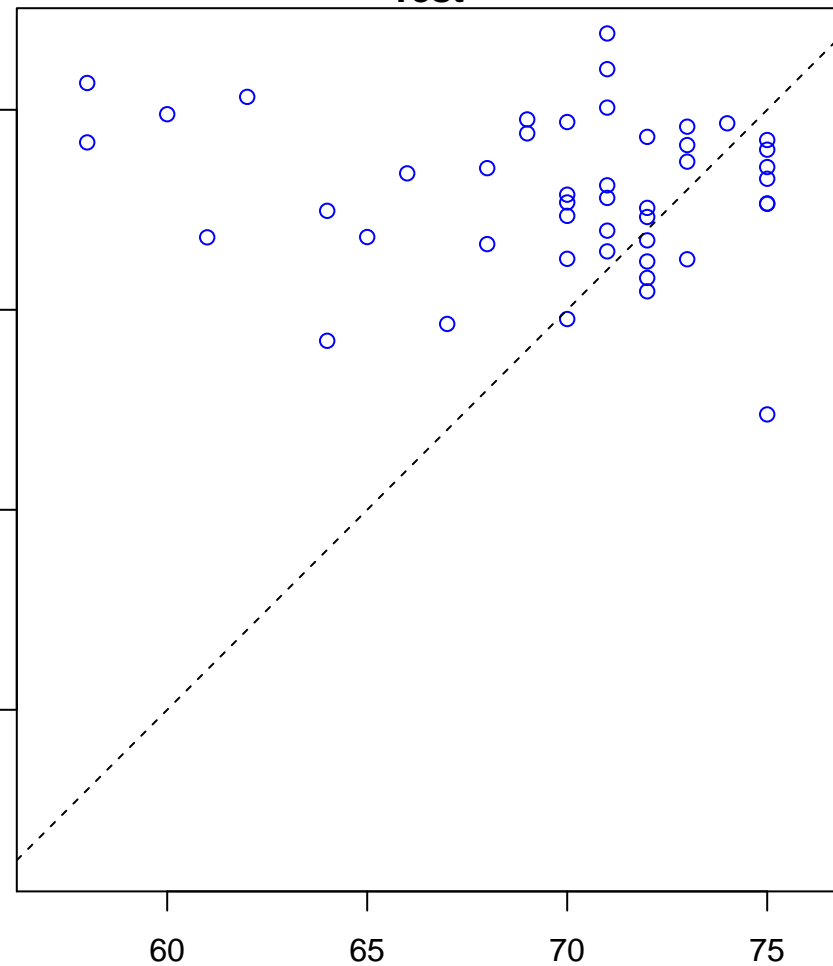


DNA-templated transcription, initiation (Score: 1.887858)

Control

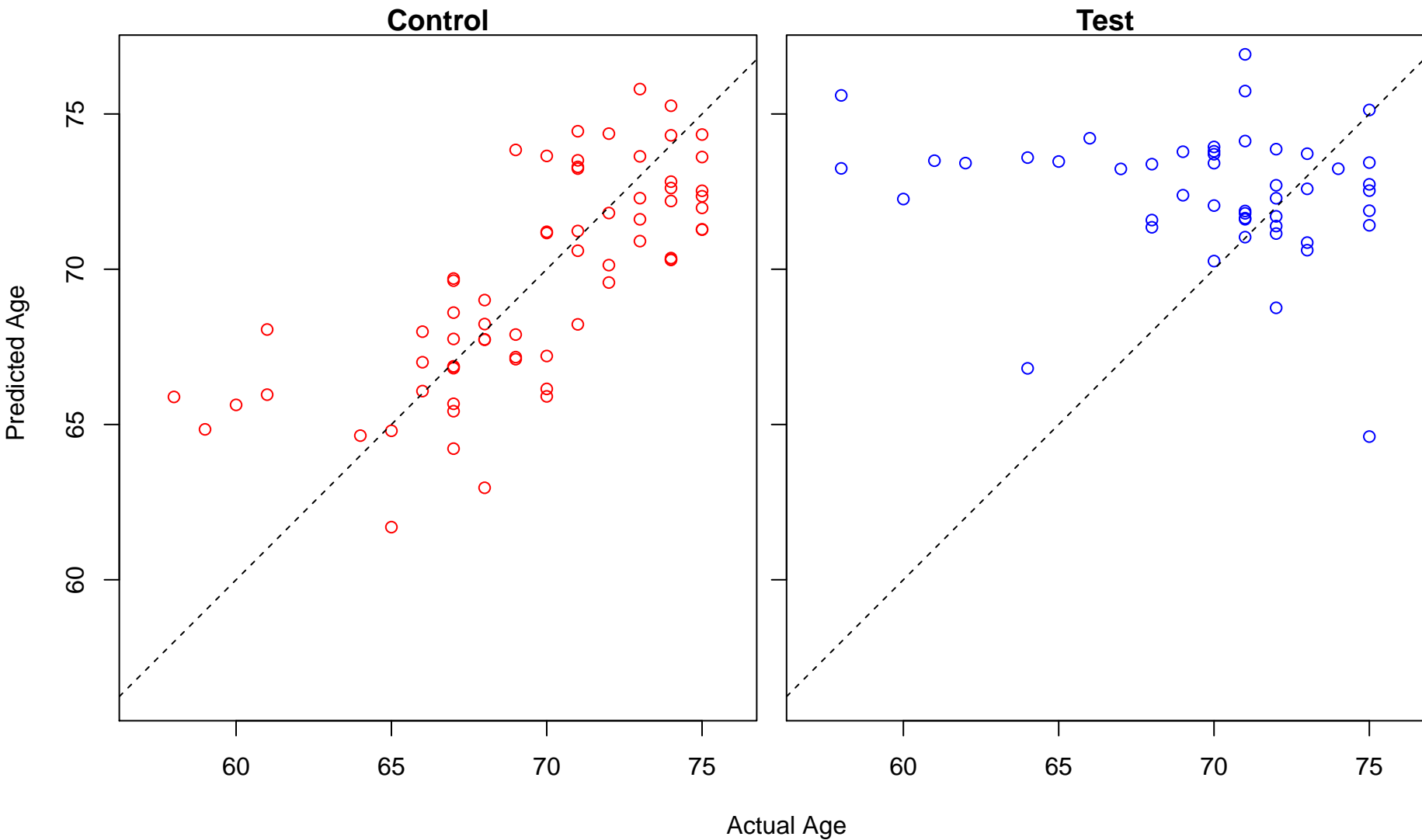


Test

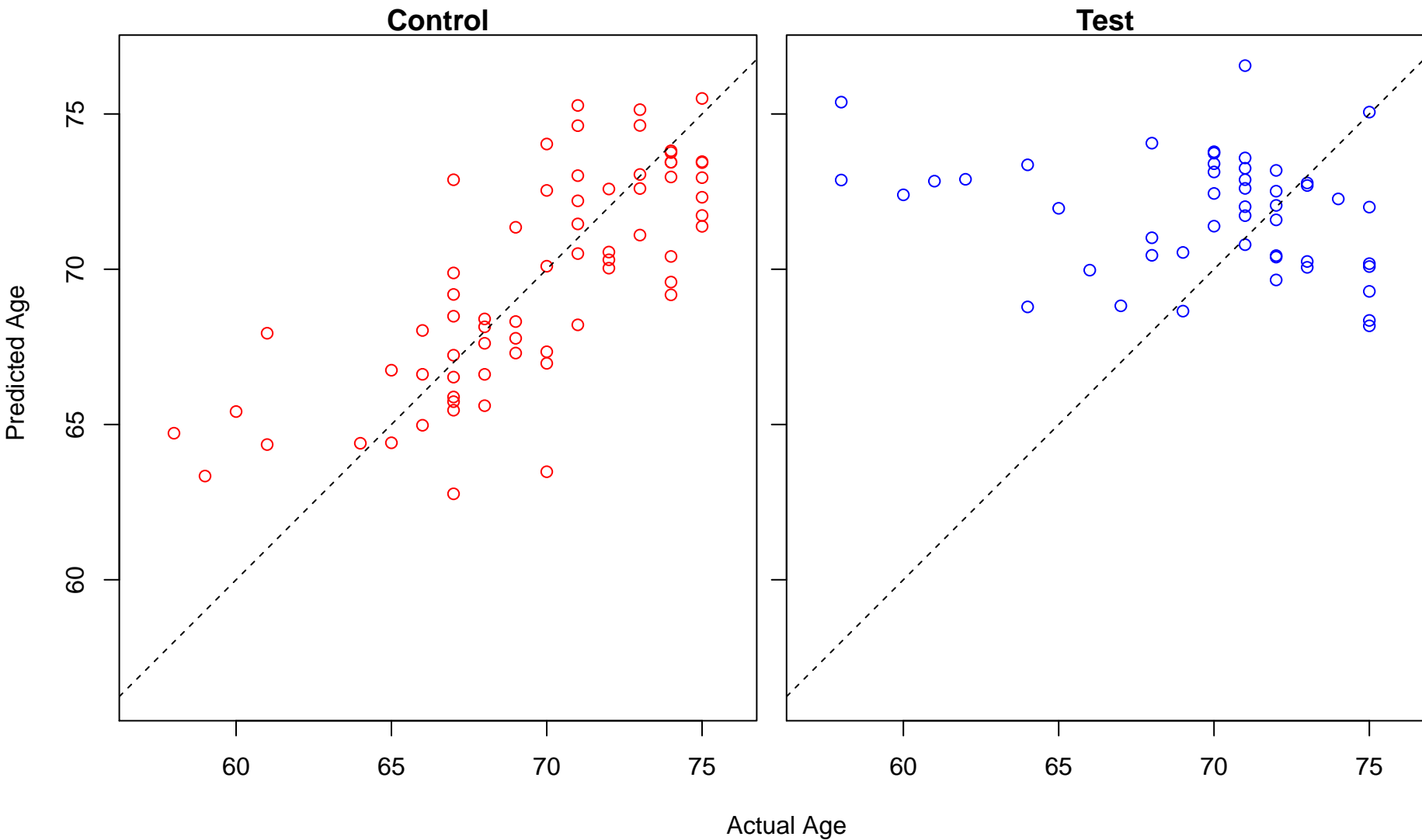


Actual Age

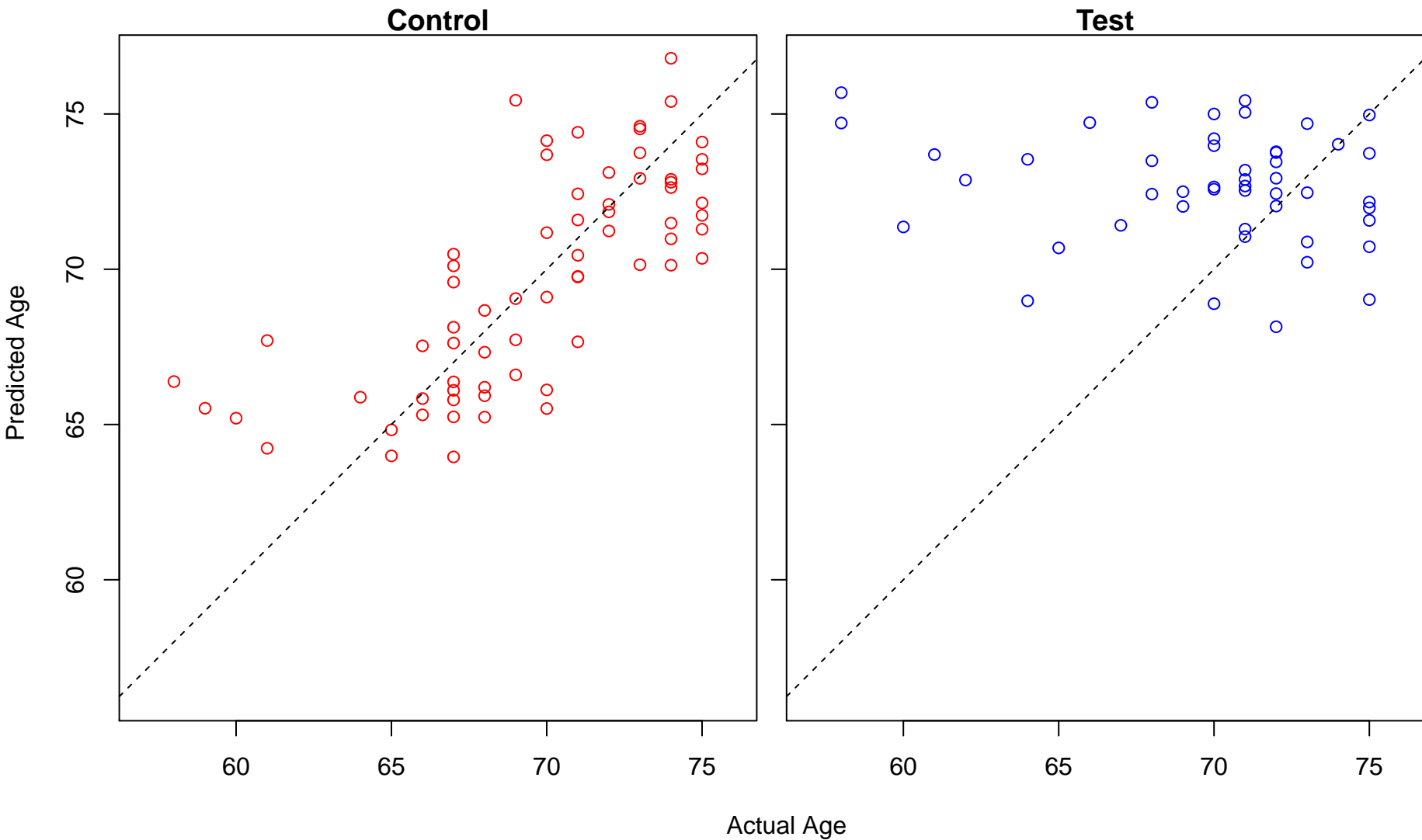
positive regulation of cell migration (Score: 1.887364)



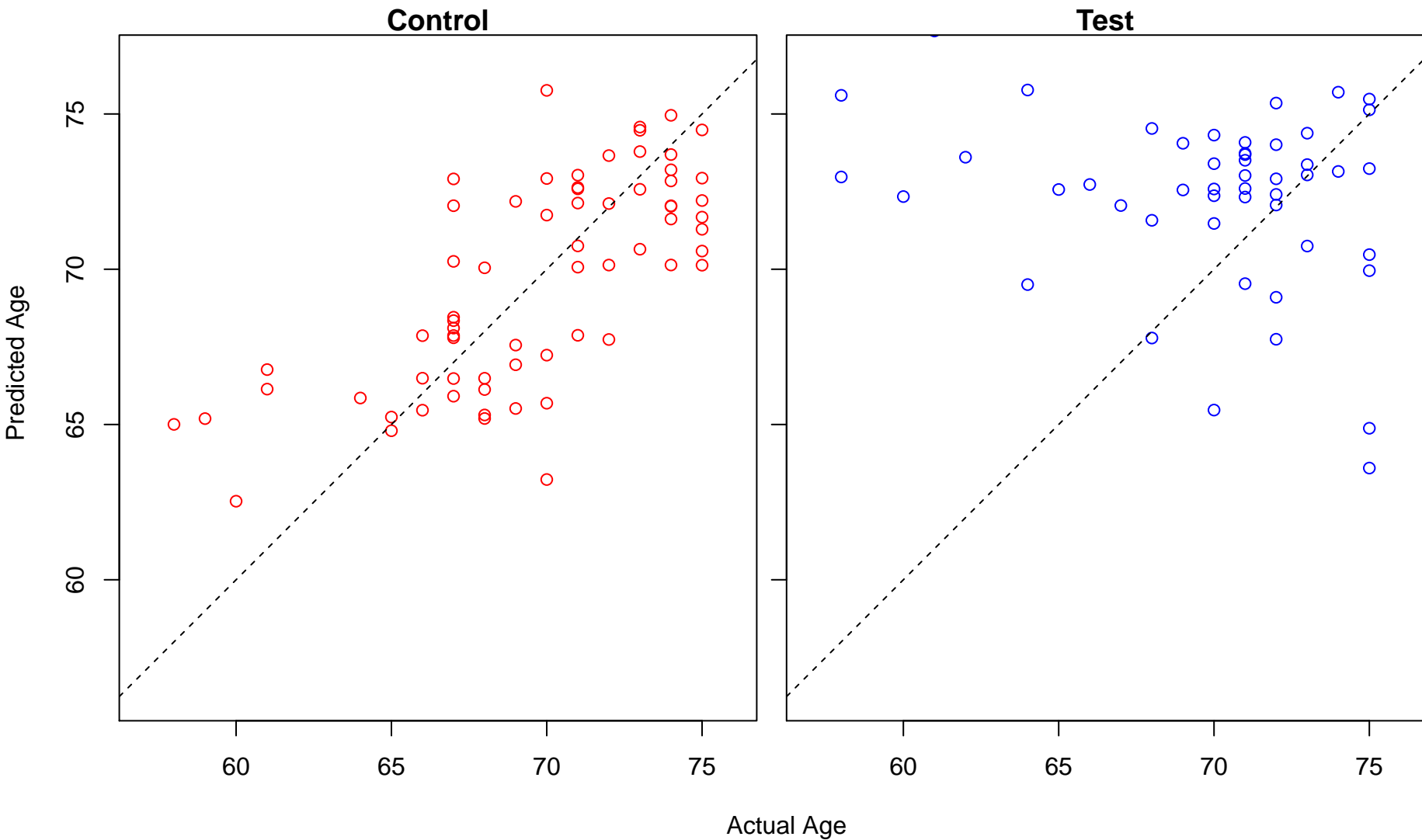
regulation of protein targeting to mitochondrion (Score: 1.886269)



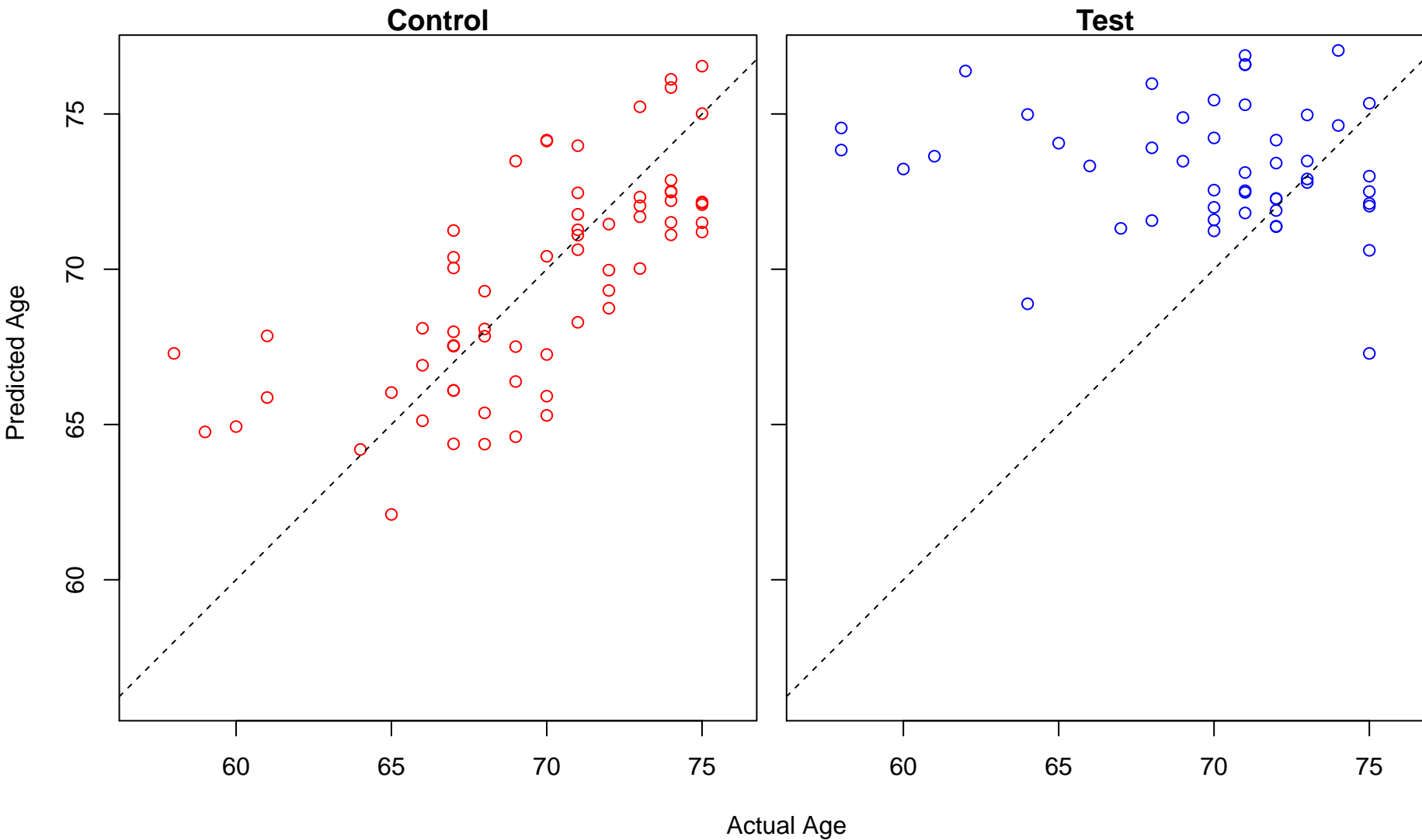
cellular cation homeostasis (Score: 1.883924)



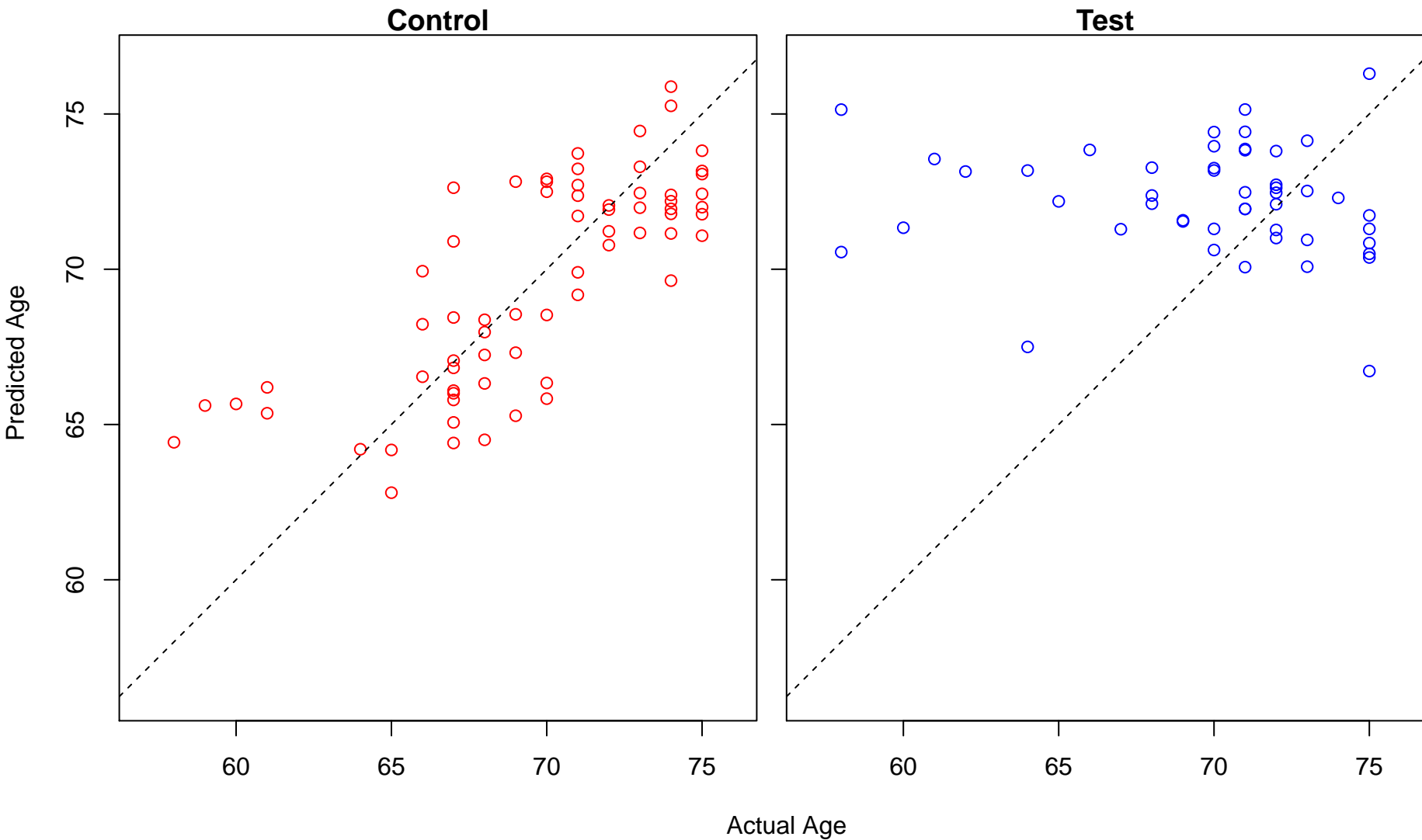
positive regulation of ion transmembrane transporter activity (Score: 1.883595)



negative regulation of intracellular signal transduction (Score: 1.883490)

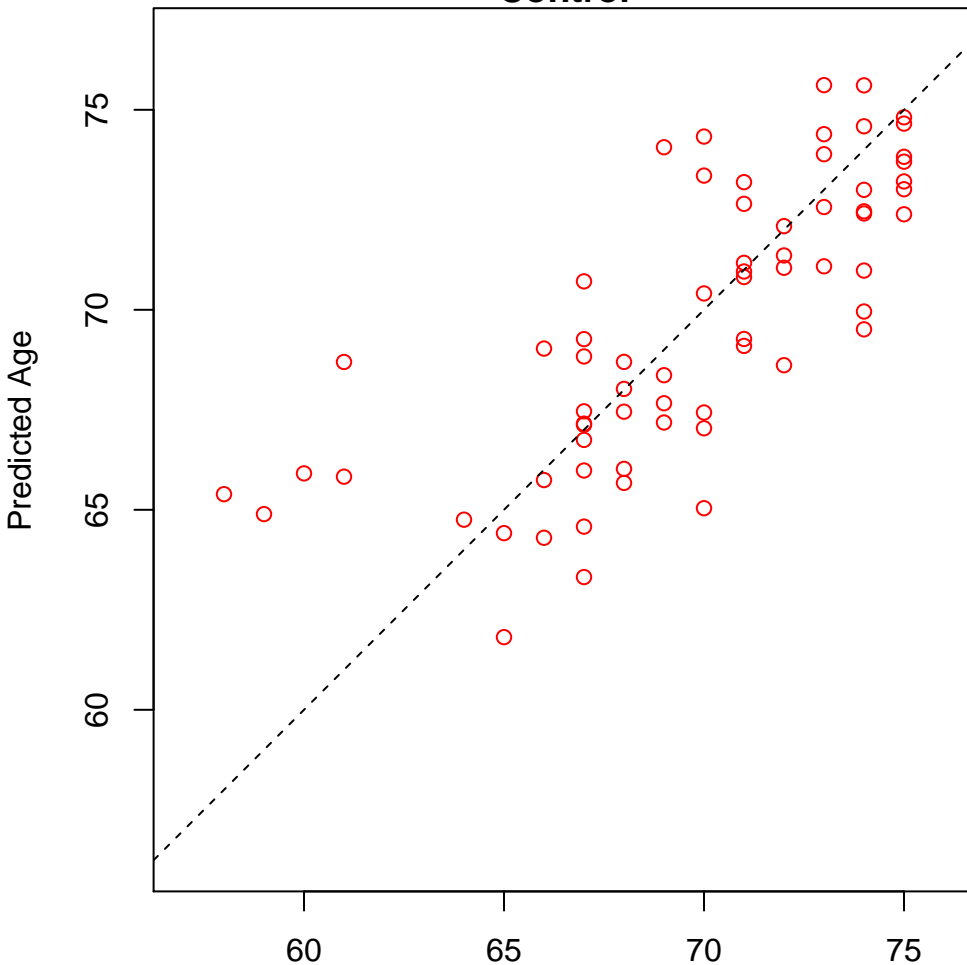


DNA packaging (Score: 1.883436)

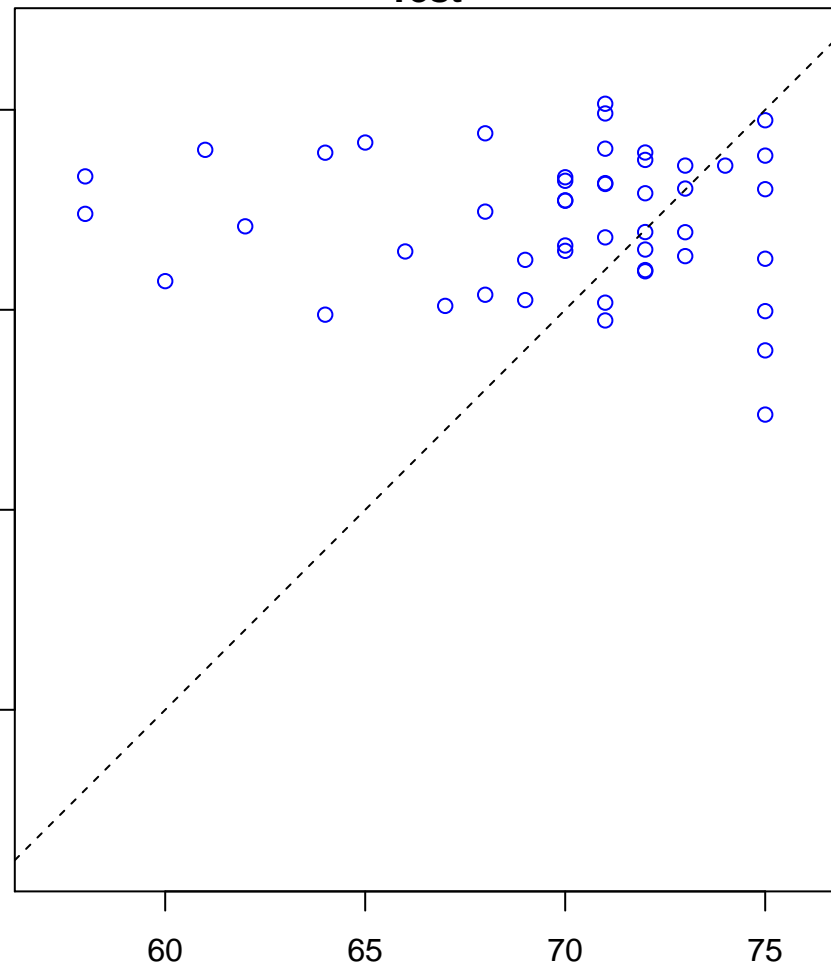


activation of protein kinase activity (Score: 1.883348)

Control

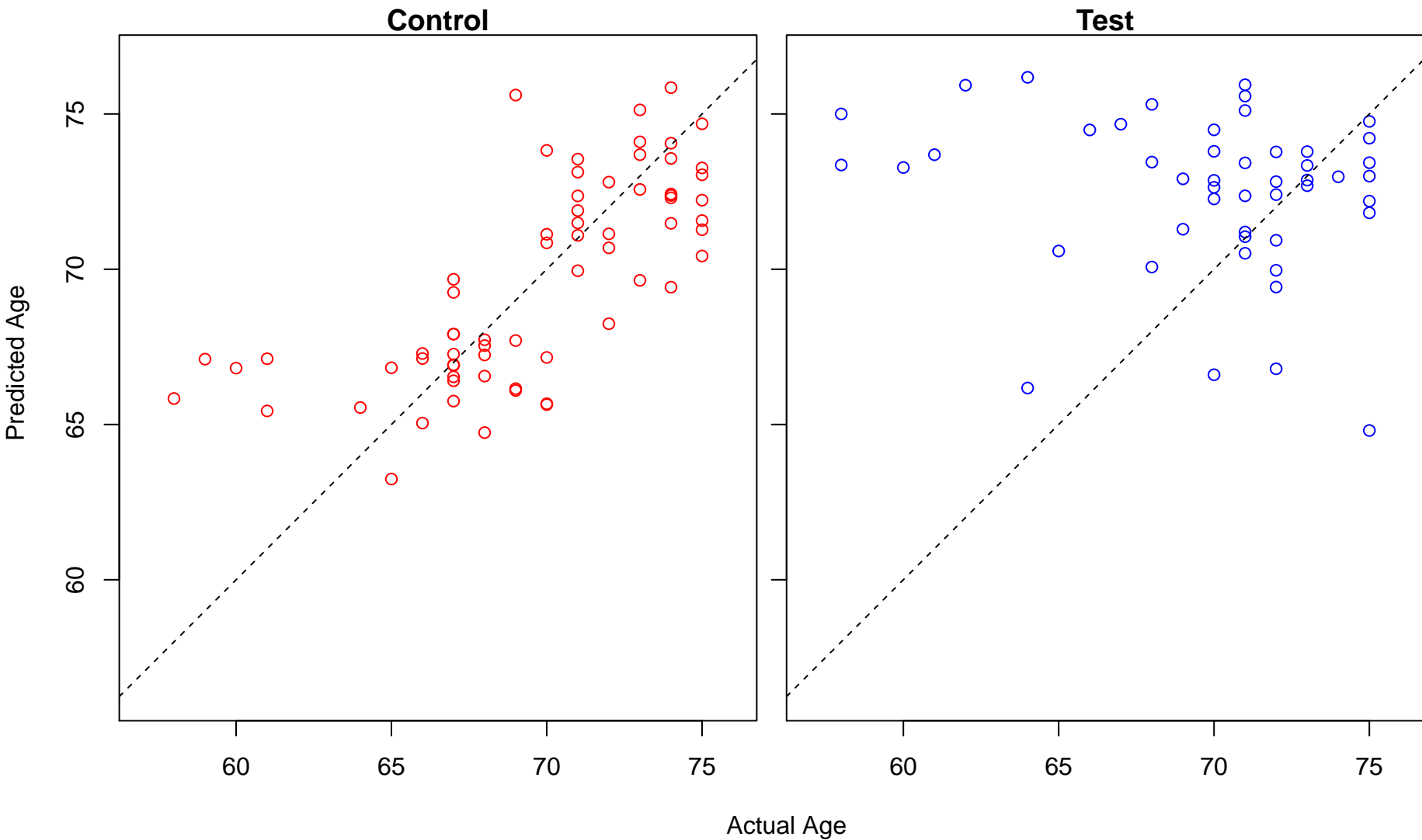


Test

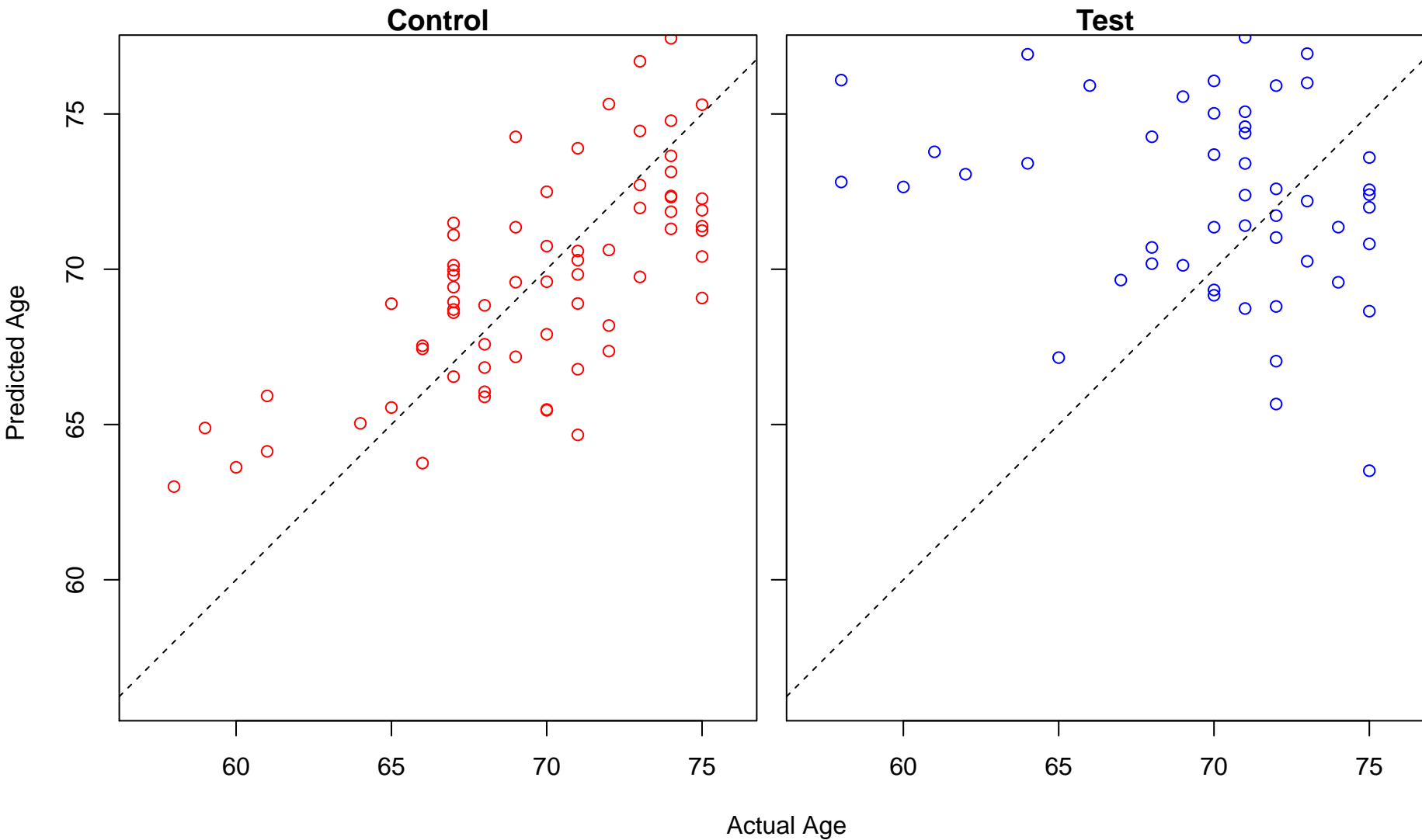


Actual Age

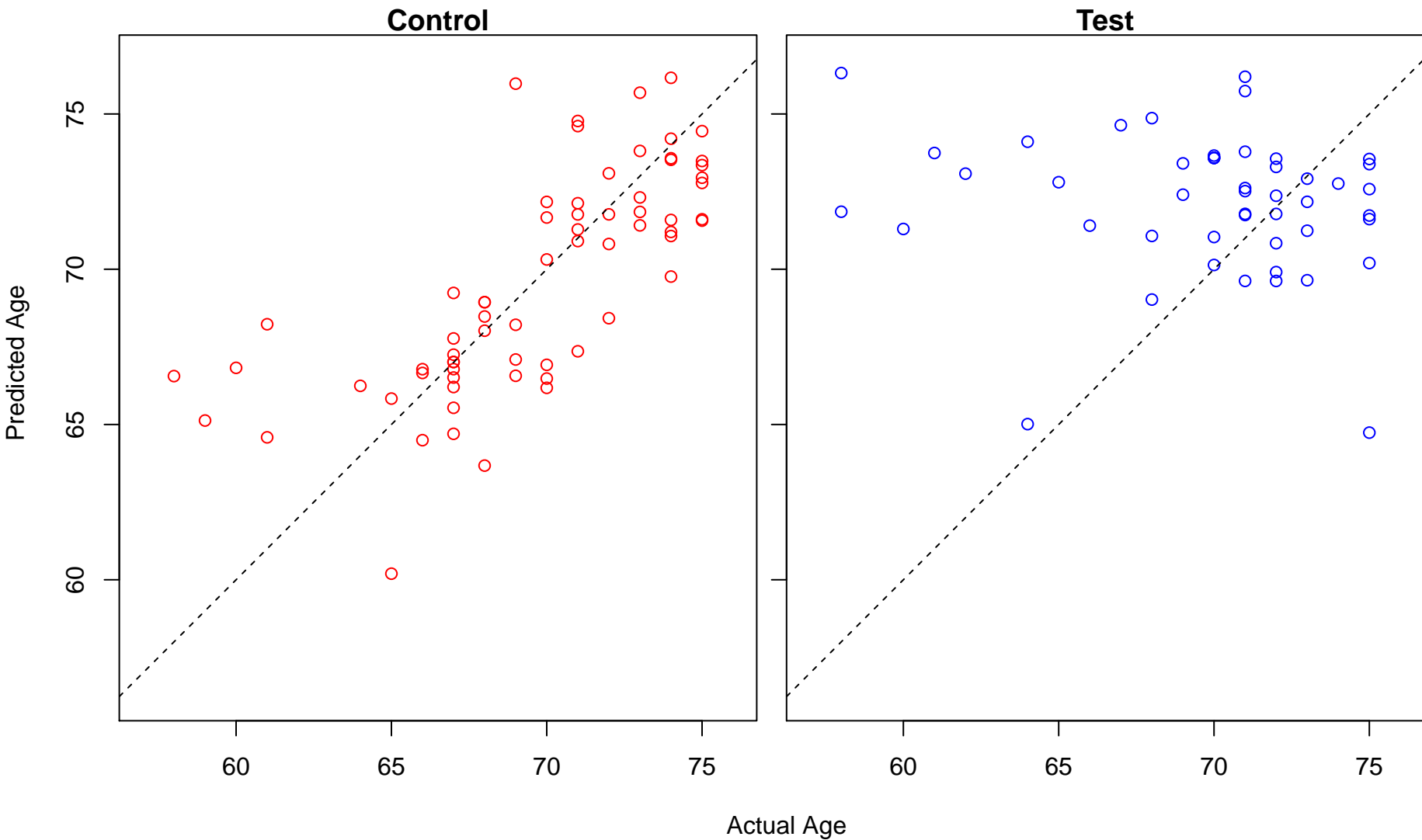
positive regulation of T cell migration (Score: 1.882950)



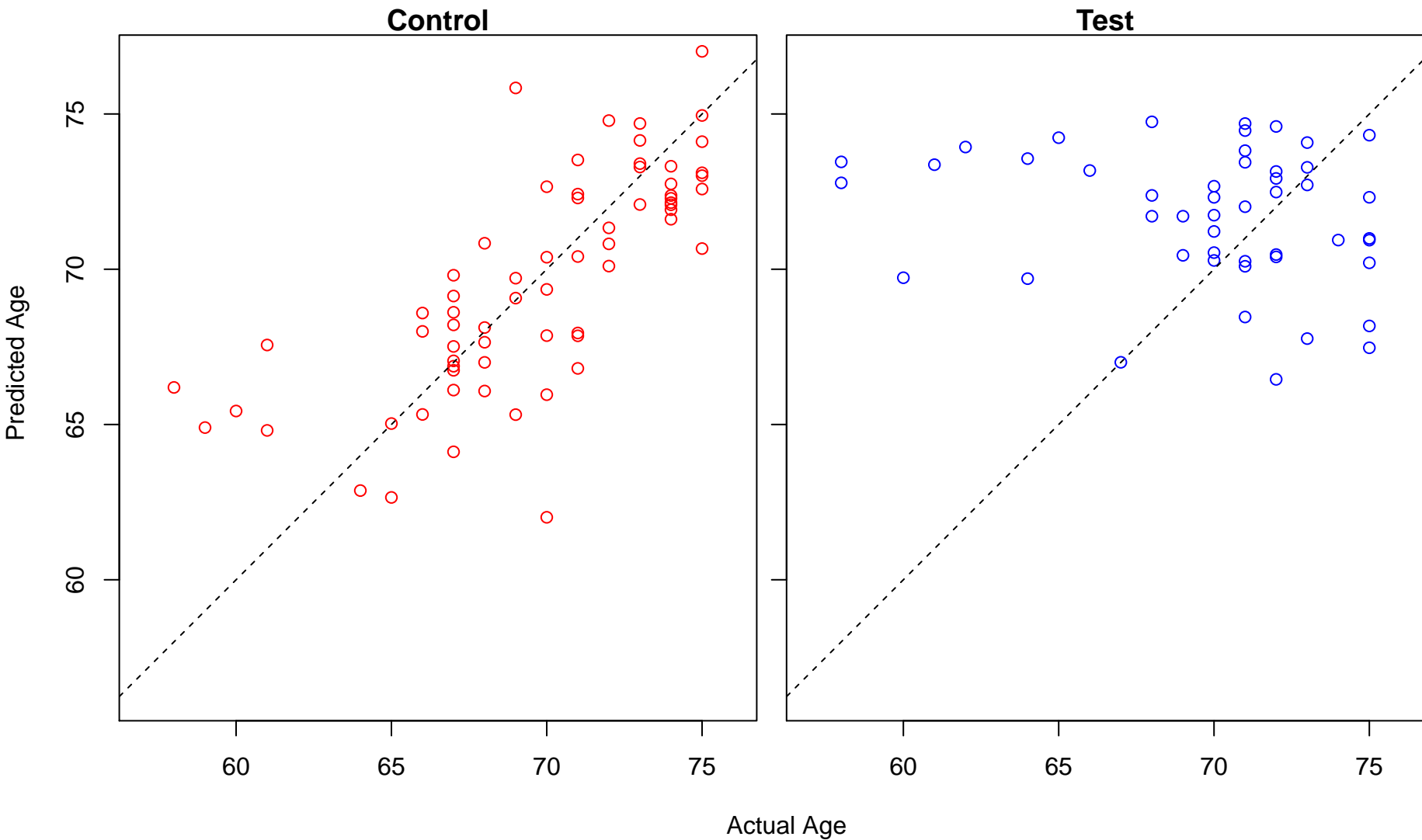
regulation of thymocyte apoptotic process (Score: 1.882814)



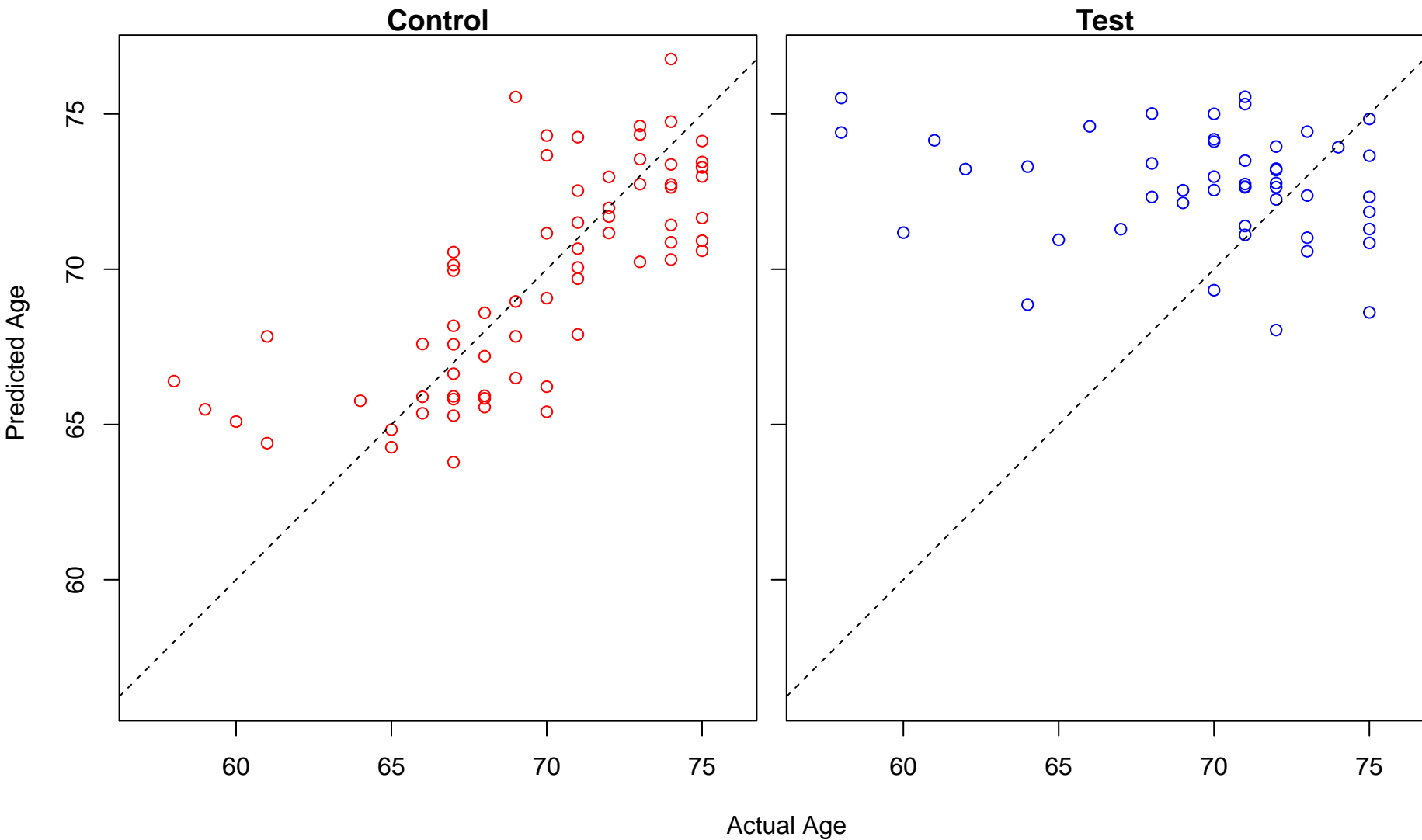
regulation of leukocyte migration (Score: 1.882398)



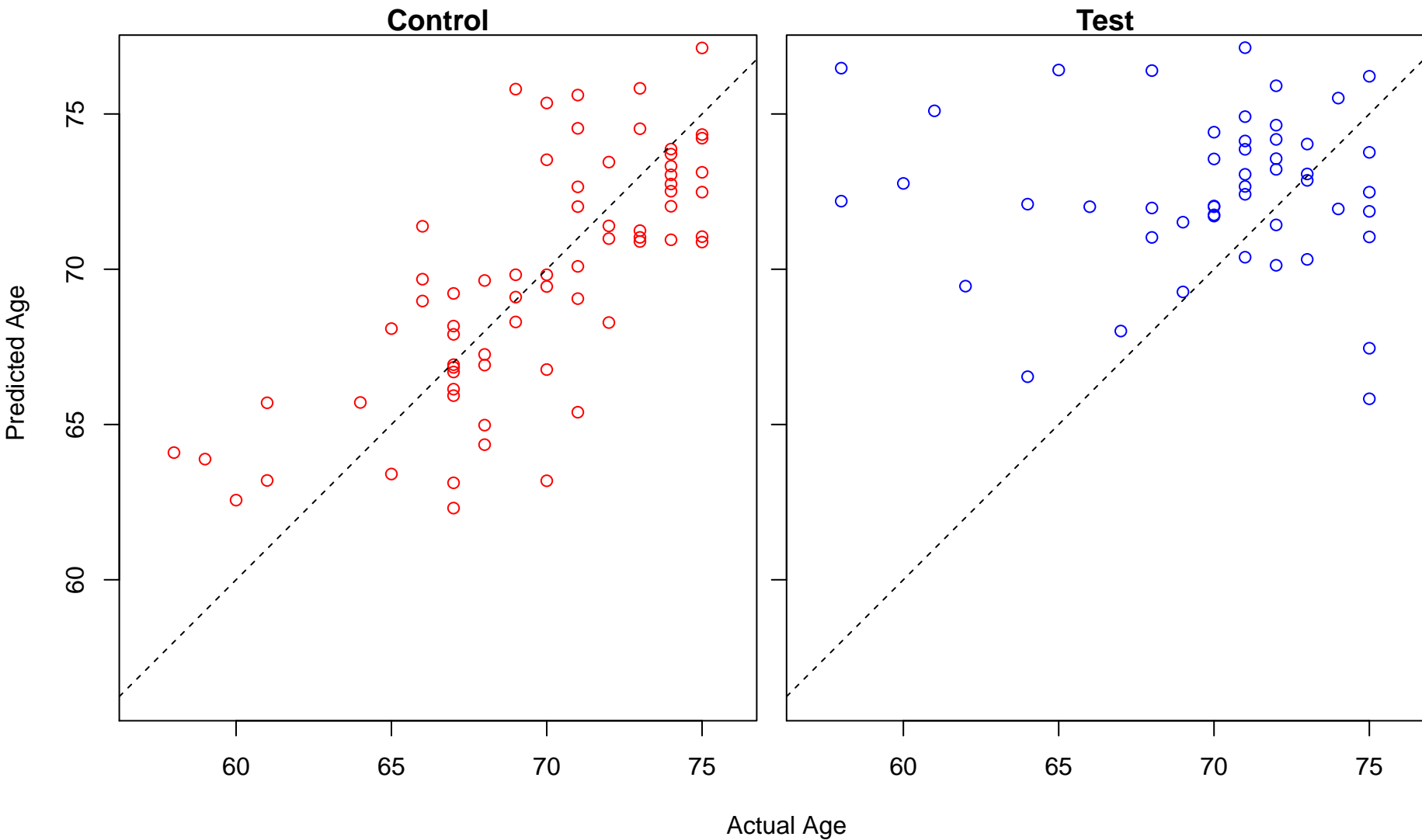
regulation of homeostatic process (Score: 1.881200)



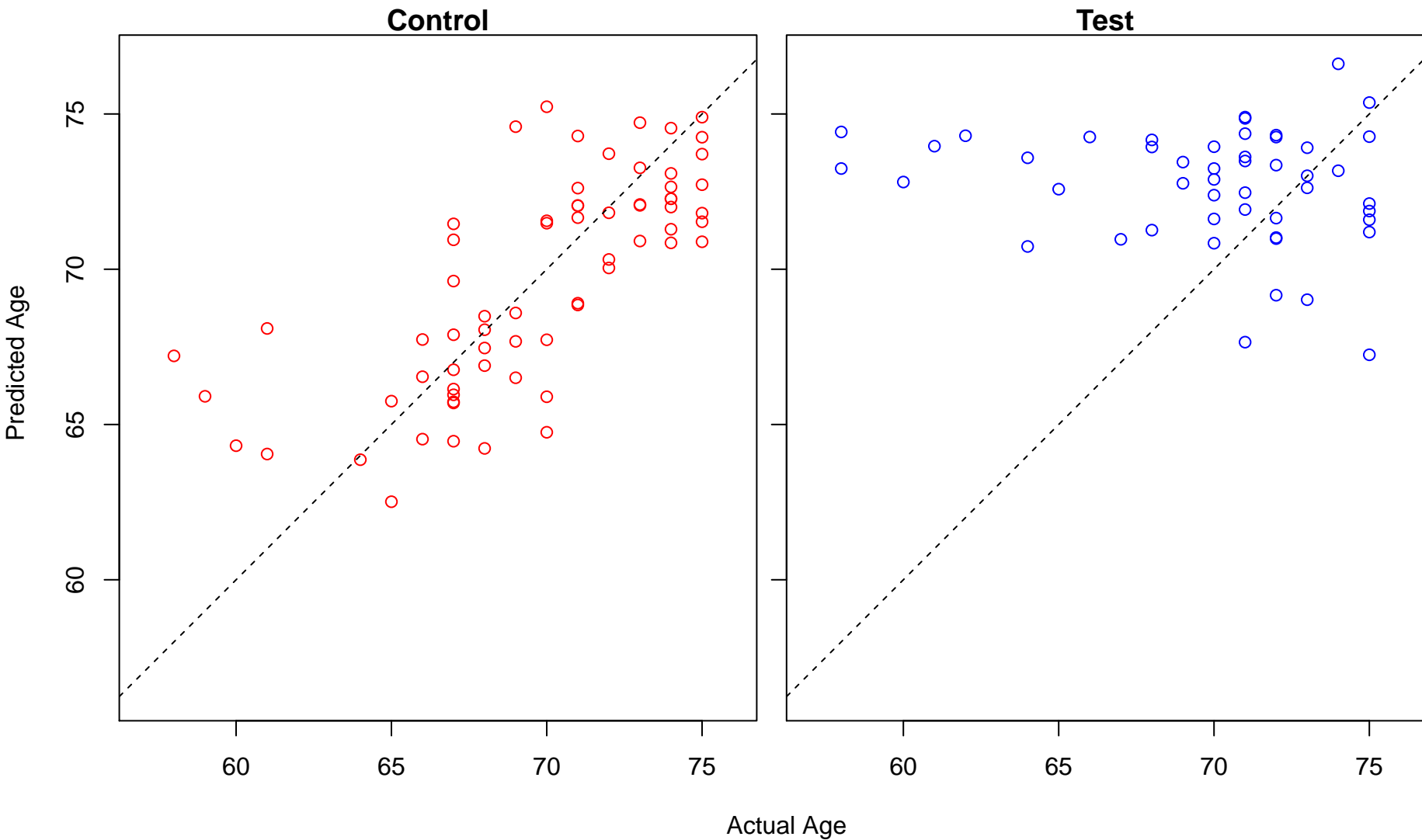
cation homeostasis (Score: 1.881086)



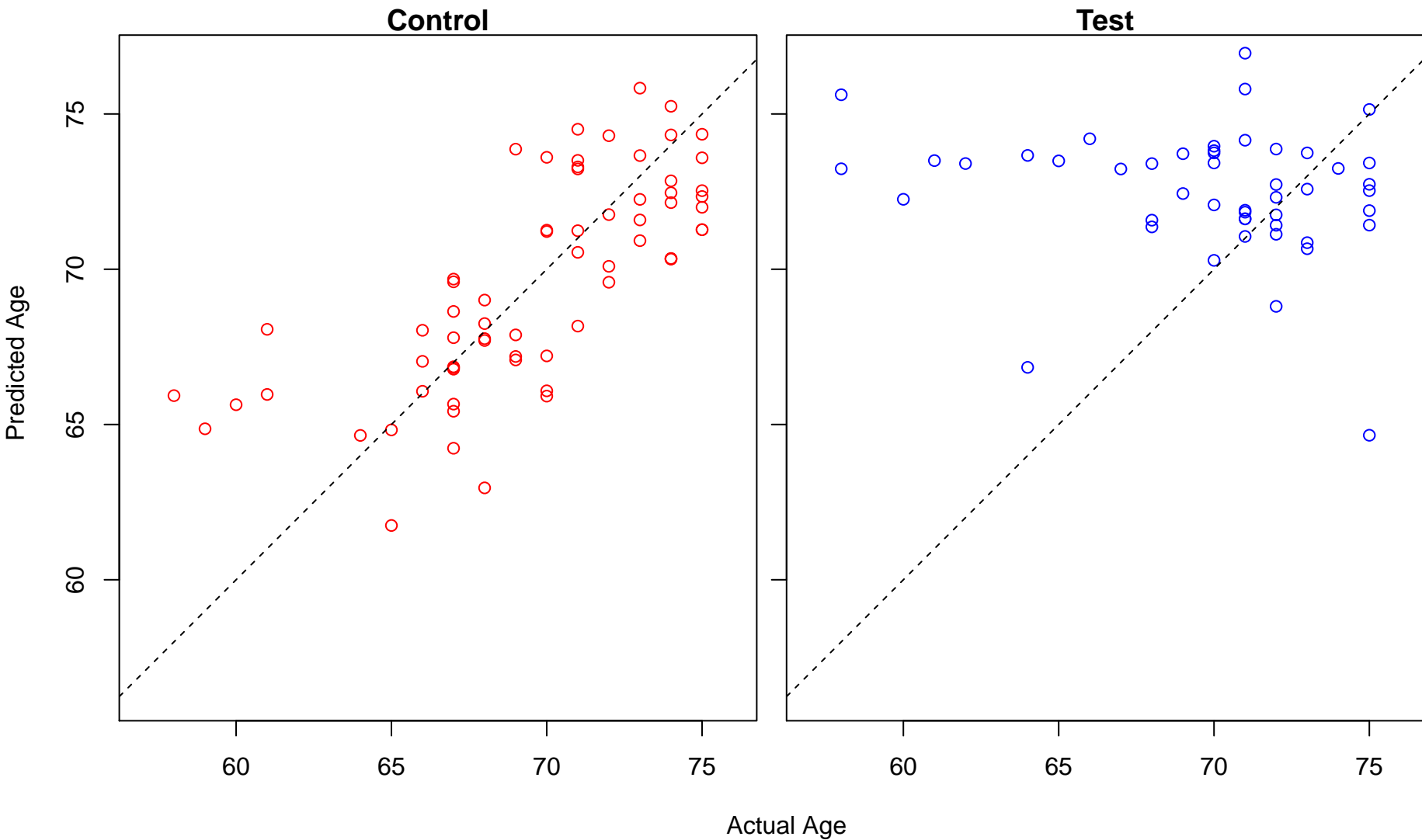
lymphocyte mediated immunity (Score: 1.880879)



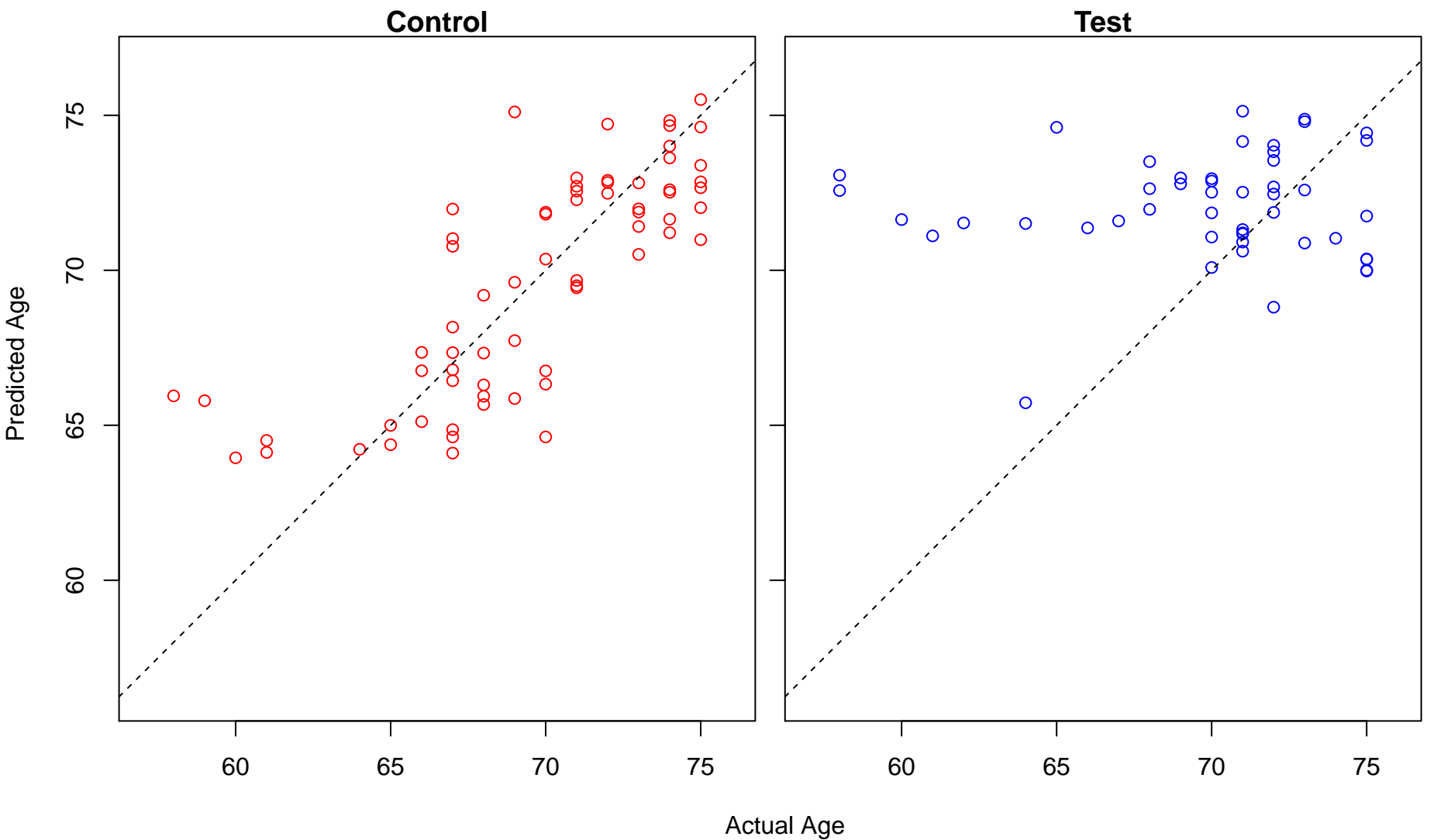
glycoprotein biosynthetic process (Score: 1.880551)



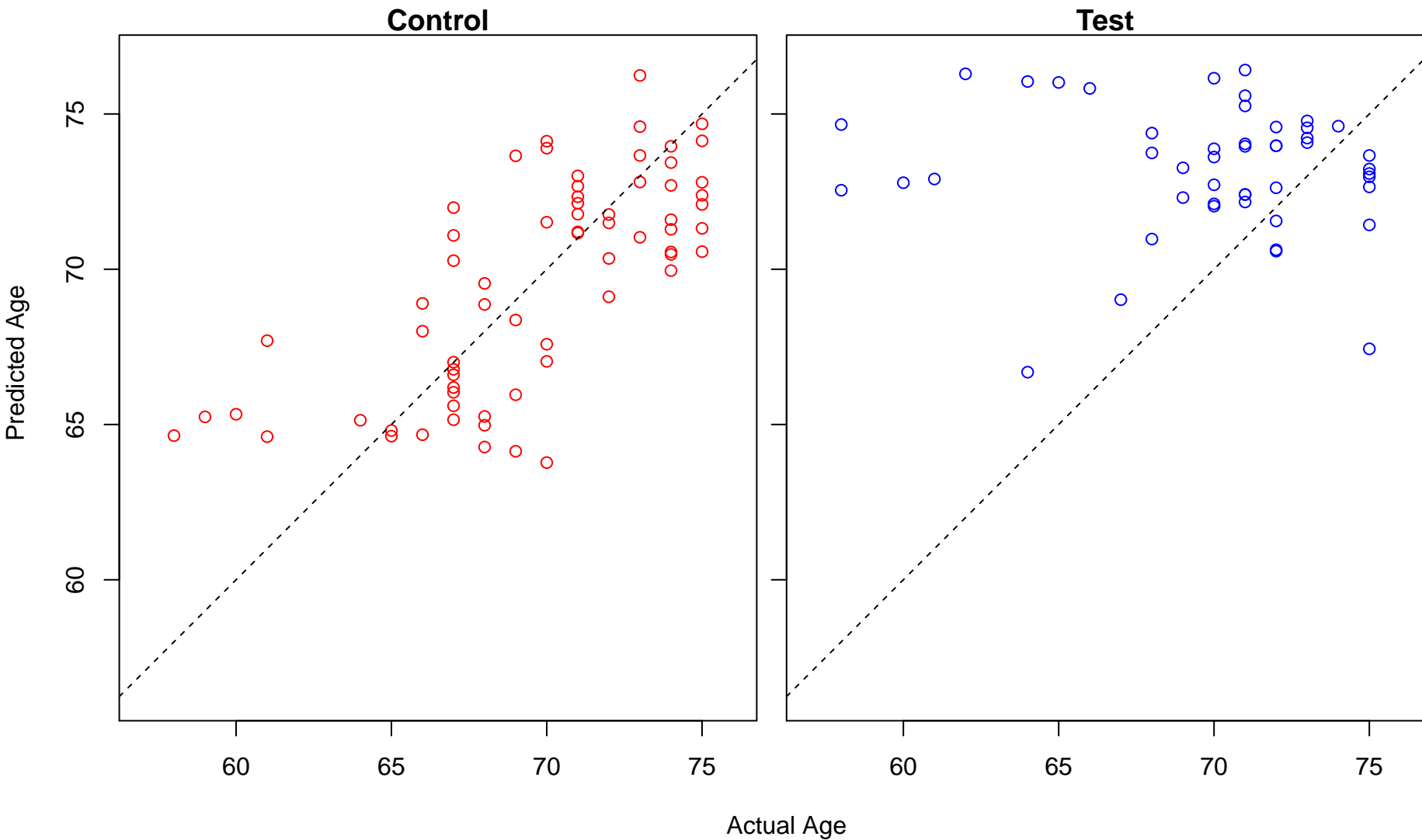
positive regulation of cell motility (Score: 1.879195)



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

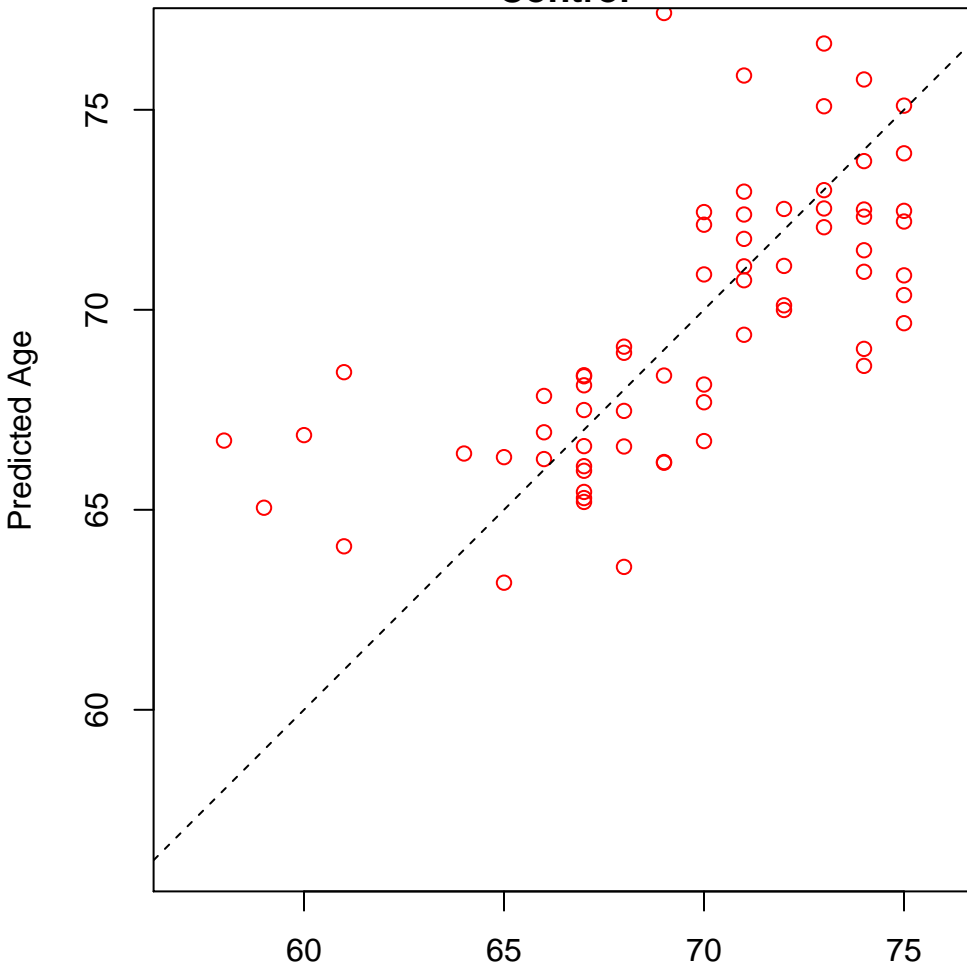


positive regulation of chromosome organization (Score: 1.878766)

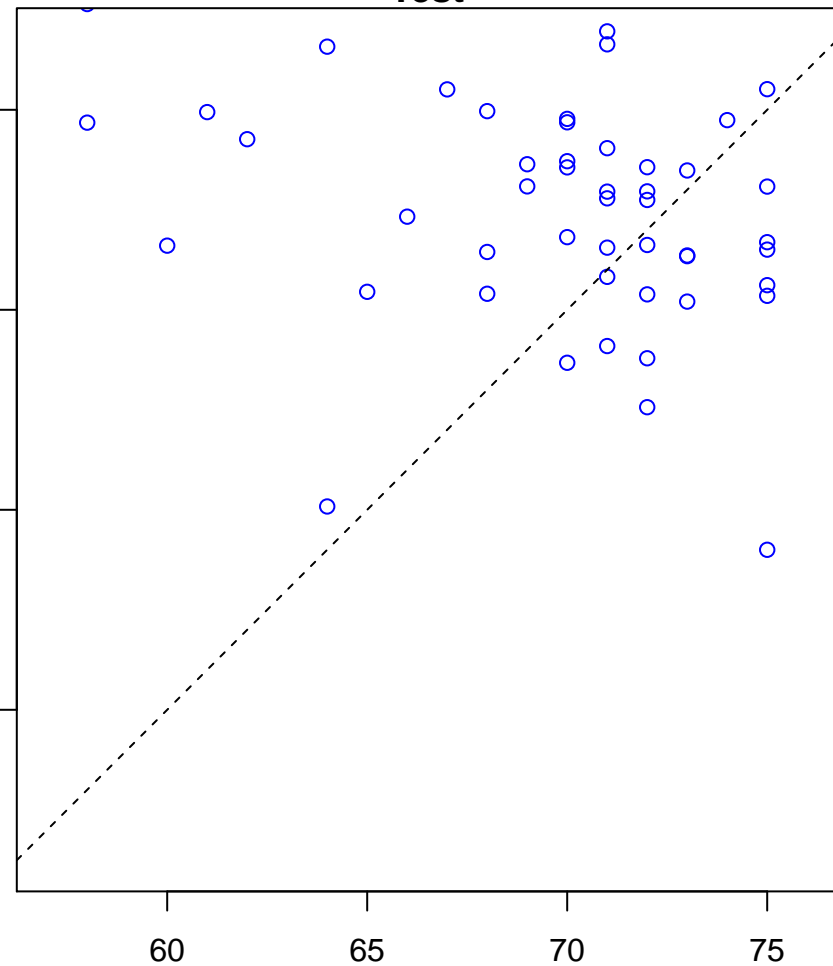


positive regulation of T cell proliferation (Score: 1.876651)

Control

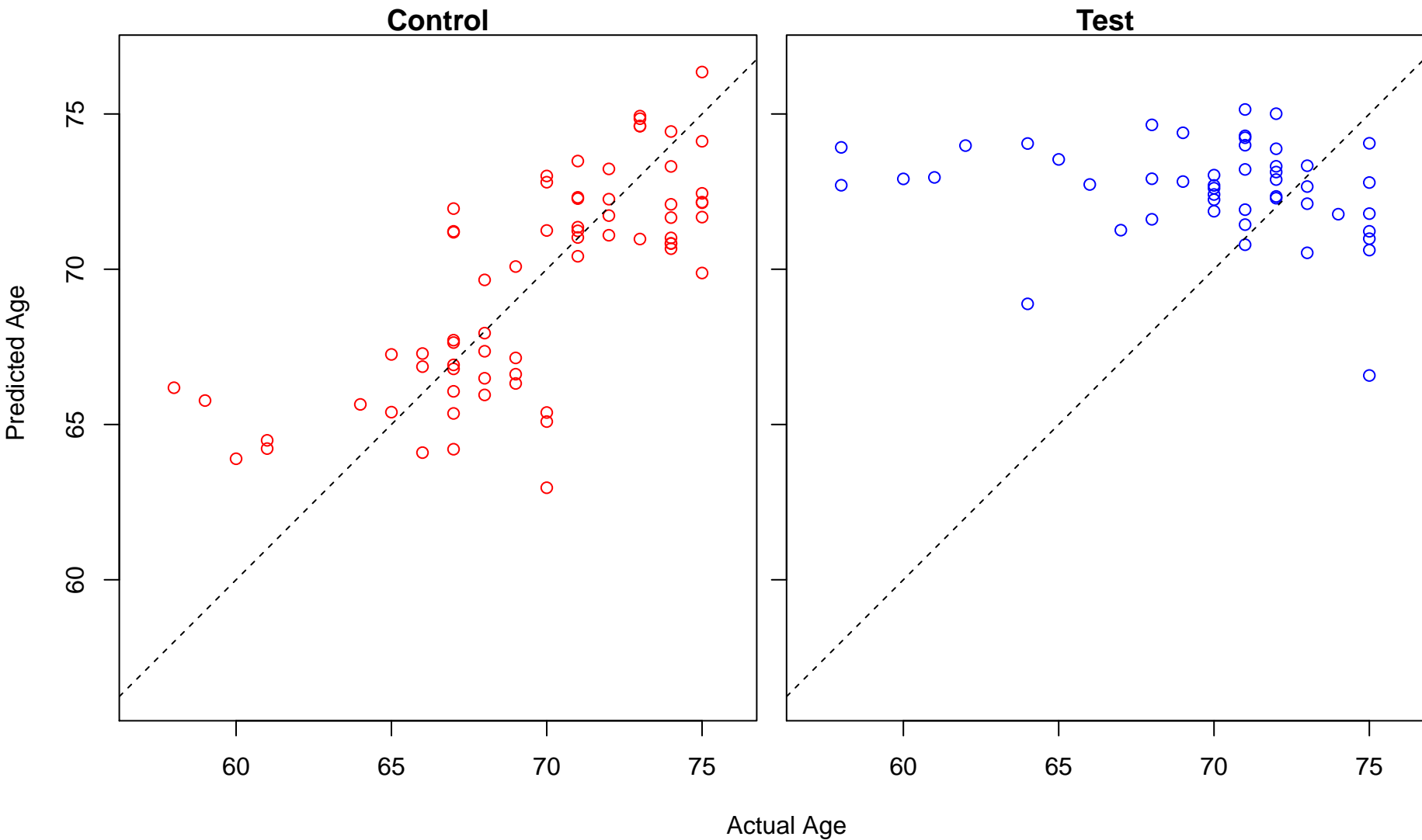


Test

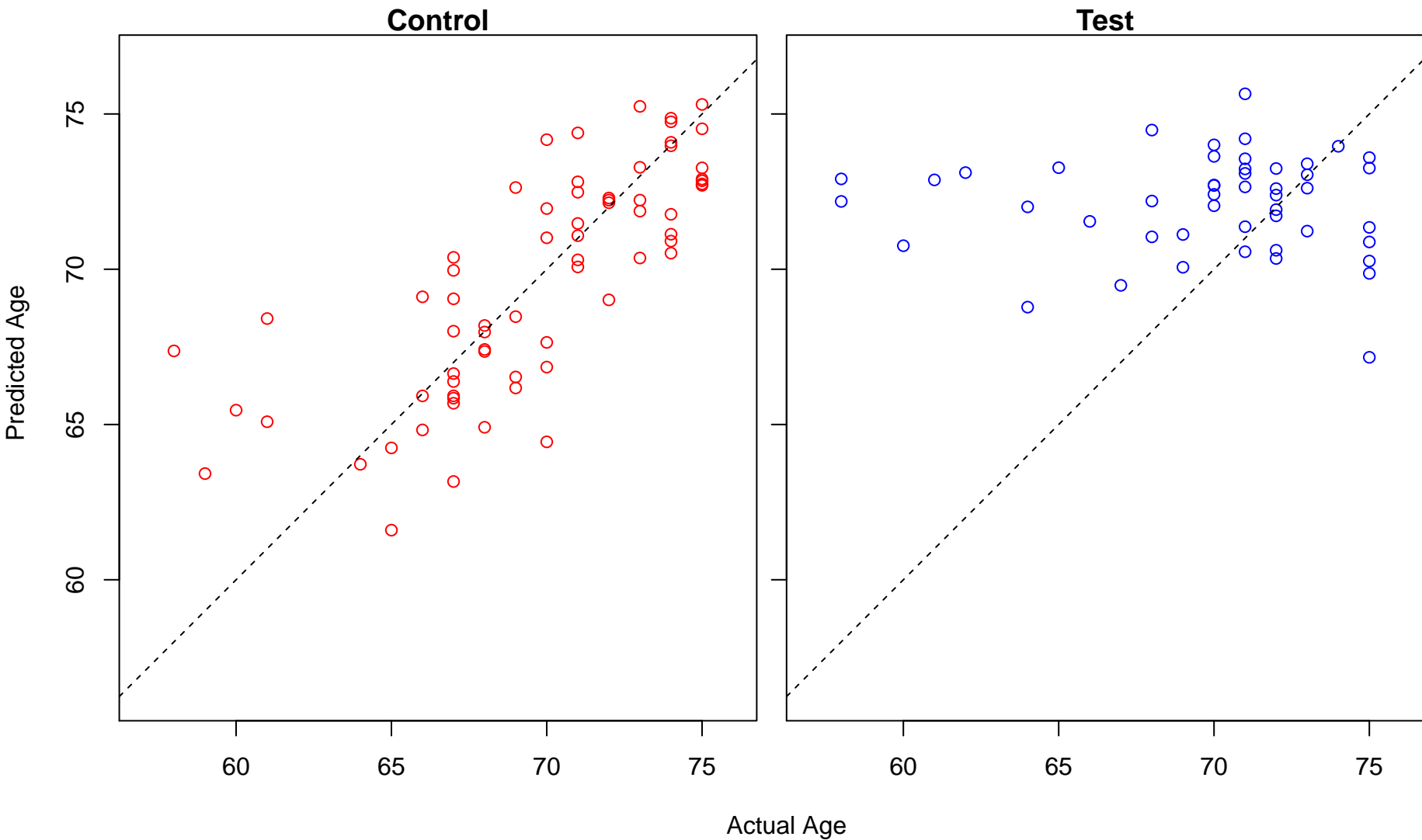


Actual Age

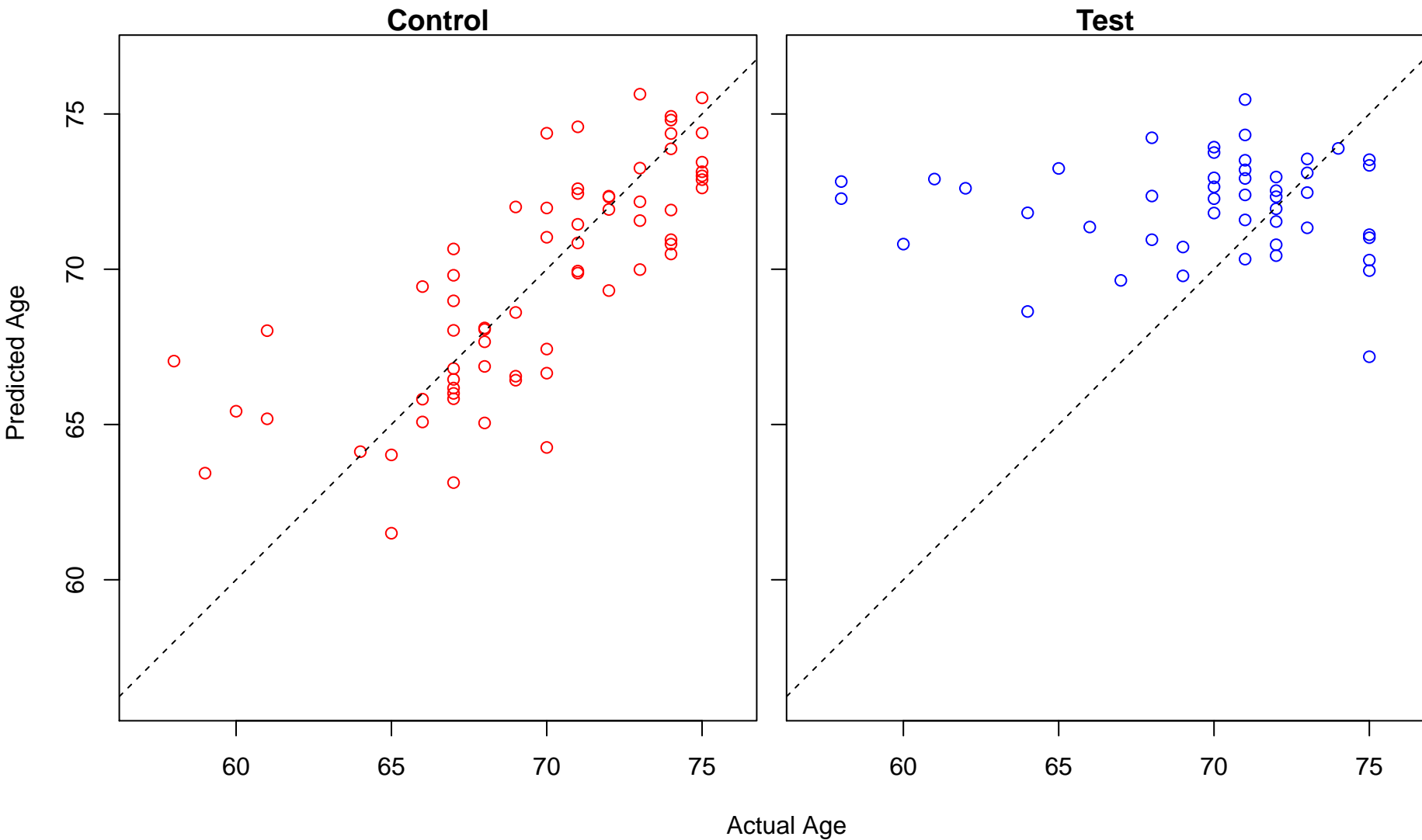
glycerolipid biosynthetic process (Score: 1.876555)



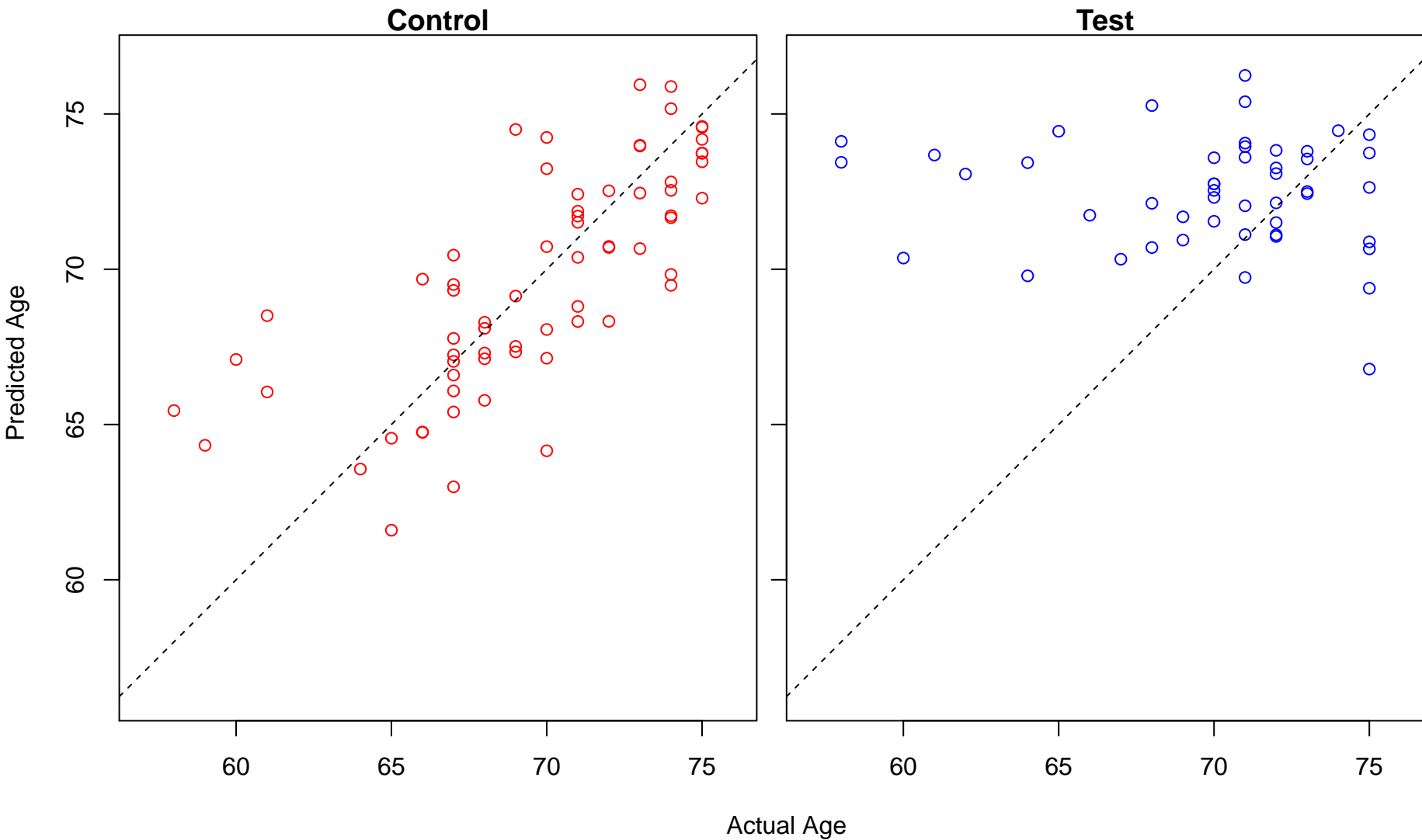
response to peptide (Score: 1.875888)



cellular response to peptide (Score: 1.875600)

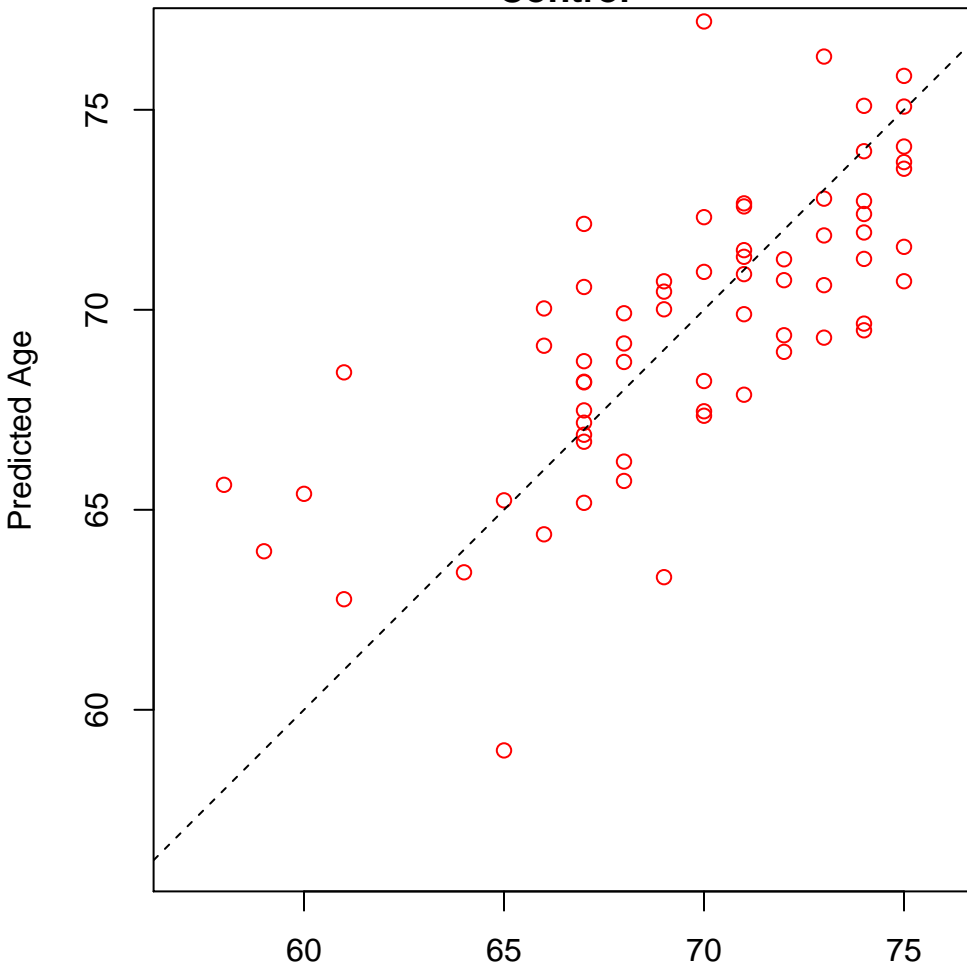


regulation of MAP kinase activity (Score: 1.875274)

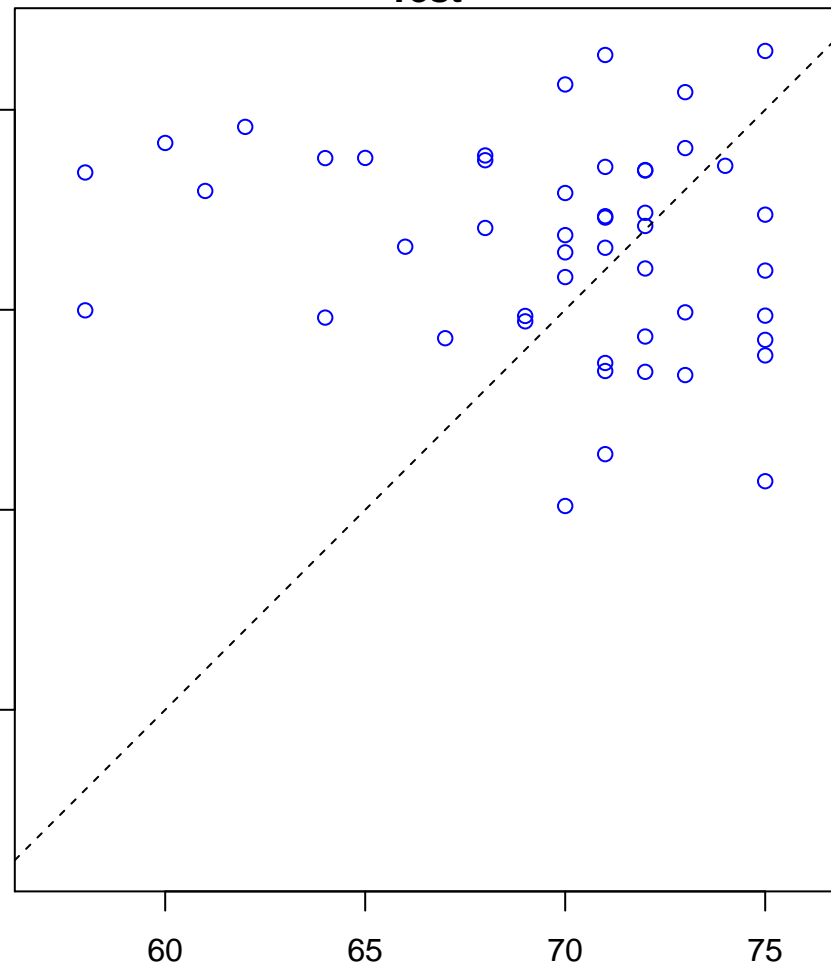


cellular response to ionizing radiation (Score: 1.873773)

Control

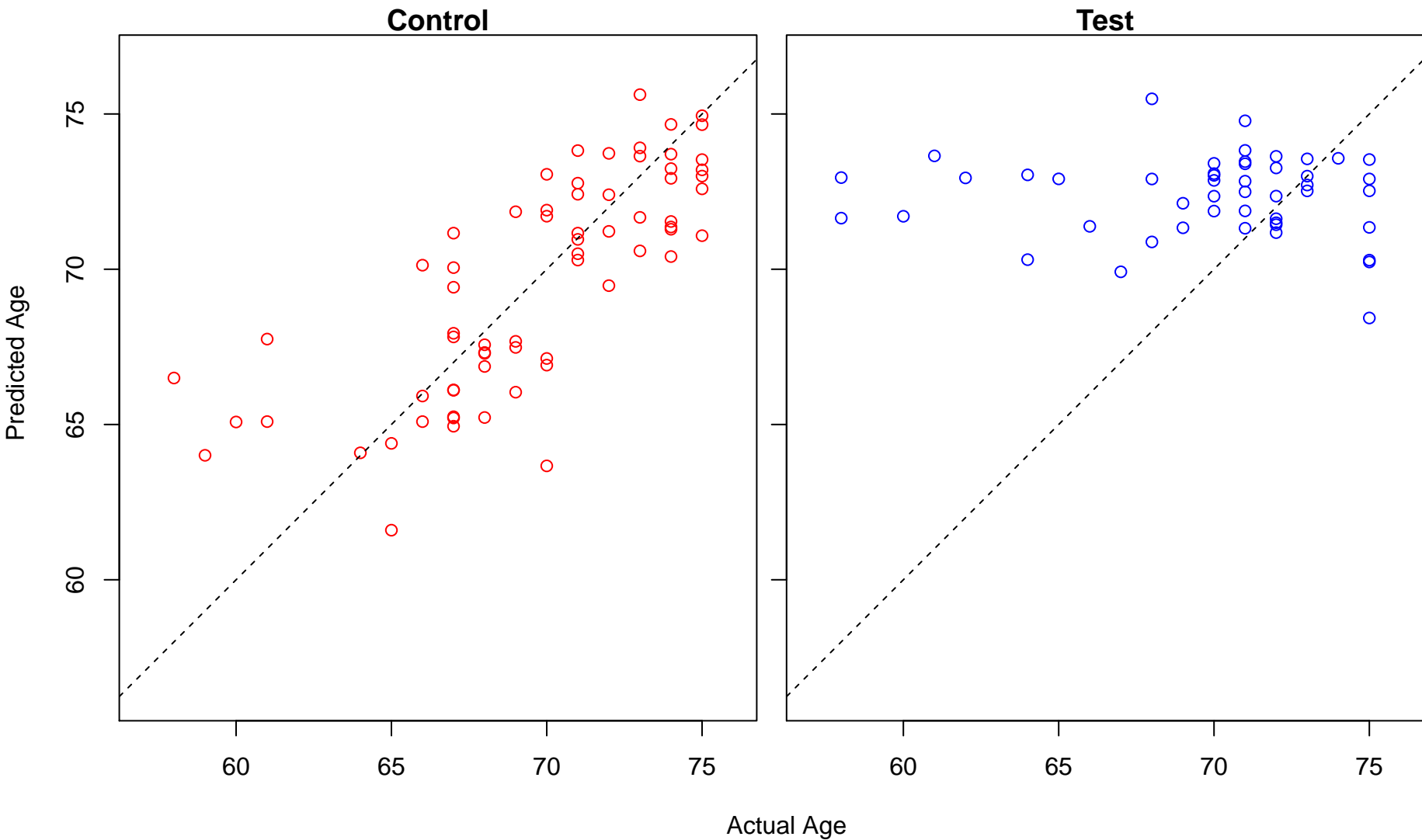


Test

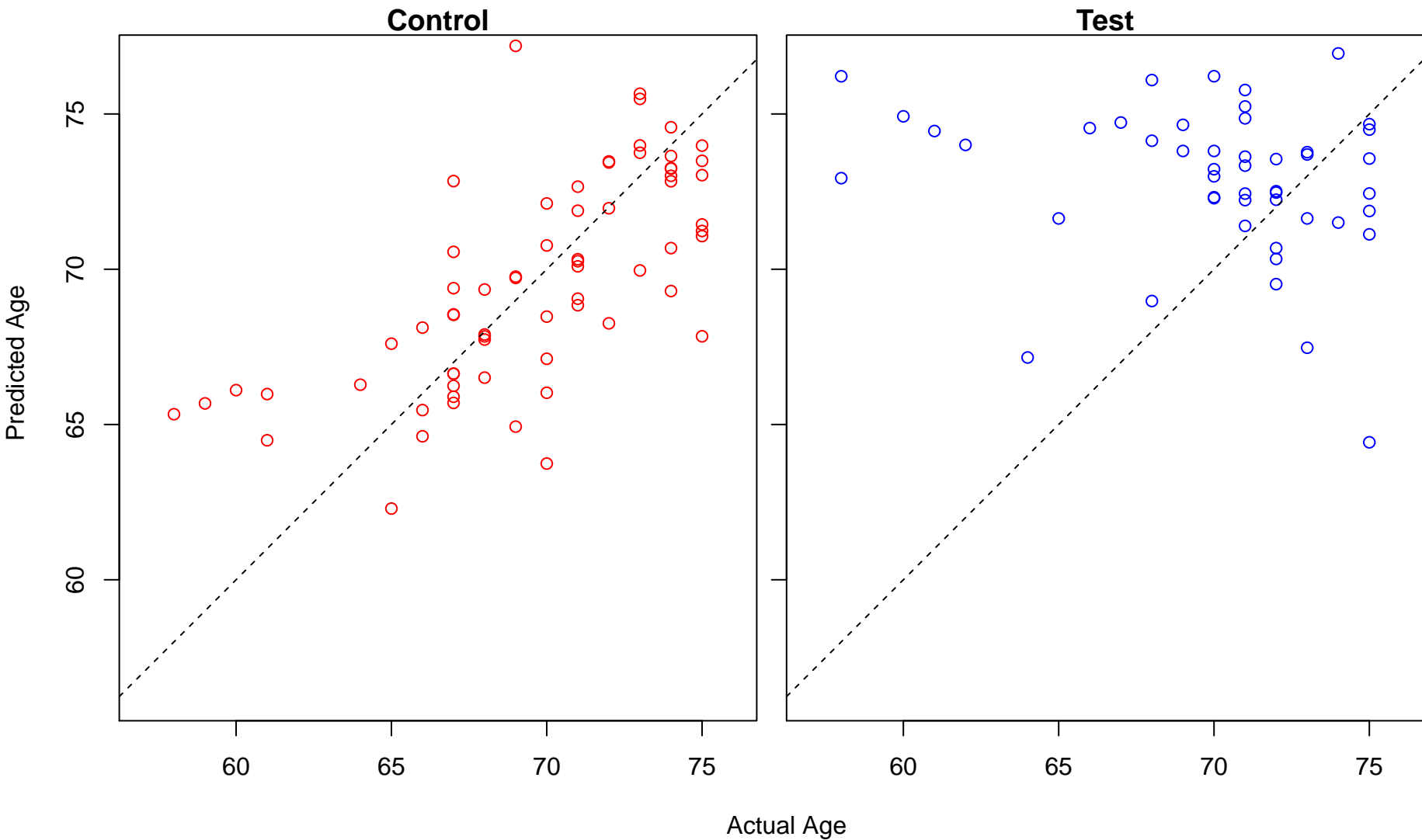


Actual Age

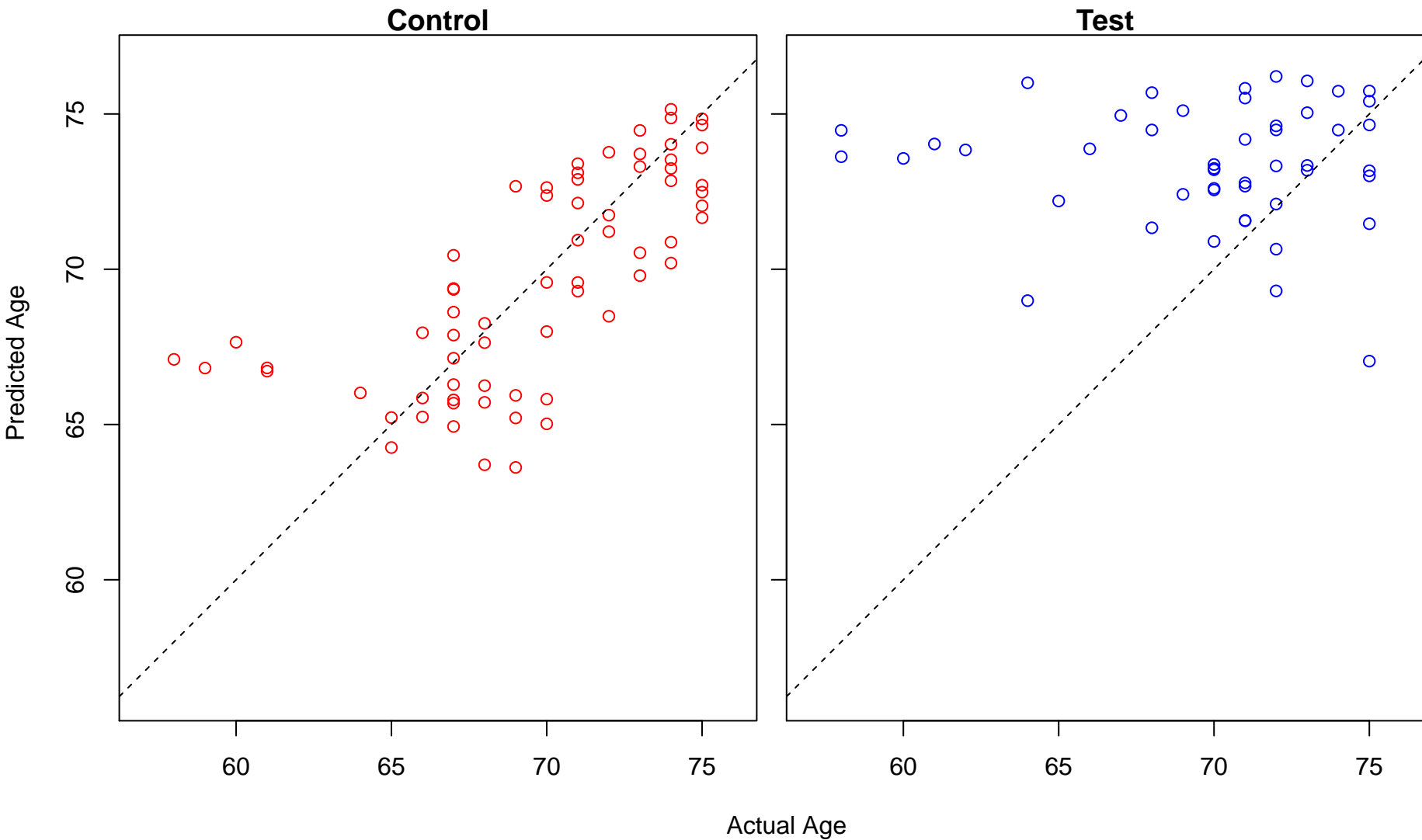
negative regulation of cell cycle (Score: 1.873483)



positive regulation of lymphocyte differentiation (Score: 1.873116)

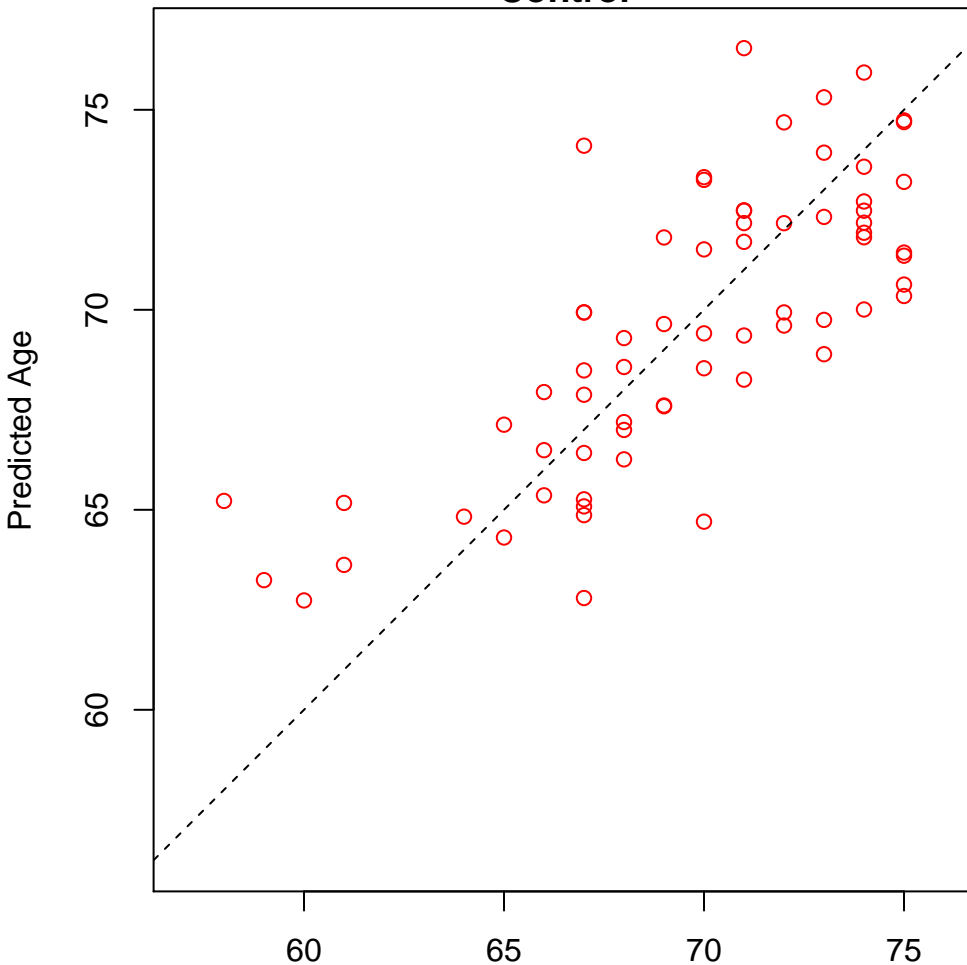


negative regulation of cellular component movement (Score: 1.871906)

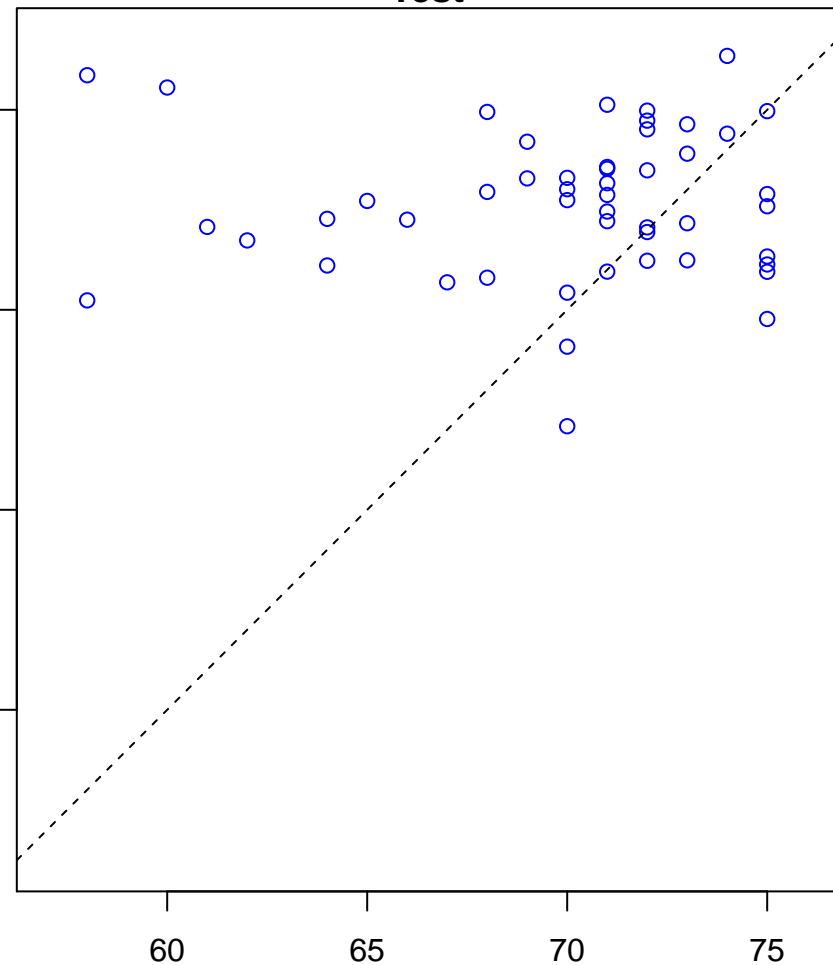


regulation of membrane permeability (Score: 1.871229)

Control

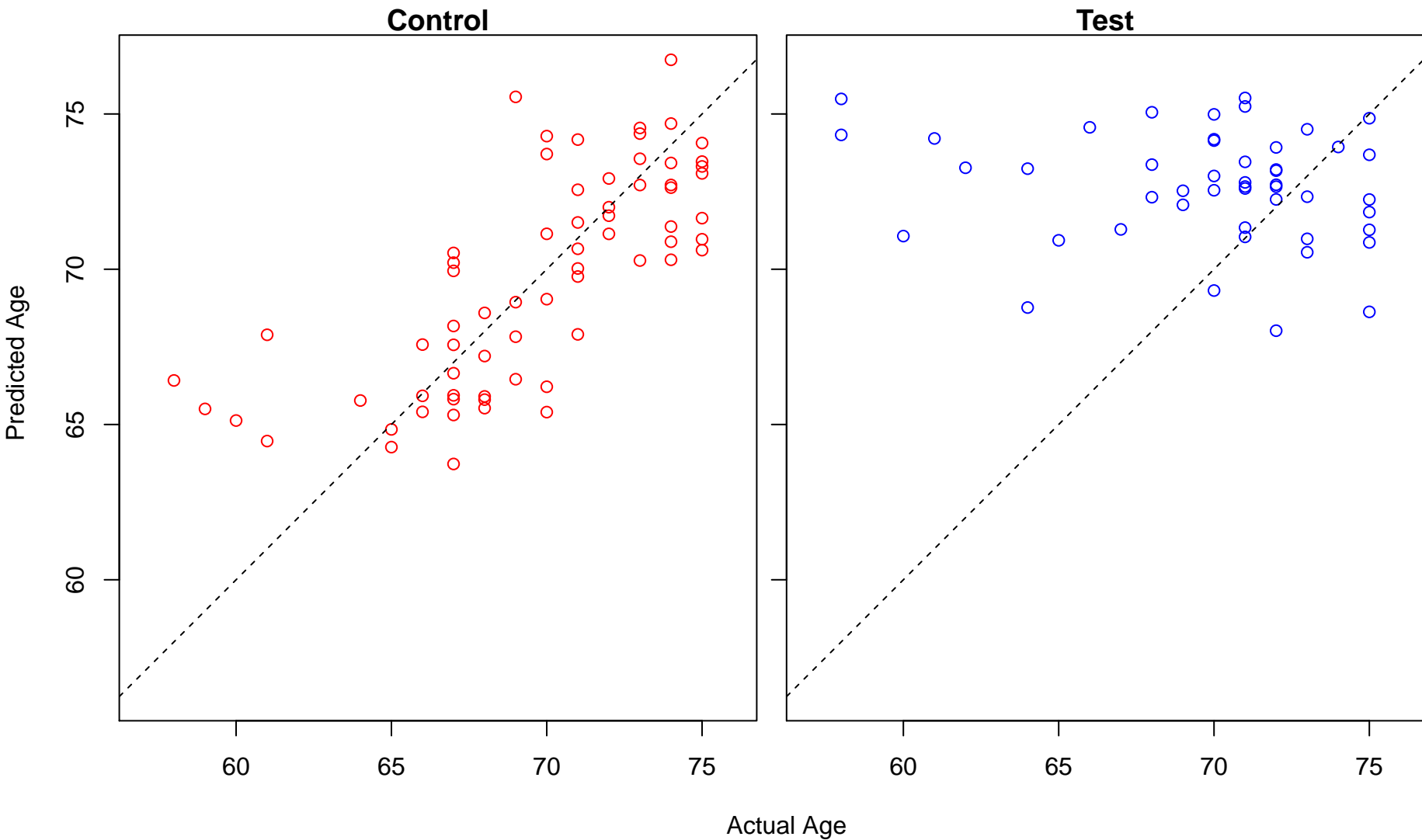


Test

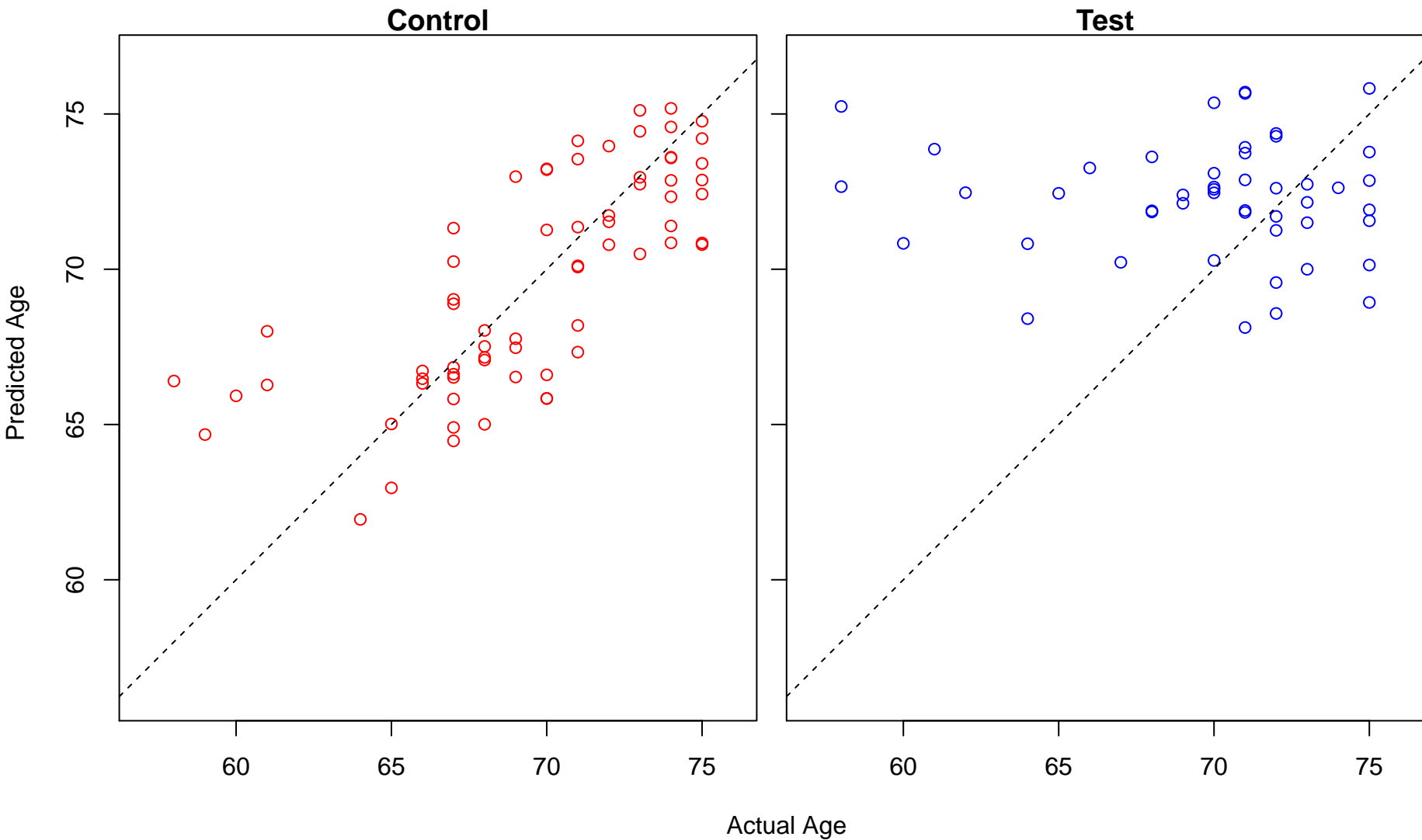


Actual Age

inorganic ion homeostasis (Score: 1.870797)

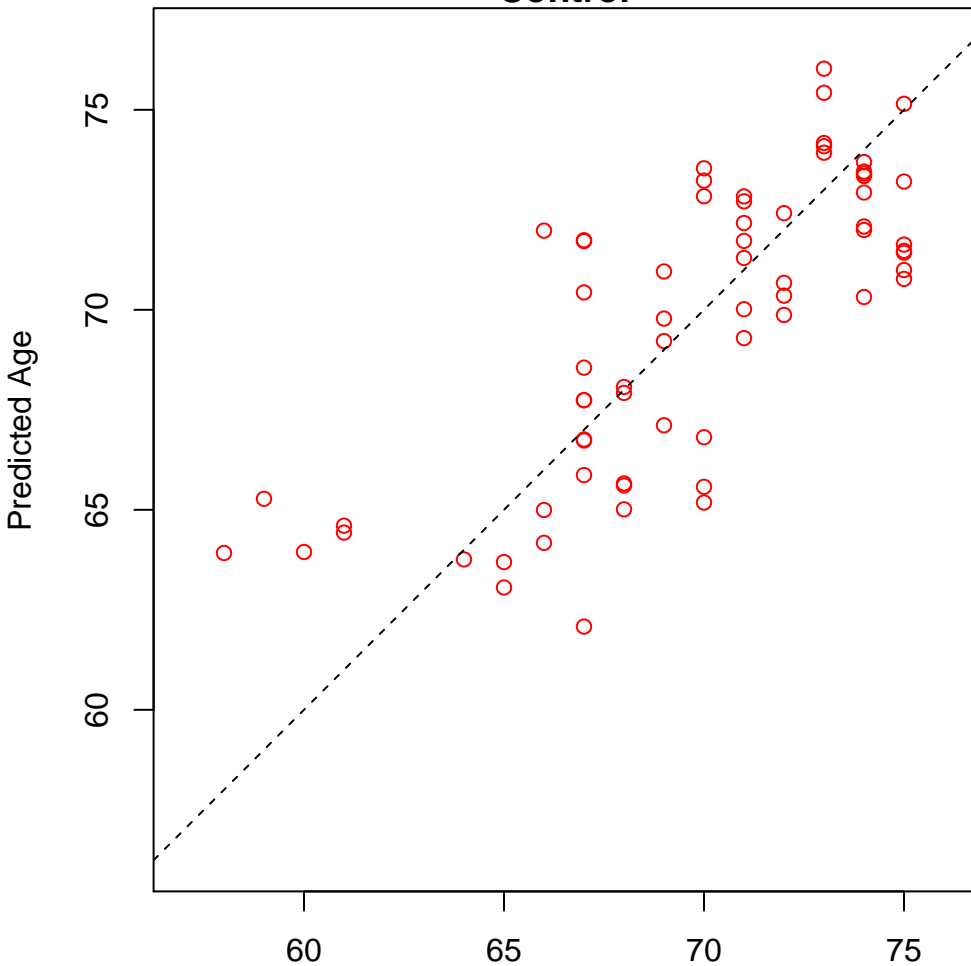


cell adhesion (Score: 1.869580)

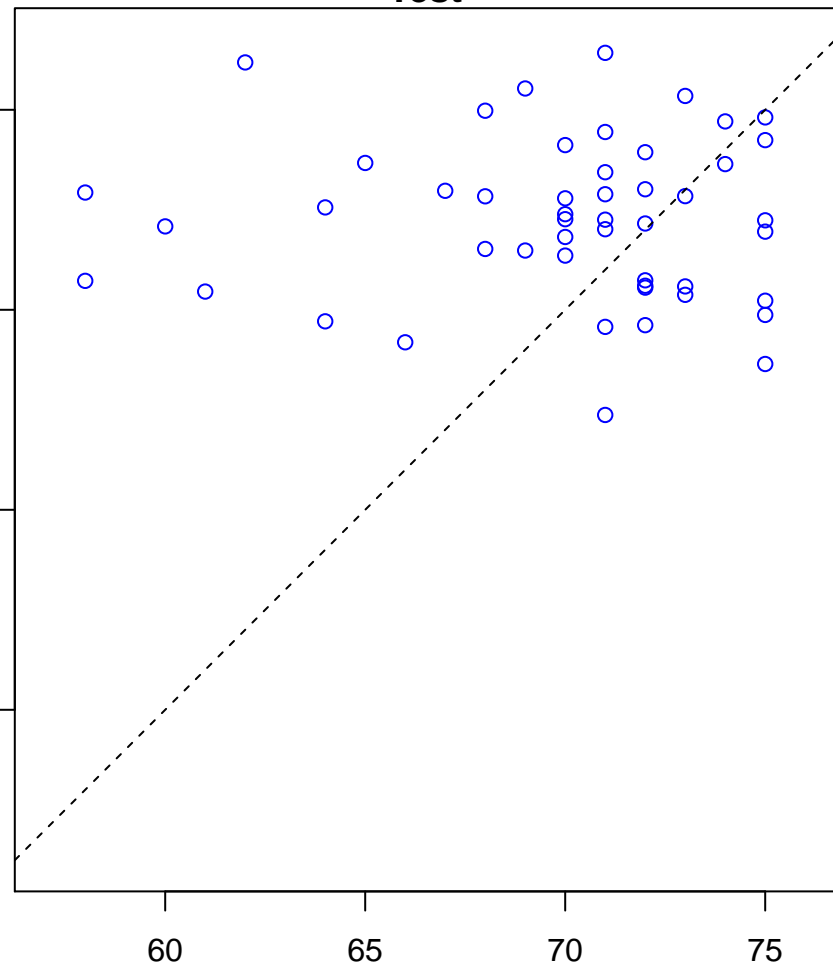


multi-organism membrane organization (Score: 1.868908)

Control

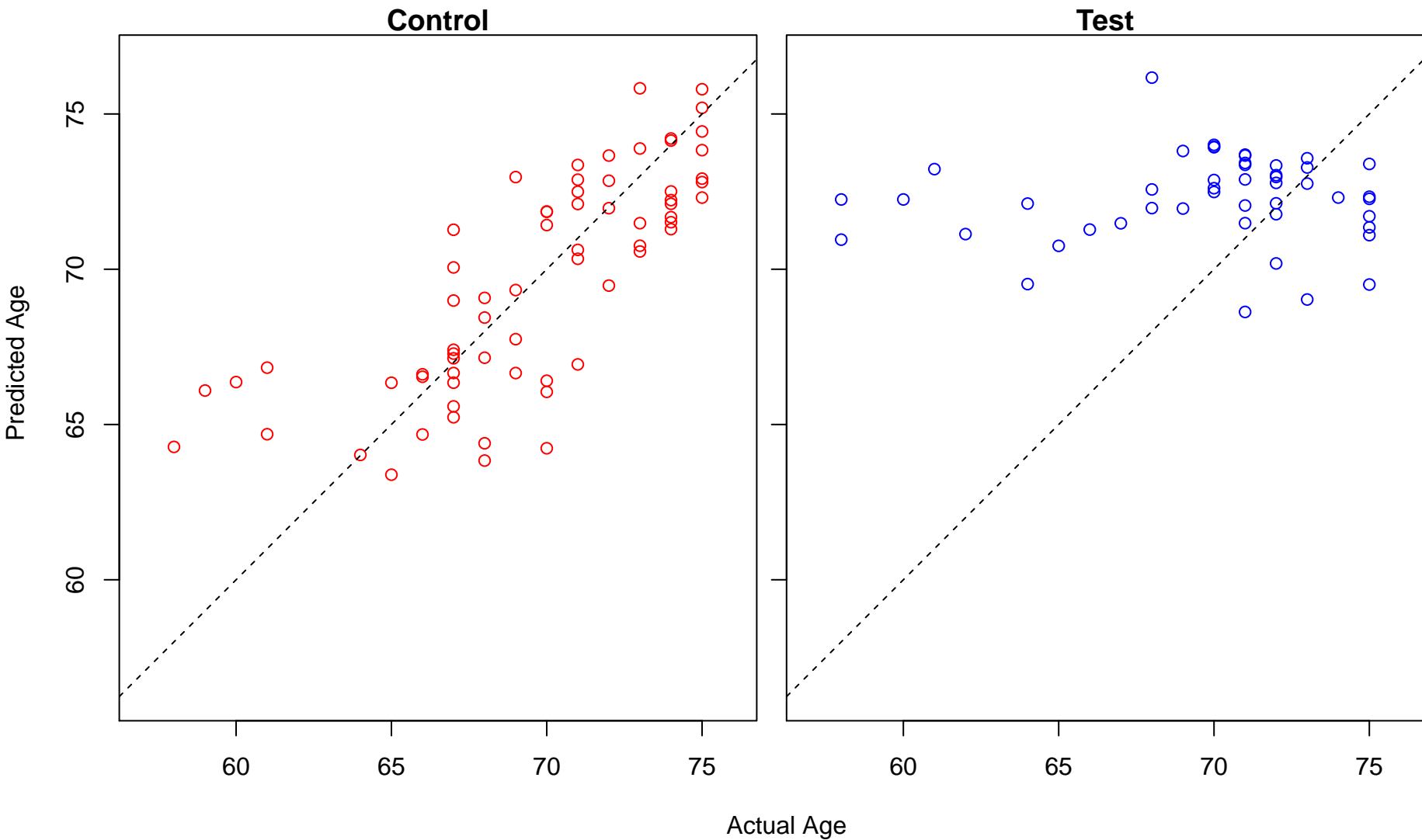


Test

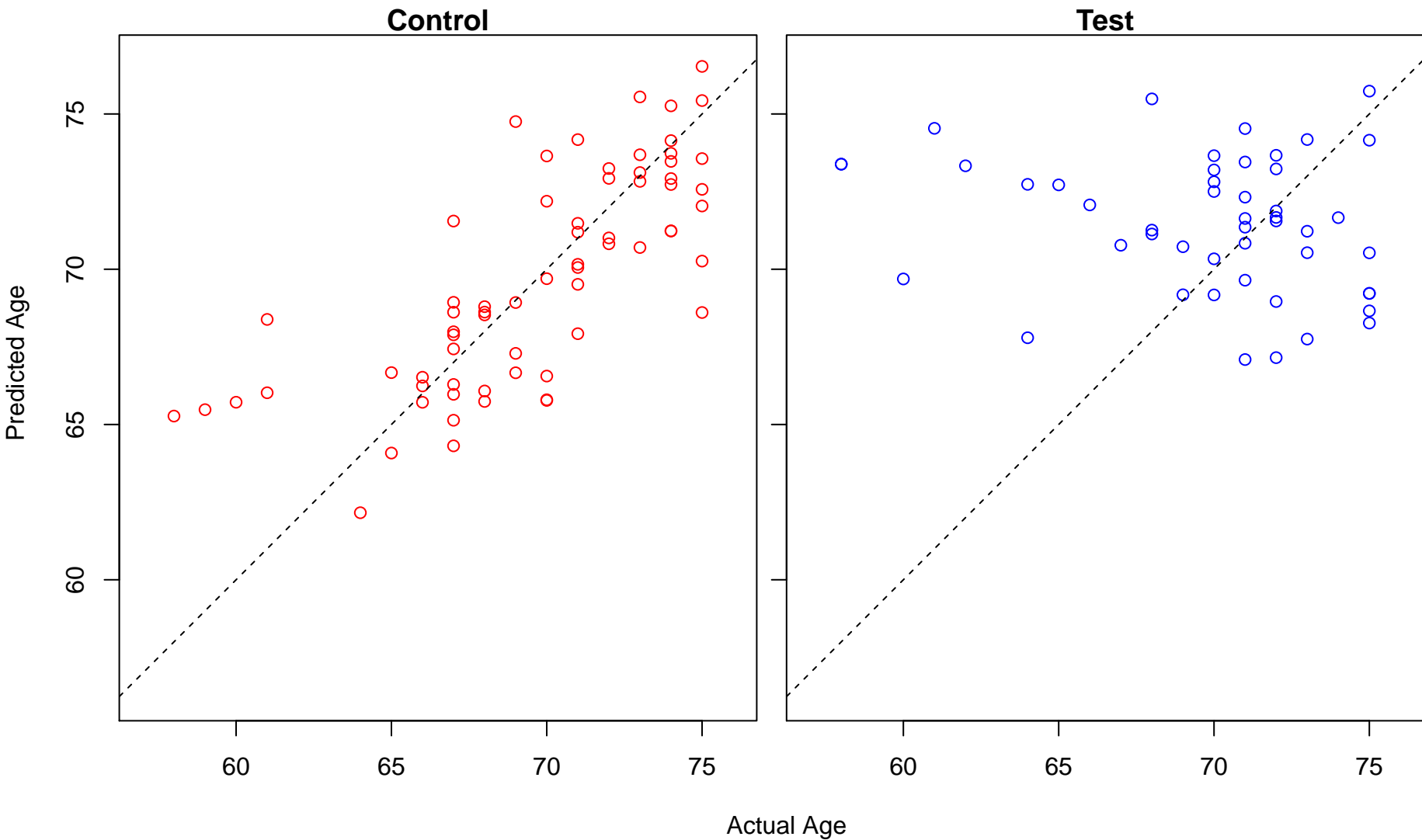


Actual Age

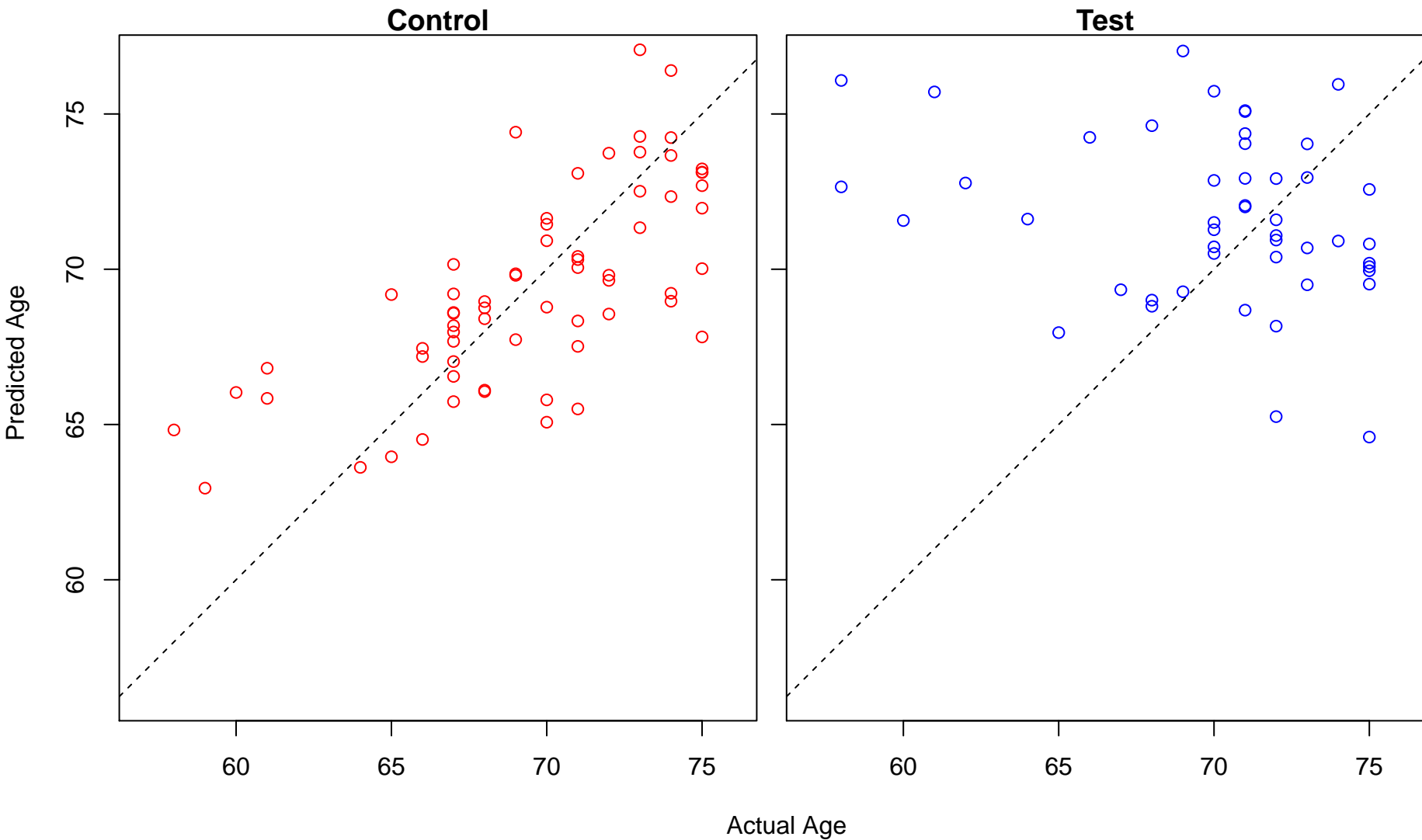
lipoprotein metabolic process (Score: 1.868907)



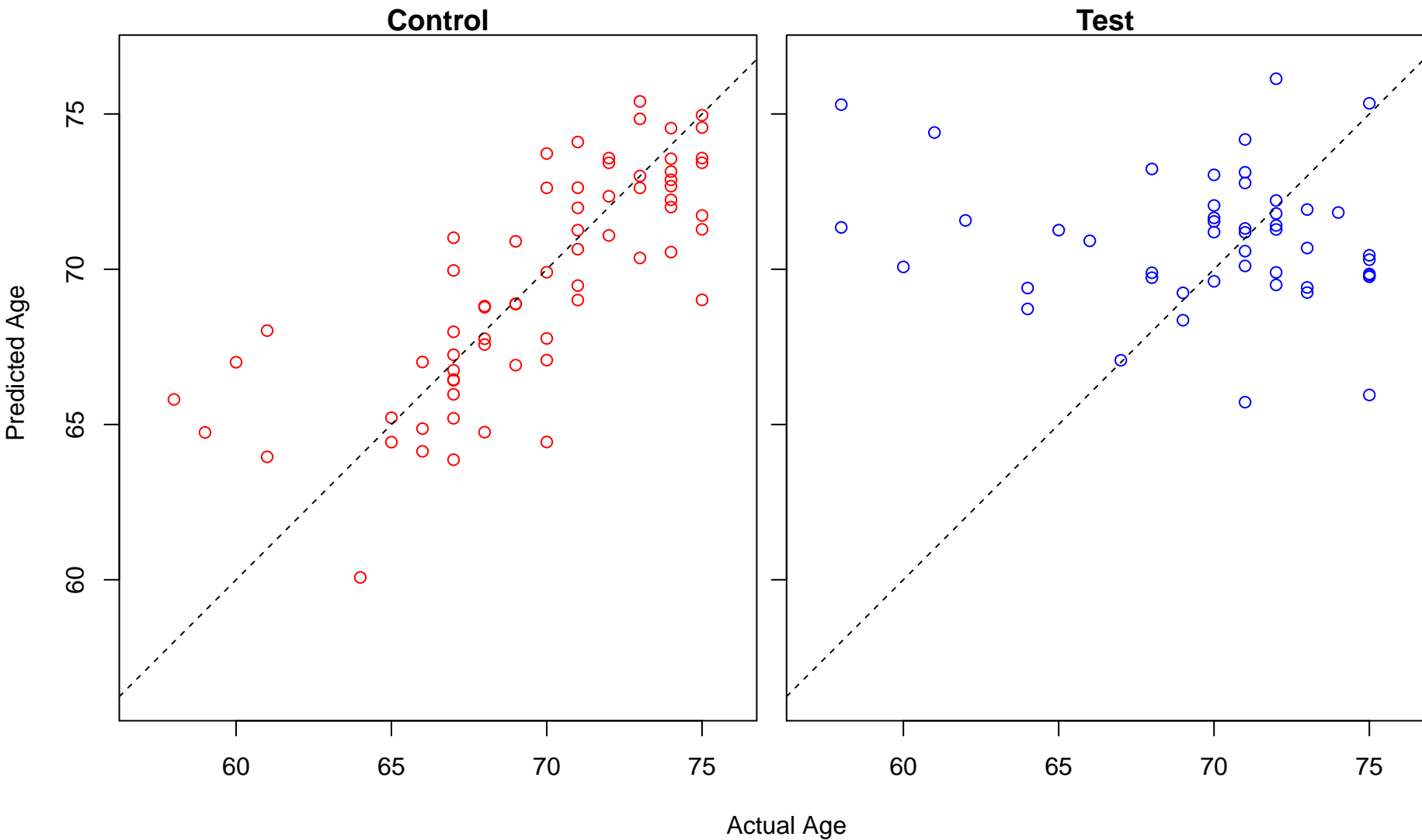
negative regulation of cysteine-type endopeptidase activity (Score: 1.867834)



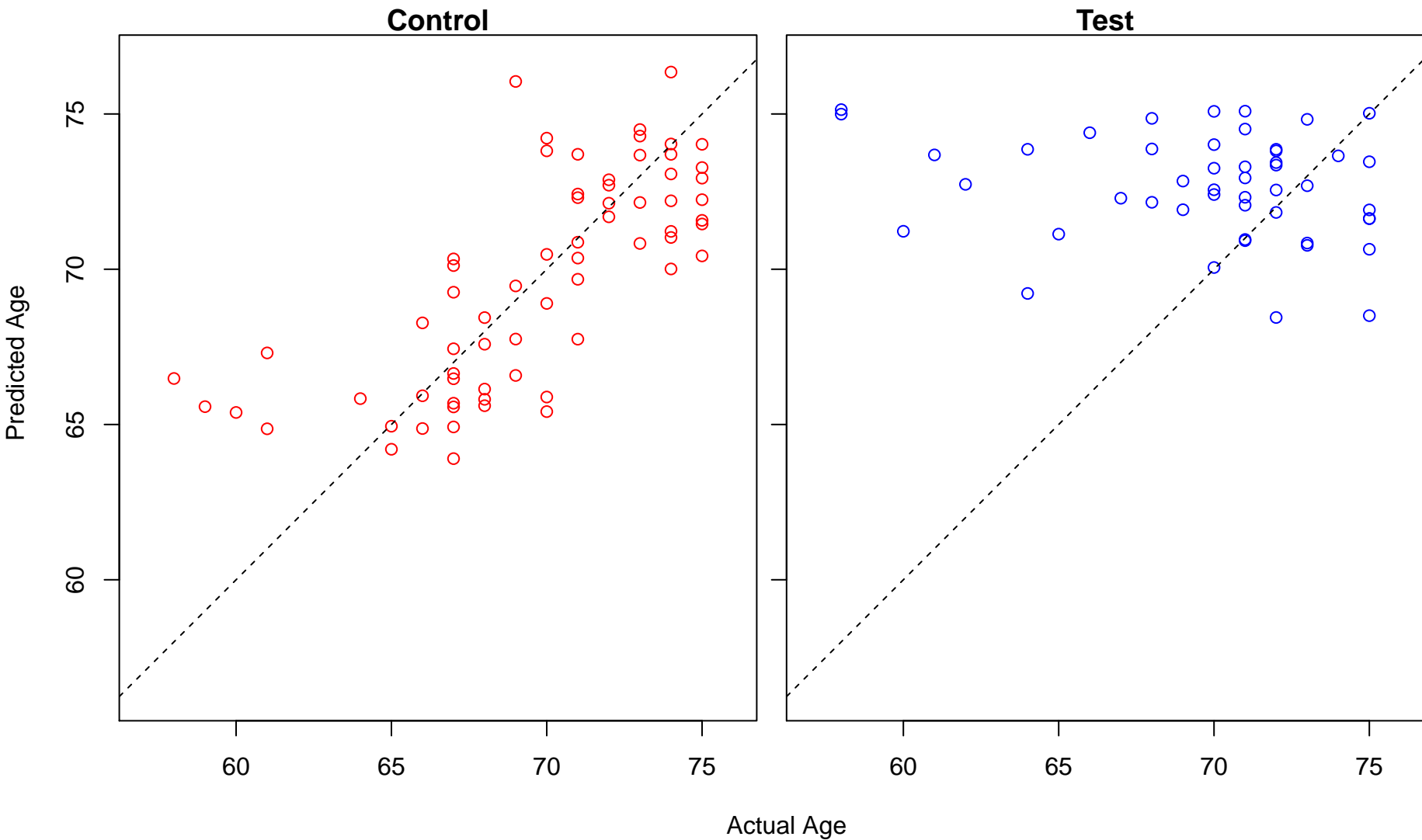
positive regulation of lymphocyte apoptotic process (Score: 1.867760)



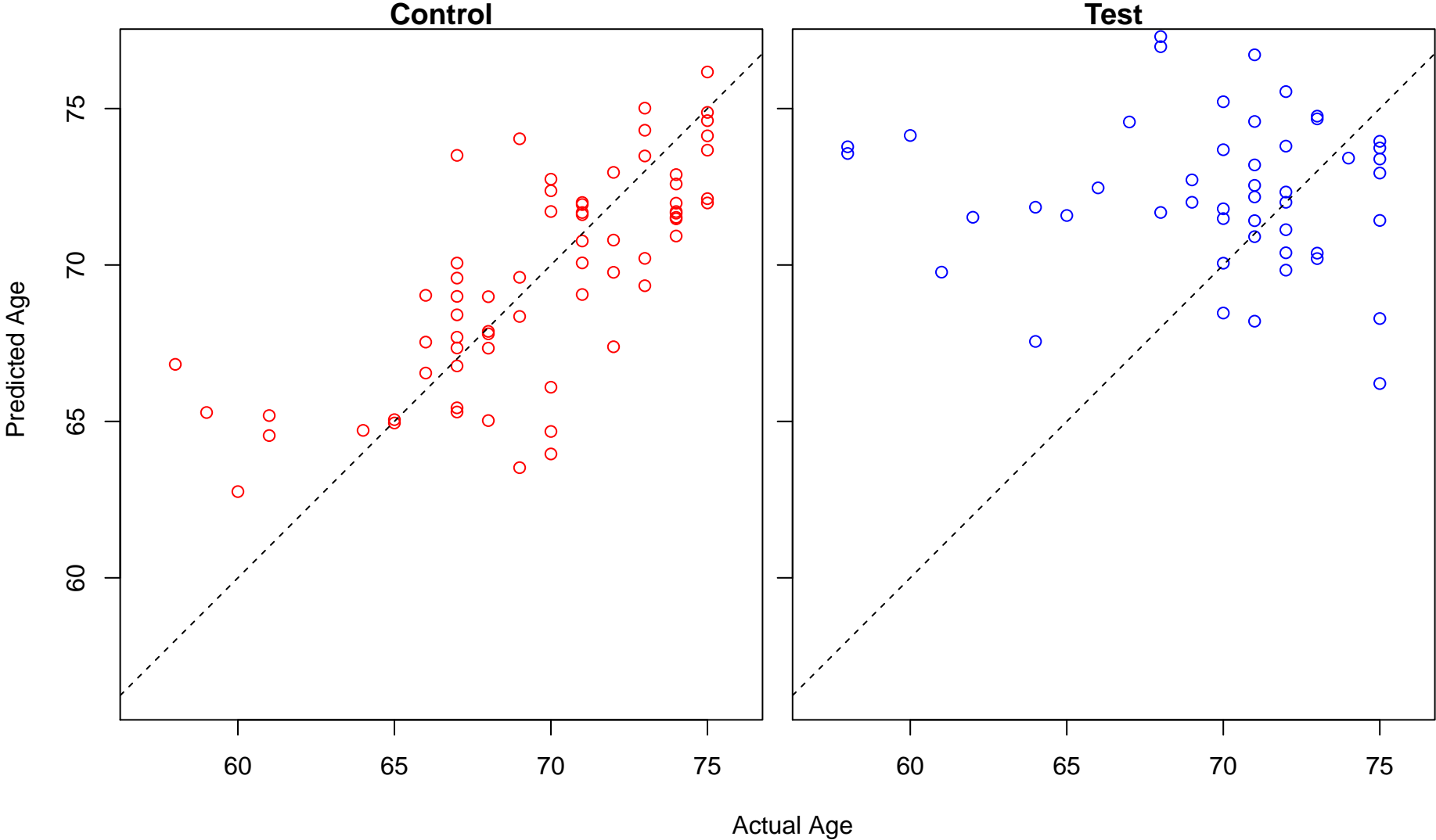
regulation of extrinsic apoptotic signaling pathway (Score: 1.867617)



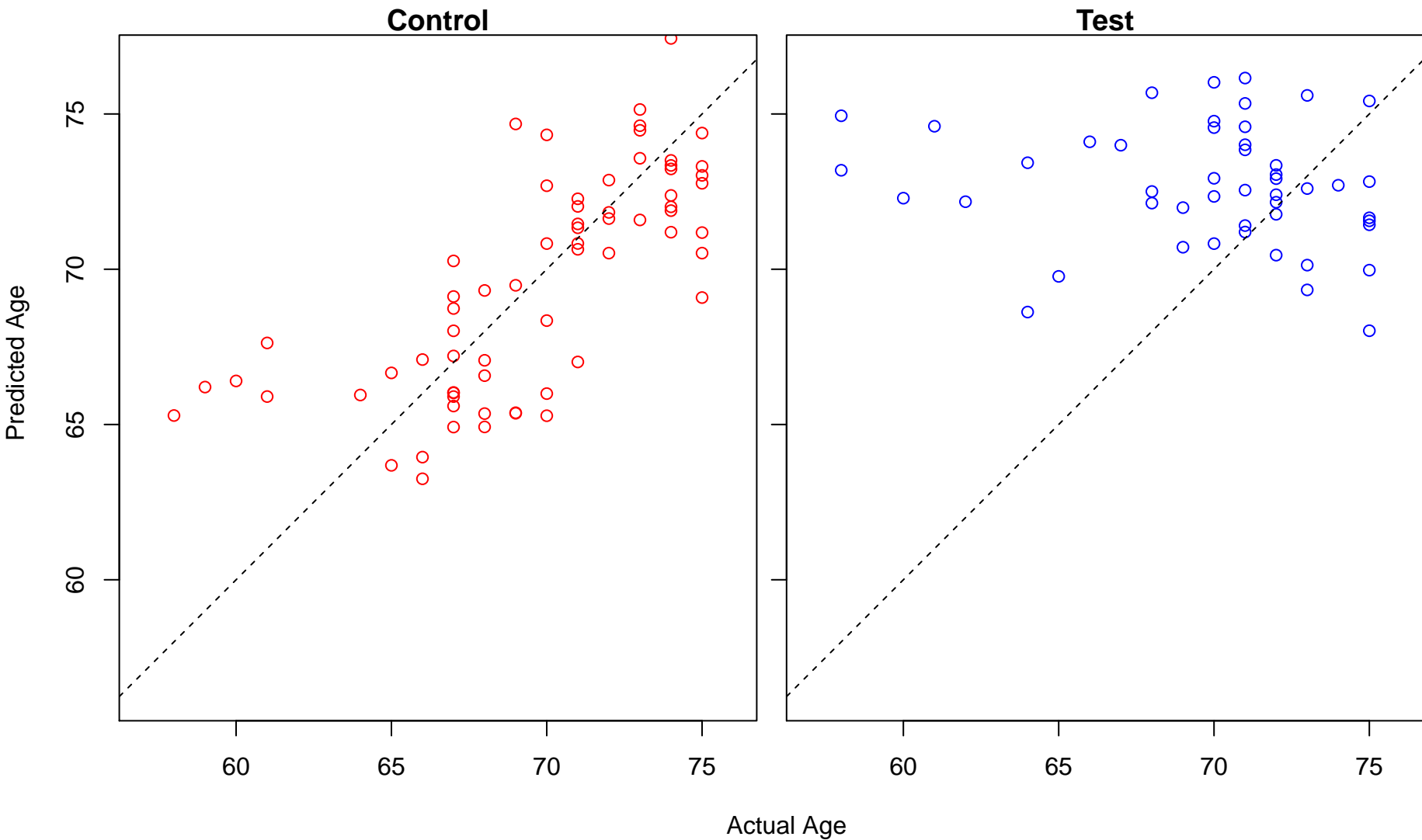
metal ion homeostasis (Score: 1.866846)



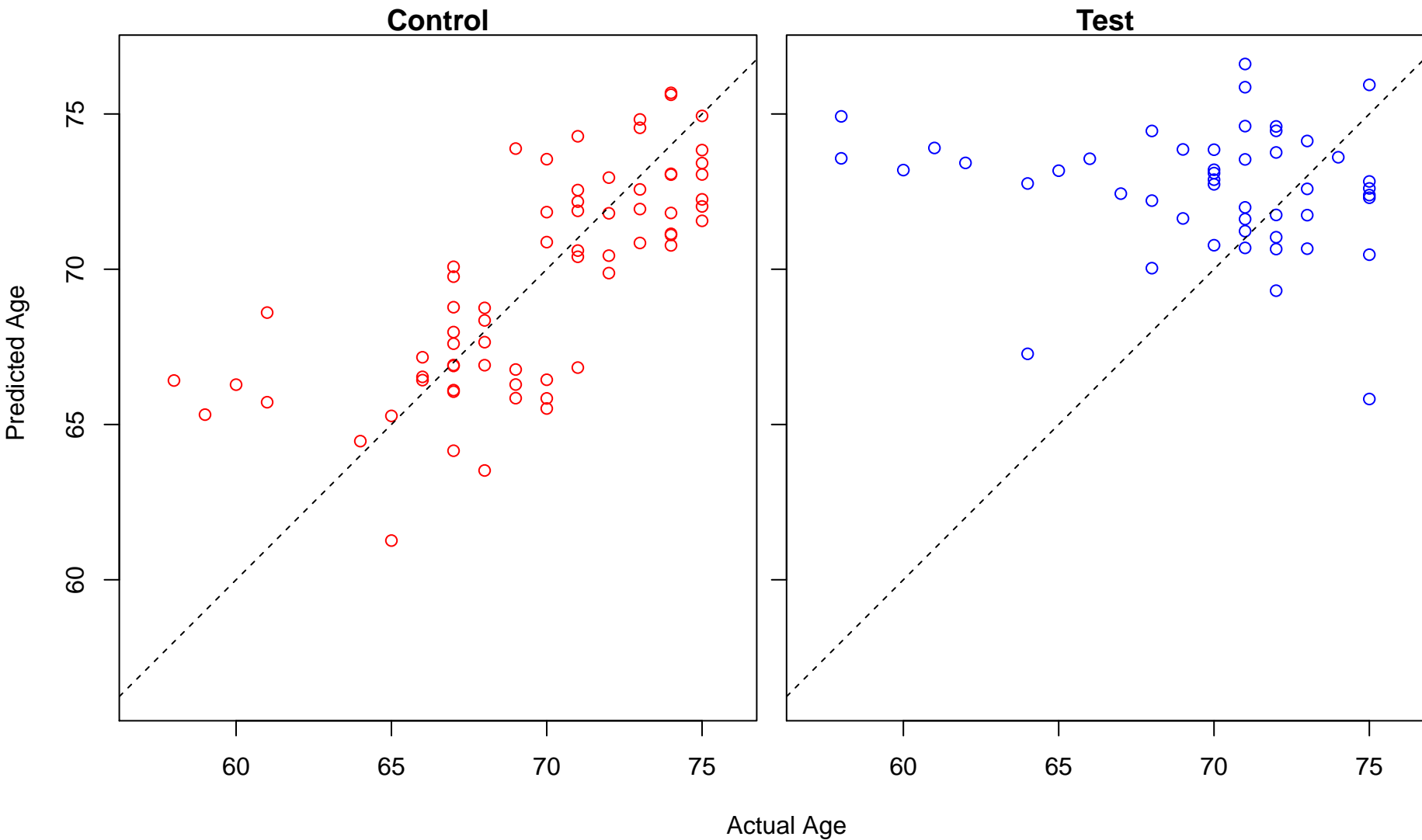
intrinsic apoptotic signaling pathway by p53 class mediator (Score: 1.866729)



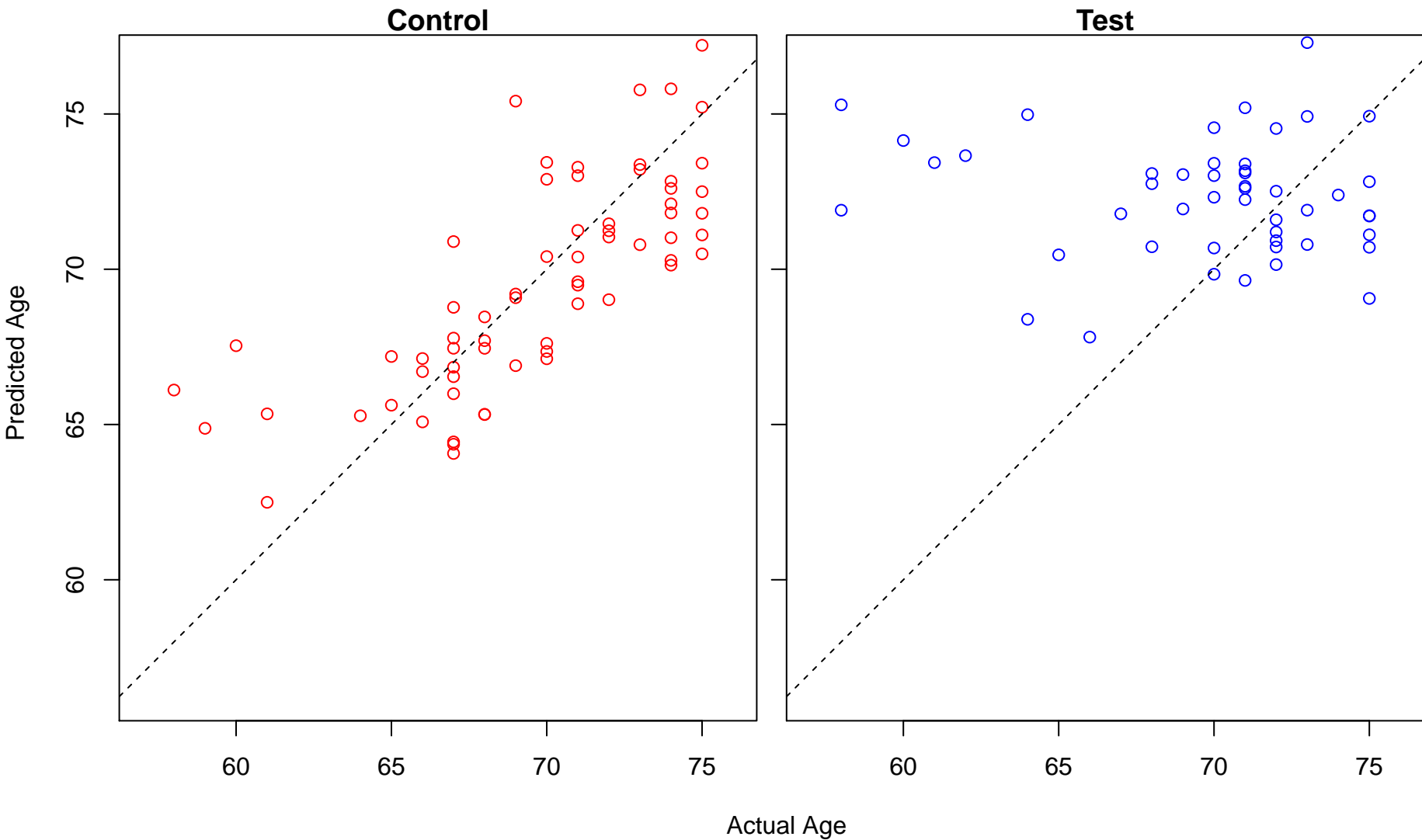
transition metal ion homeostasis (Score: 1.866058)



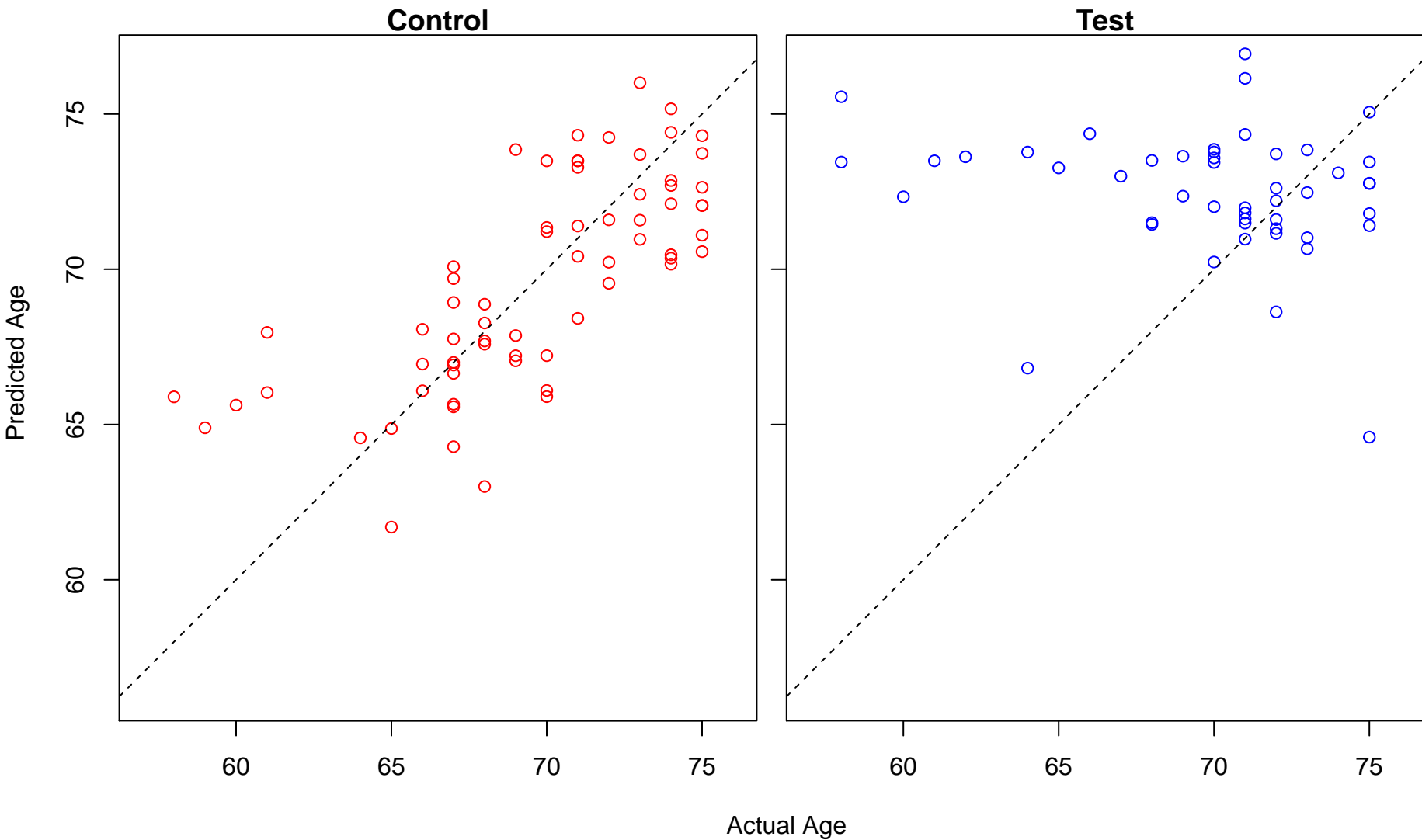
regulation of cell migration (Score: 1.865766)



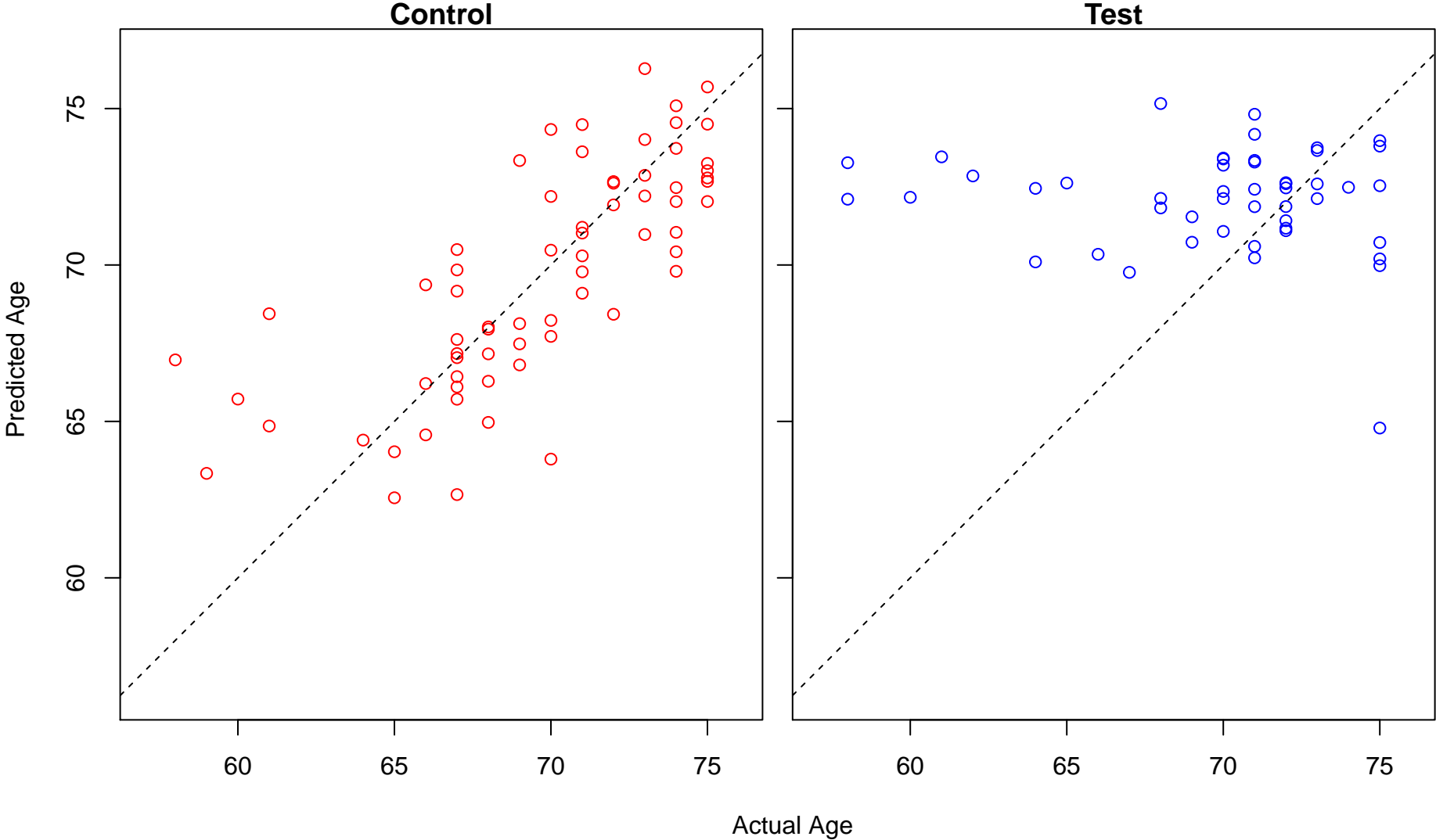
establishment of protein localization to mitochondrion (Score: 1.865477)



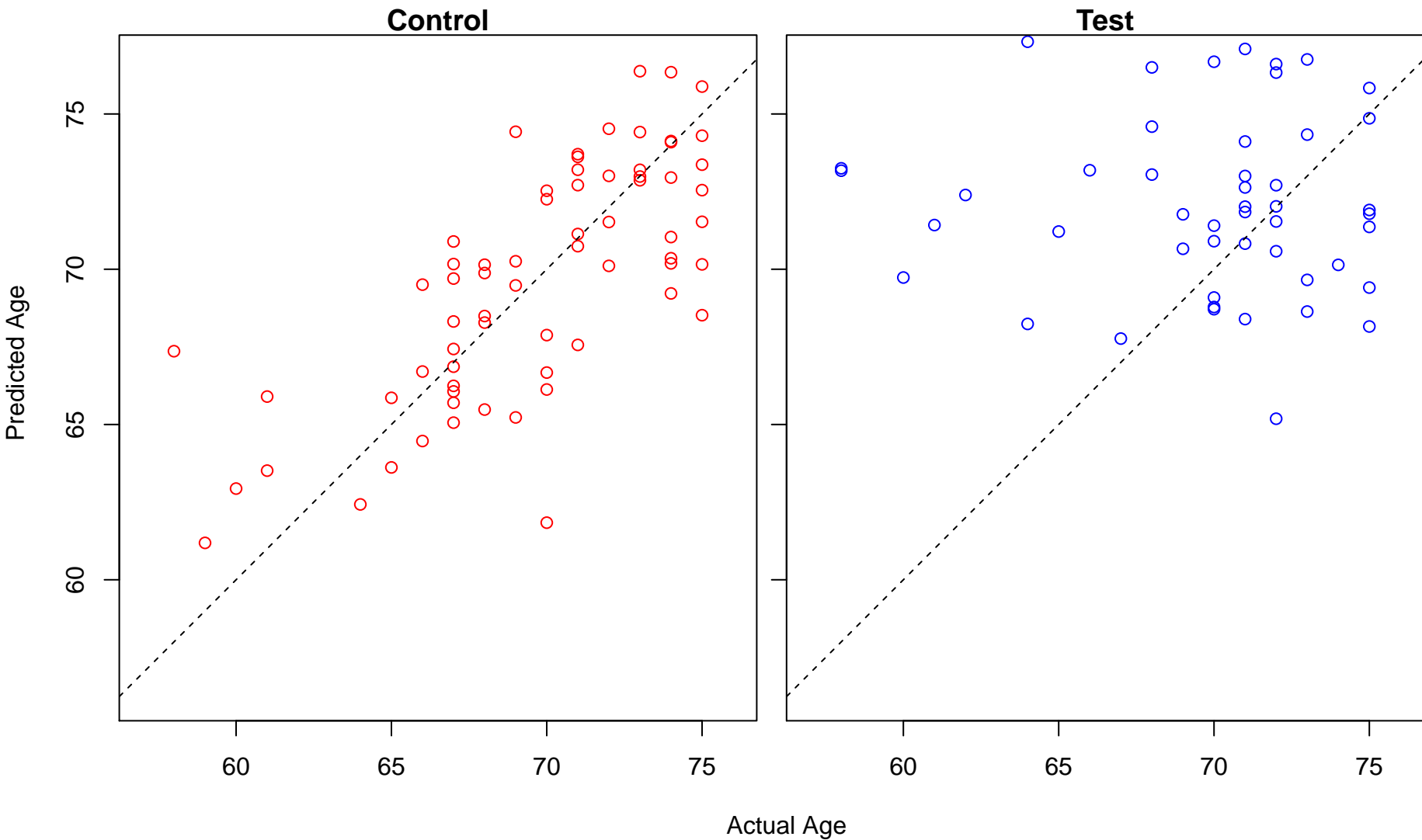
positive regulation of locomotion (Score: 1.864857)



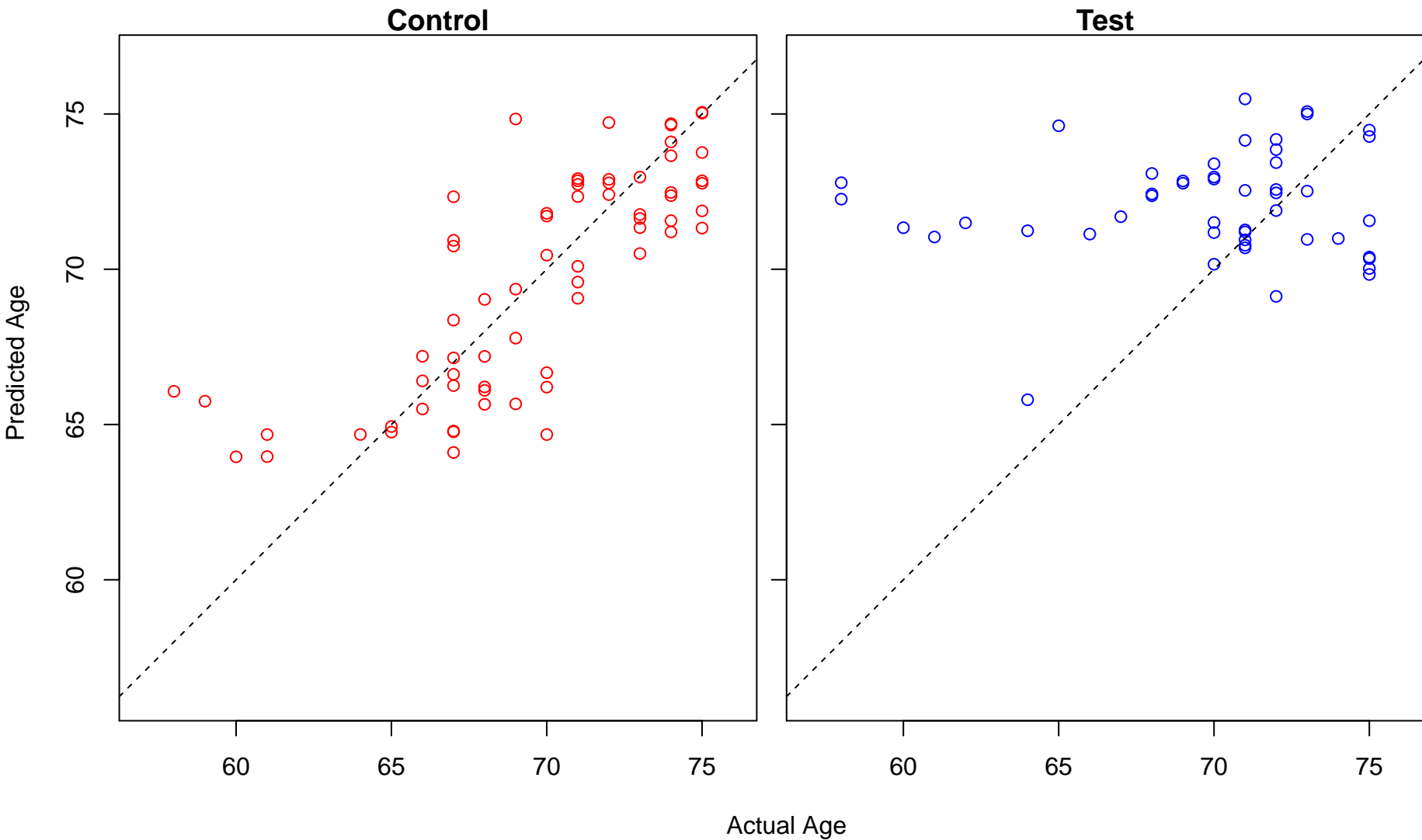
cellular response to fibroblast growth factor stimulus (Score: 1.864591)



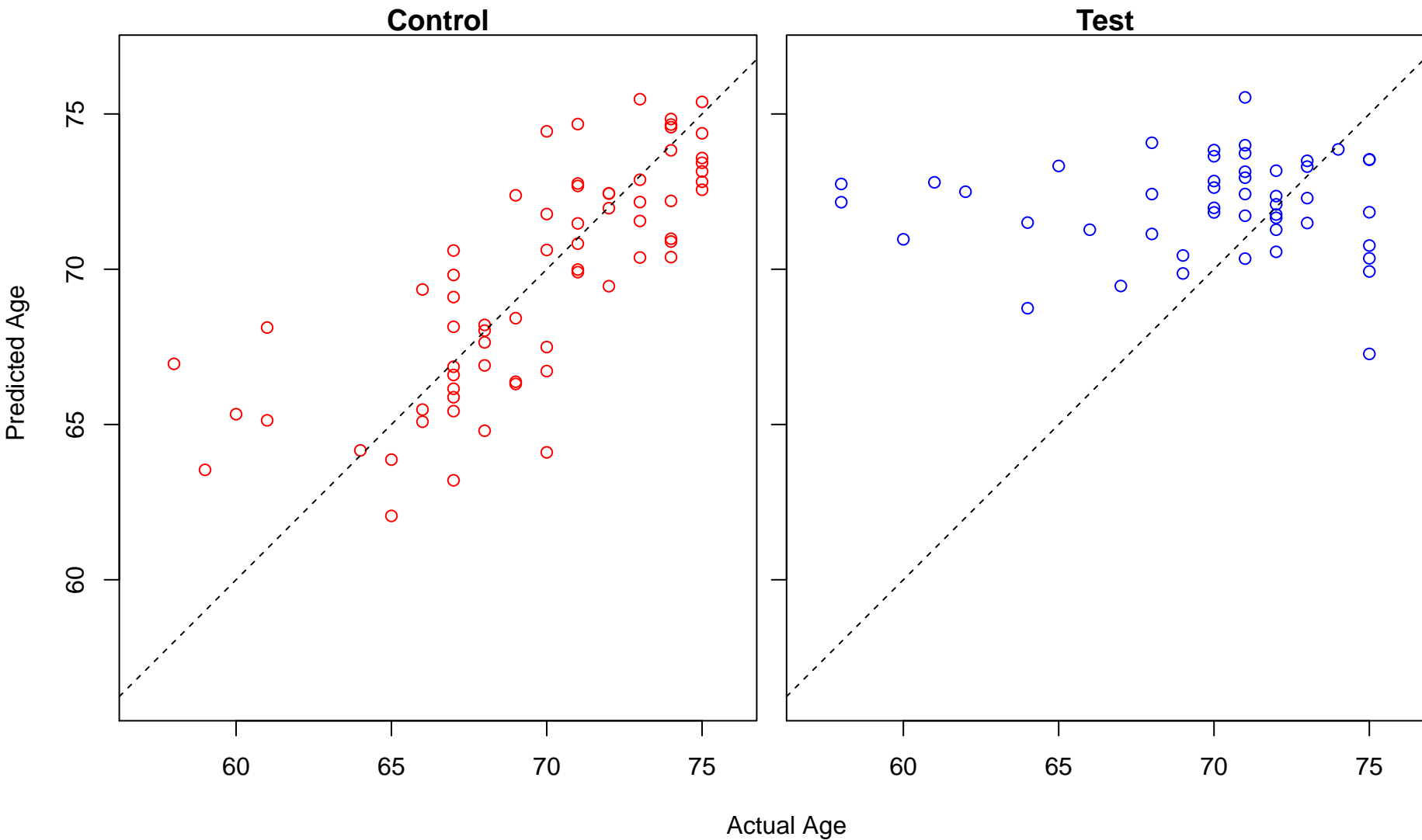
regulation of ion homeostasis (Score: 1.862406)



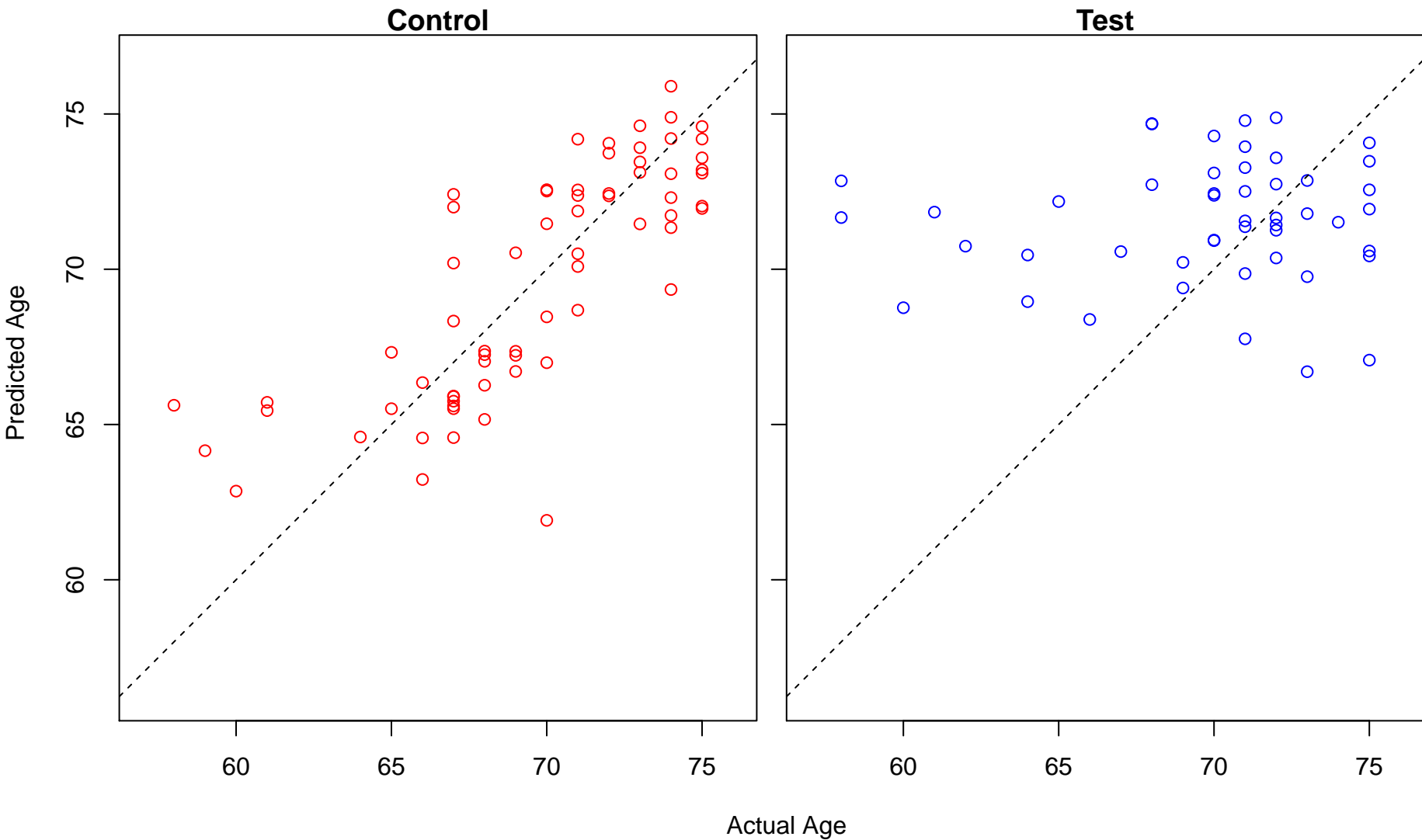
nuclear-transcribed mRNA catabolic process, exonucleolytic (Score: 1.861873)



cellular response to peptide hormone stimulus (Score: 1.861196)

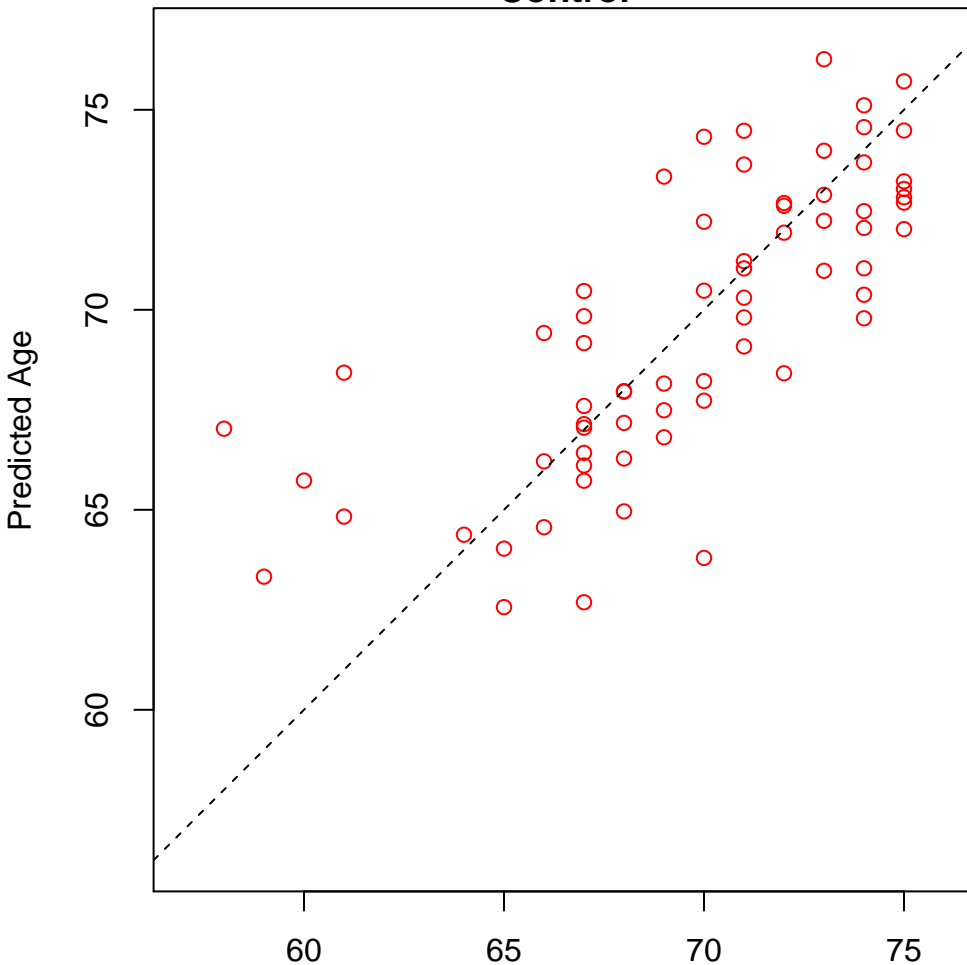


nucleoside triphosphate biosynthetic process (Score: 1.861118)

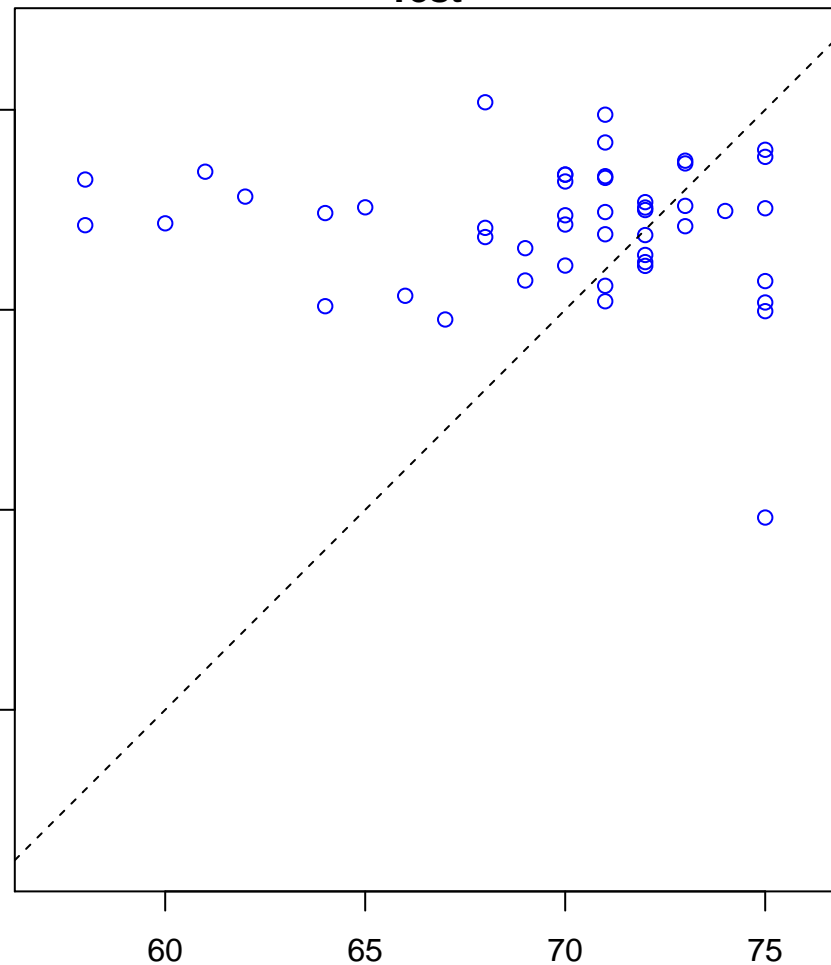


response to fibroblast growth factor (Score: 1.860743)

Control

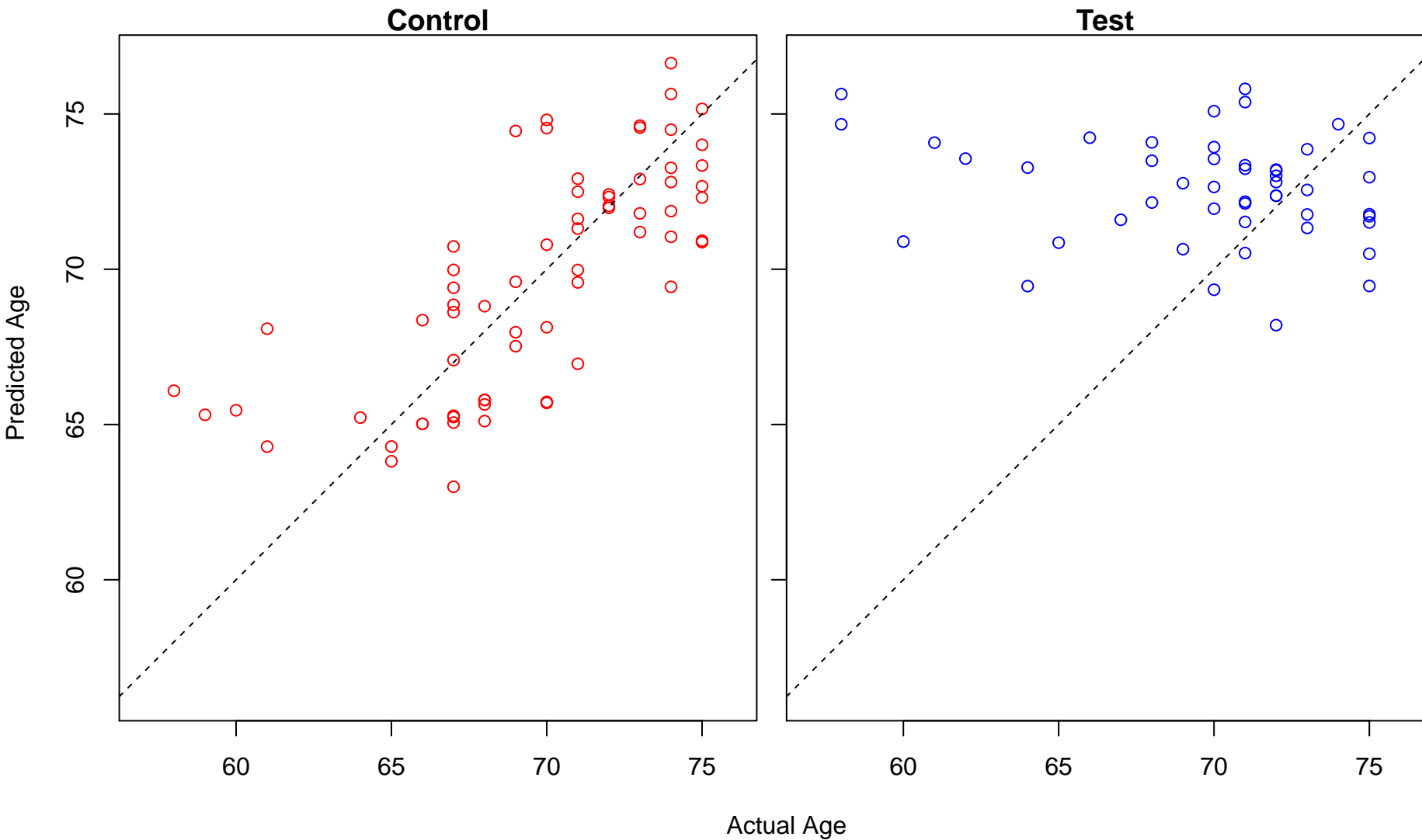


Test

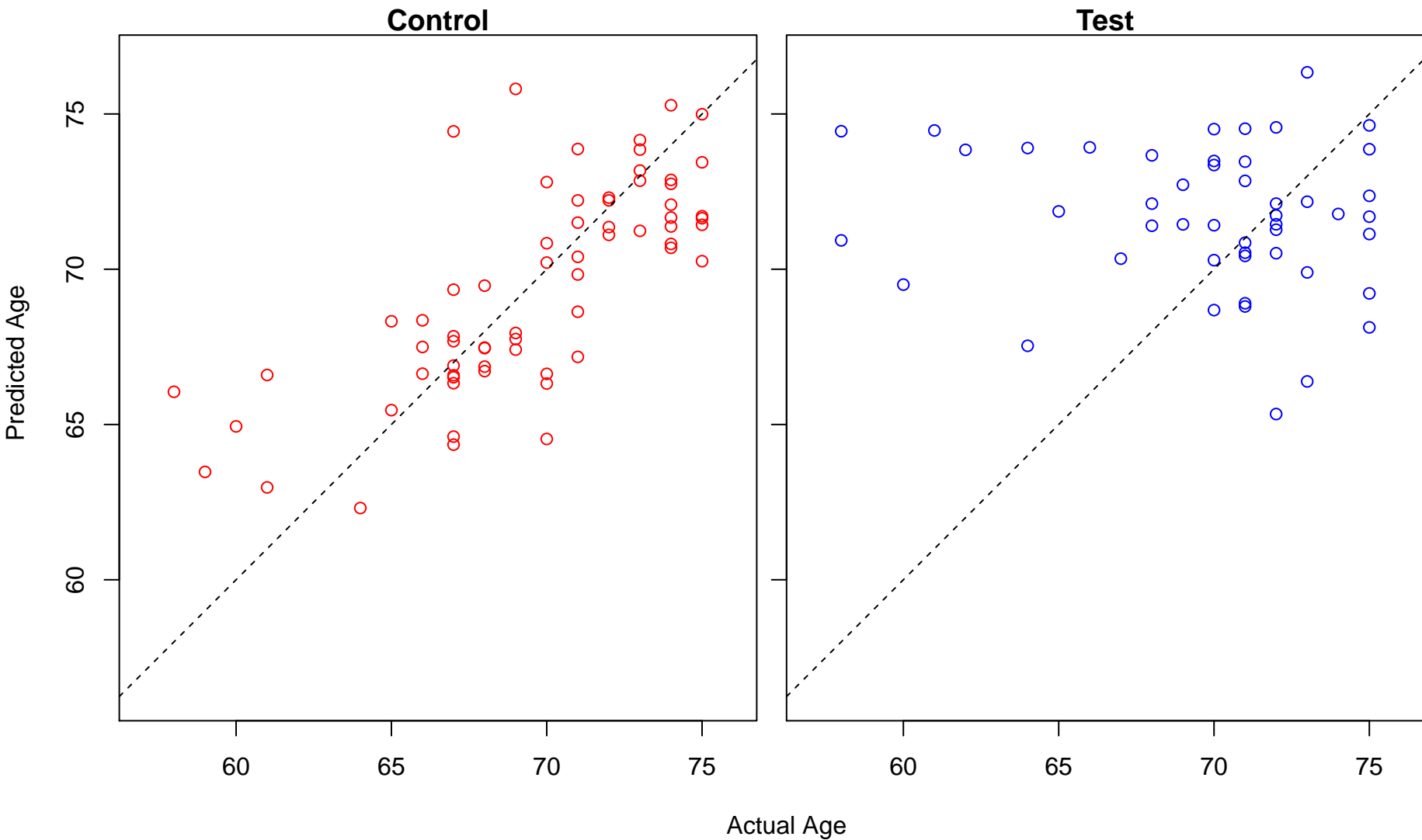


Actual Age

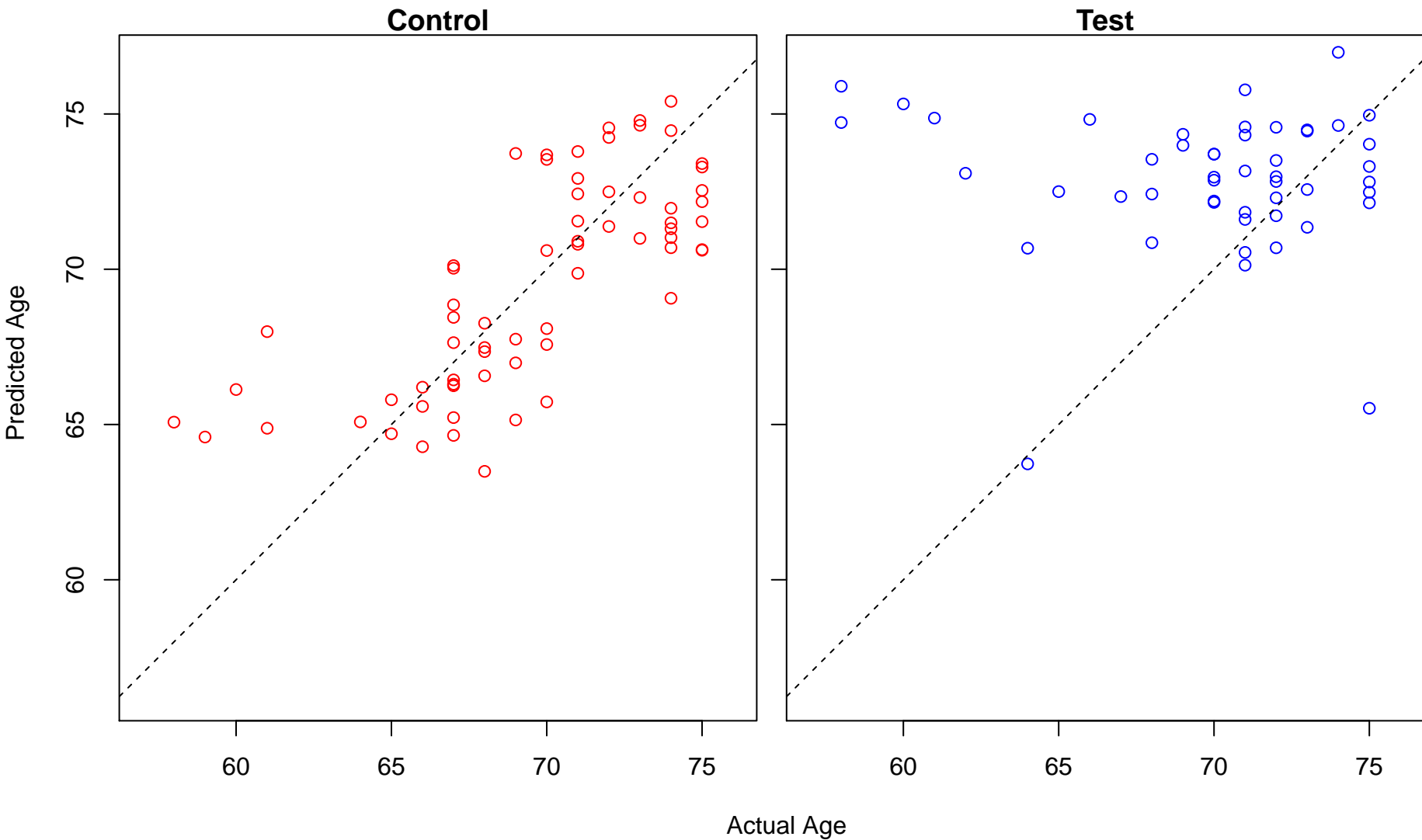
cellular metal ion homeostasis (Score: 1.860070)



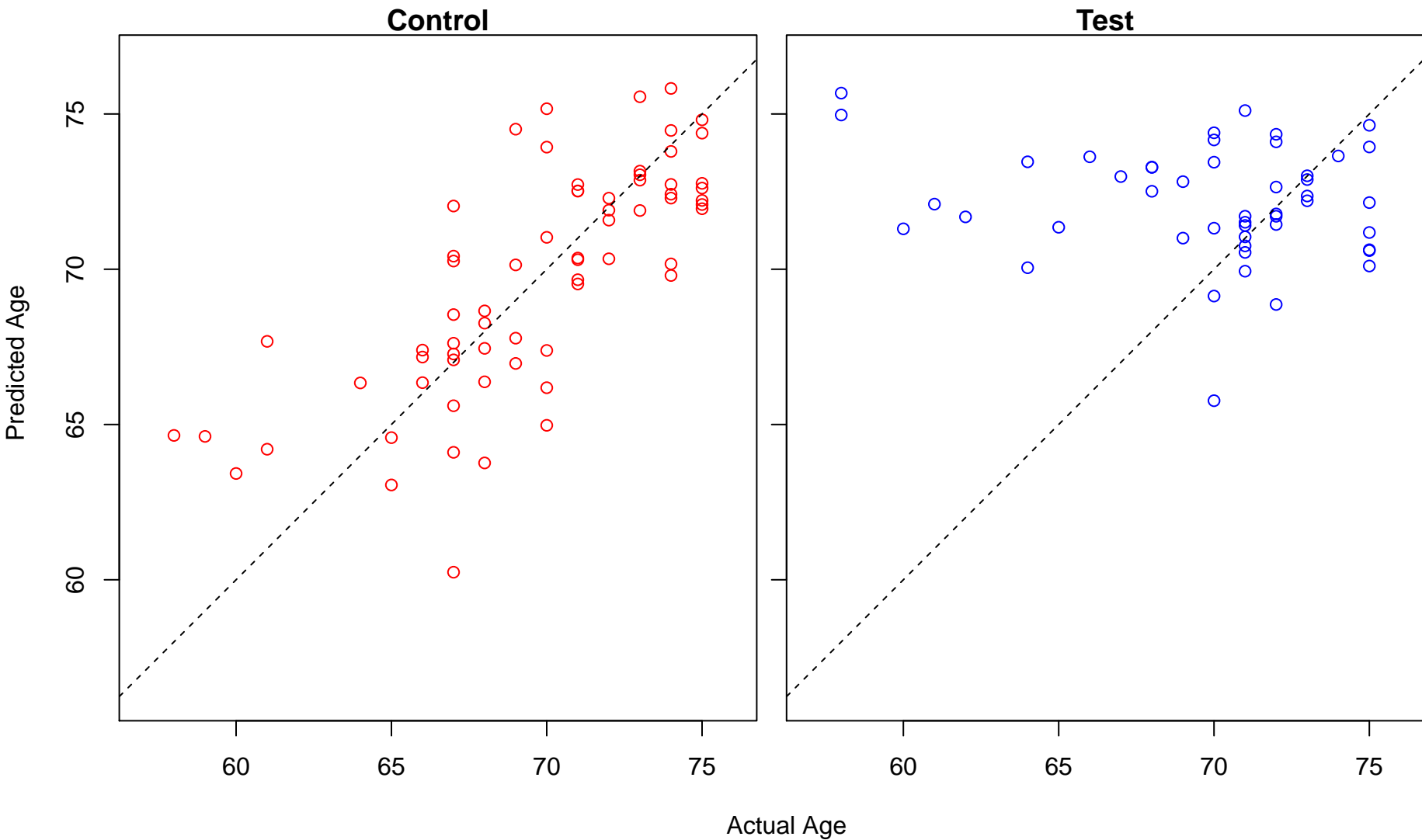
response to type I interferon (Score: 1.859596)



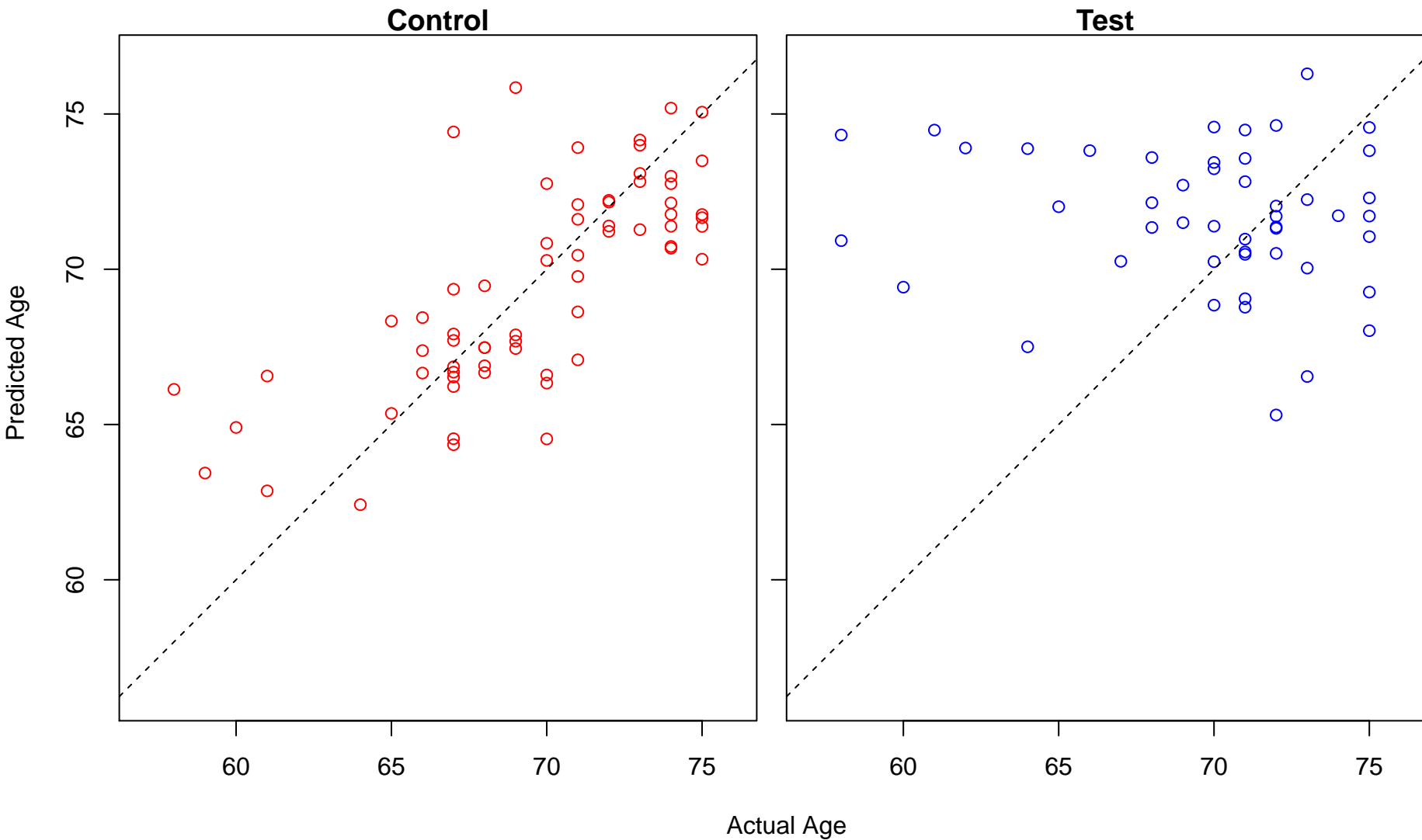
positive regulation of growth (Score: 1.859013)



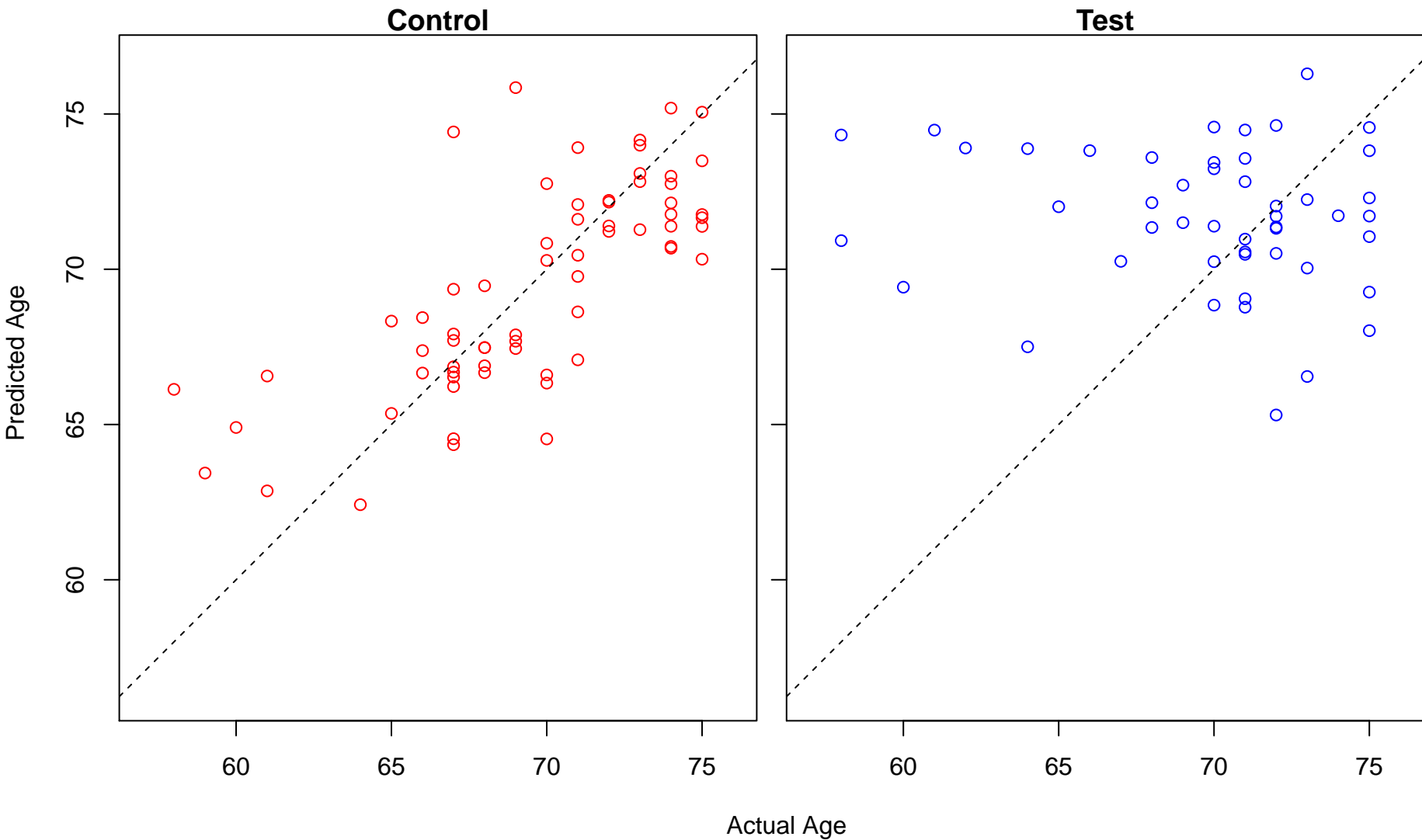
cellular divalent inorganic cation homeostasis (Score: 1.858815)



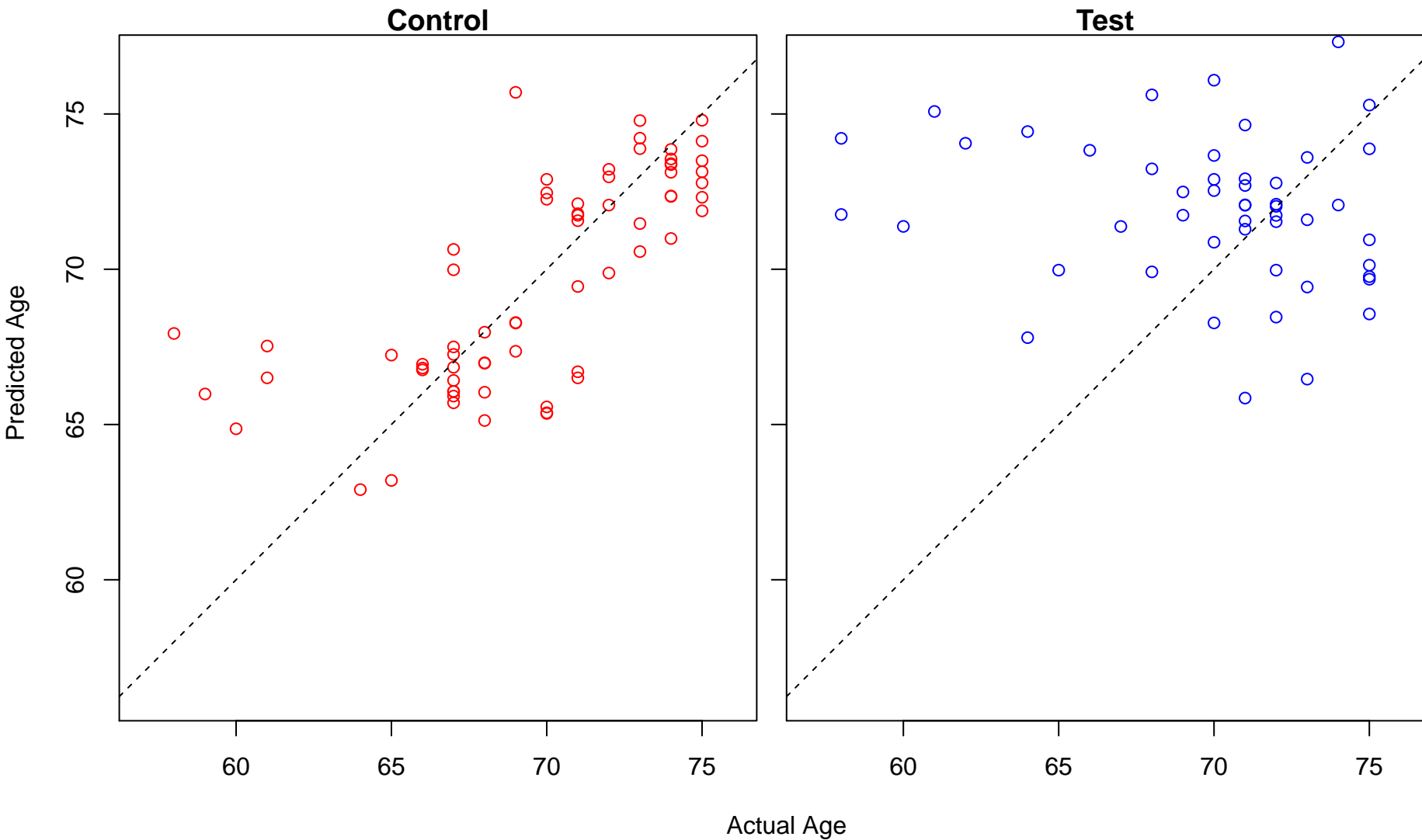
type I interferon signaling pathway (Score: 1.858717)



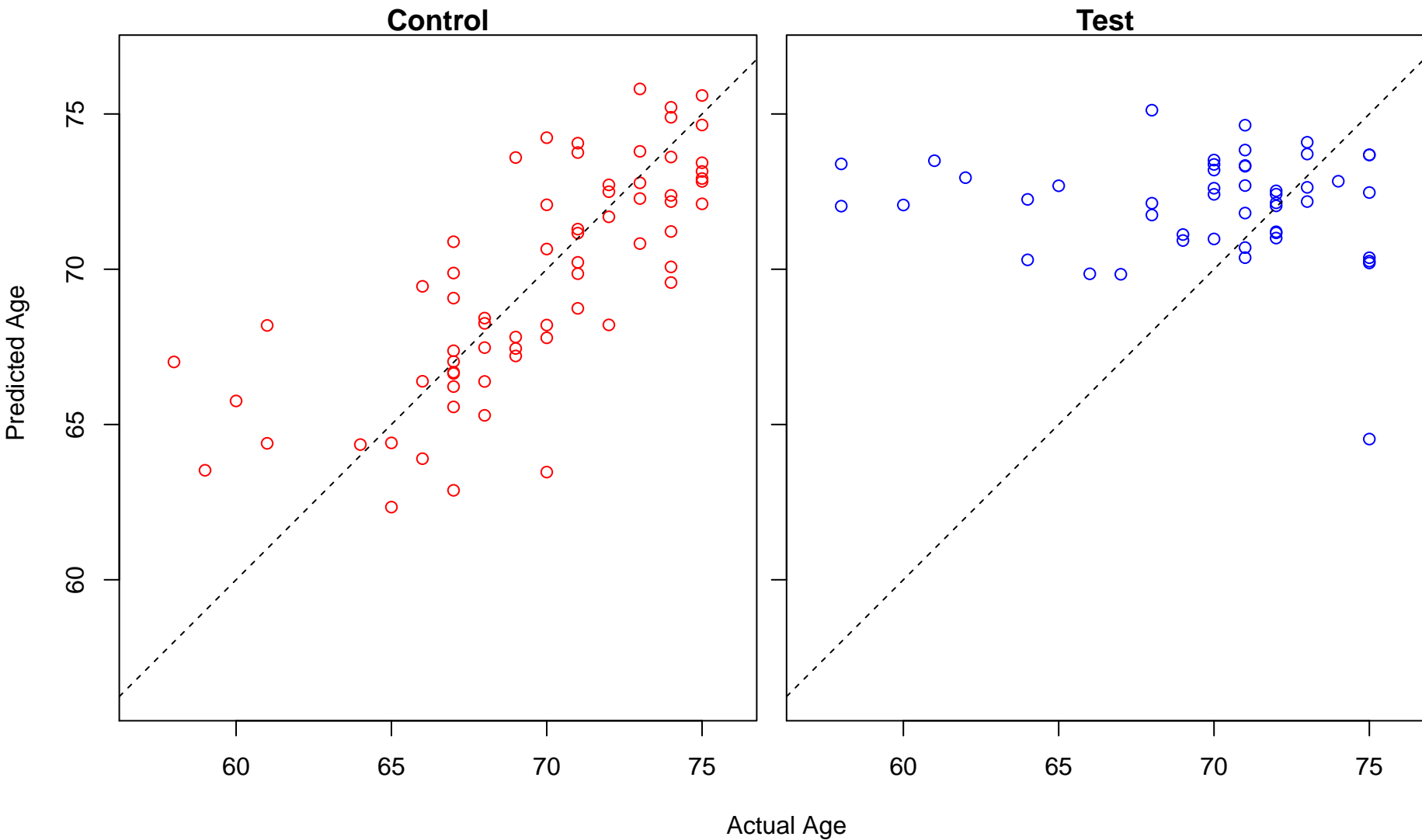
cellular response to type I interferon (Score: 1.858717)



defense response to other organism (Score: 1.858532)

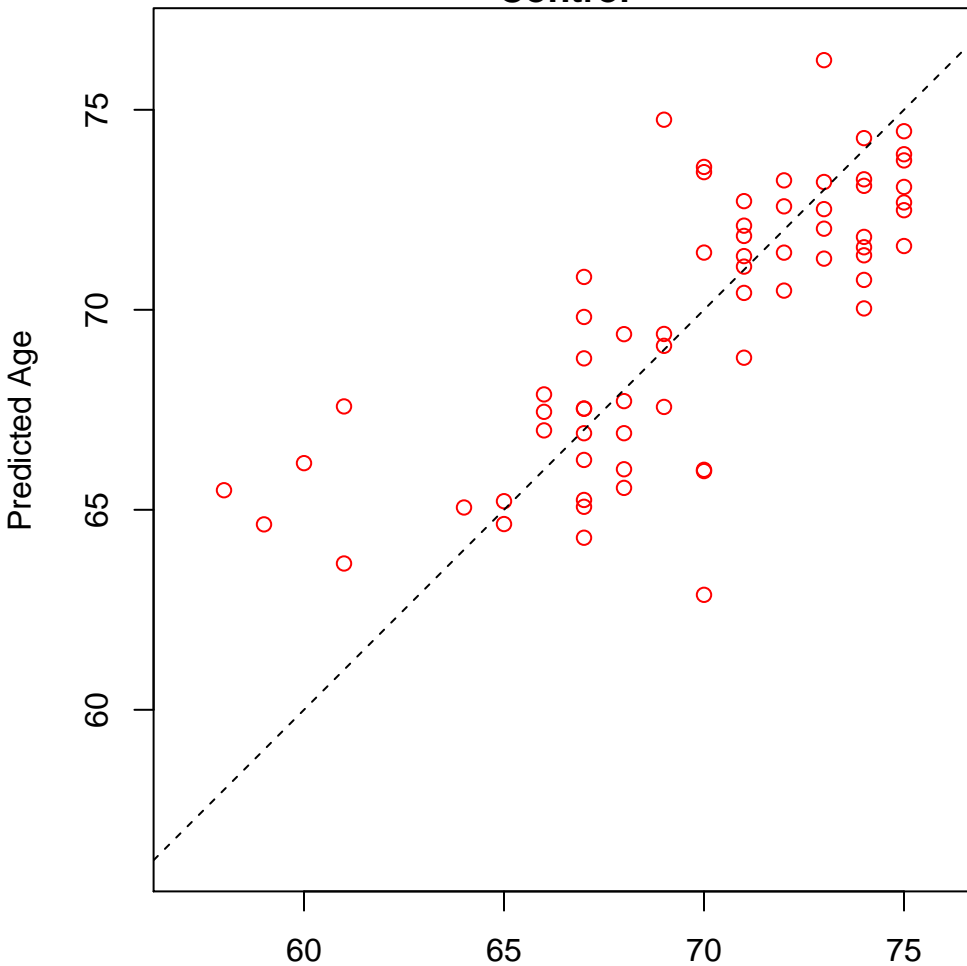


fibroblast growth factor receptor signaling pathway (Score: 1.857686)

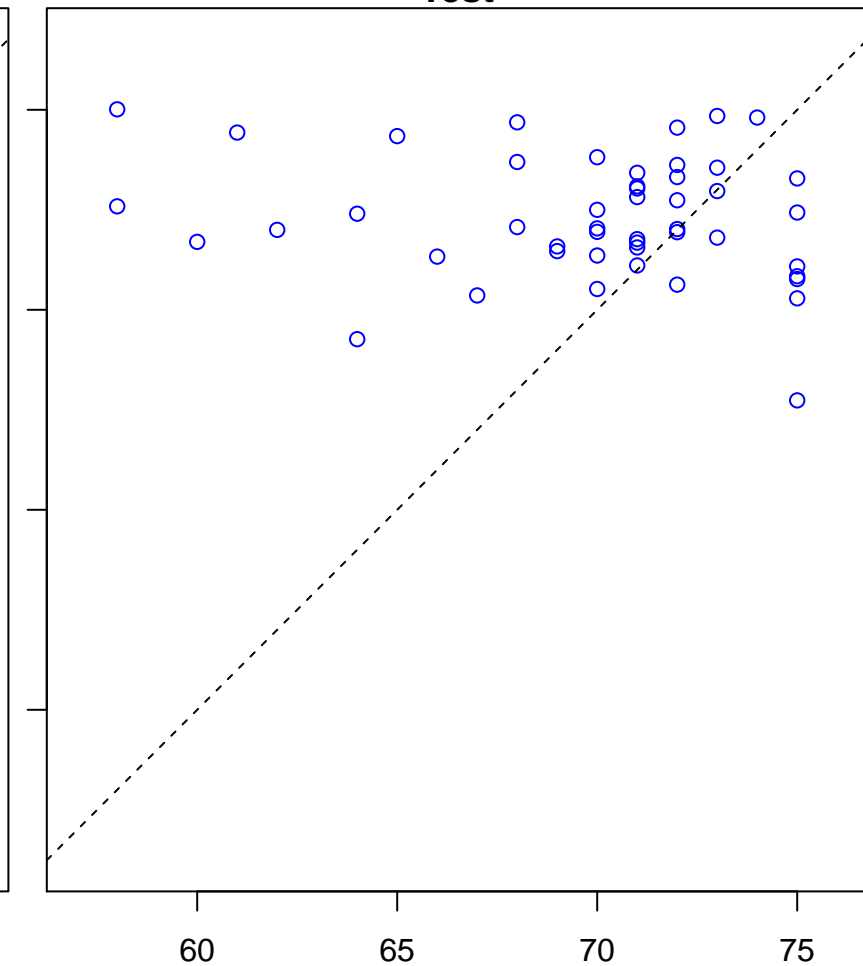


regulation of DNA metabolic process (Score: 1.857597)

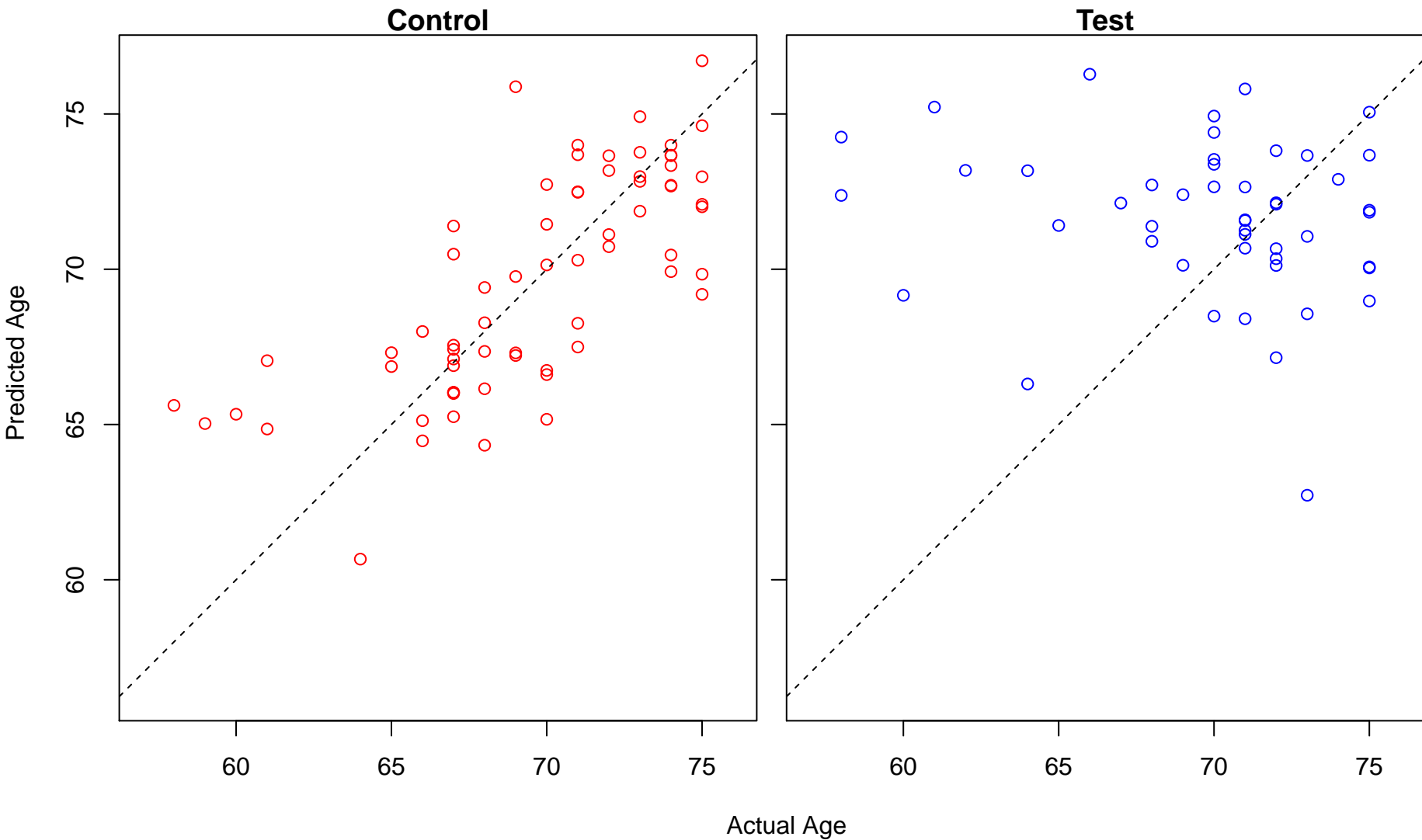
Control



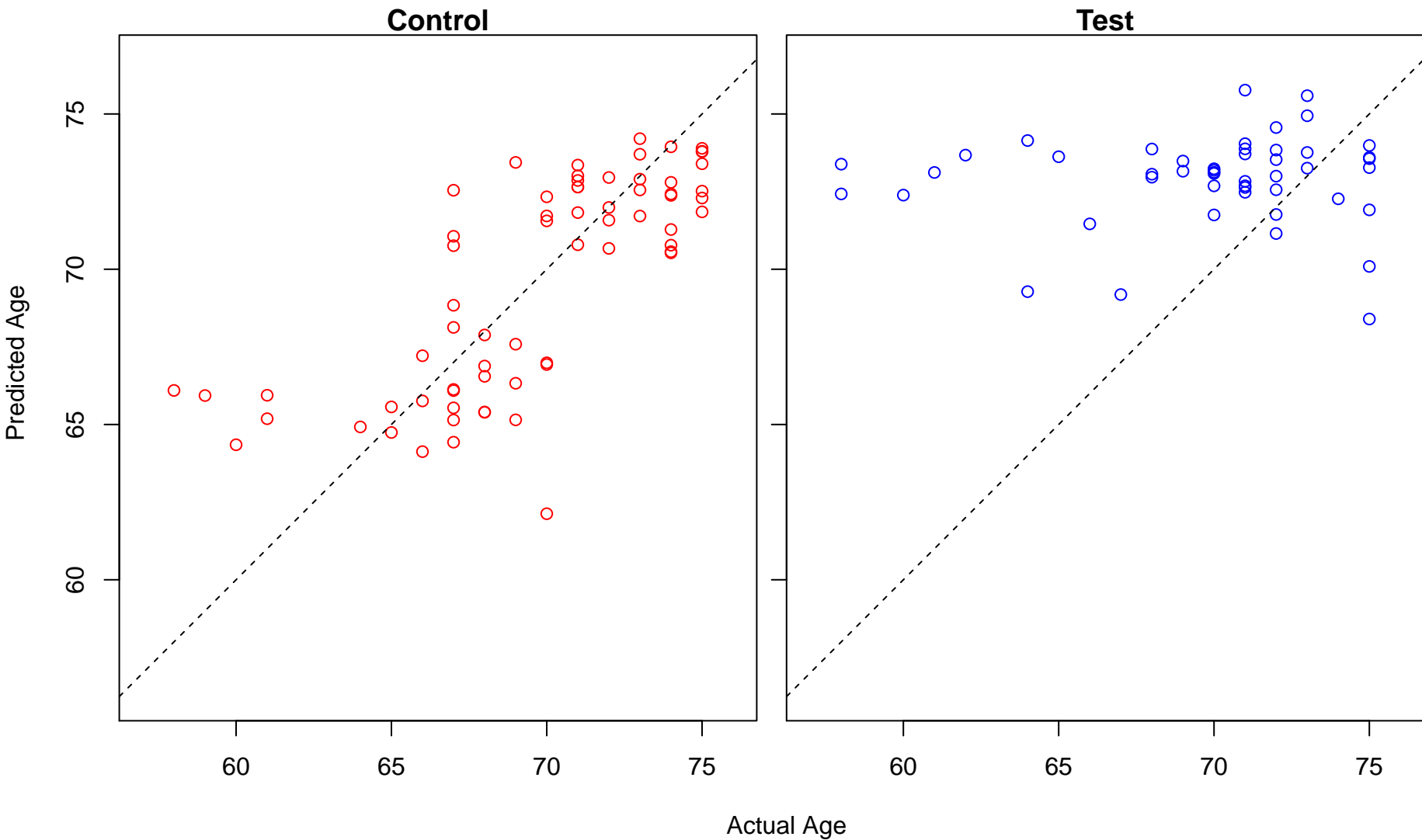
Test



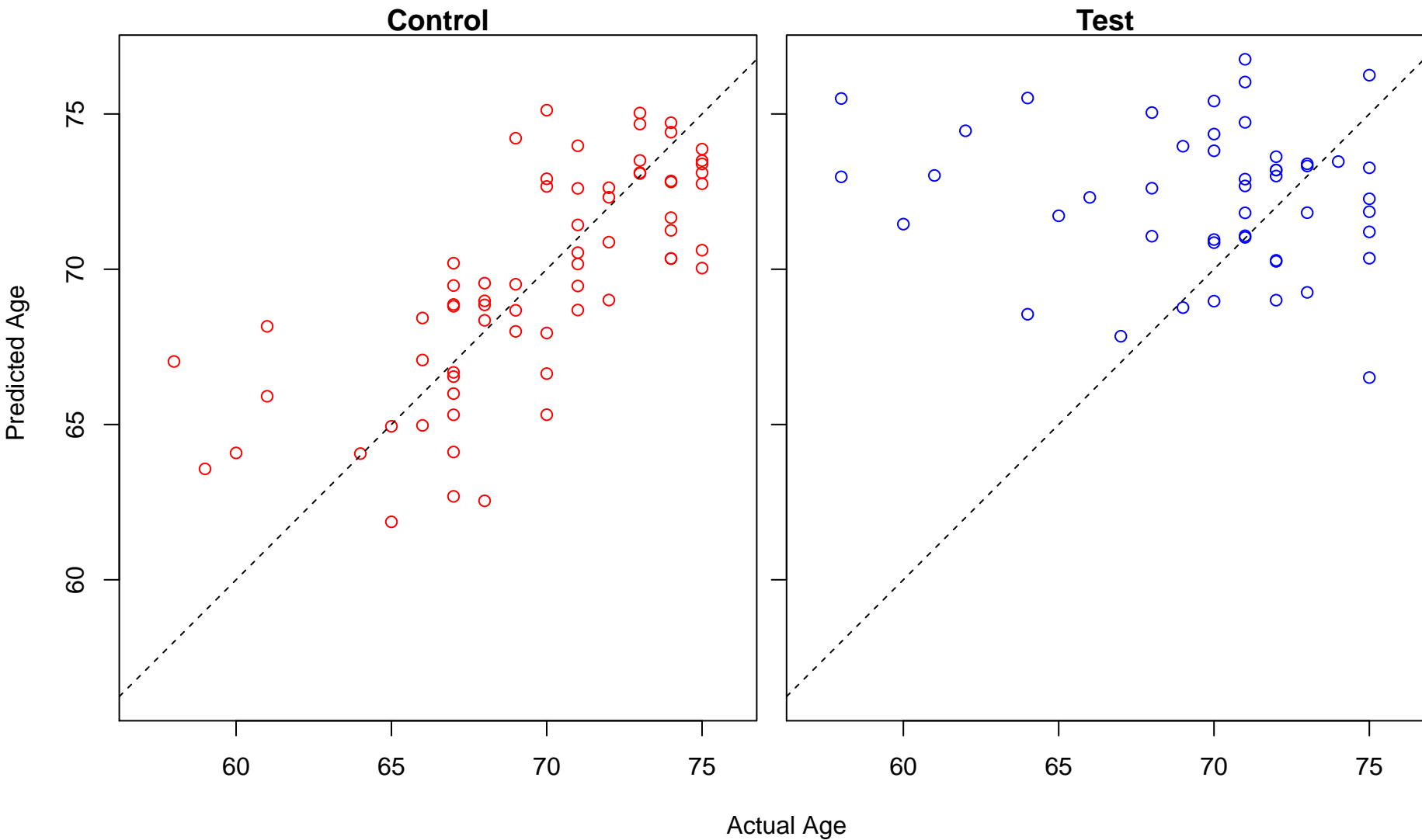
negative regulation of multi-organism process (Score: 1.857042)



cellular respiration (Score: 1.854455)

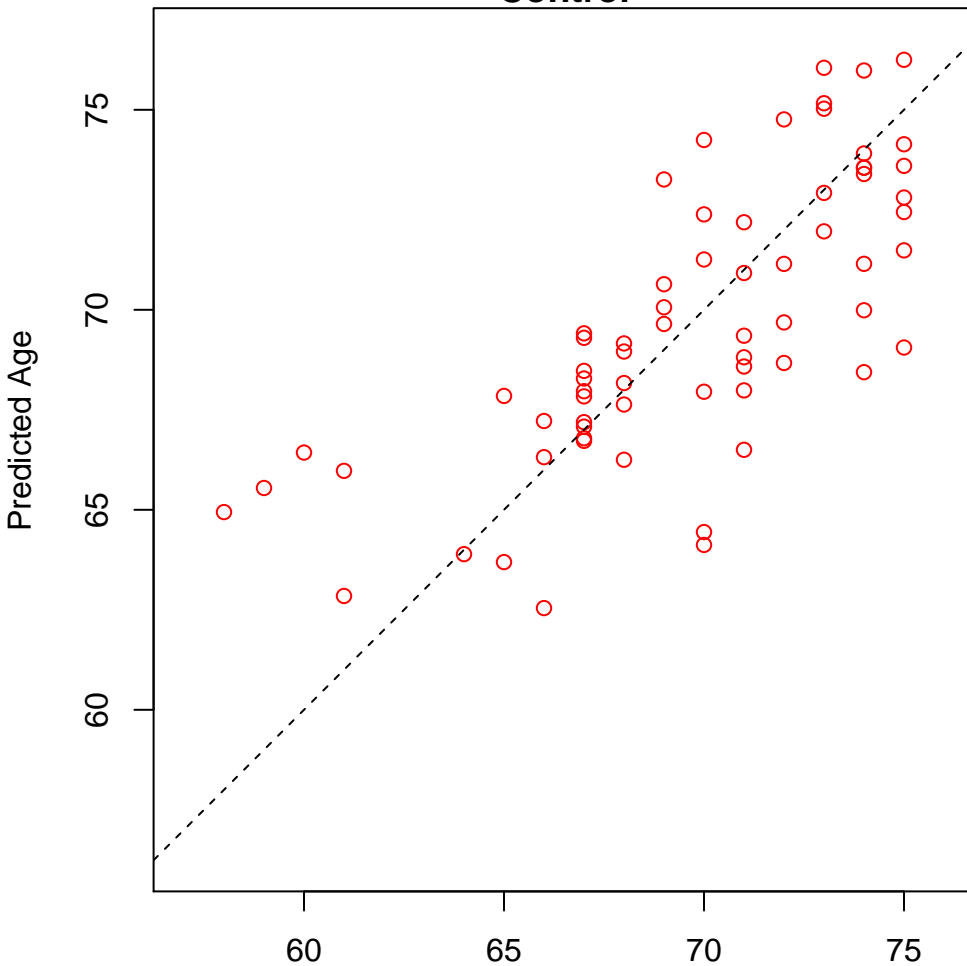


response to lipid (Score: 1.853297)

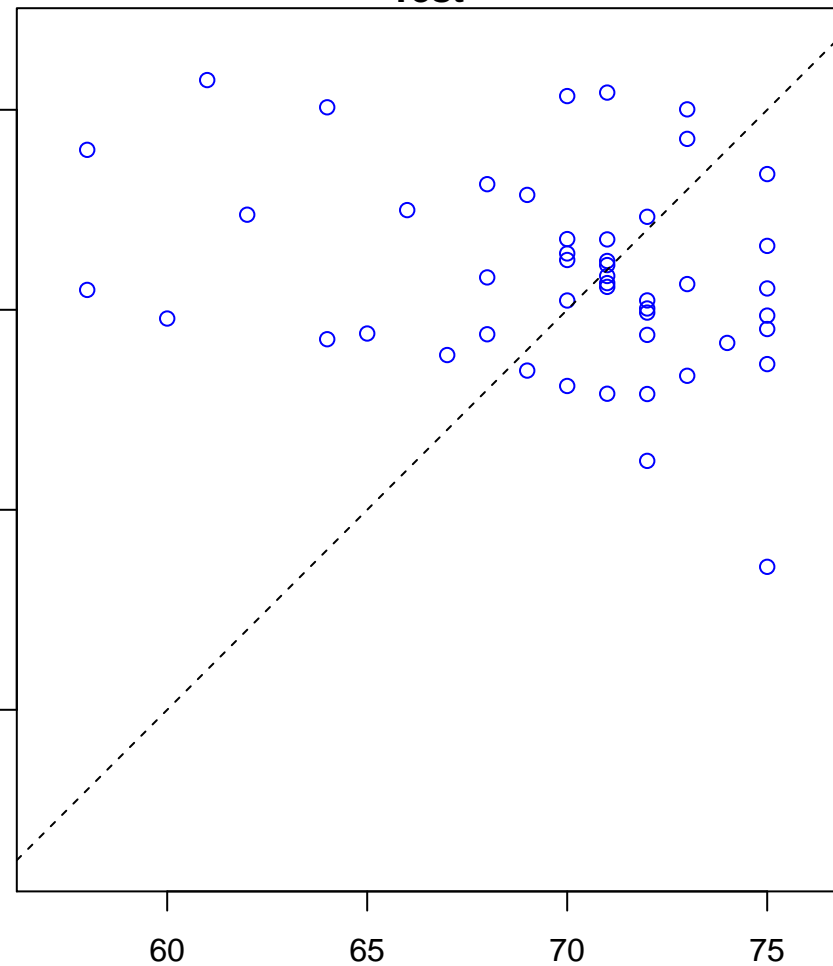


regulation of T cell apoptotic process (Score: 1.852527)

Control

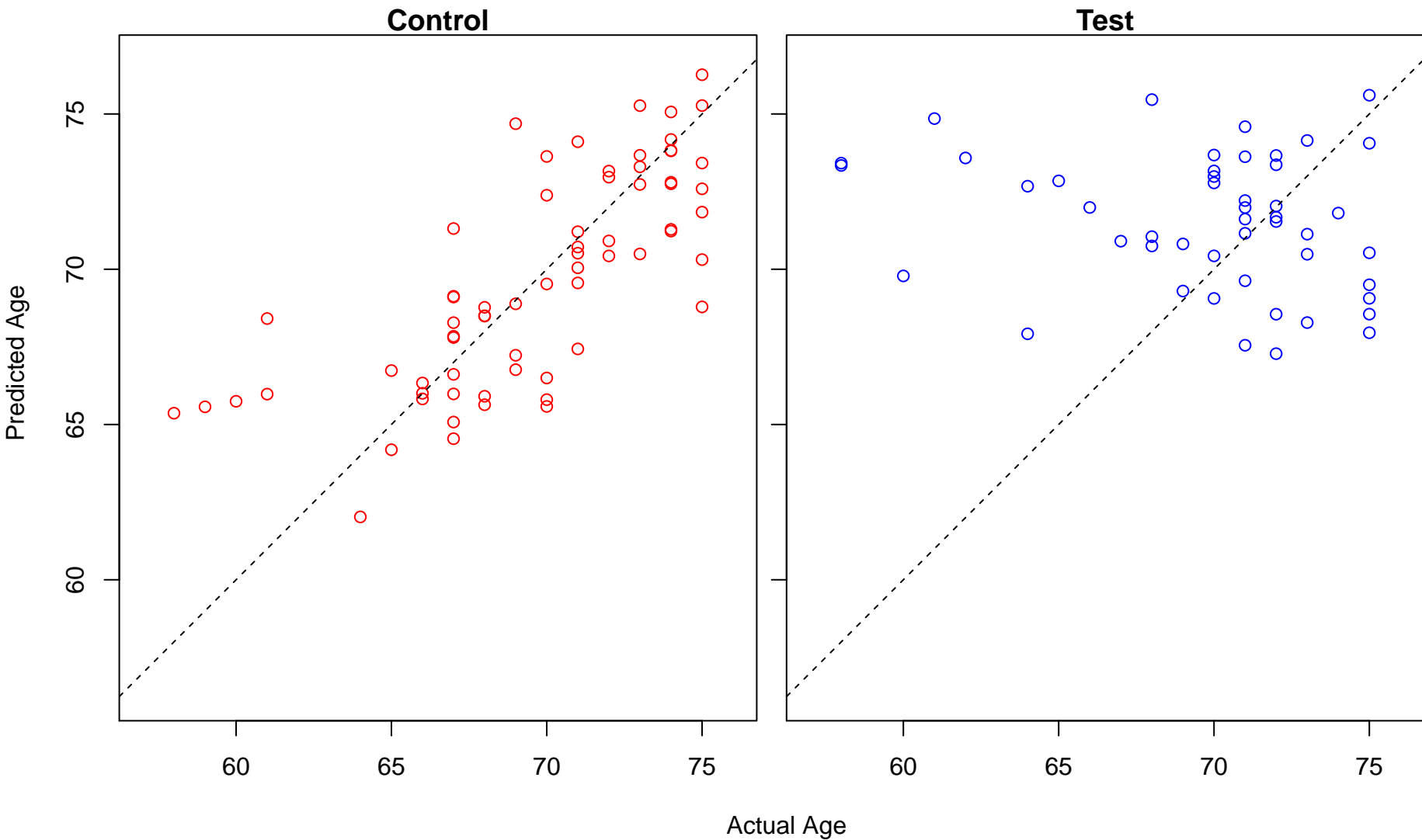


Test

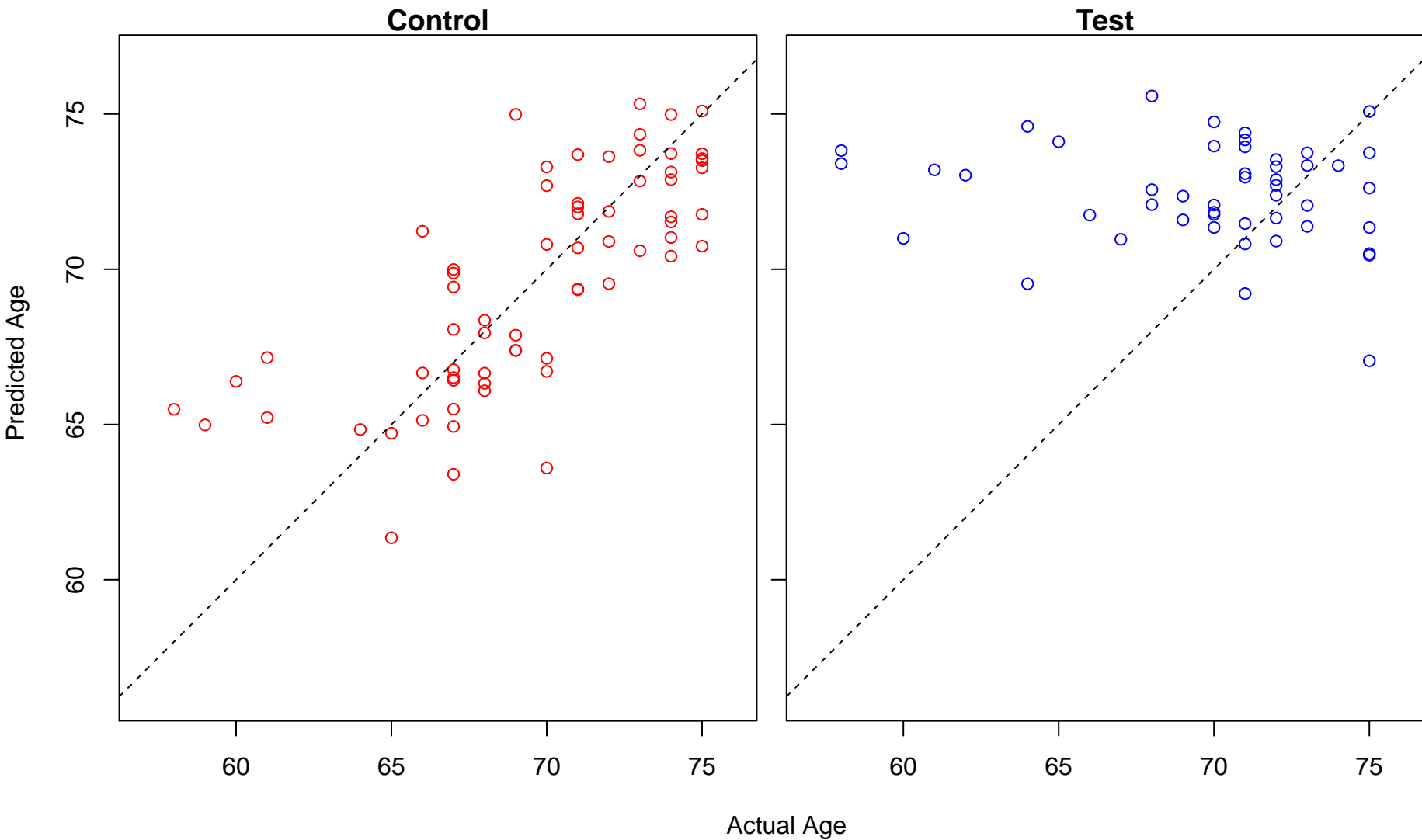


Actual Age

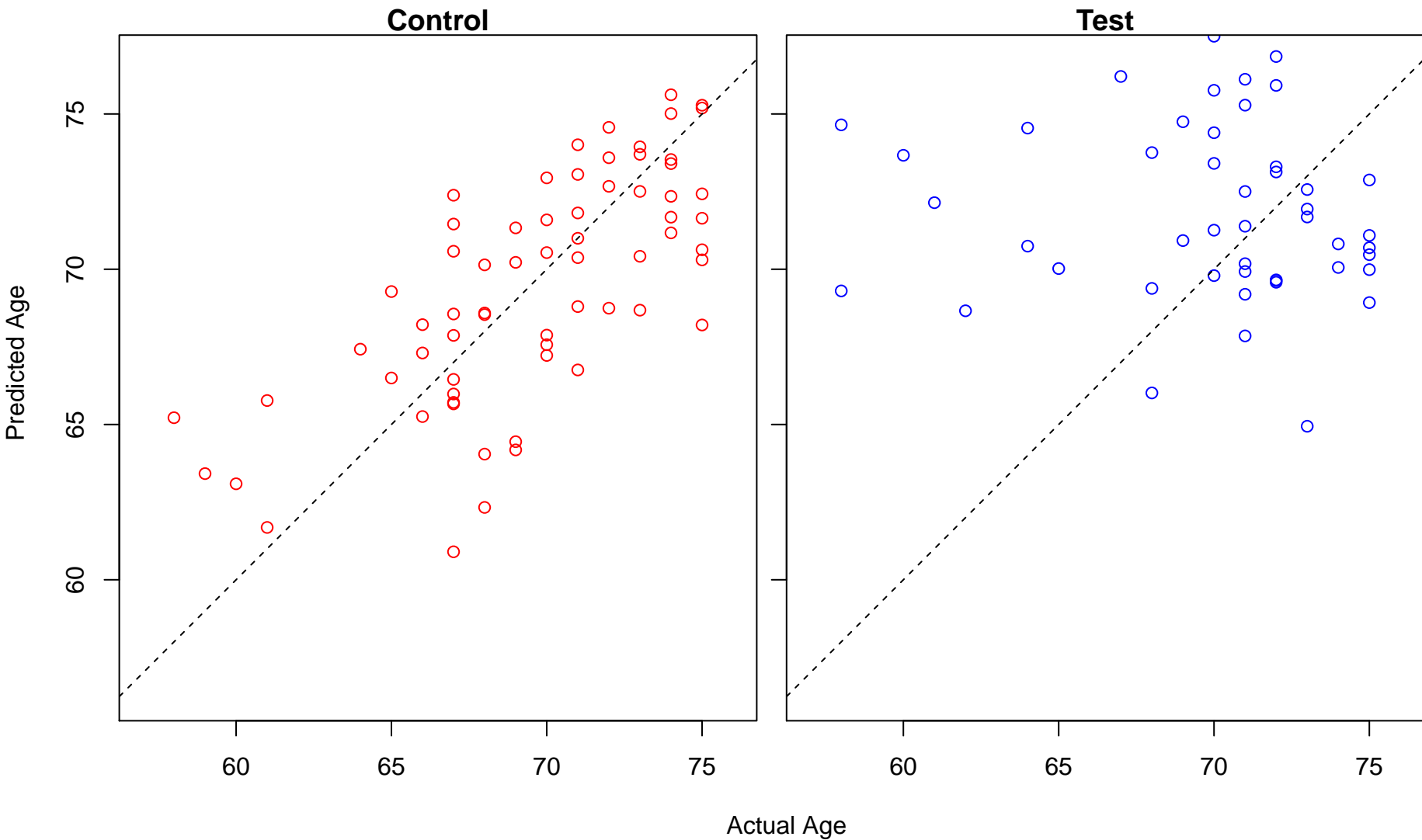
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 1.85)



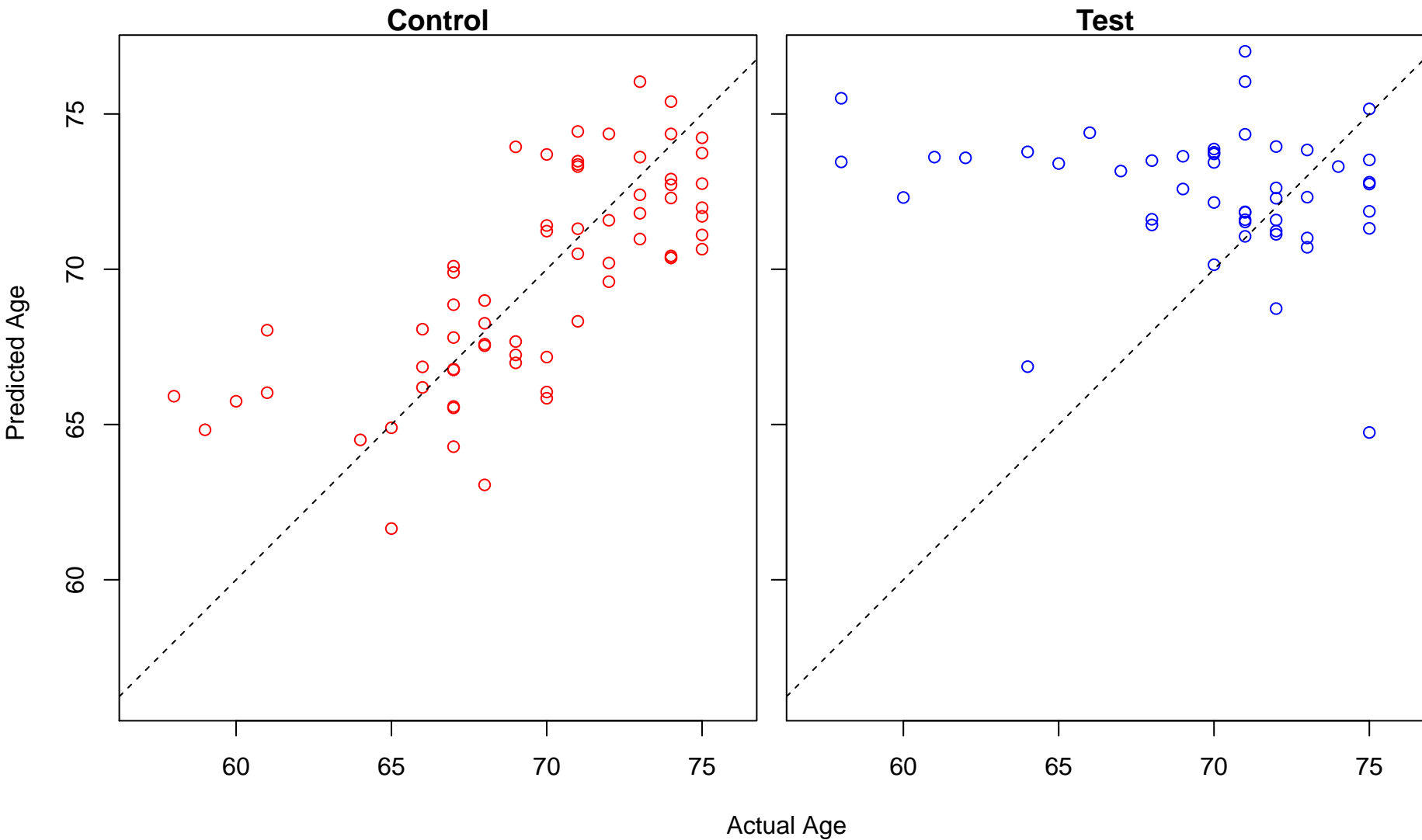
positive regulation of MAPK cascade (Score: 1.849484)



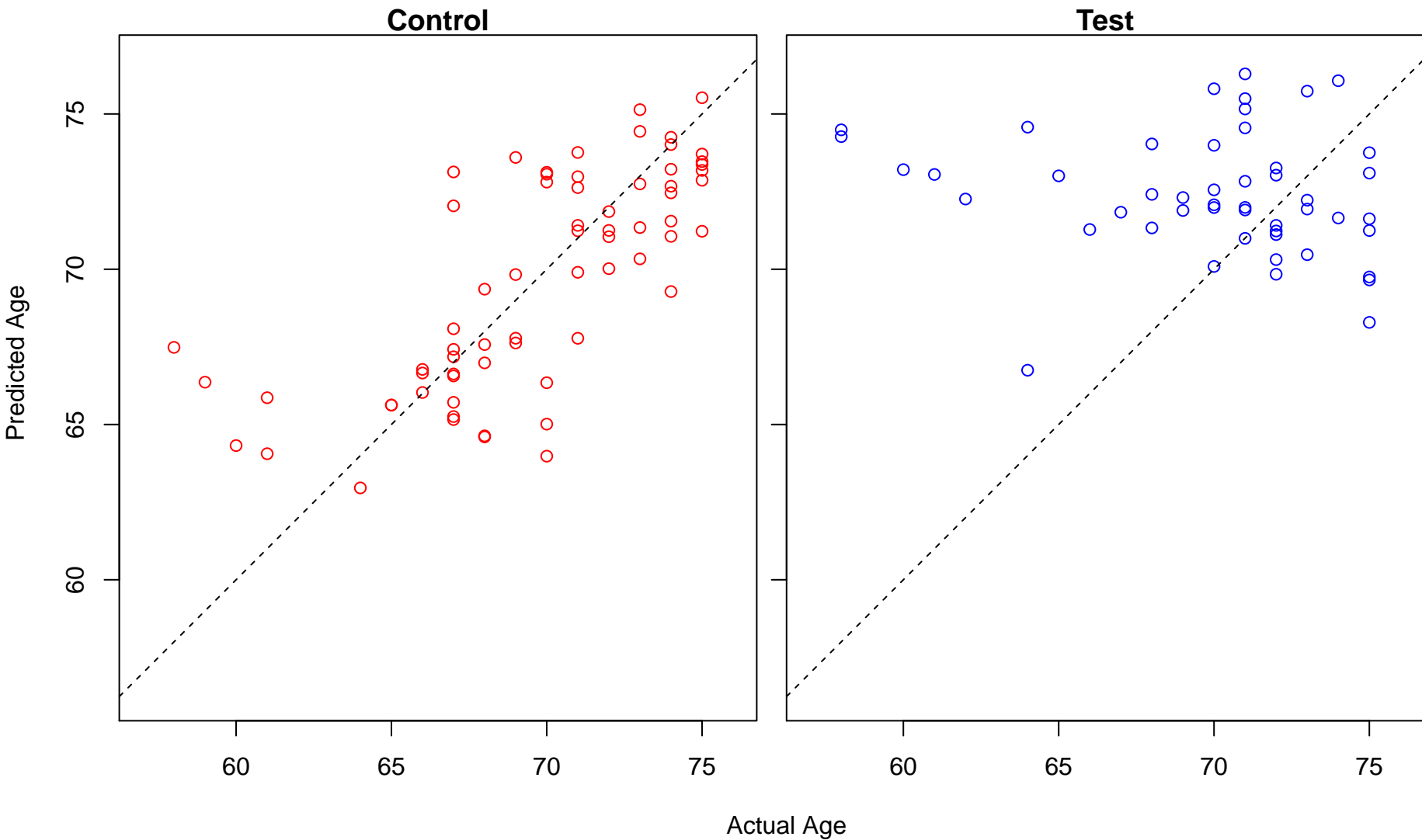
negative regulation of endothelial cell proliferation (Score: 1.849251)



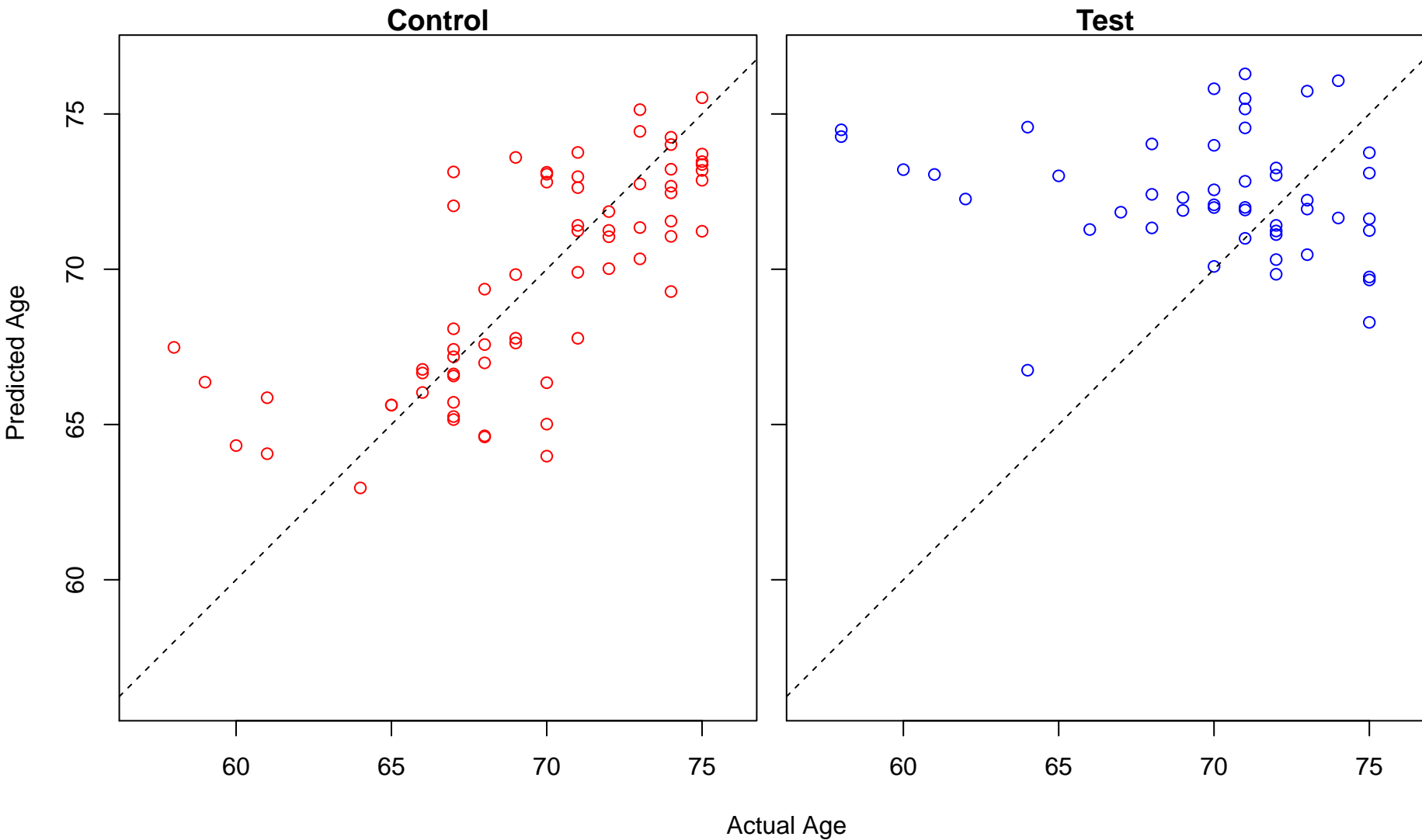
positive regulation of cellular component movement (Score: 1.848768)



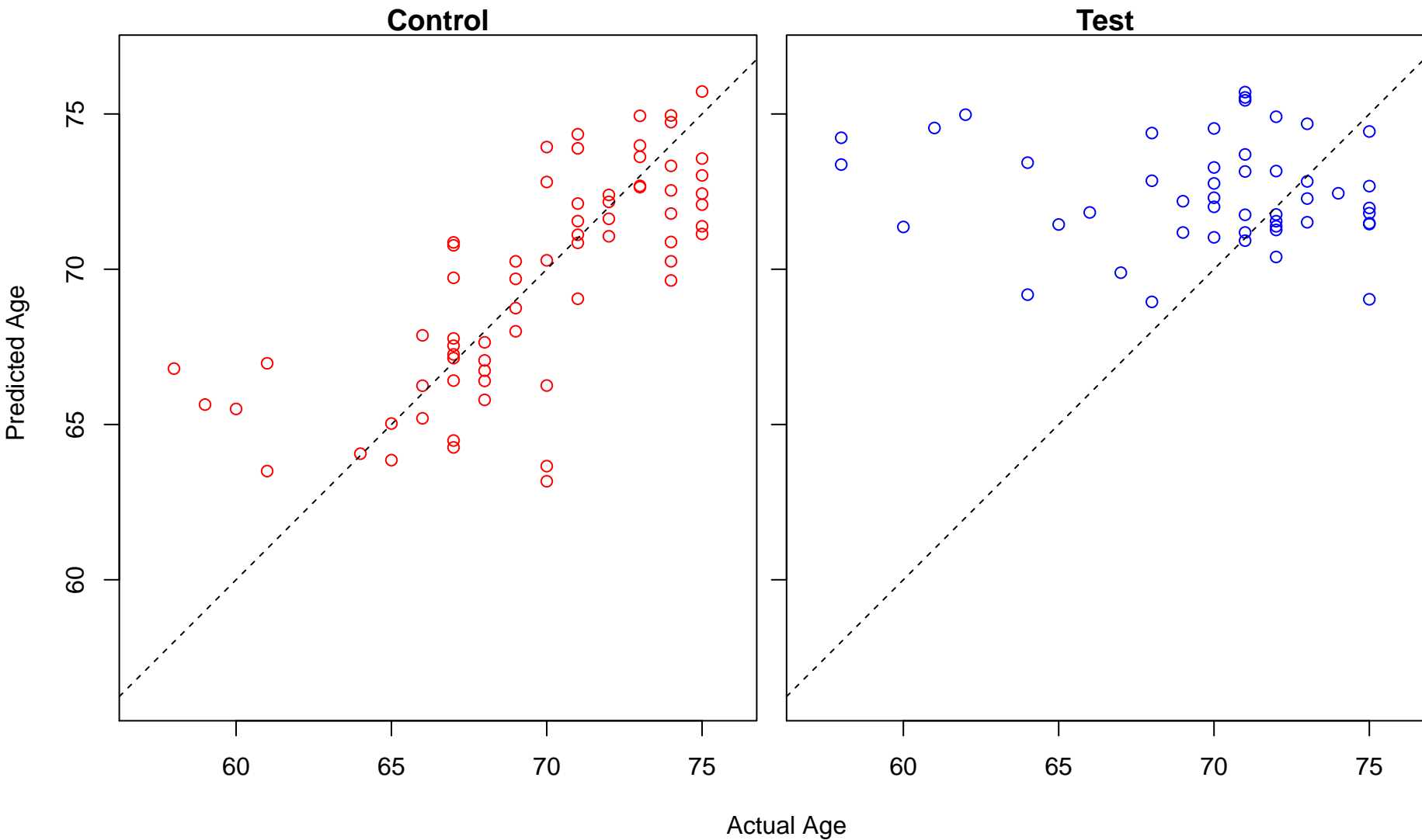
mitophagy (Score: 1.848381)



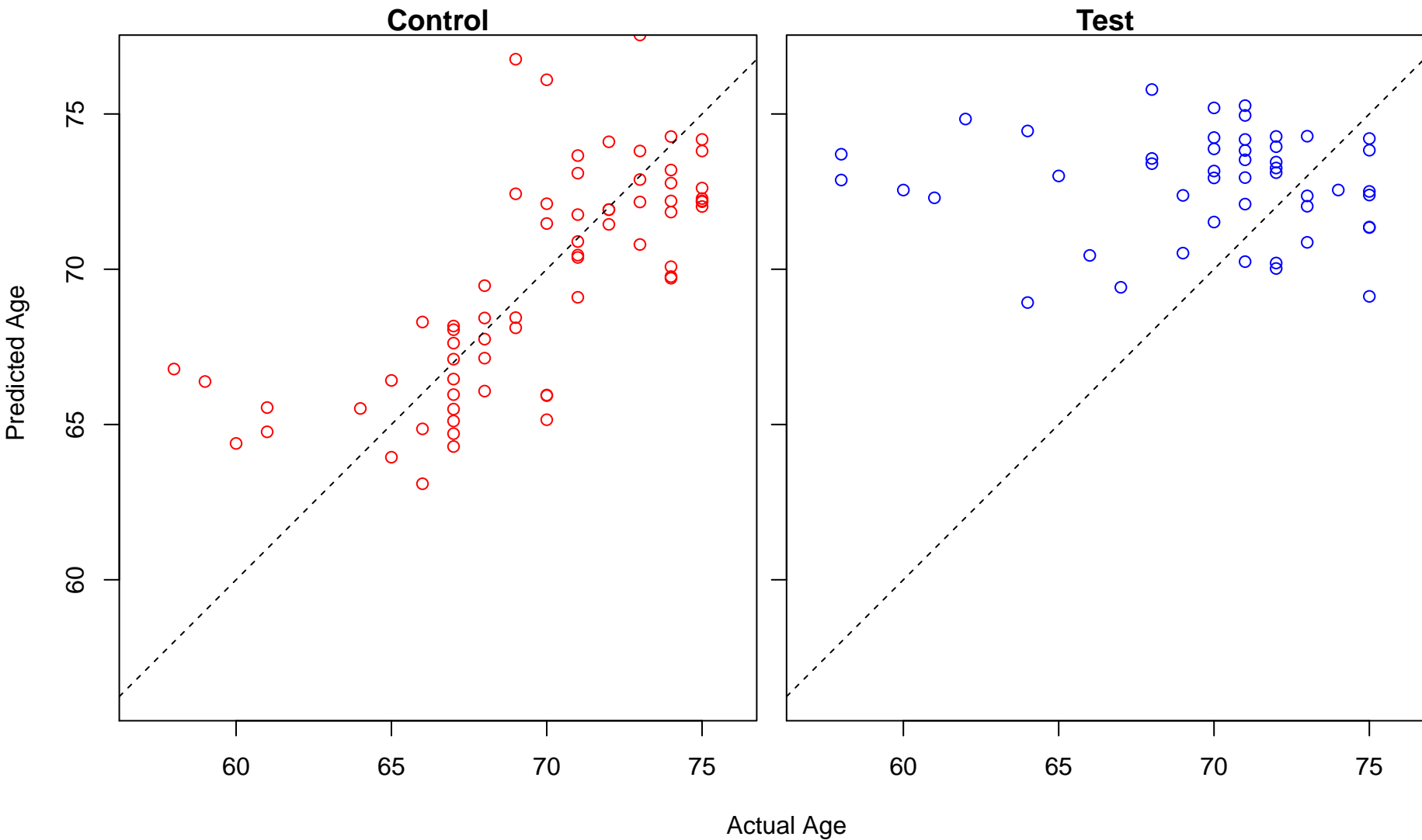
mitochondrion disassembly (Score: 1.848381)



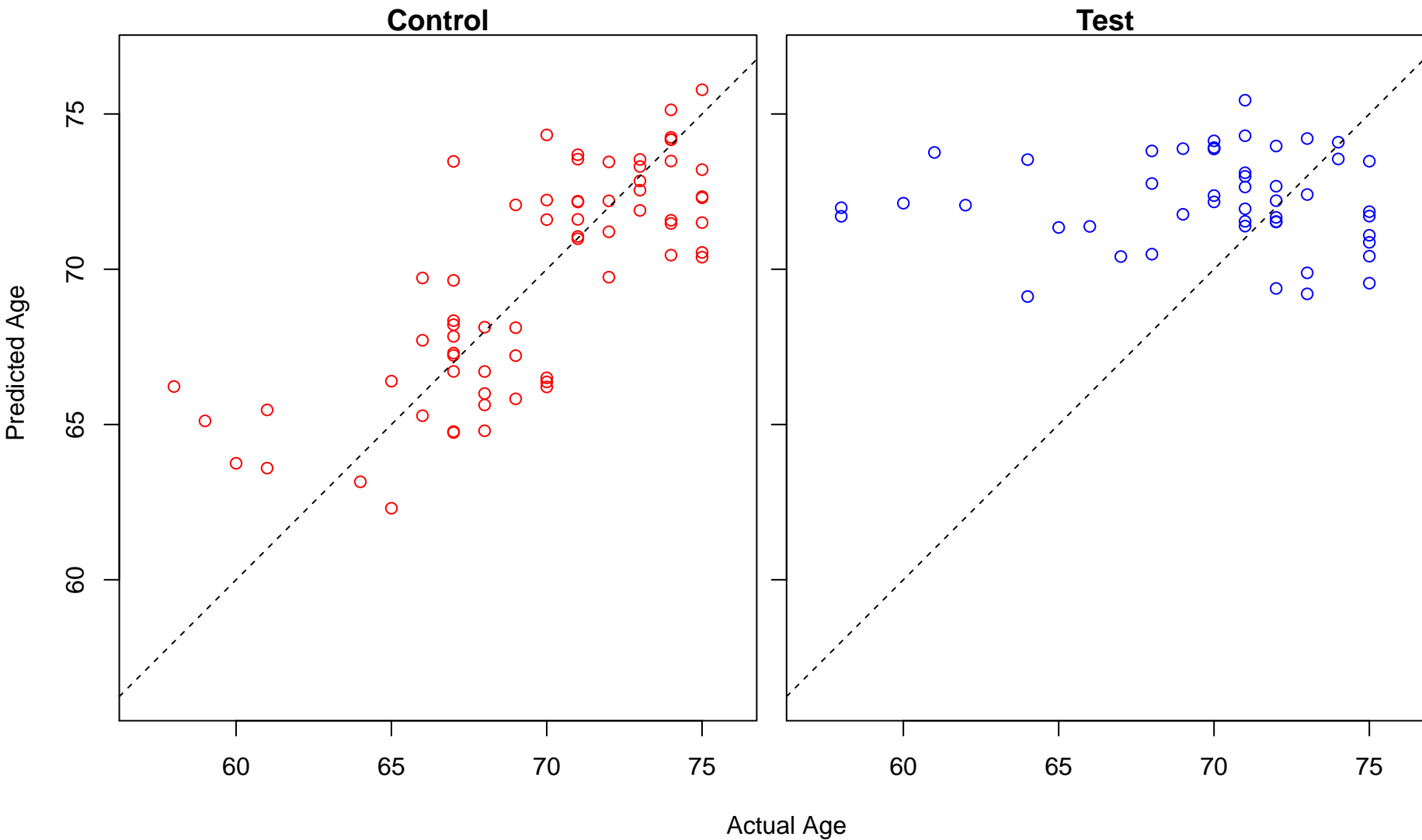
organelle assembly (Score: 1.847182)



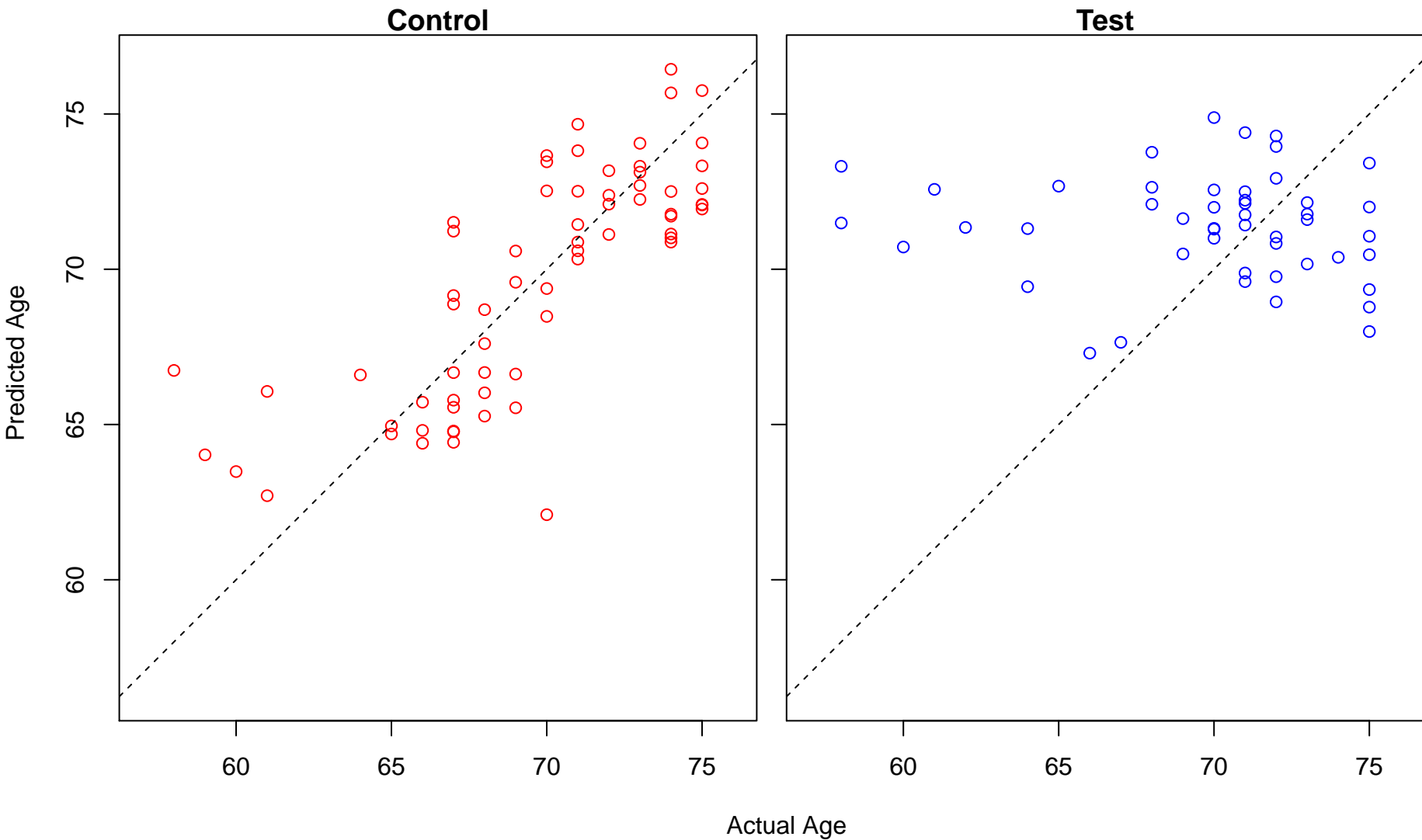
cell redox homeostasis (Score: 1.846204)



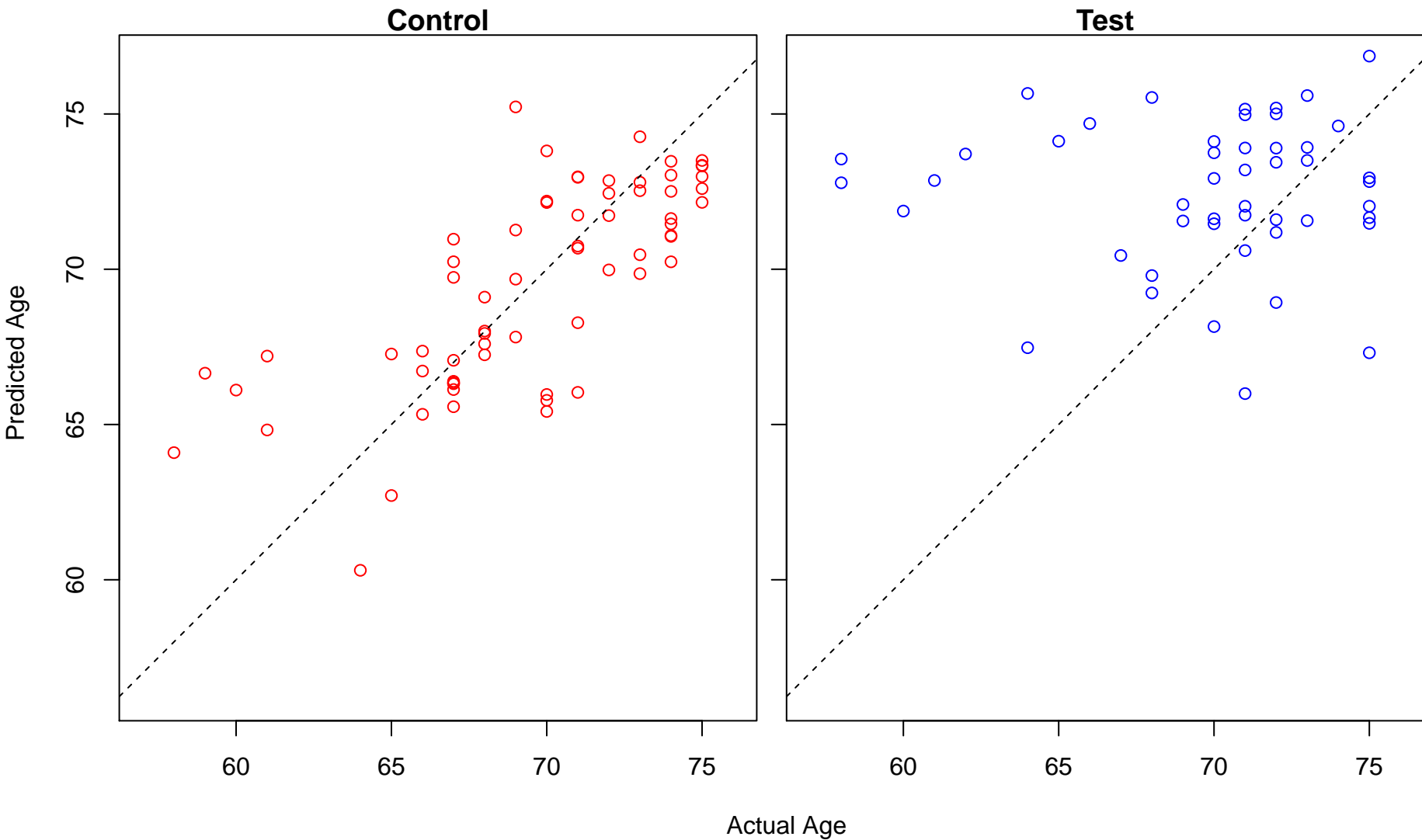
regulation of centrosome cycle (Score: 1.846116)



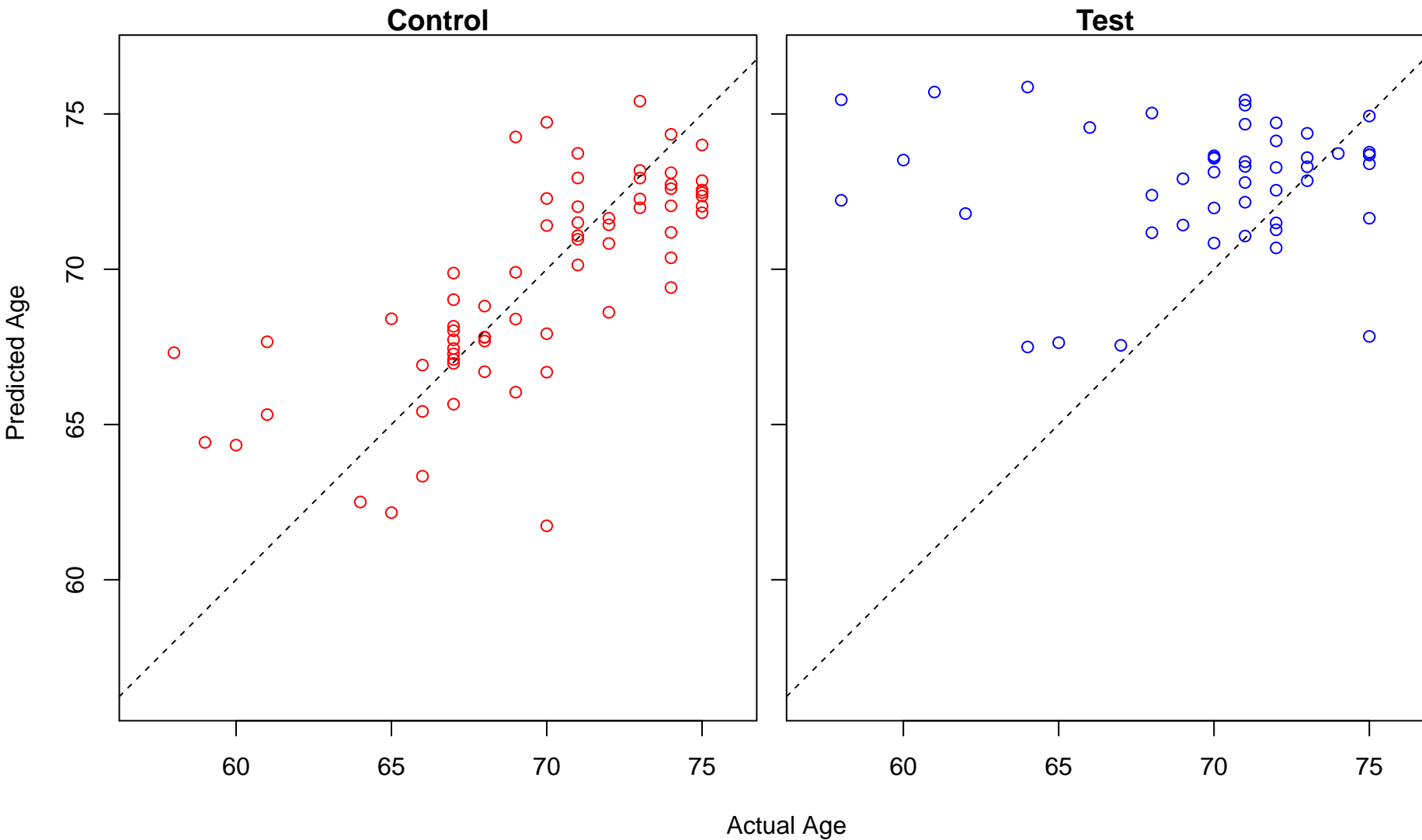
nucleoside triphosphate metabolic process (Score: 1.846017)



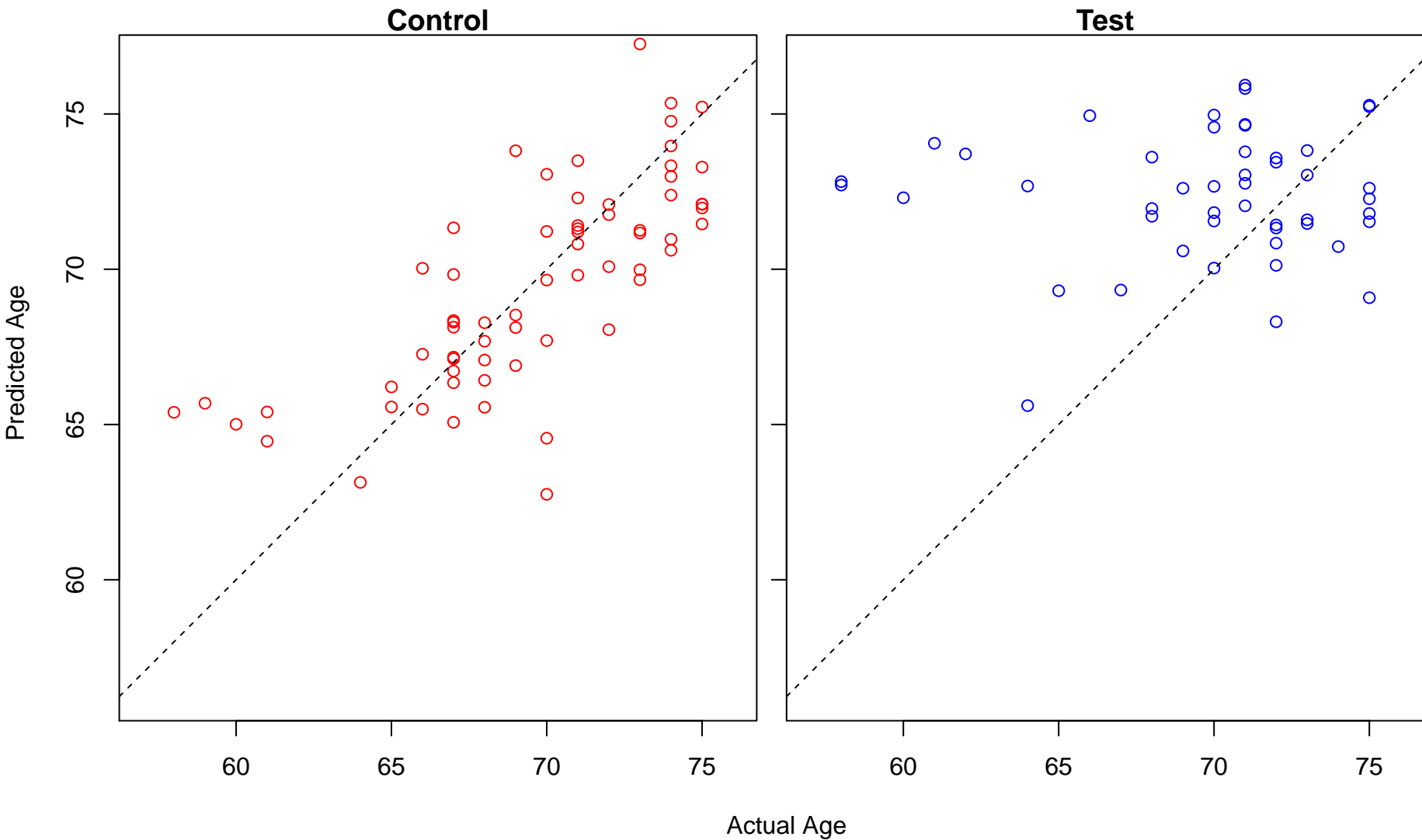
toll-like receptor 9 signaling pathway (Score: 1.846009)



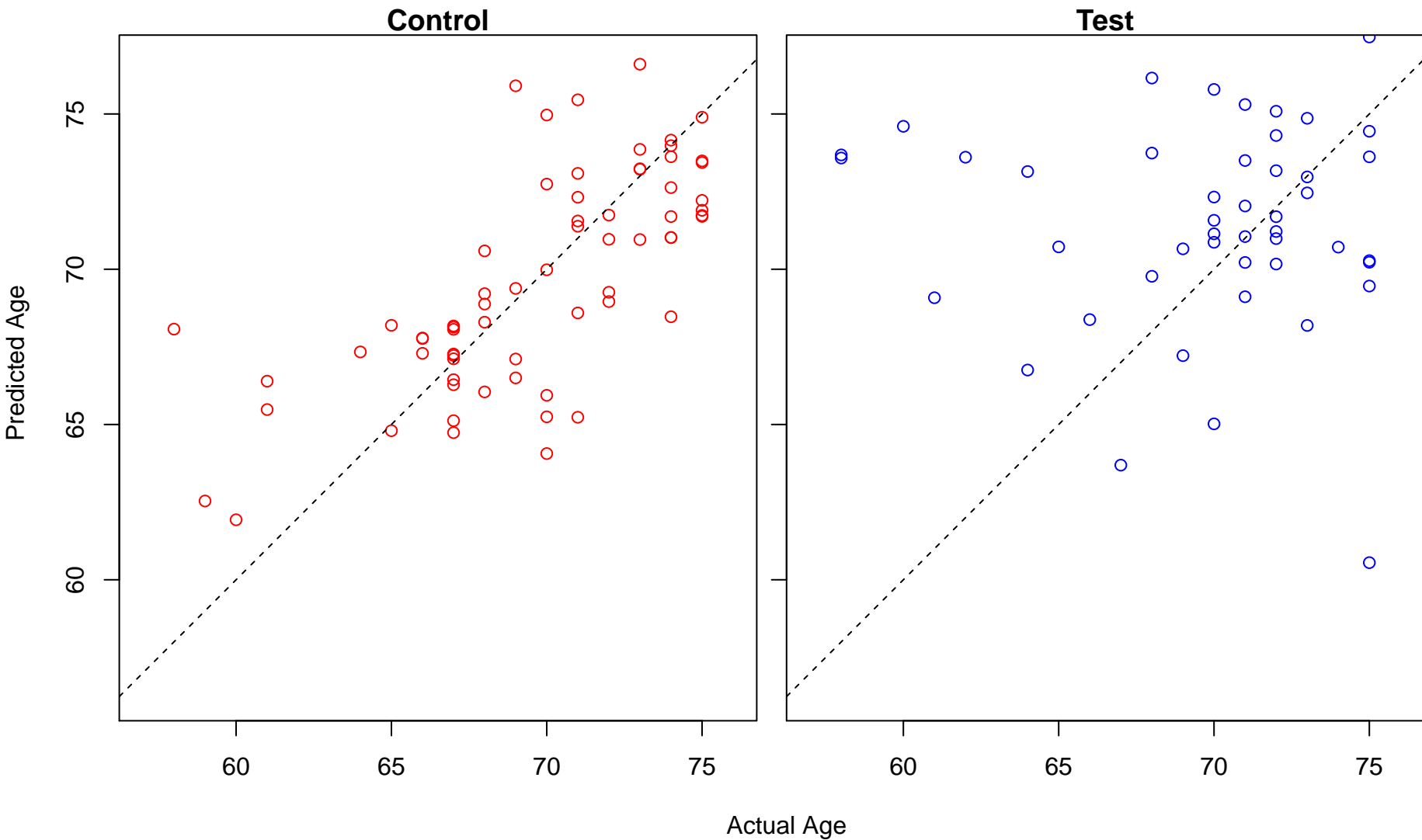
organ morphogenesis (Score: 1.845245)



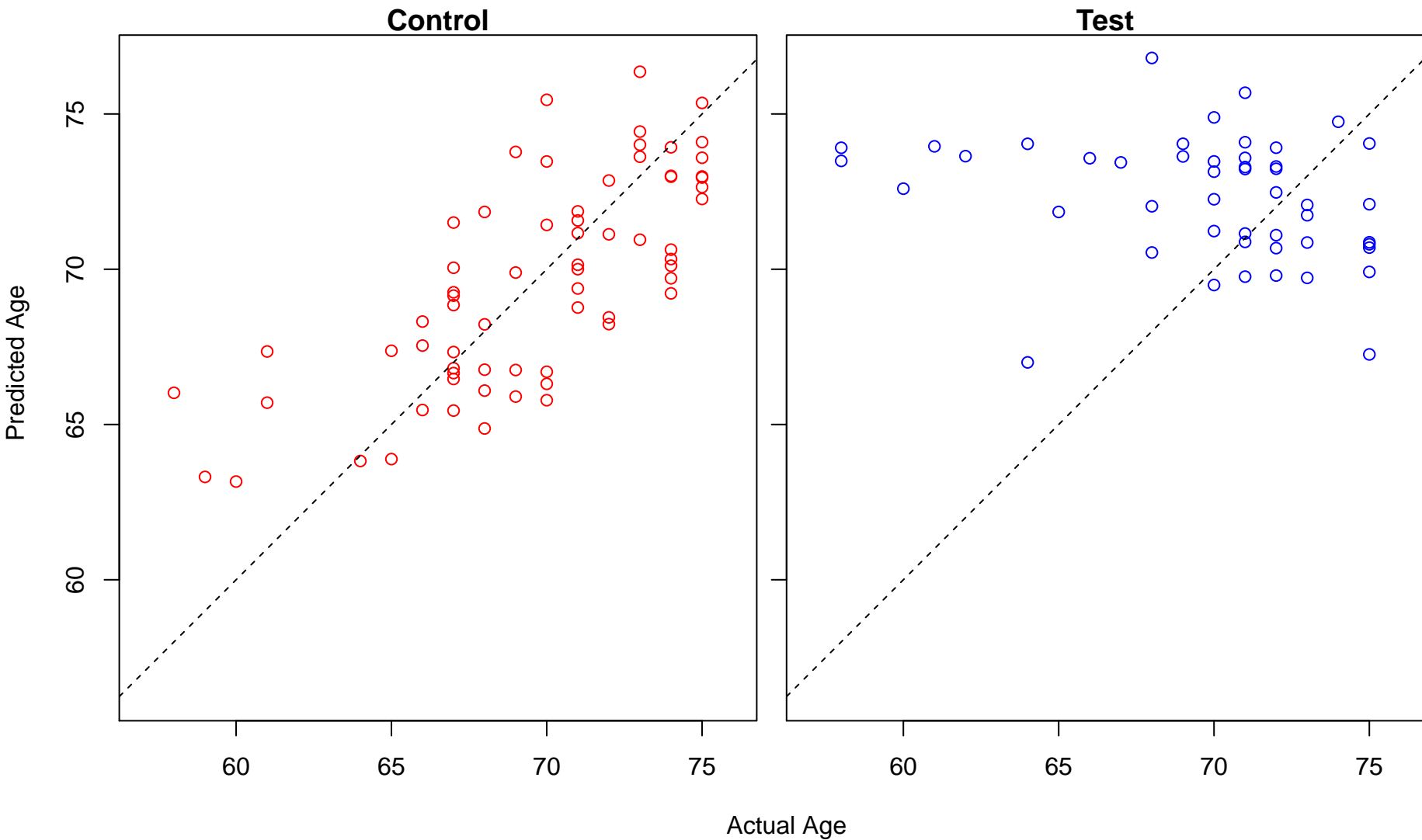
vasculature development (Score: 1.845077)



leukocyte activation involved in immune response (Score: 1.843284)

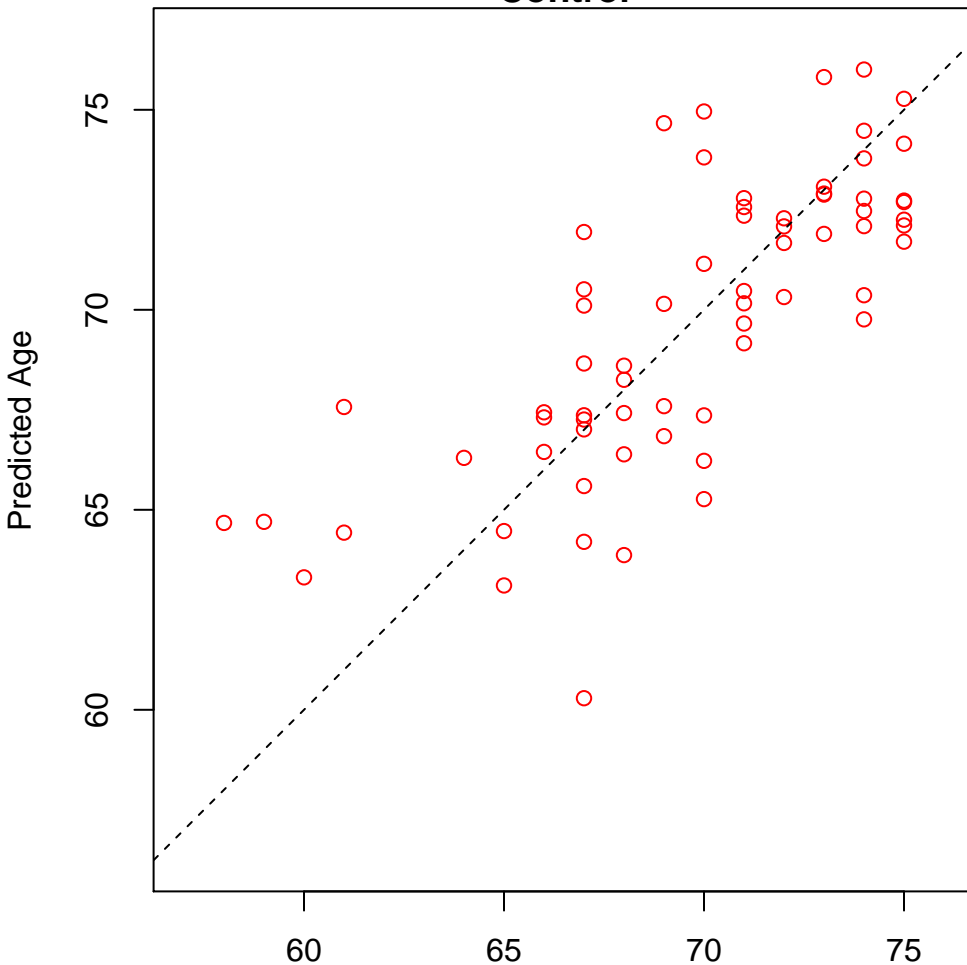


regulation of lipid metabolic process (Score: 1.843113)

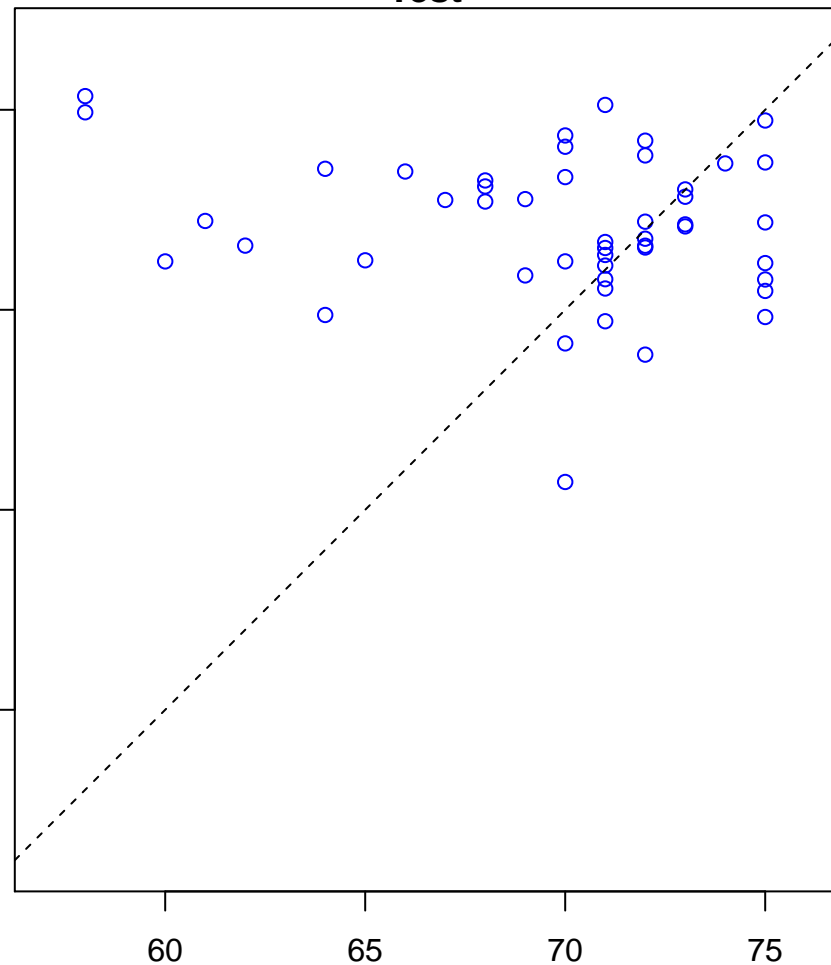


divalent inorganic cation homeostasis (Score: 1.841263)

Control

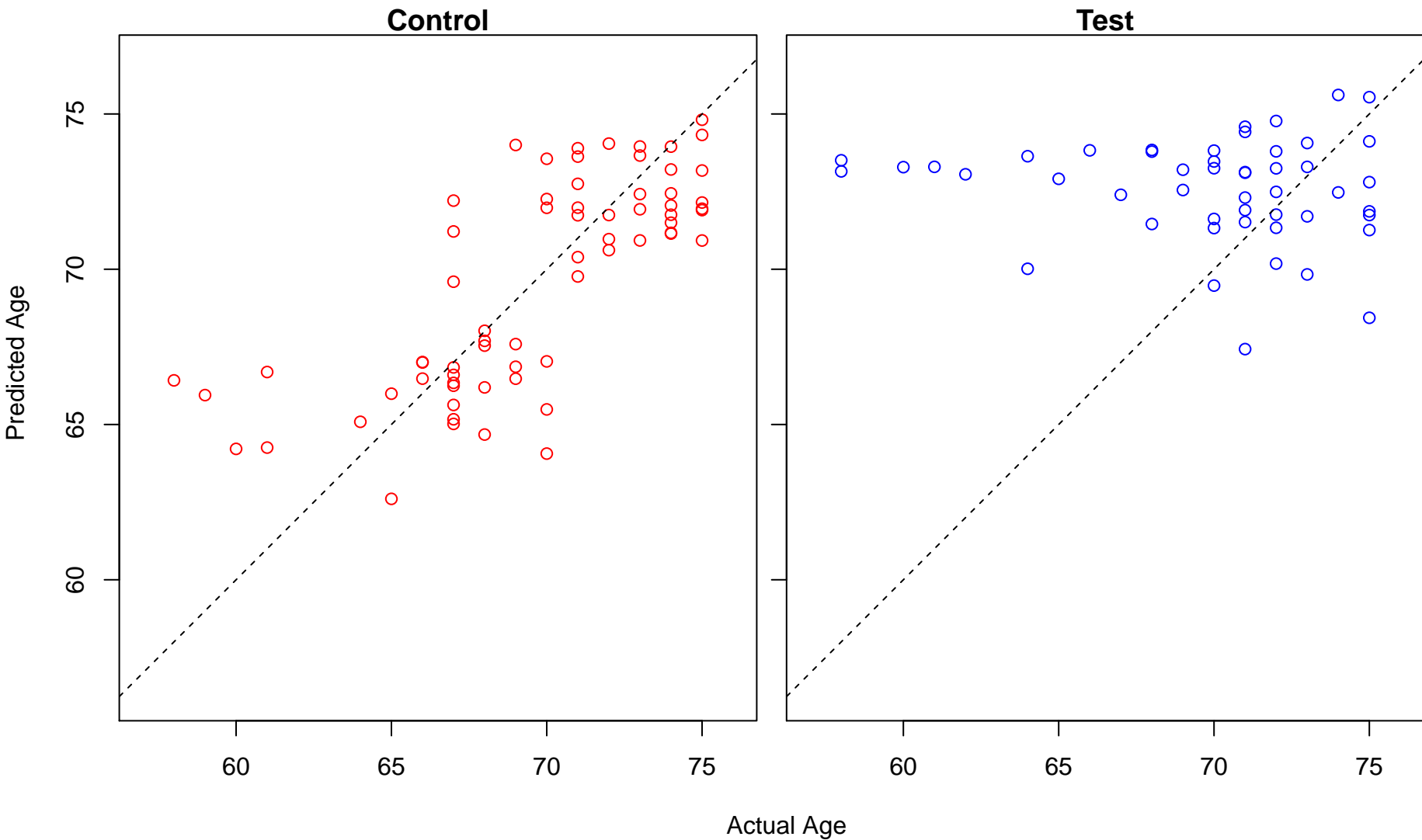


Test

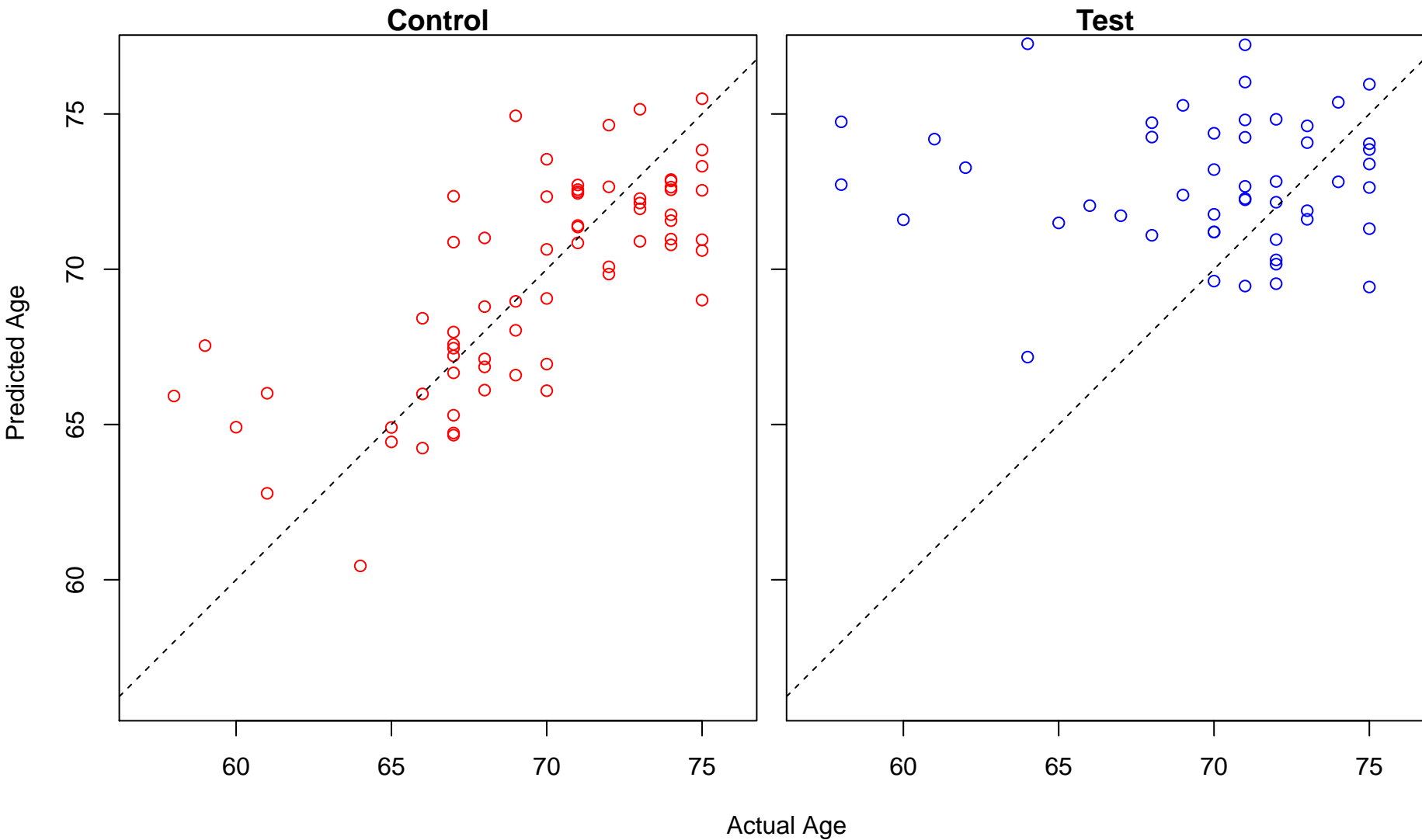


Actual Age

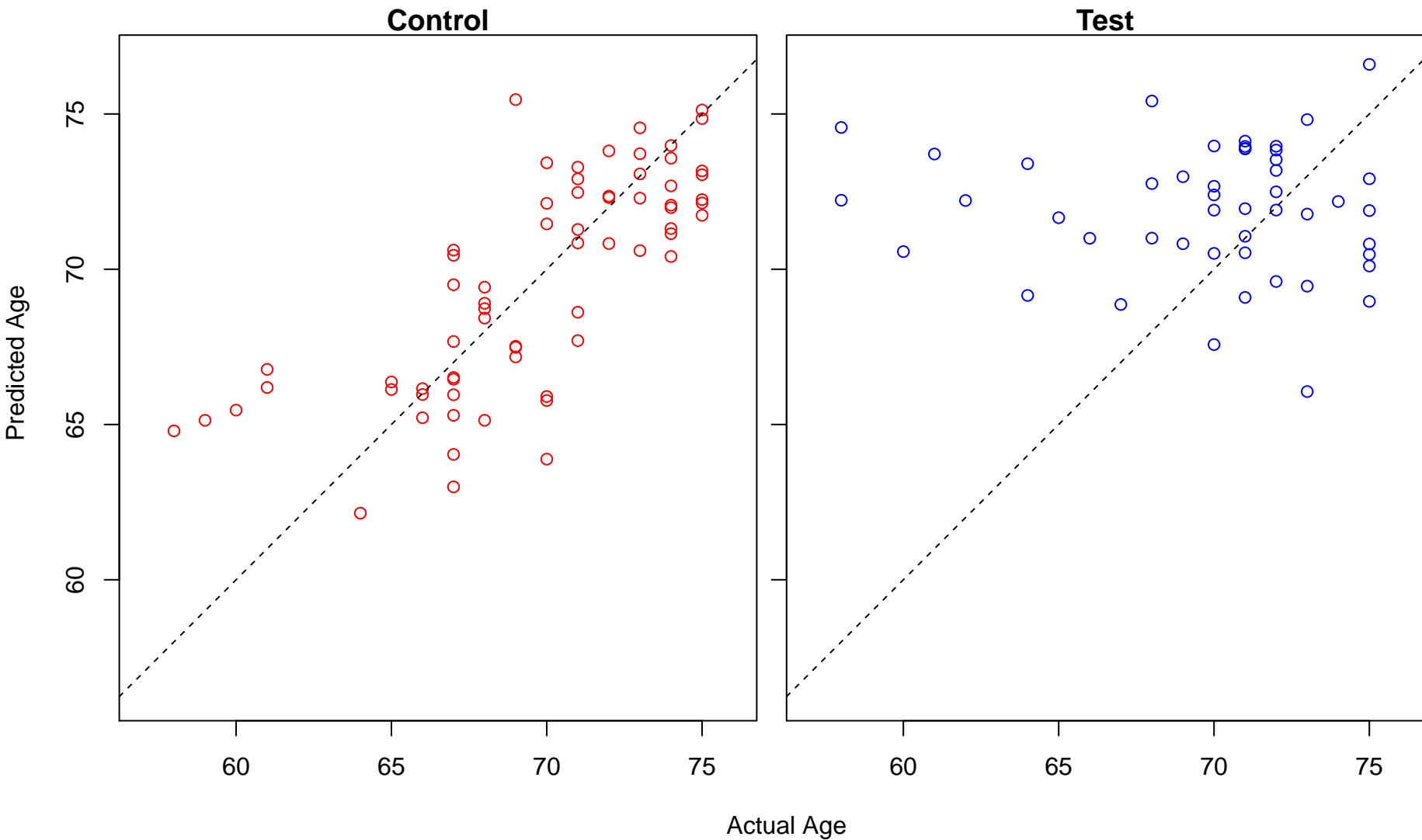
glycosylation (Score: 1.840918)



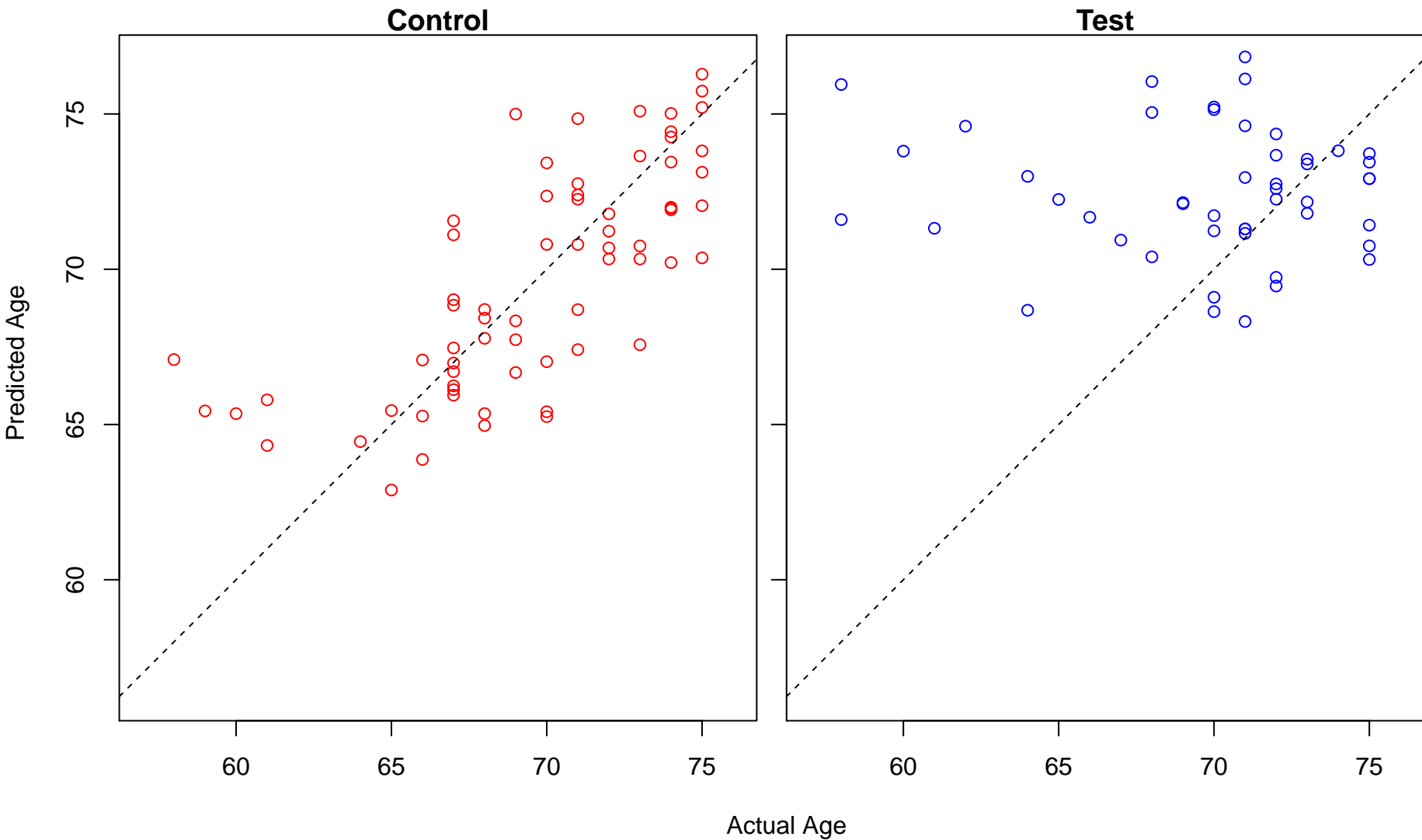
pattern specification process (Score: 1.839881)



regulation of intracellular transport (Score: 1.839504)

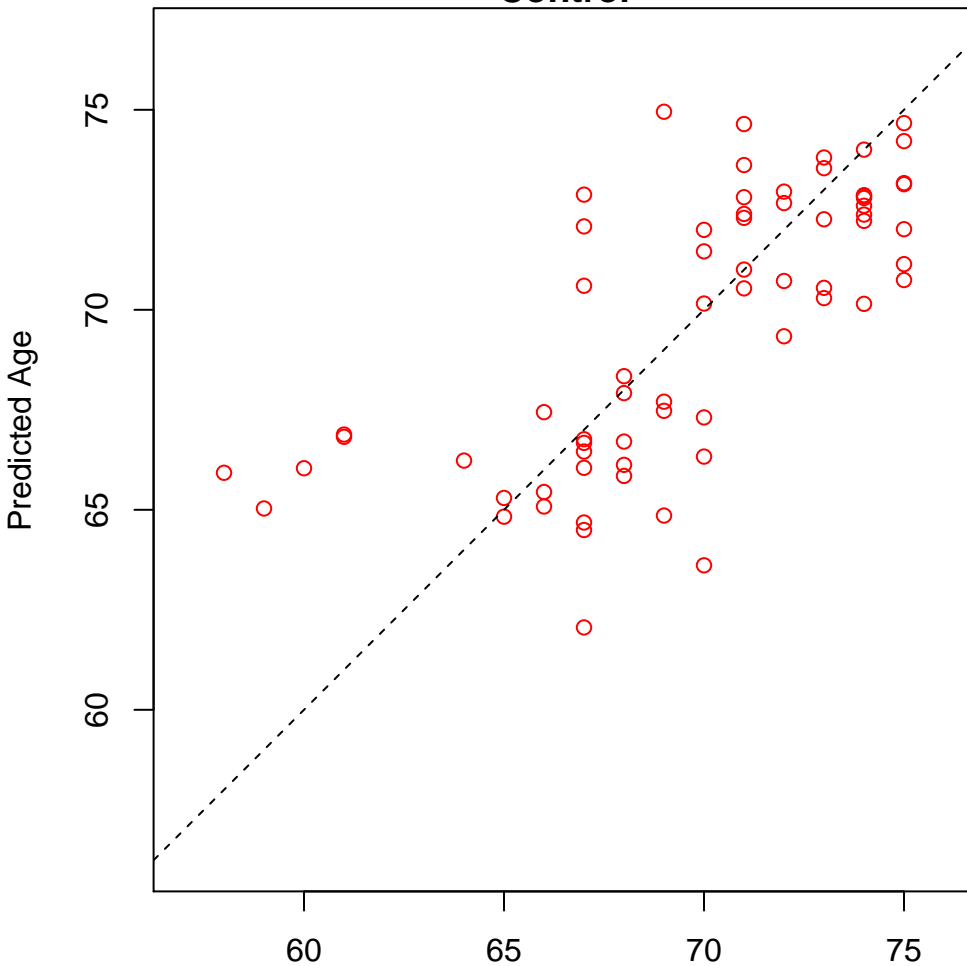


regulation of neuron death (Score: 1.839145)

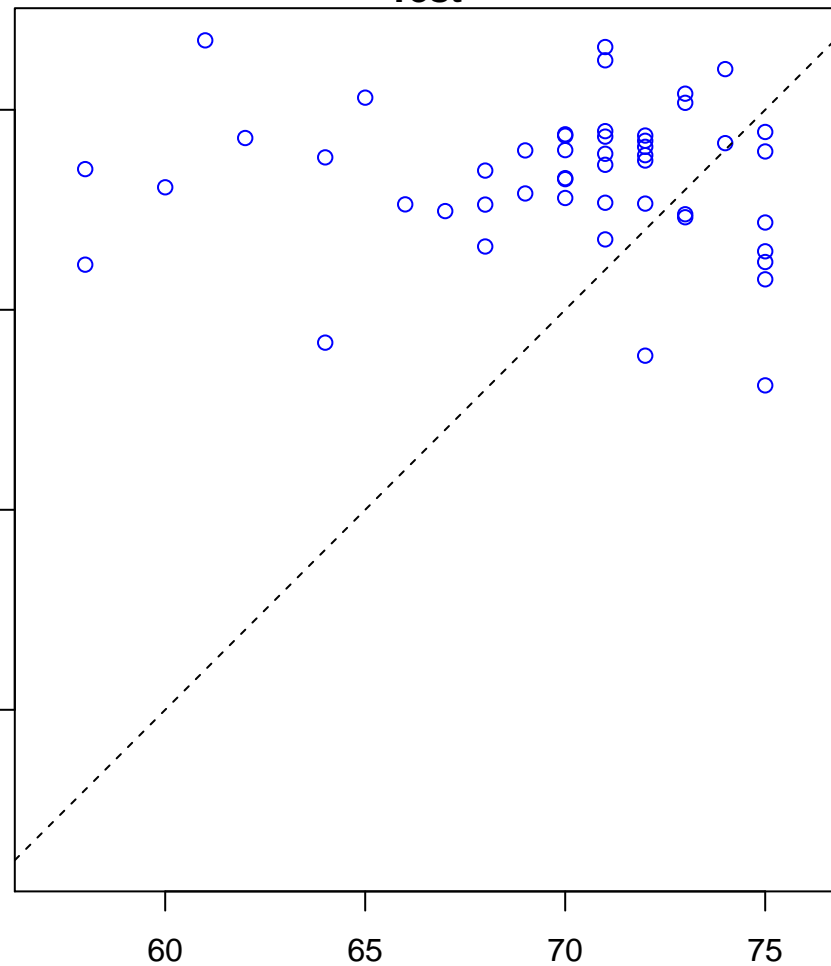


cellular amino acid metabolic process (Score: 1.837551)

Control

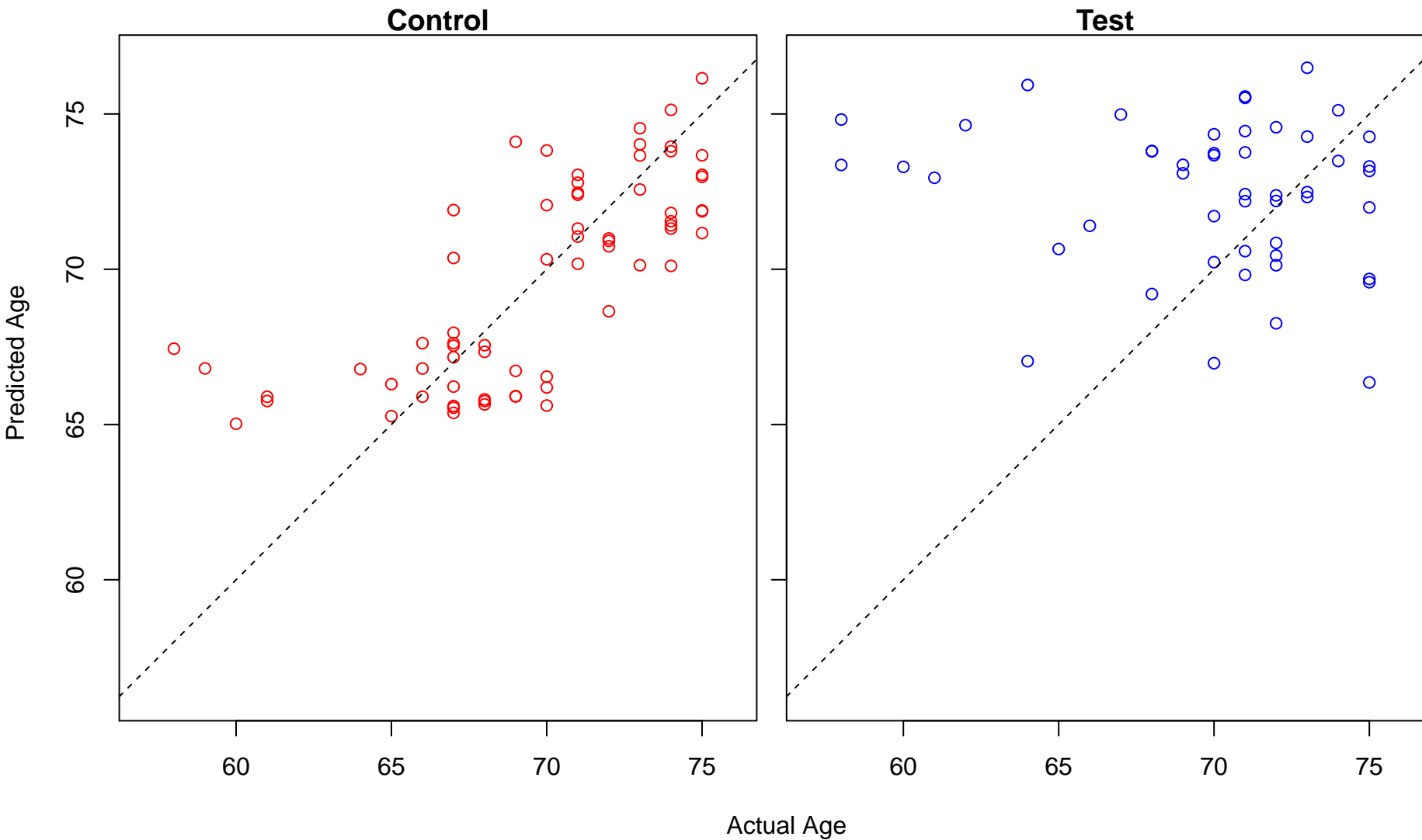


Test

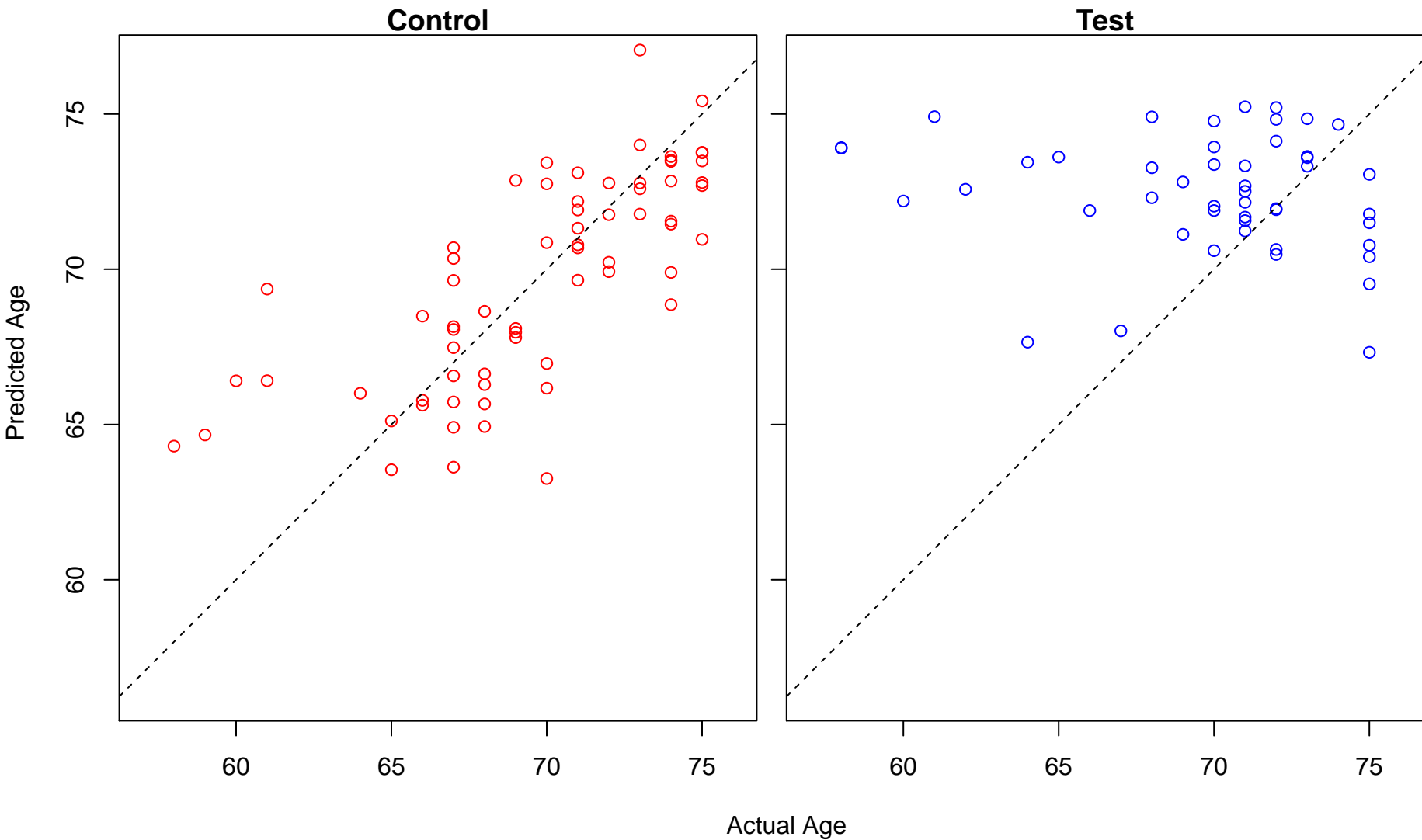


Actual Age

negative regulation of smooth muscle cell proliferation (Score: 1.836828)

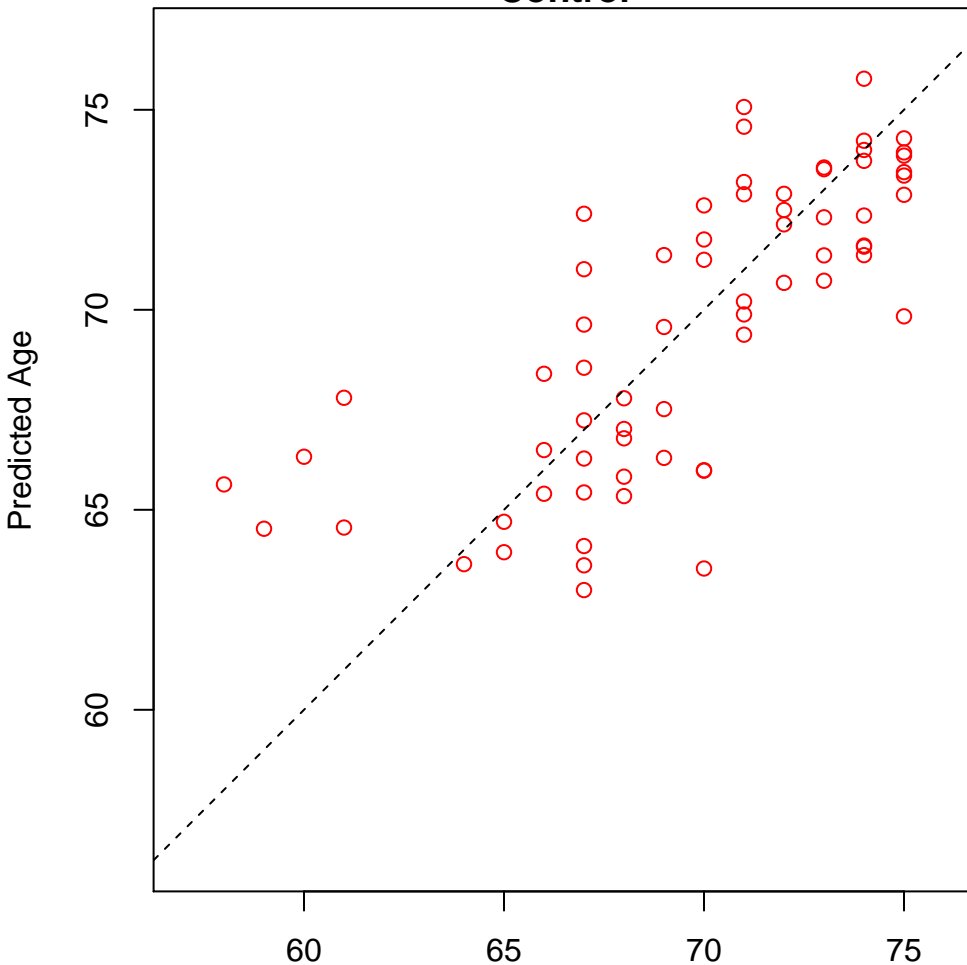


regulation of DNA replication (Score: 1.836823)

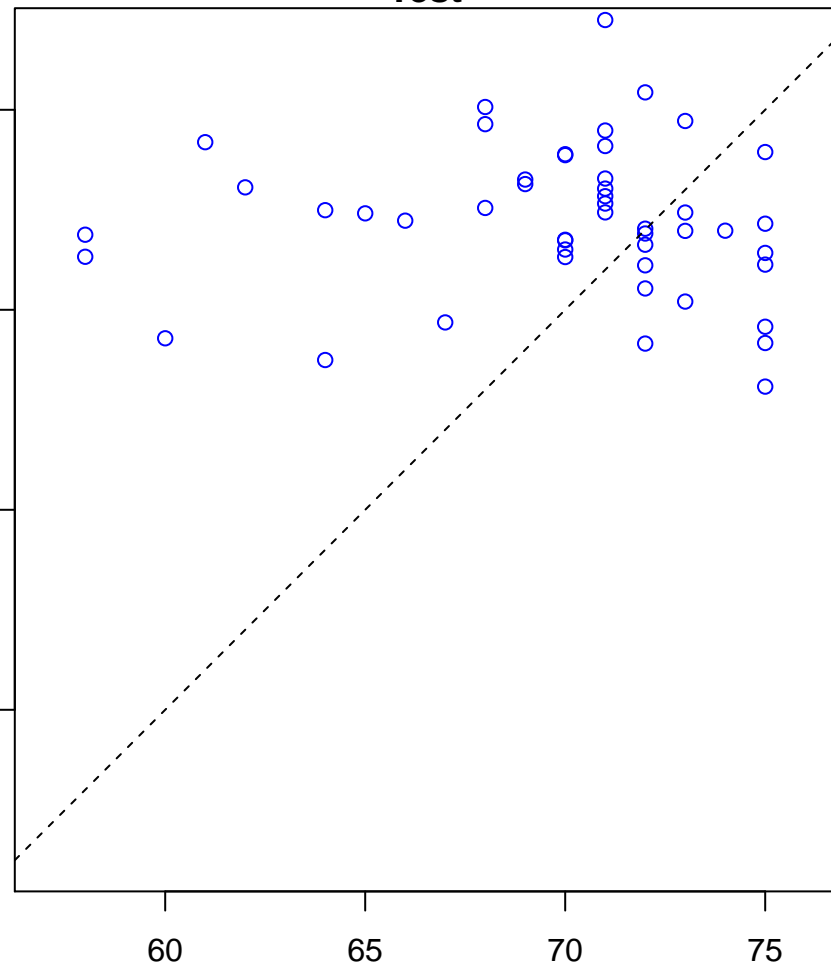


ribonucleoprotein complex biogenesis (Score: 1.836512)

Control

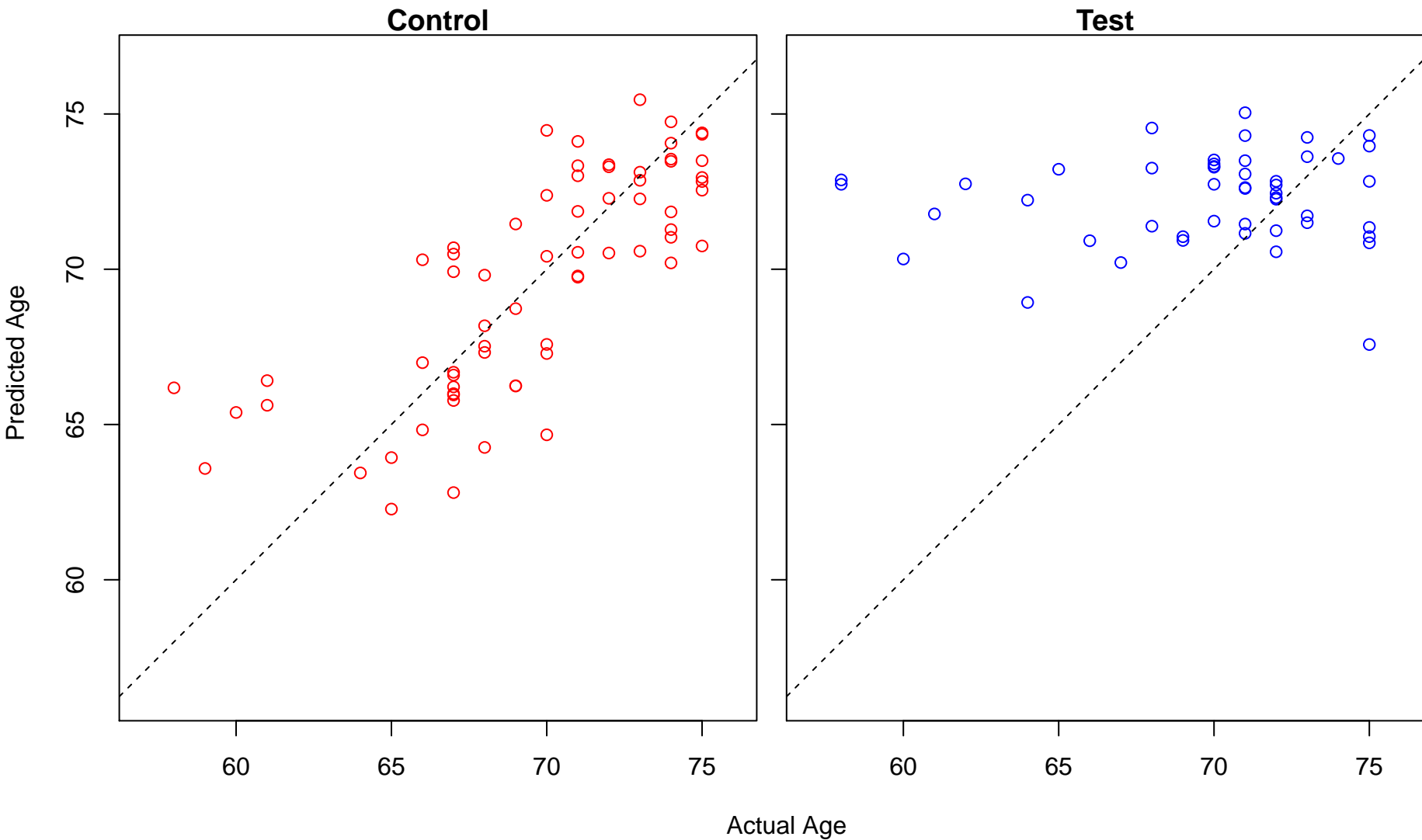


Test

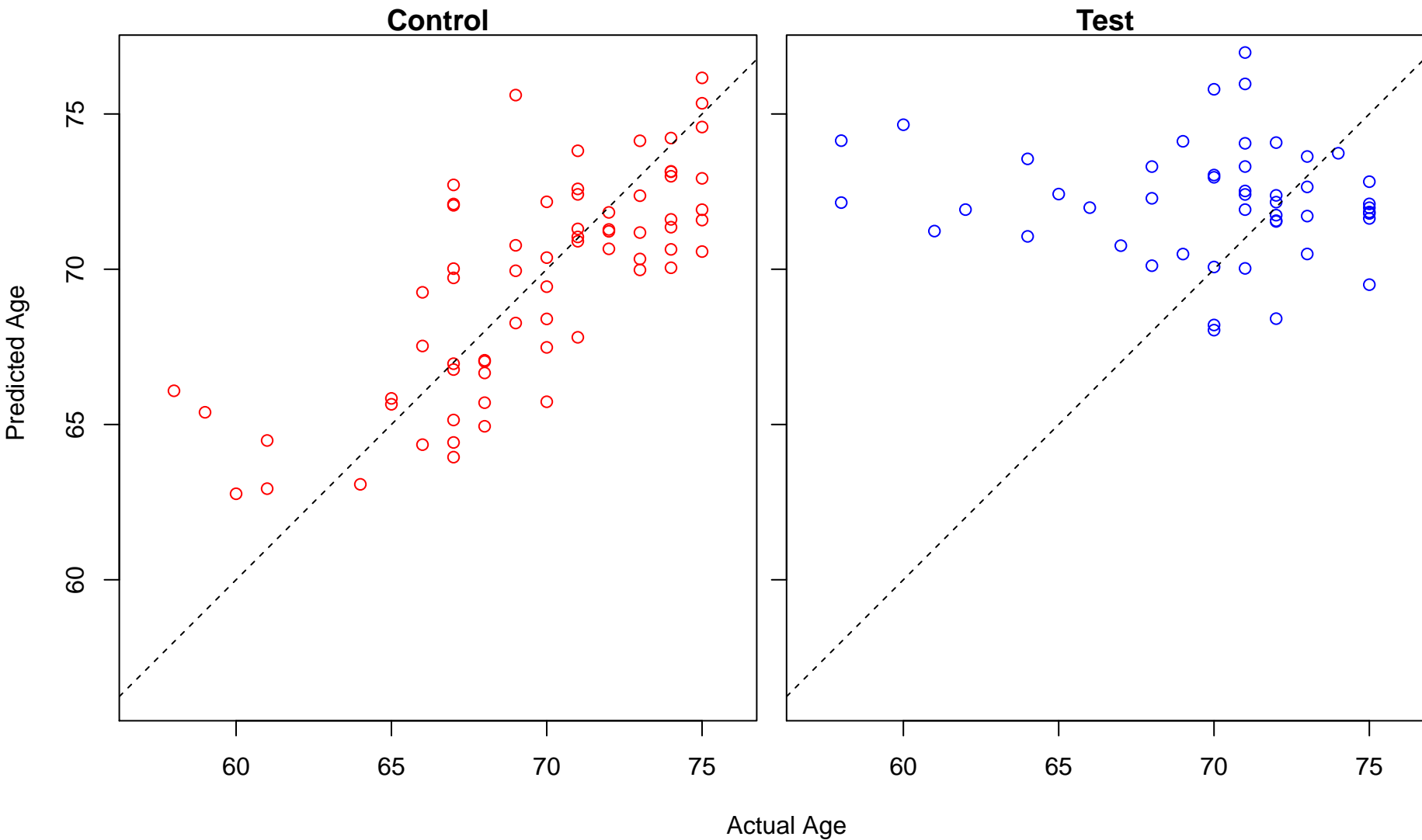


Actual Age

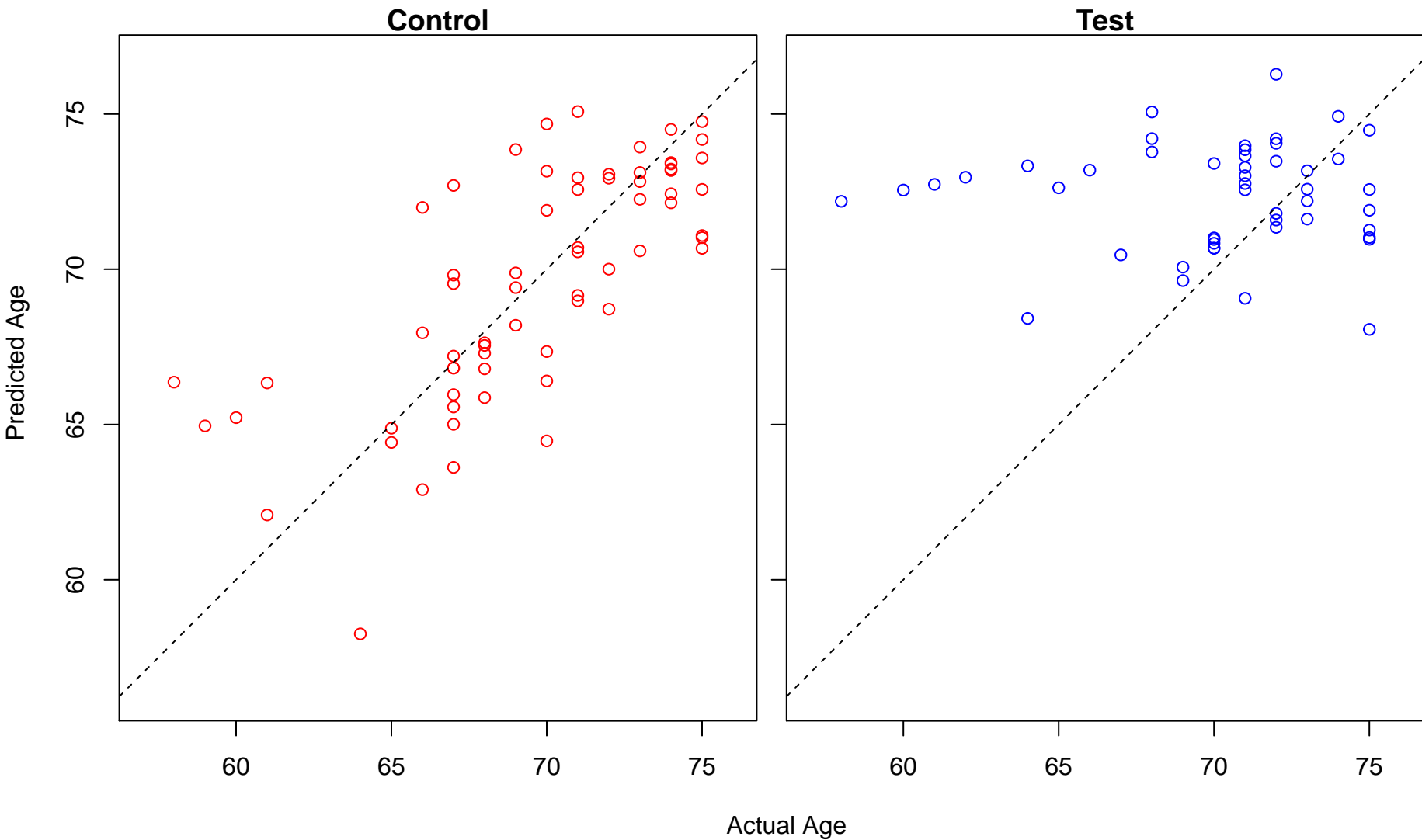
cellular response to organonitrogen compound (Score: 1.835591)



positive regulation of neuron death (Score: 1.834811)

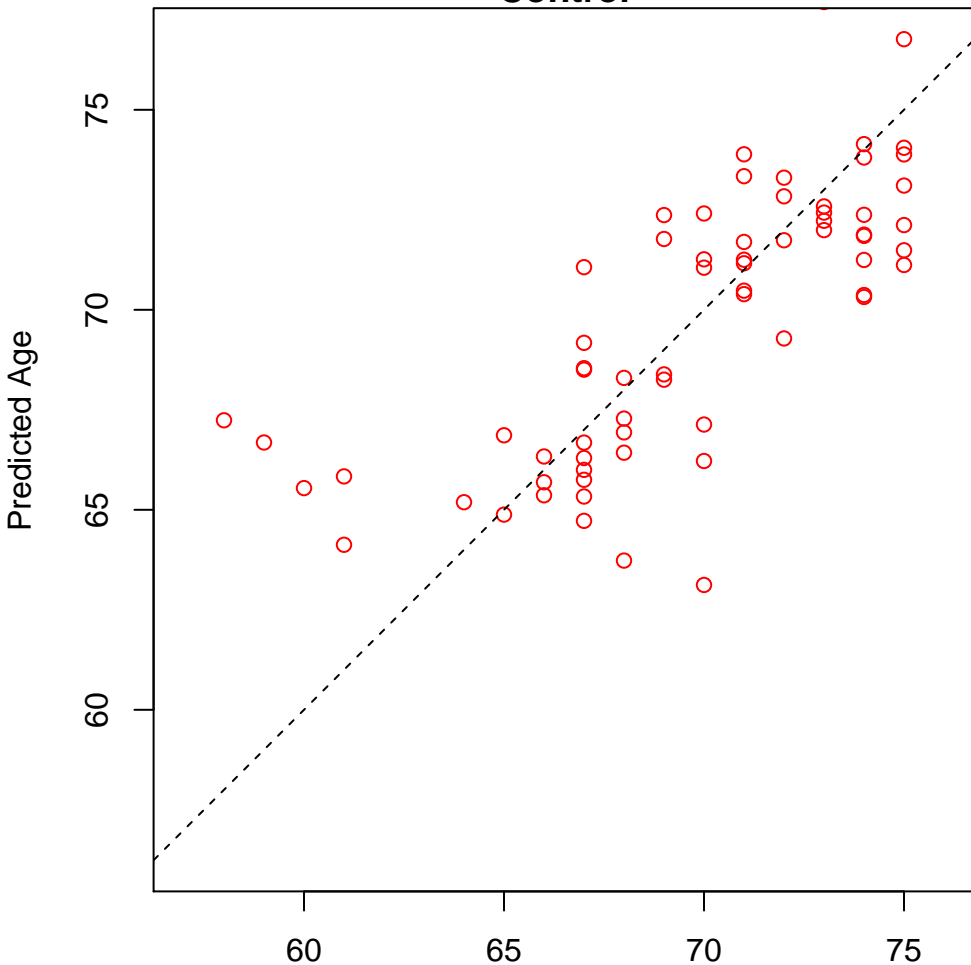


protein processing (Score: 1.834236)

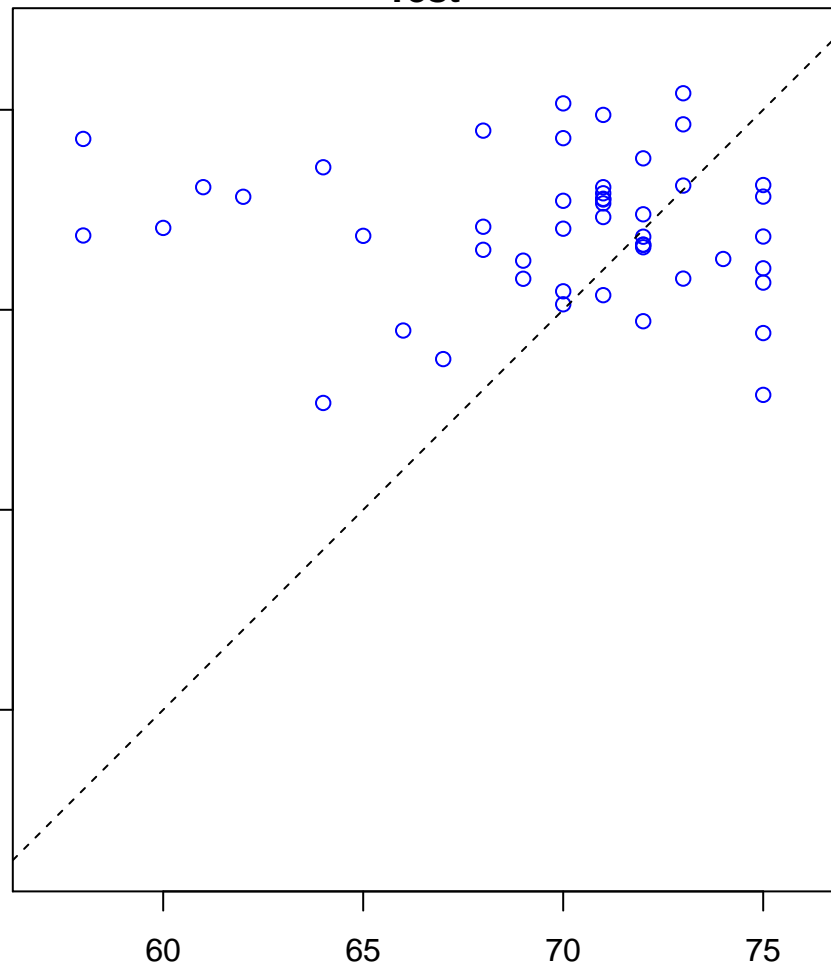


glycosyl compound metabolic process (Score: 1.834105)

Control

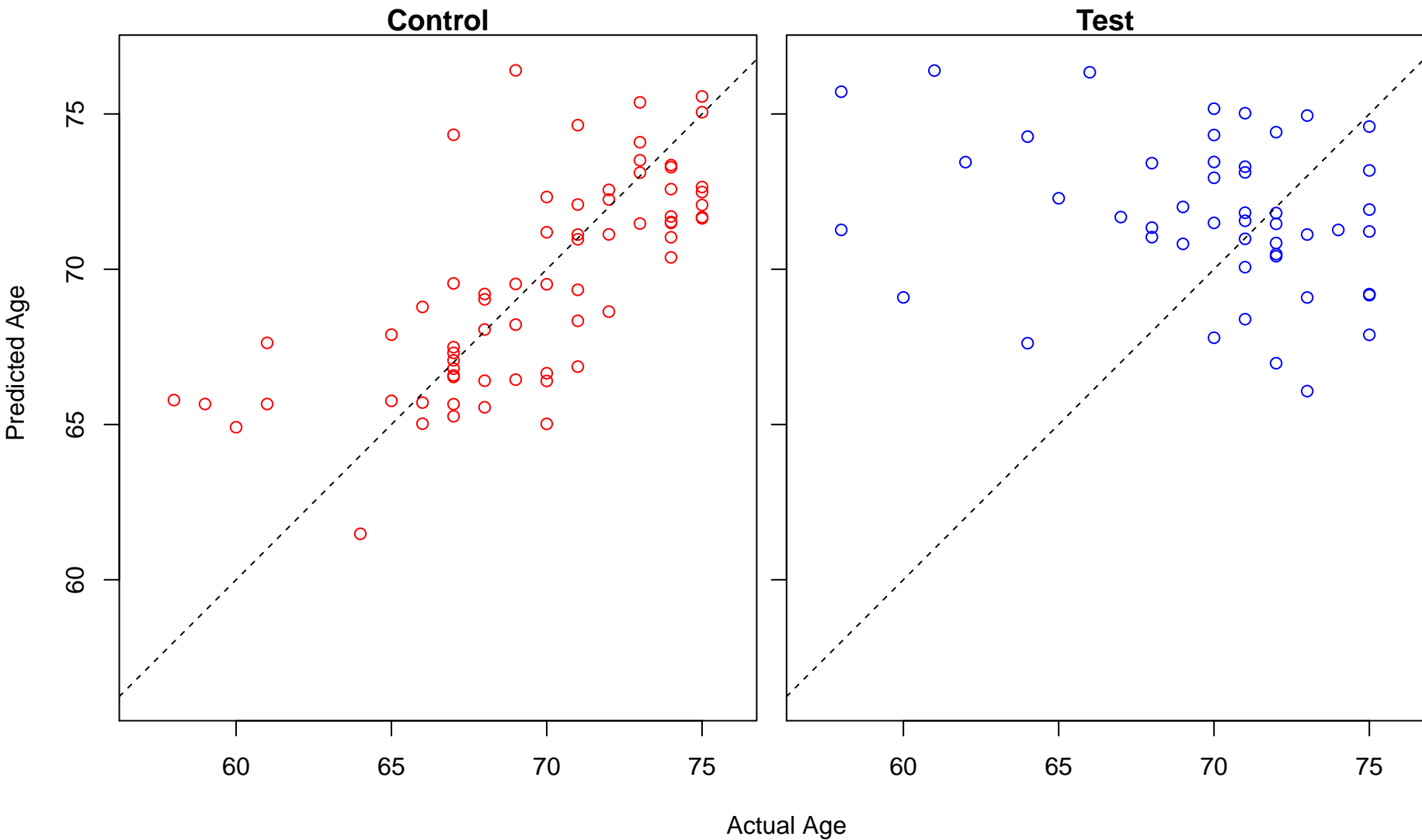


Test

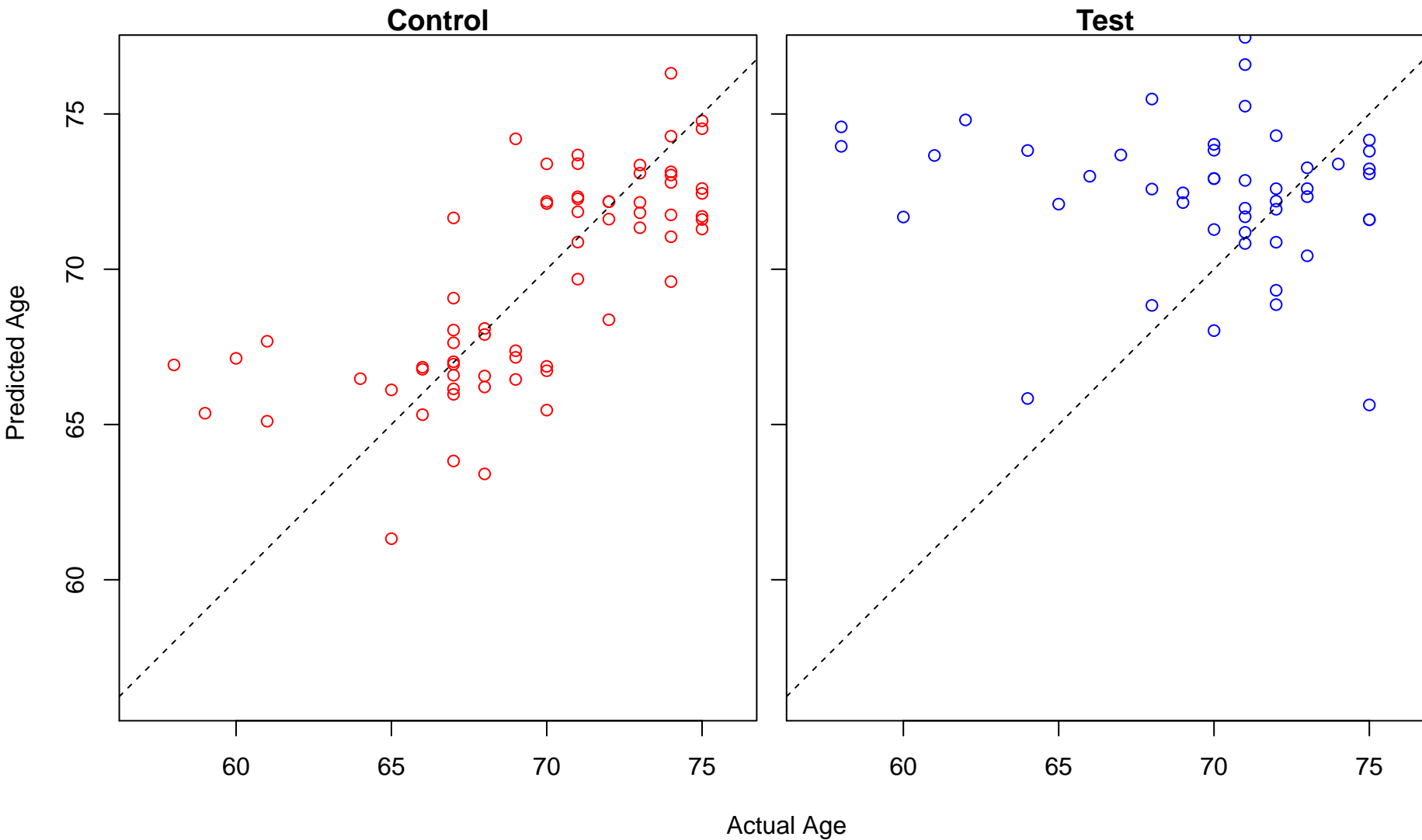


Actual Age

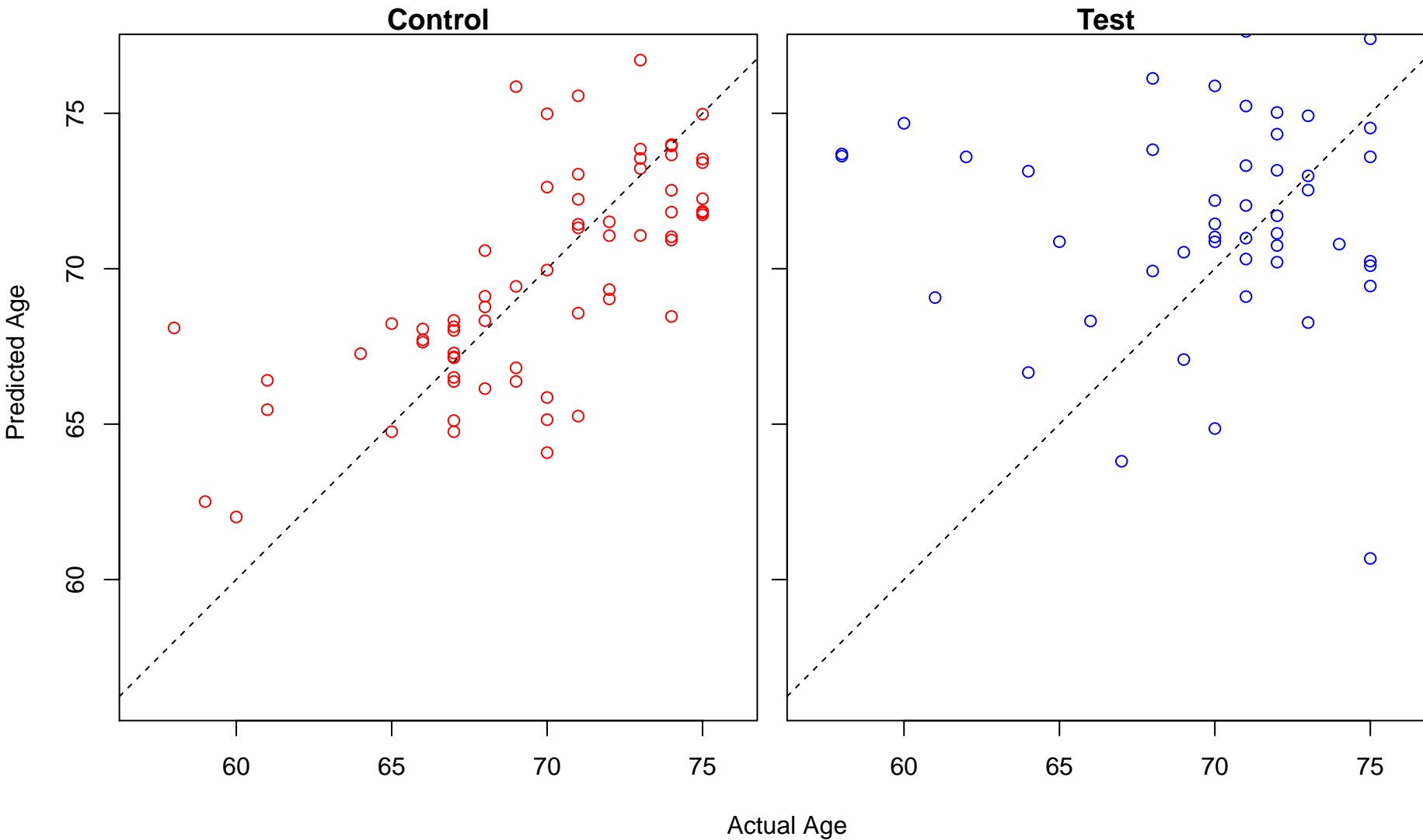
regulation of viral genome replication (Score: 1.833881)



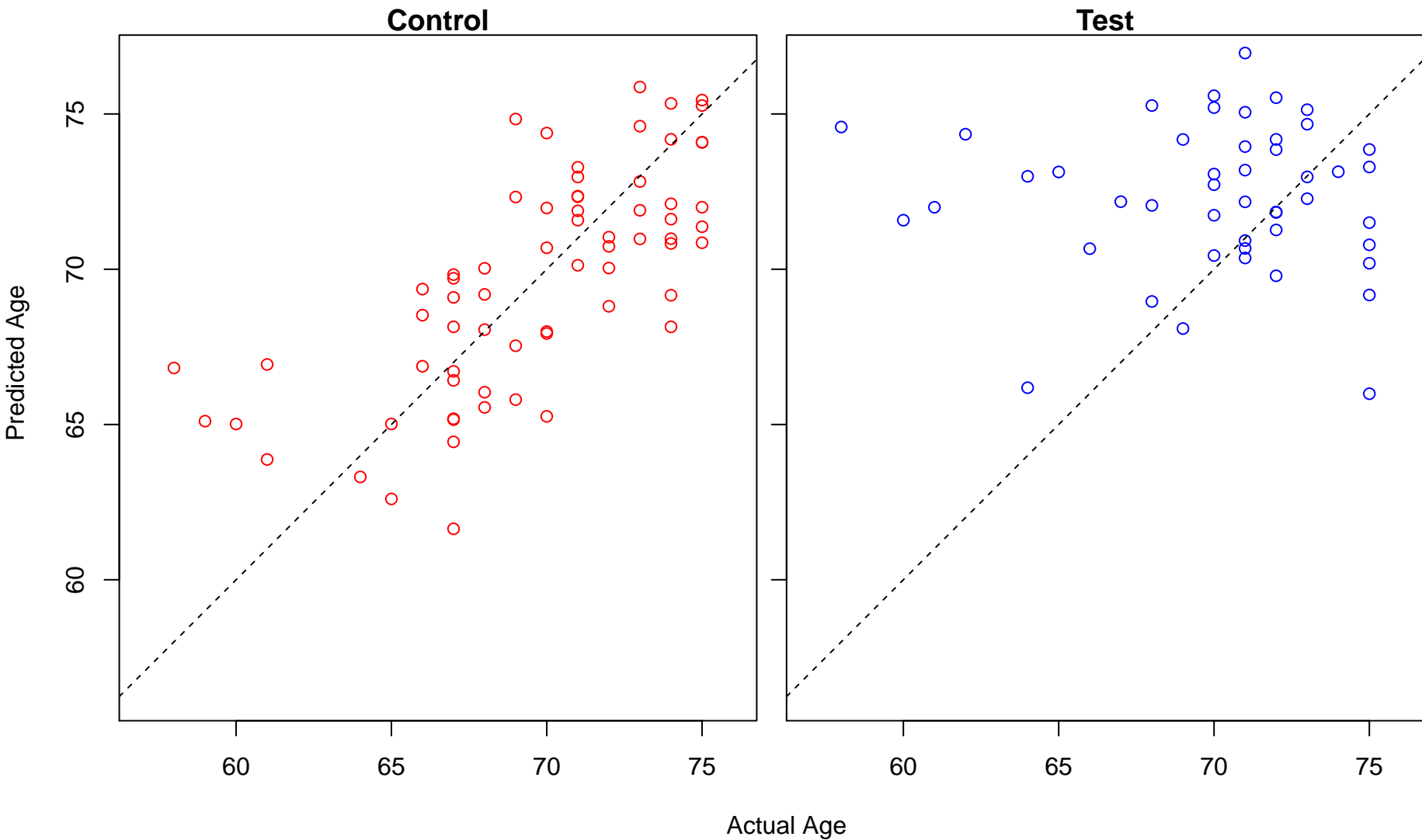
positive regulation of chemotaxis (Score: 1.833162)



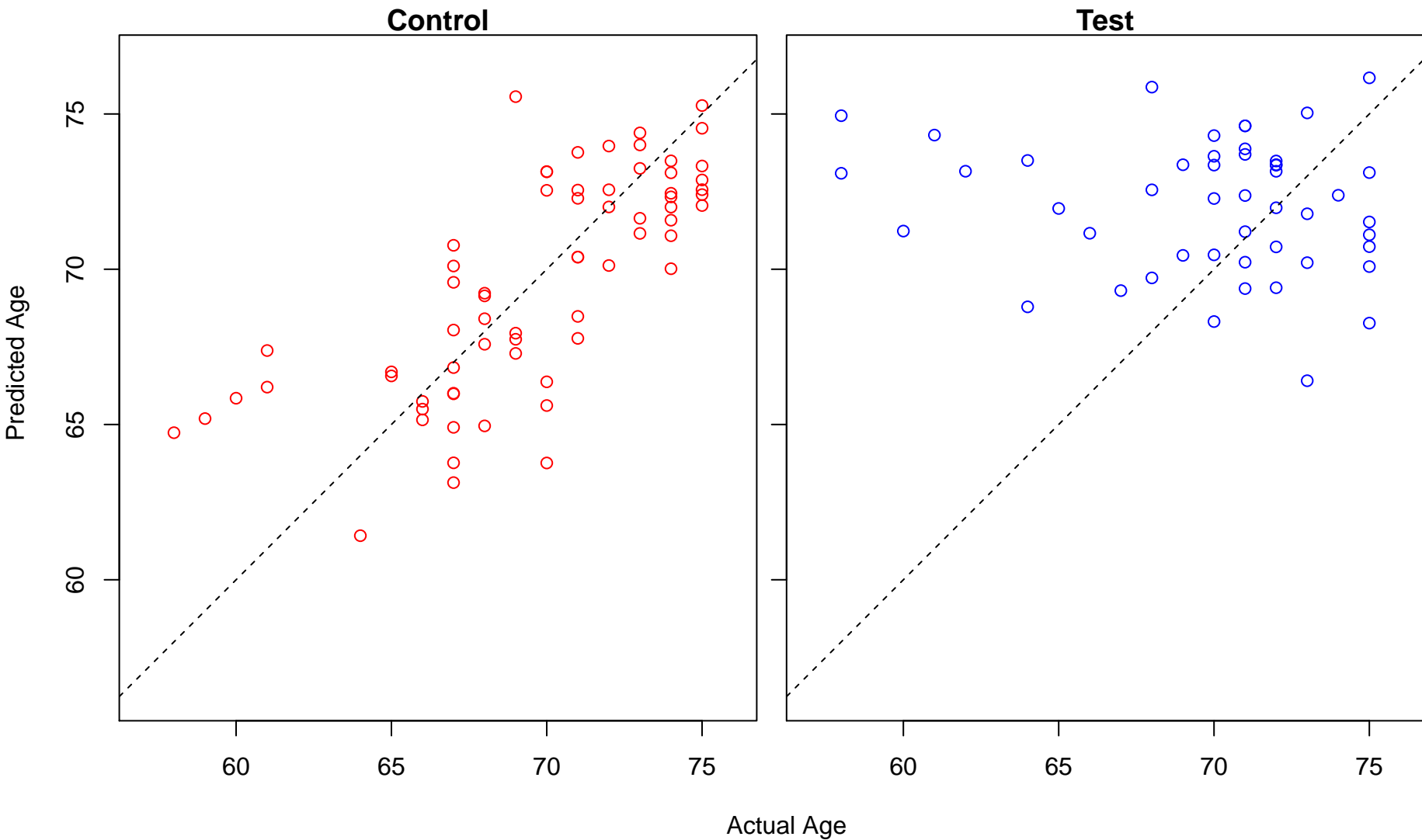
cell activation involved in immune response (Score: 1.833045)



cellular response to heat (Score: 1.831808)

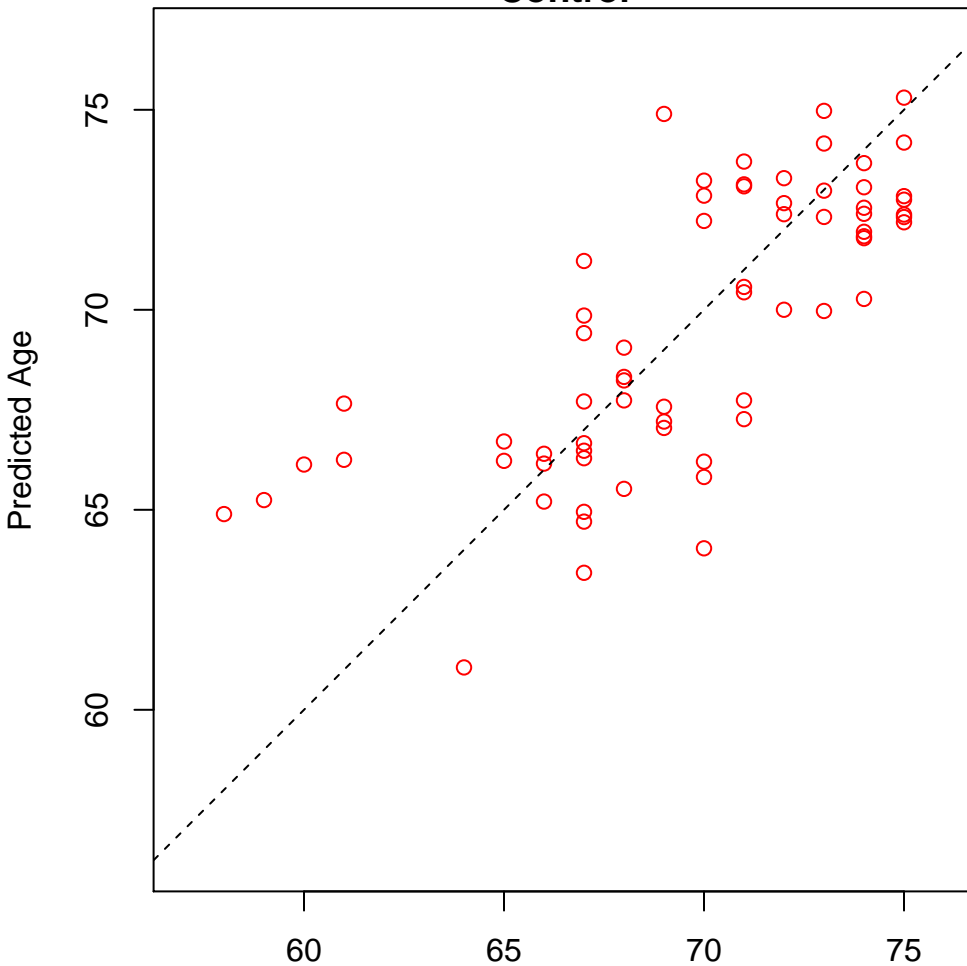


regulation of intracellular protein transport (Score: 1.831071)

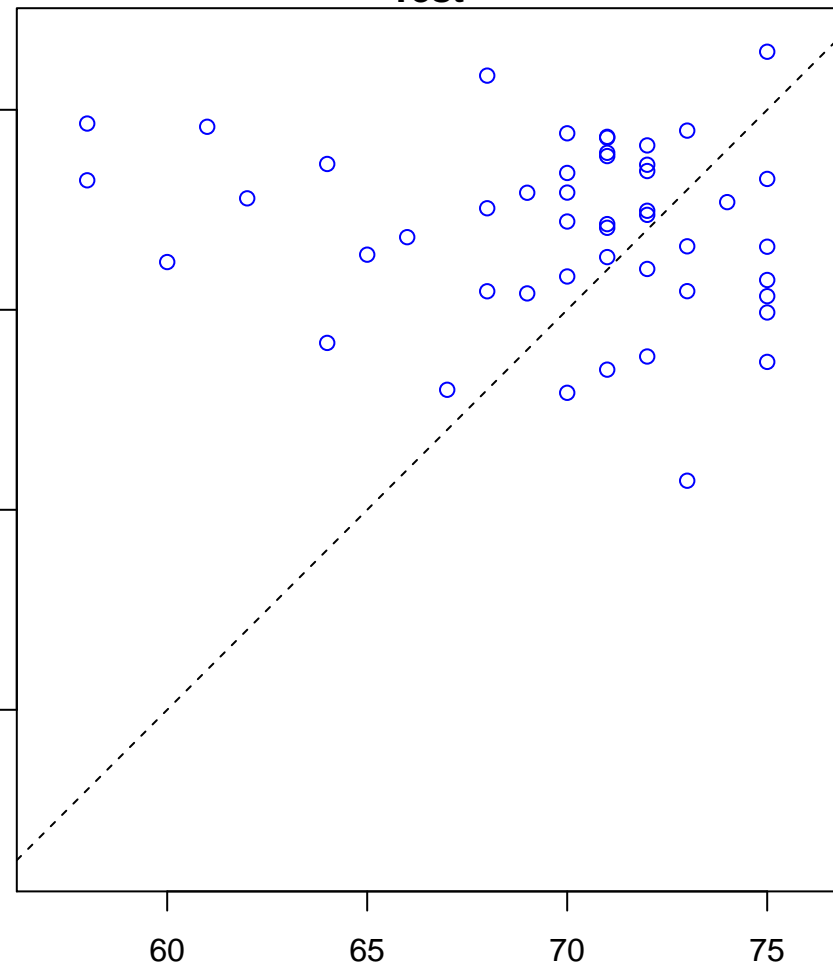


regulation of cellular protein localization (Score: 1.829860)

Control

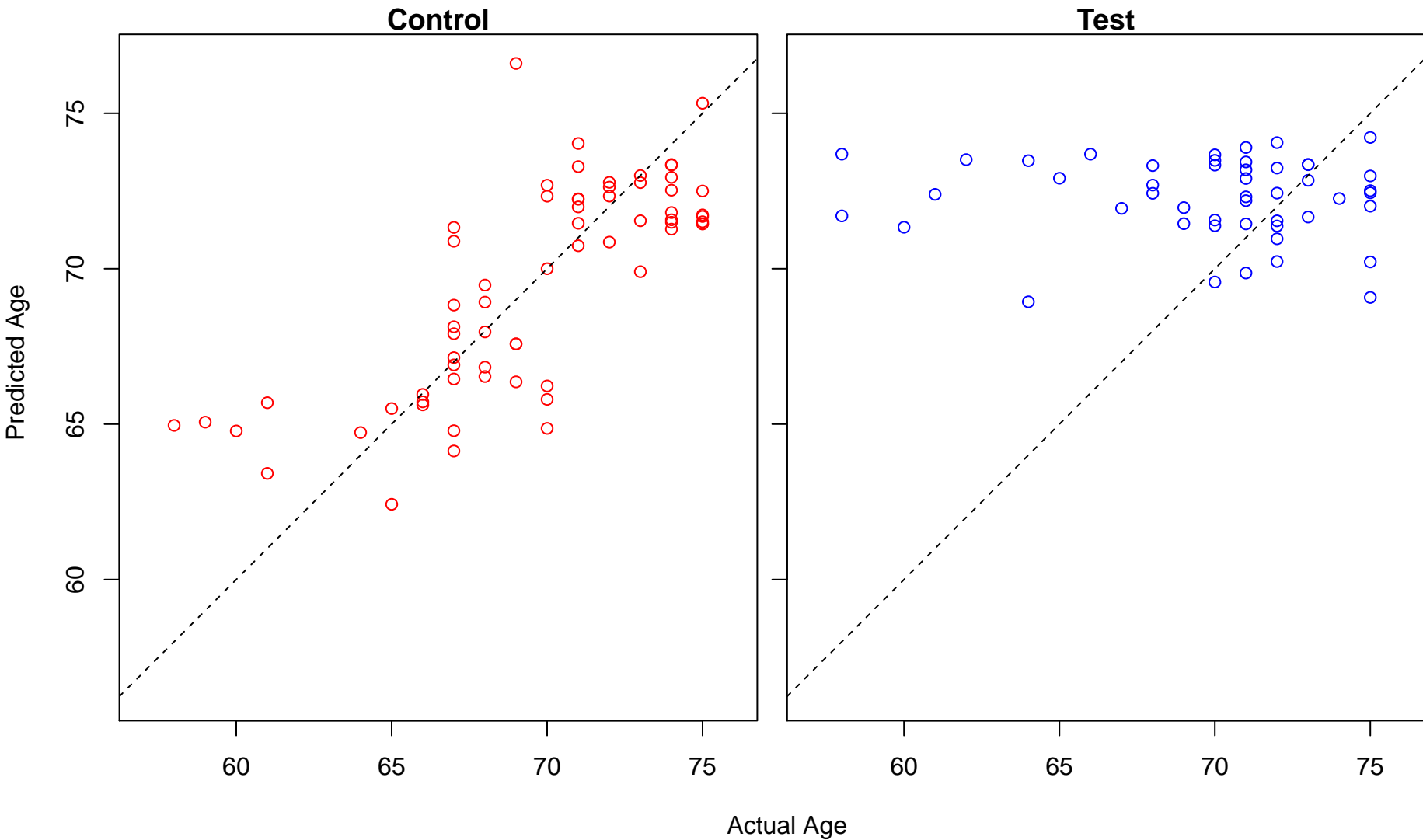


Test

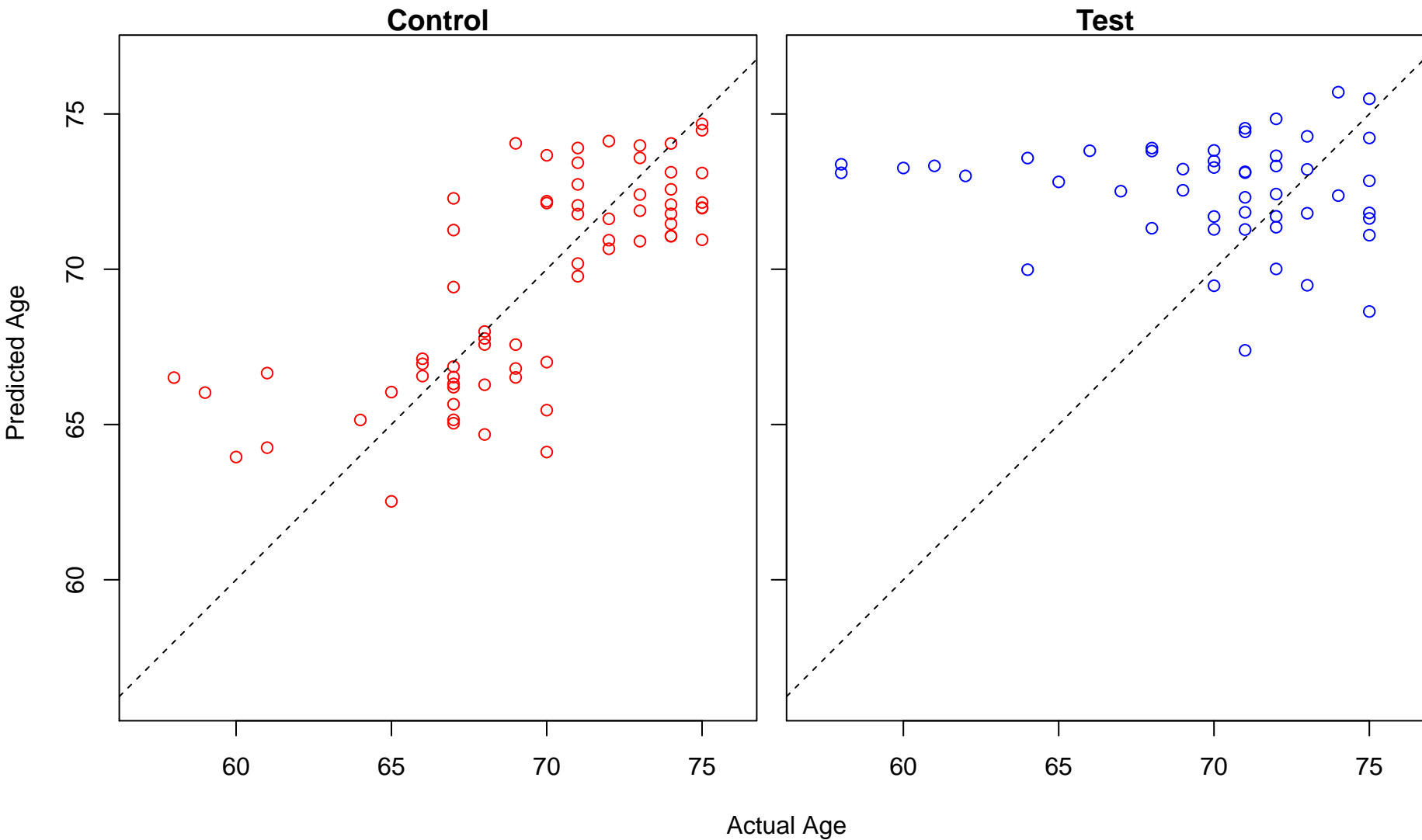


Actual Age

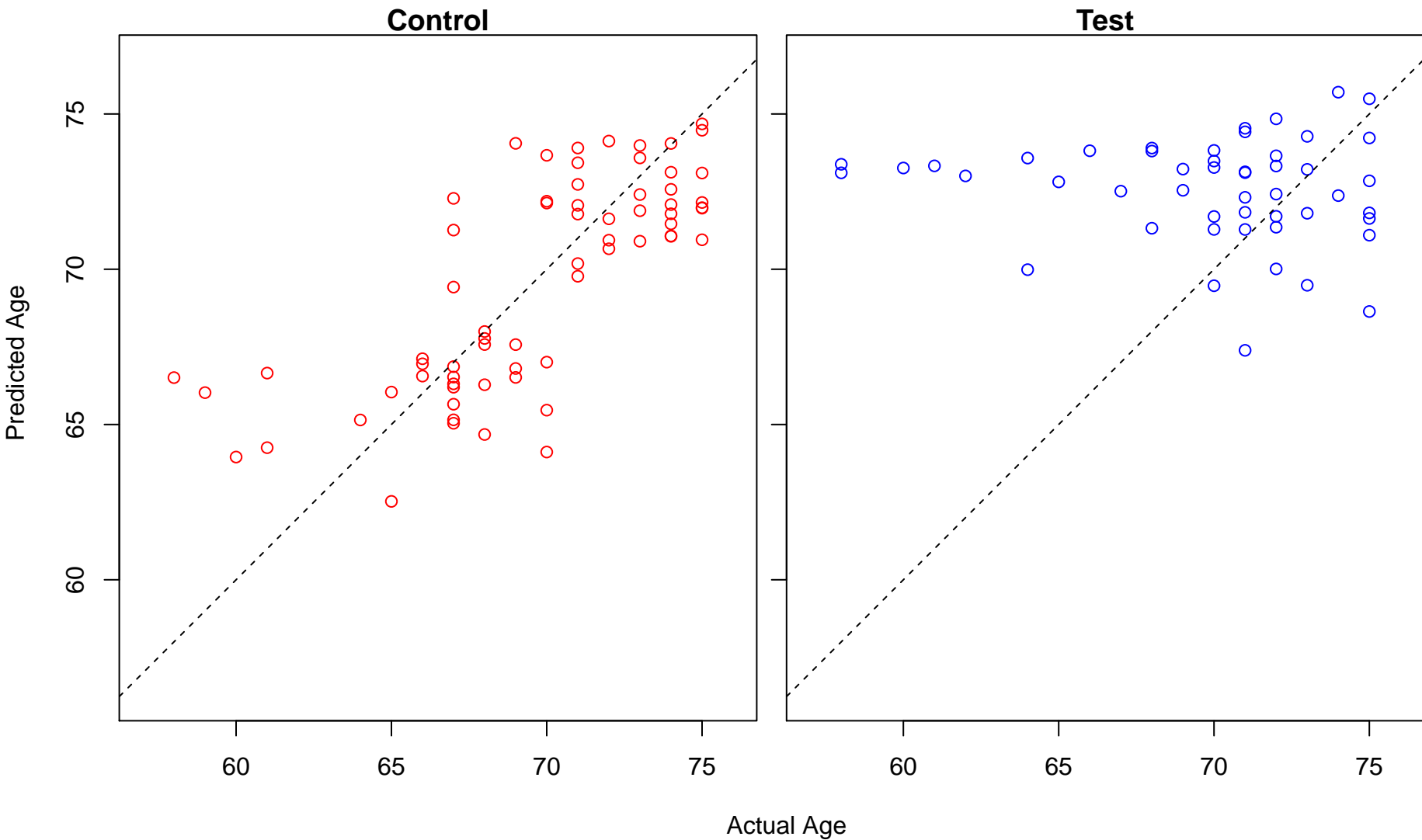
positive regulation of protein complex assembly (Score: 1.829647)



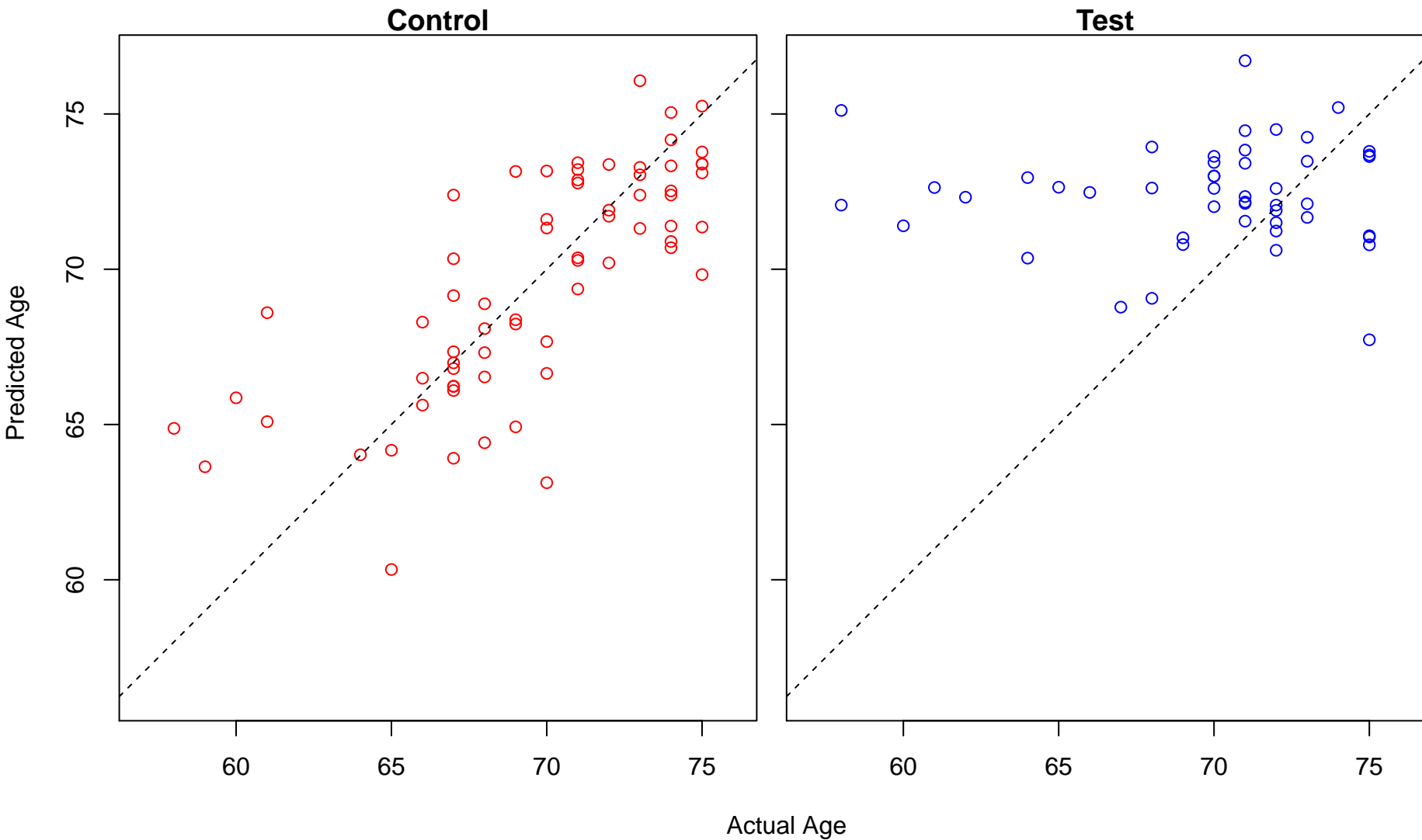
protein glycosylation (Score: 1.829592)



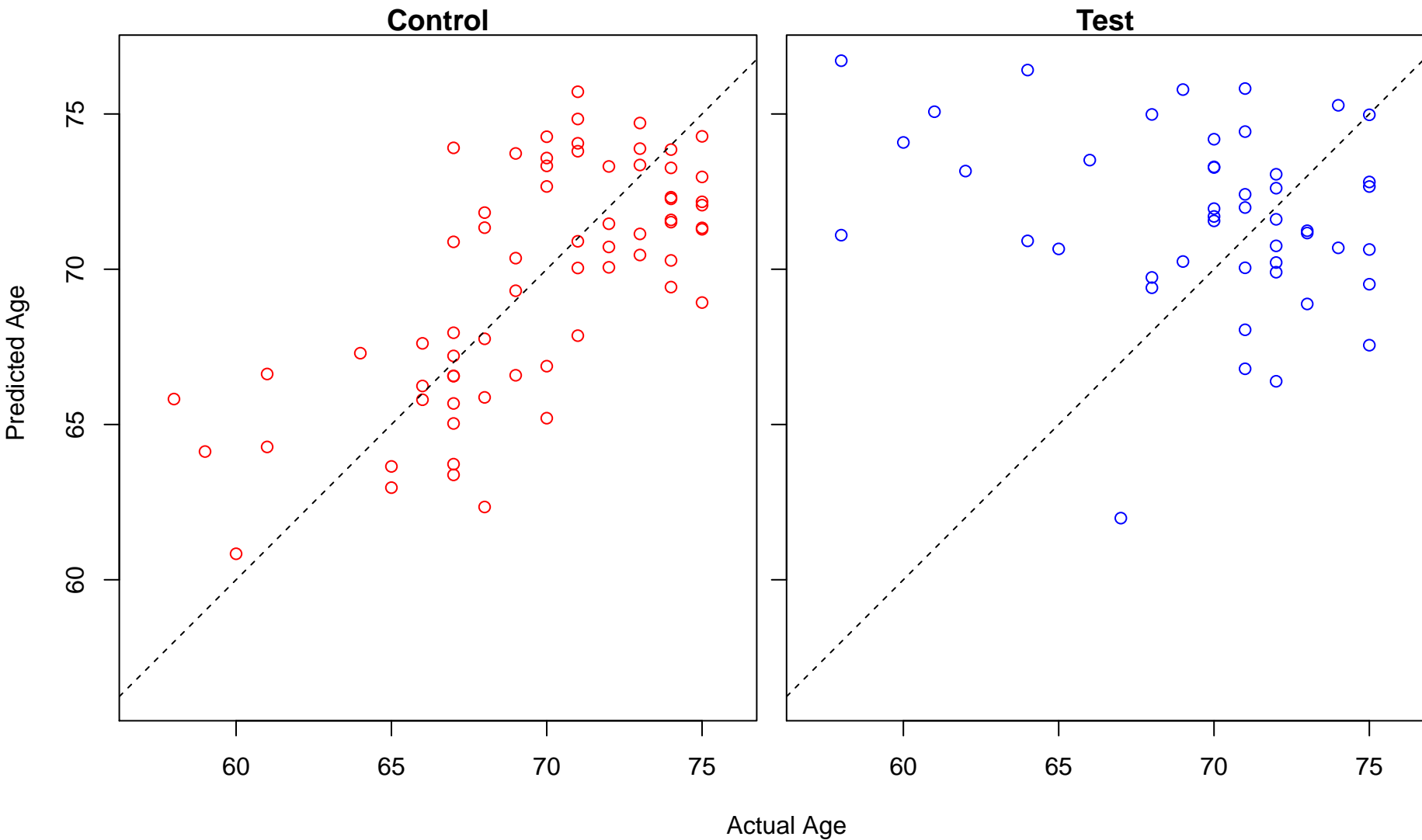
macromolecule glycosylation (Score: 1.829592)



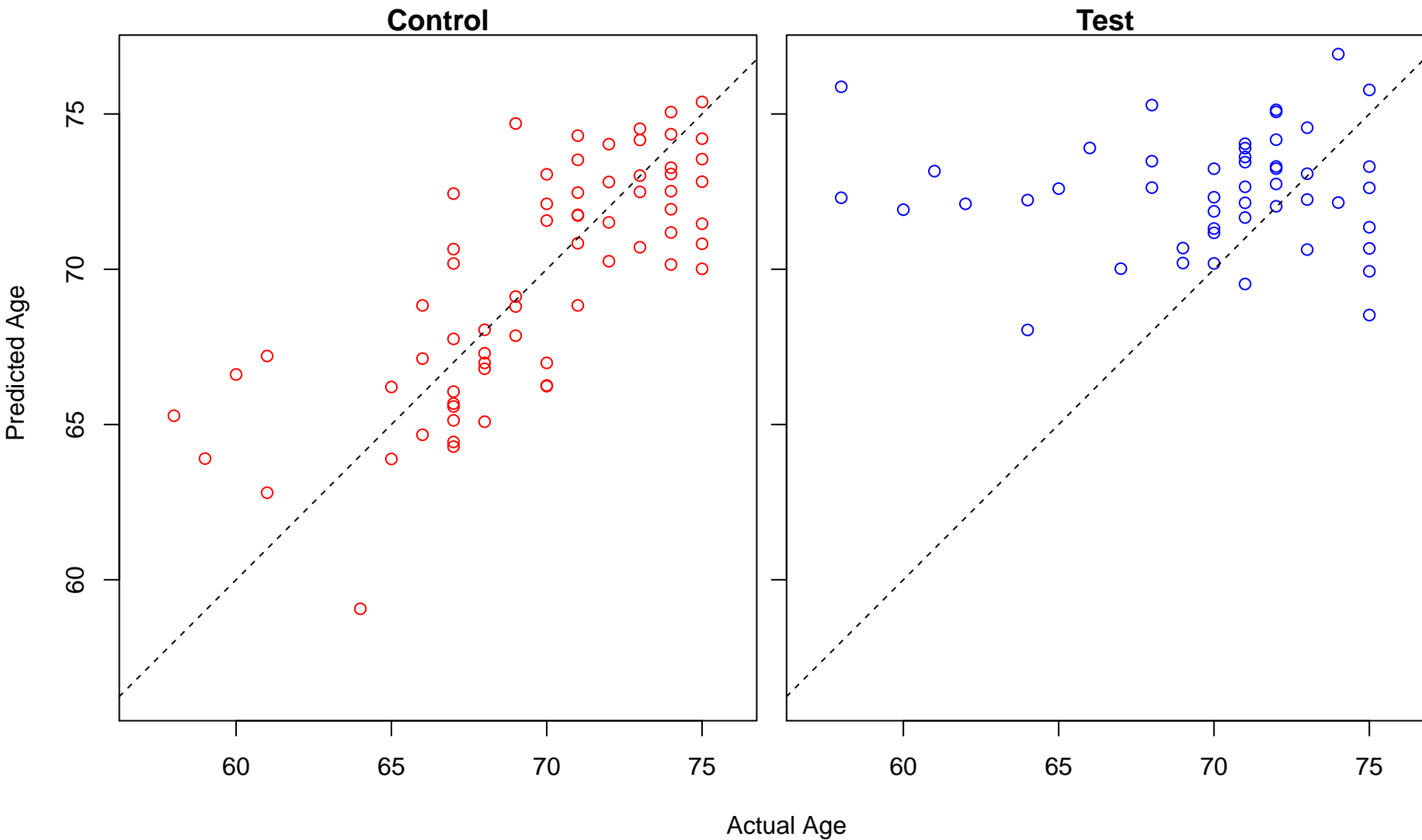
cell cycle checkpoint (Score: 1.829498)



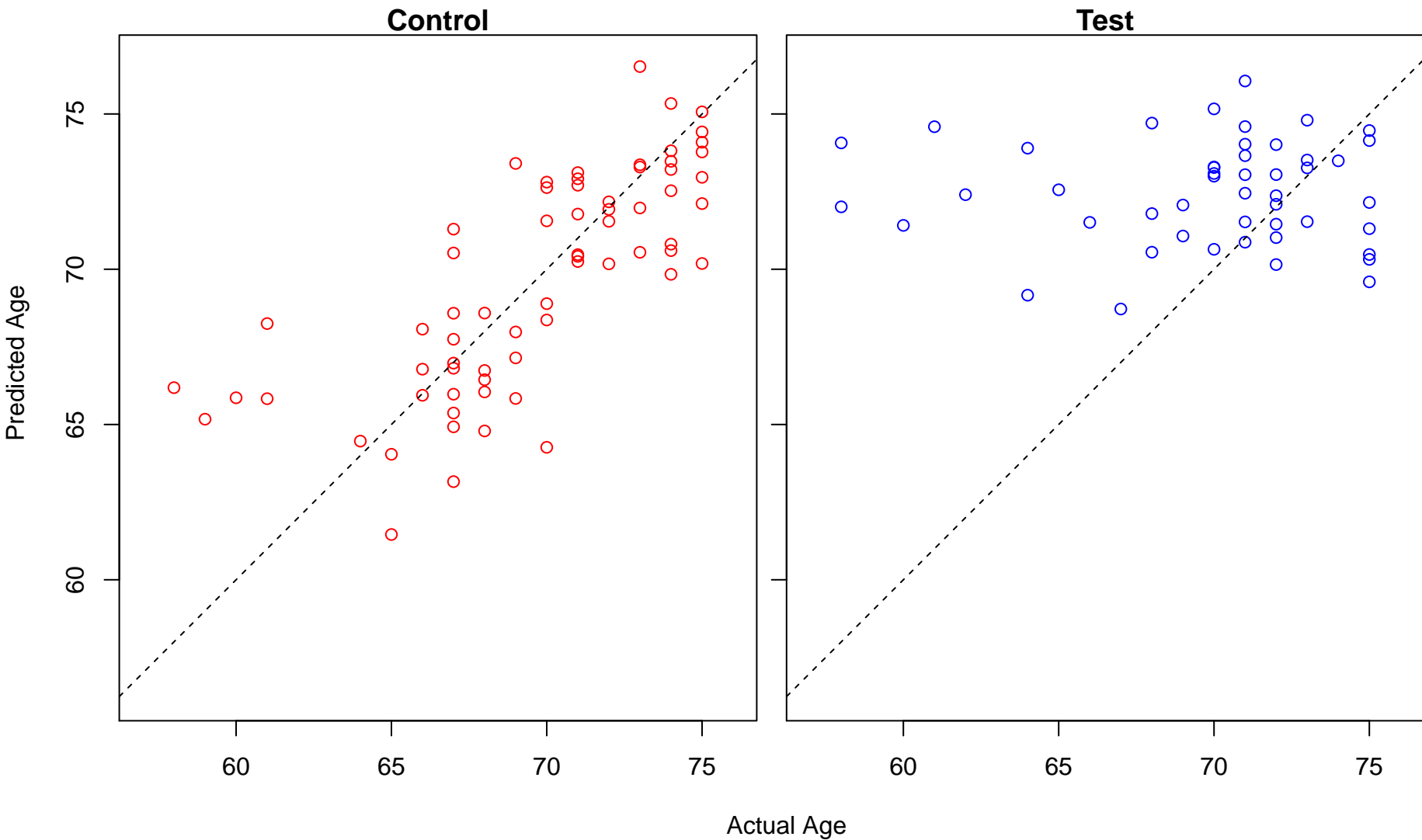
spindle organization (Score: 1.828550)



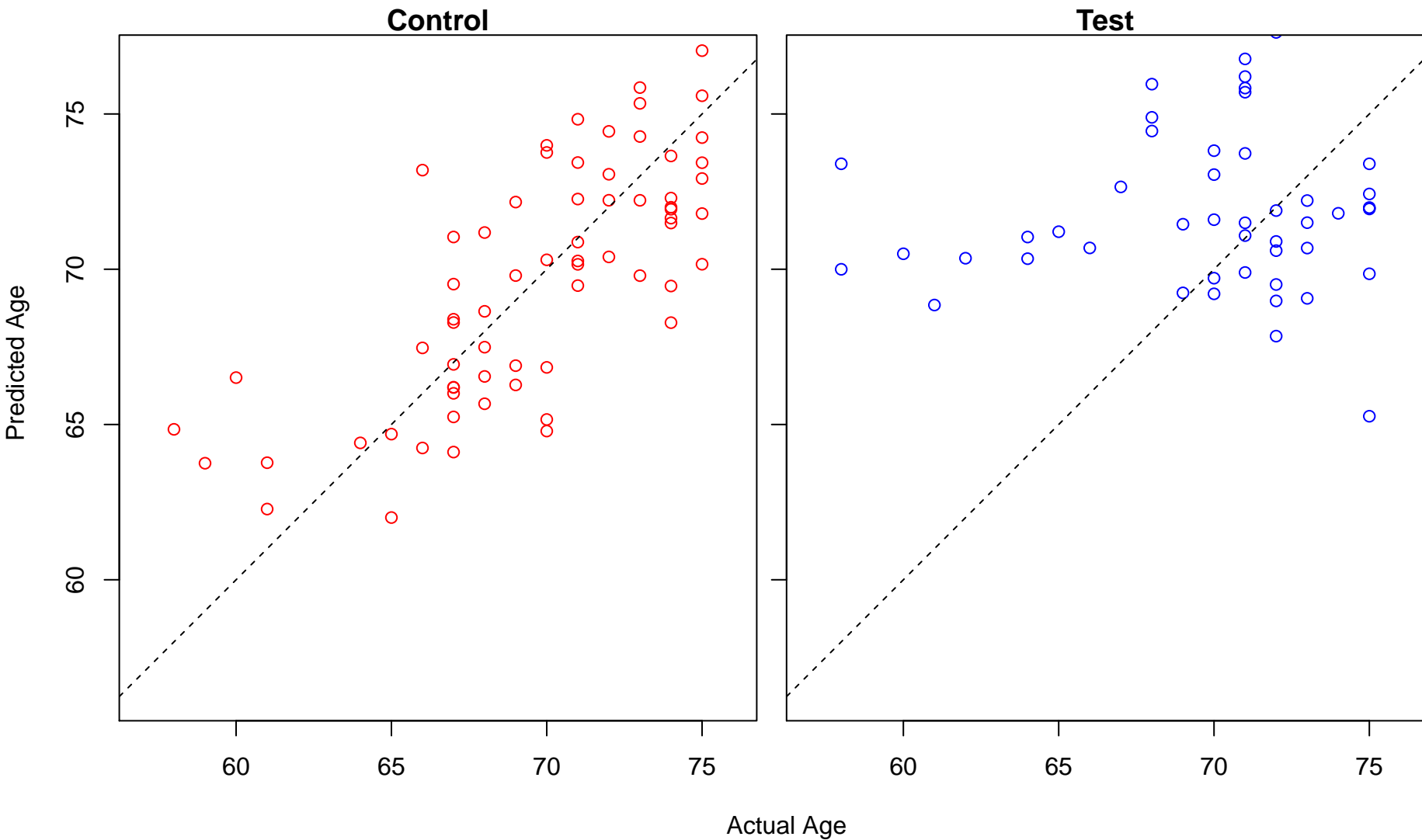
zymogen activation (Score: 1.828260)



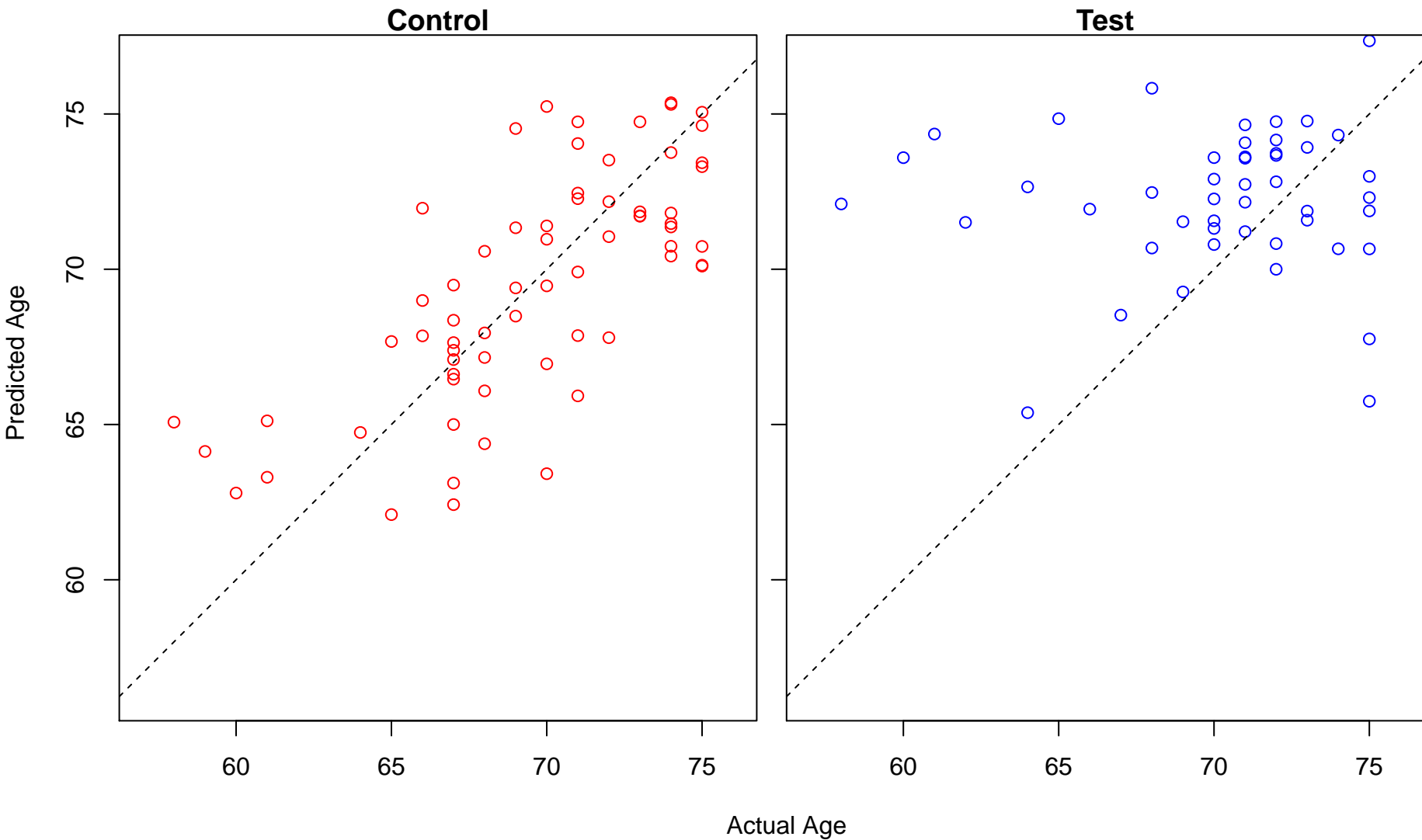
mitotic cell cycle phase transition (Score: 1.827225)



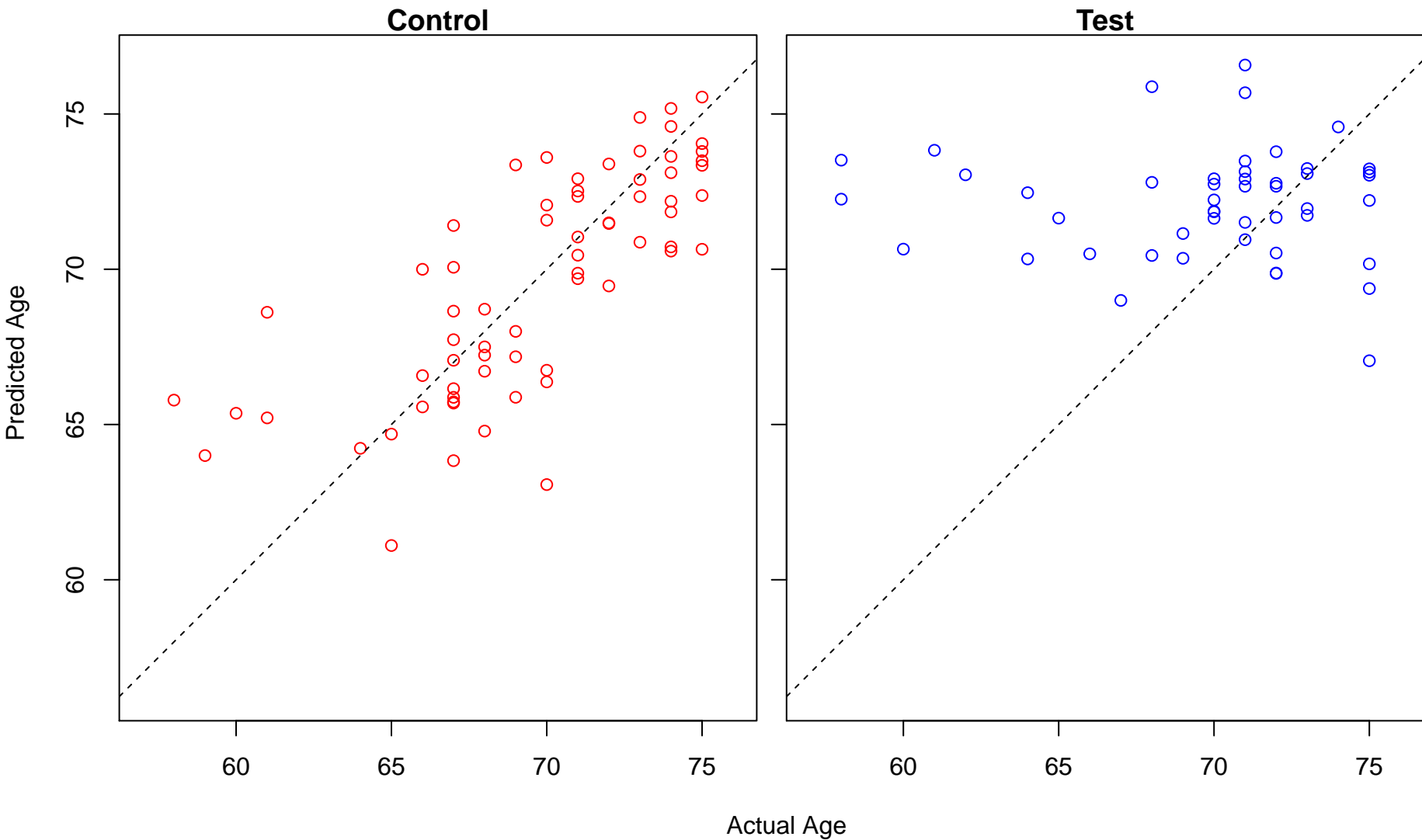
membrane lipid metabolic process (Score: 1.826742)



leukocyte mediated immunity (Score: 1.826611)

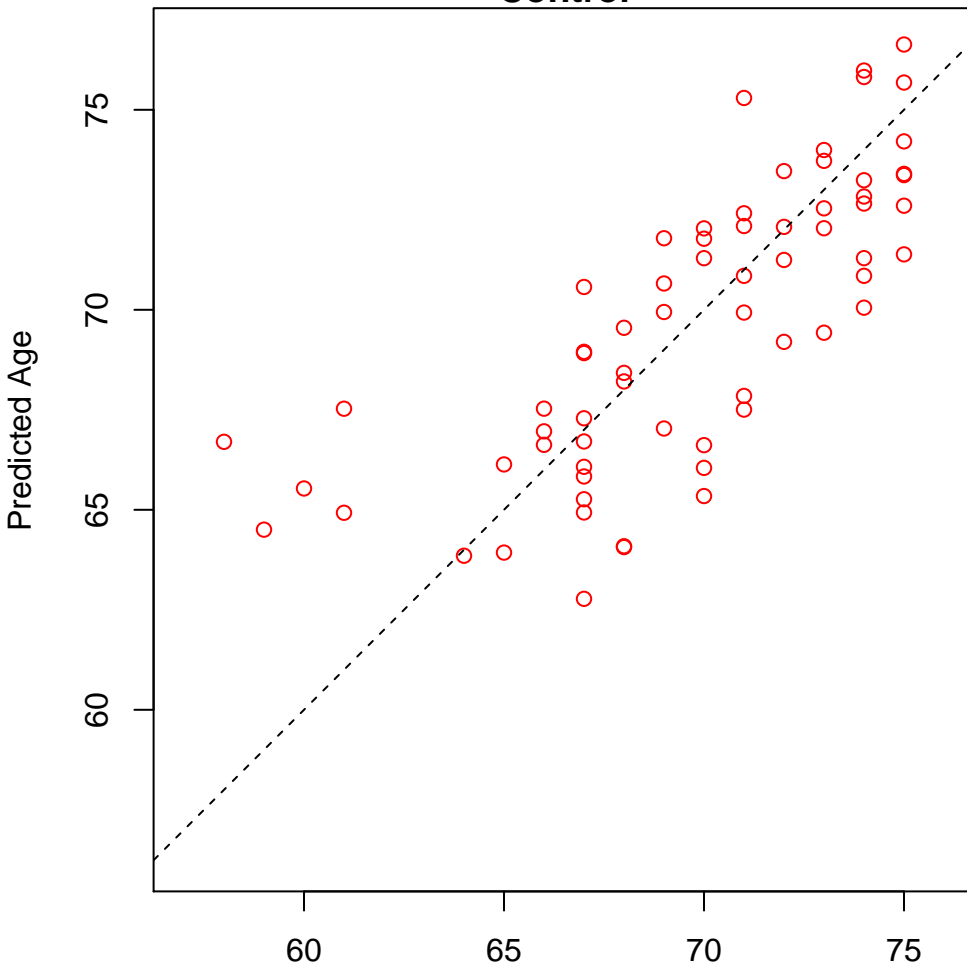


regulation of mitotic cell cycle phase transition (Score: 1.824626)

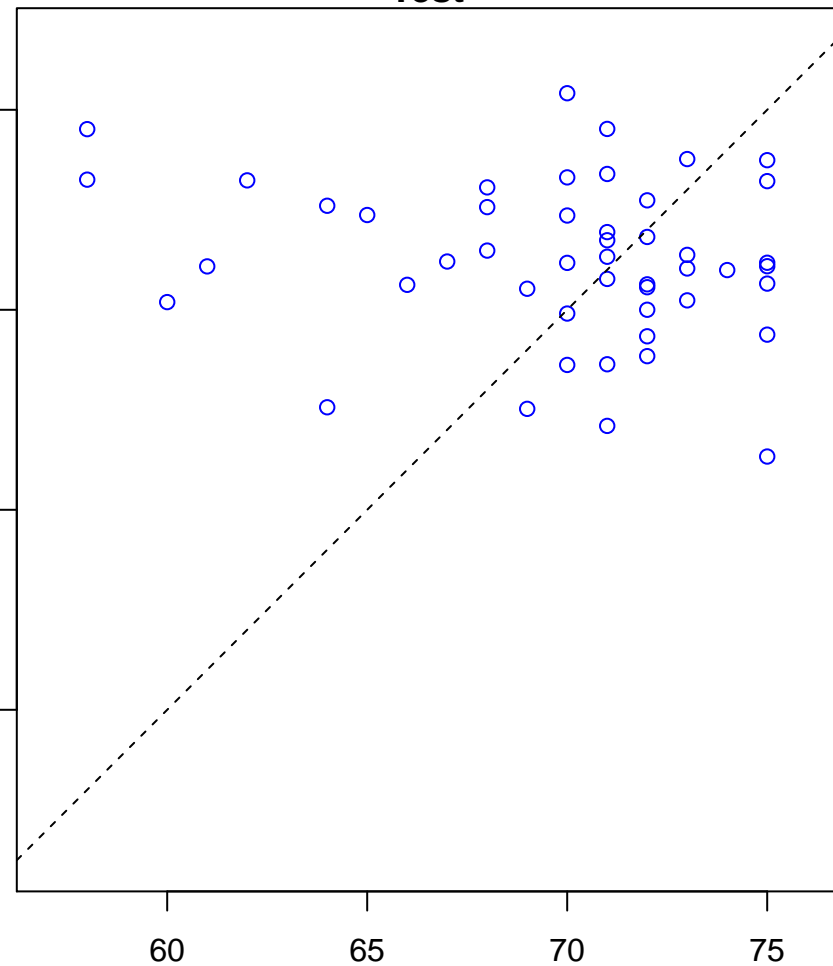


cellular response to external stimulus (Score: 1.824181)

Control

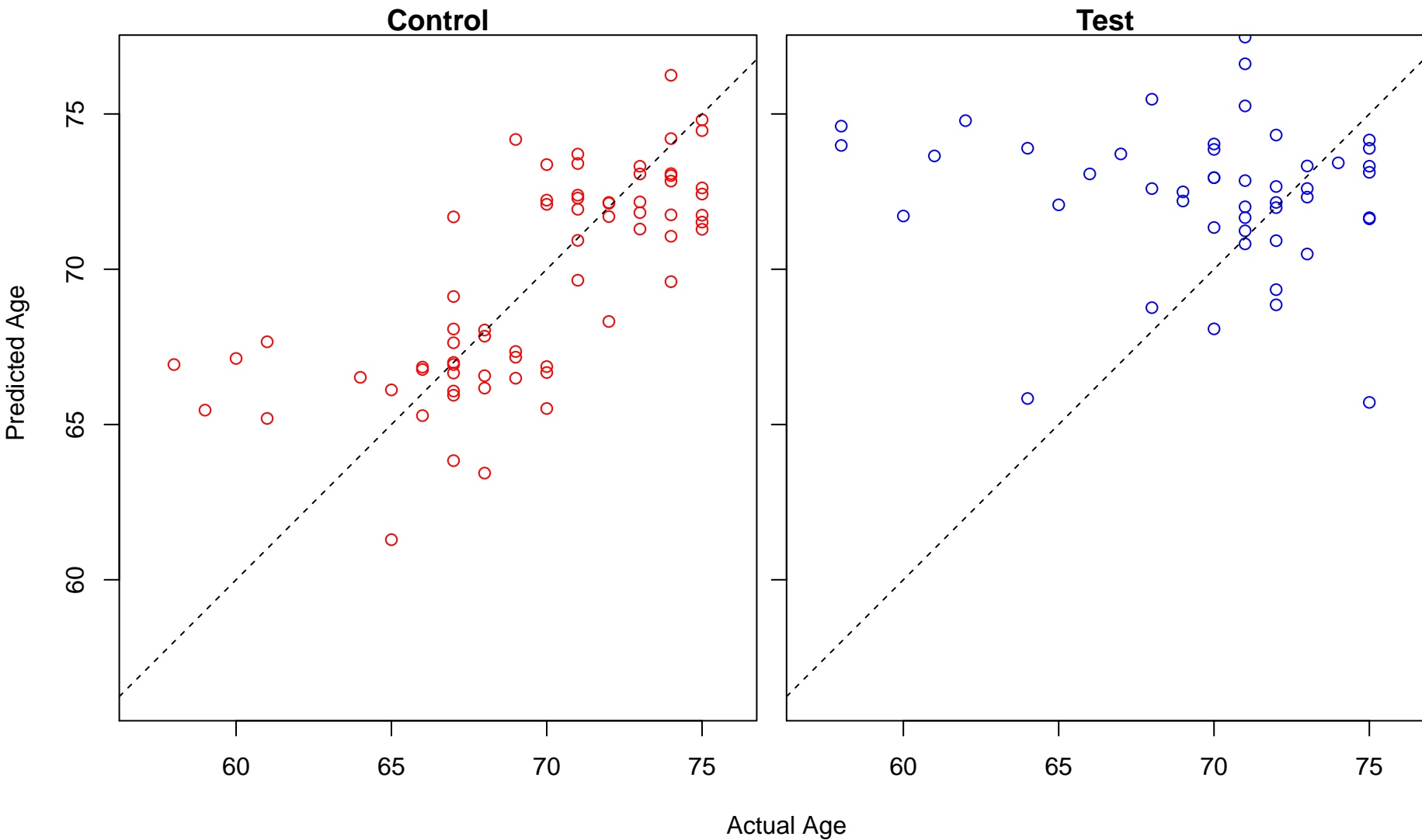


Test

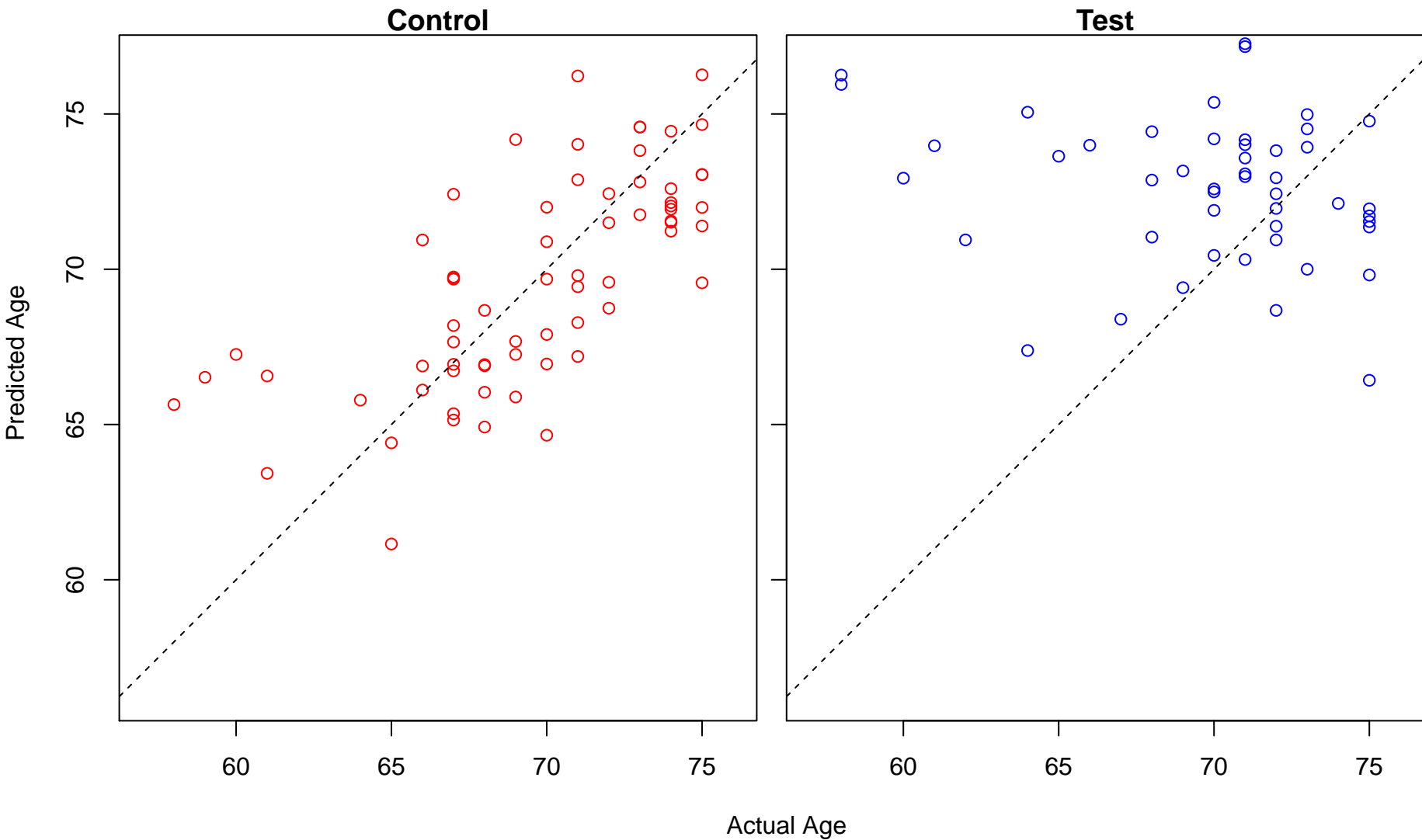


Actual Age

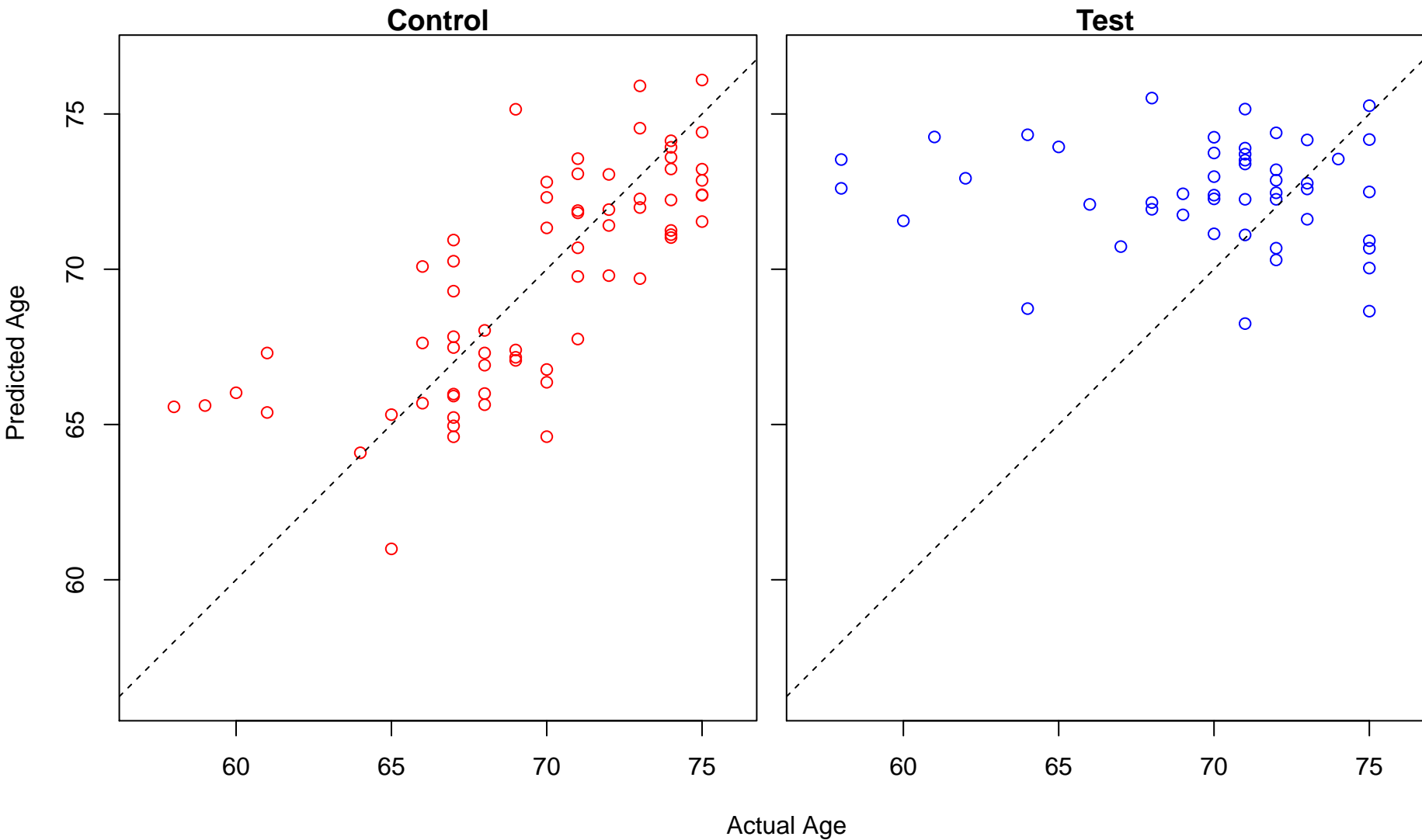
positive regulation of behavior (Score: 1.824134)



regulation of peptide transport (Score: 1.823869)

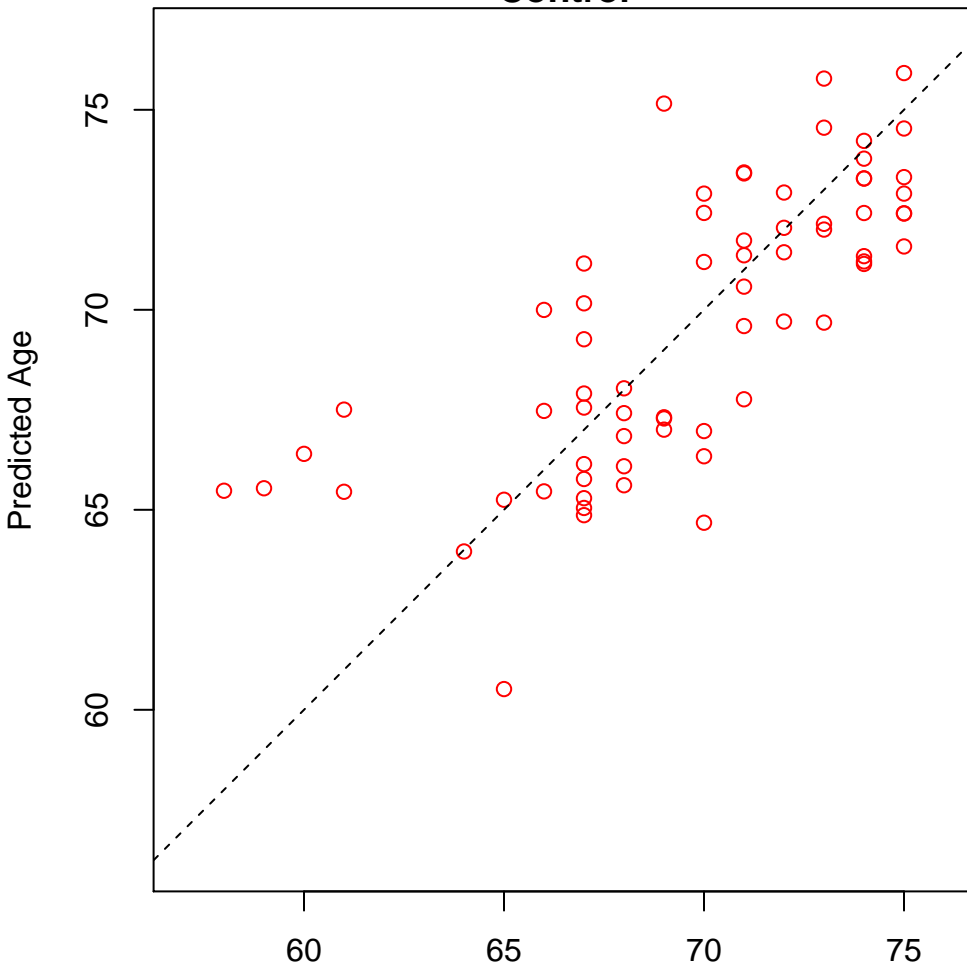


innate immune response-activating signal transduction (Score: 1.823433)

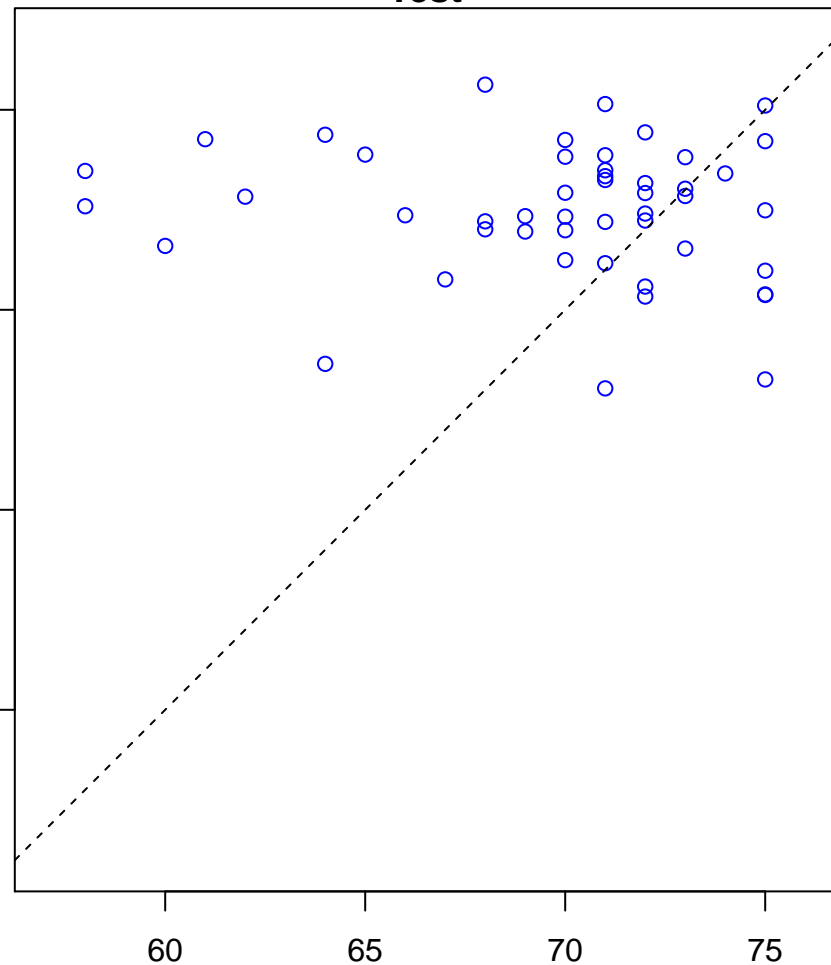


activation of innate immune response (Score: 1.820900)

Control

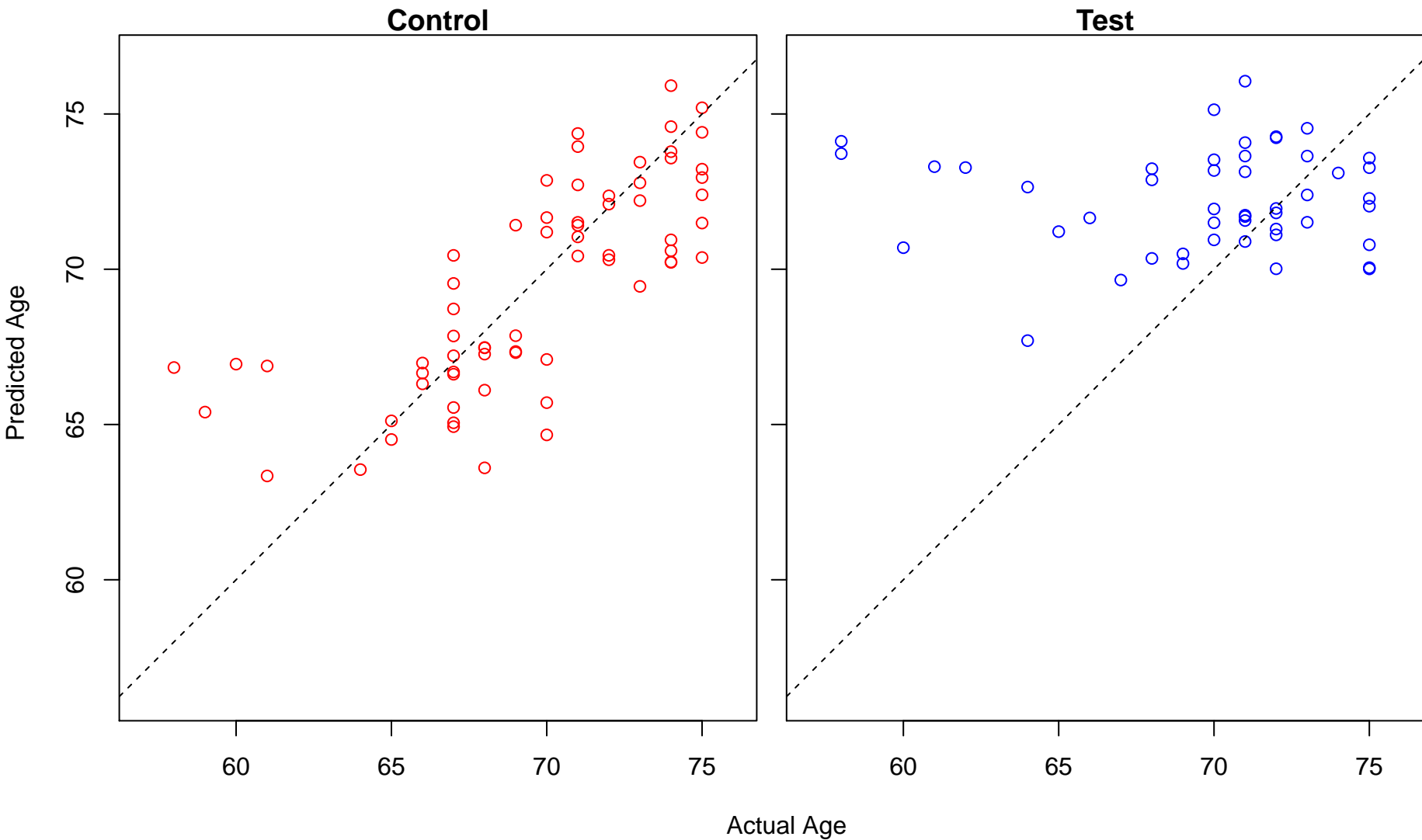


Test



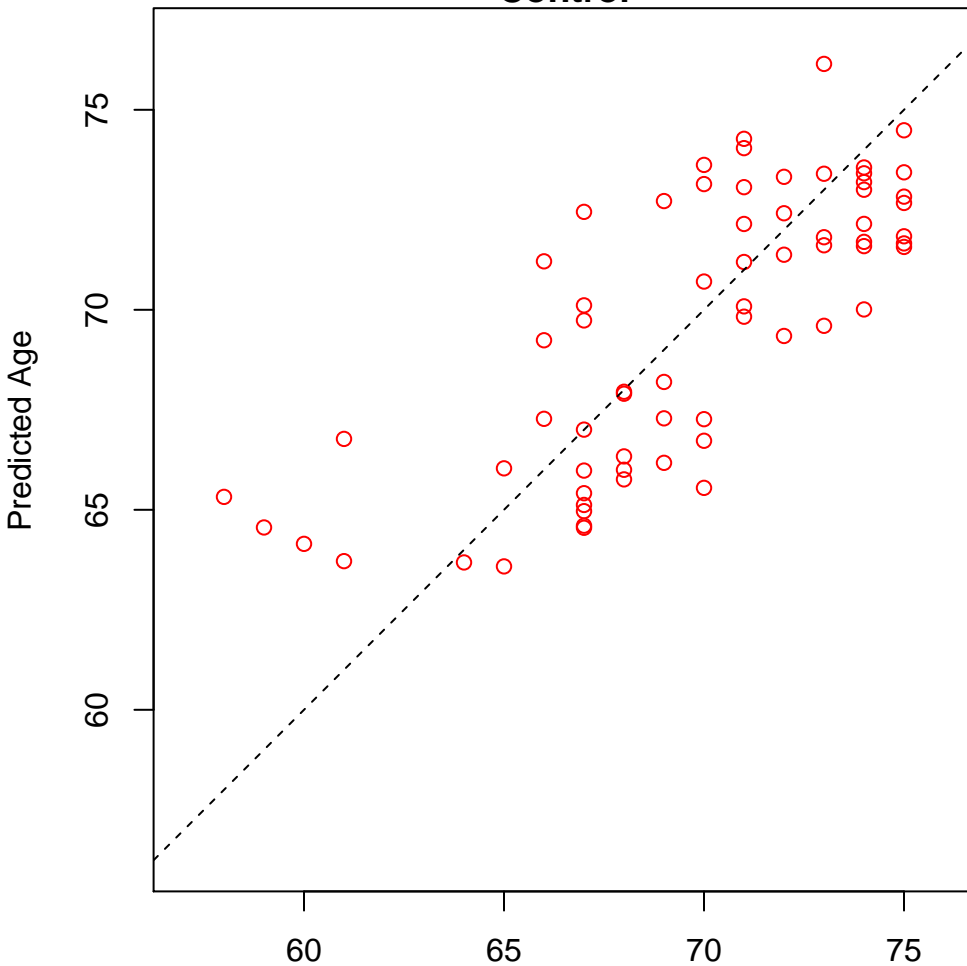
Actual Age

actin cytoskeleton organization (Score: 1.817891)

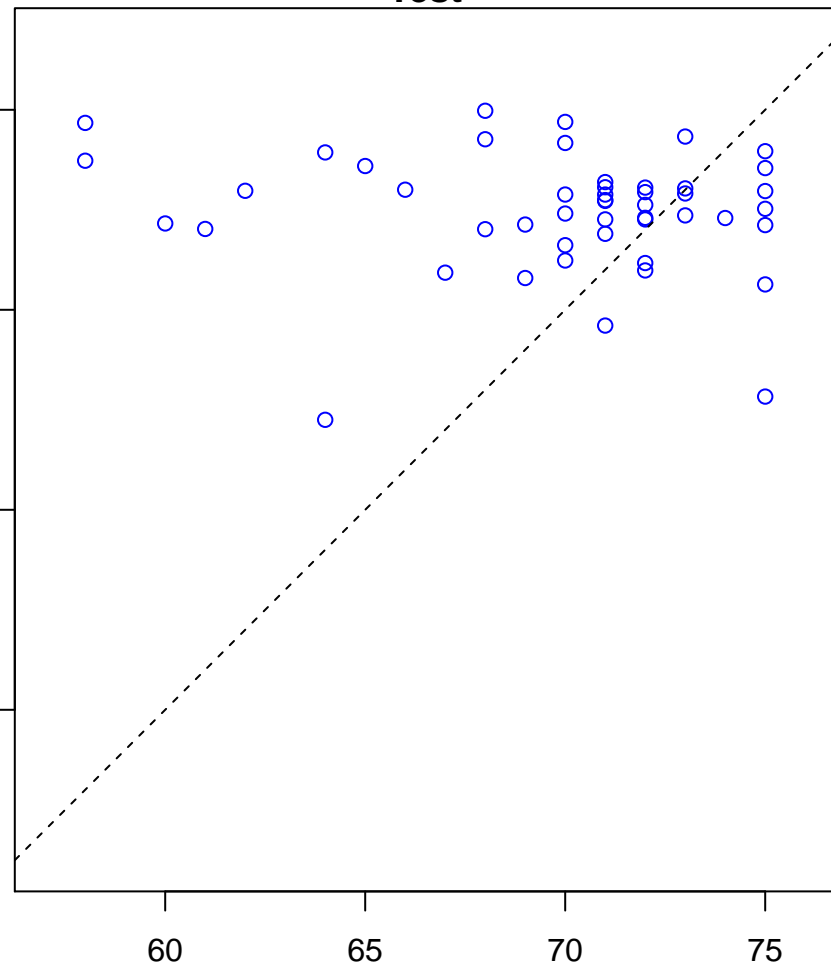


cellular response to abiotic stimulus (Score: 1.817656)

Control

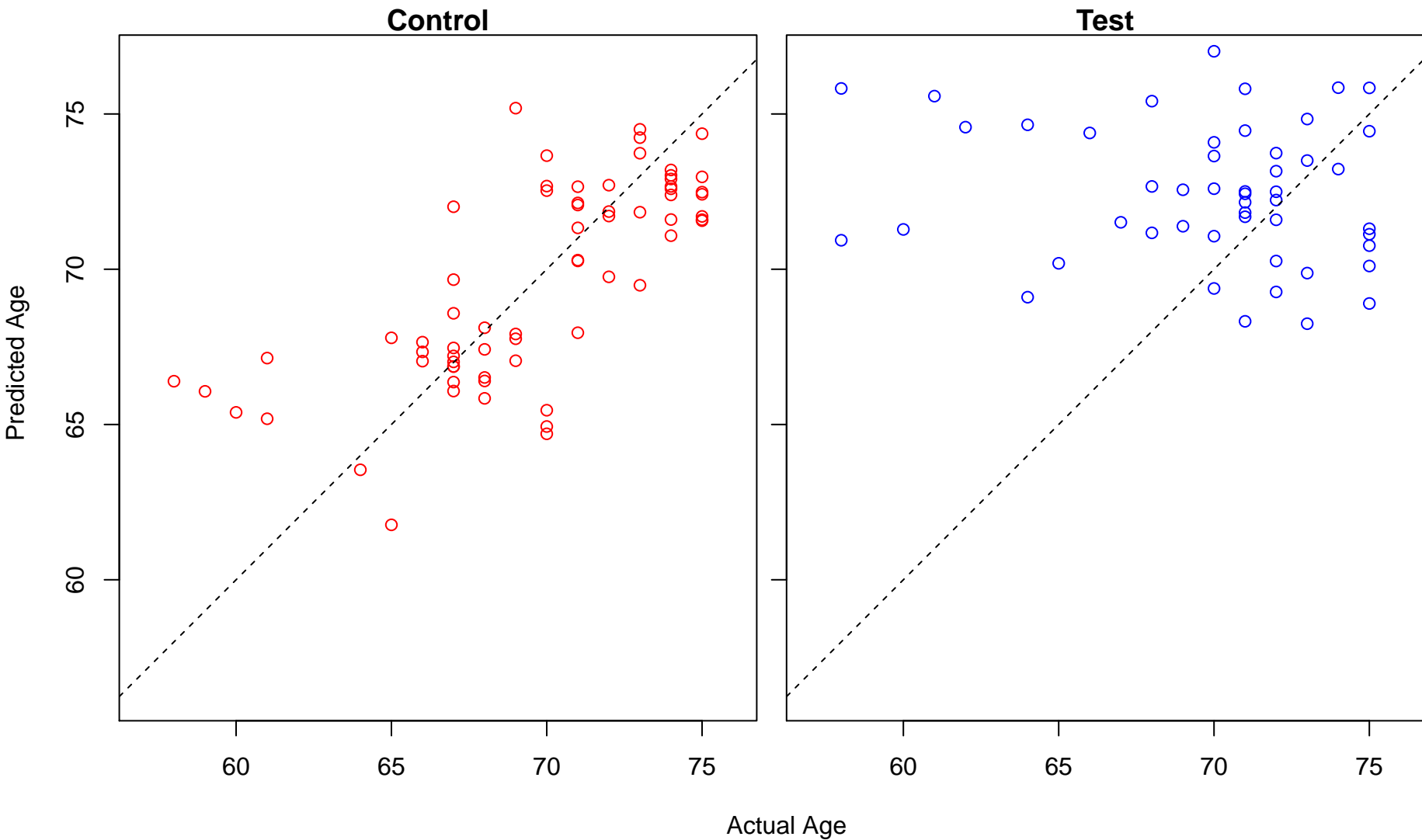


Test

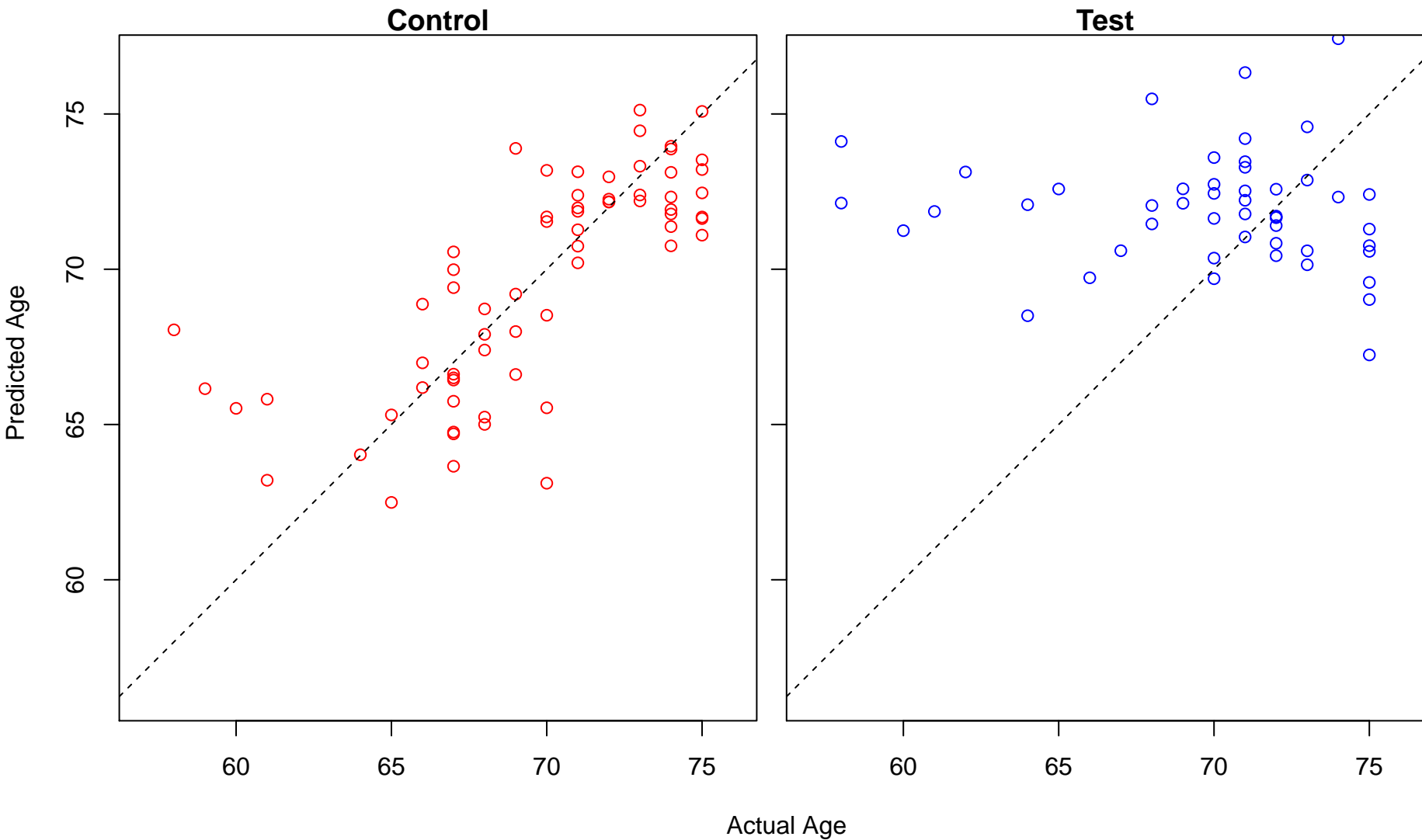


Actual Age

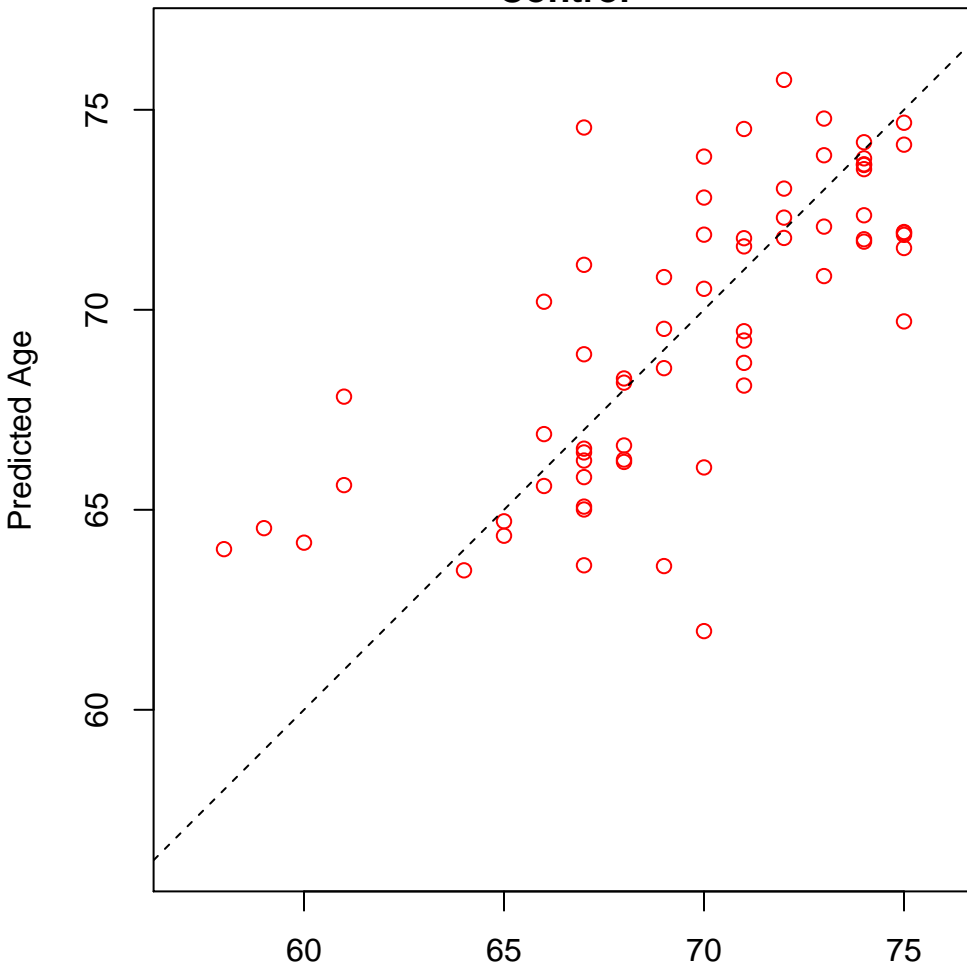
DNA biosynthetic process (Score: 1.816572)



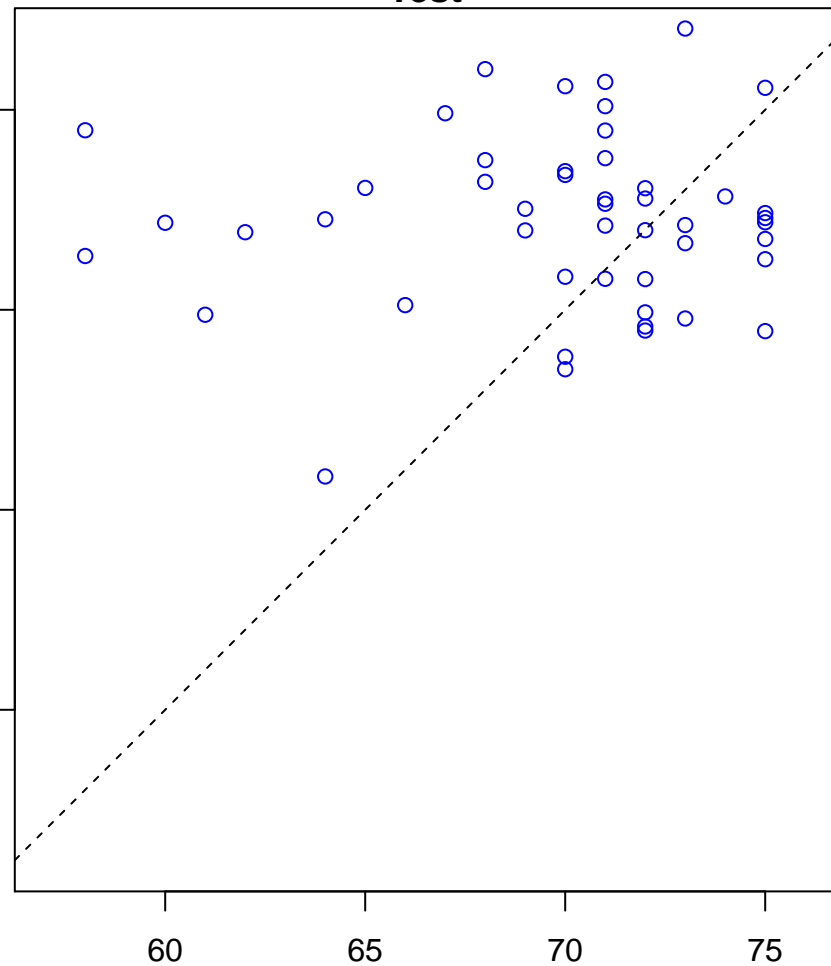
RNA processing (Score: 1.816428)



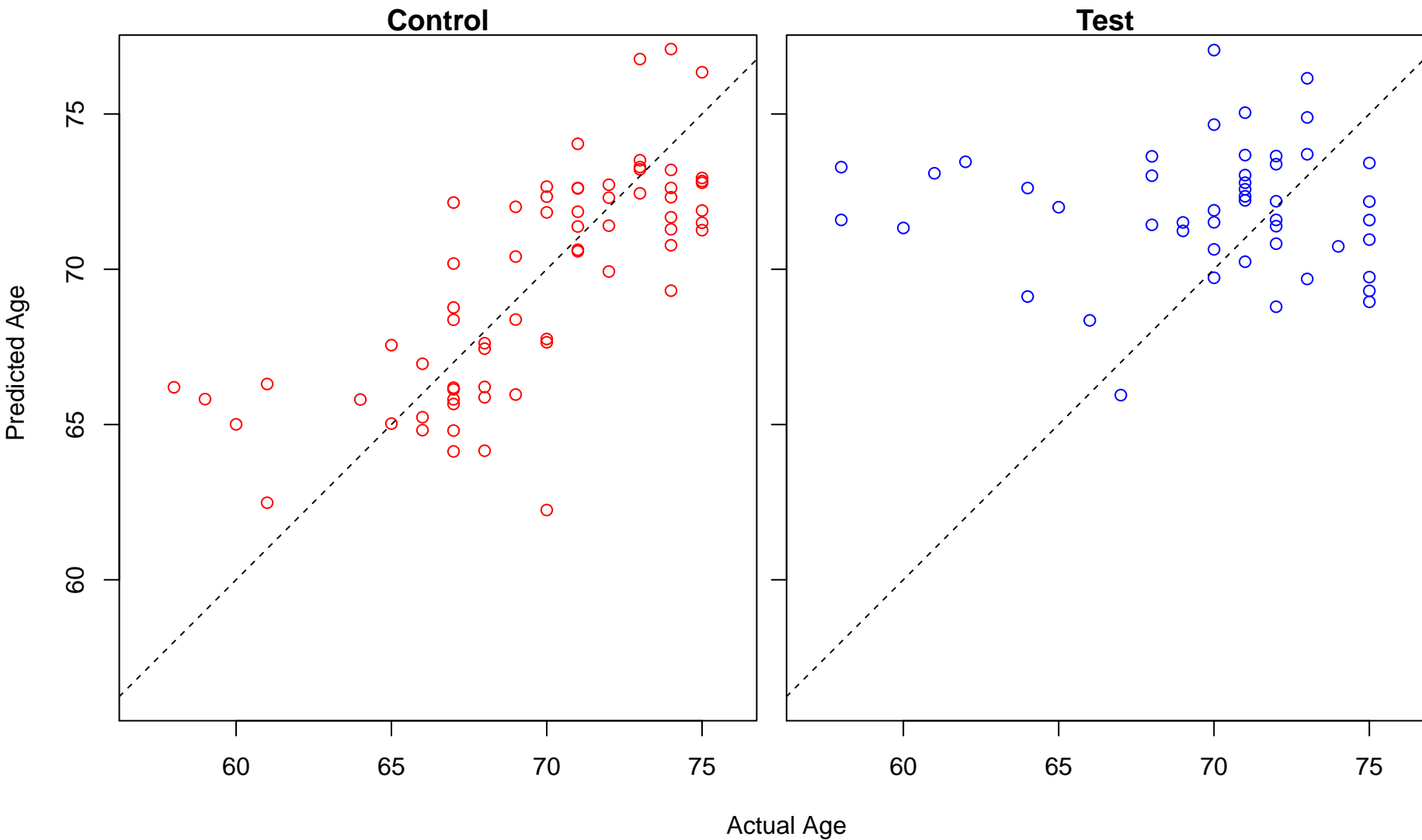
Control



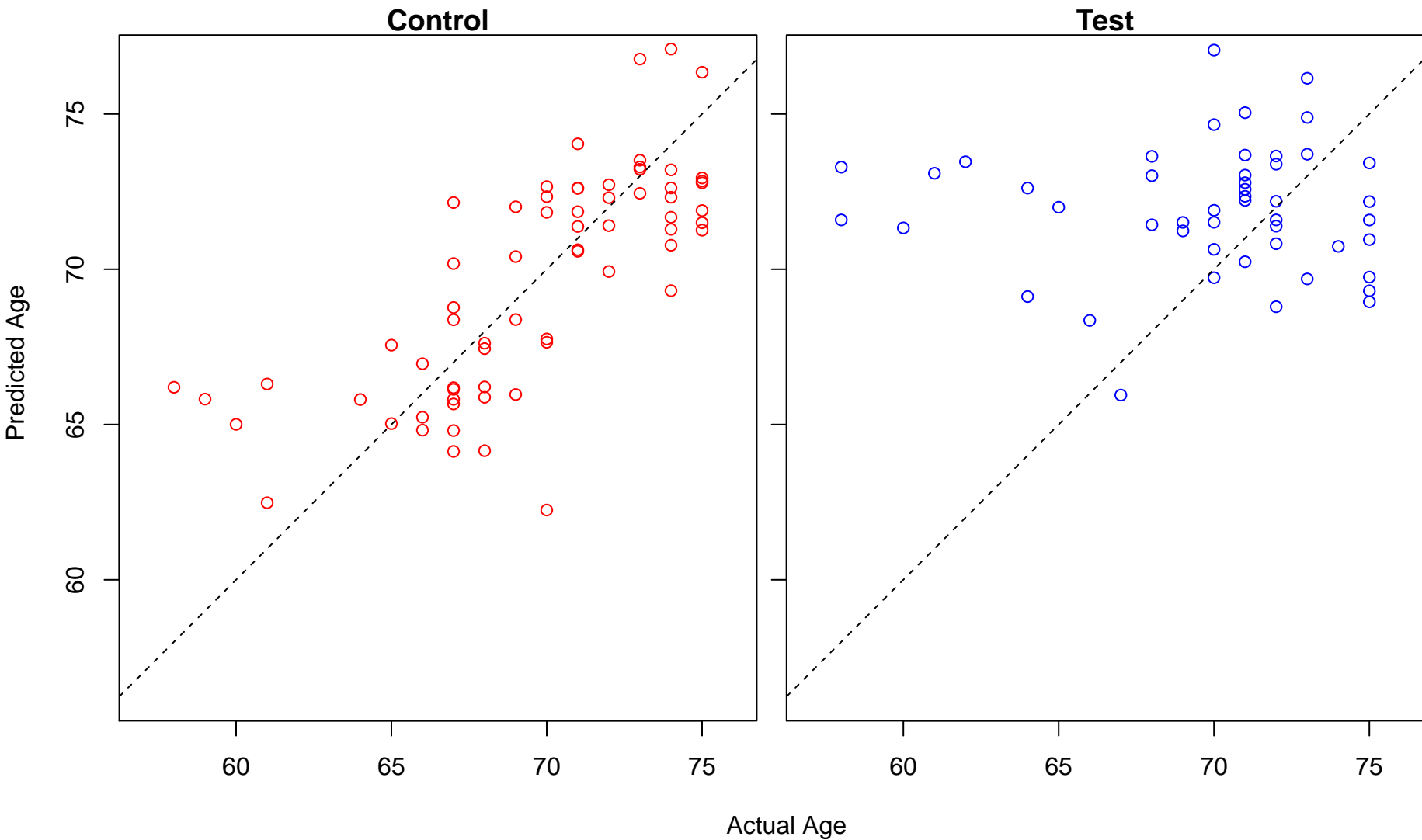
Test



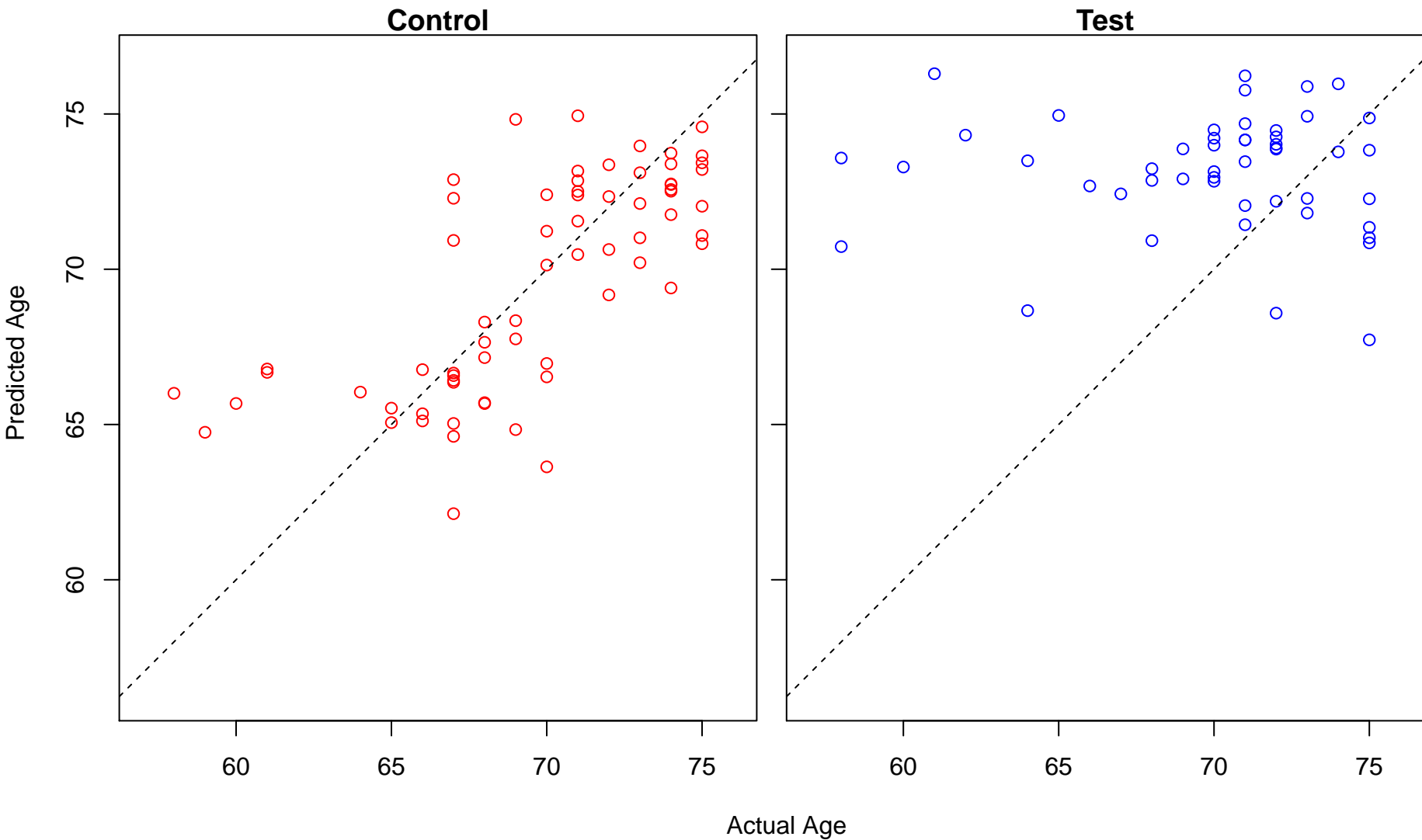
ribonucleoside triphosphate metabolic process (Score: 1.814242)



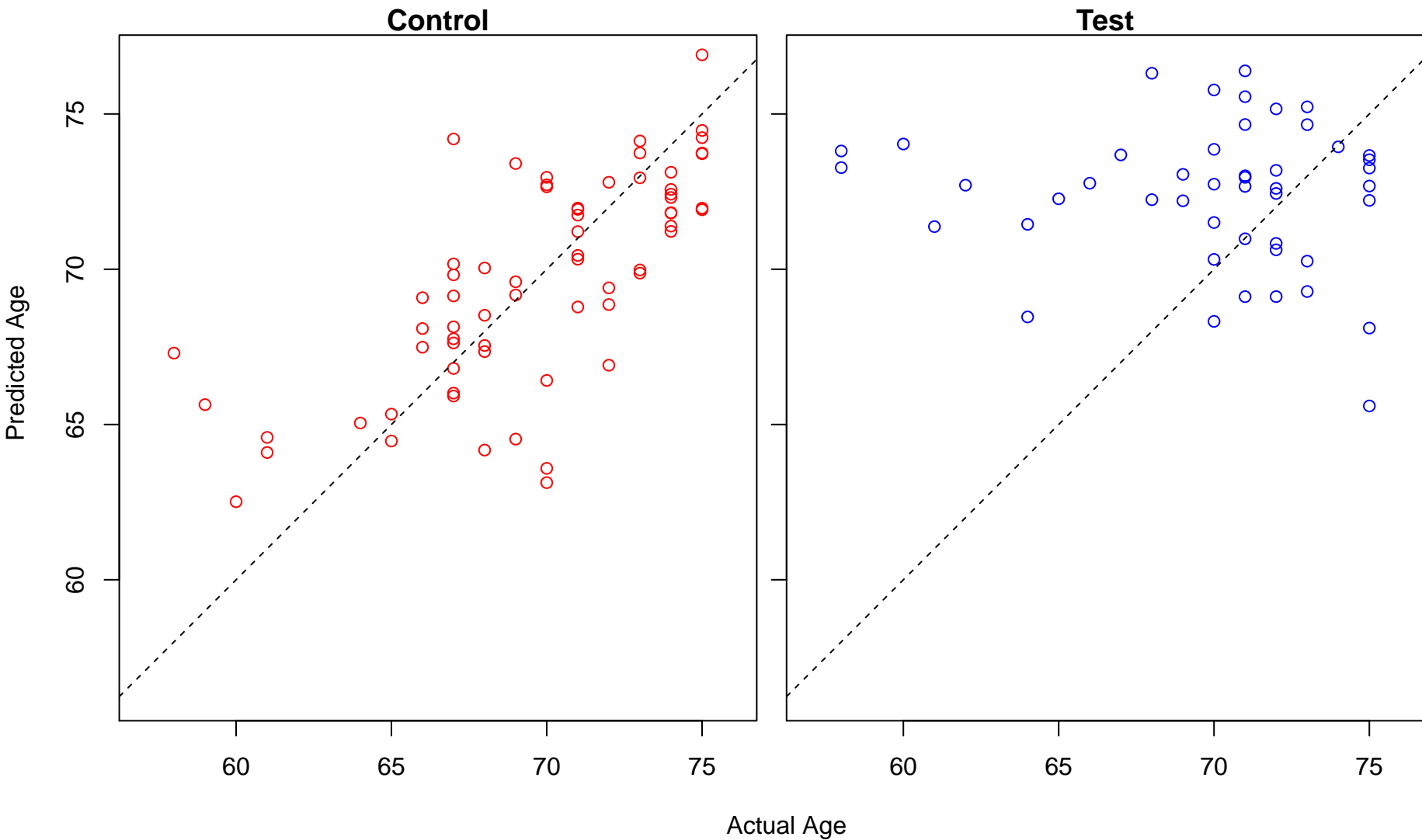
purine ribonucleoside triphosphate metabolic process (Score: 1.814242)



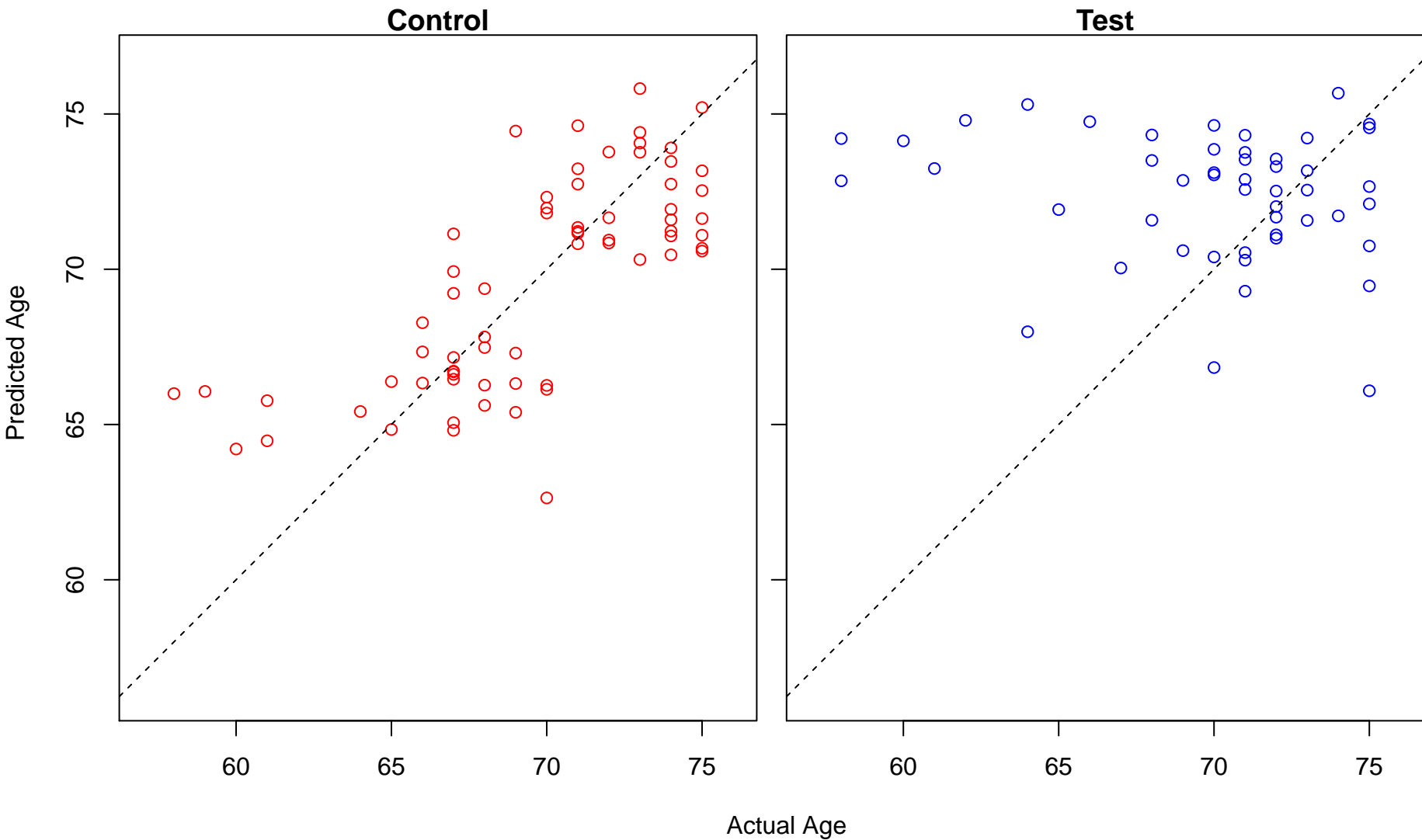
alpha-amino acid metabolic process (Score: 1.813991)



intrinsic apoptotic signaling pathway in response to DNA damage (Score: 1.813638)

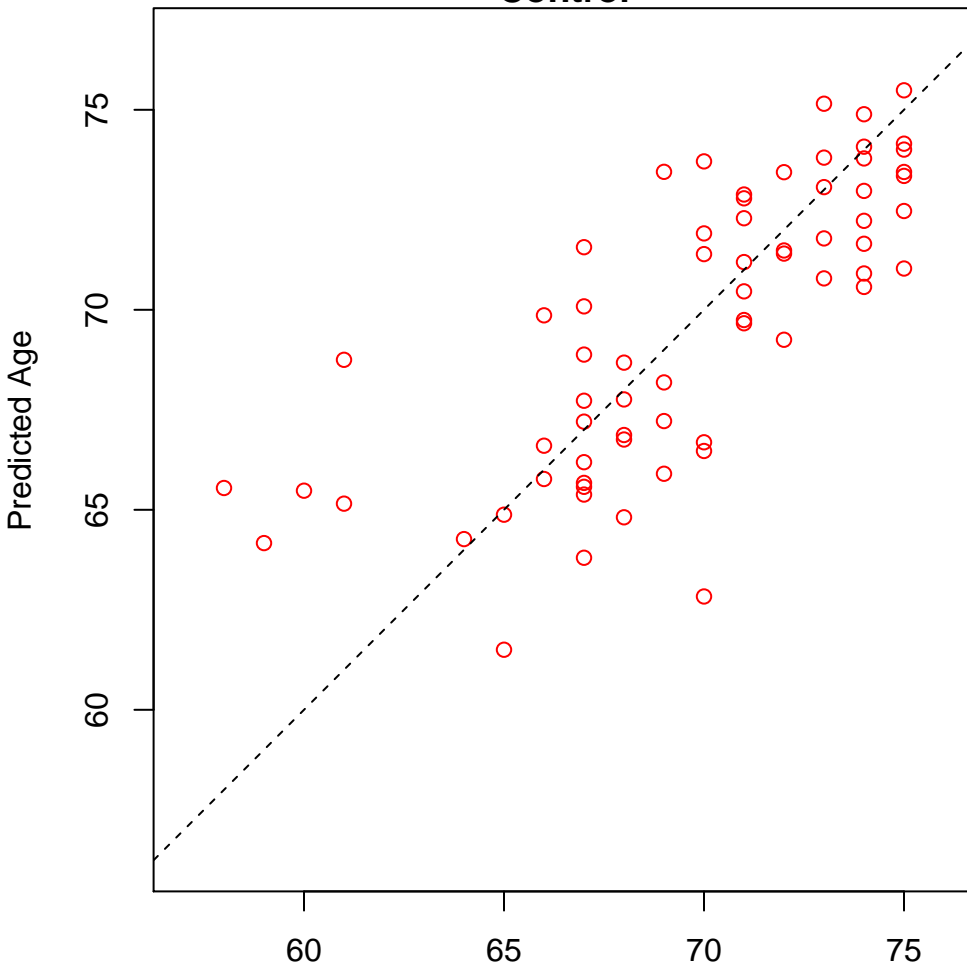


lipid modification (Score: 1.811515)

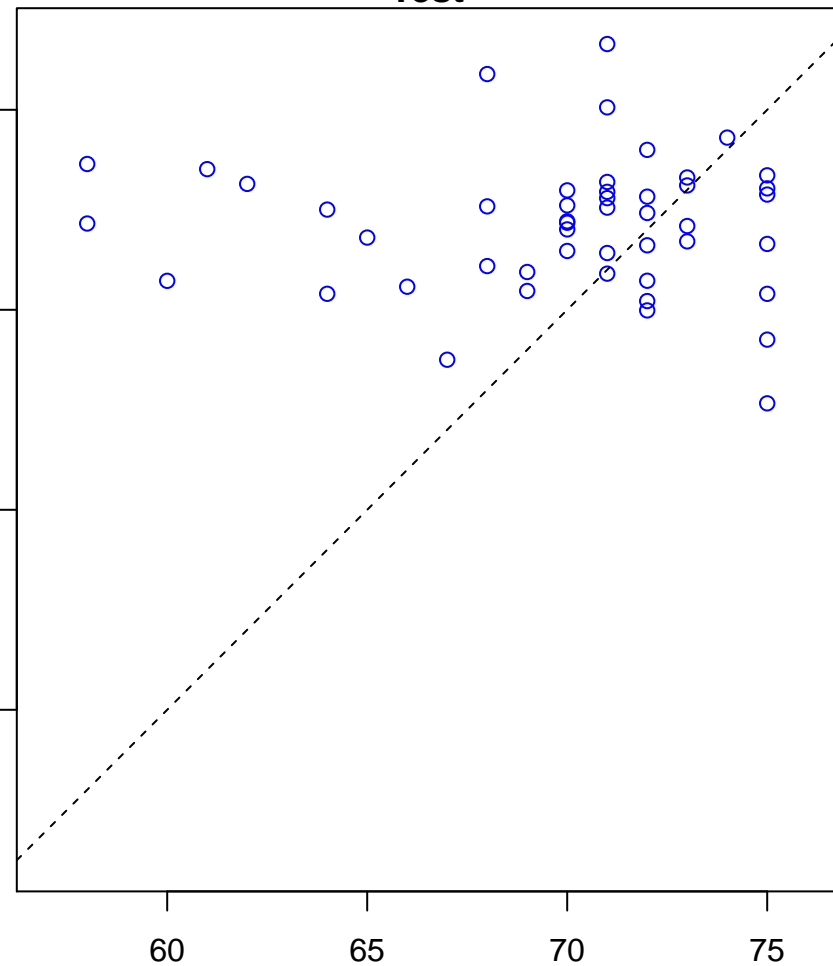


regulation of cell cycle phase transition (Score: 1.809622)

Control

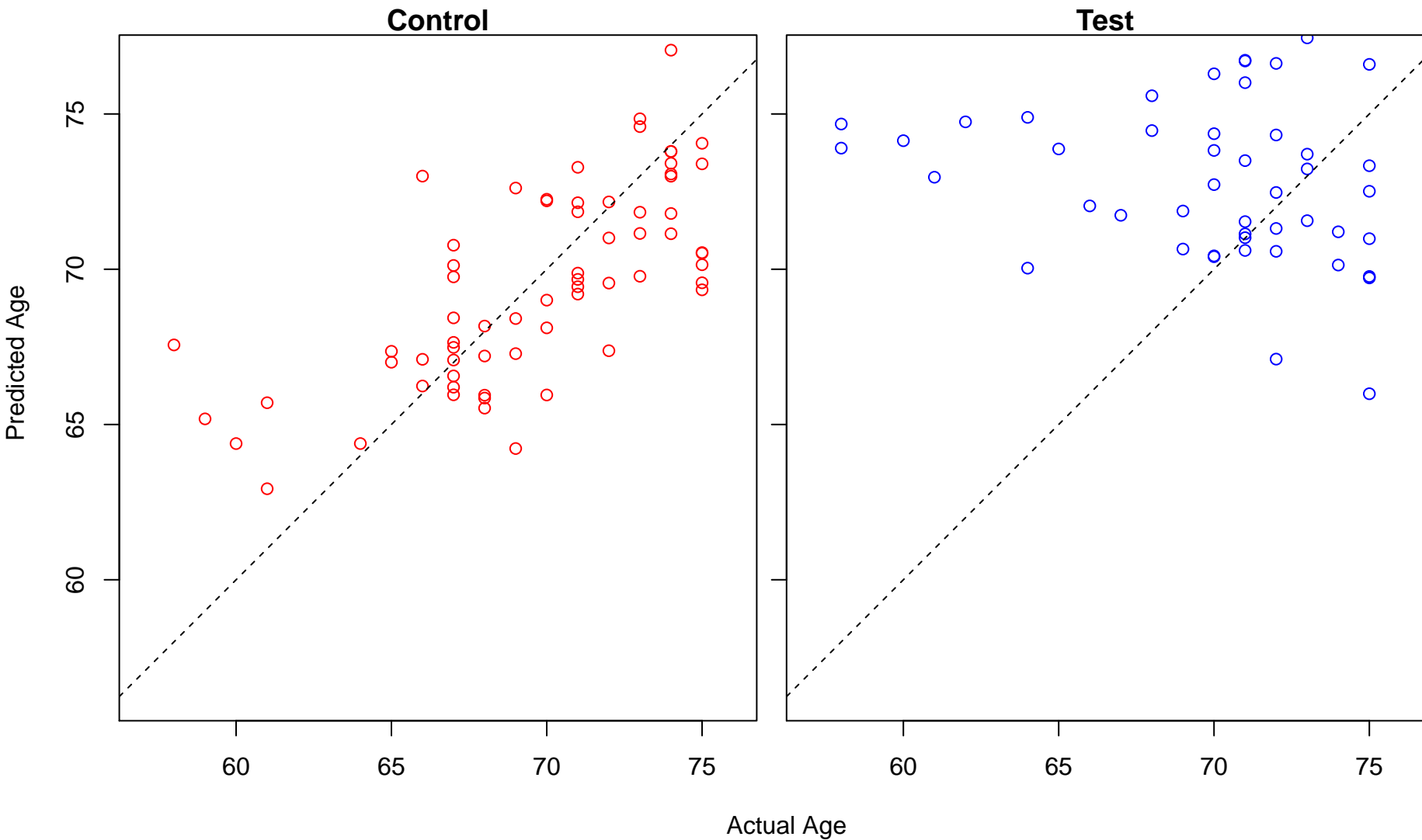


Test

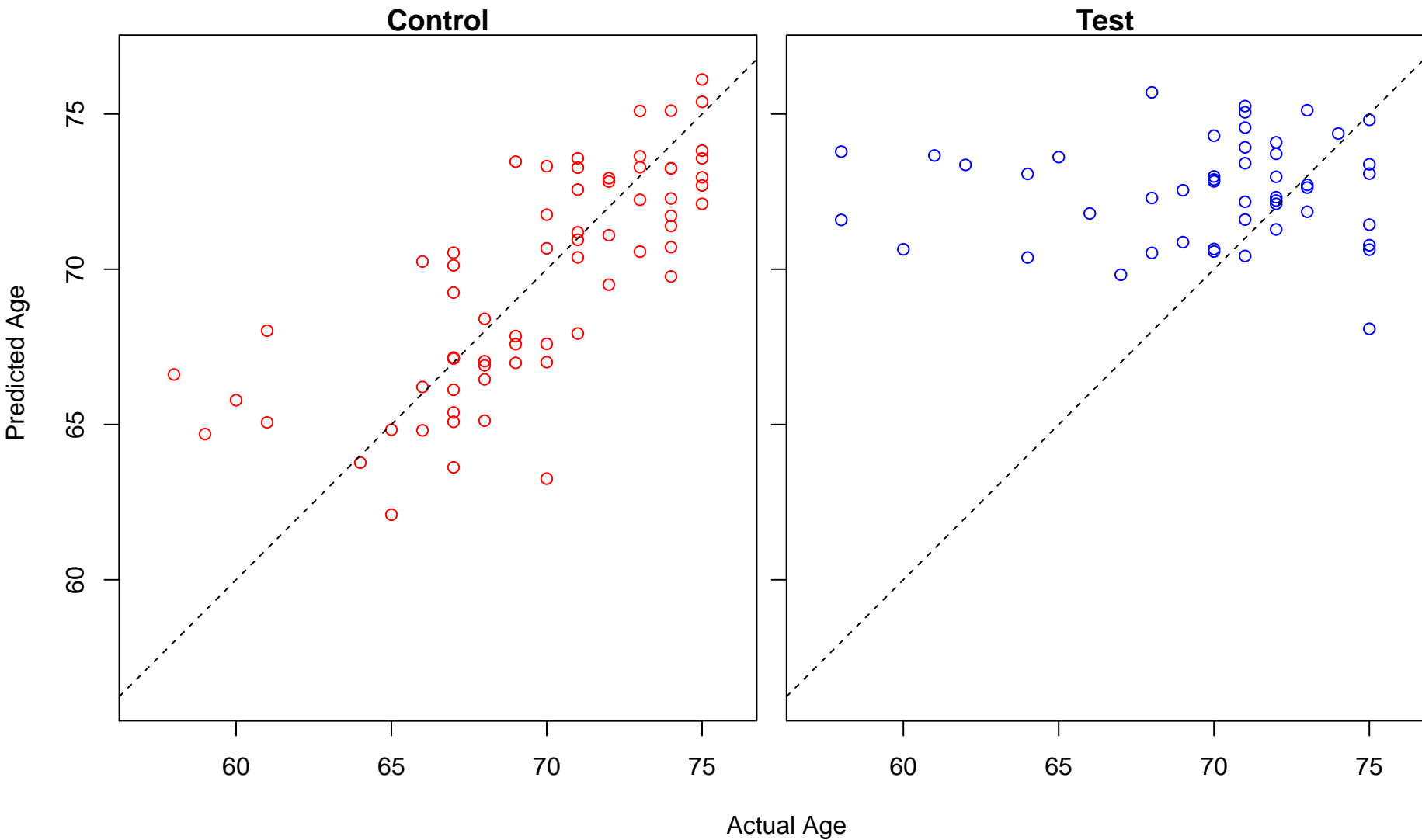


Actual Age

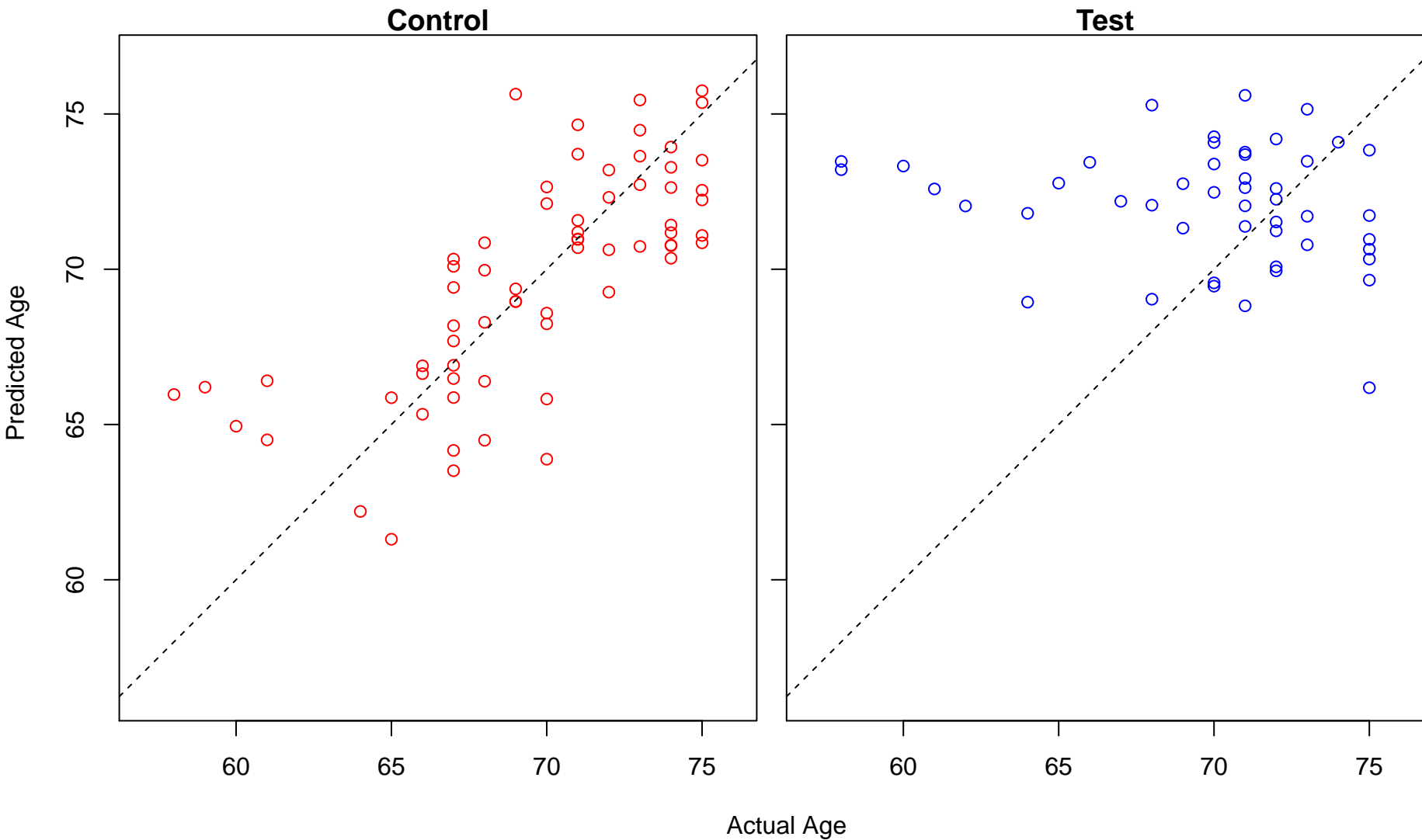
negative regulation of TOR signaling (Score: 1.809351)



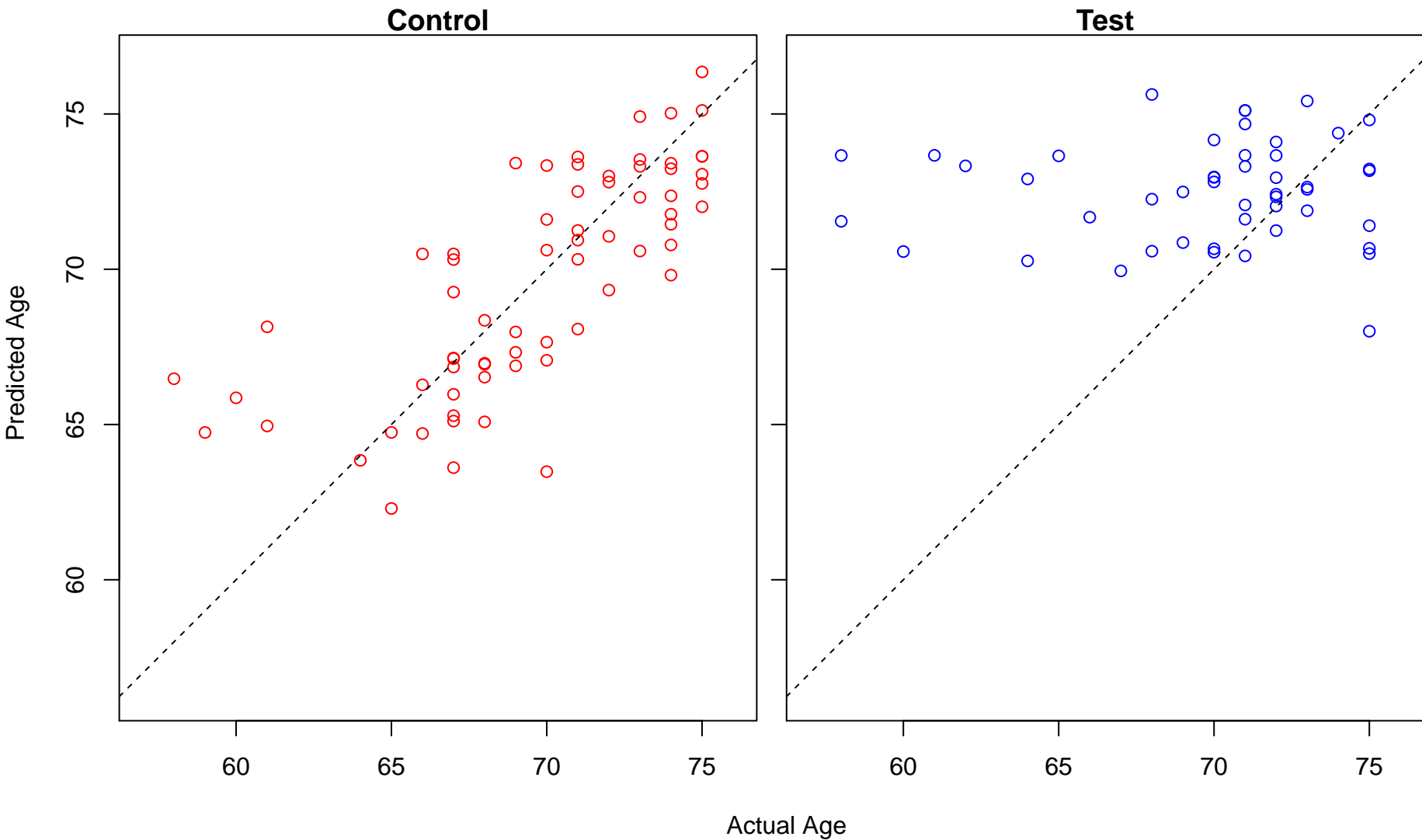
regulation of protein ubiquitination (Score: 1.809192)



tRNA processing (Score: 1.808407)

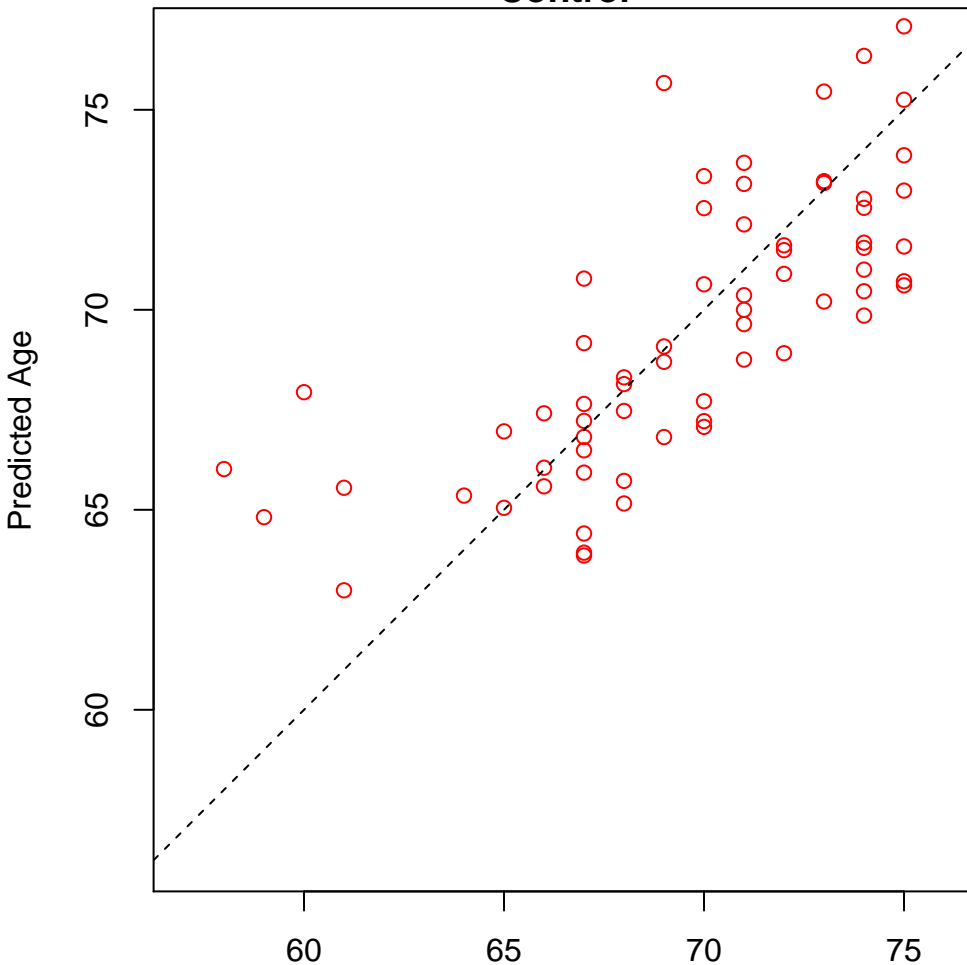


regulation of protein modification by small protein conjugation or removal (Score: 1.808272)

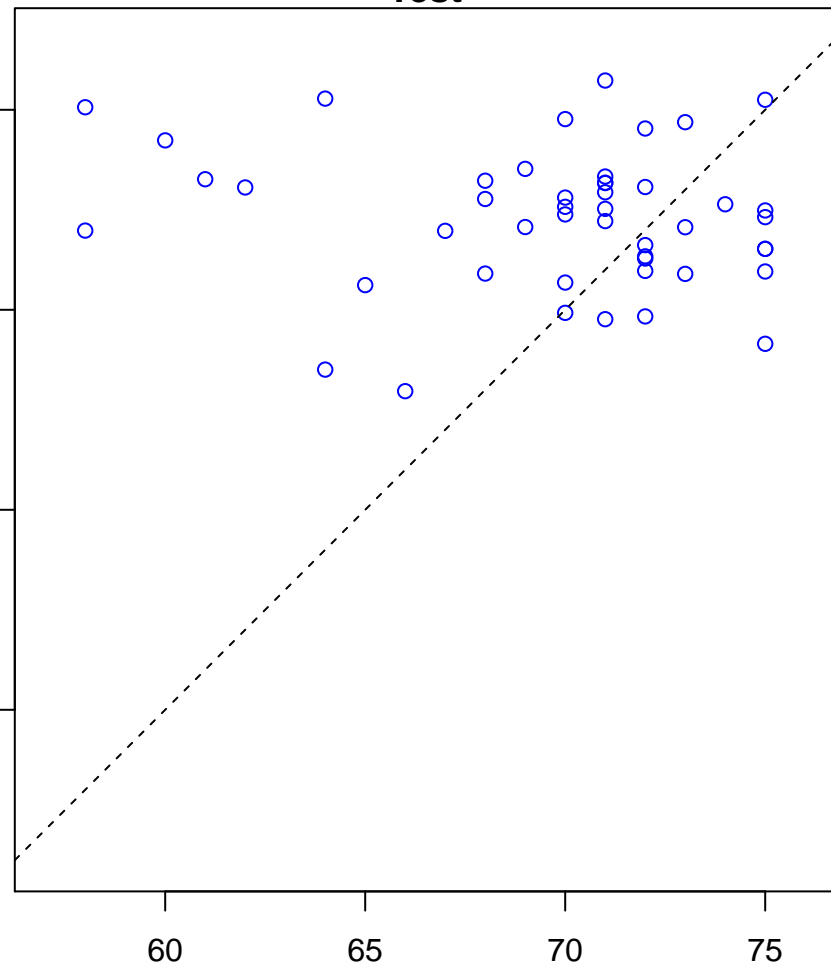


protein localization to mitochondrion (Score: 1.808015)

Control

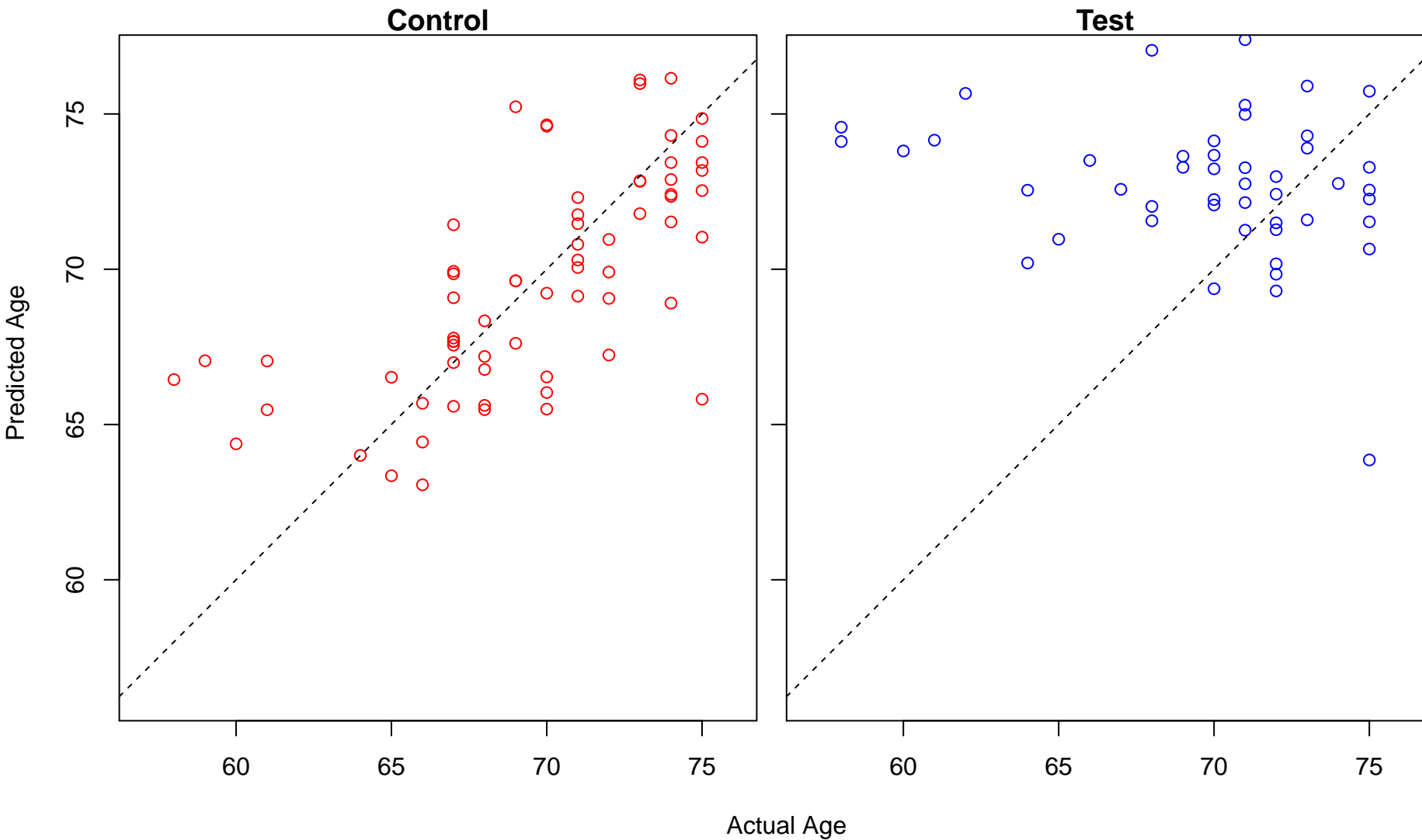


Test

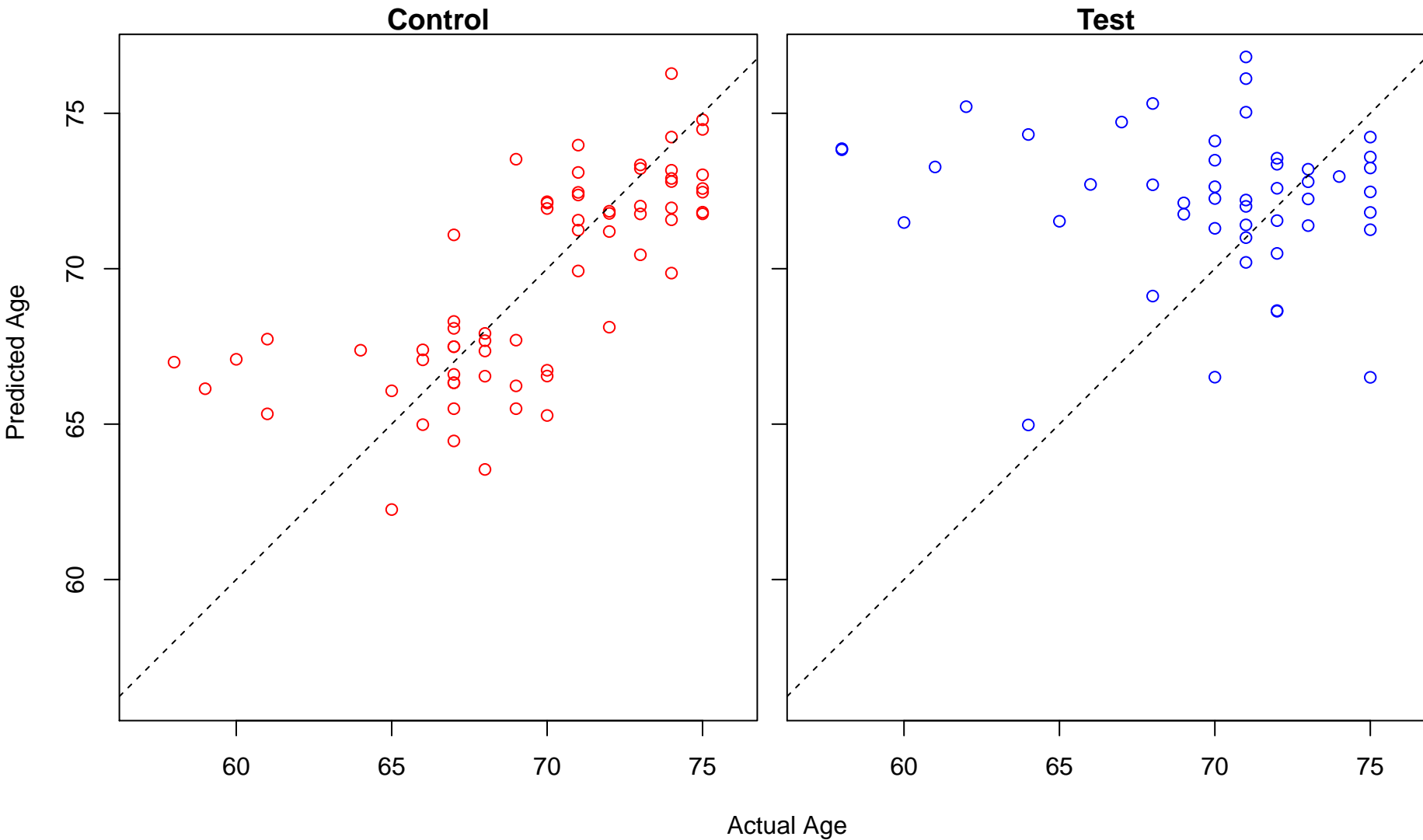


Actual Age

response to hypoxia (Score: 1.807111)

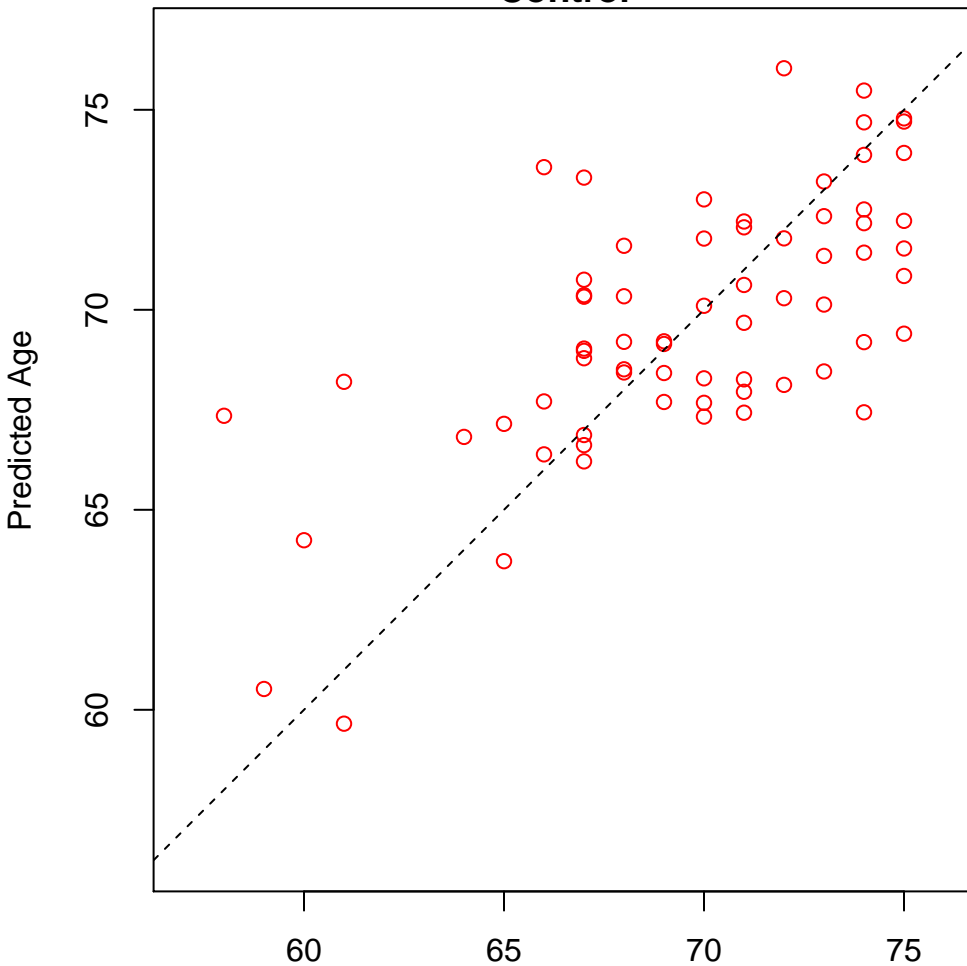


positive regulation of leukocyte chemotaxis (Score: 1.807056)

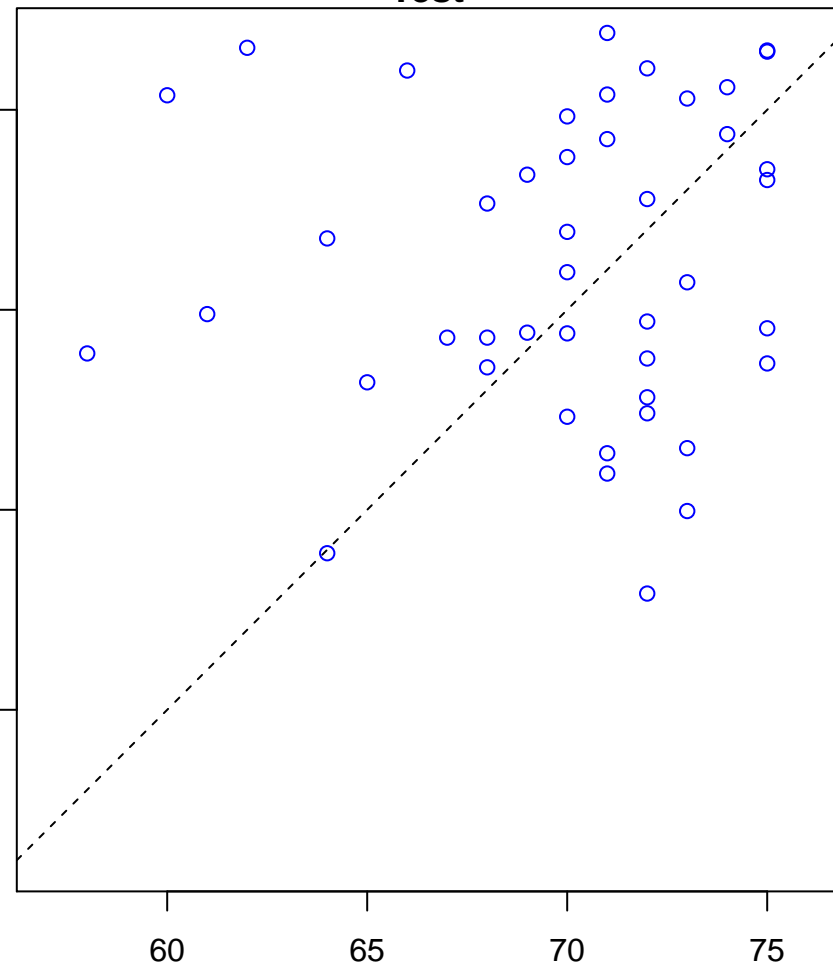


glutamate receptor signaling pathway (Score: 1.806837)

Control

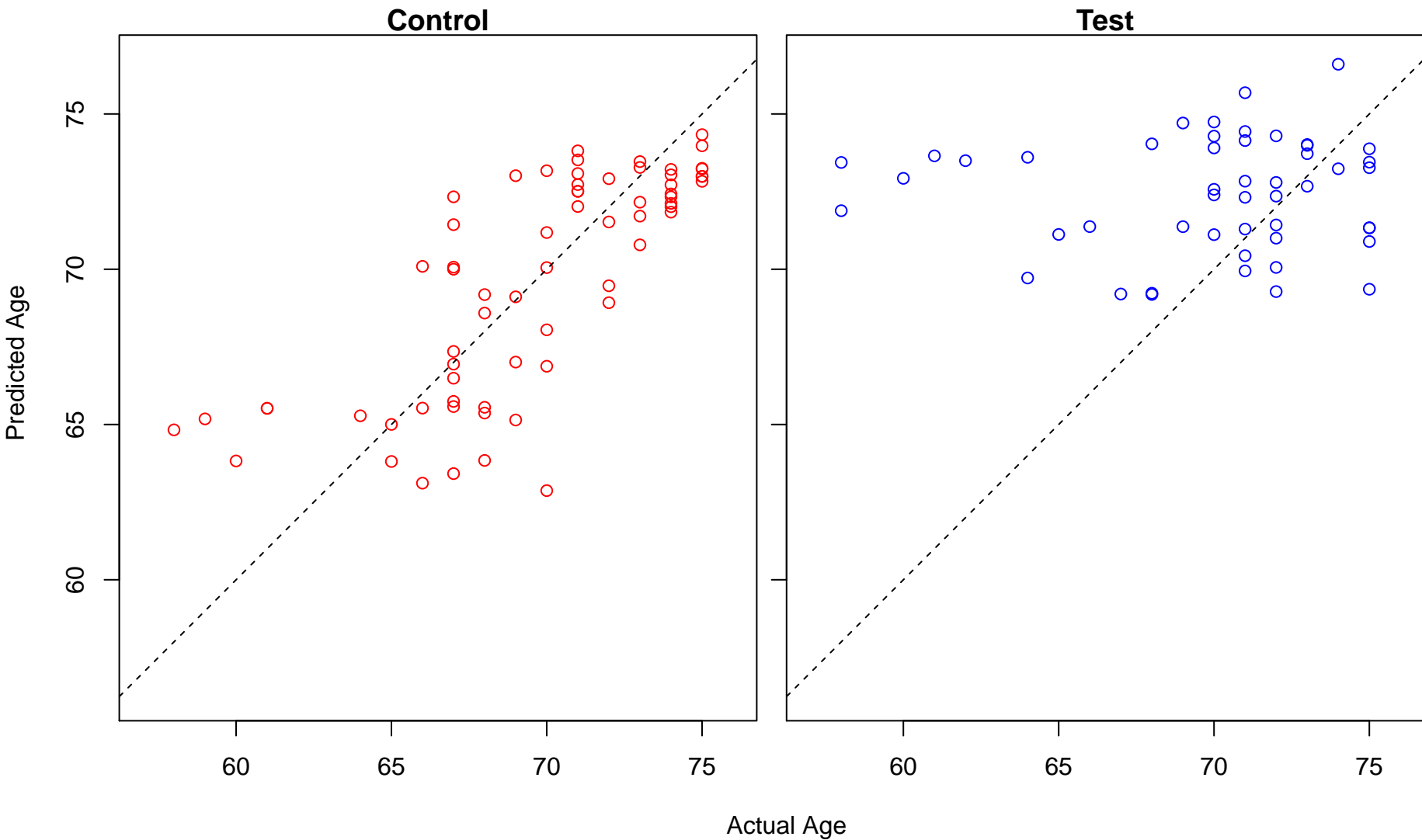


Test

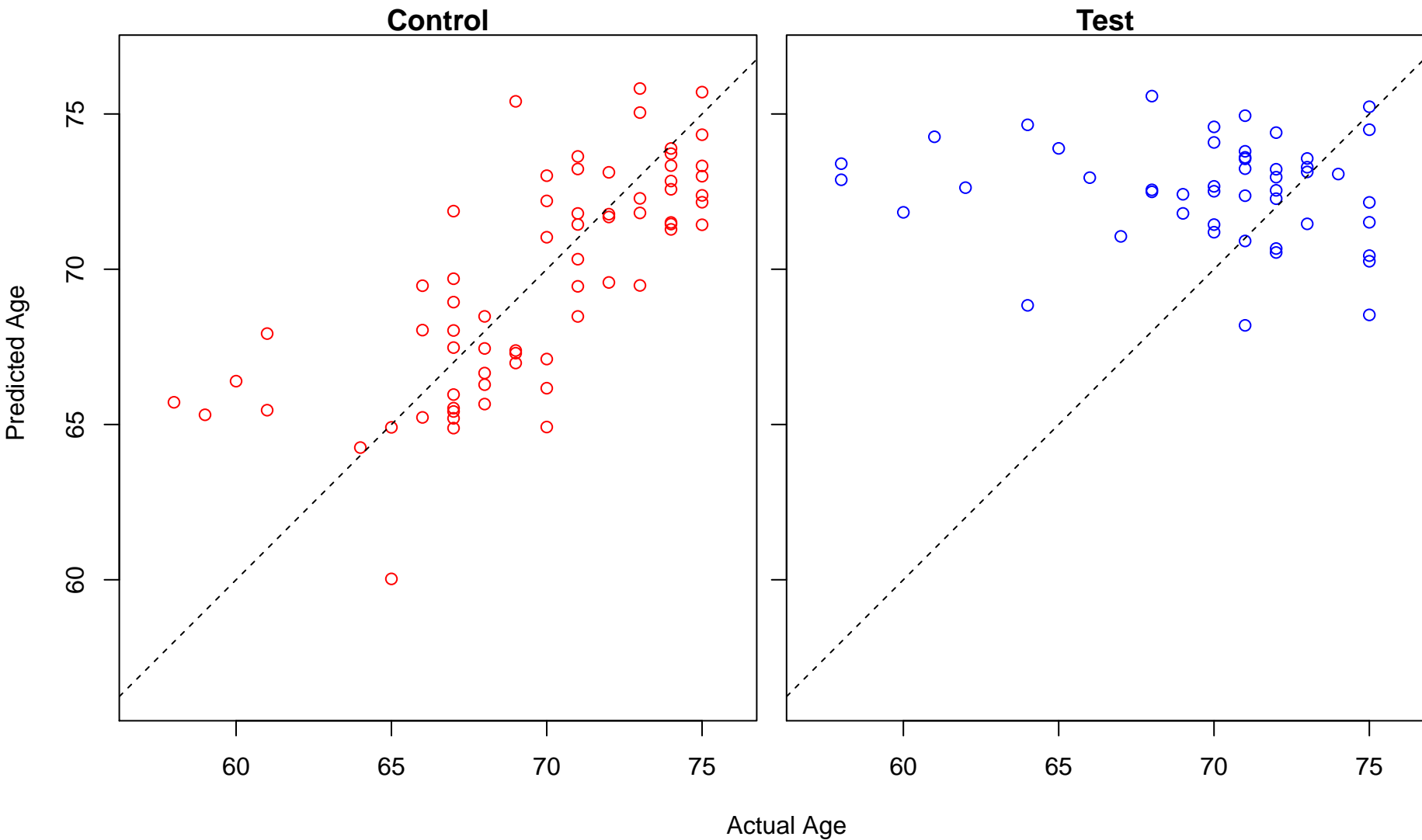


Actual Age

aerobic respiration (Score: 1.806756)

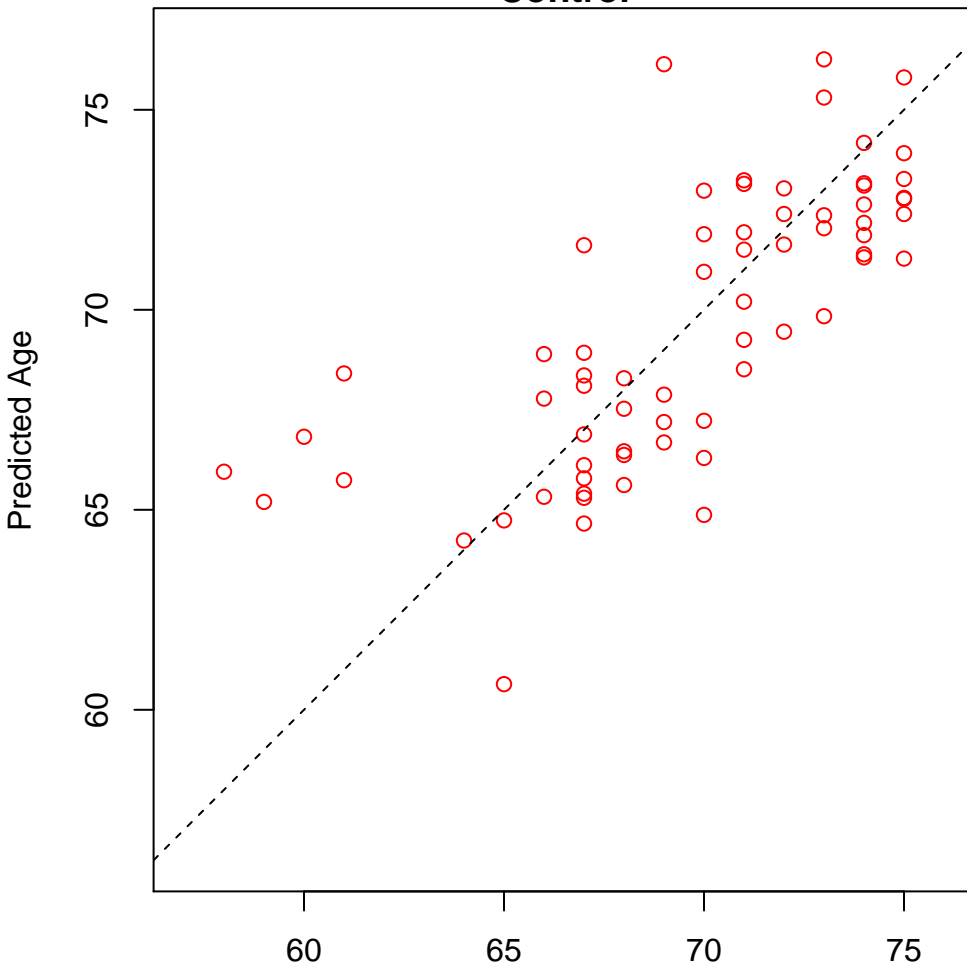


positive regulation of innate immune response (Score: 1.806141)

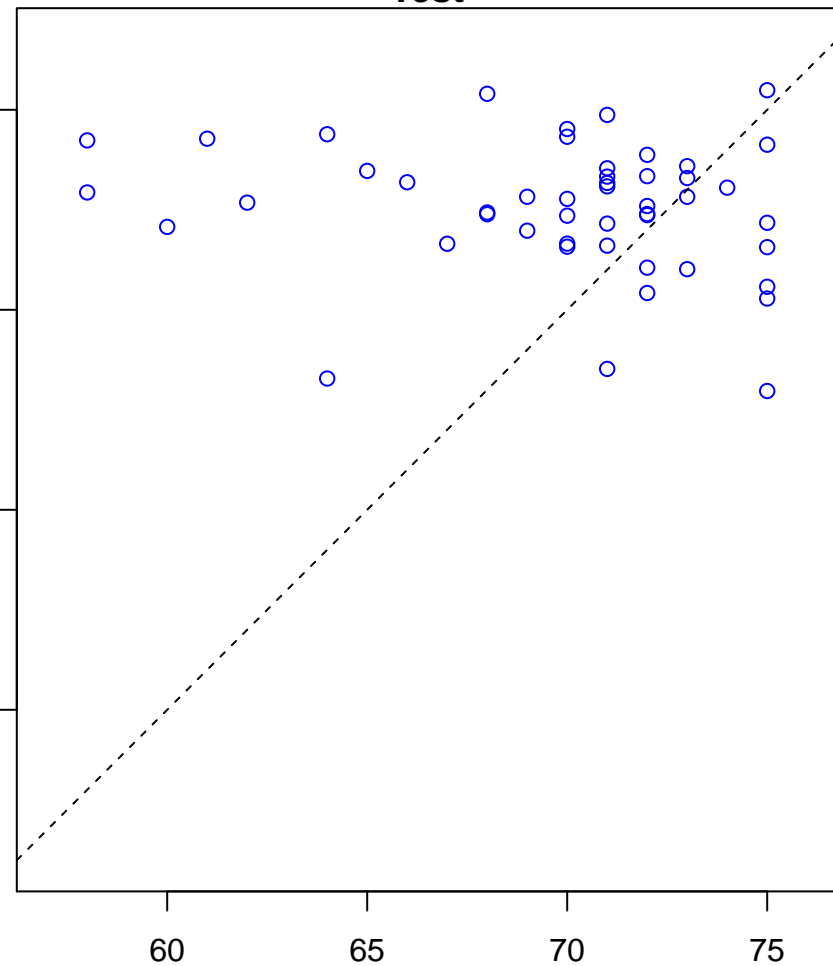


positive regulation of defense response (Score: 1.805800)

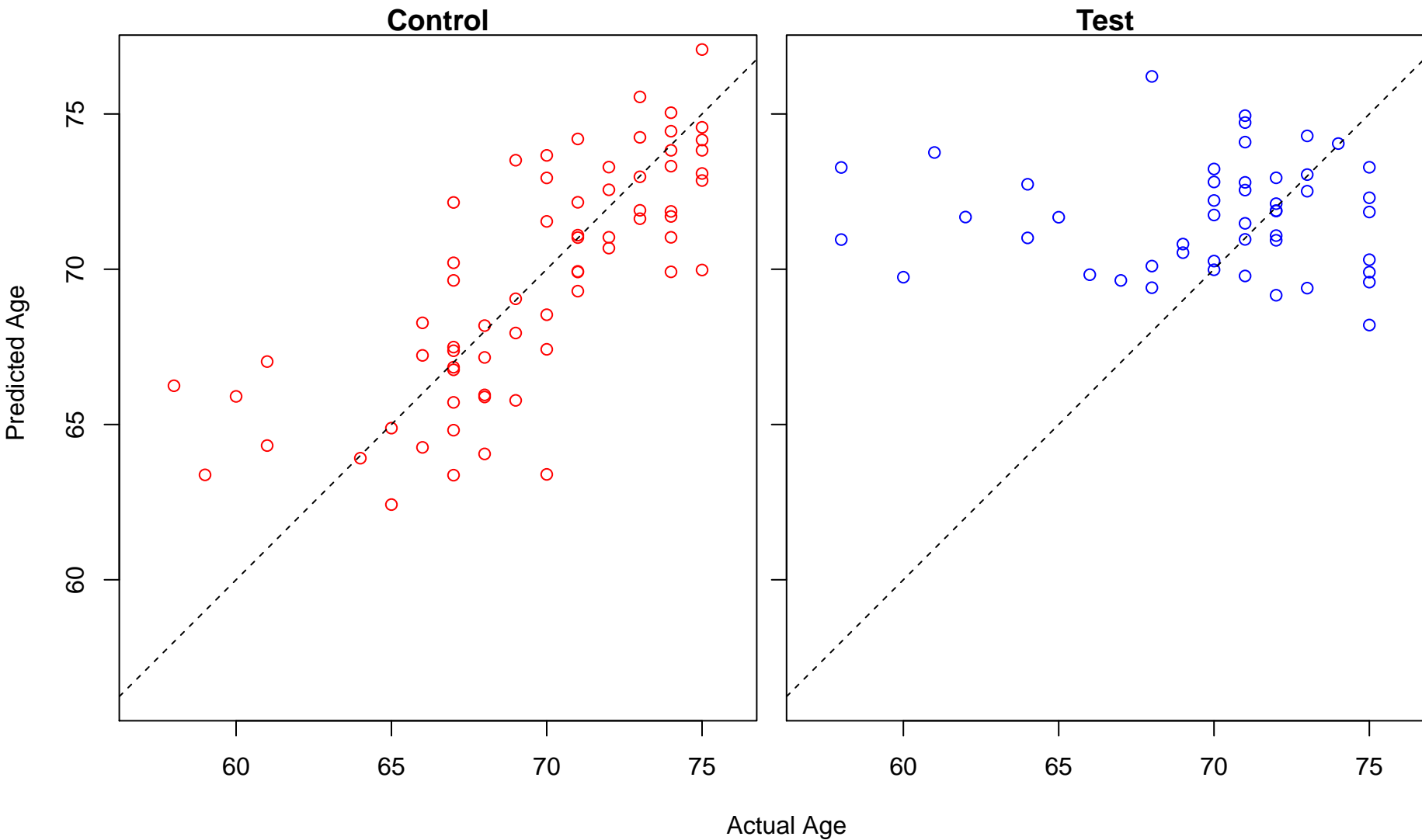
Control



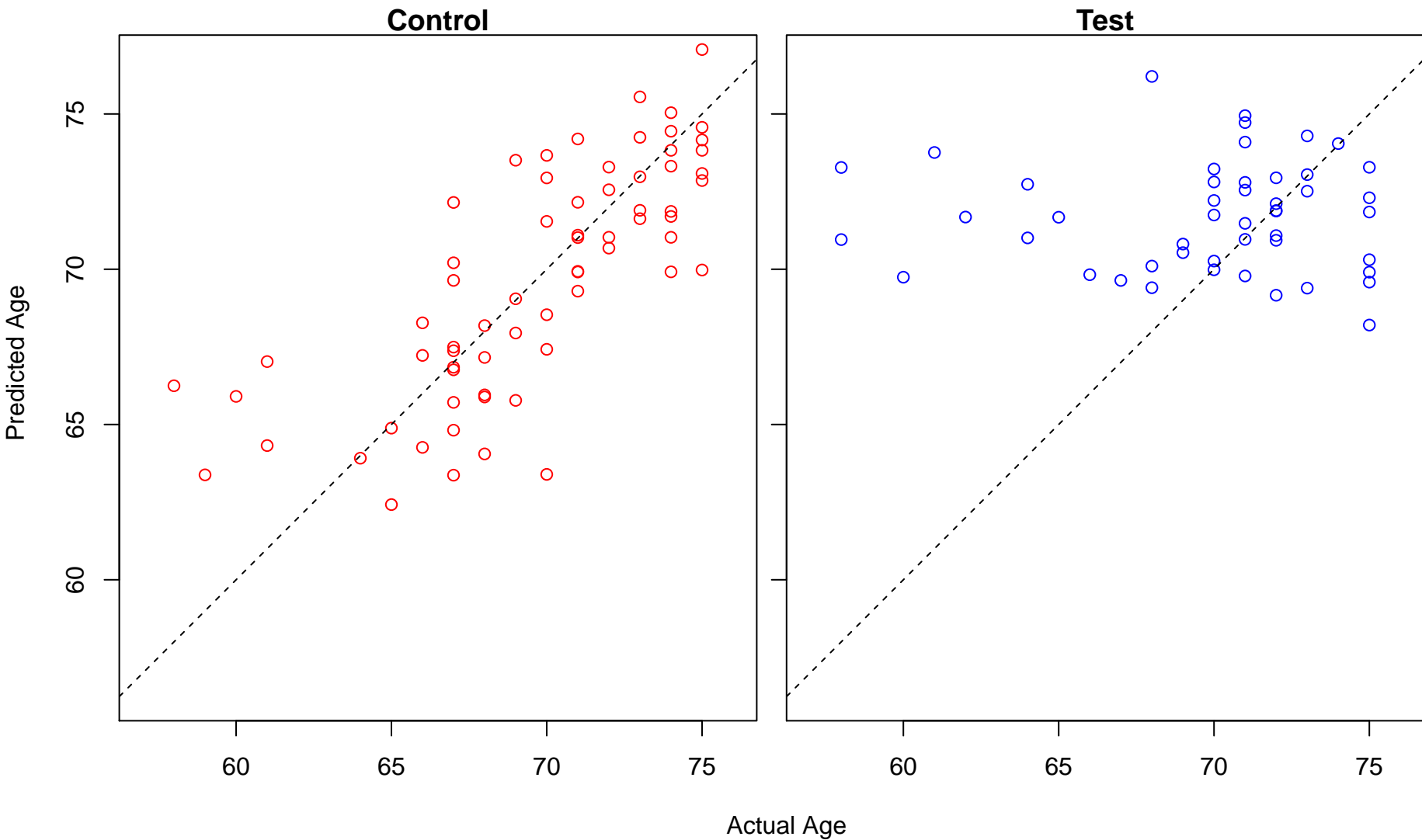
Test



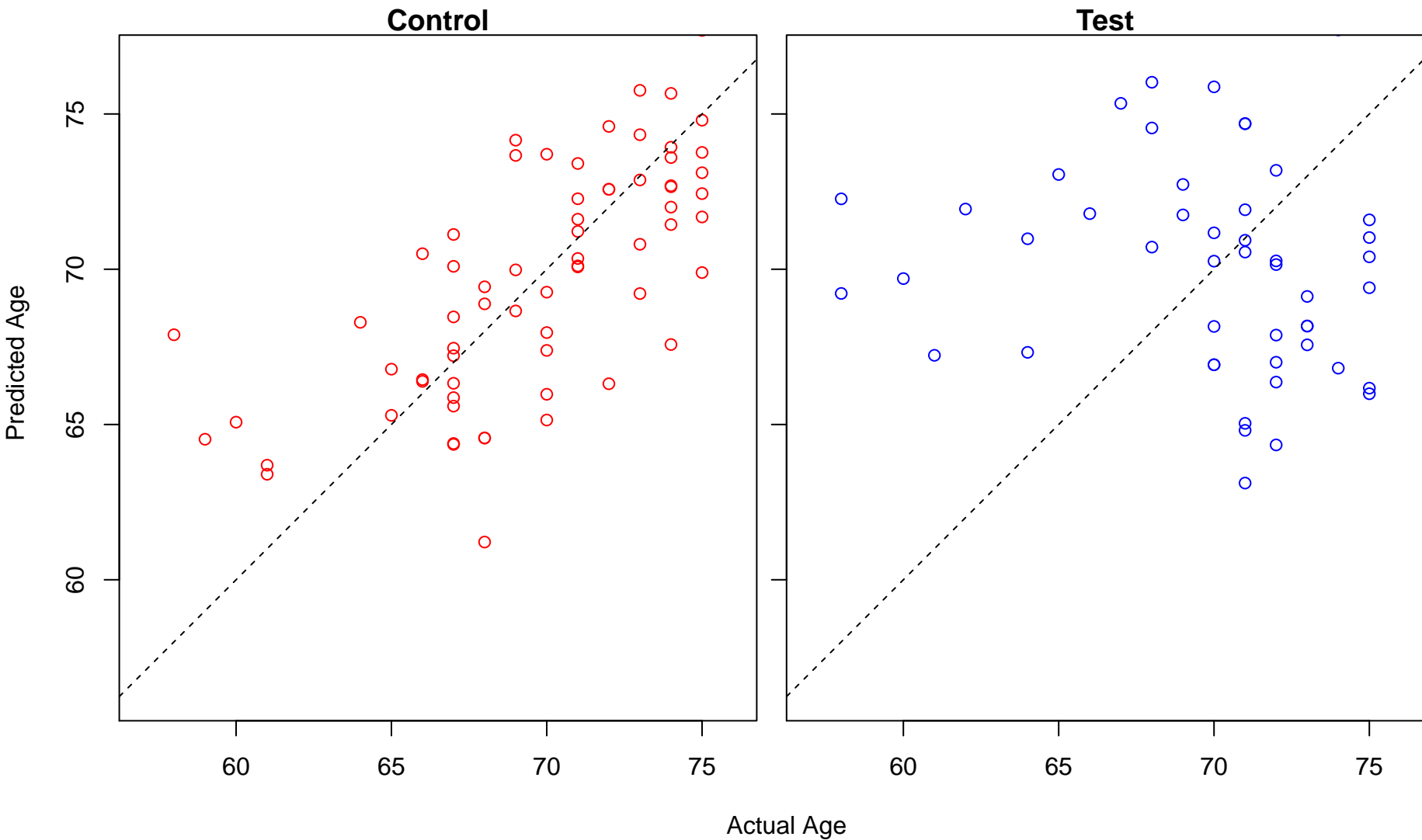
cellular biogenic amine metabolic process (Score: 1.805059)



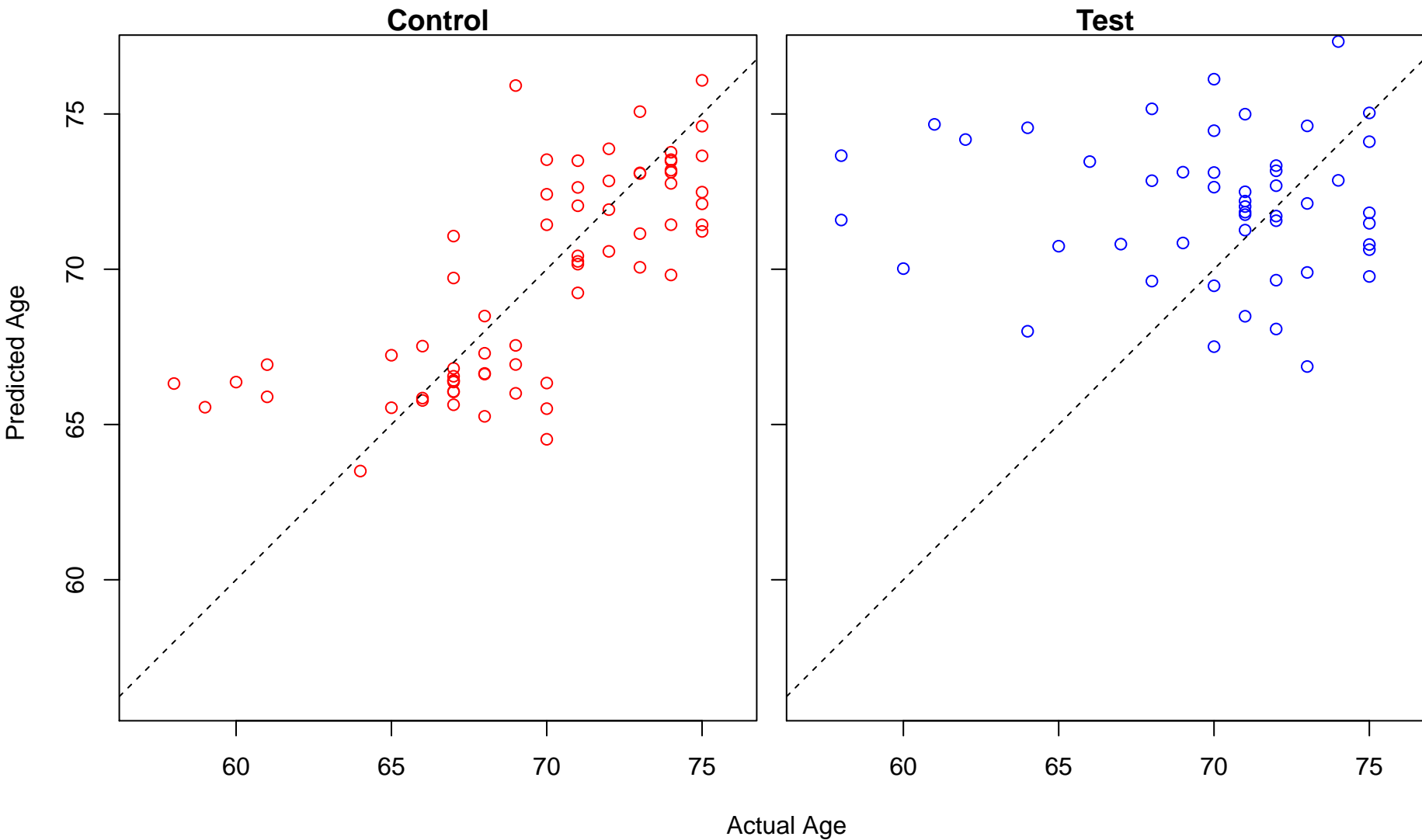
cellular amine metabolic process (Score: 1.805059)



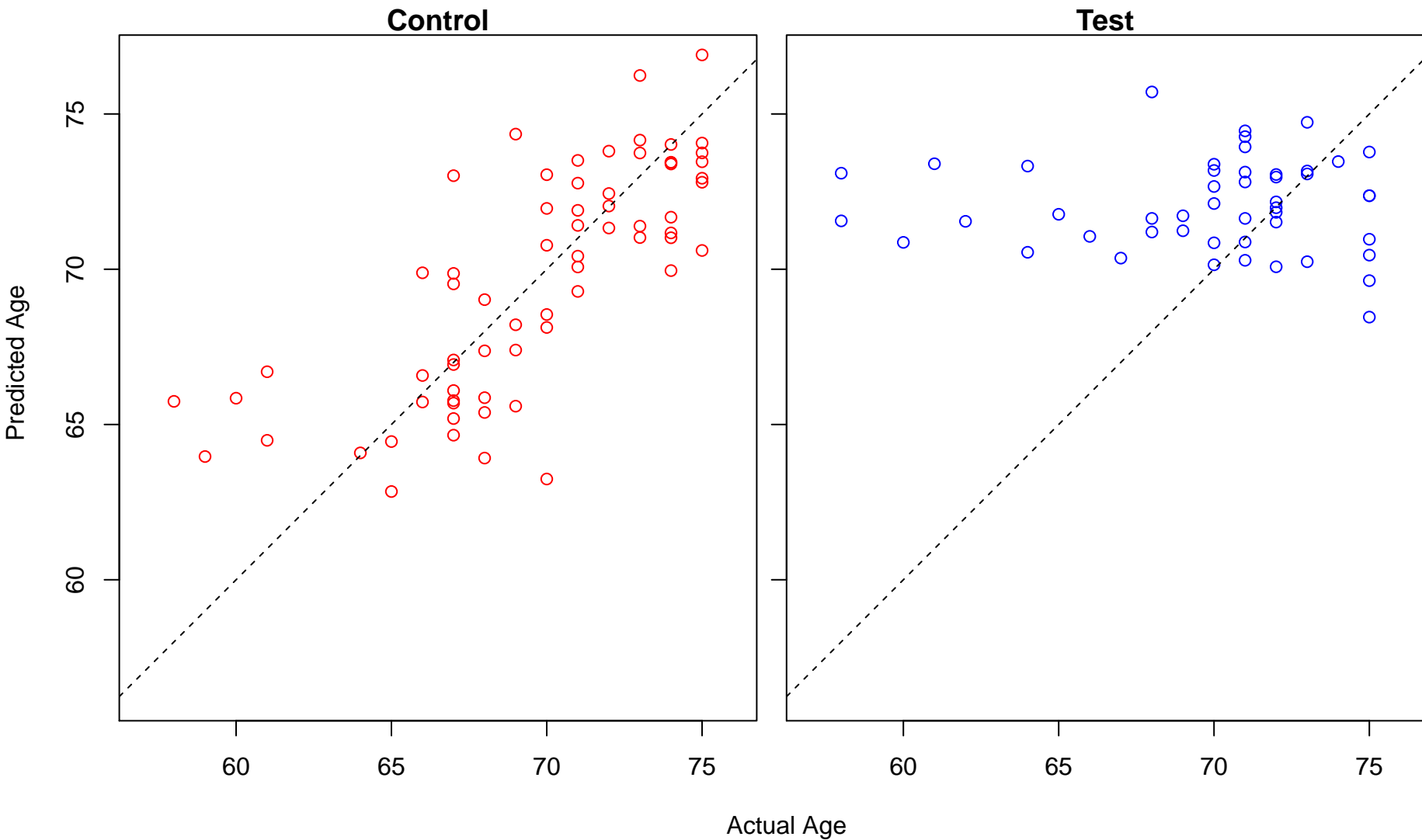
response to fungus (Score: 1.803883)



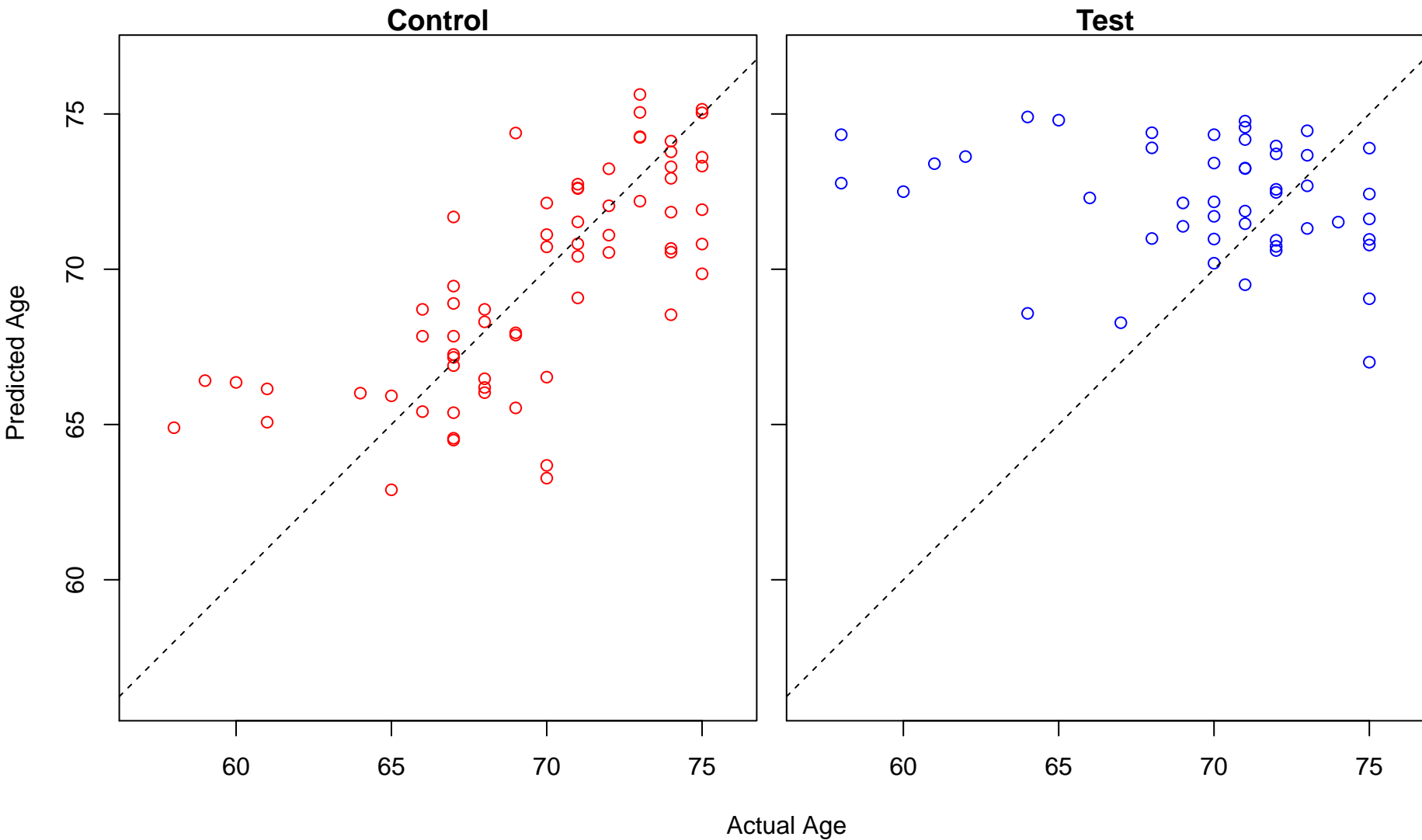
regulation of binding (Score: 1.802085)



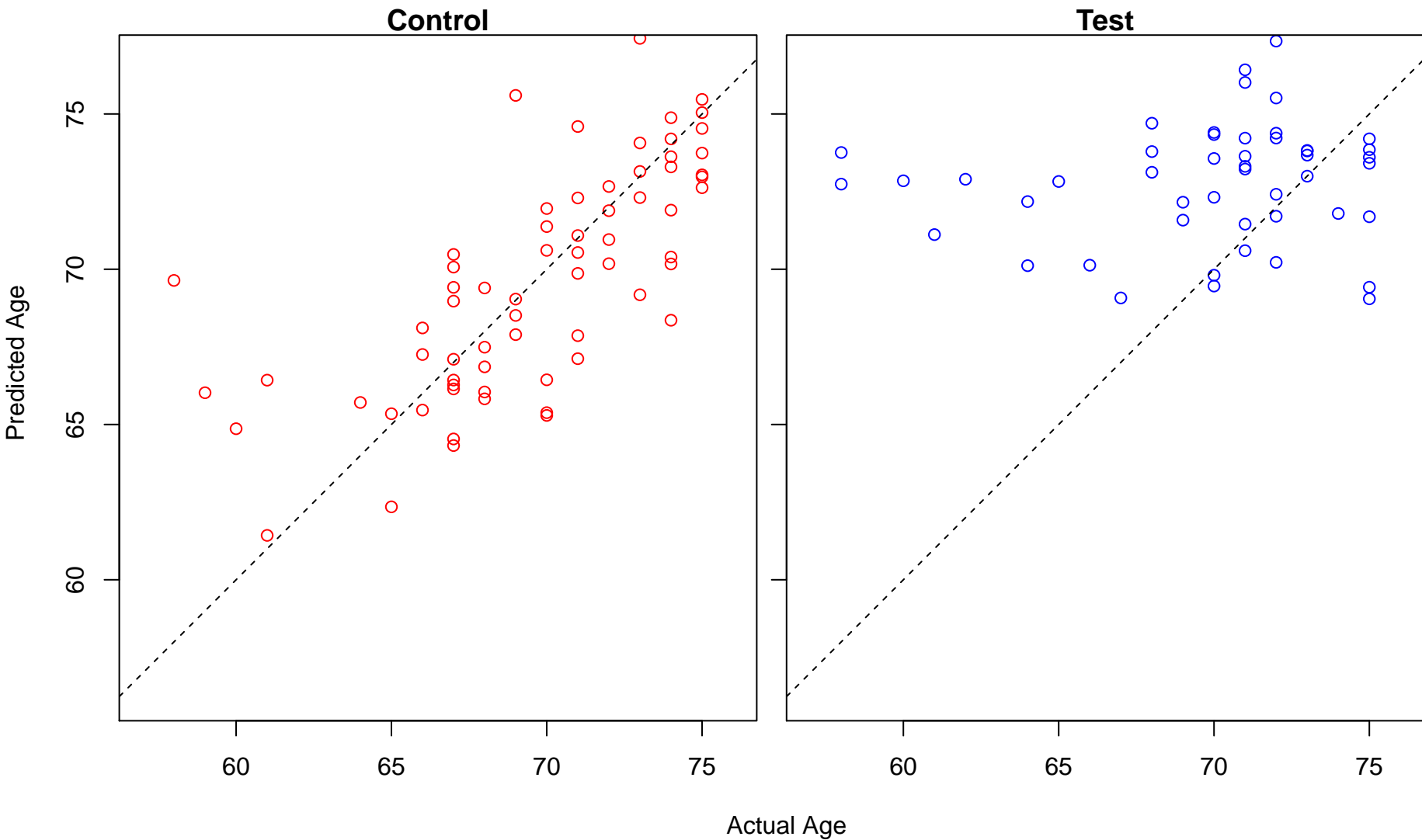
amine metabolic process (Score: 1.801724)



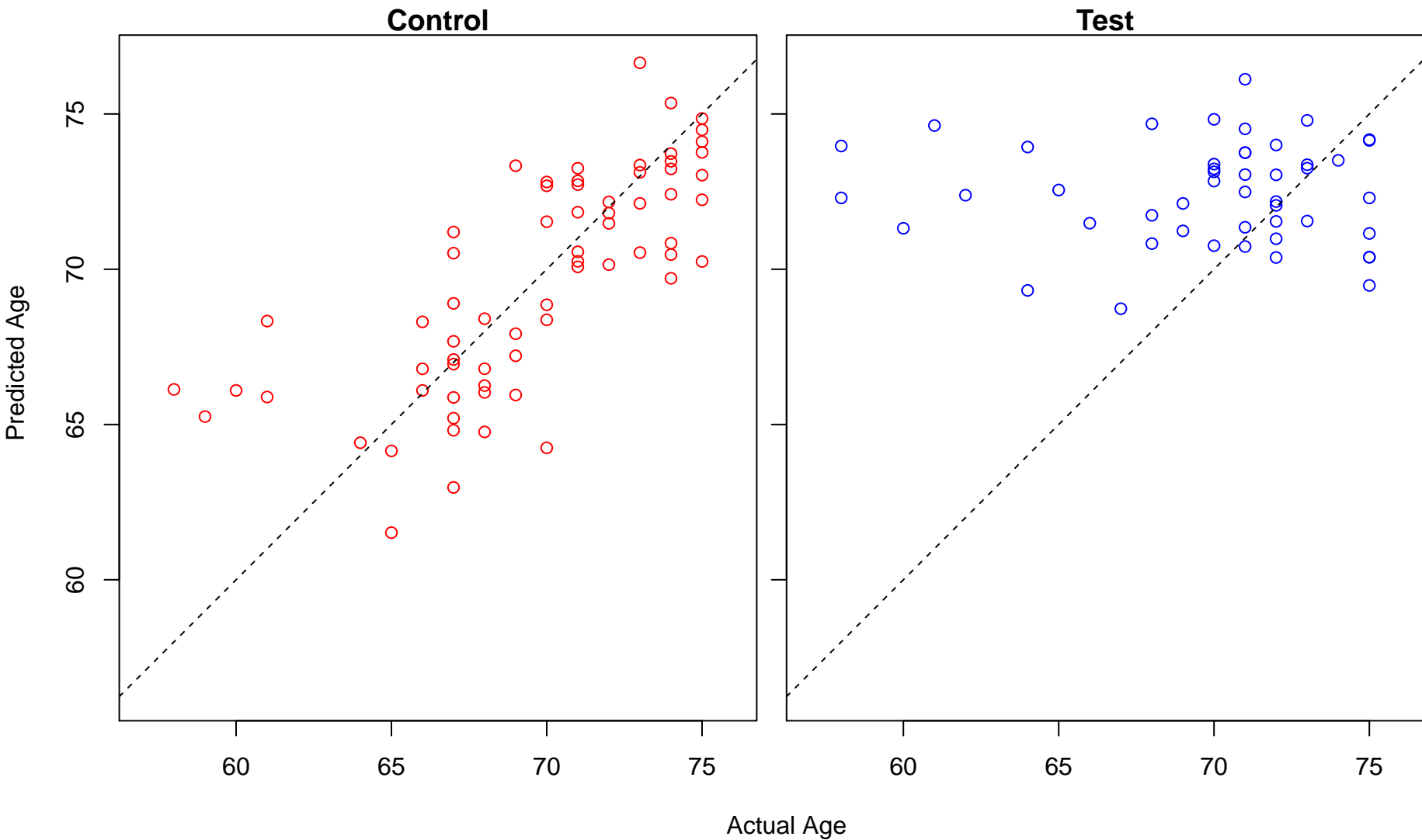
positive regulation of homeostatic process (Score: 1.801096)



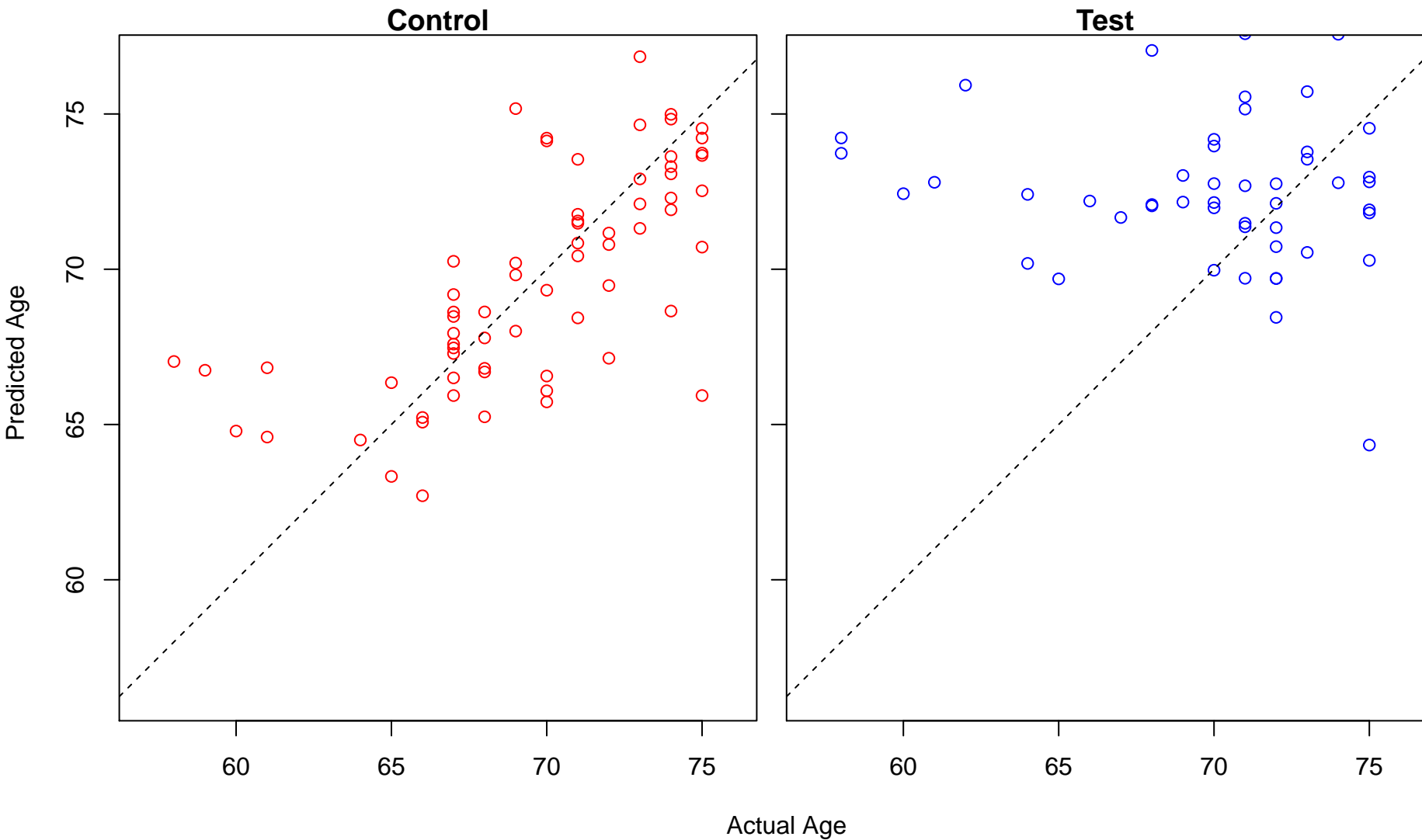
protein homooligomerization (Score: 1.800927)



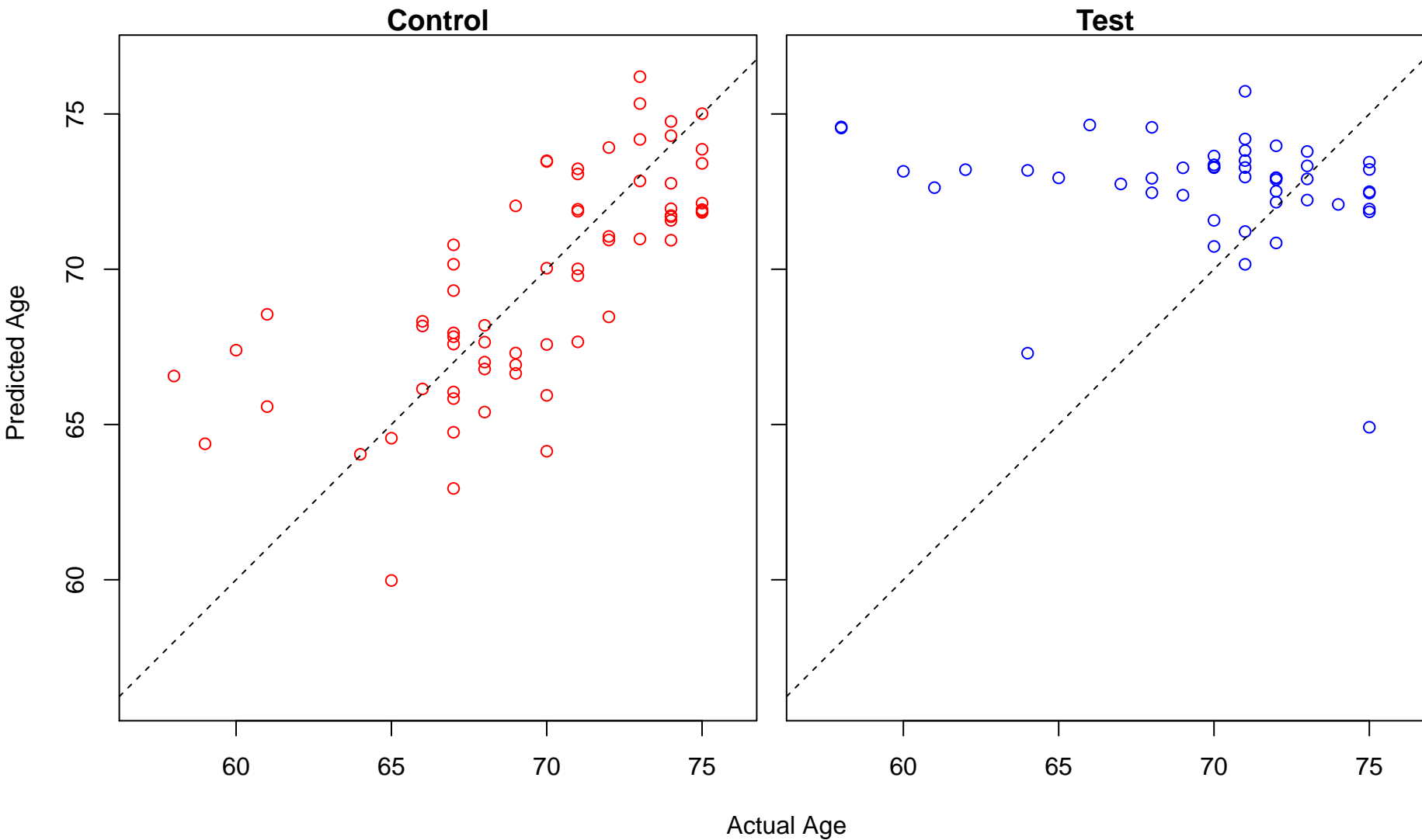
cell cycle phase transition (Score: 1.800149)



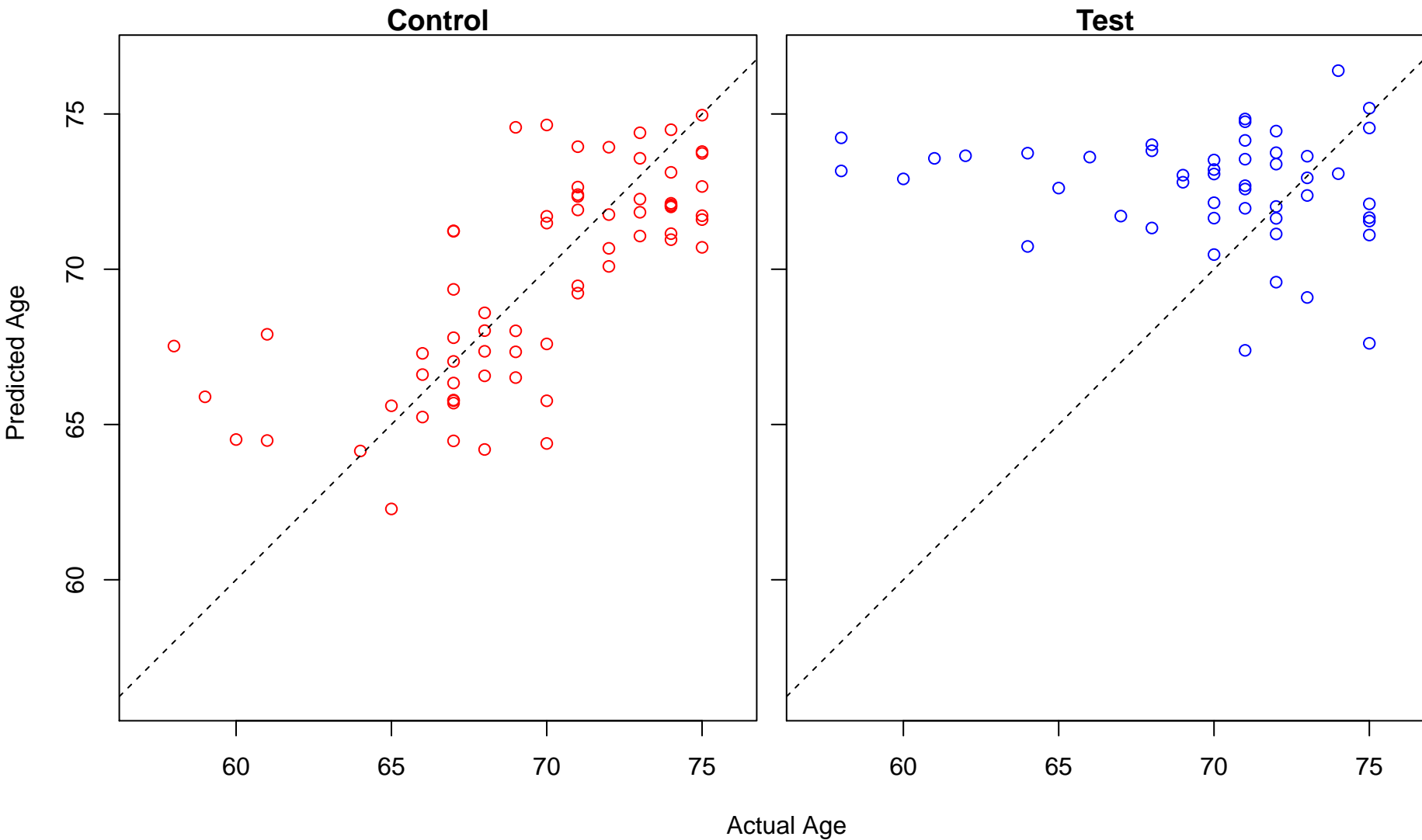
response to oxygen levels (Score: 1.799298)



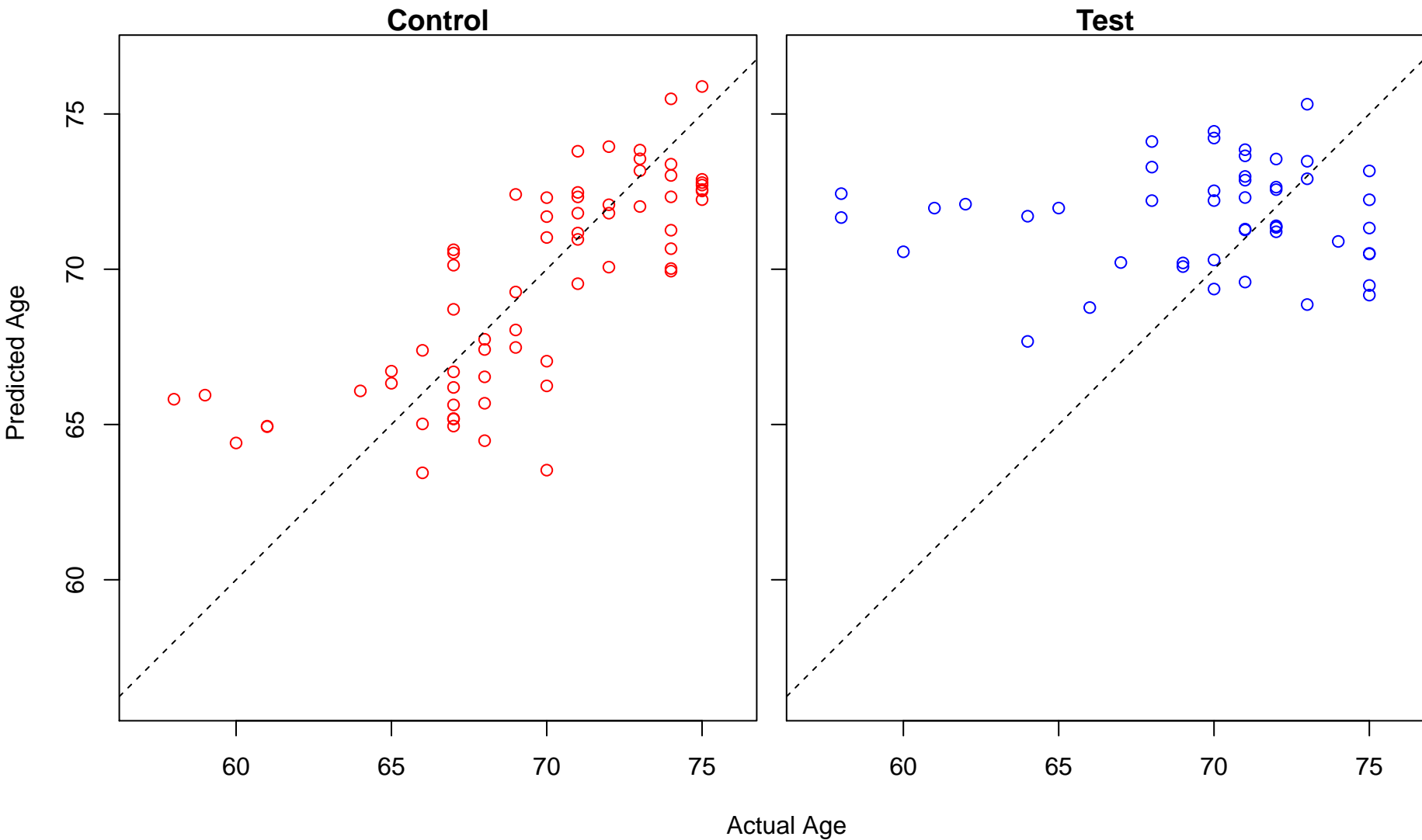
leukocyte migration (Score: 1.799123)



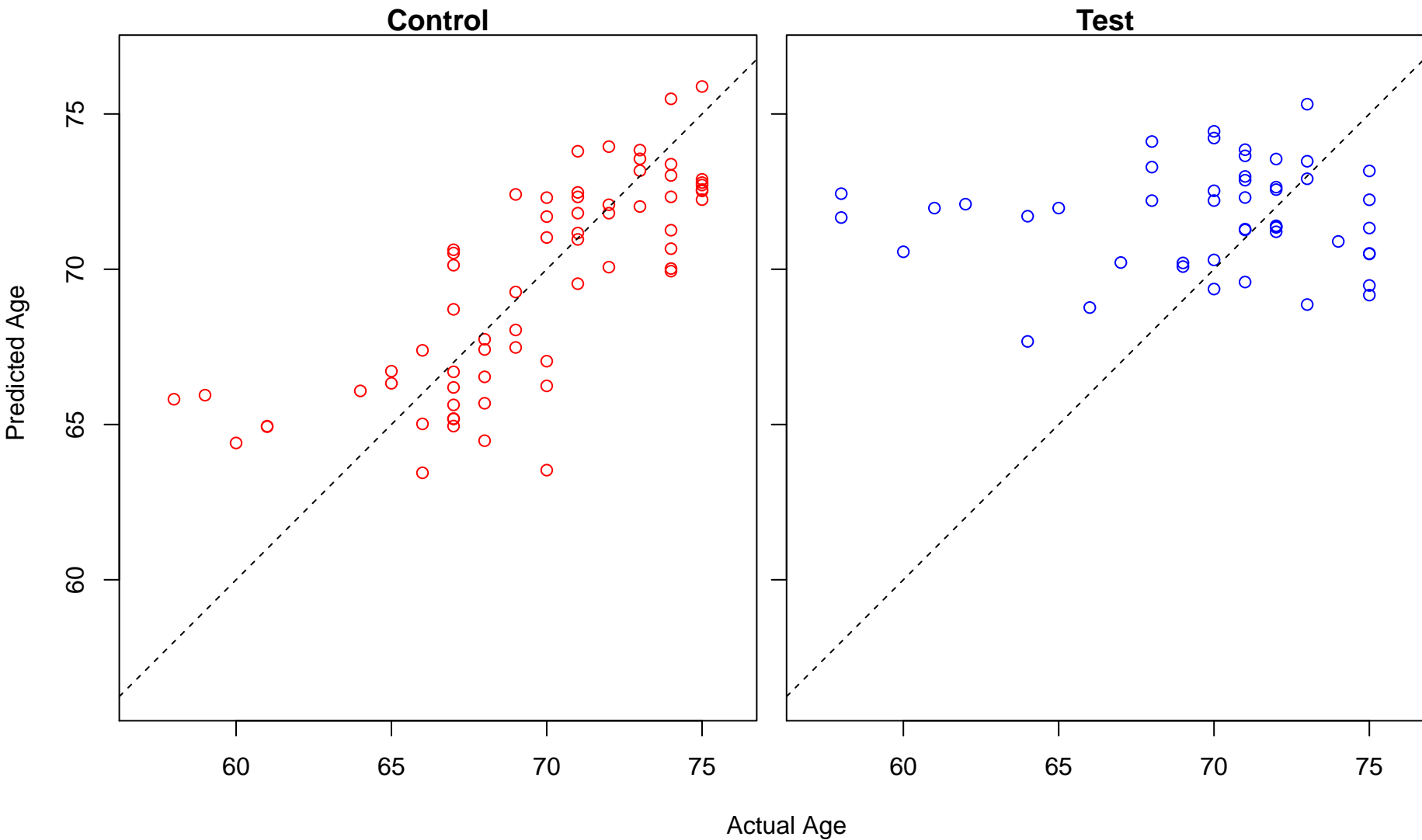
glycoprotein metabolic process (Score: 1.798792)



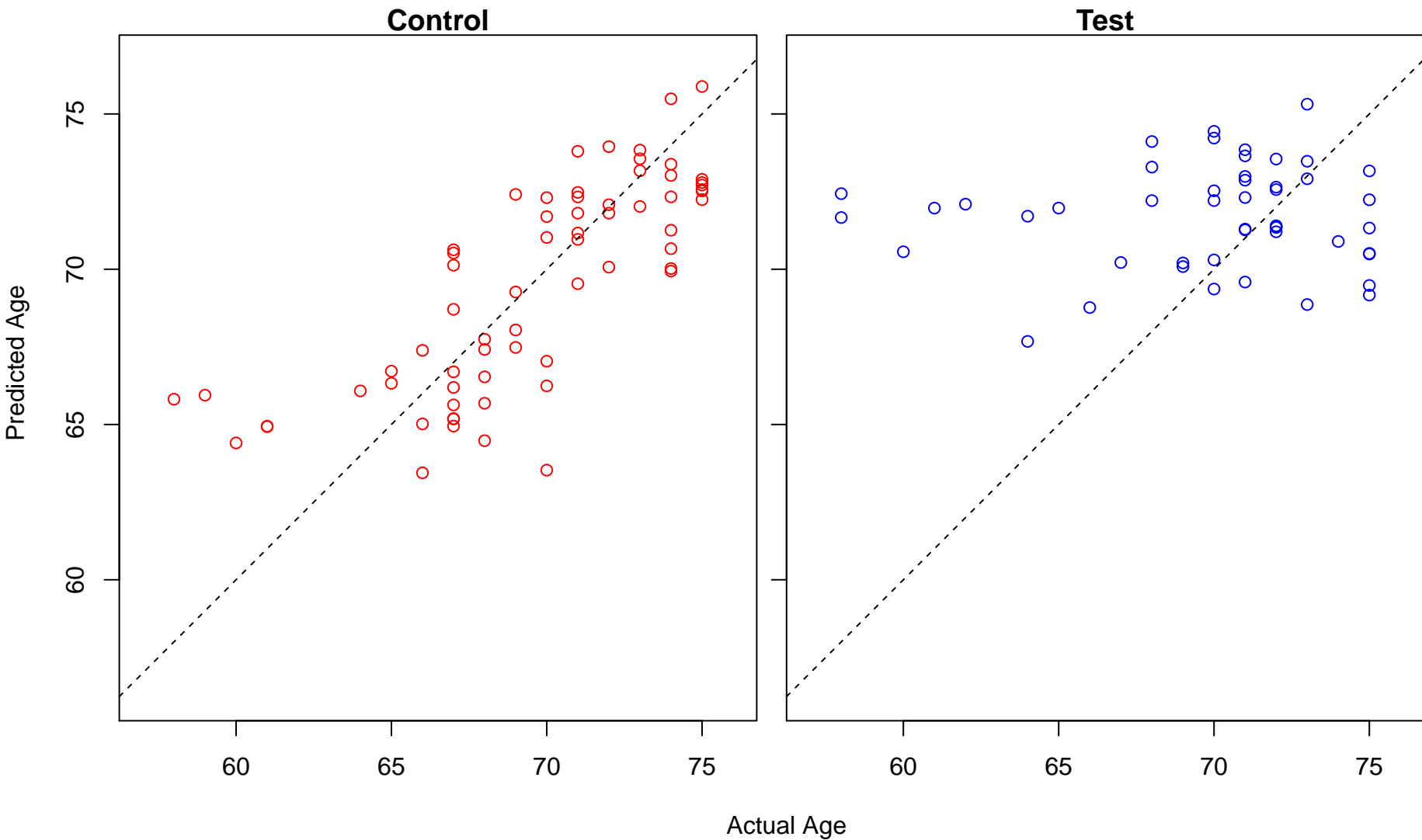
ATP biosynthetic process (Score: 1.798314)



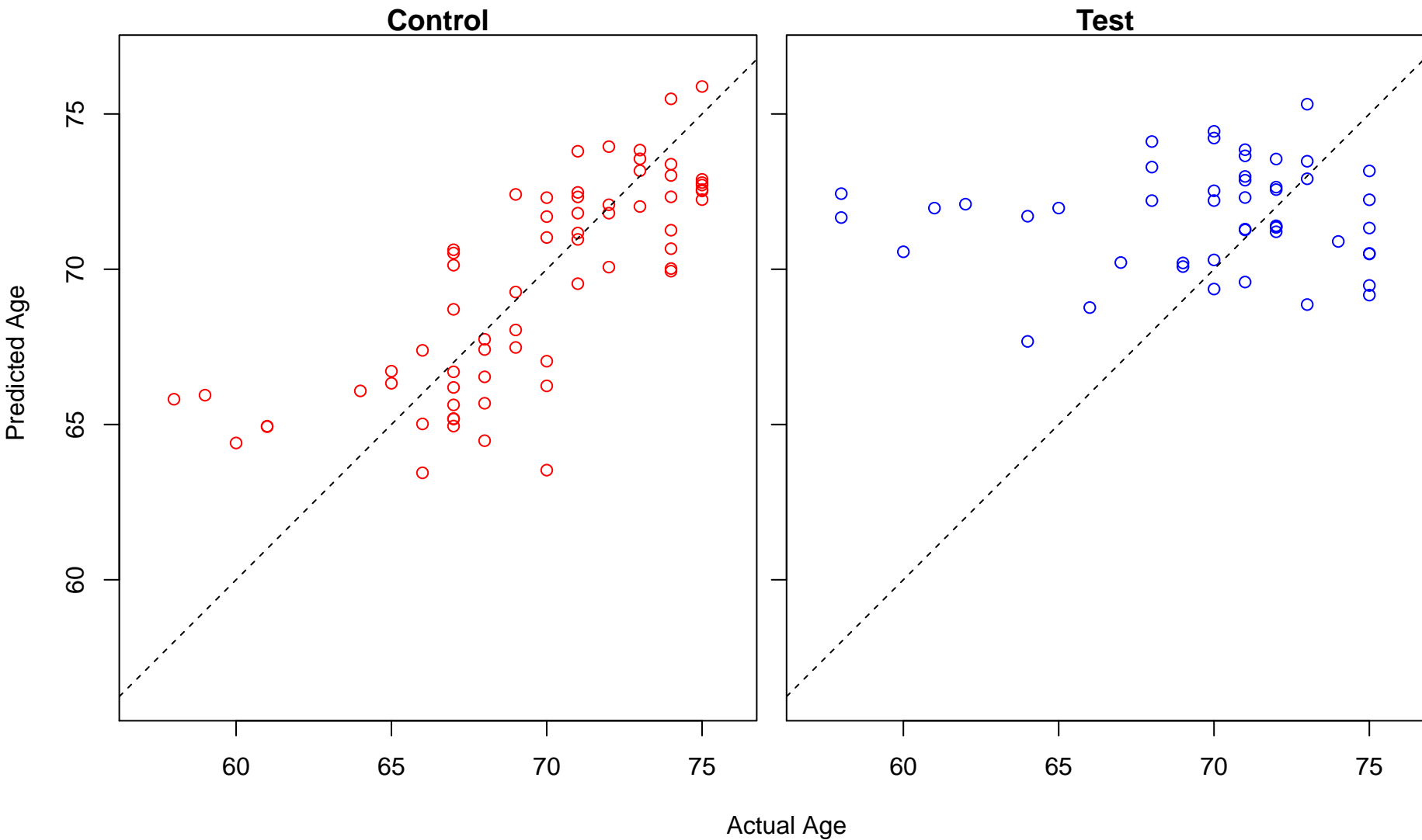
purine nucleoside triphosphate biosynthetic process (Score: 1.798314)



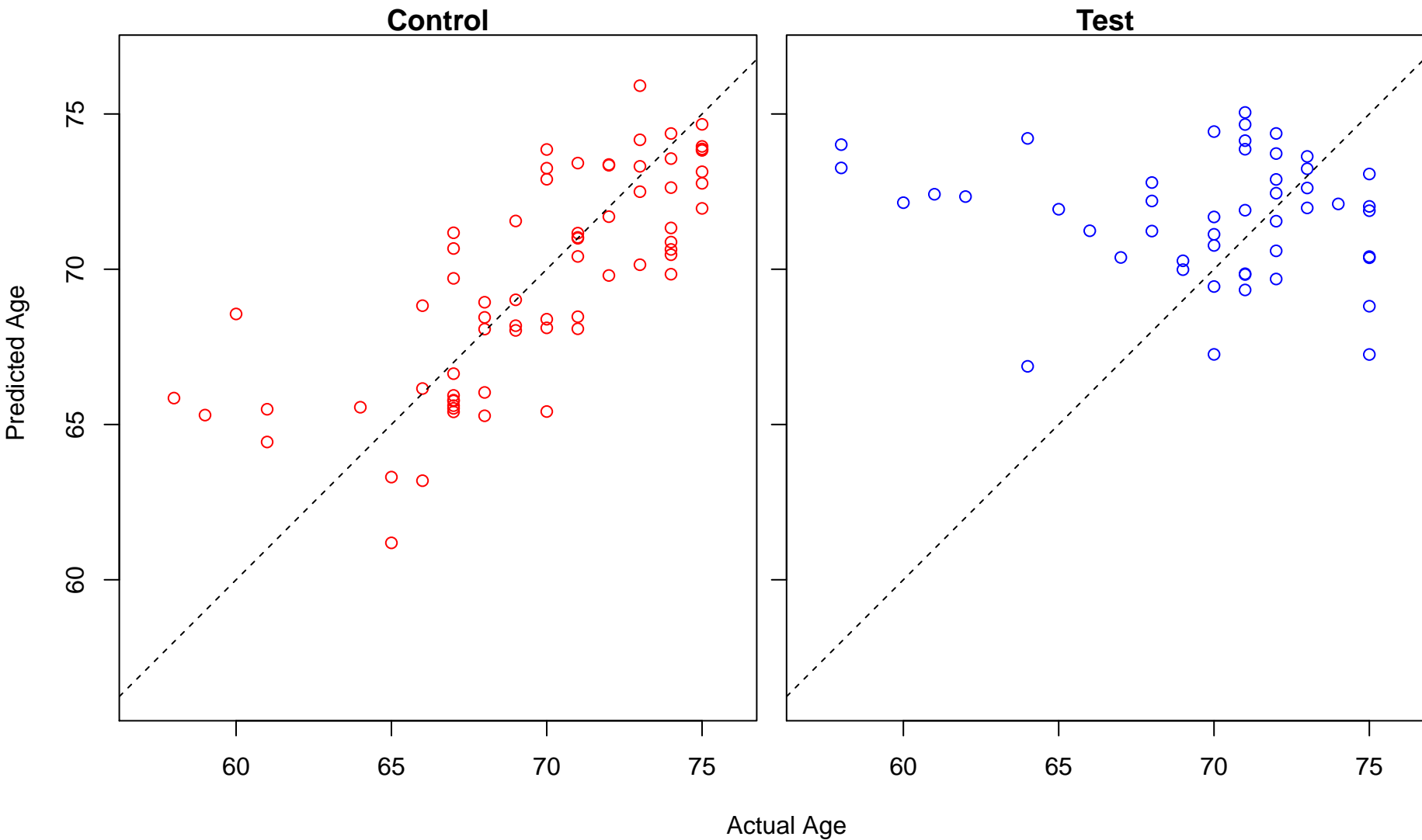
ribonucleoside triphosphate biosynthetic process (Score: 1.798314)



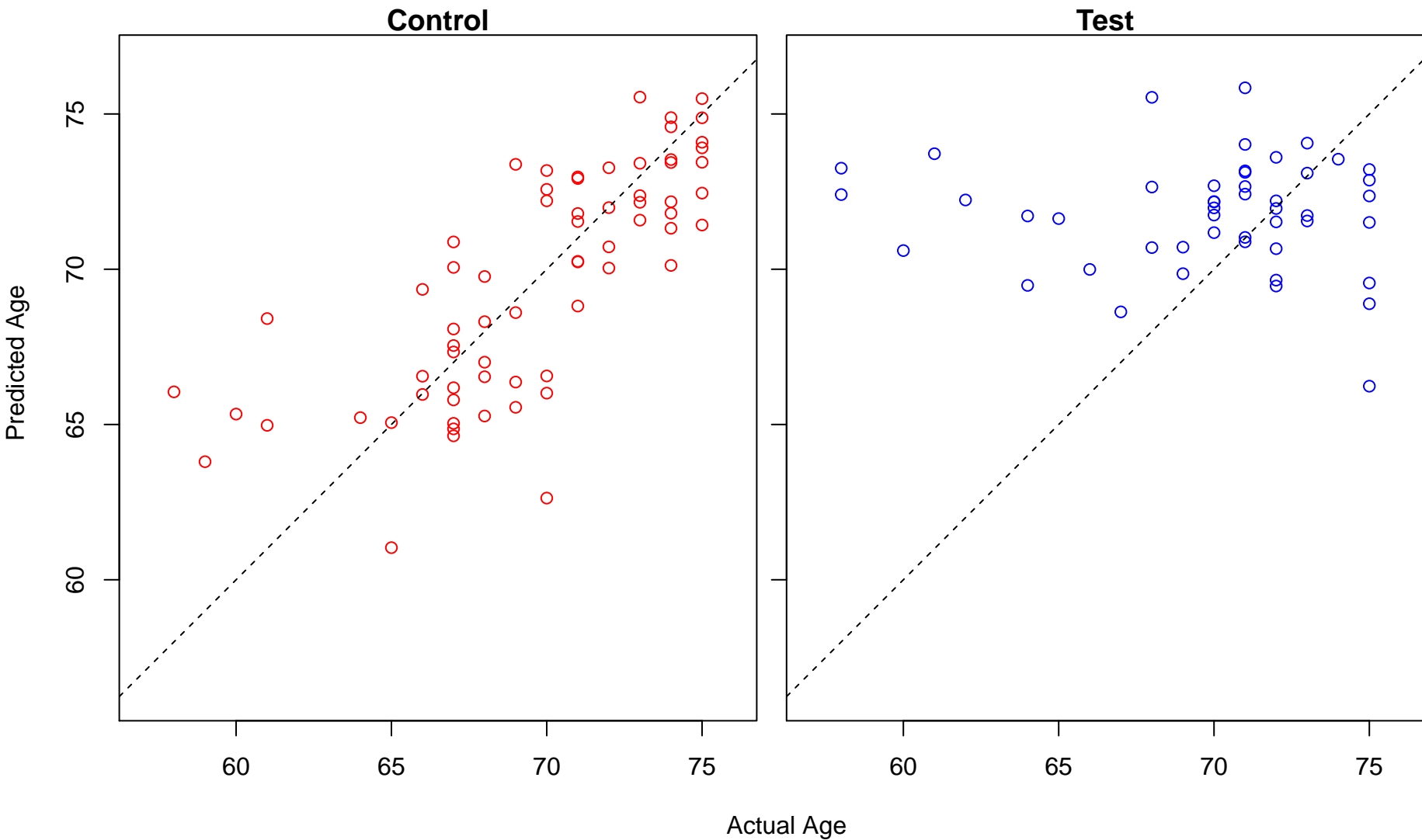
purine ribonucleoside triphosphate biosynthetic process (Score: 1.798314)



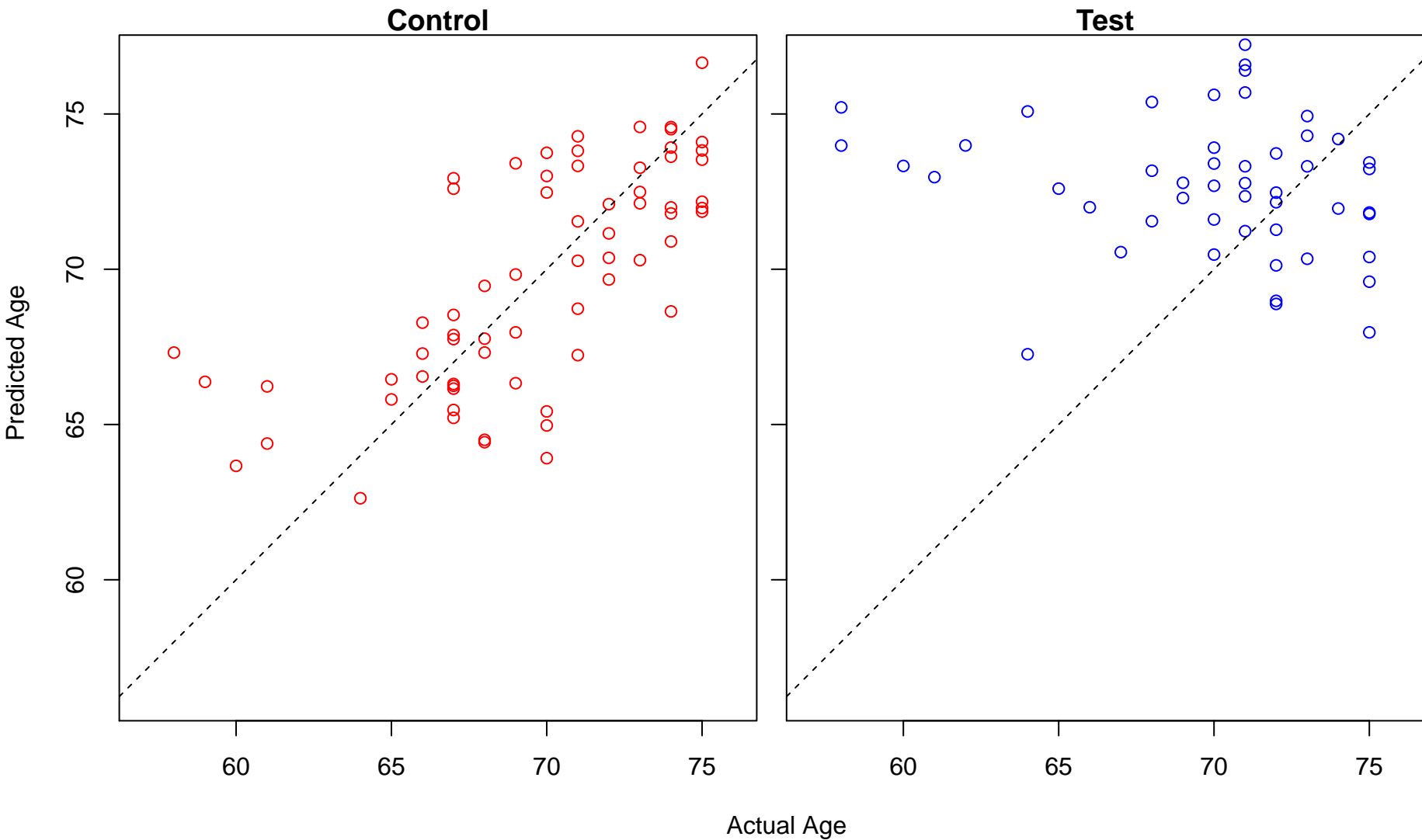
execution phase of apoptosis (Score: 1.797265)



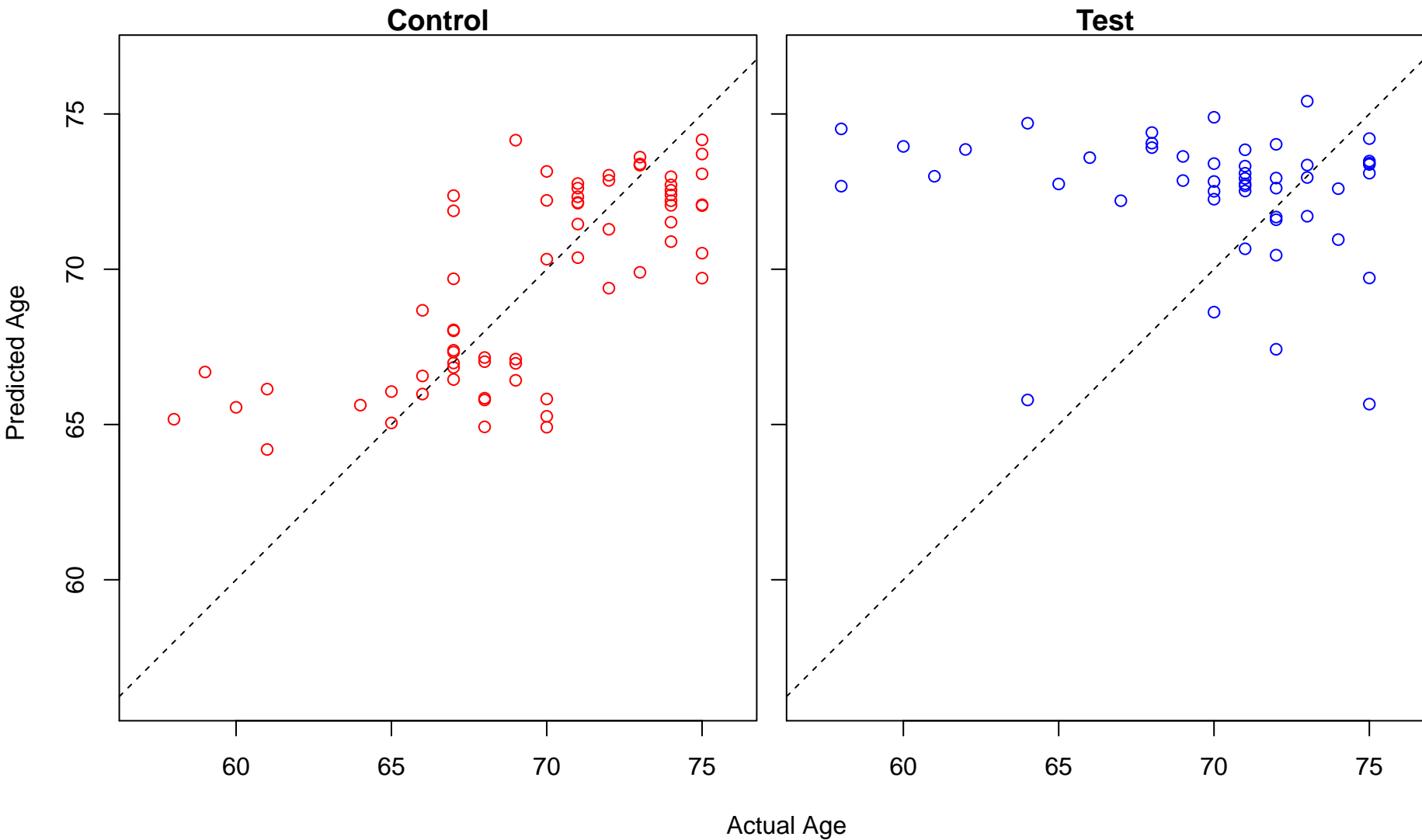
regulation of G1/S transition of mitotic cell cycle (Score: 1.796469)



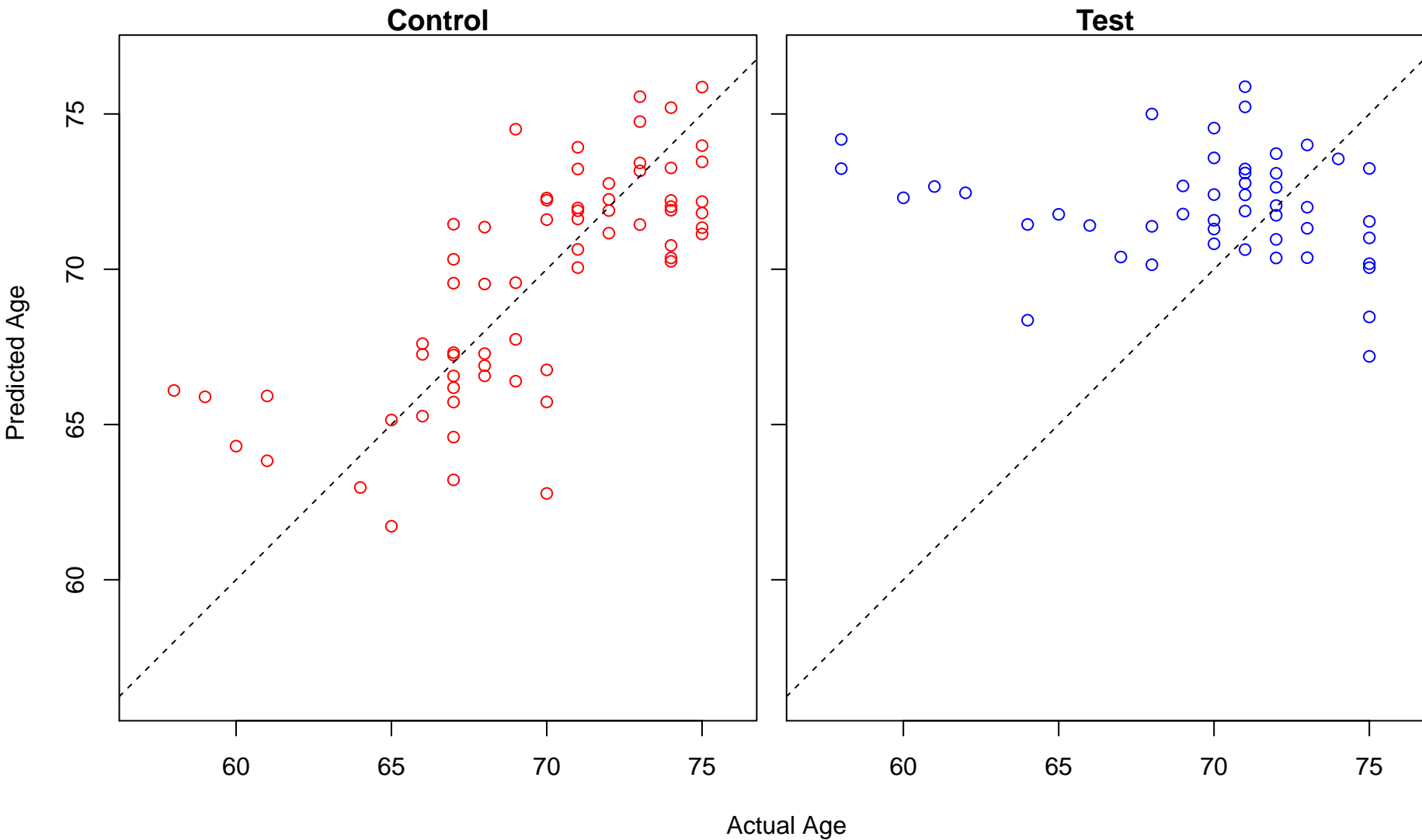
macromitophagy (Score: 1.796456)



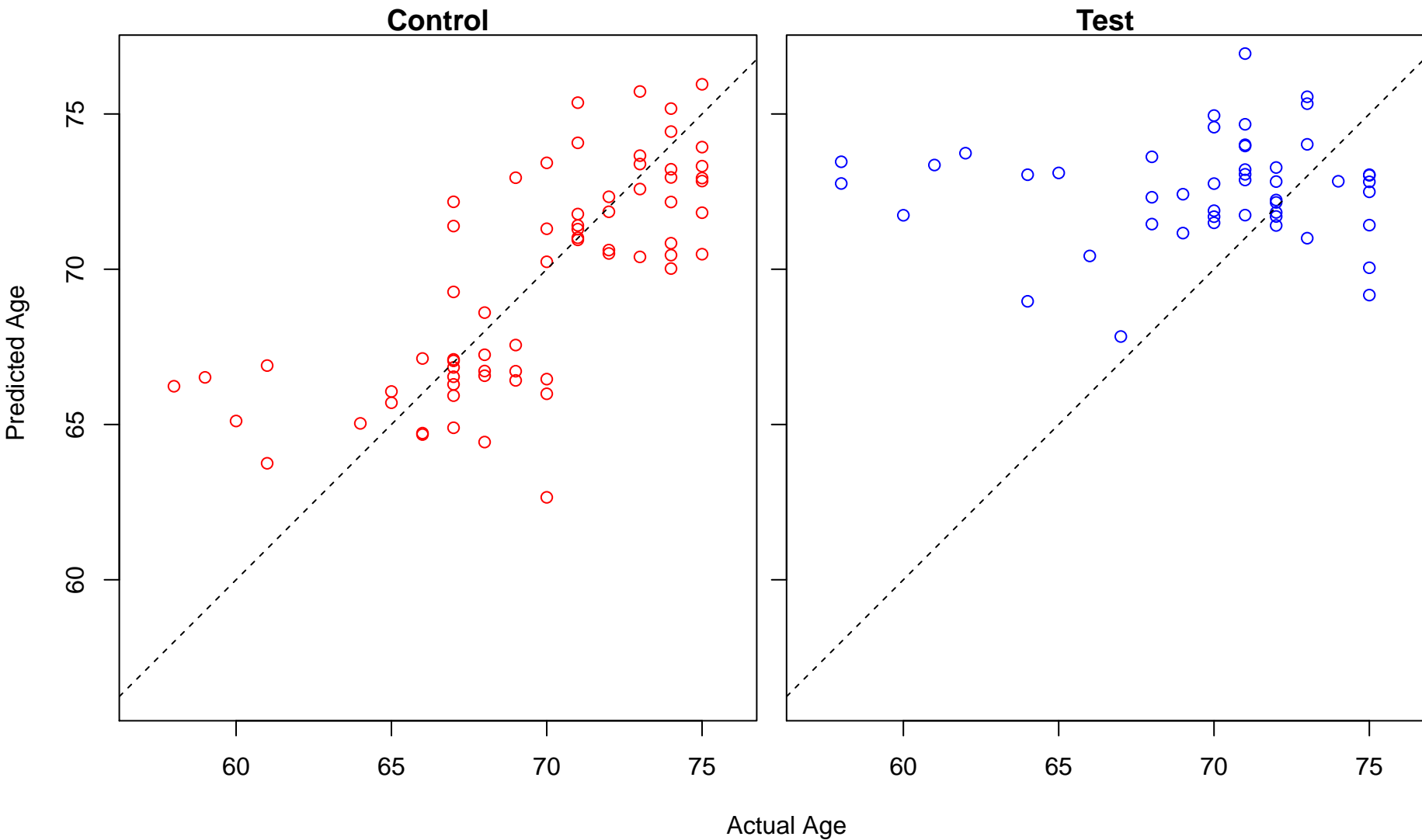
cyclic-nucleotide-mediated signaling (Score: 1.795944)



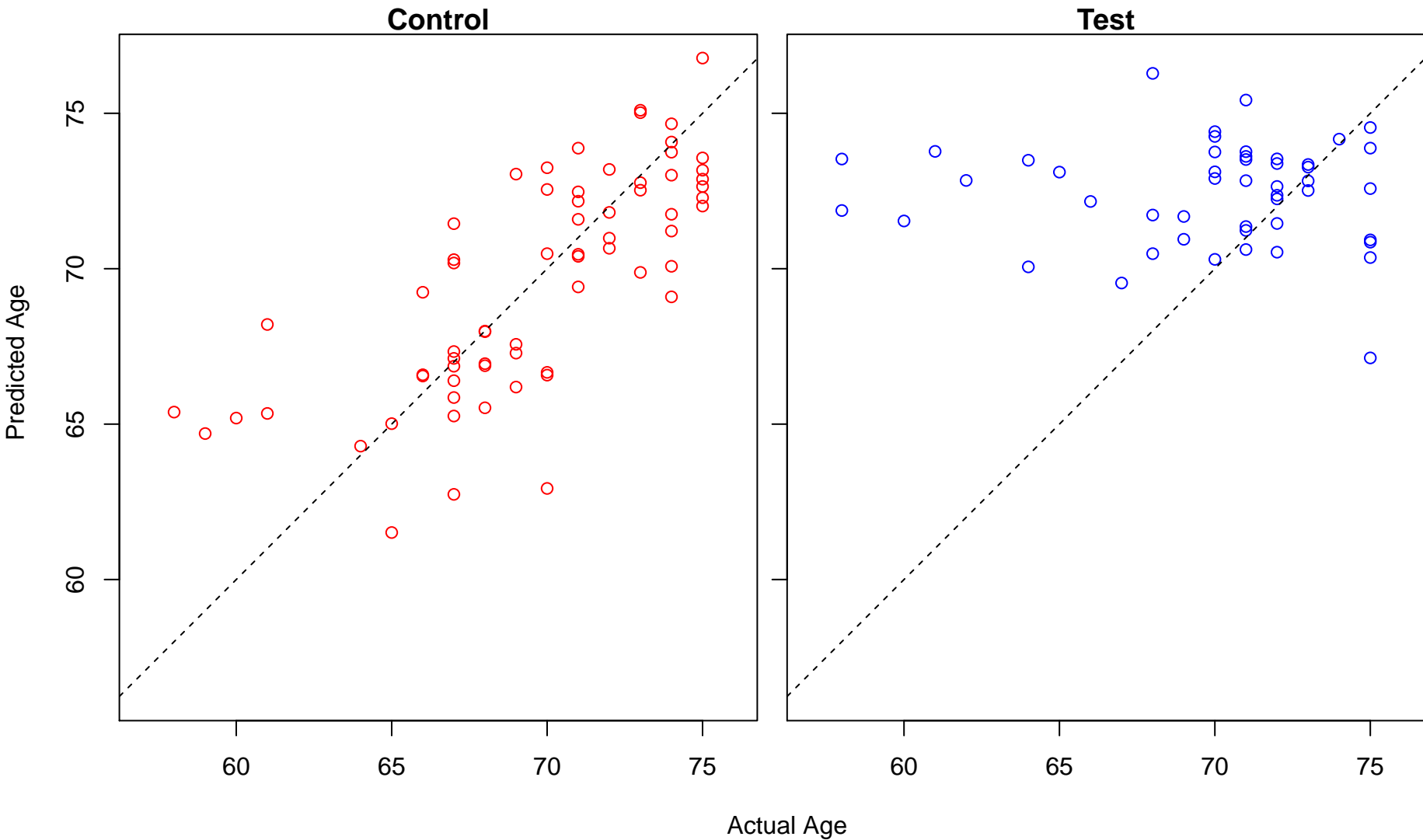
ncRNA processing (Score: 1.795917)



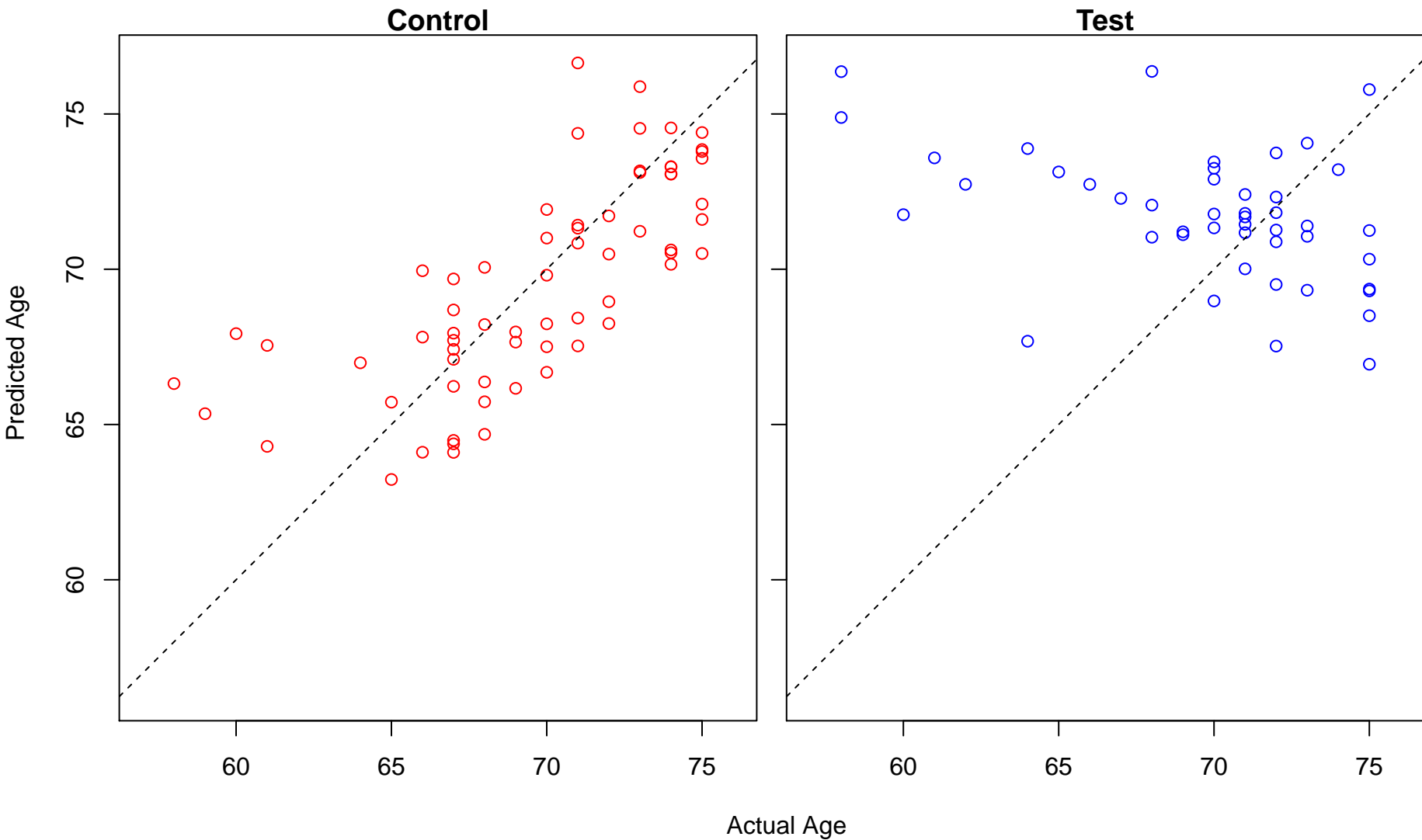
generation of precursor metabolites and energy (Score: 1.794660)



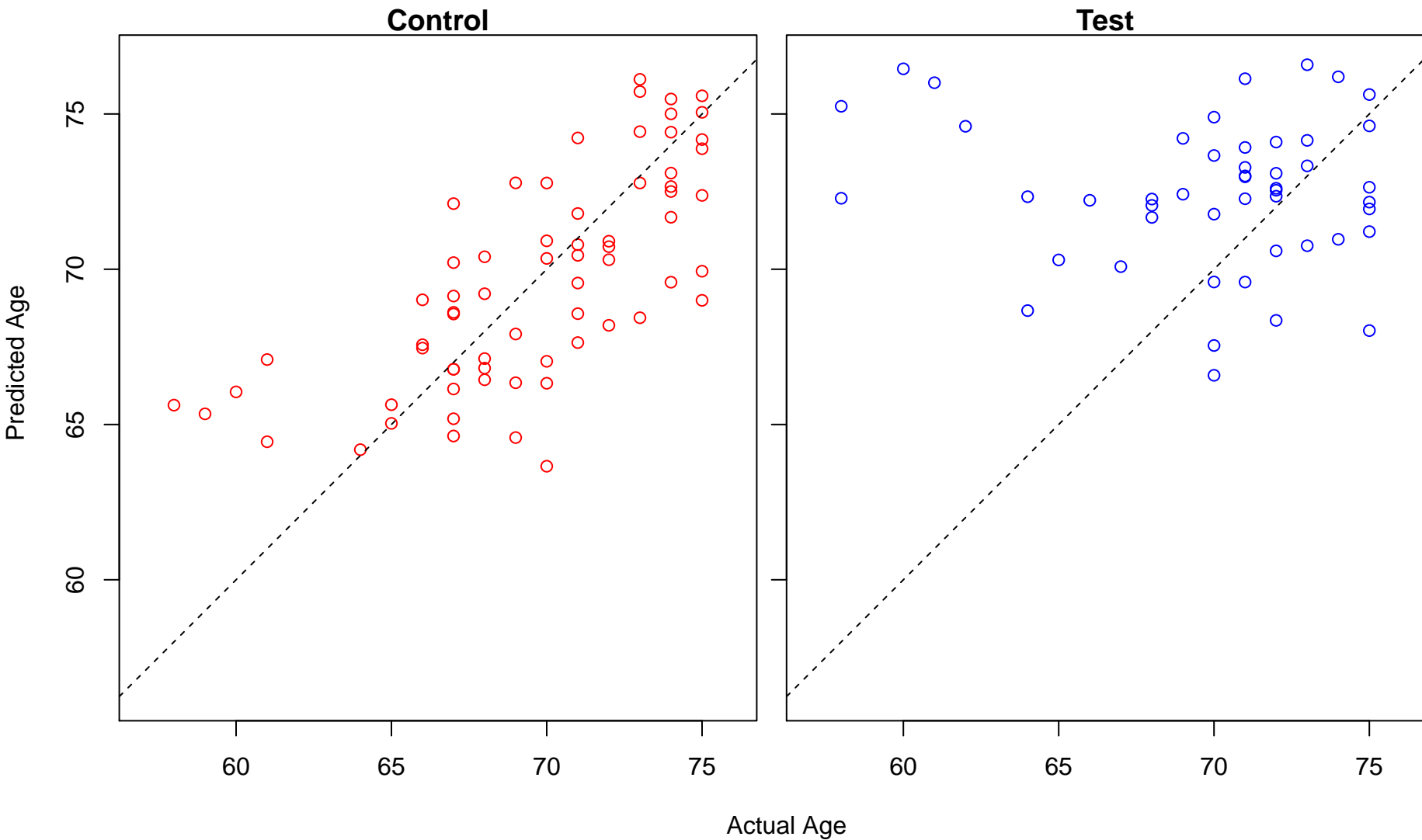
regulation of proteolysis involved in cellular protein catabolic process (Score: 1.794548)



regulation of mononuclear cell proliferation (Score: 1.794288)

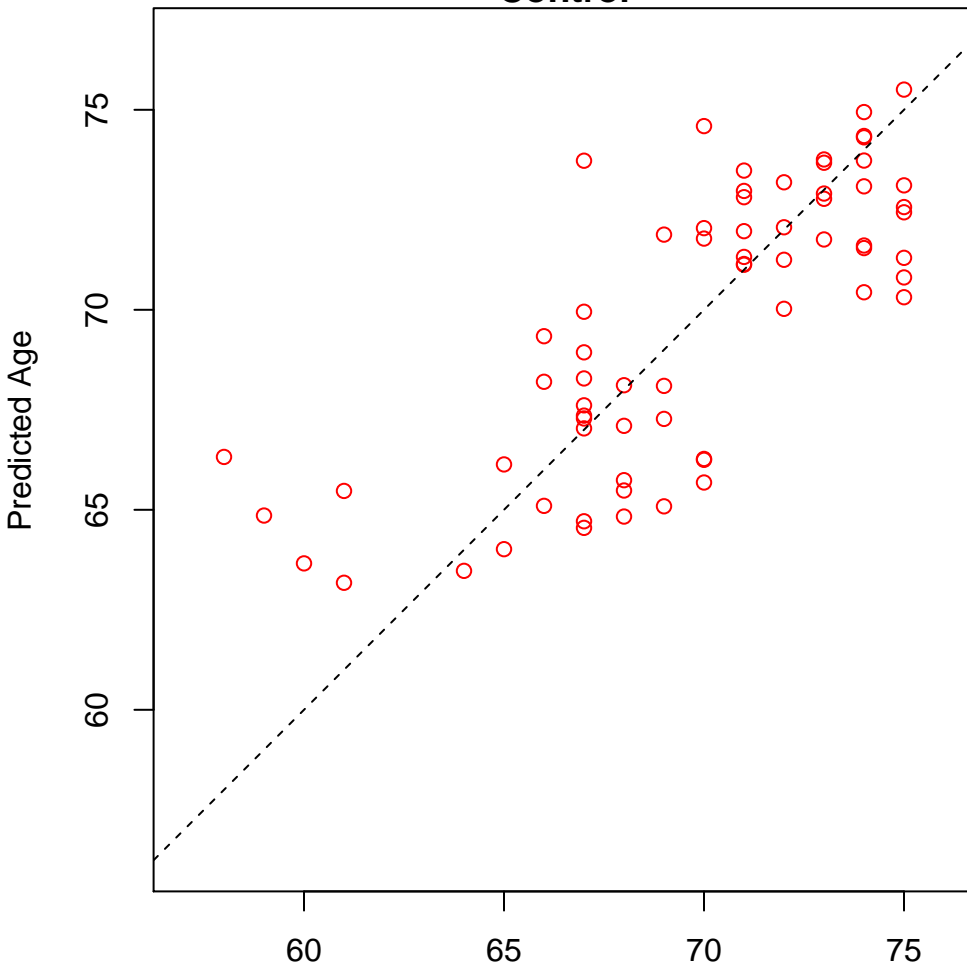


regulation of cytokinesis (Score: 1.794109)

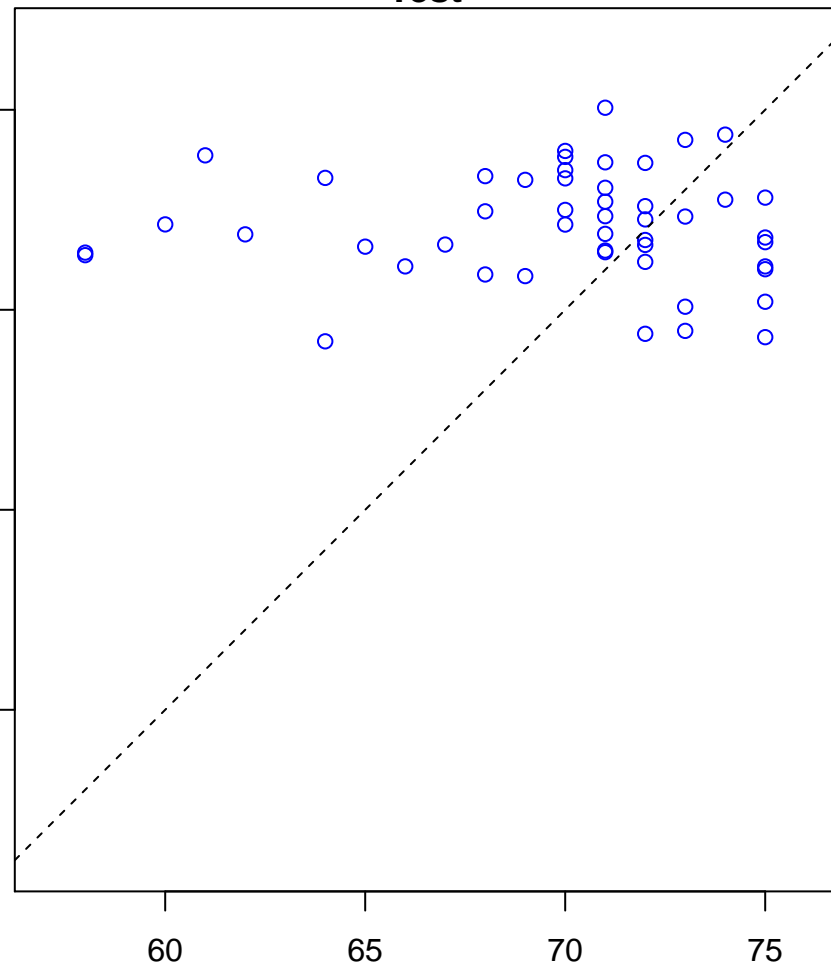


regulation of centrosome duplication (Score: 1.793695)

Control

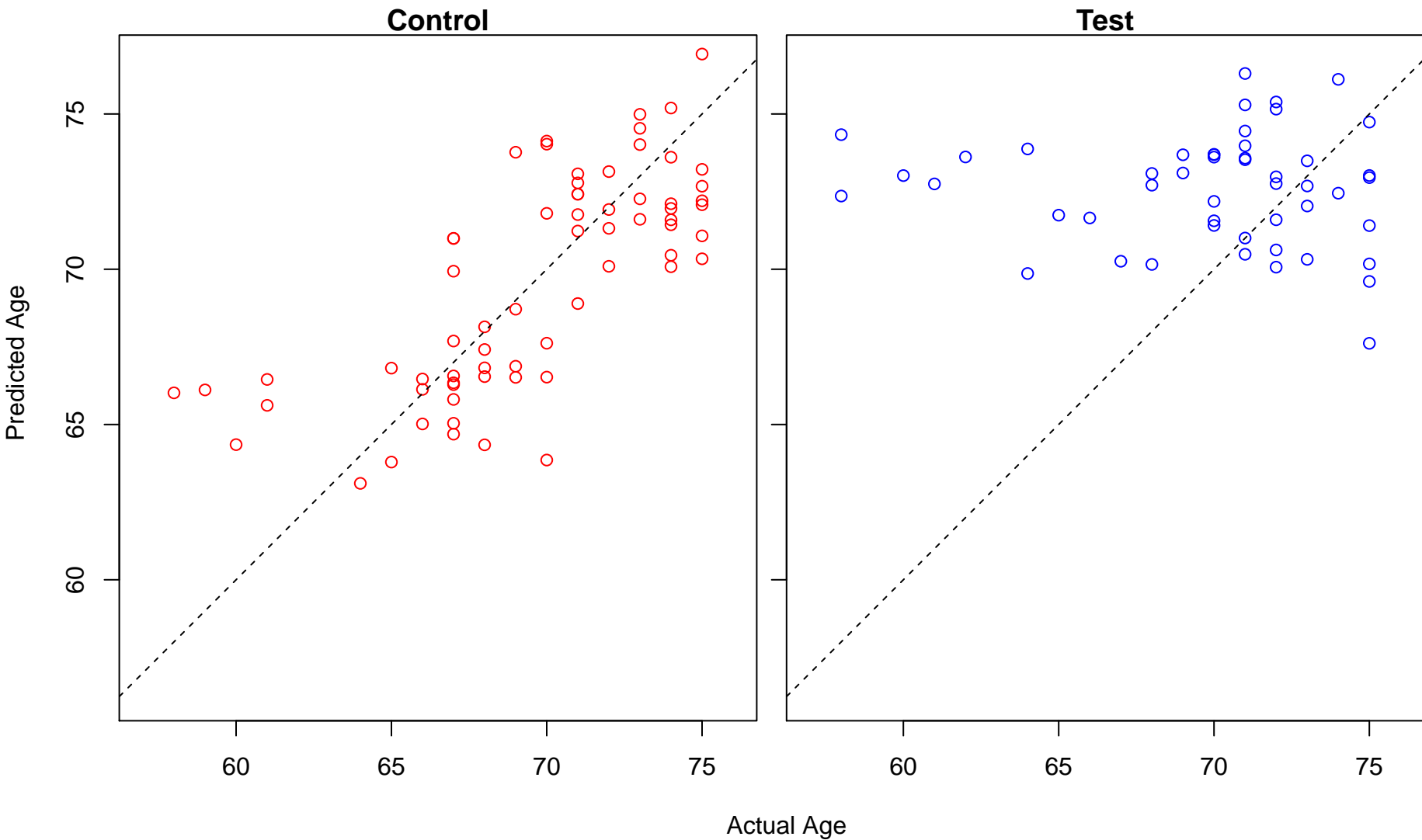


Test

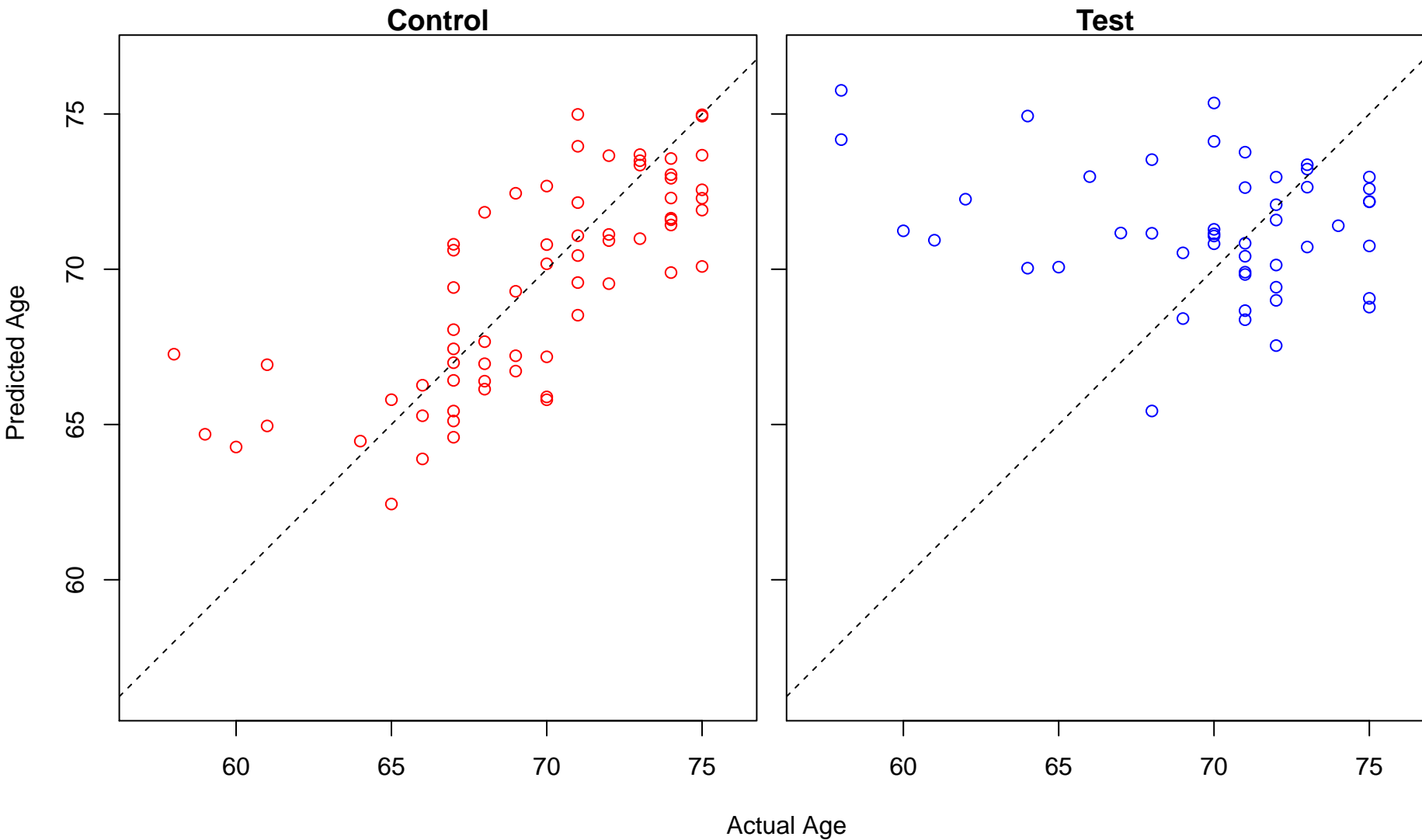


Actual Age

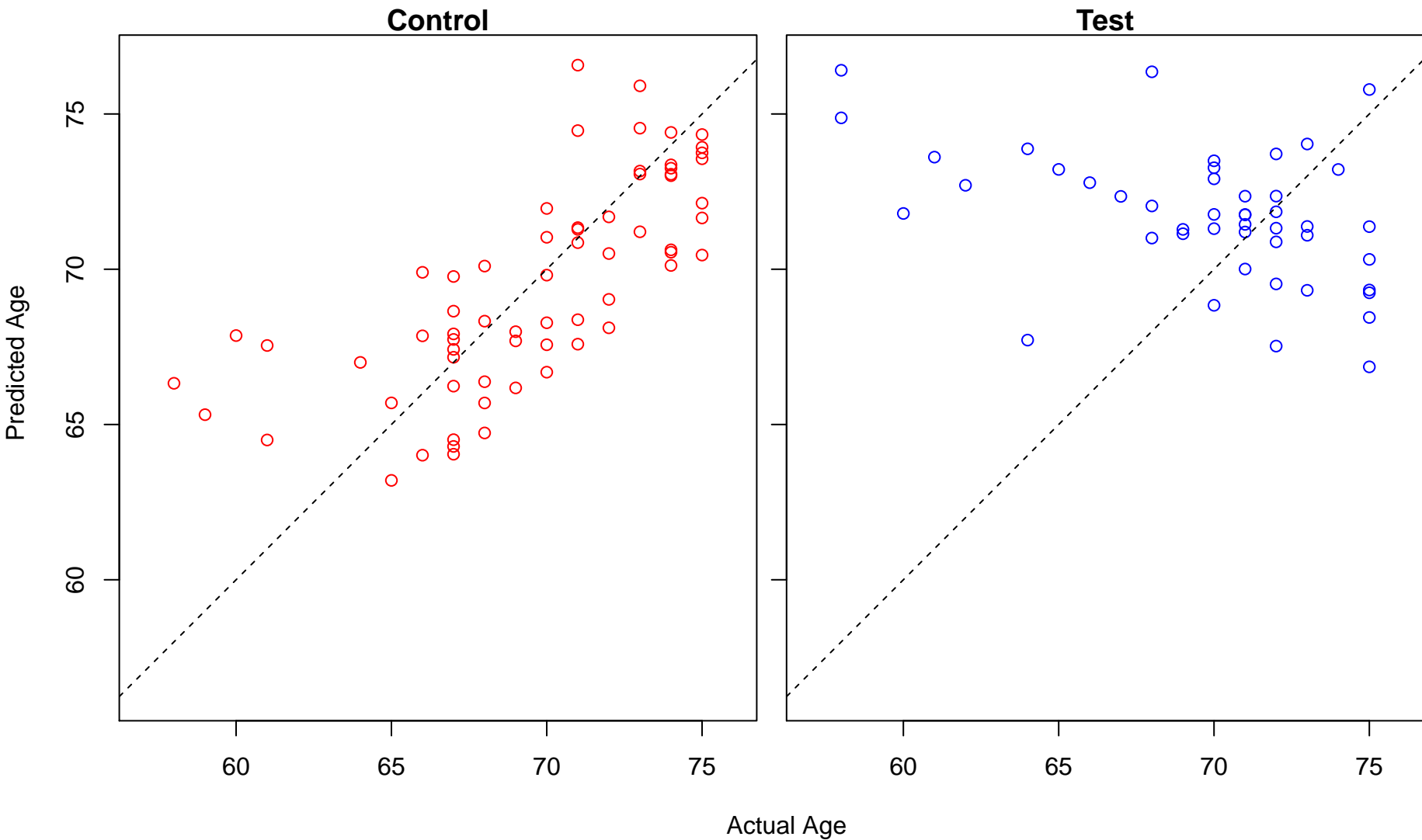
organelle localization (Score: 1.793656)



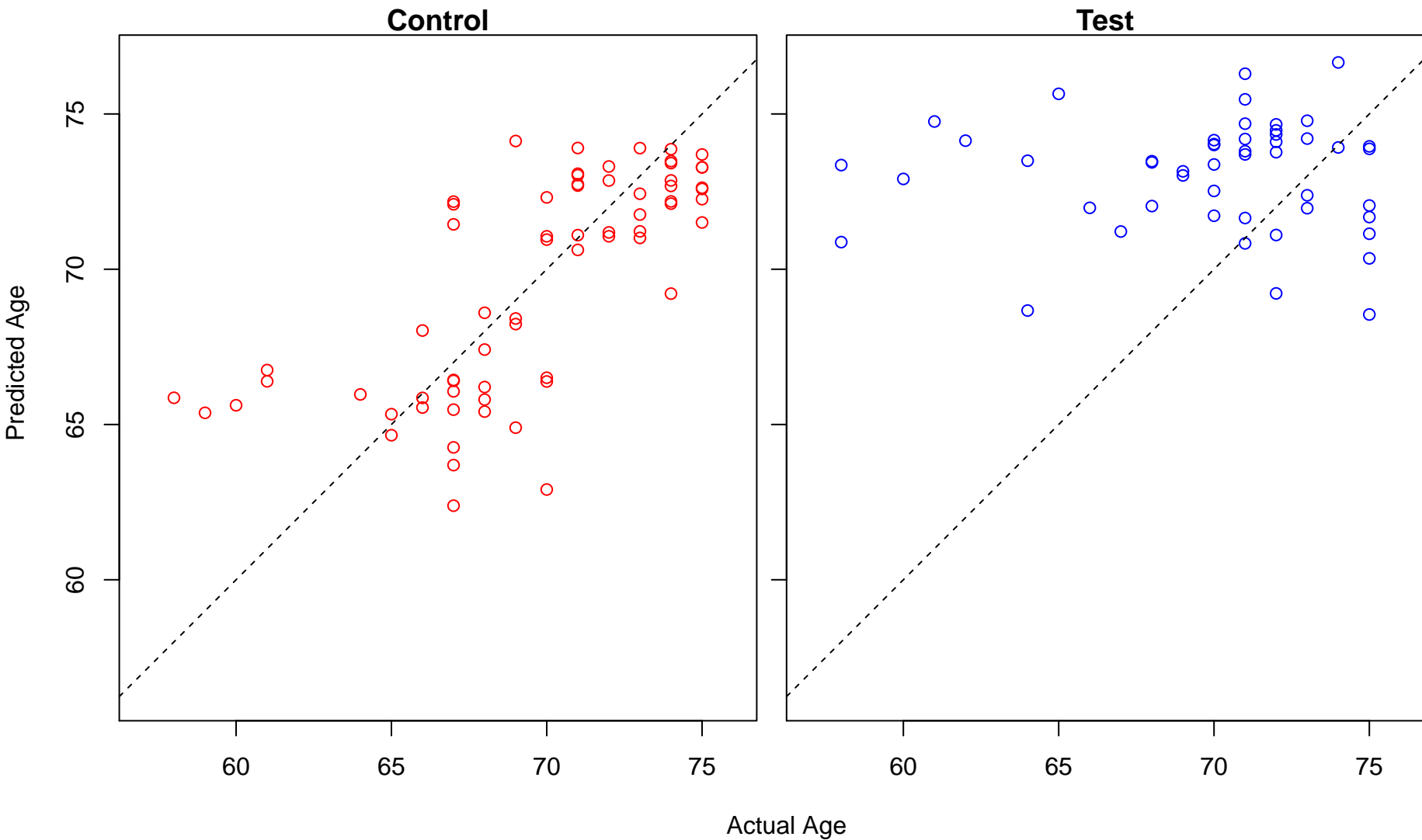
vacuolar transport (Score: 1.793375)



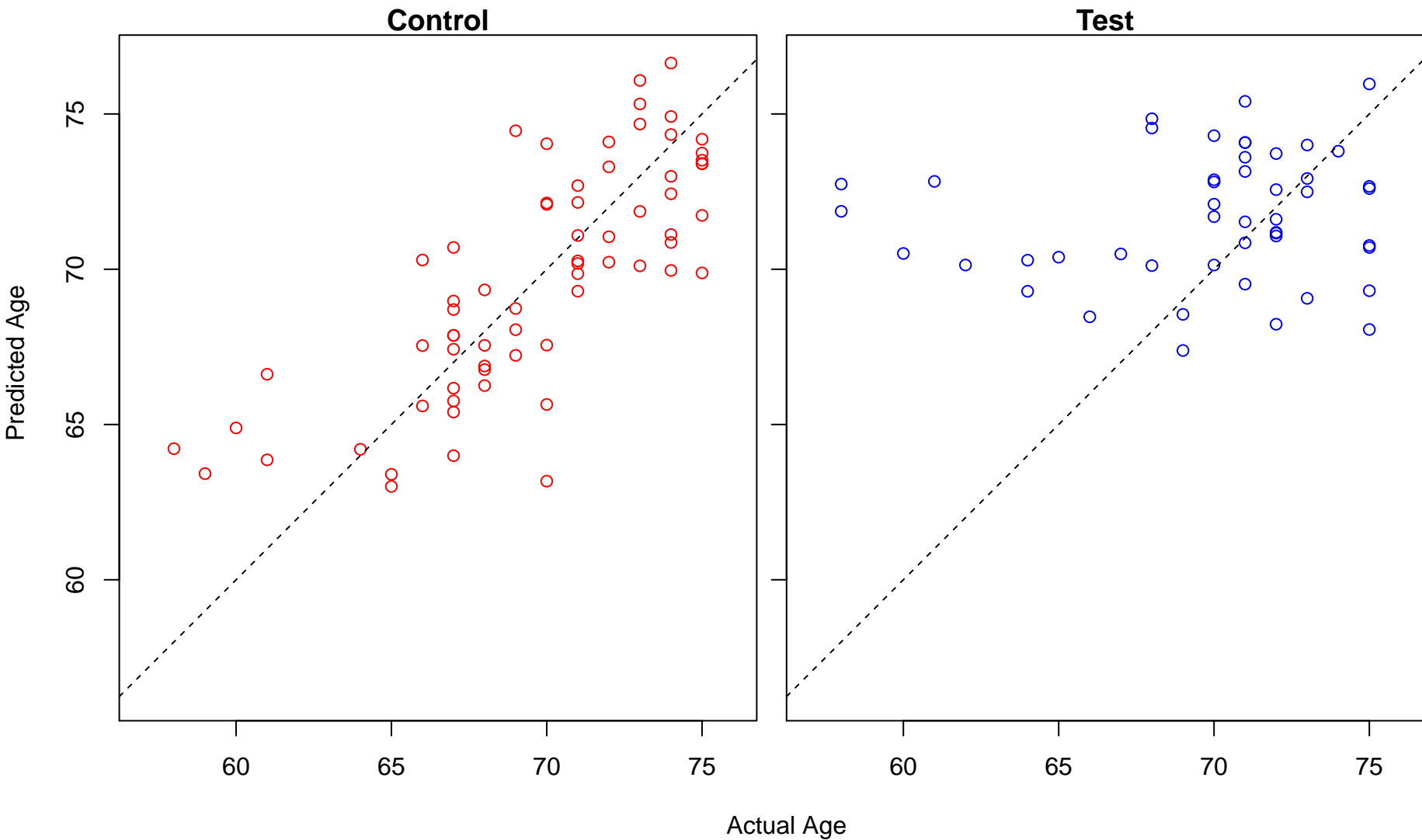
regulation of leukocyte proliferation (Score: 1.793220)



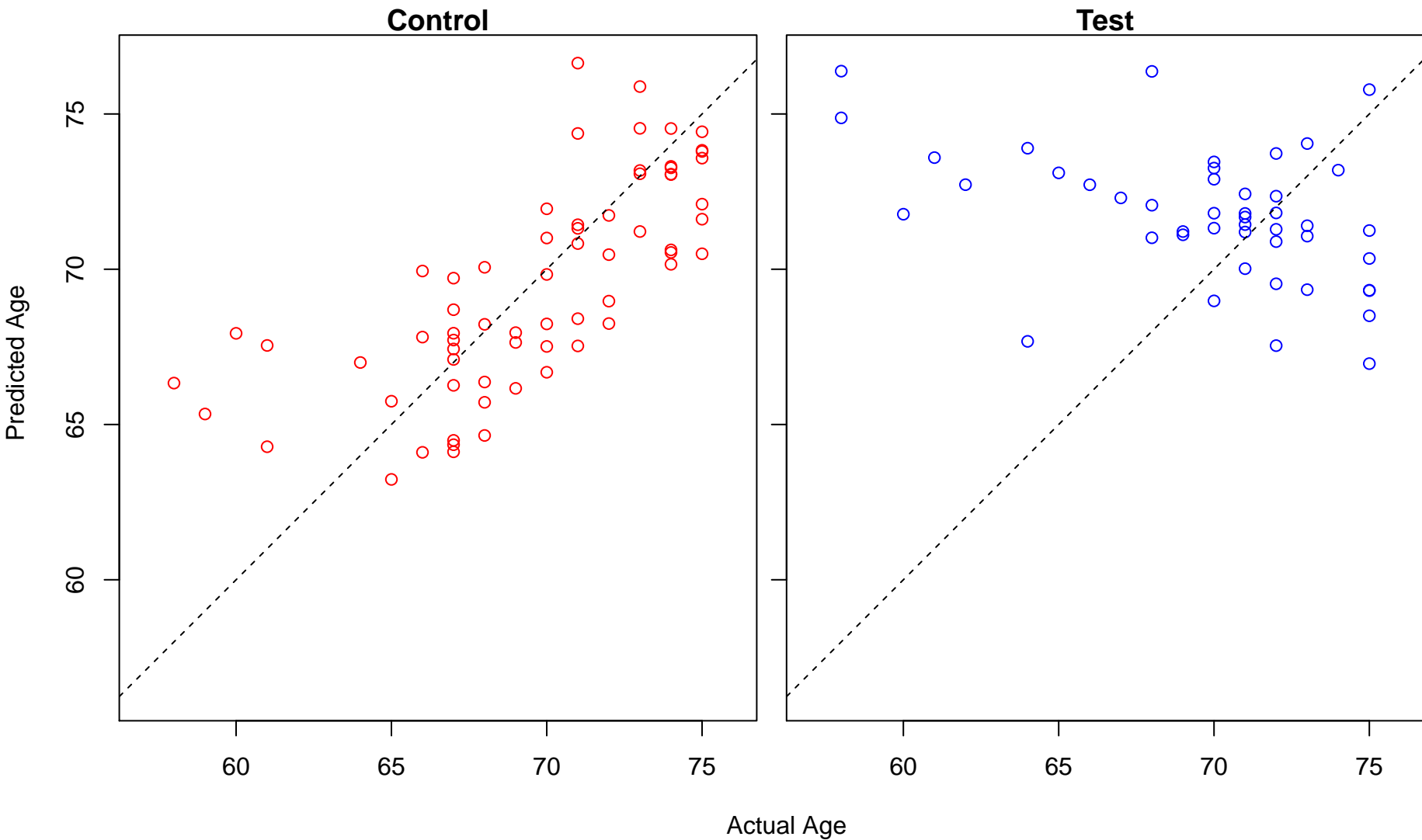
mRNA metabolic process (Score: 1.793115)



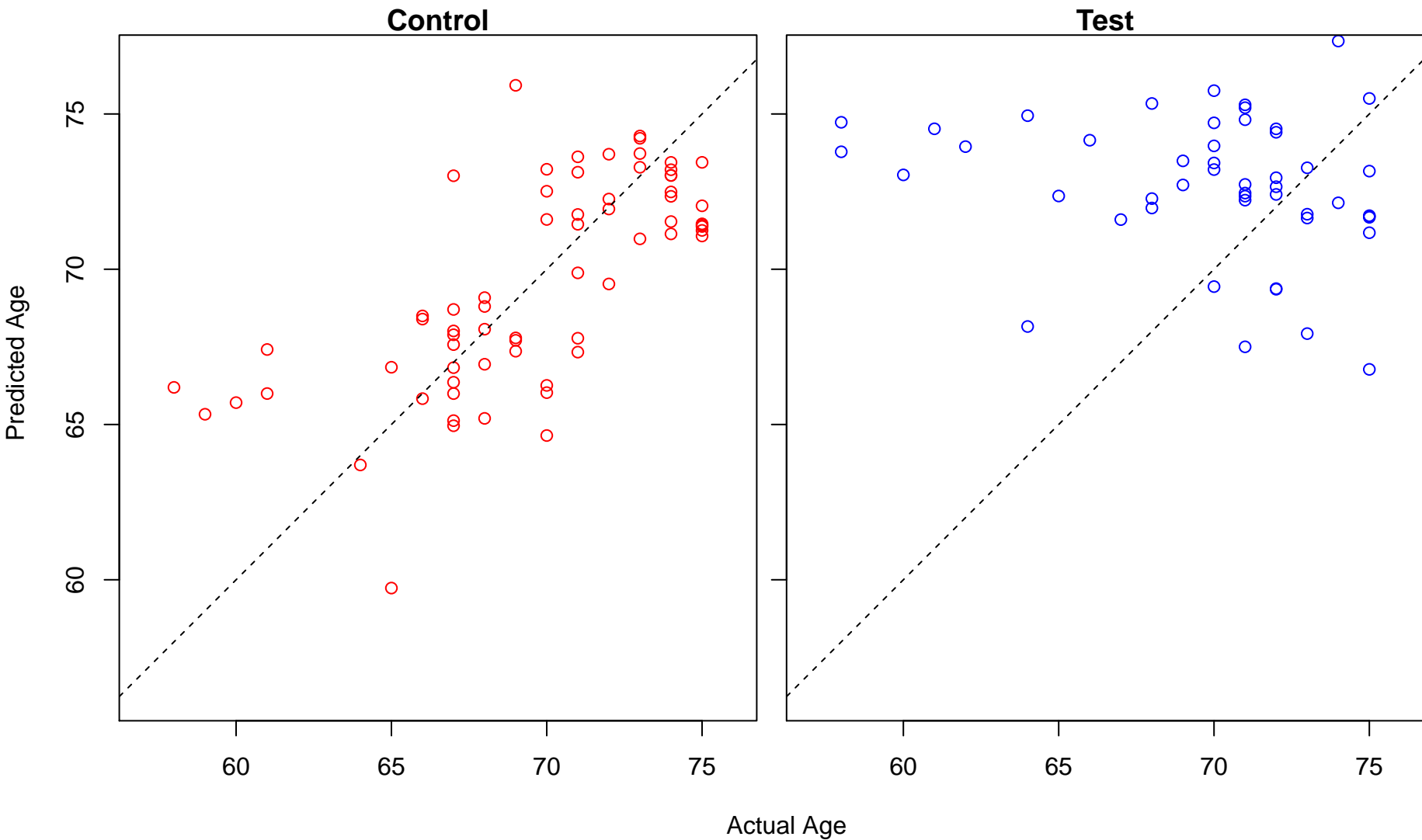
vascular endothelial growth factor receptor signaling pathway (Score: 1.791409)



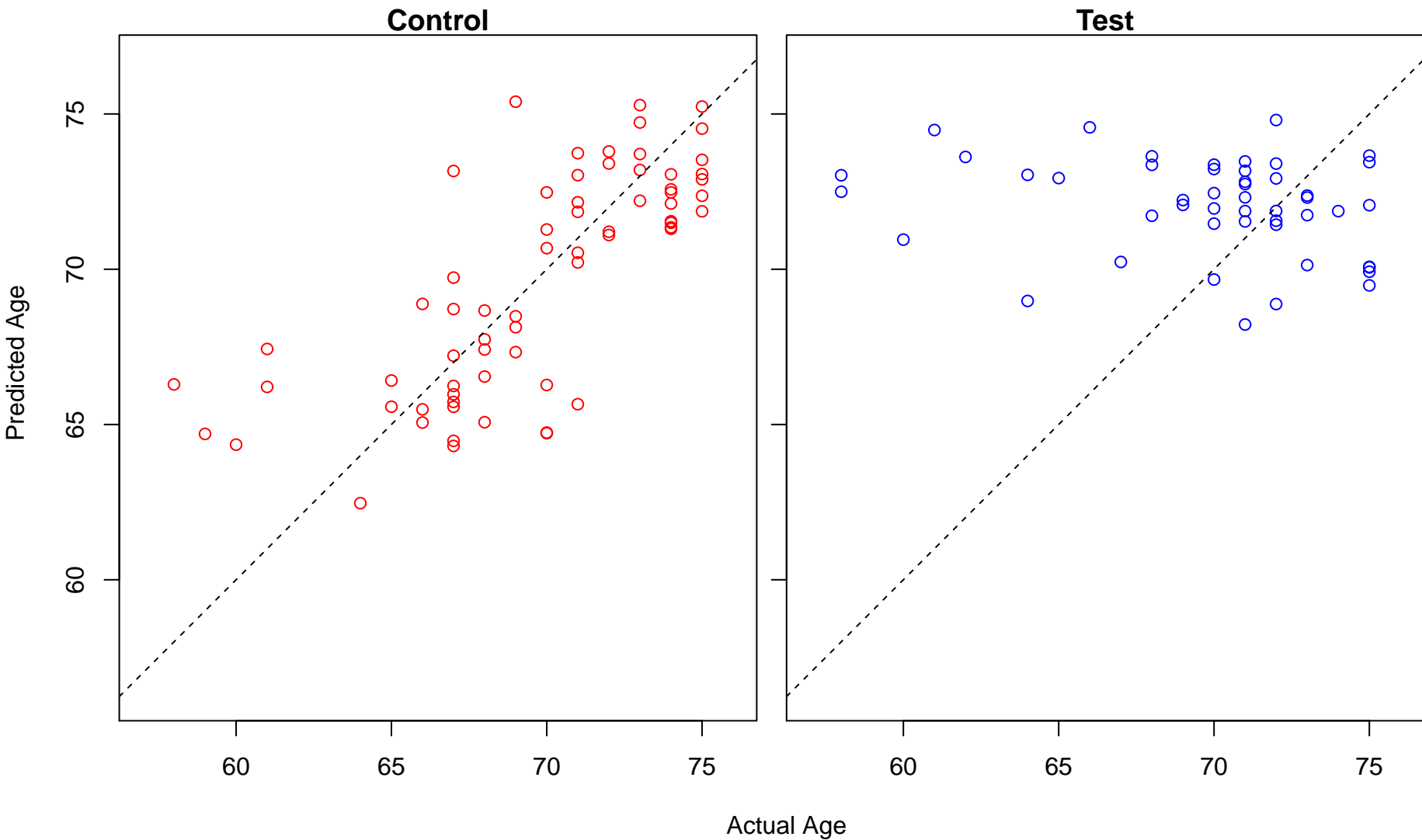
regulation of lymphocyte proliferation (Score: 1.791041)



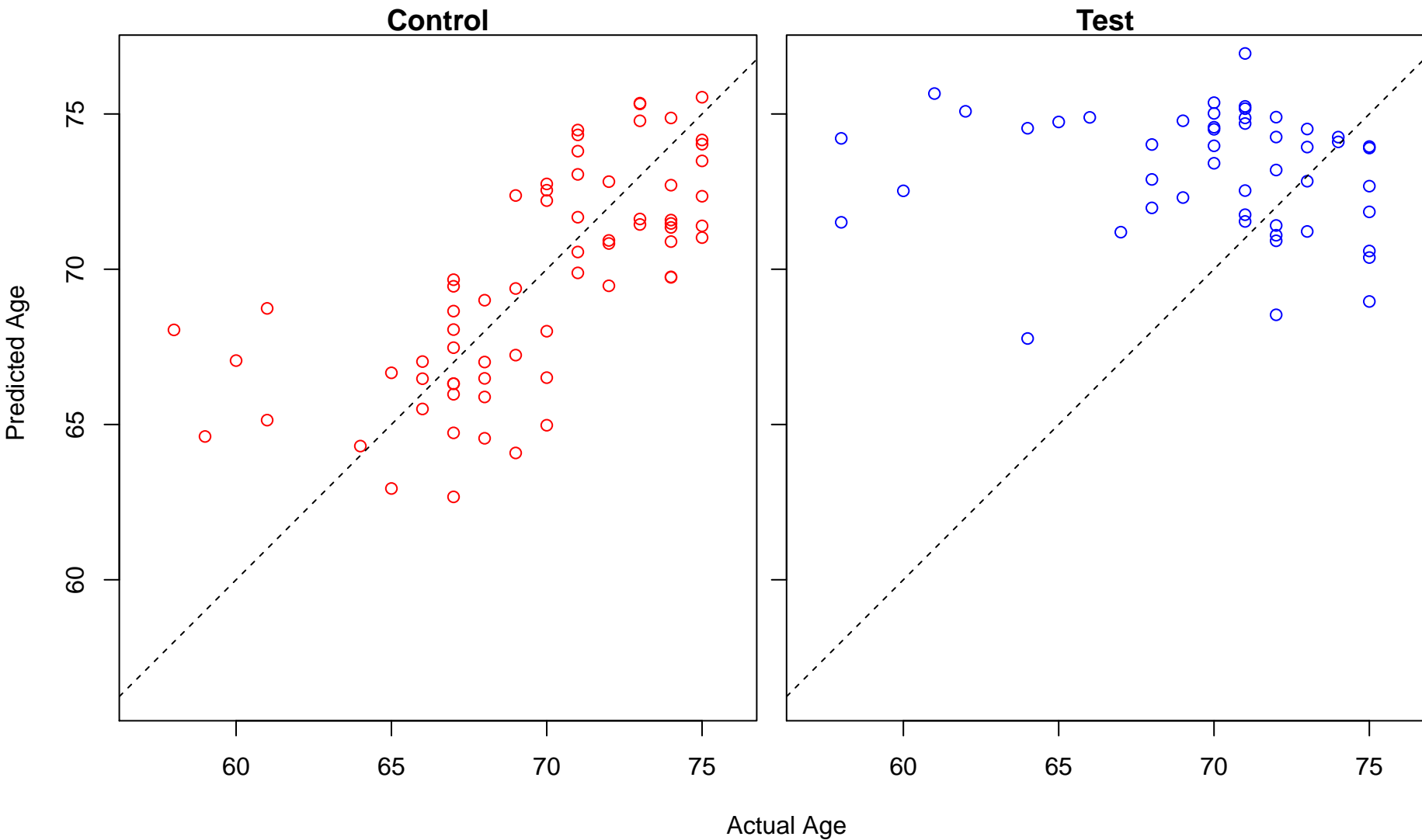
positive regulation of cytokine production (Score: 1.790996)



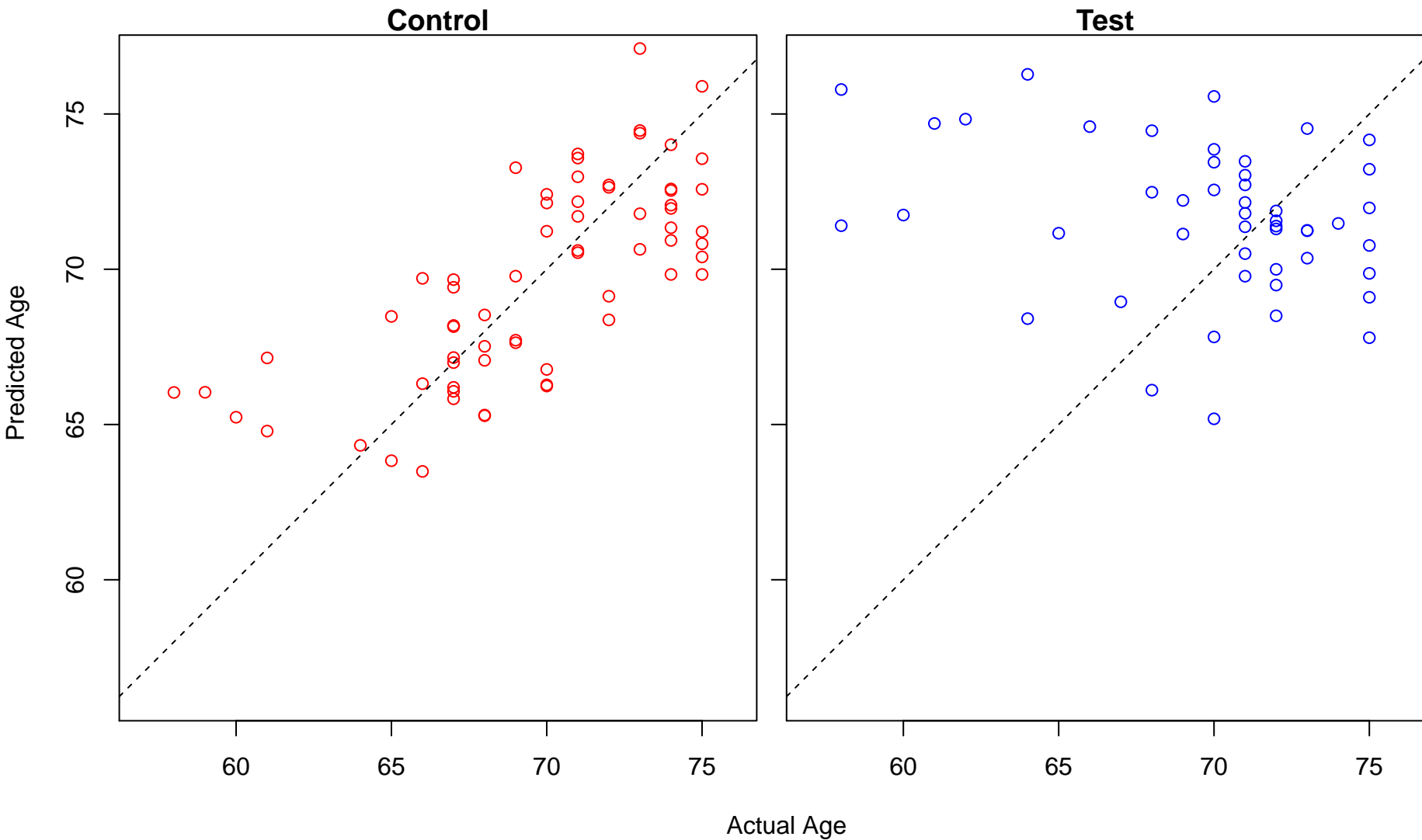
response to biotic stimulus (Score: 1.790918)



circadian rhythm (Score: 1.790821)

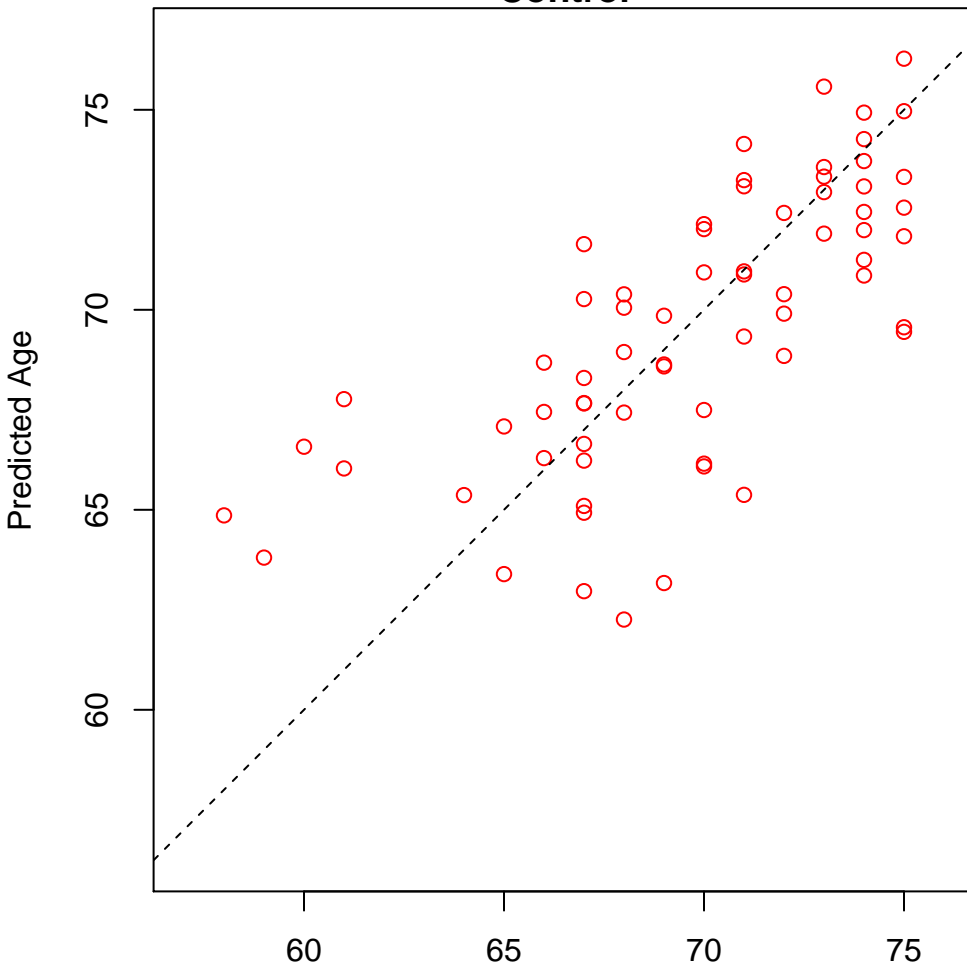


fatty acid beta-oxidation using acyl-CoA dehydrogenase (Score: 1.790626)

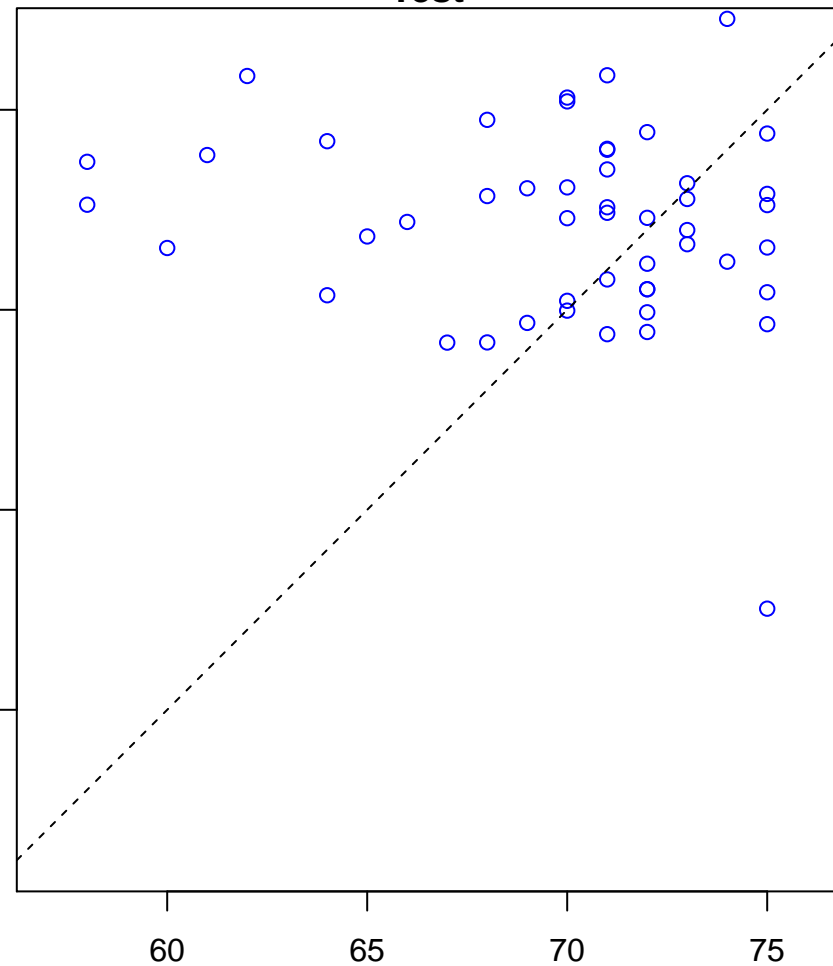


response to extracellular stimulus (Score: 1.790113)

Control

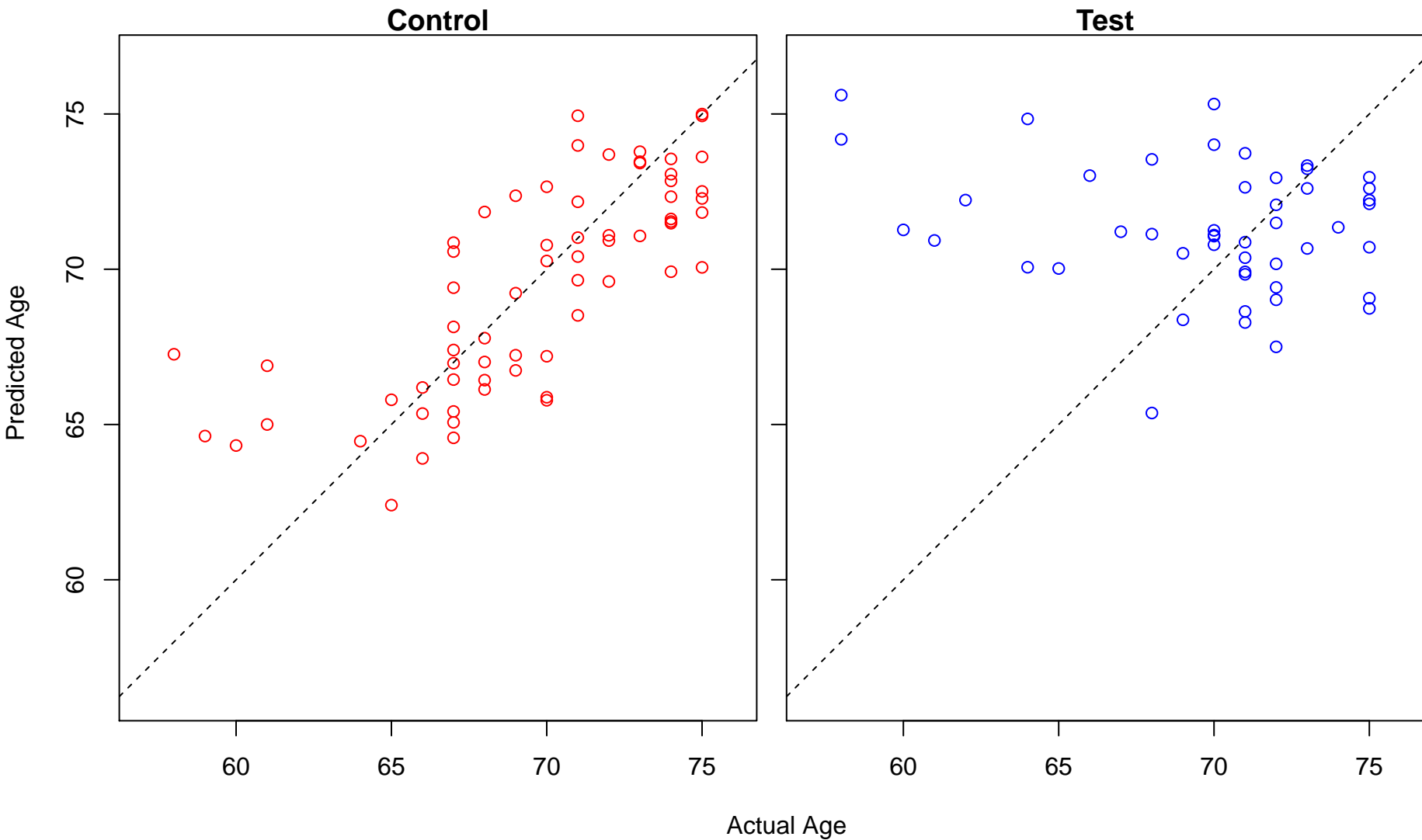


Test

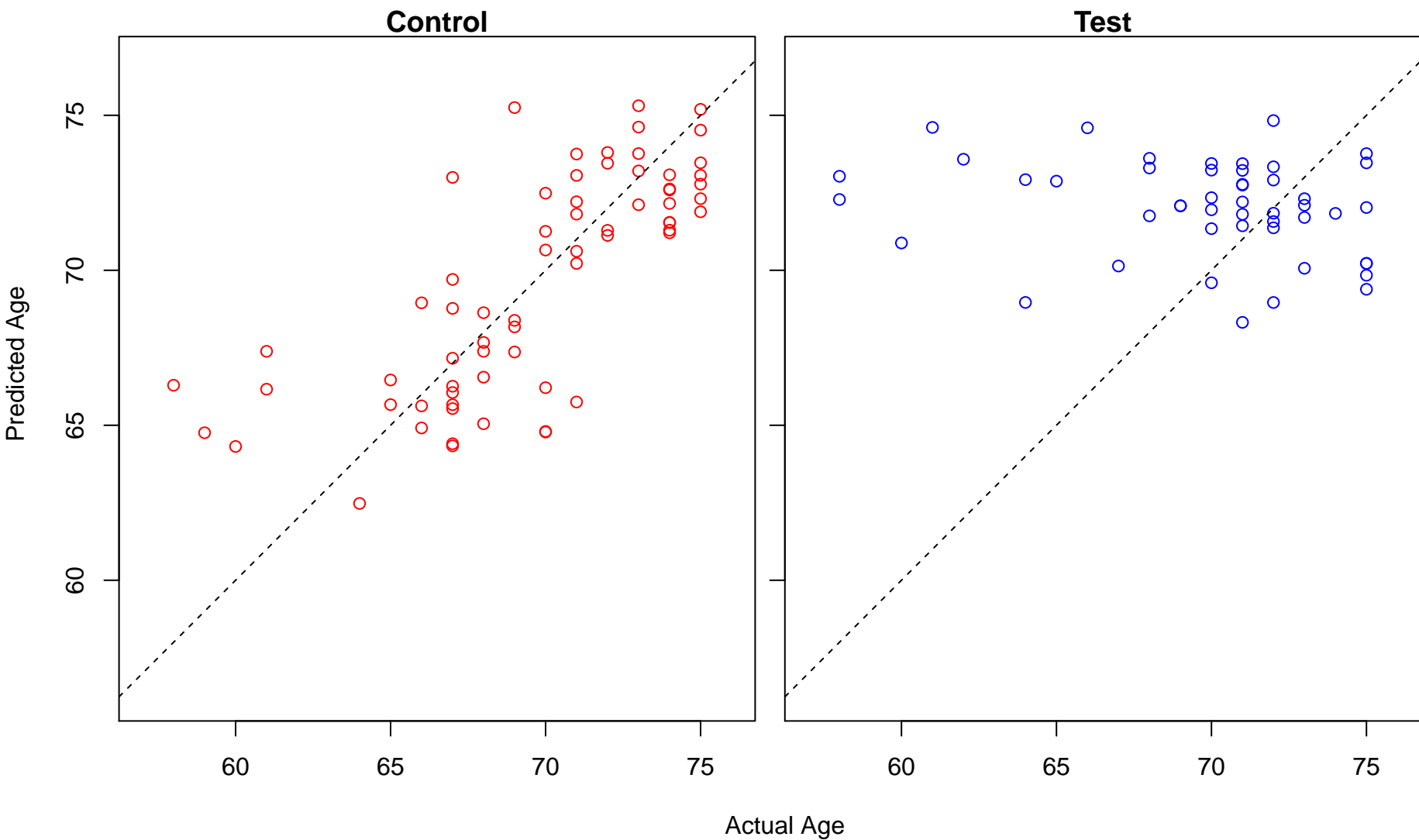


Actual Age

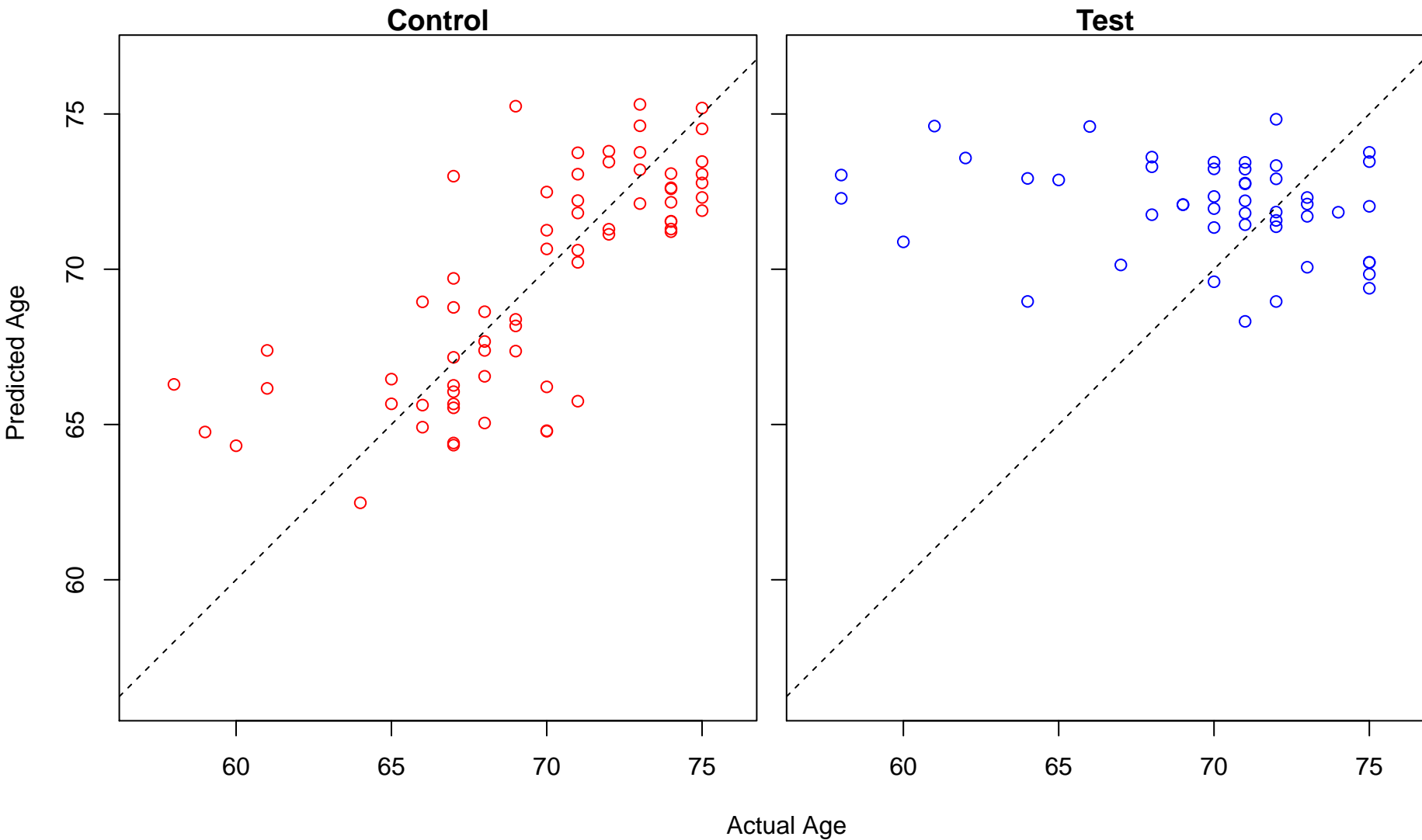
lysosomal transport (Score: 1.789532)



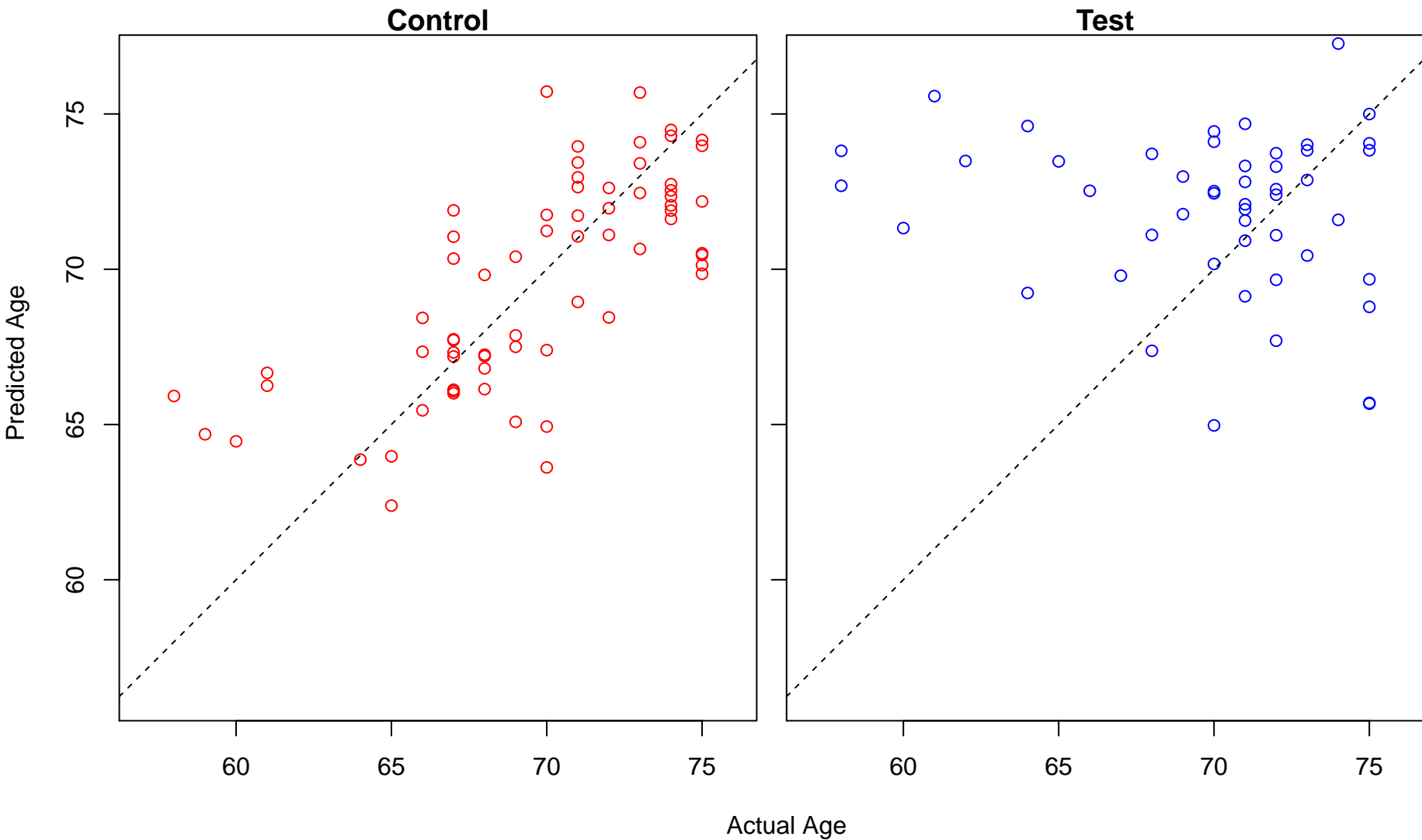
response to external biotic stimulus (Score: 1.789393)



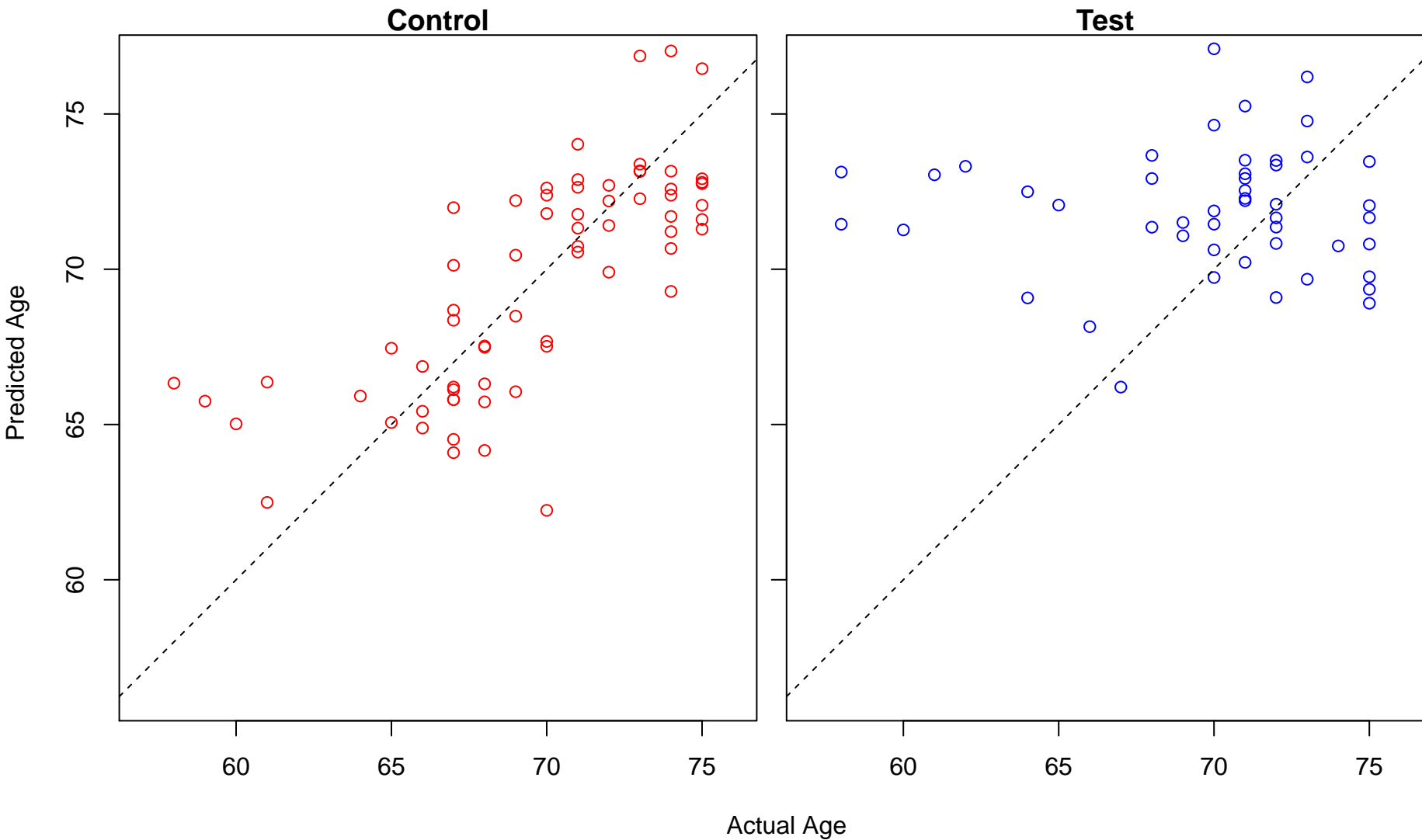
response to other organism (Score: 1.789393)



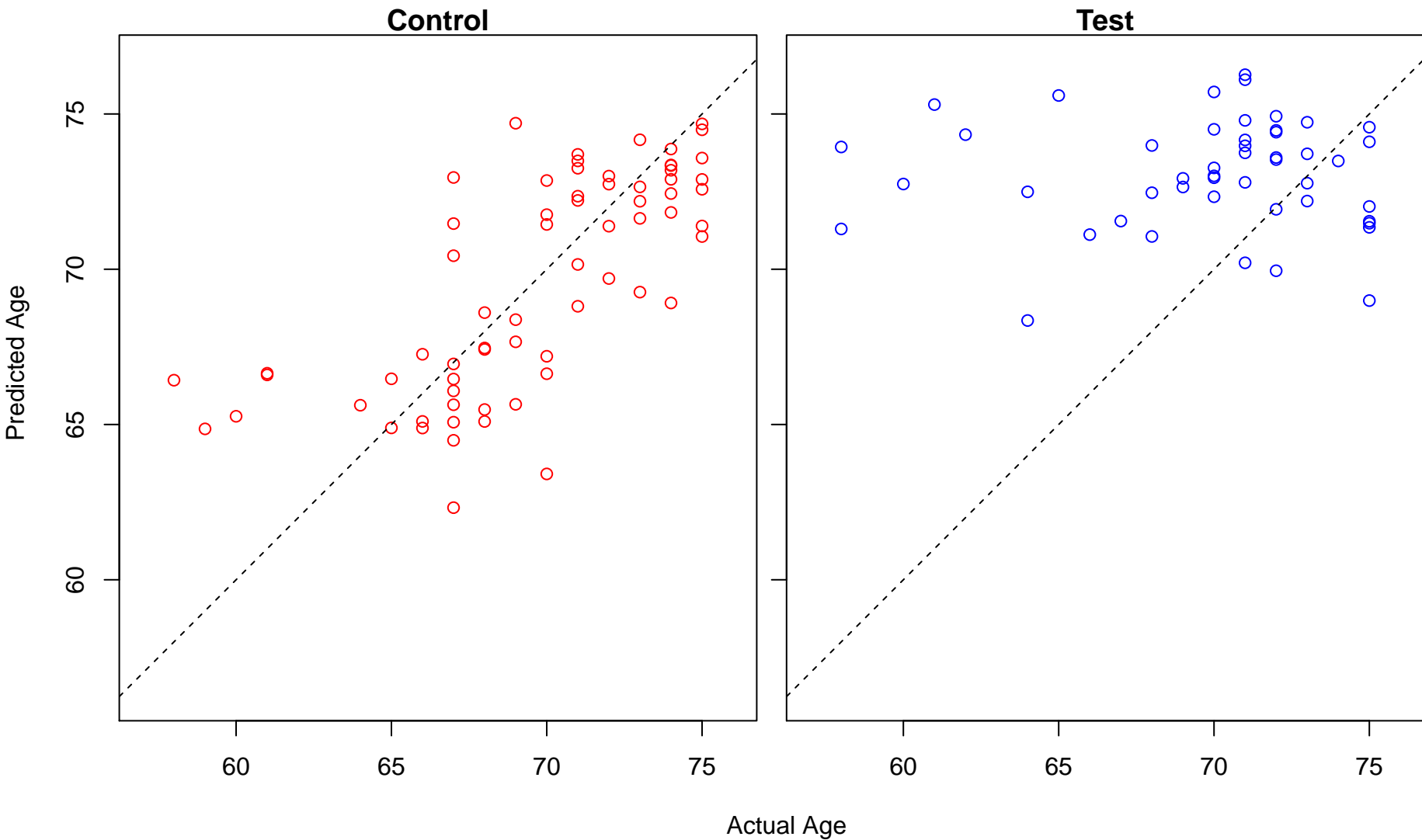
positive regulation of cation transmembrane transport (Score: 1.788739)



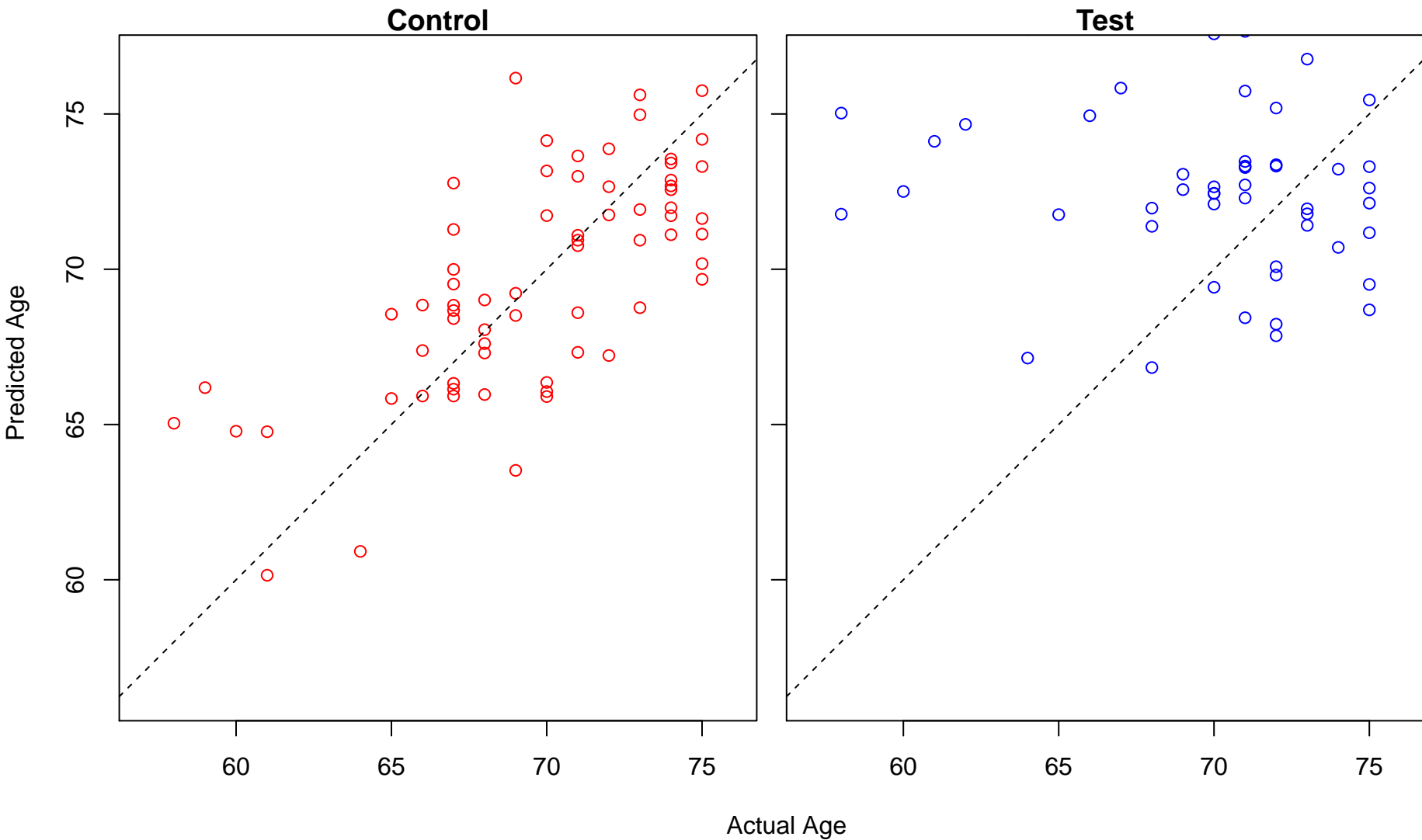
purine nucleoside triphosphate metabolic process (Score: 1.788486)



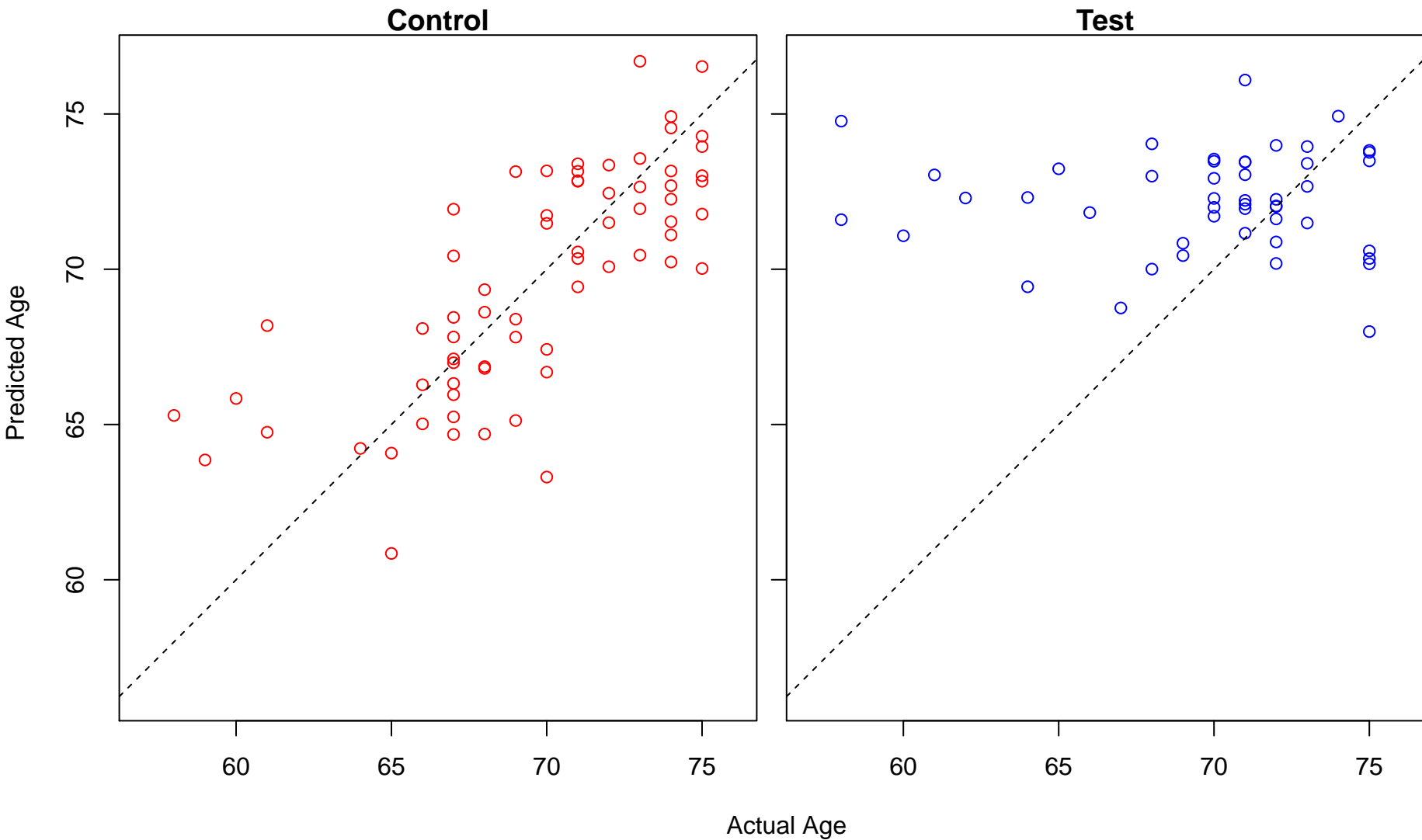
protein localization to membrane (Score: 1.788339)



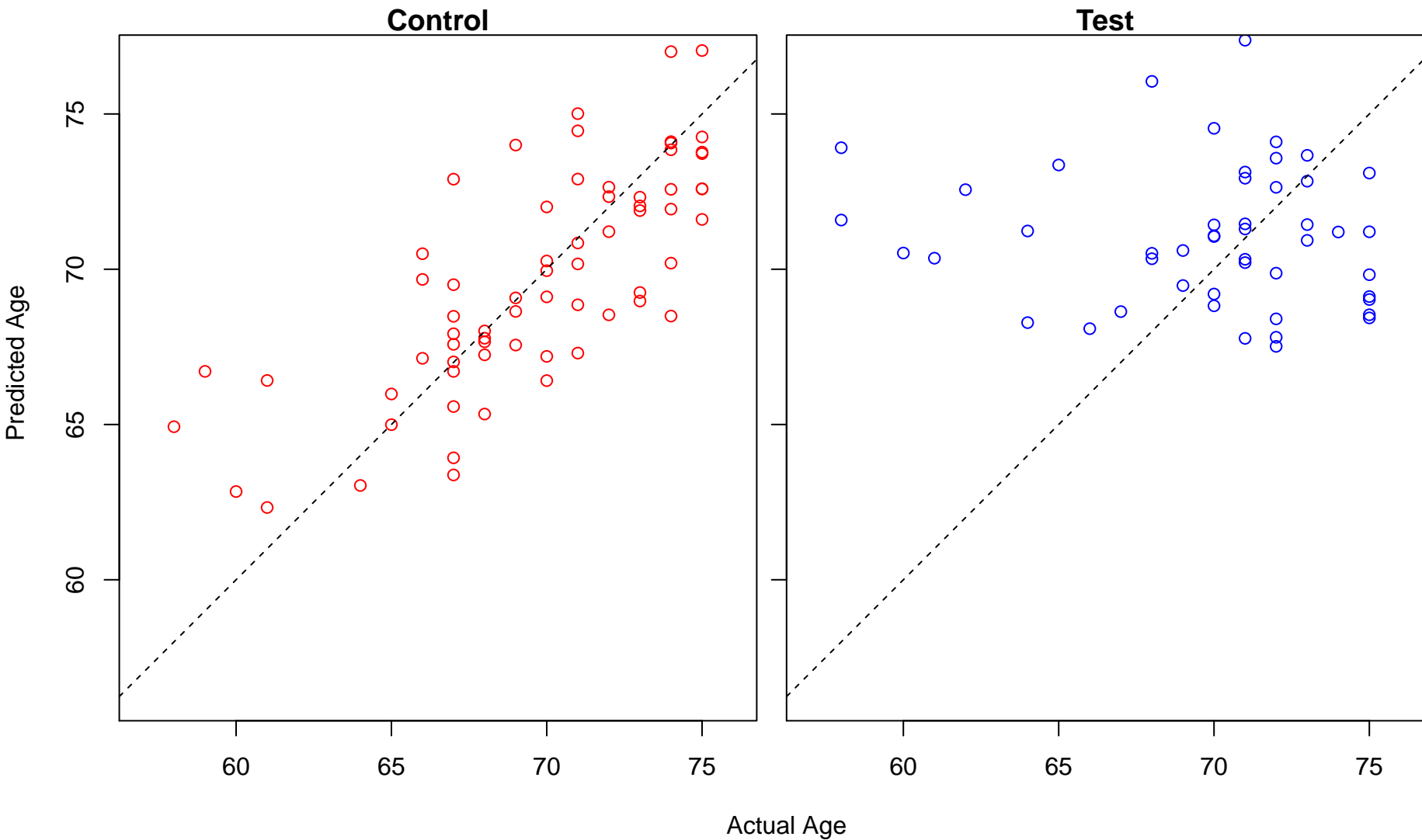
histone monoubiquitination (Score: 1.788183)



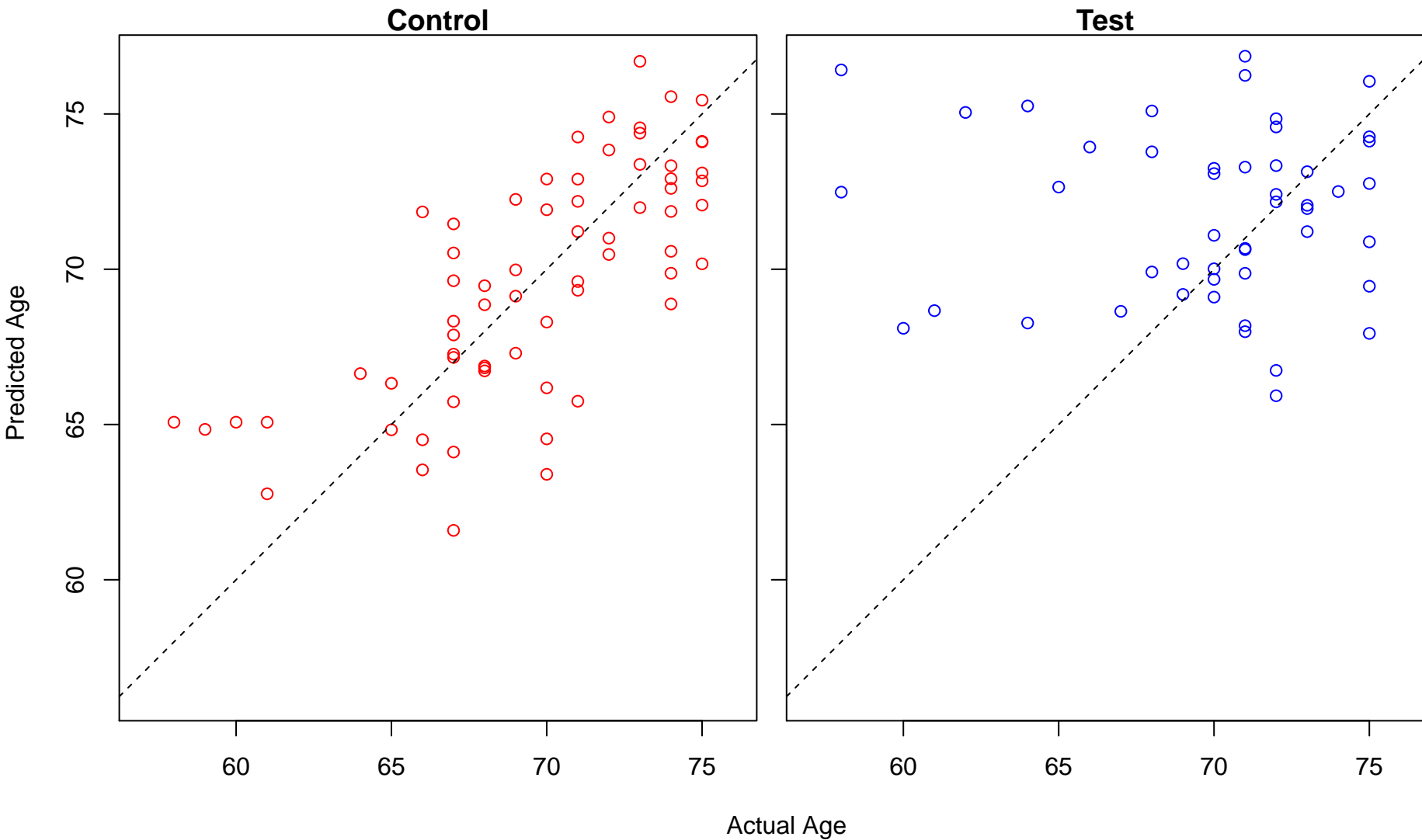
DNA damage checkpoint (Score: 1.787568)



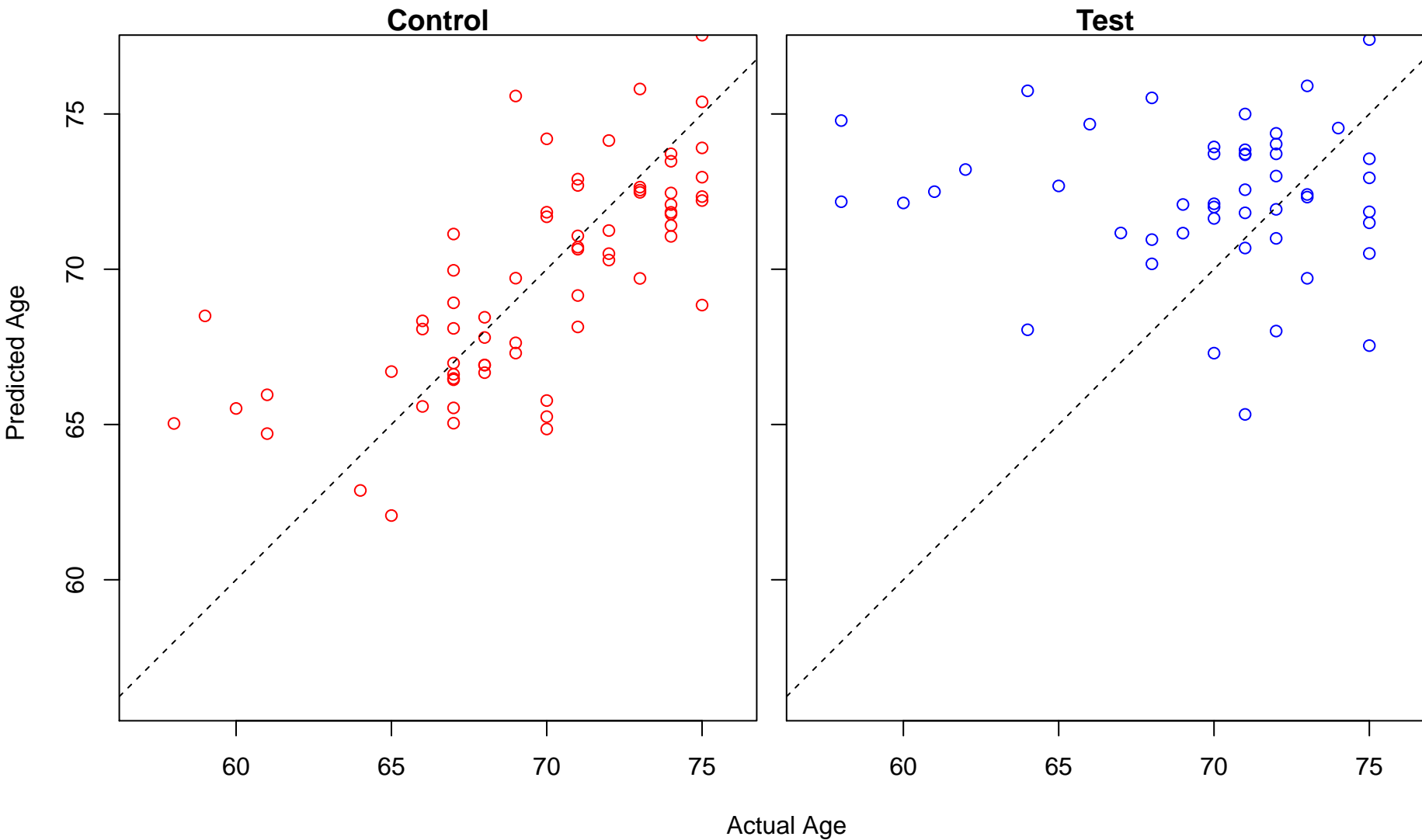
regulation of monocyte differentiation (Score: 1.787492)



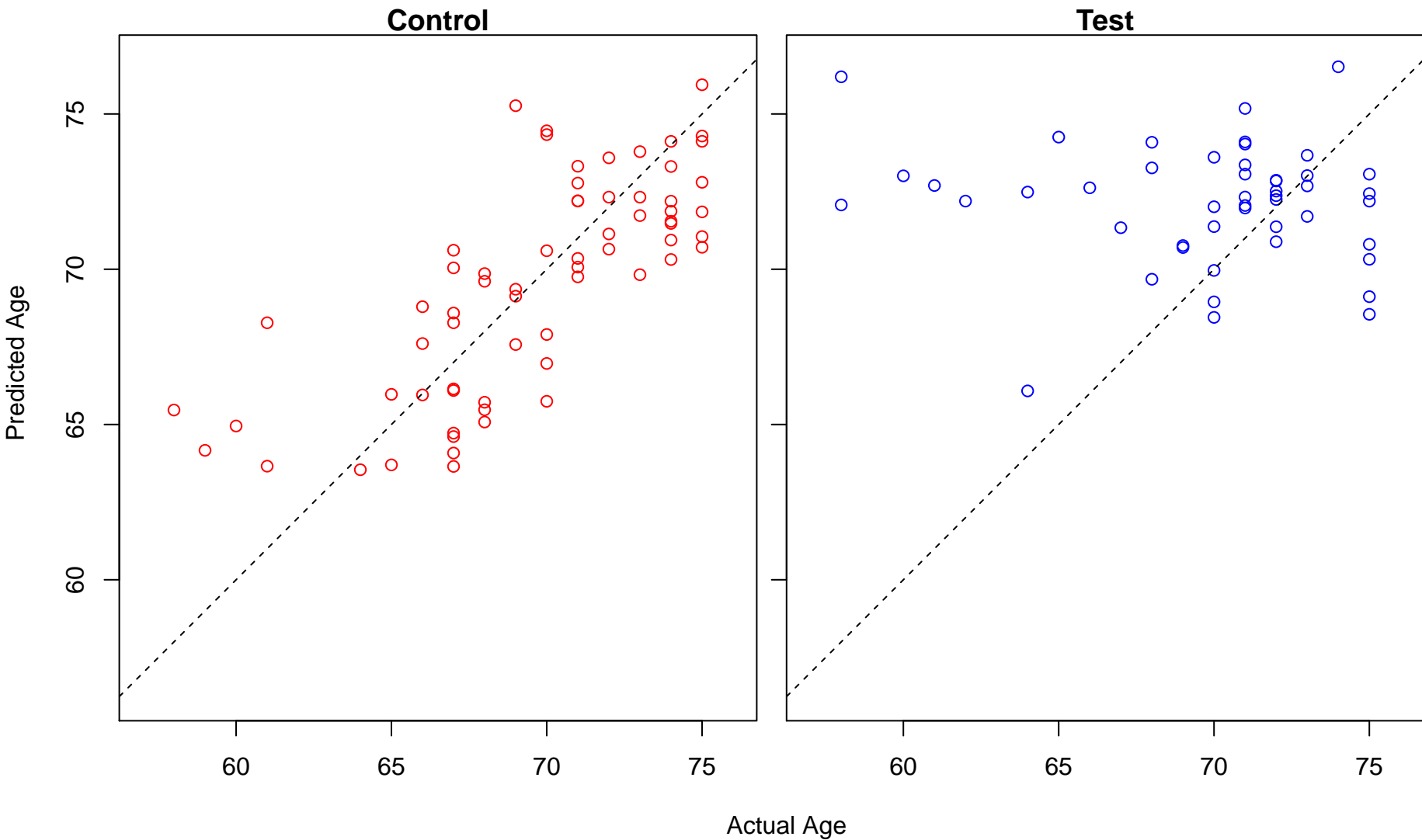
regulation of receptor activity (Score: 1.787420)



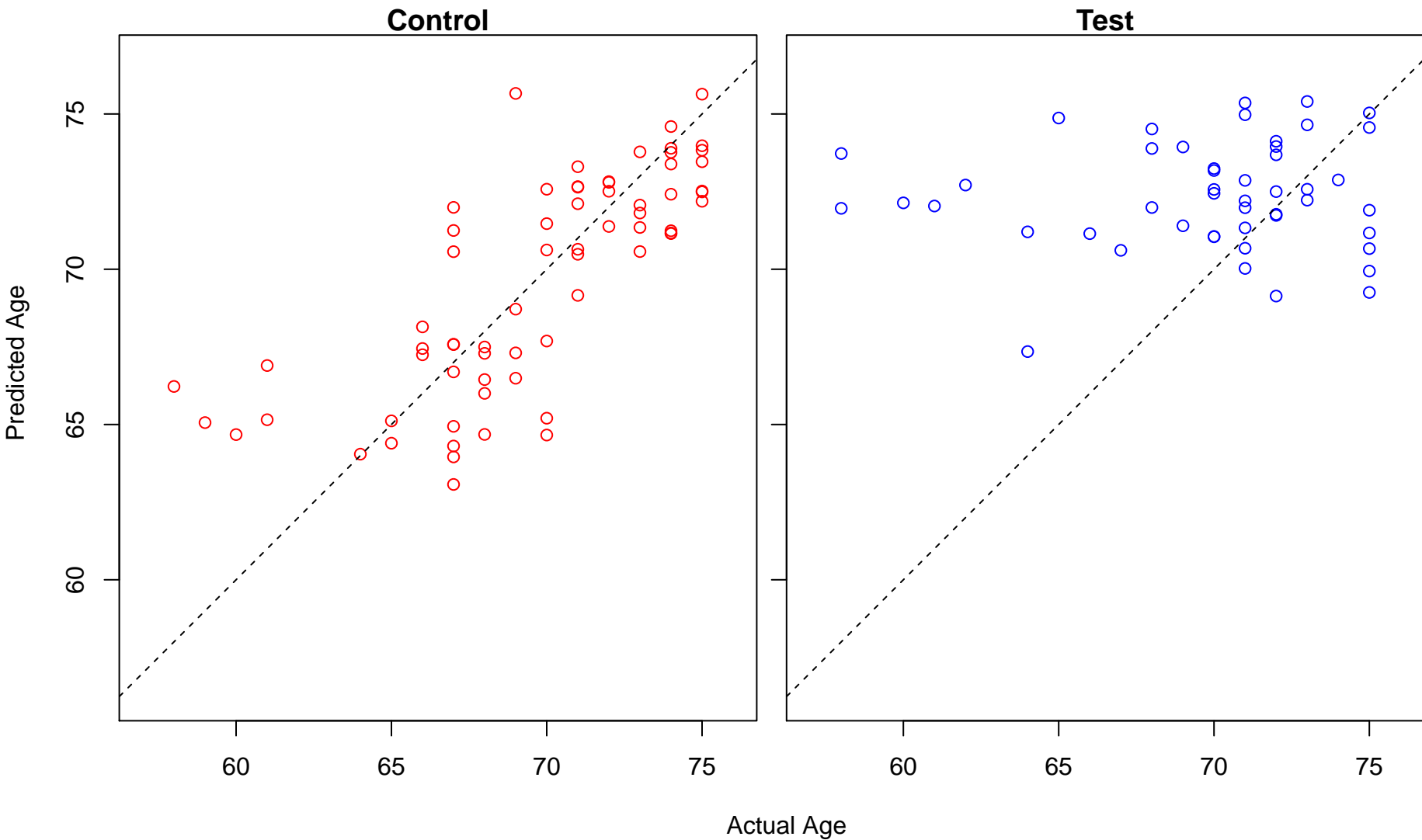
TRIF-dependent toll-like receptor signaling pathway (Score: 1.787255)



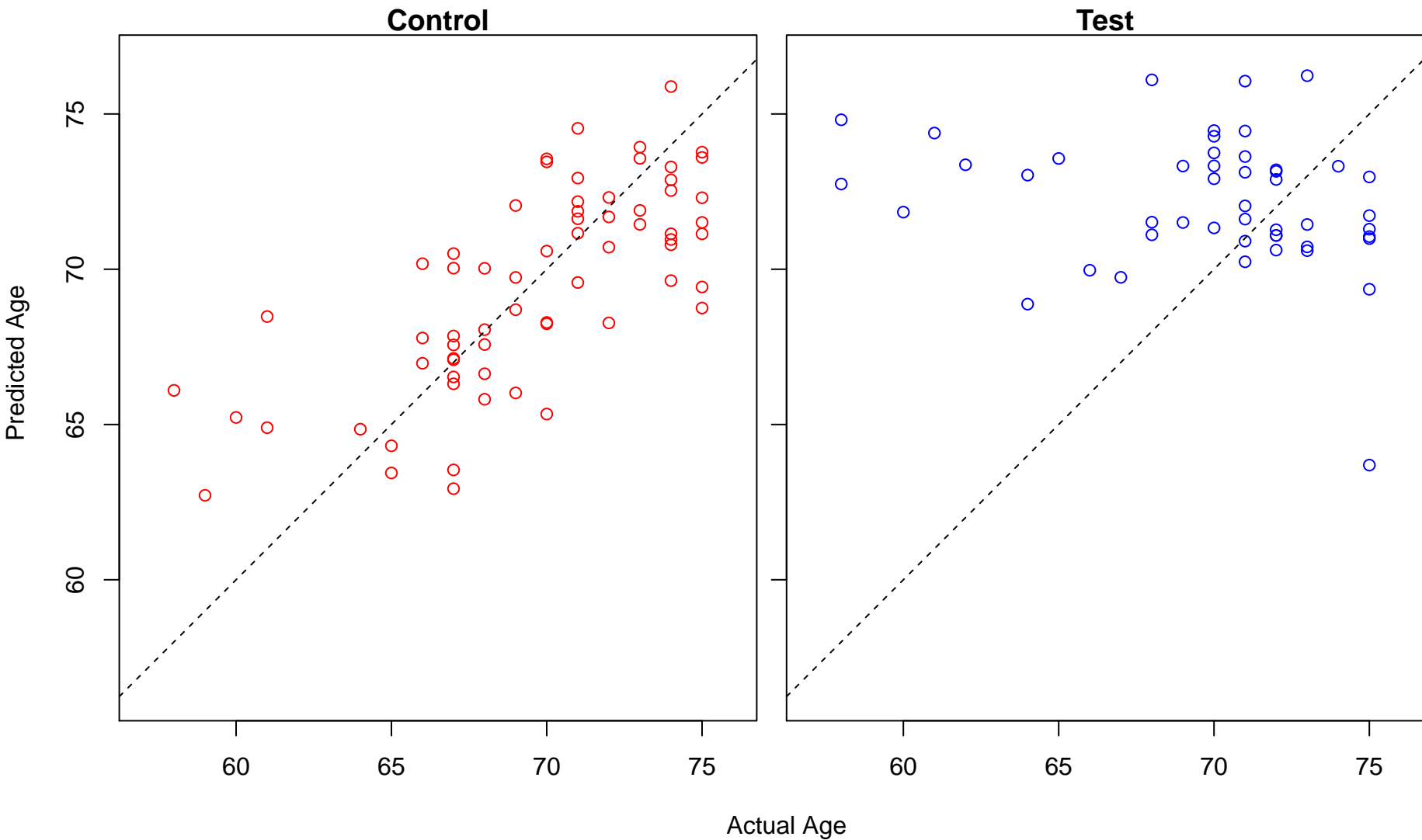
positive regulation of DNA metabolic process (Score: 1.786059)



nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay (Score: 1.785877)

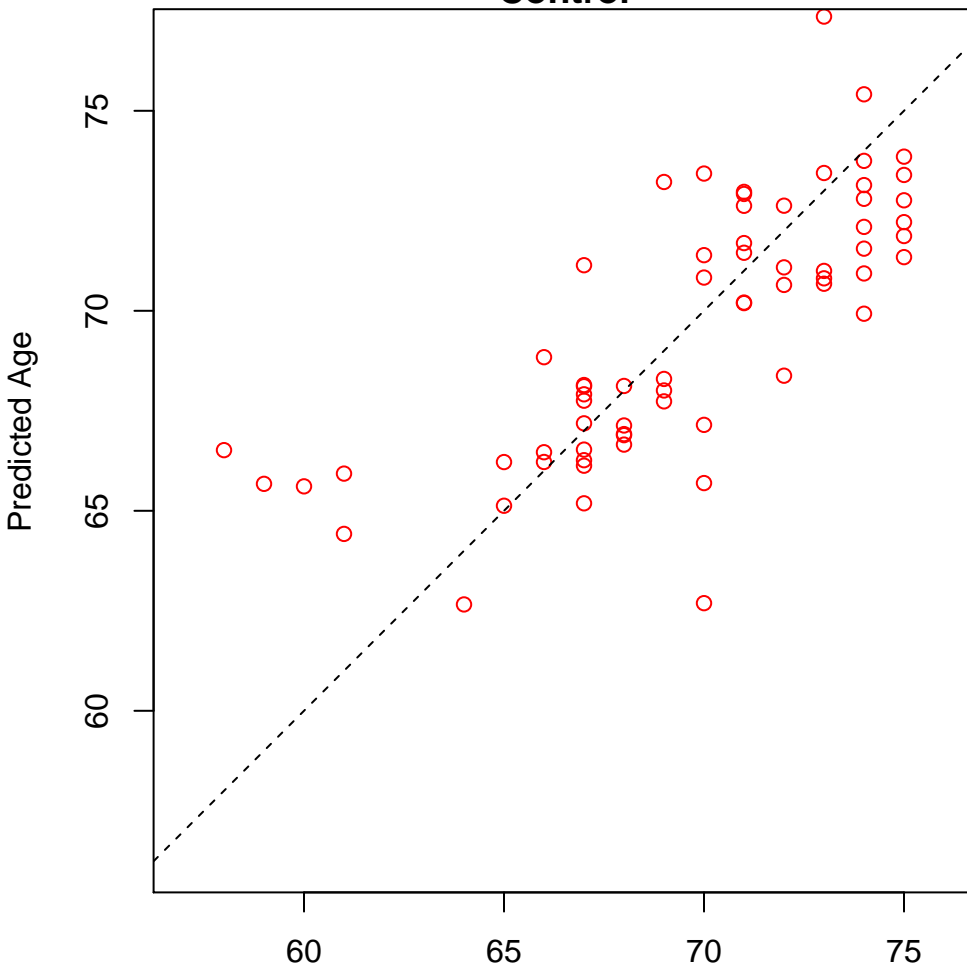


regulation of response to DNA damage stimulus (Score: 1.785563)

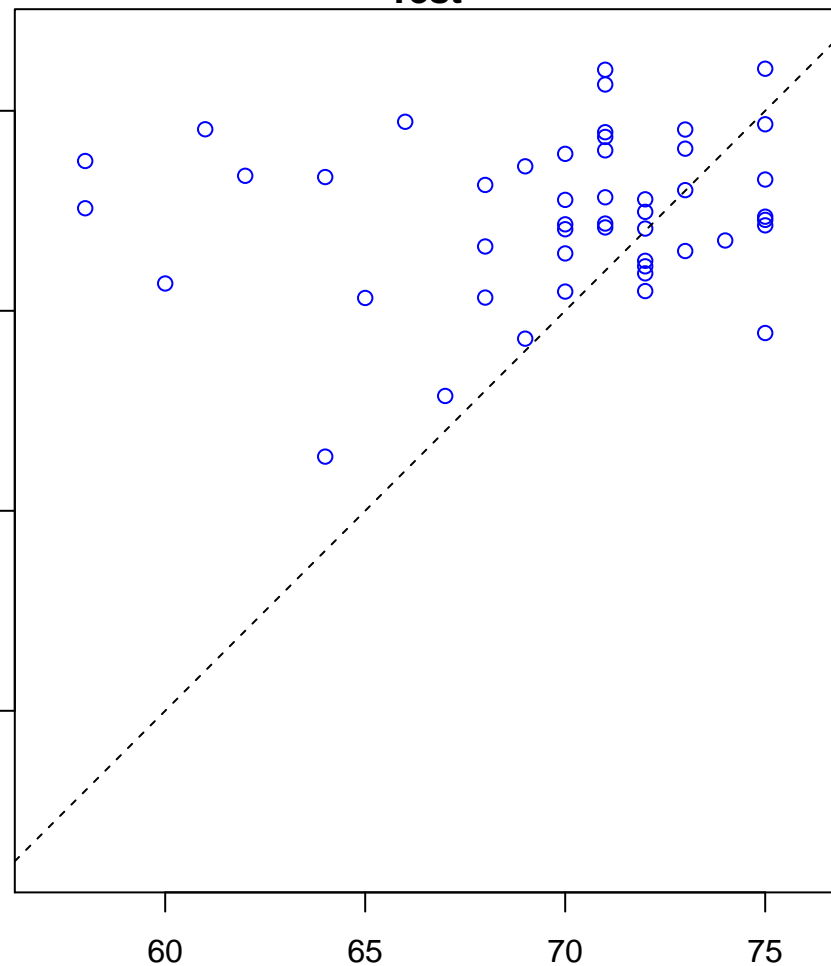


cardiovascular system development (Score: 1.784702)

Control

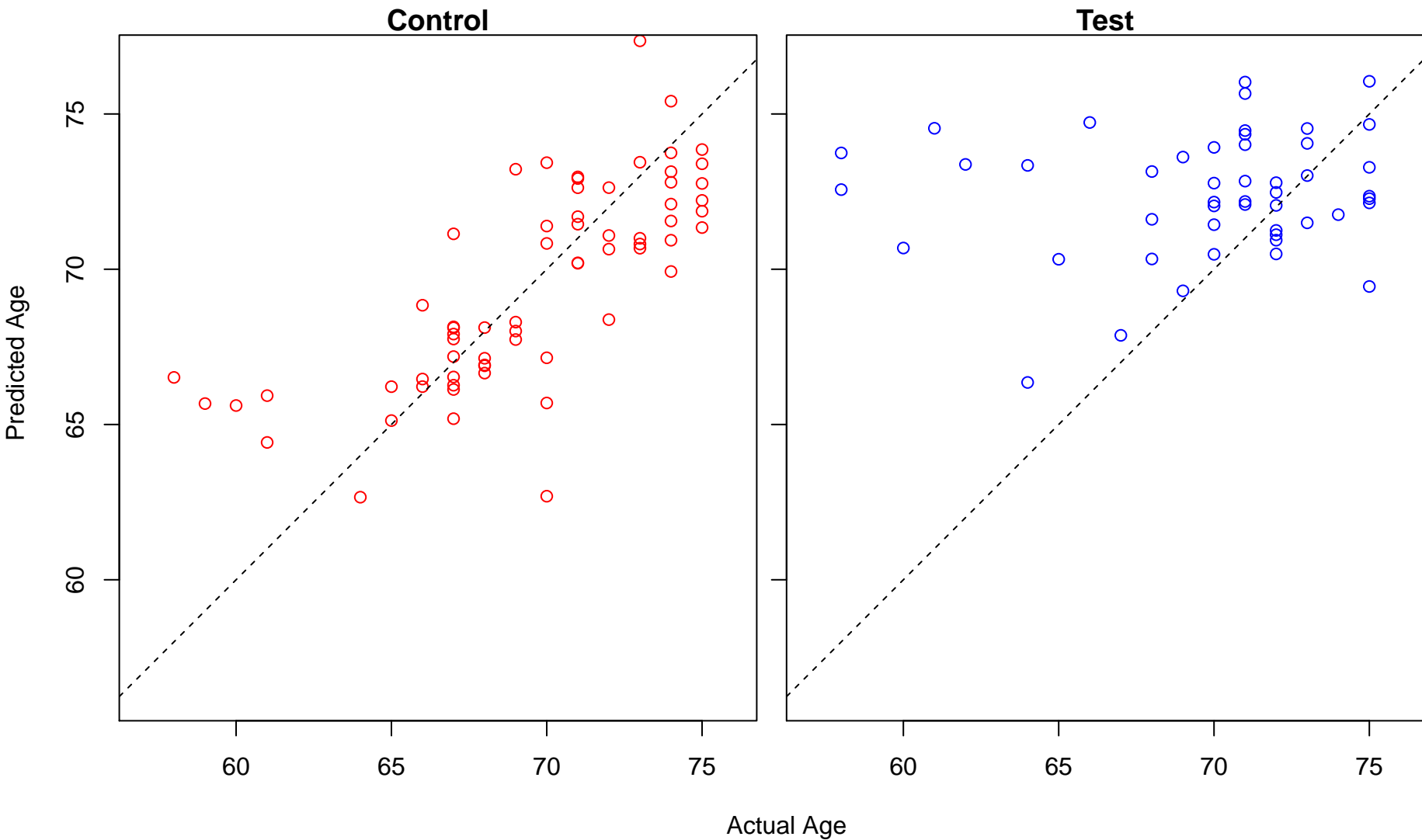


Test

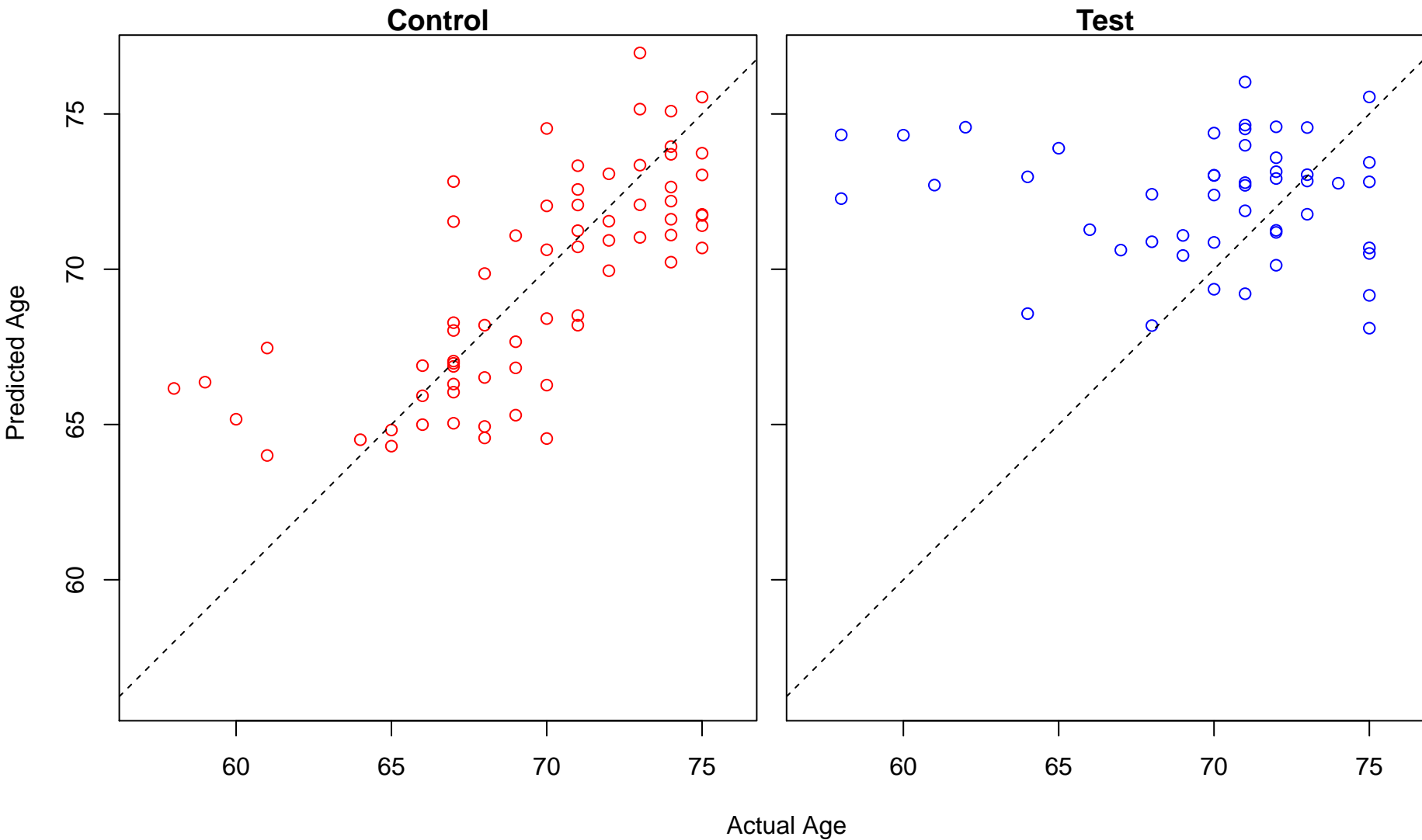


Actual Age

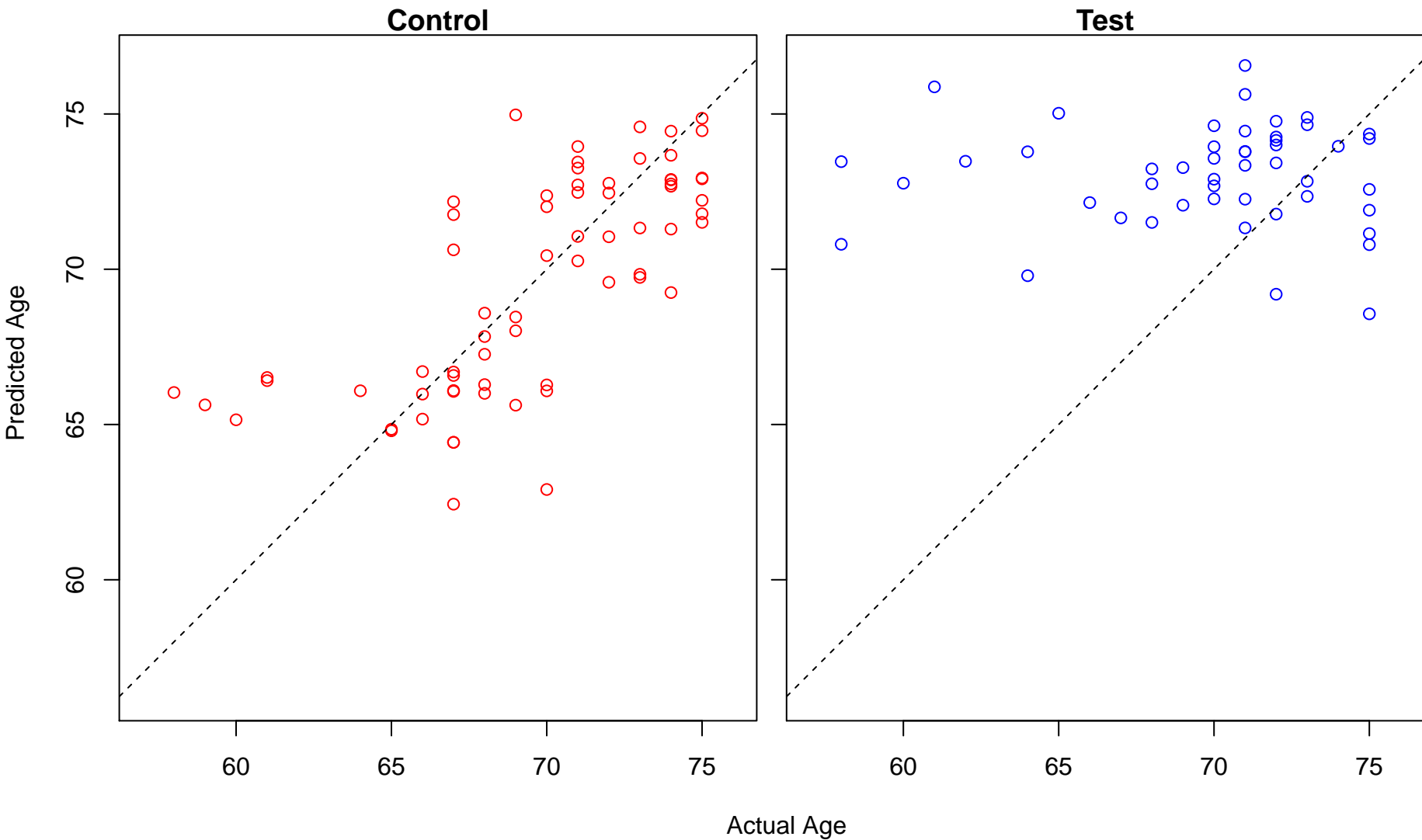
circulatory system development (Score: 1.784702)



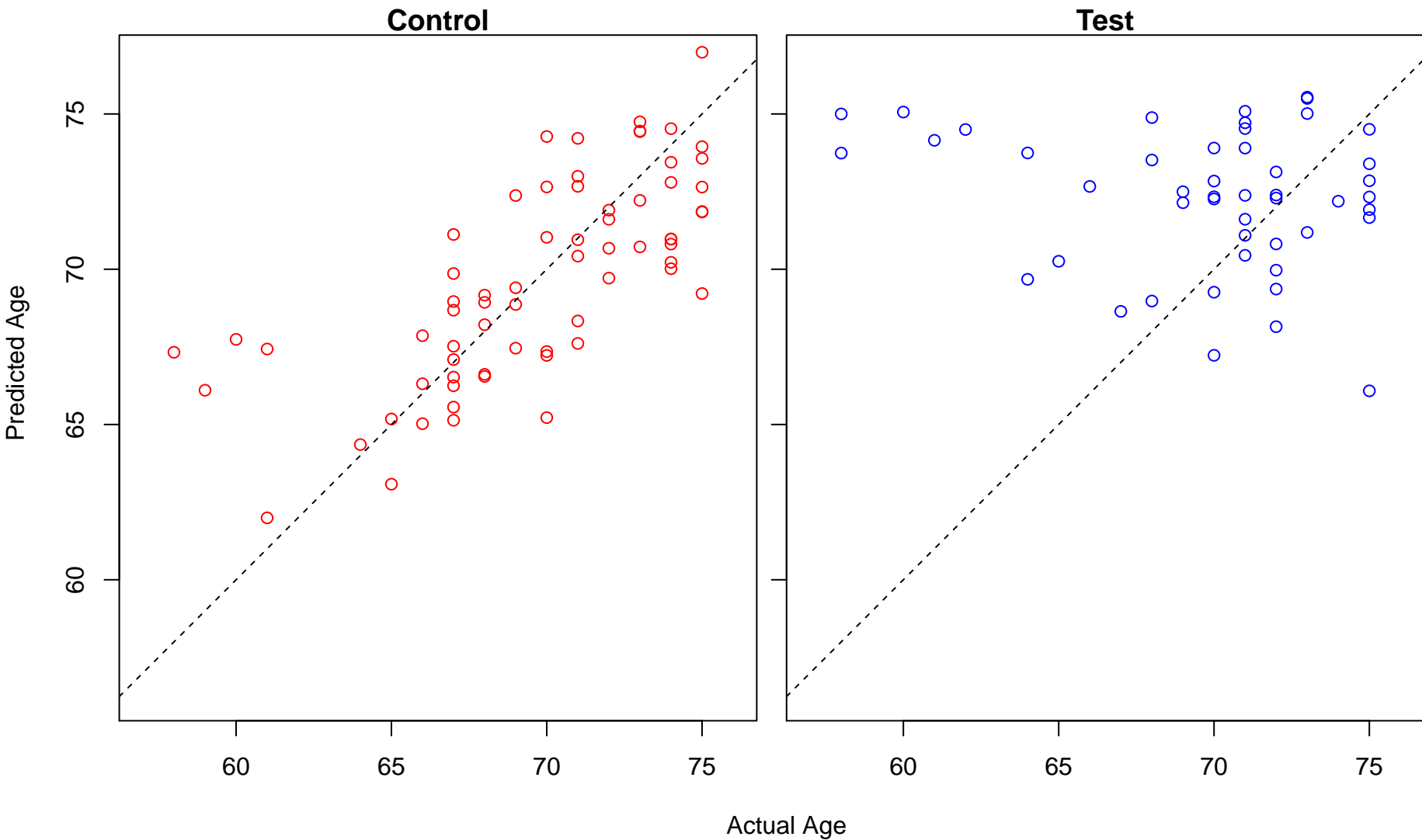
regulation of macroautophagy (Score: 1.784565)



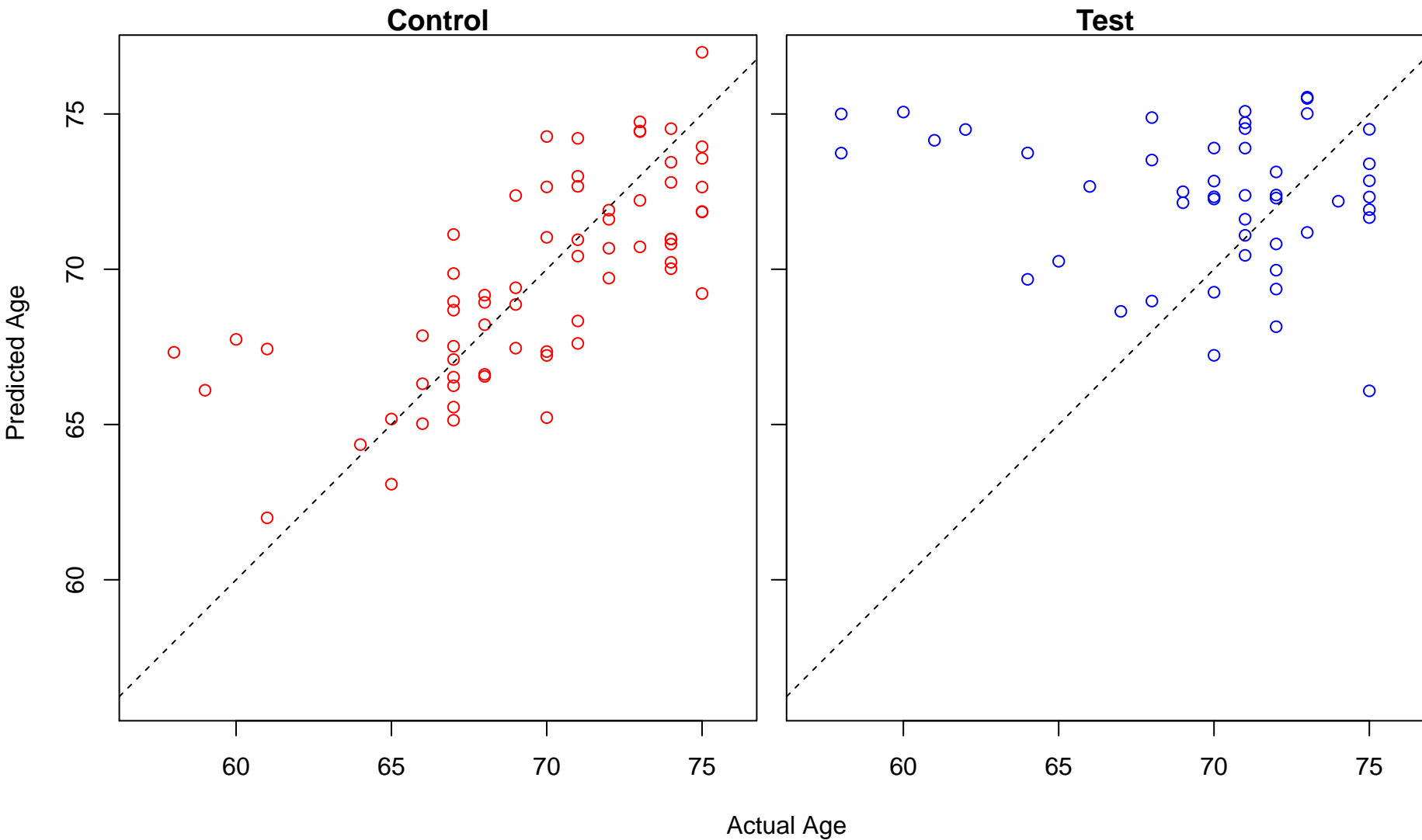
amide biosynthetic process (Score: 1.783856)



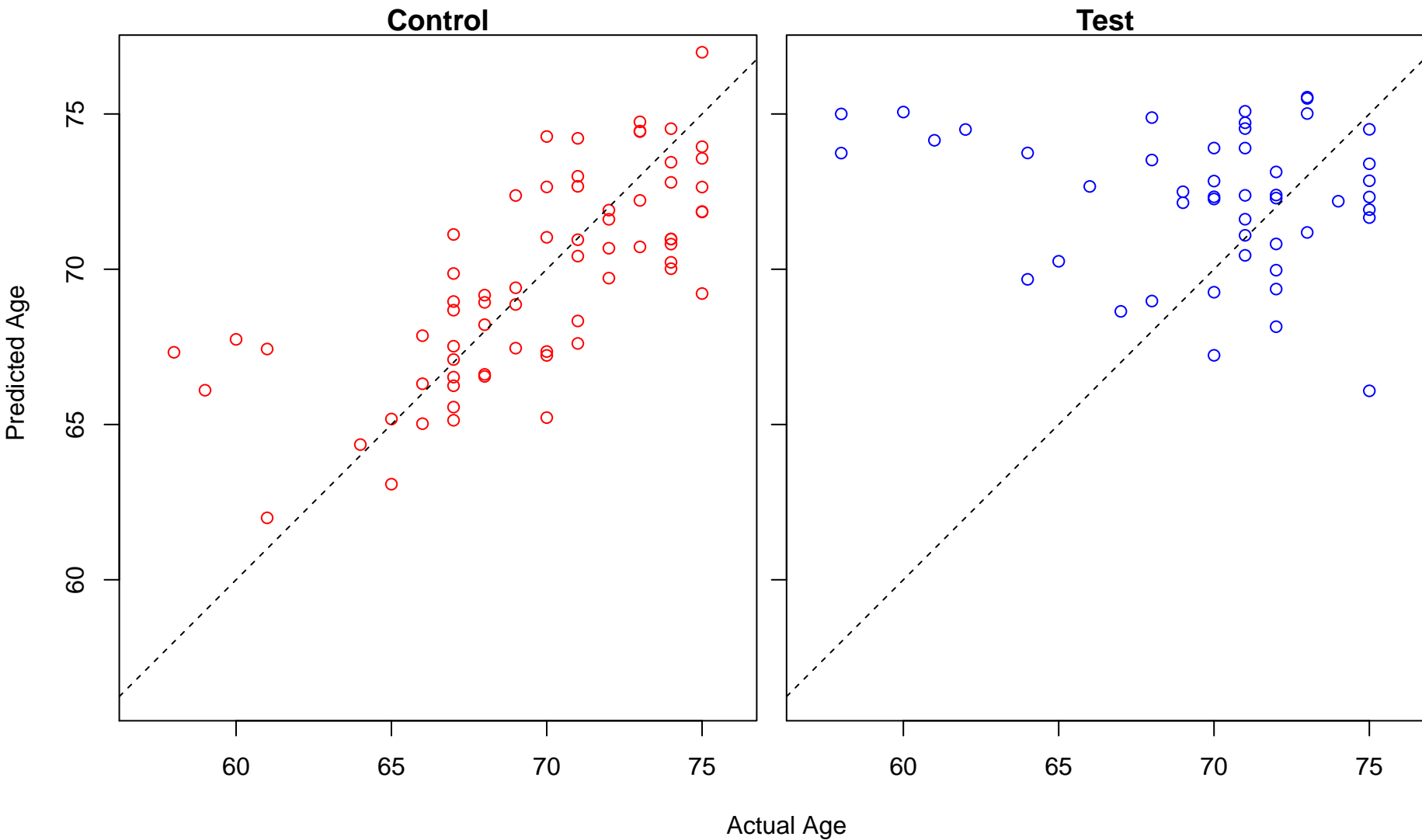
synaptic transmission (Score: 1.782950)



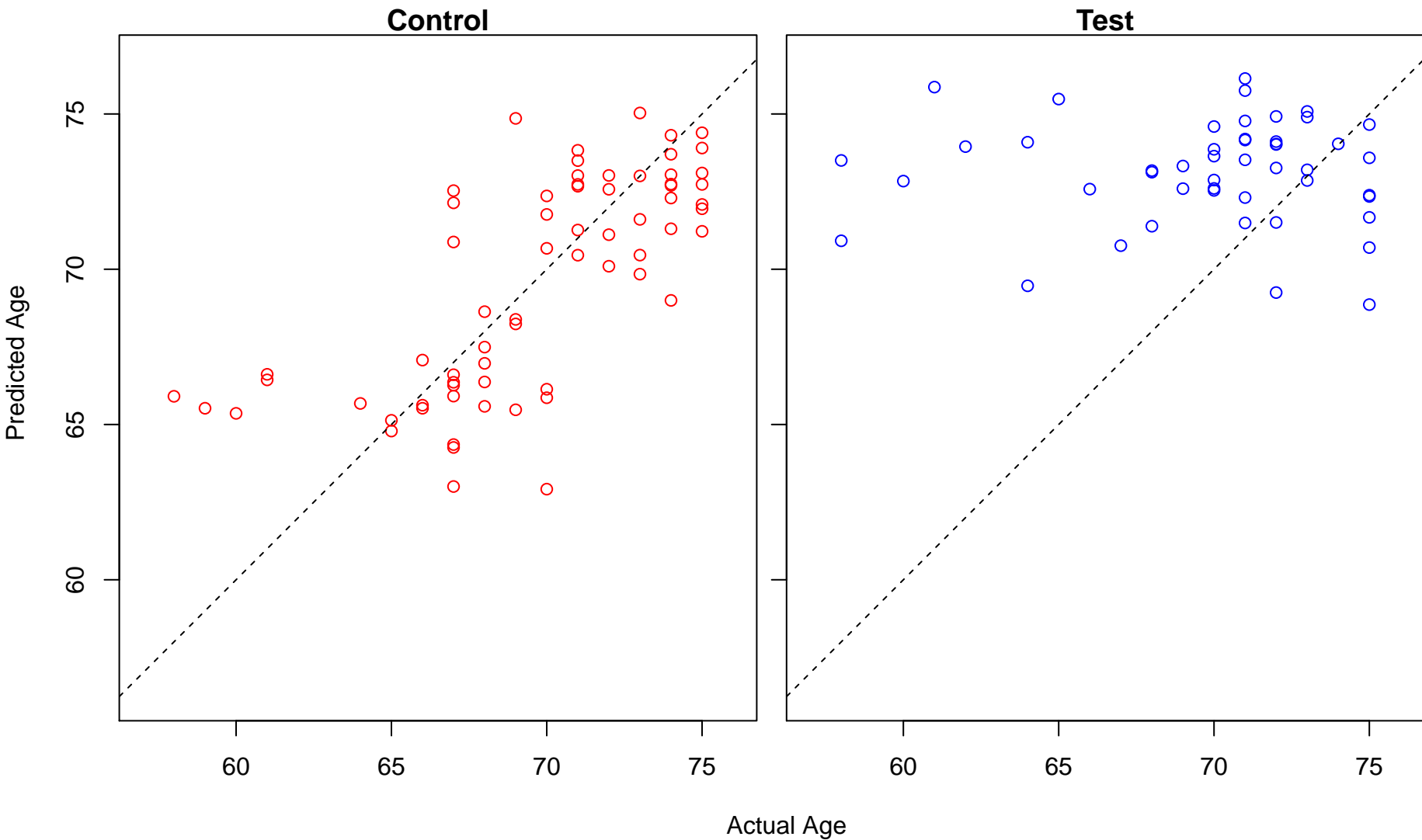
synaptic signaling (Score: 1.782950)



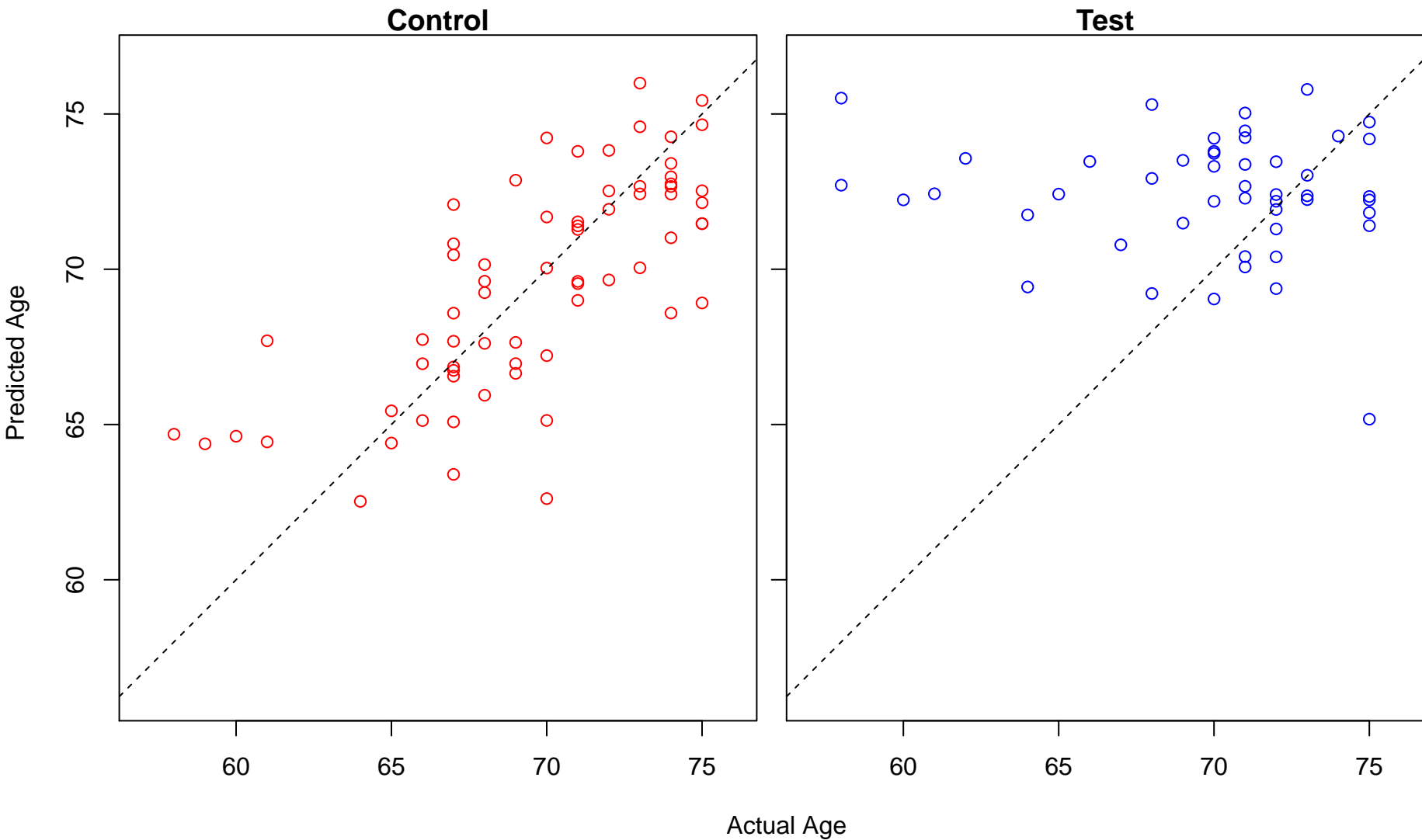
trans-synaptic signaling (Score: 1.782950)



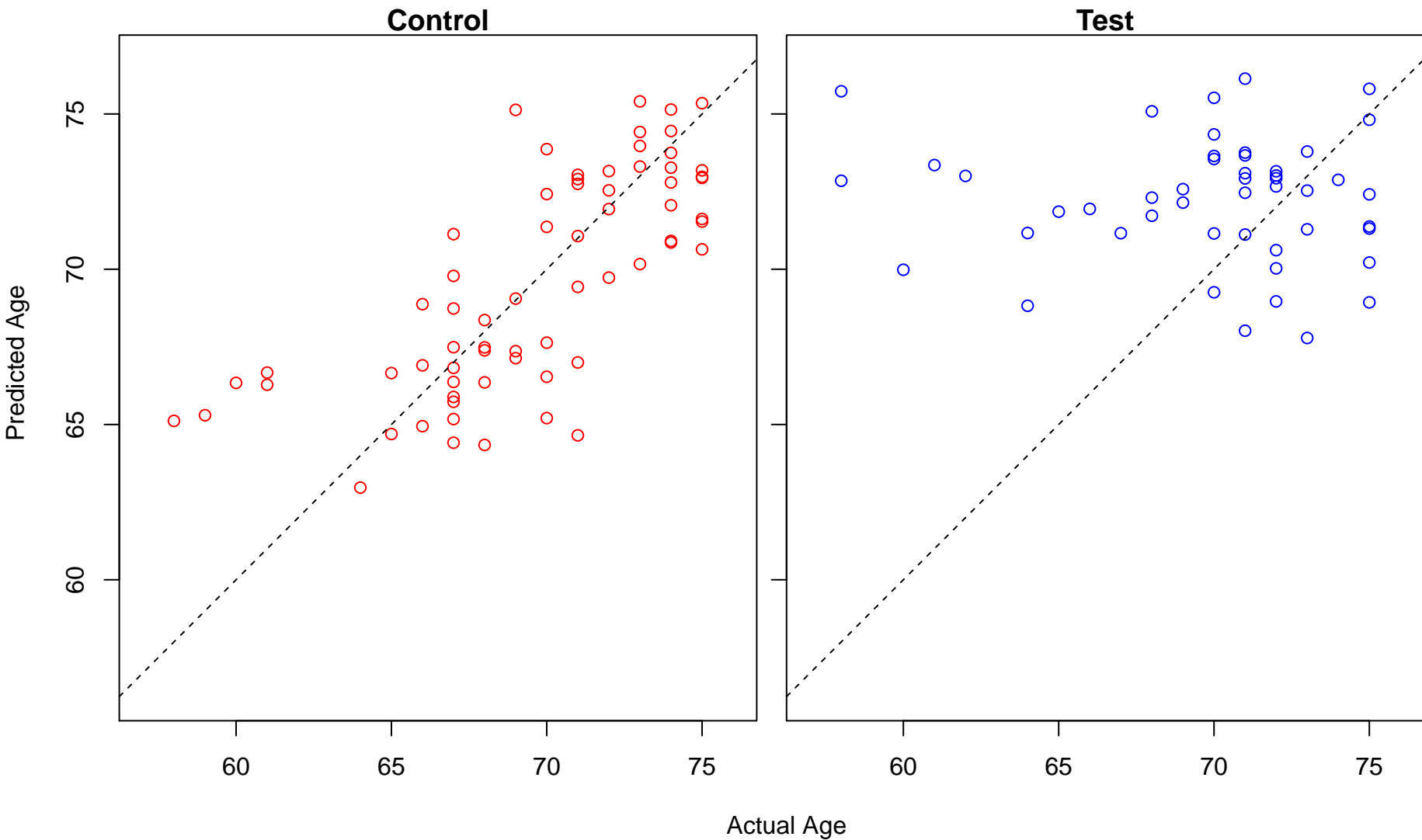
translation (Score: 1.782237)



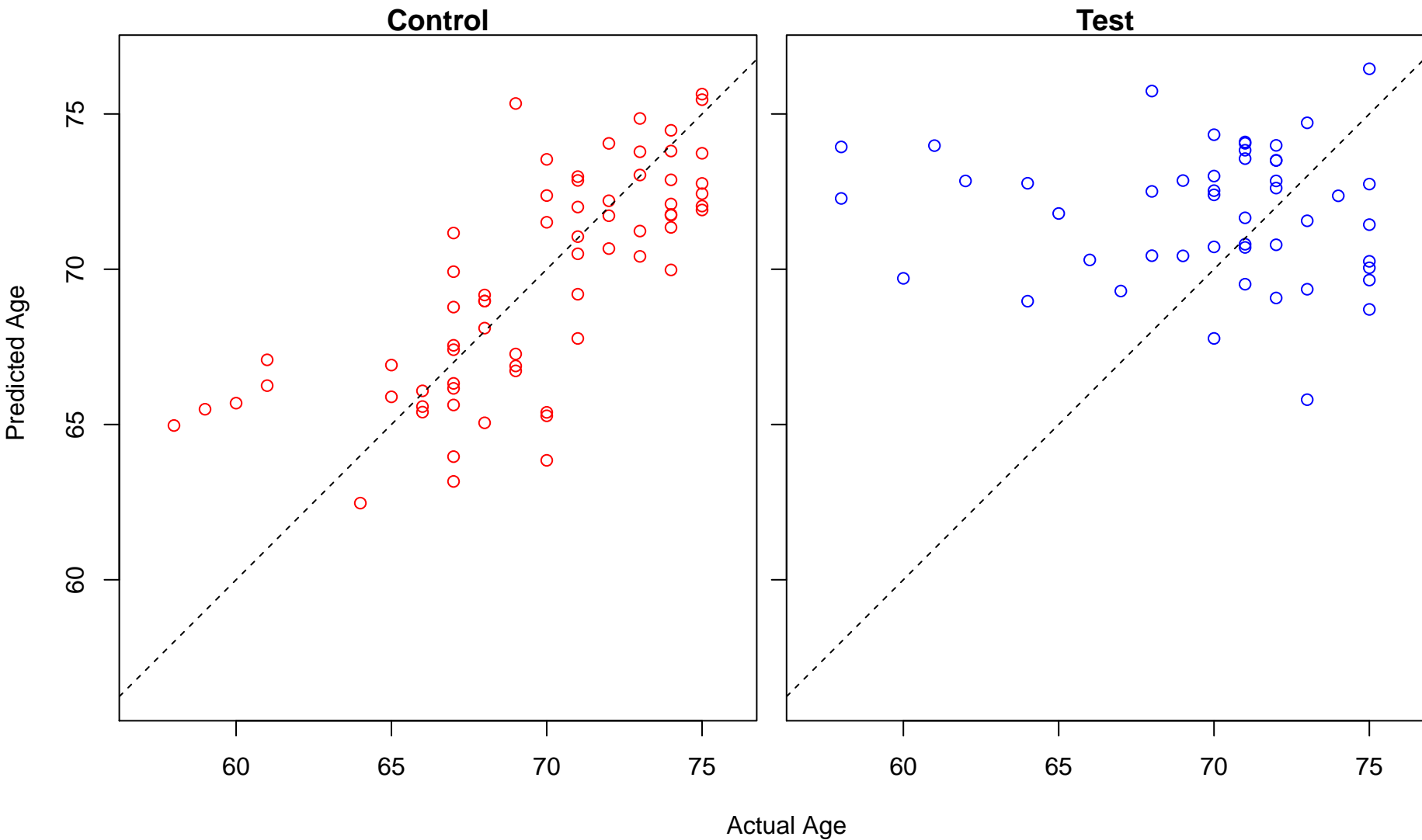
regulation of proteasomal ubiquitin-dependent protein catabolic process (Score: 1.781853)



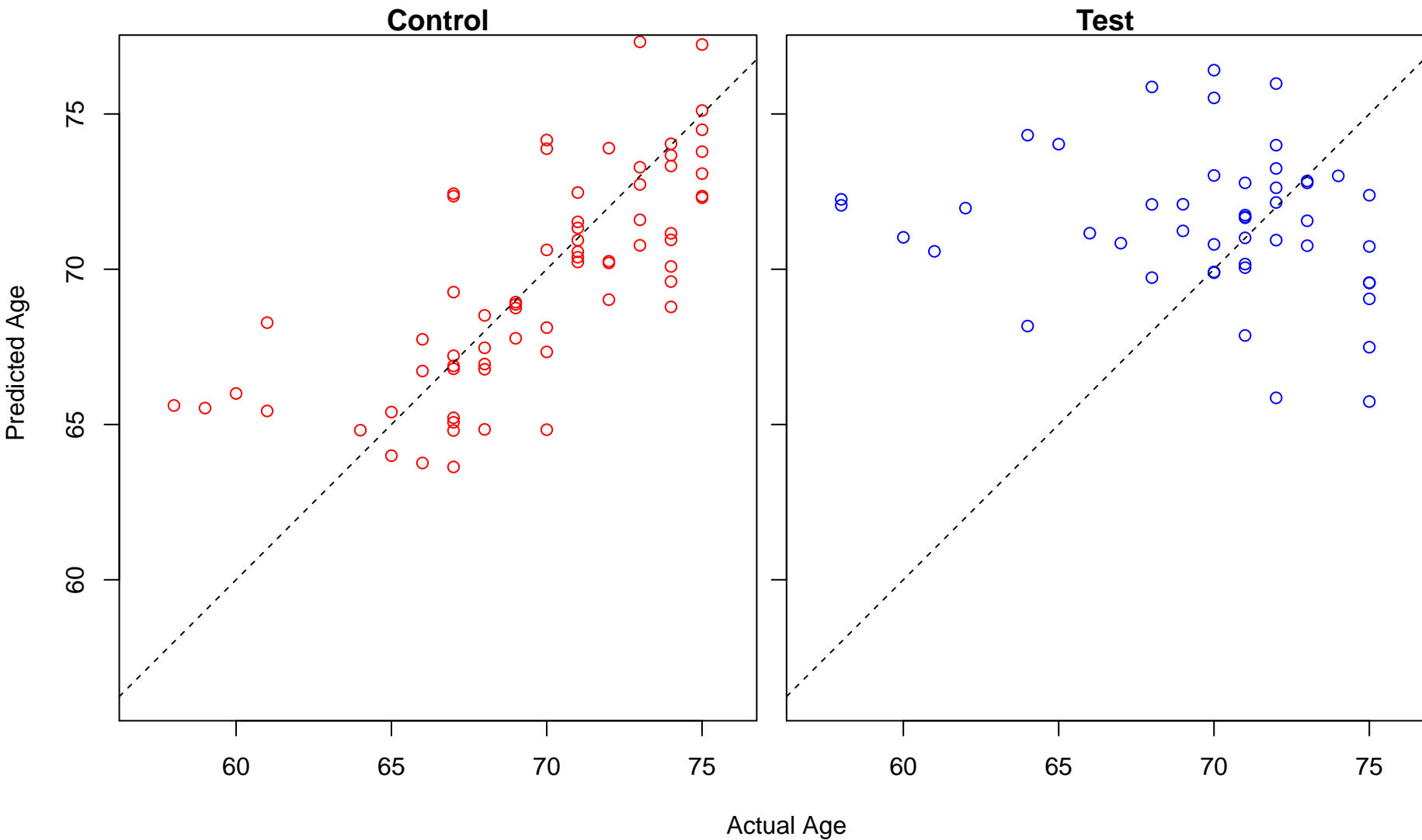
homotypic cell-cell adhesion (Score: 1.781301)



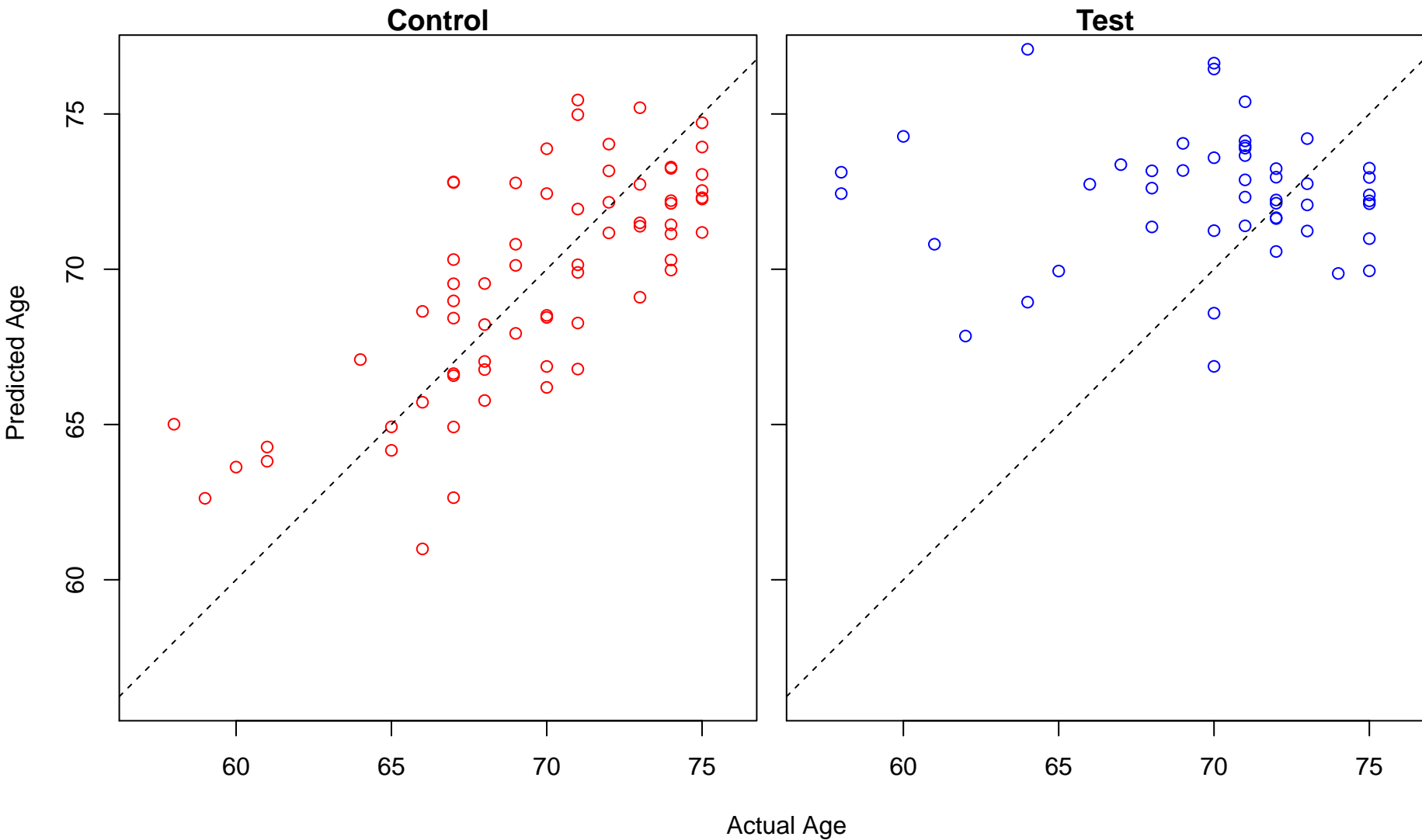
regulation of cytoplasmic transport (Score: 1.780001)



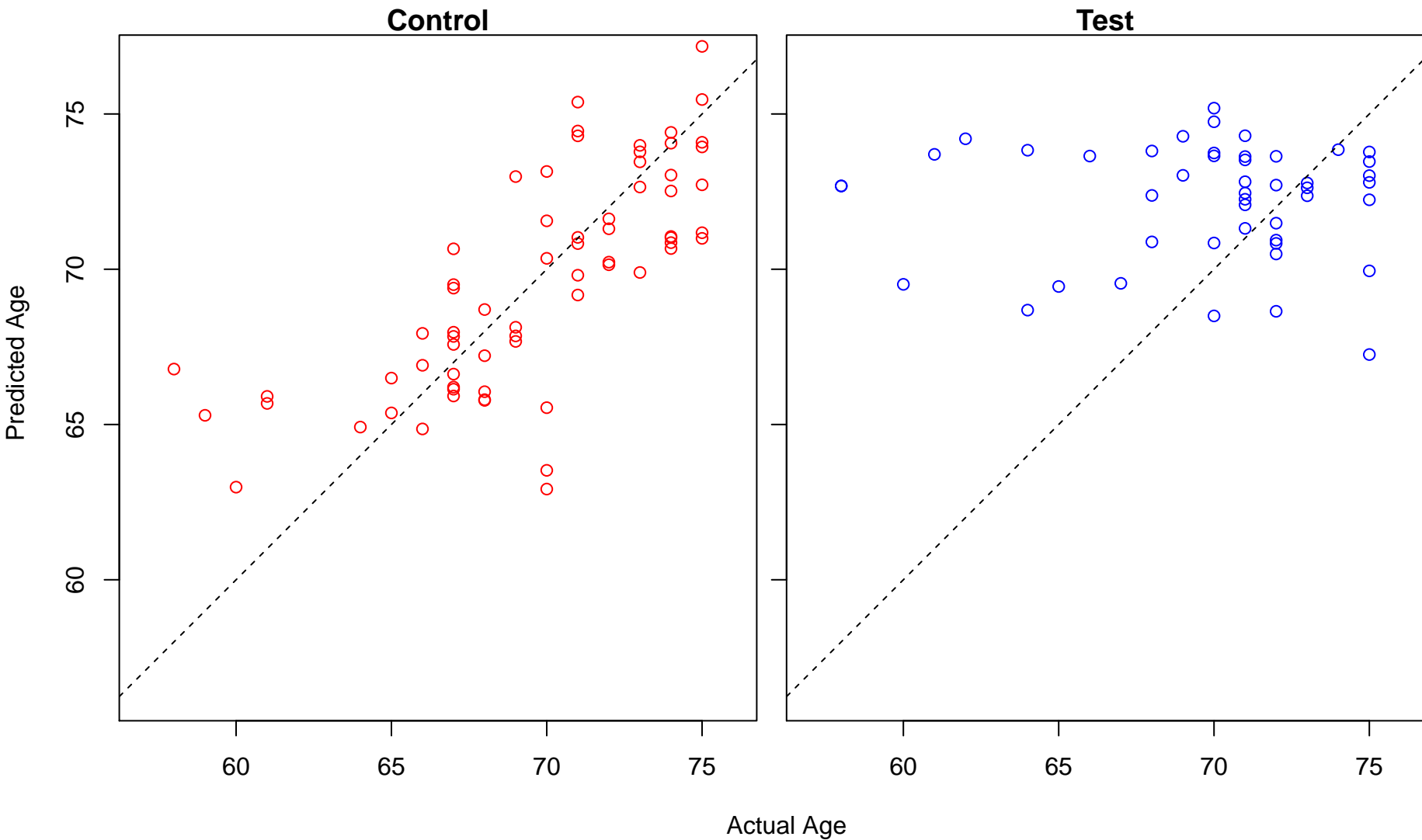
regulation of DNA-dependent DNA replication (Score: 1.779760)



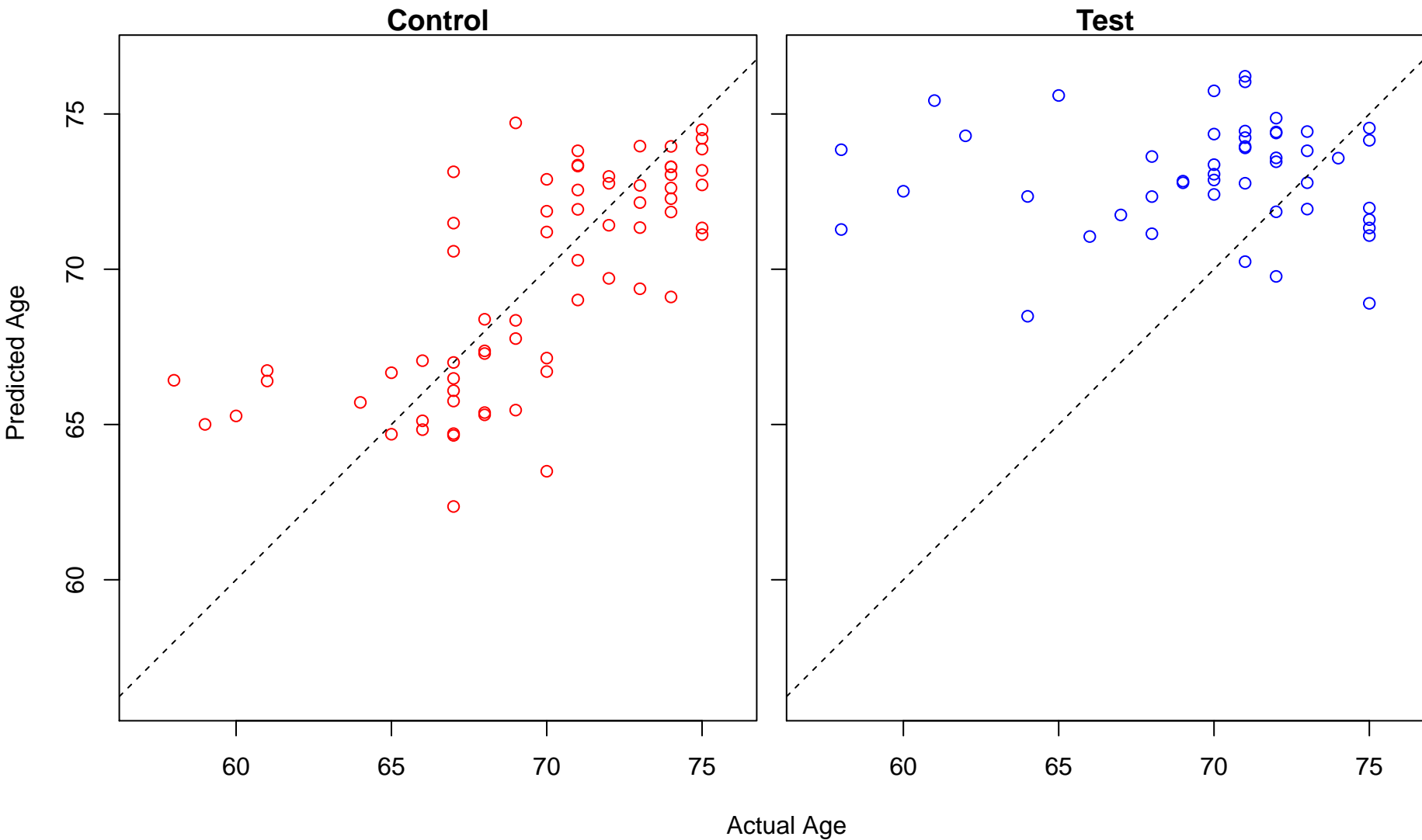
positive regulation of release of cytochrome c from mitochondria (Score: 1.779696)



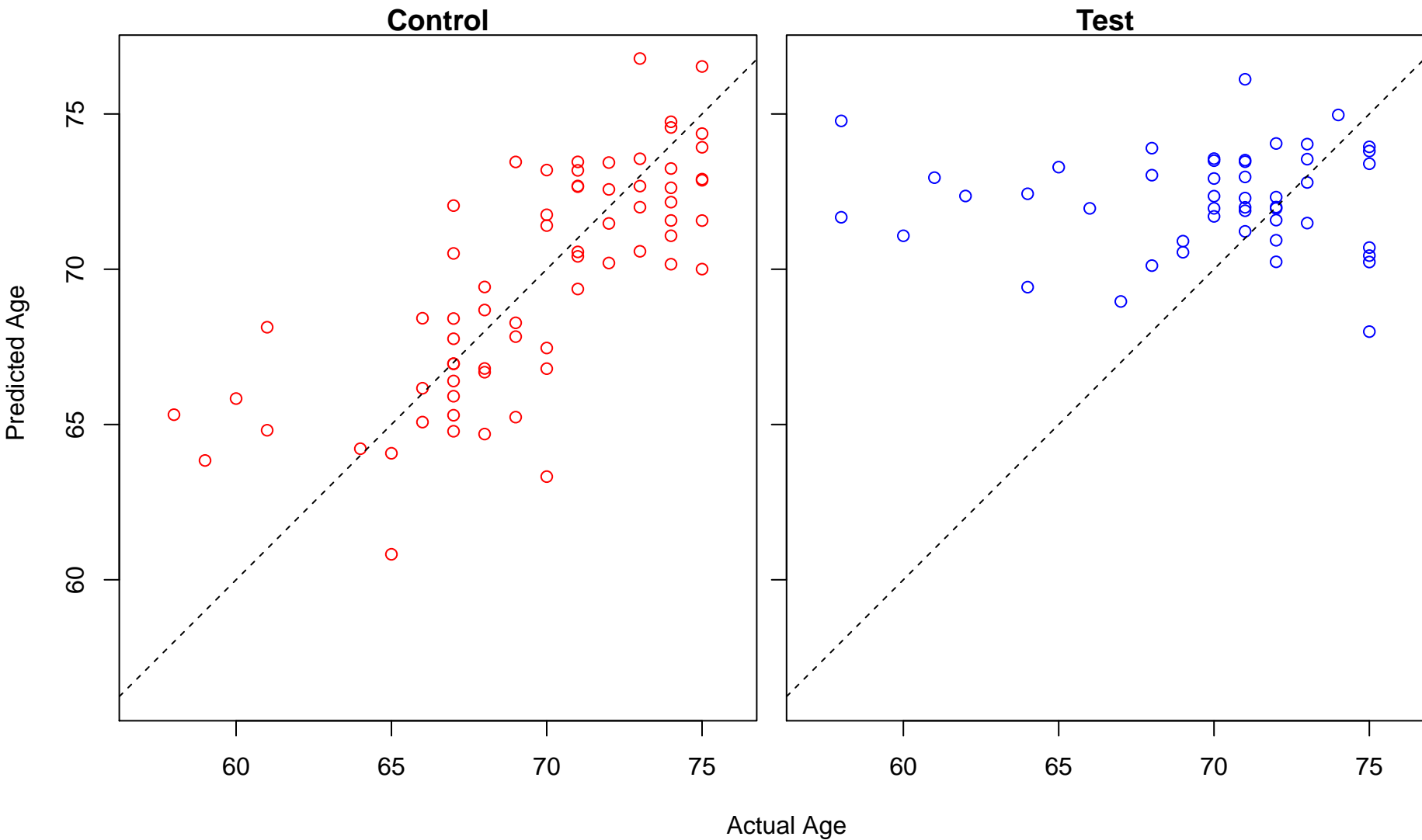
positive regulation of binding (Score: 1.778713)



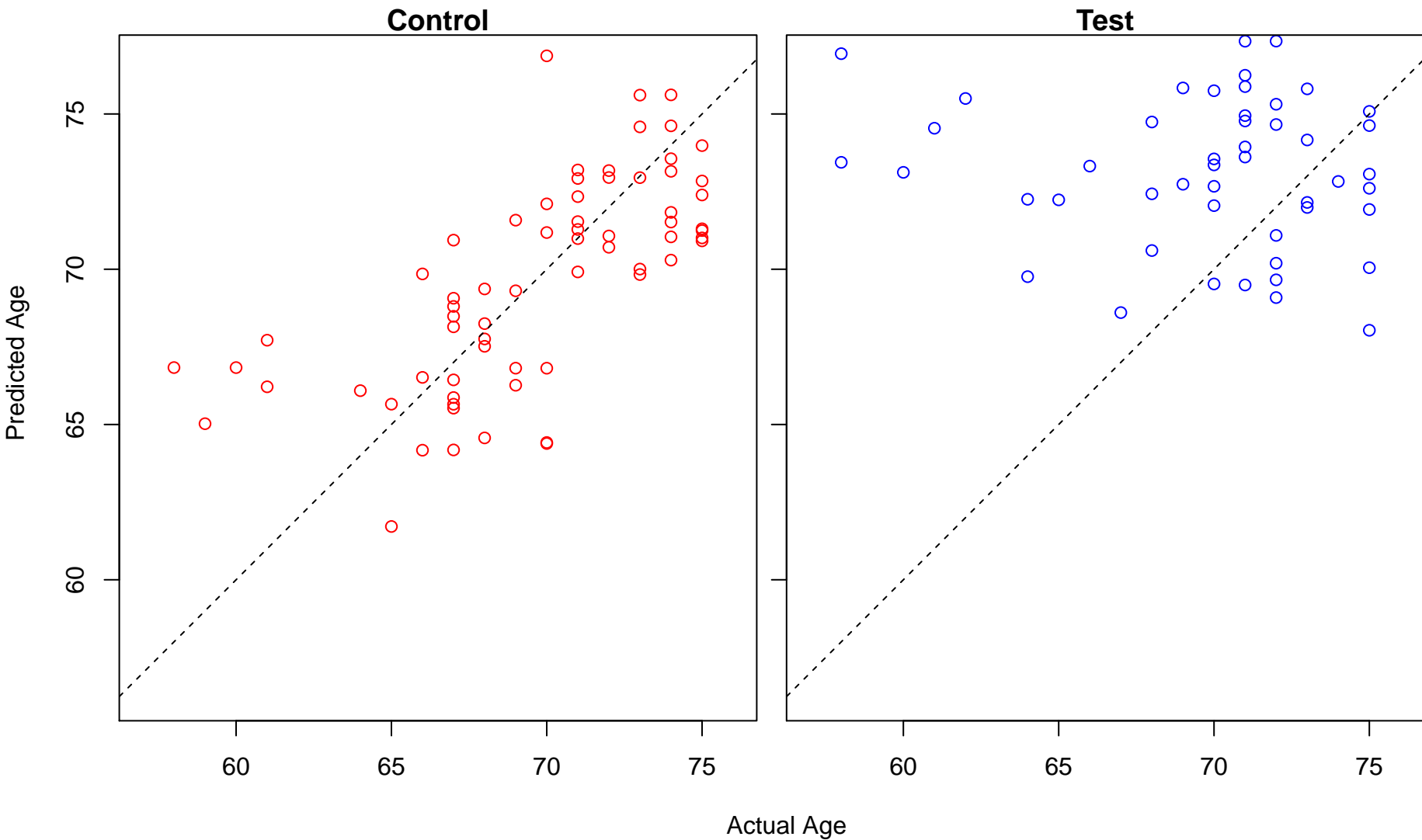
establishment of protein localization to membrane (Score: 1.778556)



DNA integrity checkpoint (Score: 1.777991)

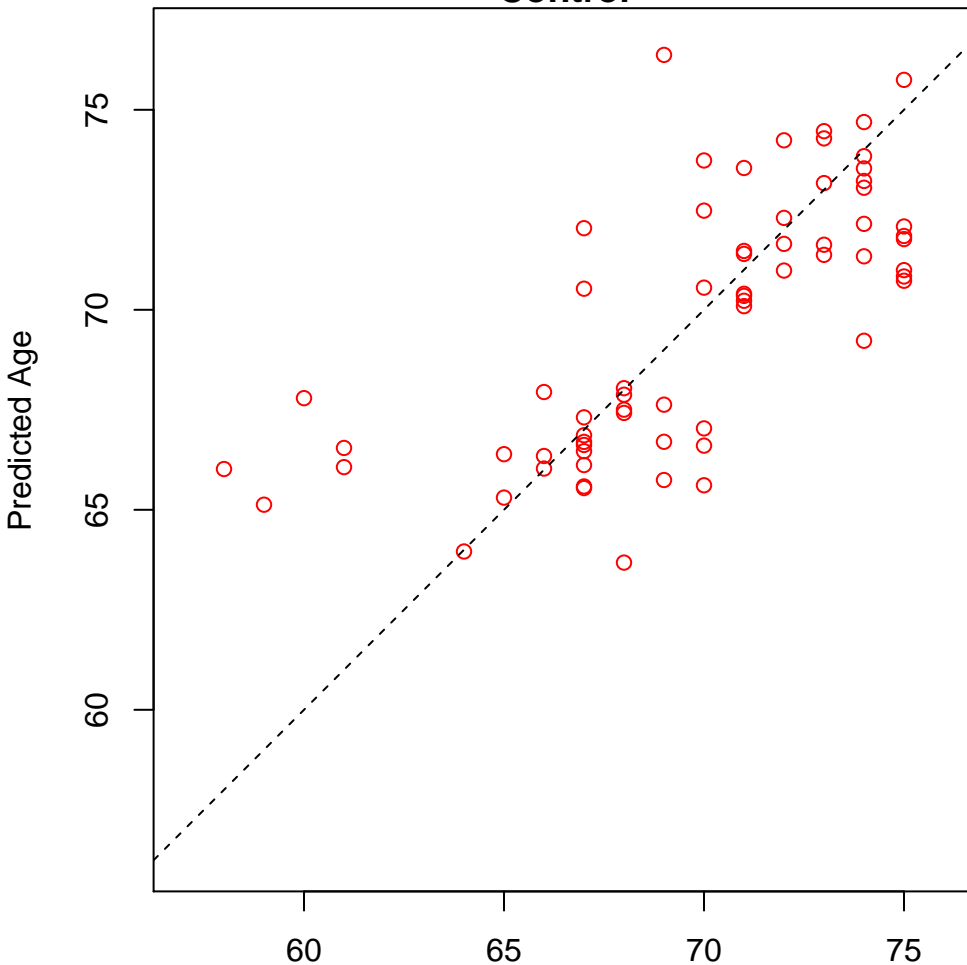


regulation of angiogenesis (Score: 1.777944)

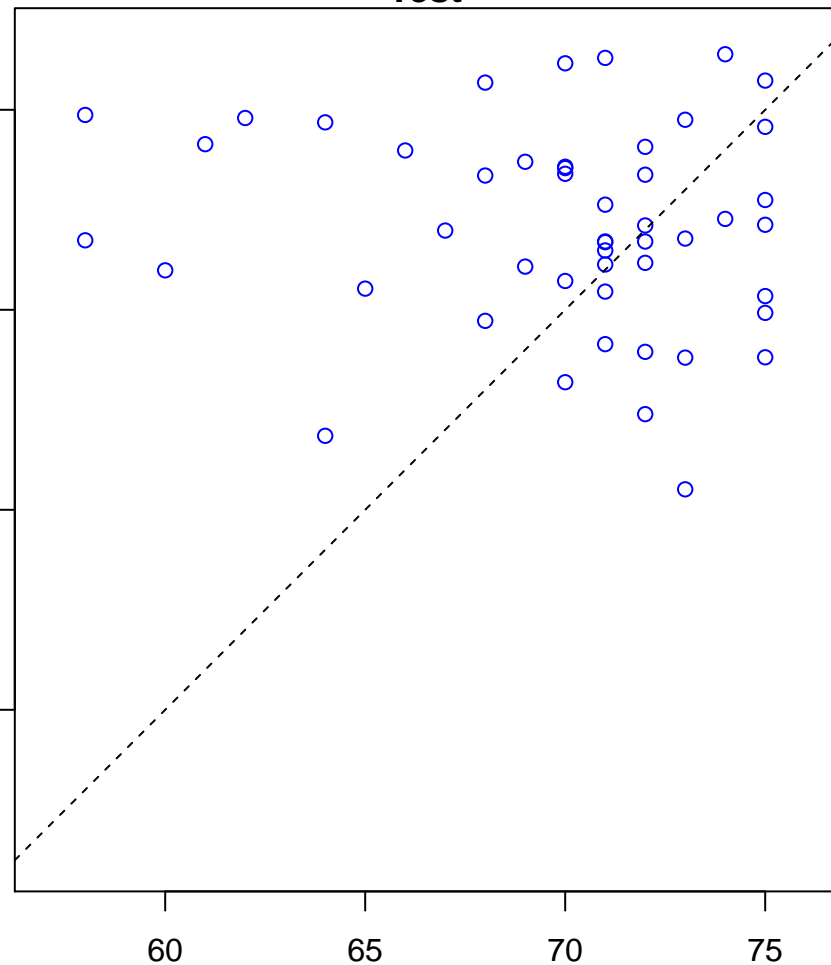


response to organic cyclic compound (Score: 1.776775)

Control

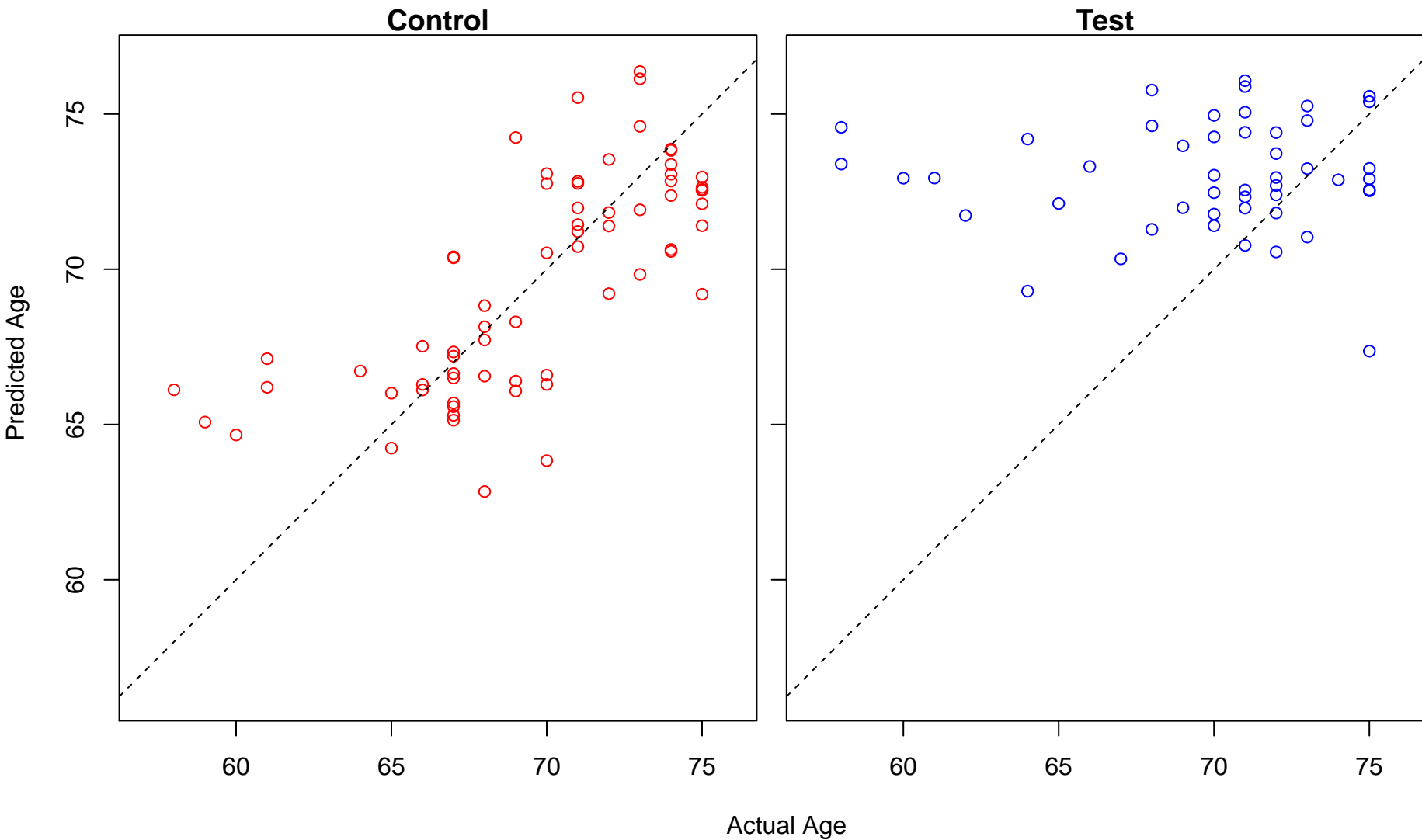


Test

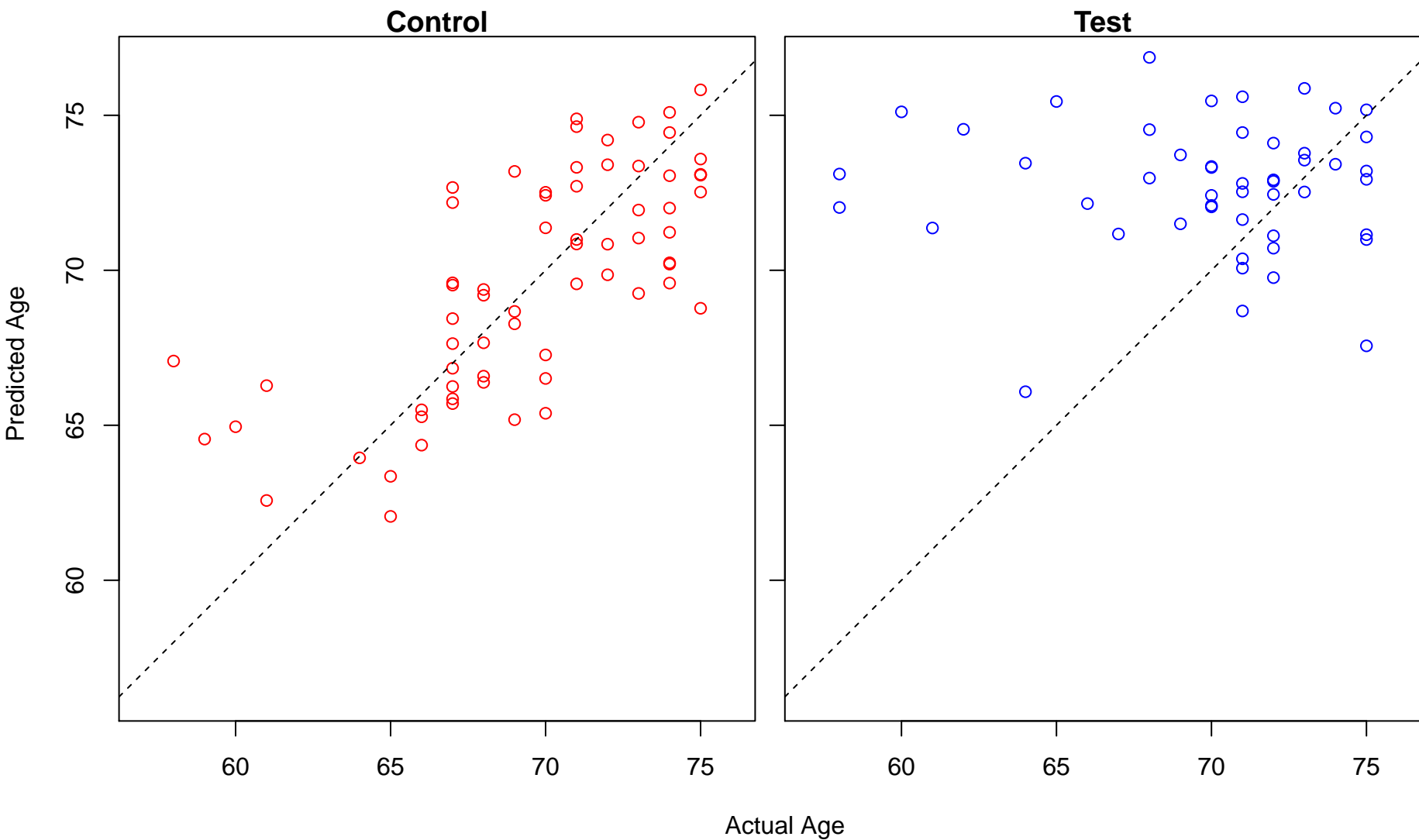


Actual Age

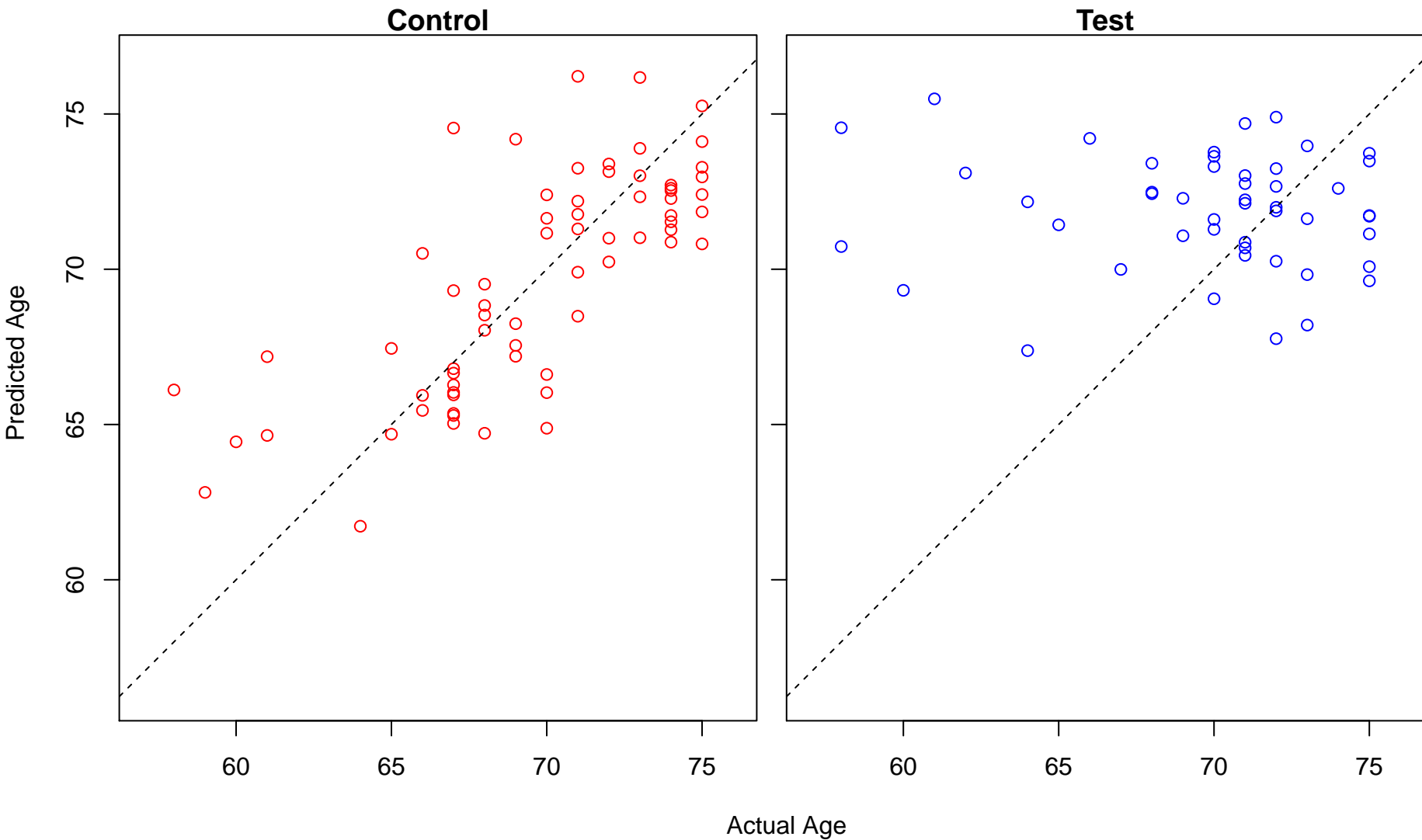
neural nucleus development (Score: 1.776015)



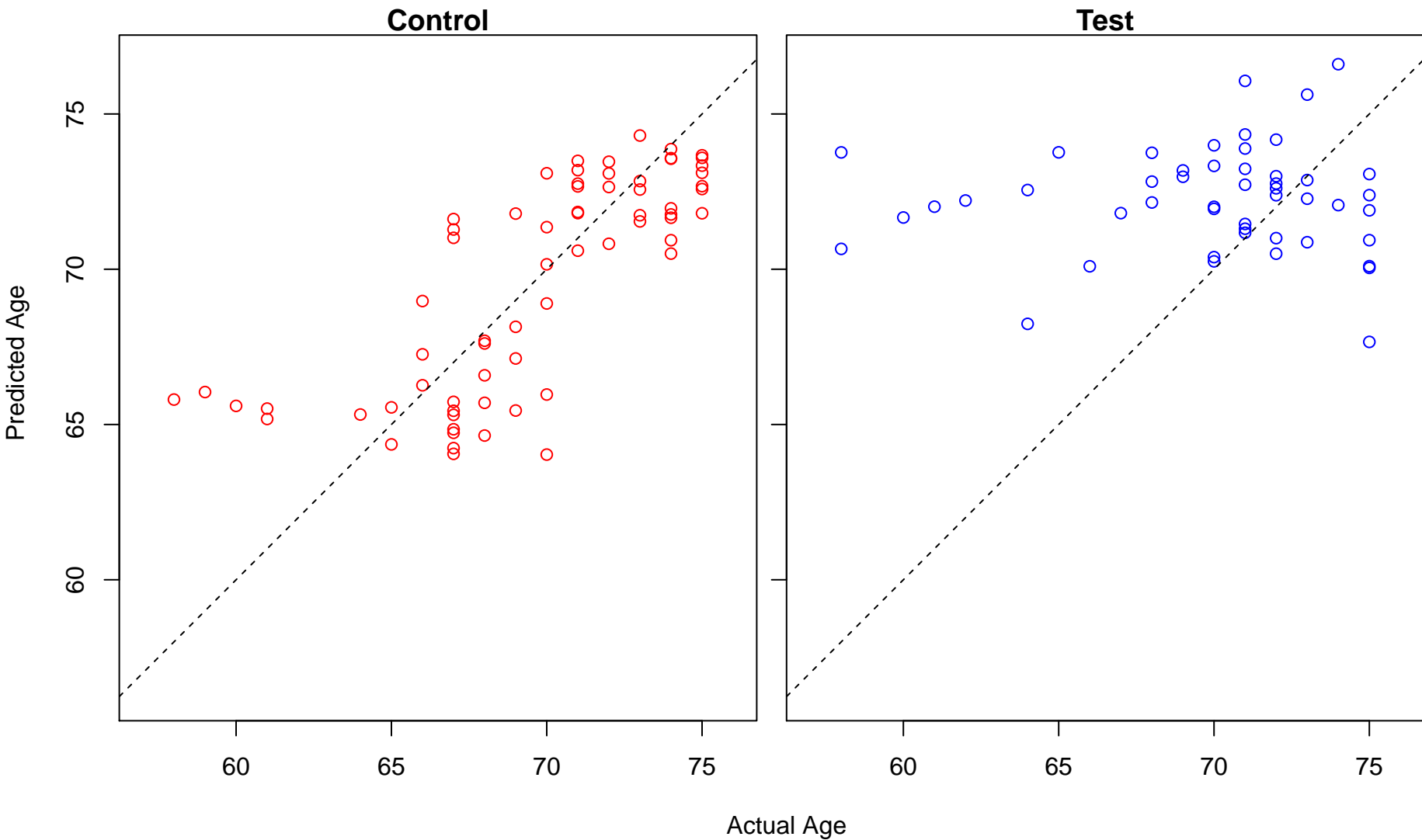
second-messenger-mediated signaling (Score: 1.775666)



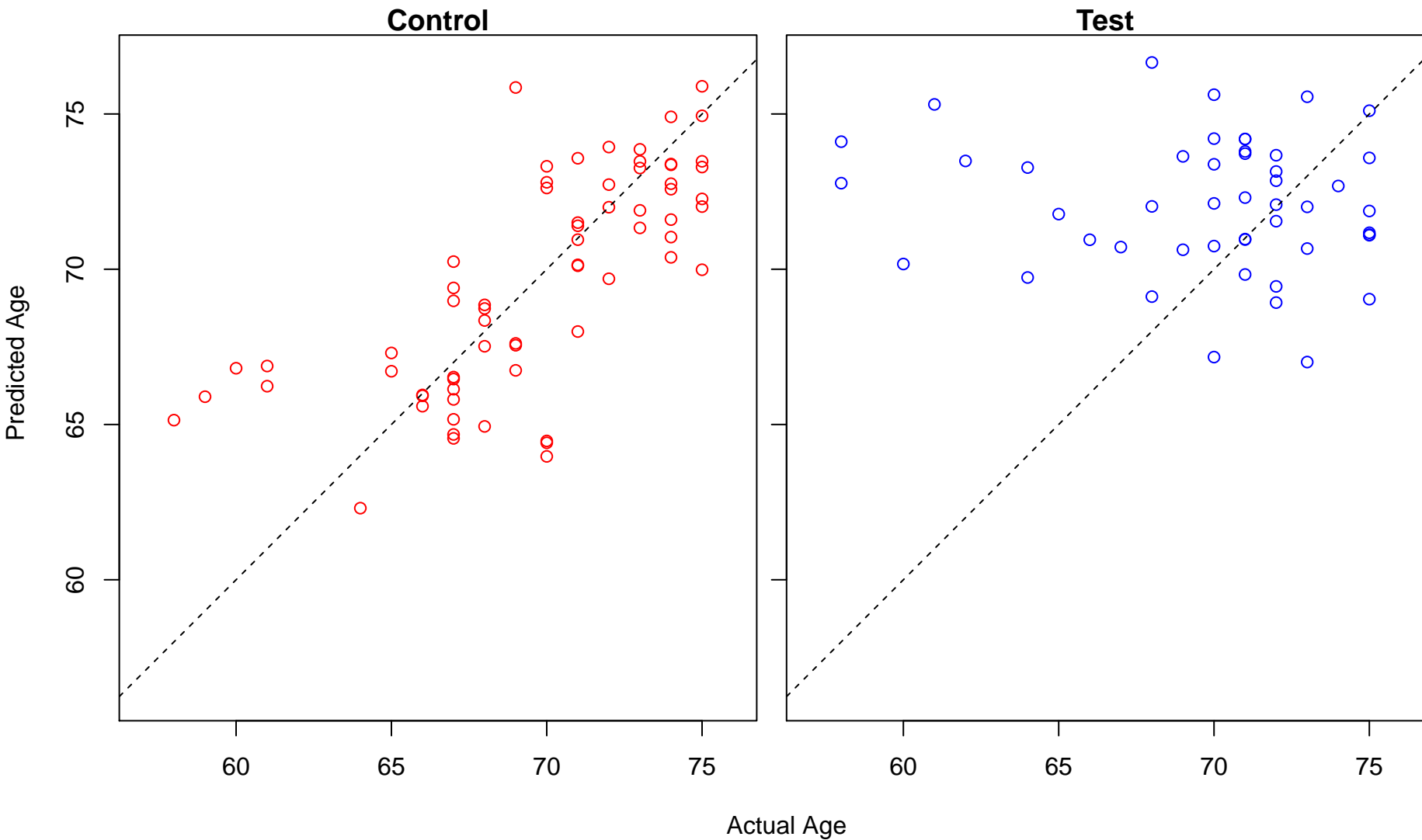
response to virus (Score: 1.775244)



mRNA processing (Score: 1.774879)

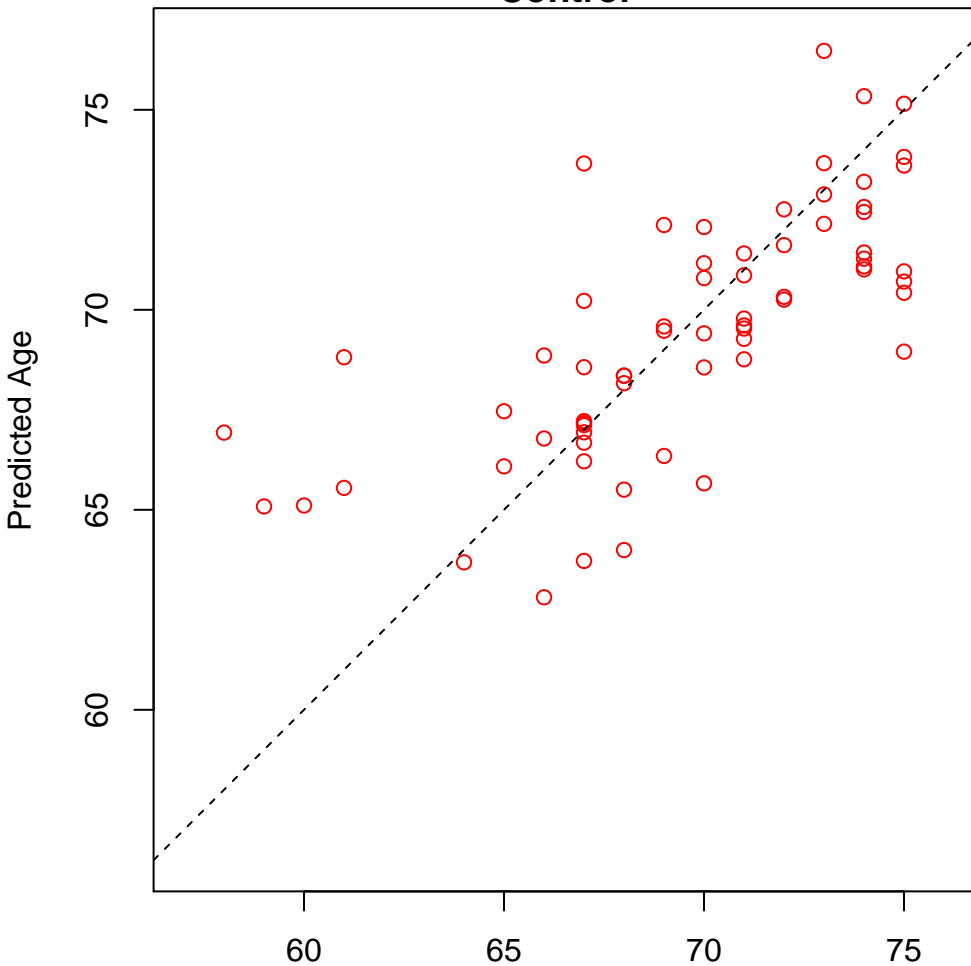


regulation of nucleocytoplasmic transport (Score: 1.773106)

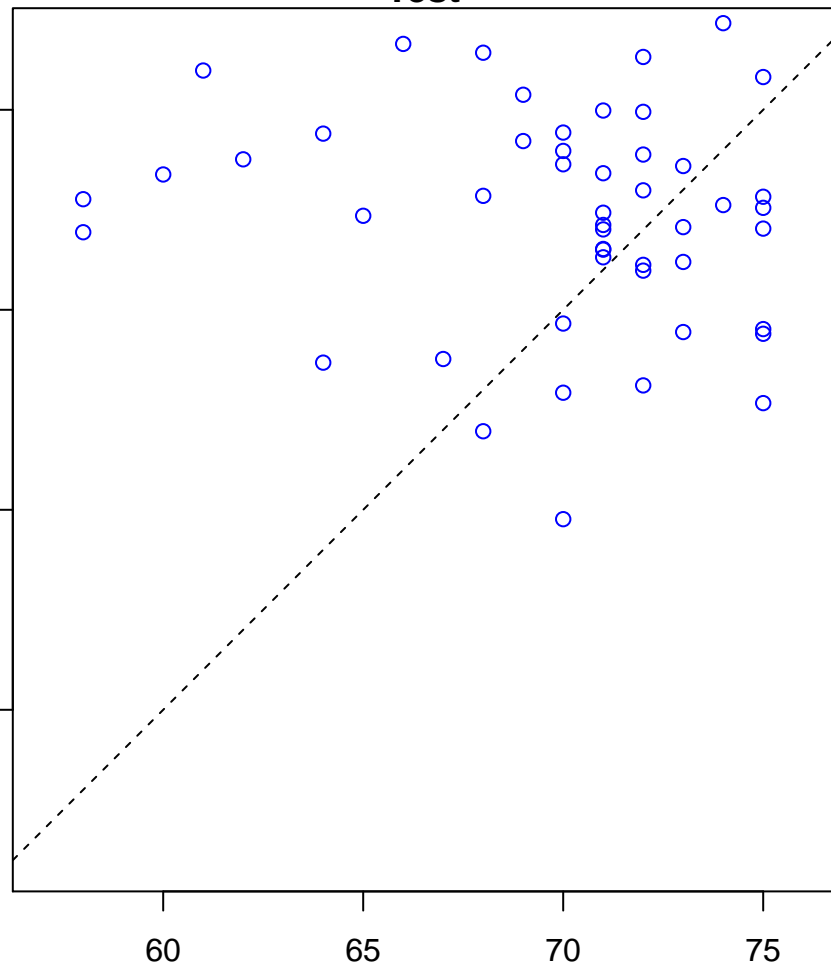


phosphatidylserine metabolic process (Score: 1.772368)

Control



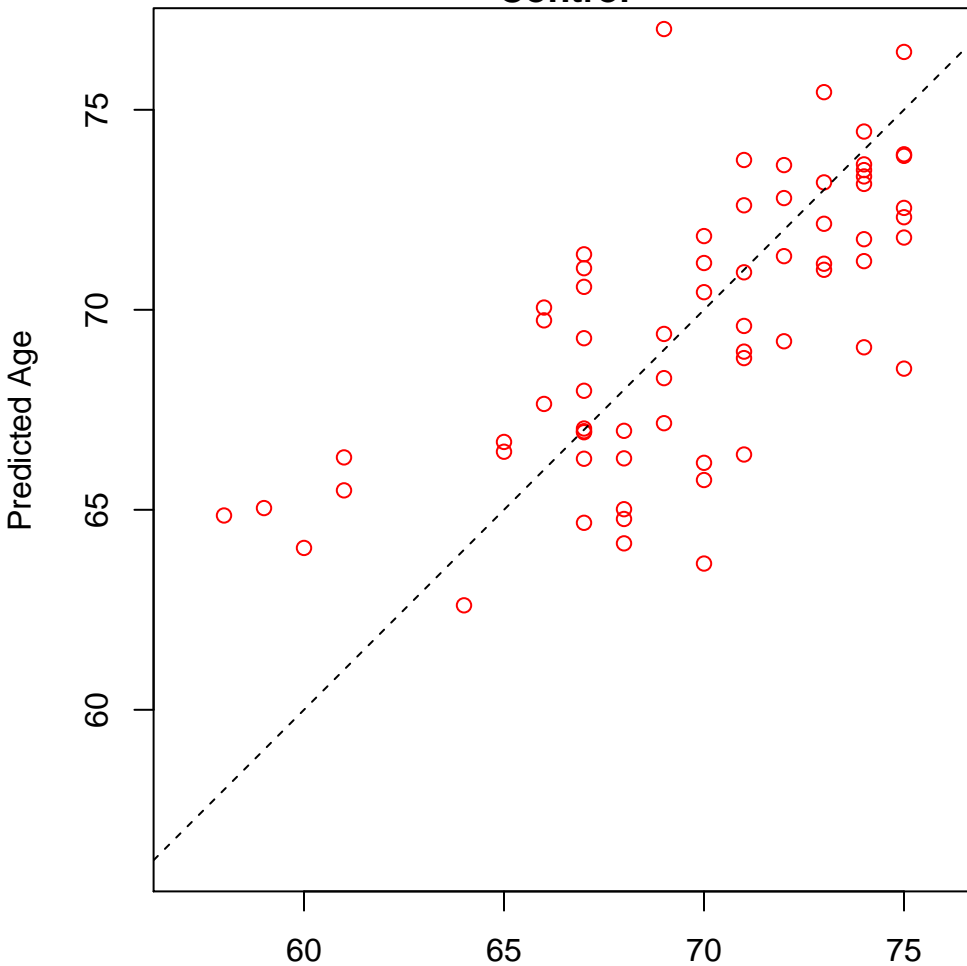
Test



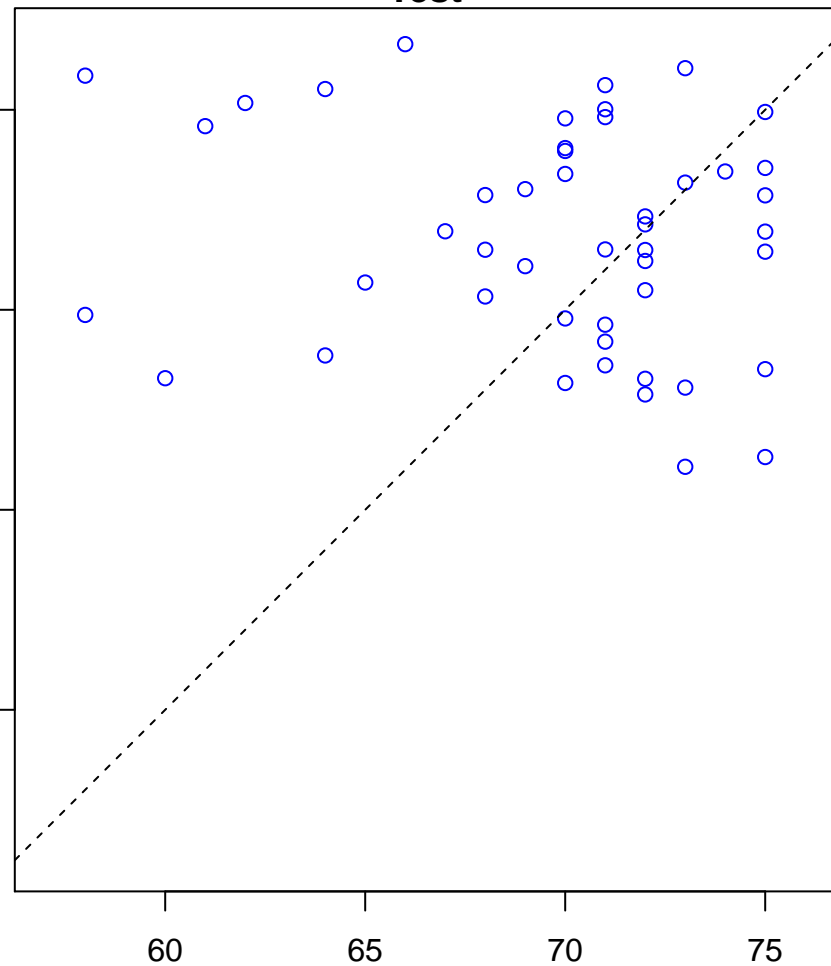
Actual Age

negative regulation of defense response (Score: 1.770888)

Control

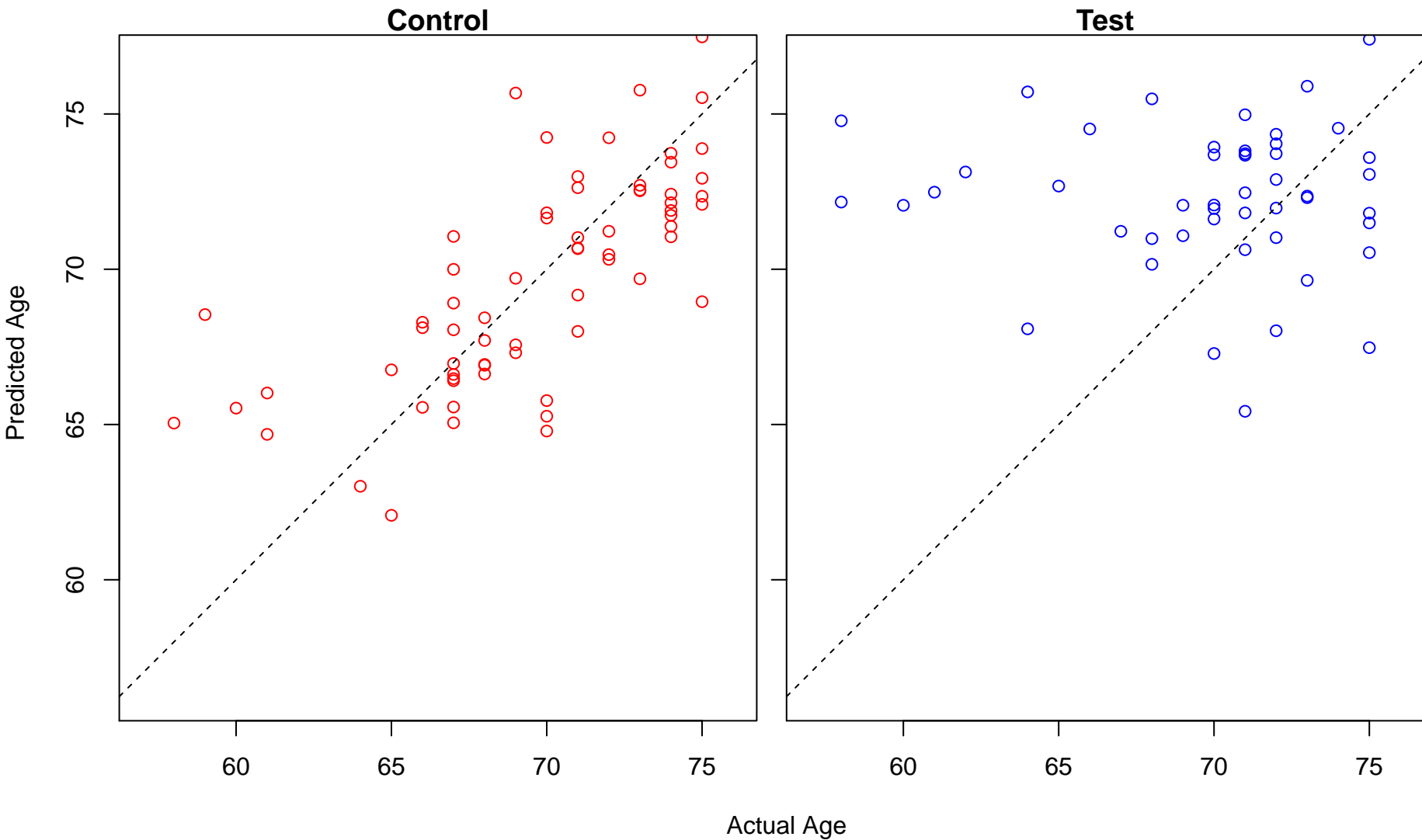


Test

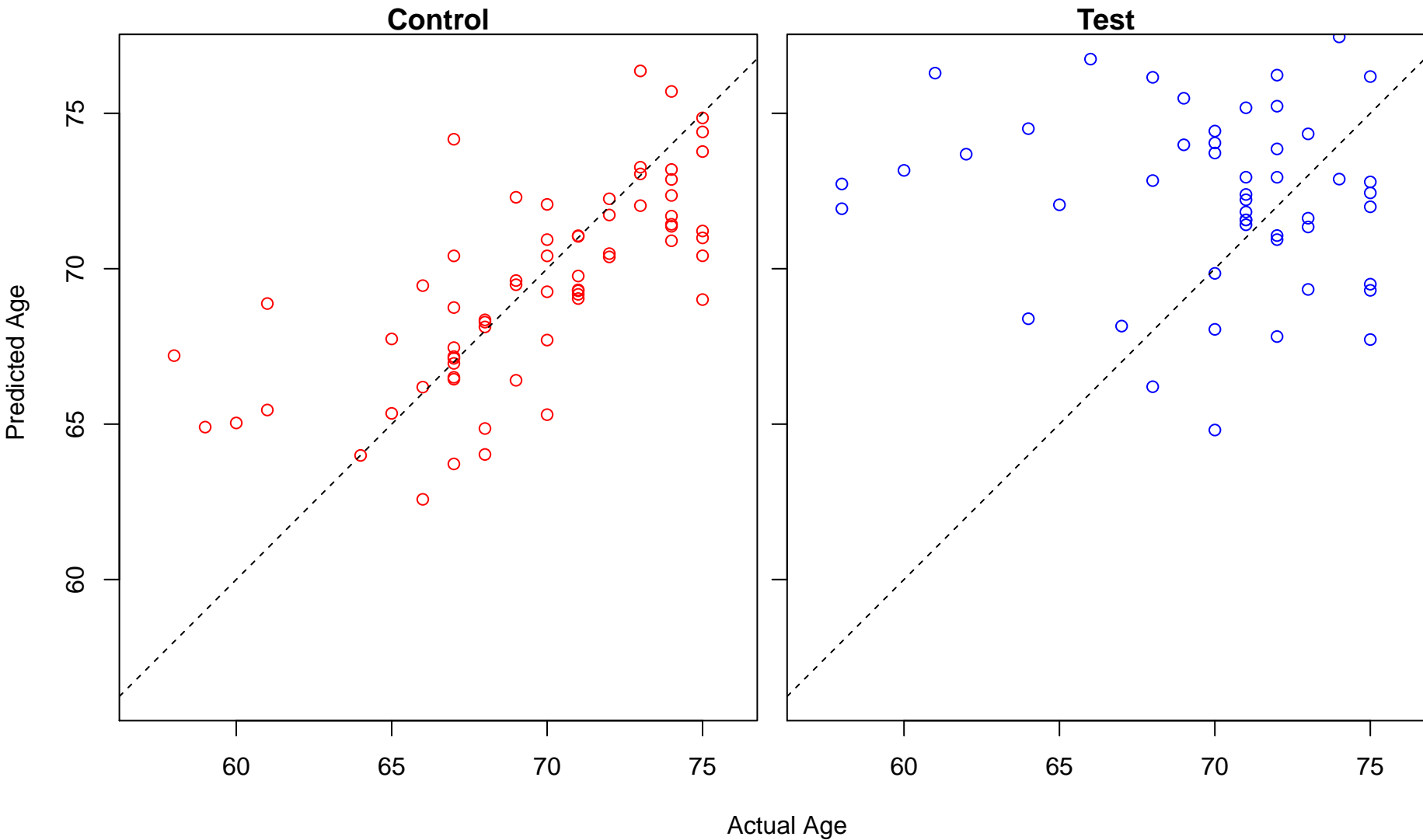


Actual Age

MyD88-independent toll-like receptor signaling pathway (Score: 1.769688)

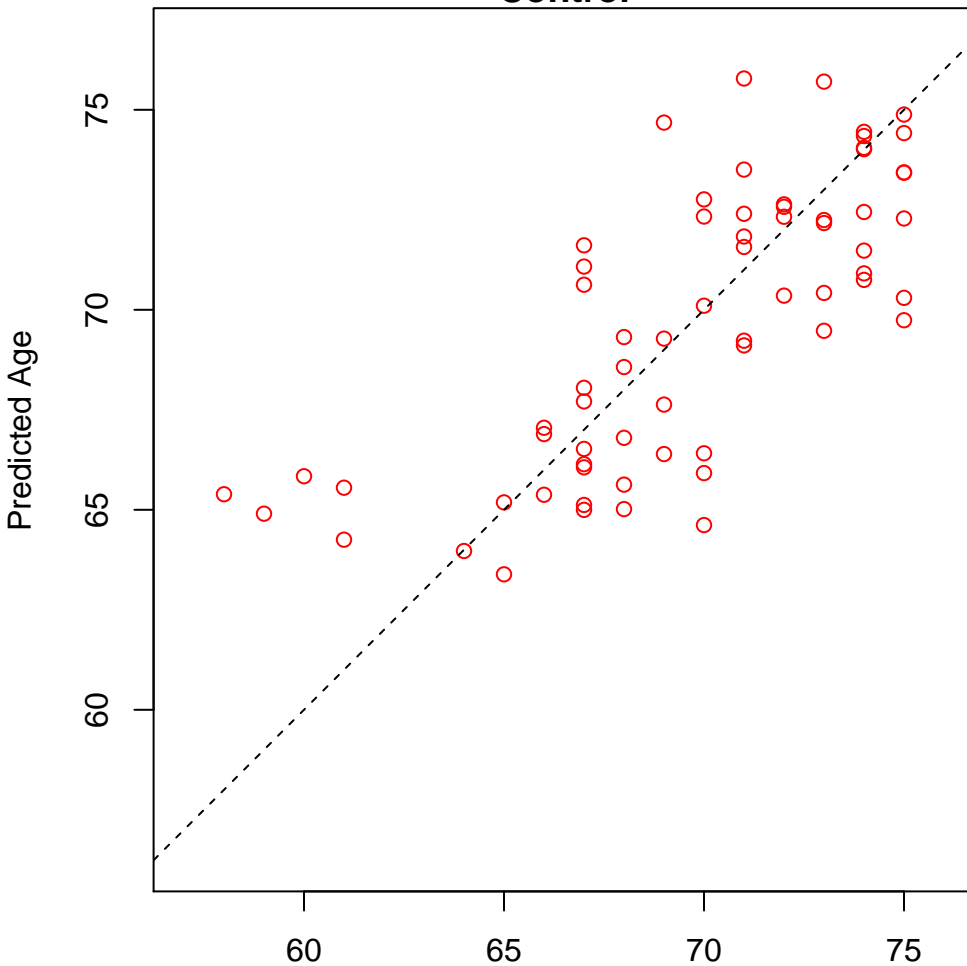


alditol phosphate metabolic process (Score: 1.769655)

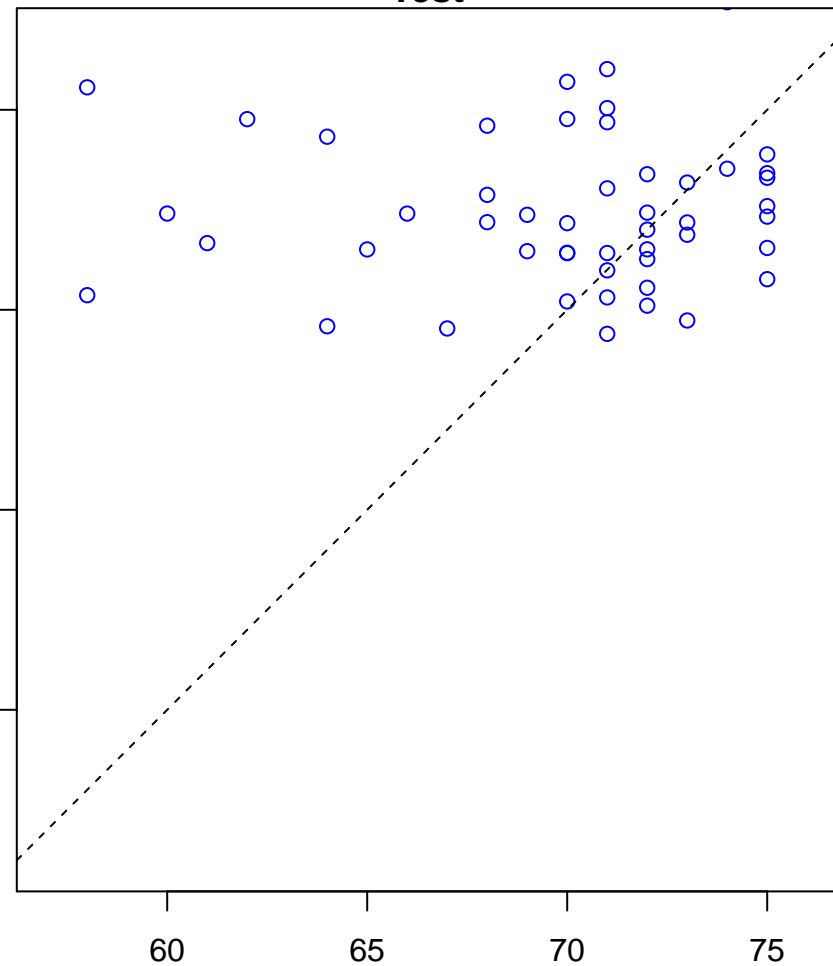


regulation of neuron apoptotic process (Score: 1.768568)

Control

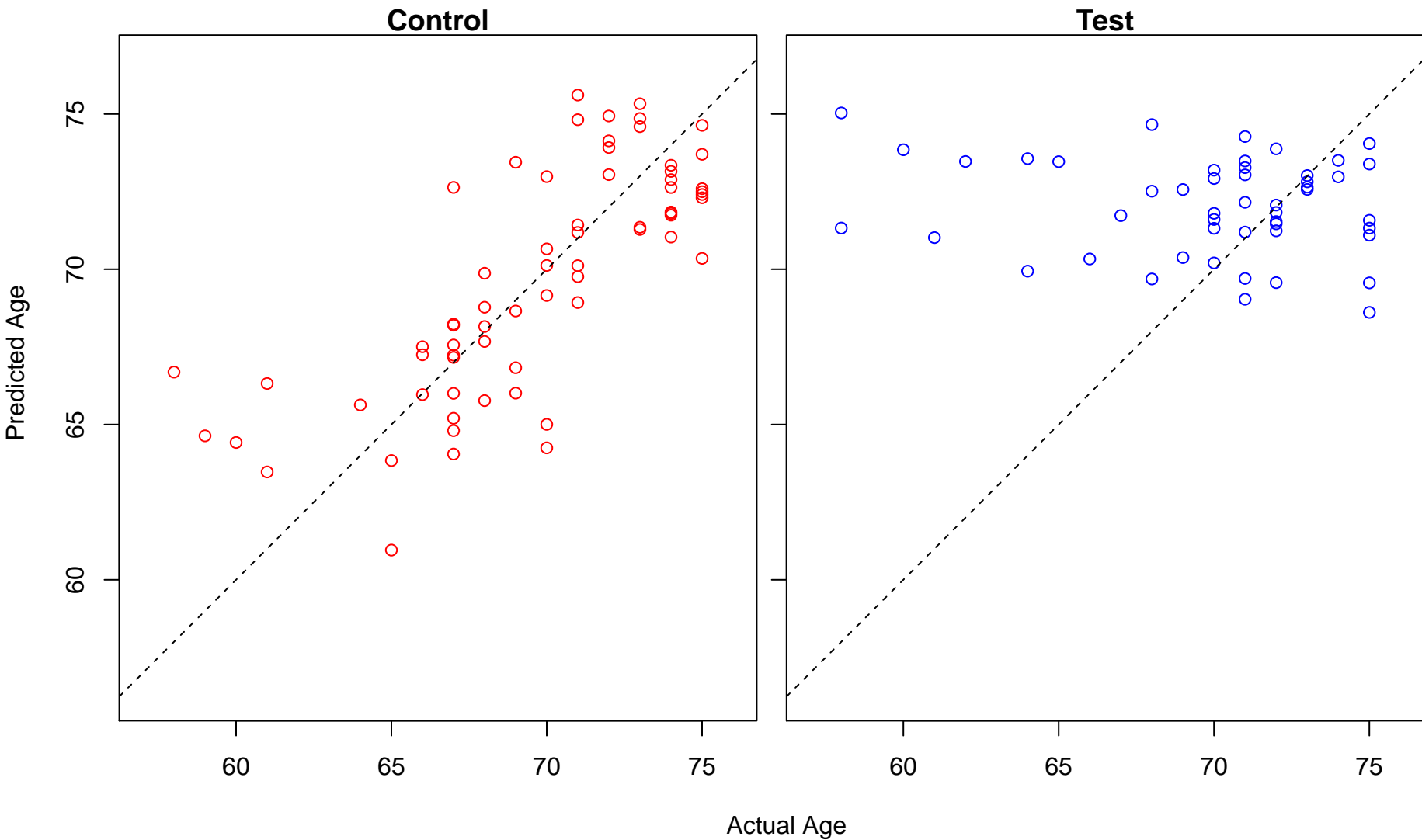


Test

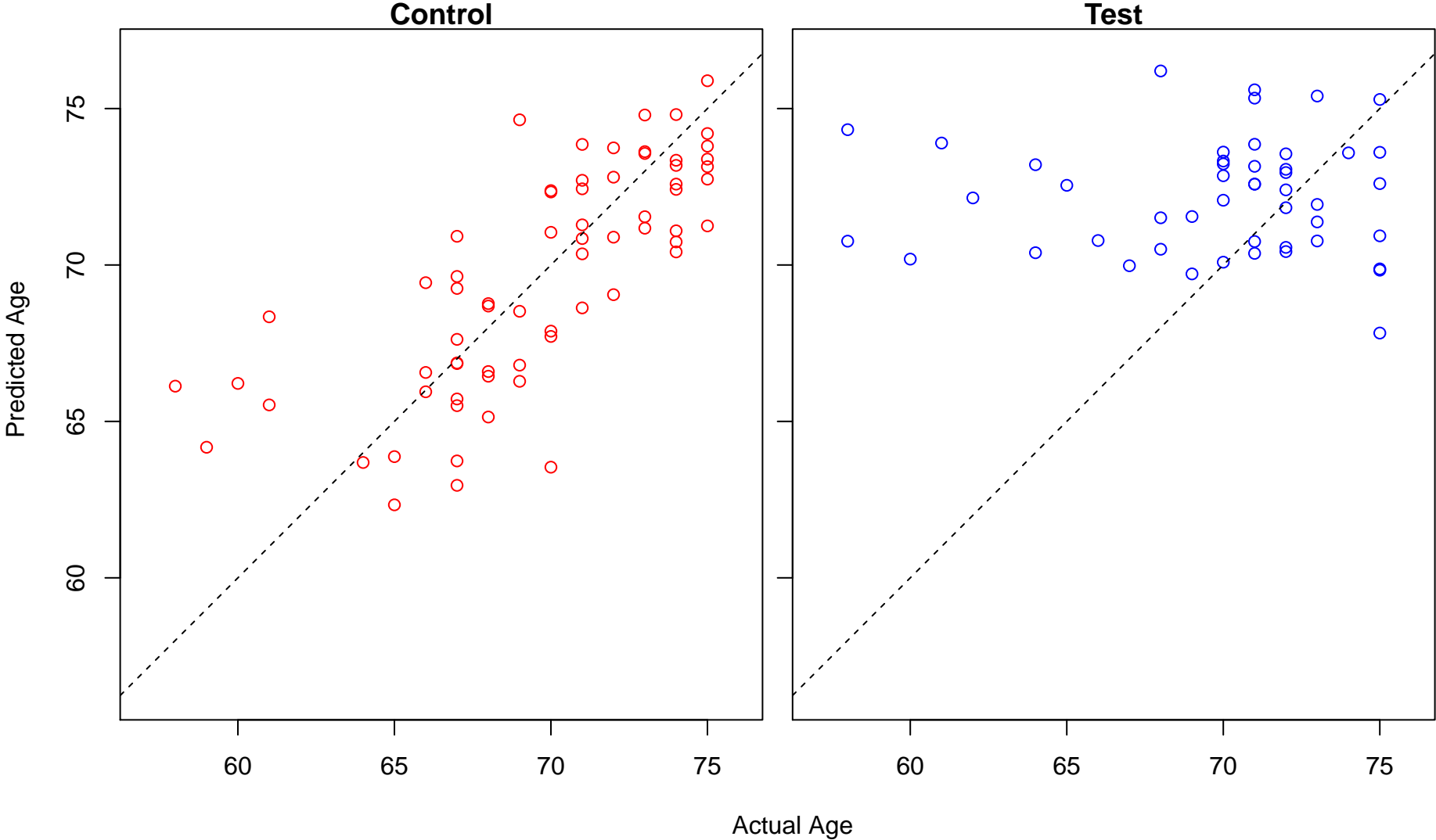


Actual Age

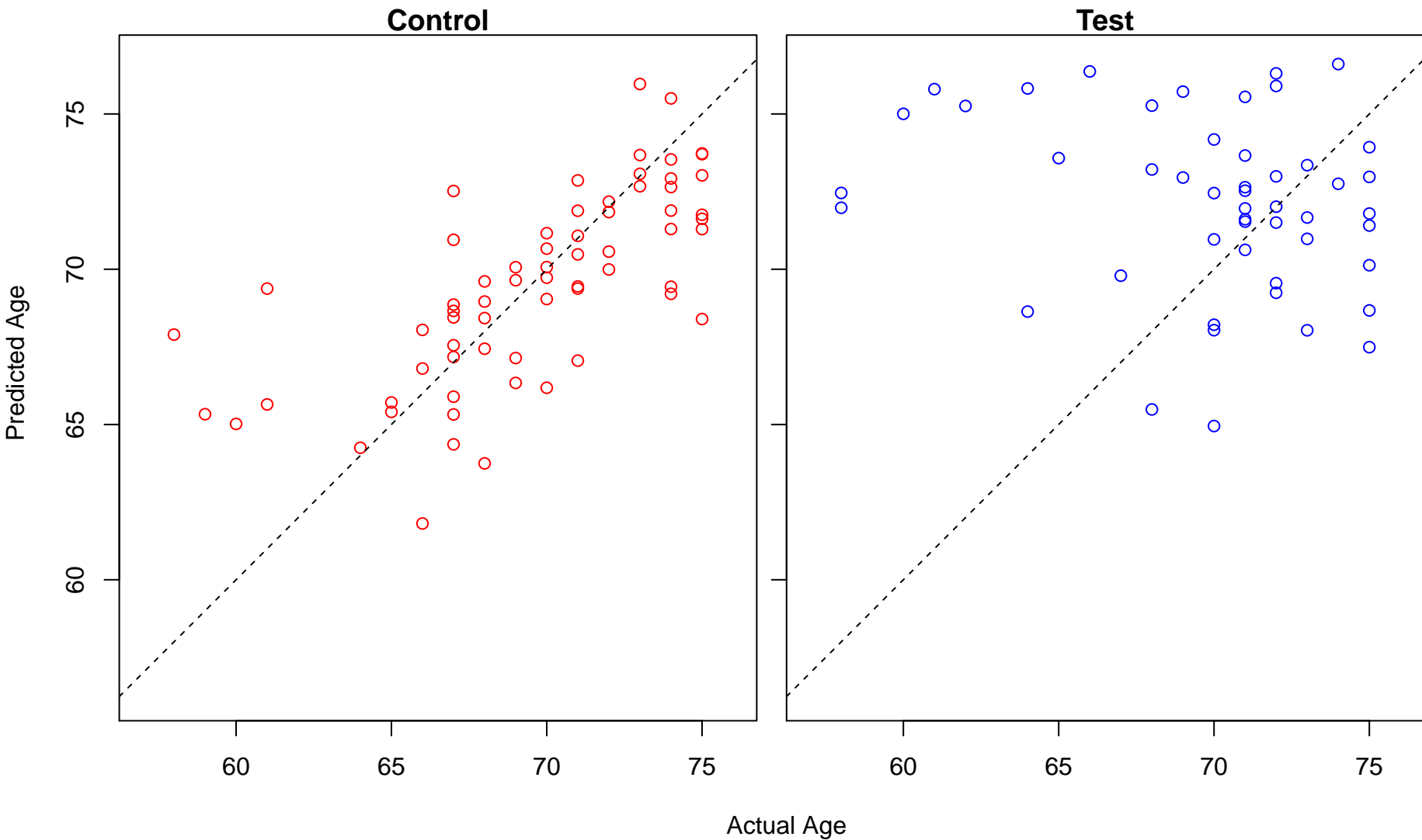
nuclear export (Score: 1.766916)



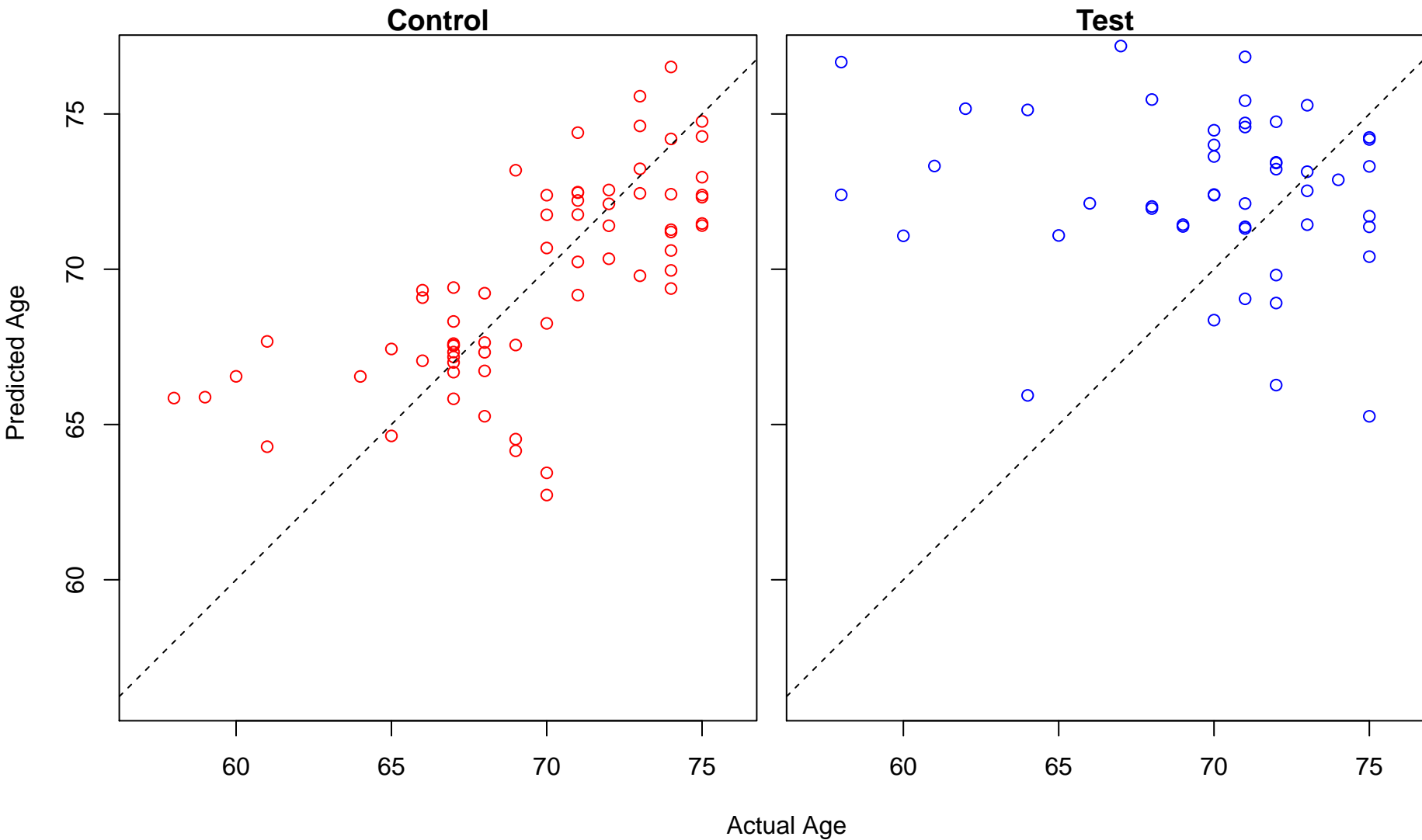
negative regulation of protein modification by small protein conjugation or removal (Score: 1.76653)



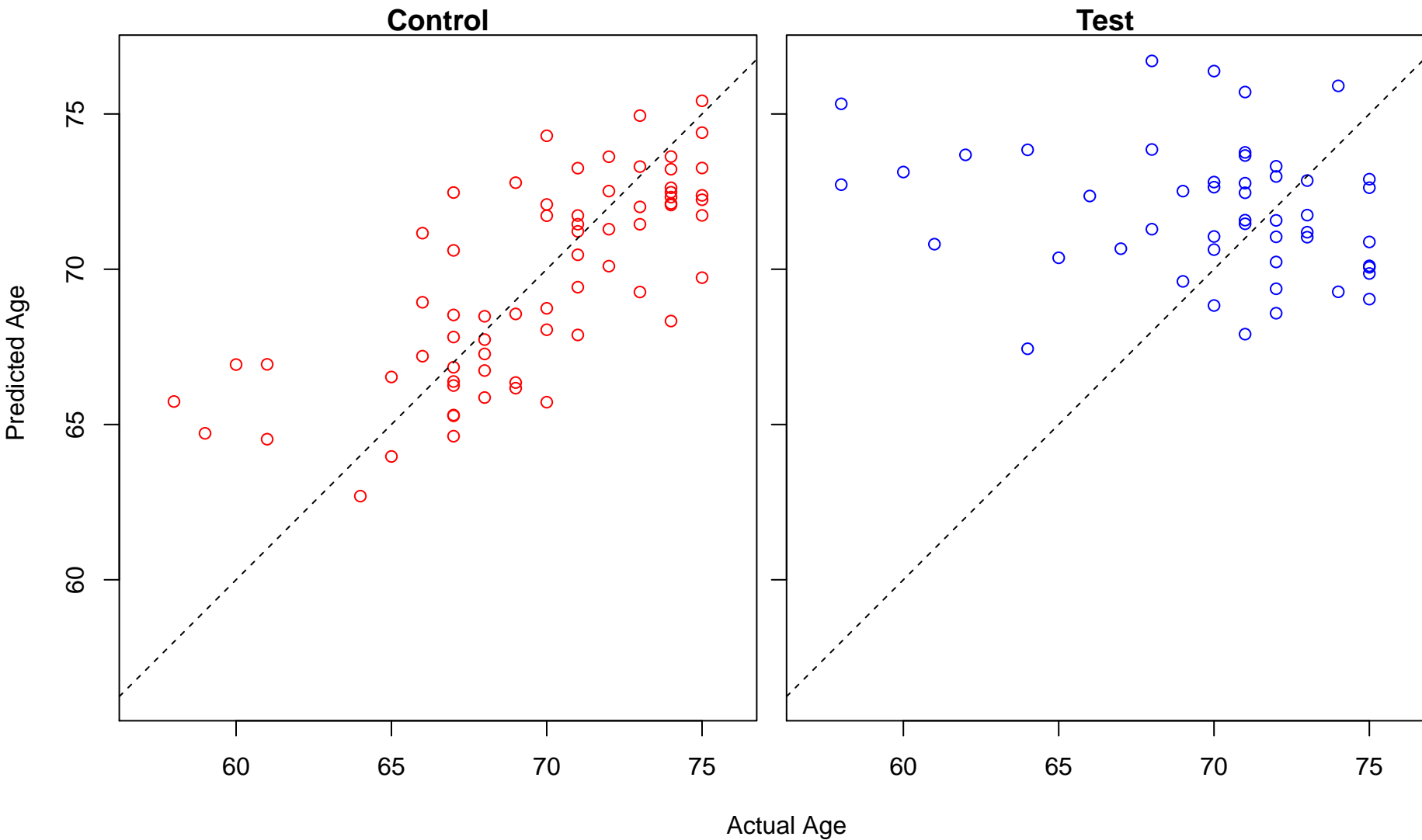
phosphatidylethanolamine acyl-chain remodeling (Score: 1.764210)



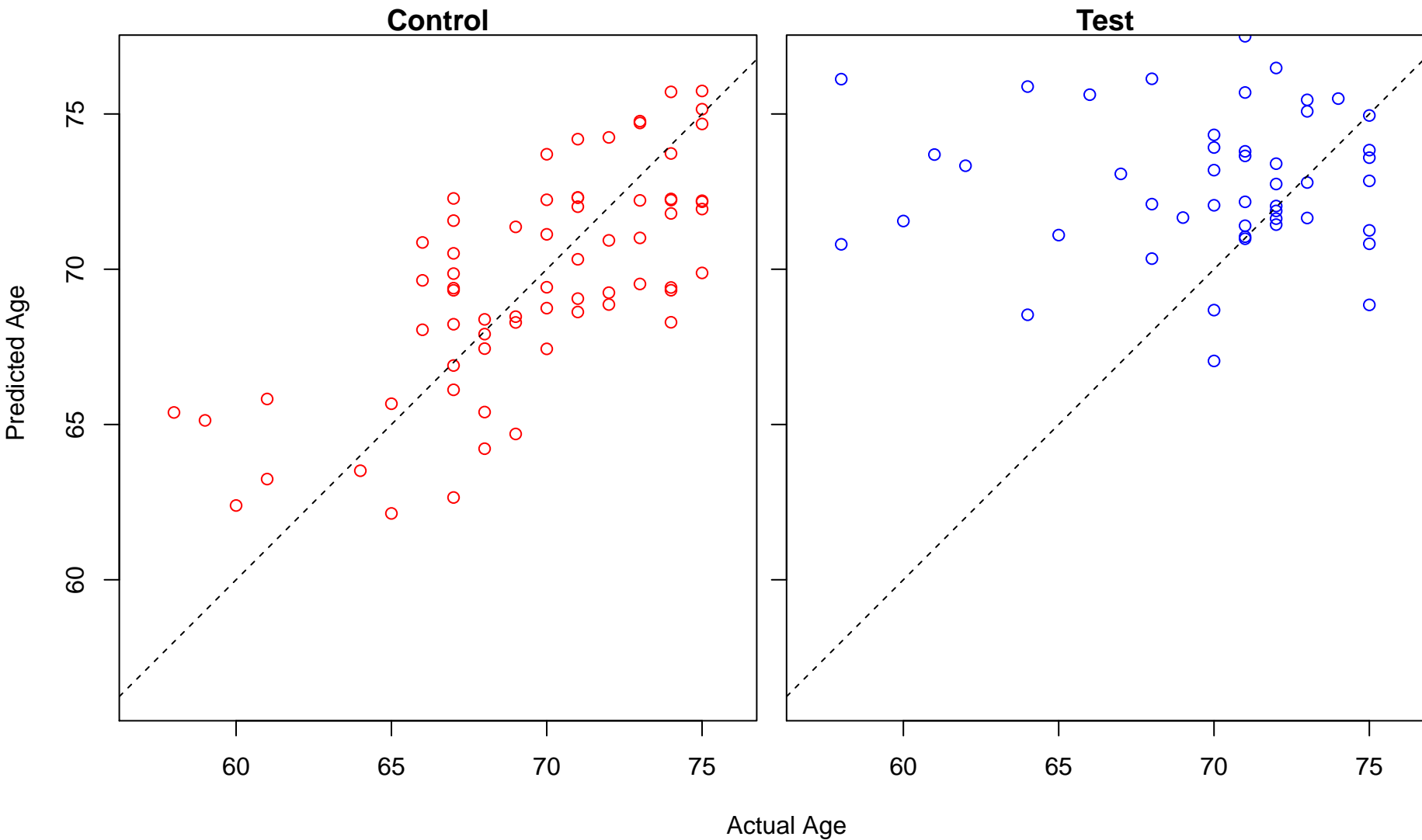
positive regulation of G1/S transition of mitotic cell cycle (Score: 1.763671)



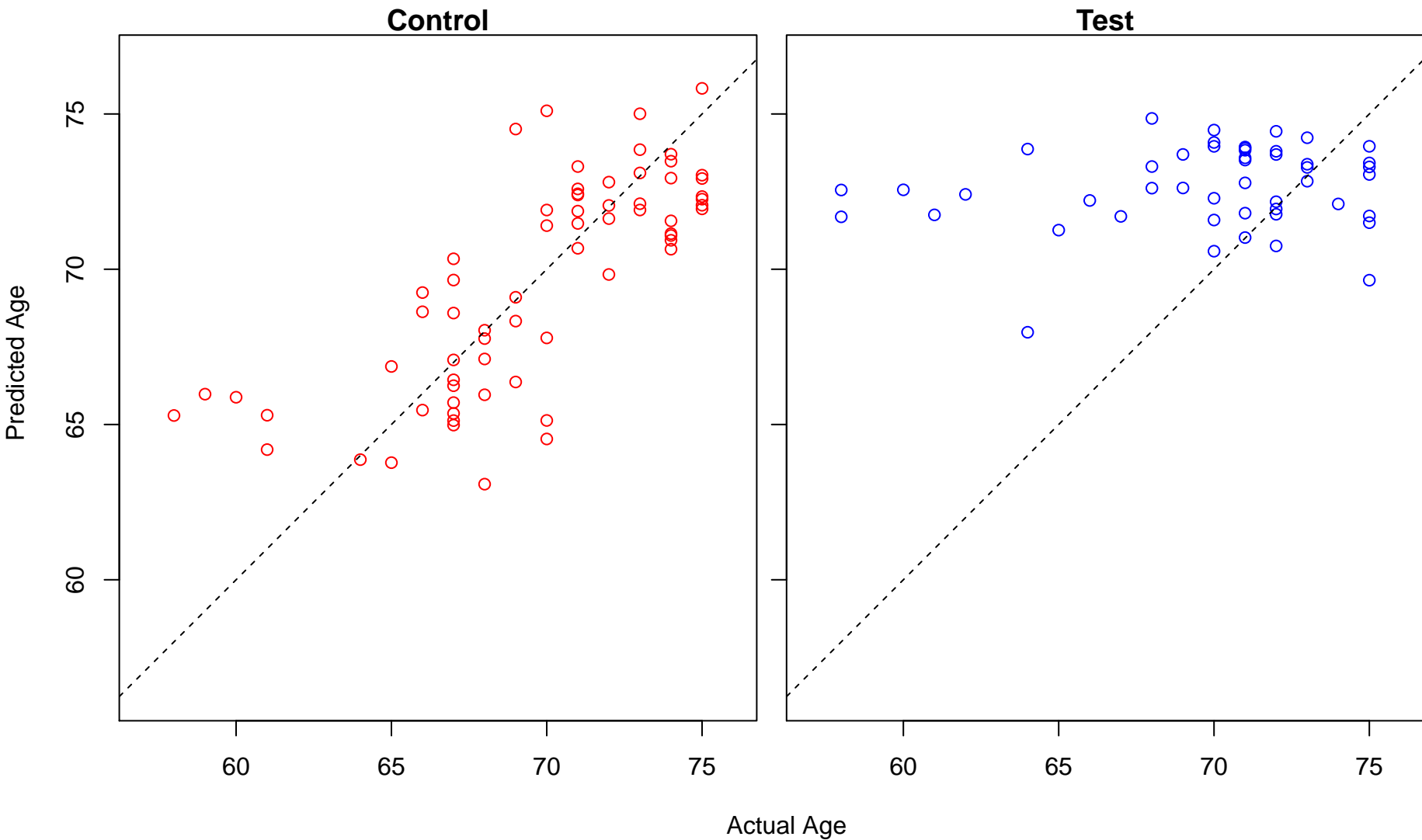
chromosome condensation (Score: 1.763625)



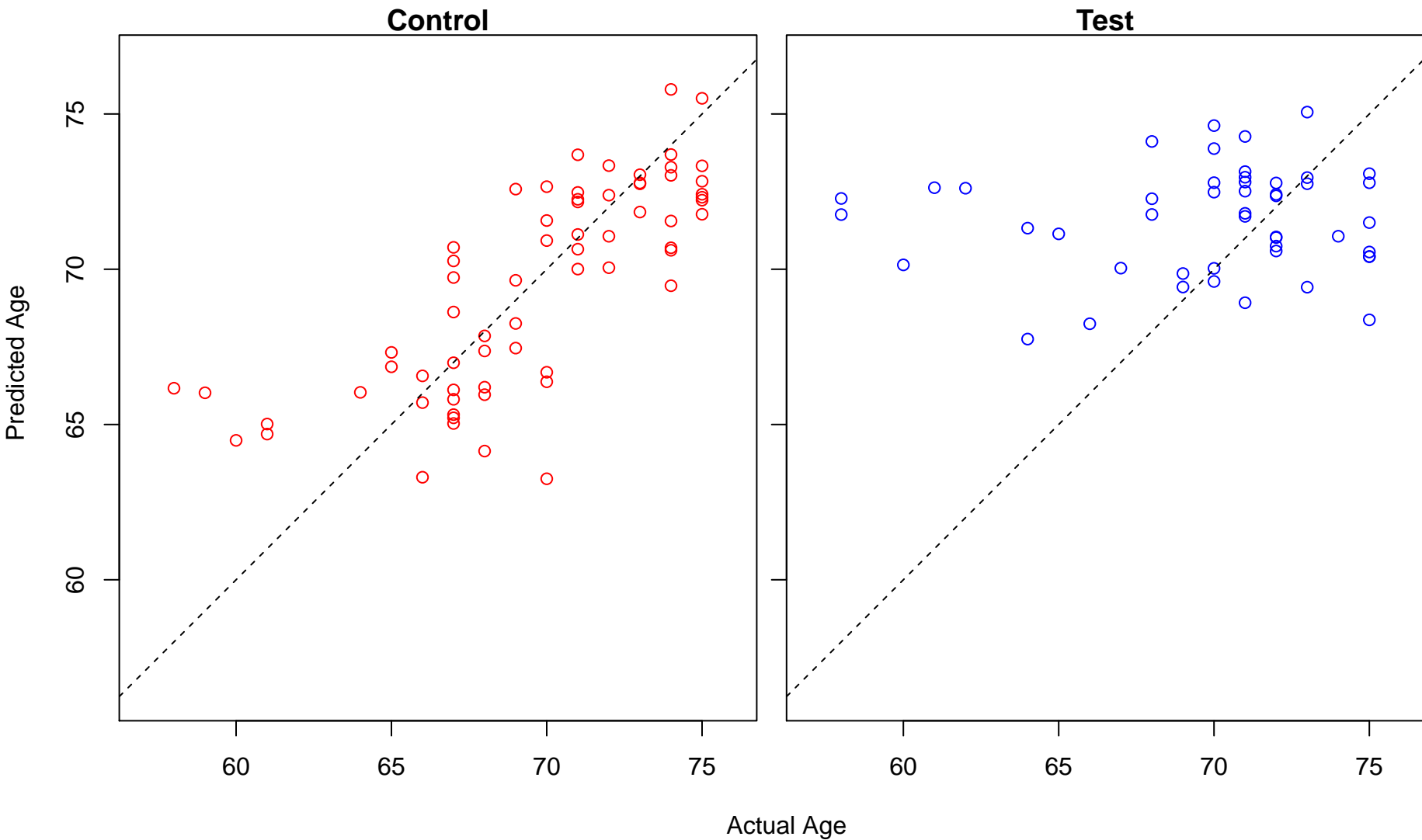
regulation of fatty acid metabolic process (Score: 1.763617)



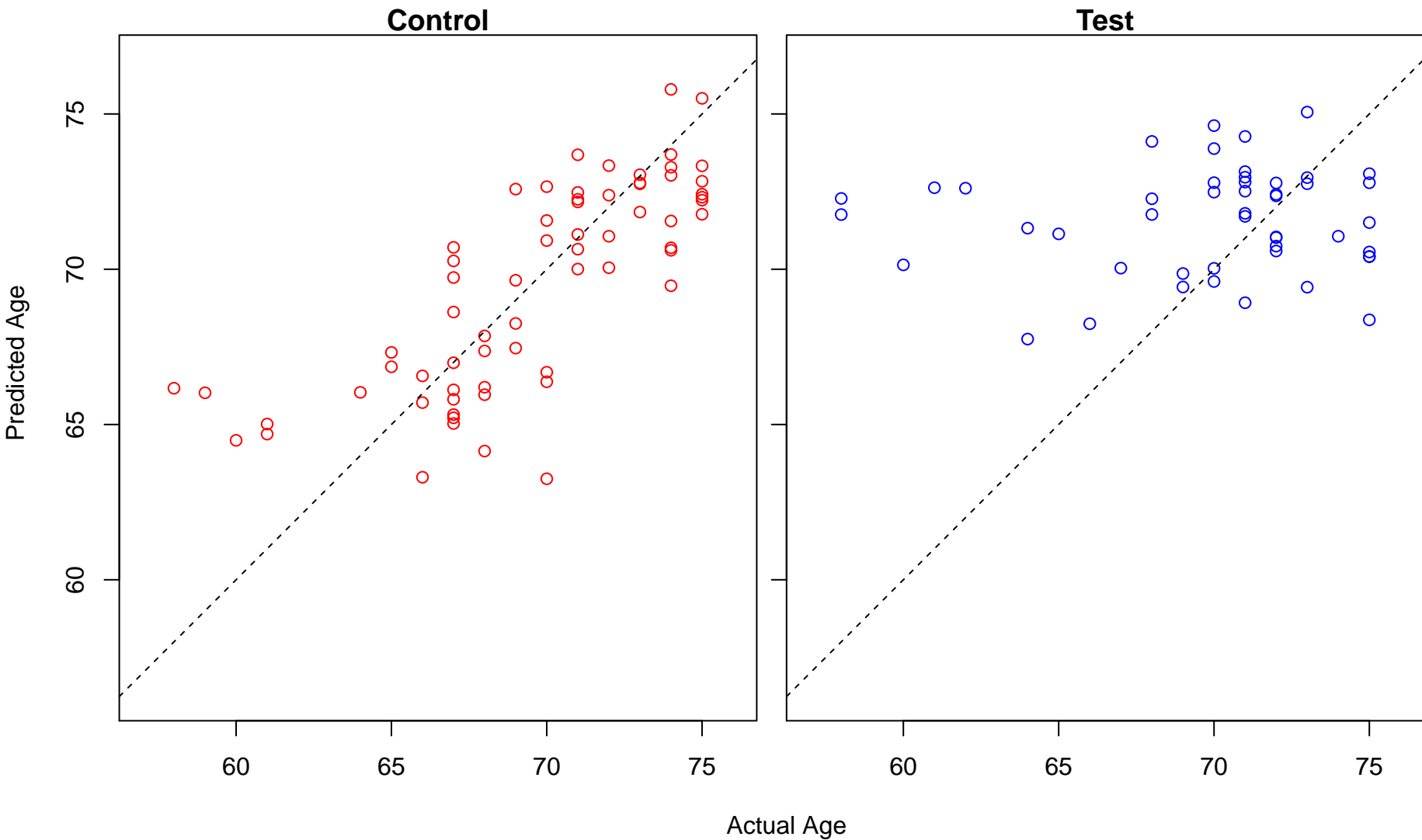
vesicle organization (Score: 1.763034)



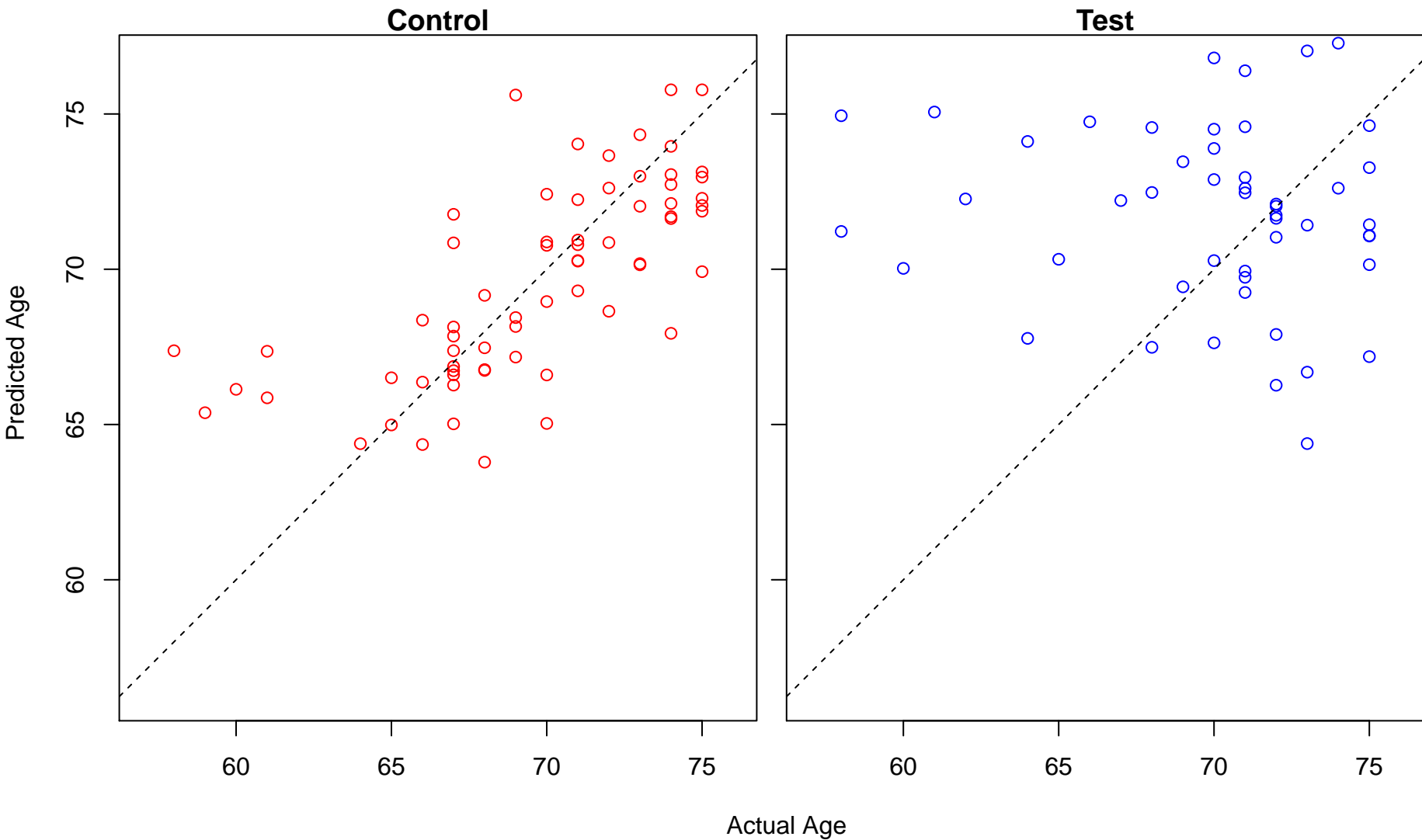
purine nucleoside monophosphate biosynthetic process (Score: 1.760993)



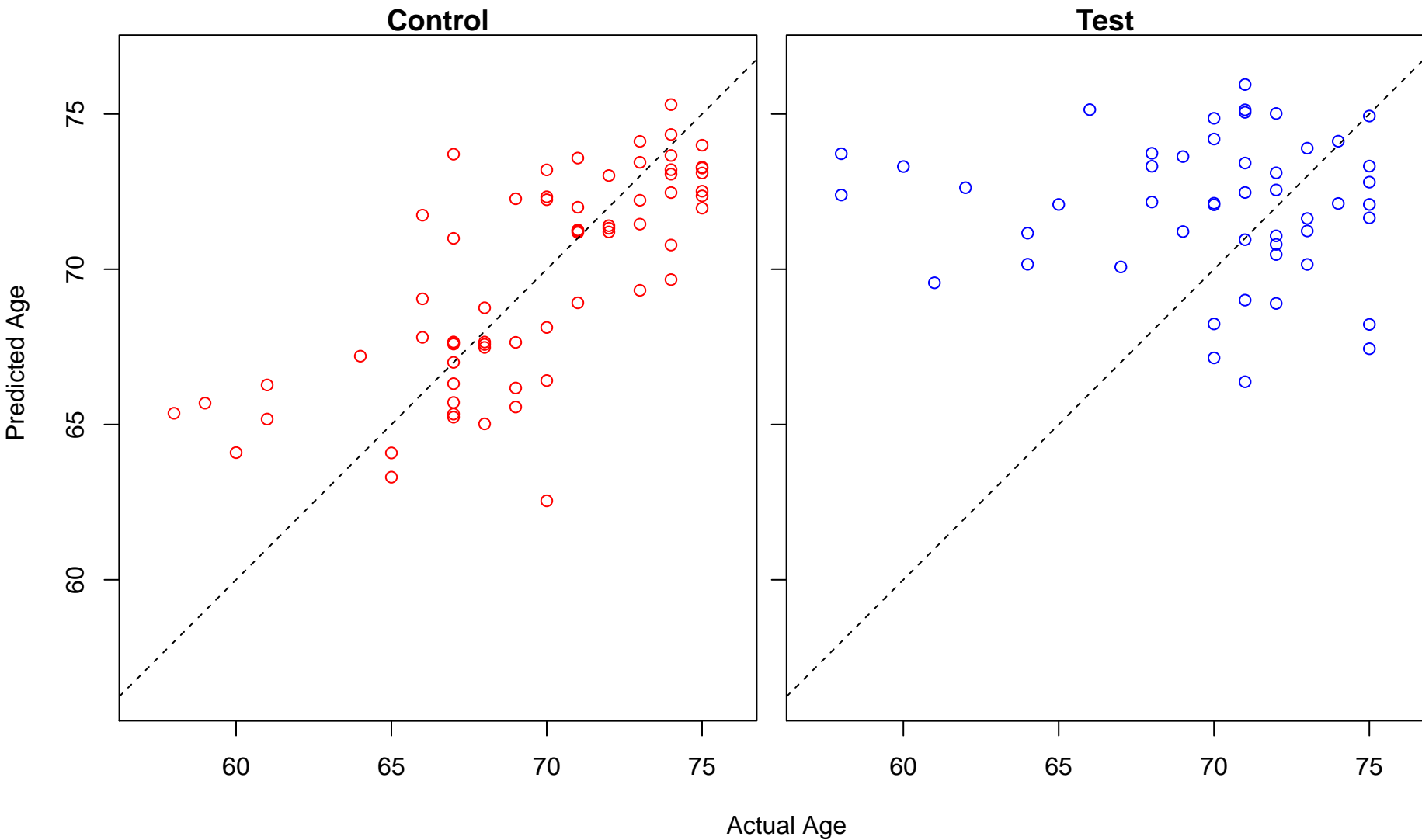
purine ribonucleoside monophosphate biosynthetic process (Score: 1.760993)



negative regulation of response to biotic stimulus (Score: 1.760481)

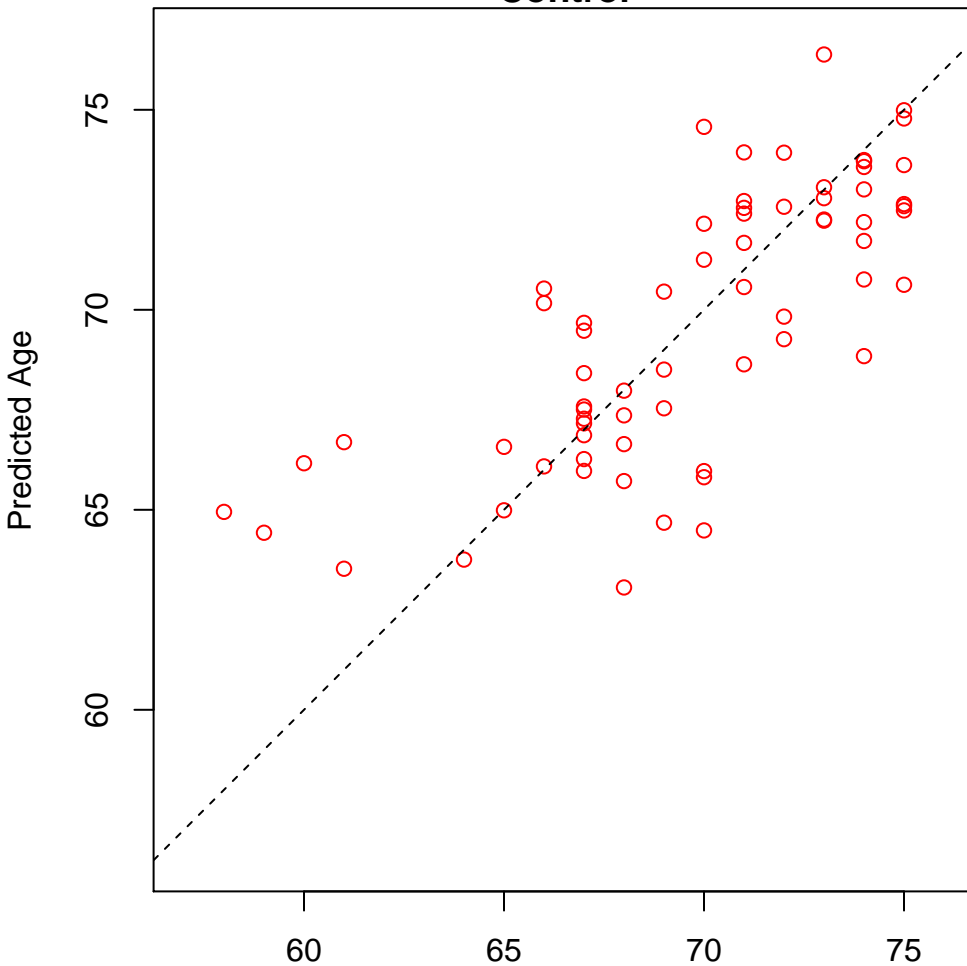


positive regulation of myeloid leukocyte differentiation (Score: 1.759564)

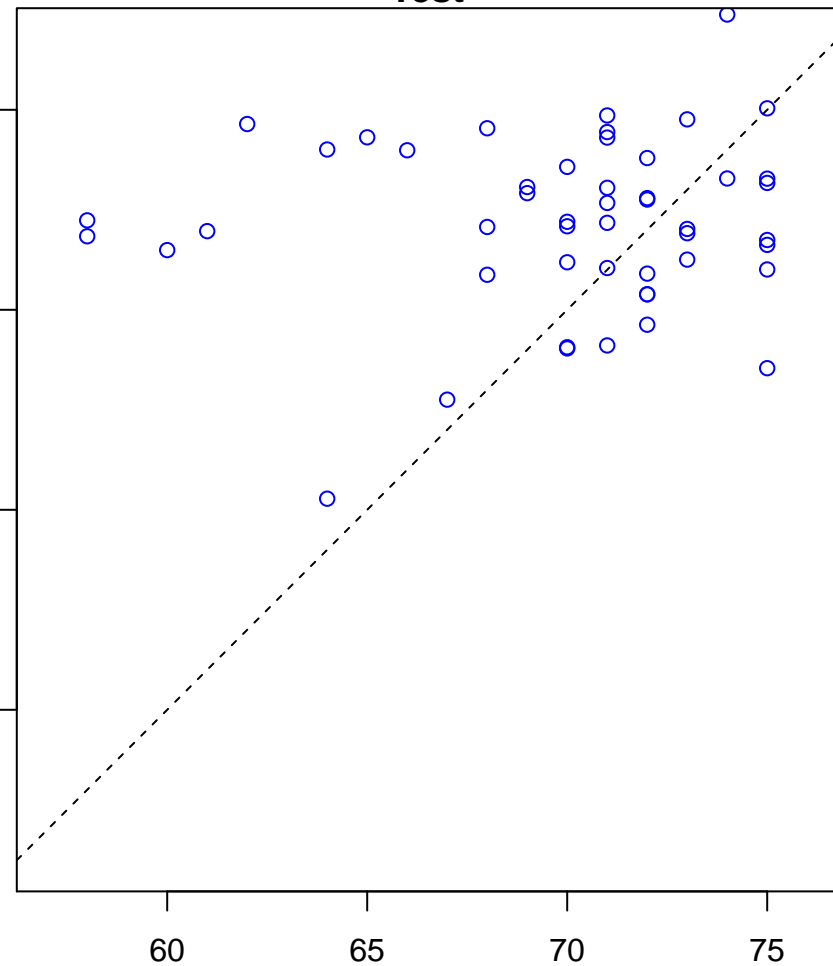


regulation of glucose metabolic process (Score: 1.759548)

Control

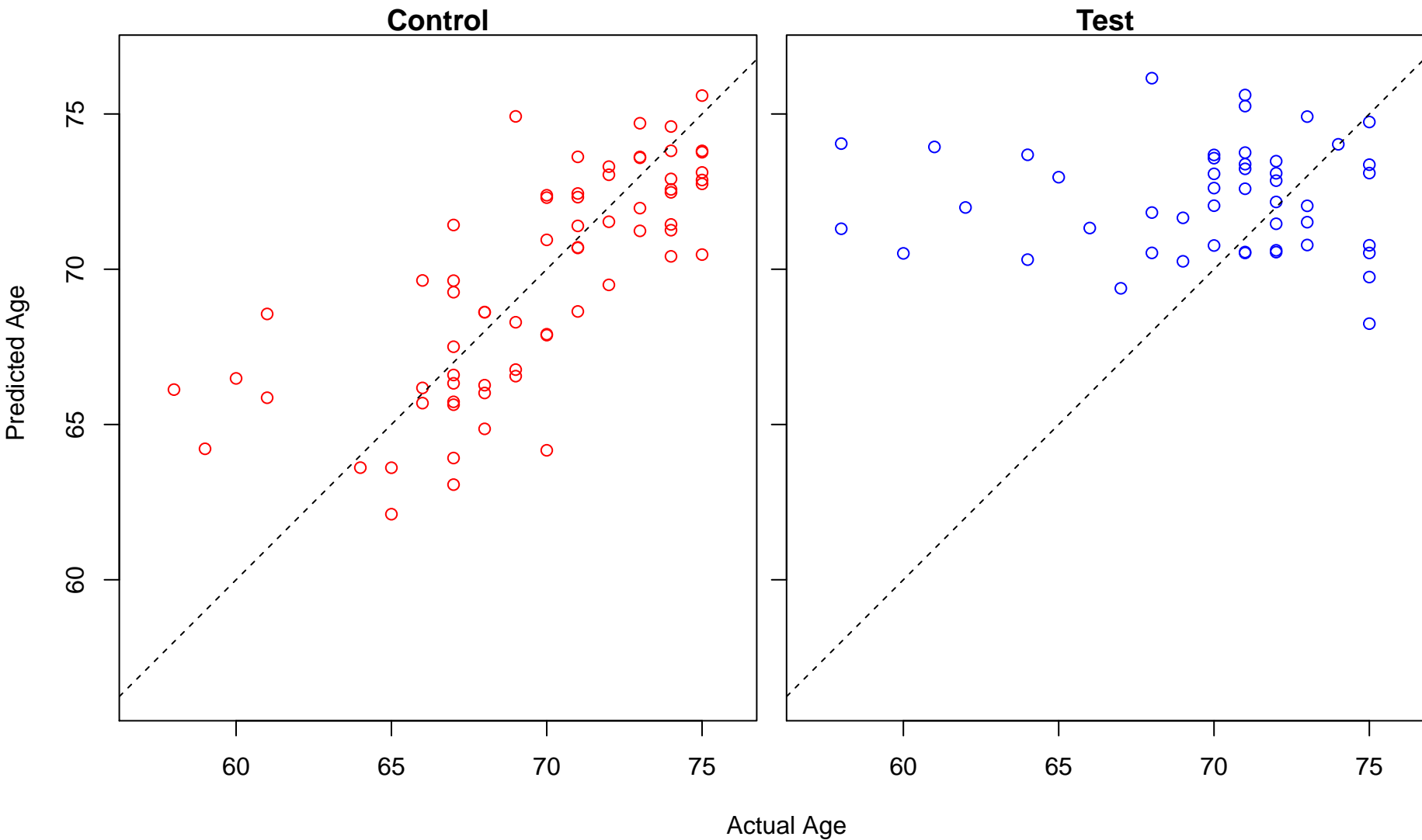


Test

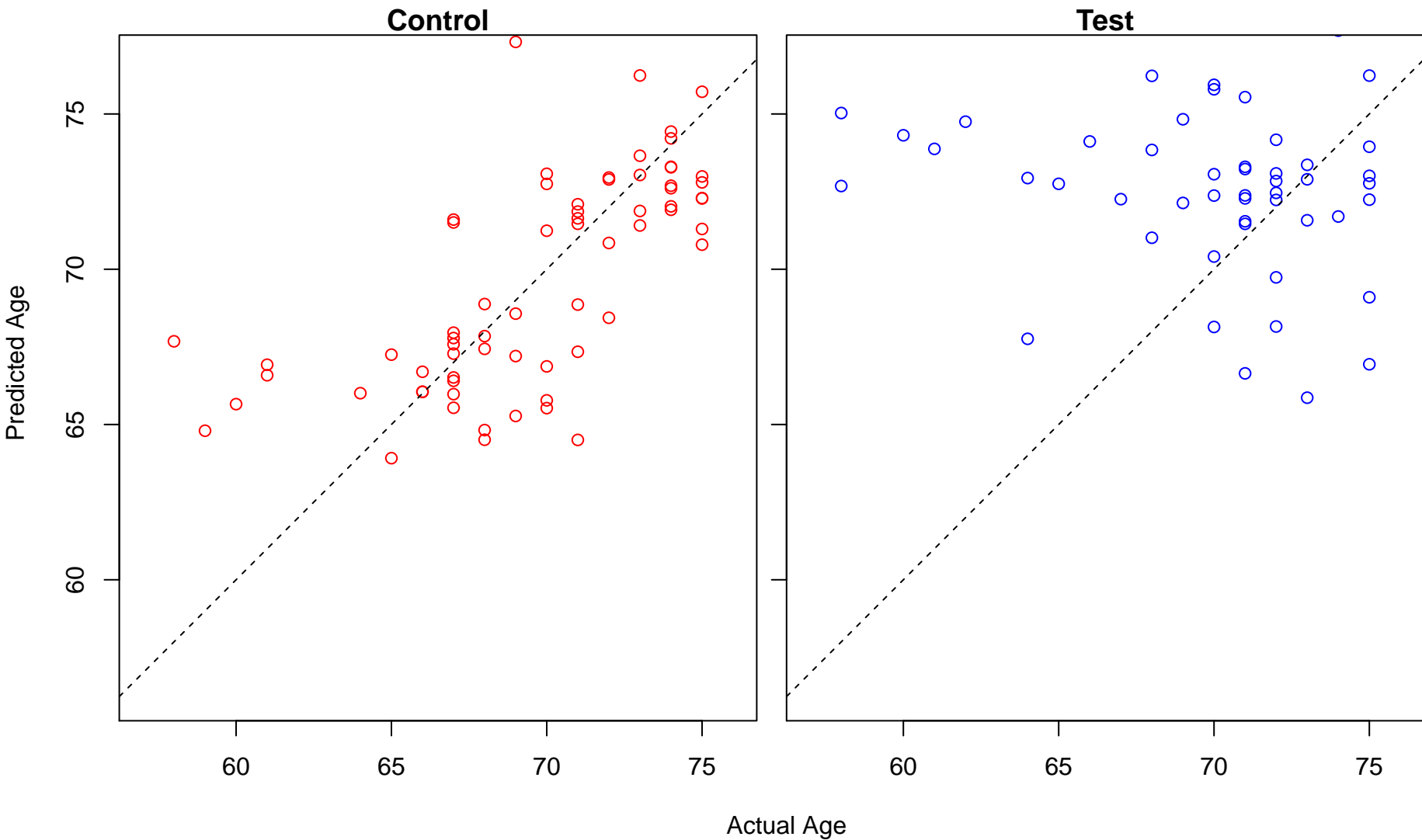


Actual Age

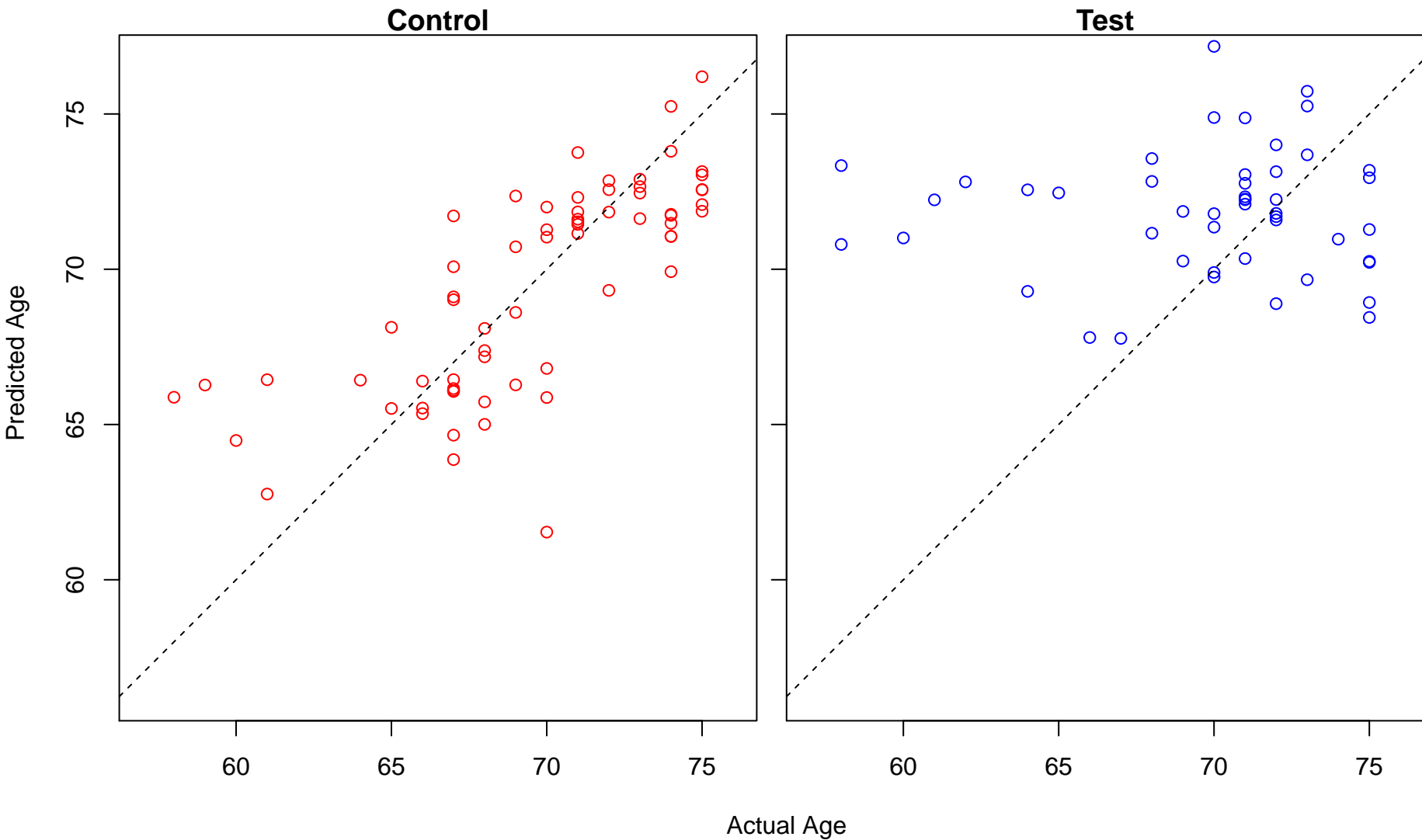
negative regulation of protein ubiquitination (Score: 1.759453)



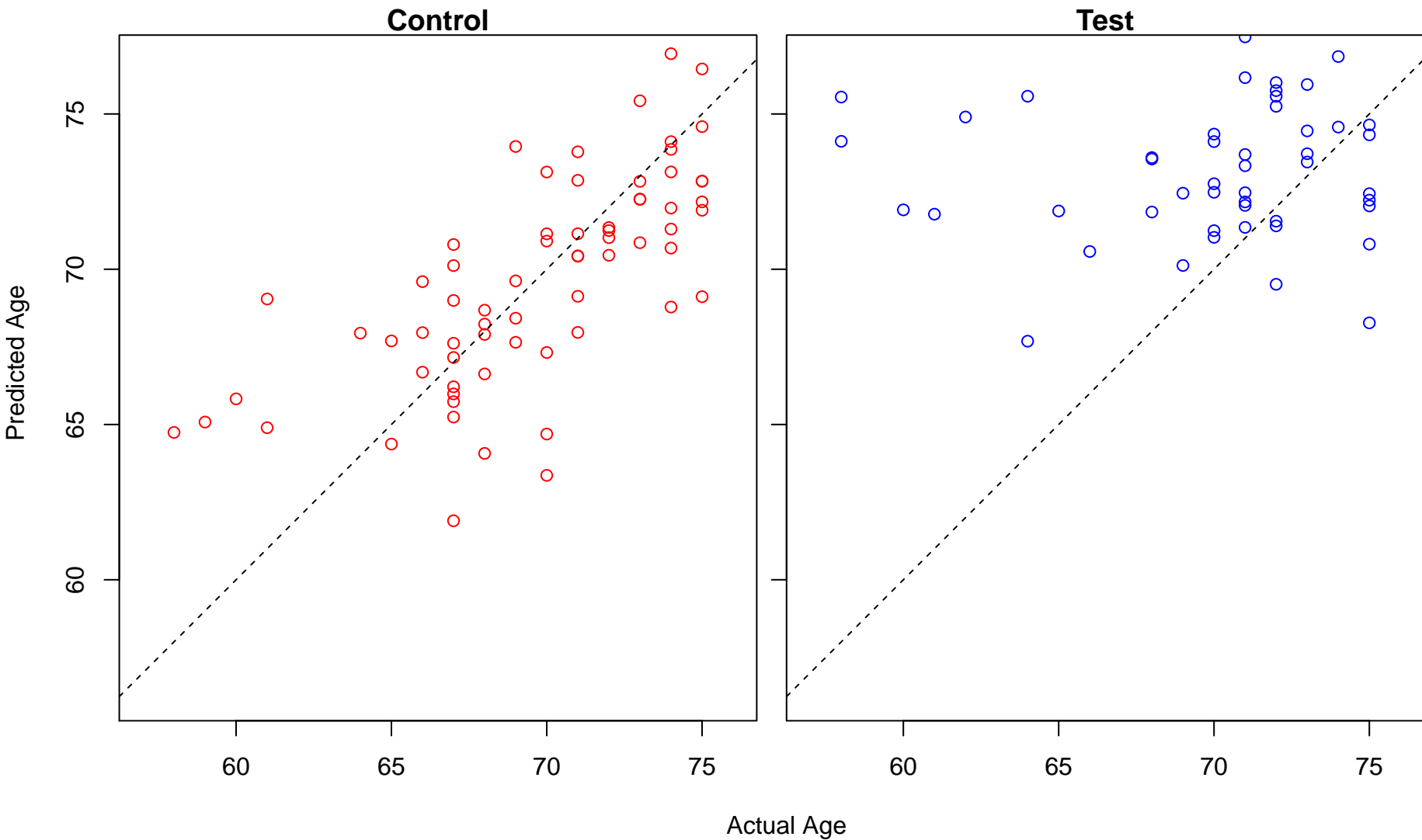
lymphocyte differentiation (Score: 1.758730)



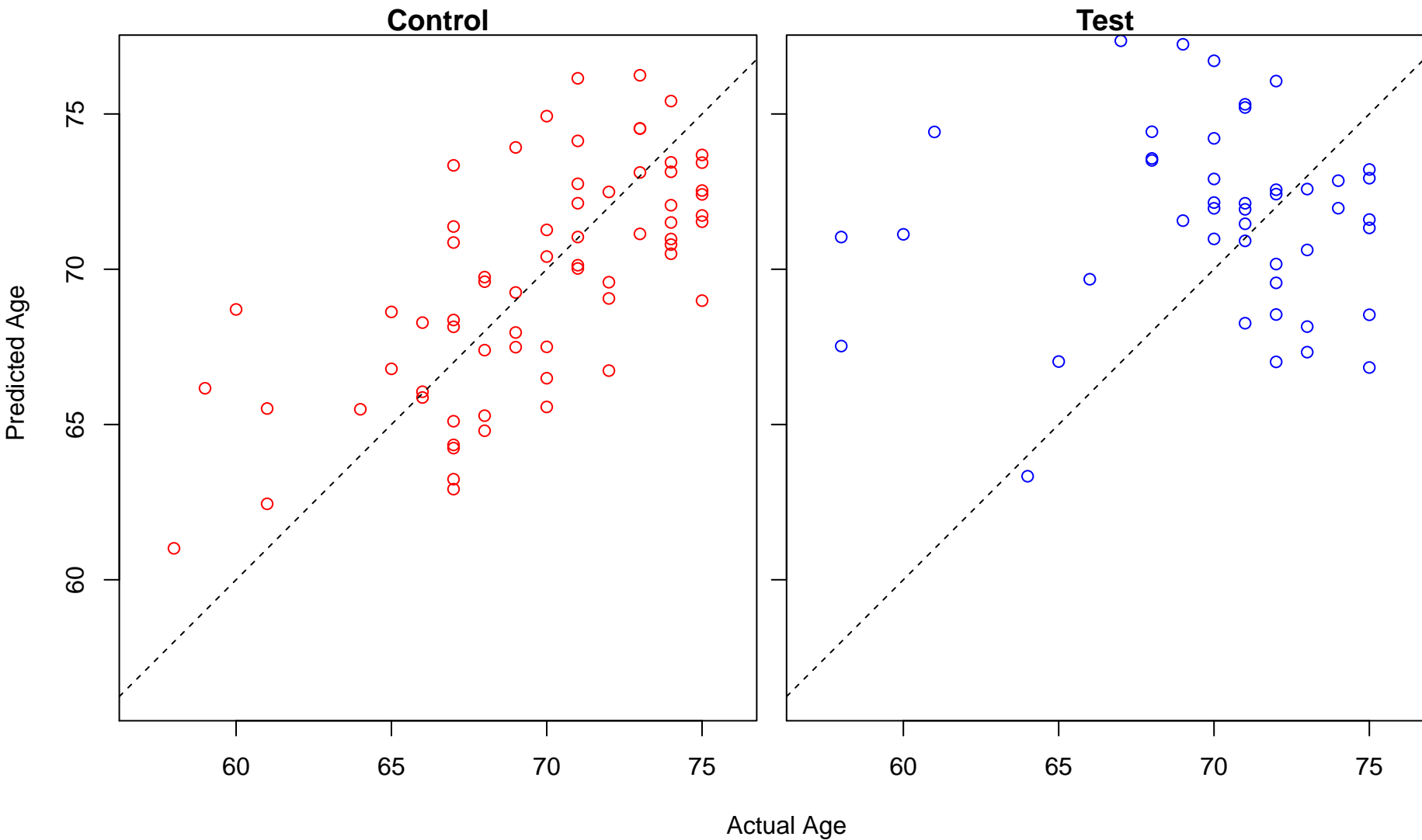
ribonucleoside monophosphate metabolic process (Score: 1.758567)



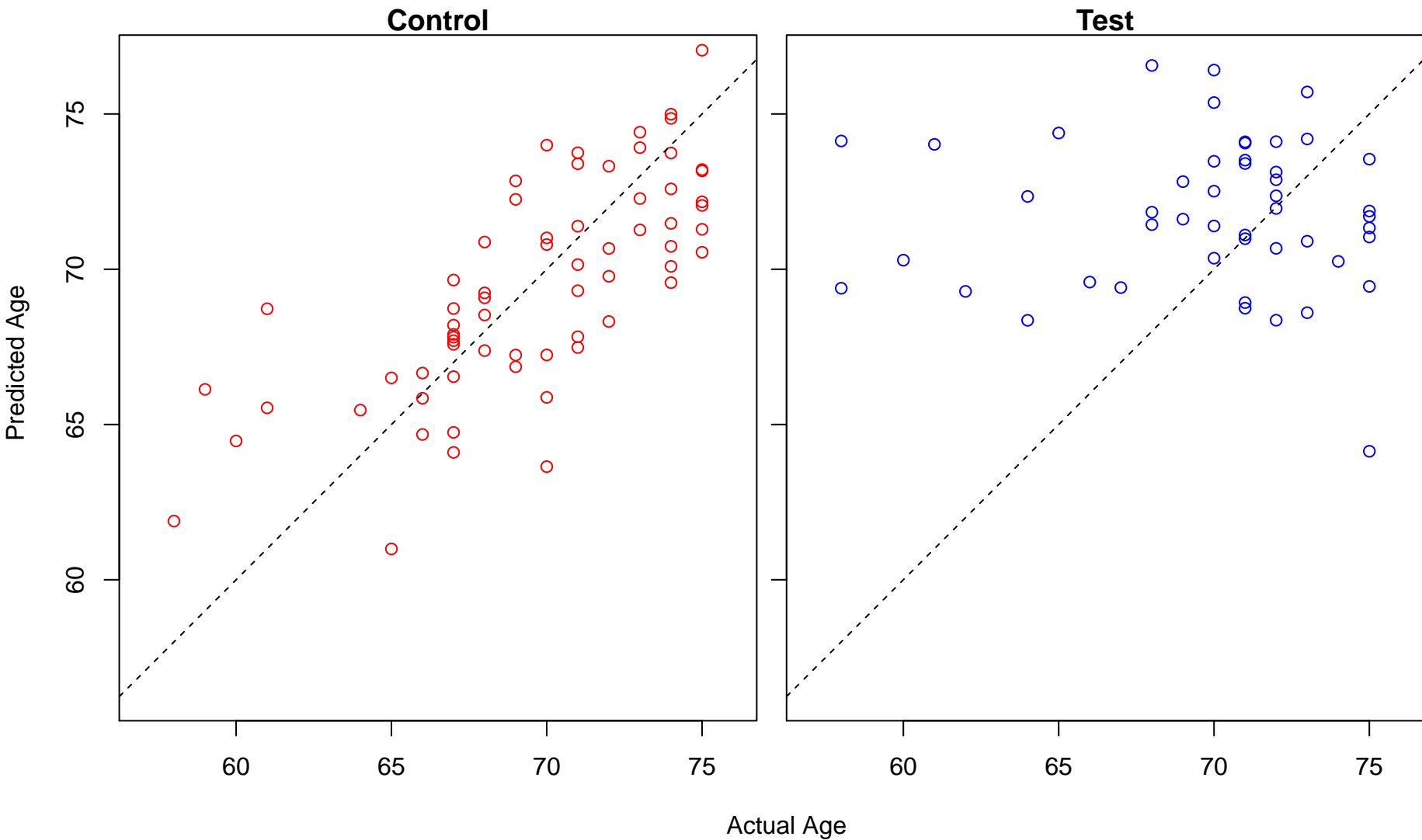
DNA duplex unwinding (Score: 1.758031)



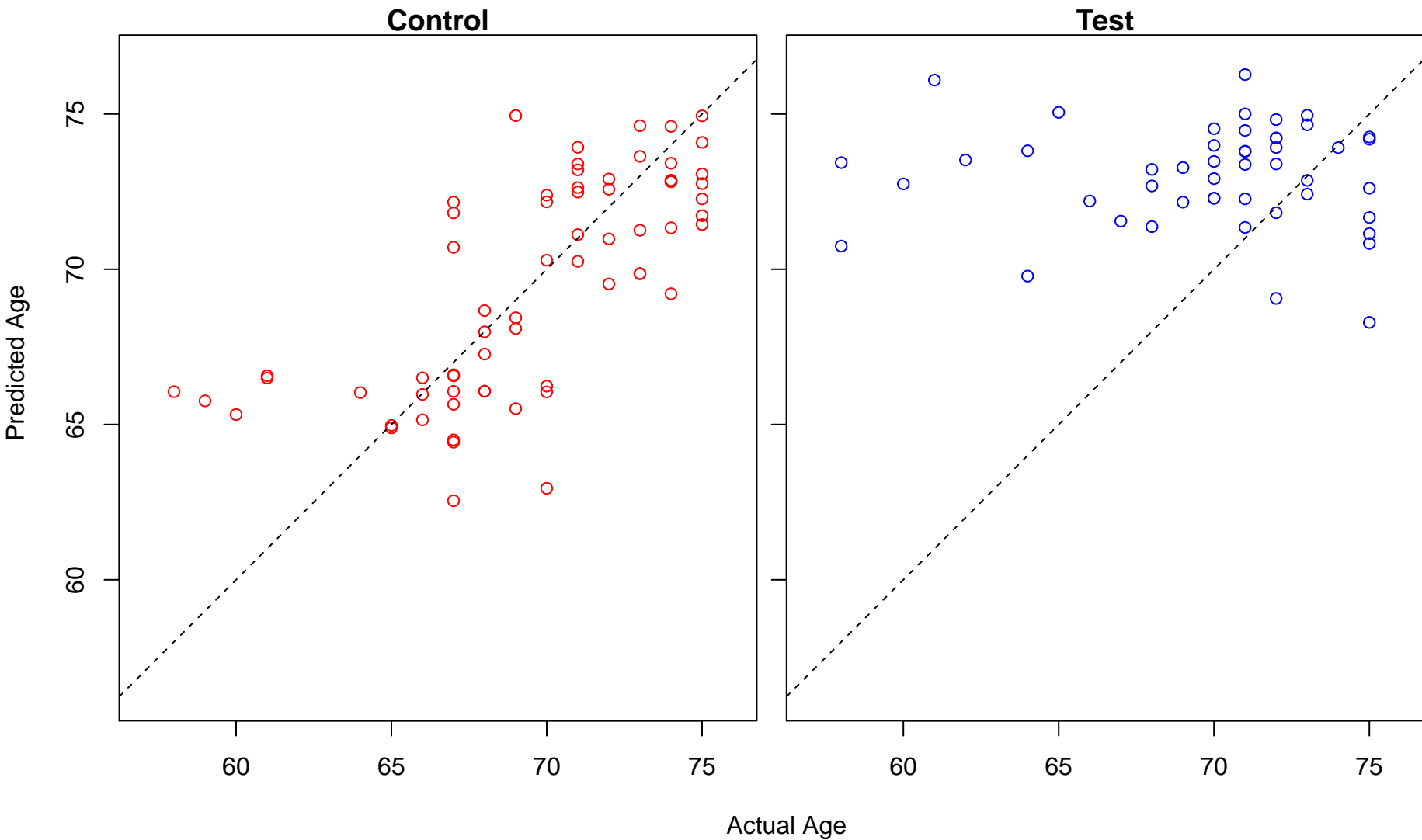
skeletal muscle tissue development (Score: 1.757568)



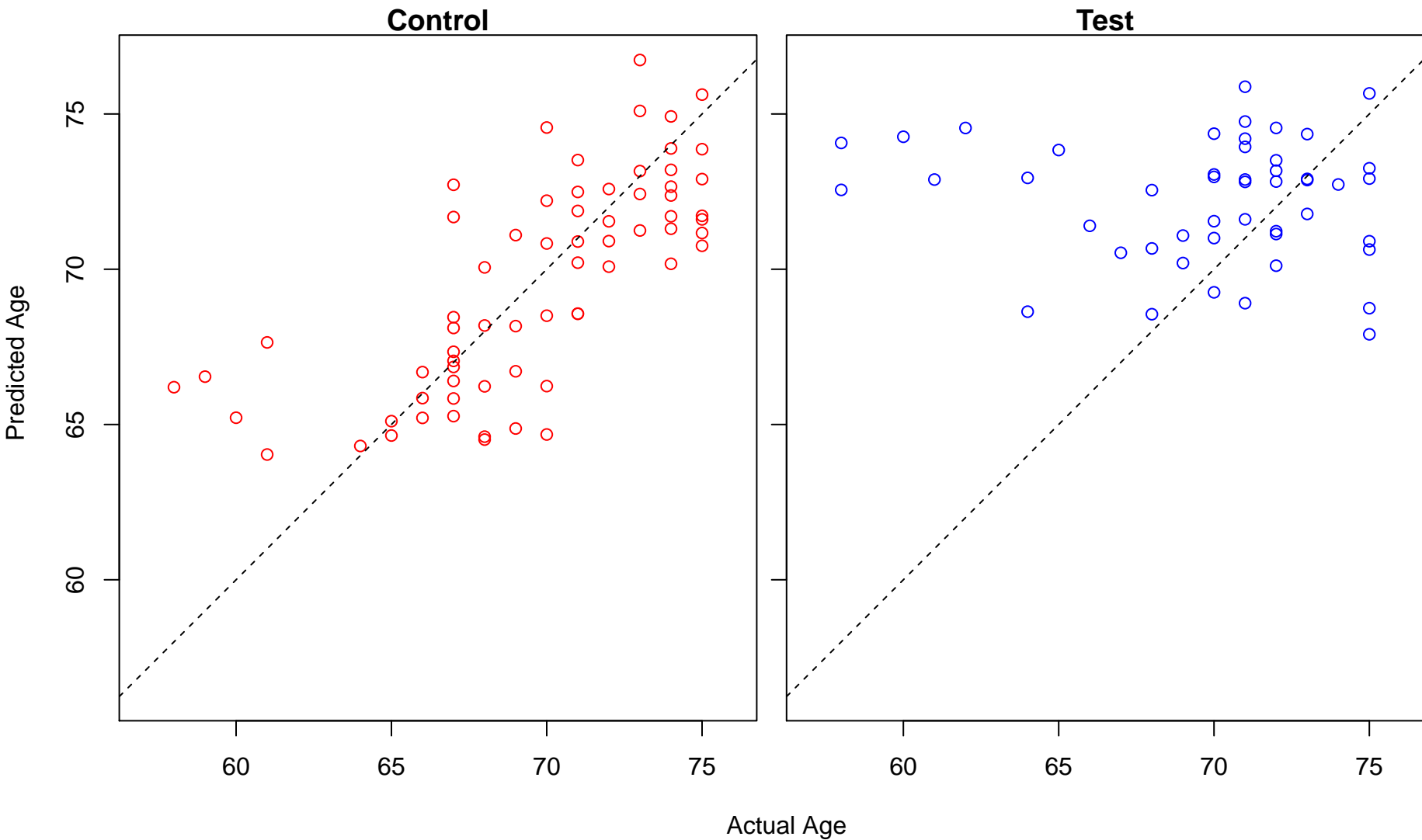
positive regulation of neutrophil migration (Score: 1.757451)



peptide biosynthetic process (Score: 1.757148)

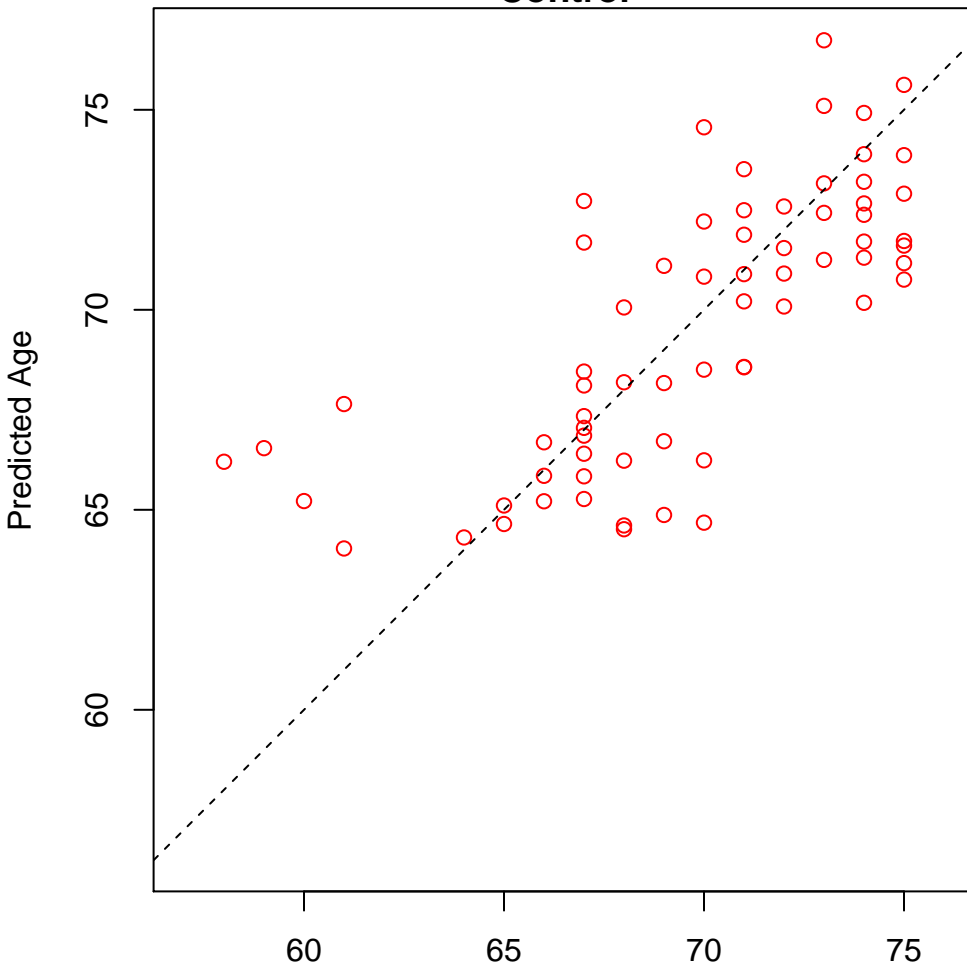


regulation of response to extracellular stimulus (Score: 1.756823)

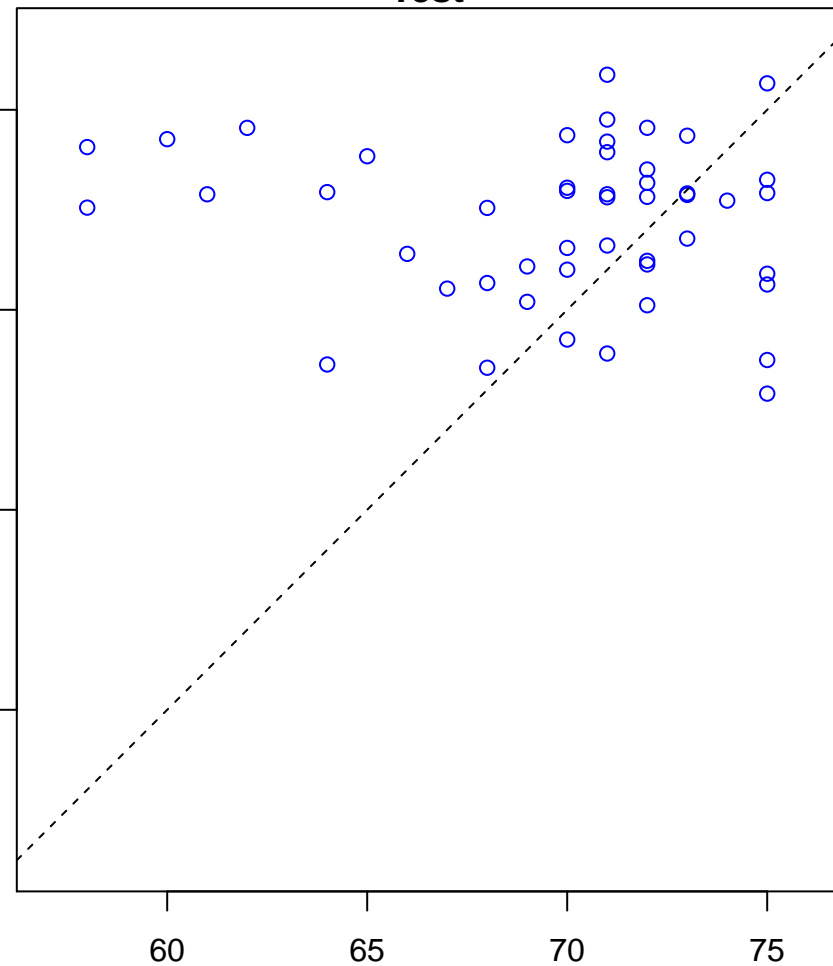


regulation of response to nutrient levels (Score: 1.756823)

Control

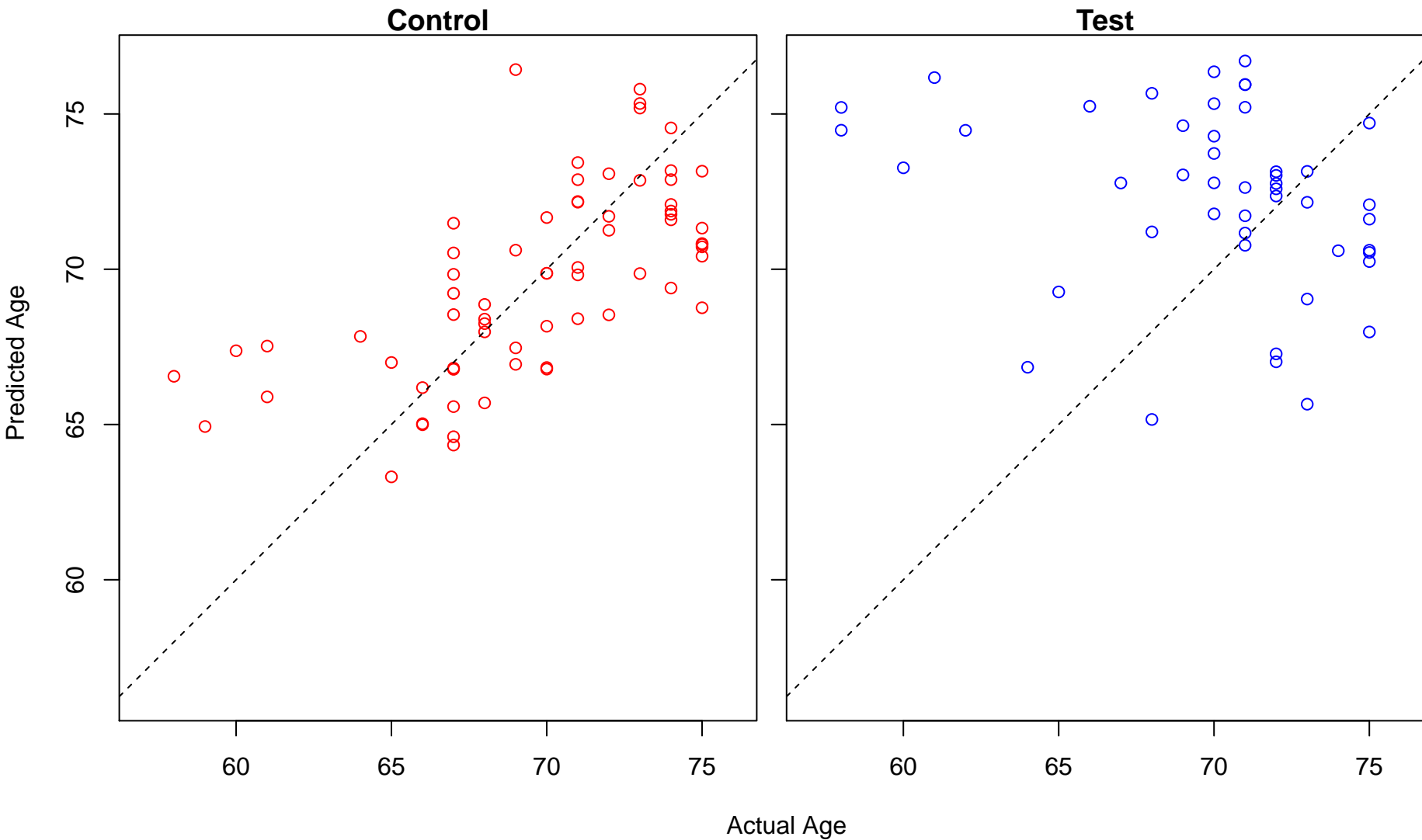


Test

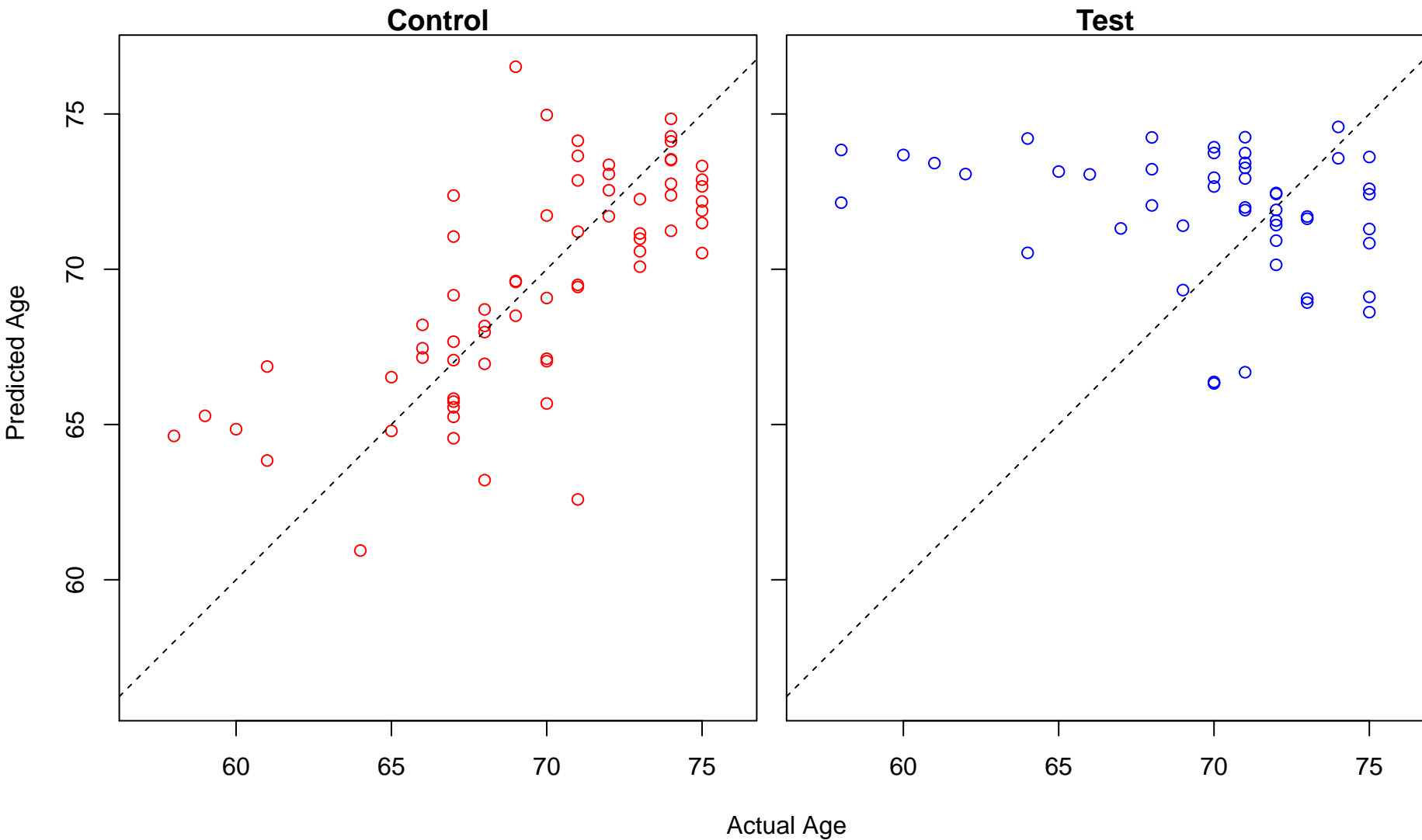


Actual Age

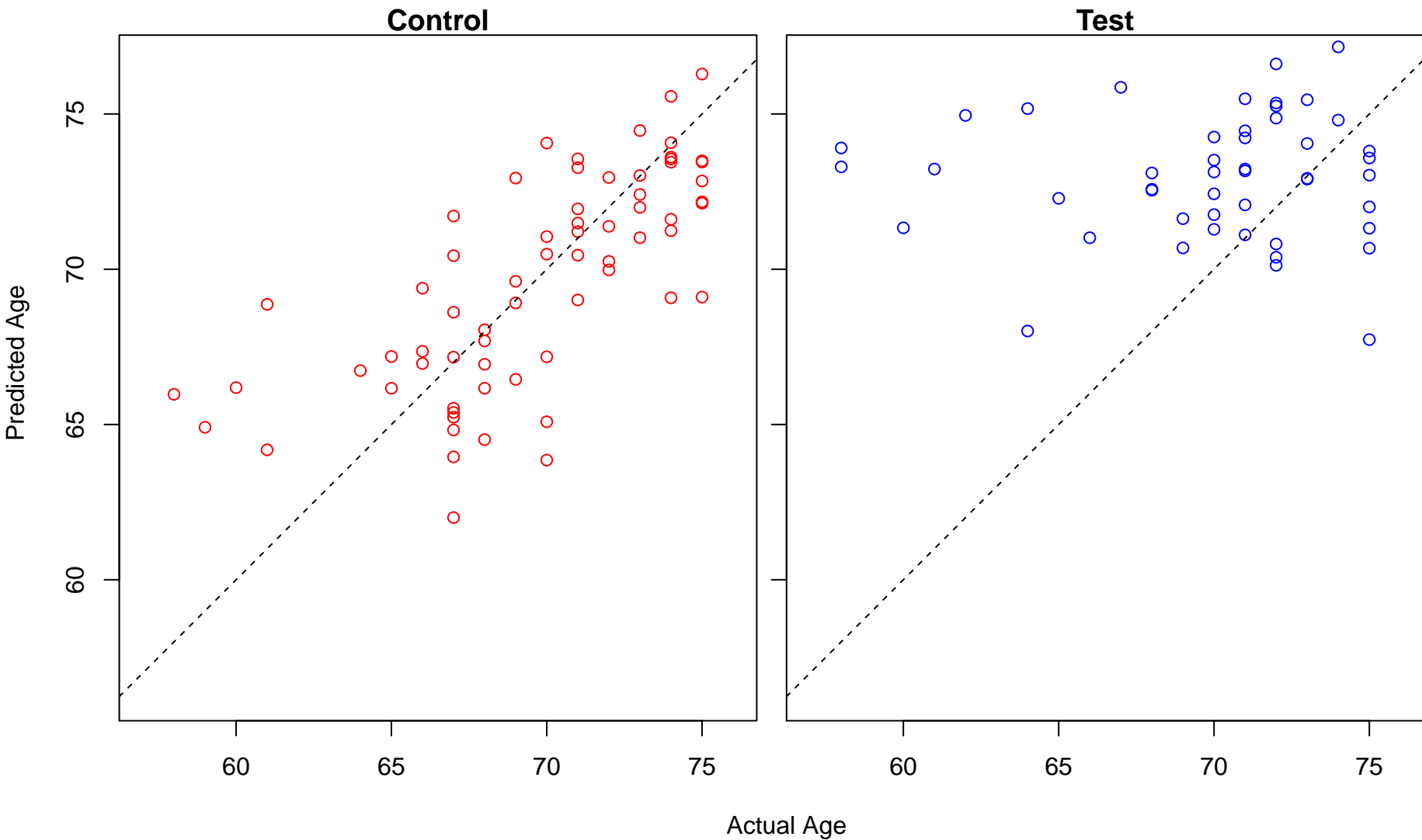
regulation of CD4-positive, alpha-beta T cell differentiation (Score: 1.755360)



regulation of nuclease activity (Score: 1.755012)

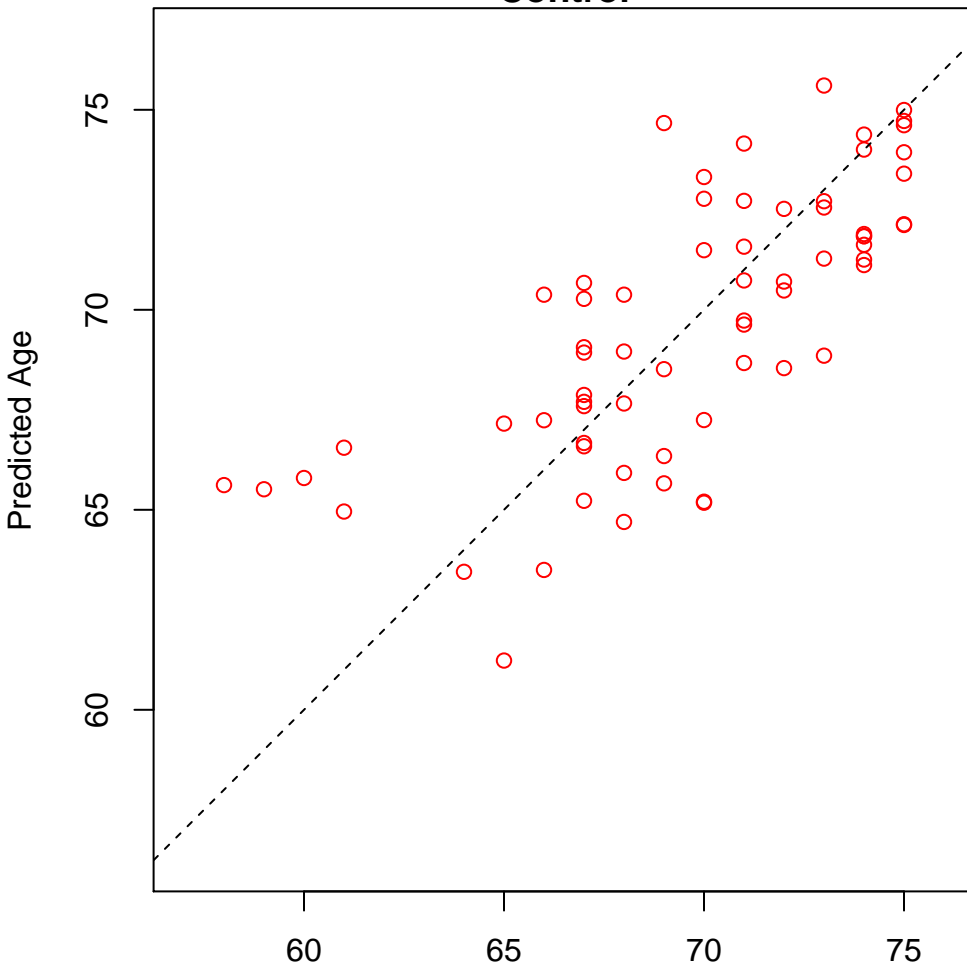


DNA geometric change (Score: 1.754955)

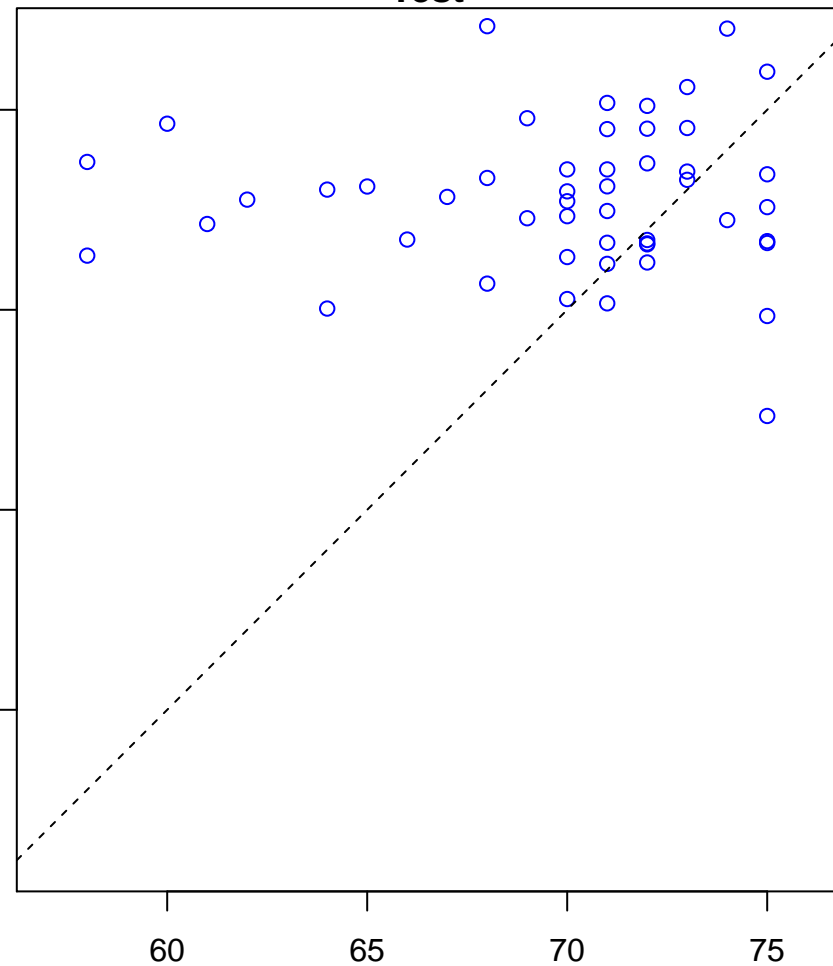


negative regulation of cell differentiation (Score: 1.754588)

Control

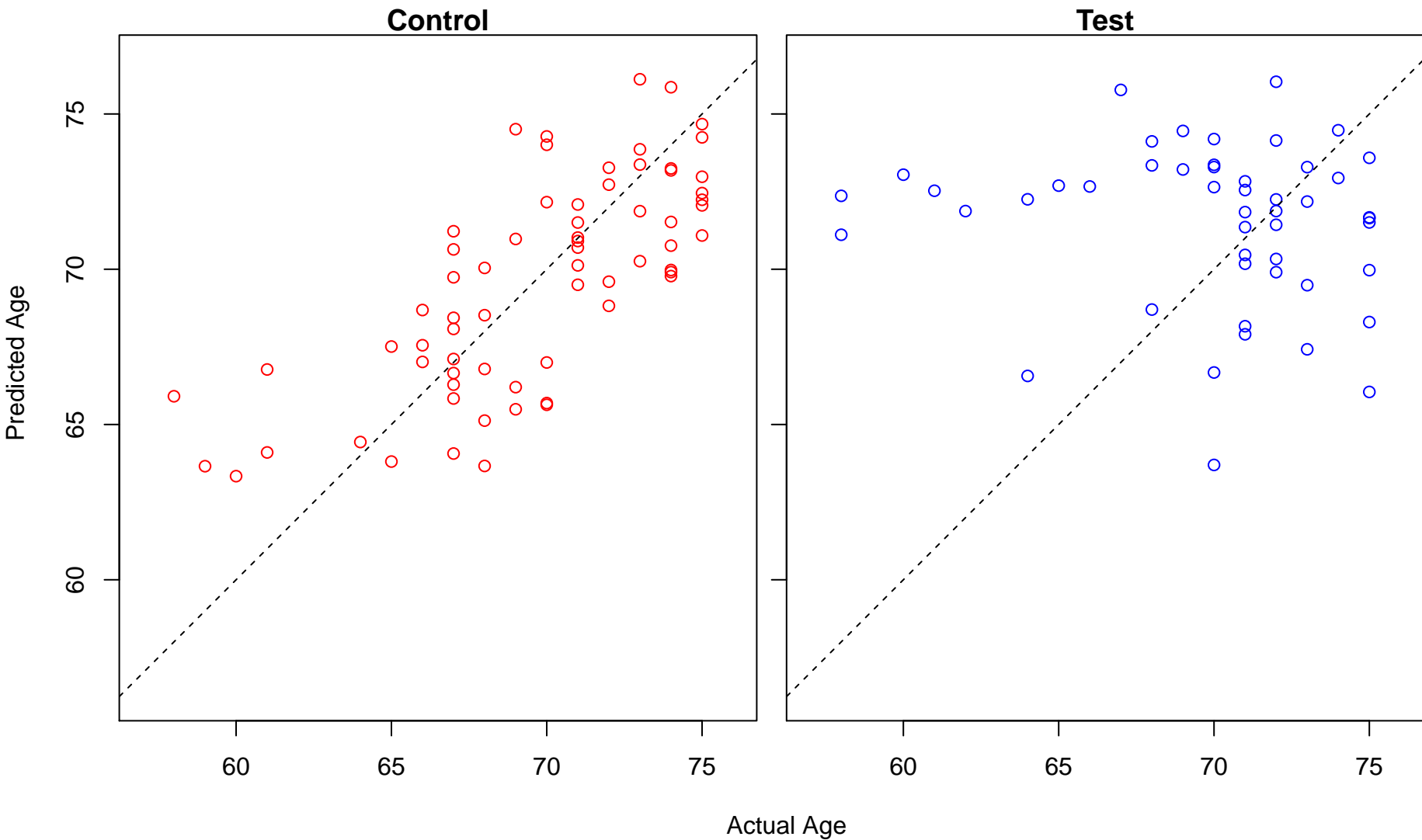


Test

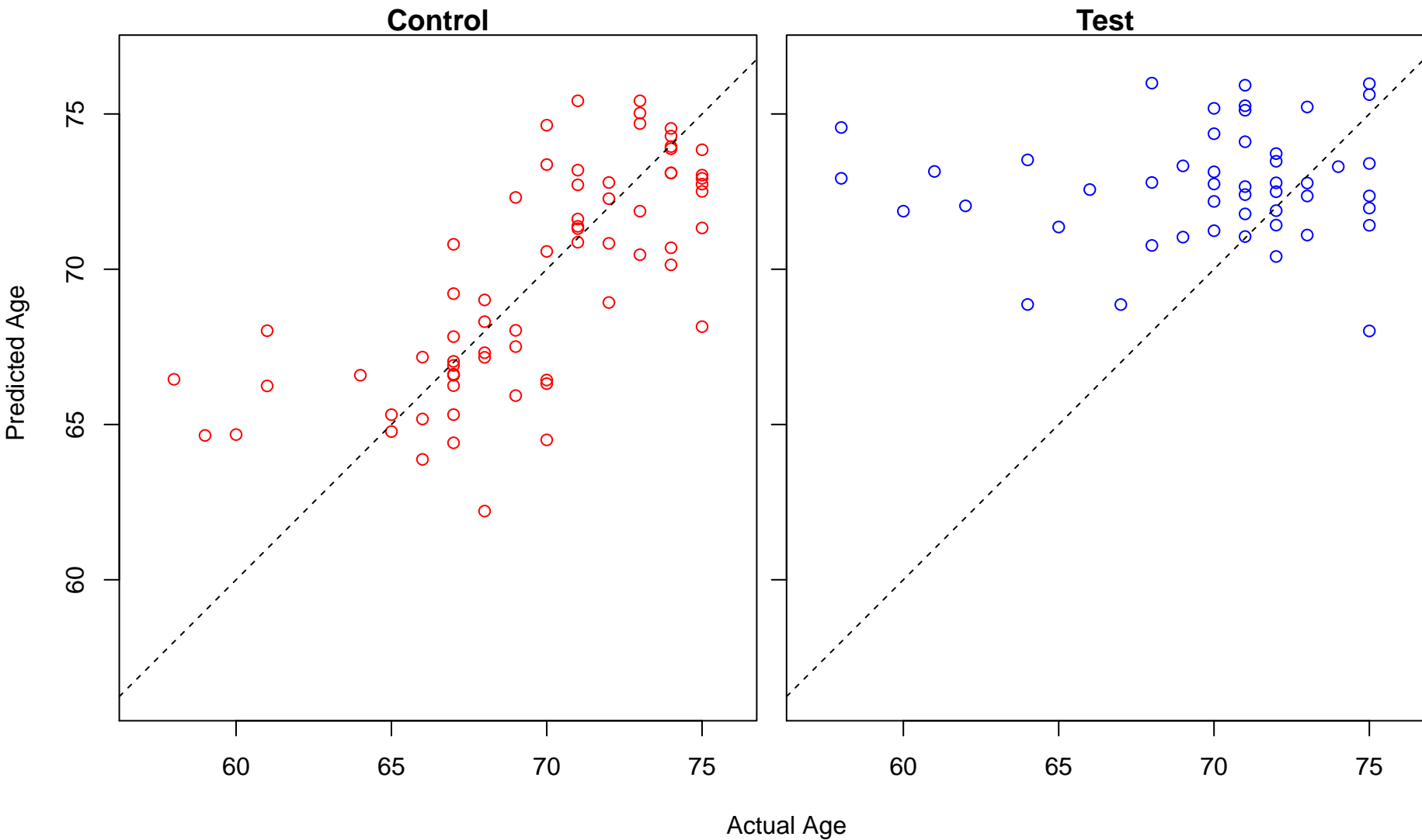


Actual Age

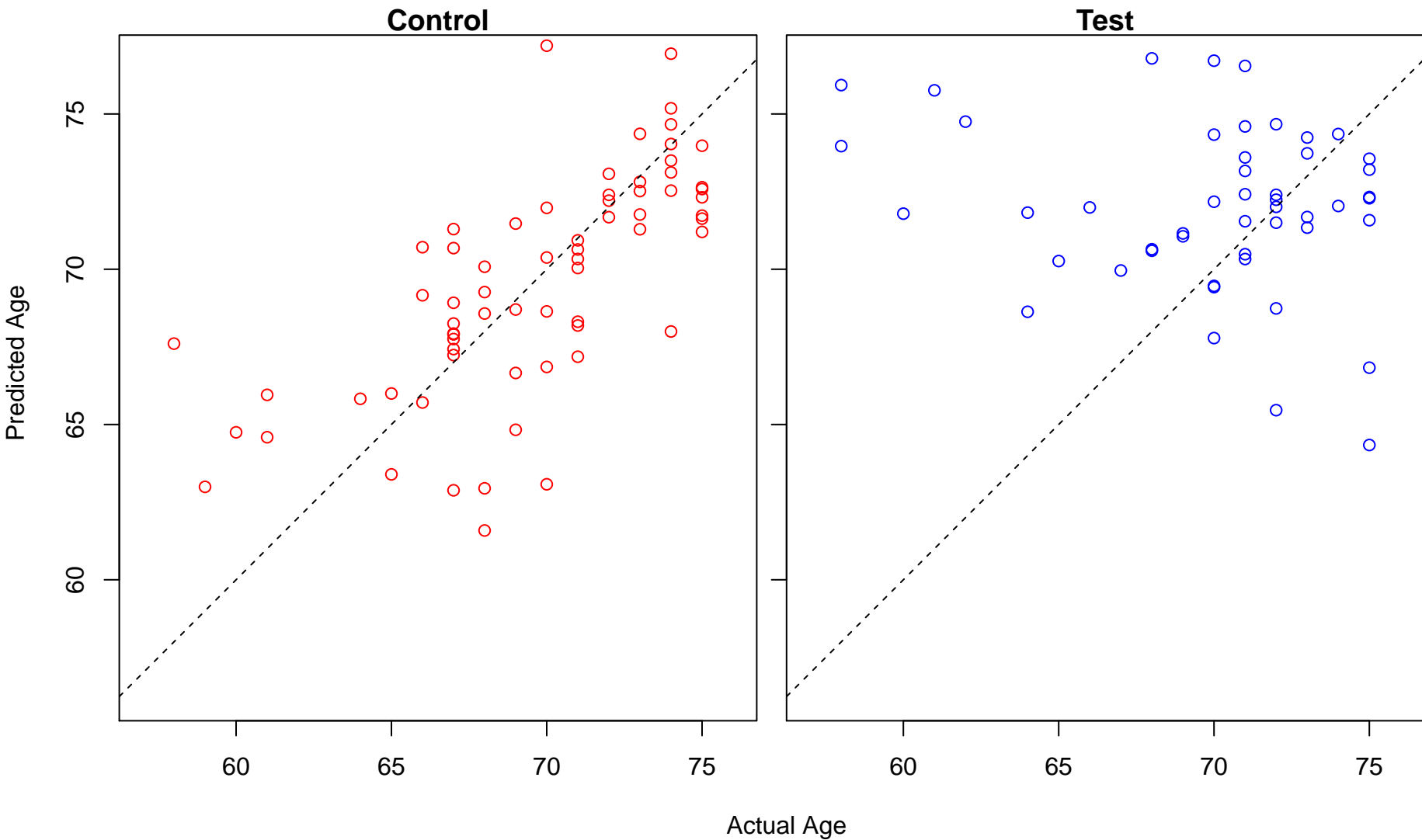
regulation of lipid biosynthetic process (Score: 1.754331)



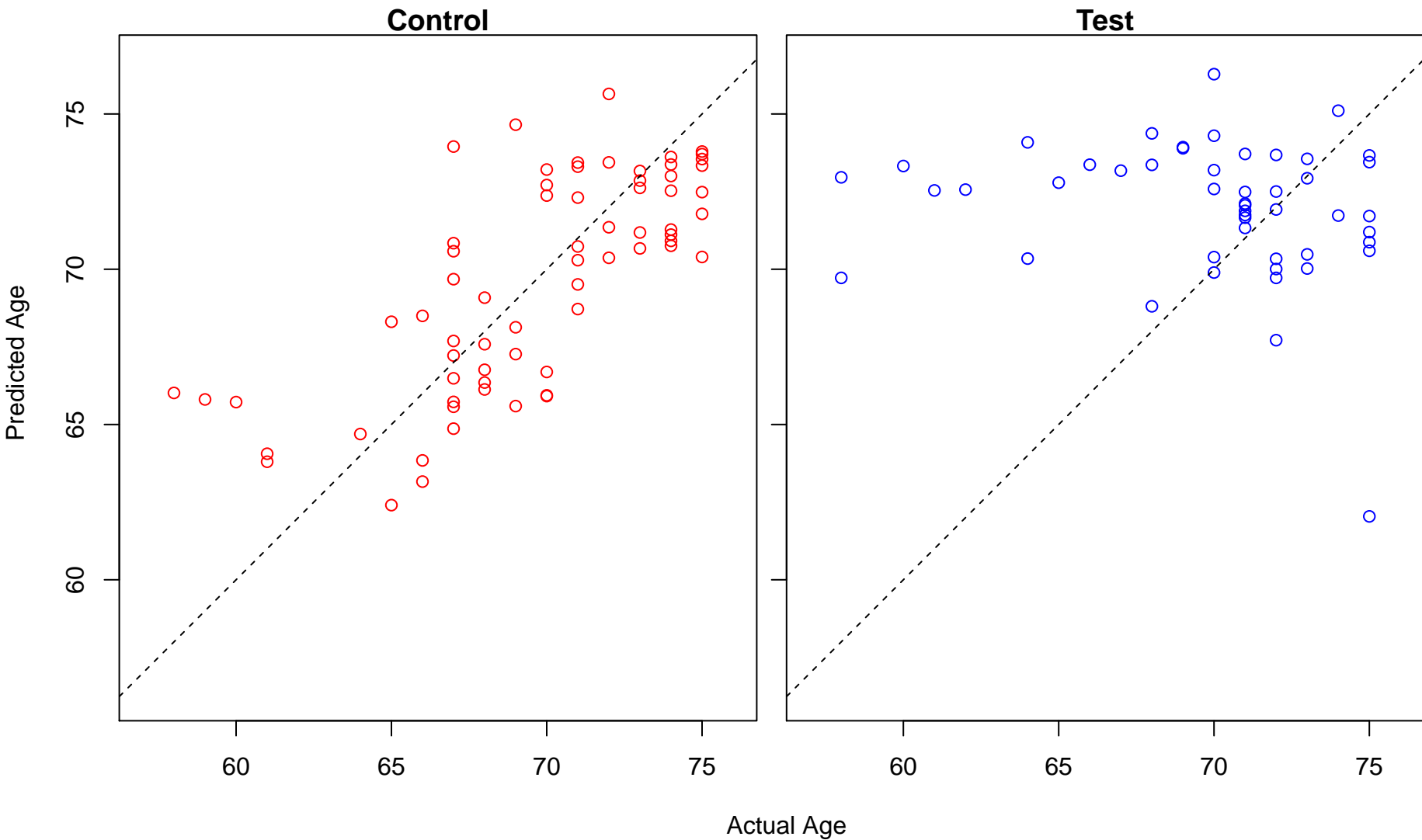
substantia nigra development (Score: 1.754189)



phosphatidylcholine biosynthetic process (Score: 1.754153)

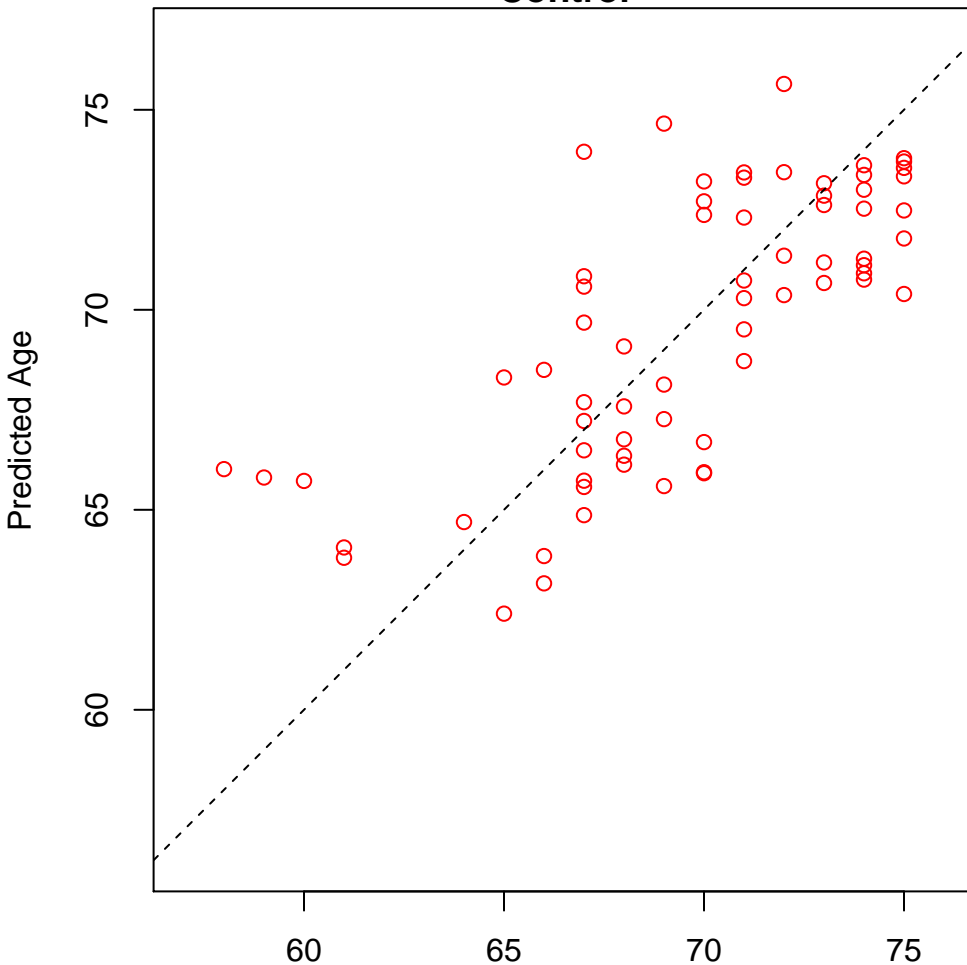


protein mannosylation (Score: 1.754113)

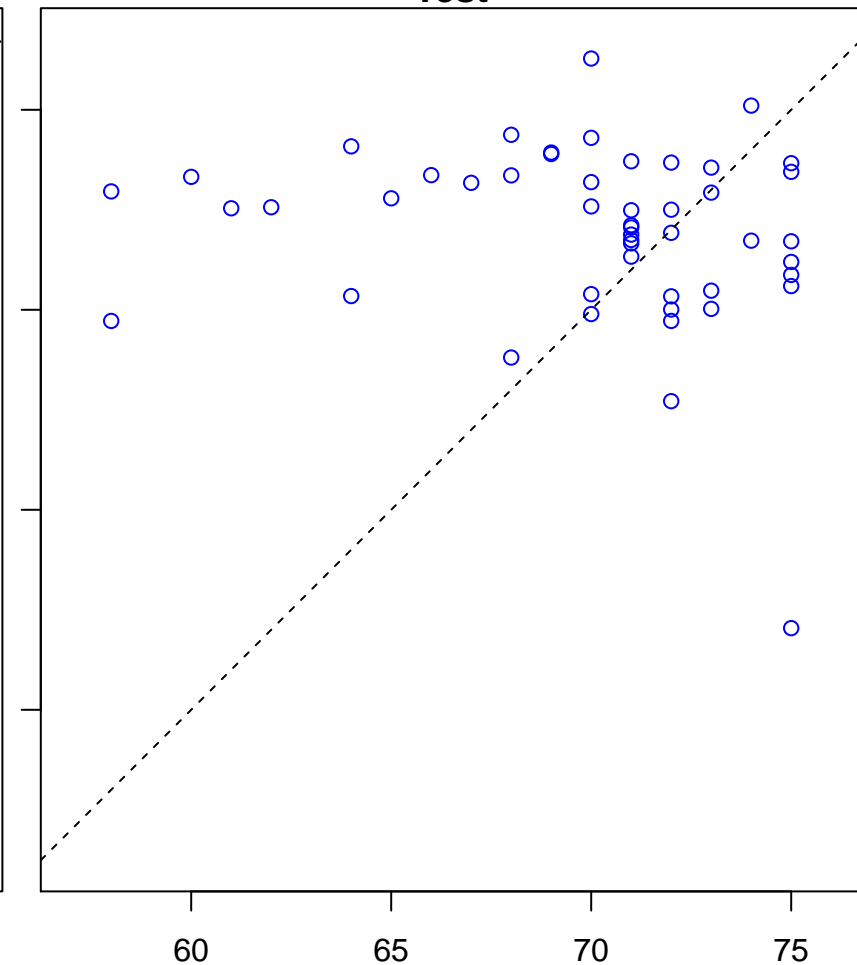


protein O-linked mannosylation (Score: 1.754113)

Control

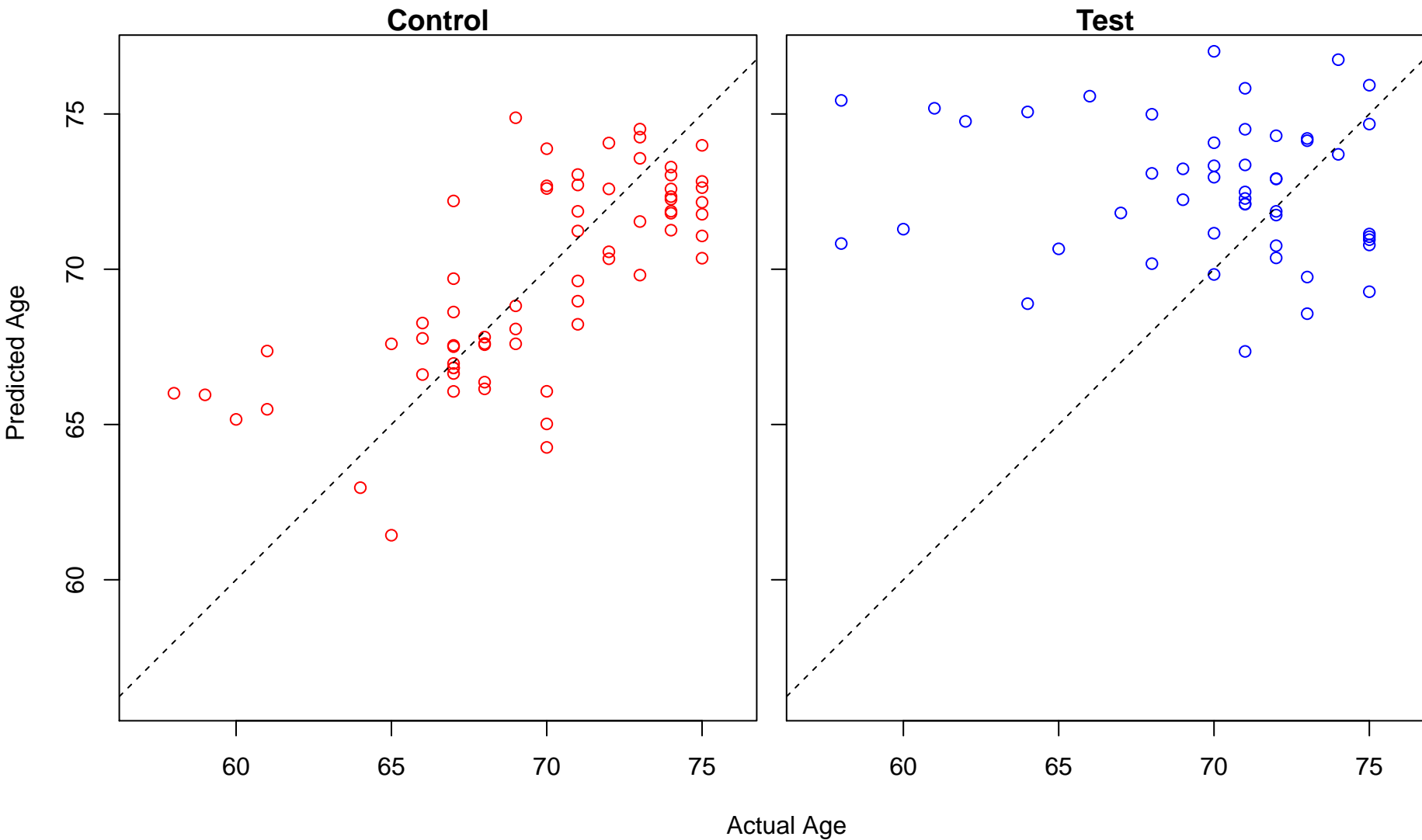


Test

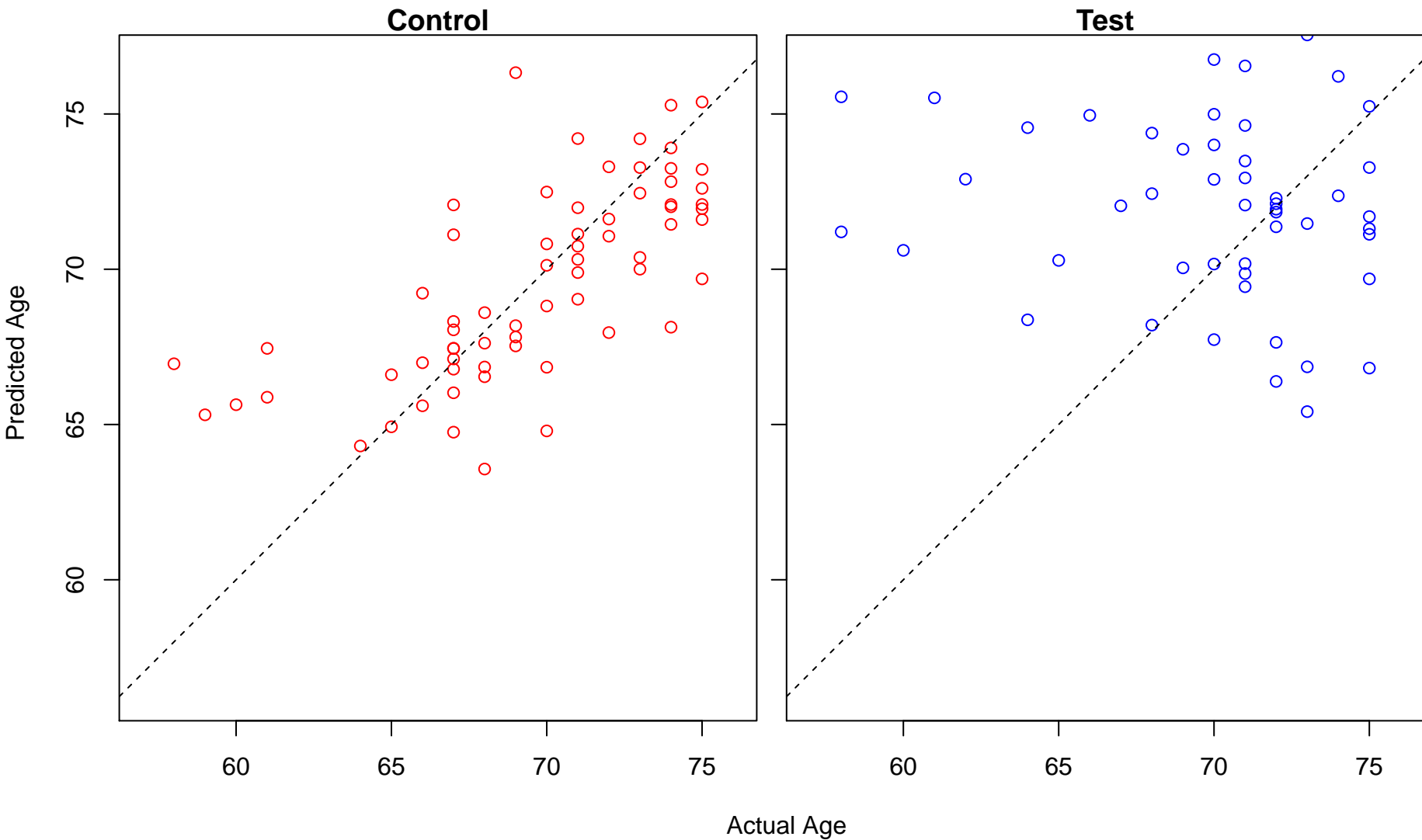


Actual Age

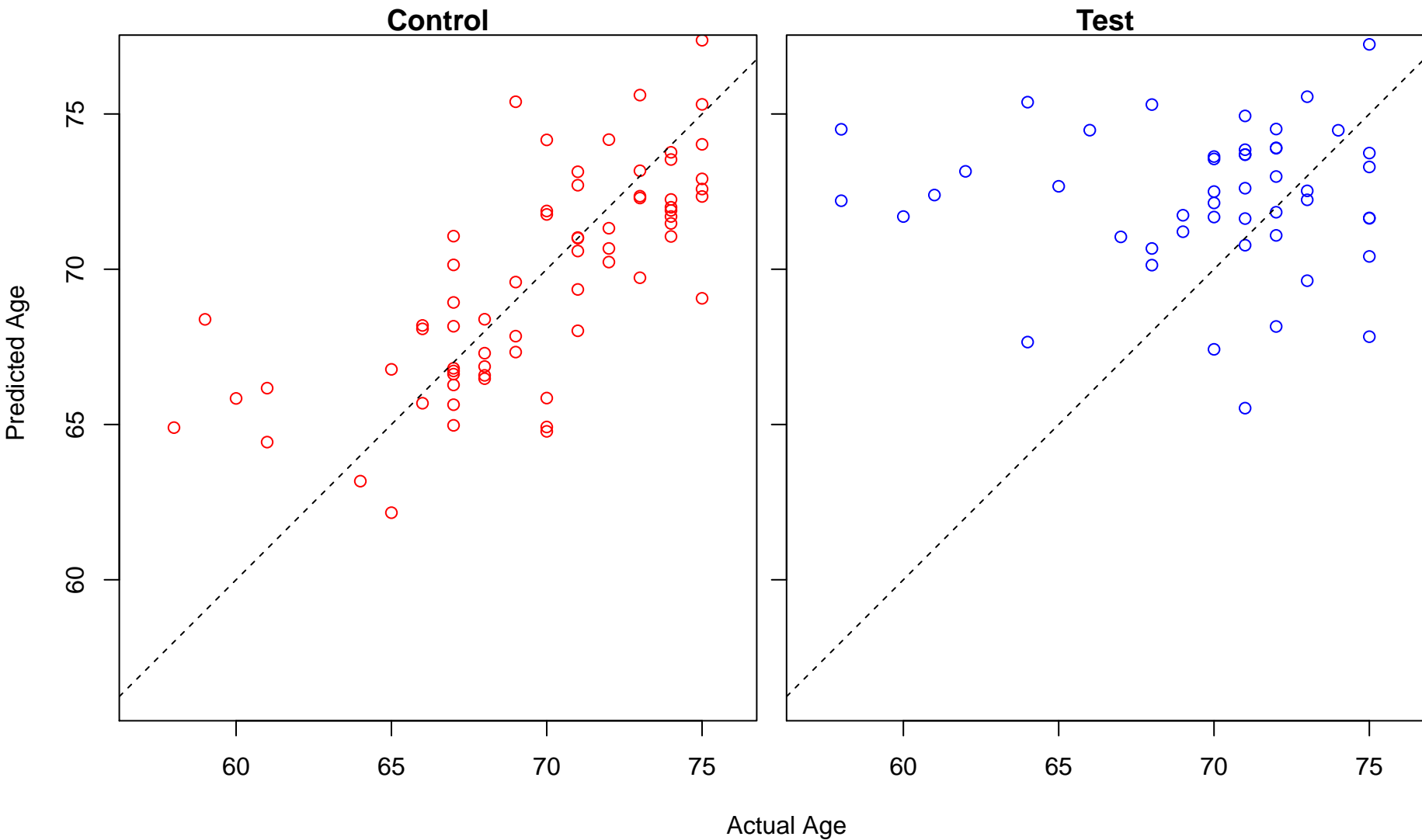
translesion synthesis (Score: 1.753824)



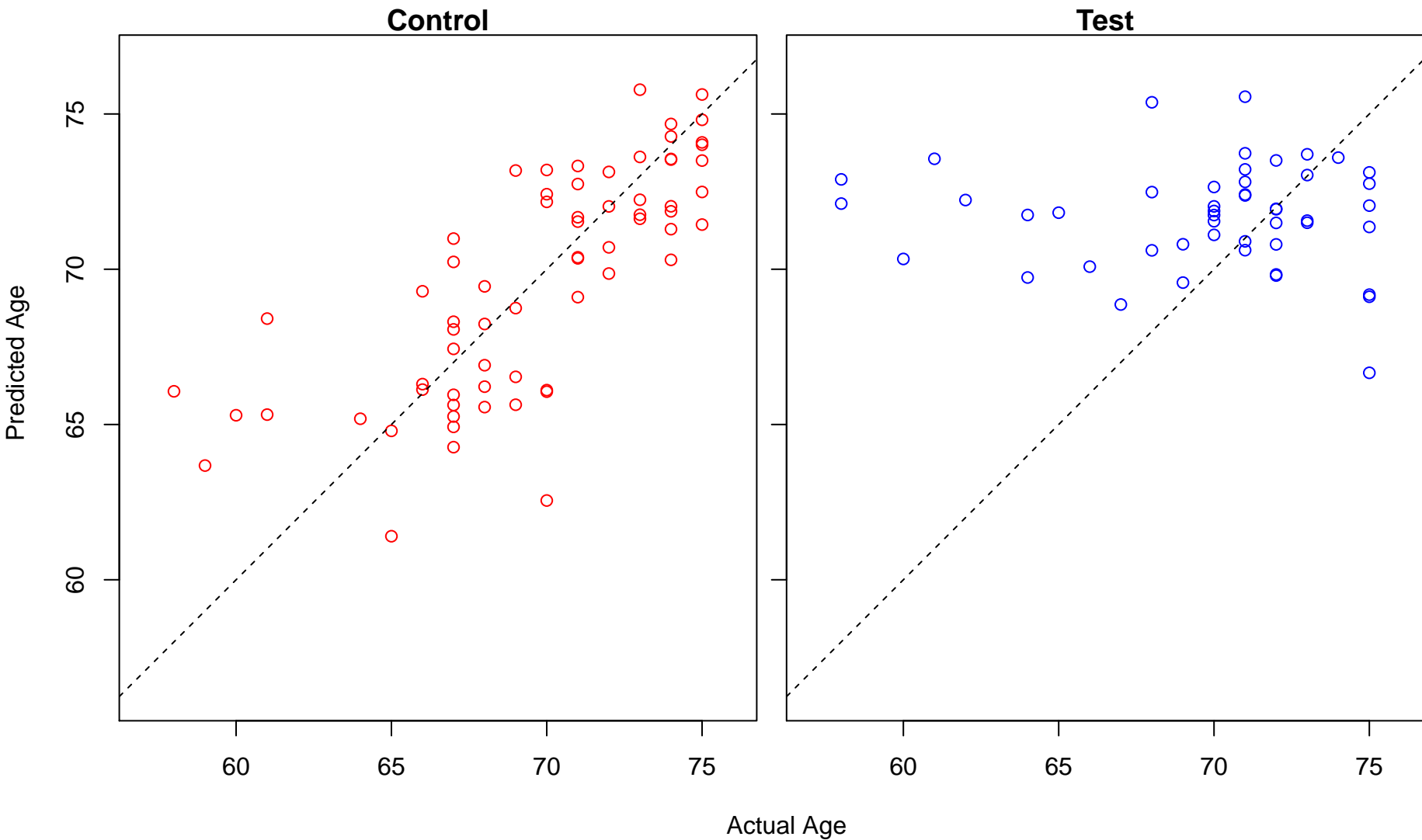
negative regulation of defense response to virus (Score: 1.753508)



toll-like receptor 3 signaling pathway (Score: 1.753445)

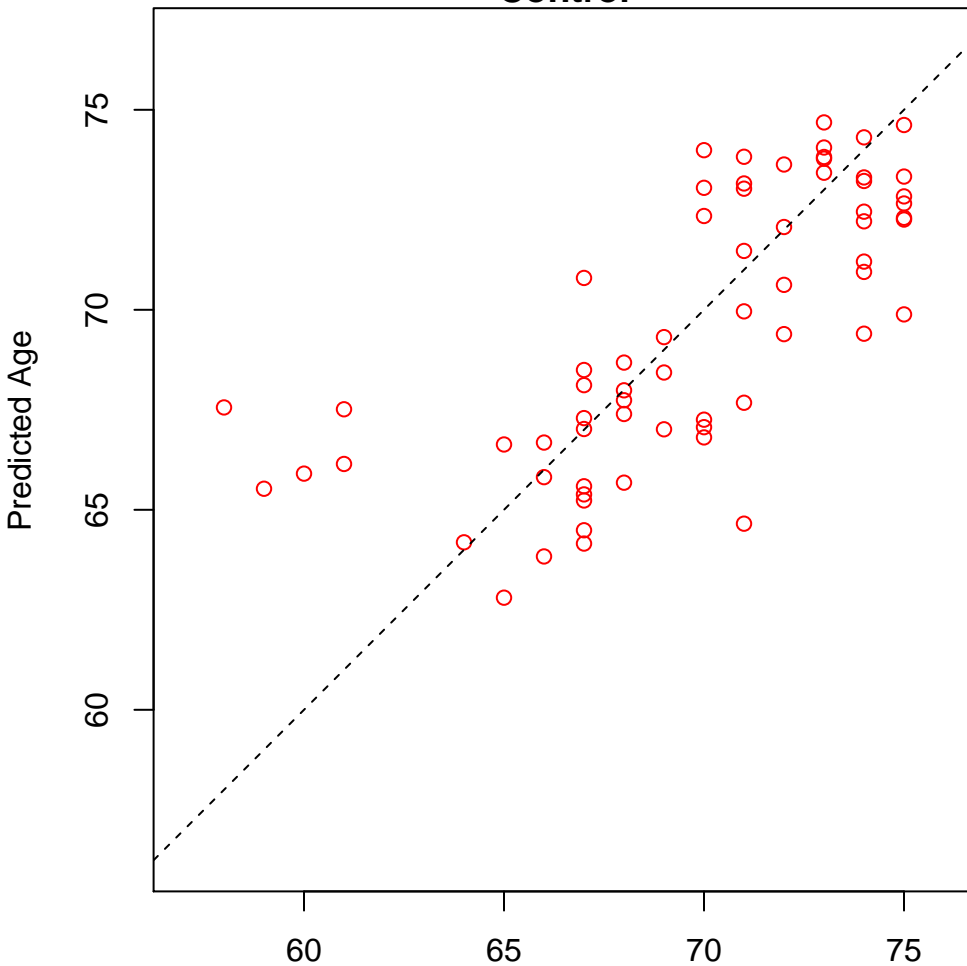


regulation of cell cycle G1/S phase transition (Score: 1.752381)

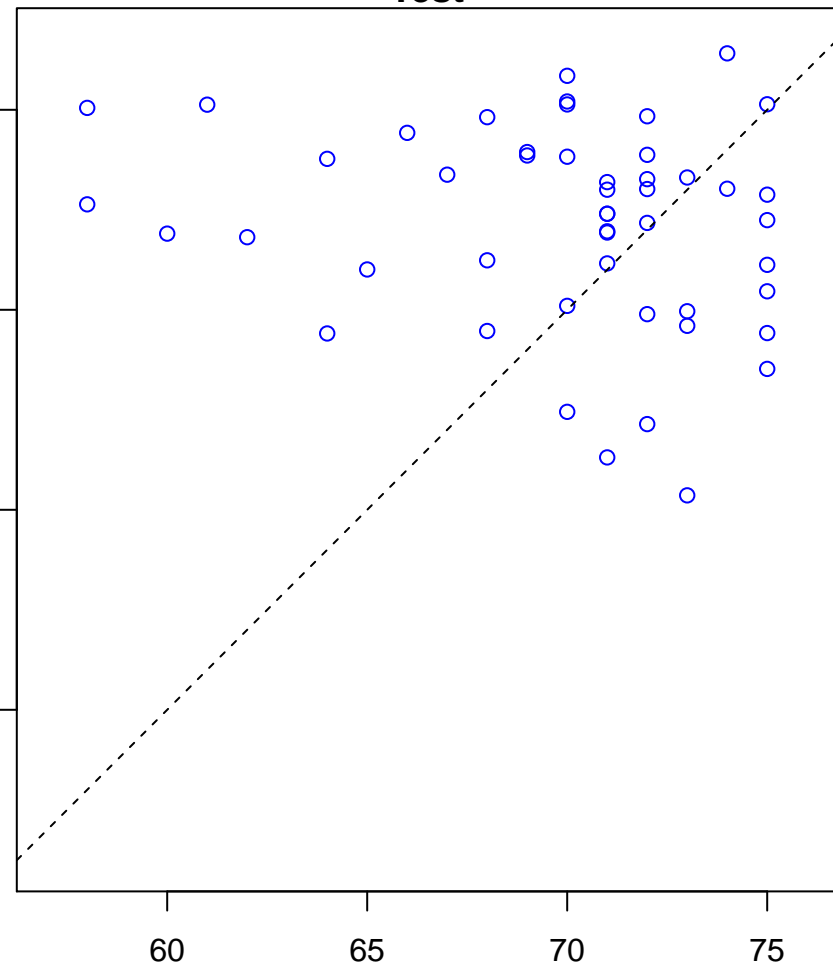


regulation of adaptive immune response (Score: 1.752083)

Control



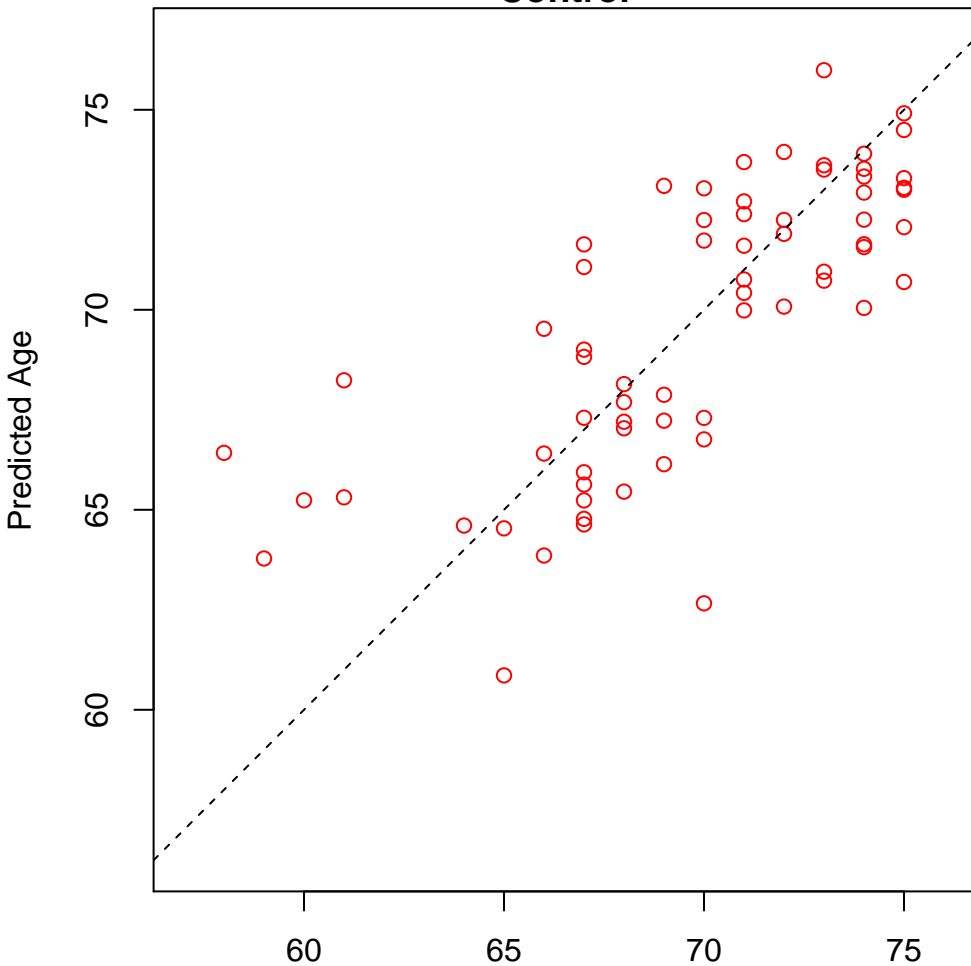
Test



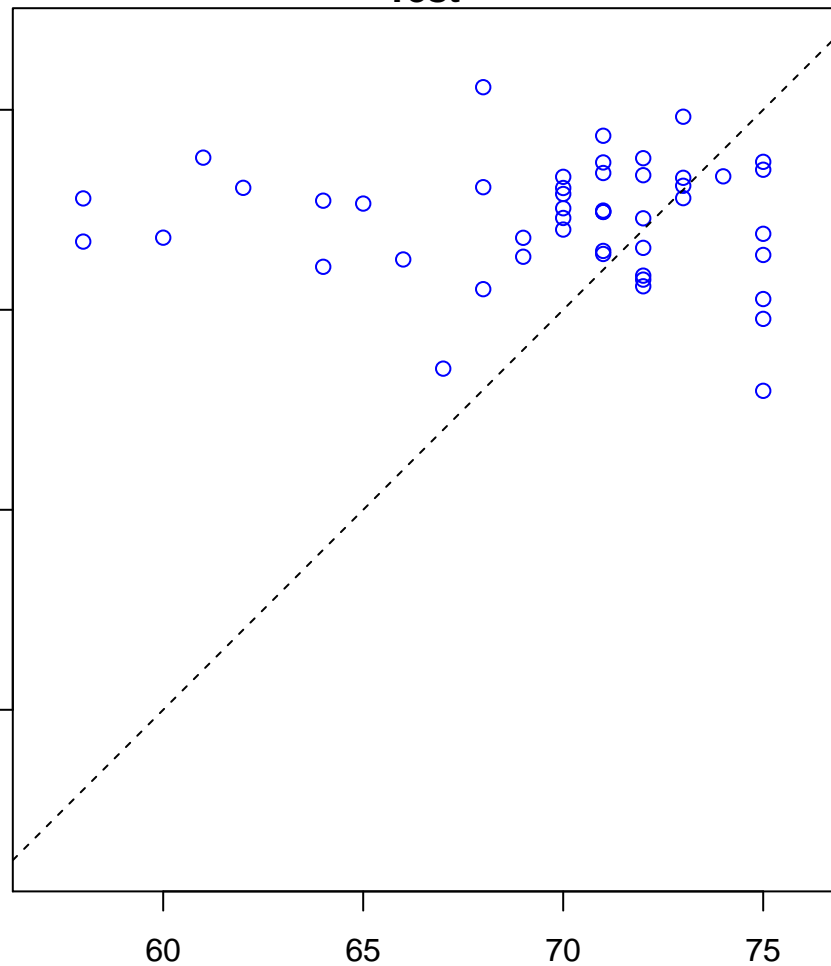
Actual Age

negative regulation of cell cycle process (Score: 1.748861)

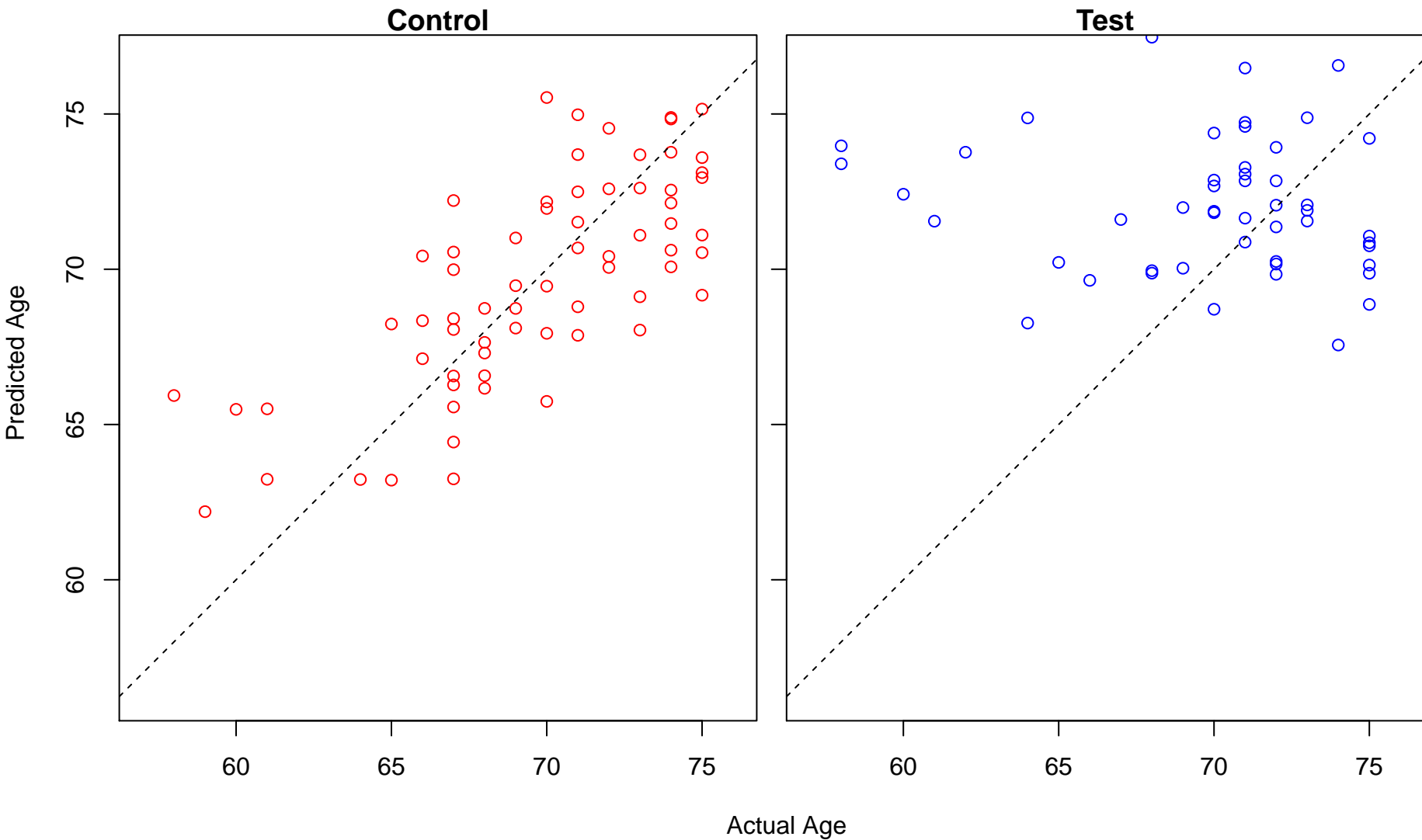
Control



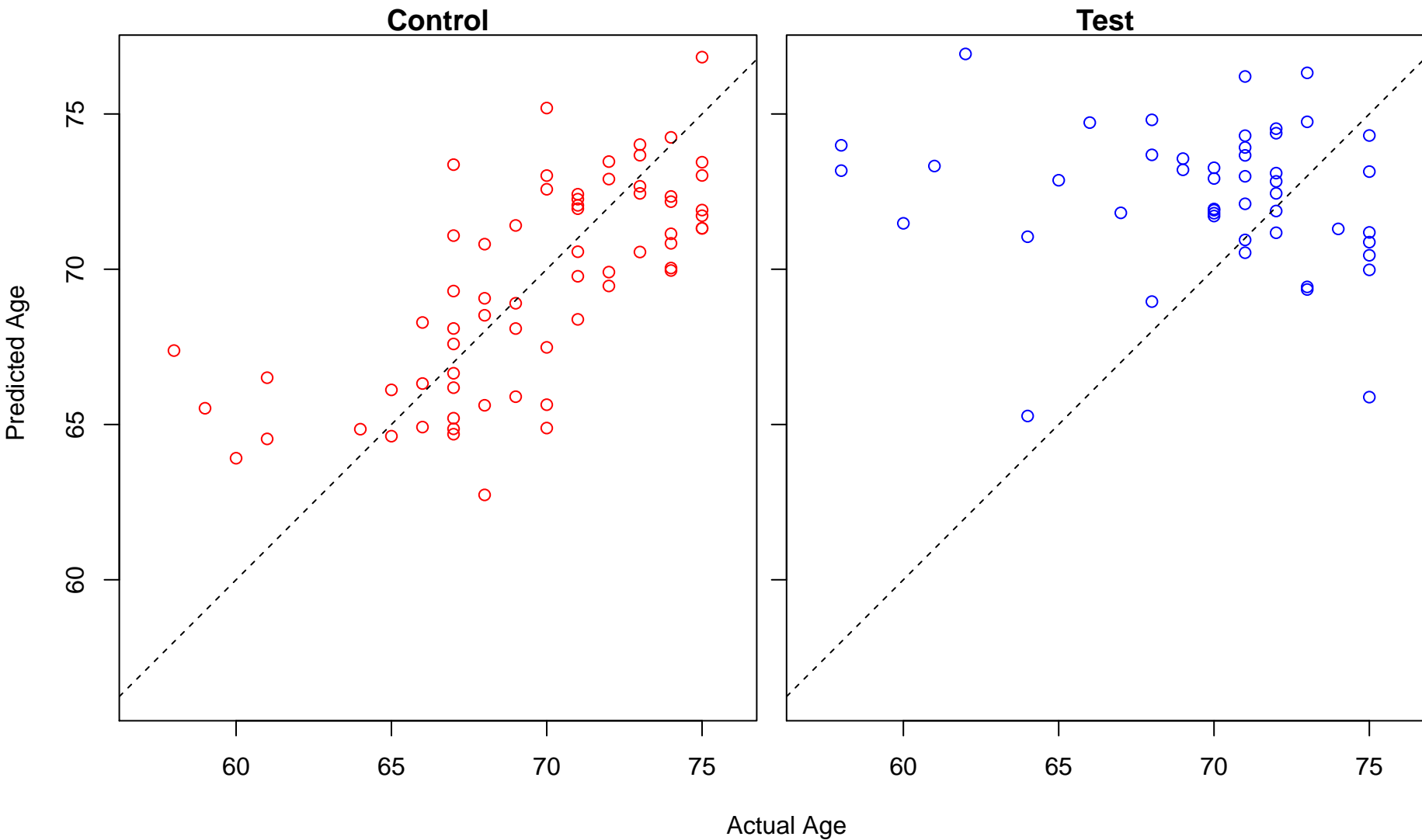
Test



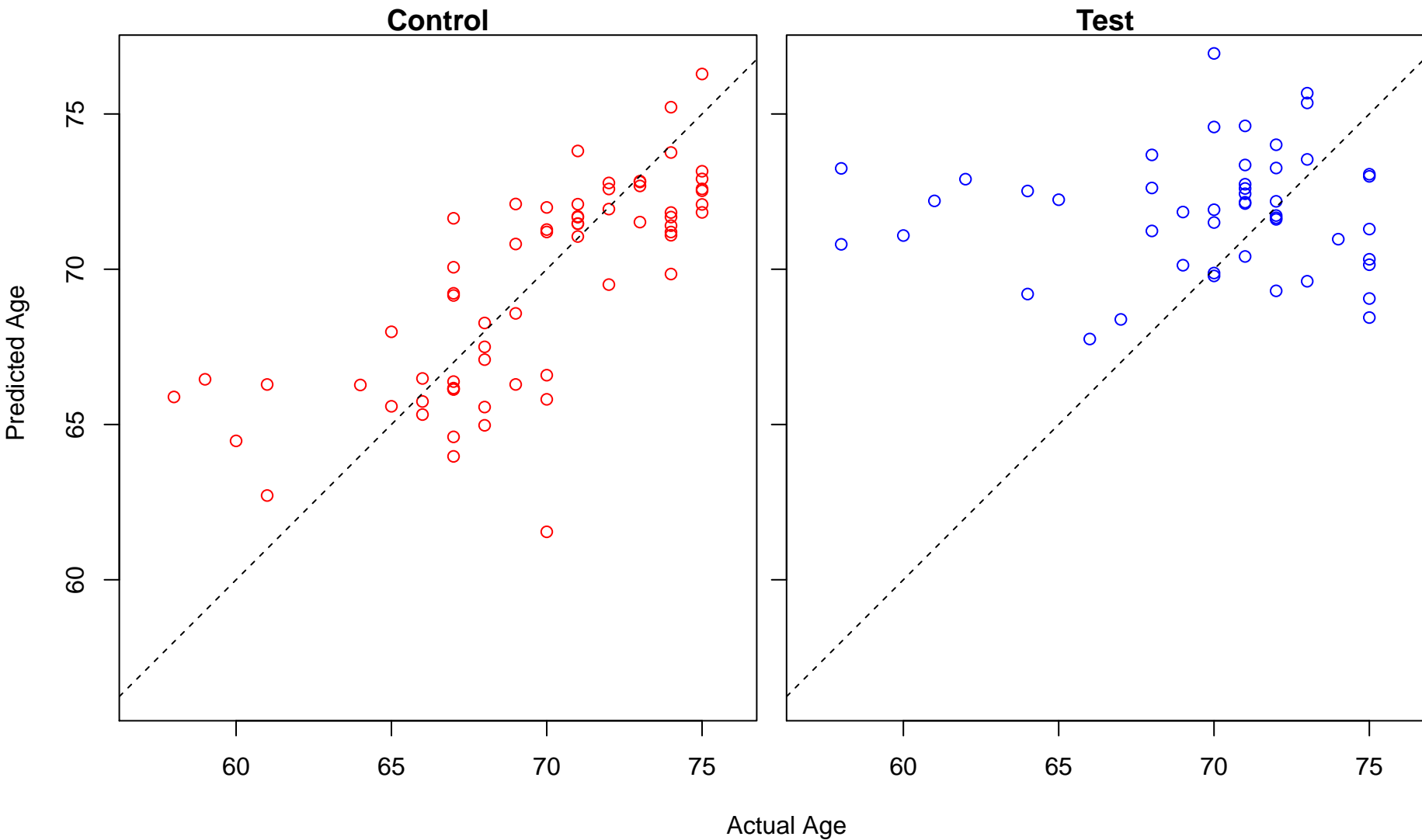
negative regulation of RNA splicing (Score: 1.747527)



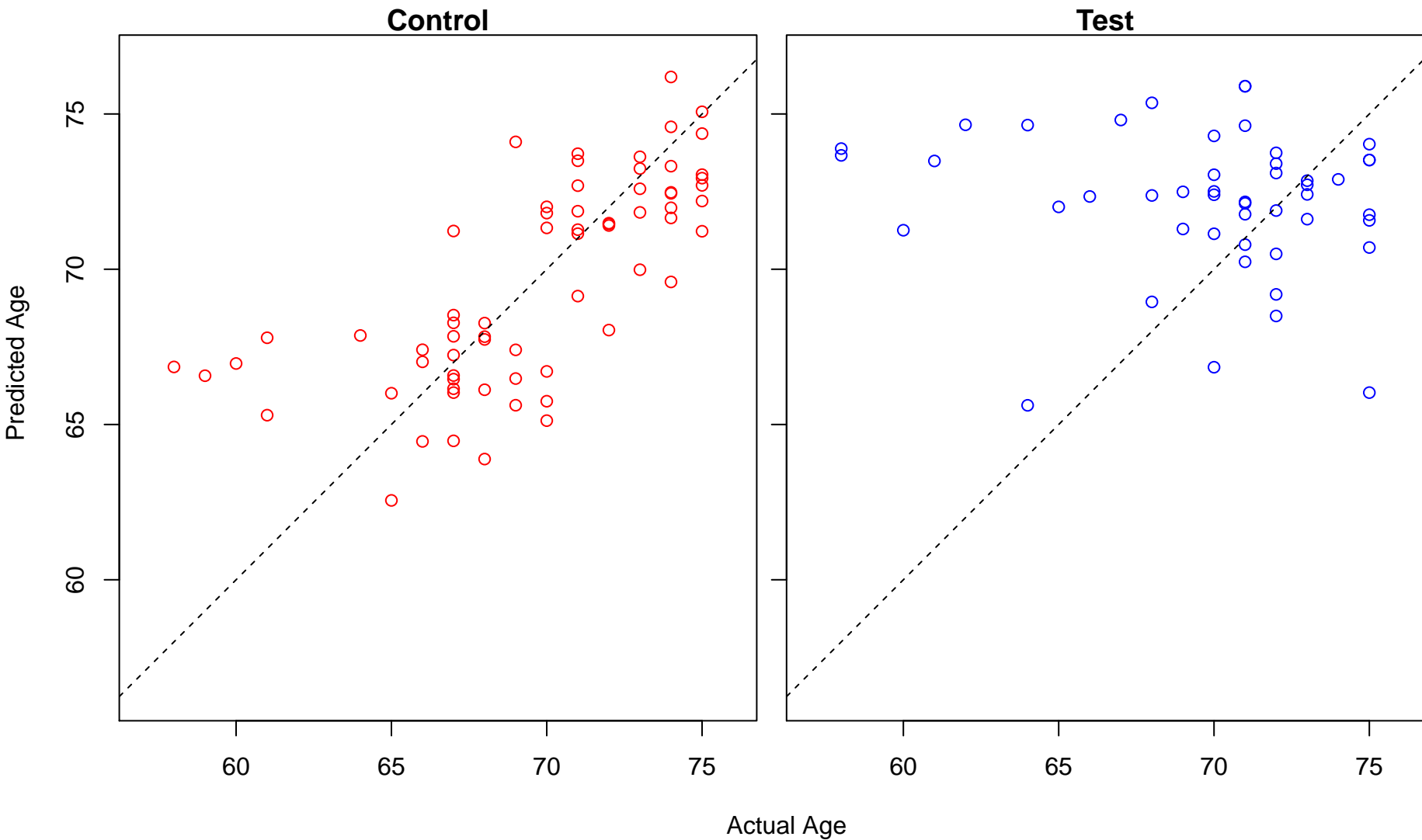
organic hydroxy compound biosynthetic process (Score: 1.746344)



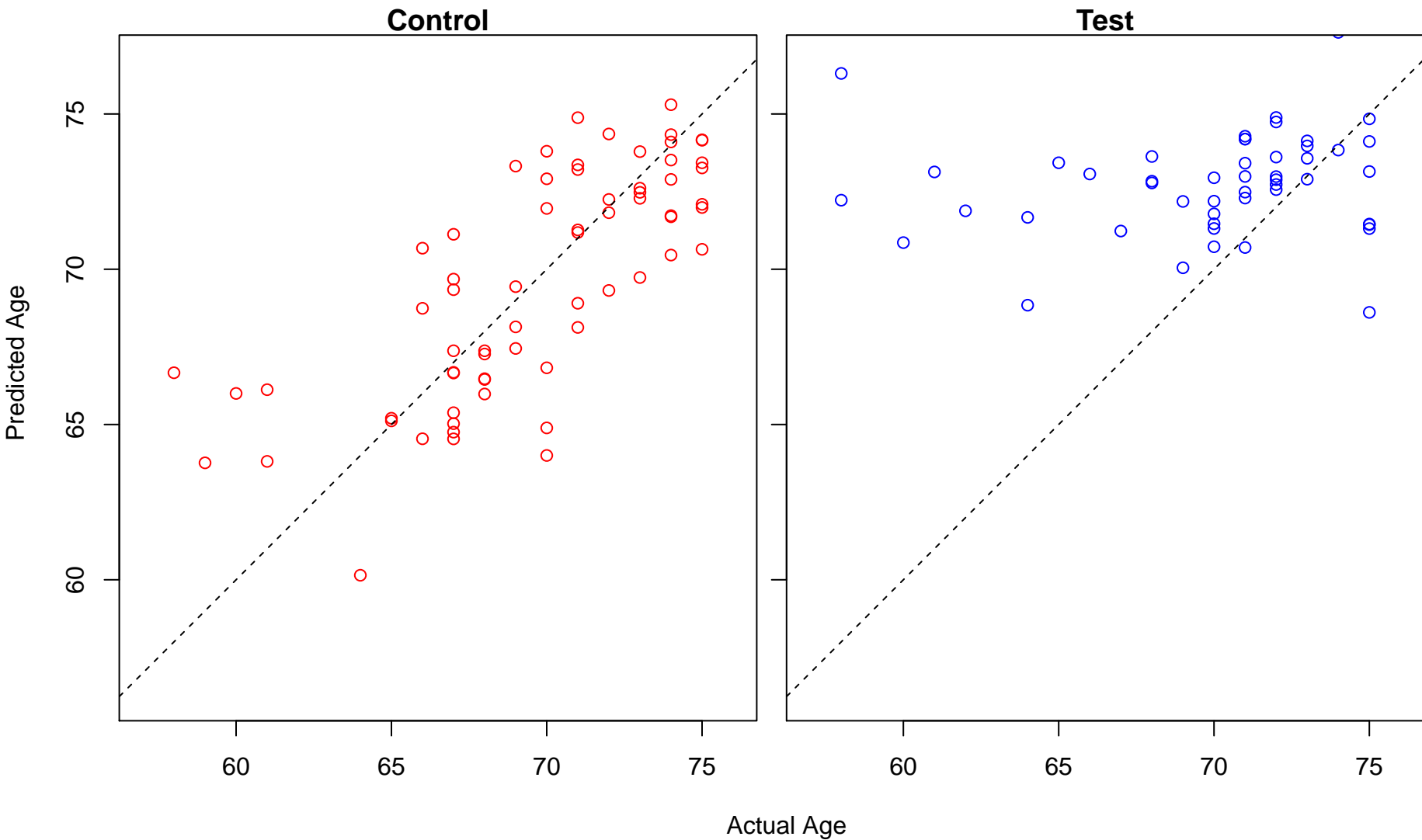
nucleoside monophosphate metabolic process (Score: 1.744467)



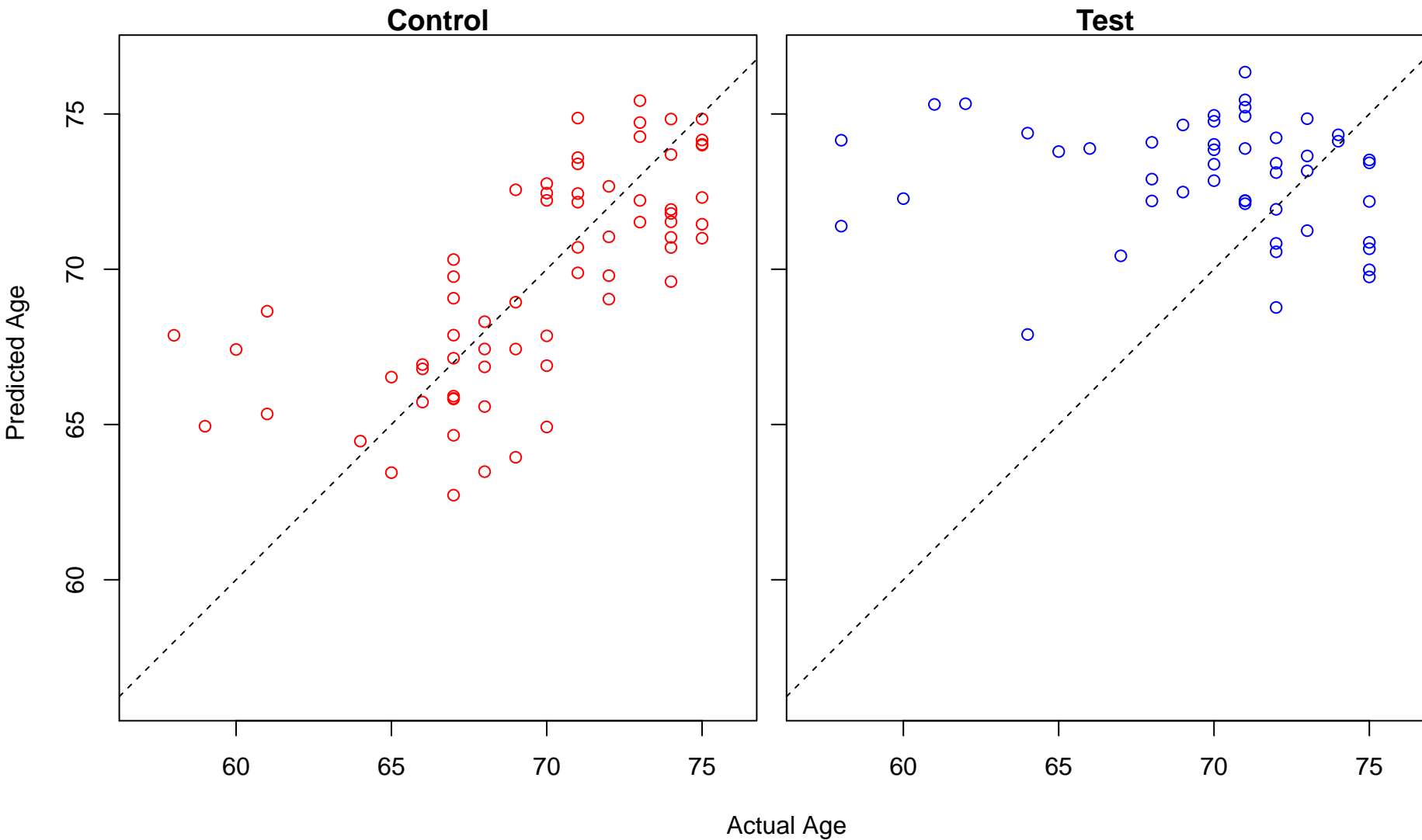
regulation of leukocyte chemotaxis (Score: 1.744463)



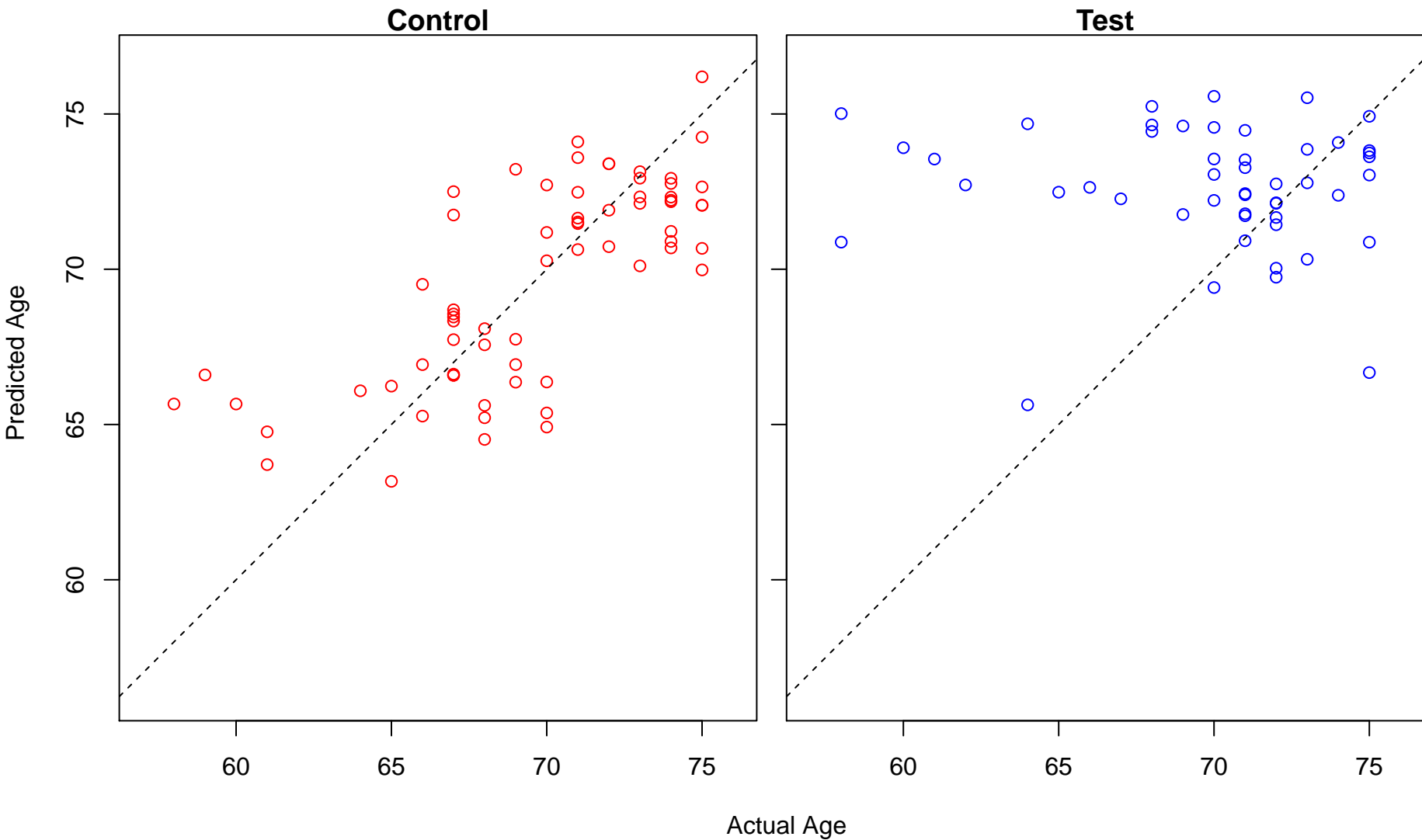
protein maturation (Score: 1.743446)



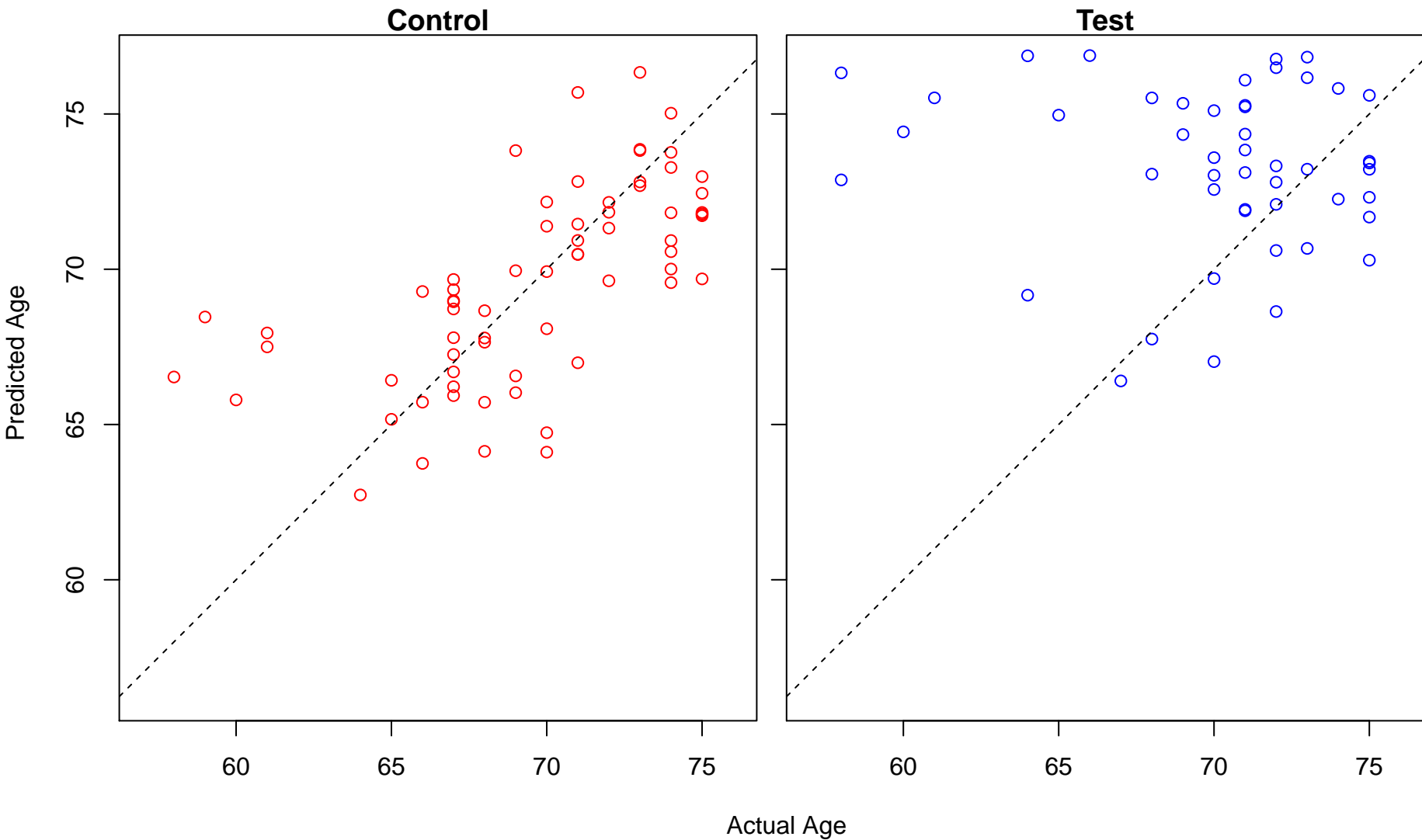
rhythmic process (Score: 1.743430)



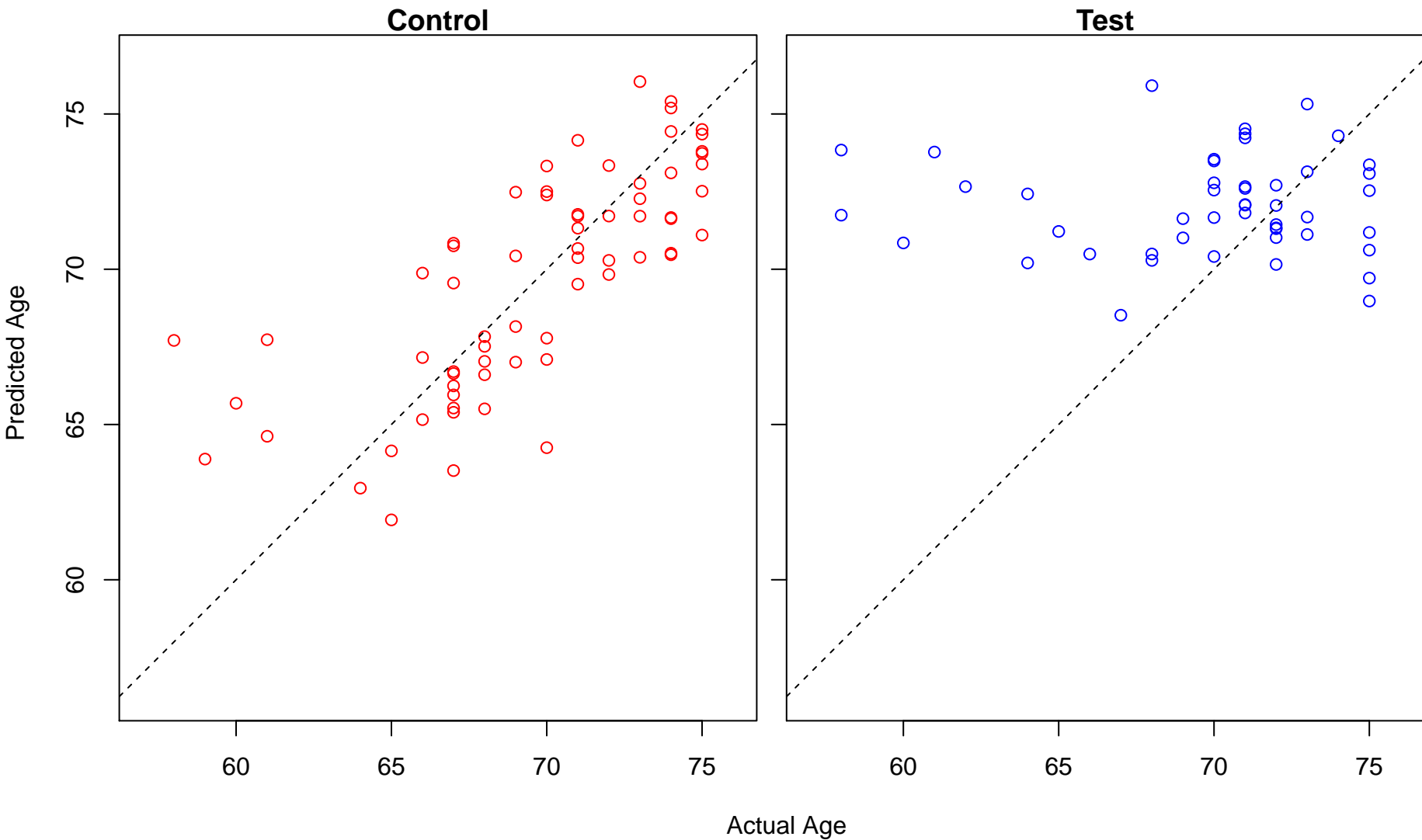
cAMP-mediated signaling (Score: 1.743349)



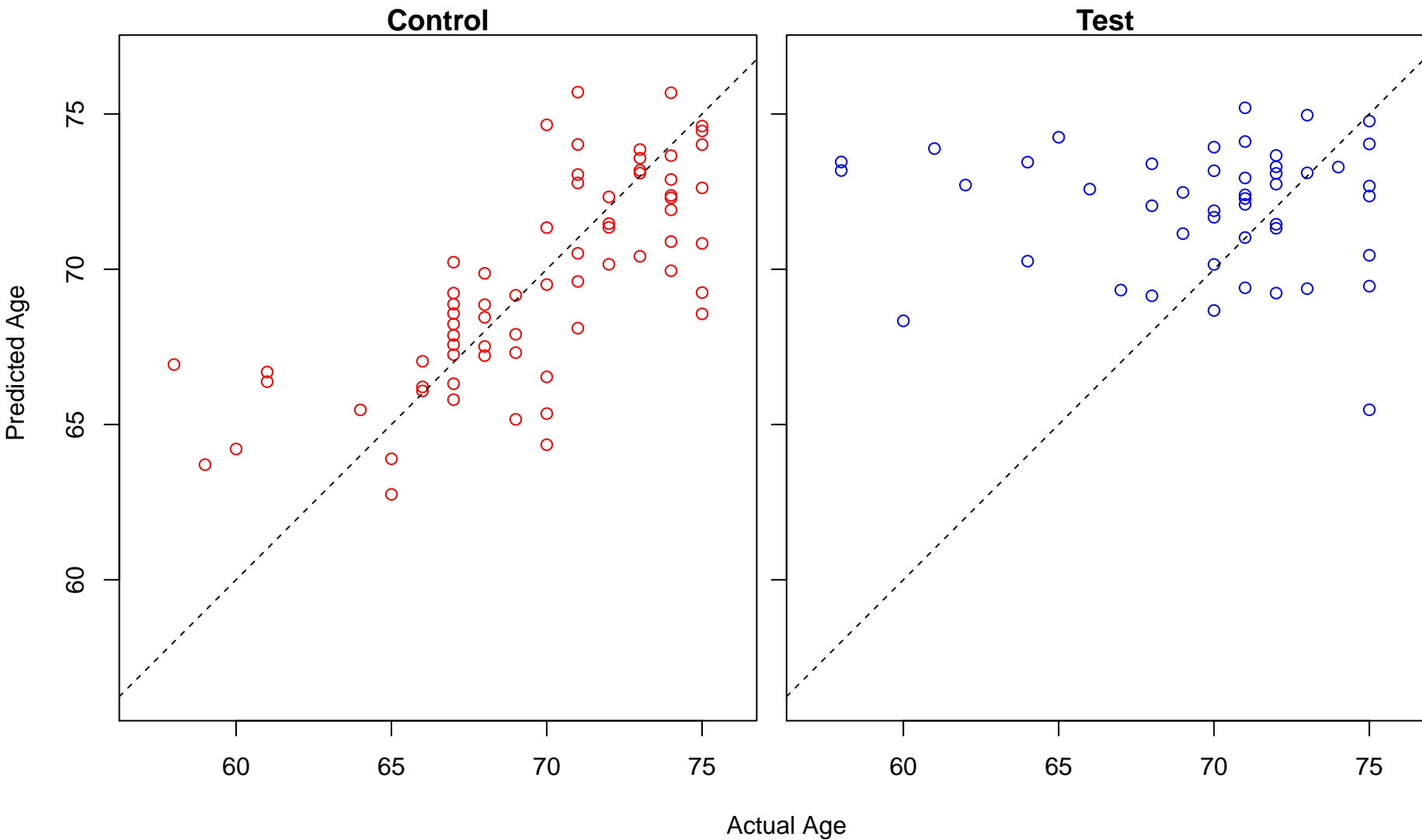
proteasome assembly (Score: 1.743066)



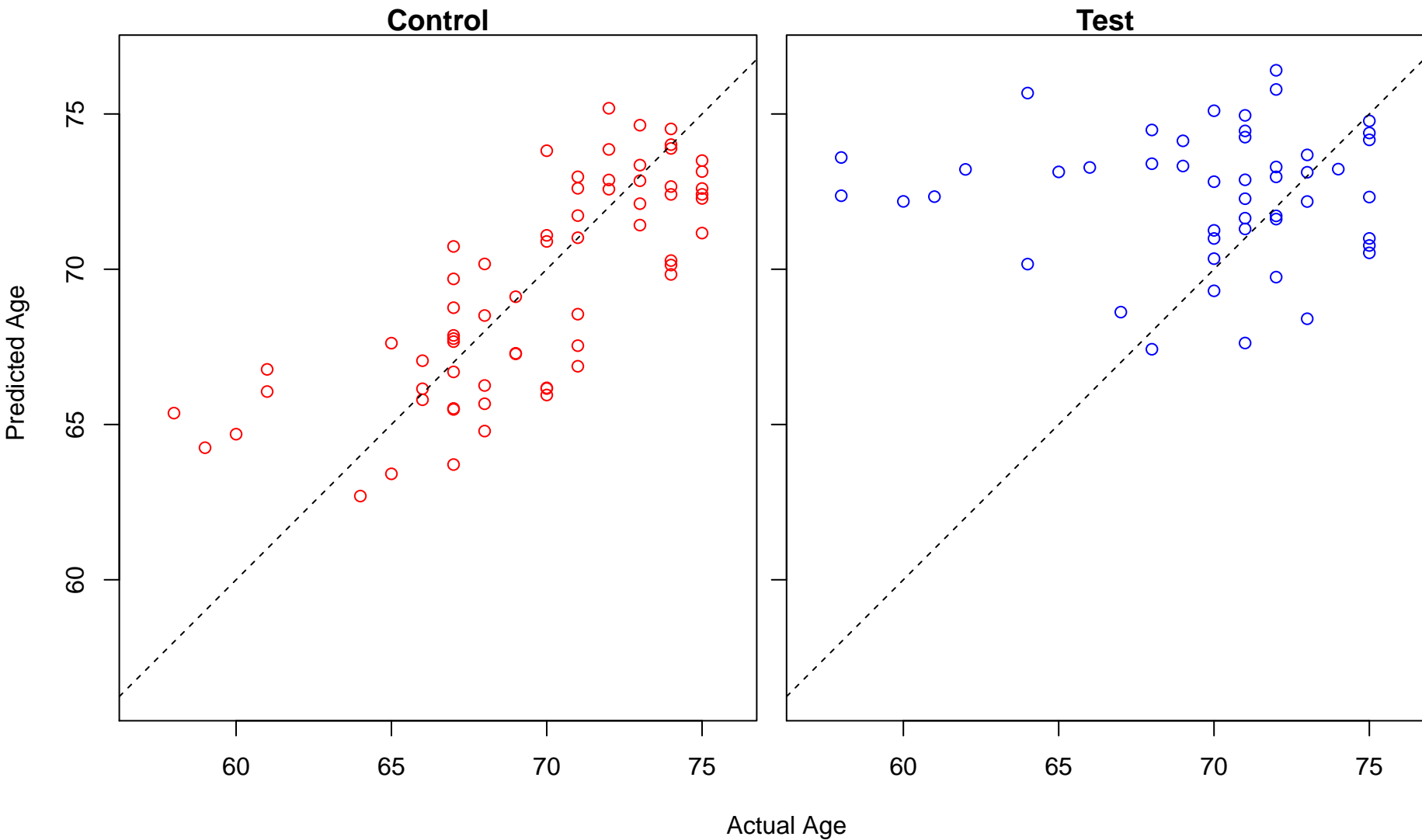
cellular protein catabolic process (Score: 1.742970)



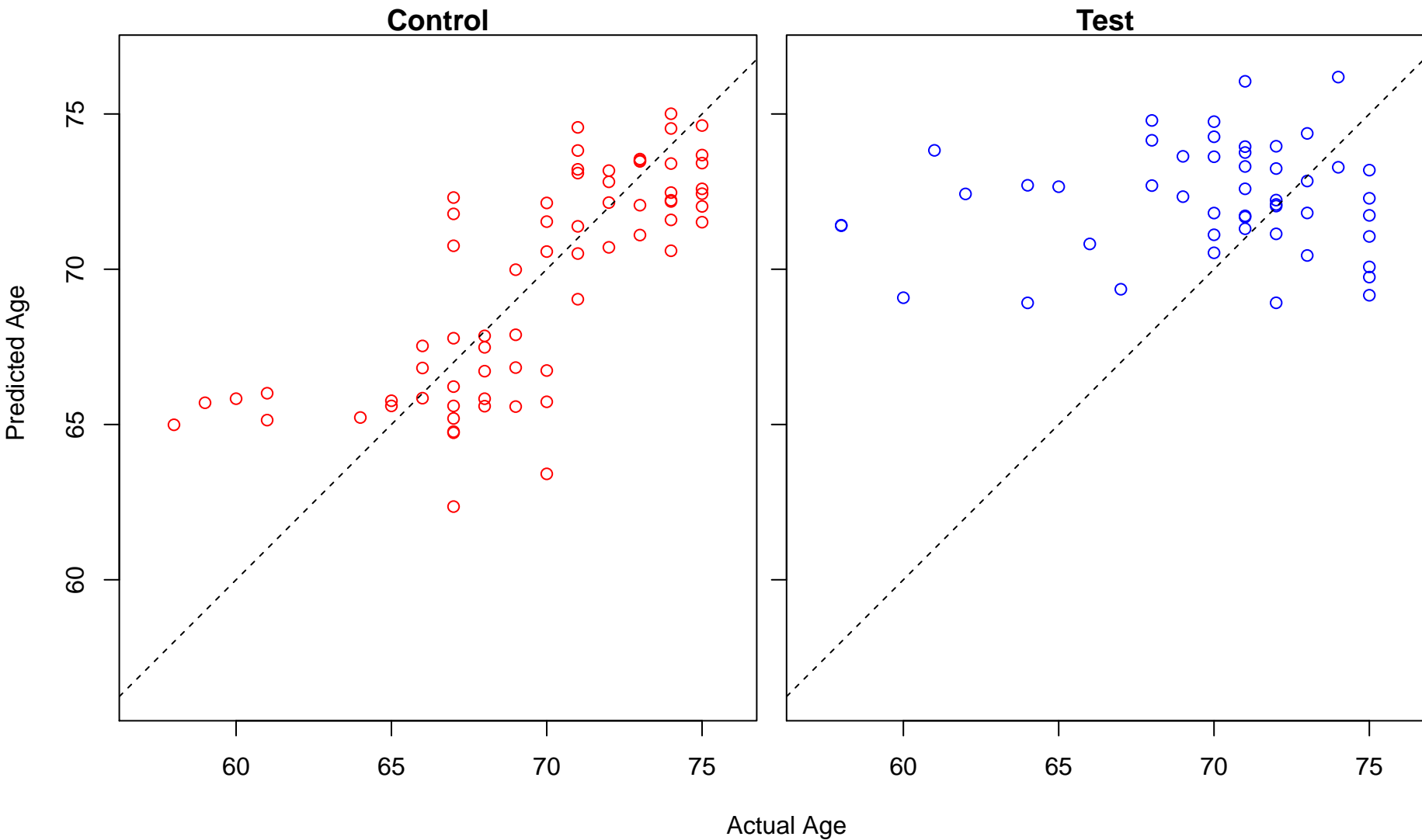
regulation of cation transmembrane transport (Score: 1.742819)



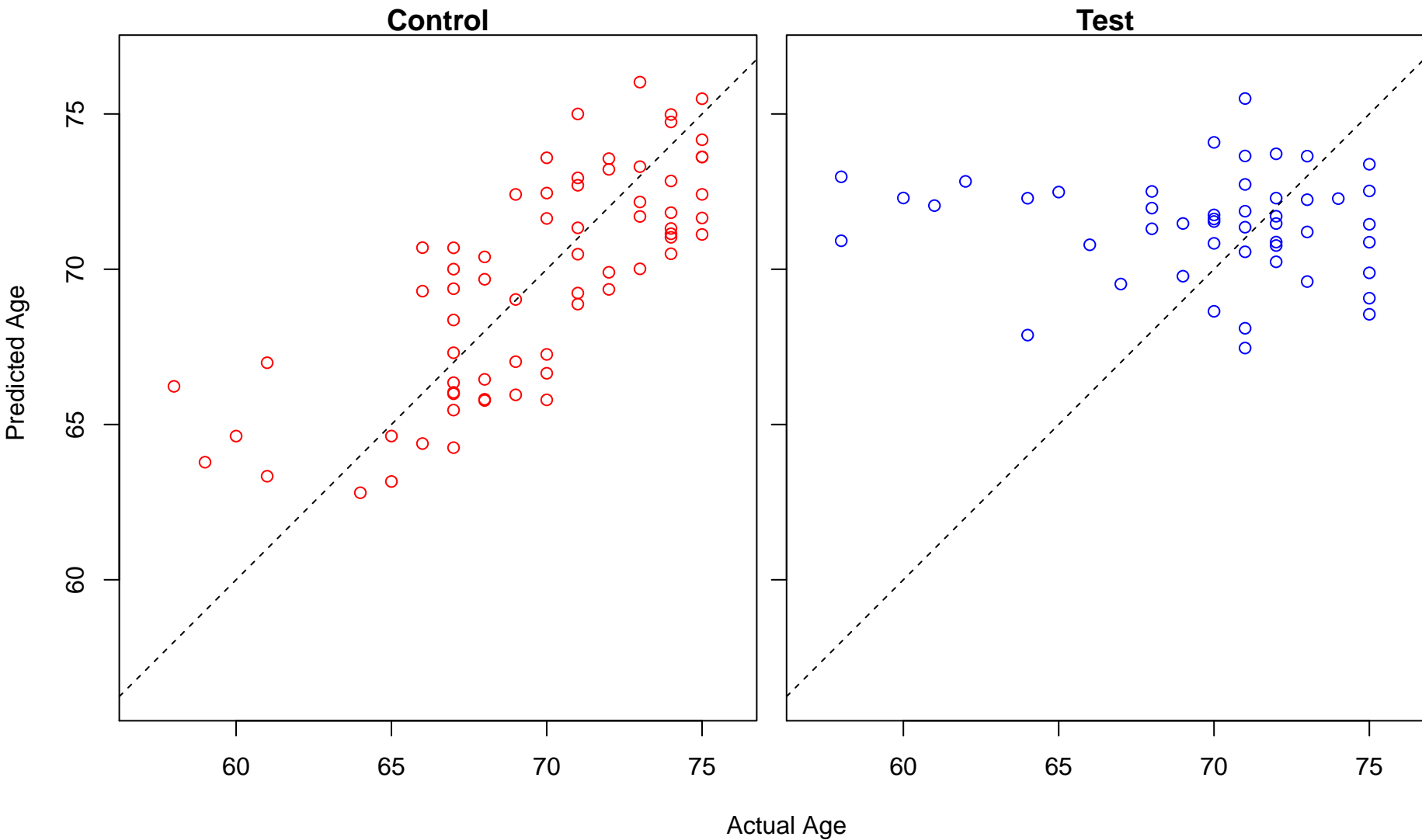
negative regulation of binding (Score: 1.742781)



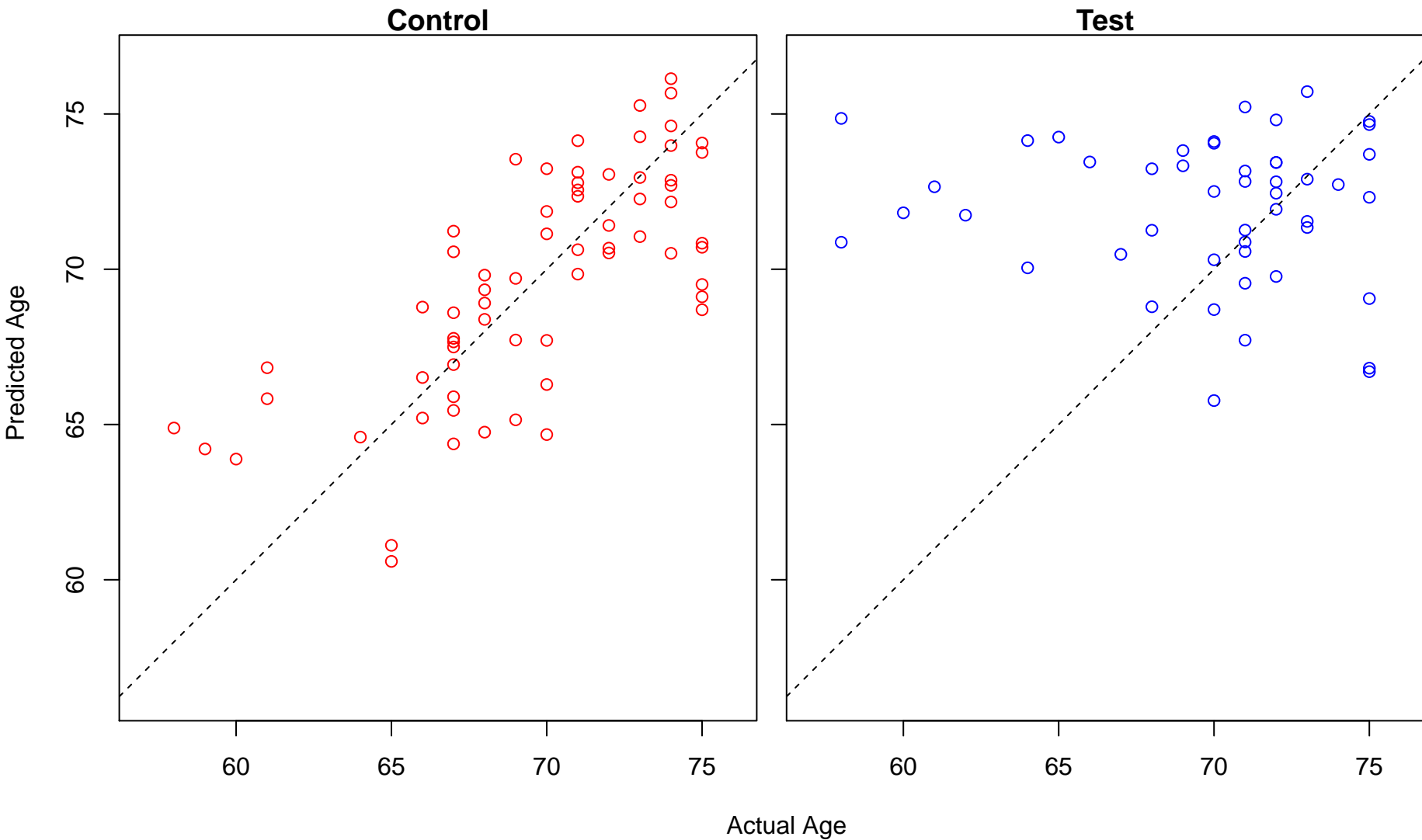
ribonucleoprotein complex subunit organization (Score: 1.742458)



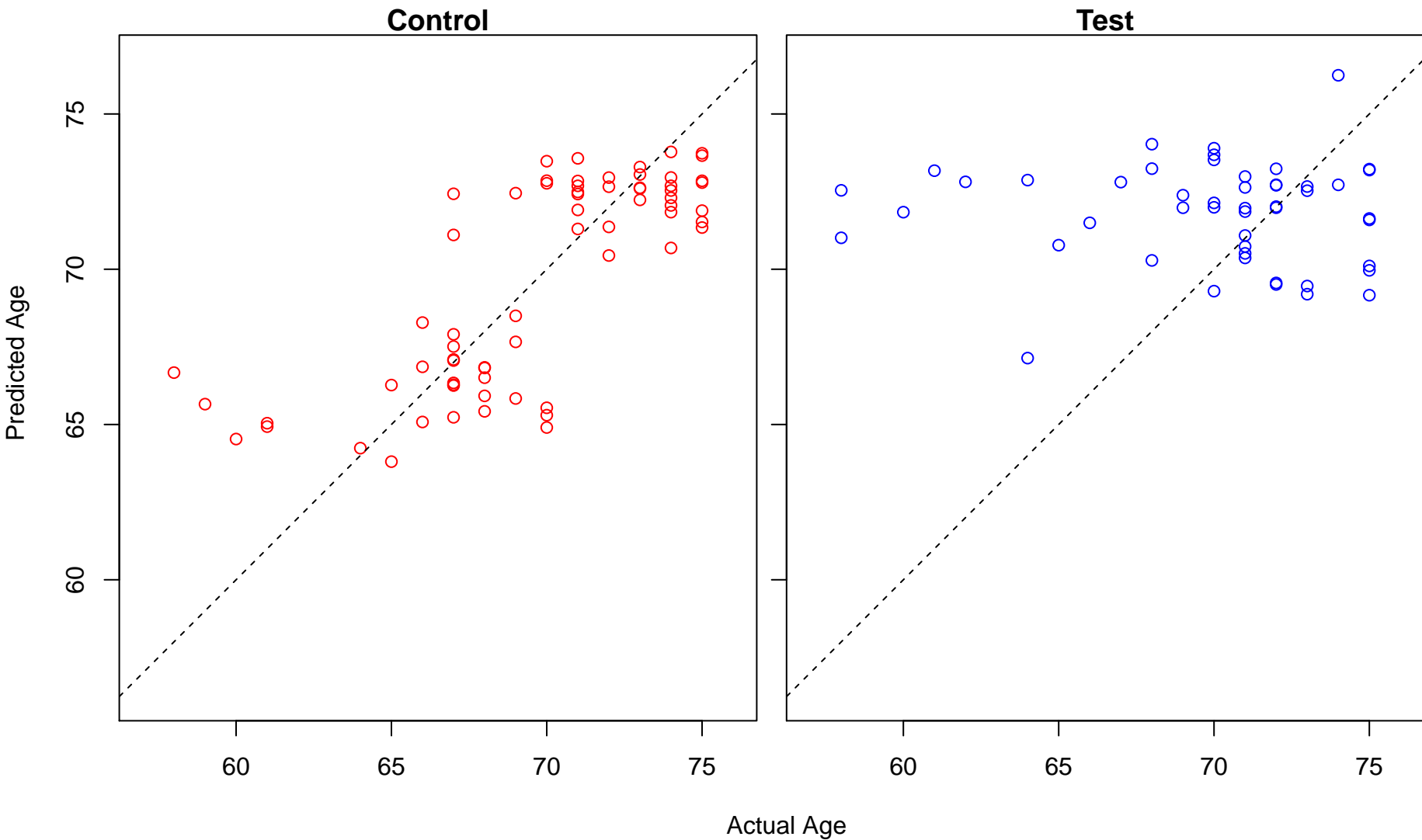
response to ionizing radiation (Score: 1.742122)



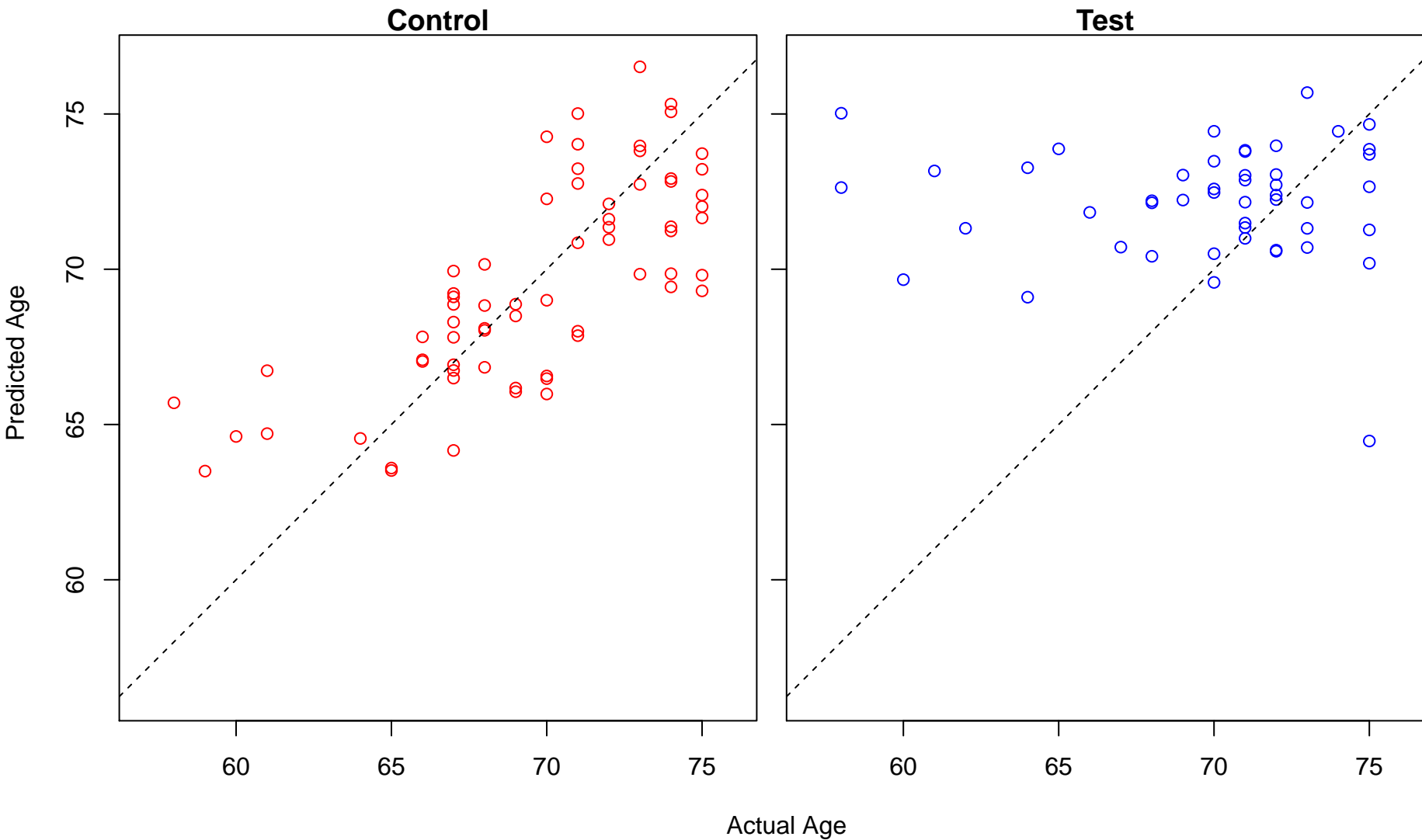
positive regulation of ion transport (Score: 1.741571)



sister chromatid segregation (Score: 1.741202)

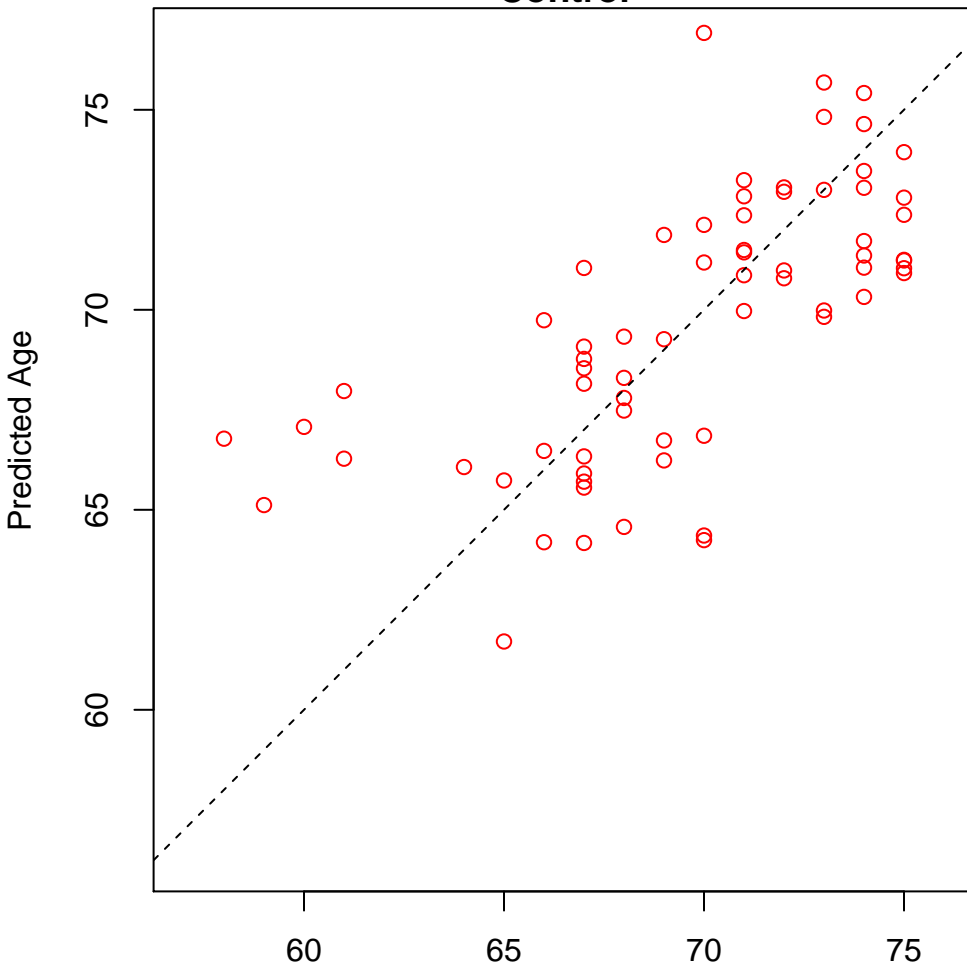


regulation of ion transmembrane transport (Score: 1.741029)

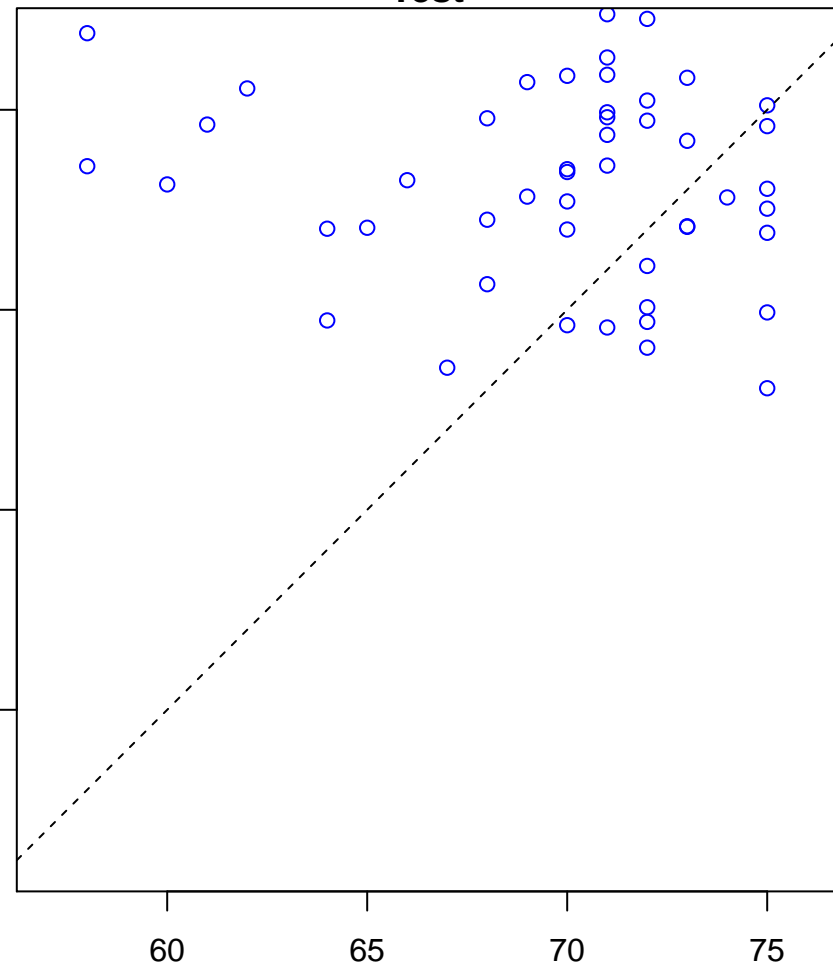


regulation of vasculature development (Score: 1.740690)

Control

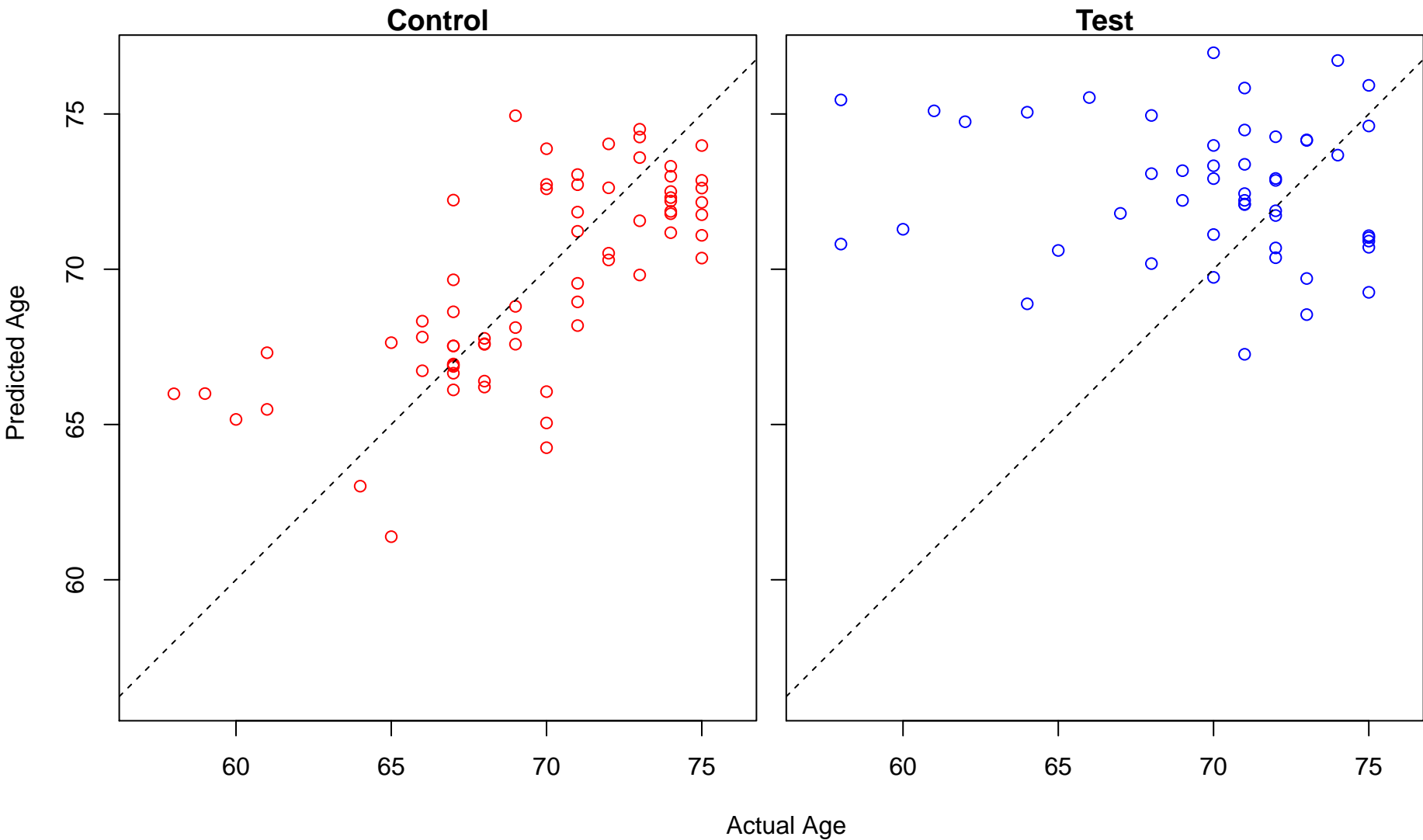


Test

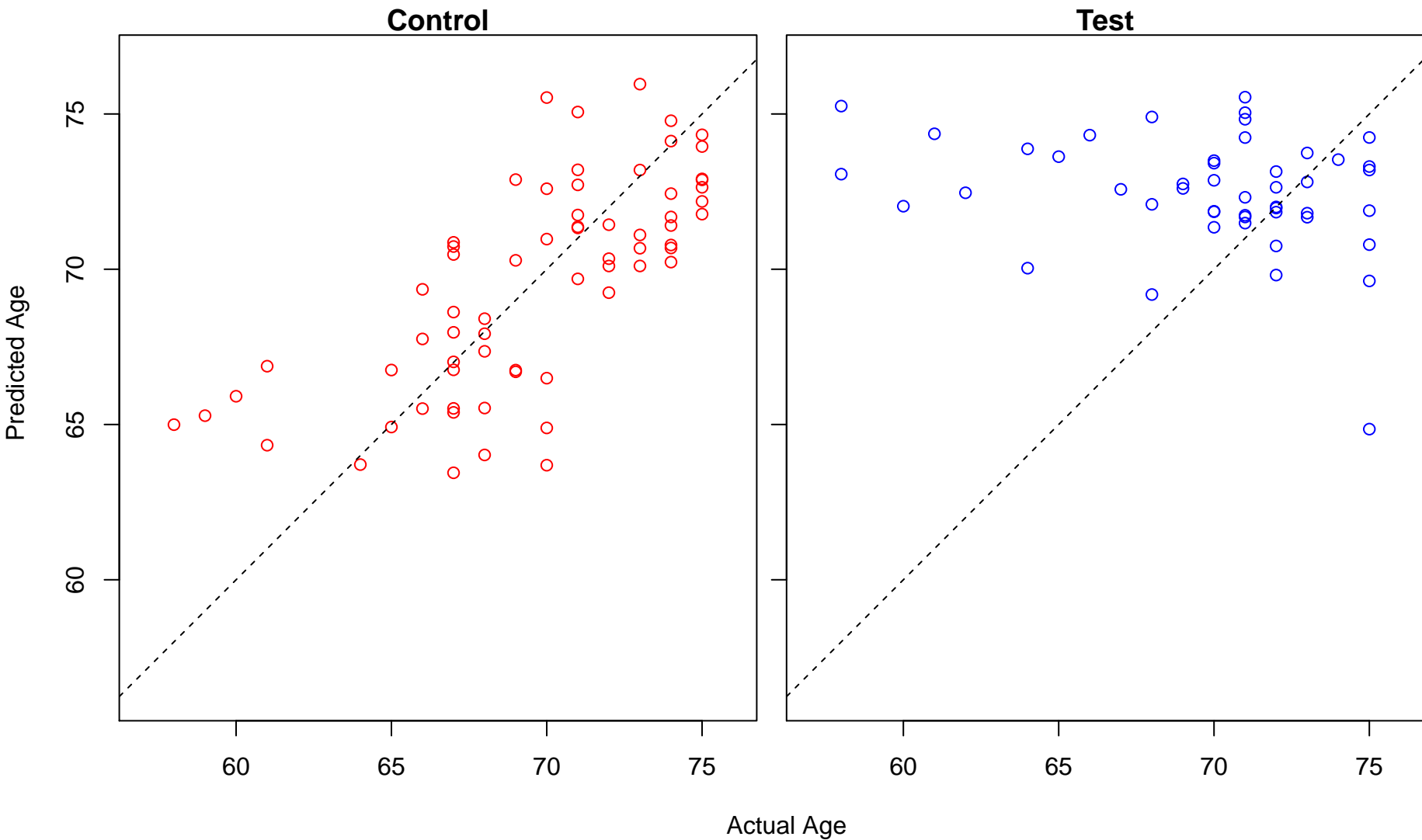


Actual Age

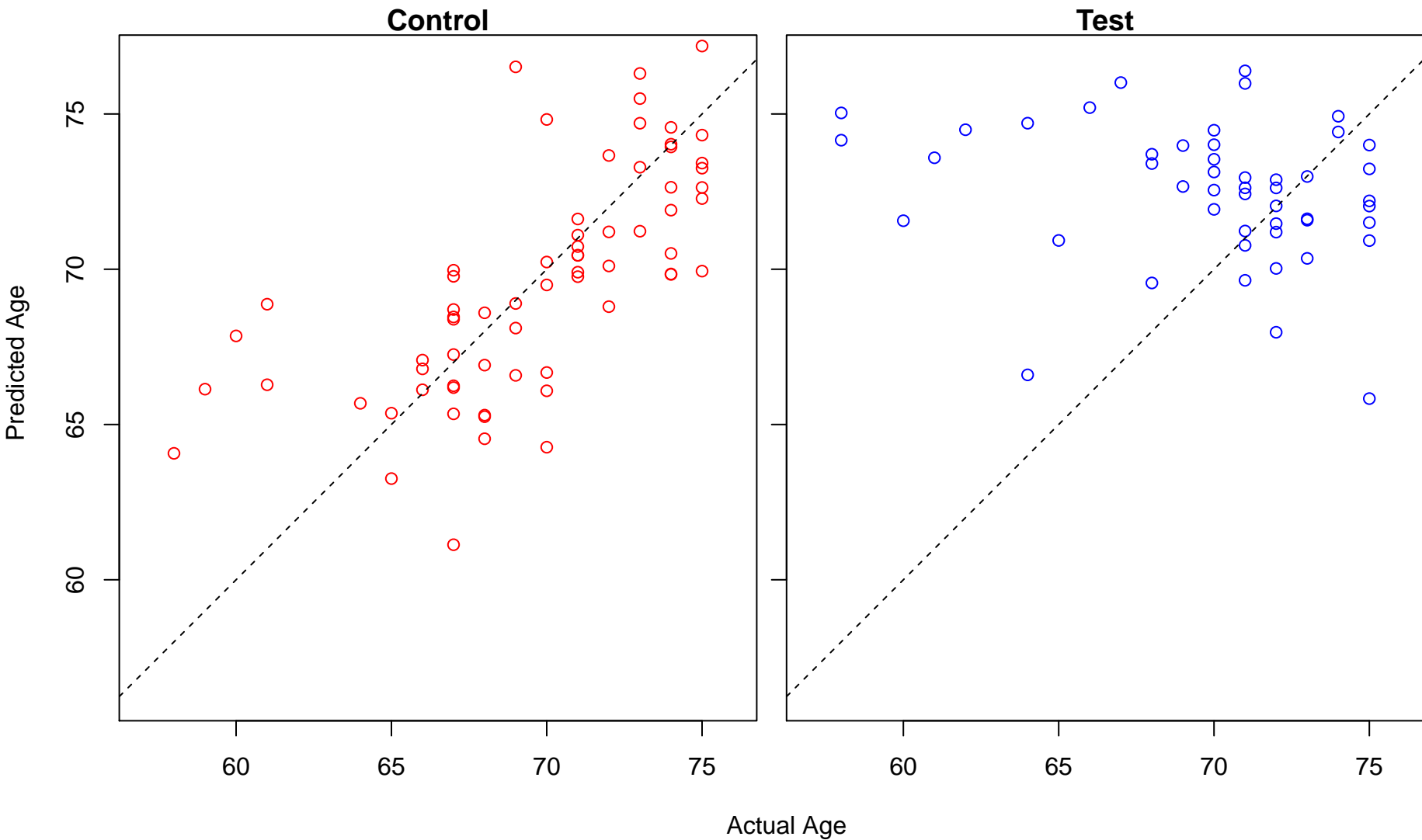
postreplication repair (Score: 1.739935)



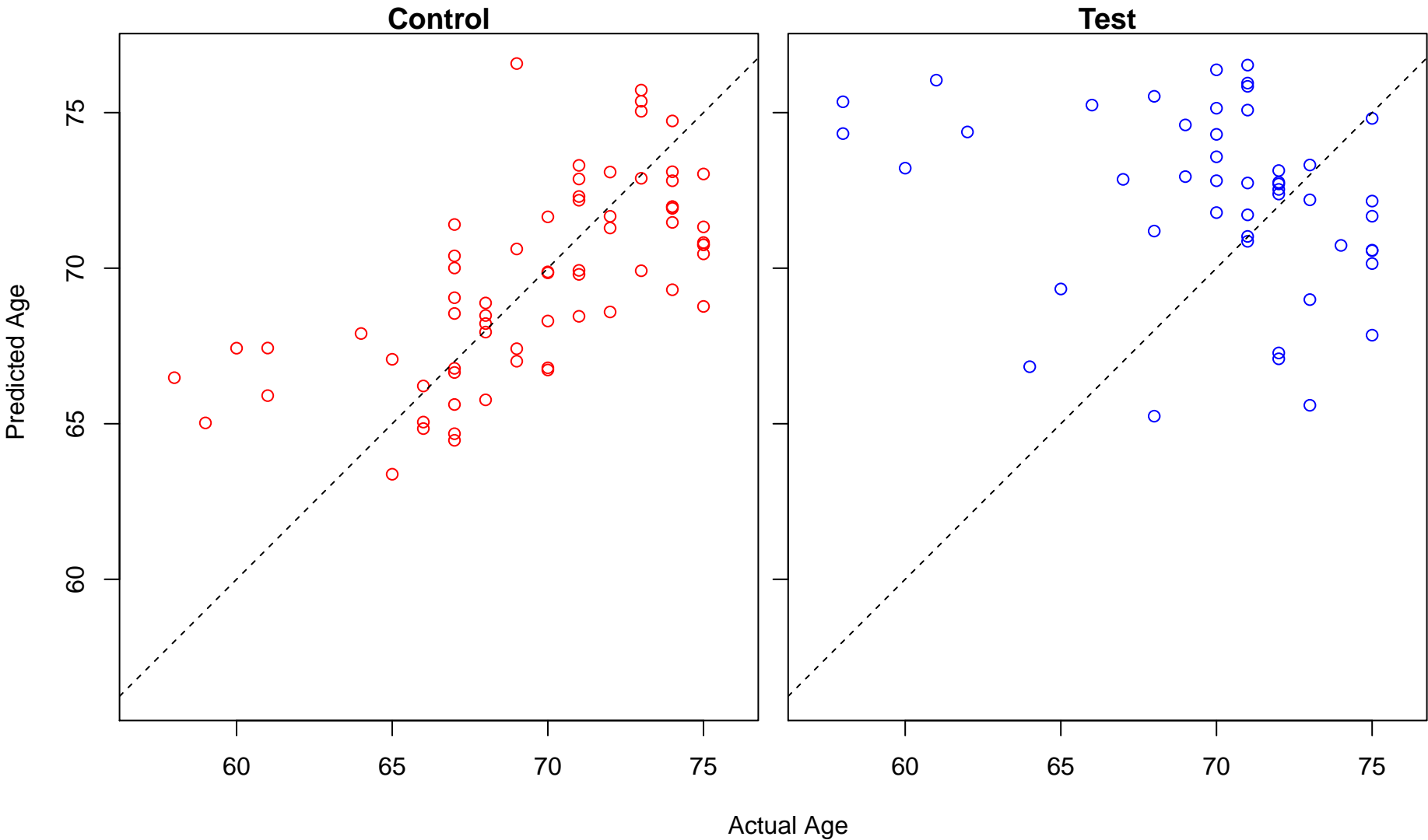
dephosphorylation (Score: 1.739736)



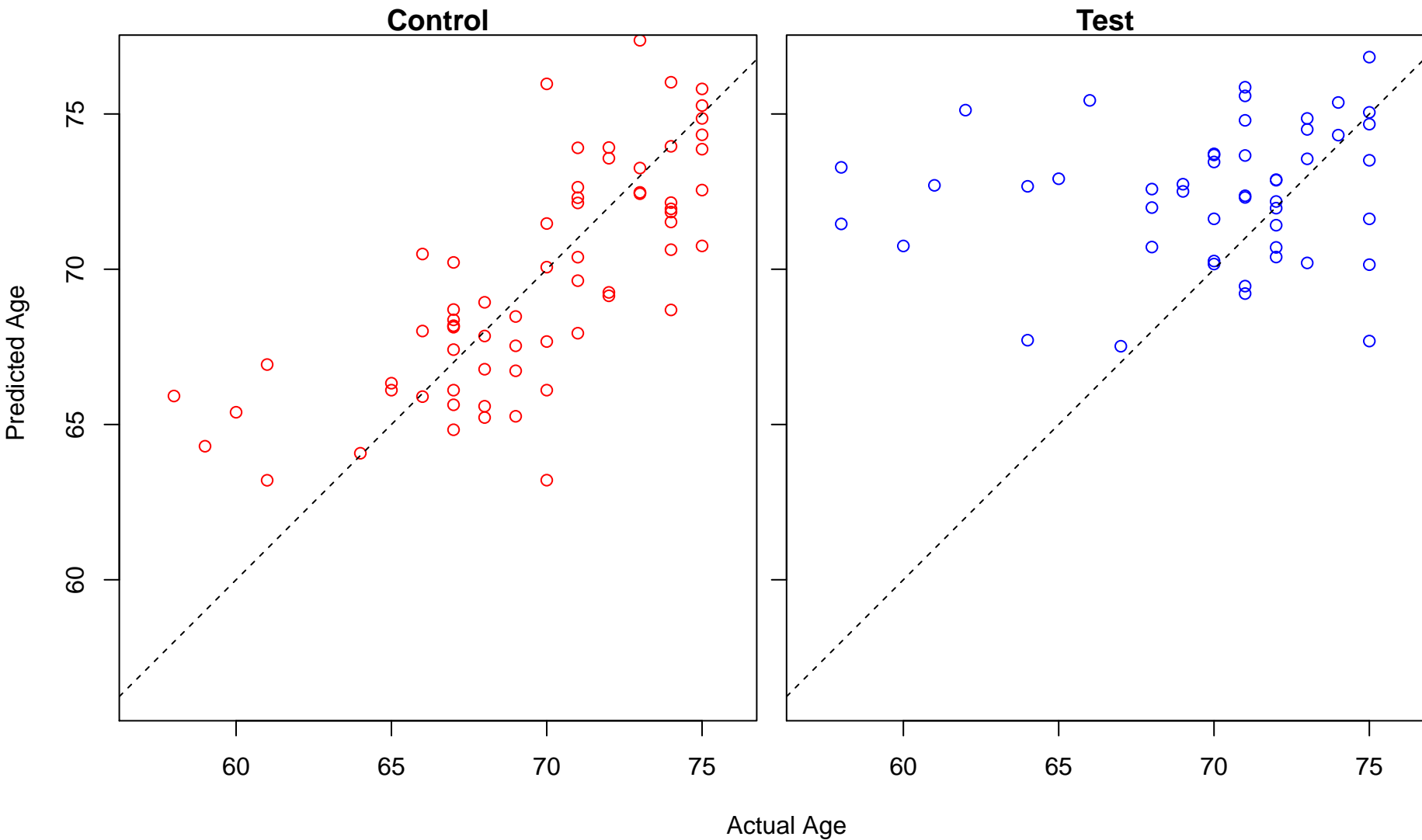
regulation of inflammatory response (Score: 1.739638)



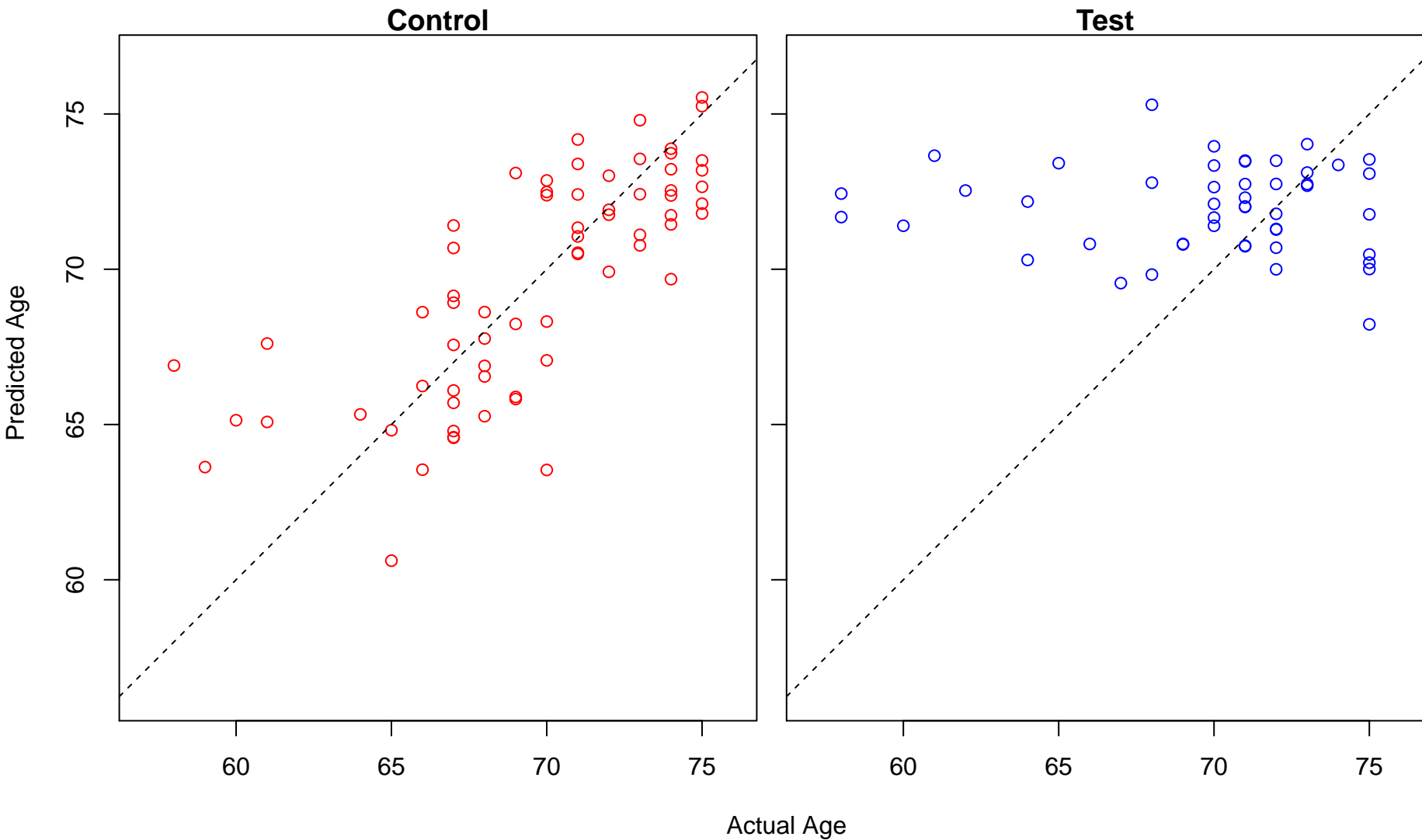
positive regulation of CD4-positive, alpha-beta T cell differentiation (Score: 1.739632)



regulation of generation of precursor metabolites and energy (Score: 1.738901)

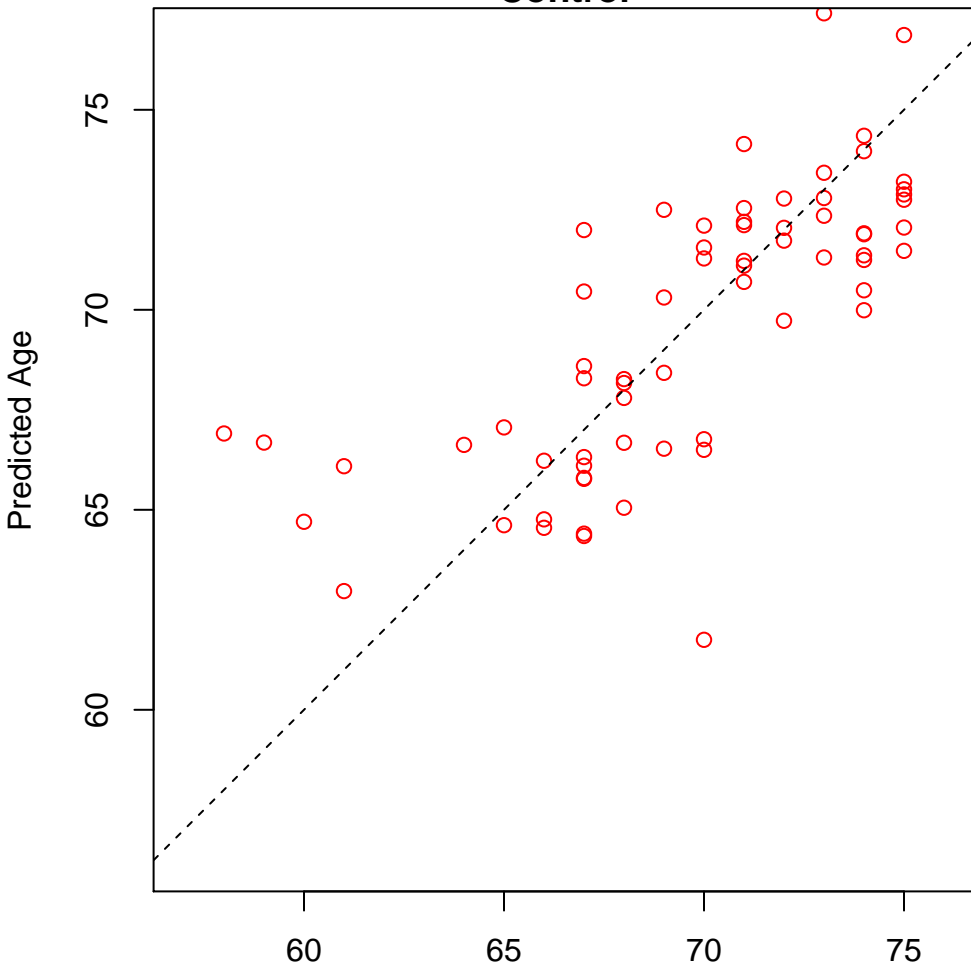


regulation of cell cycle arrest (Score: 1.738540)

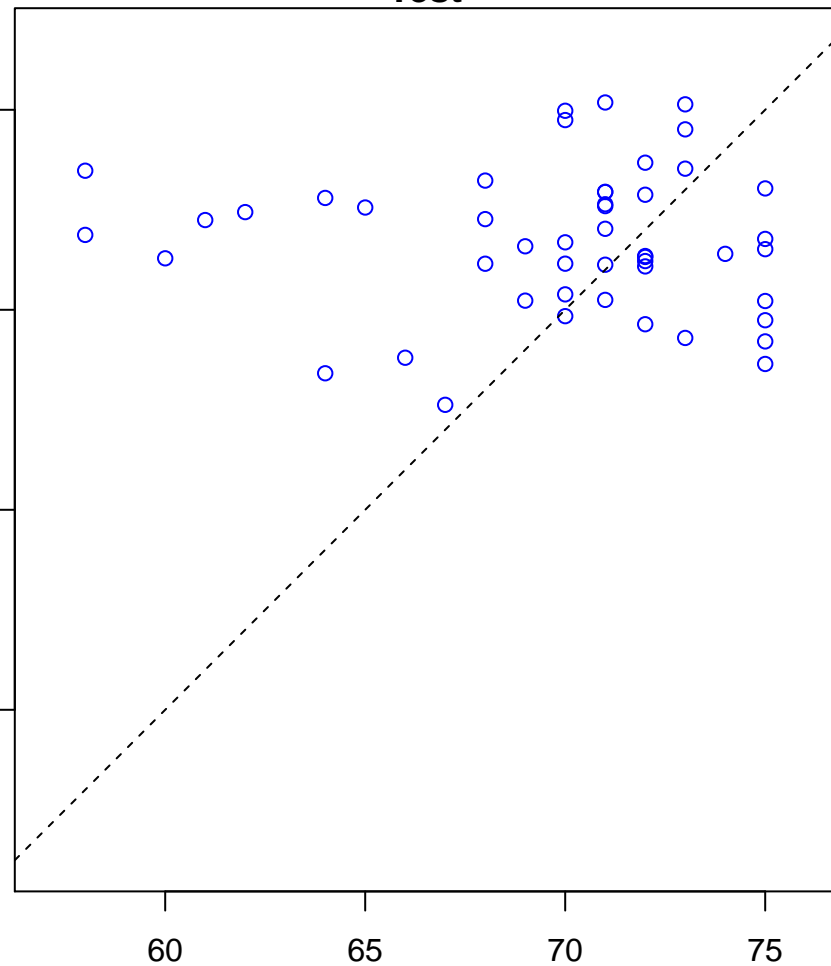


purine ribonucleotide metabolic process (Score: 1.738404)

Control

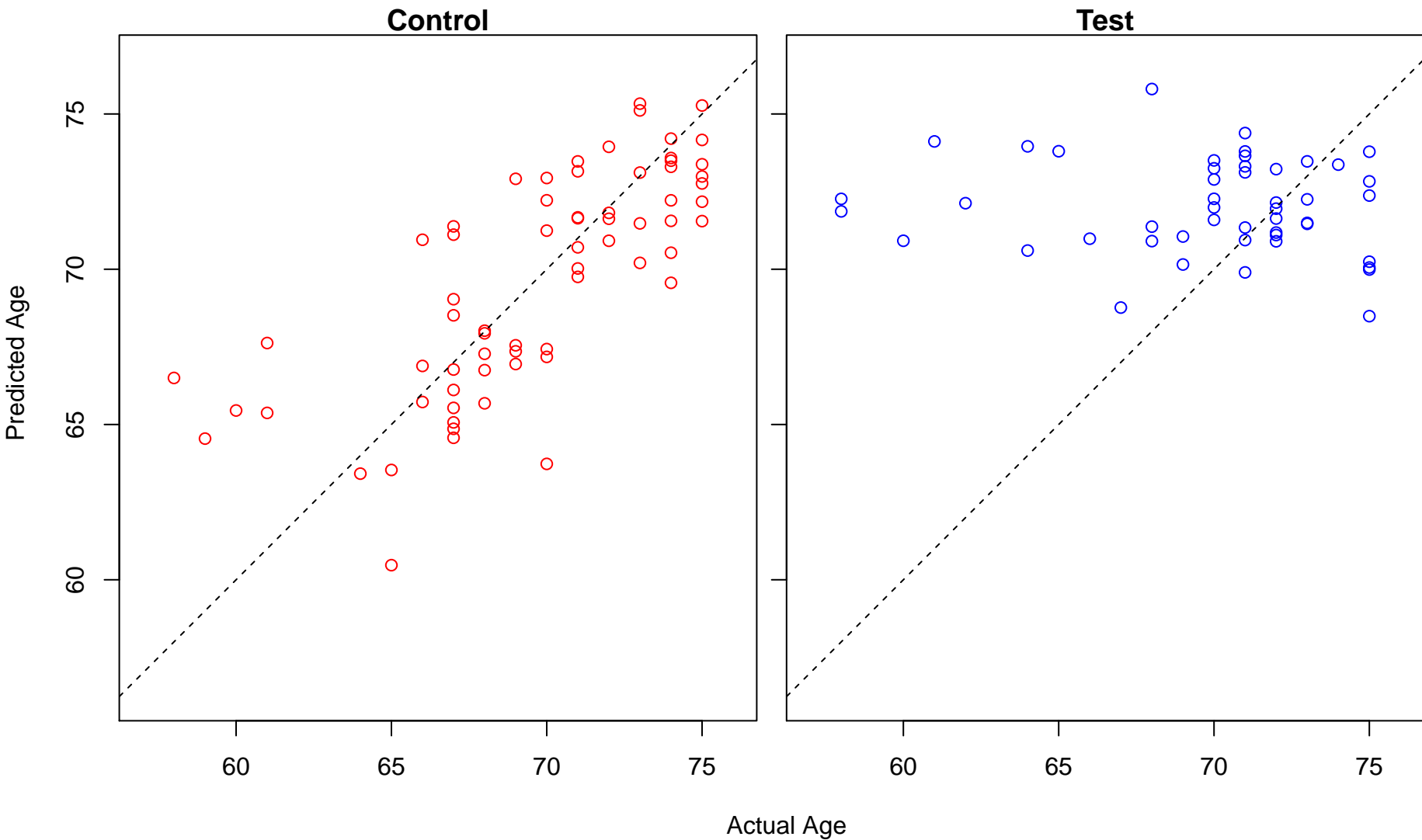


Test

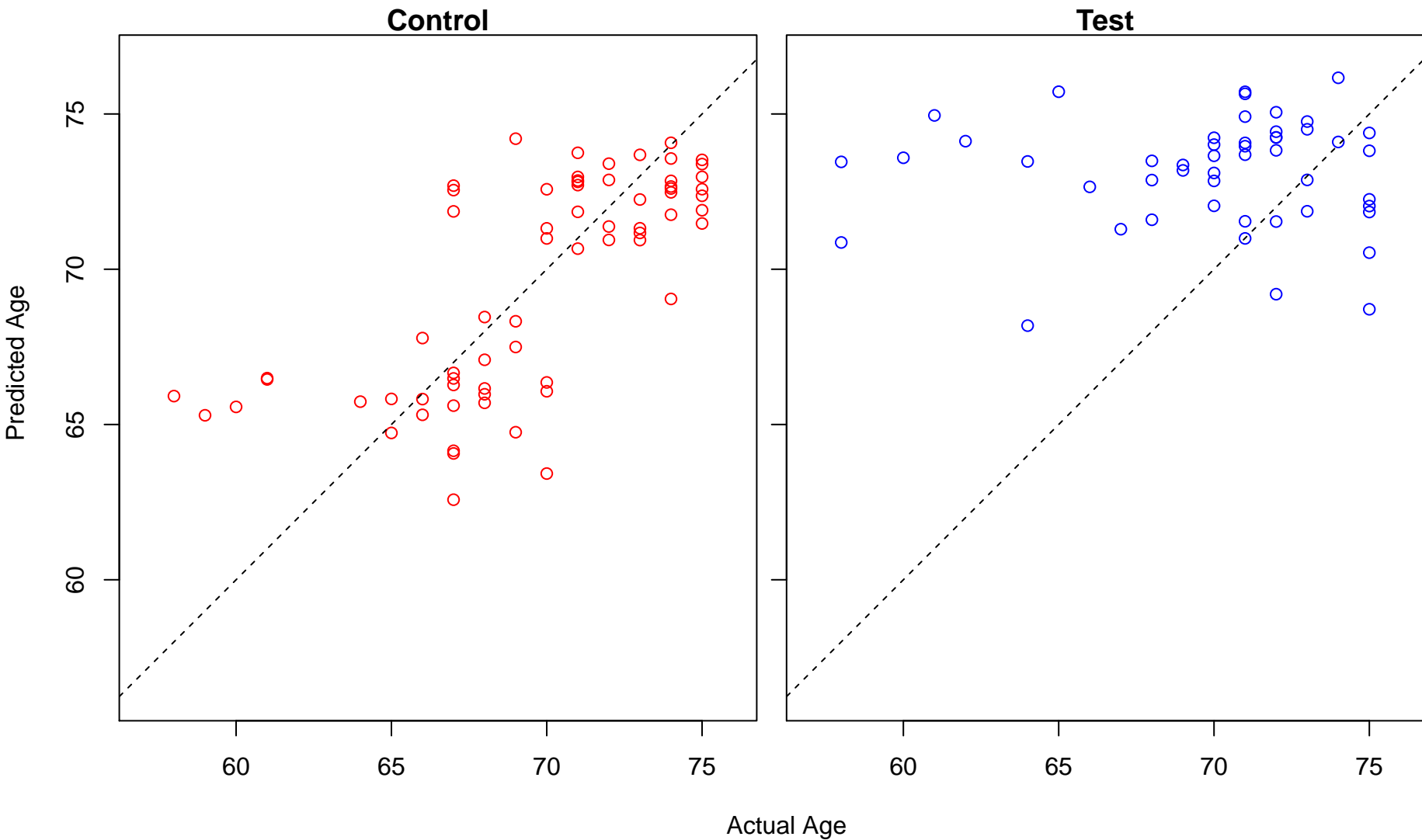


Actual Age

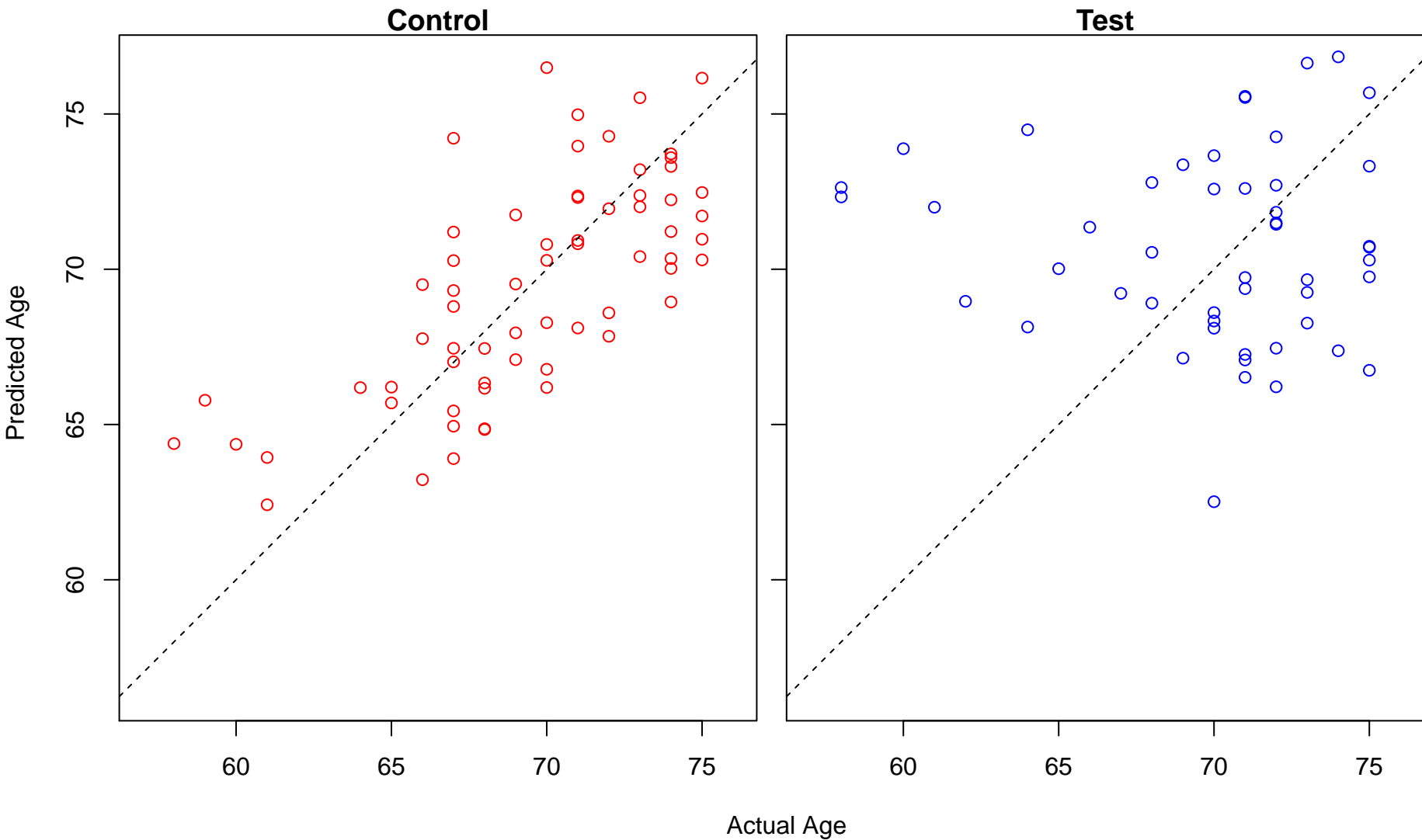
negative regulation of Wnt signaling pathway (Score: 1.738273)



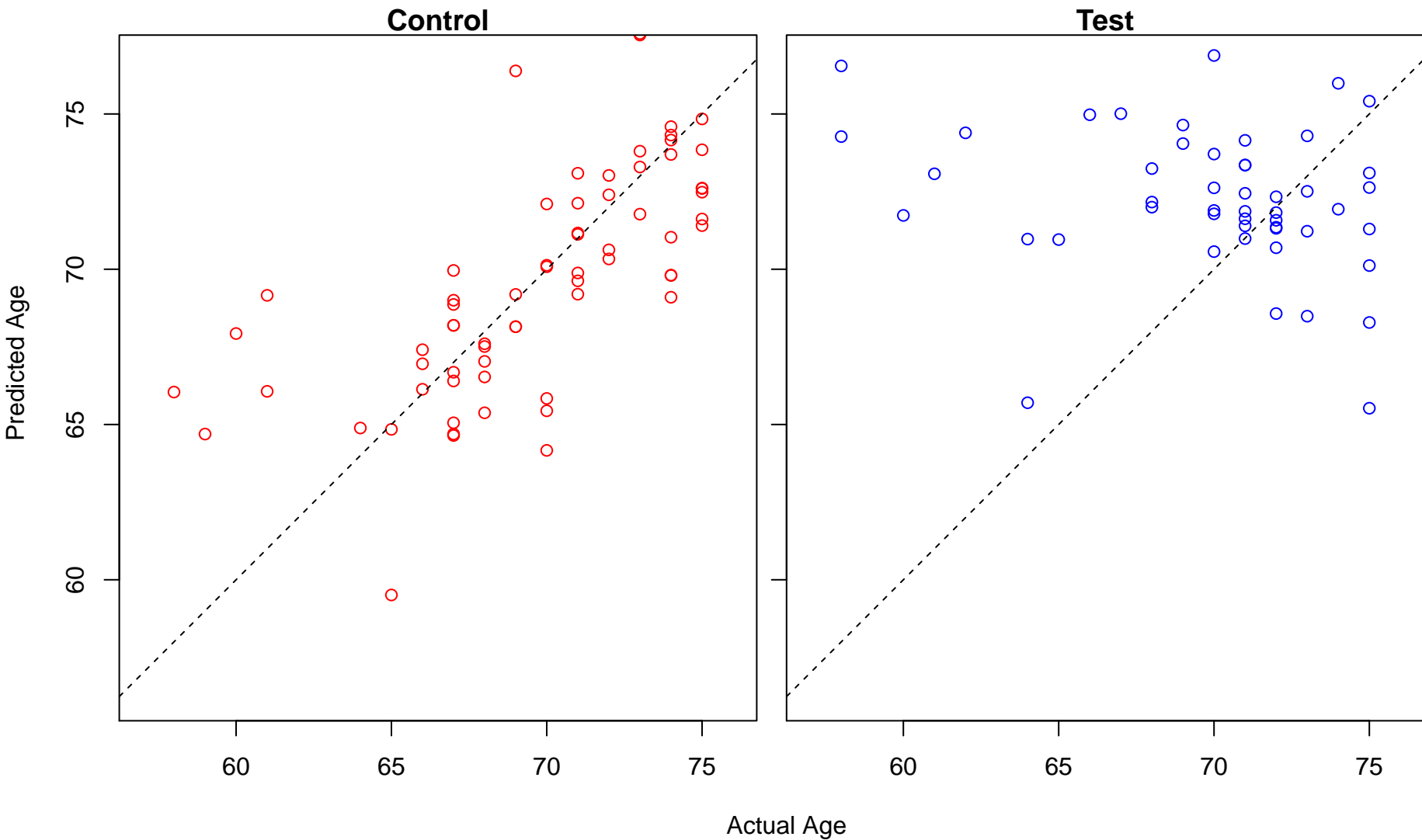
mRNA catabolic process (Score: 1.737275)



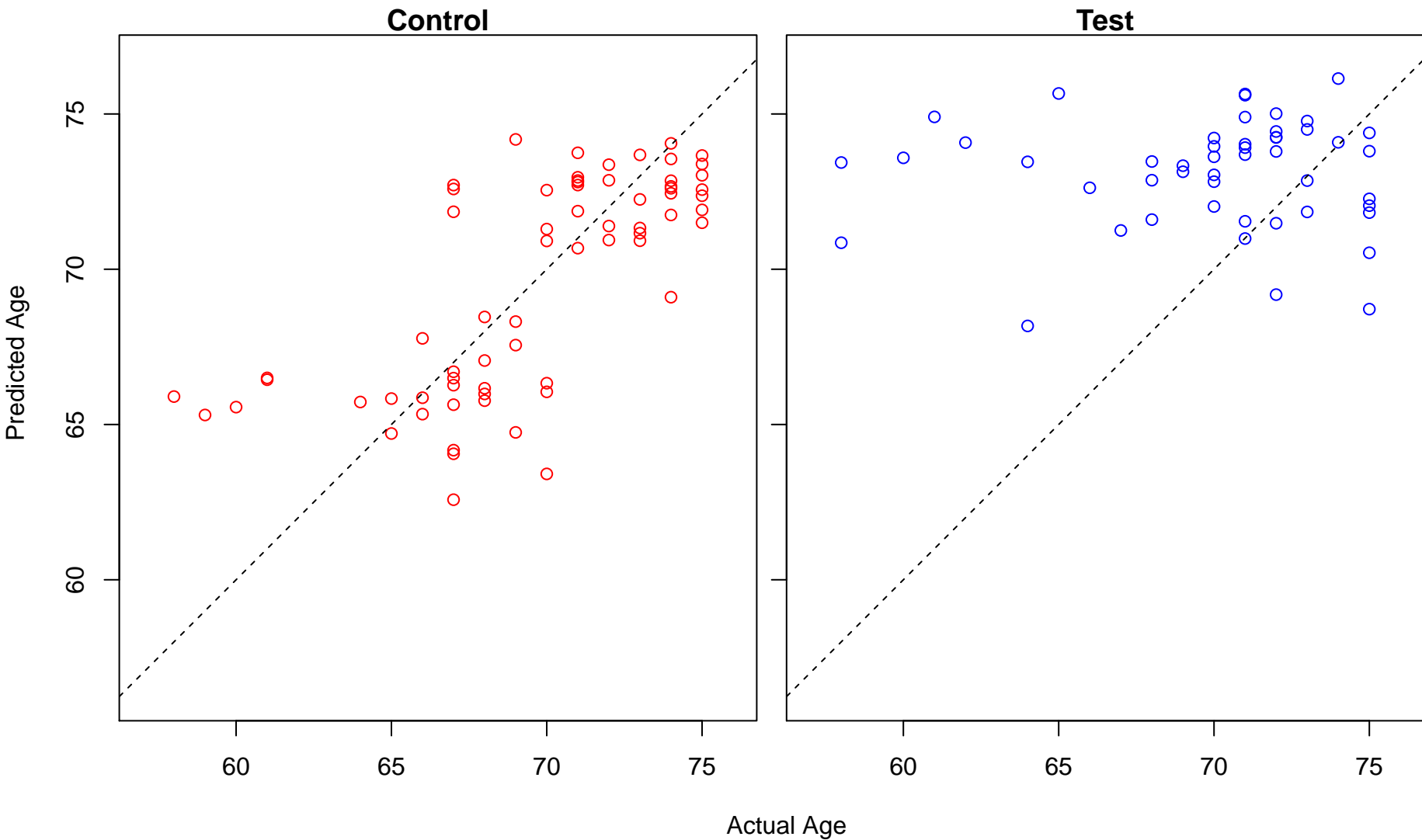
regulation of cyclase activity (Score: 1.736926)



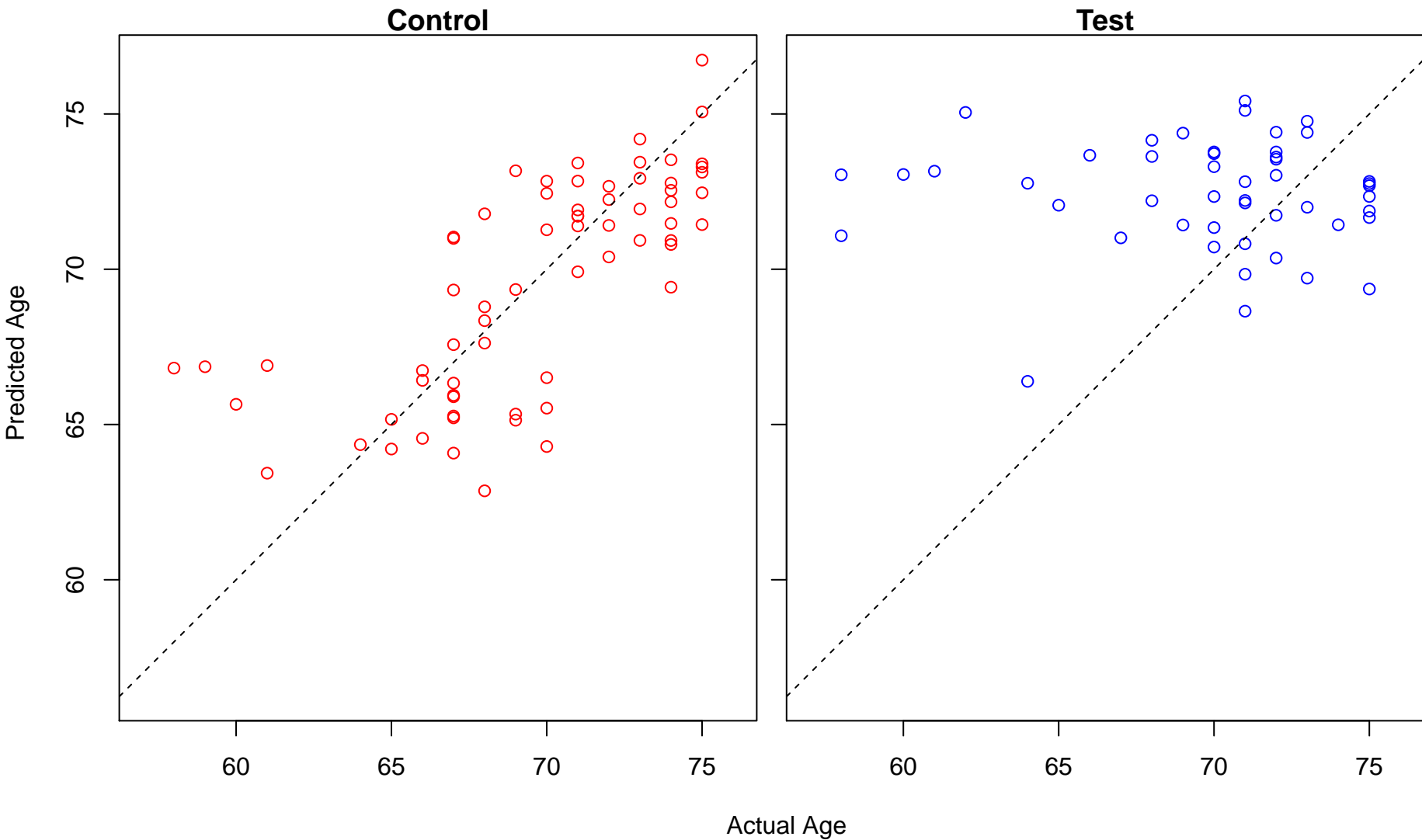
positive regulation of response to wounding (Score: 1.736841)



nuclear-transcribed mRNA catabolic process (Score: 1.735020)

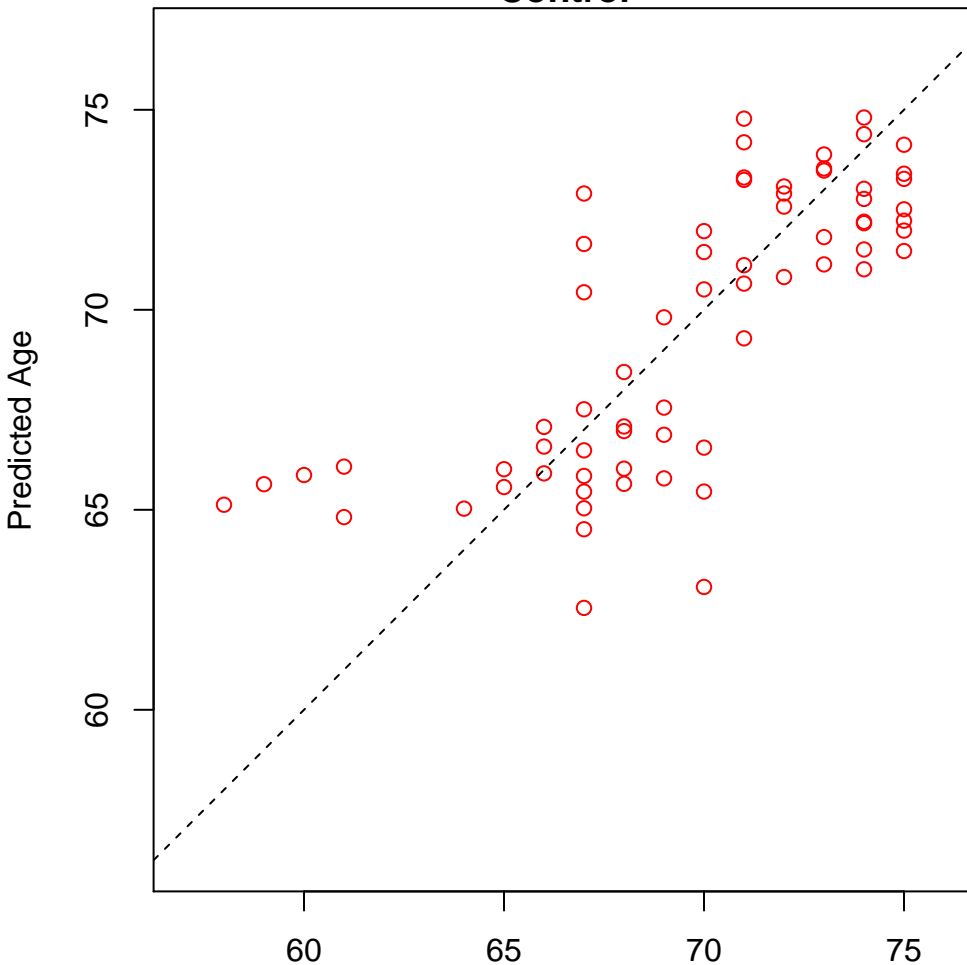


macromolecule methylation (Score: 1.734692)

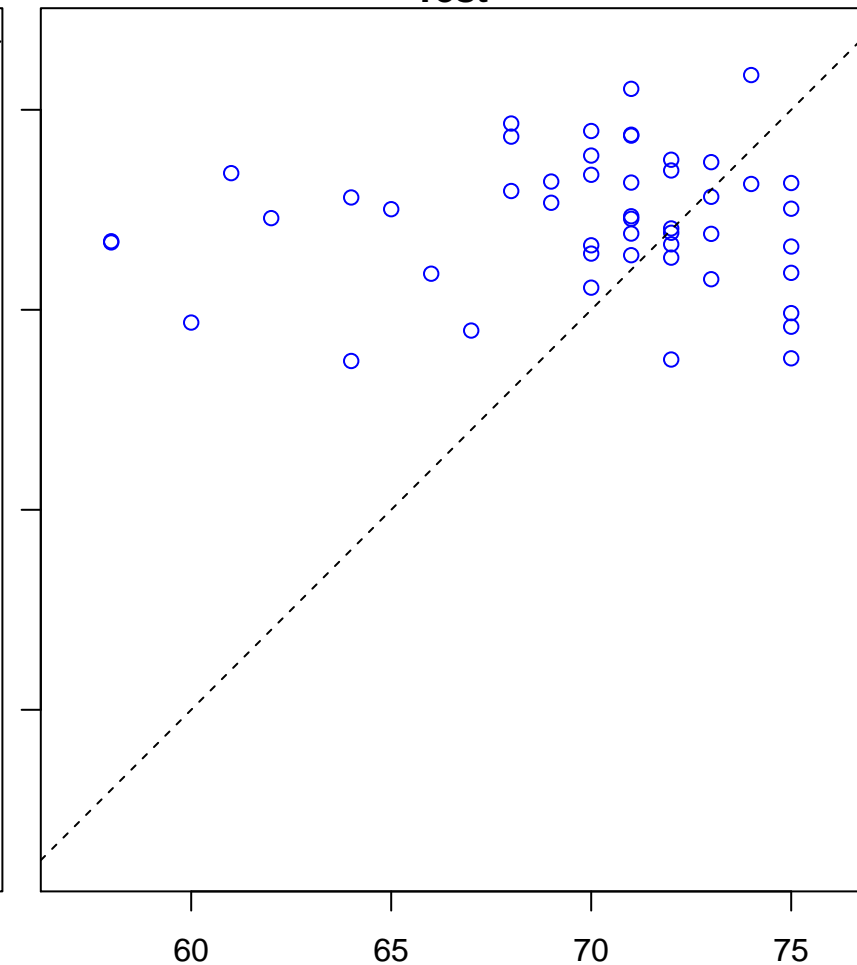


ribonucleoprotein complex assembly (Score: 1.733009)

Control

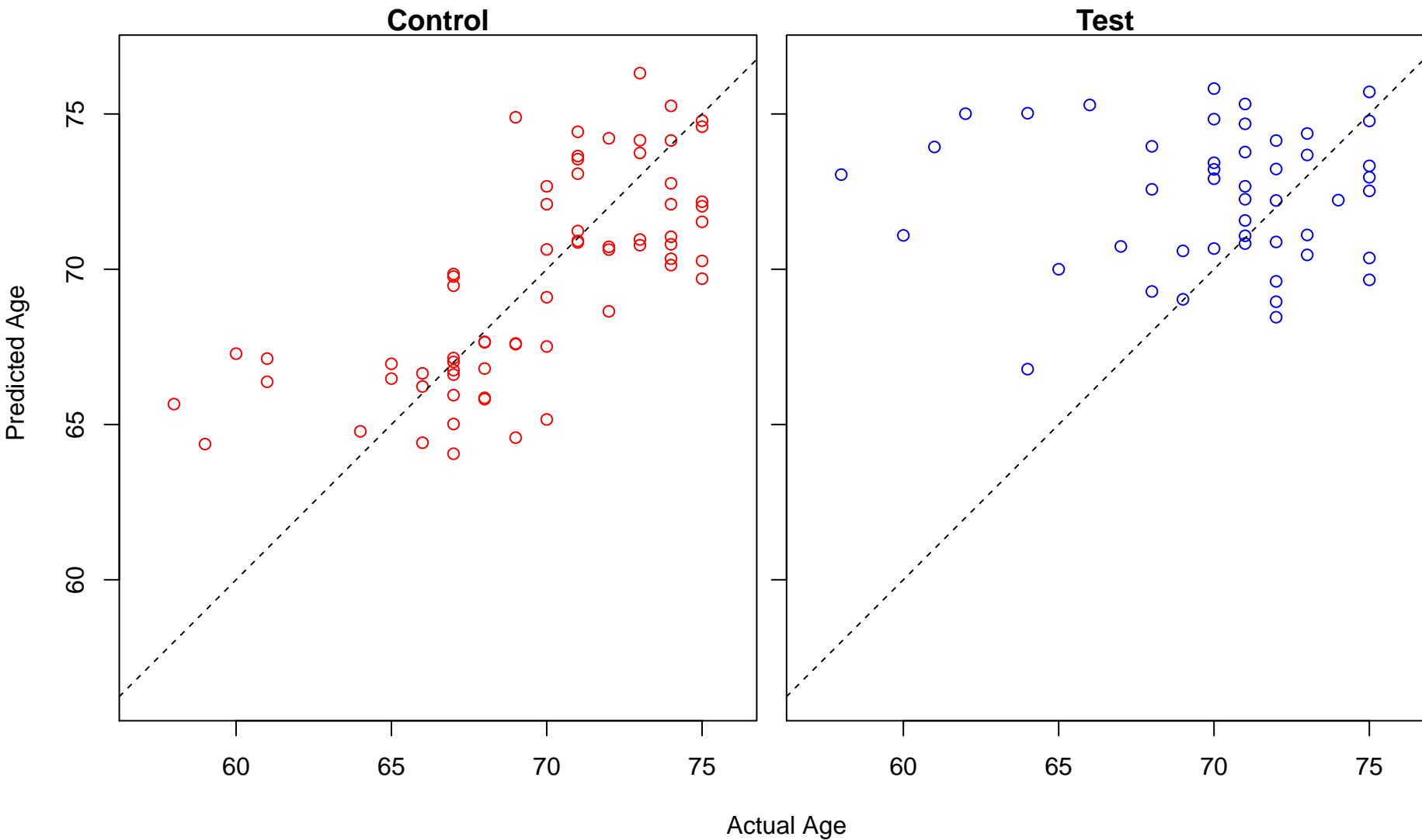


Test

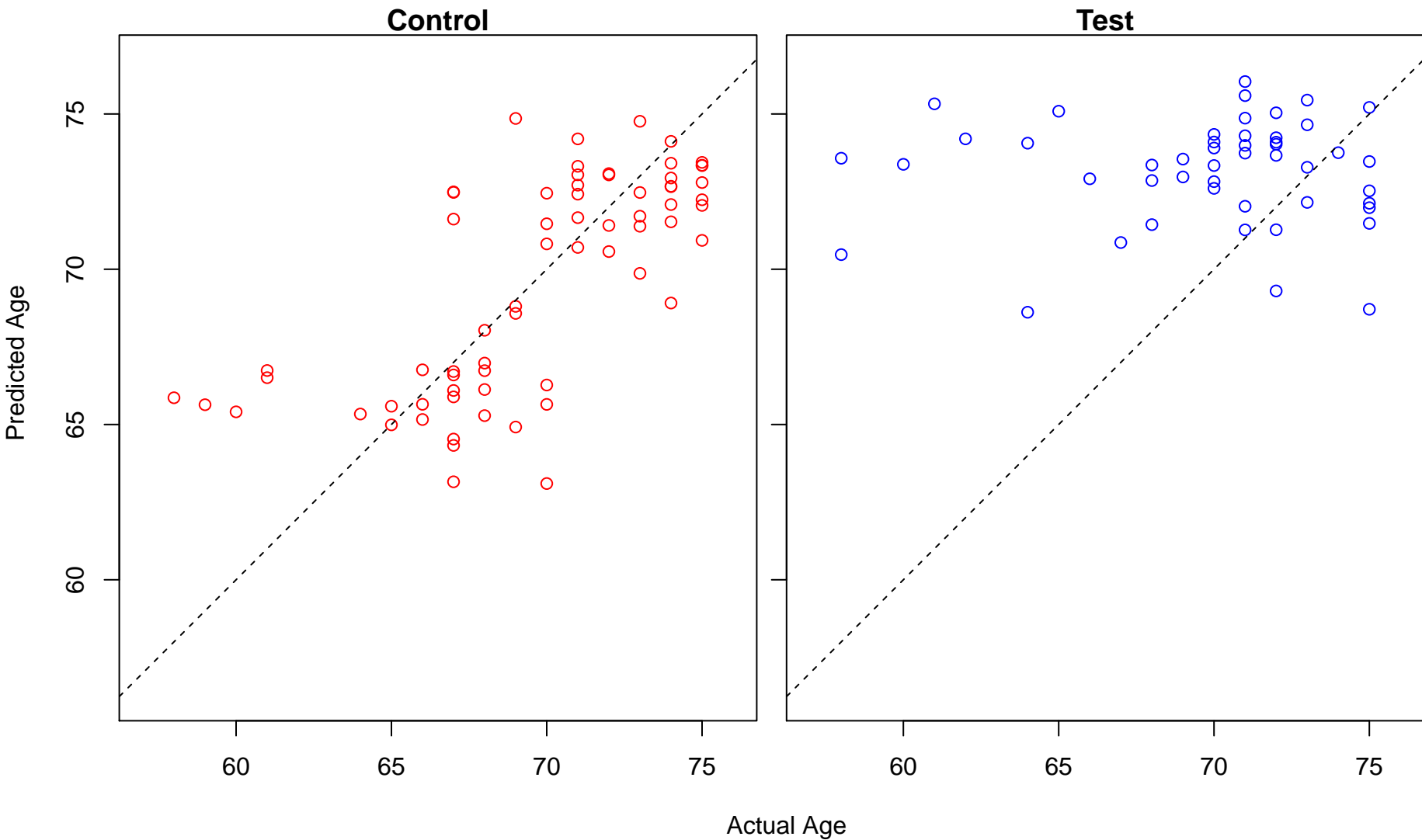


Actual Age

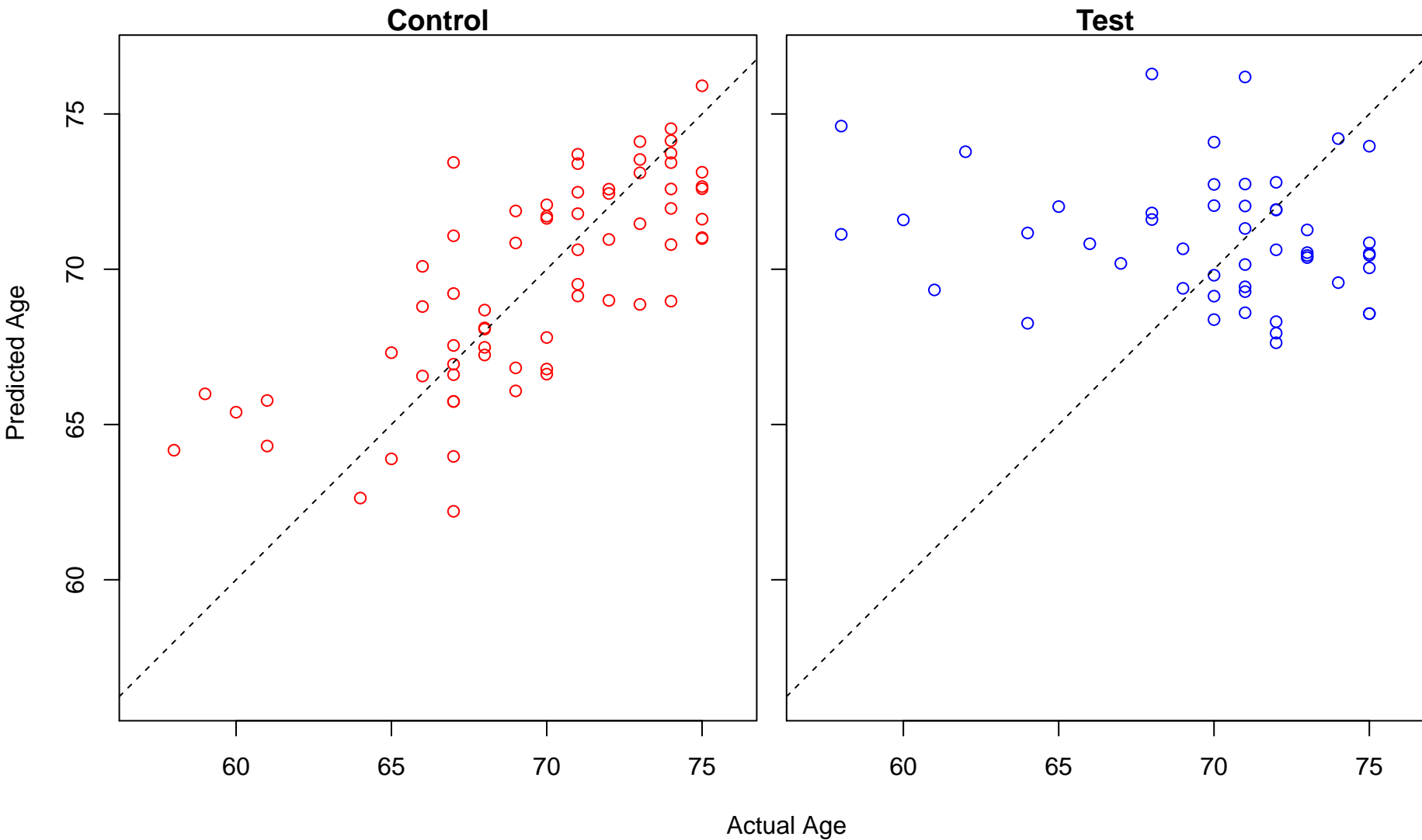
actin filament-based movement (Score: 1.732705)



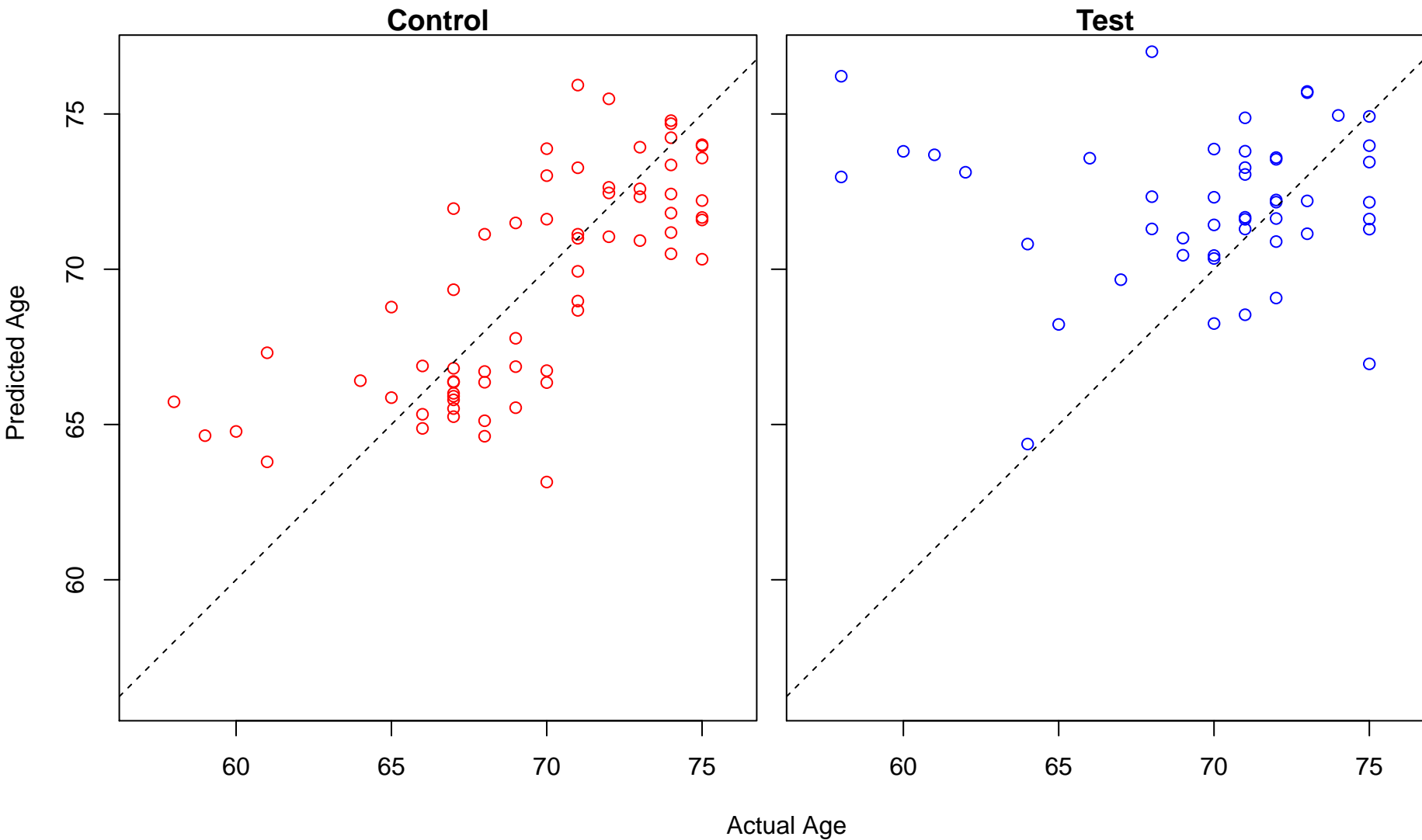
translational initiation (Score: 1.732165)



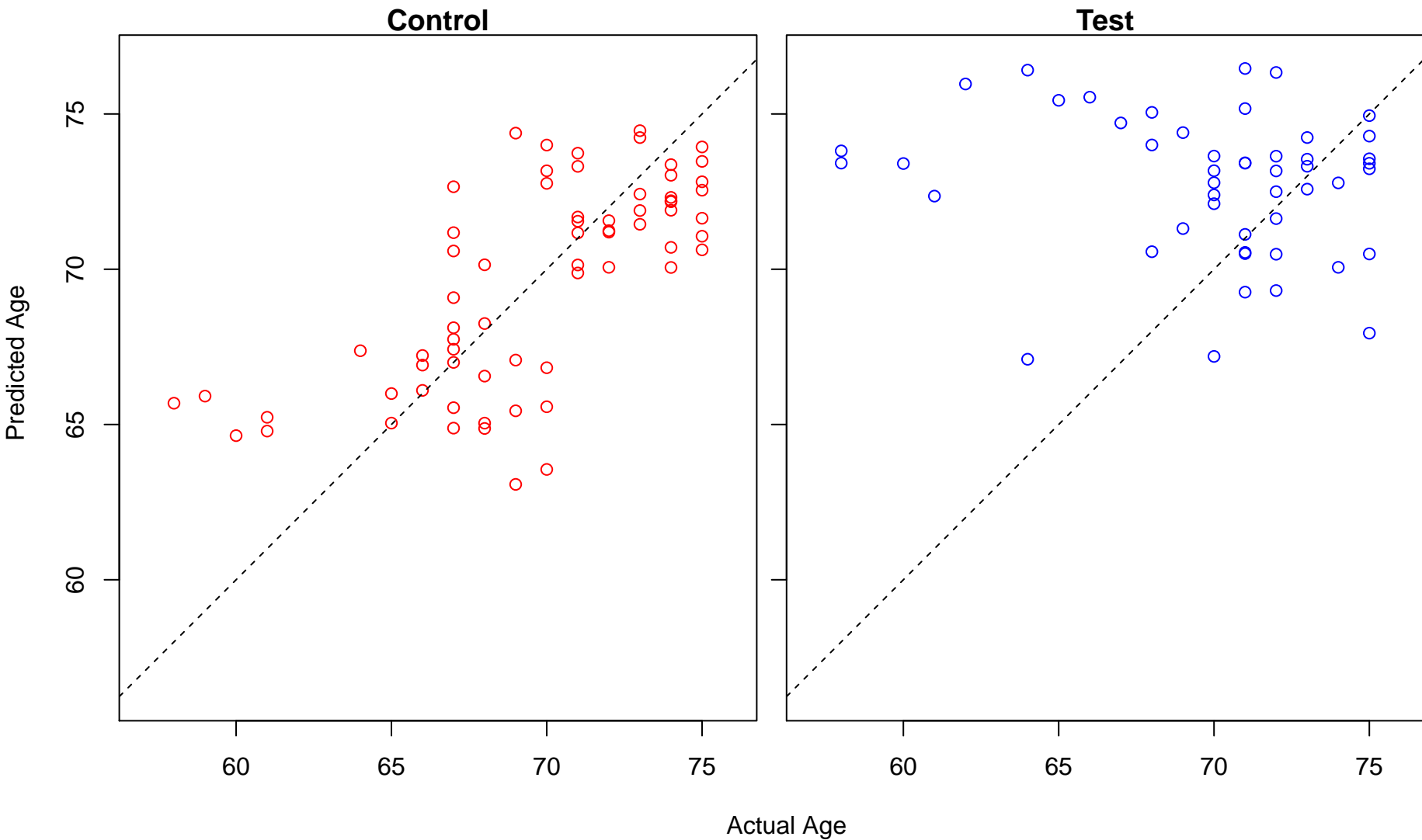
positive regulation of monocyte differentiation (Score: 1.731020)



positive regulation of cell growth (Score: 1.730484)

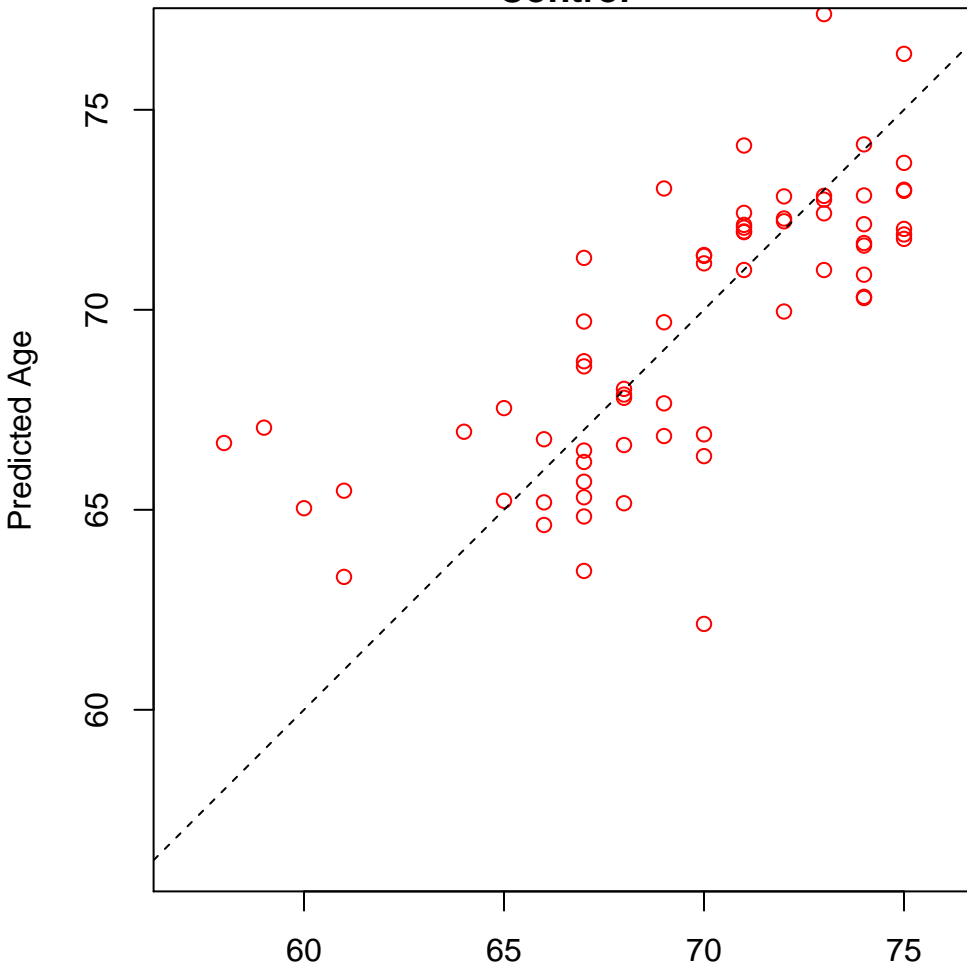


positive regulation of histone modification (Score: 1.730104)

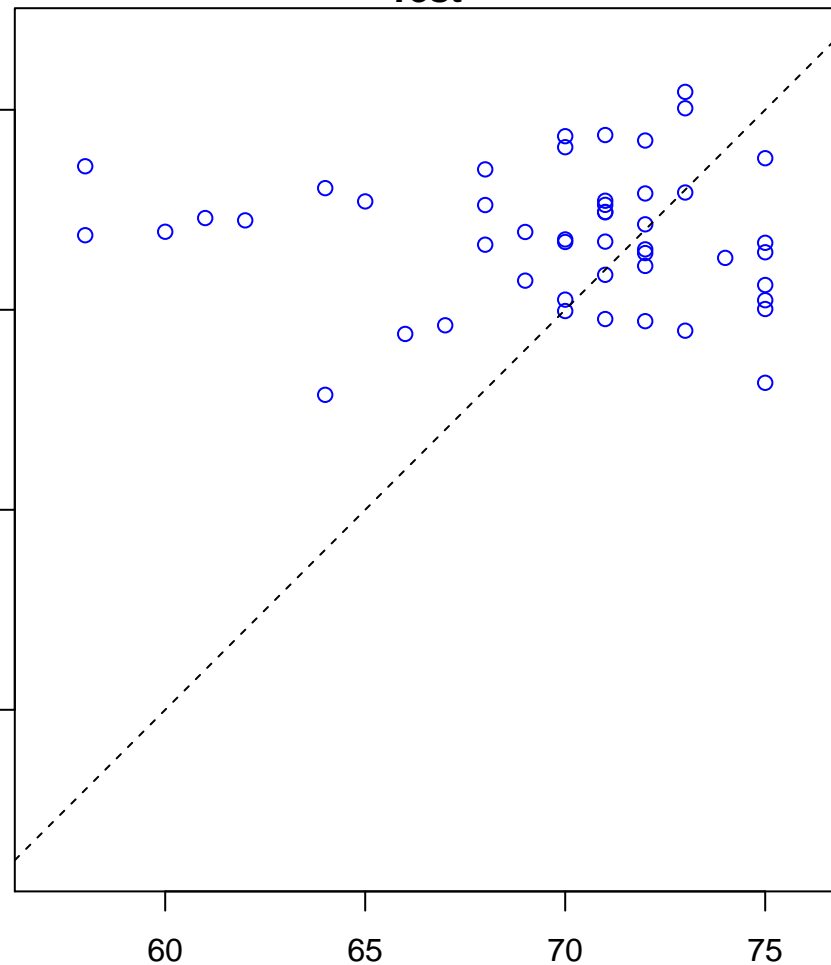


ribose phosphate metabolic process (Score: 1.729990)

Control

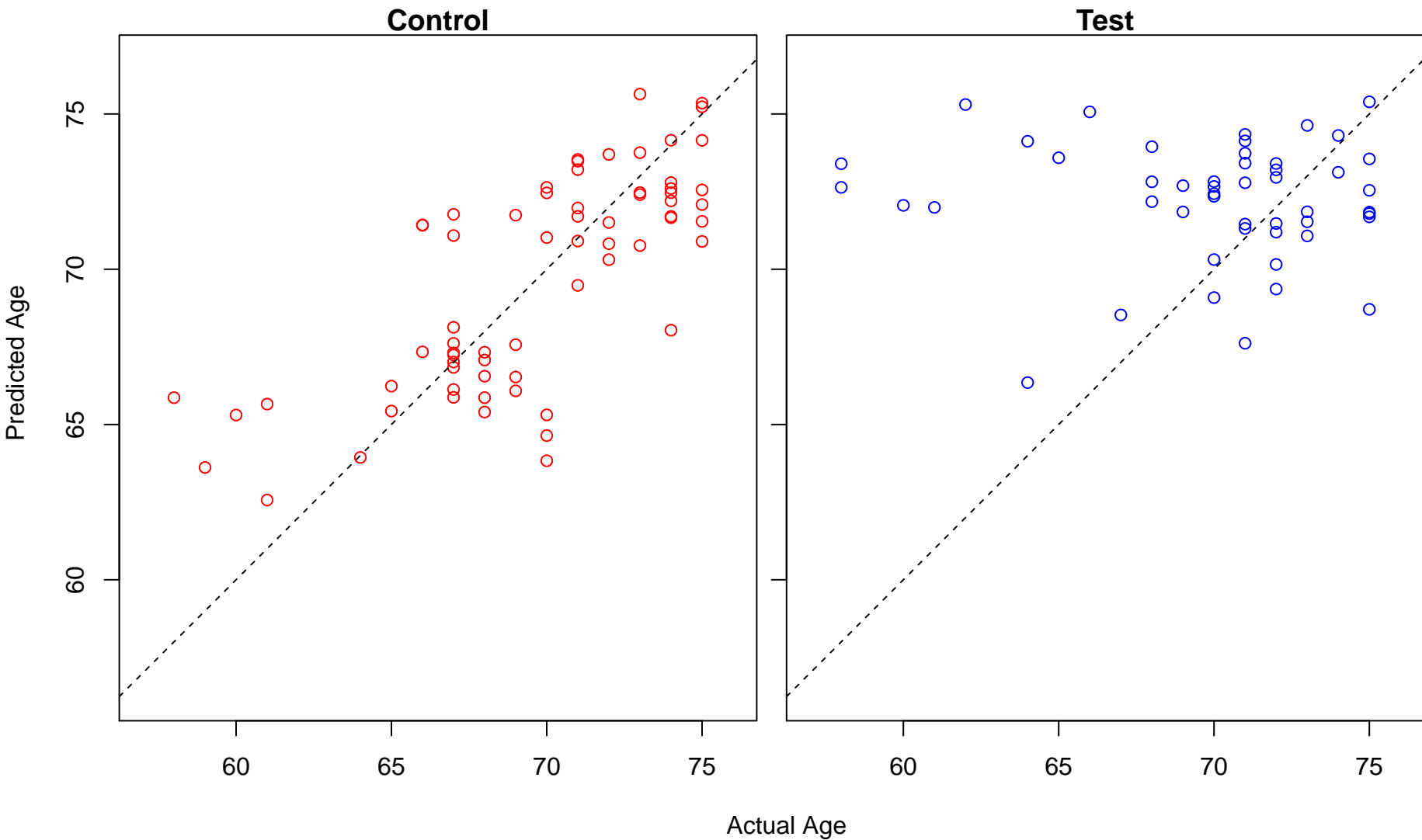


Test

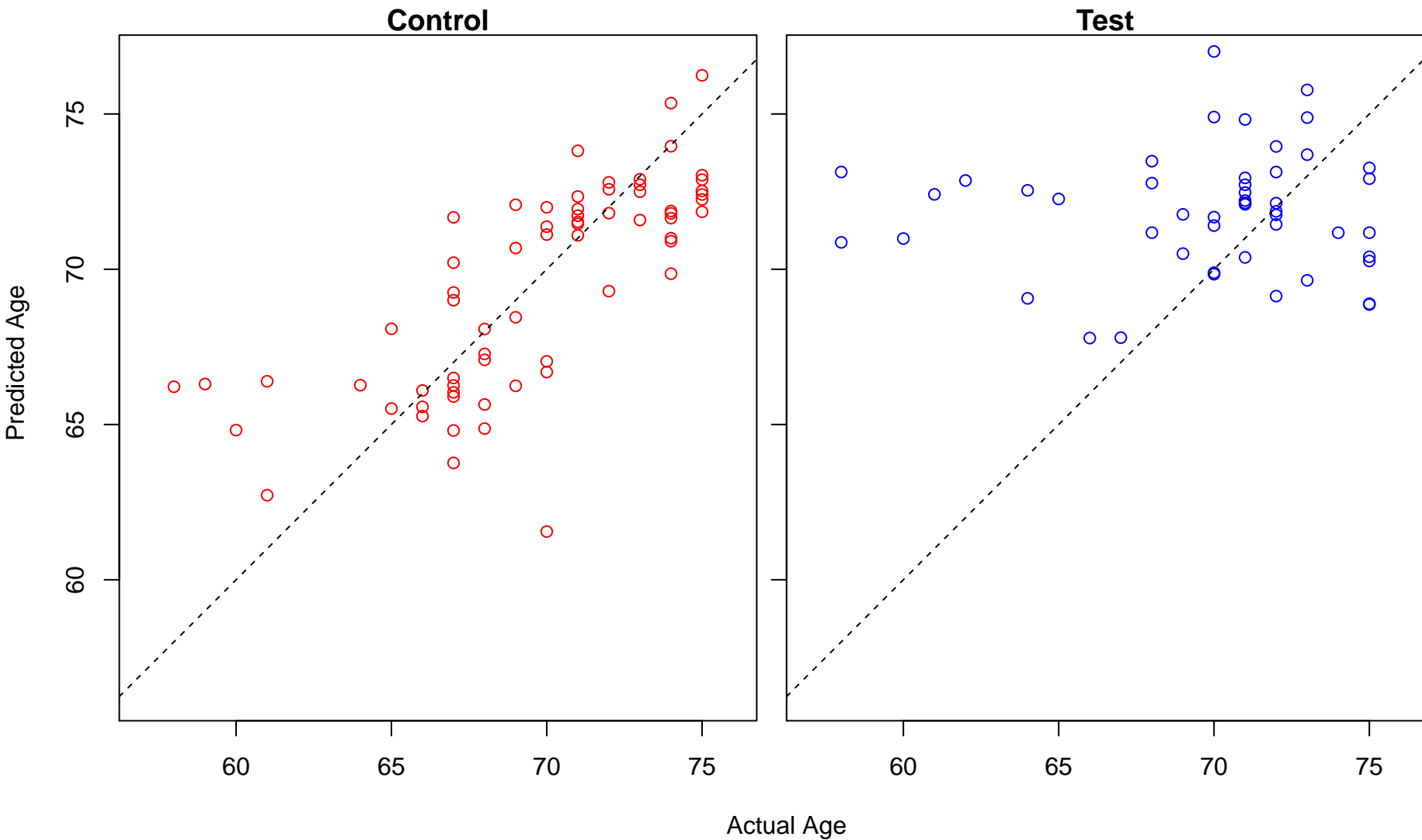


Actual Age

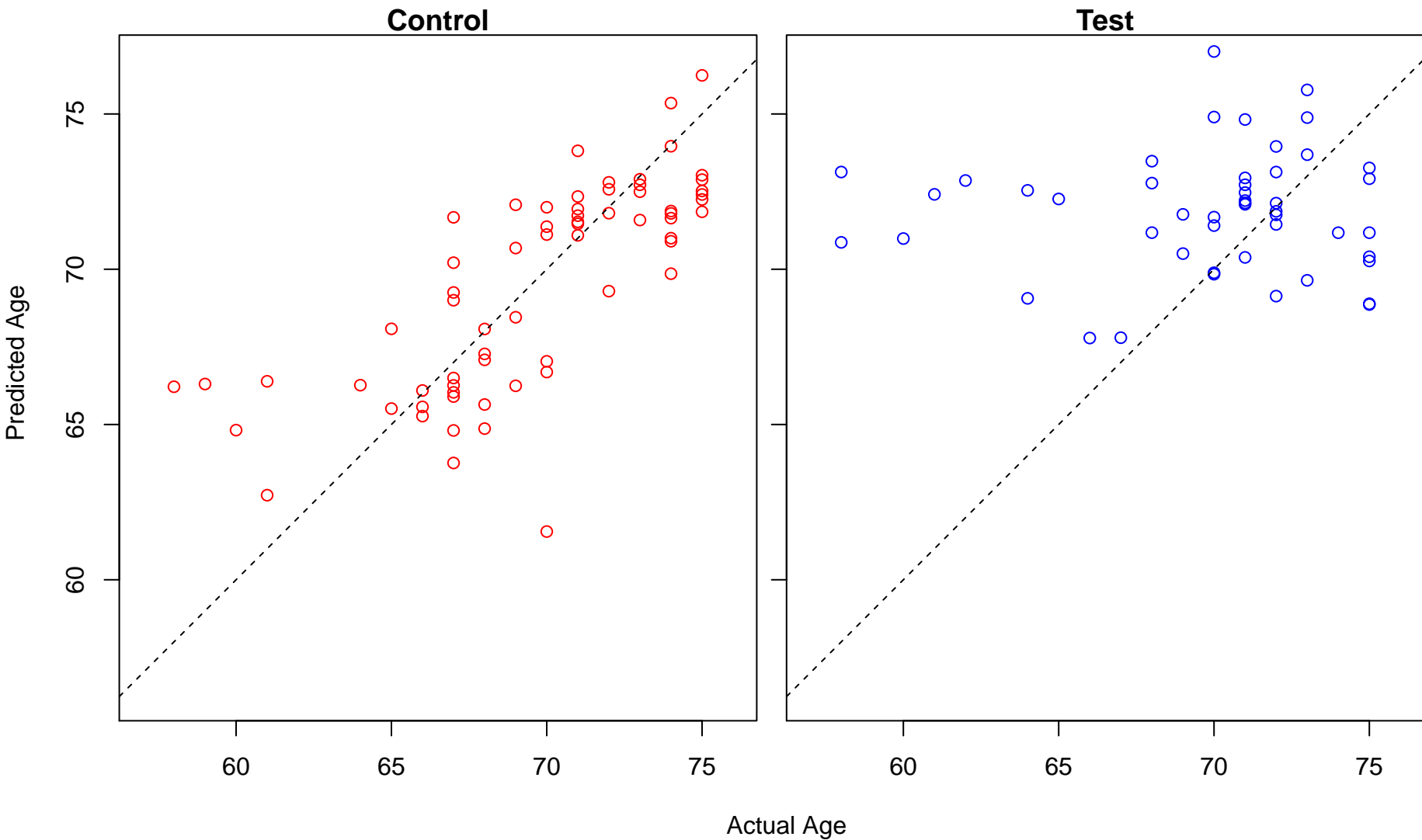
regulation of carbohydrate metabolic process (Score: 1.729888)



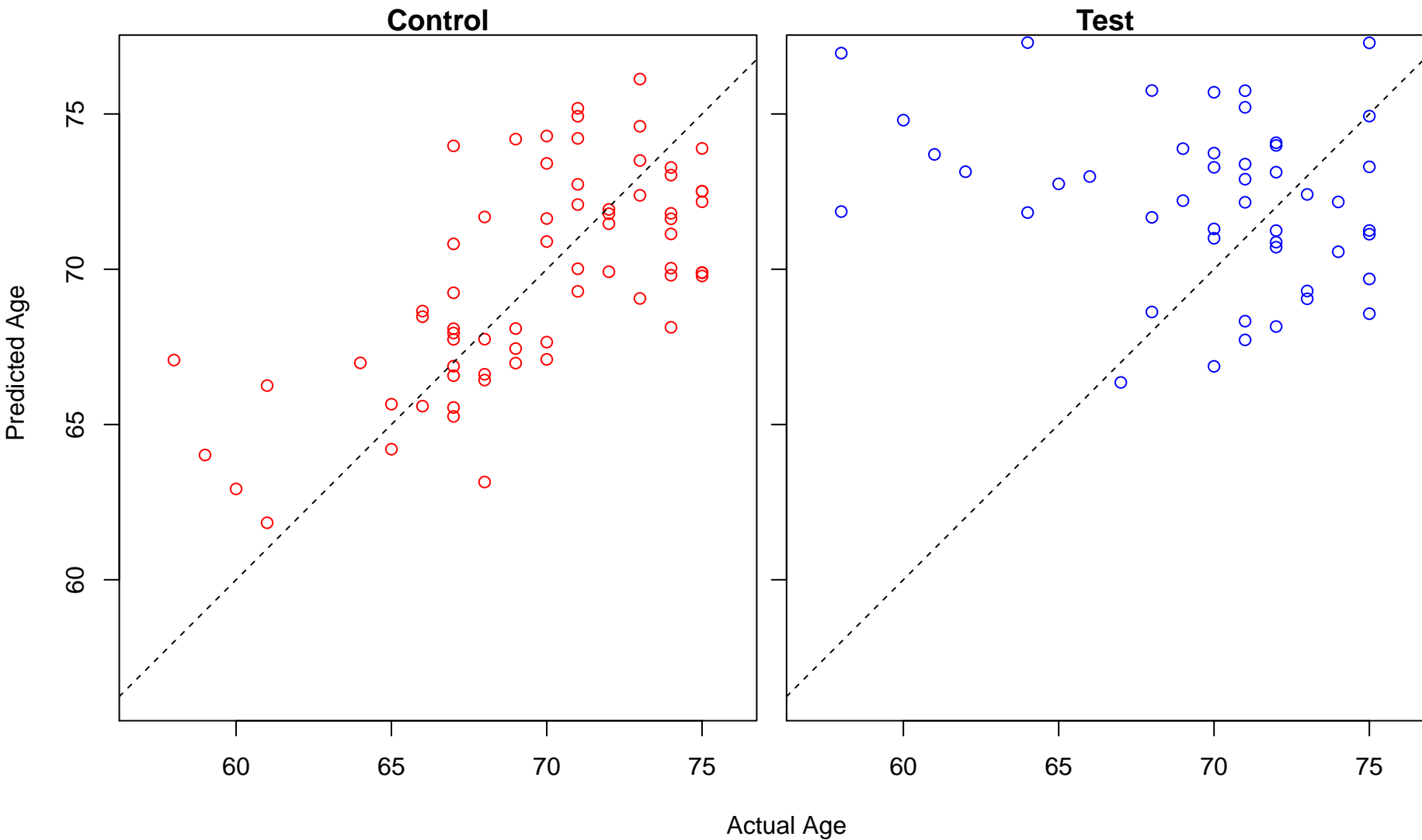
purine nucleoside monophosphate metabolic process (Score: 1.727362)



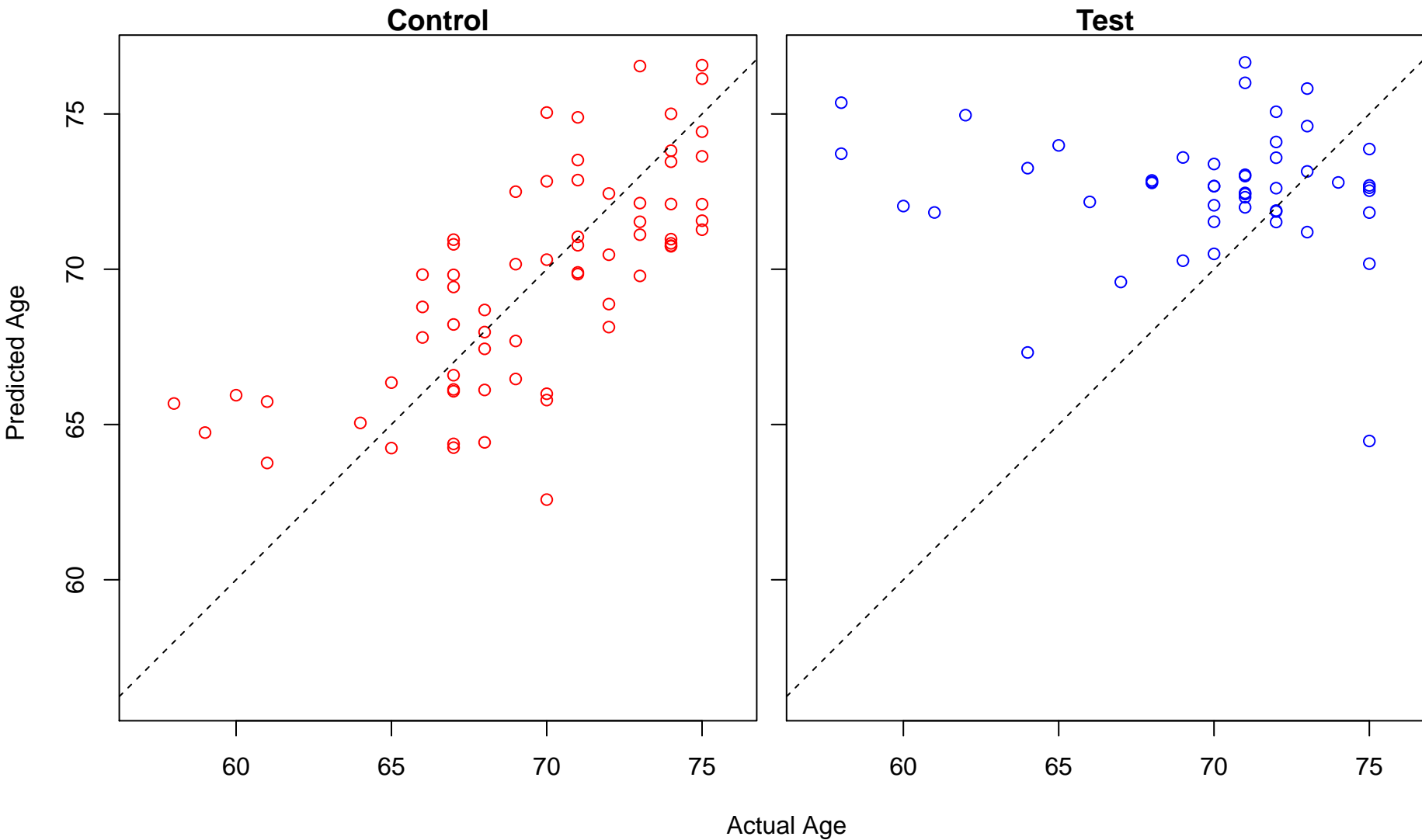
purine ribonucleoside monophosphate metabolic process (Score: 1.727362)



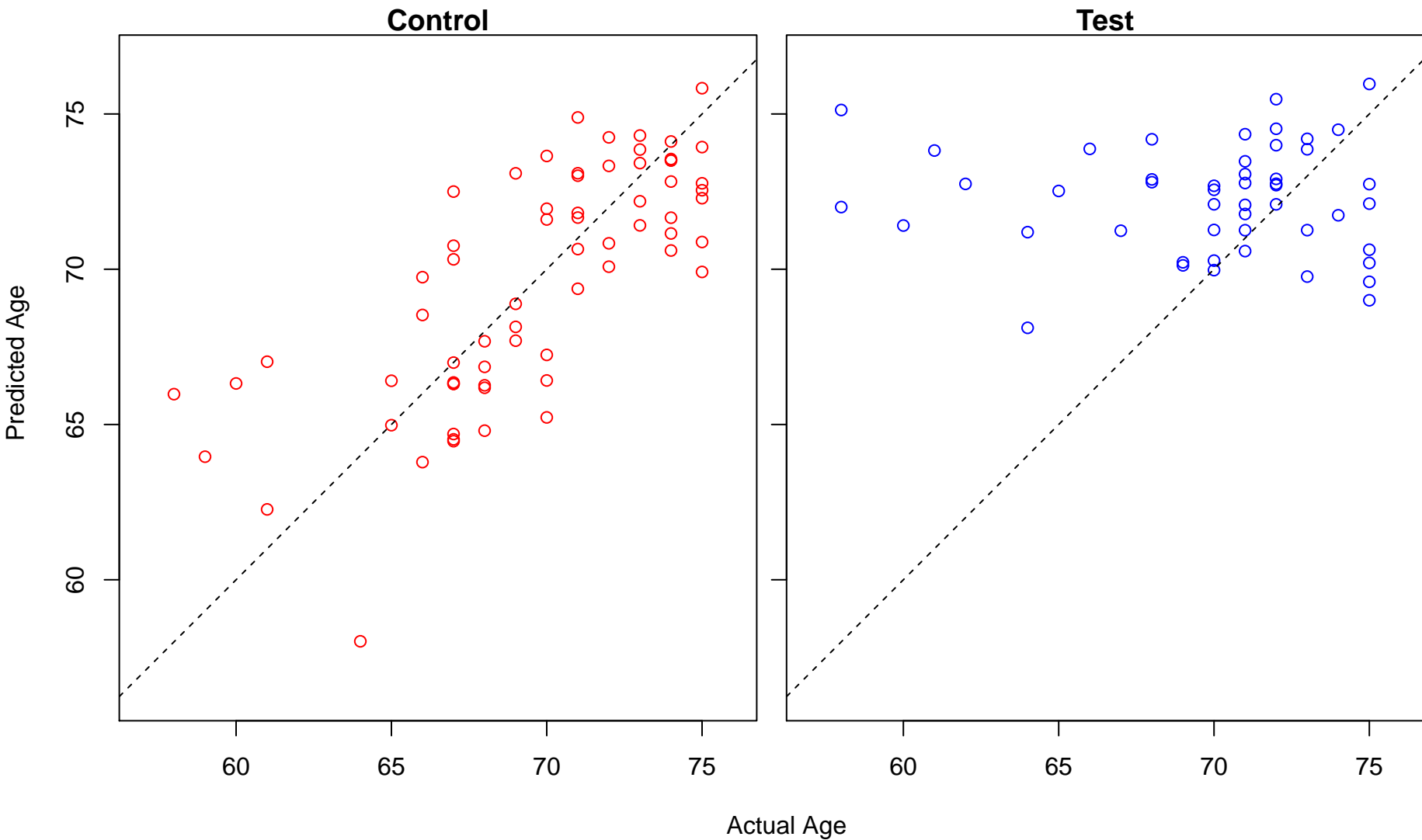
mitotic spindle organization (Score: 1.726684)



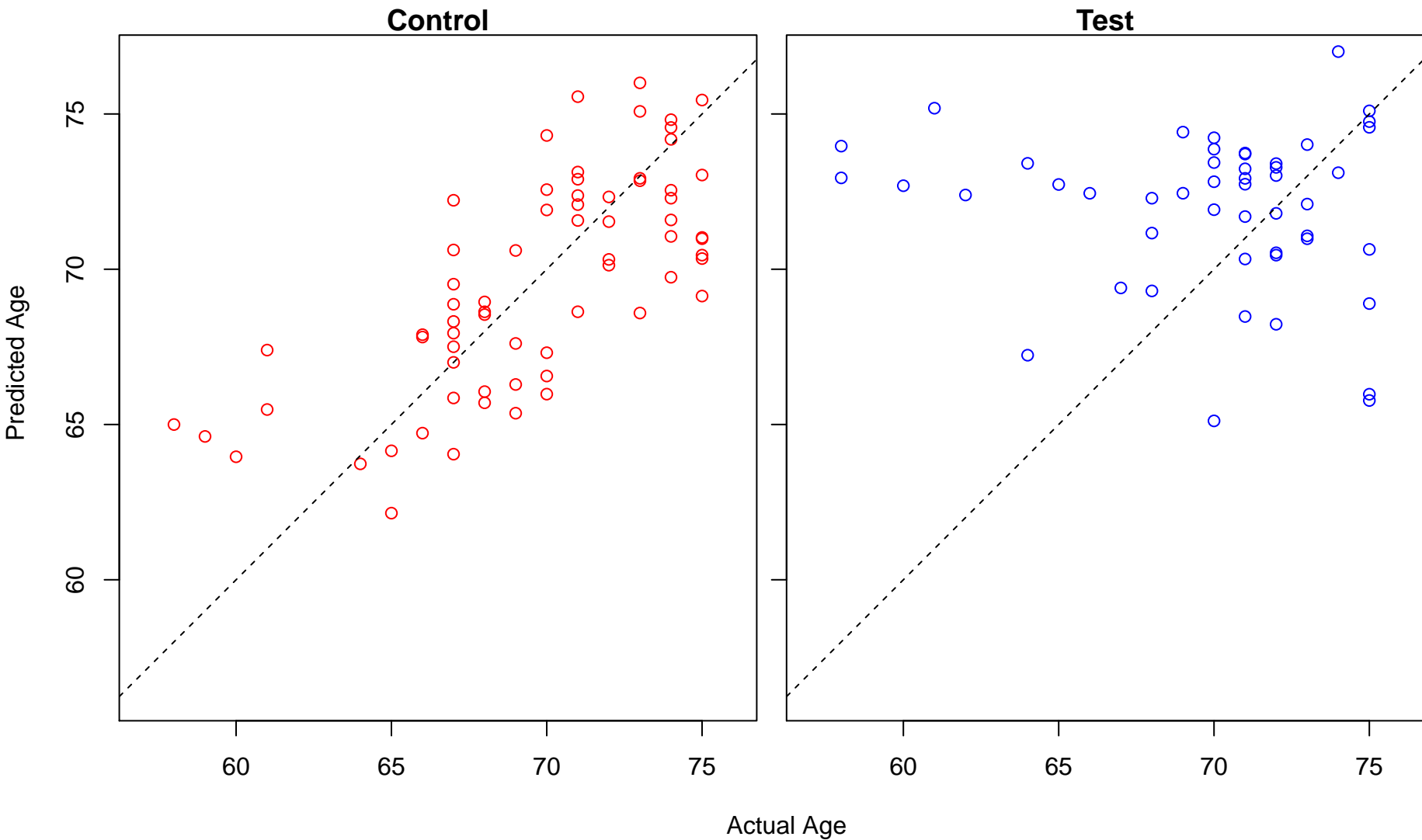
protein folding (Score: 1.726576)



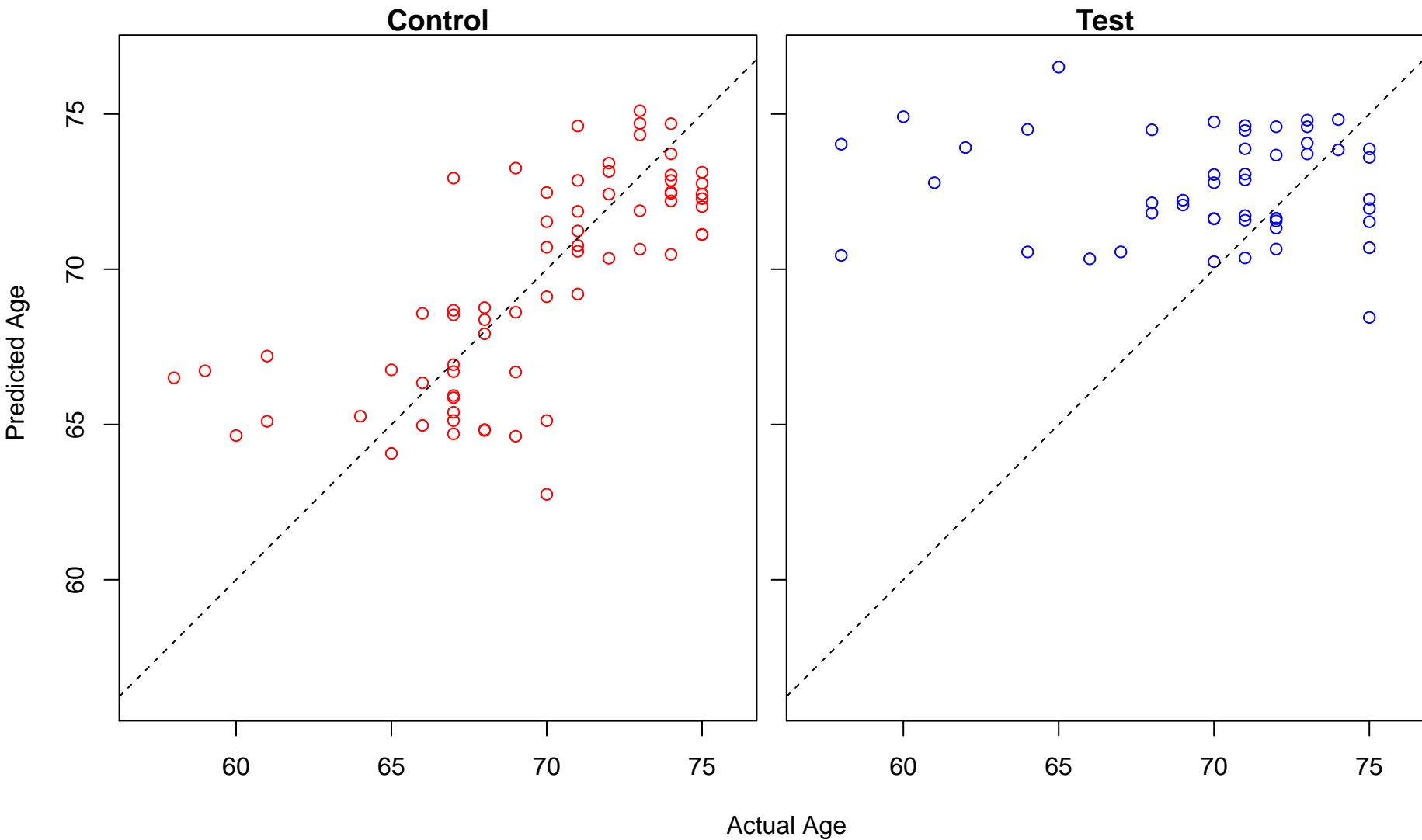
activation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 1.726427)



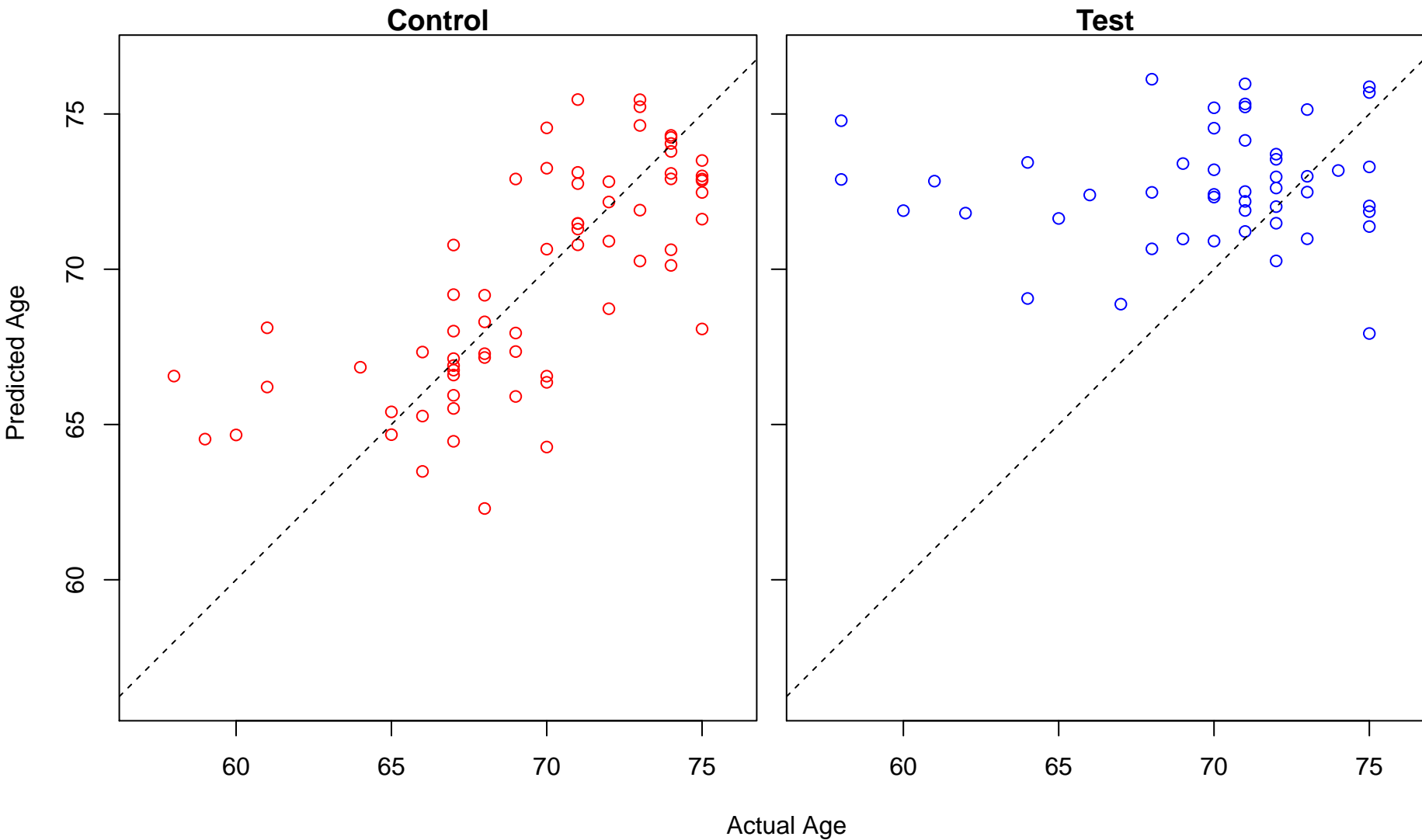
positive regulation of transmembrane transport (Score: 1.726235)



RNA localization (Score: 1.725792)

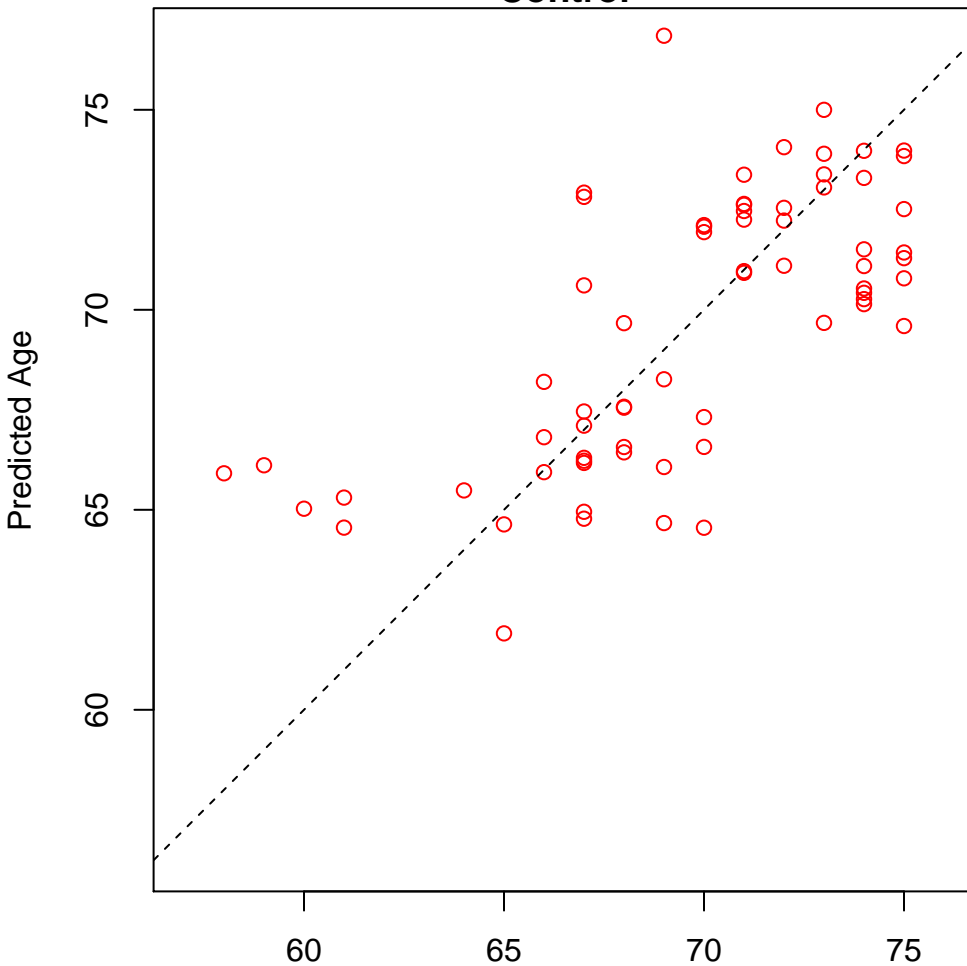


midbrain development (Score: 1.725165)

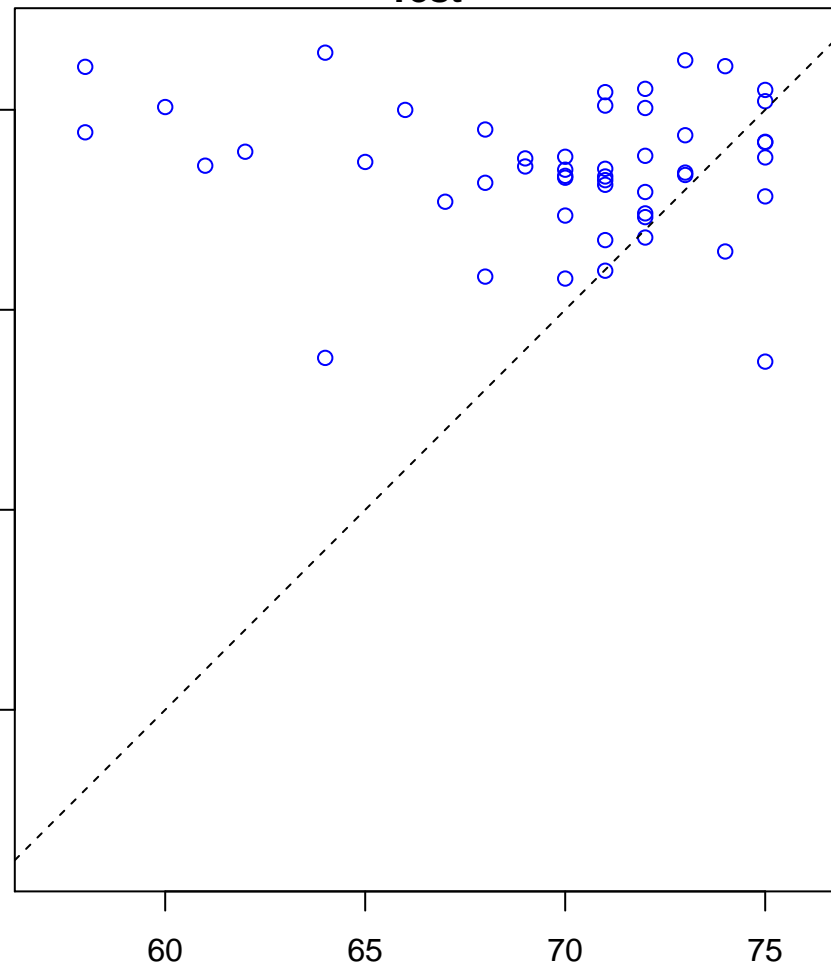


microtubule cytoskeleton organization (Score: 1.724959)

Control

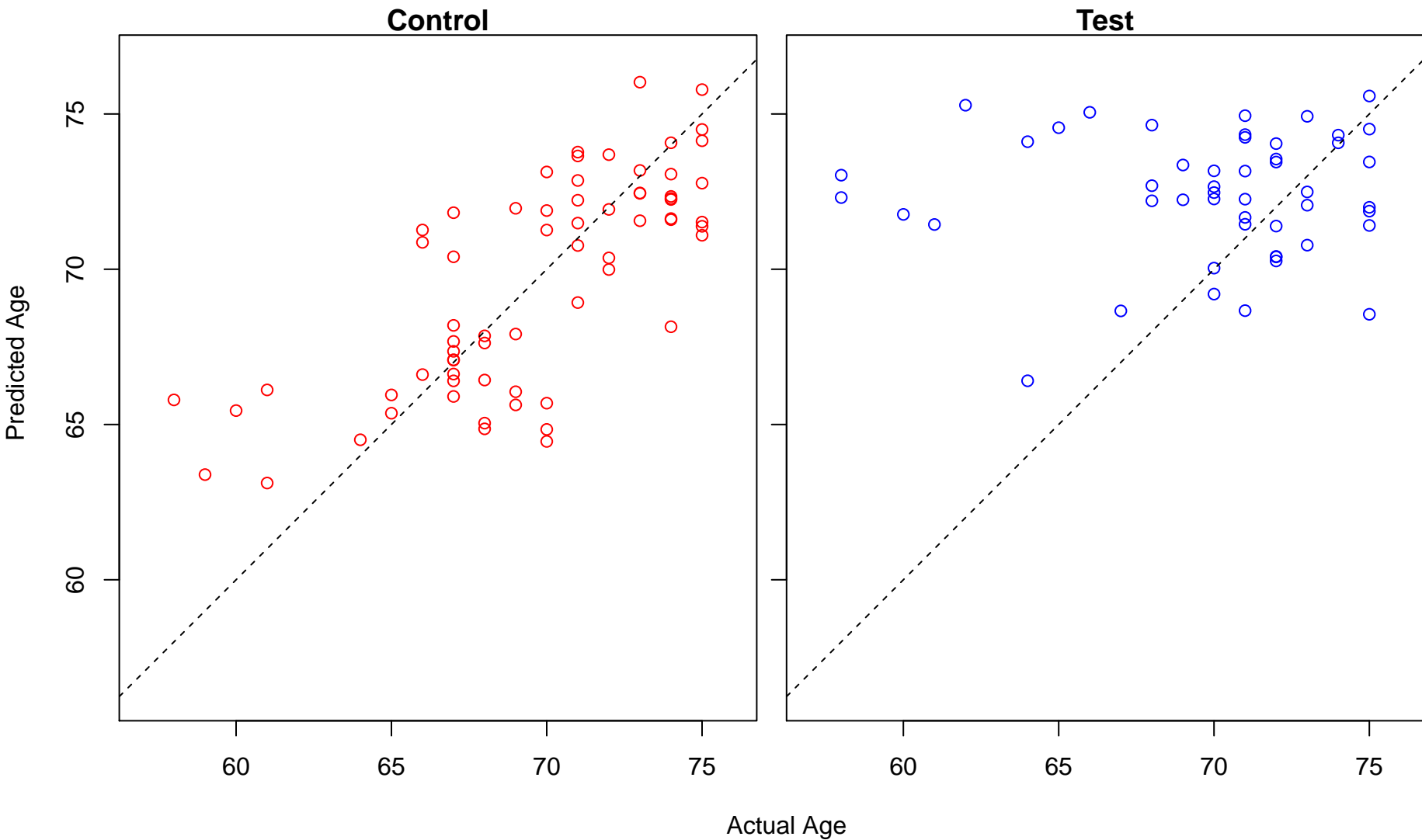


Test

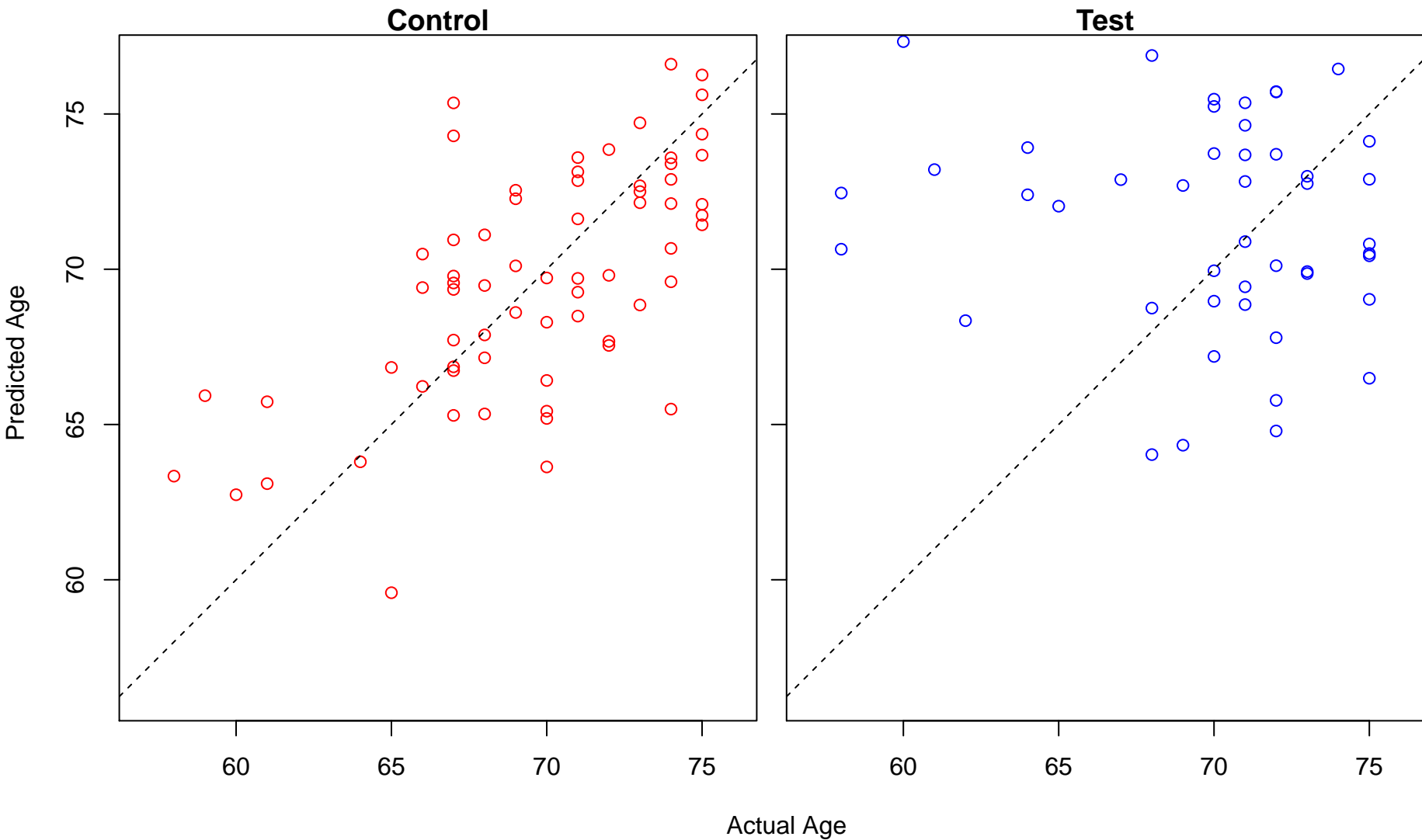


Actual Age

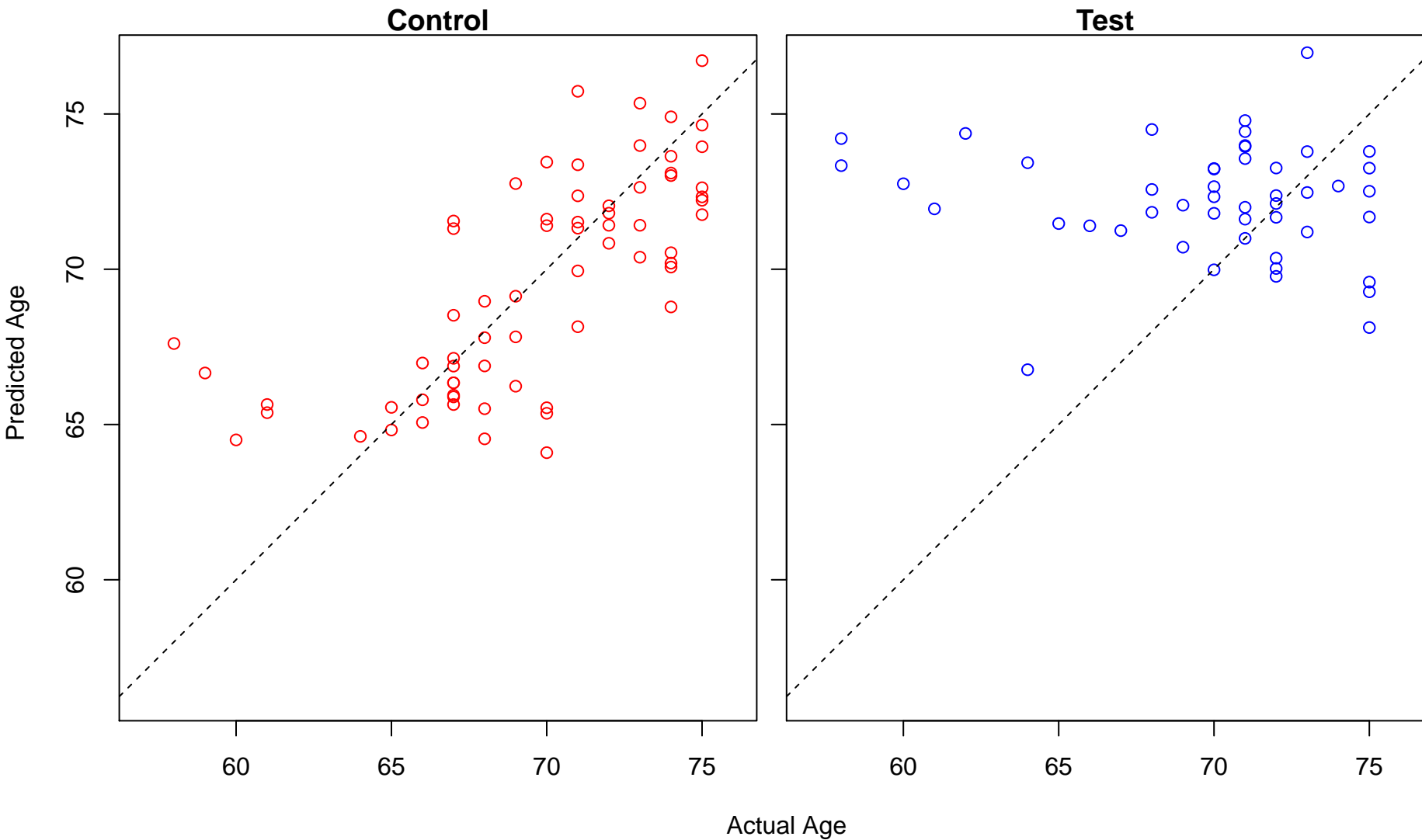
regulation of cellular carbohydrate metabolic process (Score: 1.724640)



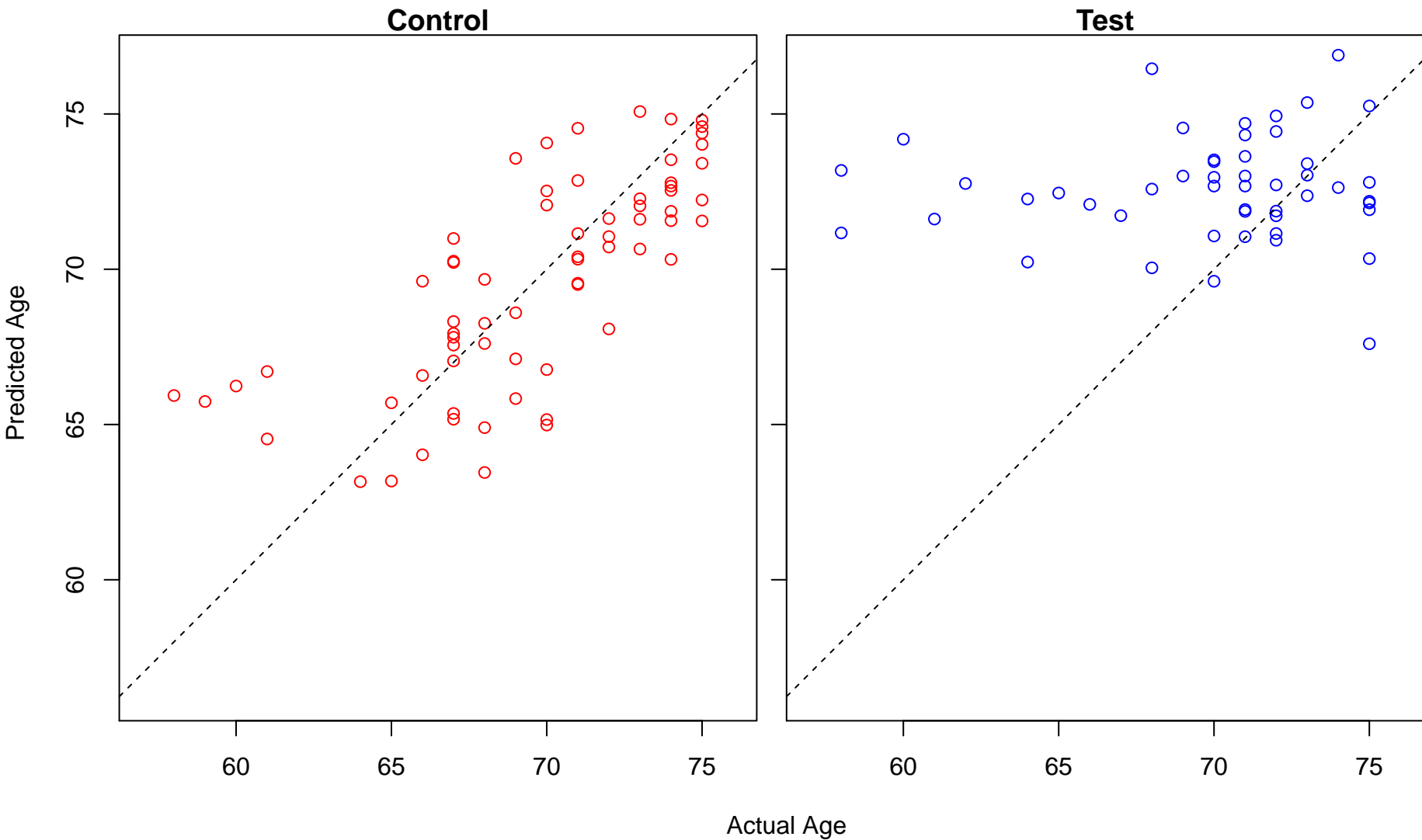
positive regulation of osteoblast differentiation (Score: 1.723733)



macroautophagy (Score: 1.722296)

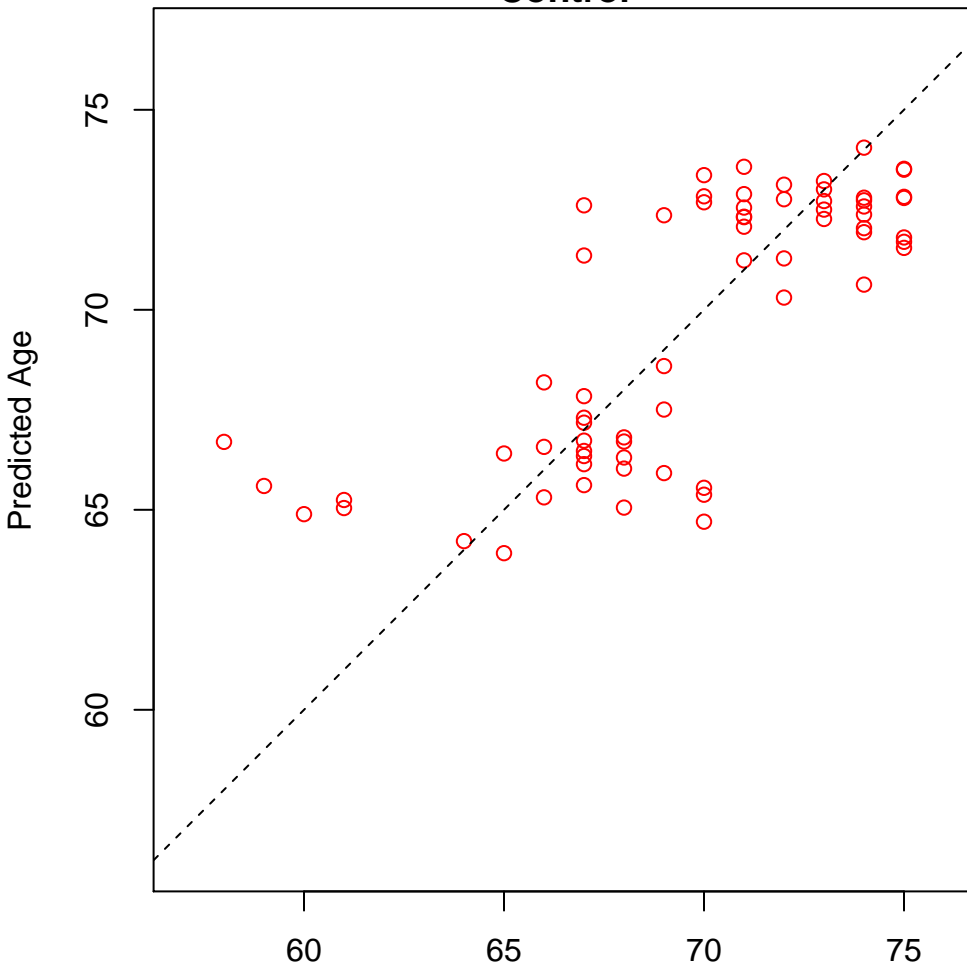


negative regulation of developmental process (Score: 1.720466)

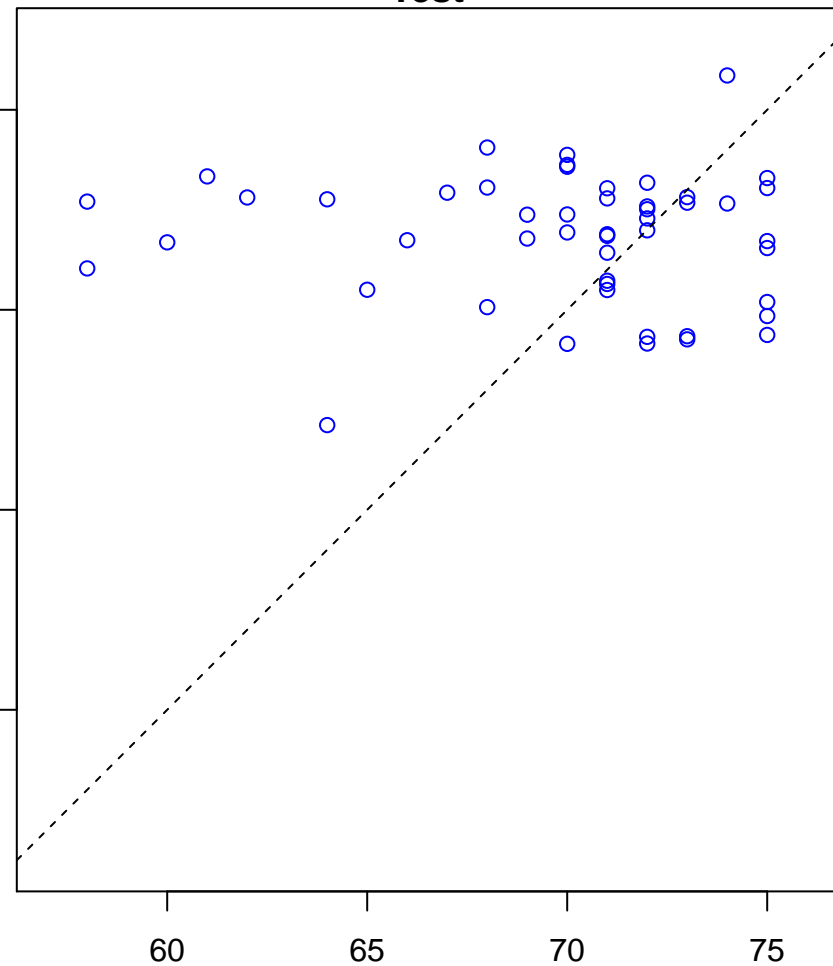


nuclear chromosome segregation (Score: 1.719620)

Control

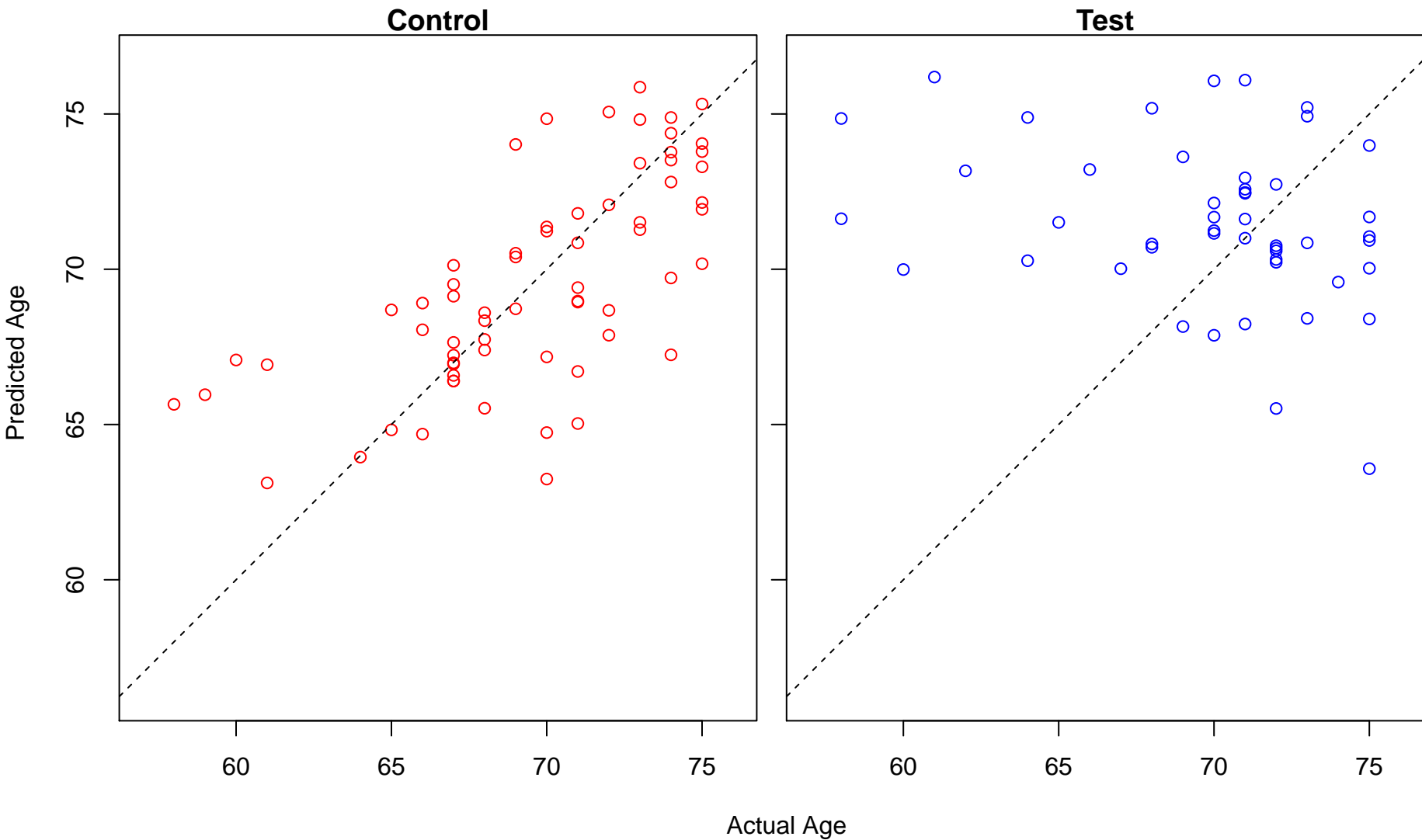


Test

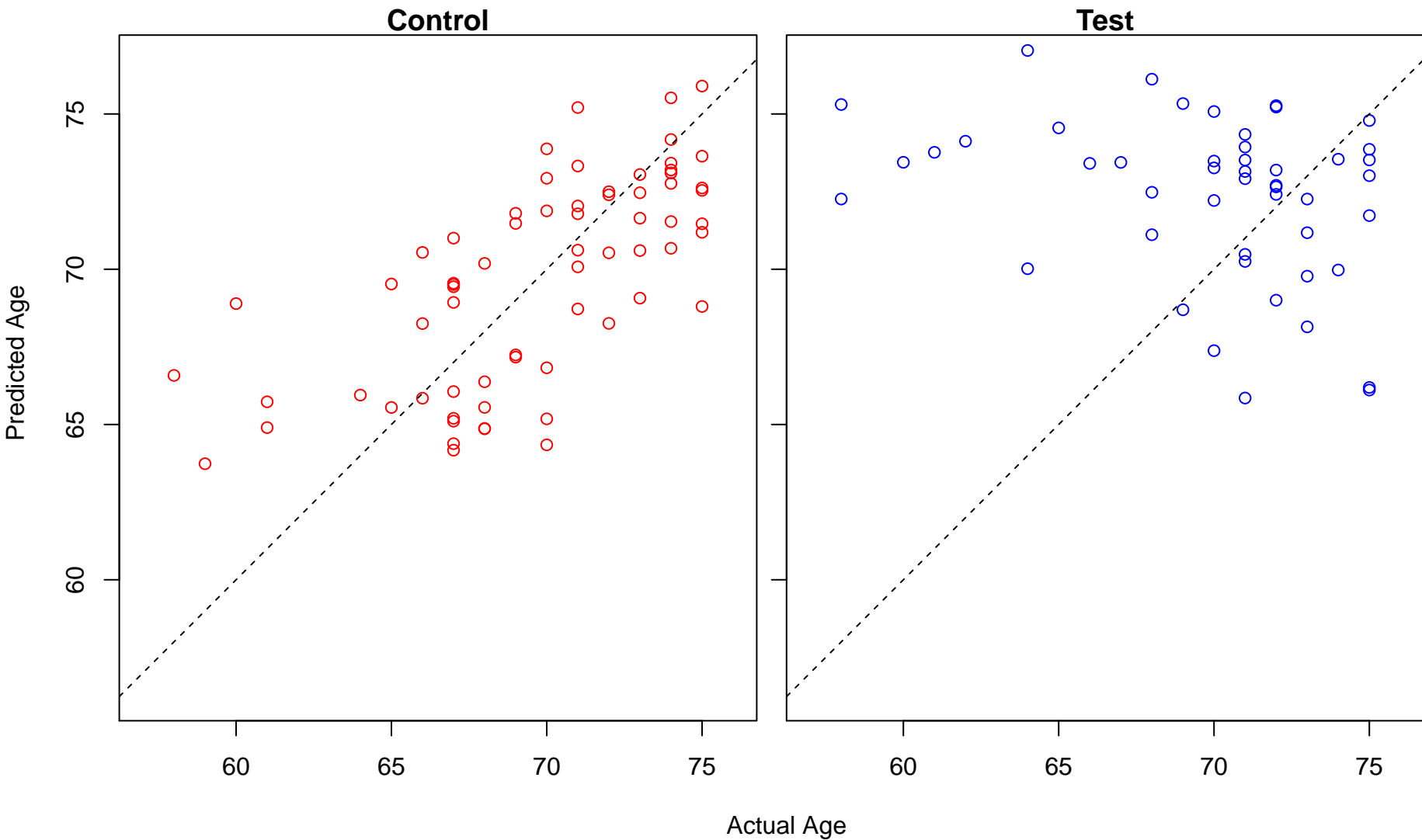


Actual Age

regulation of lymphocyte apoptotic process (Score: 1.717929)

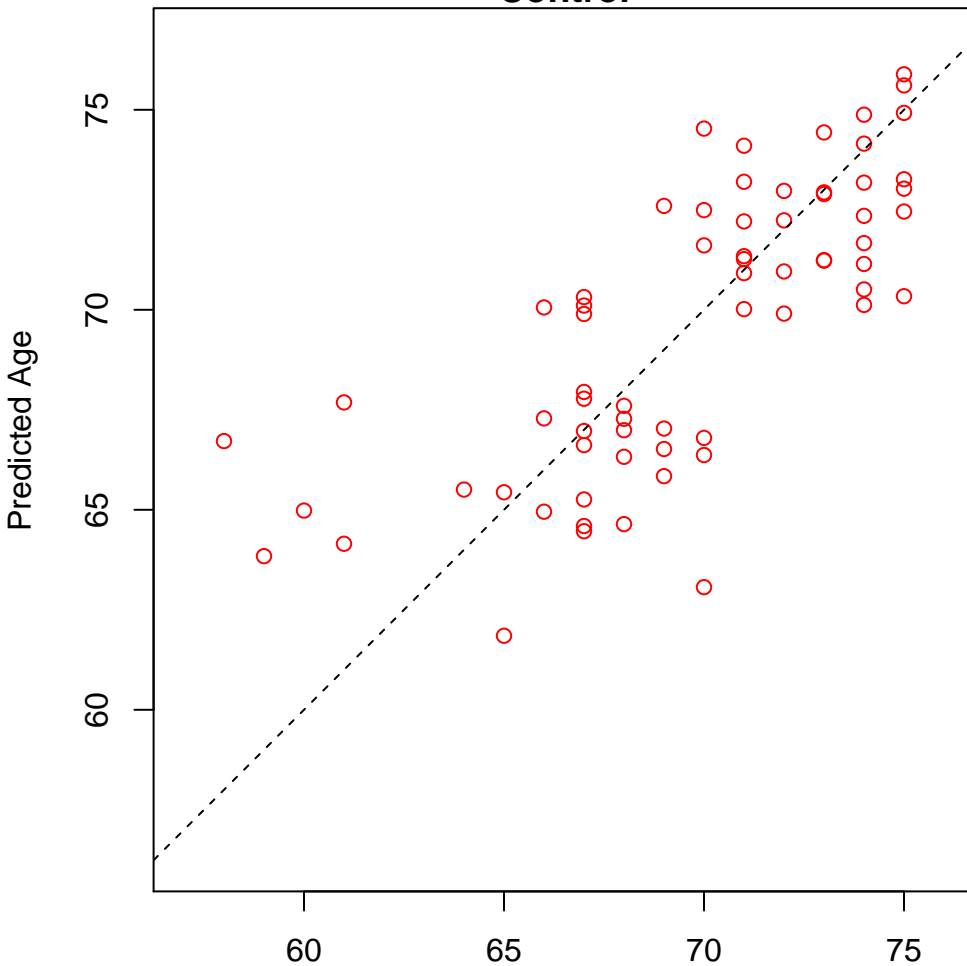


regulation of Notch signaling pathway (Score: 1.717680)

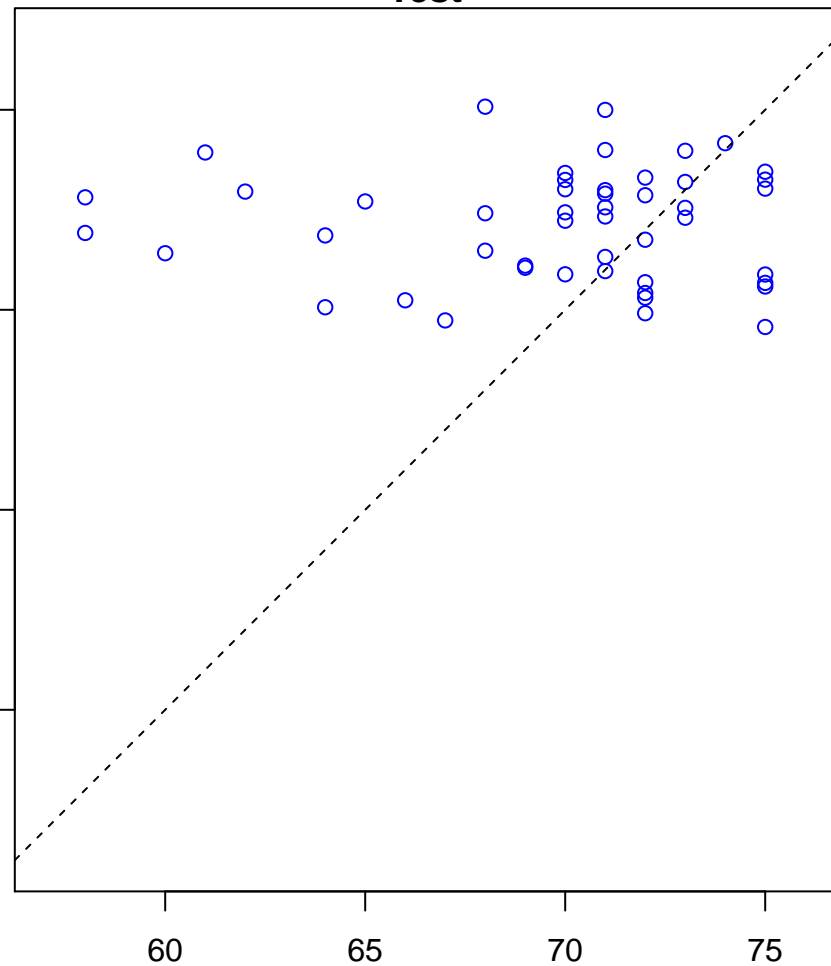


positive regulation of cell cycle process (Score: 1.717061)

Control

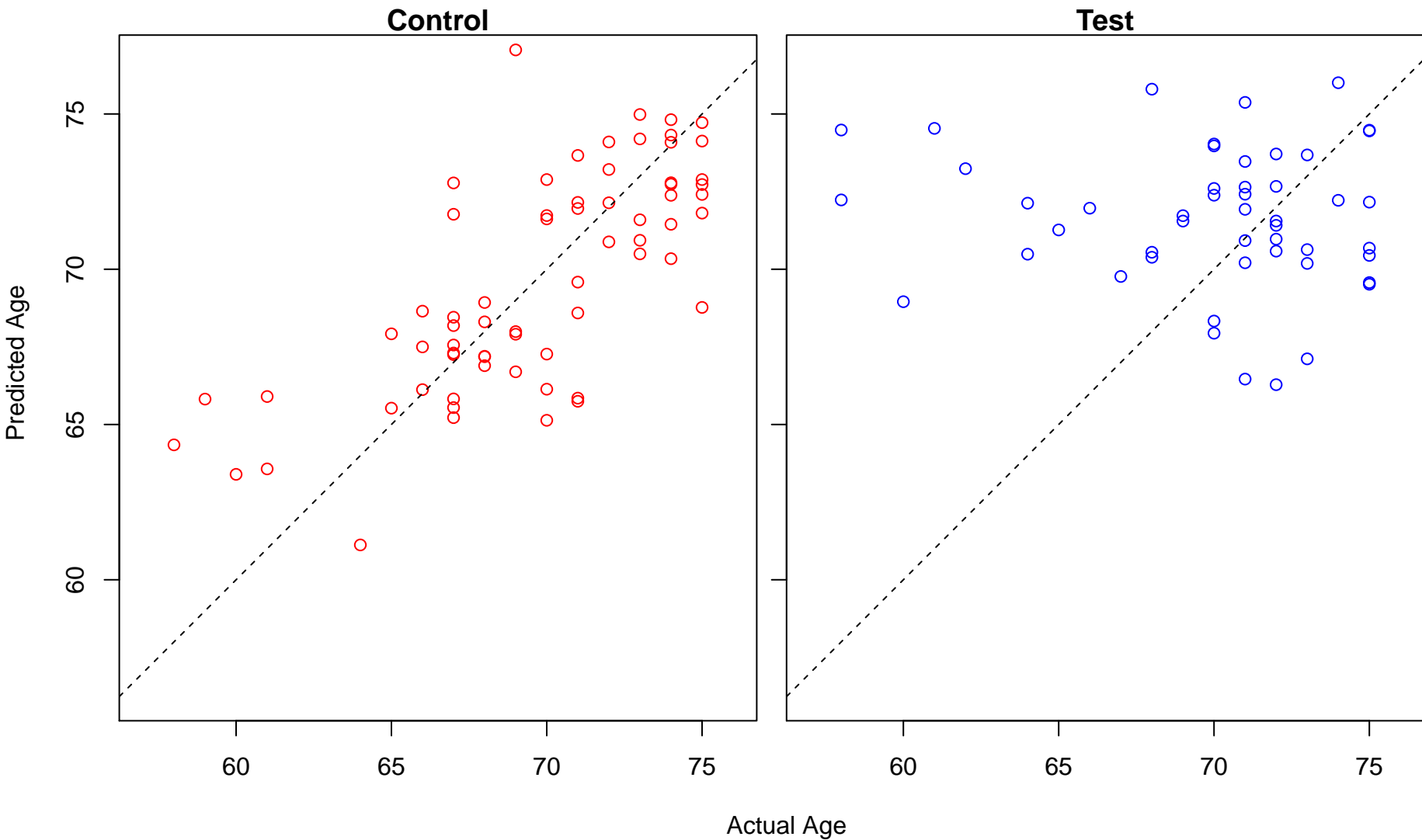


Test

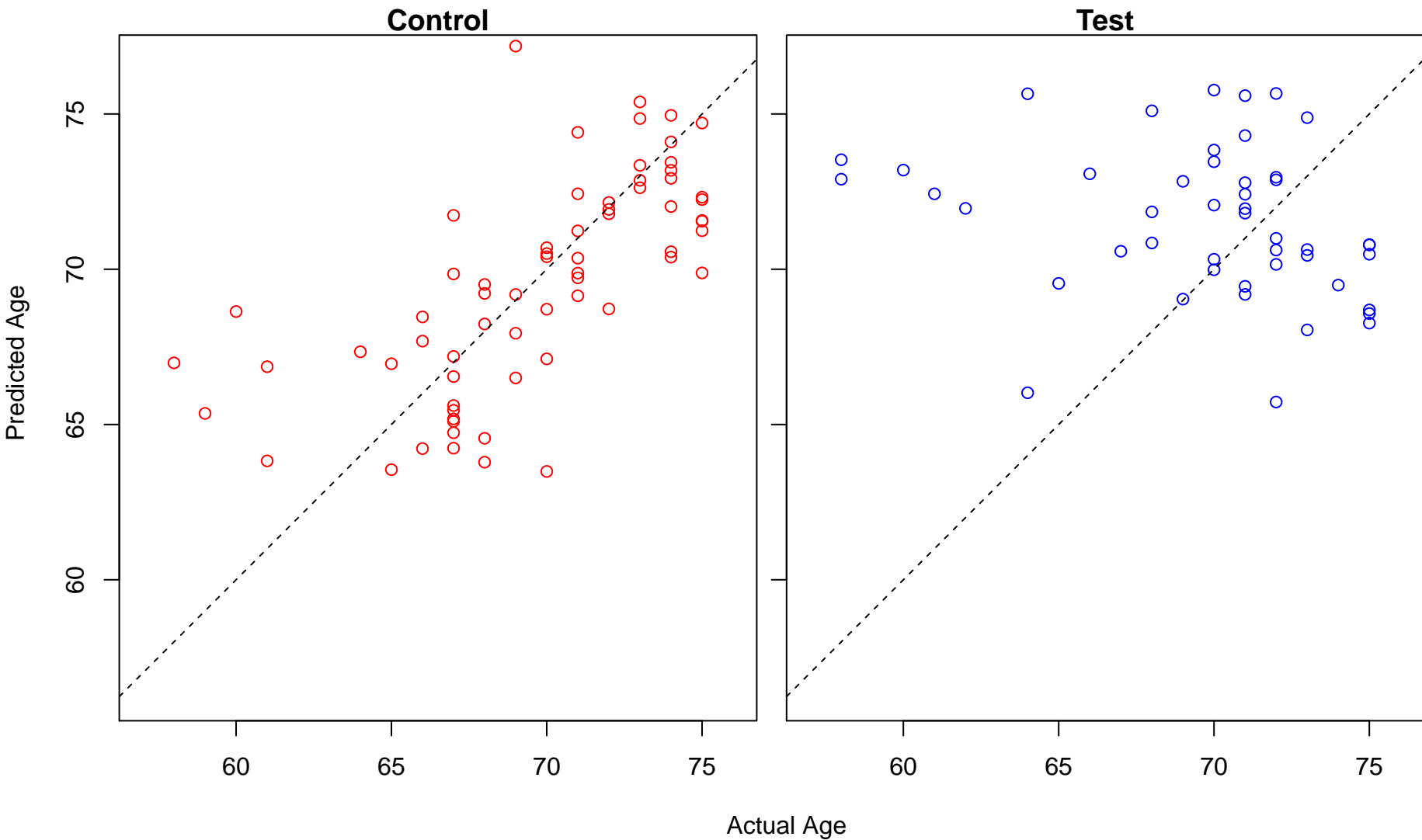


Actual Age

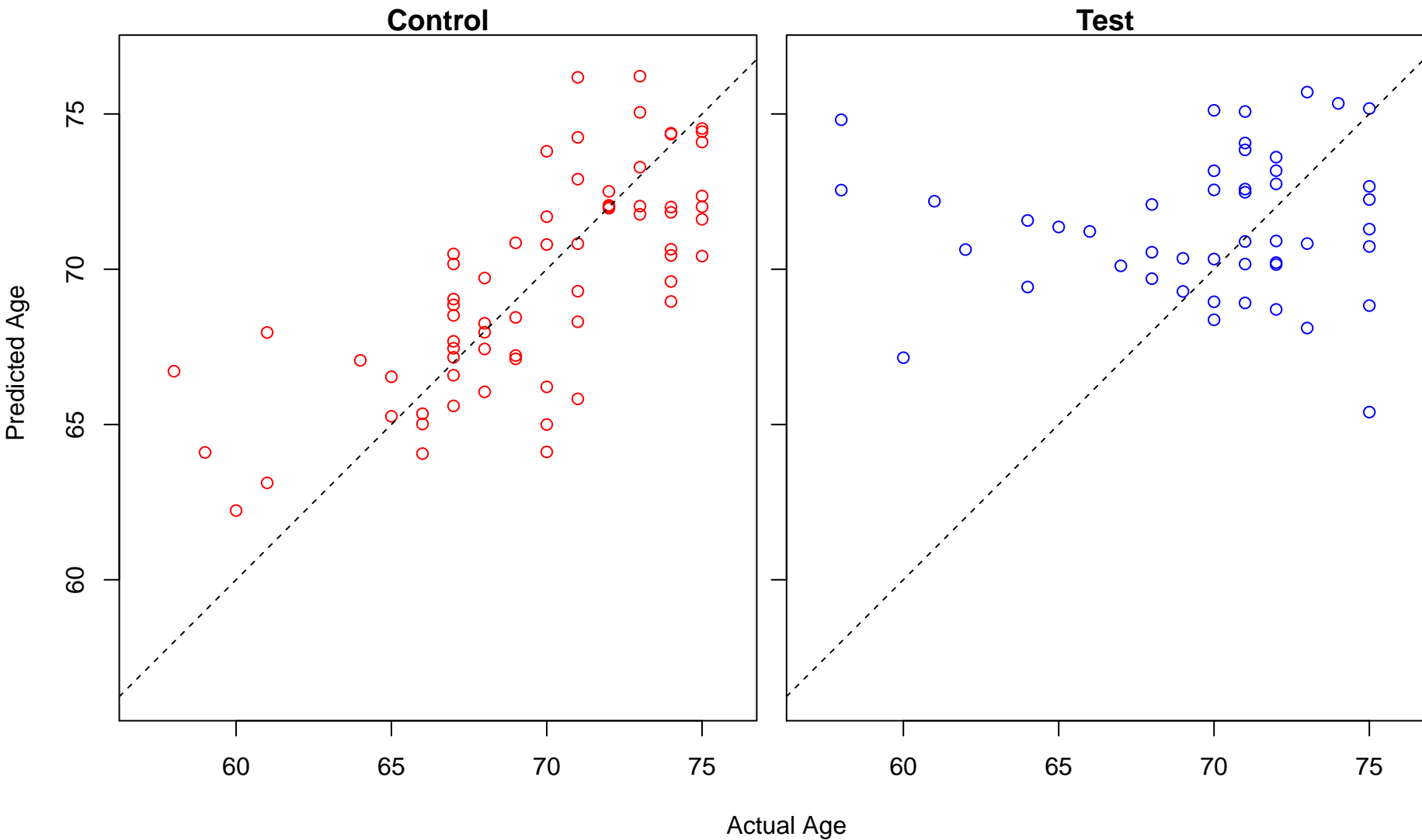
regulation of membrane potential (Score: 1.716945)



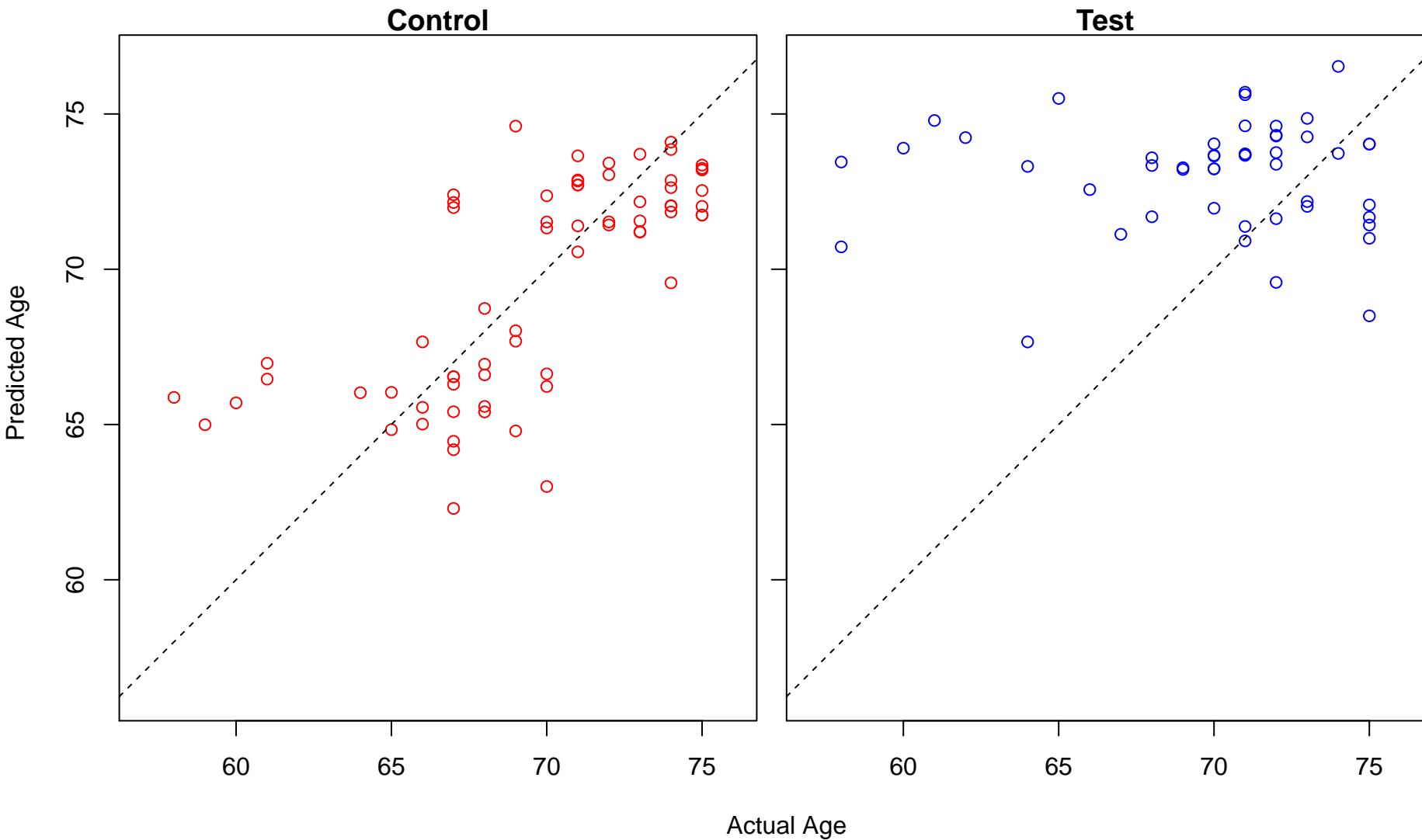
negative regulation of cell activation (Score: 1.716841)



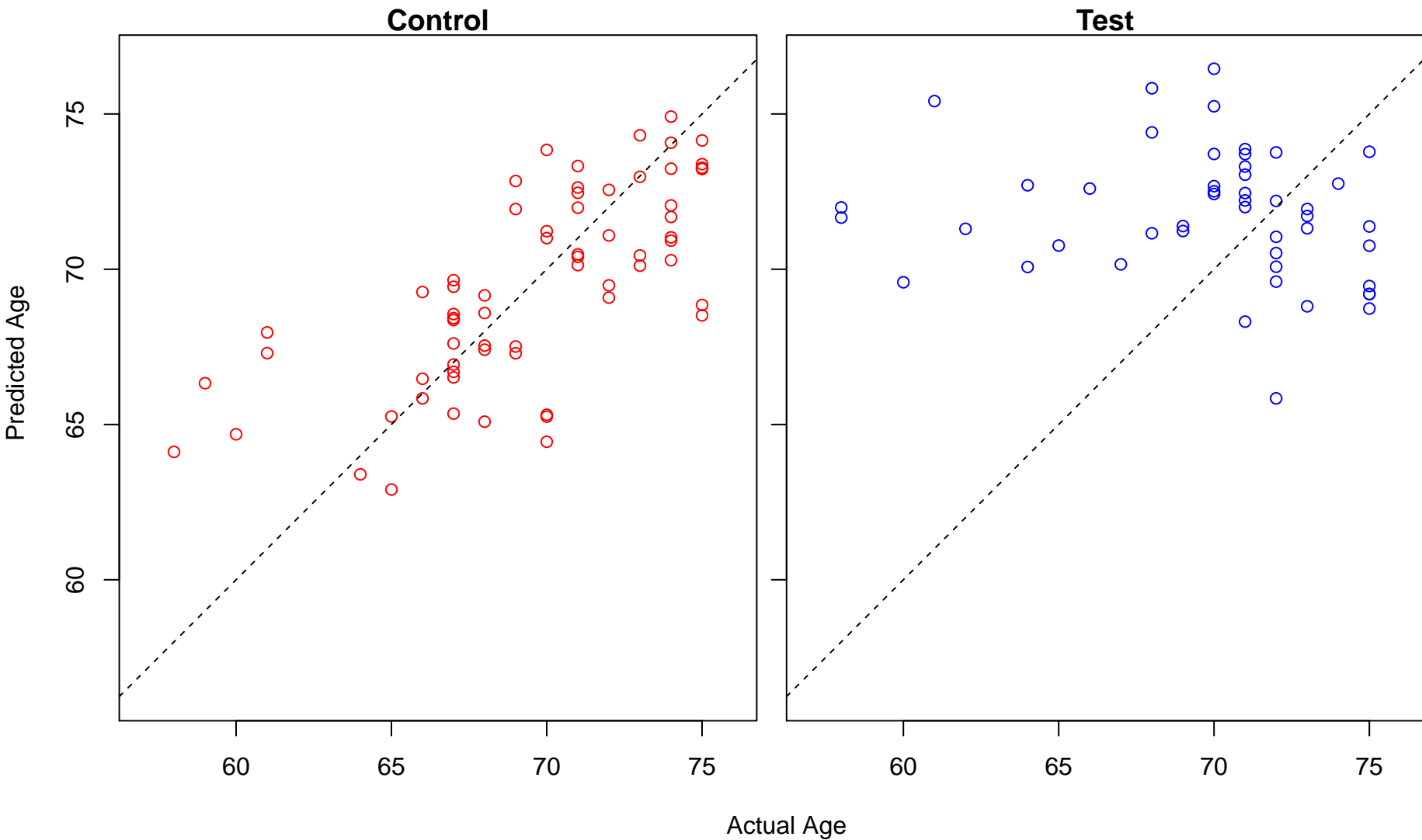
regulation of cation channel activity (Score: 1.716723)



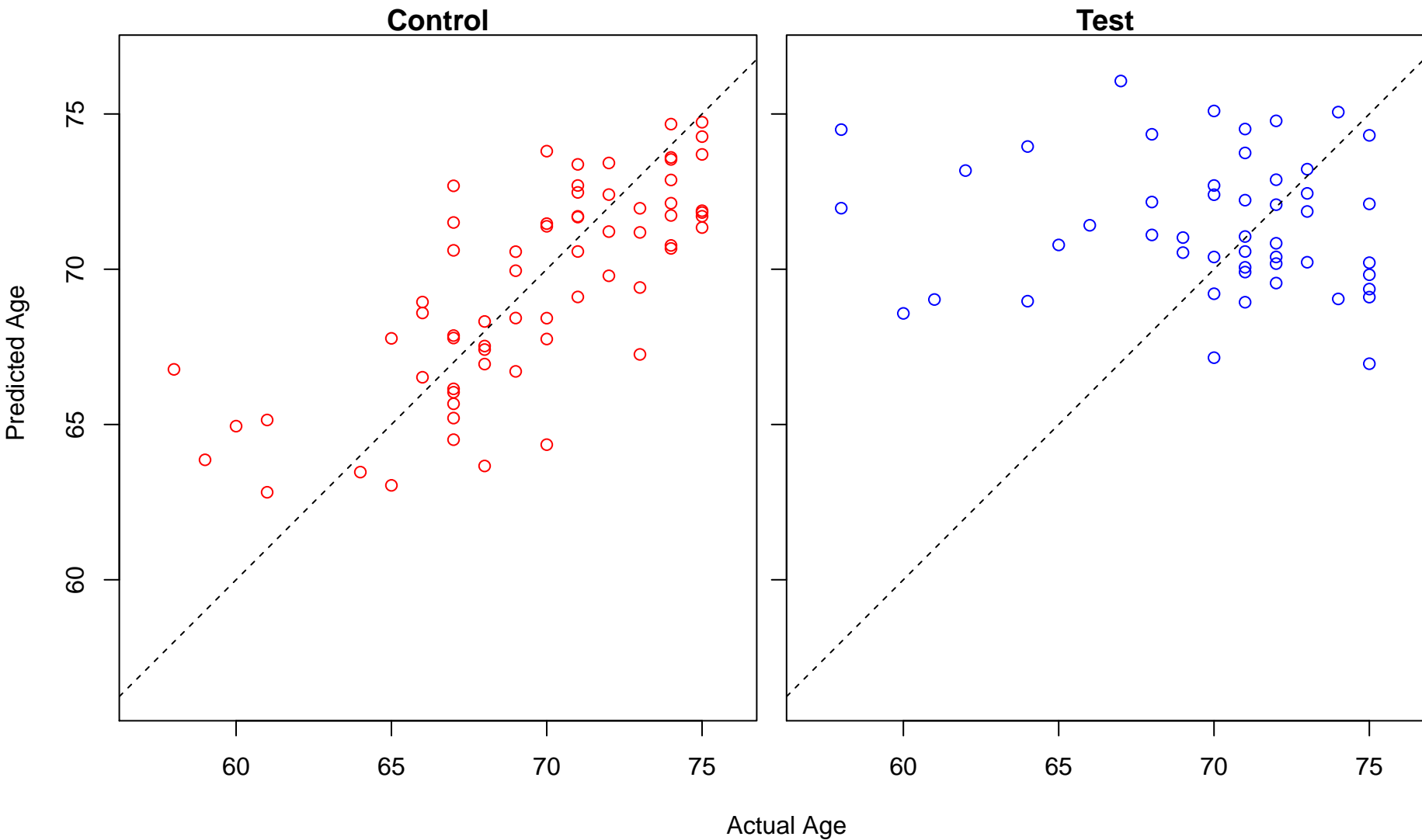
RNA catabolic process (Score: 1.715140)



extracellular matrix disassembly (Score: 1.714626)

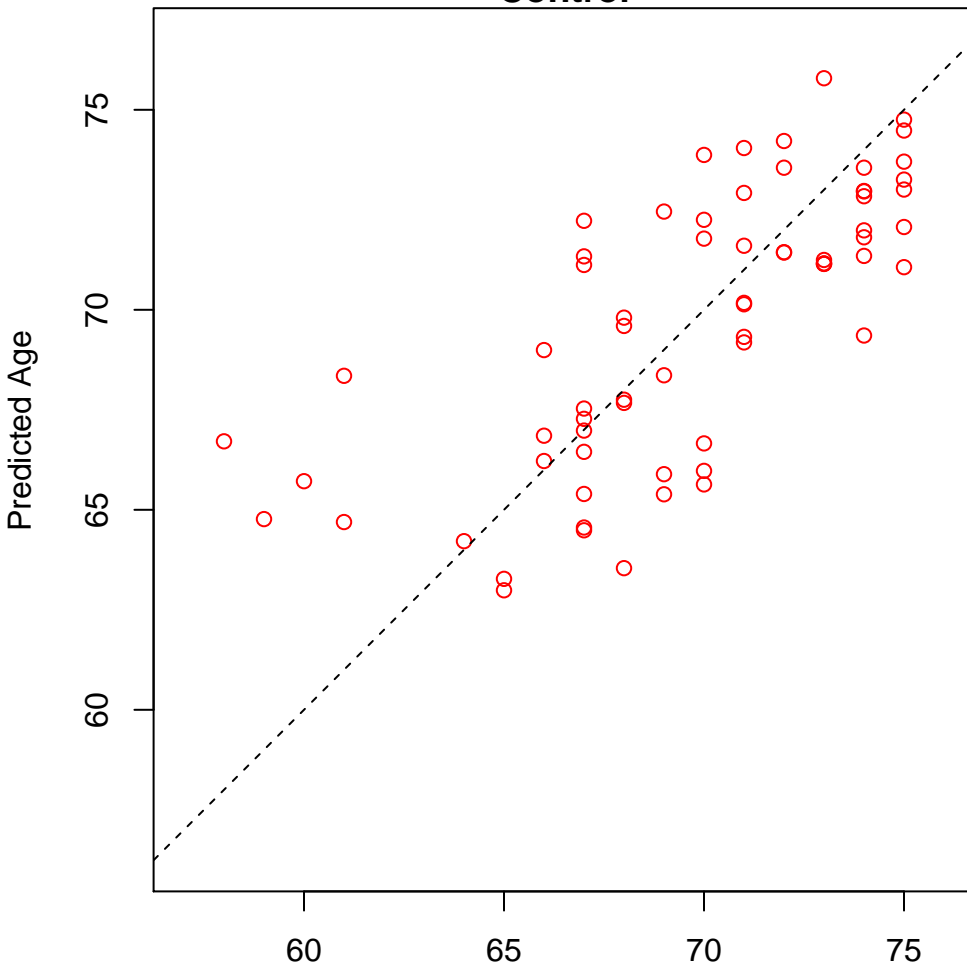


negative regulation of mRNA metabolic process (Score: 1.714592)

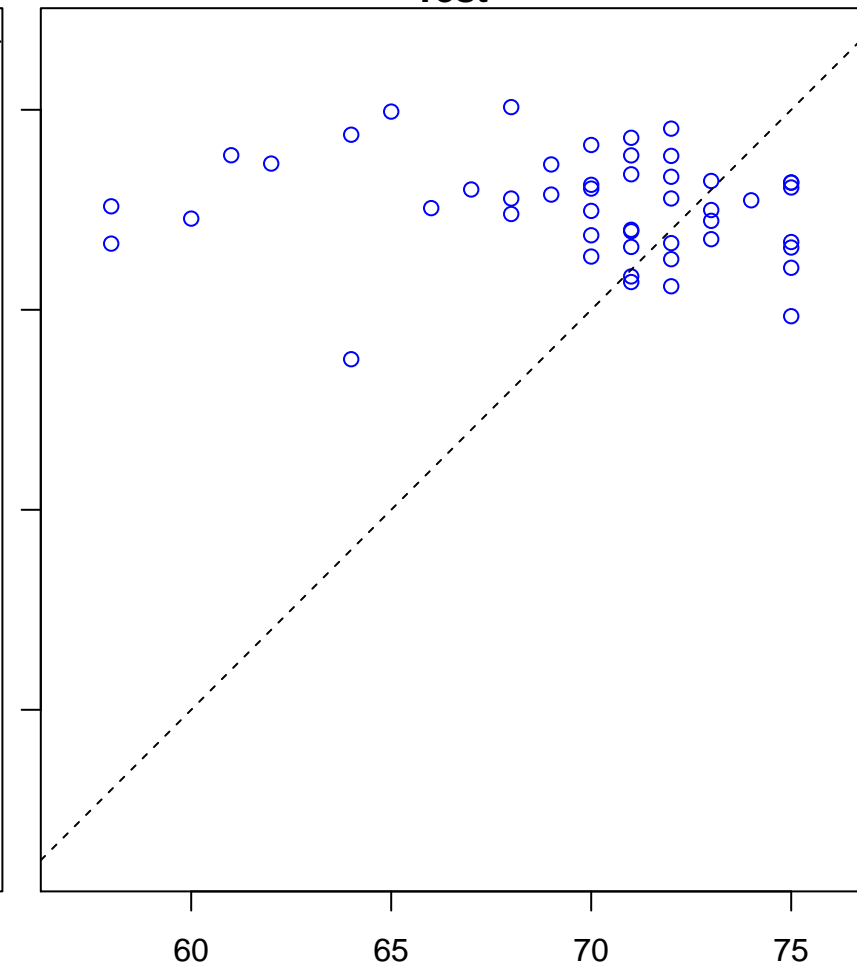


regulation of gene expression, epigenetic (Score: 1.714469)

Control

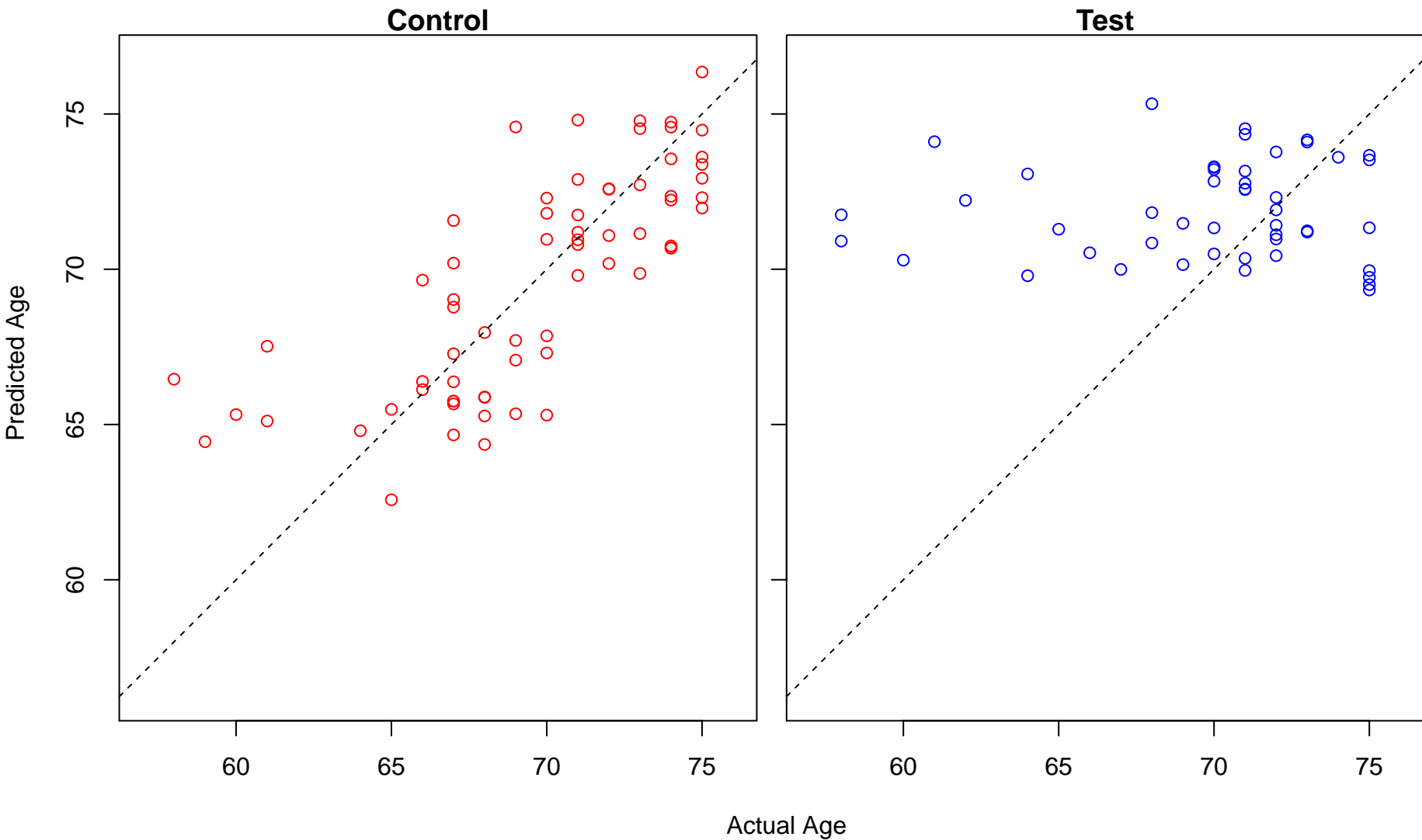


Test

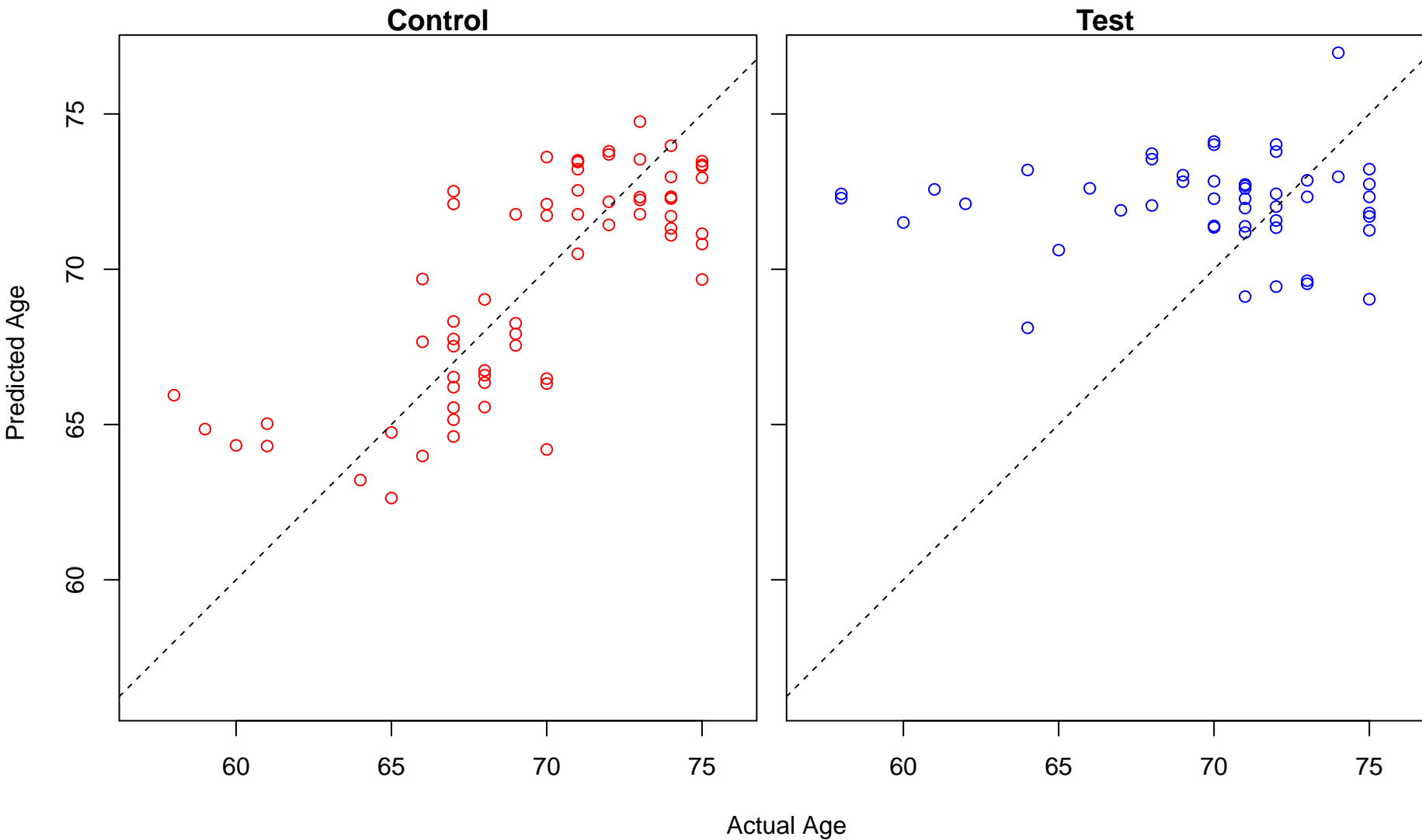


Actual Age

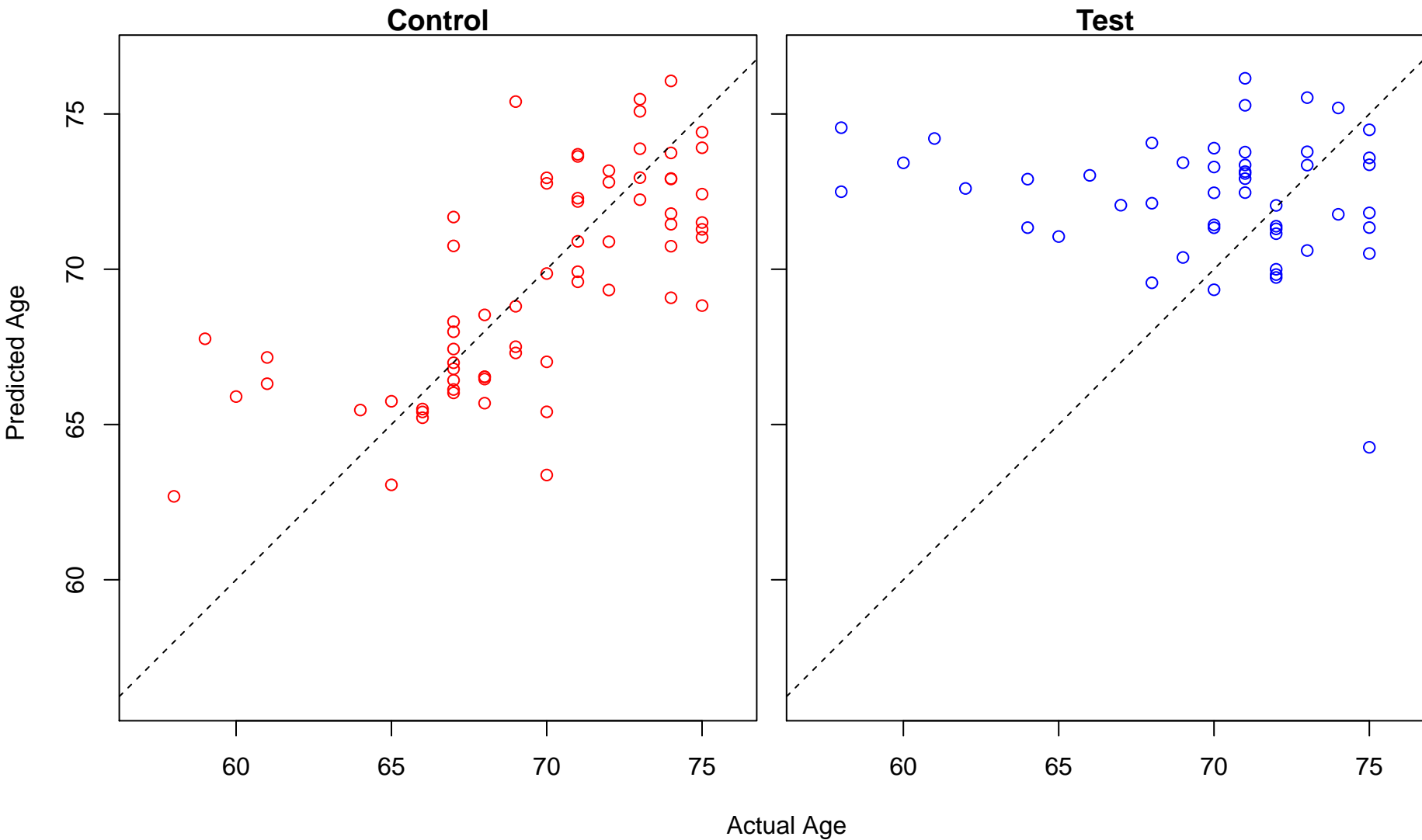
polyamine metabolic process (Score: 1.714125)



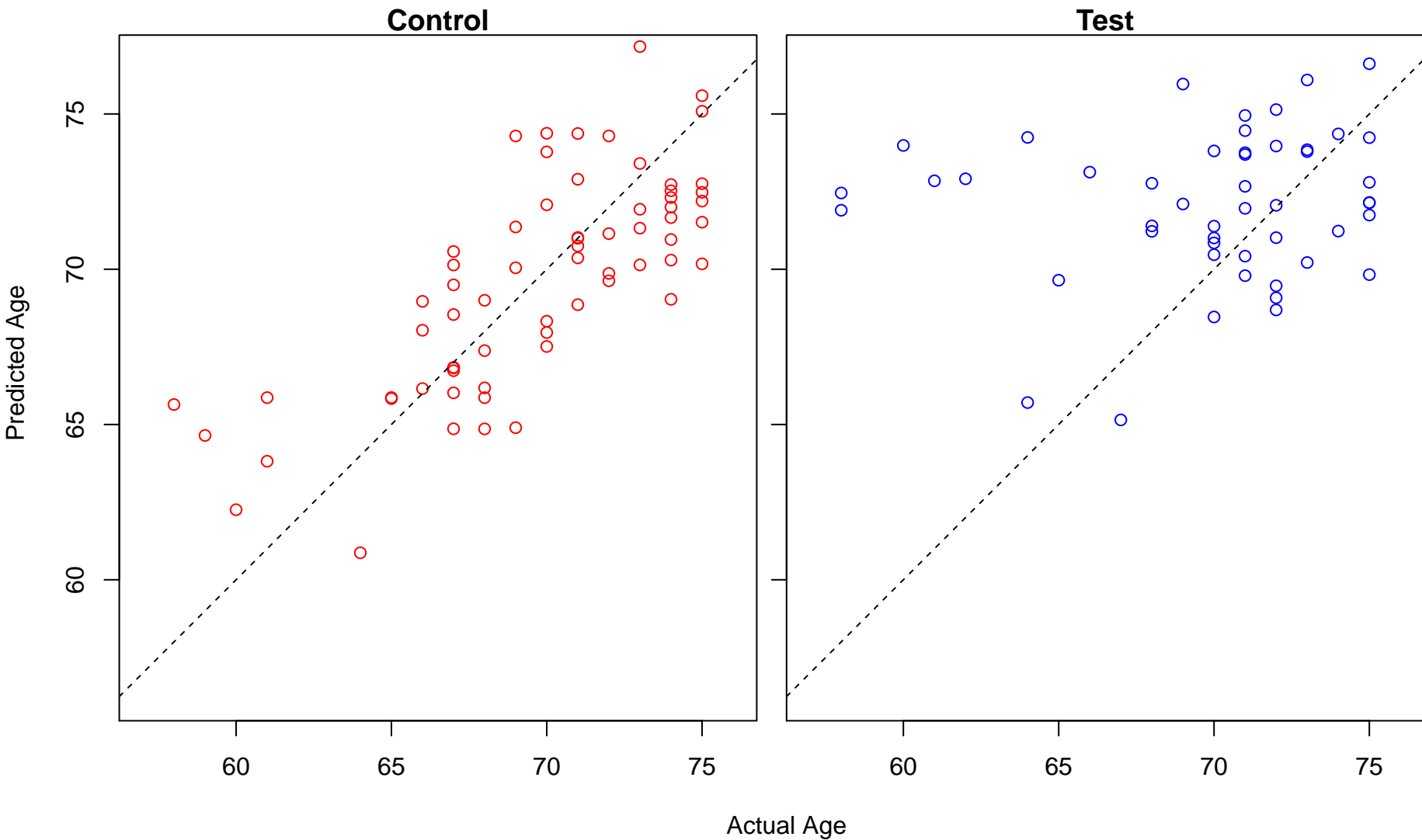
chromosome segregation (Score: 1.714087)



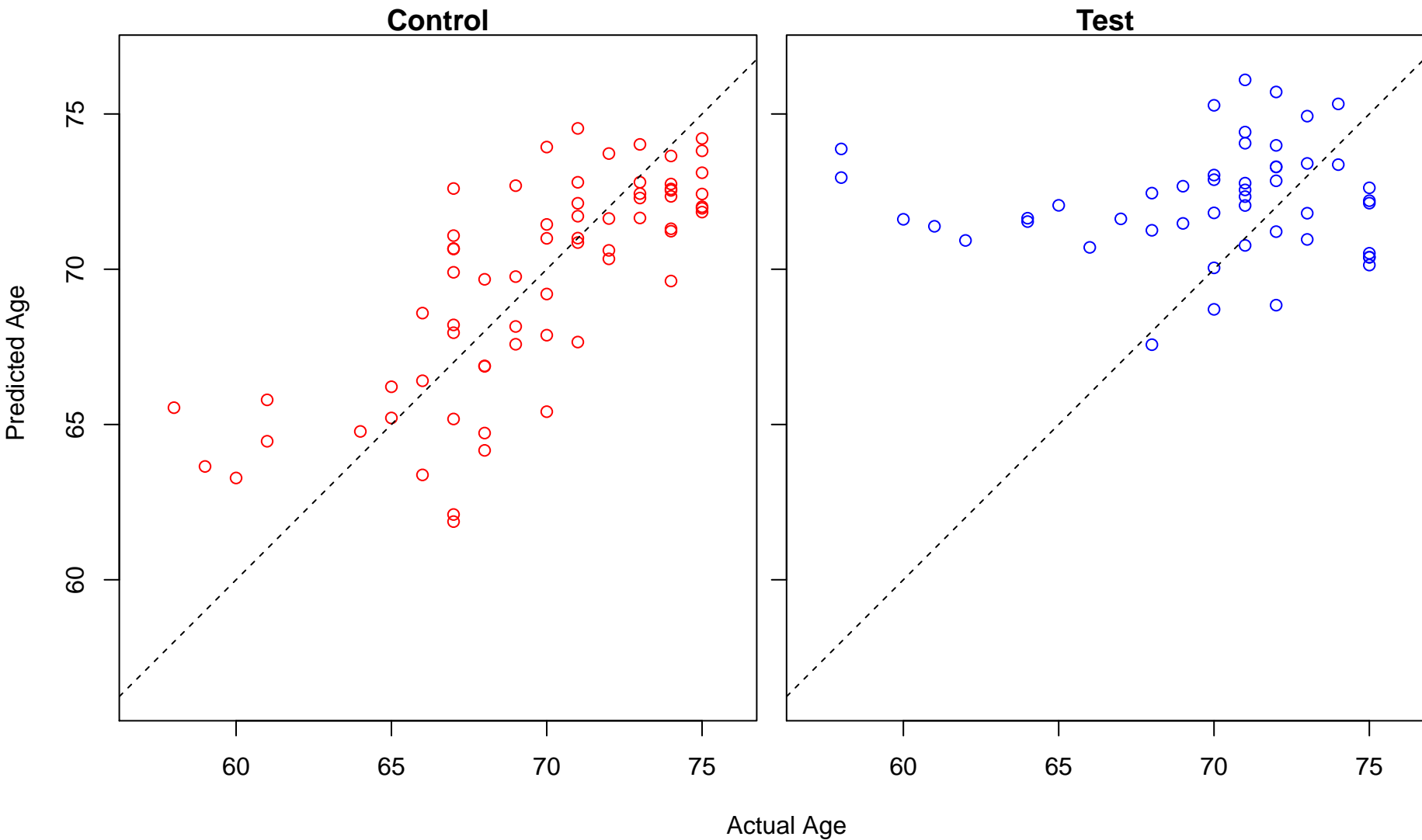
cellular response to hypoxia (Score: 1.713823)



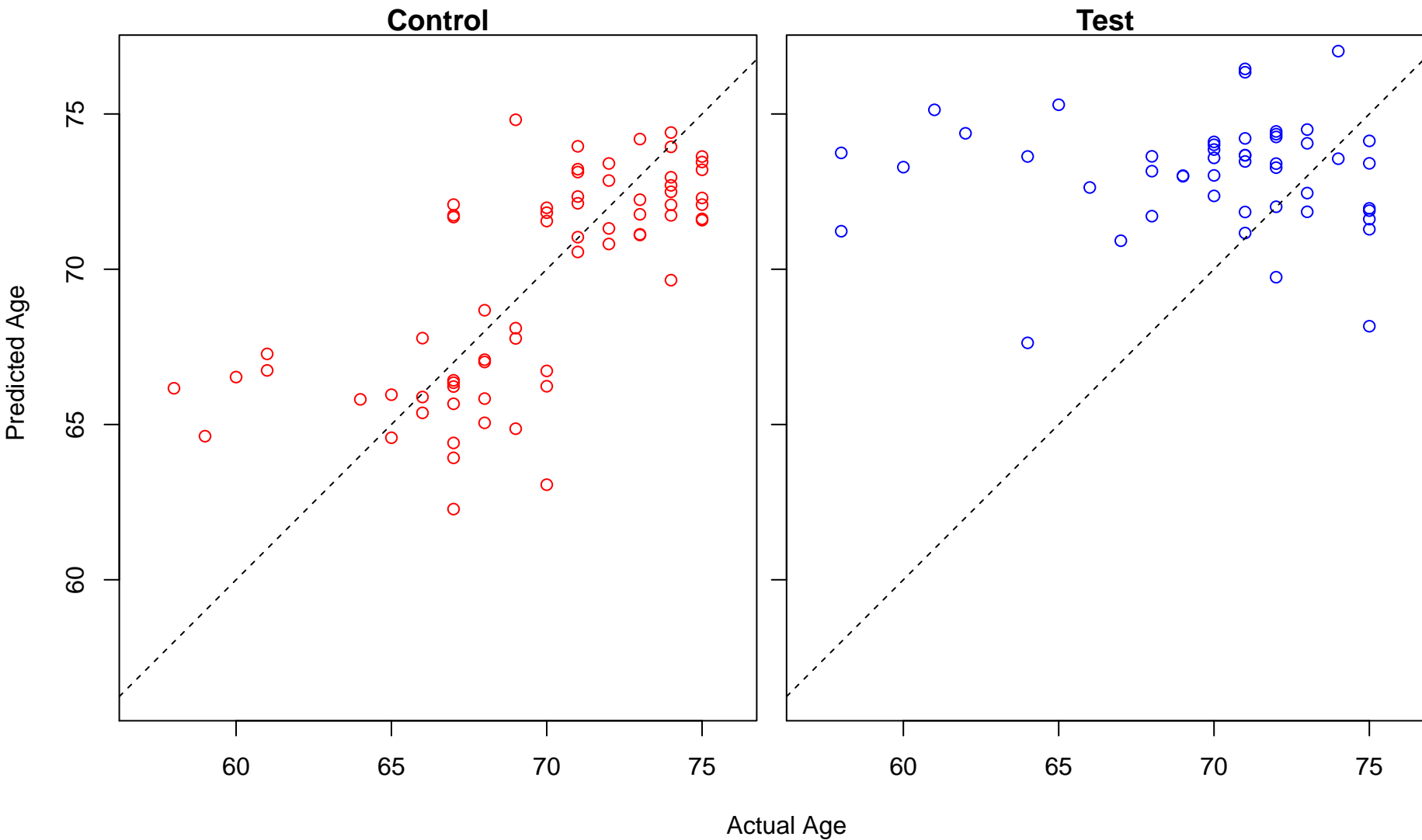
tube development (Score: 1.712052)



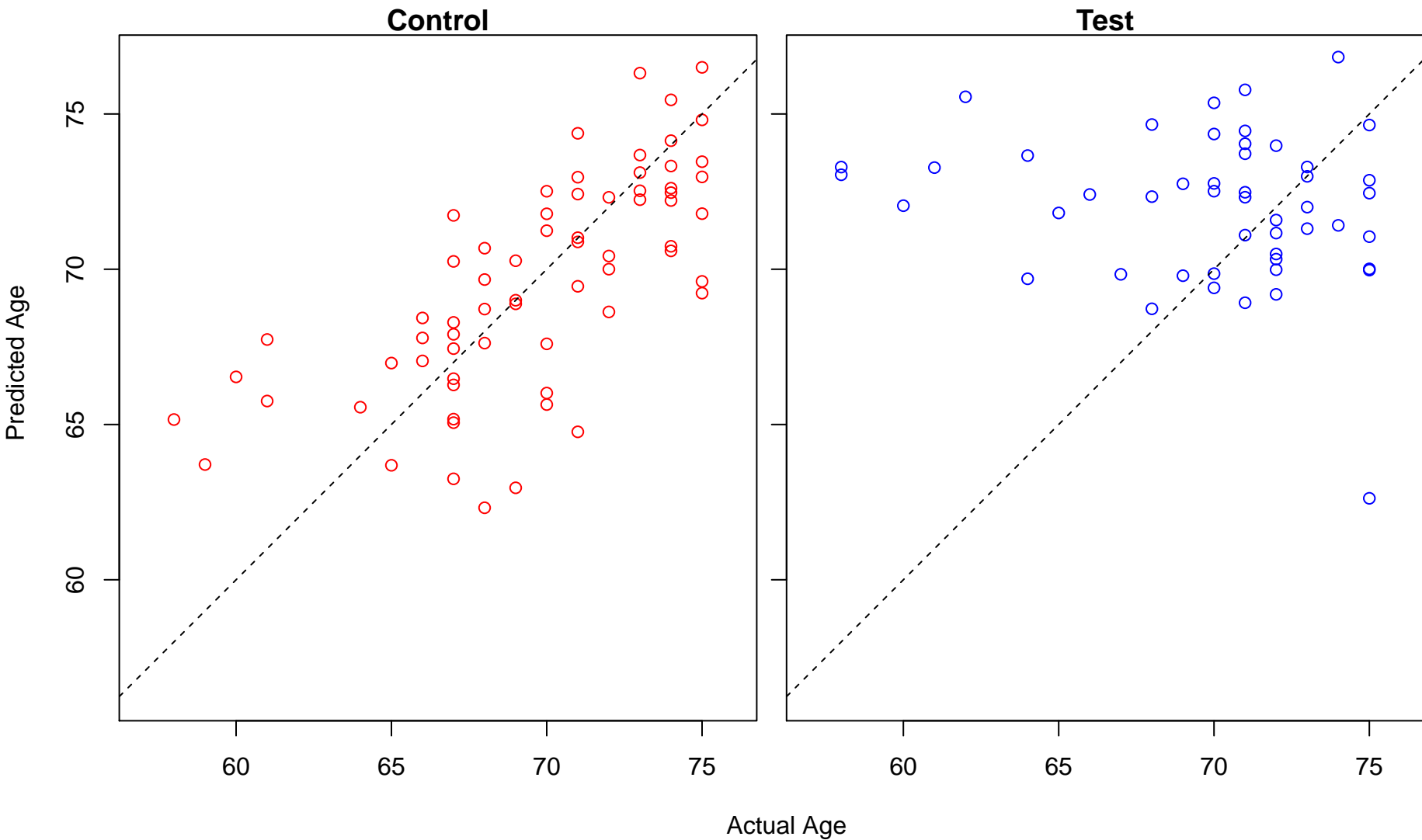
organelle fusion (Score: 1.711357)



organic cyclic compound catabolic process (Score: 1.711182)

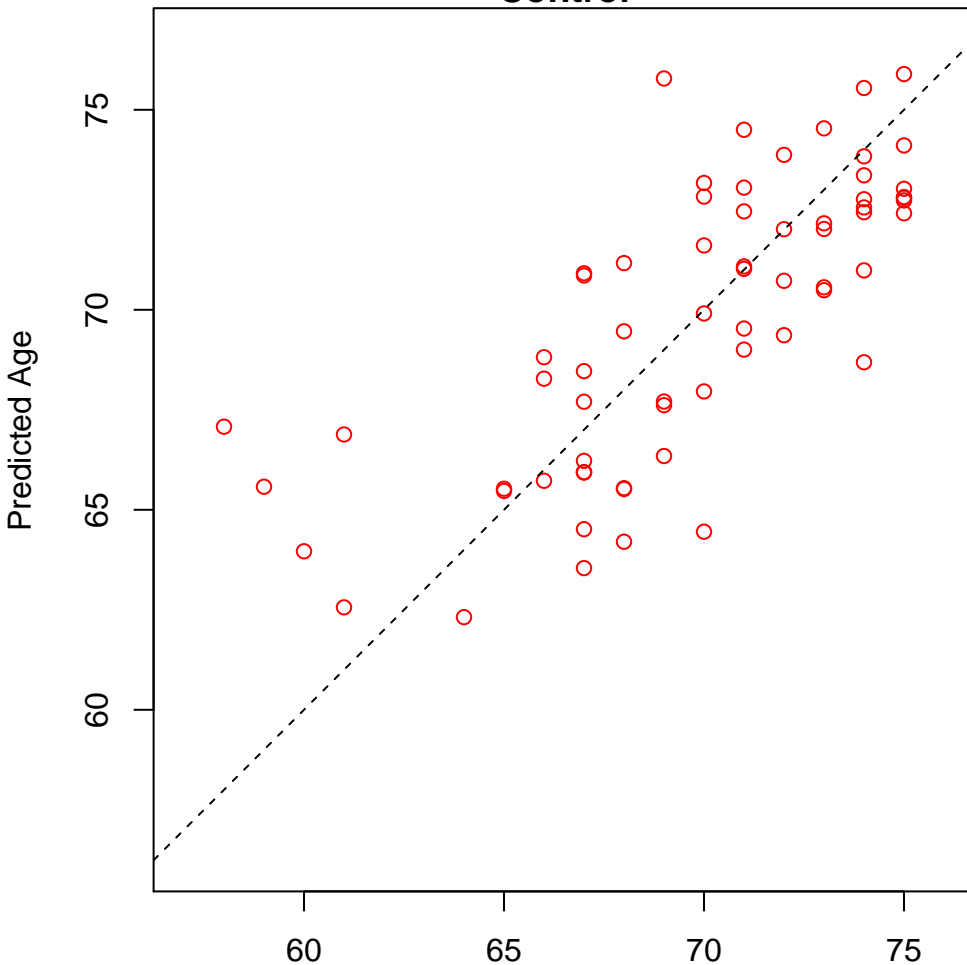


response to nutrient levels (Score: 1.709616)

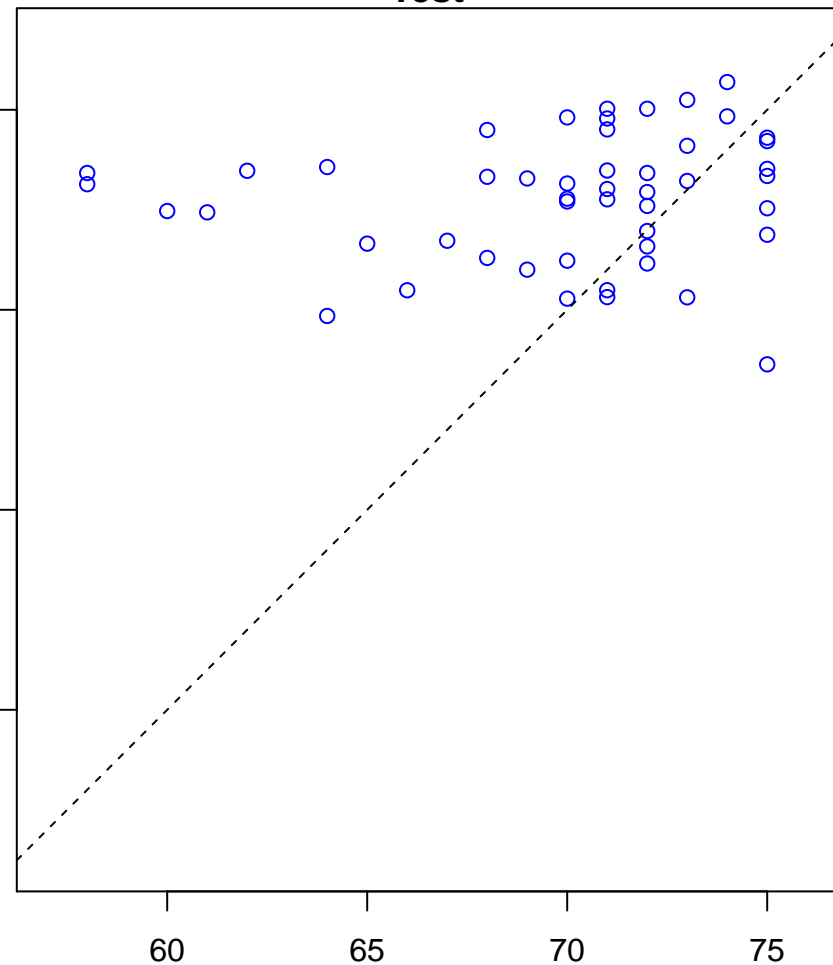


response to unfolded protein (Score: 1.709009)

Control



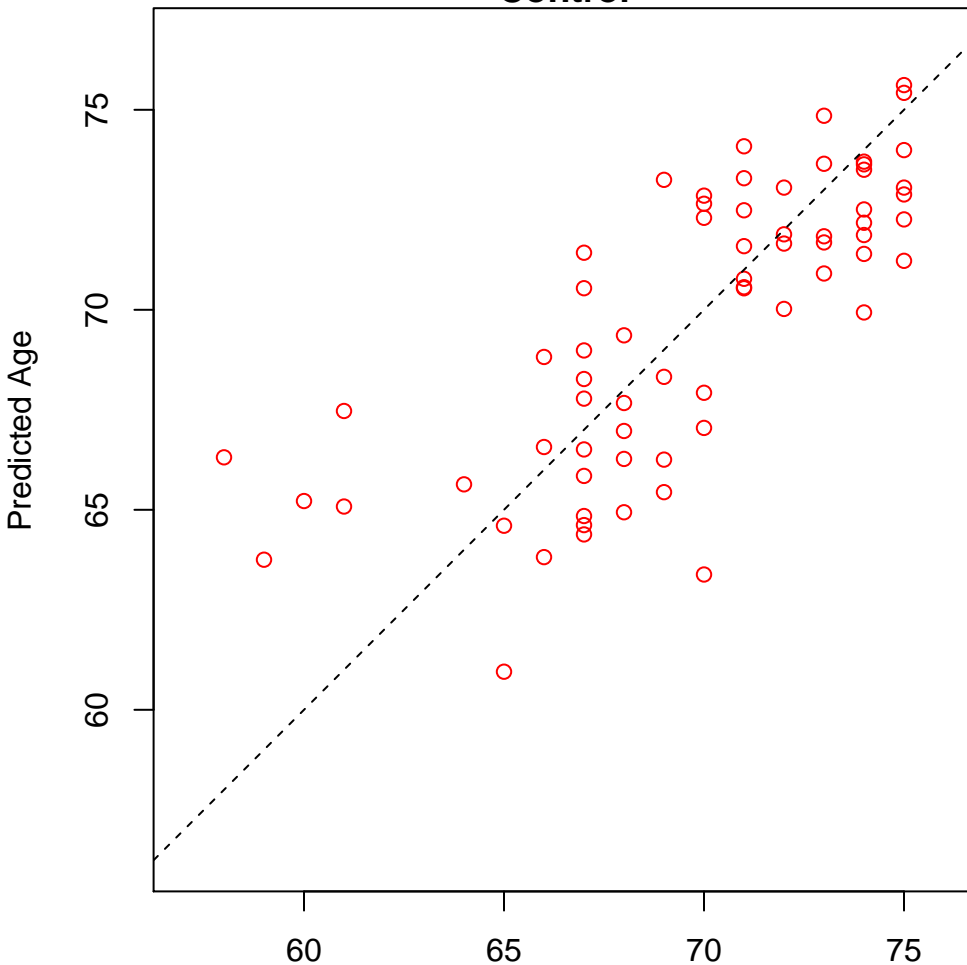
Test



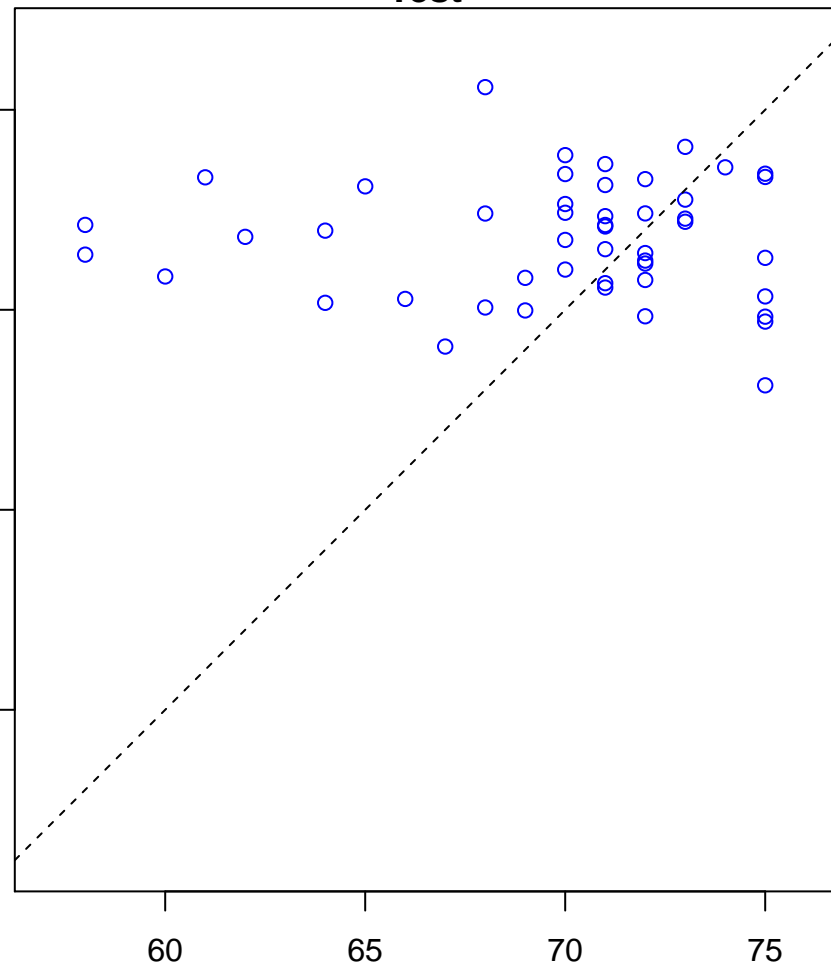
Actual Age

positive regulation of cell cycle arrest (Score: 1.708869)

Control

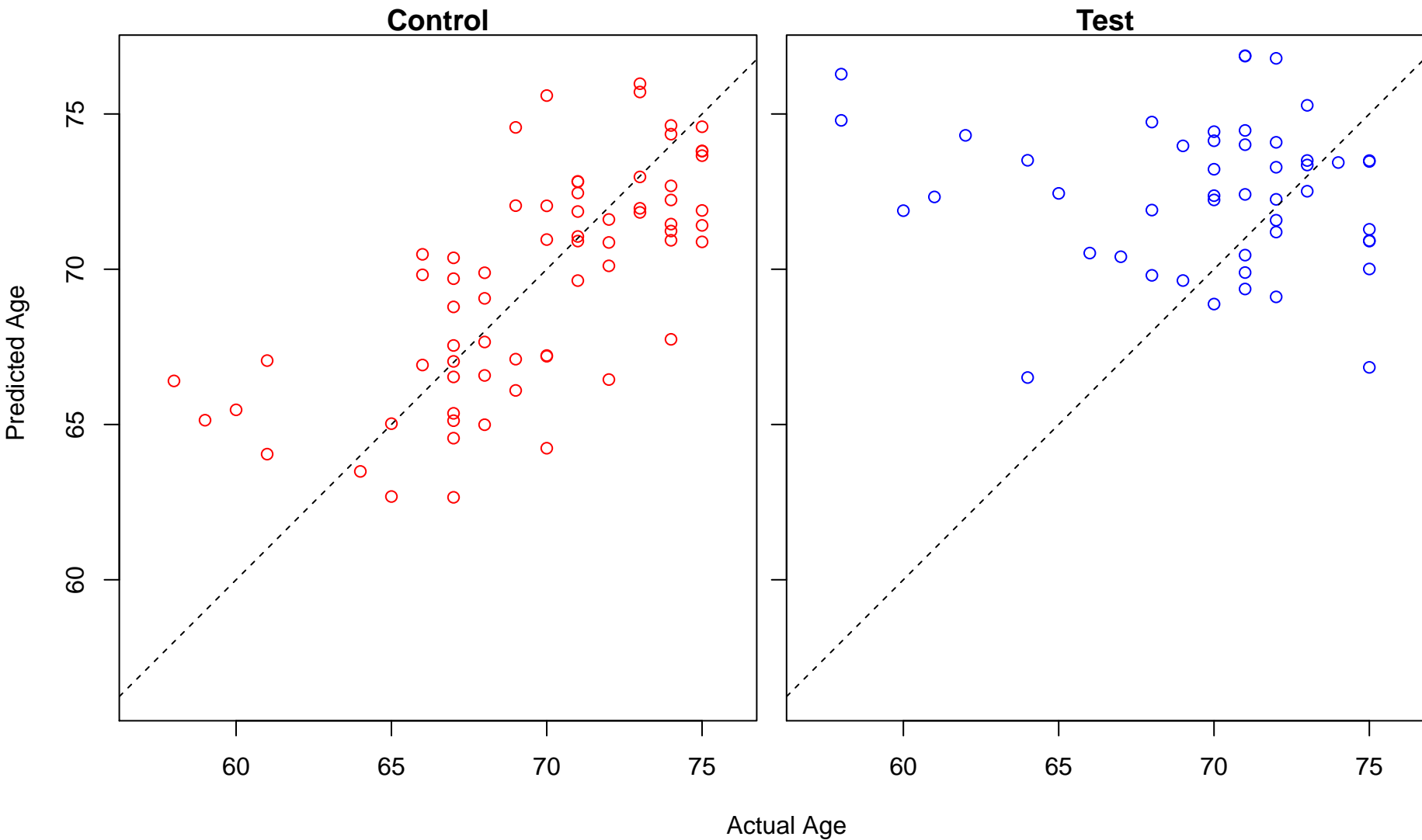


Test

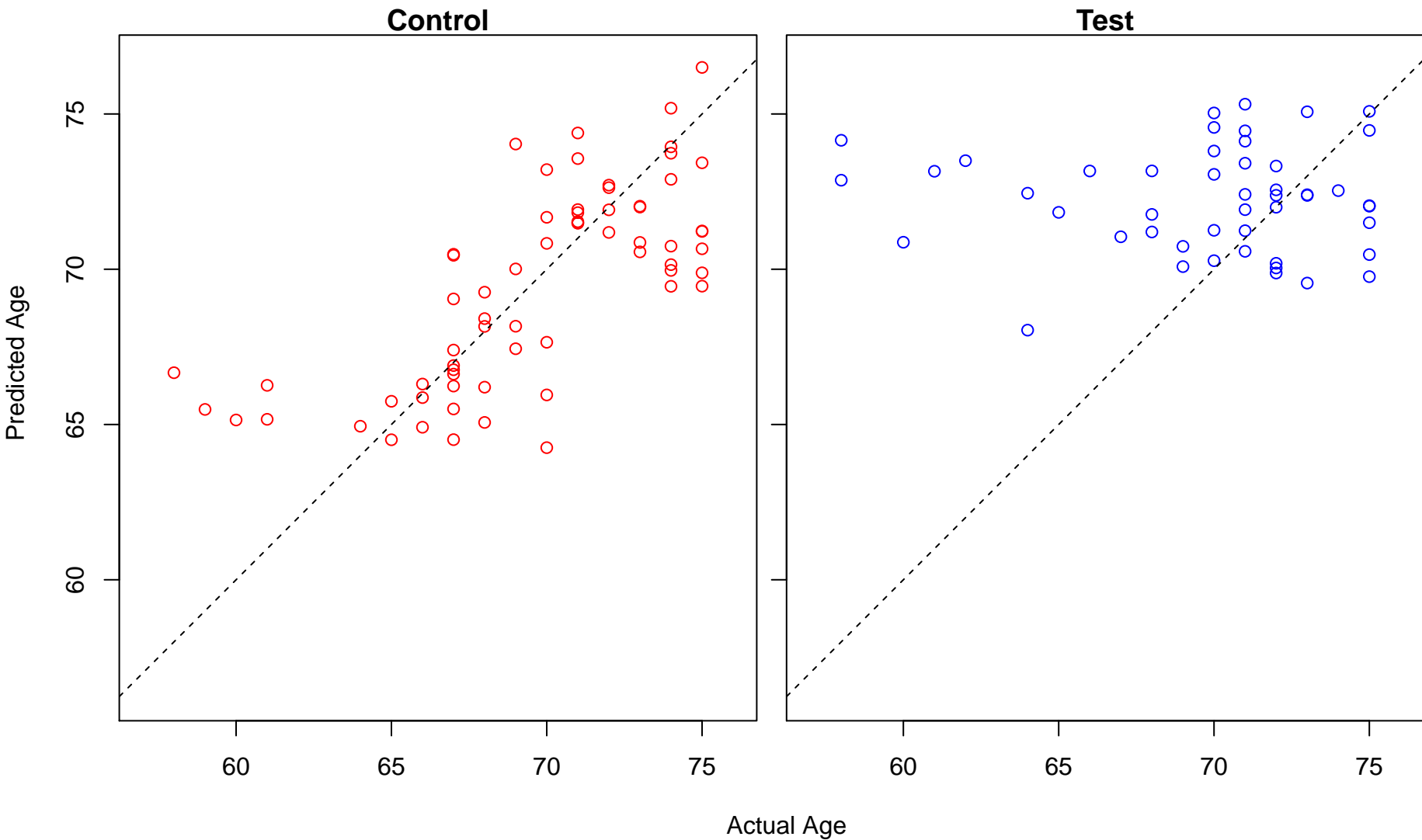


Actual Age

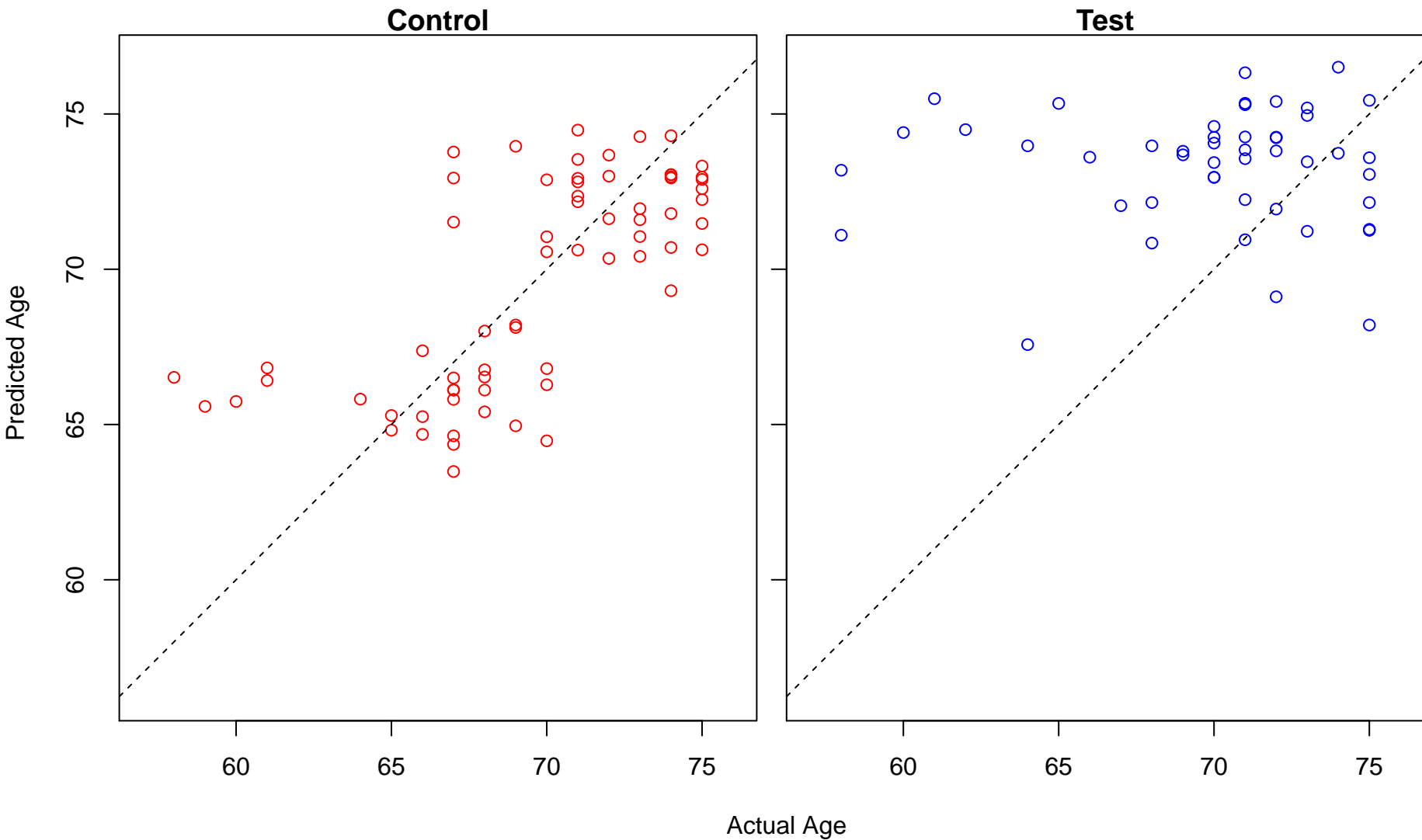
response to heat (Score: 1.708161)



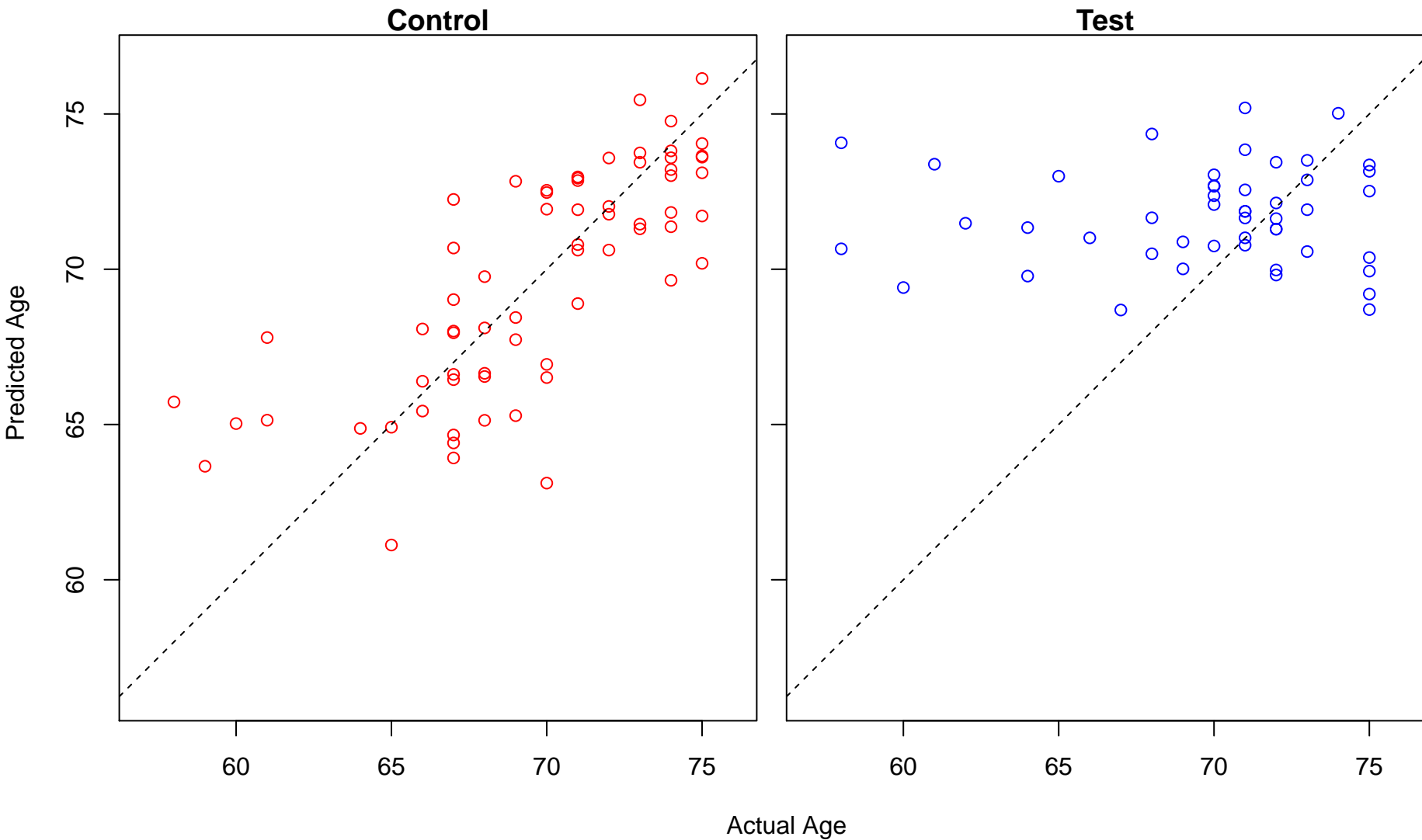
positive regulation of cytoskeleton organization (Score: 1.707497)



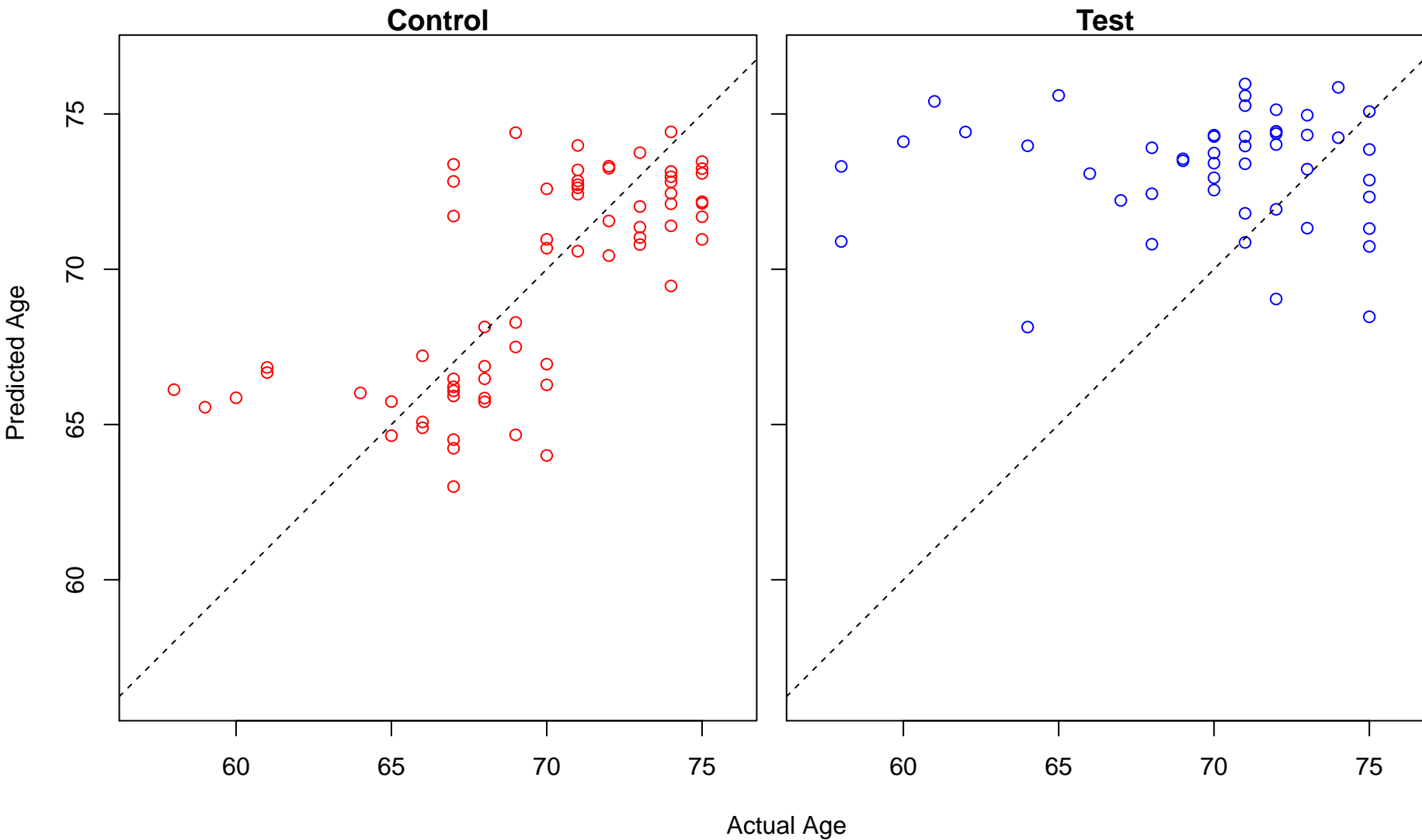
viral transcription (Score: 1.707405)



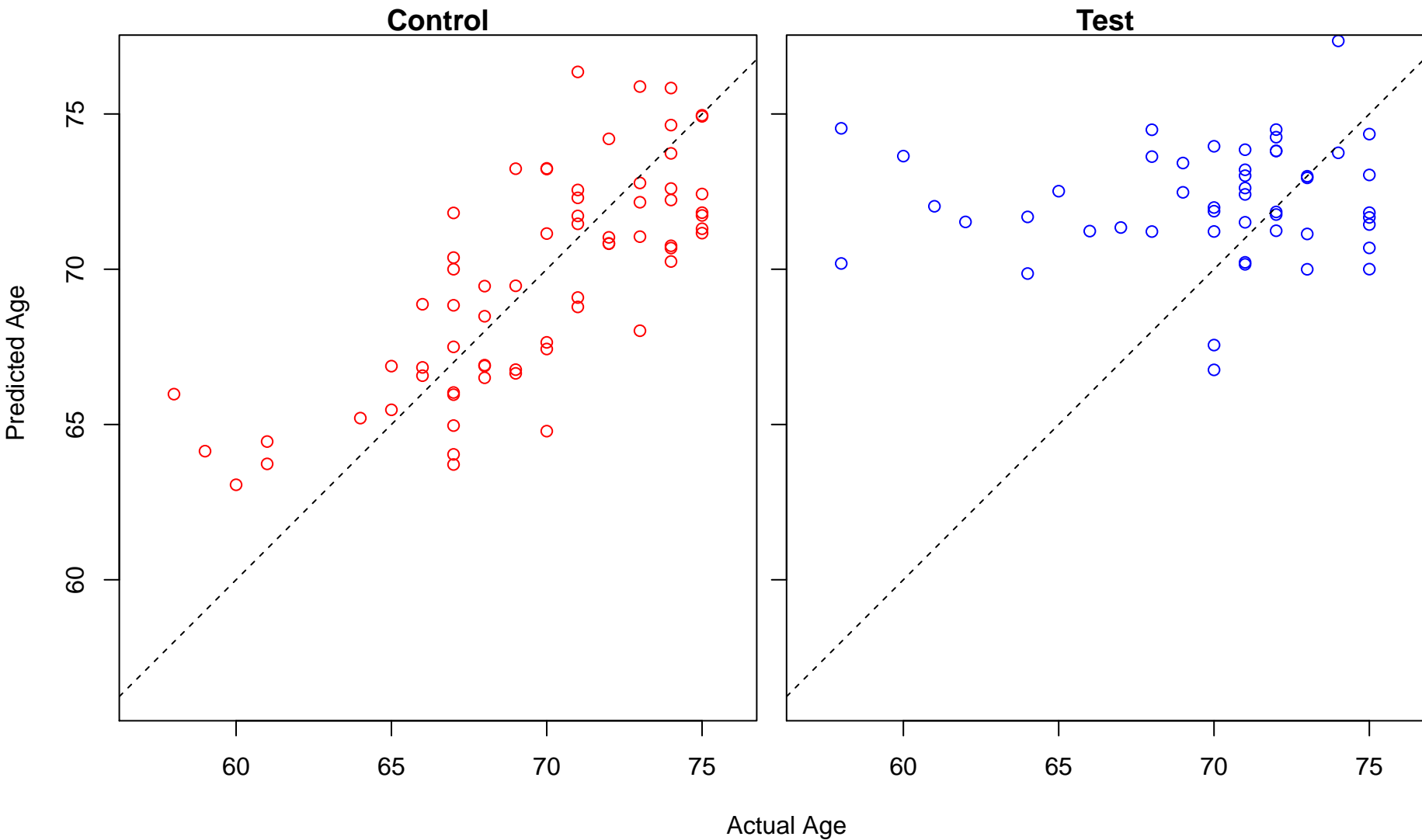
G1 DNA damage checkpoint (Score: 1.706776)



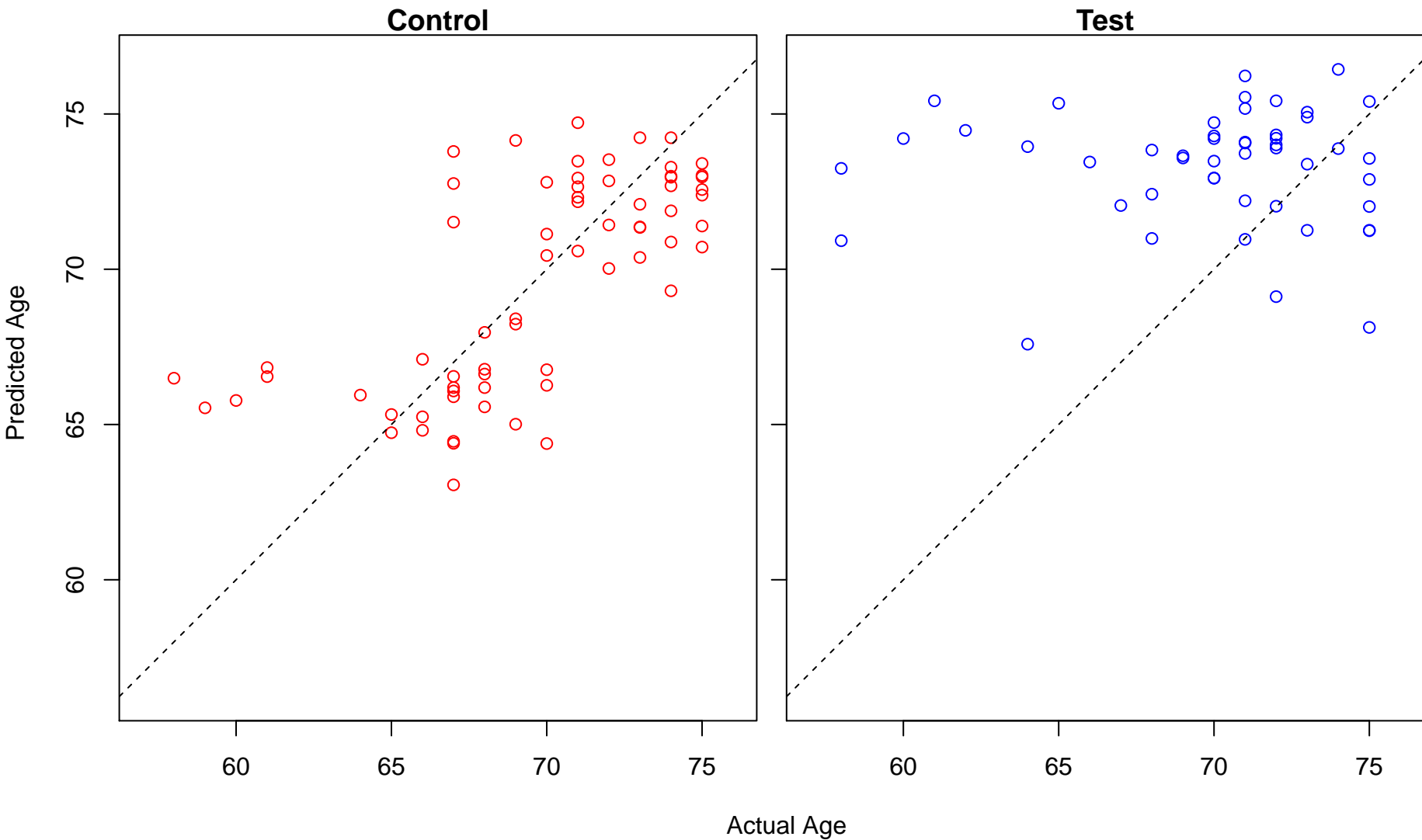
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (Score: 1.706390)



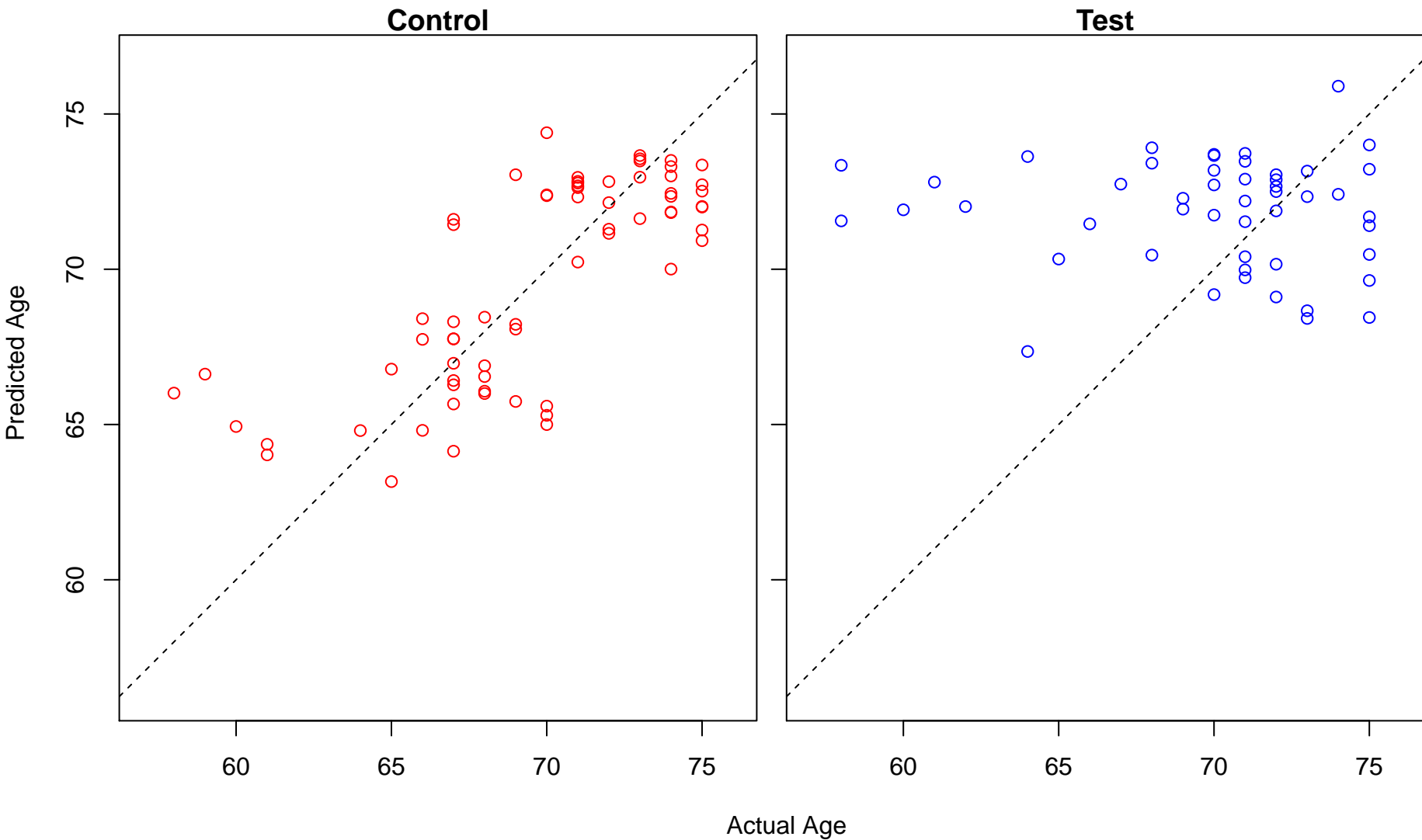
regulation of mitochondrial membrane permeability (Score: 1.706269)



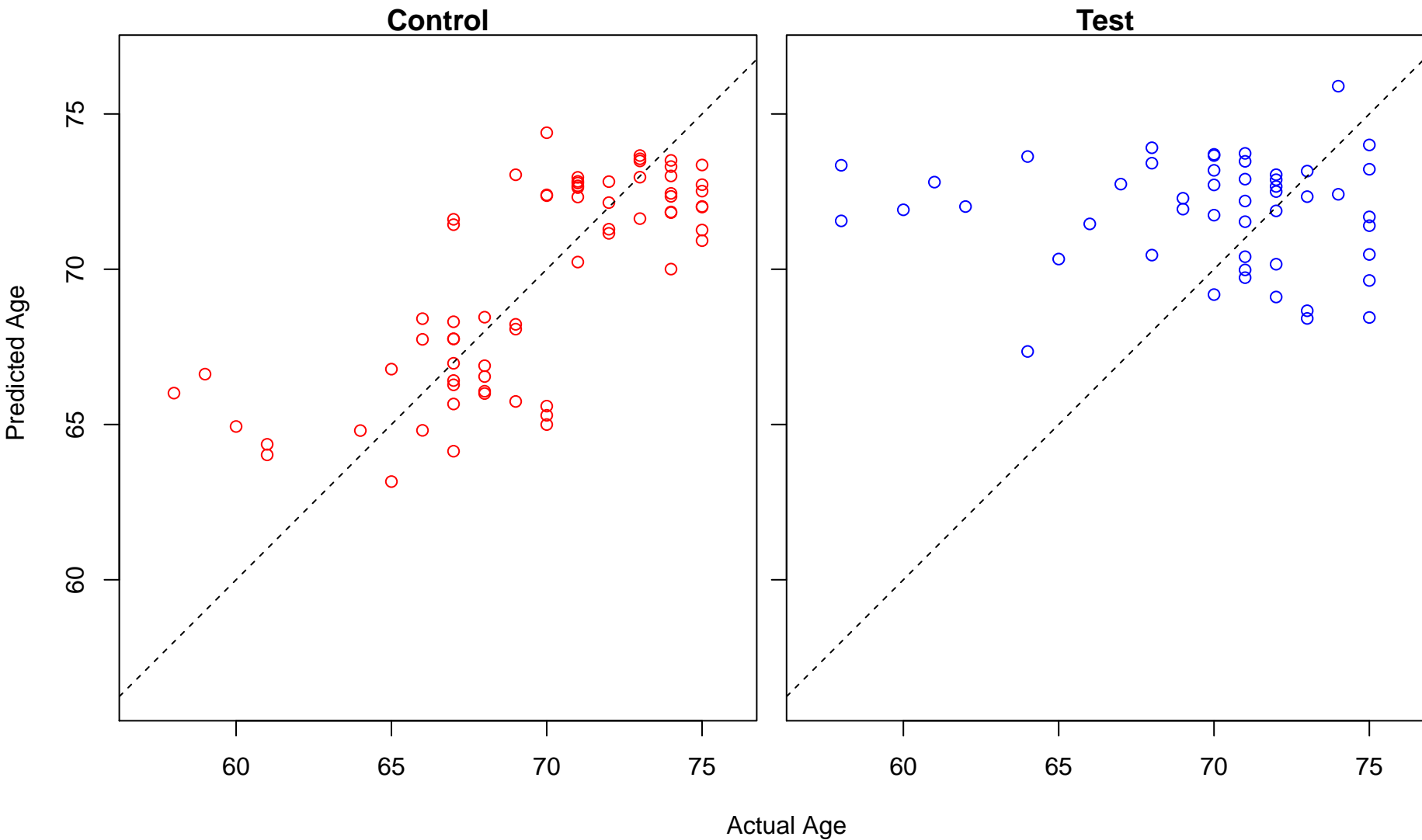
multi-organism metabolic process (Score: 1.706218)



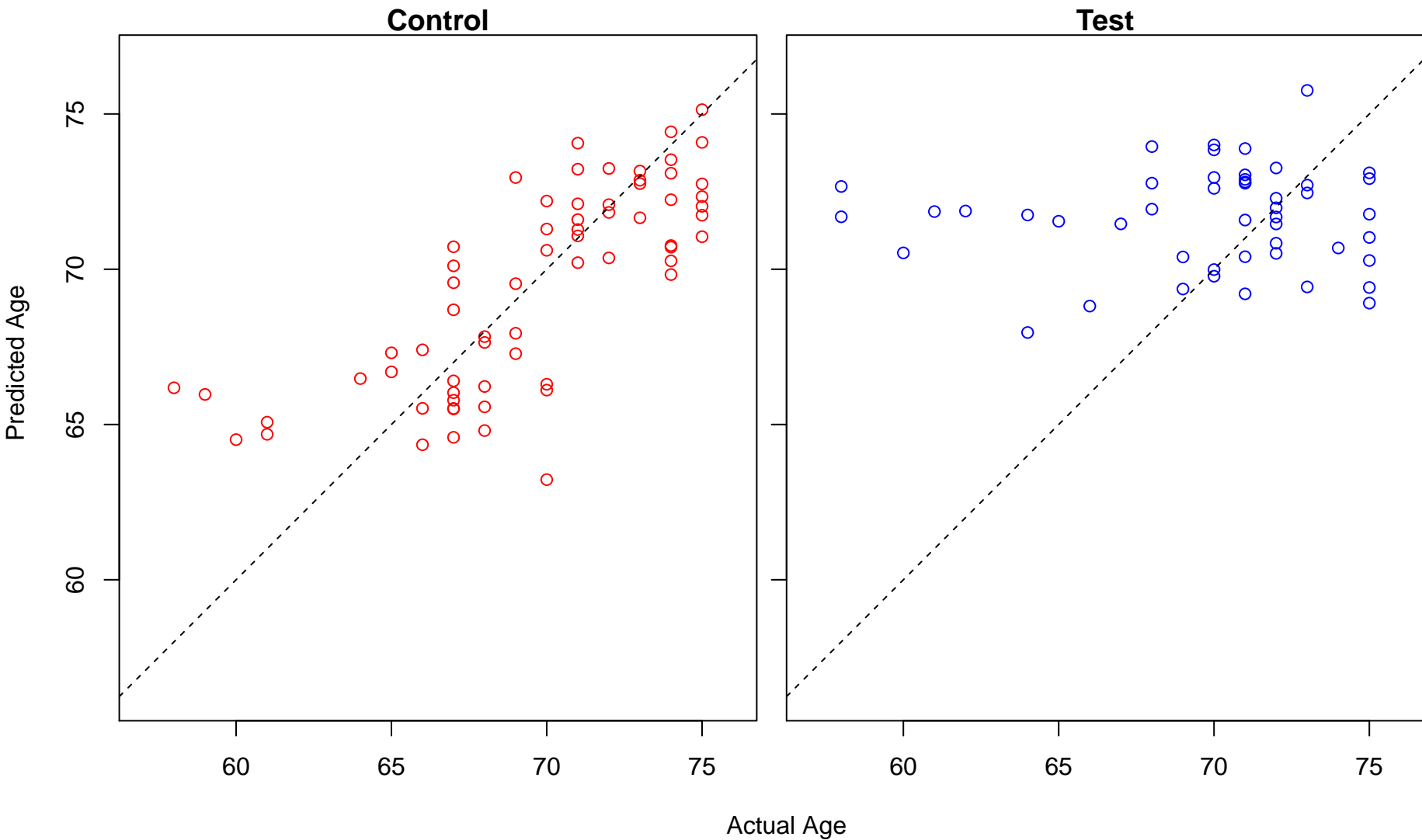
chromosome localization (Score: 1.705914)



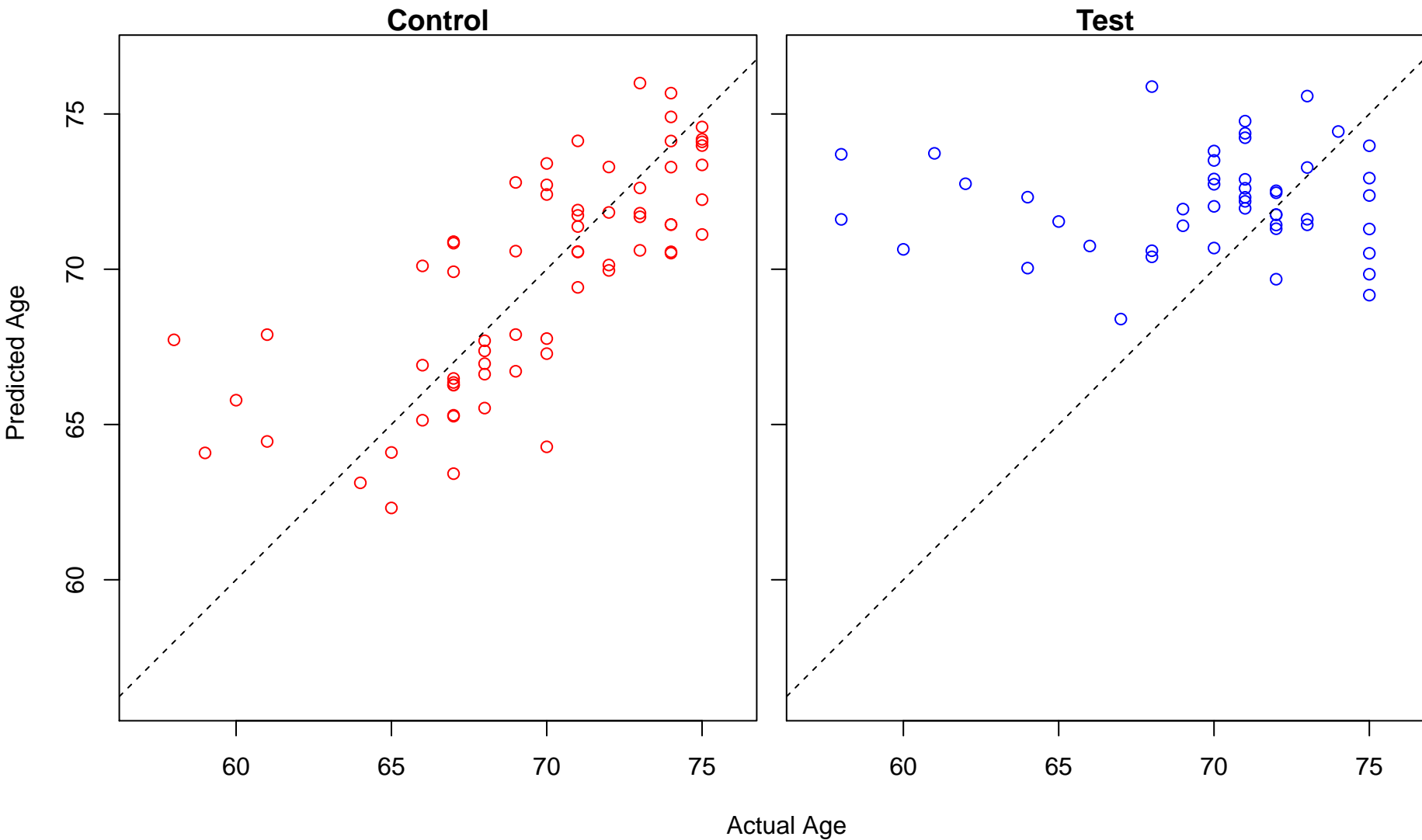
establishment of chromosome localization (Score: 1.705914)



ribonucleoside monophosphate biosynthetic process (Score: 1.705316)

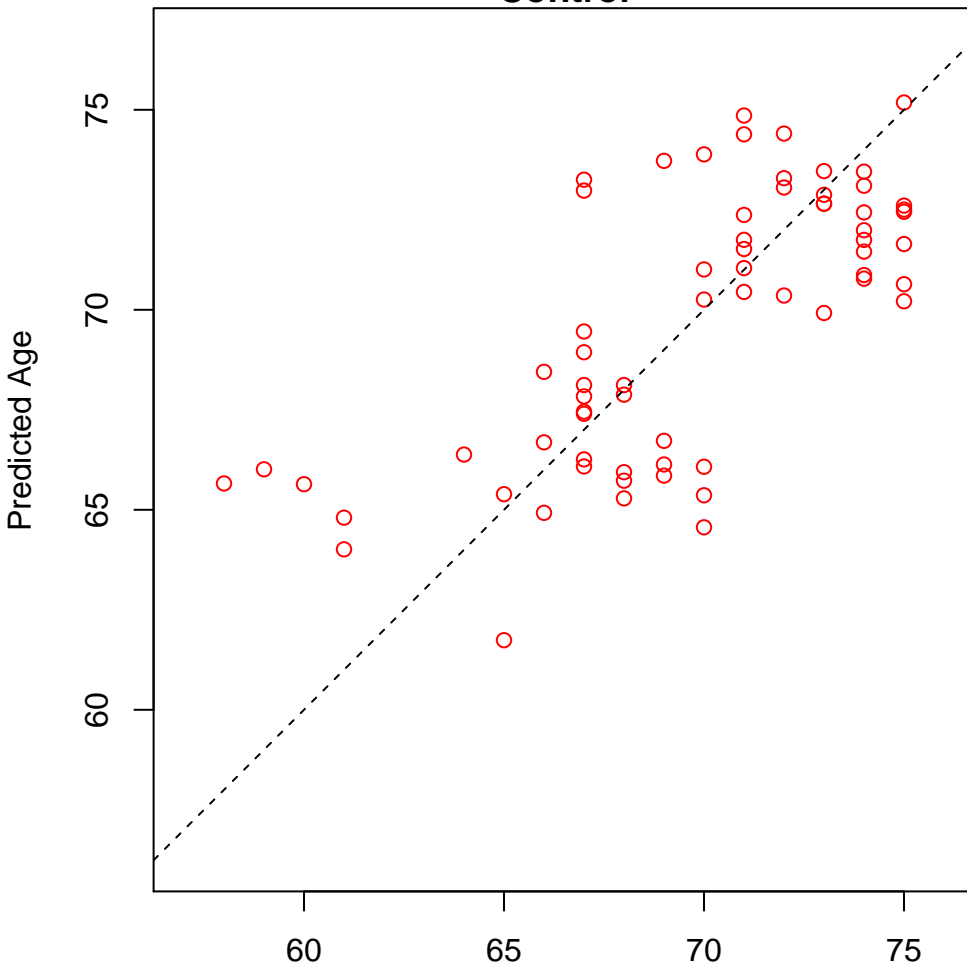


proteolysis involved in cellular protein catabolic process (Score: 1.704905)

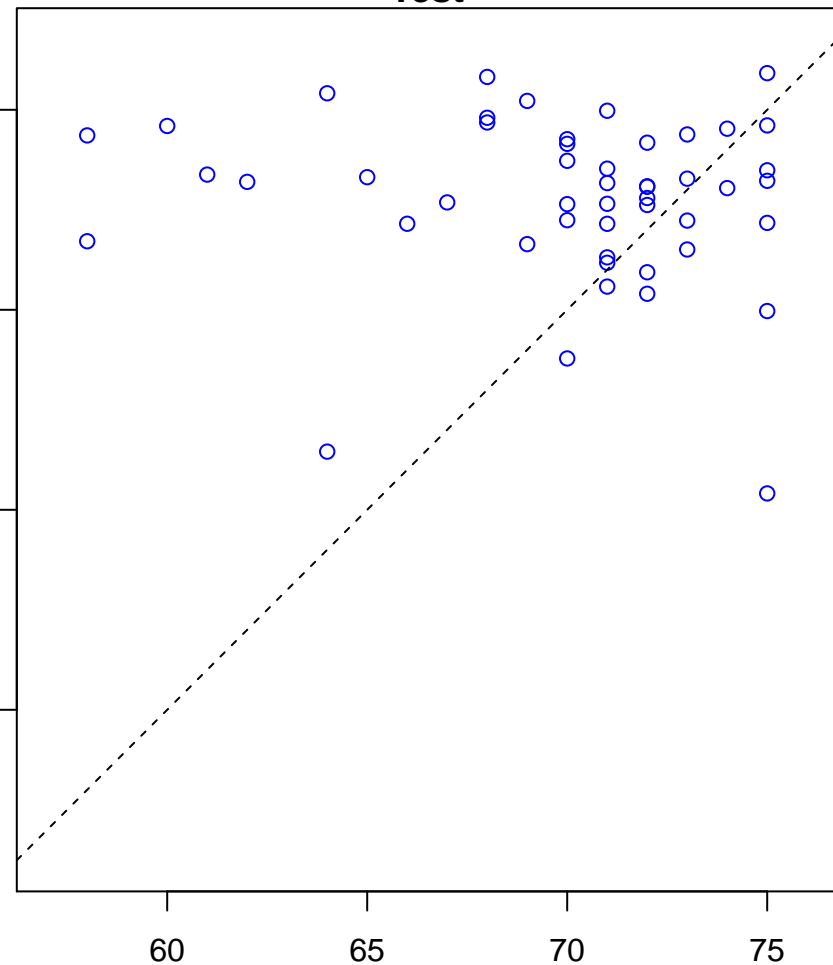


response to purine-containing compound (Score: 1.704292)

Control

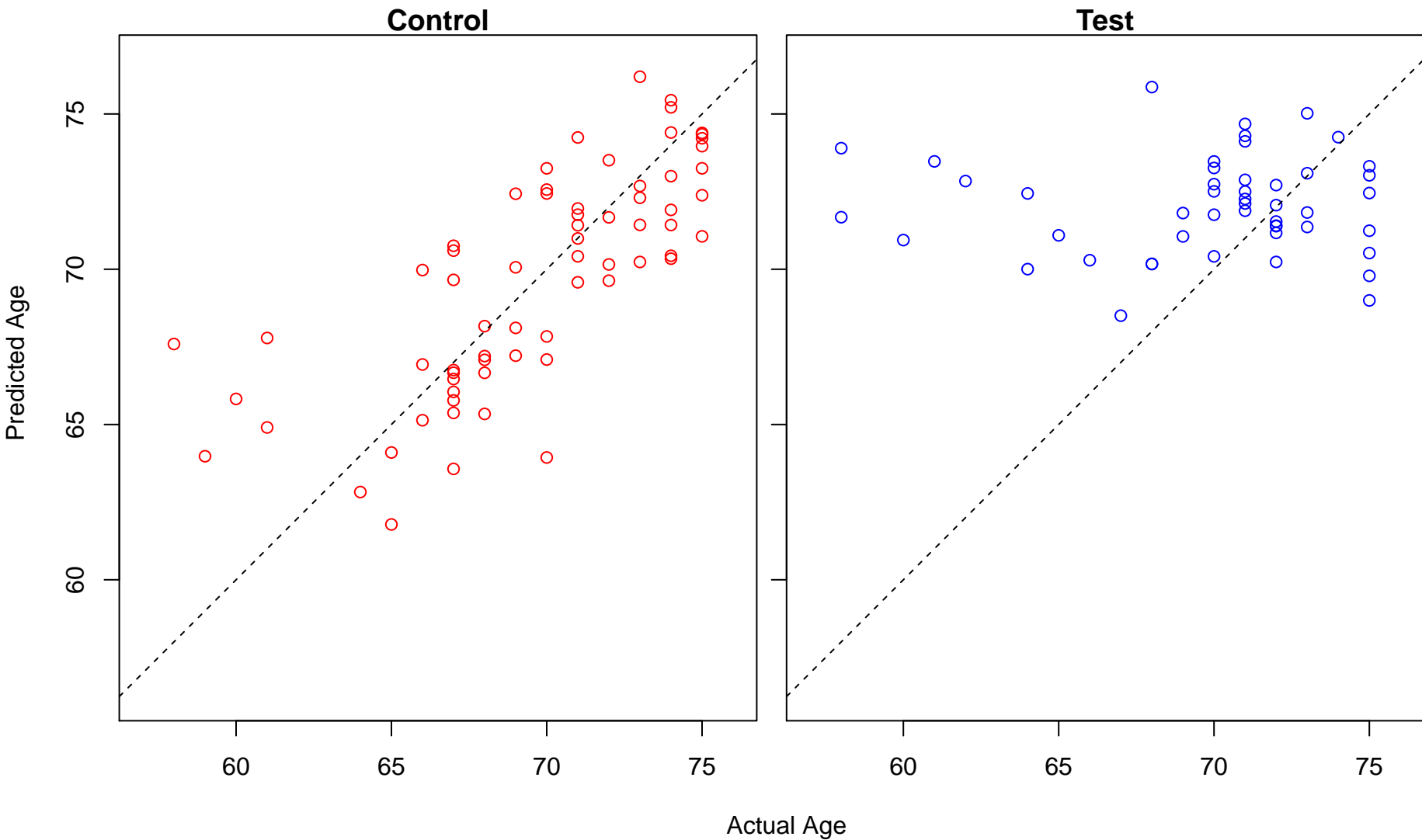


Test

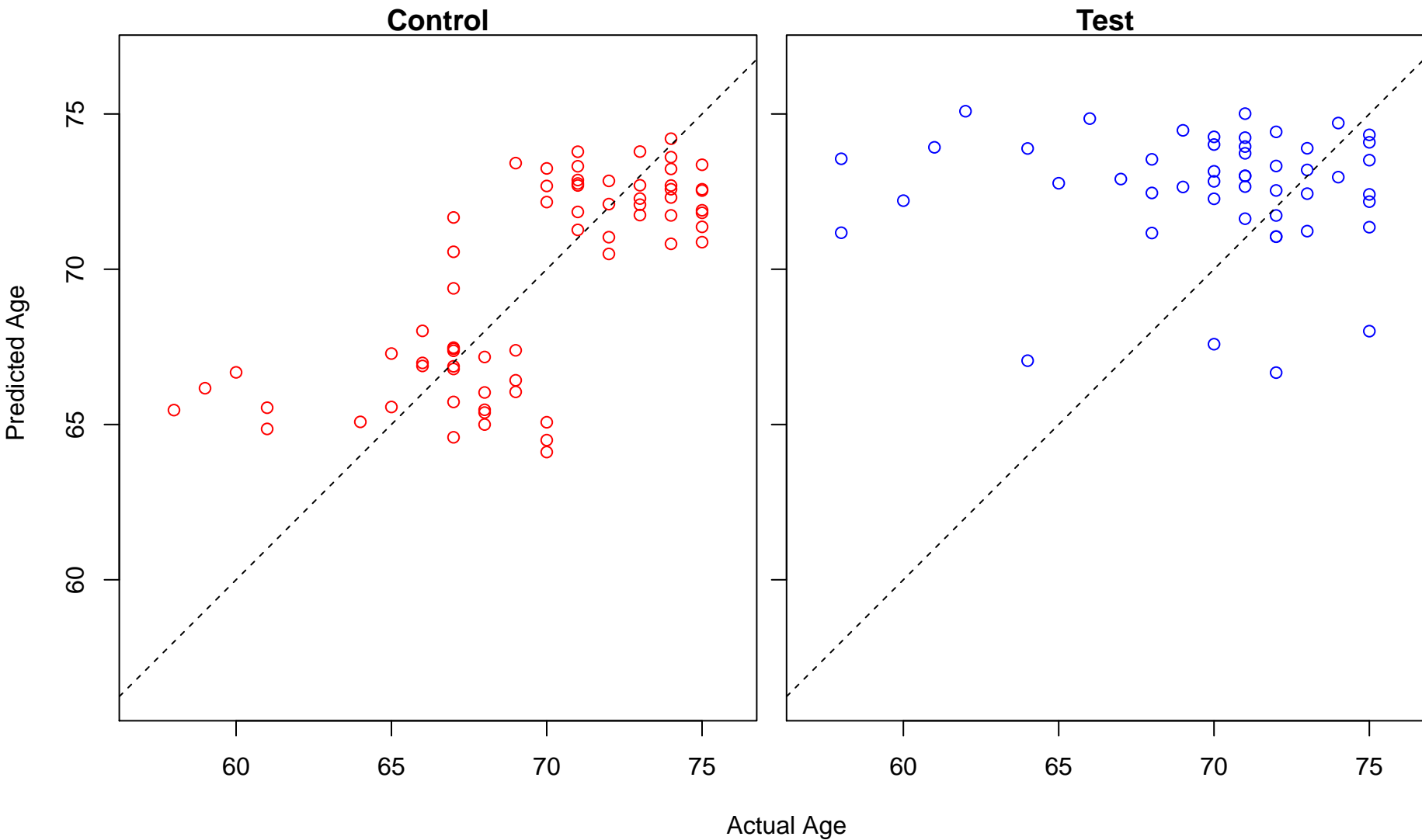


Actual Age

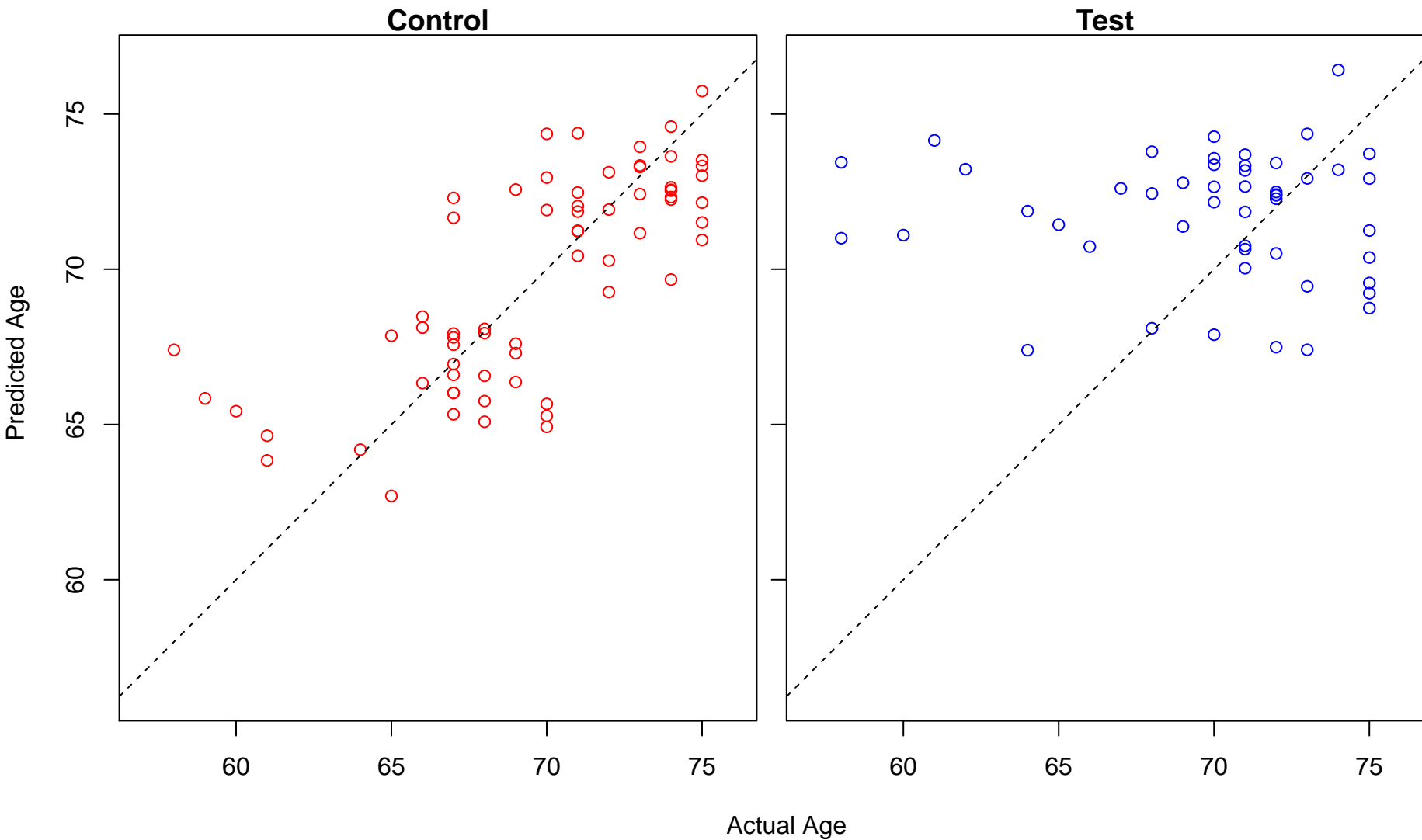
protein catabolic process (Score: 1.704180)



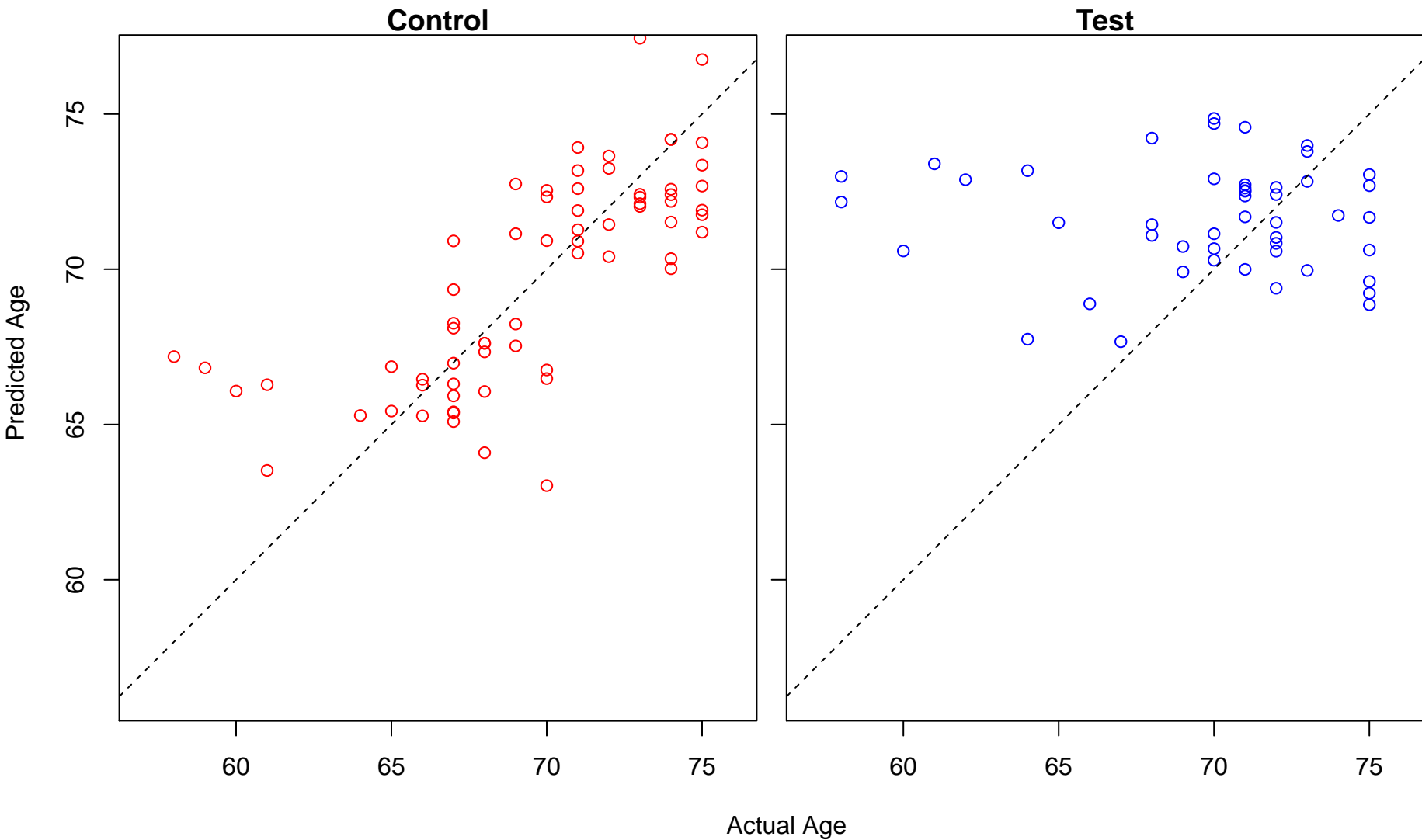
histone deubiquitination (Score: 1.704172)



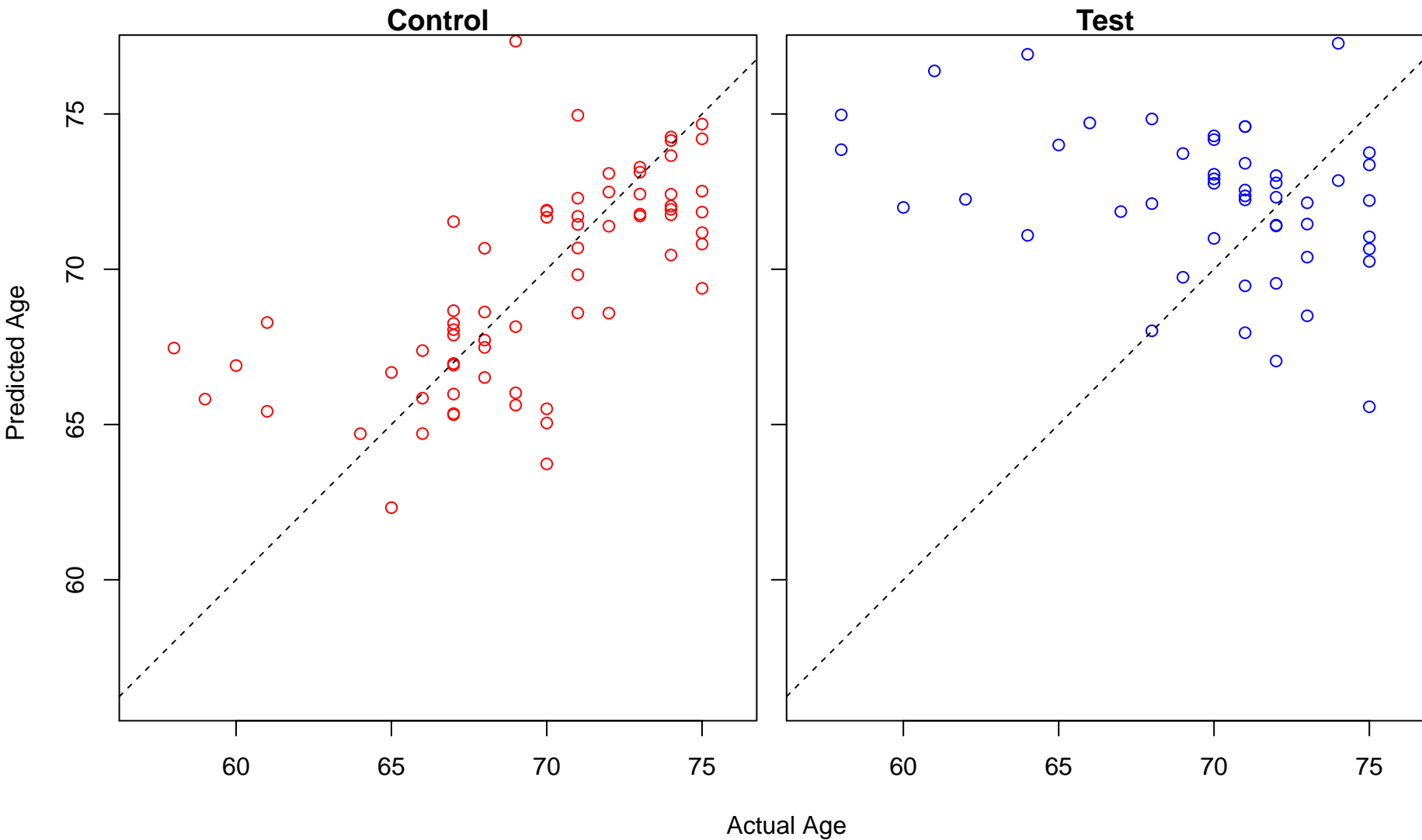
regulation of microtubule cytoskeleton organization (Score: 1.704044)



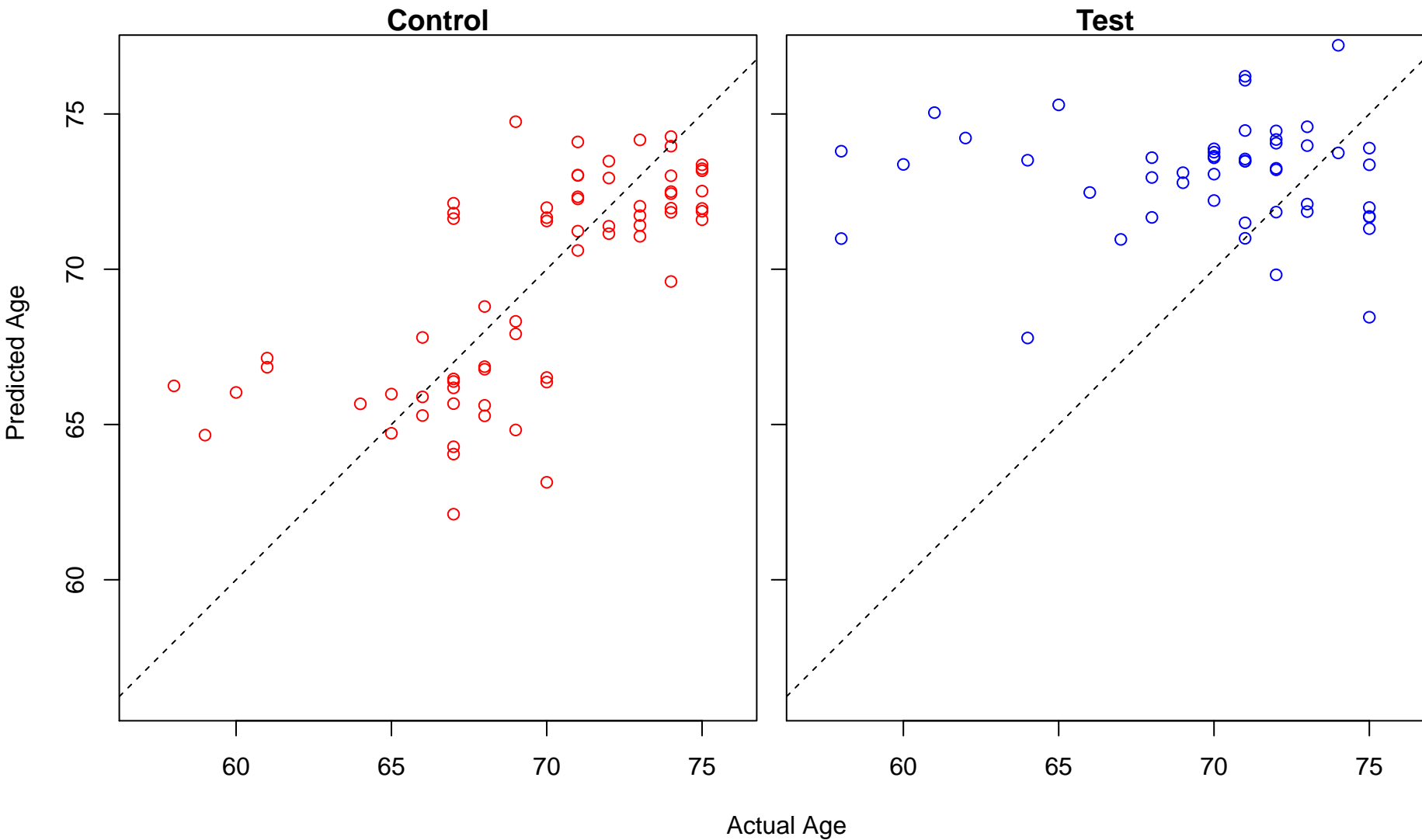
ribonucleoside metabolic process (Score: 1.703977)



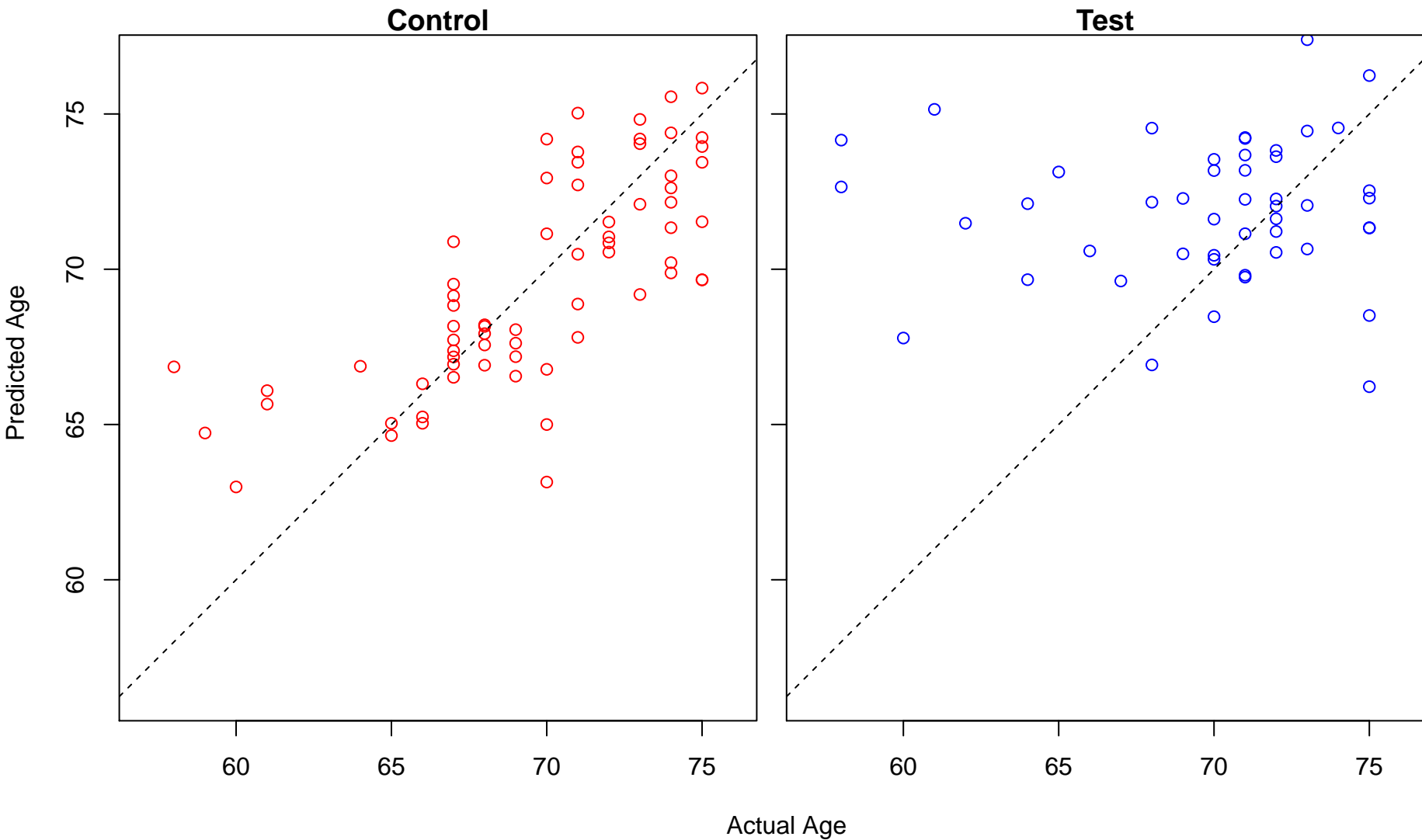
regulation of transcription factor import into nucleus (Score: 1.703965)



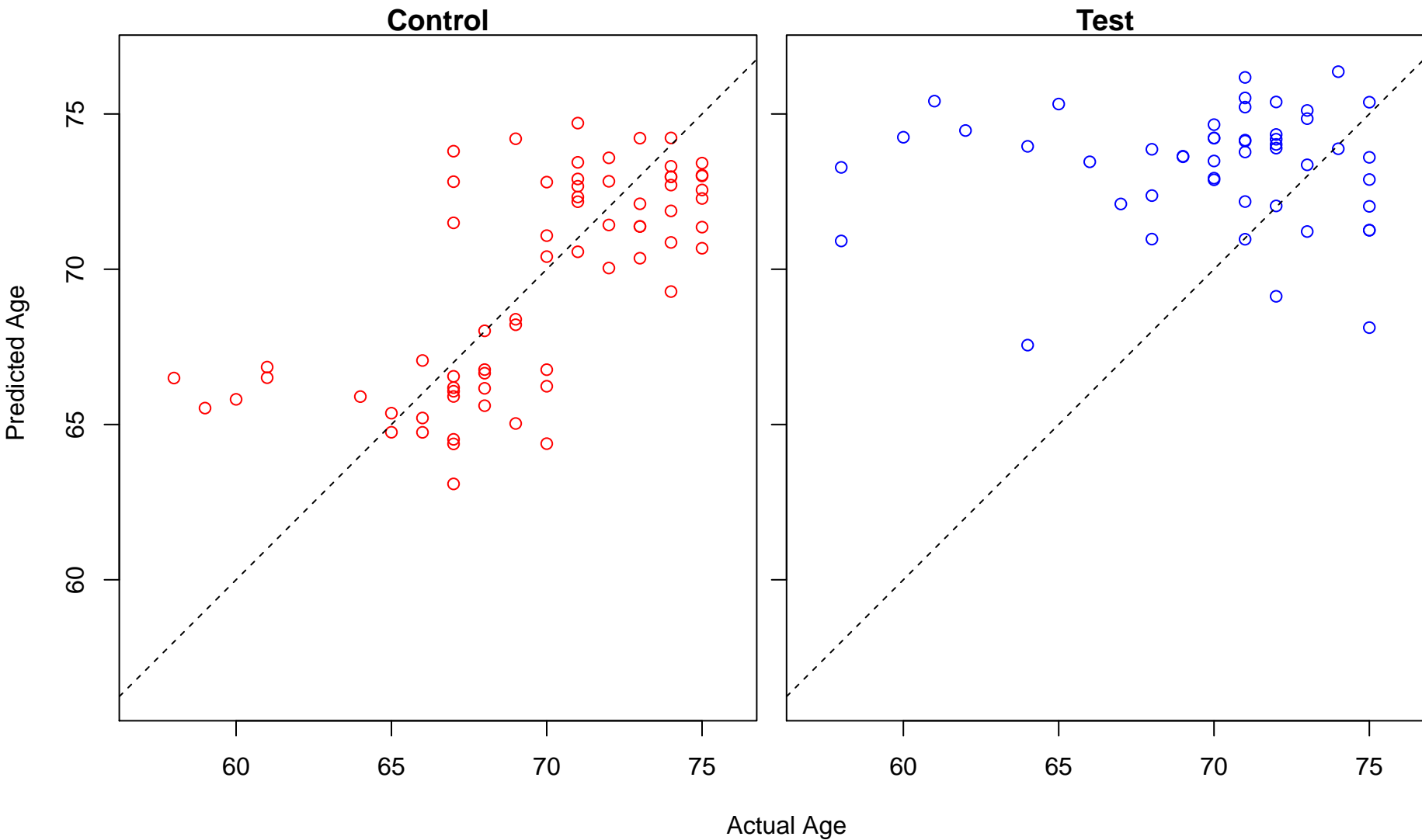
nucleobase-containing compound catabolic process (Score: 1.703400)



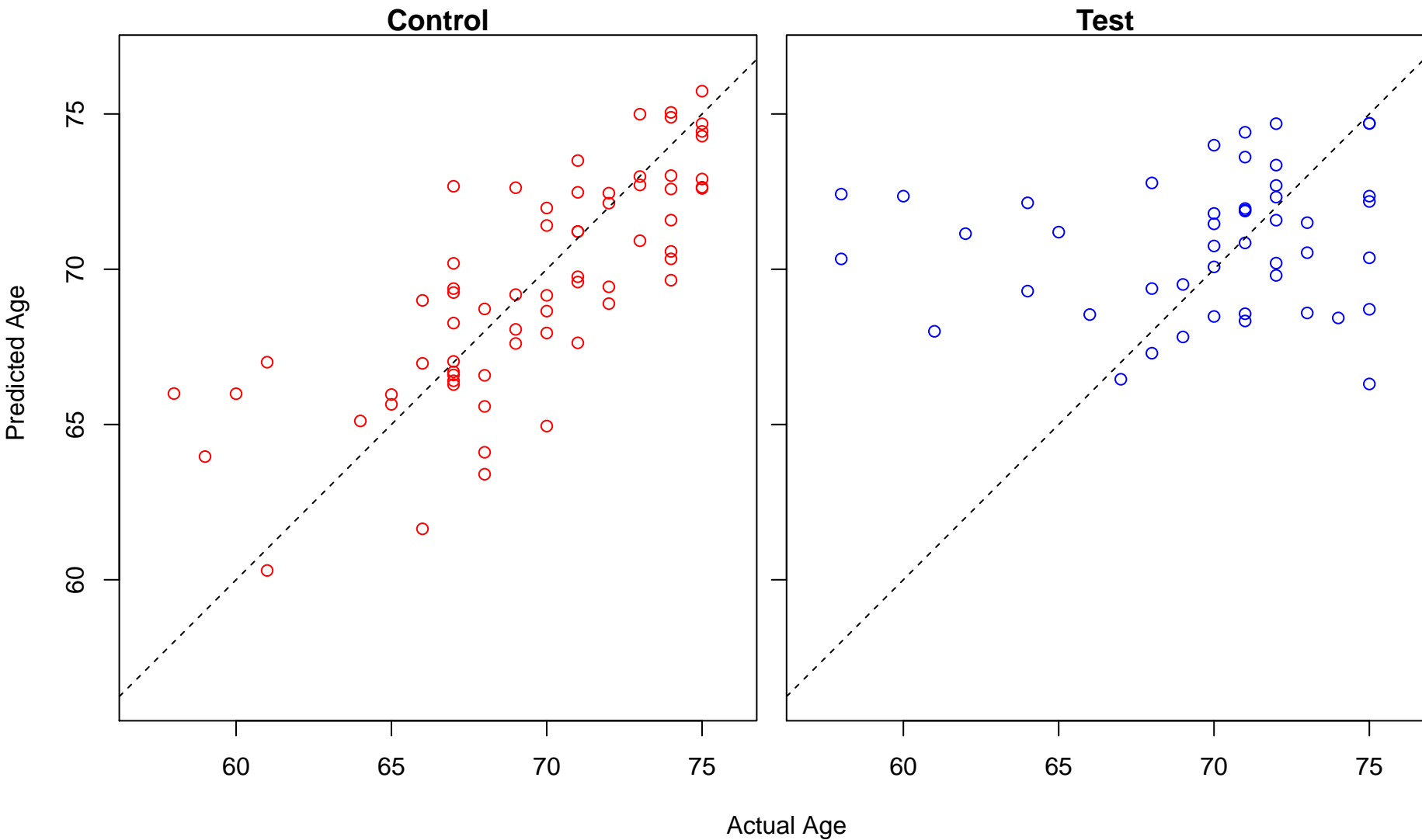
regulation of ion transmembrane transporter activity (Score: 1.703087)



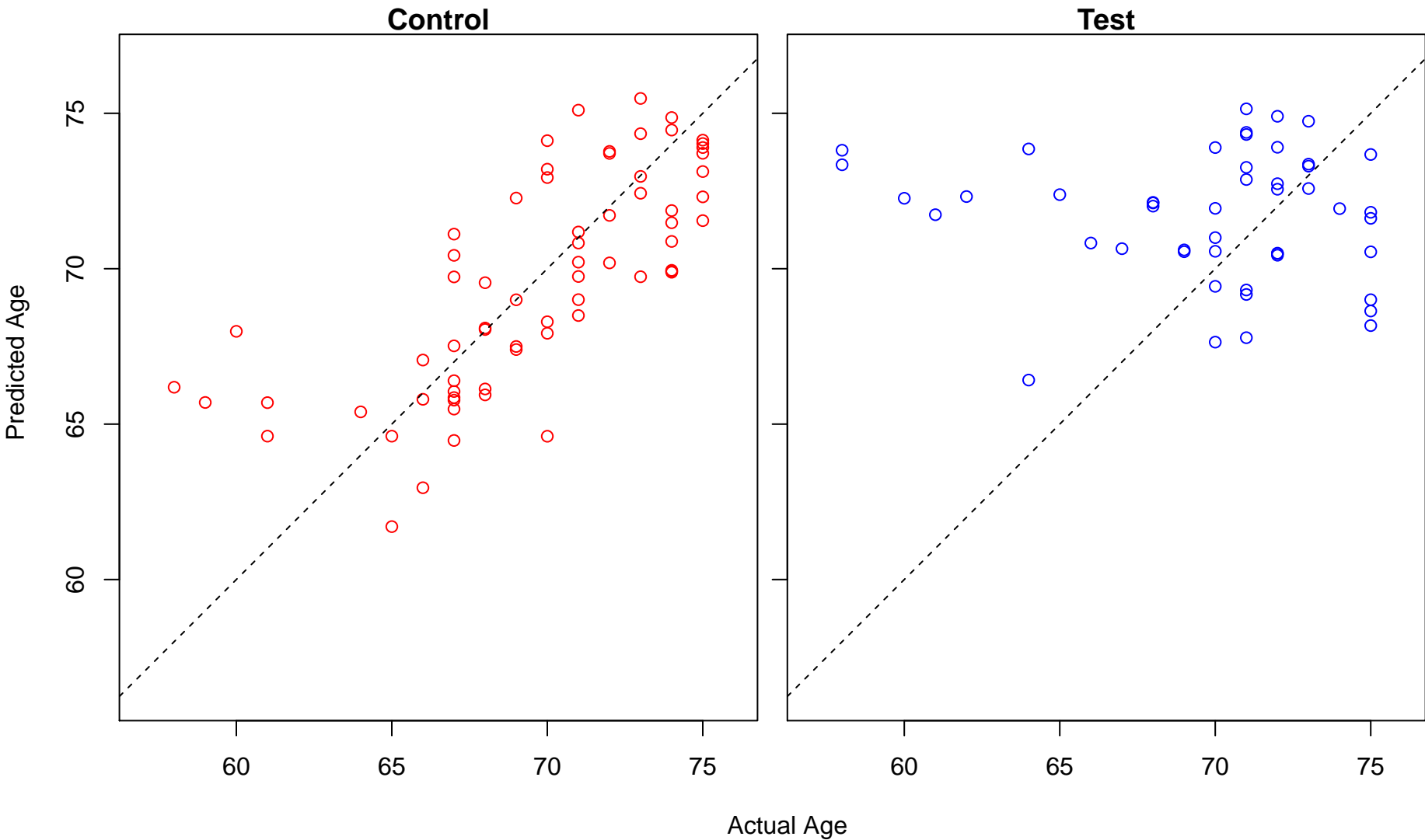
viral gene expression (Score: 1.702632)



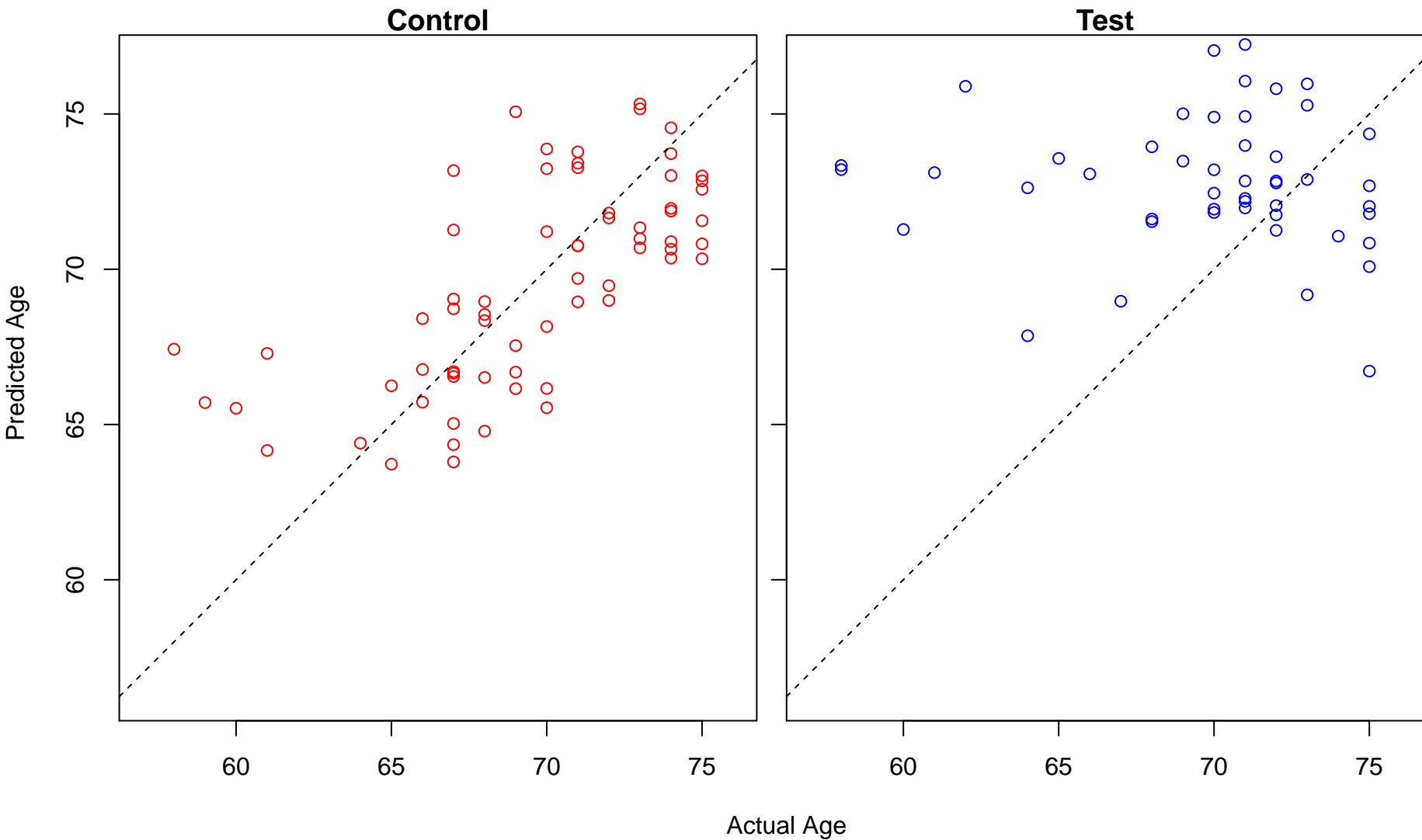
regulation of mitophagy (Score: 1.702613)



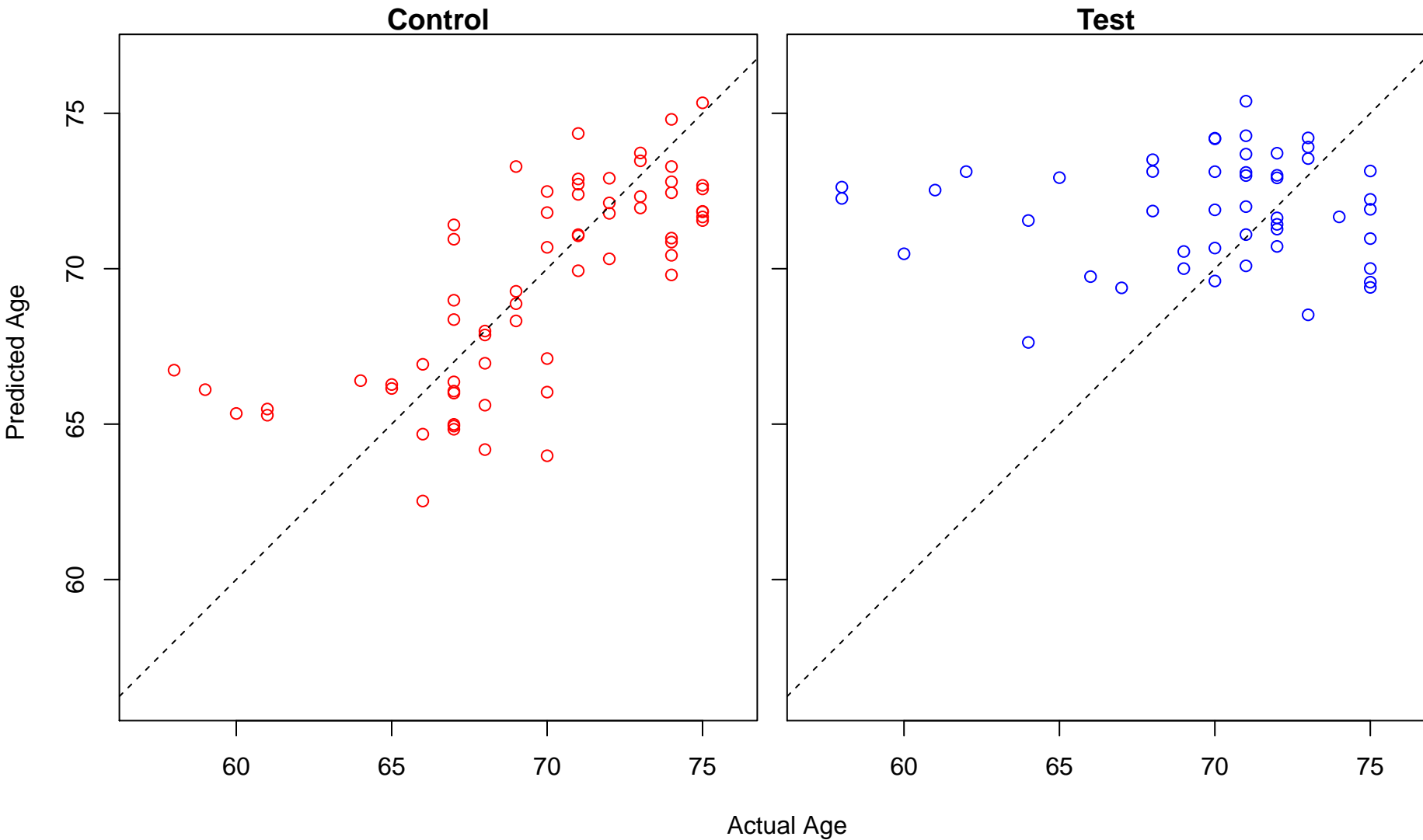
cellular component disassembly involved in execution phase of apoptosis (Score: 1.701404)



small molecule biosynthetic process (Score: 1.701057)

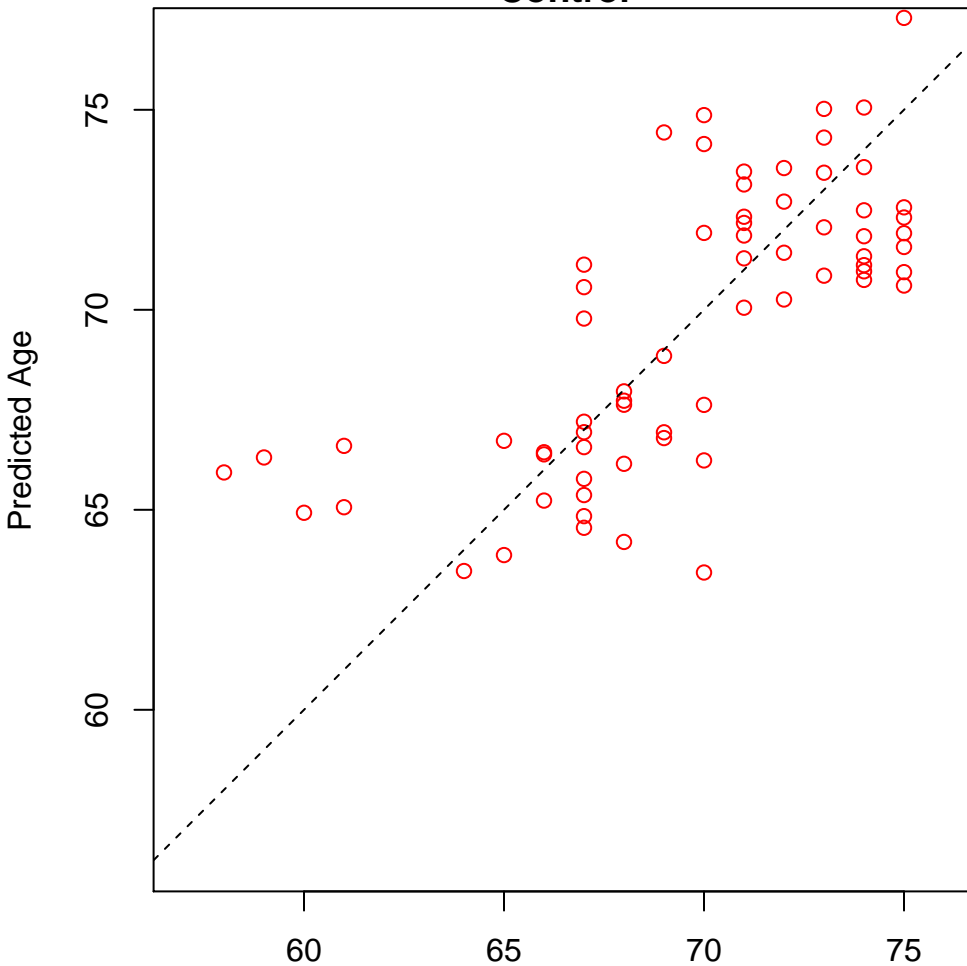


purine ribonucleotide biosynthetic process (Score: 1.701055)

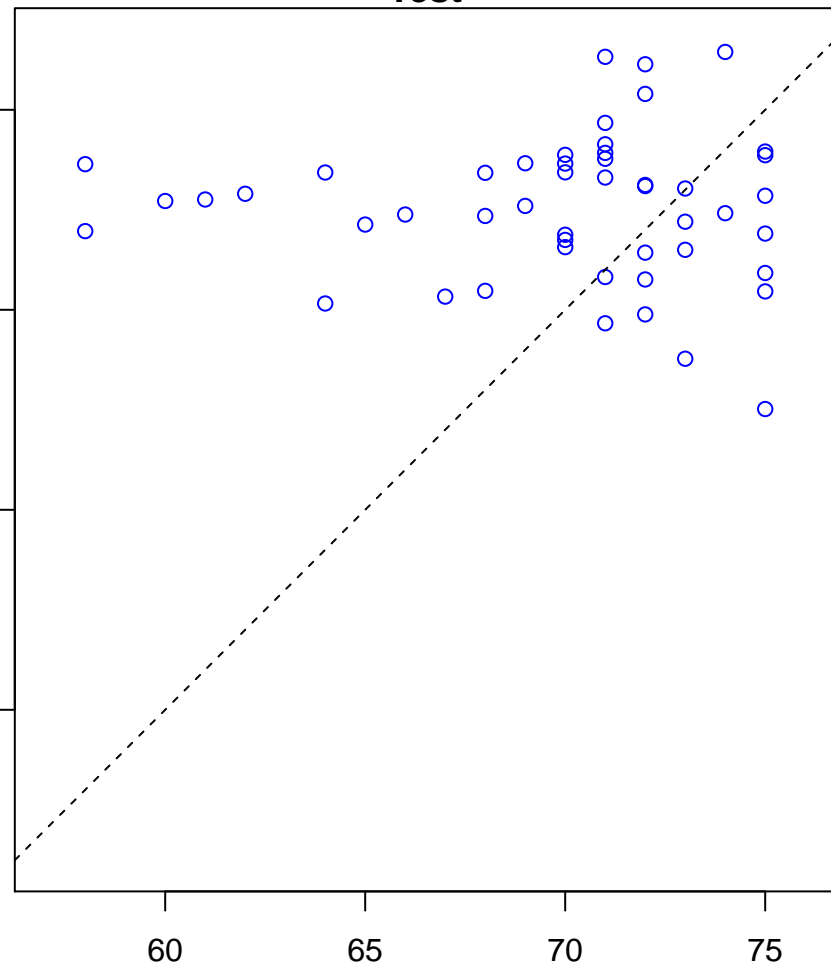


establishment of organelle localization (Score: 1.700300)

Control

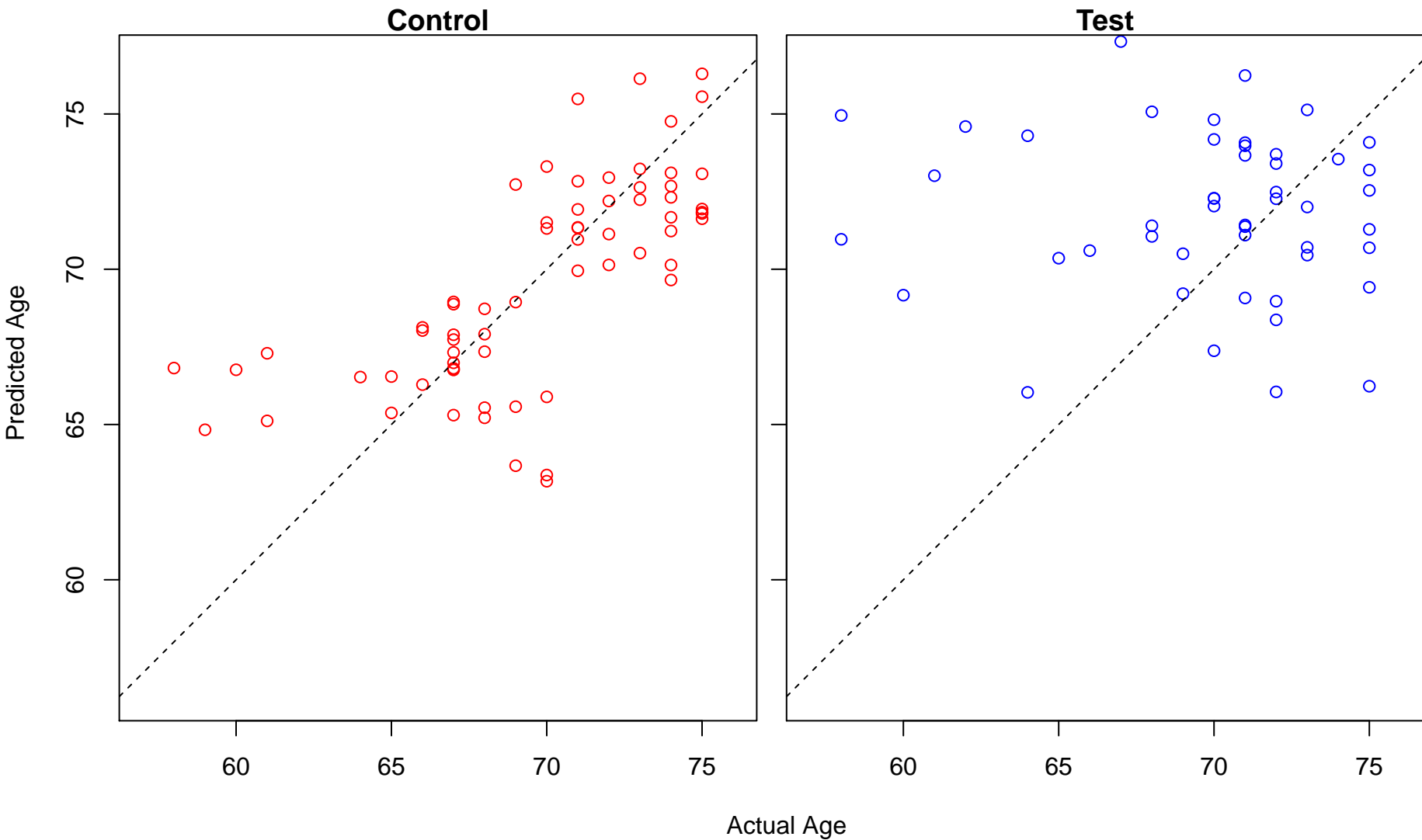


Test

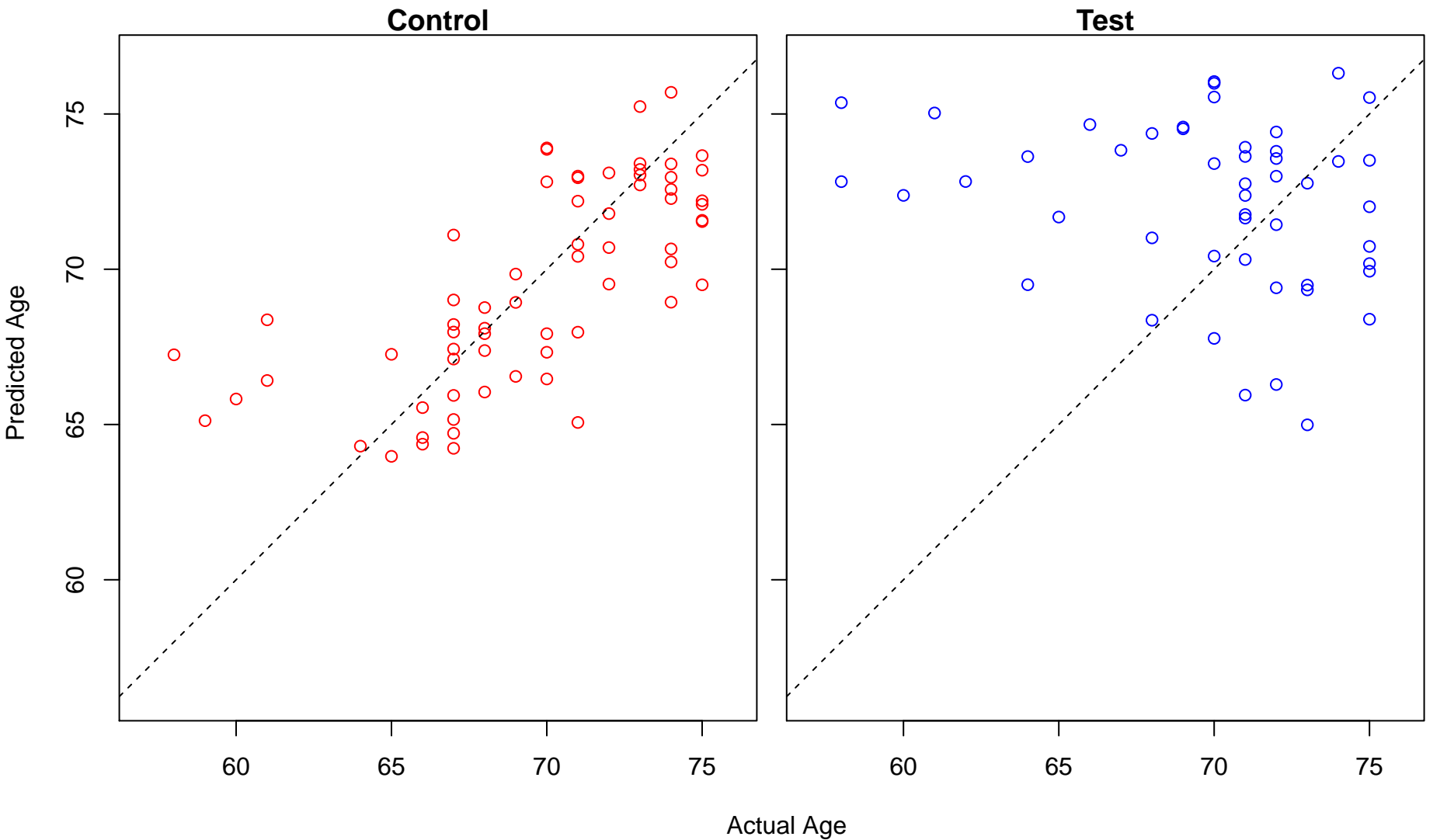


Actual Age

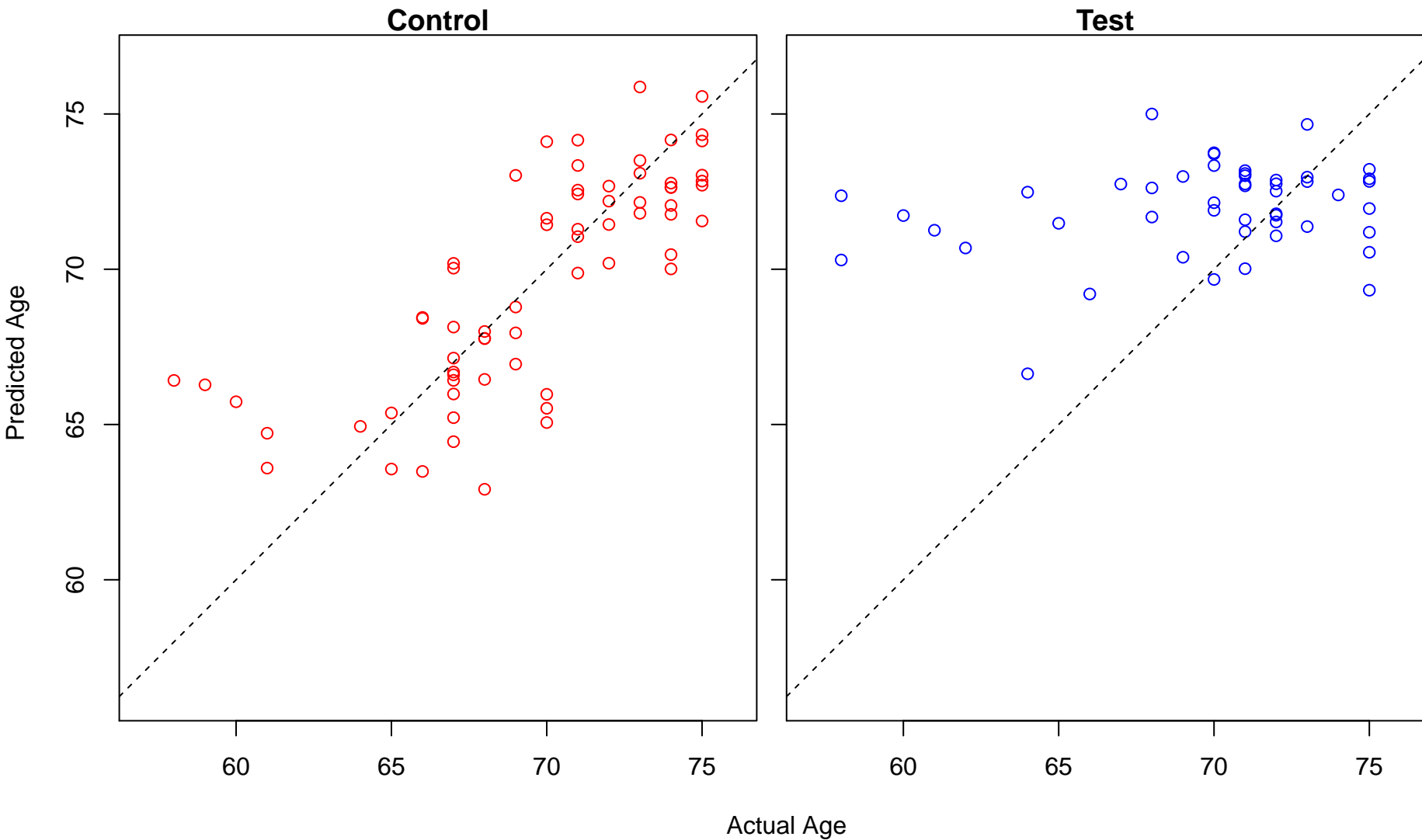
positive regulation of cell cycle G1/S phase transition (Score: 1.699912)



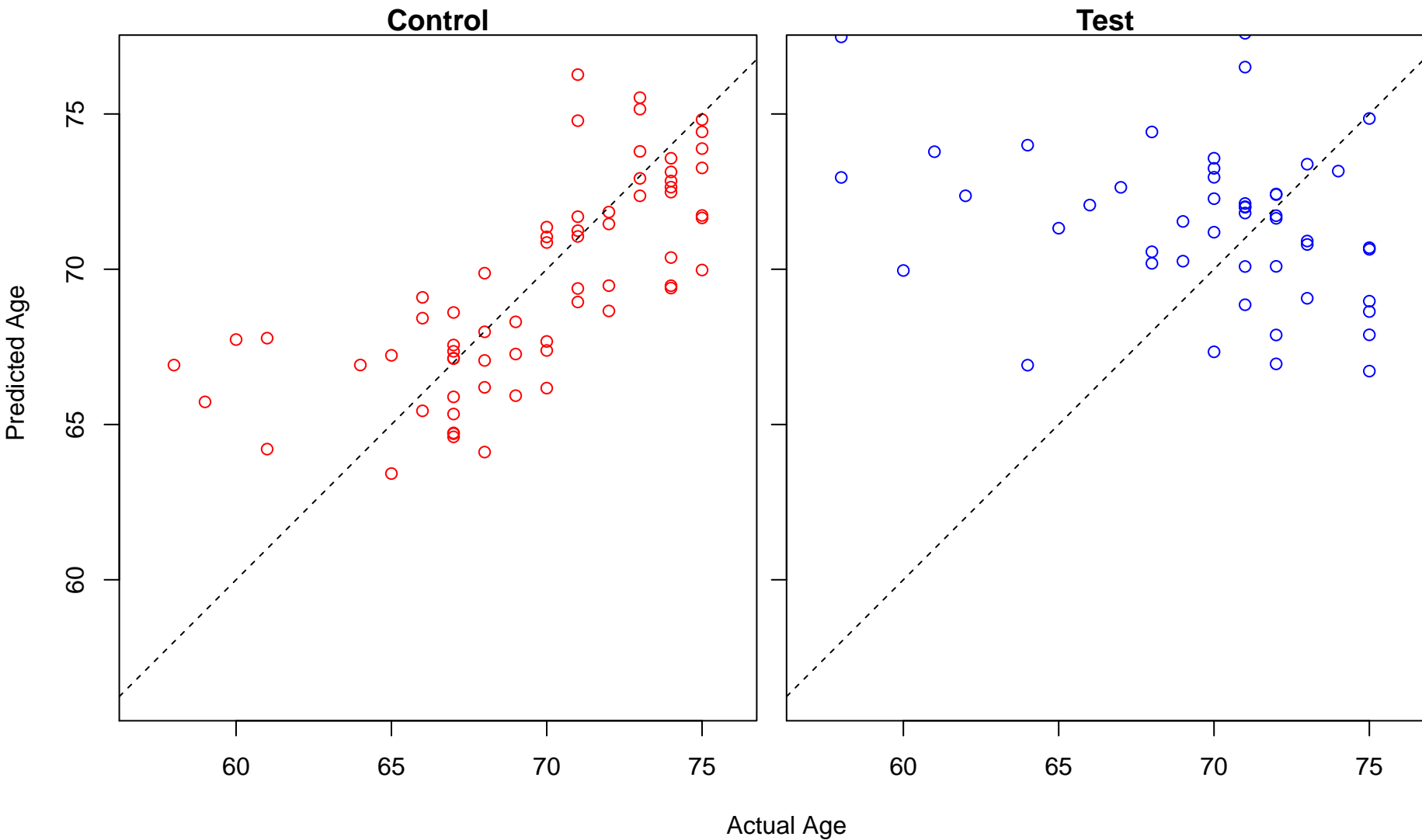
Immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily



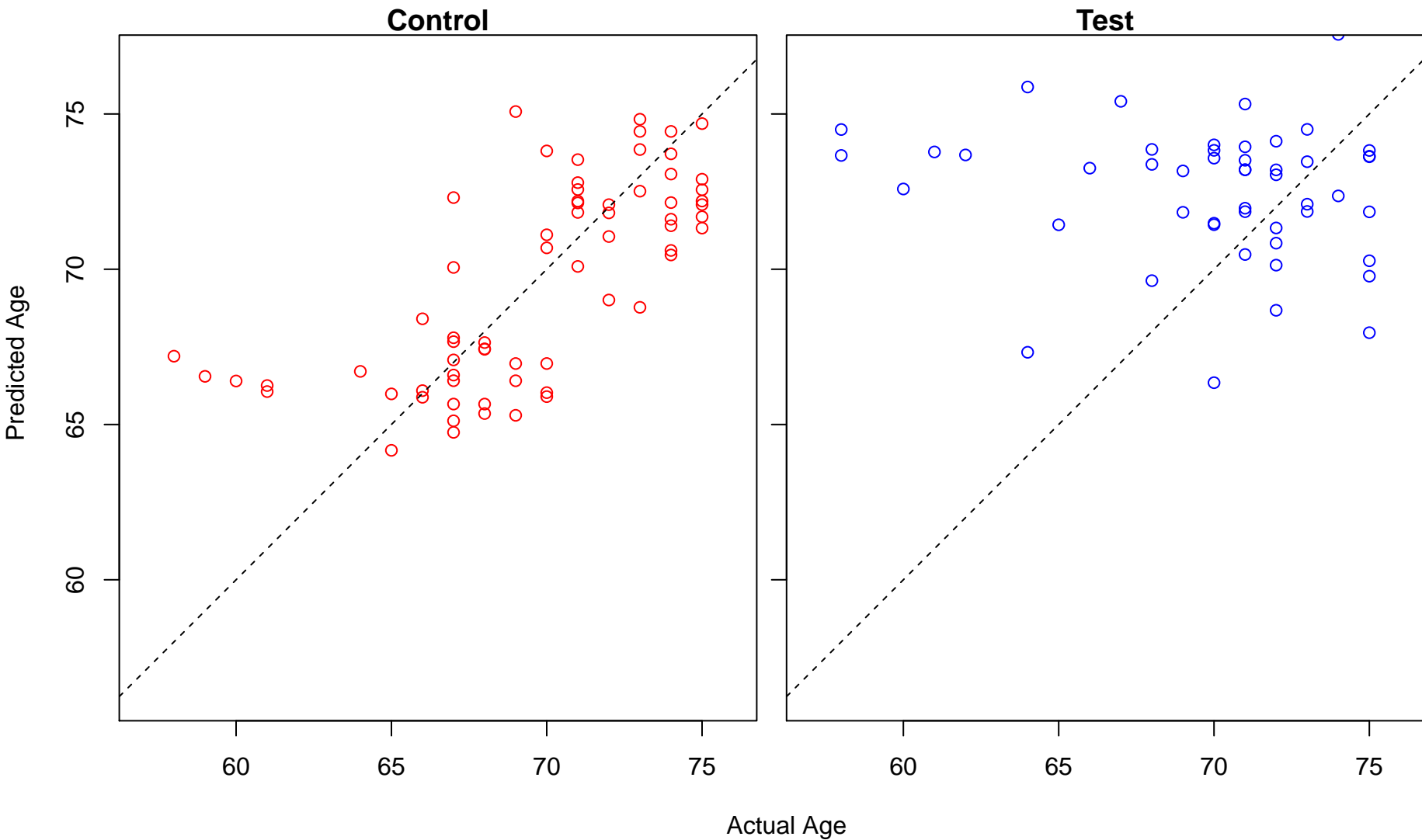
endosomal transport (Score: 1.698955)



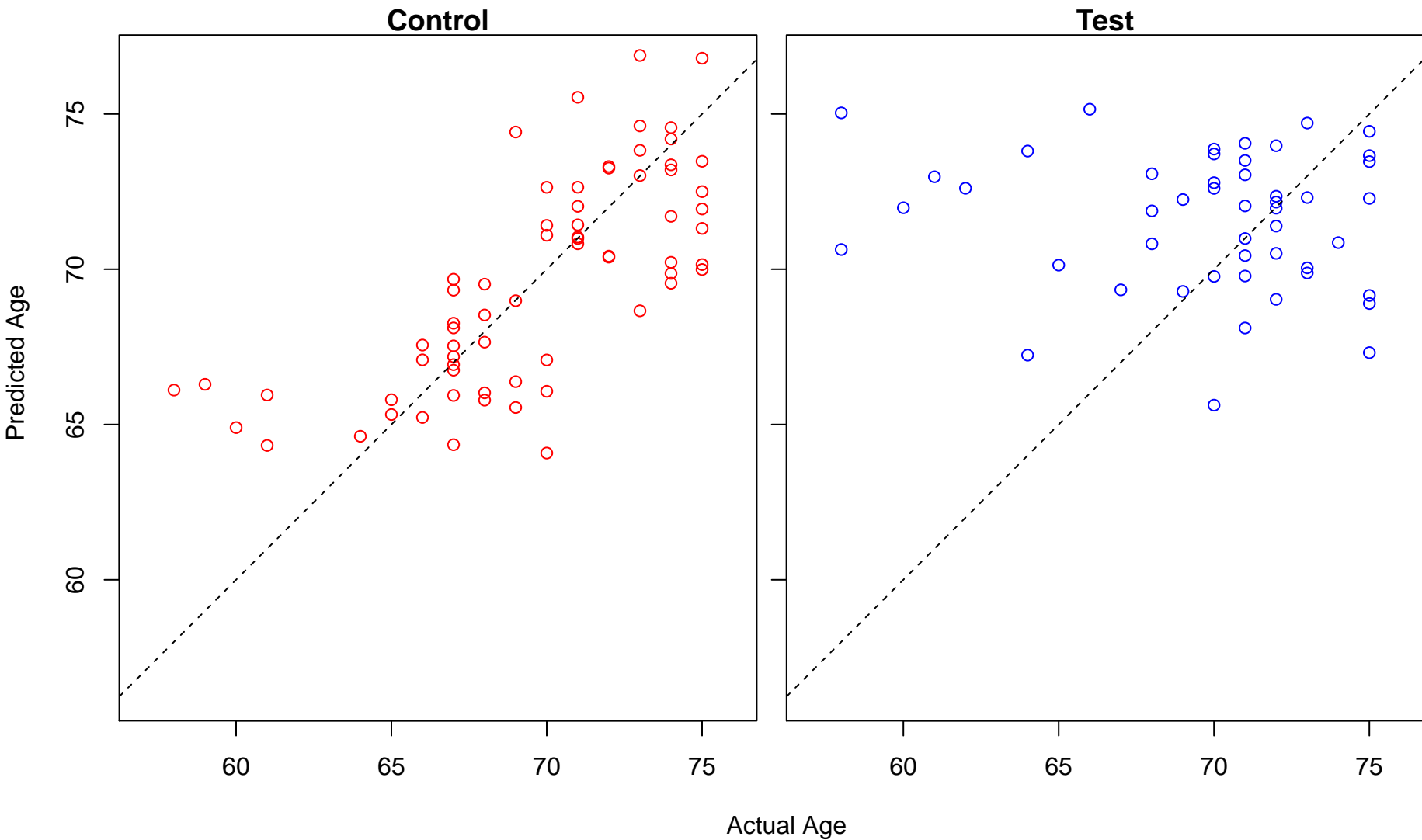
regulation of T cell proliferation (Score: 1.698206)



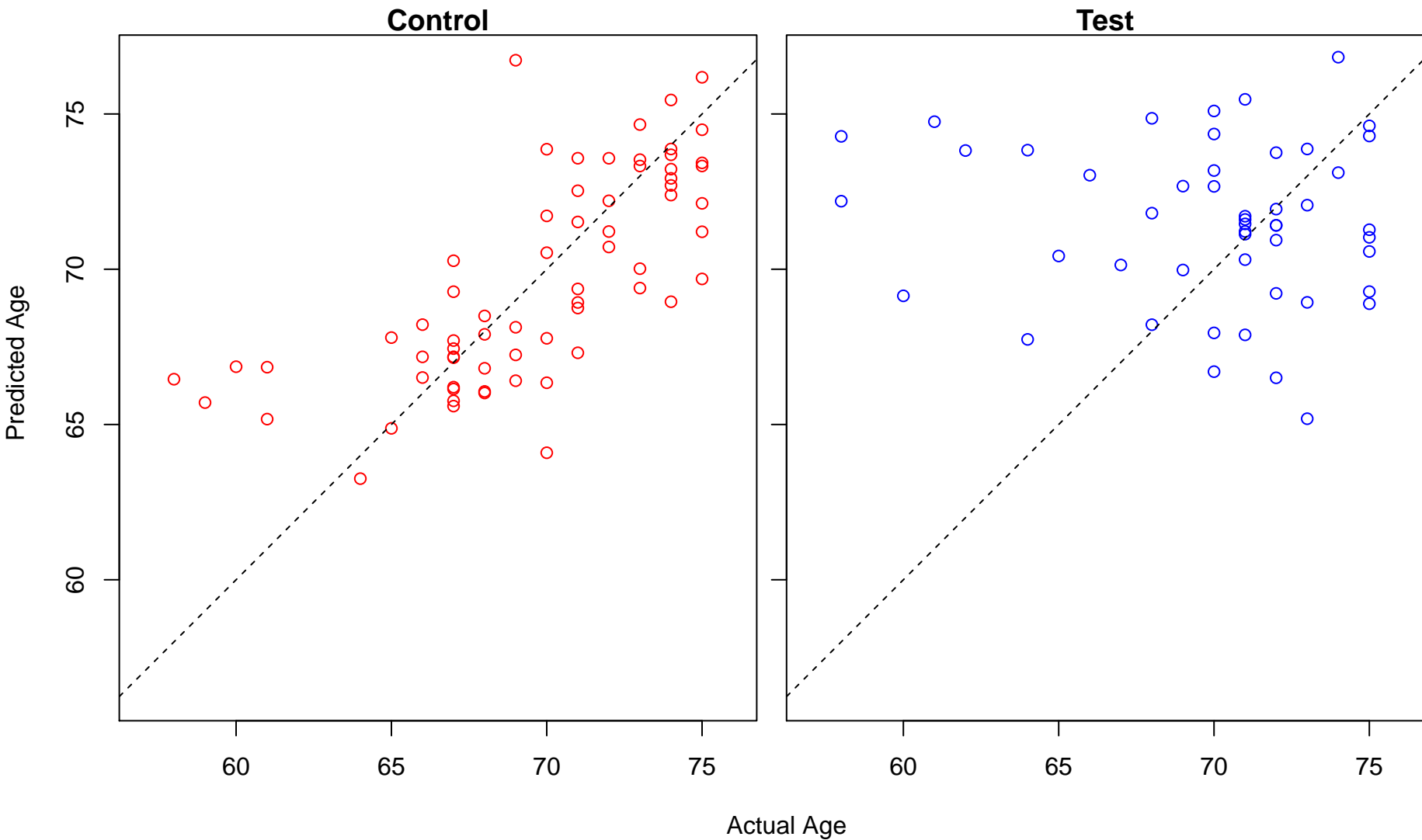
regulation of smooth muscle cell proliferation (Score: 1.698077)



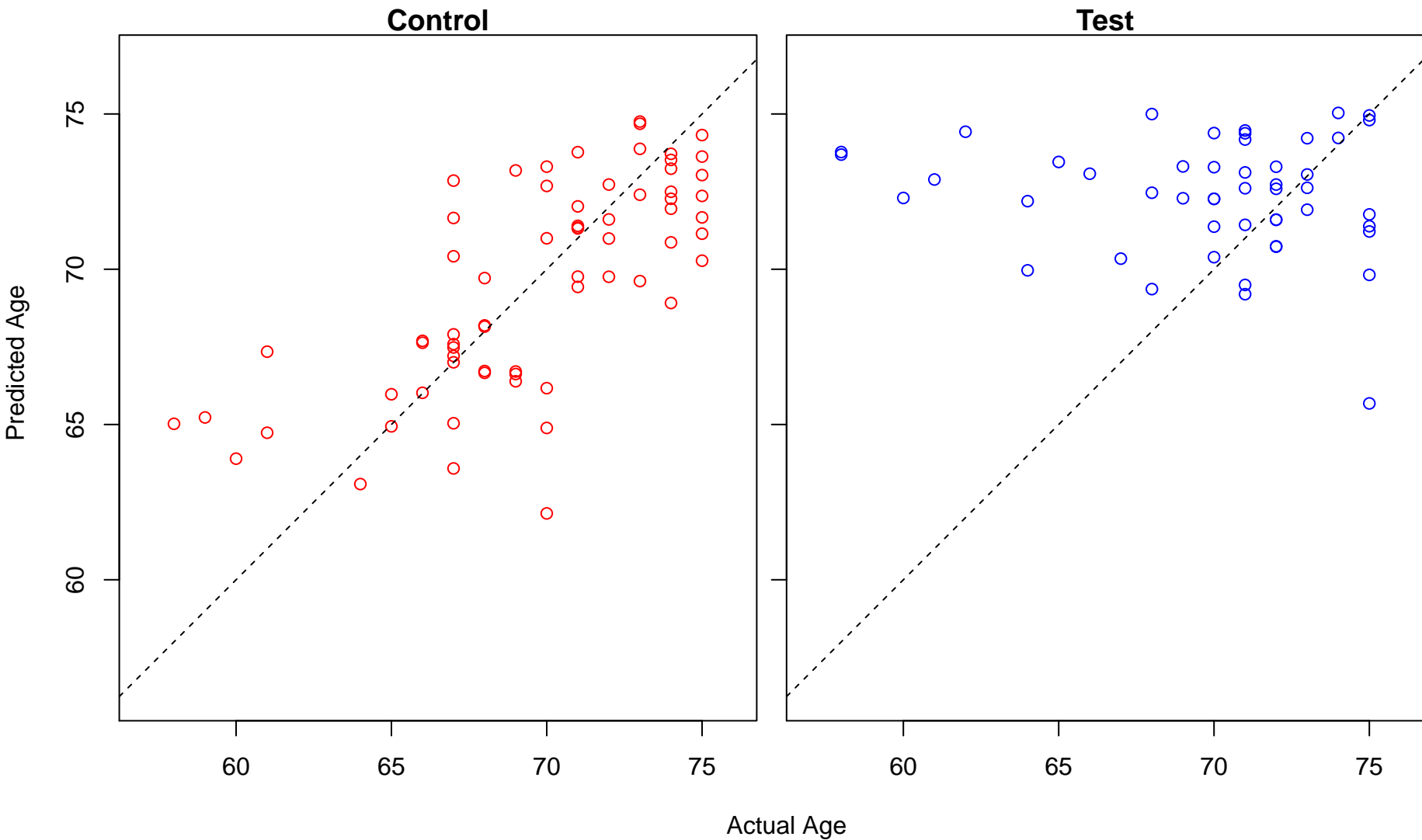
fatty acid oxidation (Score: 1.697063)



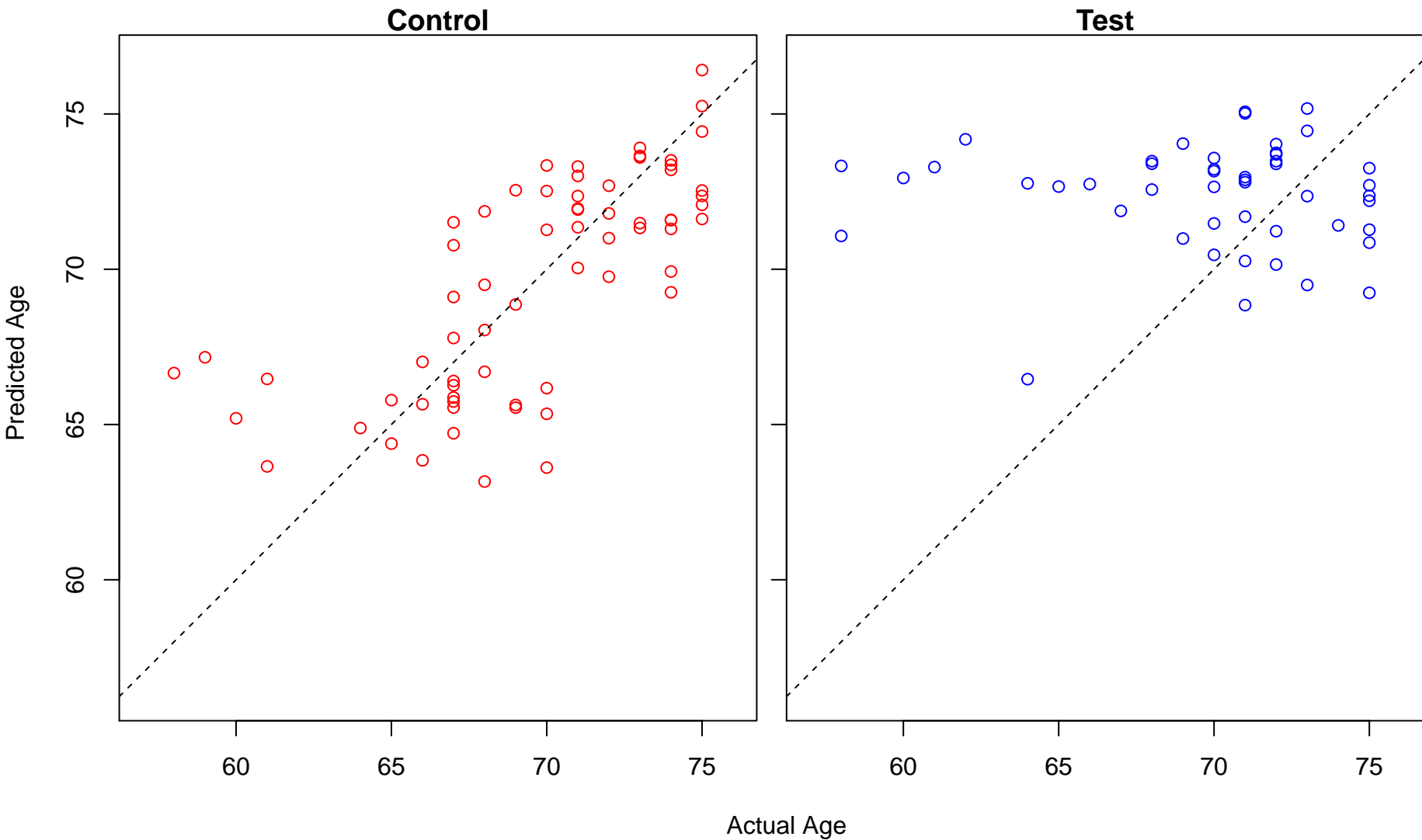
regulation of protein binding (Score: 1.696706)



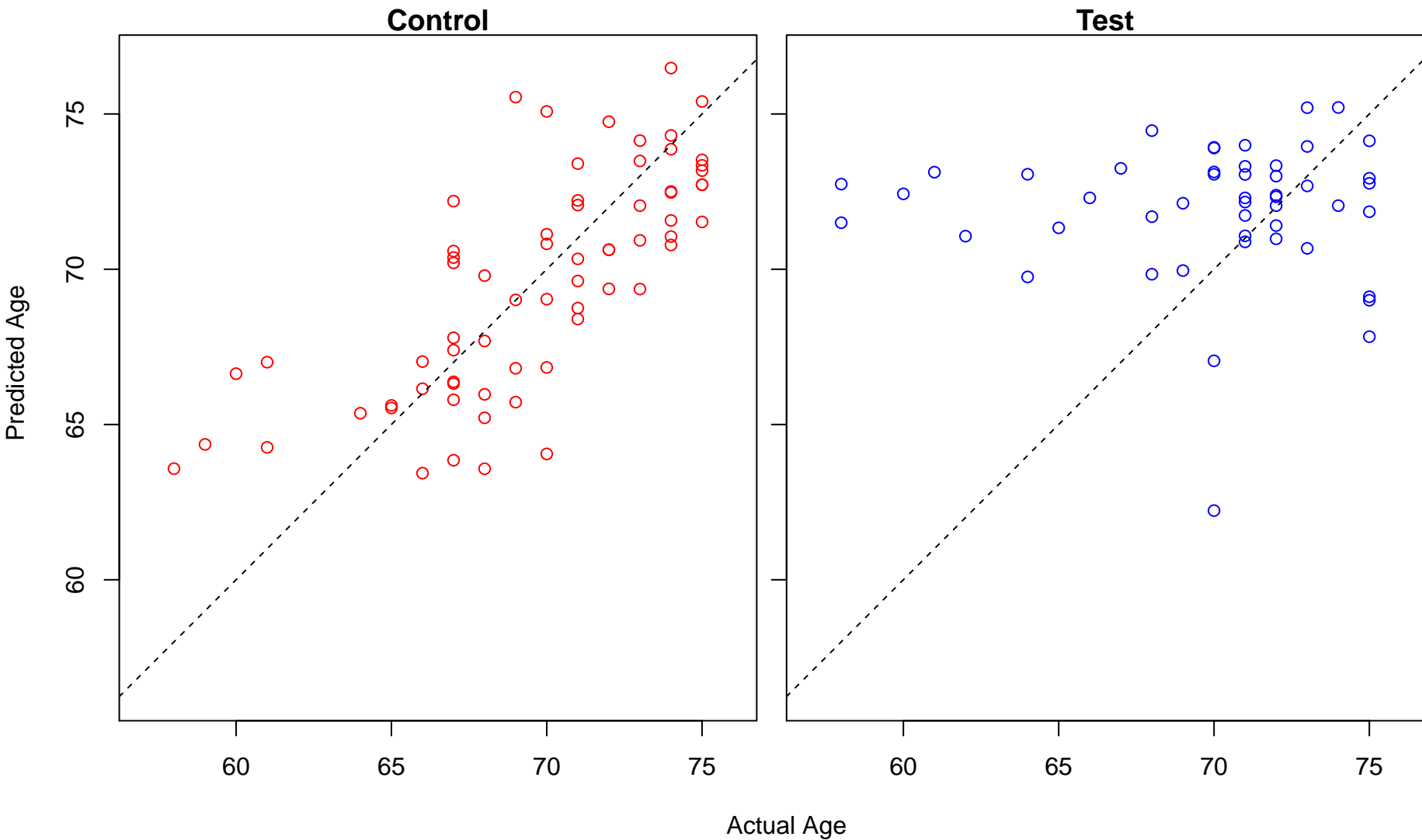
regulation of proteasomal protein catabolic process (Score: 1.696559)



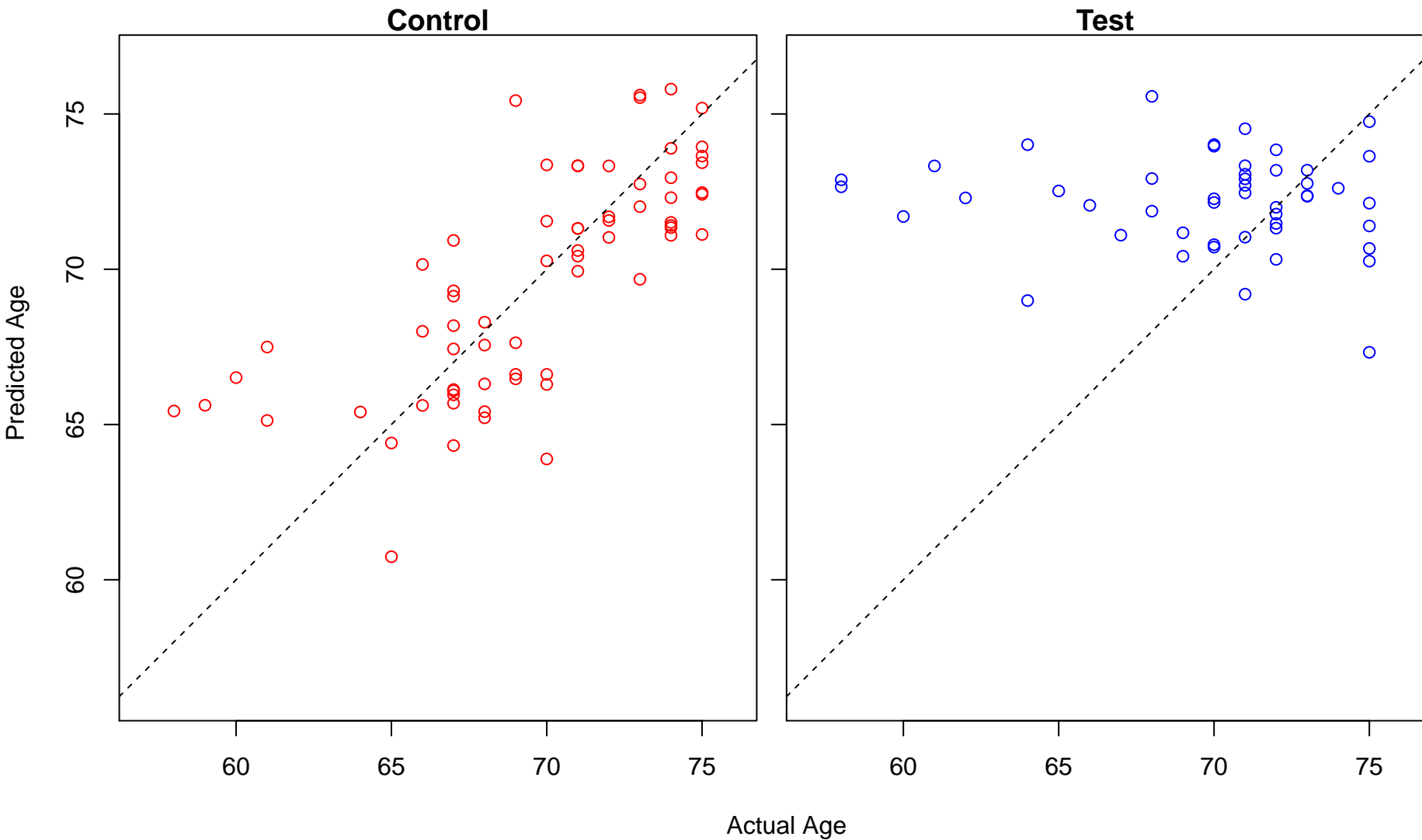
methylation (Score: 1.696061)



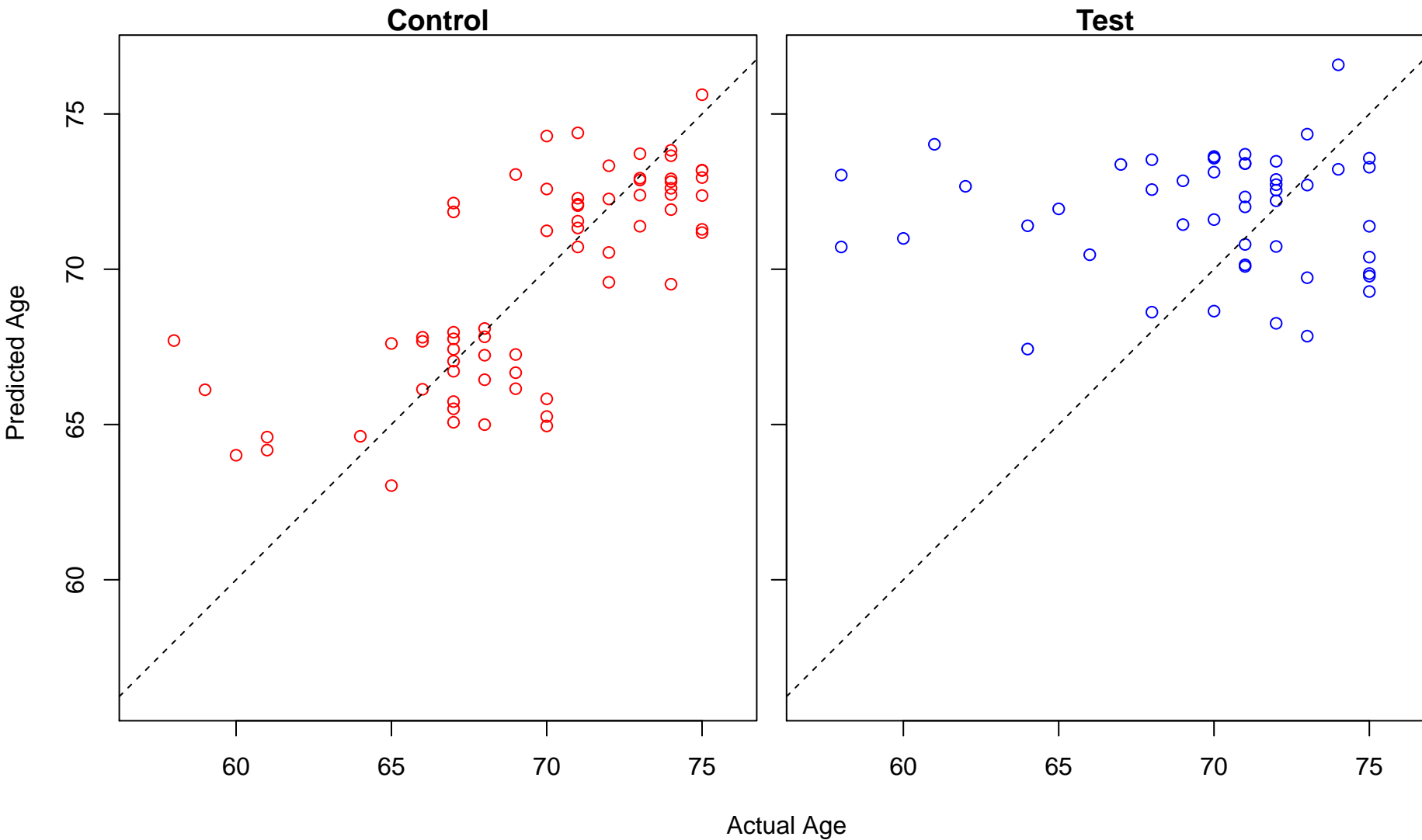
regulation of protein oligomerization (Score: 1.695601)



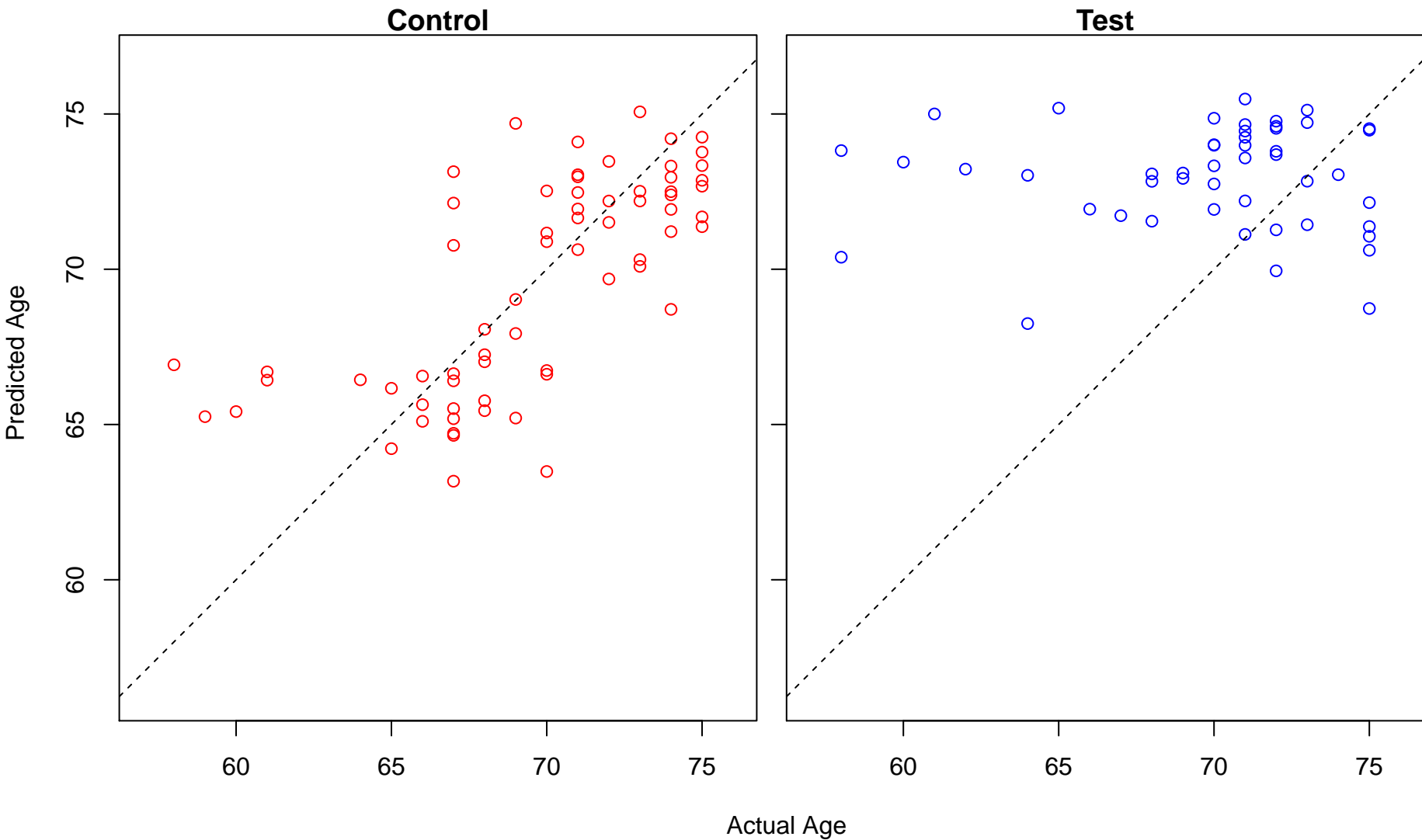
tumor necrosis factor-mediated signaling pathway (Score: 1.695359)



regulation of microtubule-based process (Score: 1.694672)

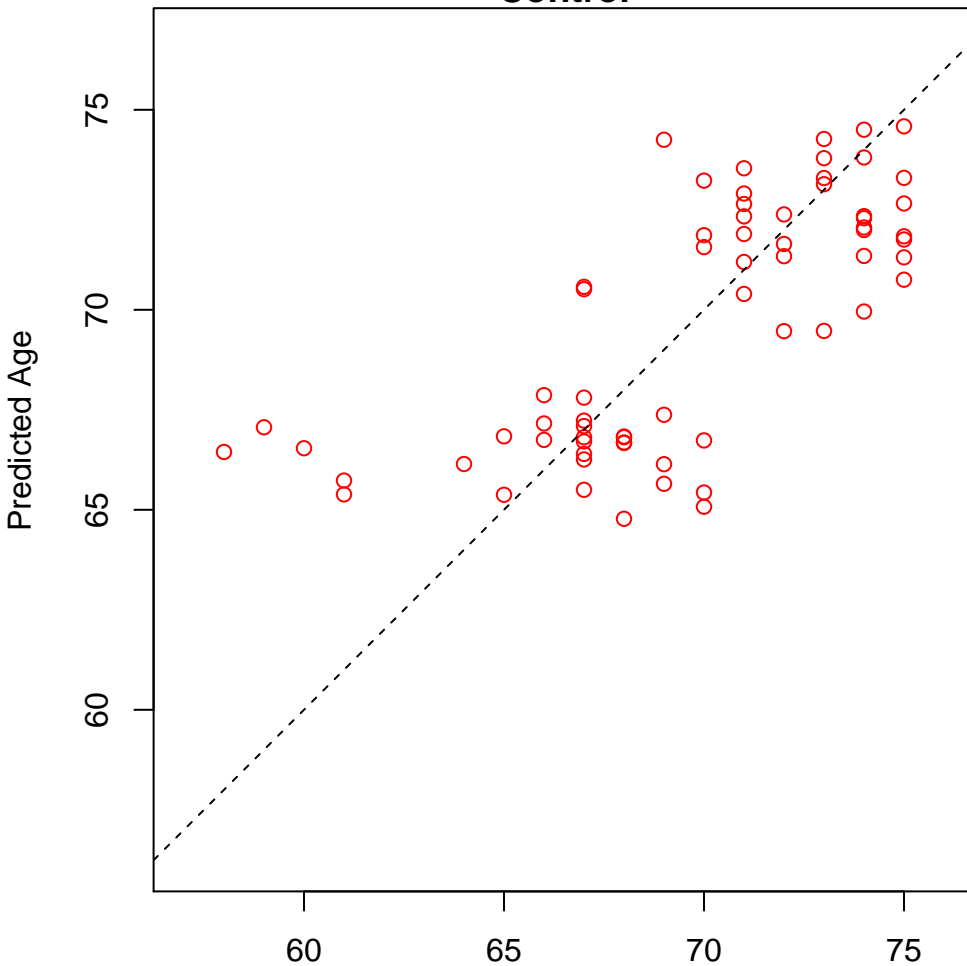


protein targeting to membrane (Score: 1.694593)

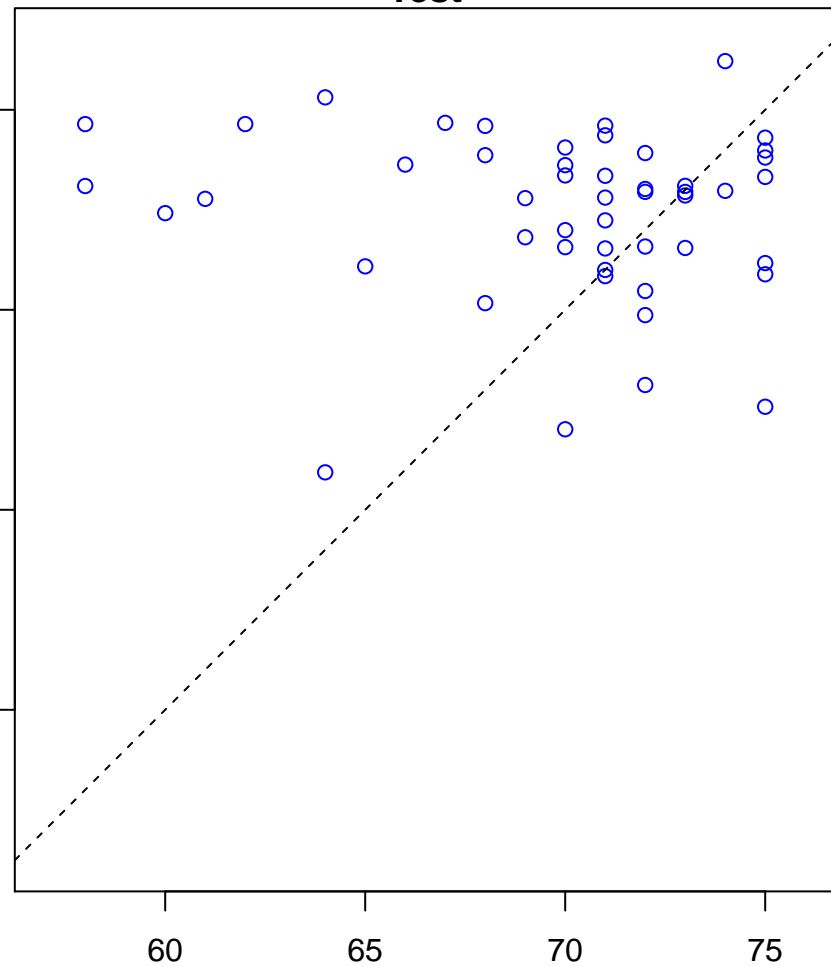


actin polymerization or depolymerization (Score: 1.694276)

Control

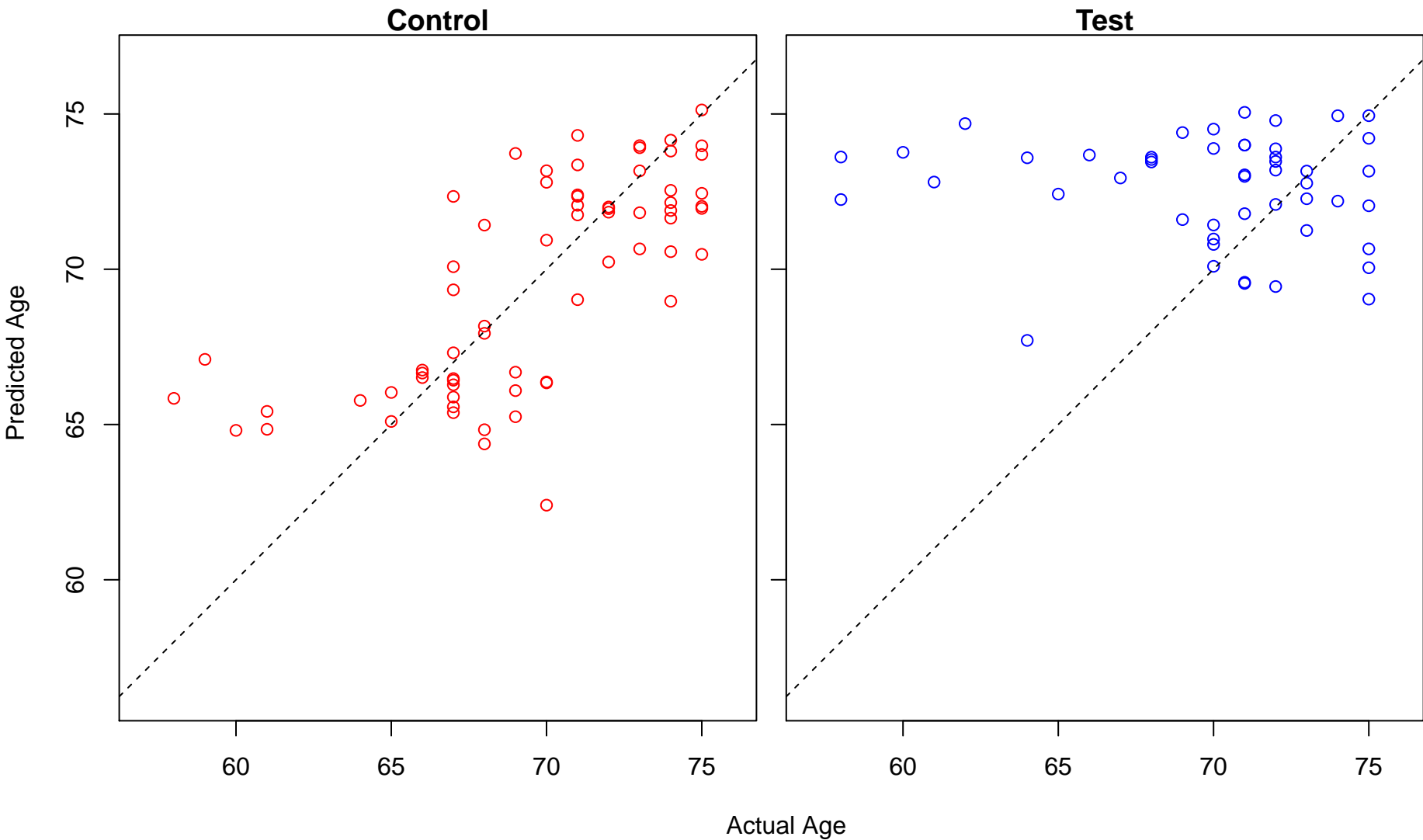


Test

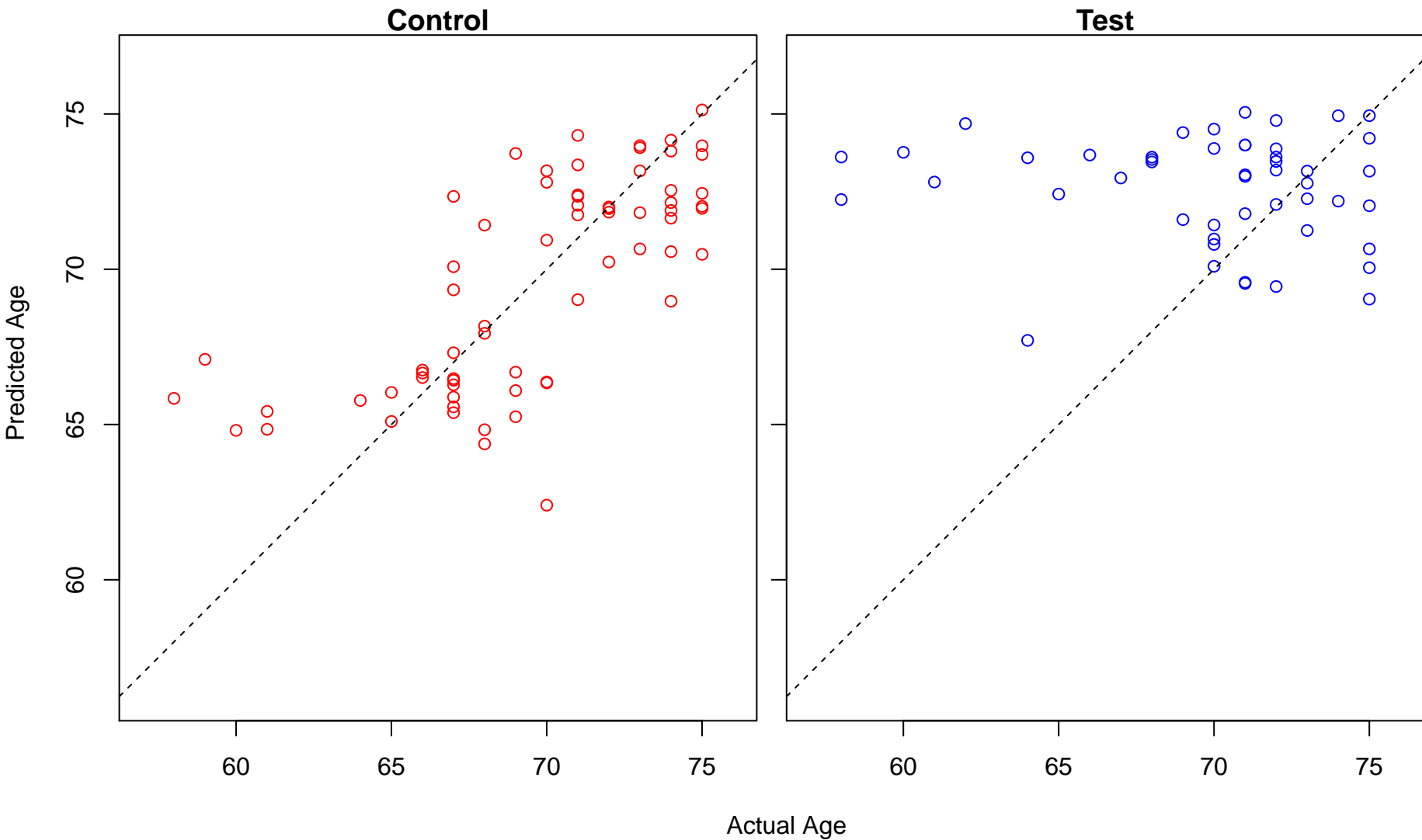


Actual Age

protein methylation (Score: 1.693763)

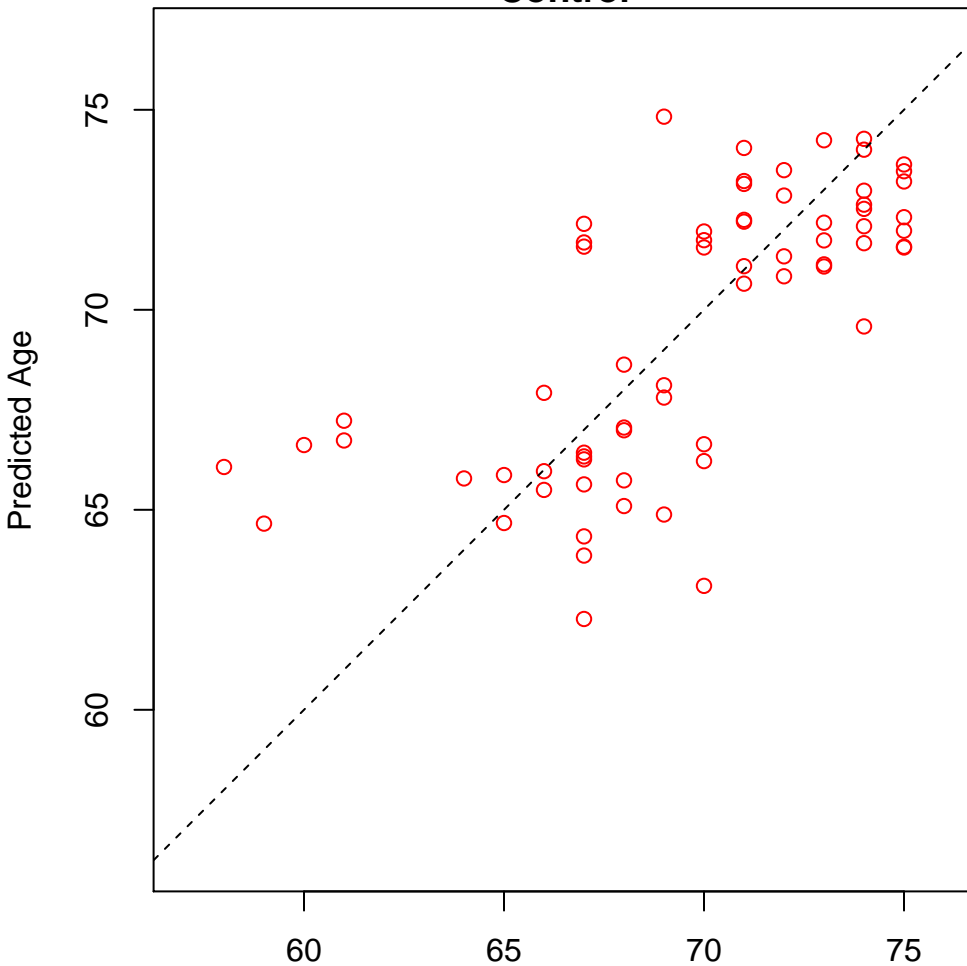


protein alkylation (Score: 1.693763)

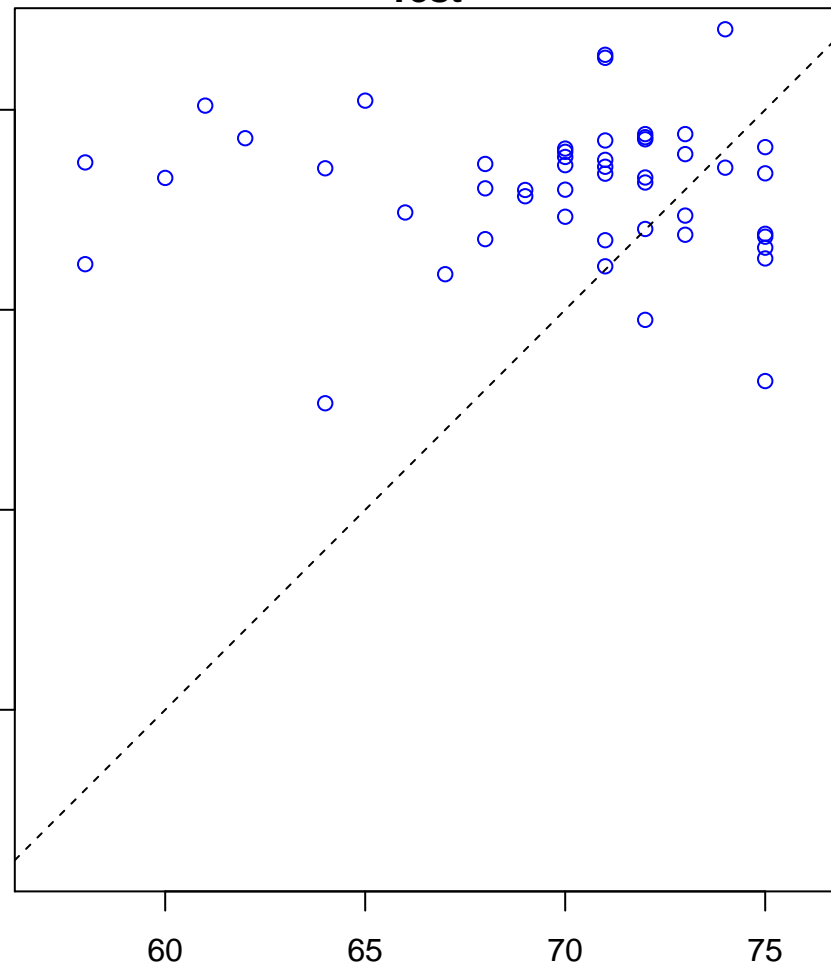


aromatic compound catabolic process (Score: 1.693528)

Control

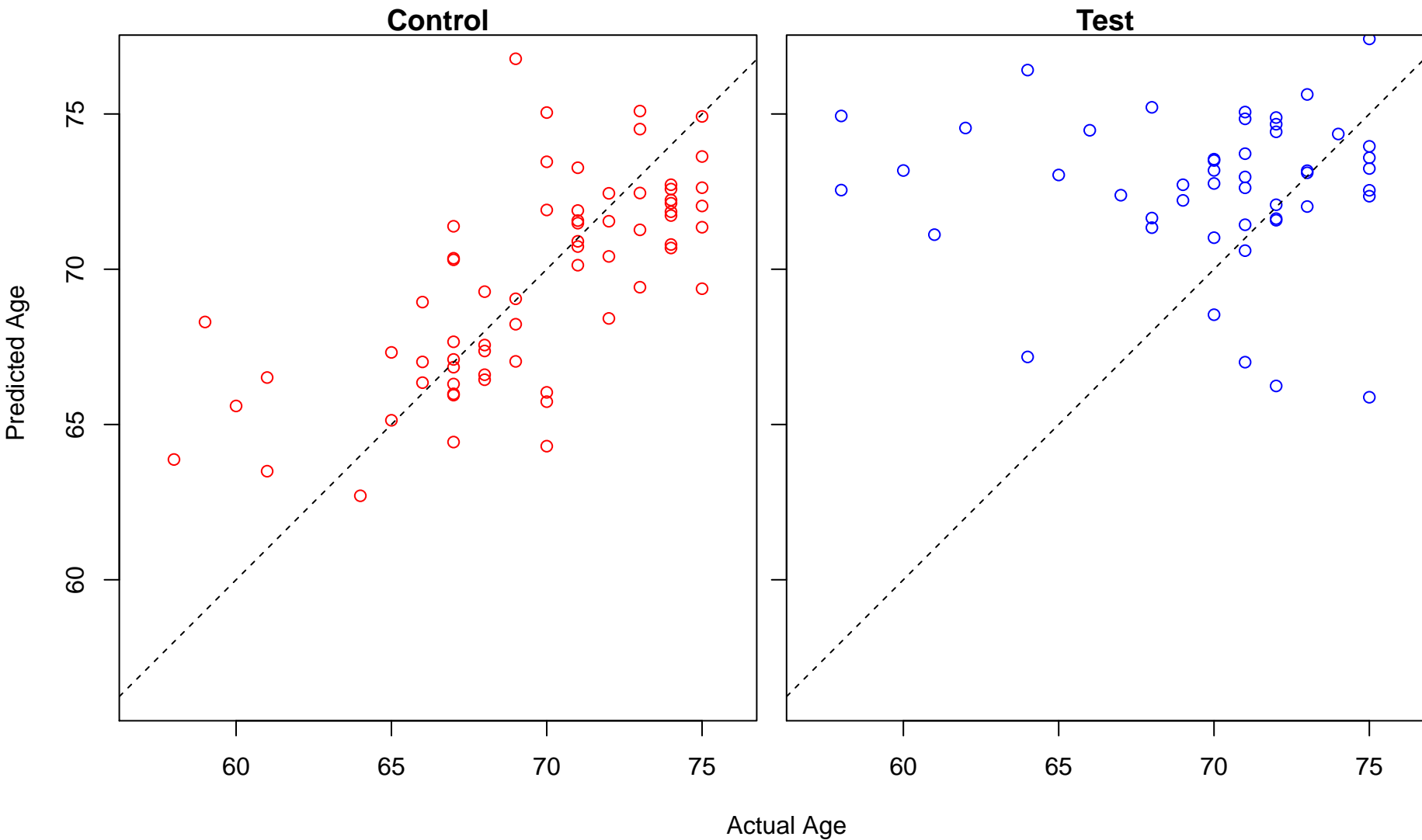


Test

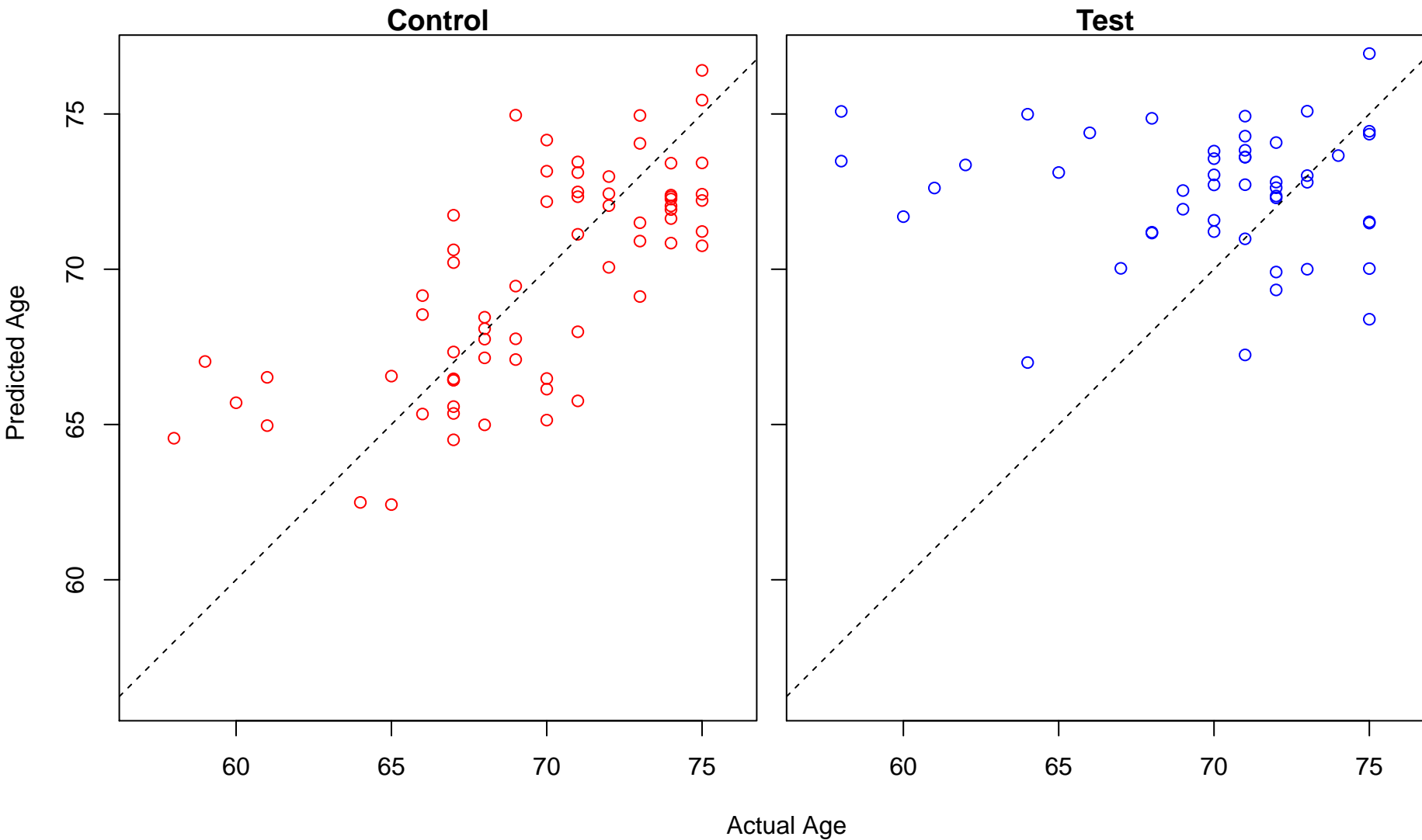


Actual Age

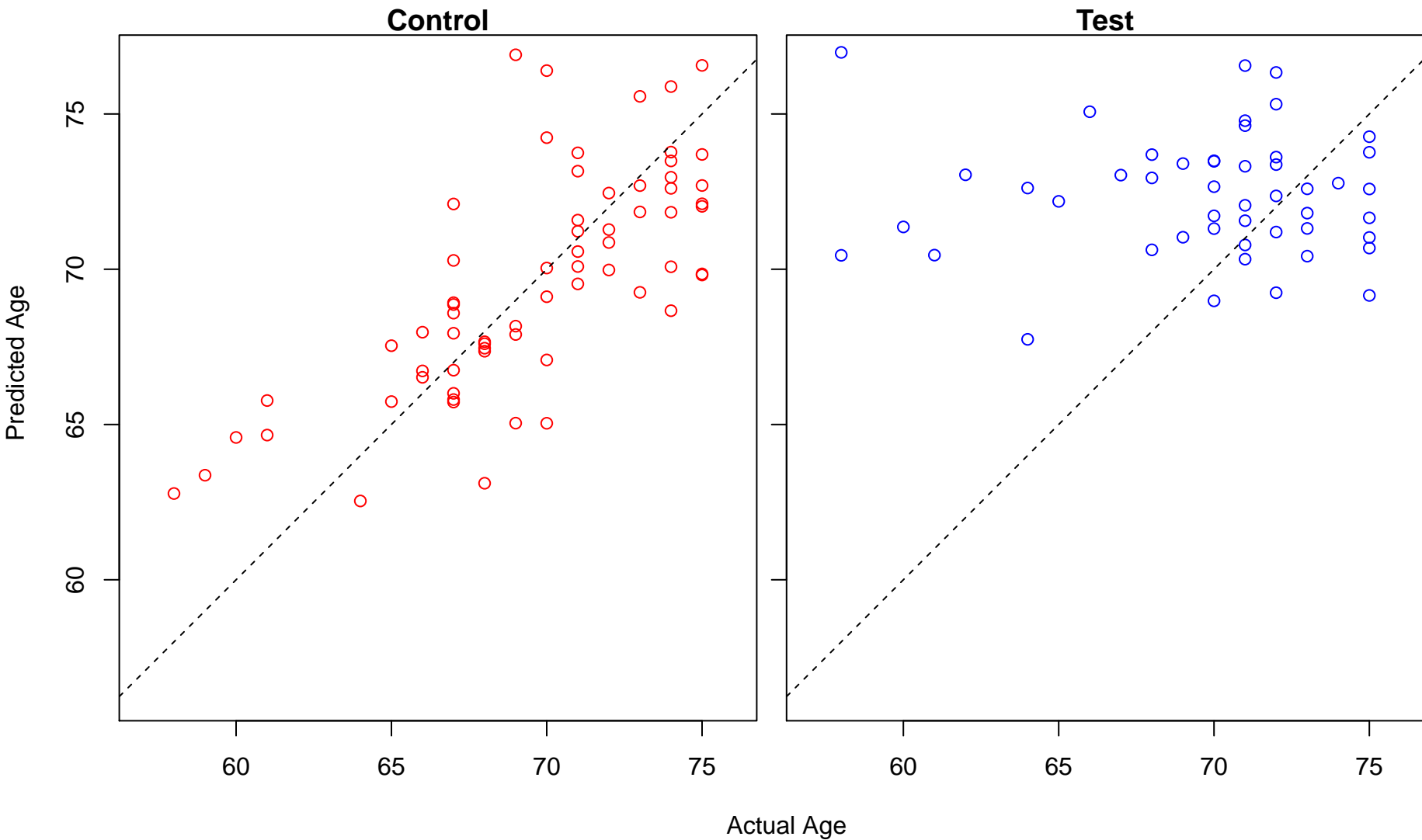
toll-like receptor 2 signaling pathway (Score: 1.692406)



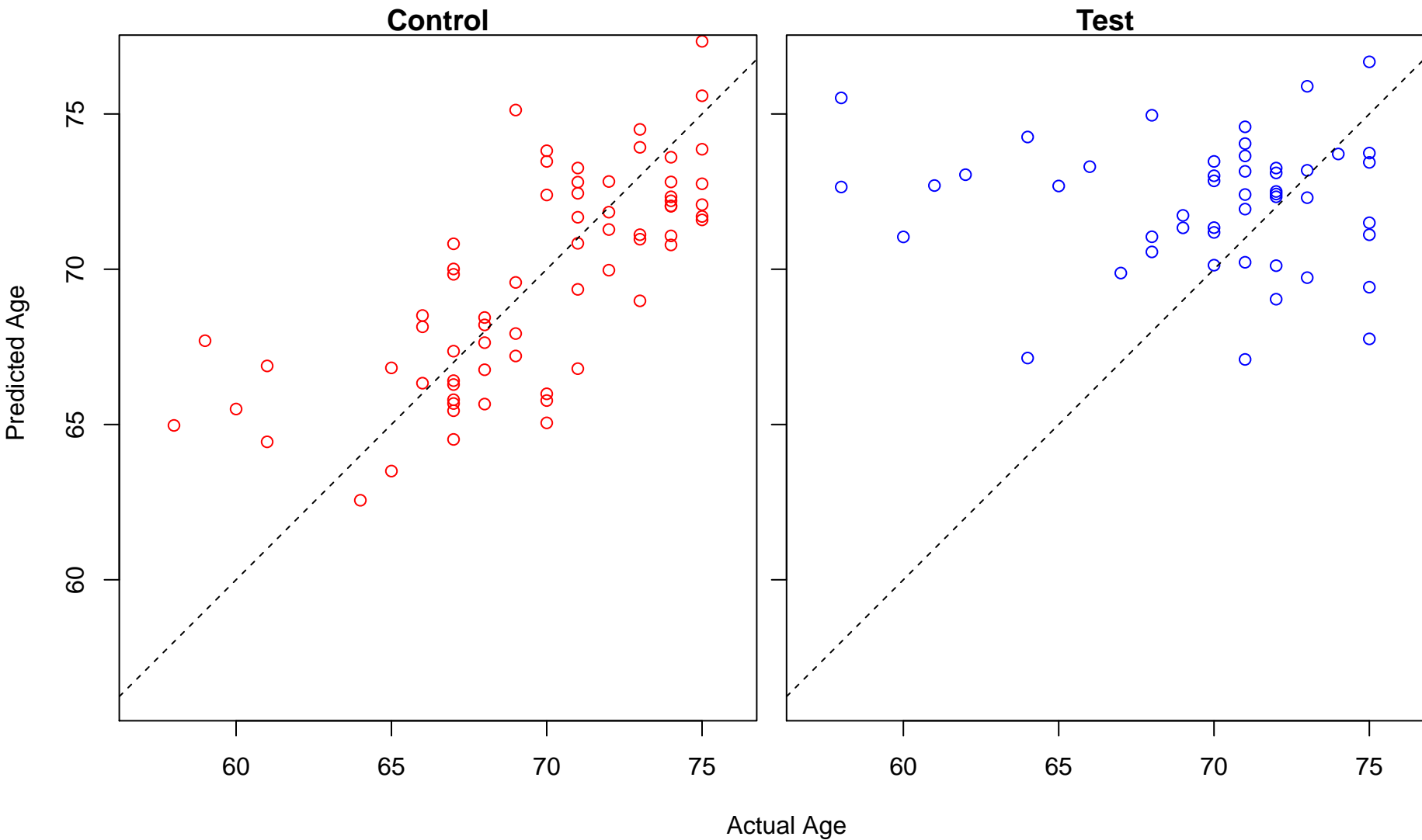
pattern recognition receptor signaling pathway (Score: 1.692045)



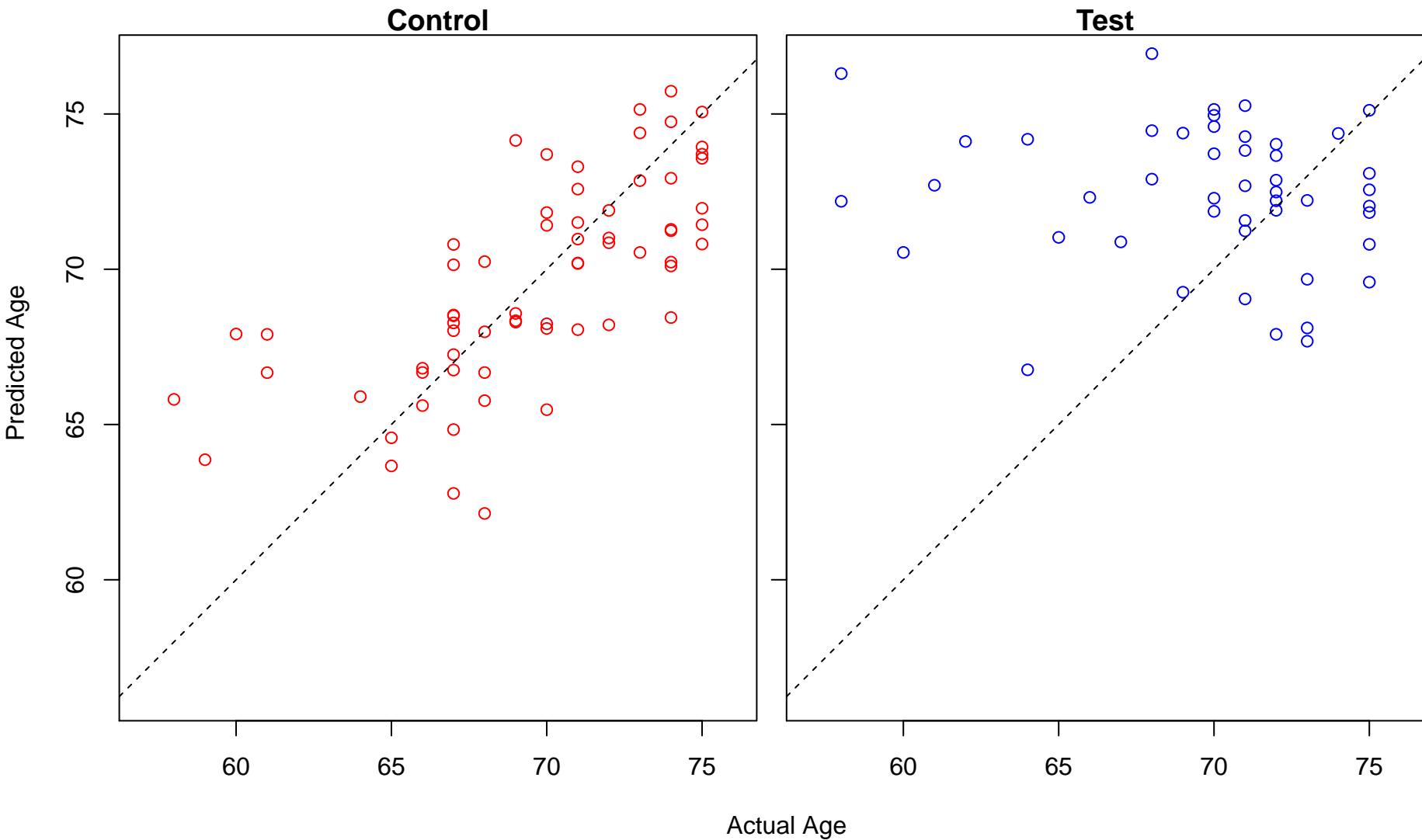
divalent metal ion transport (Score: 1.691370)



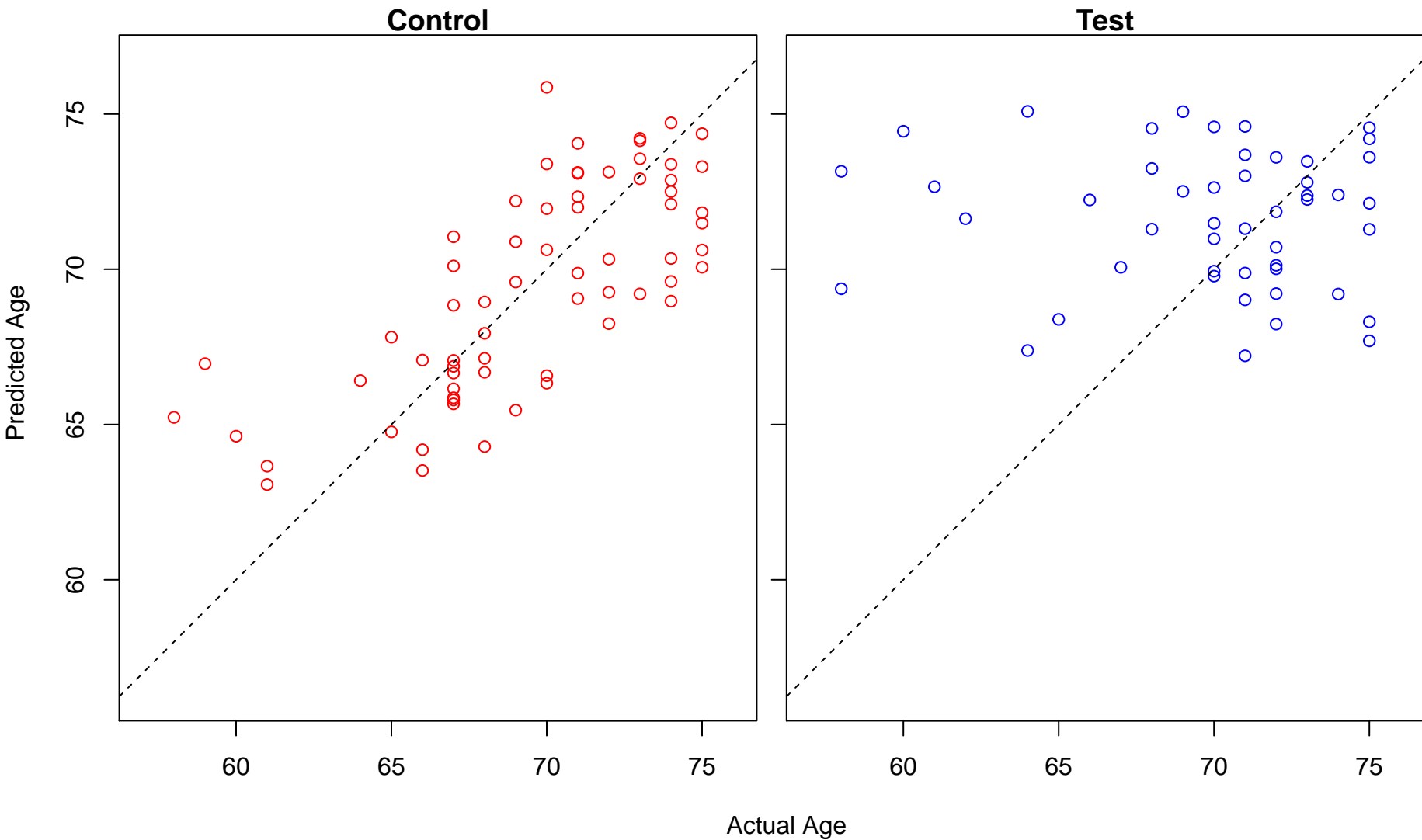
toll-like receptor signaling pathway (Score: 1.690601)



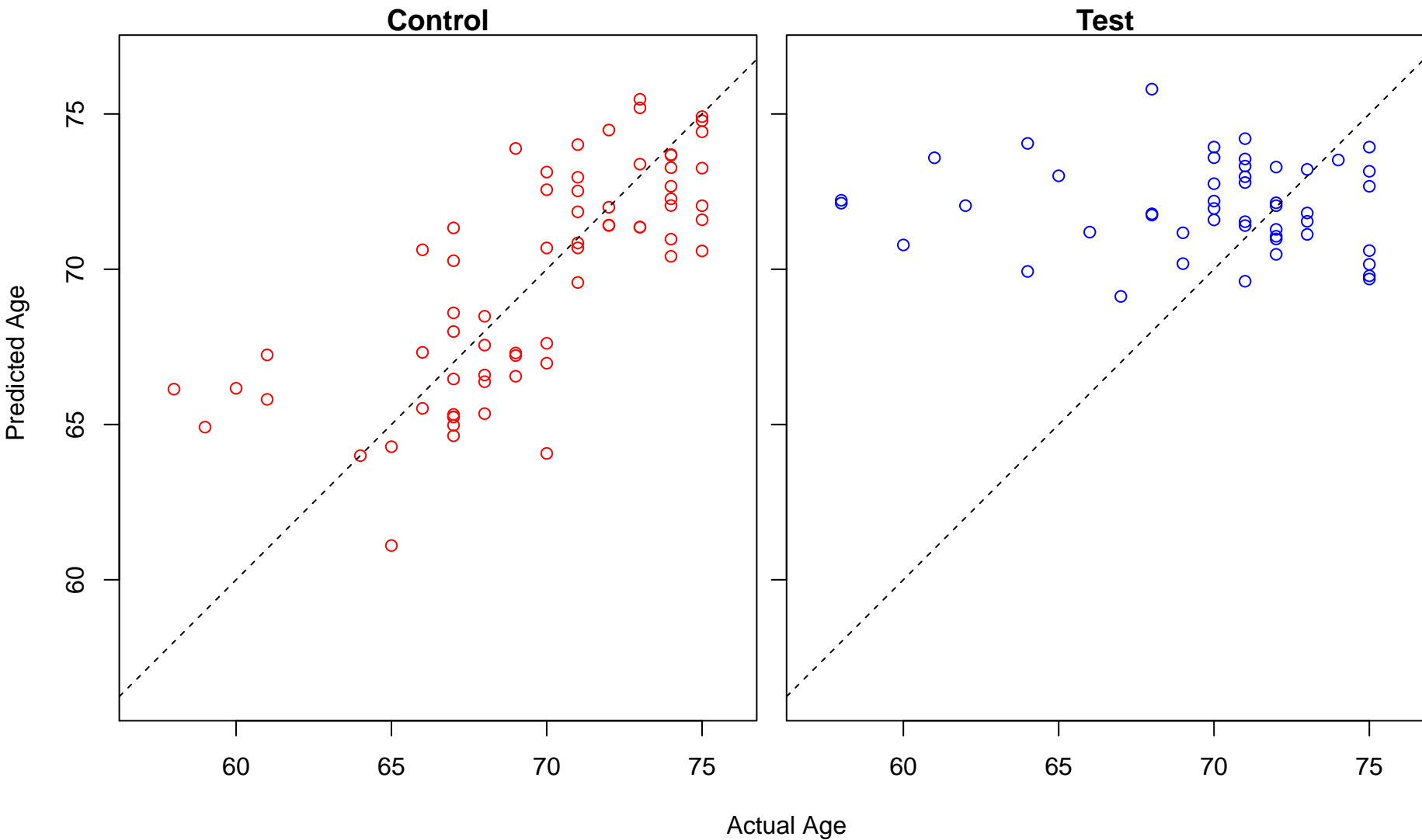
response to steroid hormone (Score: 1.690384)



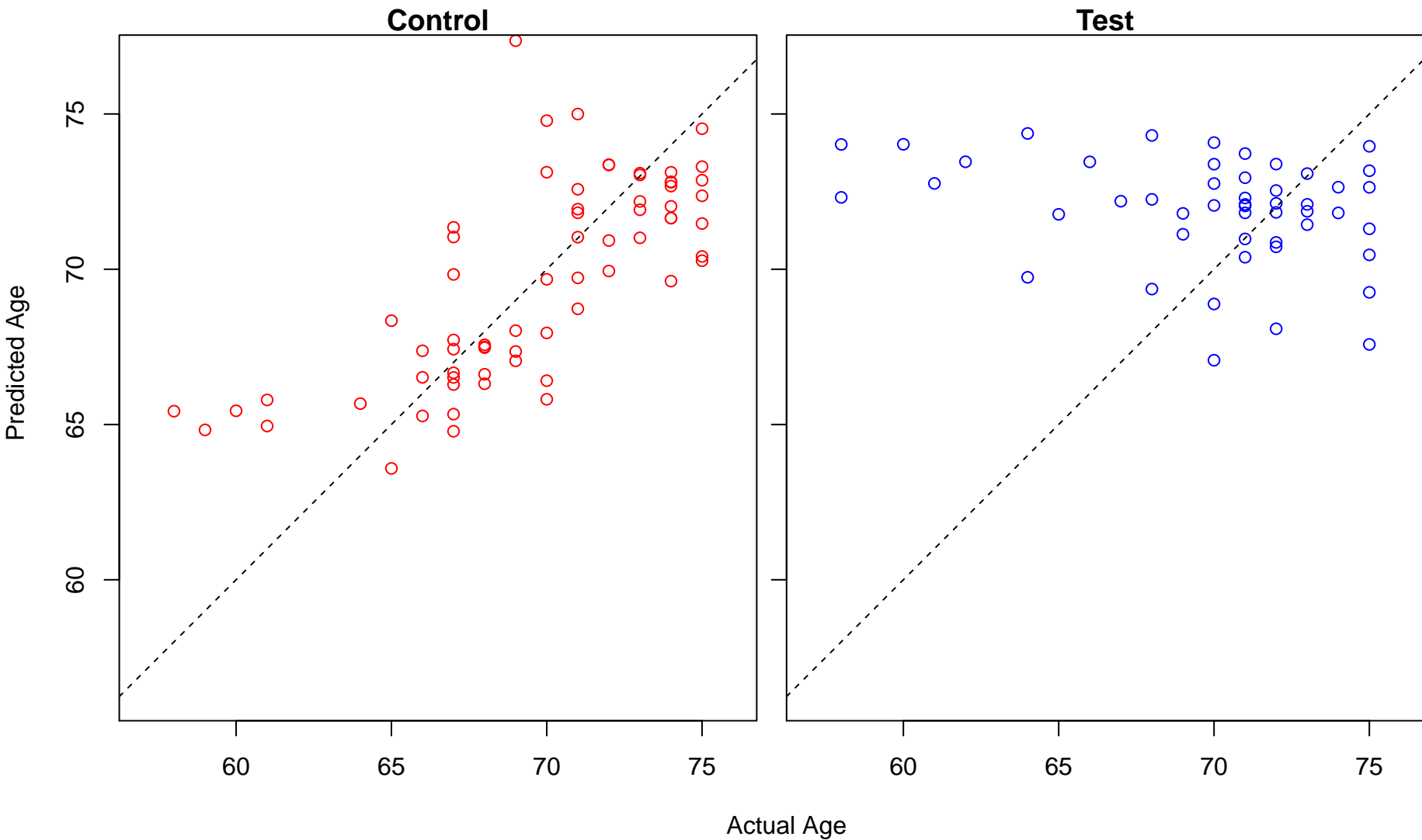
regulation of cAMP biosynthetic process (Score: 1.690206)



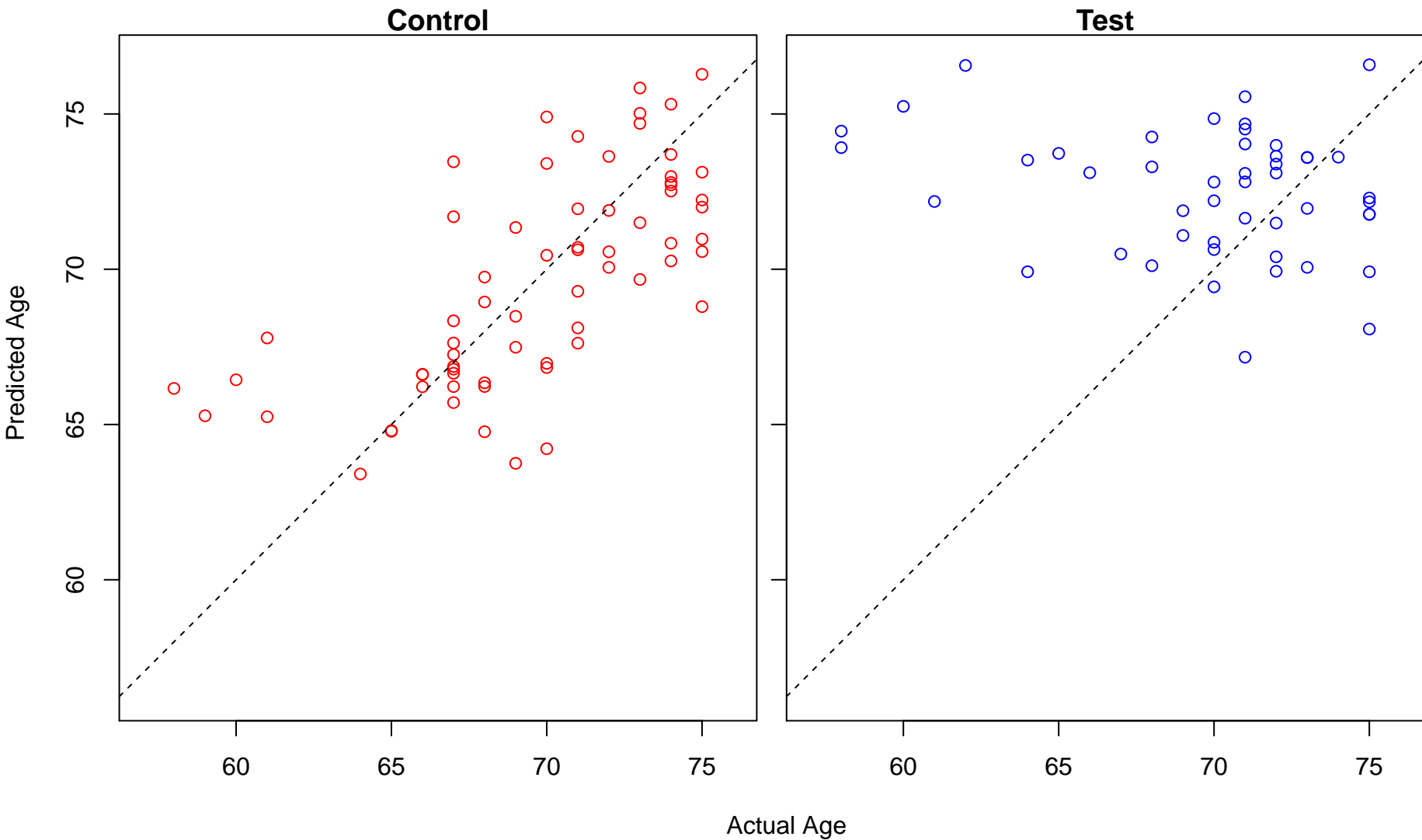
negative regulation of canonical Wnt signaling pathway (Score: 1.689820)



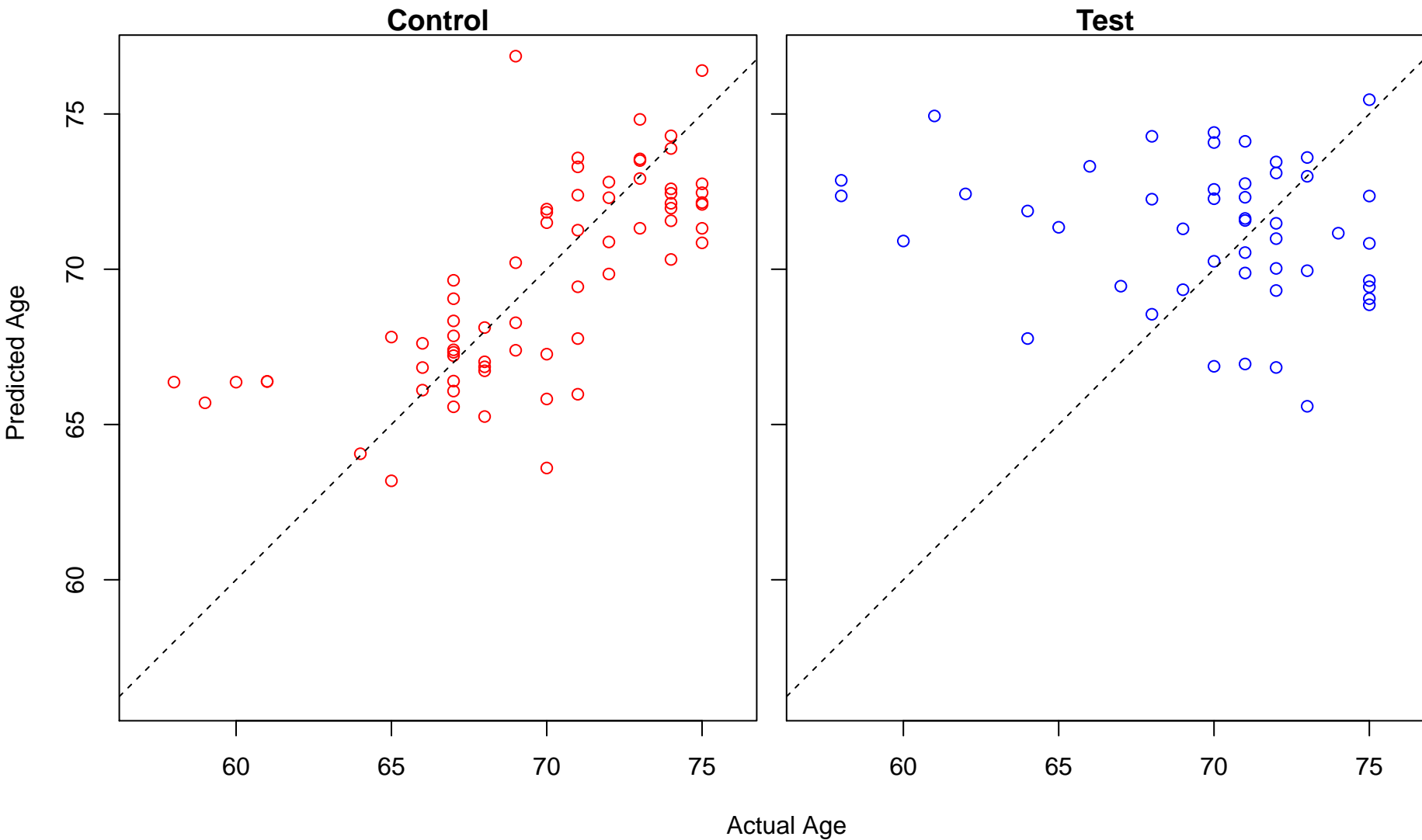
regulation of IRE1-mediated unfolded protein response (Score: 1.689665)



regulation of autophagy (Score: 1.689303)

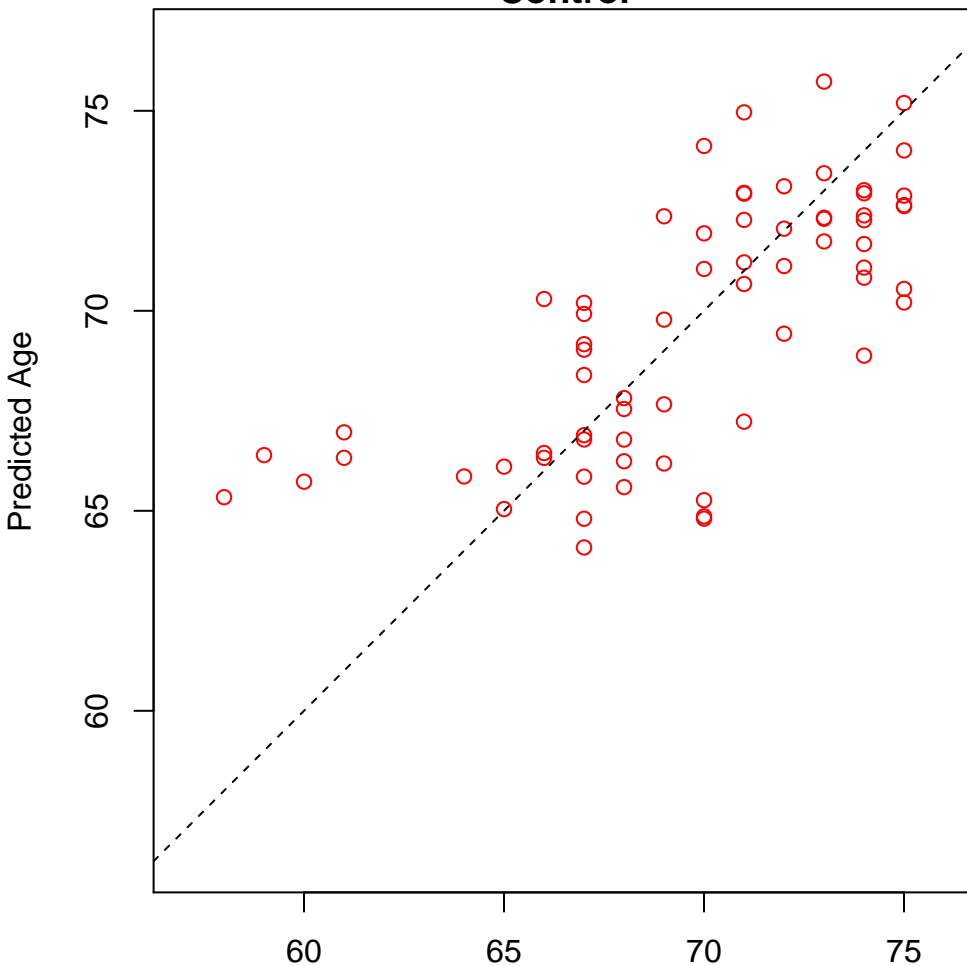


immune effector process (Score: 1.688403)

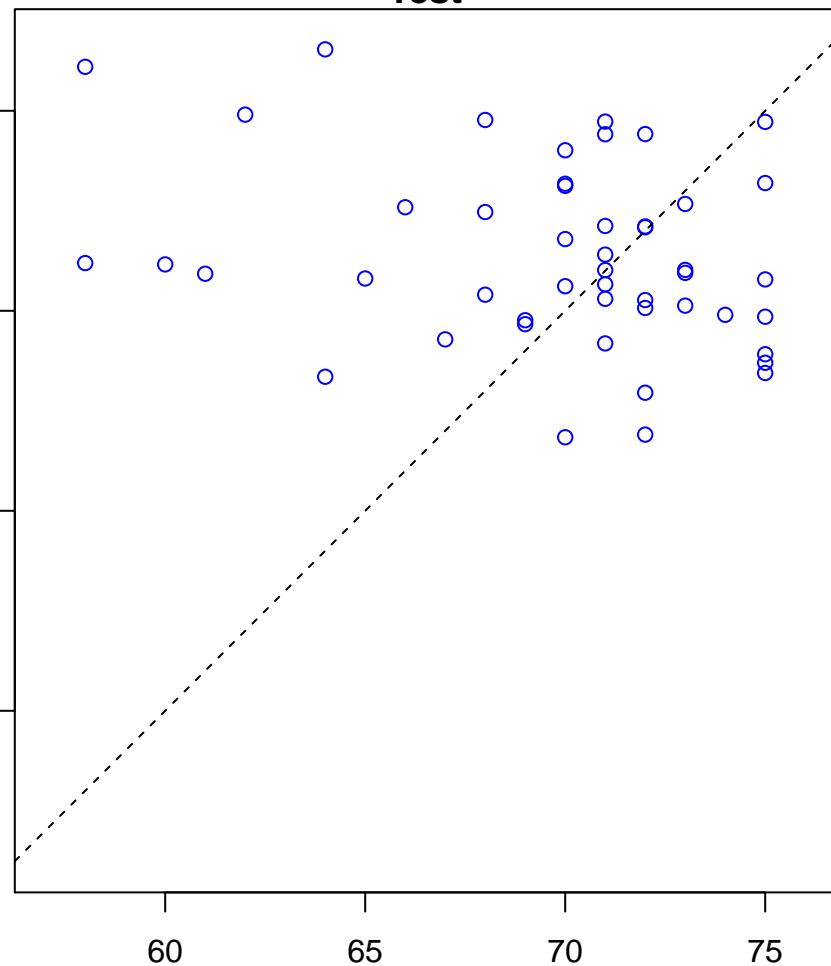


positive regulation of receptor activity (Score: 1.687788)

Control

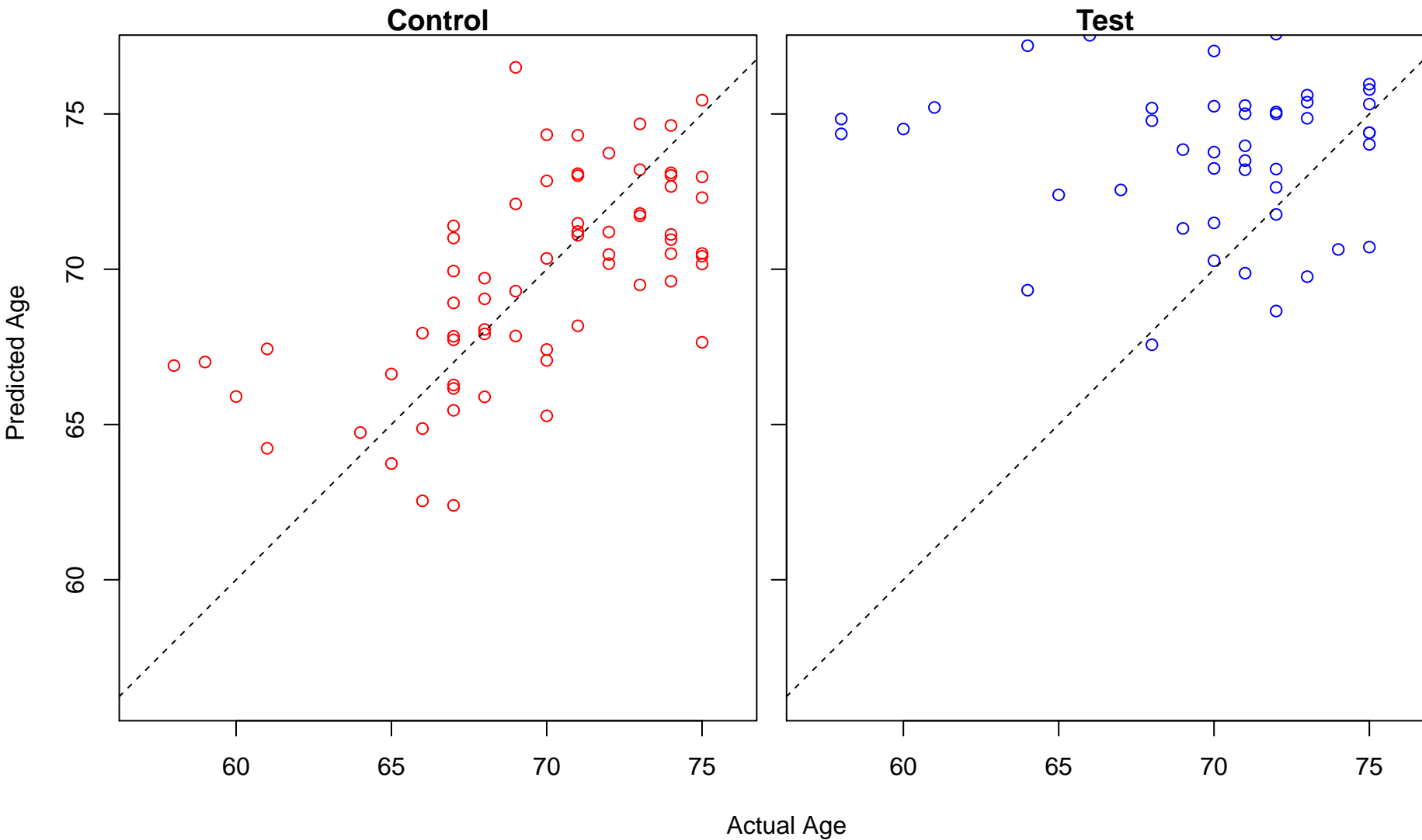


Test

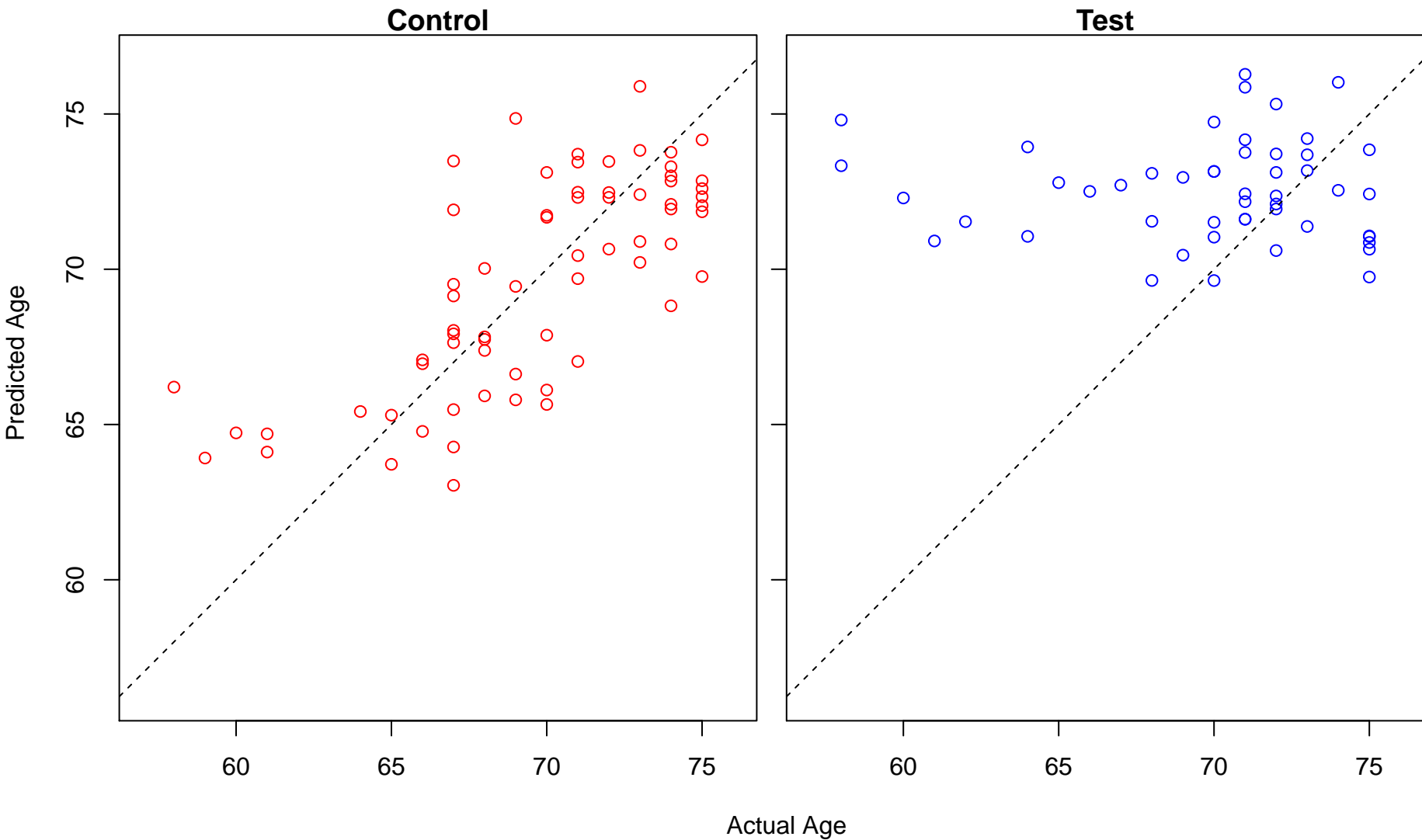


Actual Age

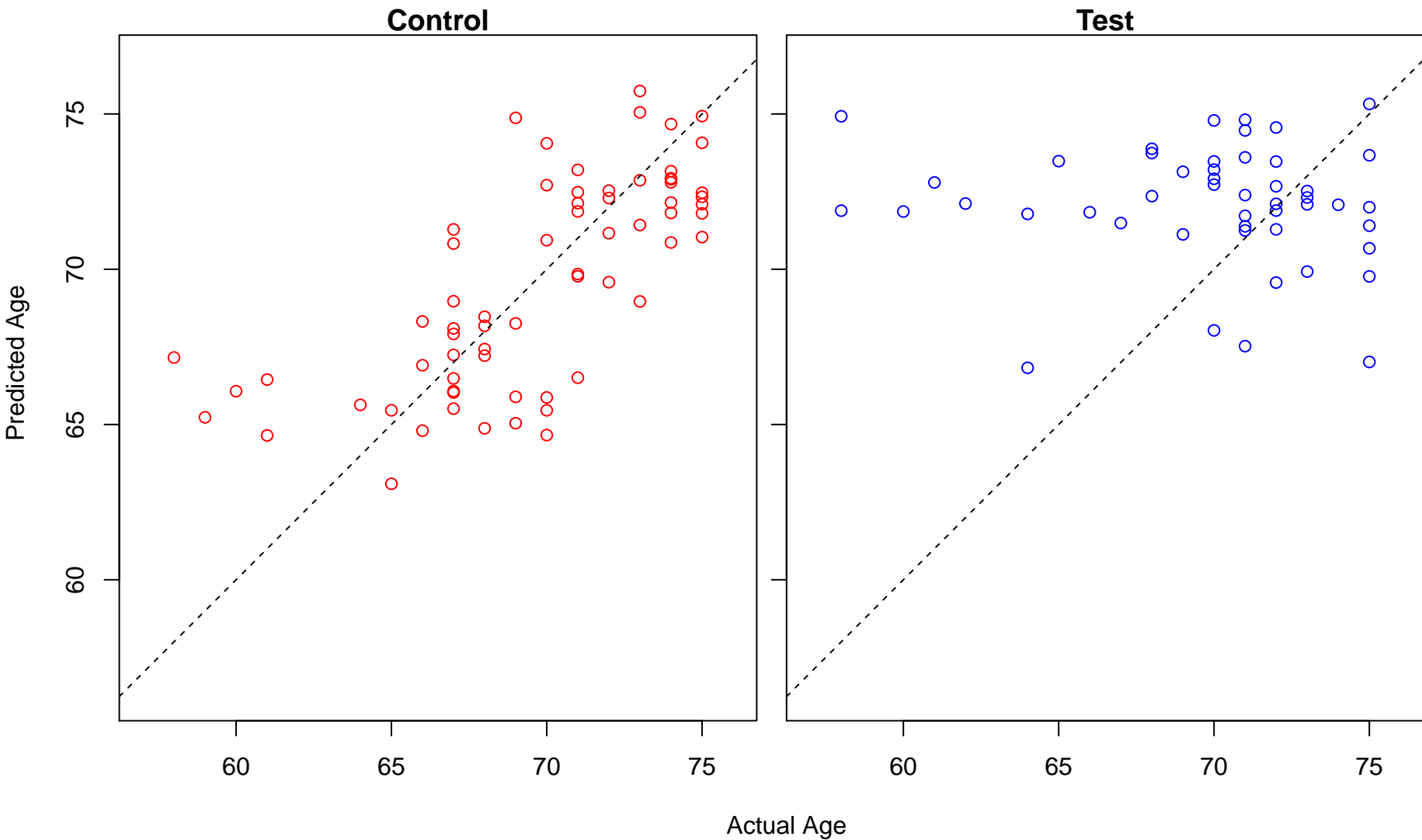
centrosome duplication (Score: 1.687716)



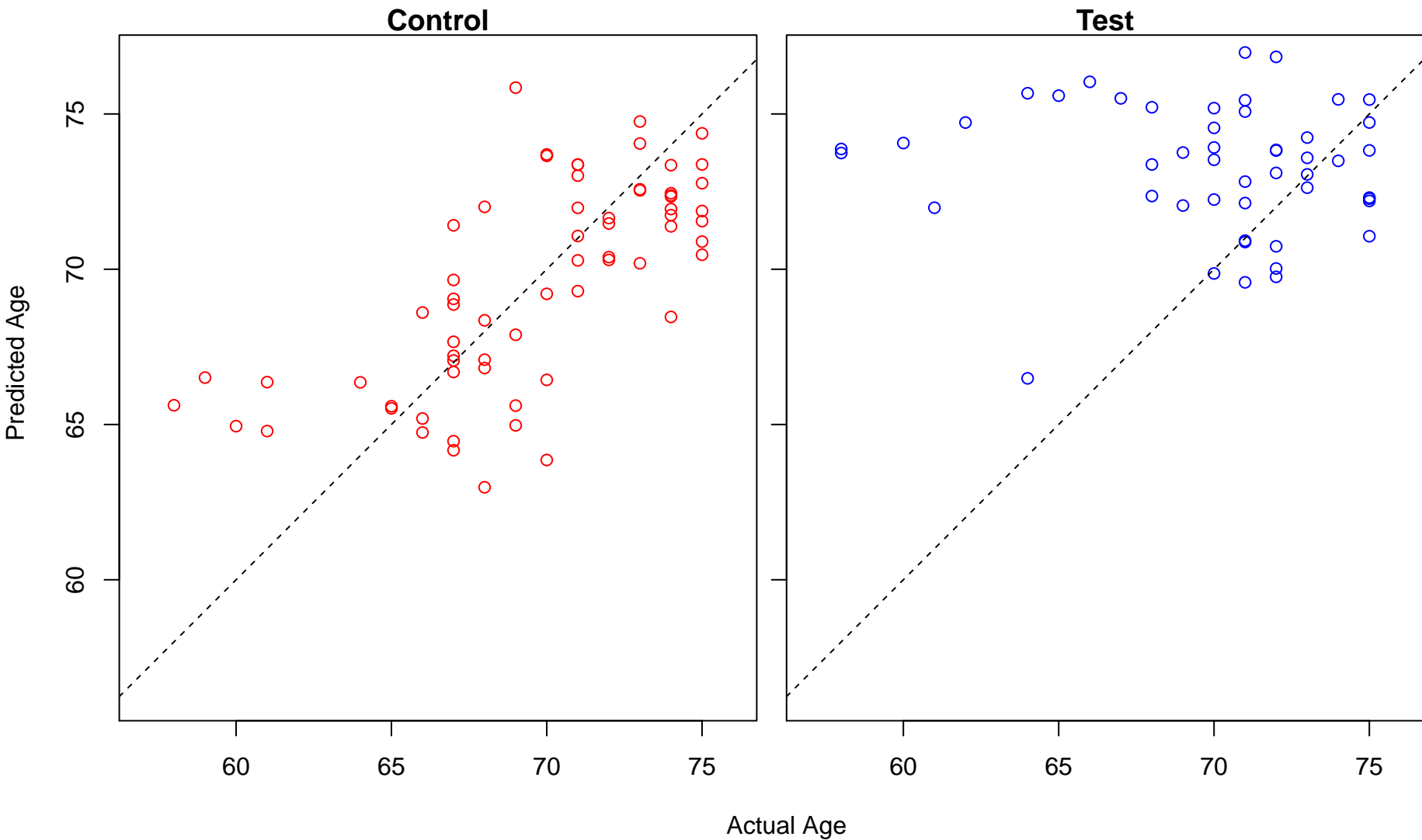
membrane fusion (Score: 1.687311)



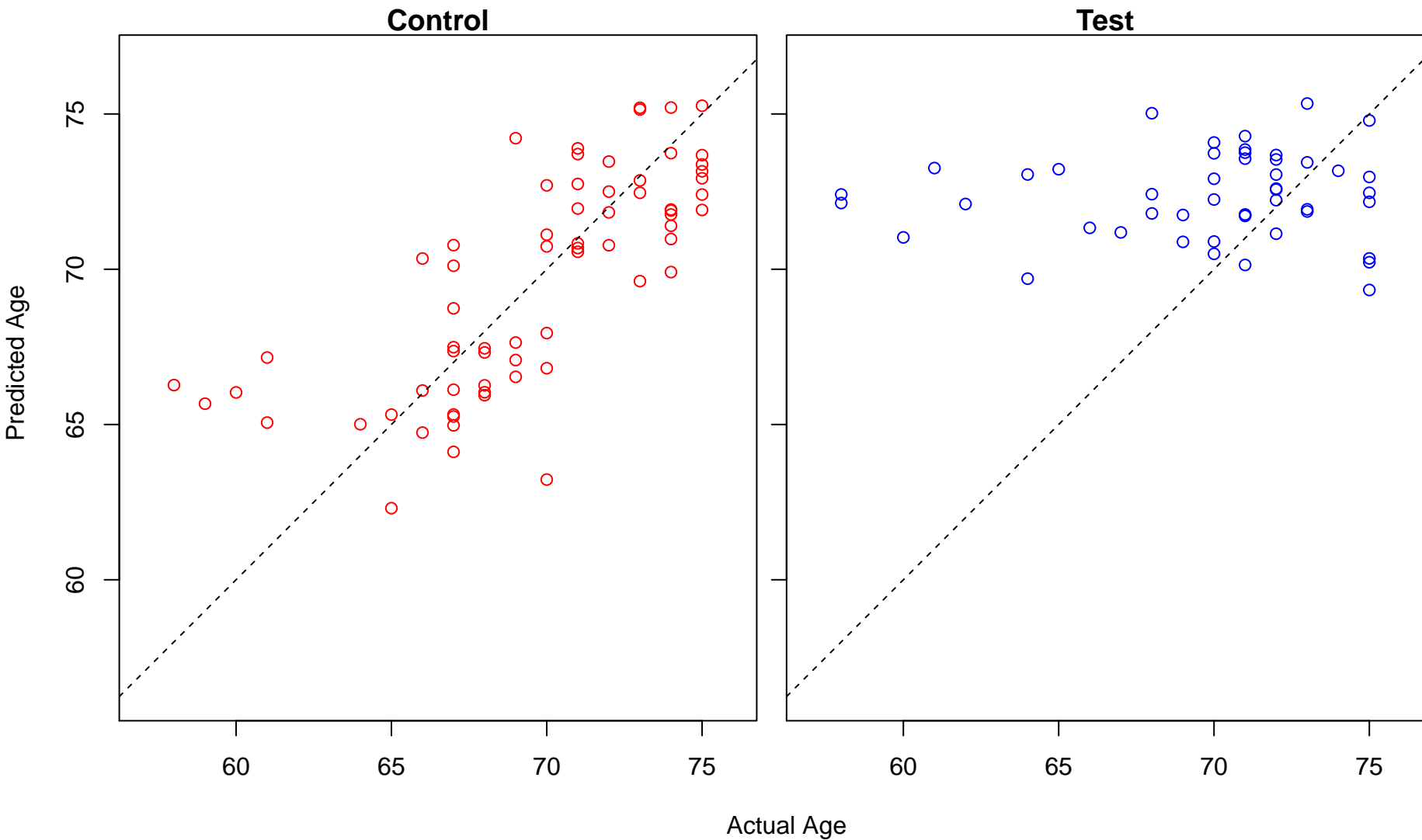
cell activation (Score: 1.686010)



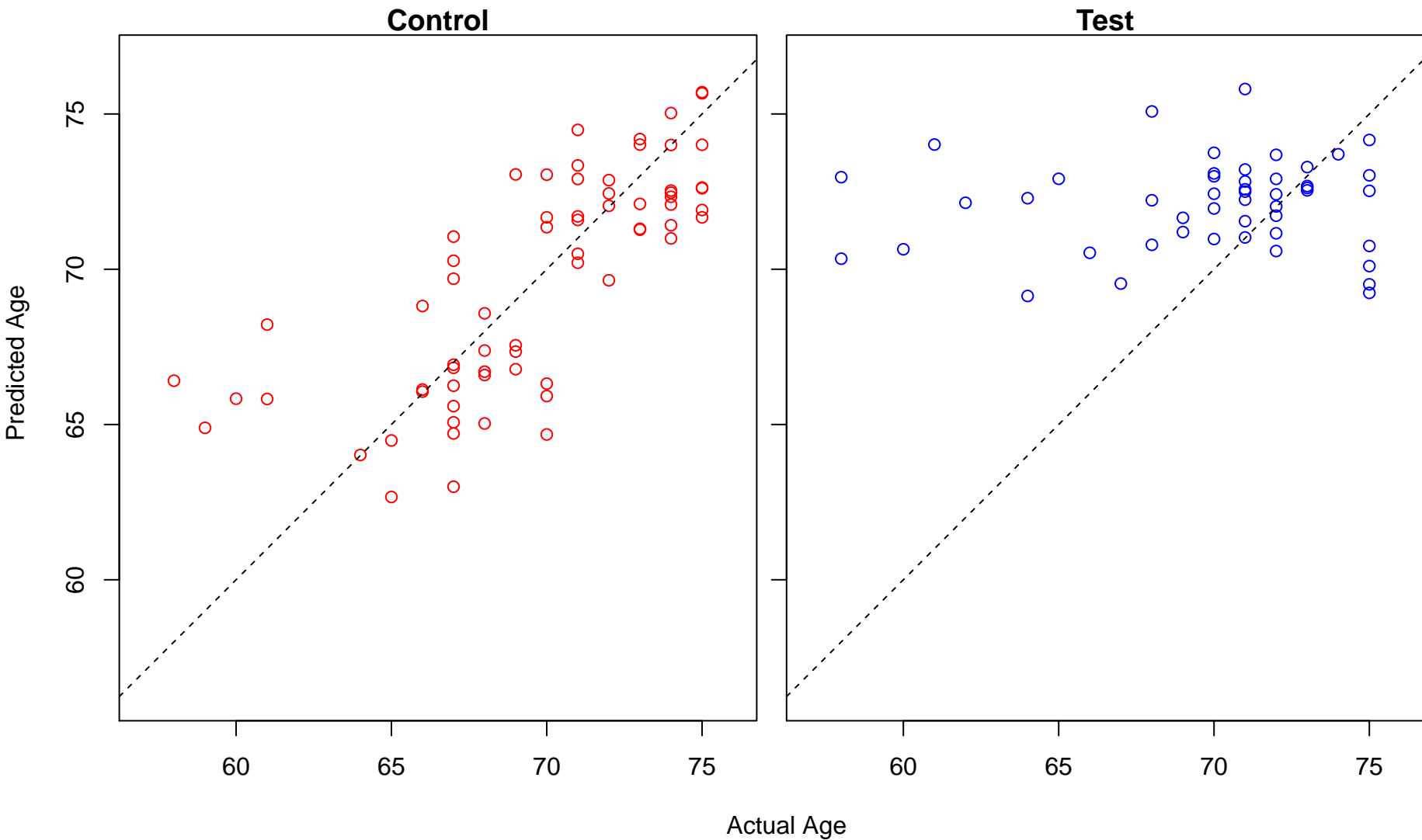
regulation of histone methylation (Score: 1.685081)



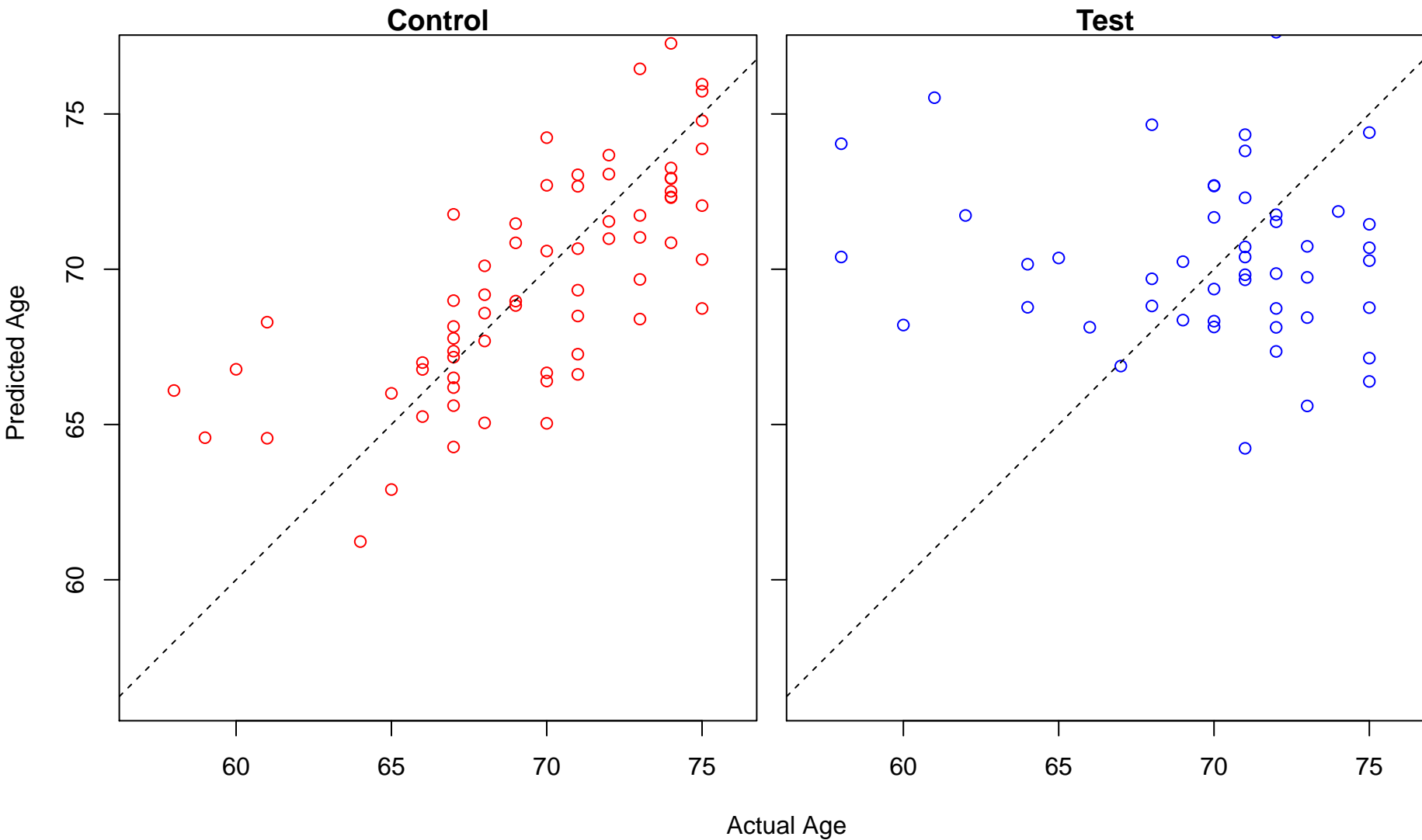
positive regulation of protein modification by small protein conjugation or removal (Score: 1.68458)



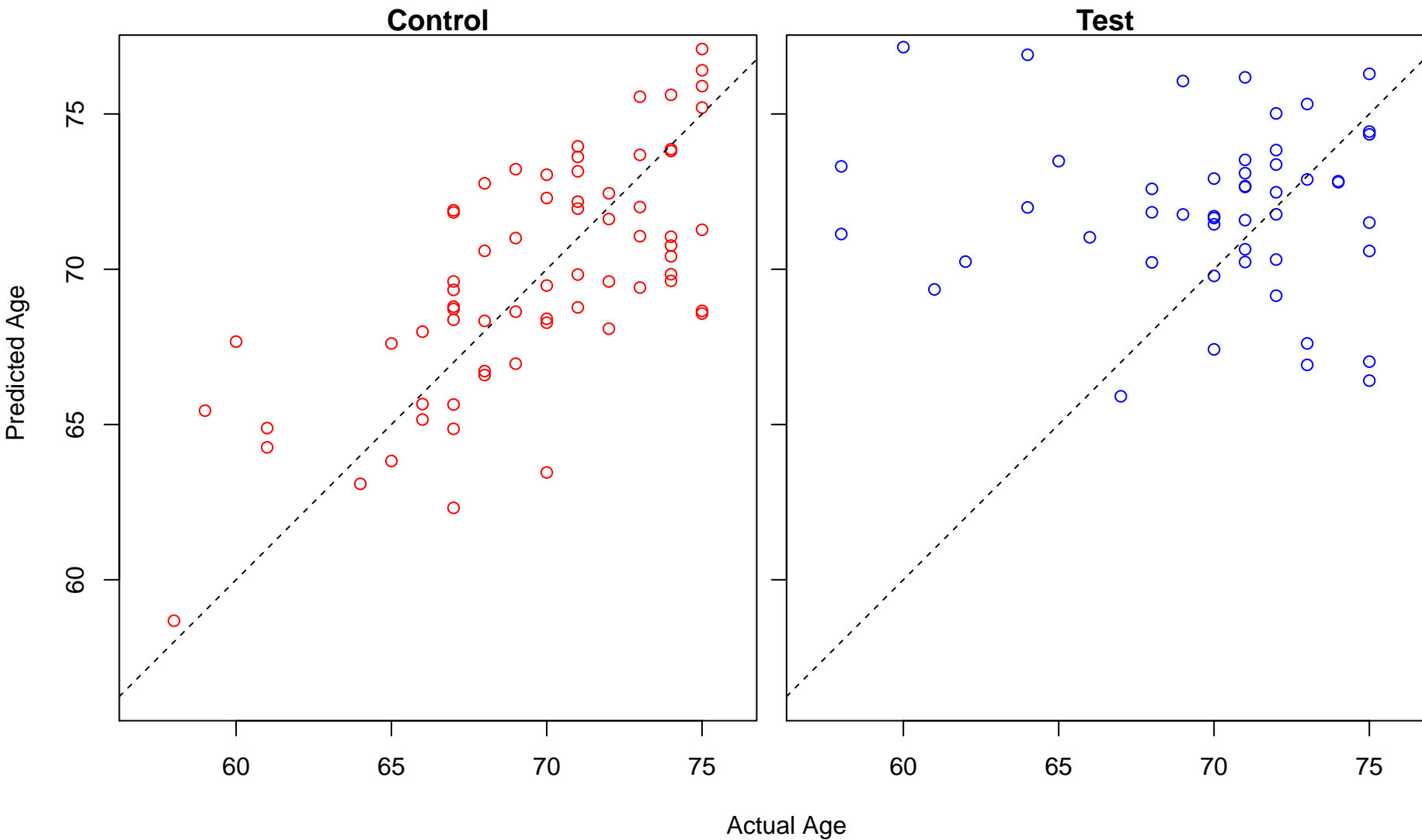
posttranscriptional regulation of gene expression (Score: 1.684011)



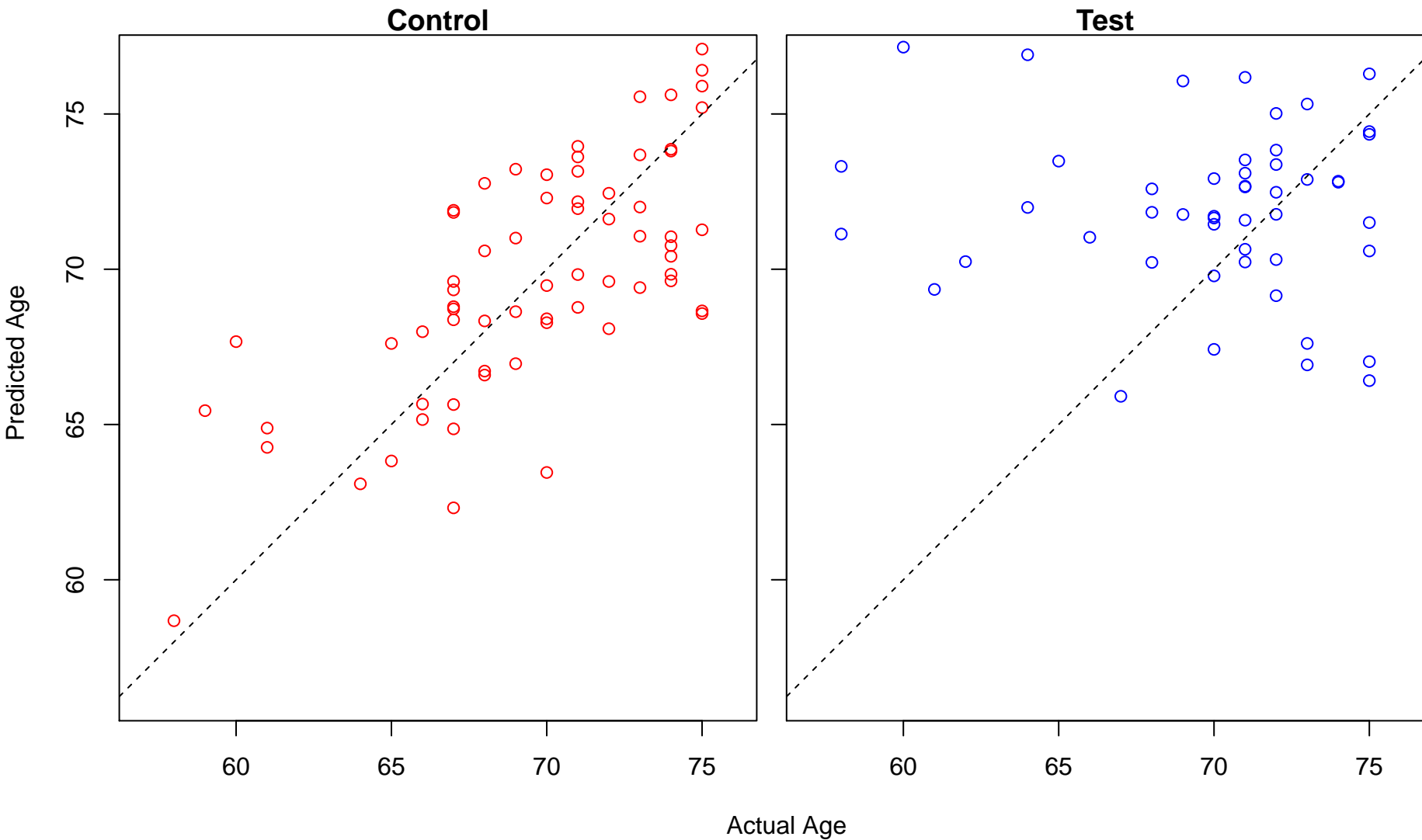
negative regulation of extrinsic apoptotic signaling pathway (Score: 1.683524)



positive regulation of nucleotide biosynthetic process (Score: 1.683069)

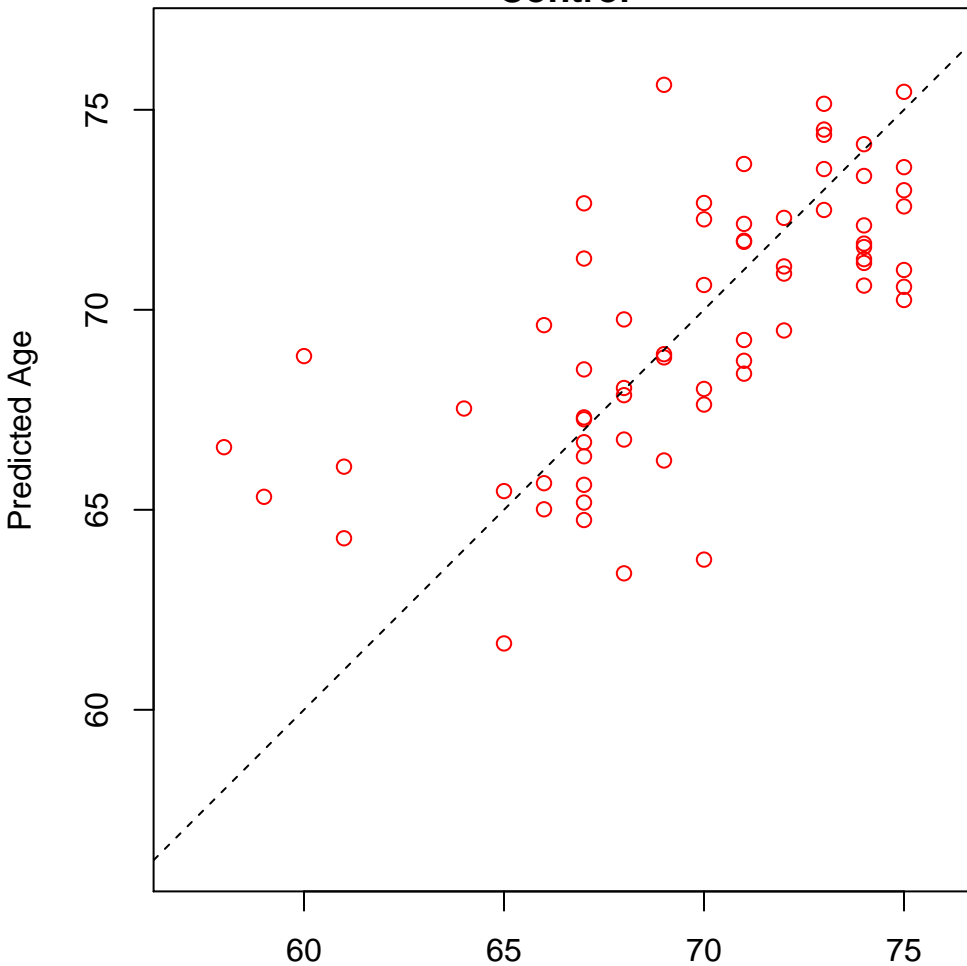


positive regulation of purine nucleotide biosynthetic process (Score: 1.683069)

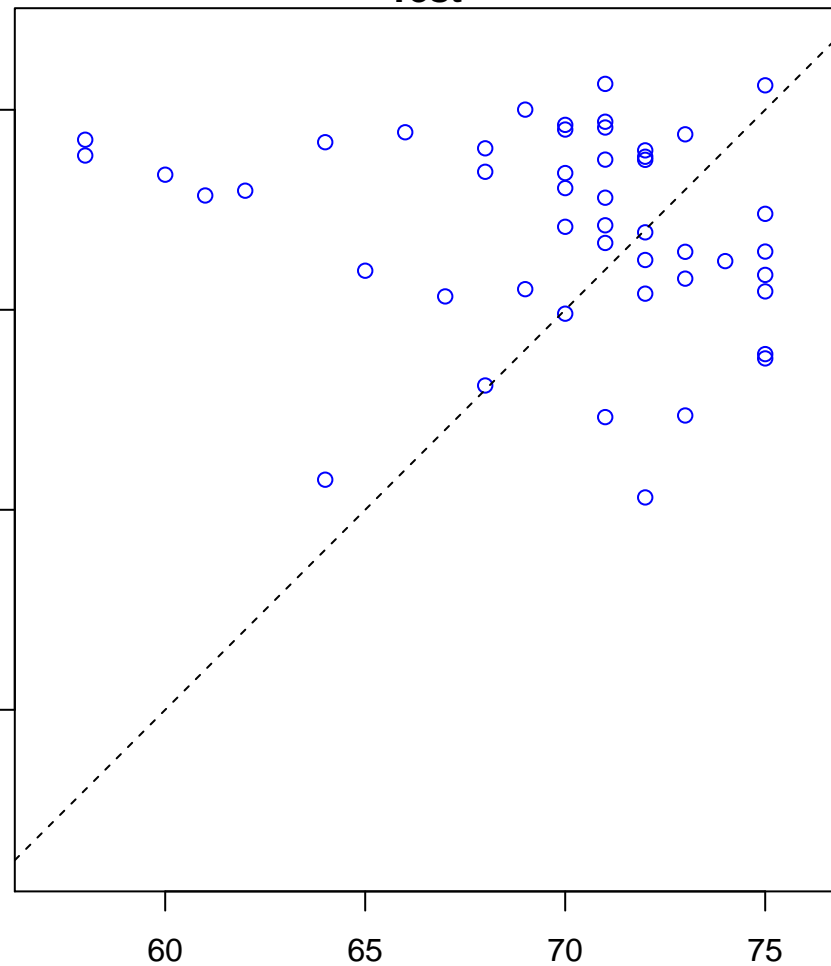


negative regulation of cell-cell adhesion (Score: 1.682822)

Control

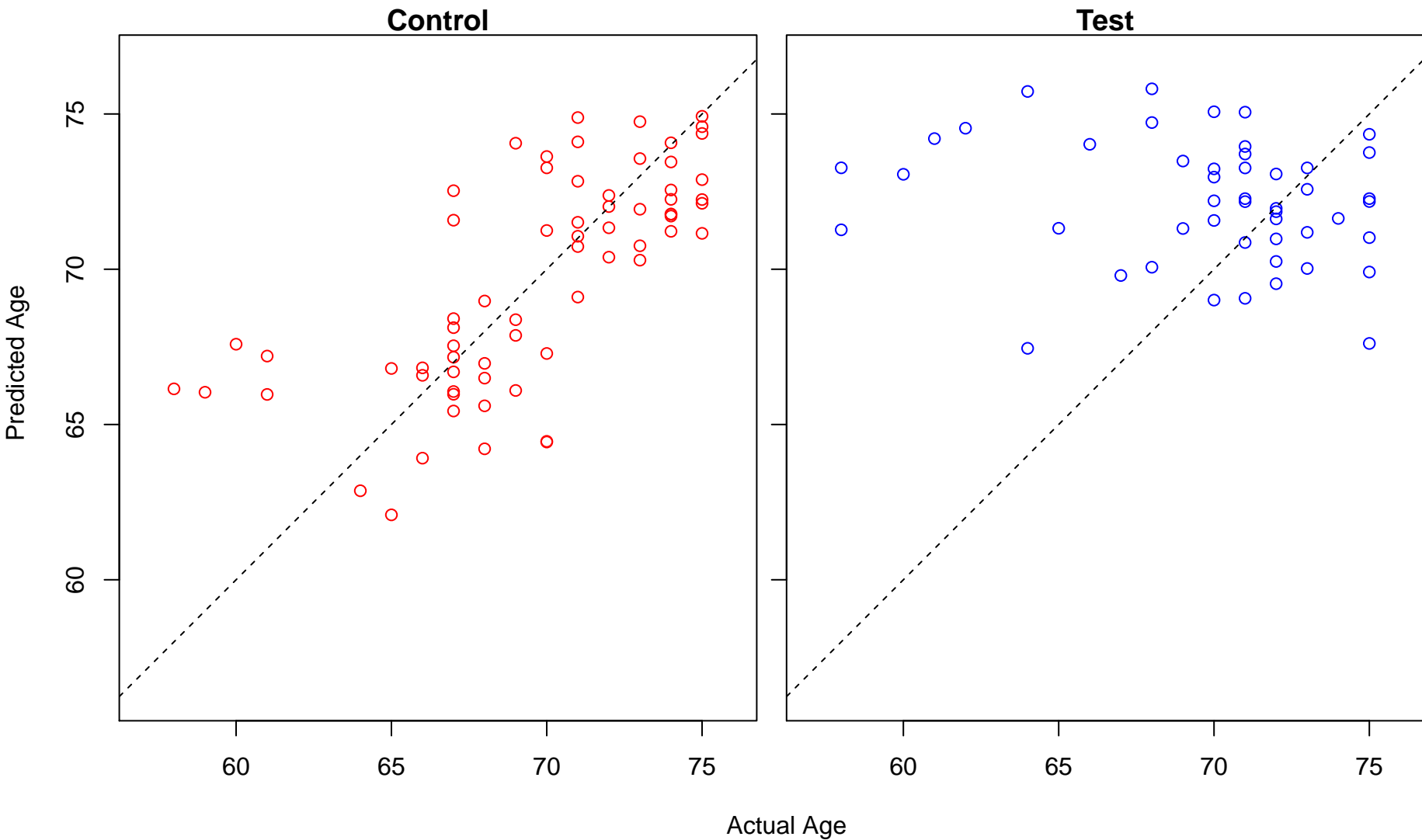


Test

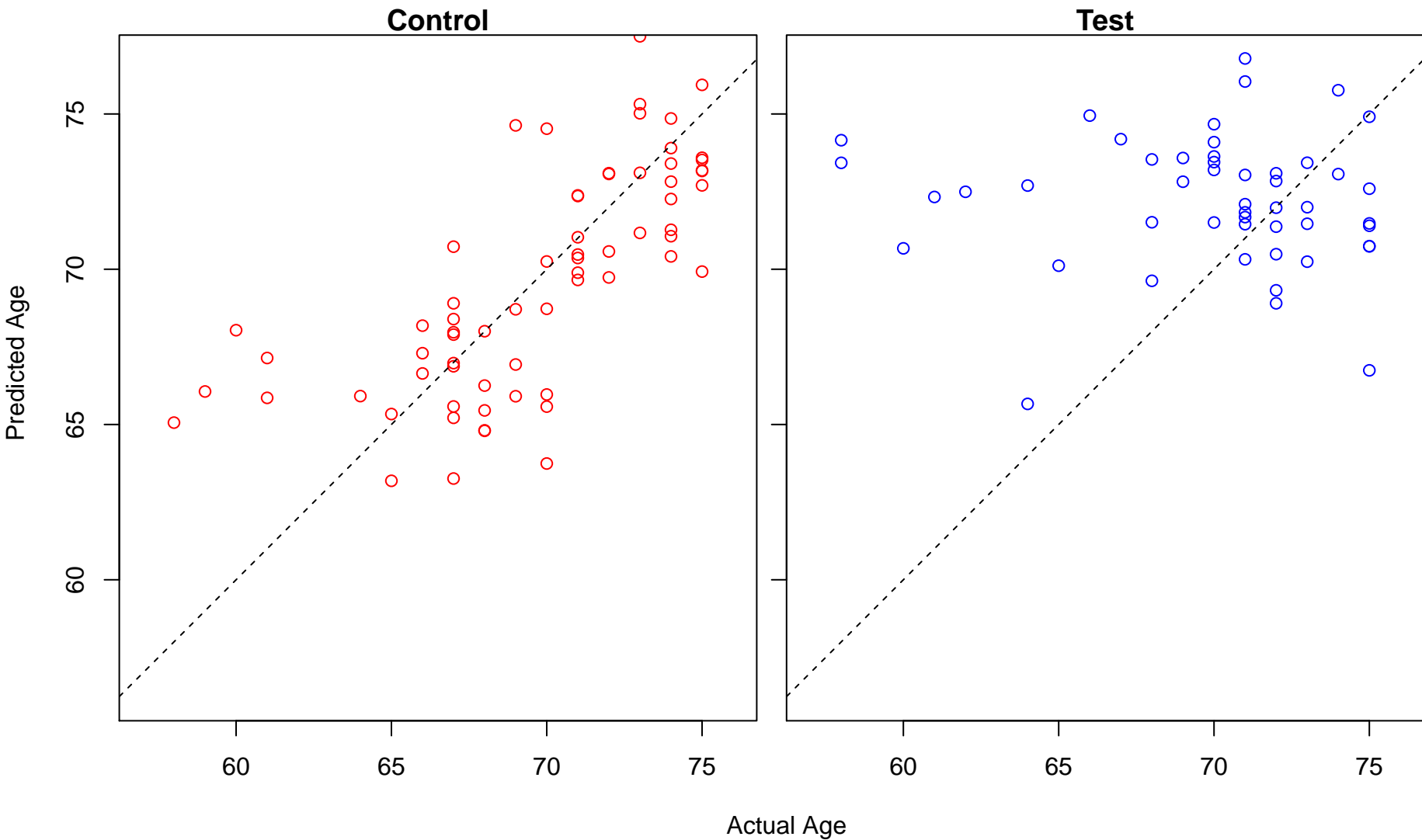


Actual Age

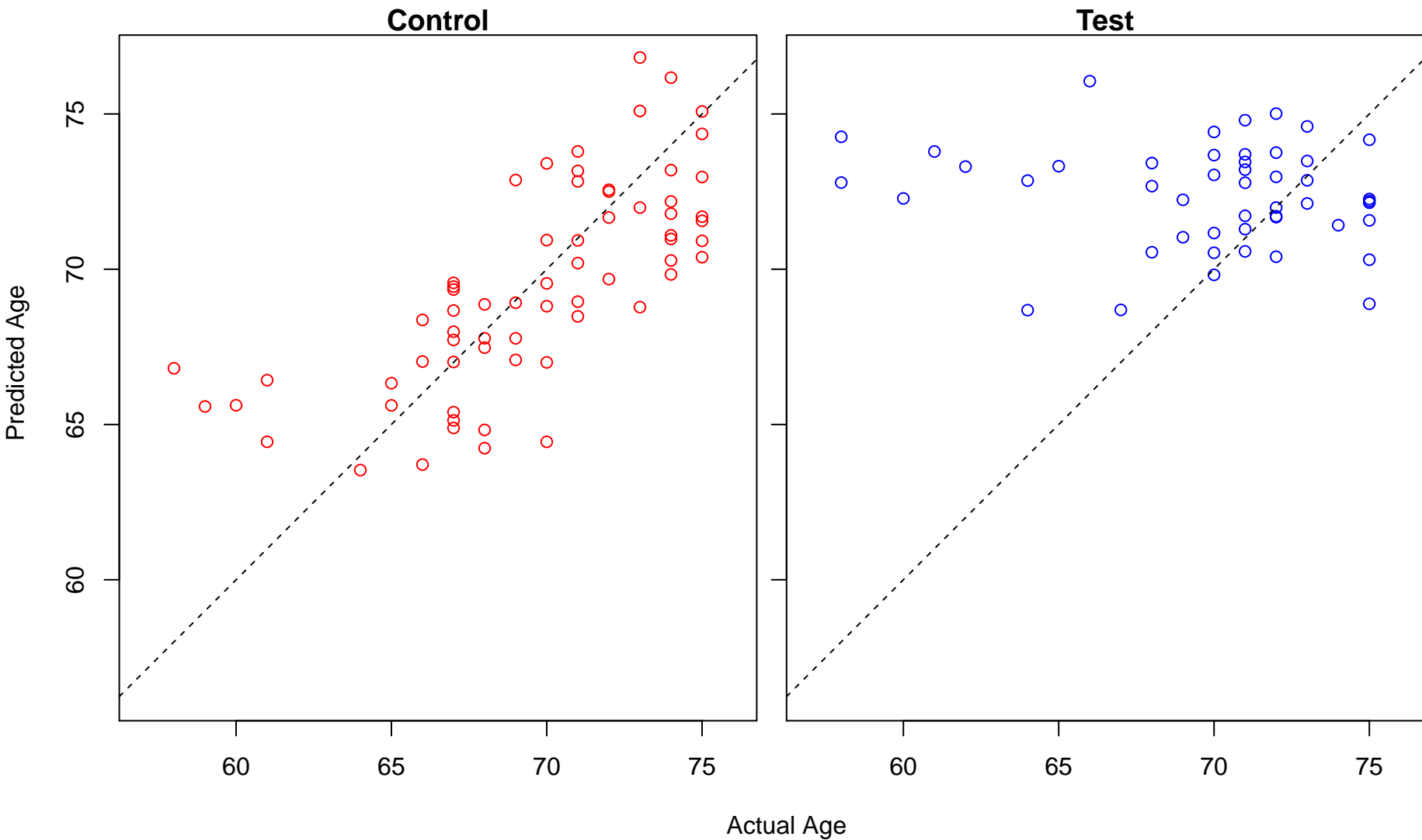
positive regulation of defense response to virus by host (Score: 1.682693)



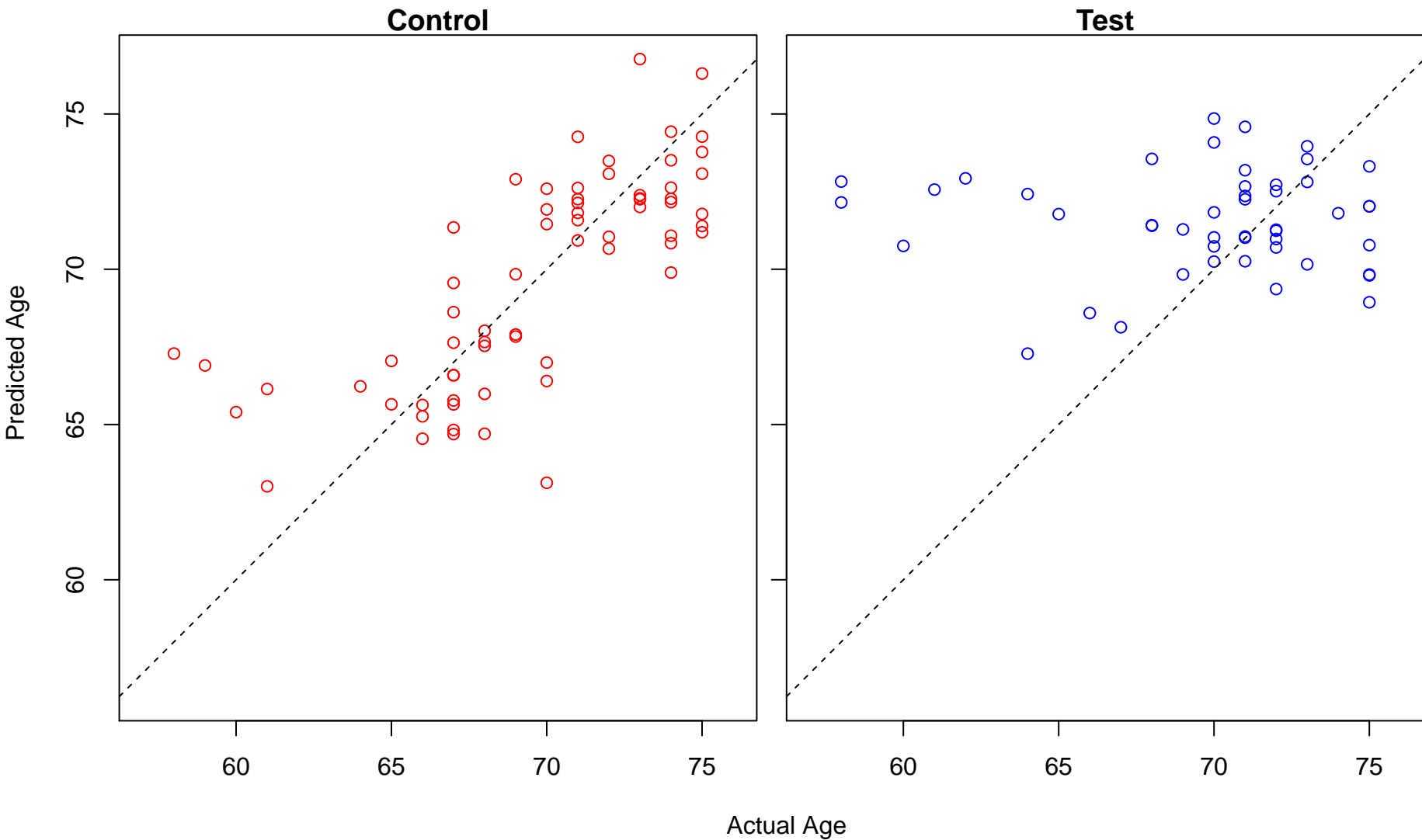
regulation of response to wounding (Score: 1.682496)



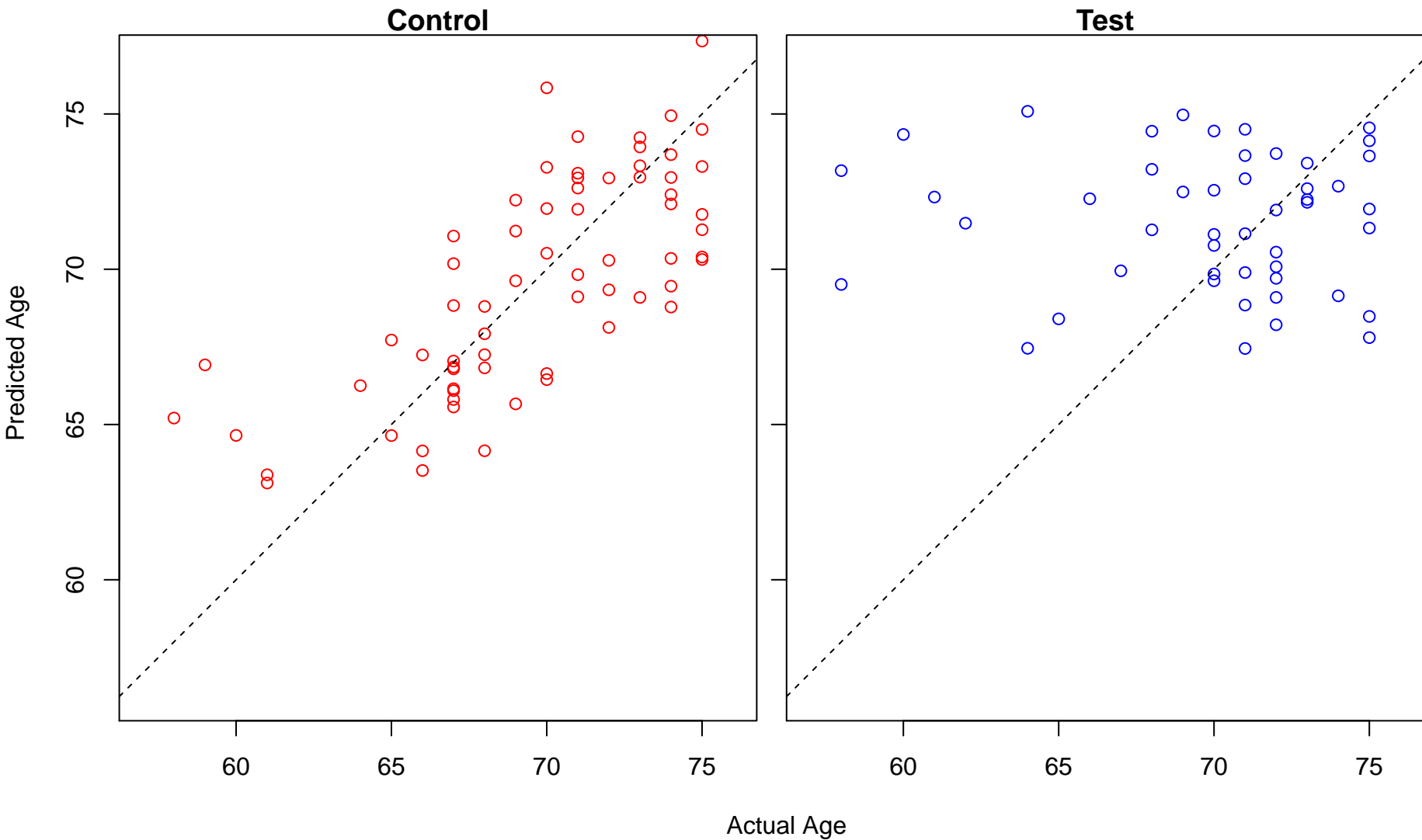
lipid catabolic process (Score: 1.682418)



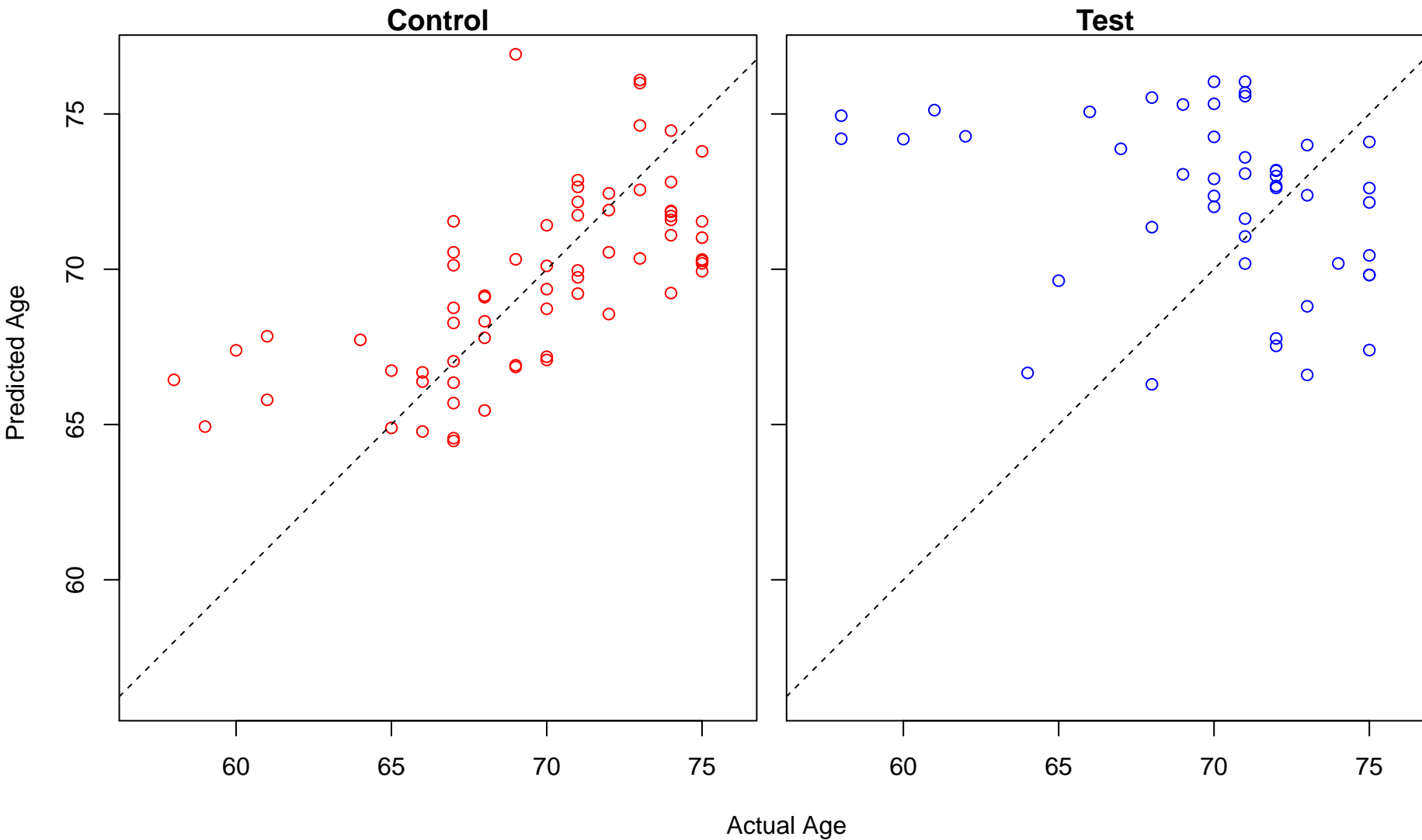
ribonucleotide metabolic process (Score: 1.682416)



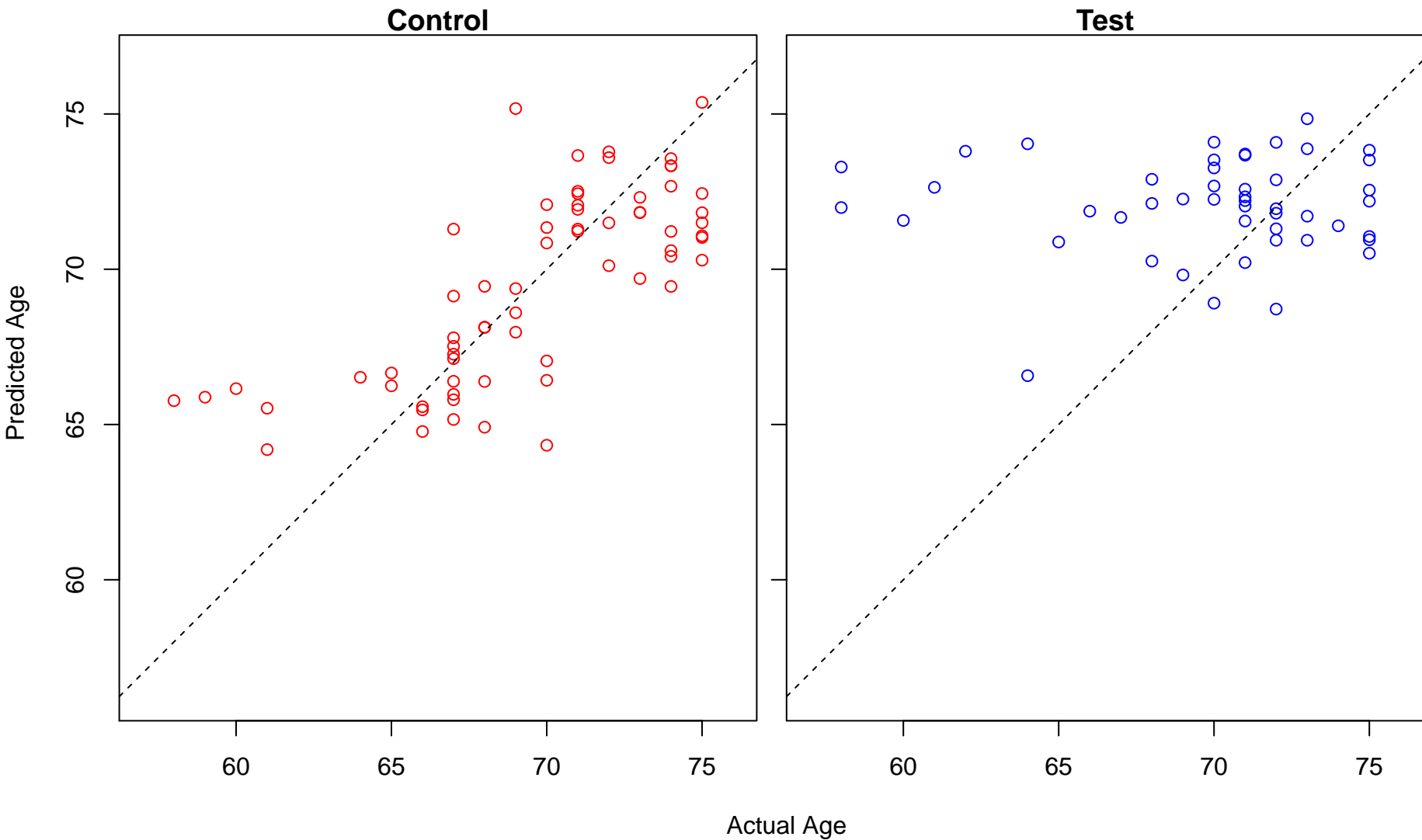
regulation of cyclic nucleotide biosynthetic process (Score: 1.681553)



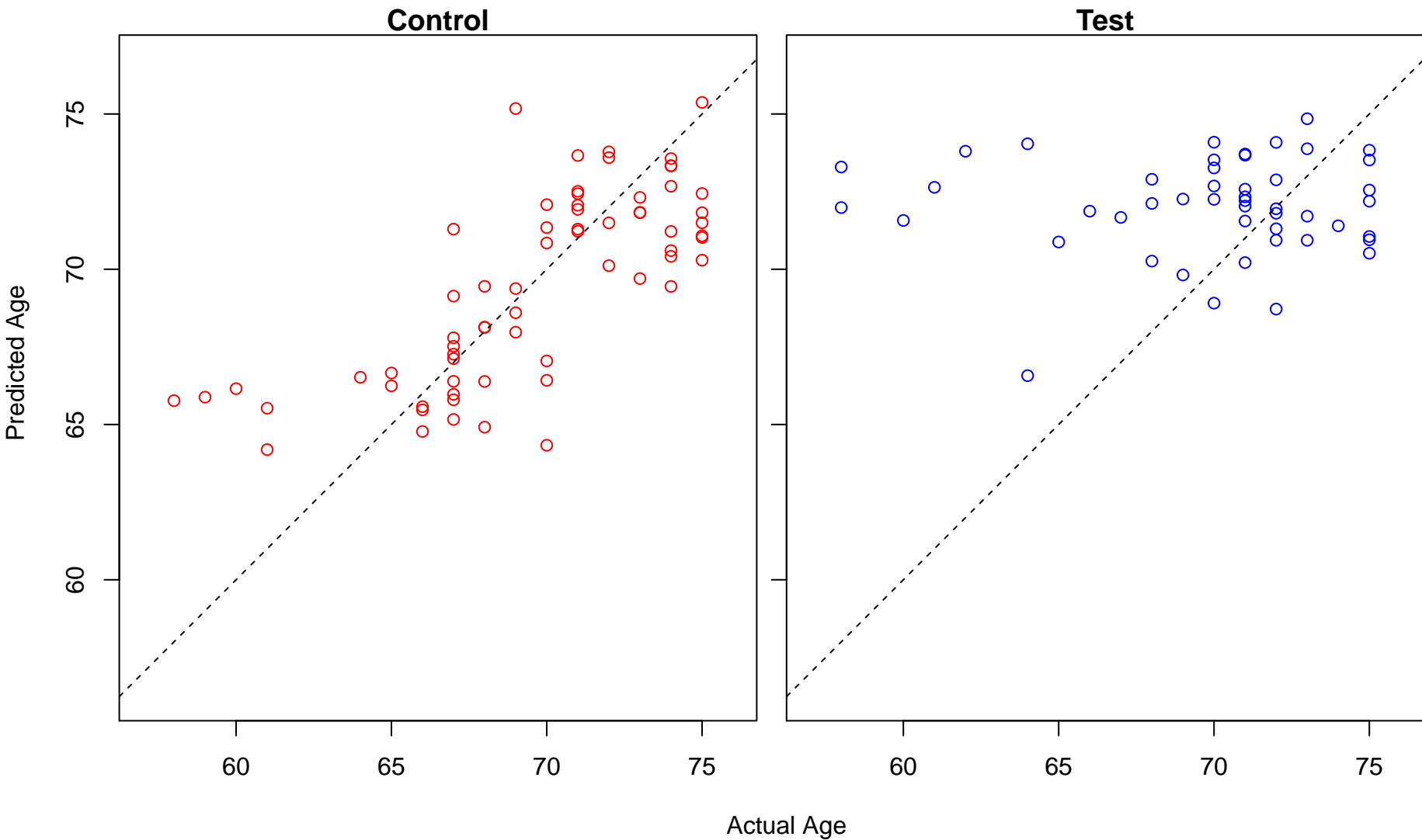
negative regulation of CD4-positive, alpha-beta T cell activation (Score: 1.681043)



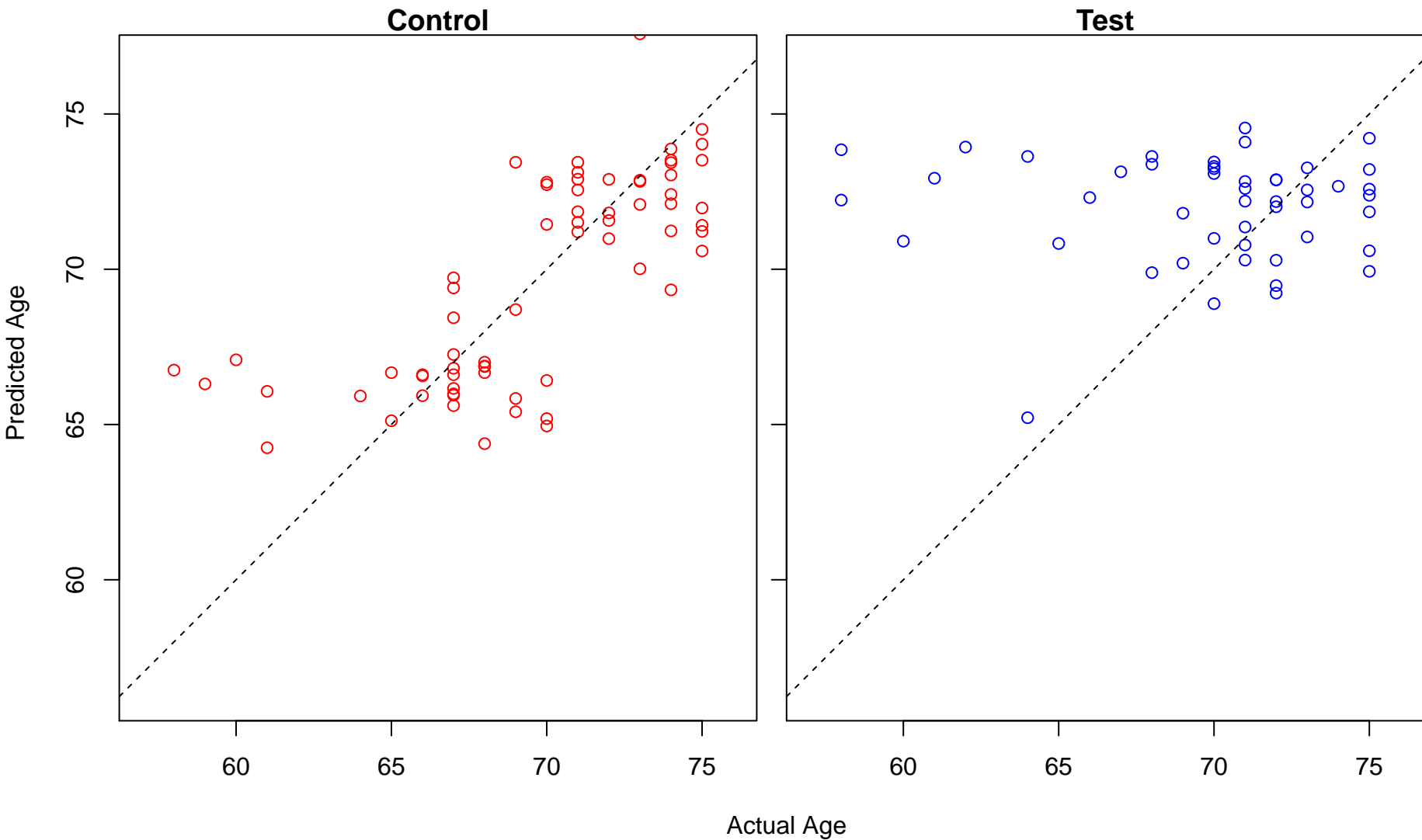
Arp2/3 complex-mediated actin nucleation (Score: 1.679546)



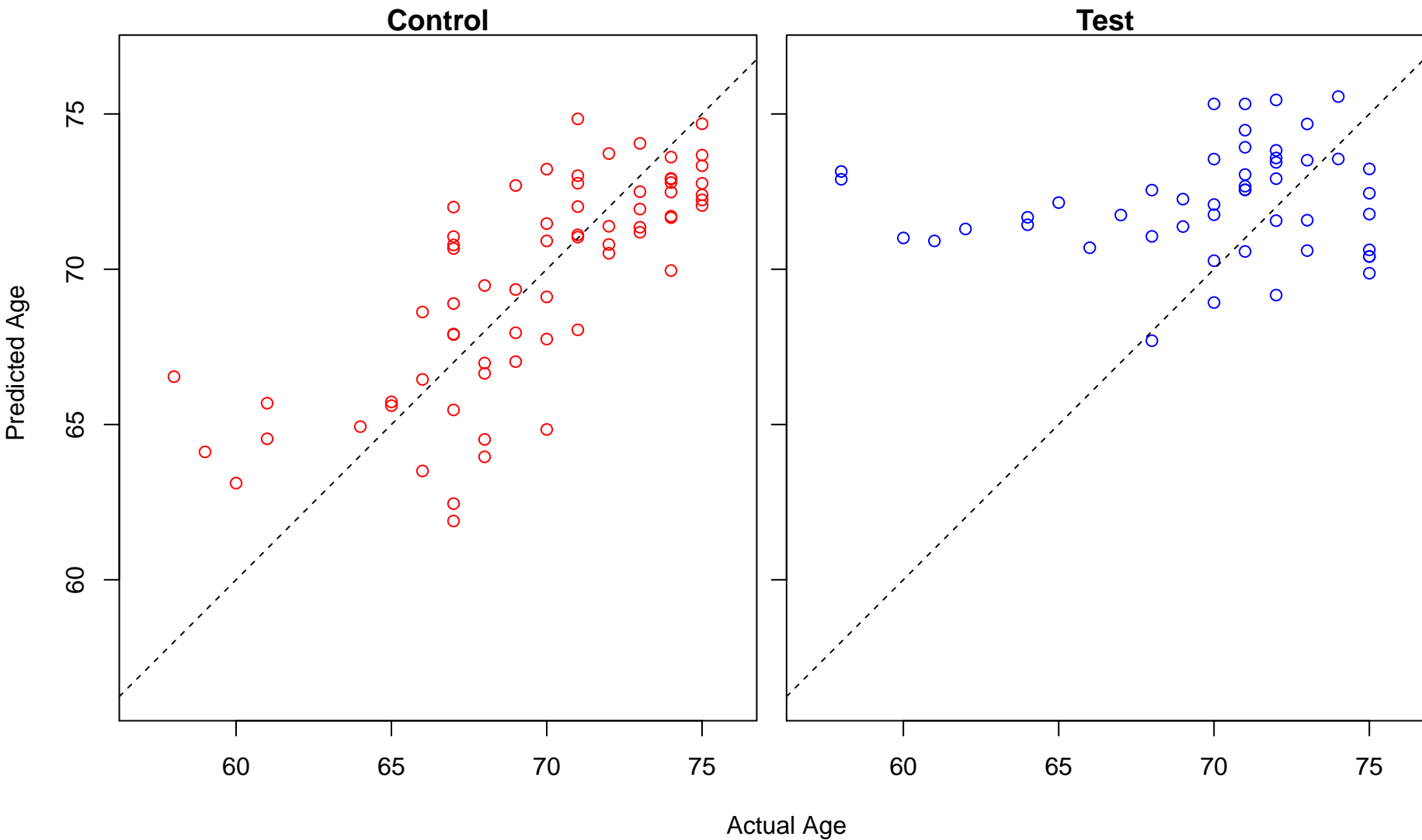
actin nucleation (Score: 1.679546)



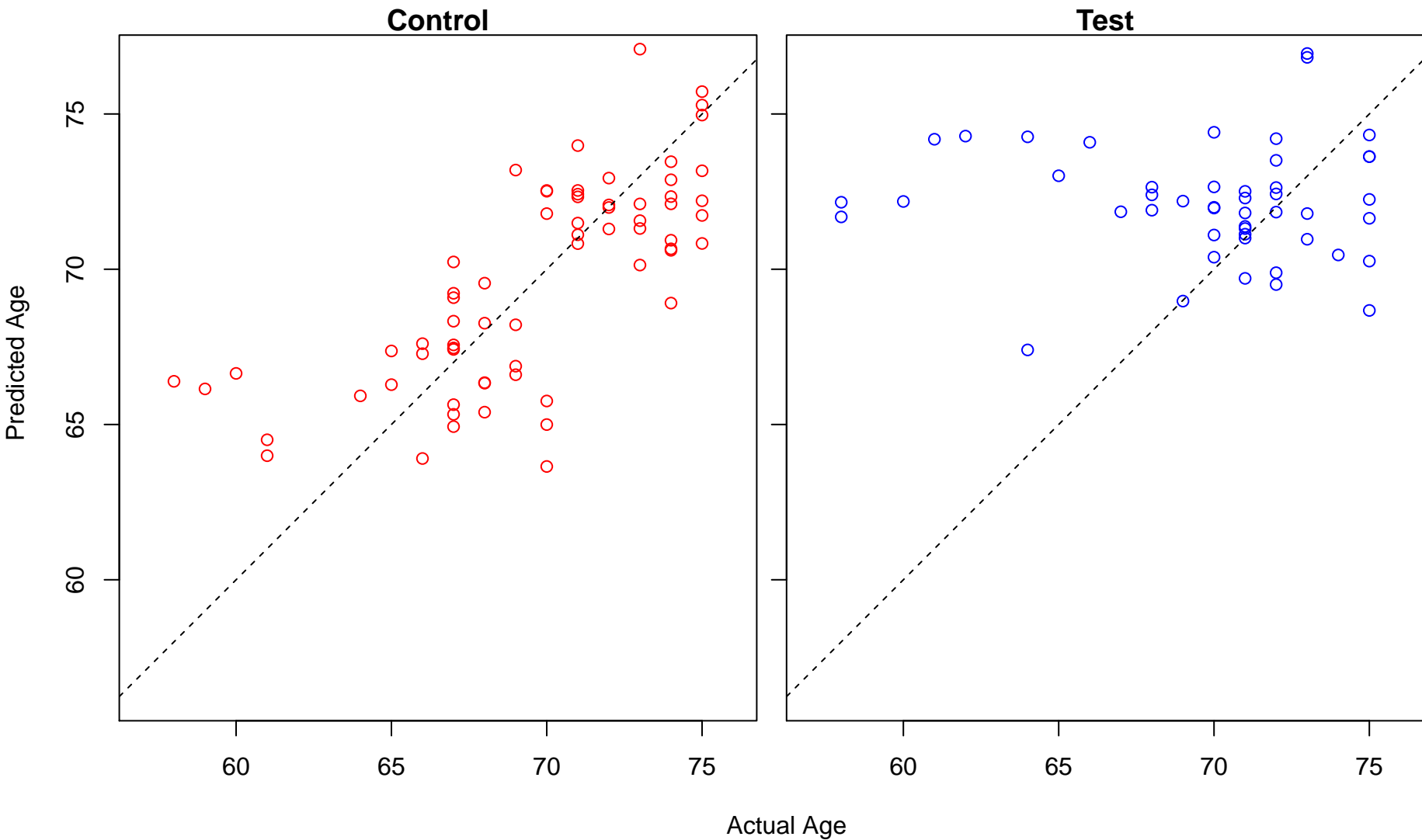
actin filament organization (Score: 1.679200)



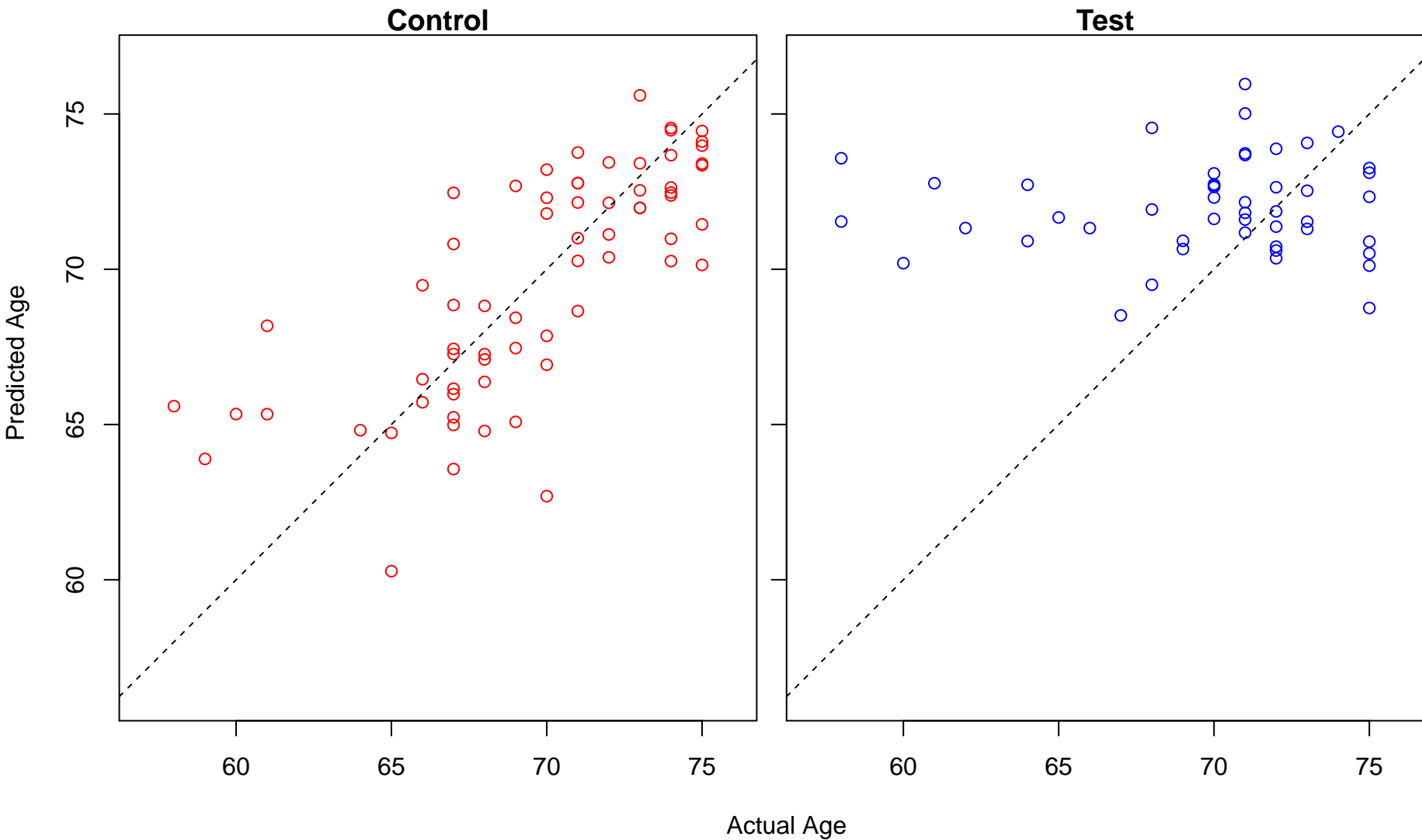
single-organism membrane fusion (Score: 1.679041)



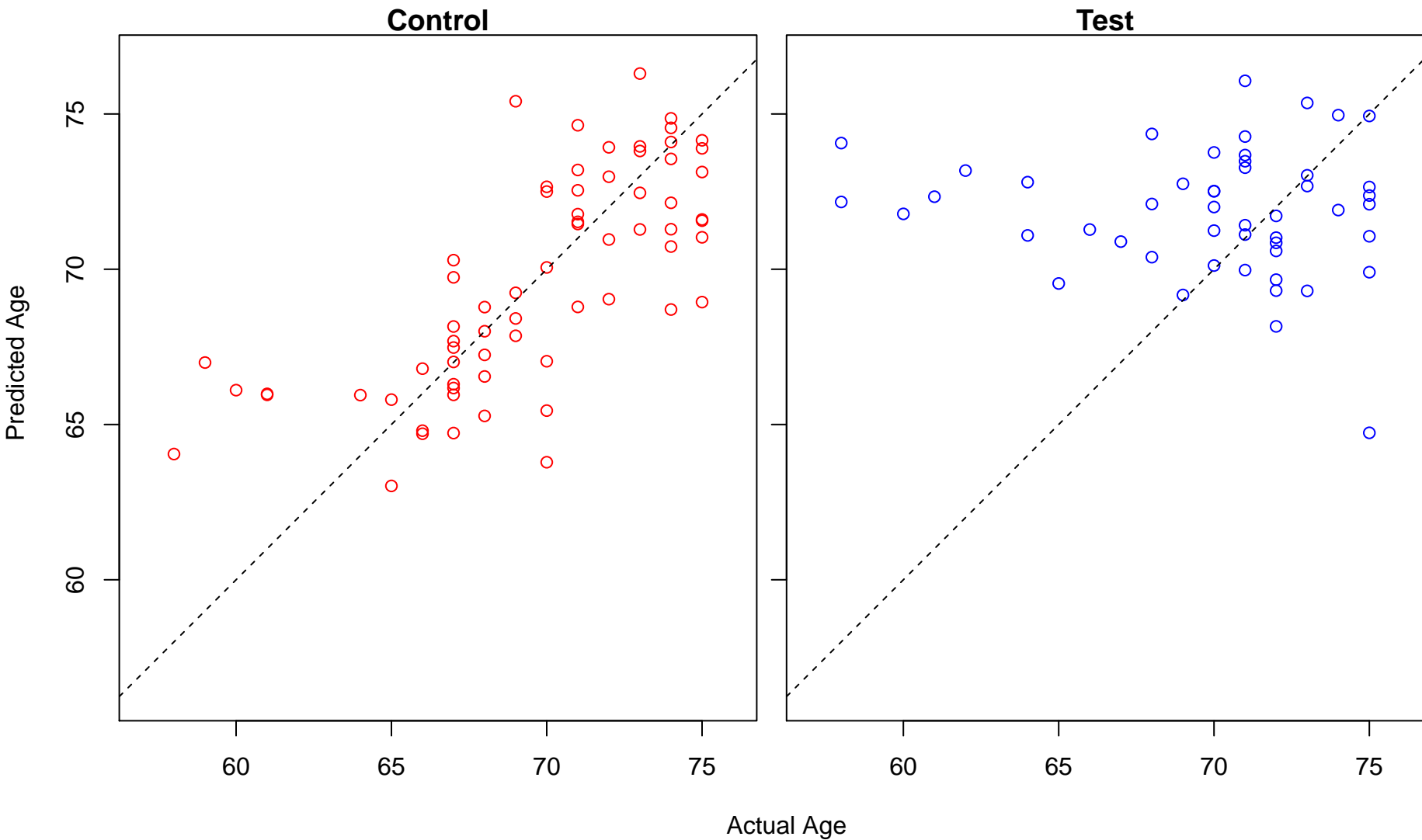
regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 1.677)



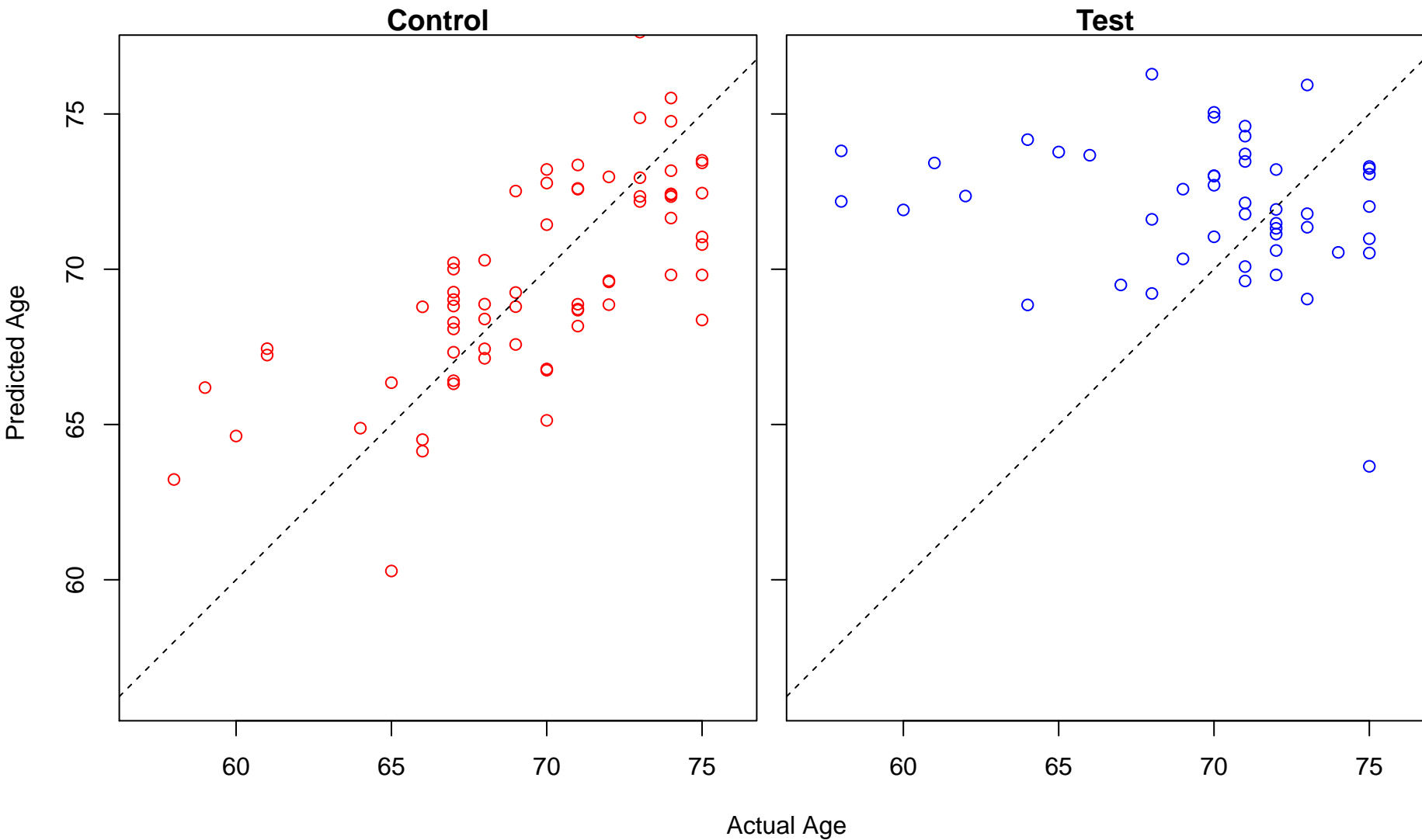
mitotic cell cycle checkpoint (Score: 1.677053)



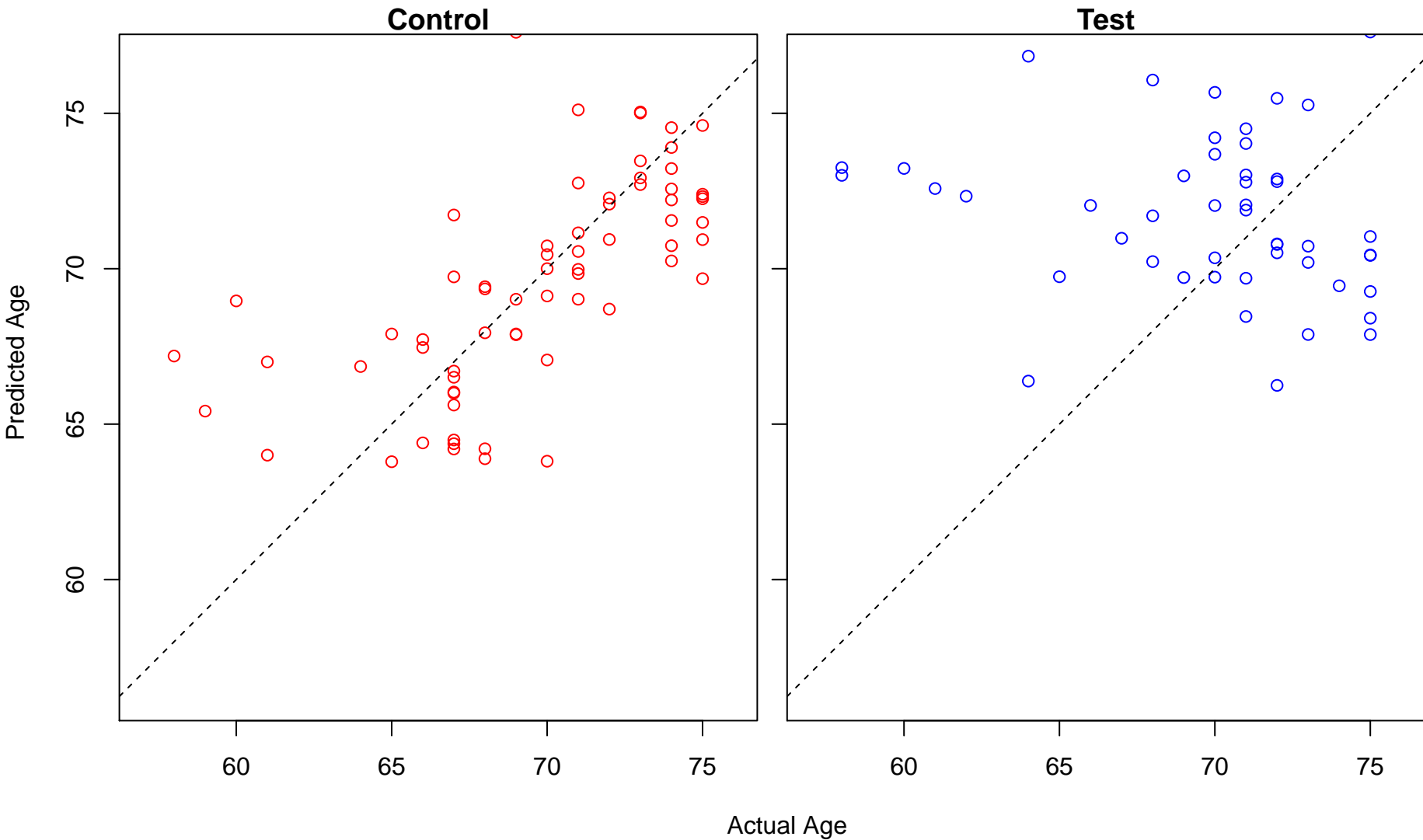
cellular response to oxygen levels (Score: 1.676688)



regulation of neutrophil migration (Score: 1.676146)

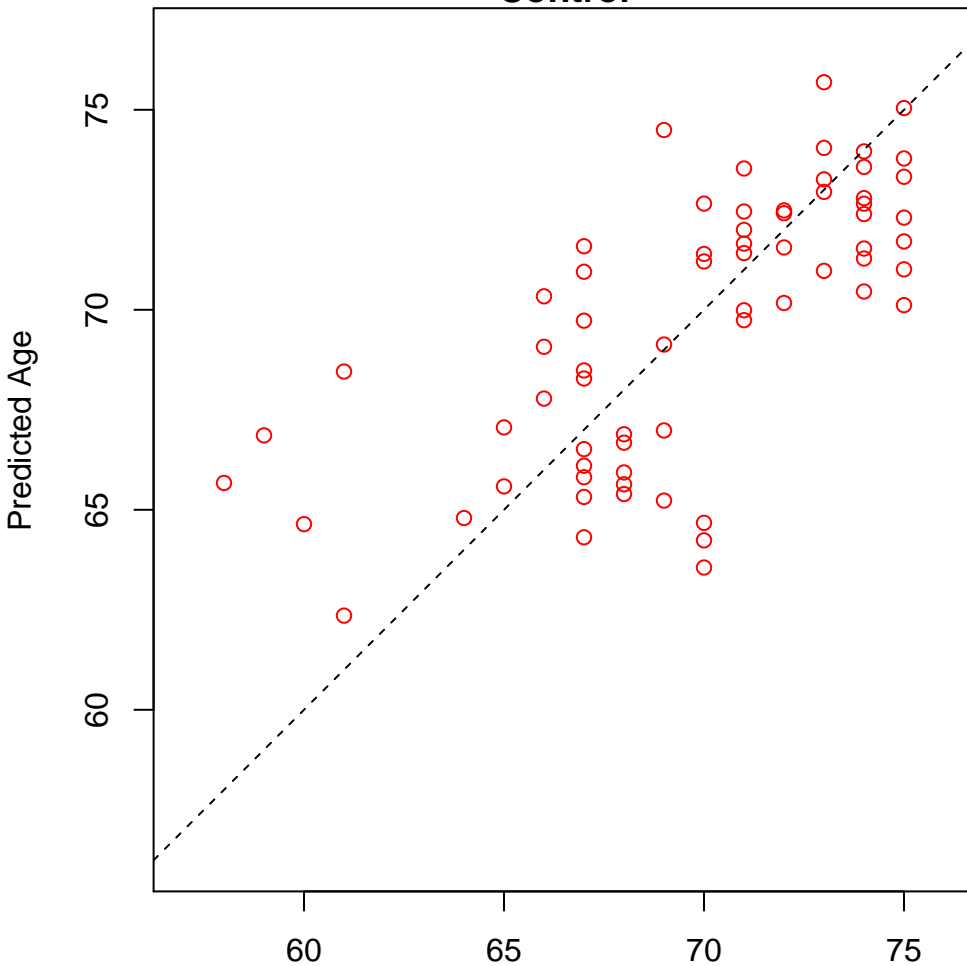


negative regulation of leukocyte activation (Score: 1.676079)

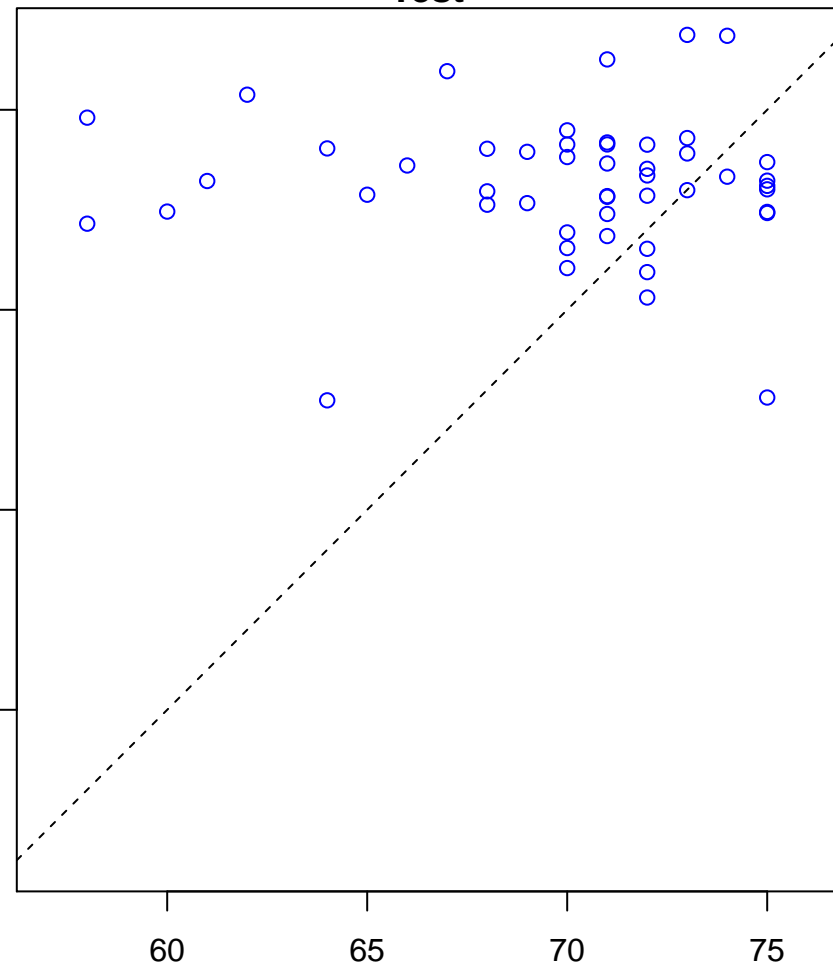


DNA-dependent DNA replication (Score: 1.675952)

Control

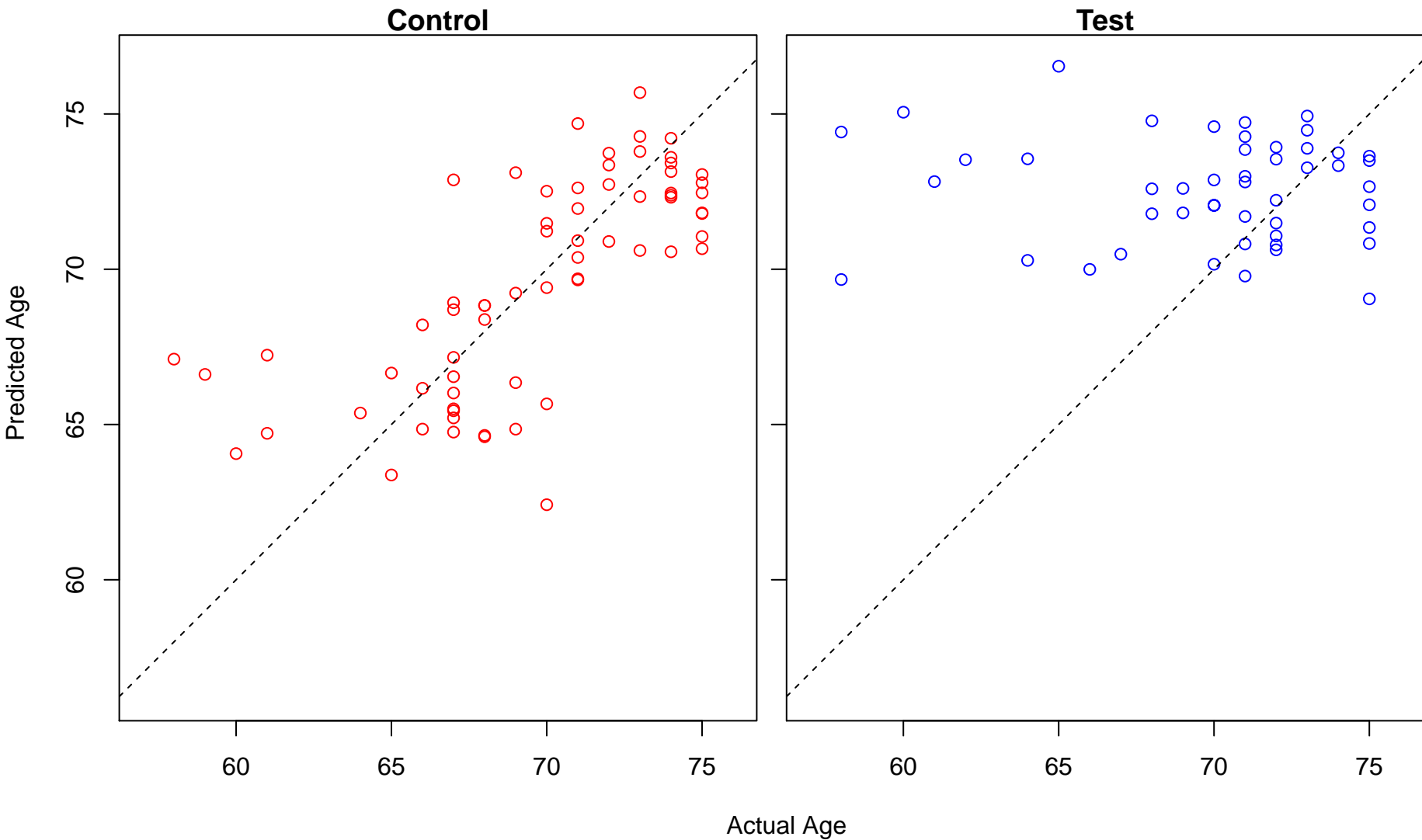


Test

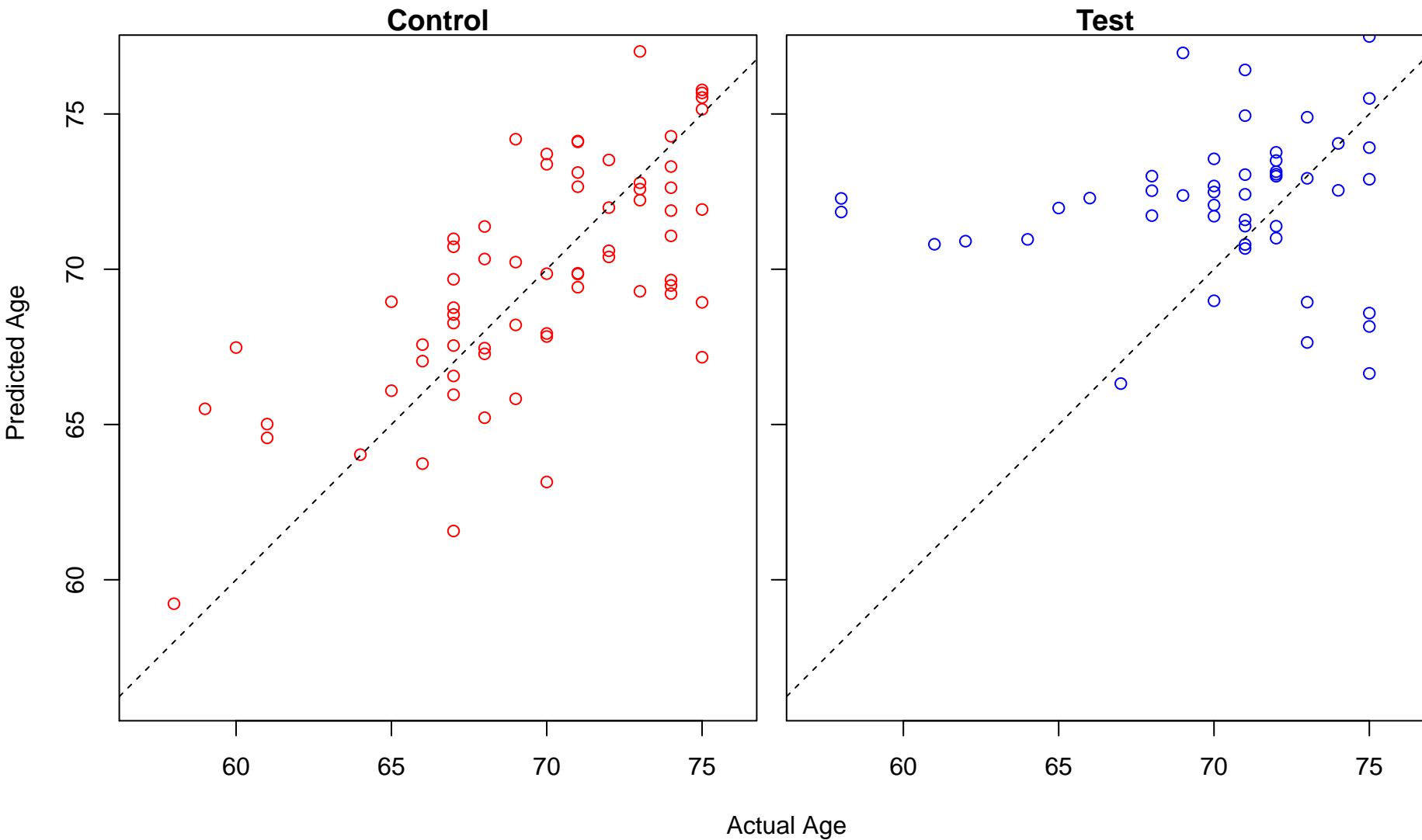


Actual Age

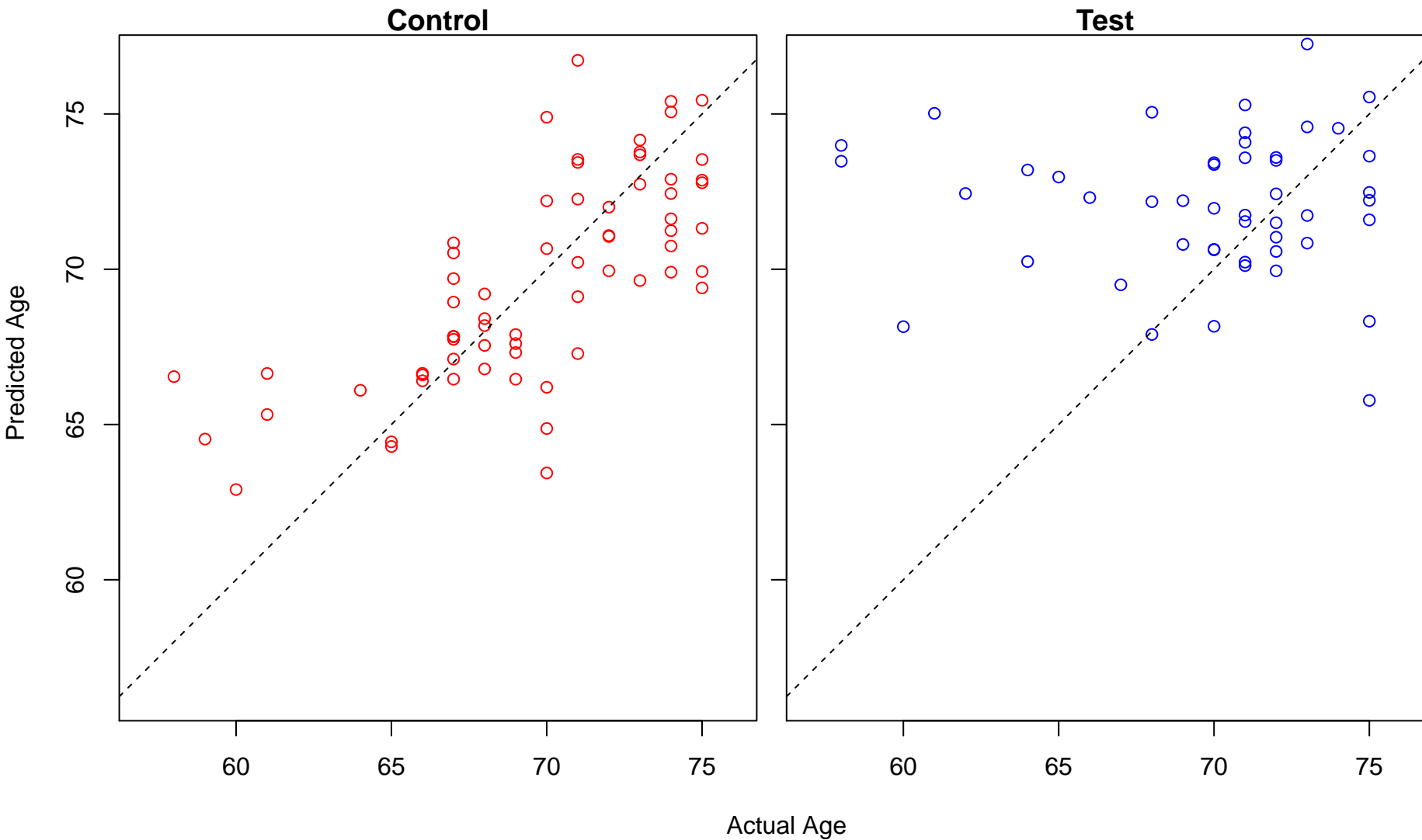
establishment of RNA localization (Score: 1.675568)



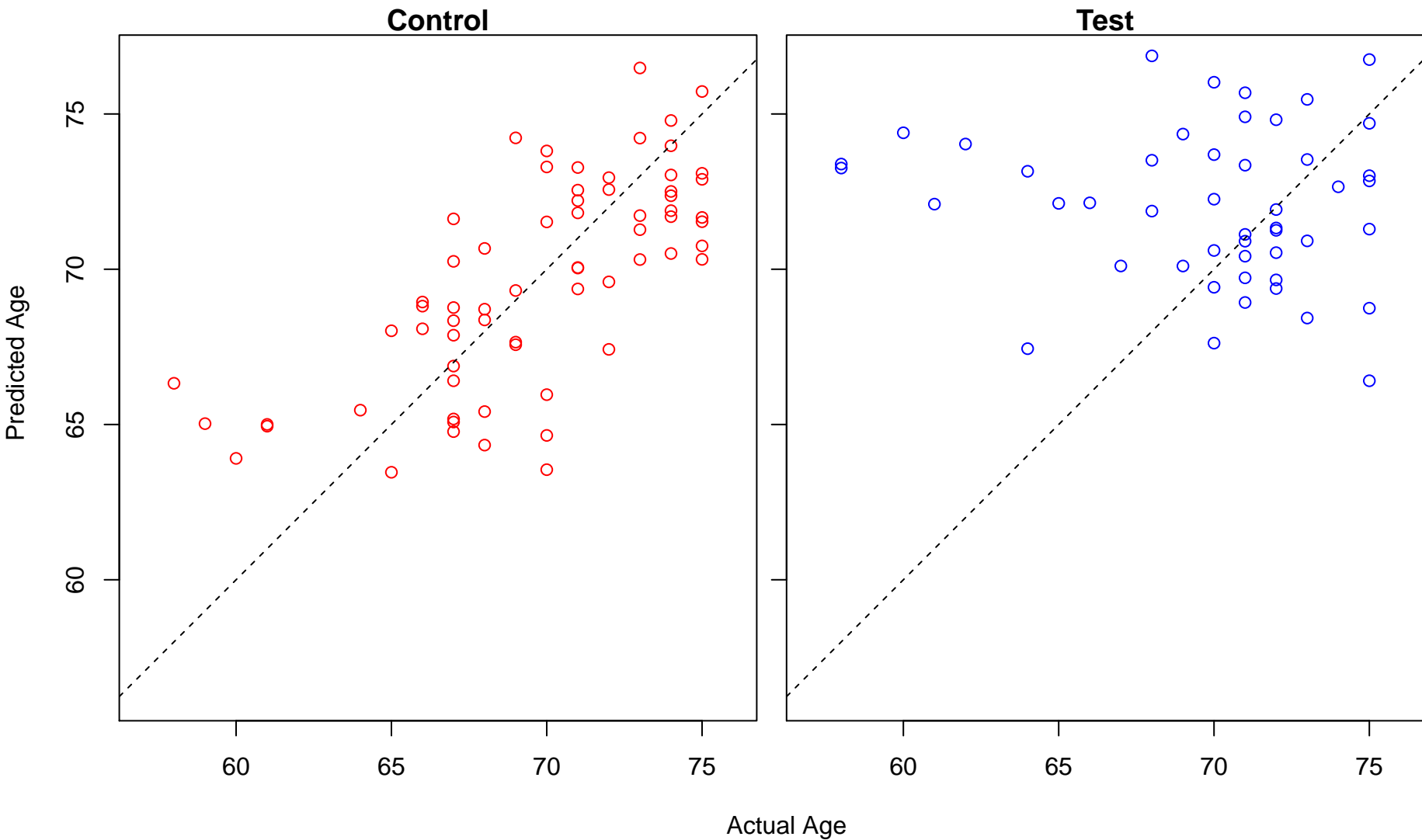
positive regulation of cAMP biosynthetic process (Score: 1.674460)



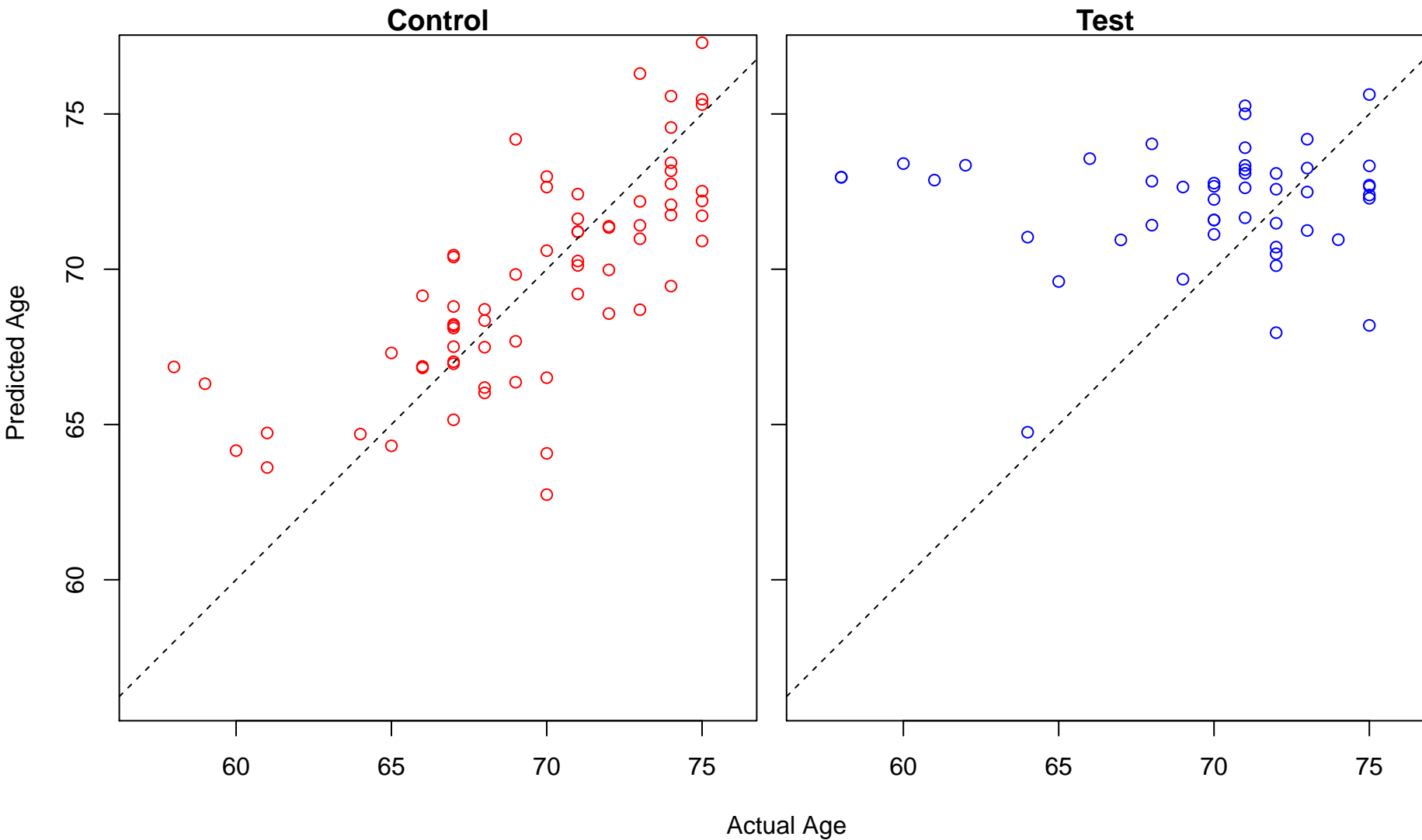
regulation of transporter activity (Score: 1.674352)



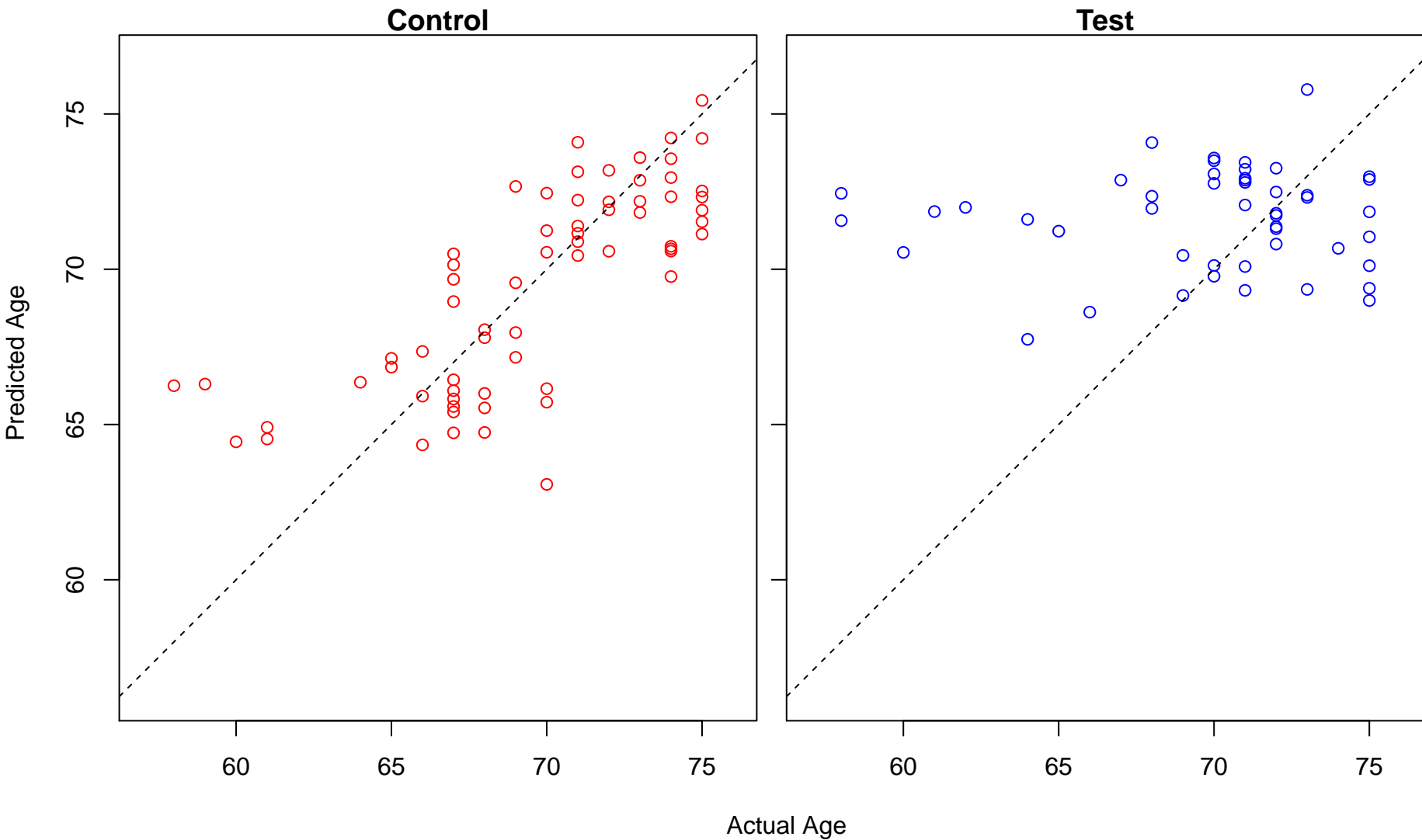
B cell activation (Score: 1.673802)



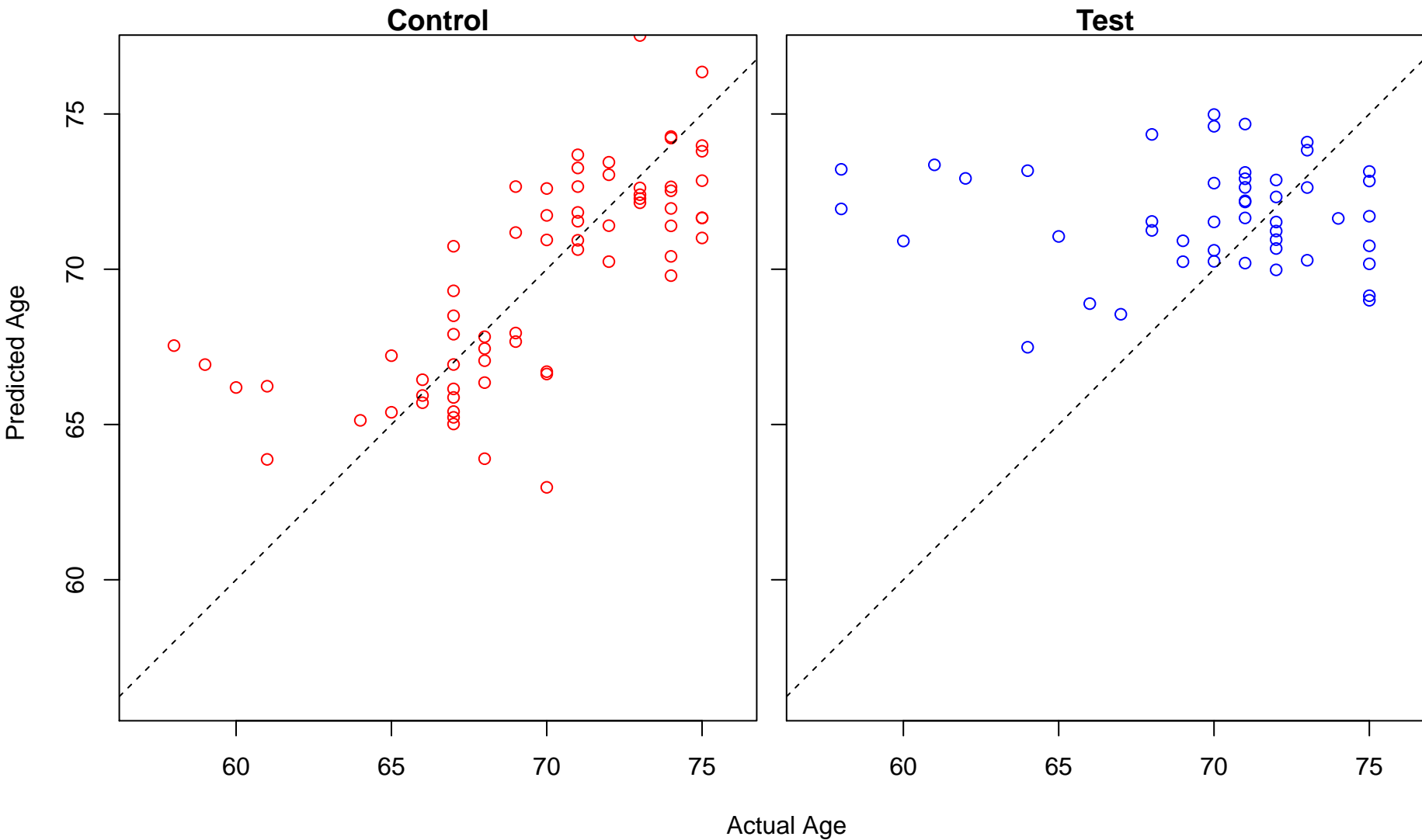
blood vessel development (Score: 1.673146)



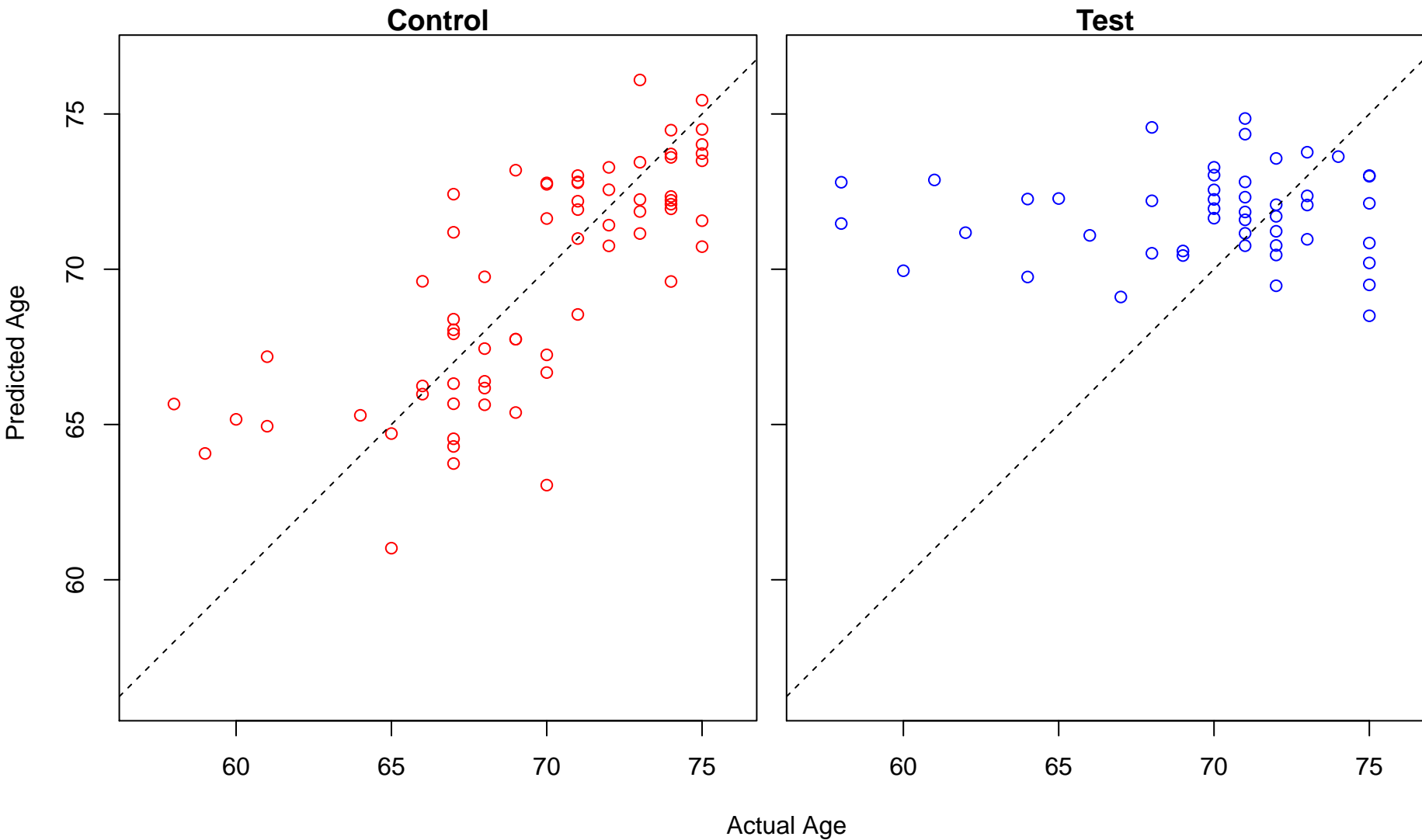
nucleoside monophosphate biosynthetic process (Score: 1.673143)



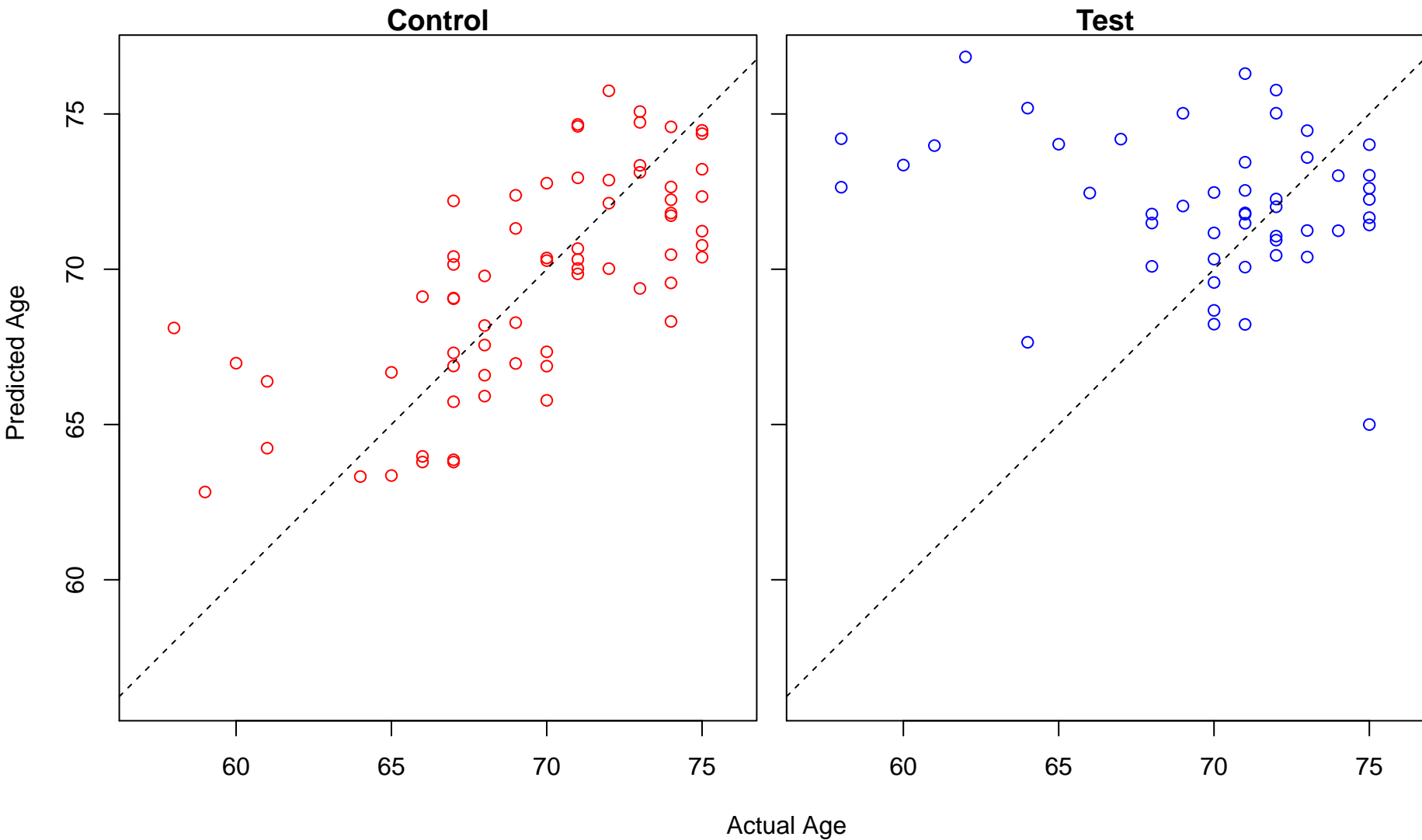
nucleoside metabolic process (Score: 1.672558)



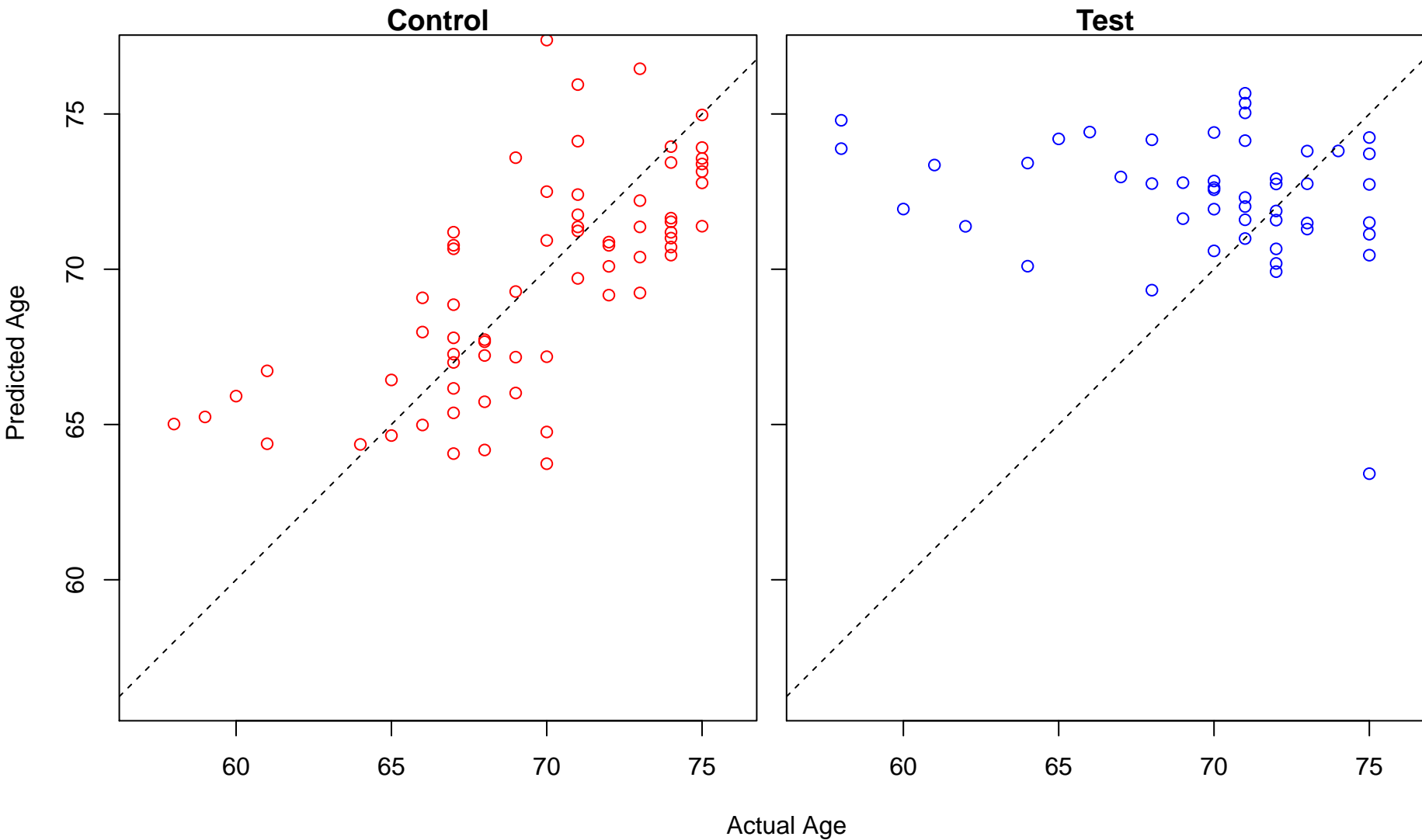
mitotic G1 DNA damage checkpoint (Score: 1.672464)



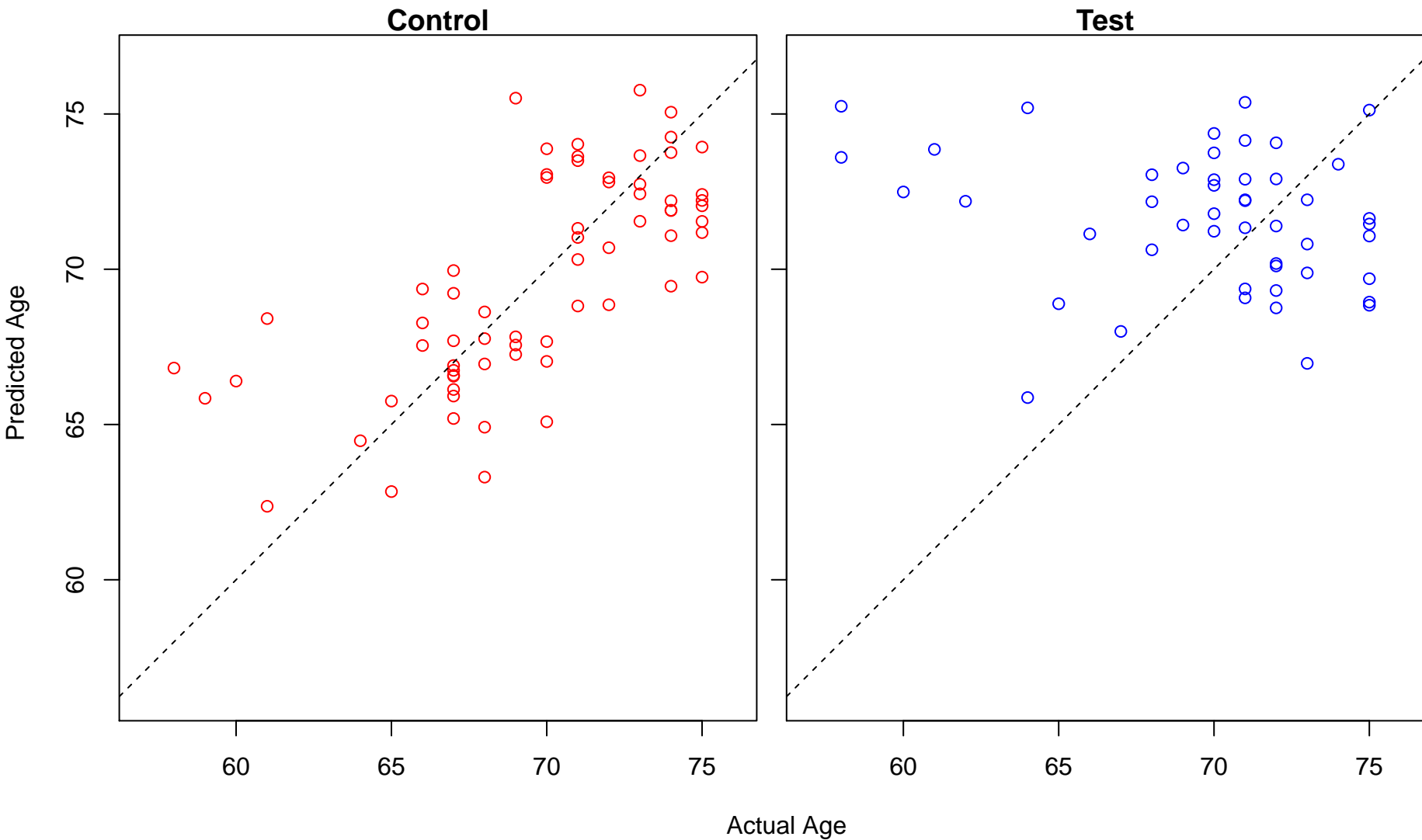
cellular extravasation (Score: 1.671828)



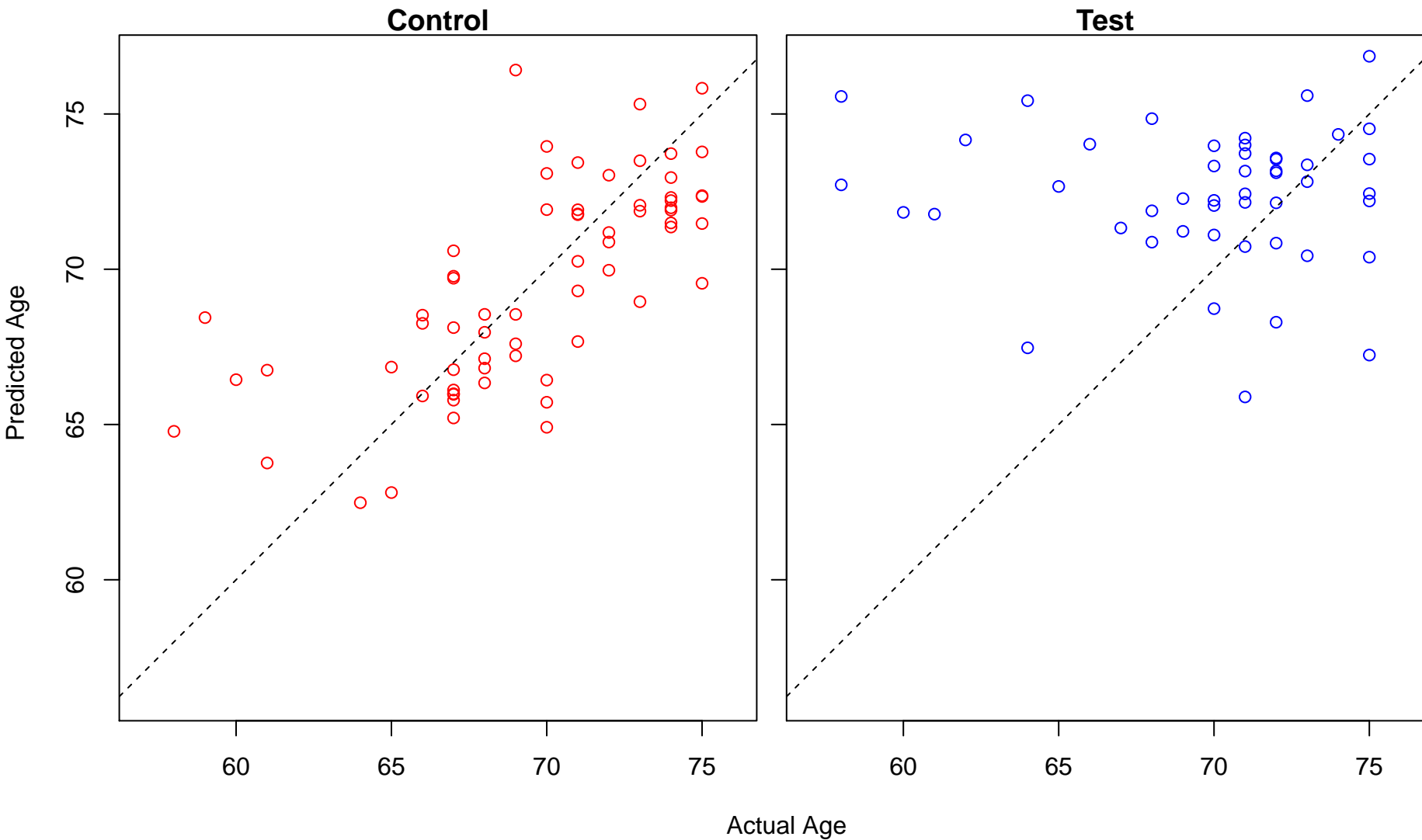
protein dephosphorylation (Score: 1.671282)



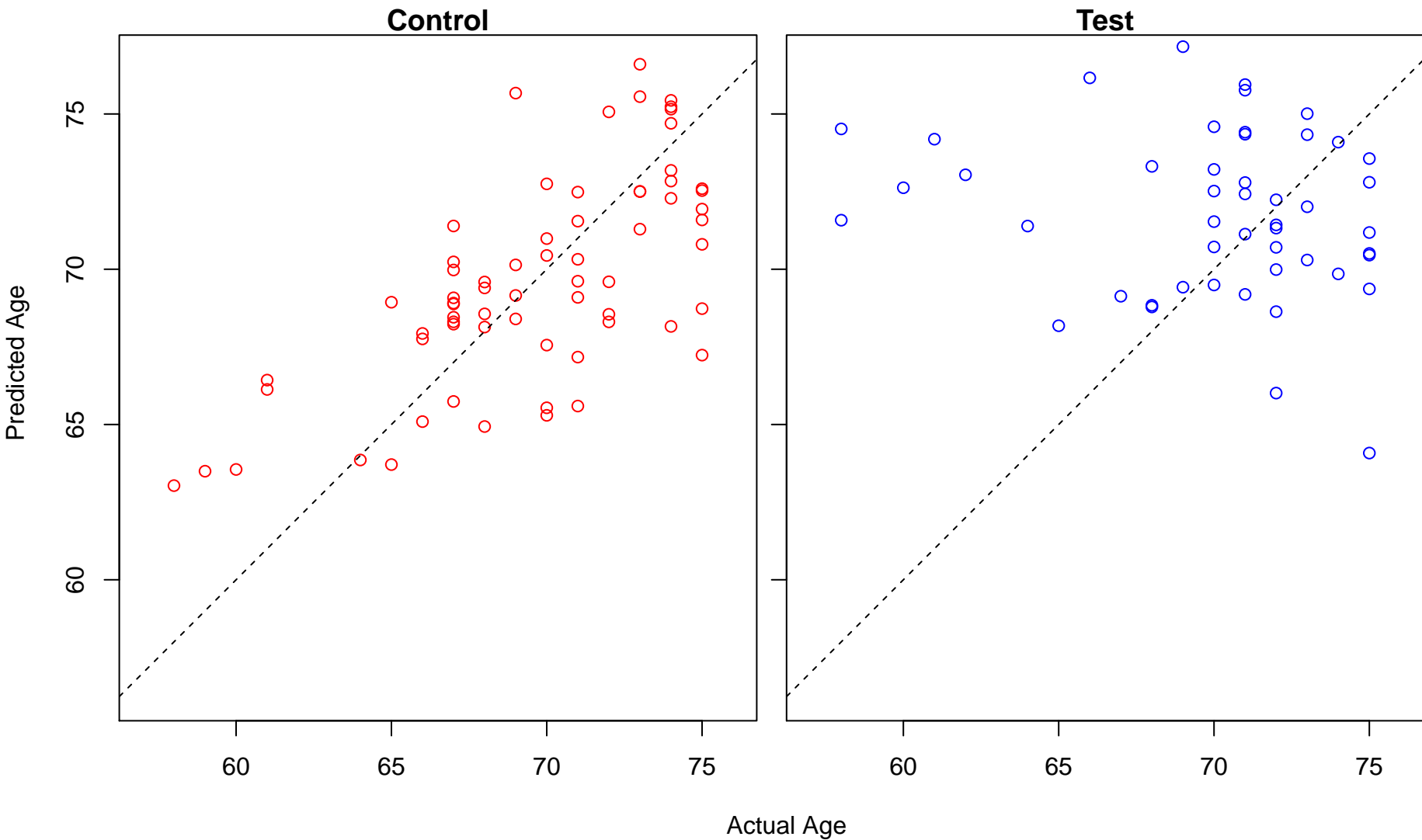
multicellular organism reproduction (Score: 1.671246)



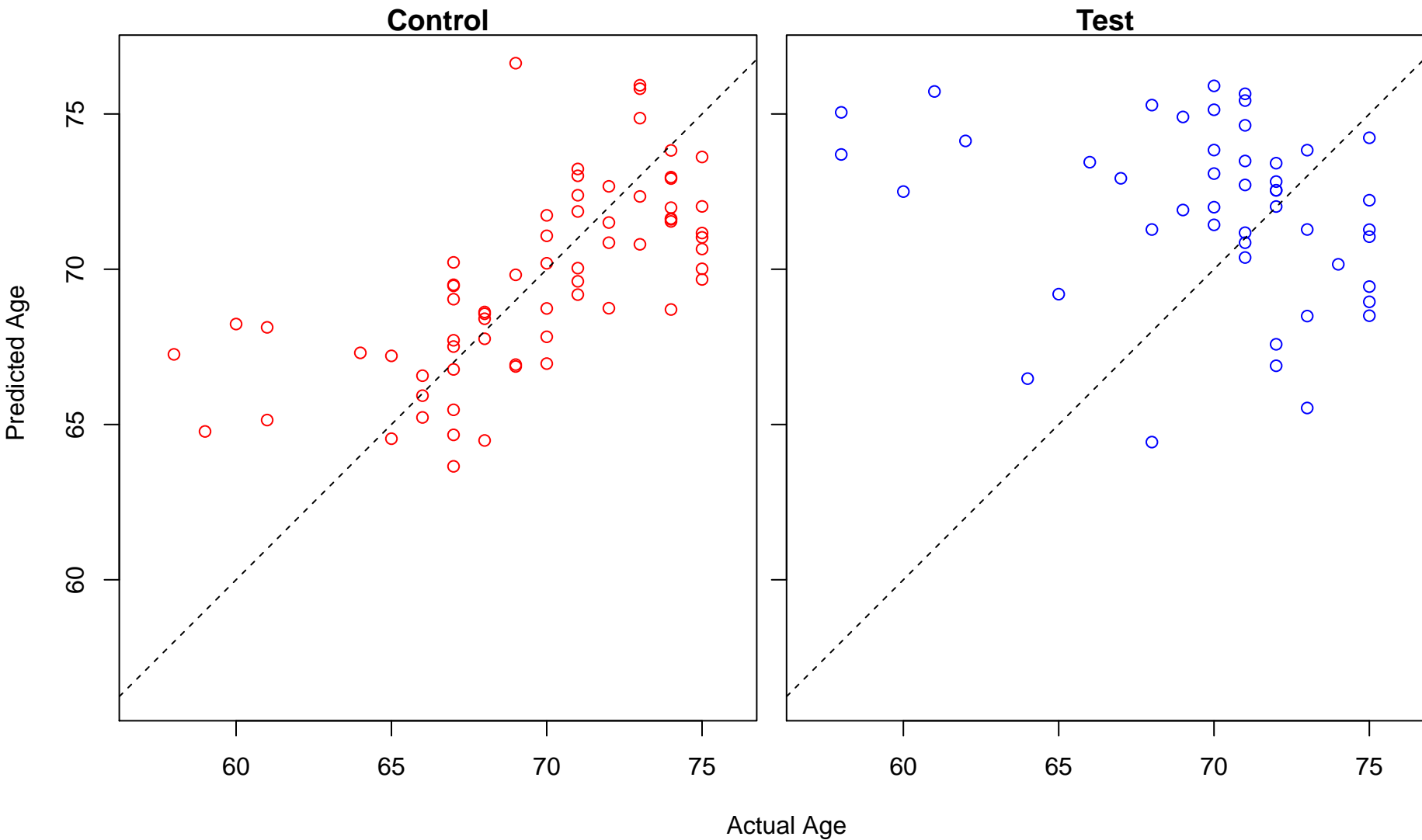
toll-like receptor 4 signaling pathway (Score: 1.671235)



positive regulation of T cell apoptotic process (Score: 1.668031)

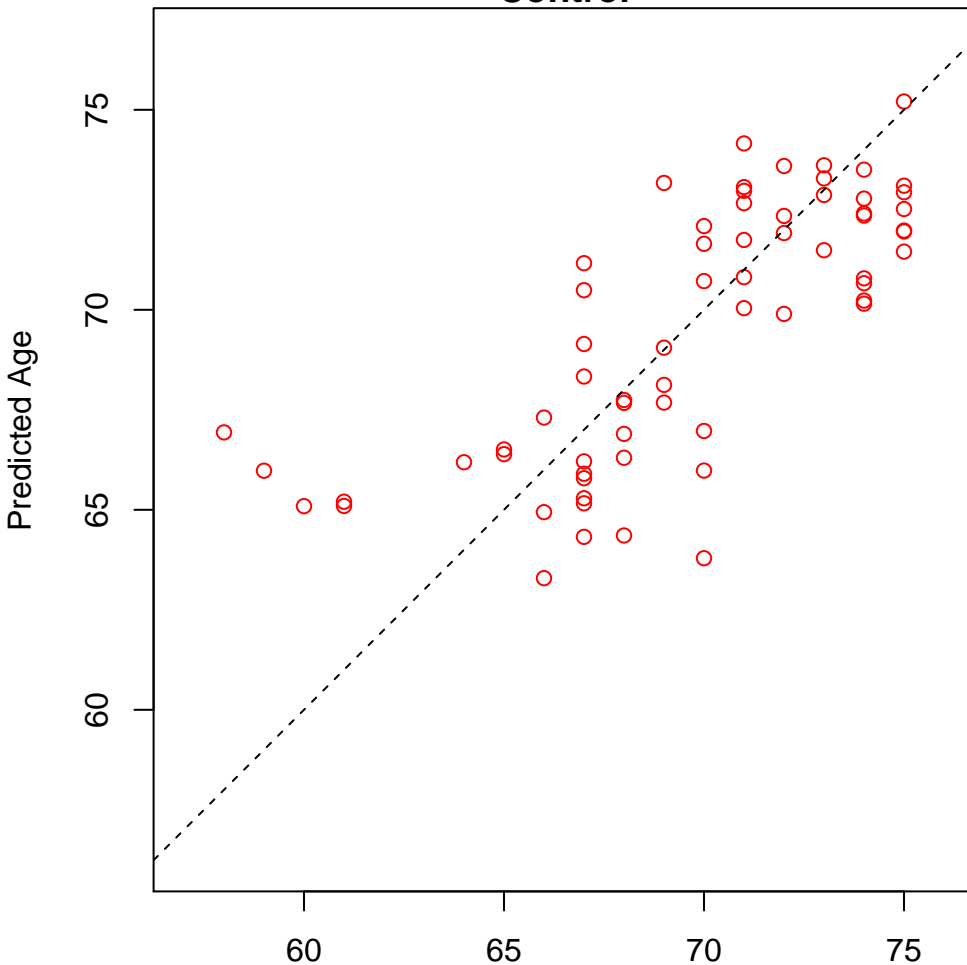


negative regulation of alpha-beta T cell activation (Score: 1.667852)

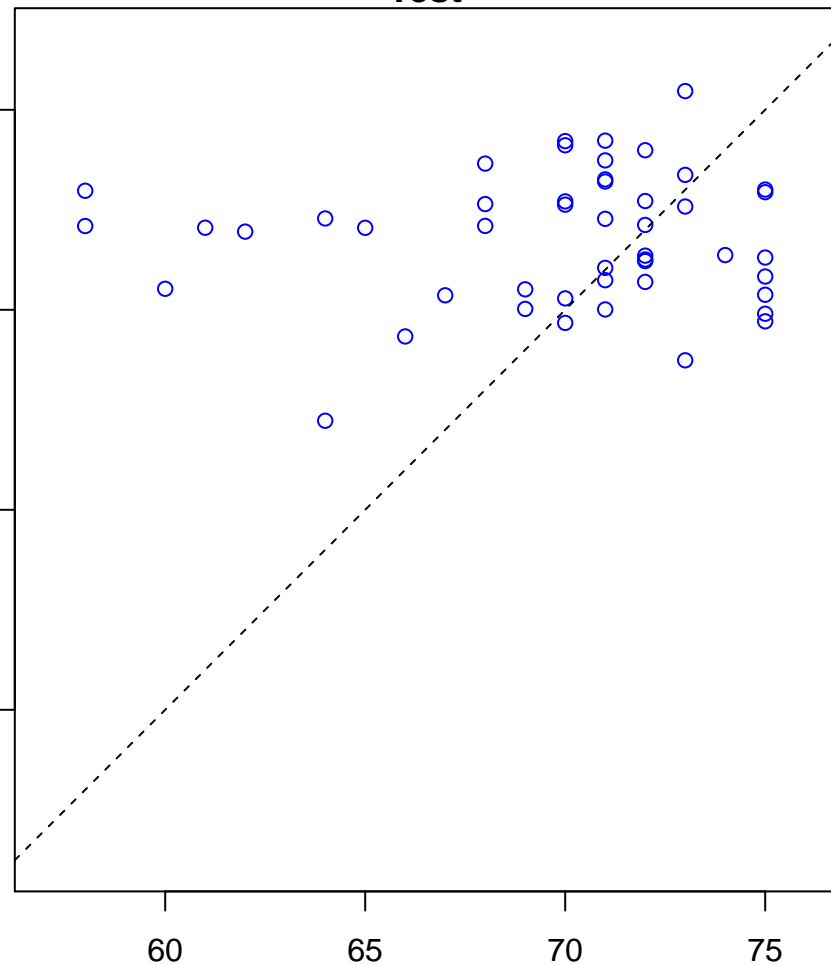


purine nucleoside biosynthetic process (Score: 1.667808)

Control

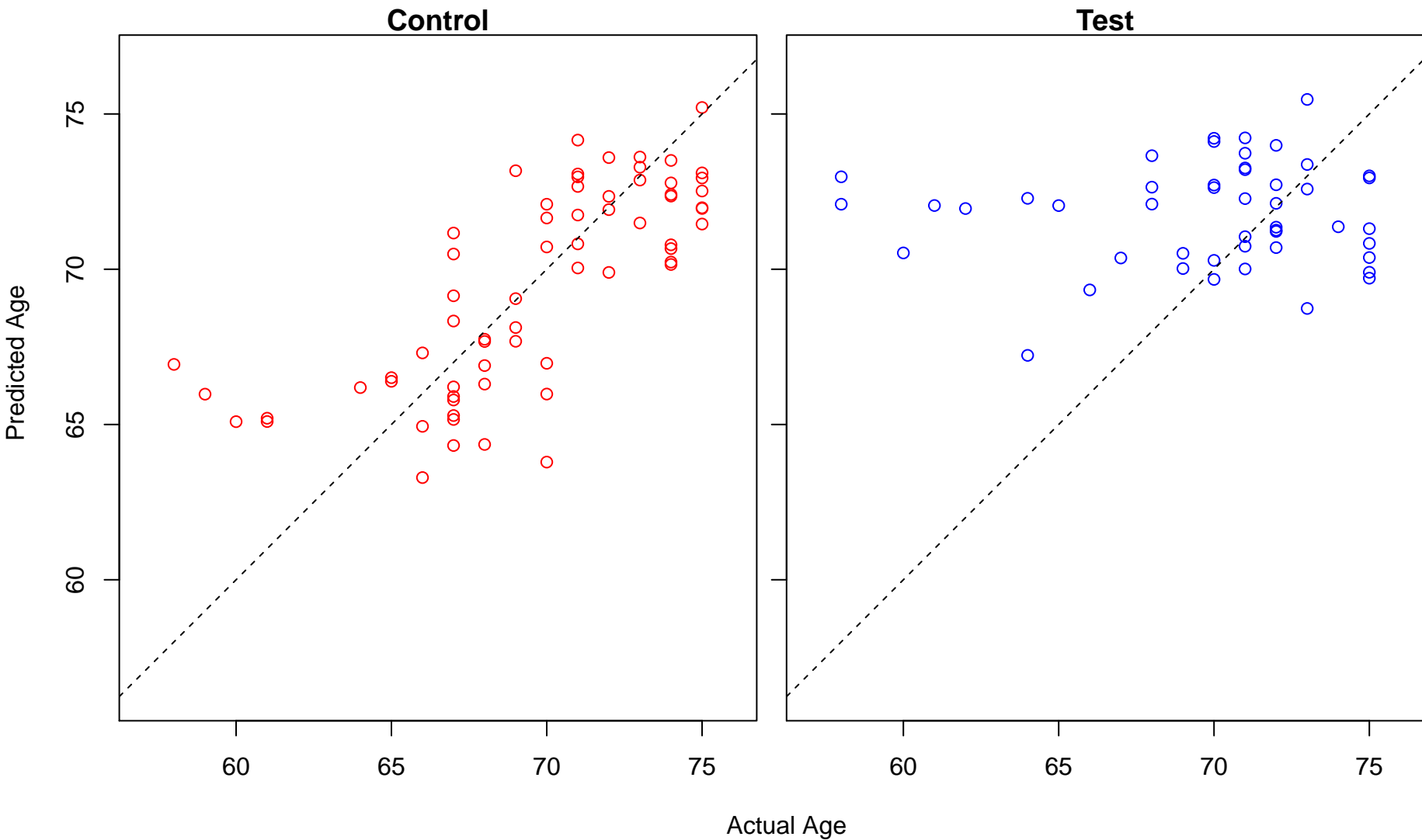


Test

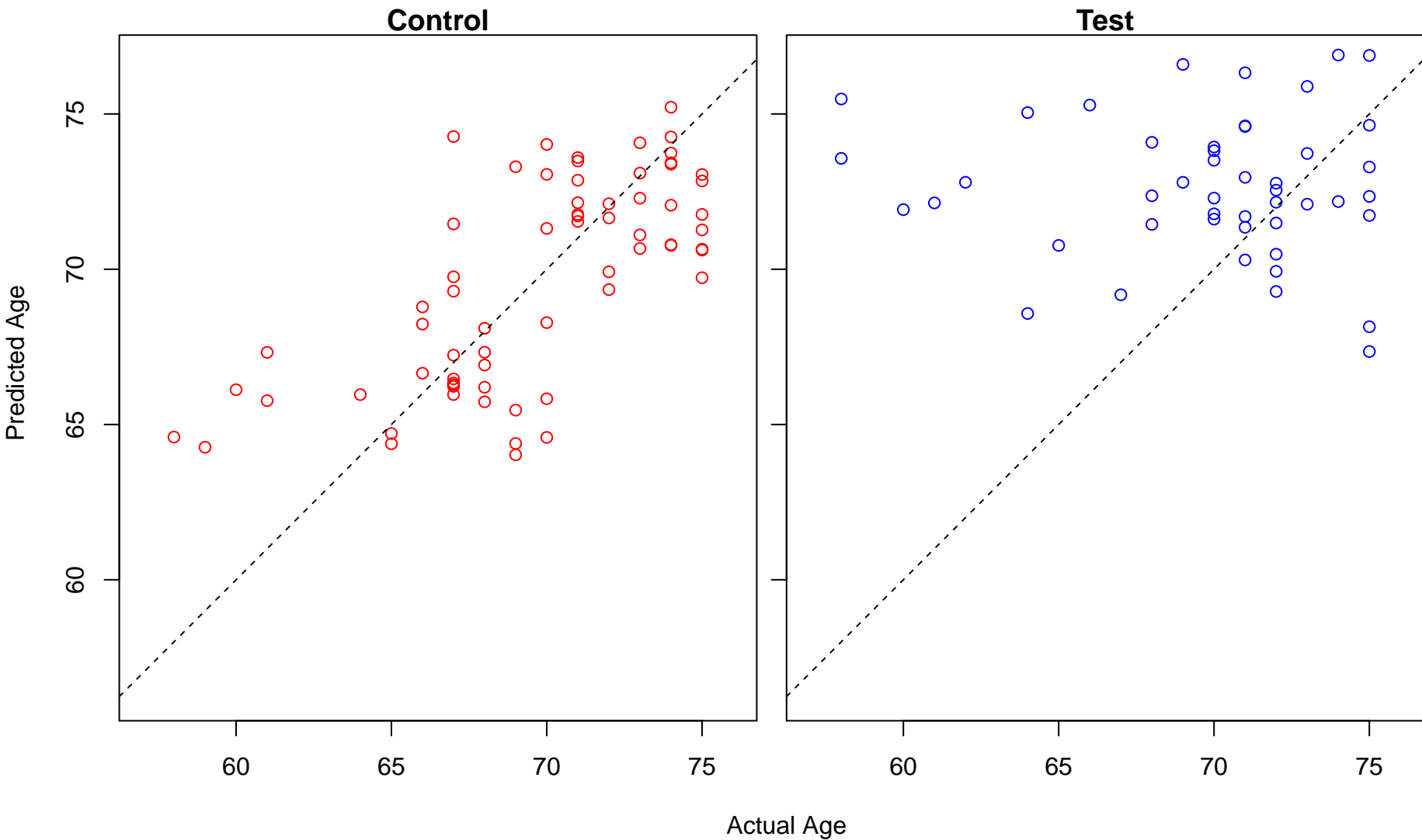


Actual Age

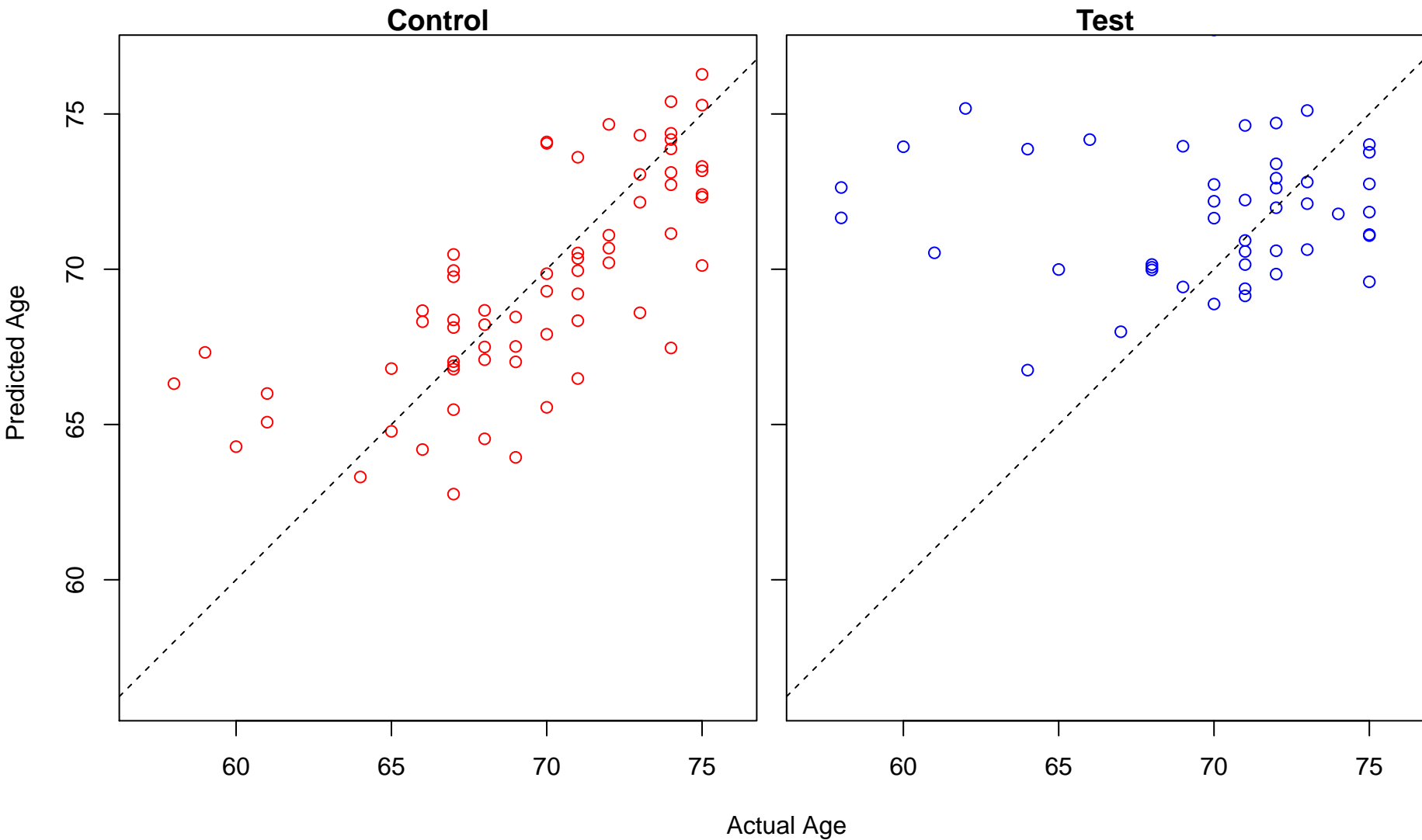
purine ribonucleoside biosynthetic process (Score: 1.667808)



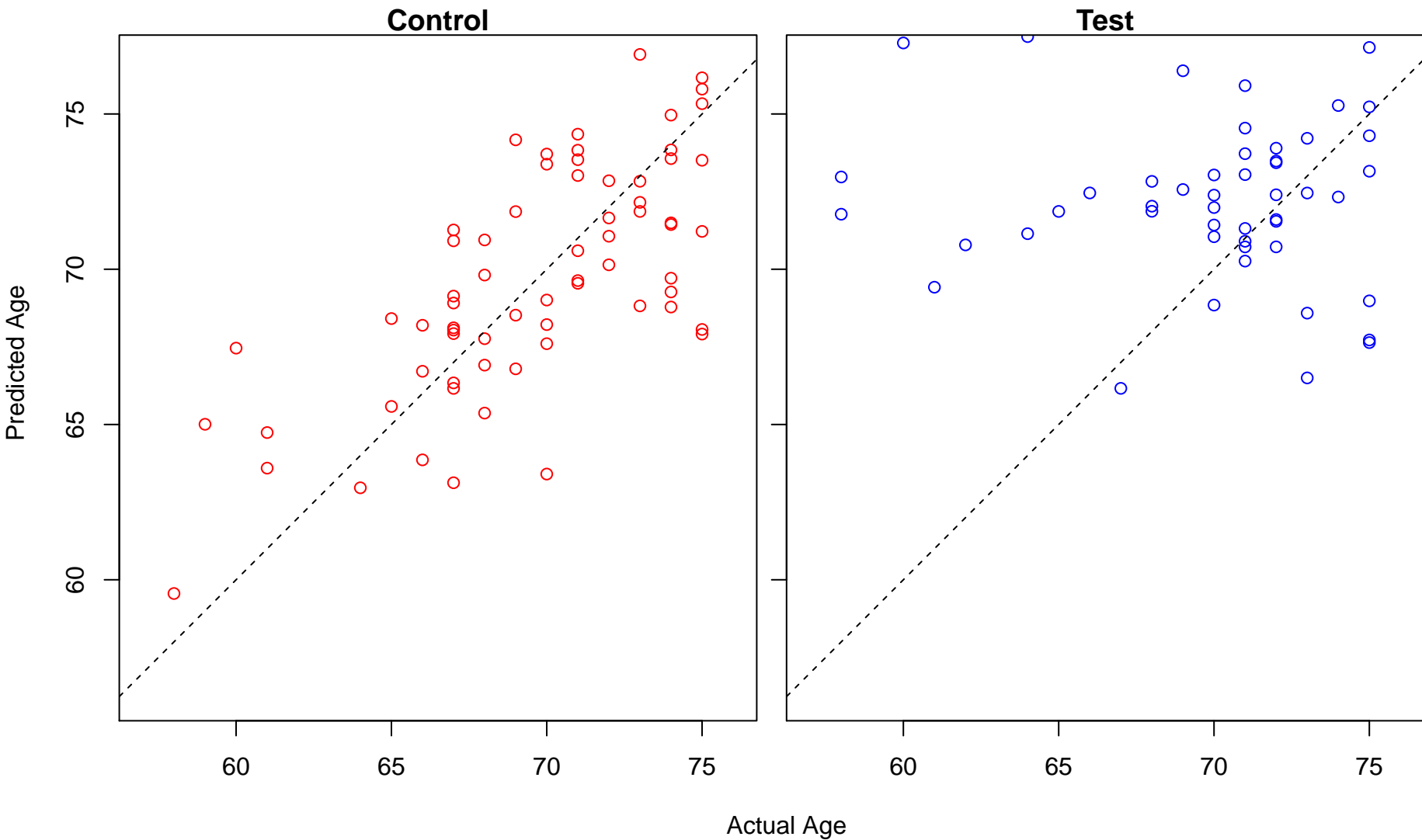
body morphogenesis (Score: 1.667801)



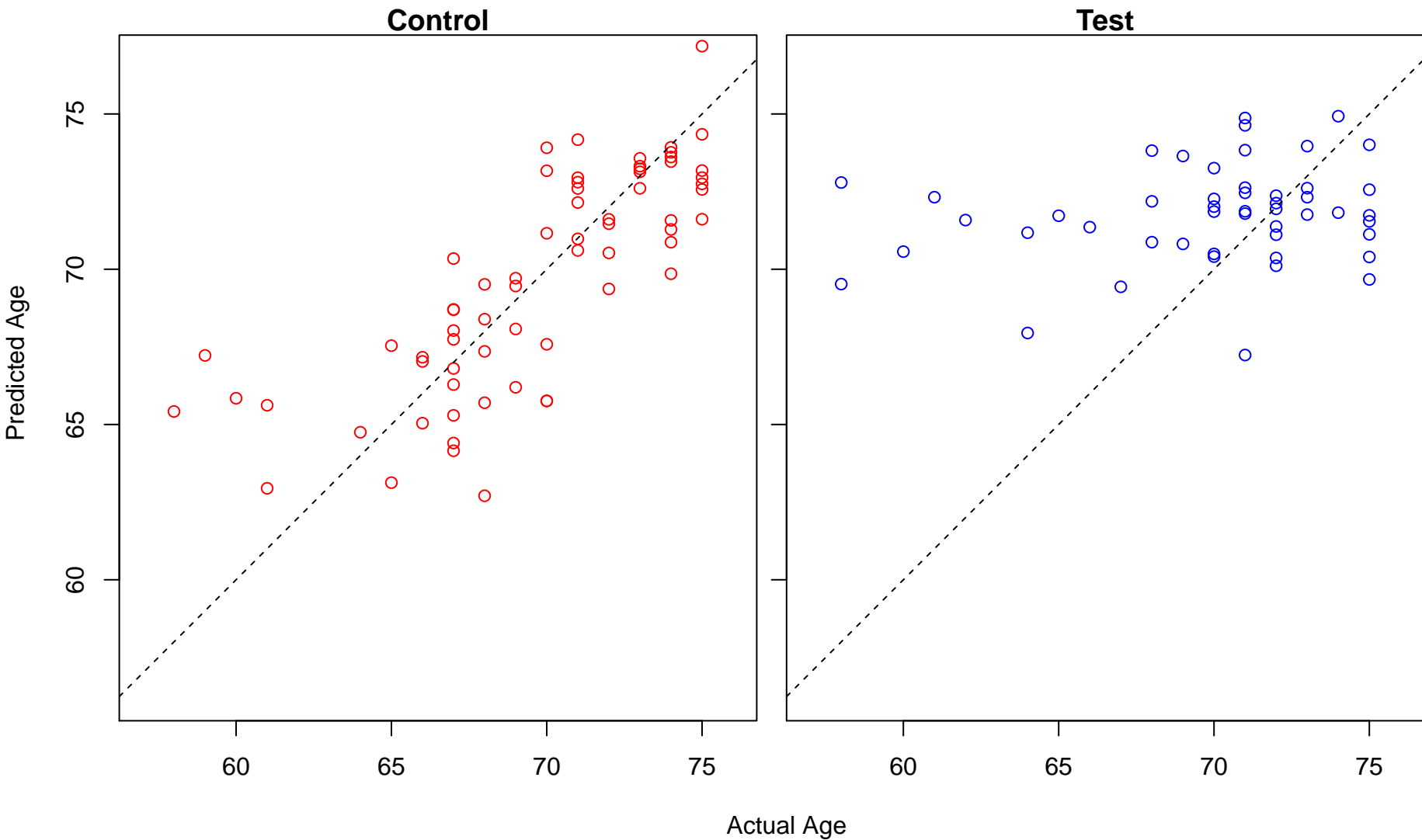
behavior (Score: 1.667656)



positive regulation of cyclic nucleotide biosynthetic process (Score: 1.667632)

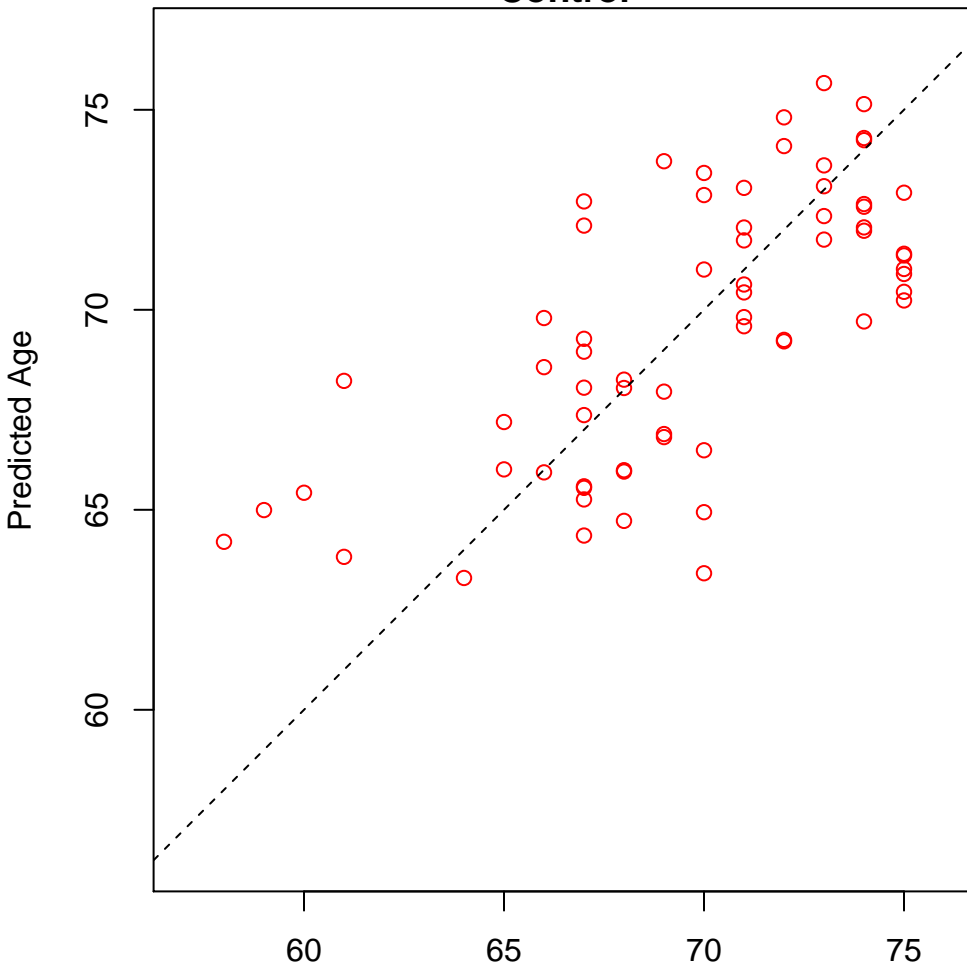


regulation of purine nucleotide metabolic process (Score: 1.667020)

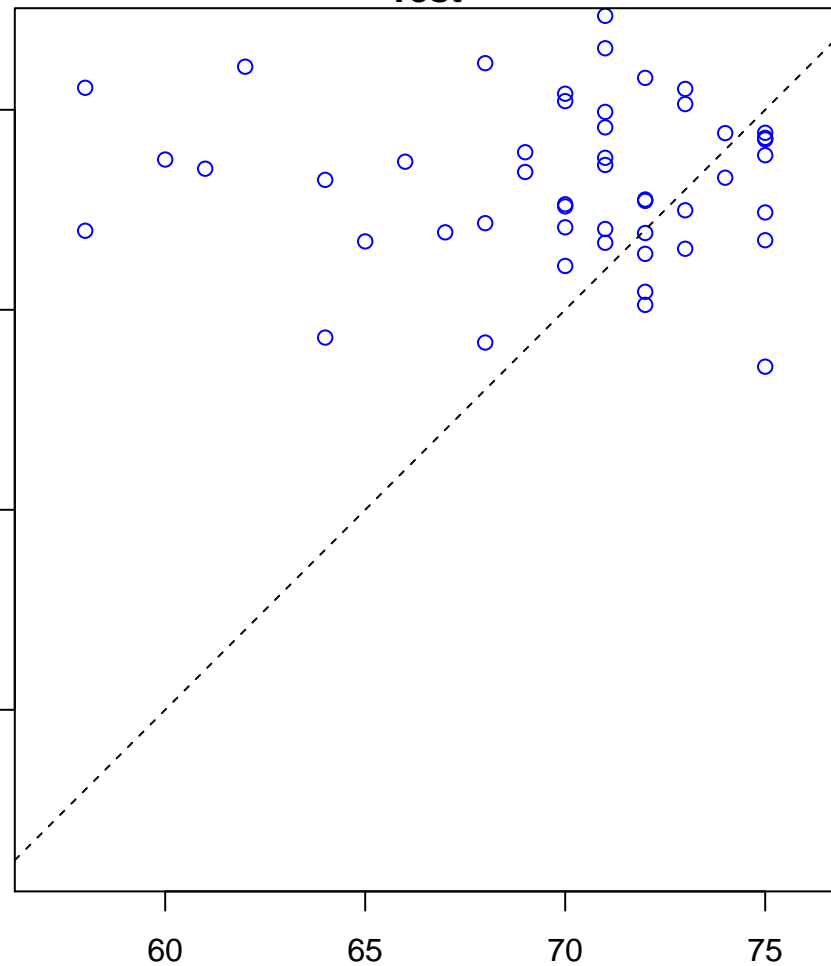


regulation of chromosome segregation (Score: 1.66688)

Control

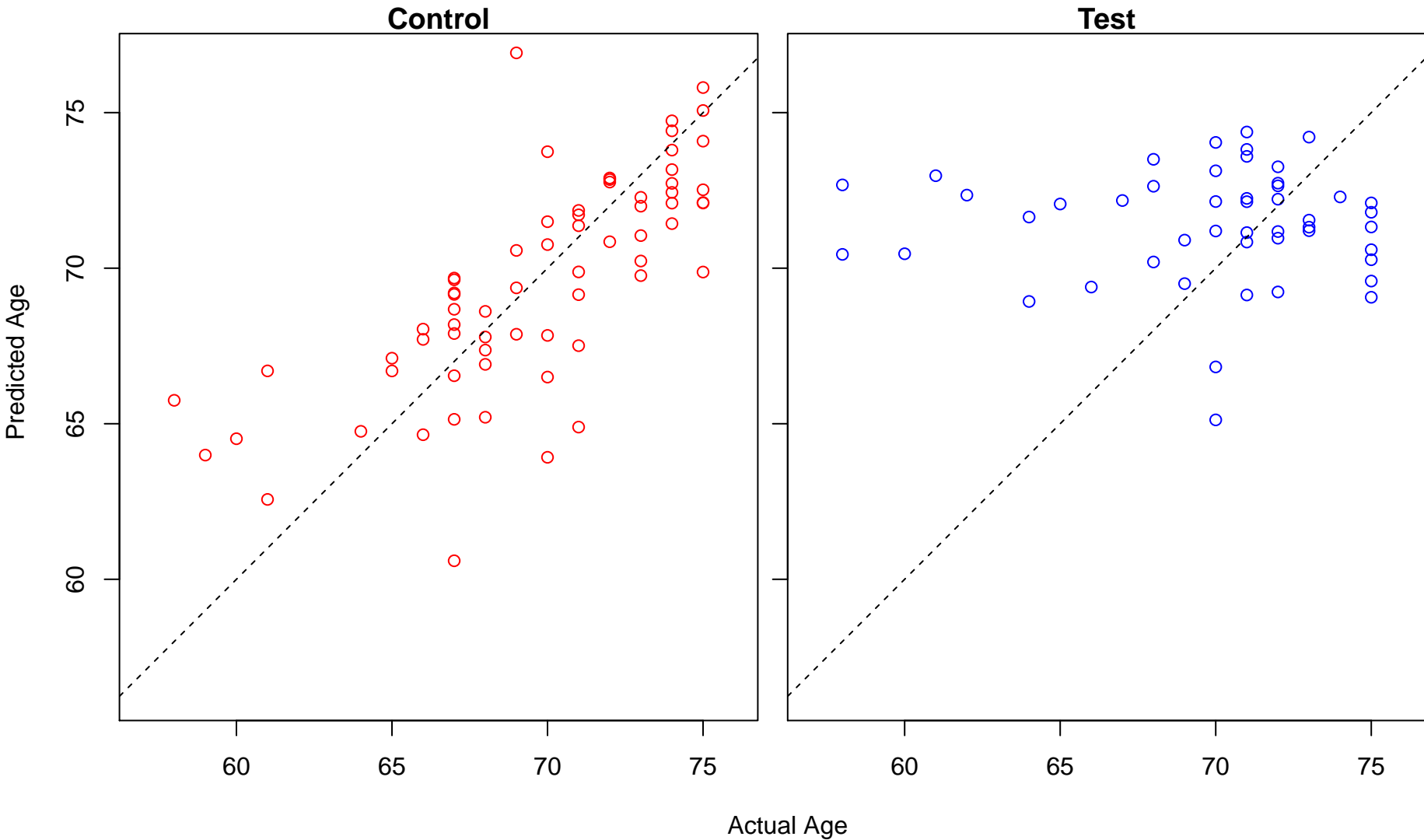


Test

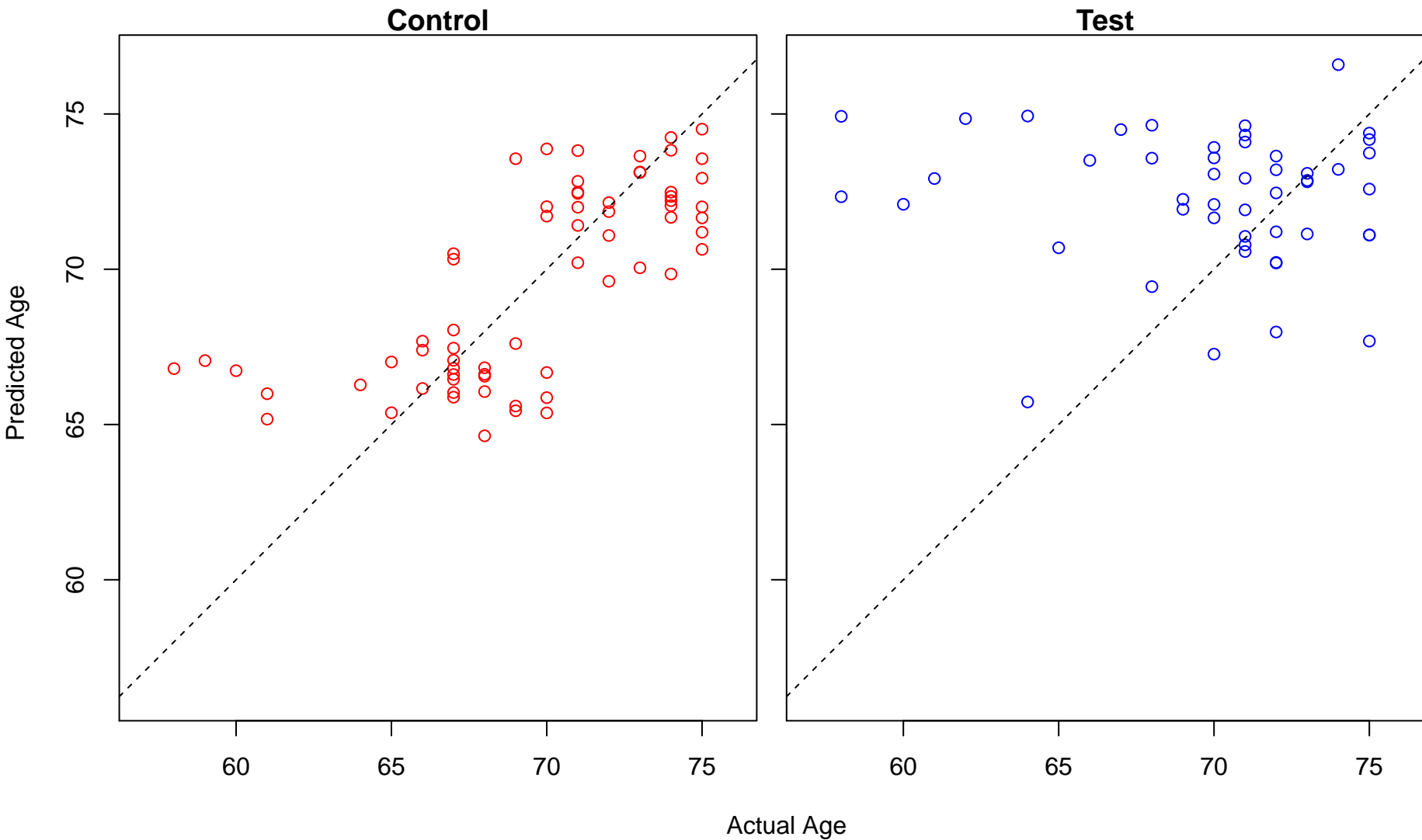


Actual Age

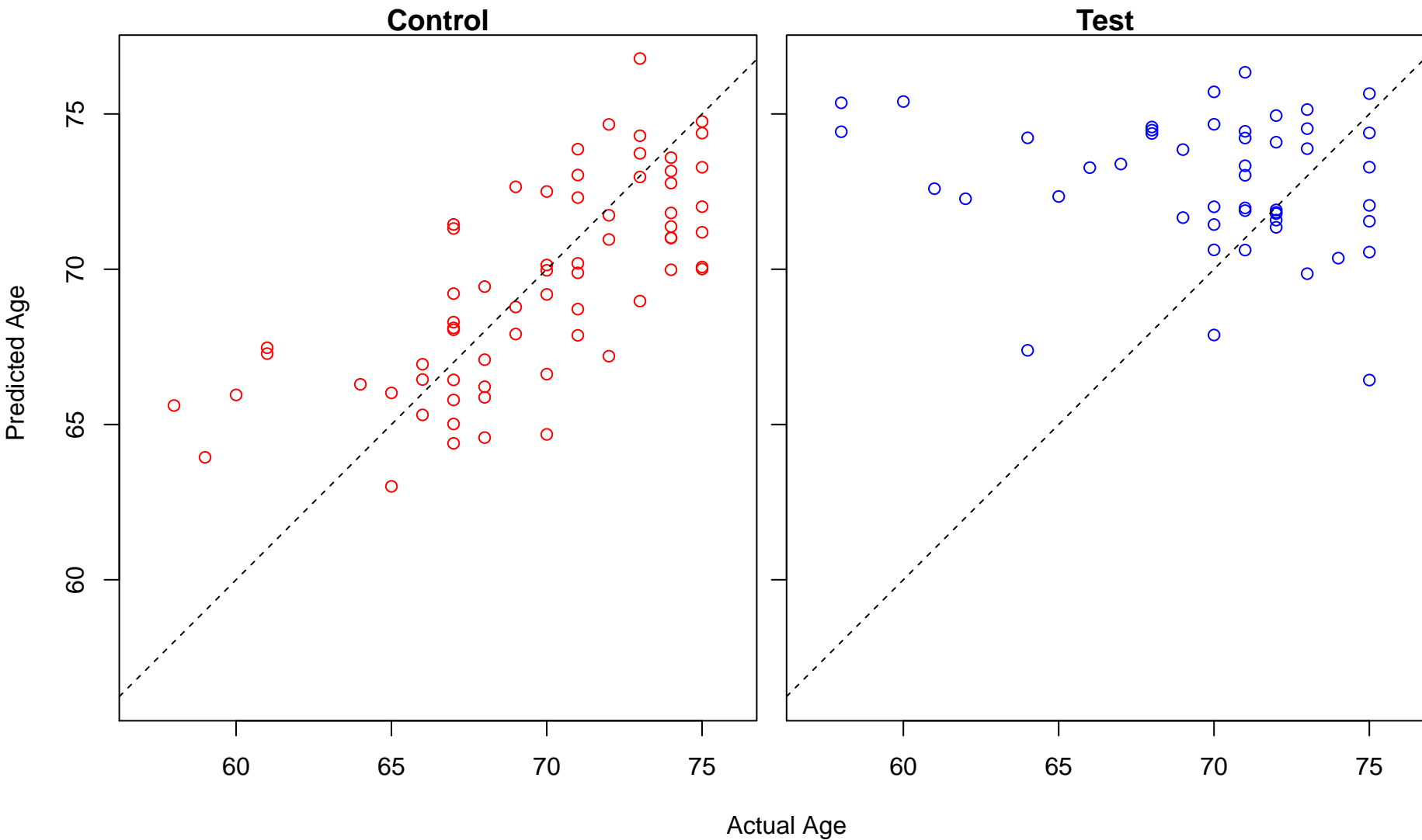
release of cytochrome c from mitochondria (Score: 1.666638)



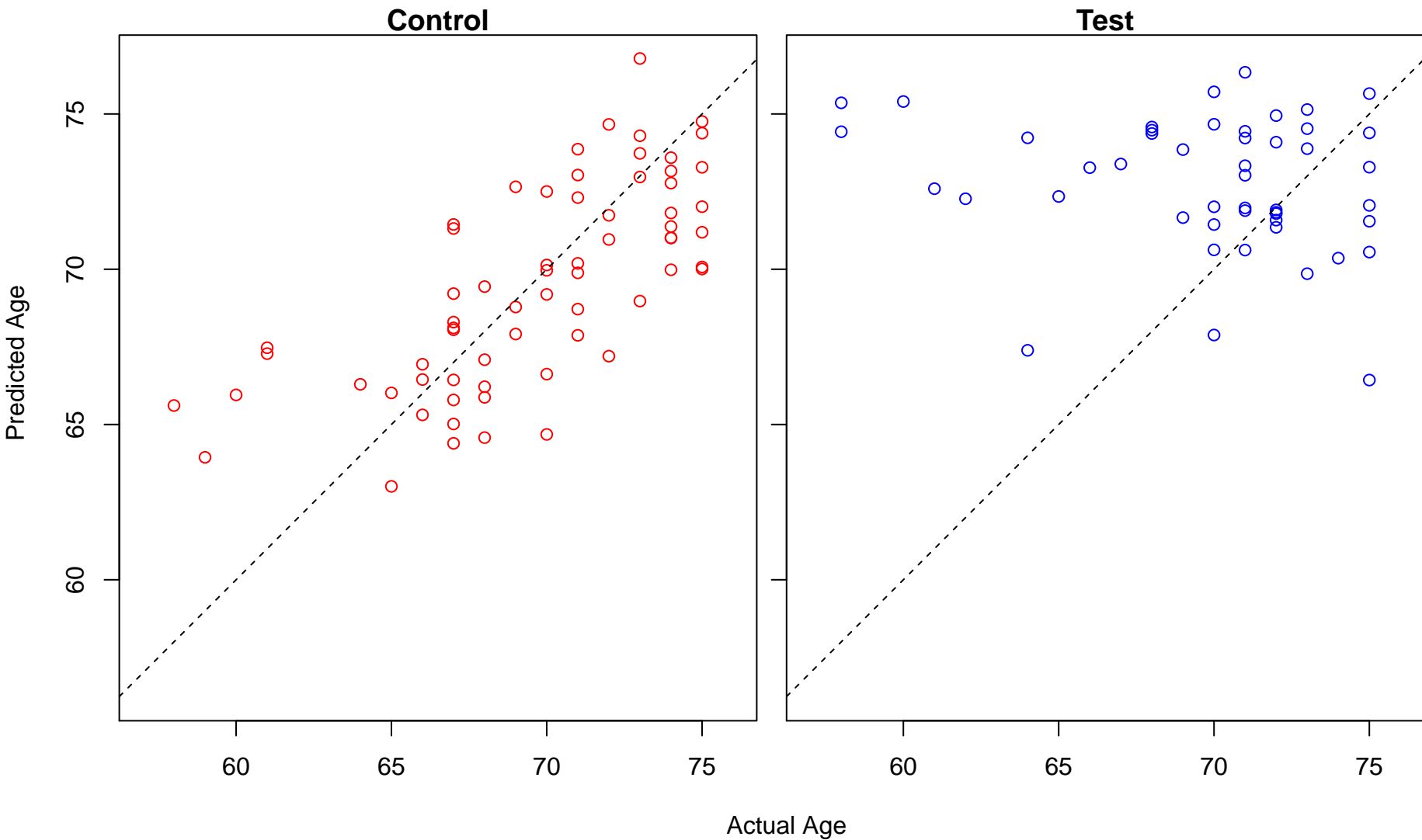
protein polymerization (Score: 1.666471)



lymphocyte costimulation (Score: 1.665786)

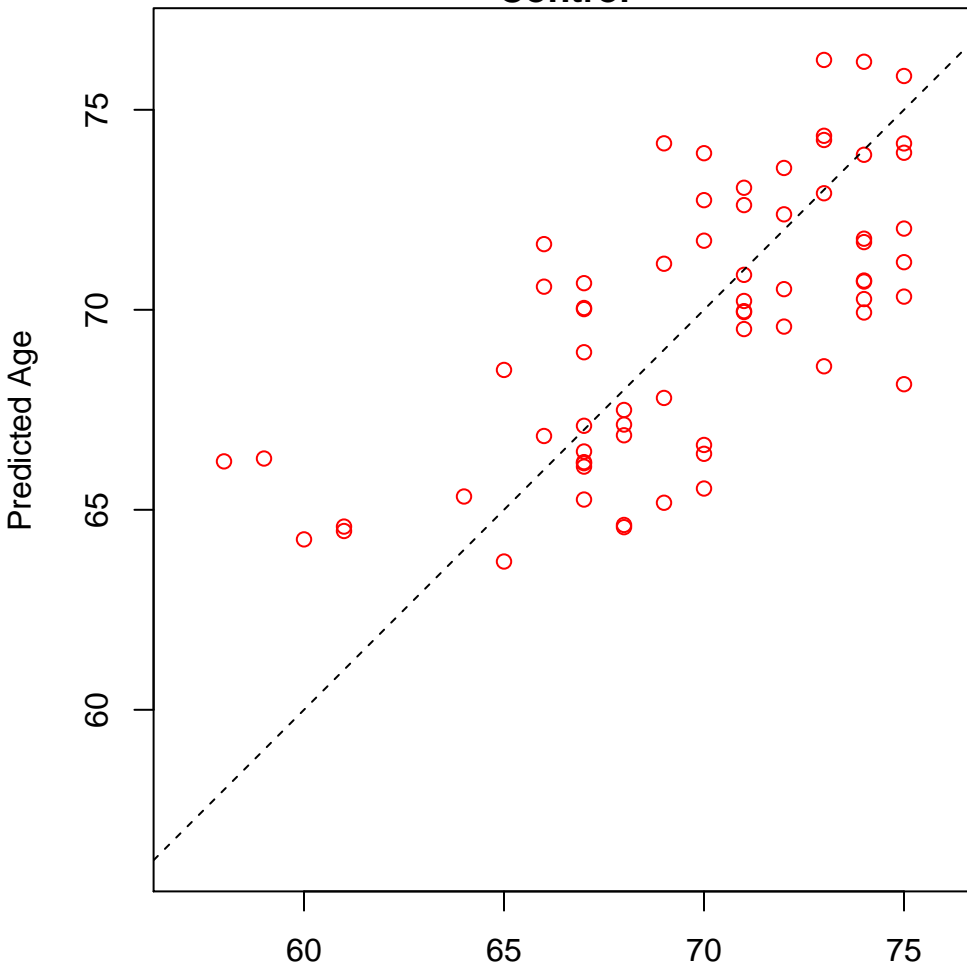


T cell costimulation (Score: 1.665786)

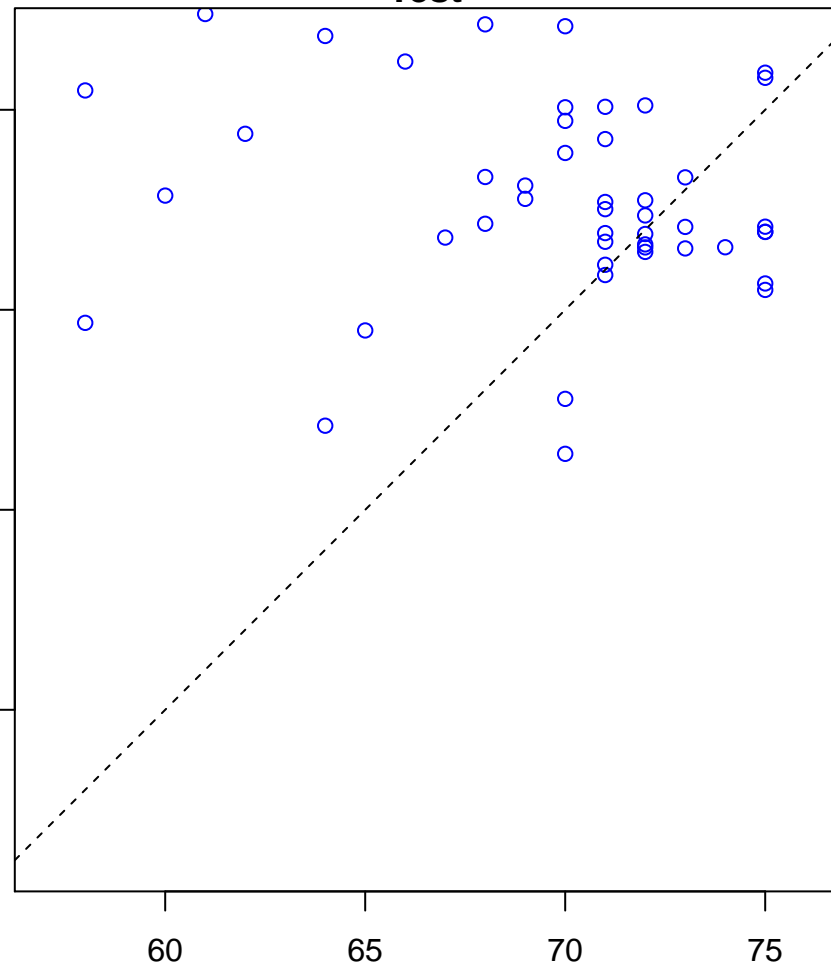


regulation of steroid metabolic process (Score: 1.665614)

Control

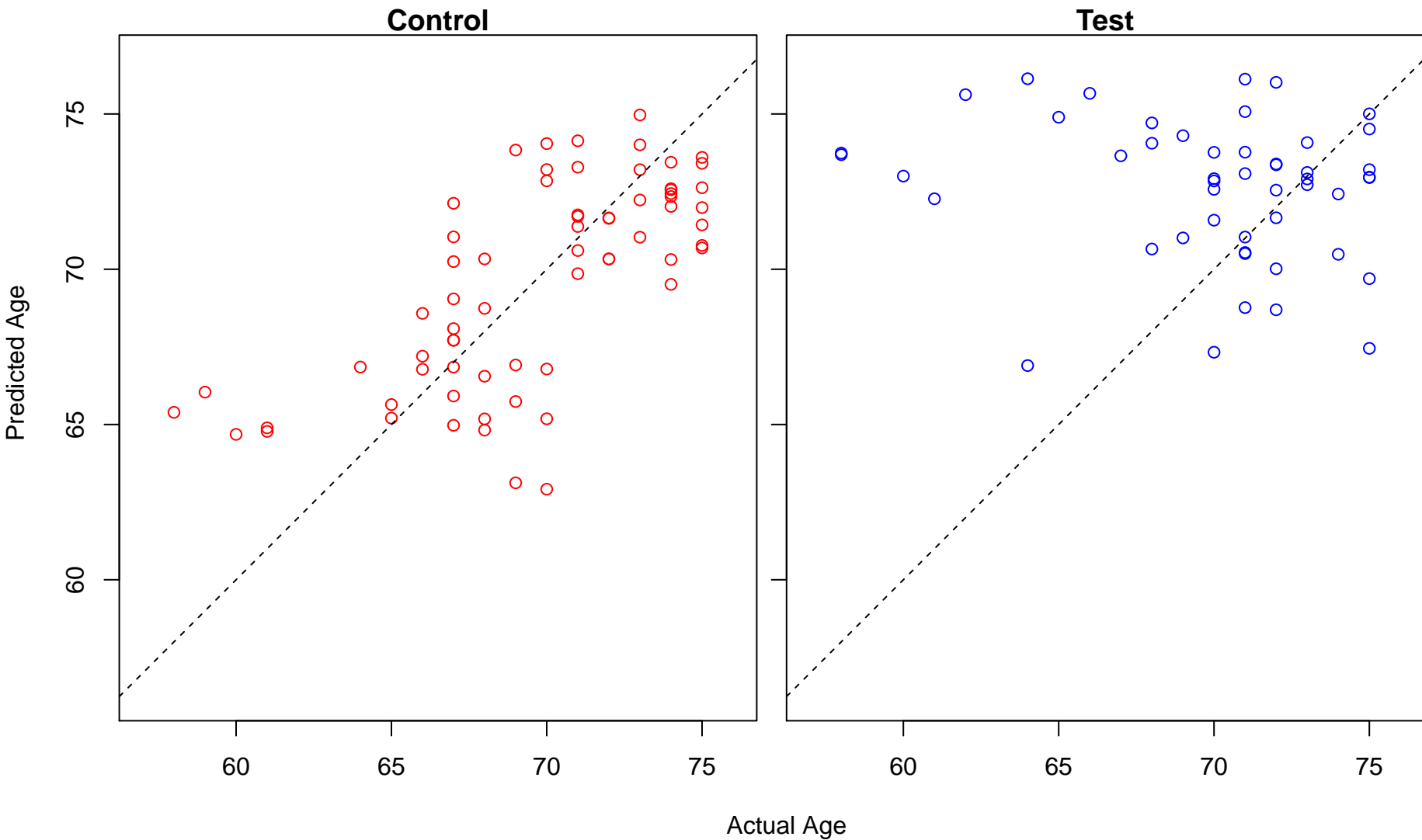


Test



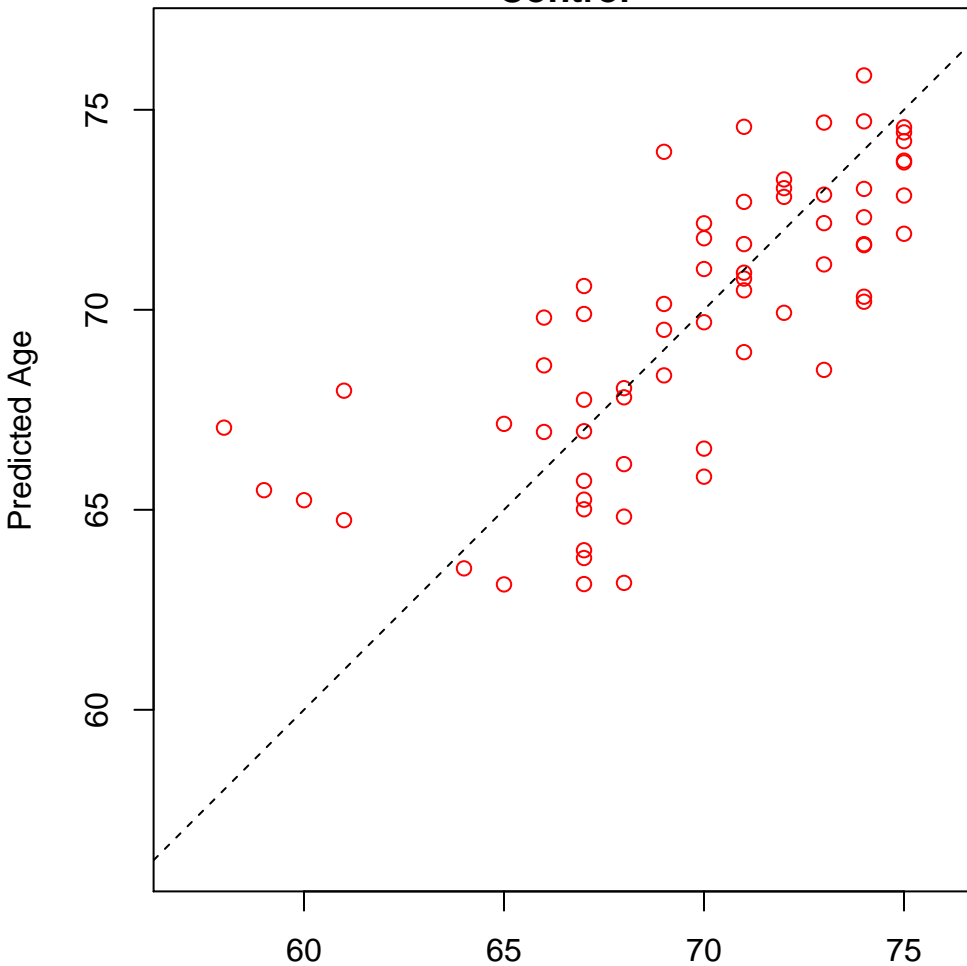
Actual Age

positive regulation of chromatin modification (Score: 1.665537)

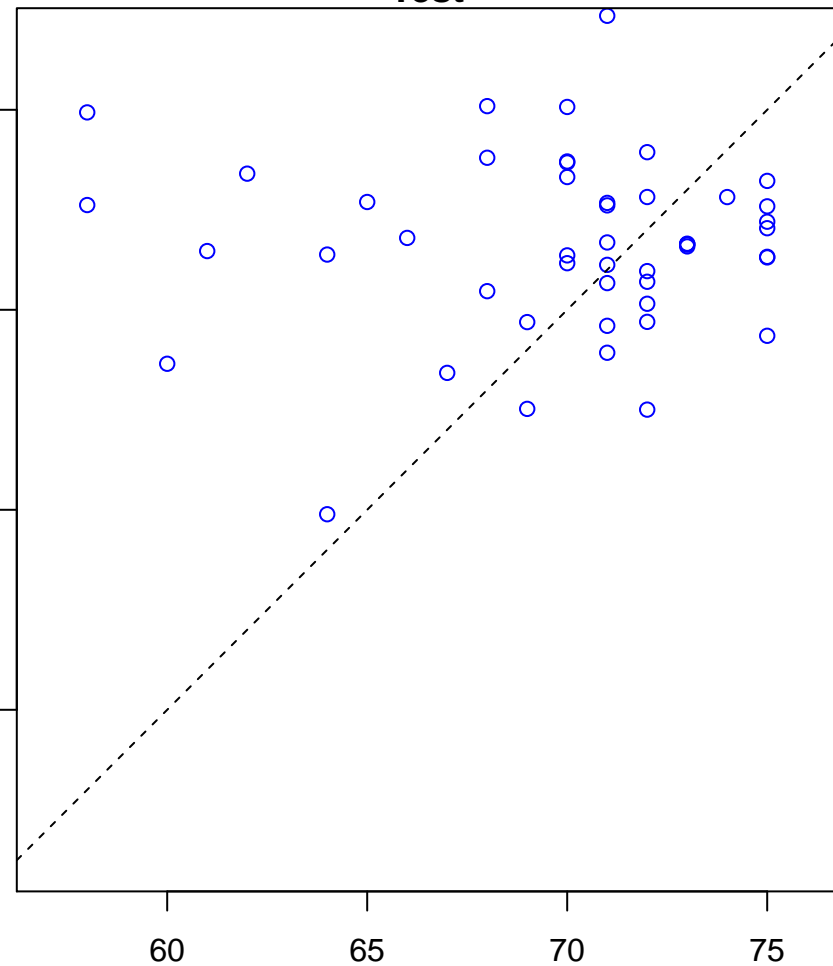


cellular response to mechanical stimulus (Score: 1.664726)

Control

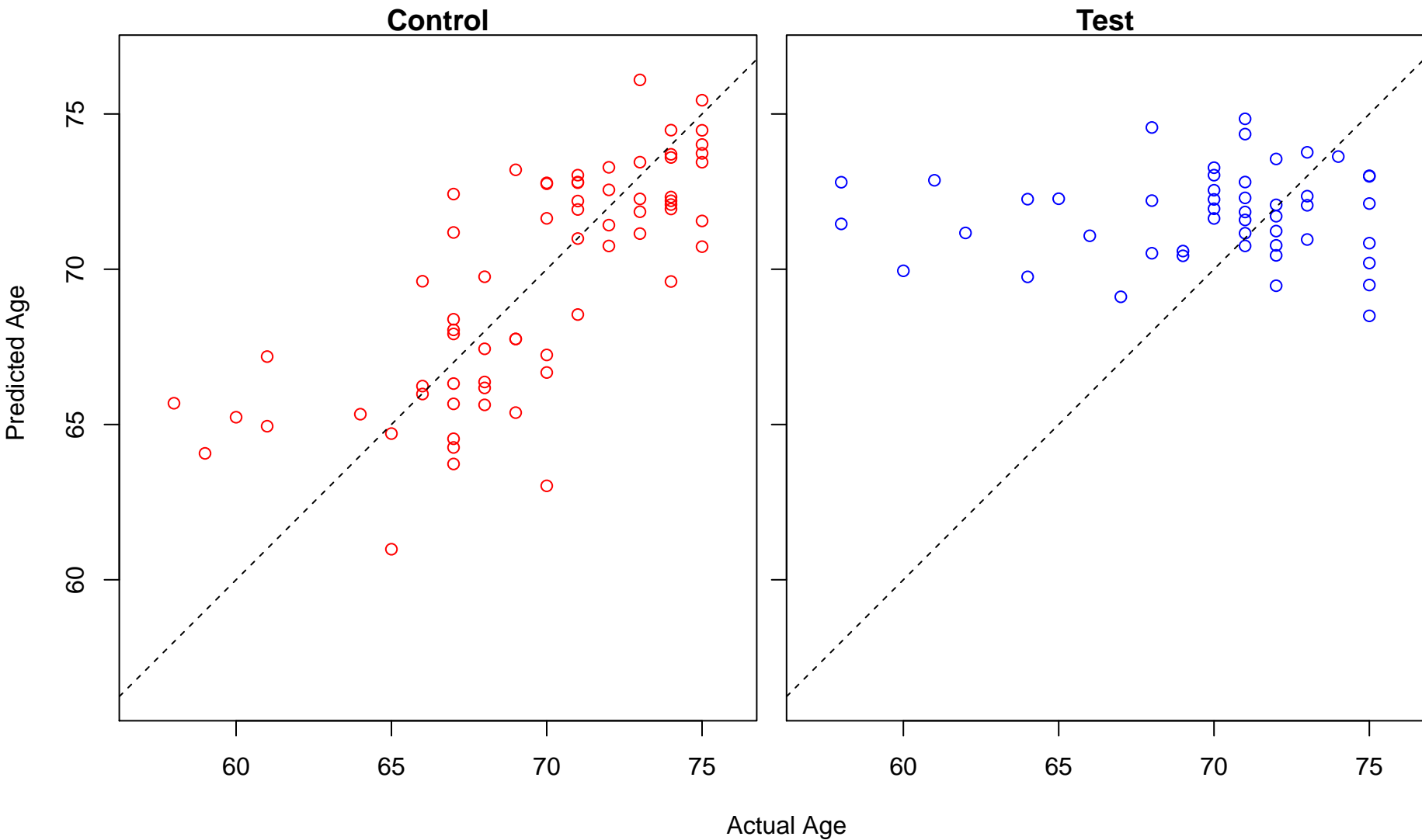


Test

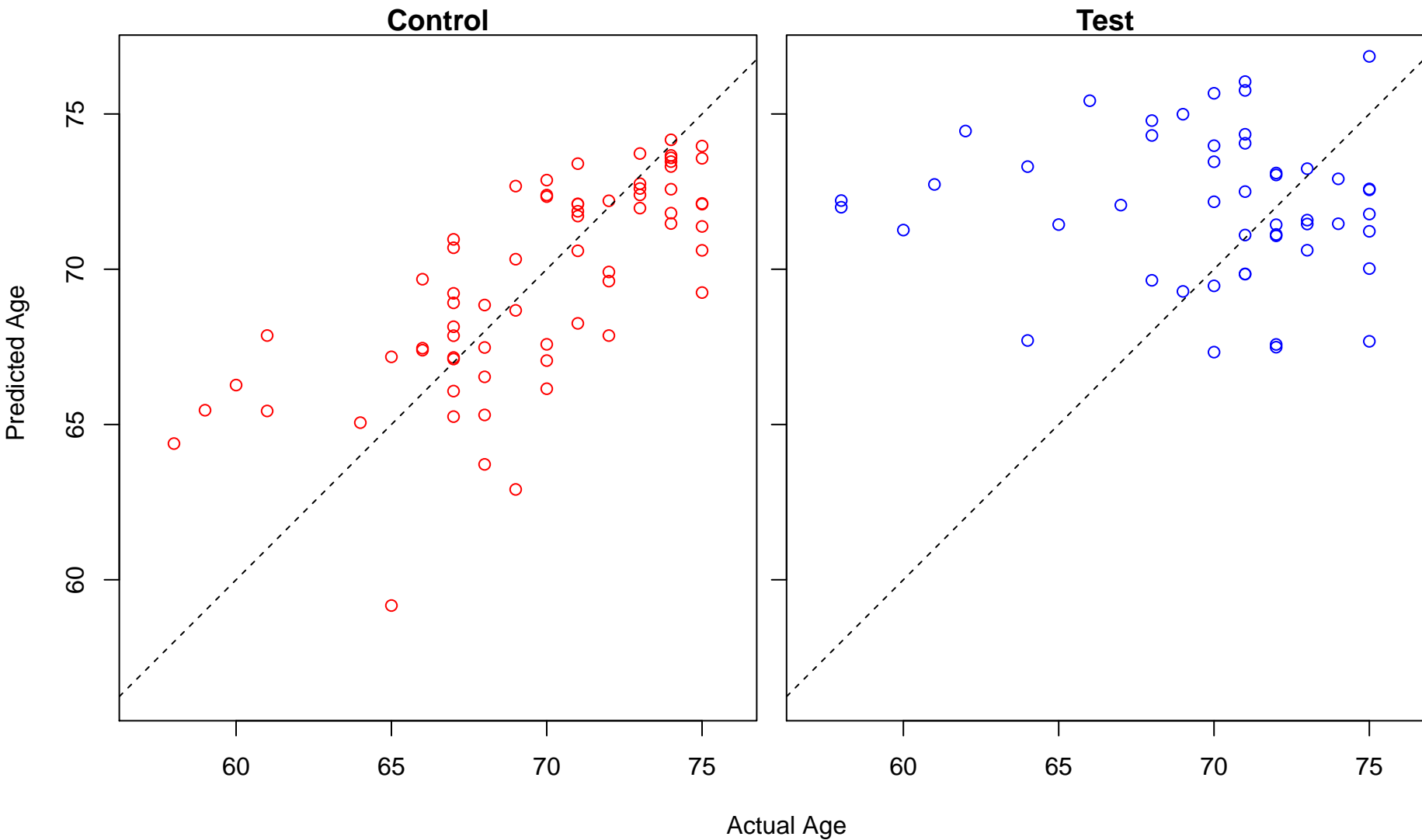


Actual Age

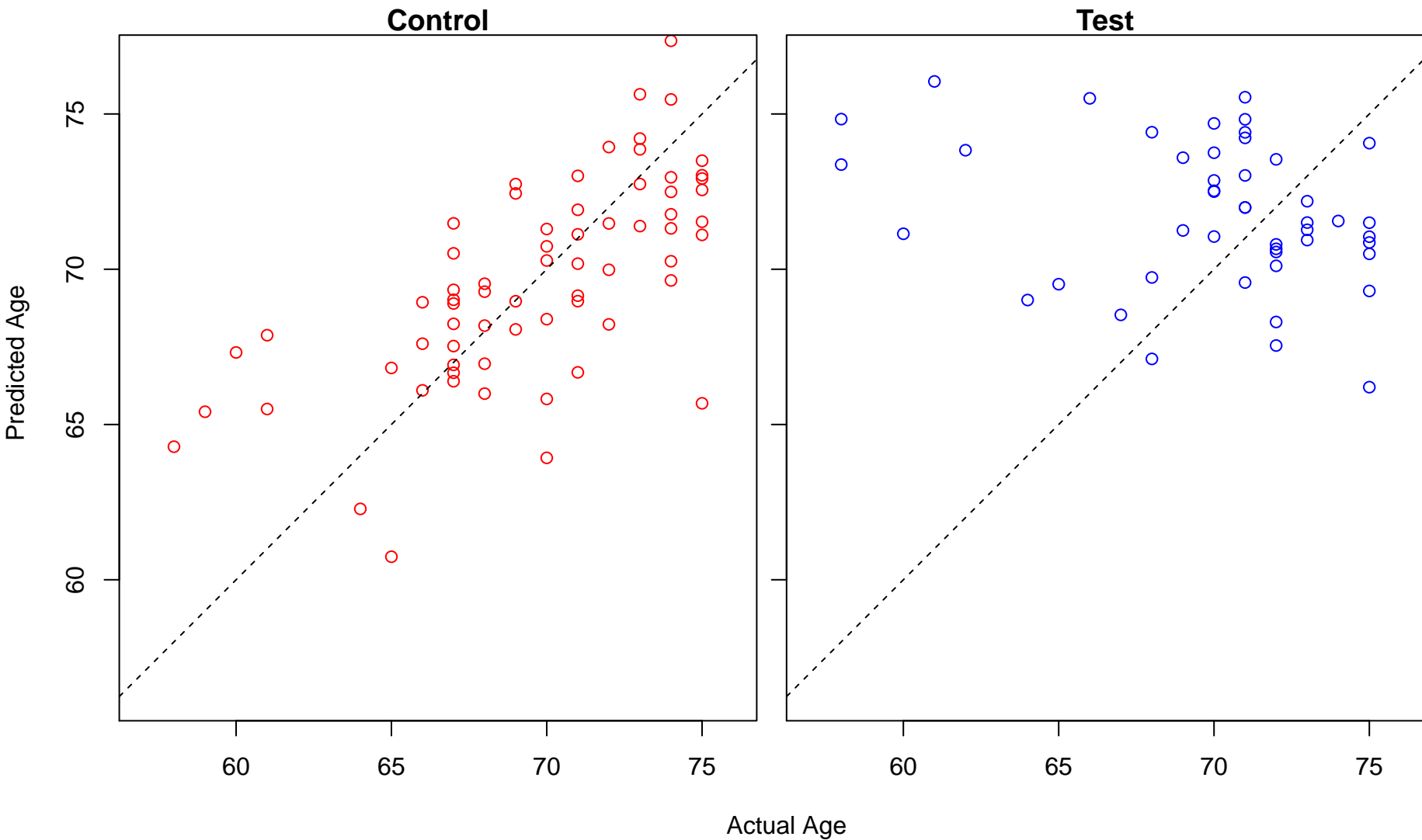
mitotic G1/S transition checkpoint (Score: 1.664469)



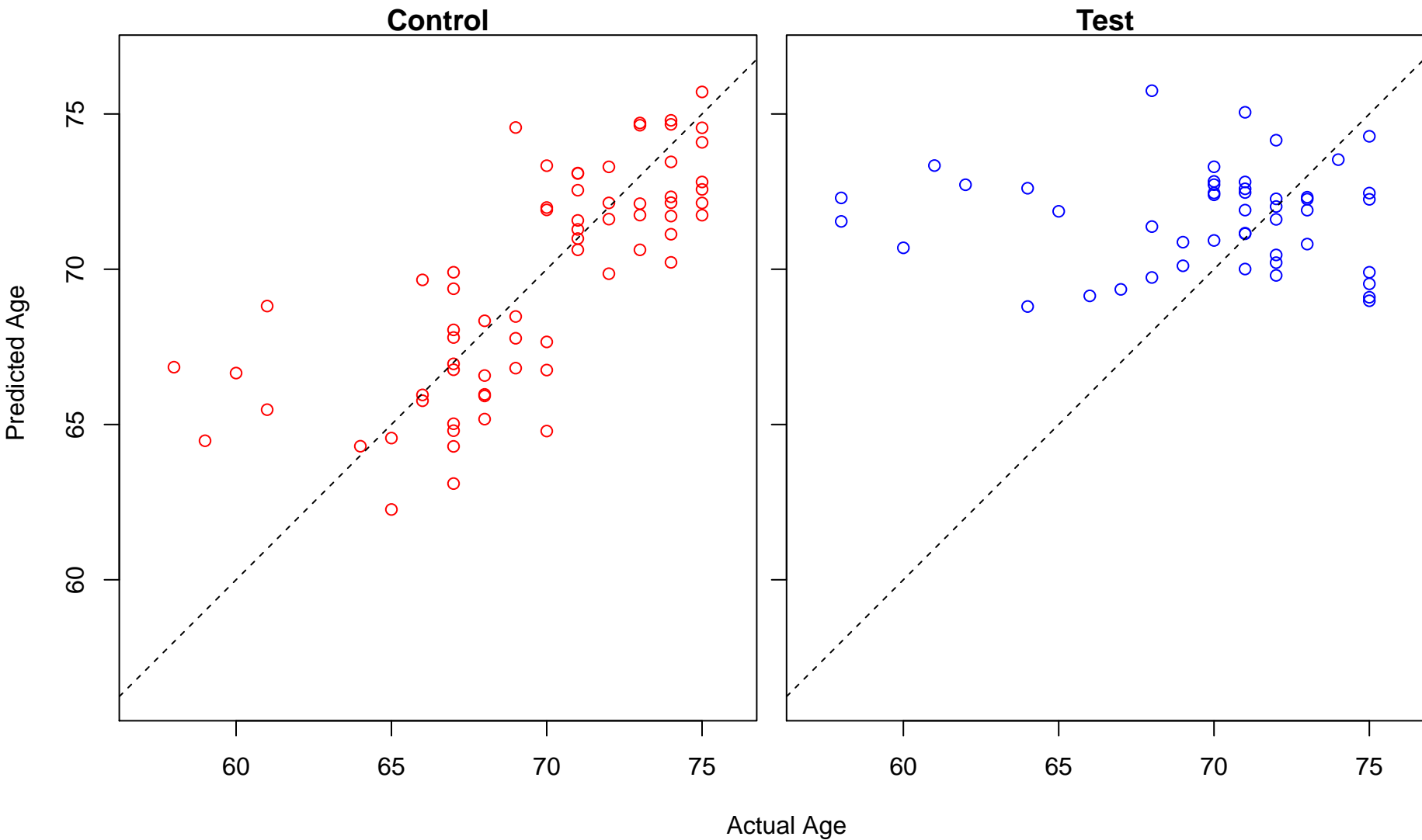
regulation of insulin receptor signaling pathway (Score: 1.664151)



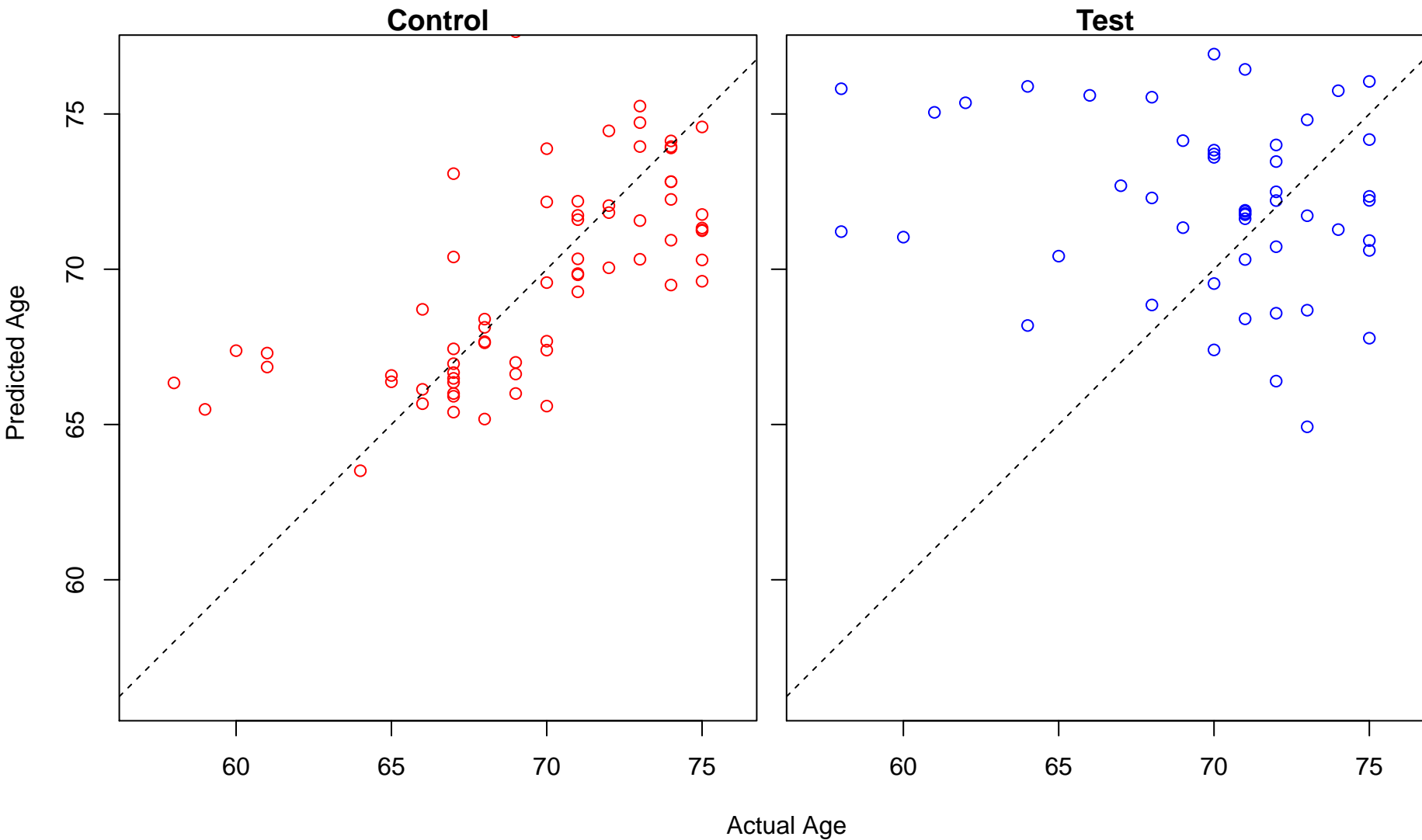
positive regulation of leukocyte apoptotic process (Score: 1.662783)



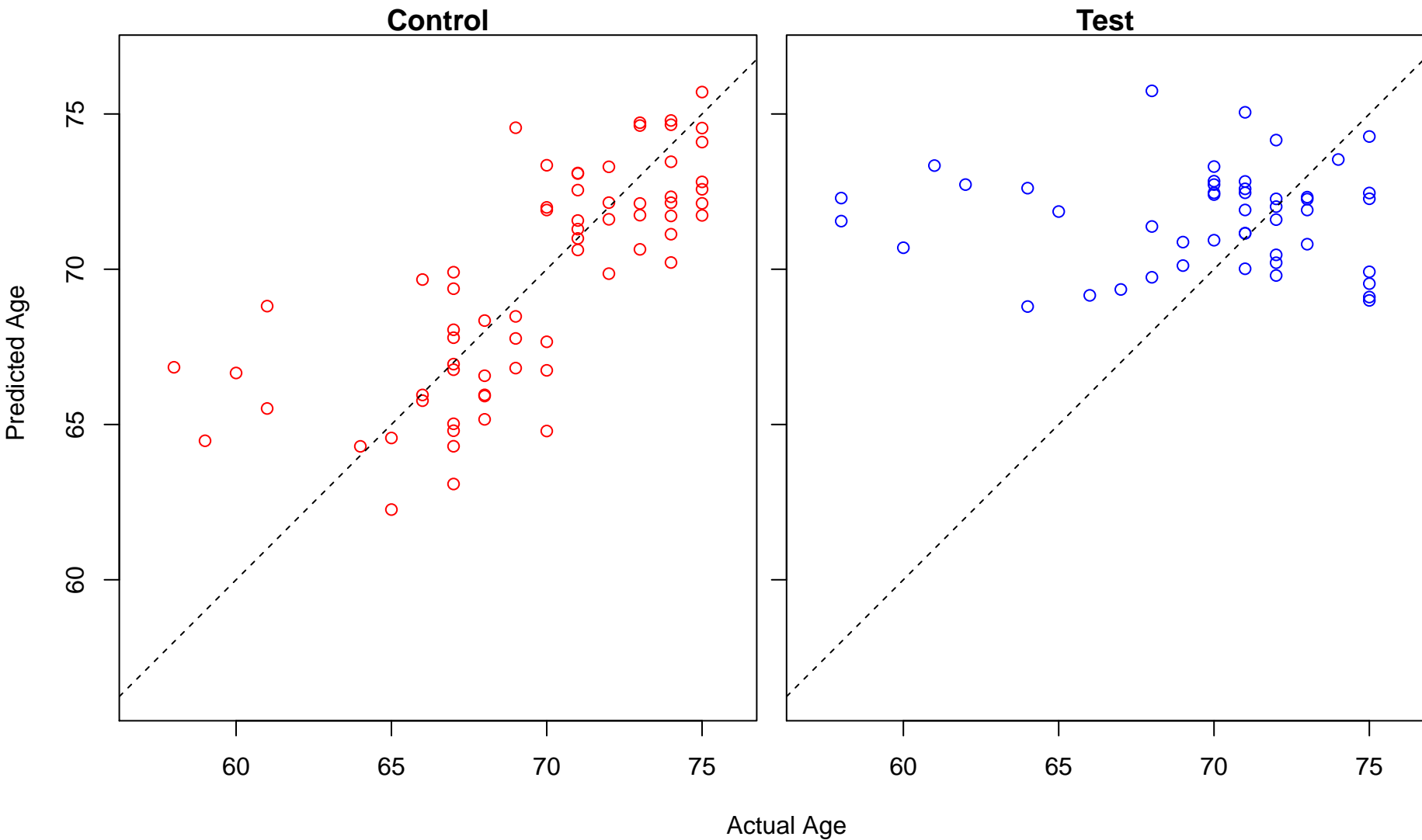
regulation of mRNA stability (Score: 1.662497)



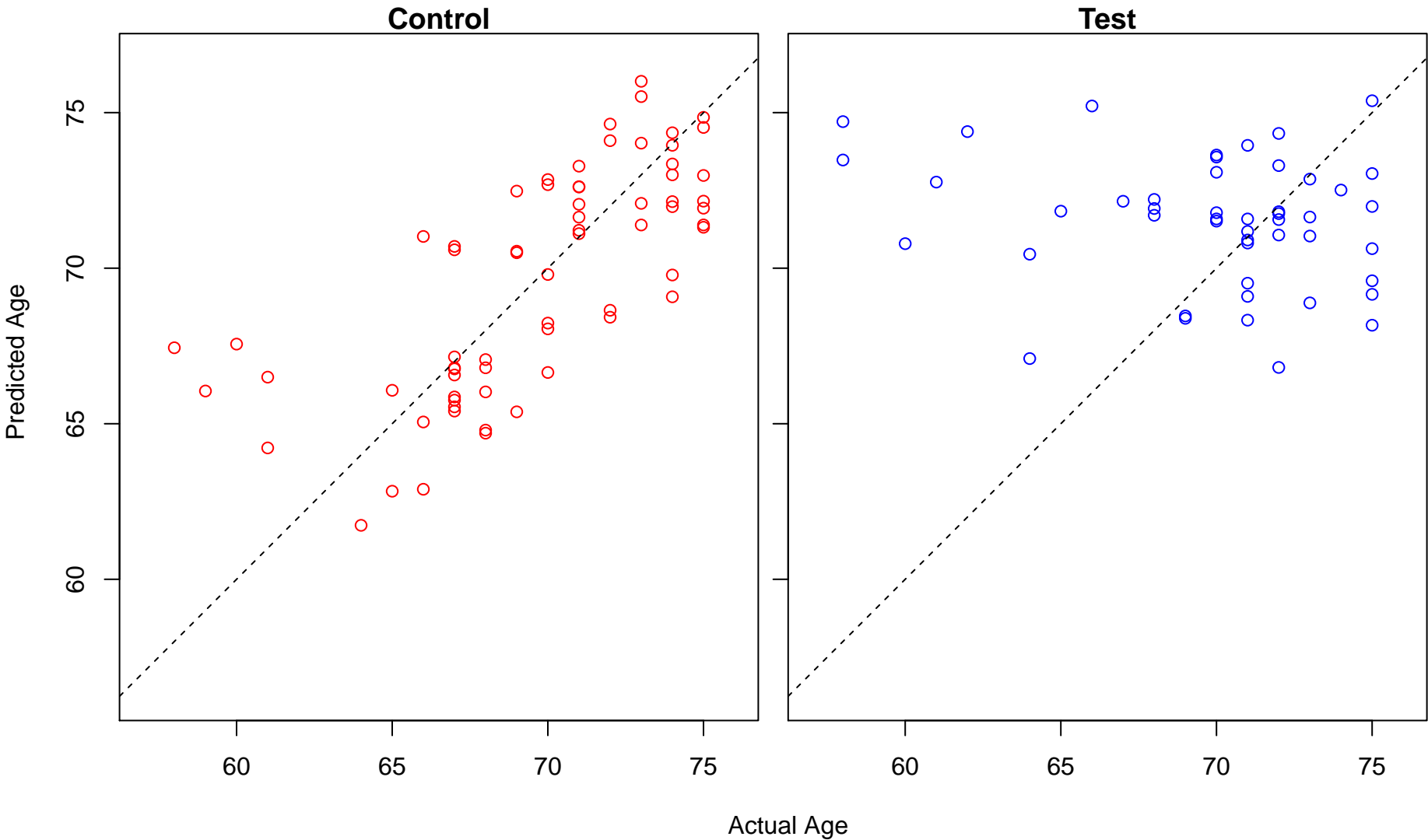
cellular response to organic cyclic compound (Score: 1.661229)



regulation of RNA stability (Score: 1.661041)

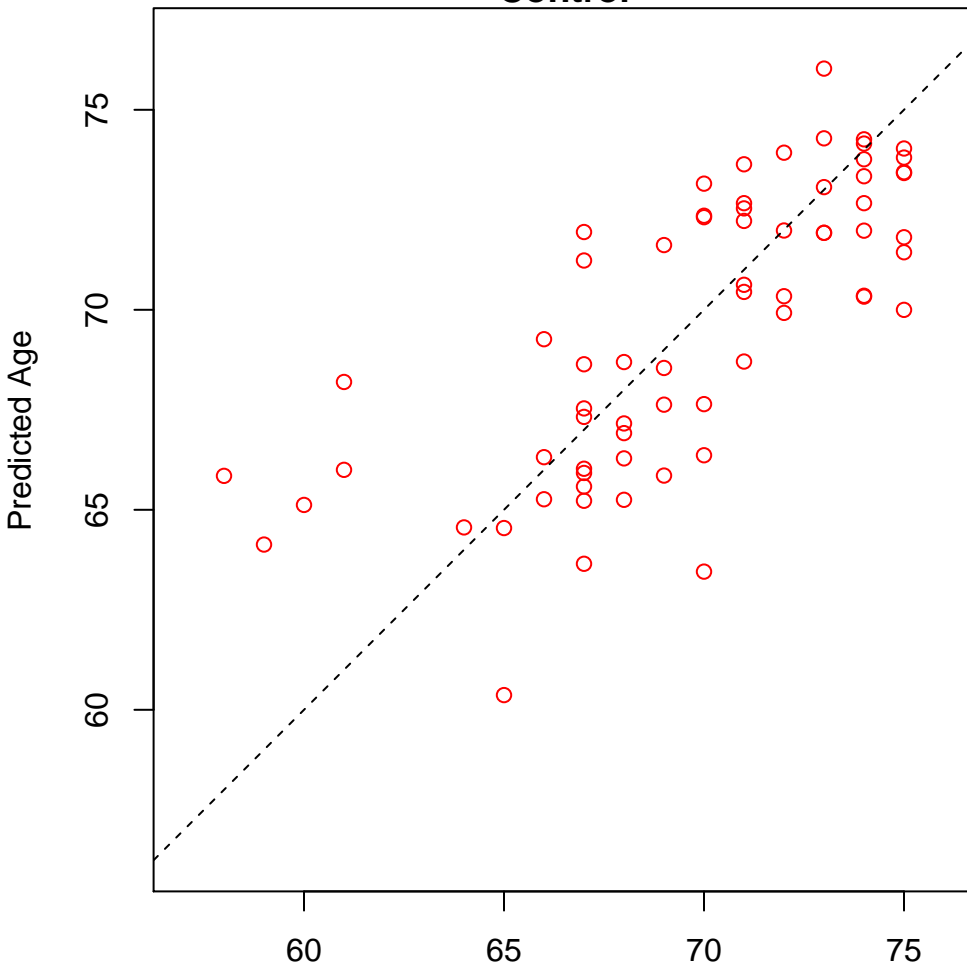


activation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 1.65)

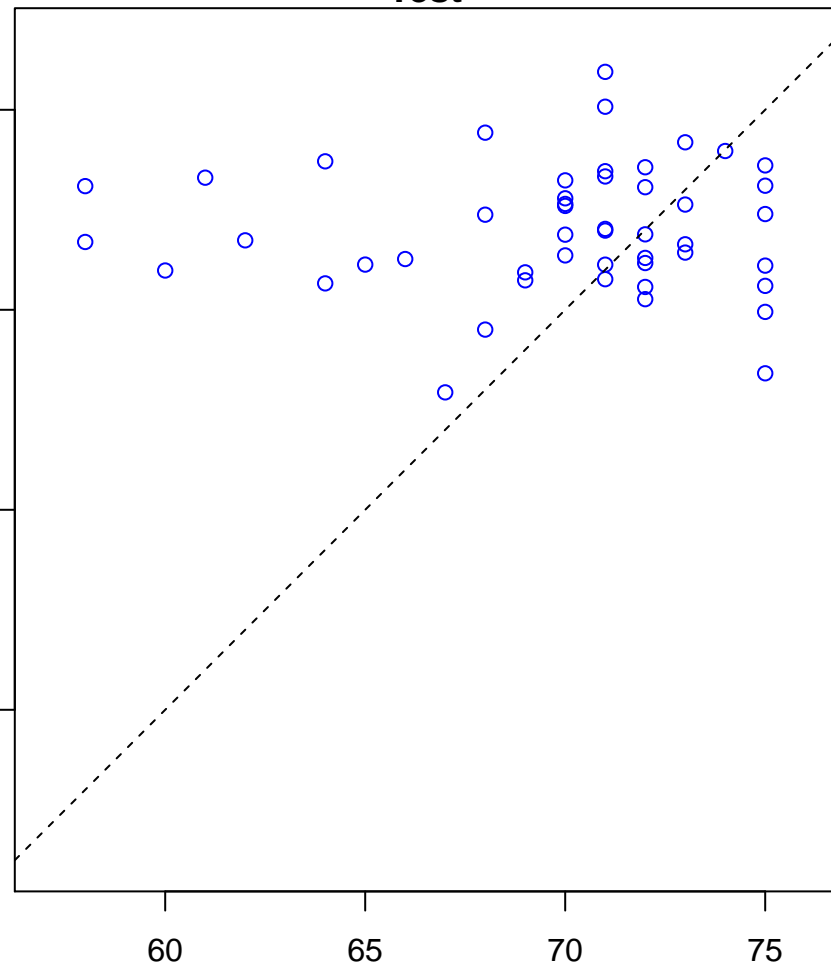


negative regulation of mitotic cell cycle (Score: 1.659489)

Control

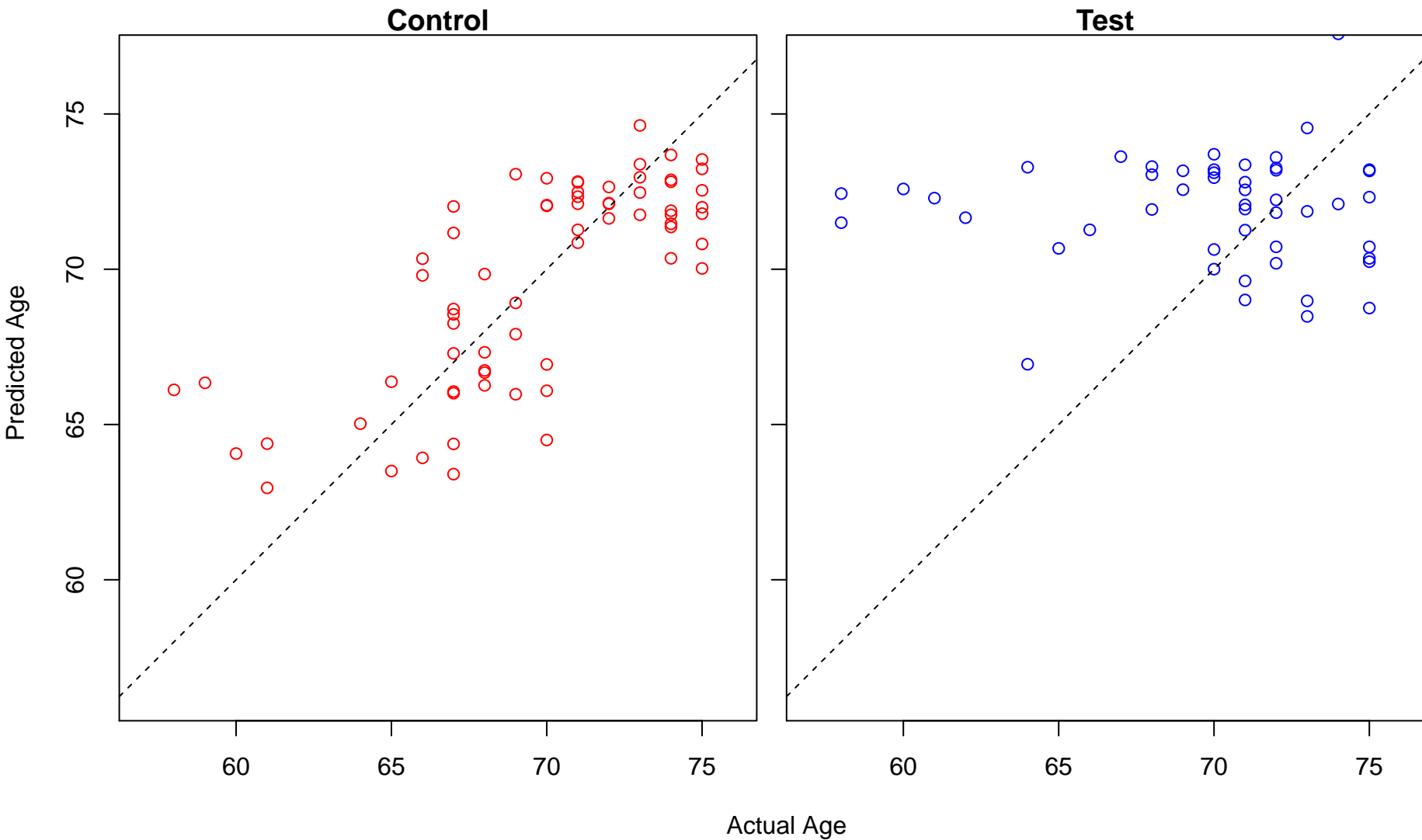


Test

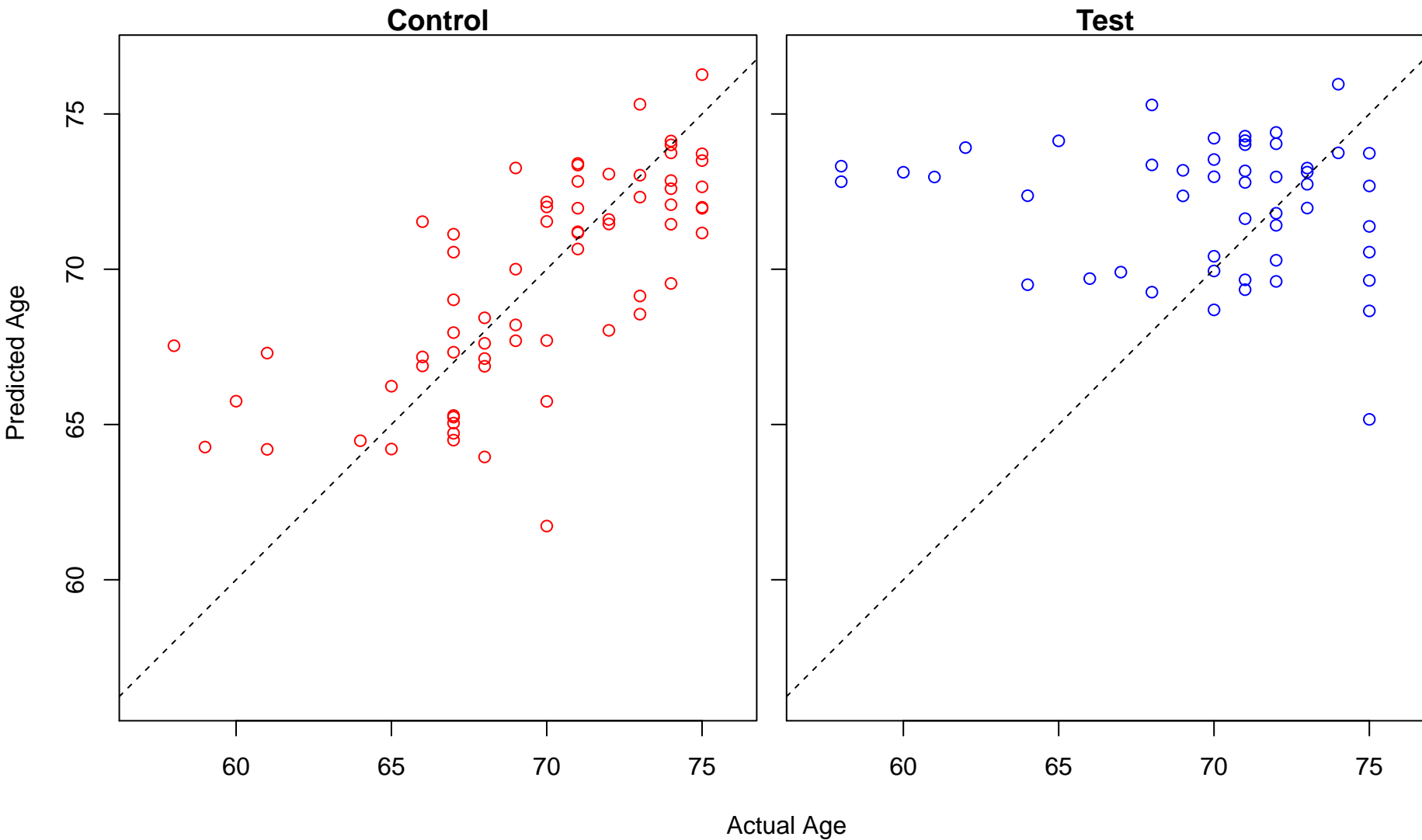


Actual Age

regulation of spindle assembly (Score: 1.658610)

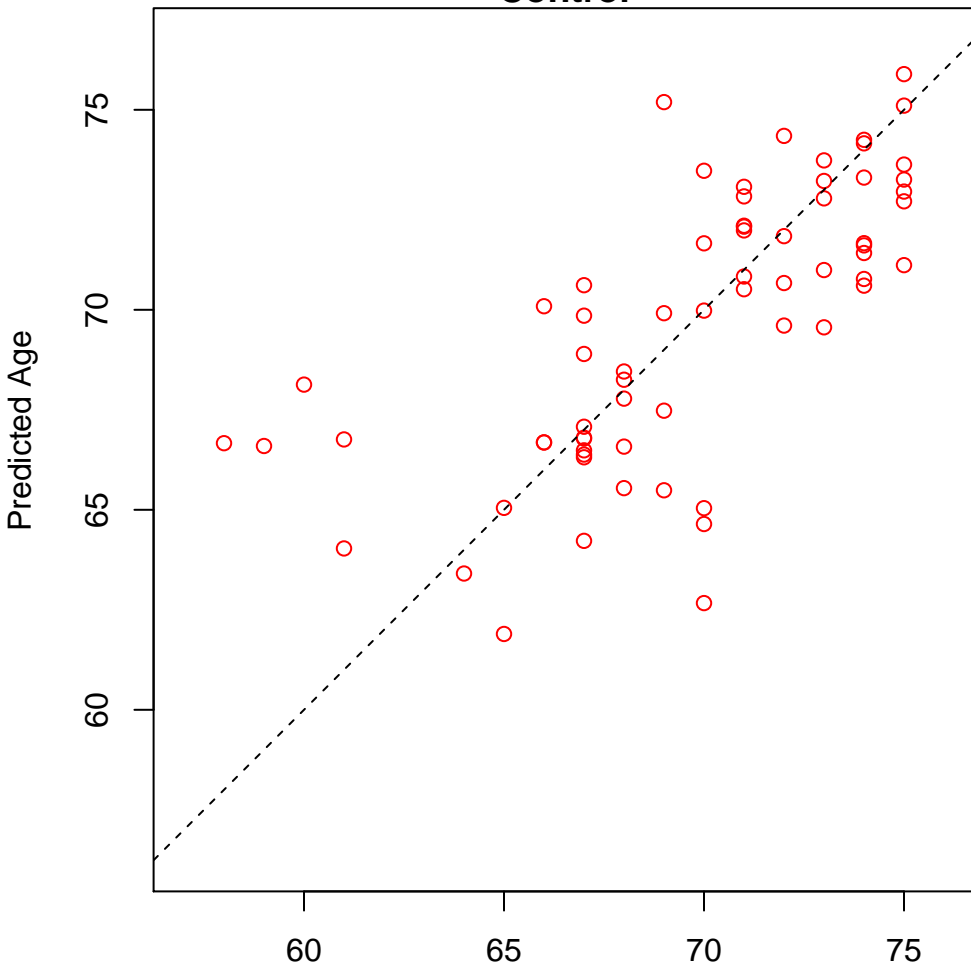


protein stabilization (Score: 1.658538)

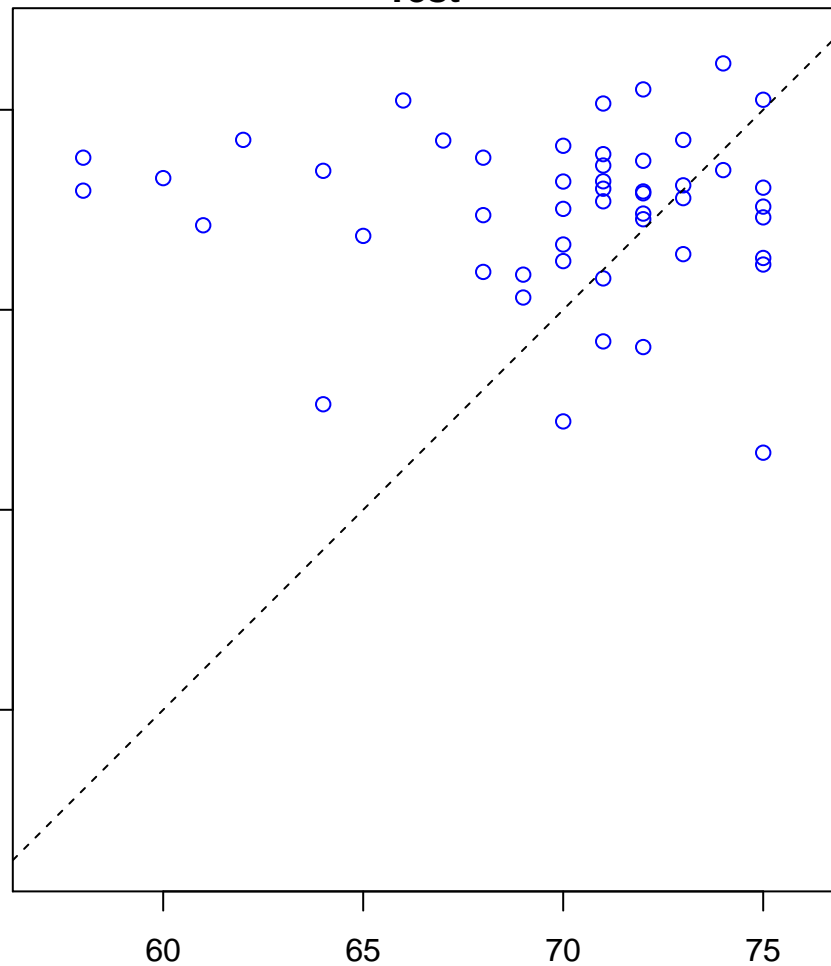


I-kappaB kinase/NF-kappaB signaling (Score: 1.657948)

Control

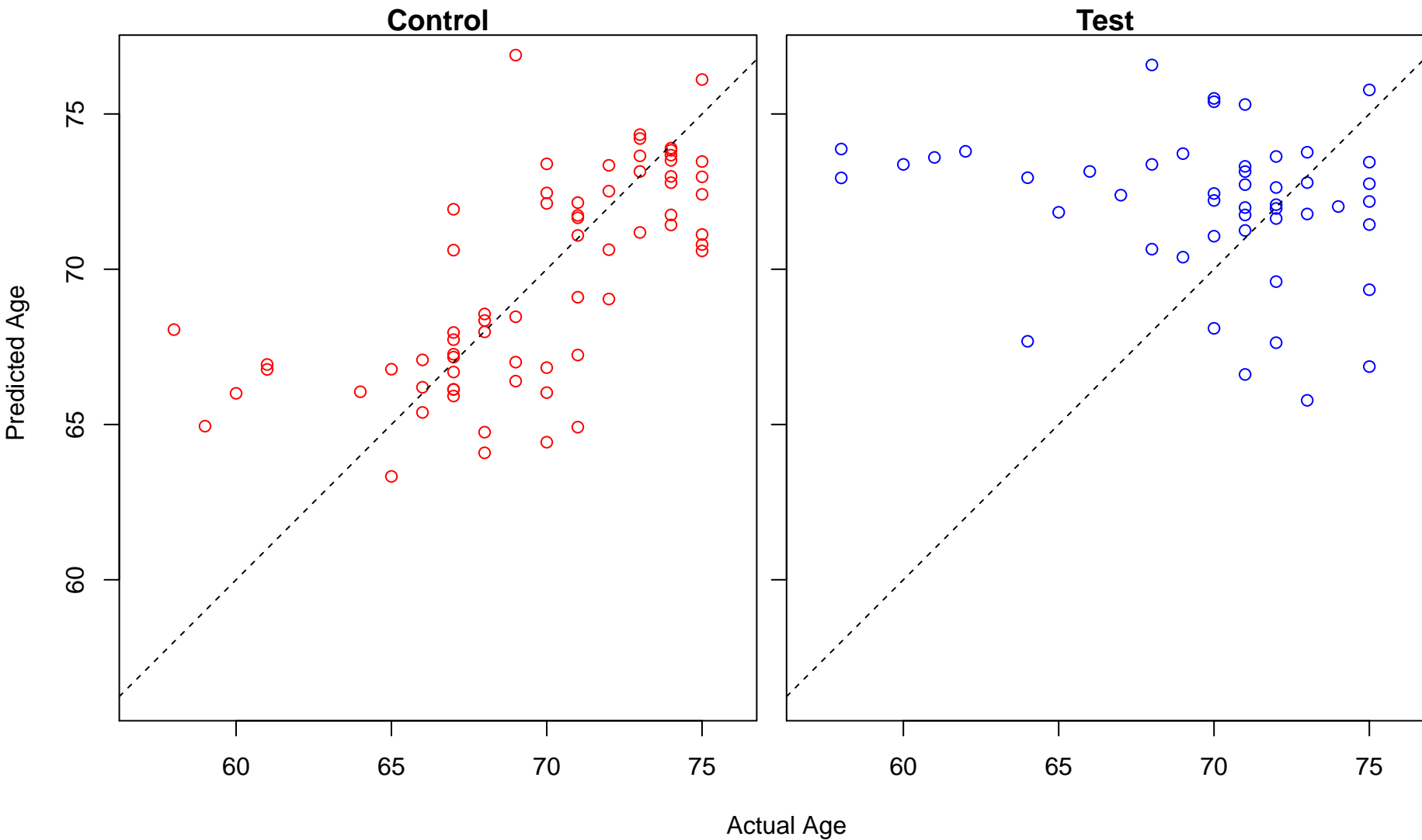


Test

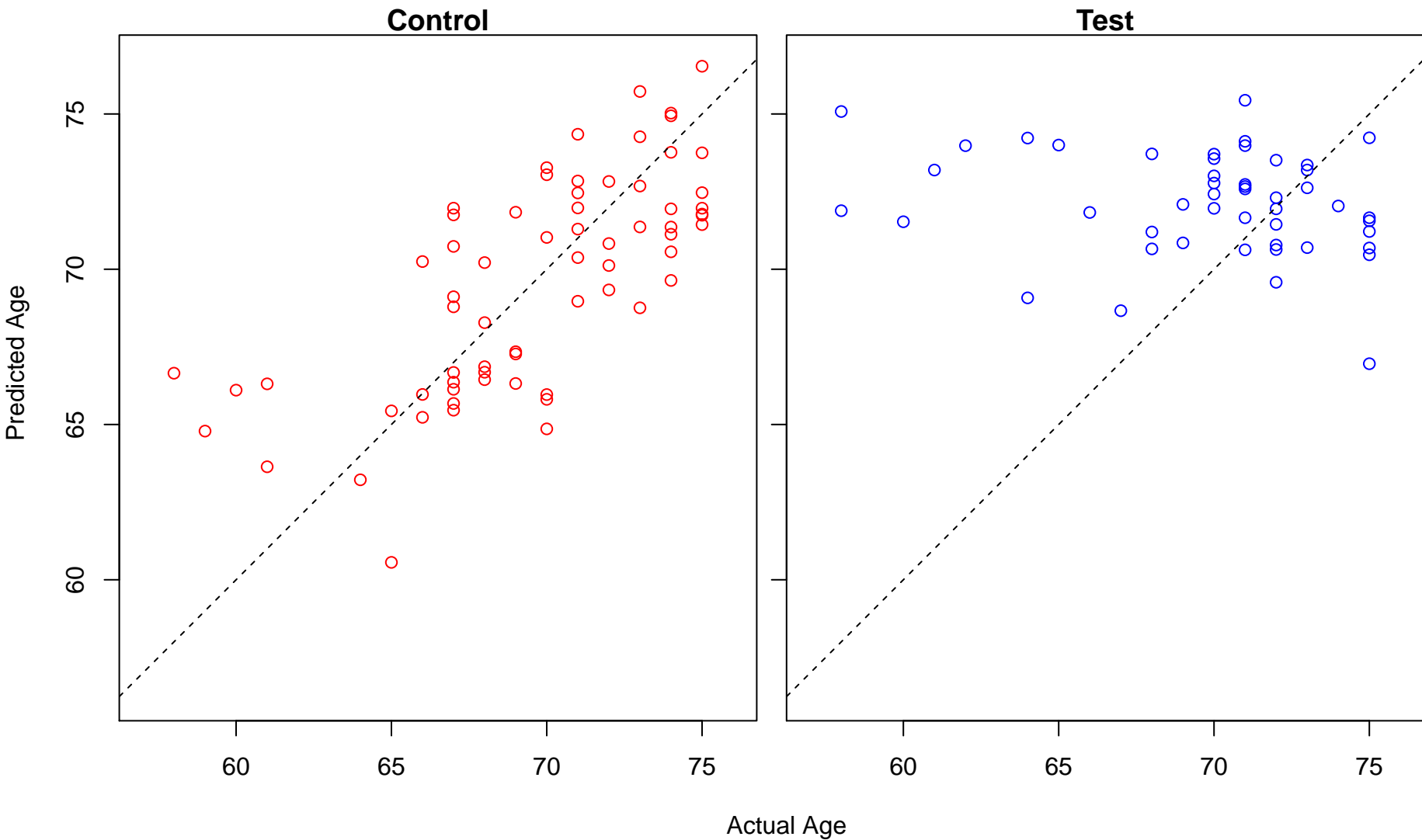


Actual Age

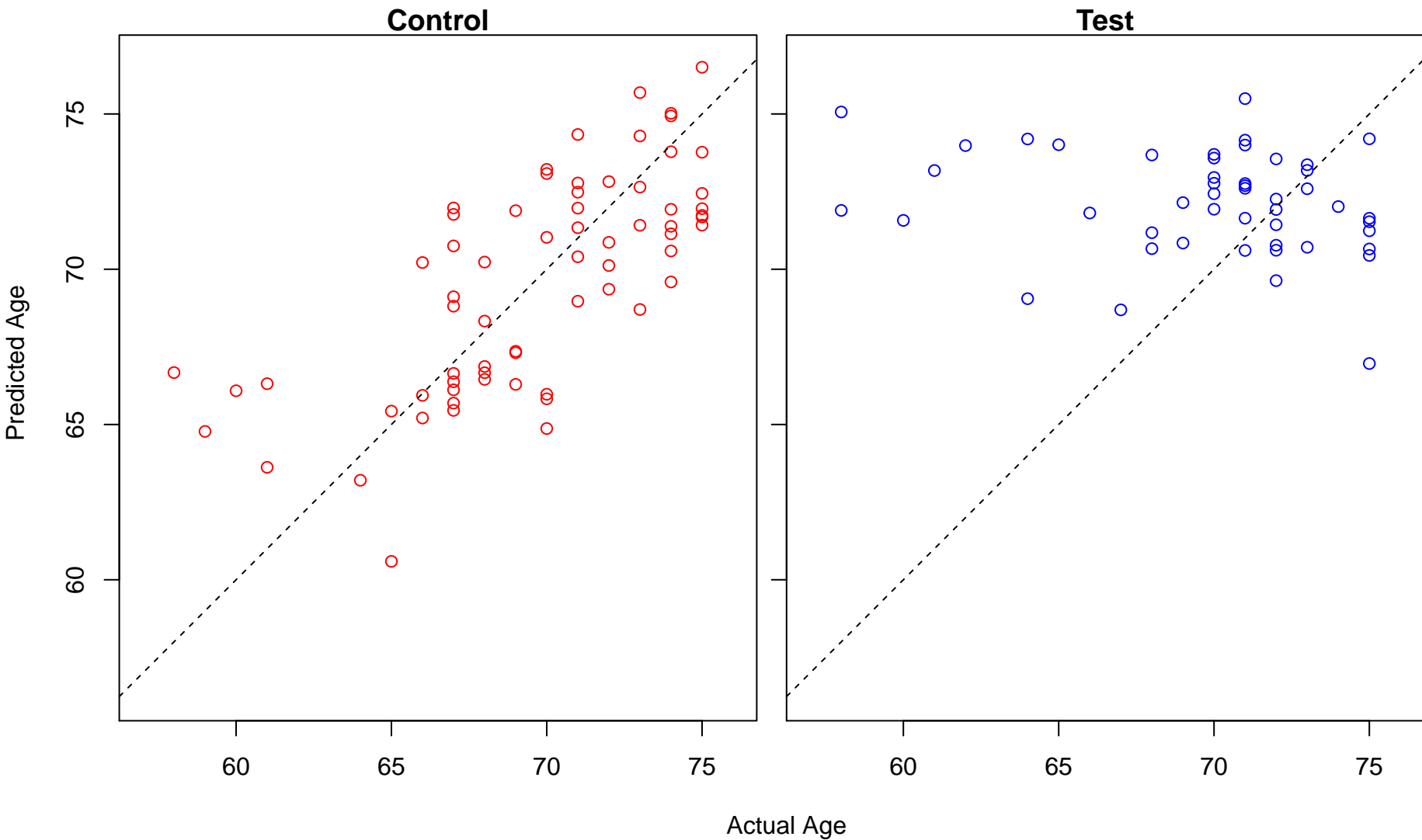
leukocyte differentiation (Score: 1.657910)



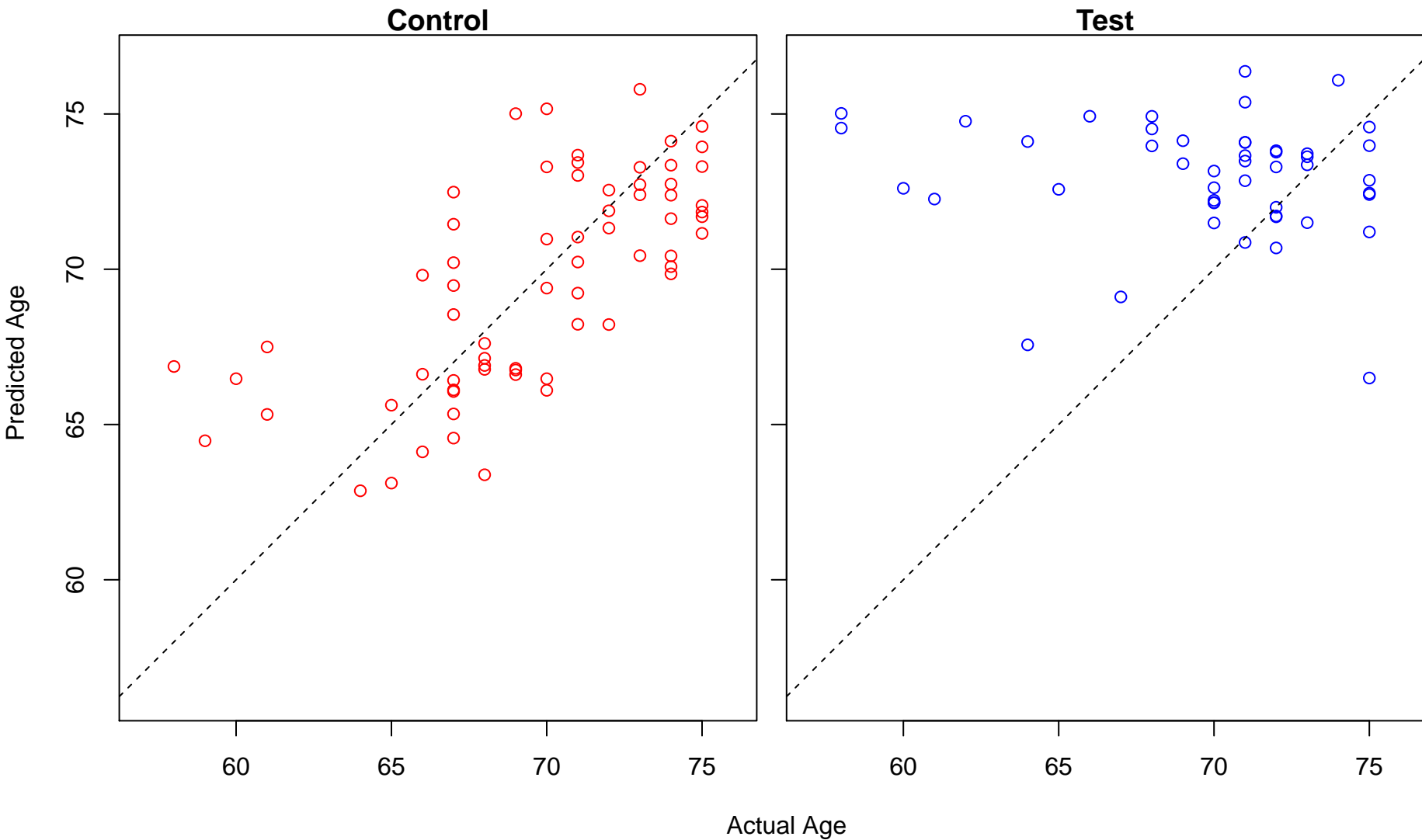
blood coagulation (Score: 1.657007)



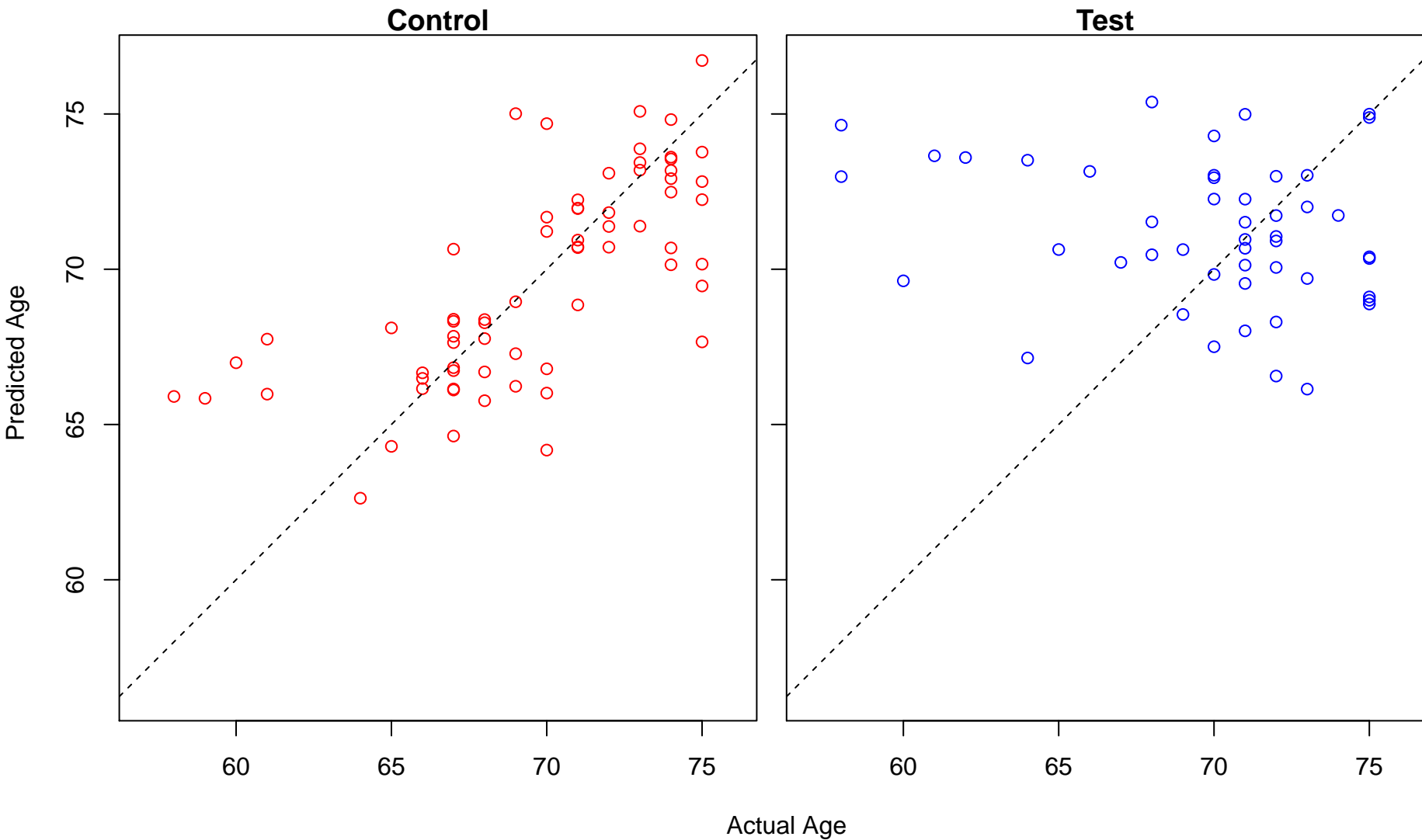
hemostasis (Score: 1.656973)



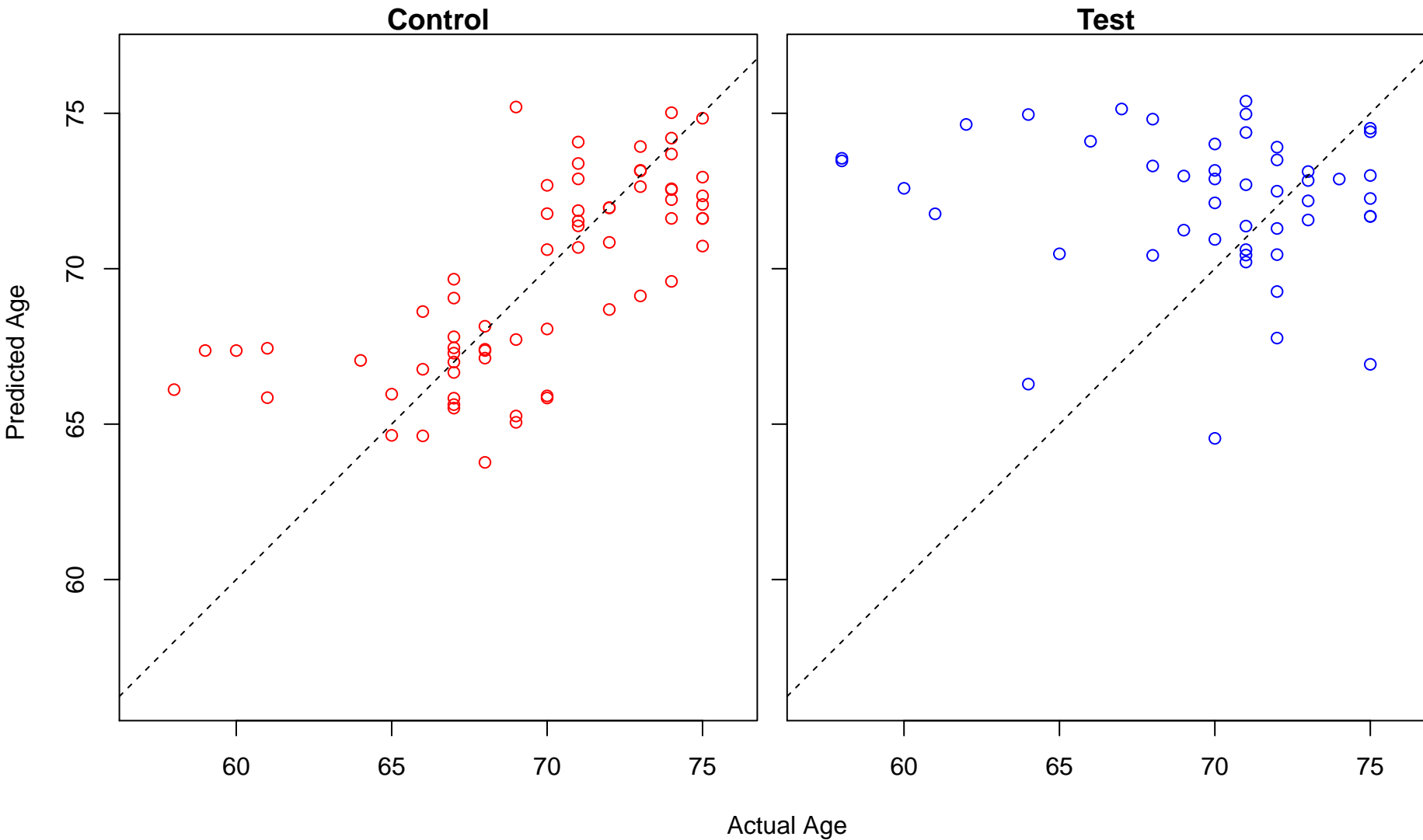
negative regulation of kinase activity (Score: 1.656926)



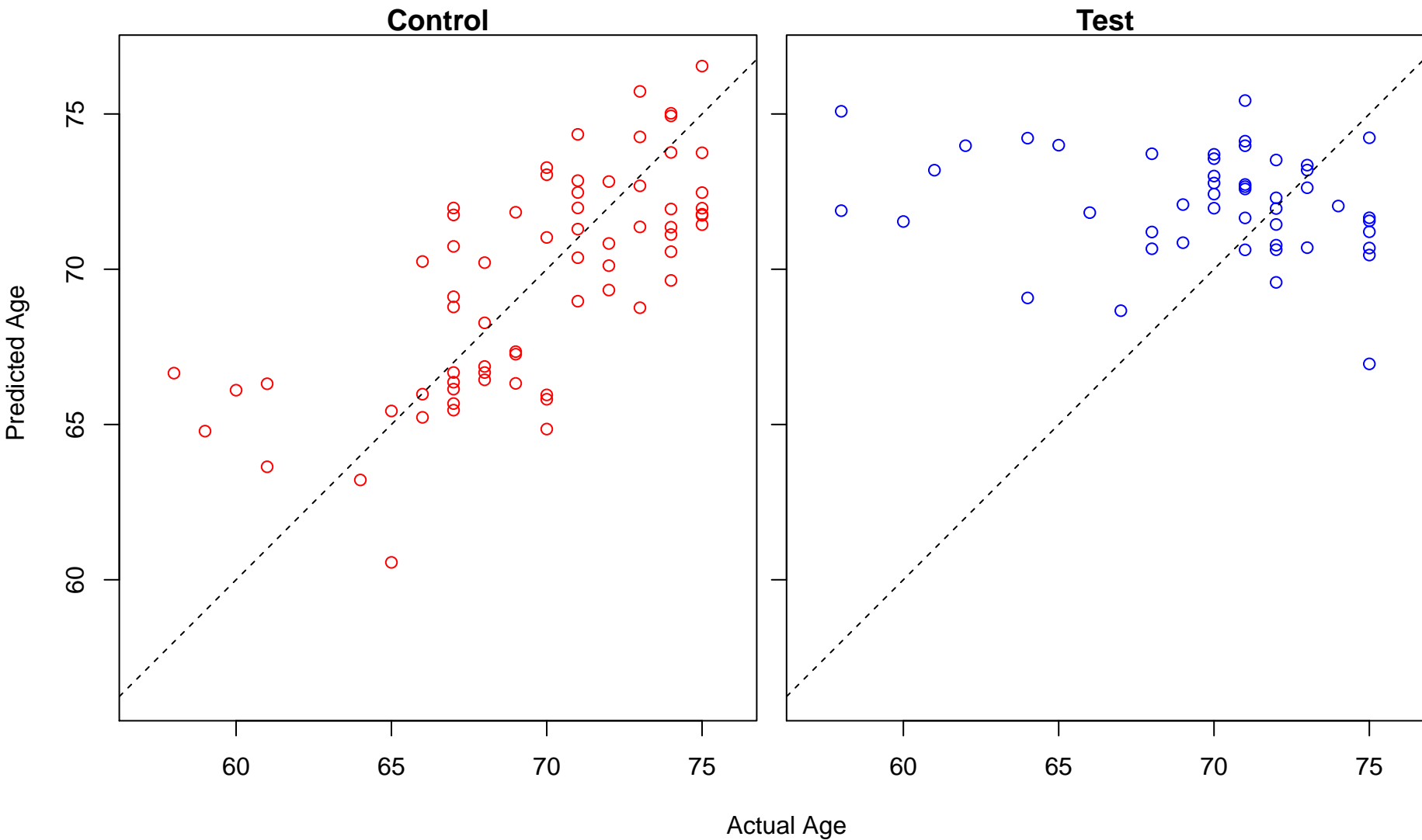
negative regulation of endopeptidase activity (Score: 1.656330)



positive regulation of monocyte chemotaxis (Score: 1.656322)

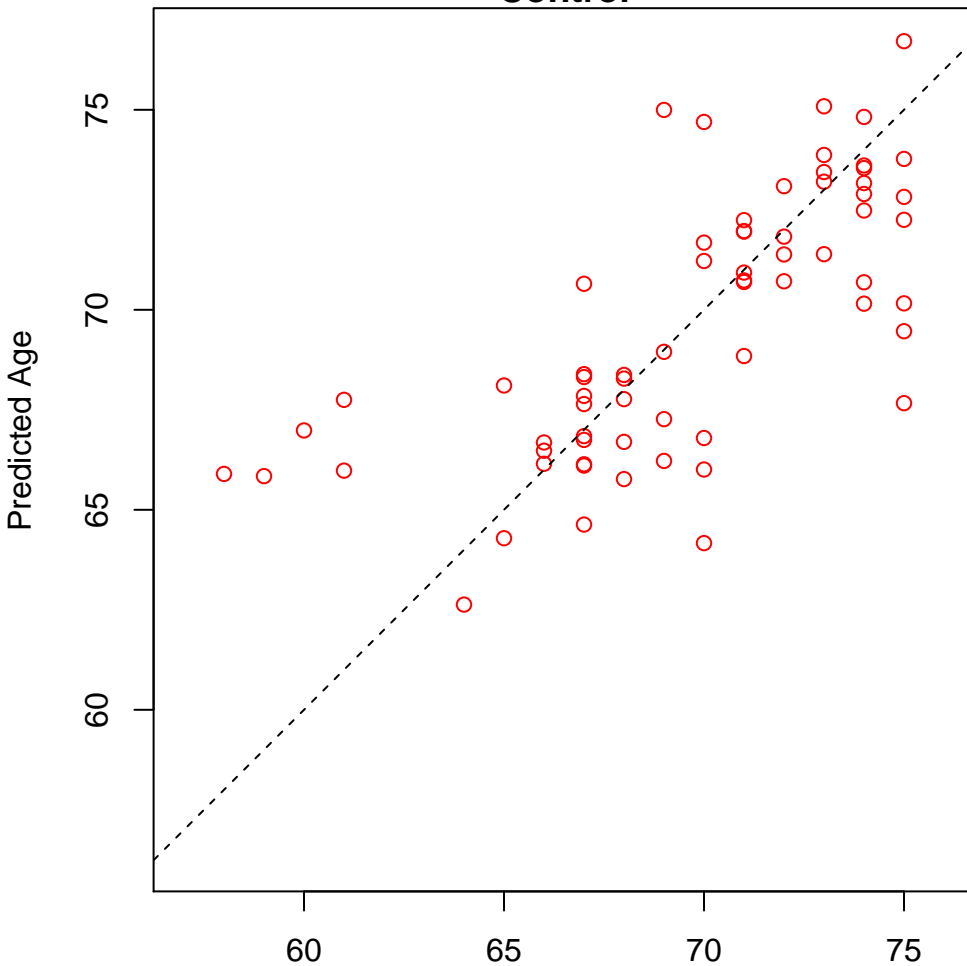


coagulation (Score: 1.656244)

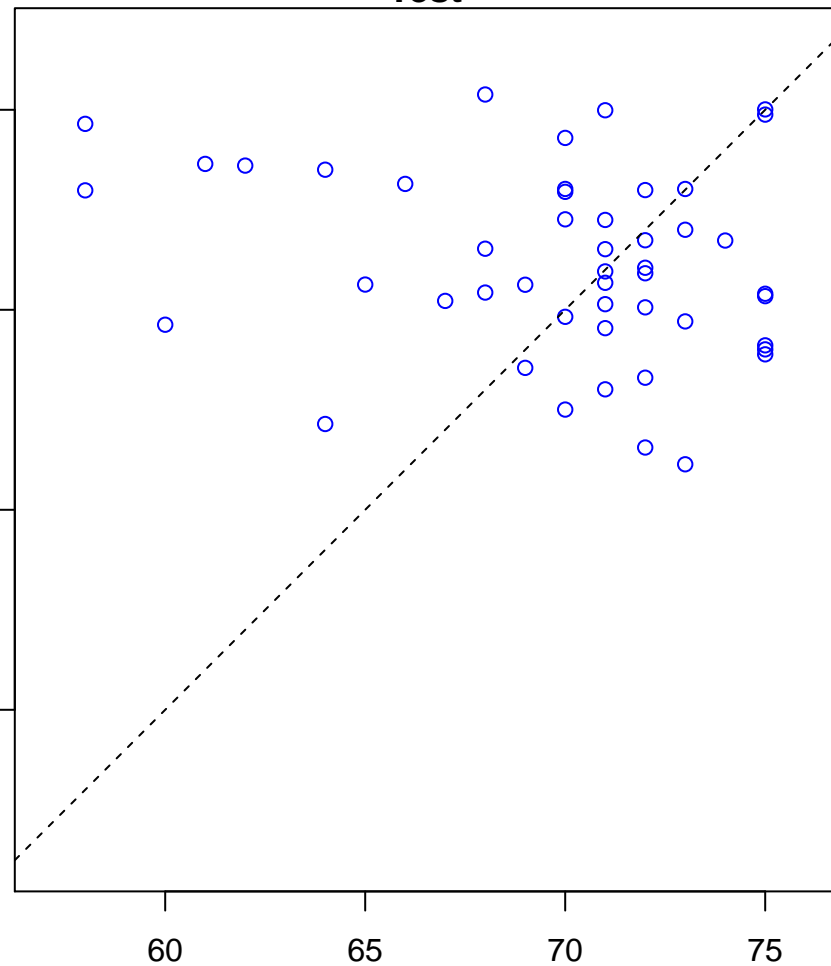


negative regulation of peptidase activity (Score: 1.656228)

Control

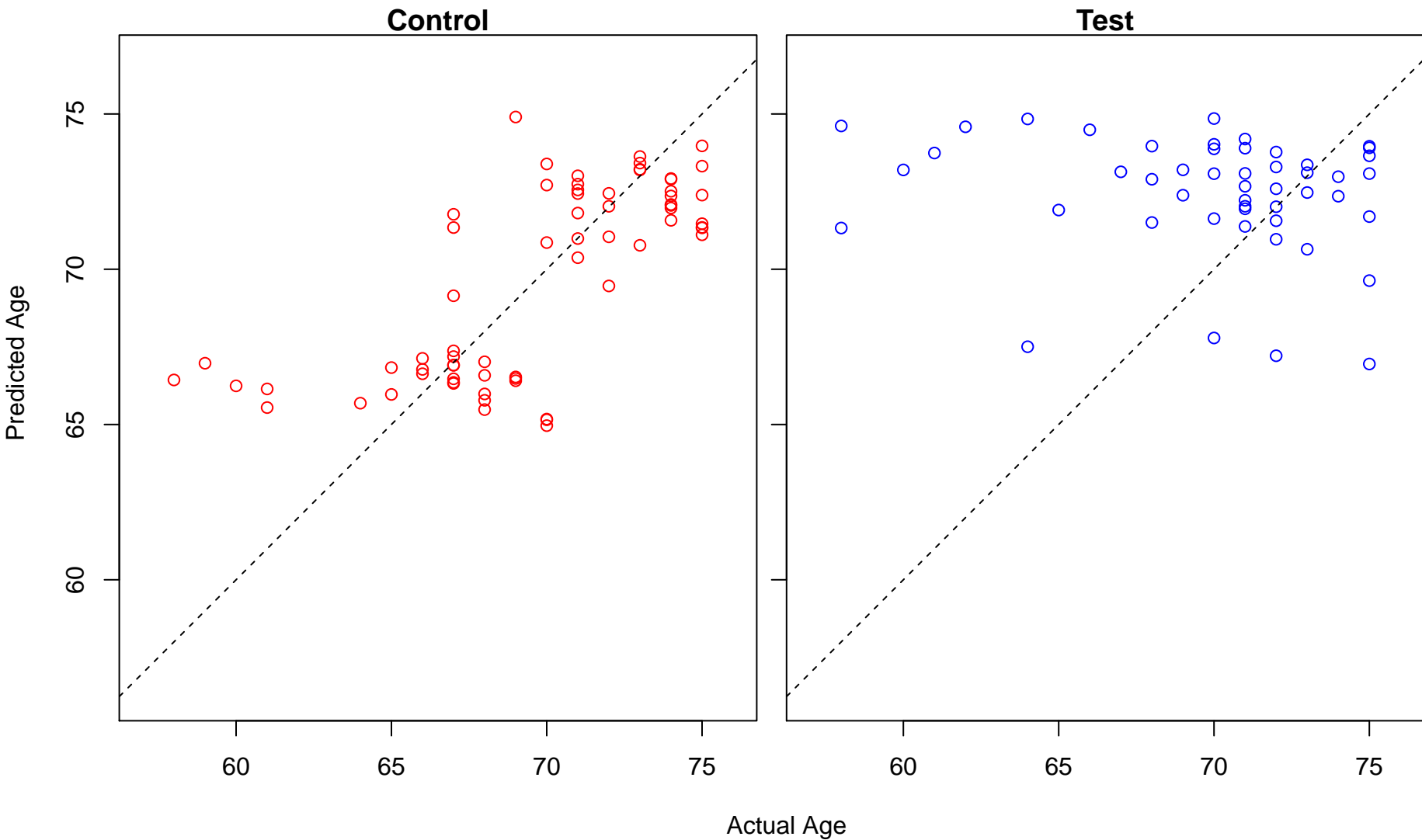


Test

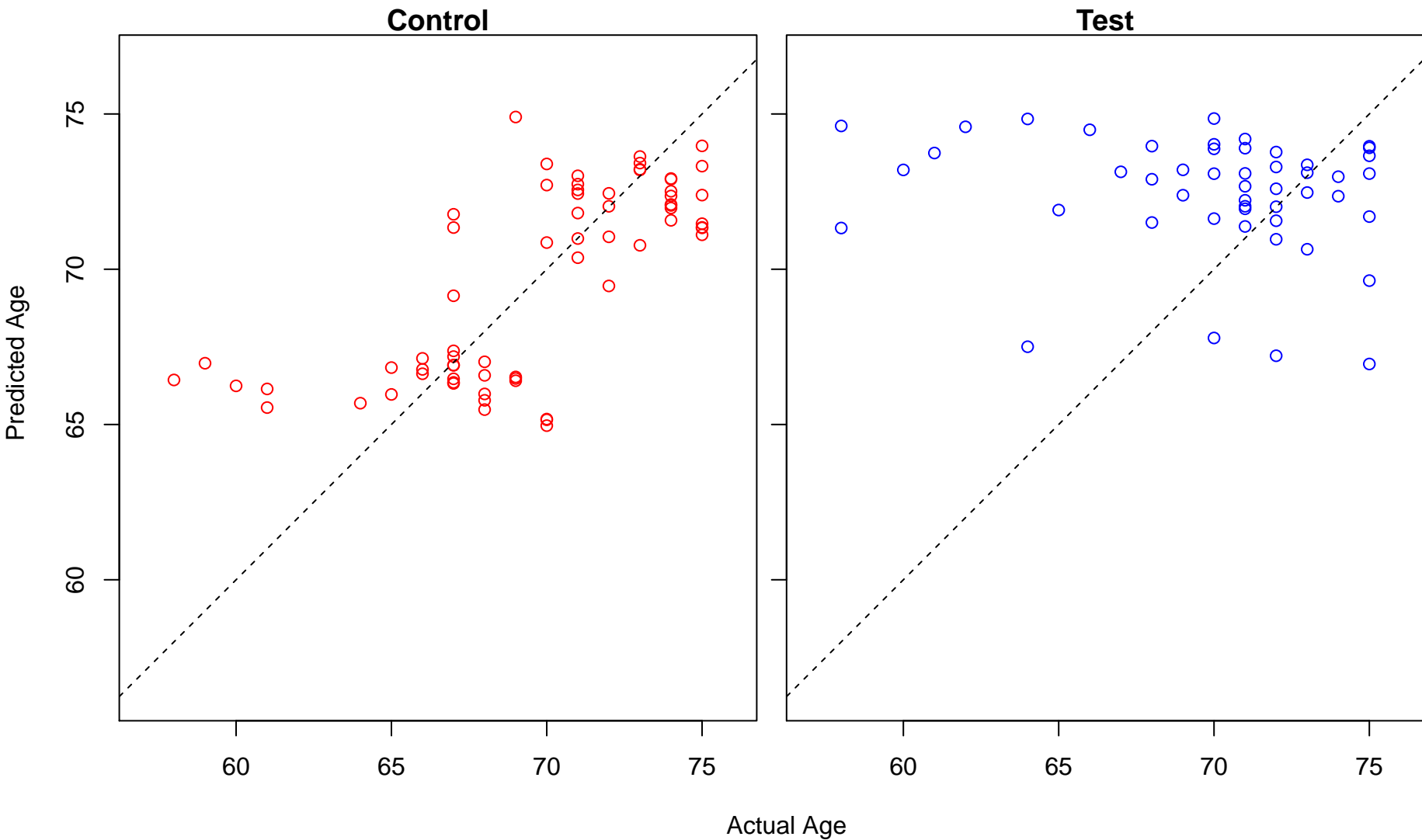


Actual Age

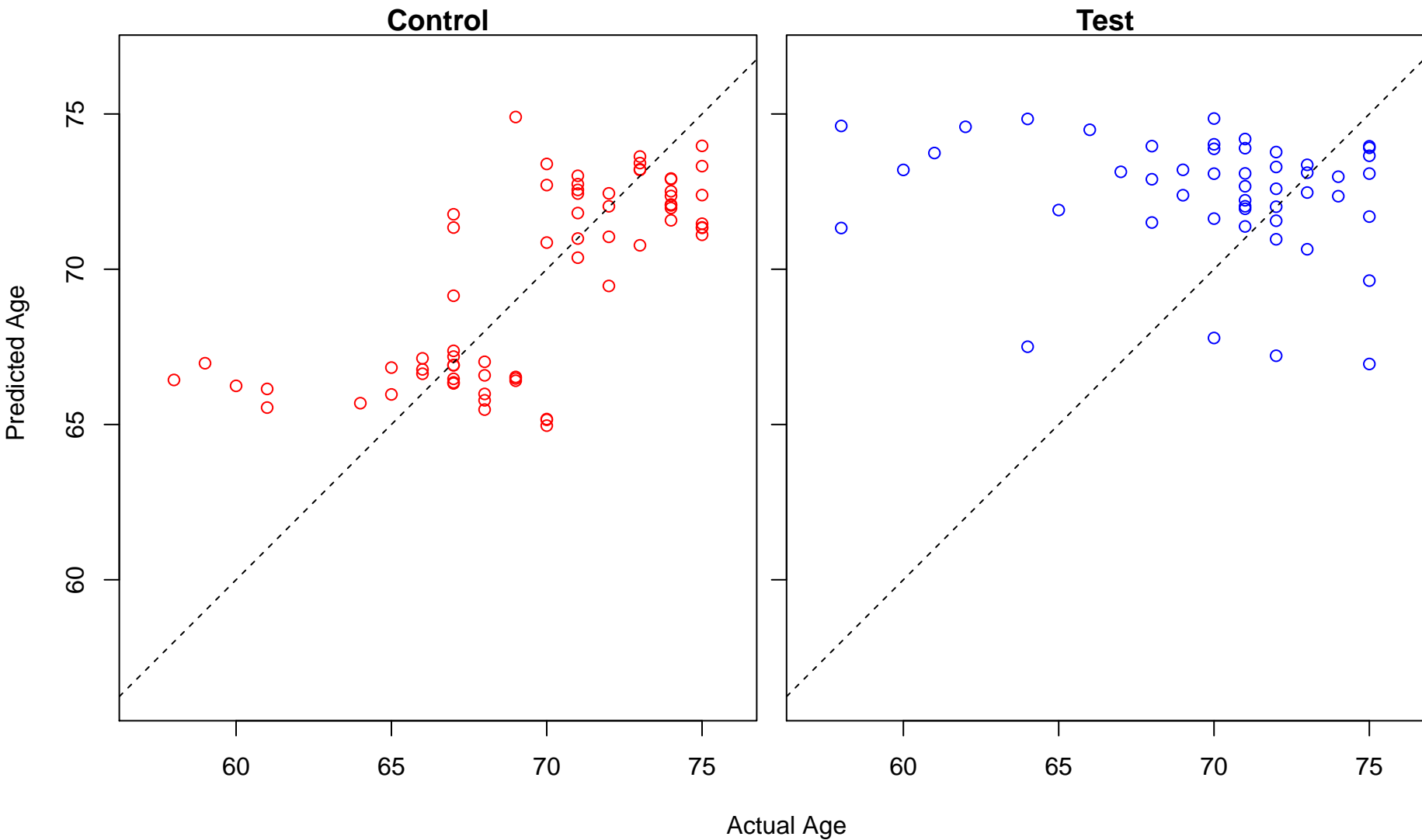
NADH dehydrogenase complex assembly (Score: 1.655821)



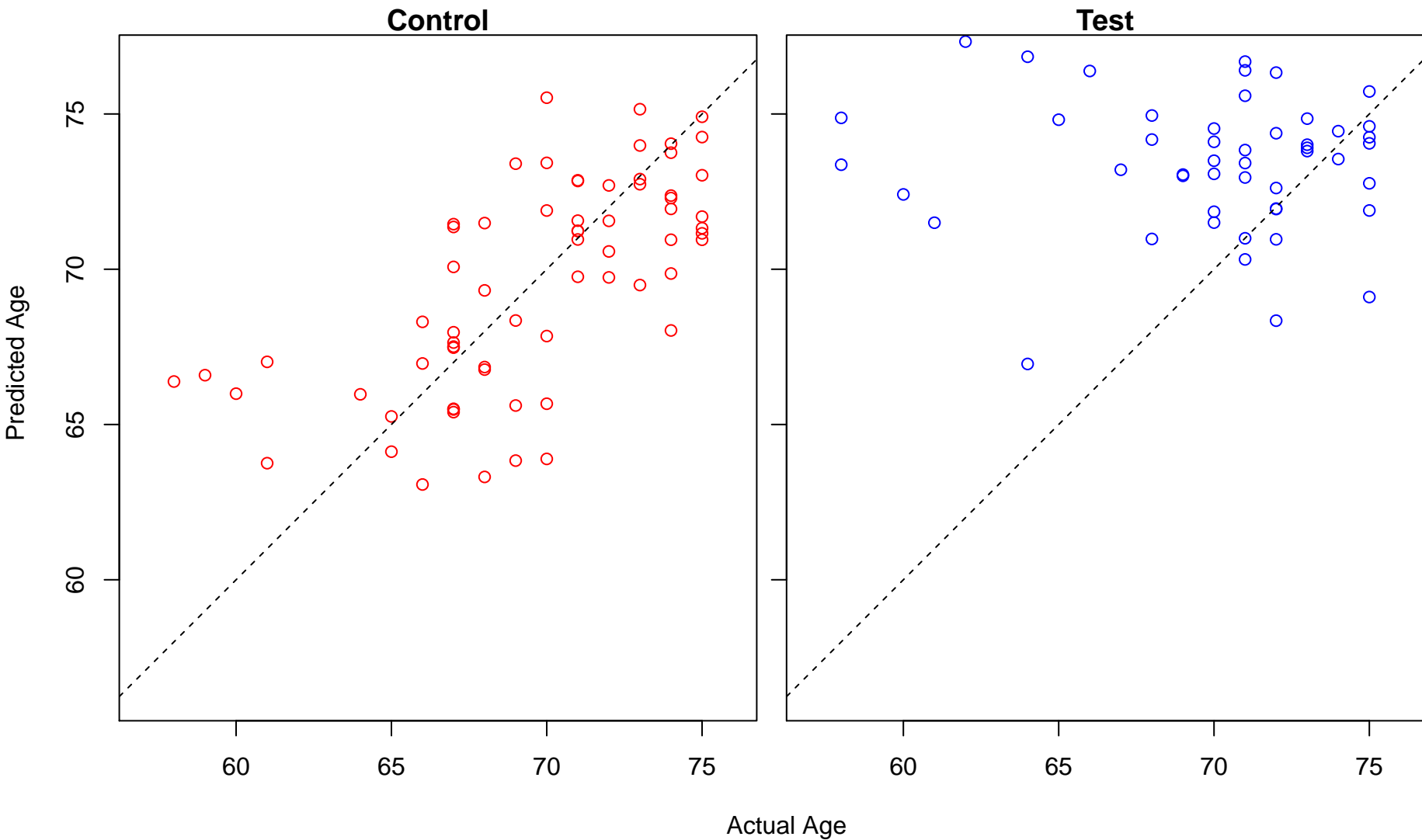
mitochondrial respiratory chain complex I assembly (Score: 1.655821)



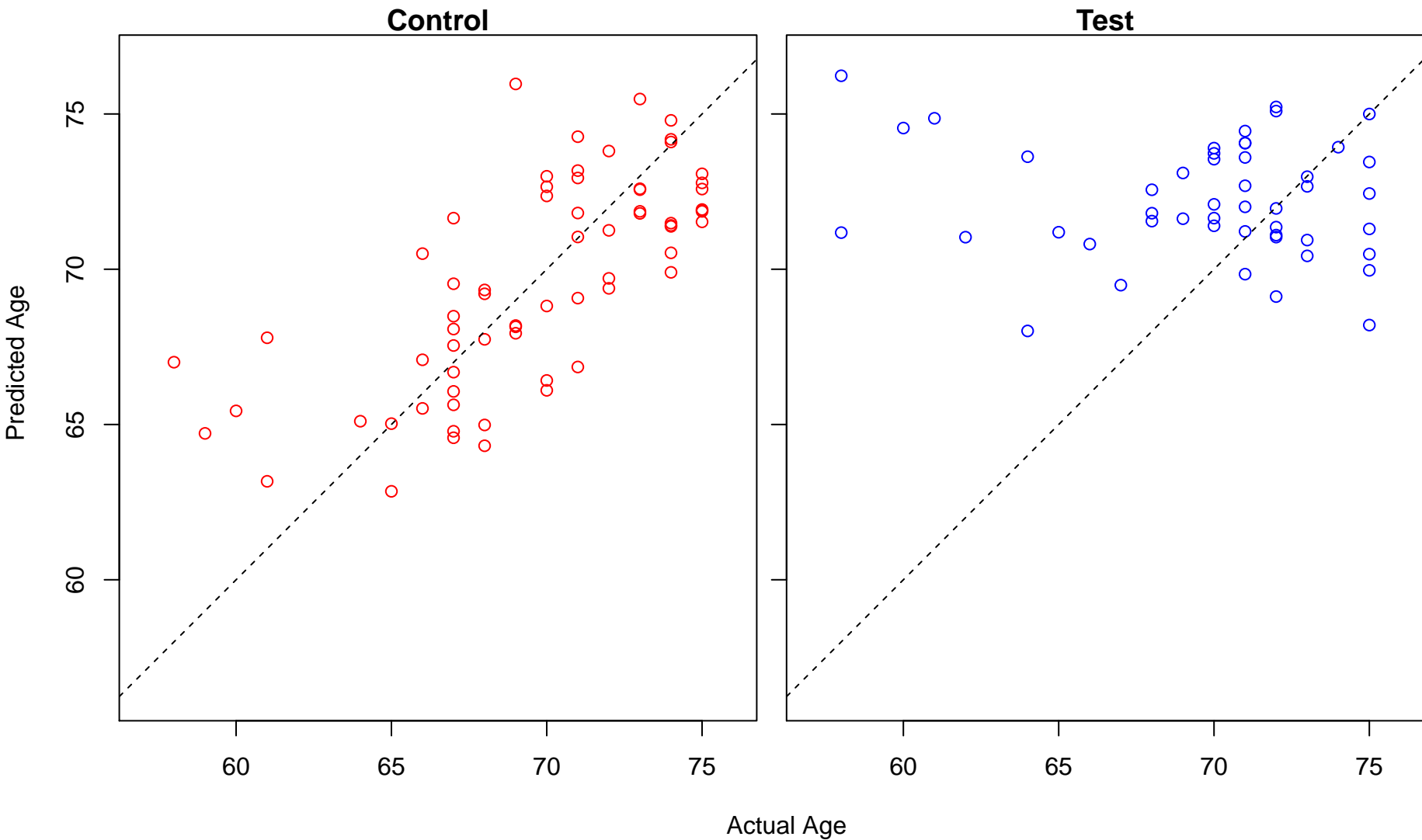
mitochondrial respiratory chain complex I biogenesis (Score: 1.655821)



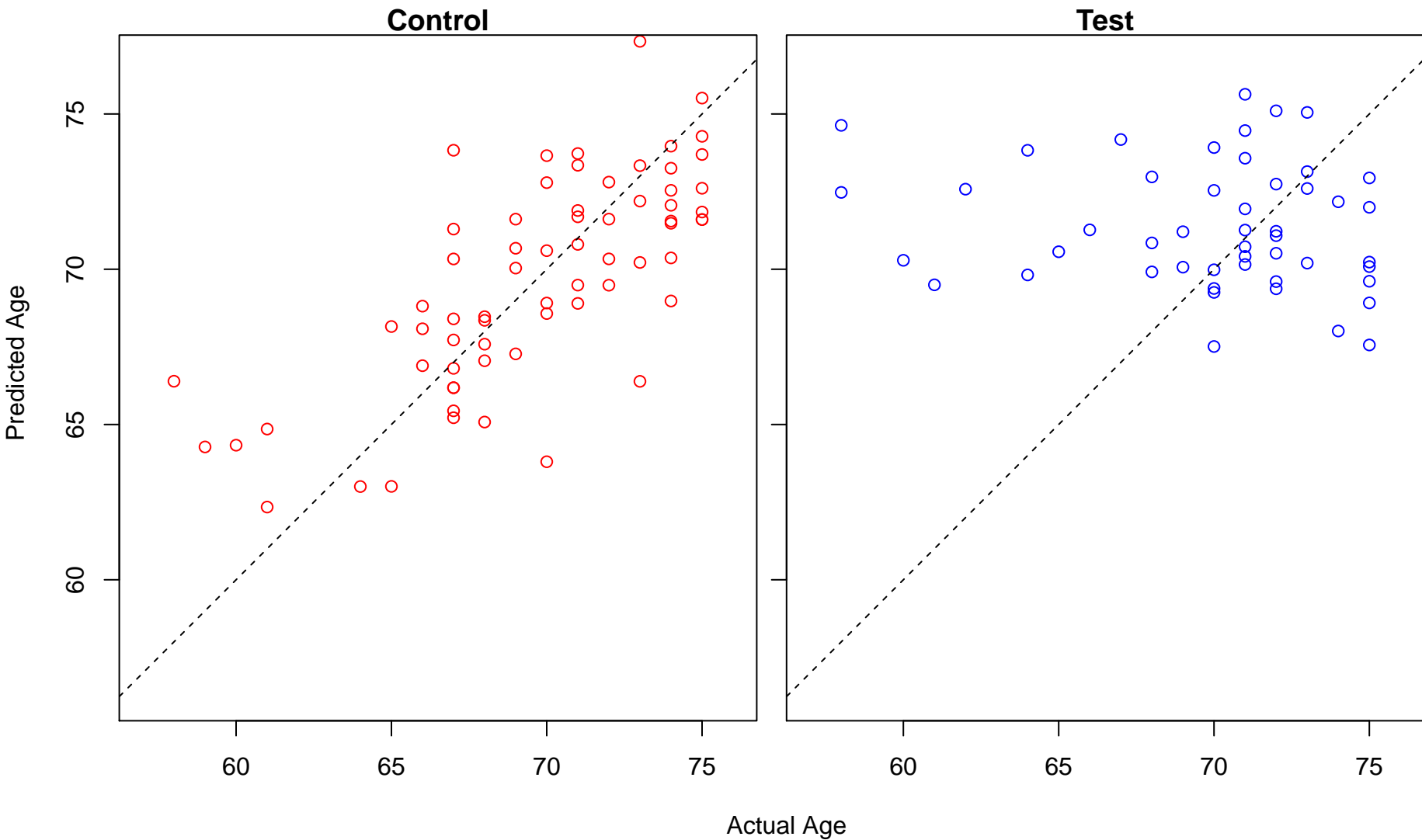
regulation of chromatin organization (Score: 1.655745)



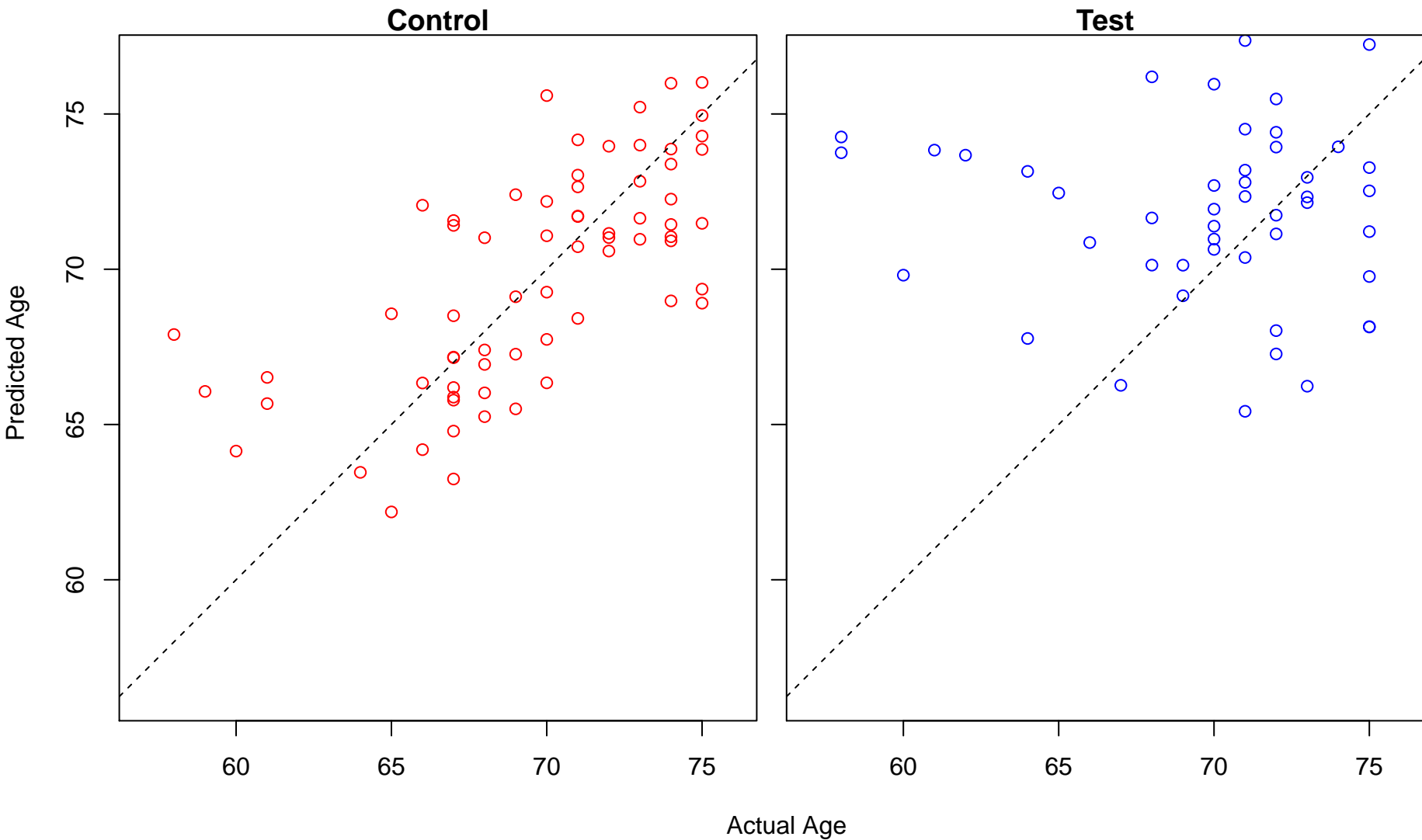
reproduction (Score: 1.654906)



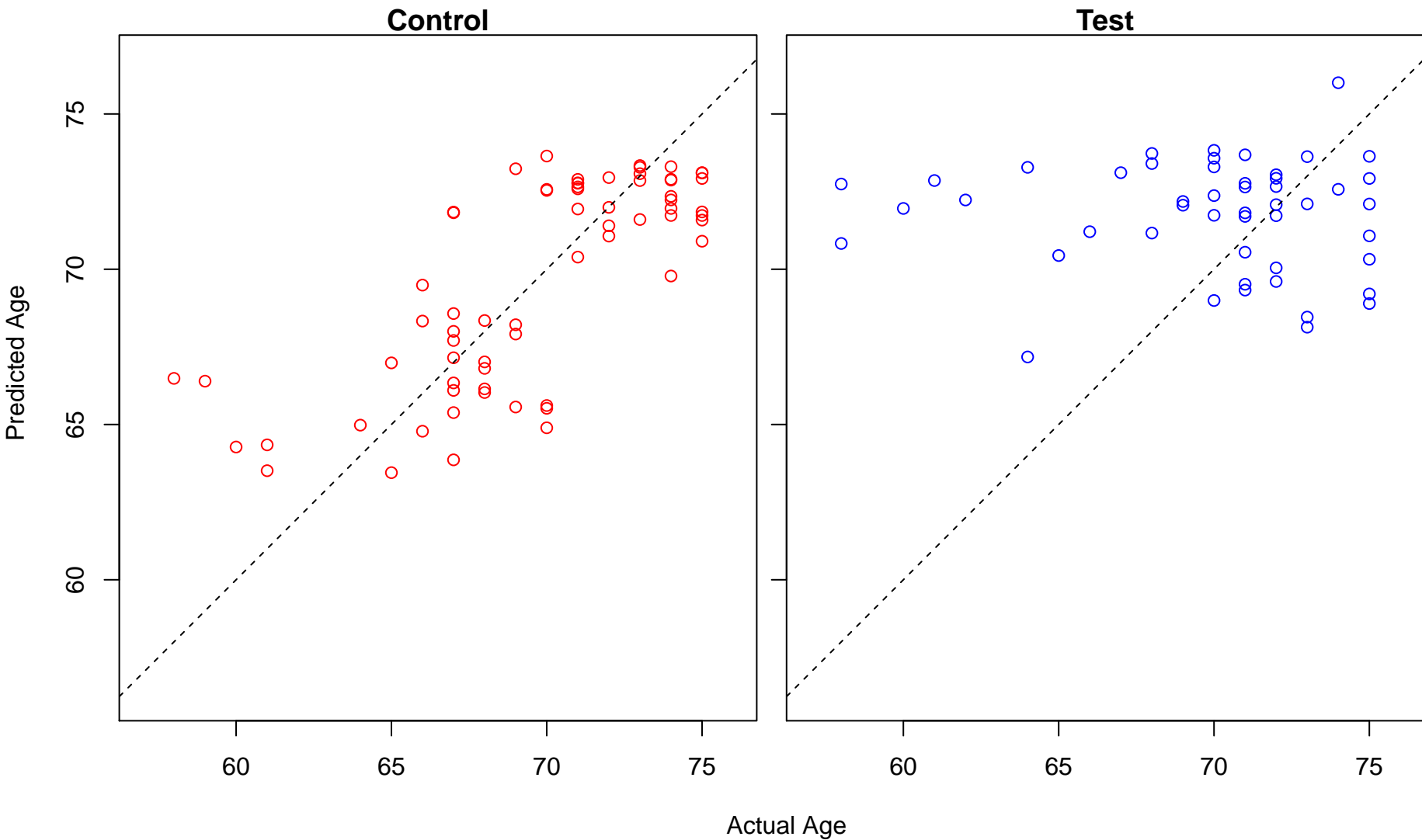
negative regulation of mRNA processing (Score: 1.654902)



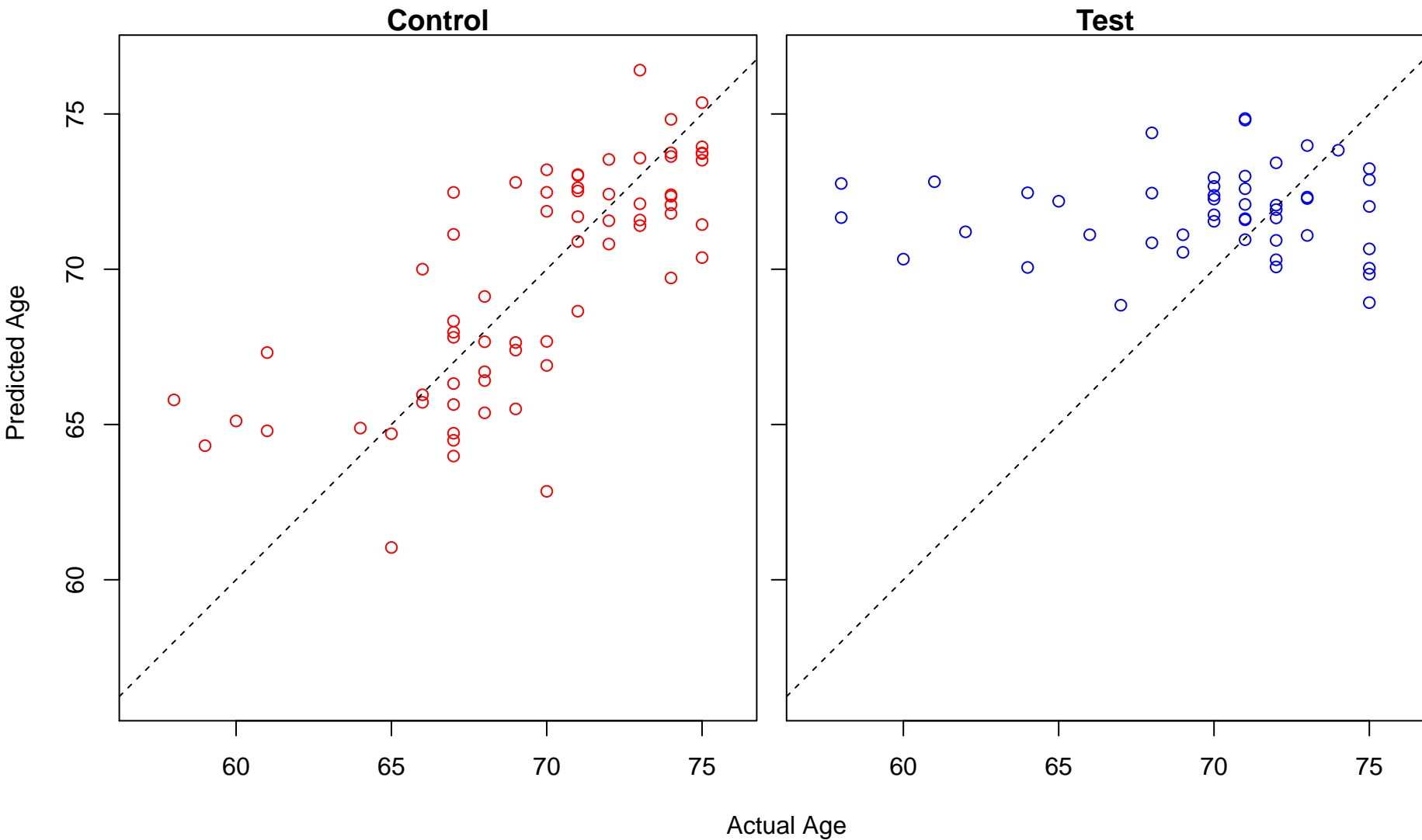
regulation of cell-substrate adhesion (Score: 1.654460)



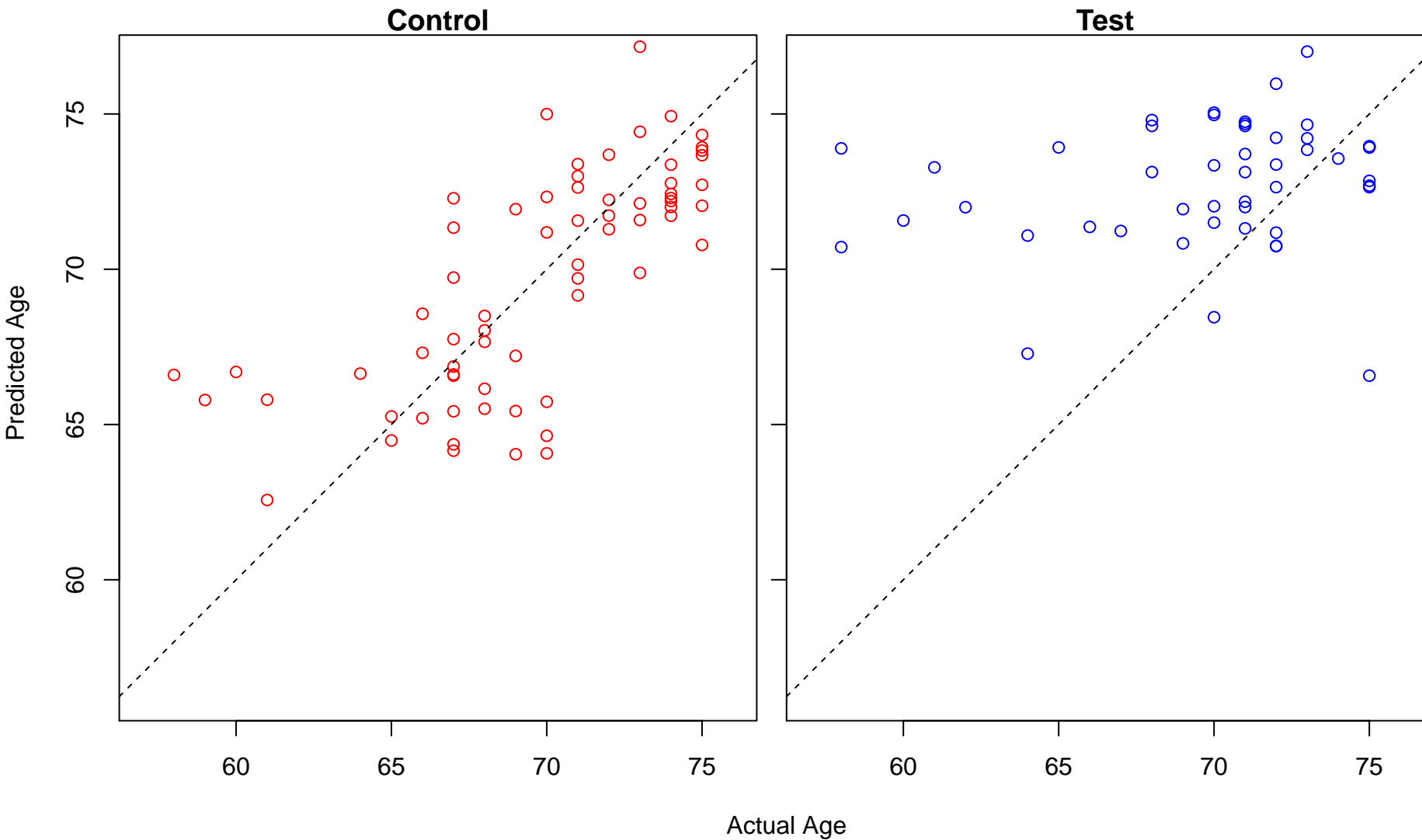
metaphase plate congression (Score: 1.653903)



mitotic DNA damage checkpoint (Score: 1.653854)

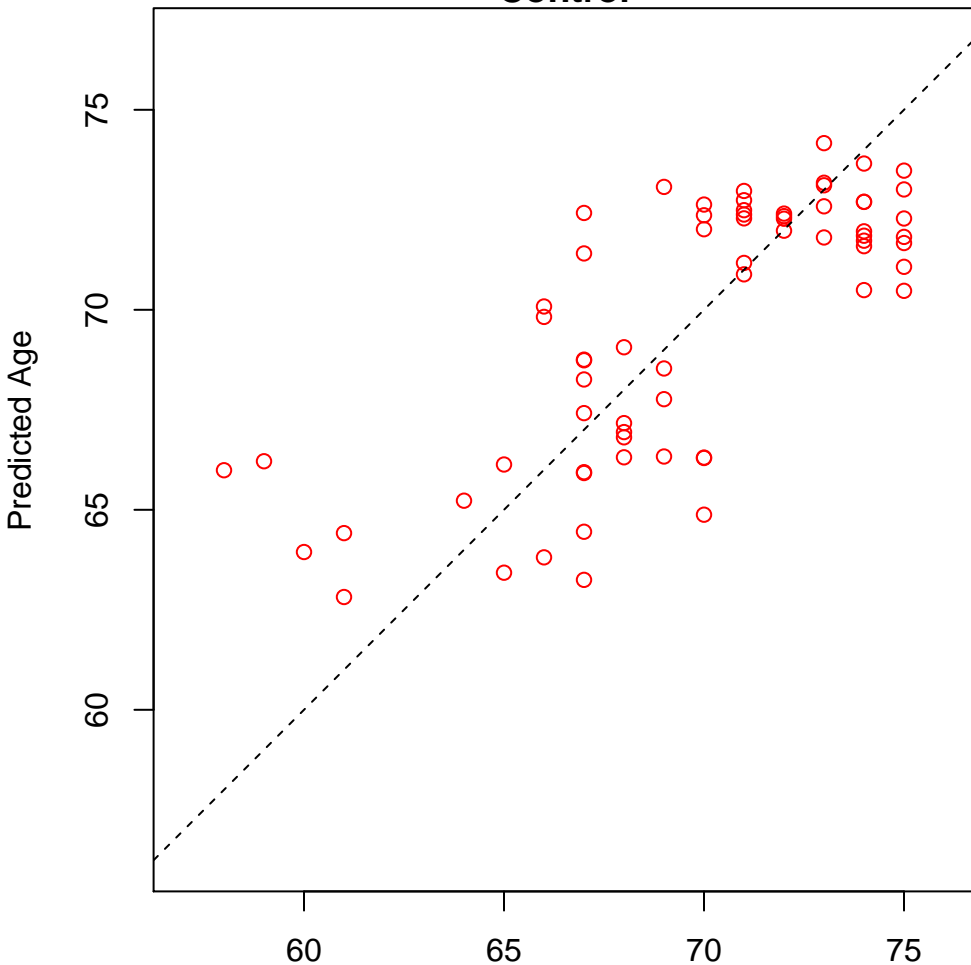


homeostasis of number of cells (Score: 1.653114)

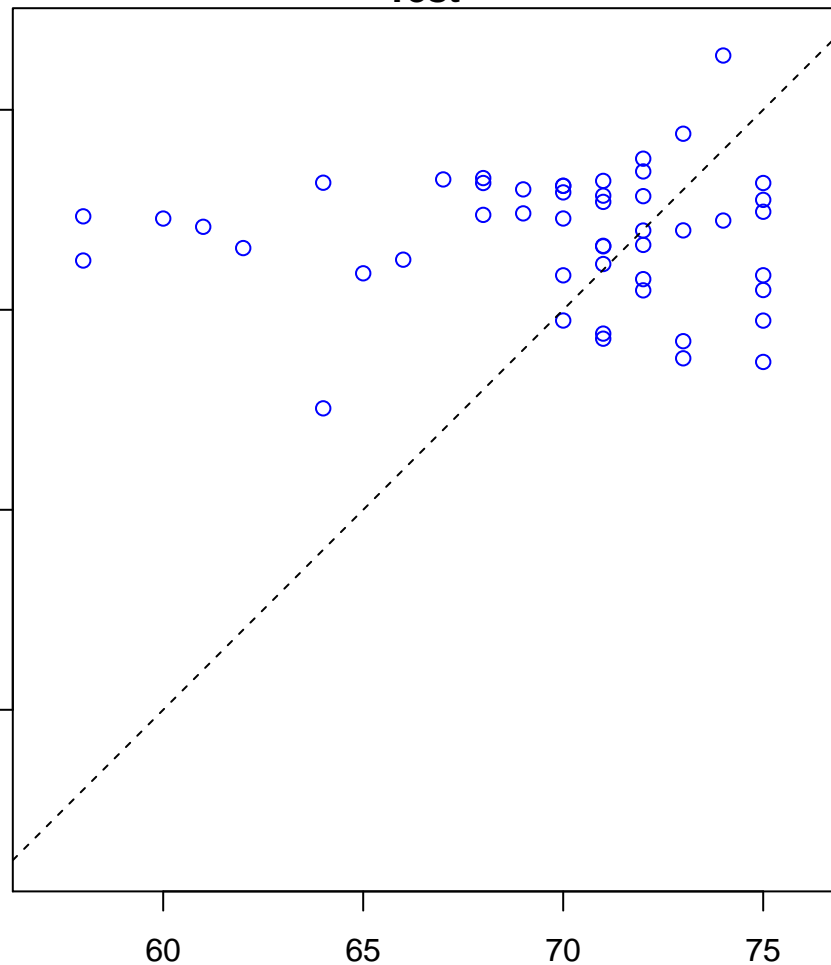


cell separation after cytokinesis (Score: 1.652834)

Control

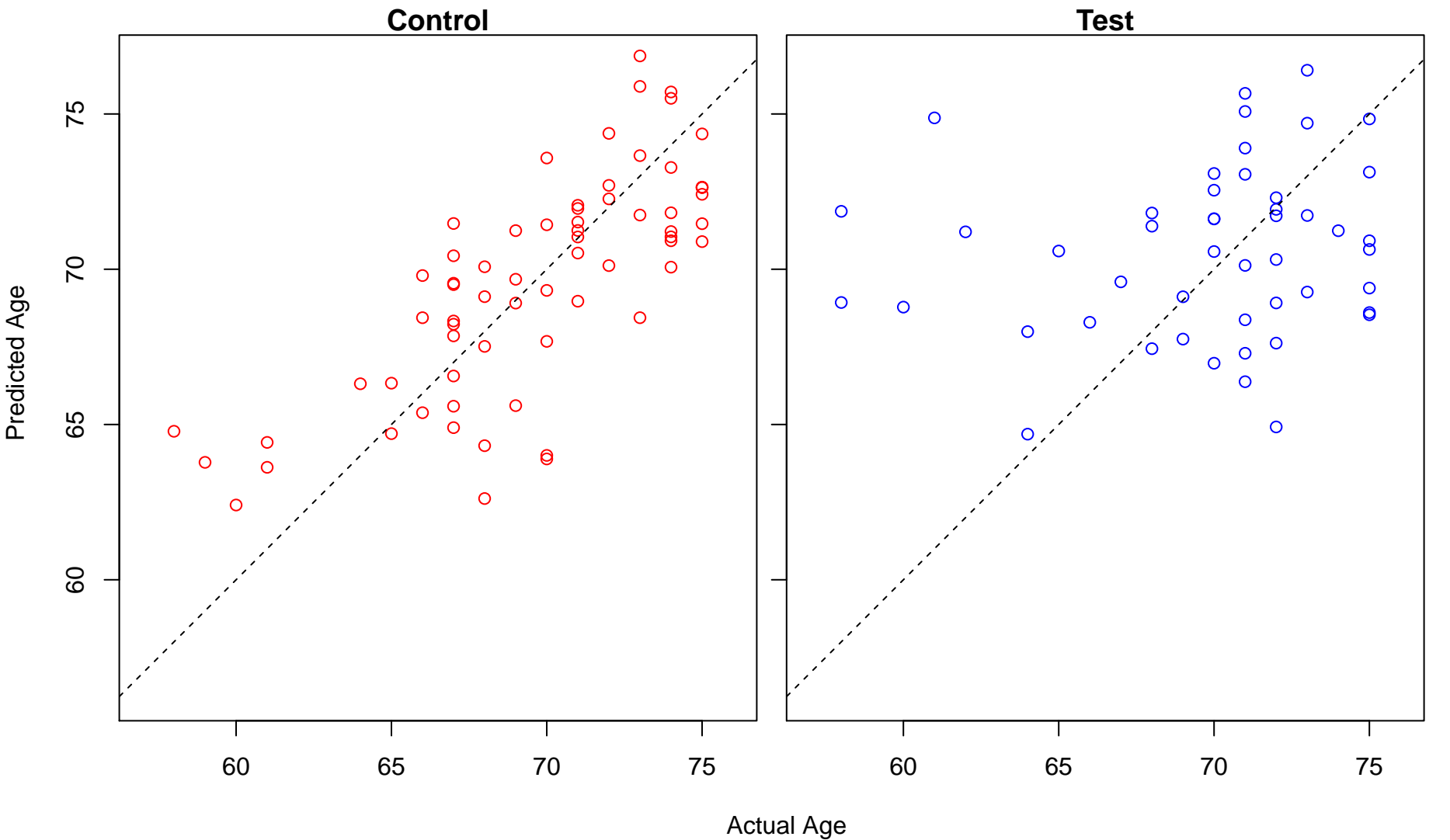


Test



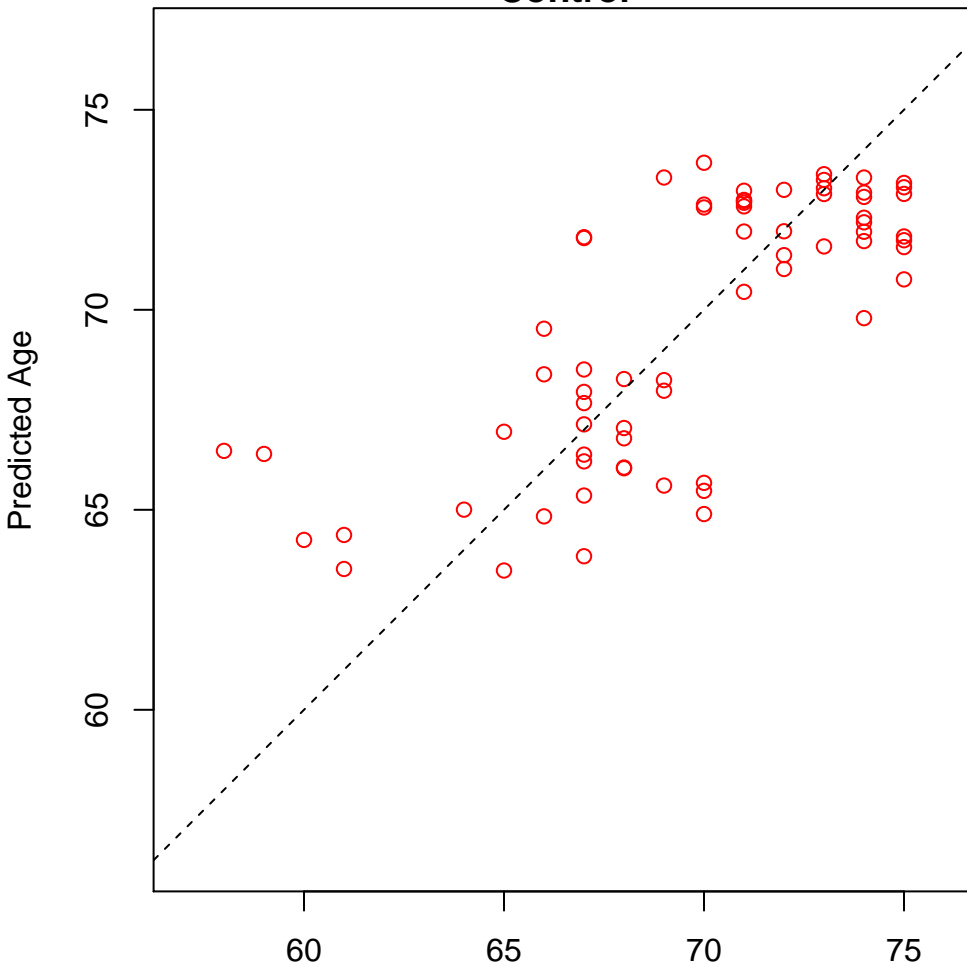
Actual Age

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

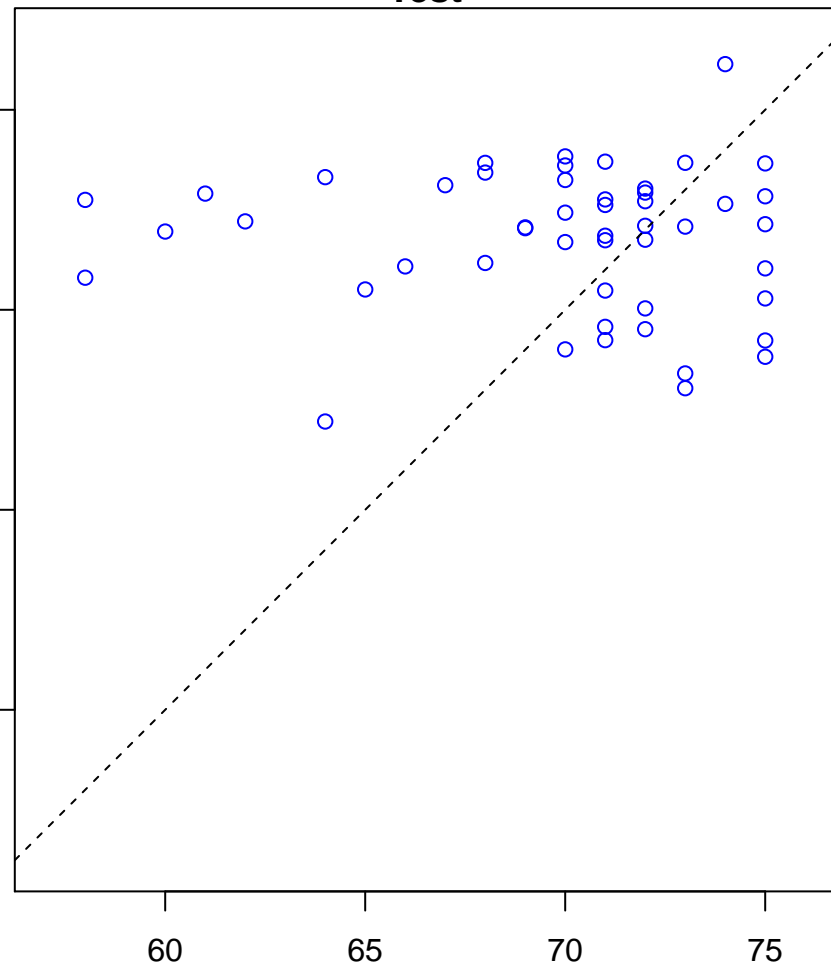


mitotic metaphase plate congruence (Score: 1.652298)

Control

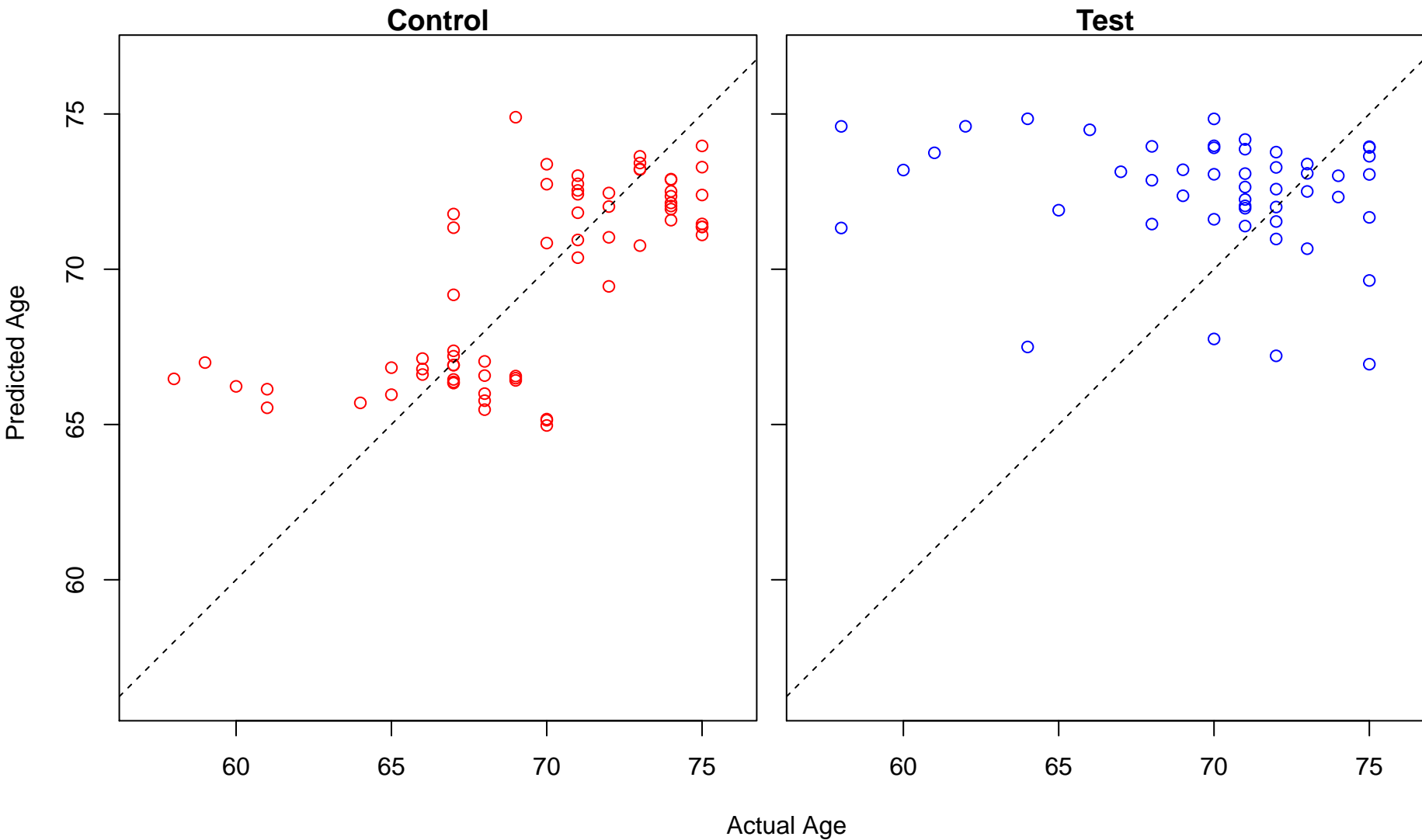


Test

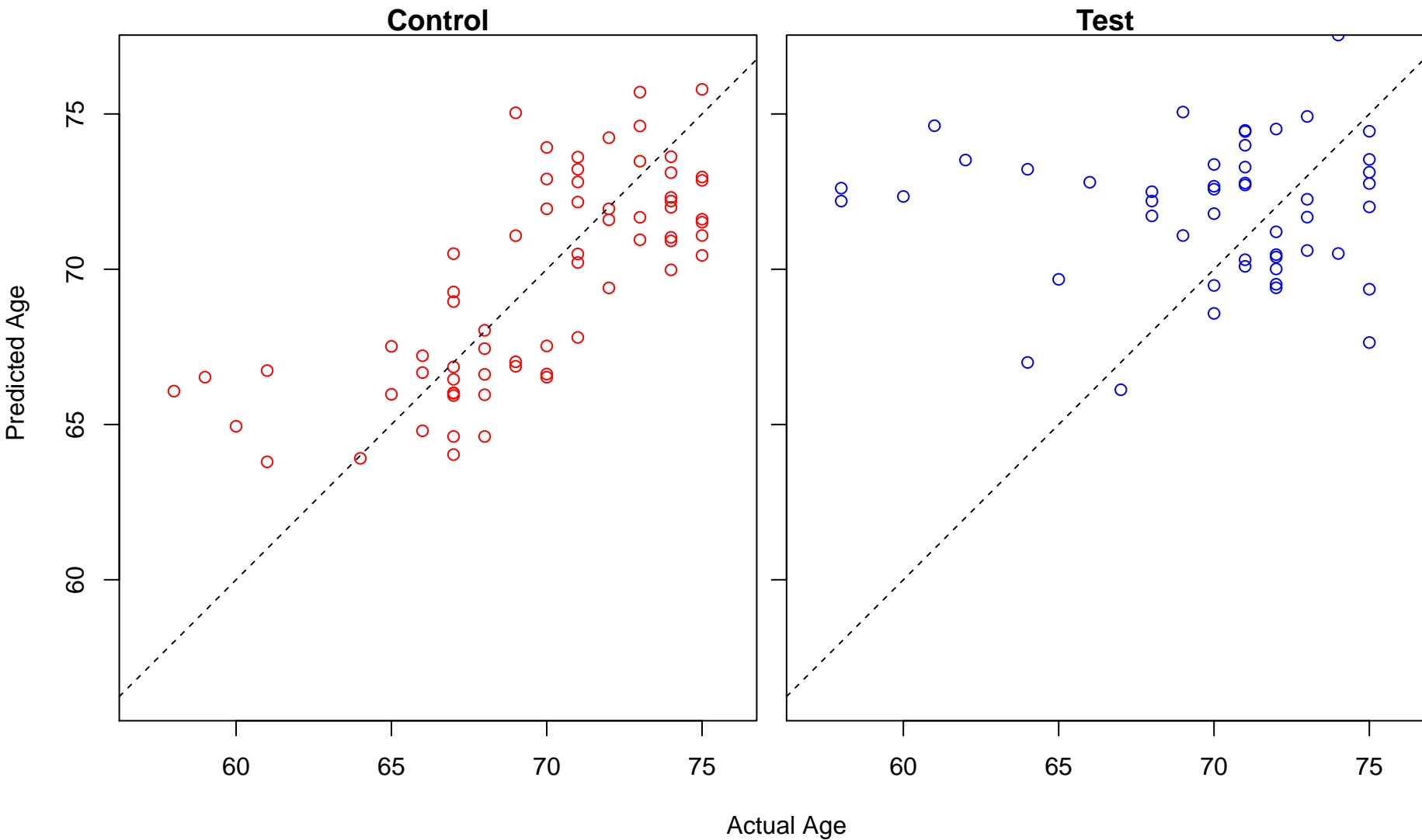


Actual Age

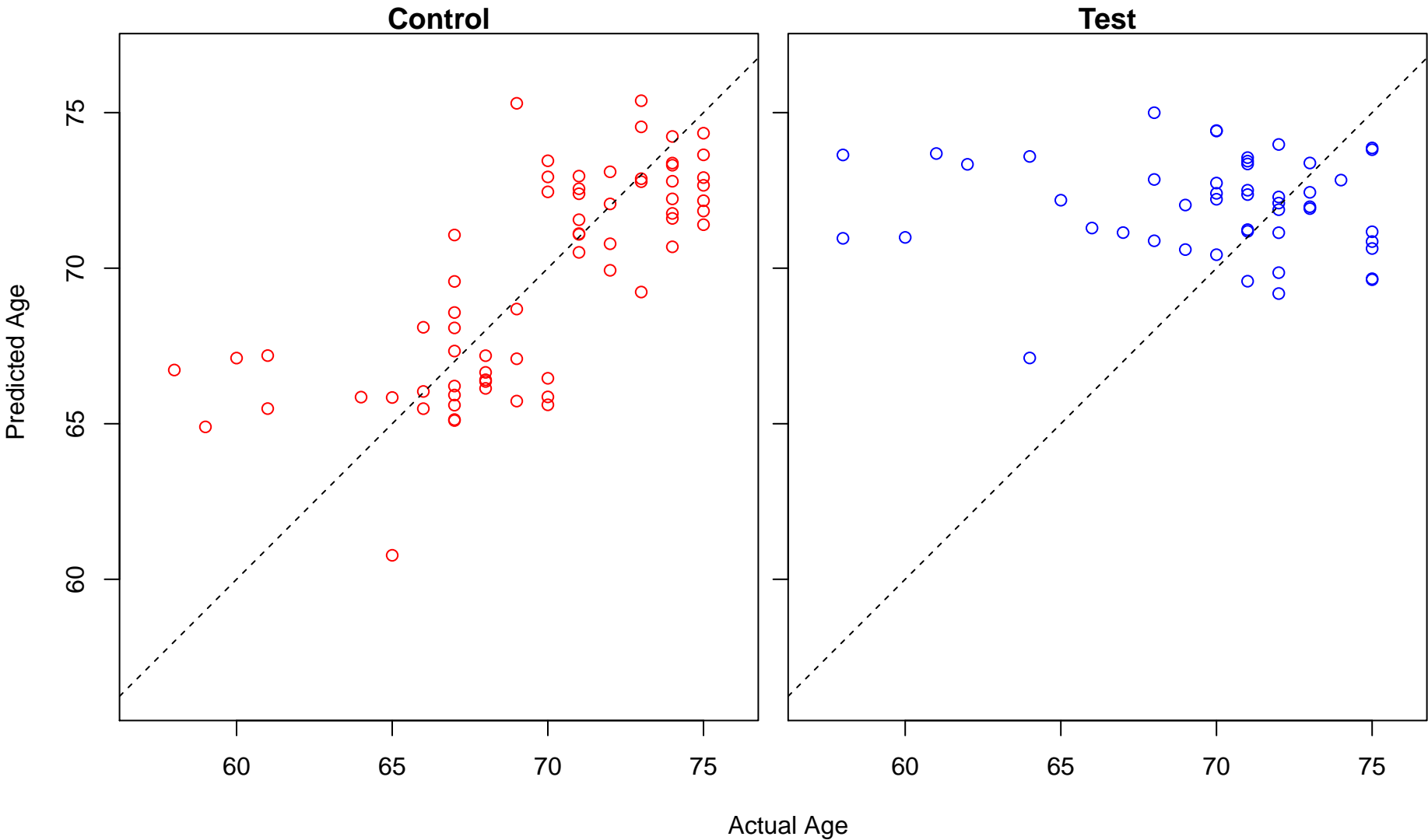
mitochondrial respiratory chain complex assembly (Score: 1.652266)



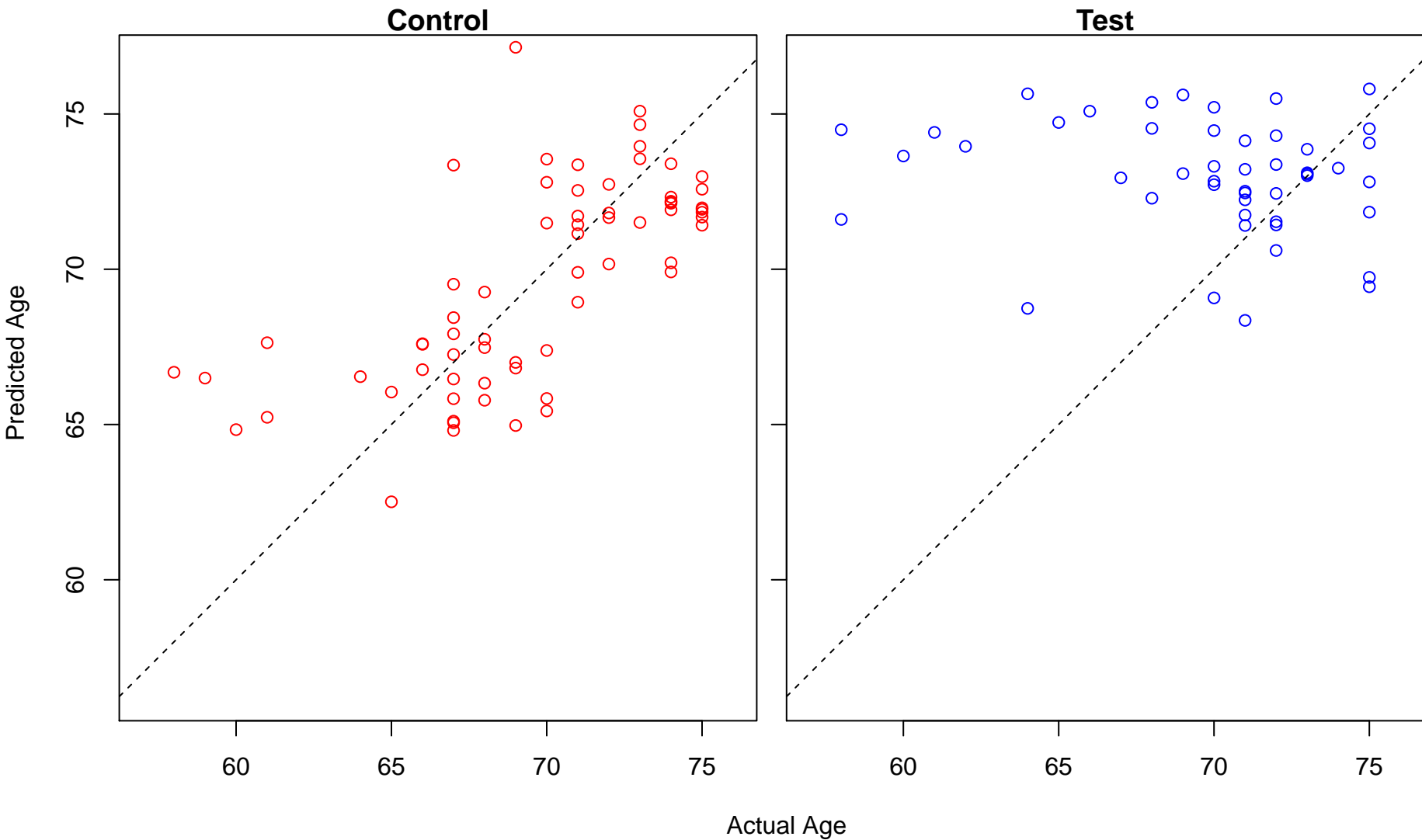
morphogenesis of an epithelium (Score: 1.651968)



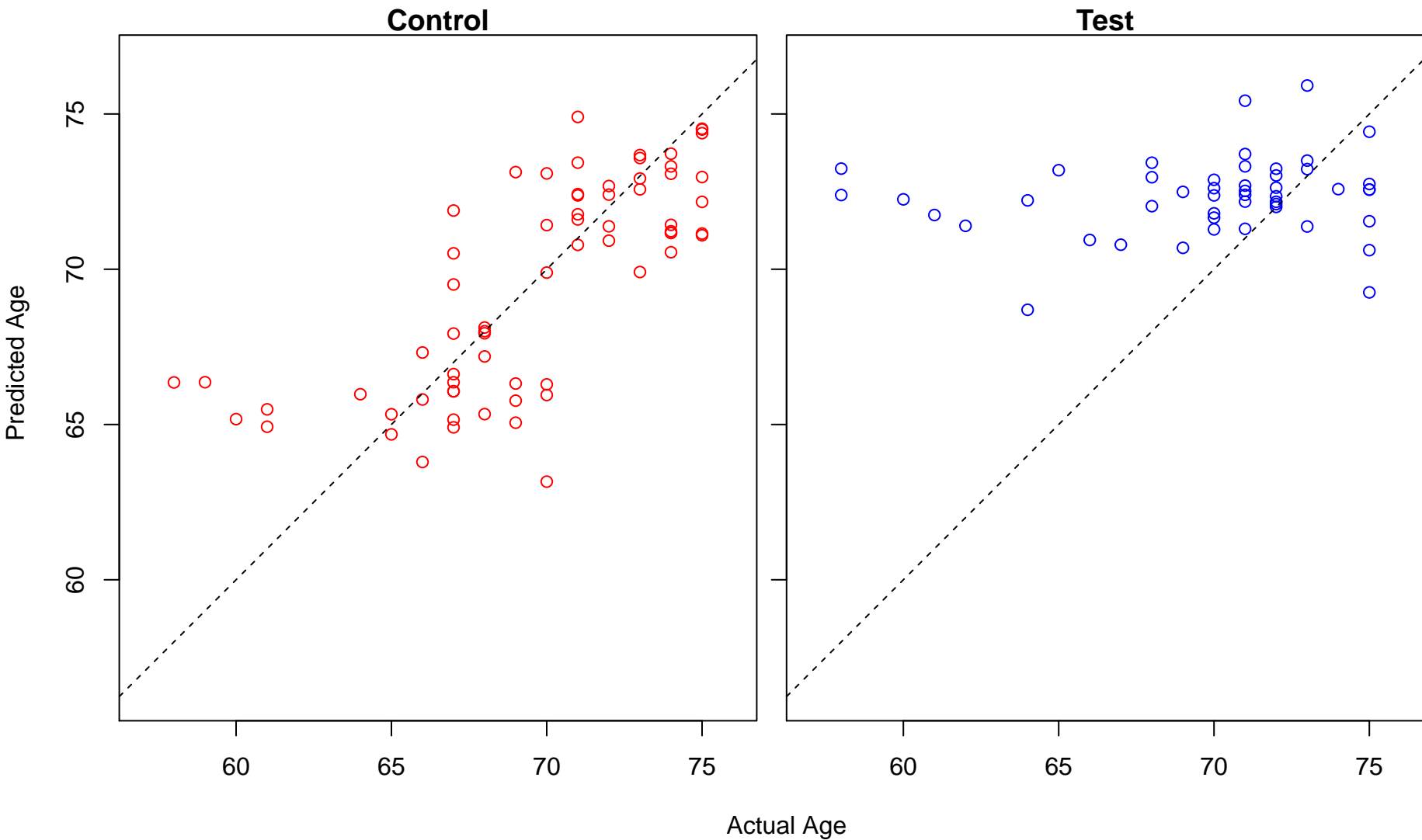
antigen processing and presentation of exogenous peptide antigen via MHC class I (Score: 1.65188)



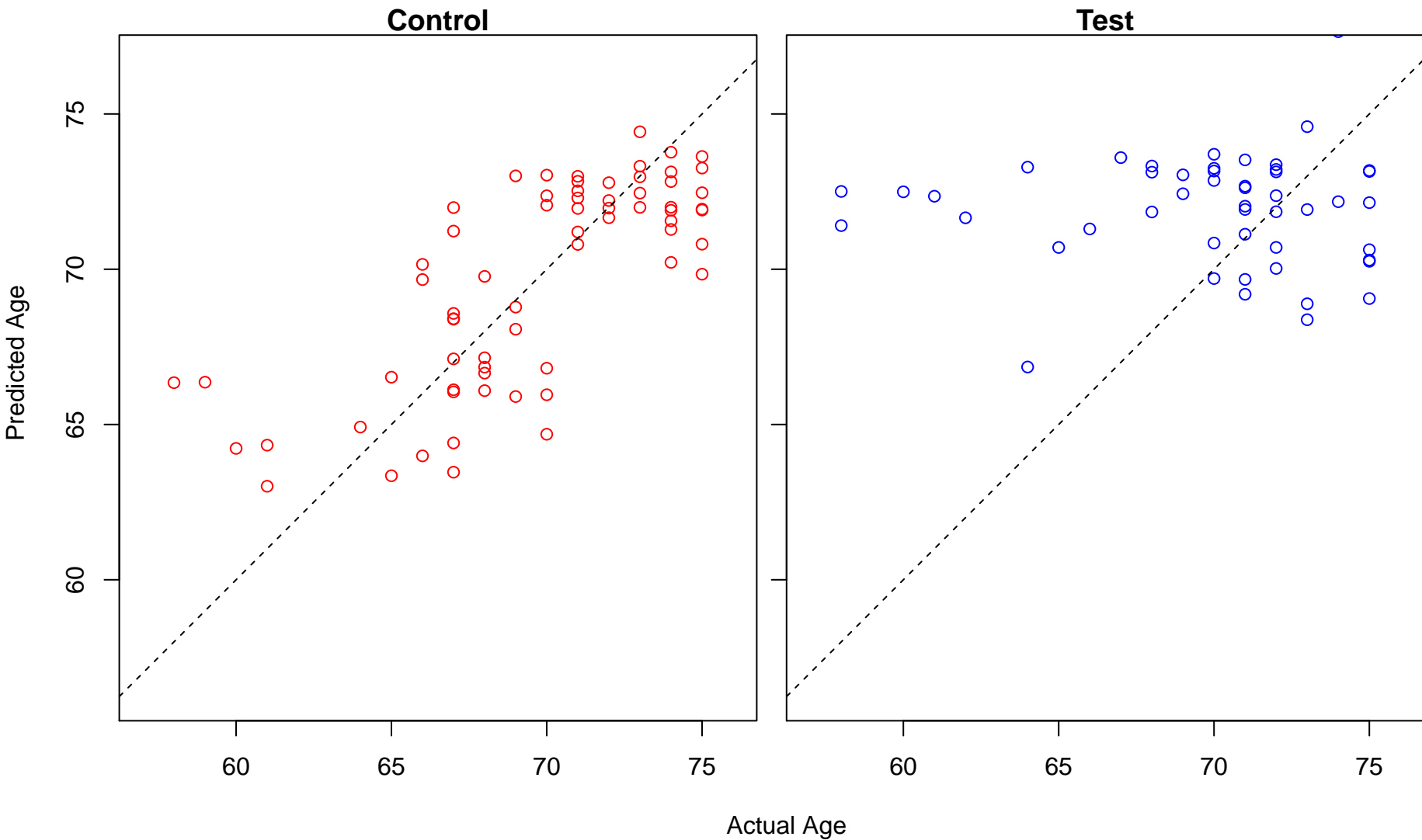
telomere organization (Score: 1.651617)



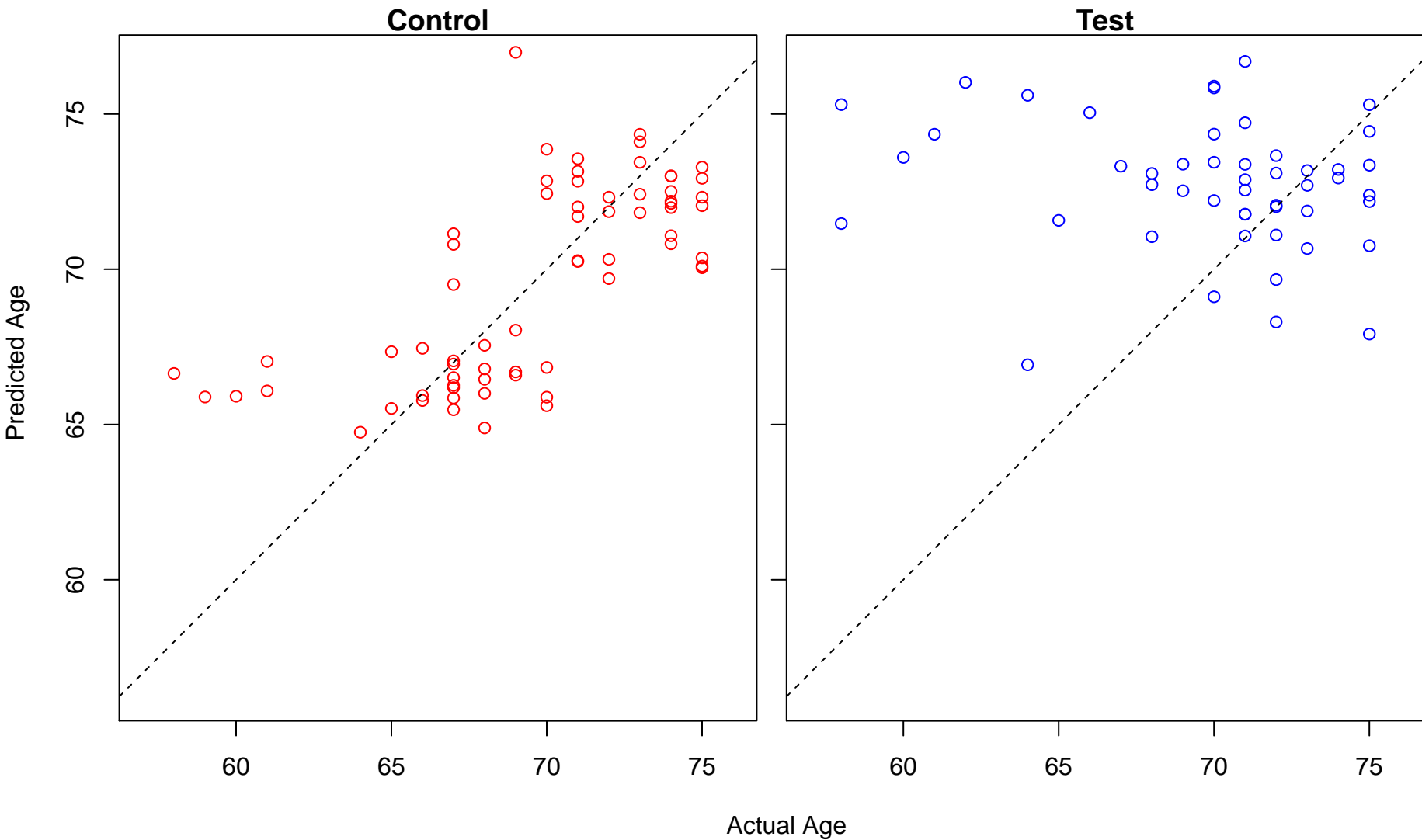
energy derivation by oxidation of organic compounds (Score: 1.651272)



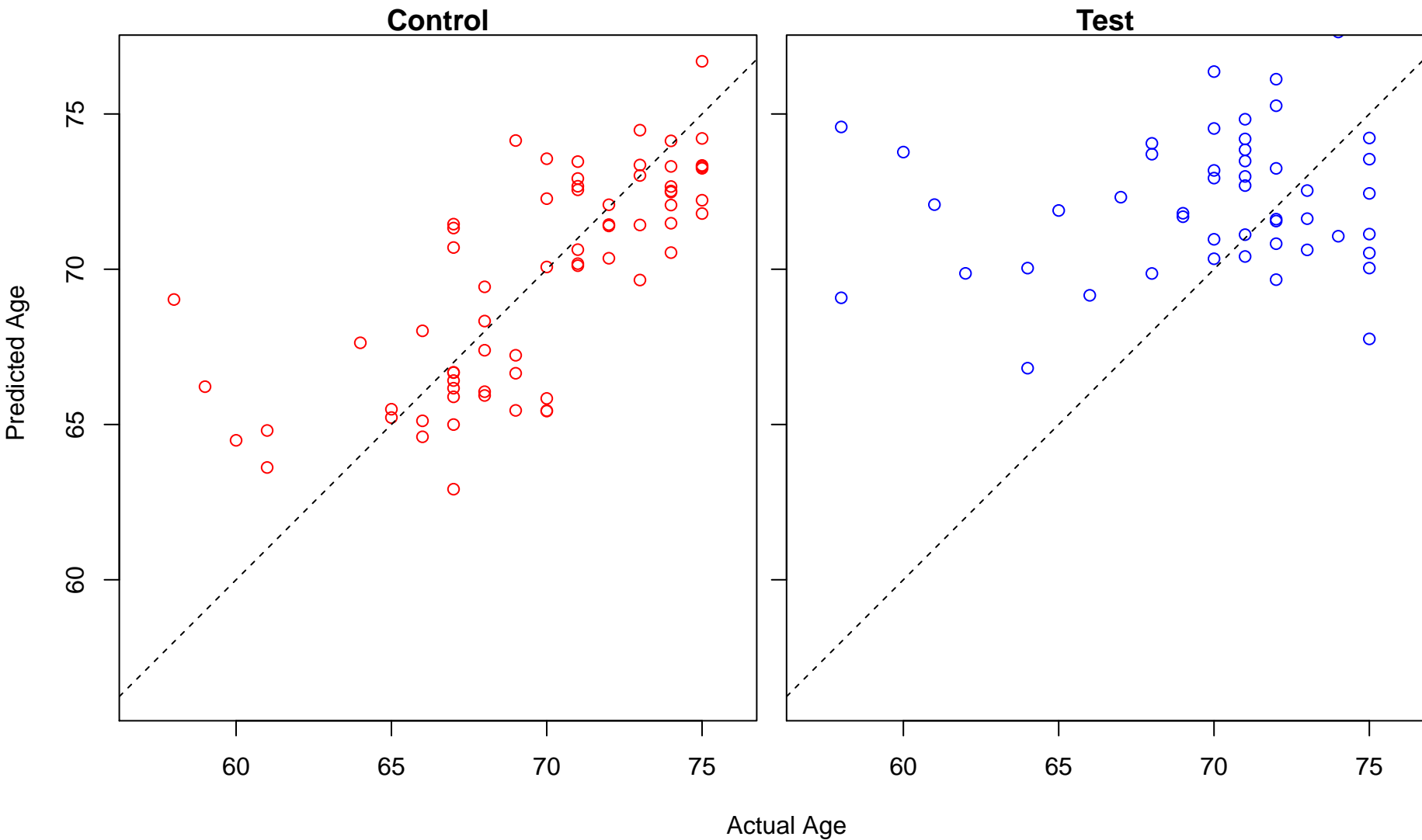
regulation of spindle organization (Score: 1.650718)



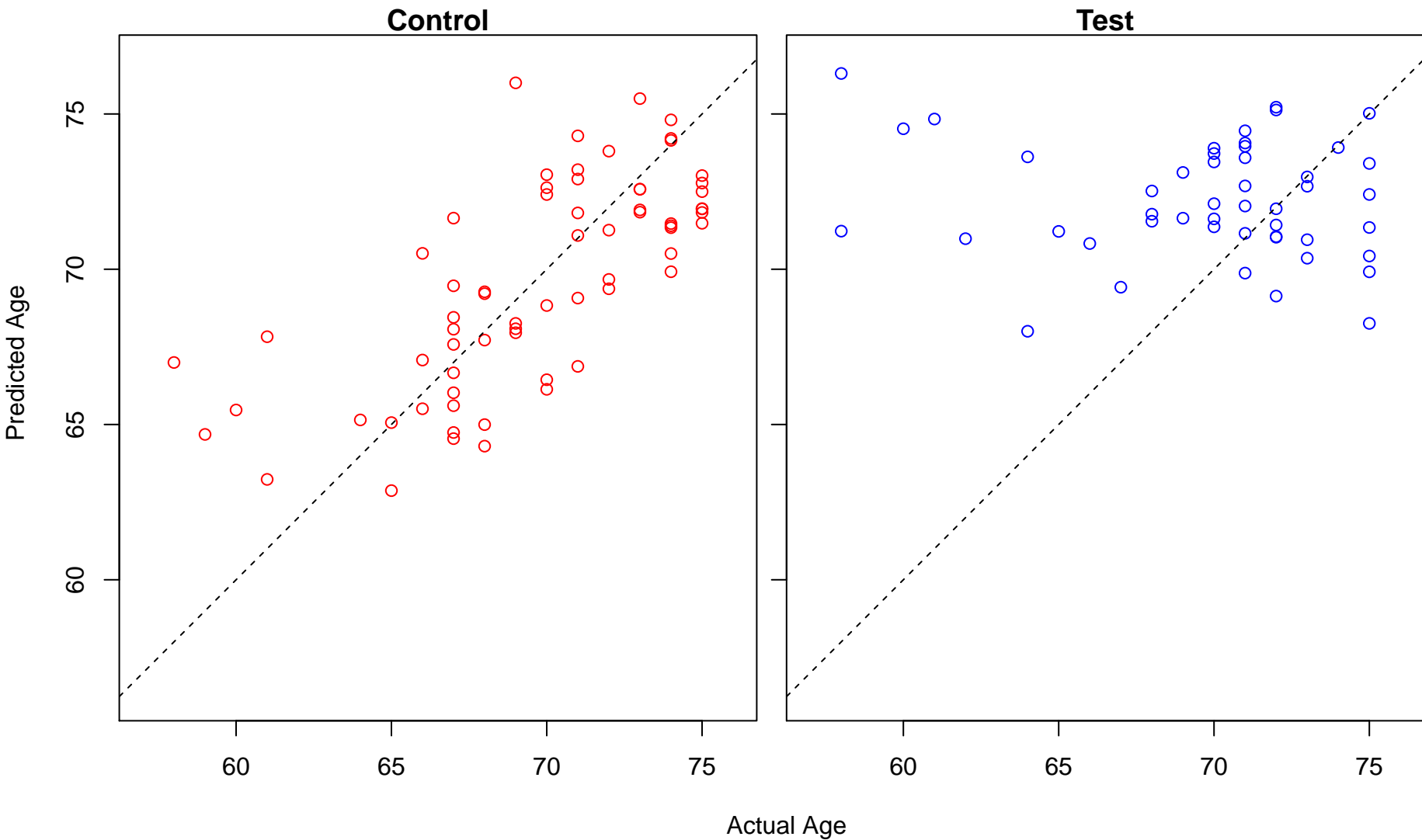
transition metal ion transport (Score: 1.650251)



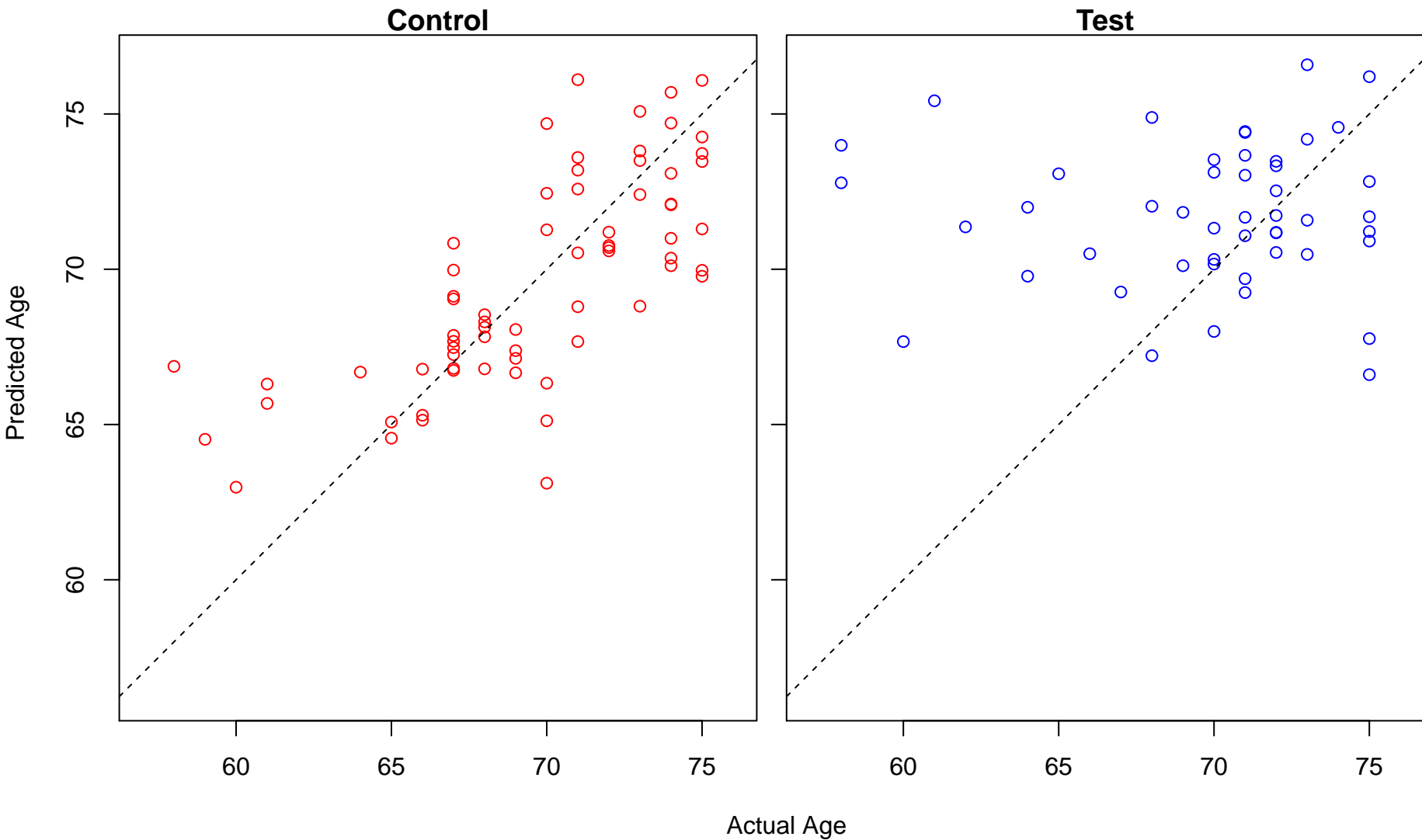
erythrocyte homeostasis (Score: 1.649280)



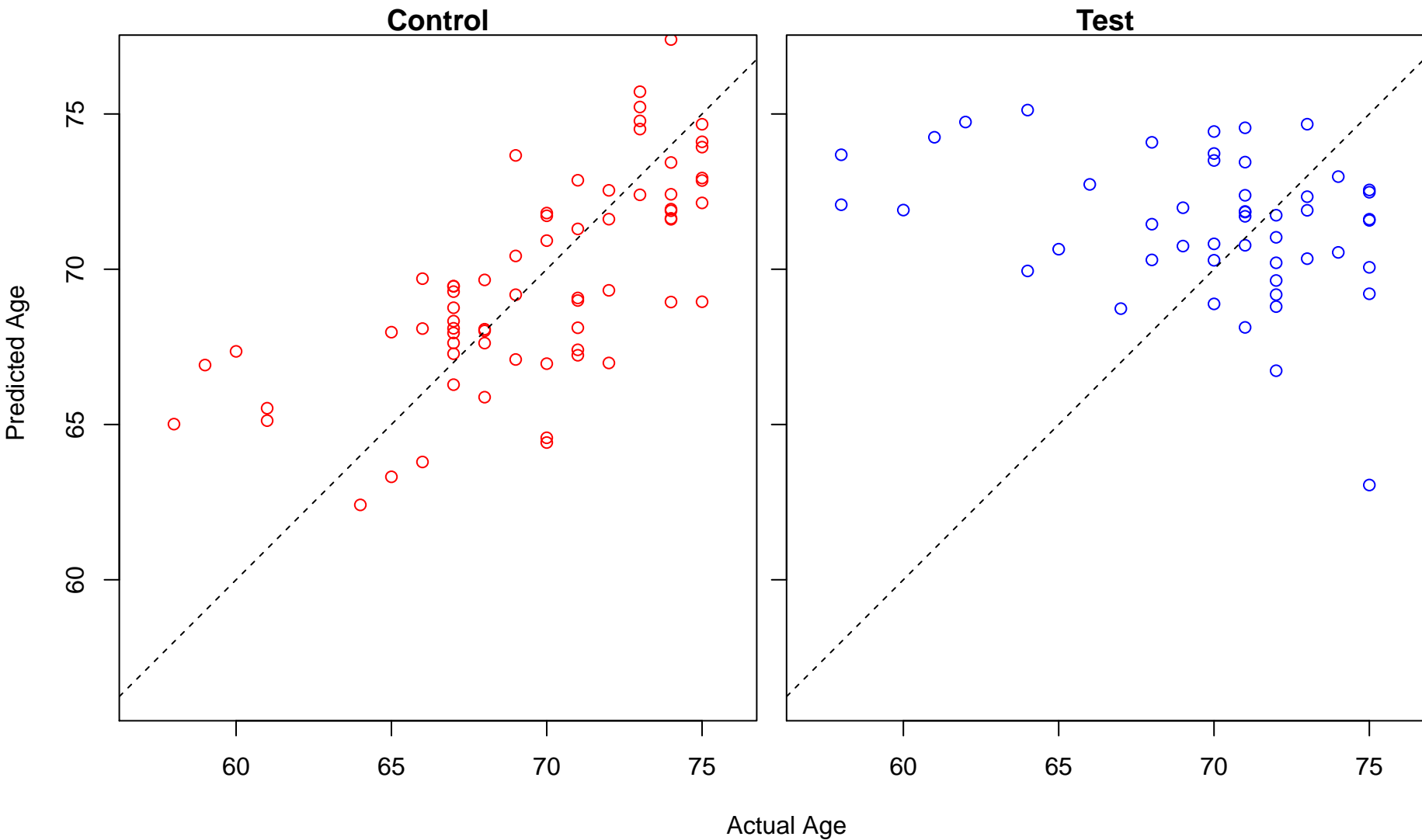
reproductive process (Score: 1.649237)



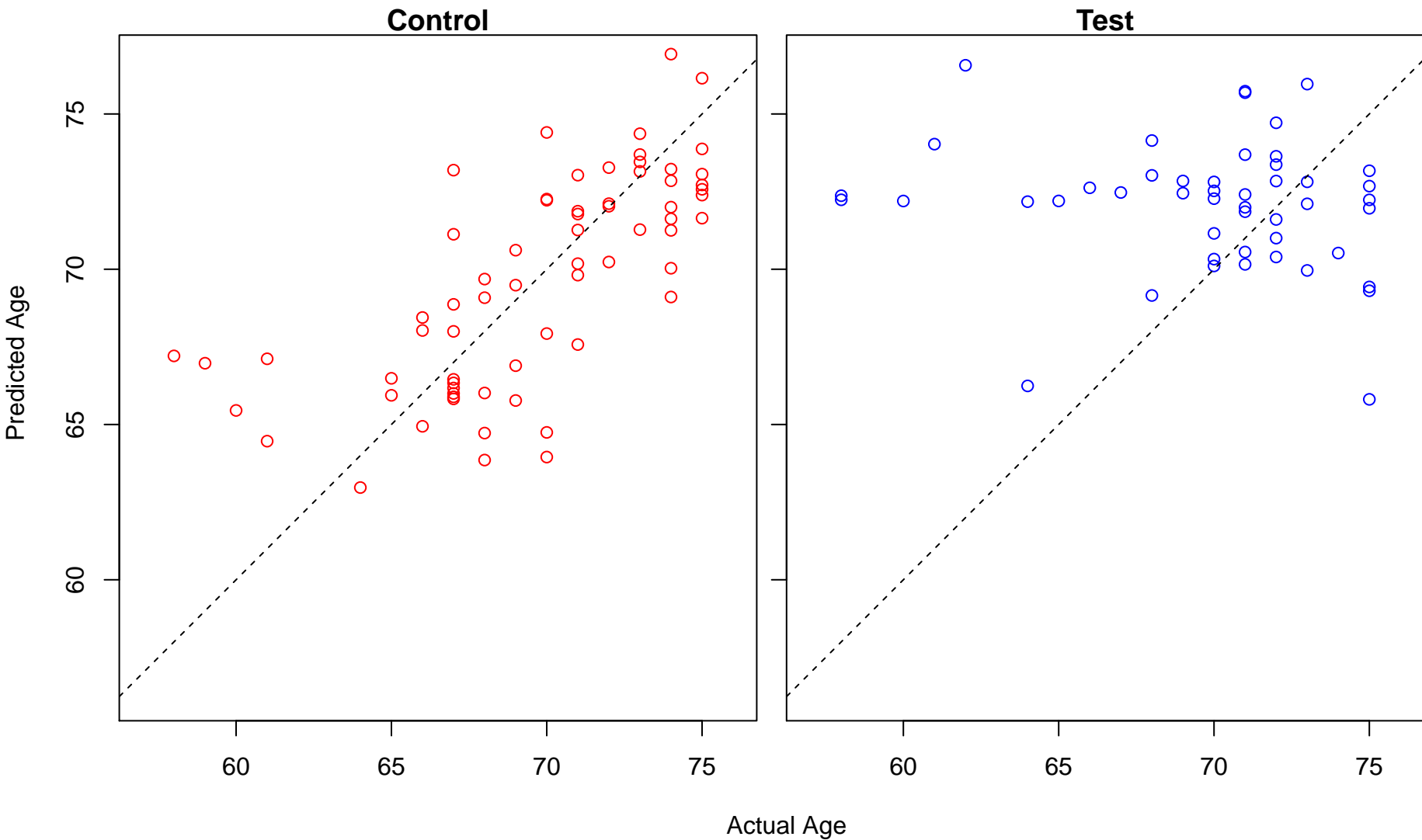
regulation of transmembrane transporter activity (Score: 1.648447)



regulation of cellular extravasation (Score: 1.647741)

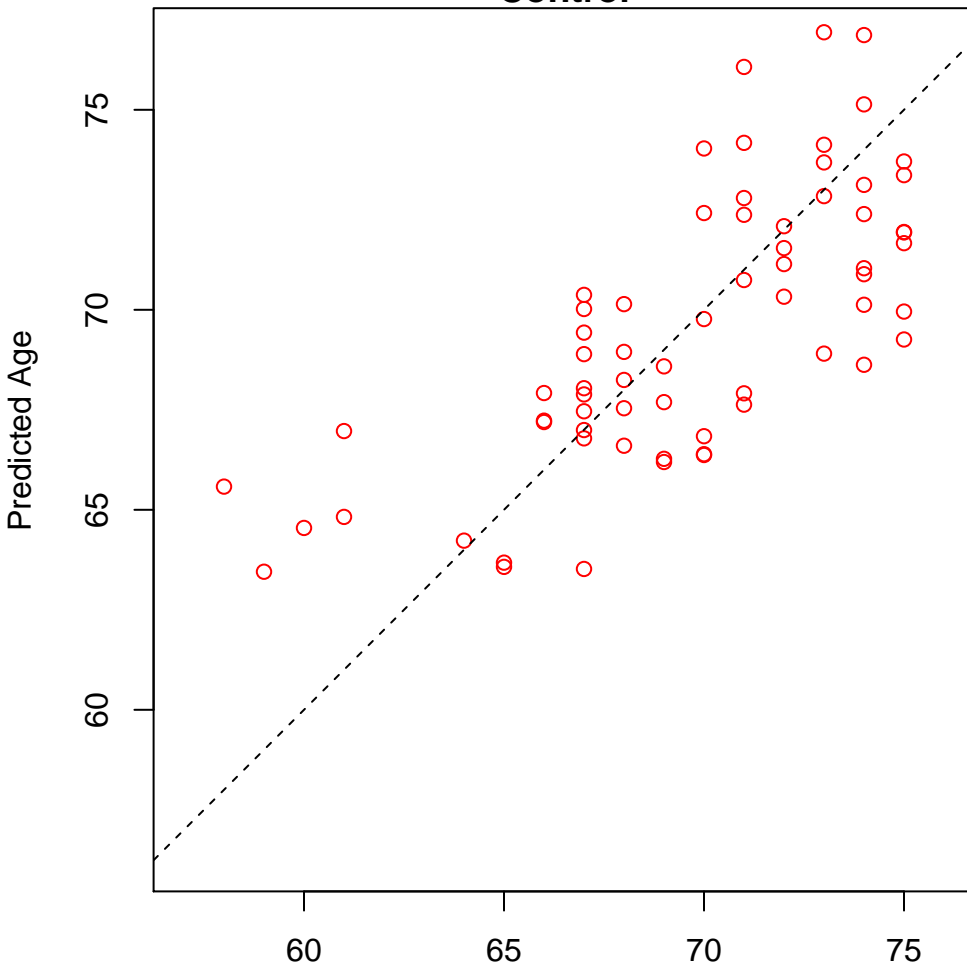


alcohol biosynthetic process (Score: 1.647561)

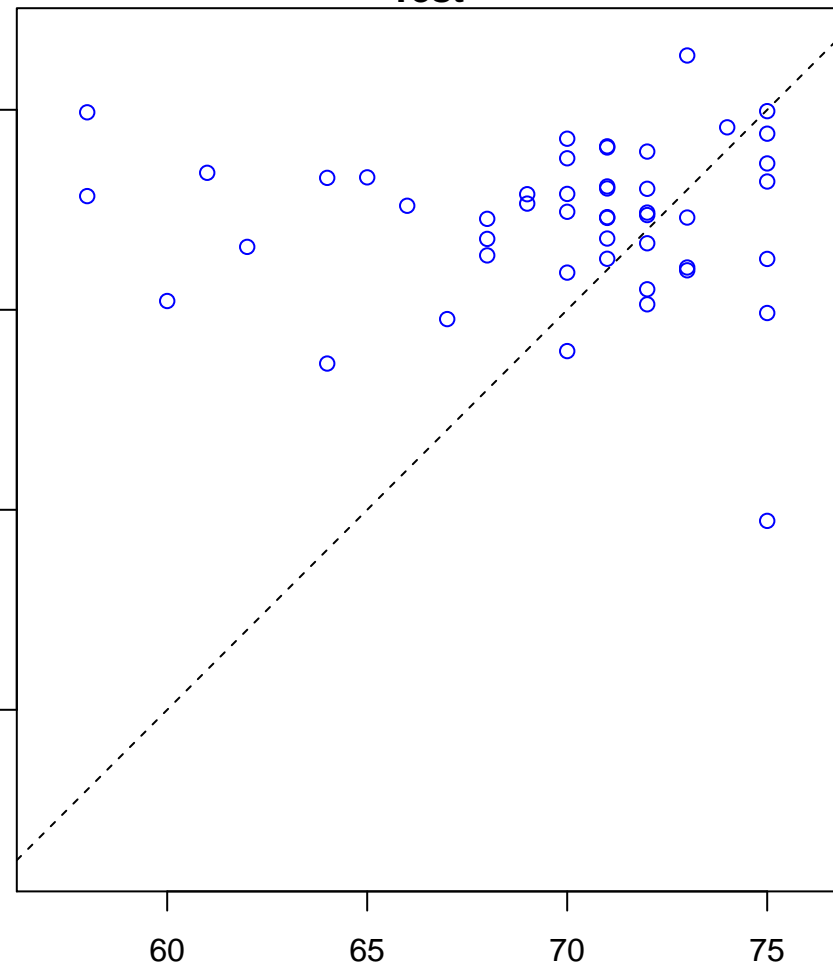


regulation of transmembrane transport (Score: 1.647386)

Control

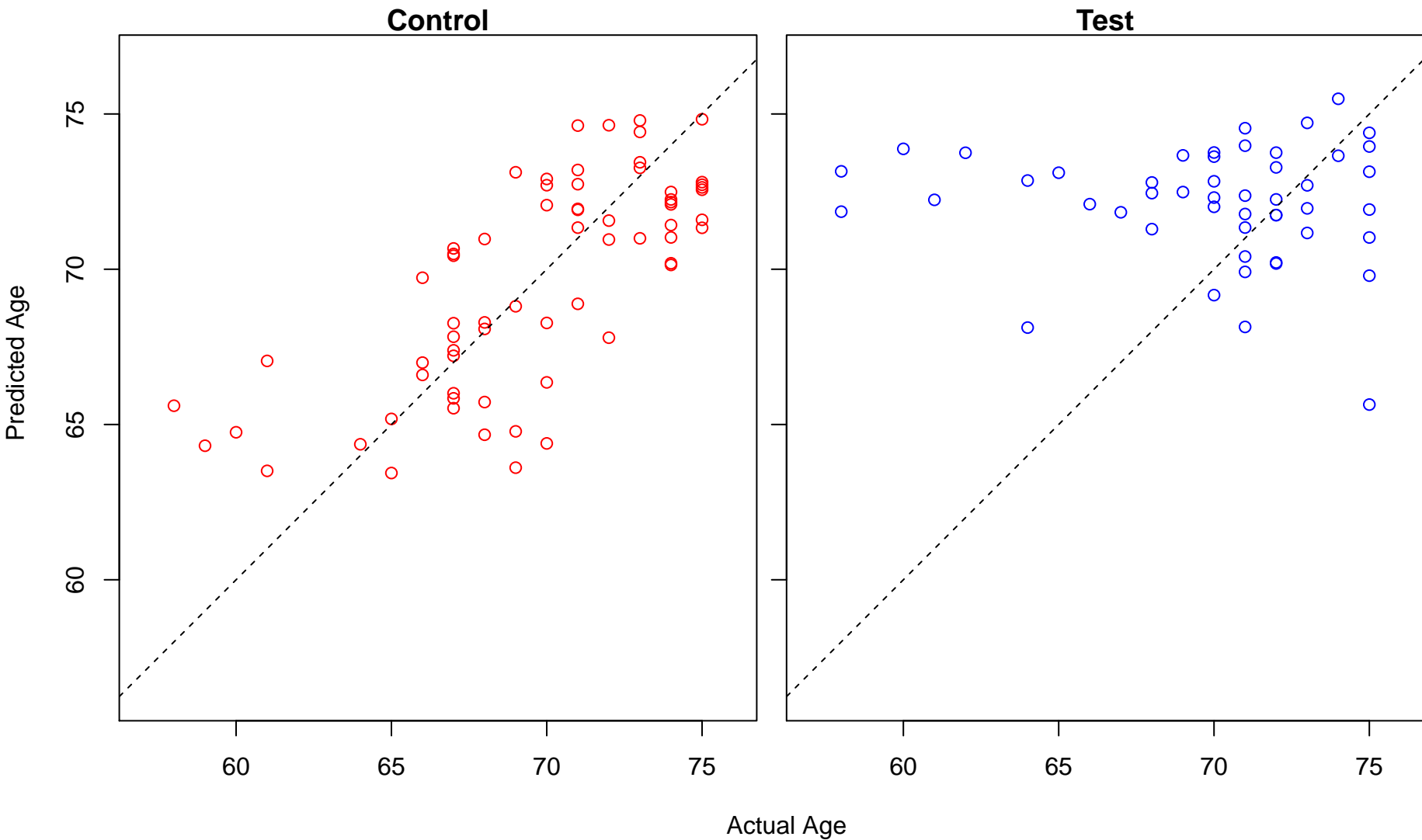


Test

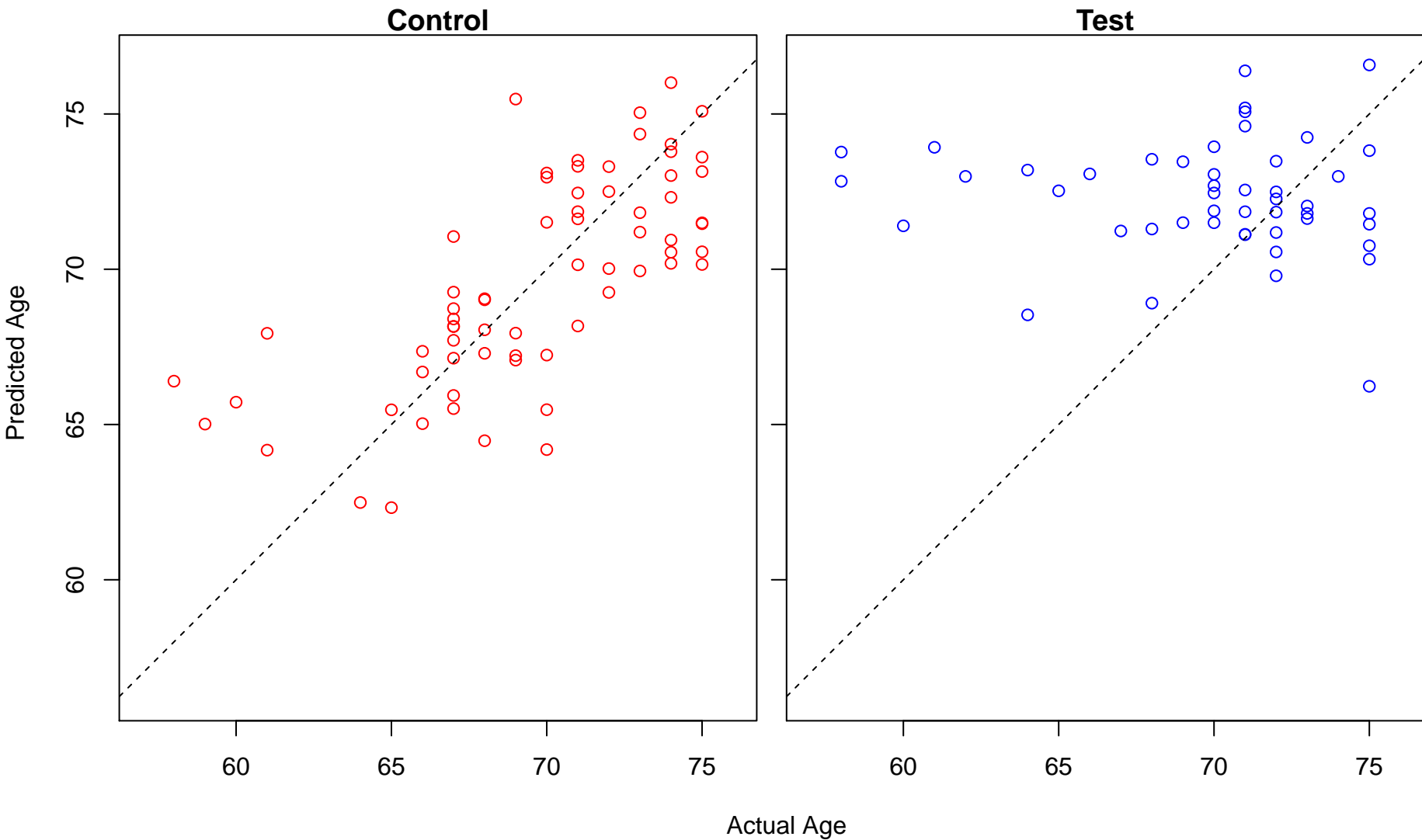


Actual Age

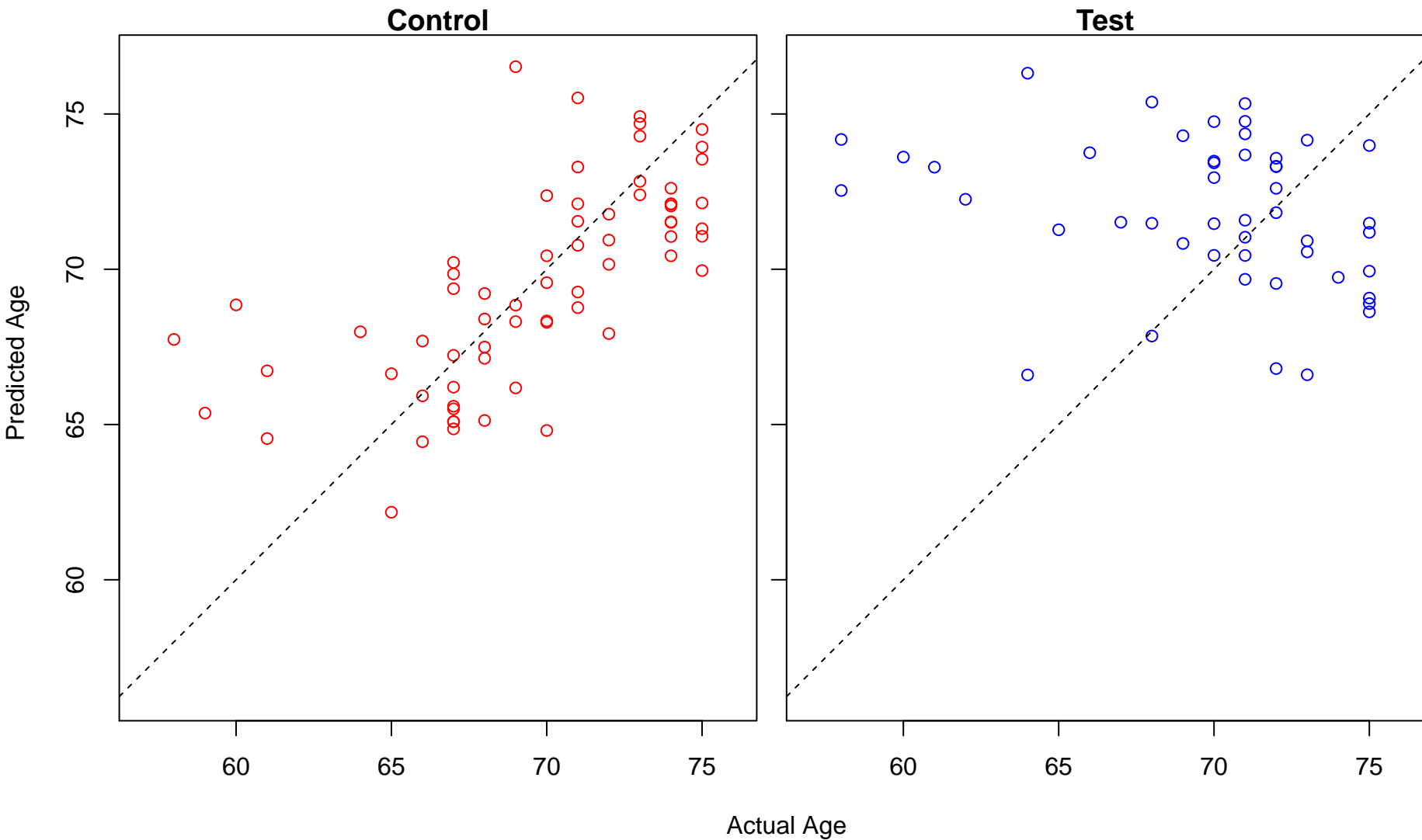
phosphatidylinositol-mediated signaling (Score: 1.646439)



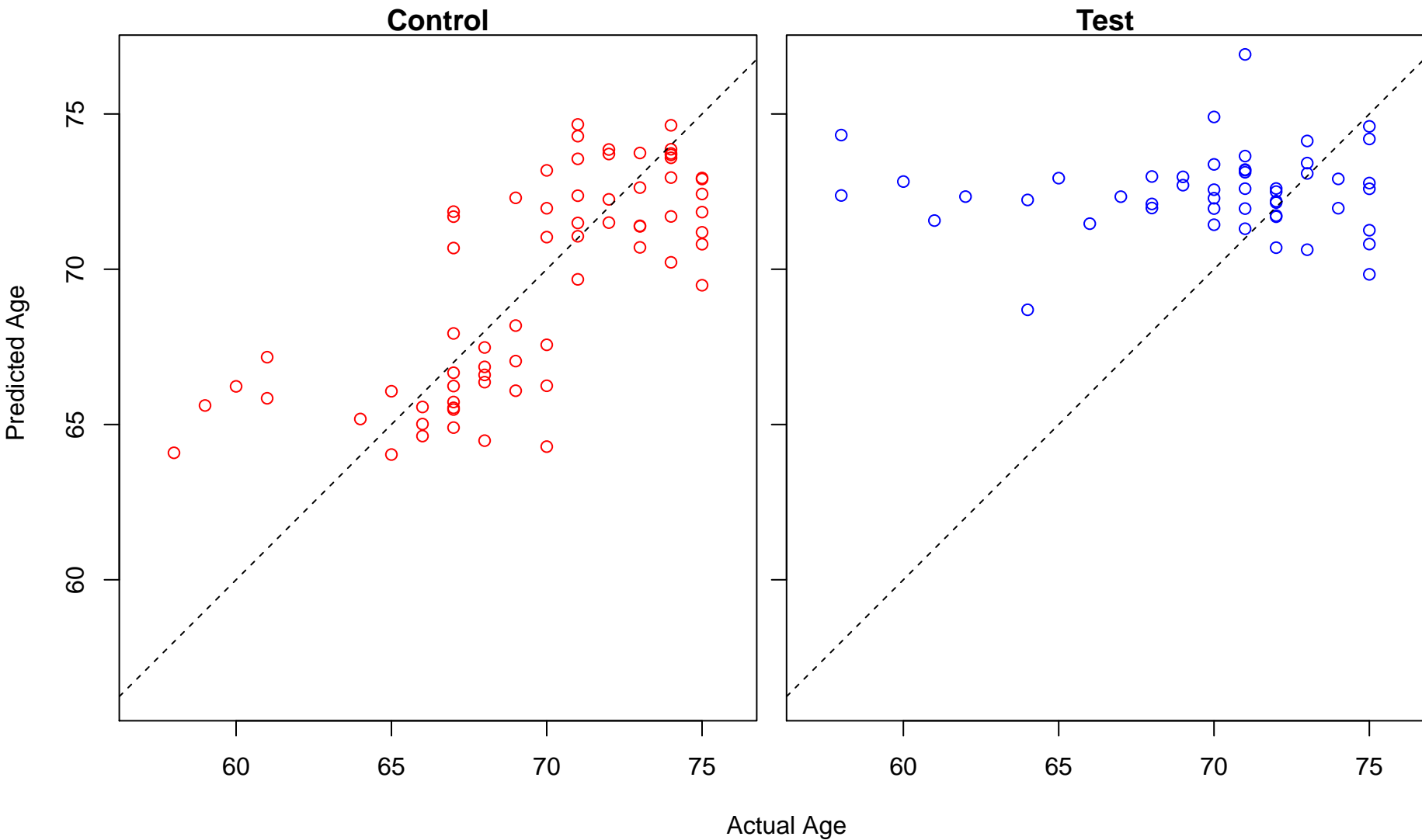
anatomical structure formation involved in morphogenesis (Score: 1.646202)



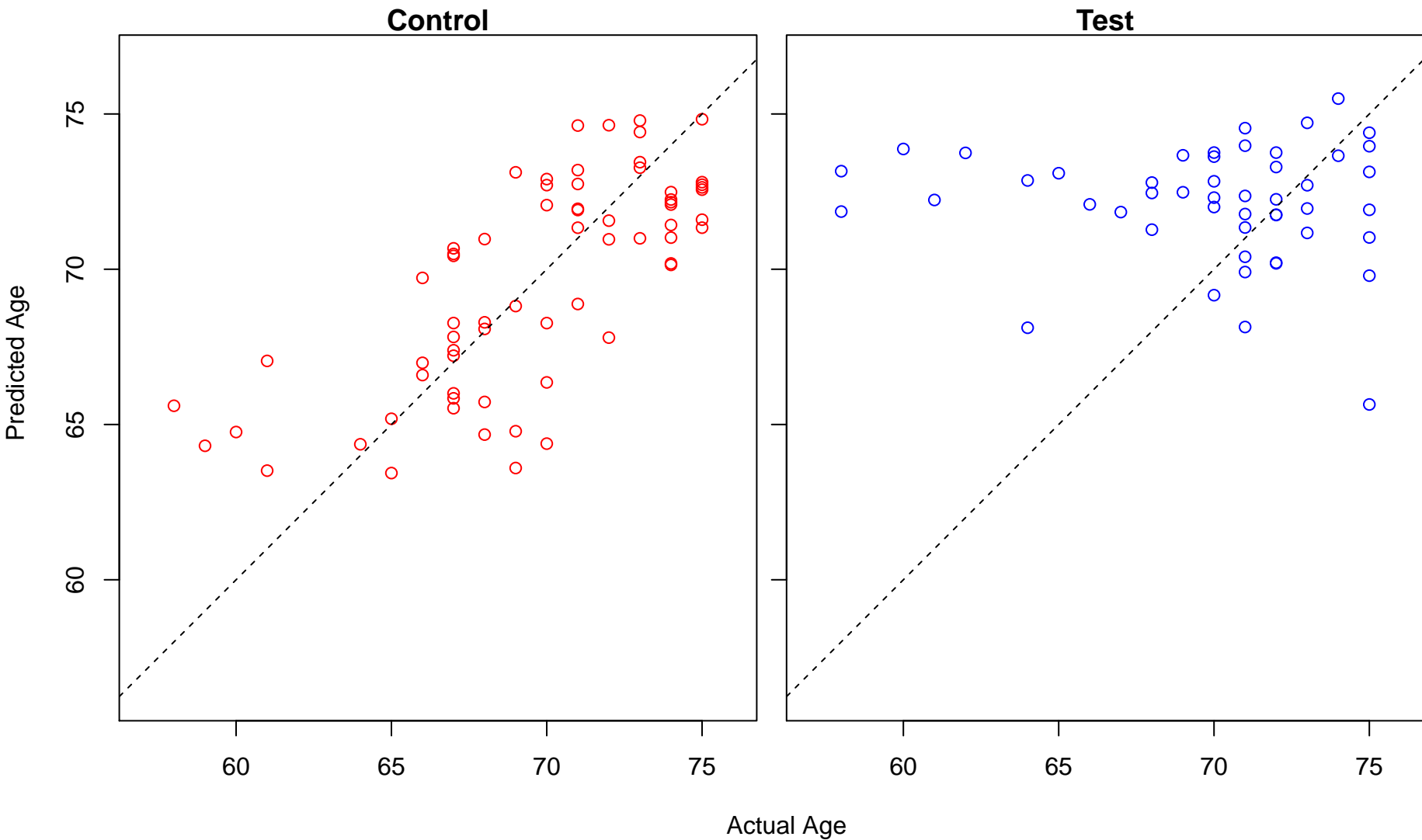
negative regulation of T cell activation (Score: 1.646055)



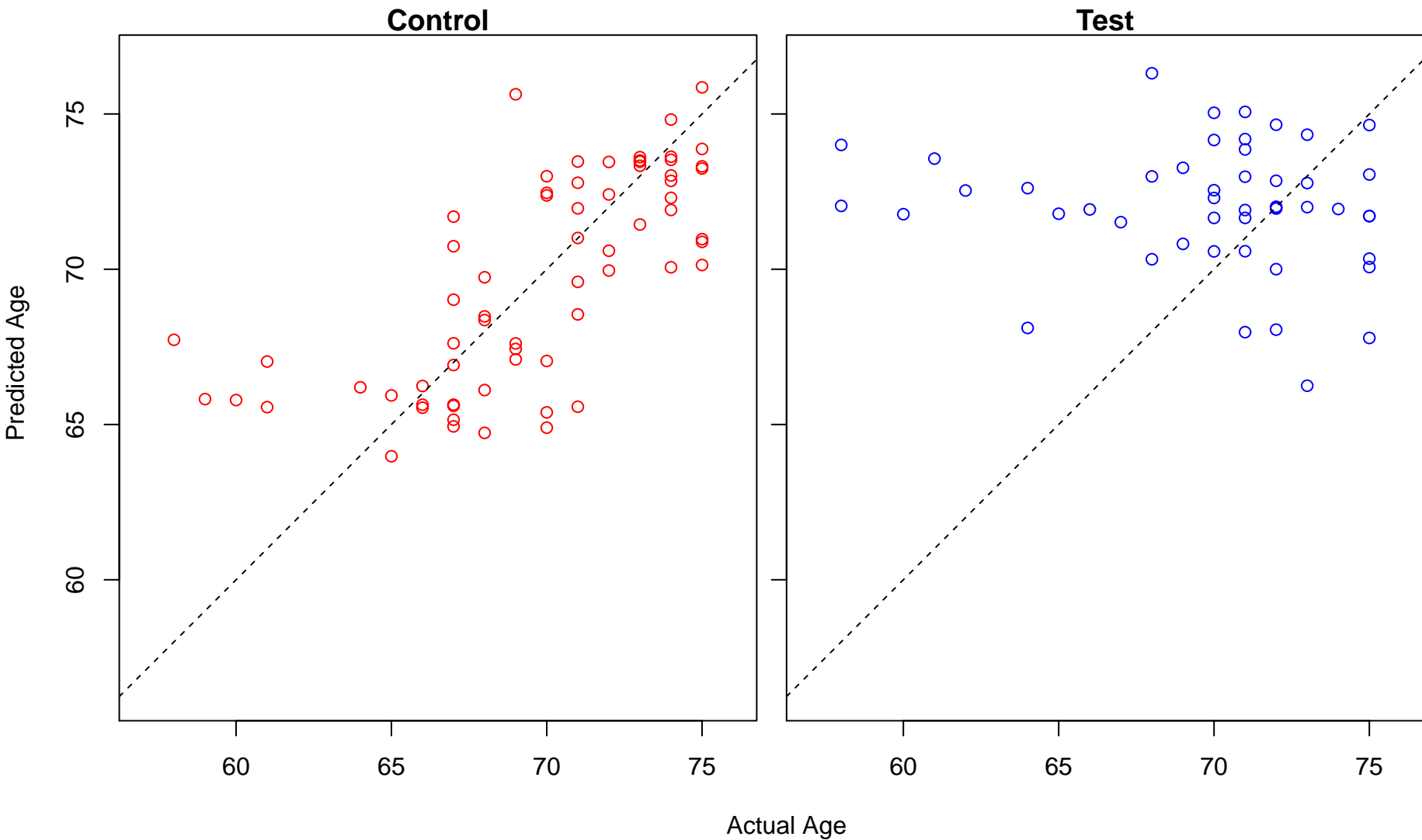
mRNA 3'-end processing (Score: 1.645722)



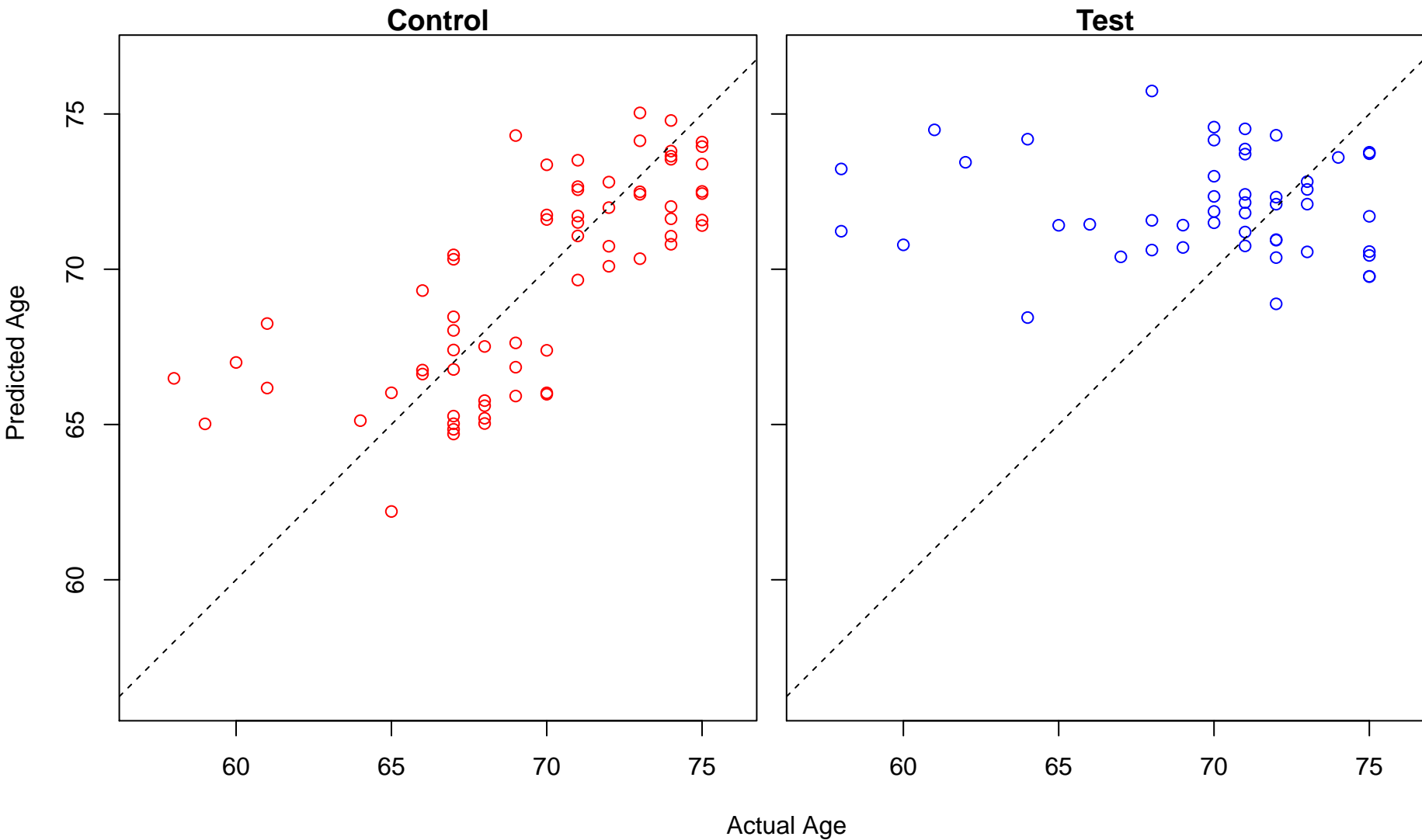
inositol lipid-mediated signaling (Score: 1.645707)



immune system development (Score: 1.645491)

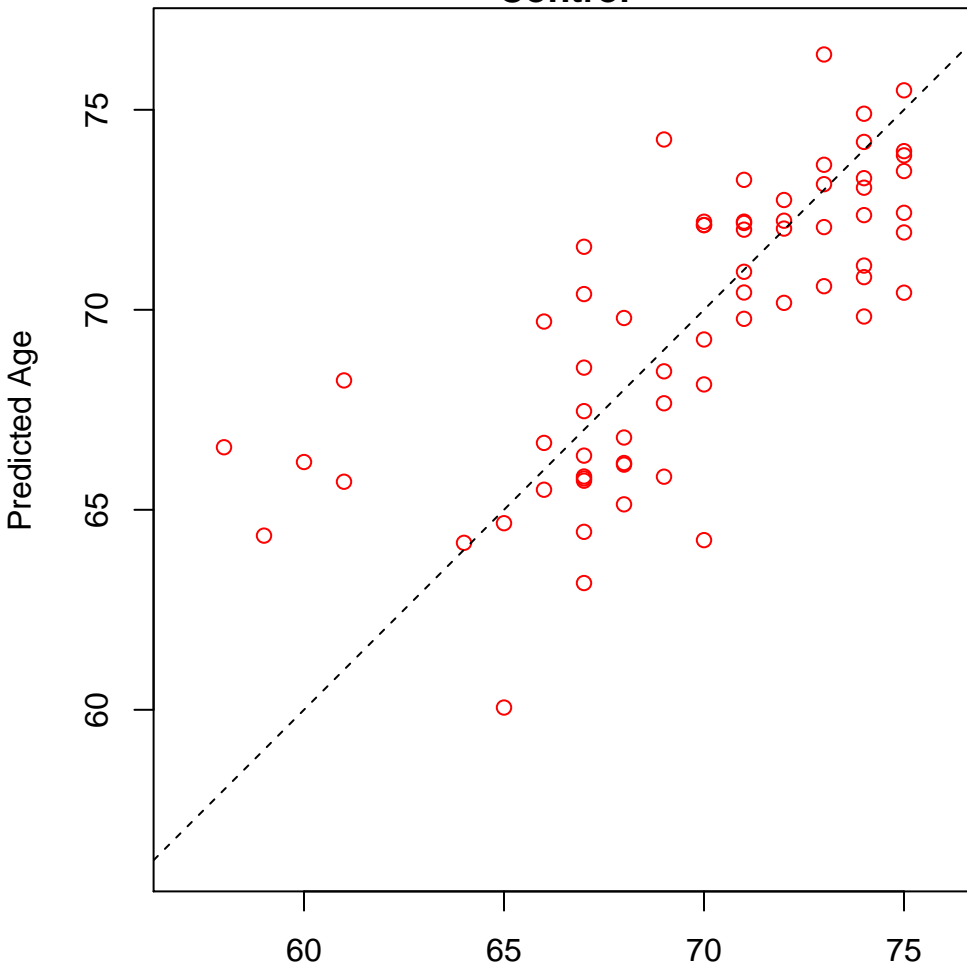


regulation of cellular amino acid metabolic process (Score: 1.645193)

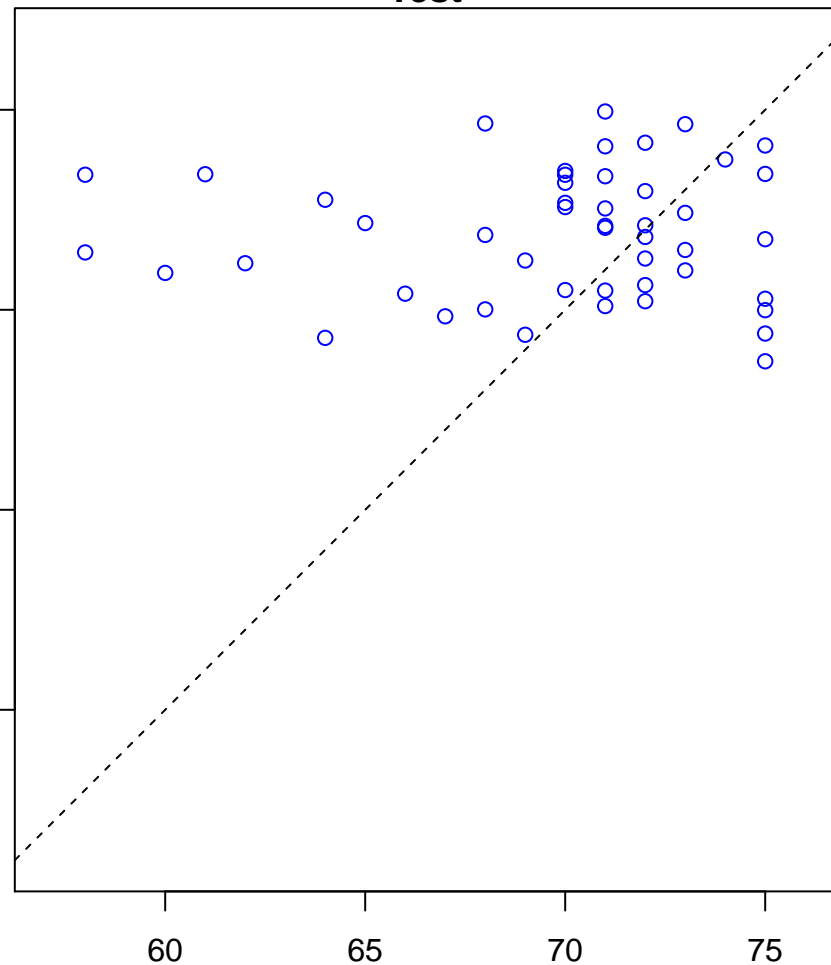


G1/S transition of mitotic cell cycle (Score: 1.644851)

Control

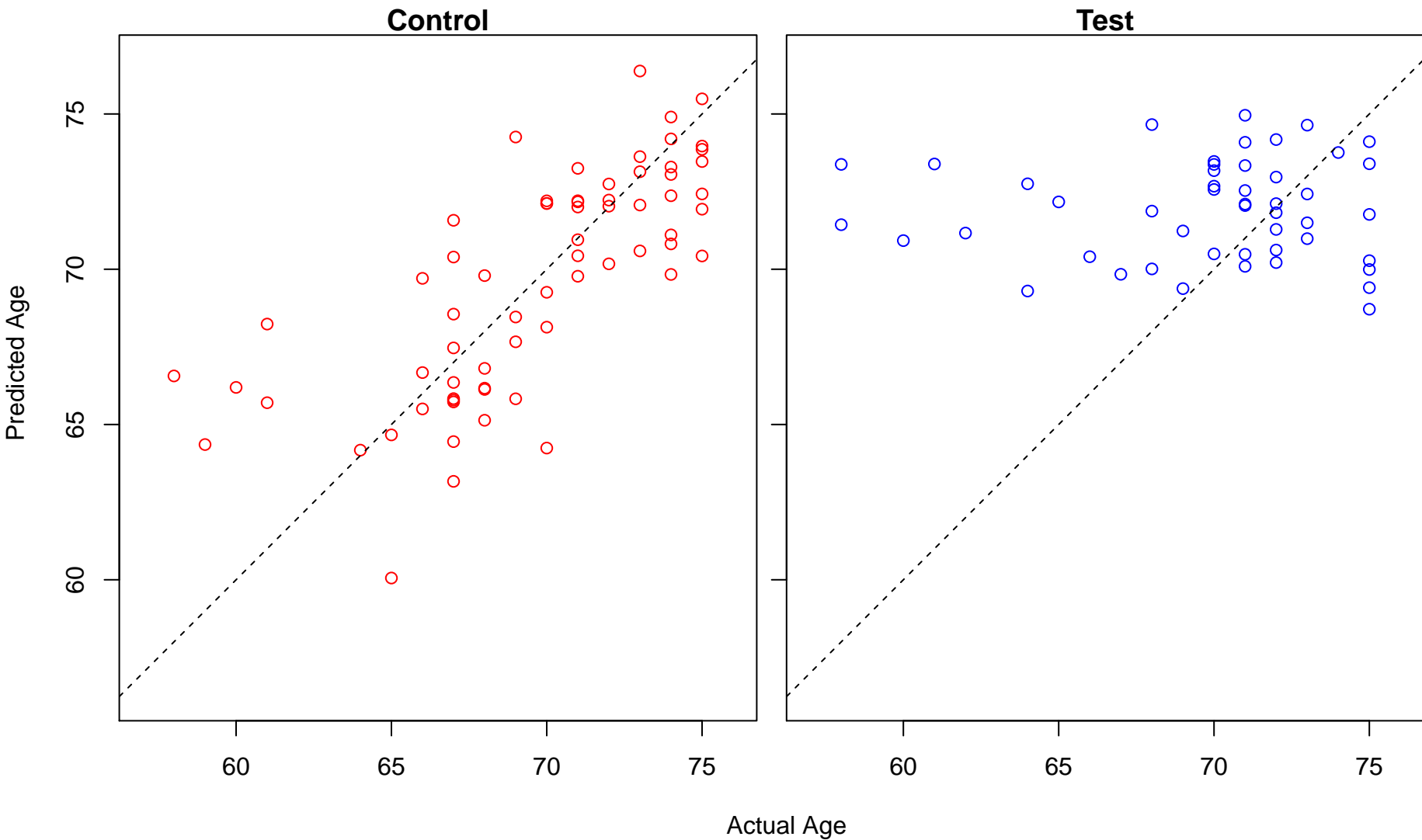


Test

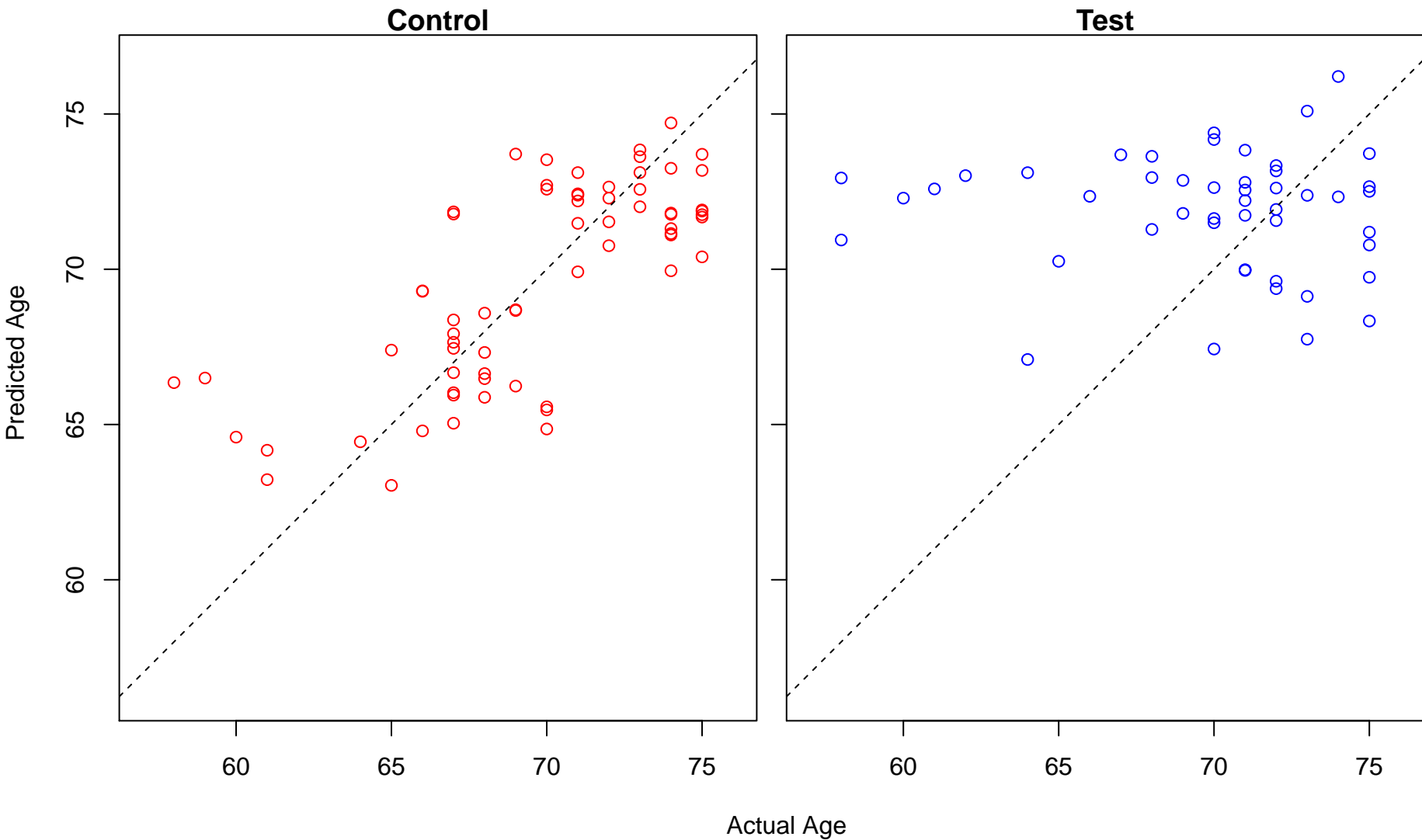


Actual Age

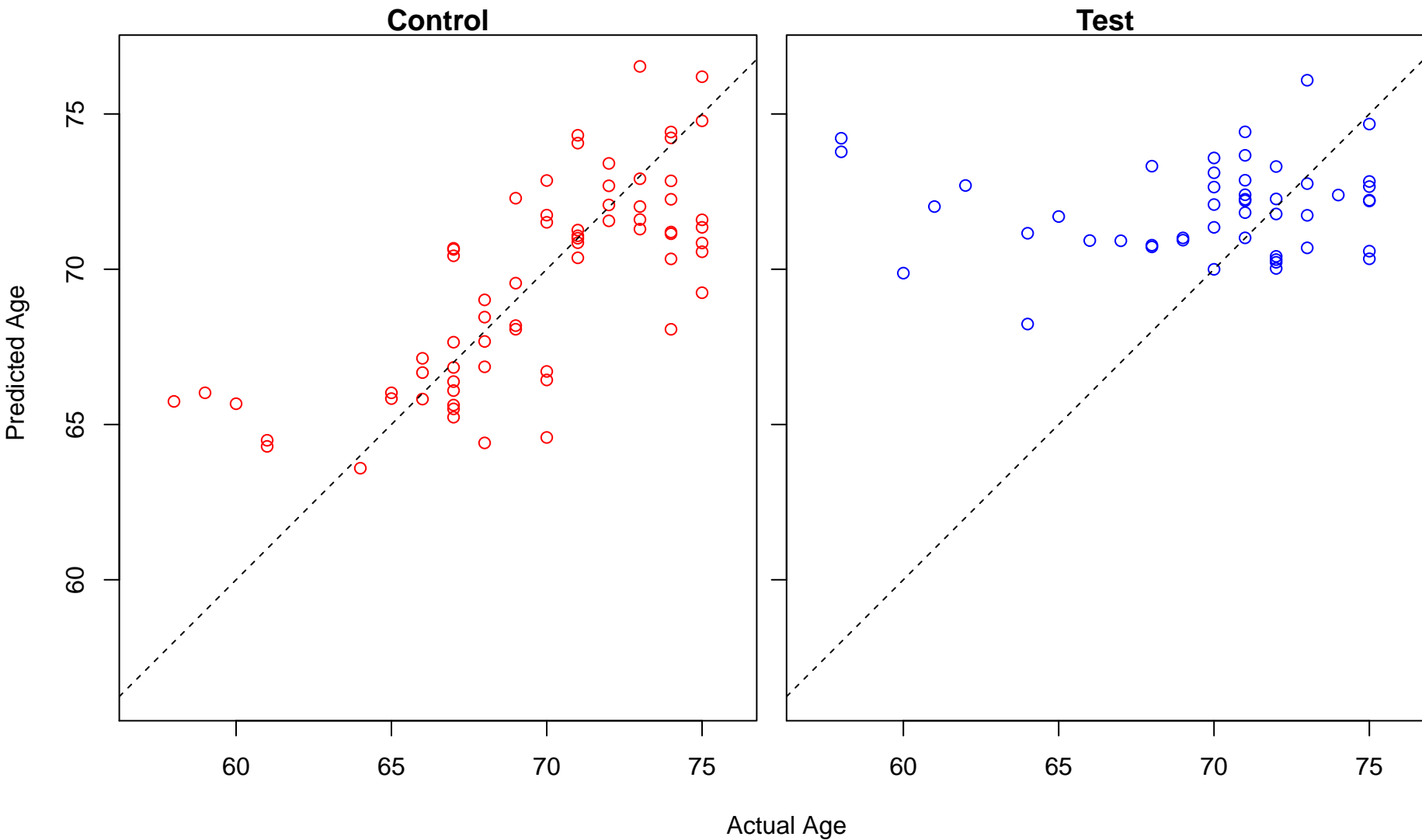
cell cycle G1/S phase transition (Score: 1.644851)



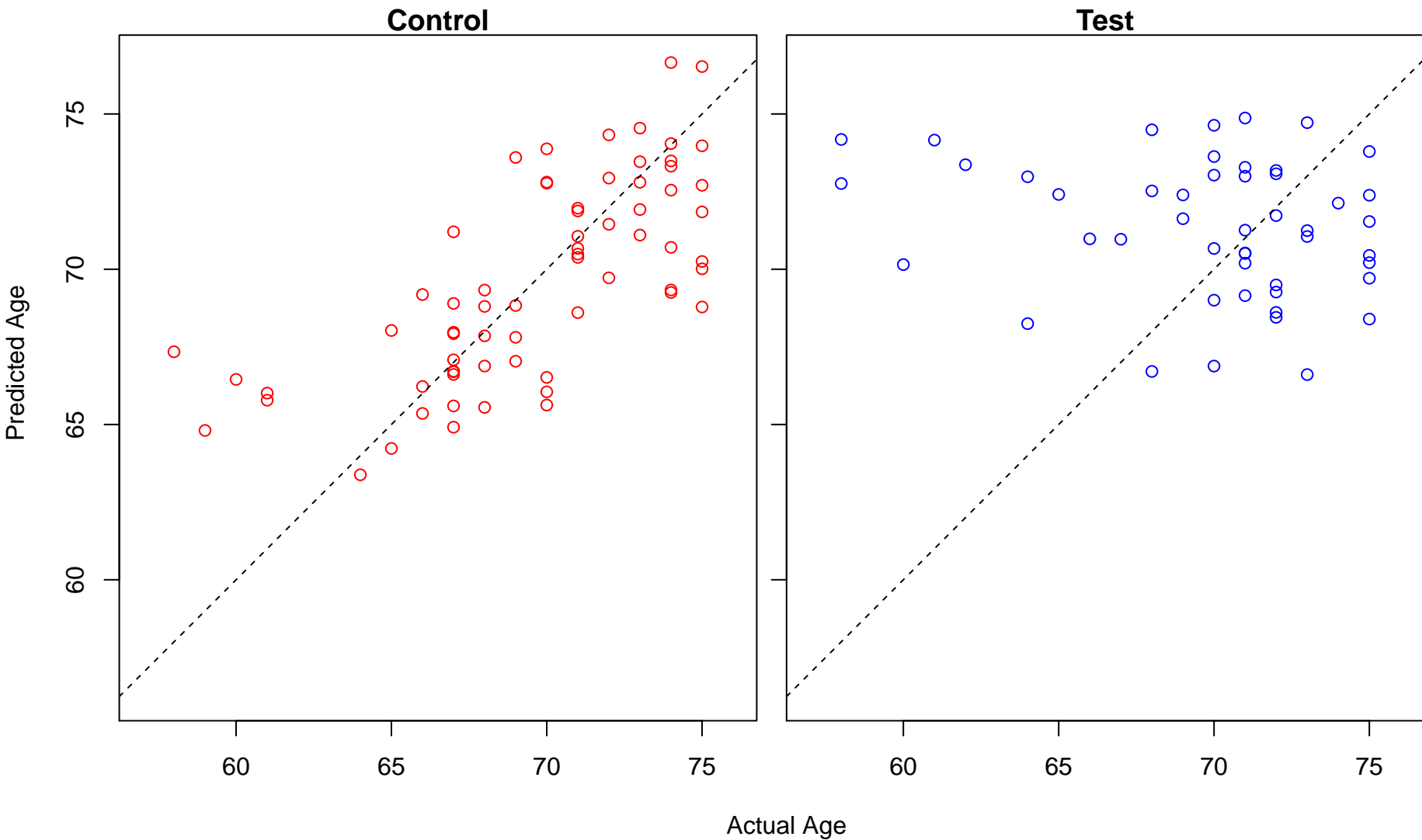
virion assembly (Score: 1.644722)



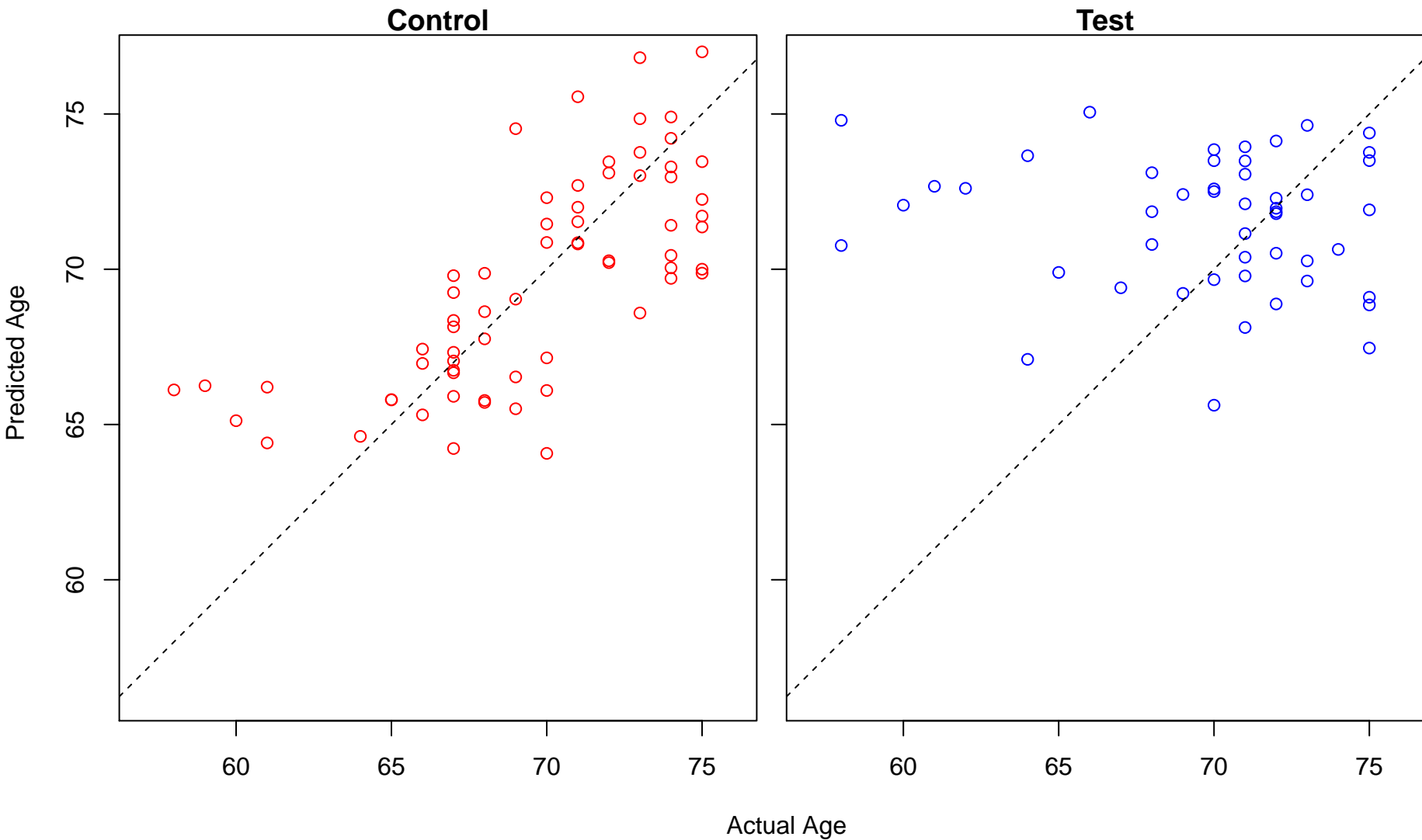
regulation of actin filament-based process (Score: 1.644691)



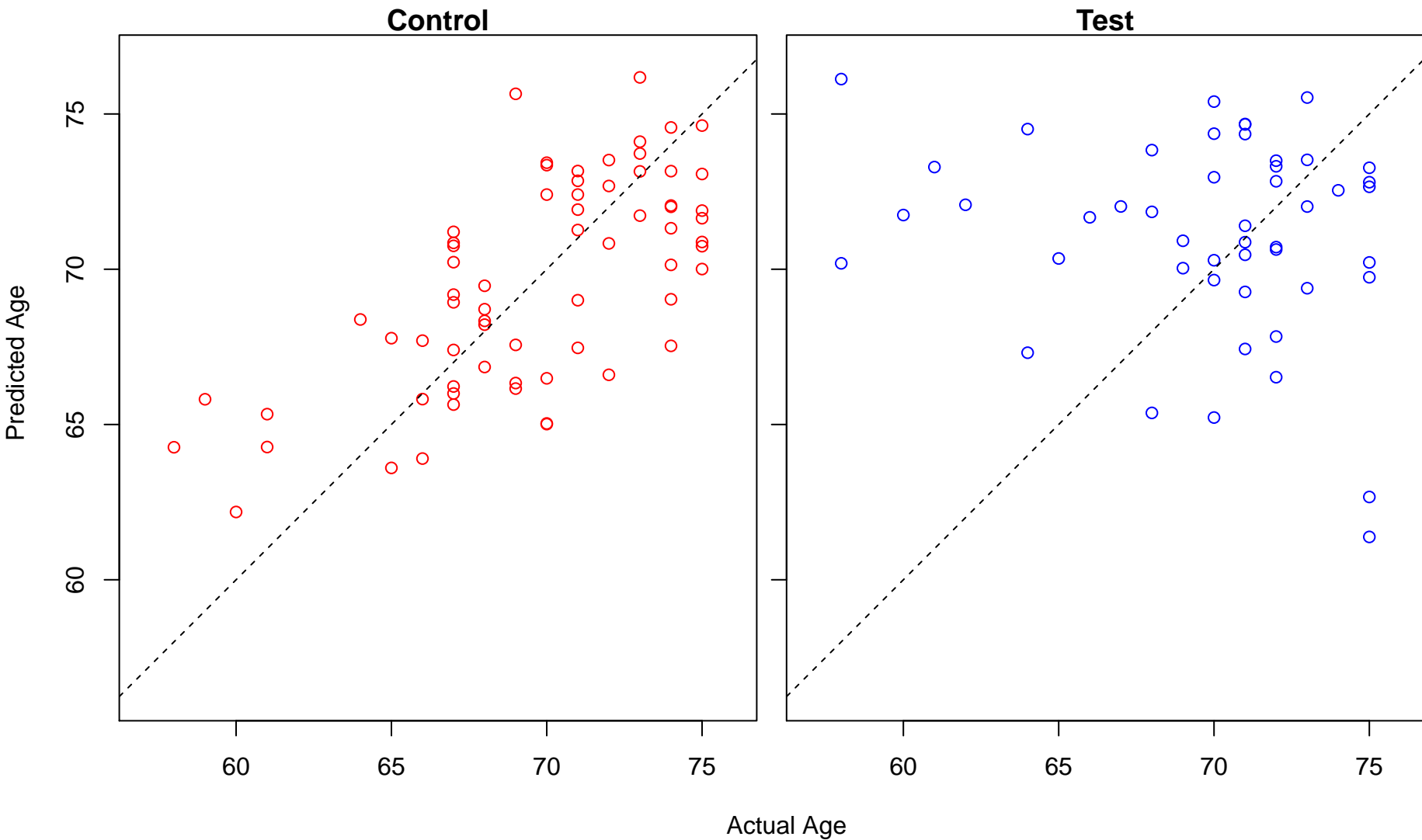
positive regulation of protein localization to nucleus (Score: 1.644611)



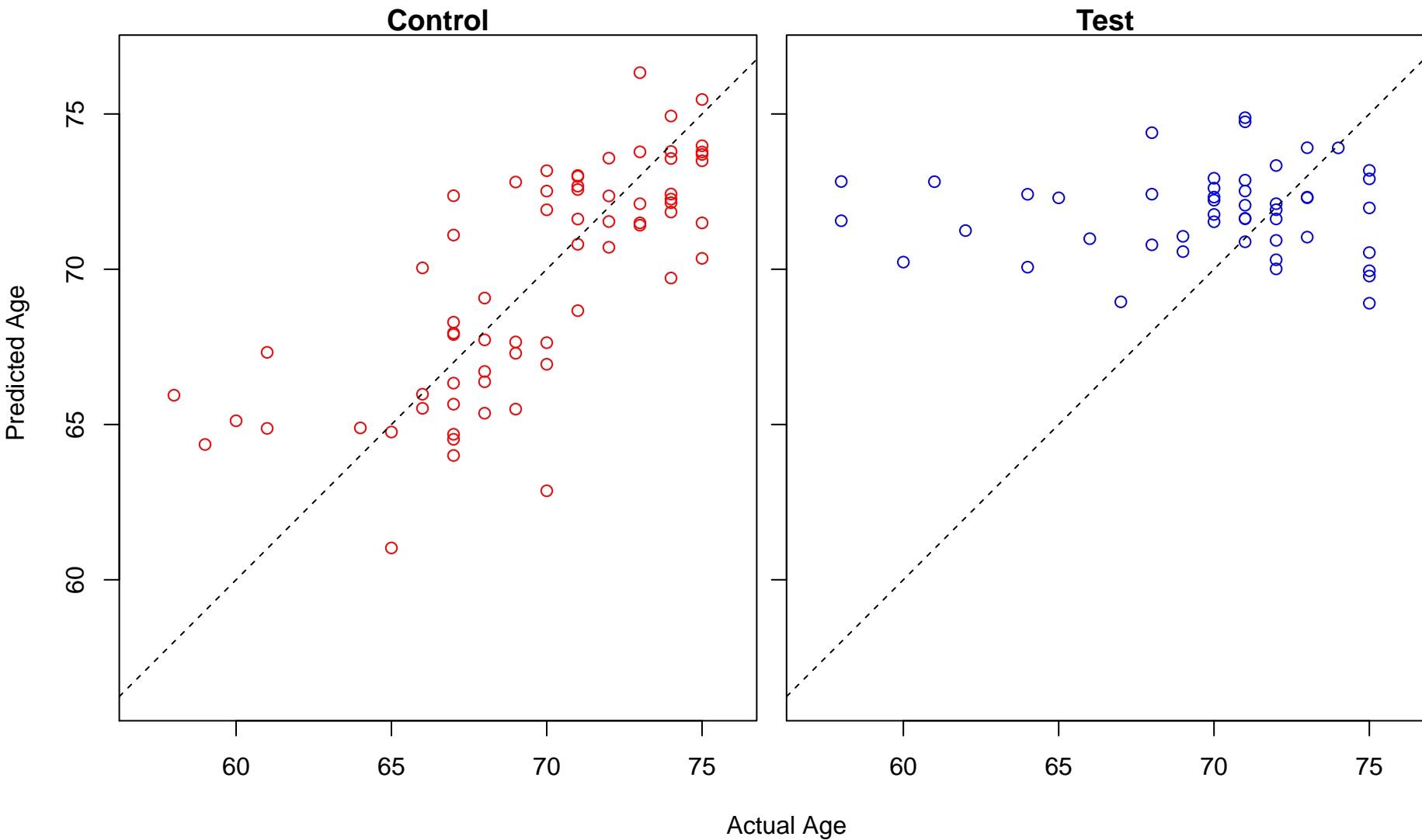
lipid oxidation (Score: 1.644542)



positive regulation of cation channel activity (Score: 1.643874)

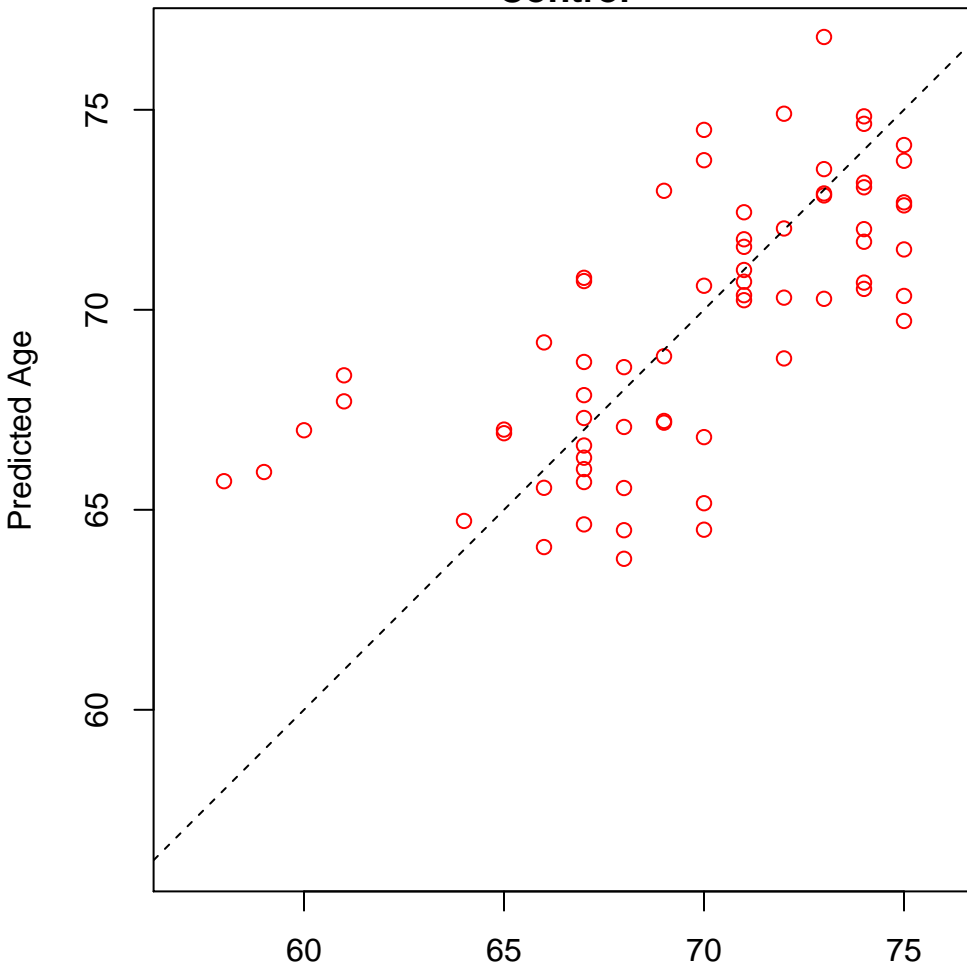


mitotic DNA integrity checkpoint (Score: 1.643145)

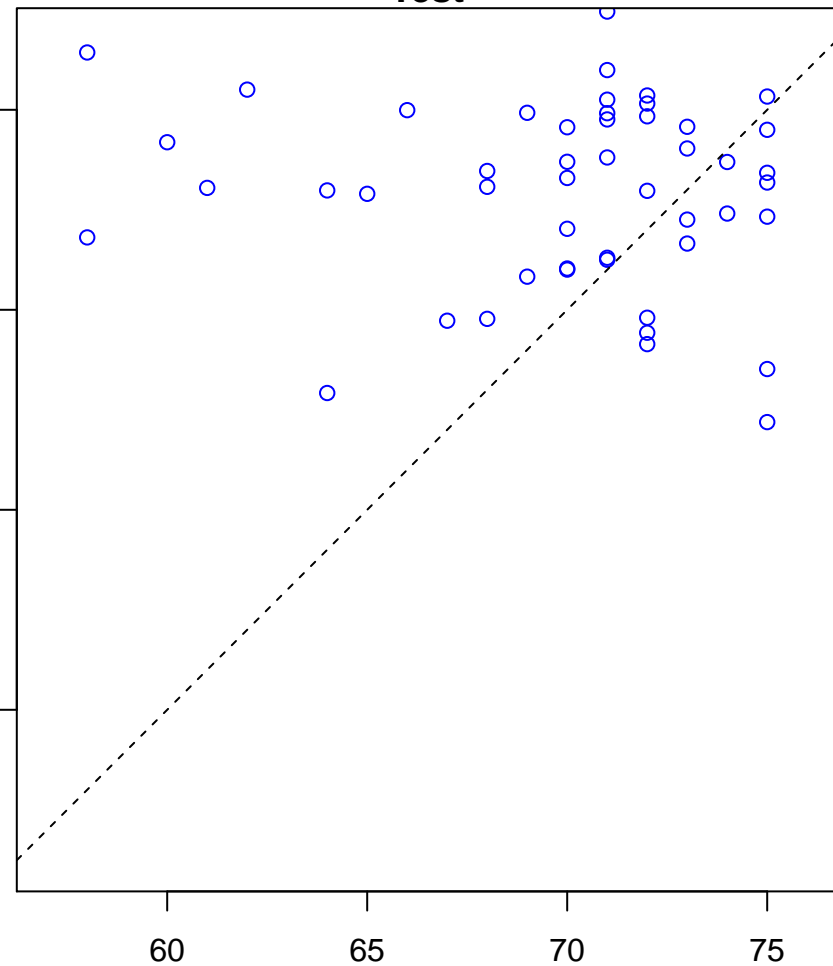


regulation of endothelial cell migration (Score: 1.642946)

Control

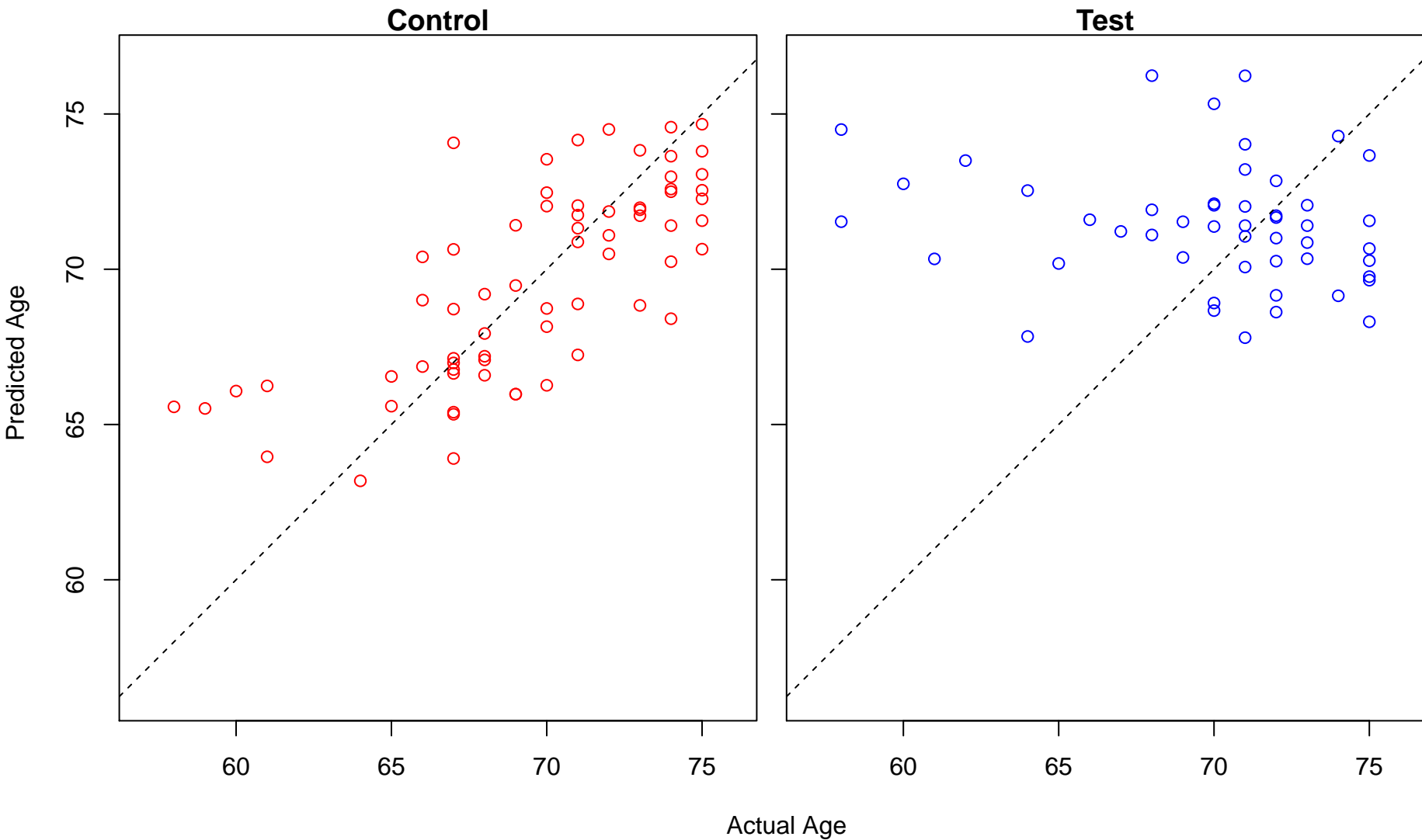


Test

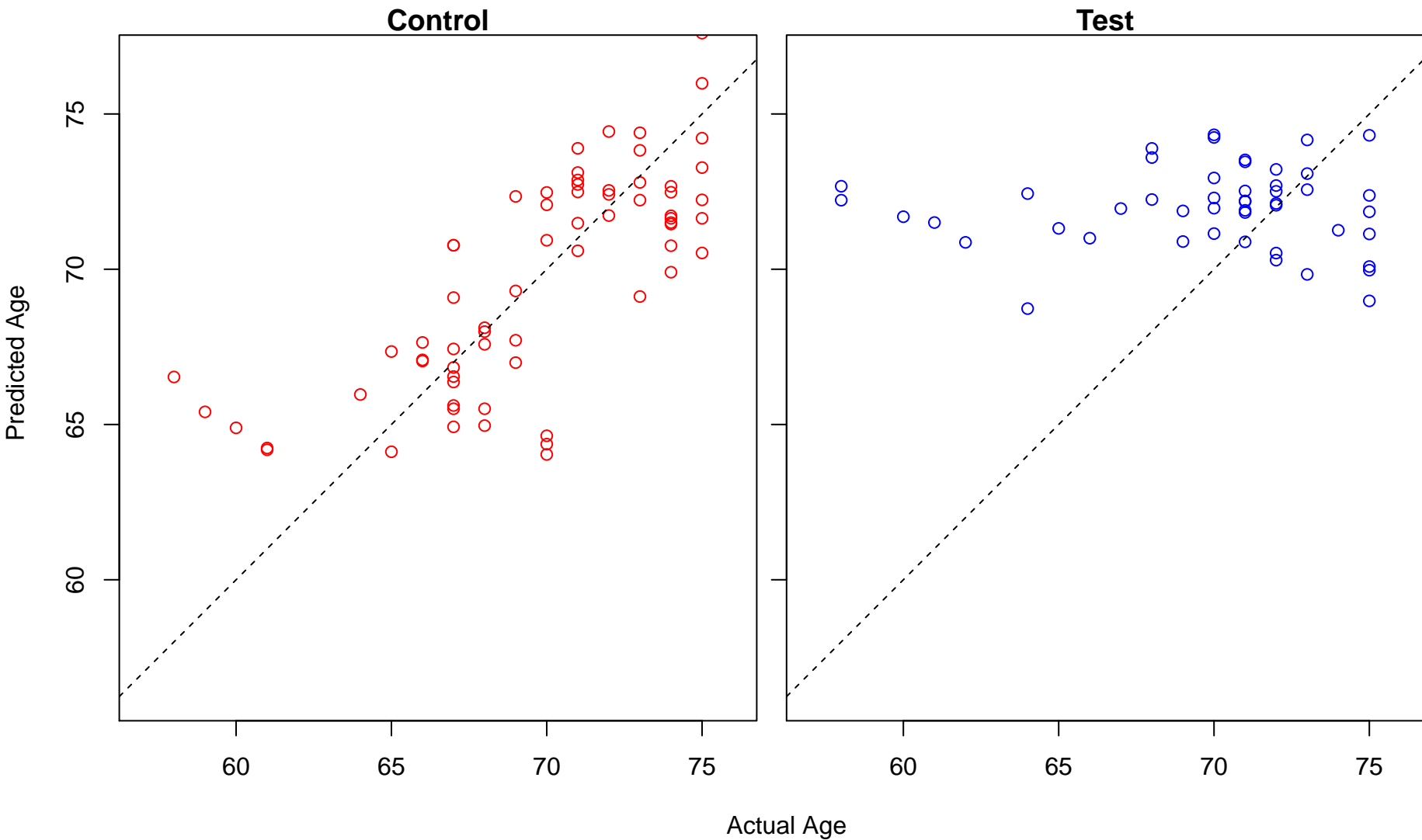


Actual Age

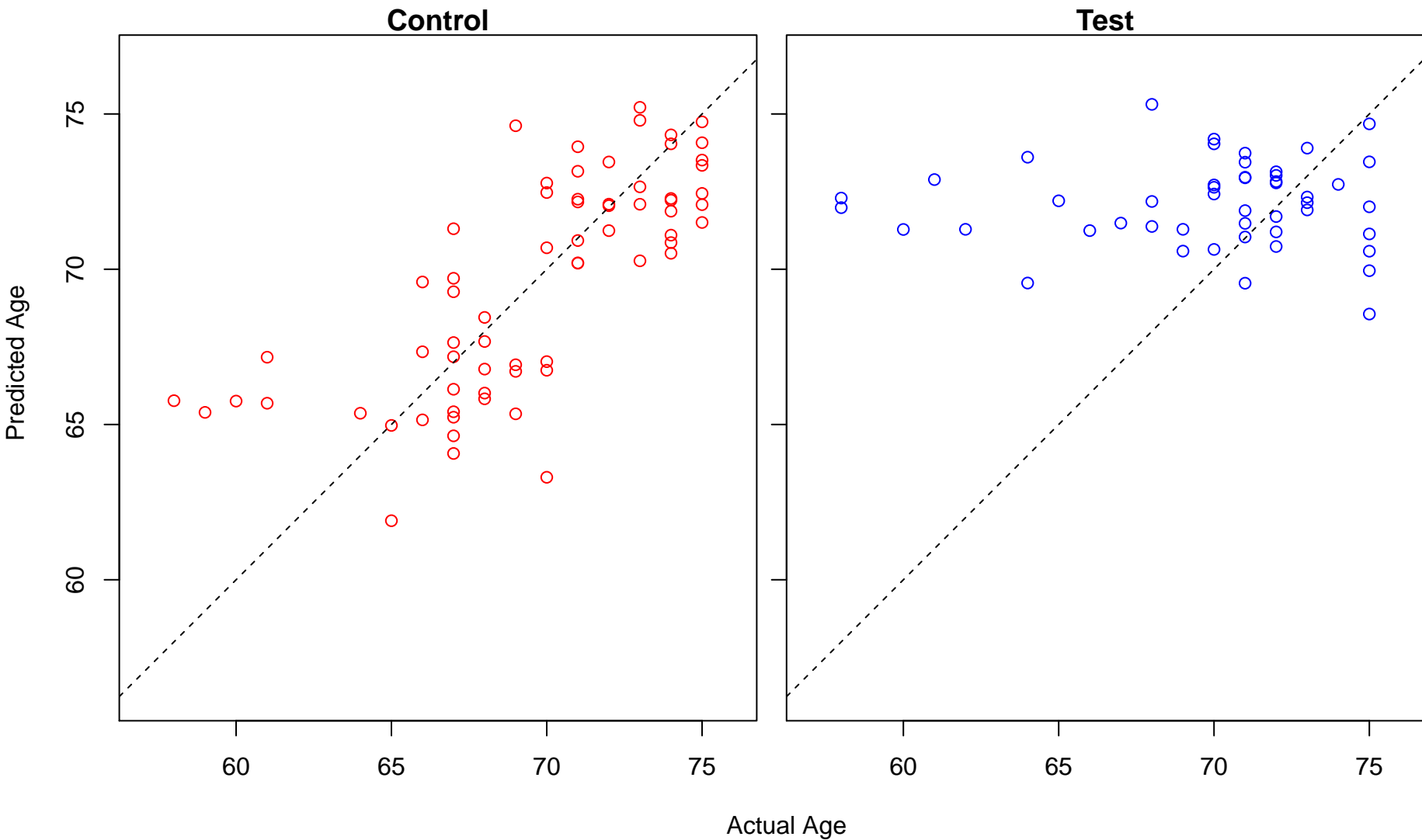
apoptotic chromosome condensation (Score: 1.642919)



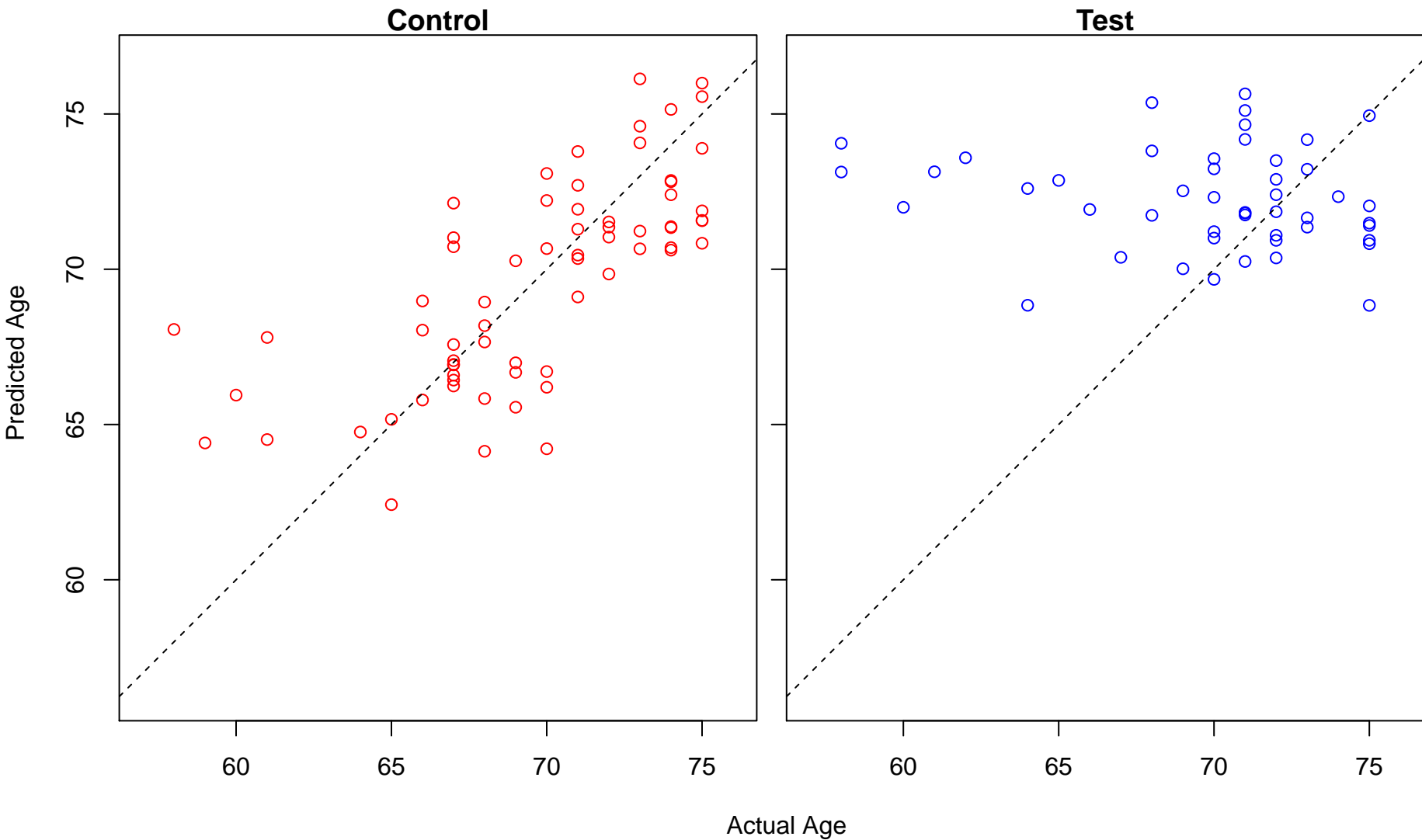
glycolipid biosynthetic process (Score: 1.642376)



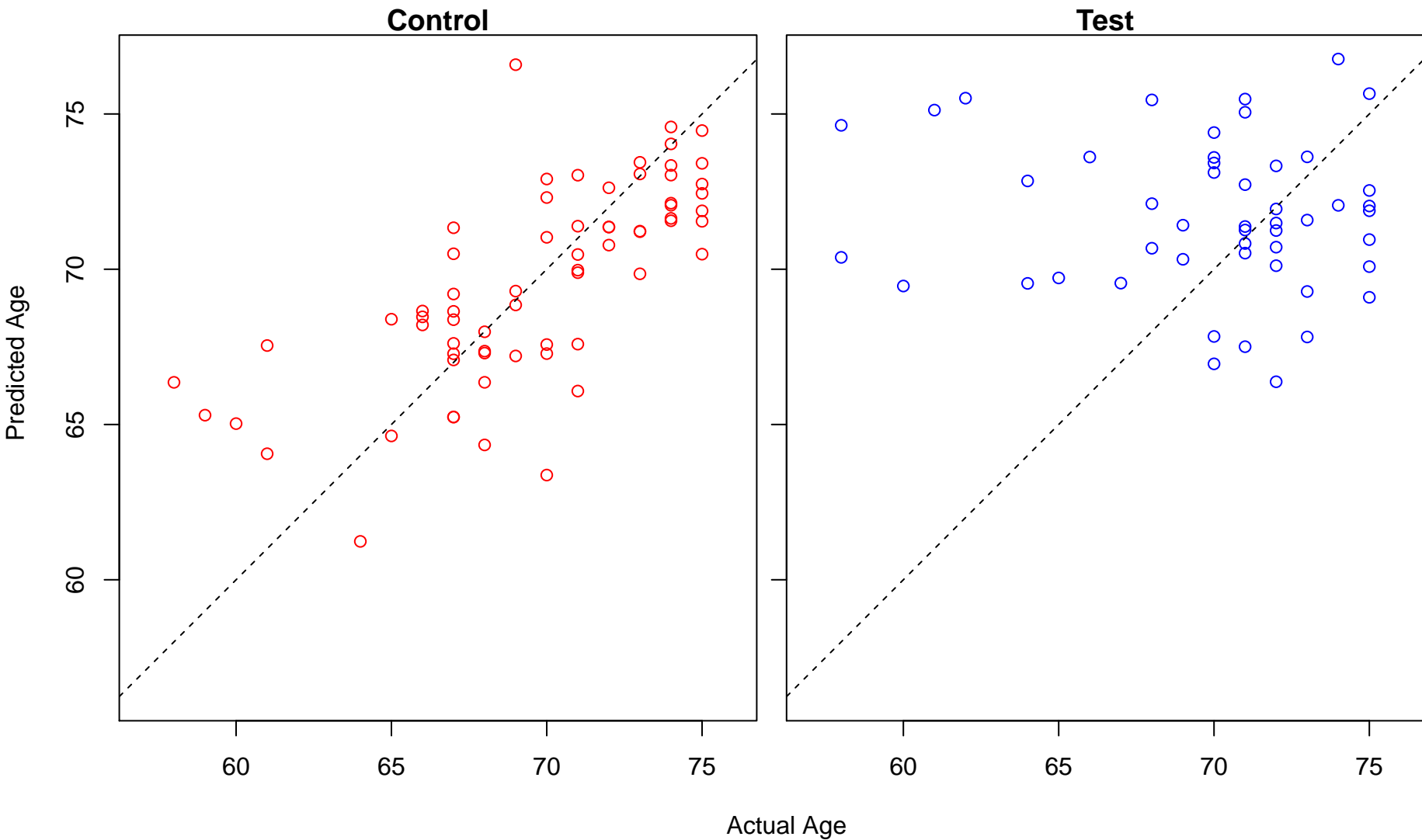
positive regulation of cellular protein catabolic process (Score: 1.642168)



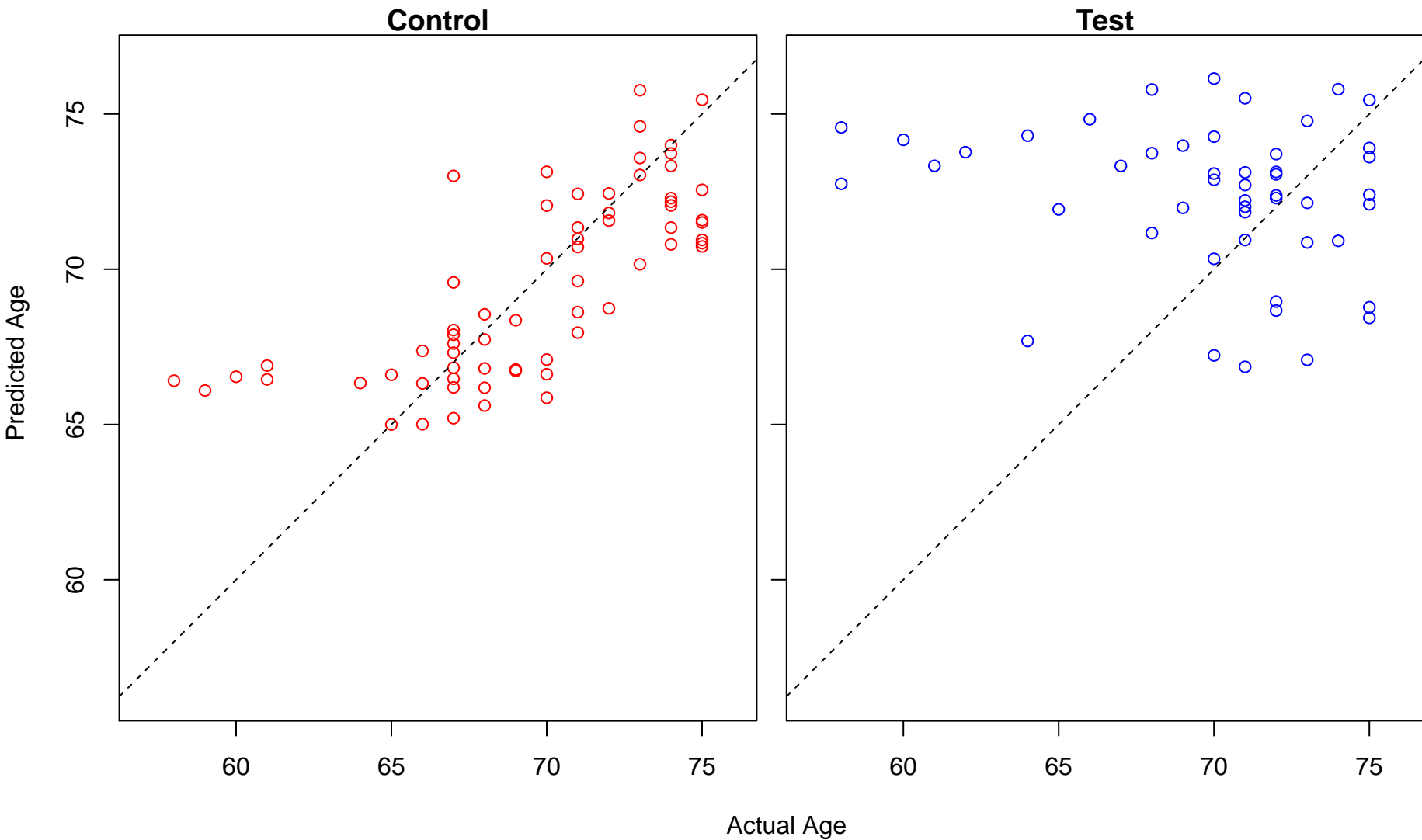
regulation of GTPase activity (Score: 1.642088)



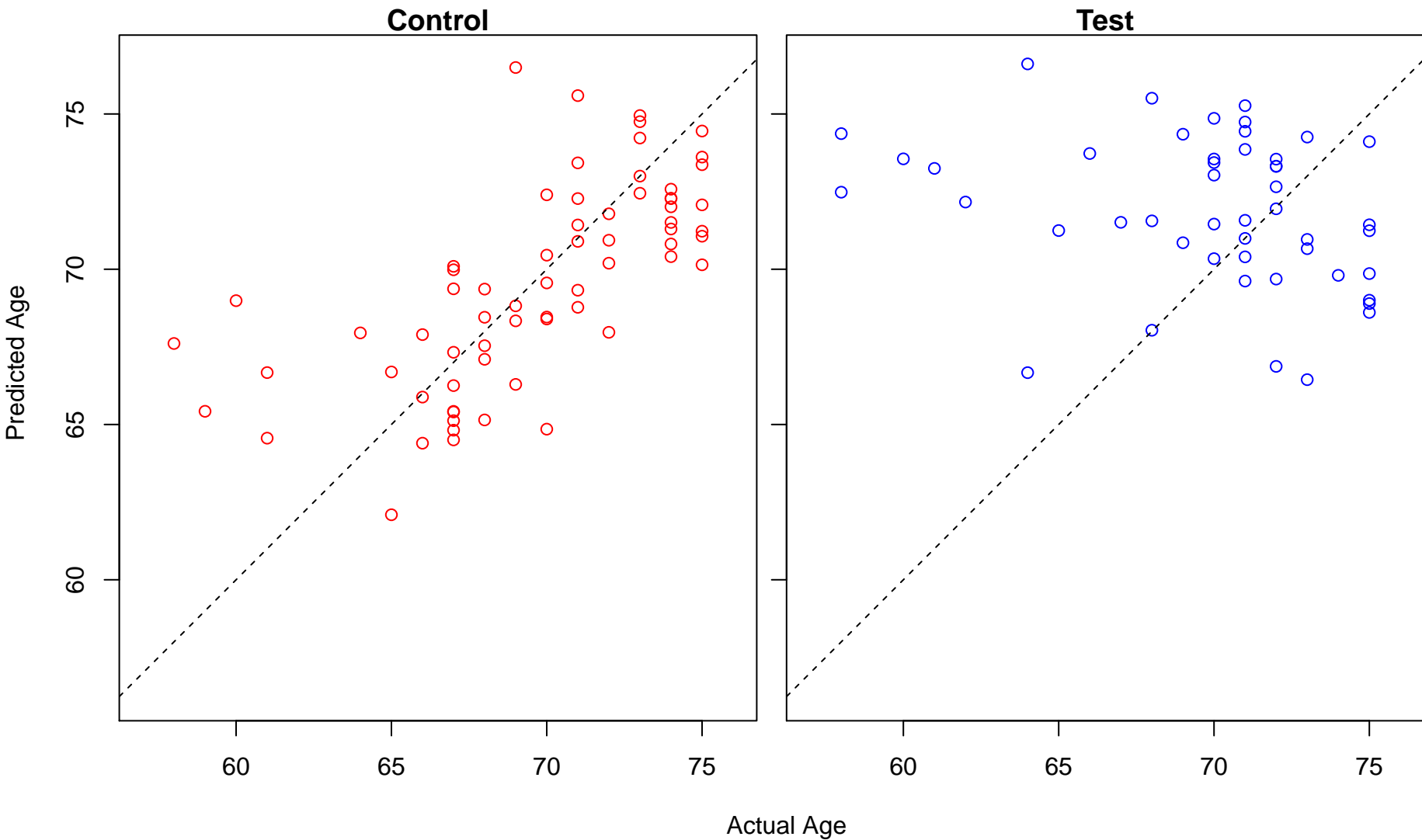
regulation of mitochondrial membrane potential (Score: 1.641837)



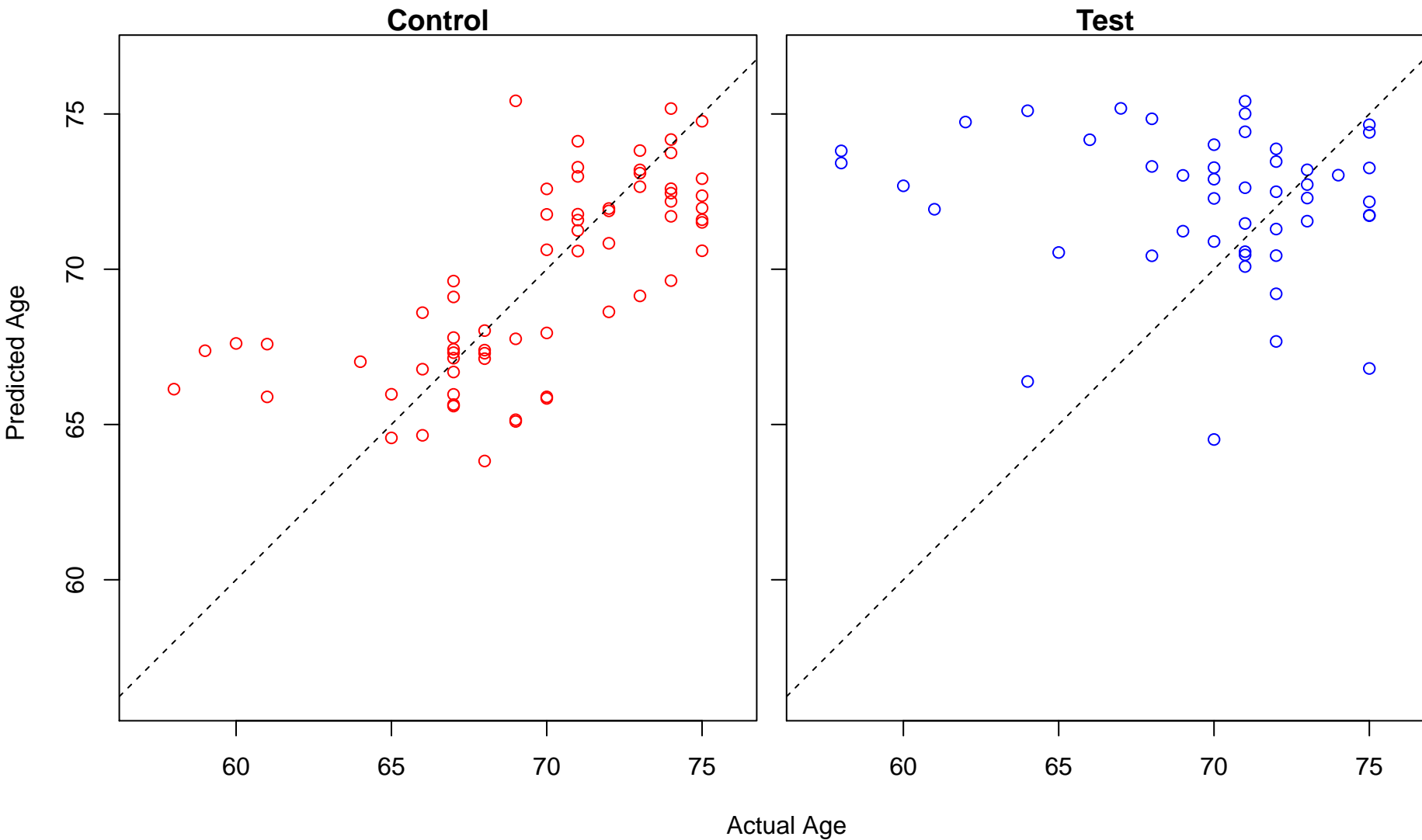
T cell differentiation (Score: 1.641662)



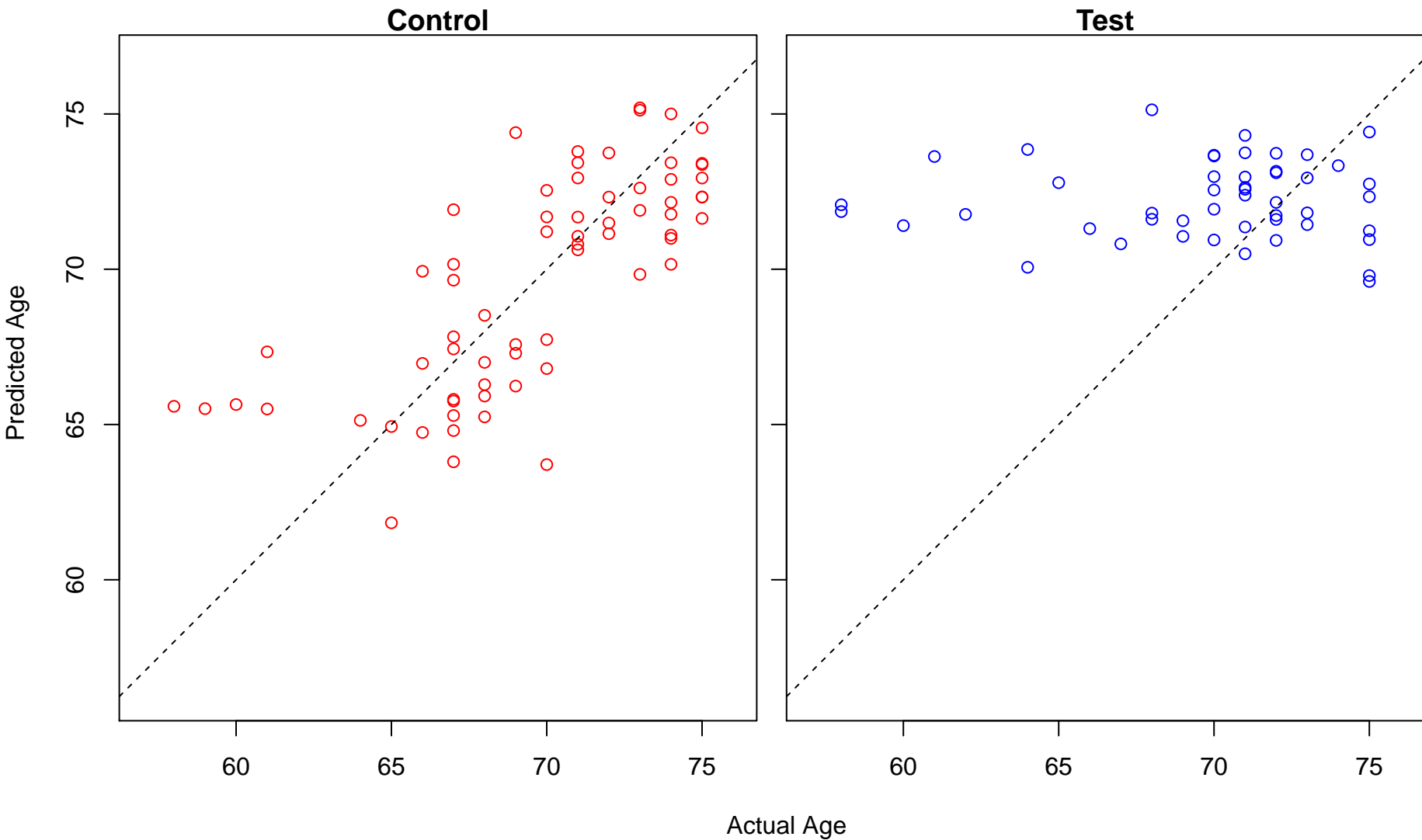
negative regulation of leukocyte cell-cell adhesion (Score: 1.641584)



regulation of monocyte chemotaxis (Score: 1.641482)

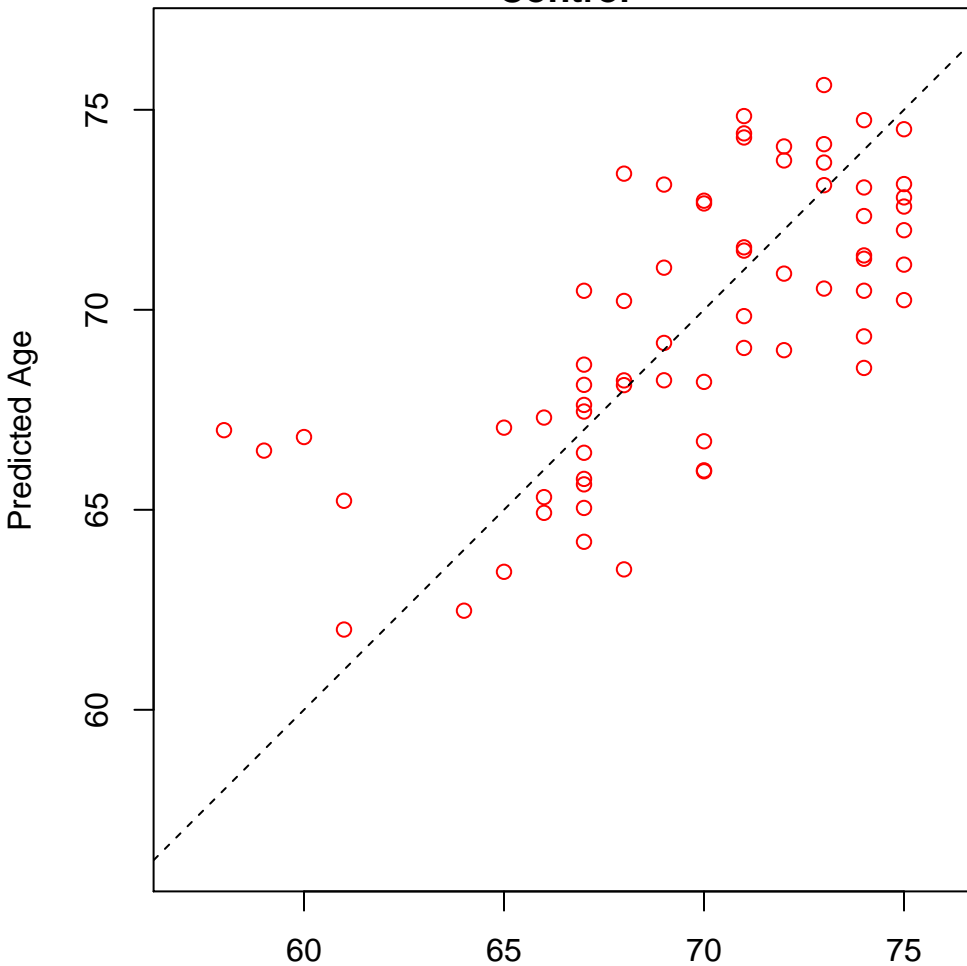


positive regulation of ligase activity (Score: 1.640381)

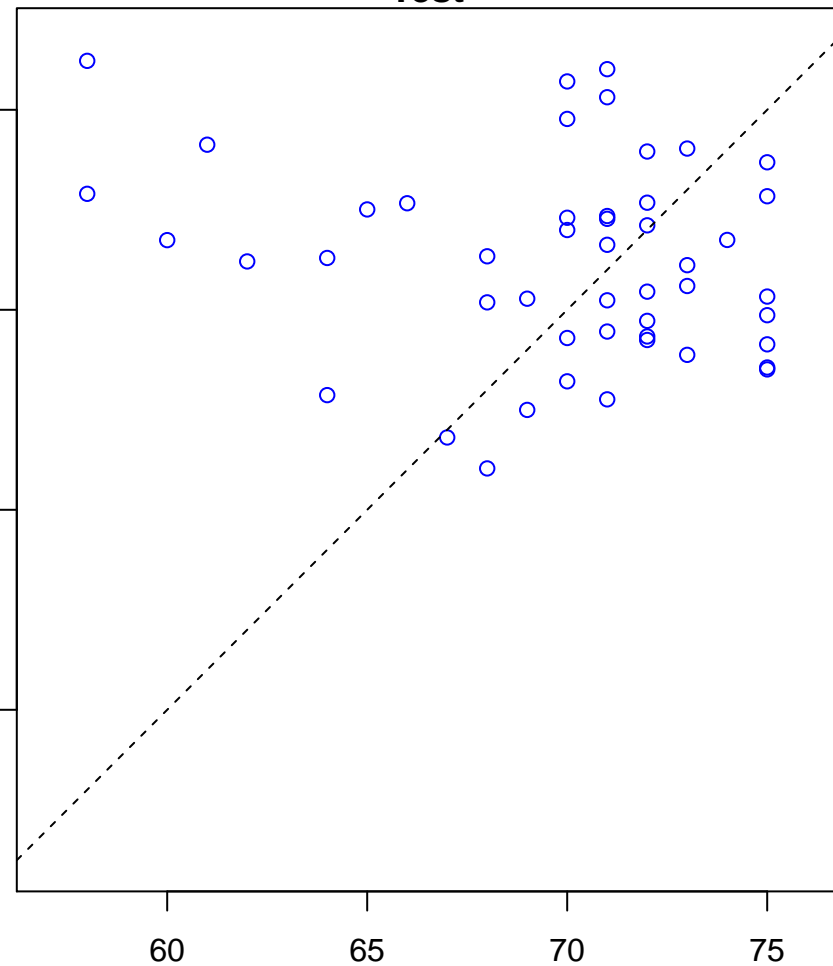


mitotic nuclear envelope disassembly (Score: 1.639103)

Control

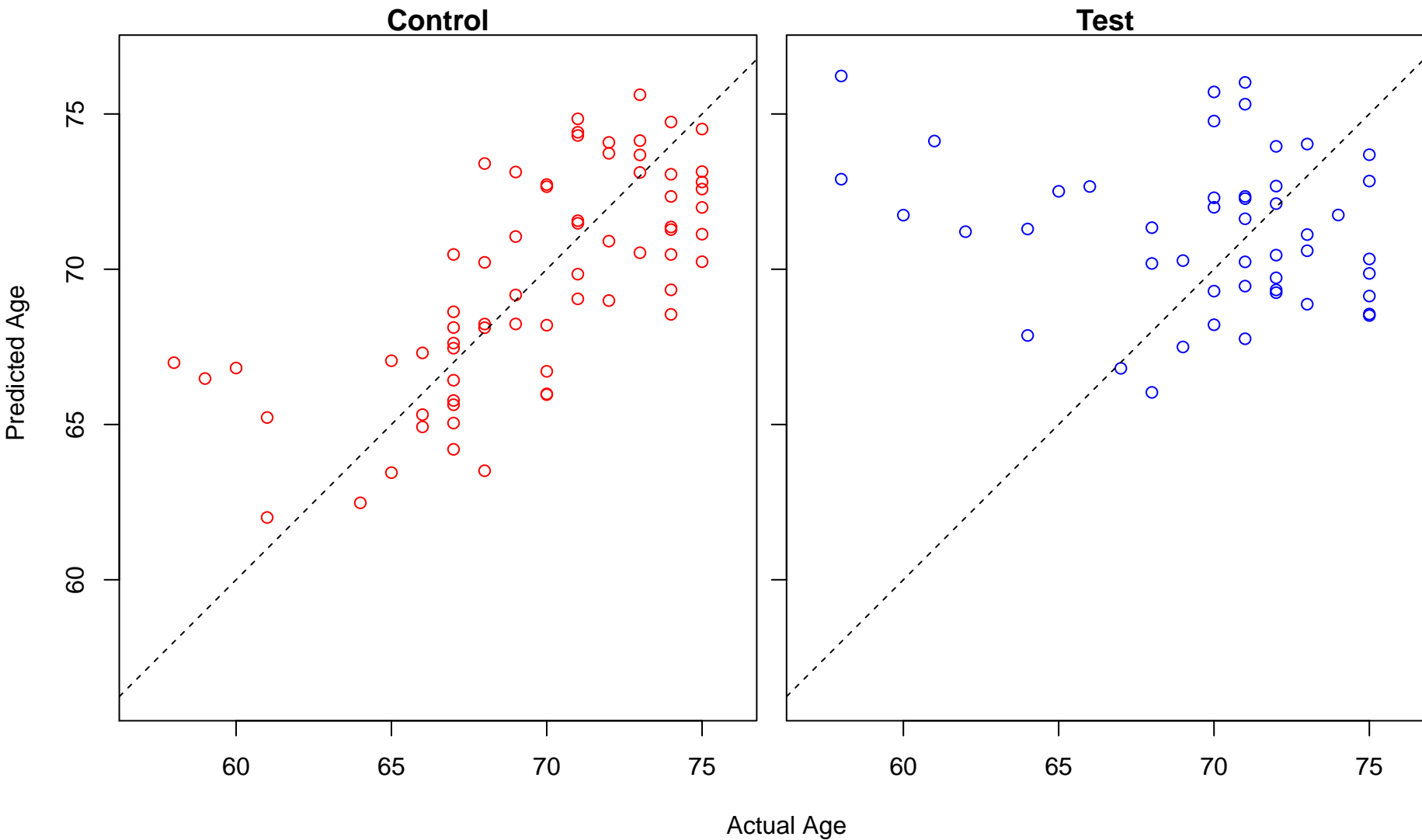


Test

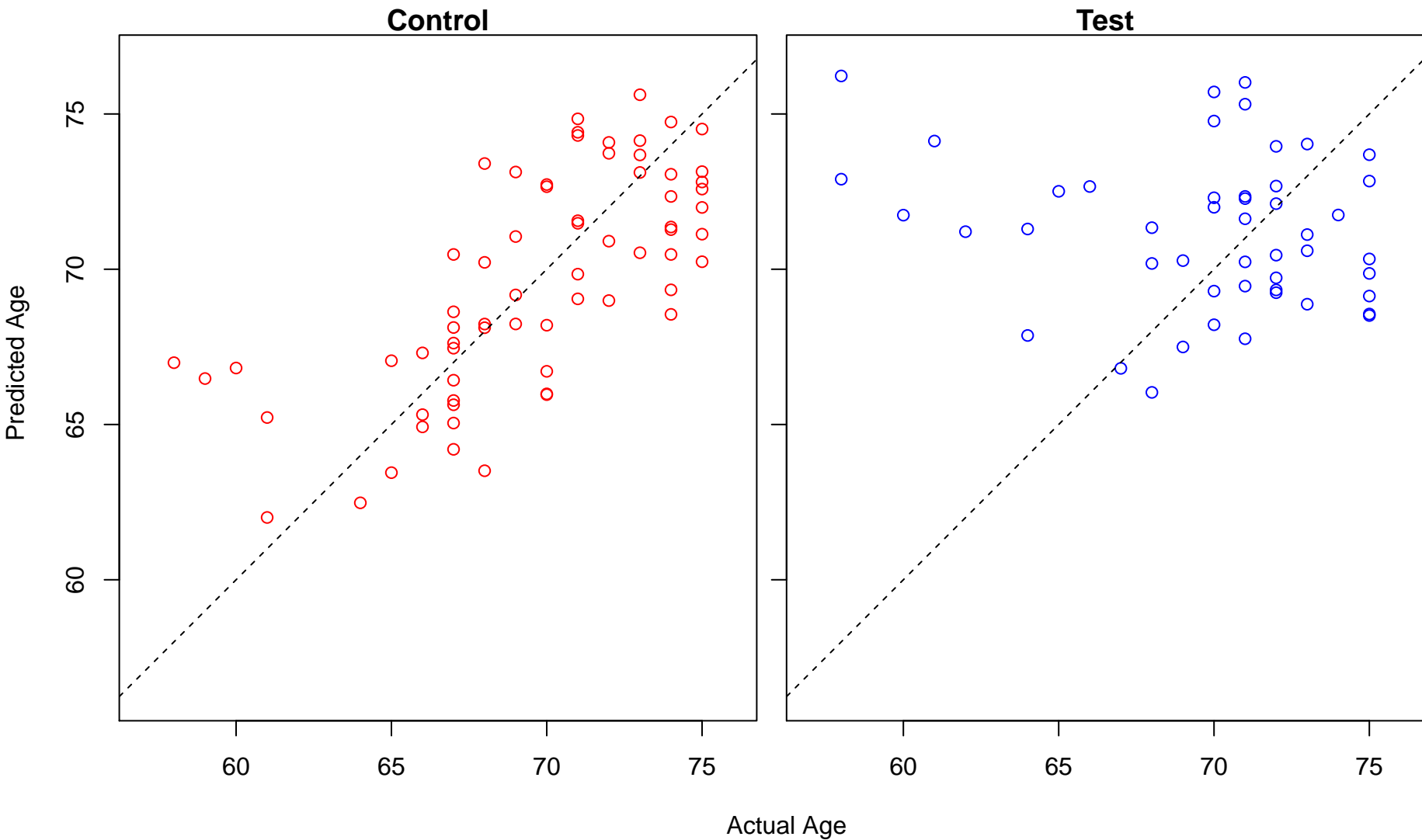


Actual Age

membrane disassembly (Score: 1.639103)

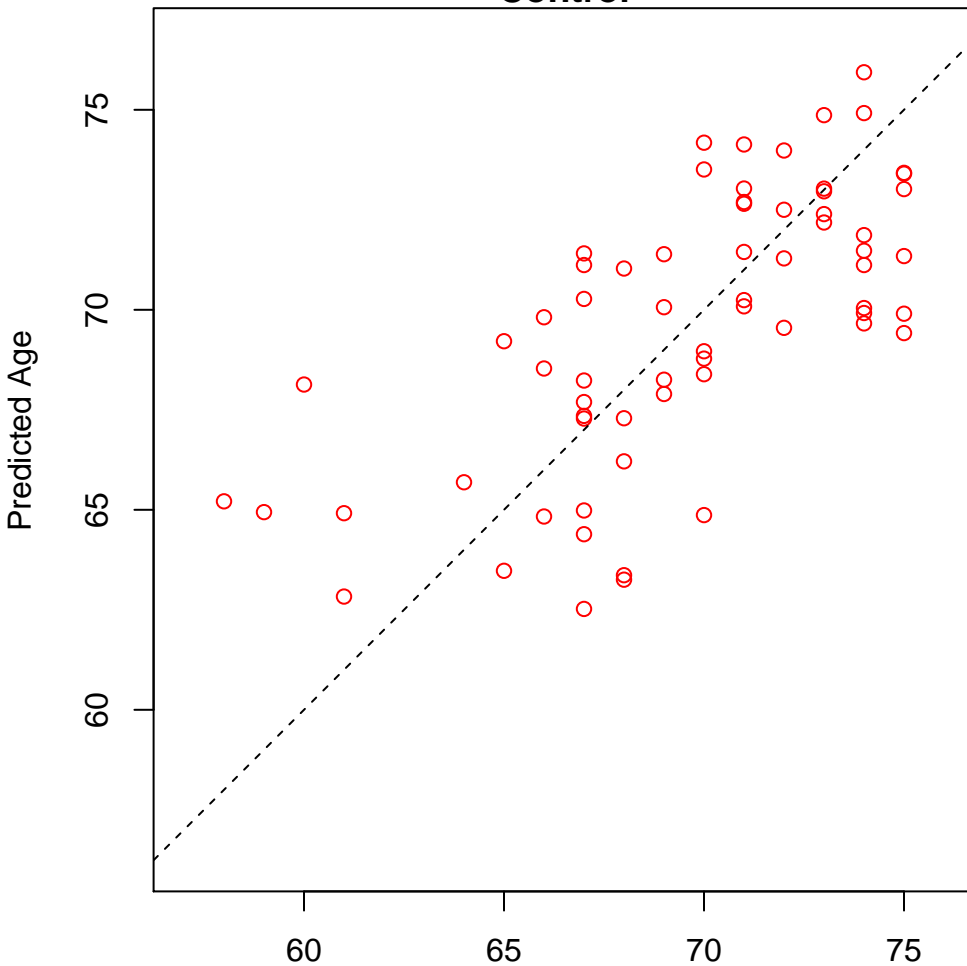


nuclear envelope disassembly (Score: 1.639103)

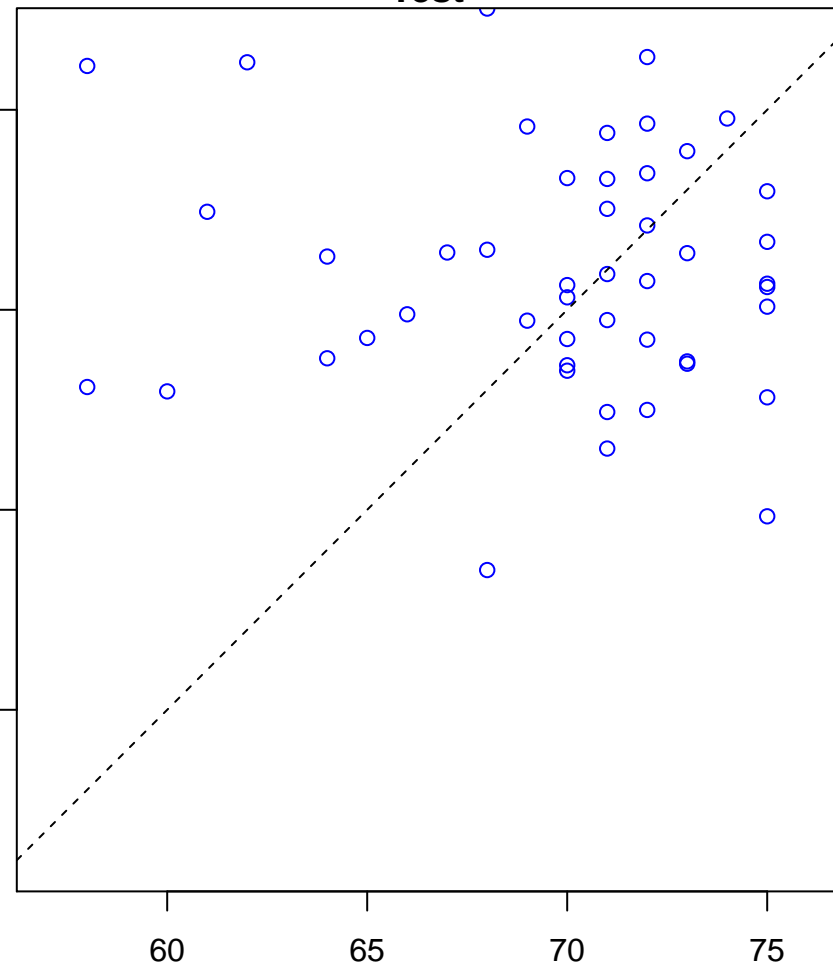


organic acid transmembrane transport (Score: 1.638504)

Control

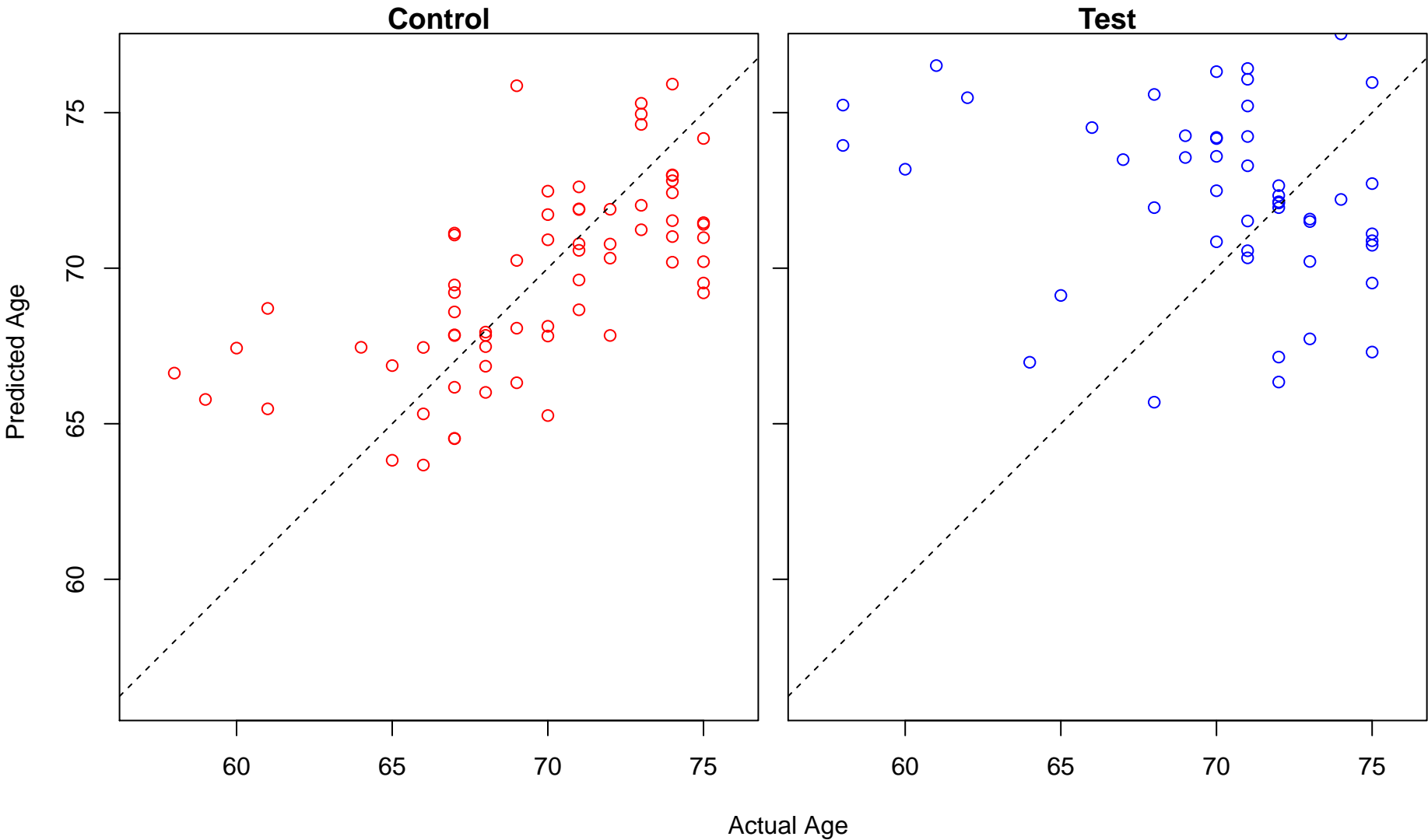


Test

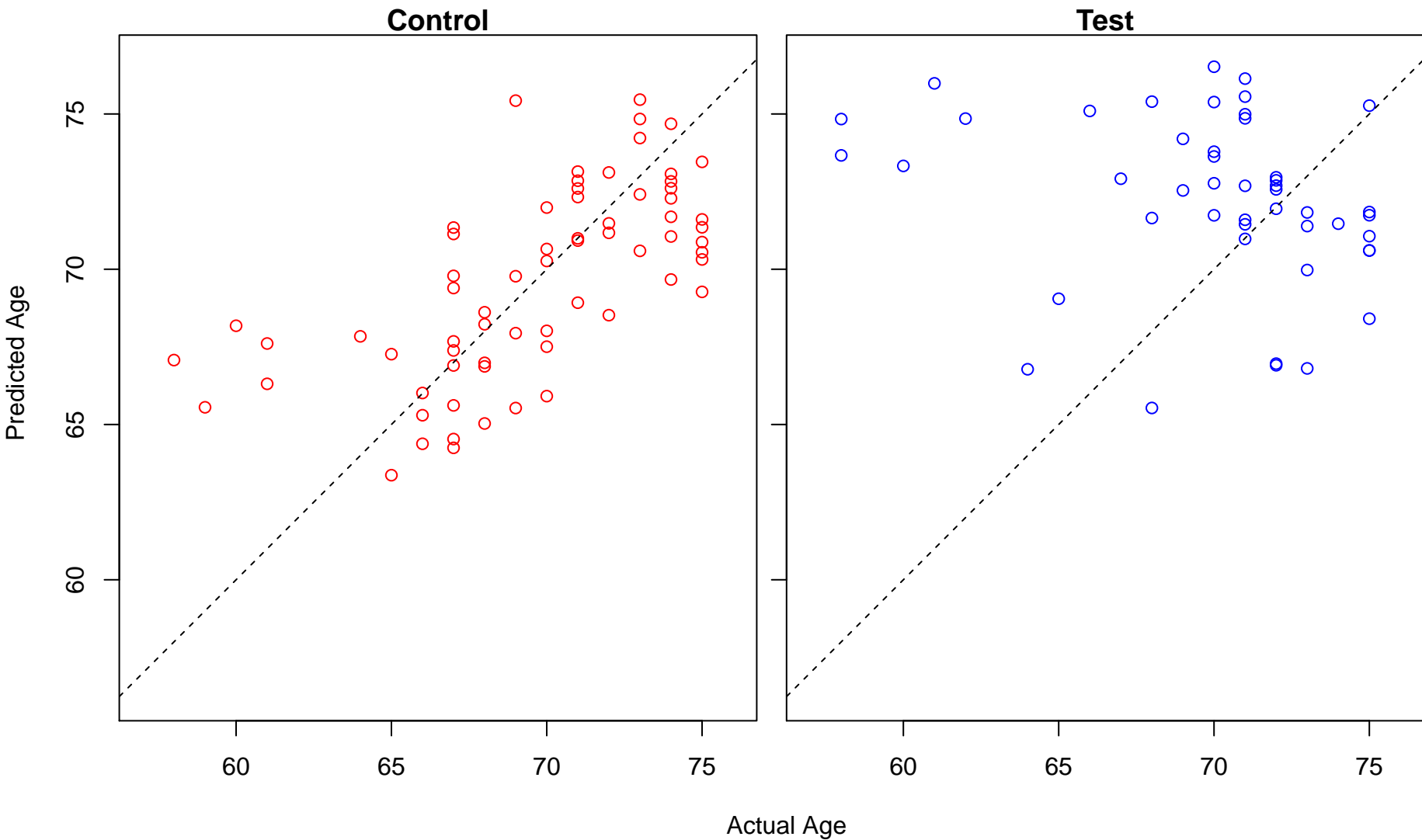


Actual Age

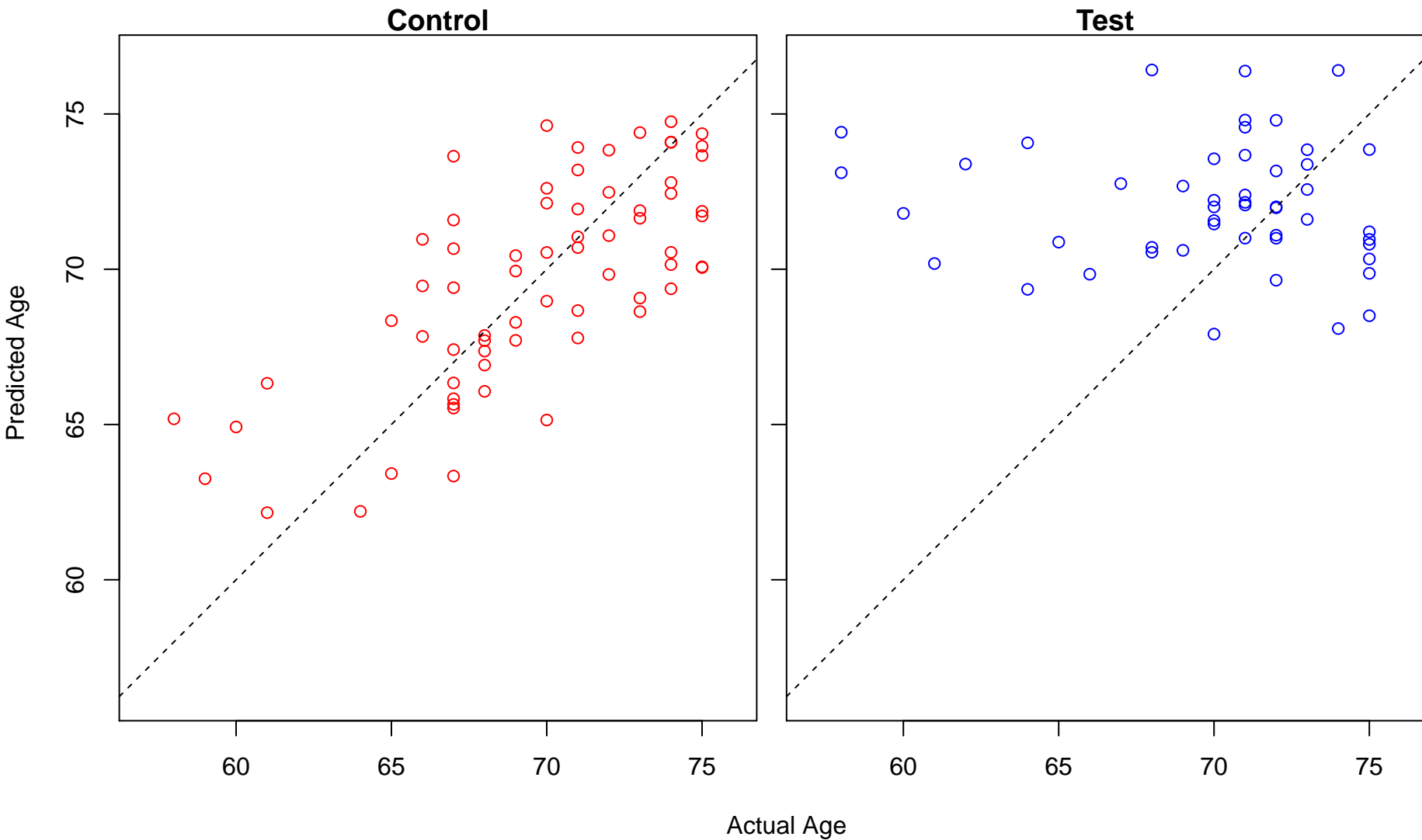
positive regulation of CD4-positive, alpha-beta T cell activation (Score: 1.637844)



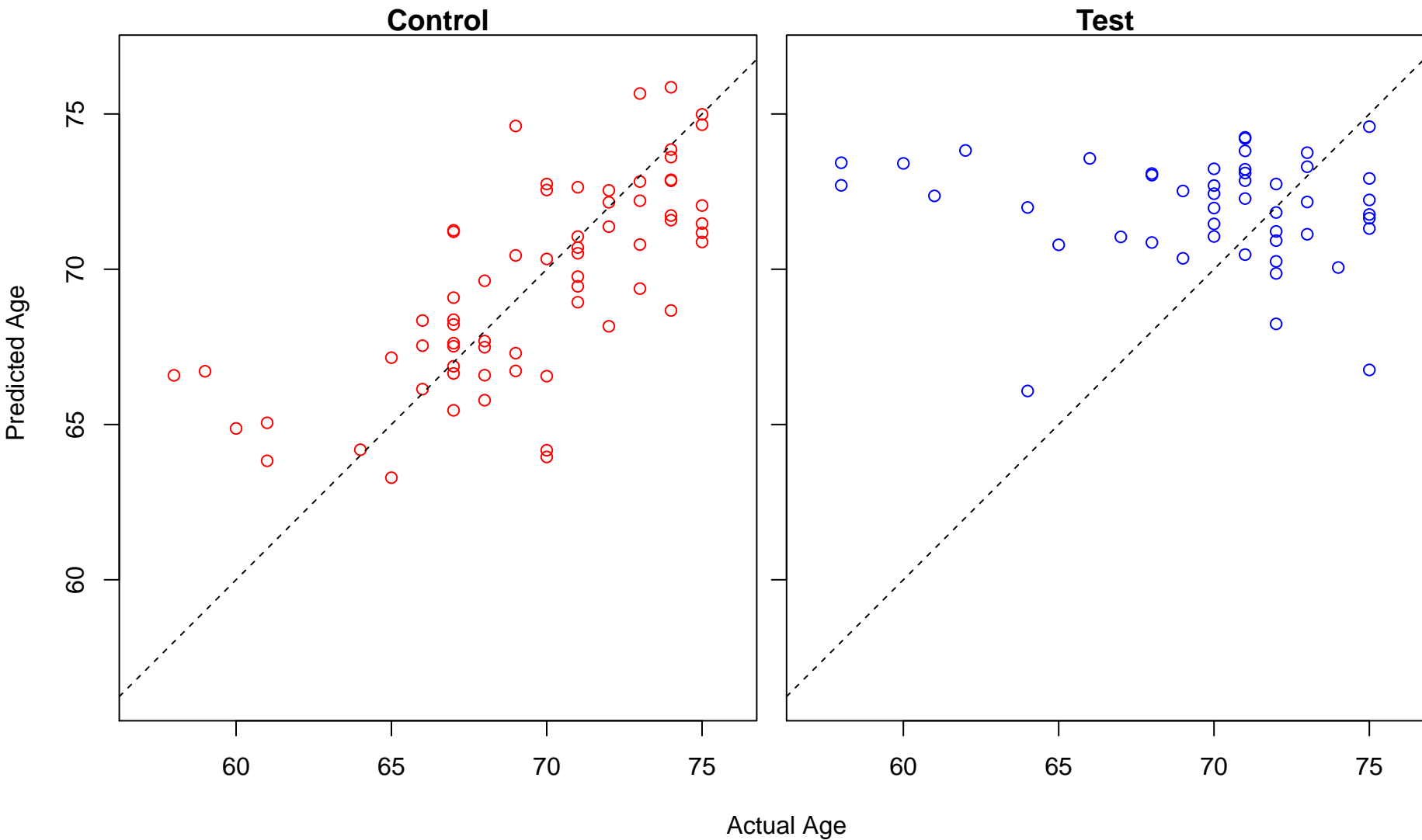
regulation of alpha-beta T cell differentiation (Score: 1.637843)



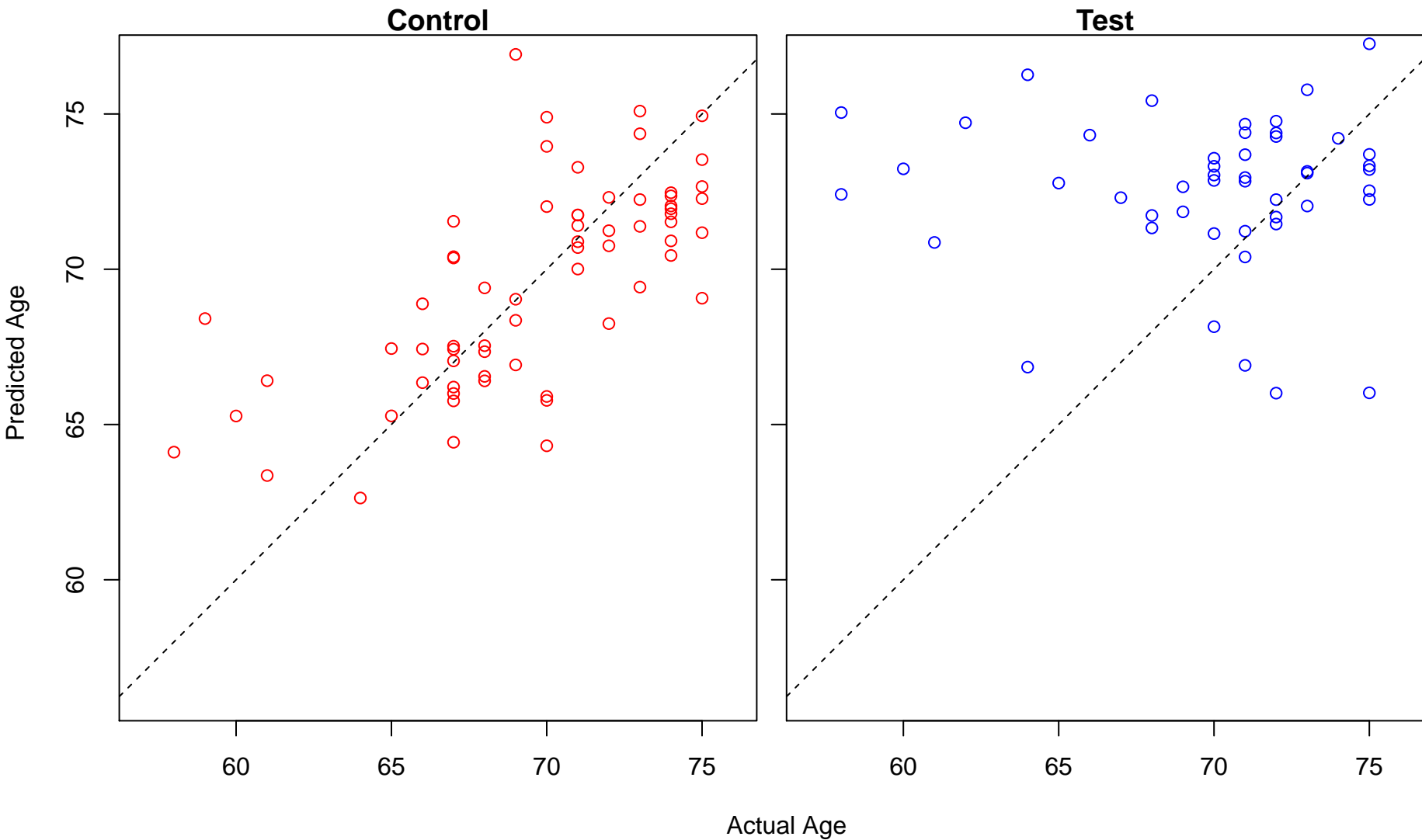
negative regulation of mRNA splicing, via spliceosome (Score: 1.637839)



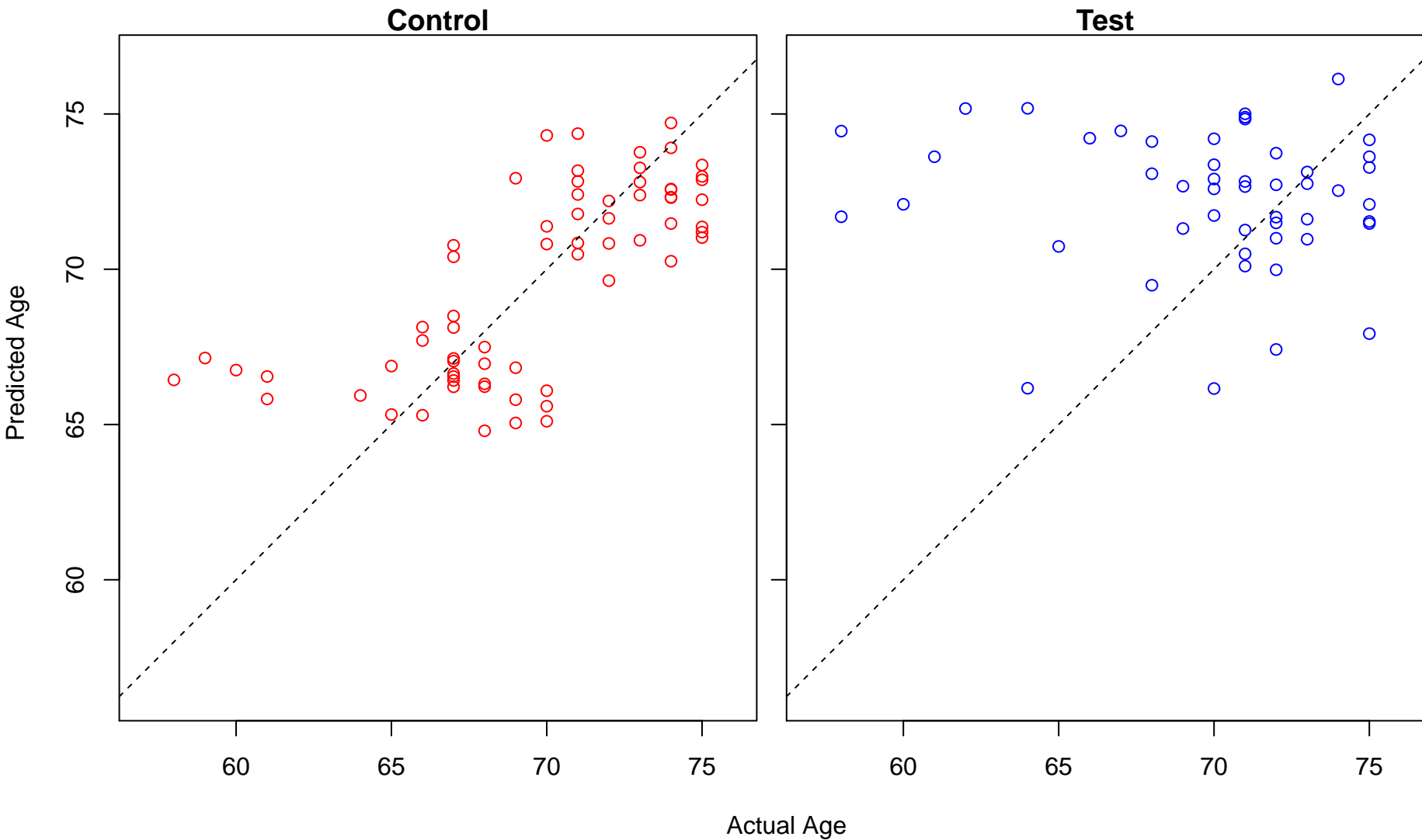
blood vessel morphogenesis (Score: 1.637346)



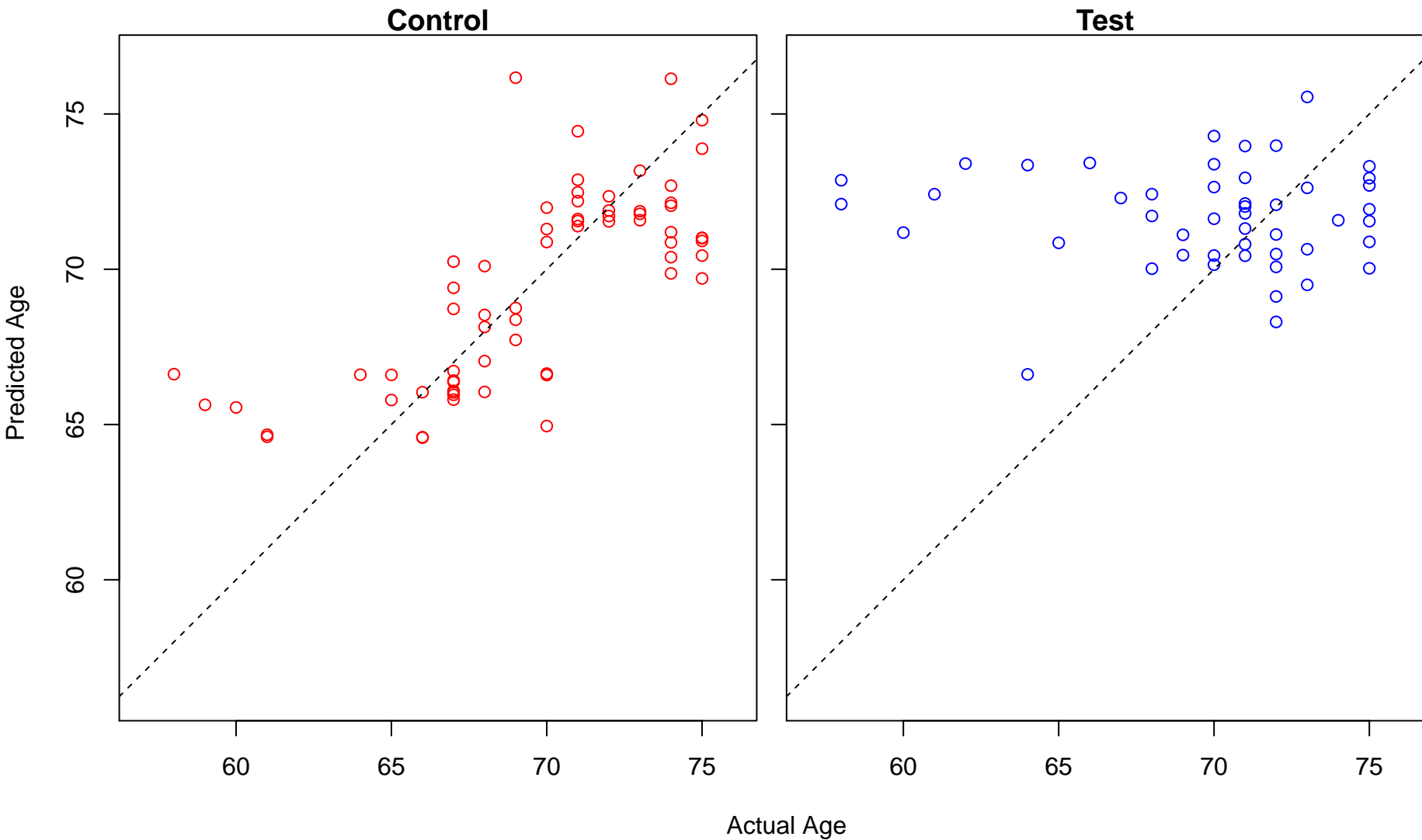
toll-like receptor TLR1:TLR2 signaling pathway (Score: 1.636934)



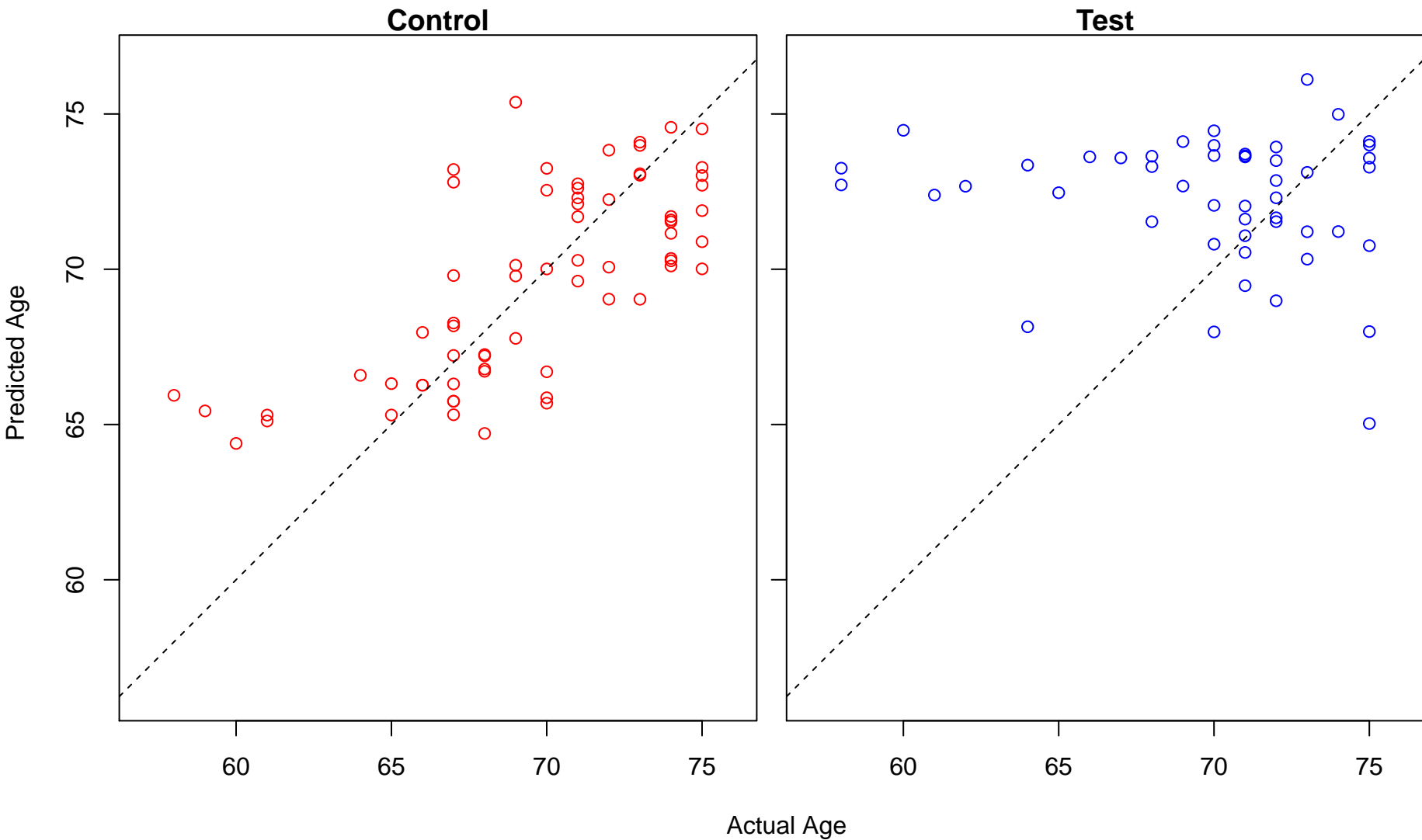
regulation of lymphocyte migration (Score: 1.636926)



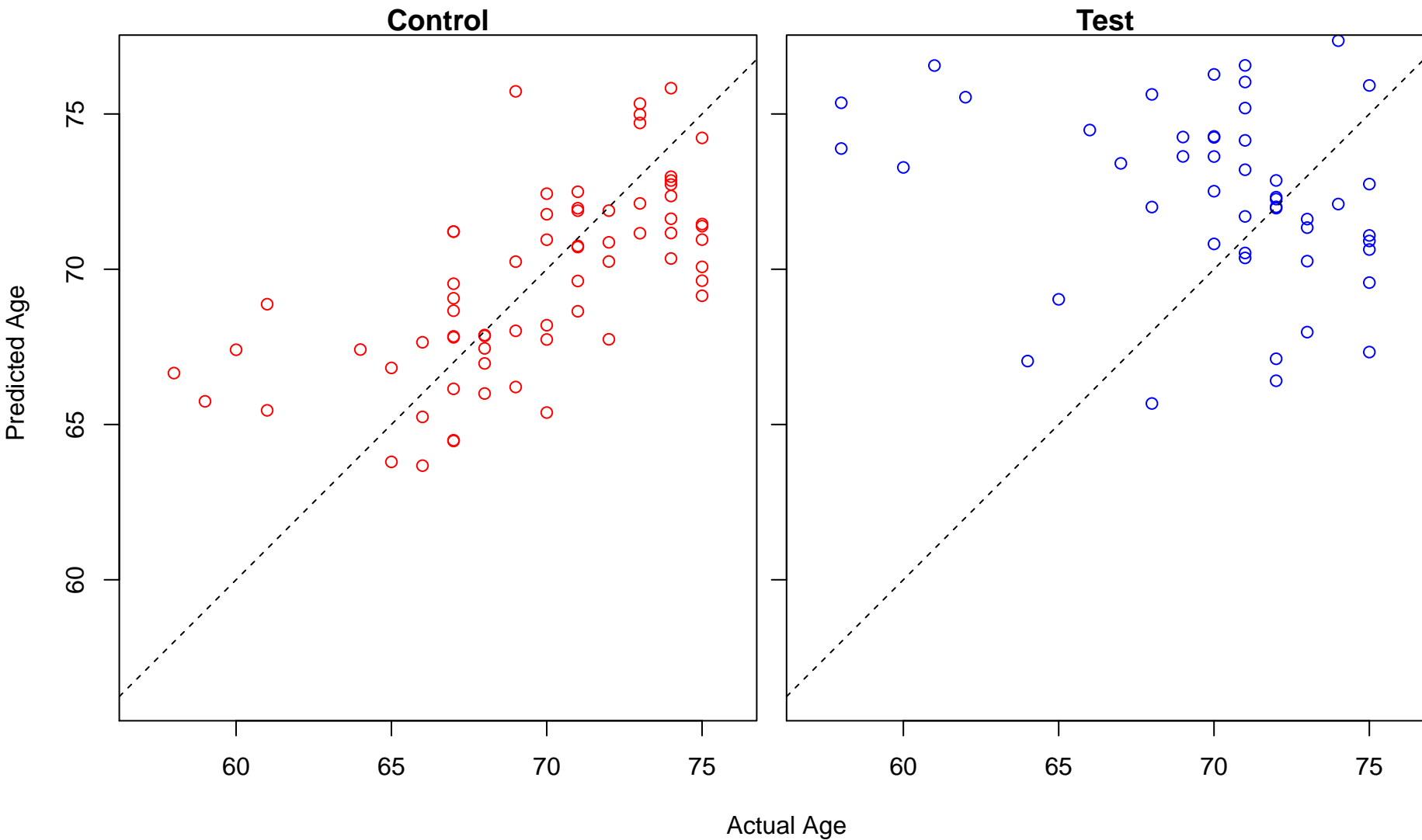
positive regulation of actin filament polymerization (Score: 1.636294)



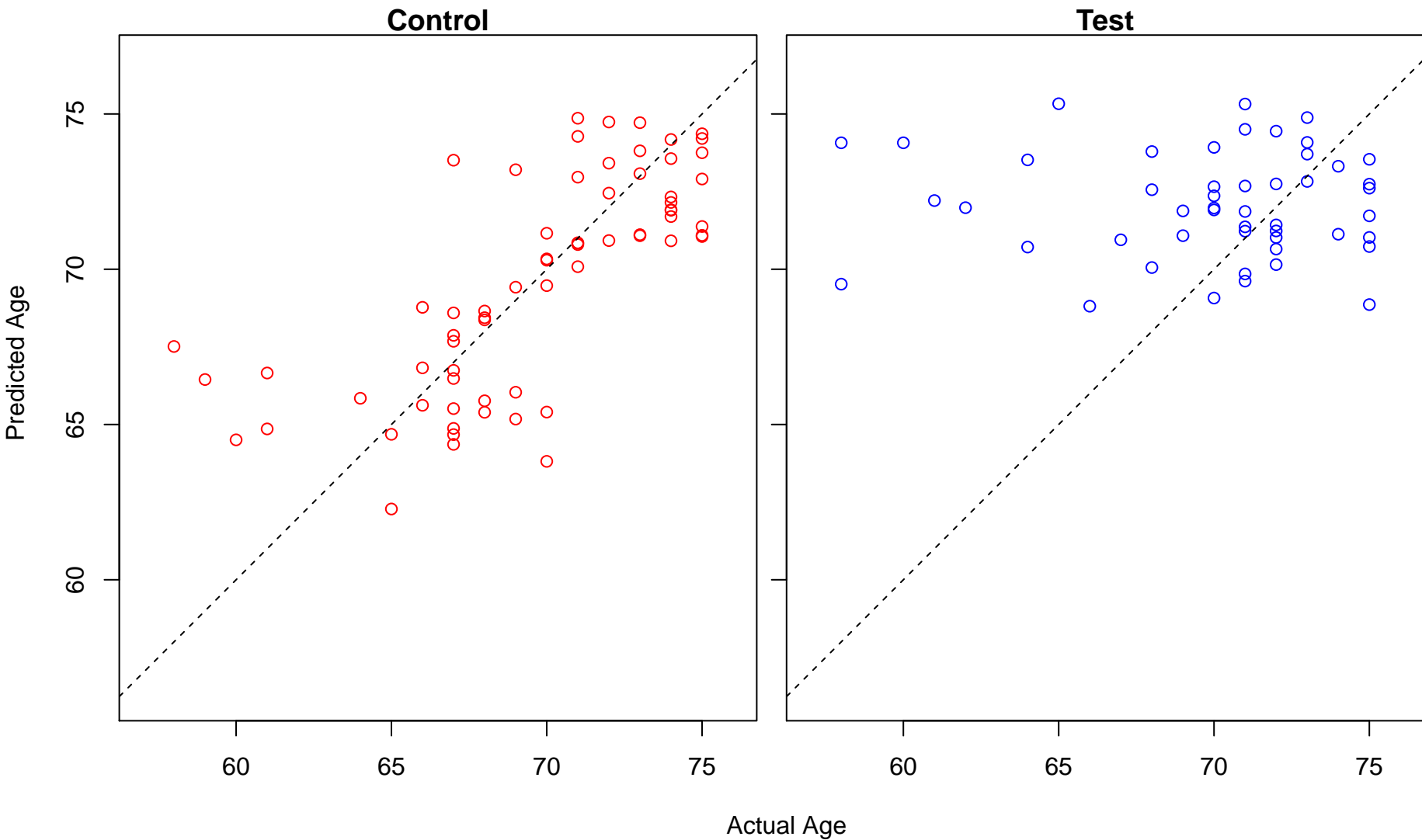
polyprenol metabolic process (Score: 1.635923)



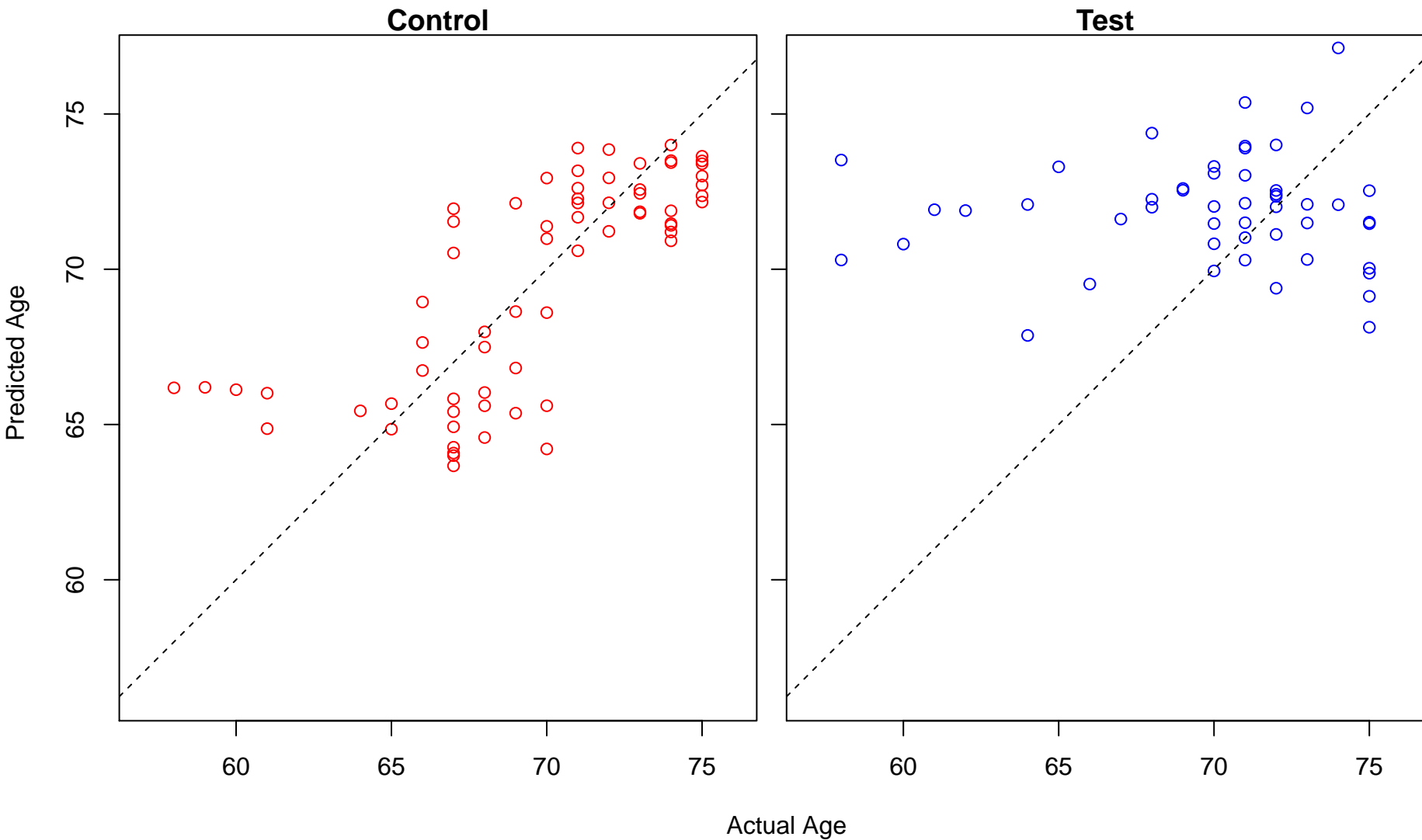
regulation of CD4-positive, alpha-beta T cell activation (Score: 1.635335)



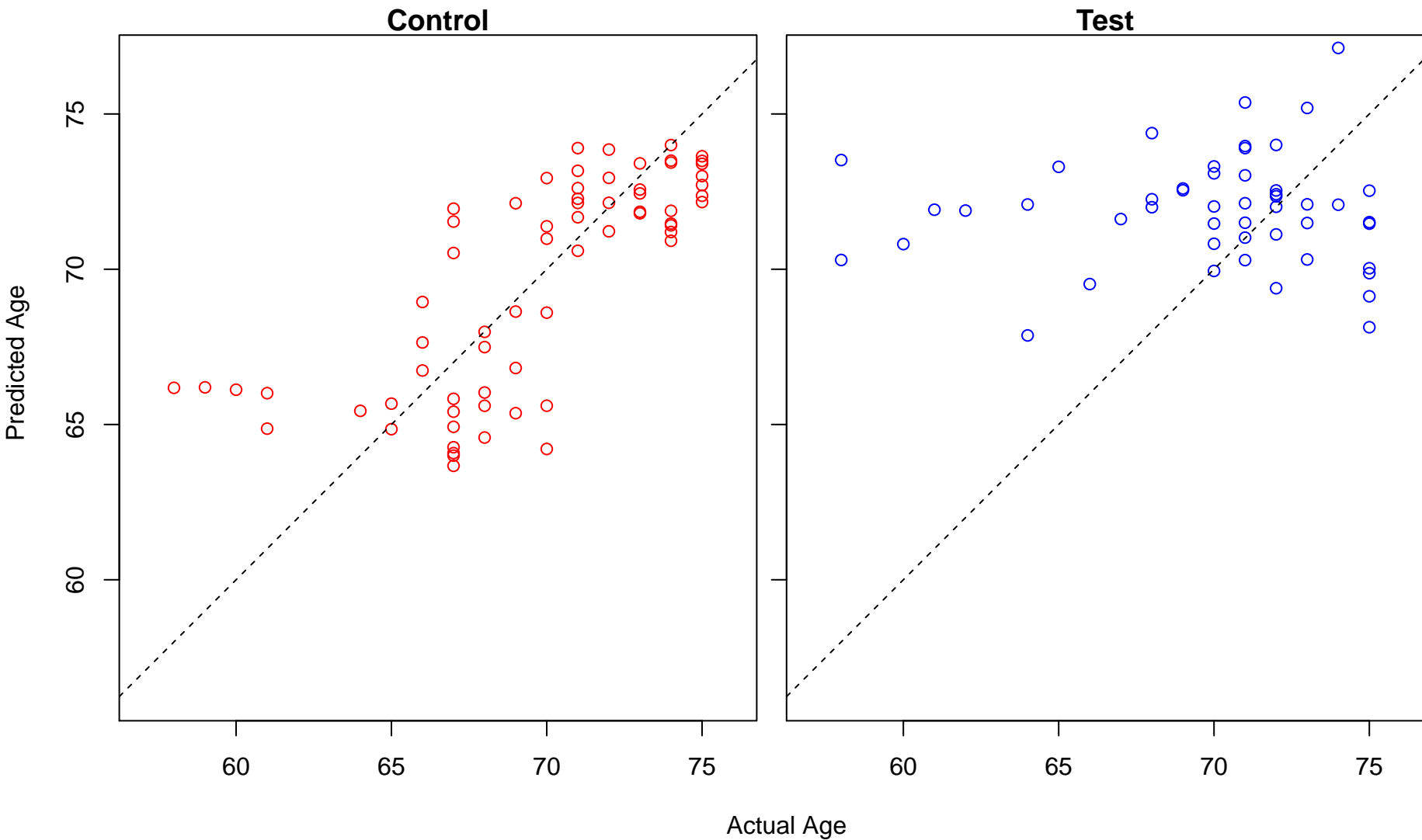
ribonucleoprotein complex export from nucleus (Score: 1.635207)



RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (Score: 1.63510)

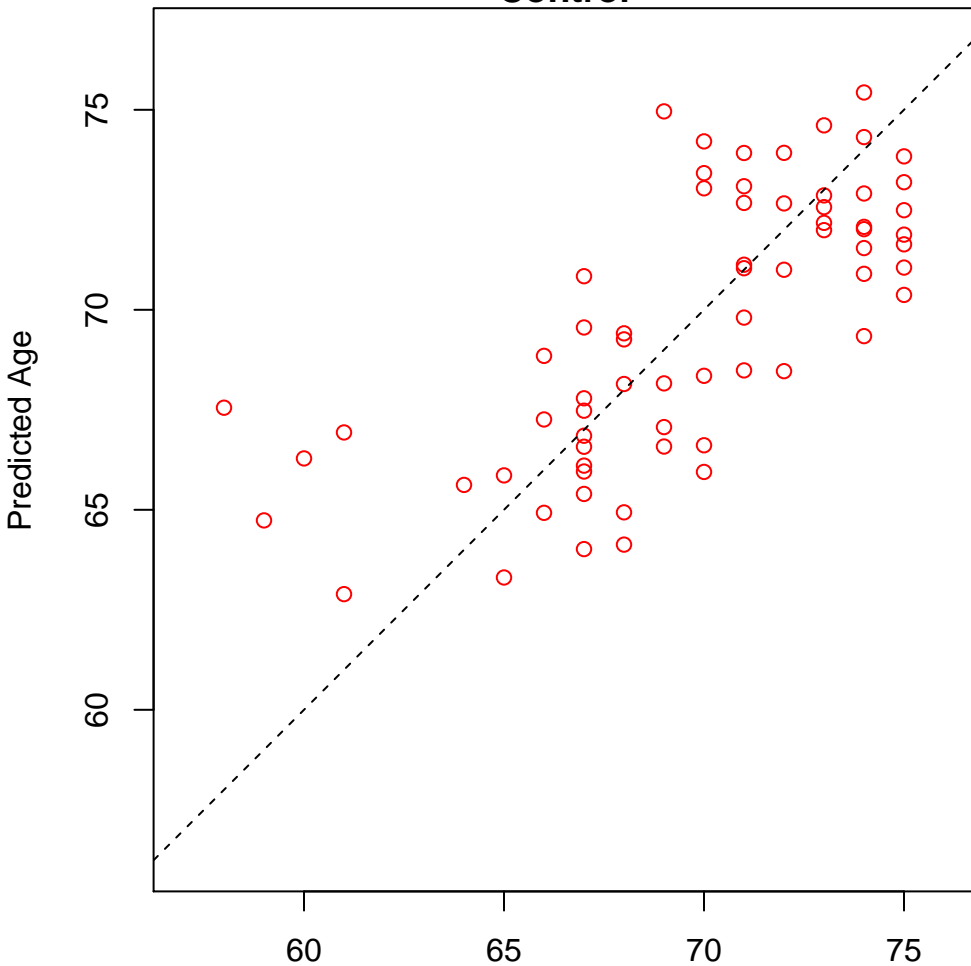


mRNA splicing, via spliceosome (Score: 1.635101)

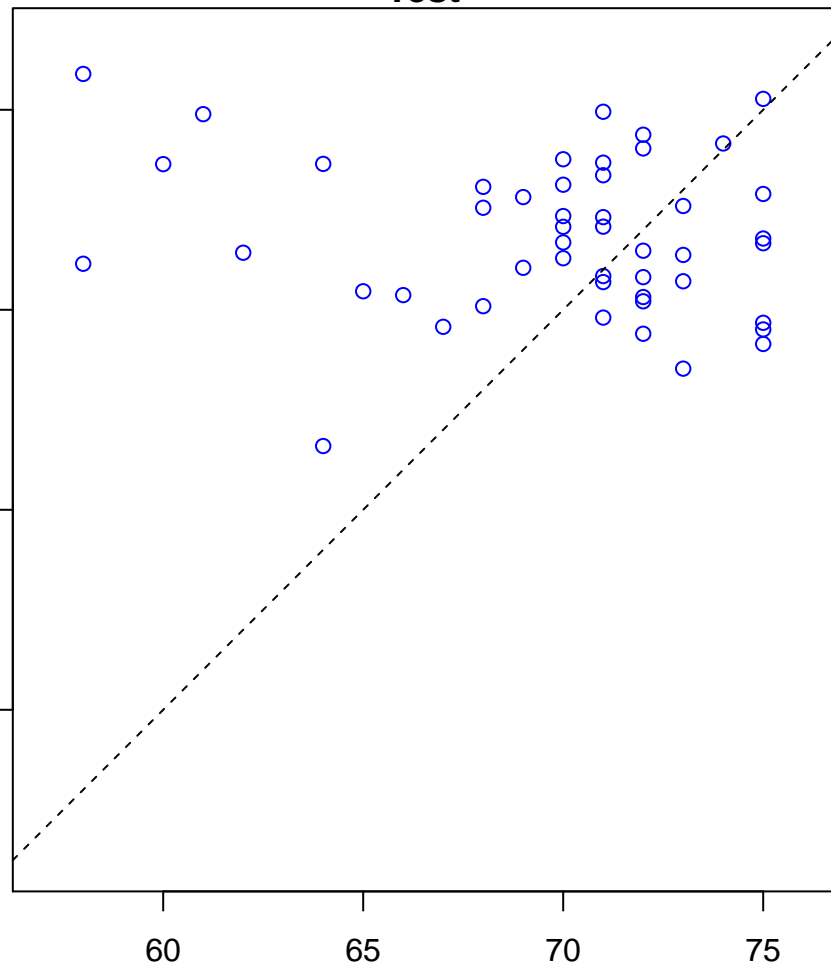


single organism reproductive process (Score: 1.635083)

Control



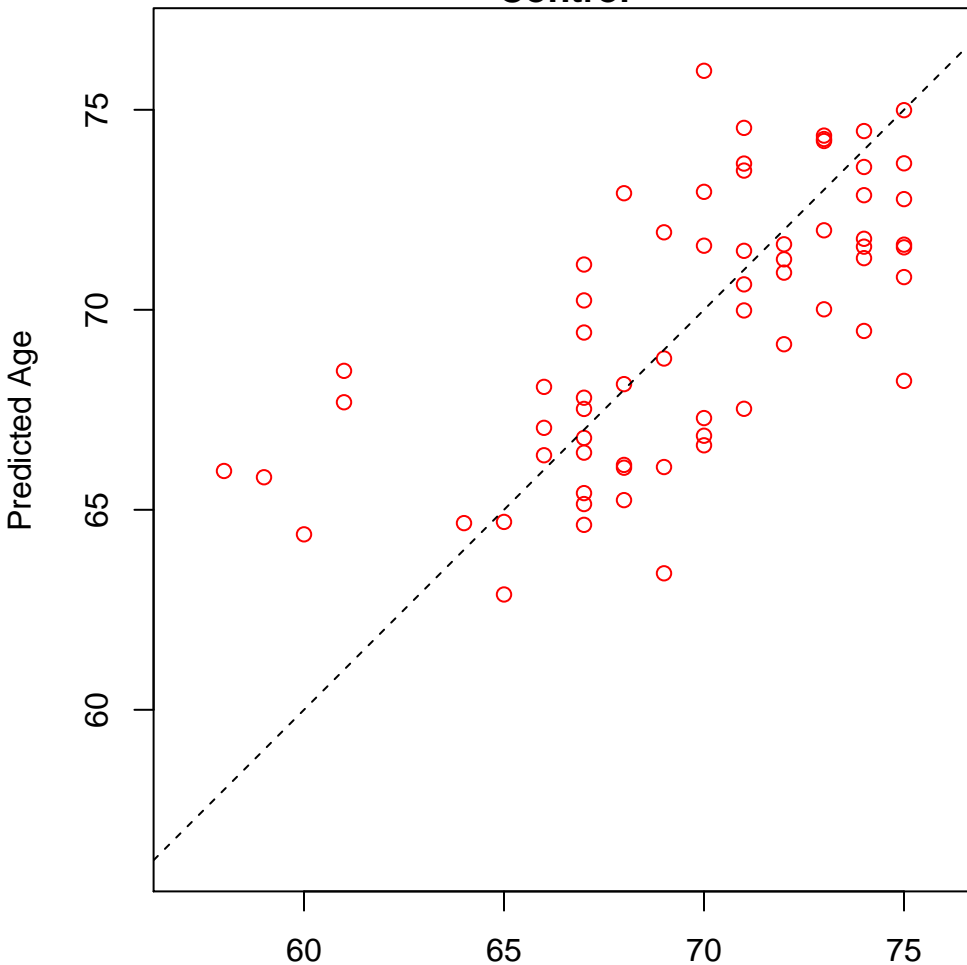
Test



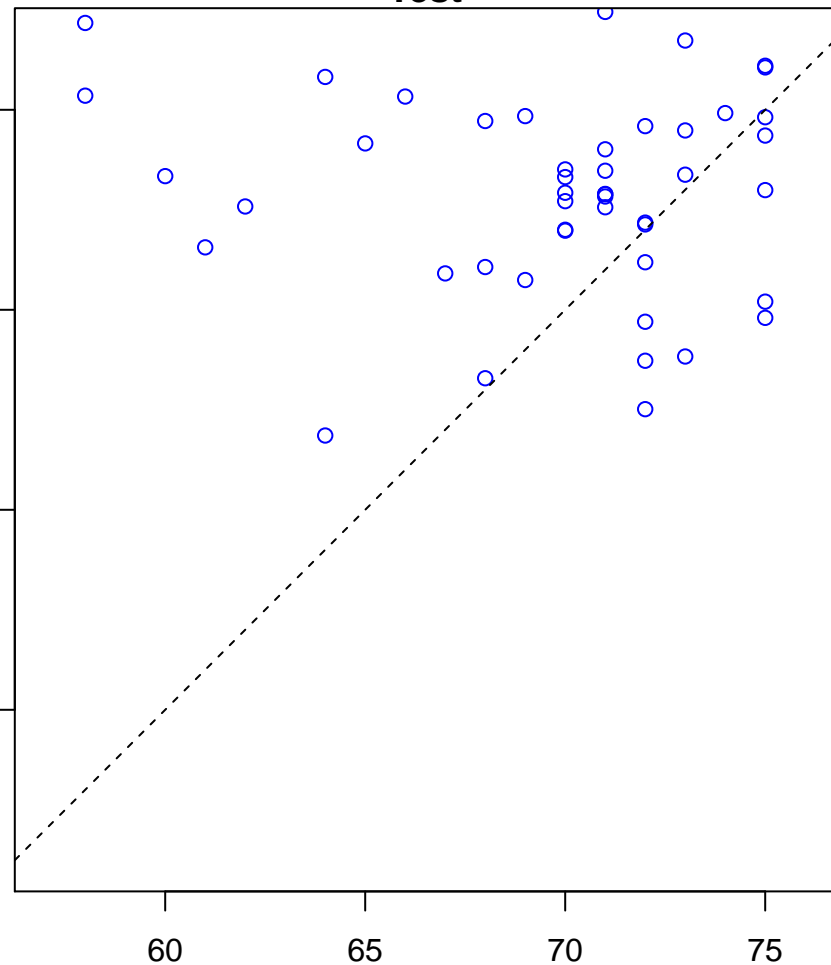
Actual Age

regulation of dendrite development (Score: 1.634660)

Control

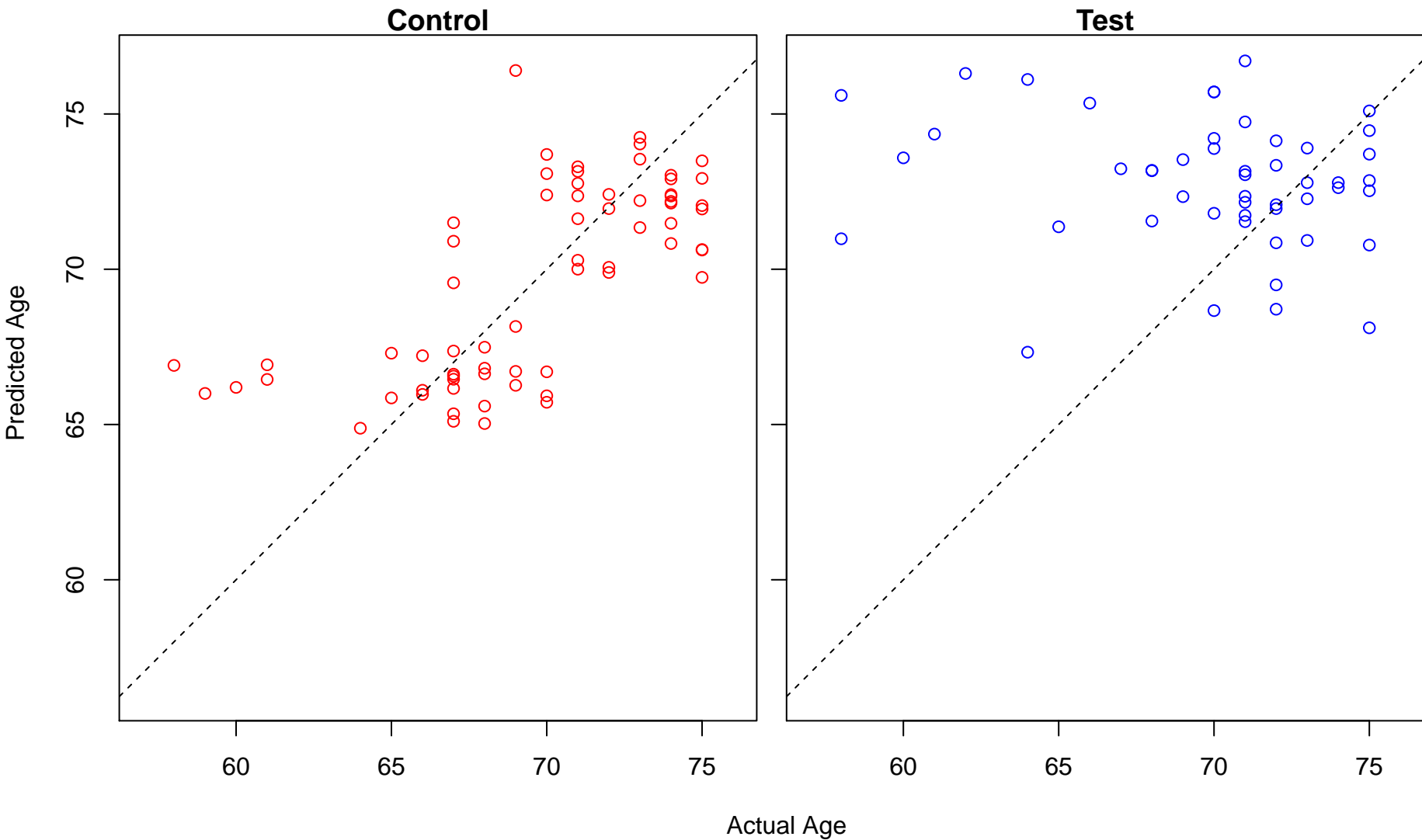


Test

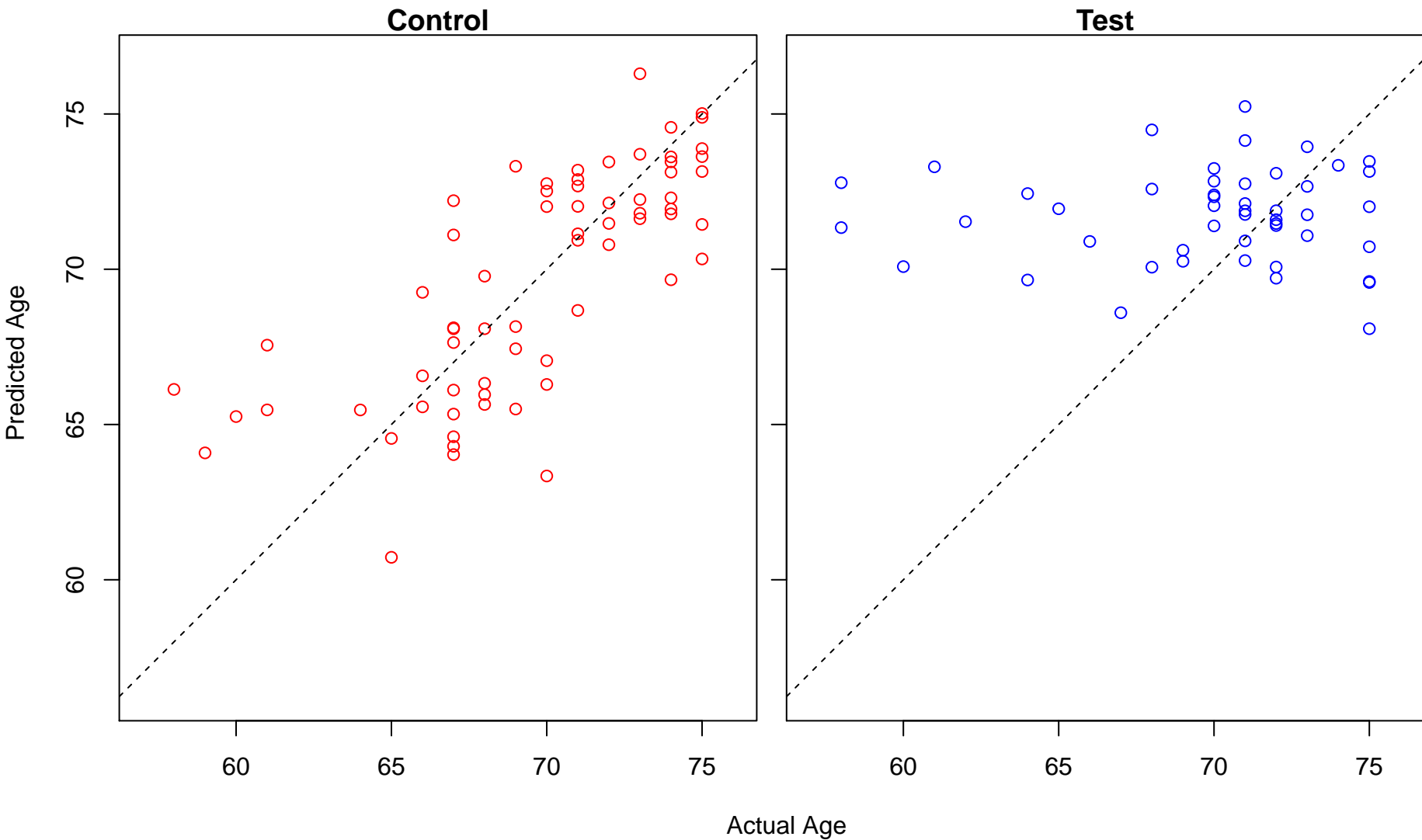


Actual Age

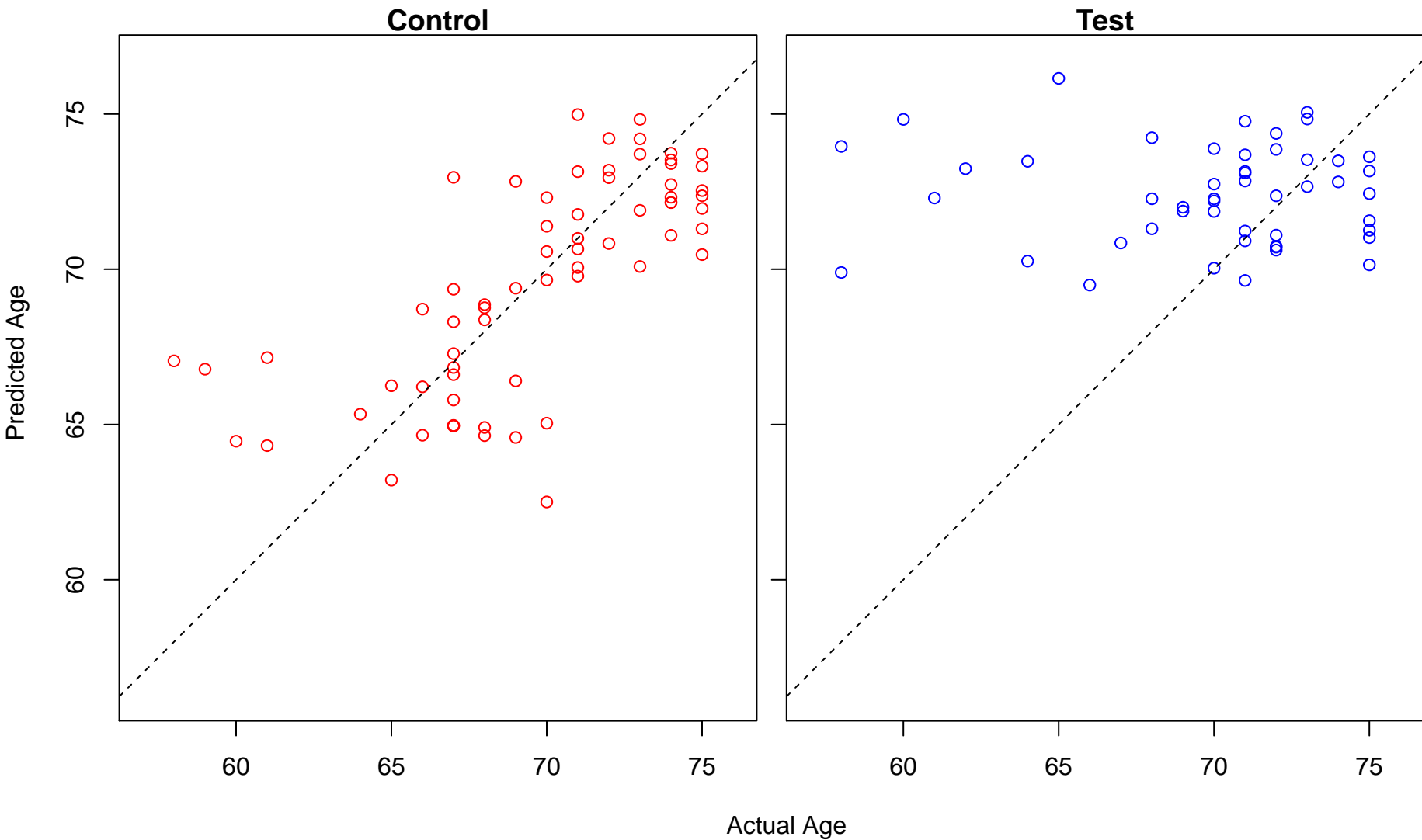
iron ion transport (Score: 1.633576)



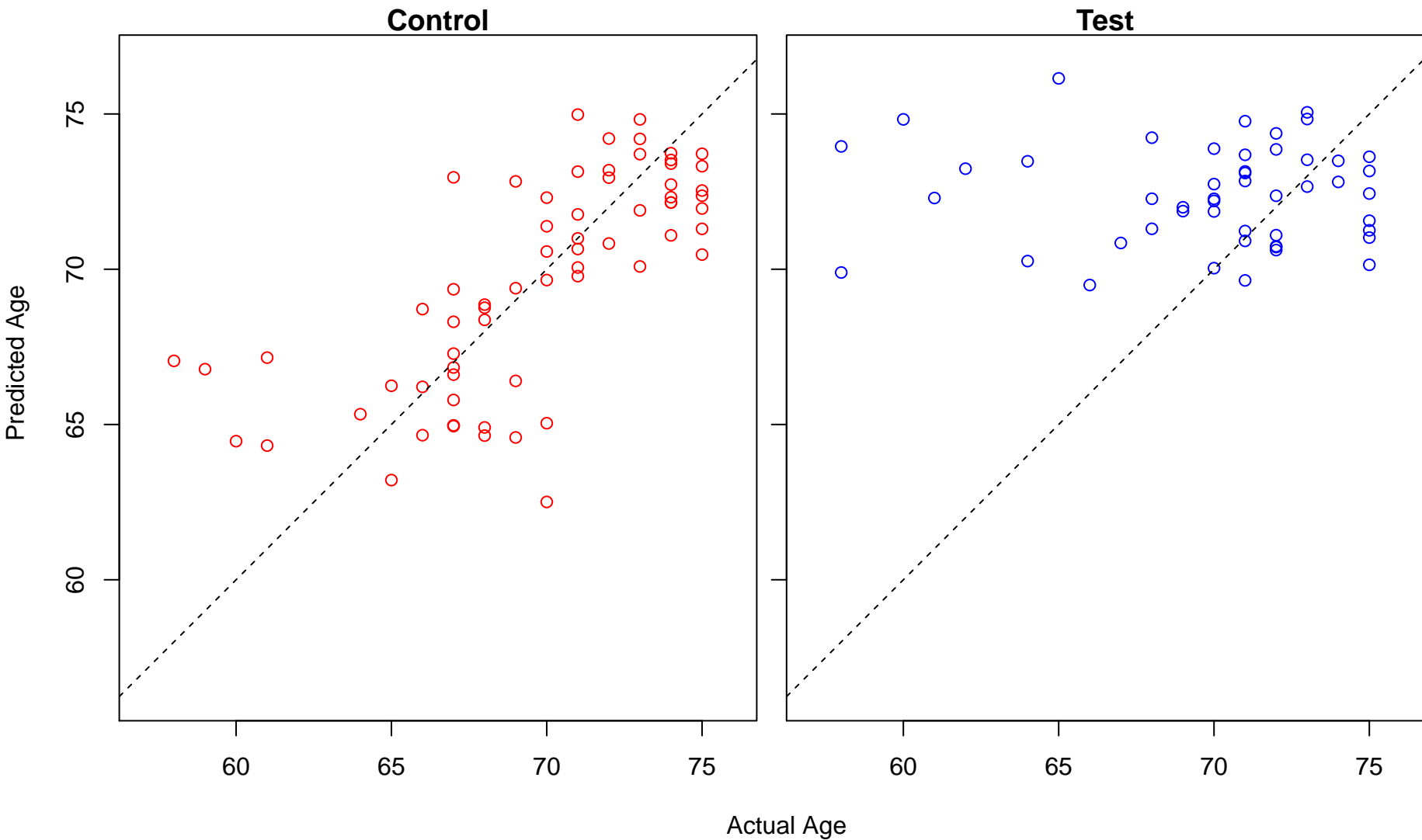
negative regulation of G1/S transition of mitotic cell cycle (Score: 1.632644)



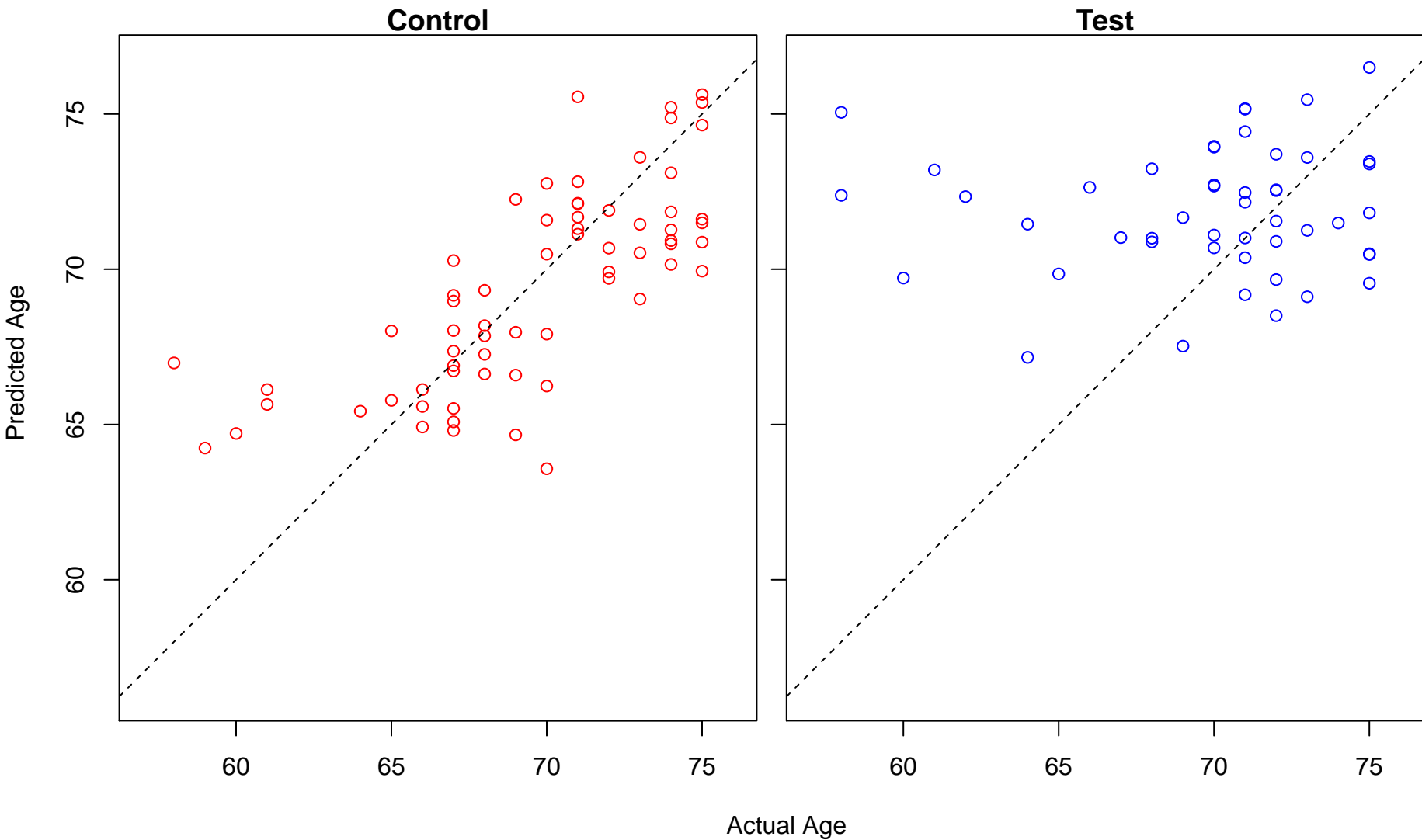
nucleic acid transport (Score: 1.632259)



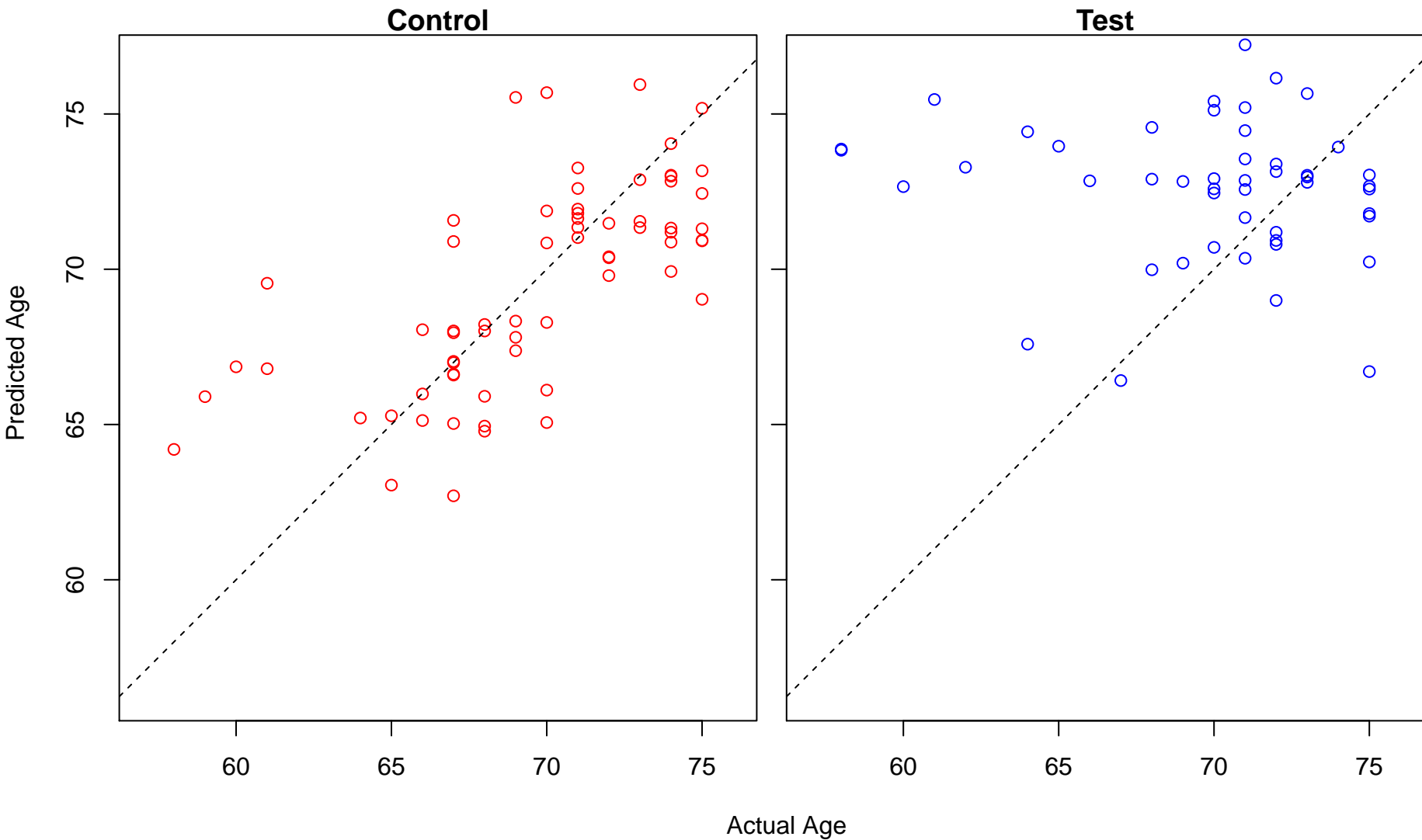
RNA transport (Score: 1.632259)



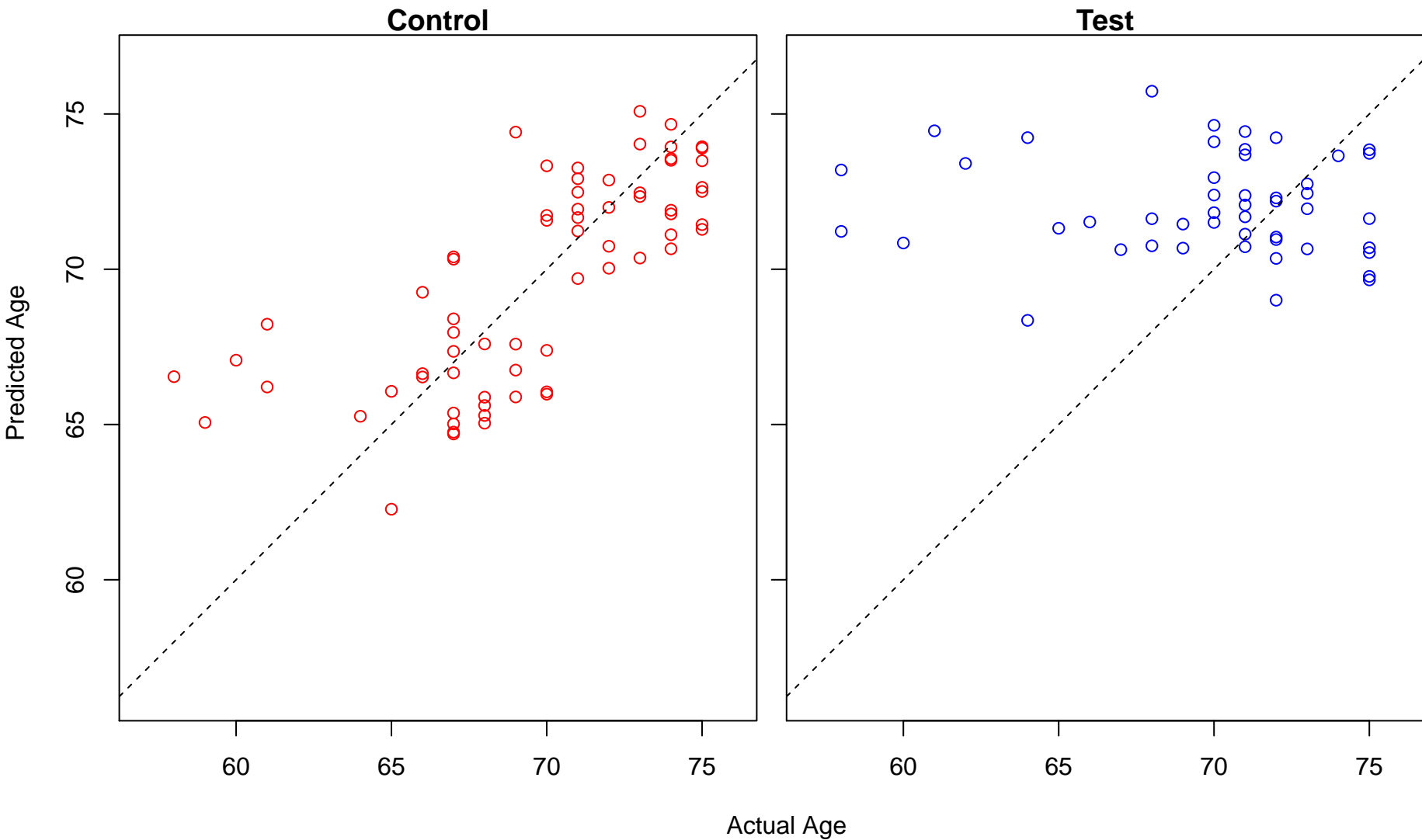
muscle contraction (Score: 1.631323)



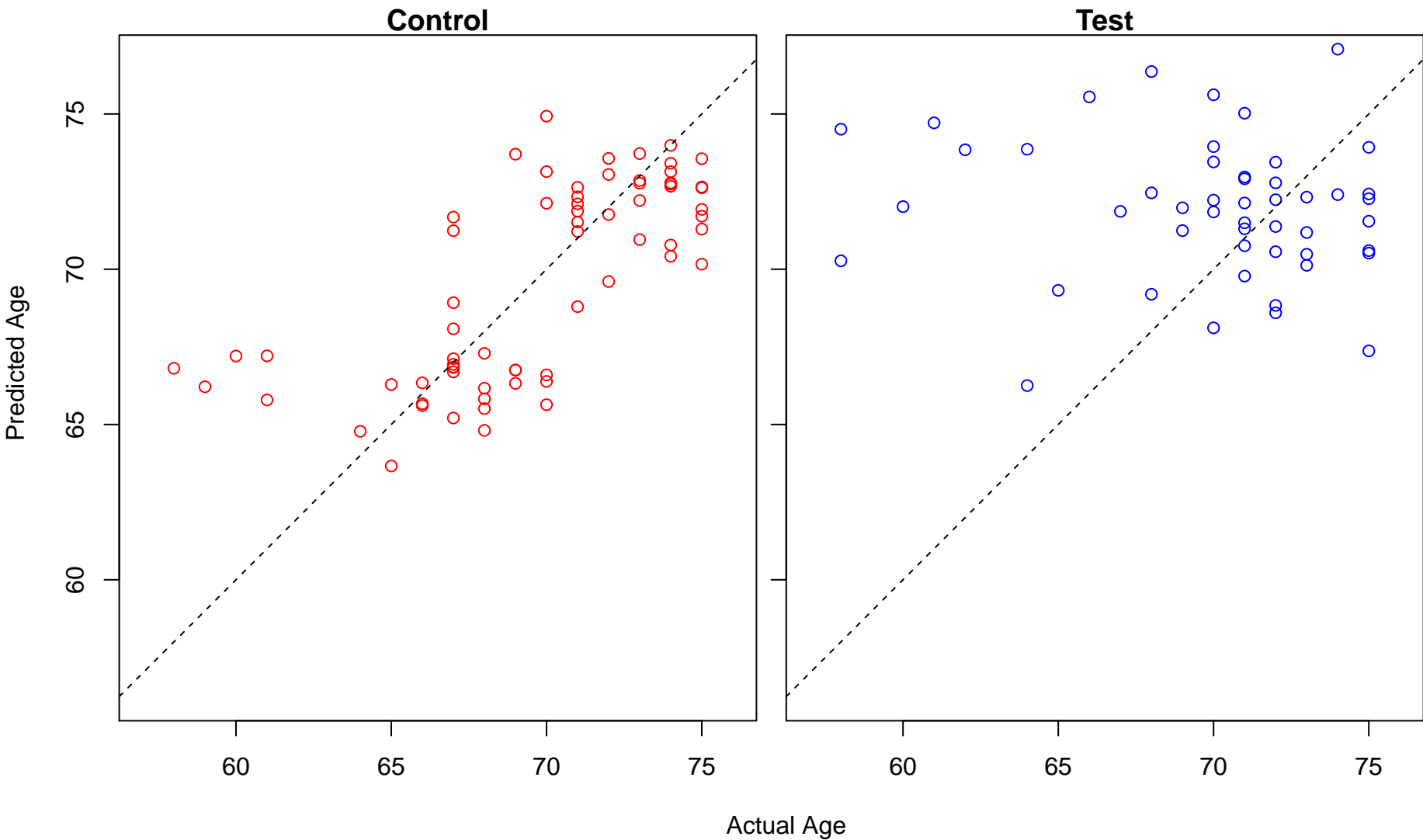
regulation of telomere maintenance via telomere lengthening (Score: 1.630416)



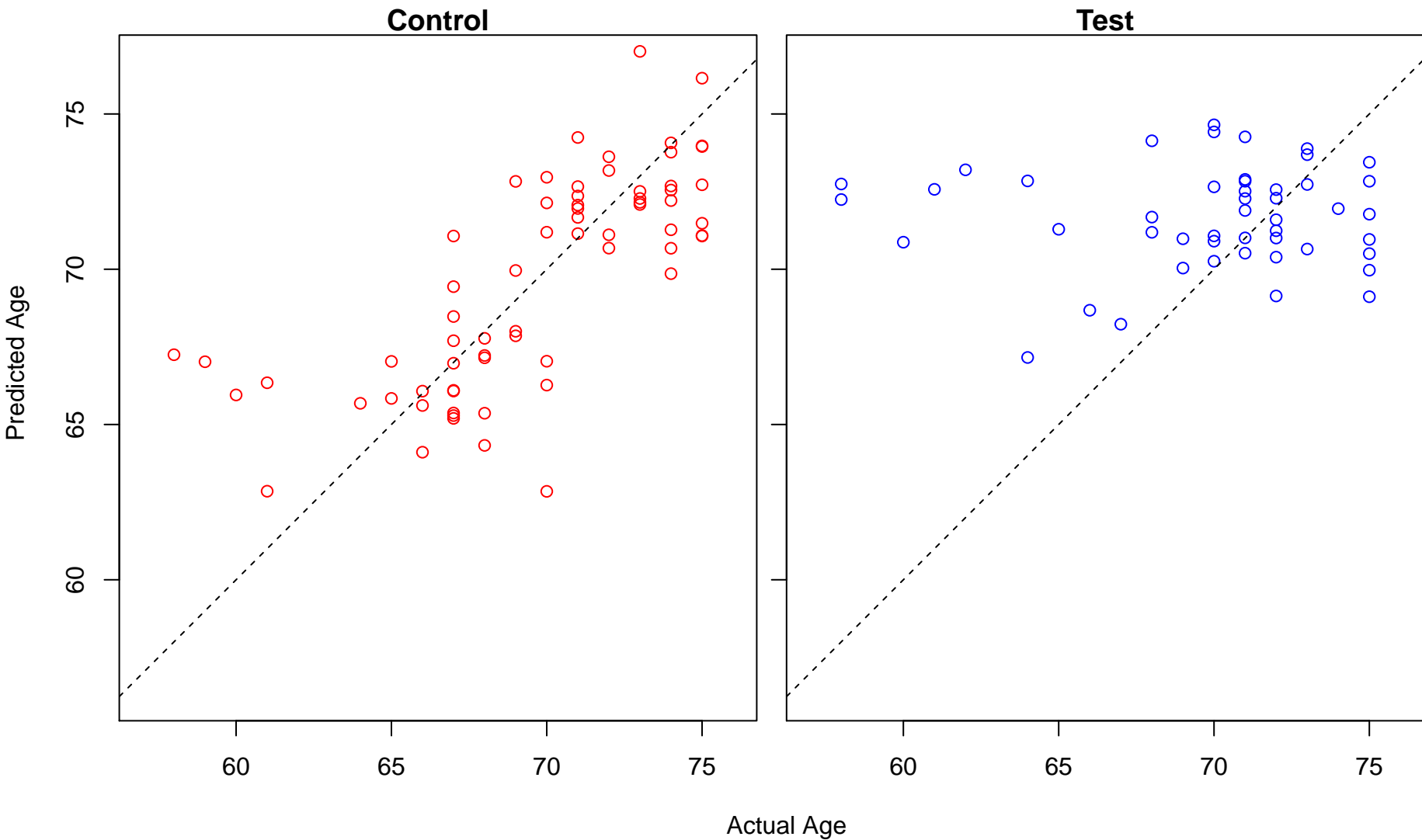
regulation of cellular amine metabolic process (Score: 1.630318)



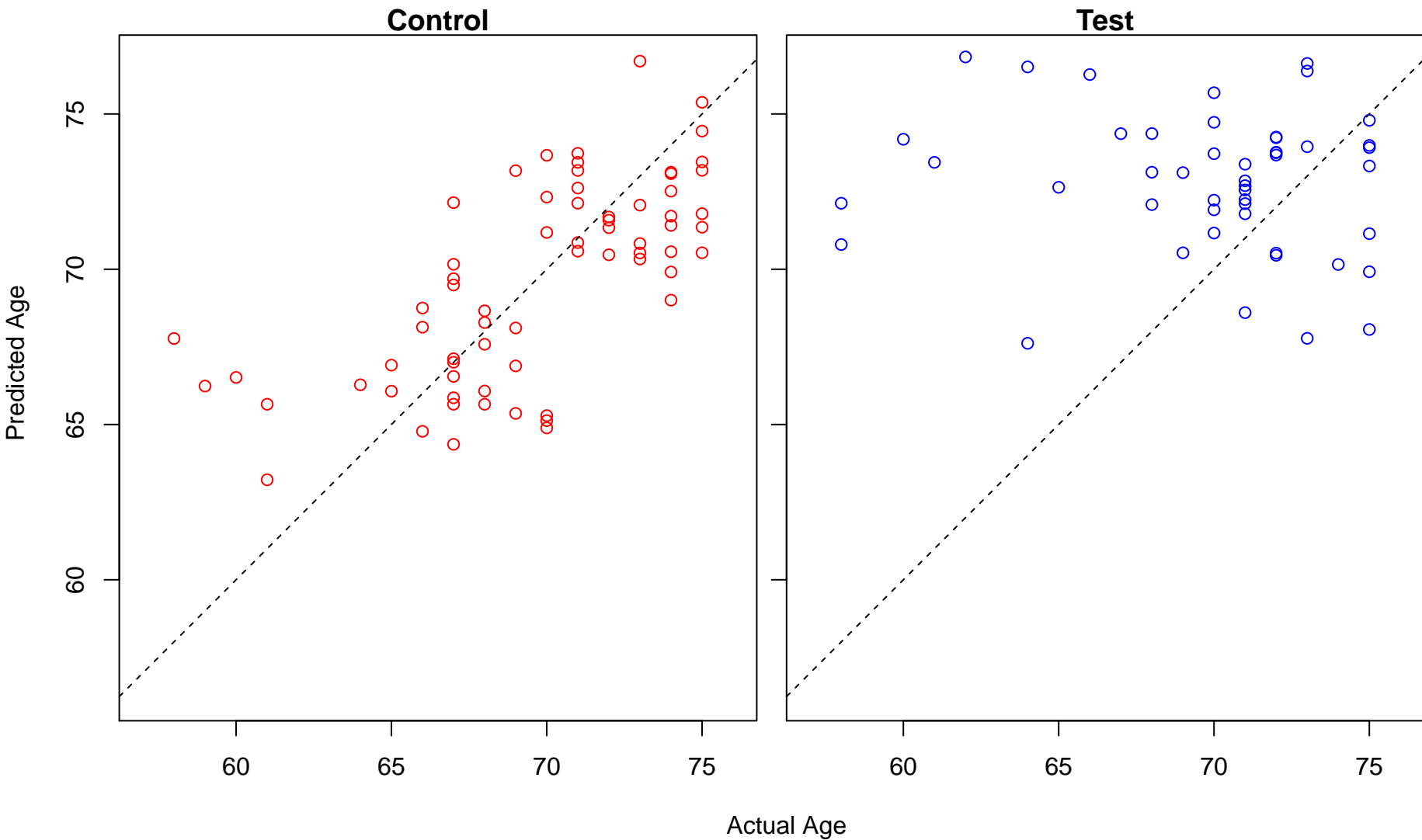
response to drug (Score: 1.630252)



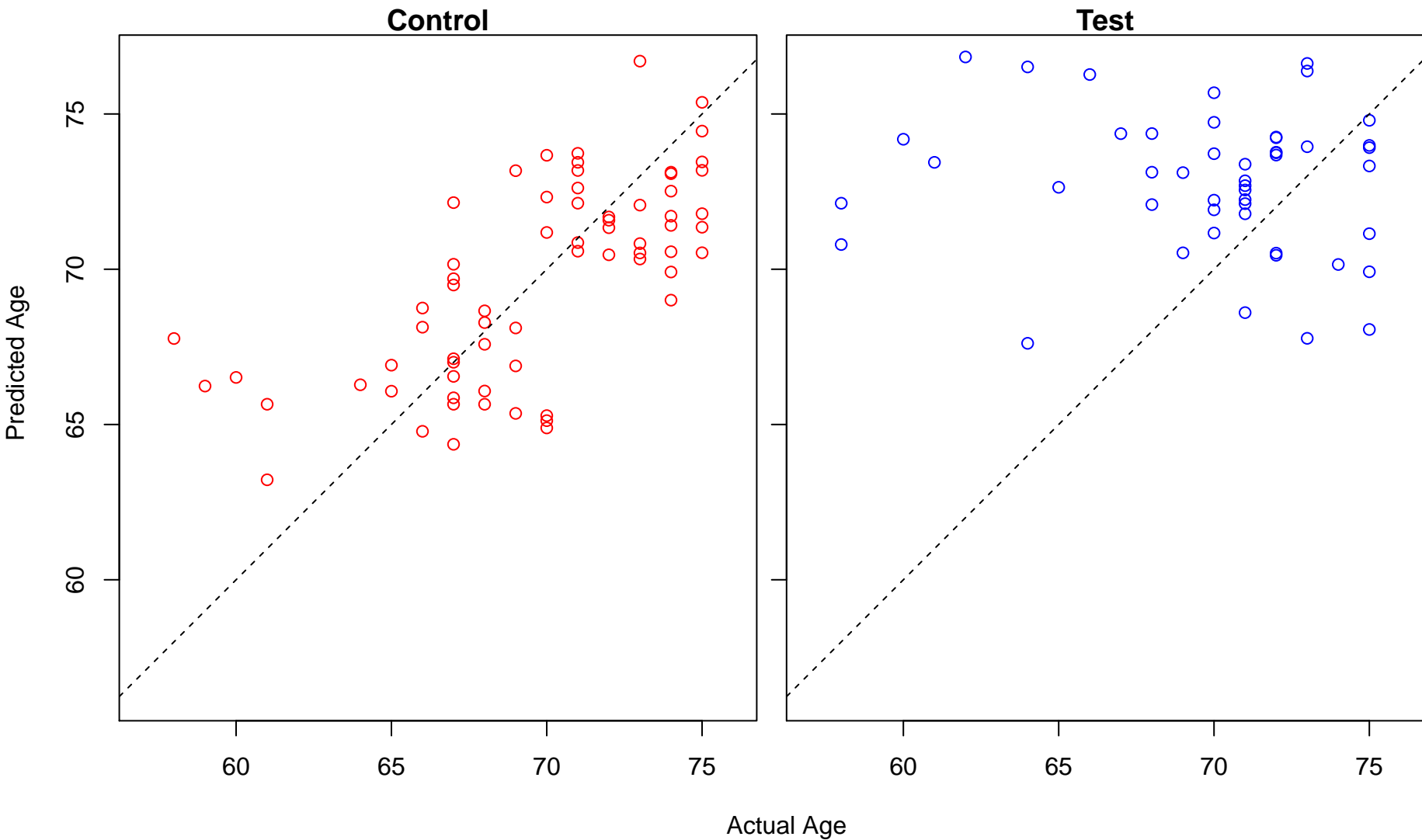
purine nucleoside metabolic process (Score: 1.629886)



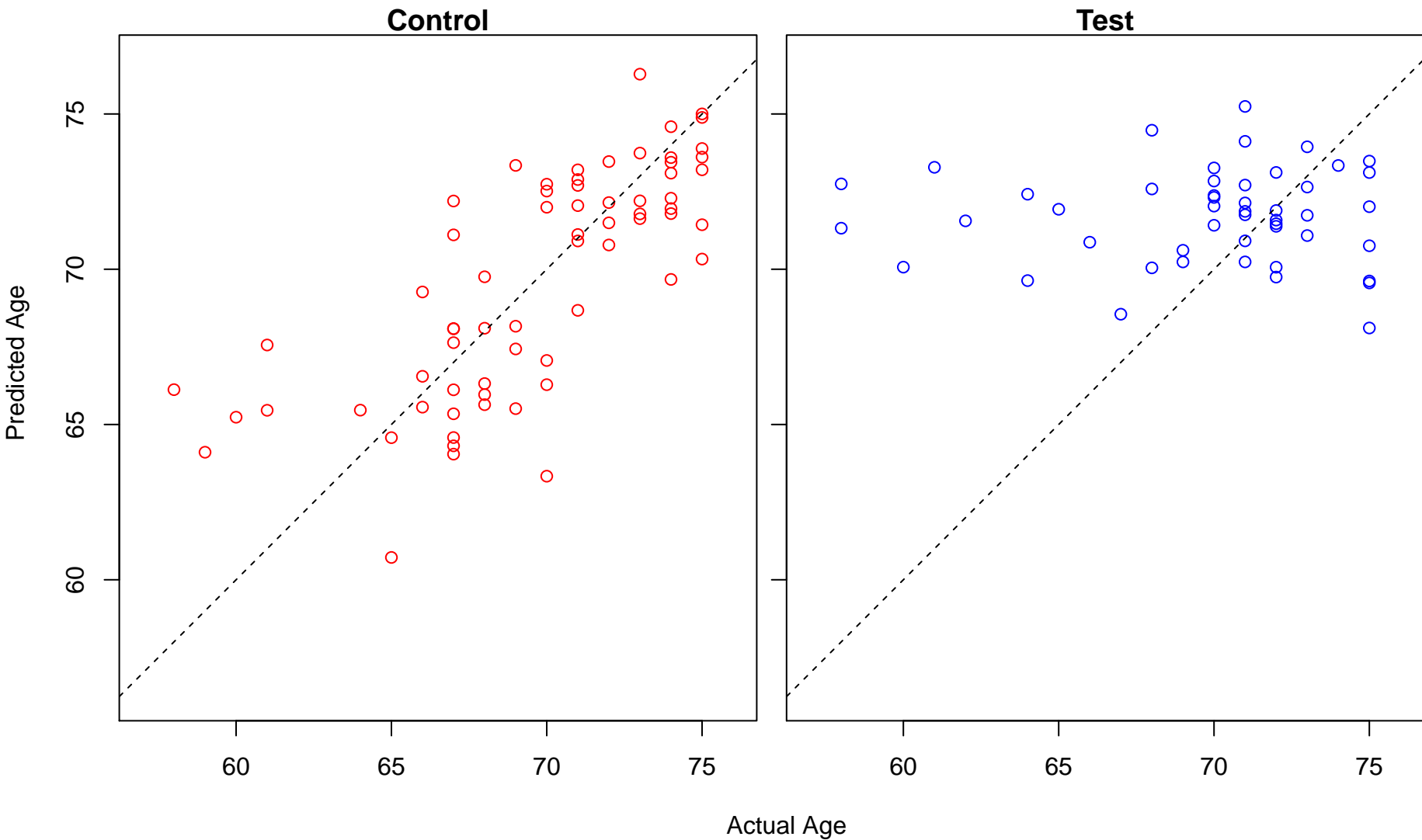
regulation of transforming growth factor beta receptor signaling pathway (Score: 1.629761)



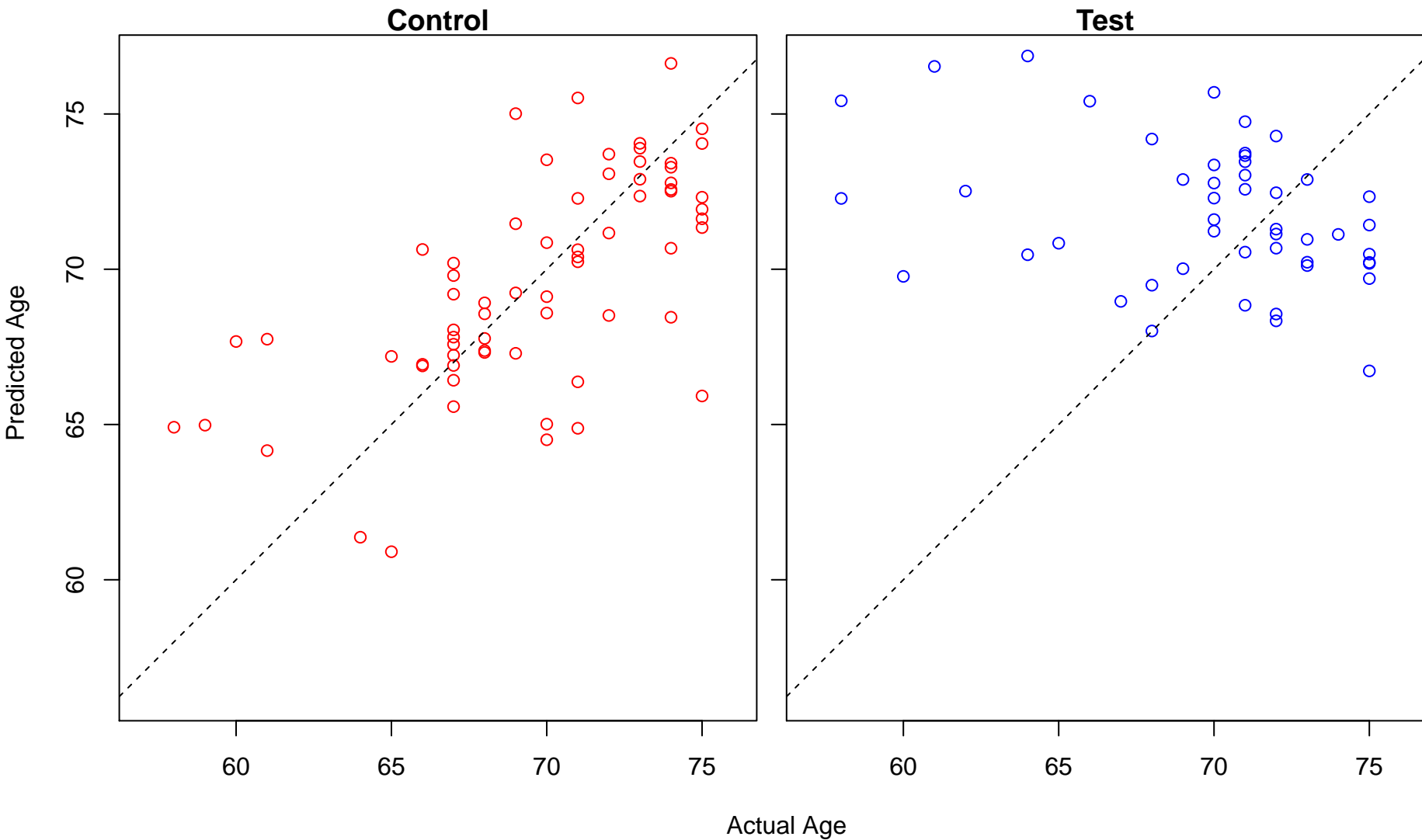
regulation of cellular response to transforming growth factor beta stimulus (Score: 1.629761)



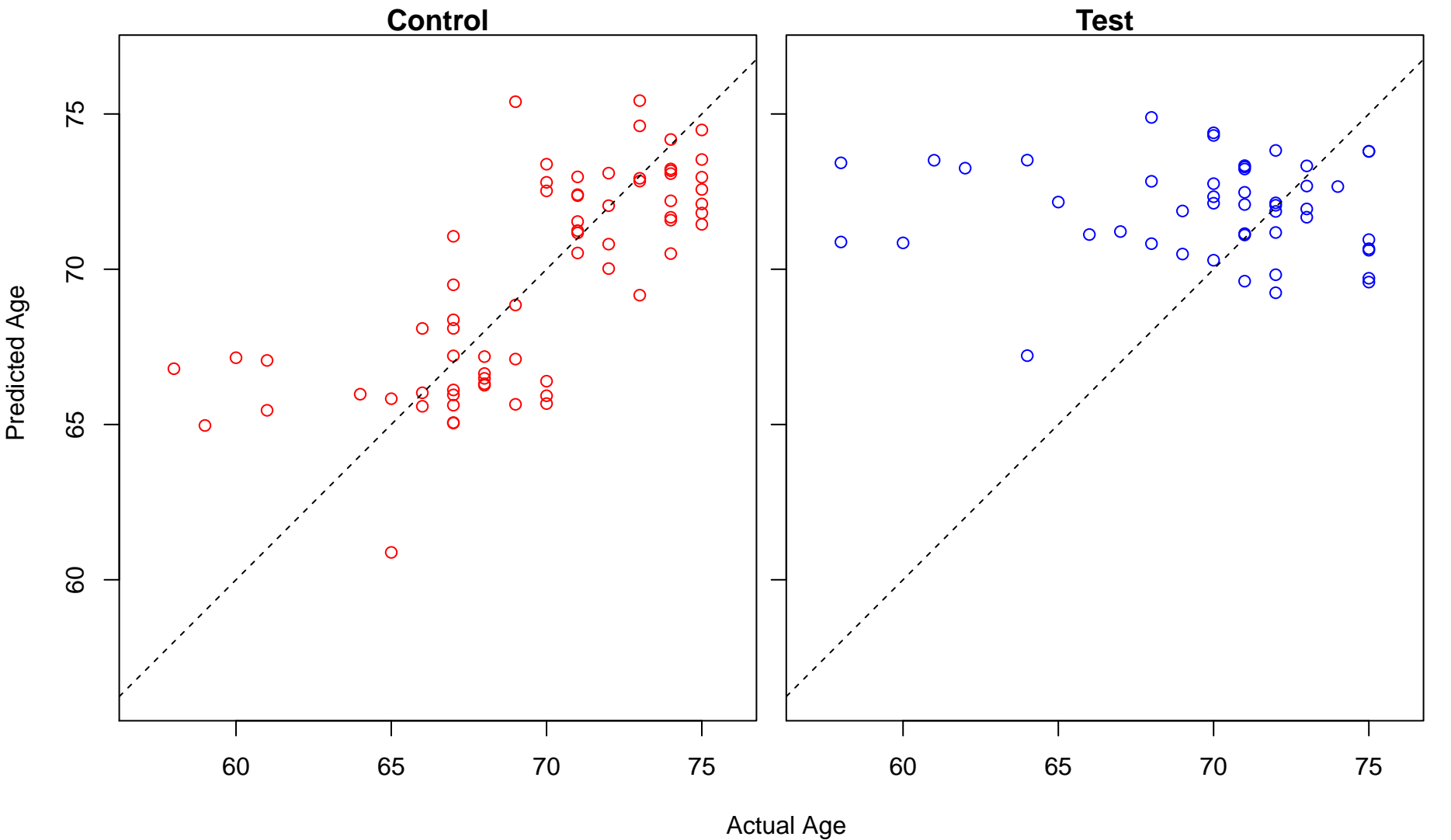
negative regulation of cell cycle G1/S phase transition (Score: 1.629650)



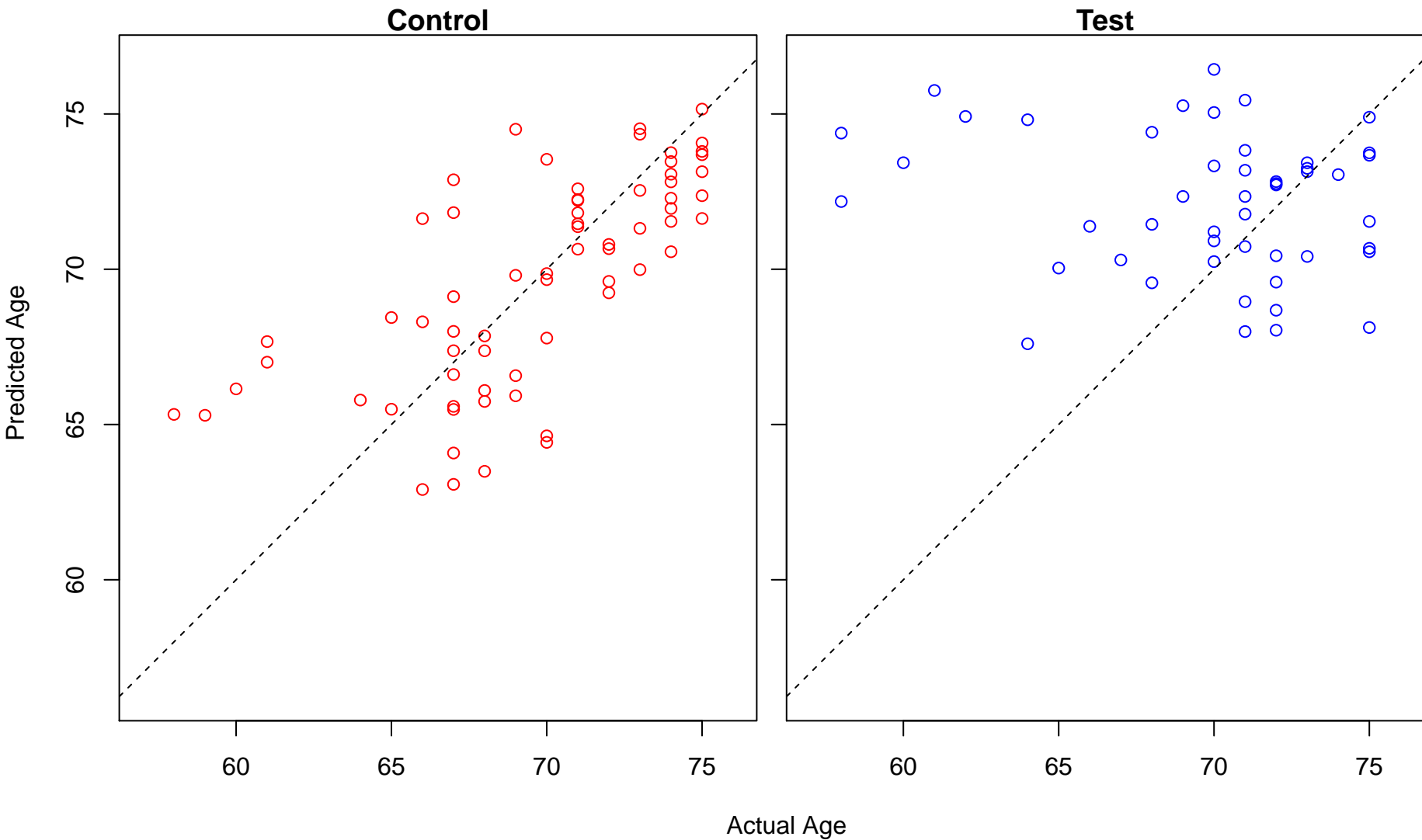
regulation of leukocyte apoptotic process (Score: 1.629510)



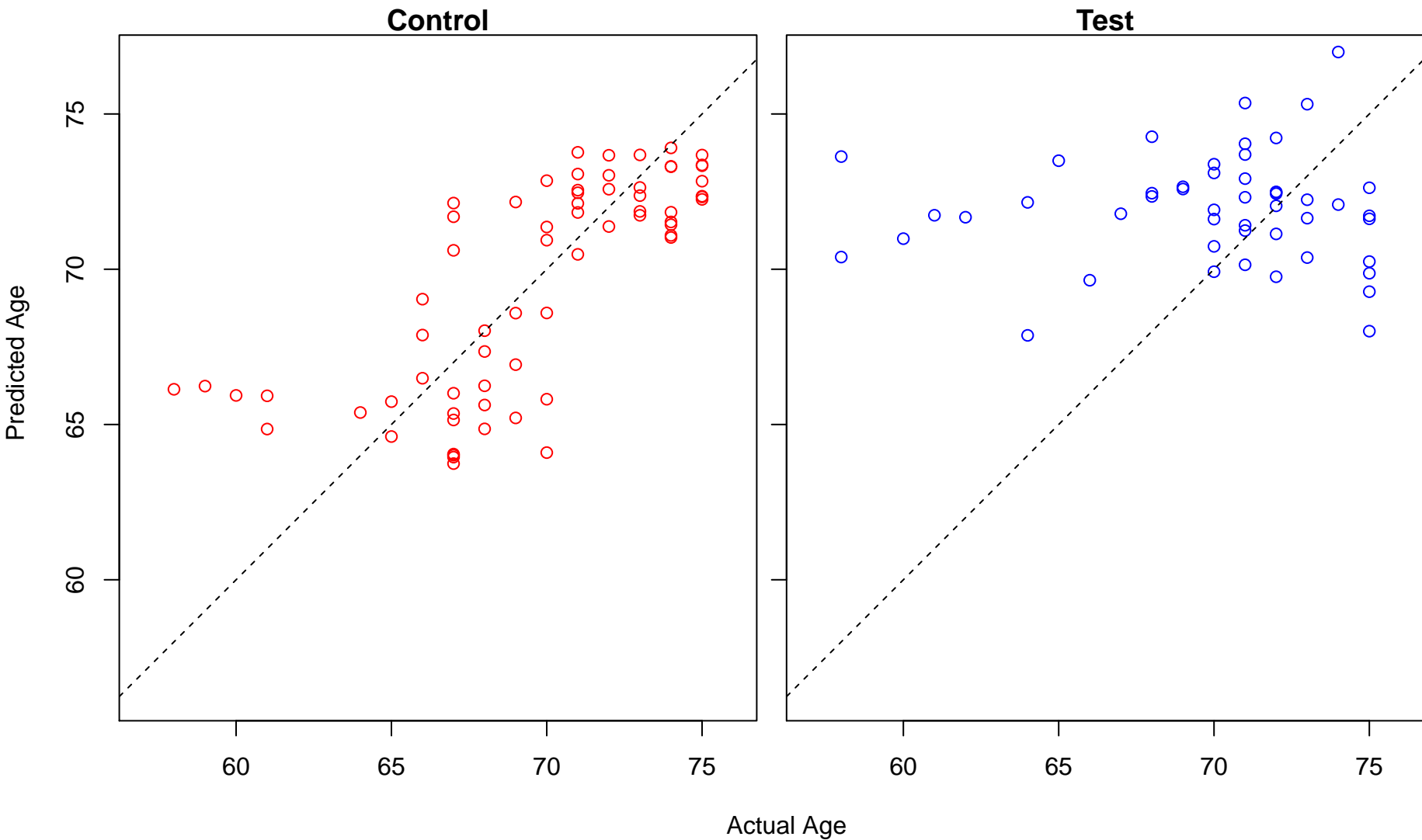
Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (Score



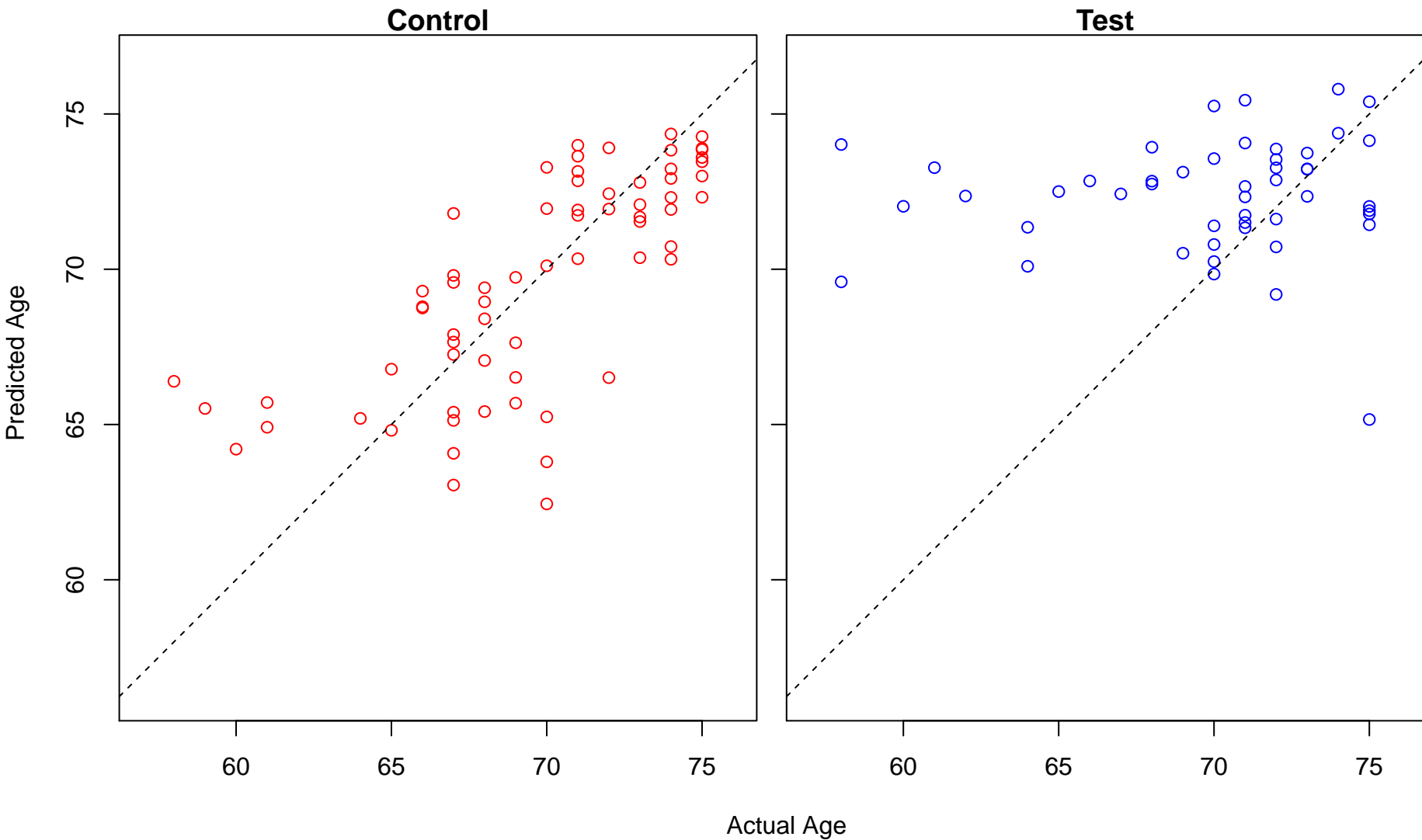
citrate metabolic process (Score: 1.628979)



RNA splicing, via transesterification reactions (Score: 1.628921)

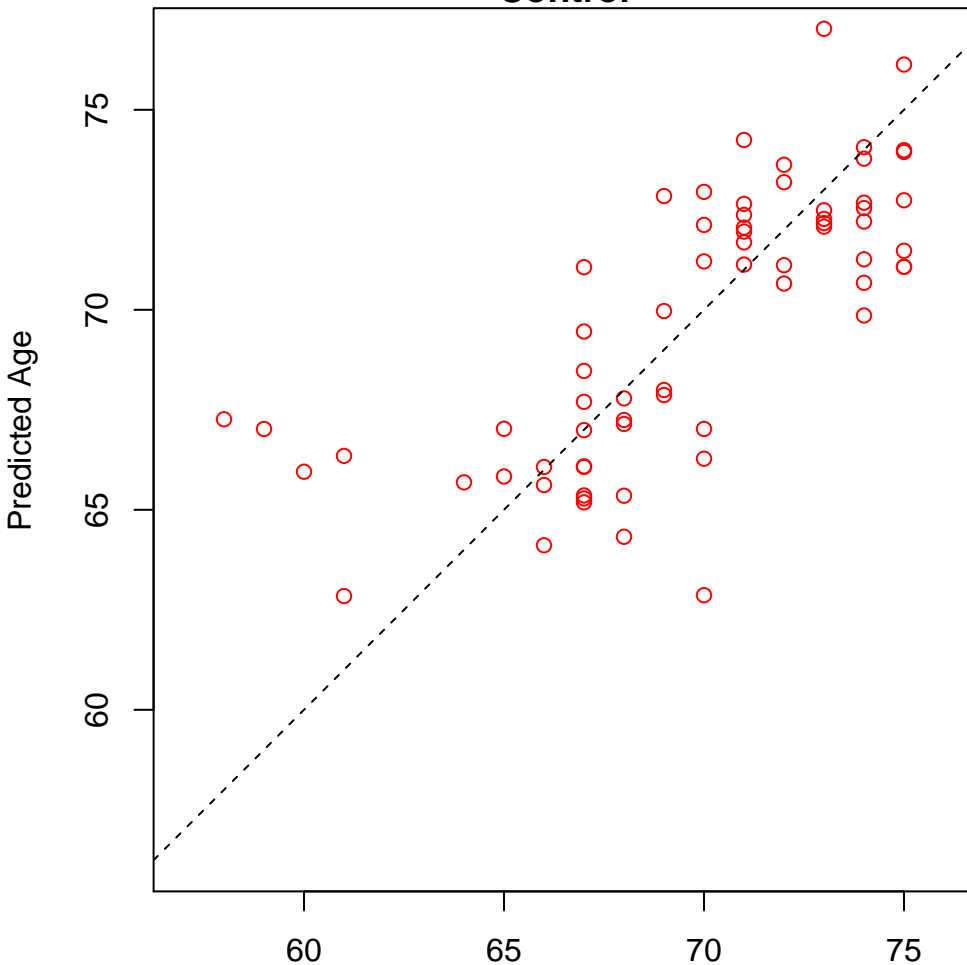


positive regulation of translation (Score: 1.628809)

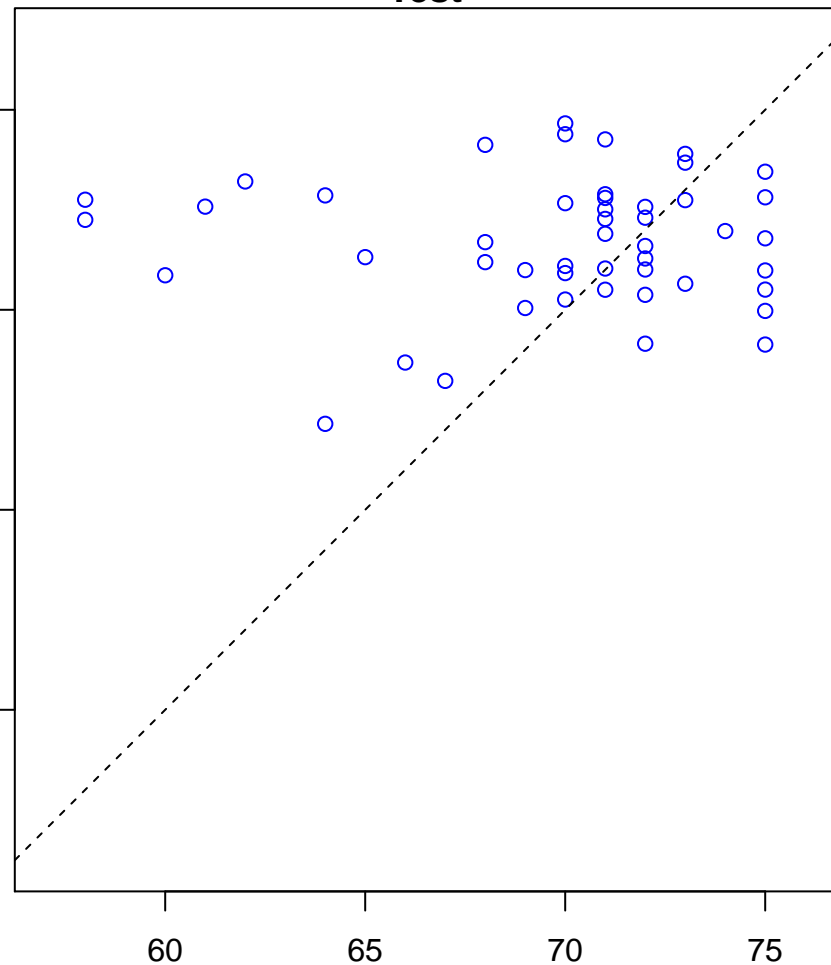


purine ribonucleoside metabolic process (Score: 1.628780)

Control

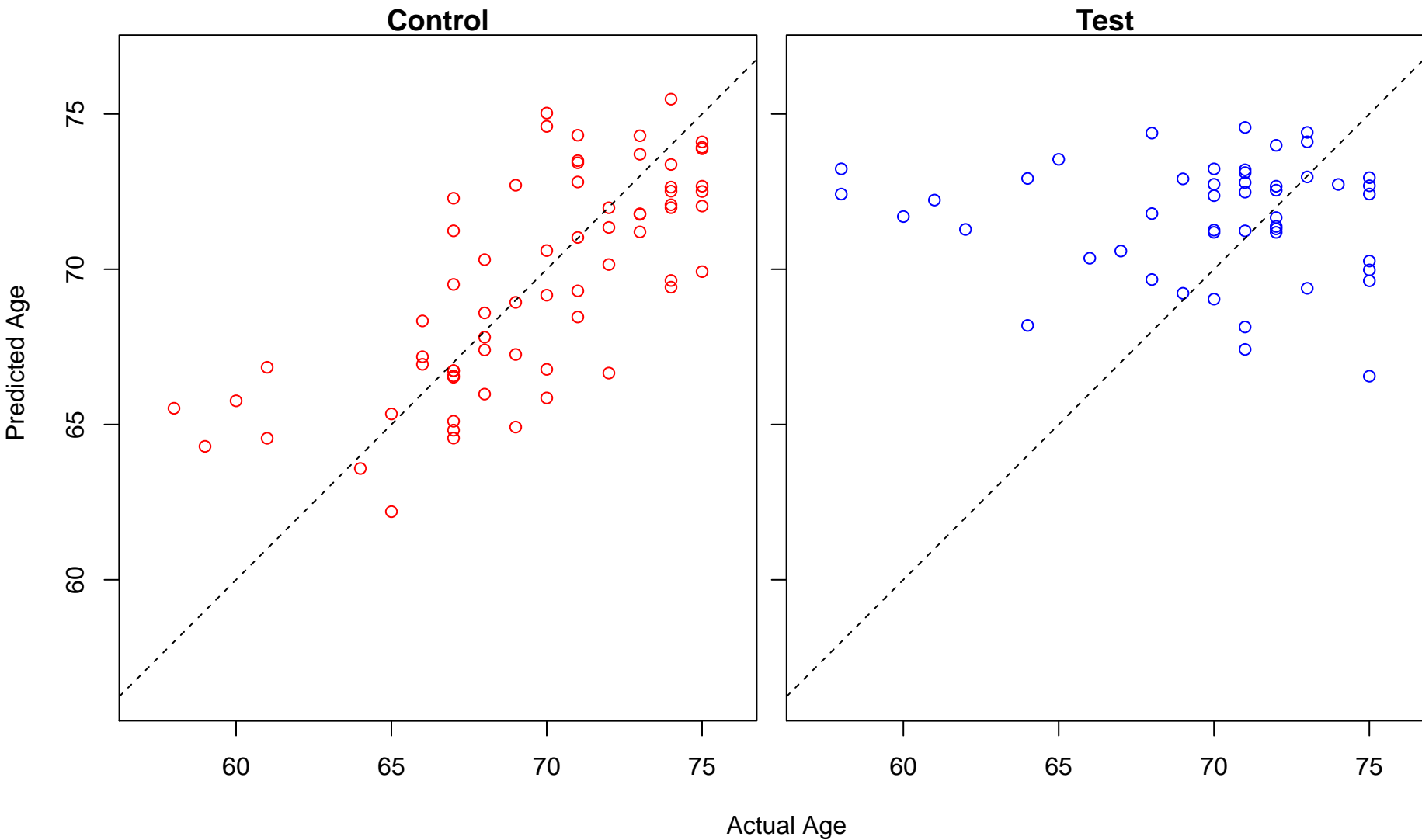


Test

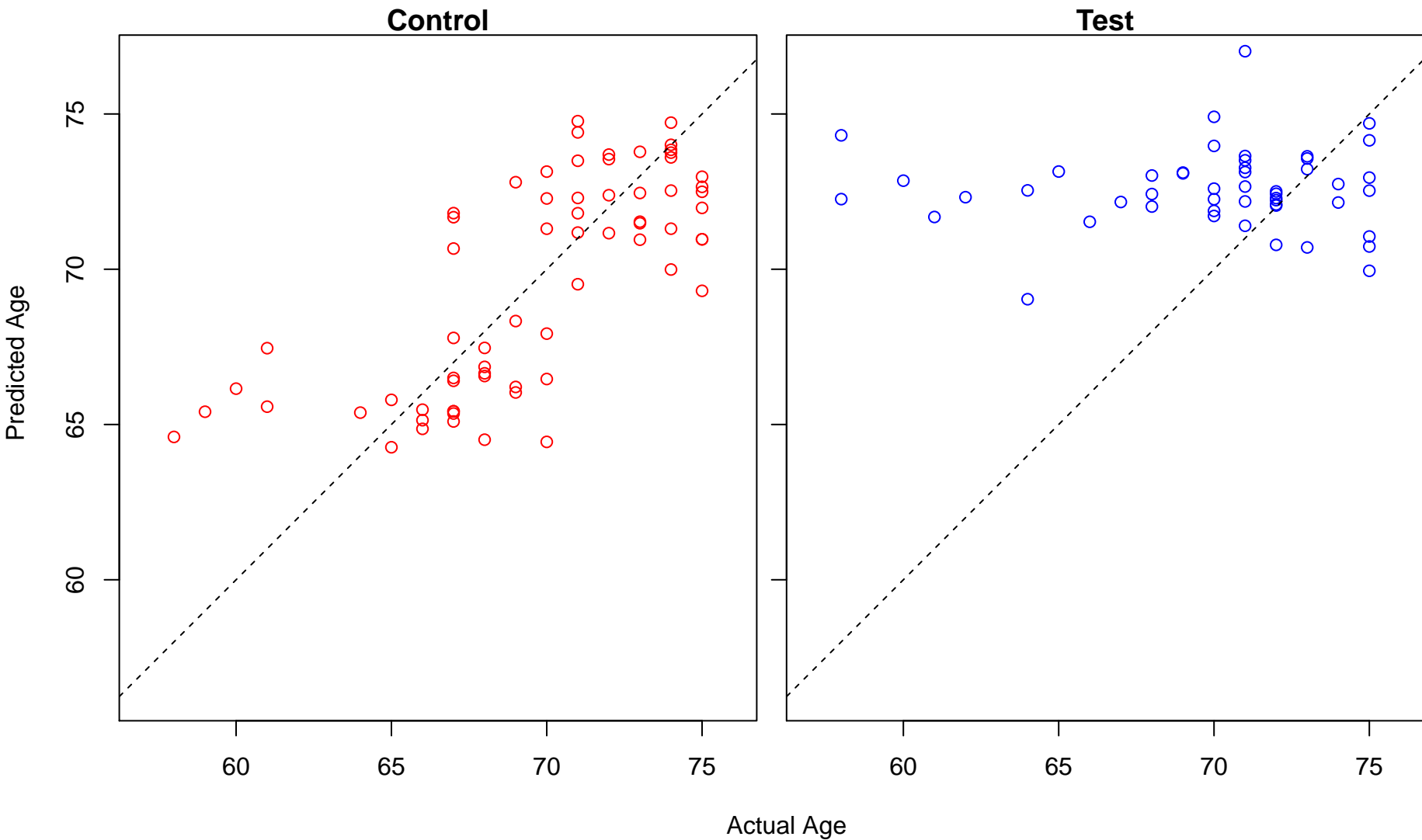


Actual Age

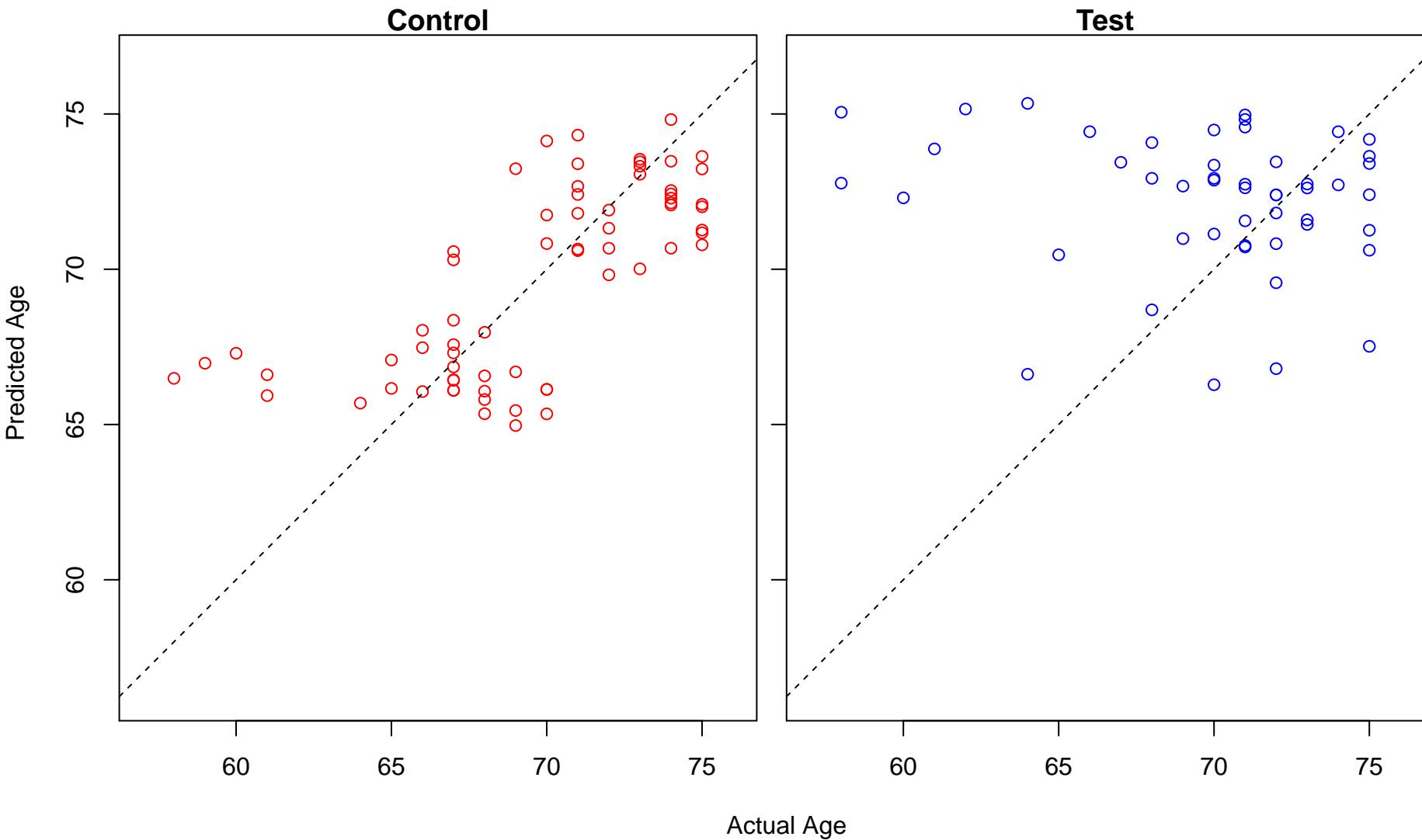
cellular response to radiation (Score: 1.628698)



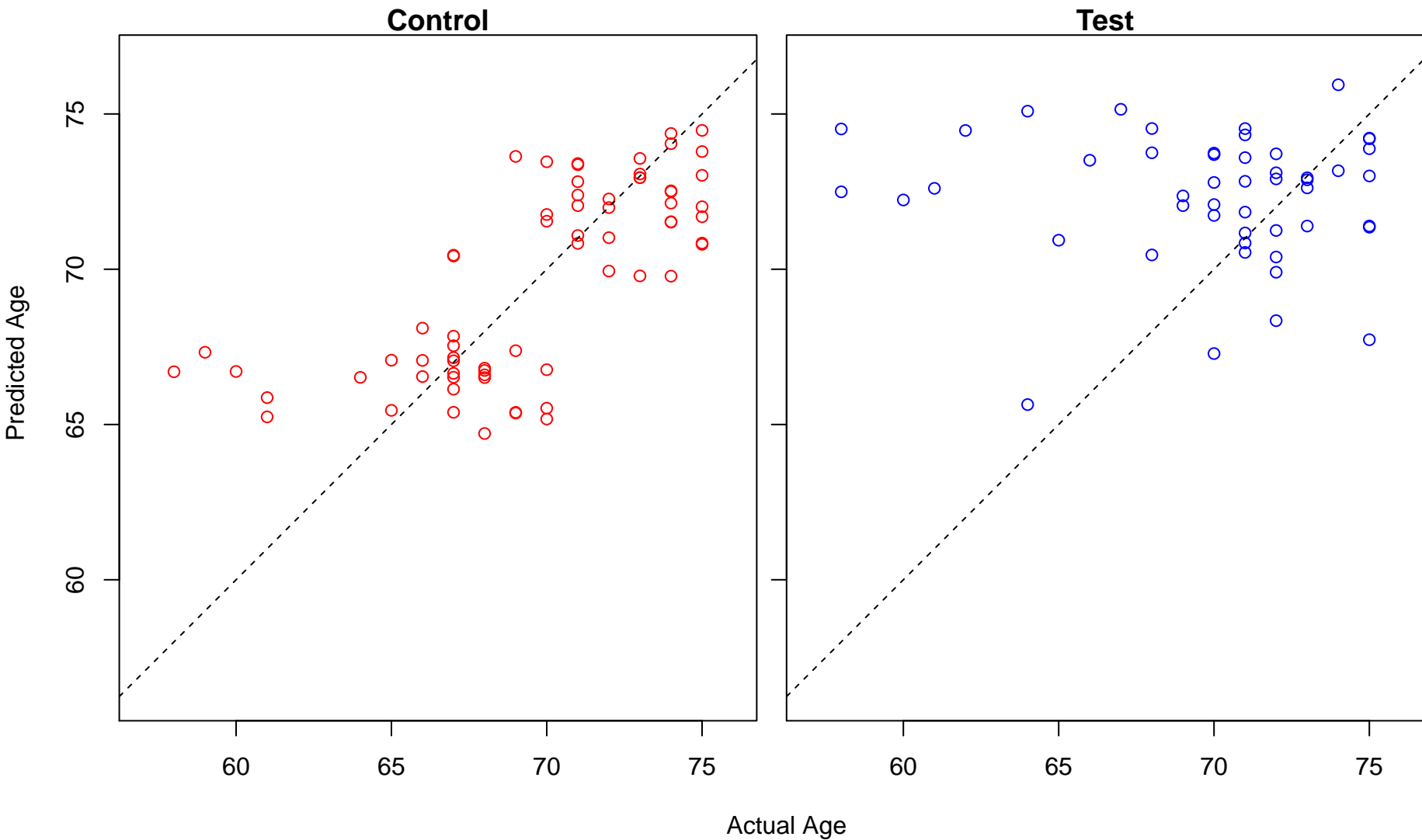
RNA 3'-end processing (Score: 1.628609)



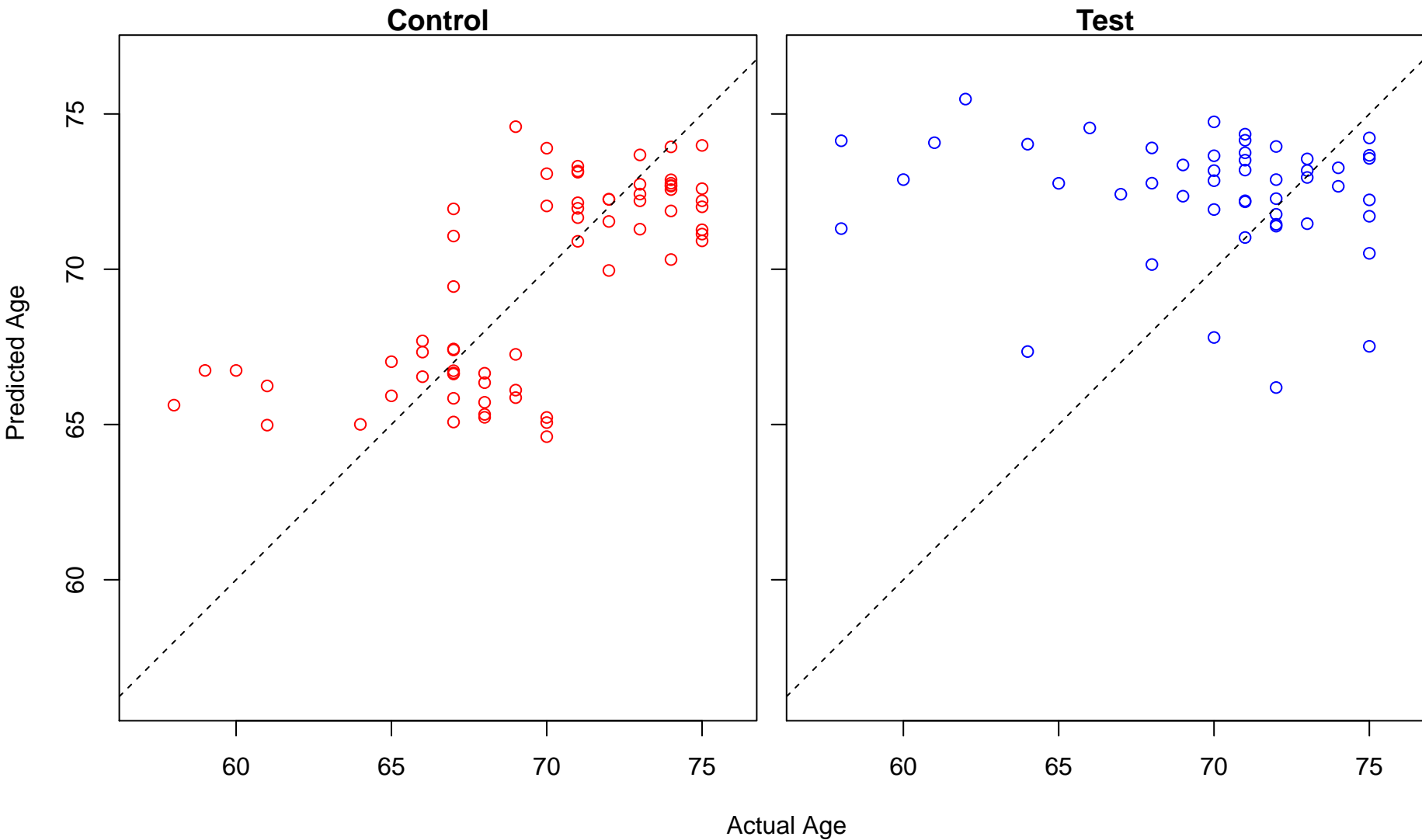
regulation of smooth muscle cell migration (Score: 1.628218)



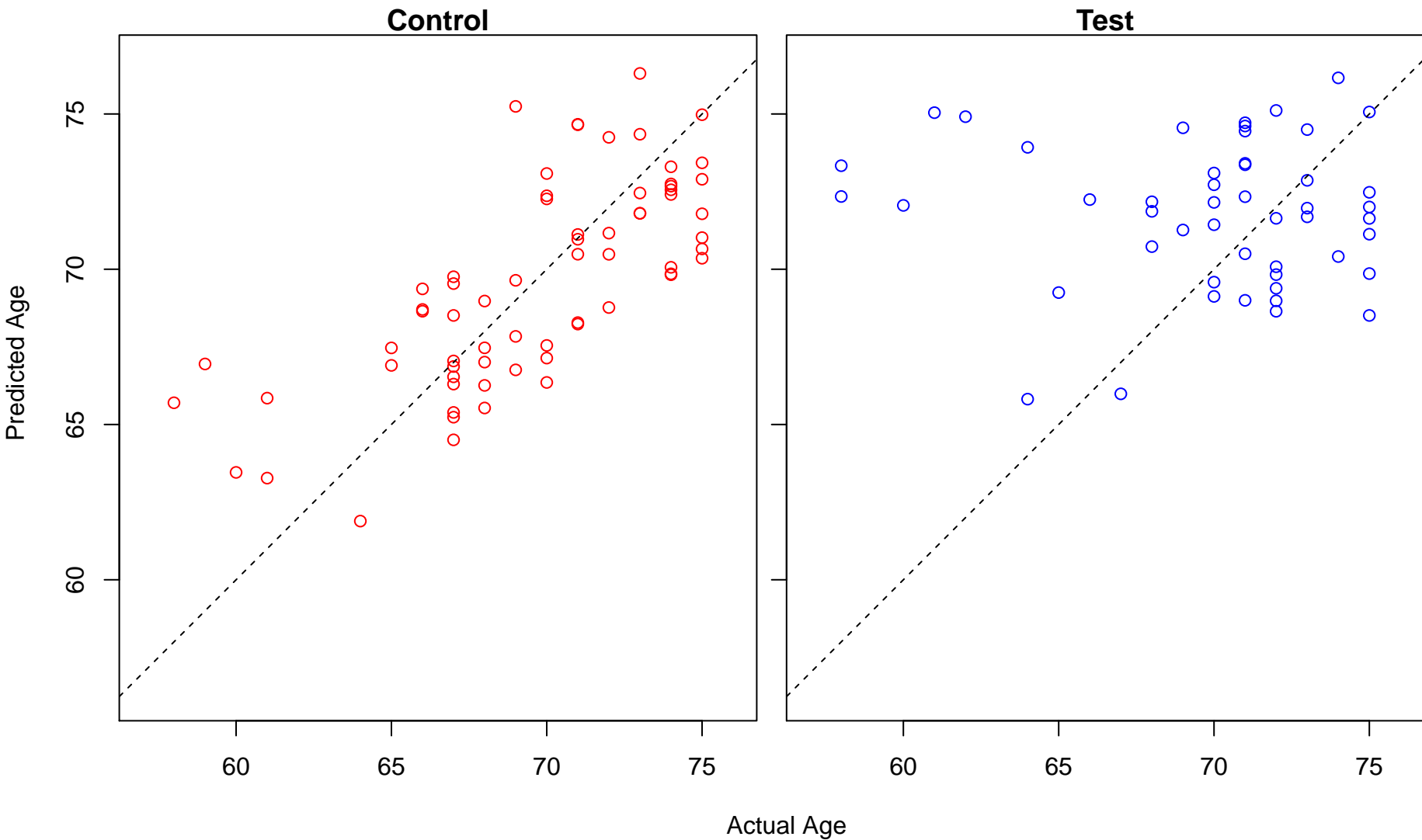
actin filament polymerization (Score: 1.627437)



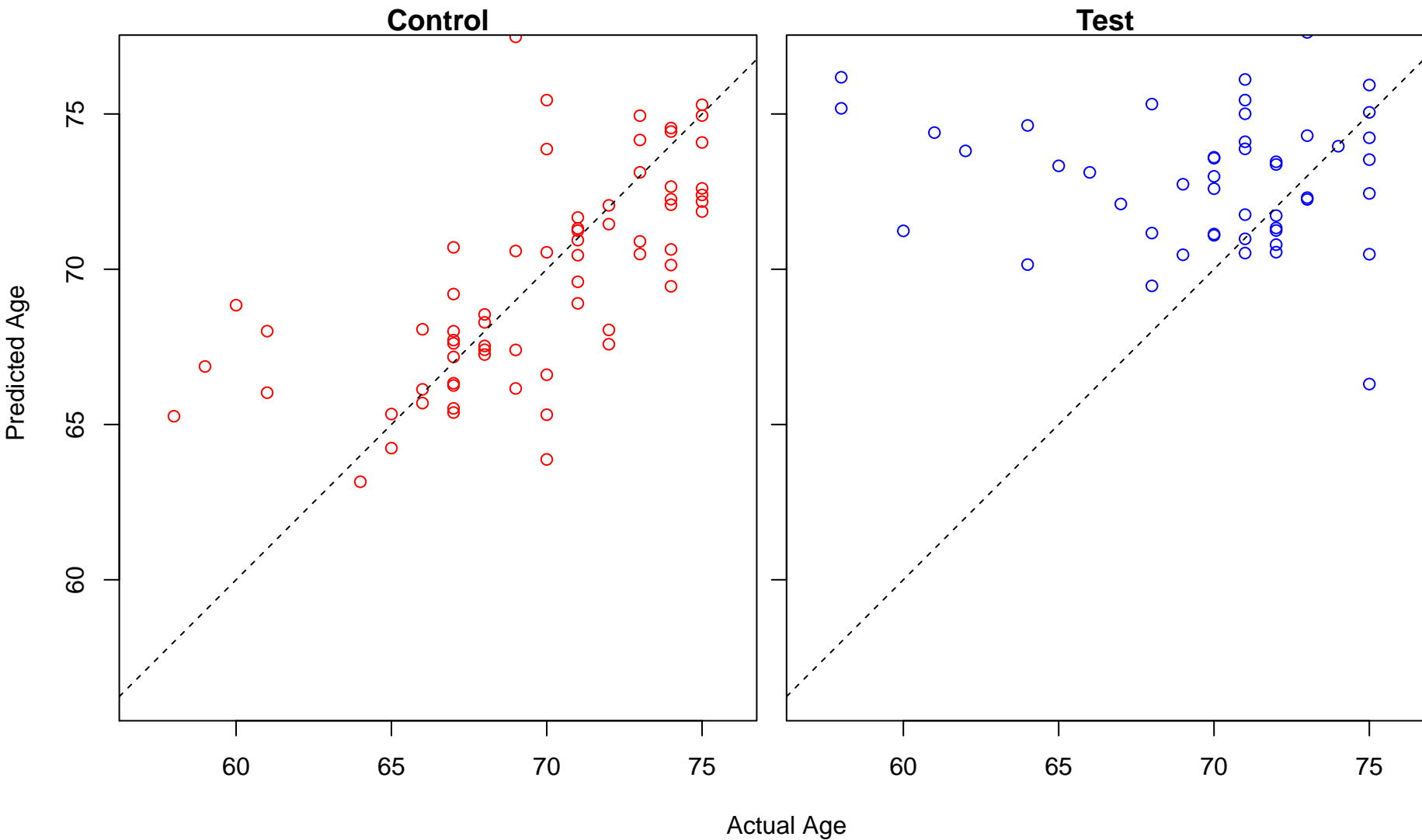
protein deubiquitination (Score: 1.627404)



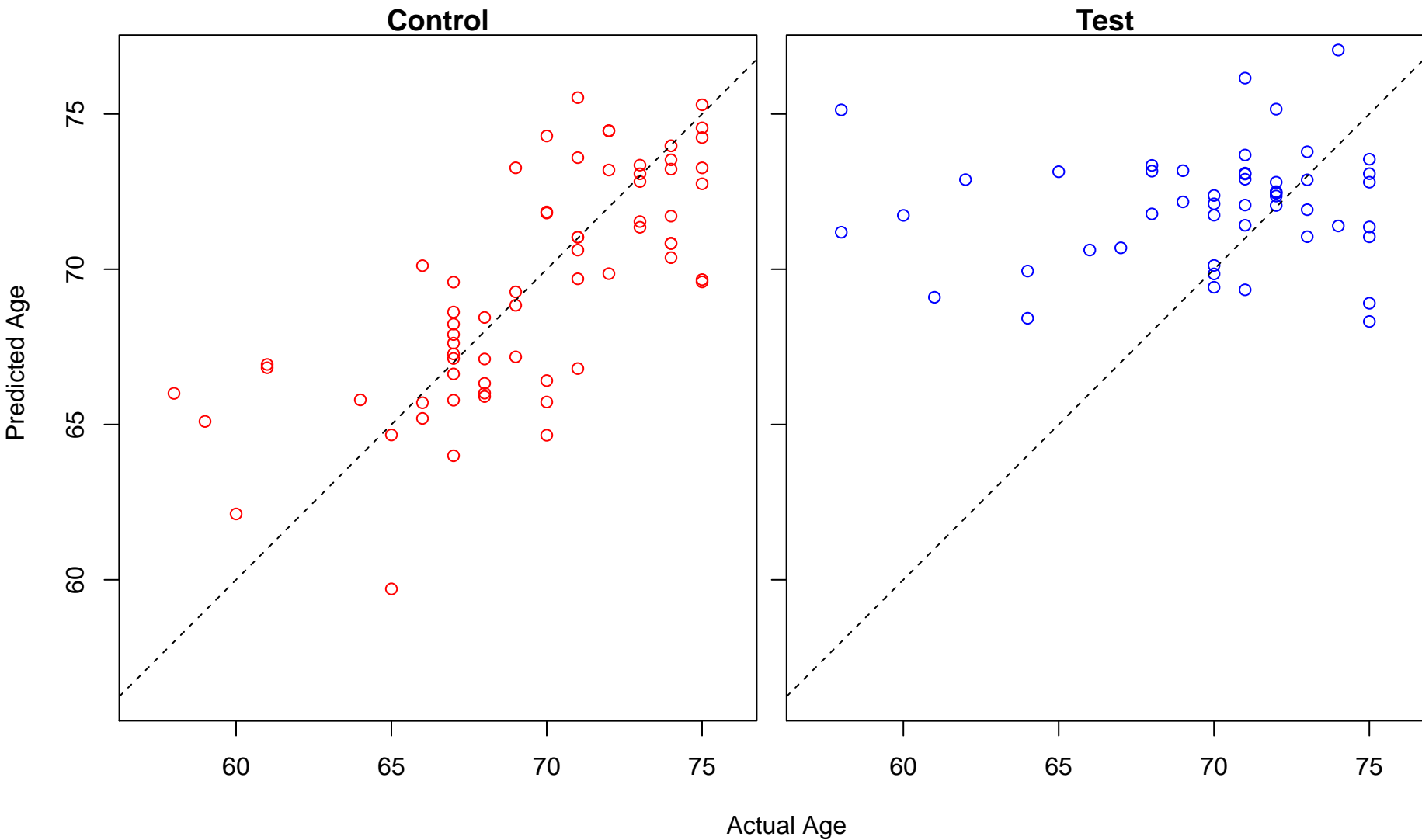
epithelial tube morphogenesis (Score: 1.627069)



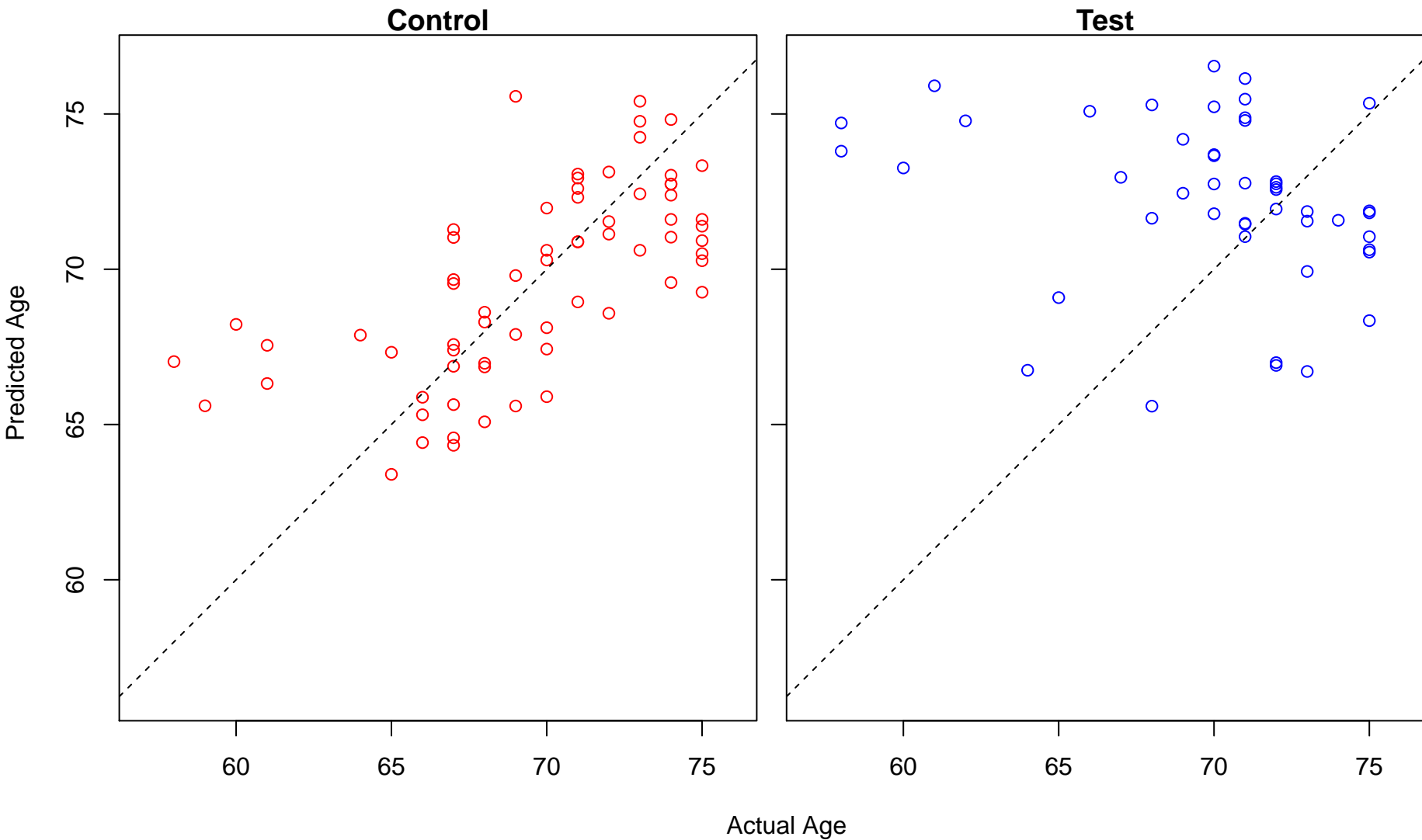
positive regulation of protein serine/threonine kinase activity (Score: 1.626922)



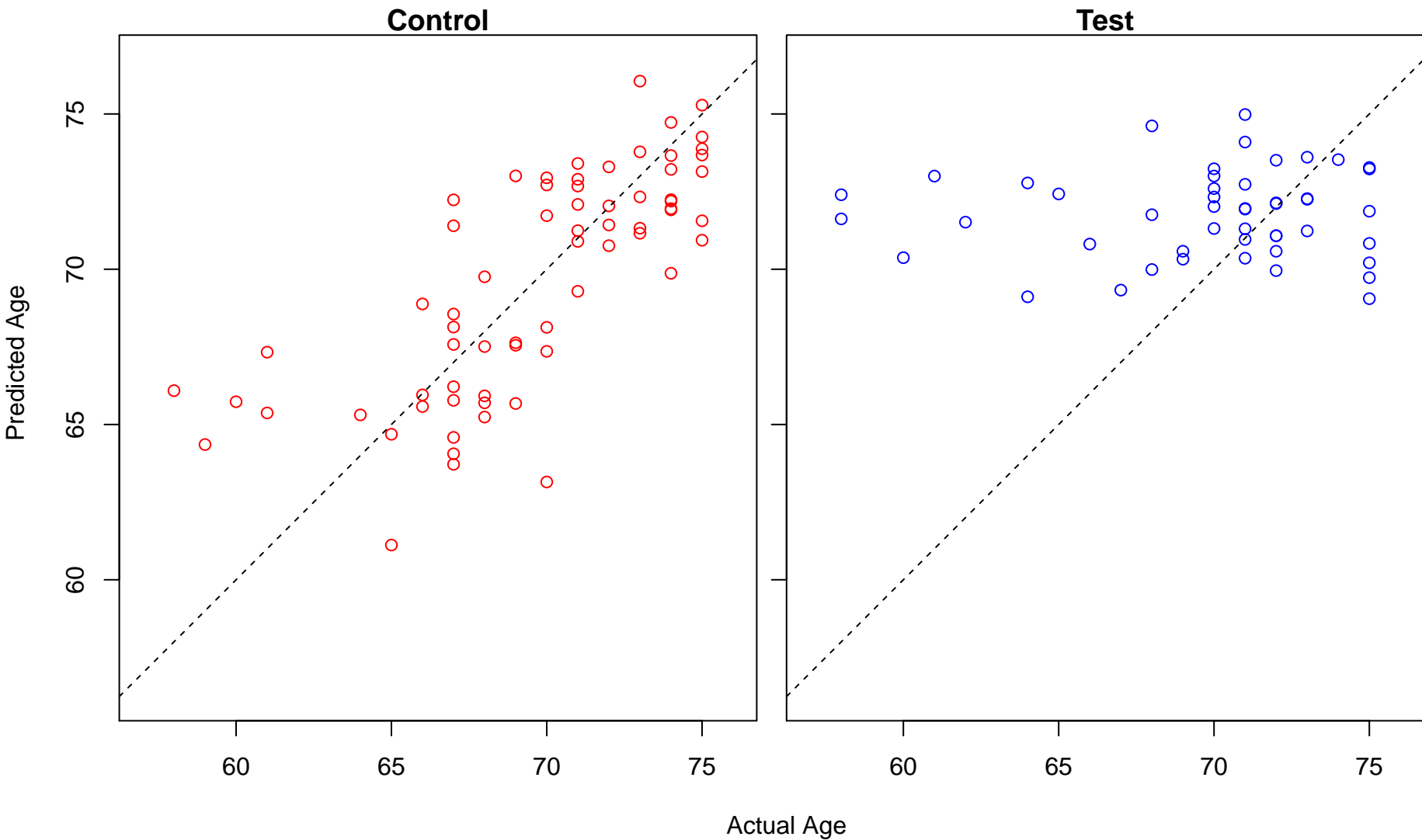
protein localization to nucleus (Score: 1.626920)



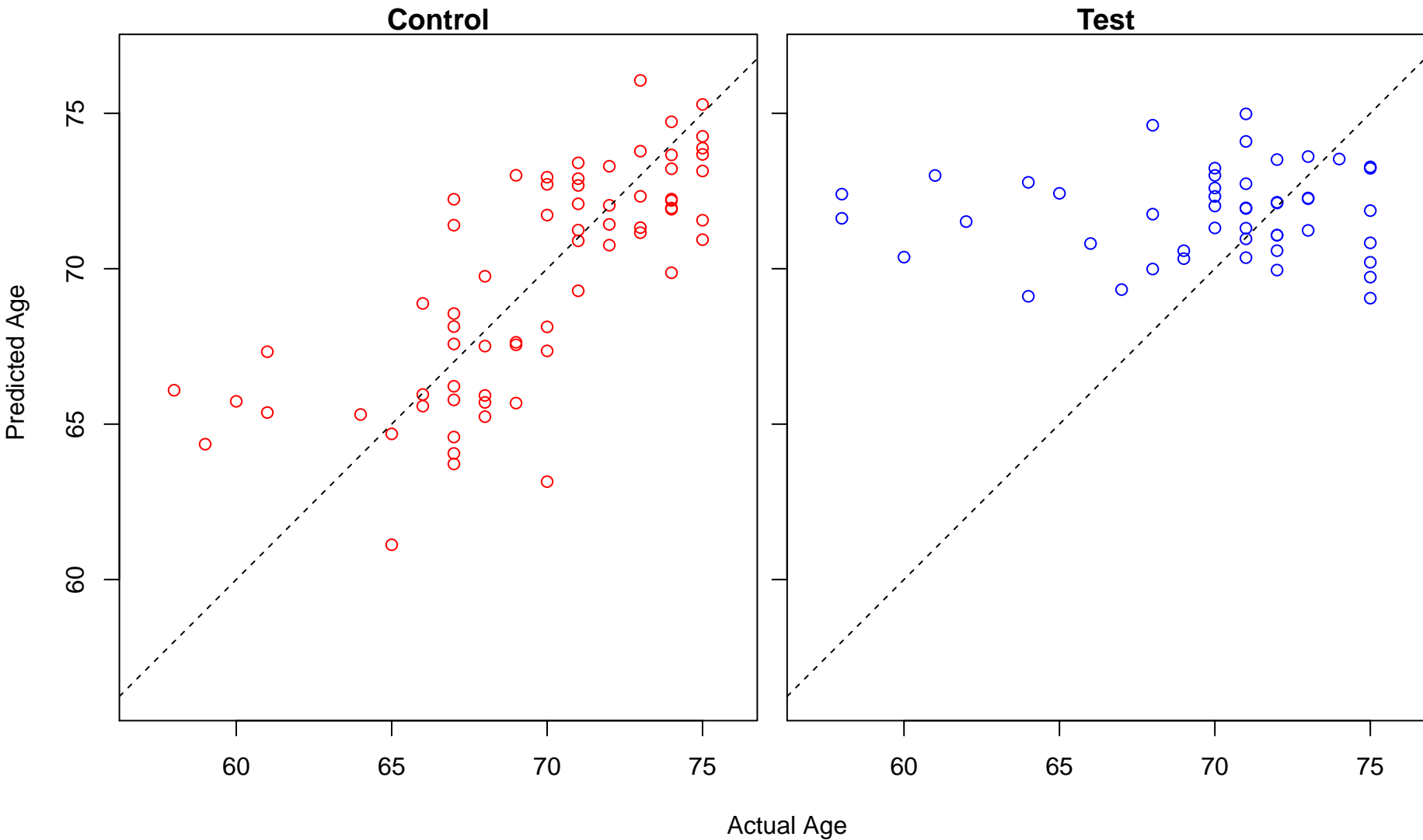
positive regulation of alpha-beta T cell differentiation (Score: 1.626656)



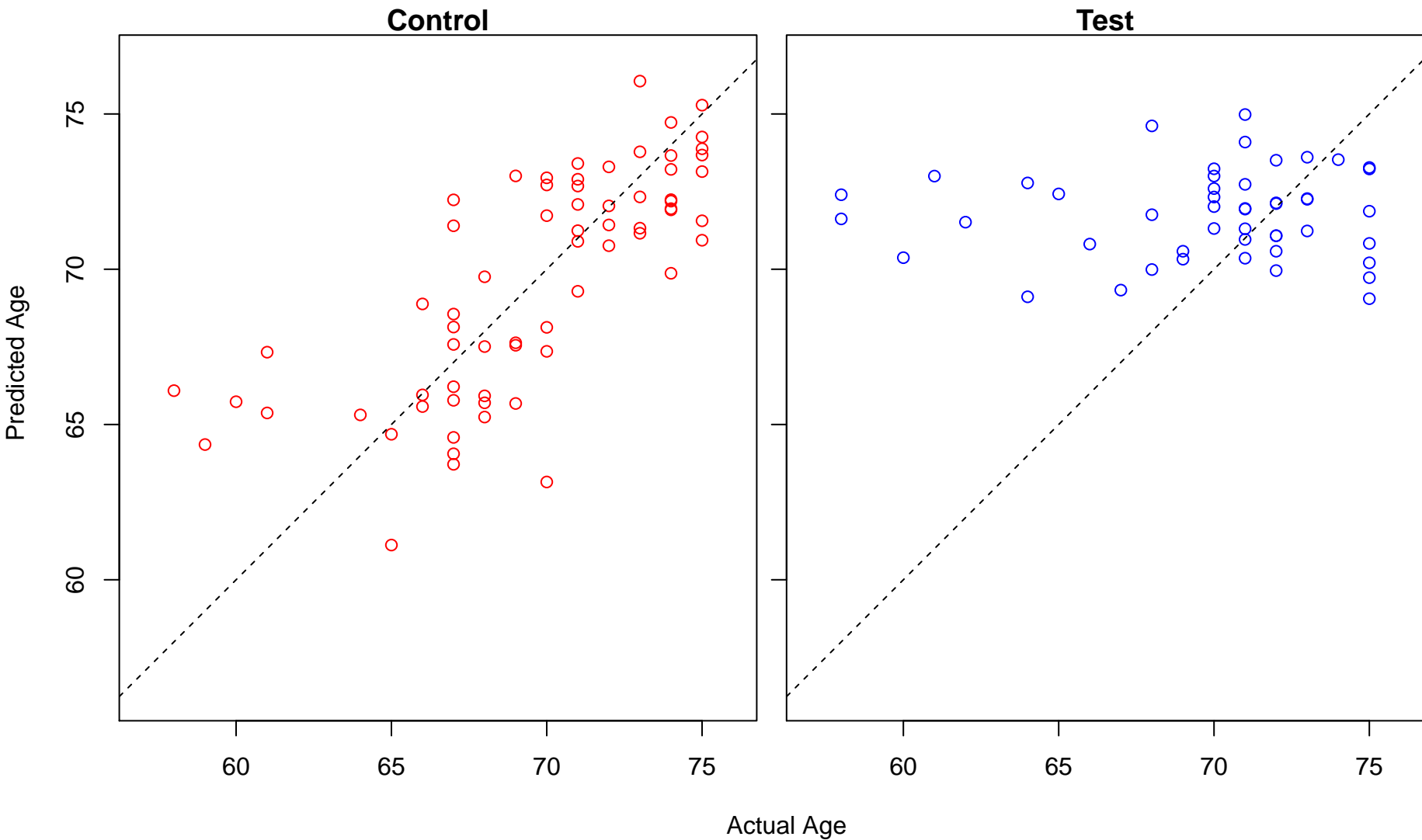
signal transduction involved in mitotic cell cycle checkpoint (Score: 1.626612)



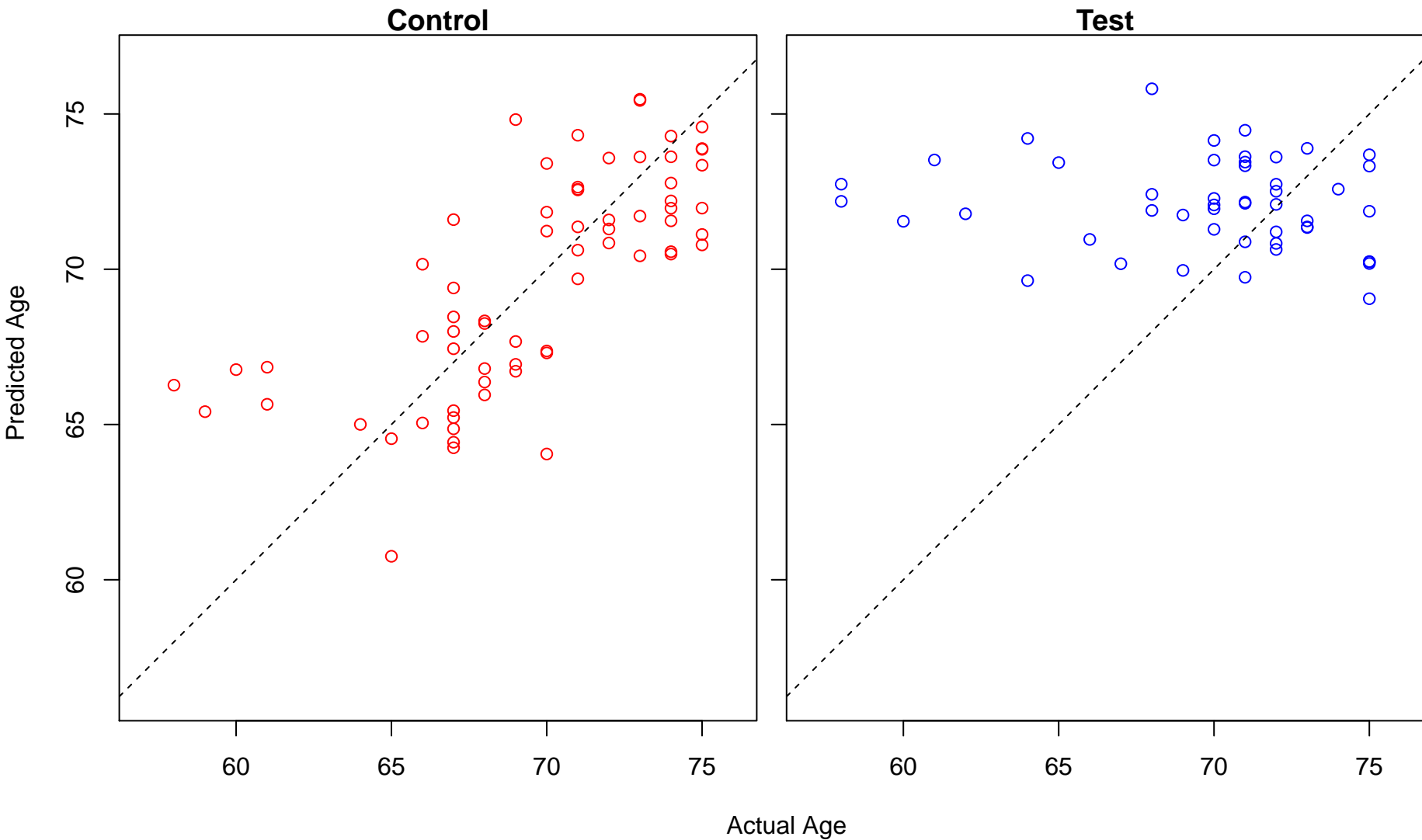
signal transduction involved in mitotic DNA damage checkpoint (Score: 1.626612)



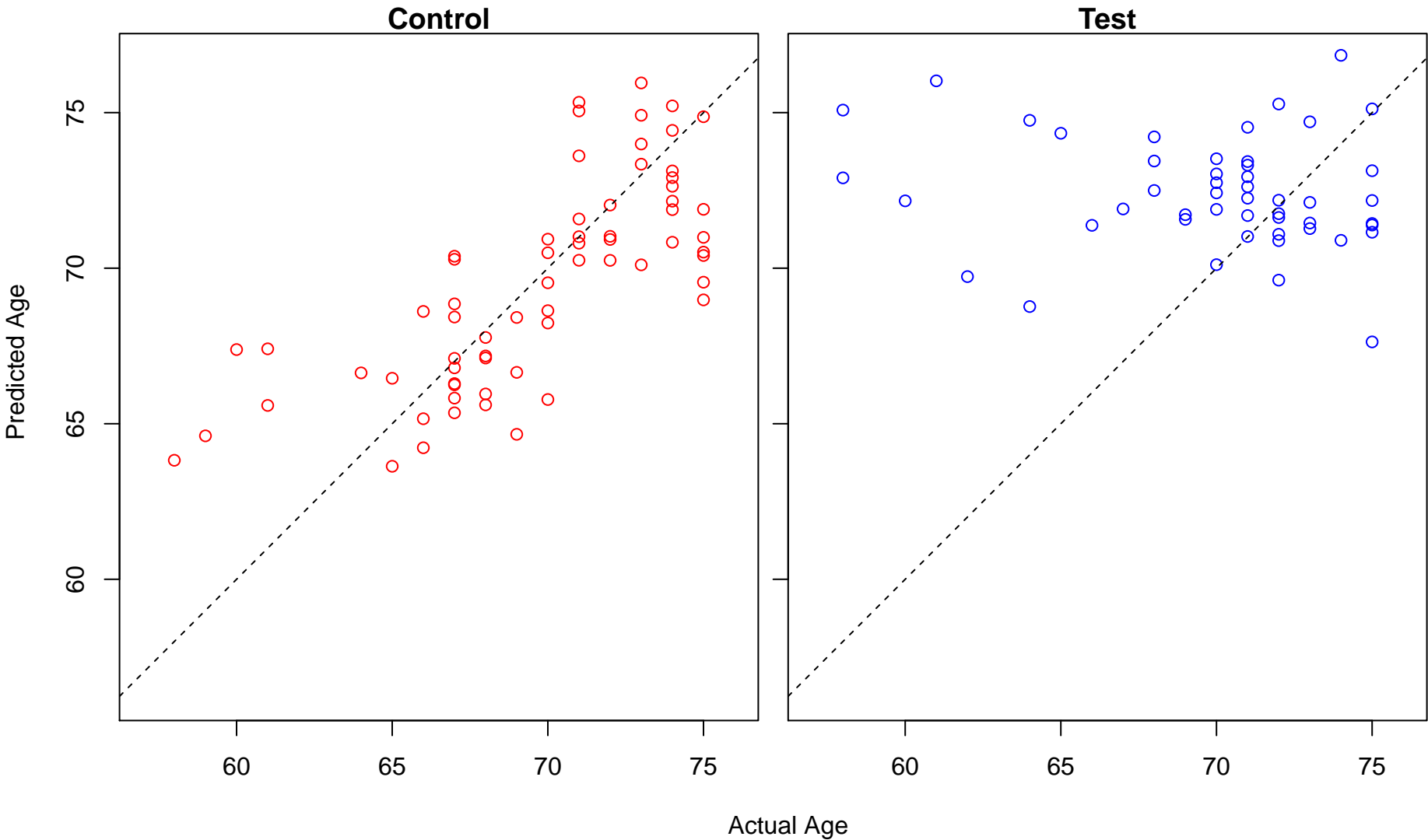
signal transduction involved in mitotic DNA integrity checkpoint (Score: 1.626612)



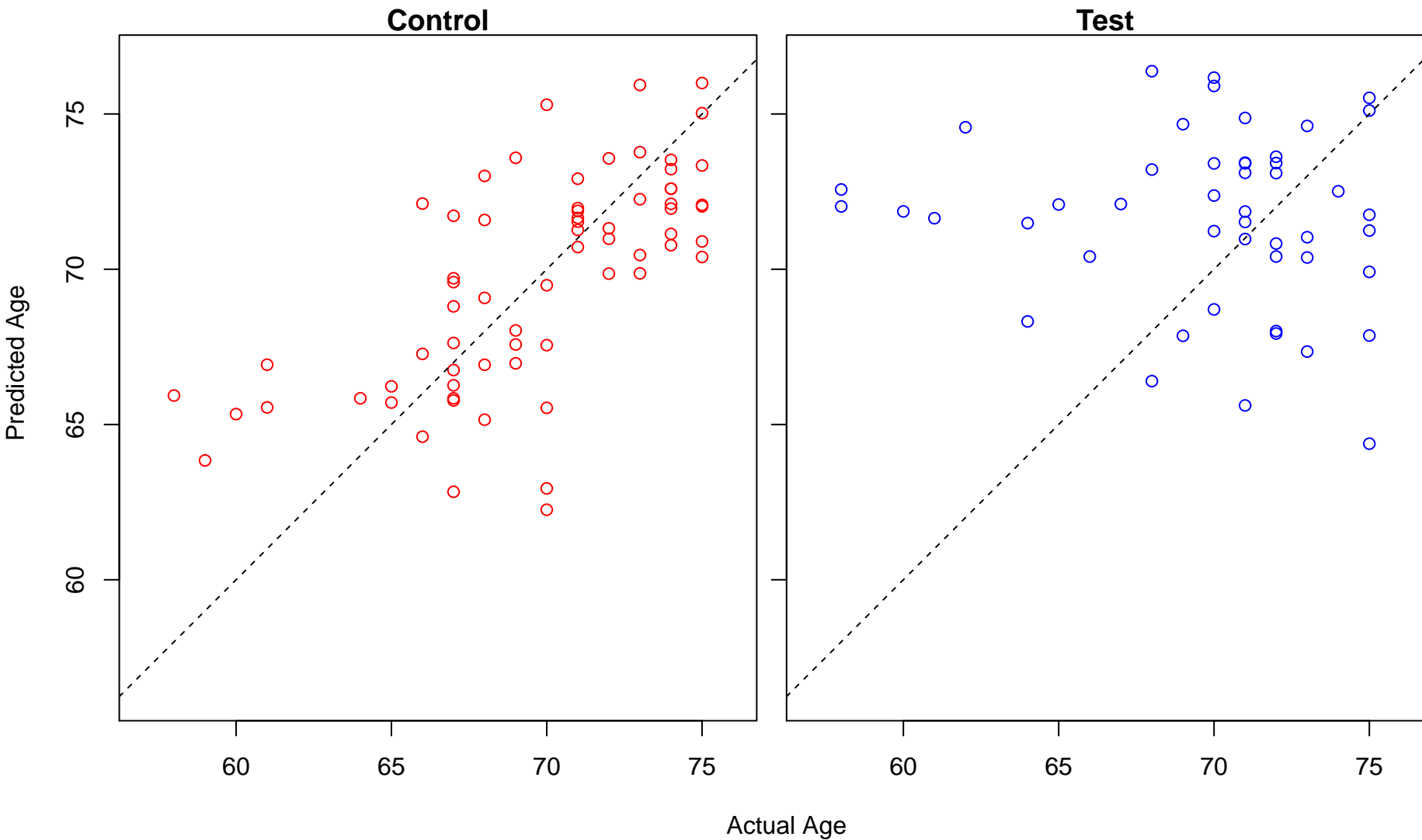
regulation of canonical Wnt signaling pathway (Score: 1.625467)



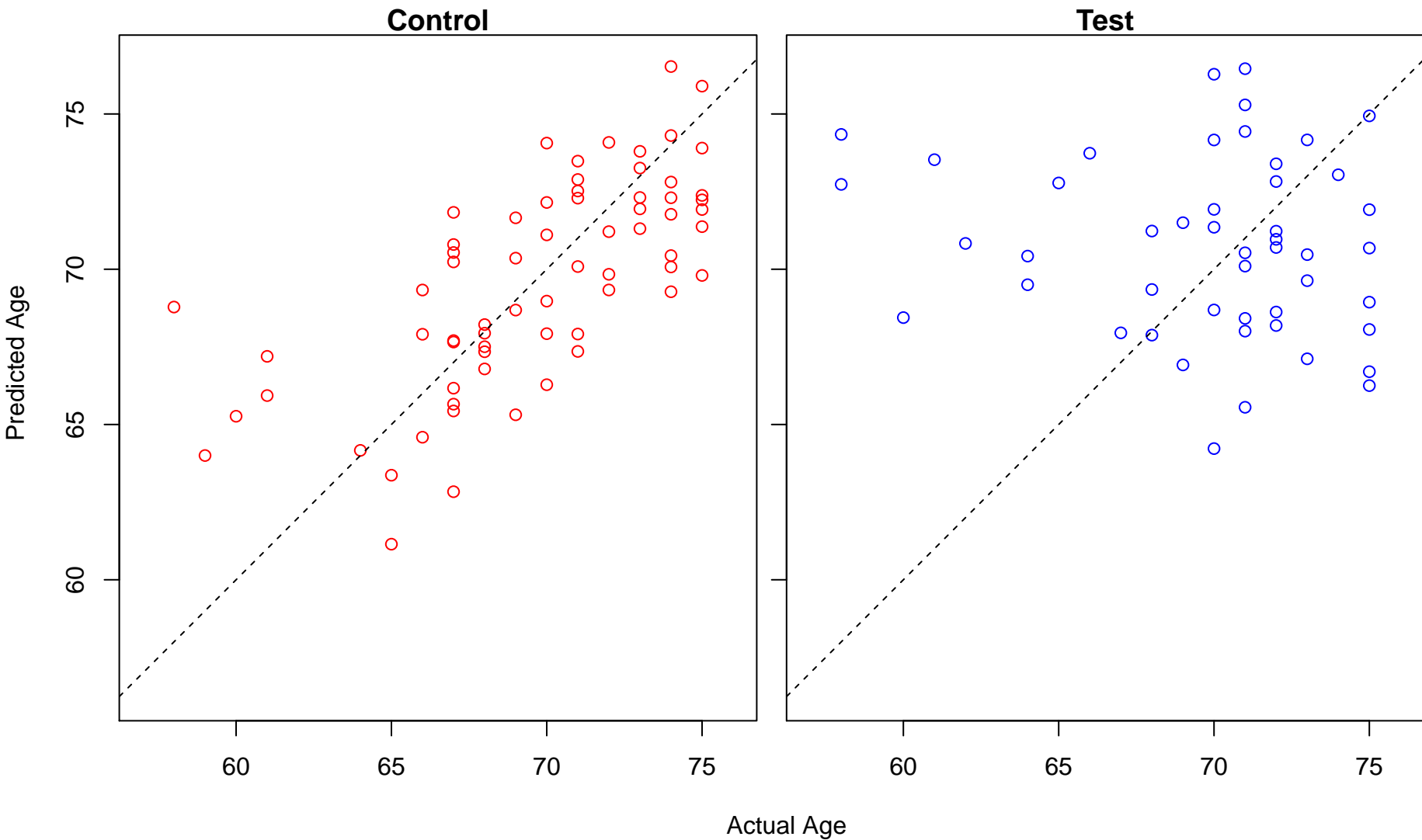
branched-chain amino acid metabolic process (Score: 1.625232)



B cell differentiation (Score: 1.624835)

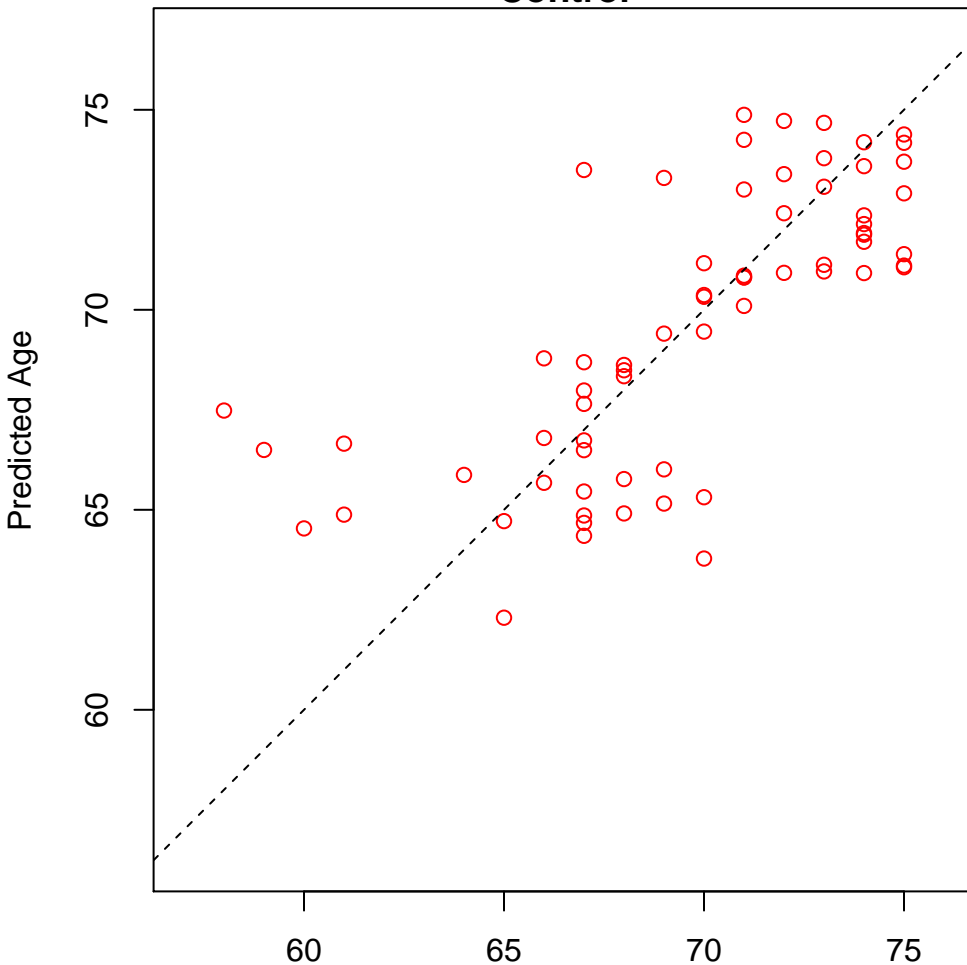


positive regulation of focal adhesion assembly (Score: 1.624802)

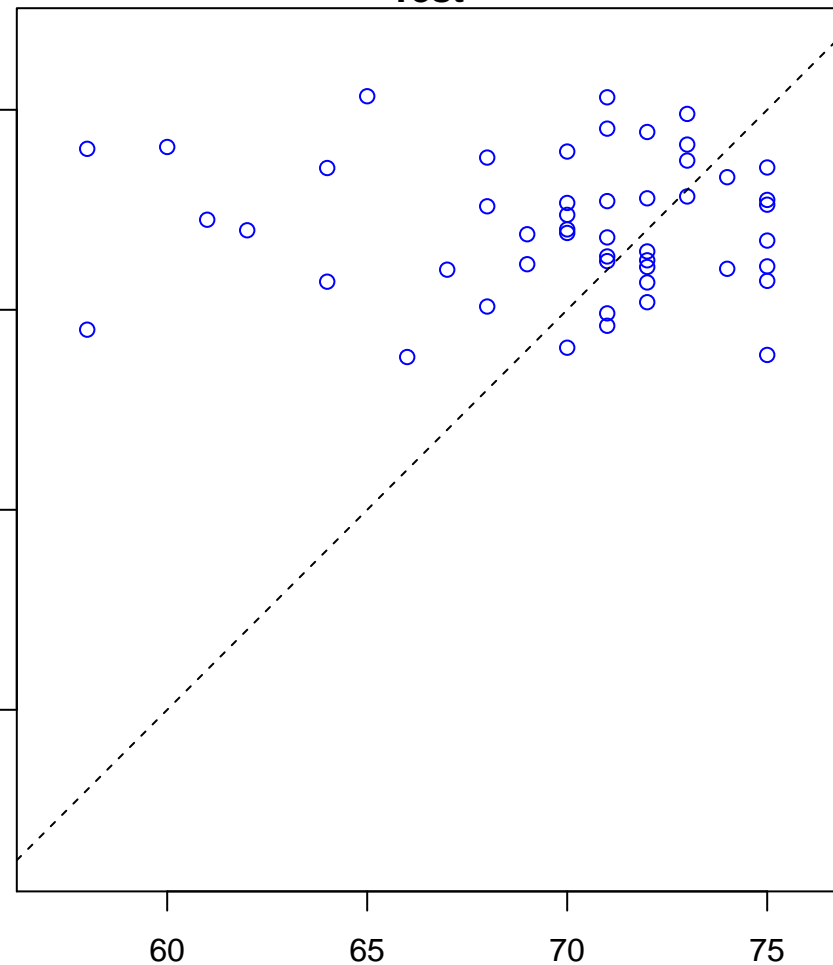


ribonucleoprotein complex localization (Score: 1.624626)

Control

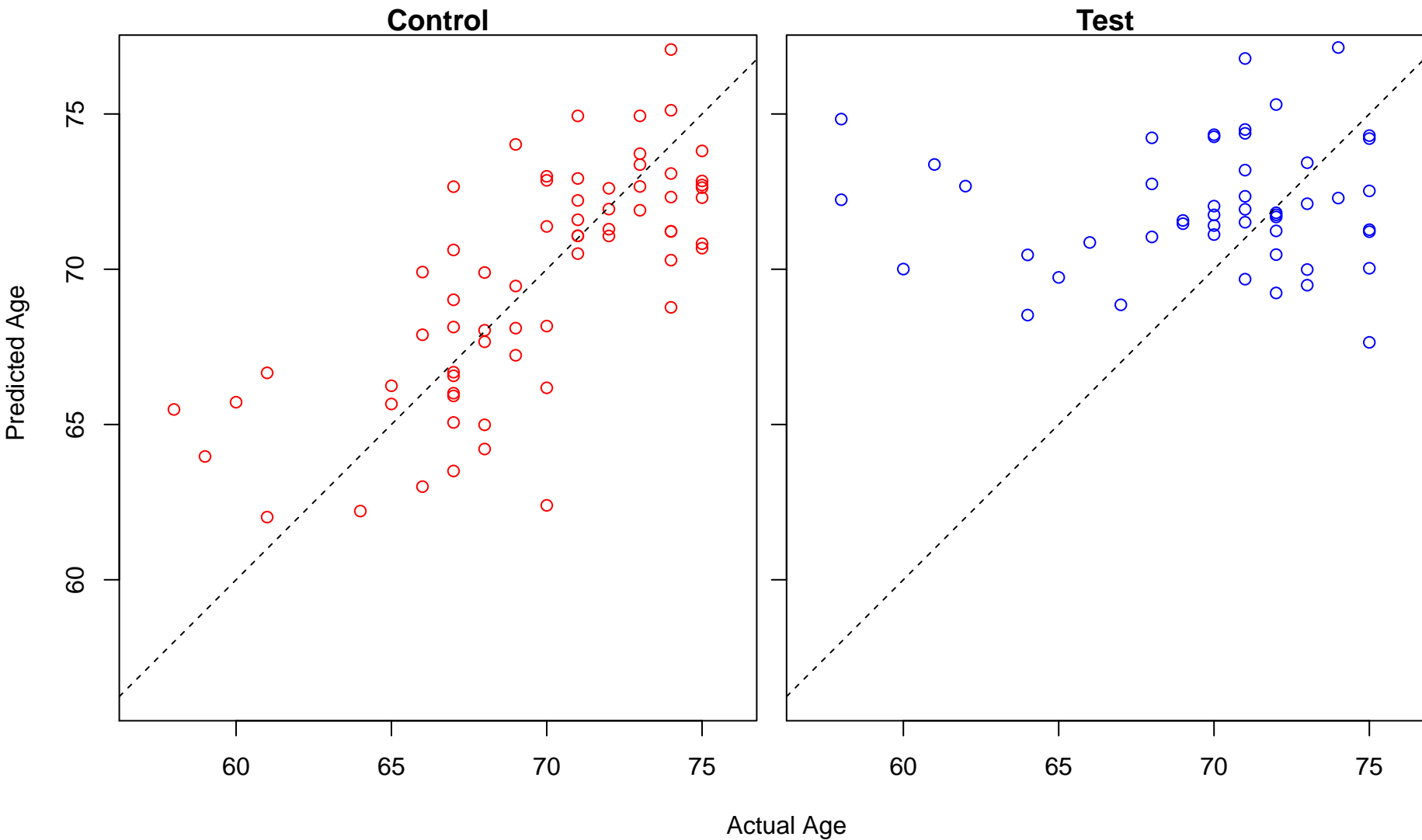


Test

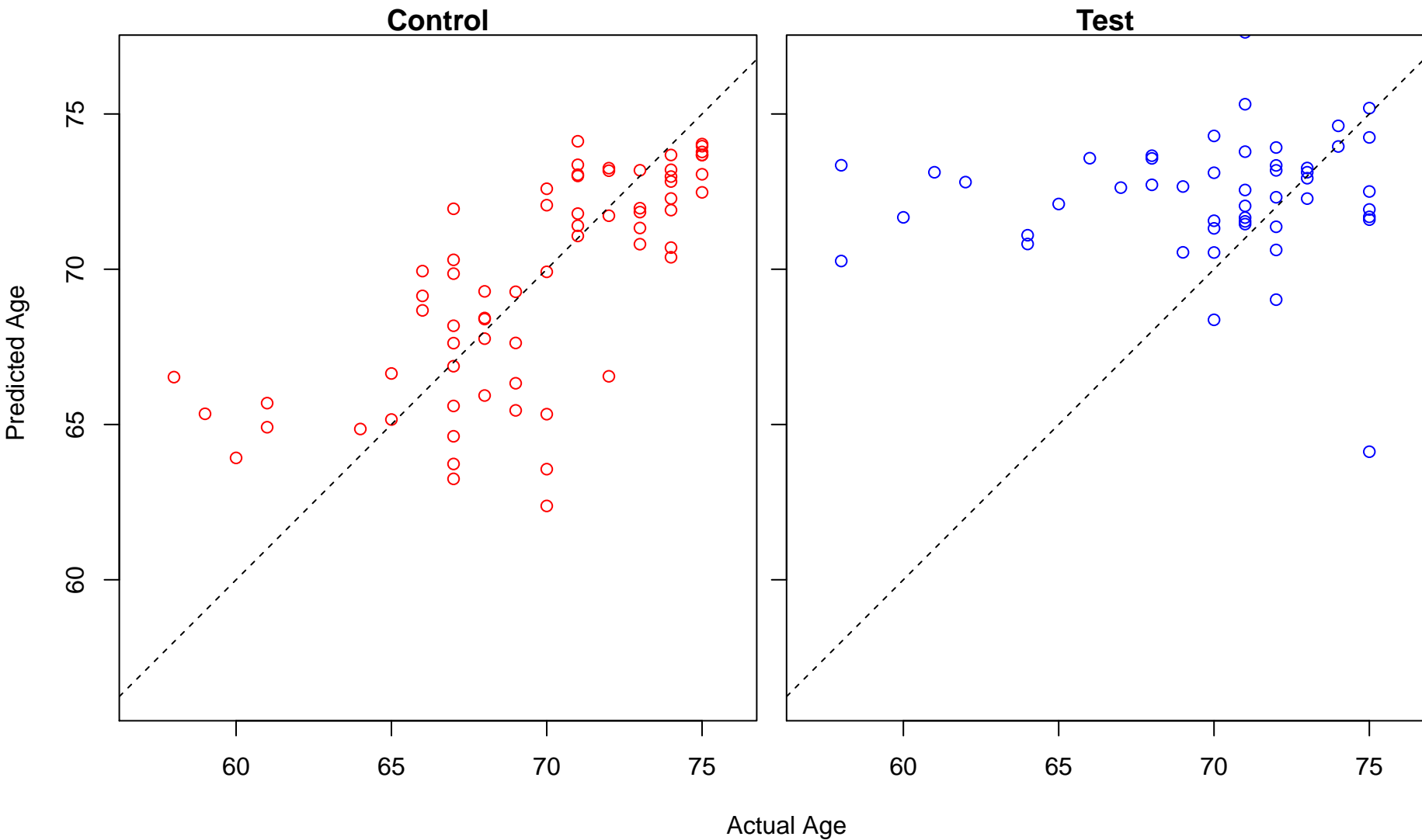


Actual Age

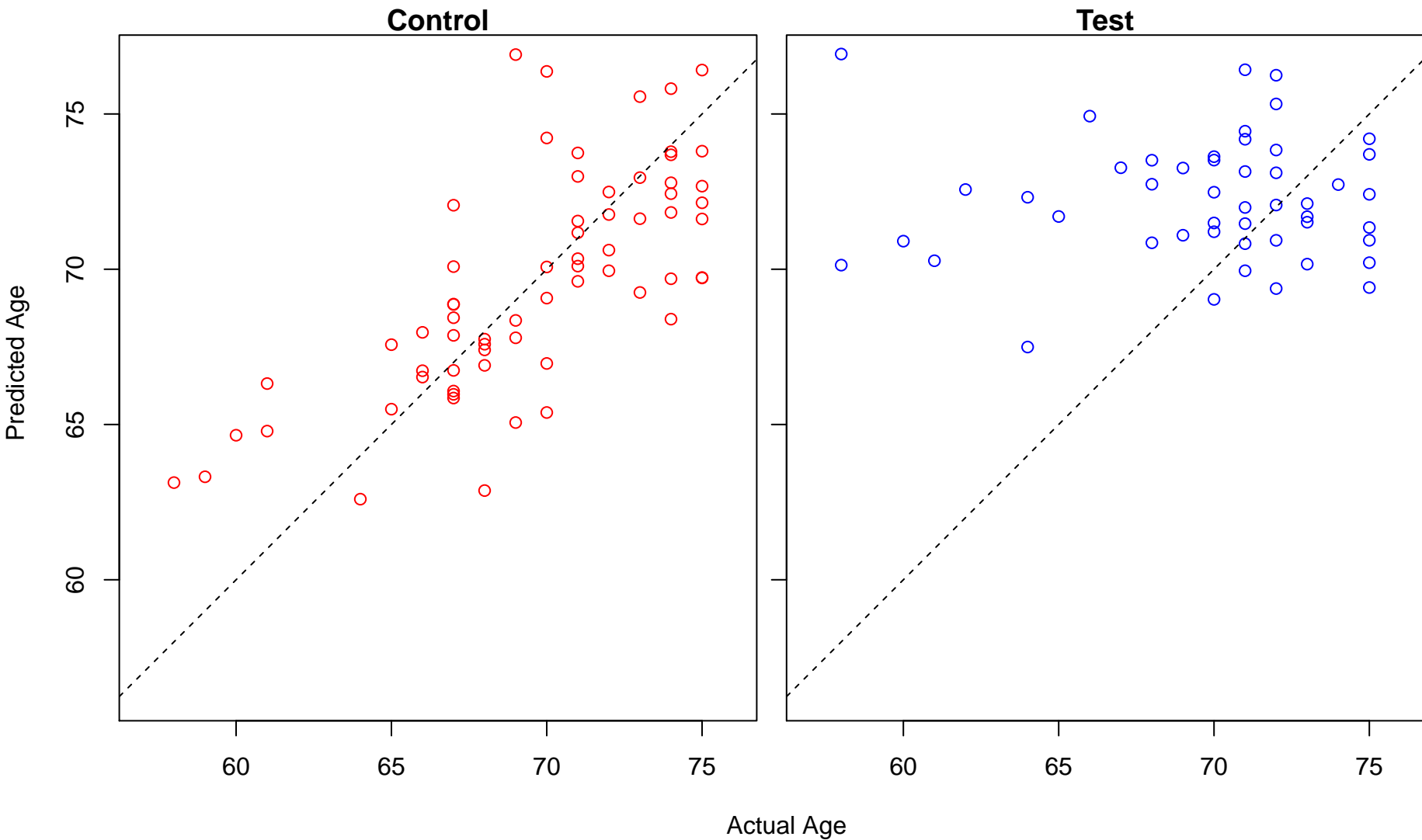
nucleotide-excision repair (Score: 1.624410)



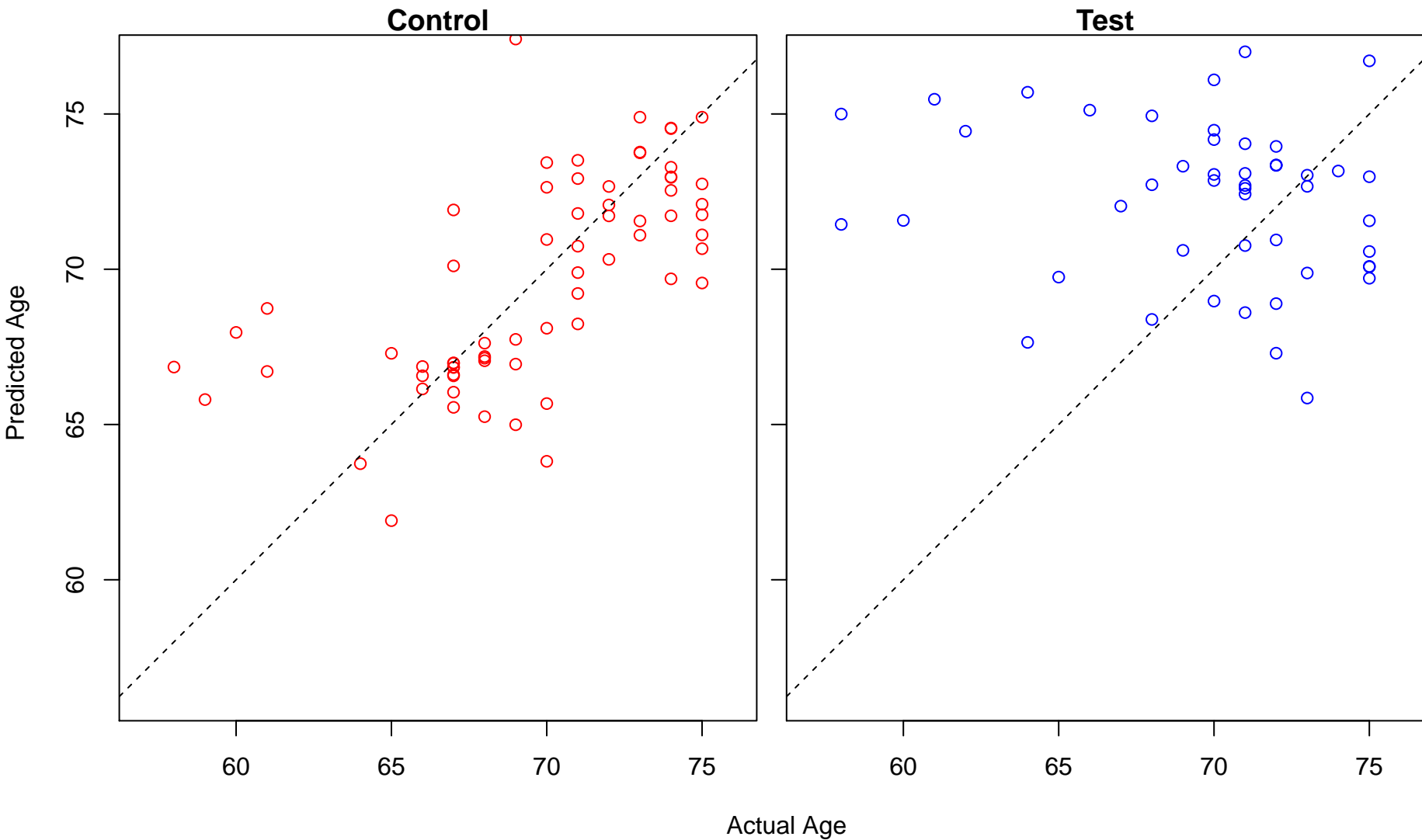
positive regulation of cellular amide metabolic process (Score: 1.624070)



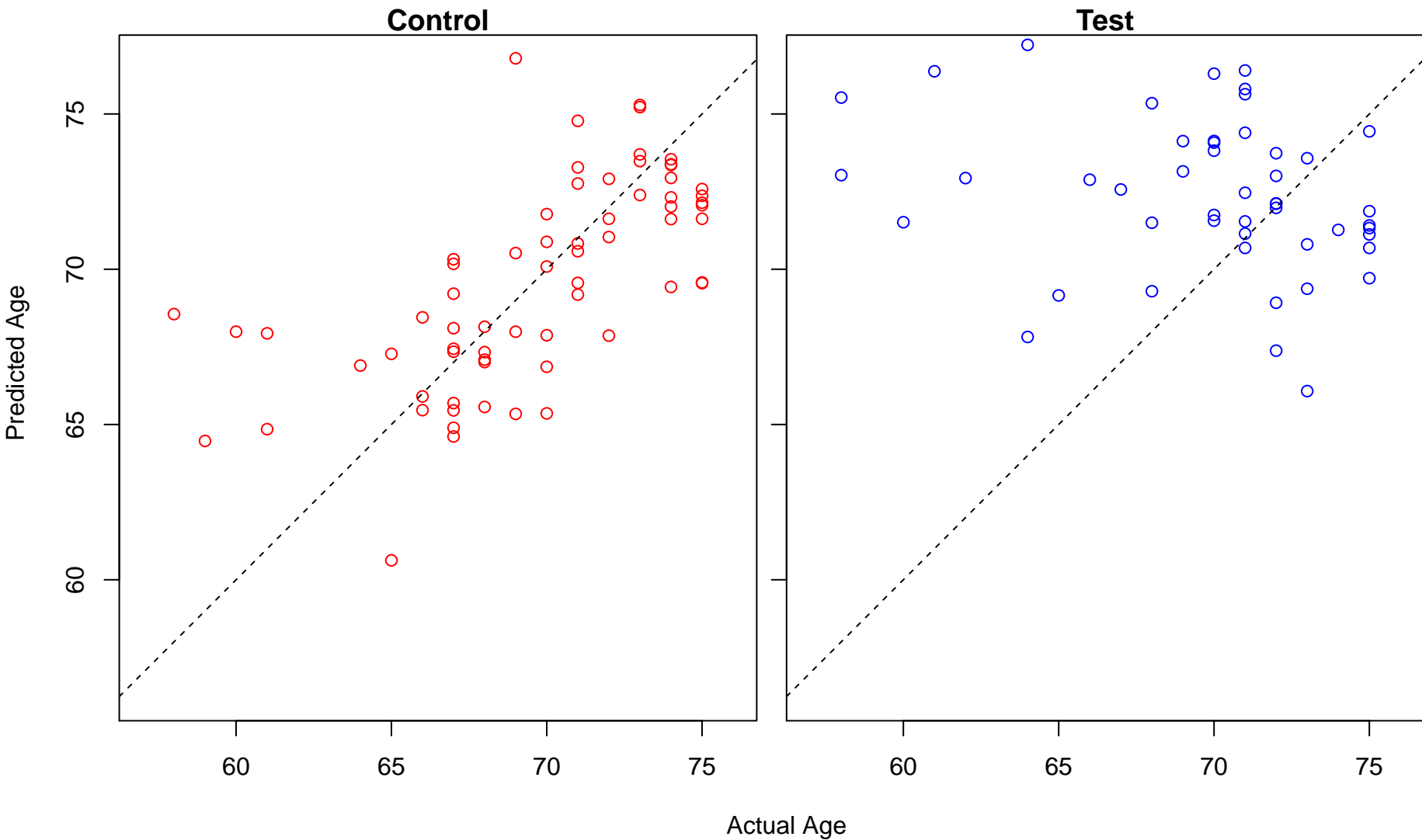
divalent inorganic cation transport (Score: 1.623563)



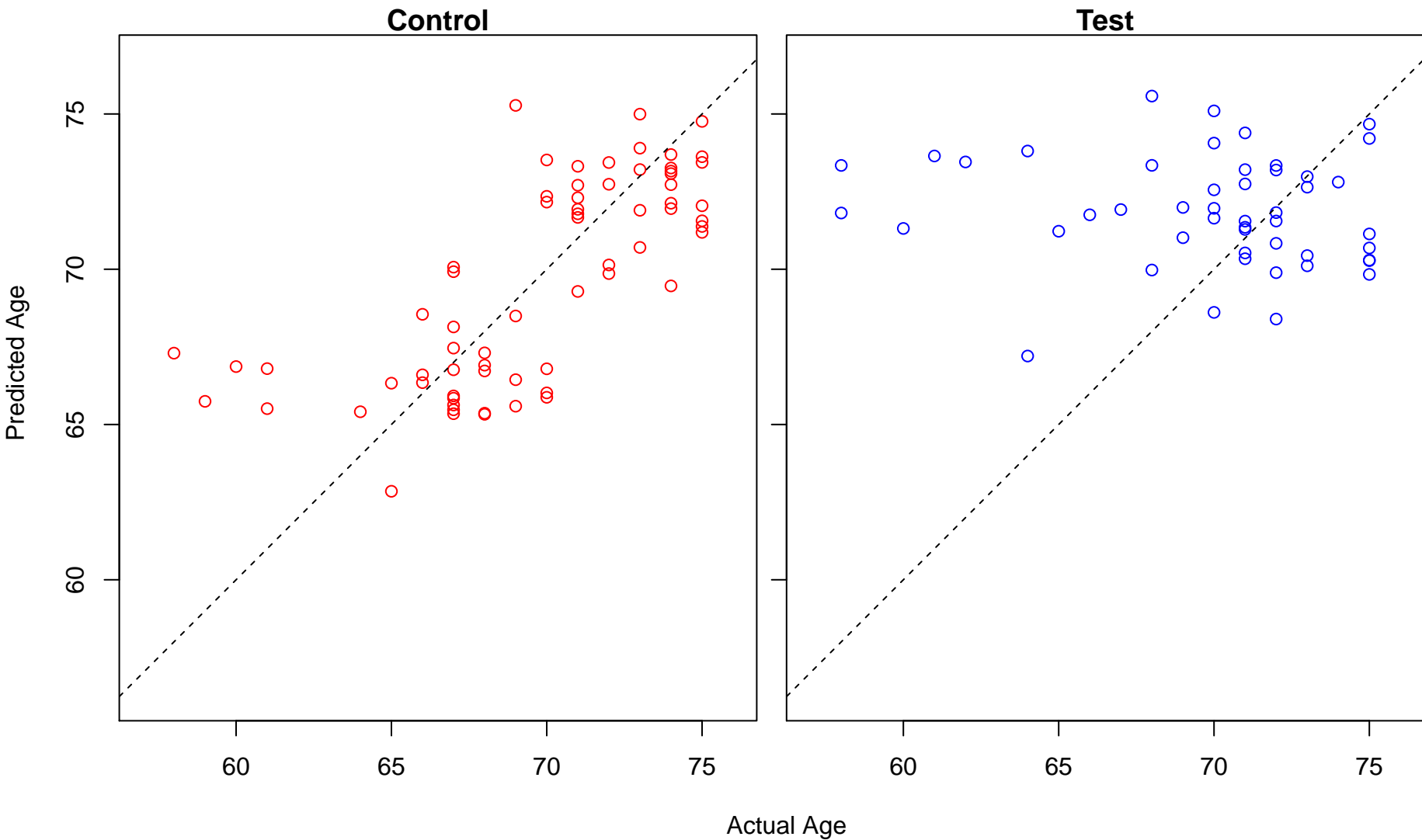
negative regulation of cytokine production (Score: 1.623404)



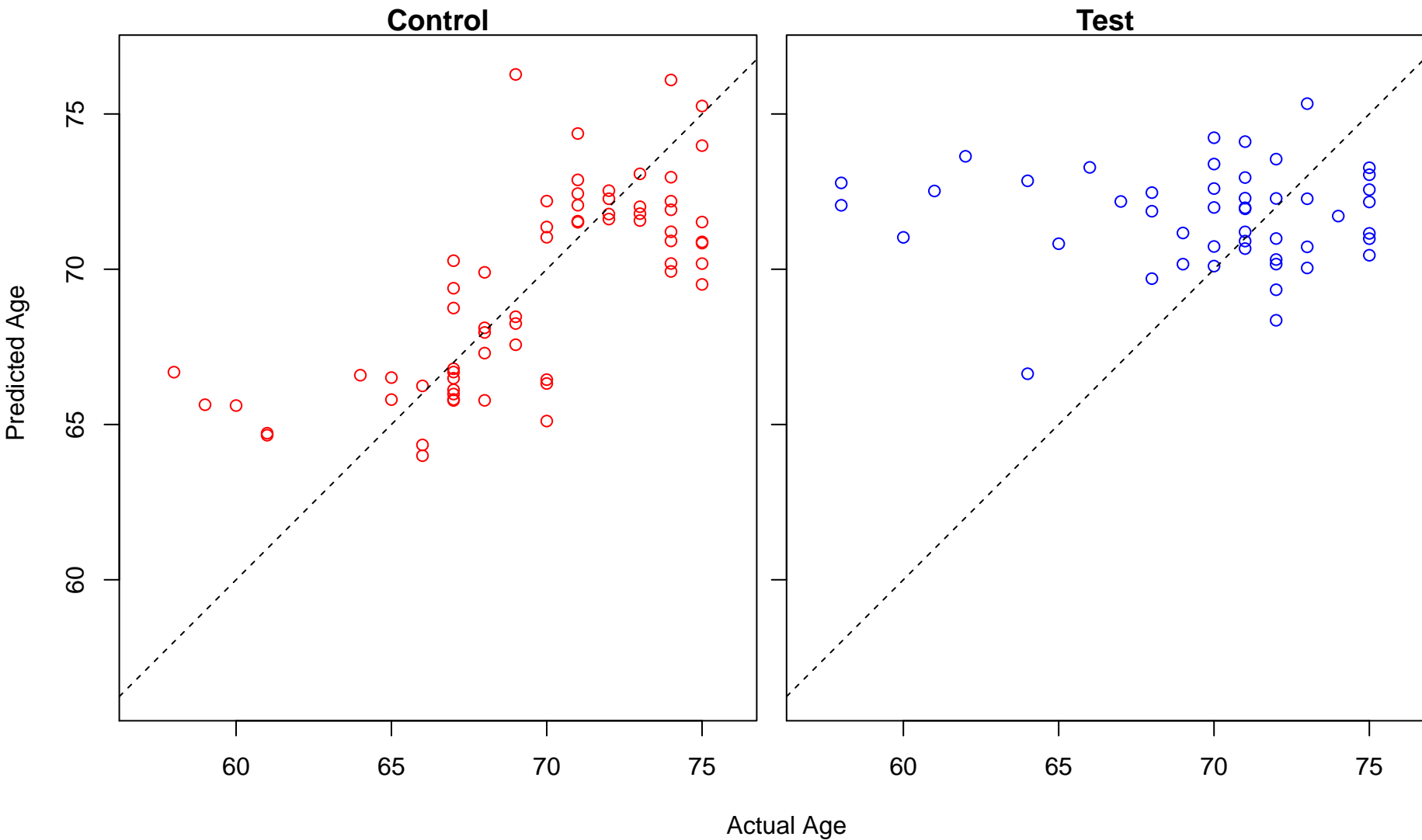
regulation of alpha-beta T cell activation (Score: 1.623312)



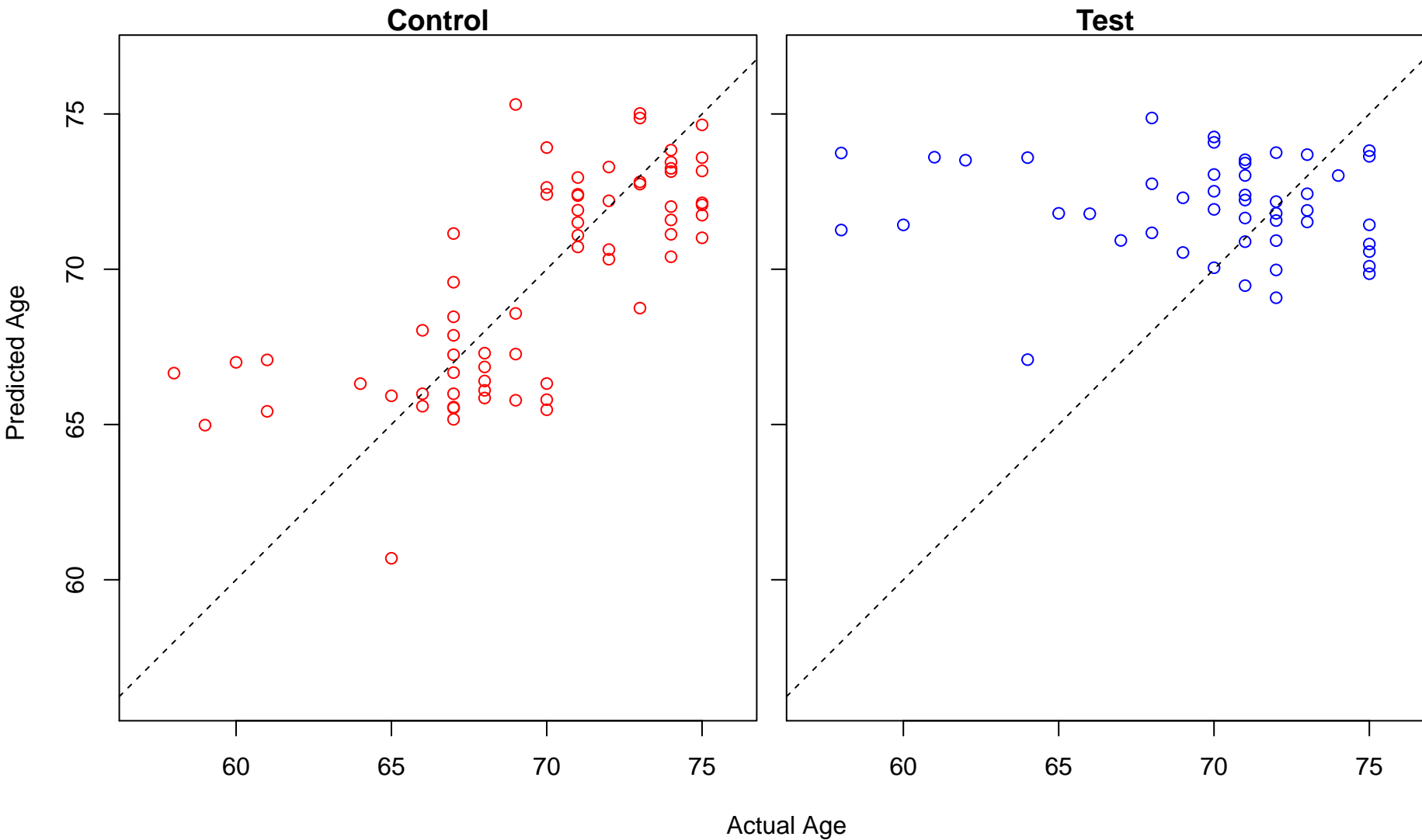
innate immune response activating cell surface receptor signaling pathway (Score: 1.623236)



positive regulation of protein polymerization (Score: 1.622364)

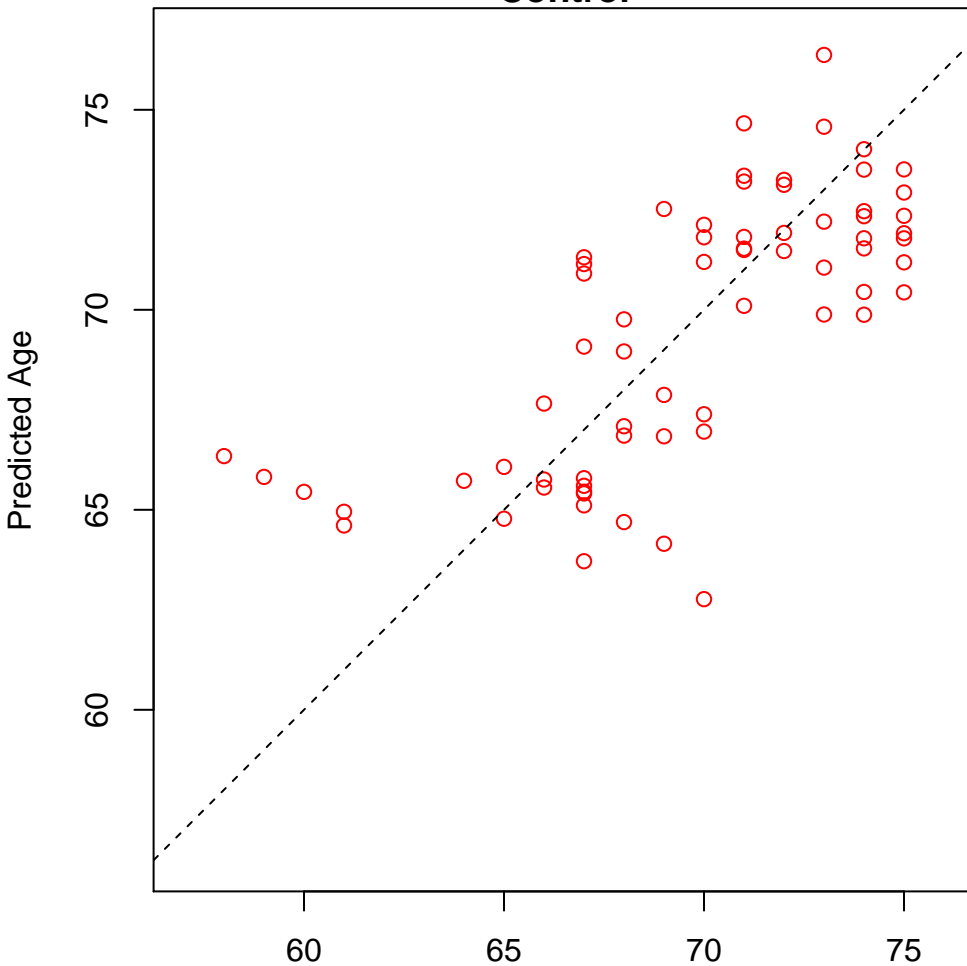


antigen processing and presentation of peptide antigen via MHC class I (Score: 1.622331)

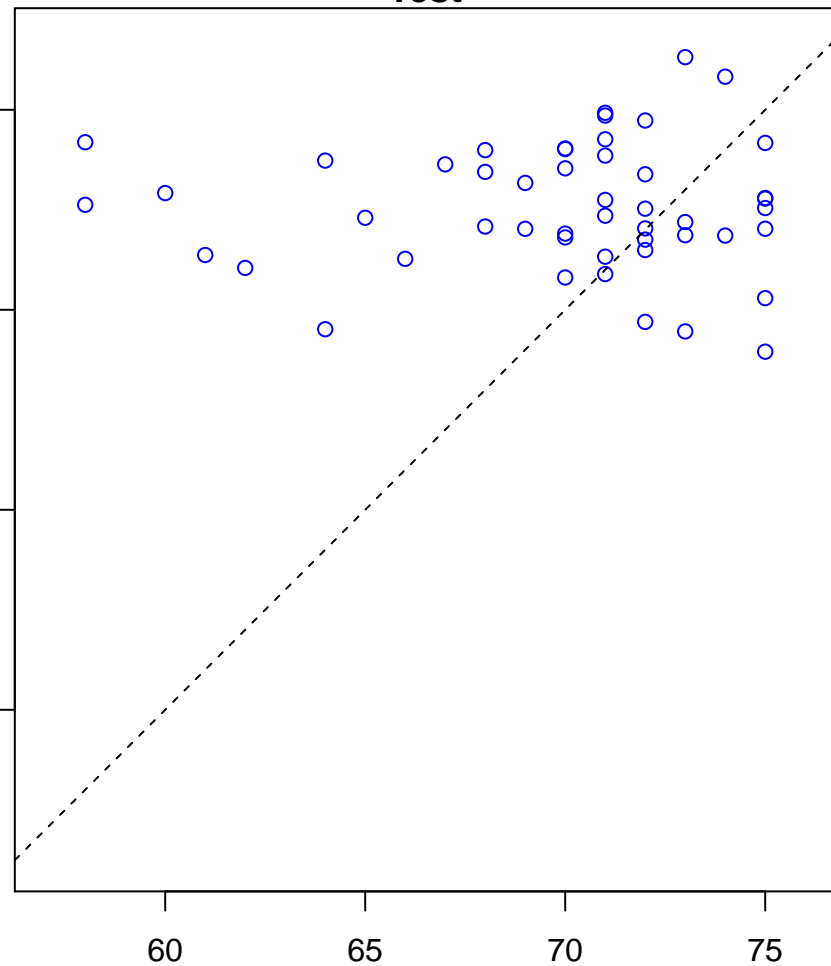


DNA-templated transcription, termination (Score: 1.618686)

Control

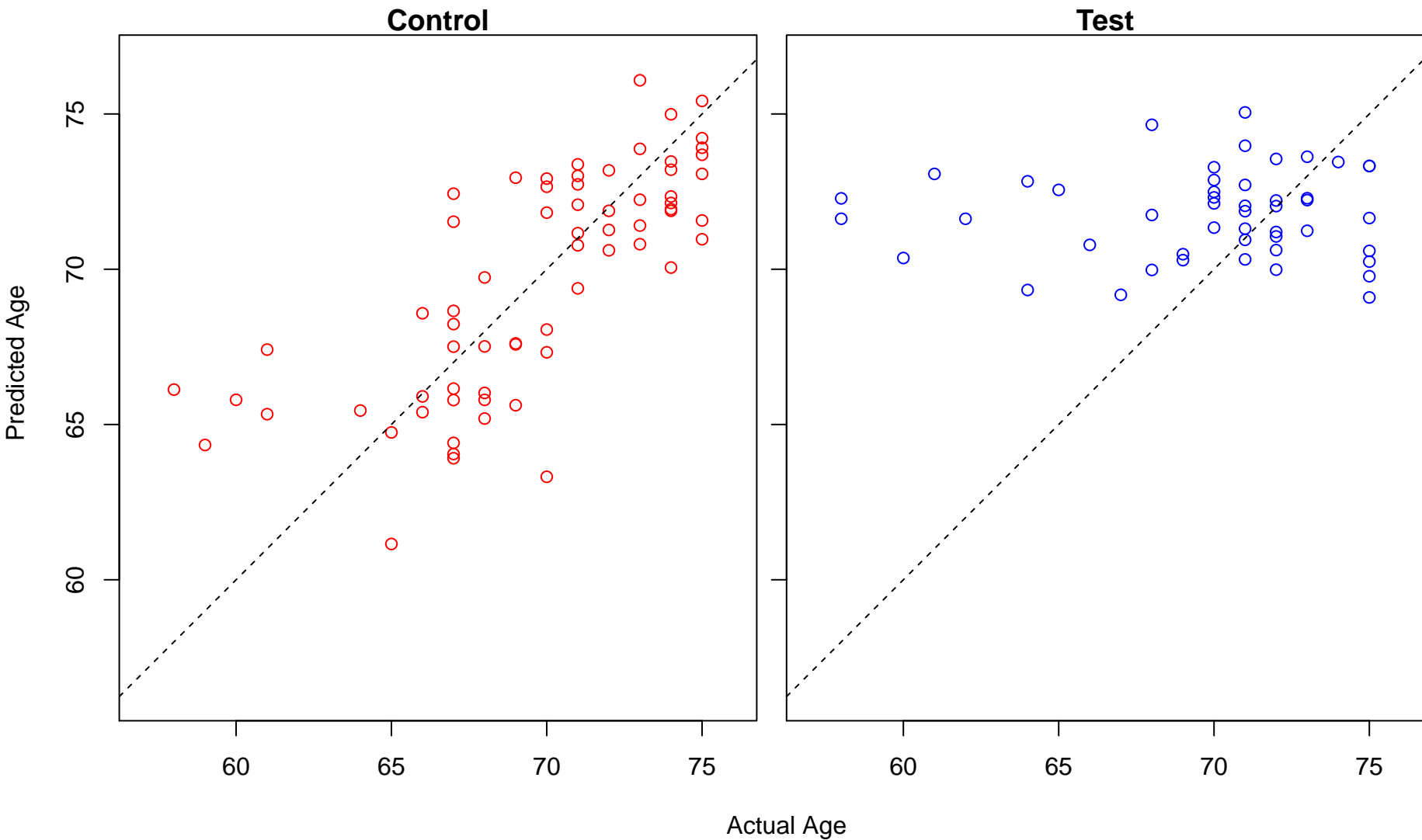


Test

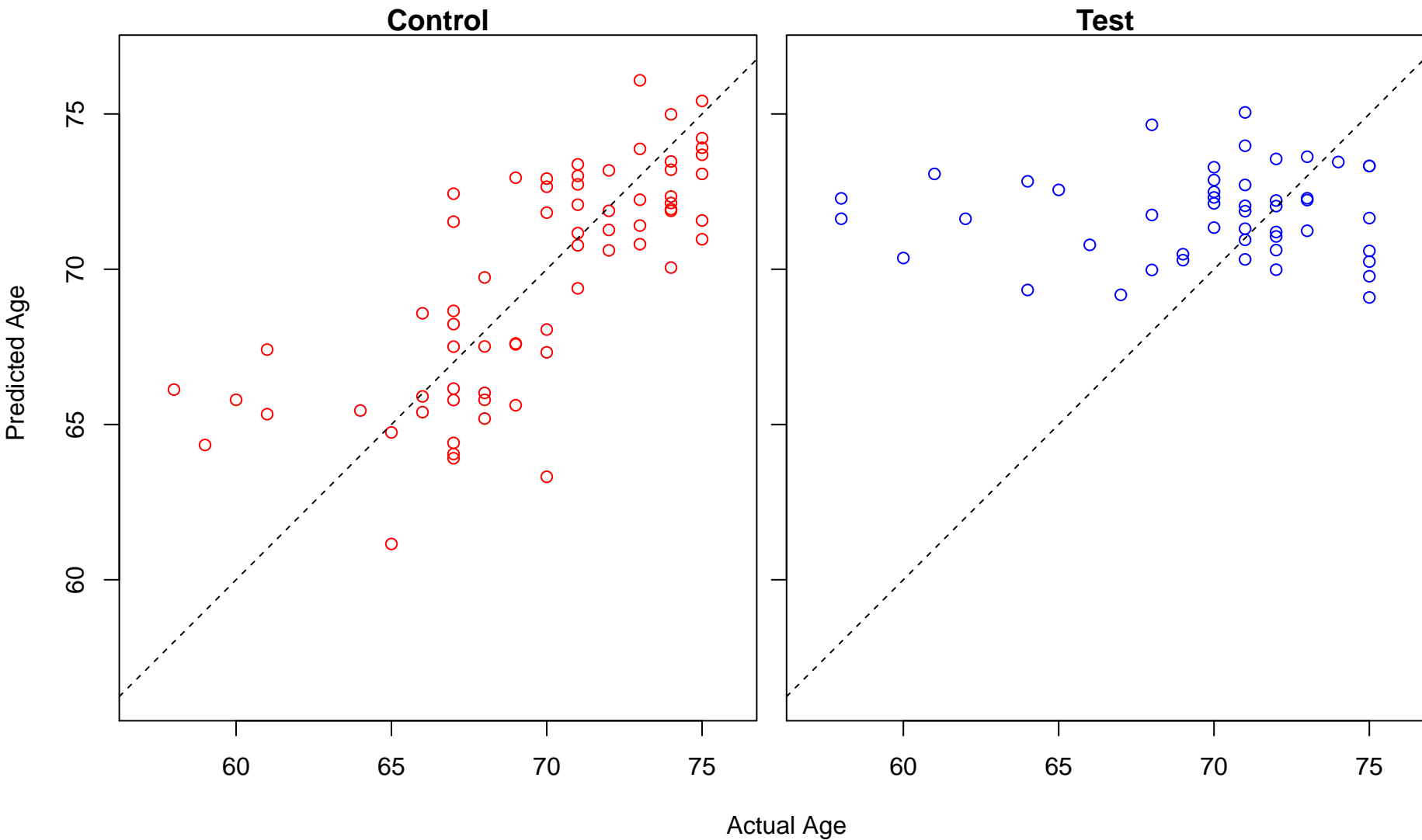


Actual Age

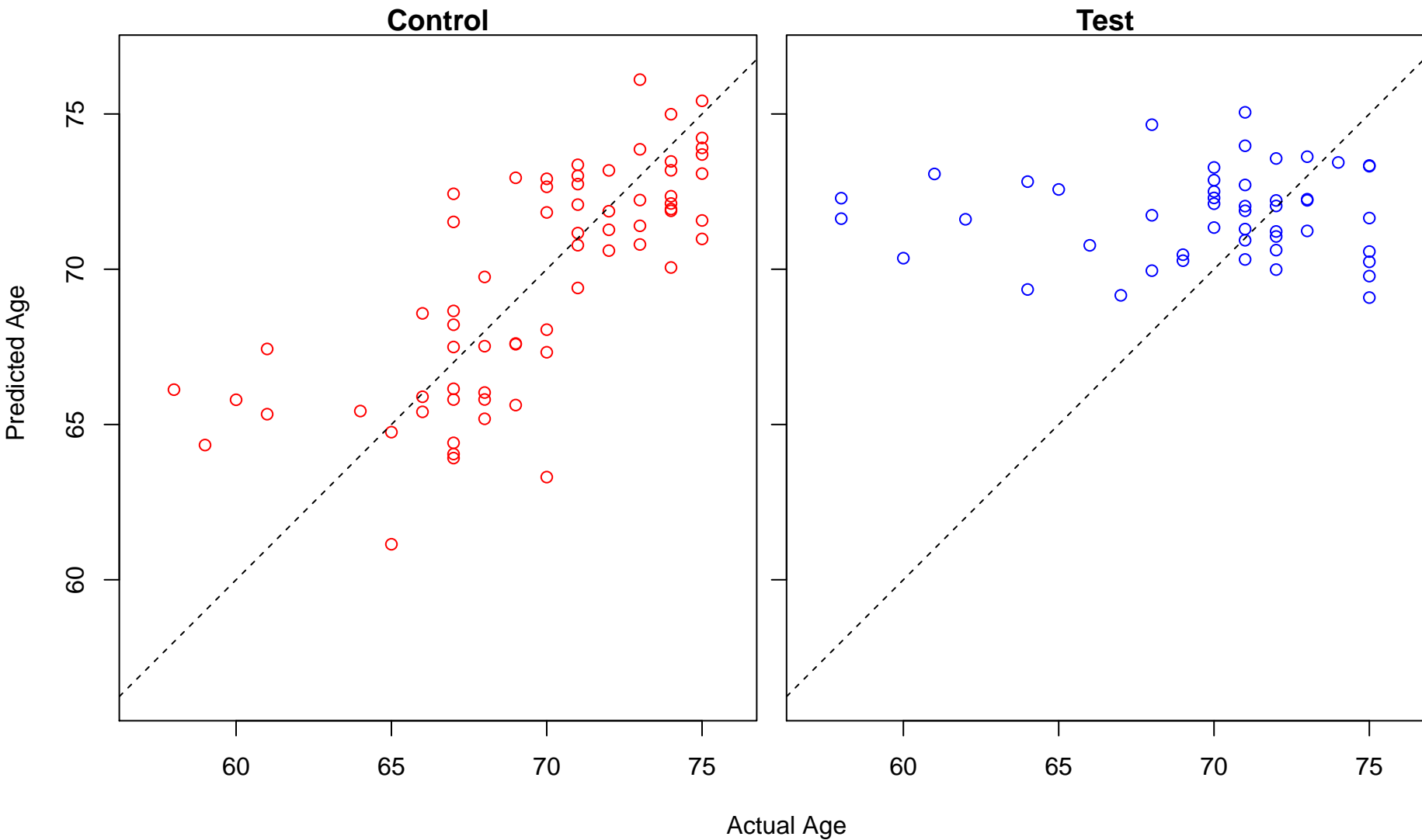
signal transduction involved in DNA integrity checkpoint (Score: 1.617727)



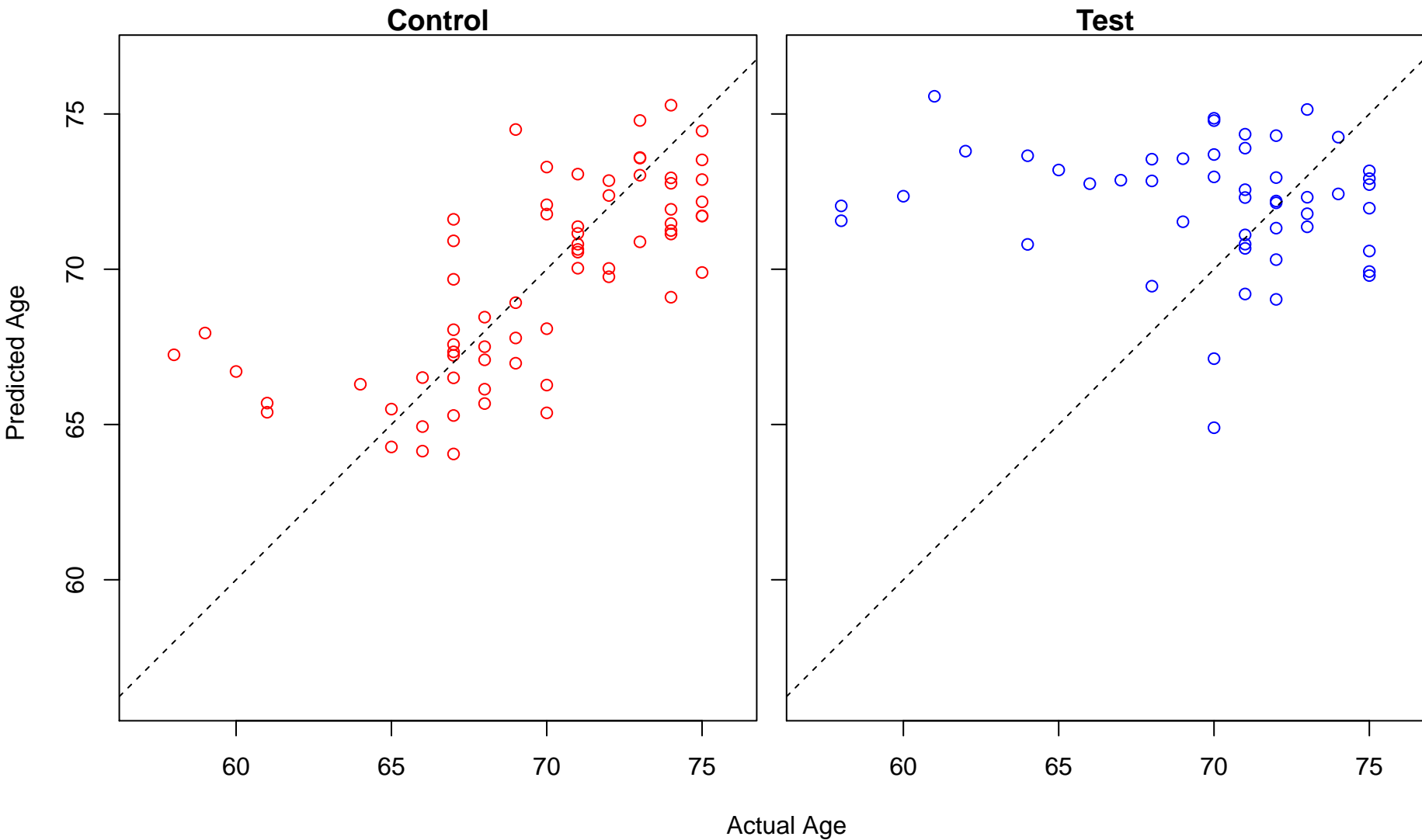
signal transduction involved in DNA damage checkpoint (Score: 1.617727)



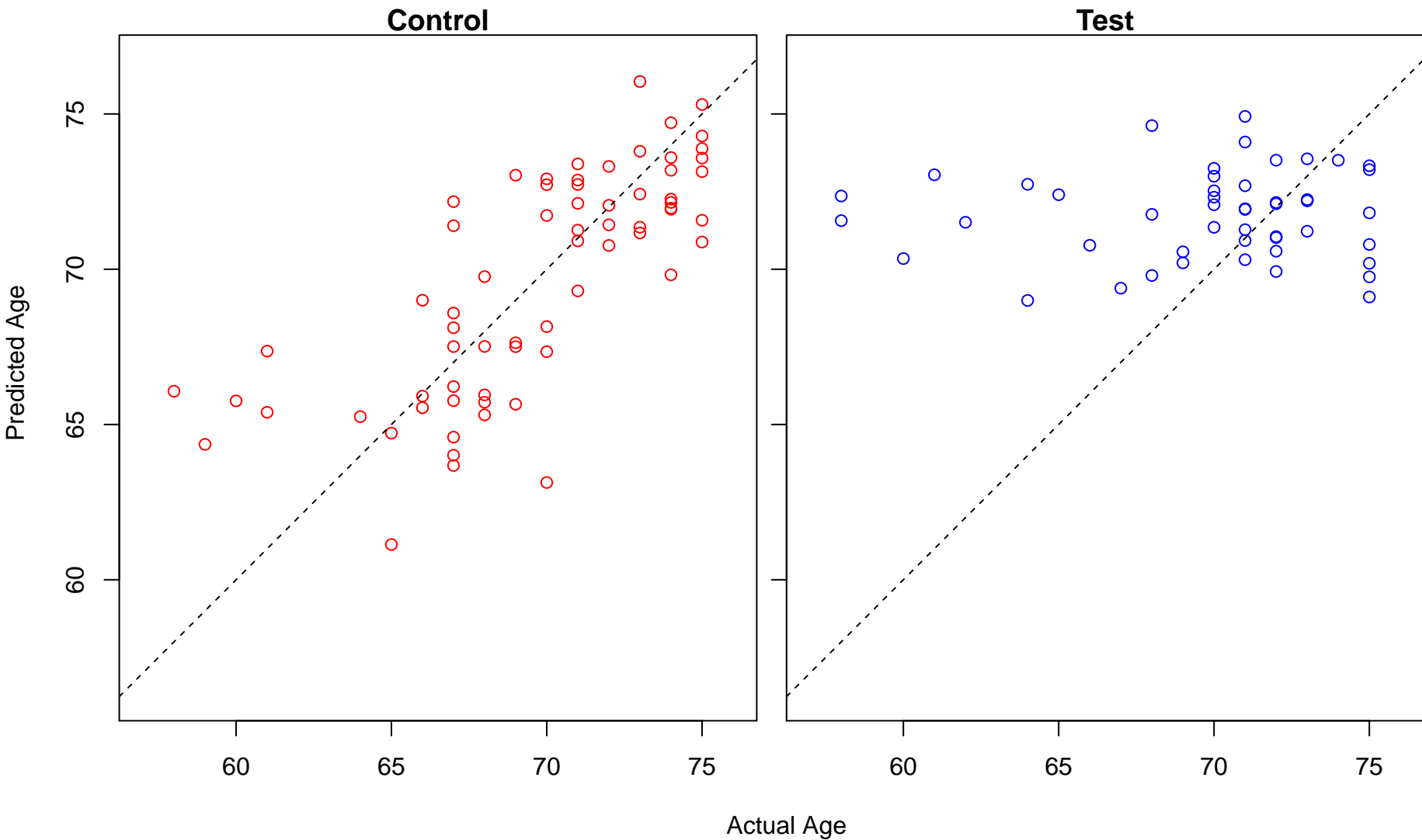
signal transduction involved in cell cycle checkpoint (Score: 1.617719)



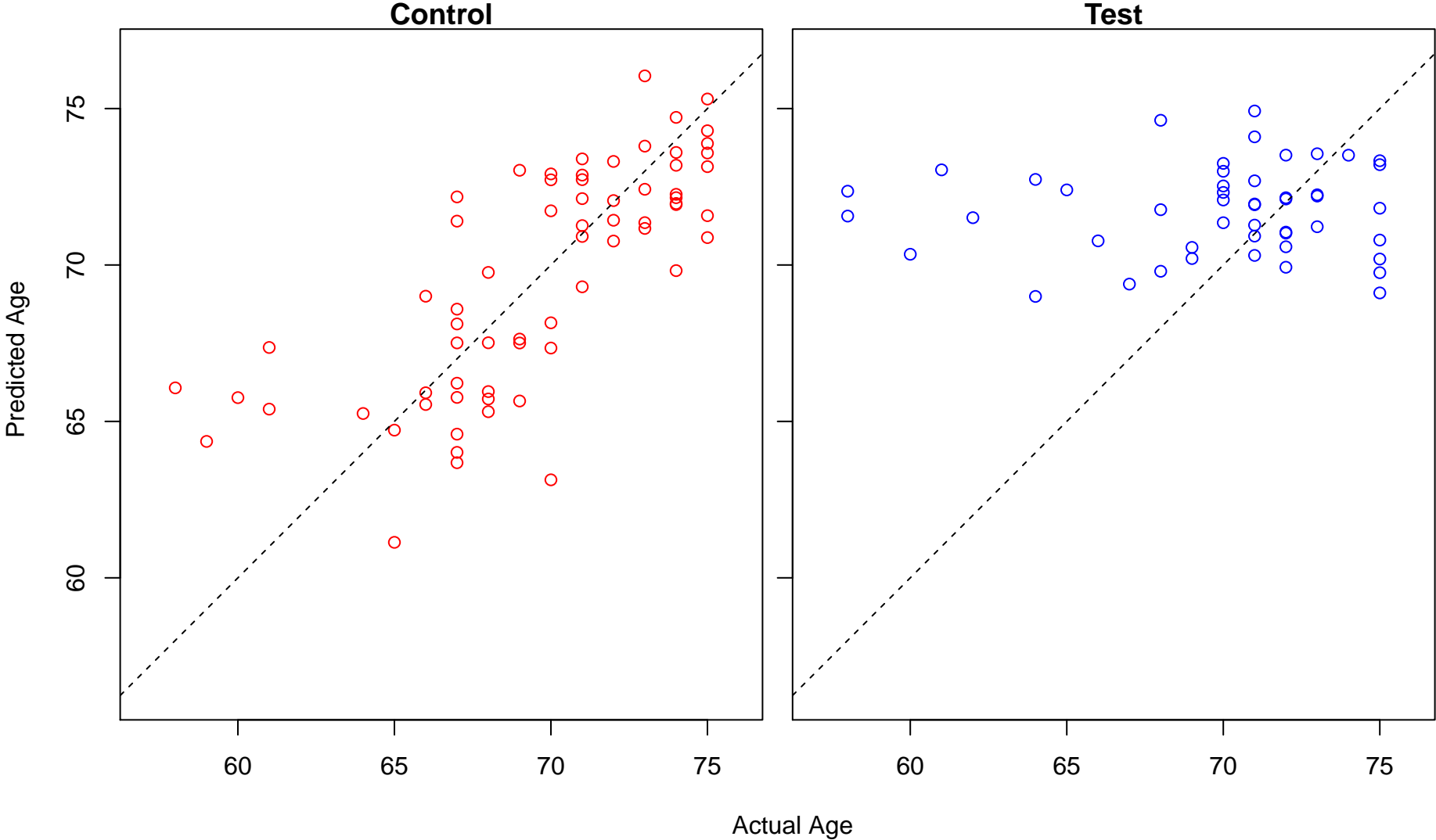
histone H2A acetylation (Score: 1.617255)



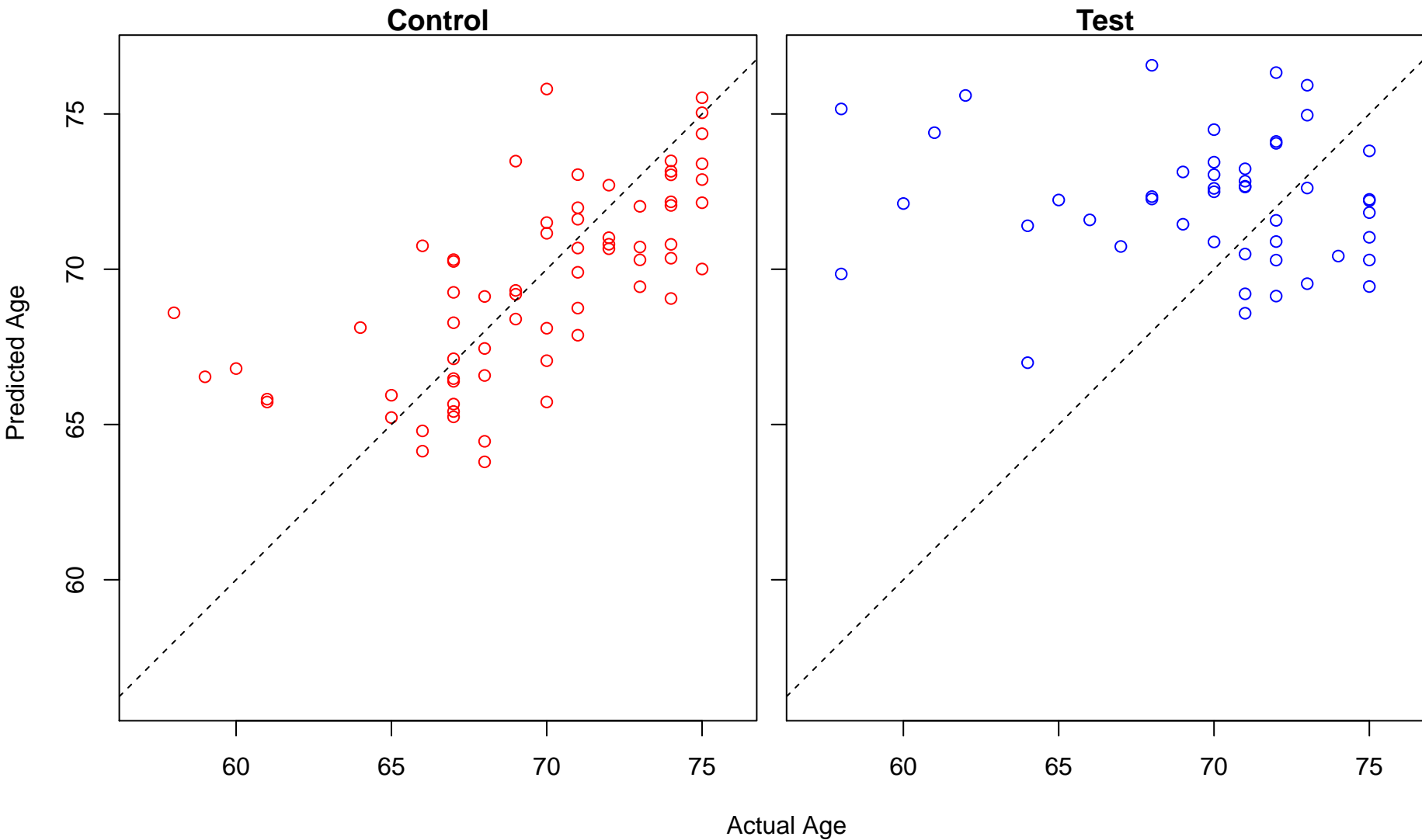
signal transduction involved in mitotic G1 DNA damage checkpoint (Score: 1.617158)



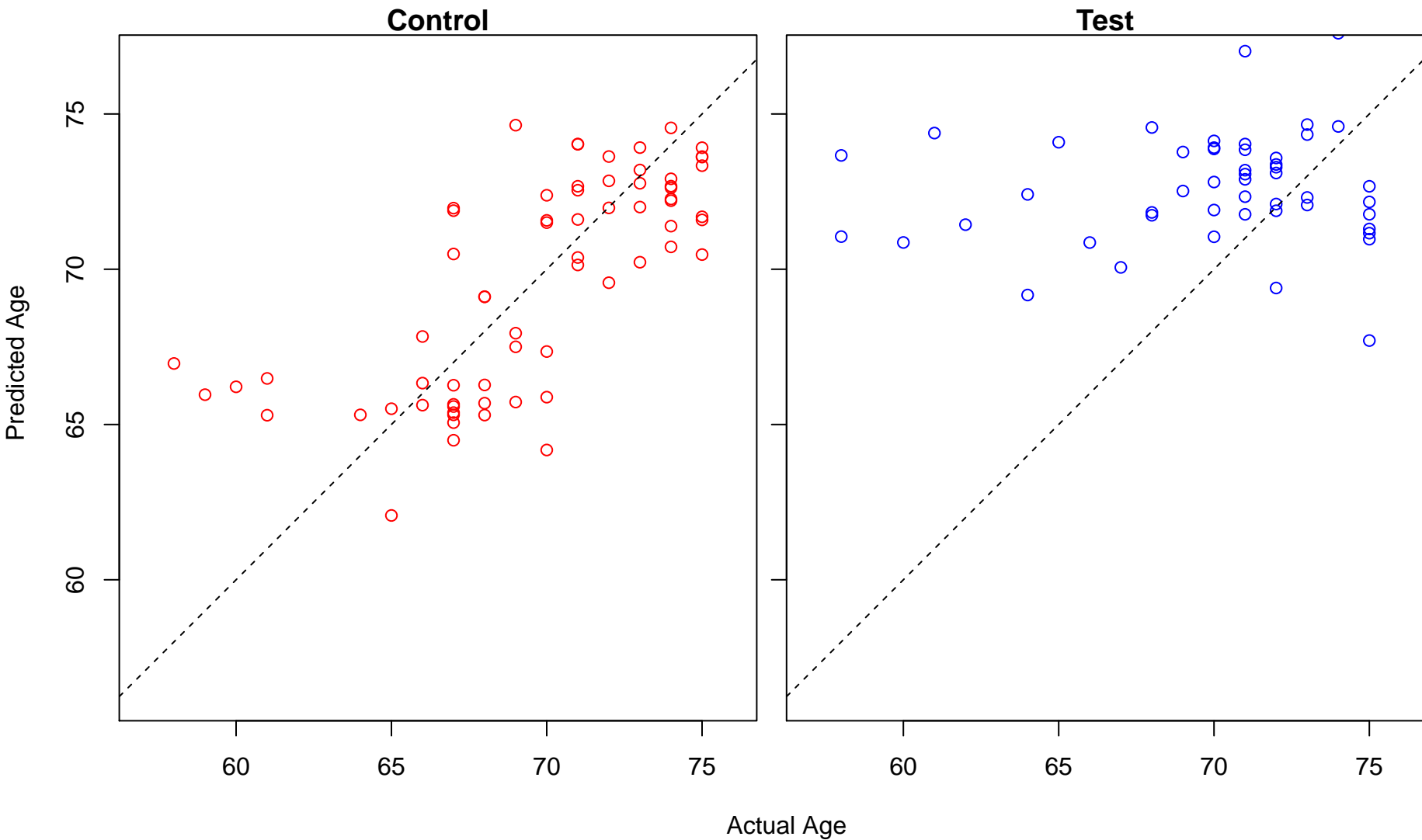
intracellular signal transduction involved in G1 DNA damage checkpoint (Score: 1.617158)



superoxide metabolic process (Score: 1.616465)

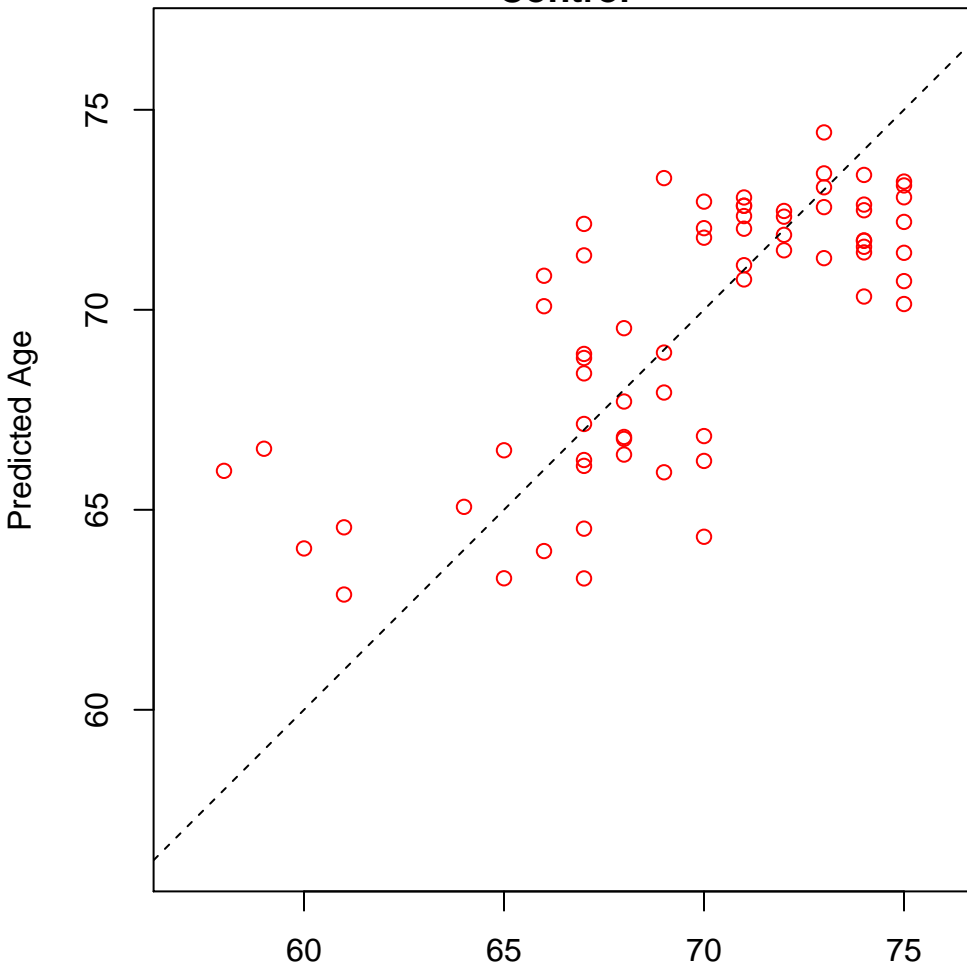


ncRNA metabolic process (Score: 1.616277)

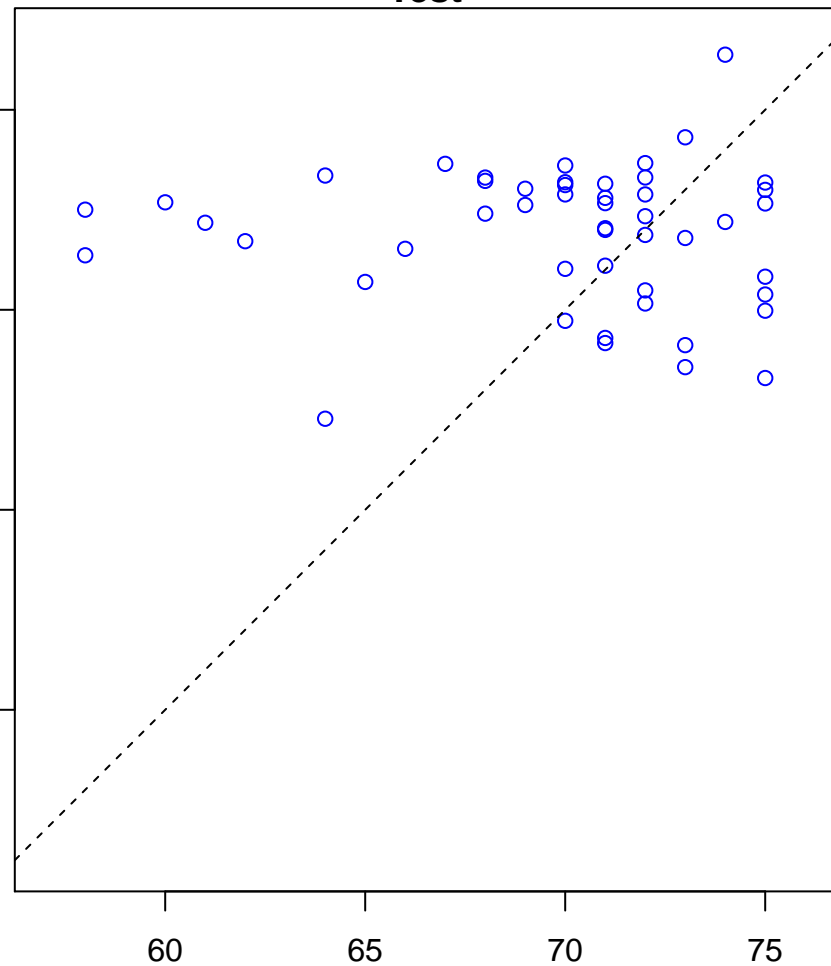


regulation of mitotic spindle assembly (Score: 1.615896)

Control



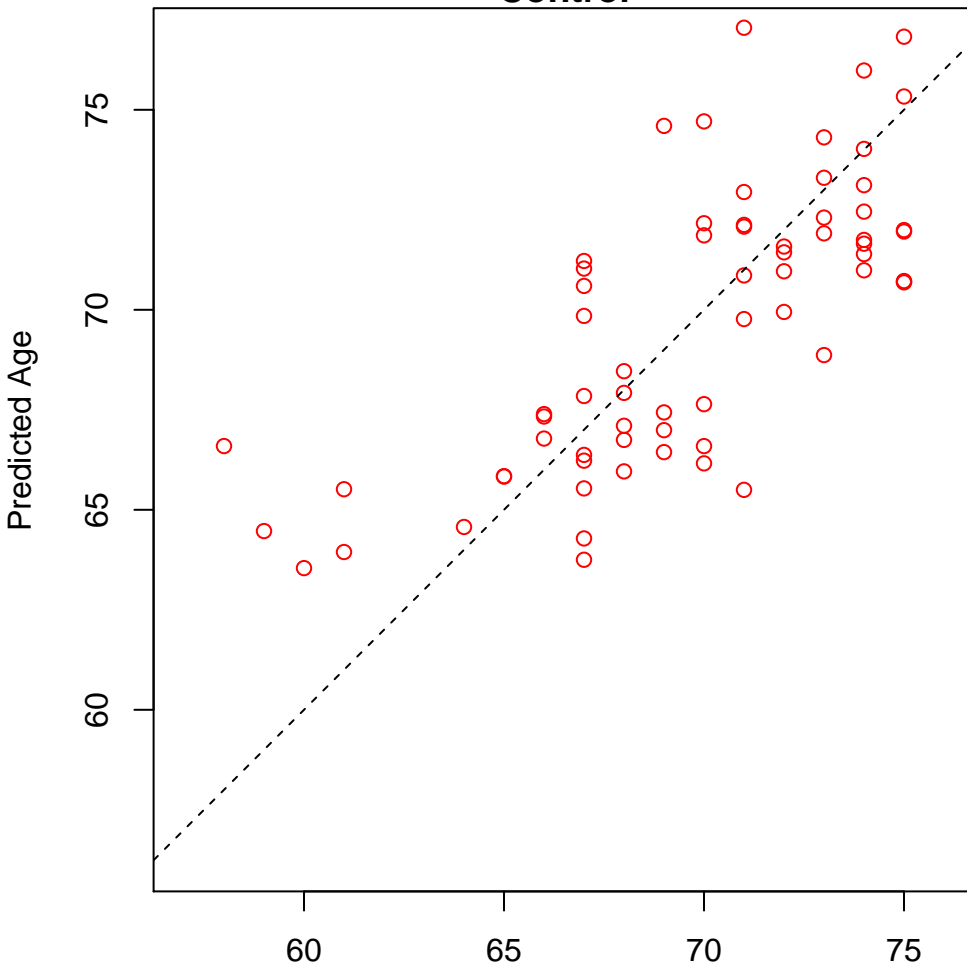
Test



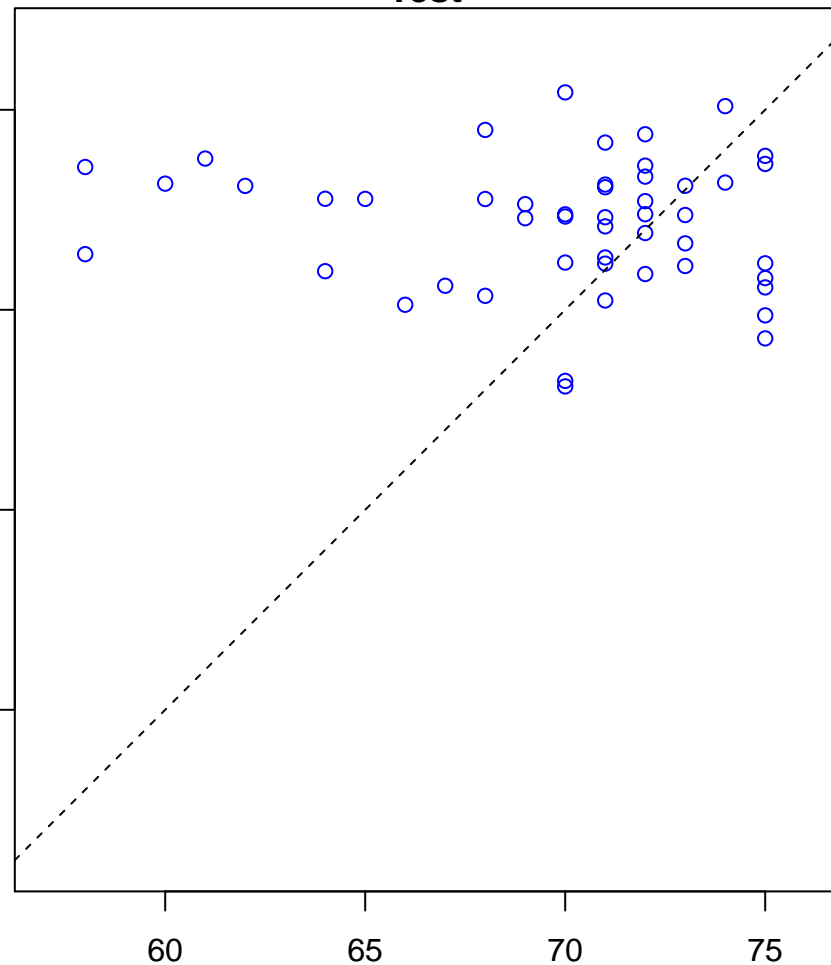
Actual Age

mitochondrial membrane organization (Score: 1.615272)

Control



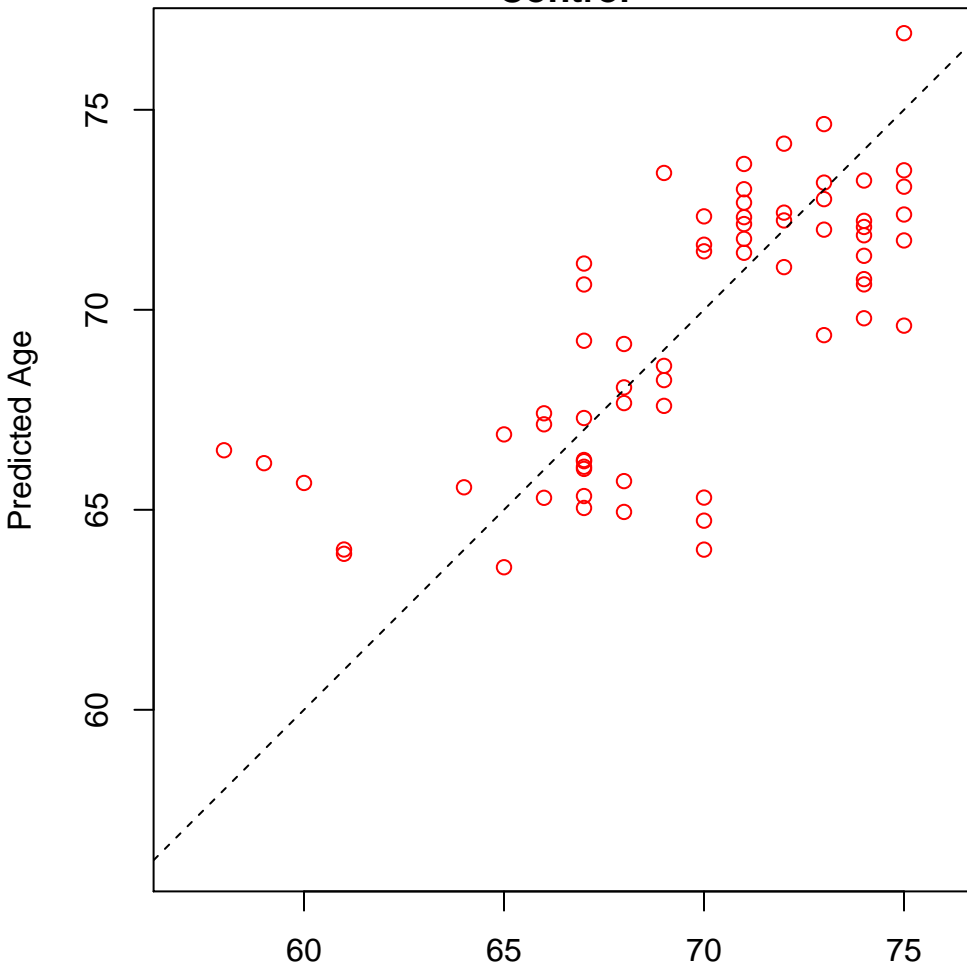
Test



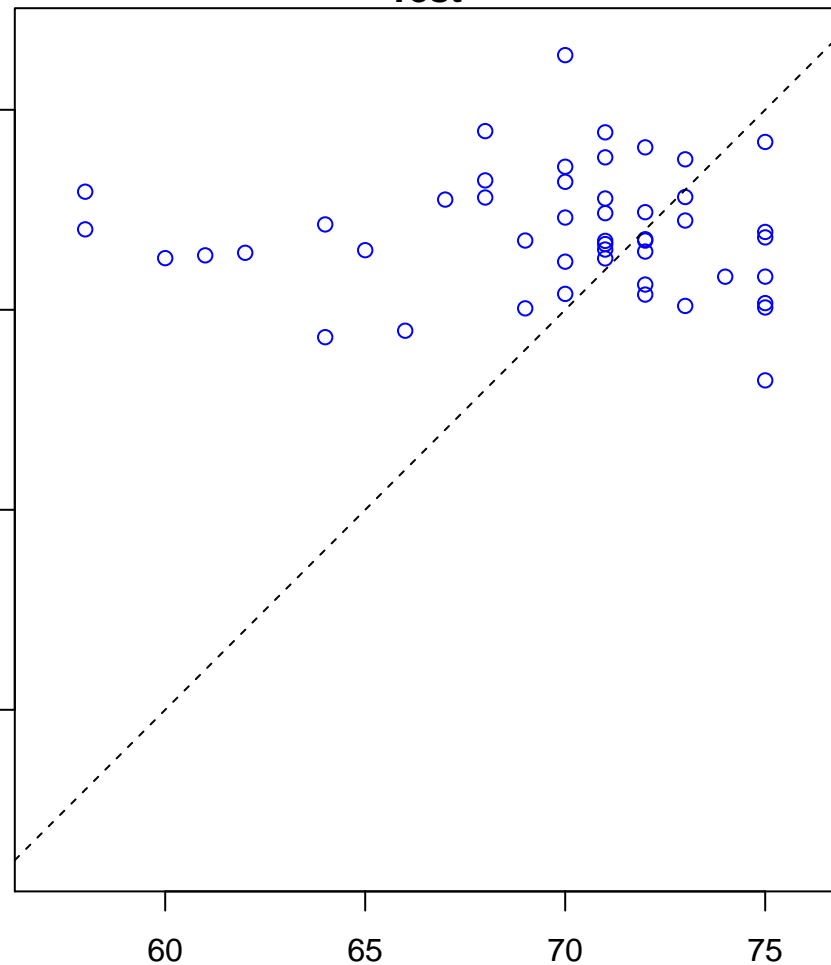
Actual Age

membrane lipid biosynthetic process (Score: 1.615222)

Control



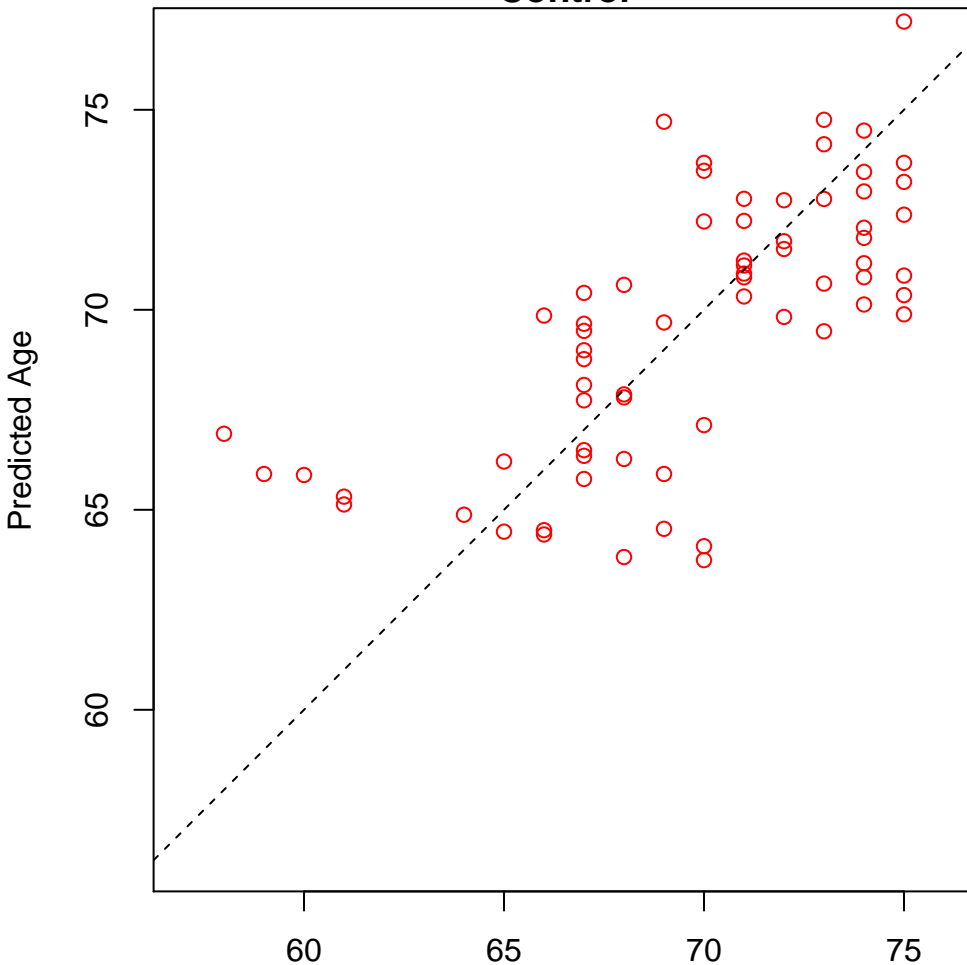
Test



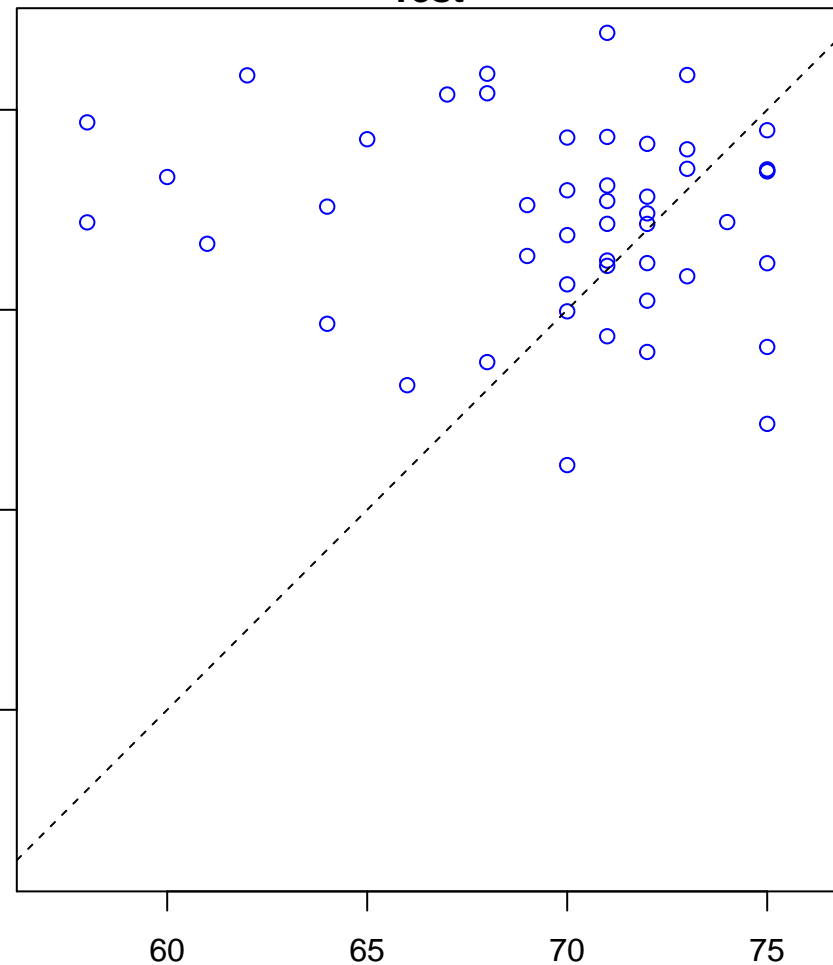
Actual Age

regulation of muscle cell differentiation (Score: 1.615078)

Control

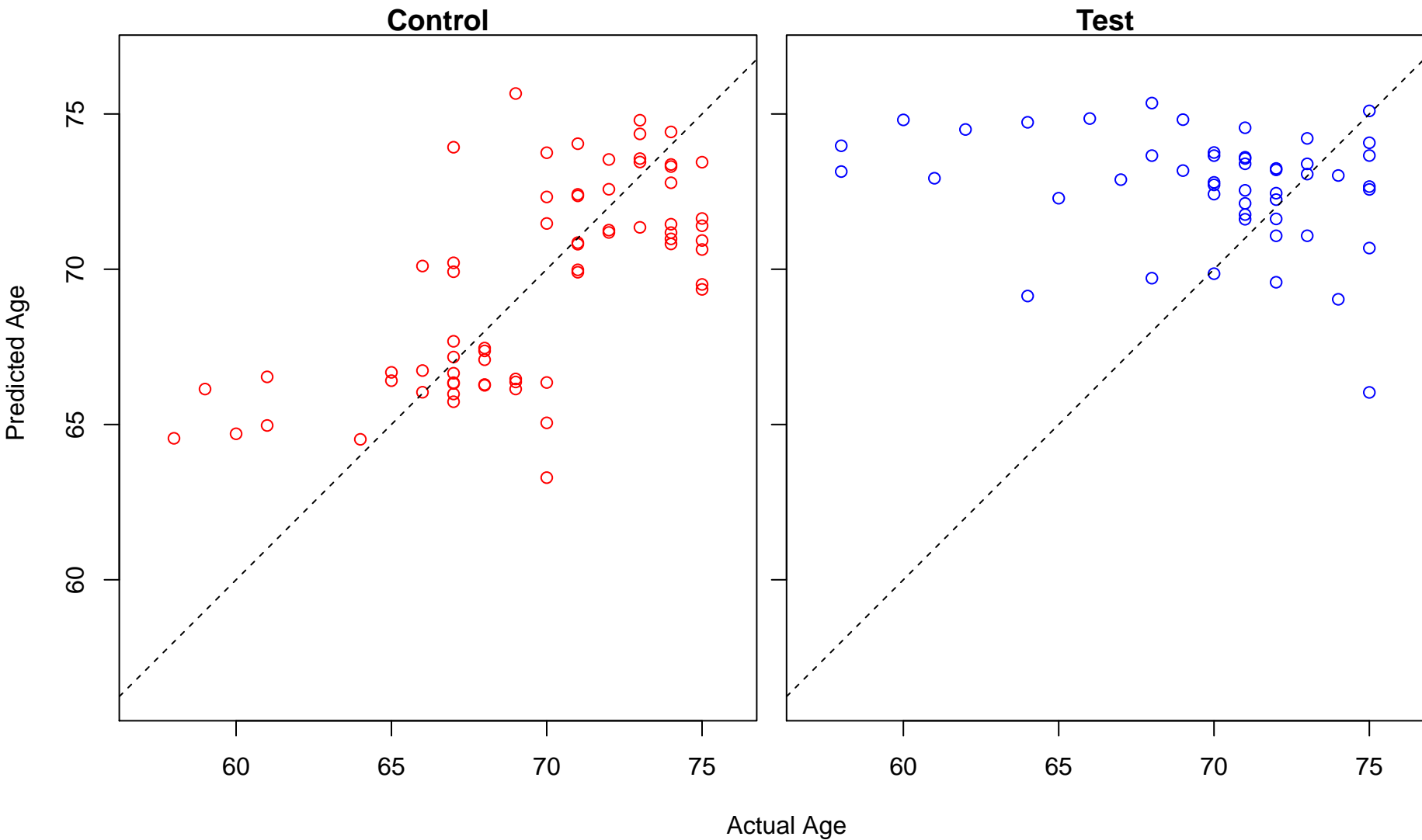


Test

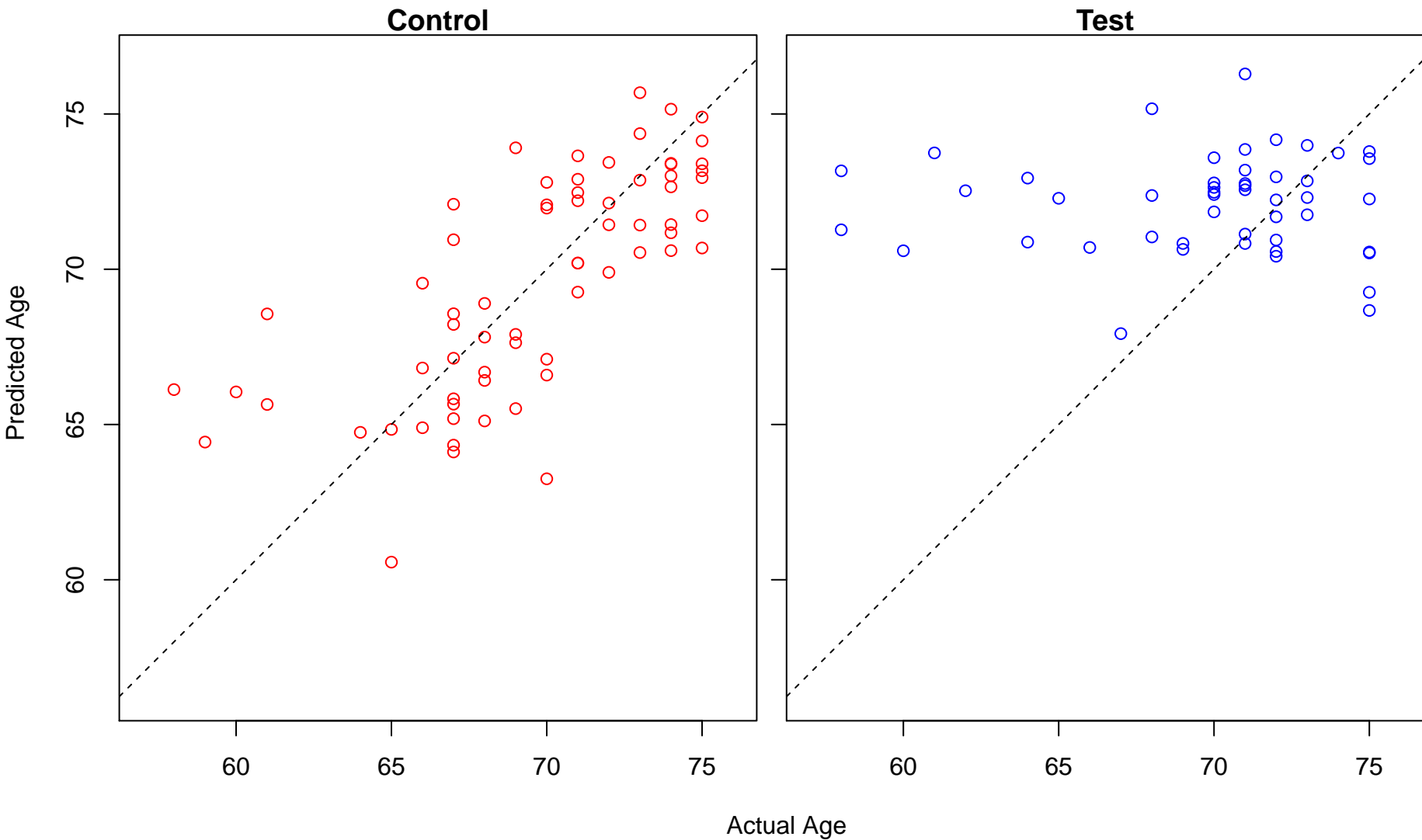


Actual Age

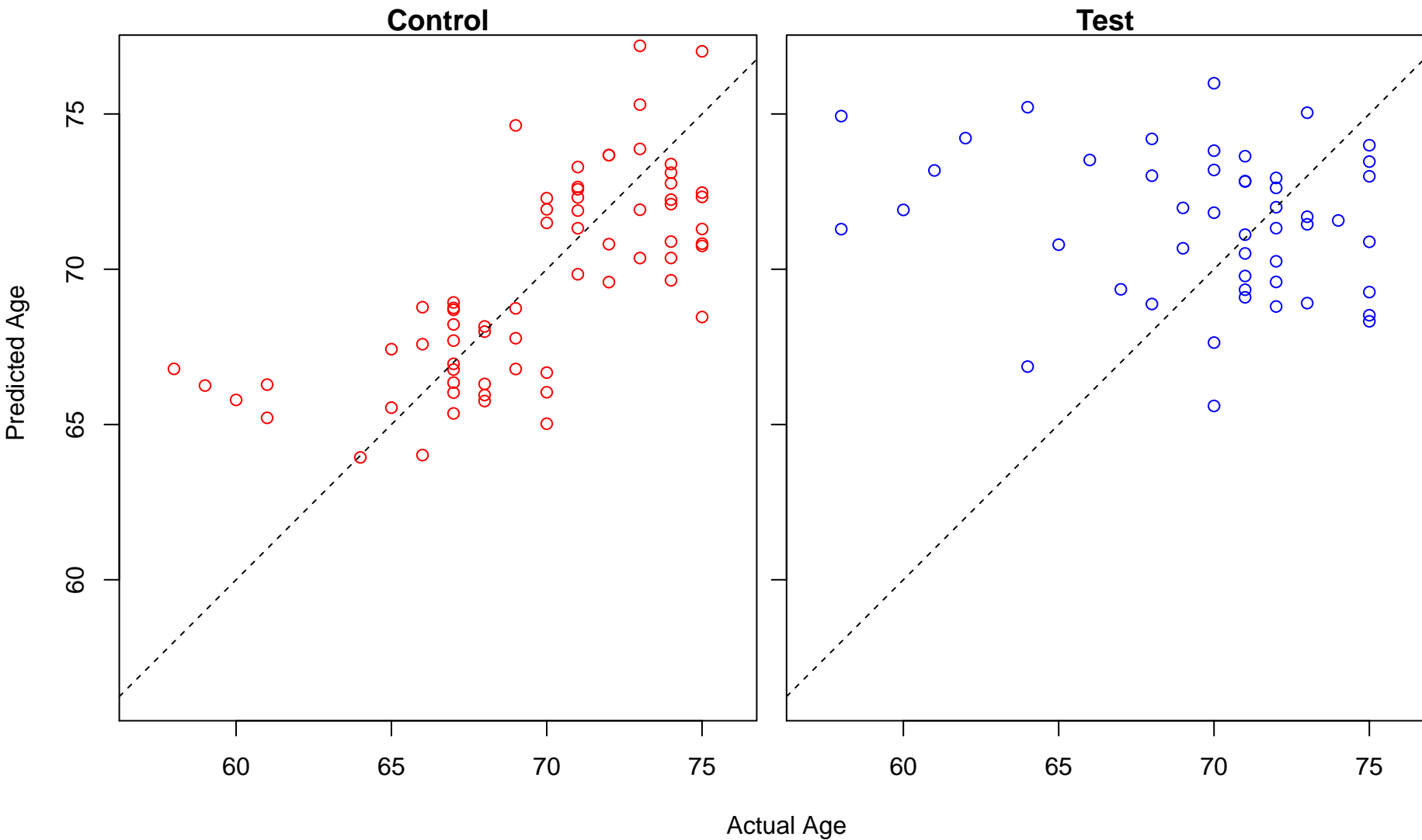
regulation of mitotic metaphase/anaphase transition (Score: 1.614345)



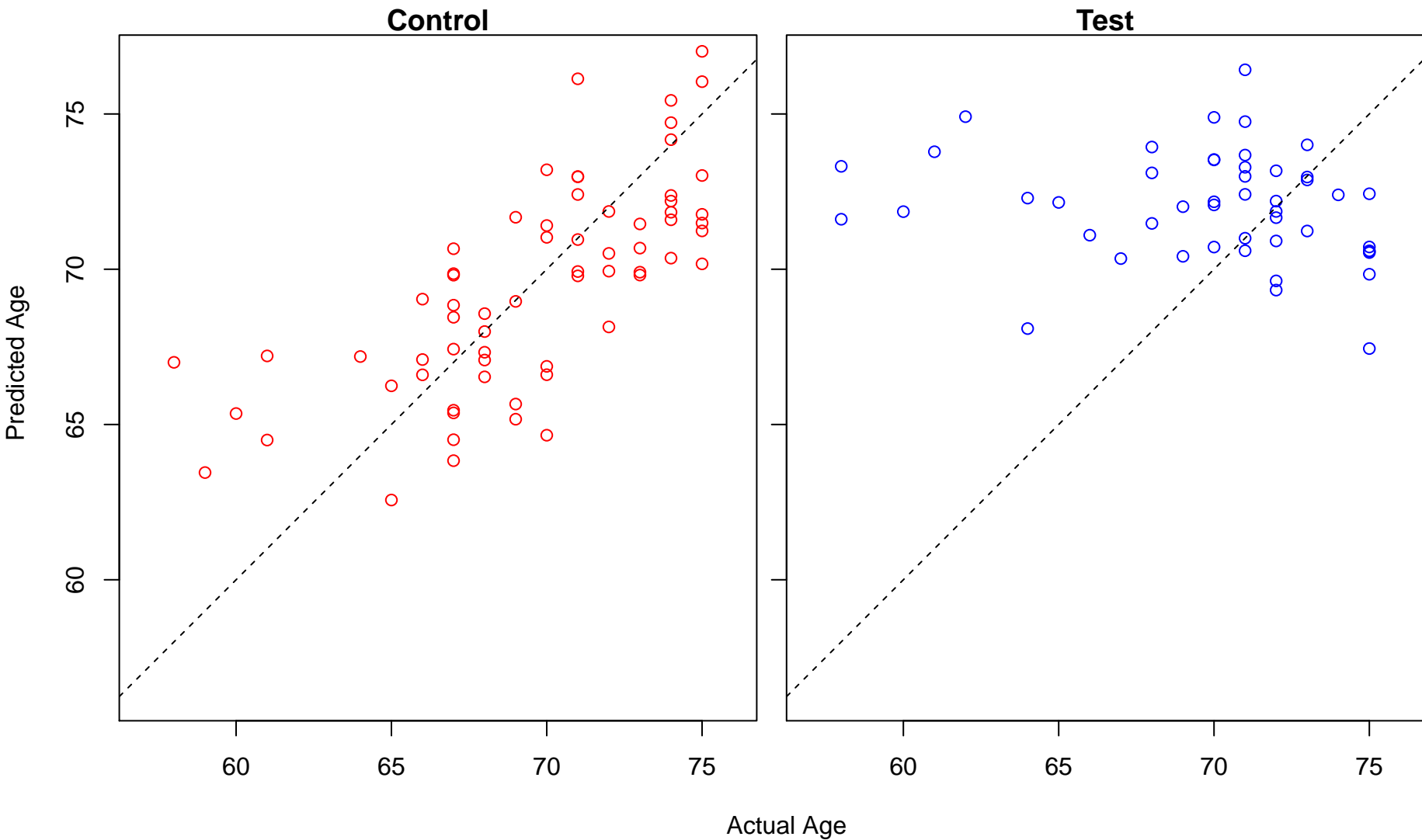
negative regulation of cell cycle phase transition (Score: 1.614163)



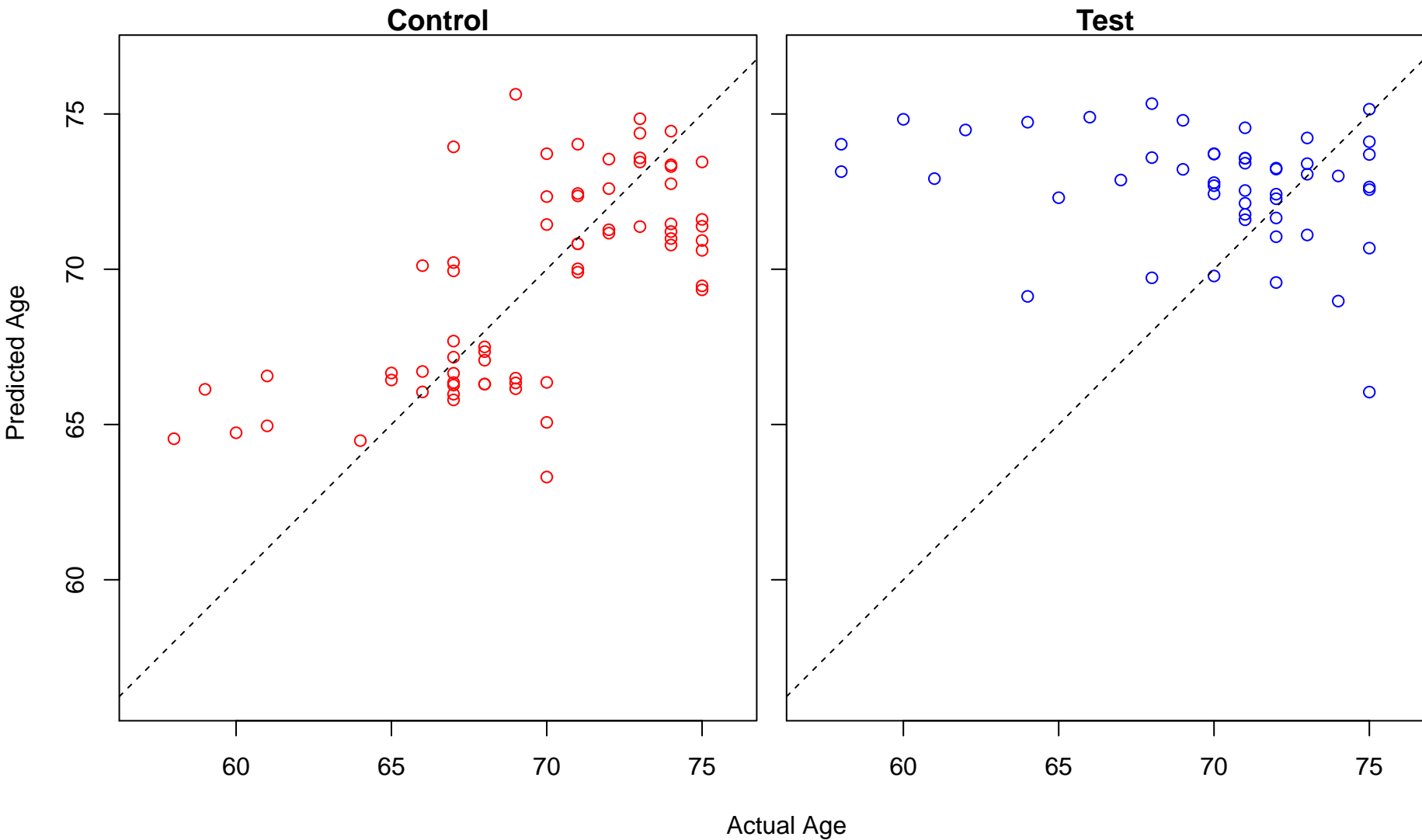
fatty acid catabolic process (Score: 1.613887)



negative regulation of intrinsic apoptotic signaling pathway (Score: 1.613771)

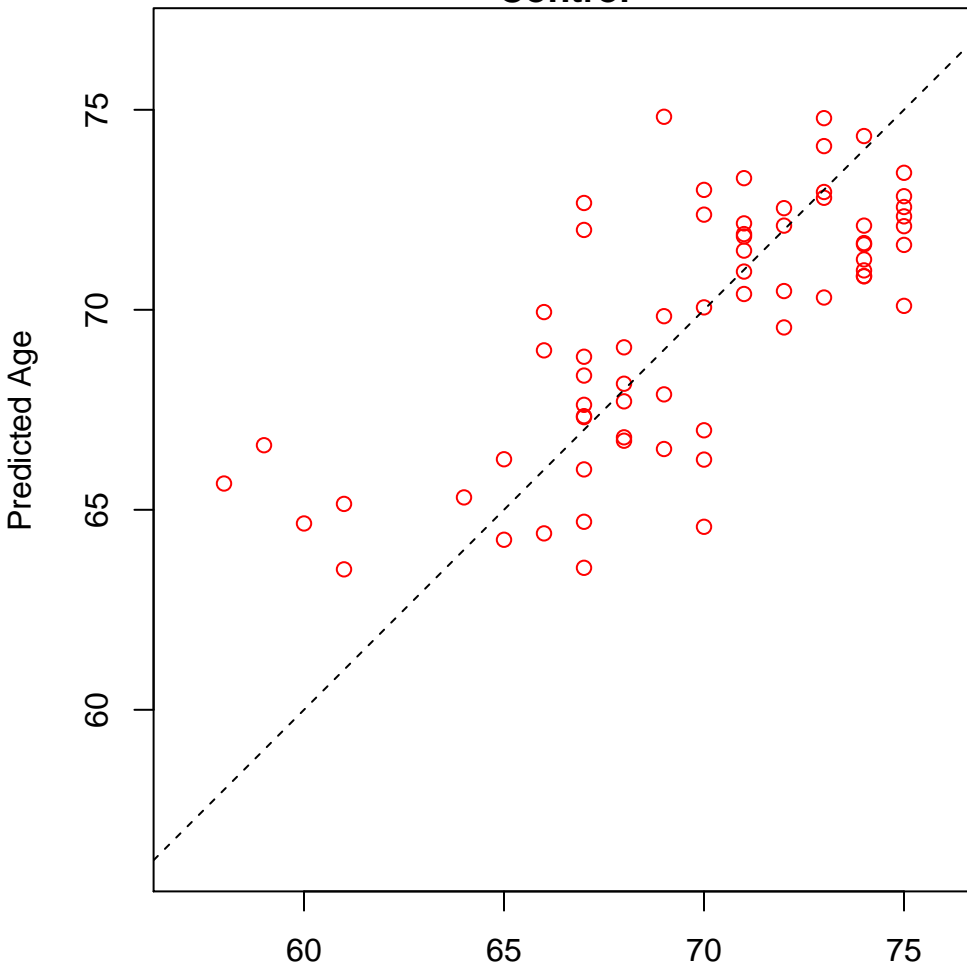


regulation of metaphase/anaphase transition of cell cycle (Score: 1.613485)

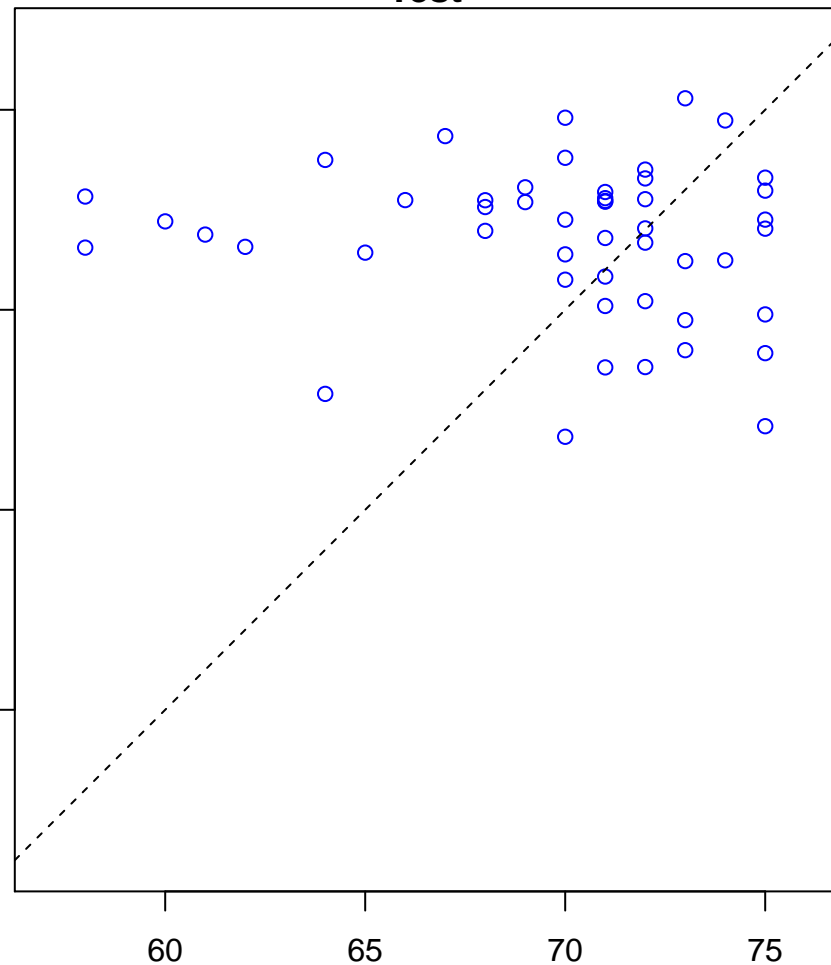


multivesicular body sorting pathway (Score: 1.613451)

Control

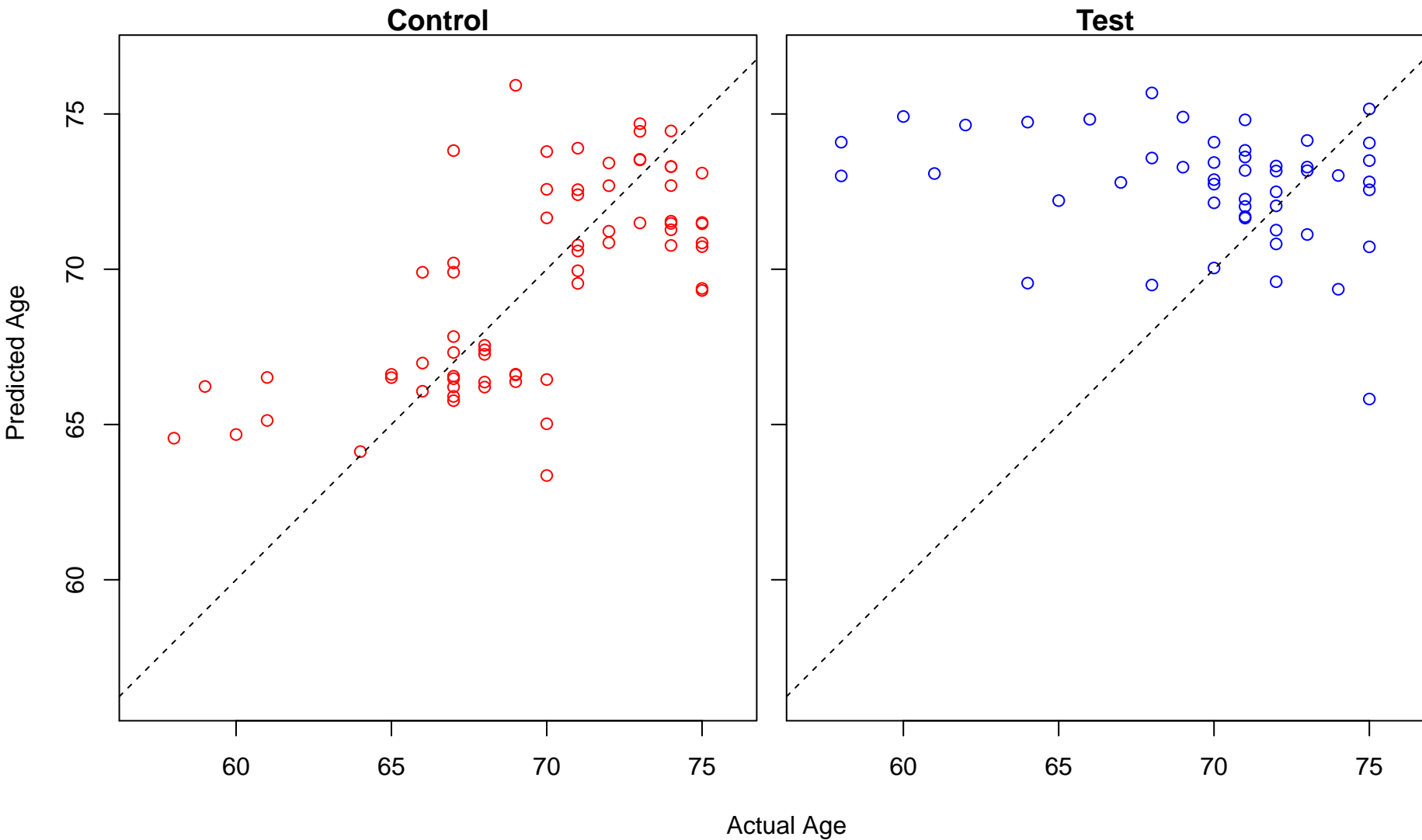


Test

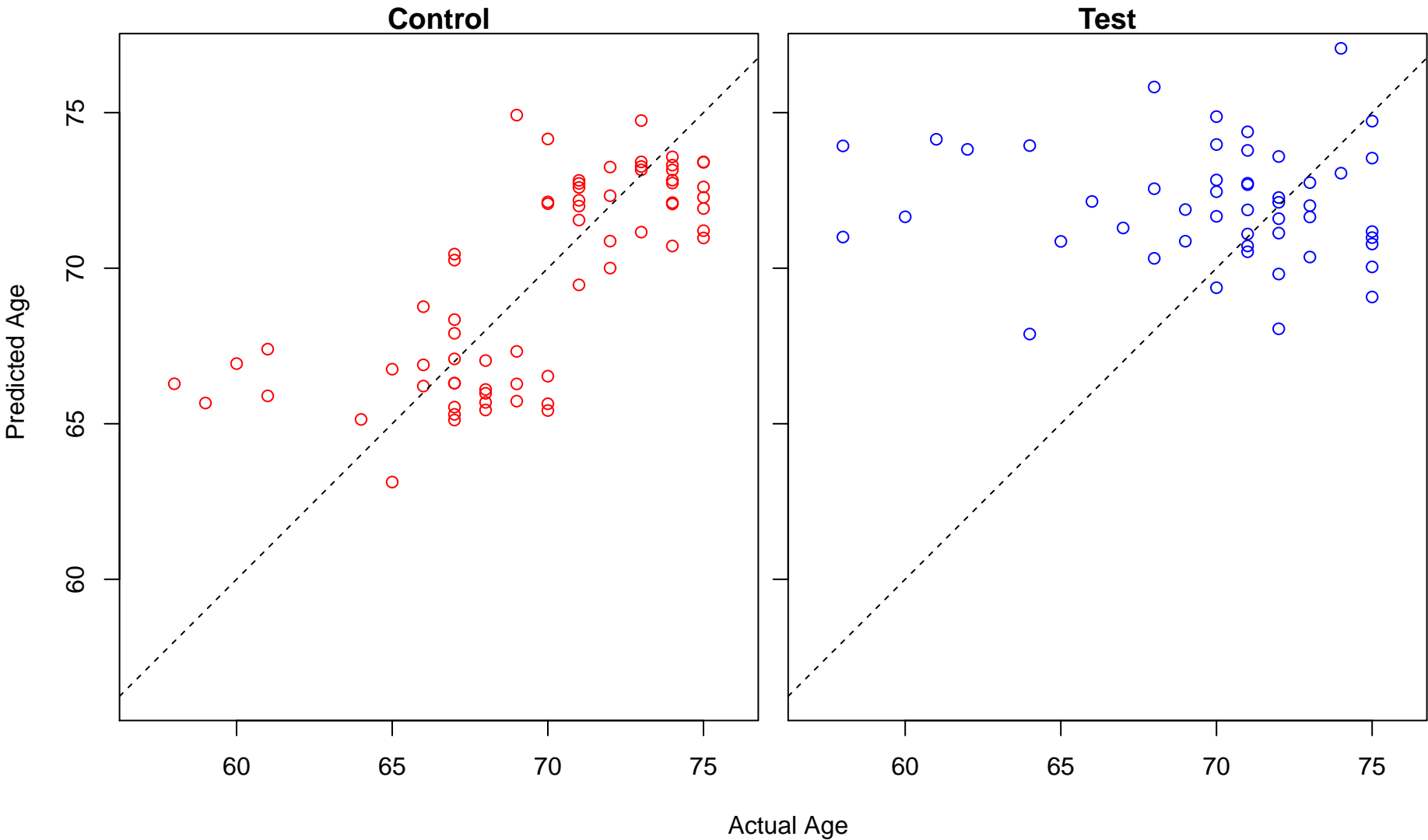


Actual Age

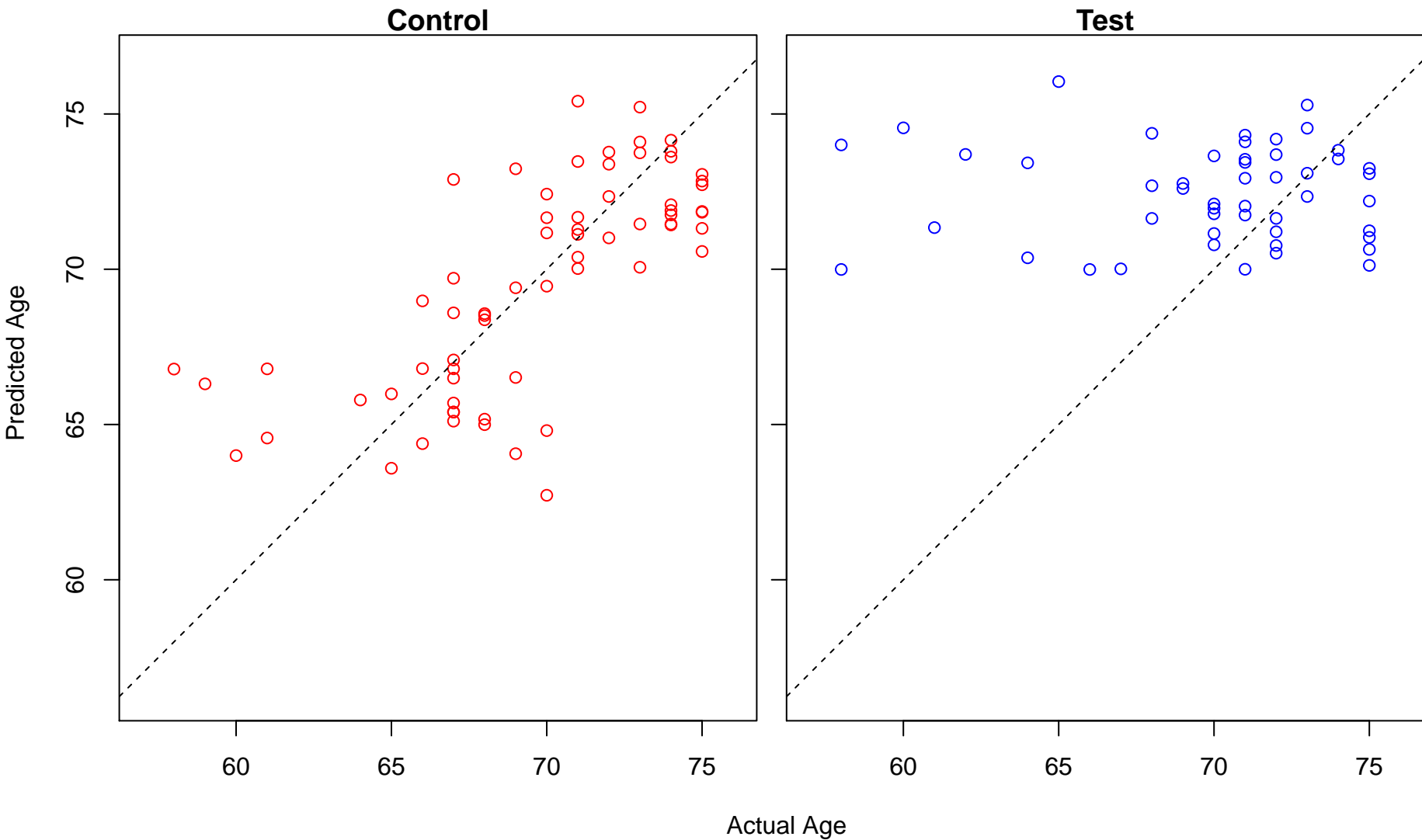
regulation of ubiquitin protein ligase activity (Score: 1.613358)



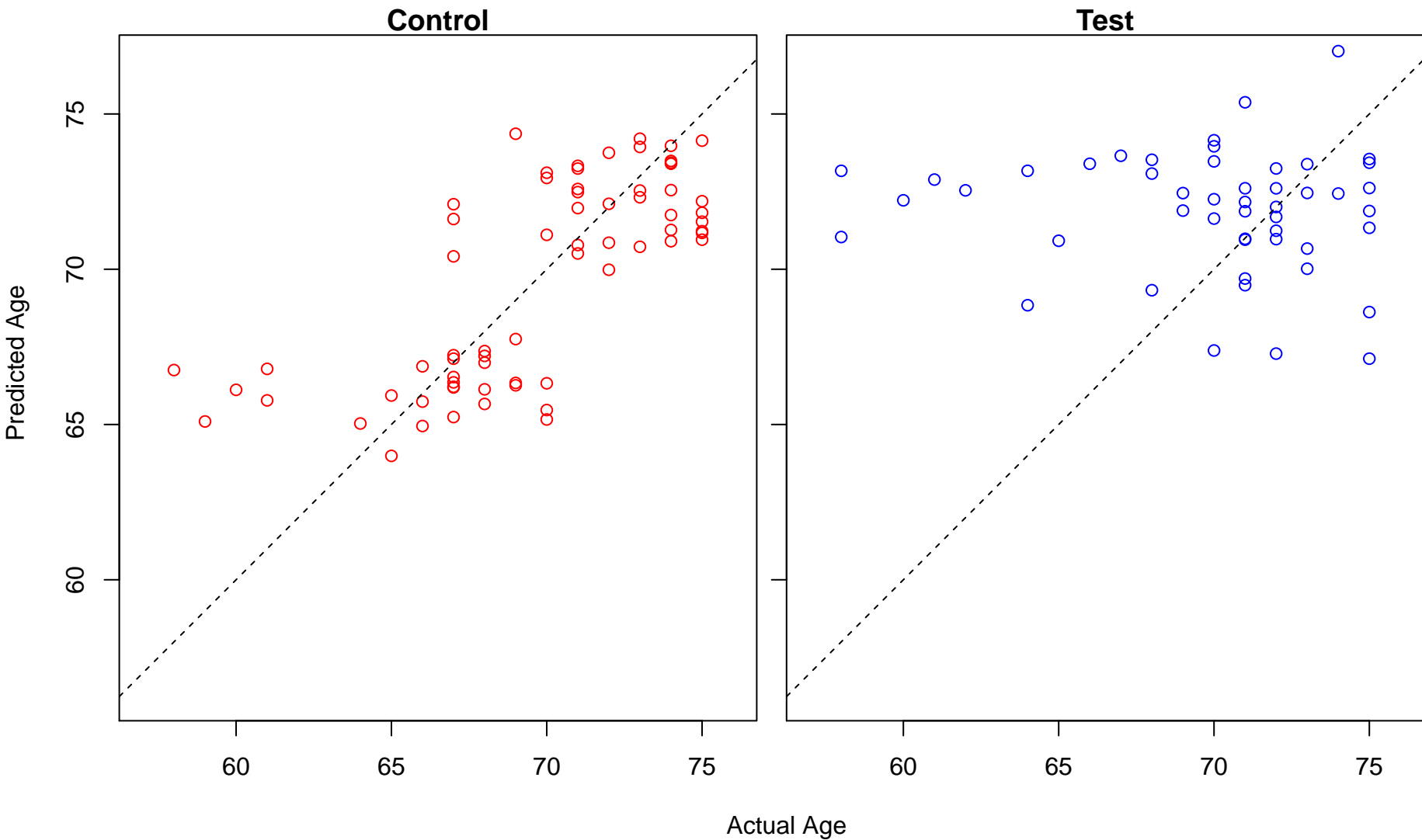
negative regulation of ubiquitin–protein ligase activity involved in mitotic cell cycle (Score: 1.61332)



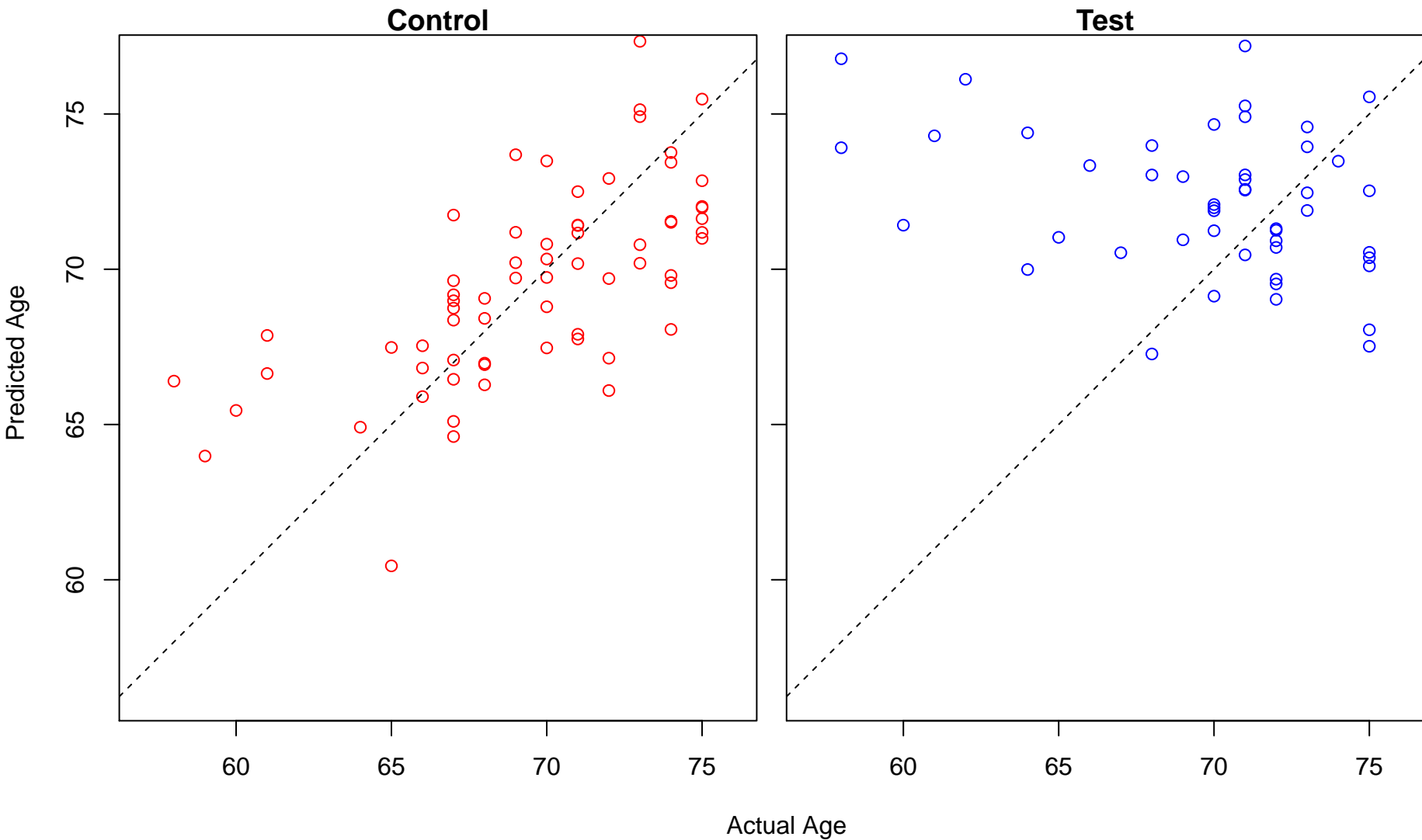
nucleobase-containing compound transport (Score: 1.612962)



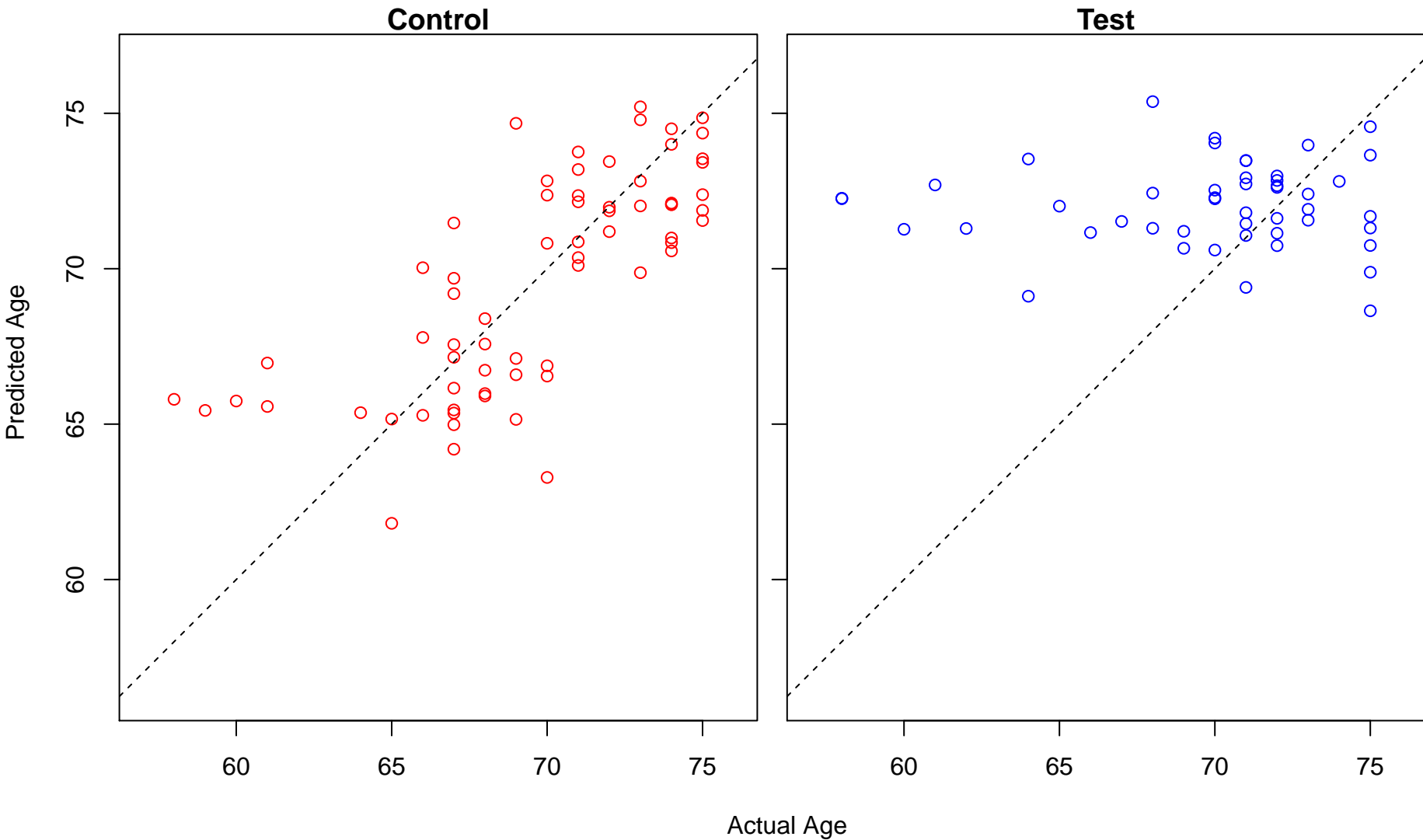
tRNA modification (Score: 1.612876)



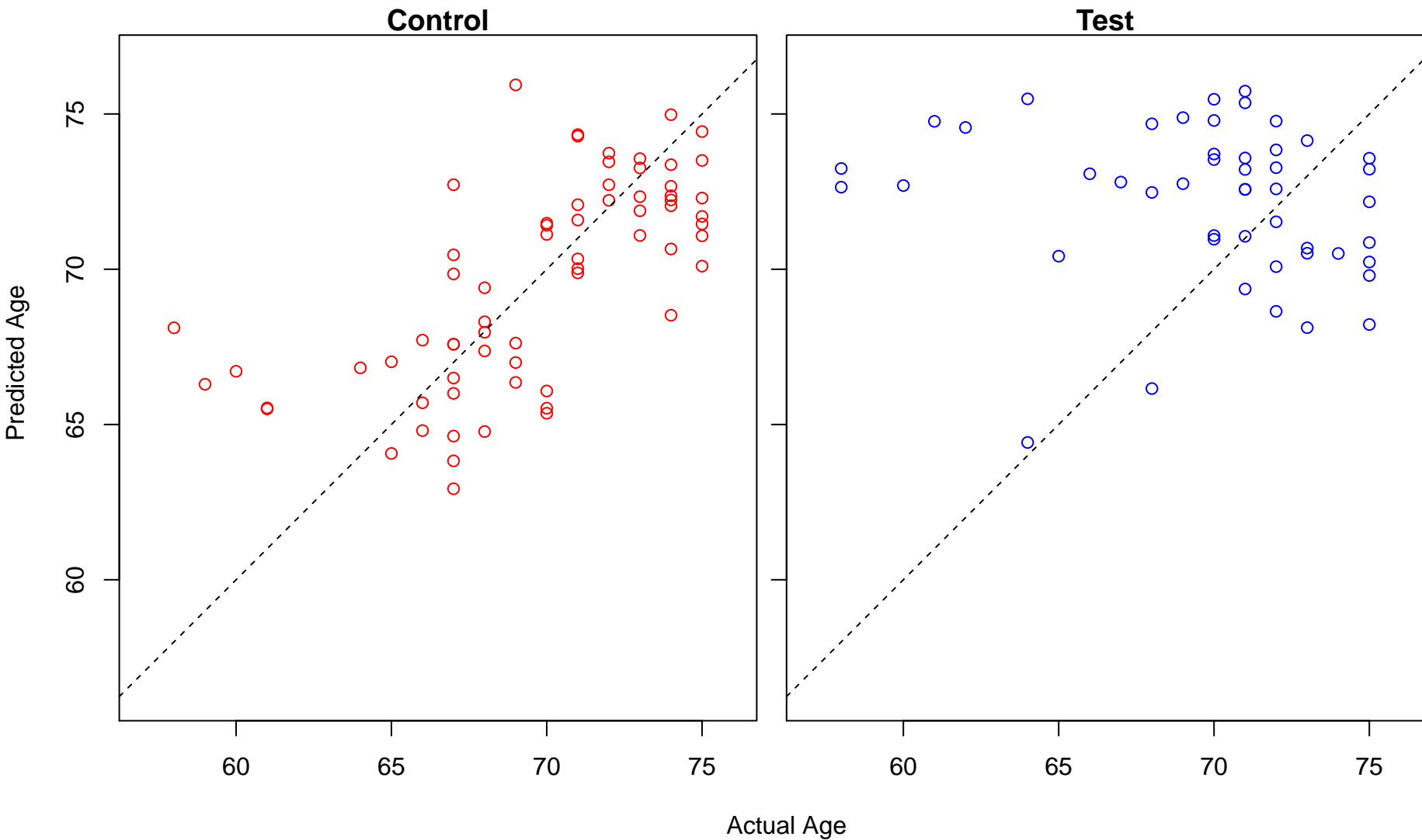
negative regulation of Ras protein signal transduction (Score: 1.612655)



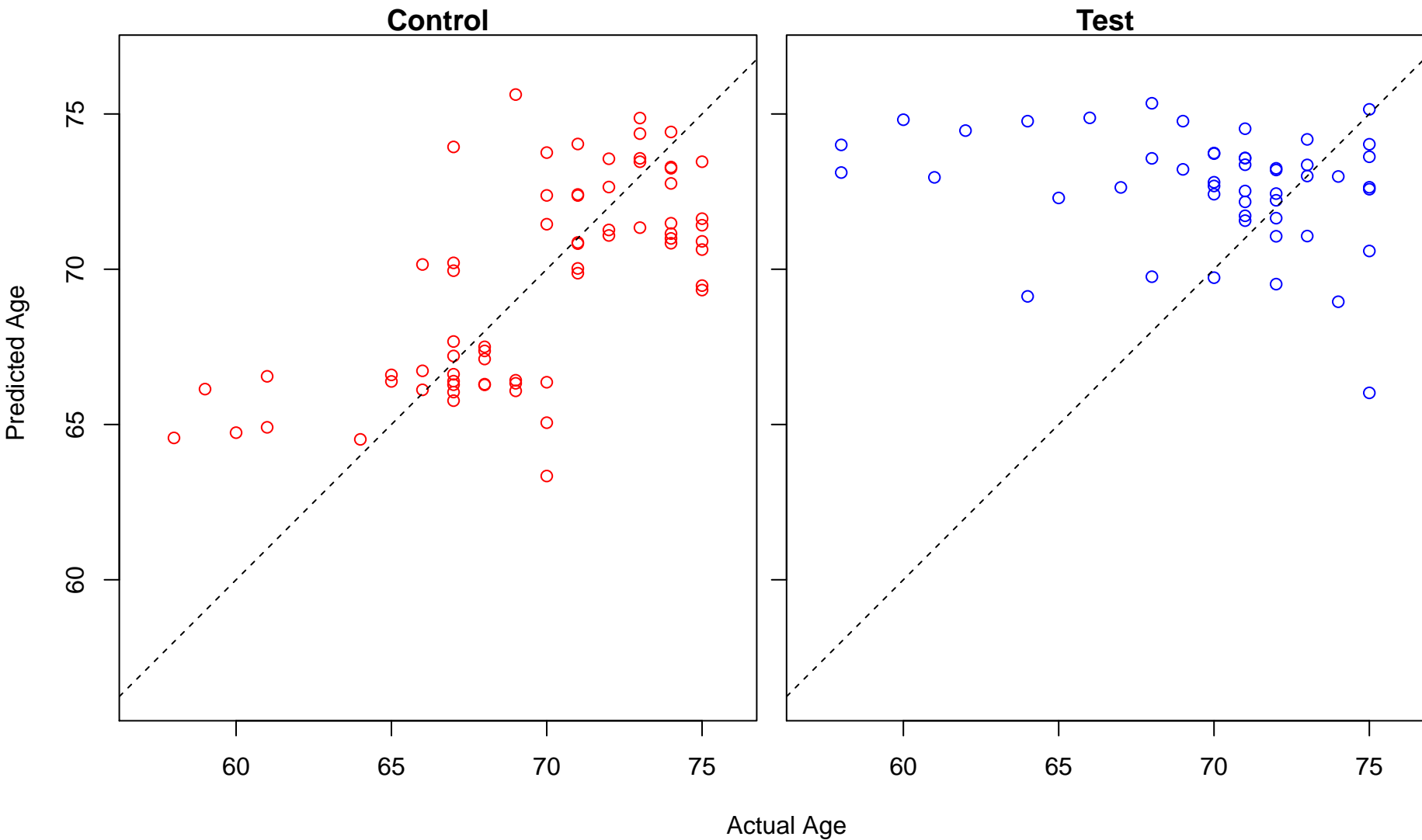
positive regulation of proteolysis involved in cellular protein catabolic process (Score: 1.611113)



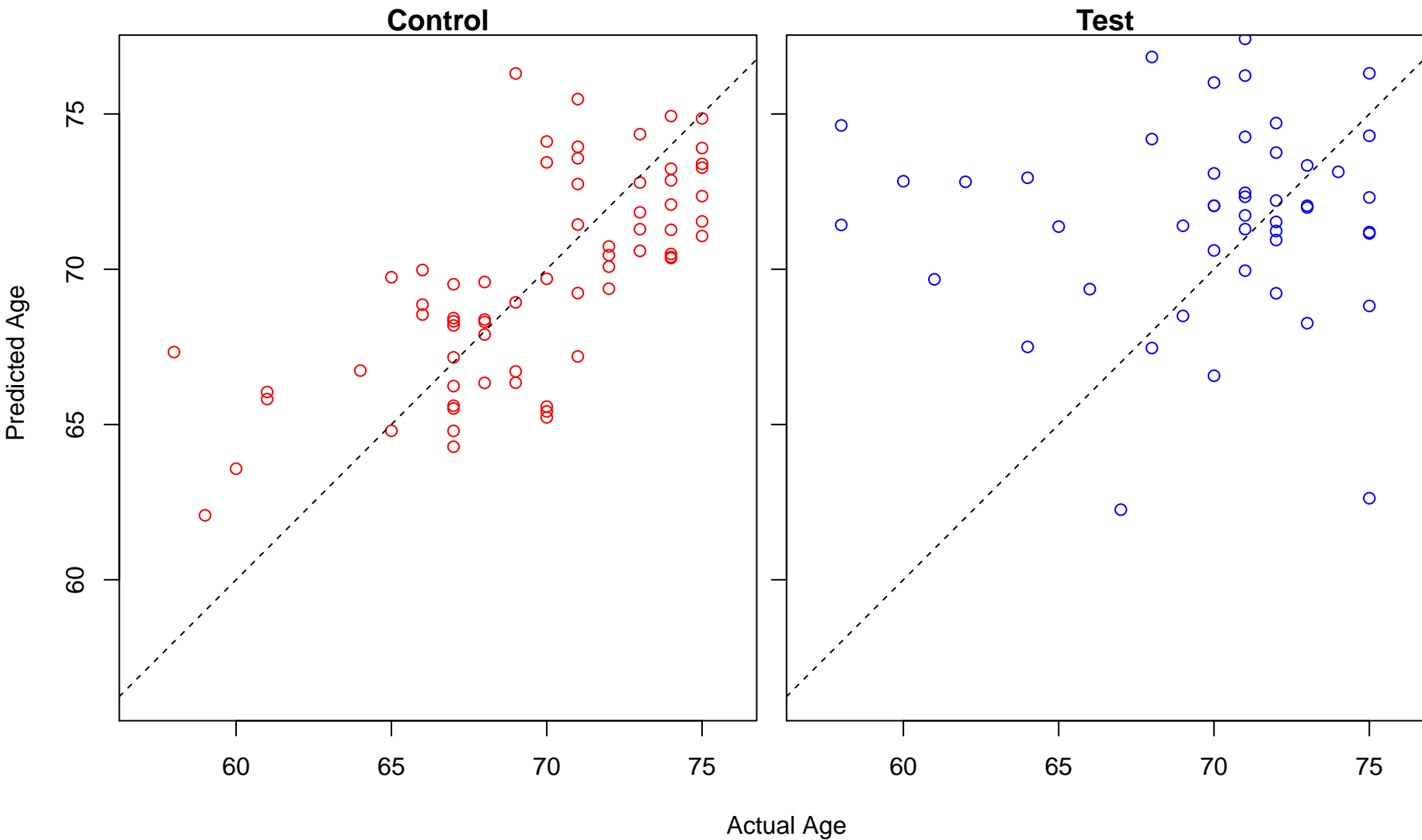
regulation of interleukin-8 production (Score: 1.609970)



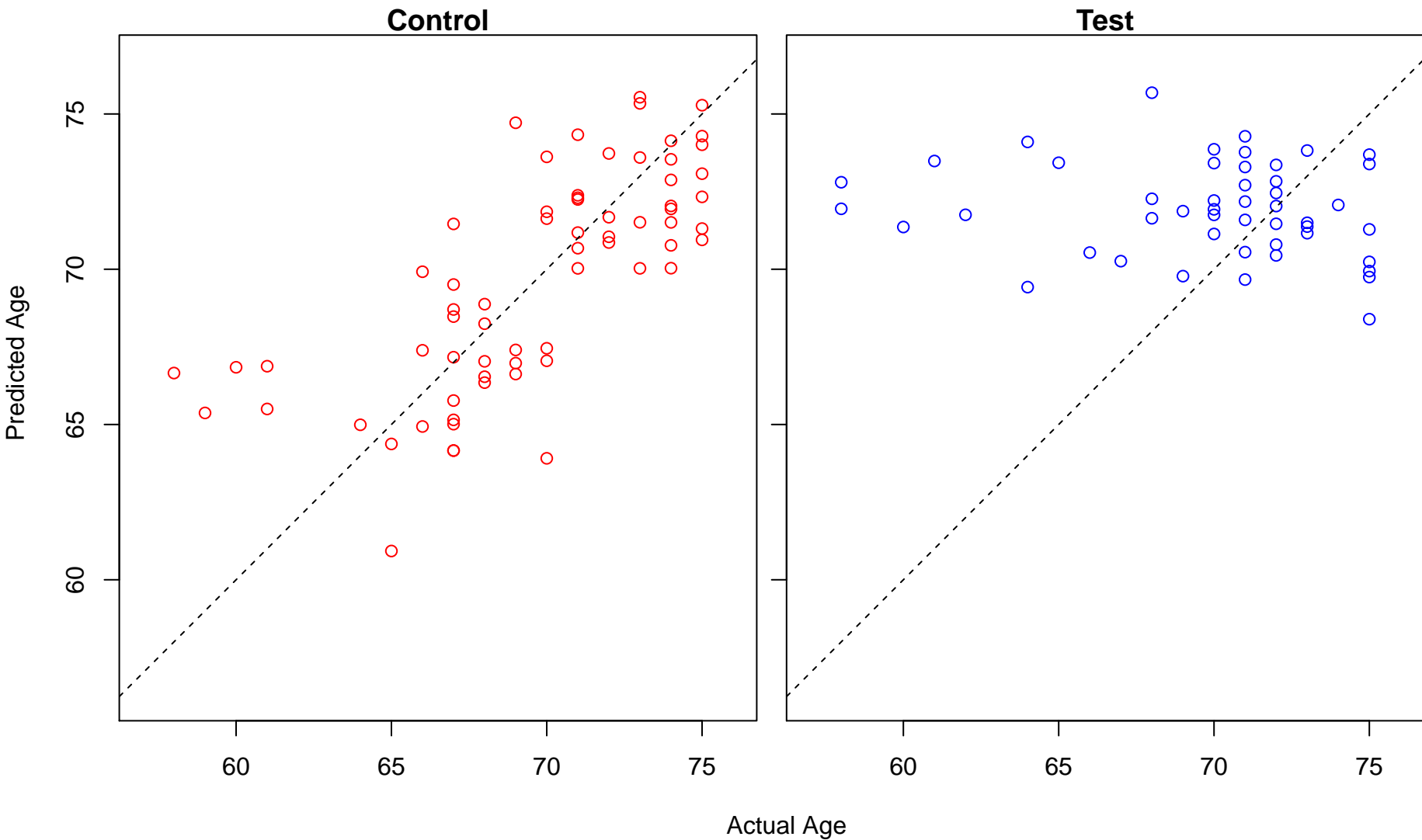
regulation of mitotic sister chromatid separation (Score: 1.609063)



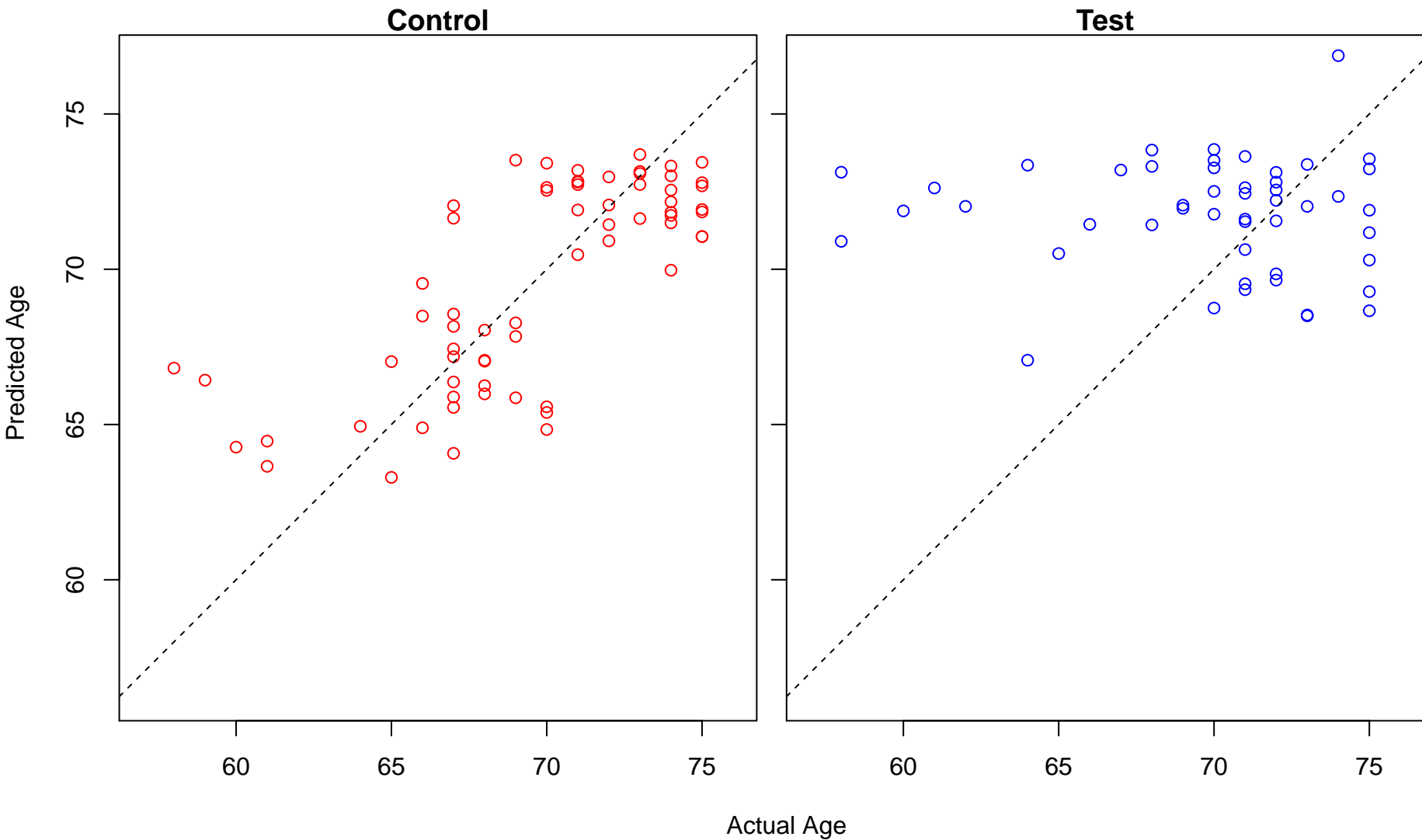
lymphocyte activation involved in immune response (Score: 1.608715)



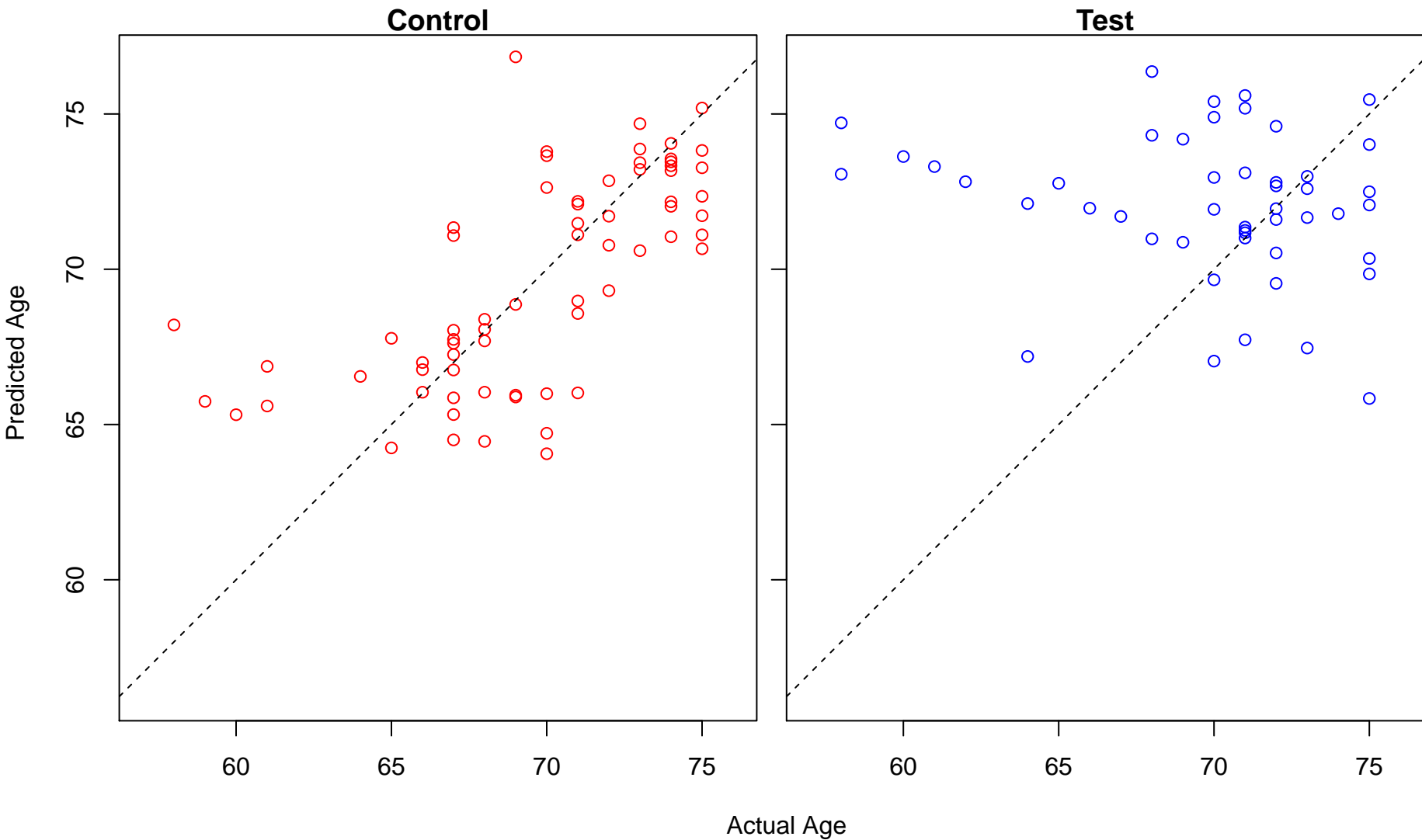
regulation of Wnt signaling pathway (Score: 1.608348)



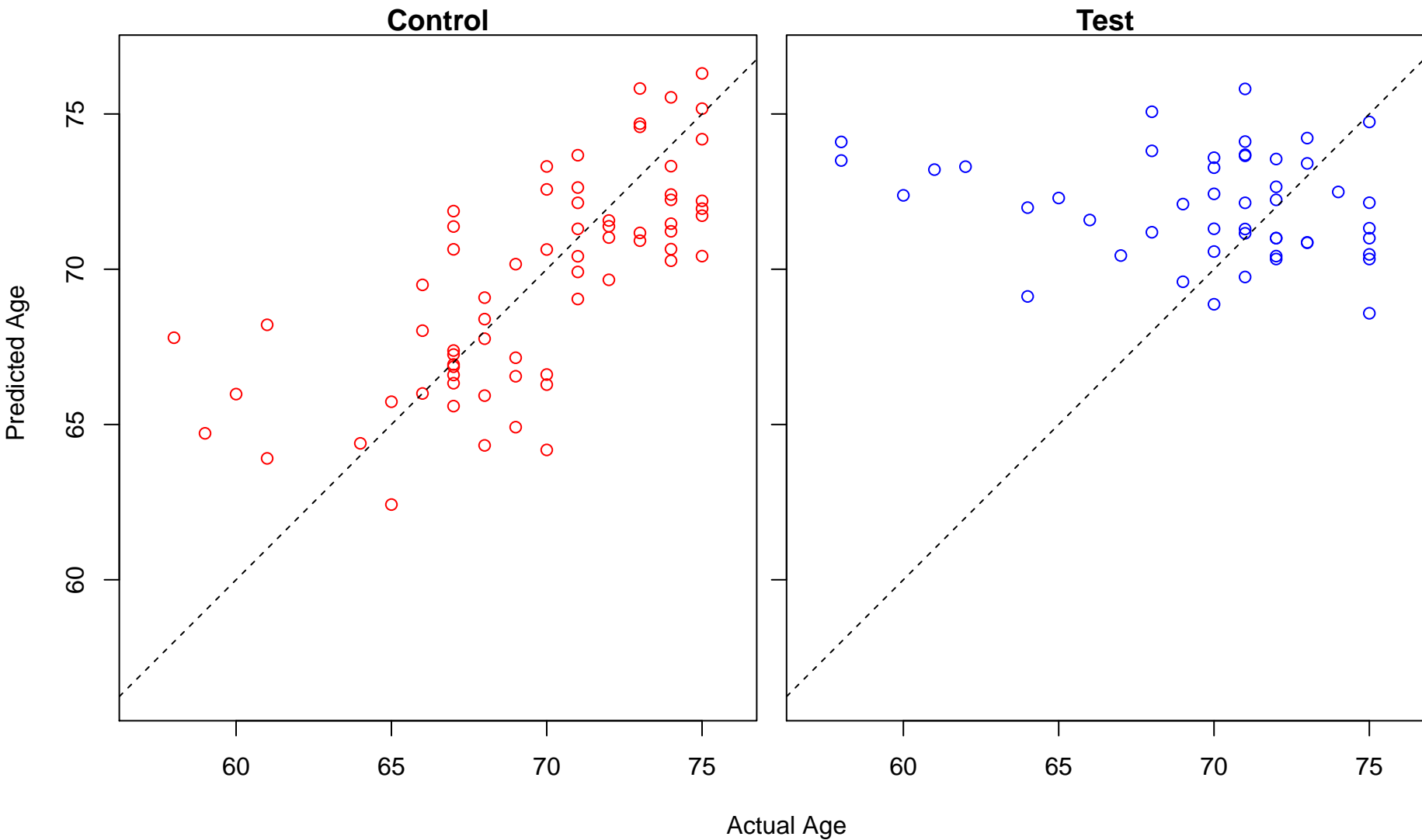
mitotic sister chromatid segregation (Score: 1.608290)



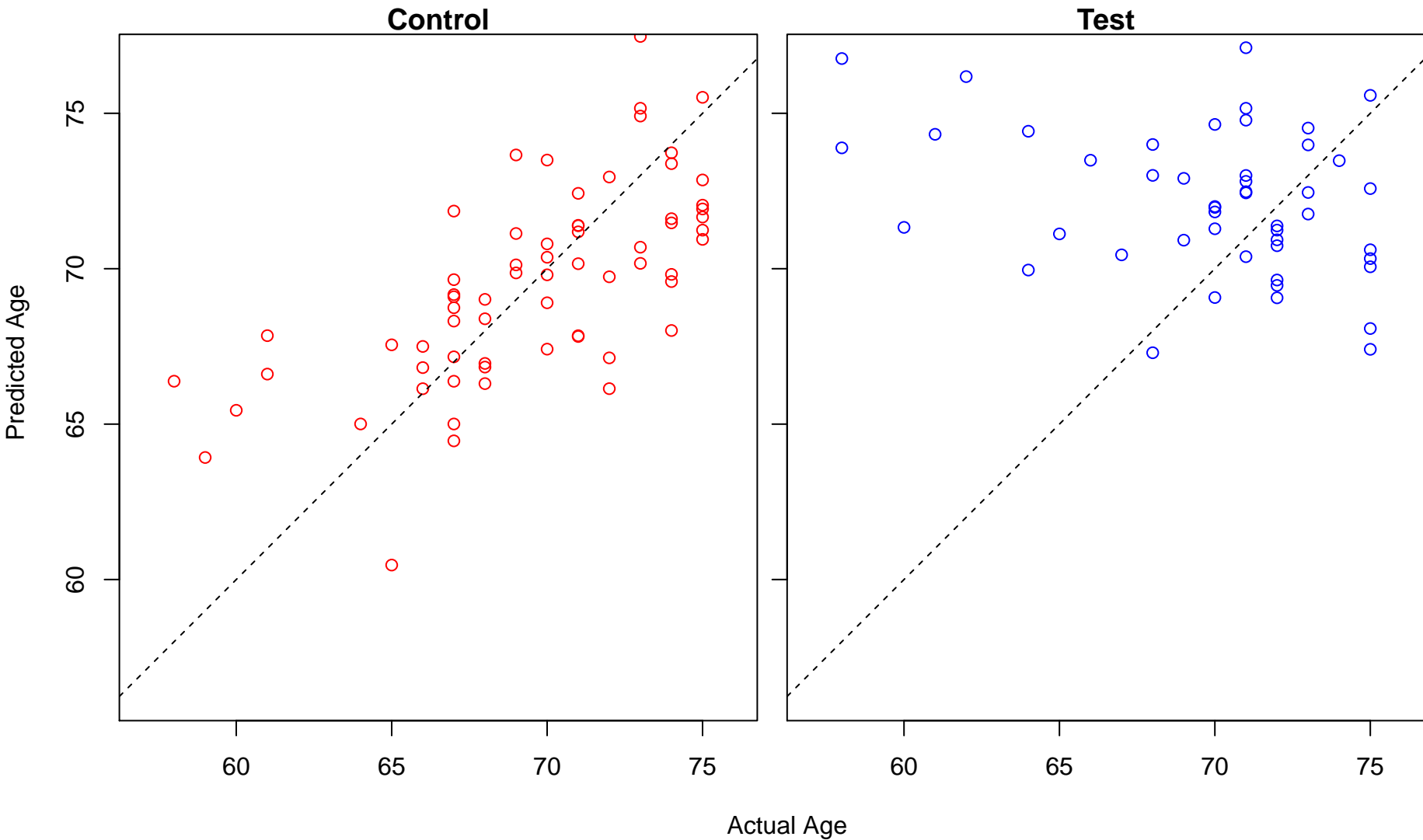
leukocyte activation (Score: 1.607771)



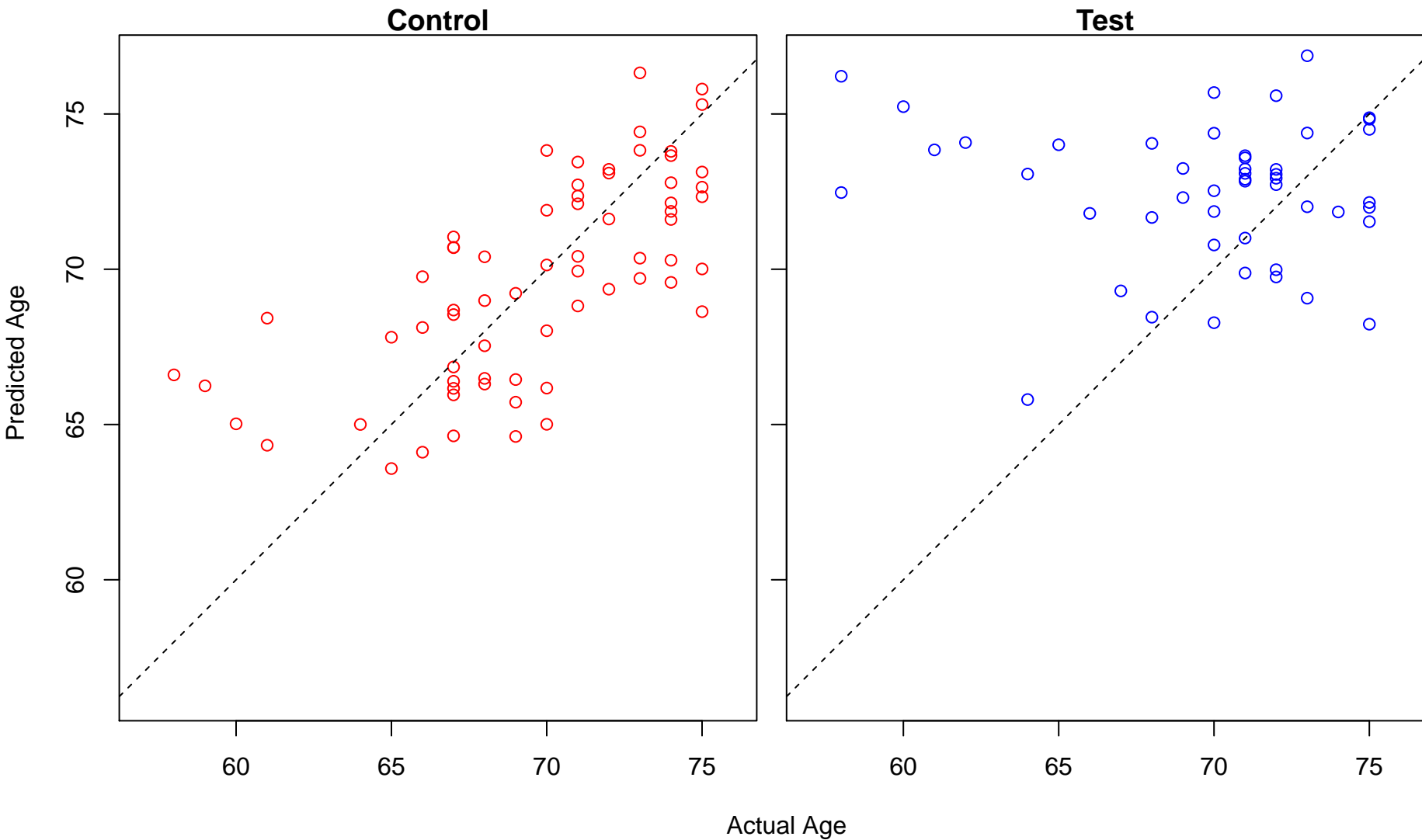
positive regulation of GTPase activity (Score: 1.607329)



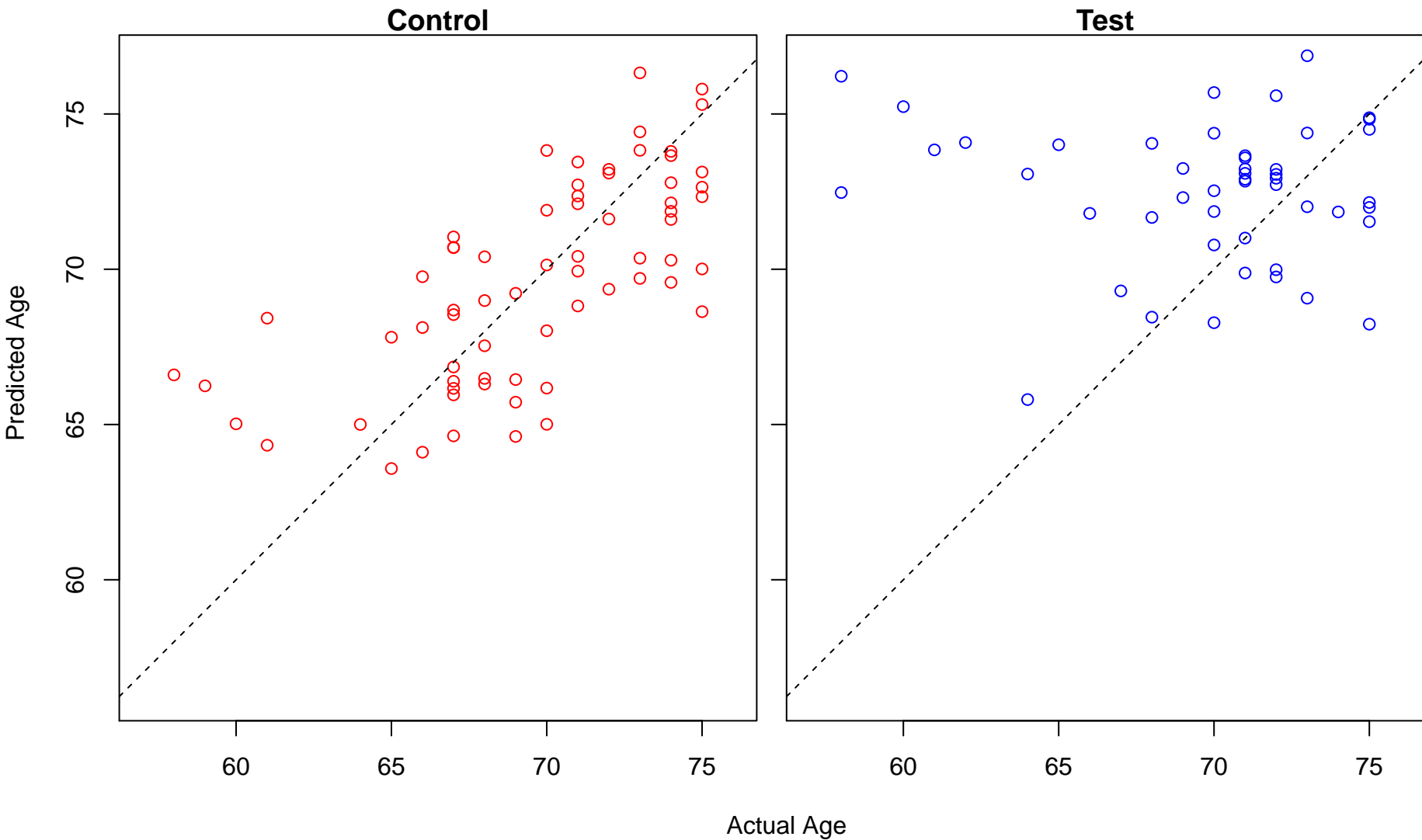
negative regulation of small GTPase mediated signal transduction (Score: 1.606987)



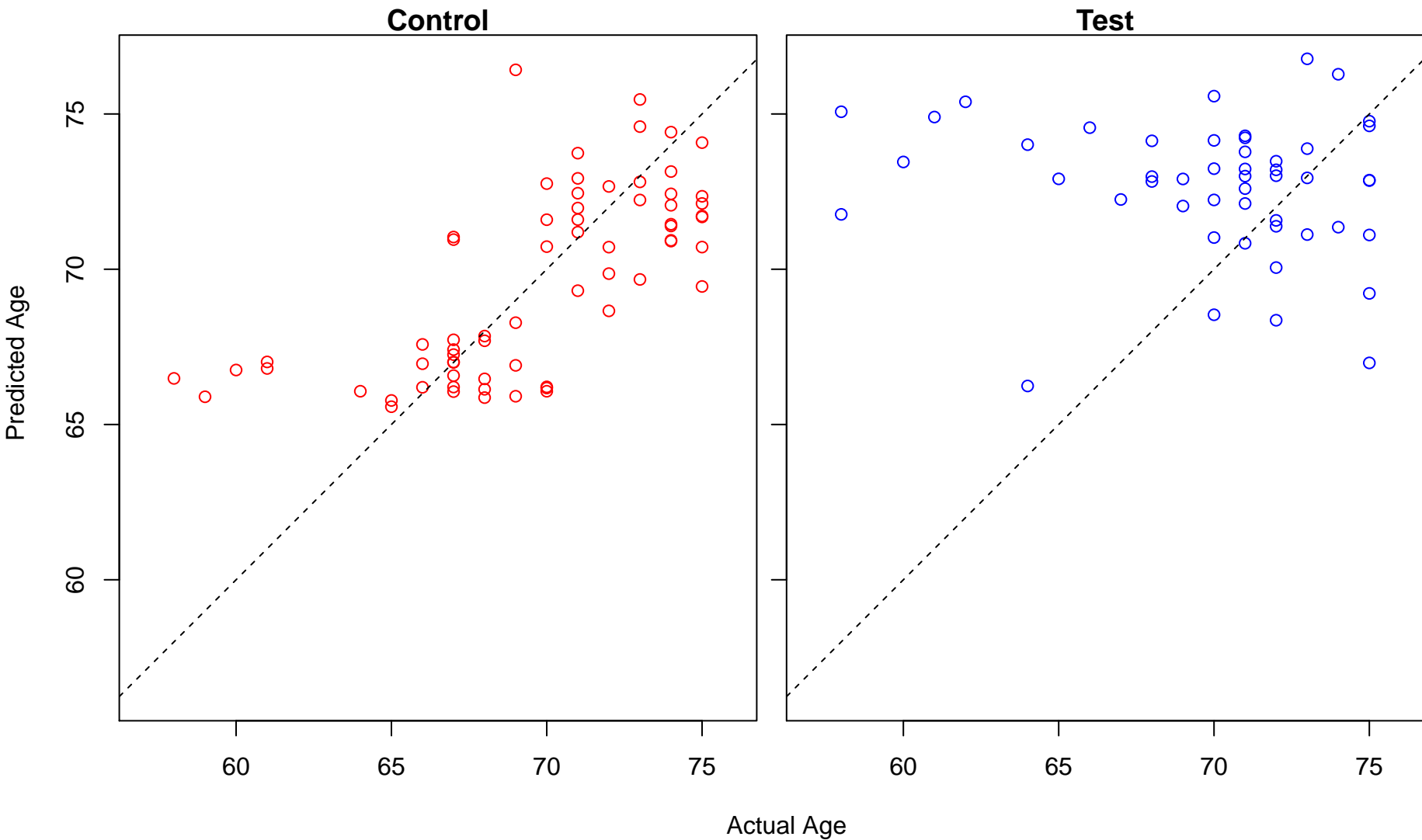
acyl-CoA metabolic process (Score: 1.606516)



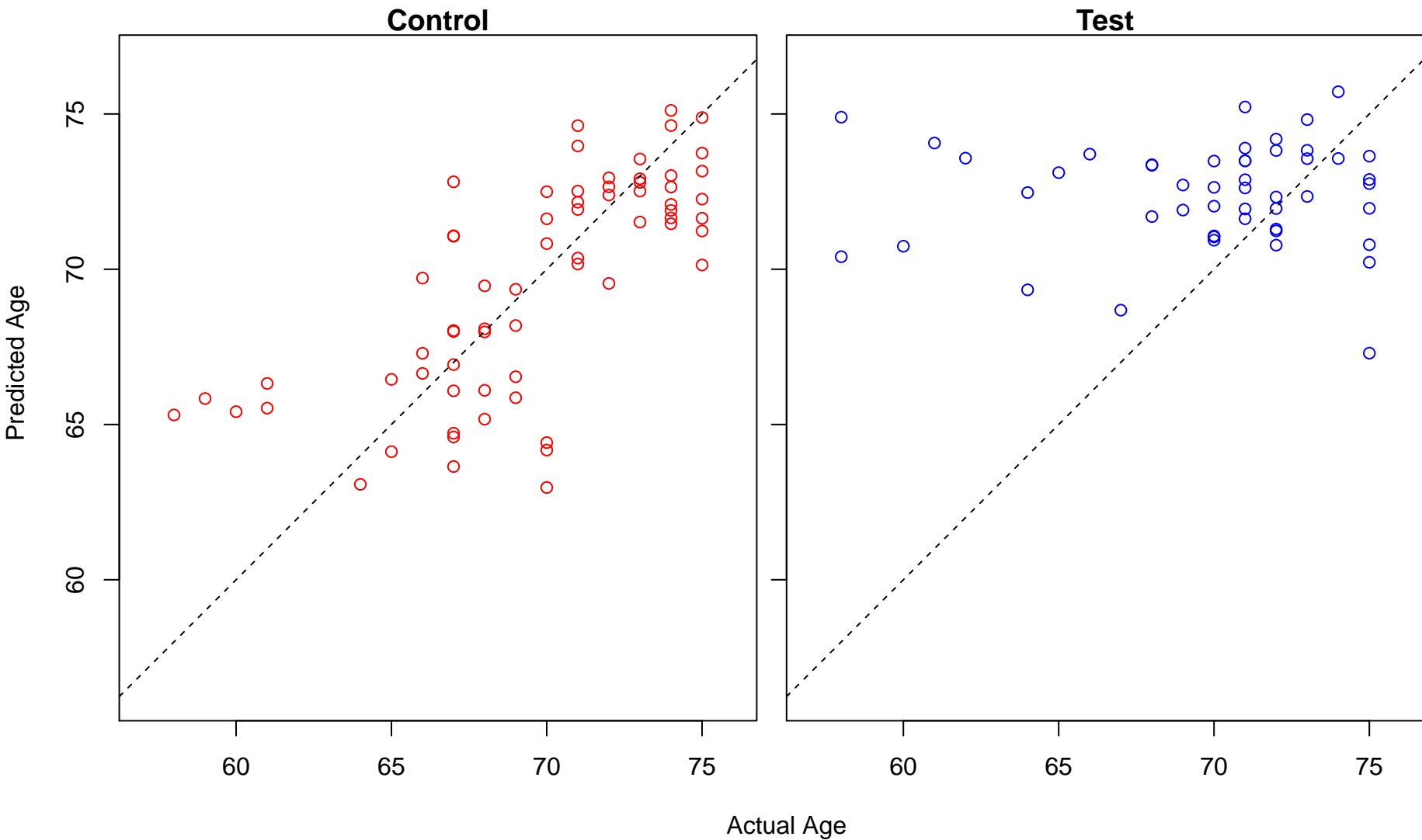
thioester metabolic process (Score: 1.606516)



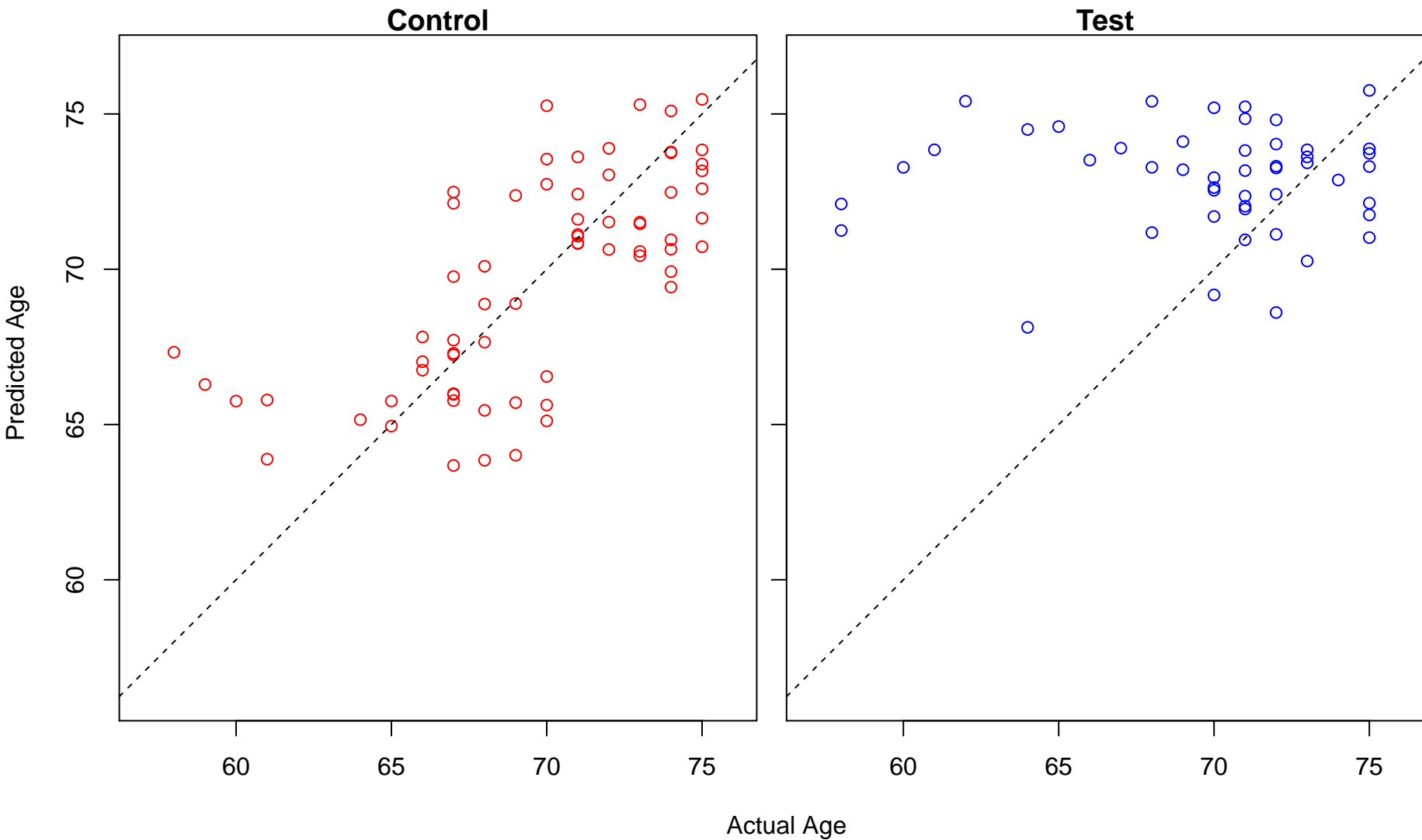
reactive oxygen species metabolic process (Score: 1.606091)



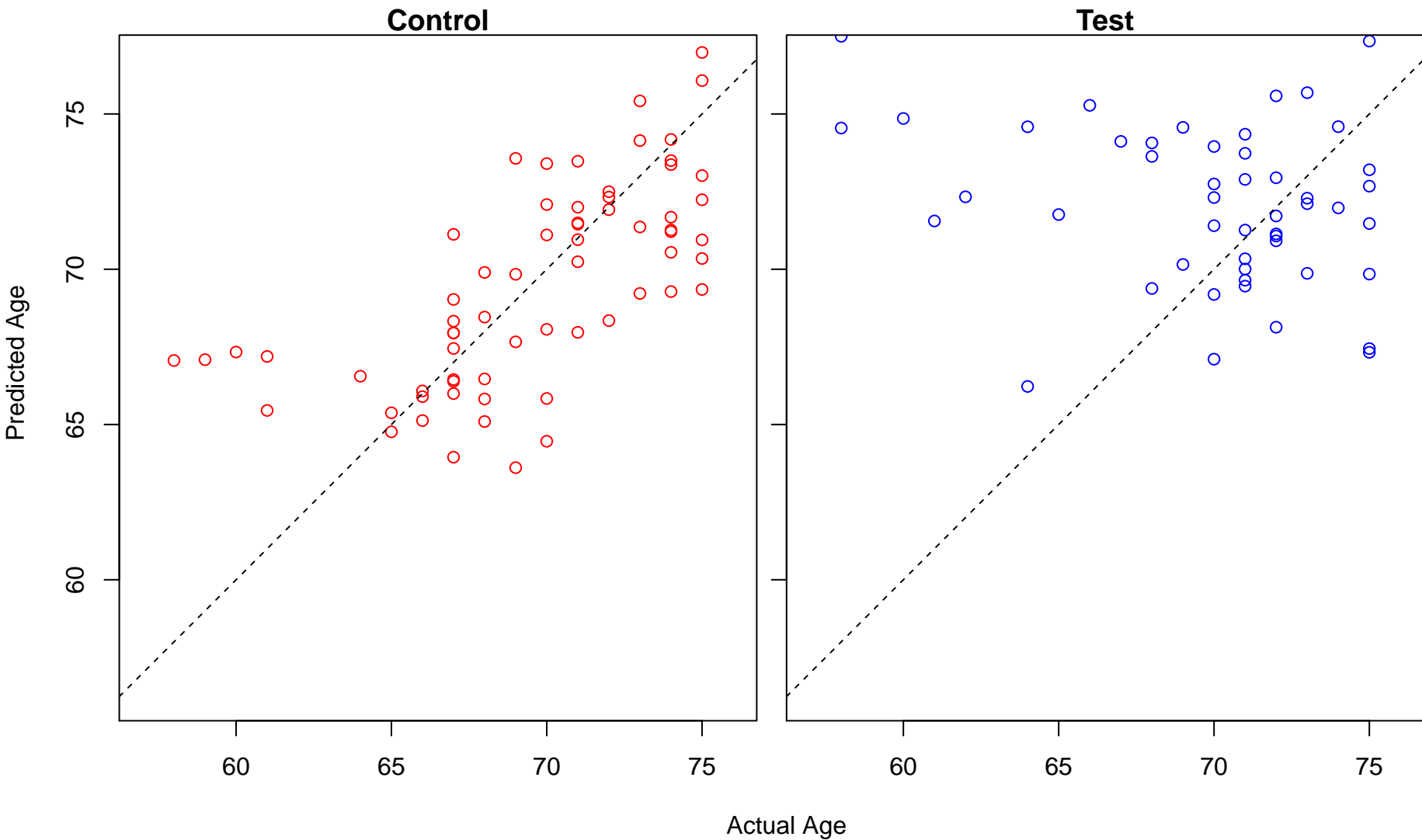
regulation of cellular amide metabolic process (Score: 1.606085)



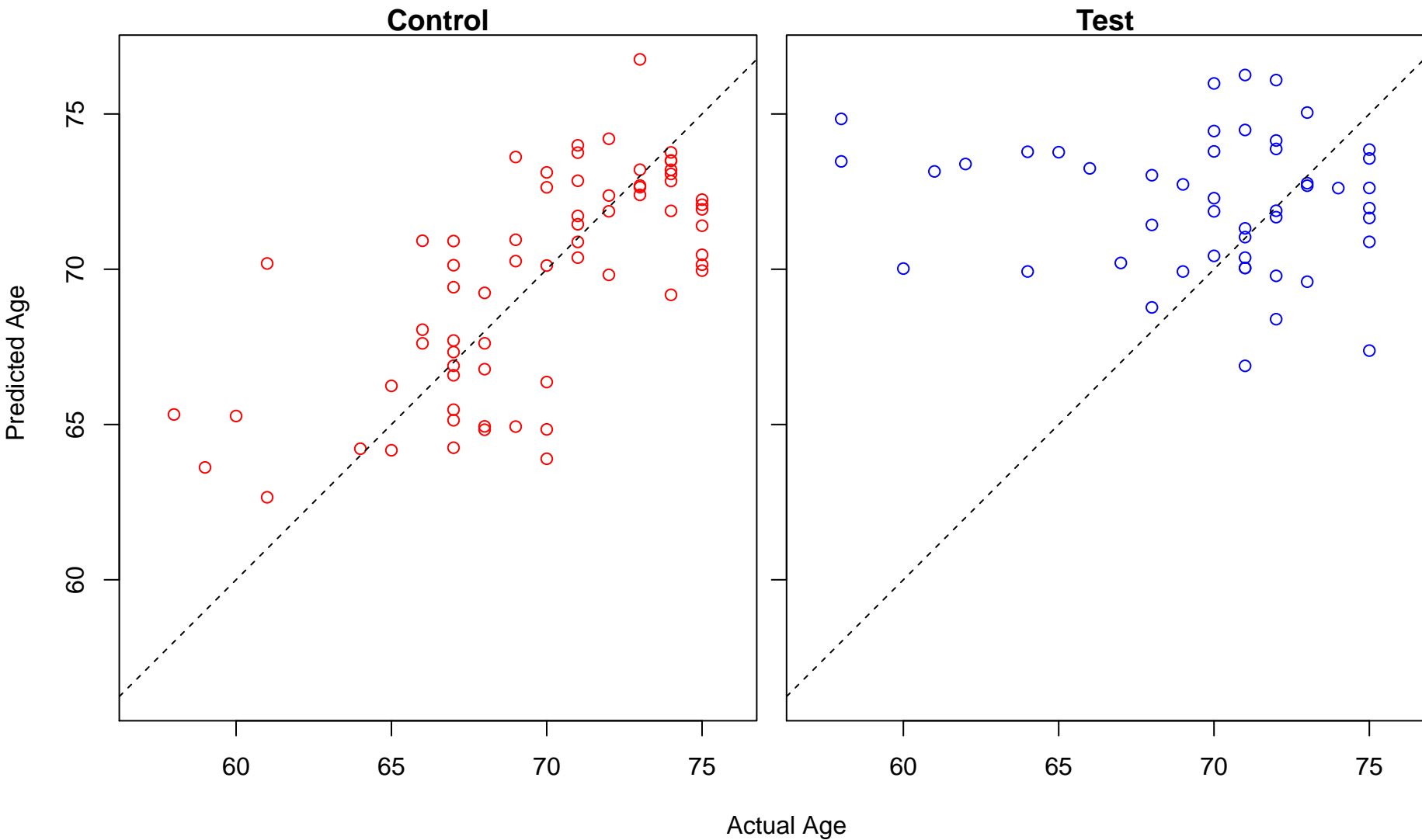
negative regulation of gene expression, epigenetic (Score: 1.606075)



maintenance of location (Score: 1.605796)

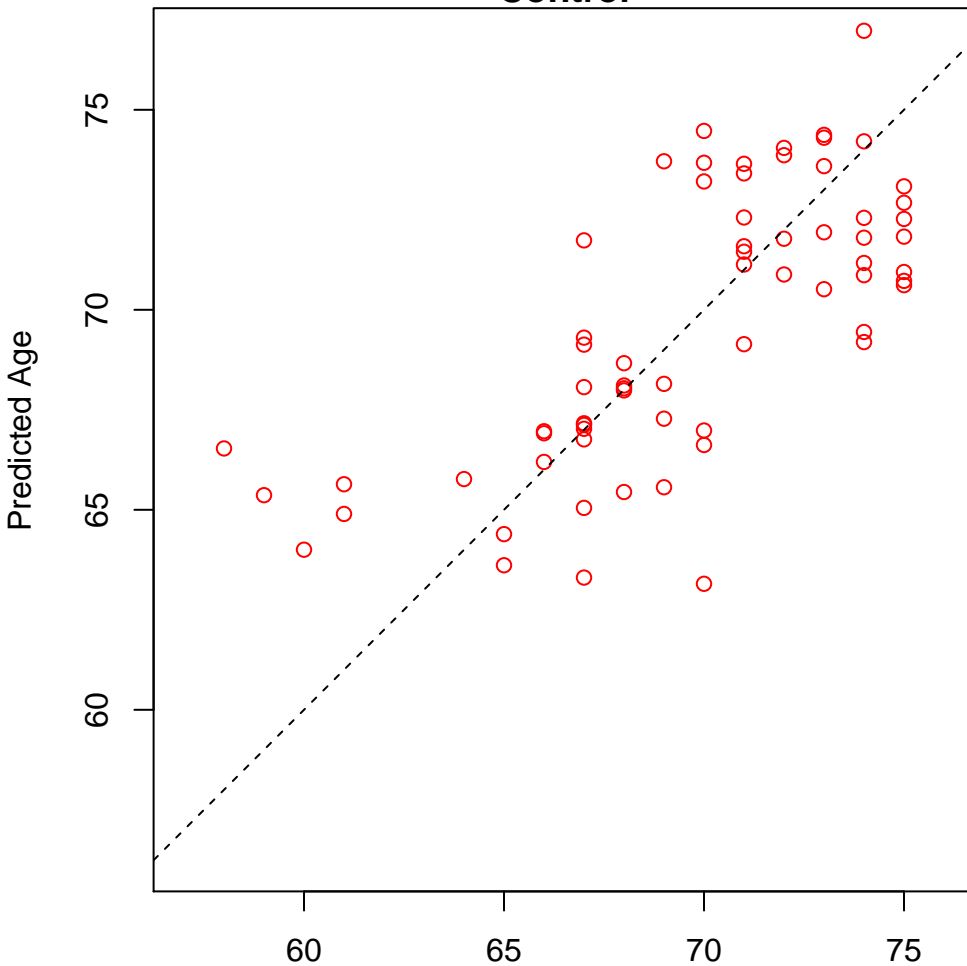


regulation of DNA repair (Score: 1.605781)

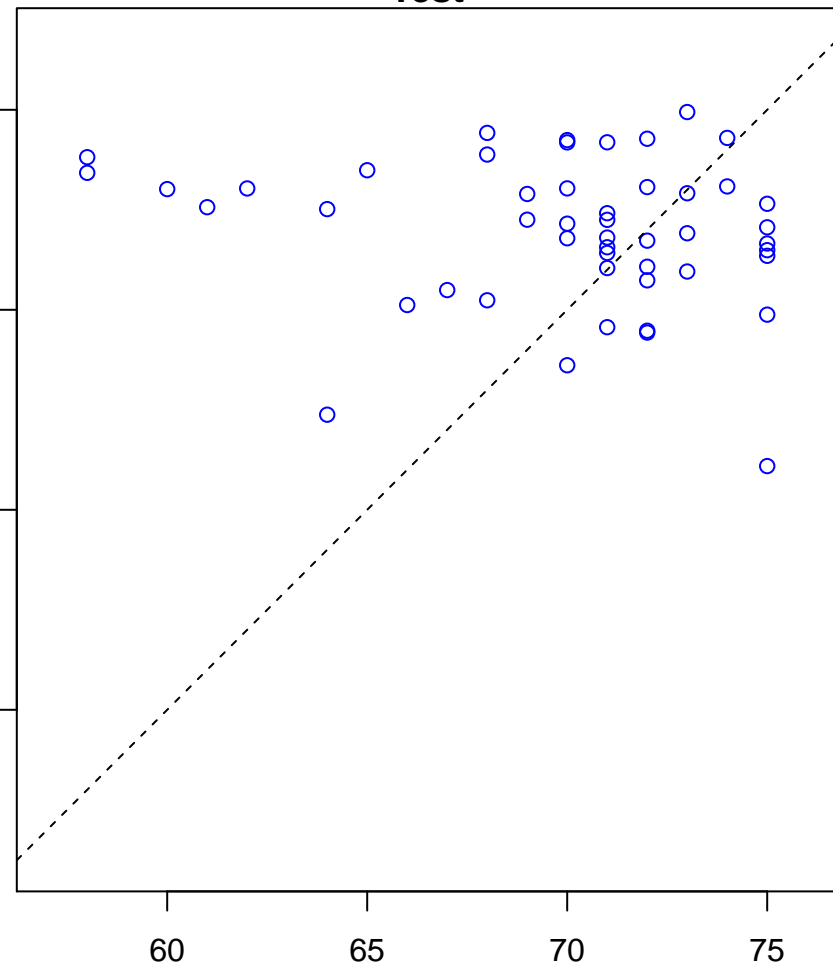


positive regulation of viral transcription (Score: 1.605391)

Control

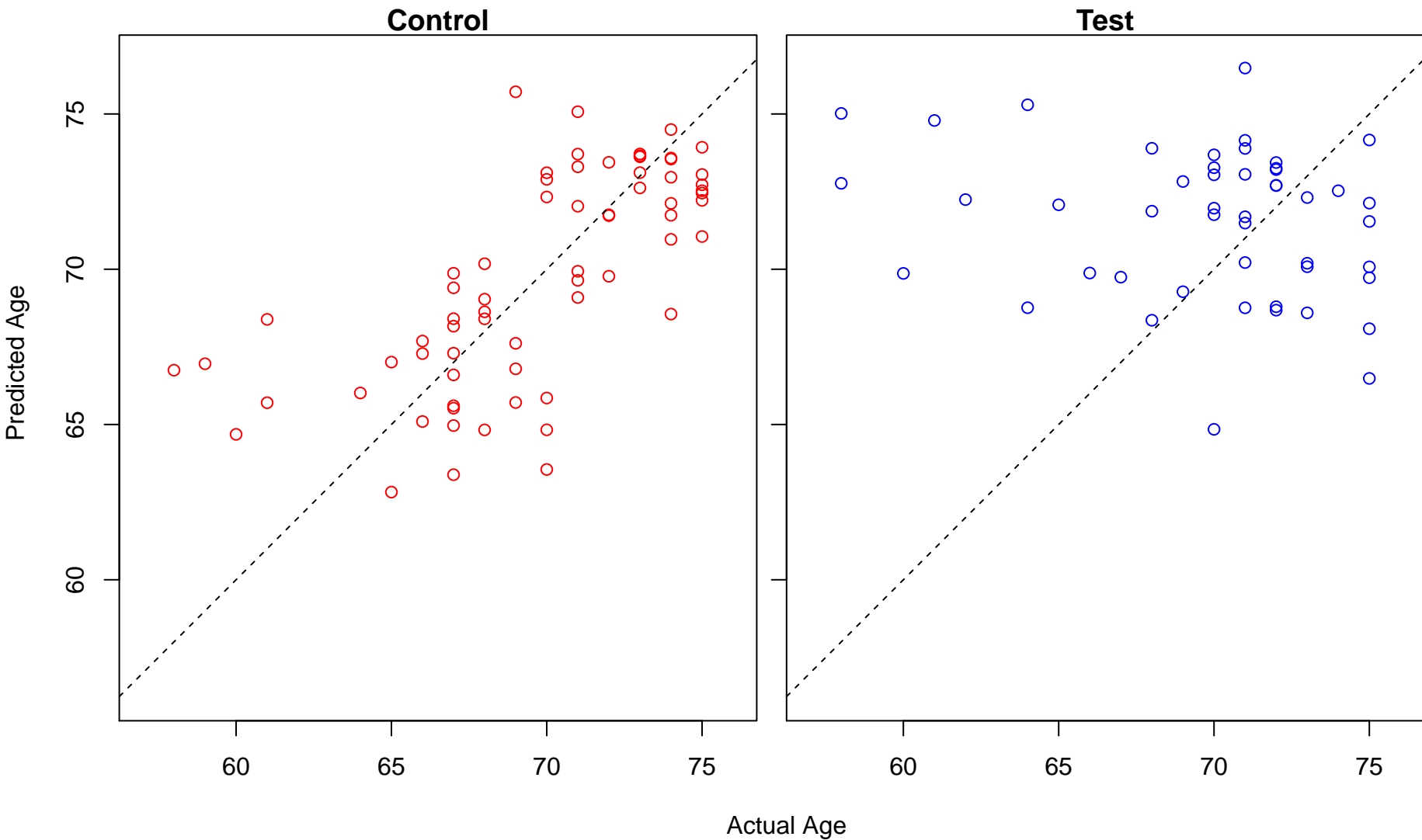


Test

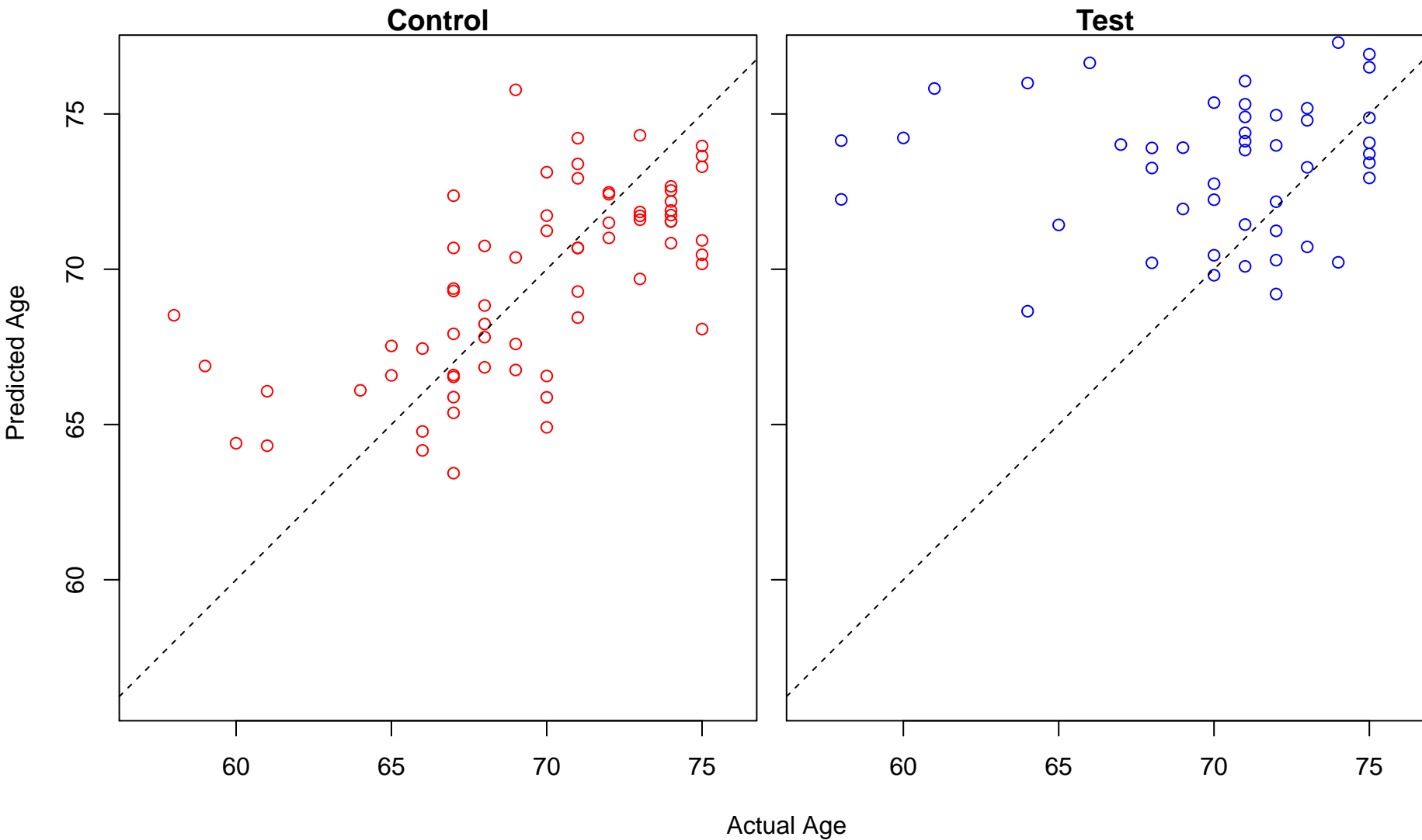


Actual Age

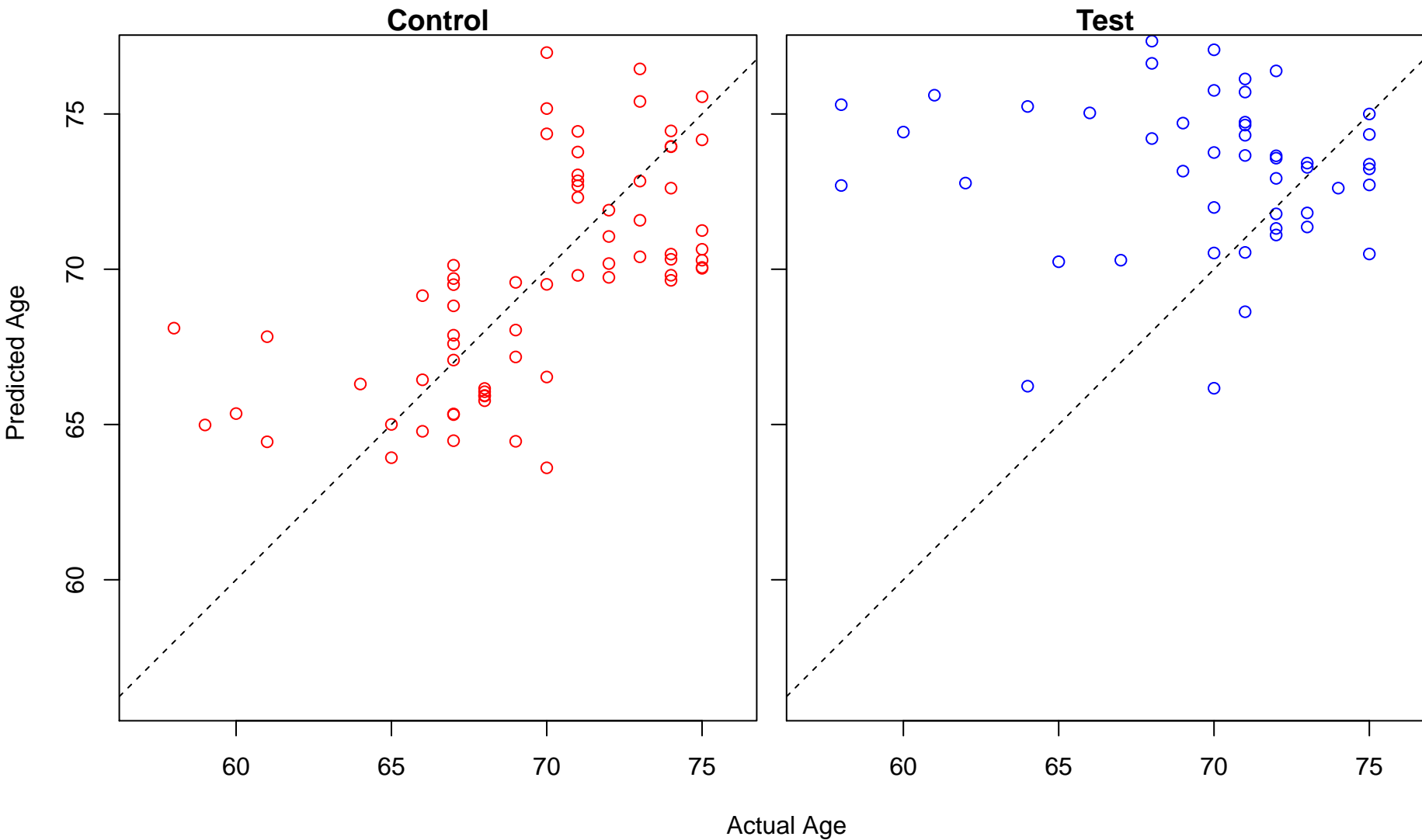
response to lipopolysaccharide (Score: 1.605303)



centriole assembly (Score: 1.604981)

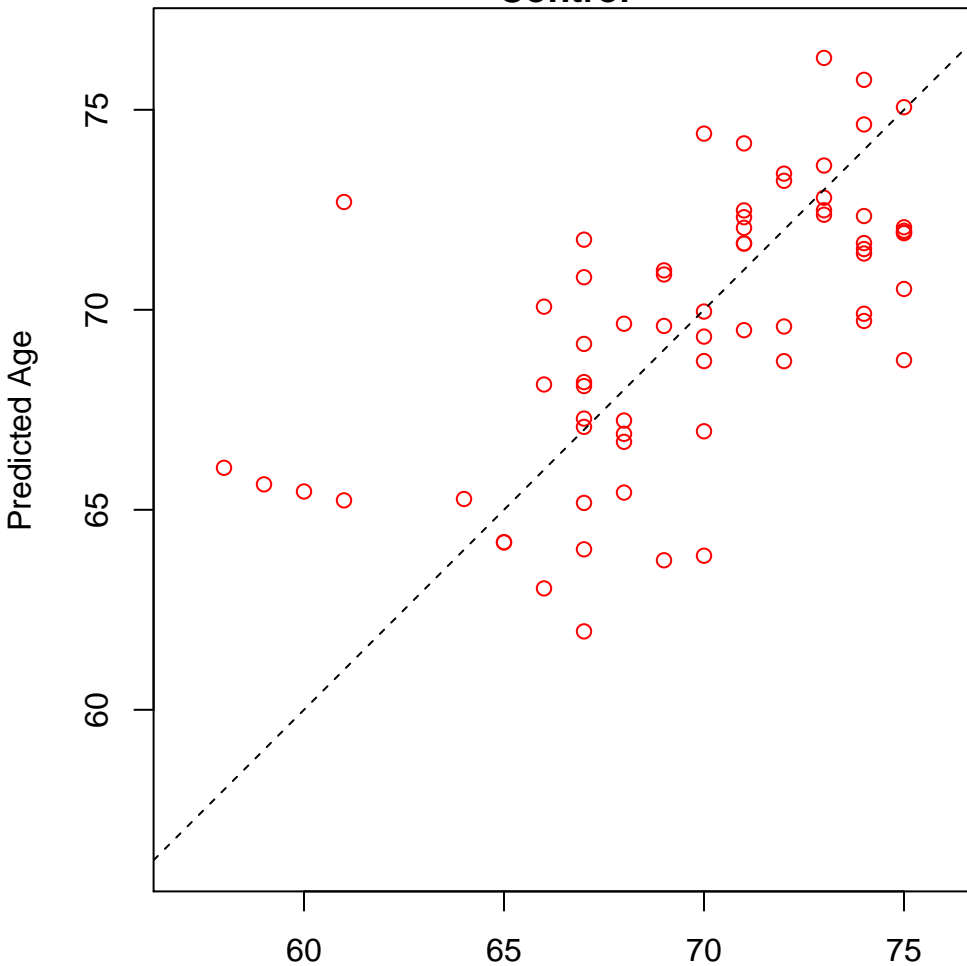


epithelial cell differentiation (Score: 1.604719)

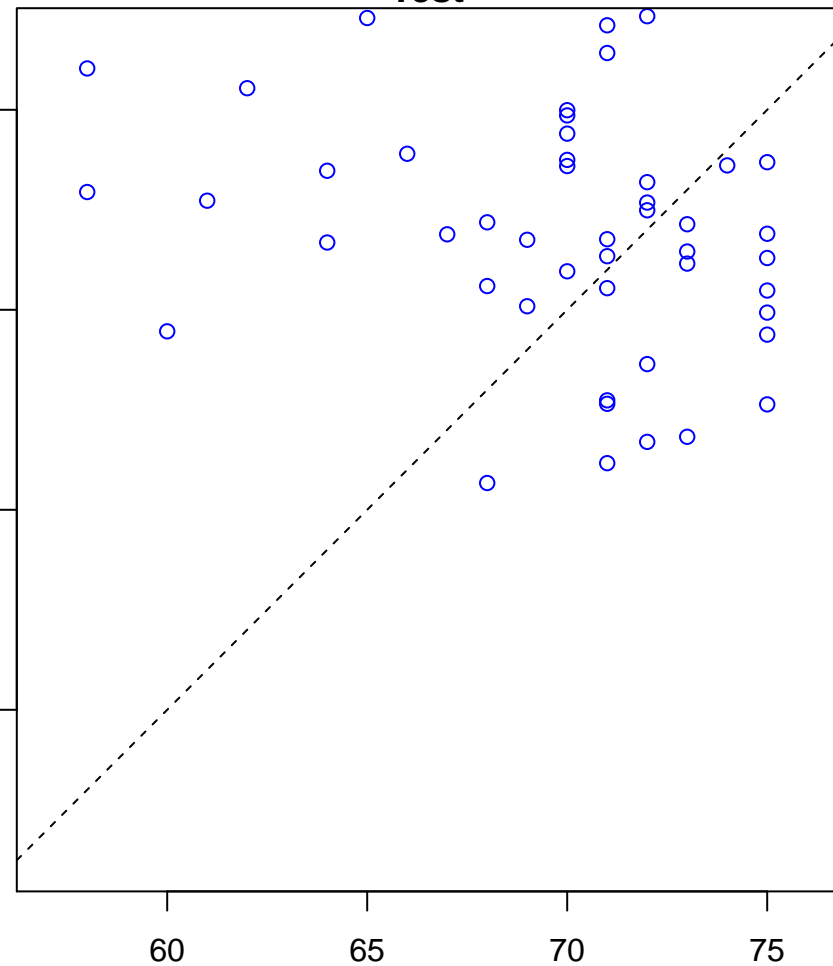


regulation of double-strand break repair (Score: 1.604470)

Control

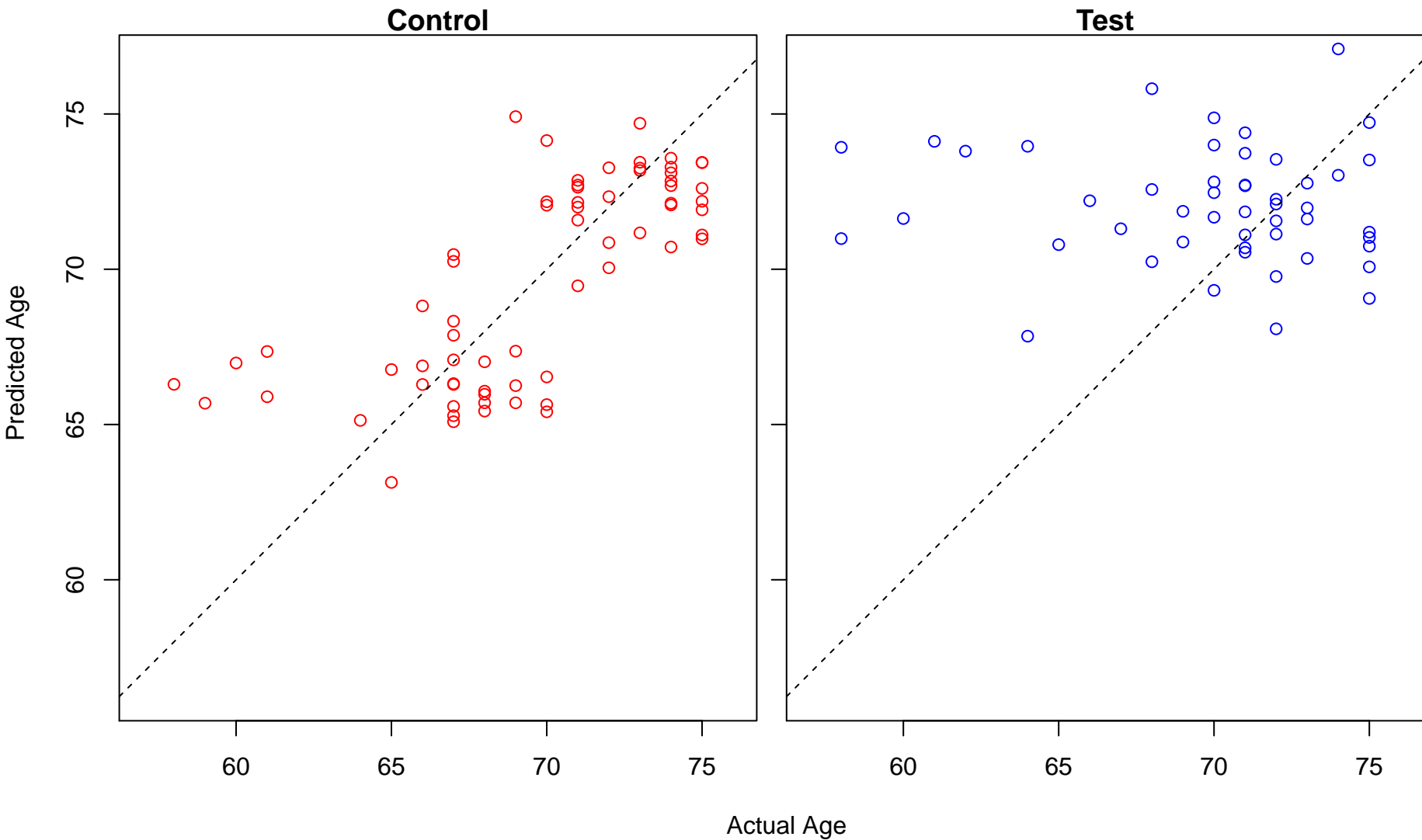


Test

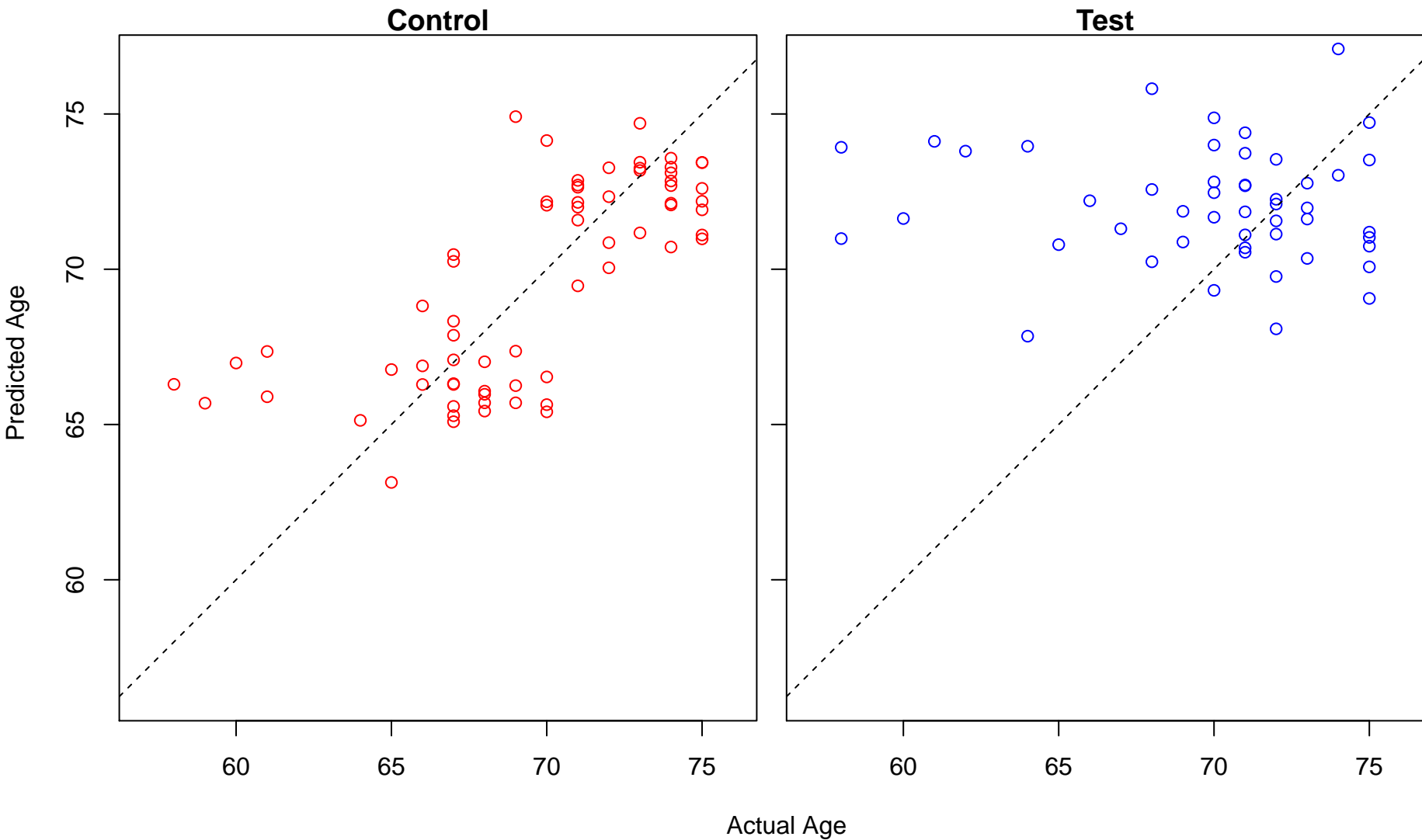


Actual Age

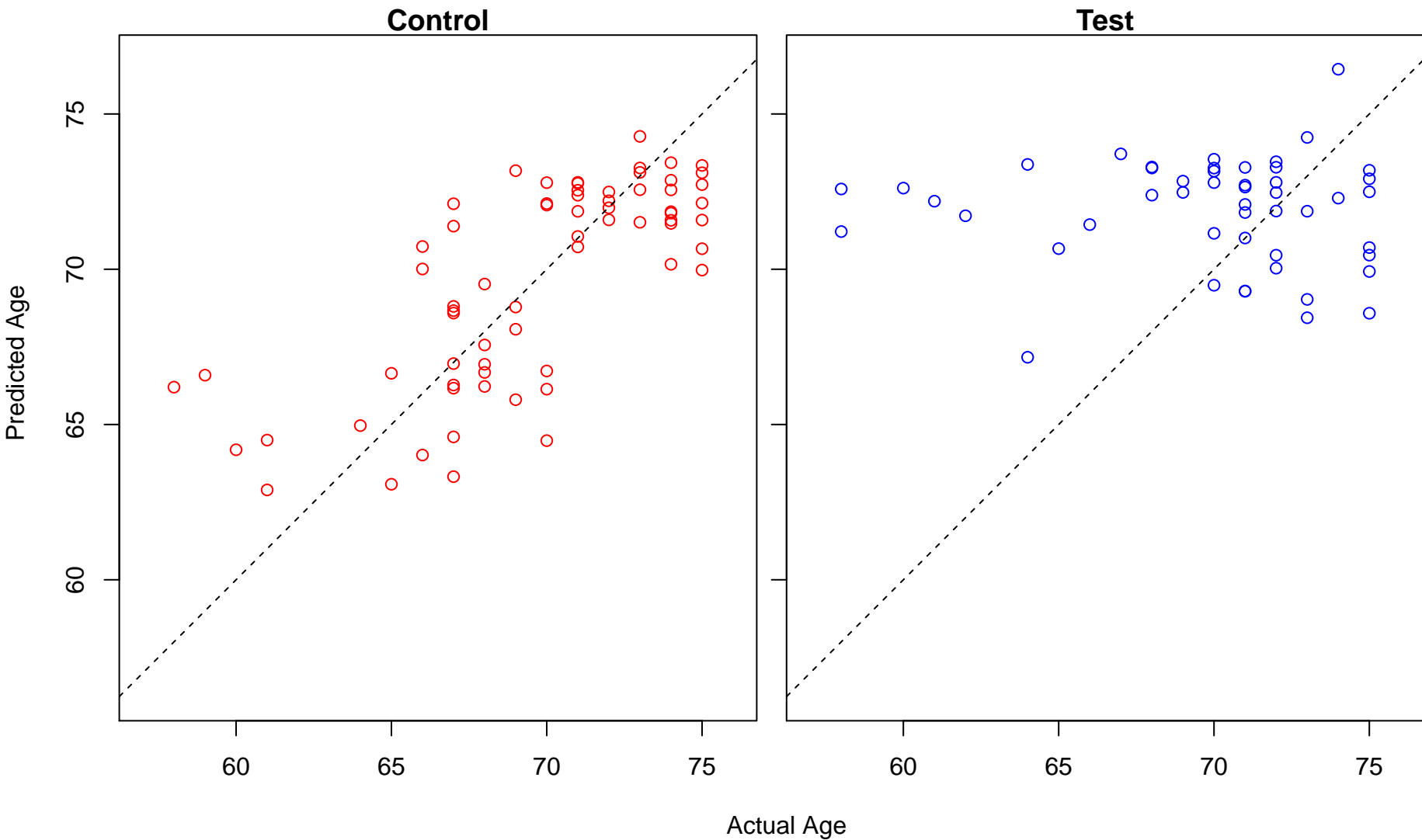
negative regulation of ligase activity (Score: 1.604301)



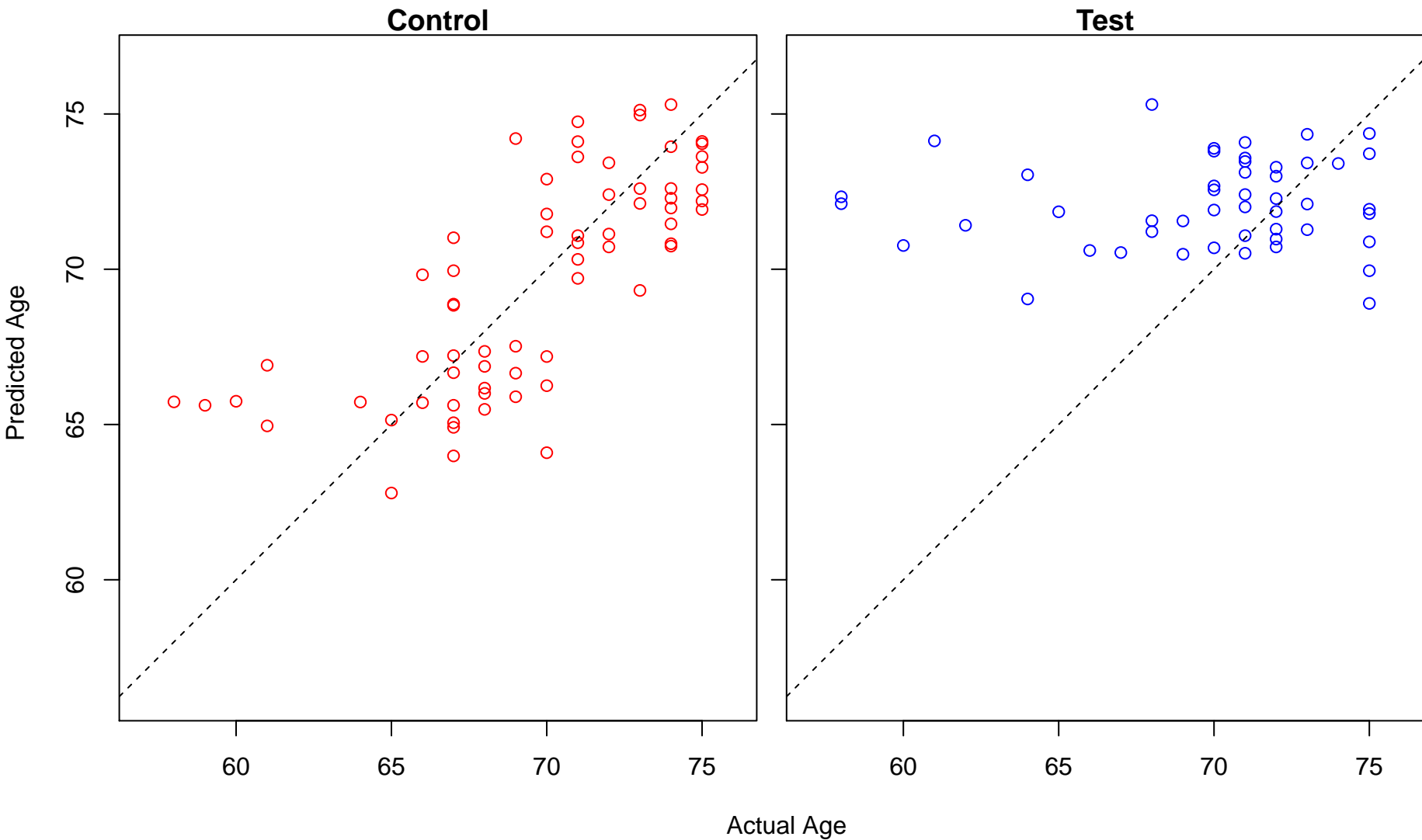
negative regulation of ubiquitin–protein transferase activity (Score: 1.604301)



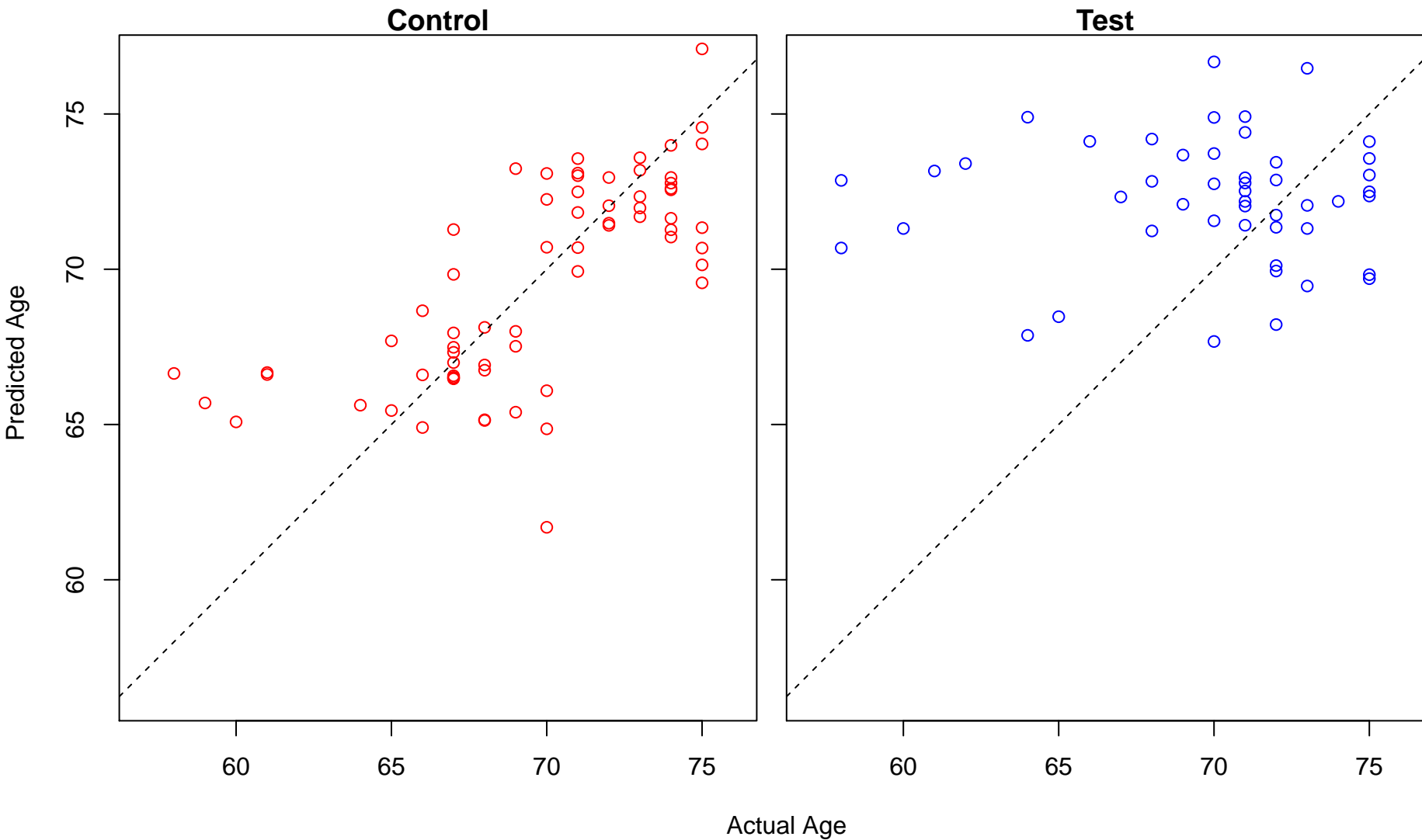
regulation of mitotic spindle organization (Score: 1.604293)



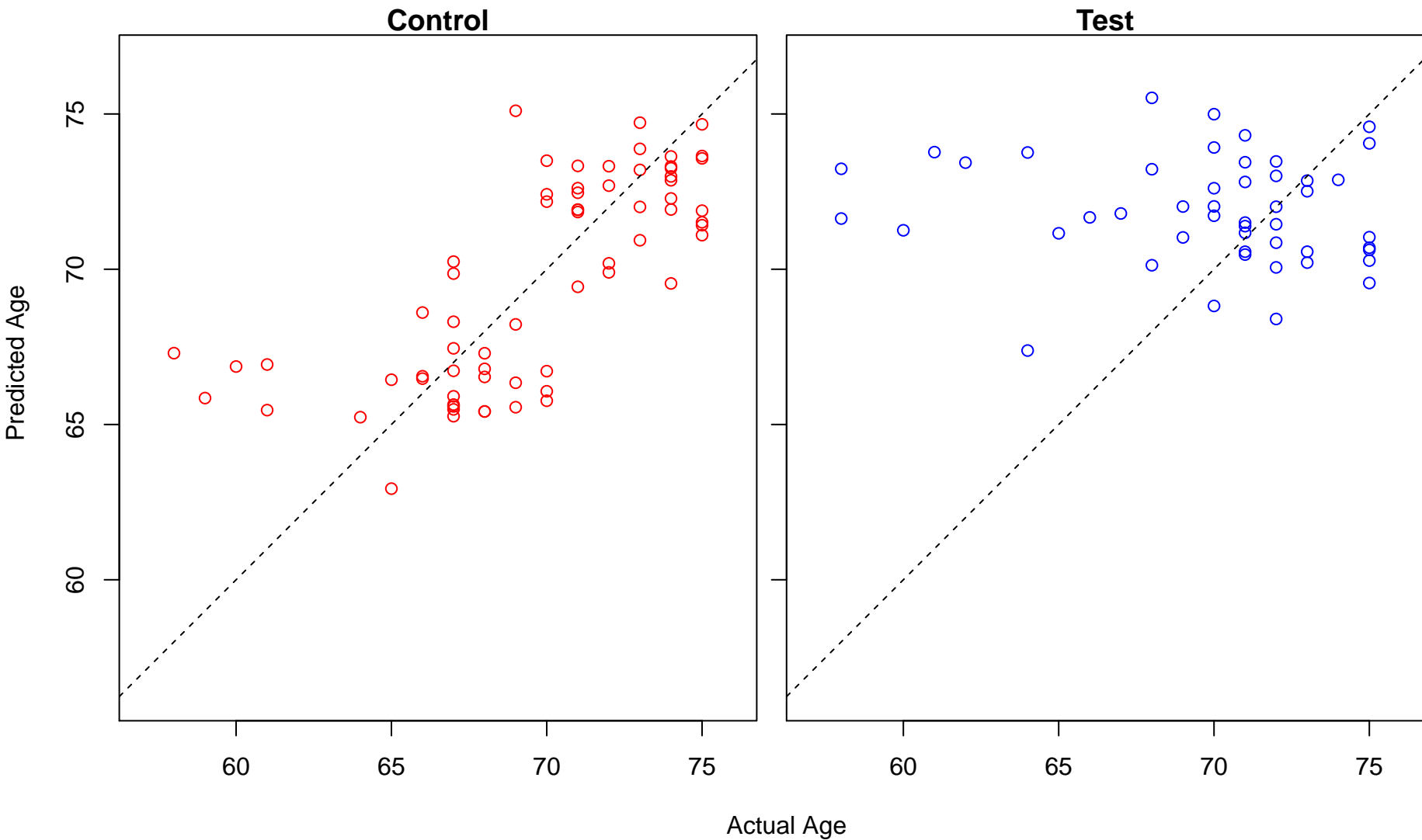
protein polyubiquitination (Score: 1.604274)



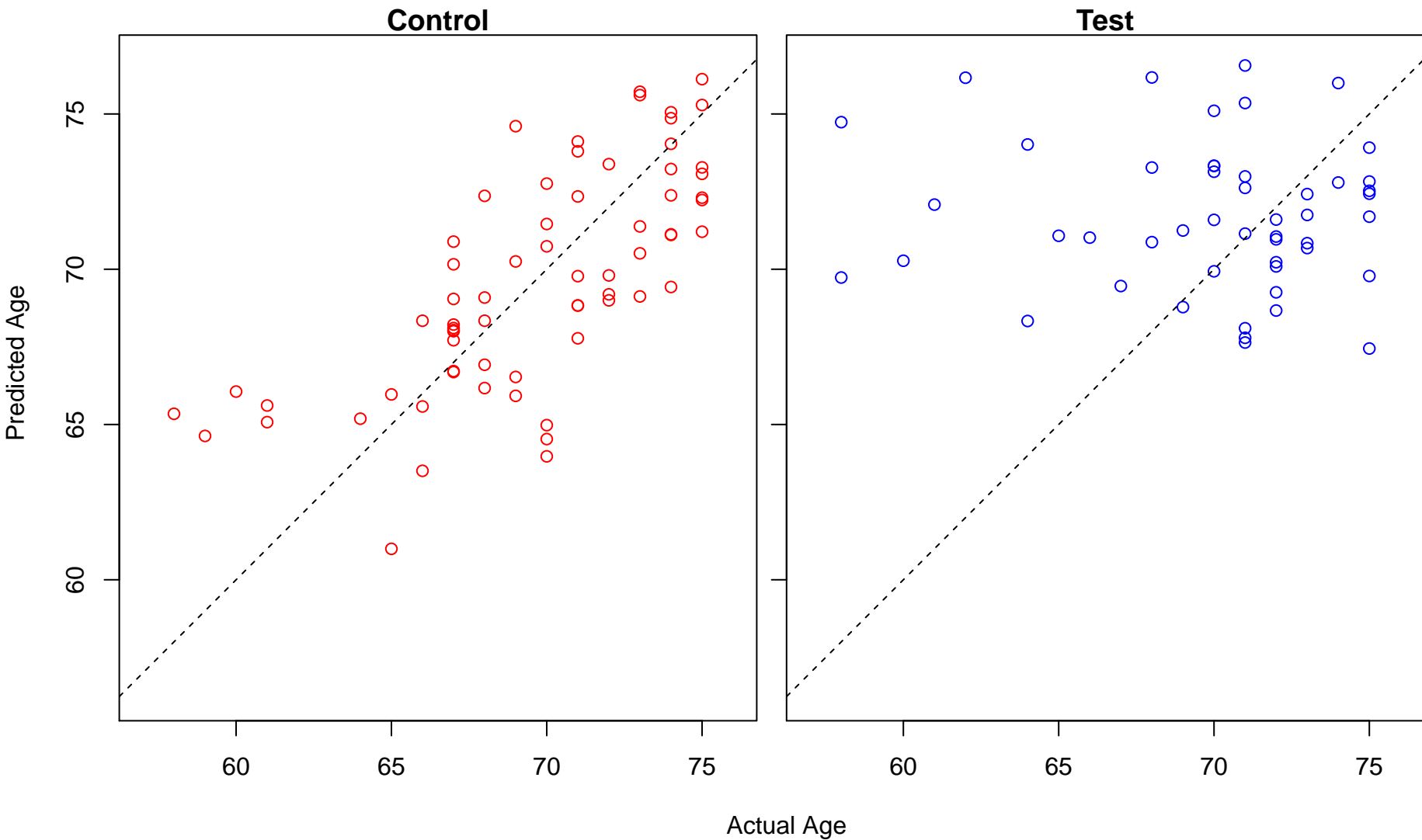
positive regulation of DNA binding (Score: 1.604043)



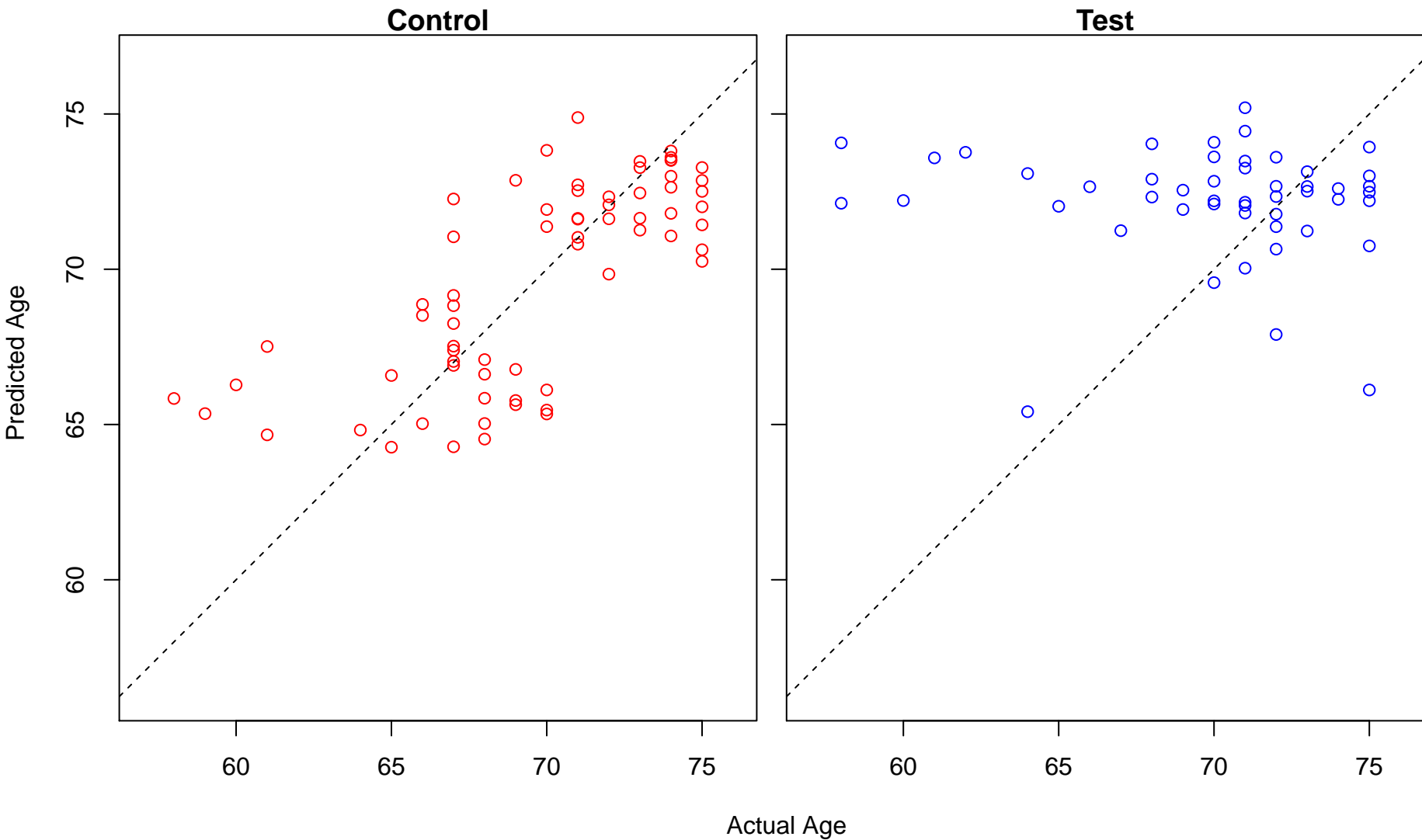
stimulatory C-type lectin receptor signaling pathway (Score: 1.603580)



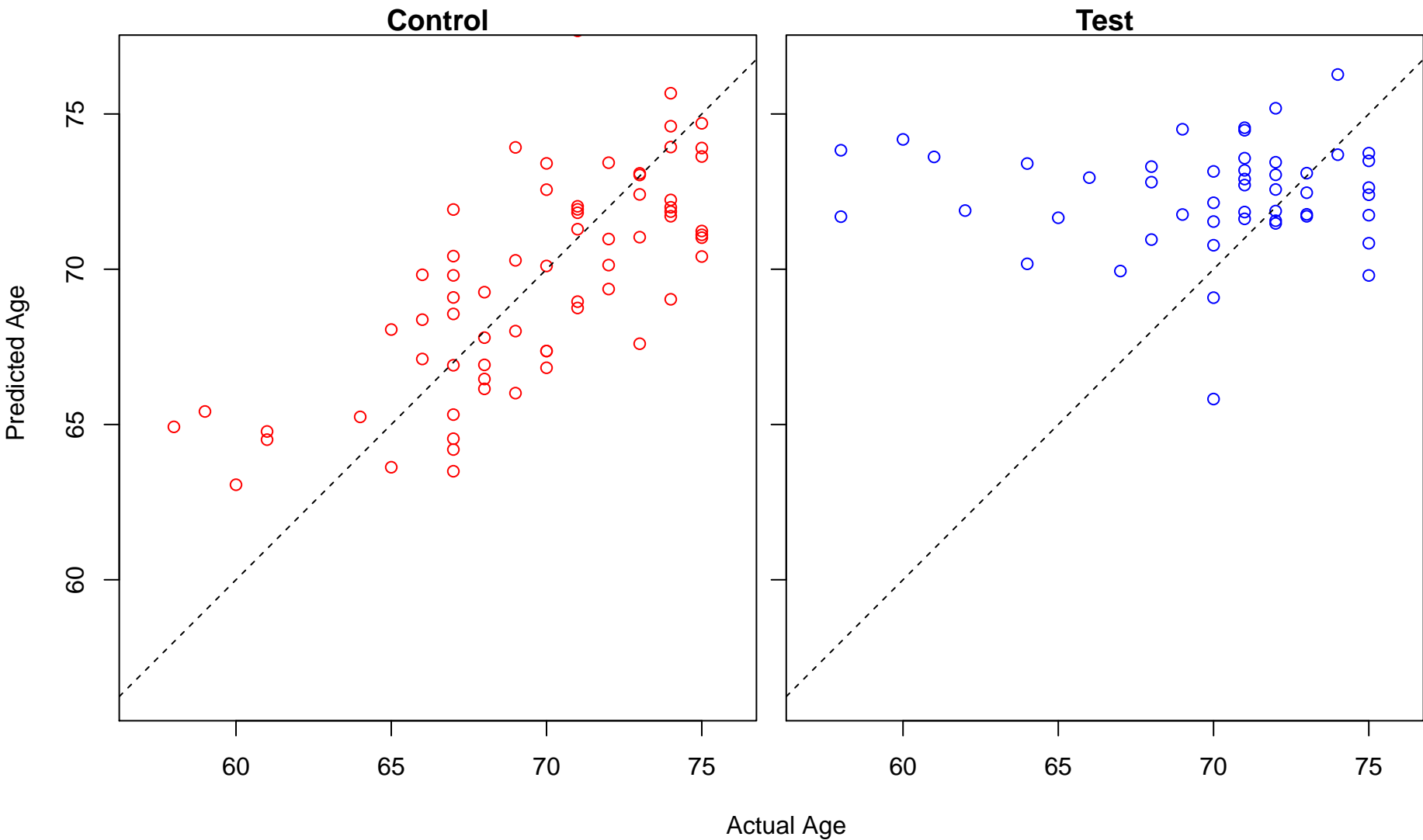
negative regulation of neuron apoptotic process (Score: 1.603207)



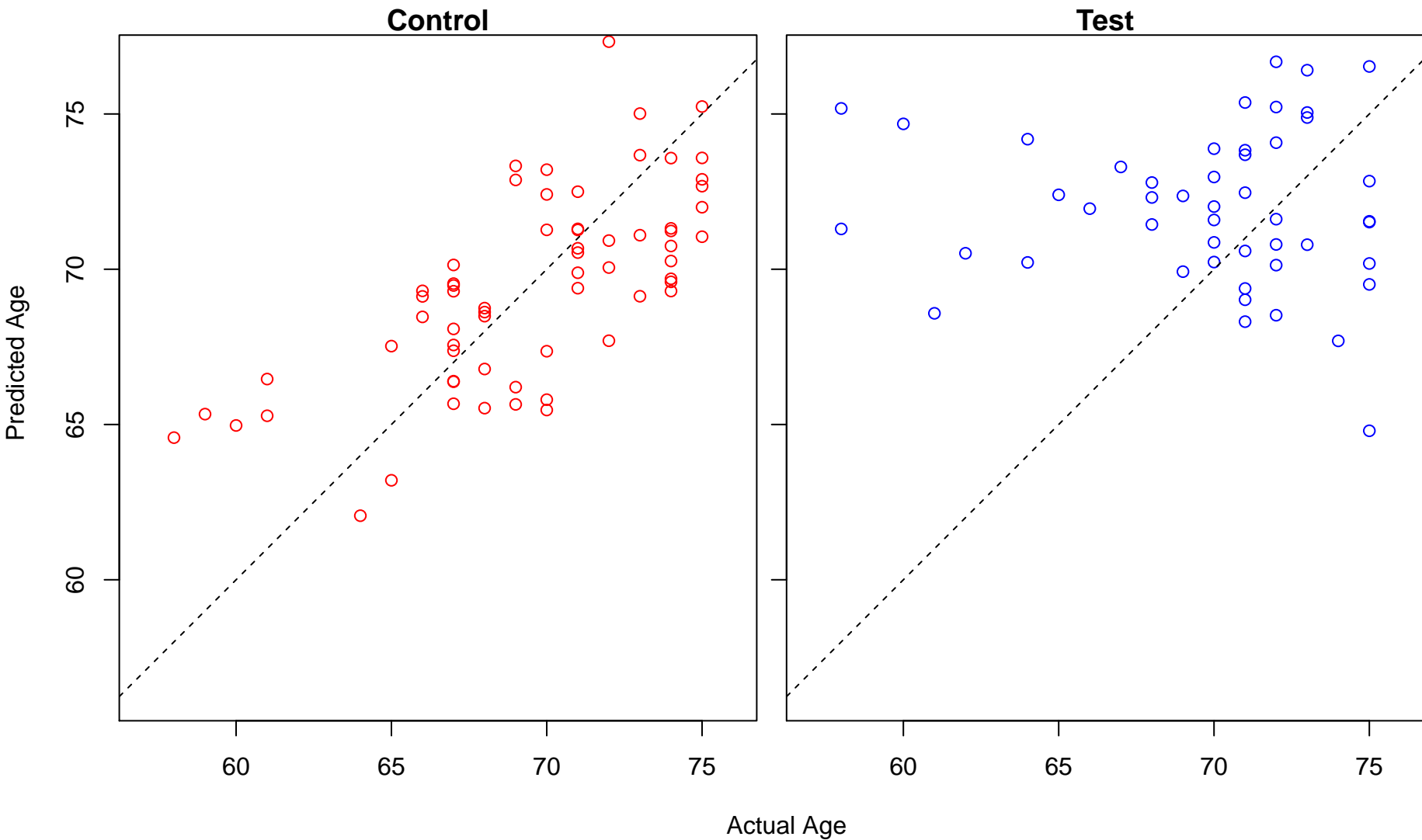
positive regulation of fibroblast proliferation (Score: 1.602946)



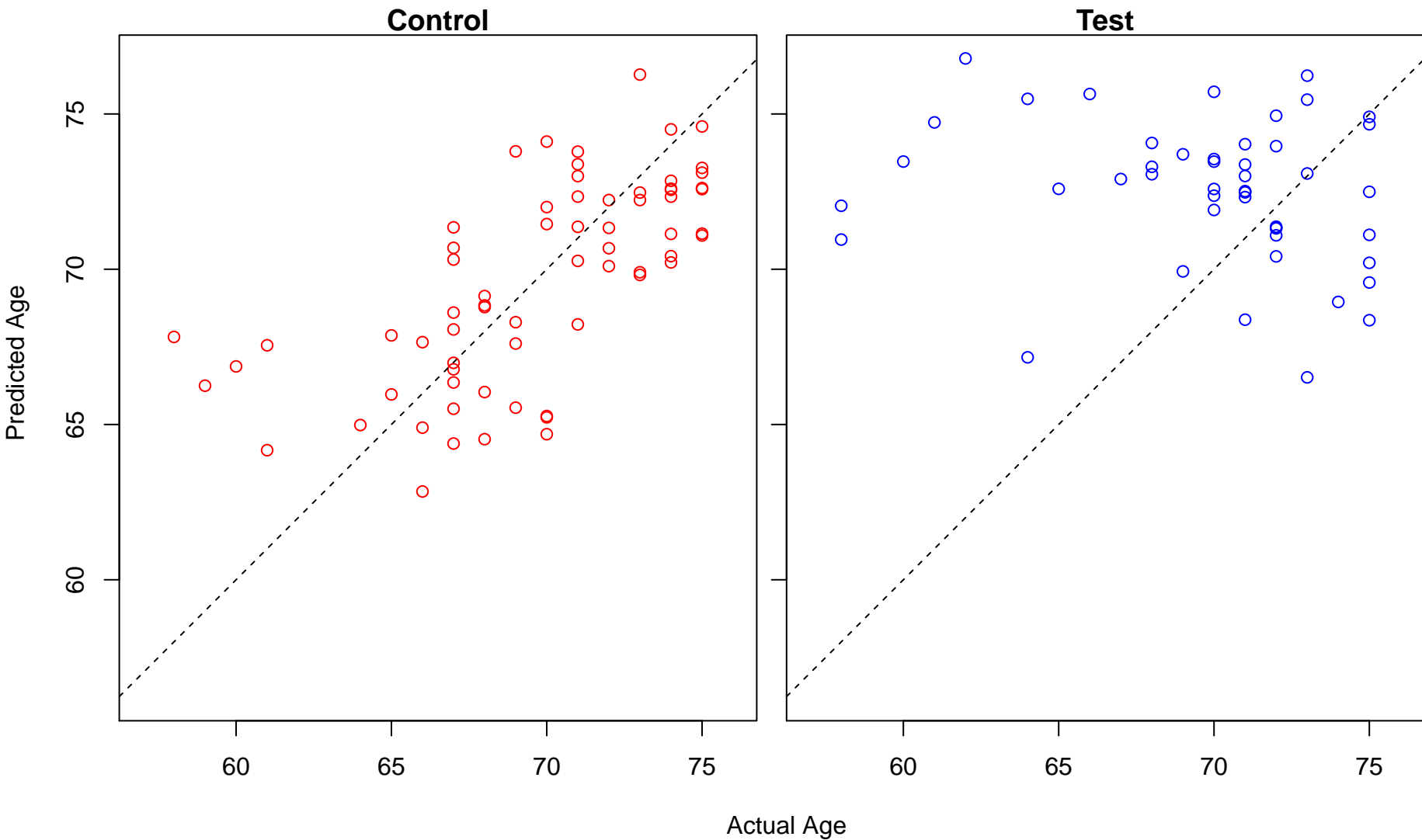
Regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (S



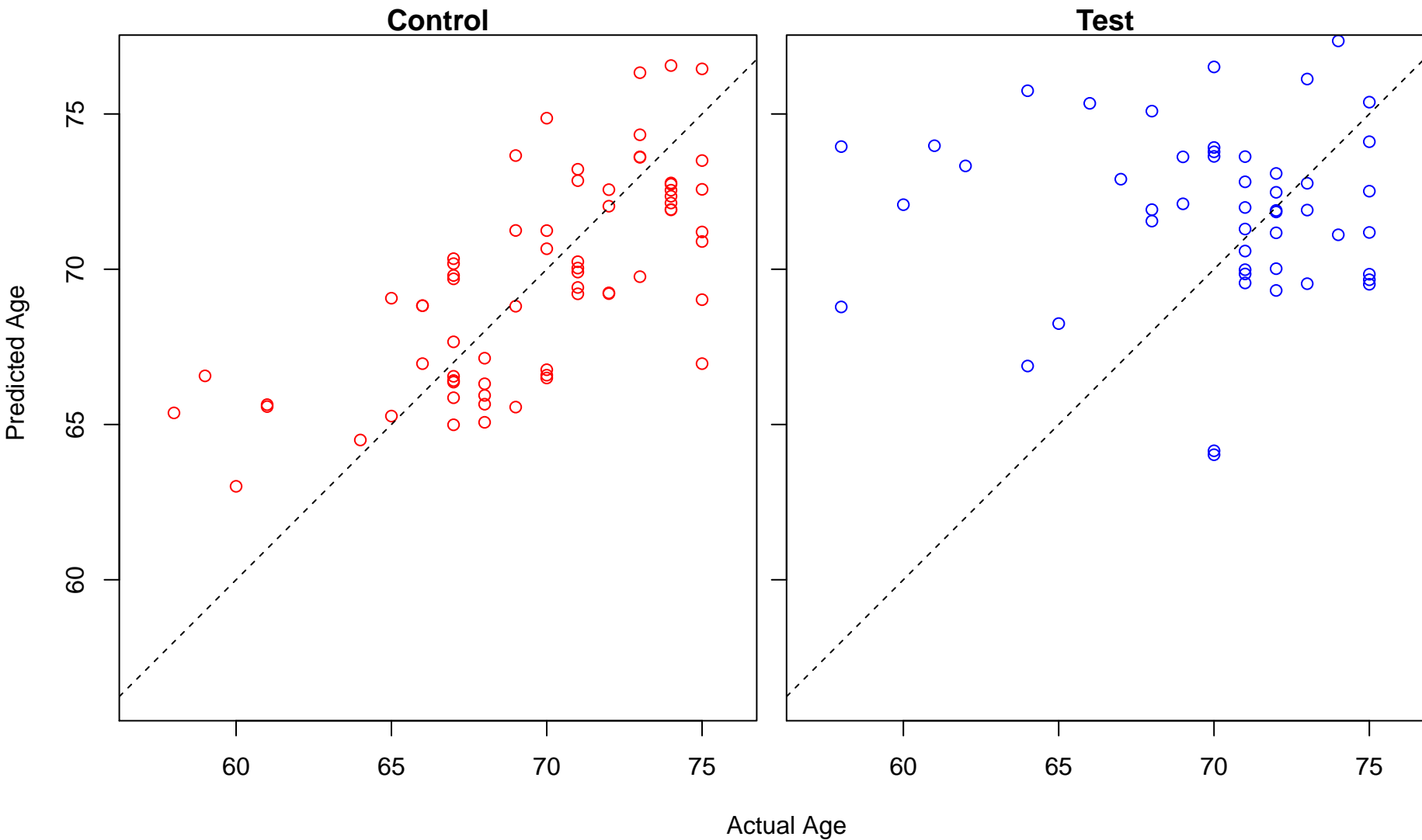
regulation of defense response to virus by virus (Score: 1.602612)



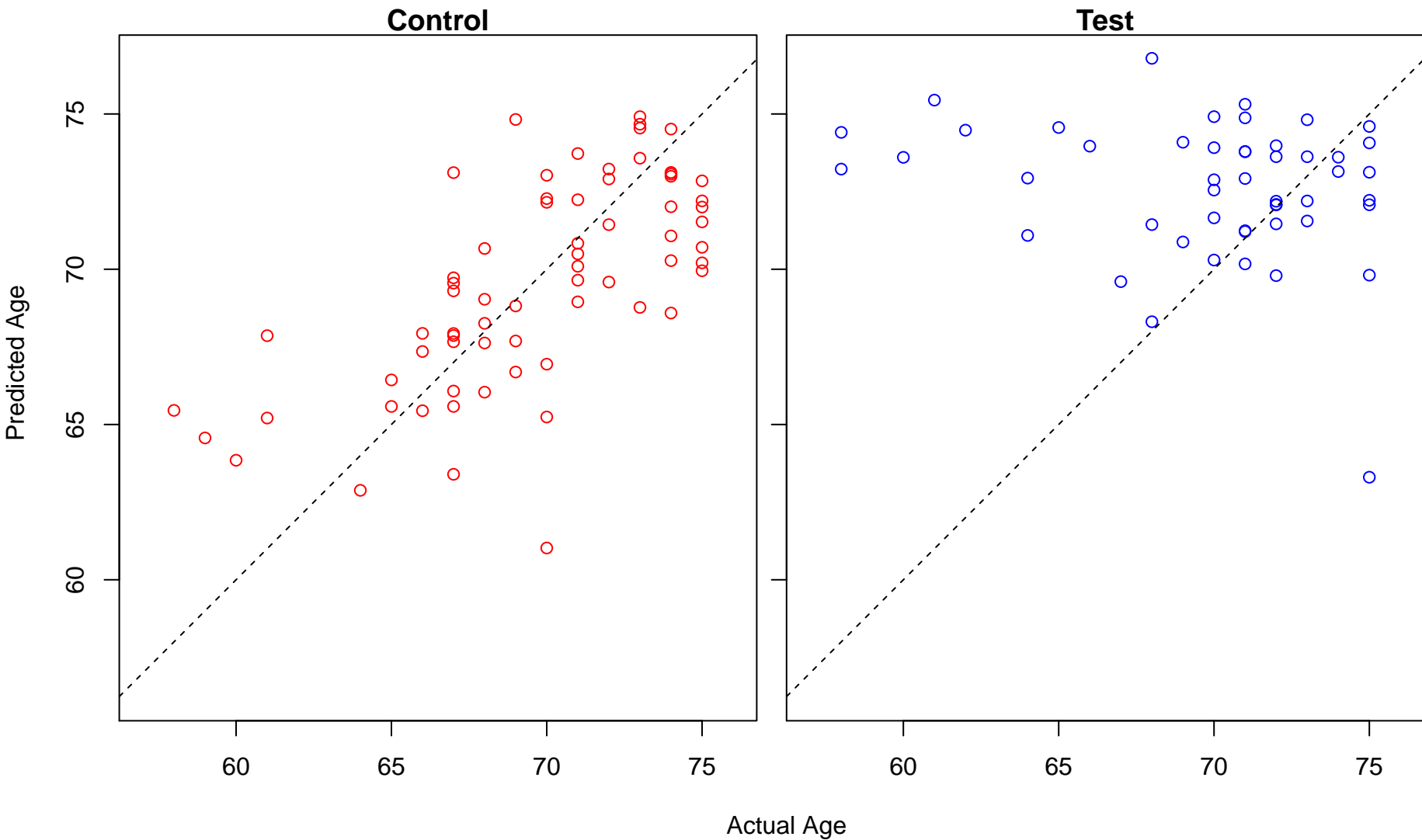
Negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 0.99)



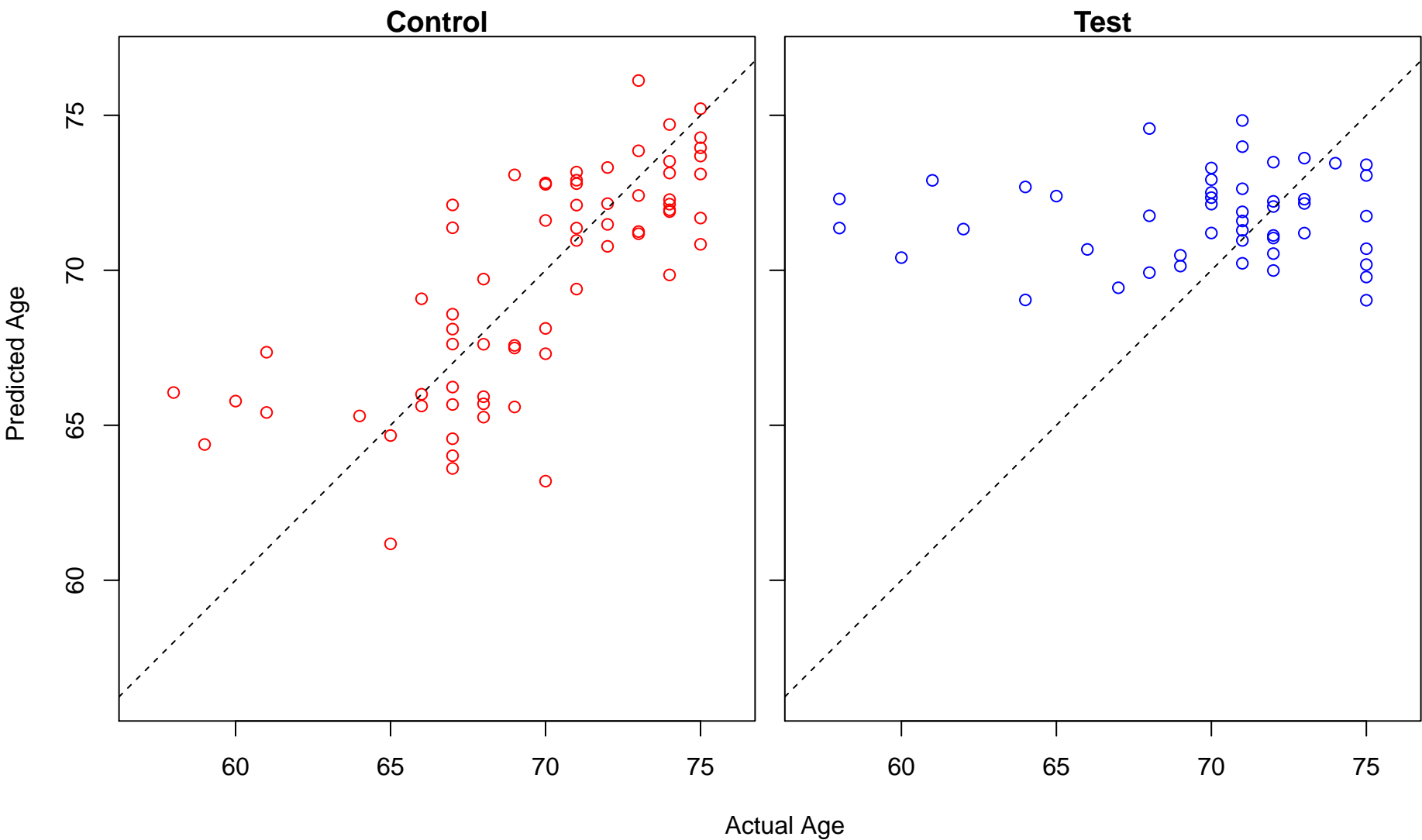
regulation of cholesterol metabolic process (Score: 1.602449)



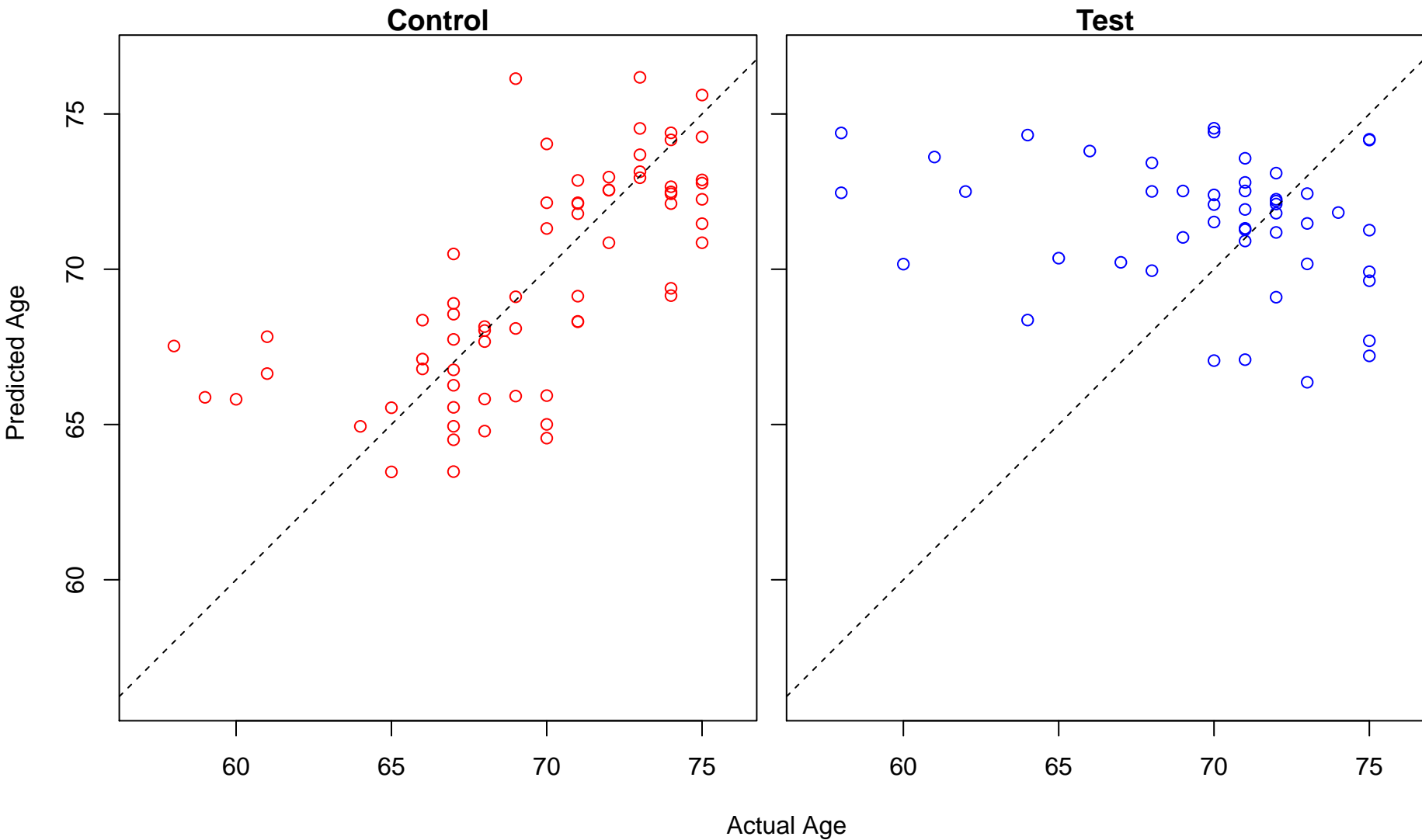
negative regulation of proteasomal protein catabolic process (Score: 1.602004)



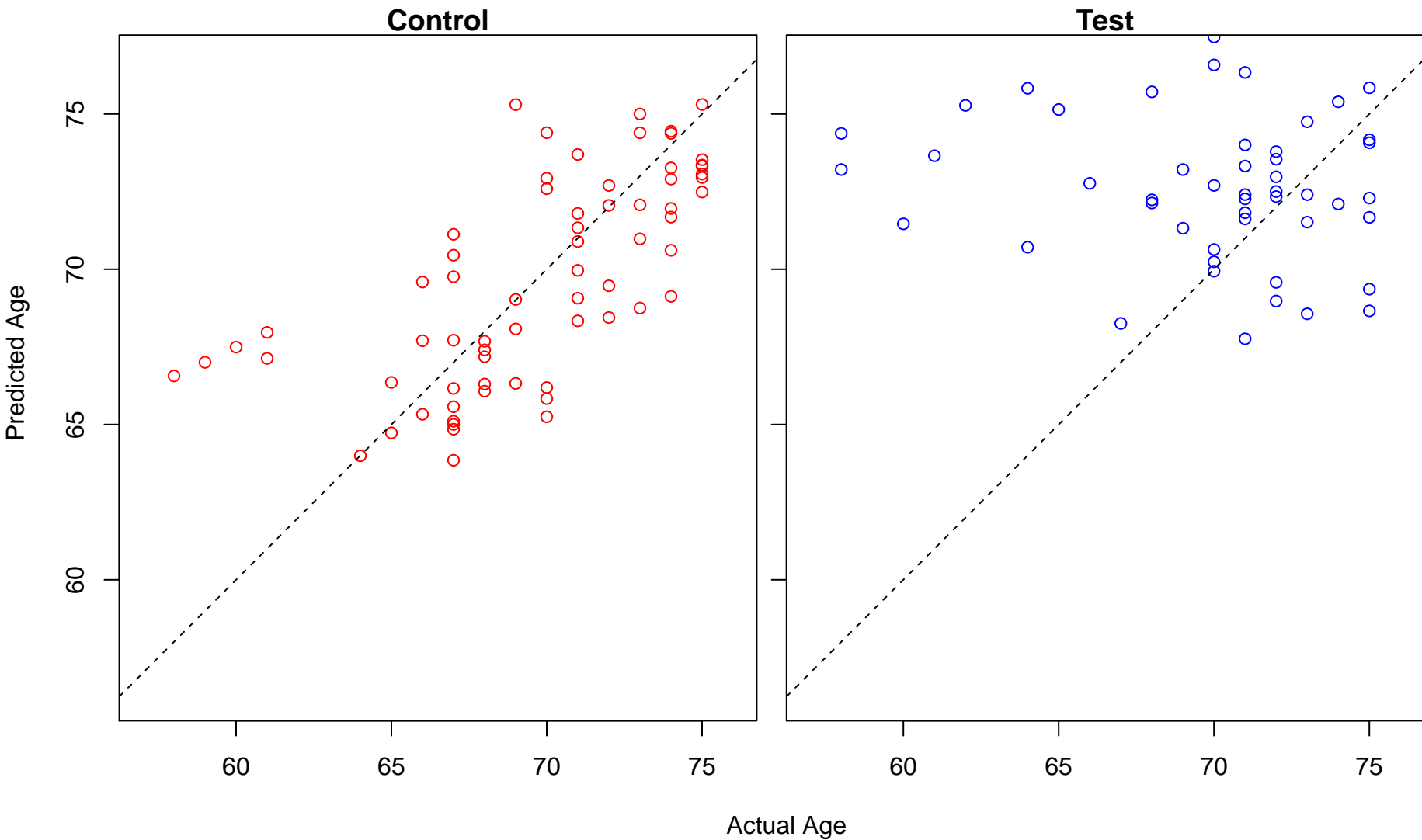
DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (Score: 1).



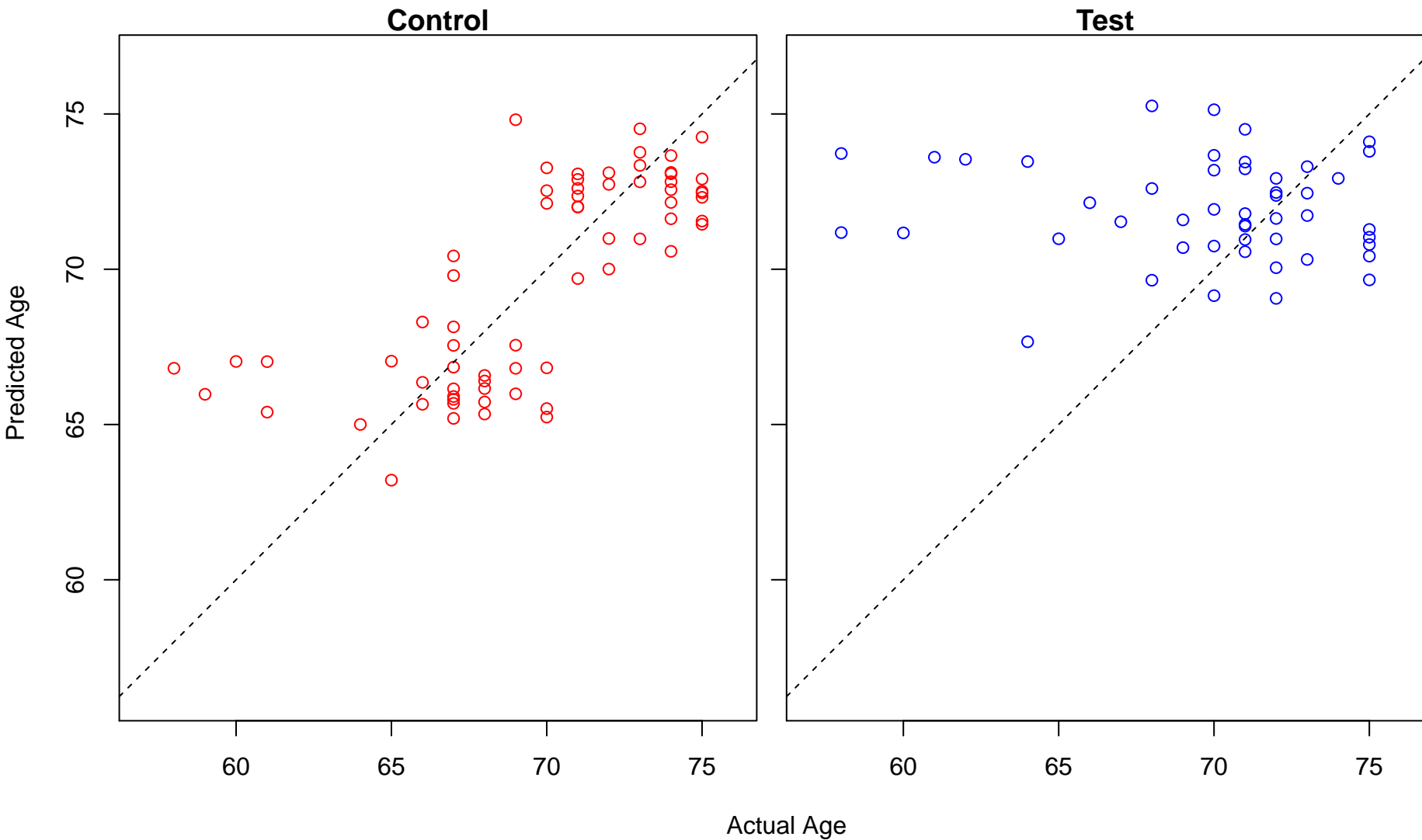
response to bacterium (Score: 1.600184)



positive regulation of stress-activated MAPK cascade (Score: 1.600004)

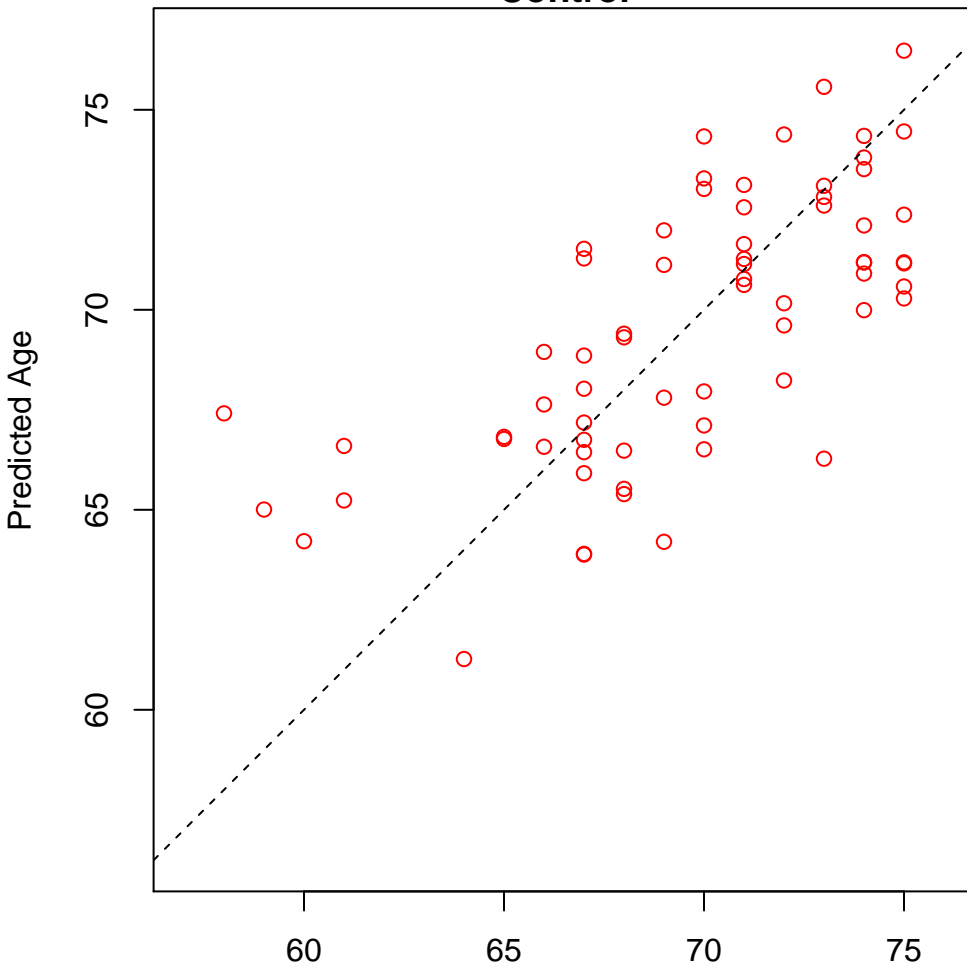


positive regulation of protein ubiquitination (Score: 1.599524)

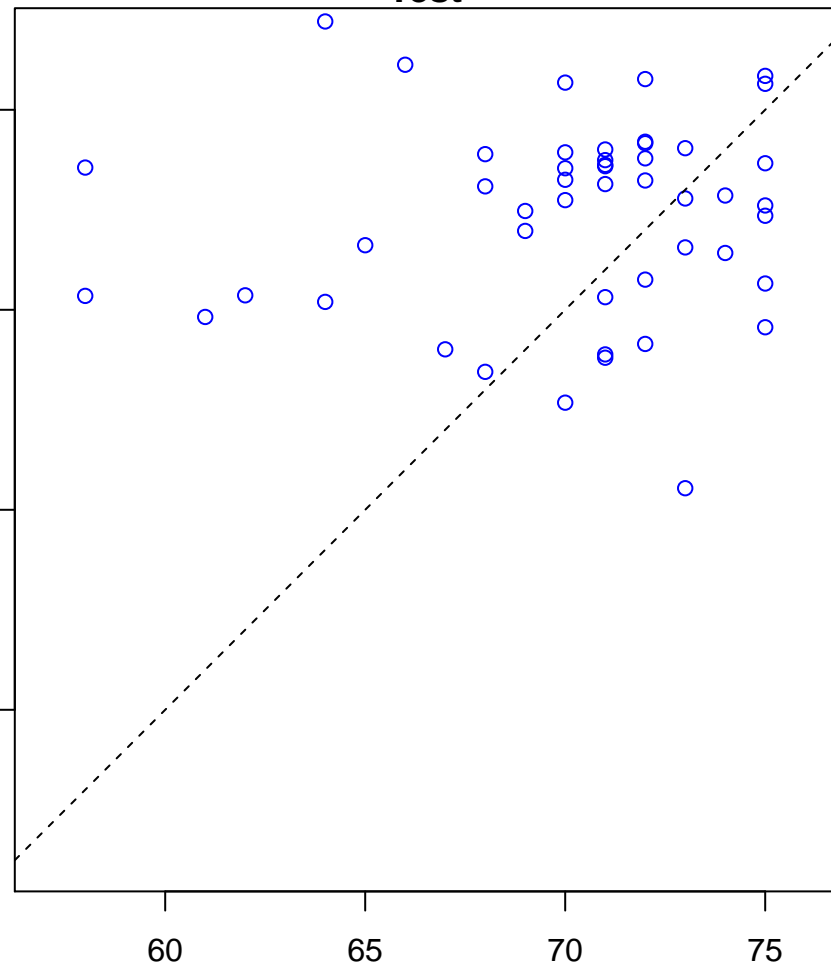


regulation of epithelial cell proliferation (Score: 1.599301)

Control

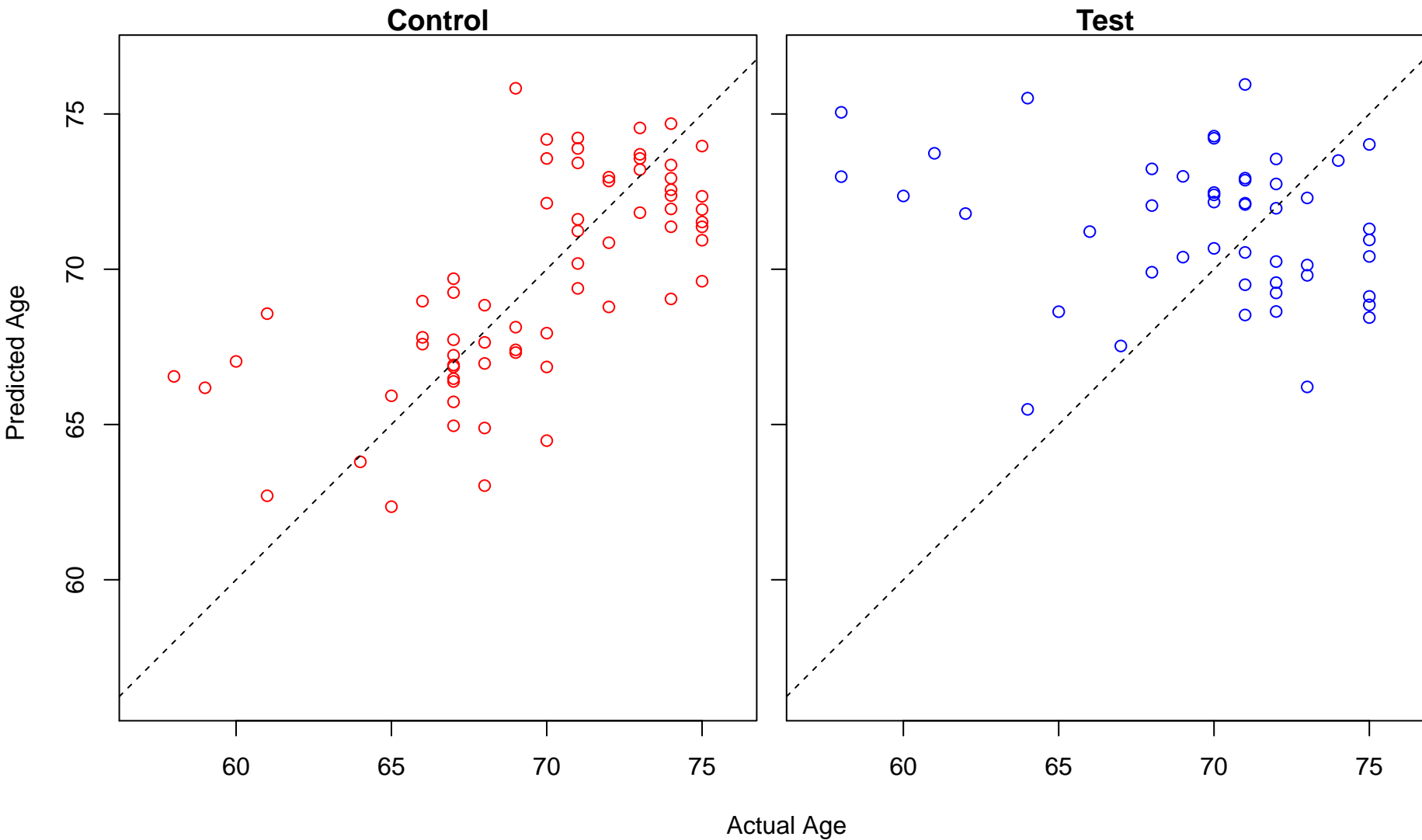


Test

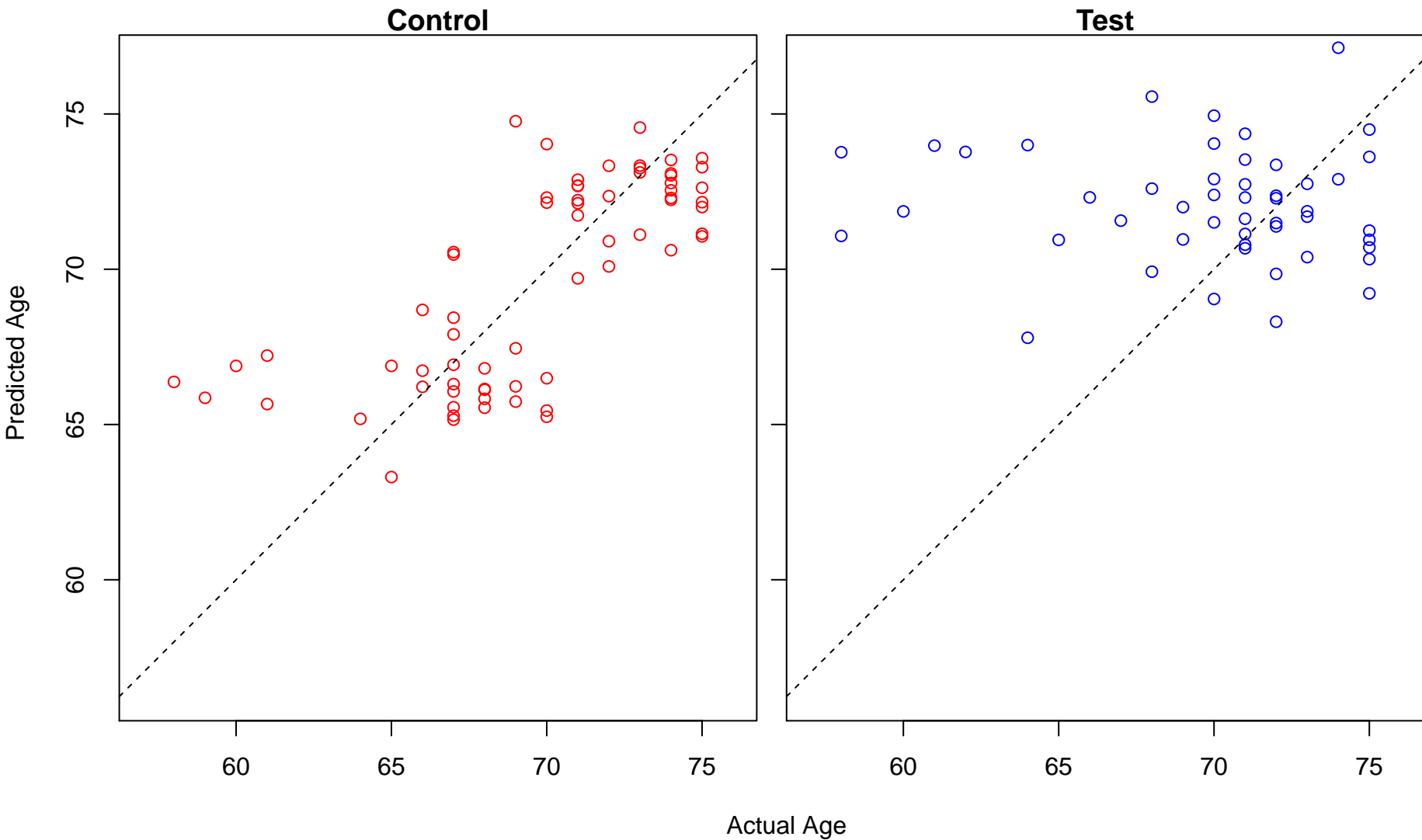


Actual Age

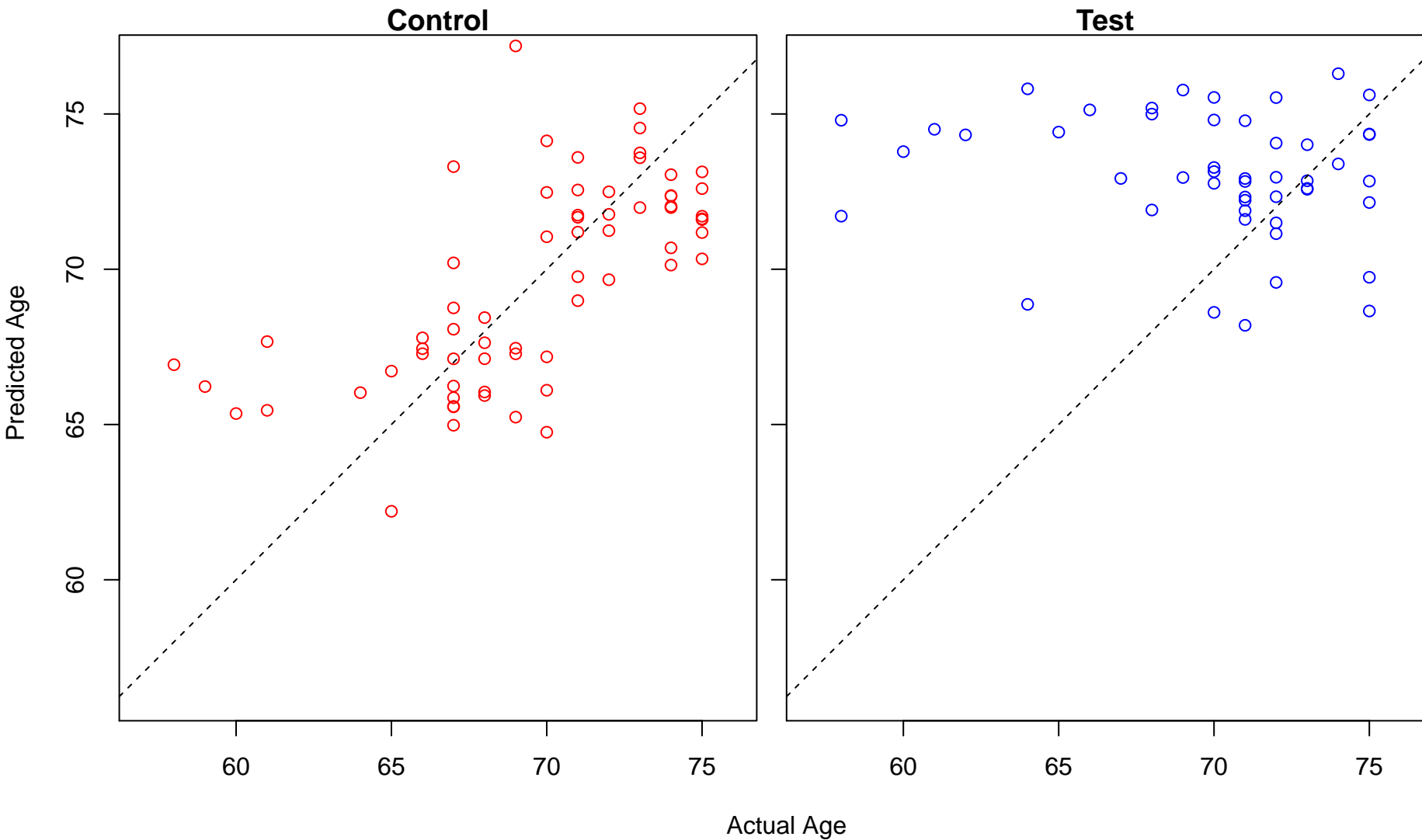
multicellular organismal reproductive process (Score: 1.598873)



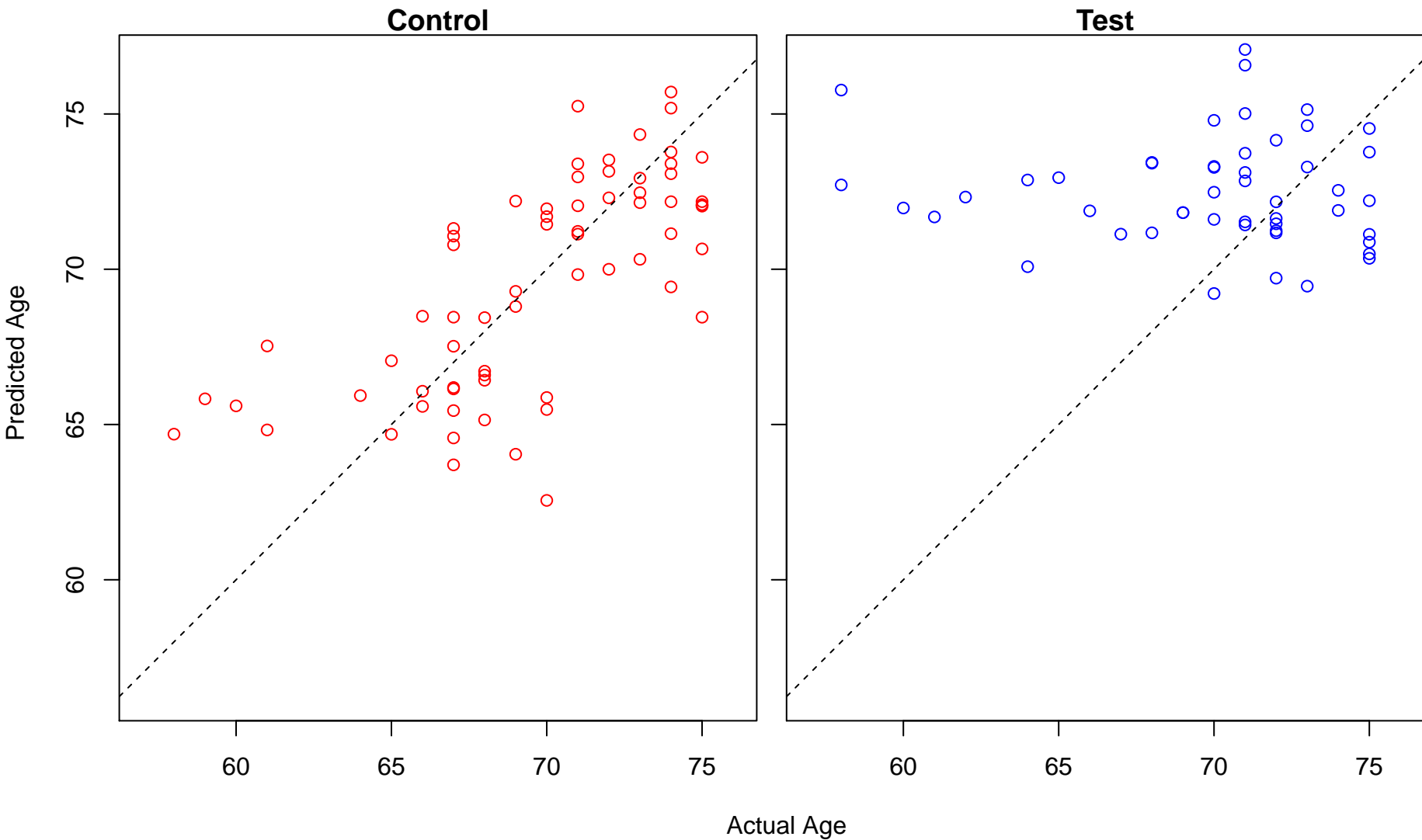
regulation of ubiquitin–protein transferase activity (Score: 1.598801)



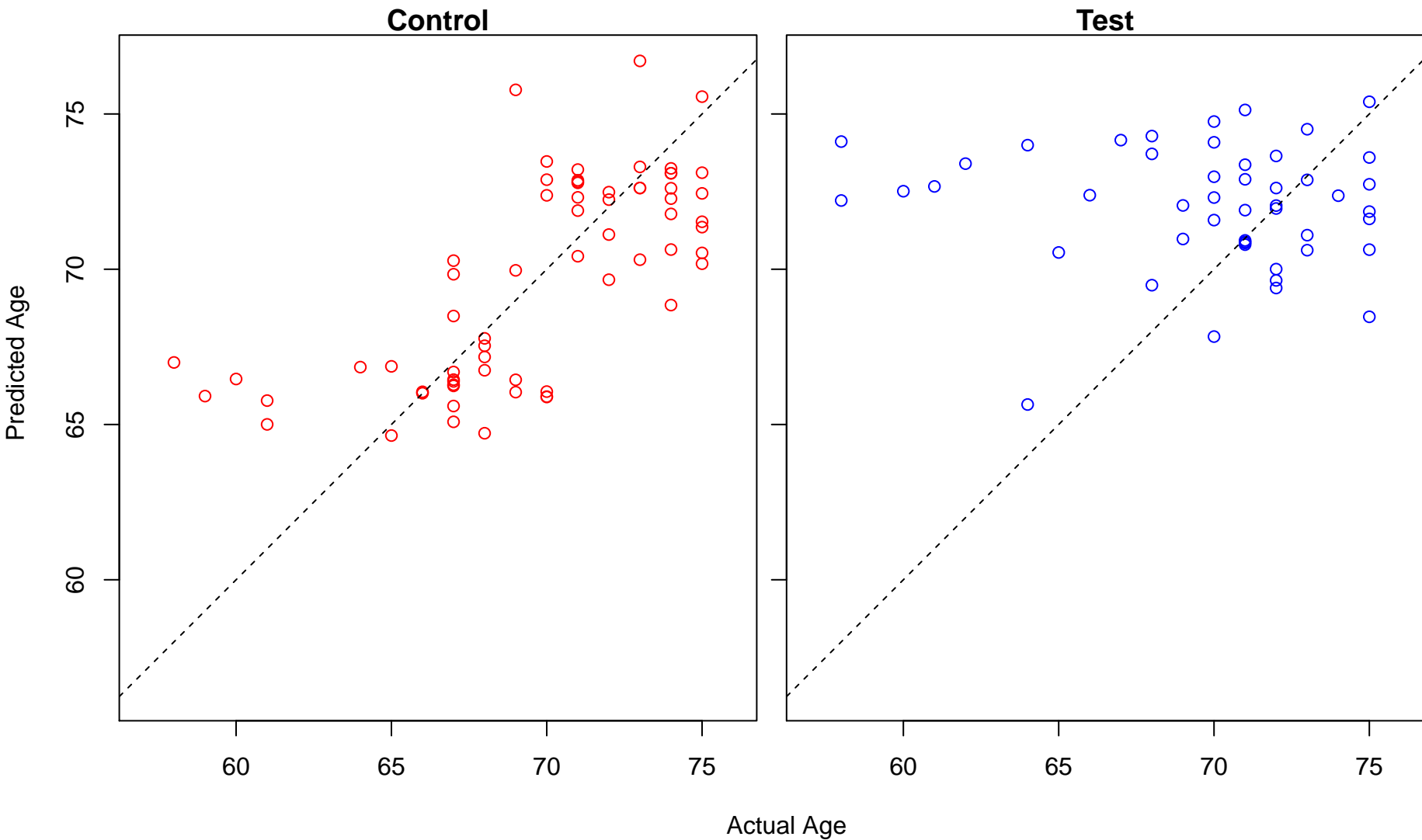
telomere maintenance (Score: 1.598473)



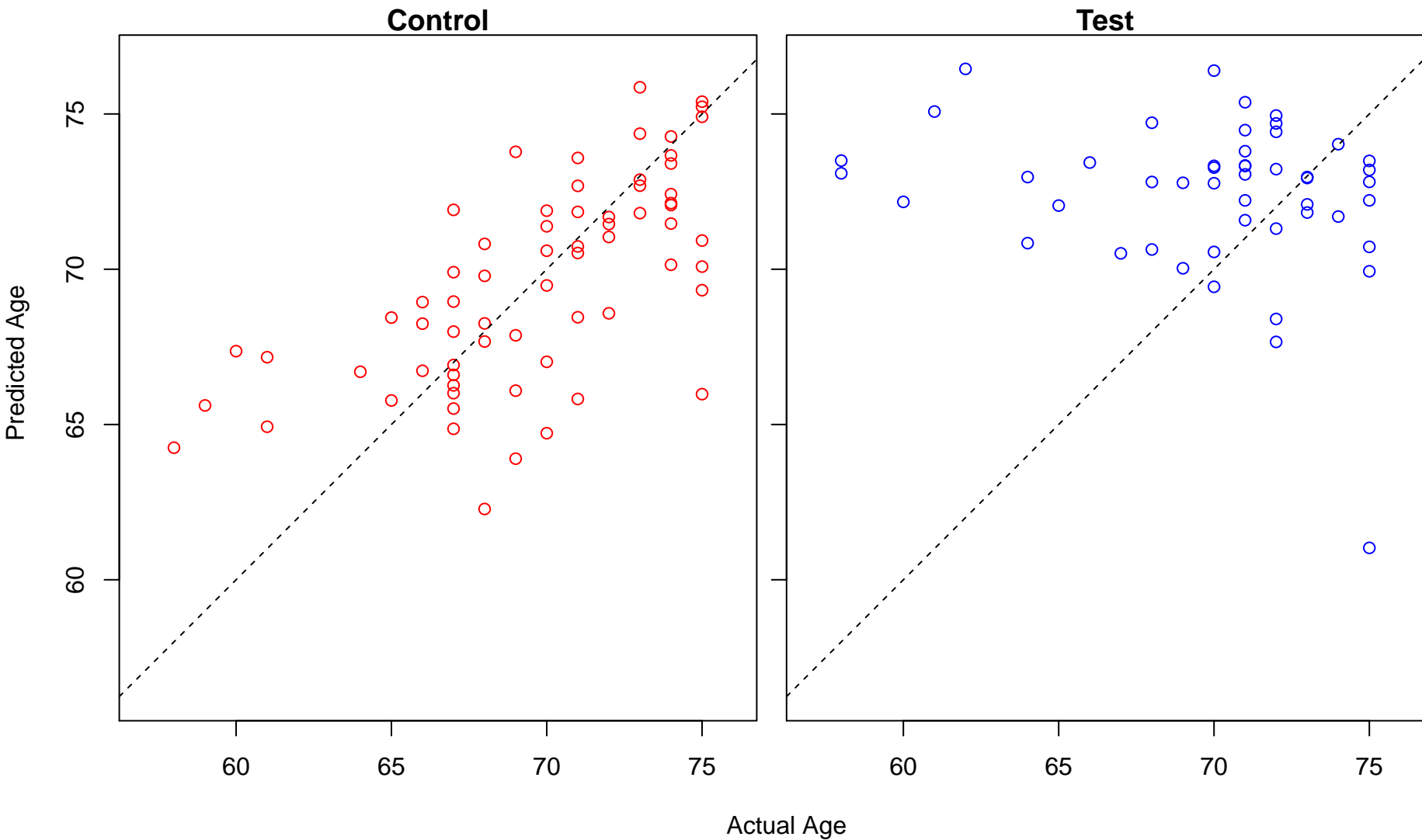
termination of RNA polymerase II transcription (Score: 1.598301)



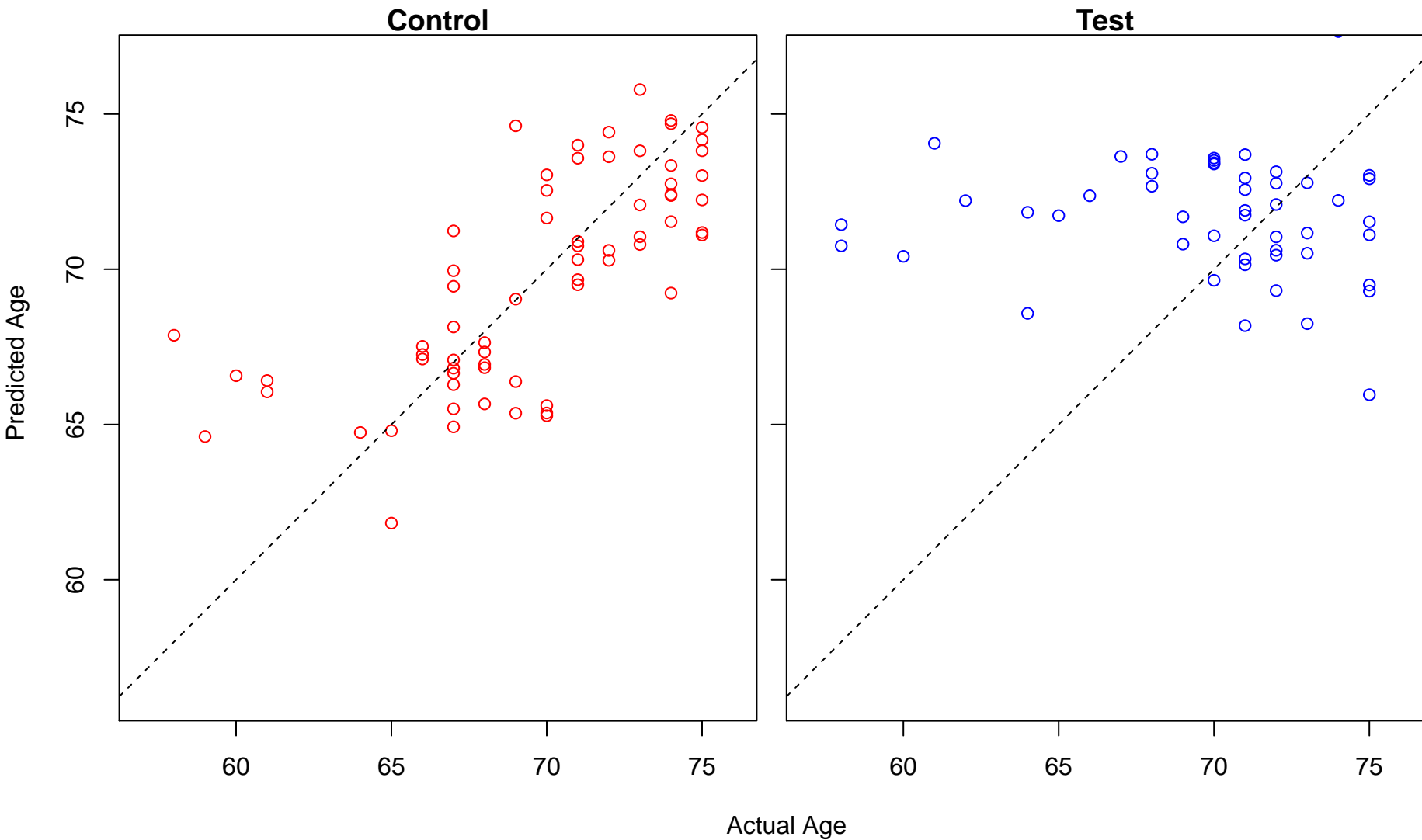
phagocytosis (Score: 1.598222)



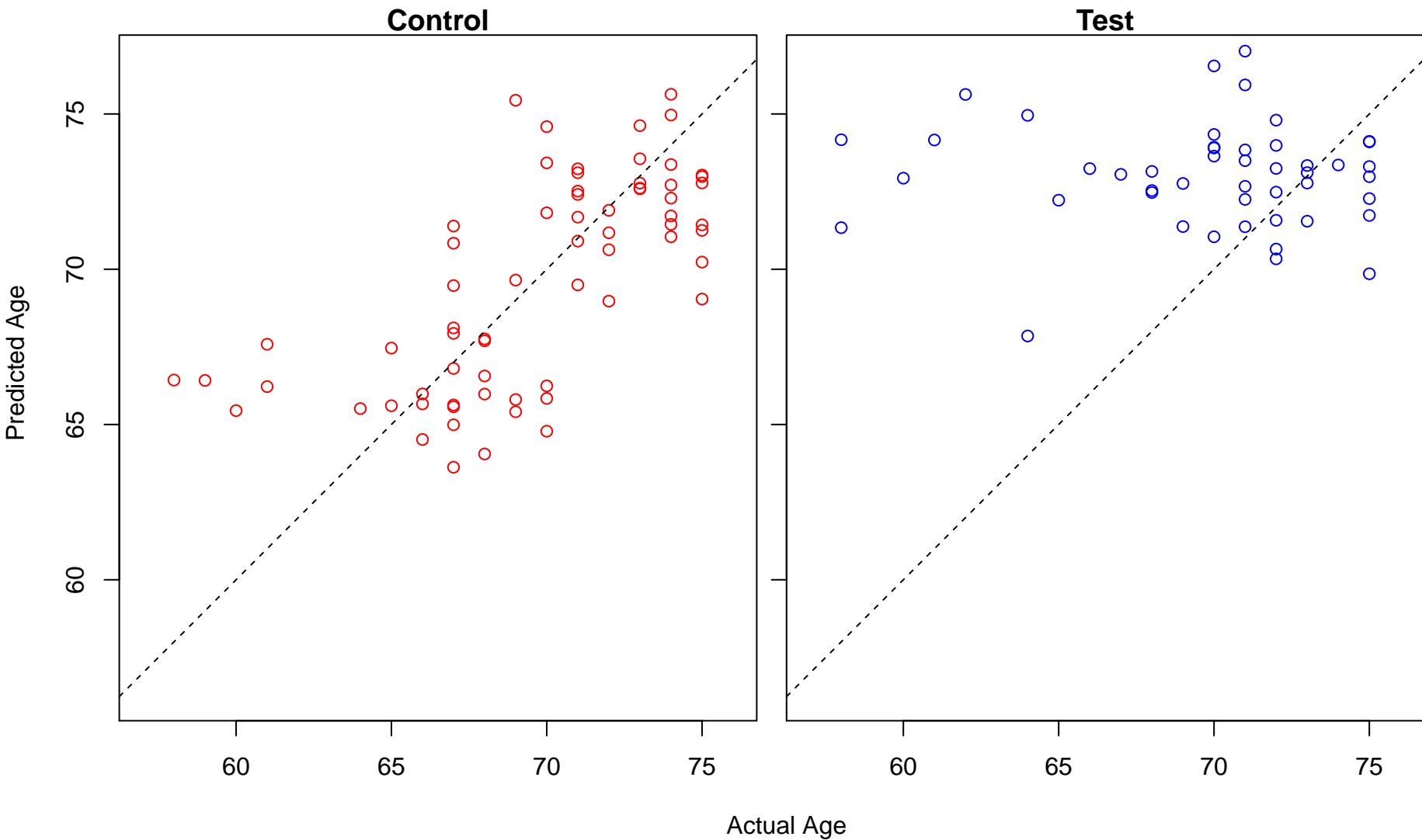
response to nutrient (Score: 1.597810)



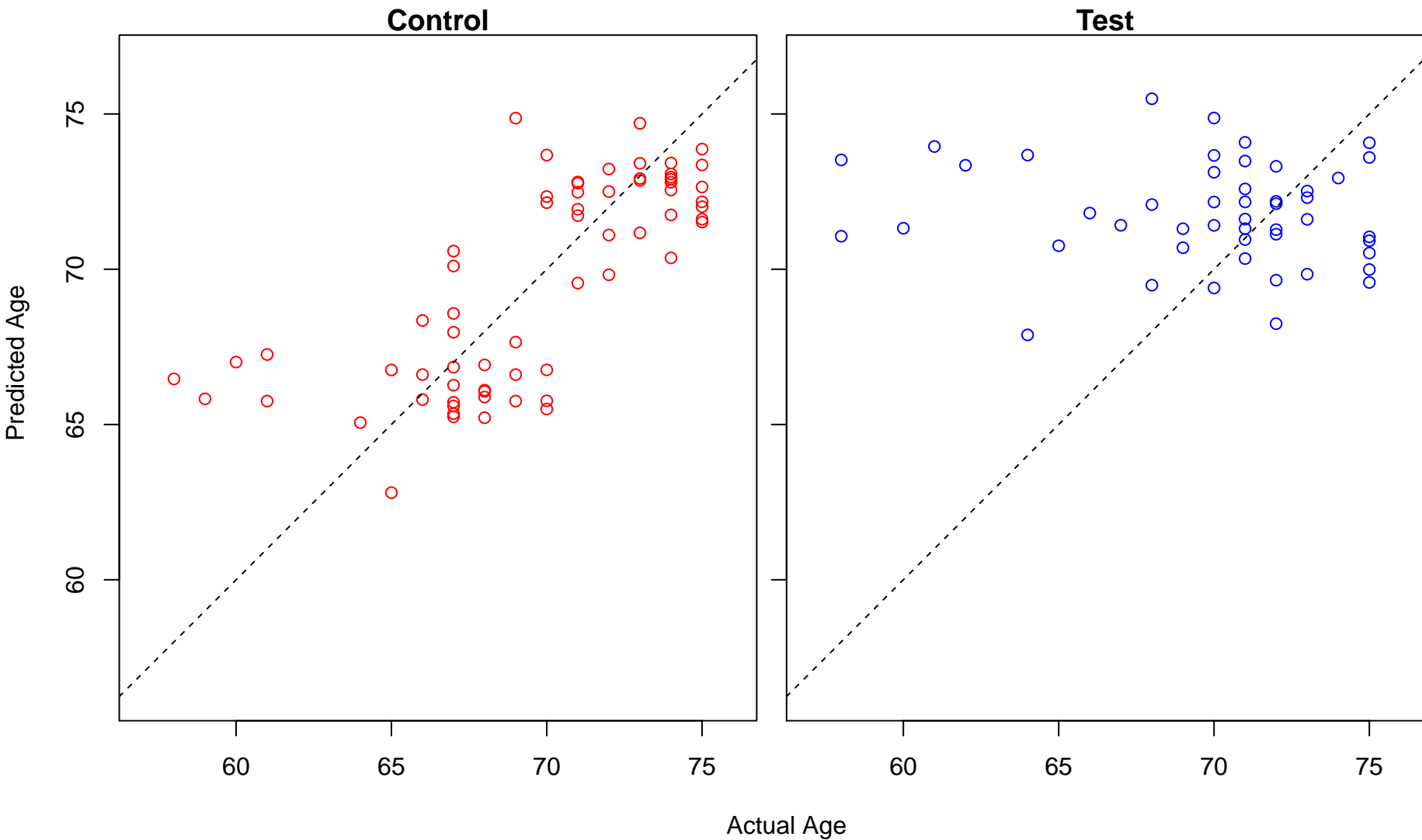
RNA modification (Score: 1.597748)



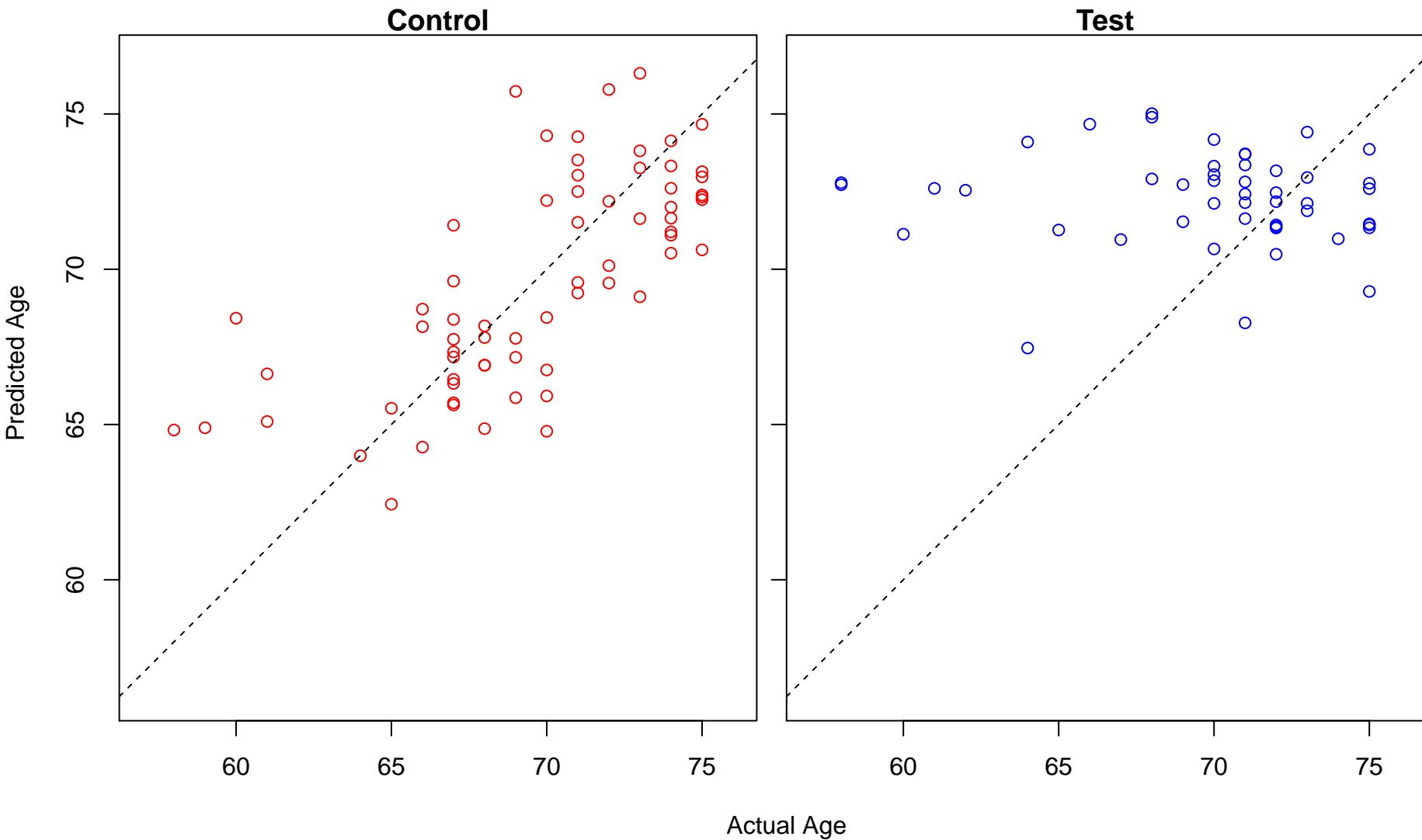
cellular iron ion homeostasis (Score: 1.597646)



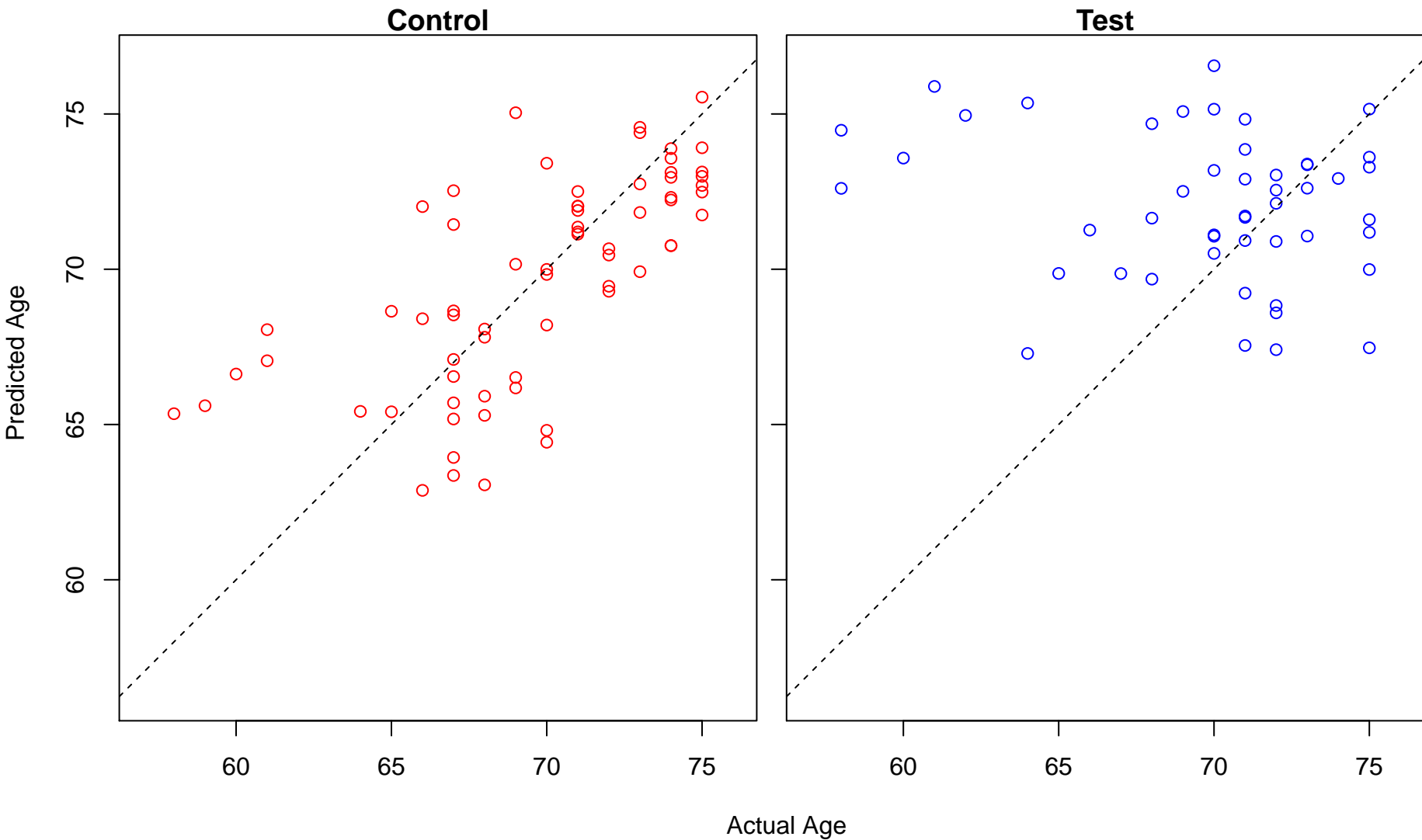
positive regulation of ubiquitin–protein transferase activity (Score: 1.597617)



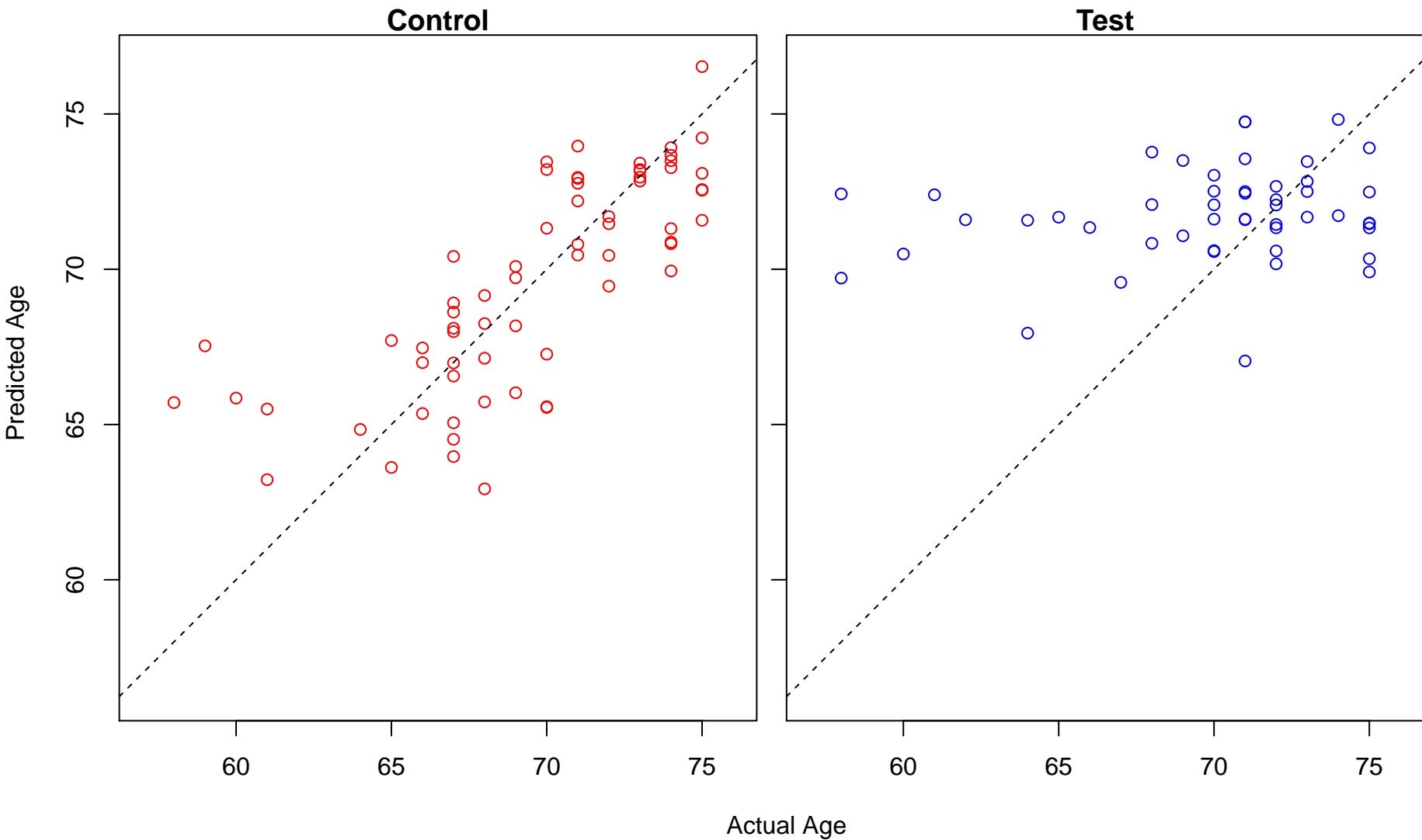
secretion by cell (Score: 1.597292)



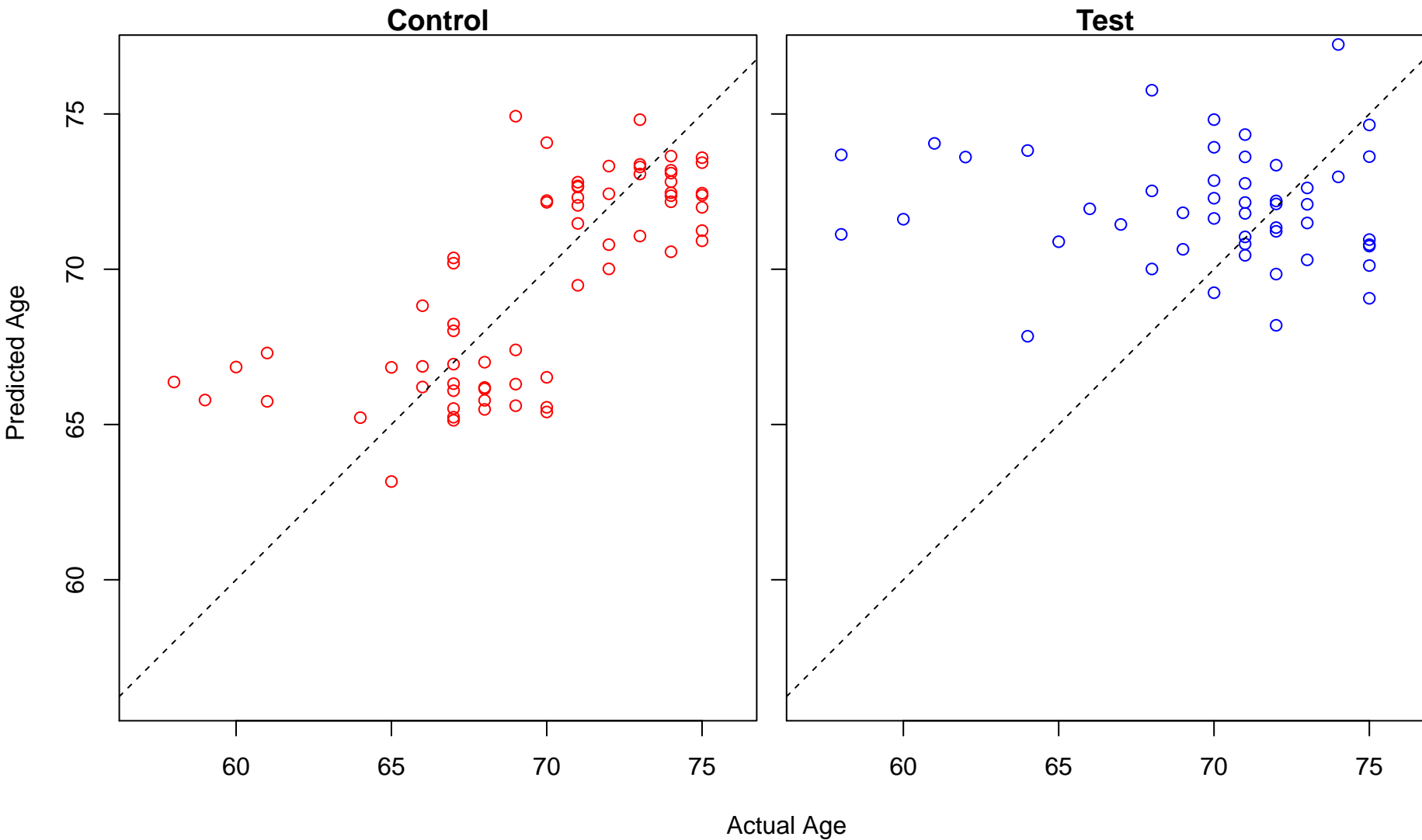
tricarboxylic acid metabolic process (Score: 1.597262)



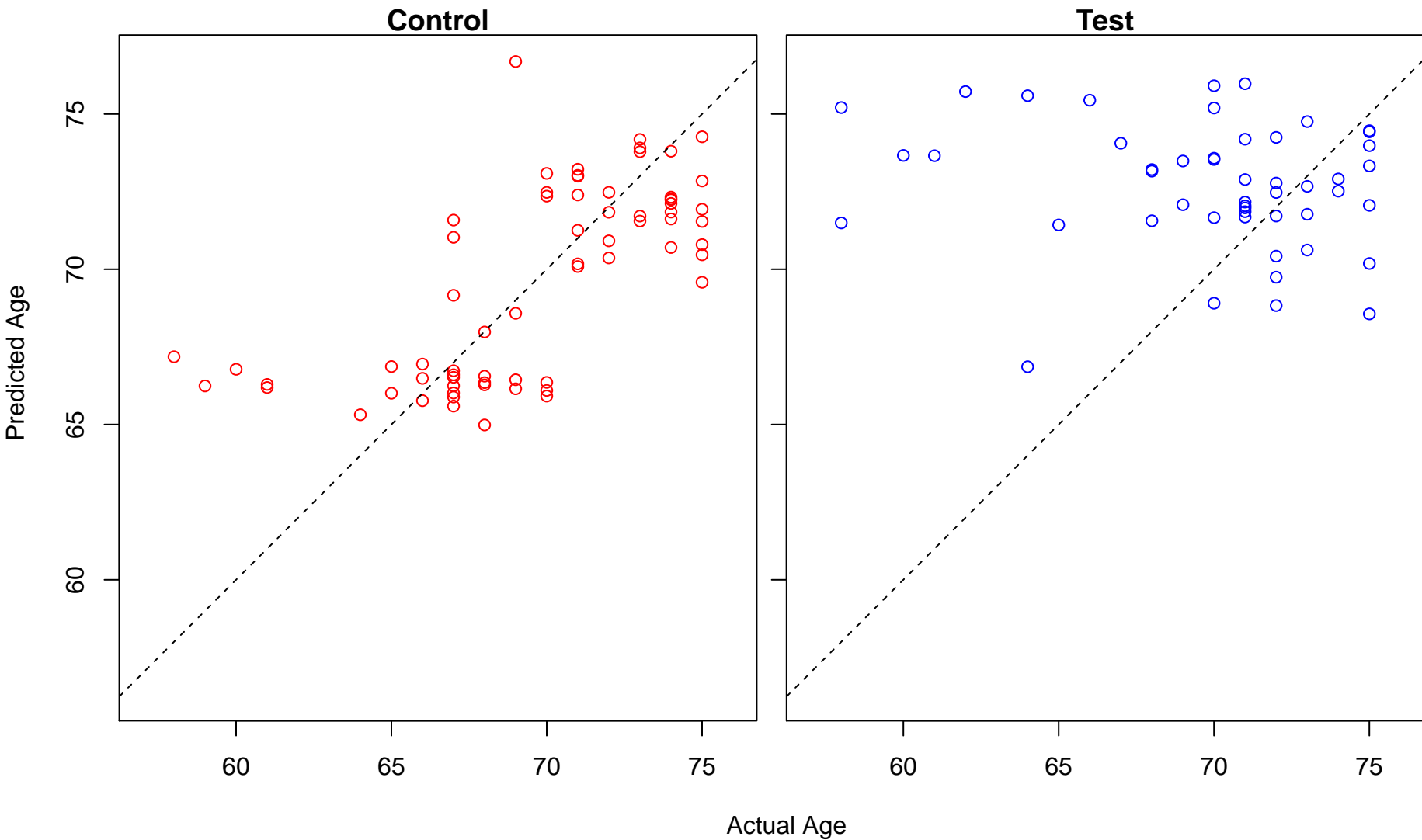
regulation of nucleotide metabolic process (Score: 1.596744)



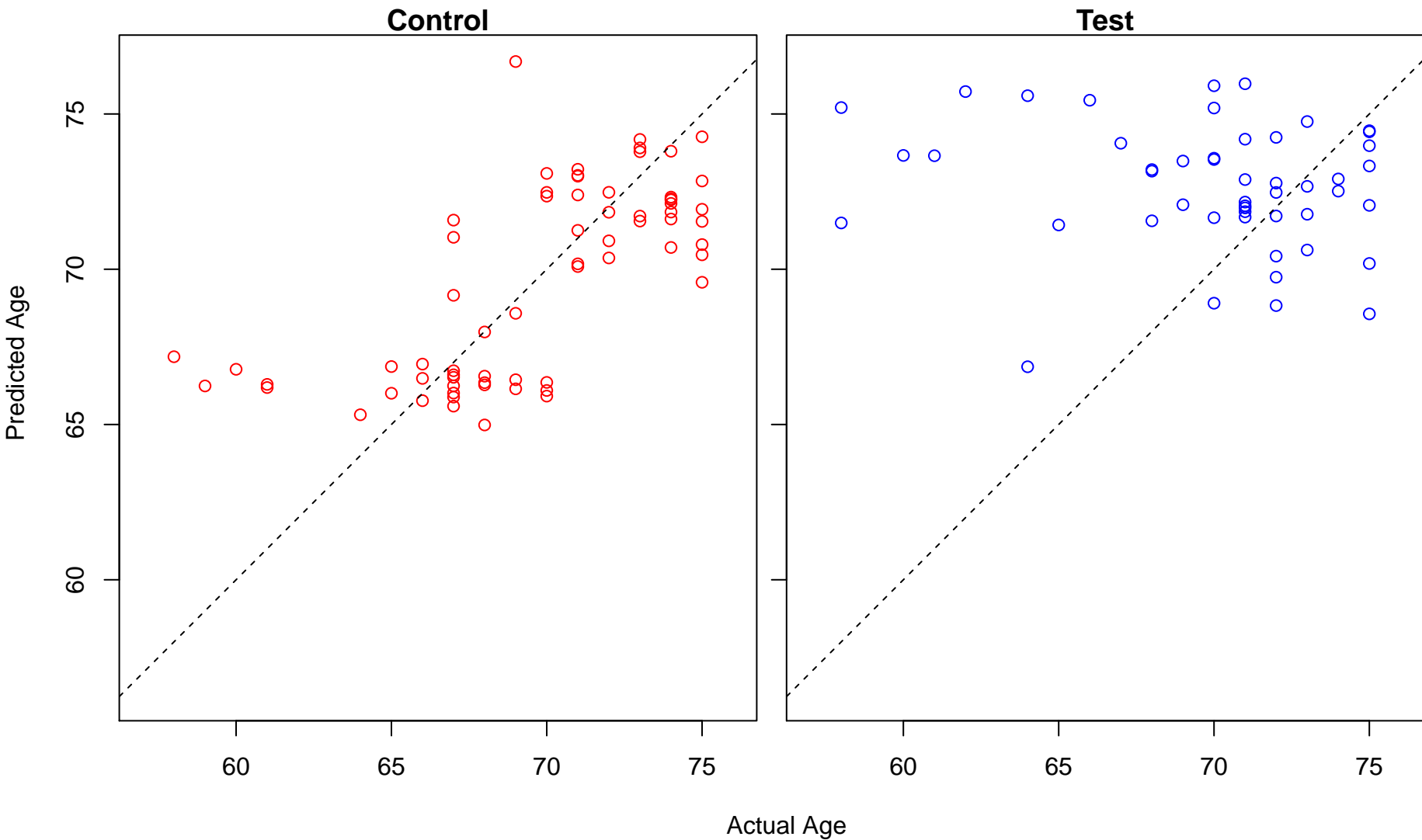
regulation of ubiquitin–protein ligase activity involved in mitotic cell cycle (Score: 1.595158)



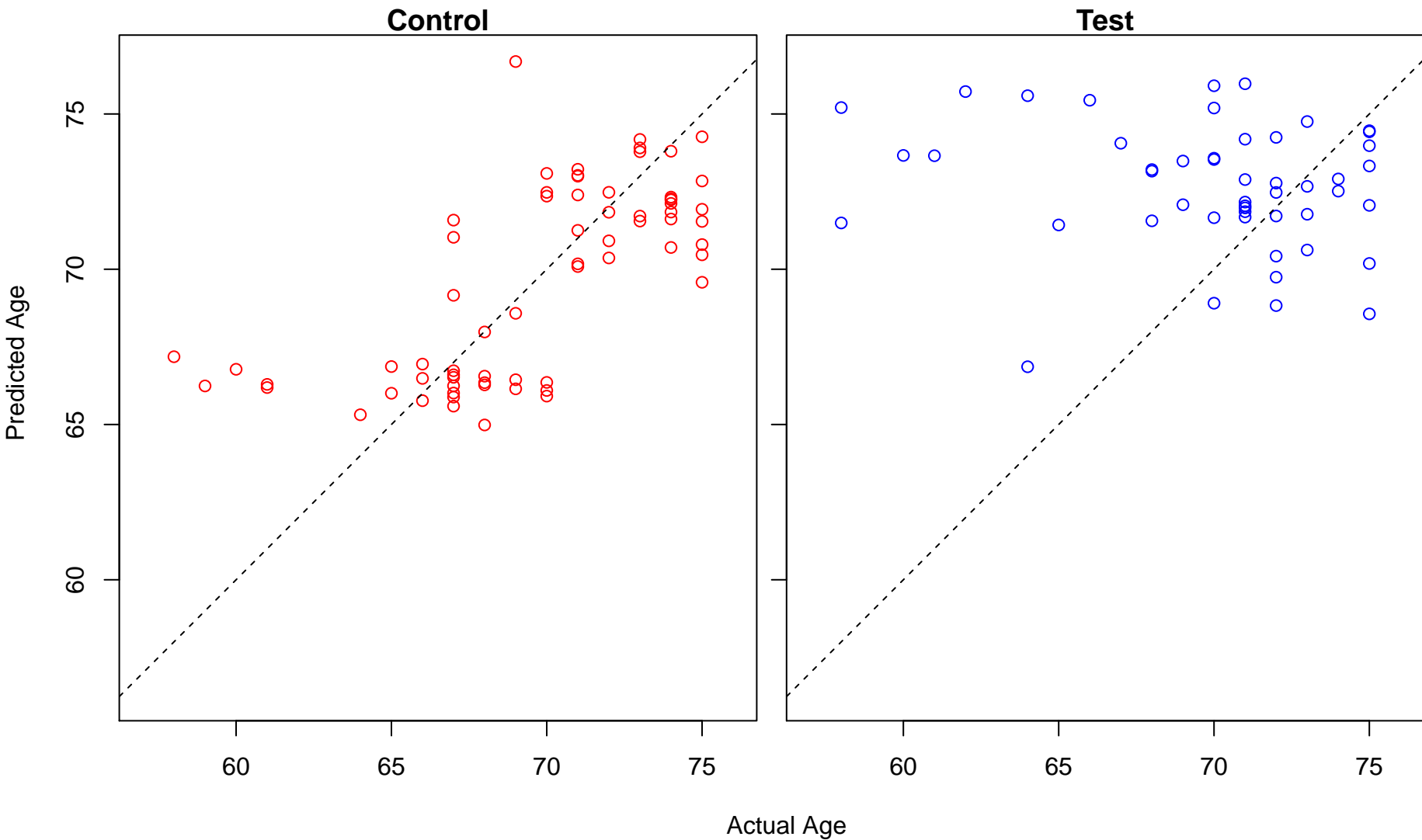
ferric iron transport (Score: 1.594589)



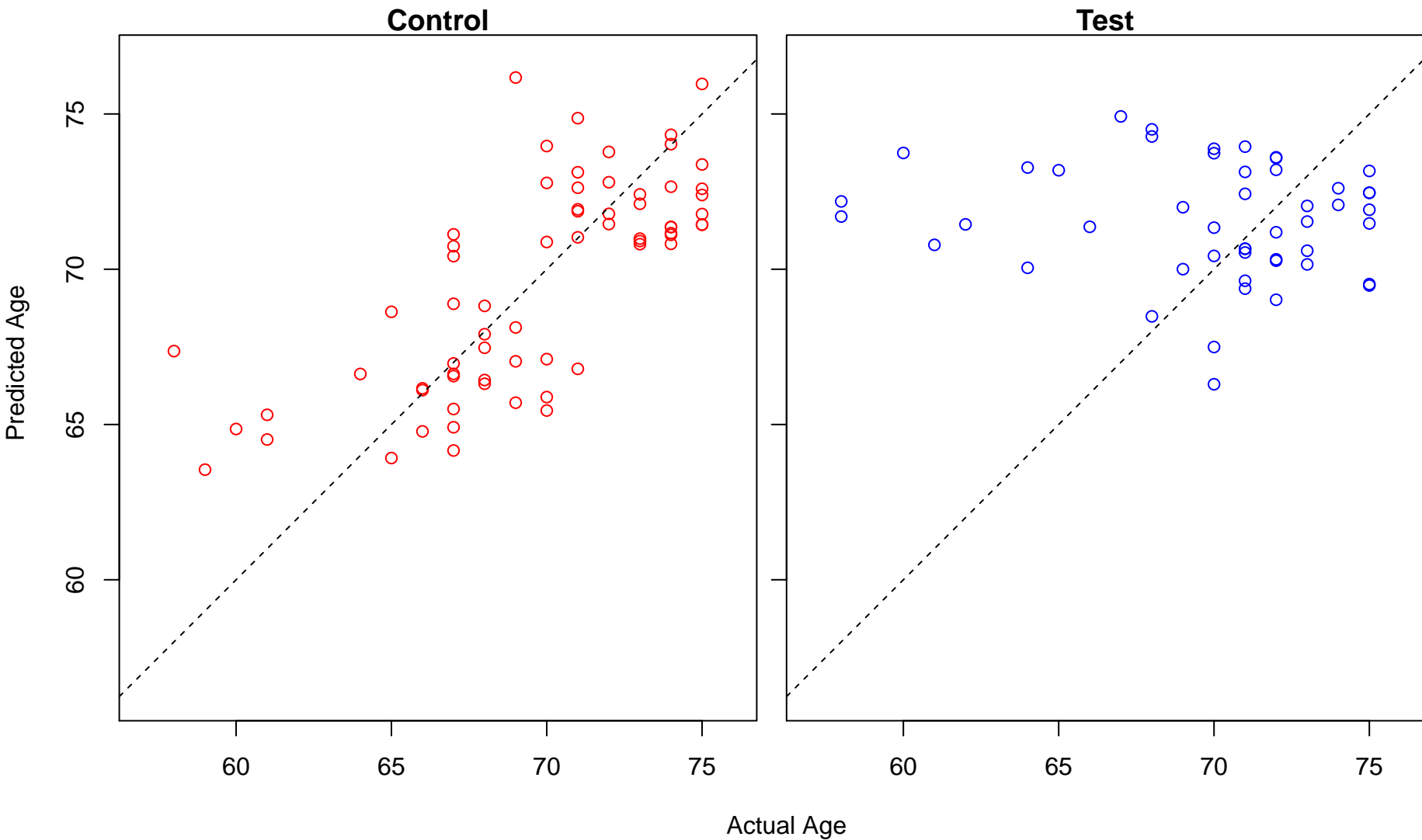
transferrin transport (Score: 1.594589)



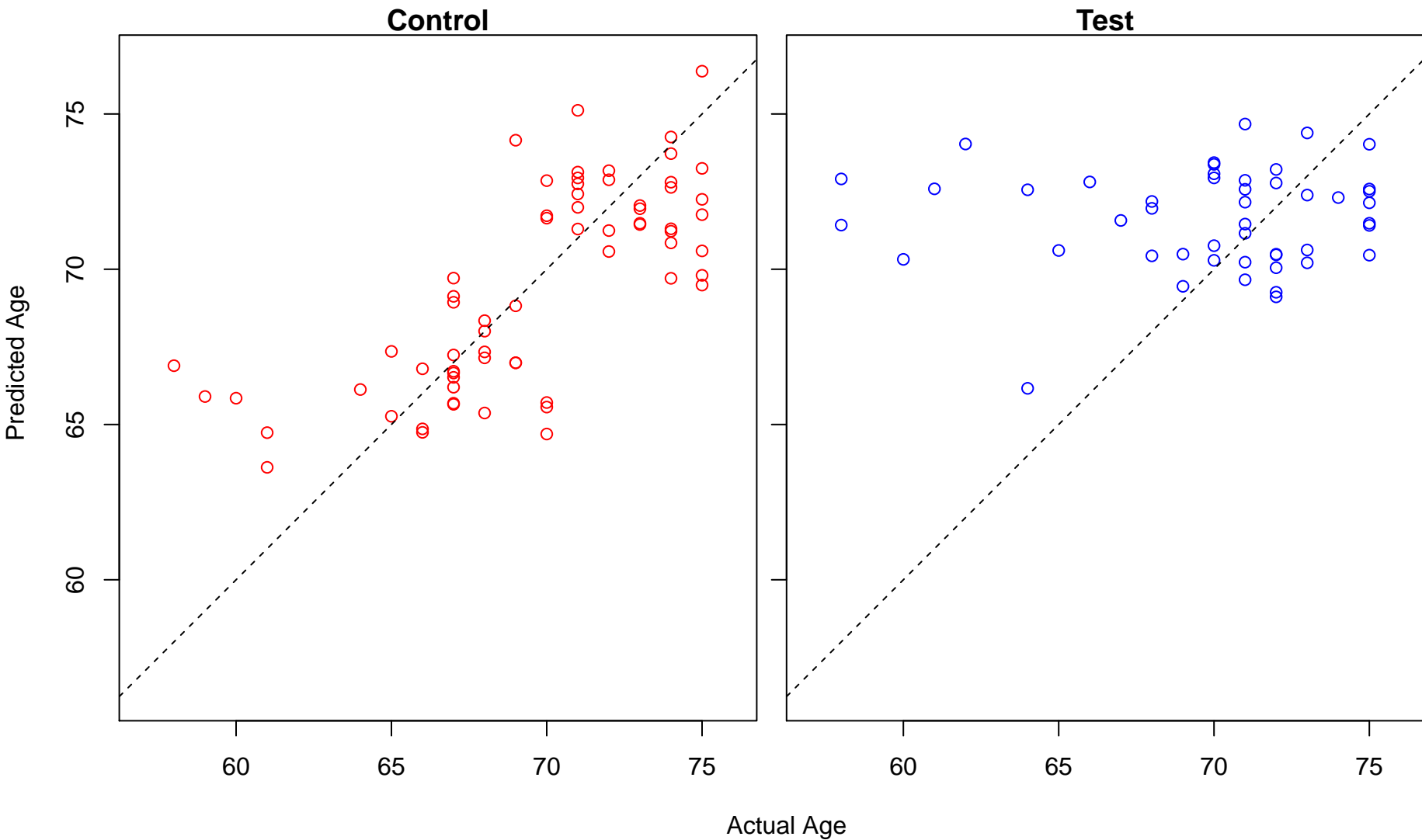
trivalent inorganic cation transport (Score: 1.594589)



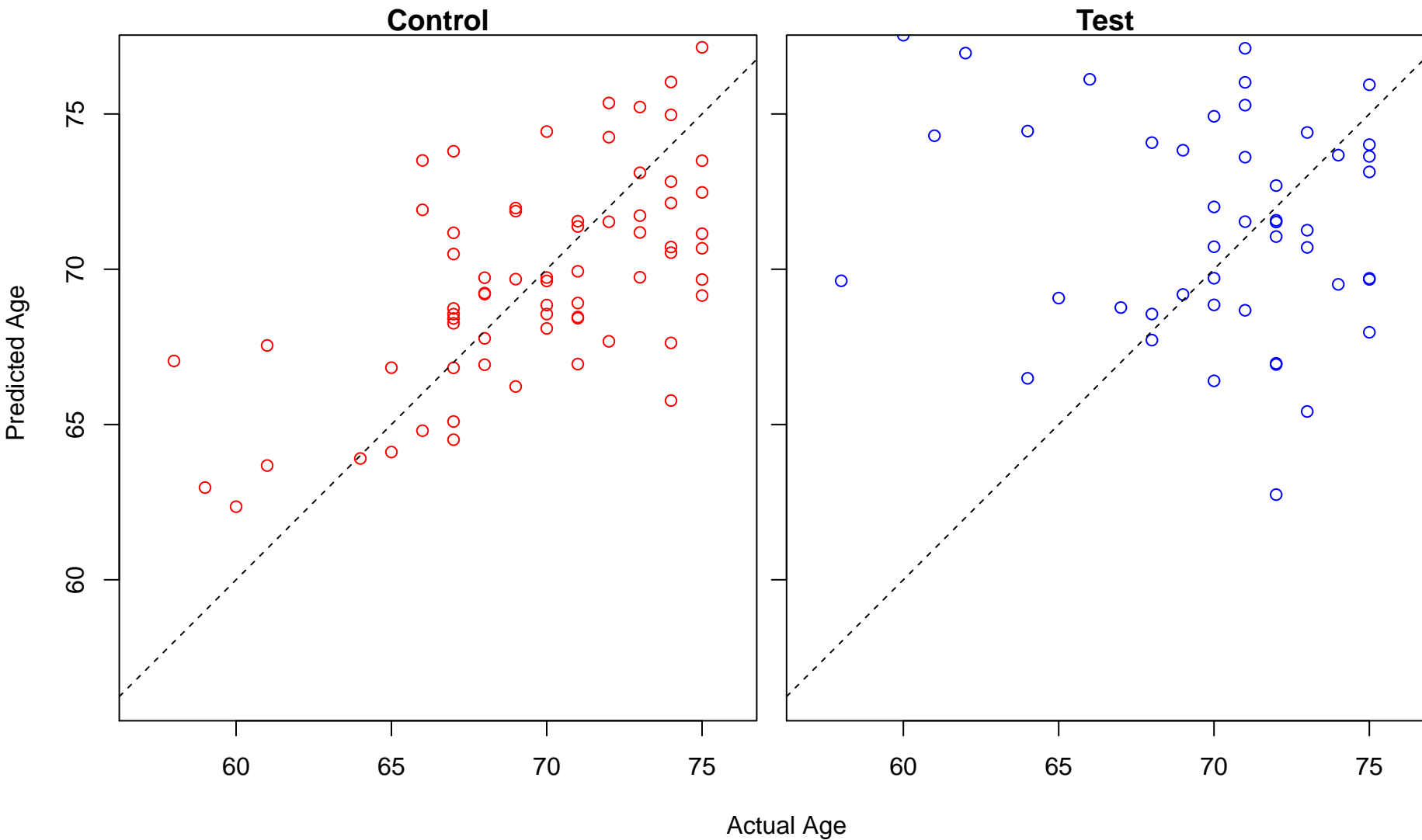
regulation of endoplasmic reticulum unfolded protein response (Score: 1.593680)



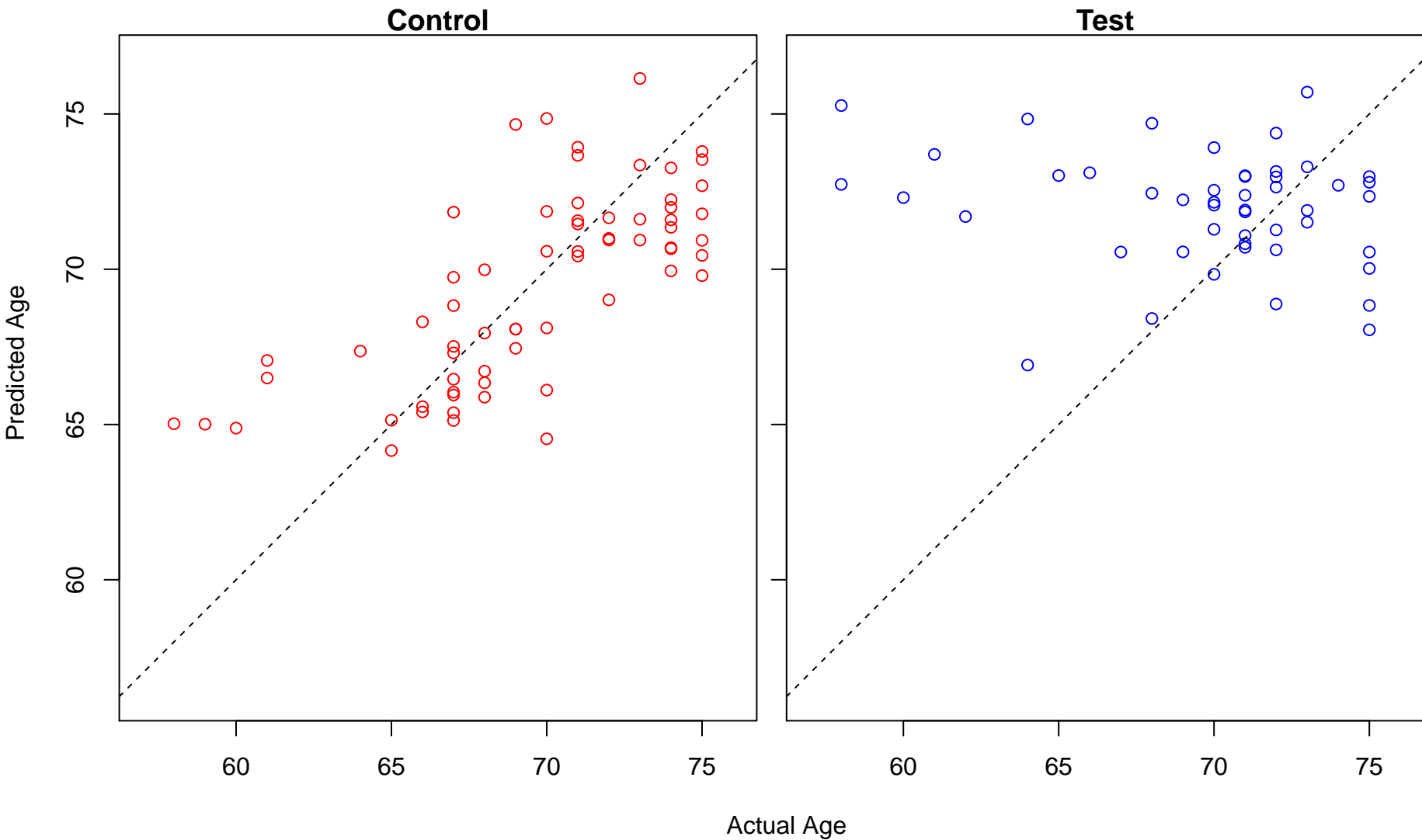
regulation of actin filament polymerization (Score: 1.592625)



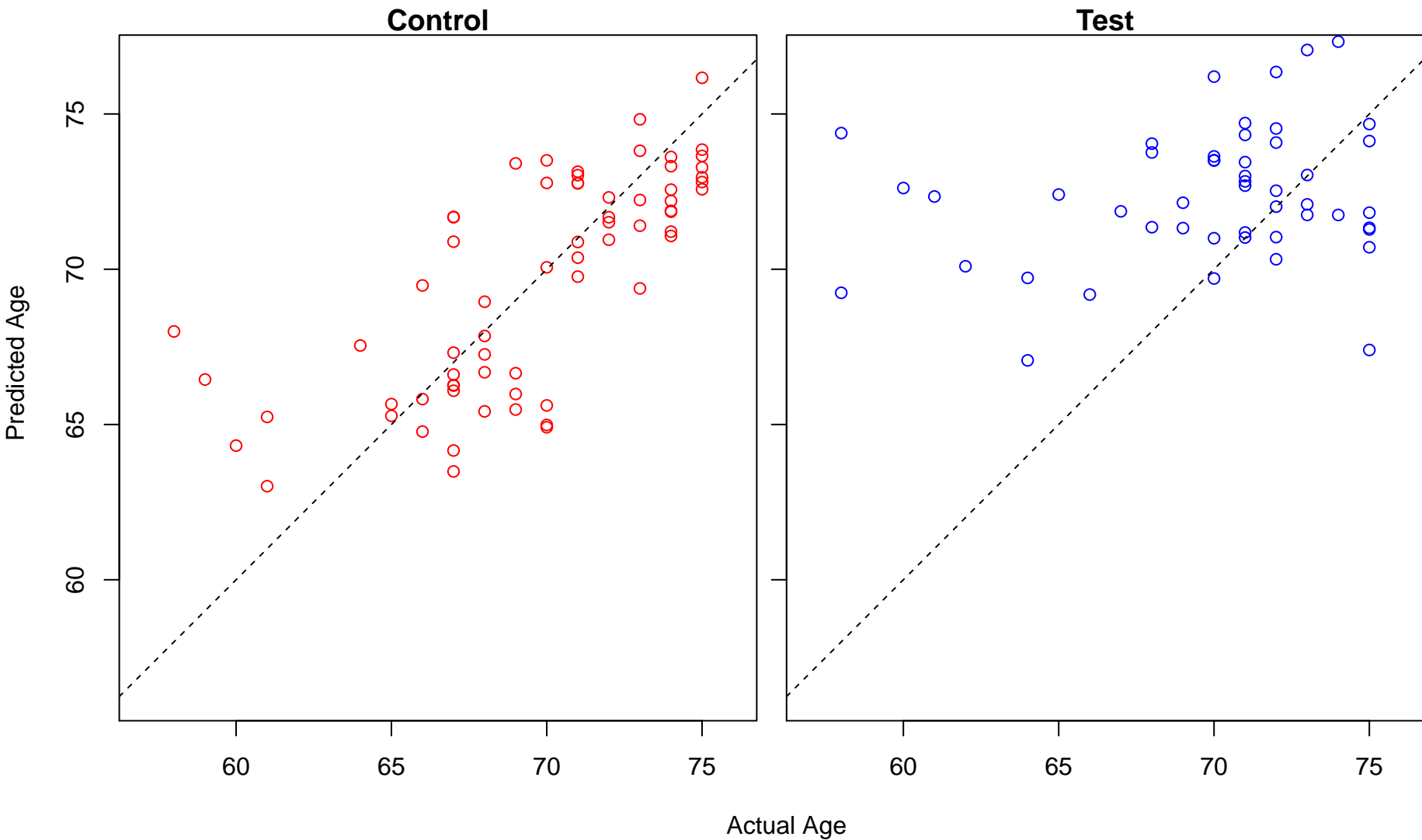
ionotropic glutamate receptor signaling pathway (Score: 1.591925)



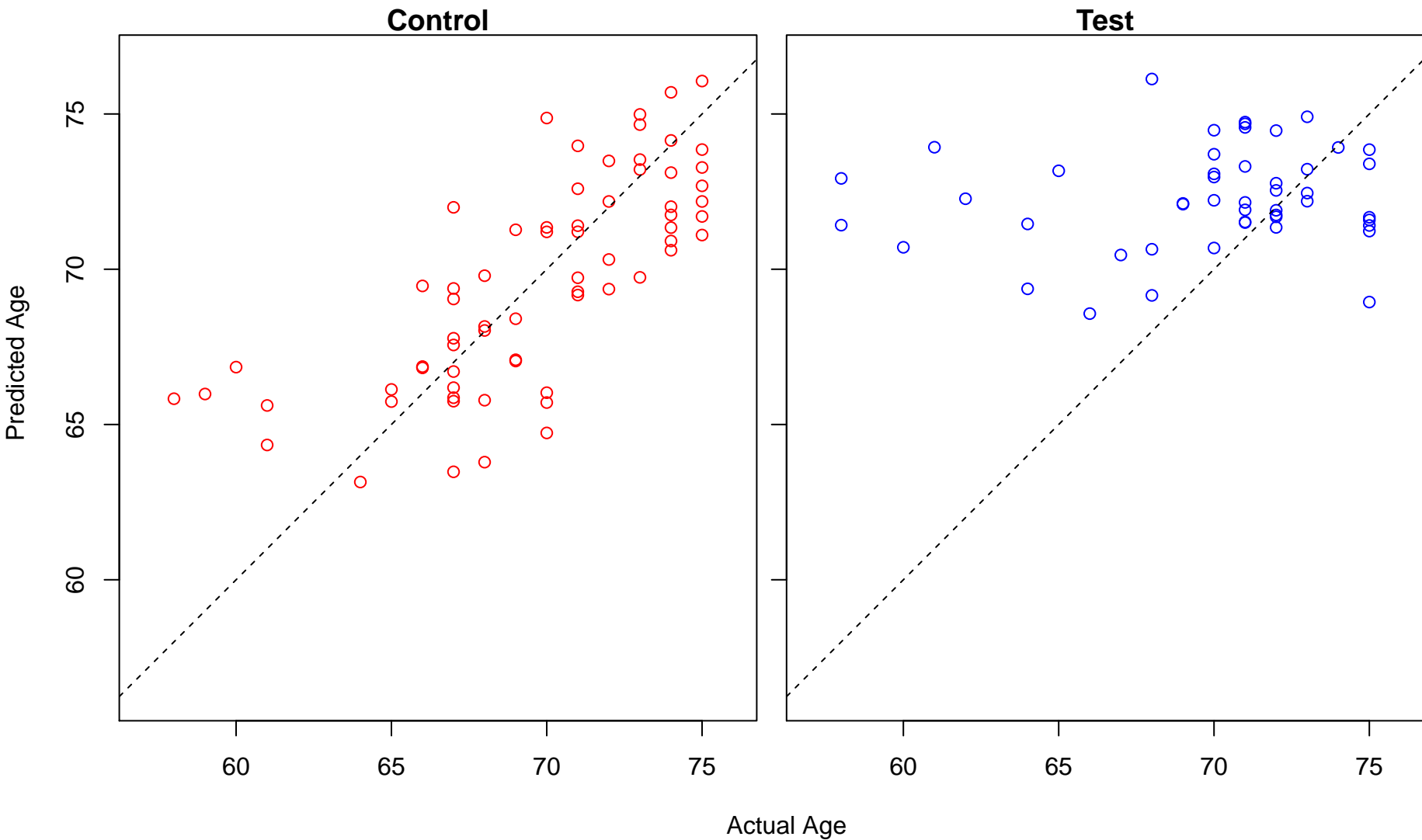
positive regulation of DNA replication (Score: 1.591715)



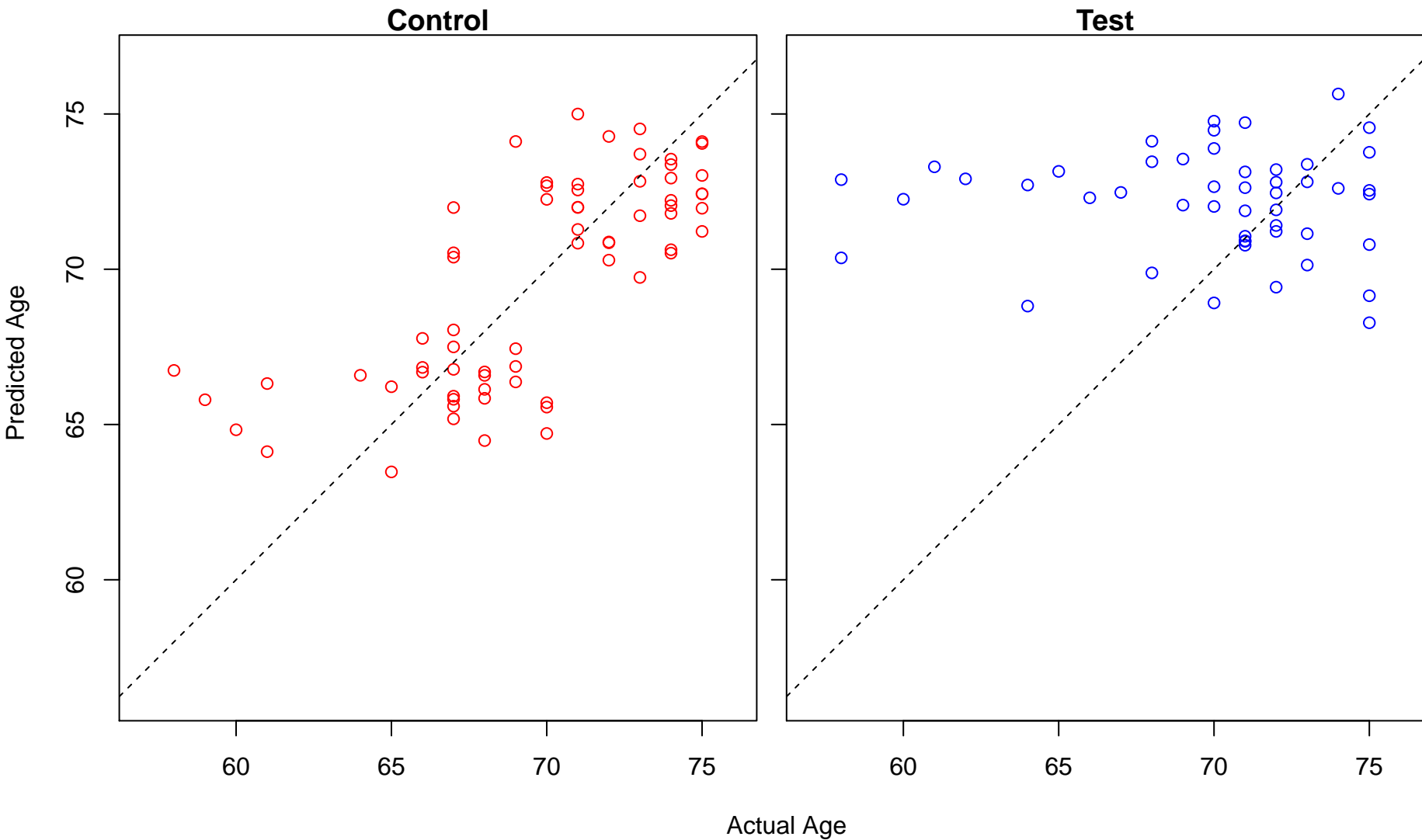
myeloid cell homeostasis (Score: 1.591554)



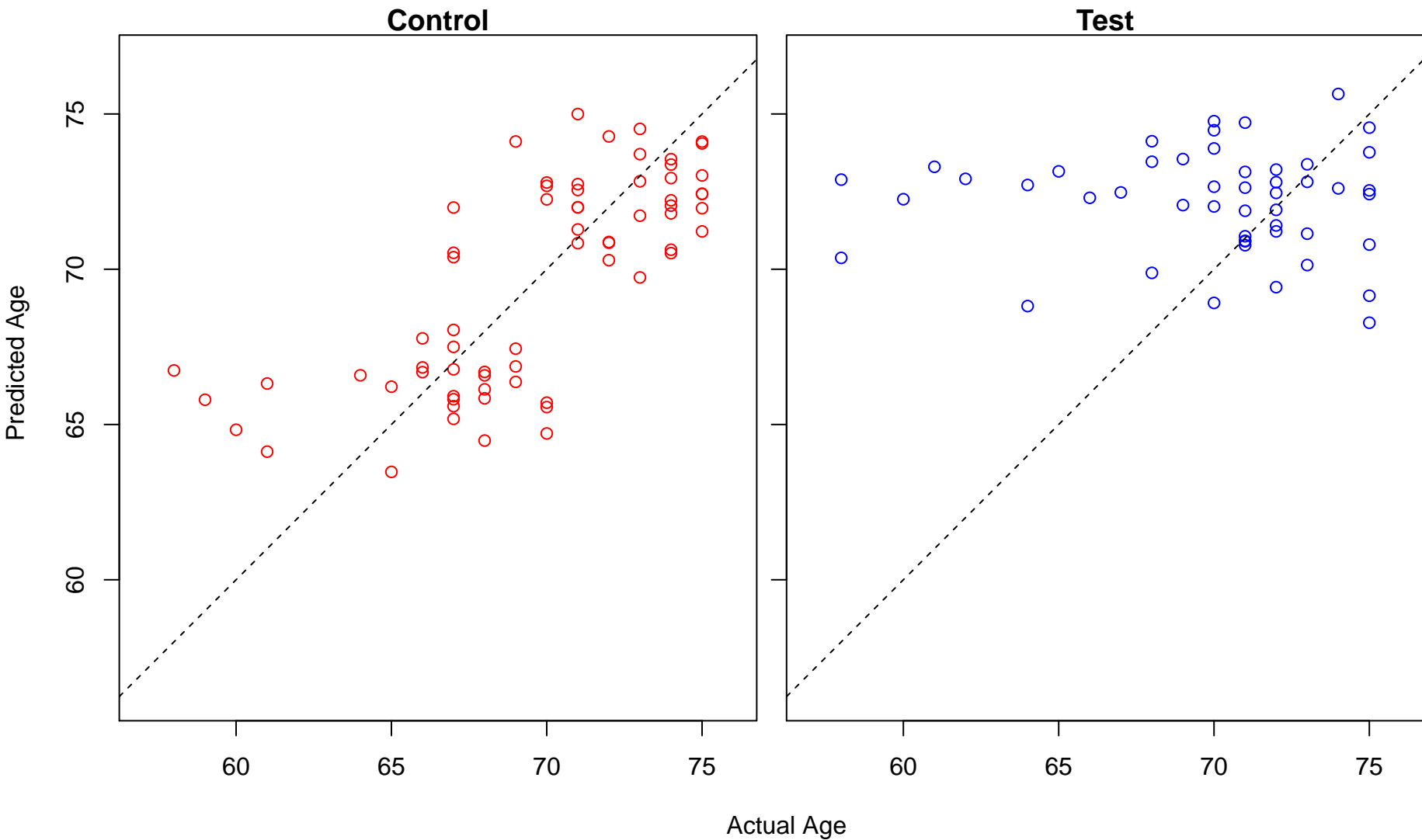
endomembrane system organization (Score: 1.591527)



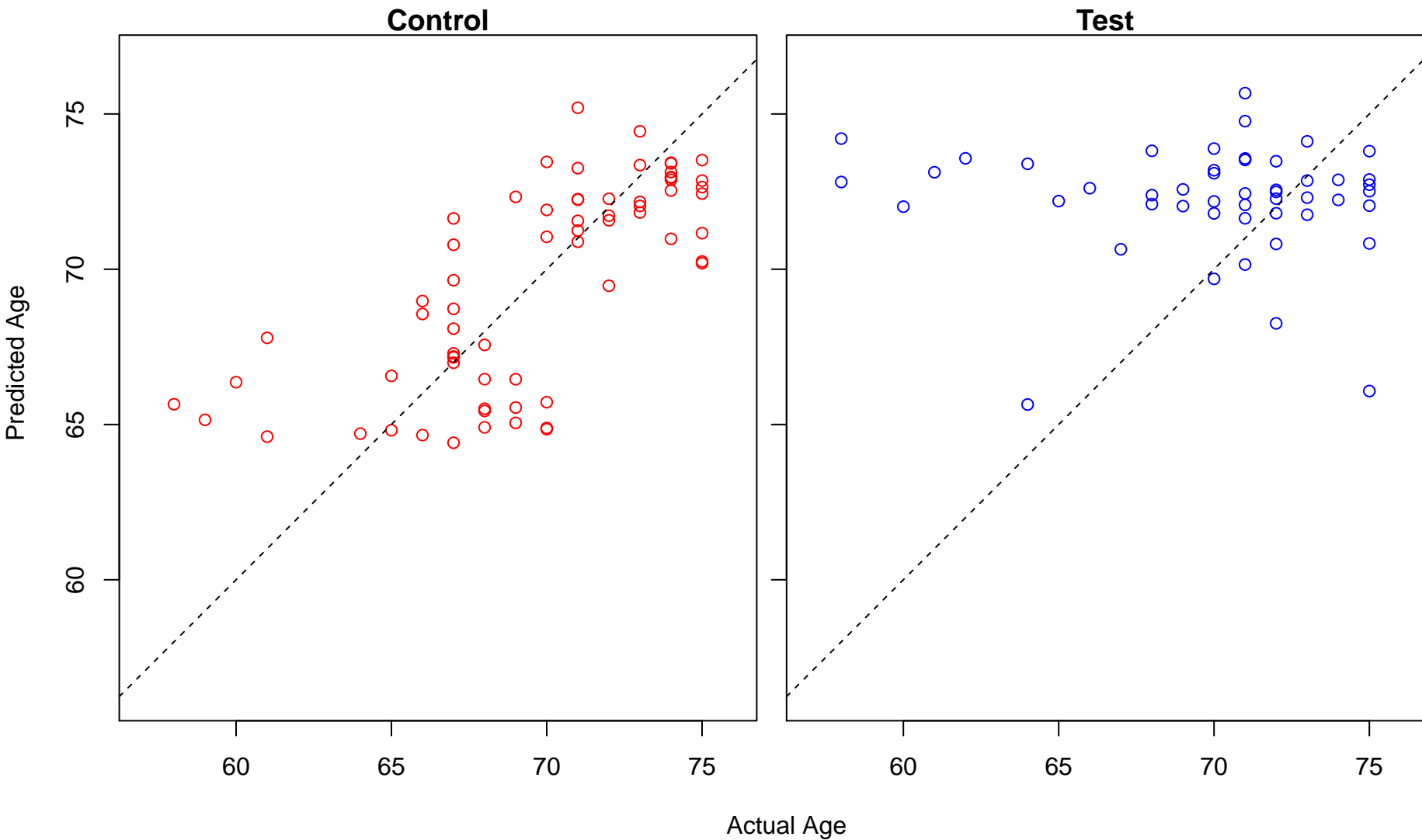
dolichol-linked oligosaccharide biosynthetic process (Score: 1.591498)



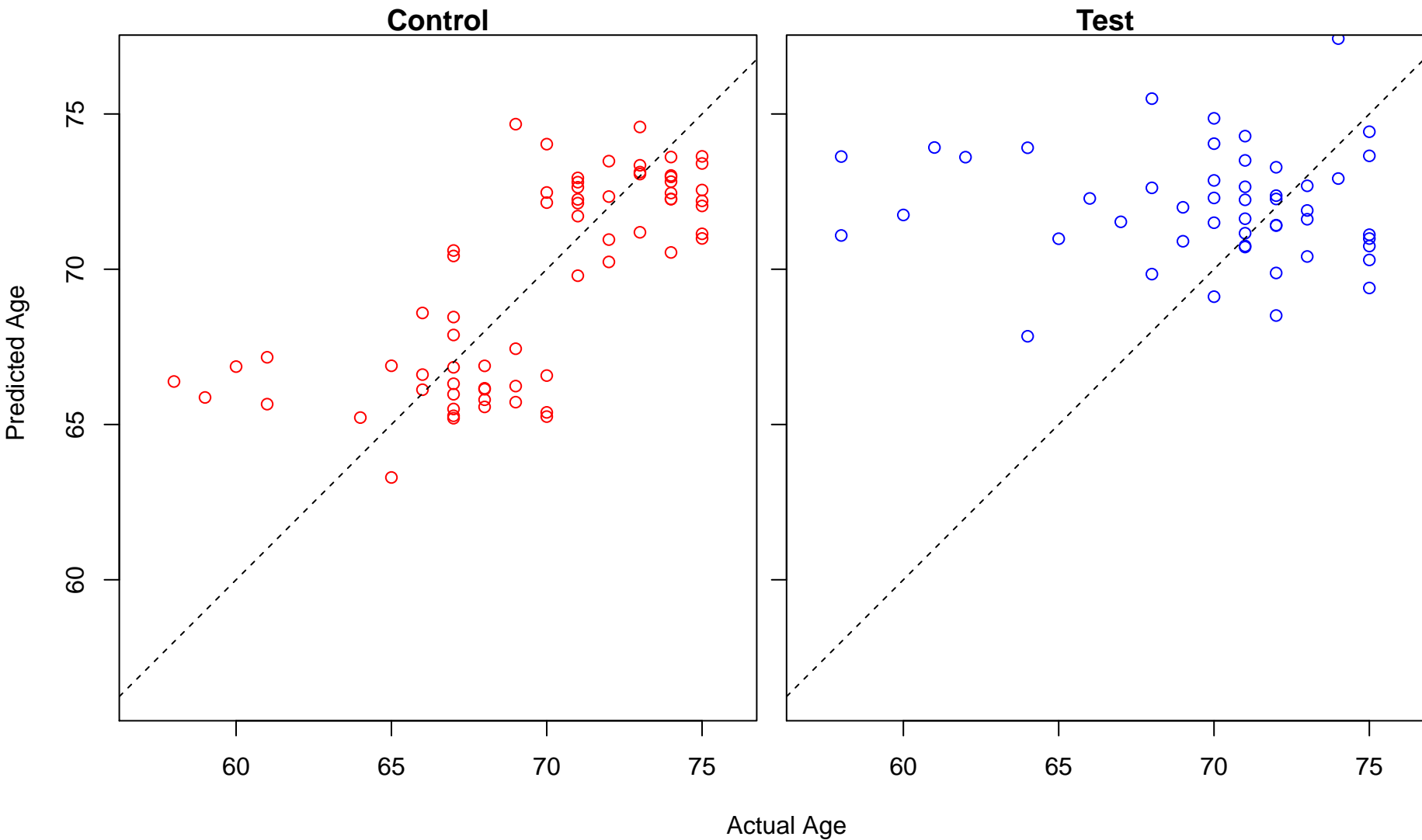
oligosaccharide–lipid intermediate biosynthetic process (Score: 1.591498)



regulation of fibroblast proliferation (Score: 1.591143)

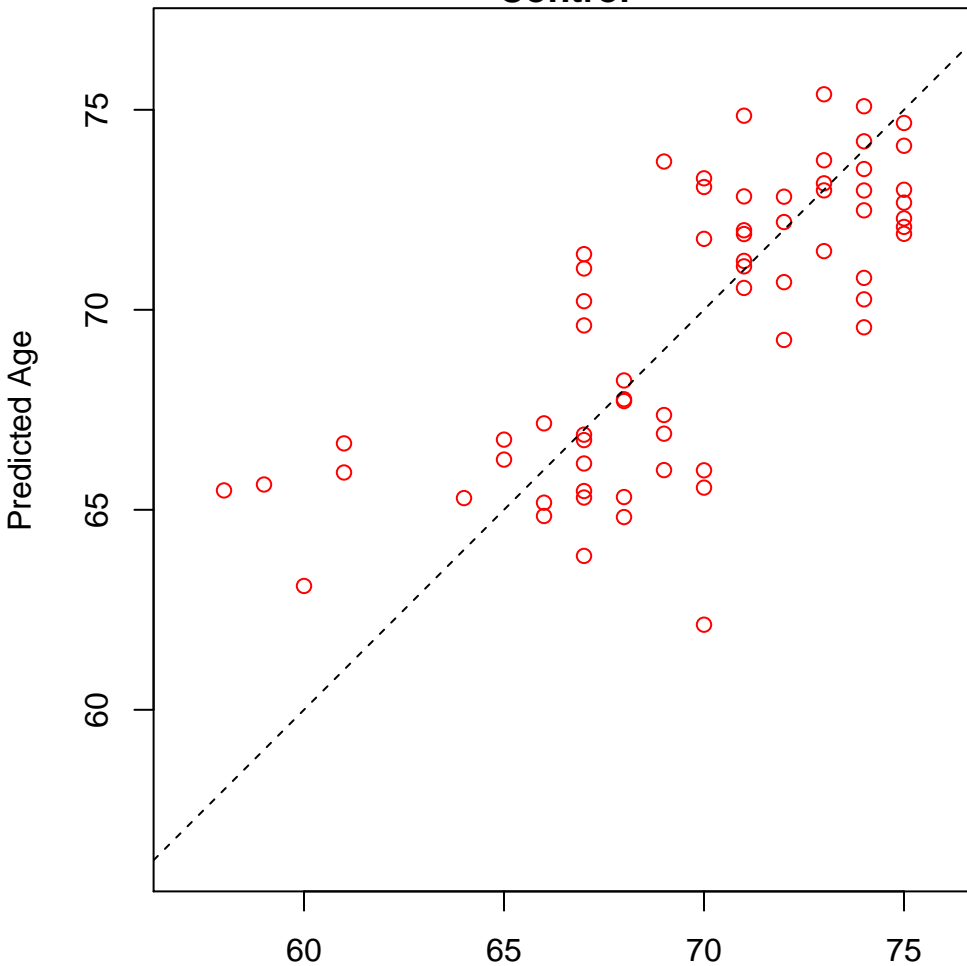


regulation of ligase activity (Score: 1.590847)

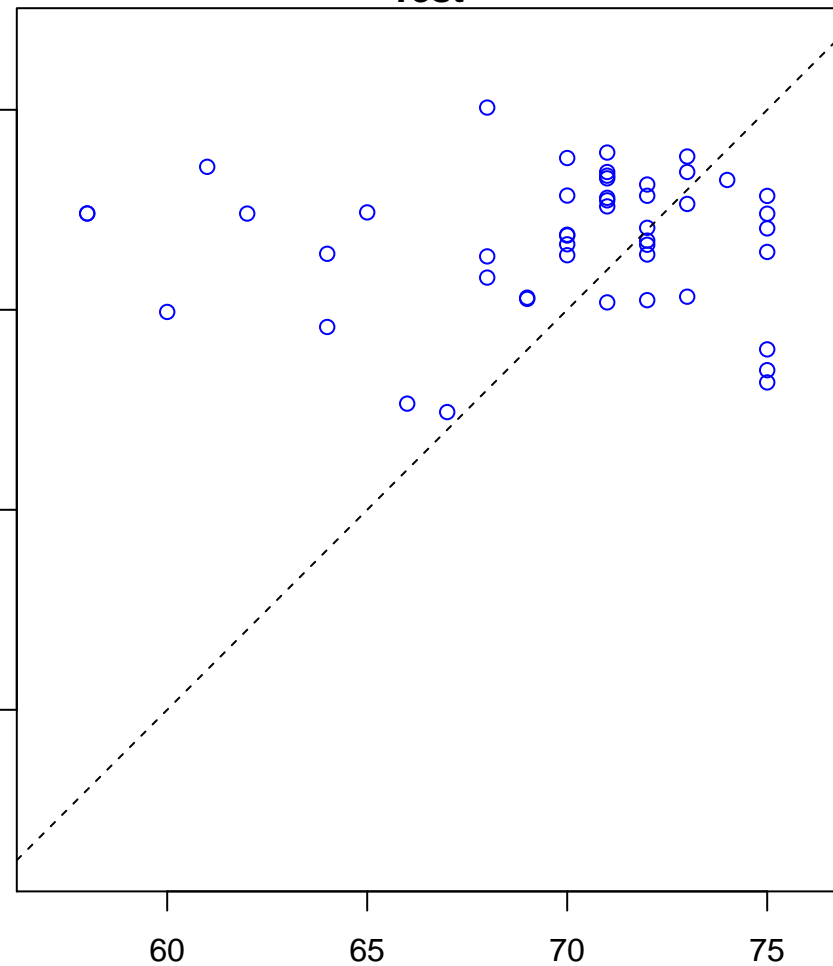


hydrogen ion transmembrane transport (Score: 1.590422)

Control

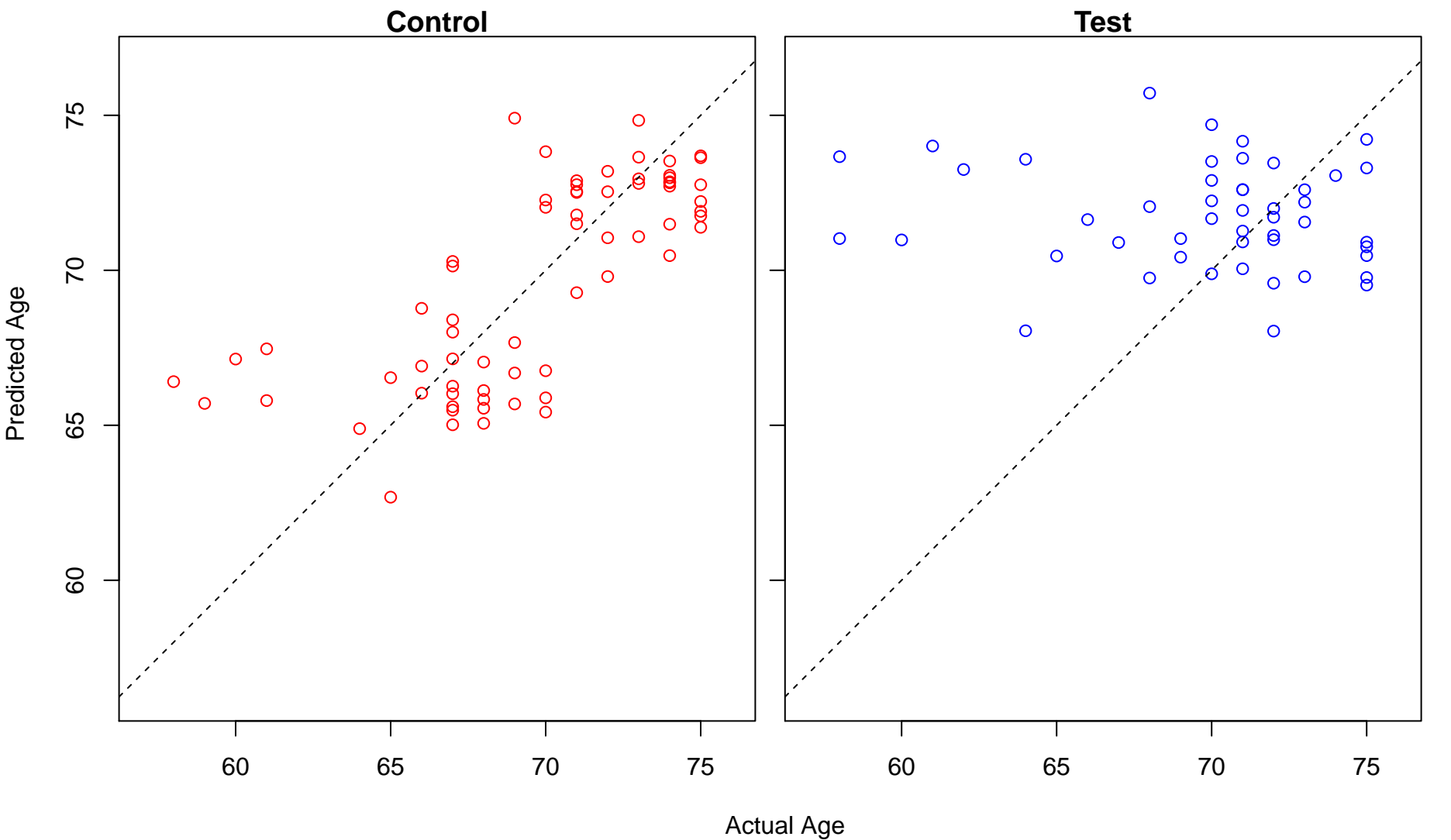


Test



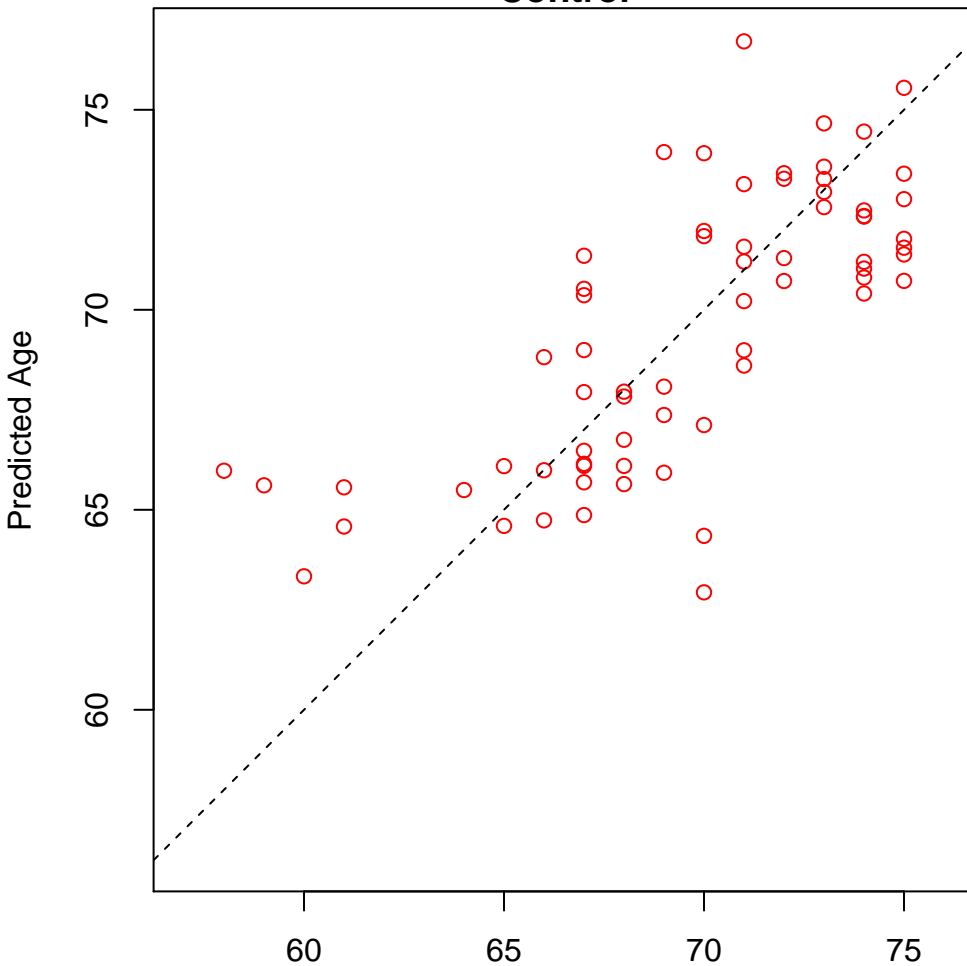
Actual Age

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

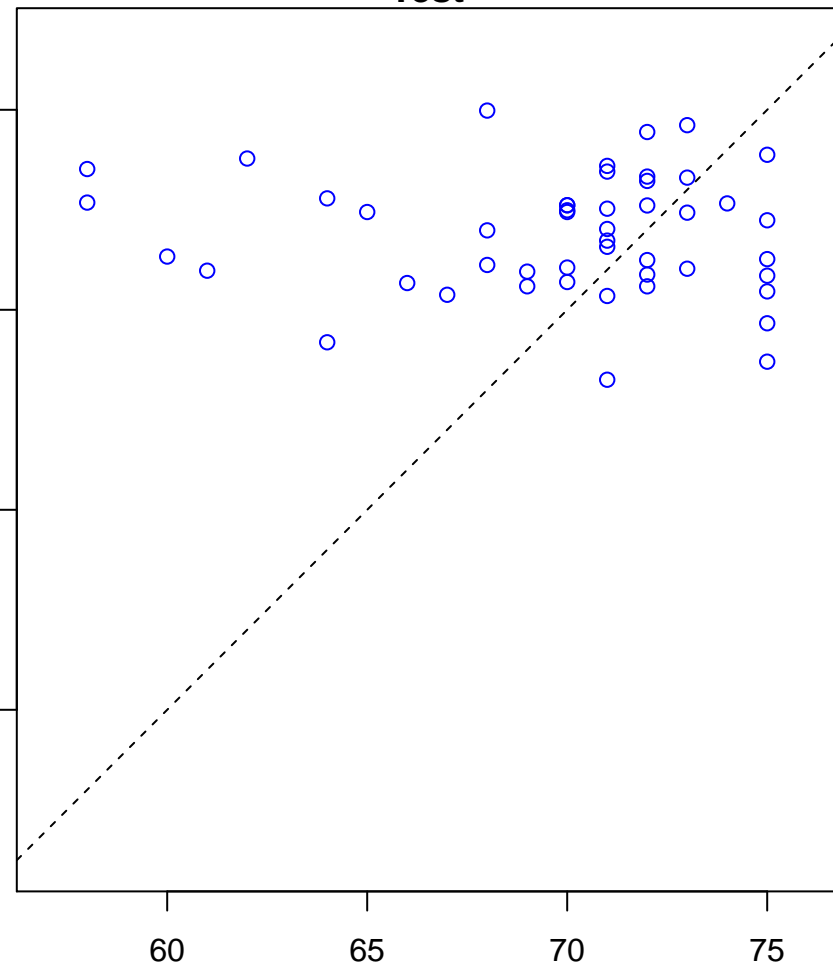


mitochondrial transmembrane transport (Score: 1.590079)

Control

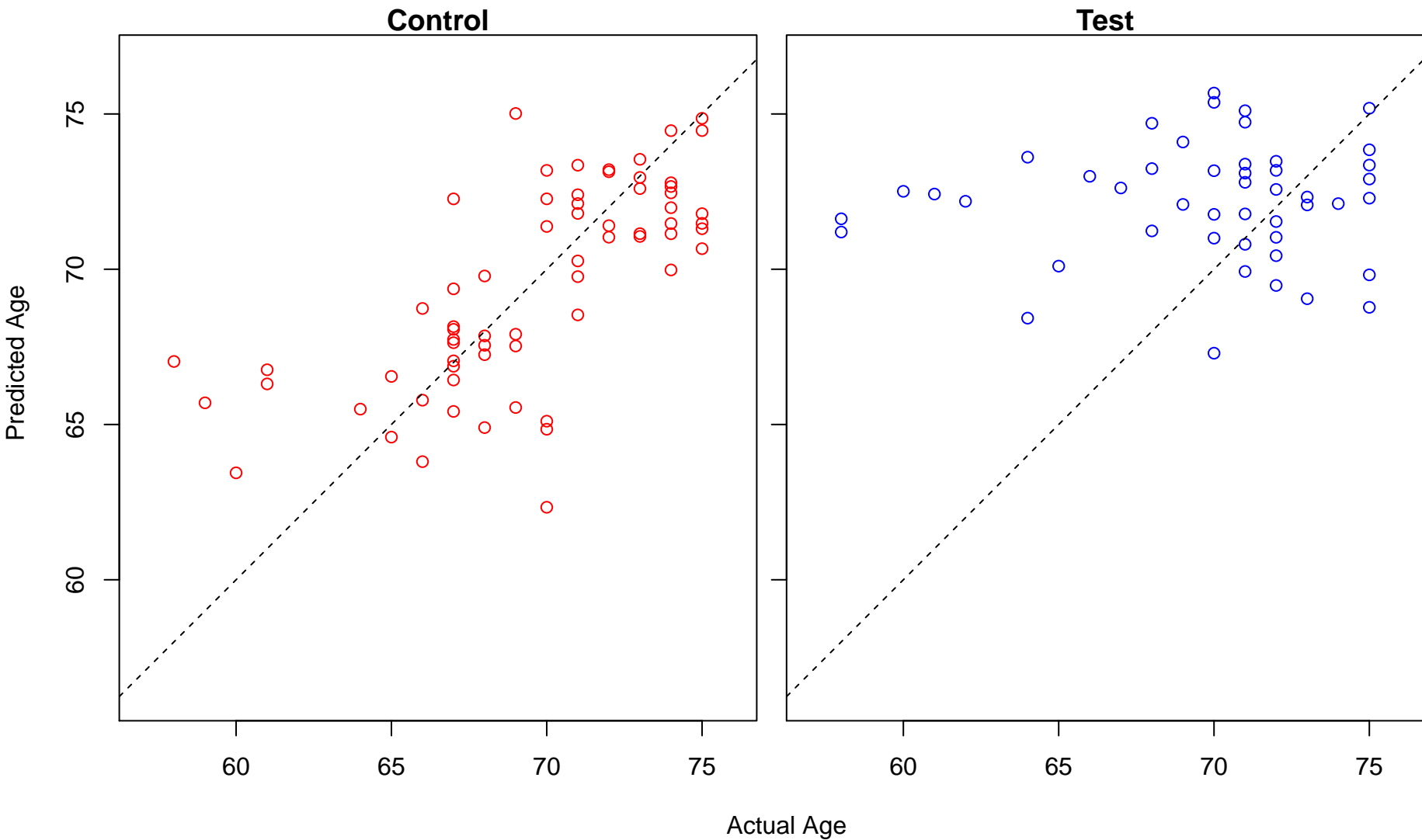


Test

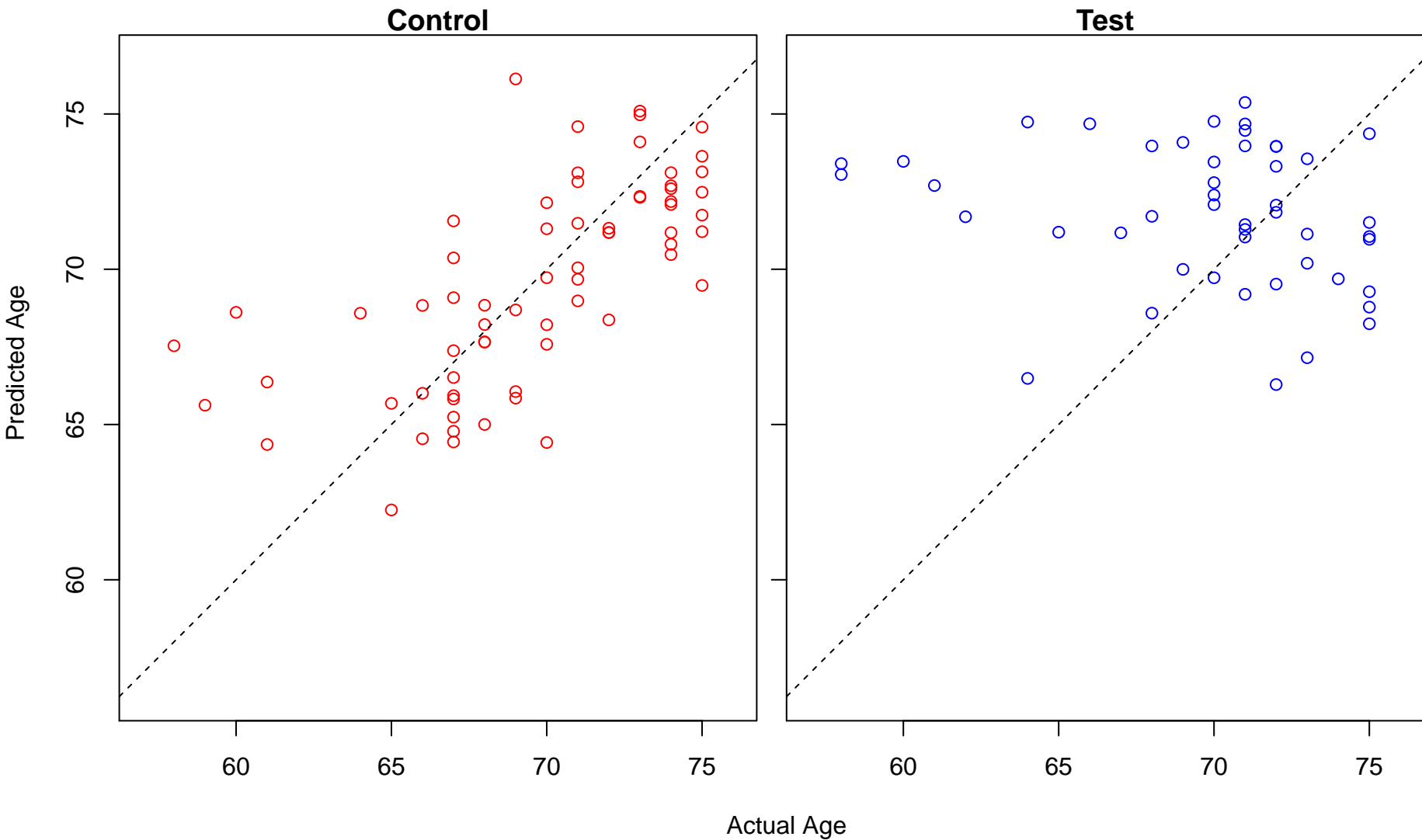


Actual Age

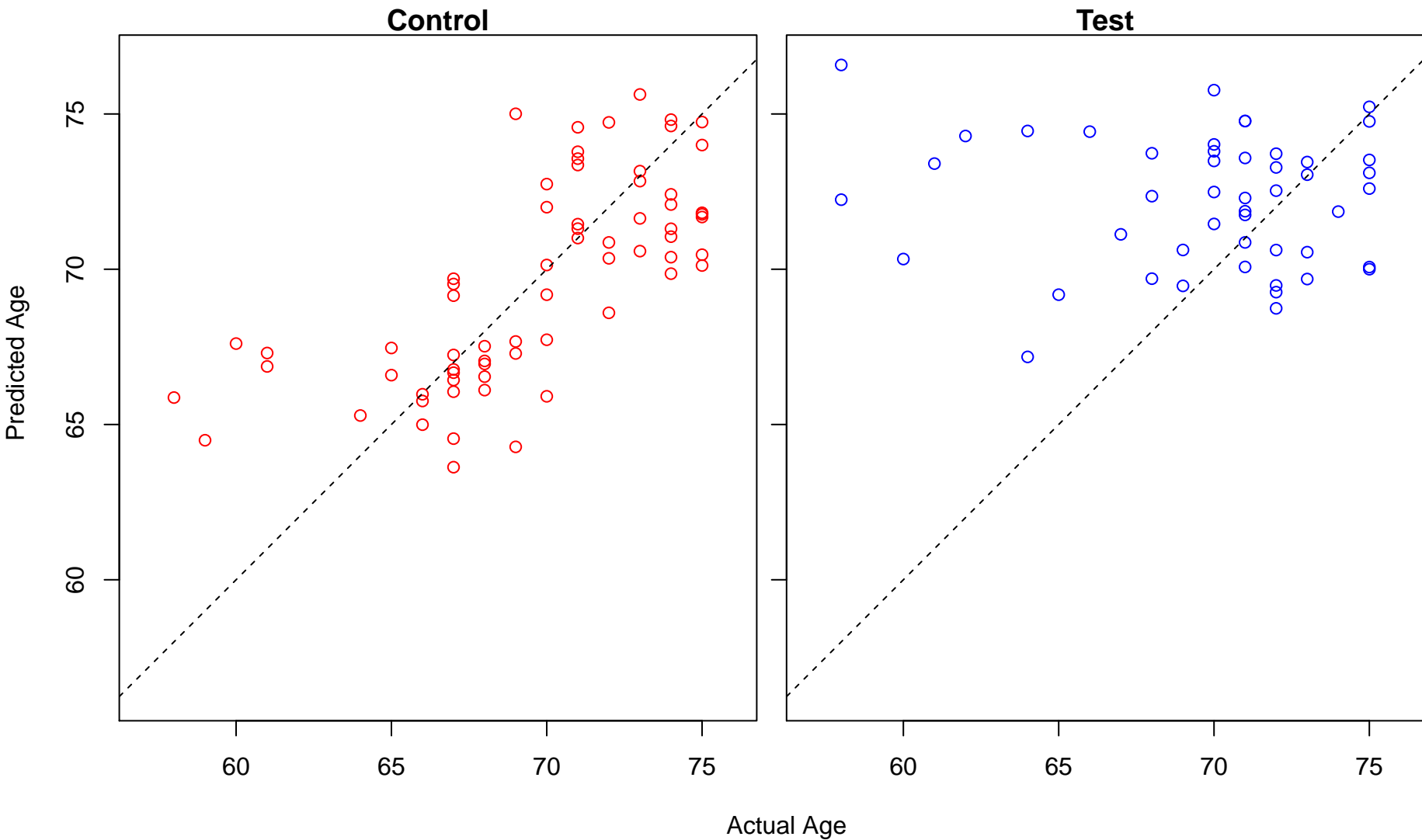
regulation of DNA binding (Score: 1.589288)



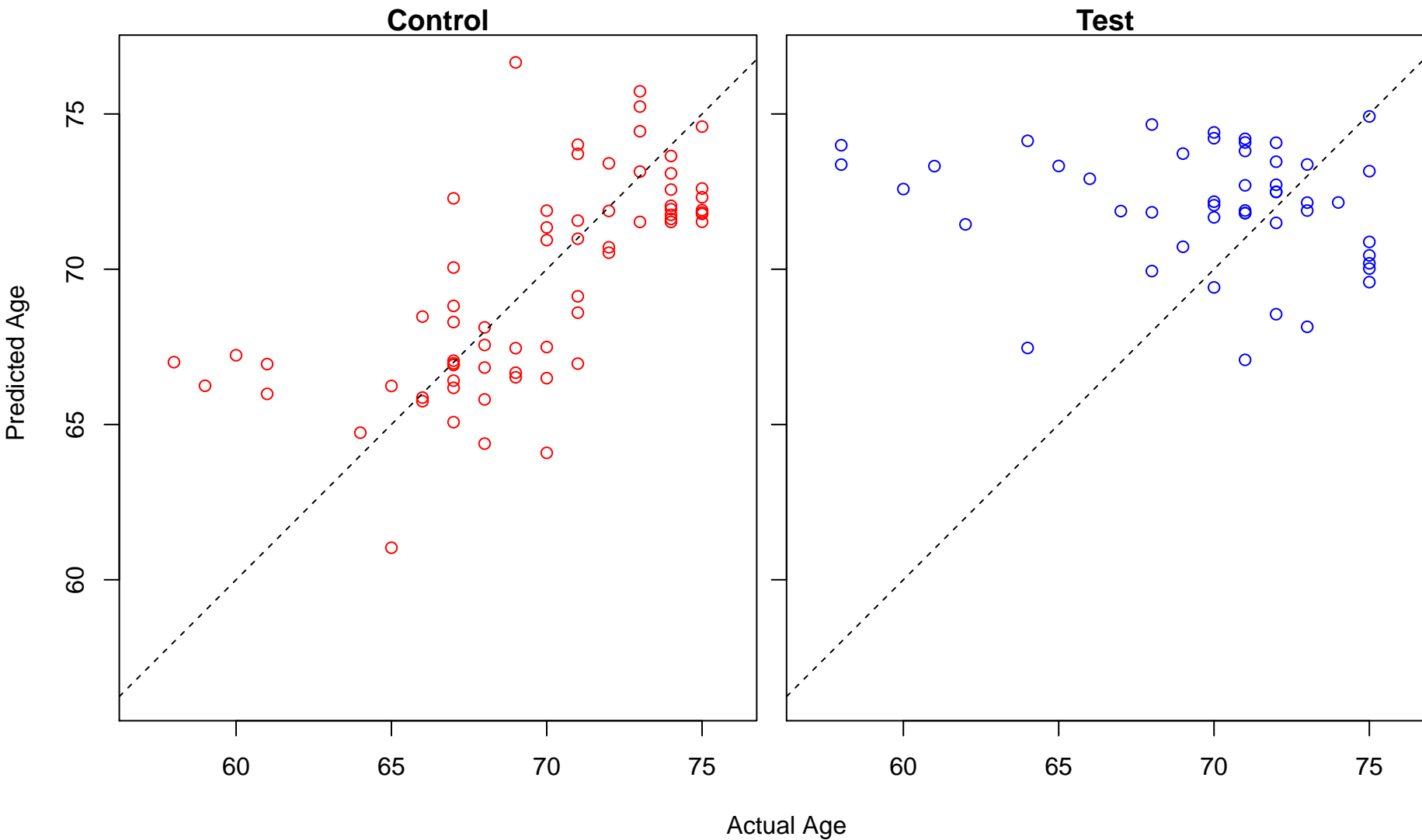
negative regulation of homotypic cell–cell adhesion (Score: 1.588933)



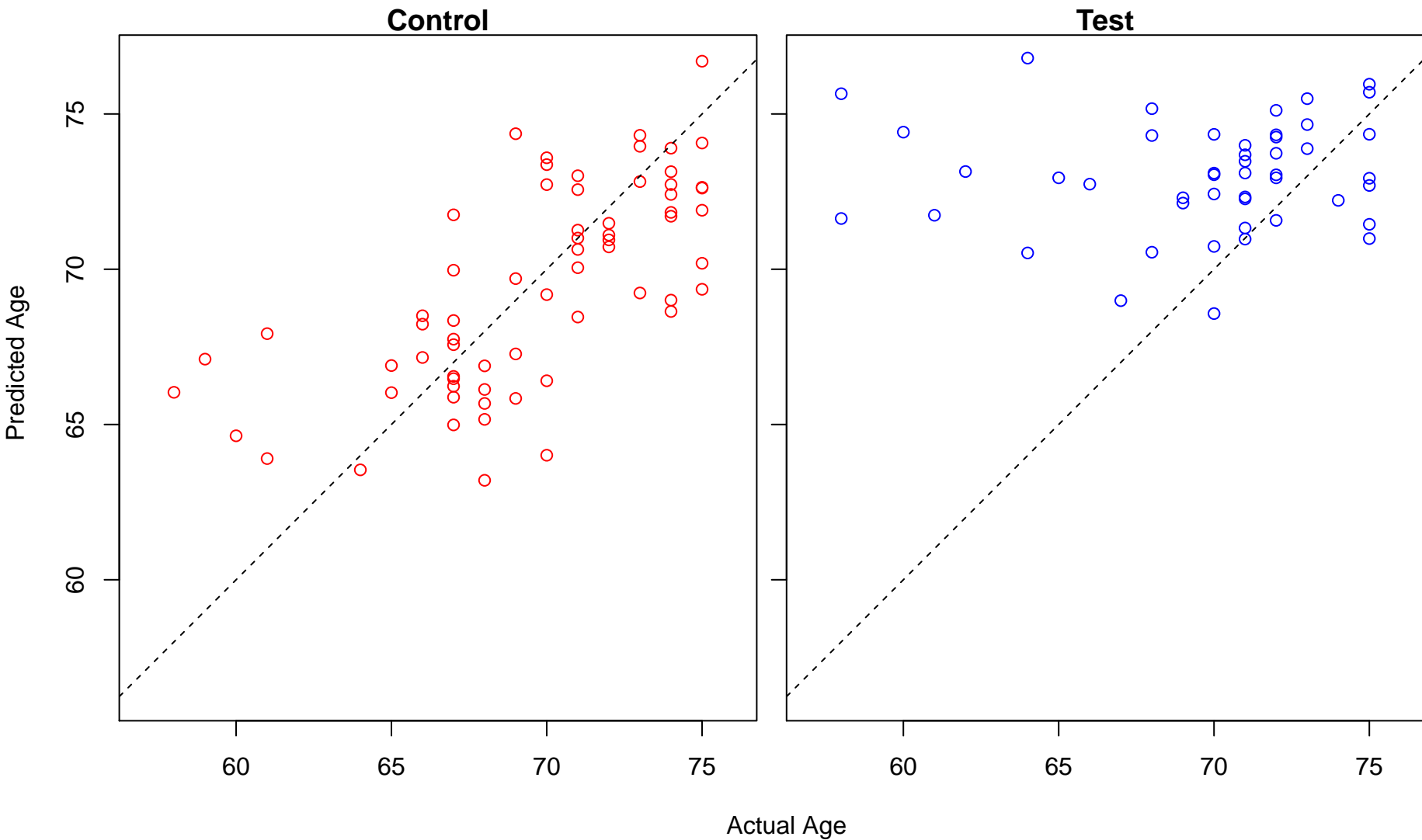
actin-mediated cell contraction (Score: 1.588587)



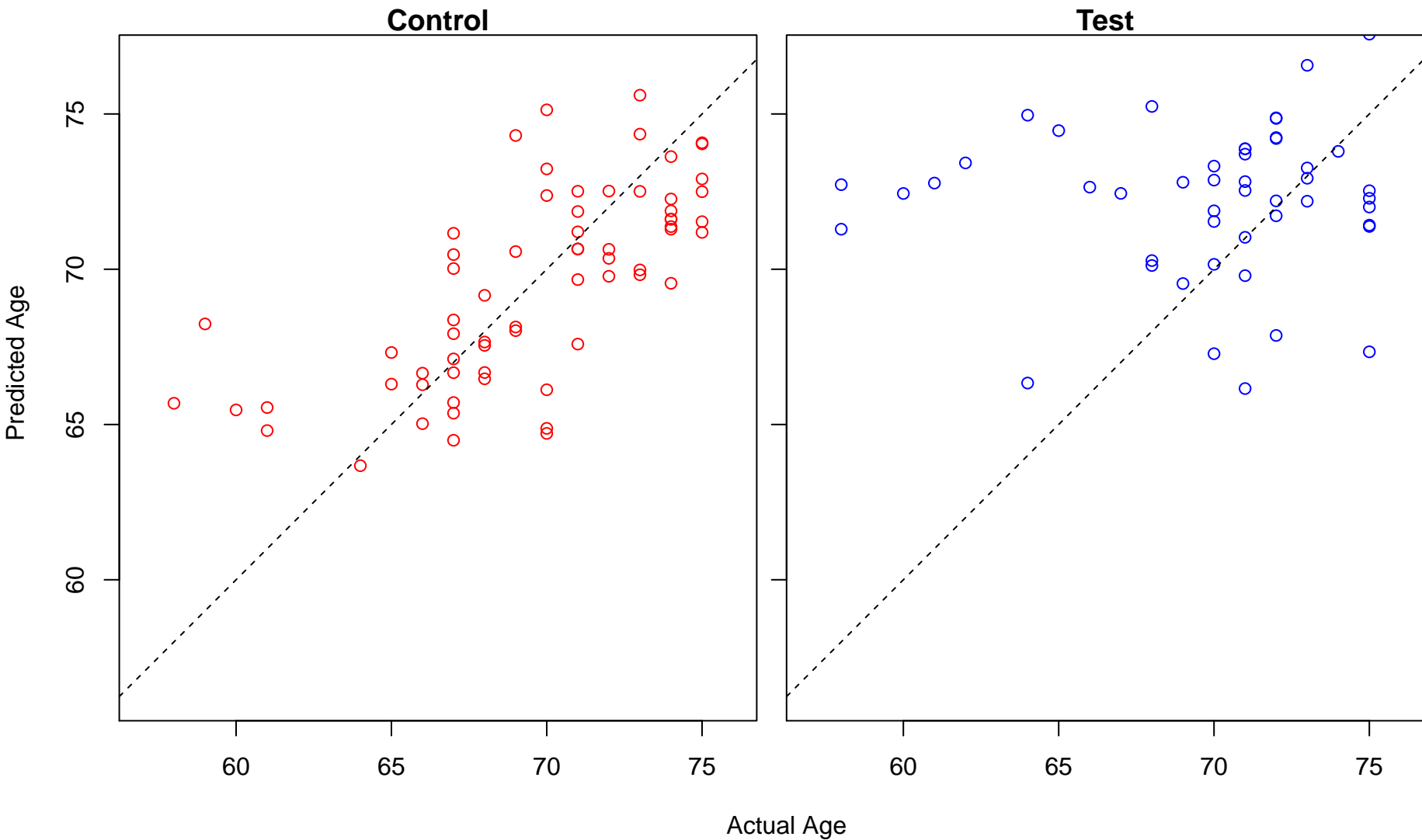
regulation of secretion (Score: 1.587850)



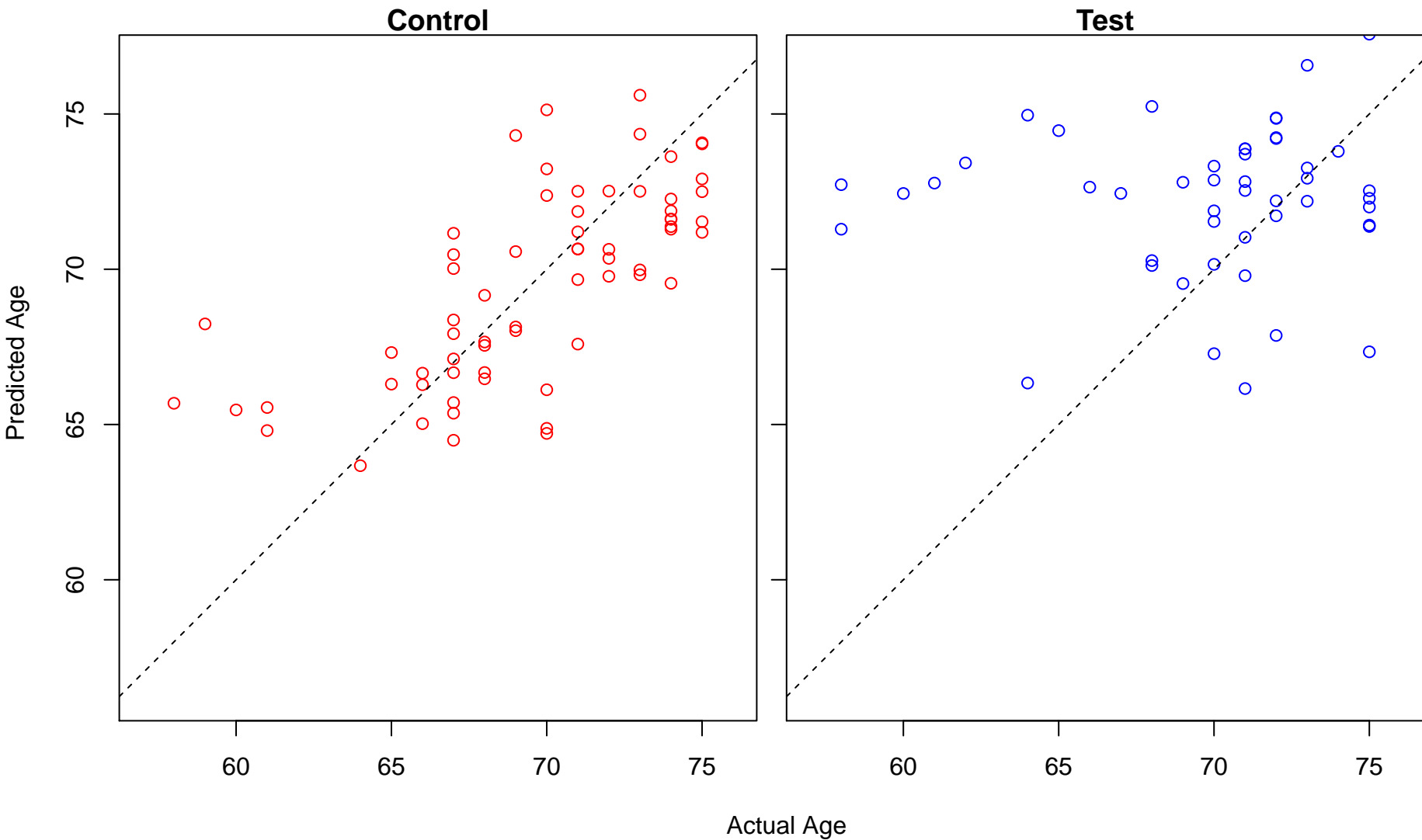
IRE1-mediated unfolded protein response (Score: 1.586760)



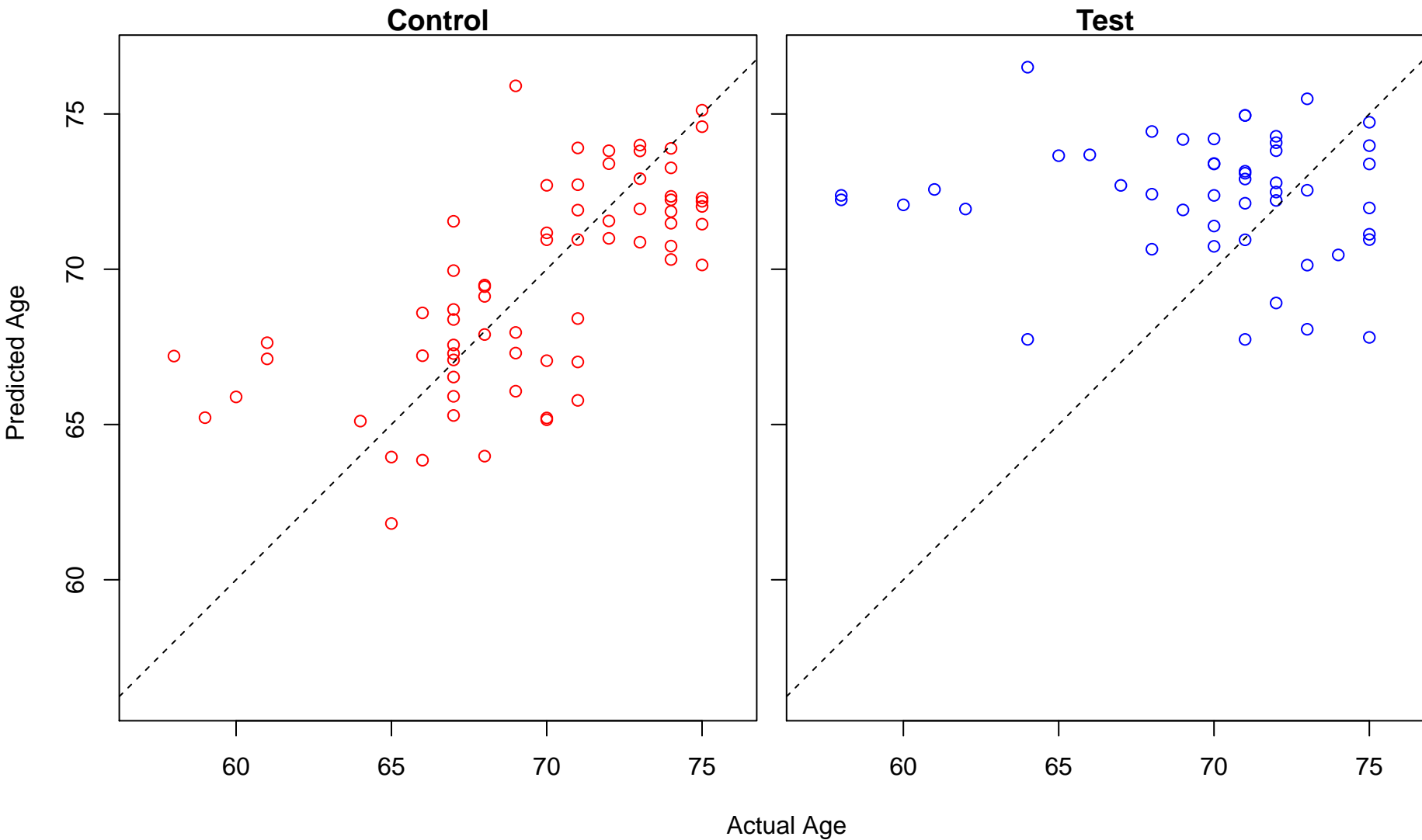
toll-like receptor 5 signaling pathway (Score: 1.586283)



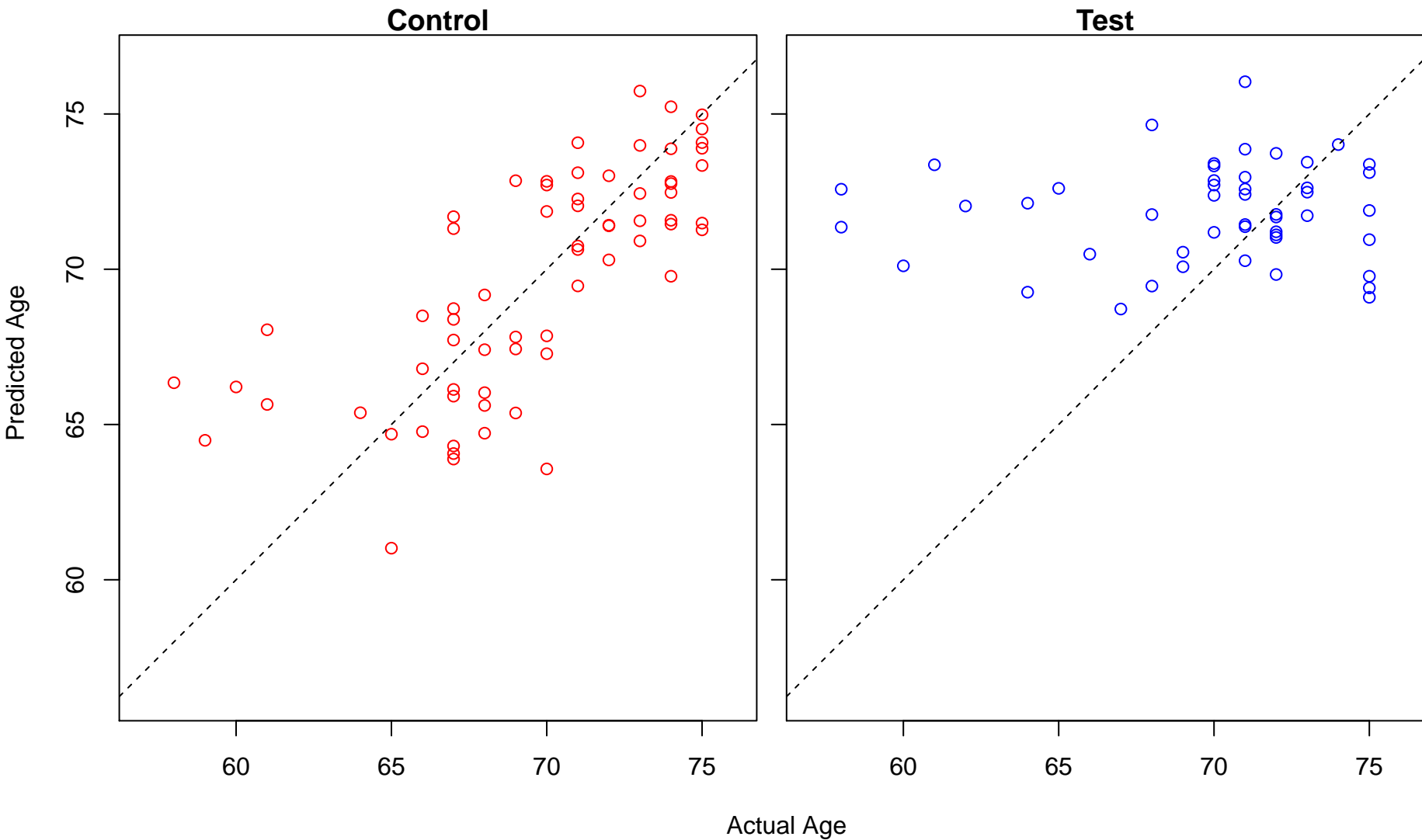
toll-like receptor 10 signaling pathway (Score: 1.586283)



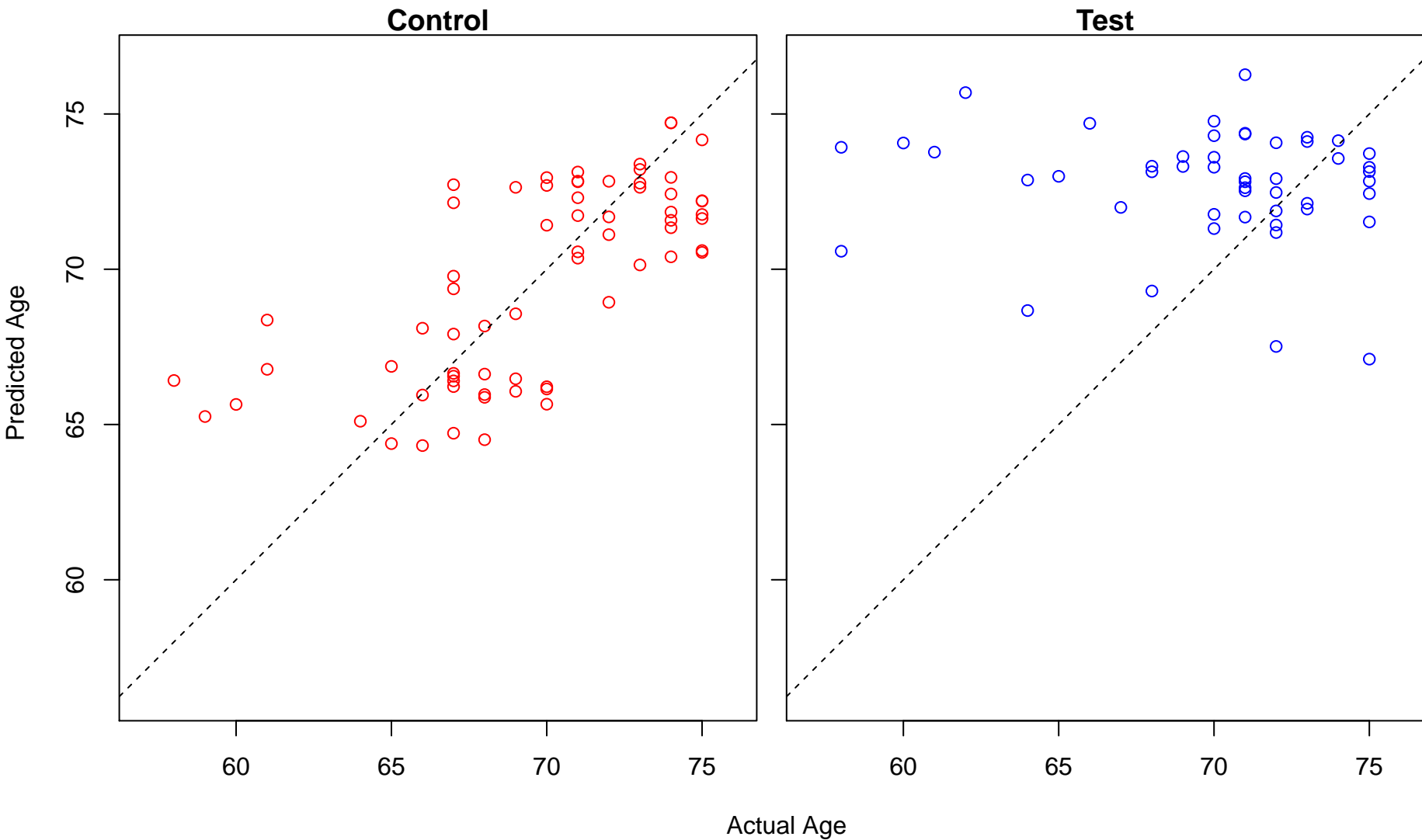
negative regulation of transport (Score: 1.585442)



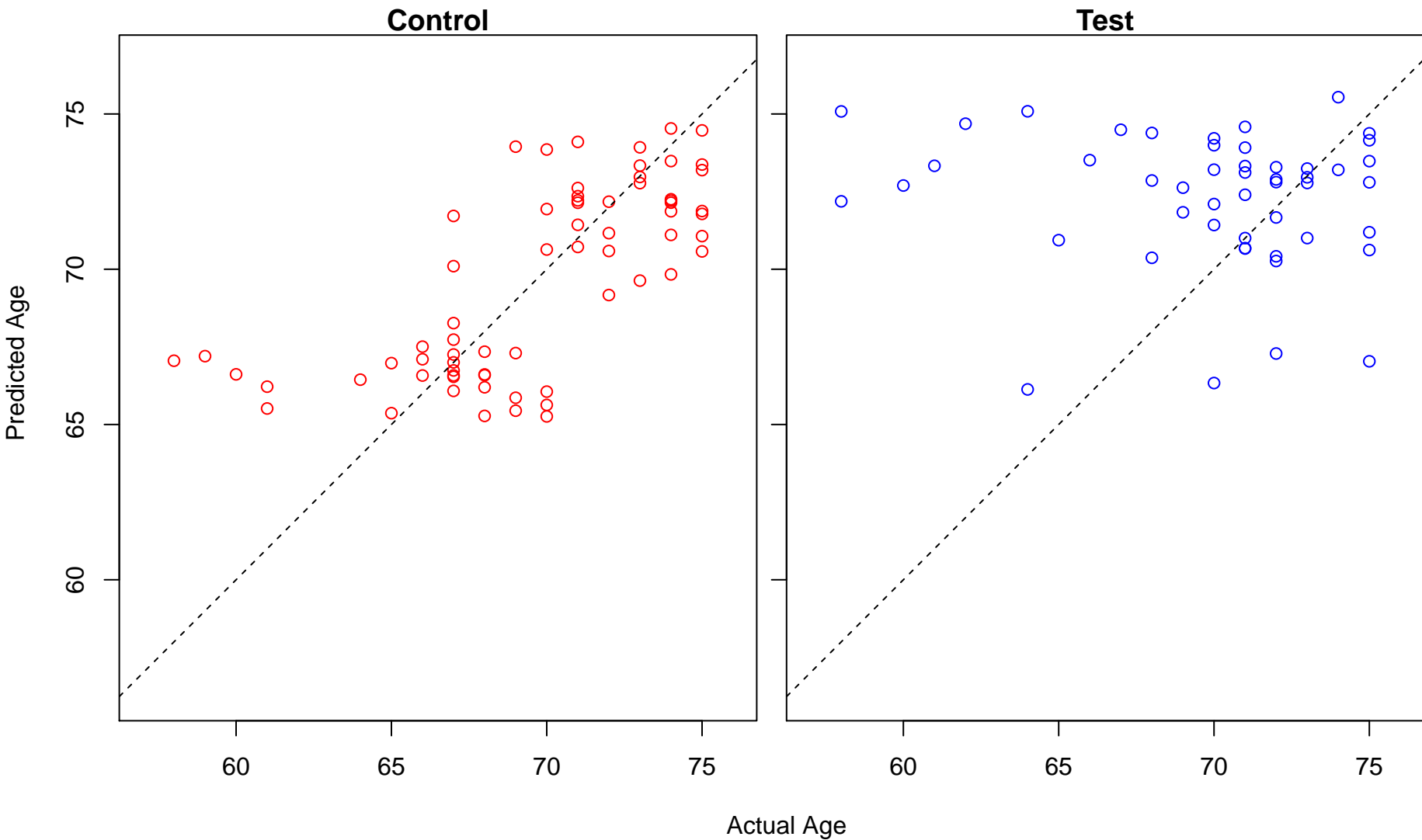
DNA damage response, signal transduction by p53 class mediator (Score: 1.585196)



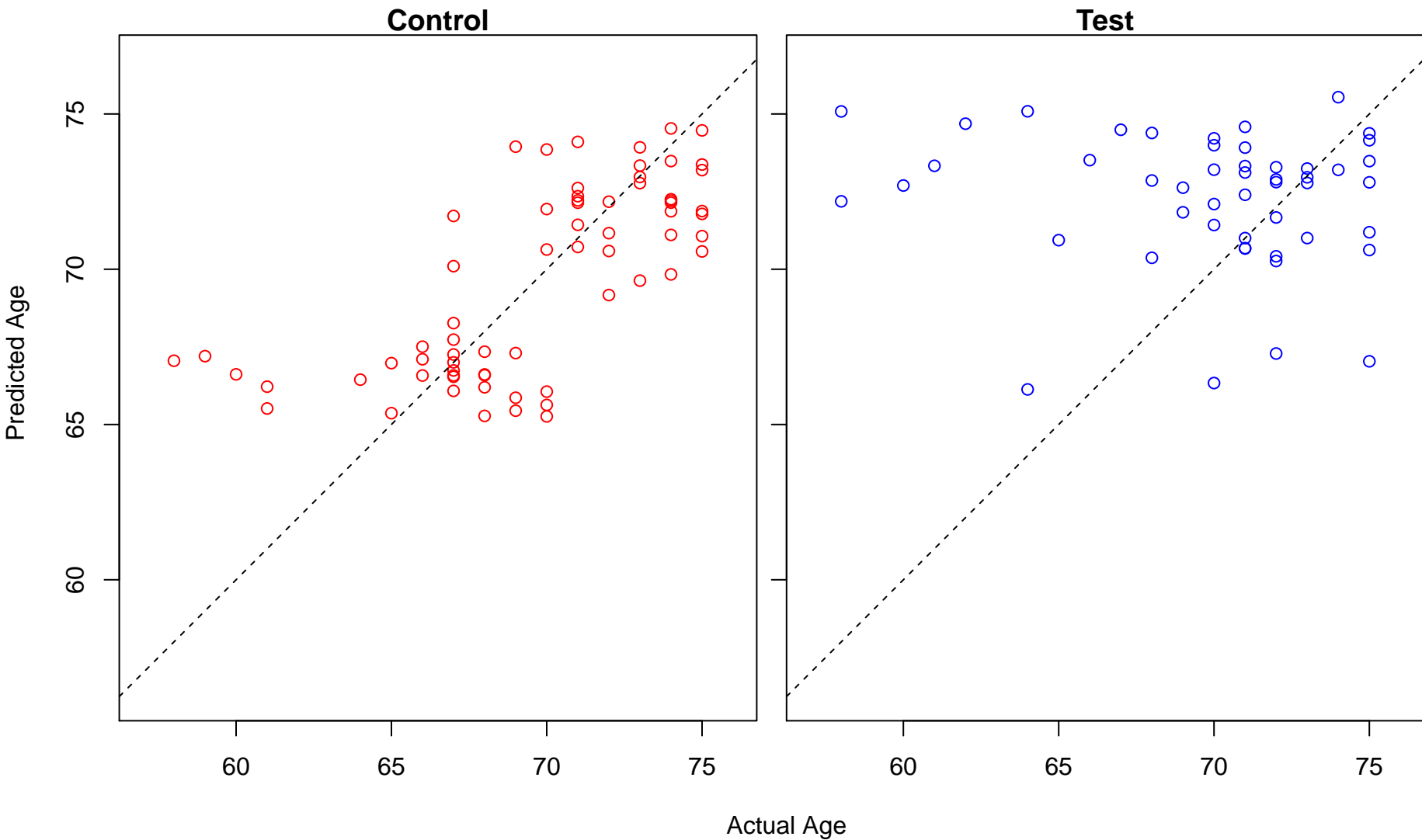
protein localization to cytoplasmic stress granule (Score: 1.584656)



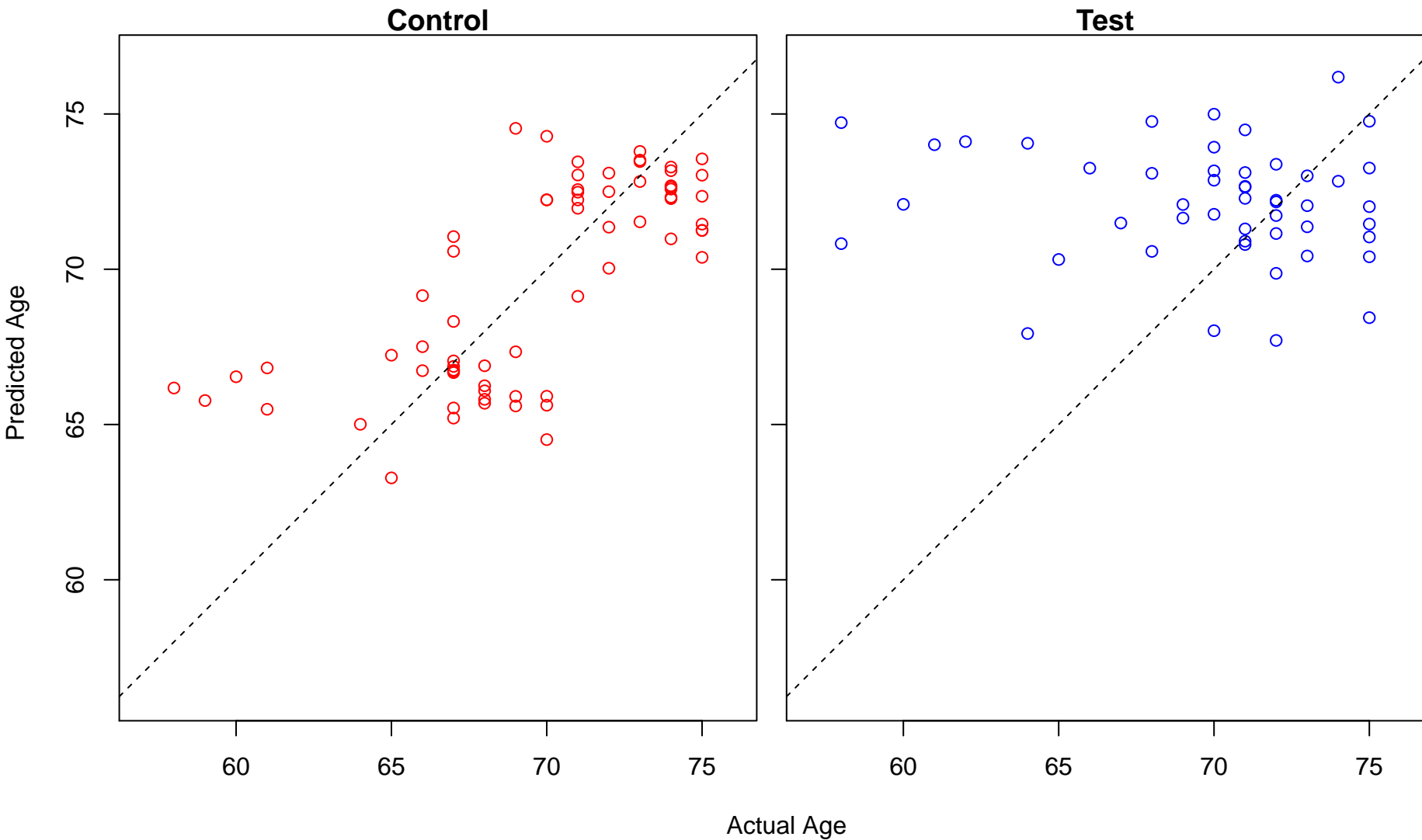
actin filament bundle assembly (Score: 1.584067)



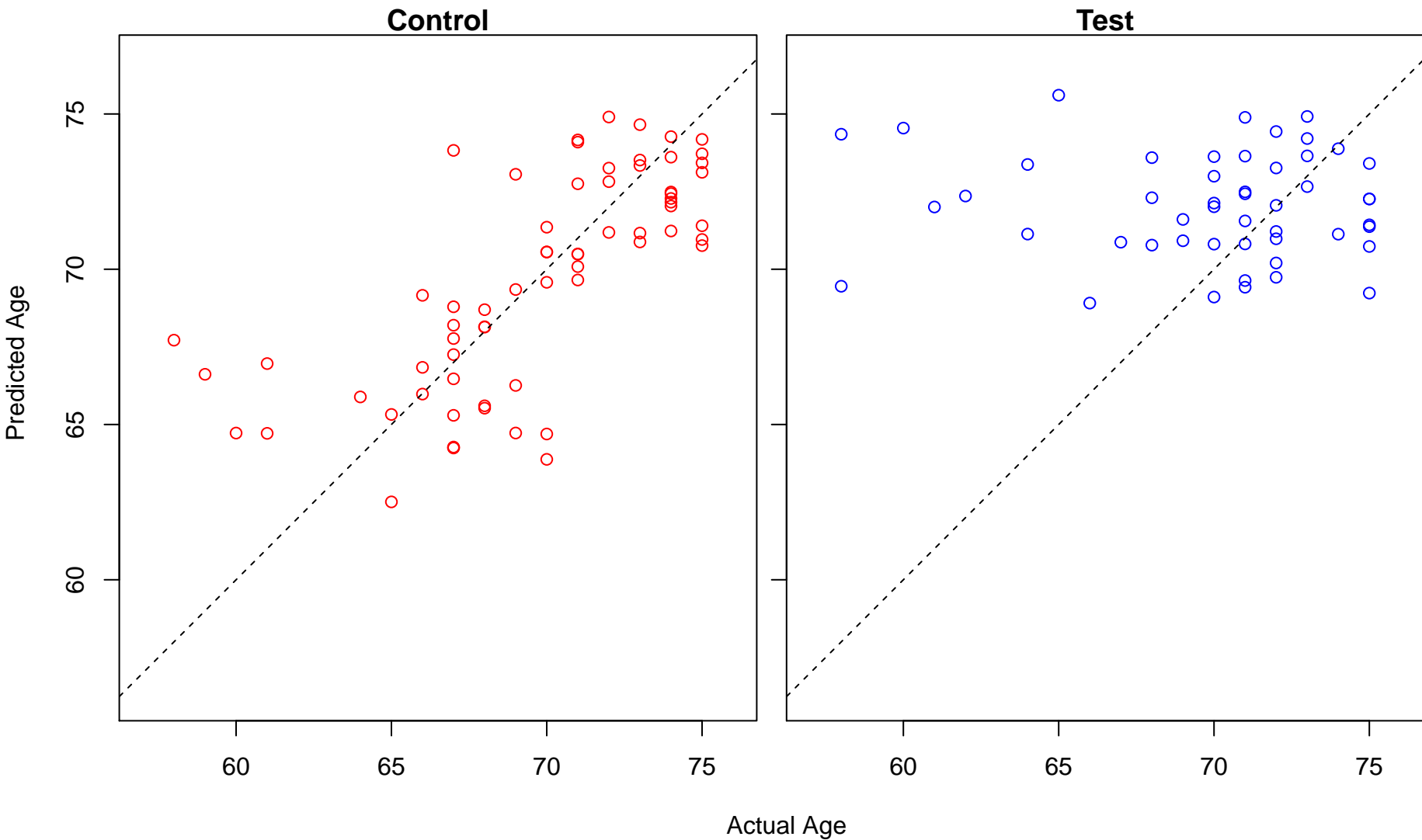
actin filament bundle organization (Score: 1.584067)



negative regulation of mitotic cell cycle phase transition (Score: 1.583421)

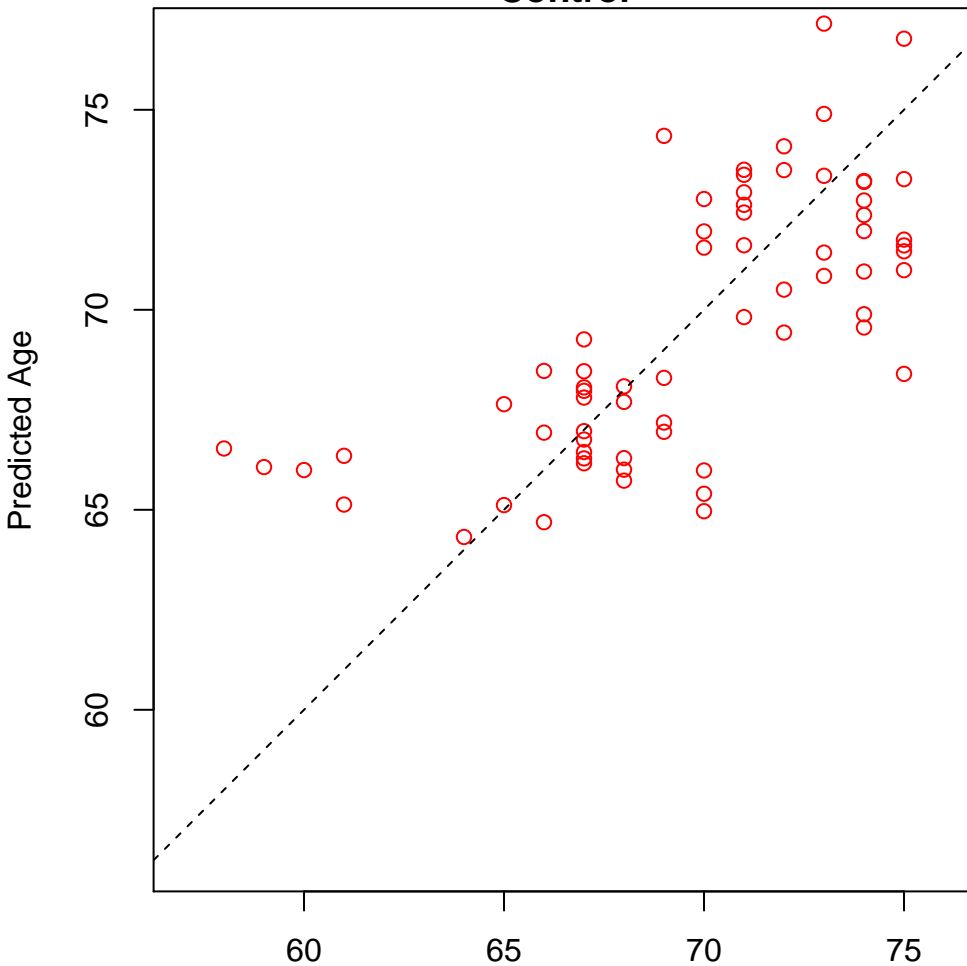


RNA export from nucleus (Score: 1.583287)

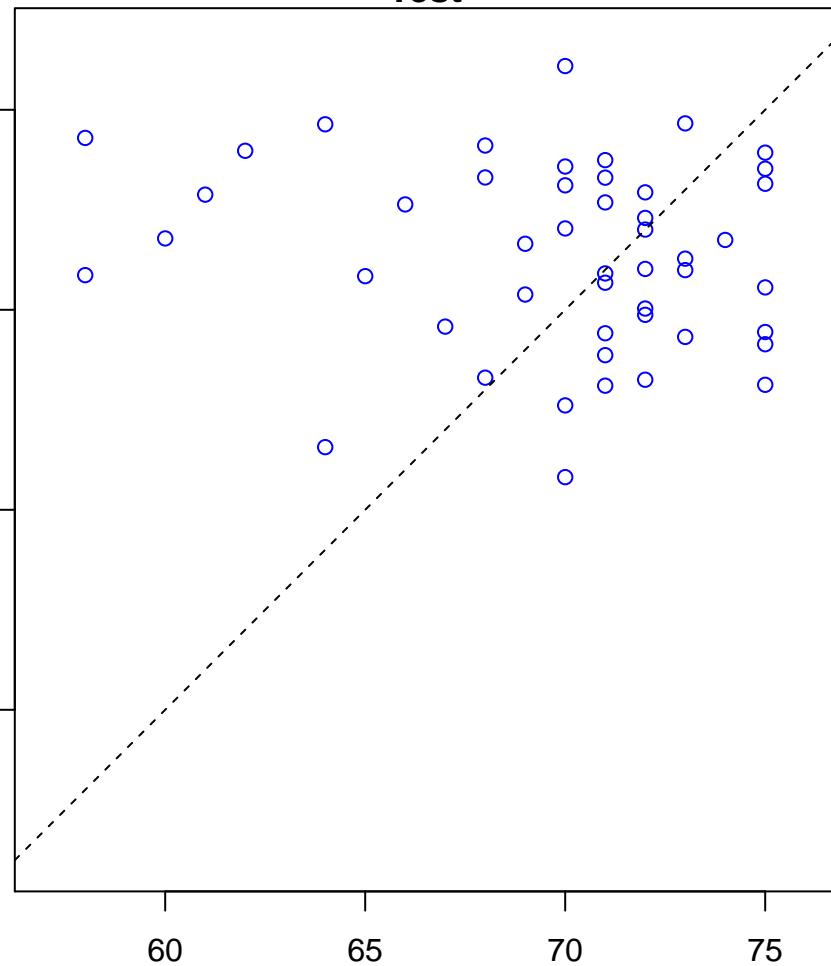


monocarboxylic acid catabolic process (Score: 1.583023)

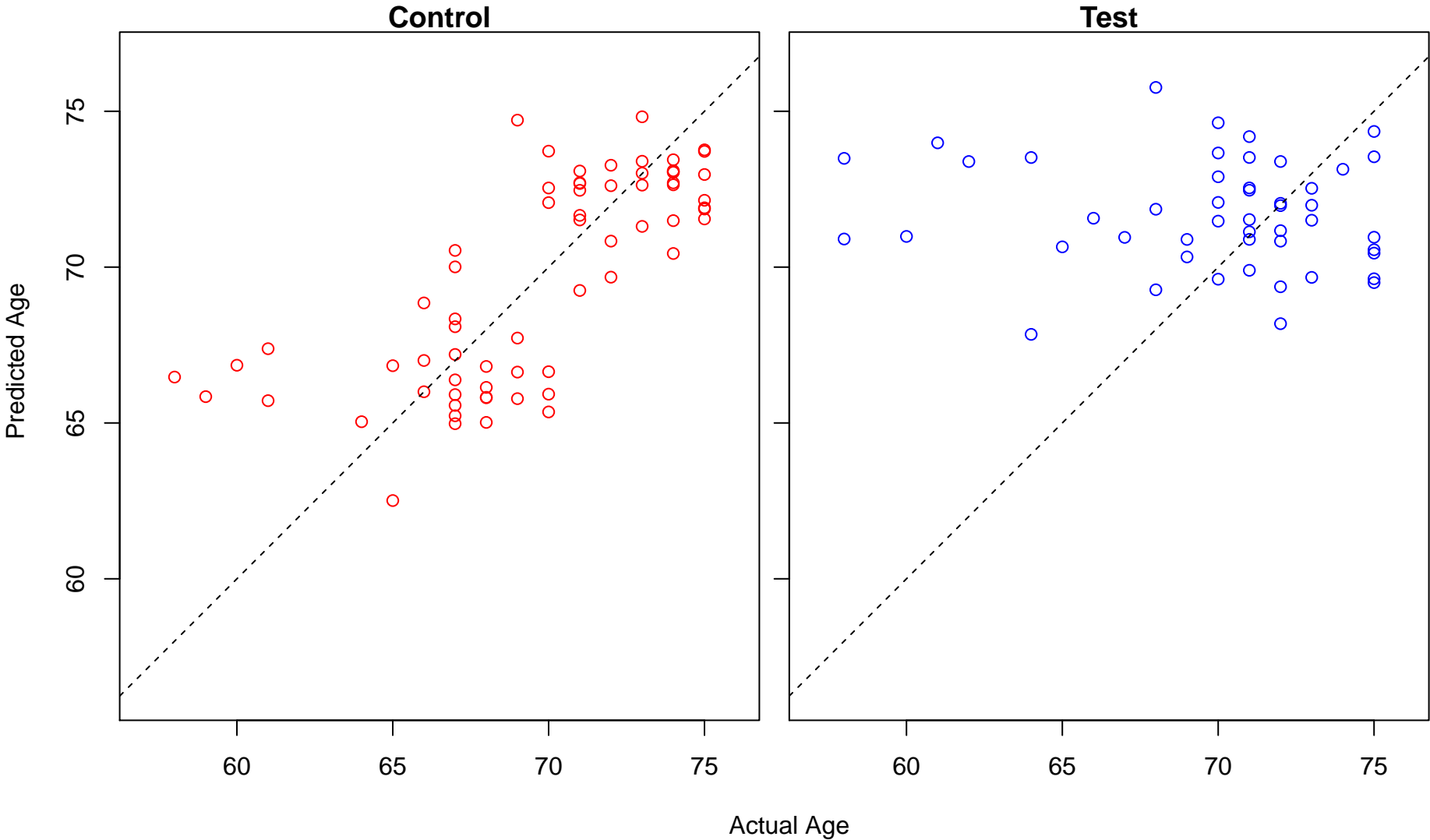
Control



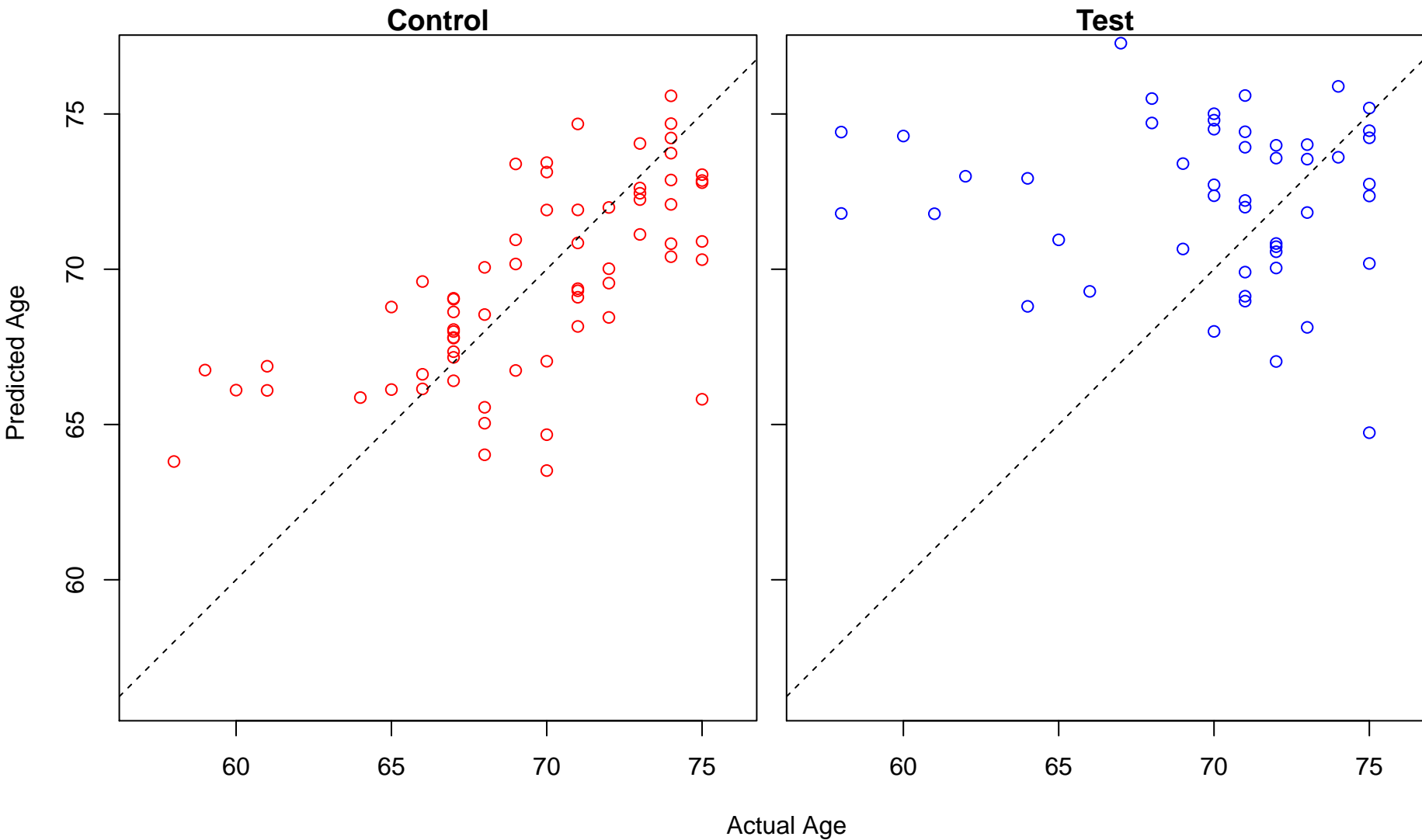
Test



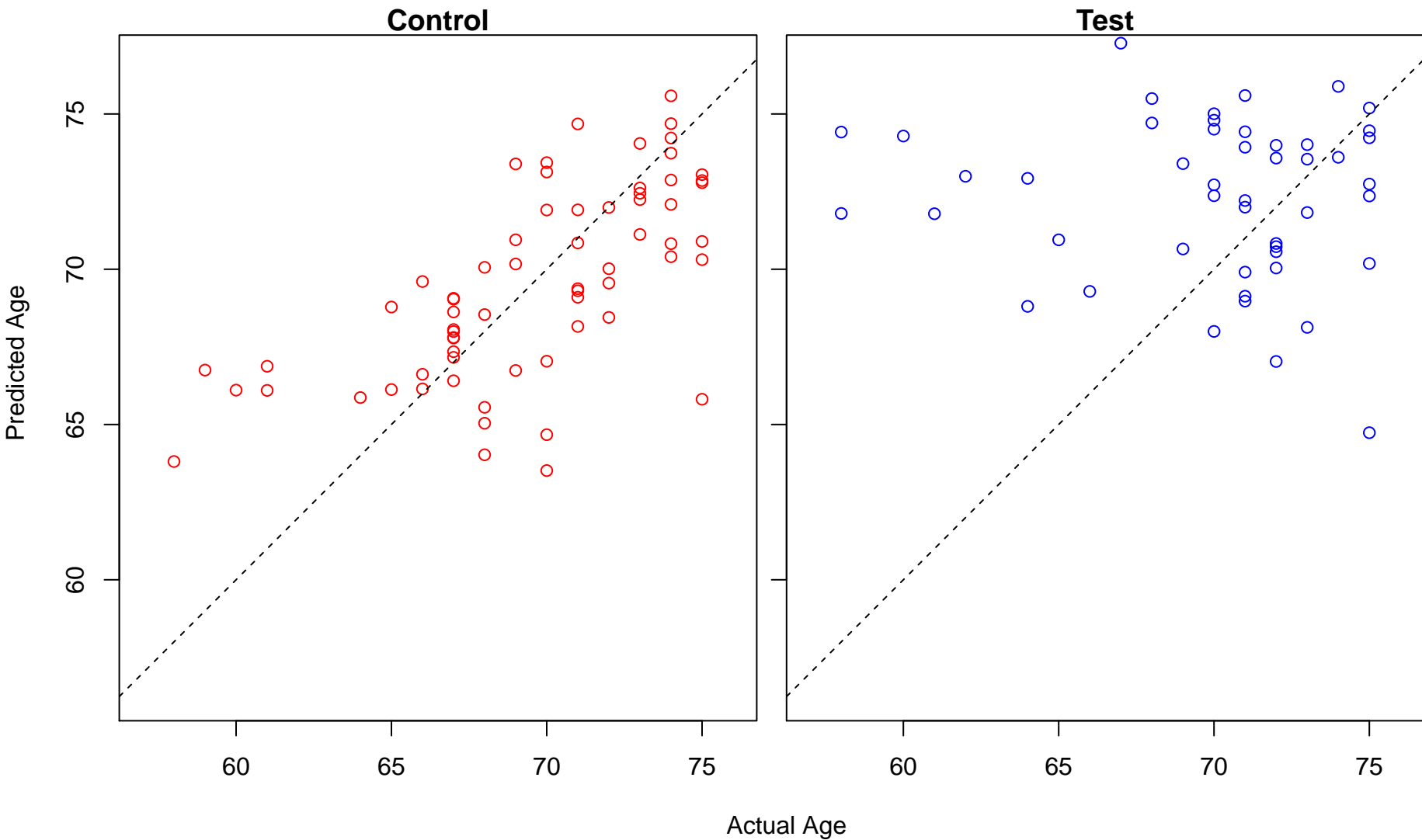
Actual Age



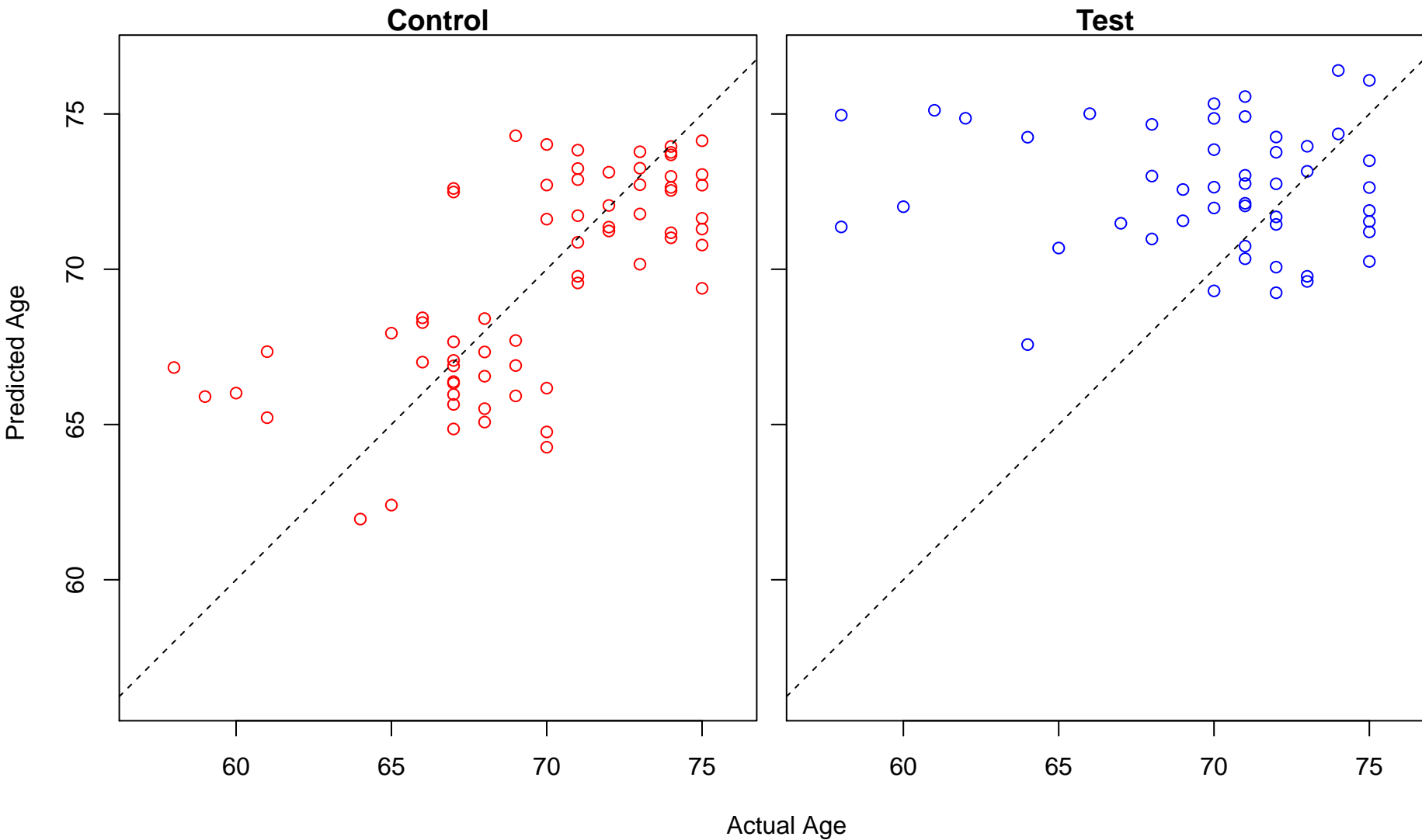
cholesterol homeostasis (Score: 1.582591)



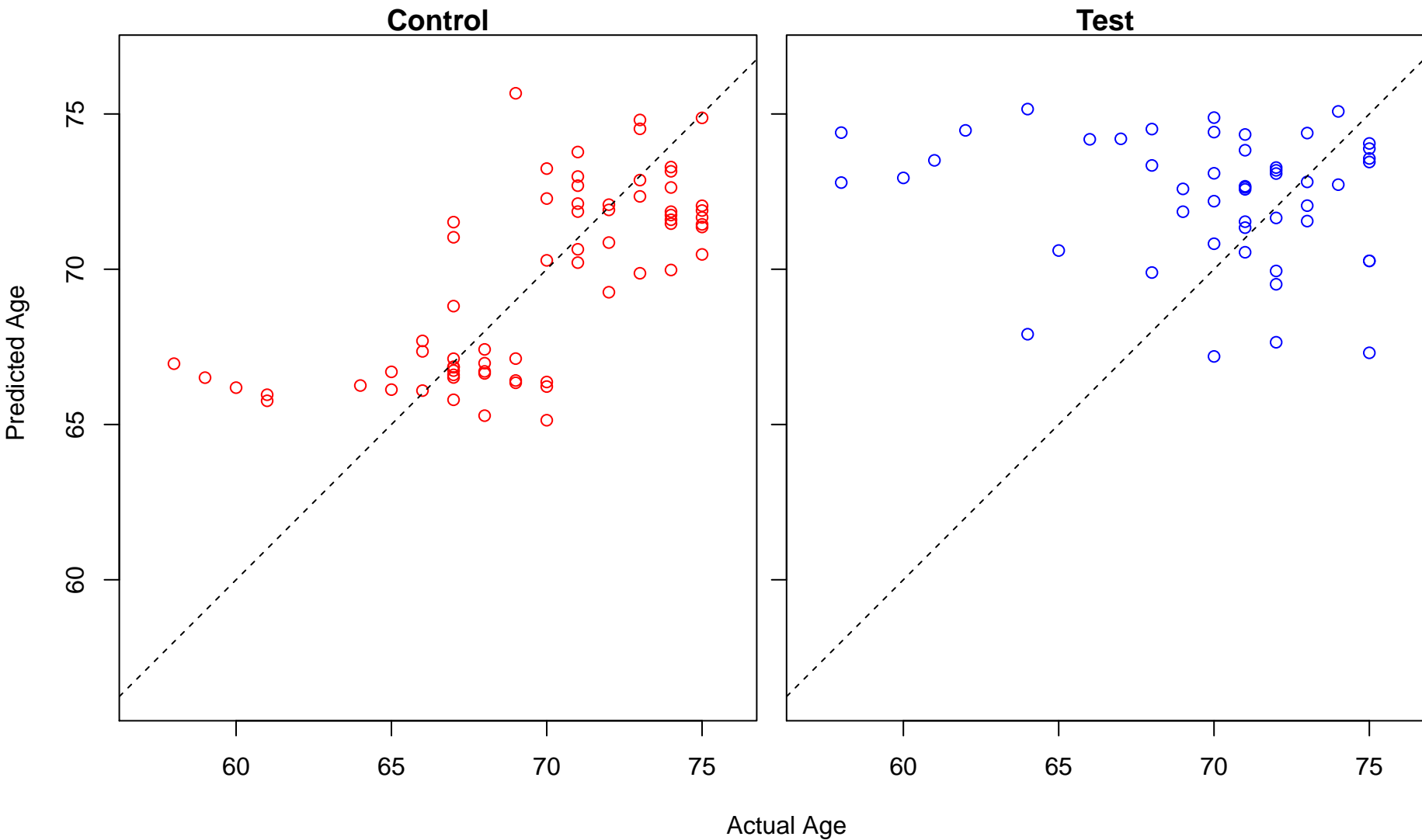
sterol homeostasis (Score: 1.582591)



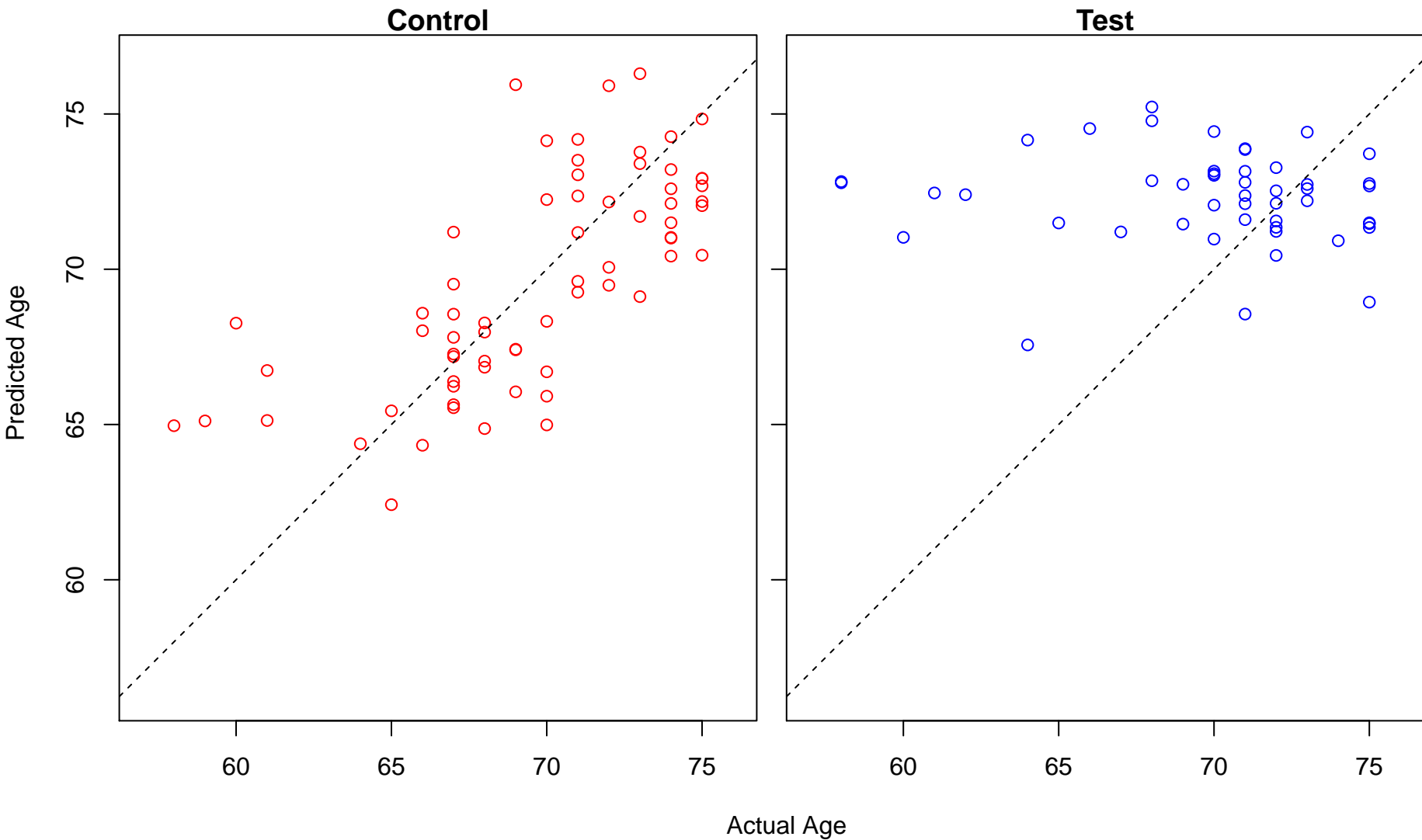
regulation of type I interferon production (Score: 1.582309)



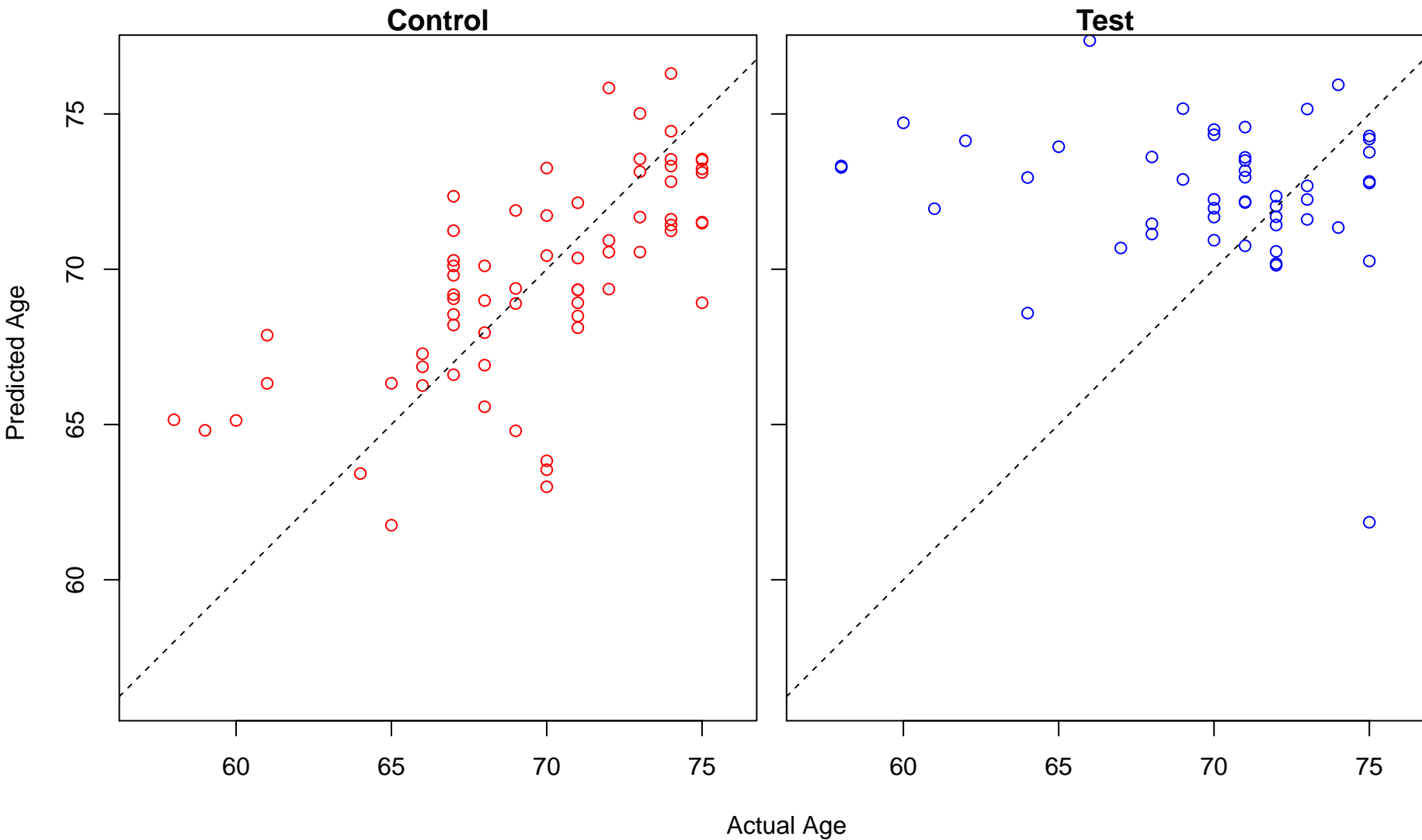
cell projection assembly (Score: 1.581396)



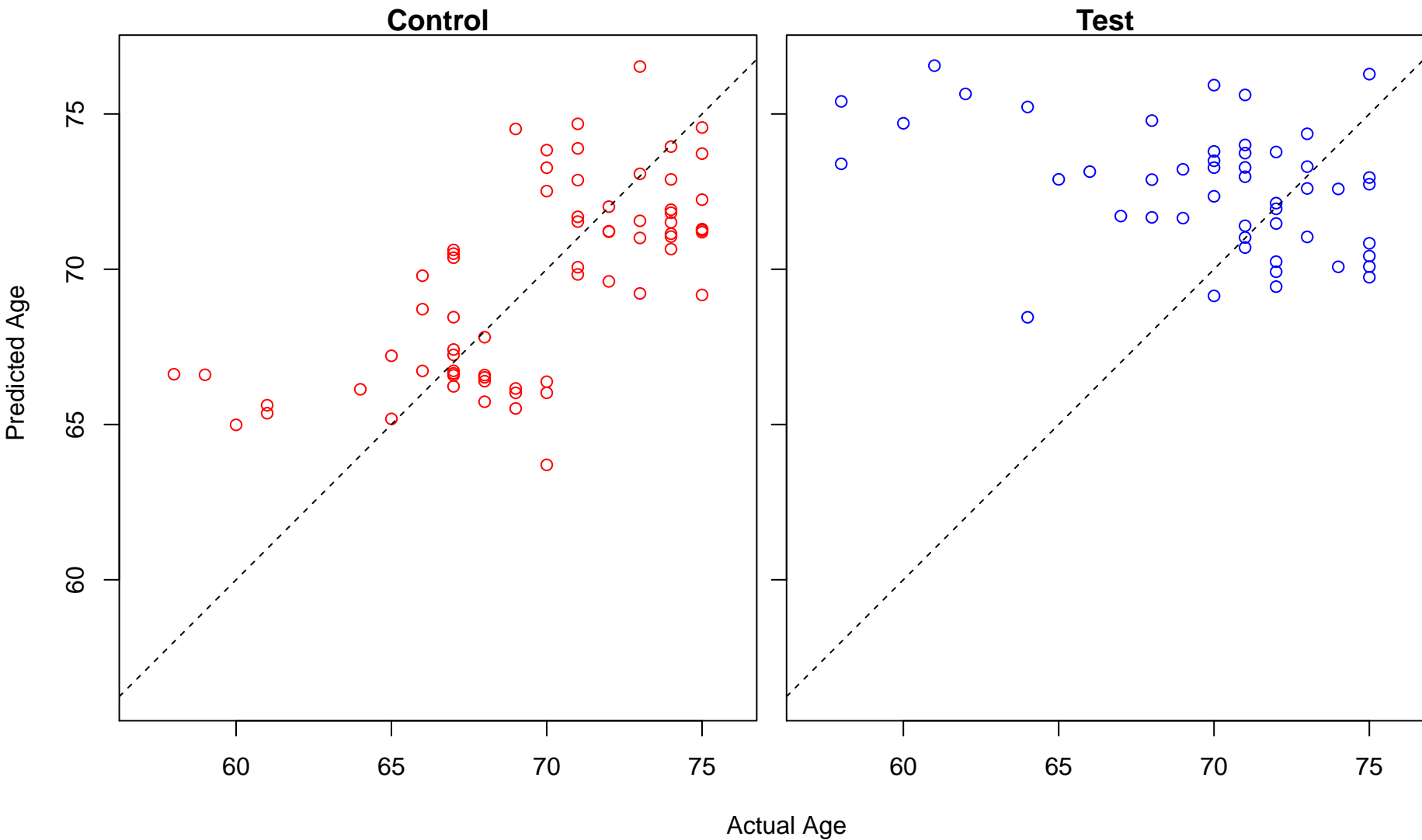
secretion (Score: 1.581235)



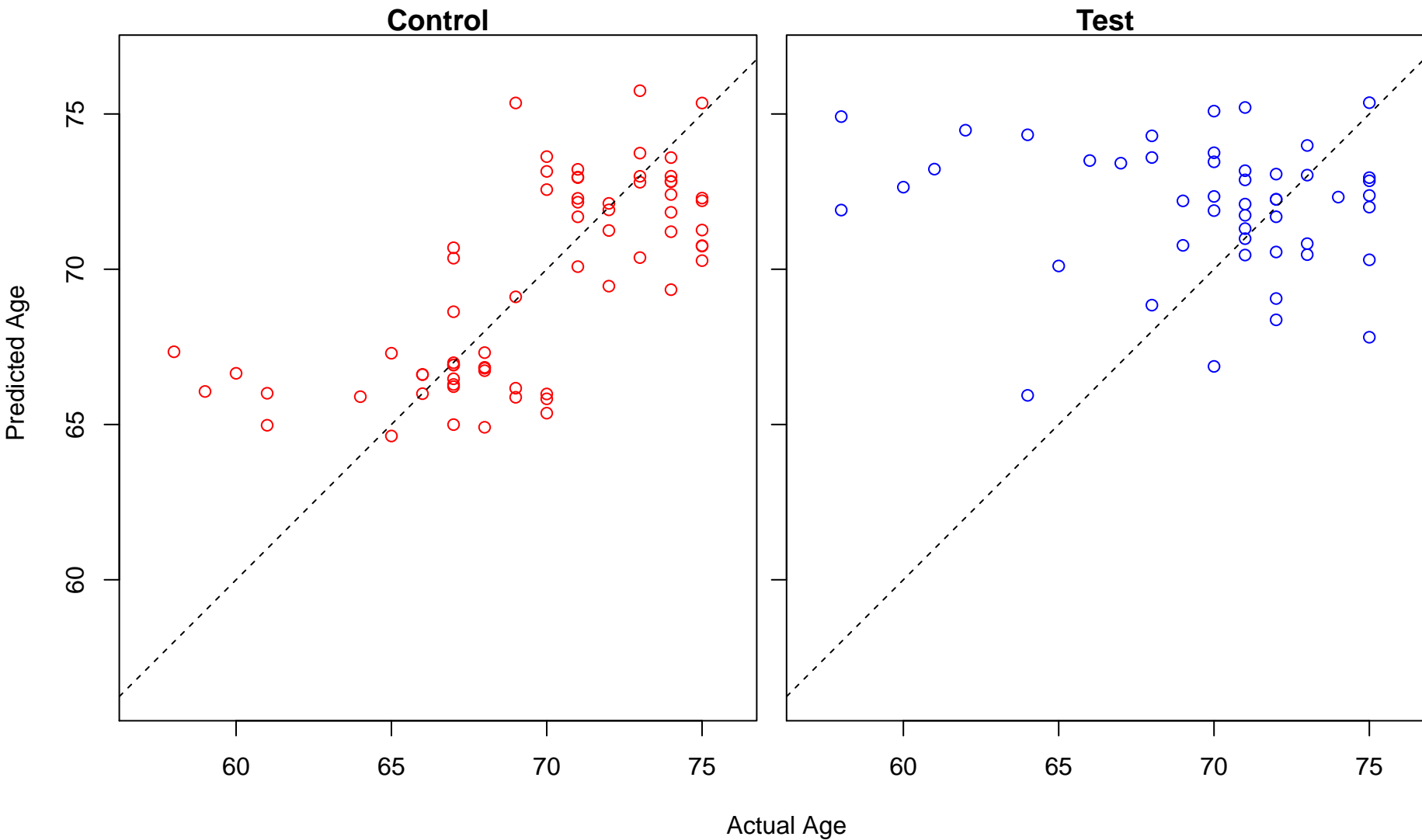
regulation of bone remodeling (Score: 1.581112)



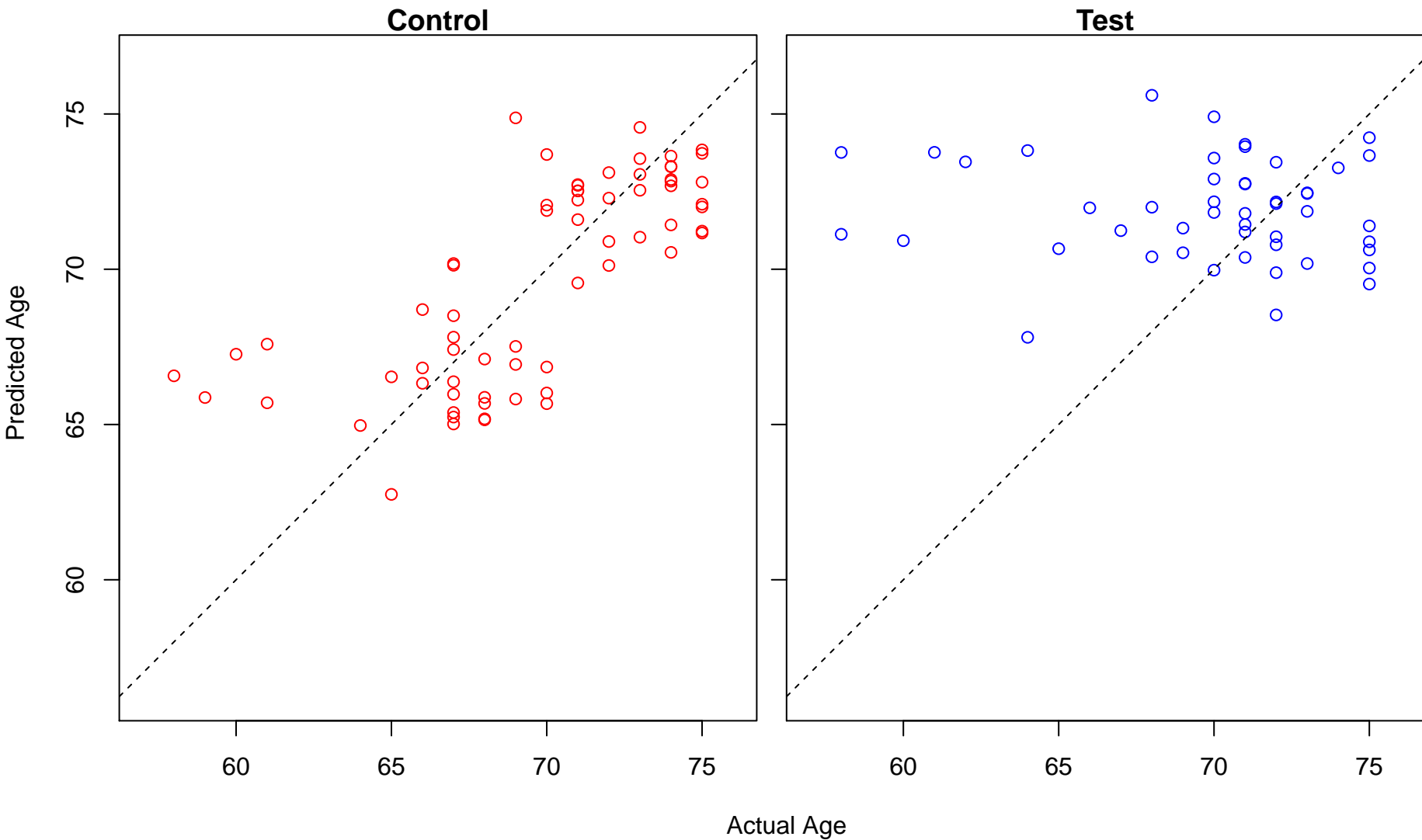
renal water homeostasis (Score: 1.581018)



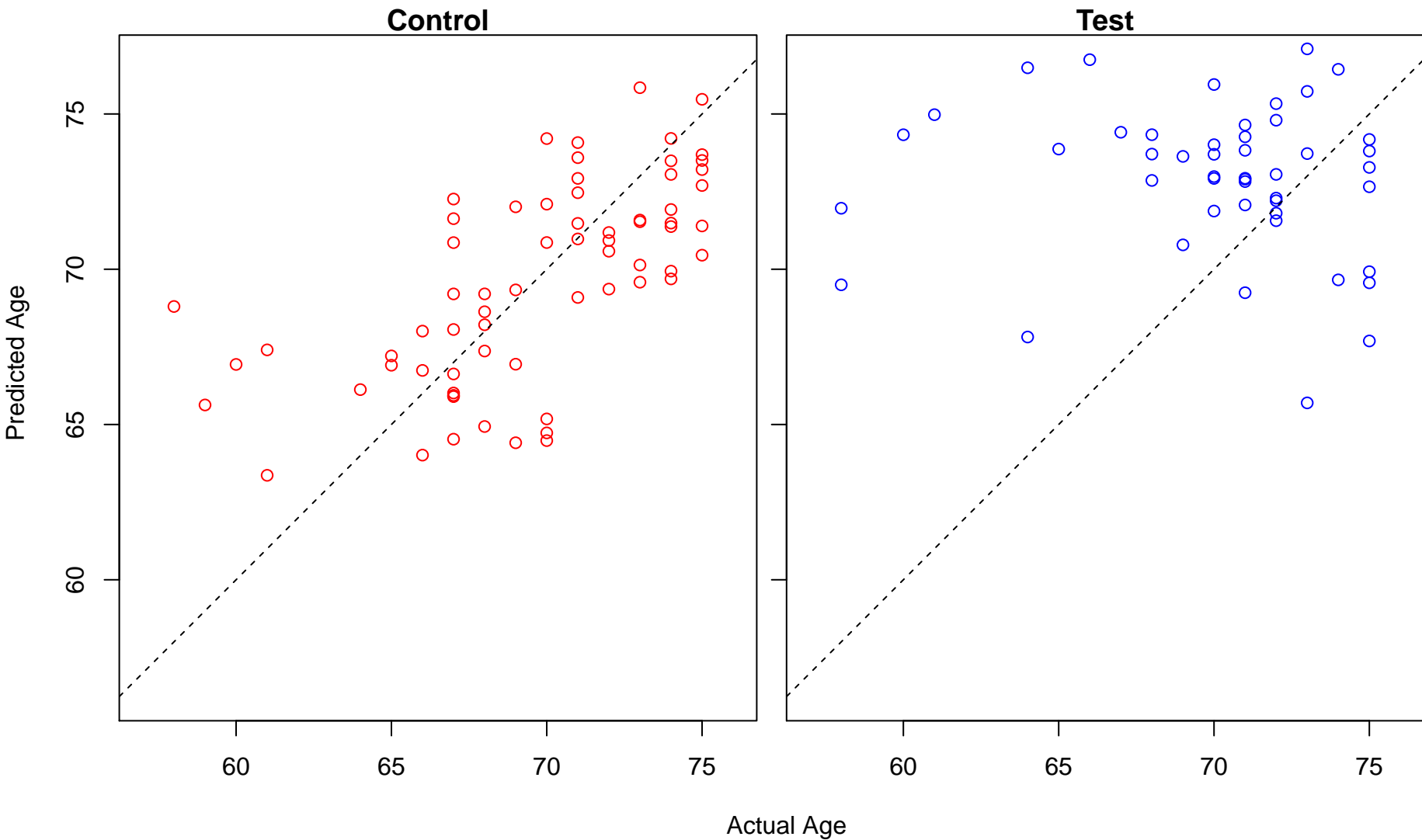
endocytosis (Score: 1.580655)



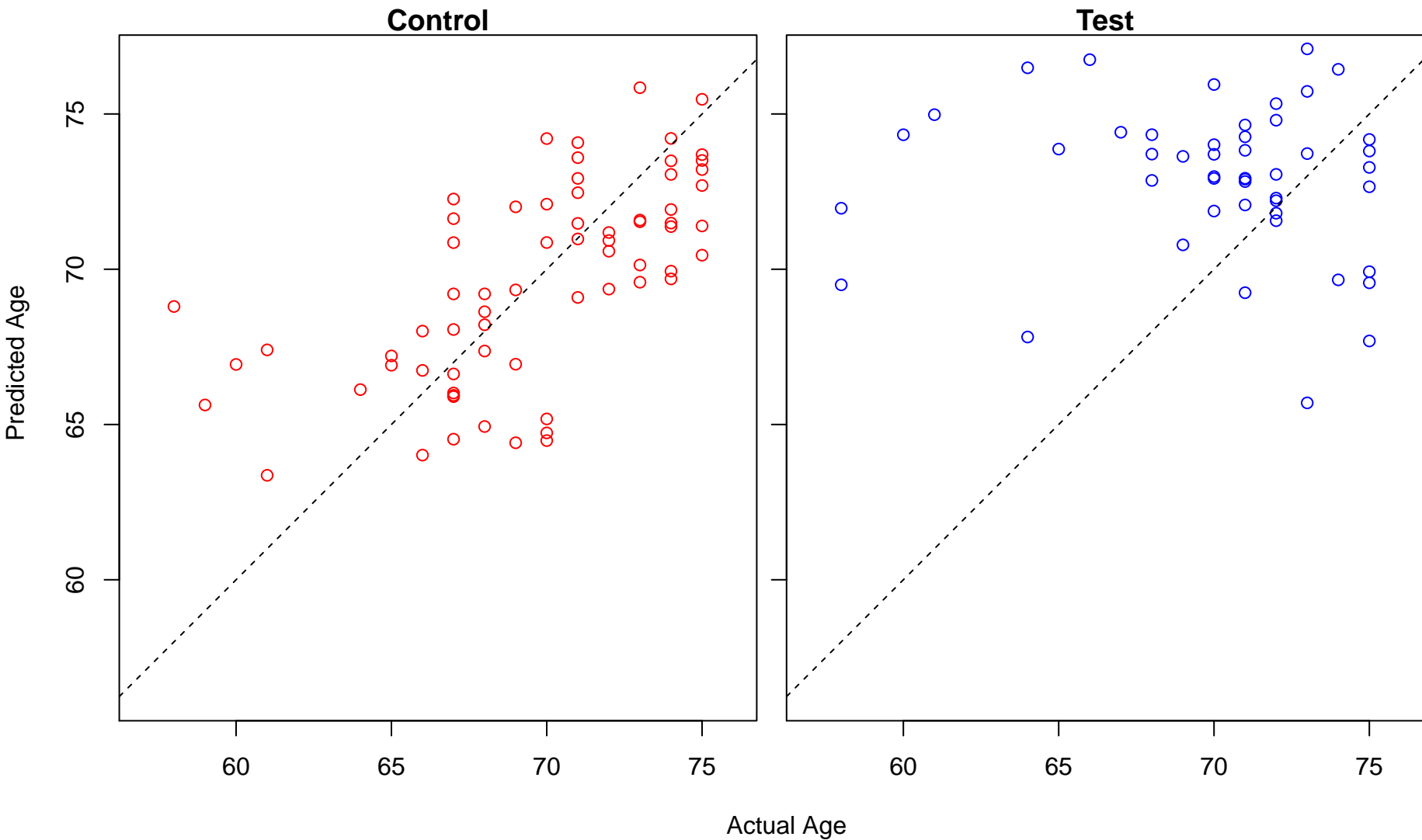
NIK/NF-kappaB signaling (Score: 1.580537)



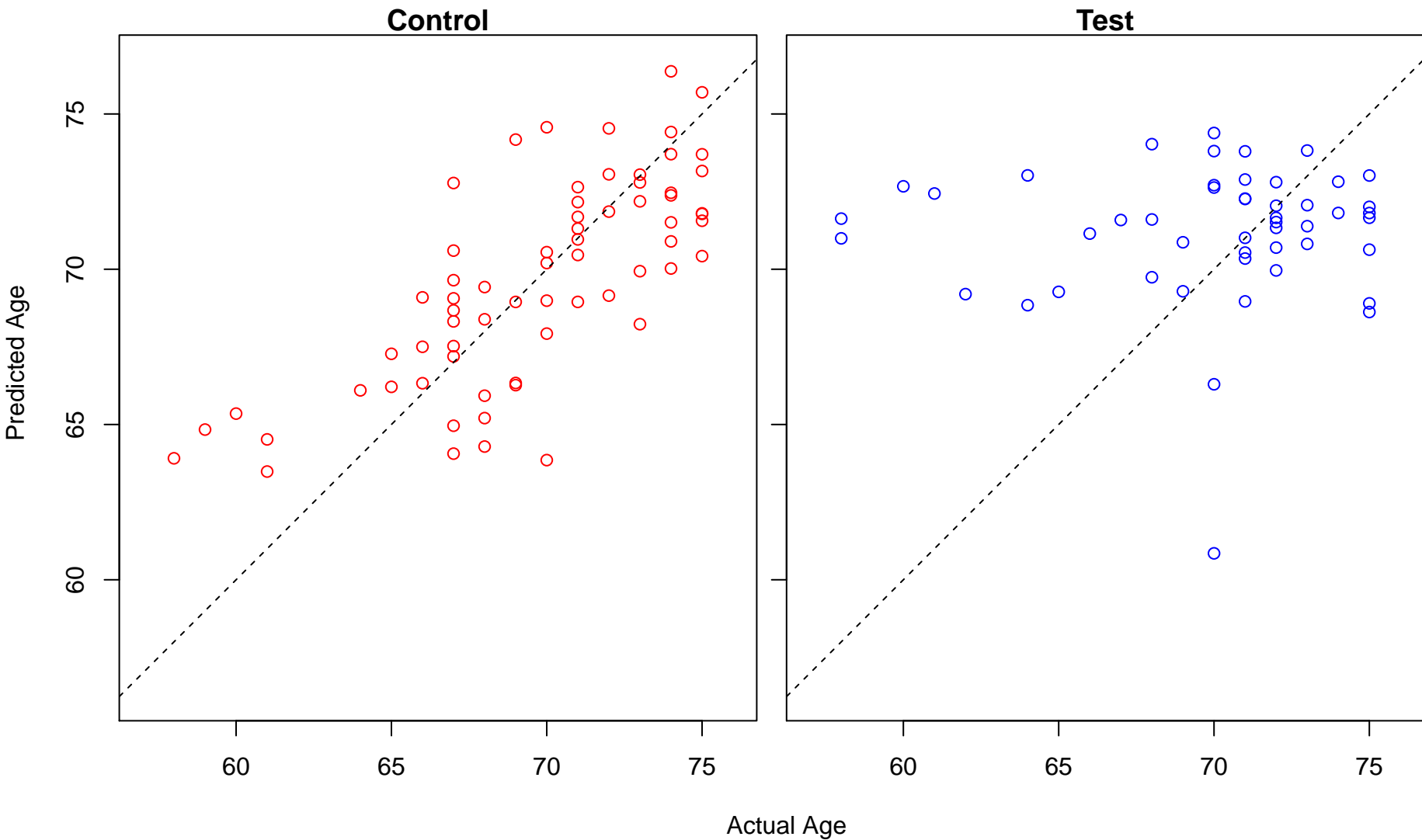
negative regulation of transforming growth factor beta receptor signaling pathway (Score: 1.58047)



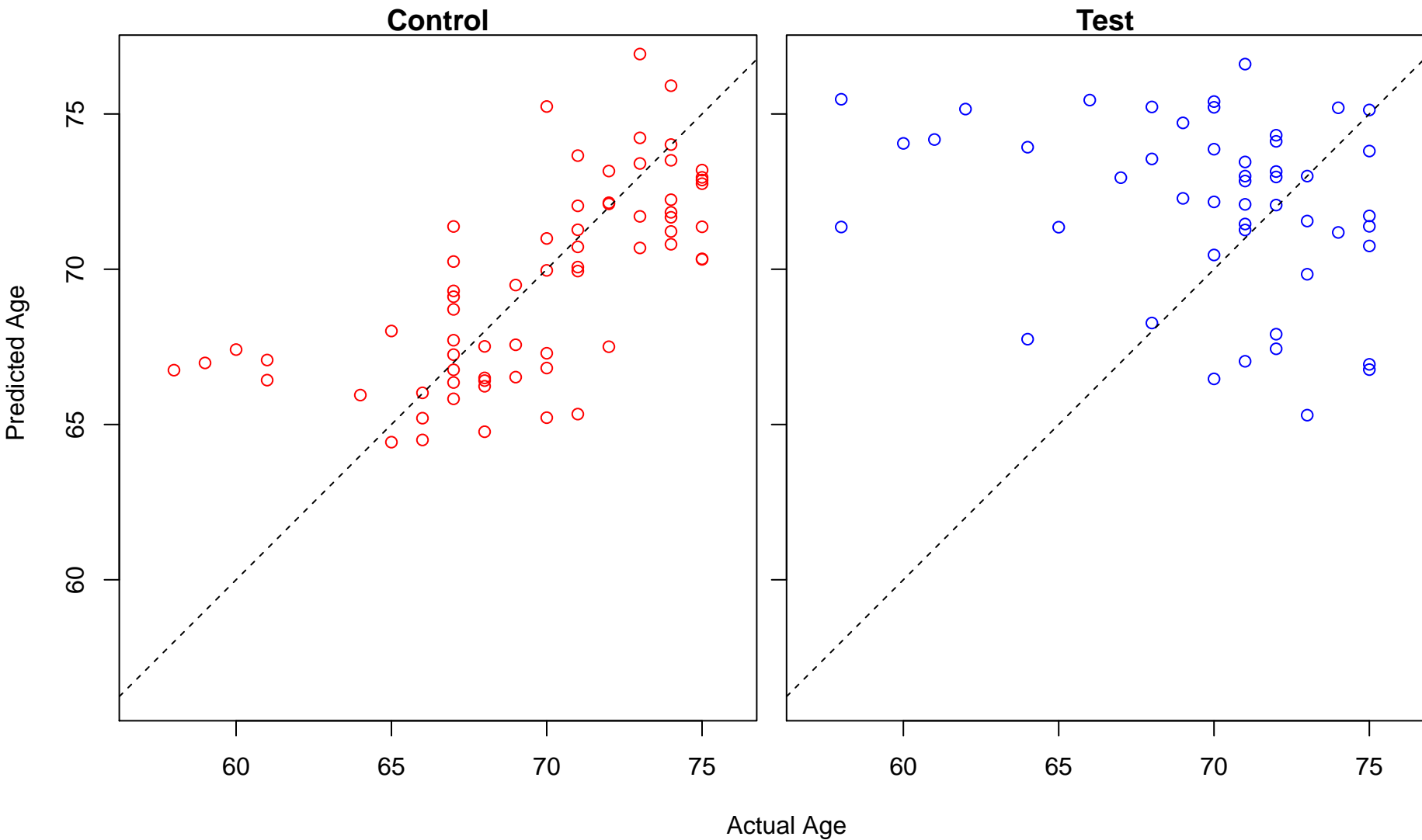
negative regulation of cellular response to transforming growth factor beta stimulus (Score: 1.58047)



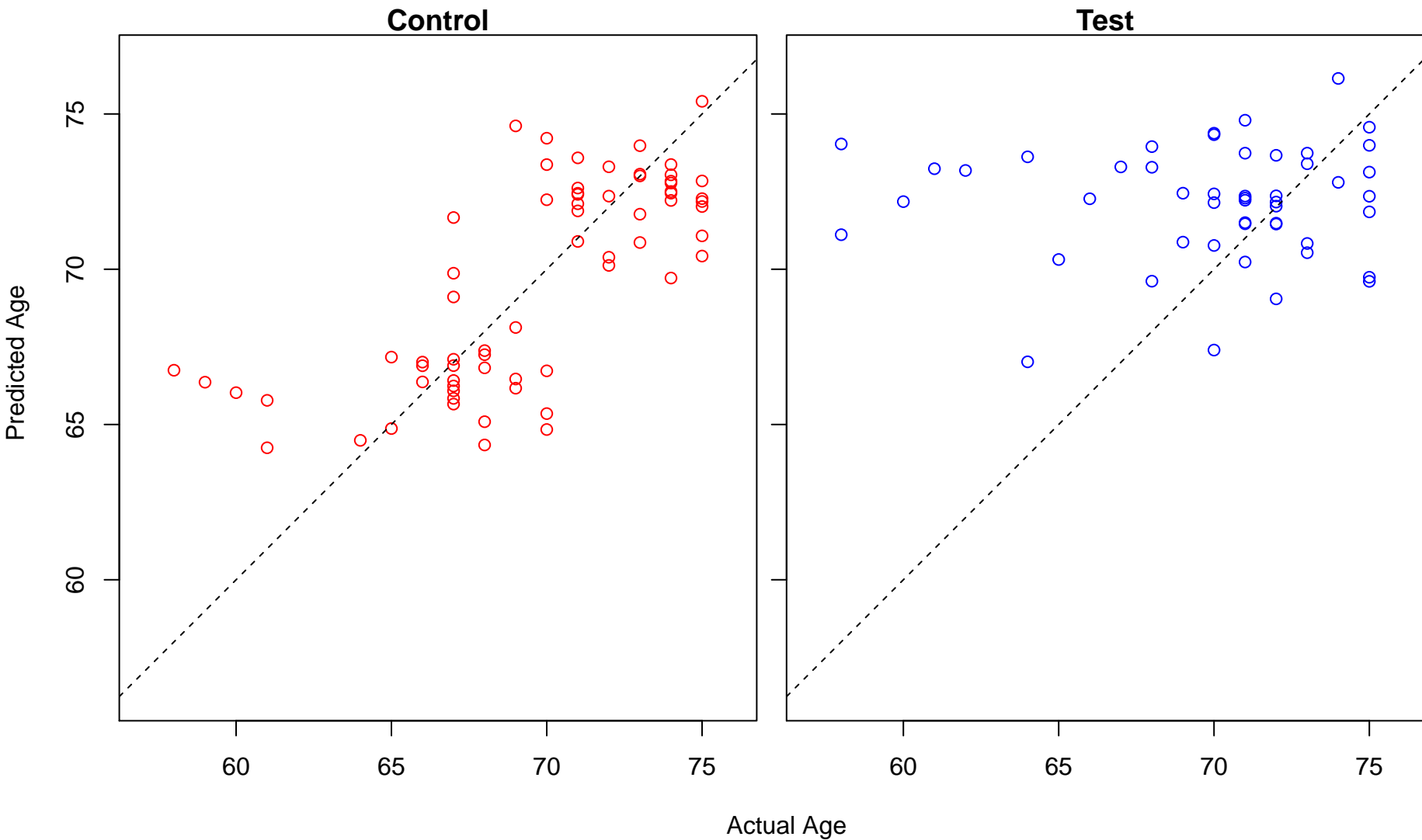
positive regulation of protein oligomerization (Score: 1.579421)



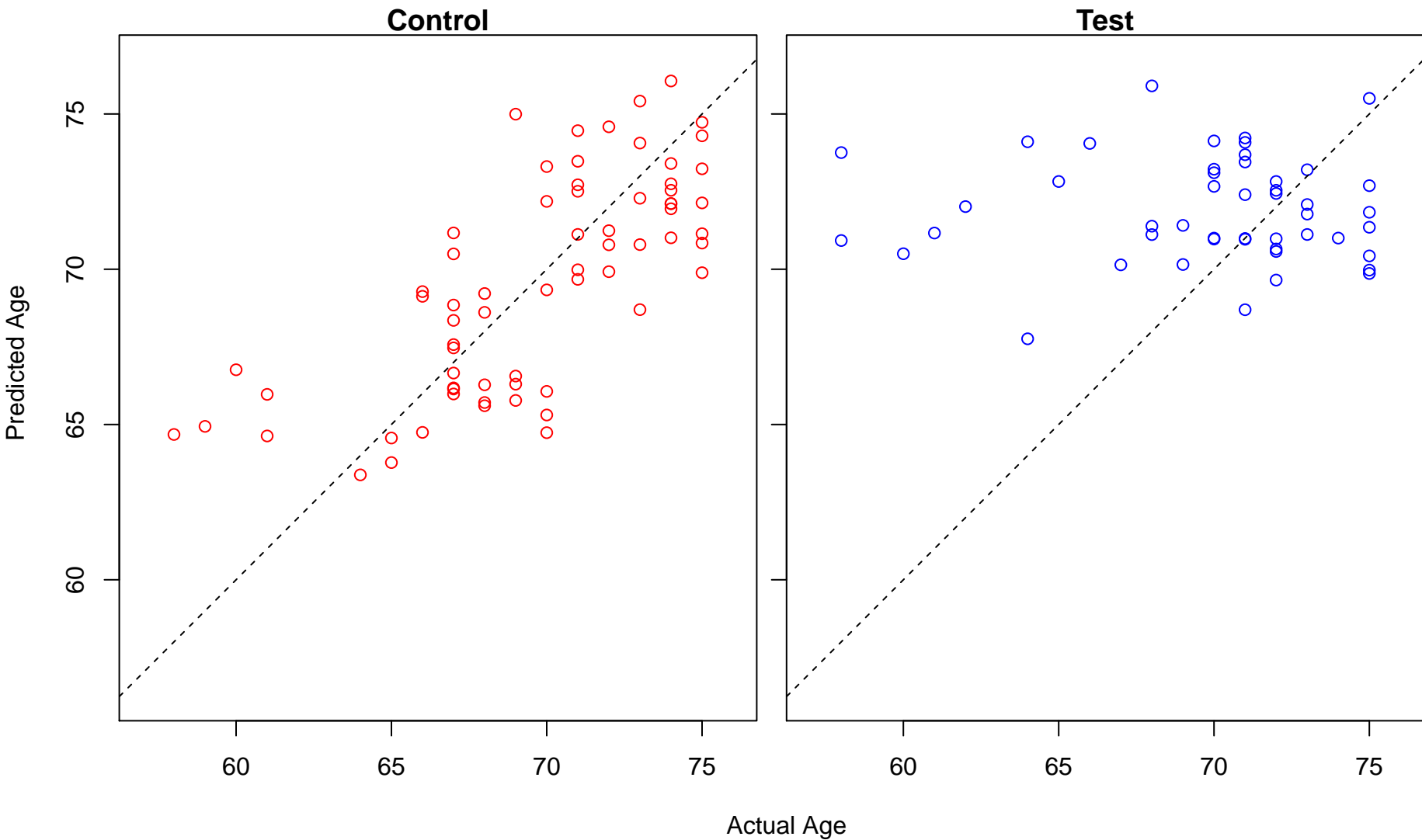
alpha-beta T cell differentiation (Score: 1.578942)



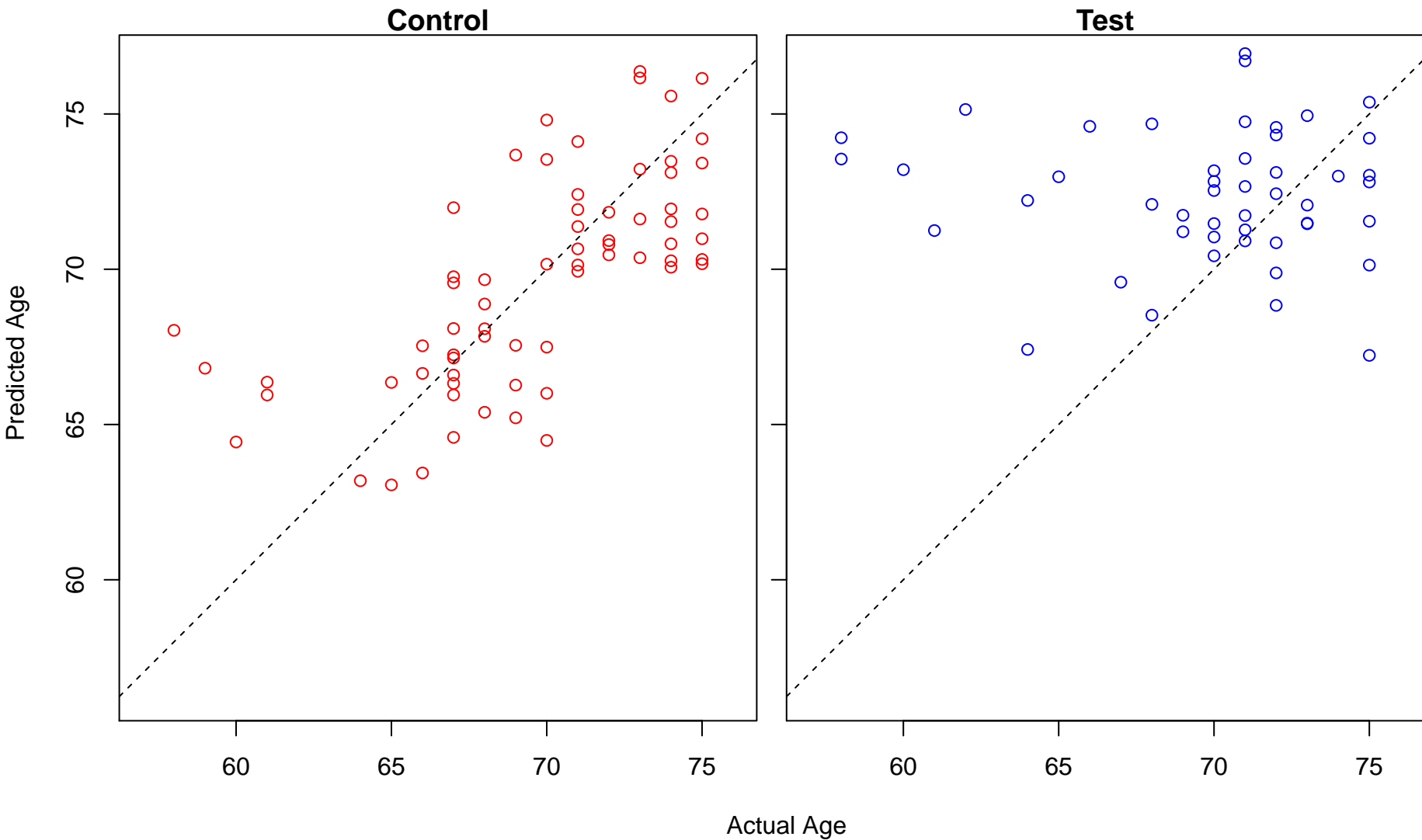
response to topologically incorrect protein (Score: 1.578589)



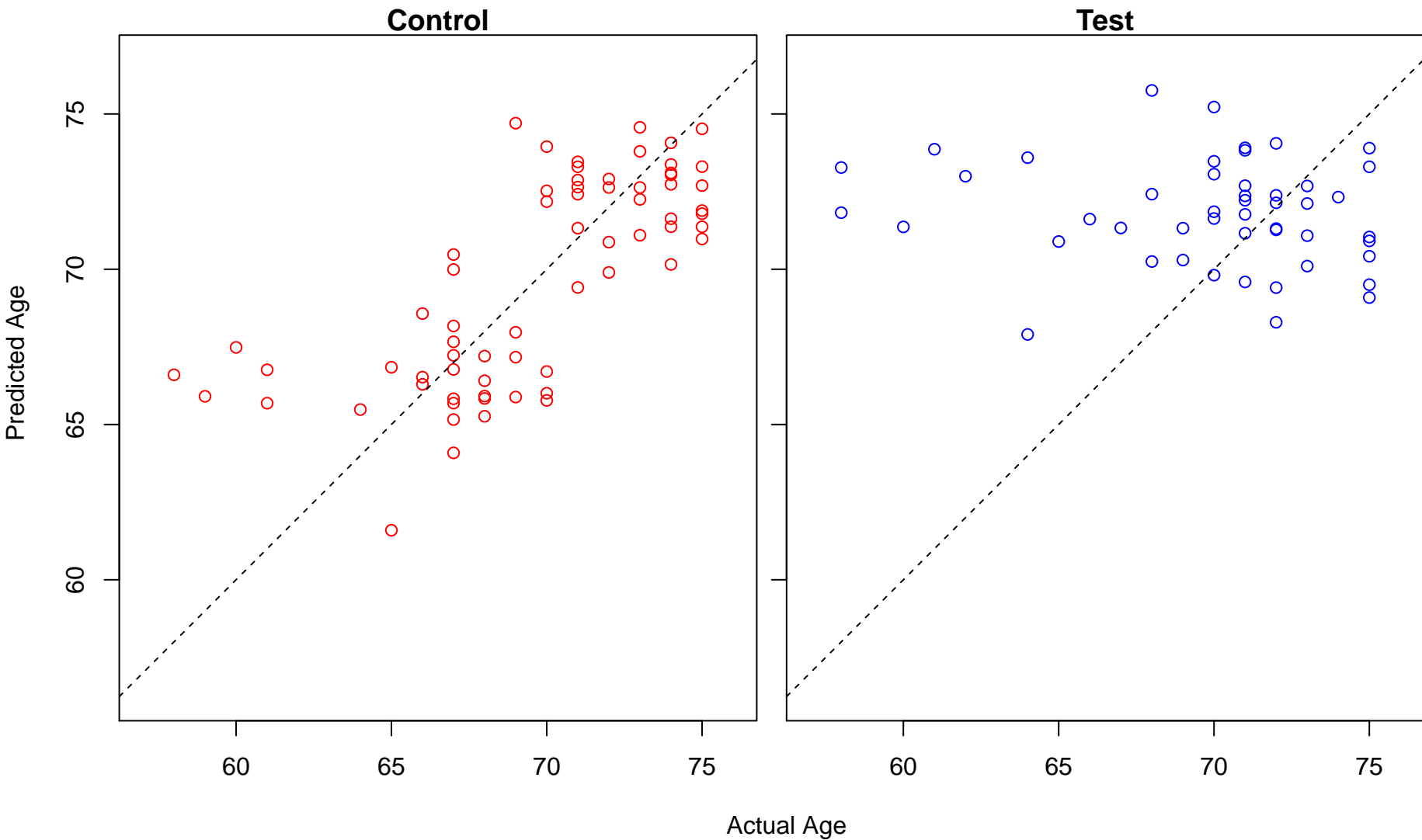
exocytosis (Score: 1.578554)



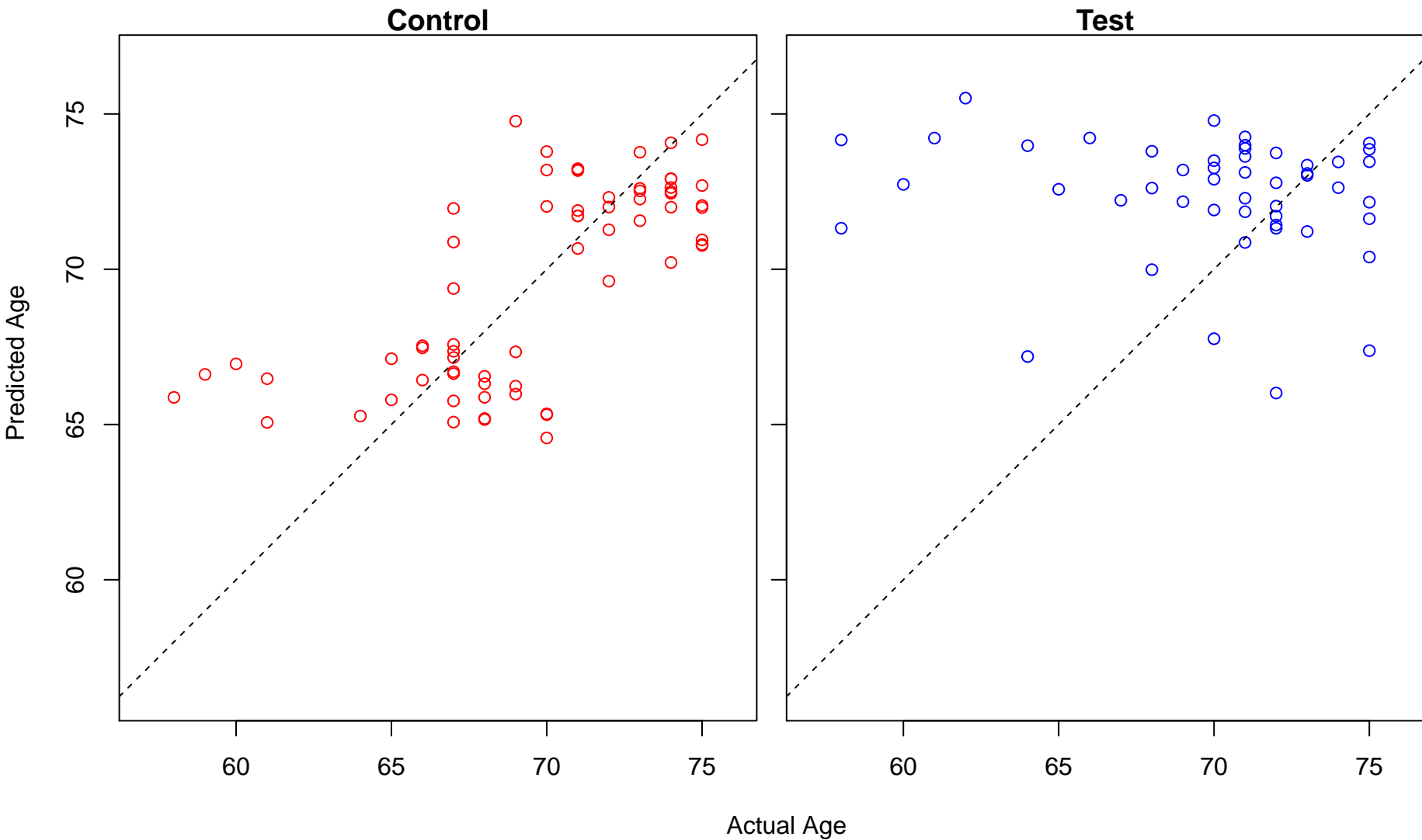
regulation of cell development (Score: 1.578255)



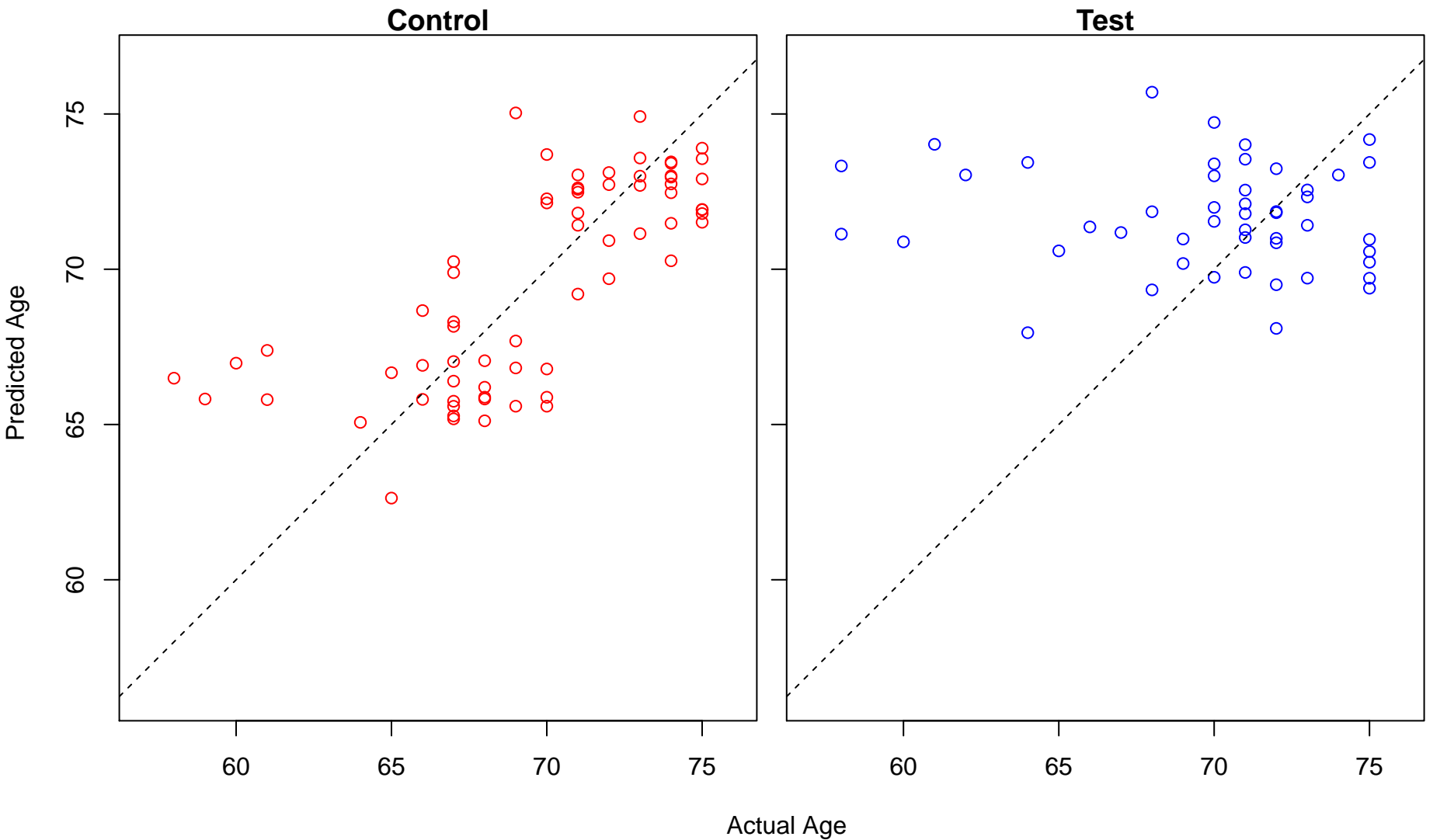
positive regulation of canonical Wnt signaling pathway (Score: 1.578232)



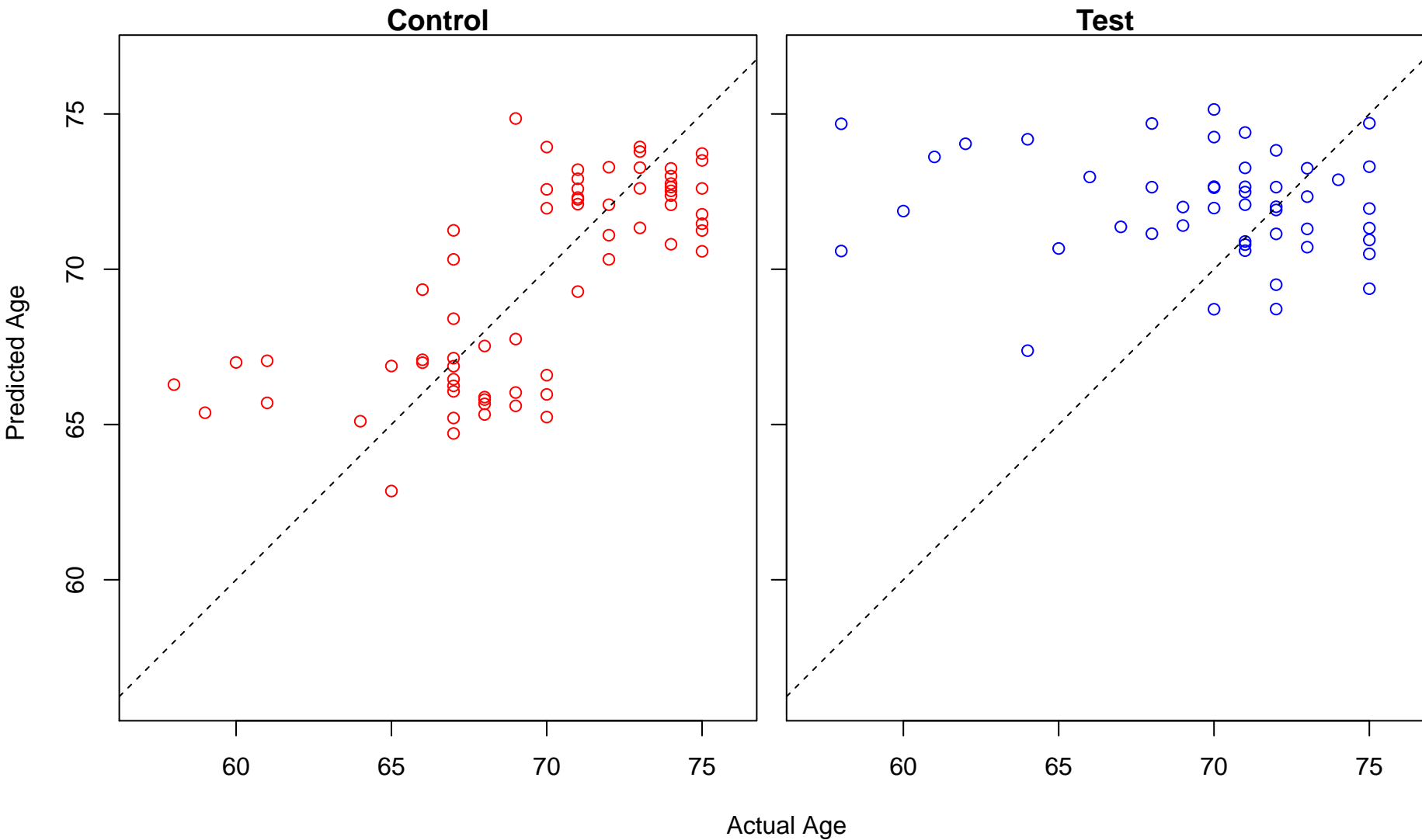
protein modification by small protein removal (Score: 1.578104)



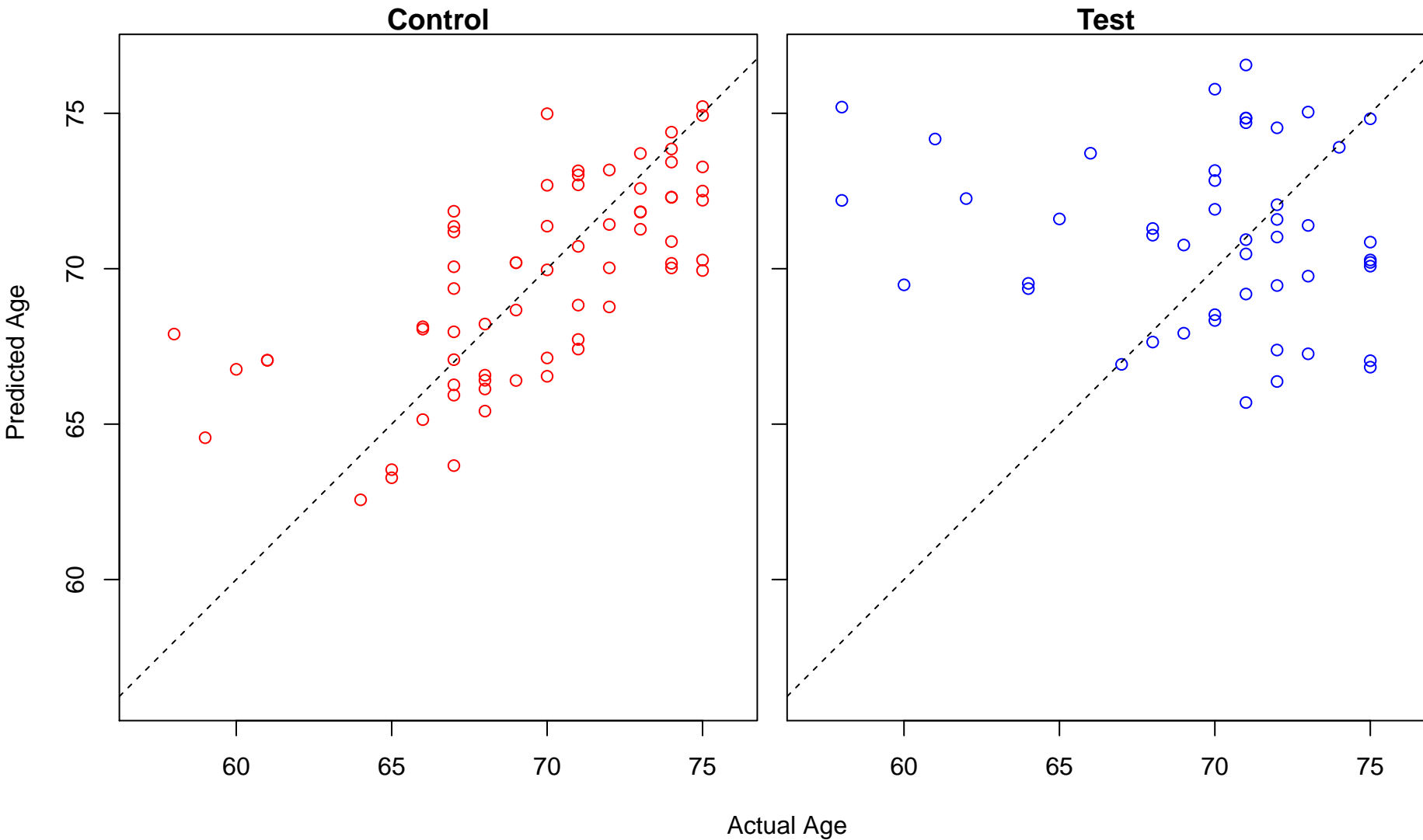
Positive regulation of ubiquitin–protein ligase activity involved in regulation of mitotic cell cycle transition (Score)



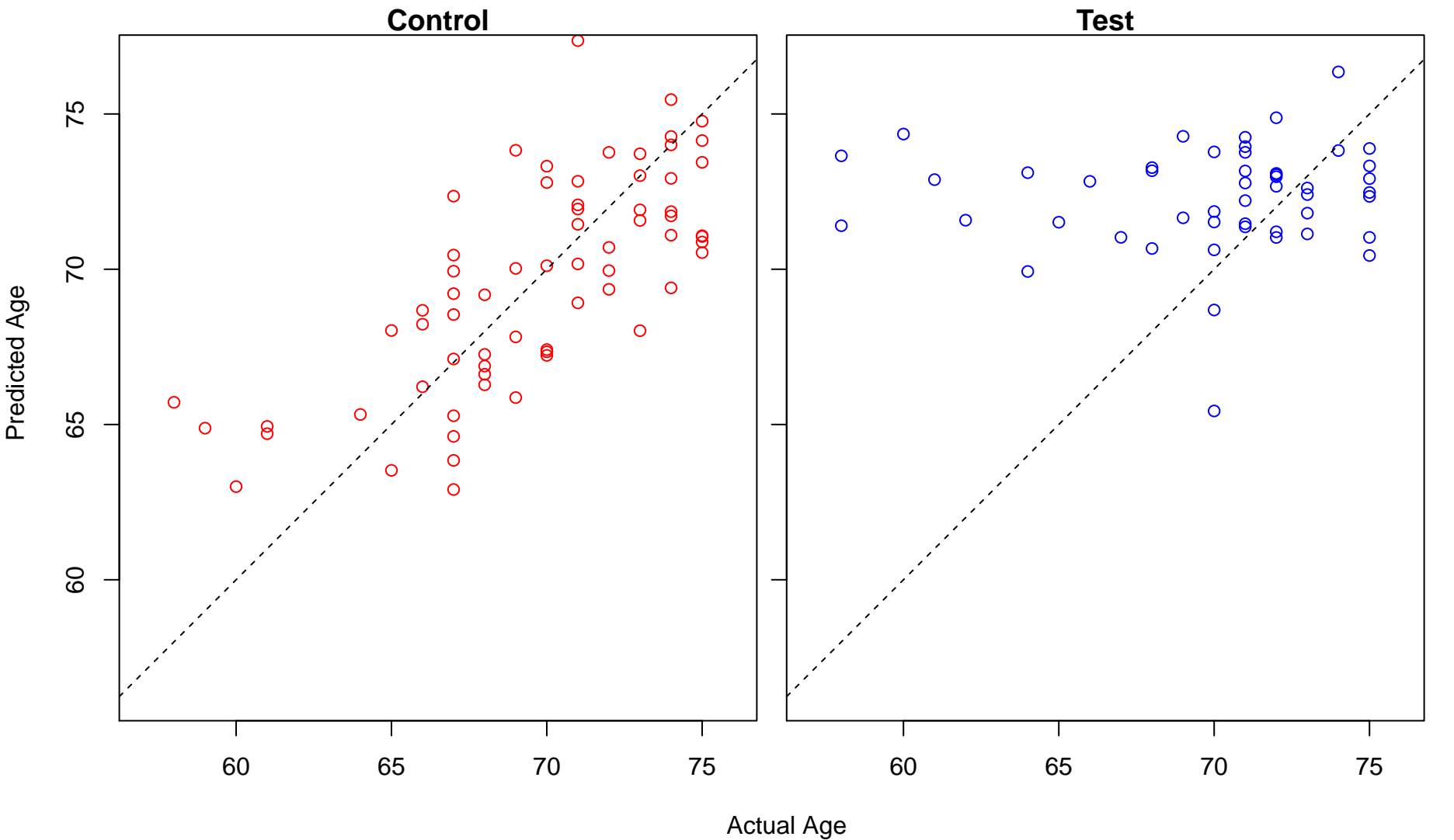
signal transduction in response to DNA damage (Score: 1.577997)



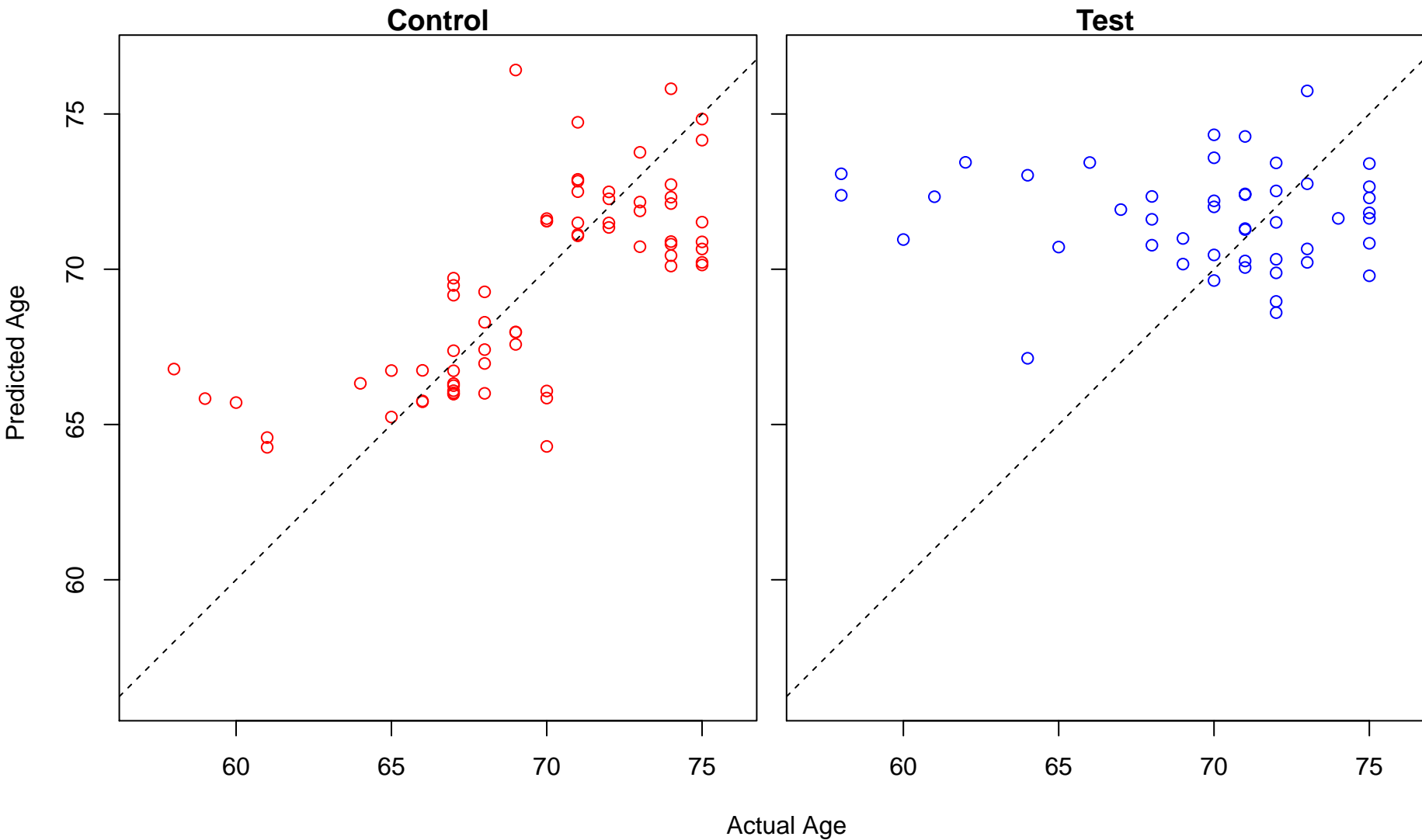
positive regulation of adherens junction organization (Score: 1.577901)



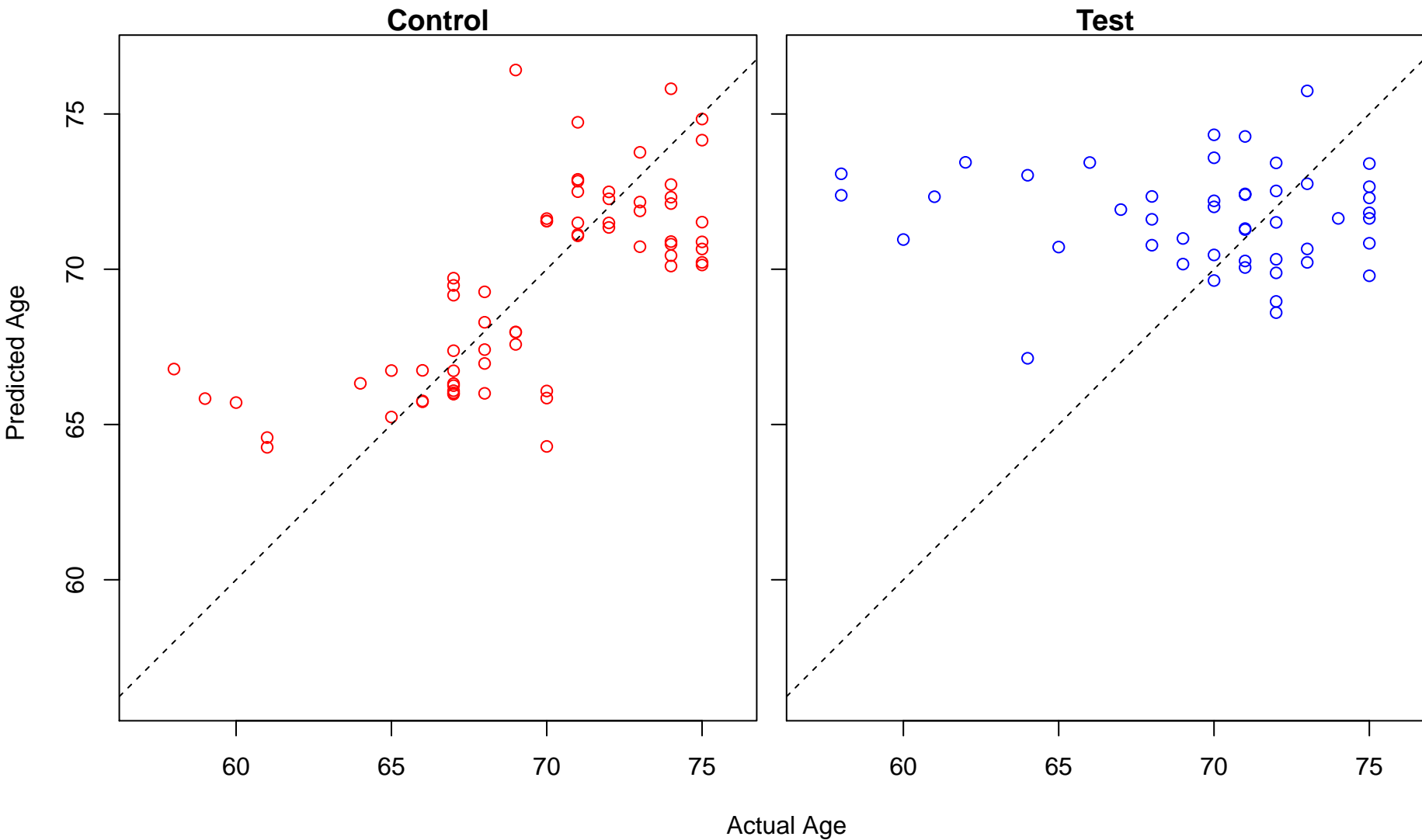
Regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (Score



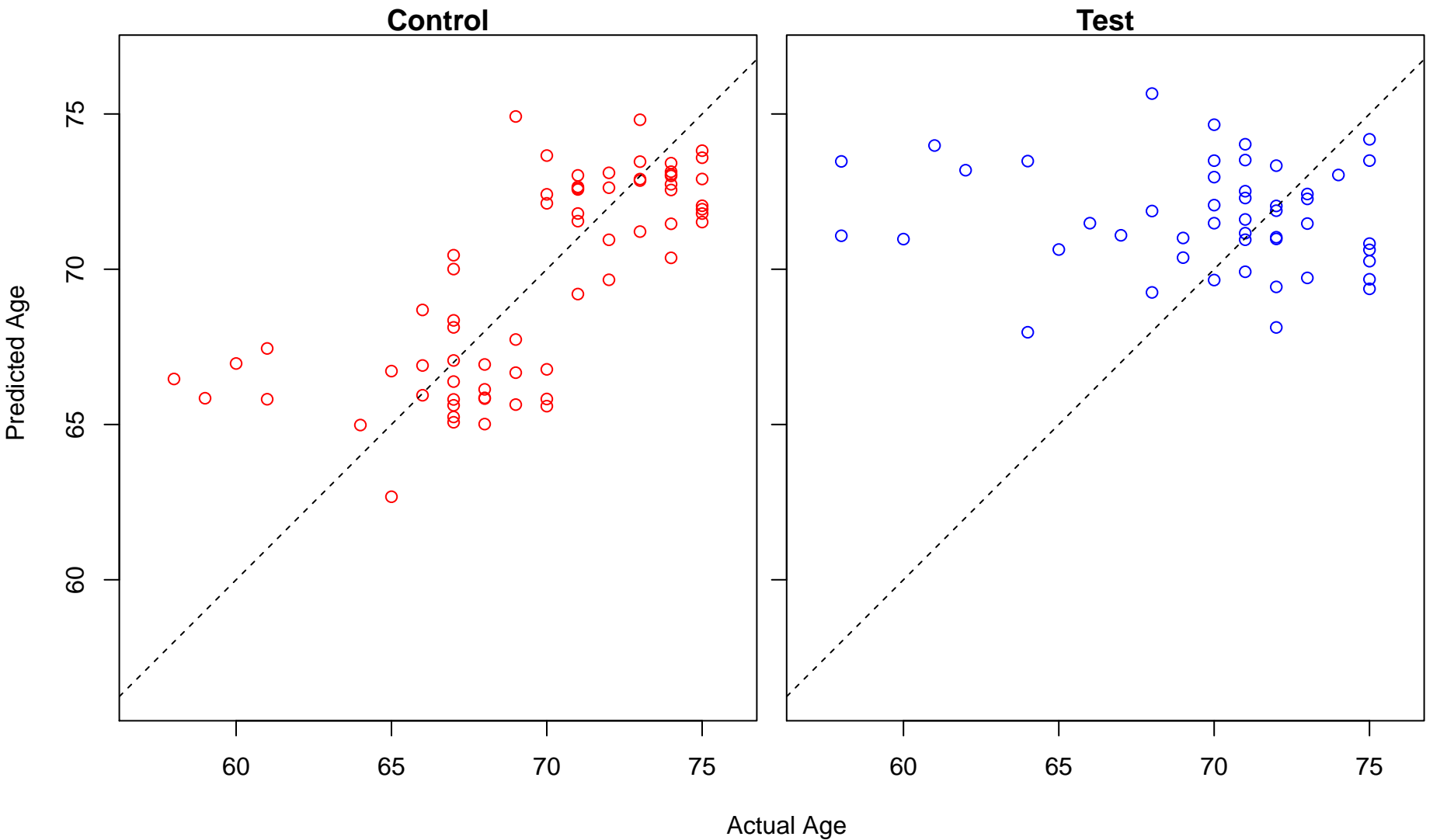
regulation of actin polymerization or depolymerization (Score: 1.576979)



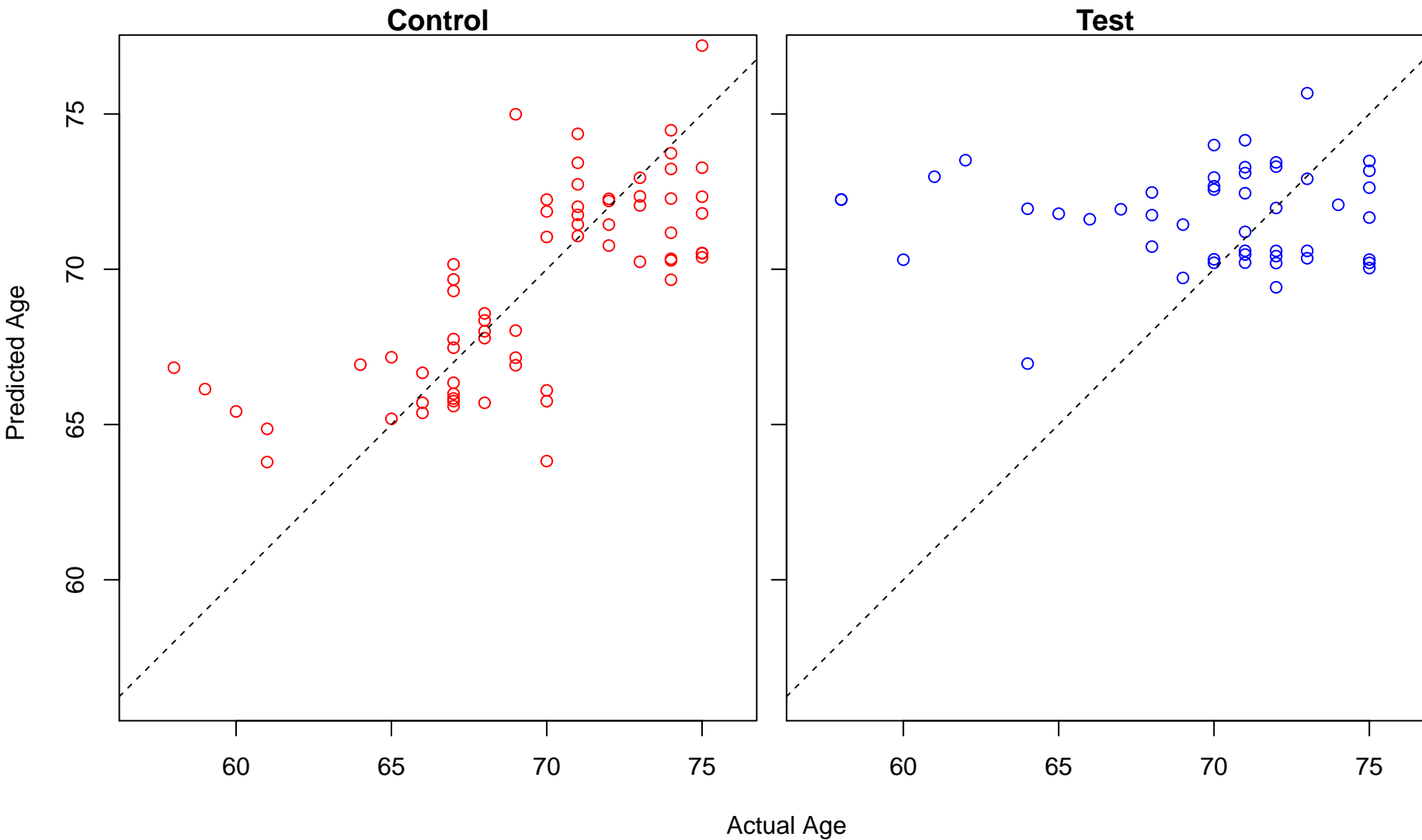
regulation of actin filament length (Score: 1.576979)



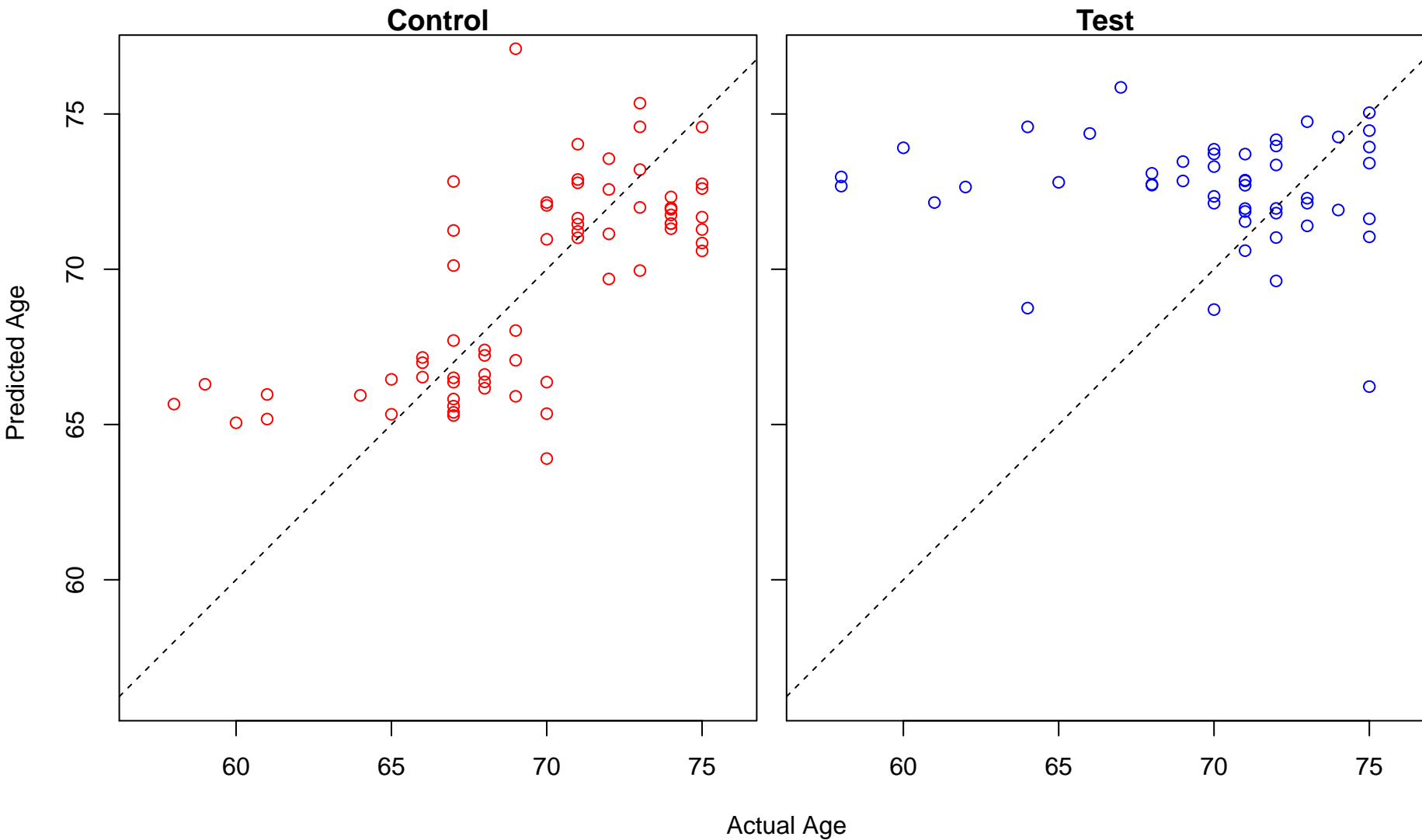
Positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score



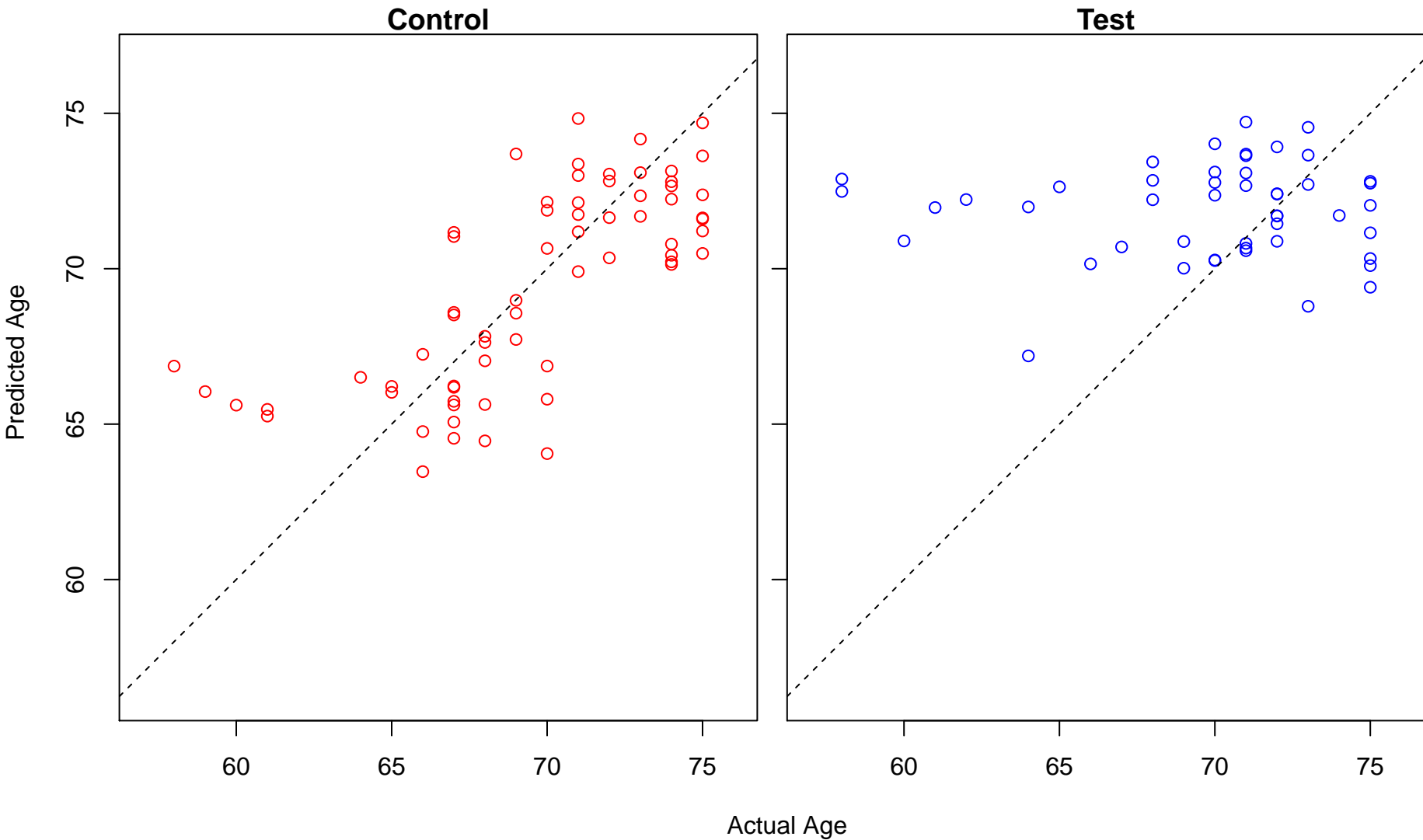
regulation of protein polymerization (Score: 1.575836)



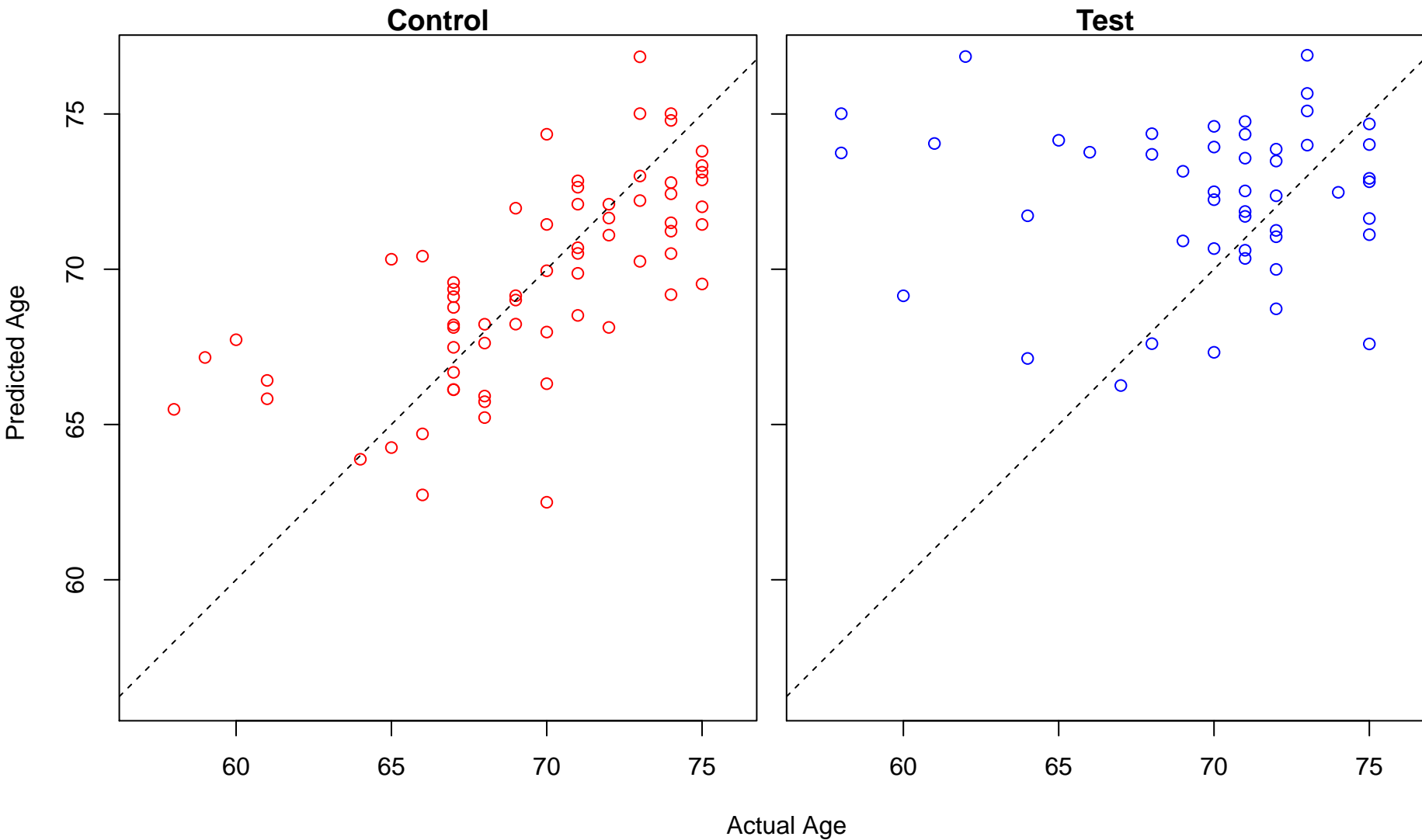
mitochondrial translational initiation (Score: 1.575789)



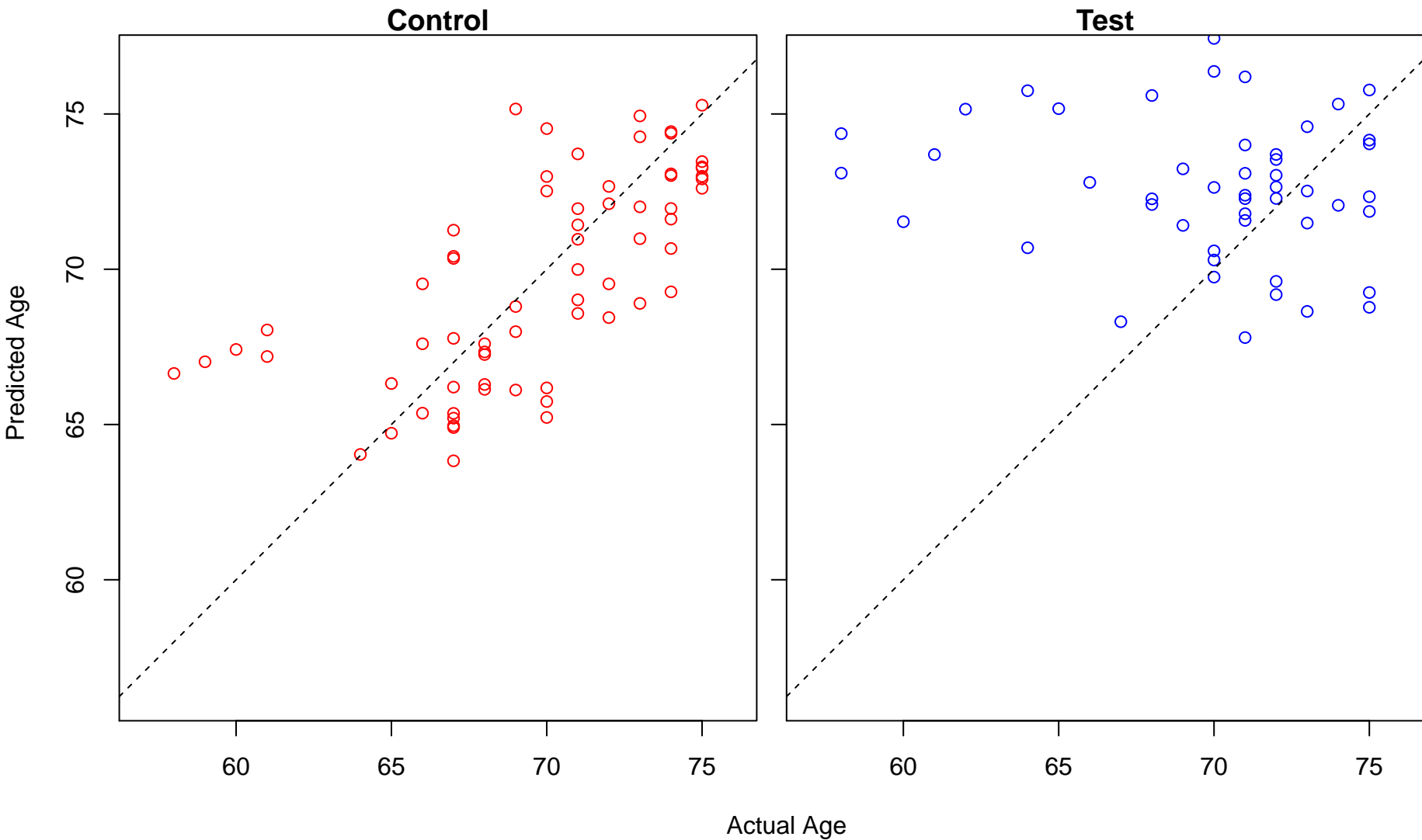
ribonucleotide biosynthetic process (Score: 1.575695)



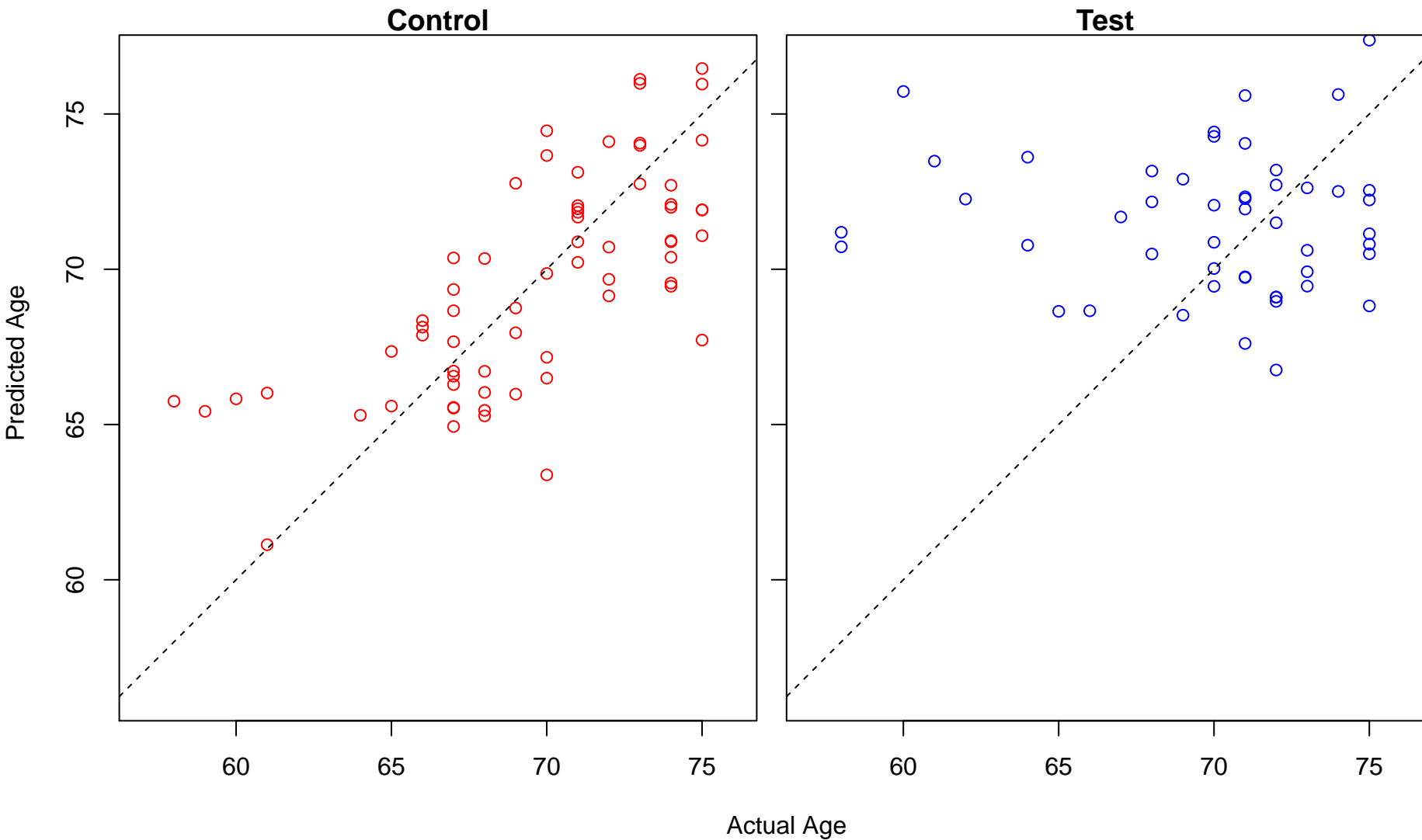
trabecula morphogenesis (Score: 1.575597)



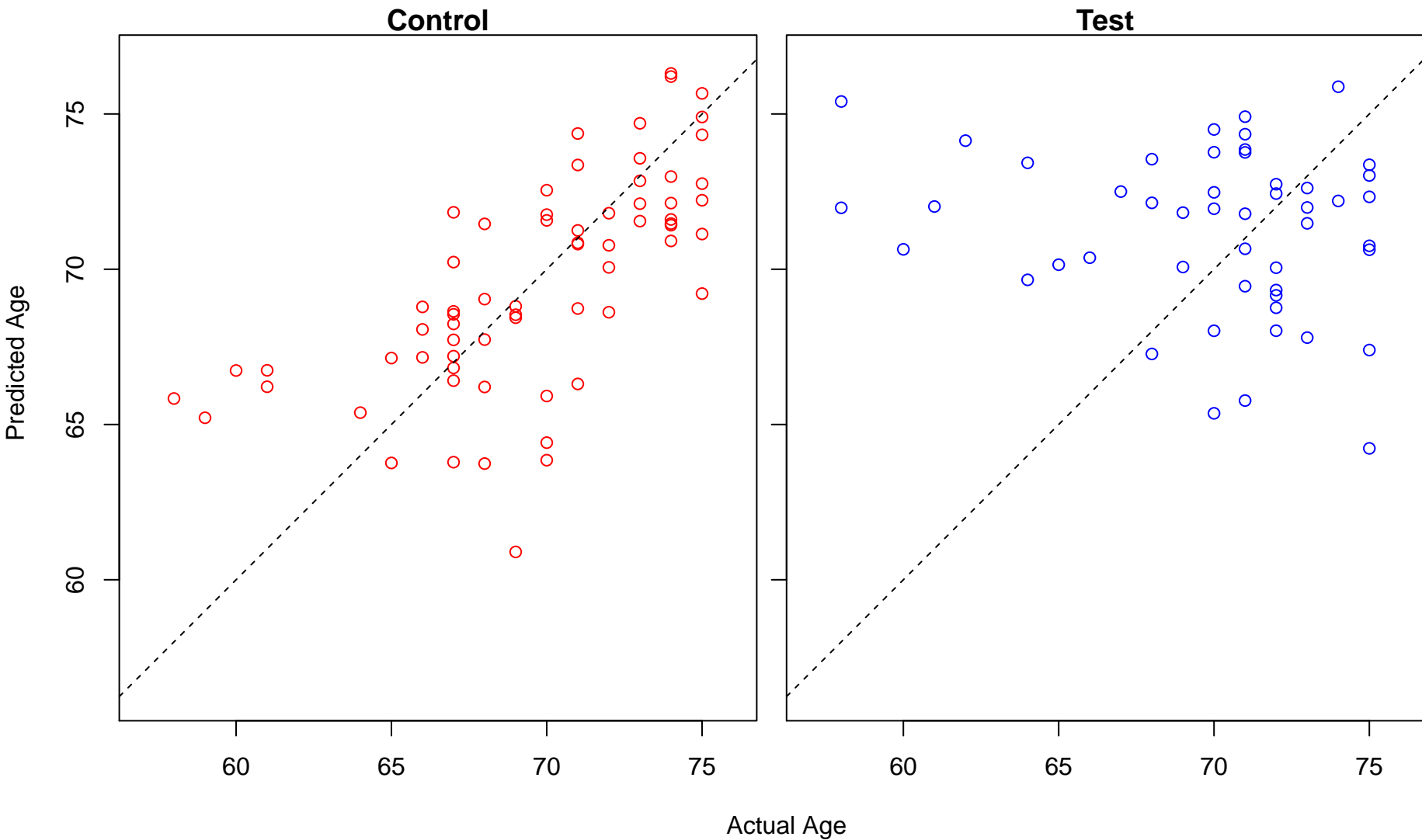
positive regulation of stress-activated protein kinase signaling cascade (Score: 1.574719)



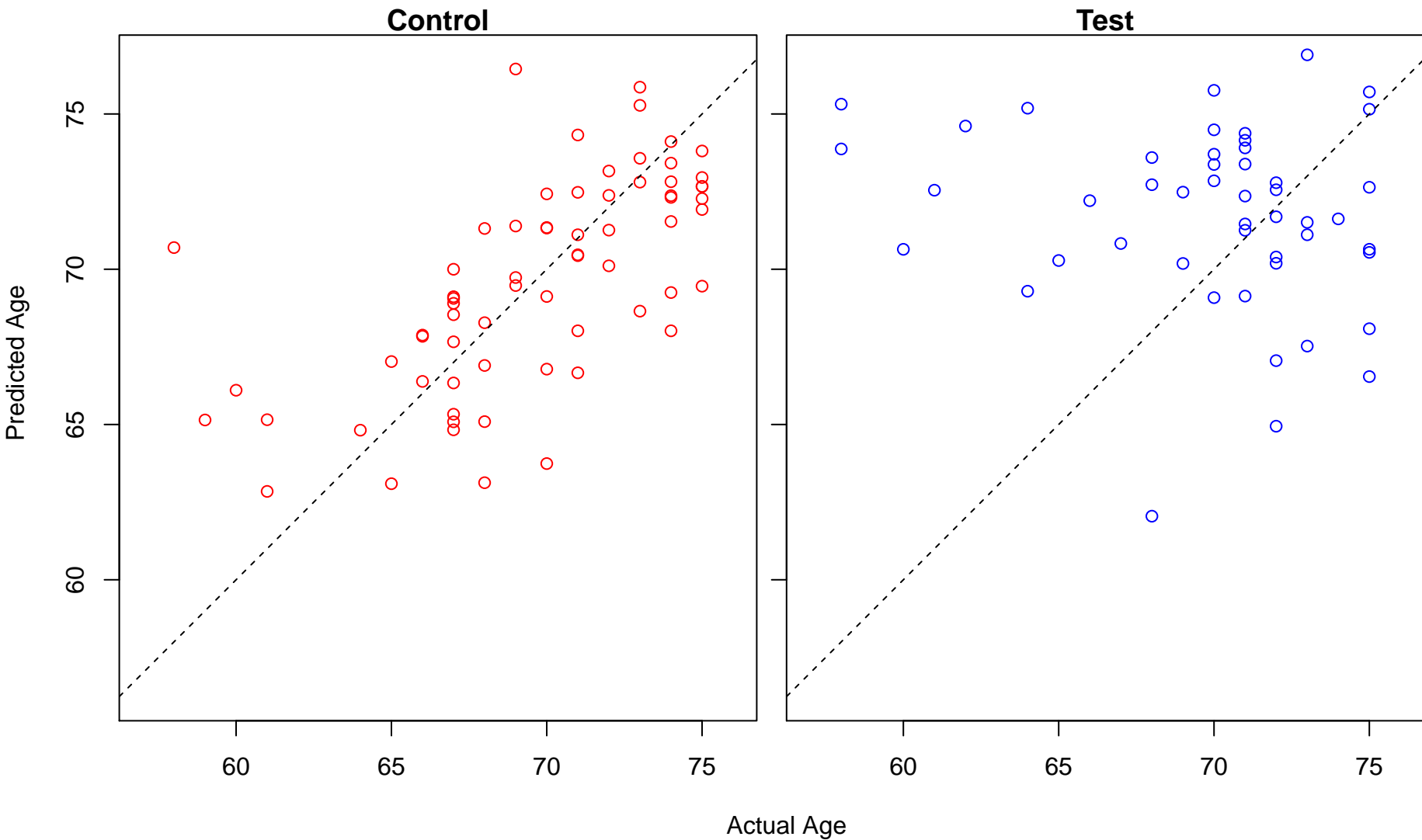
positive regulation of cell division (Score: 1.573656)



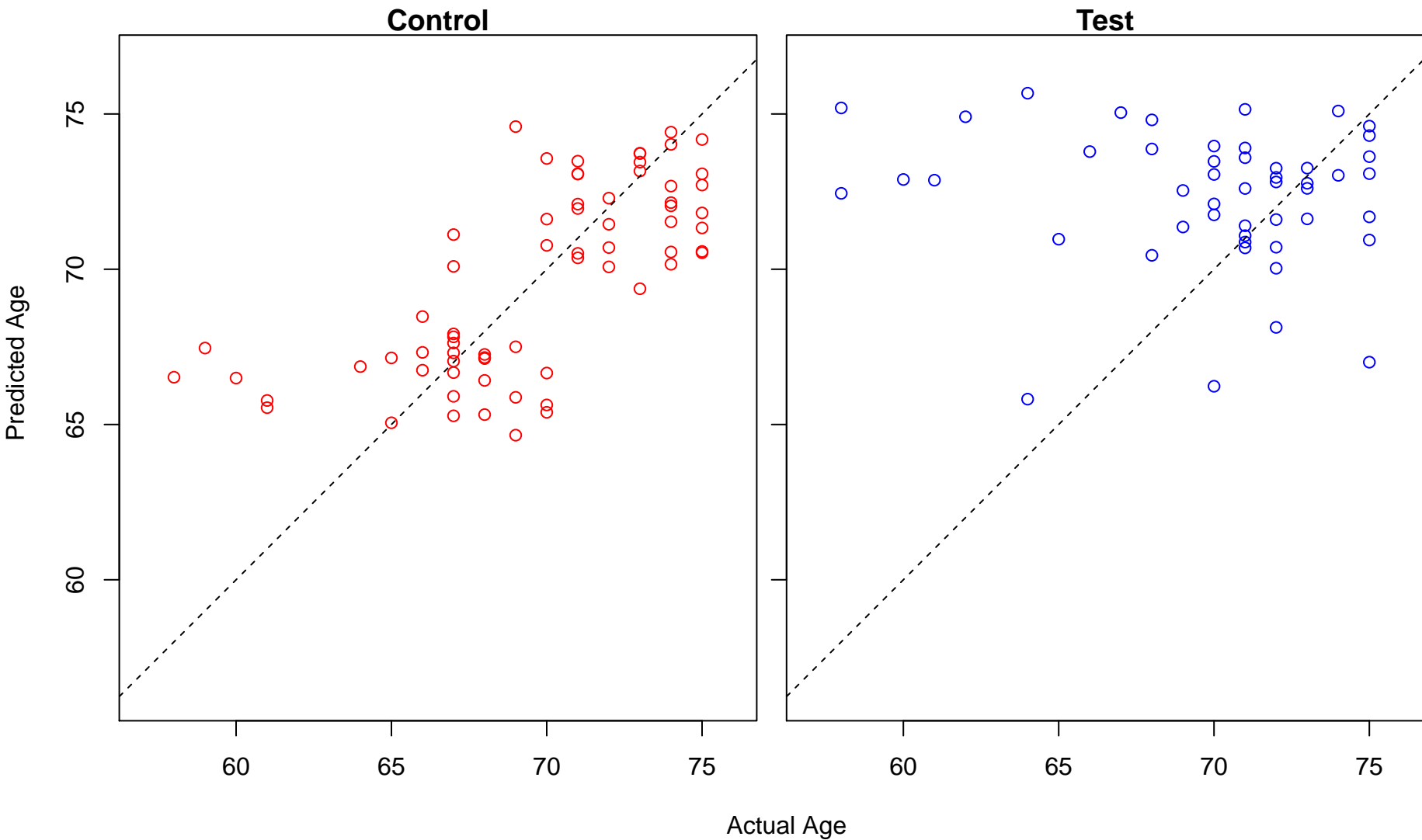
cellular response to extracellular stimulus (Score: 1.573188)



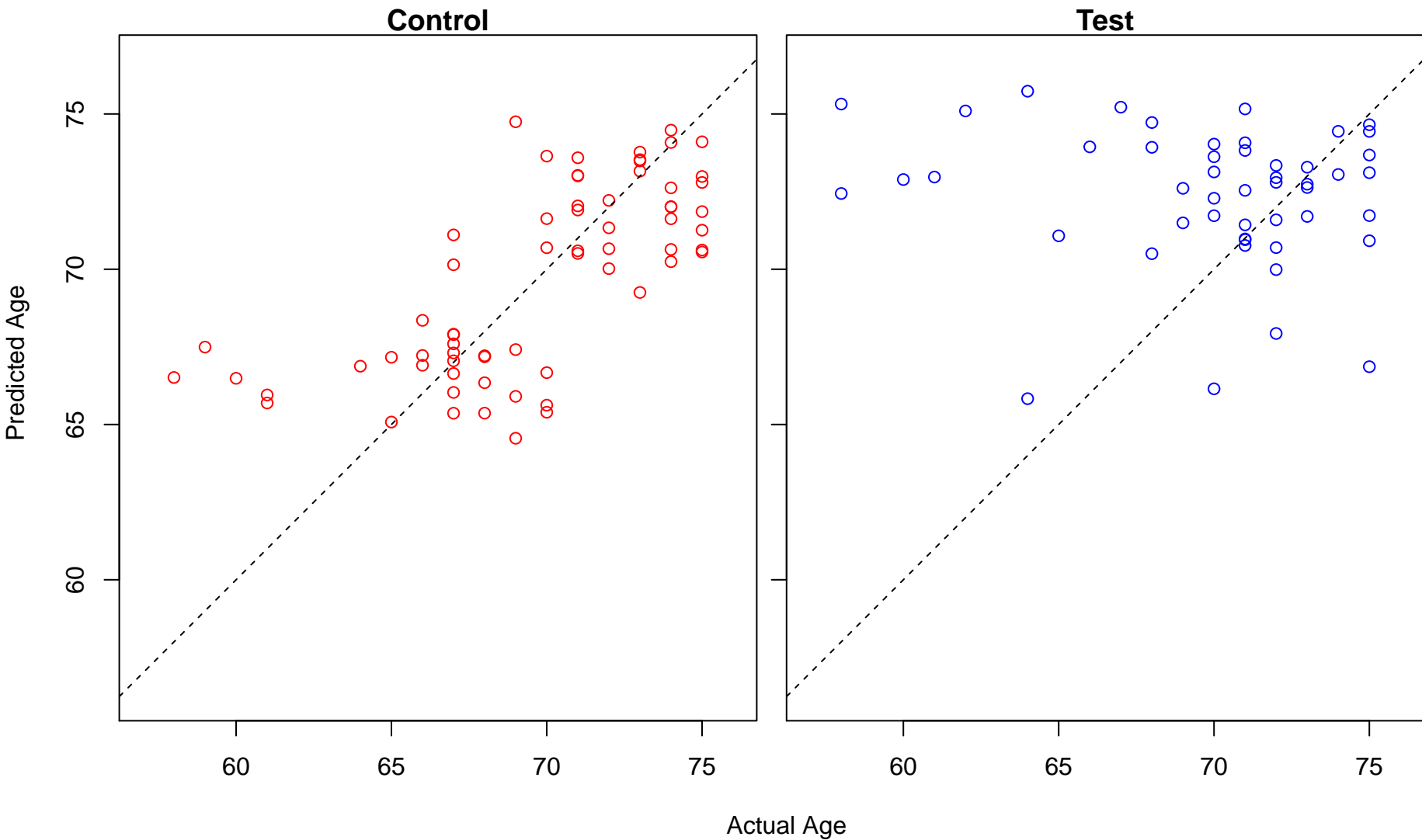
regulation of natural killer cell mediated cytotoxicity (Score: 1.573176)



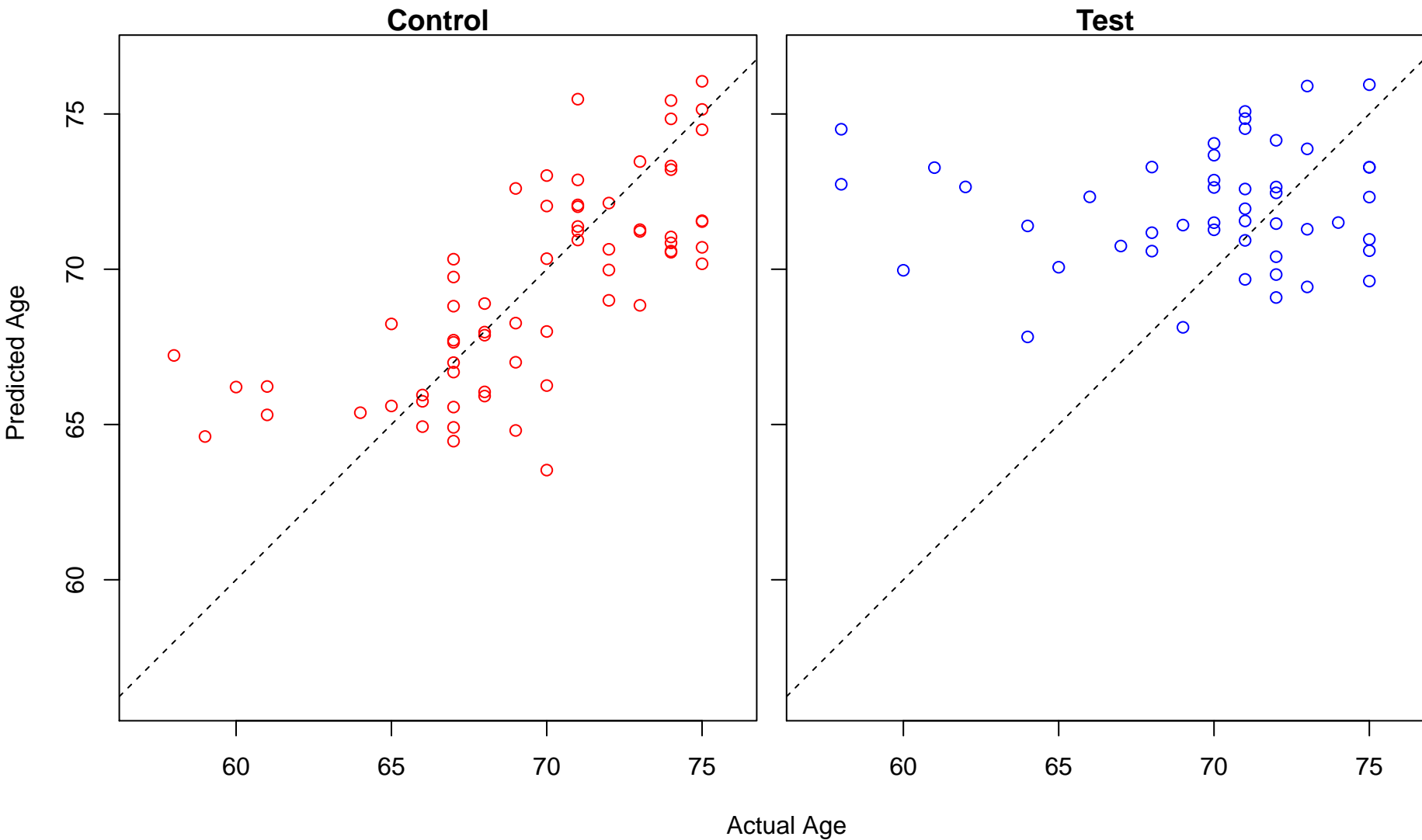
membrane invagination (Score: 1.572541)



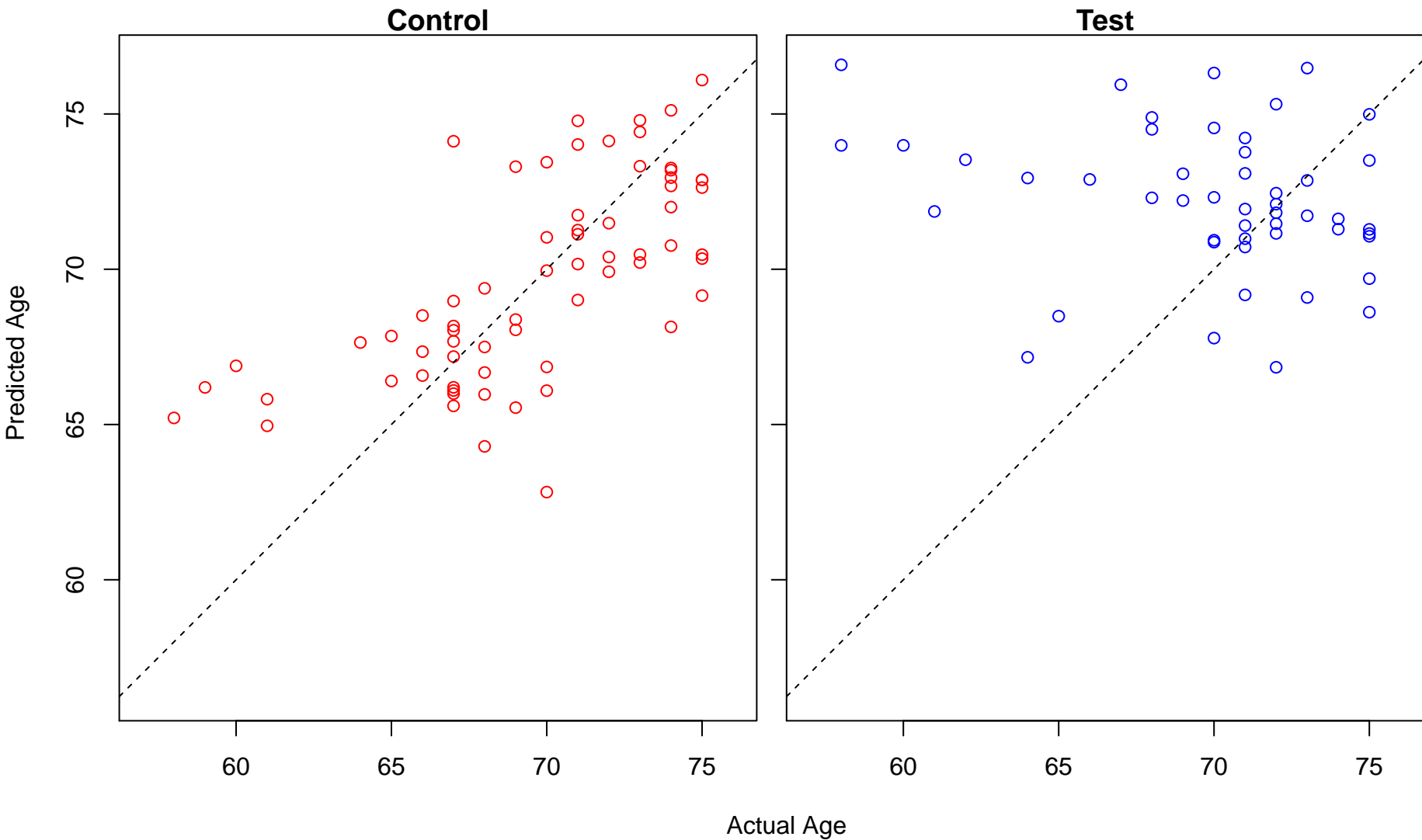
phagocytosis, engulfment (Score: 1.572100)



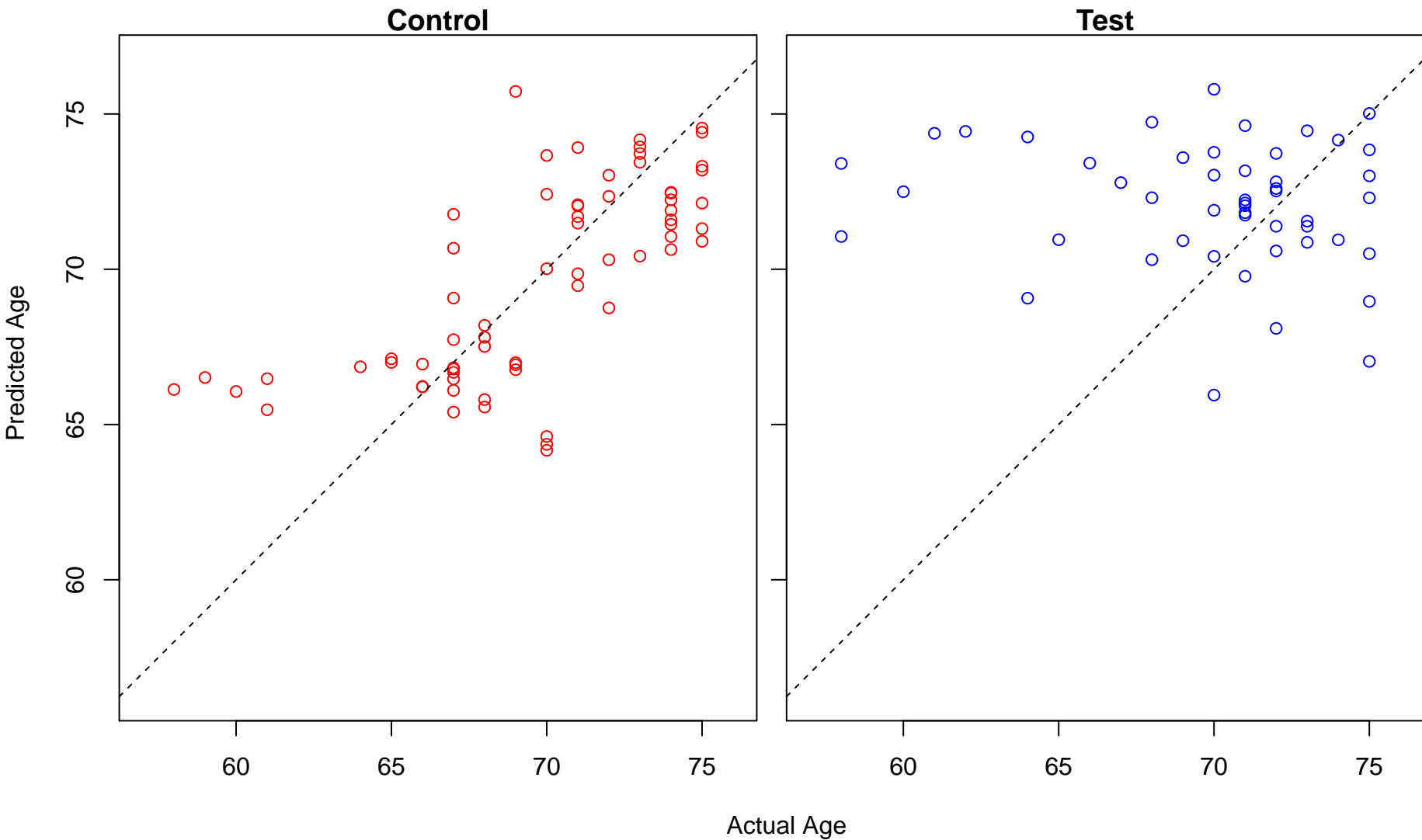
muscle system process (Score: 1.571313)



sequestering of metal ion (Score: 1.571207)

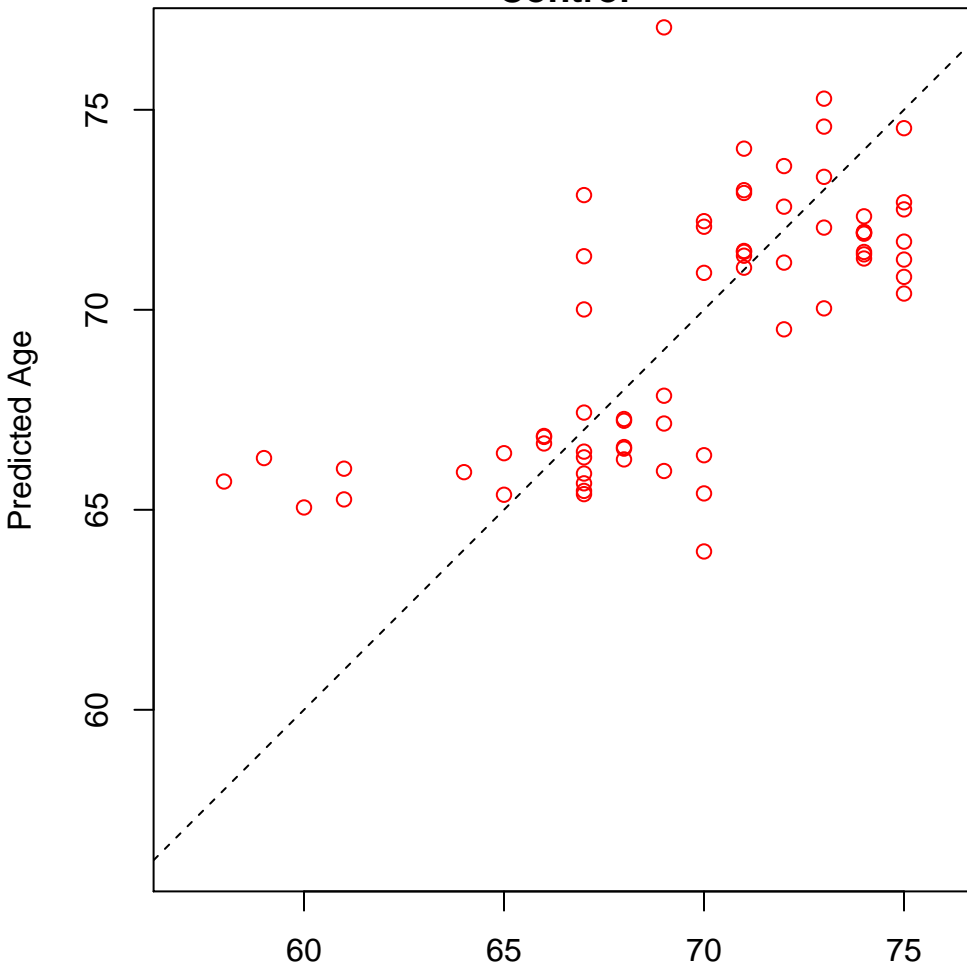


regulation of hydrogen peroxide-induced cell death (Score: 1.570955)

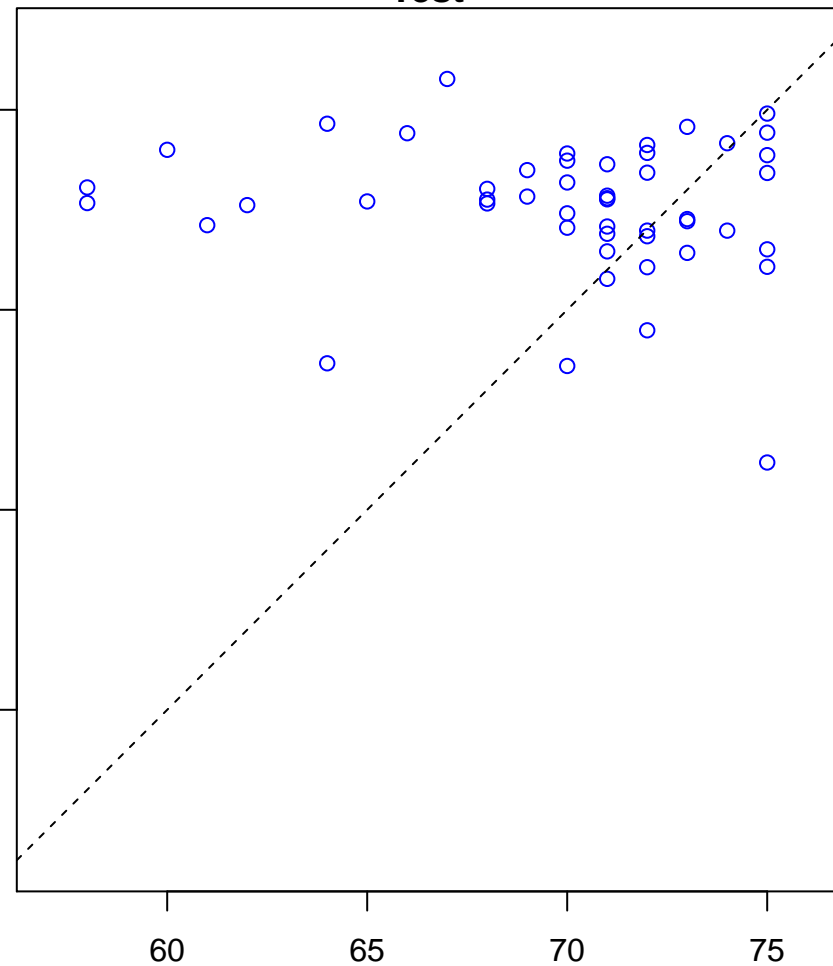


mitochondrial translational termination (Score: 1.570608)

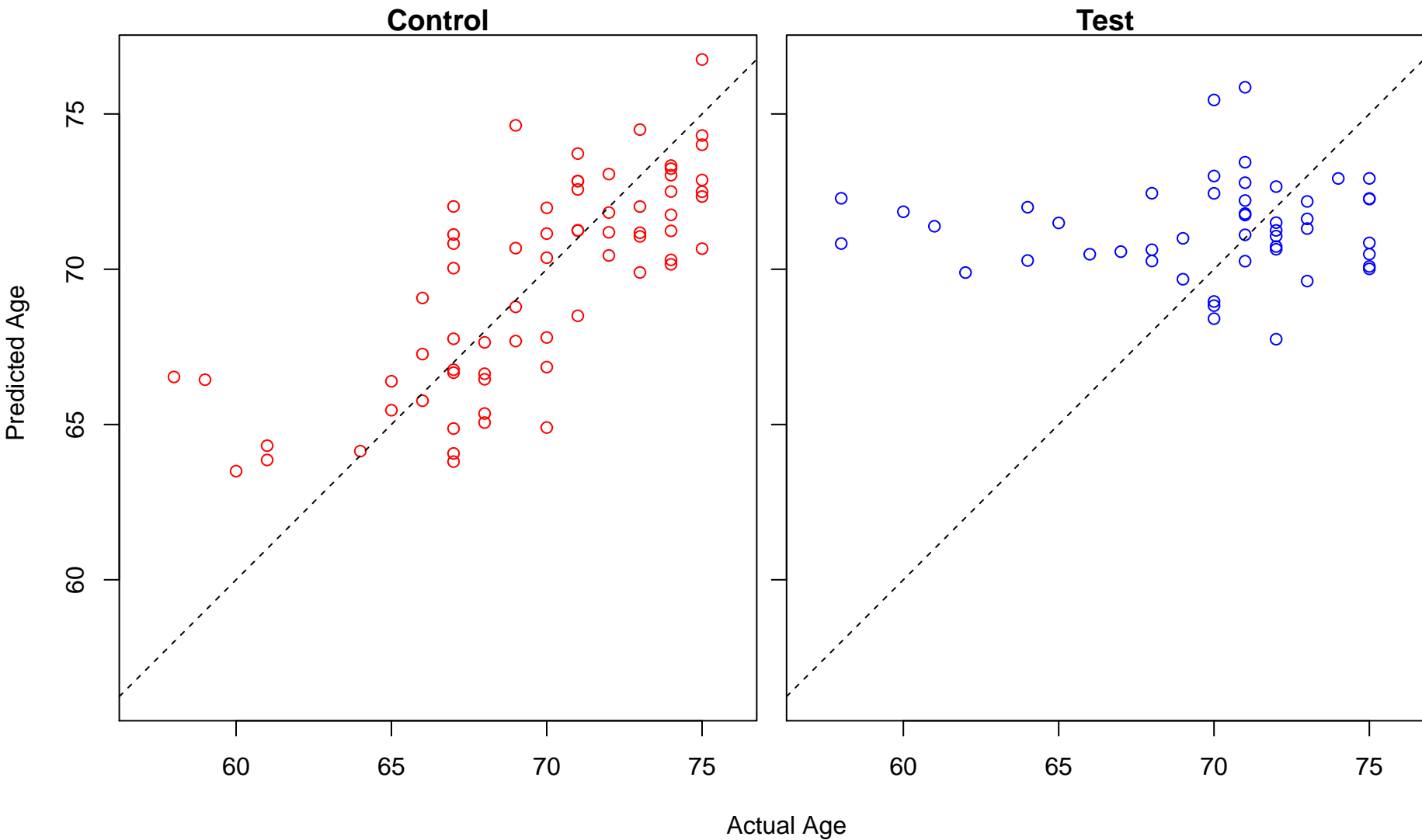
Control



Test

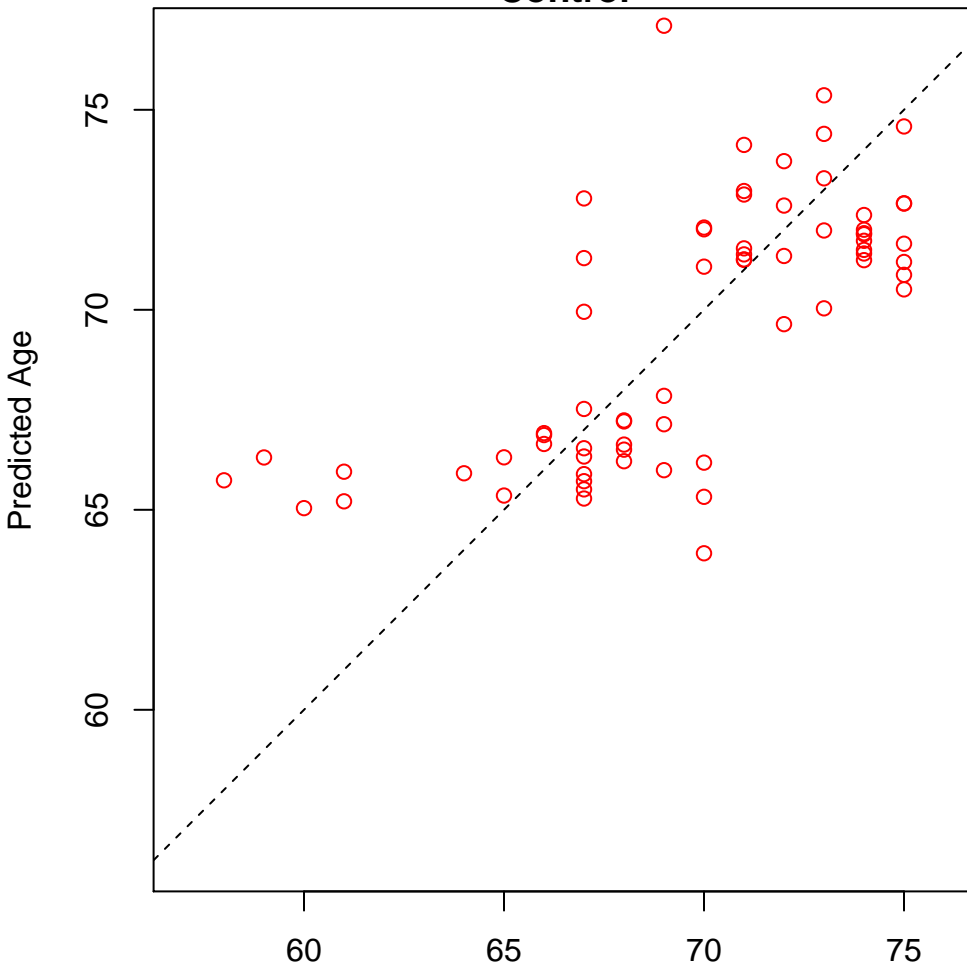


positive regulation of neuron apoptotic process (Score: 1.570429)

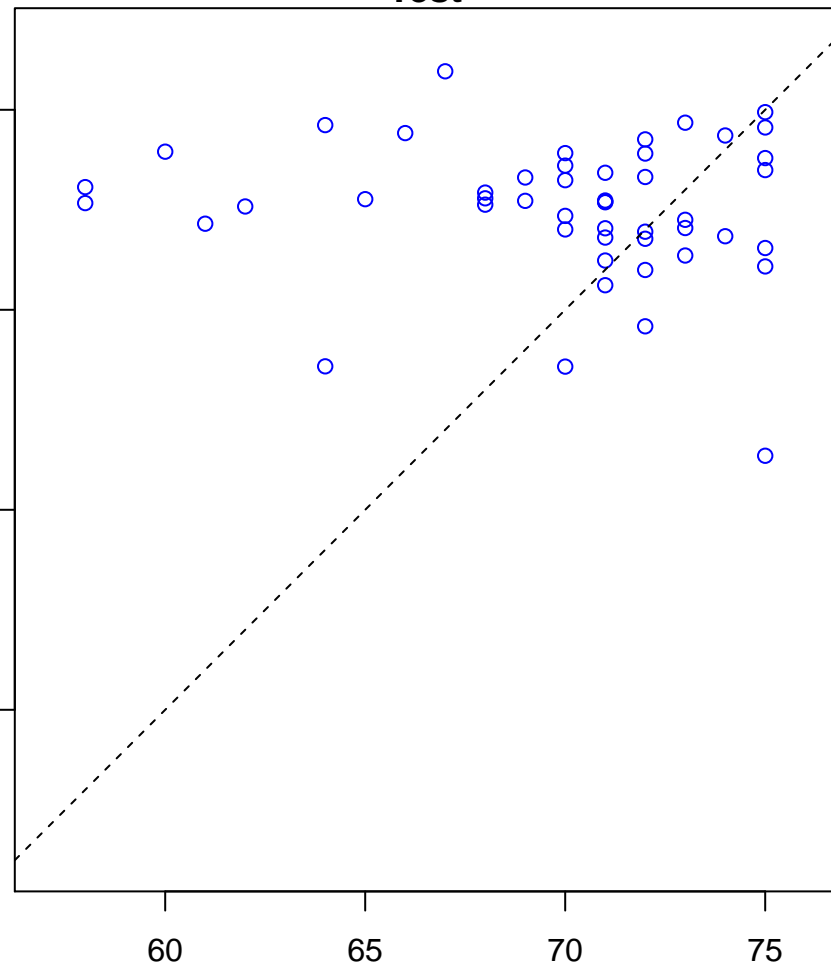


mitochondrial translational elongation (Score: 1.569800)

Control

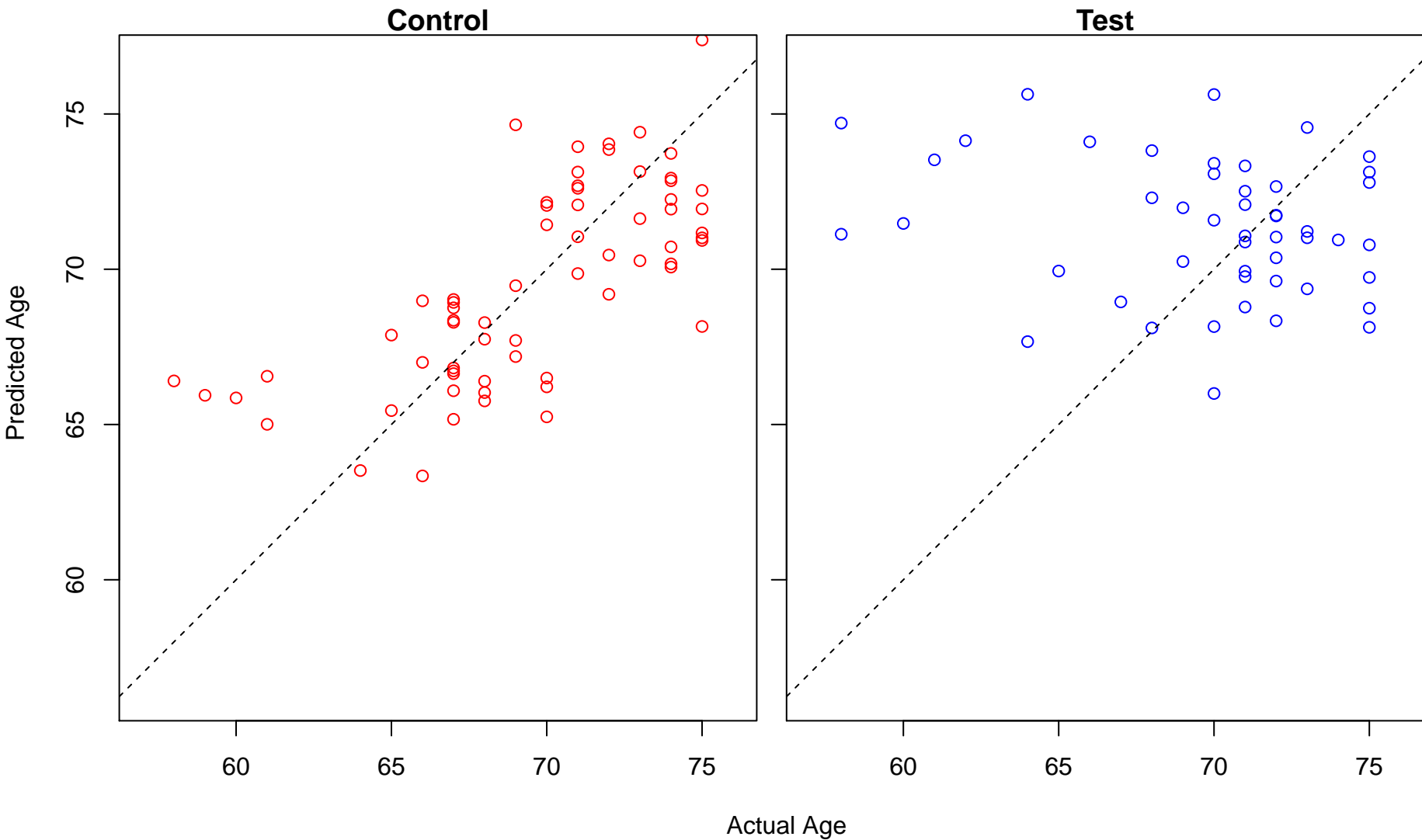


Test

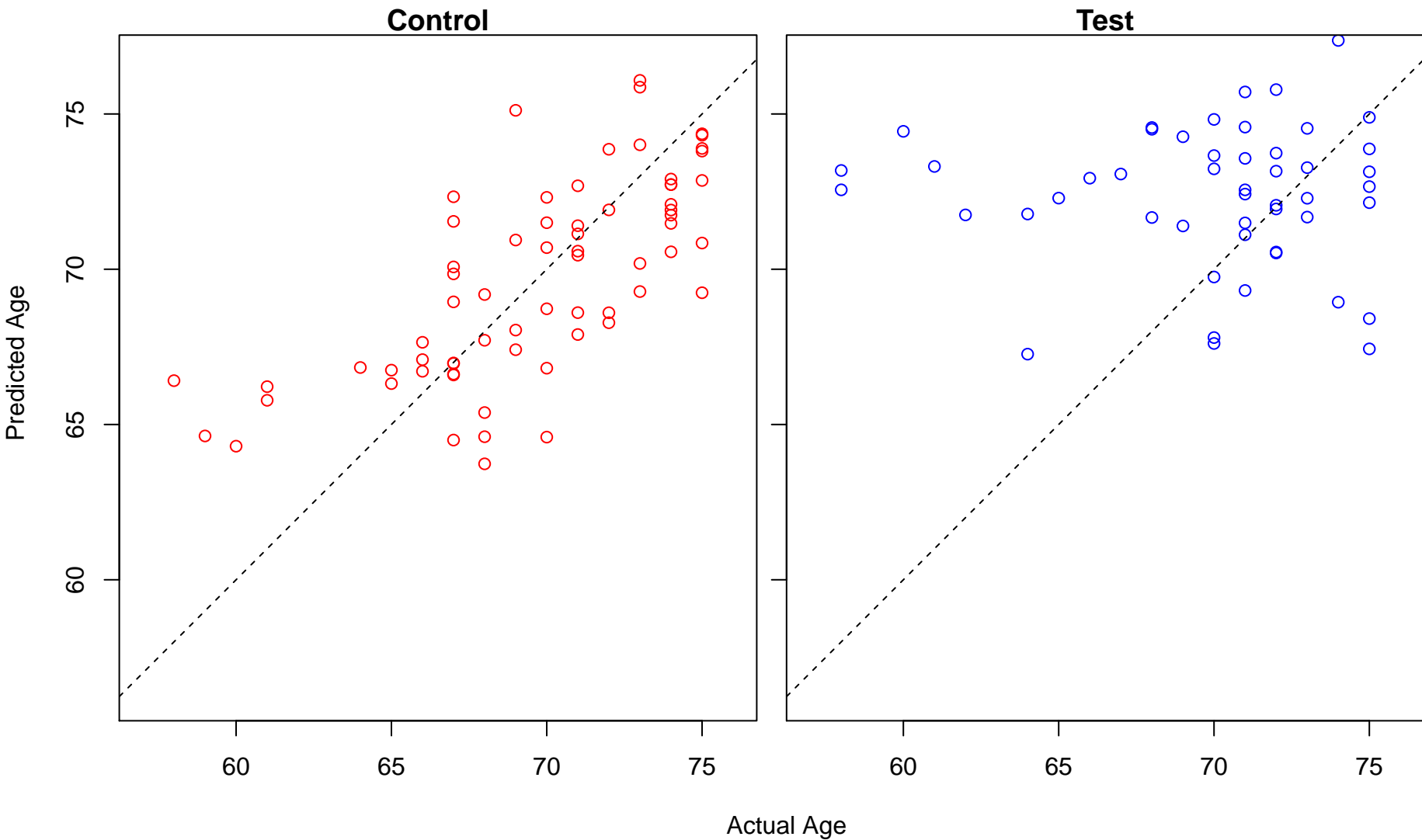


Actual Age

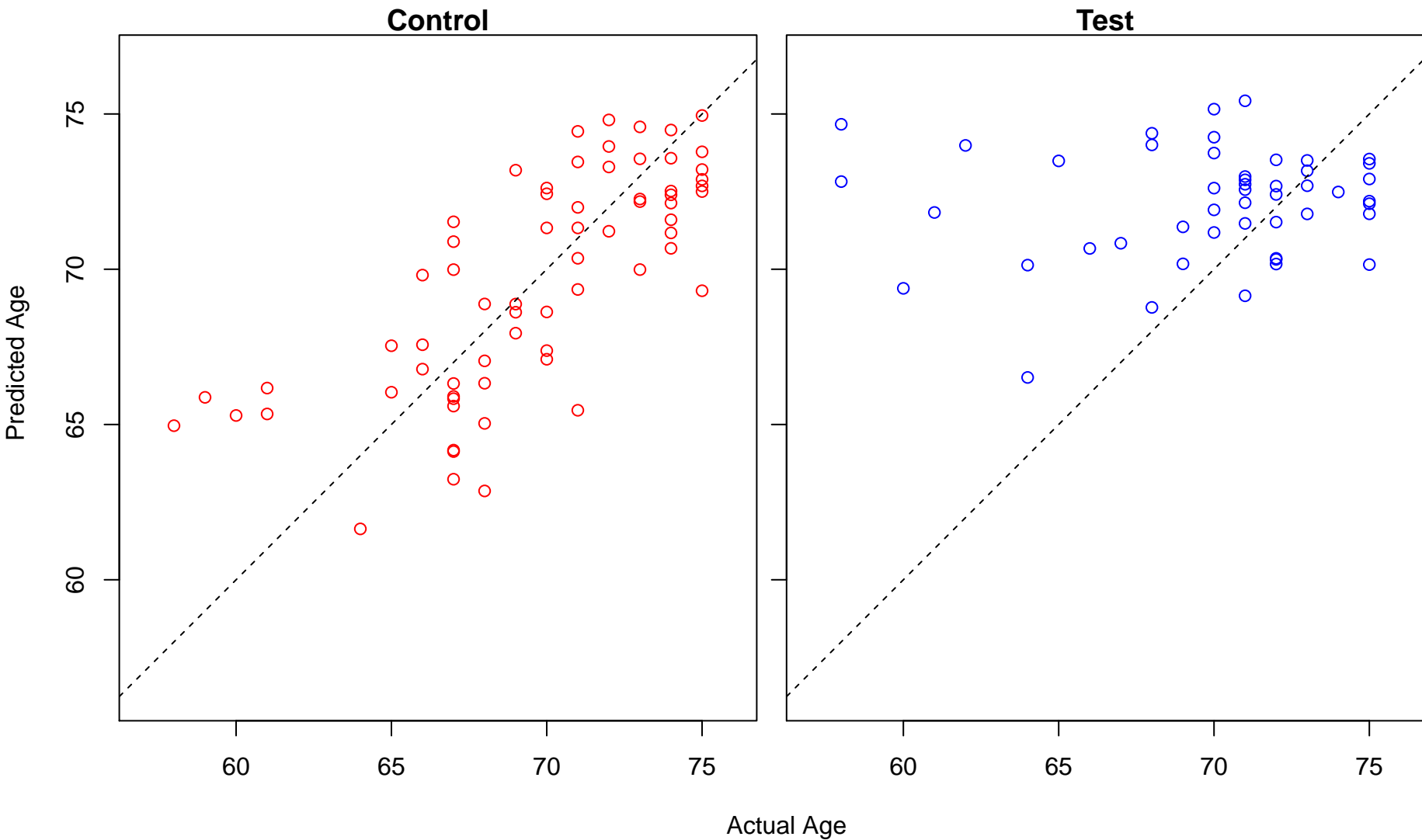
fatty acid beta-oxidation (Score: 1.569595)



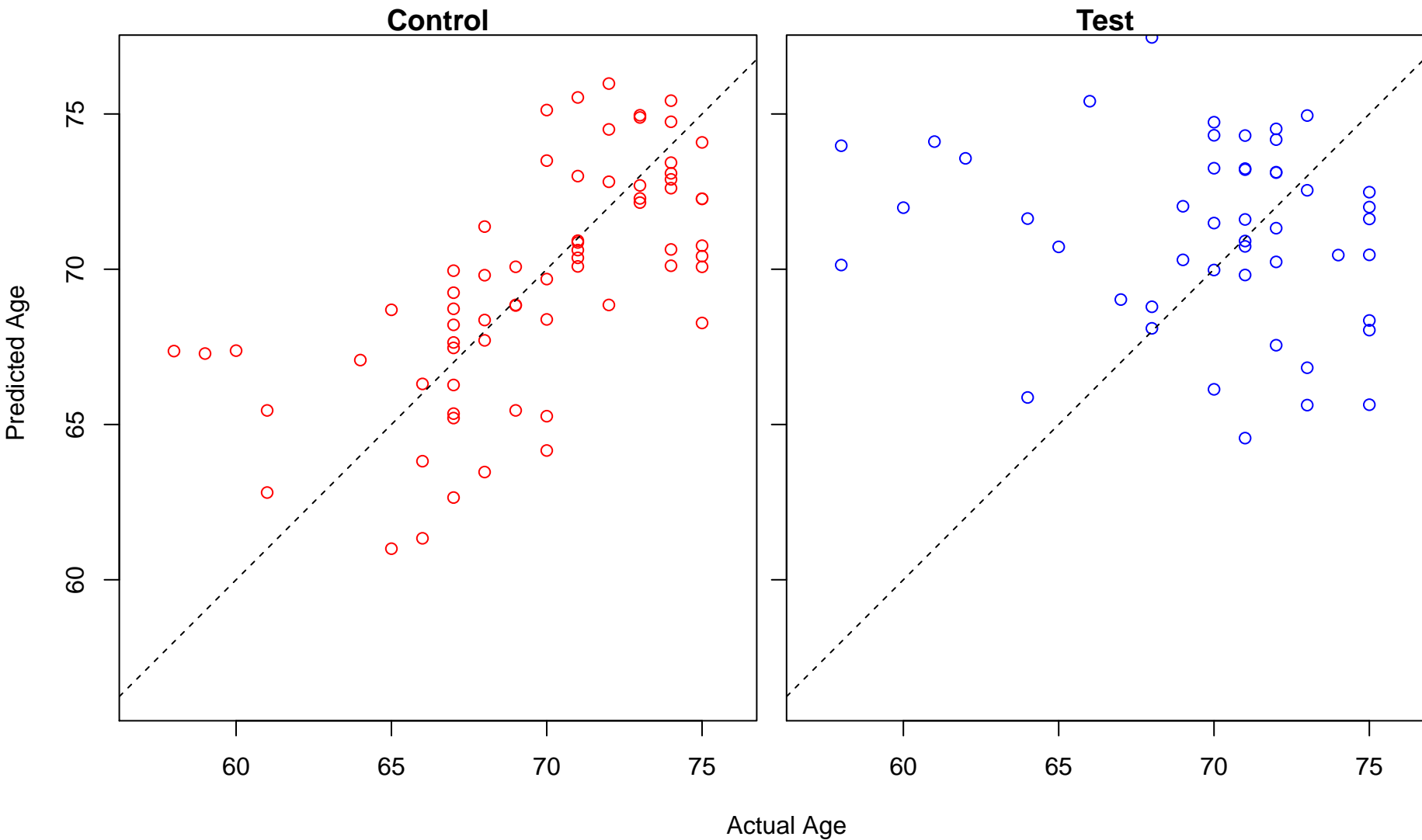
thymic T cell selection (Score: 1.569556)



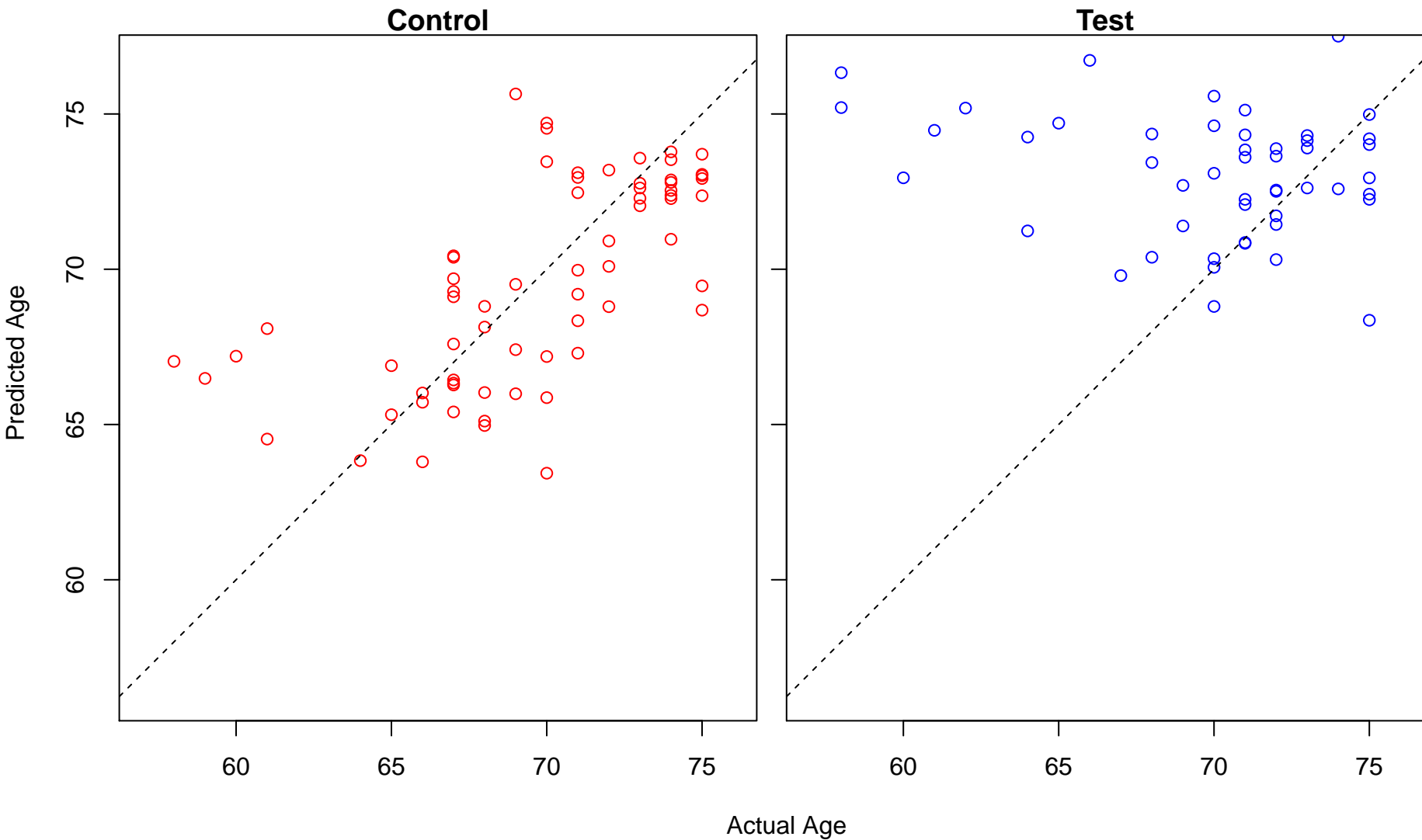
response to mechanical stimulus (Score: 1.568537)



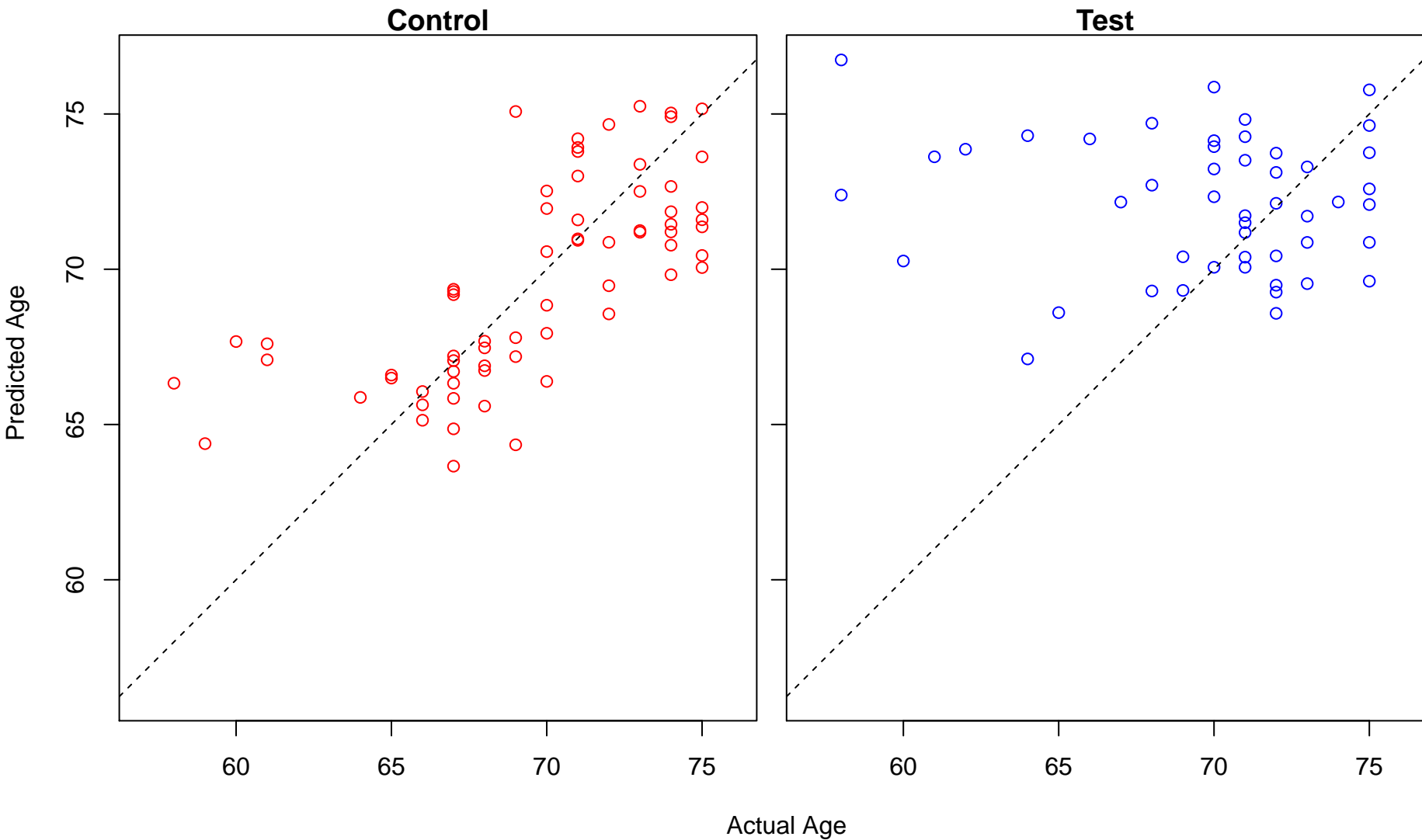
positive regulation of interleukin-1 production (Score: 1.568458)



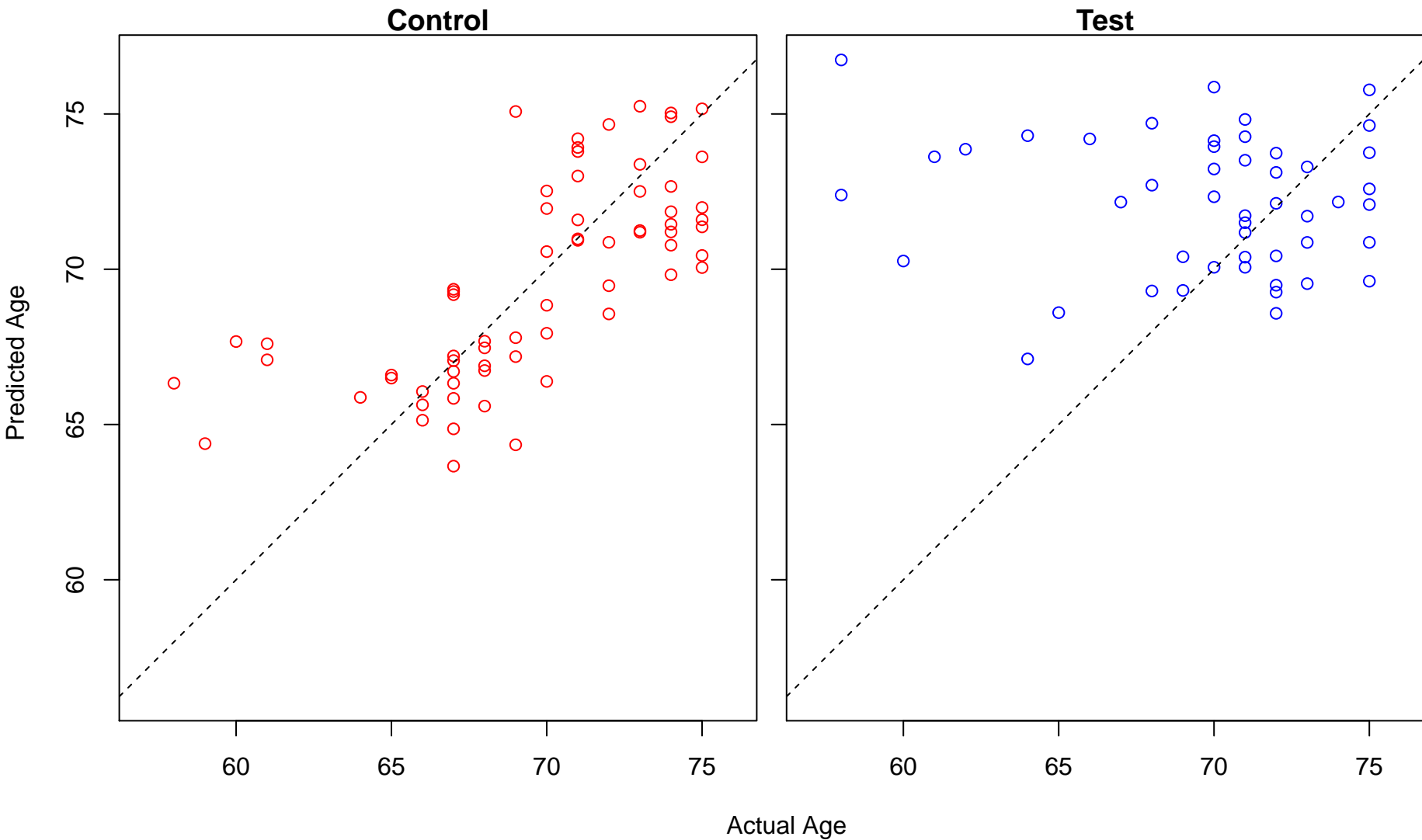
regulation of type I interferon-mediated signaling pathway (Score: 1.567074)



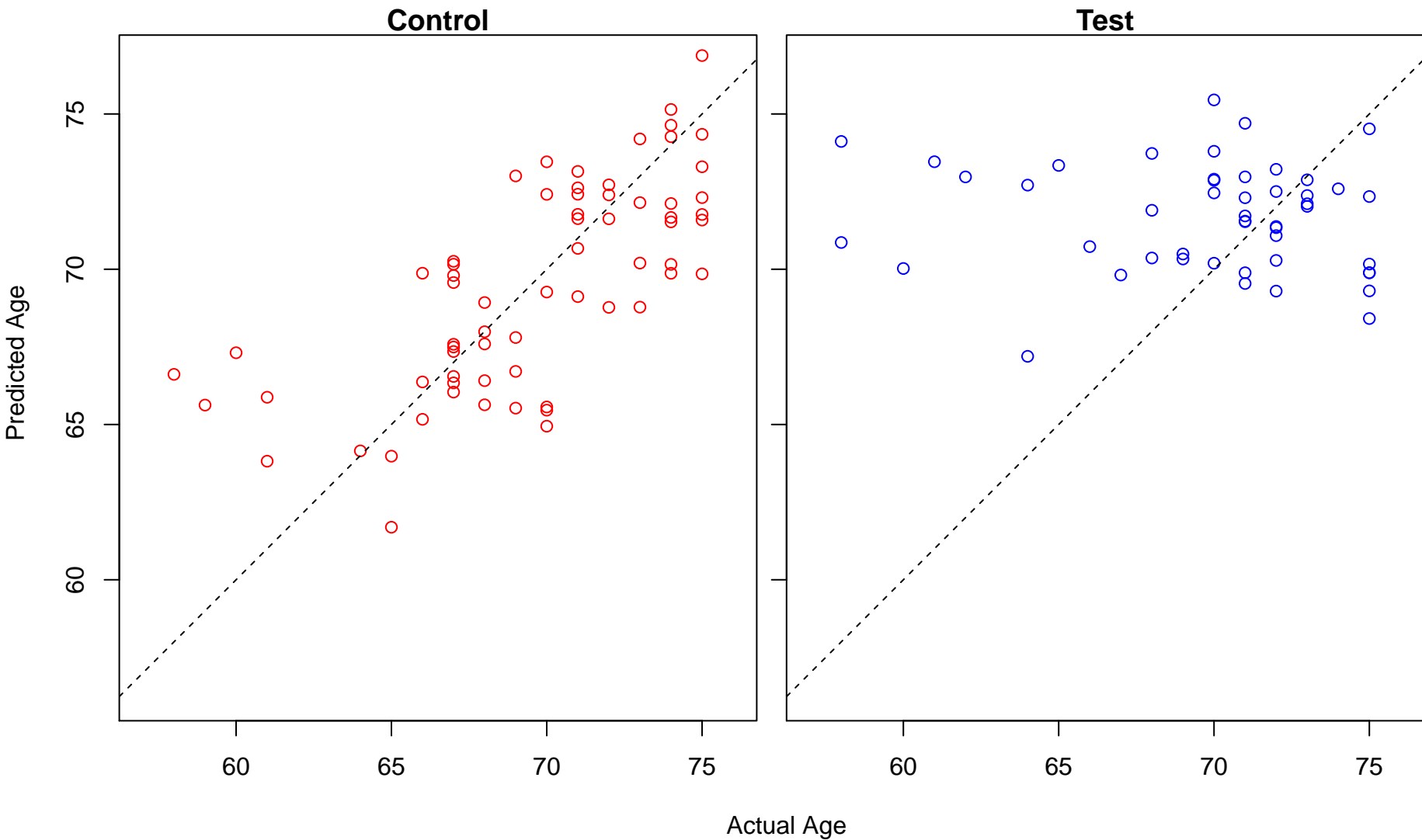
muscle filament sliding (Score: 1.567060)



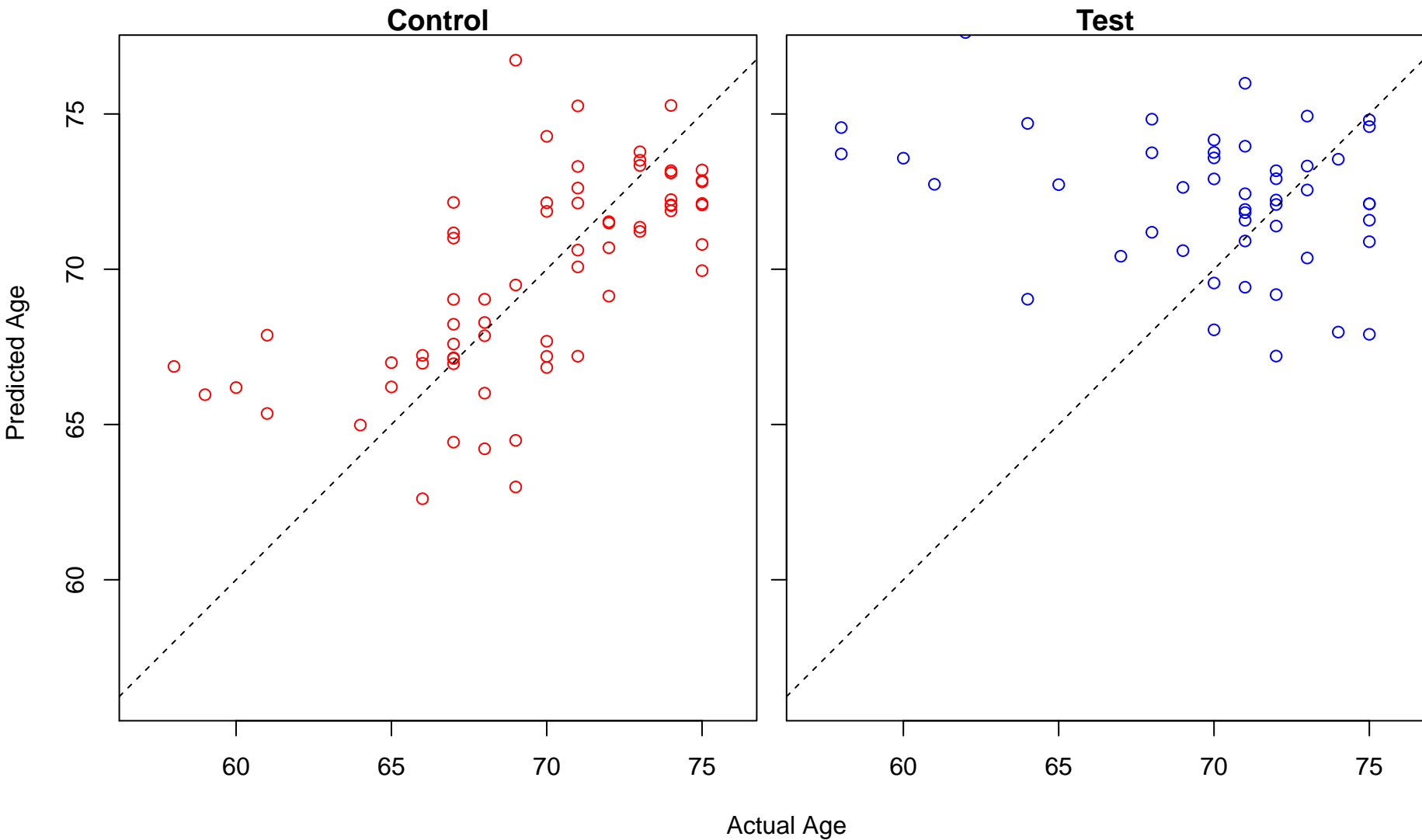
actin-myosin filament sliding (Score: 1.567060)



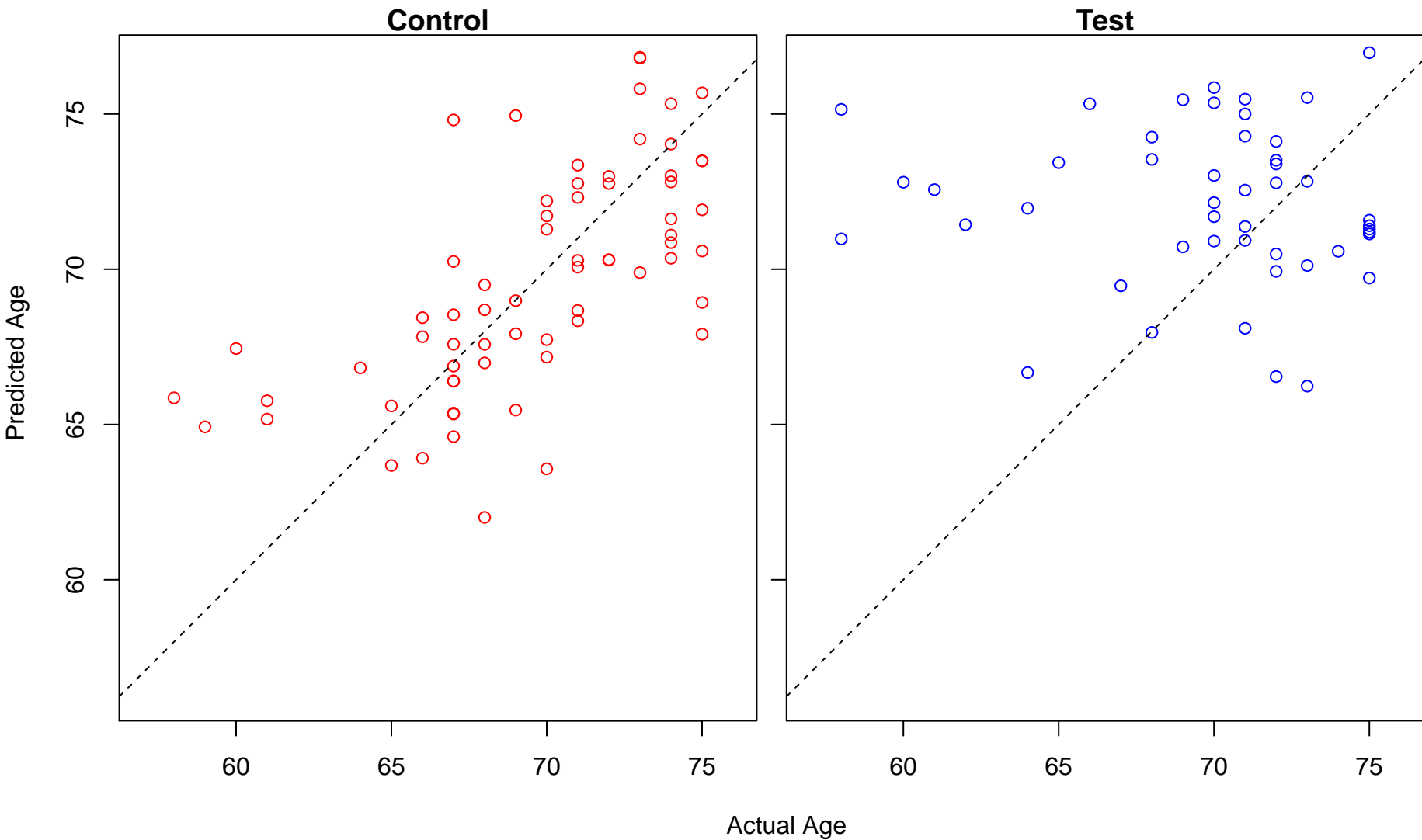
platelet activation (Score: 1.567007)



peptidyl-lysine trimethylation (Score: 1.566884)

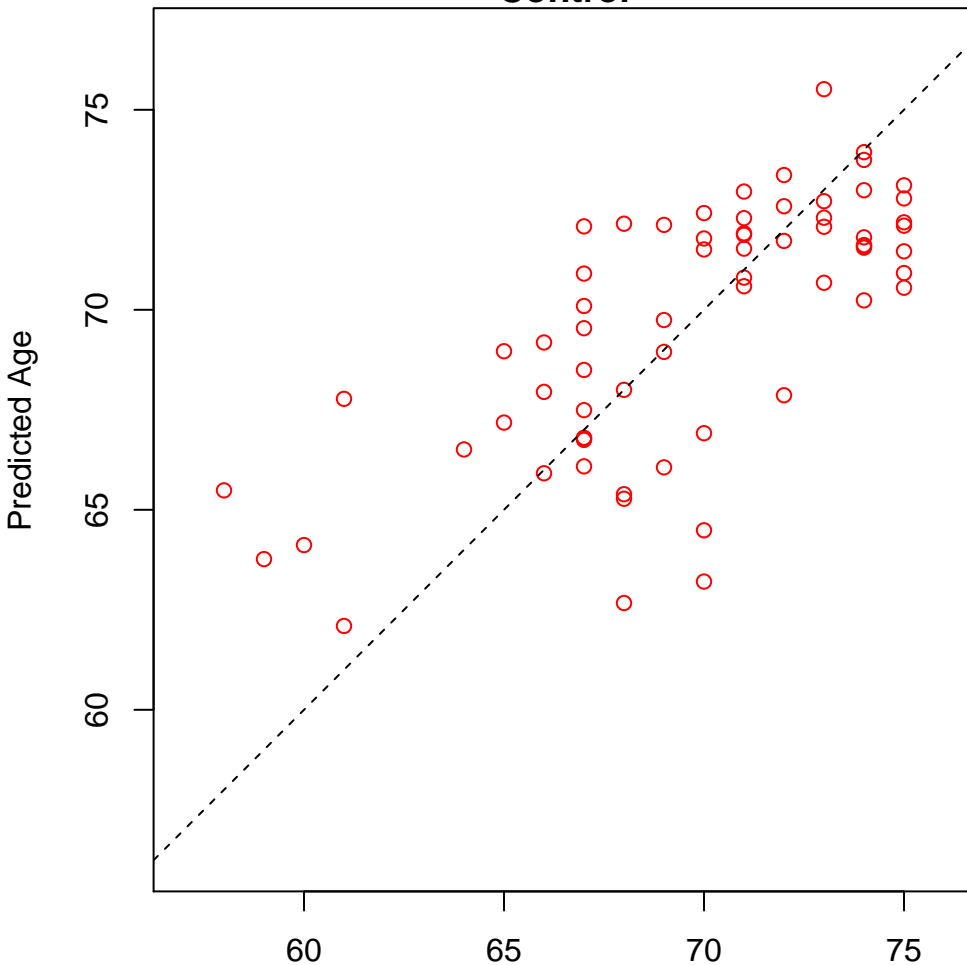


negative regulation of cell adhesion (Score: 1.566504)

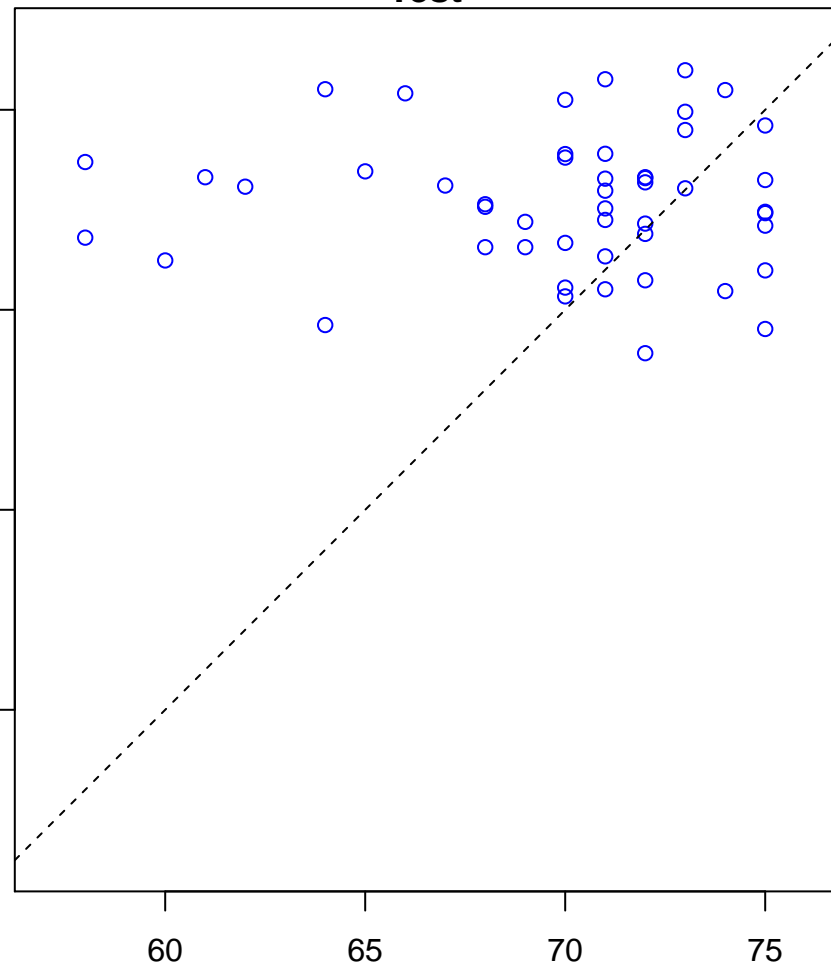


DNA double-strand break processing (Score: 1.565306)

Control

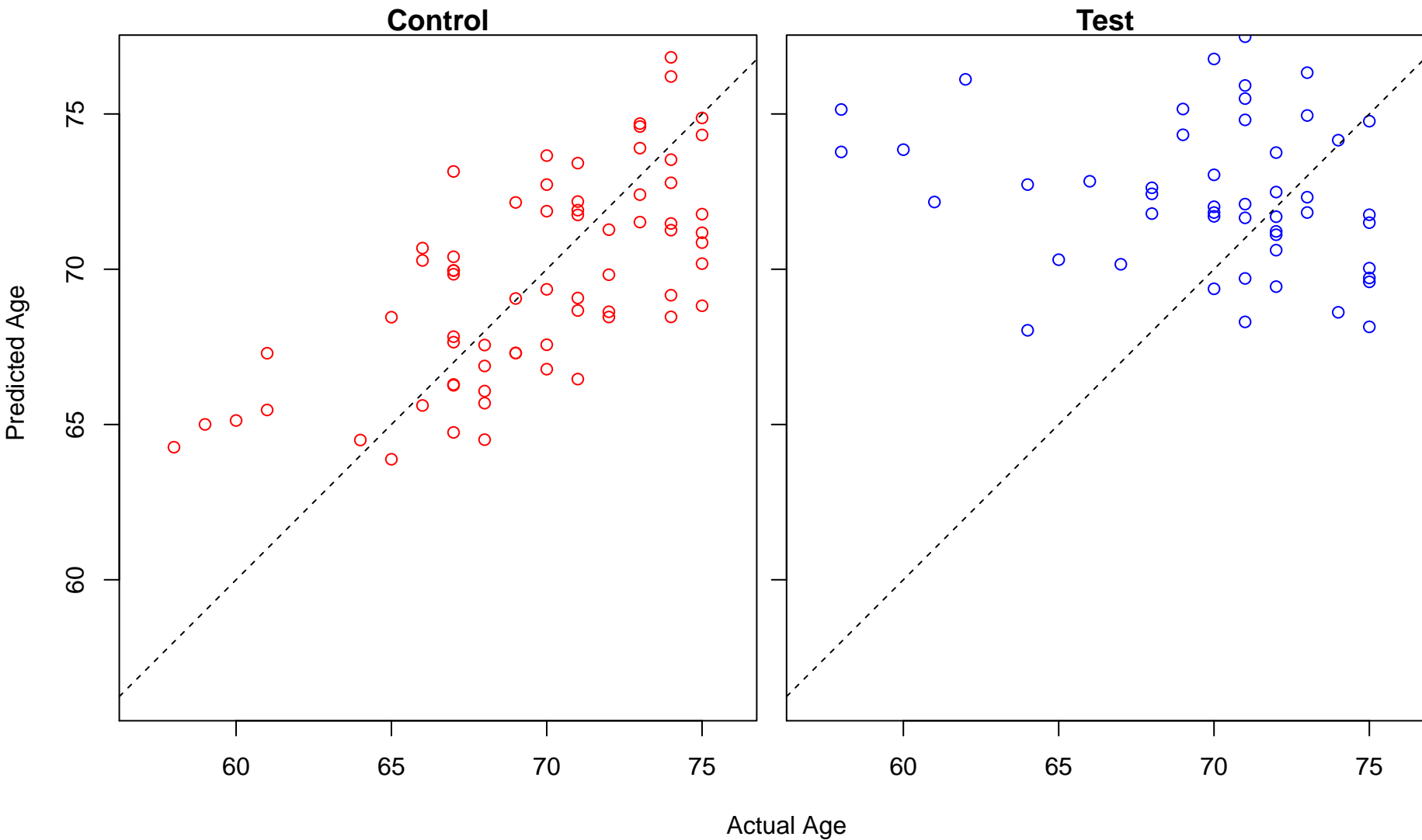


Test

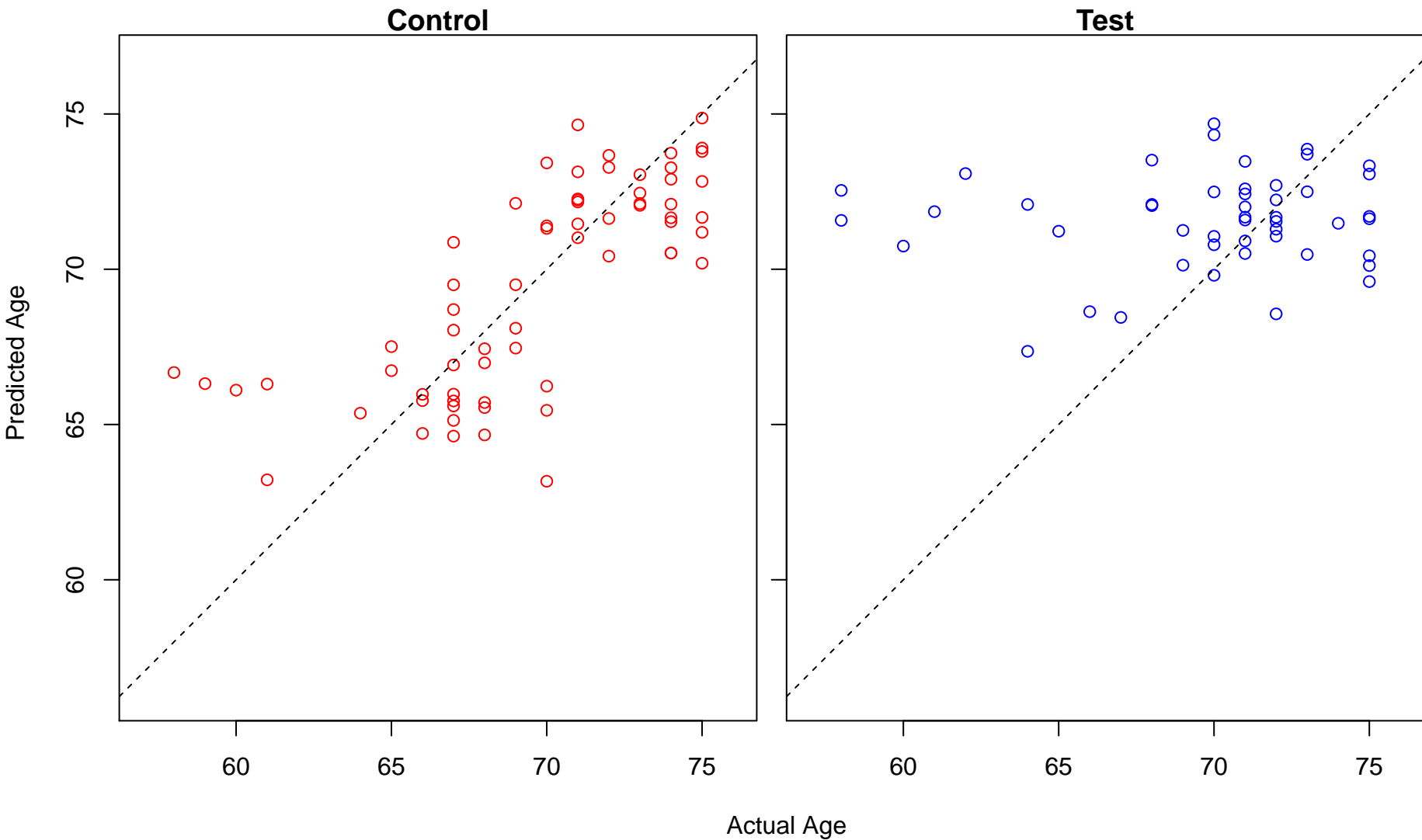


Actual Age

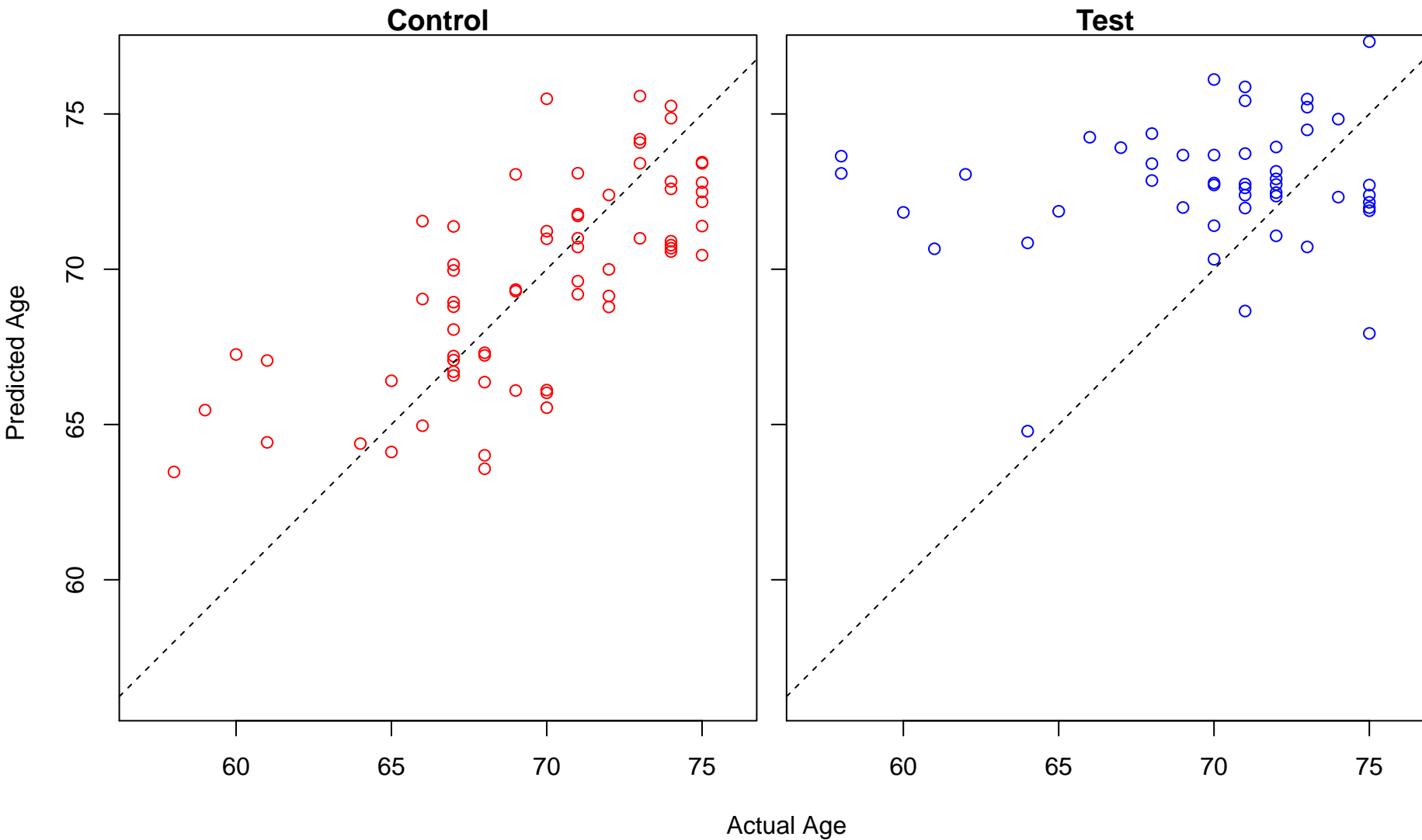
mitochondrion localization (Score: 1.564560)



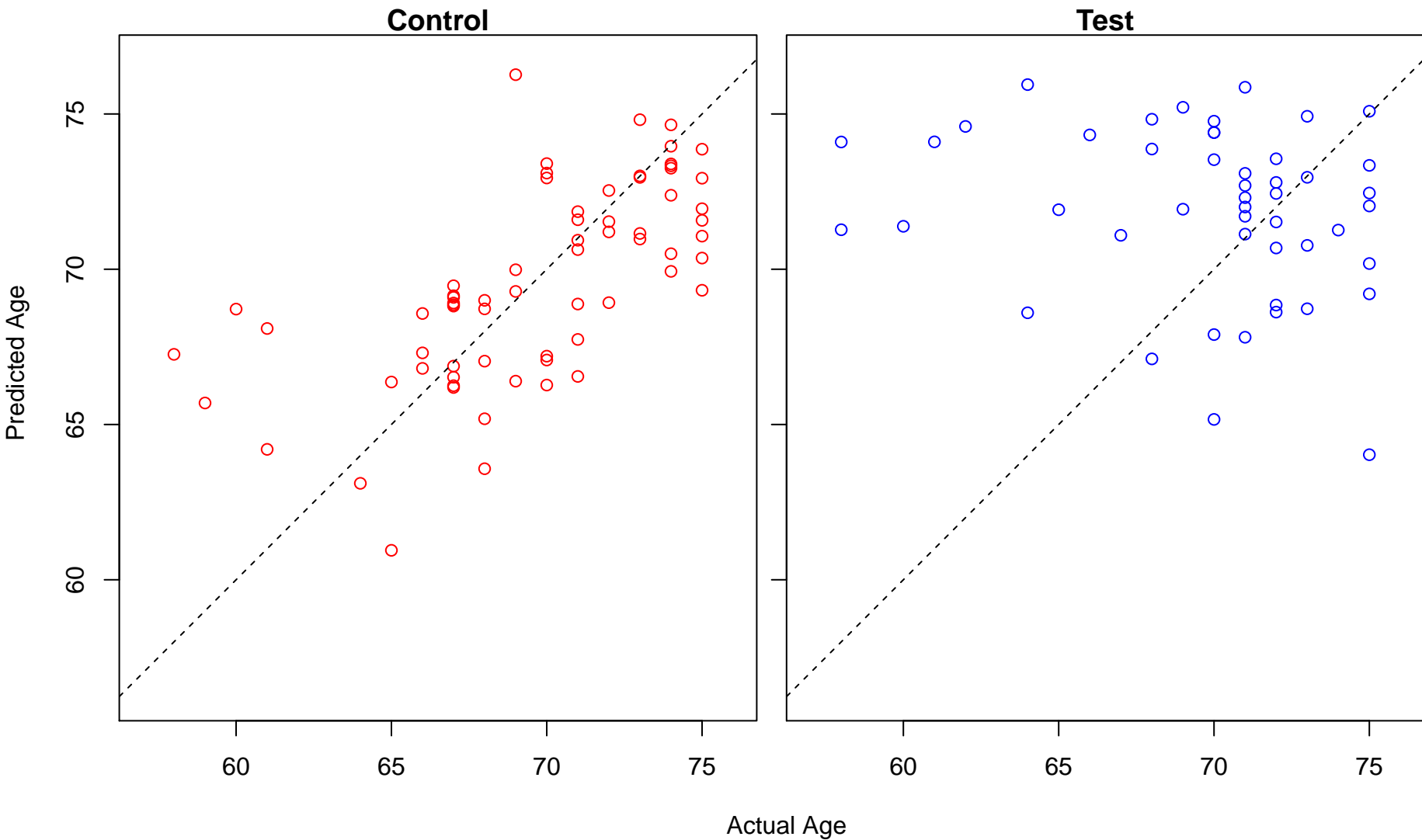
ATP metabolic process (Score: 1.564390)



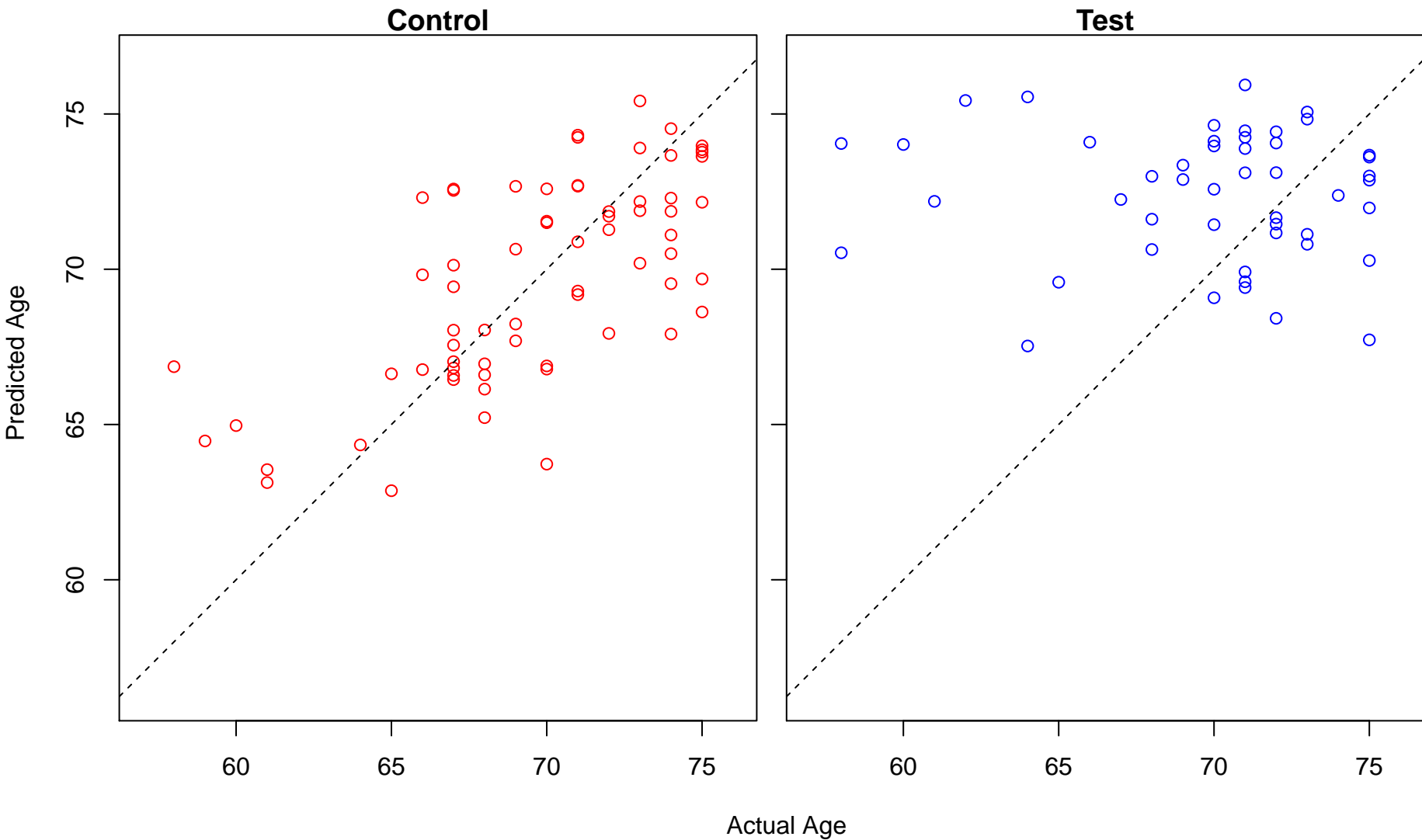
Golgi to endosome transport (Score: 1.564098)



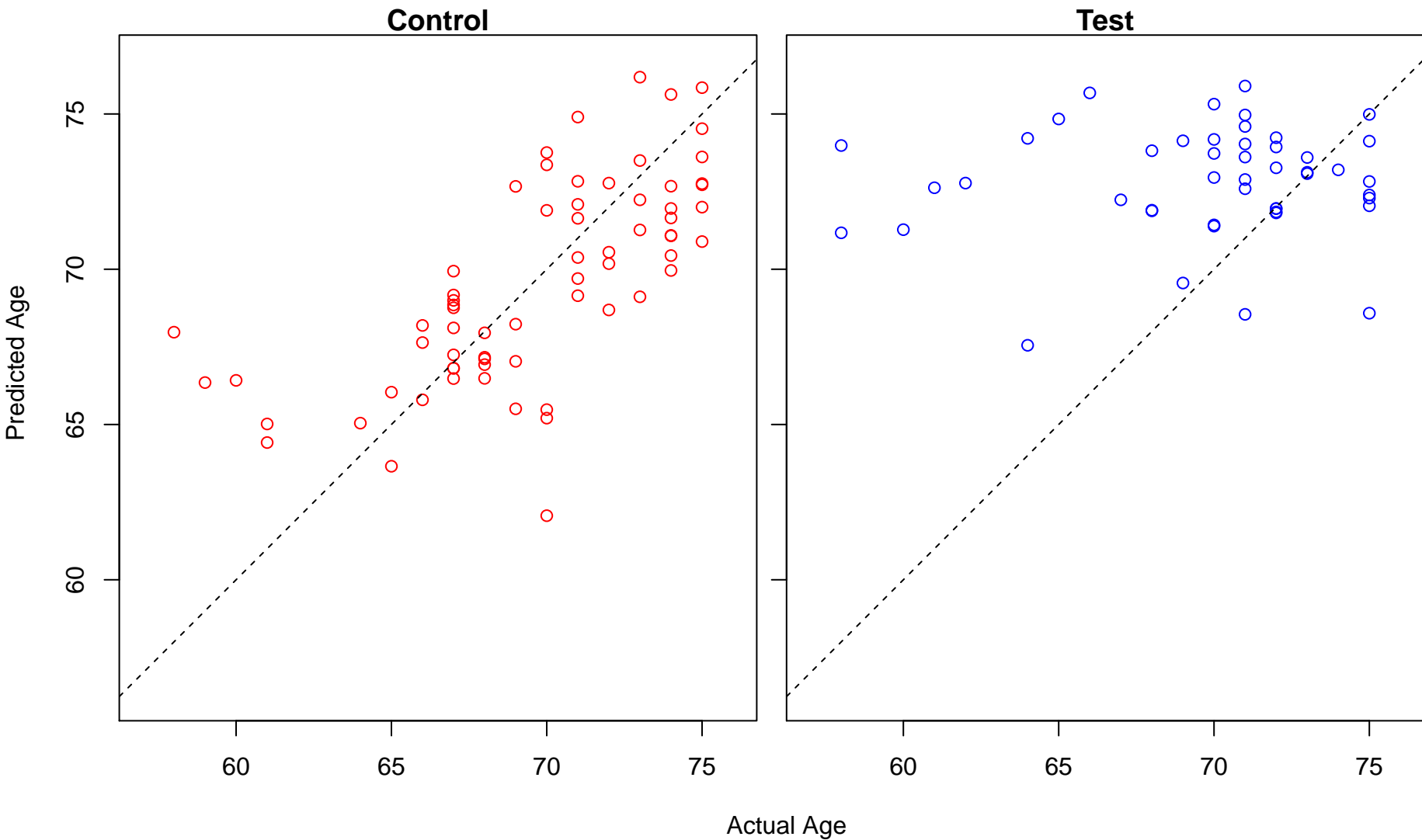
negative regulation of innate immune response (Score: 1.564031)



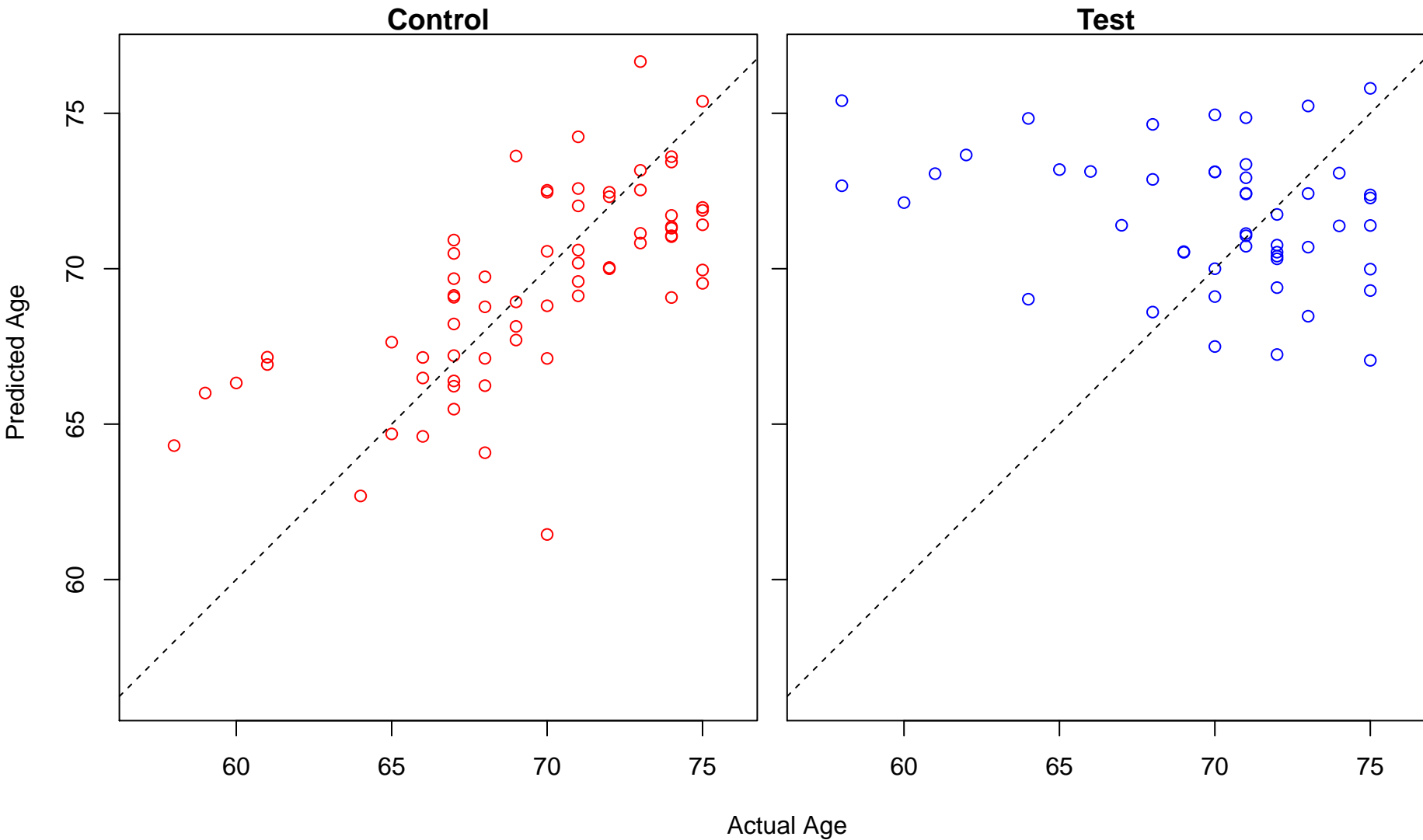
regulation of epidermal growth factor receptor signaling pathway (Score: 1.563493)



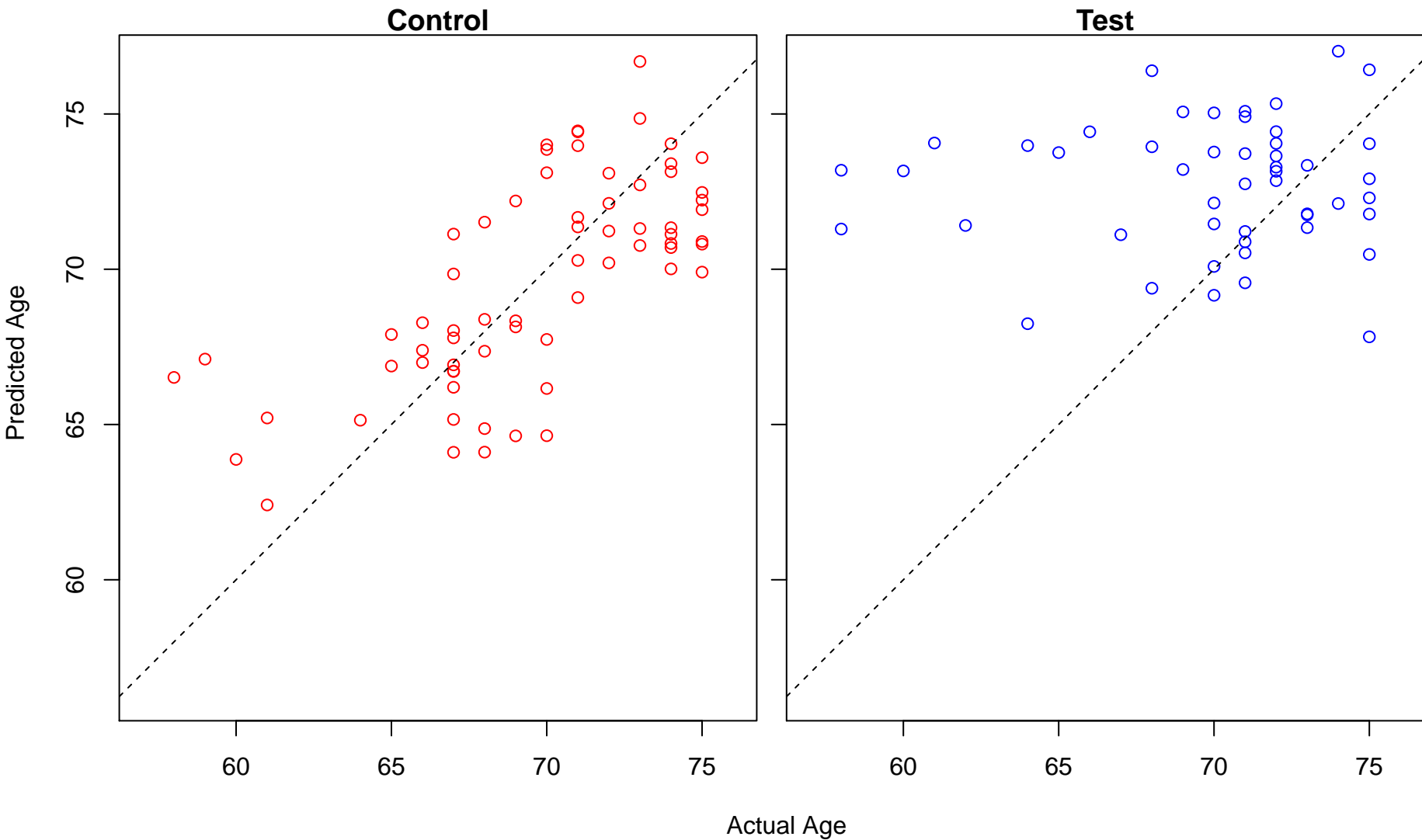
transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 1.563381)



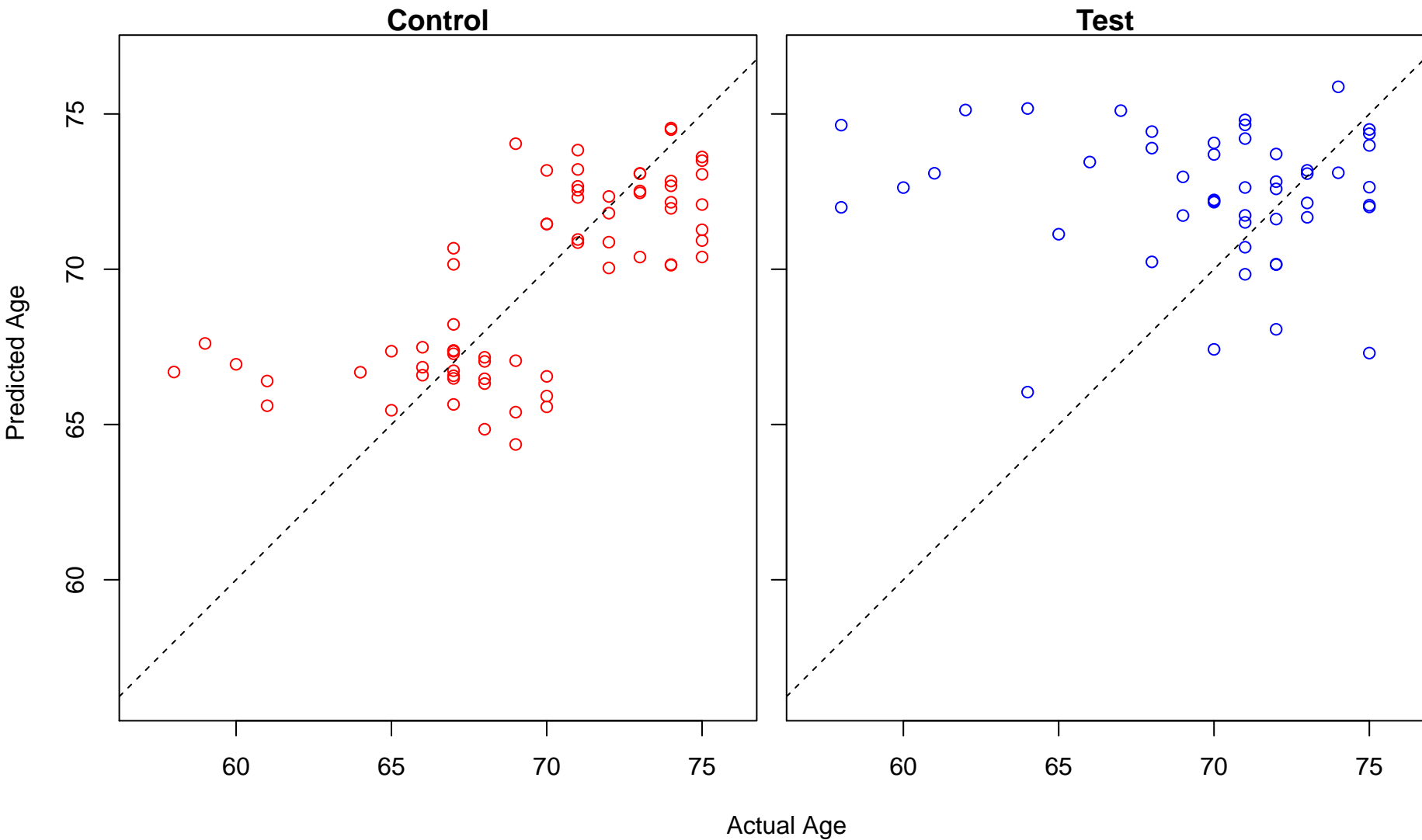
preassembly of GPI anchor in ER membrane (Score: 1.562977)



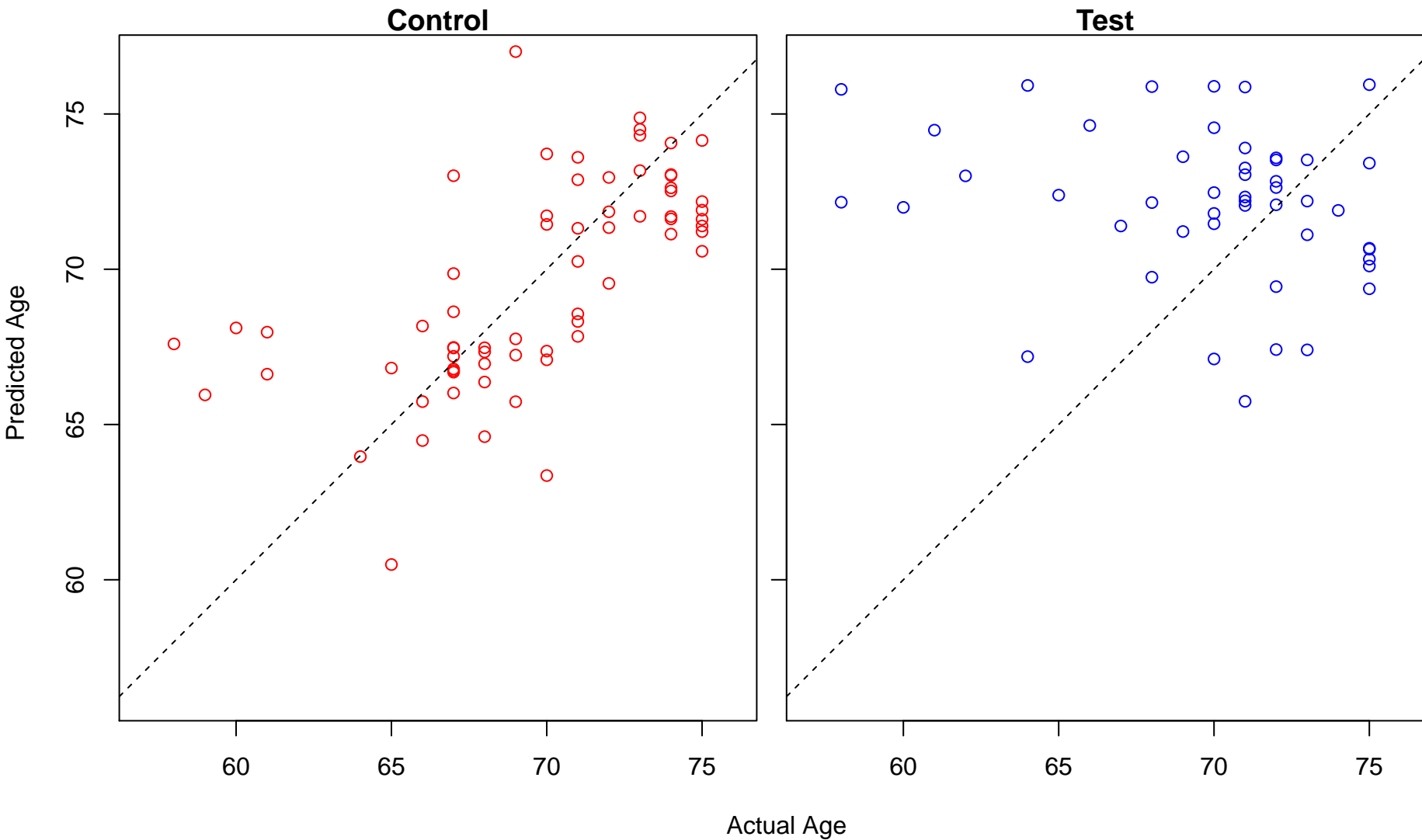
chromatin silencing (Score: 1.562780)



negative regulation of behavior (Score: 1.562551)

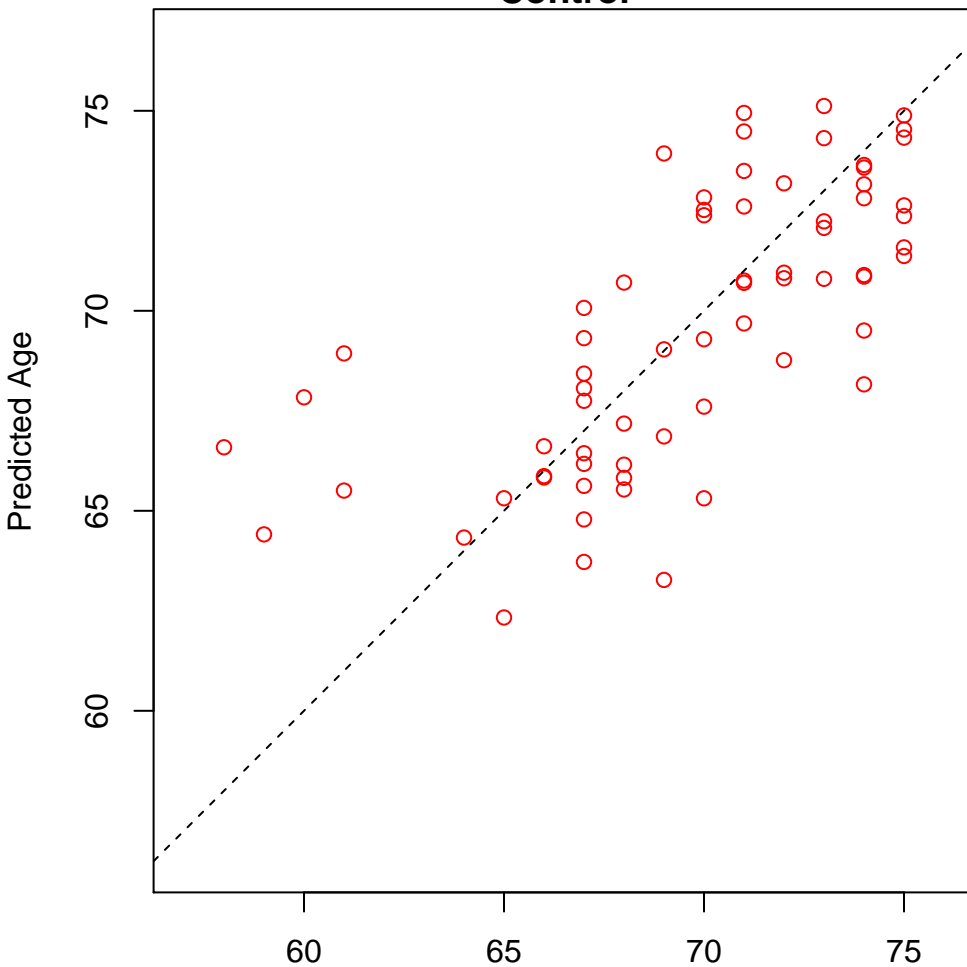


regulation of protein secretion (Score: 1.561909)

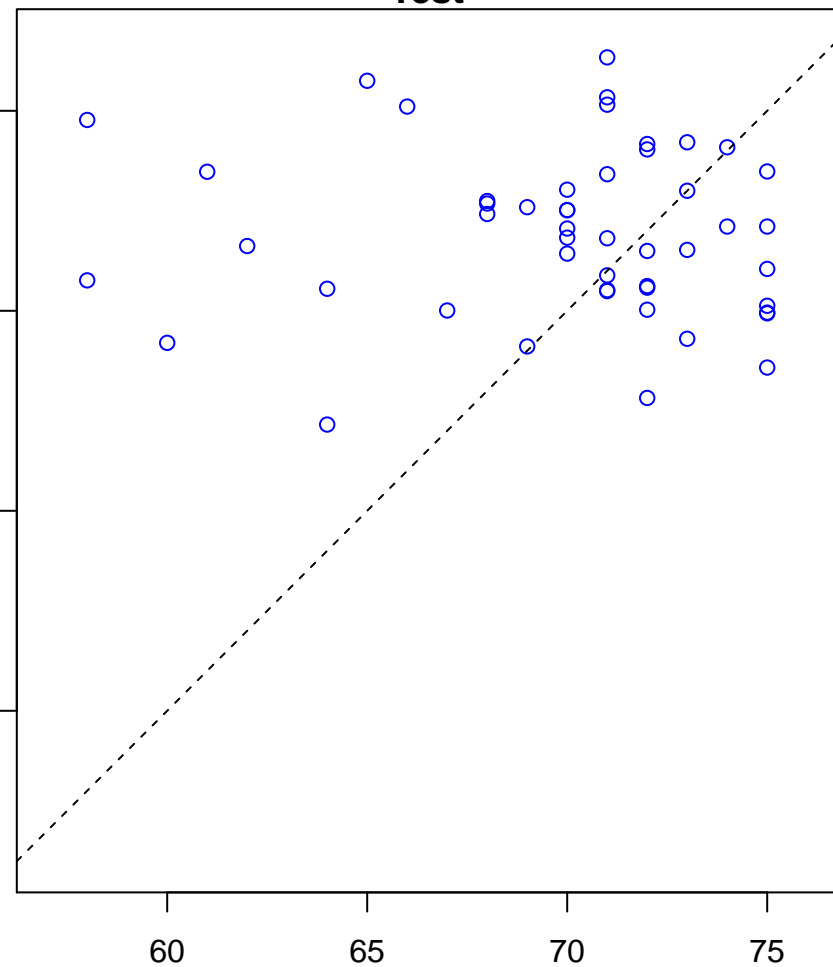


circadian regulation of gene expression (Score: 1.561188)

Control

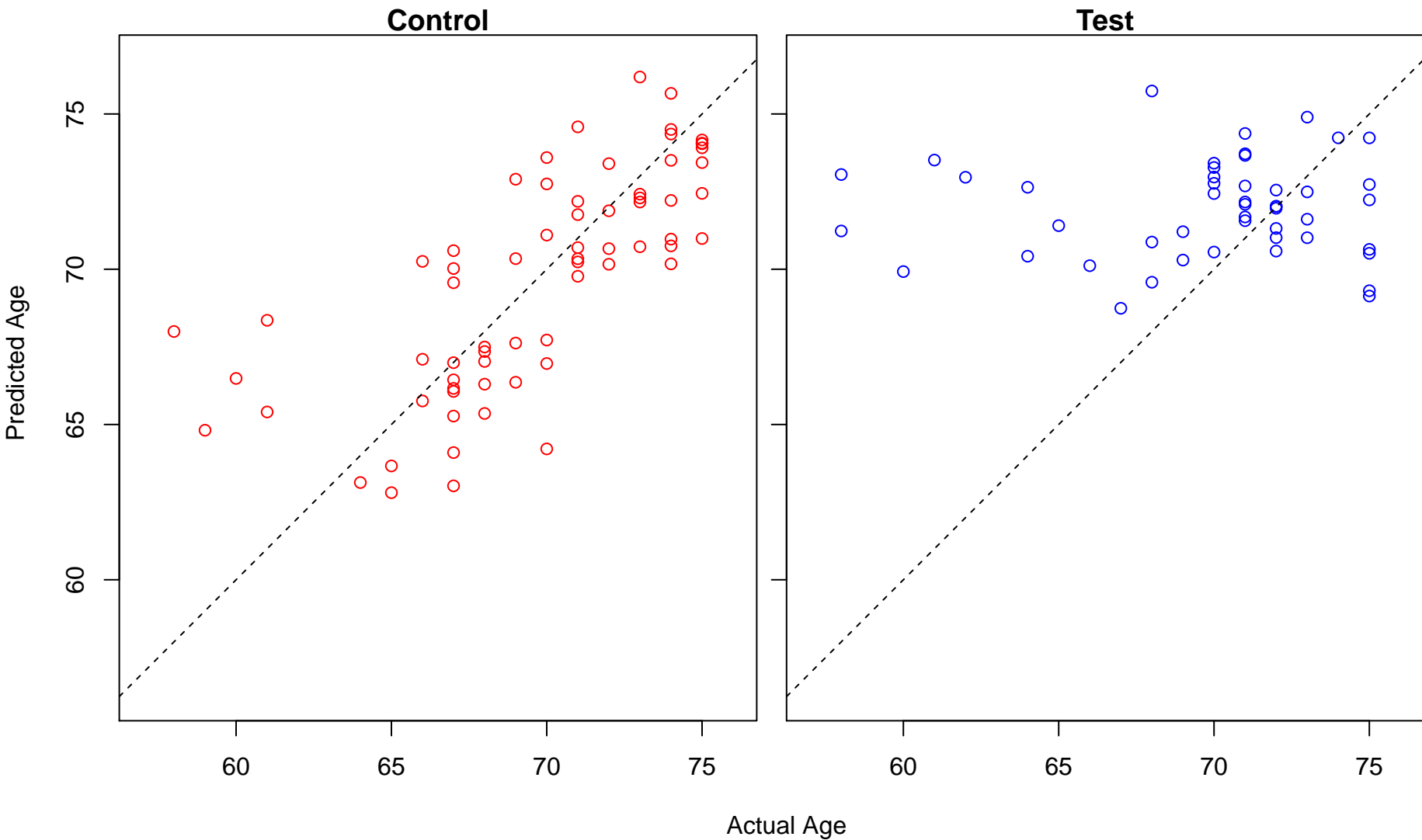


Test



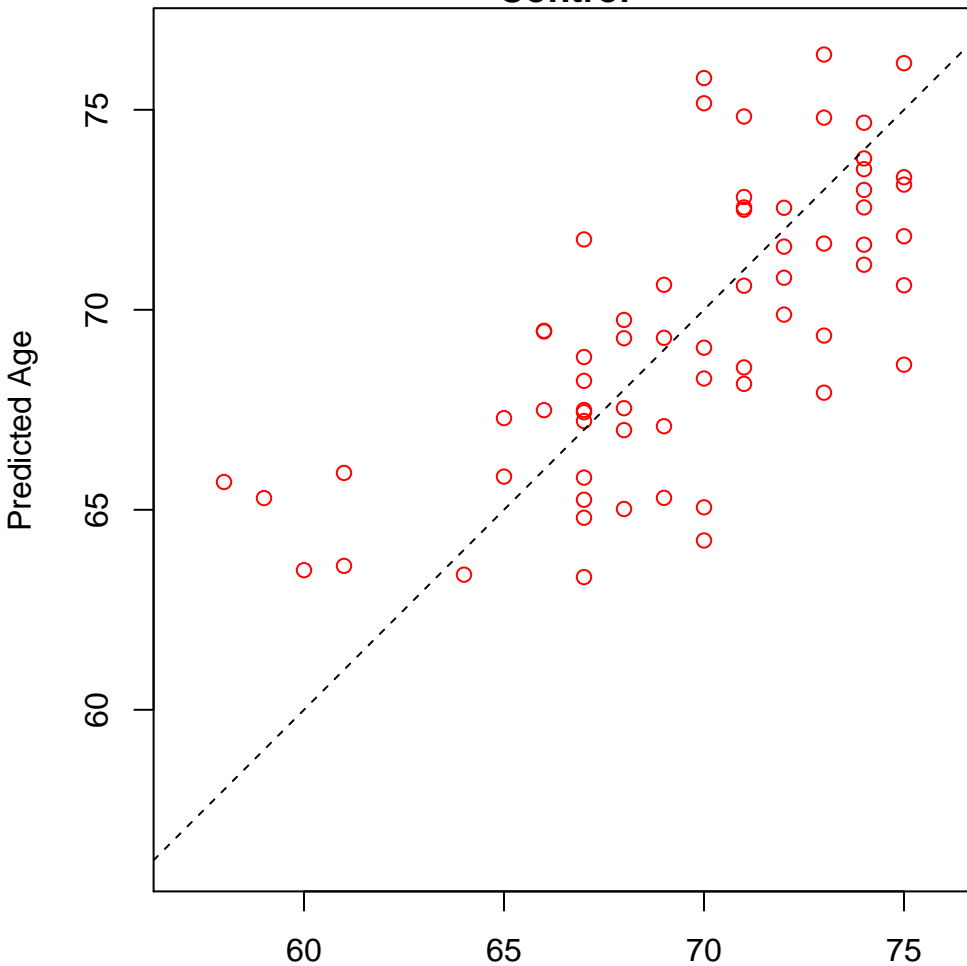
Actual Age

modification-dependent macromolecule catabolic process (Score: 1.561049)

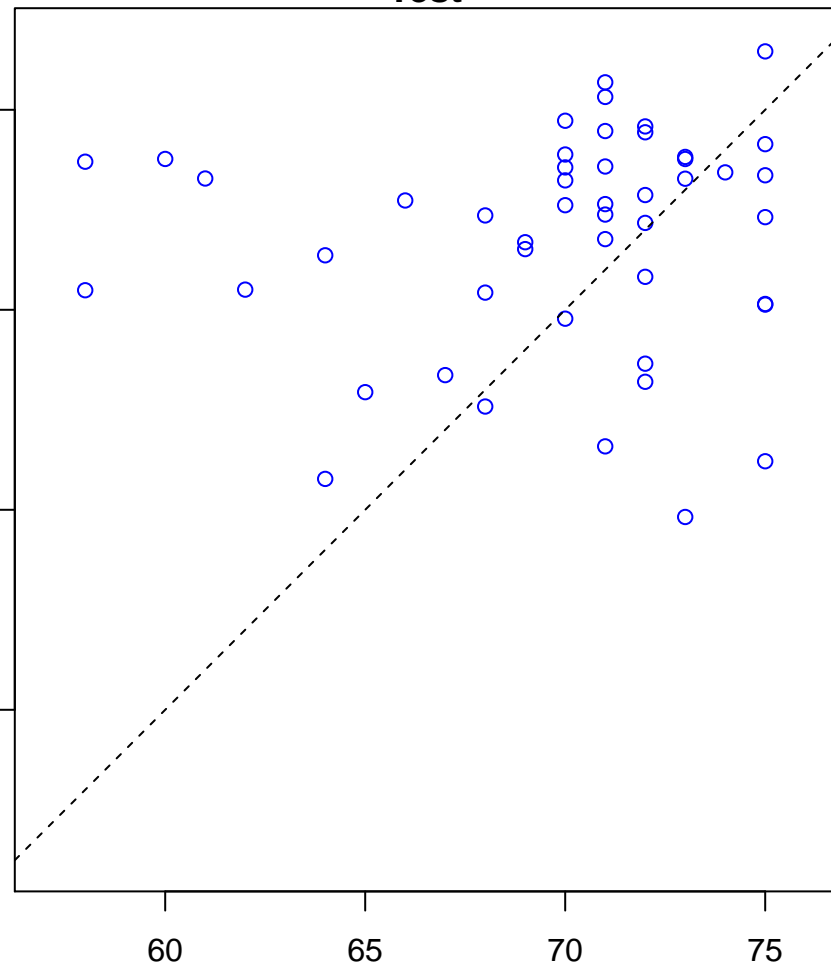


regulation of endothelial cell proliferation (Score: 1.560133)

Control

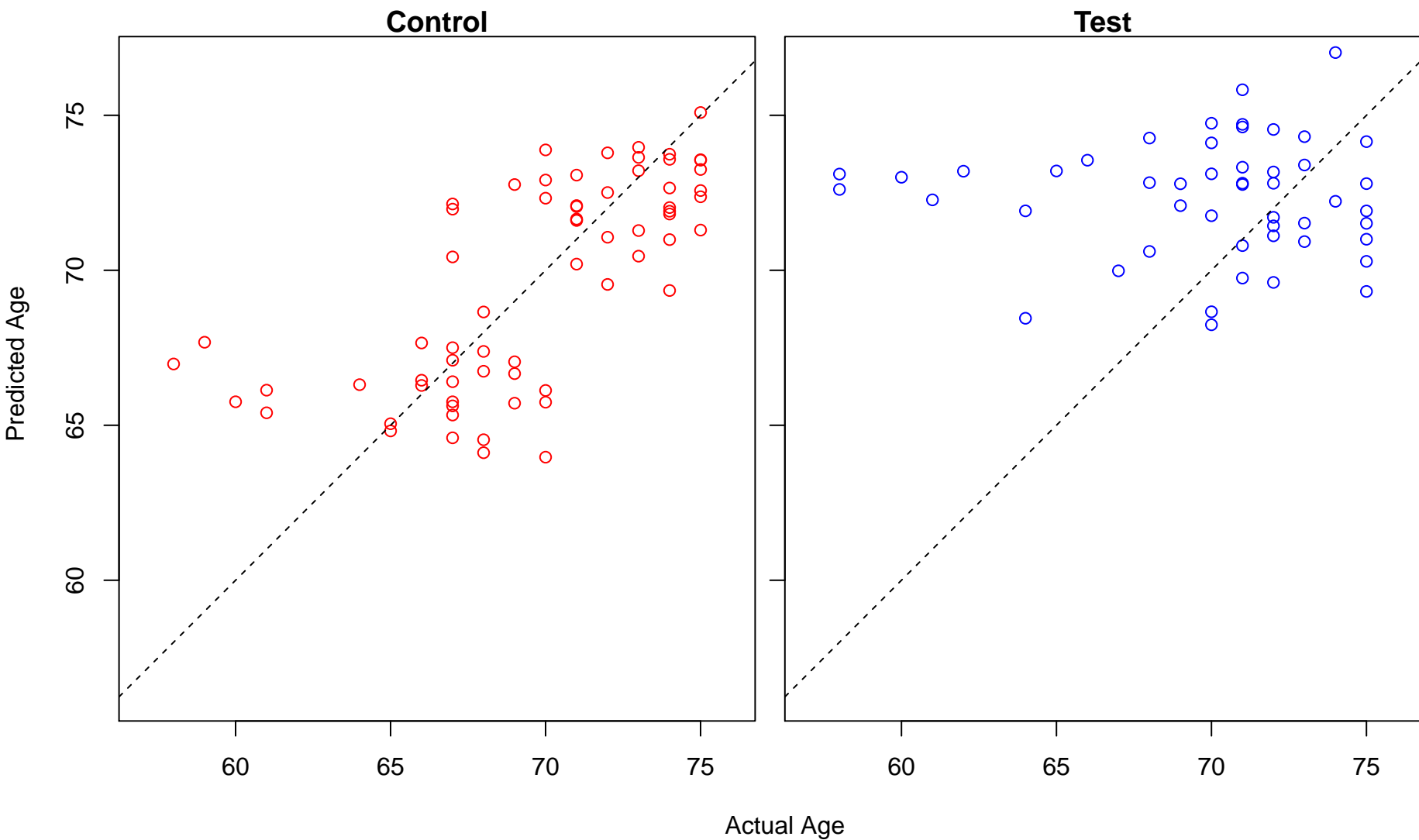


Test

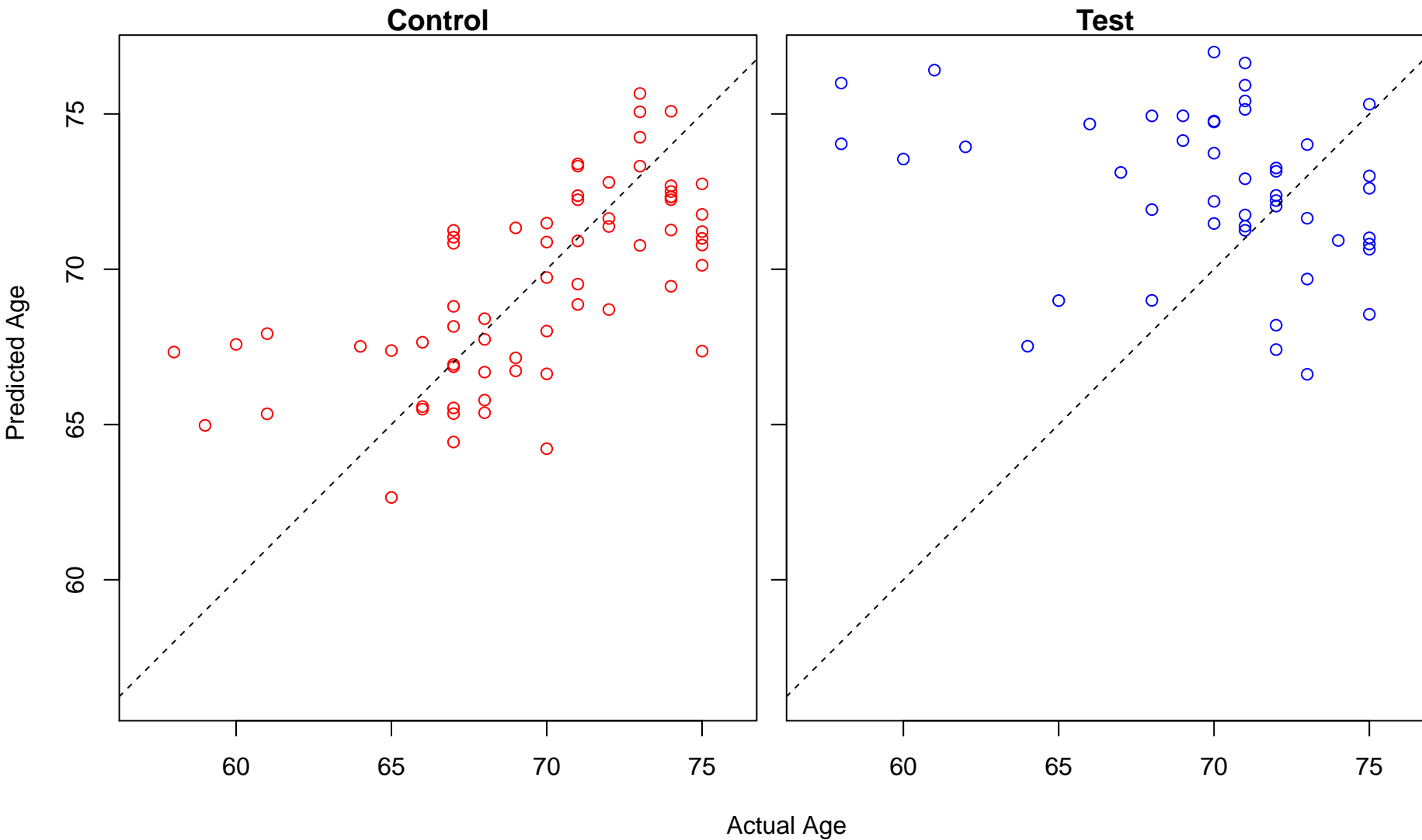


Actual Age

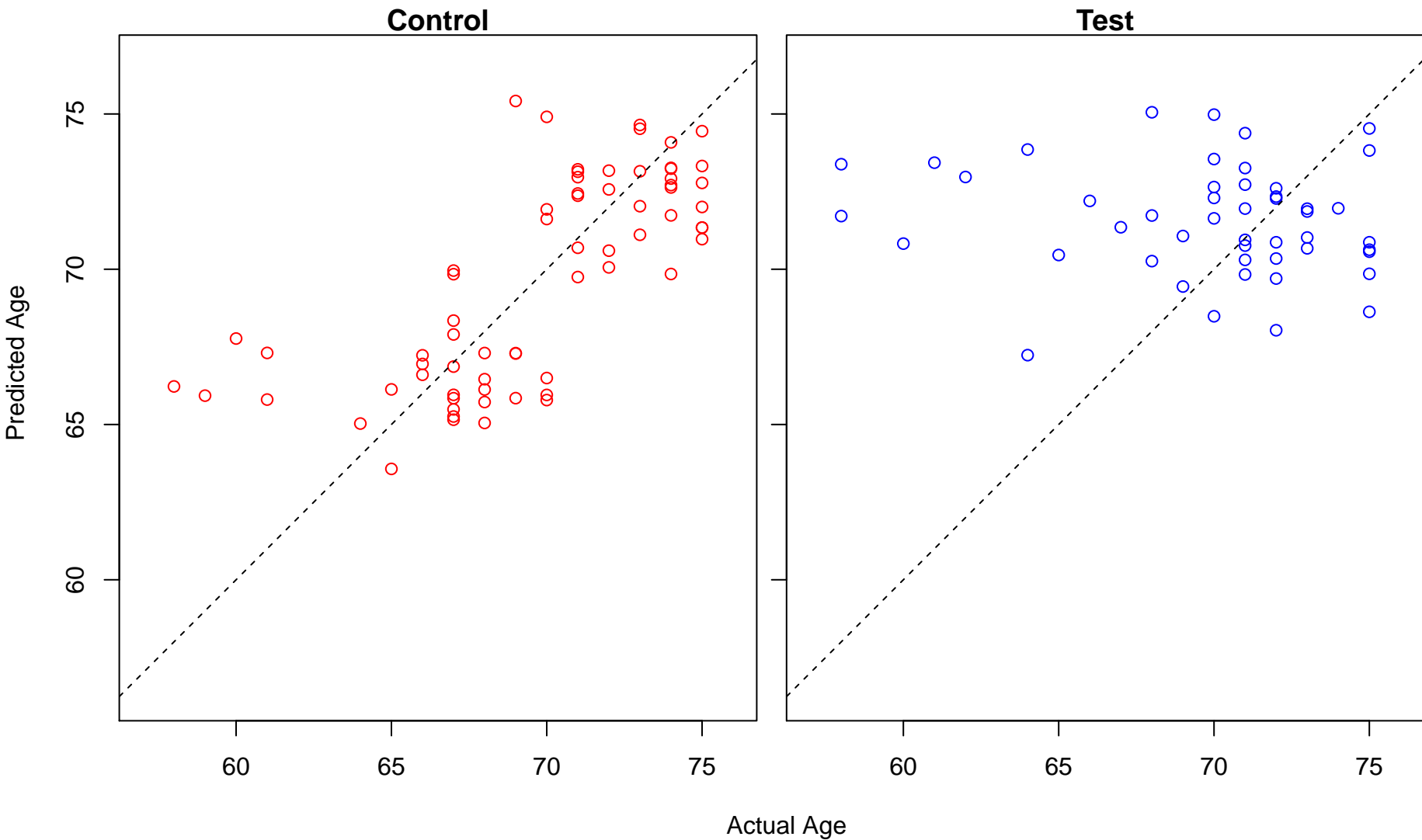
positive regulation of myeloid cell differentiation (Score: 1.559019)



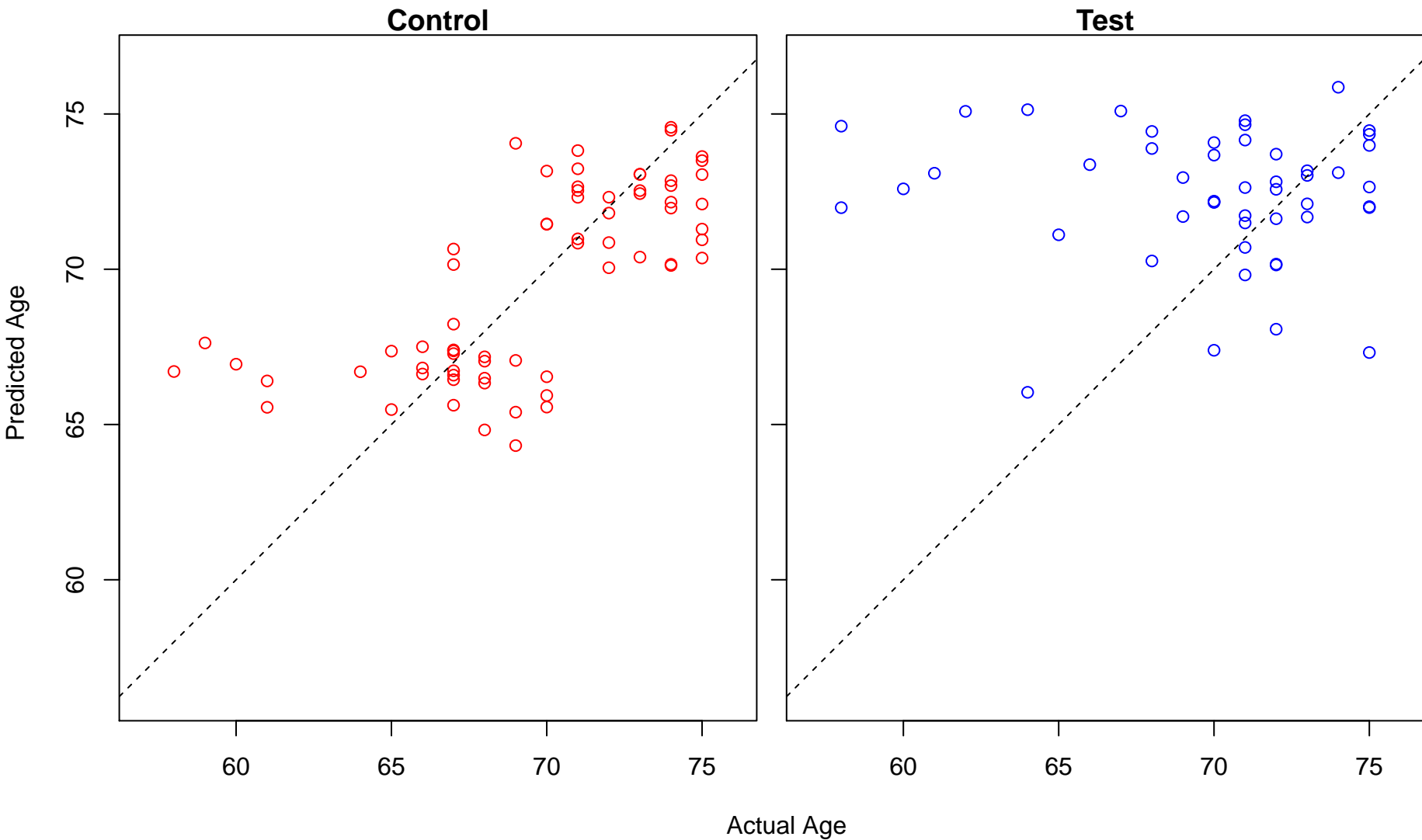
positive regulation of alpha-beta T cell activation (Score: 1.558829)



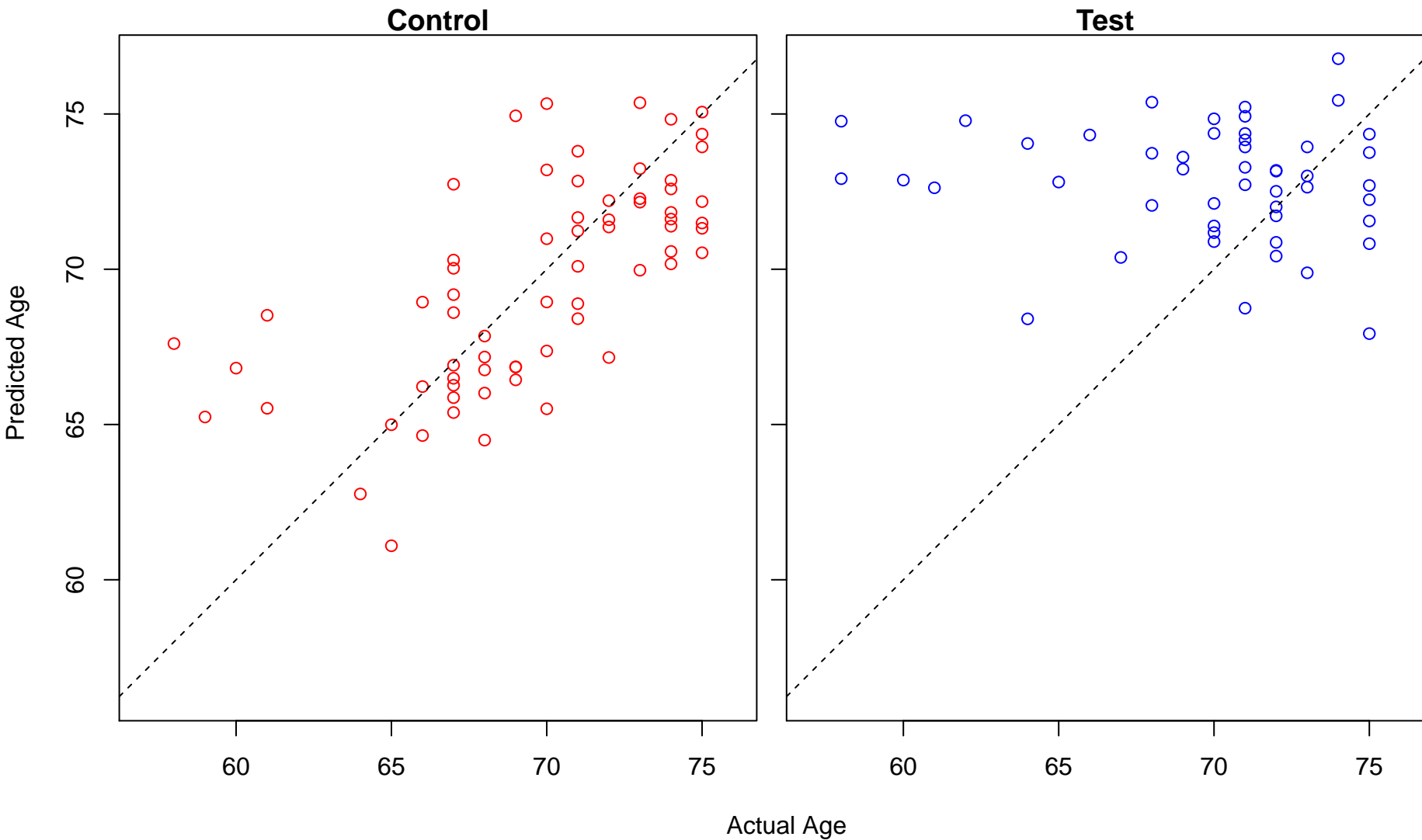
cellular response to tumor necrosis factor (Score: 1.558087)



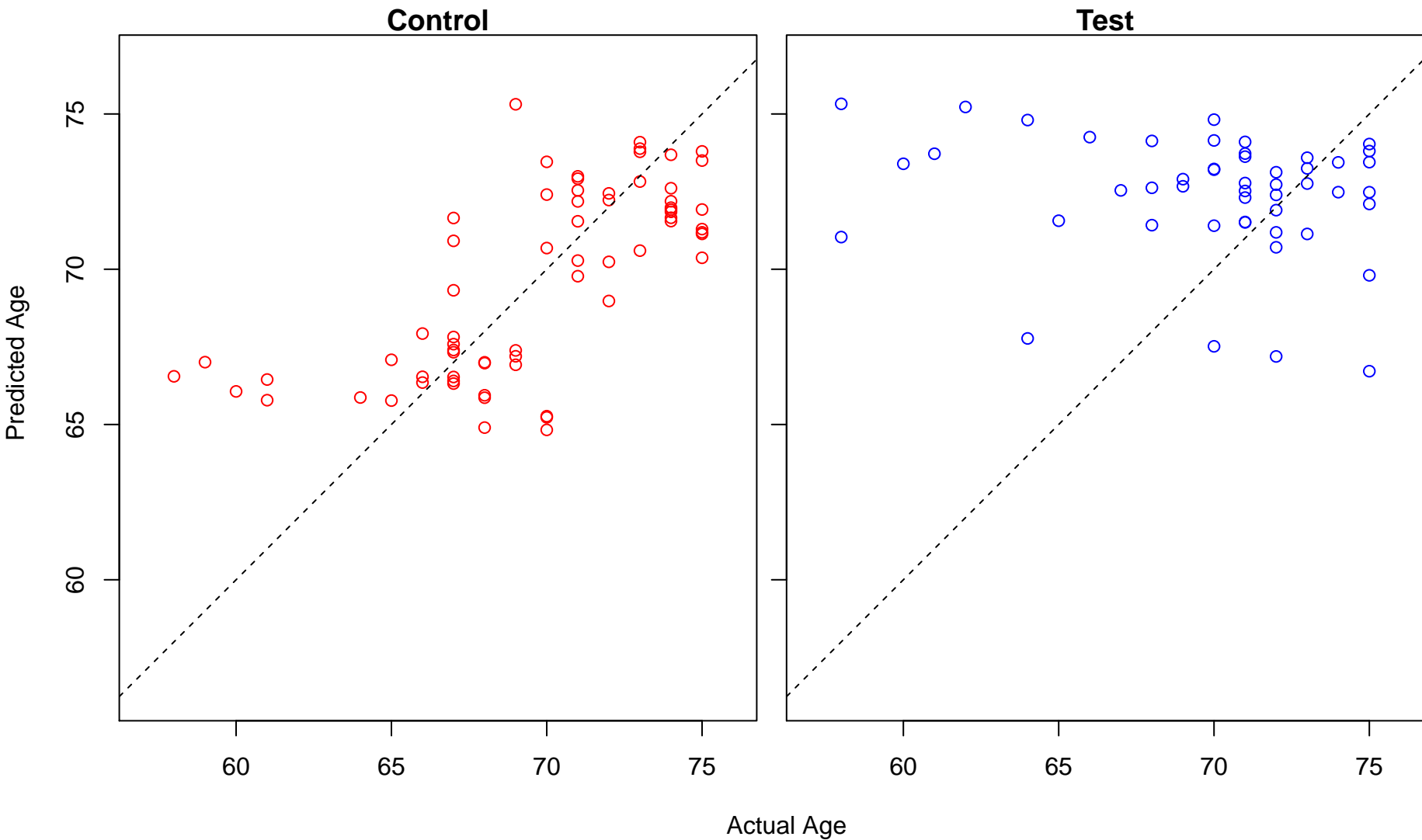
negative regulation of chemotaxis (Score: 1.557624)



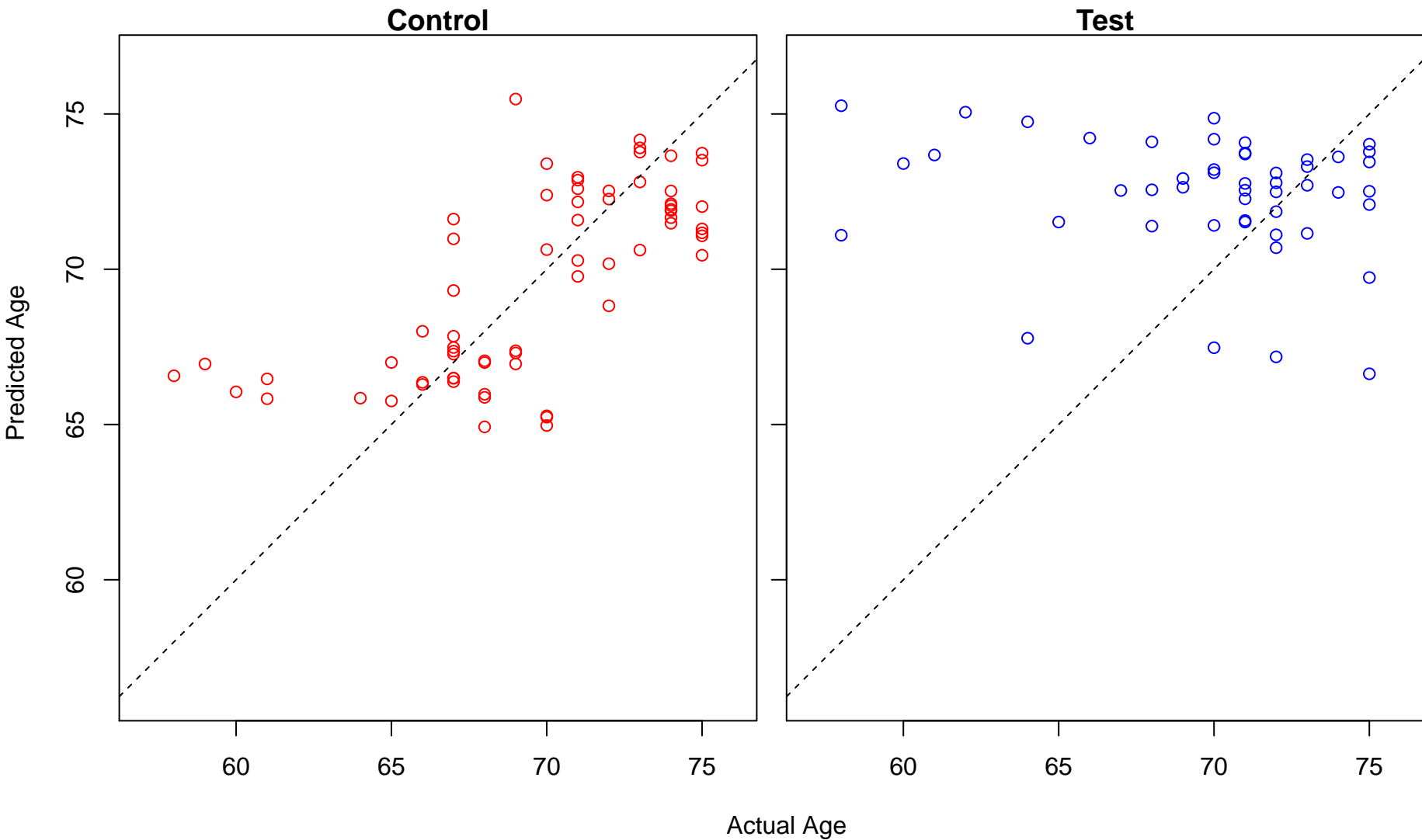
negative regulation of protein phosphorylation (Score: 1.557557)



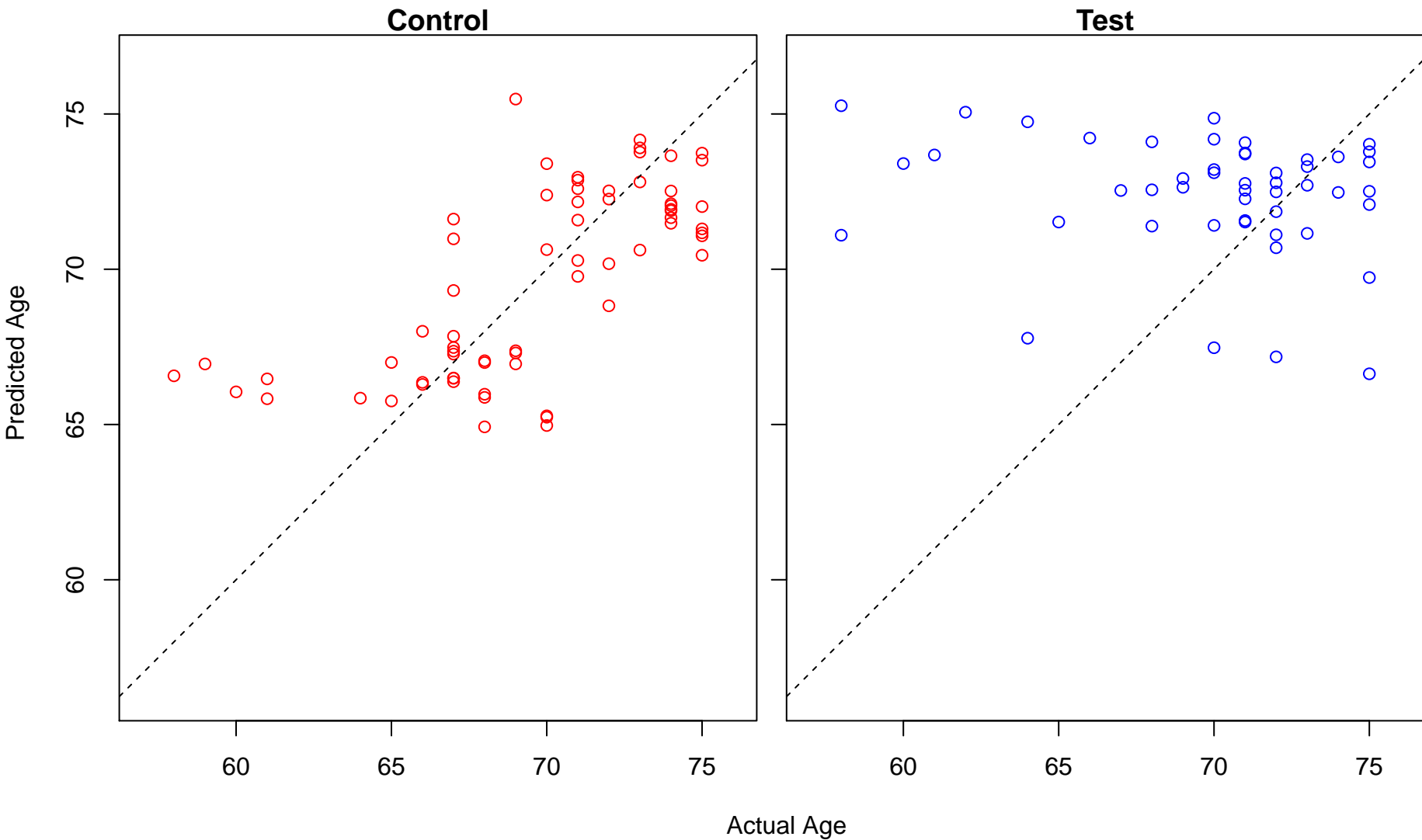
ribose phosphate biosynthetic process (Score: 1.556816)



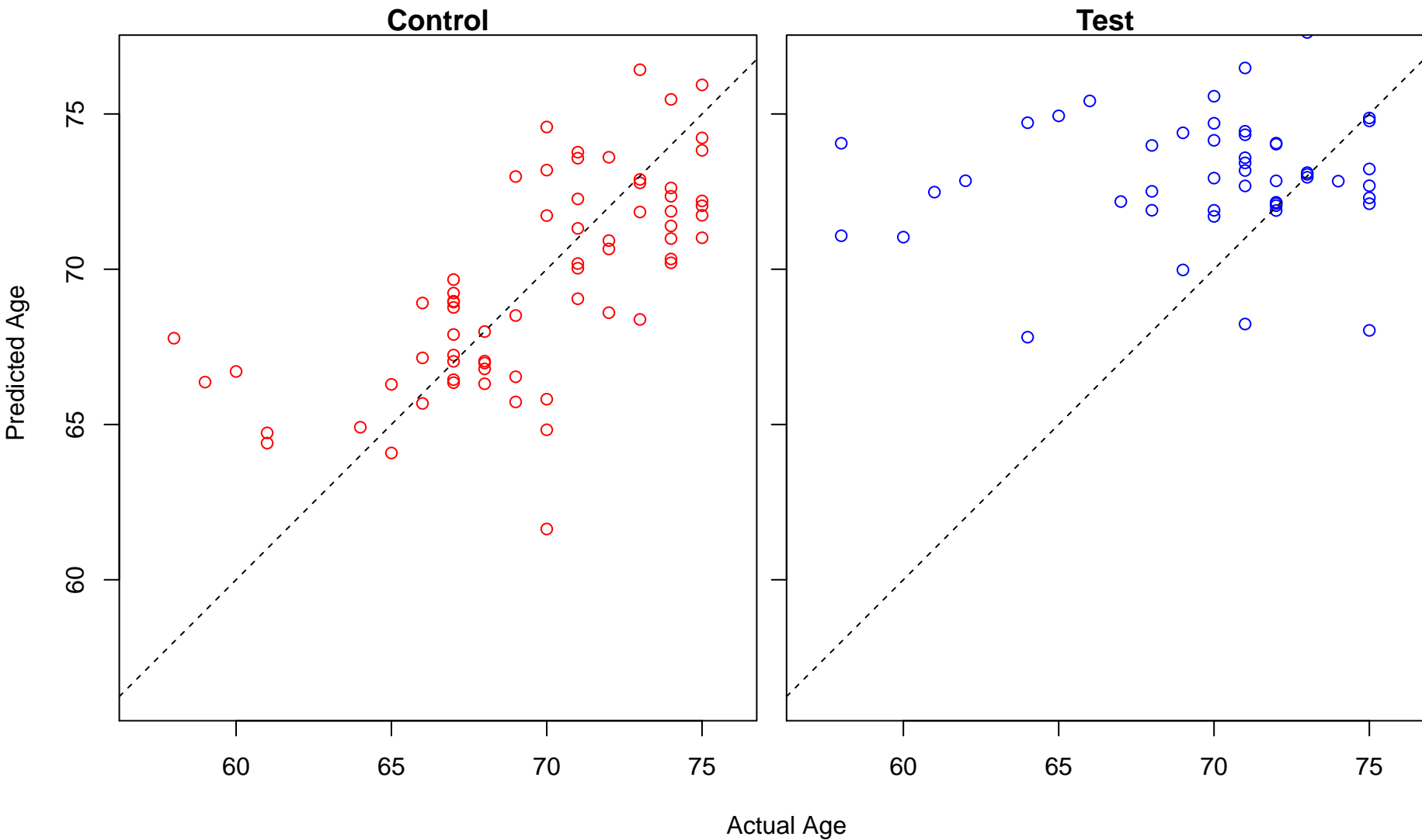
nucleoside biosynthetic process (Score: 1.556790)



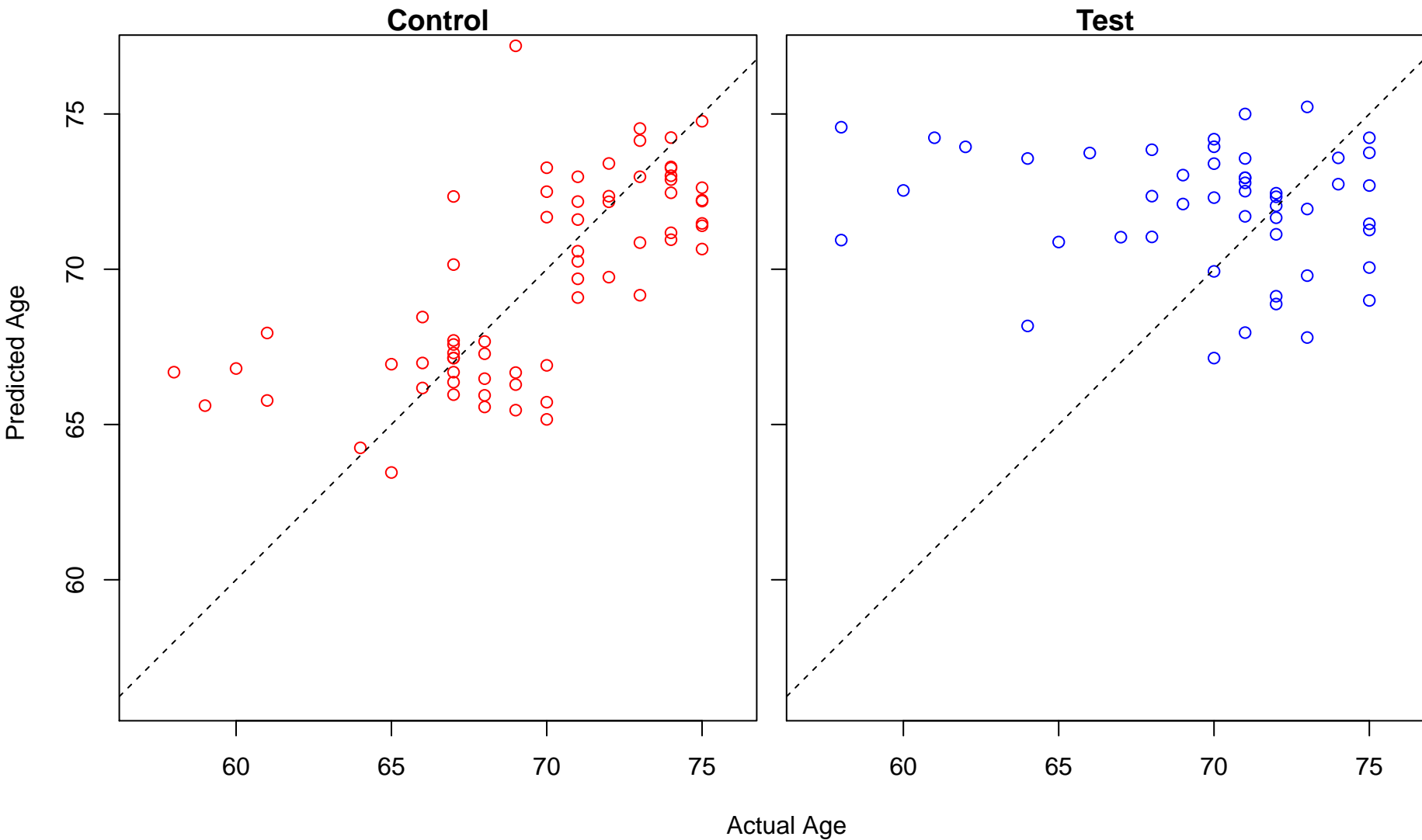
glycosyl compound biosynthetic process (Score: 1.556790)



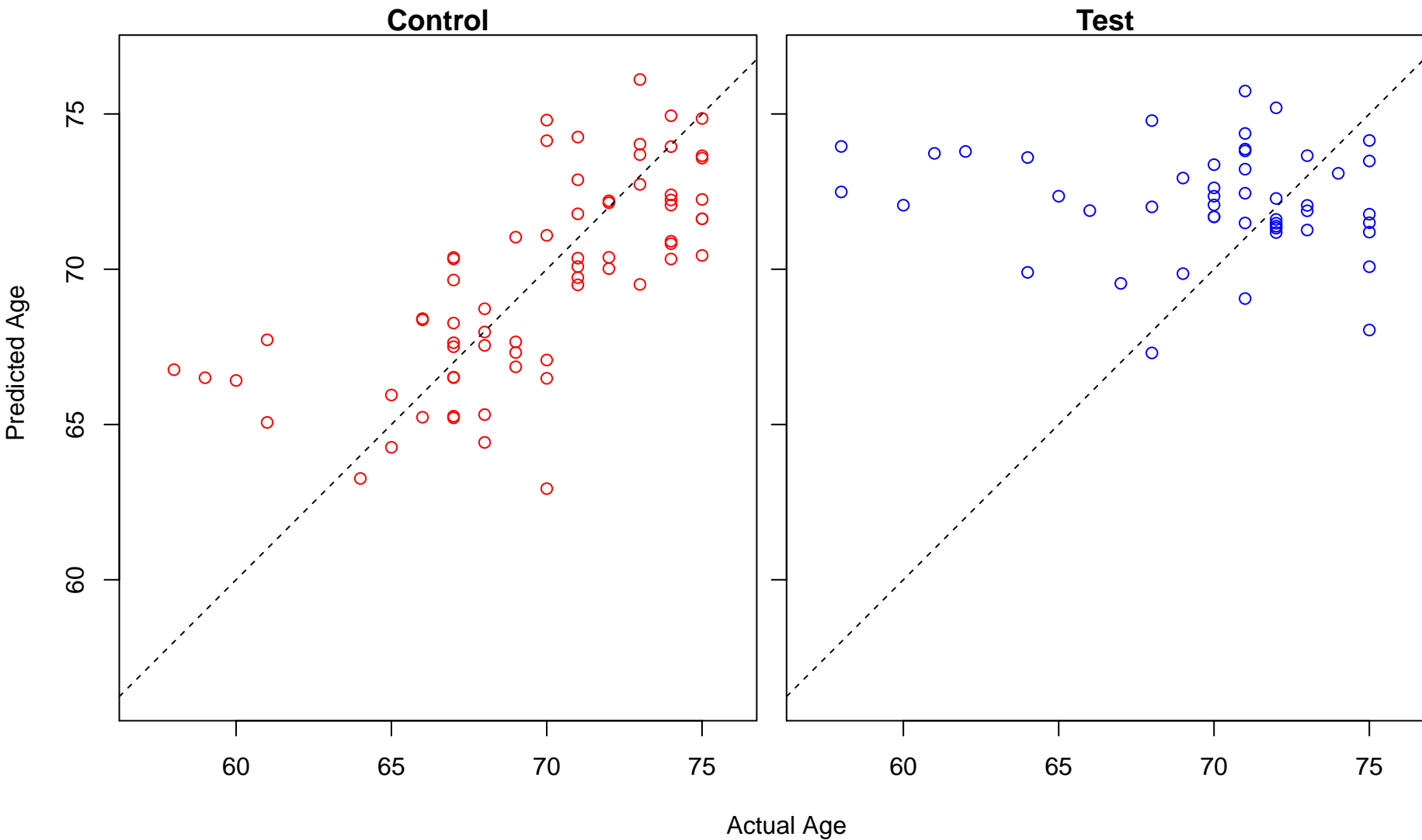
transforming growth factor beta receptor signaling pathway (Score: 1.555533)



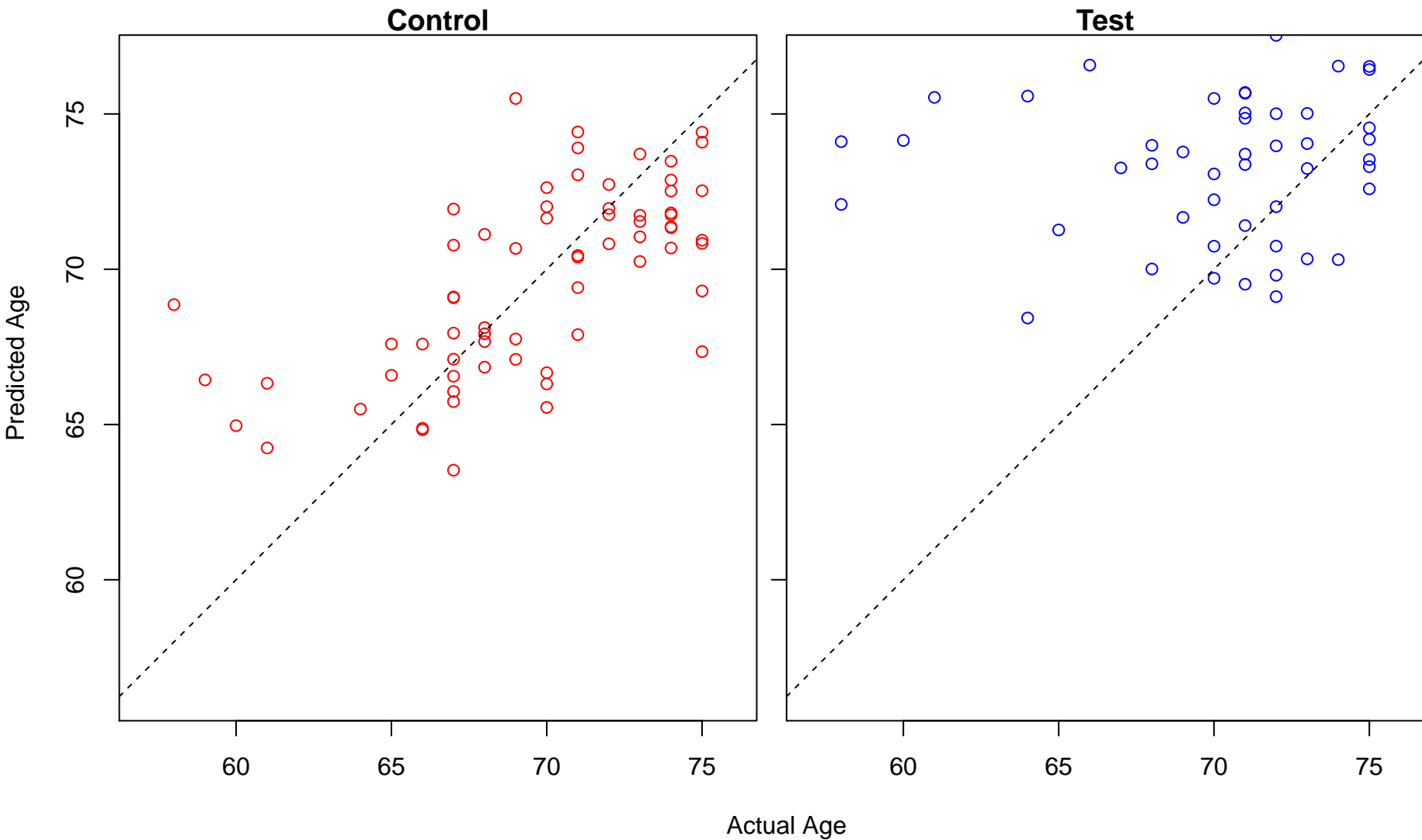
regulation of cyclin-dependent protein kinase activity (Score: 1.555401)



negative regulation of cellular component organization (Score: 1.555338)

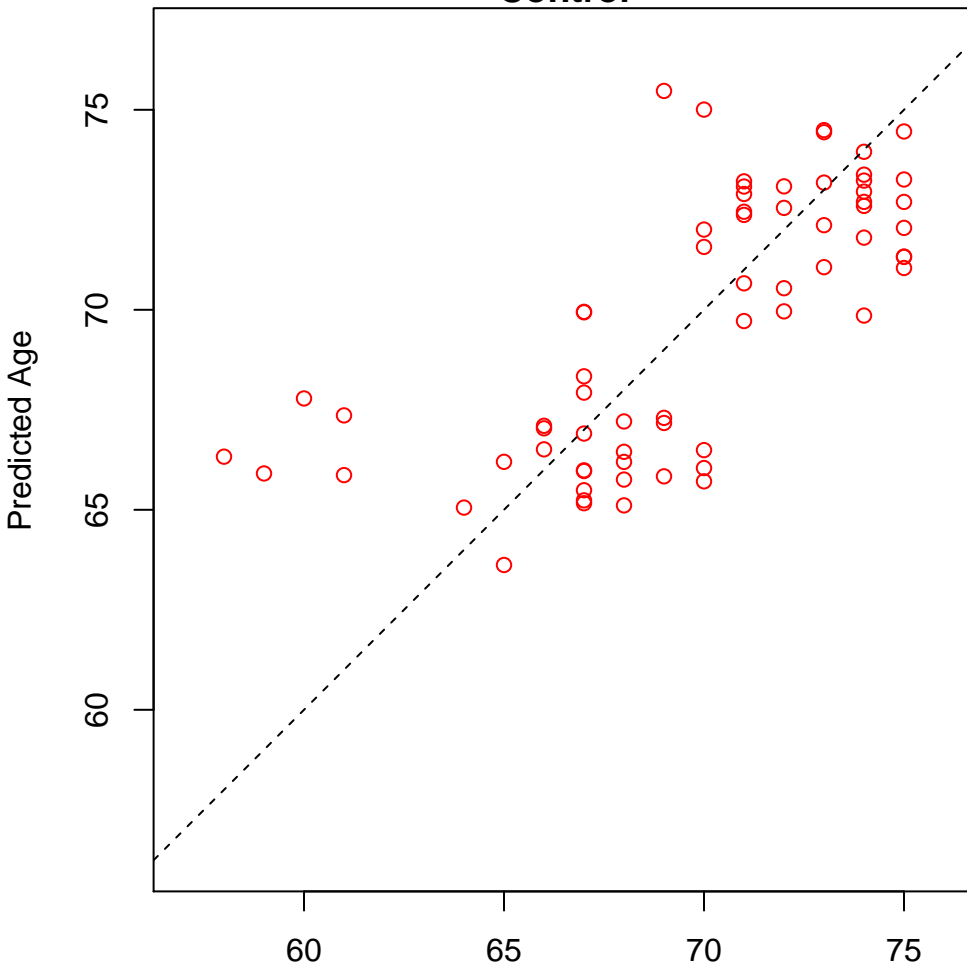


centriole replication (Score: 1.55251)

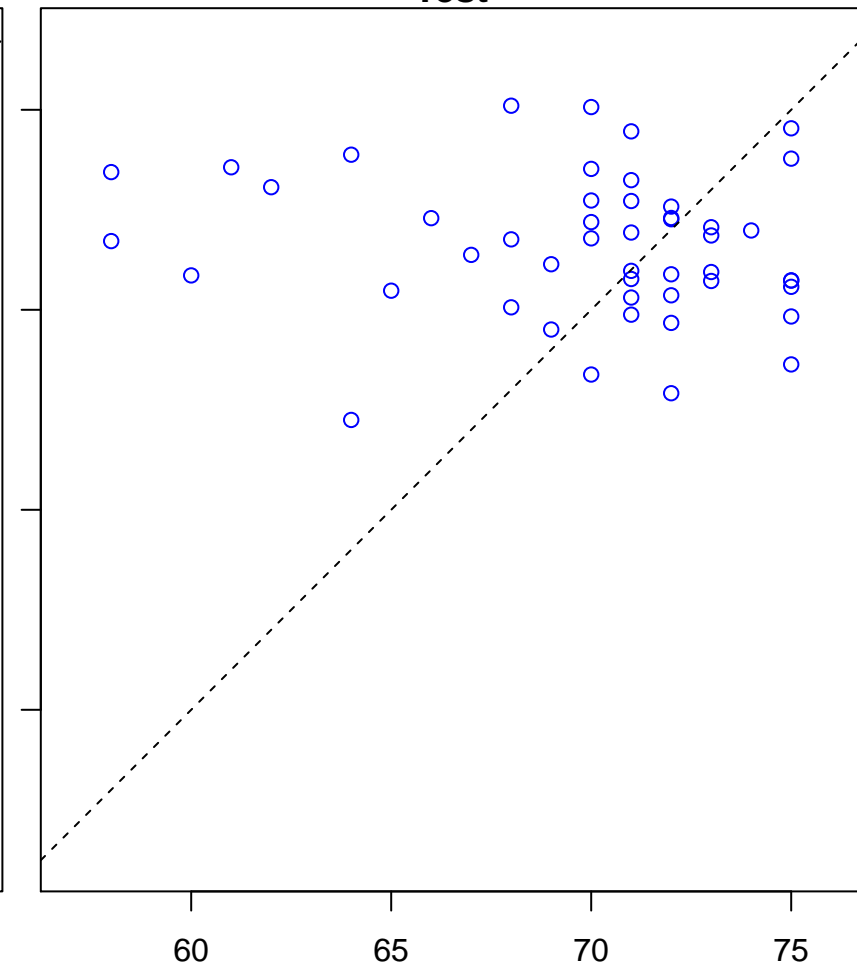


response to tumor necrosis factor (Score: 1.555134)

Control

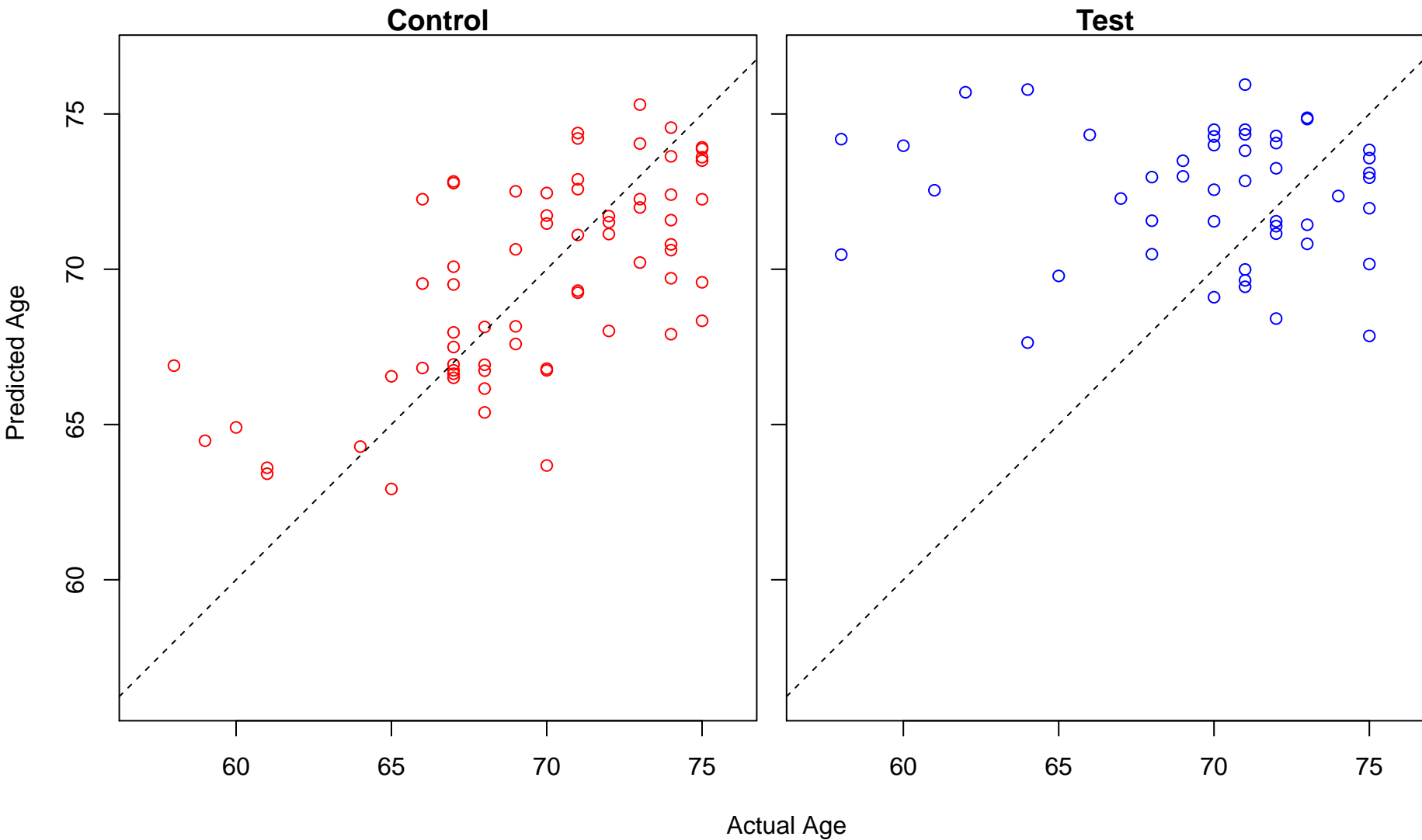


Test

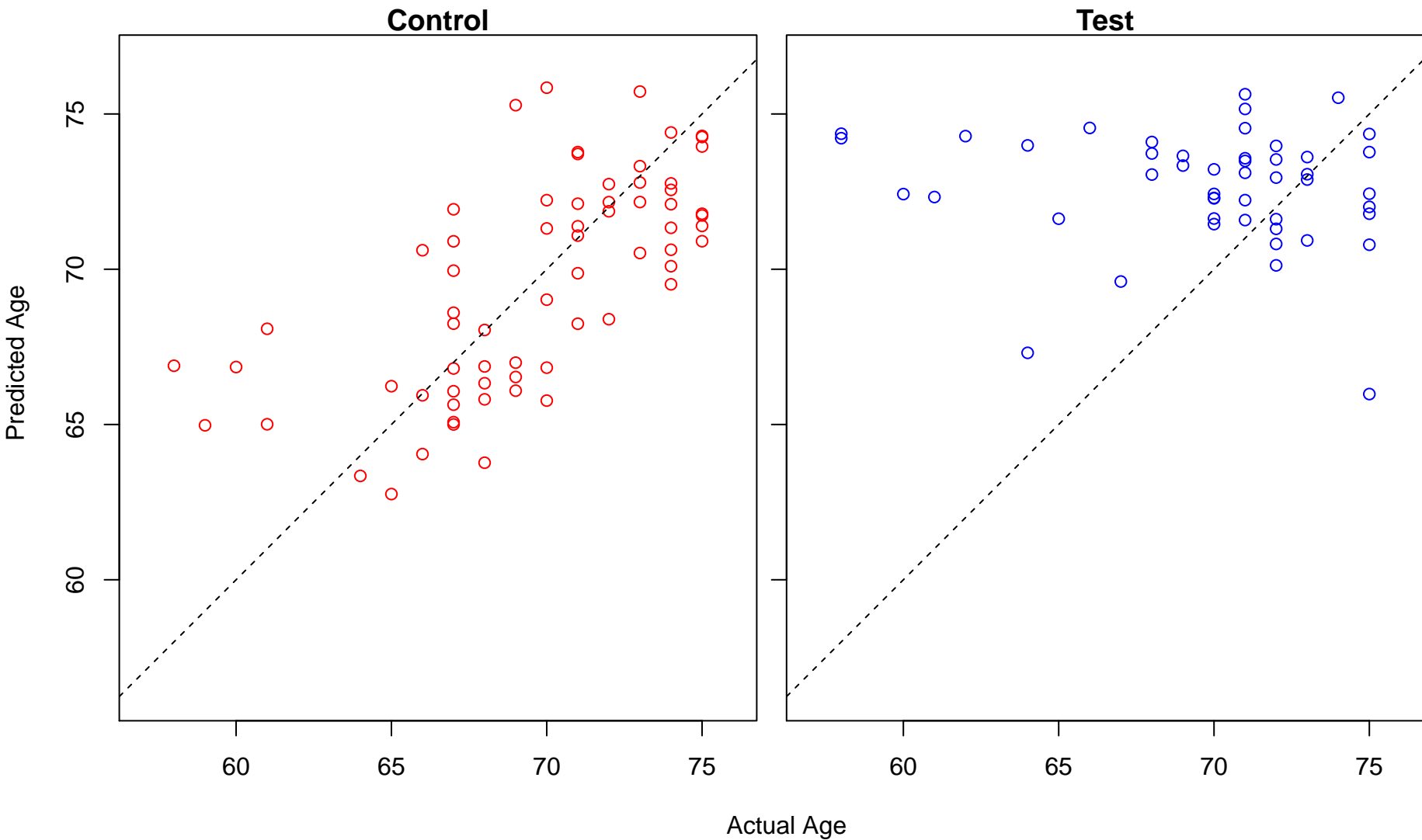


Actual Age

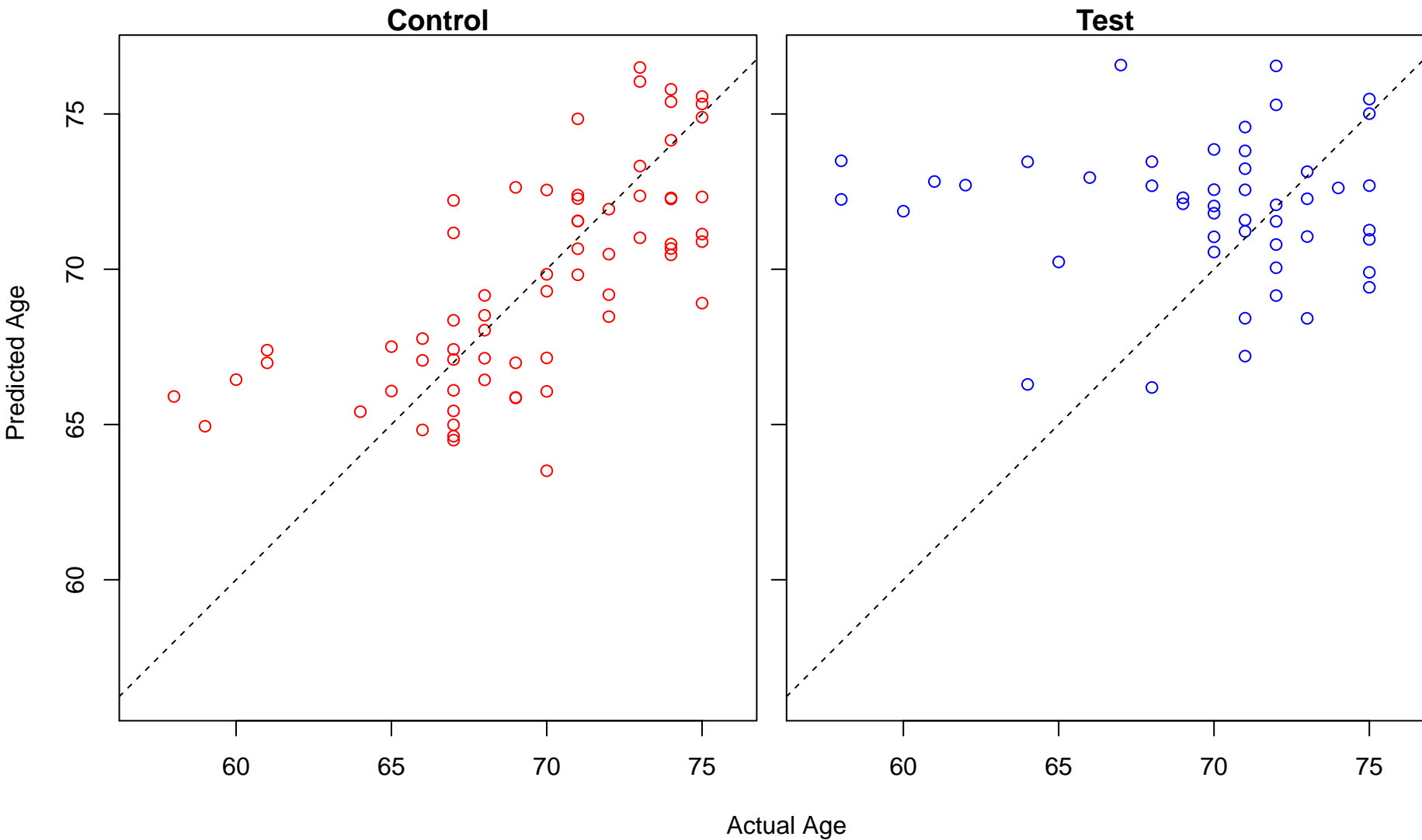
regulation of ERBB signaling pathway (Score: 1.554196)



negative regulation of protein kinase activity (Score: 1.553682)

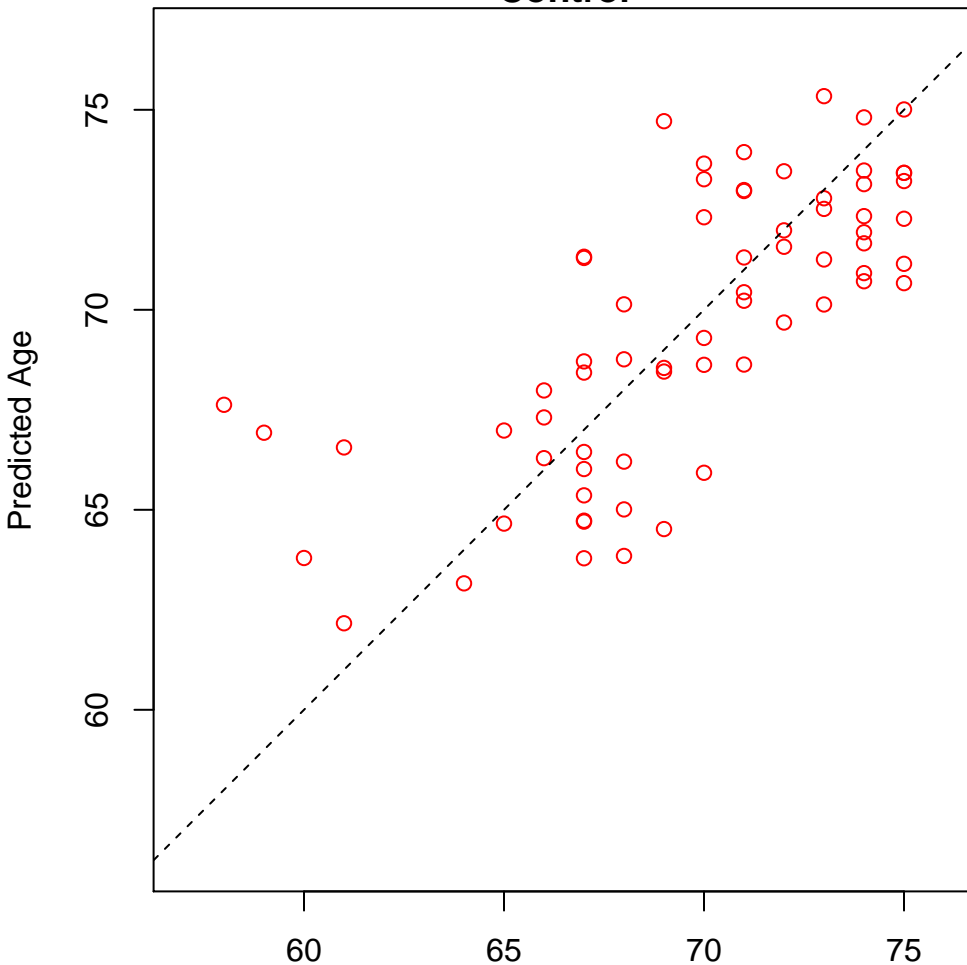


nucleotide catabolic process (Score: 1.553001)

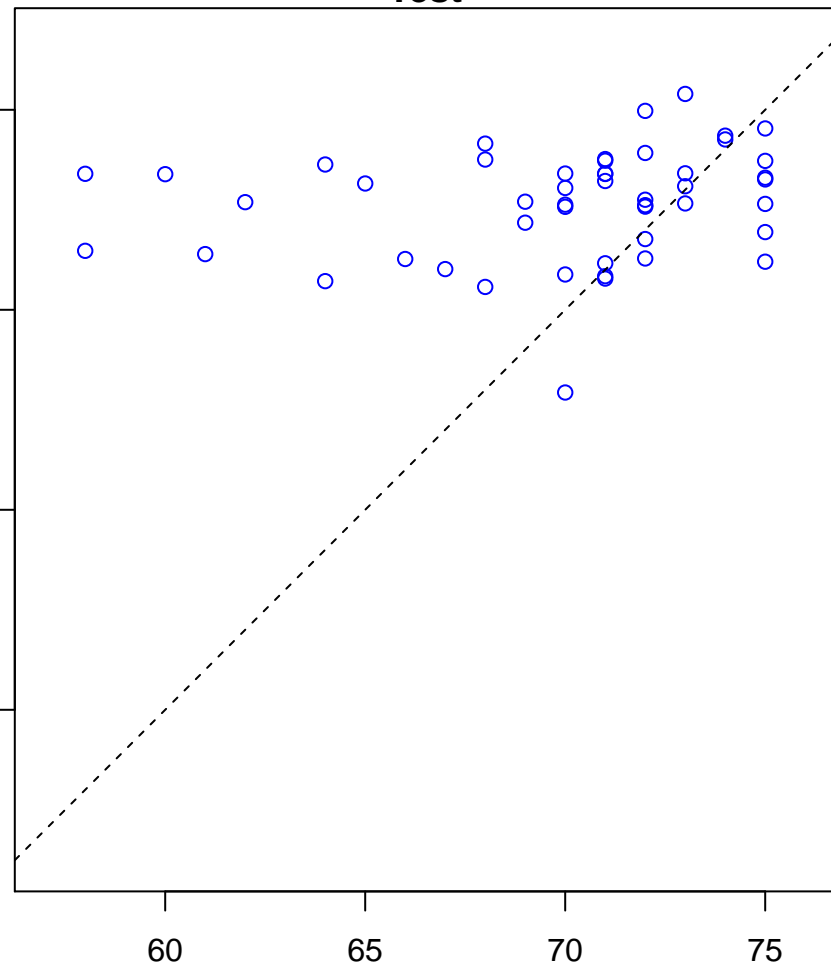


cellular response to unfolded protein (Score: 1.552868)

Control

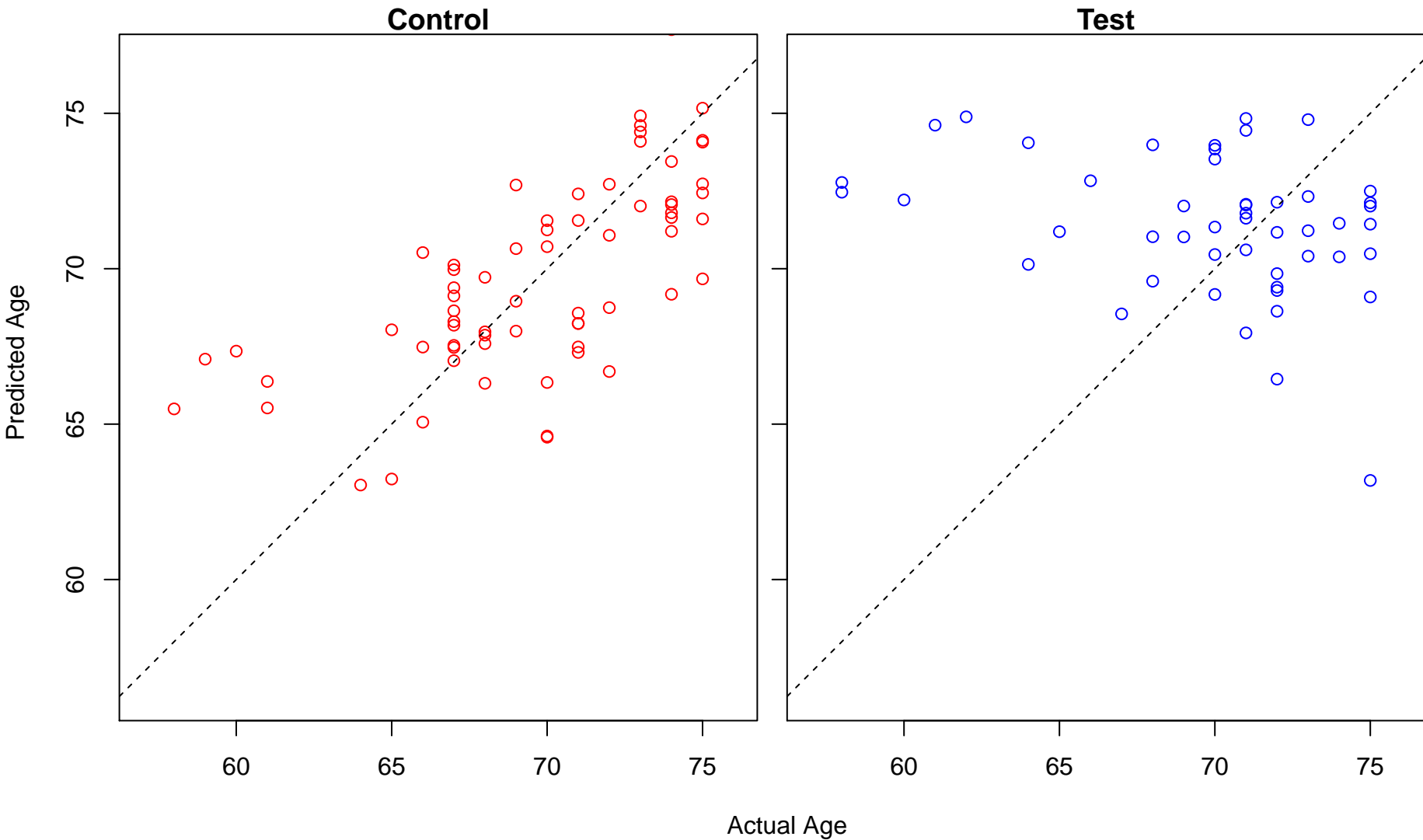


Test

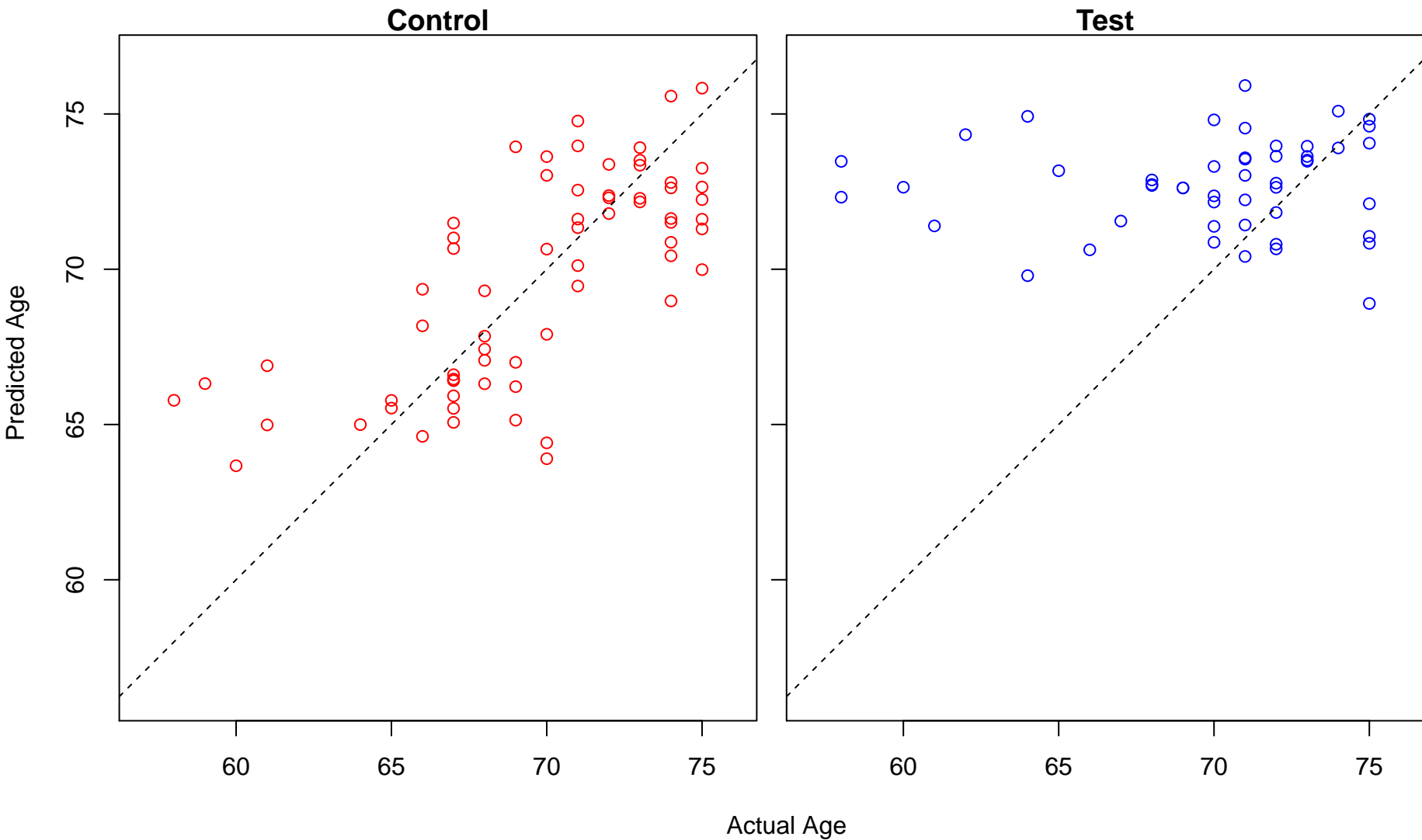


Actual Age

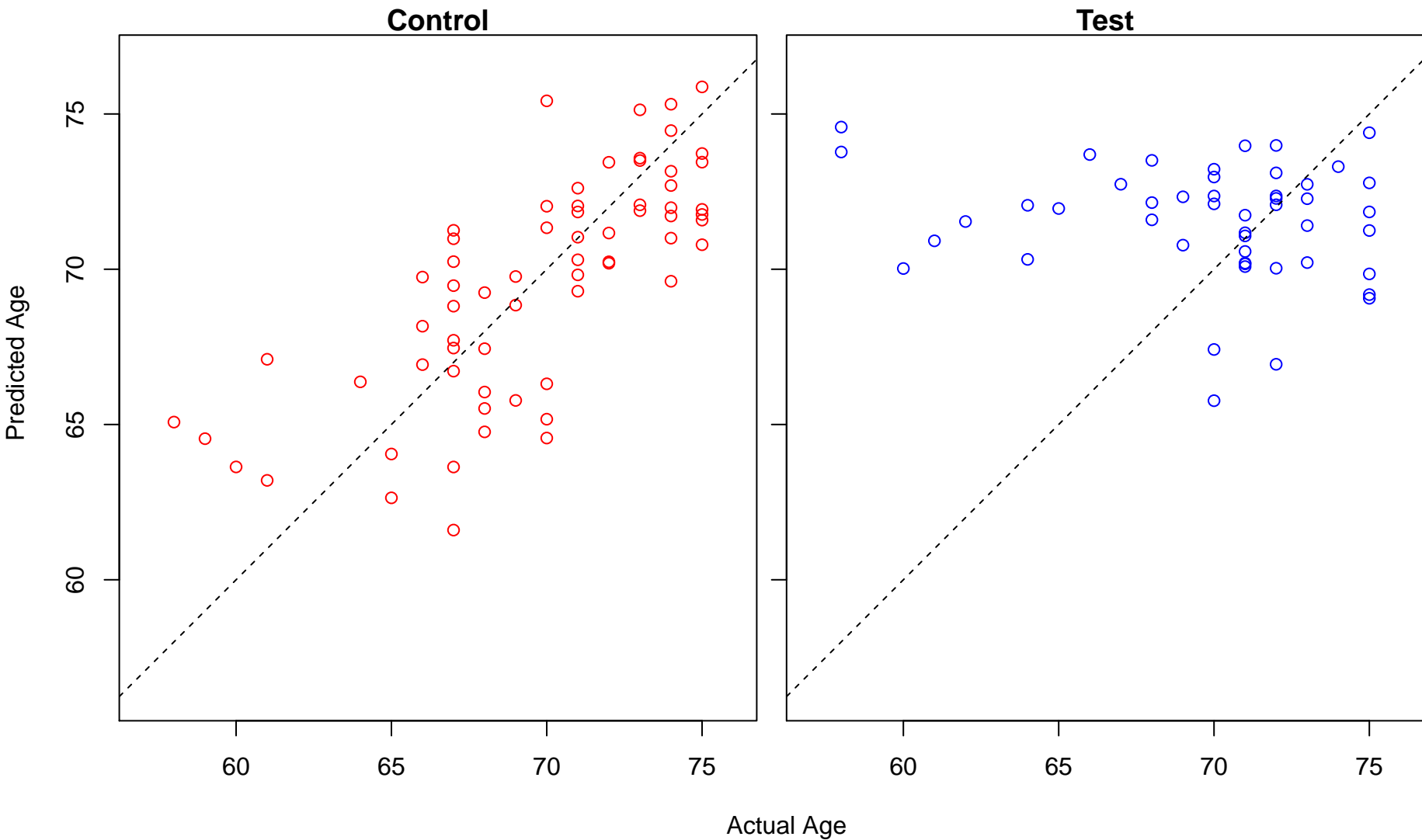
positive regulation of cellular extravasation (Score: 1.552733)



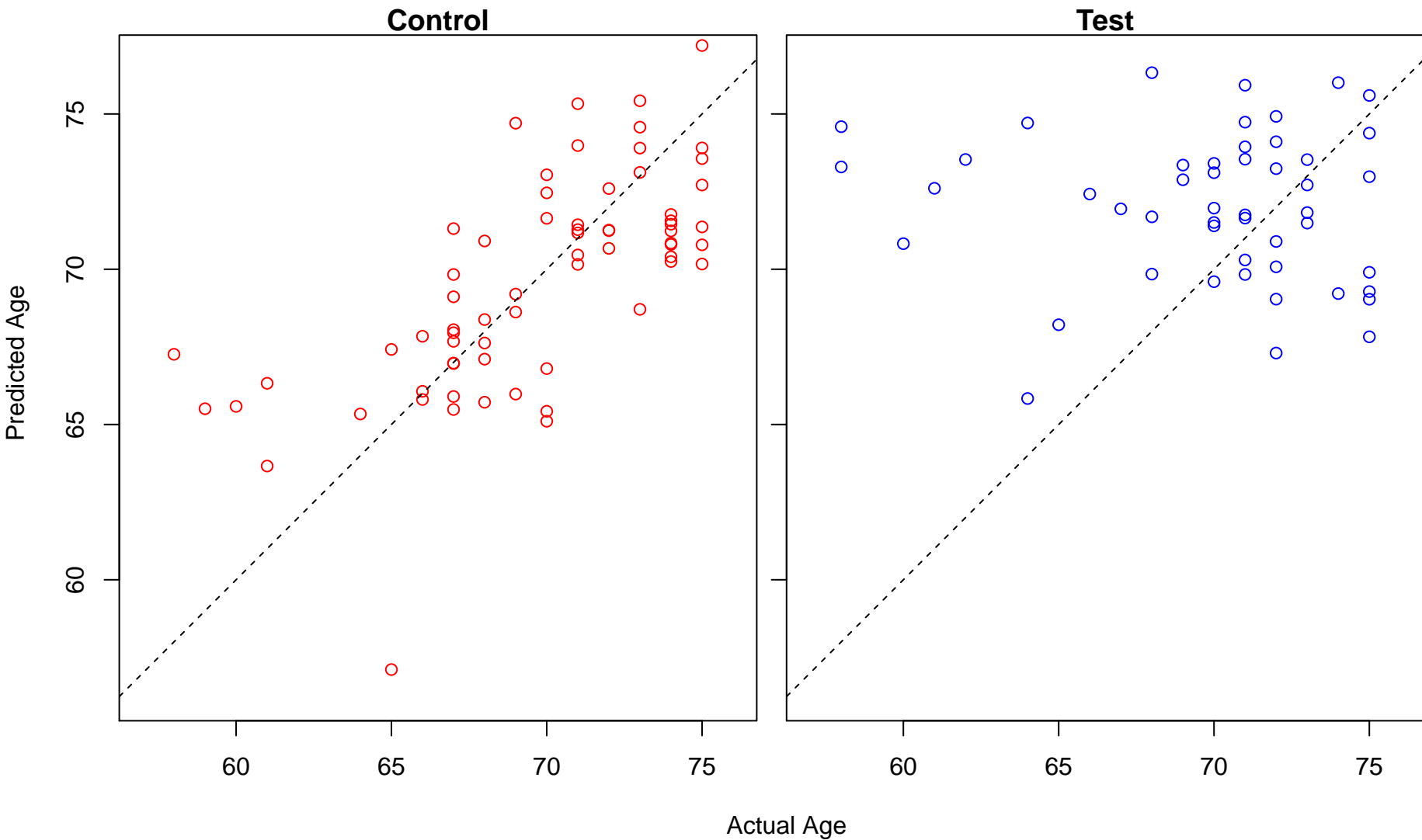
nitrogen compound transport (Score: 1.551958)



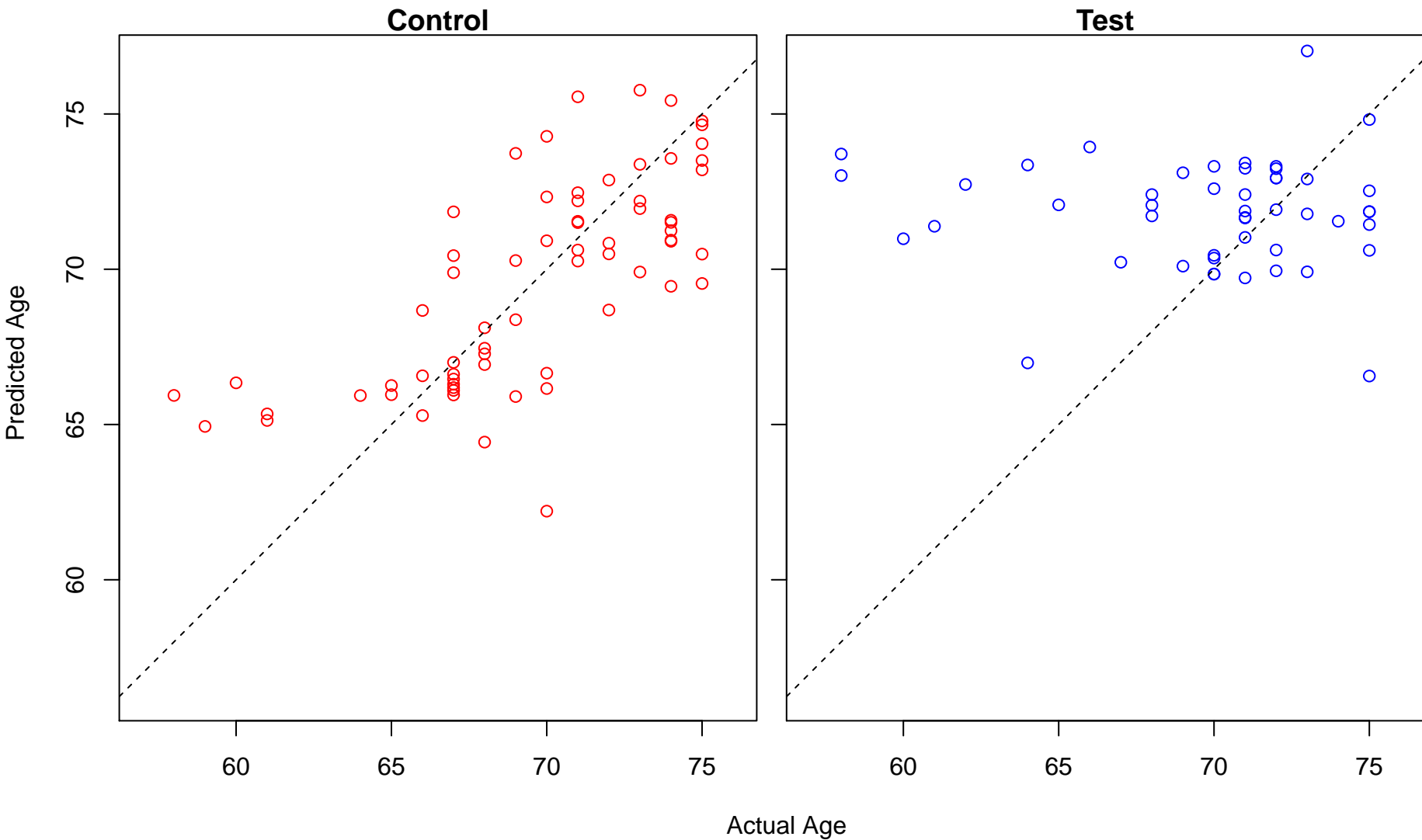
cellular calcium ion homeostasis (Score: 1.551017)



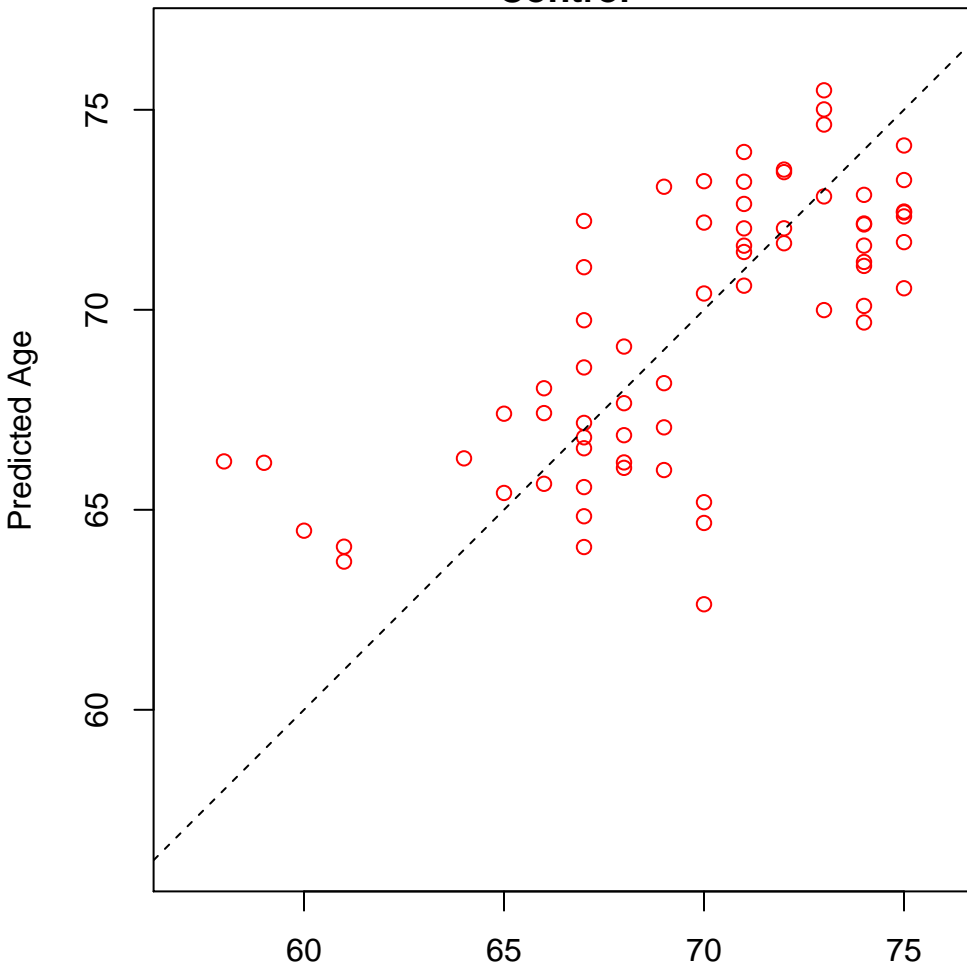
protein export from nucleus (Score: 1.550830)



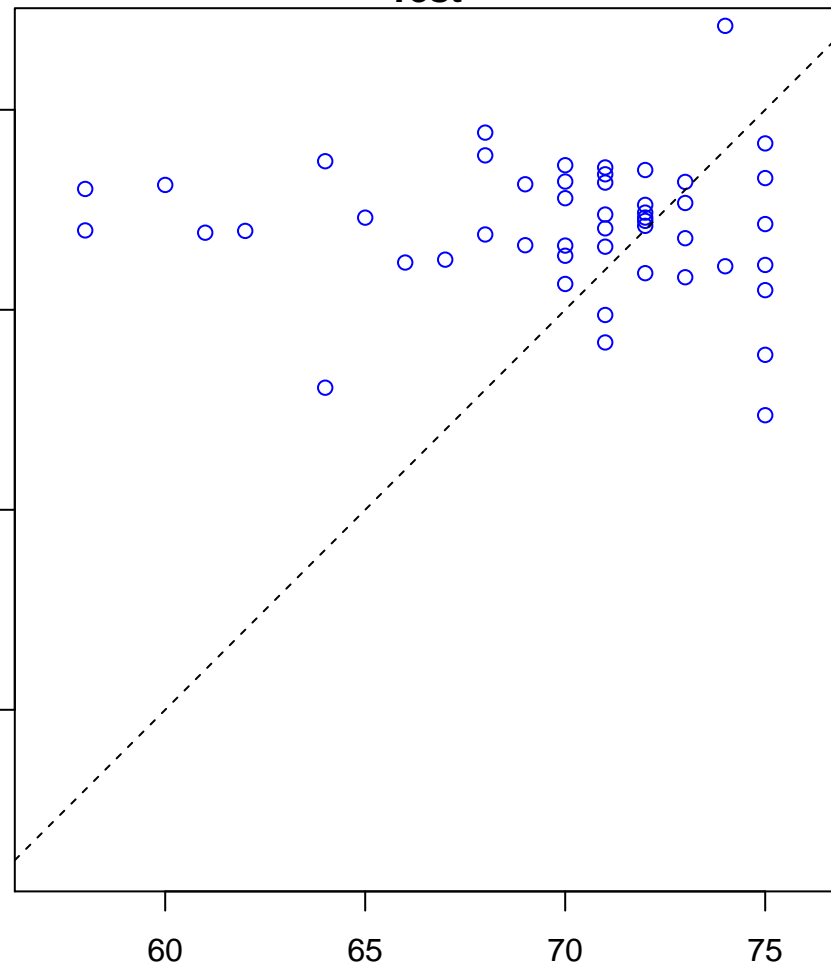
'de novo' protein folding (Score: 1.550765)



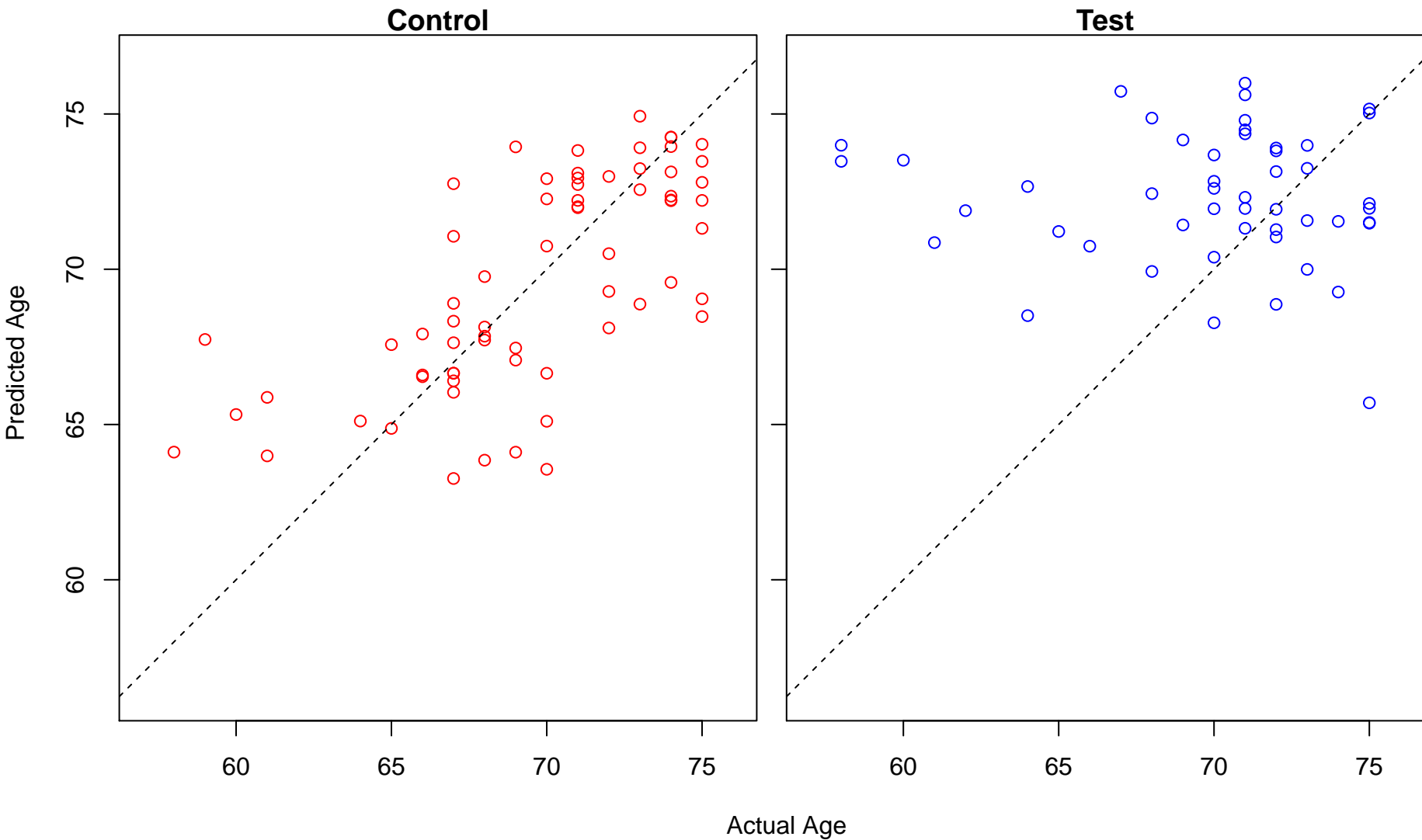
Control



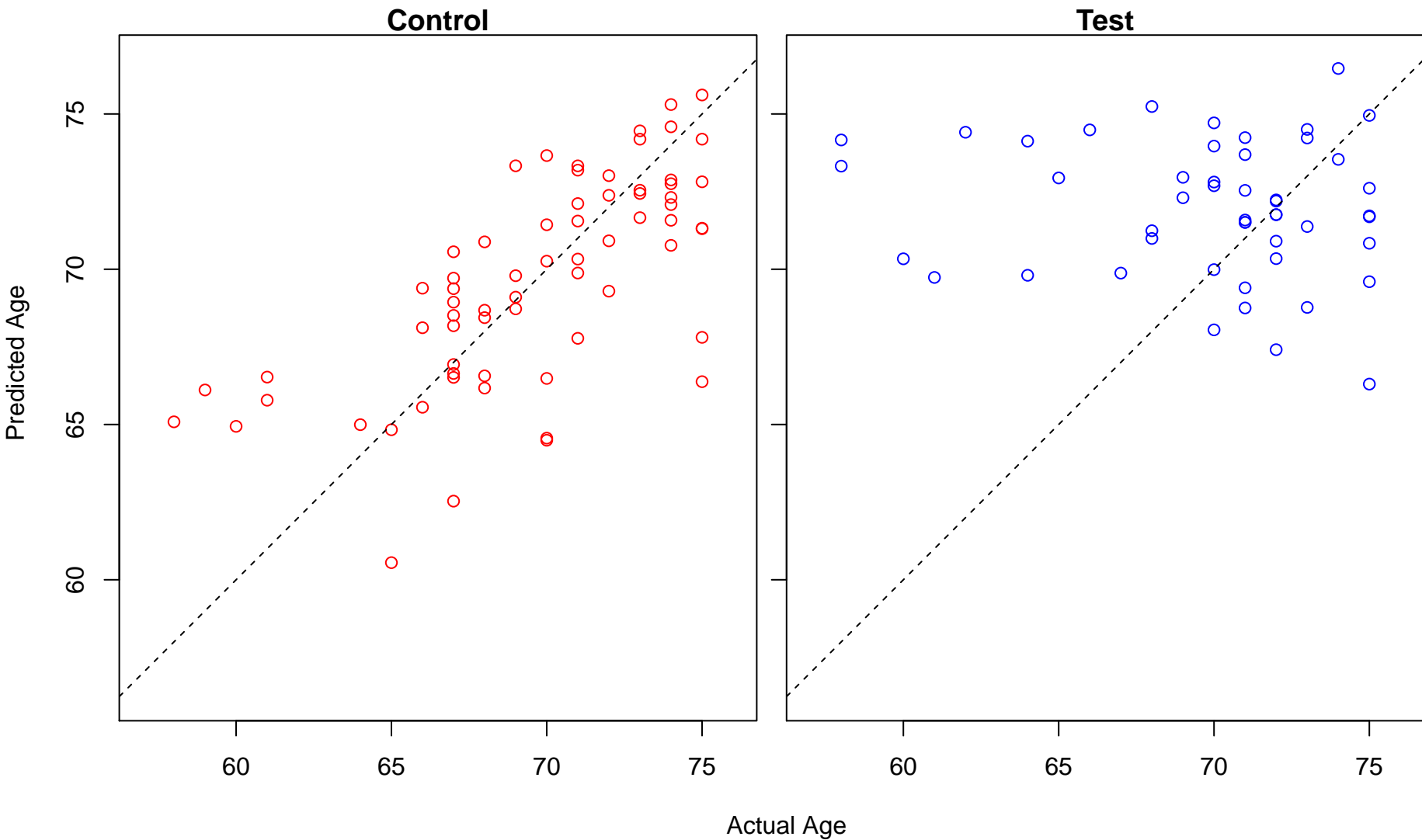
Test



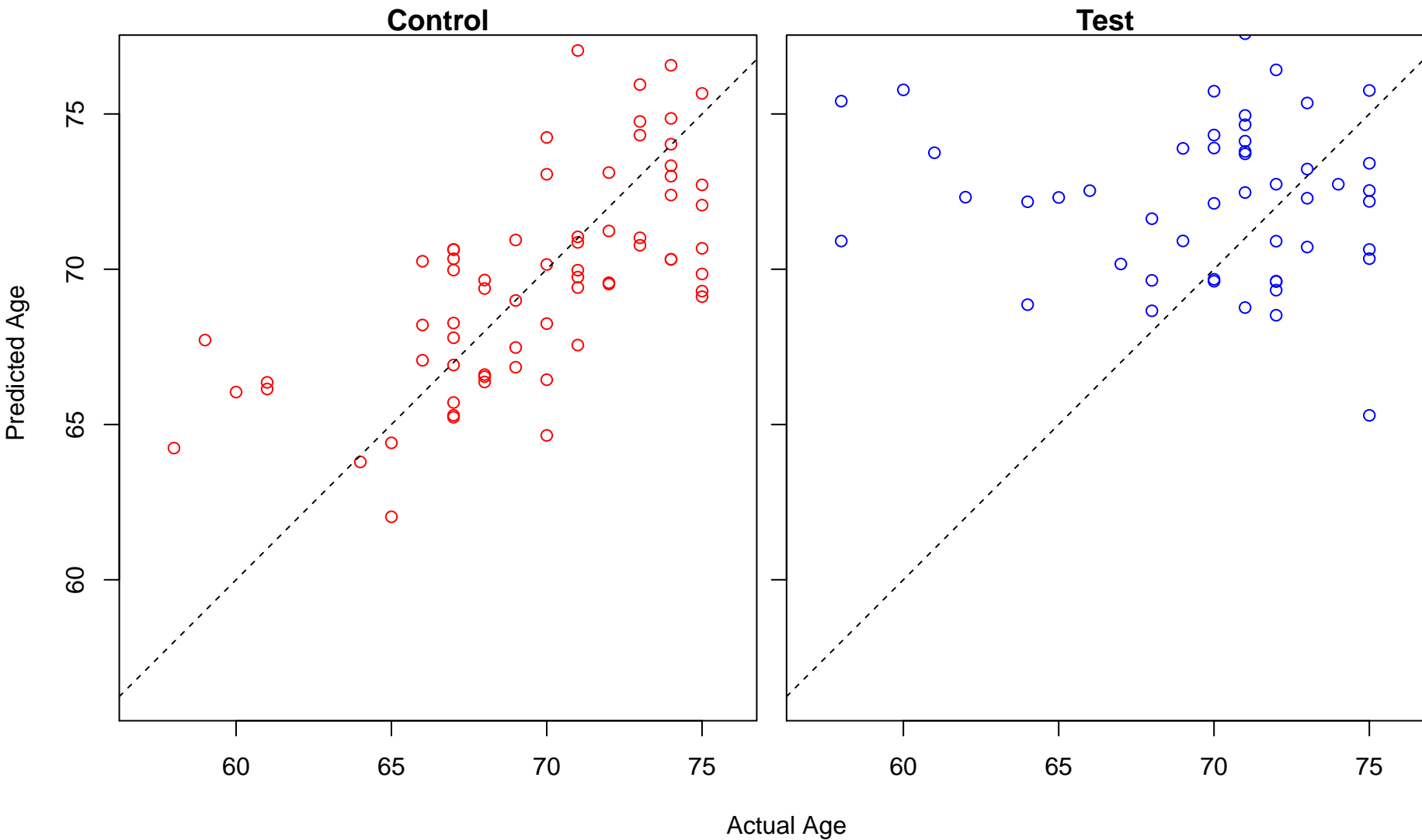
regulation of transcription from RNA polymerase II promoter in response to stress (Score: 1.54982)



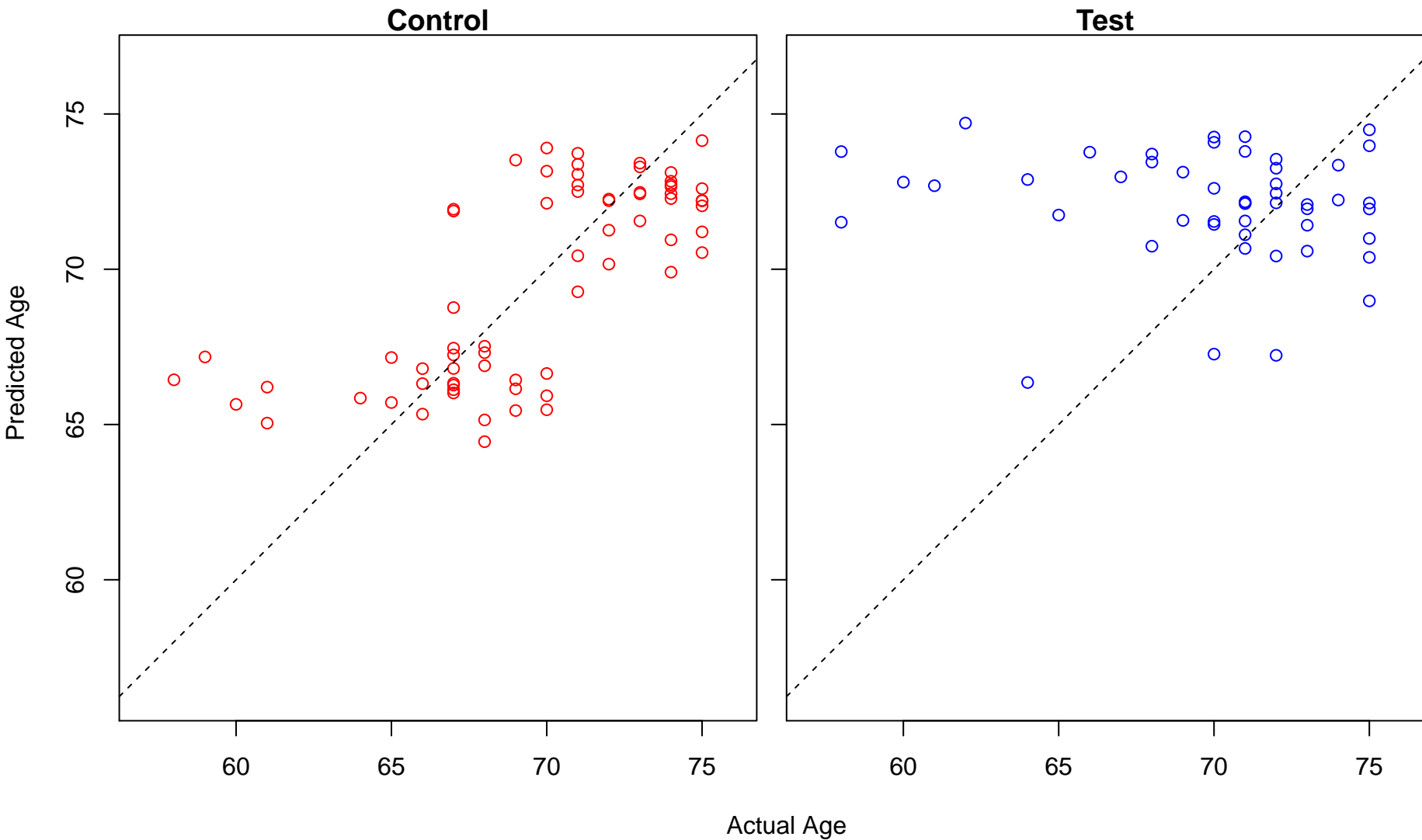
positive regulation of ERK1 and ERK2 cascade (Score: 1.549223)



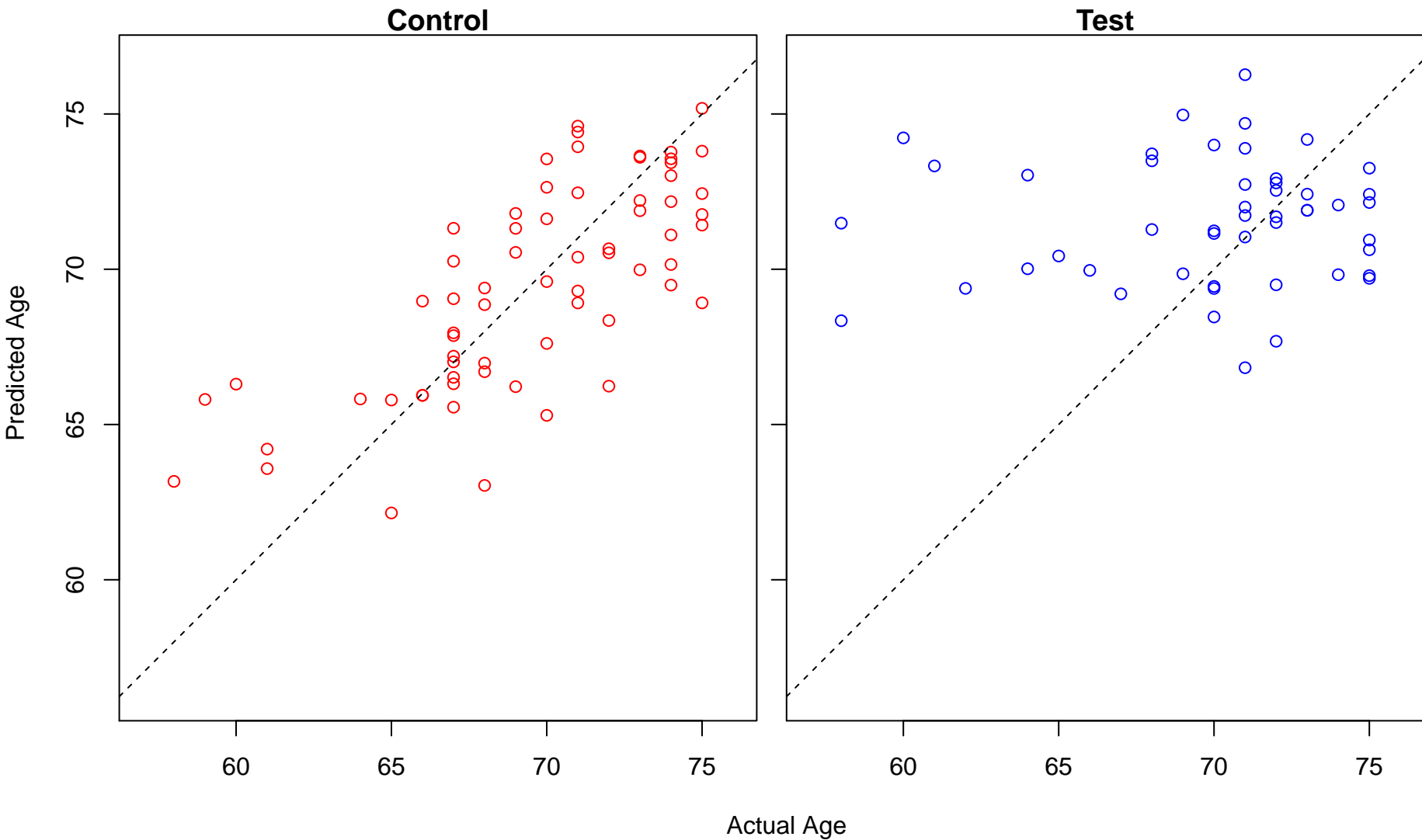
positive regulation of macroautophagy (Score: 1.549042)



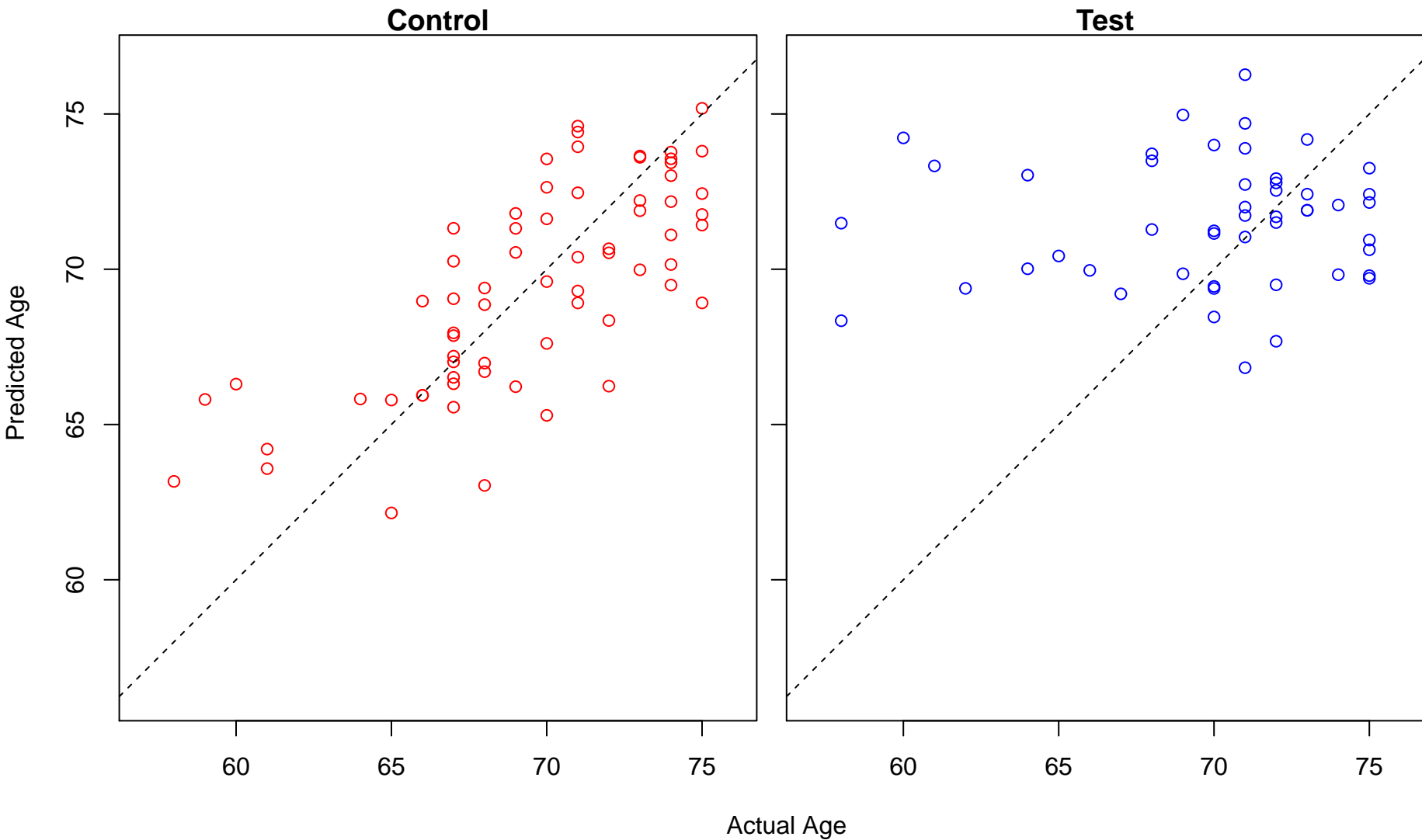
histone H3-K4 methylation (Score: 1.548626)



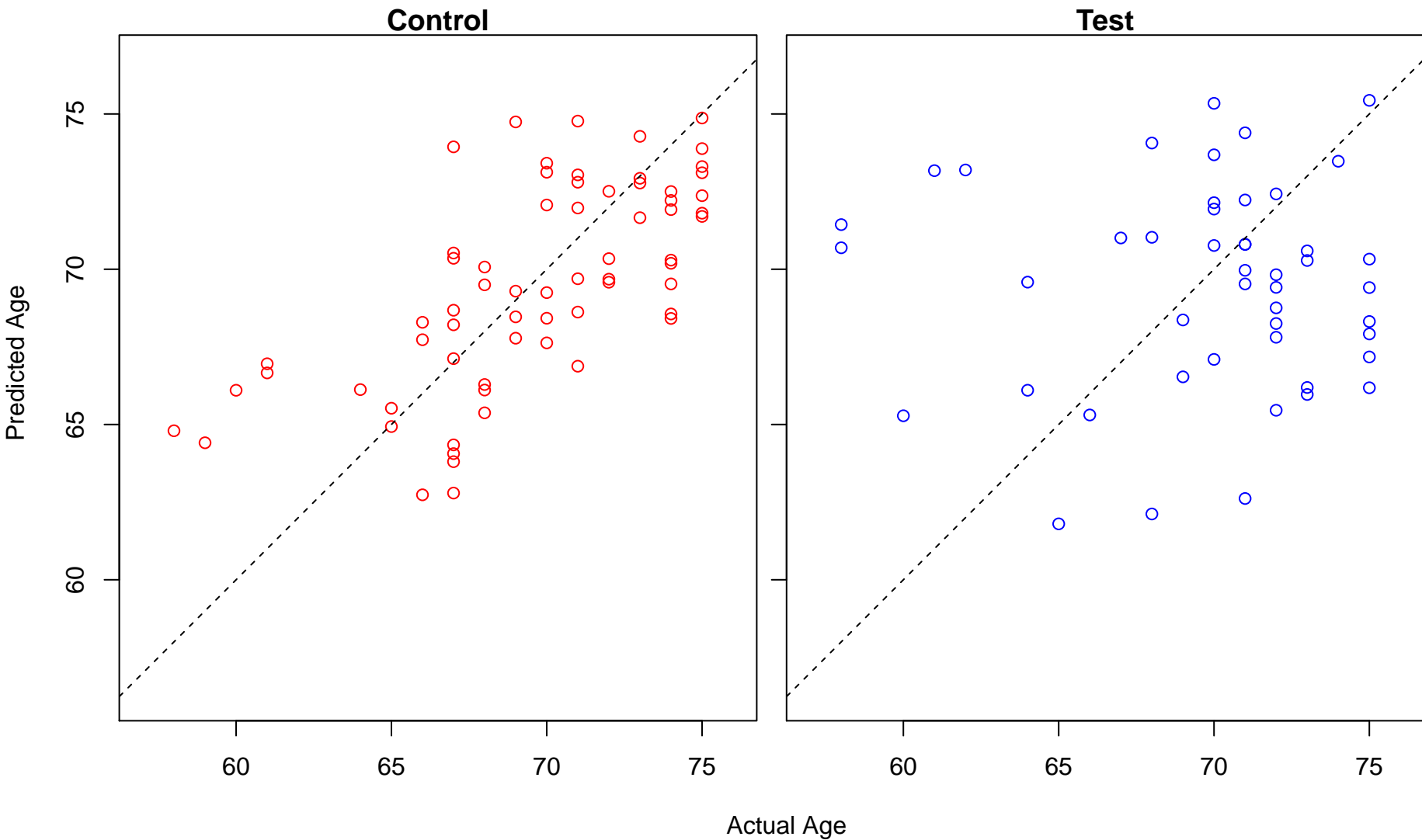
regulation of nucleotide biosynthetic process (Score: 1.548382)



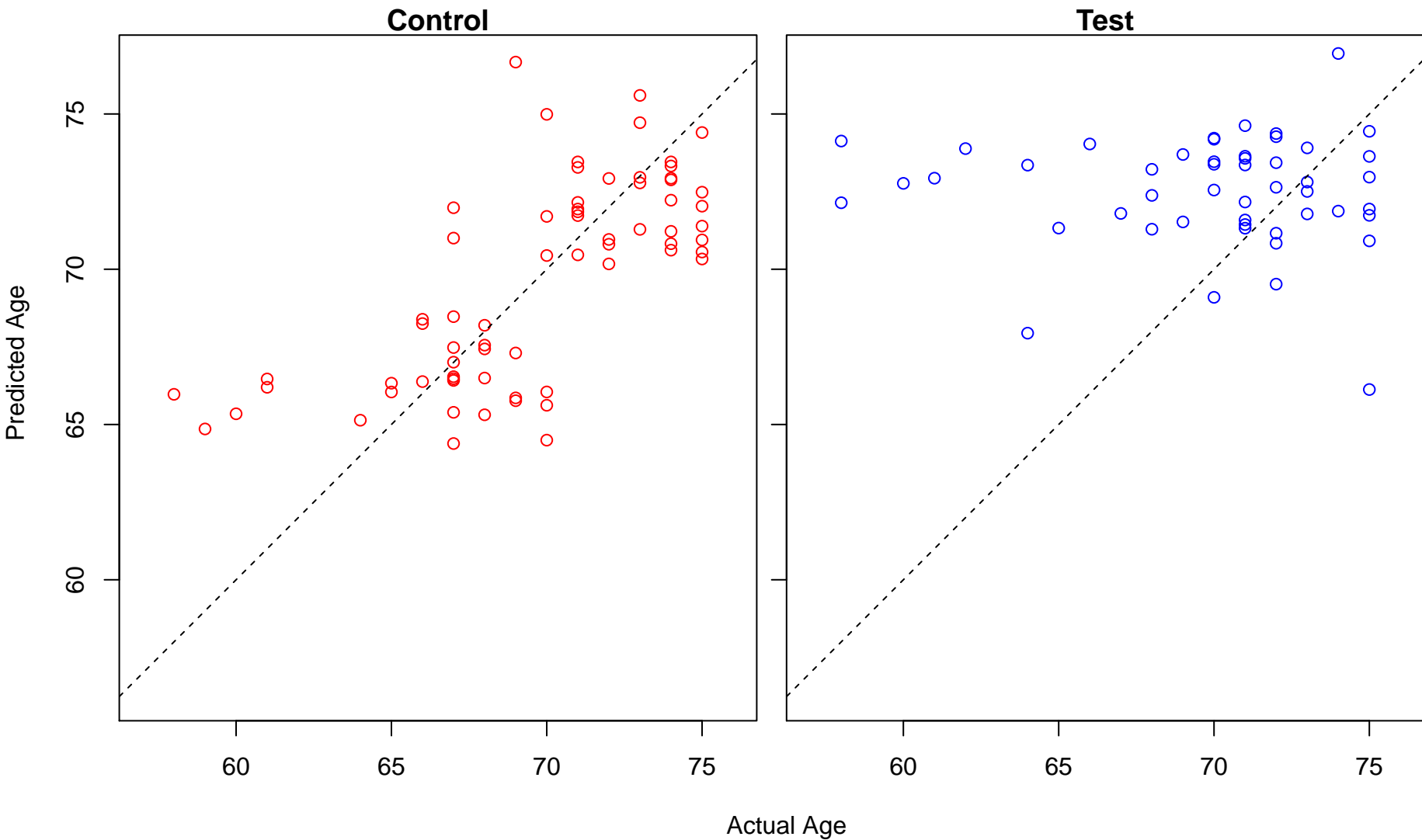
regulation of purine nucleotide biosynthetic process (Score: 1.548382)



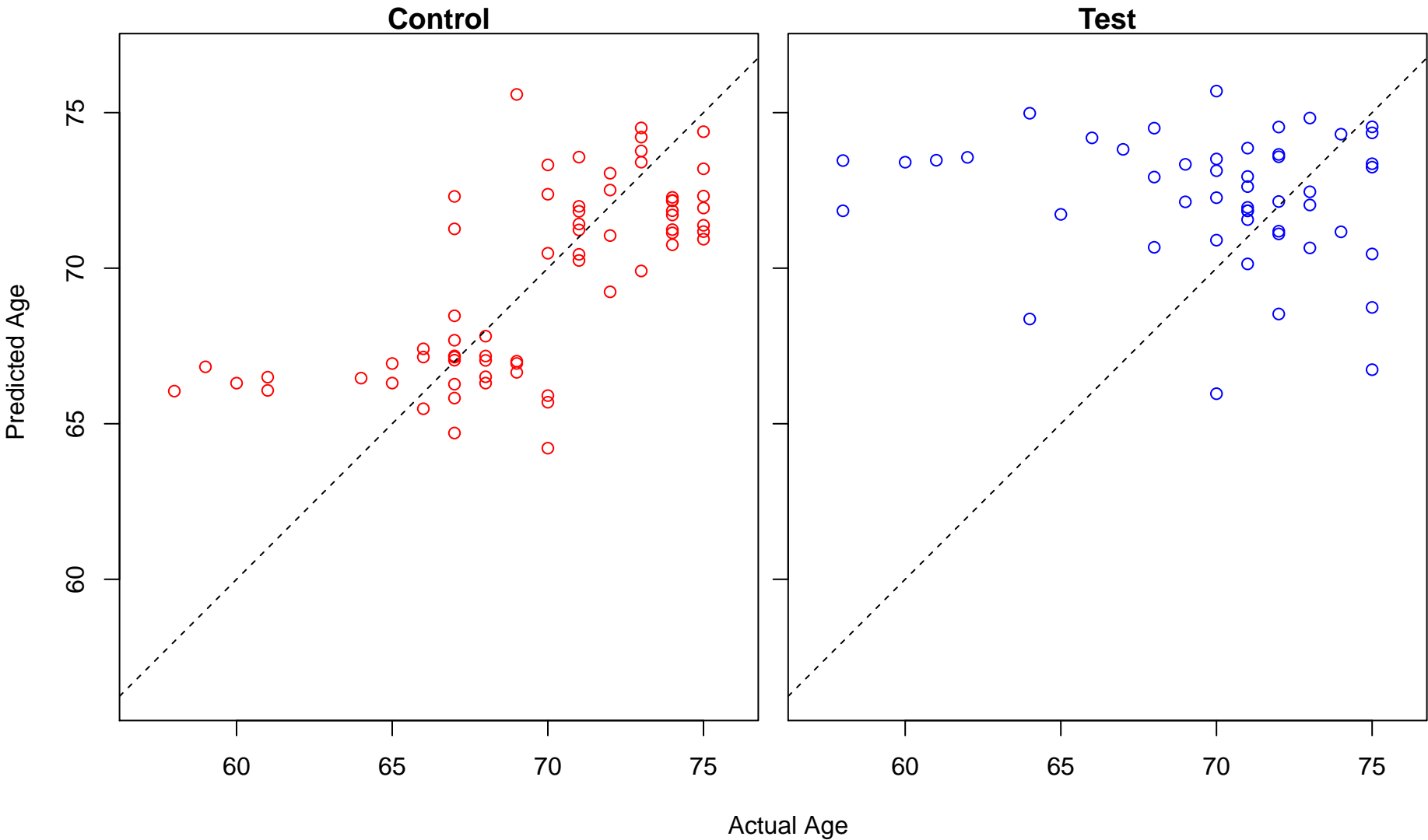
regulation of exit from mitosis (Score: 1.548212)



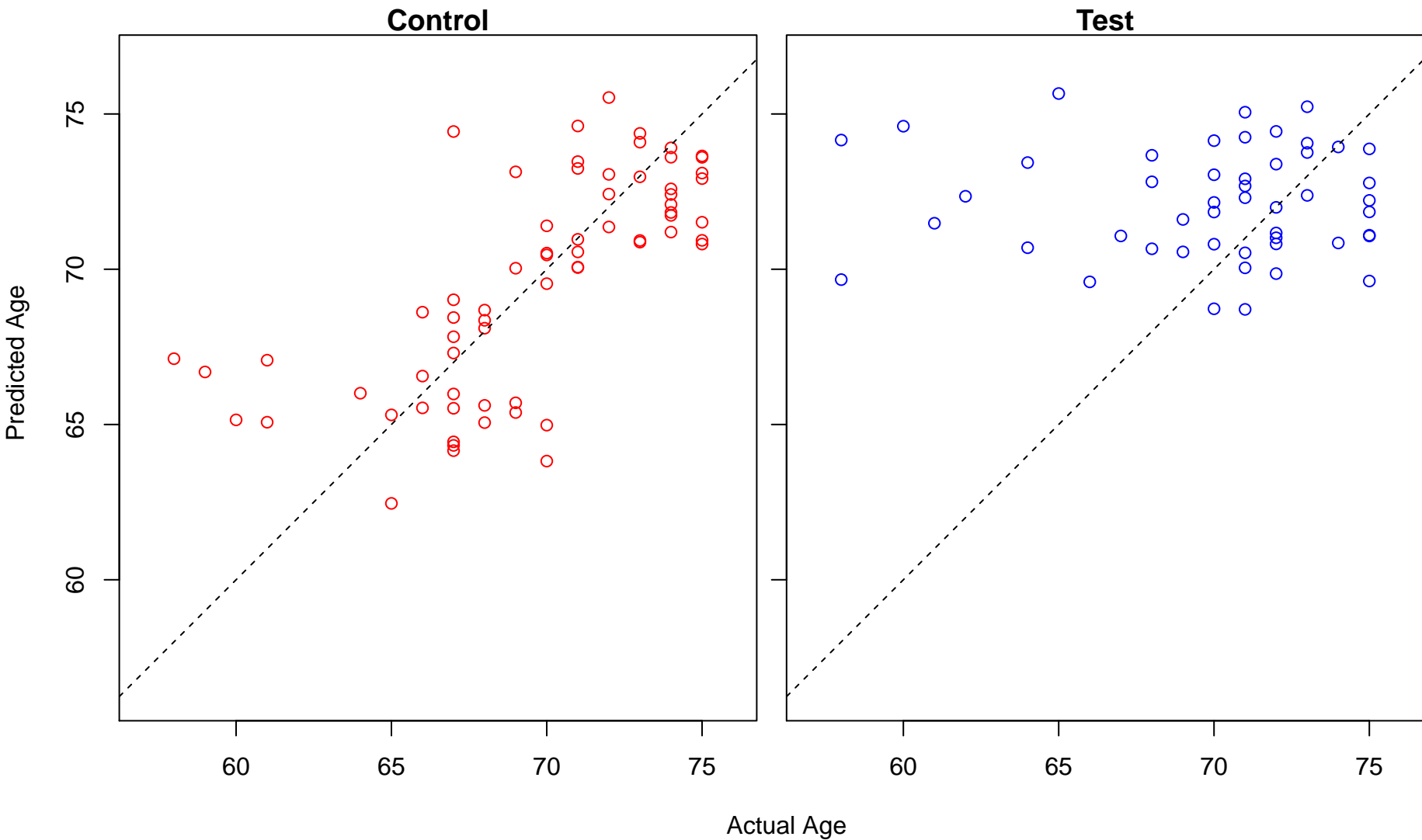
ossification (Score: 1.548132)



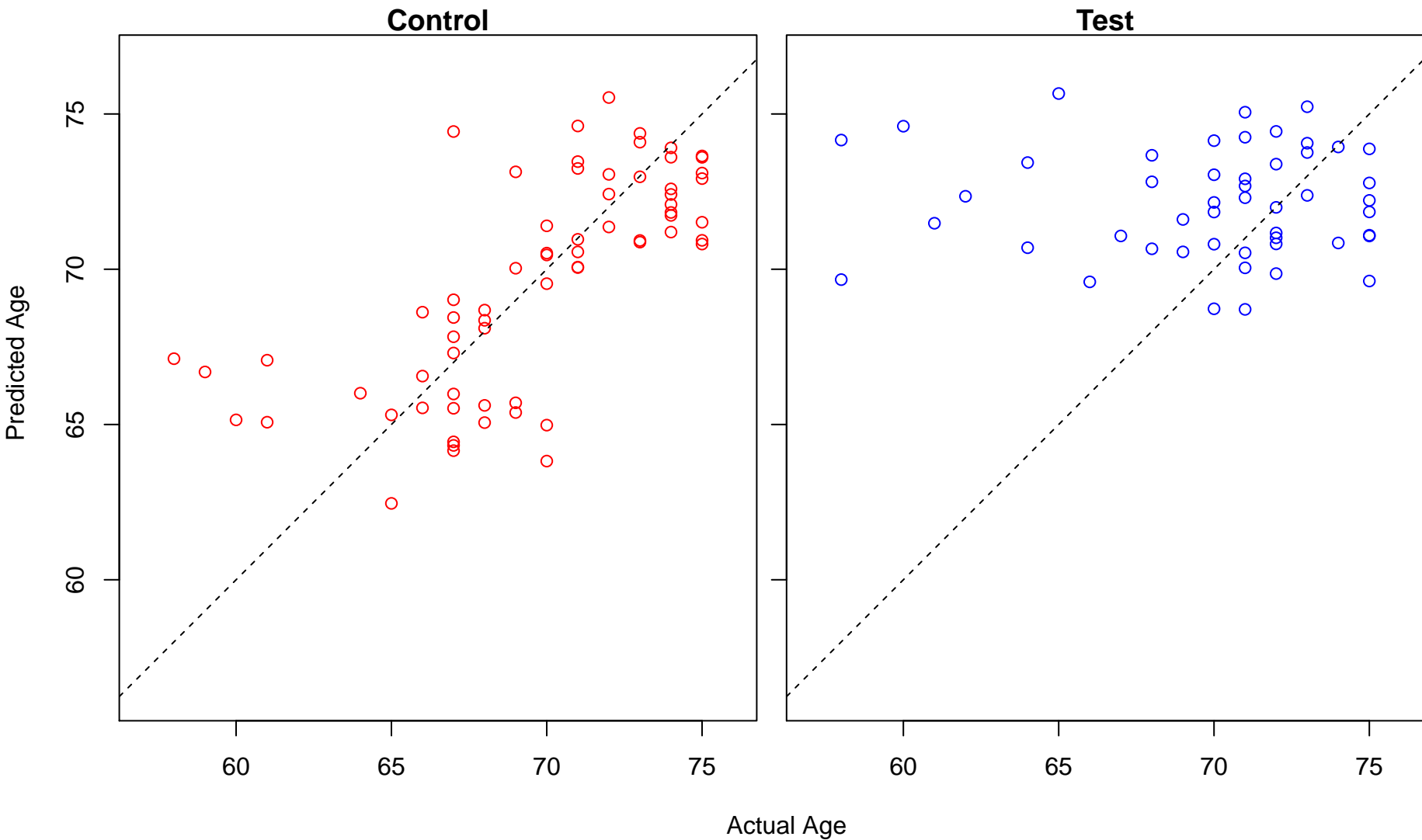
nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway (Score: 1.5480)



mRNA export from nucleus (Score: 1.547232)

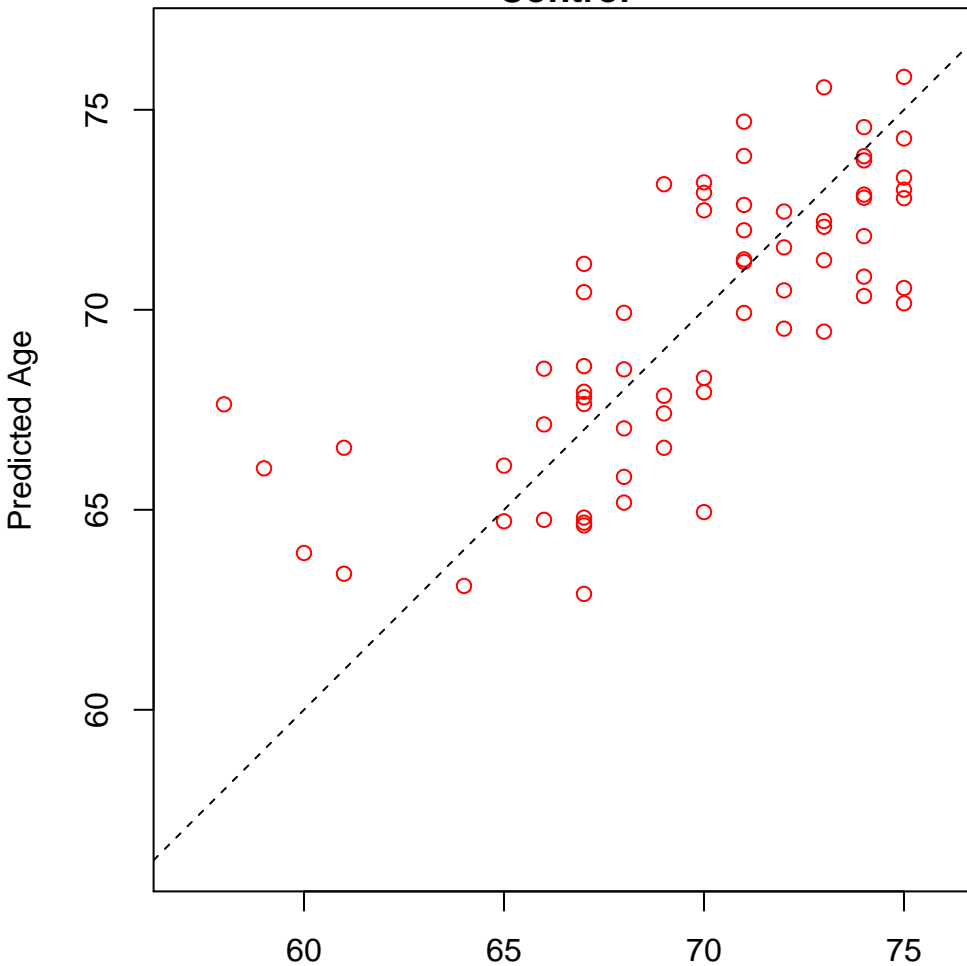


mRNA-containing ribonucleoprotein complex export from nucleus (Score: 1.547232)

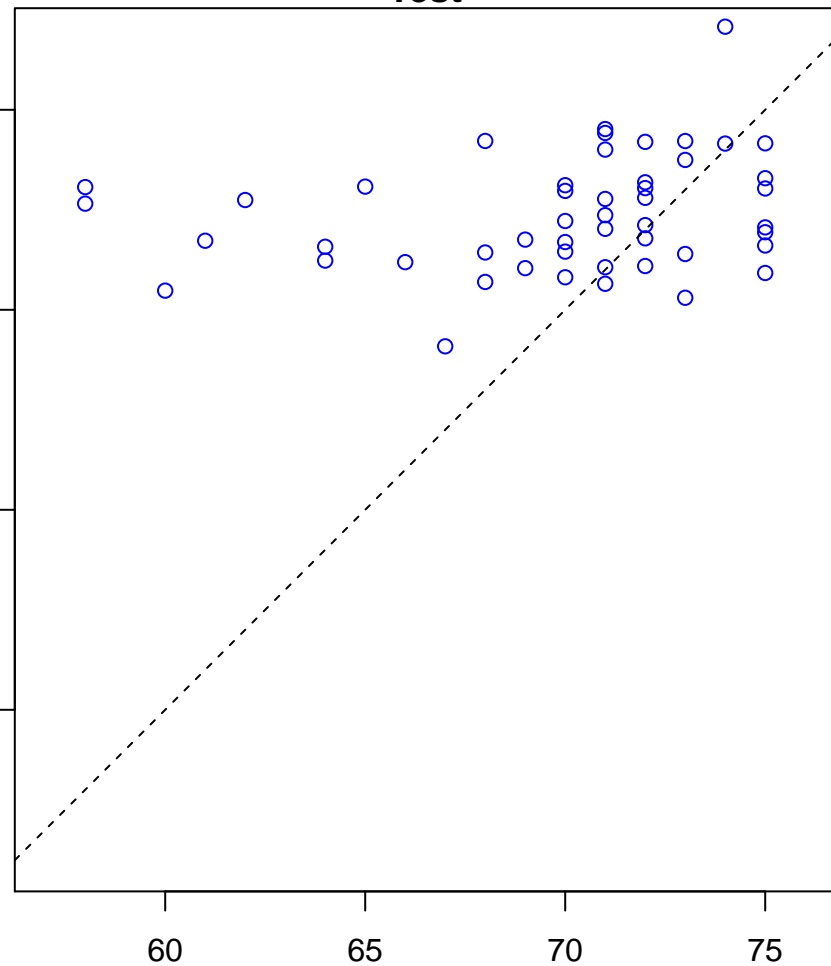


response to endoplasmic reticulum stress (Score: 1.547109)

Control

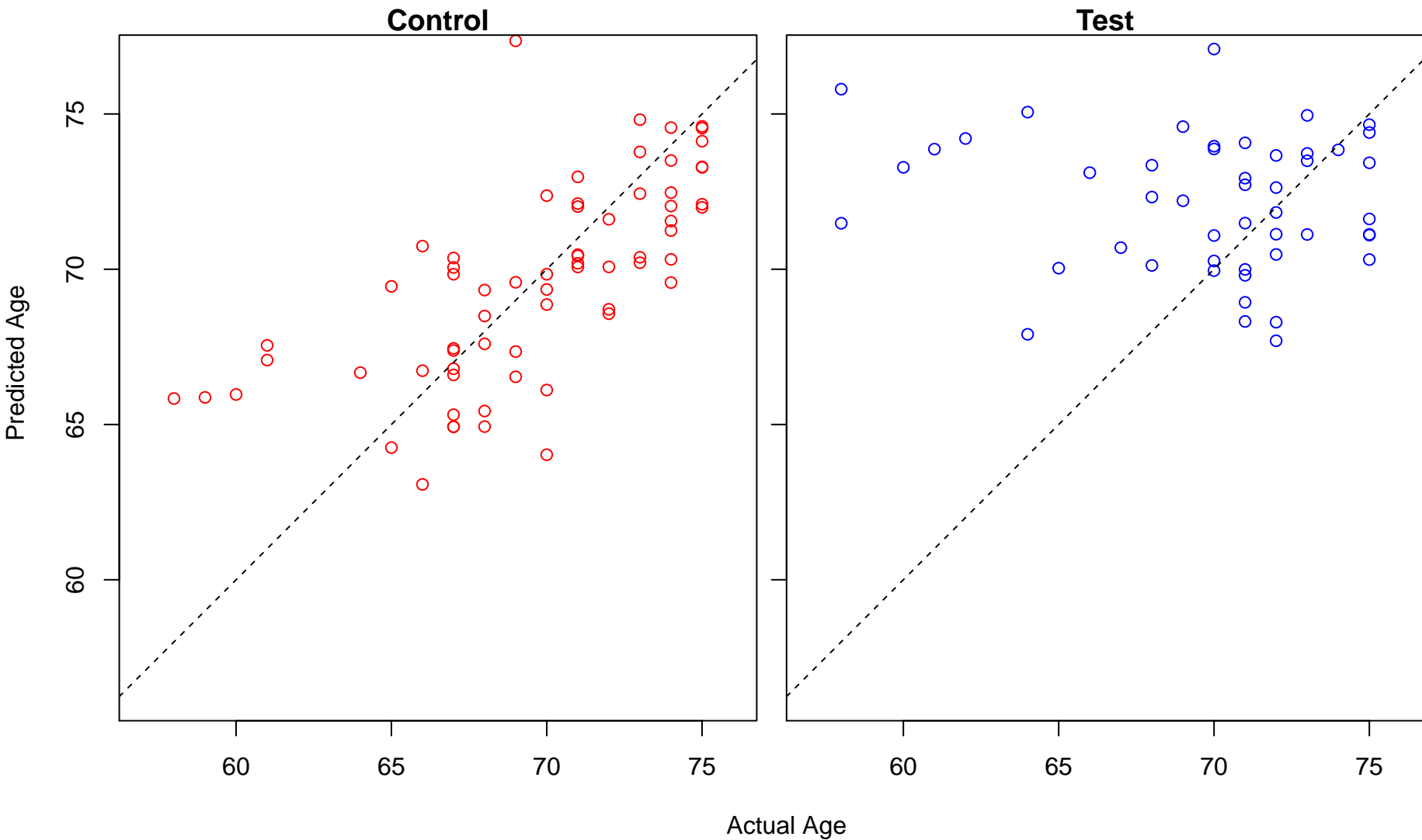


Test

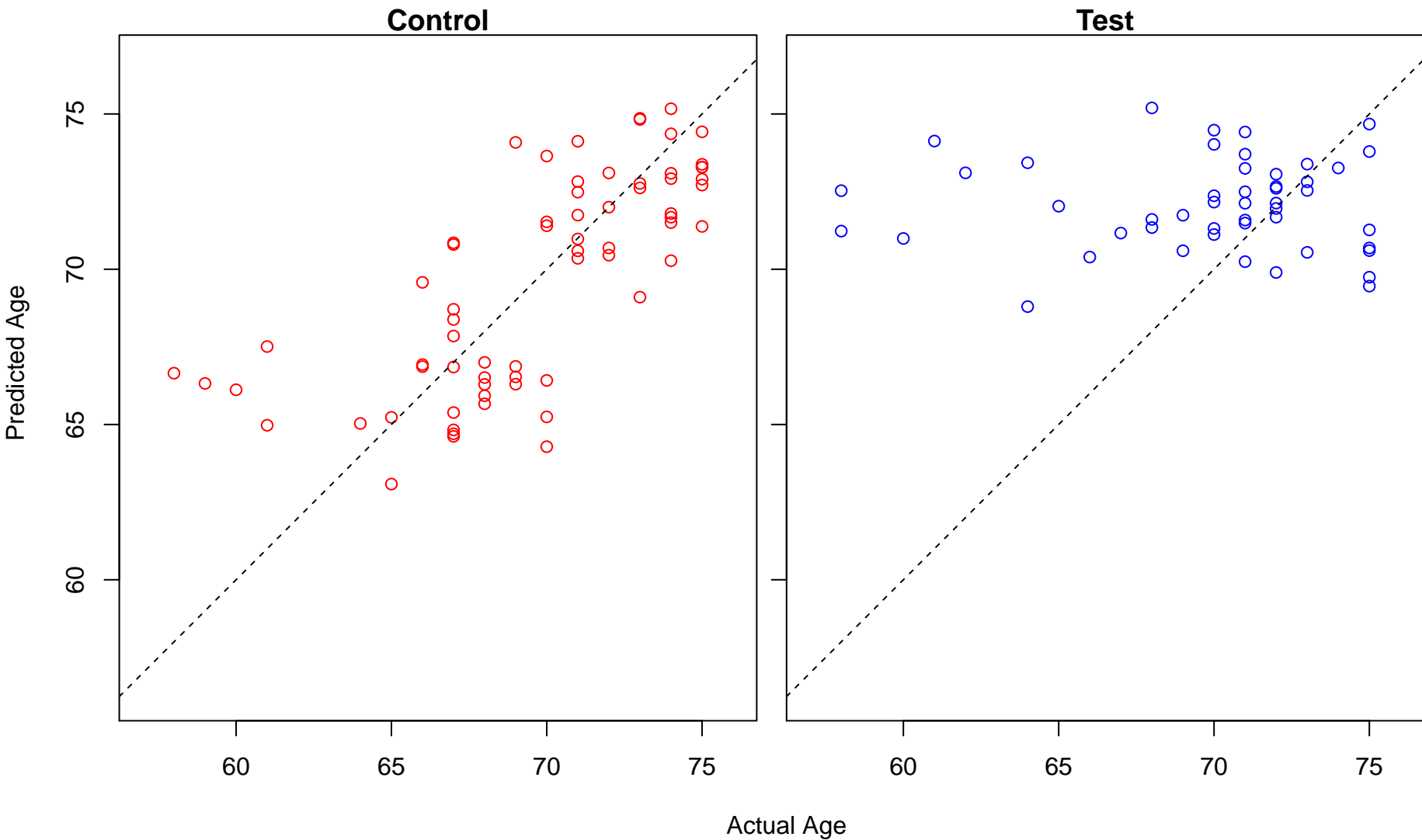


Actual Age

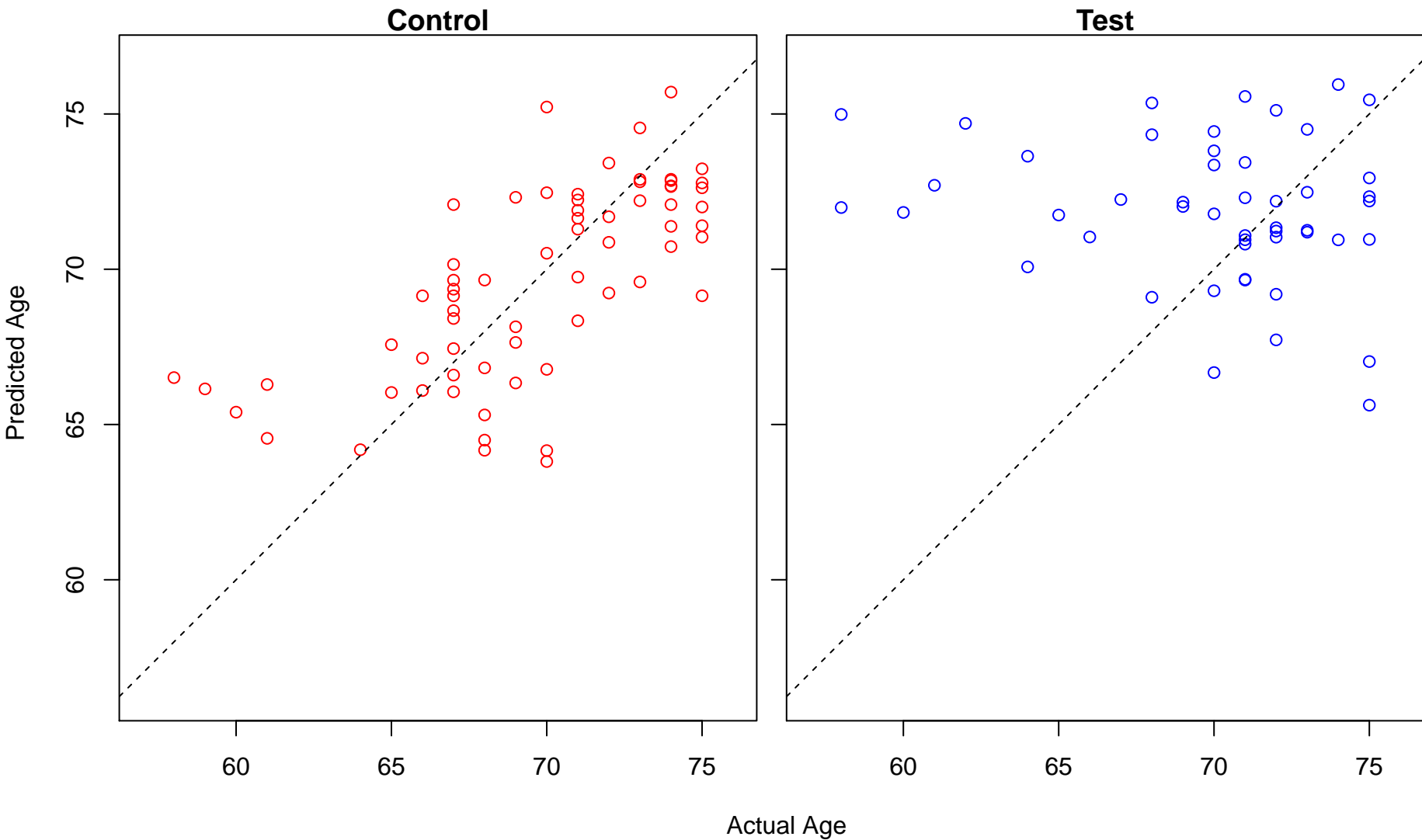
tricarboxylic acid cycle (Score: 1.546782)



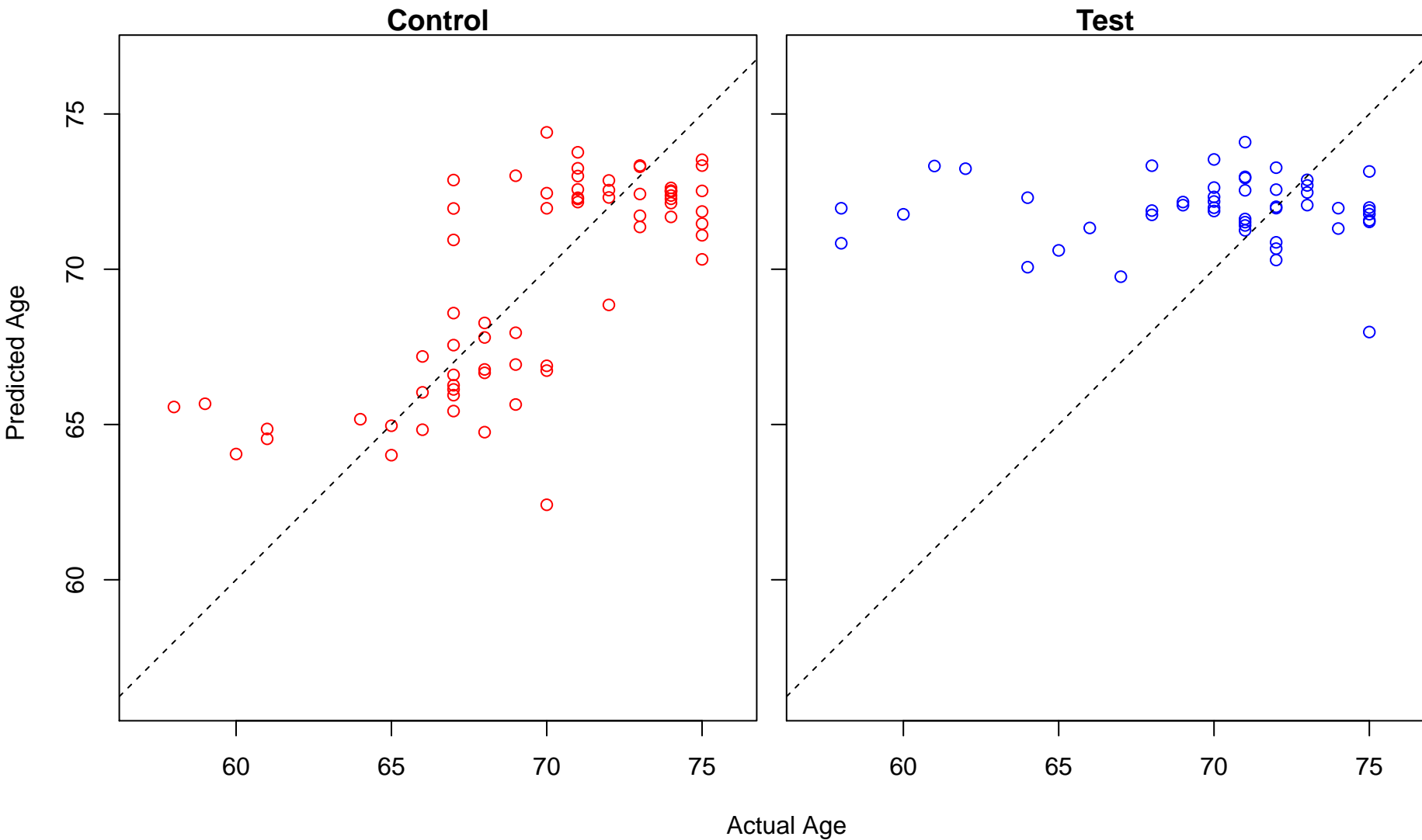
modification-dependent protein catabolic process (Score: 1.546494)



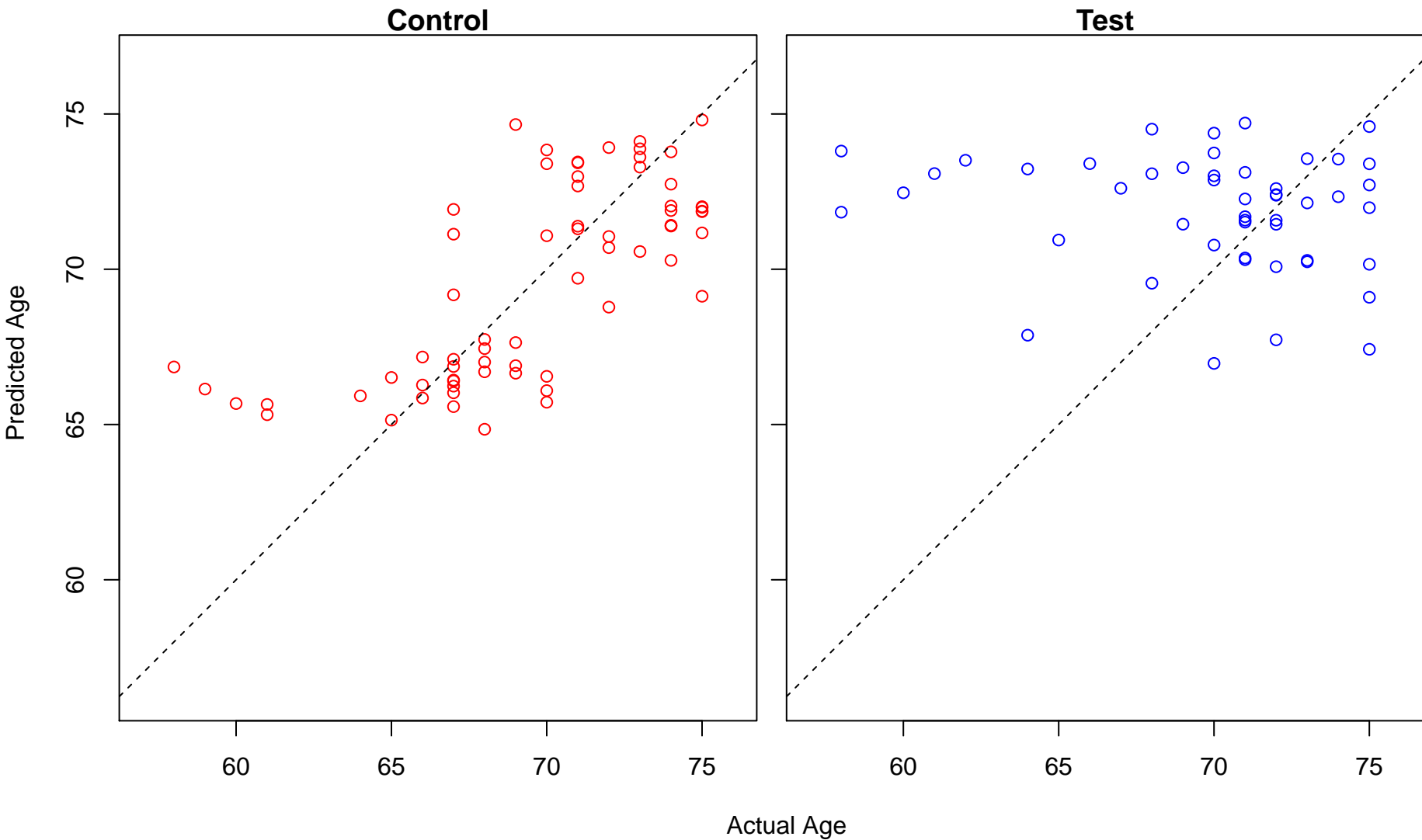
negative regulation of muscle cell differentiation (Score: 1.546441)



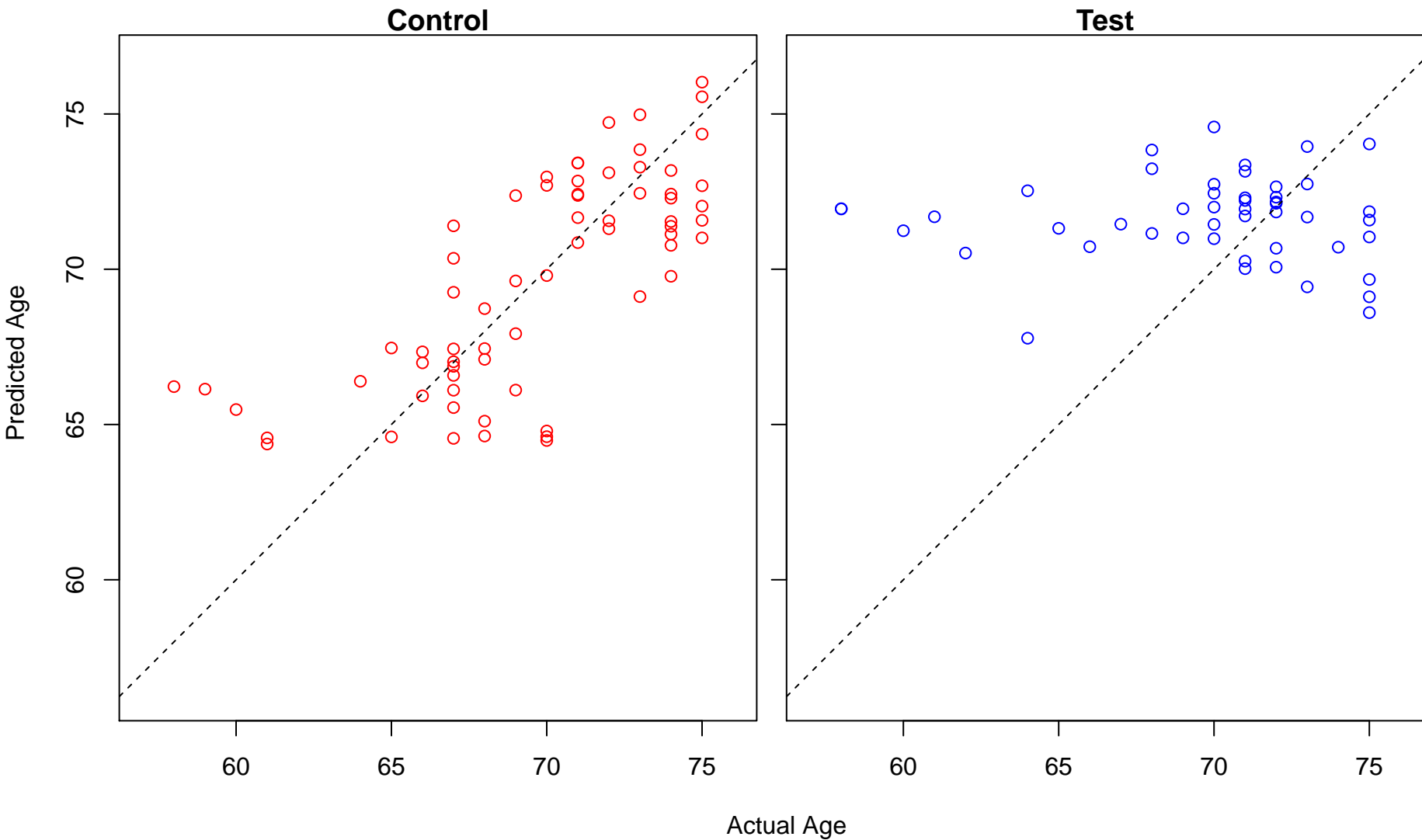
oxidative phosphorylation (Score: 1.546198)



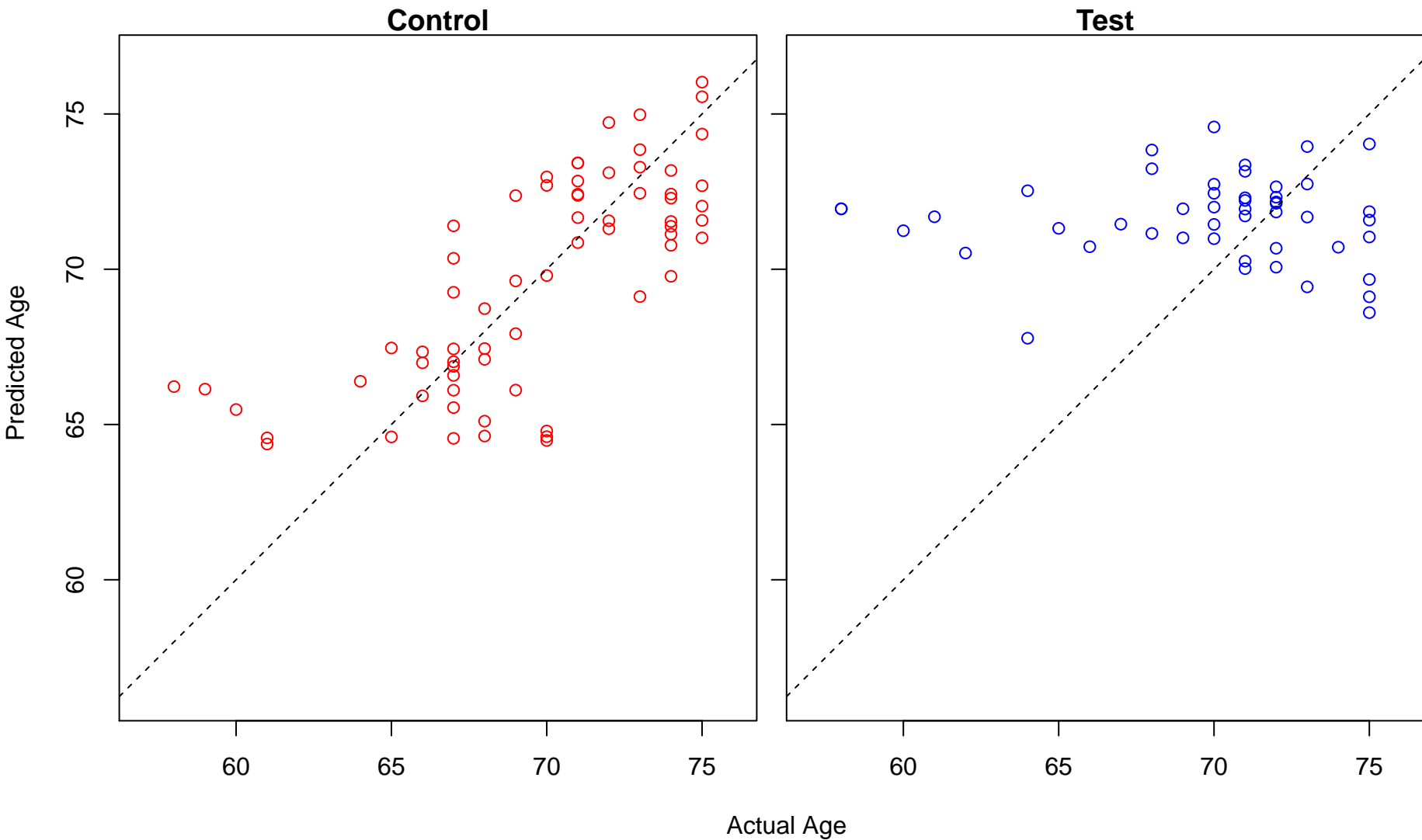
protein O-linked glycosylation (Score: 1.546191)



GPI anchor metabolic process (Score: 1.545815)

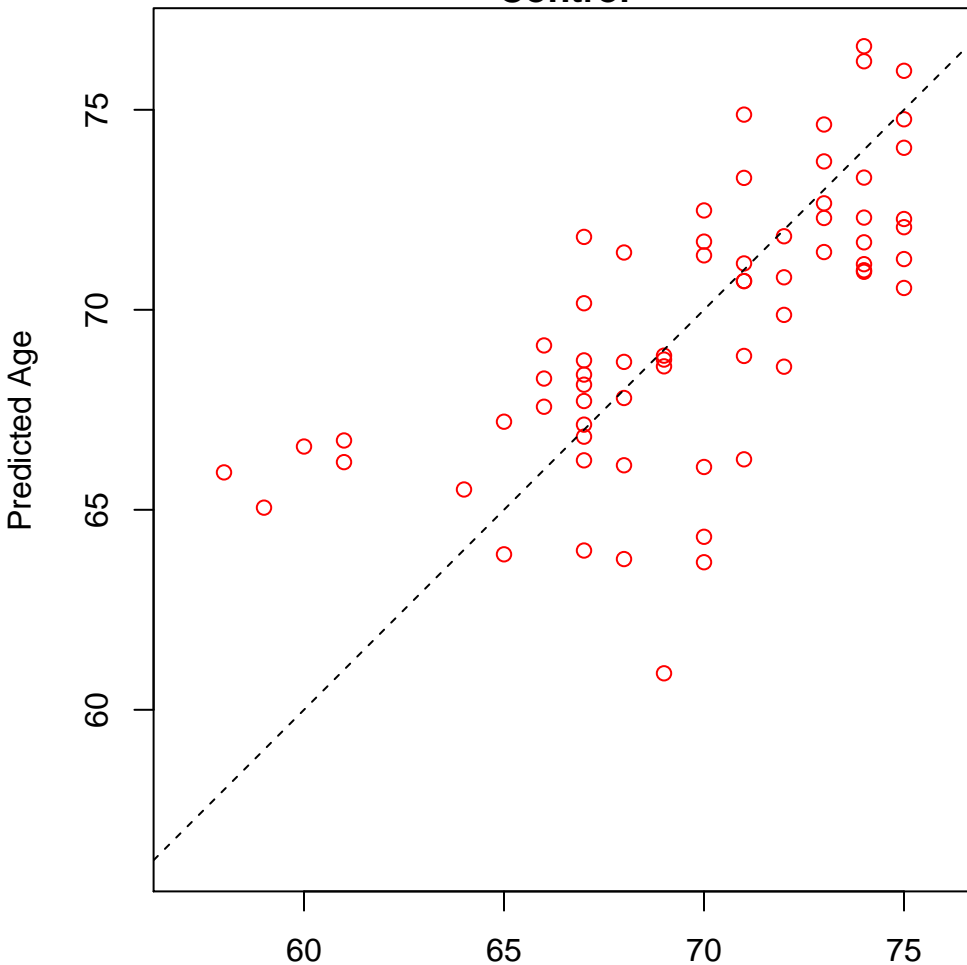


GPI anchor biosynthetic process (Score: 1.545815)

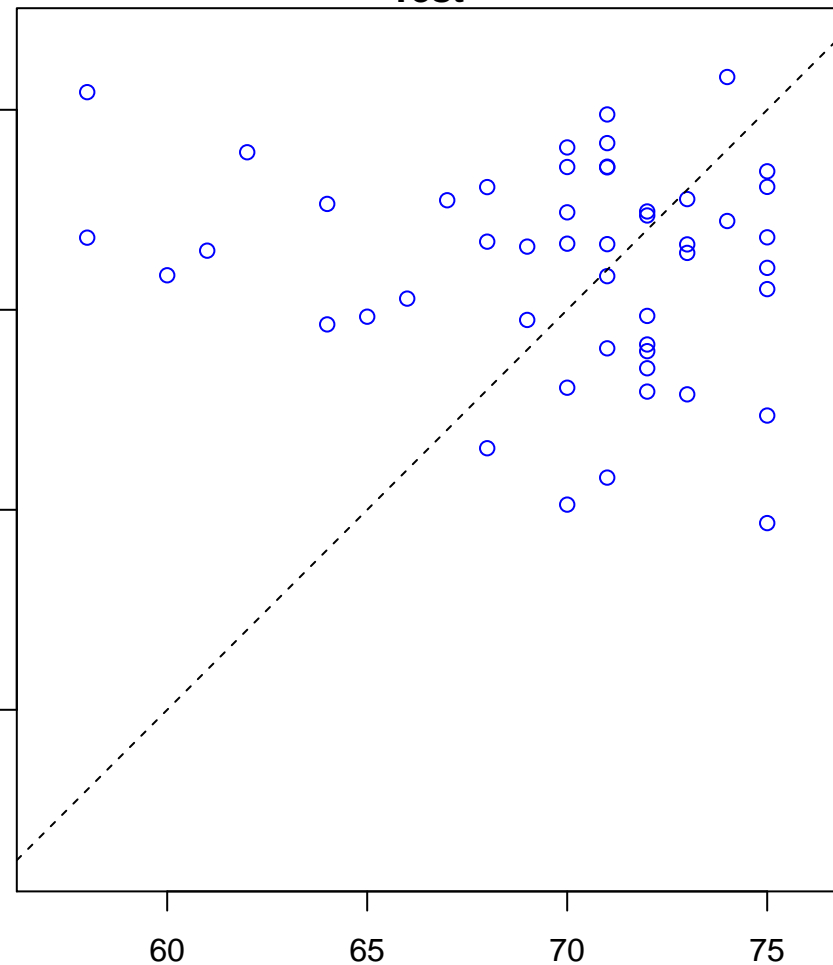


cellular response to nutrient levels (Score: 1.545539)

Control

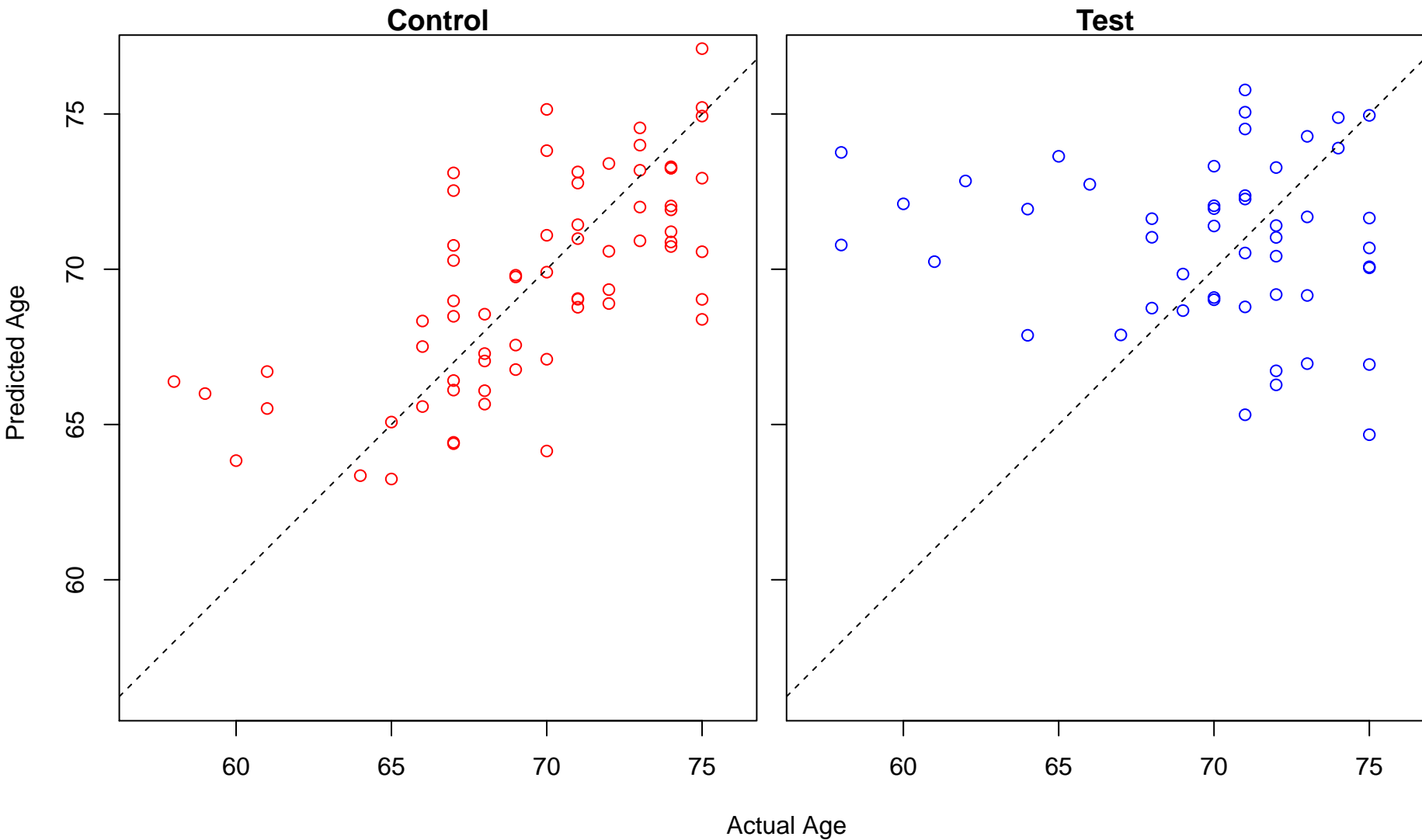


Test

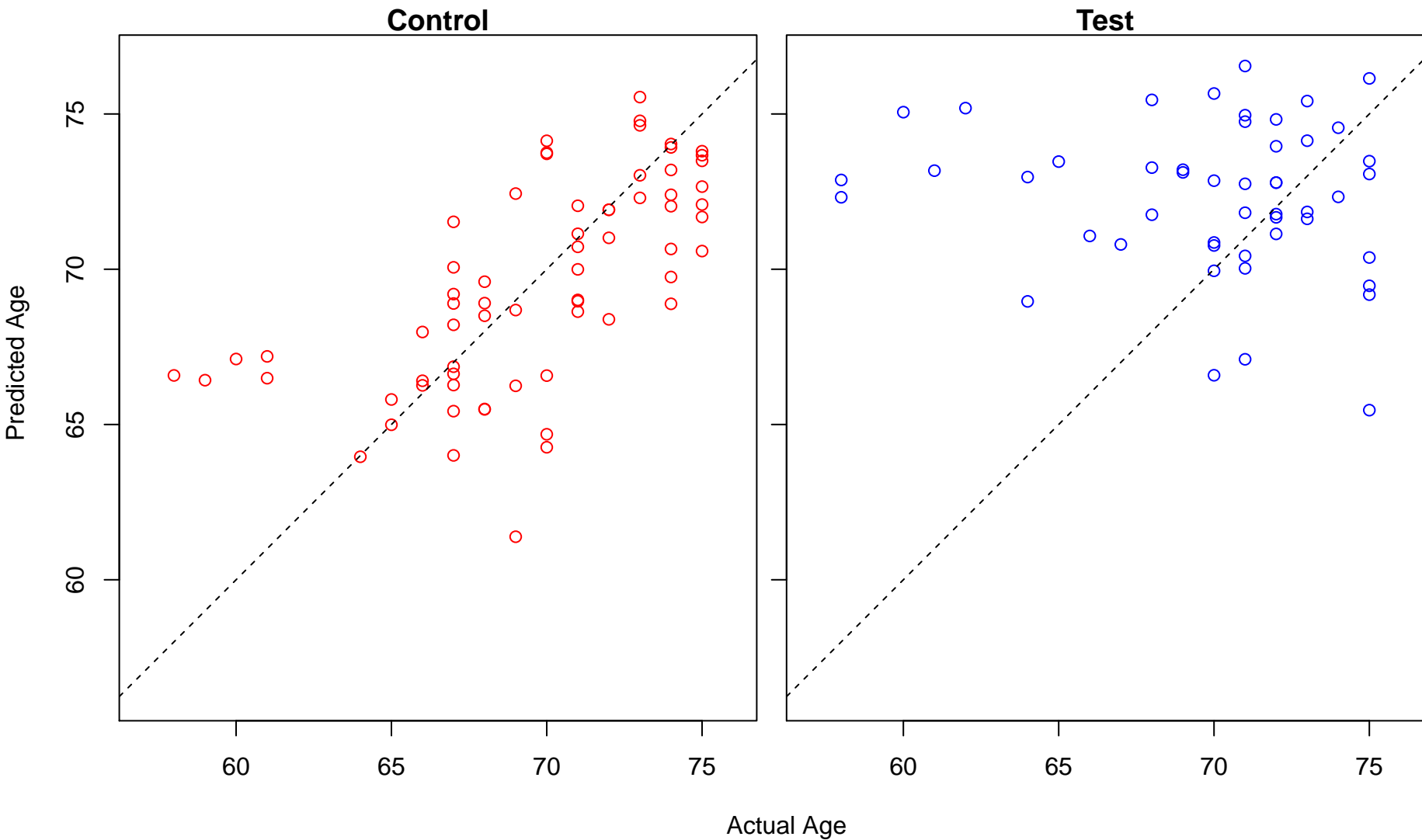


Actual Age

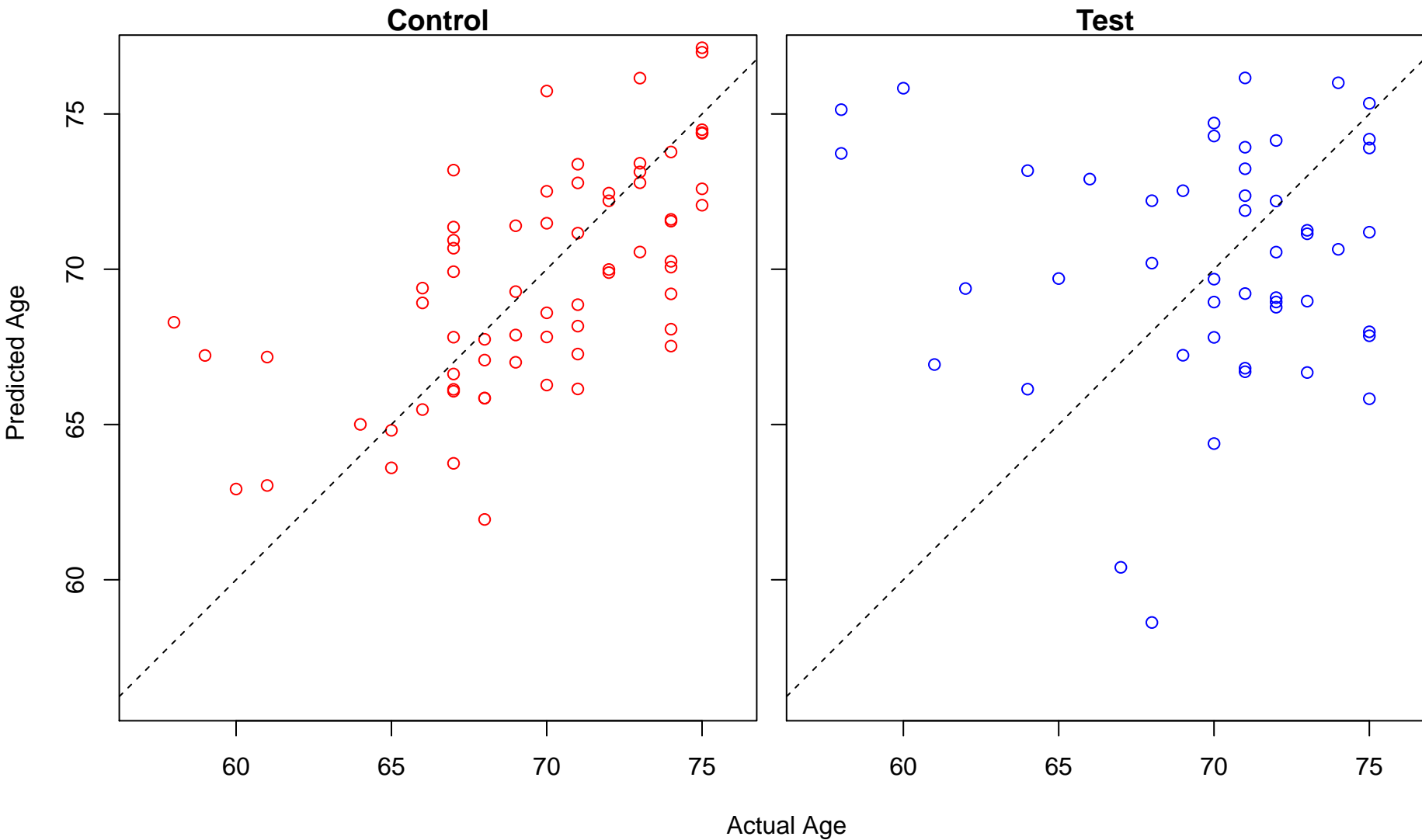
positive regulation of cell–matrix adhesion (Score: 1.545296)



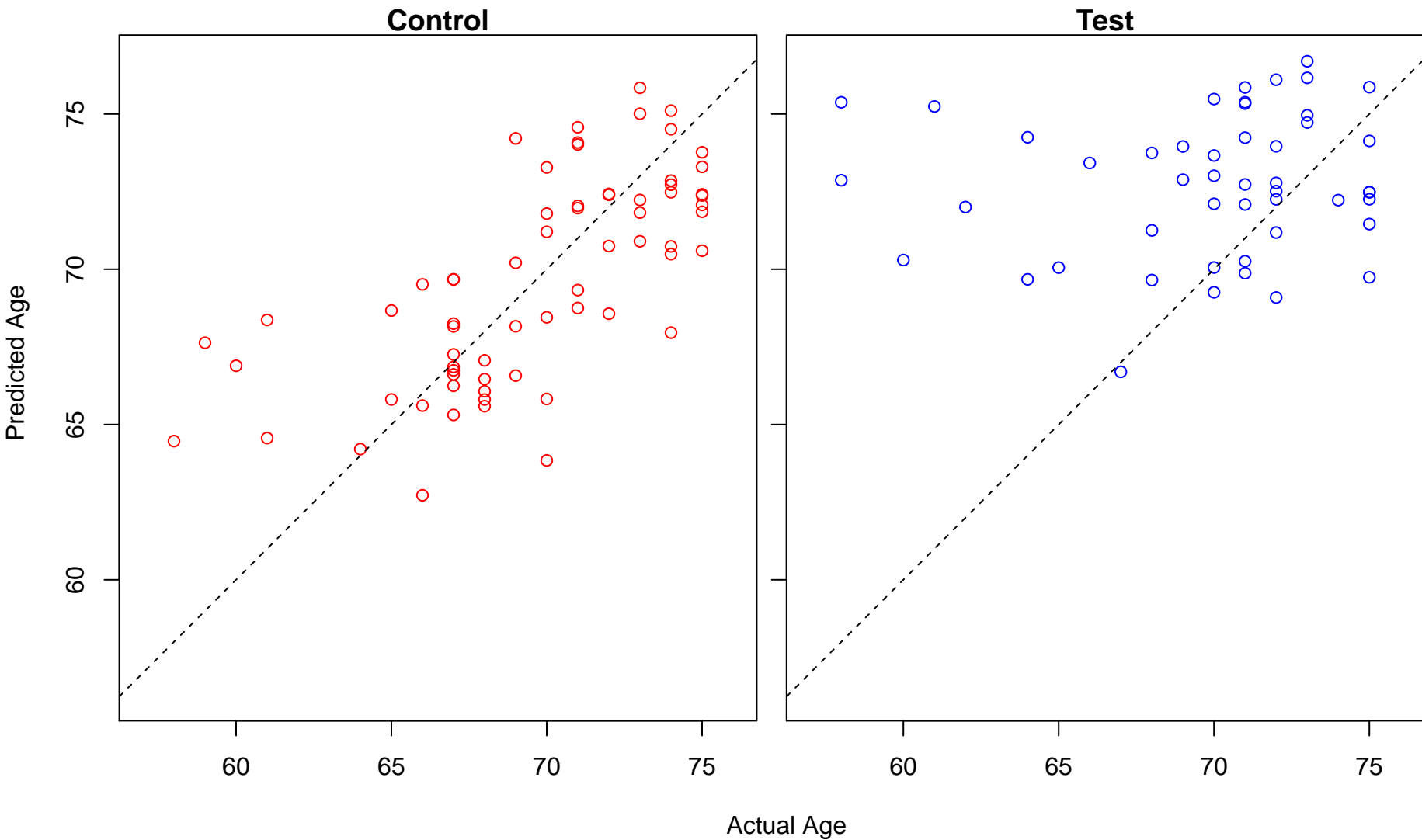
protein autophosphorylation (Score: 1.544864)



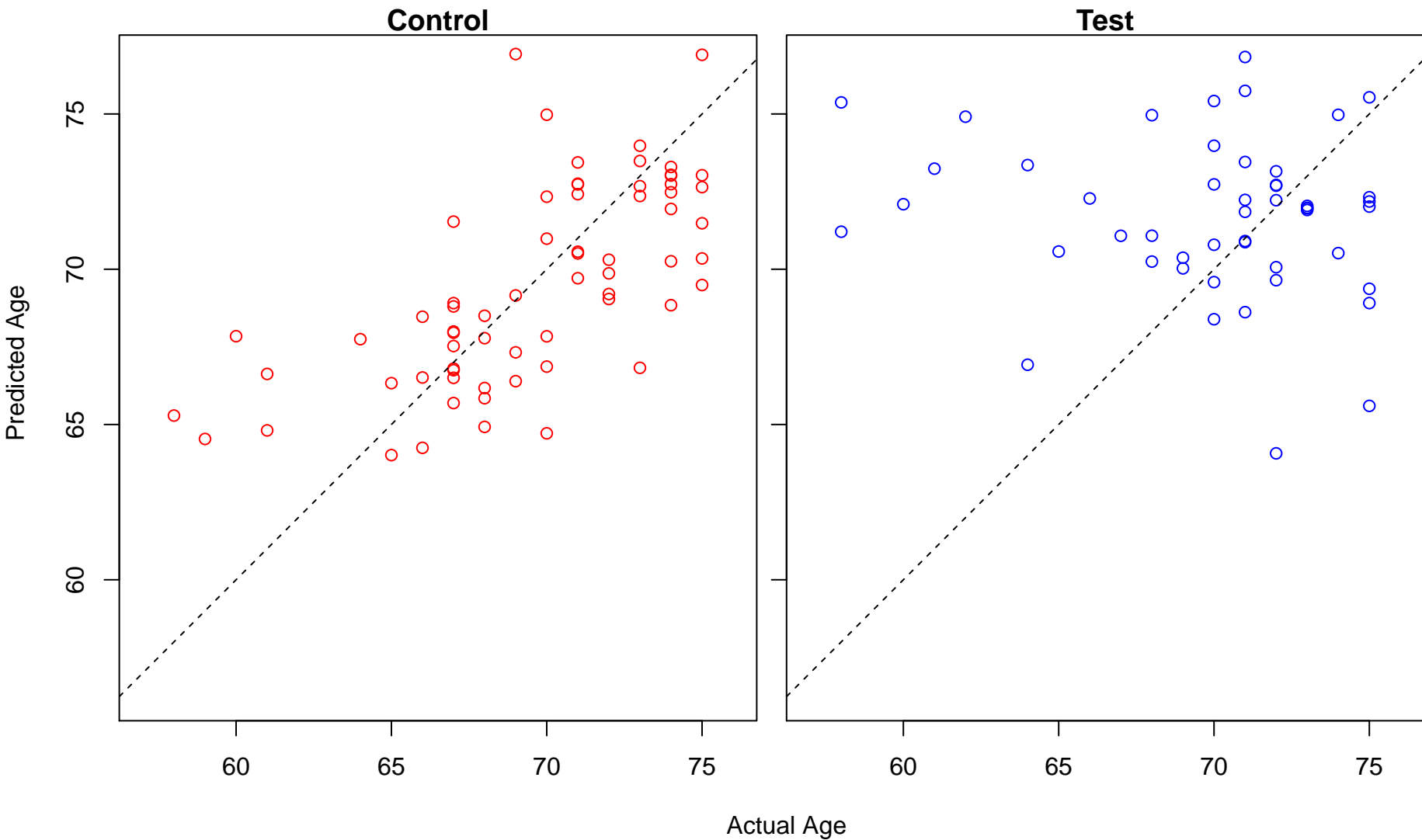
stem cell proliferation (Score: 1.544803)



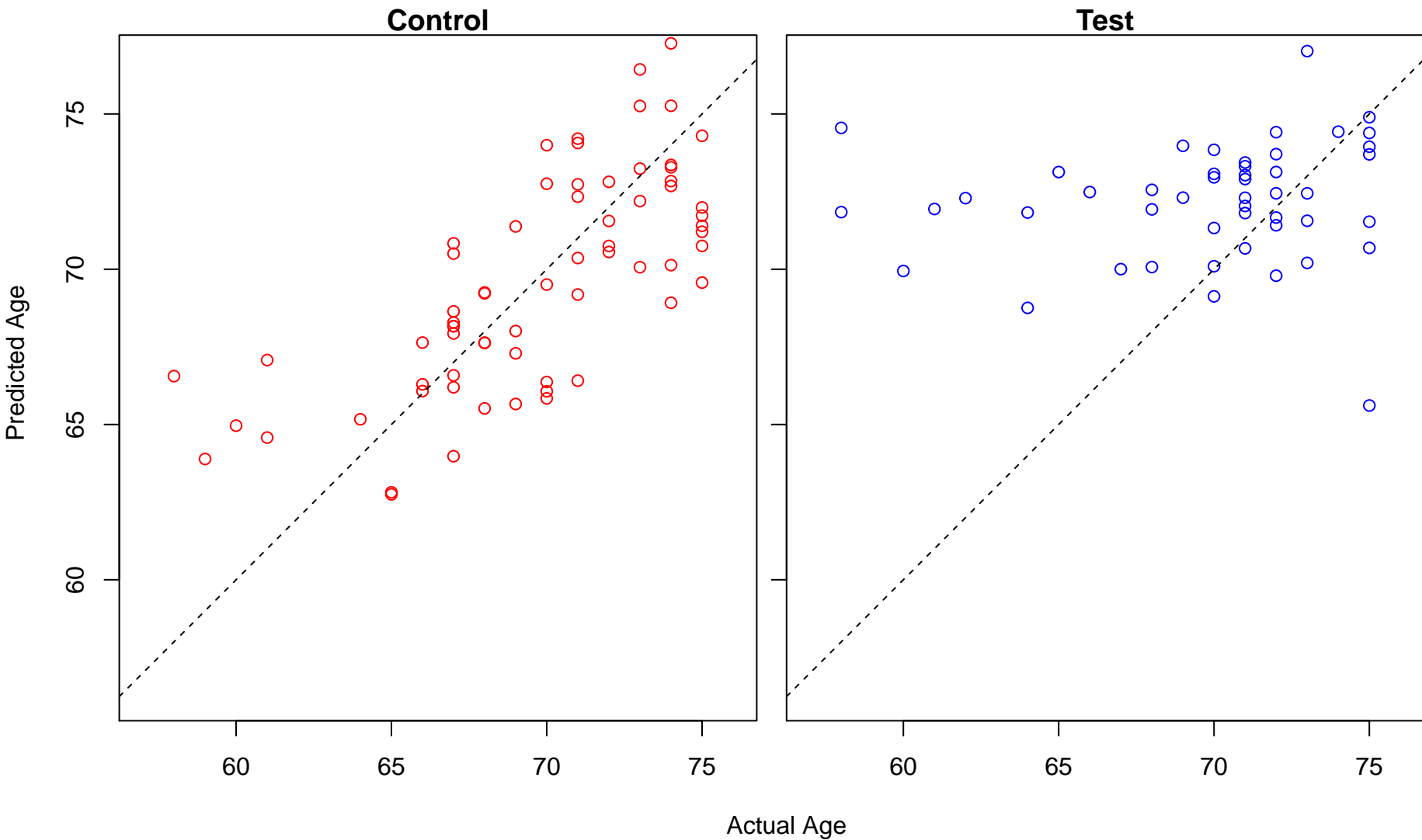
cardiac chamber development (Score: 1.544755)



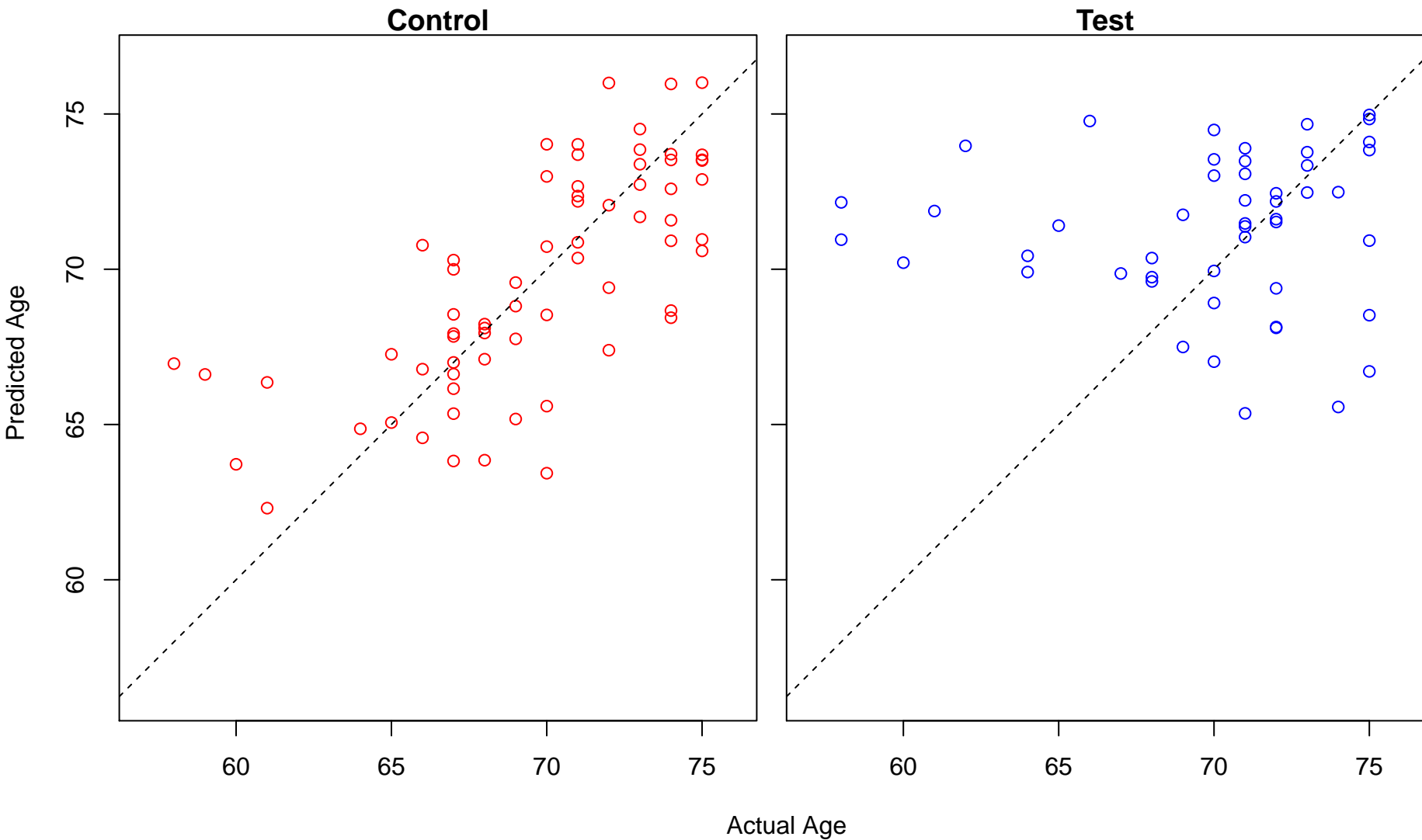
protein deneddylation (Score: 1.543423)



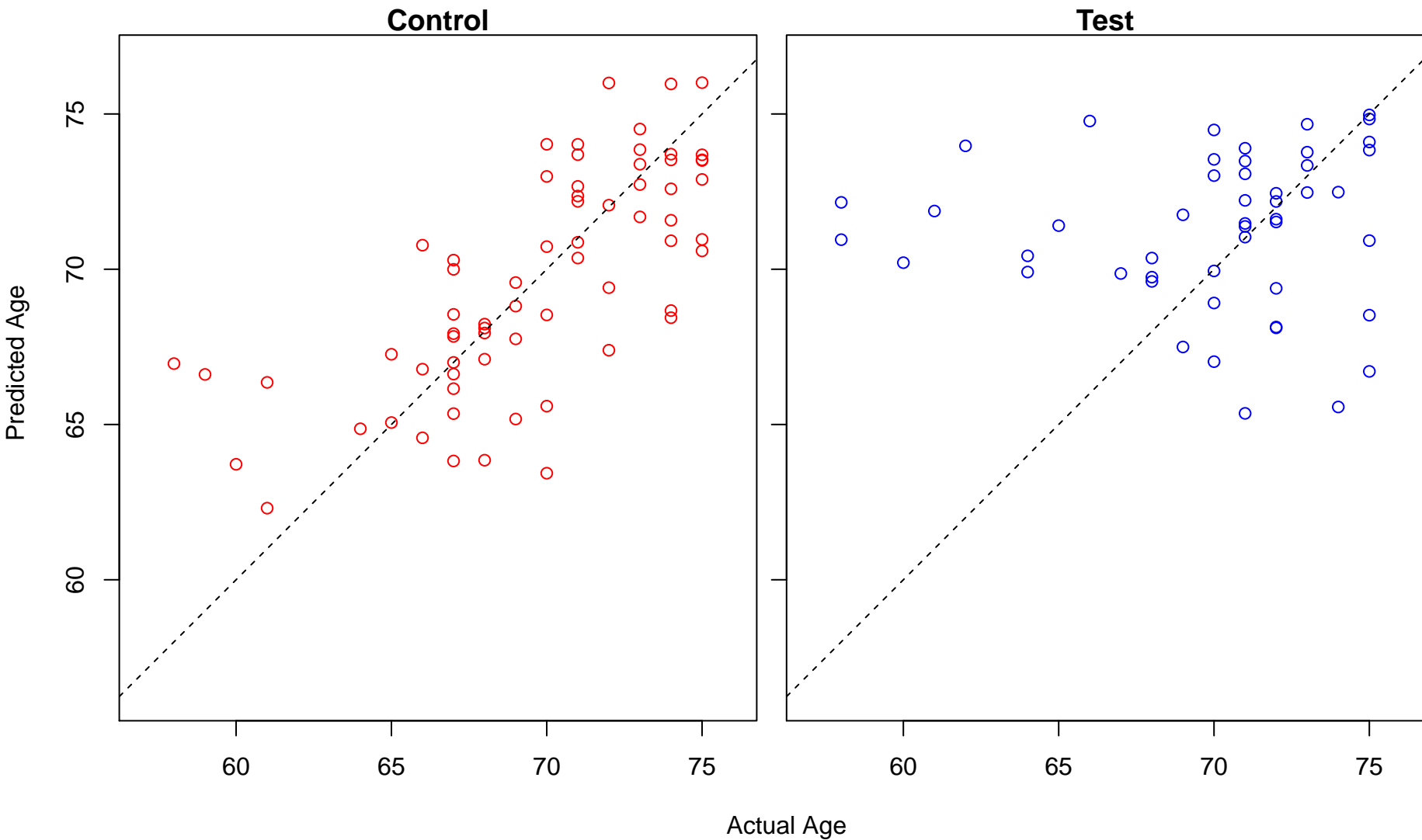
regulation of ion transport (Score: 1.543069)



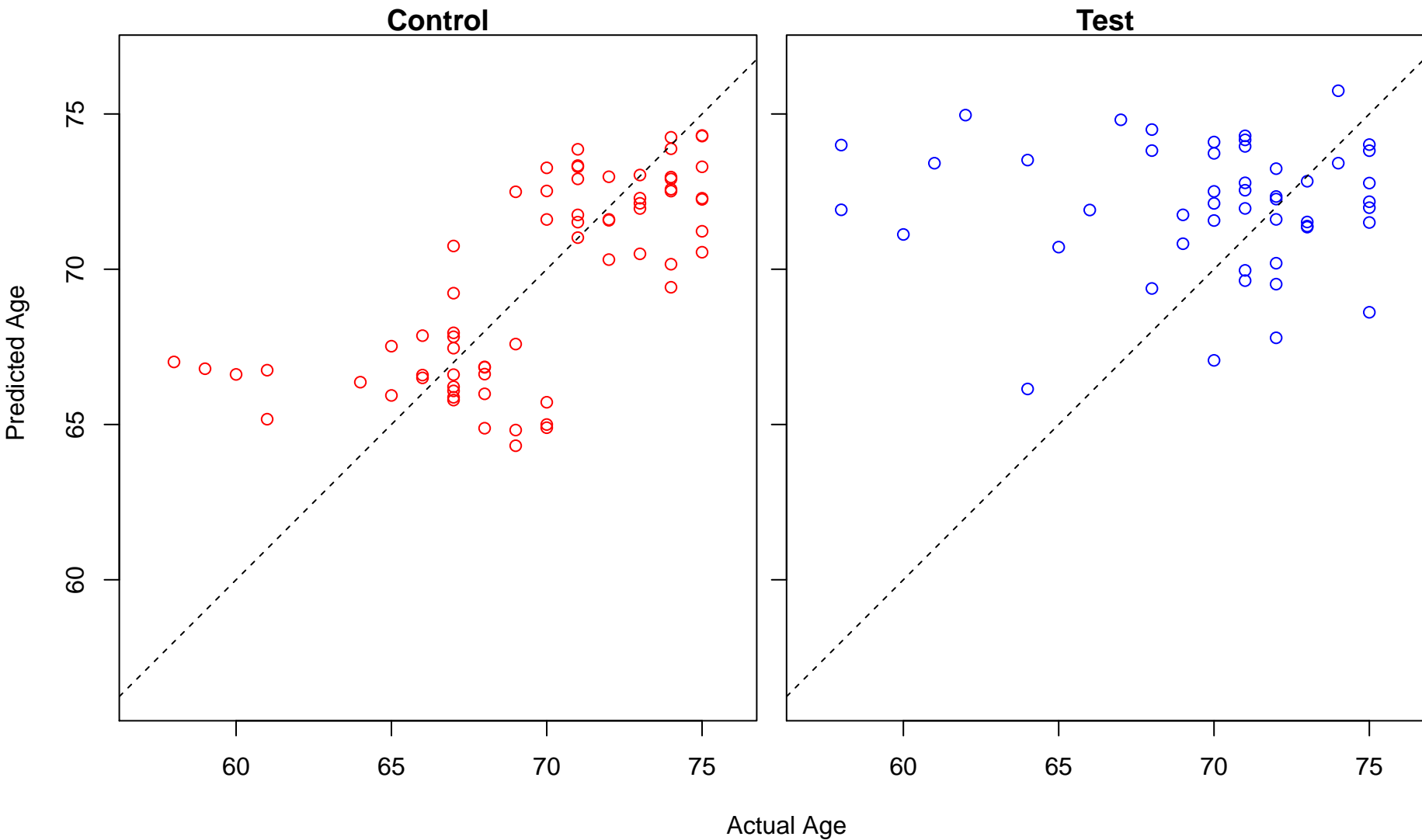
regulation of nucleoside metabolic process (Score: 1.543062)



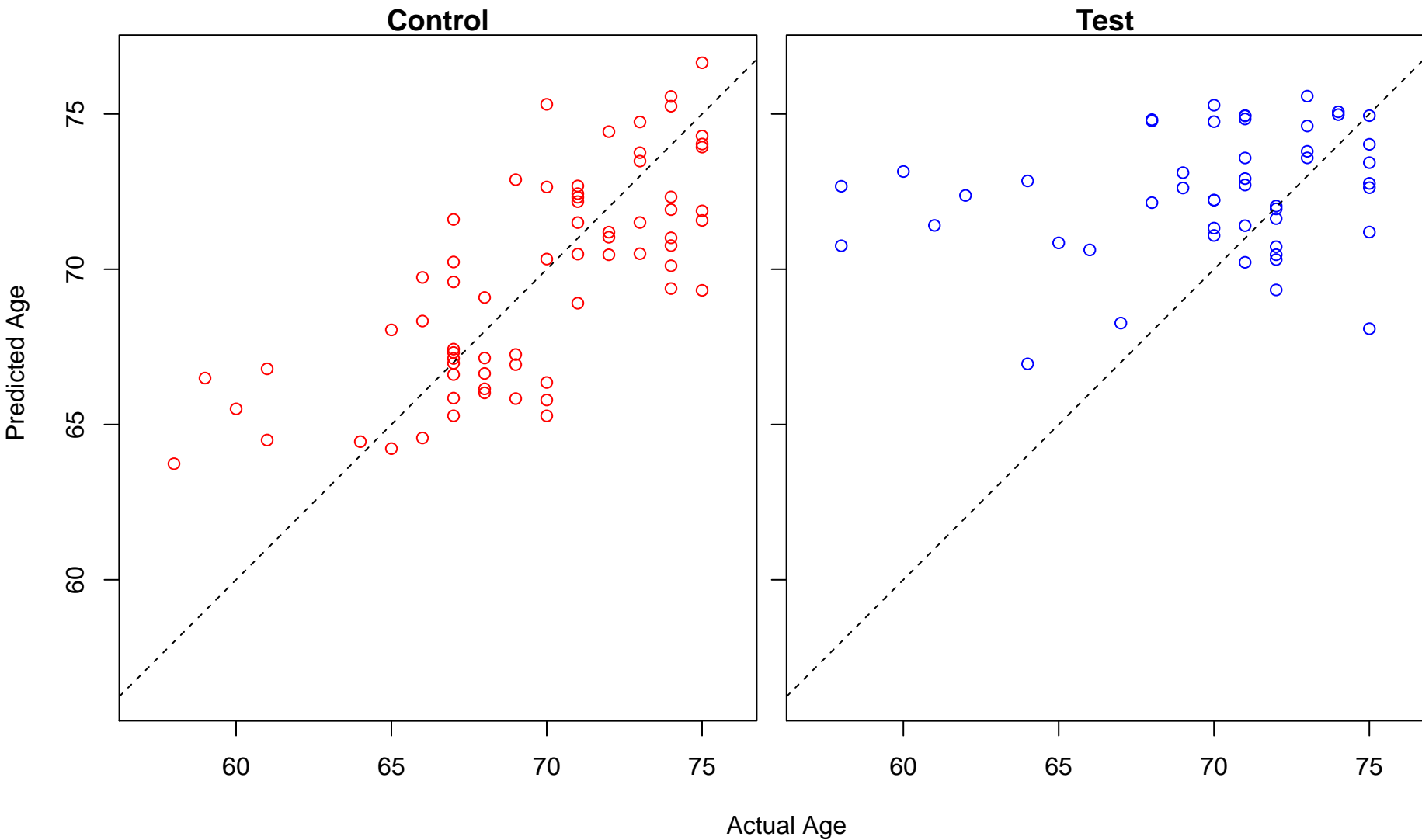
regulation of ATP metabolic process (Score: 1.543062)



positive regulation of cell cycle phase transition (Score: 1.542826)

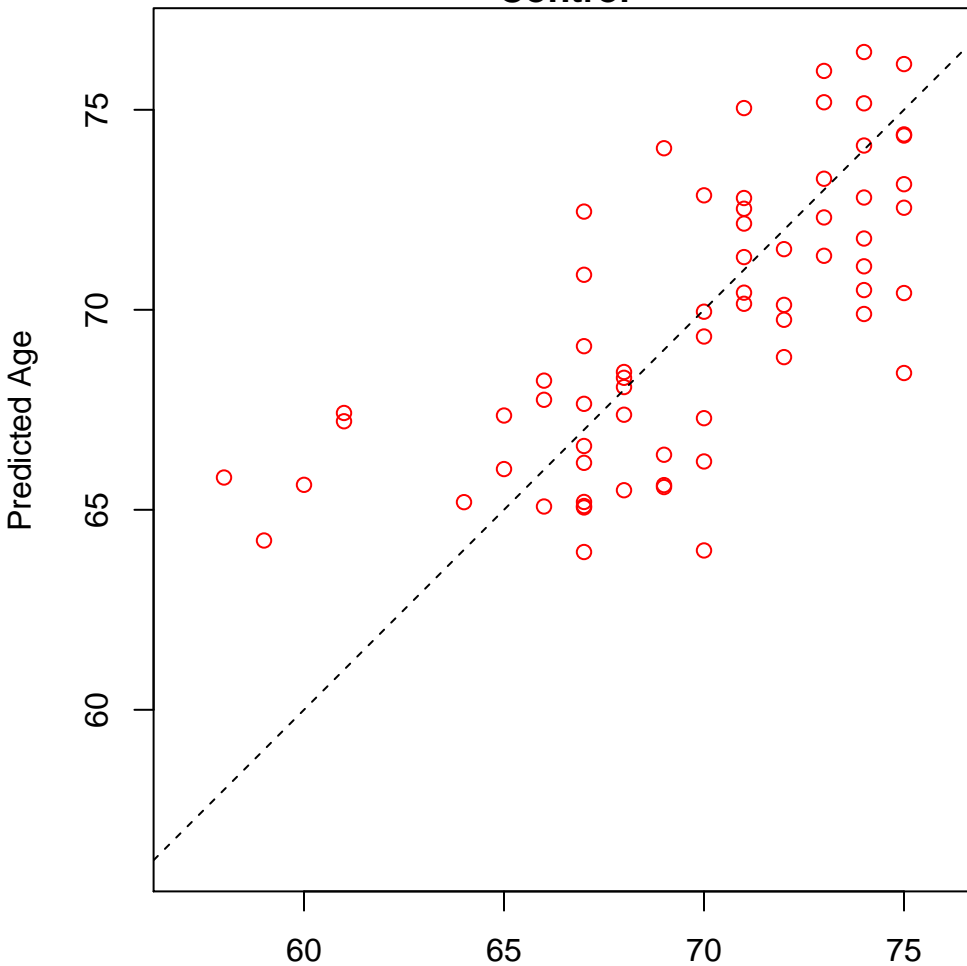


organic anion transport (Score: 1.542199)

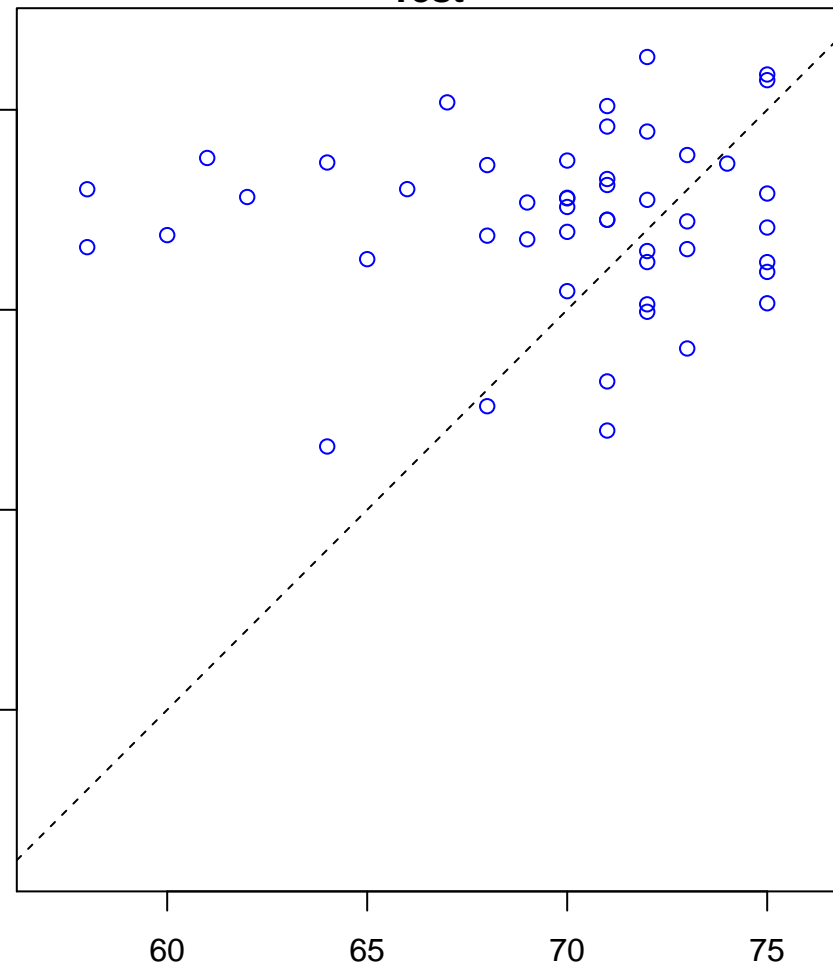


nucleoside phosphate catabolic process (Score: 1.541785)

Control

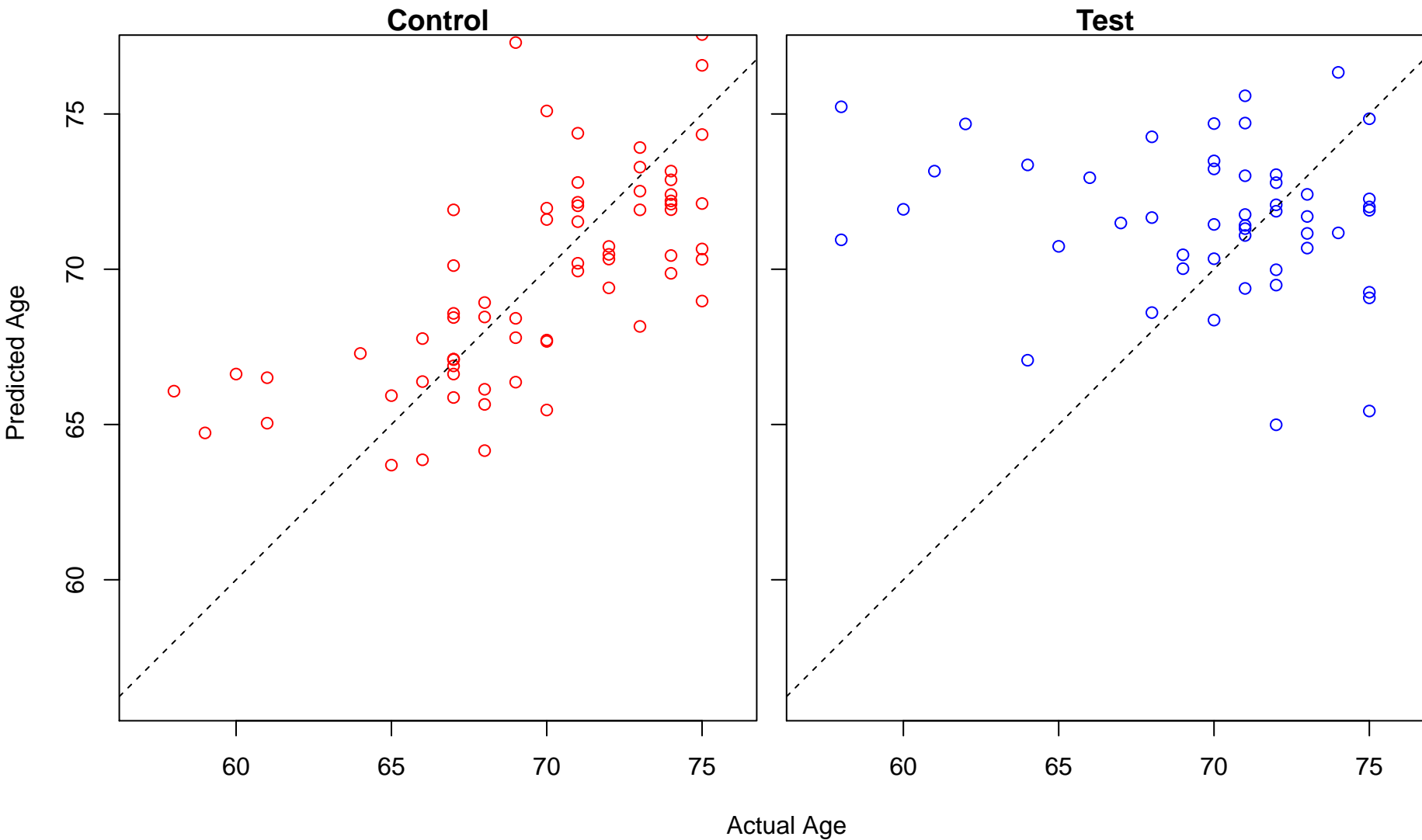


Test

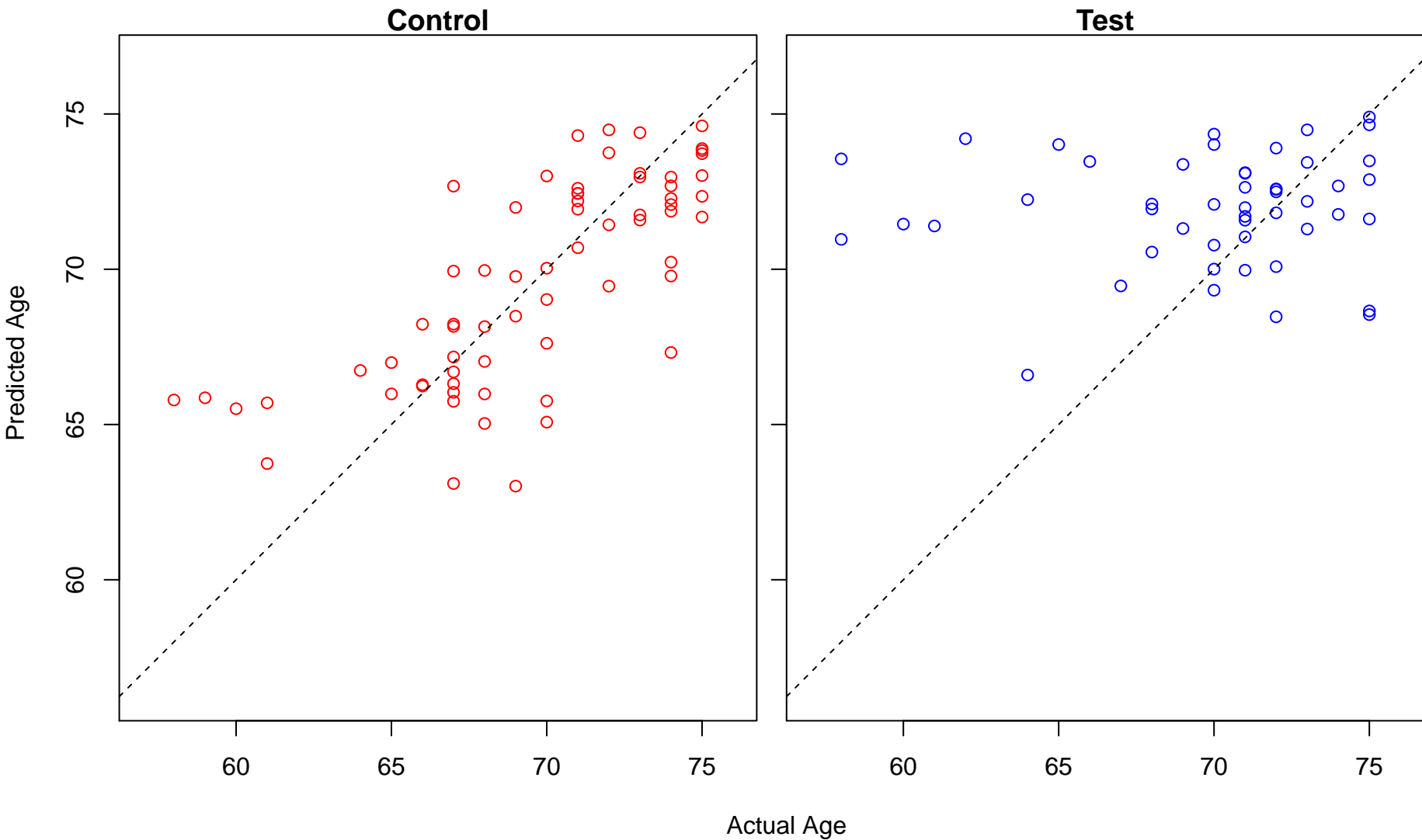


Actual Age

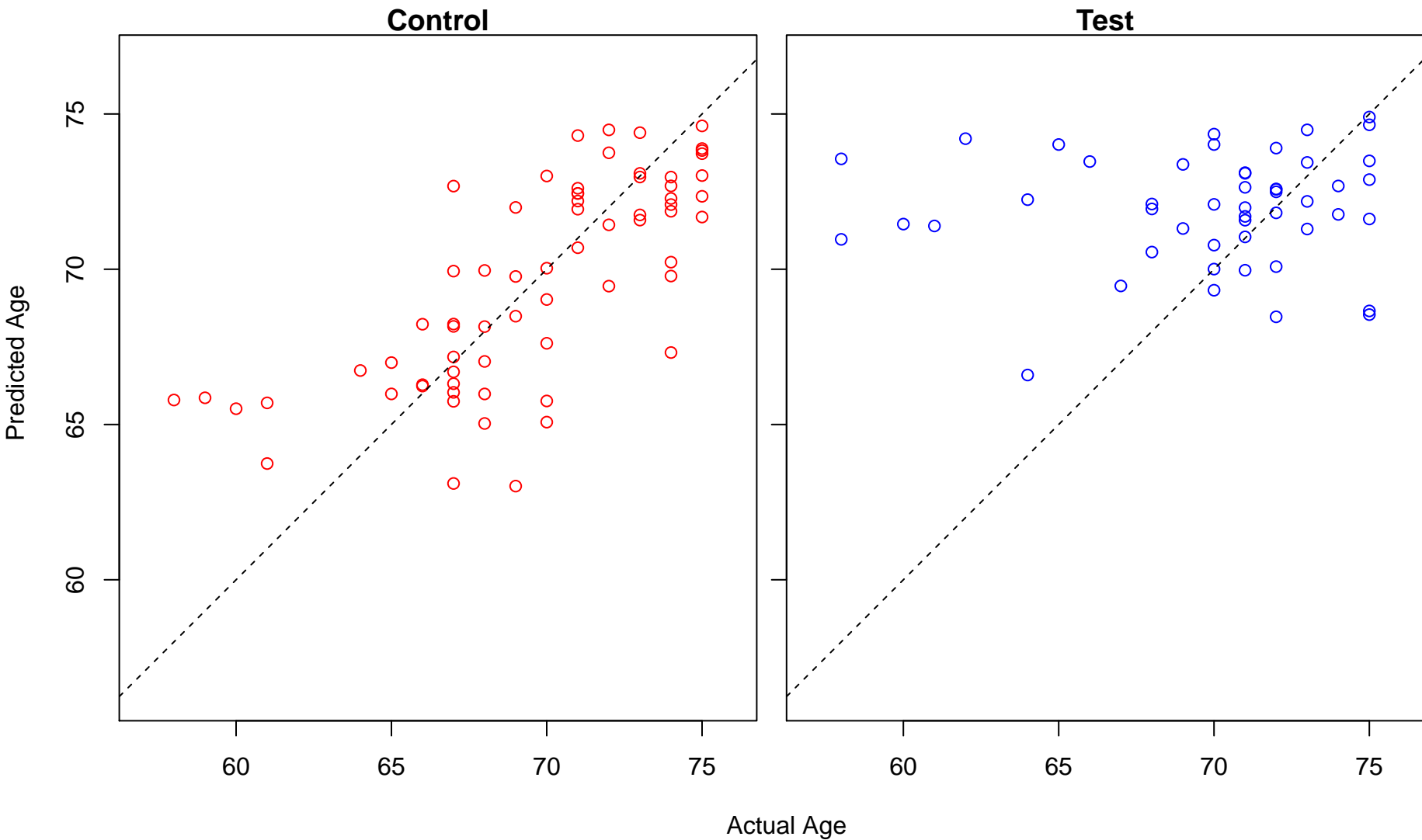
cullin deneddylation (Score: 1.541345)



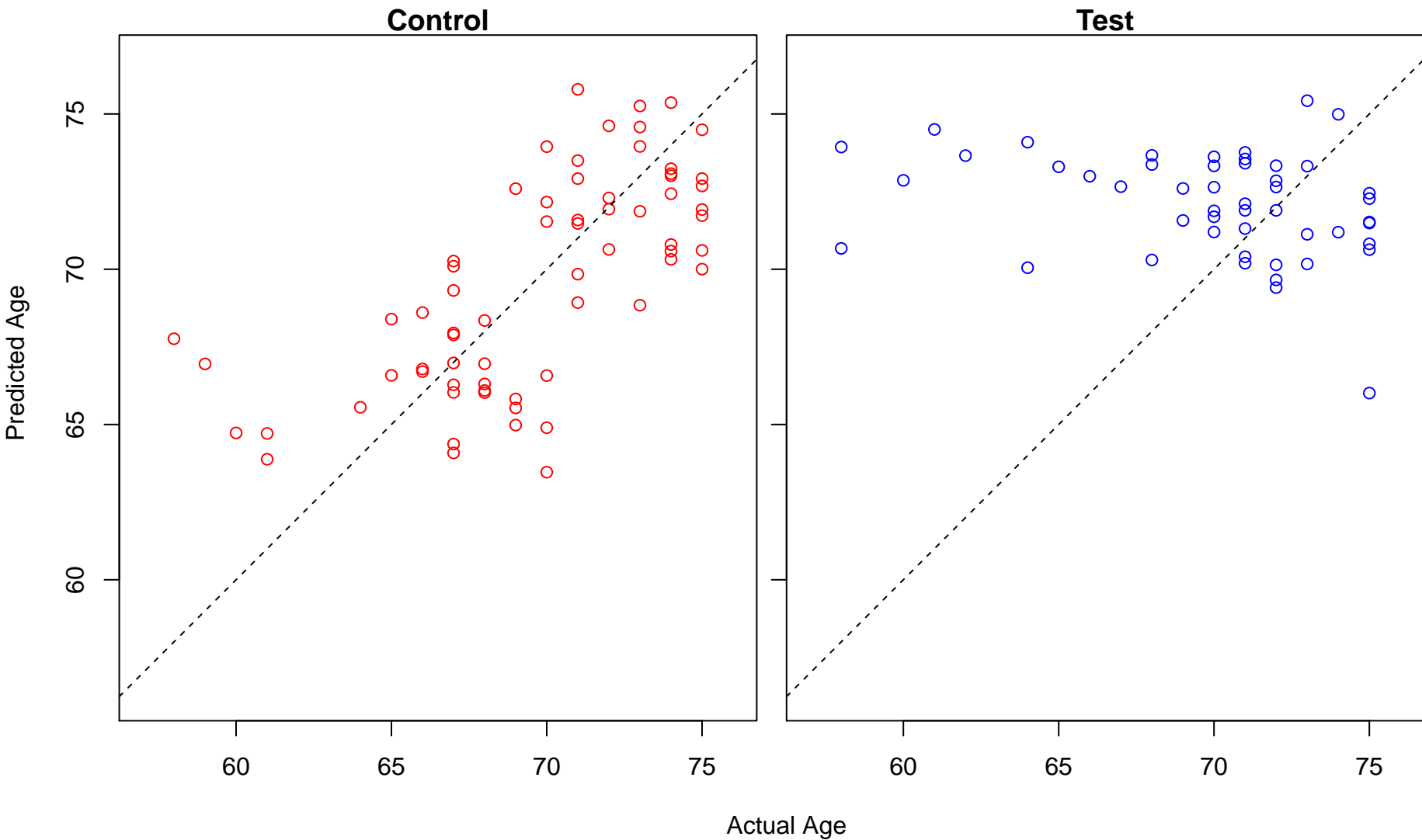
regulation of cofactor metabolic process (Score: 1.540810)



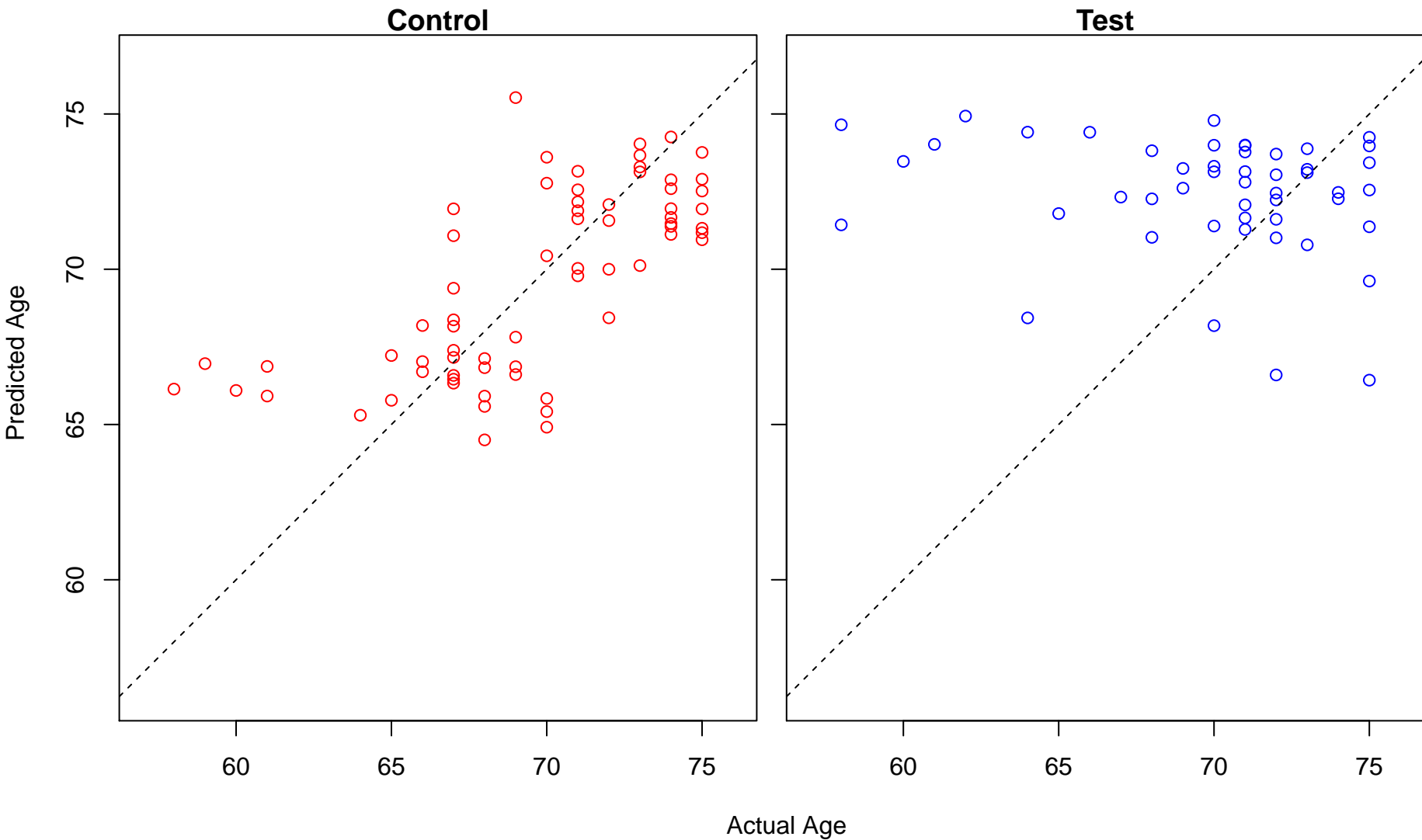
regulation of coenzyme metabolic process (Score: 1.540810)



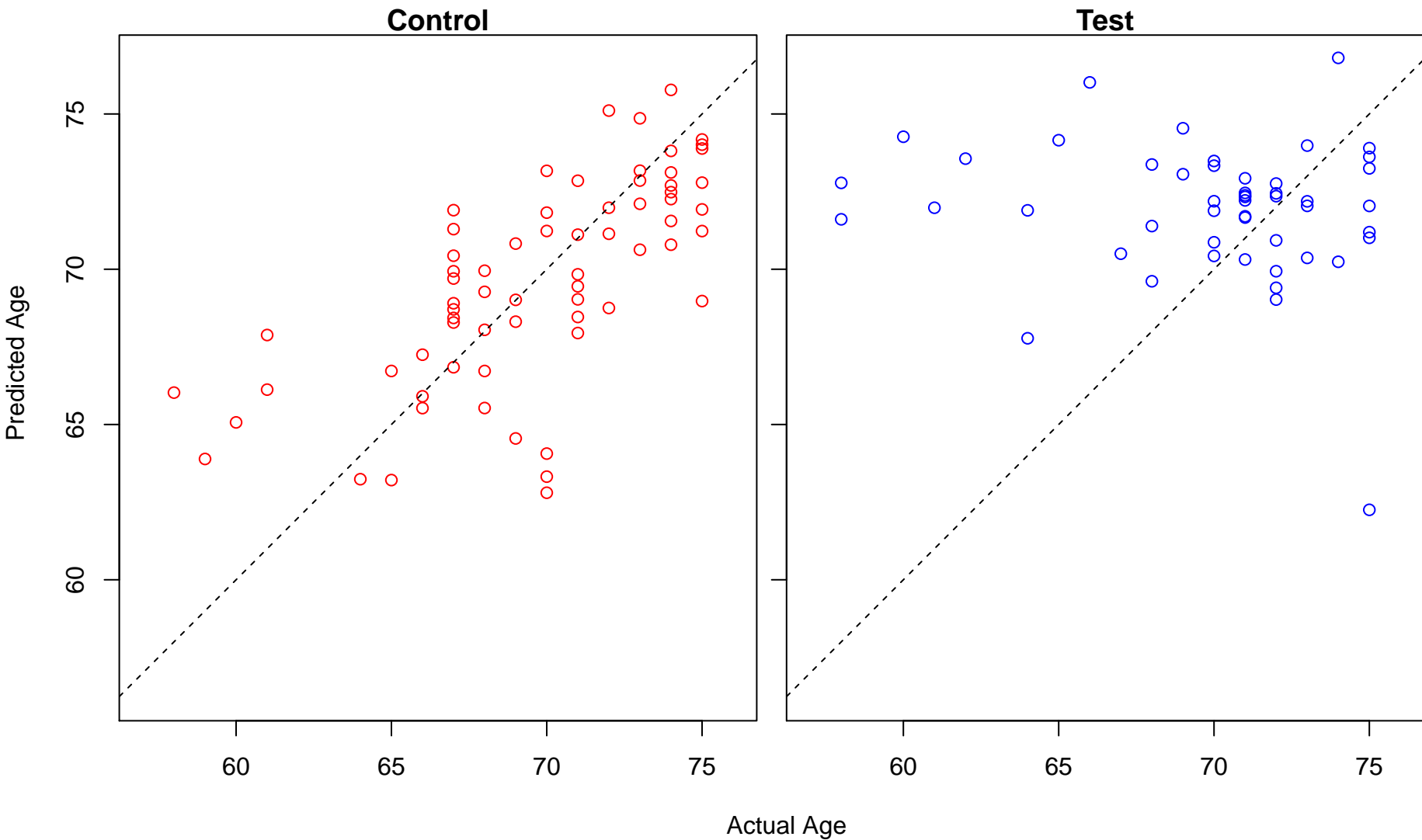
negative regulation of growth (Score: 1.540427)



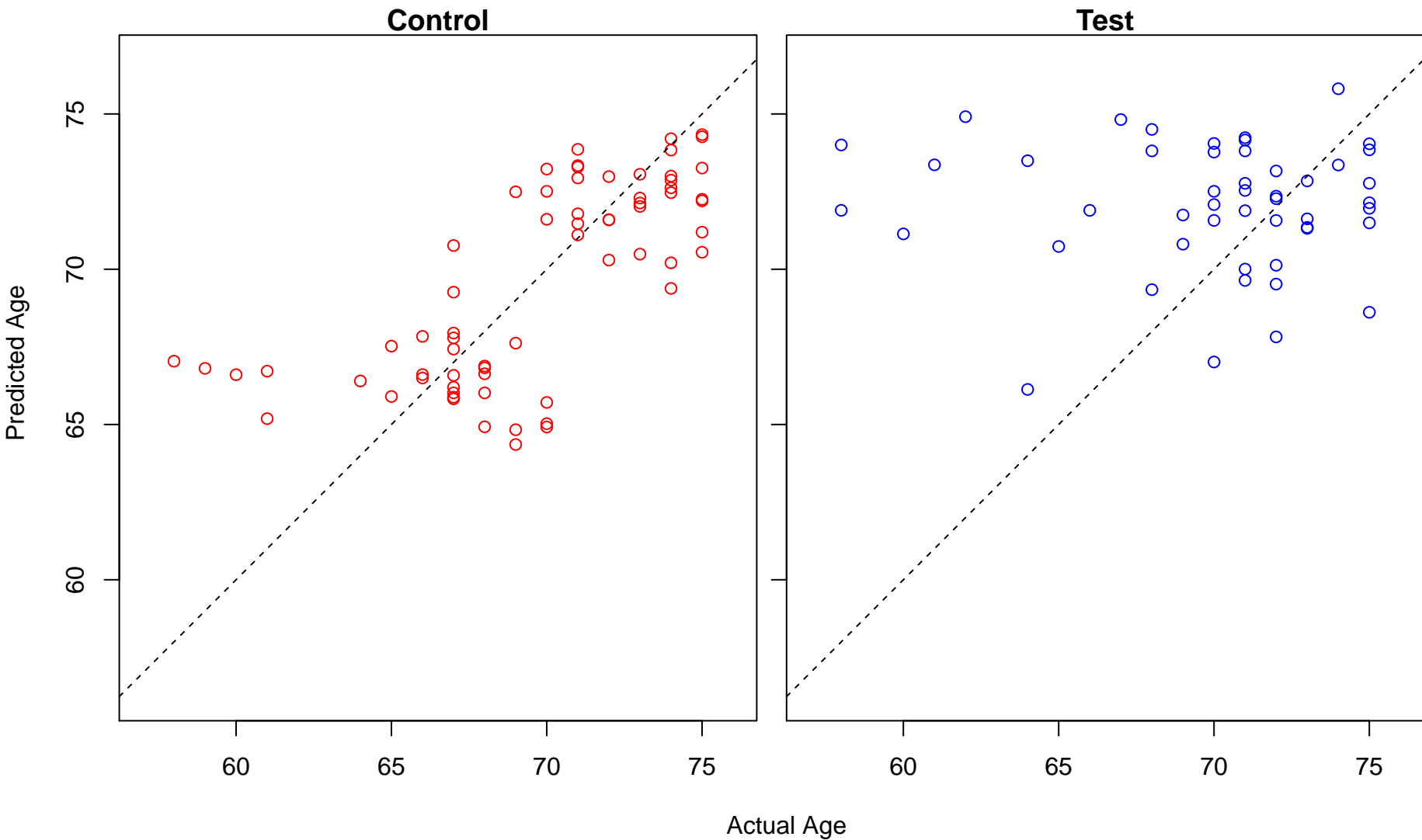
mitochondrial translation (Score: 1.540039)



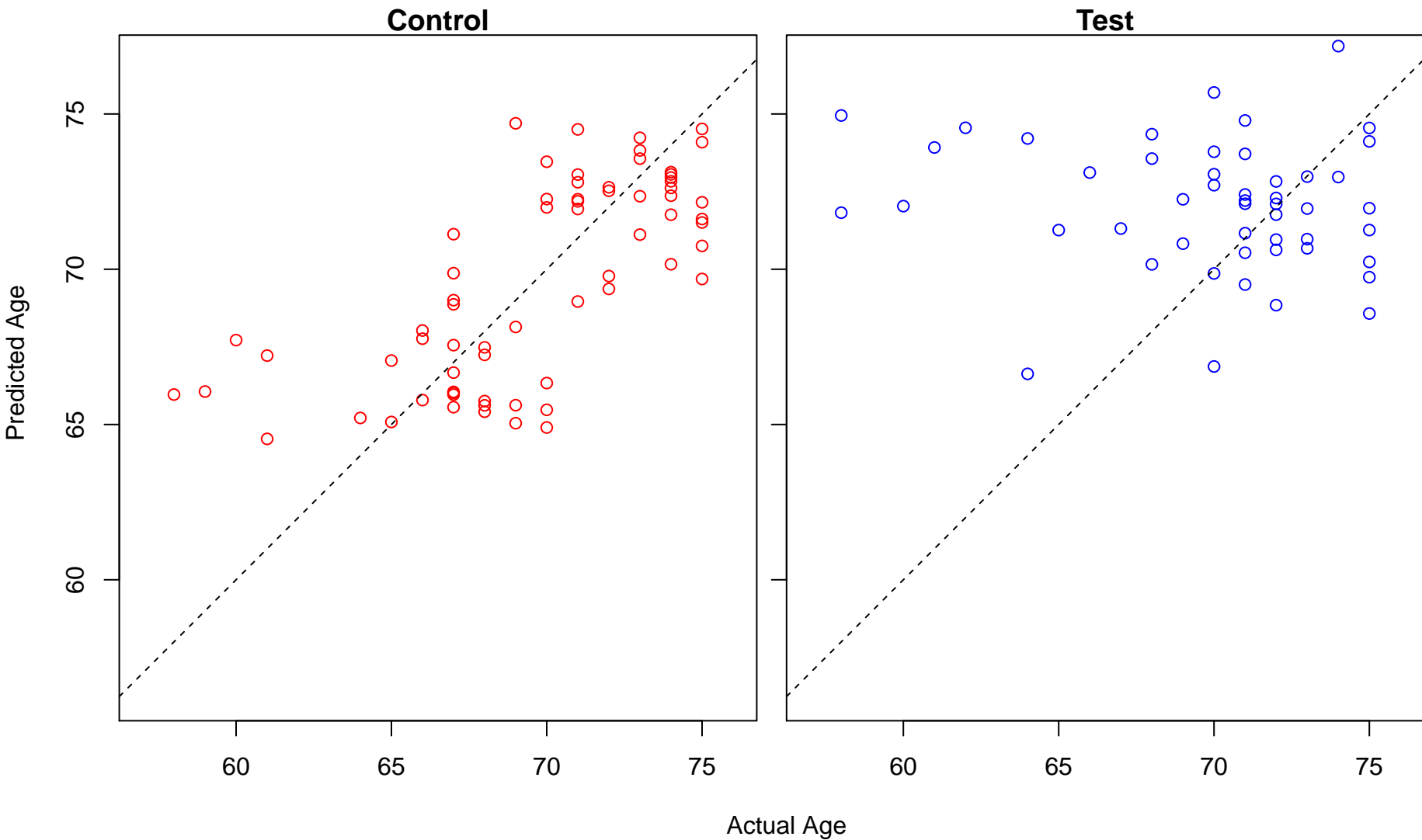
regulation of bone resorption (Score: 1.538801)



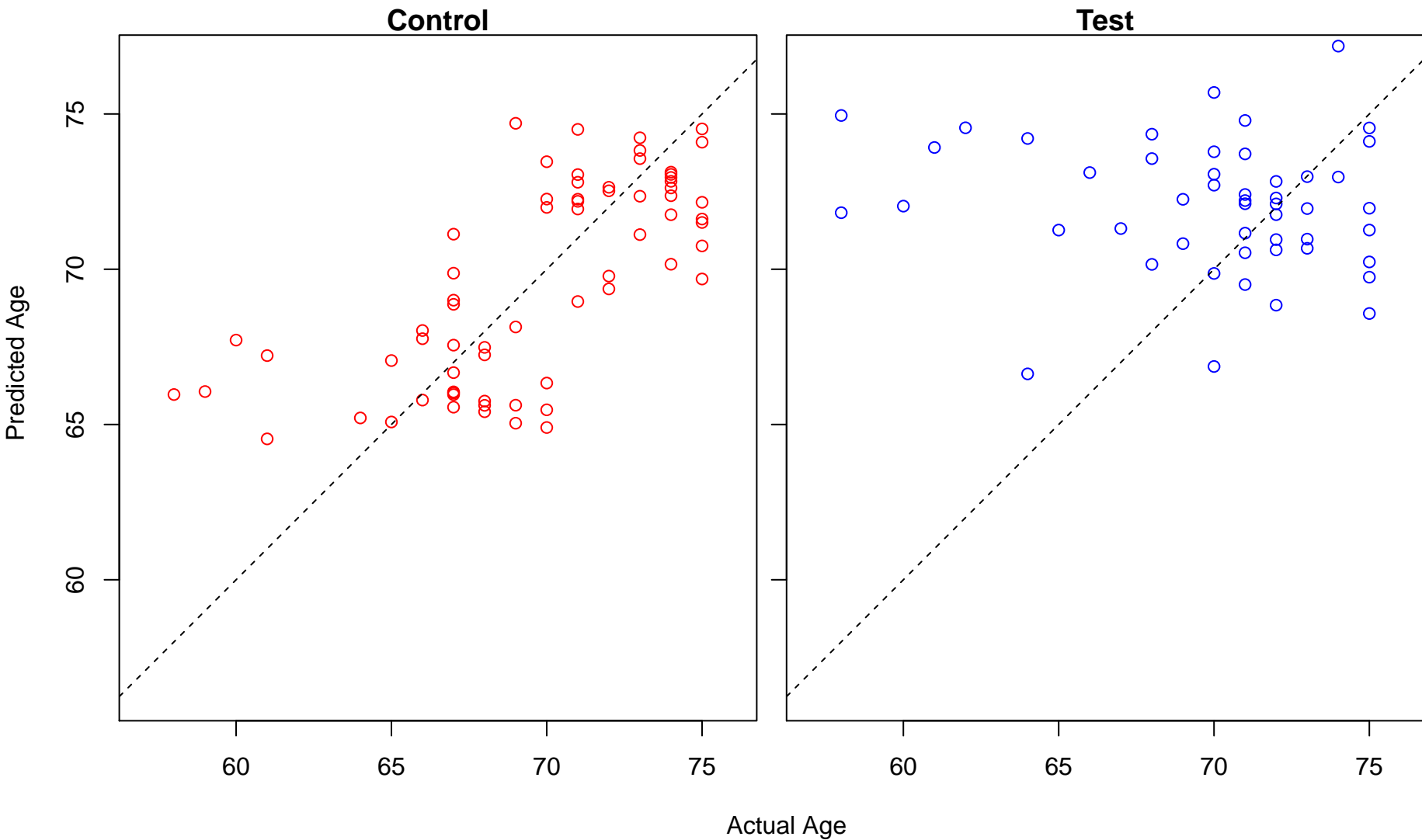
positive regulation of mitotic cell cycle phase transition (Score: 1.538637)



organic acid catabolic process (Score: 1.538382)

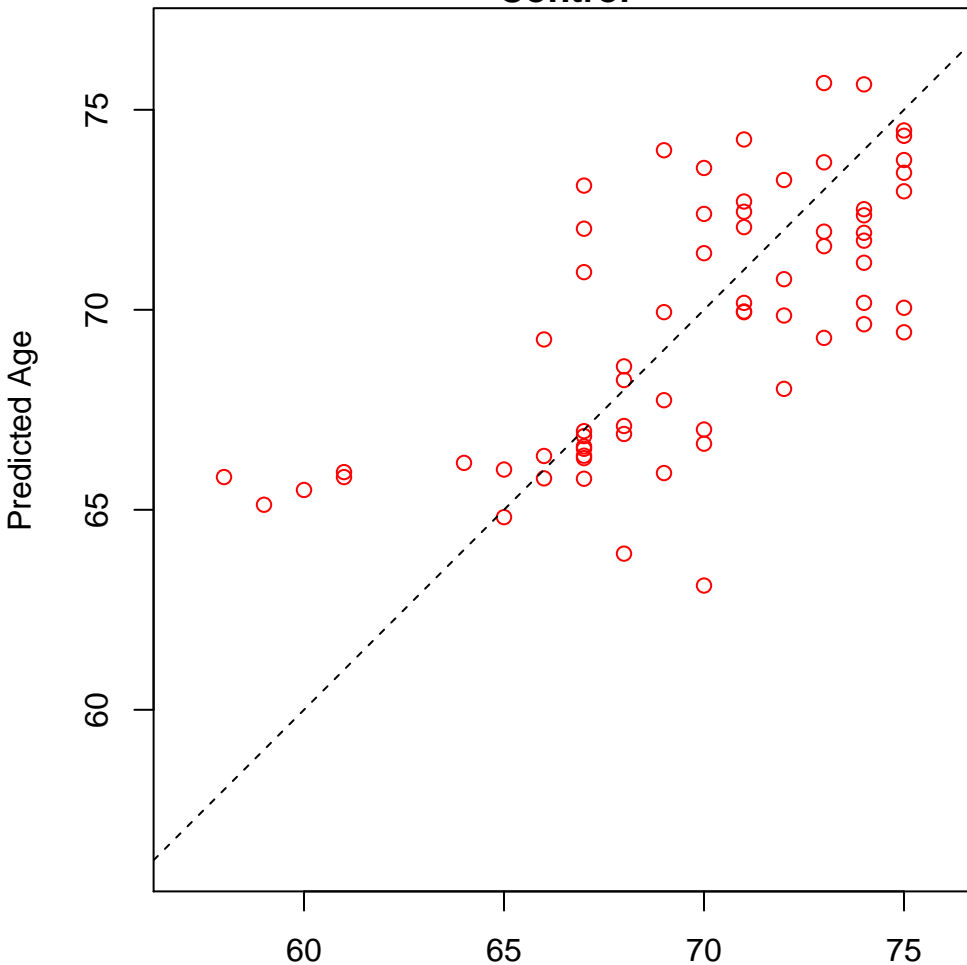


carboxylic acid catabolic process (Score: 1.538382)

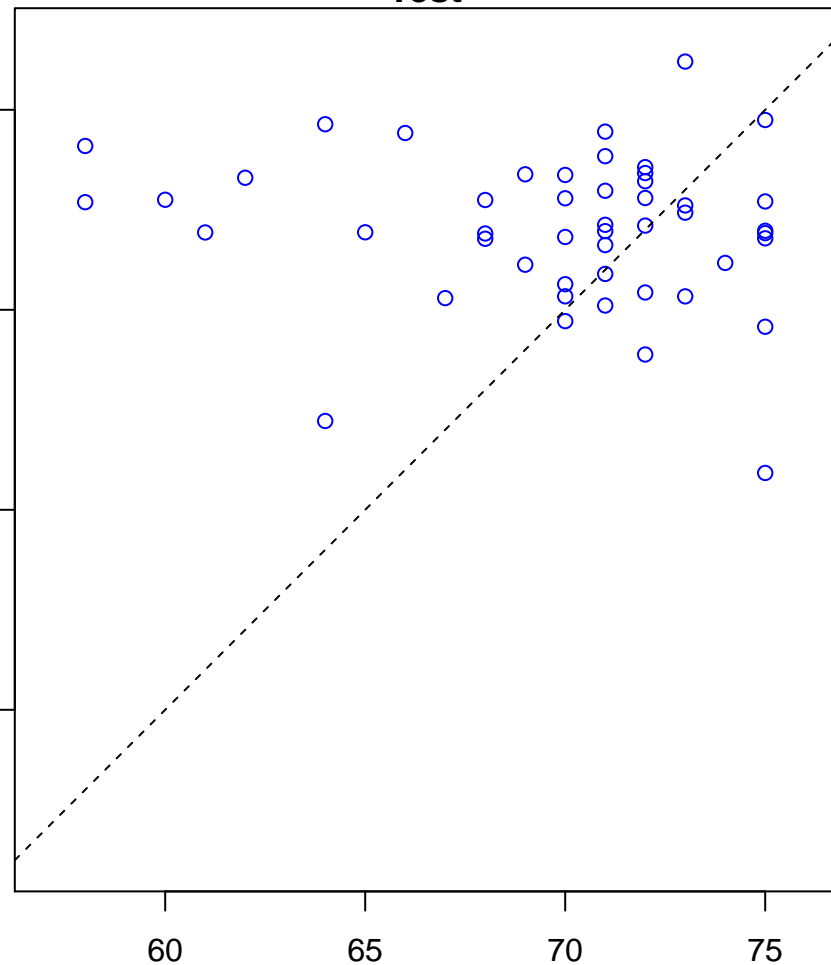


'de novo' posttranslational protein folding (Score: 1.538364)

Control

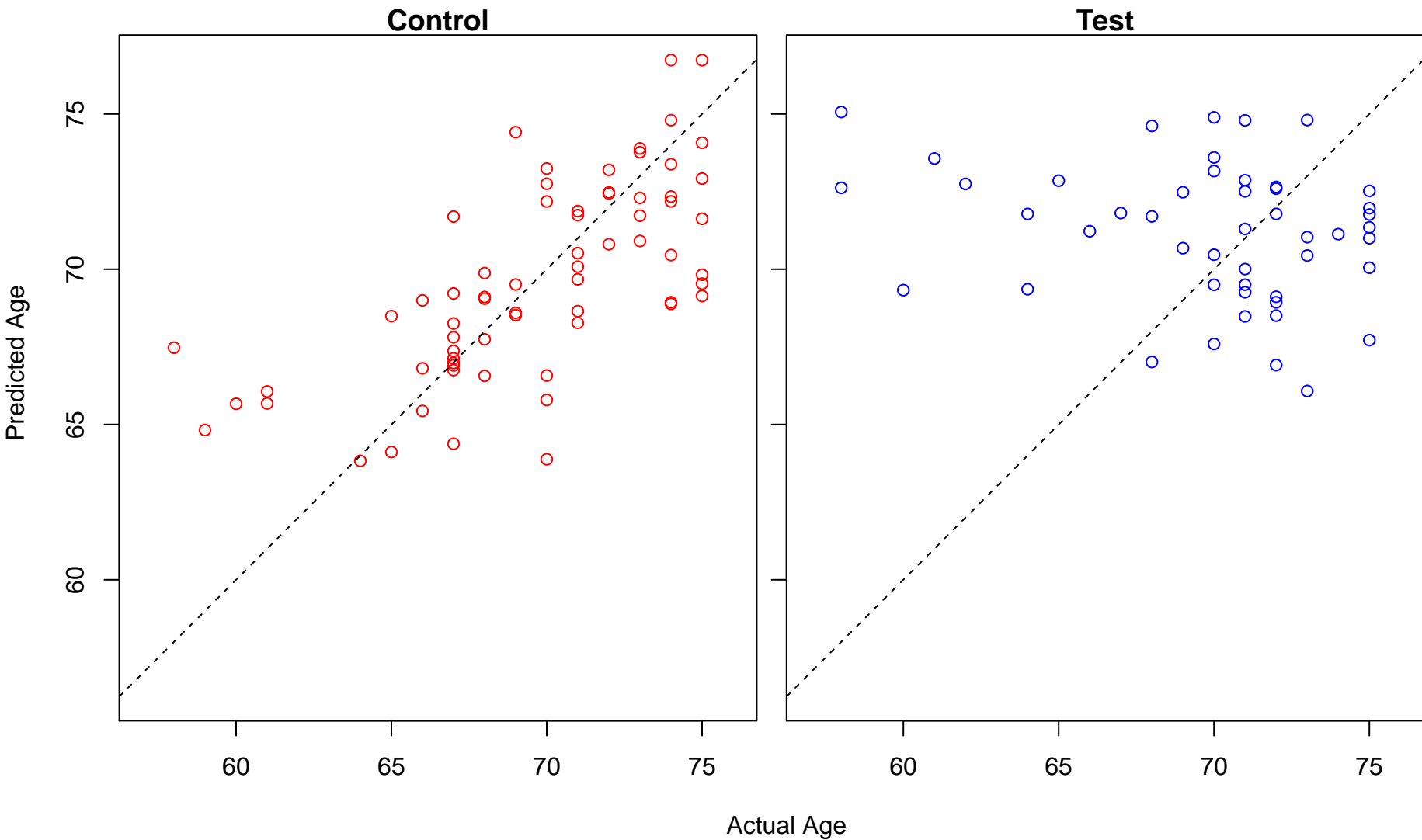


Test



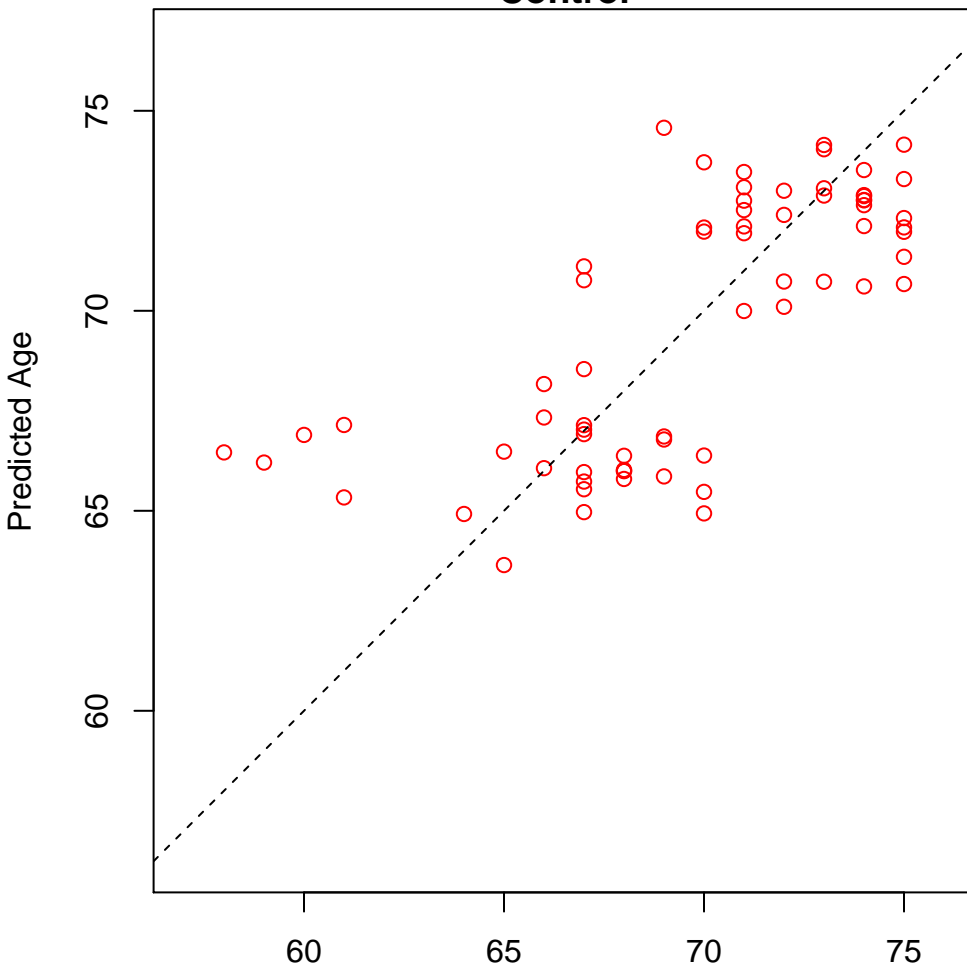
Actual Age

positive regulation of protein import (Score: 1.538335)

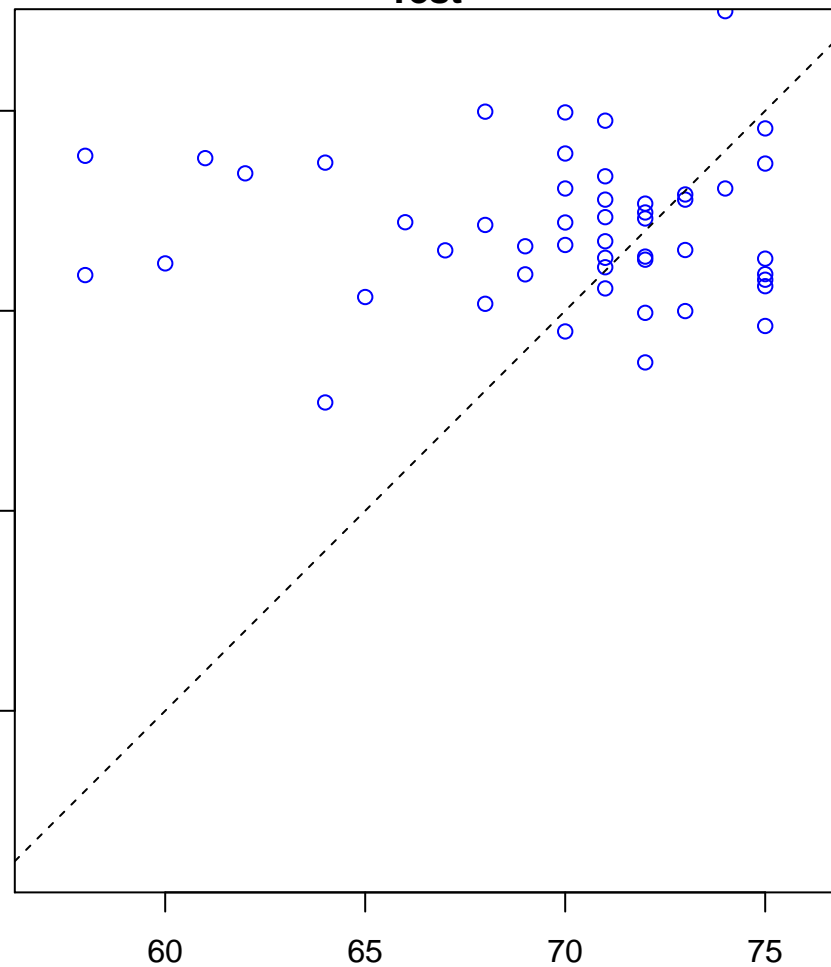


proteasomal protein catabolic process (Score: 1.538297)

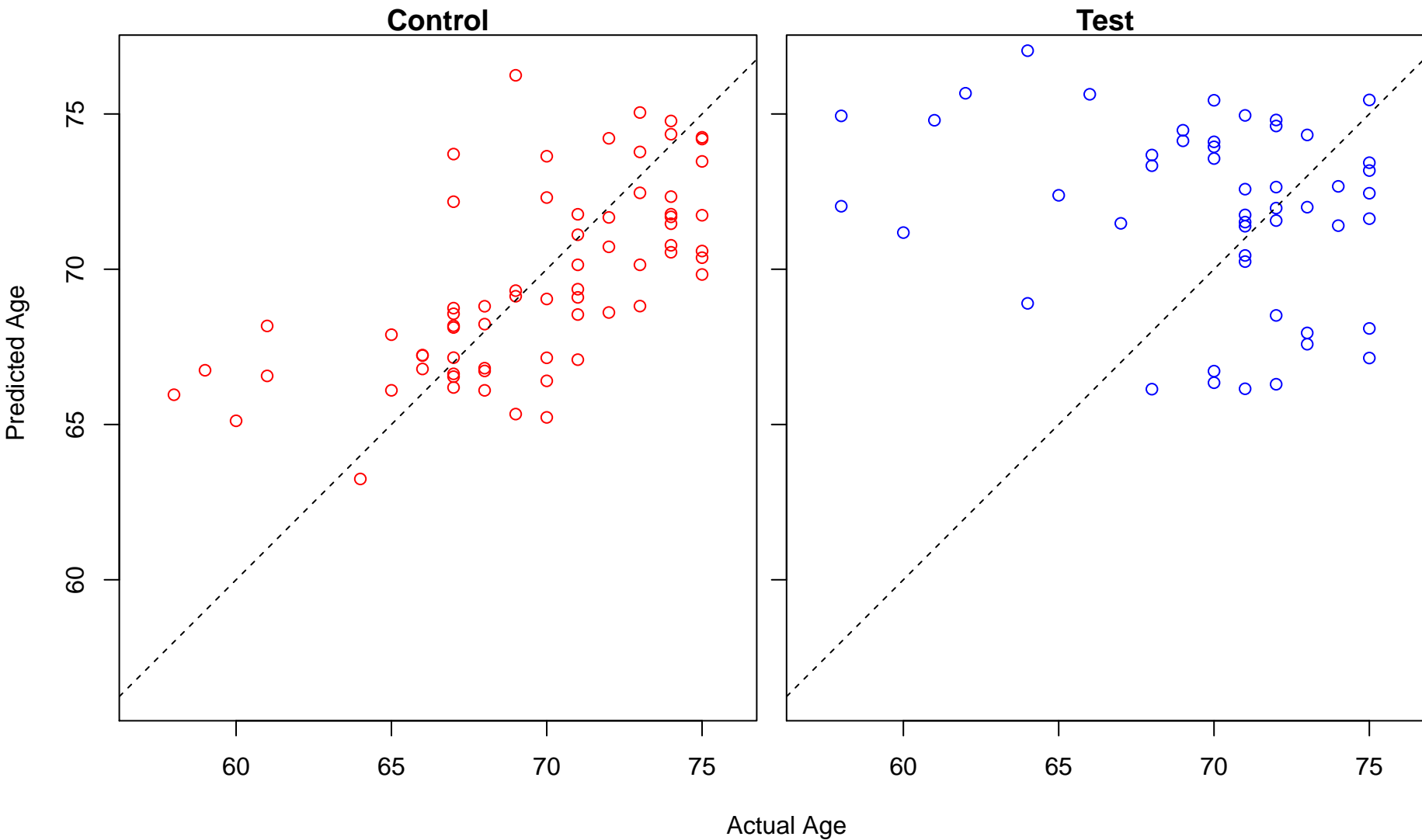
Control



Test

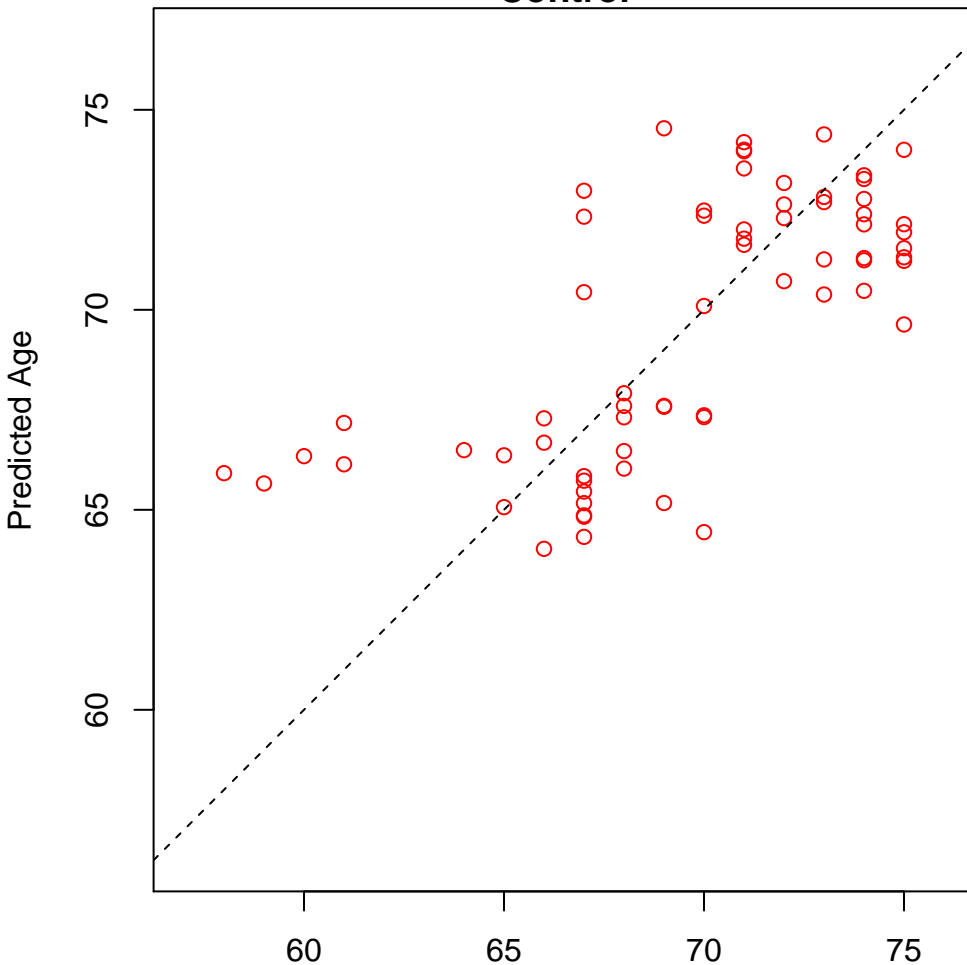


response to dsRNA (Score: 1.538200)

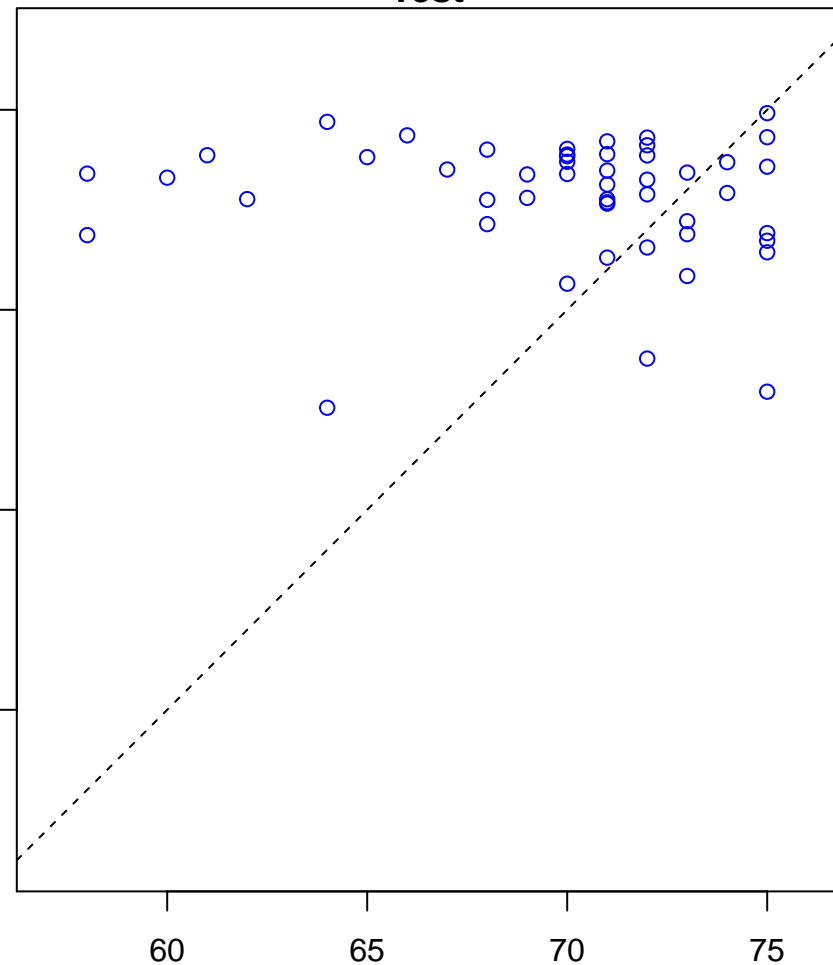


selenocysteine metabolic process (Score: 1.537989)

Control

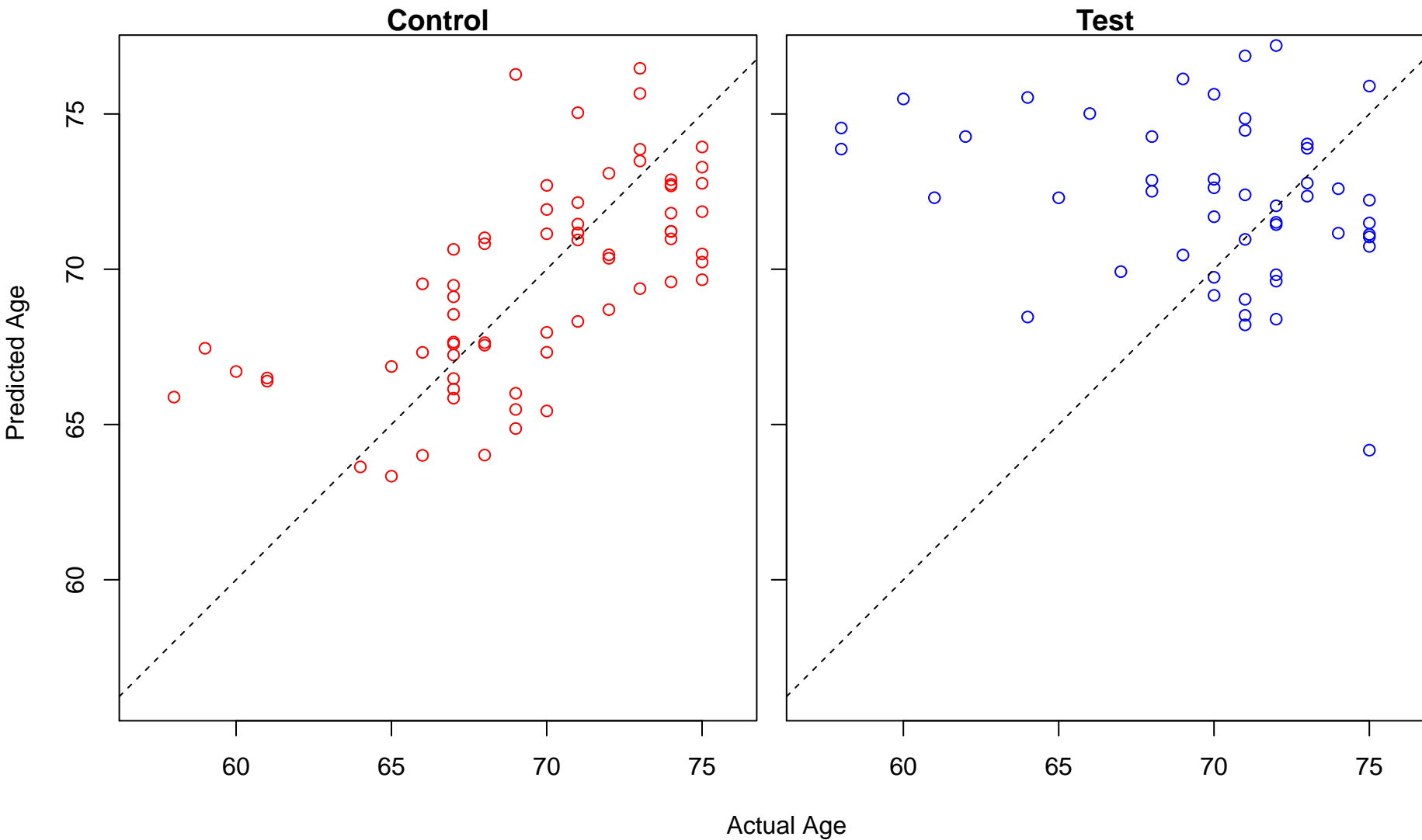


Test

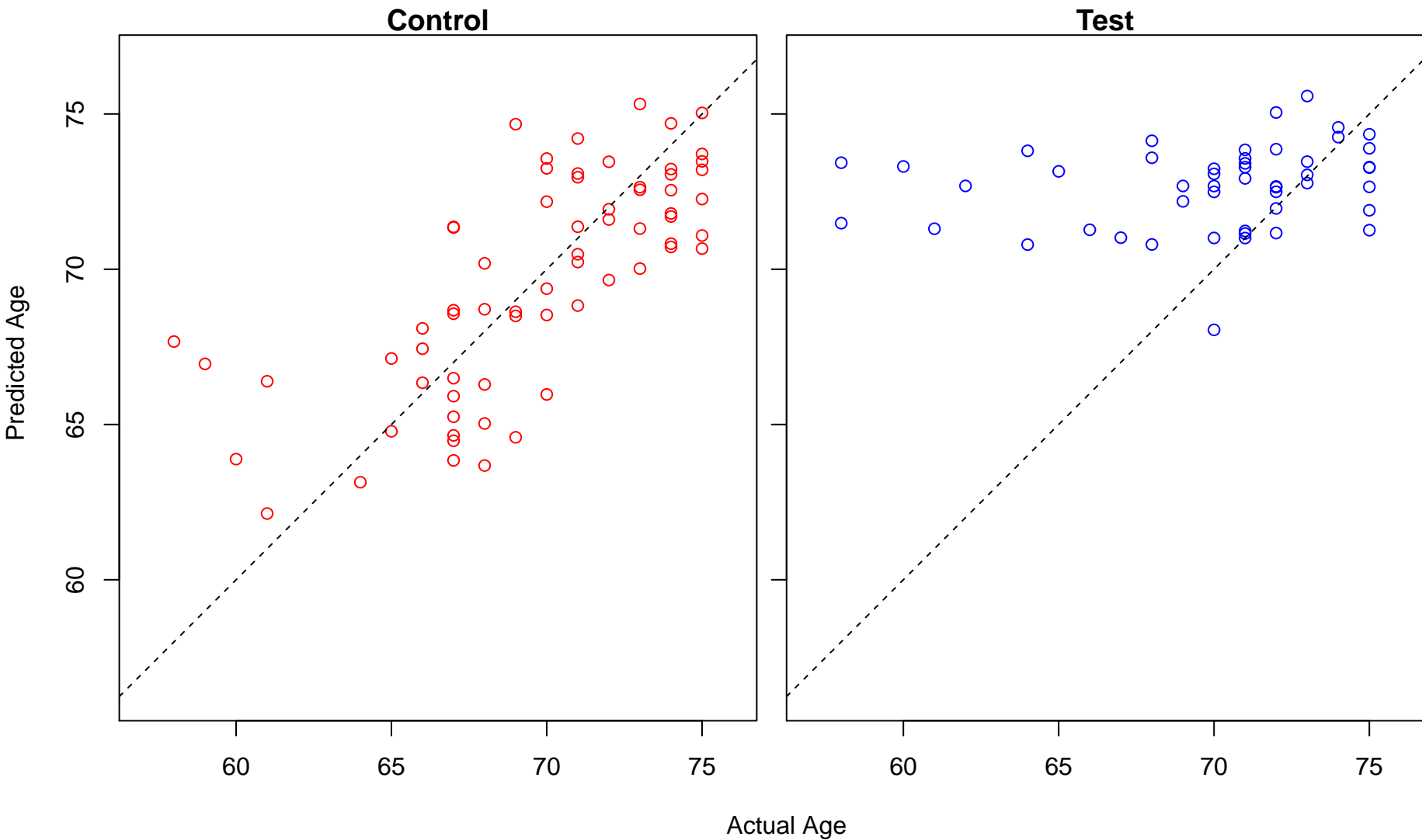


Actual Age

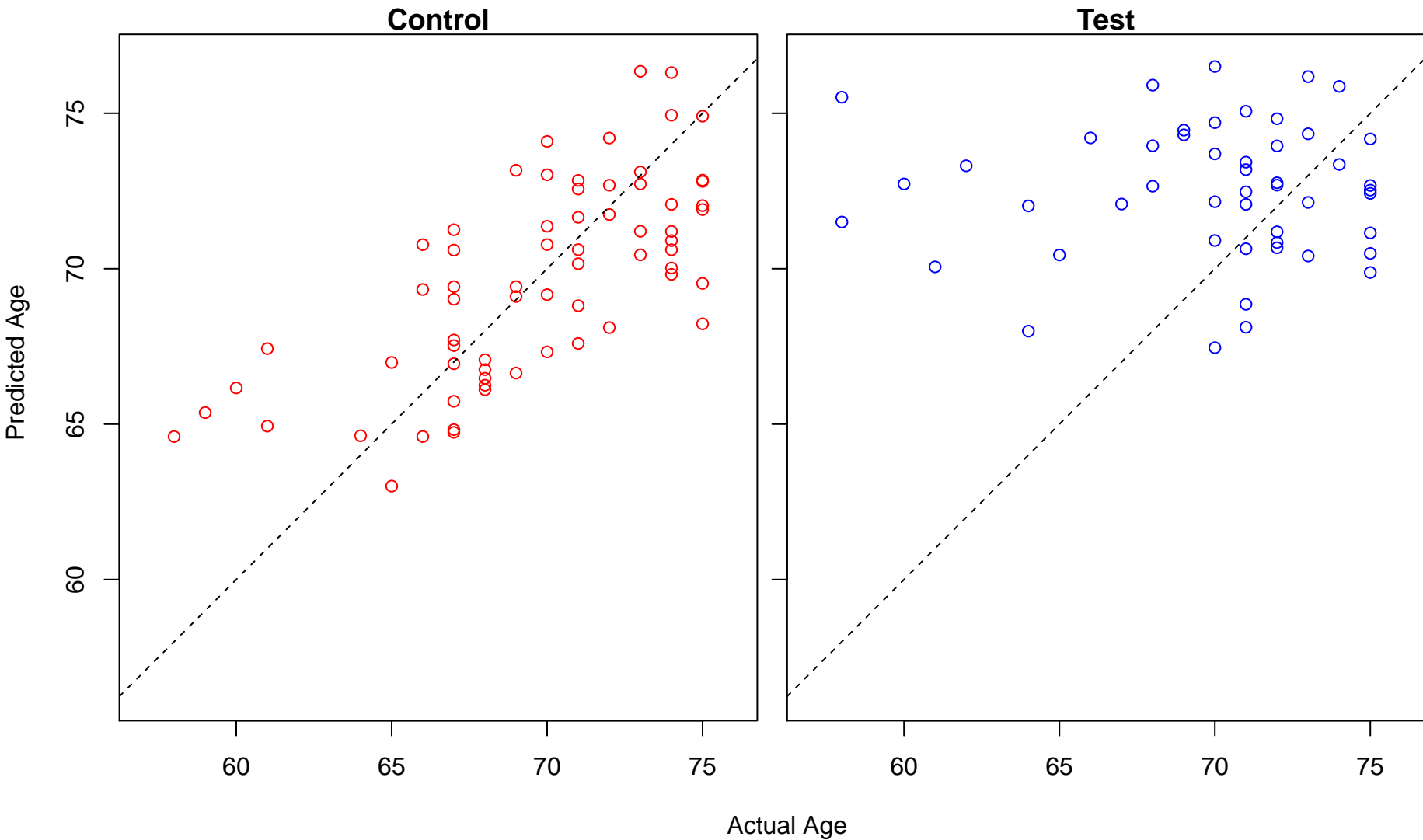
regulation of stem cell differentiation (Score: 1.537751)



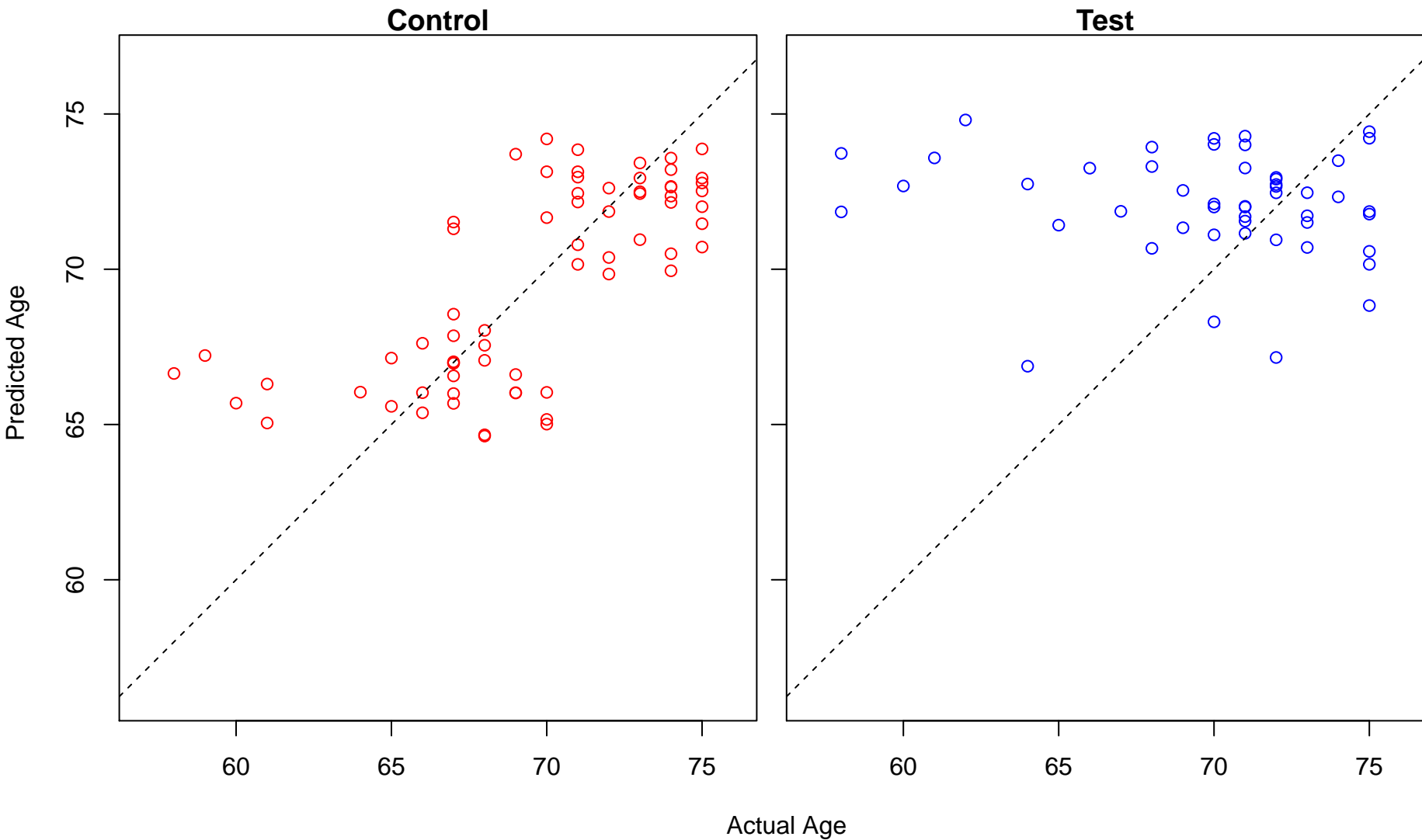
endoplasmic reticulum unfolded protein response (Score: 1.537722)



positive regulation of mitochondrial membrane permeability (Score: 1.537542)

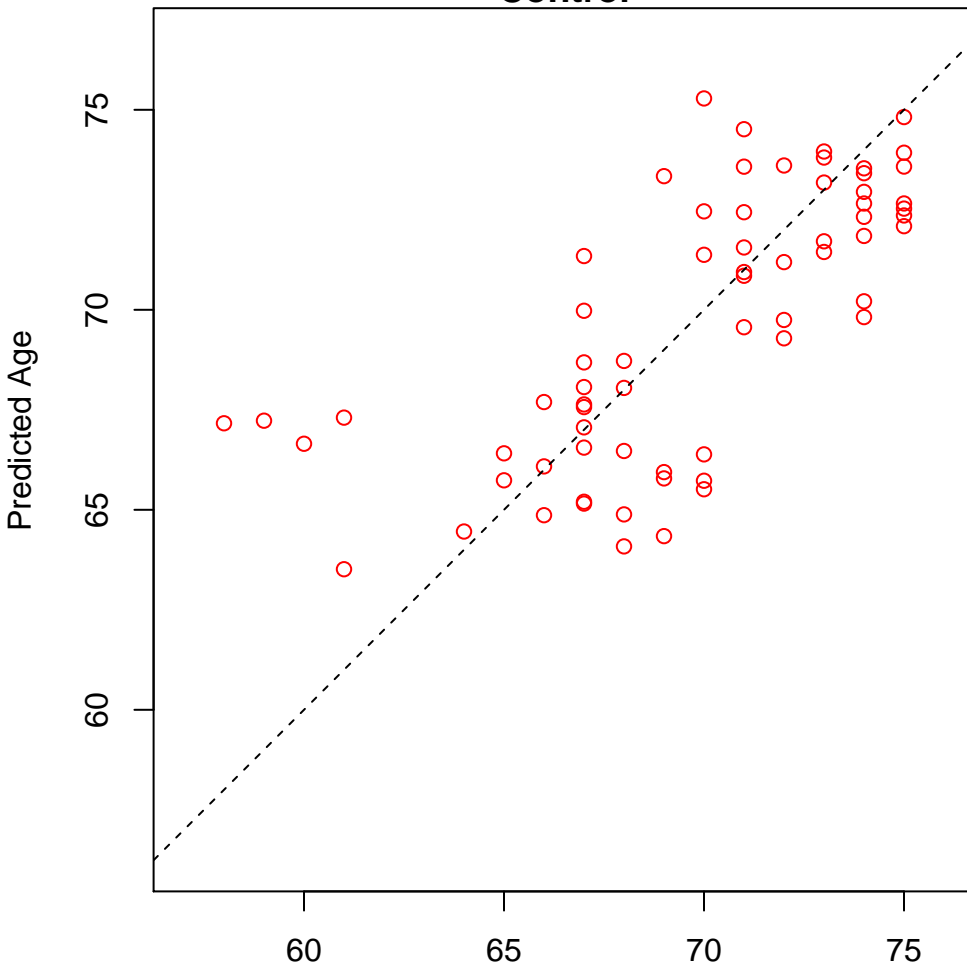


histone methylation (Score: 1.537329)

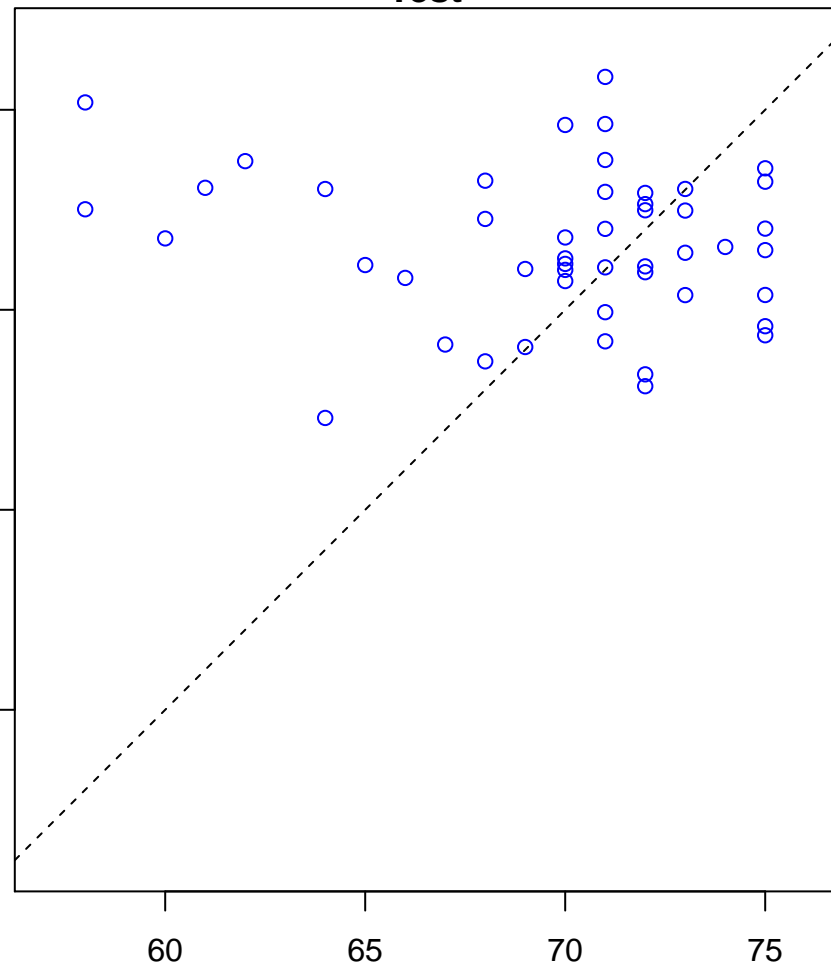


retrograde transport, endosome to Golgi (Score: 1.536918)

Control

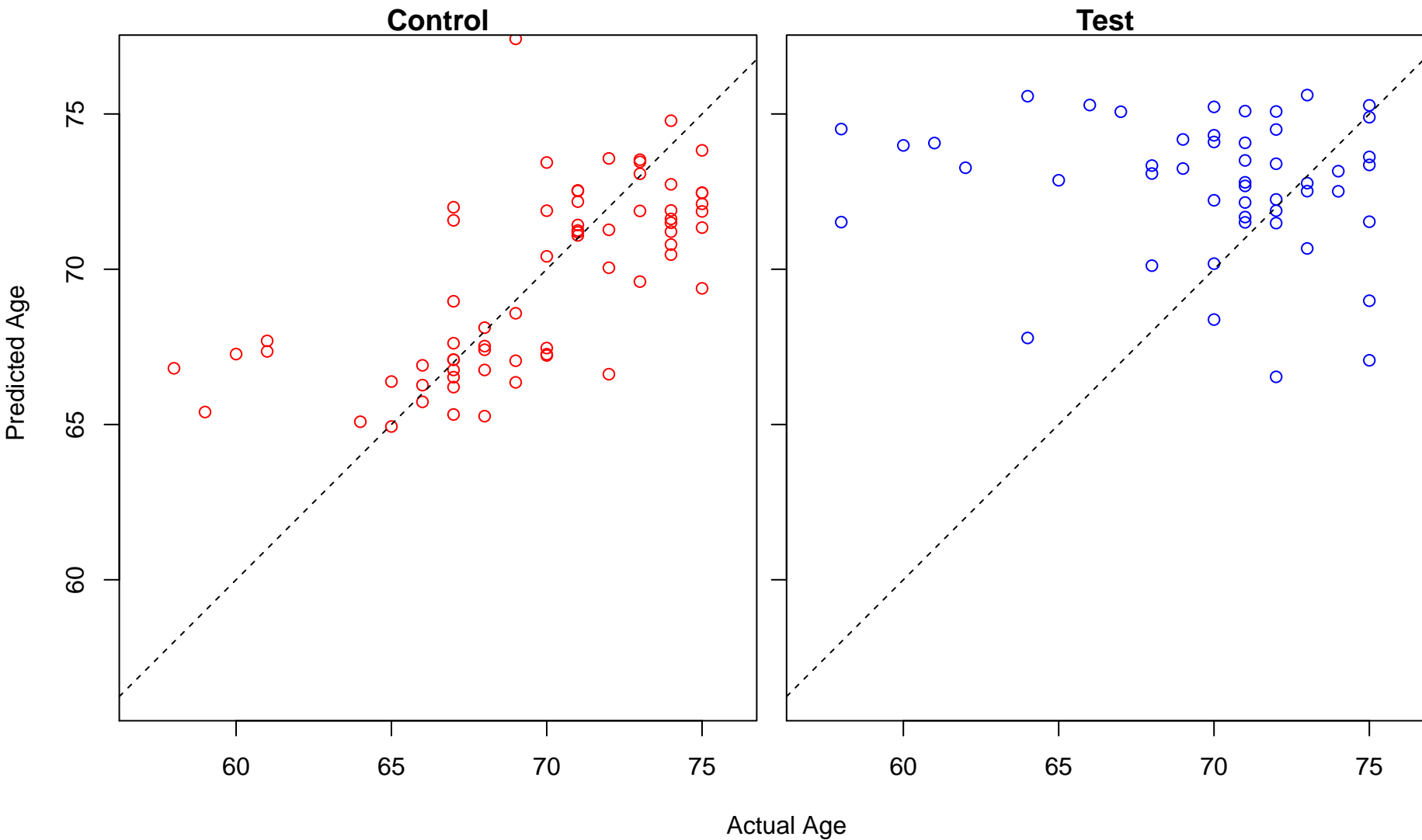


Test

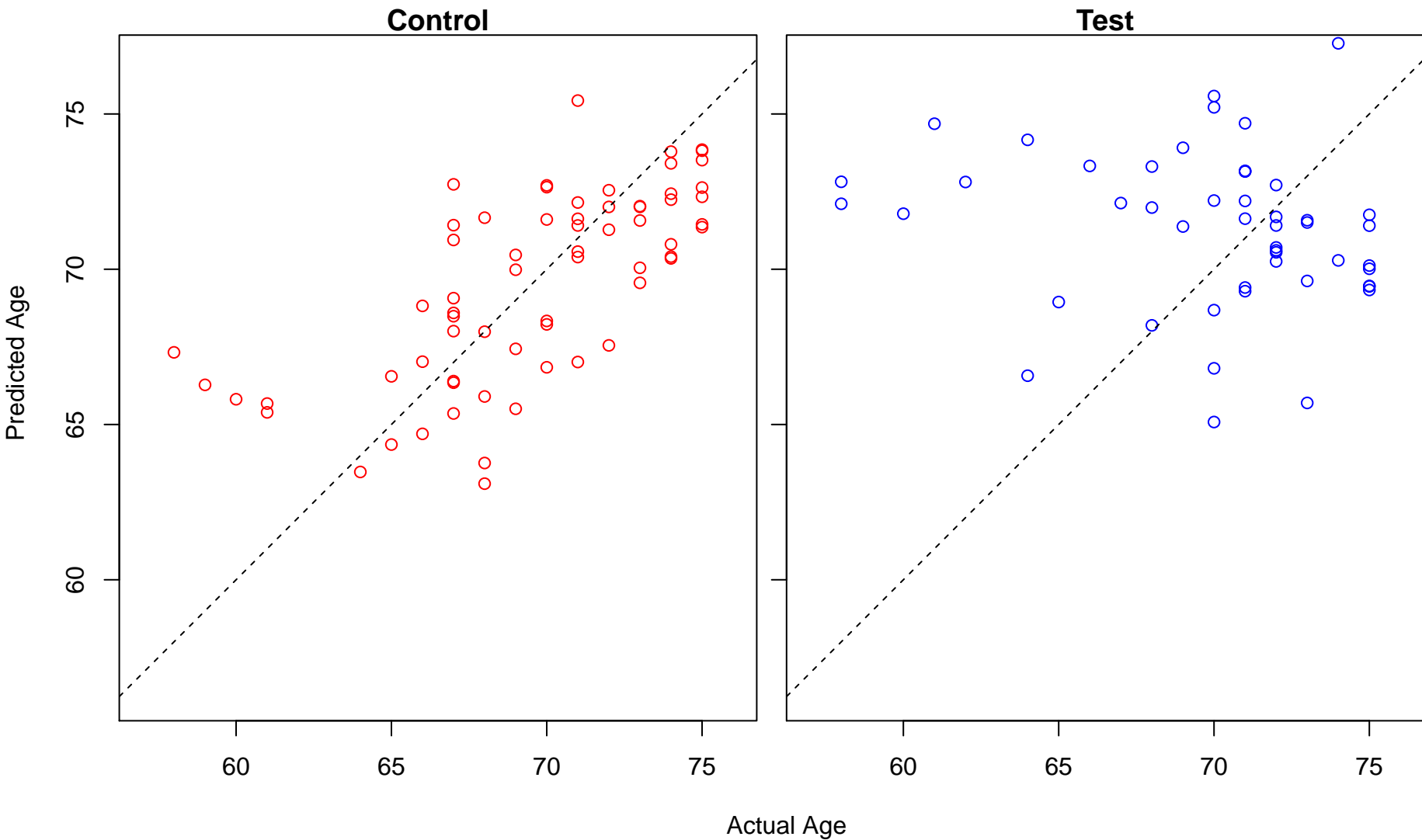


Actual Age

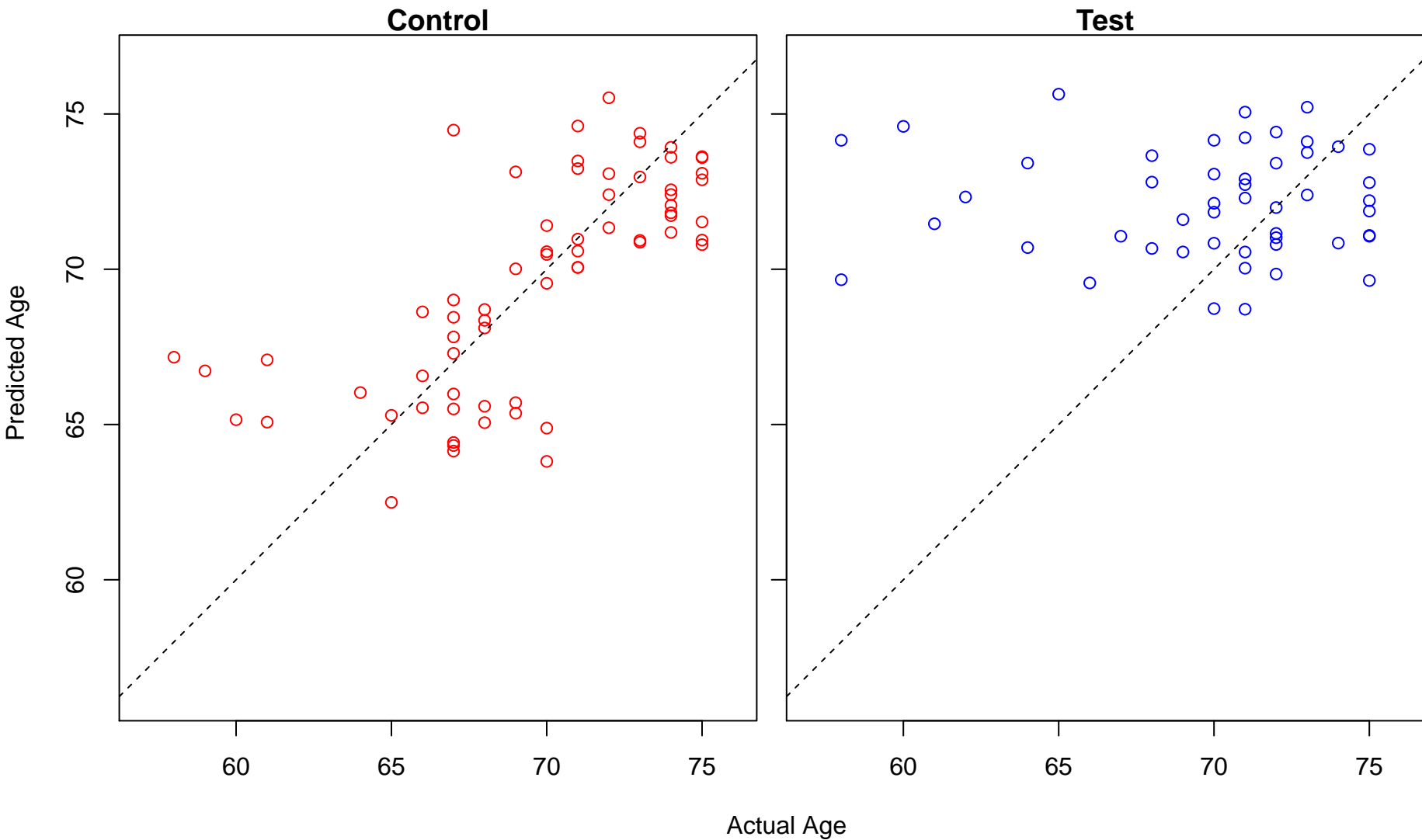
negative regulation of JUN kinase activity (Score: 1.536602)



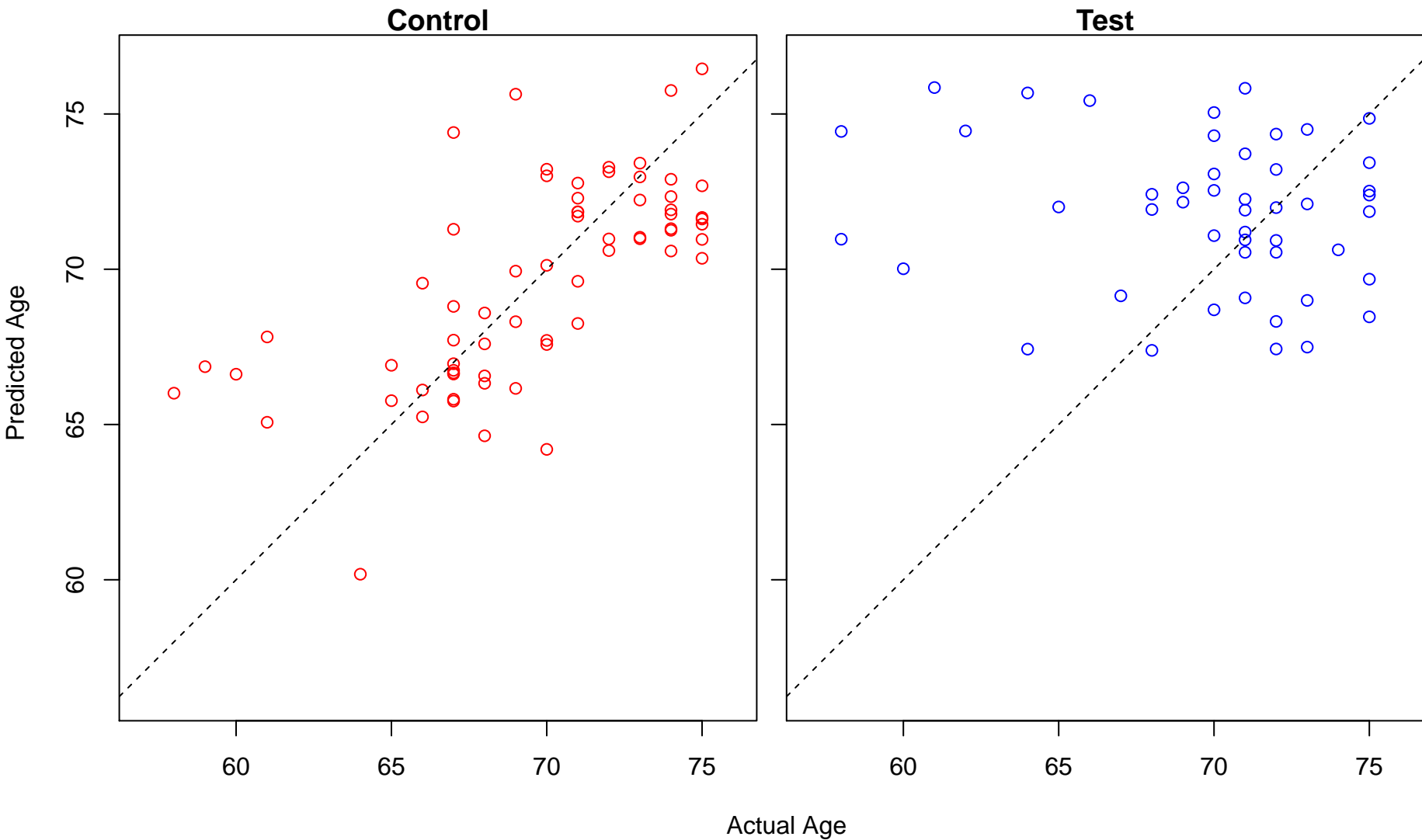
CDP-choline pathway (Score: 1.536505)



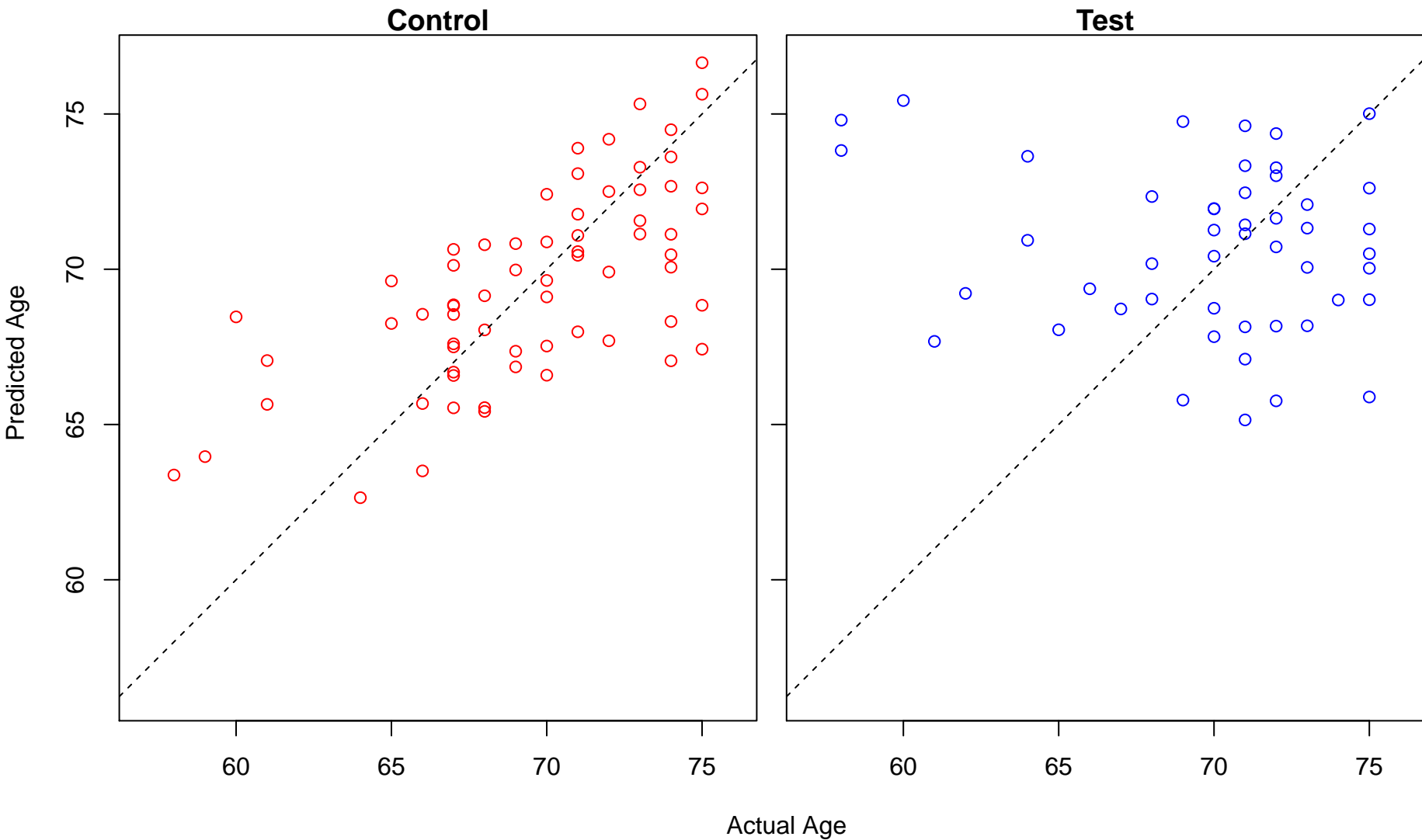
mRNA transport (Score: 1.536043)



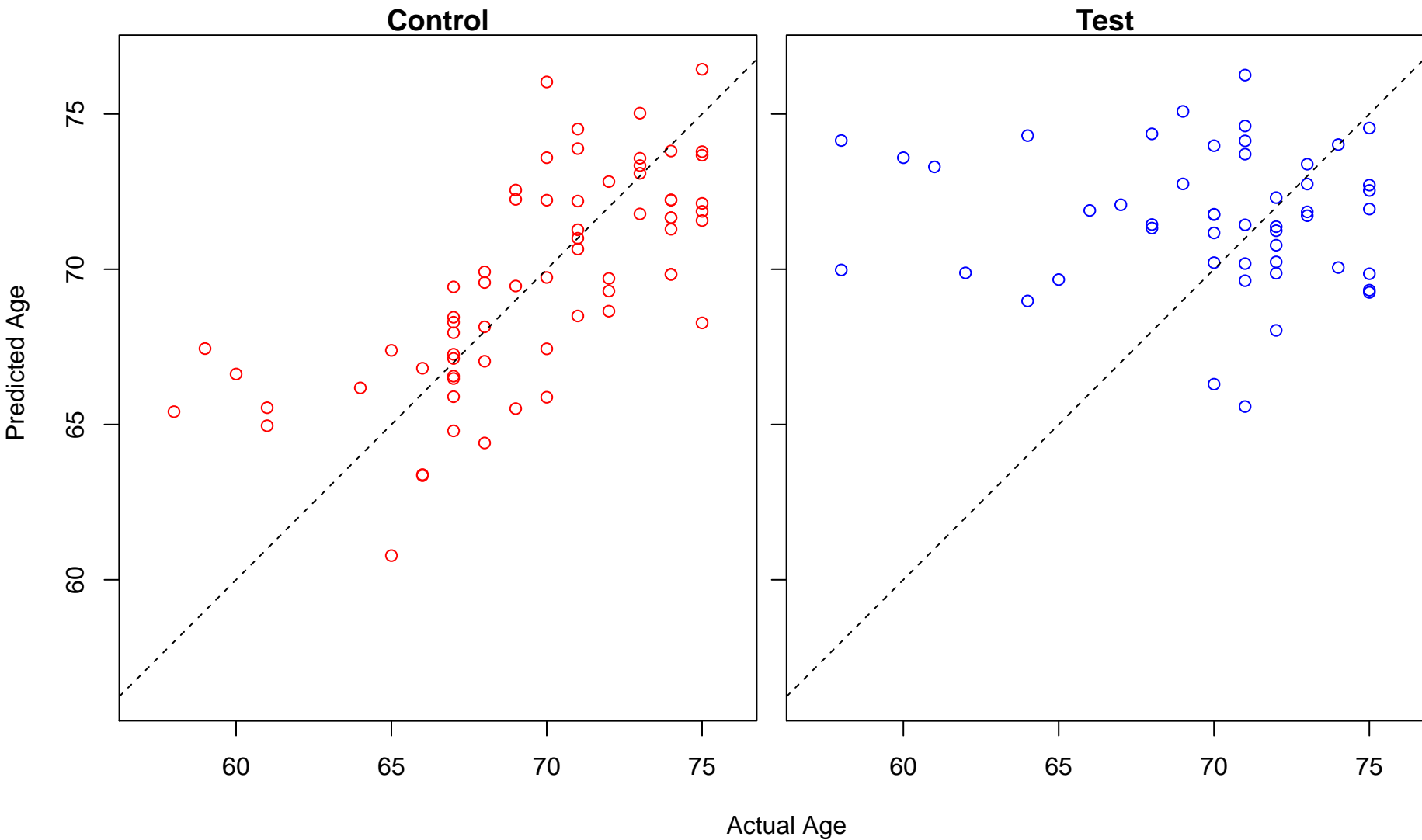
positive regulation of viral genome replication (Score: 1.535217)



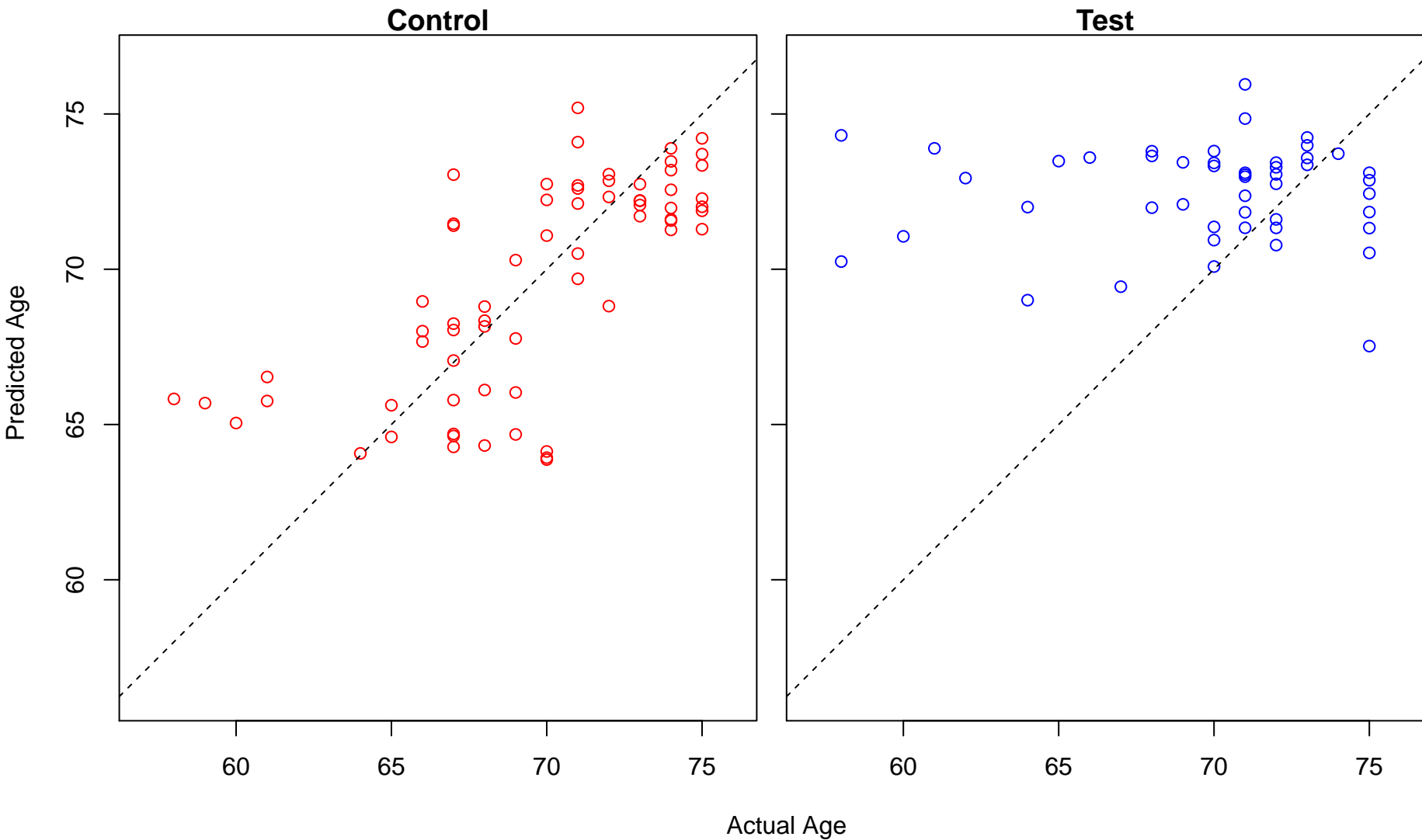
positive regulation of cyclase activity (Score: 1.535105)



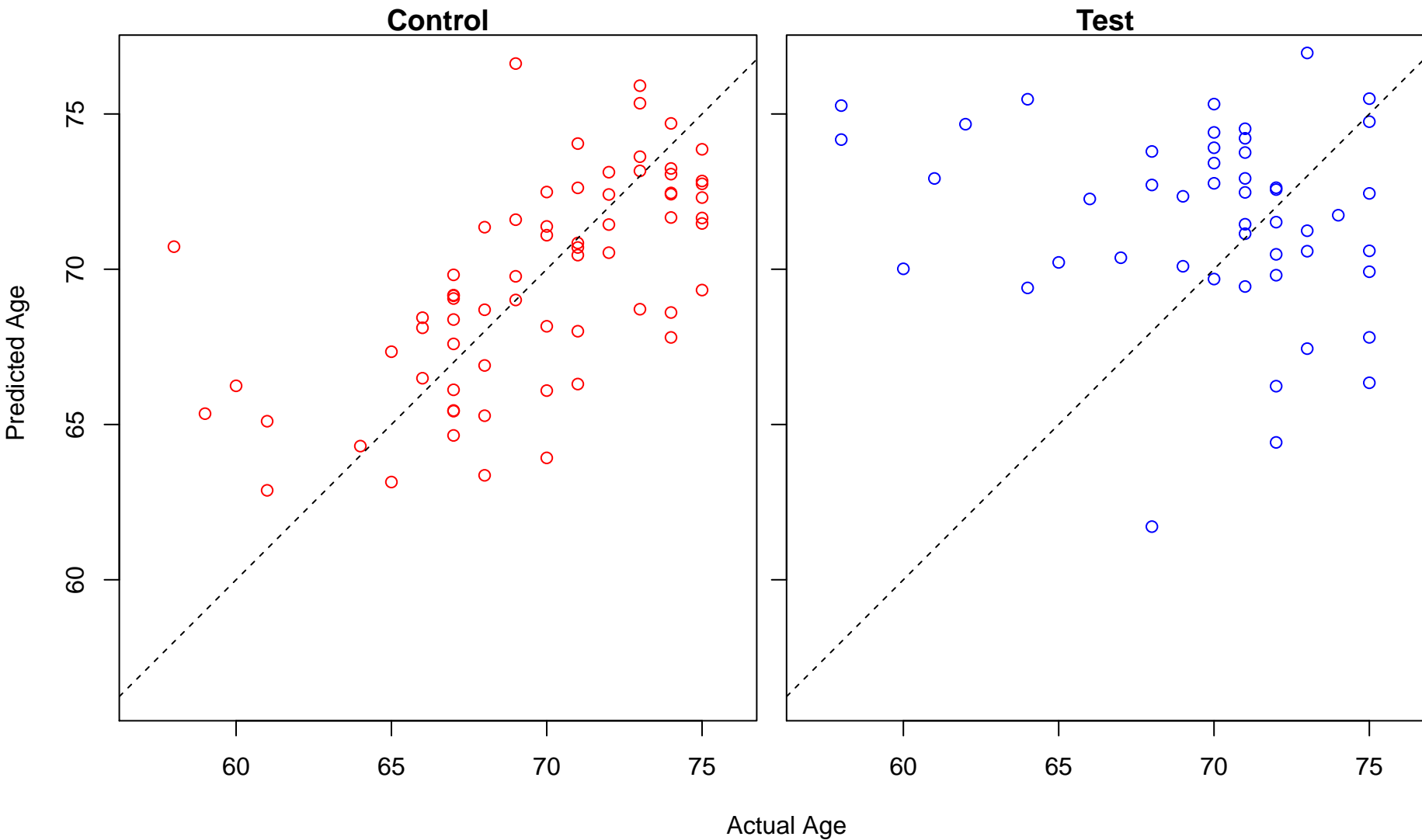
regulation of cAMP metabolic process (Score: 1.534019)



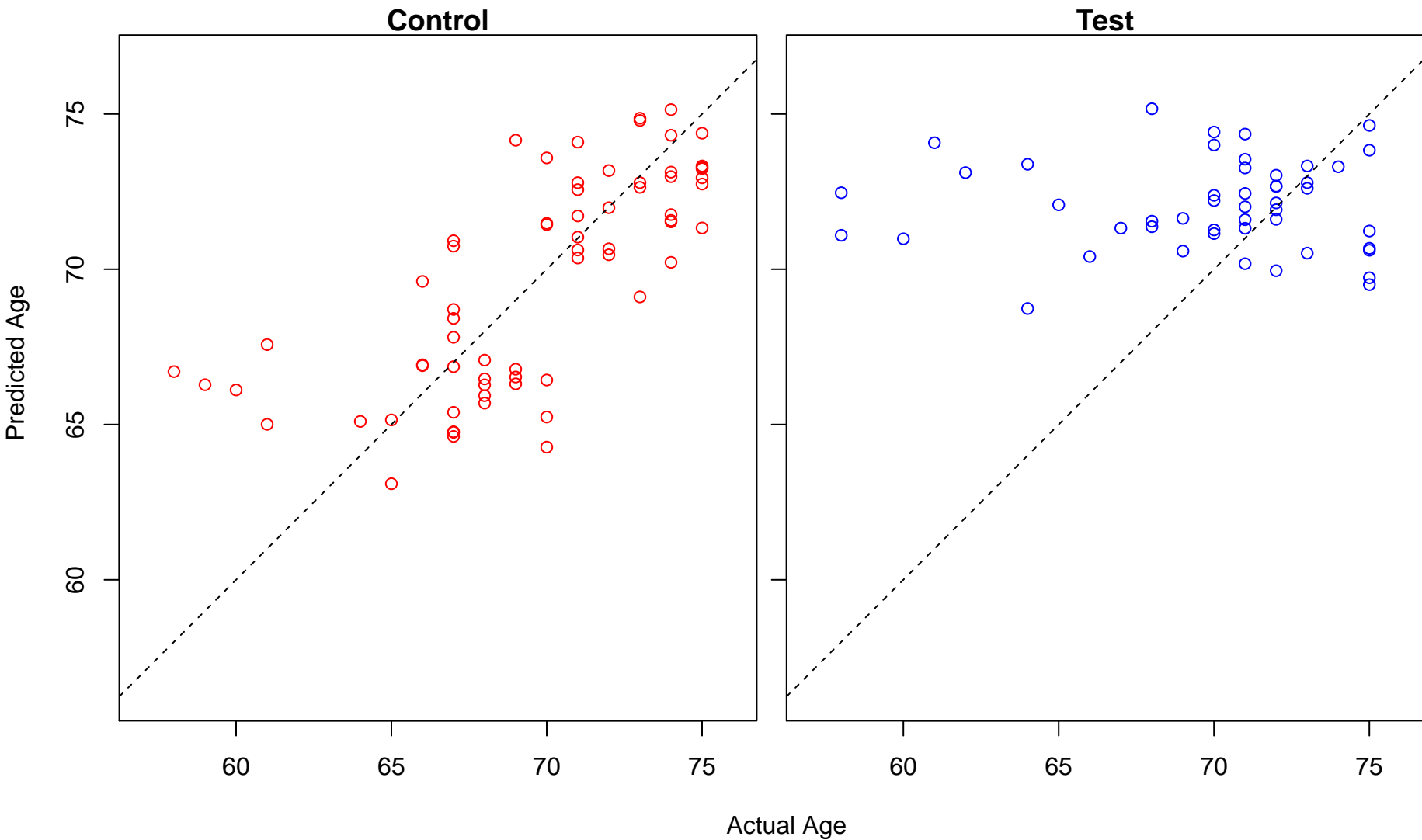
regulation of translation (Score: 1.533057)



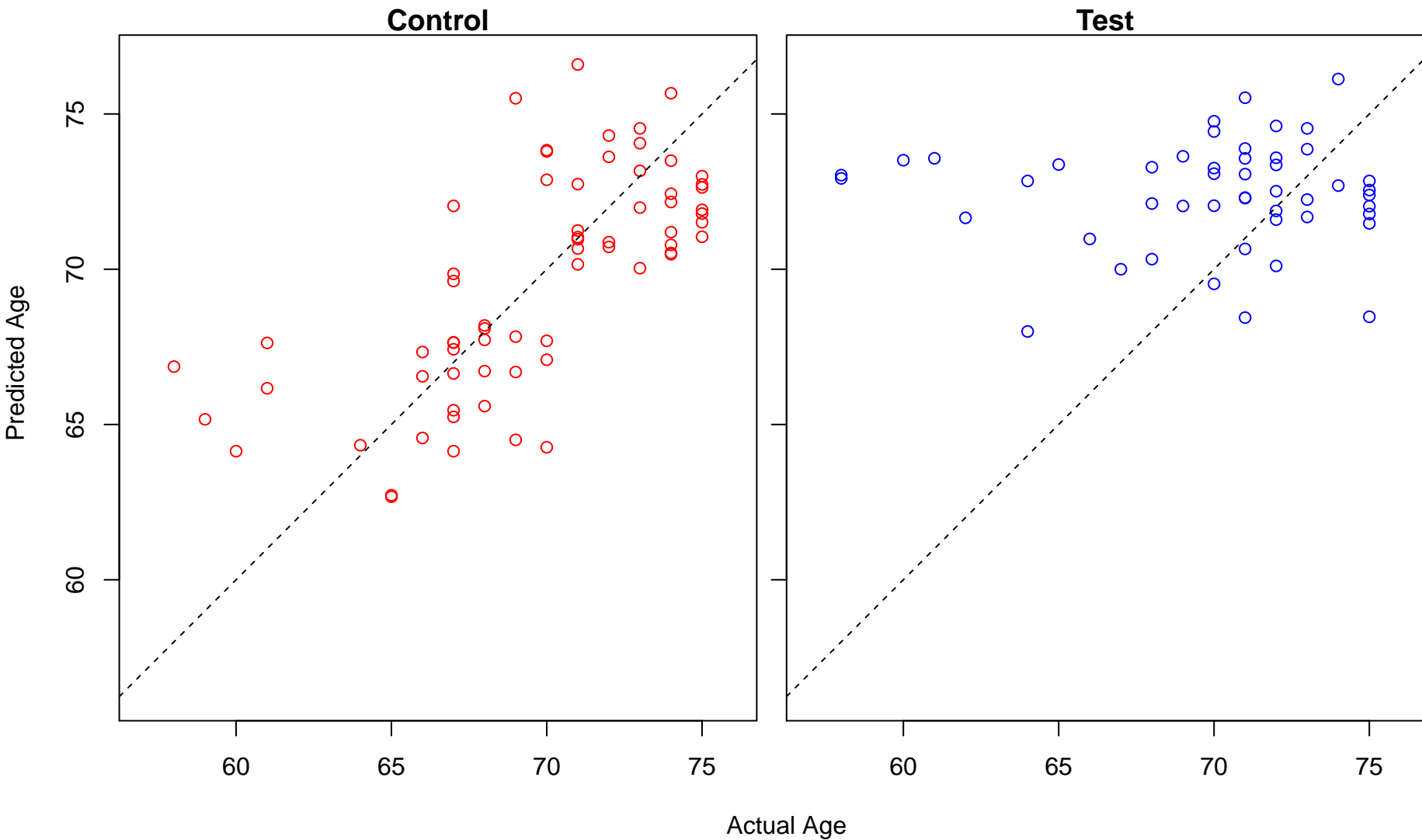
regulation of natural killer cell mediated immunity (Score: 1.531830)



ubiquitin-dependent protein catabolic process (Score: 1.531764)

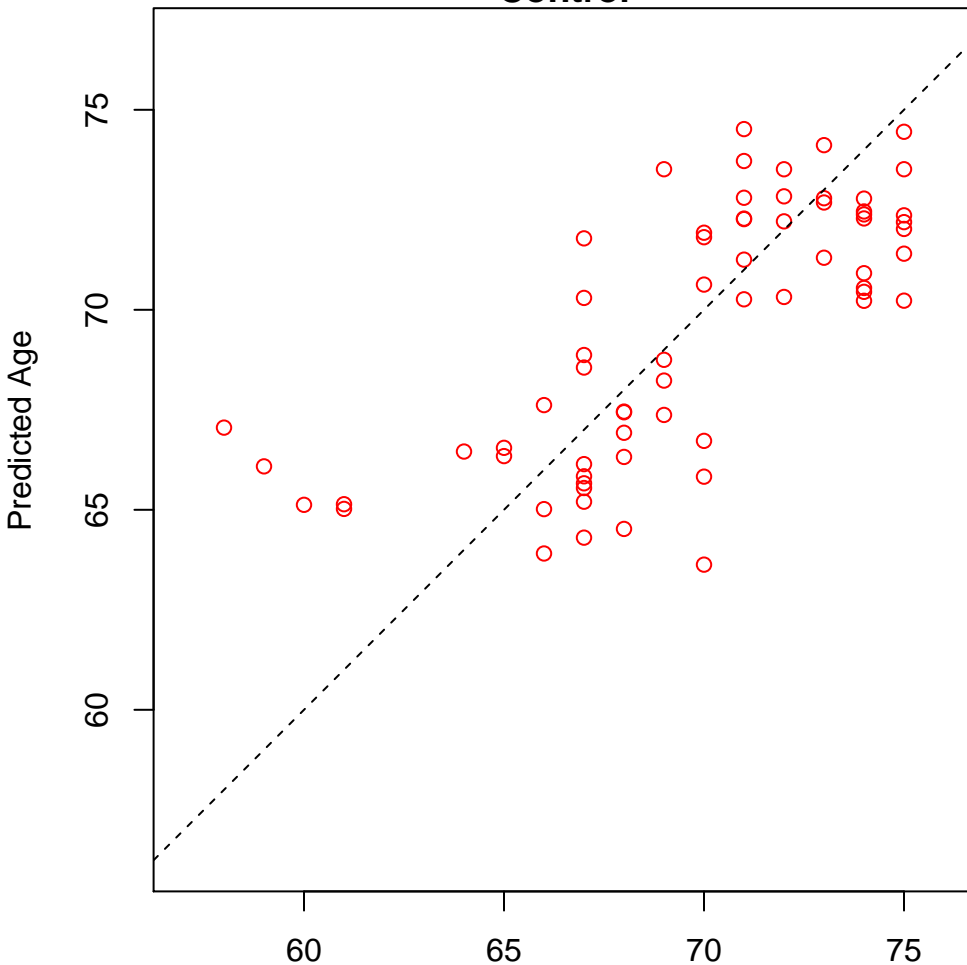


regulation of viral transcription (Score: 1.531743)

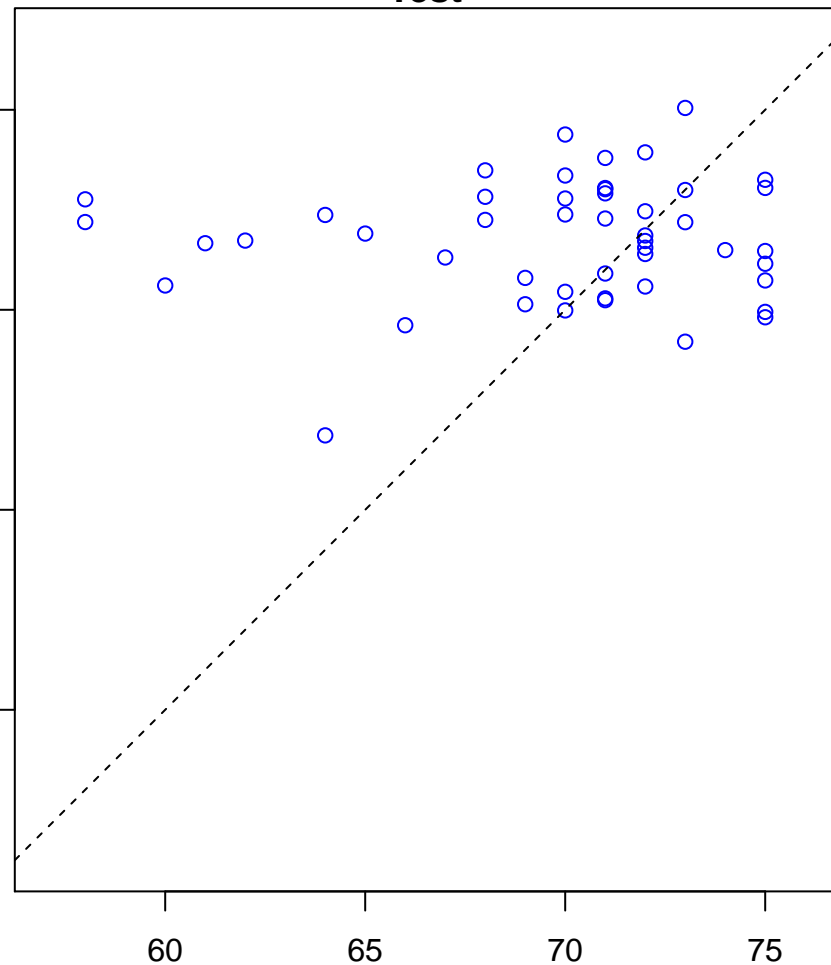


ribonucleoside biosynthetic process (Score: 1.531411)

Control

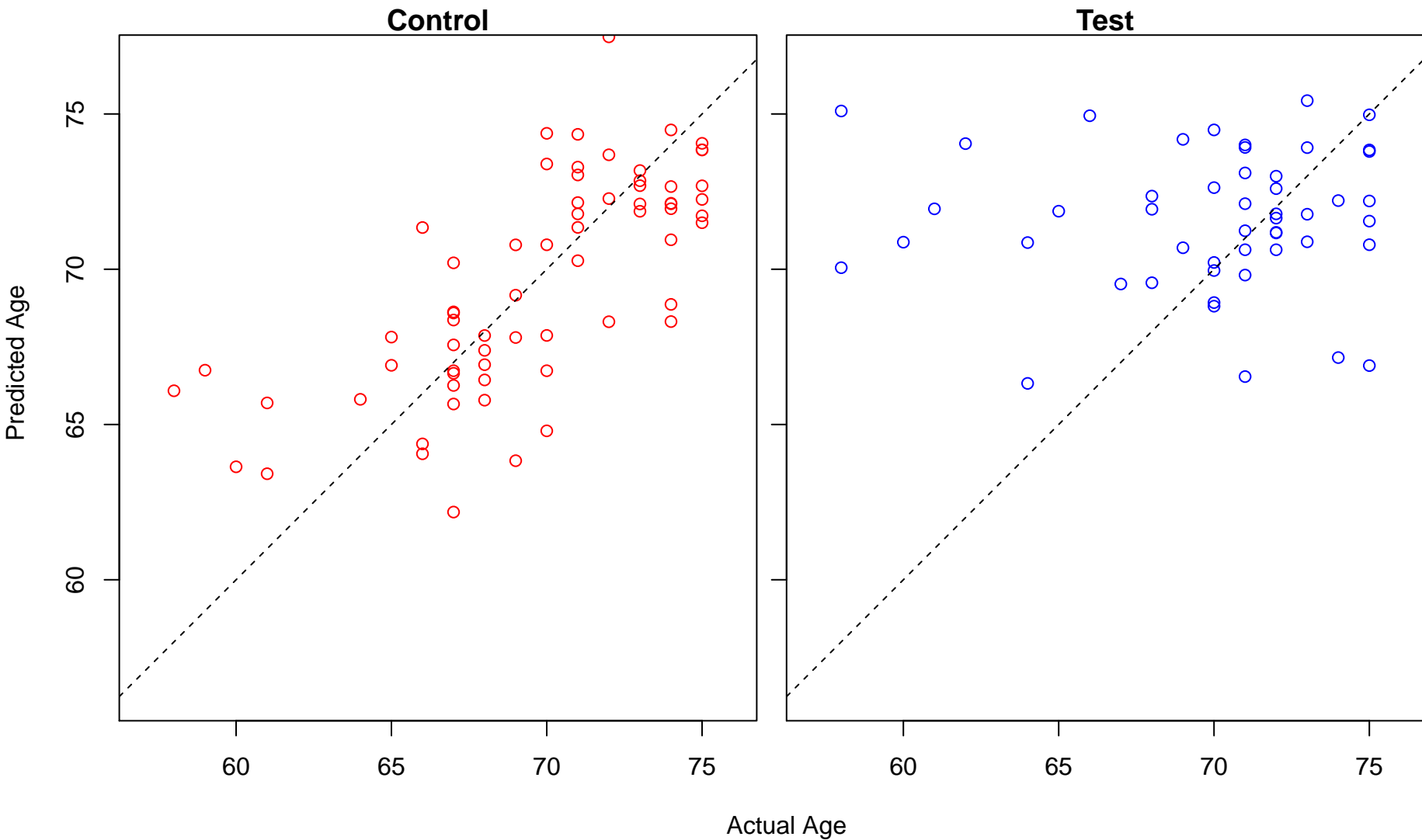


Test

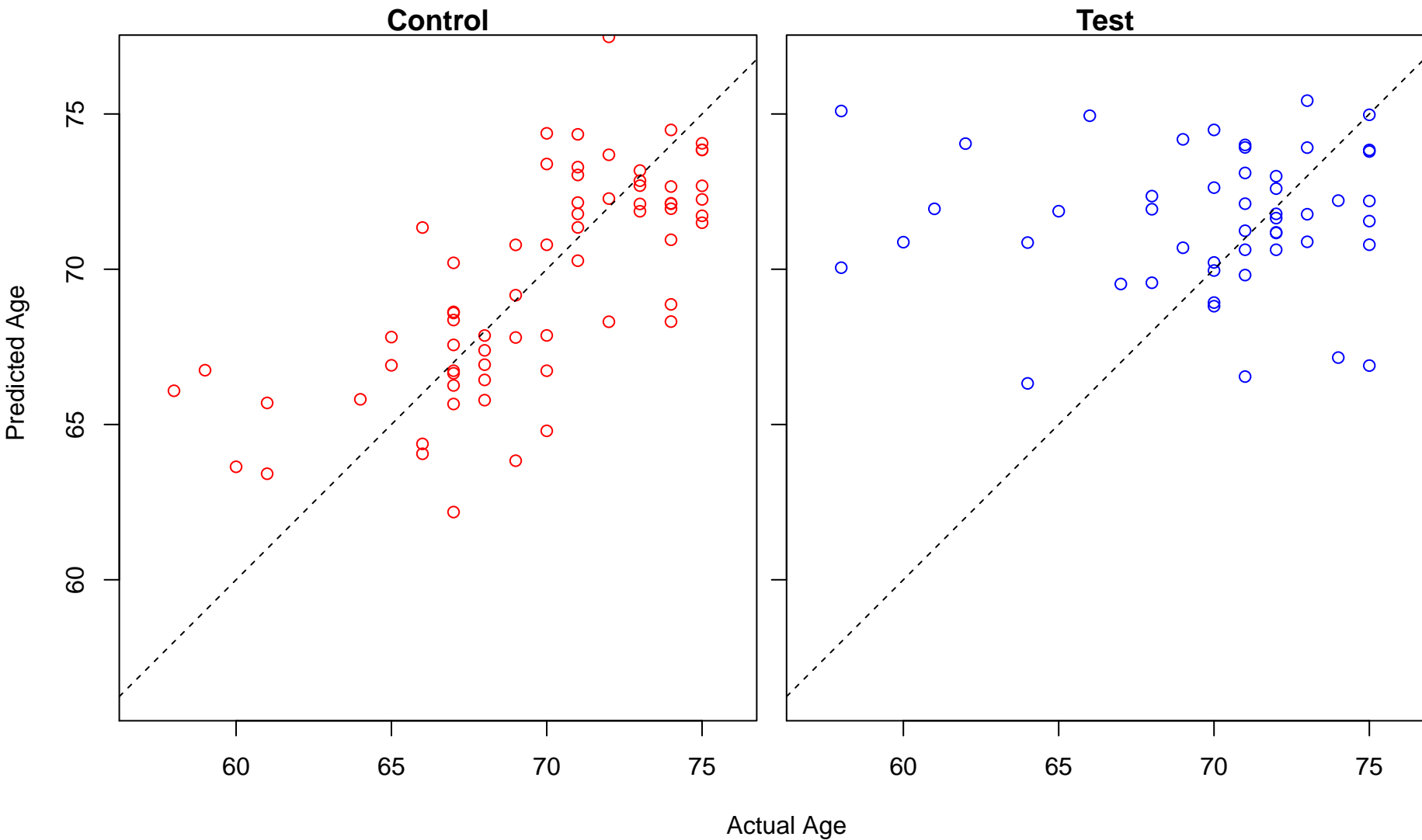


Actual Age

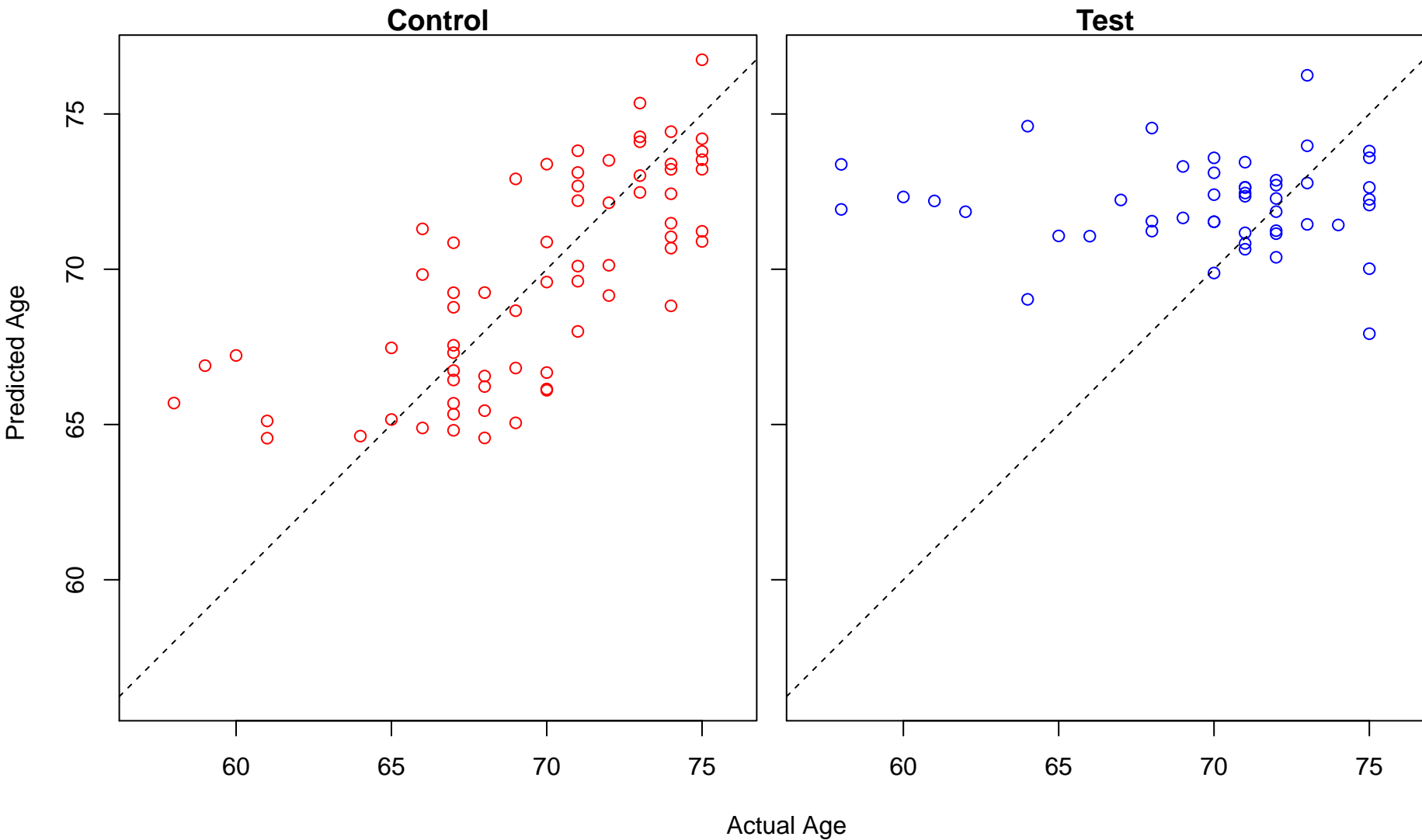
regulation of carbohydrate catabolic process (Score: 1.530419)



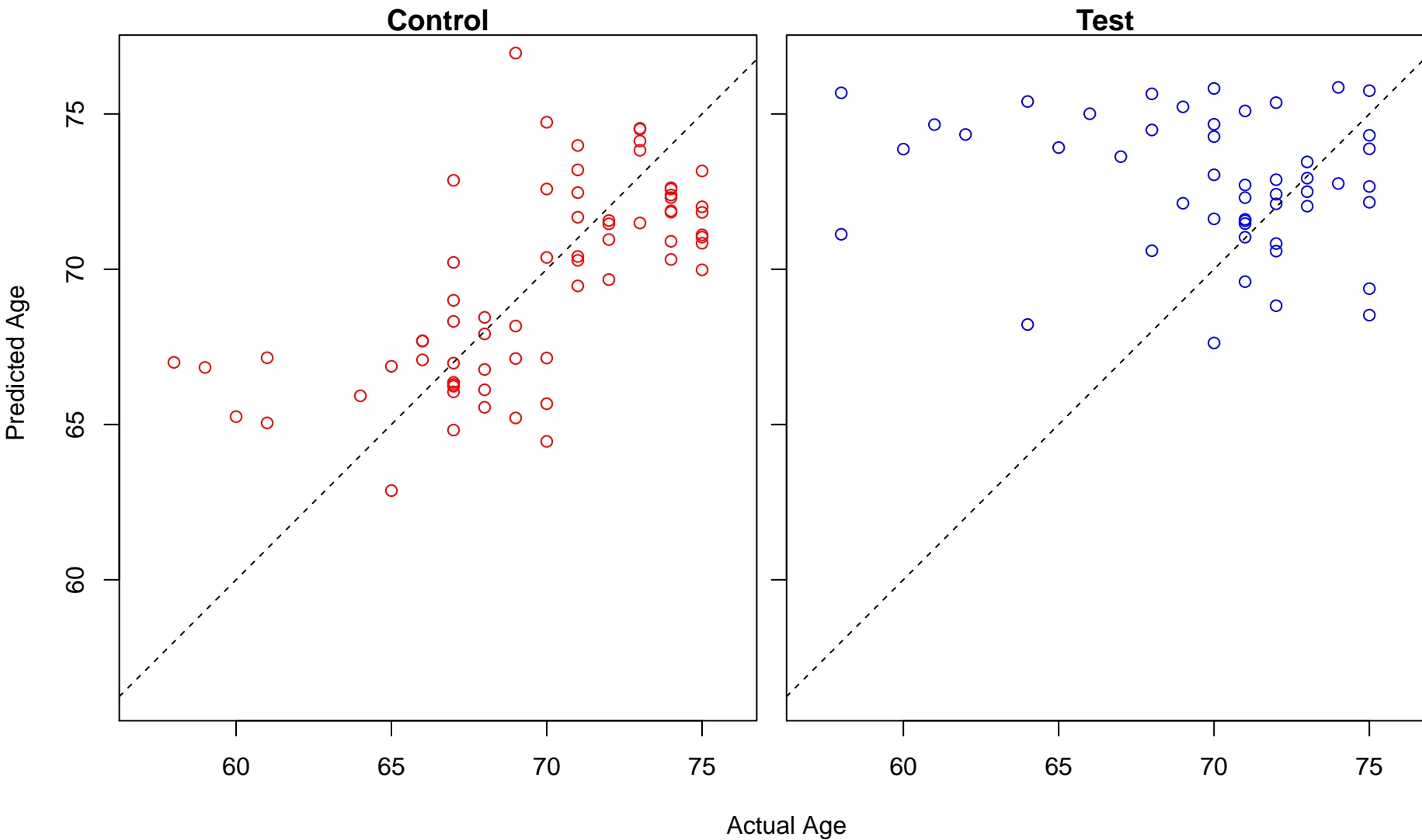
regulation of cellular carbohydrate catabolic process (Score: 1.530419)



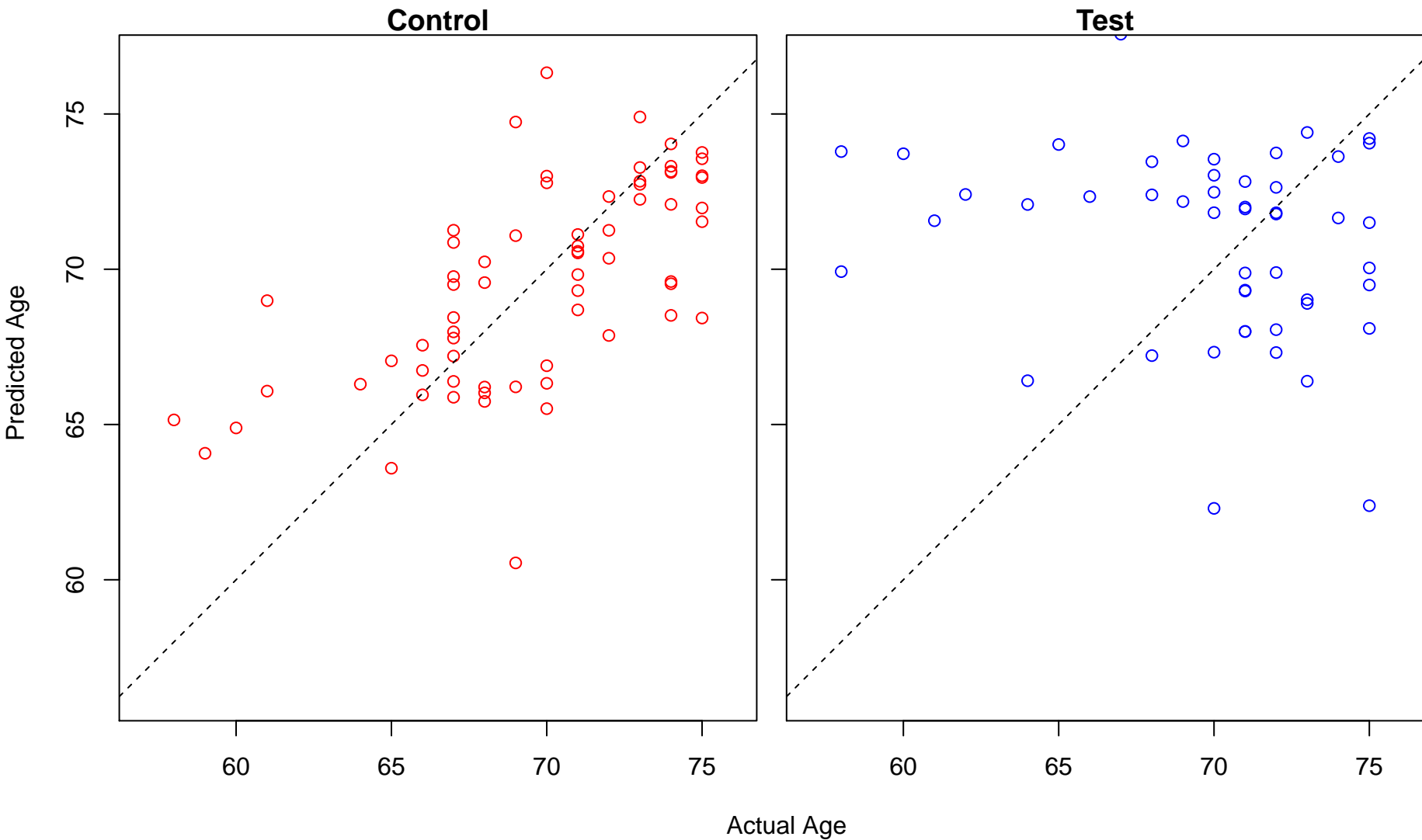
anion transmembrane transport (Score: 1.529962)



telomere maintenance via telomere lengthening (Score: 1.529904)

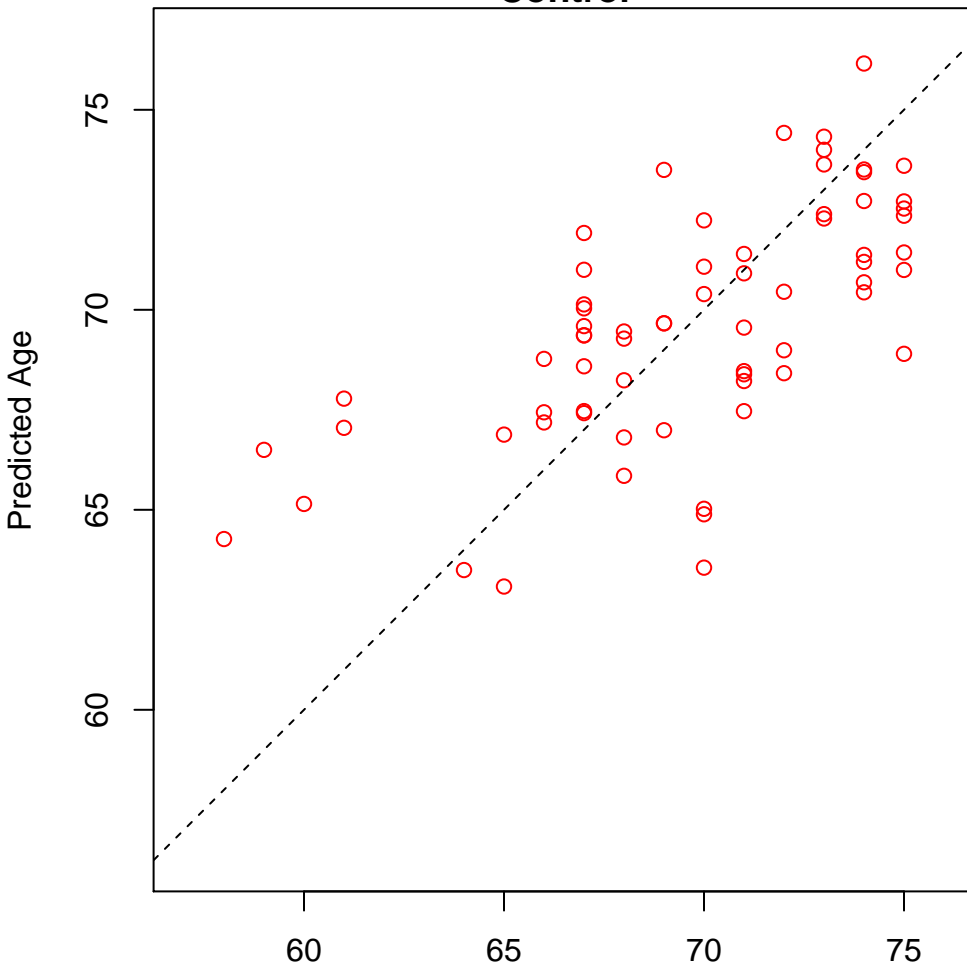


positive regulation of lipid biosynthetic process (Score: 1.529259)

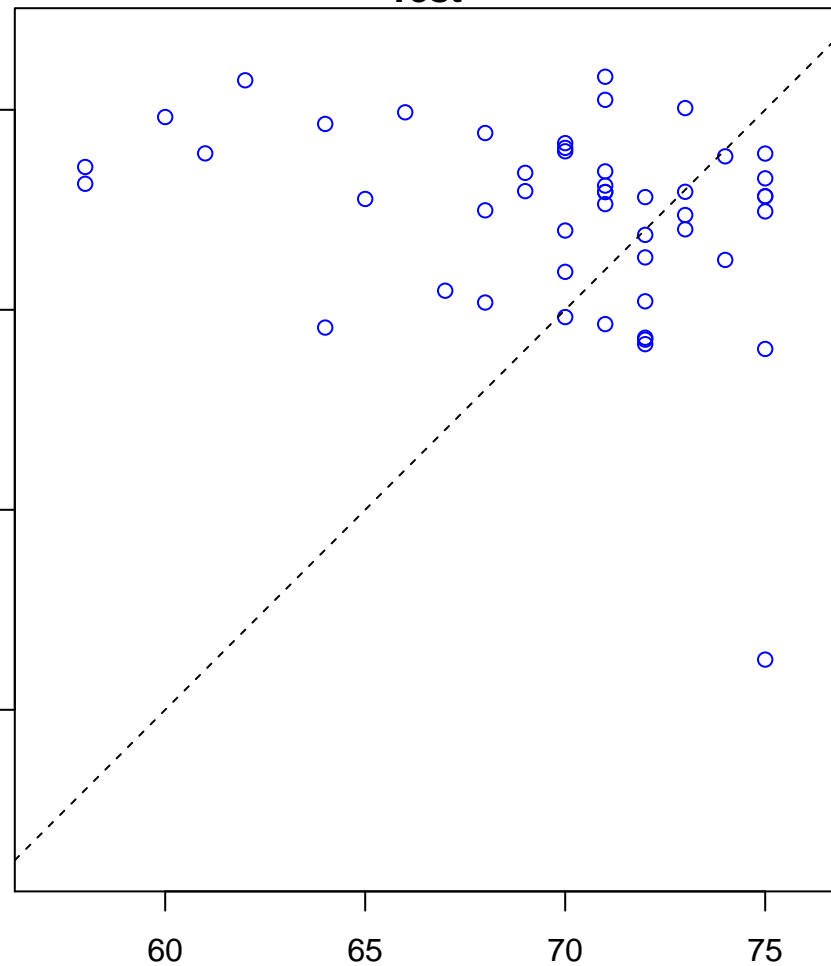


positive regulation of bone resorption (Score: 1.529132)

Control



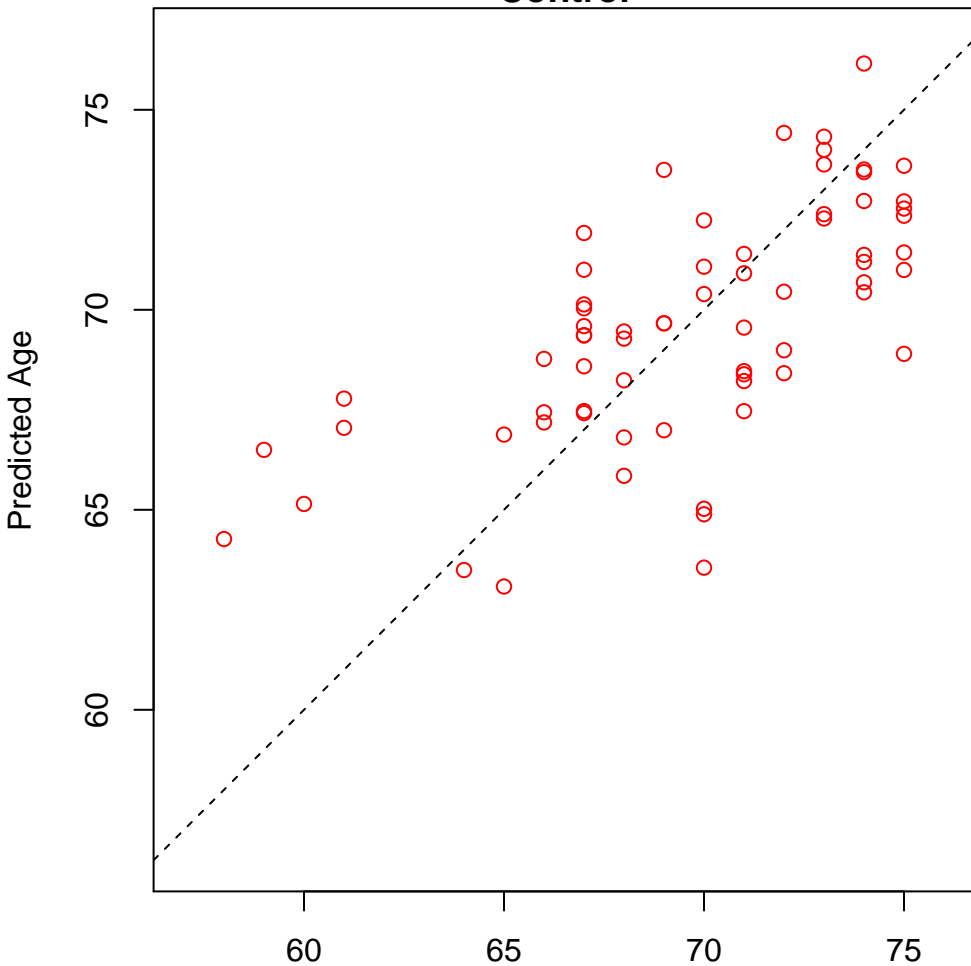
Test



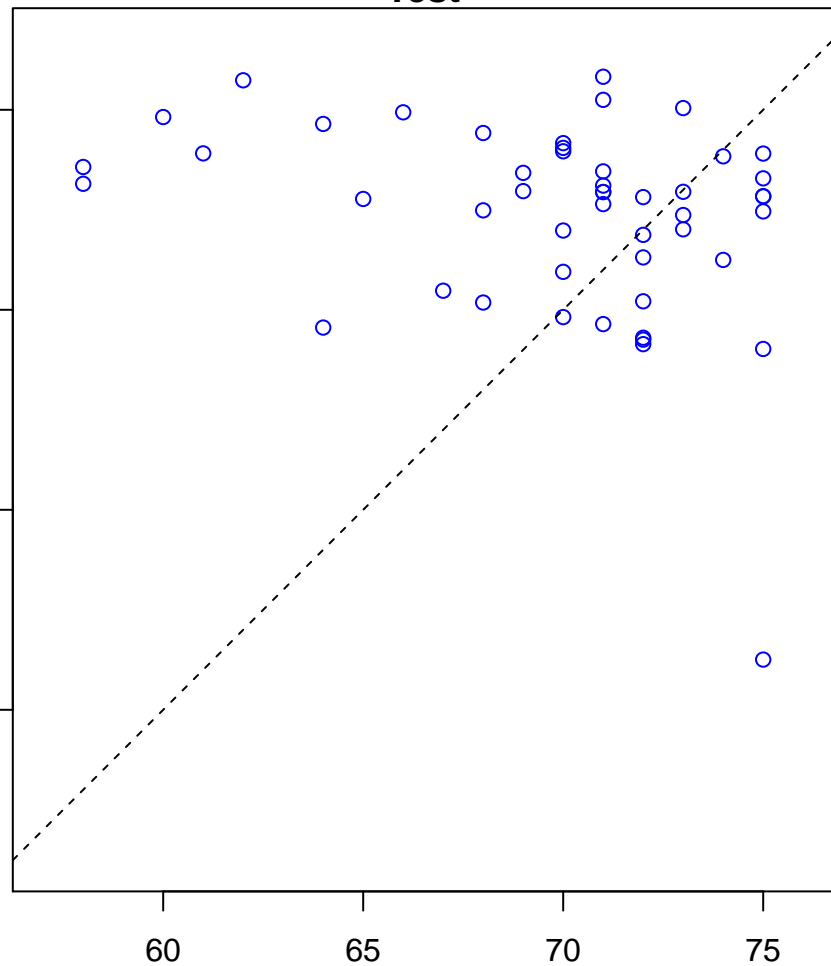
Actual Age

positive regulation of bone remodeling (Score: 1.529132)

Control

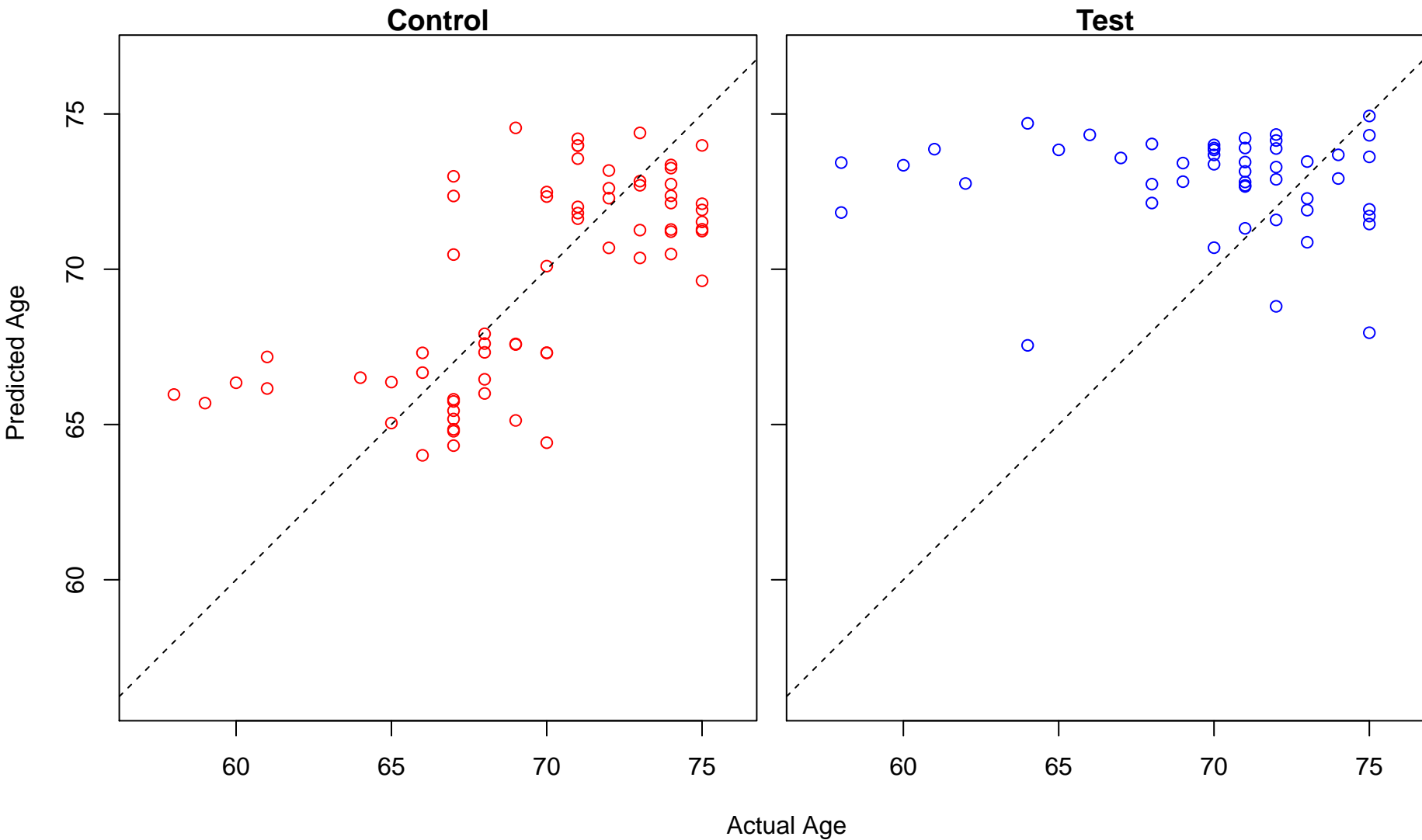


Test

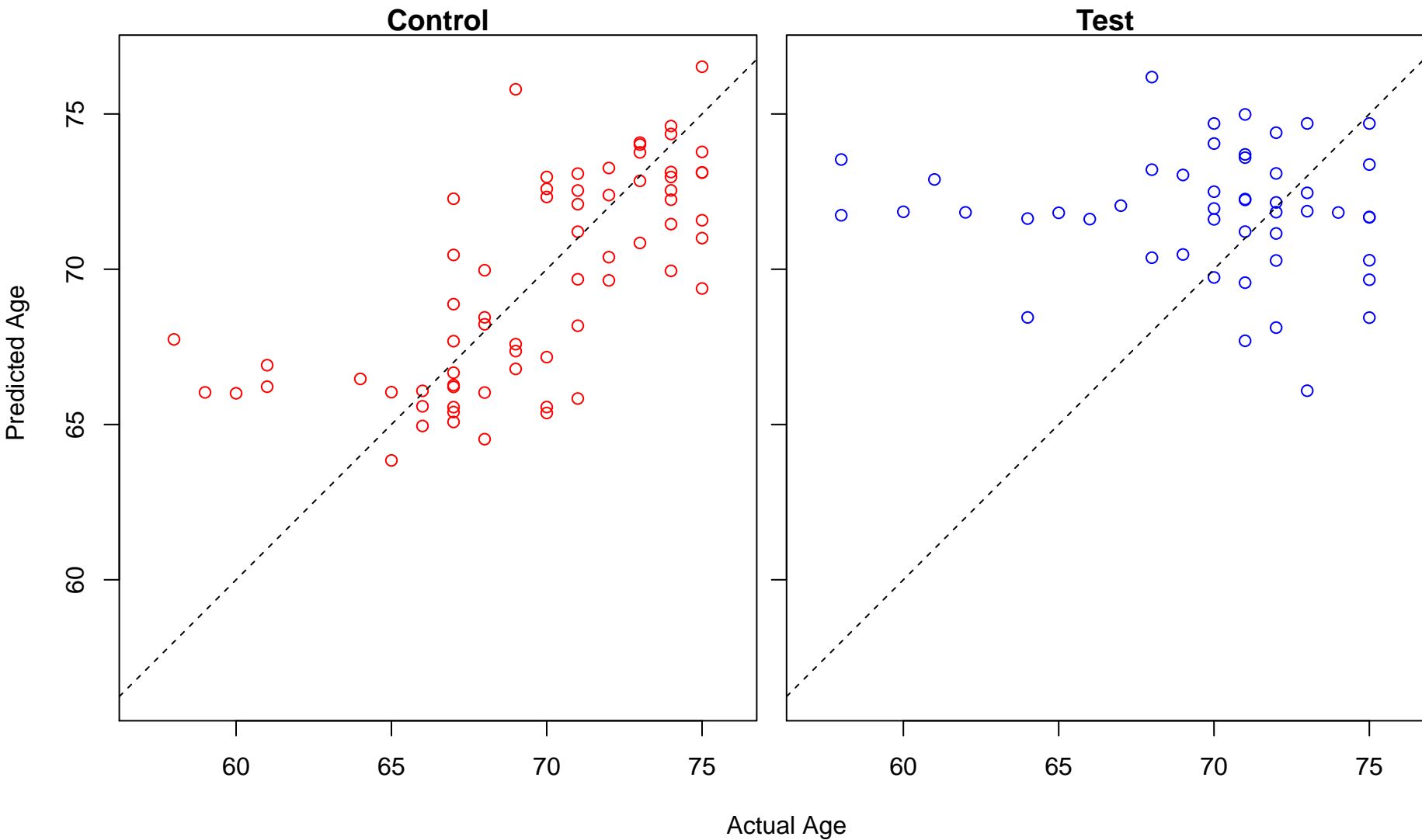


Actual Age

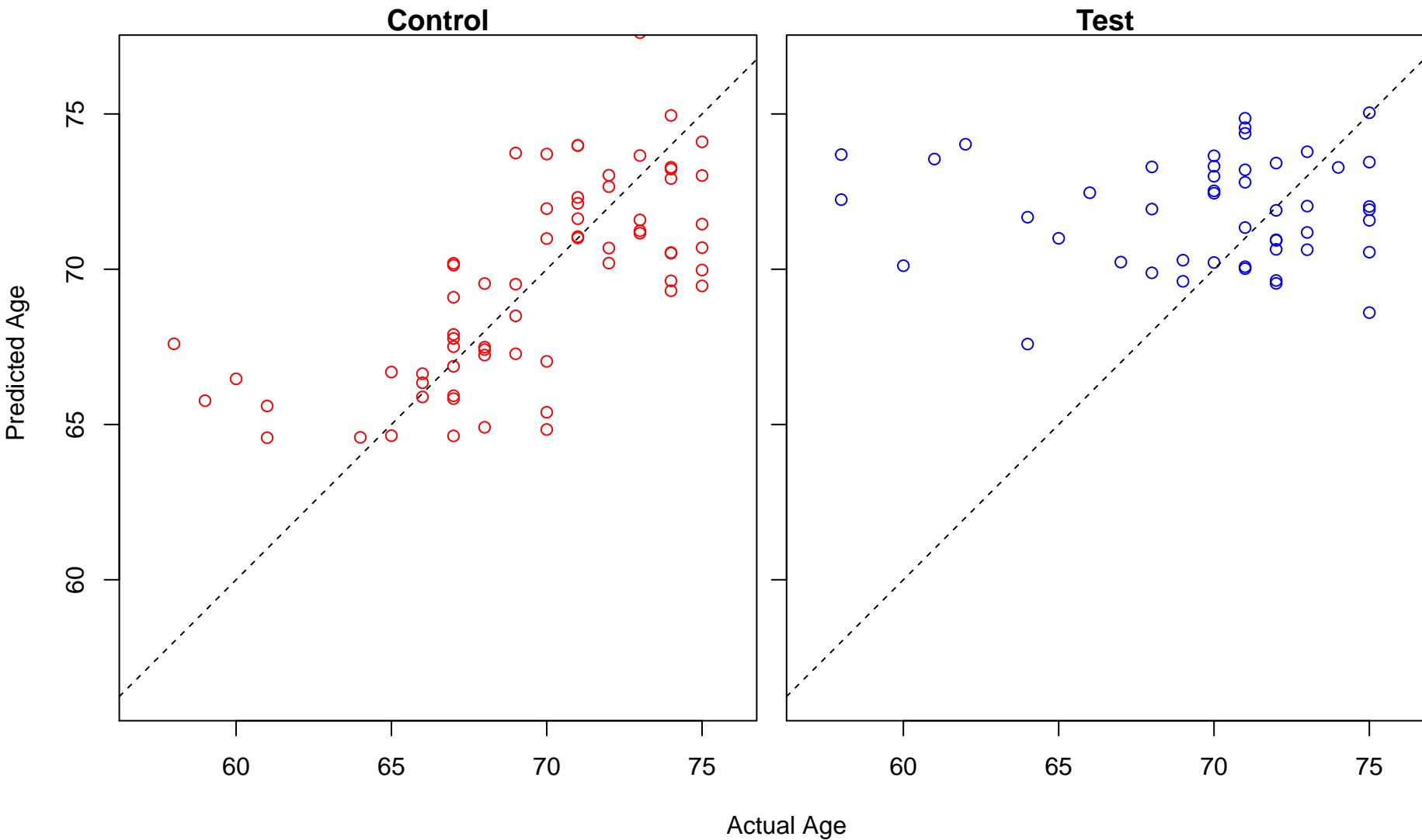
serine family amino acid metabolic process (Score: 1.528667)



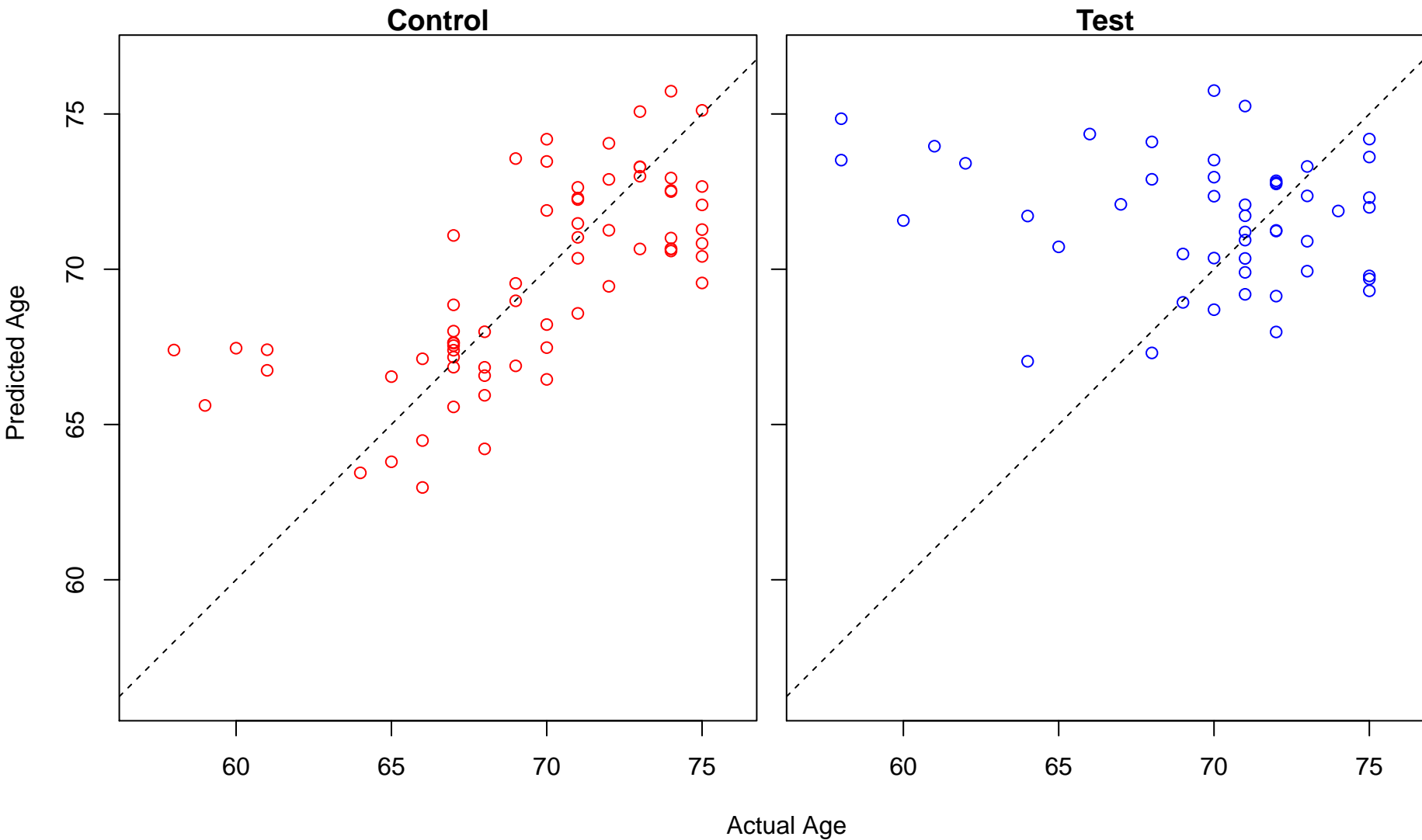
hematopoietic or lymphoid organ development (Score: 1.528580)



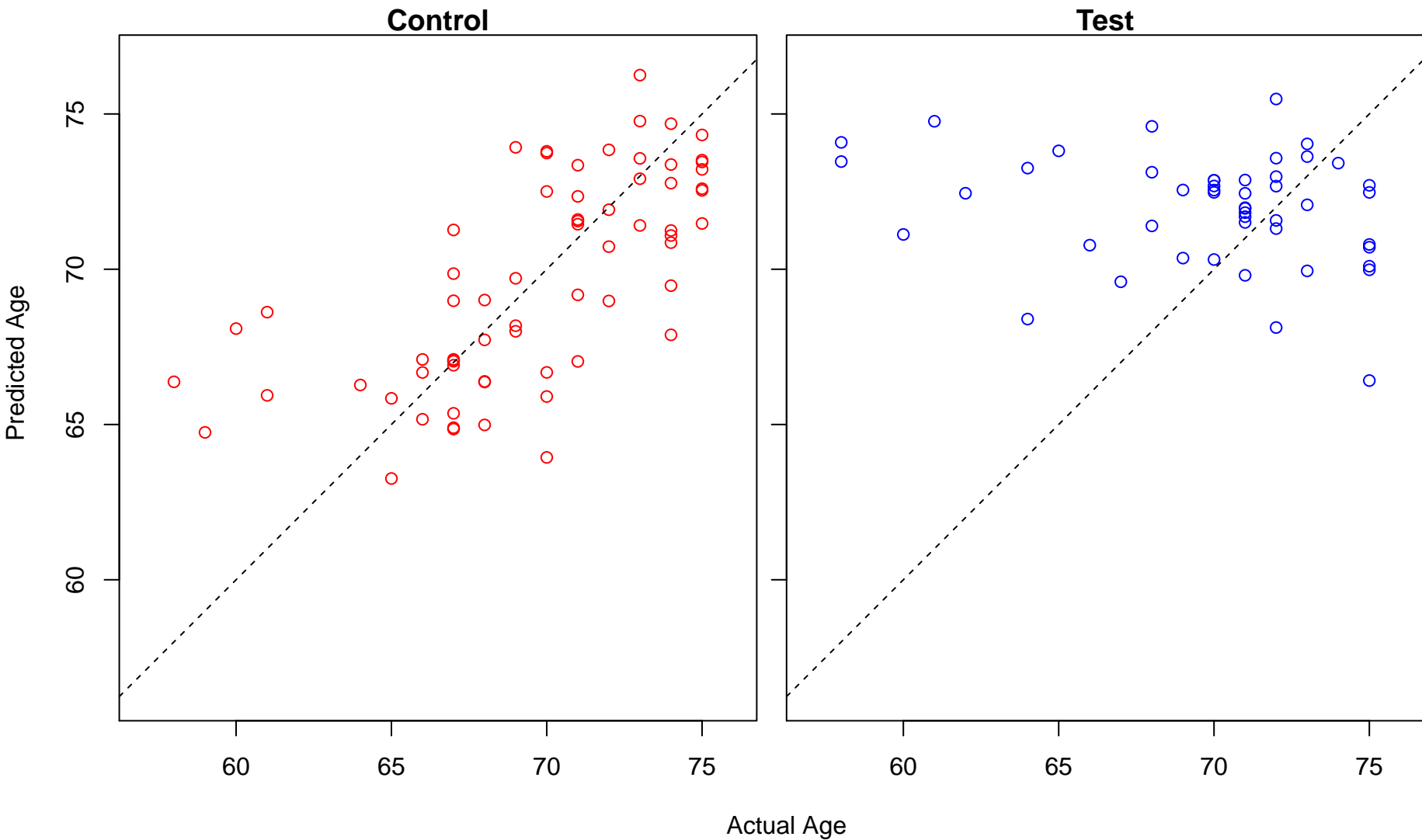
regulation of actin cytoskeleton organization (Score: 1.528182)



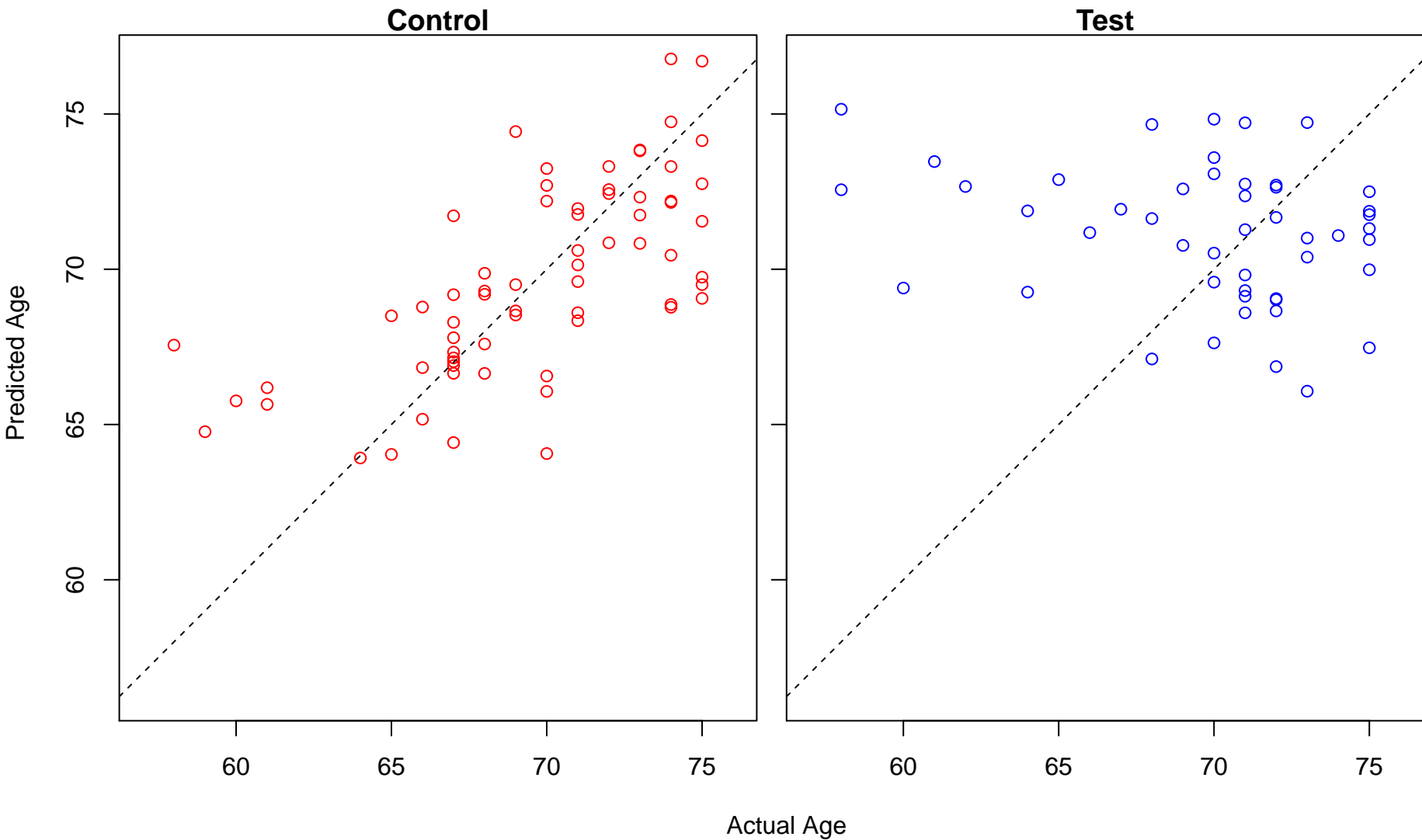
regulation of extrinsic apoptotic signaling pathway via death domain receptors (Score: 1.526971)



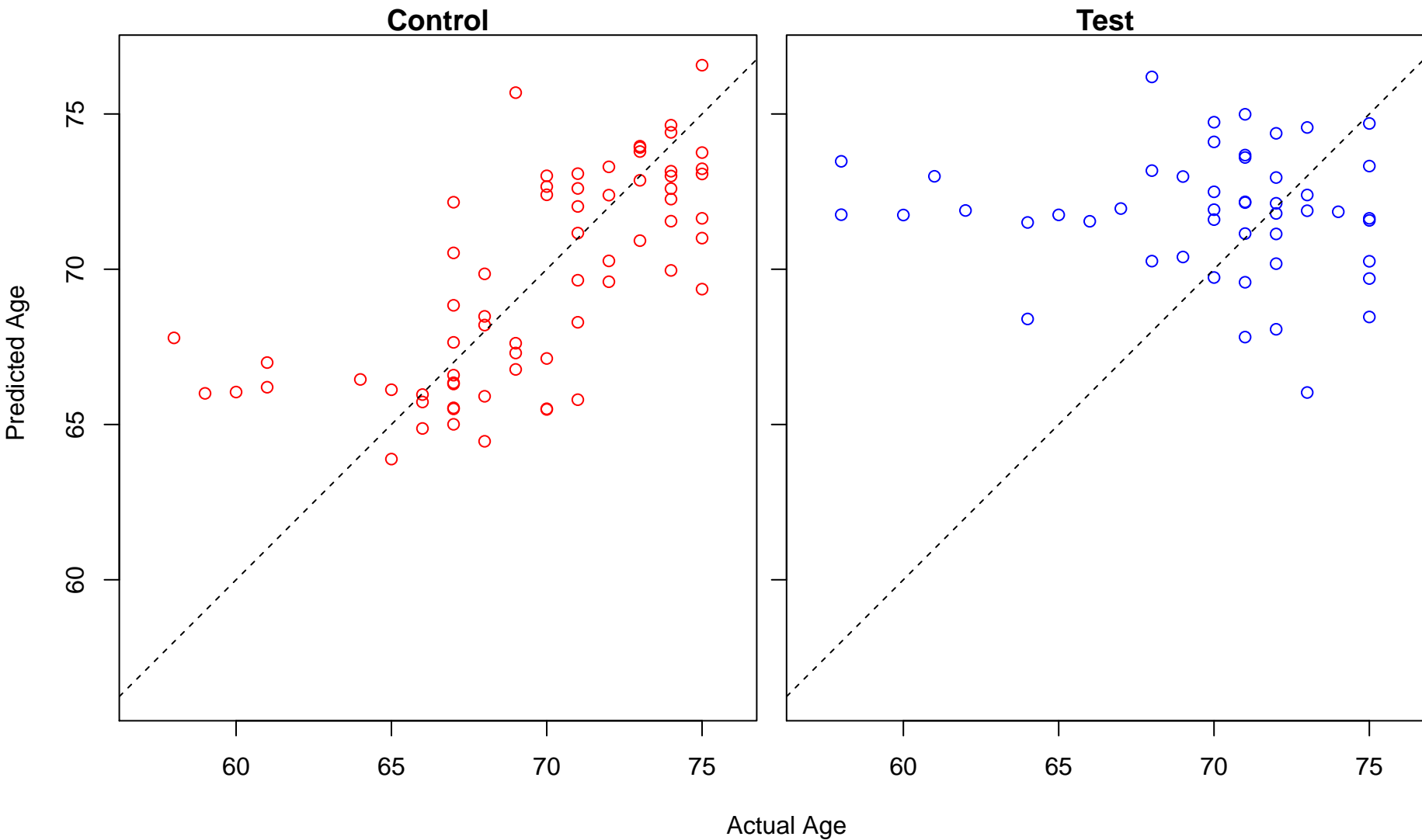
negative regulation of DNA metabolic process (Score: 1.526639)



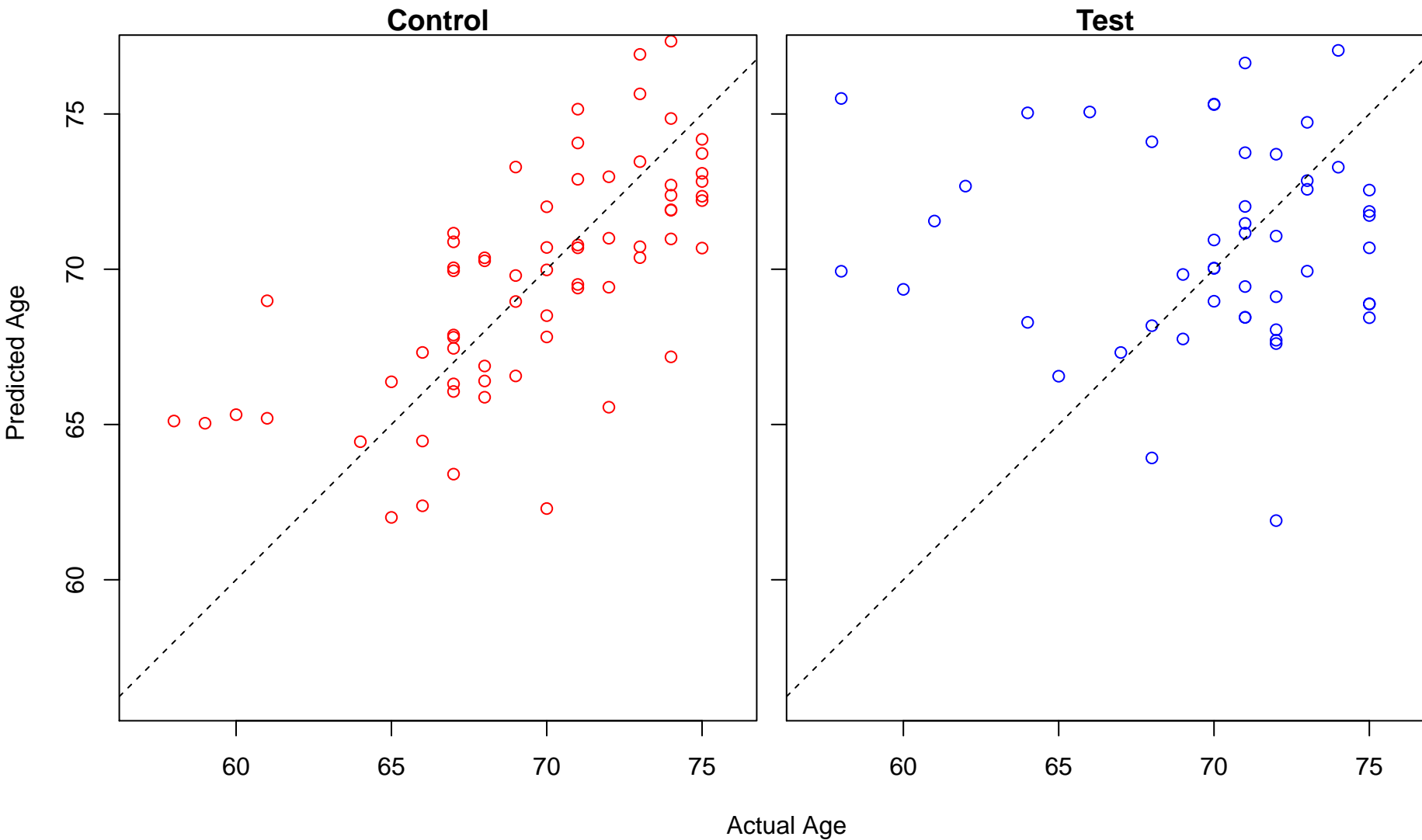
positive regulation of protein import into nucleus (Score: 1.526410)



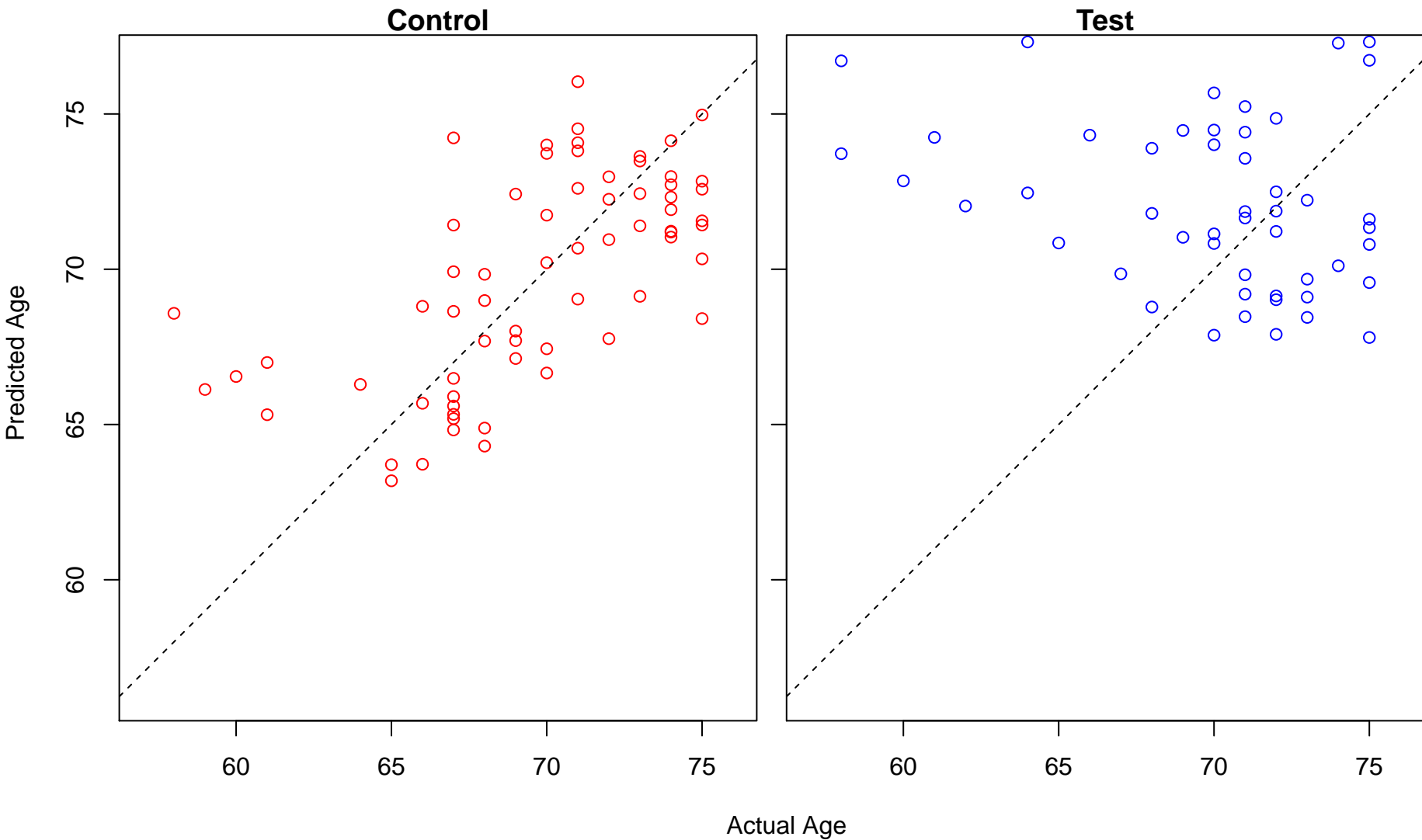
hemopoiesis (Score: 1.525991)



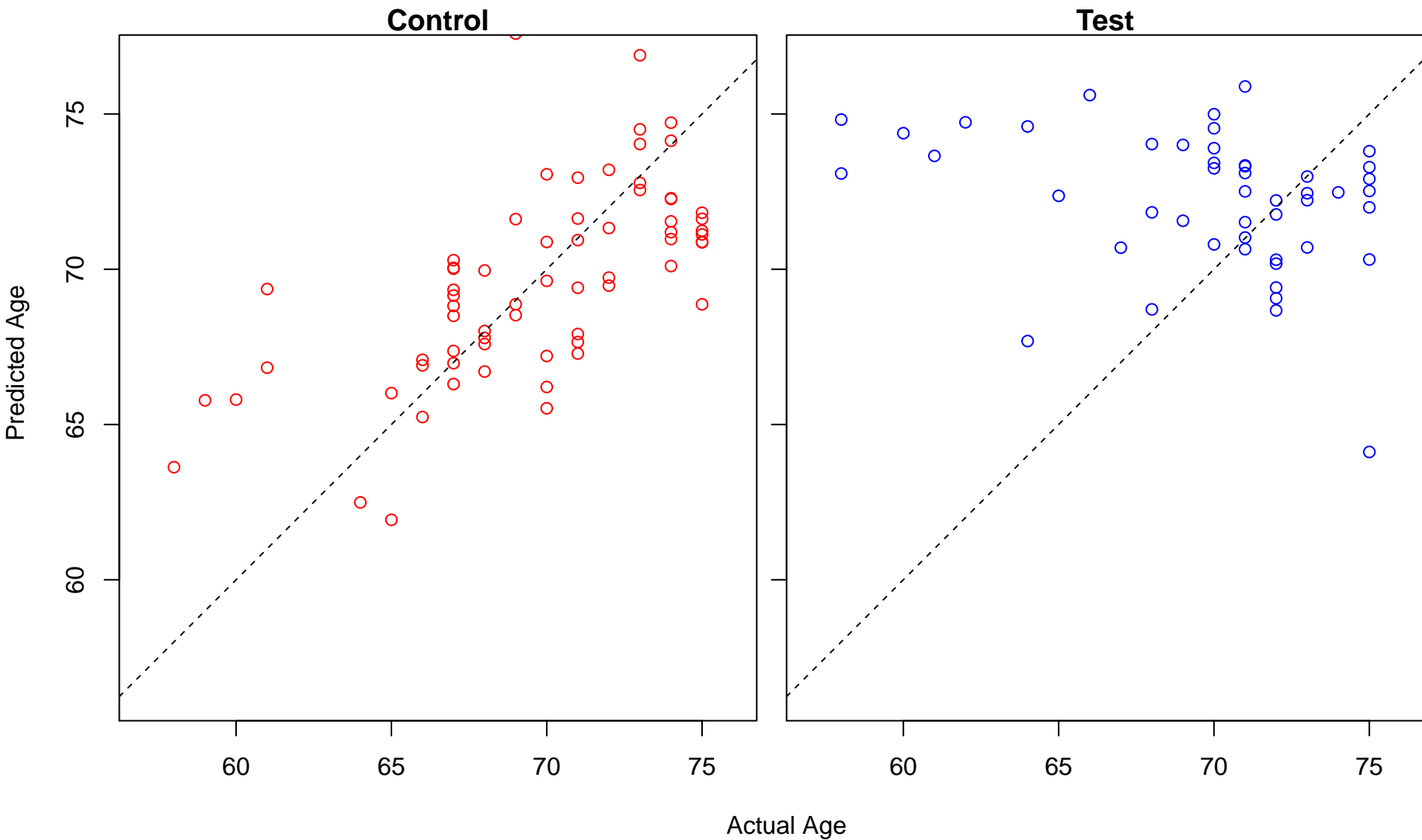
endosome to lysosome transport (Score: 1.525983)



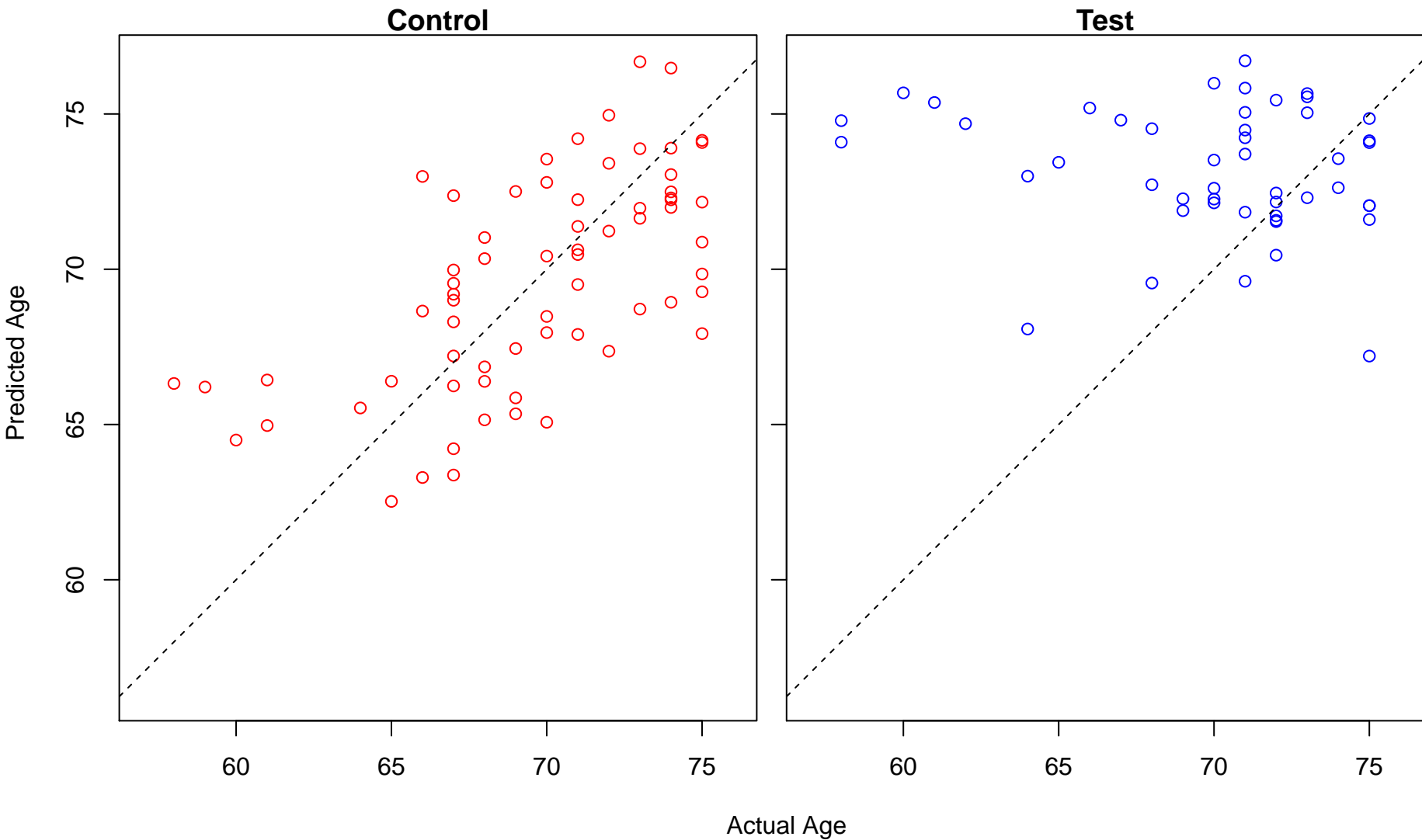
spindle assembly (Score: 1.525980)



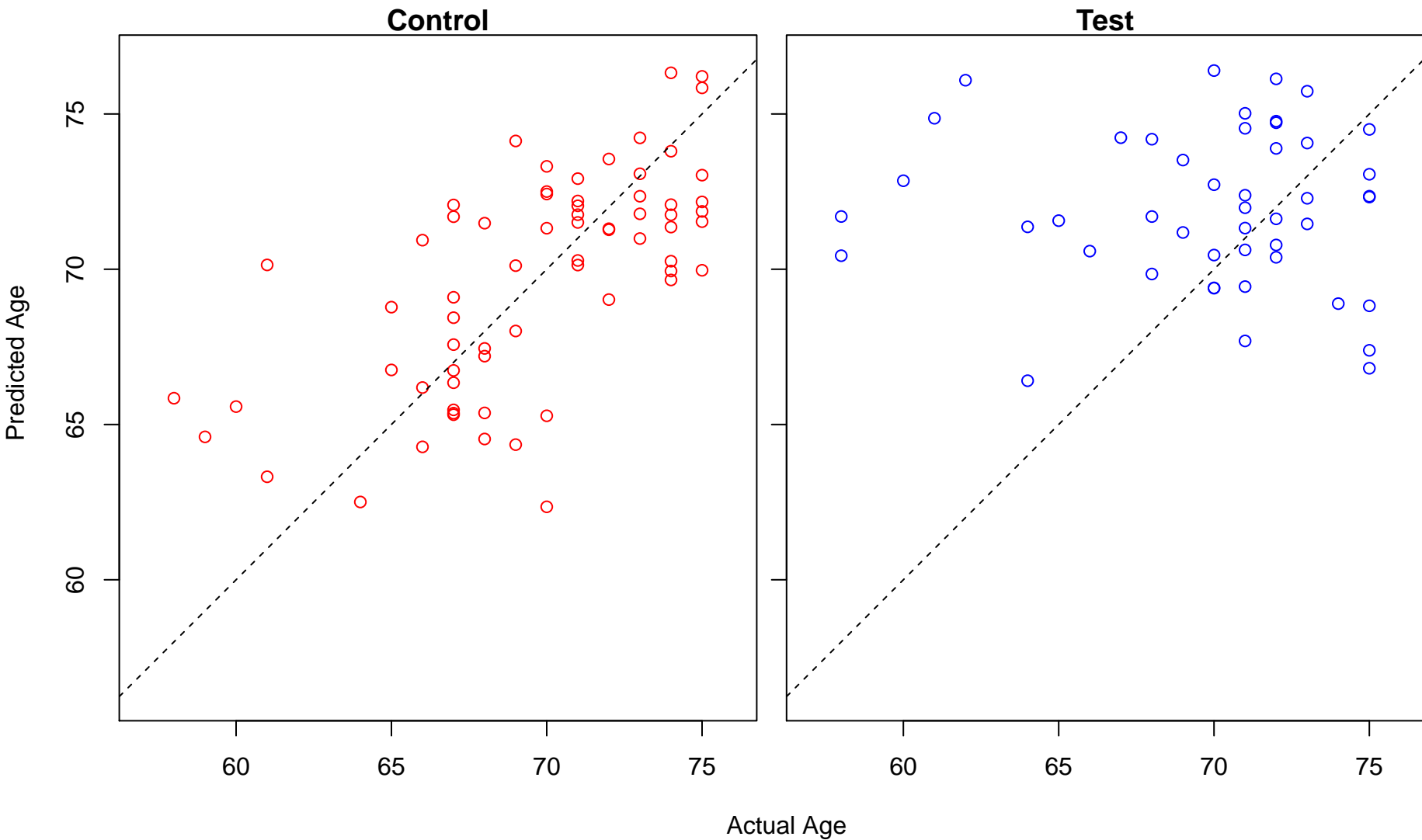
positive regulation of acute inflammatory response (Score: 1.525078)



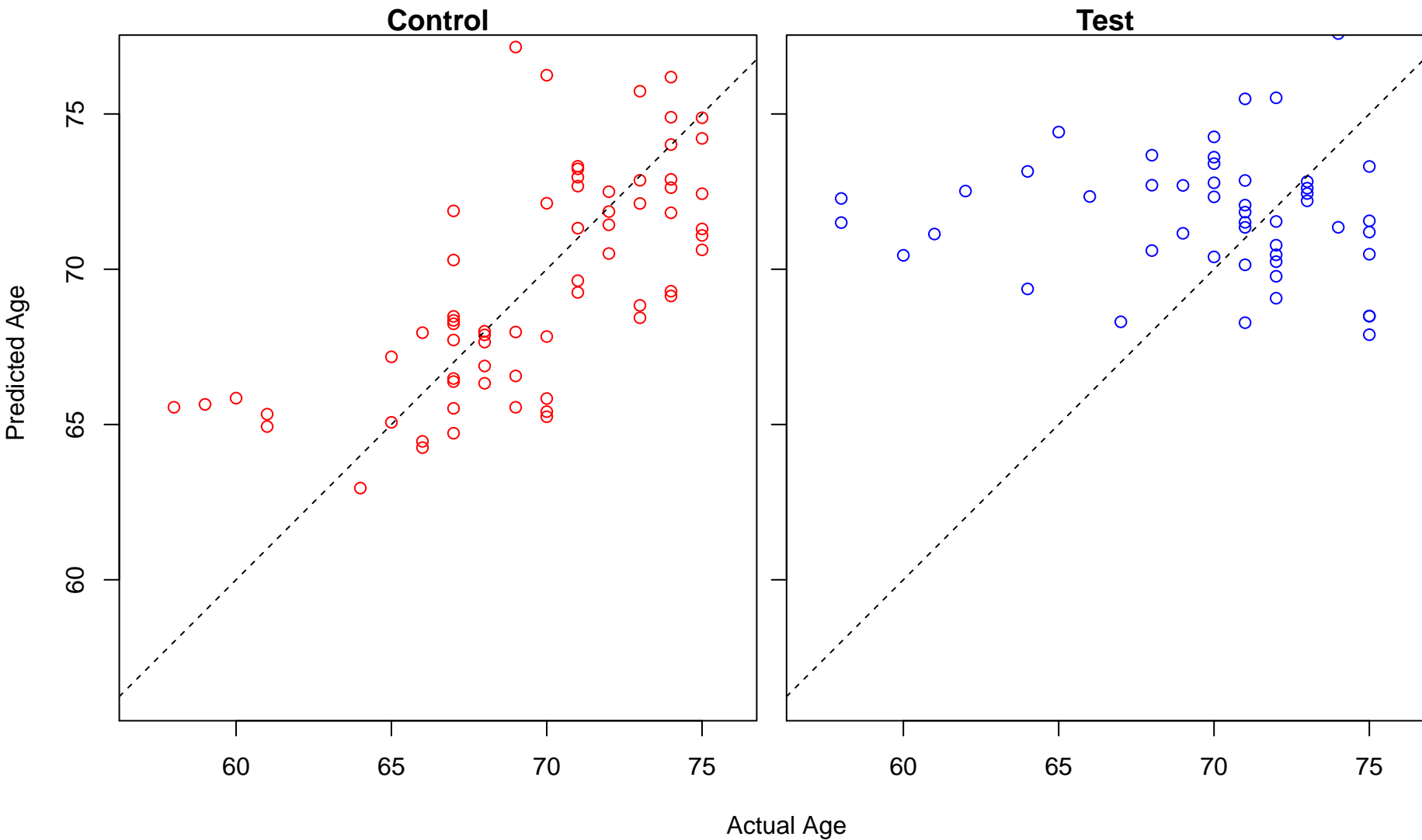
cognition (Score: 1.525020)



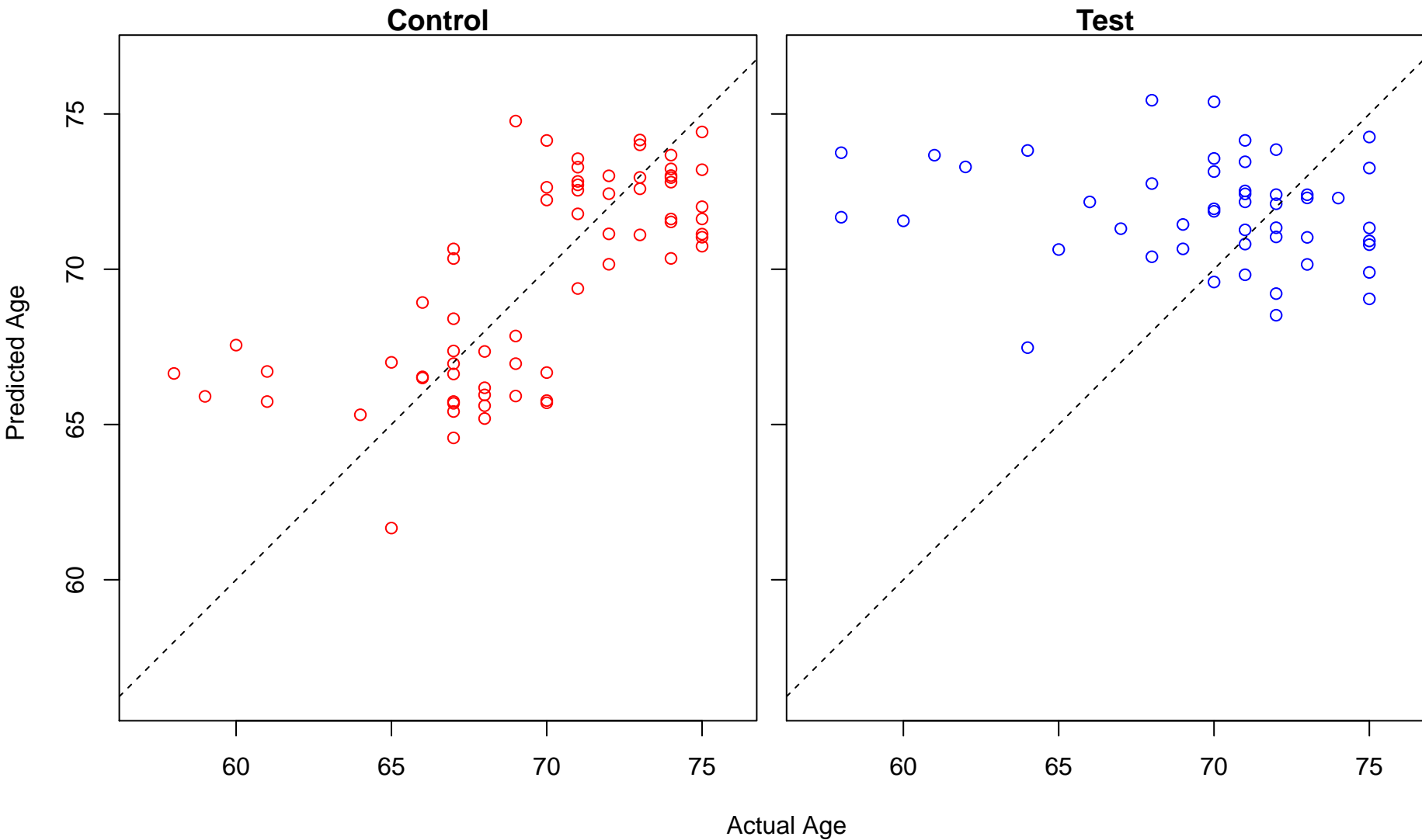
steroid biosynthetic process (Score: 1.524301)



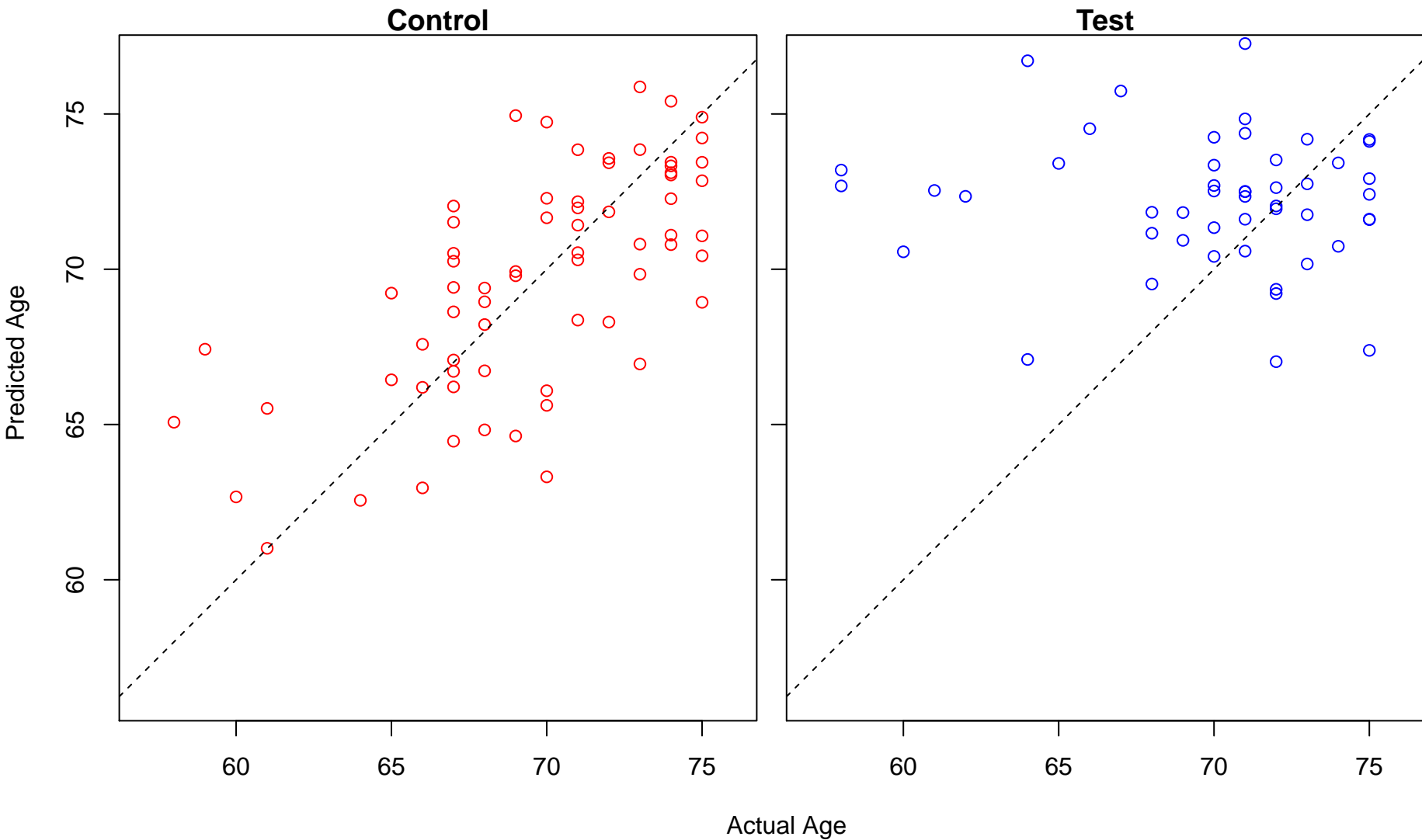
platelet degranulation (Score: 1.523150)



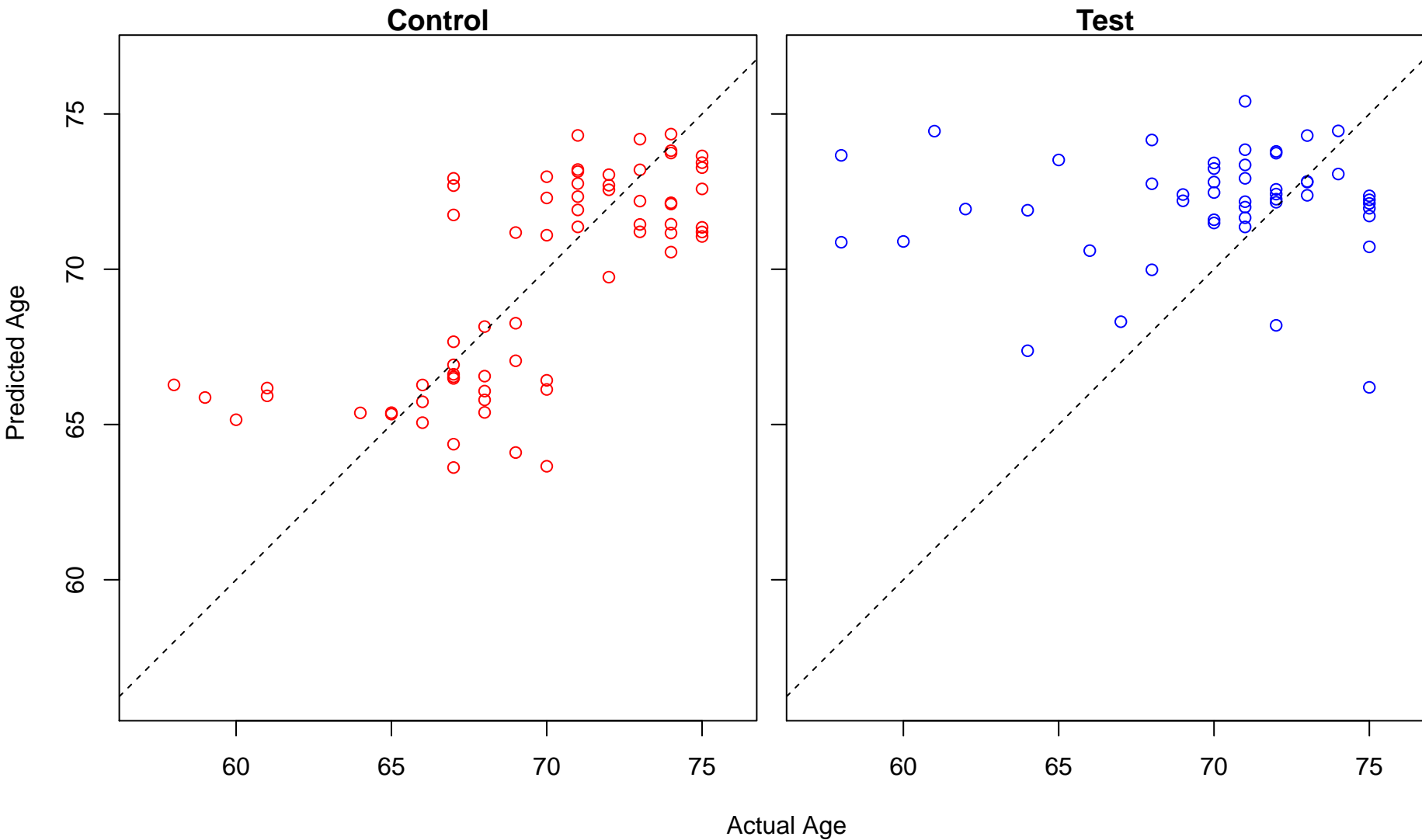
positive regulation of Wnt signaling pathway (Score: 1.522338)



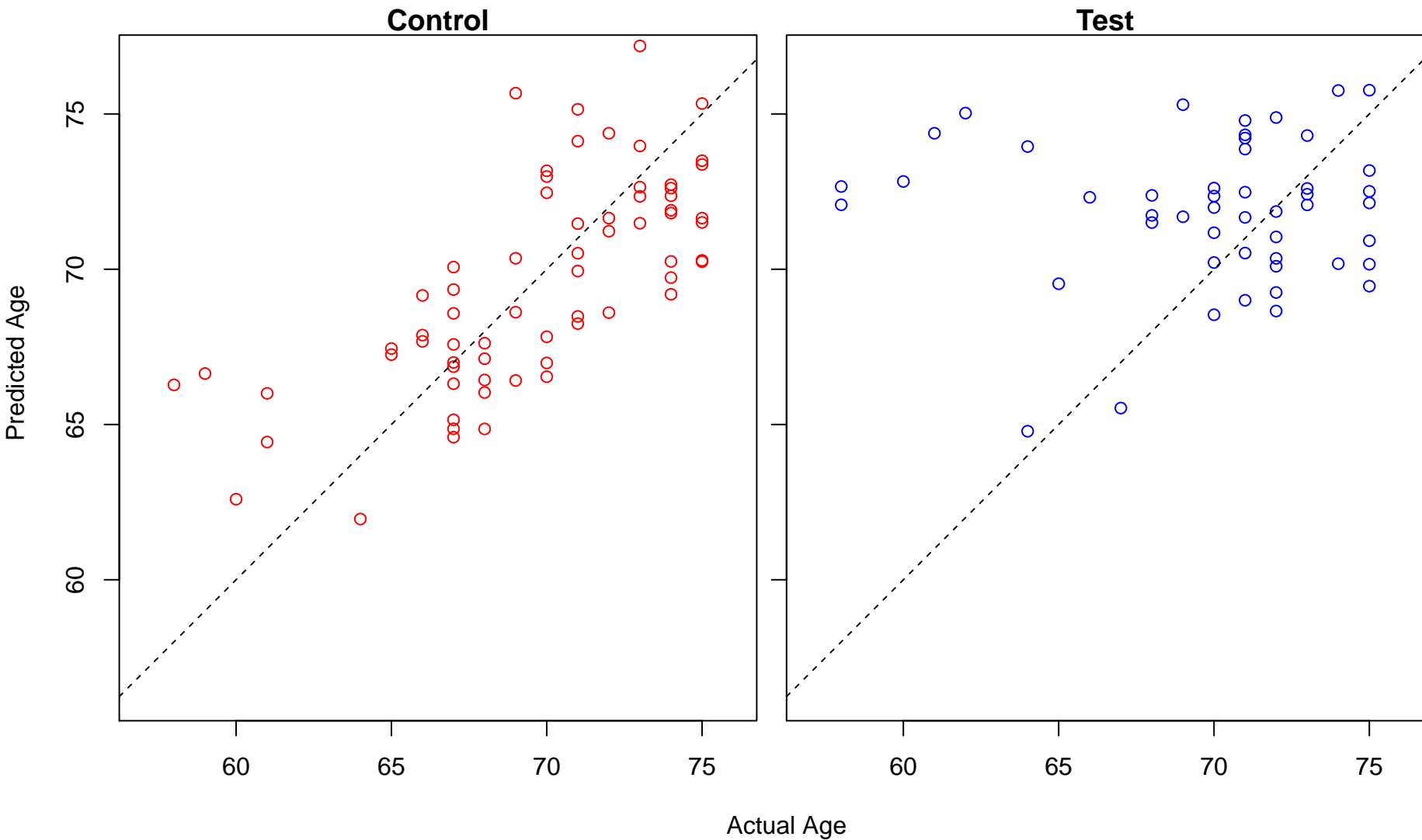
histone ubiquitination (Score: 1.522313)



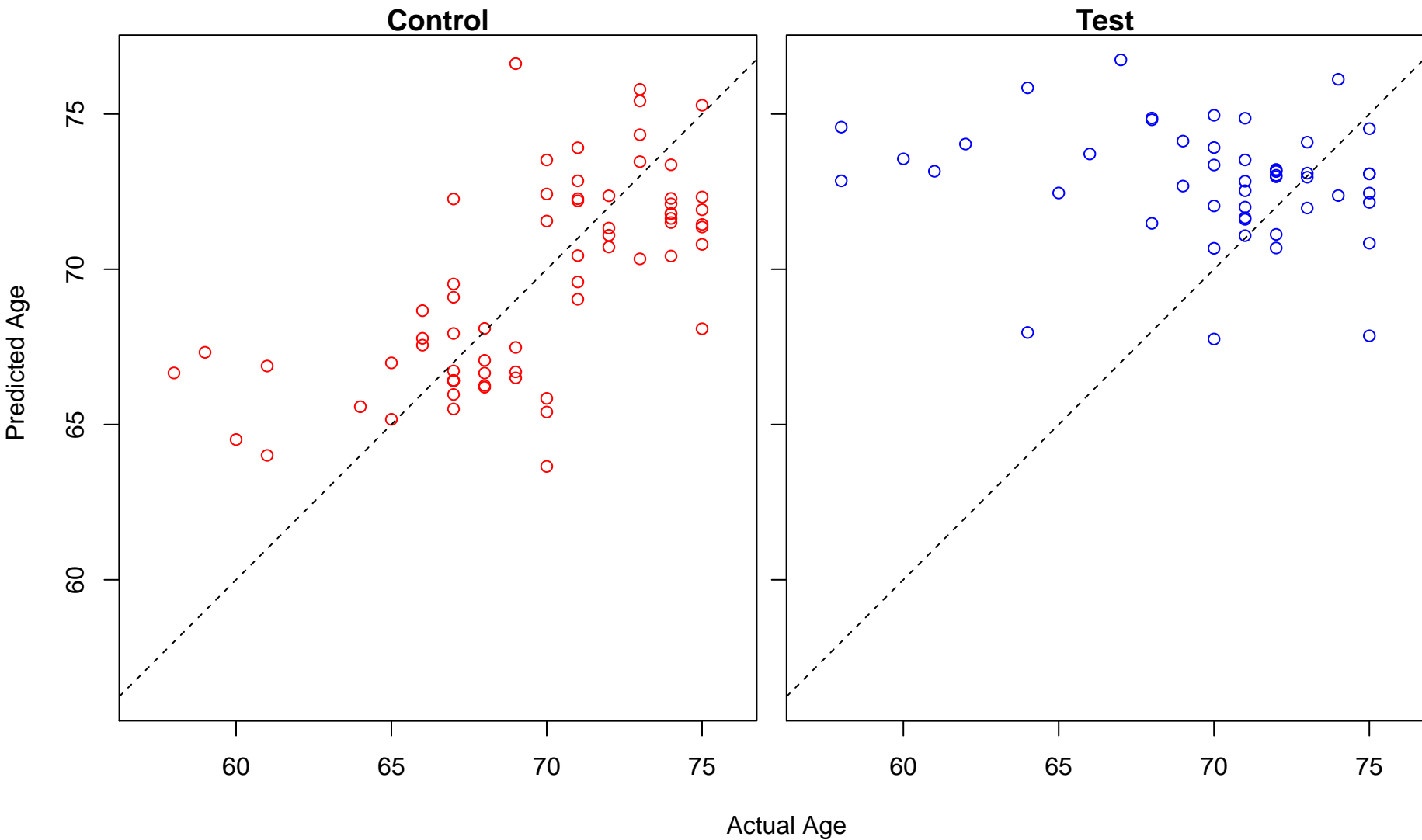
ribosome biogenesis (Score: 1.521941)



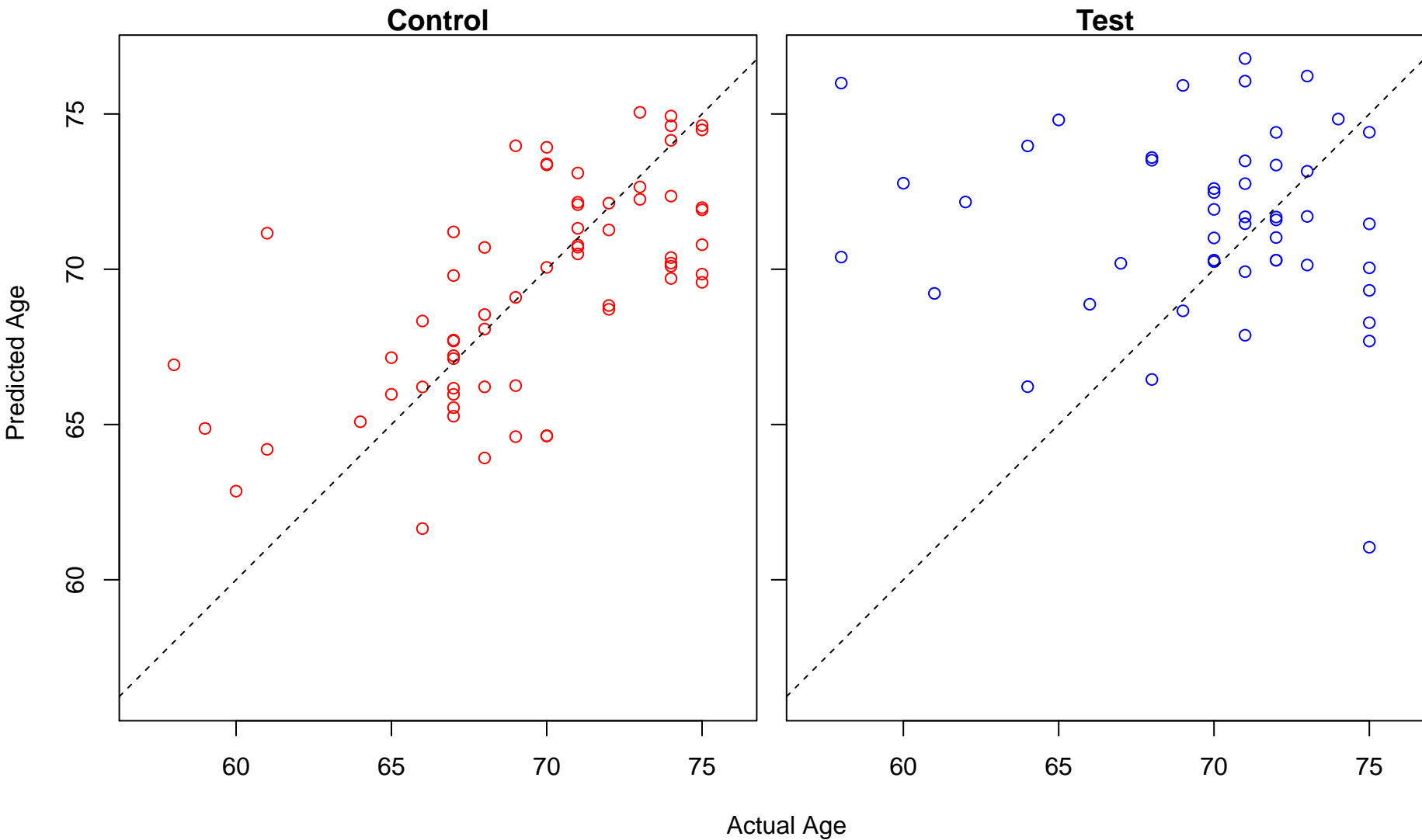
tube morphogenesis (Score: 1.521362)



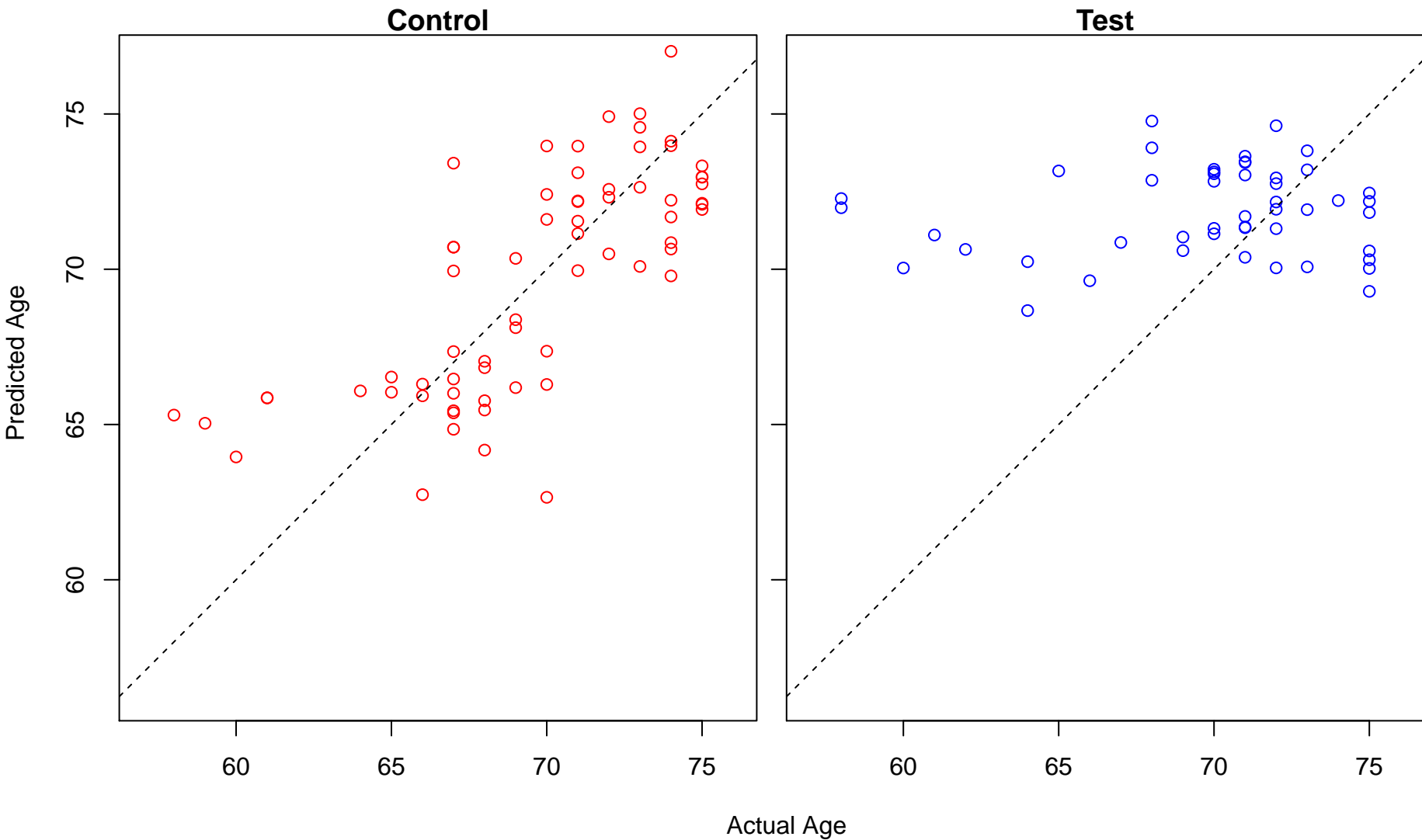
DNA replication (Score: 1.521361)



positive regulation of response to DNA damage stimulus (Score: 1.521138)

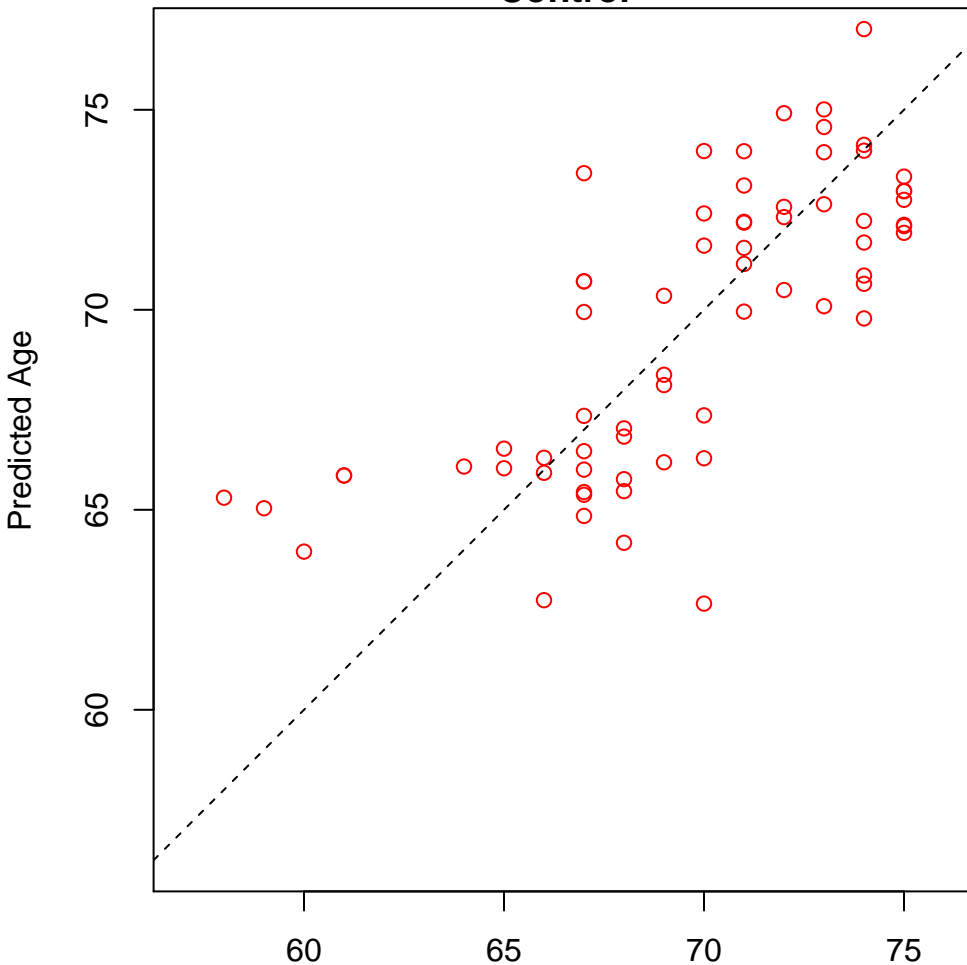


energy coupled proton transport, down electrochemical gradient (Score: 1.520606)

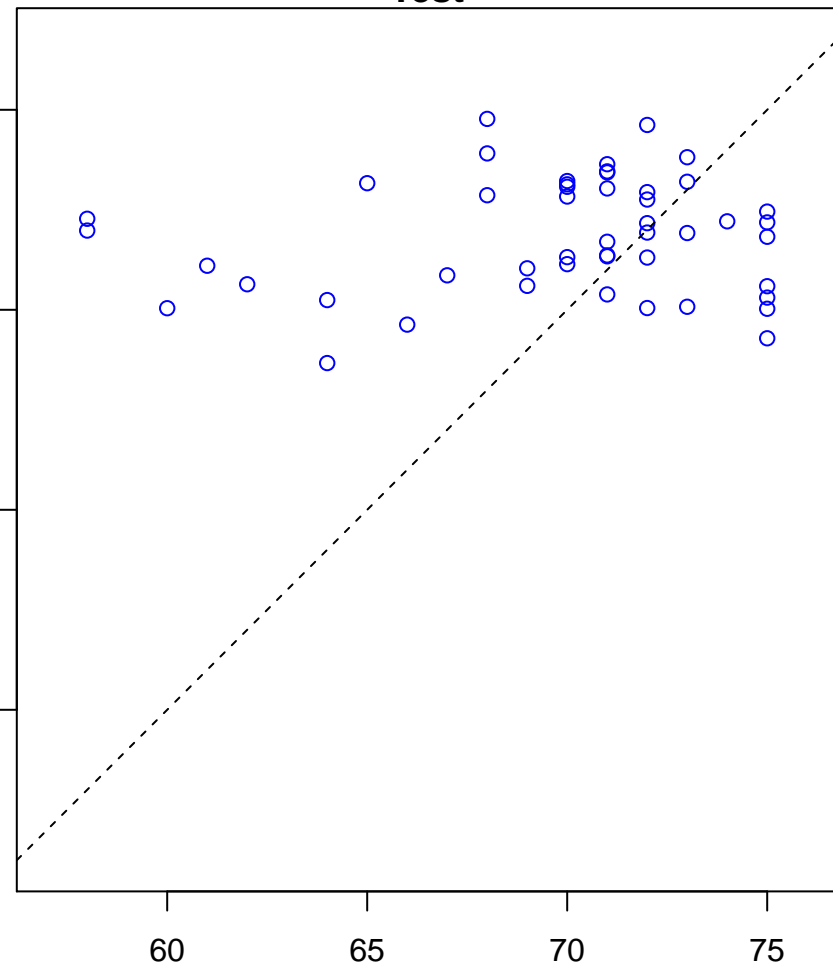


ATP synthesis coupled proton transport (Score: 1.520606)

Control

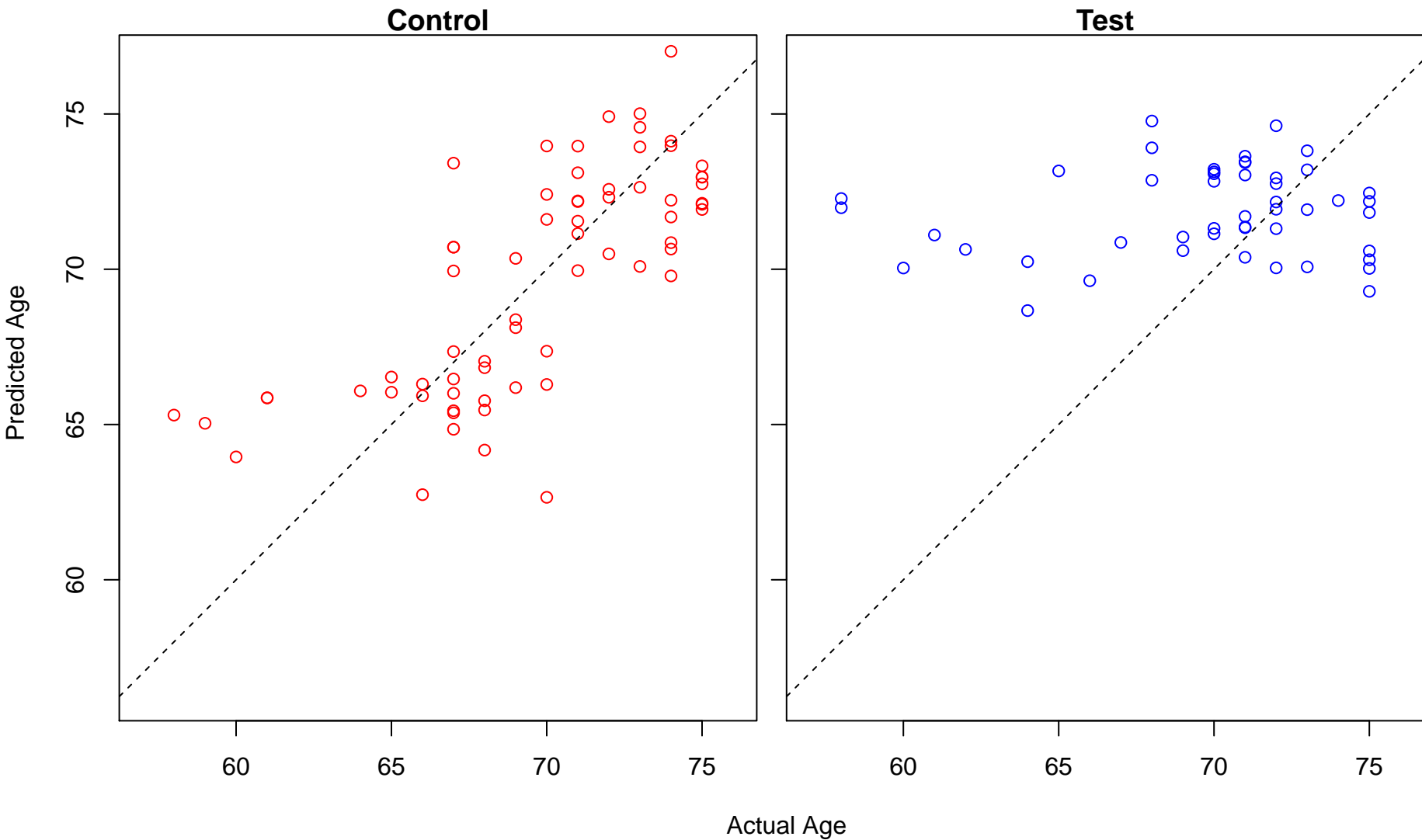


Test

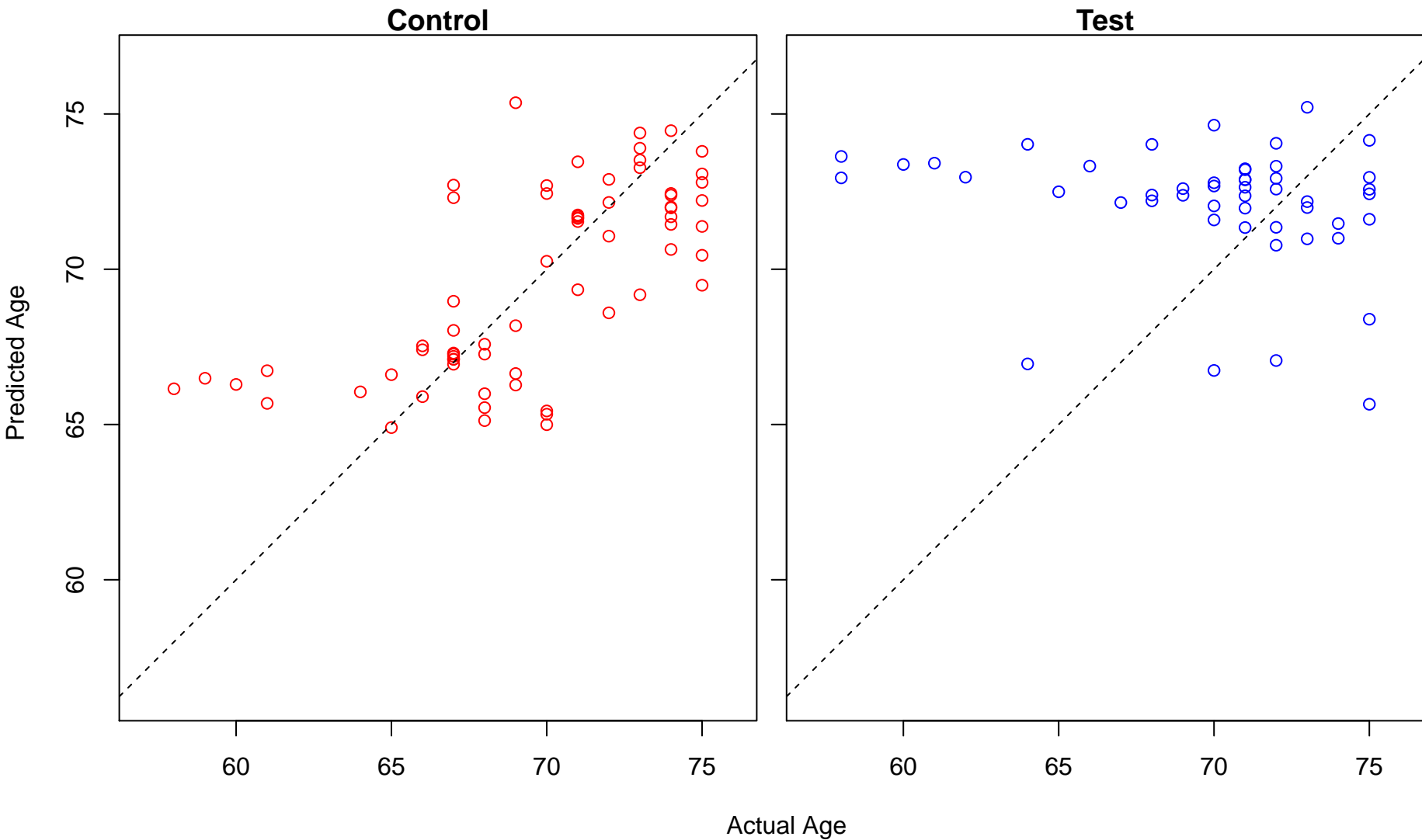


Actual Age

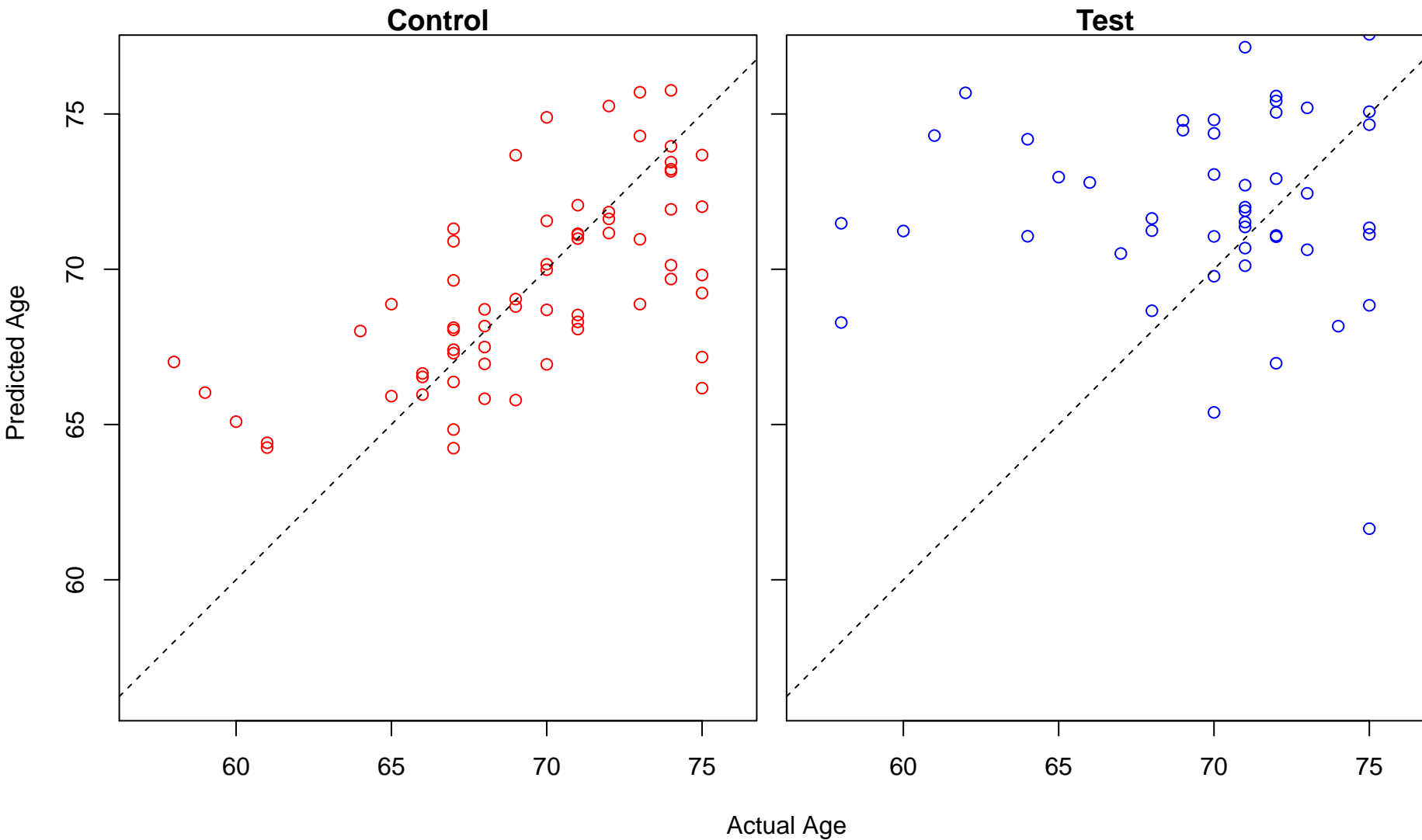
mitochondrial ATP synthesis coupled proton transport (Score: 1.520606)



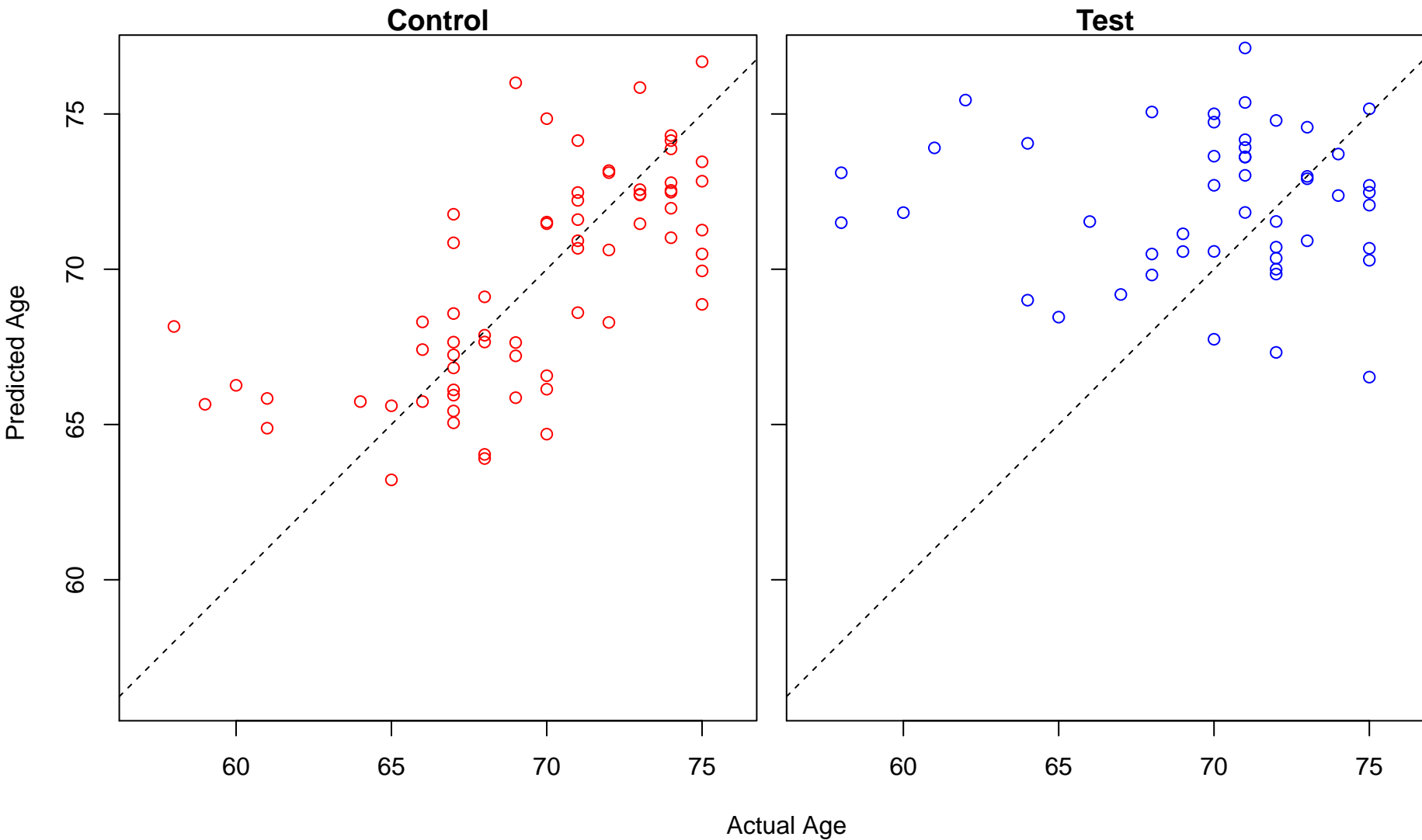
response to cAMP (Score: 1.520488)



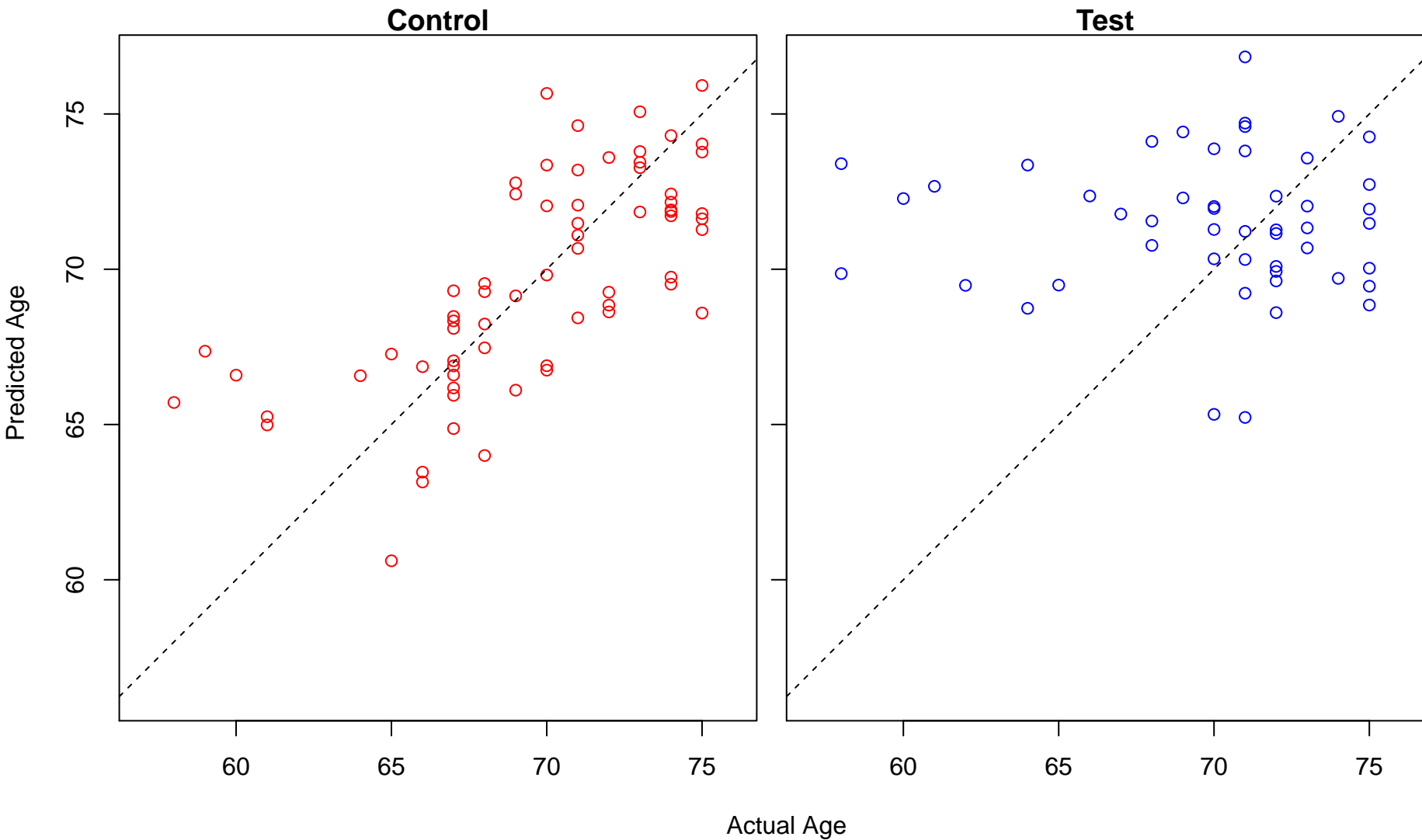
muscle cell cellular homeostasis (Score: 1.518679)



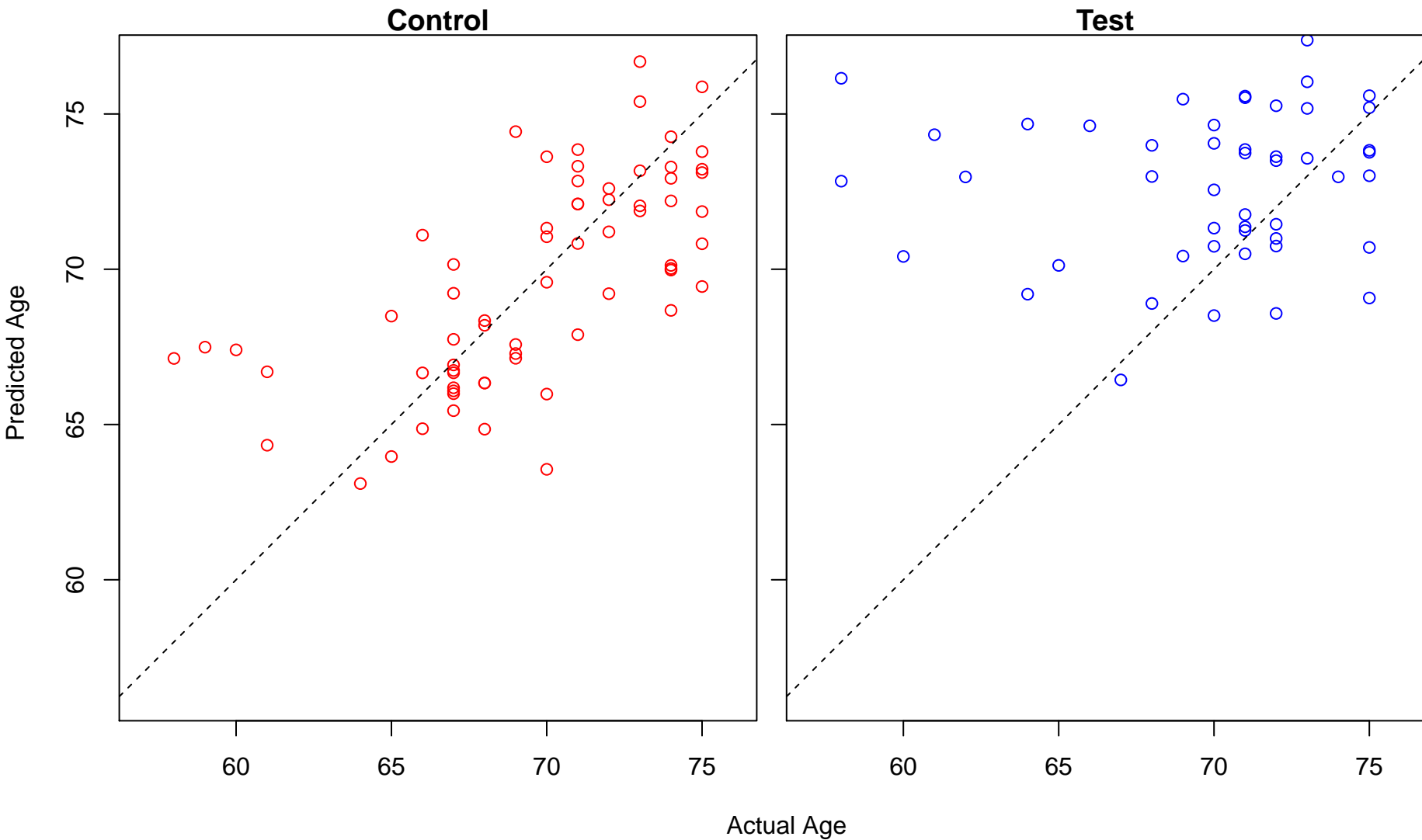
protein transmembrane transport (Score: 1.516635)



regulation of cyclic nucleotide metabolic process (Score: 1.515176)

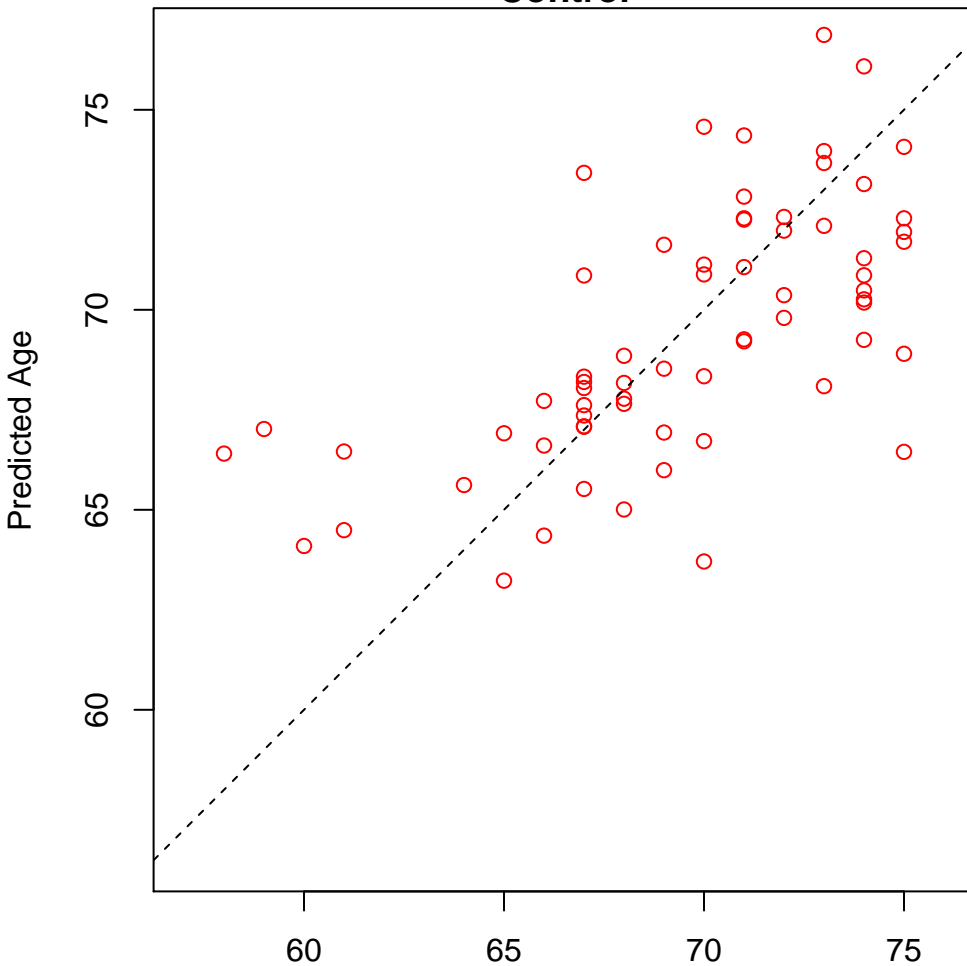


heart development (Score: 1.514992)

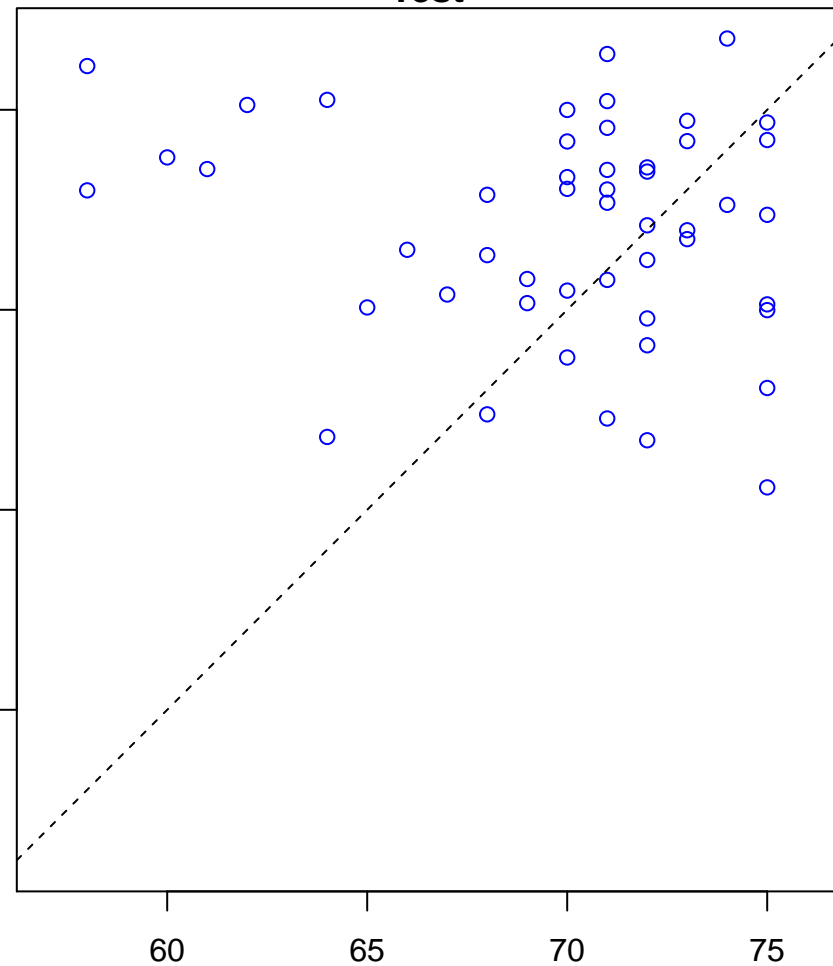


regulation of vacuole organization (Score: 1.514785)

Control

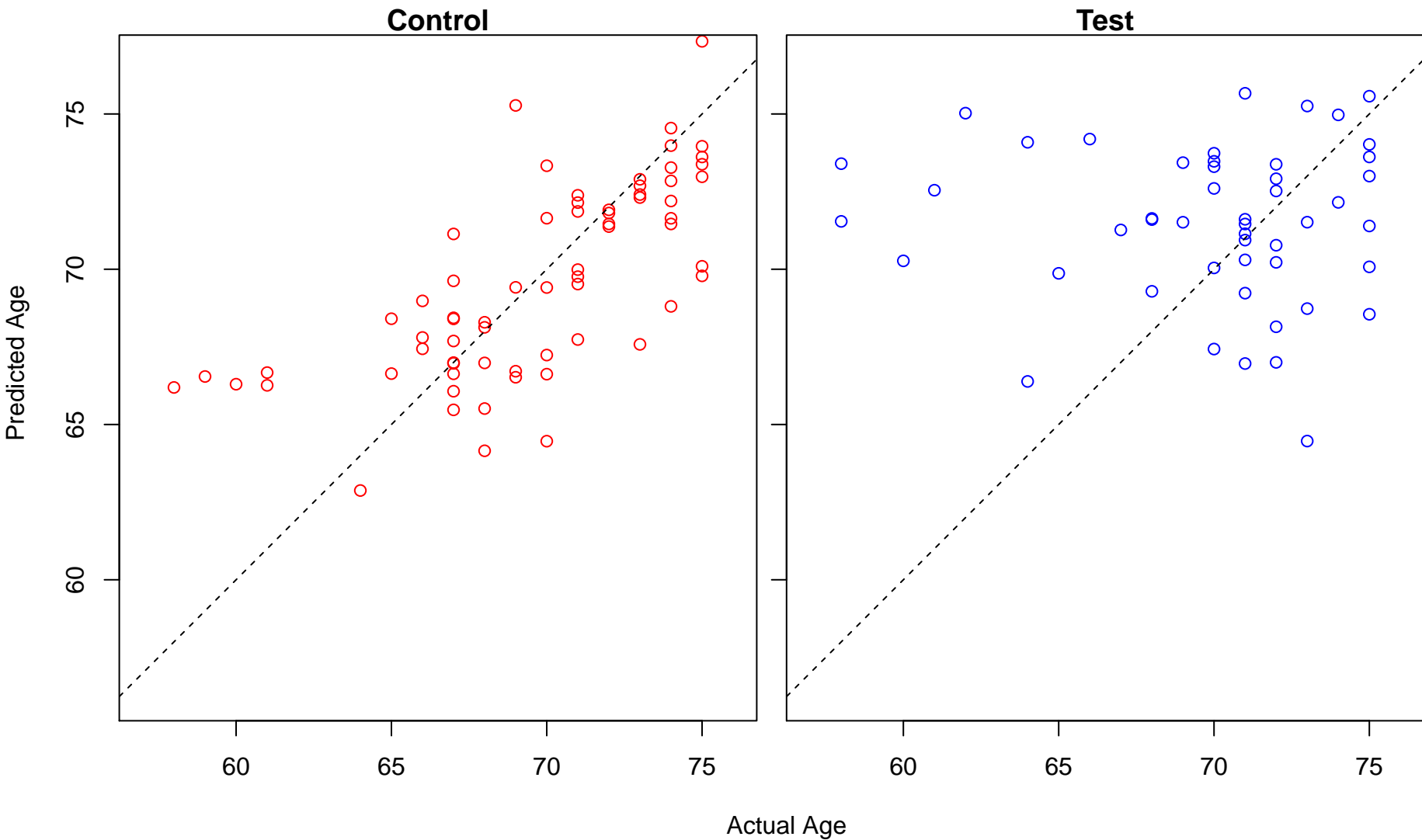


Test

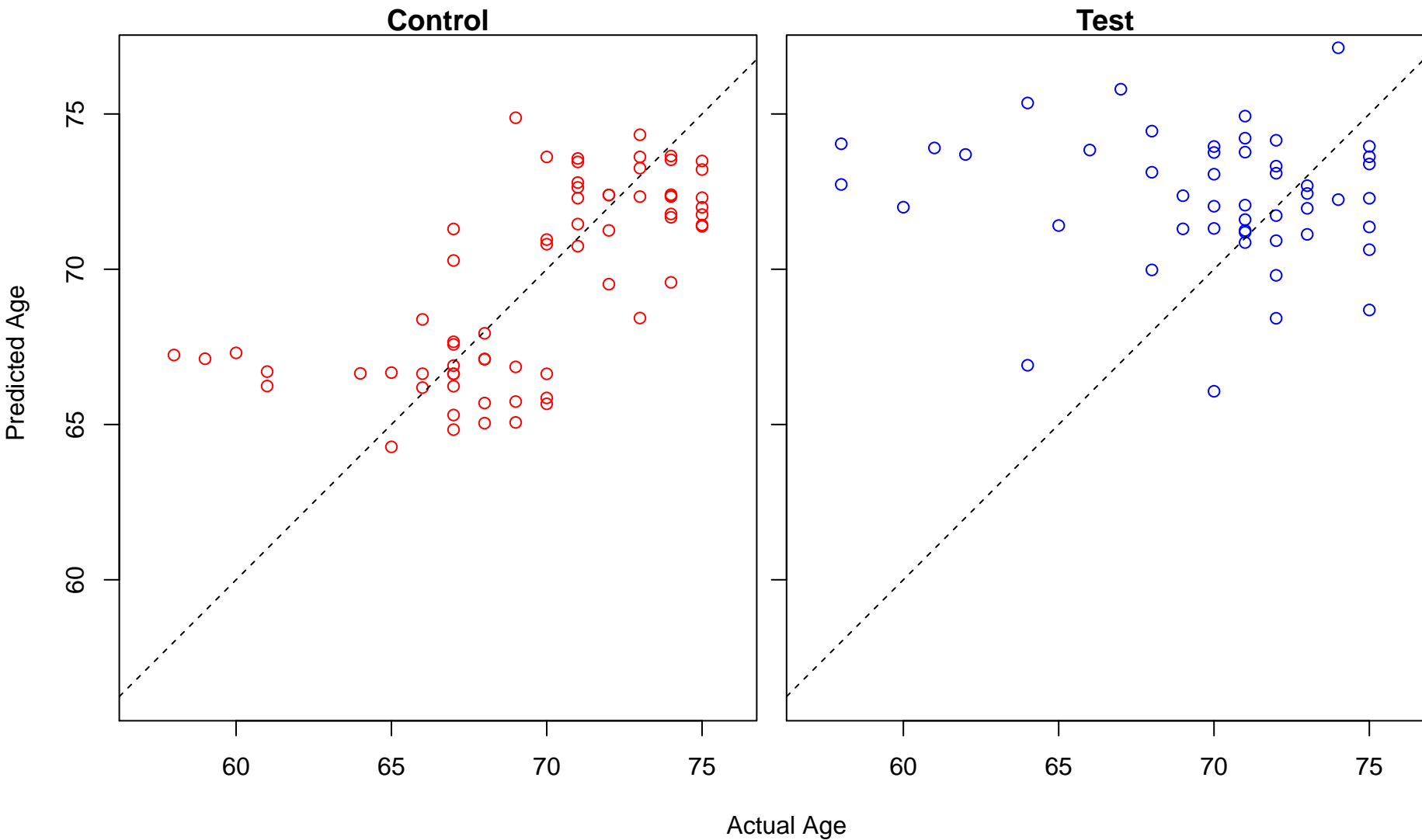


Actual Age

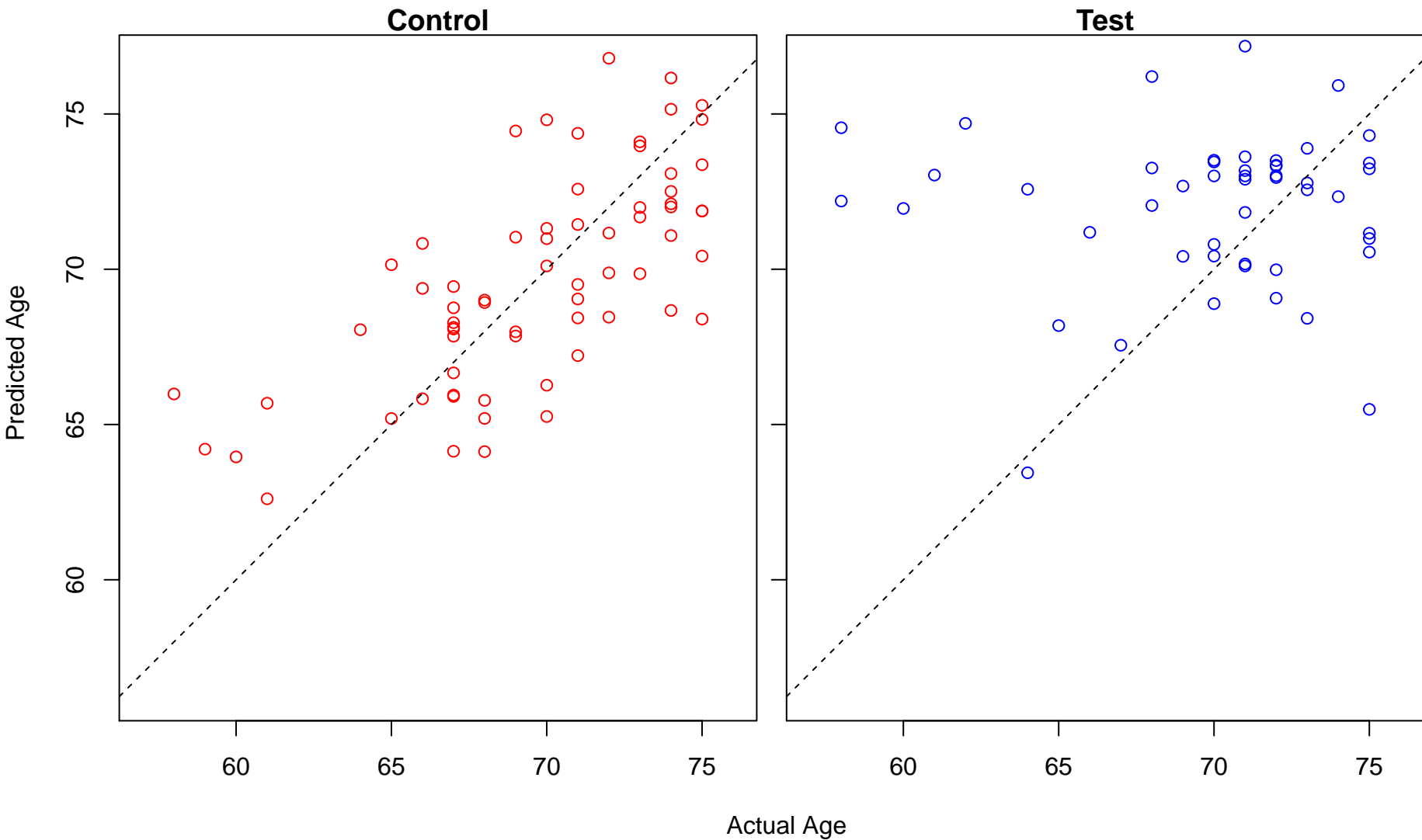
regulation by virus of viral protein levels in host cell (Score: 1.514719)



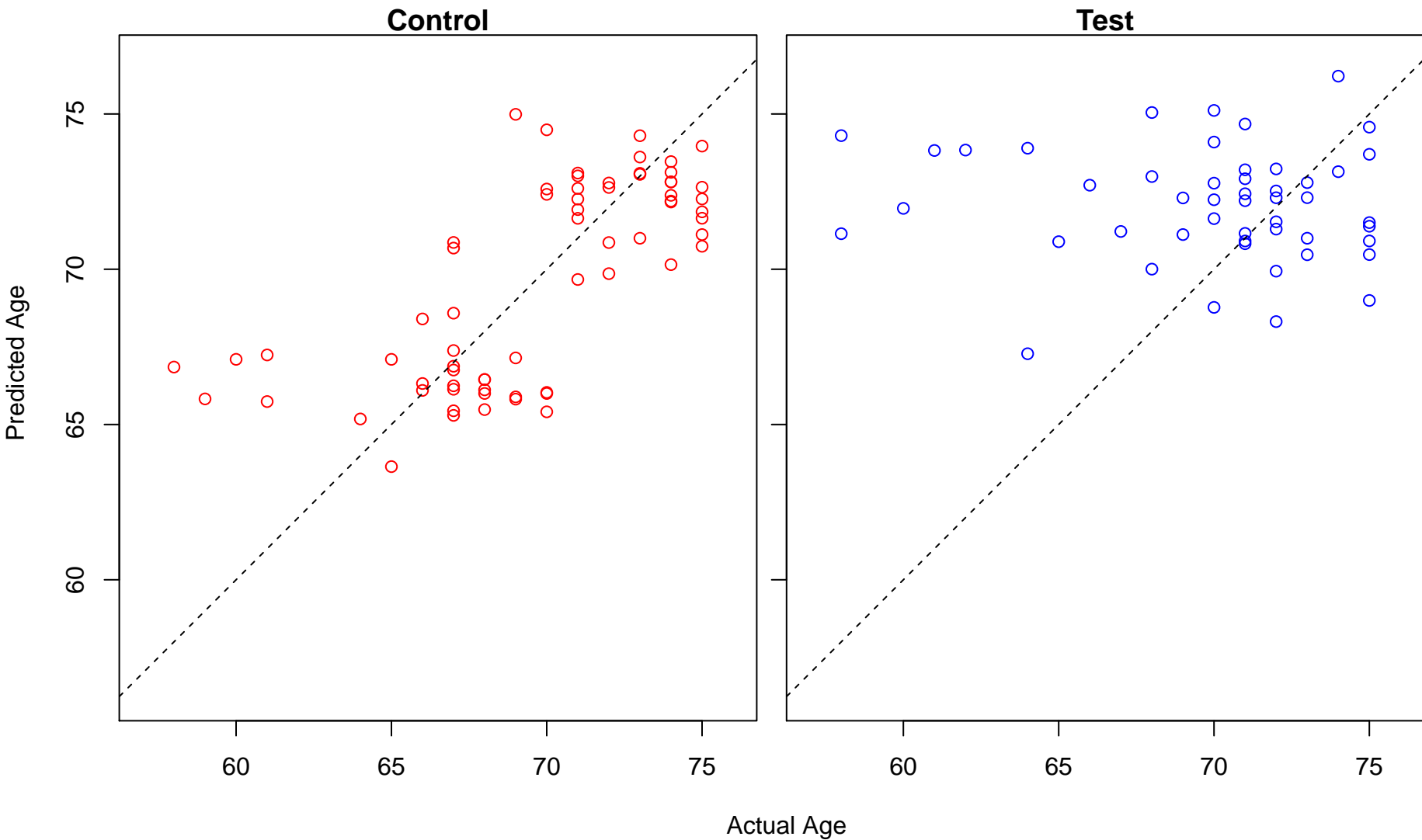
positive regulation of smooth muscle cell proliferation (Score: 1.514591)



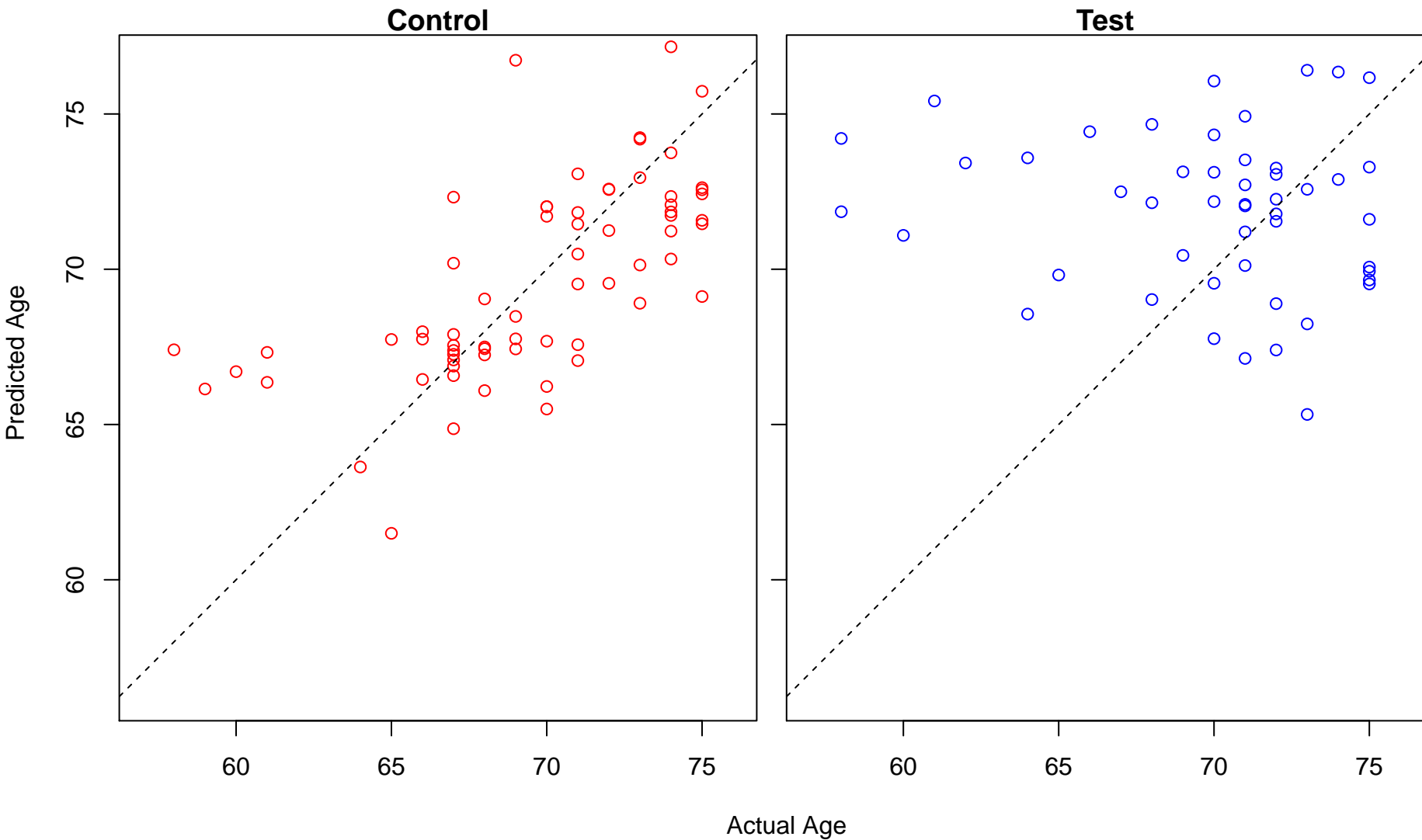
T cell mediated immunity (Score: 1.514055)



negative regulation of transferase activity (Score: 1.513866)

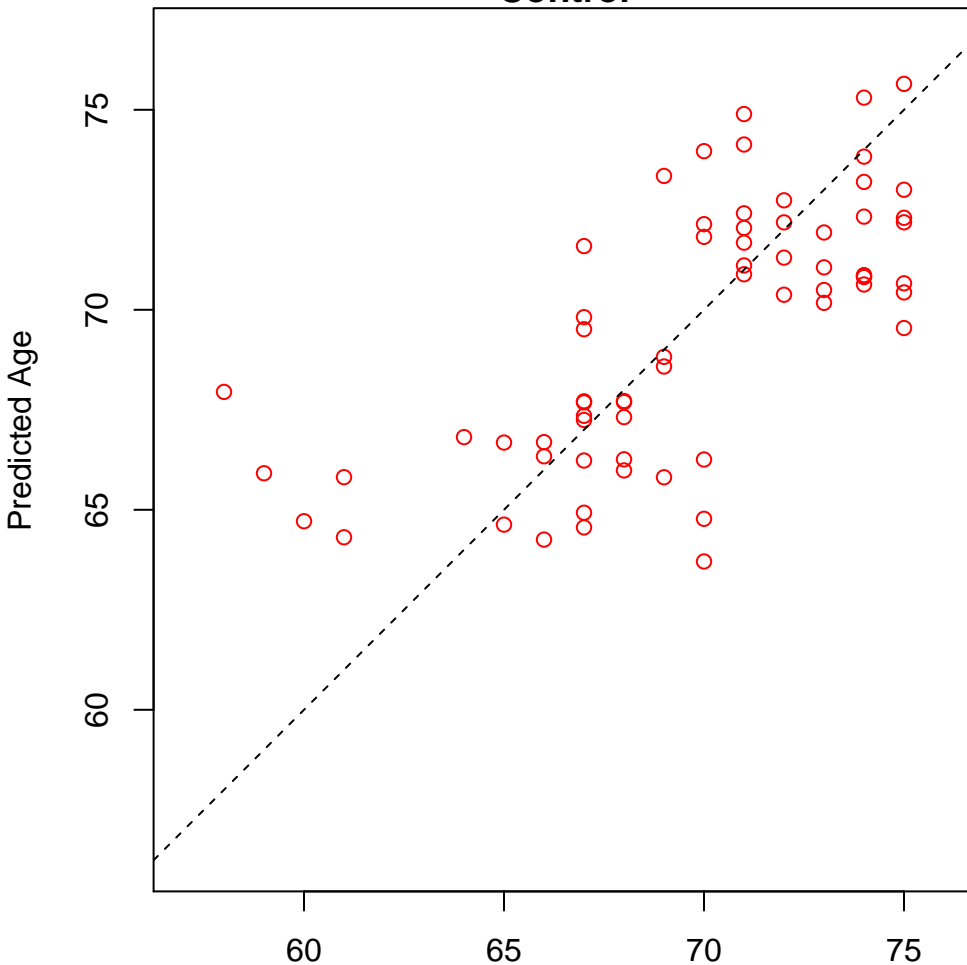


negative regulation of type I interferon production (Score: 1.513013)

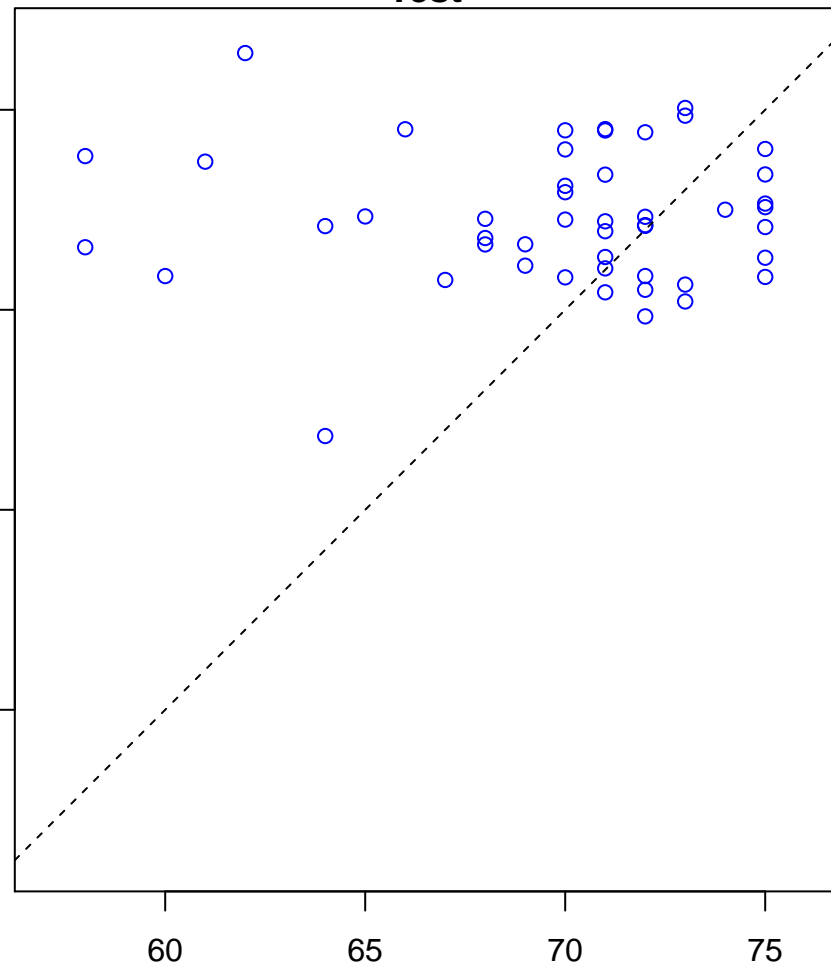


regulation of anatomical structure size (Score: 1.512913)

Control

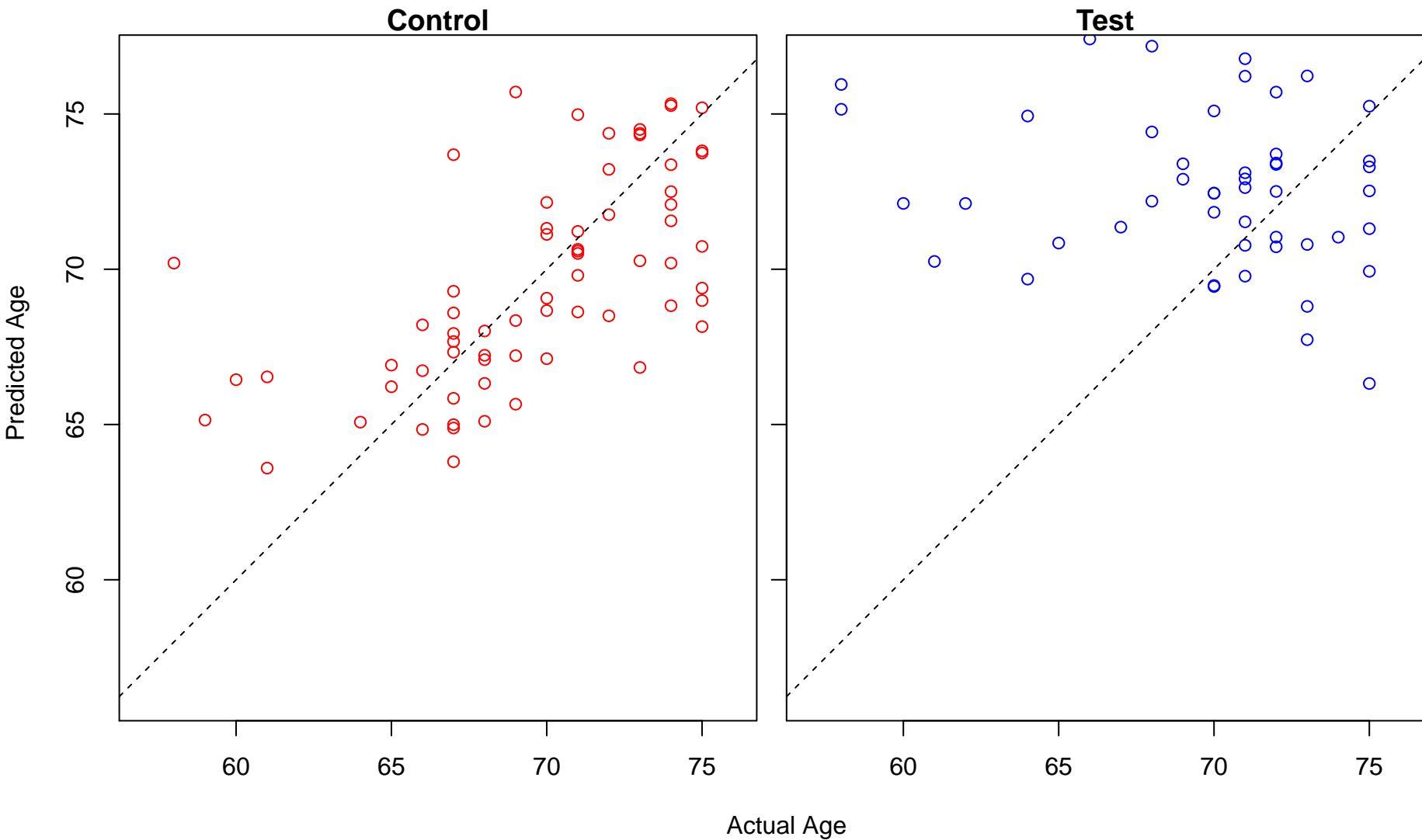


Test

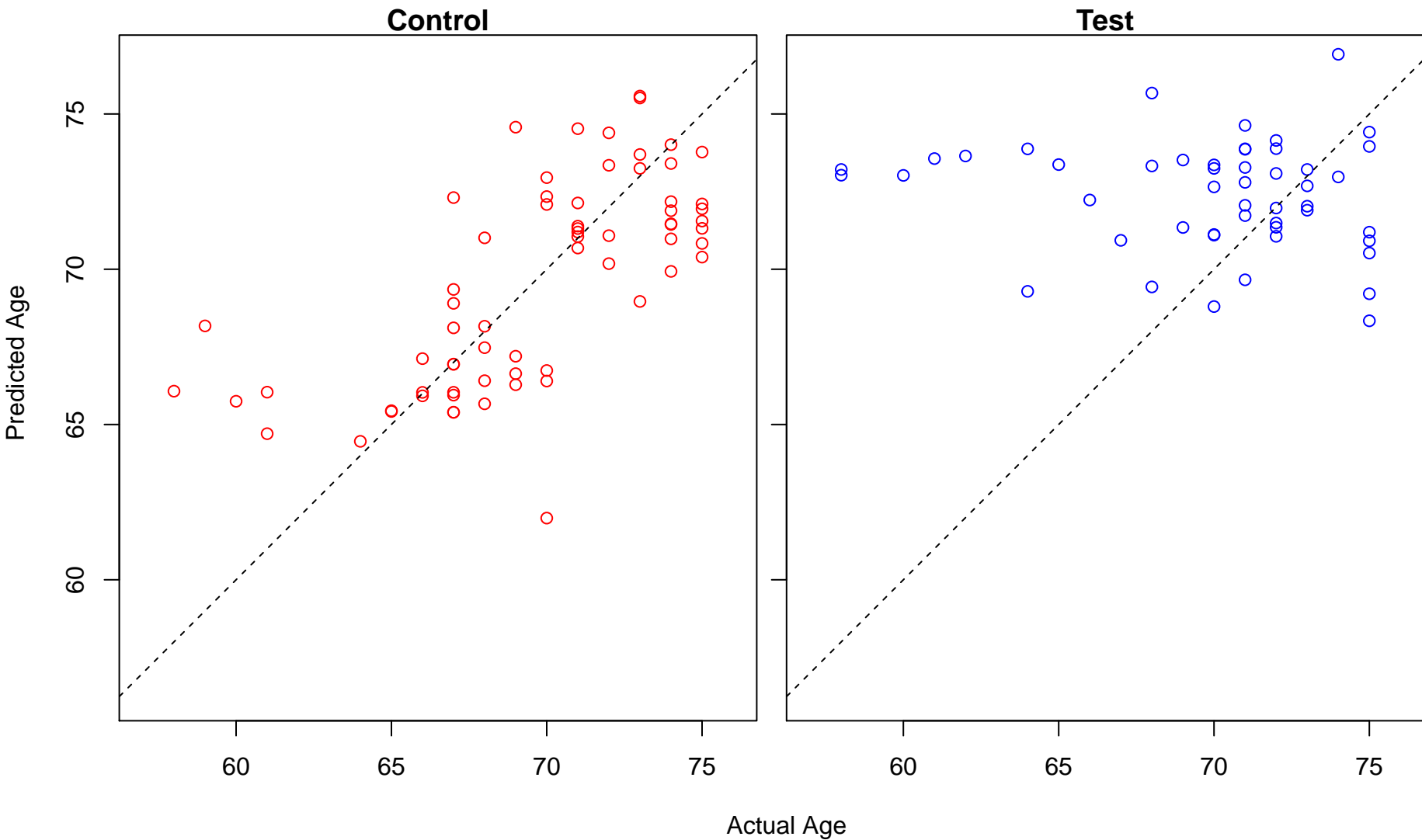


Actual Age

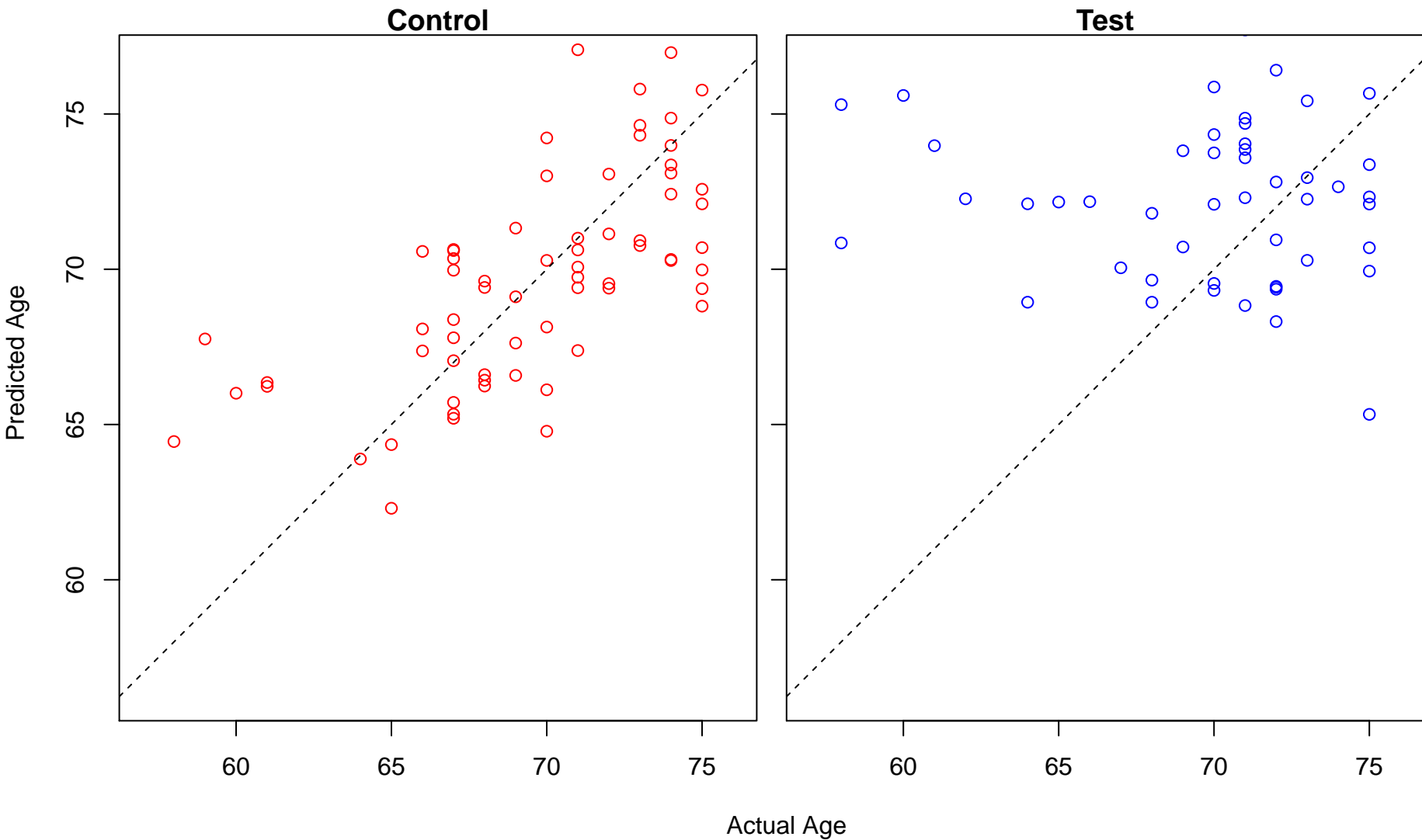
response to metal ion (Score: 1.512828)



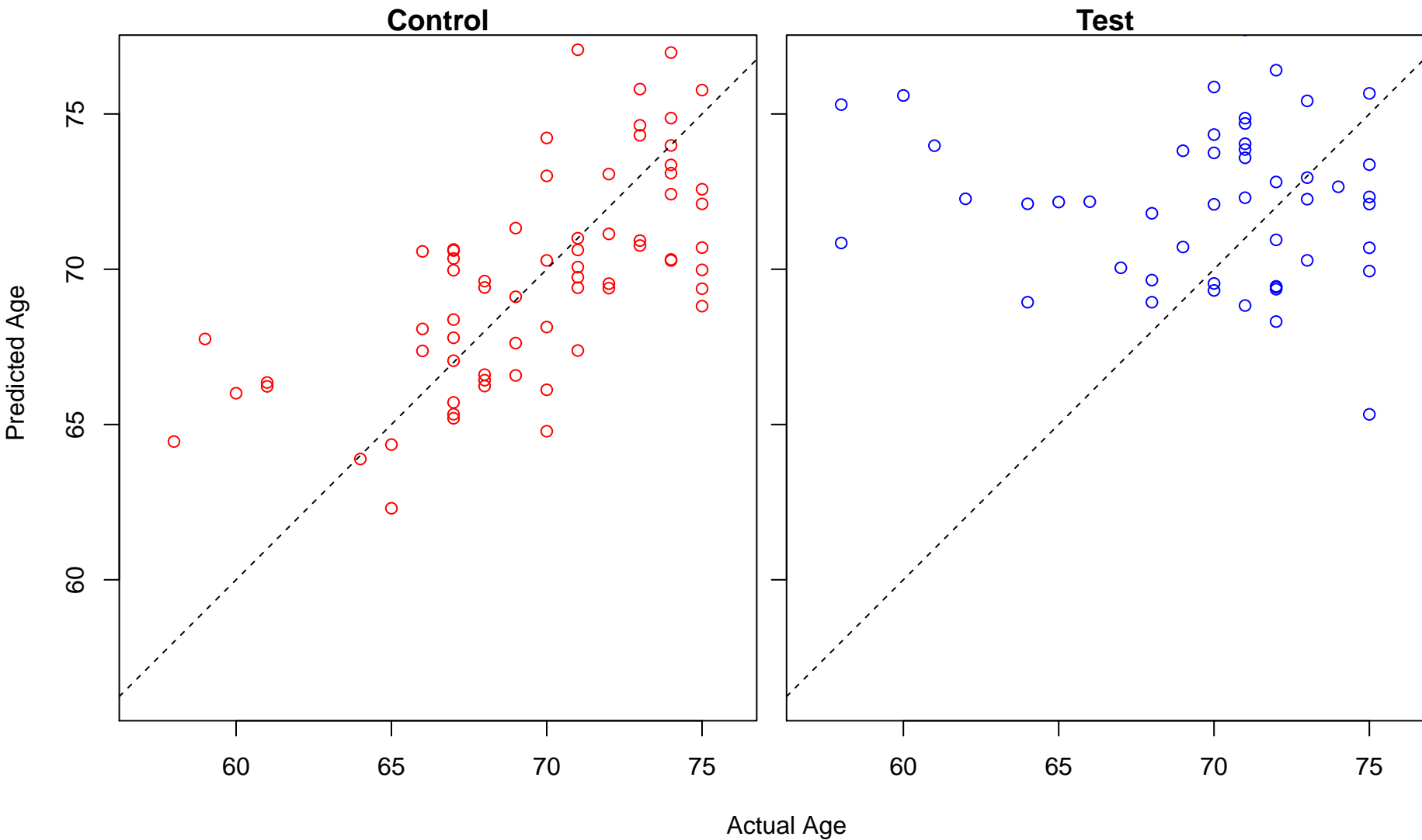
negative regulation of protein catabolic process (Score: 1.512781)



positive regulation of response to extracellular stimulus (Score: 1.512565)

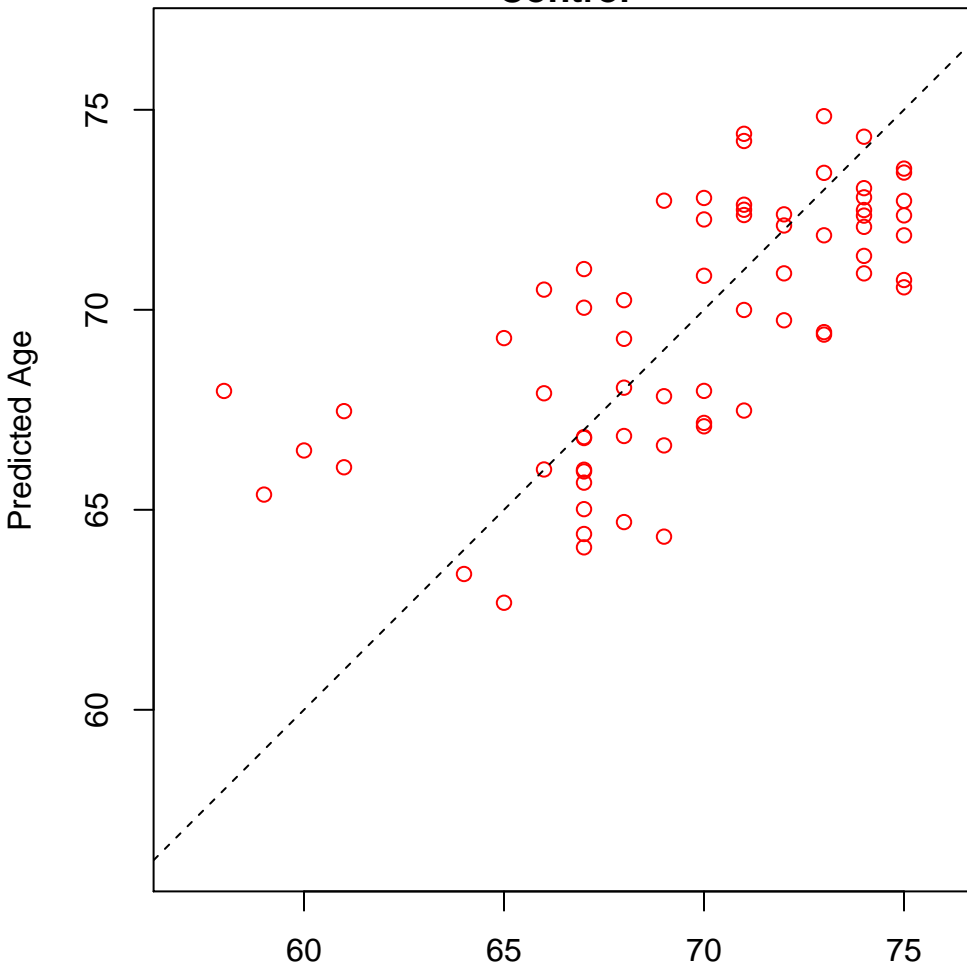


positive regulation of response to nutrient levels (Score: 1.512565)

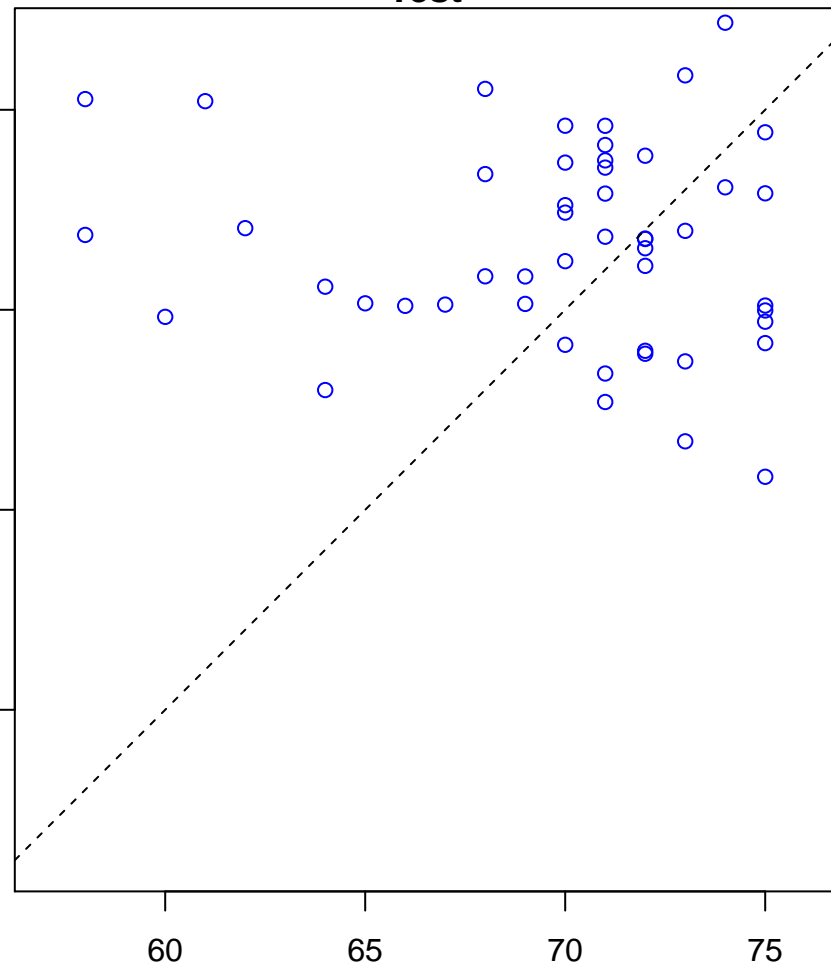


regulation of interferon-beta production (Score: 1.512498)

Control

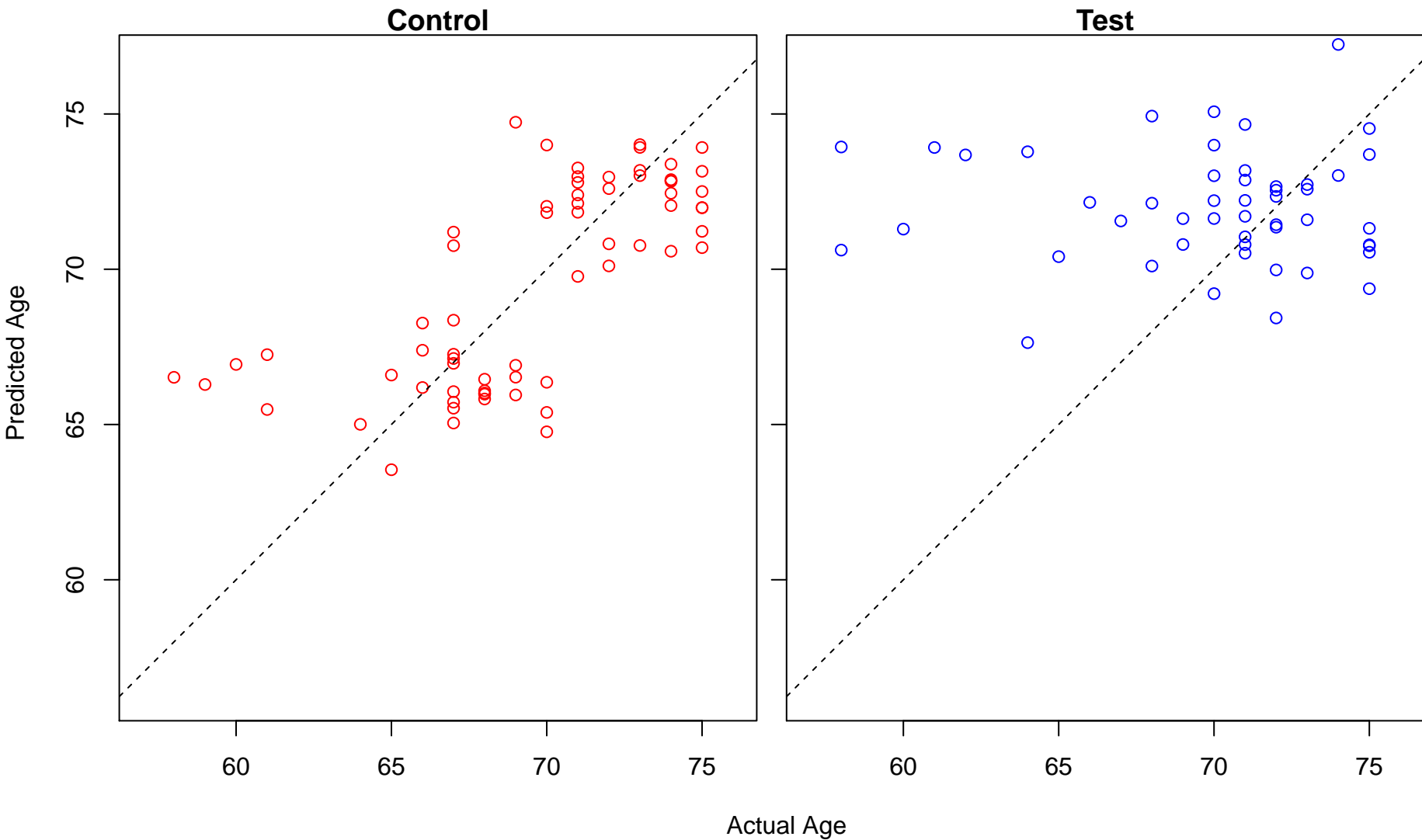


Test

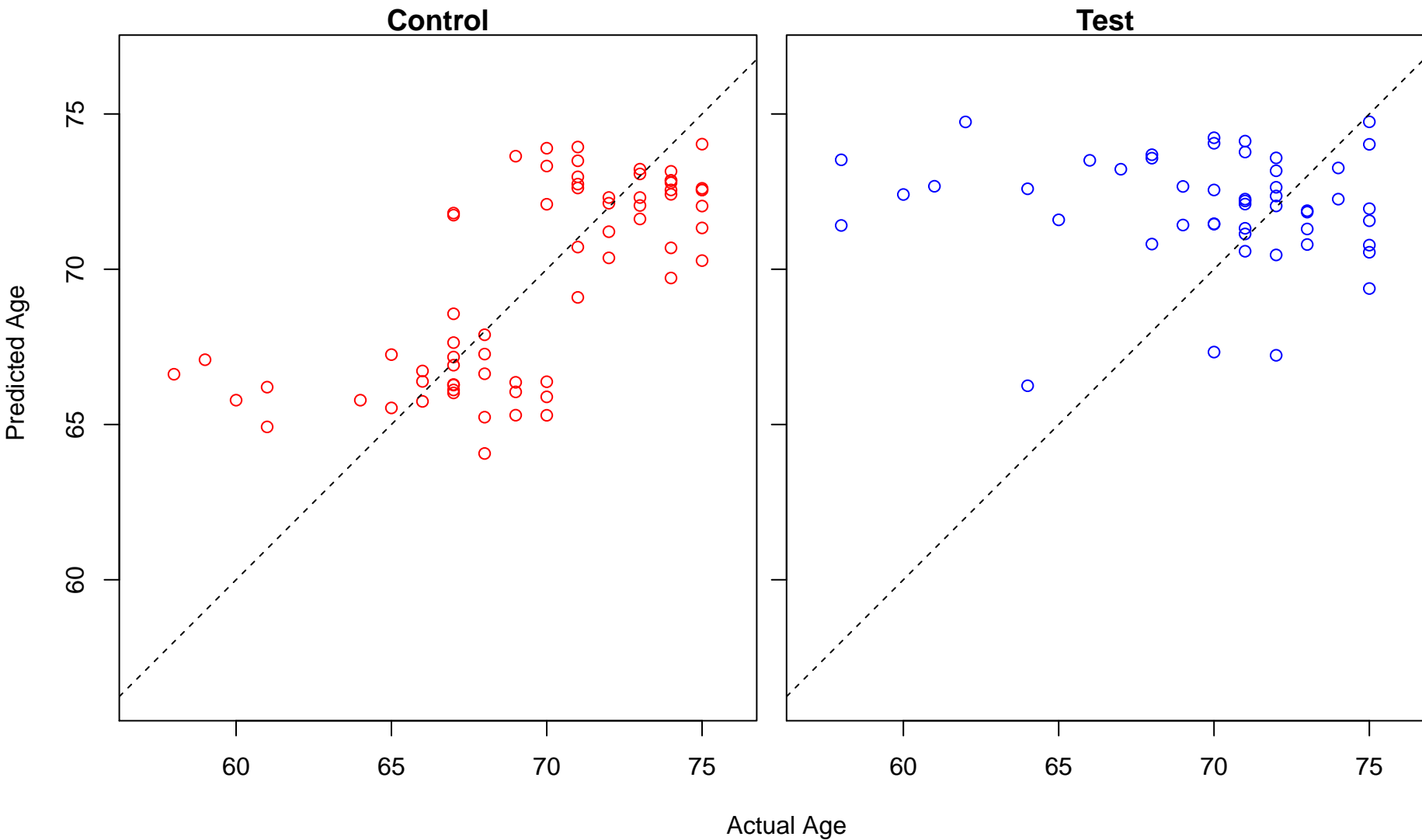


Actual Age

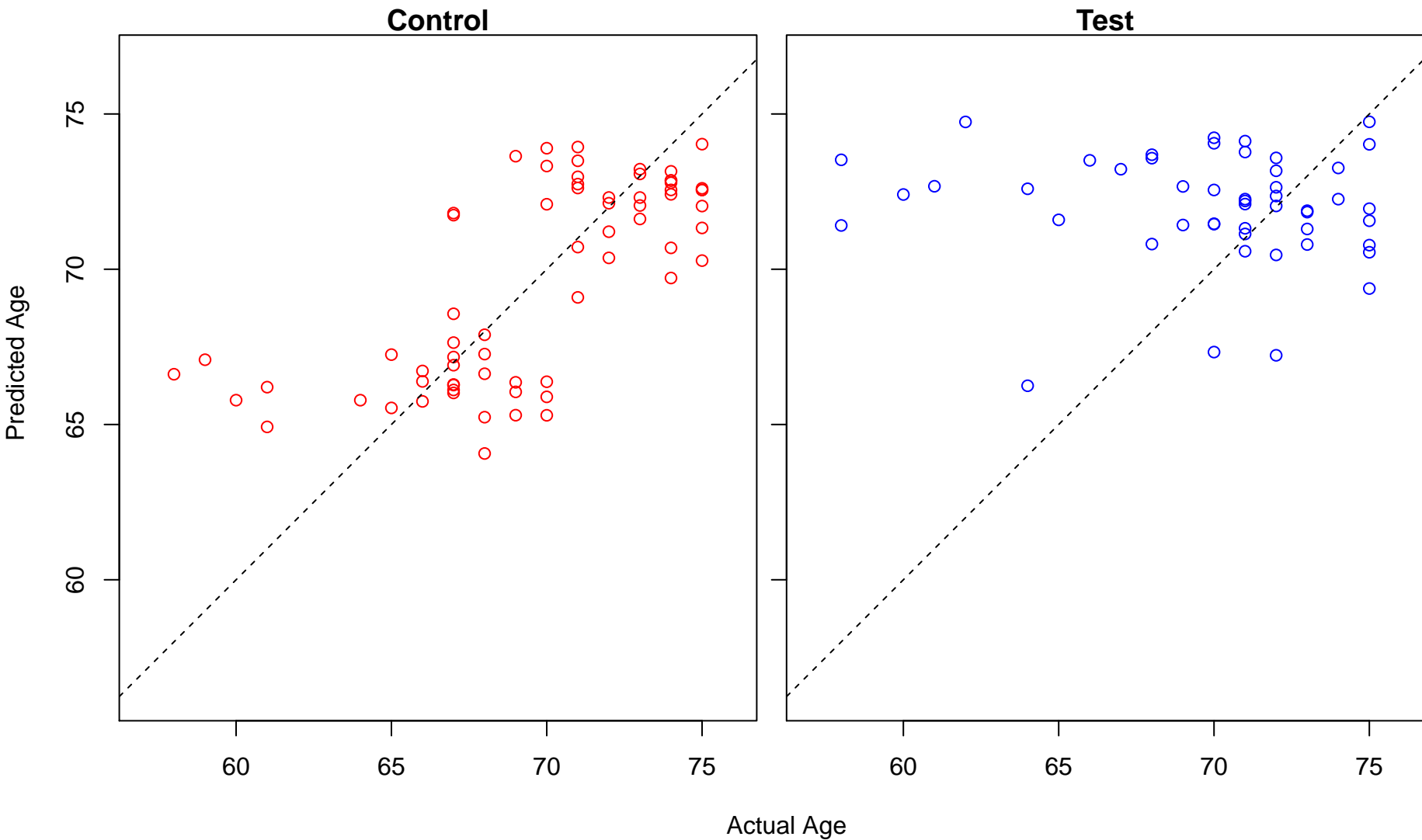
proteasome-mediated ubiquitin-dependent protein catabolic process (Score: 1.512453)



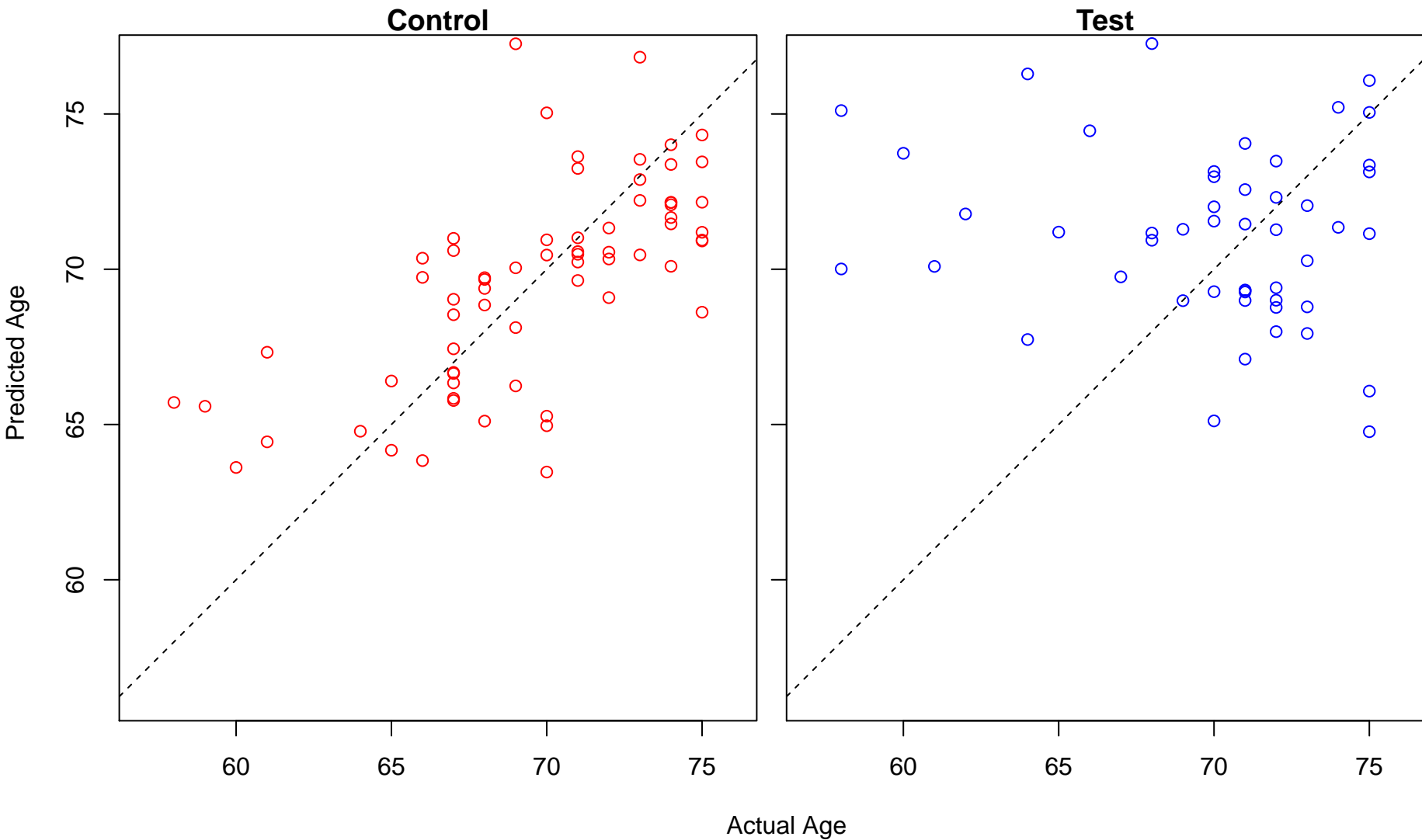
histone lysine methylation (Score: 1.512003)



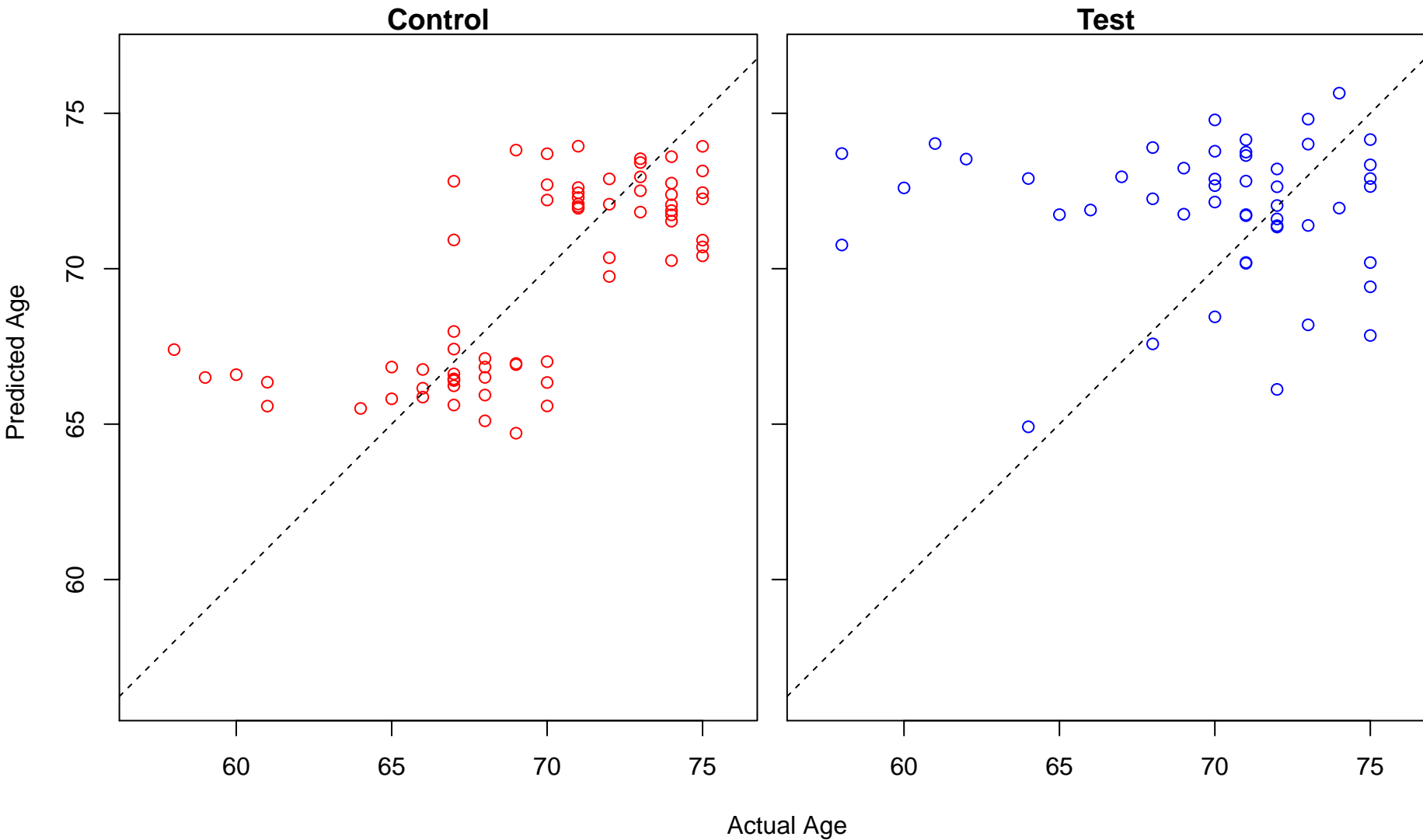
peptidyl-lysine methylation (Score: 1.512003)



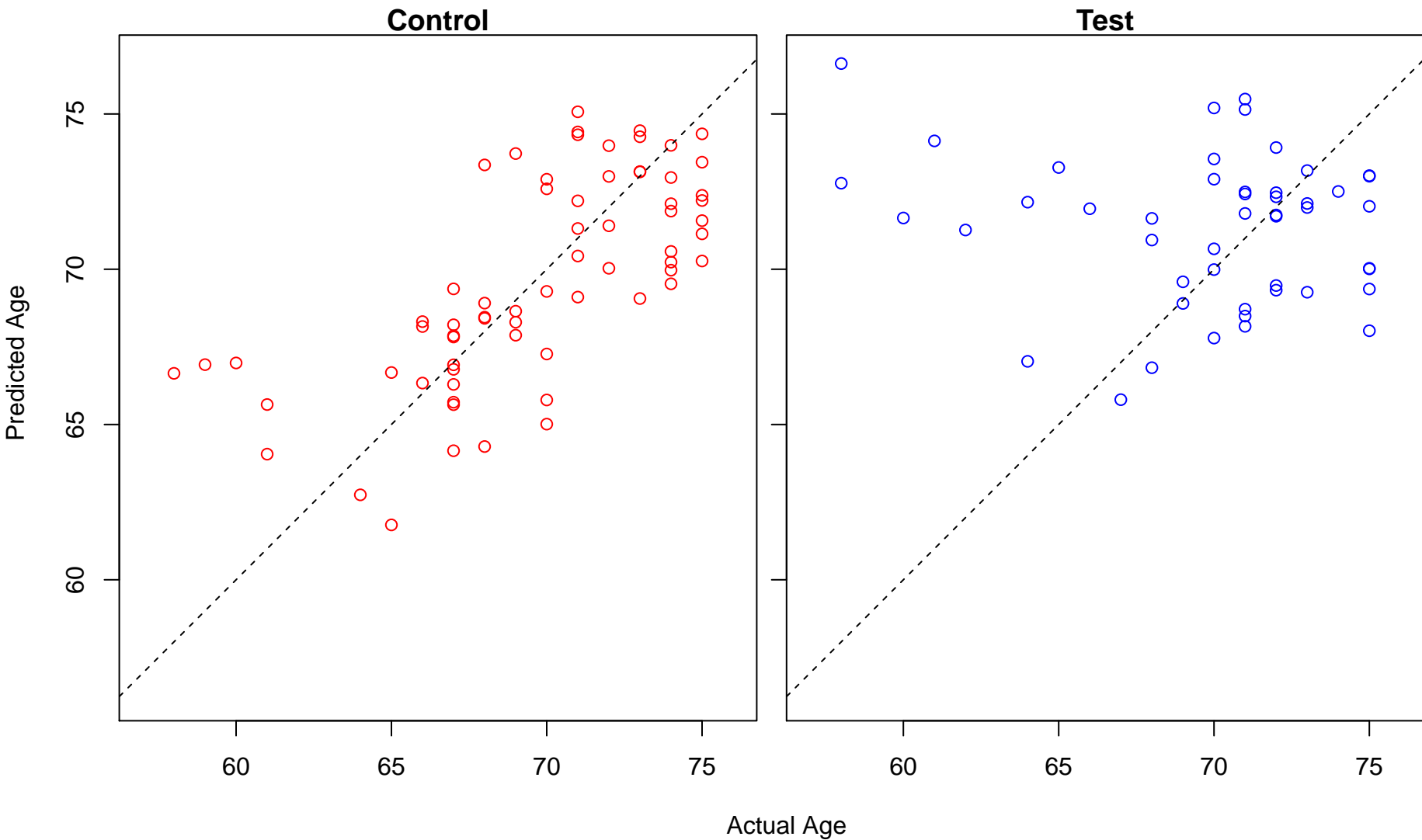
B cell activation involved in immune response (Score: 1.511763)



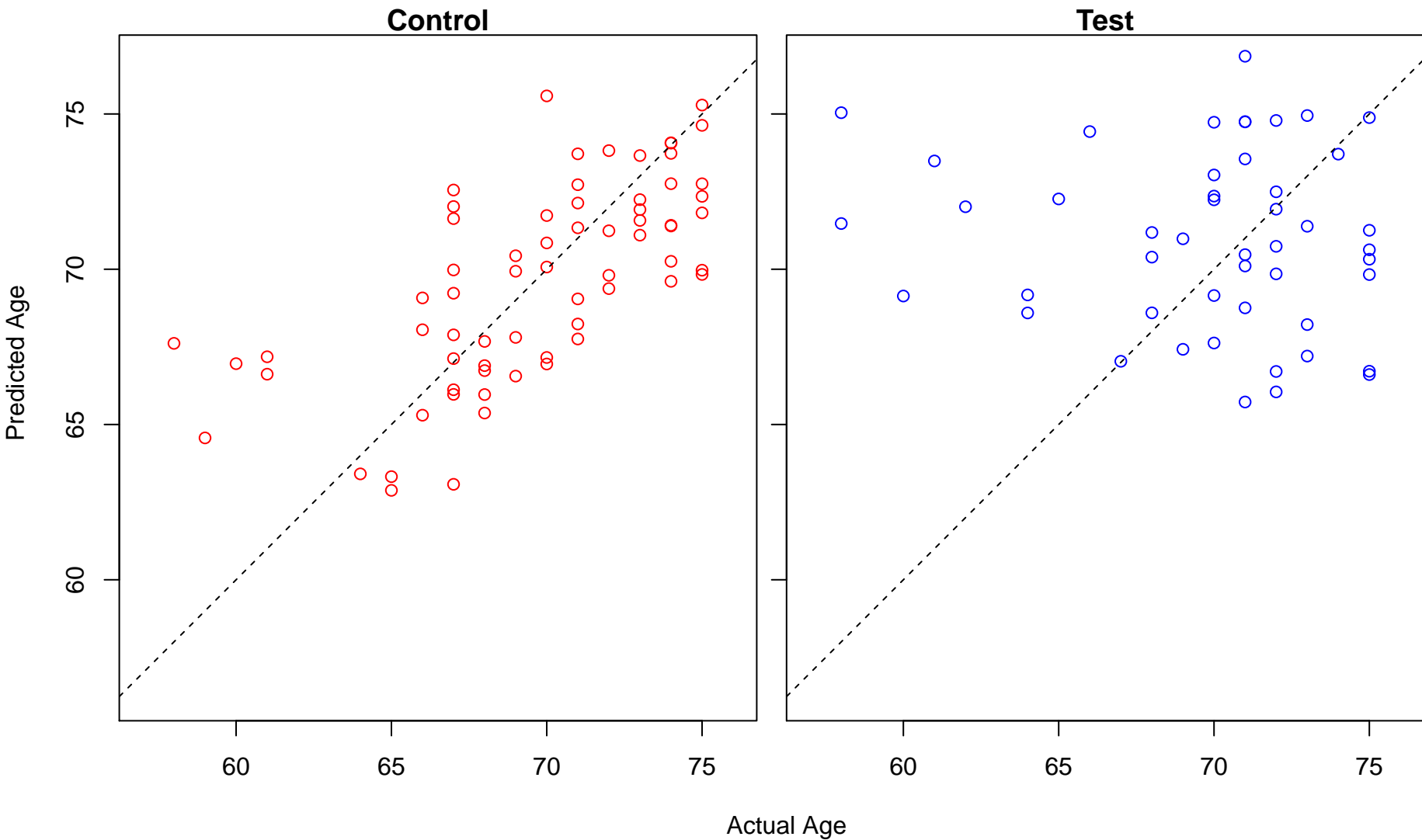
alternative mRNA splicing, via spliceosome (Score: 1.511705)



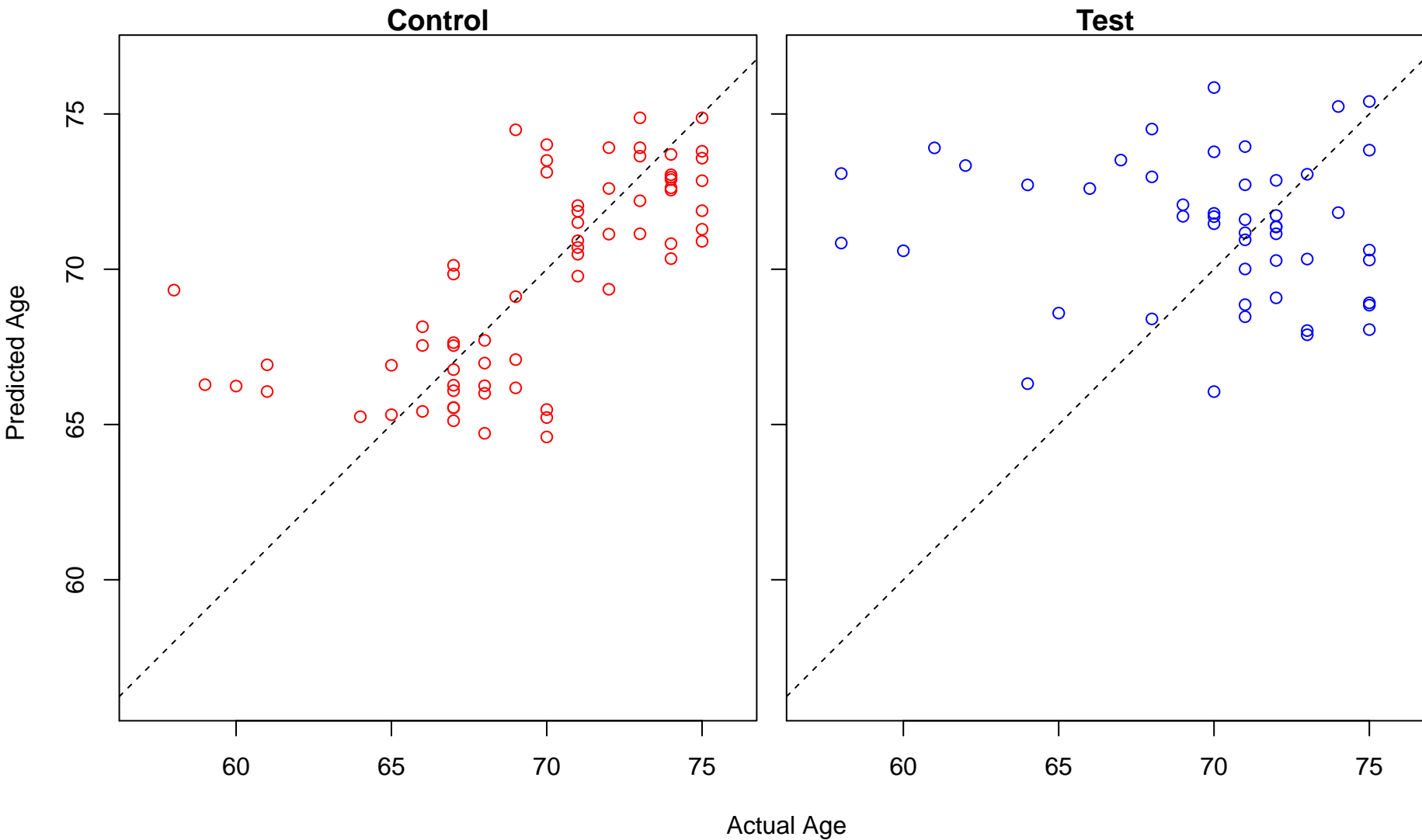
nuclear envelope organization (Score: 1.511630)



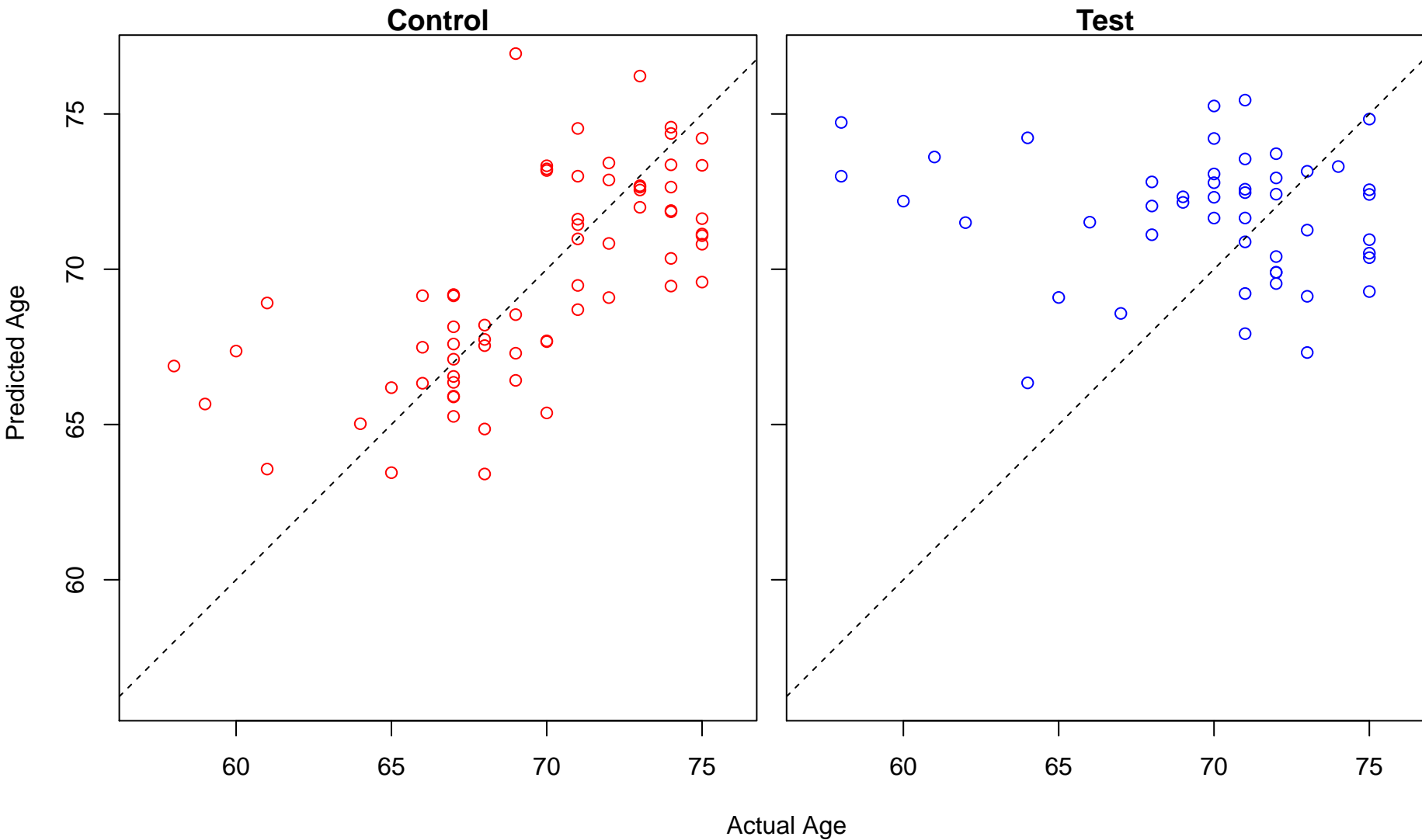
positive regulation of cell junction assembly (Score: 1.510121)



defense response to bacterium (Score: 1.510076)

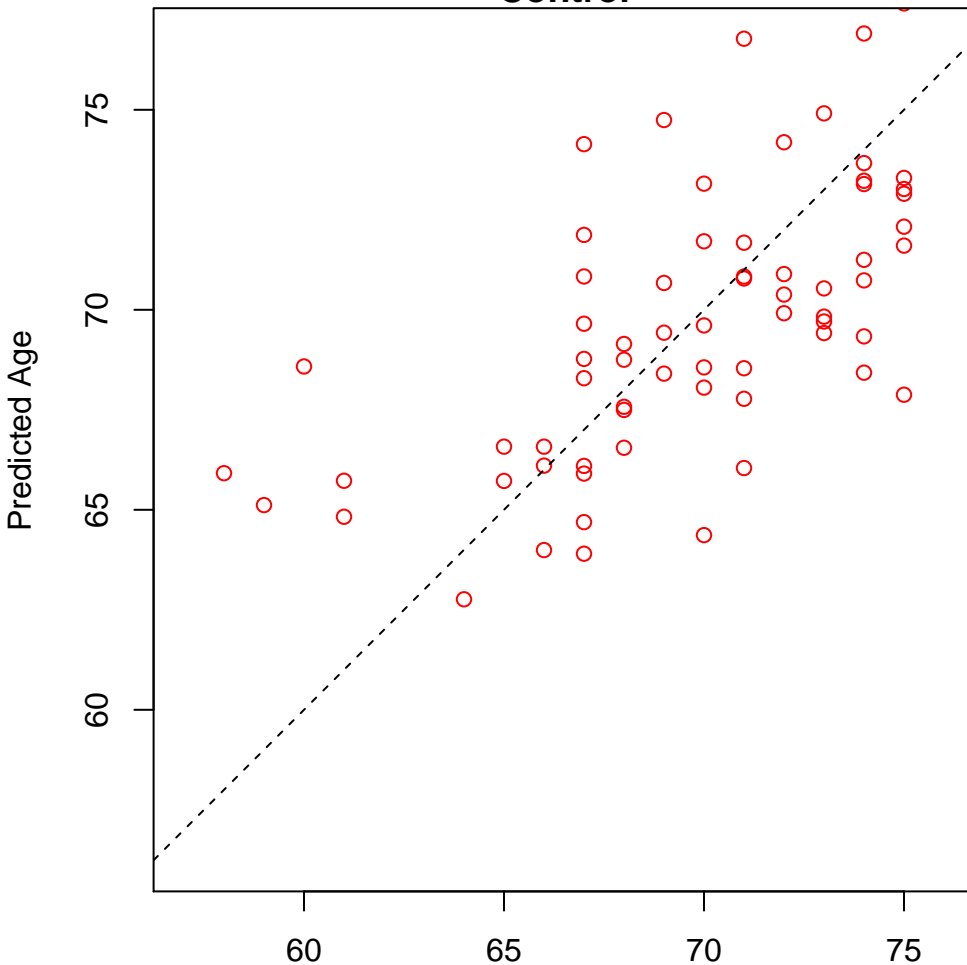


multi-organism reproductive process (Score: 1.509588)

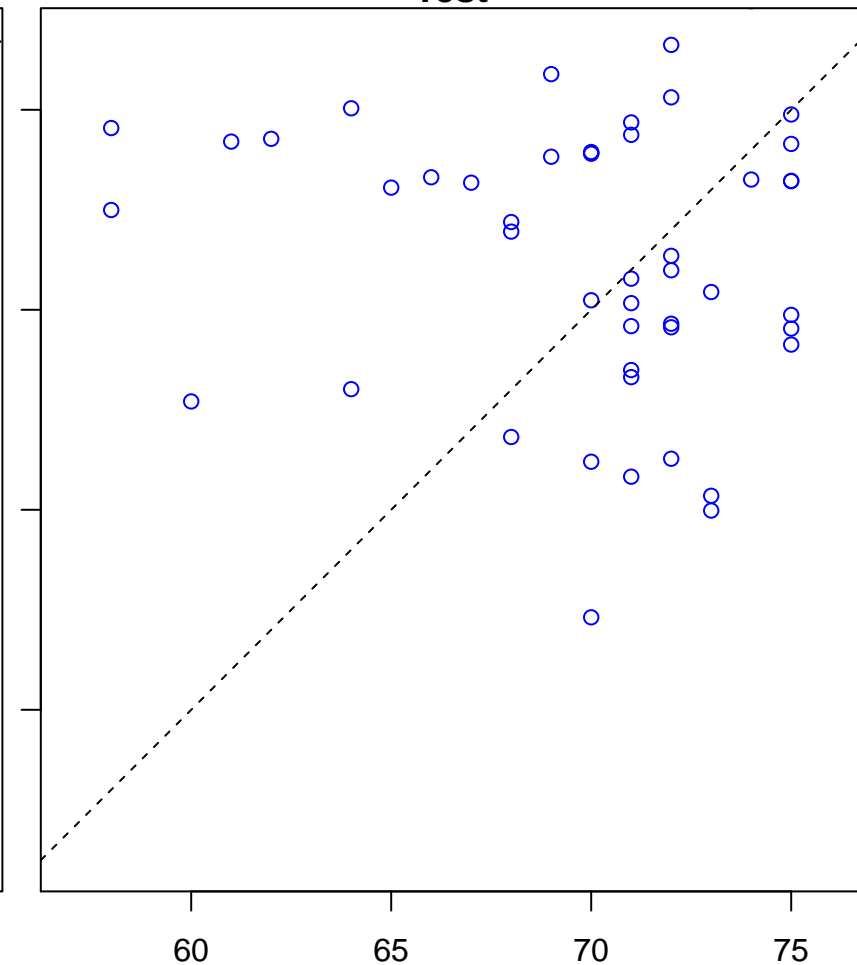


response to exogenous dsRNA (Score: 1.509355)

Control

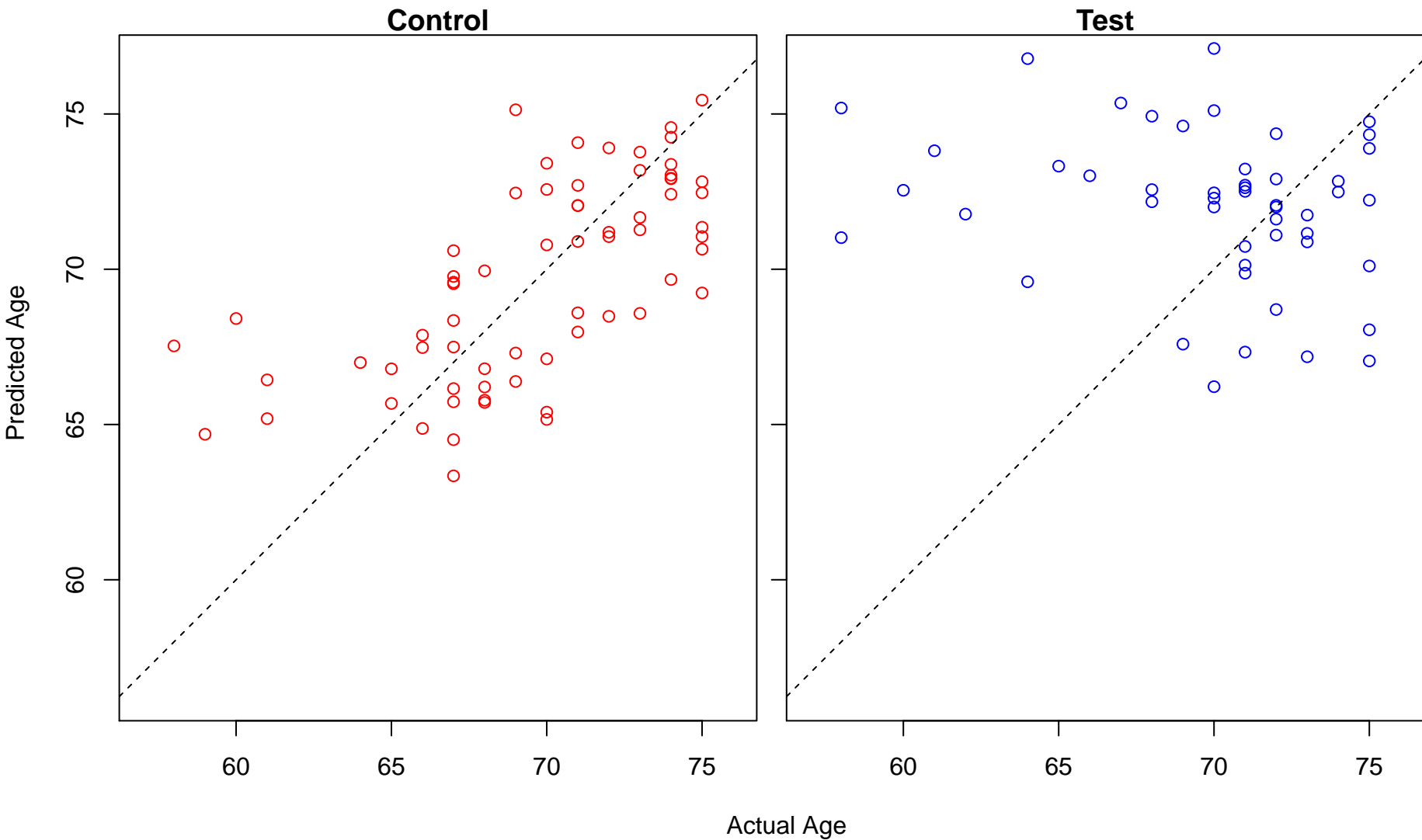


Test

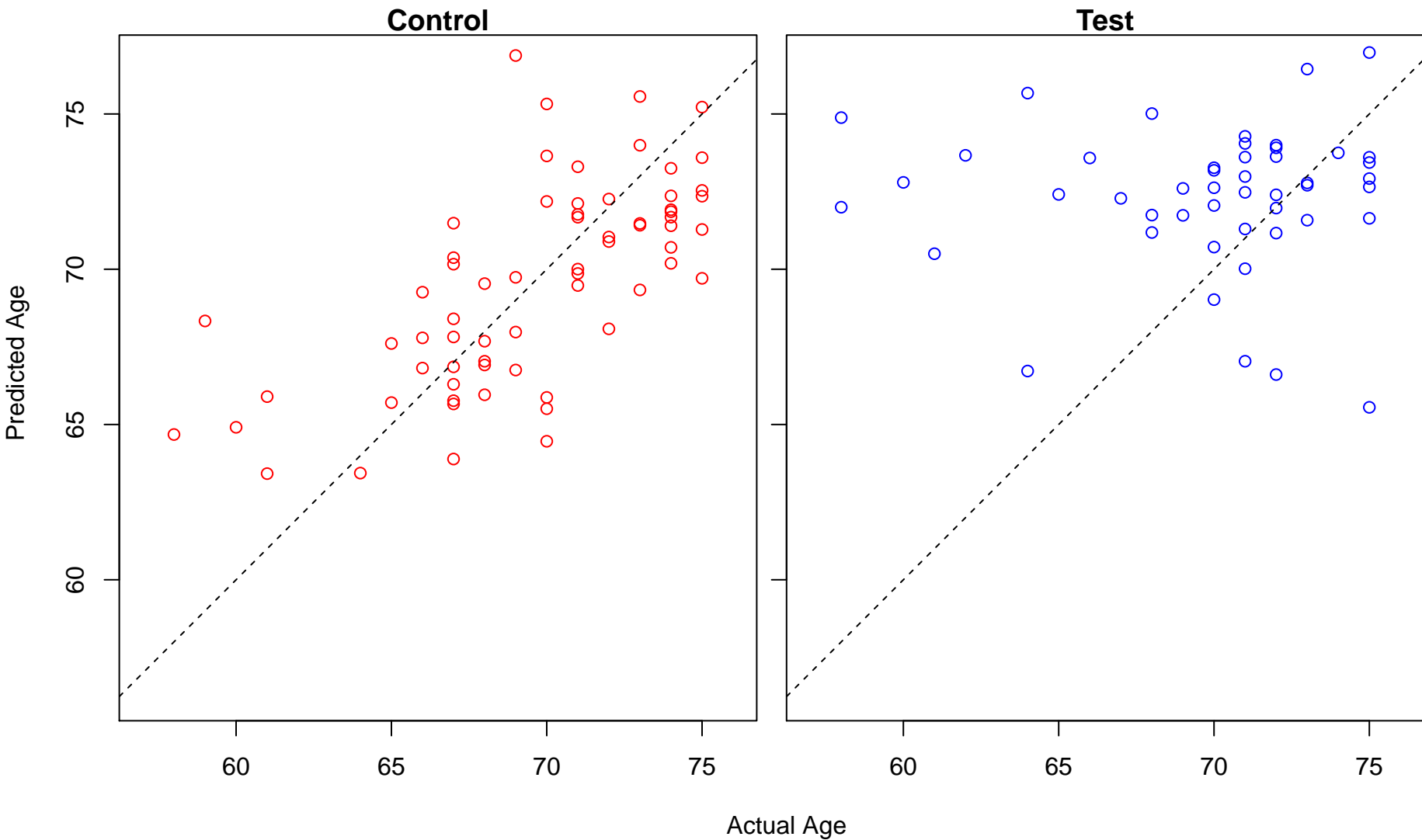


Actual Age

positive regulation of Notch signaling pathway (Score: 1.509272)

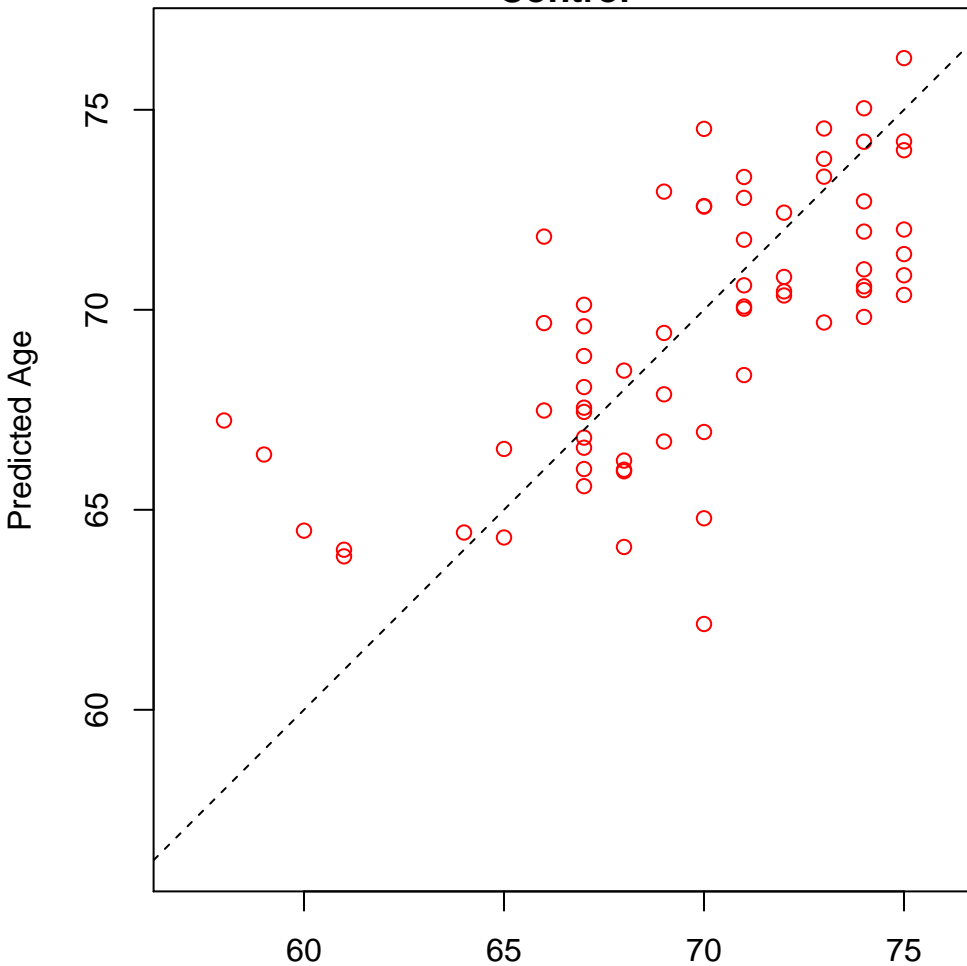


MyD88-dependent toll-like receptor signaling pathway (Score: 1.507476)

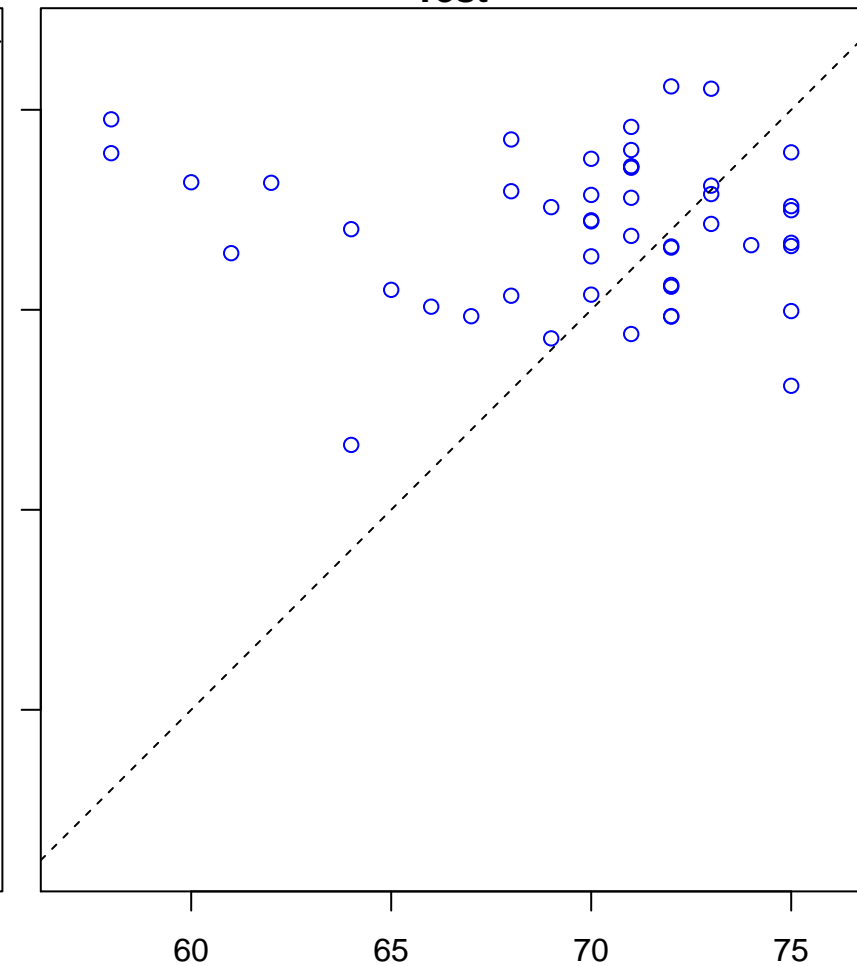


post-Golgi vesicle-mediated transport (Score: 1.507260)

Control

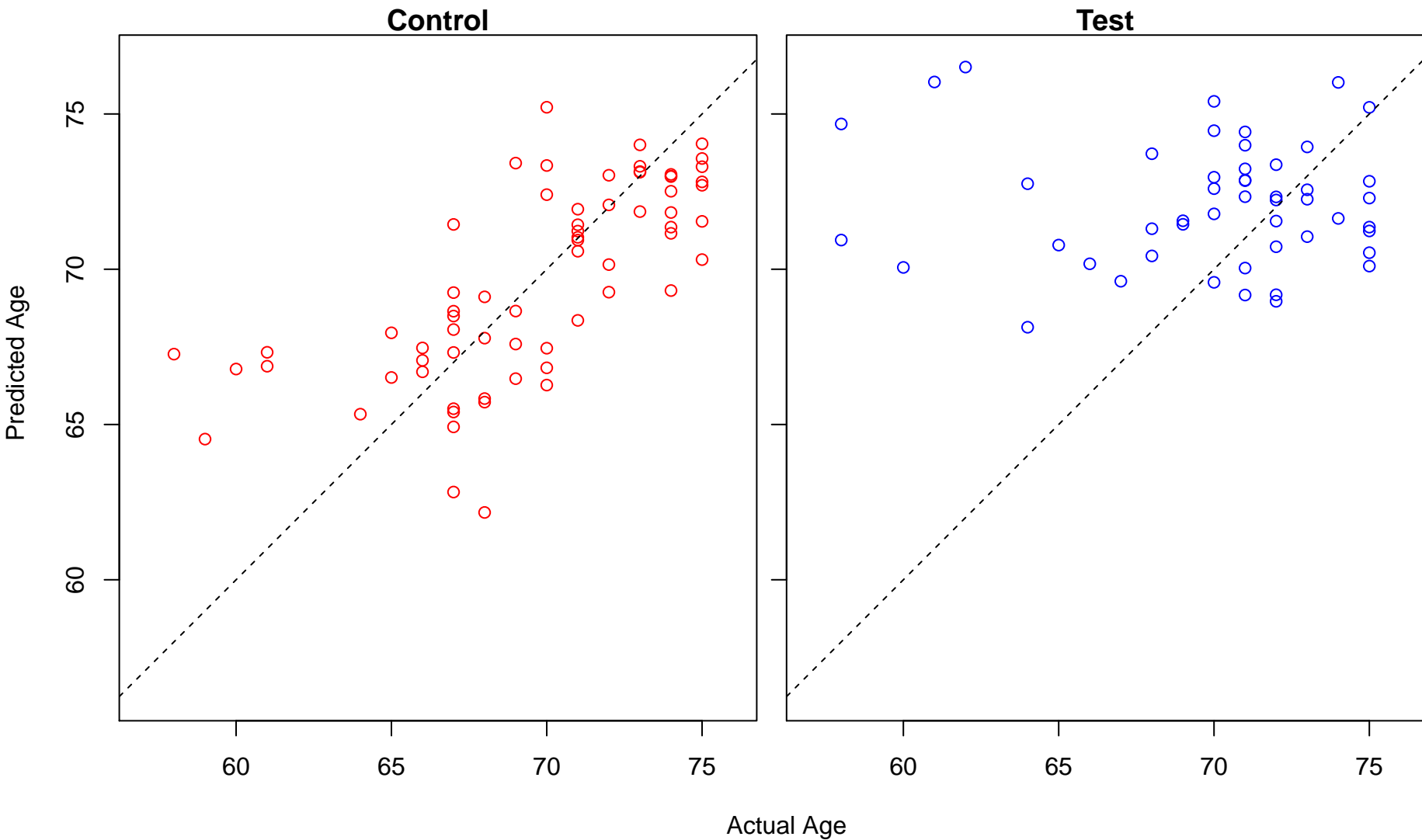


Test

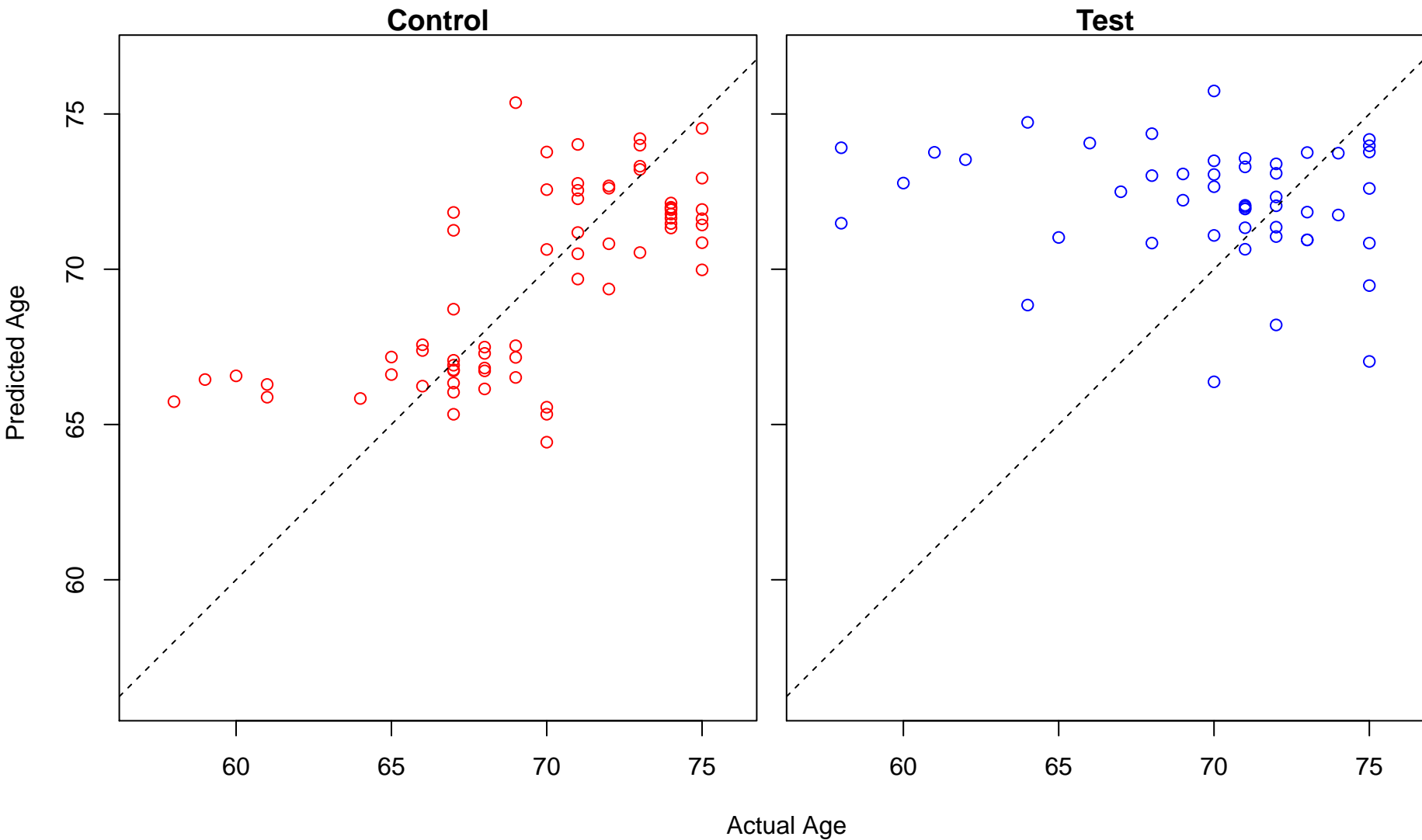


Actual Age

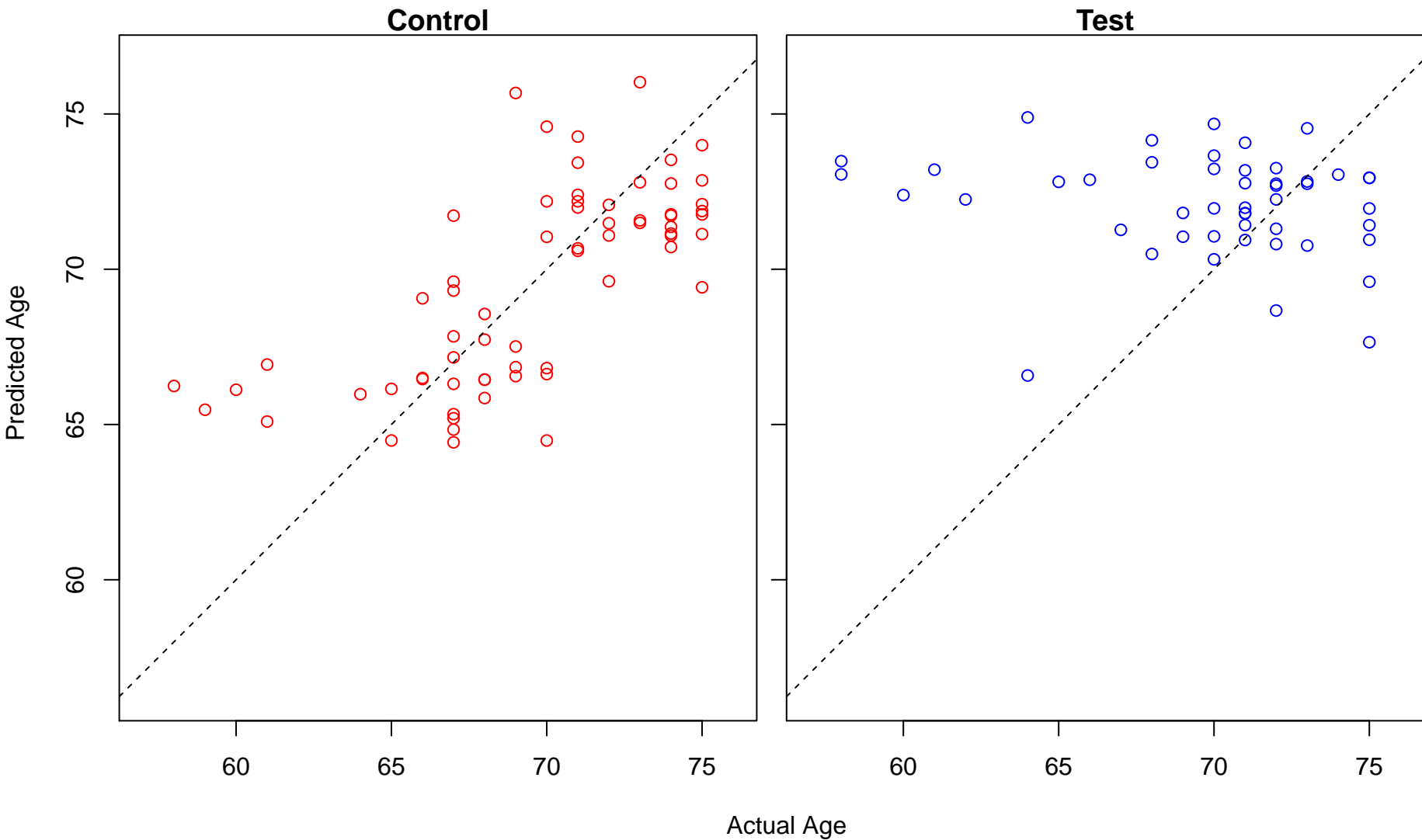
response to alcohol (Score: 1.507254)



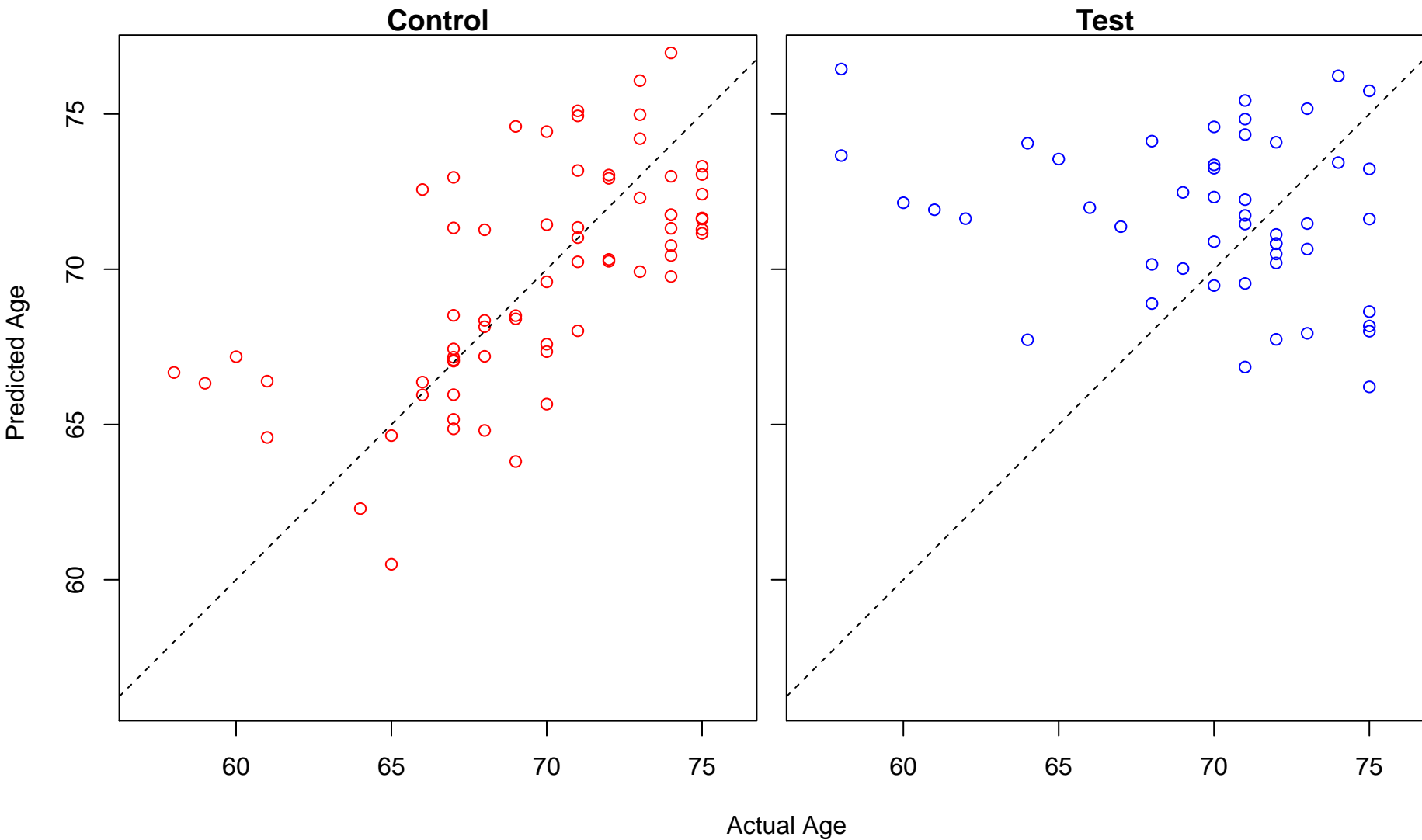
regulation of peptidyl-serine phosphorylation (Score: 1.507161)



positive regulation of telomere maintenance (Score: 1.507007)

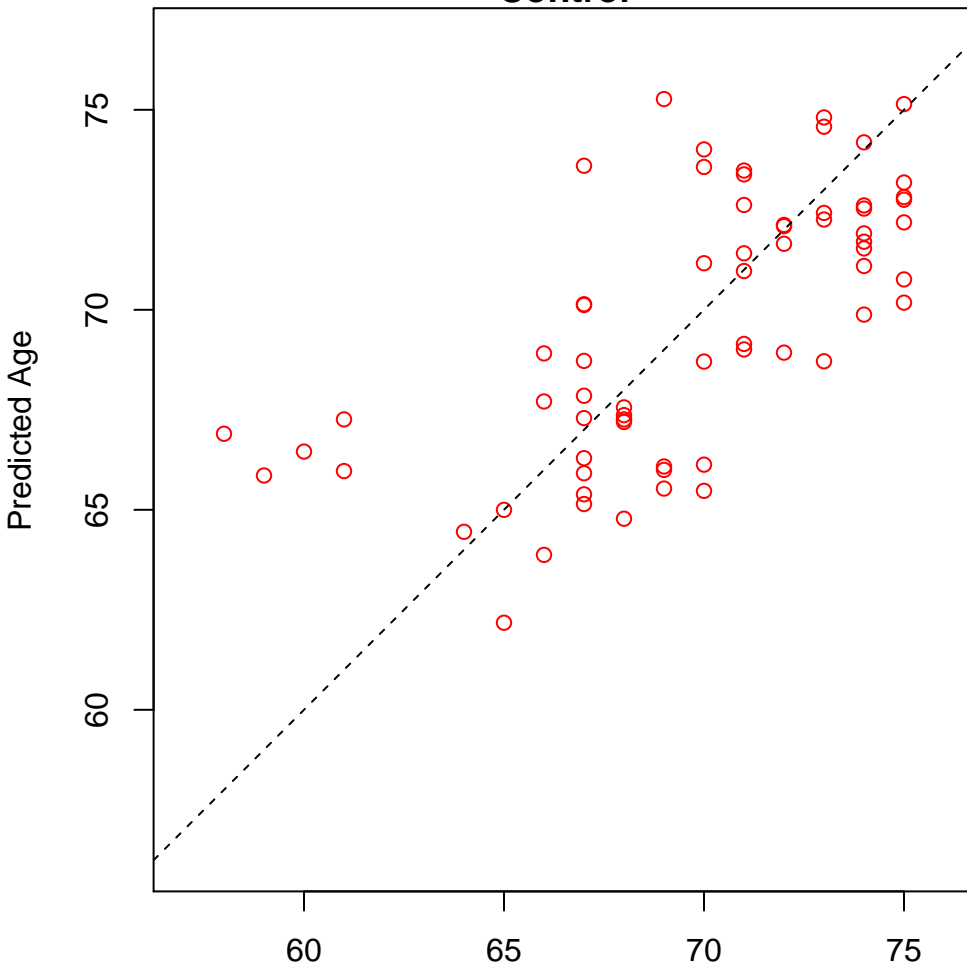


modification by symbiont of host morphology or physiology (Score: 1.506760)

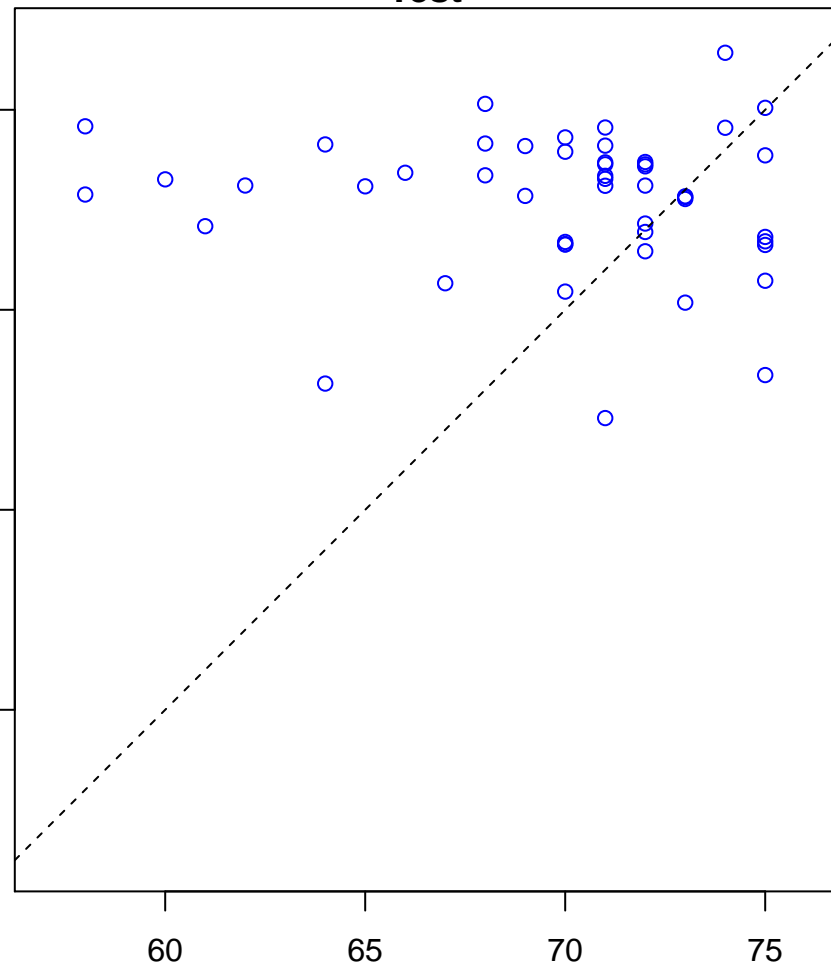


negative regulation of phosphorylation (Score: 1.506037)

Control

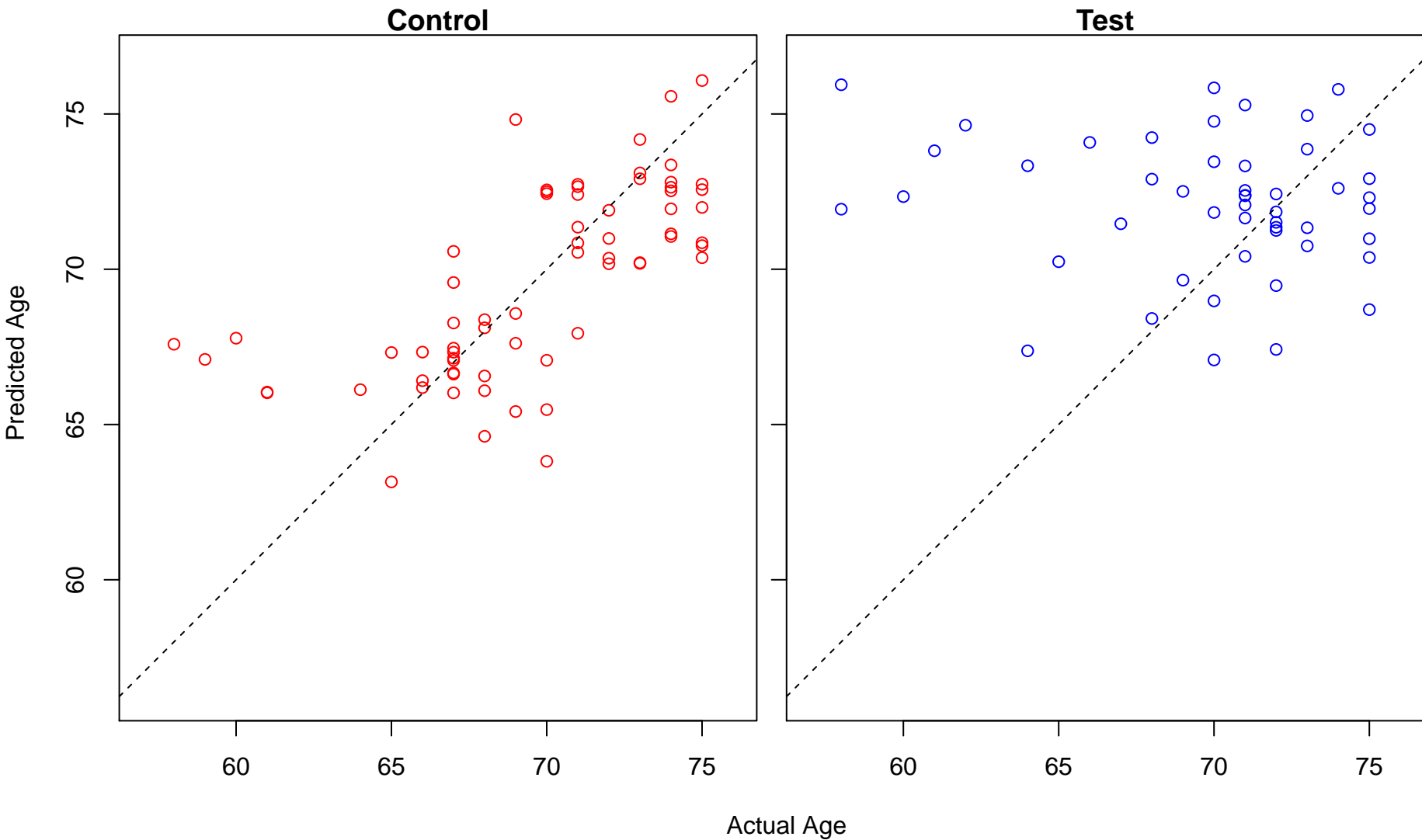


Test

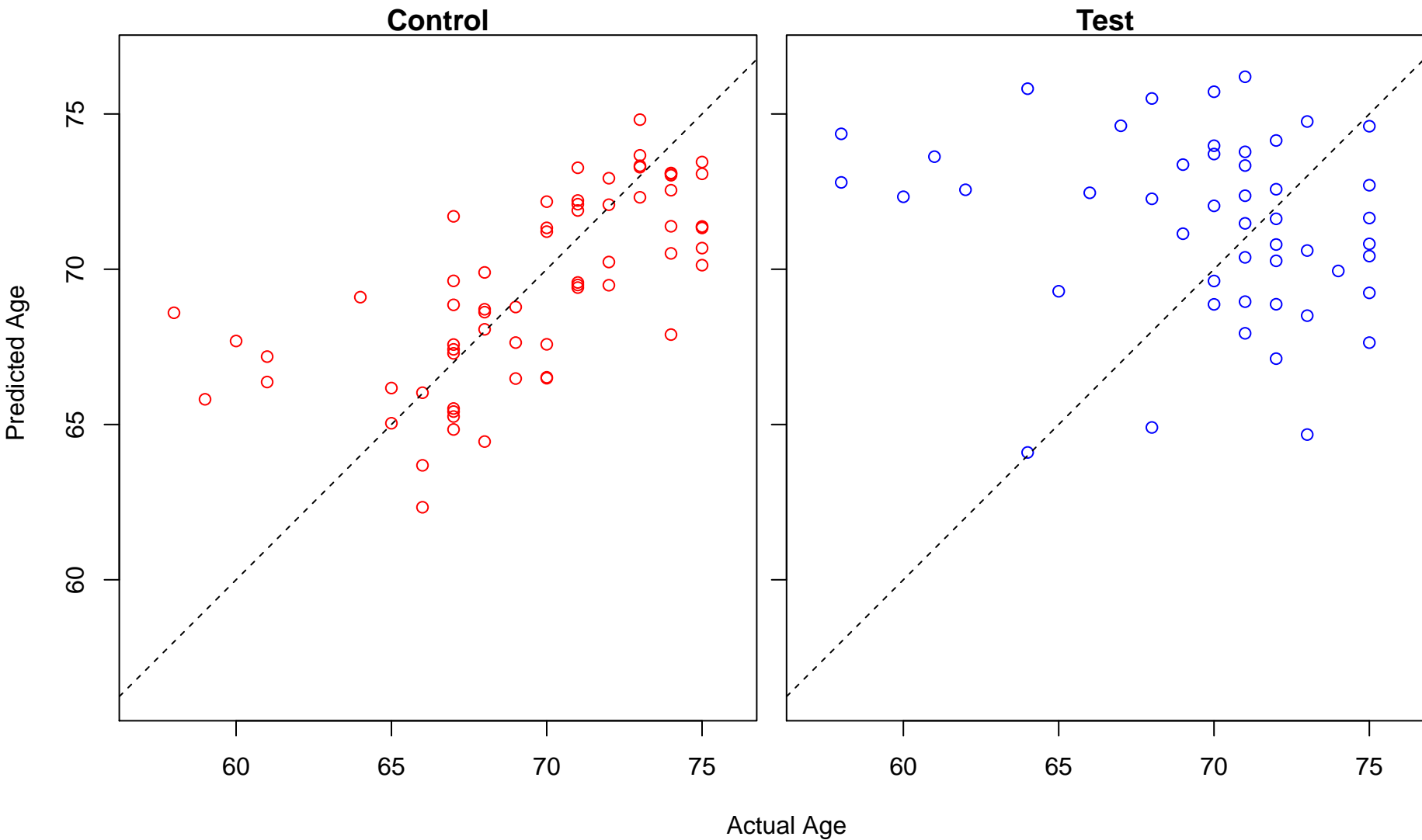


Actual Age

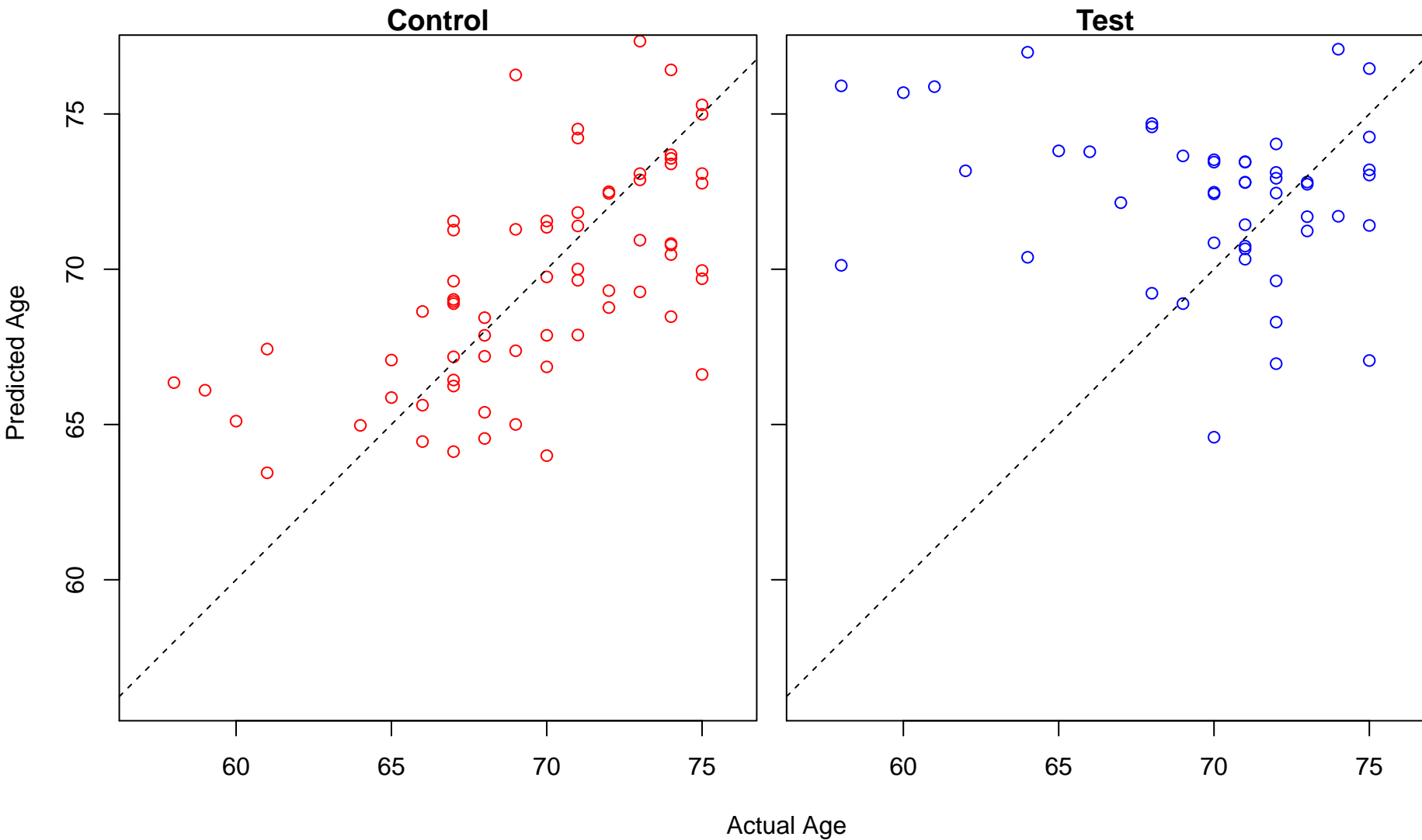
negative regulation of neuron death (Score: 1.505757)



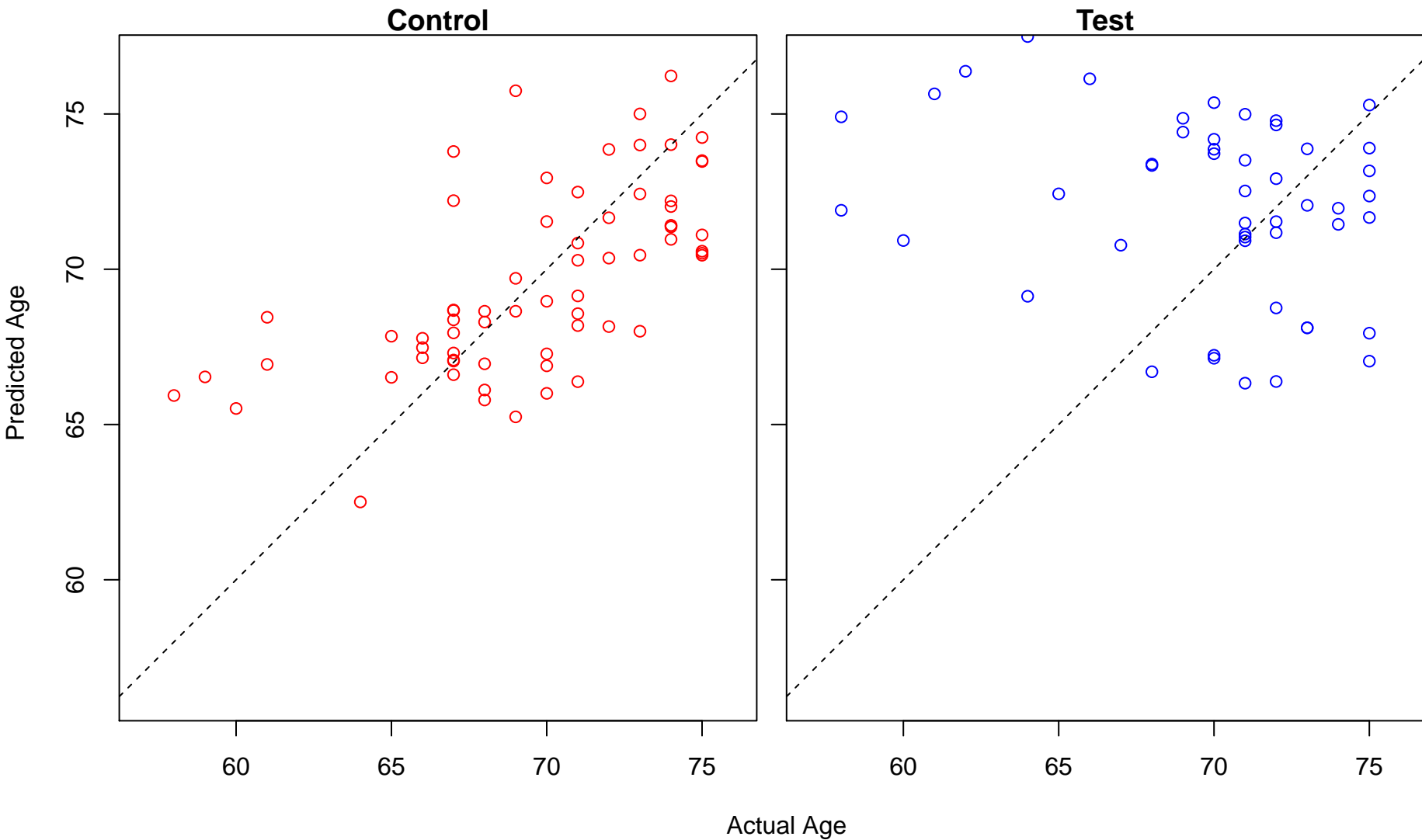
regulation of interleukin-8 secretion (Score: 1.505373)



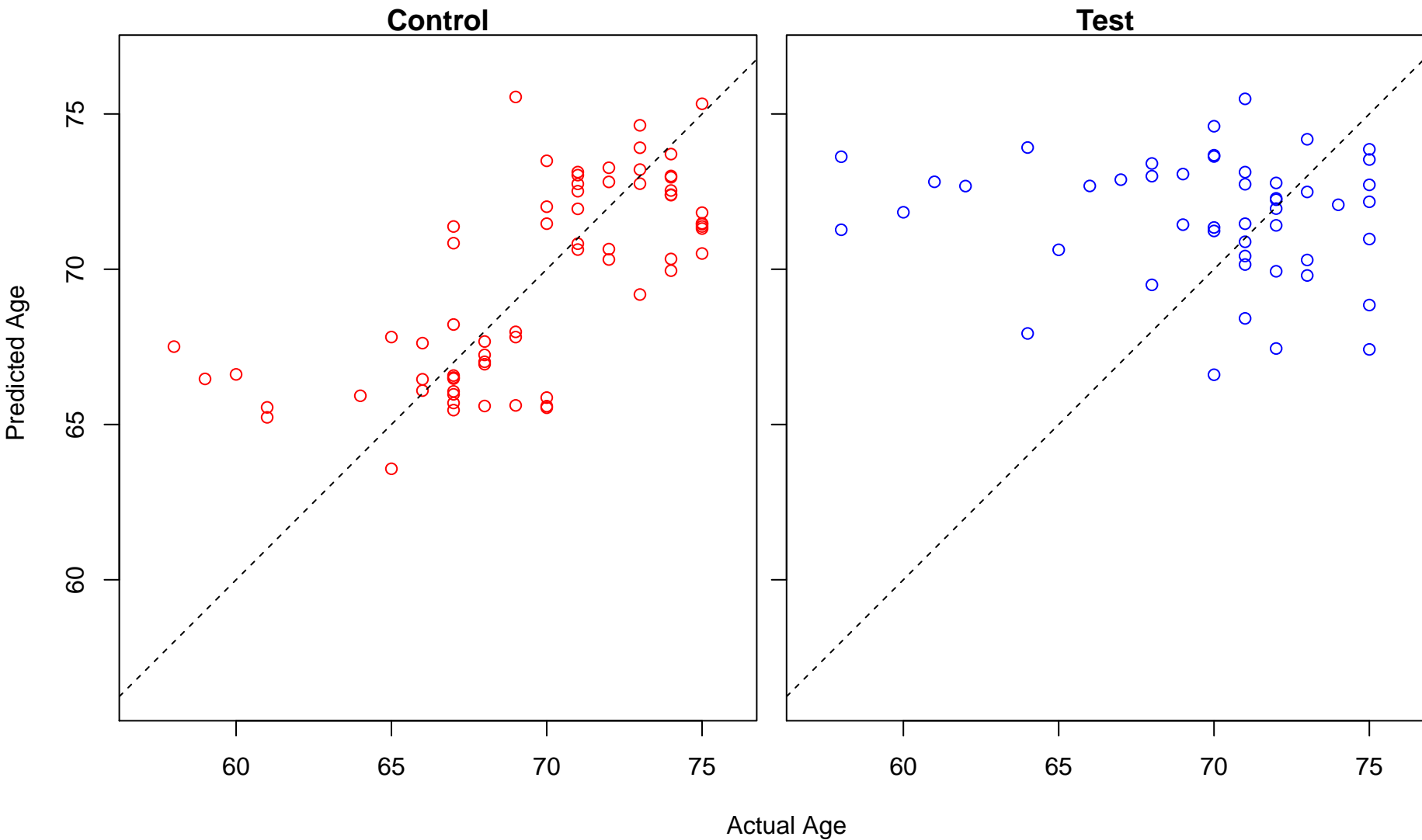
epithelial cell proliferation (Score: 1.505205)



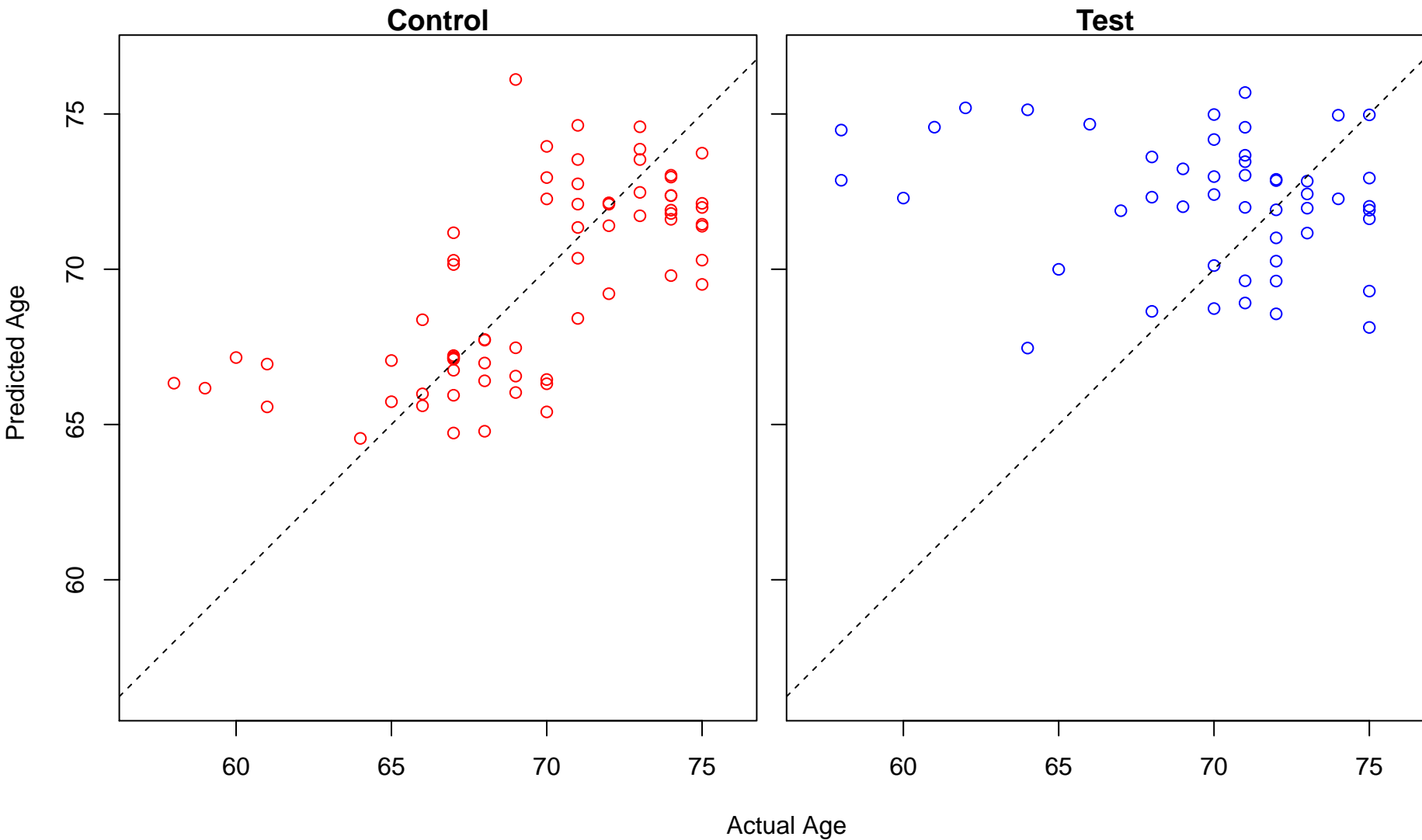
cellular response to dsRNA (Score: 1.504897)



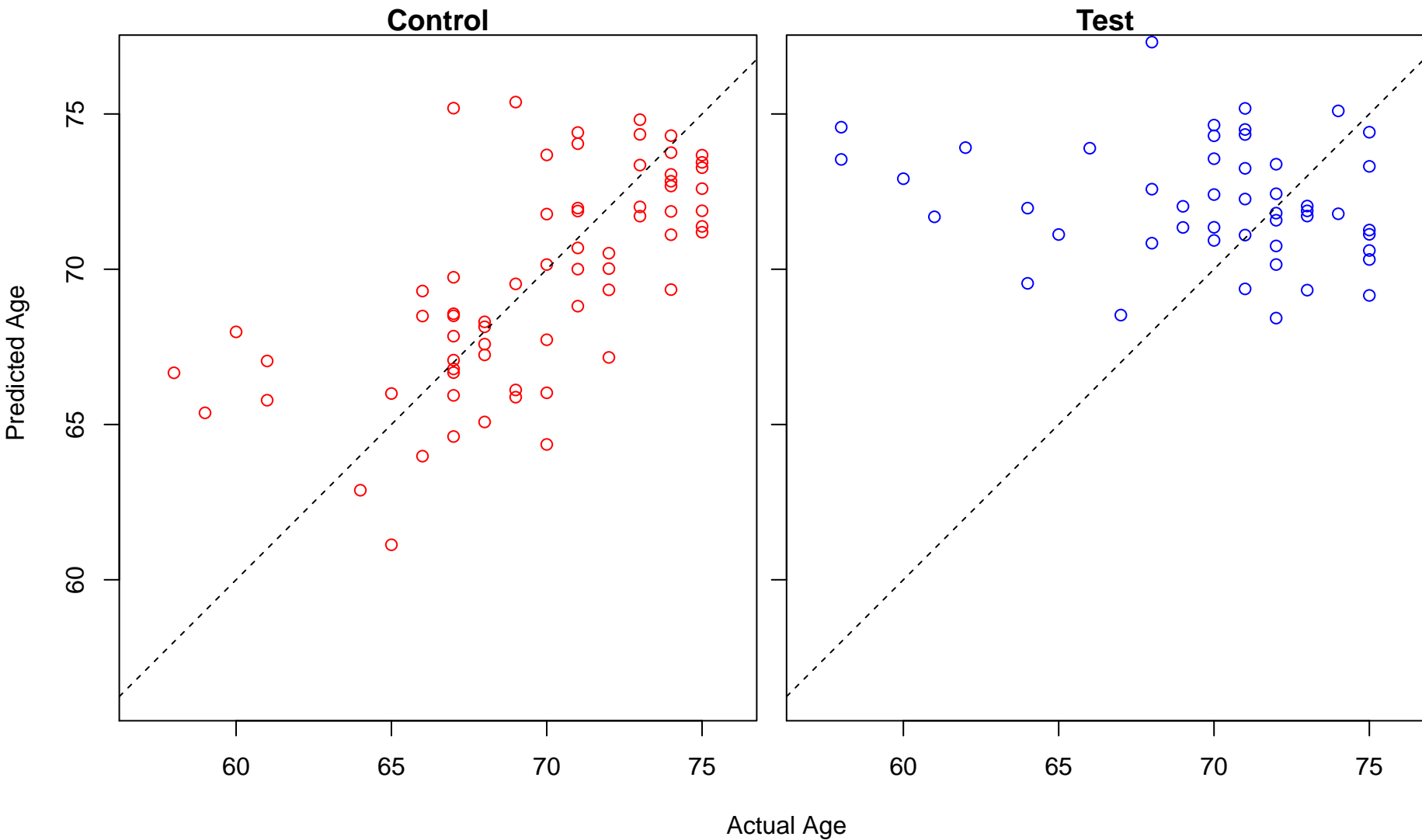
tRNA metabolic process (Score: 1.504621)



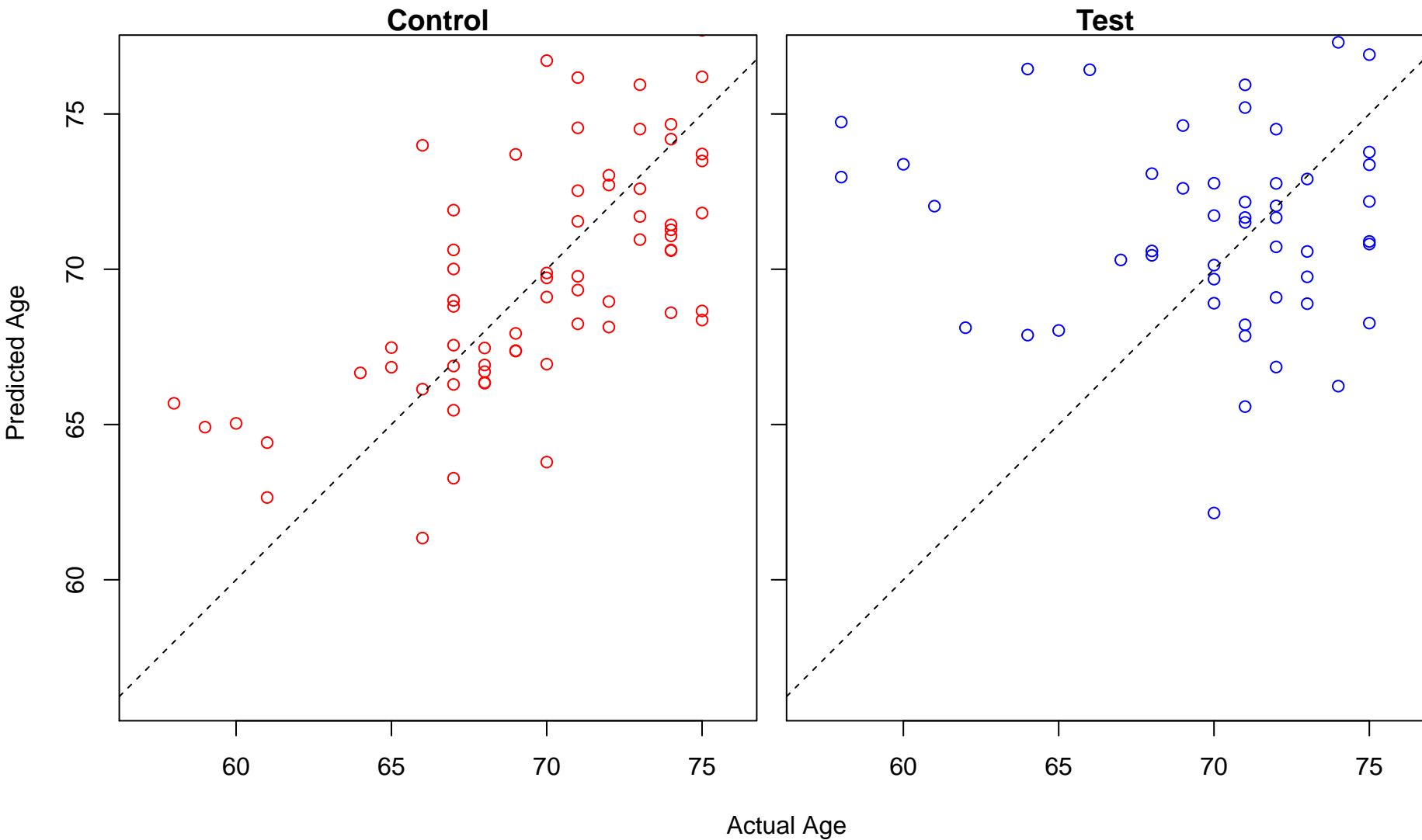
cilium morphogenesis (Score: 1.504608)



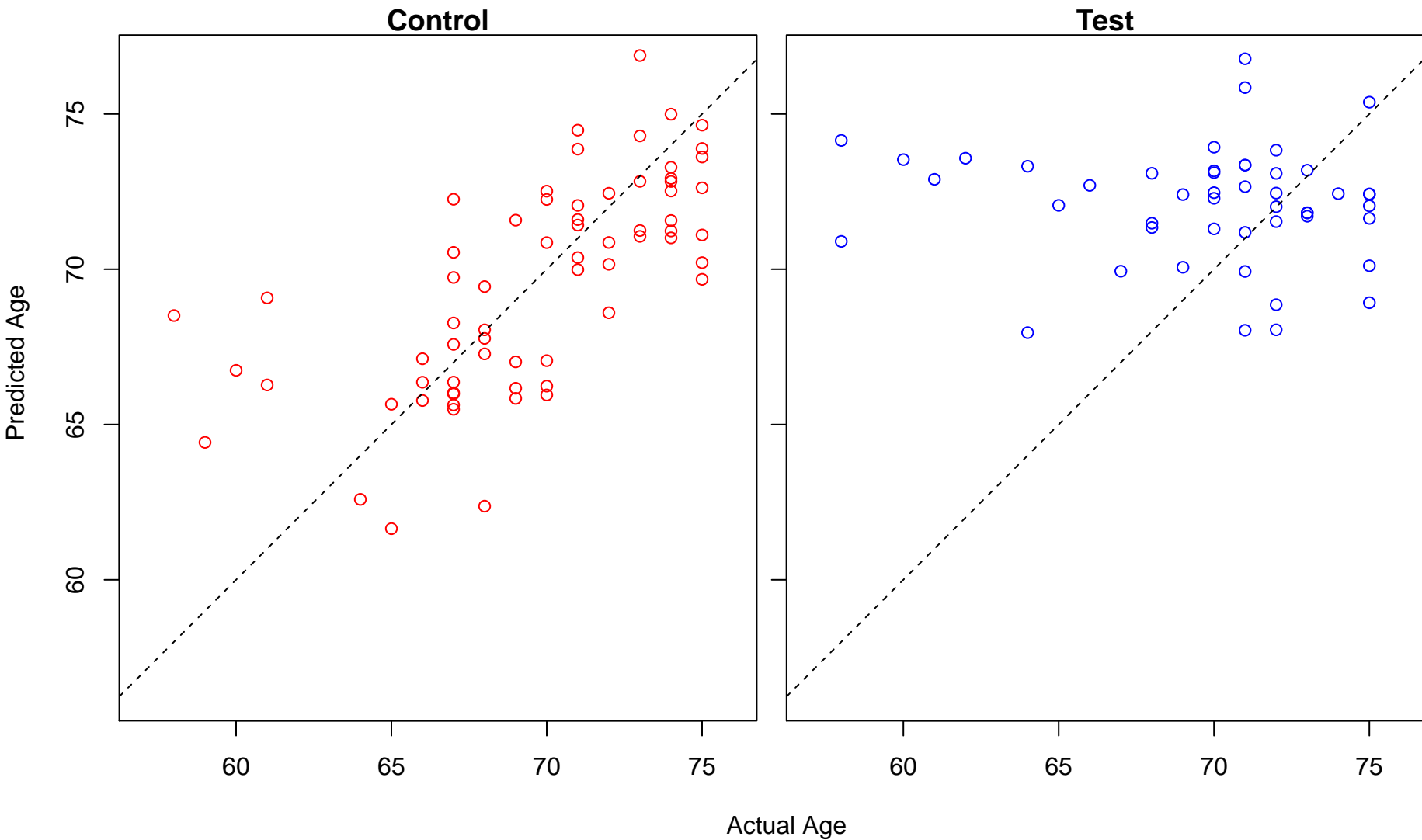
negative regulation of hemopoiesis (Score: 1.504046)



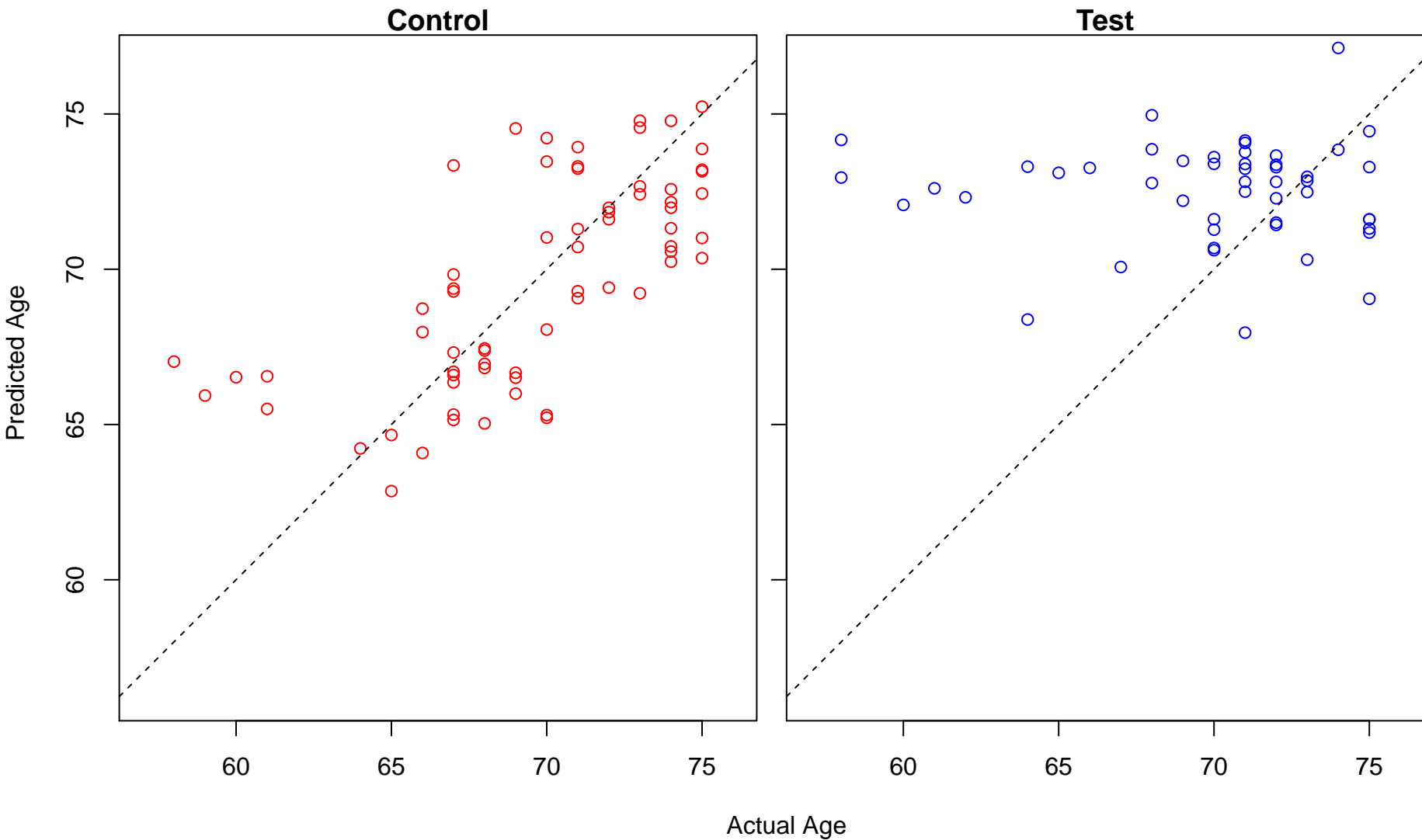
regulation of lyase activity (Score: 1.503992)



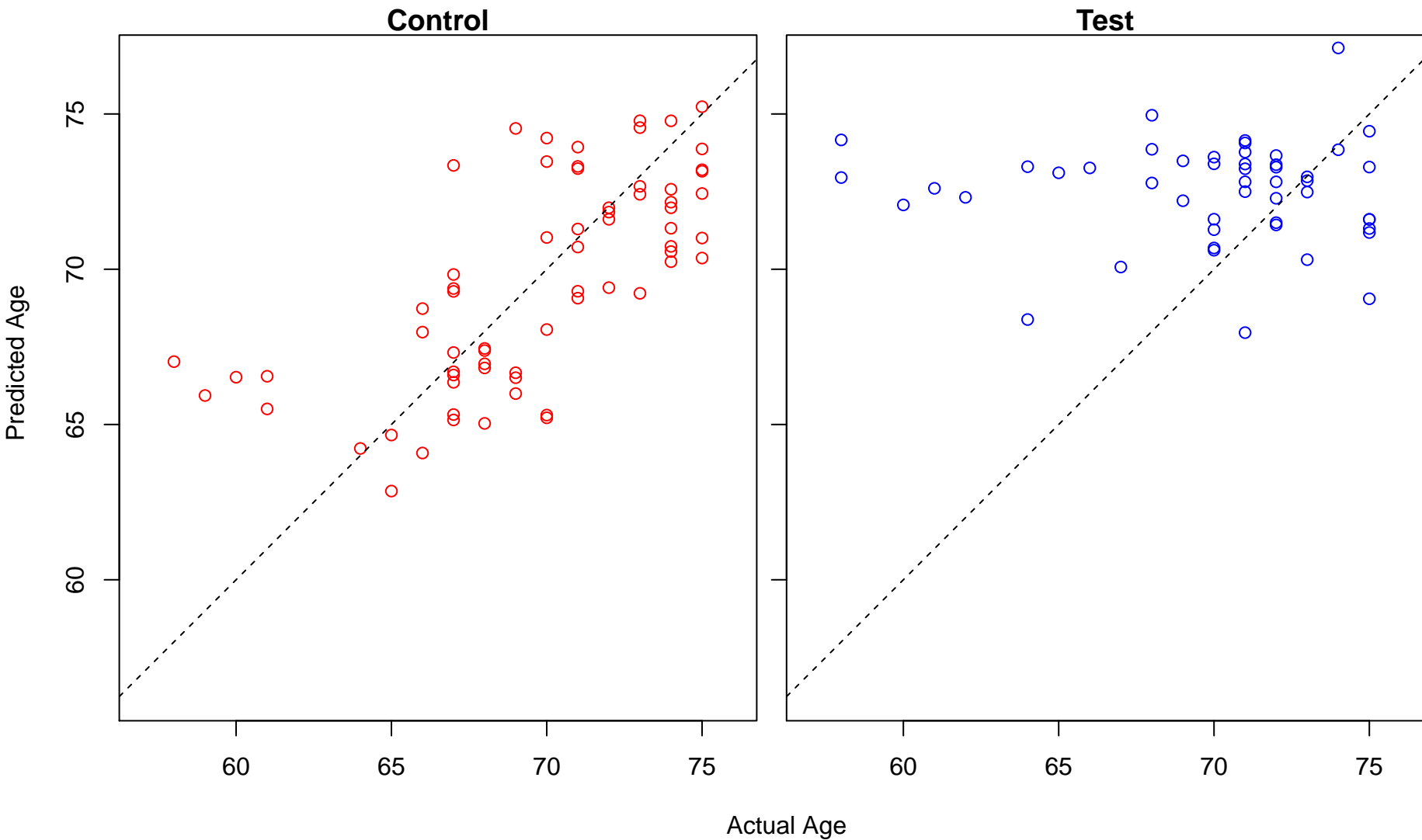
regulation of cell morphogenesis (Score: 1.503767)



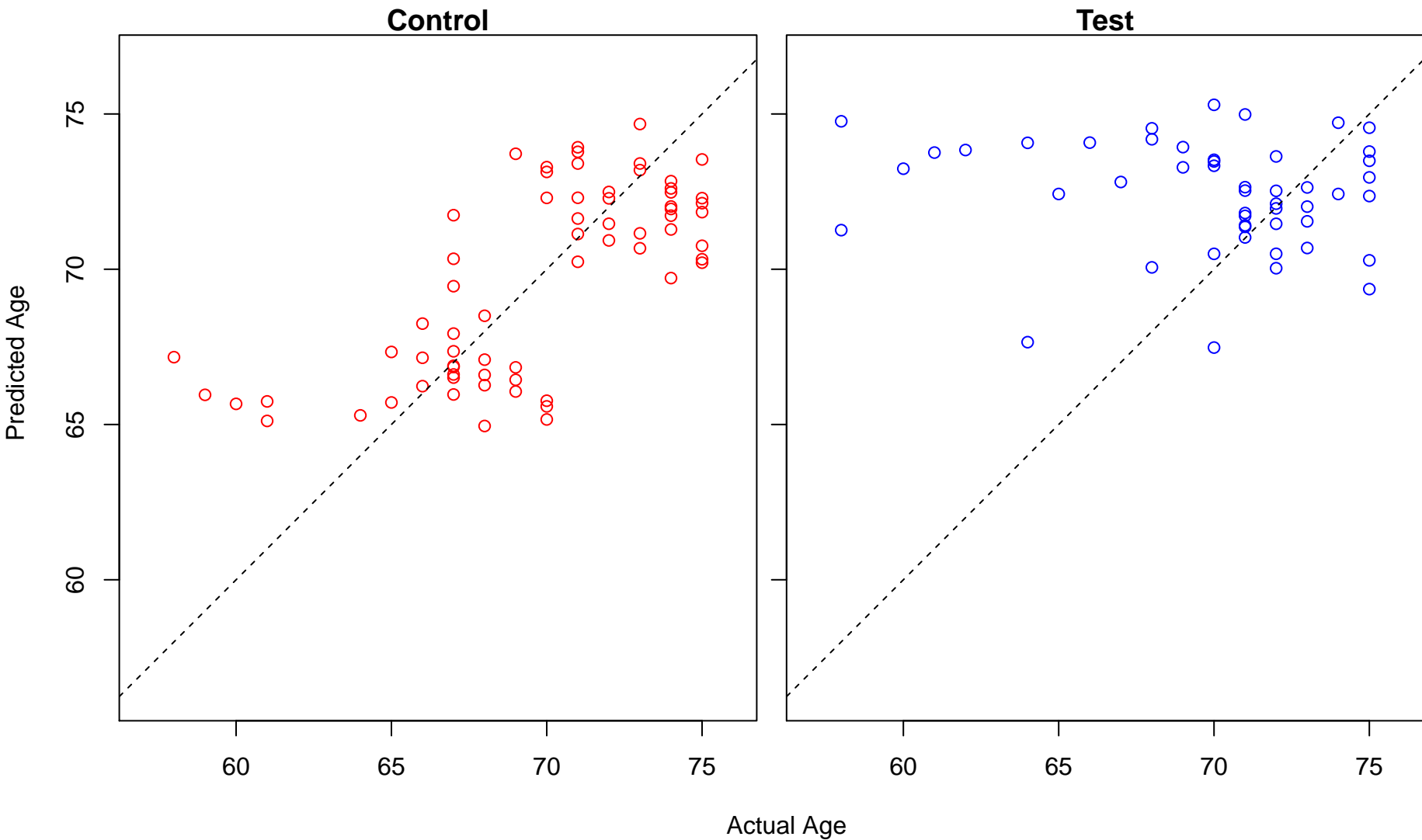
negative regulation of phosphorus metabolic process (Score: 1.502541)



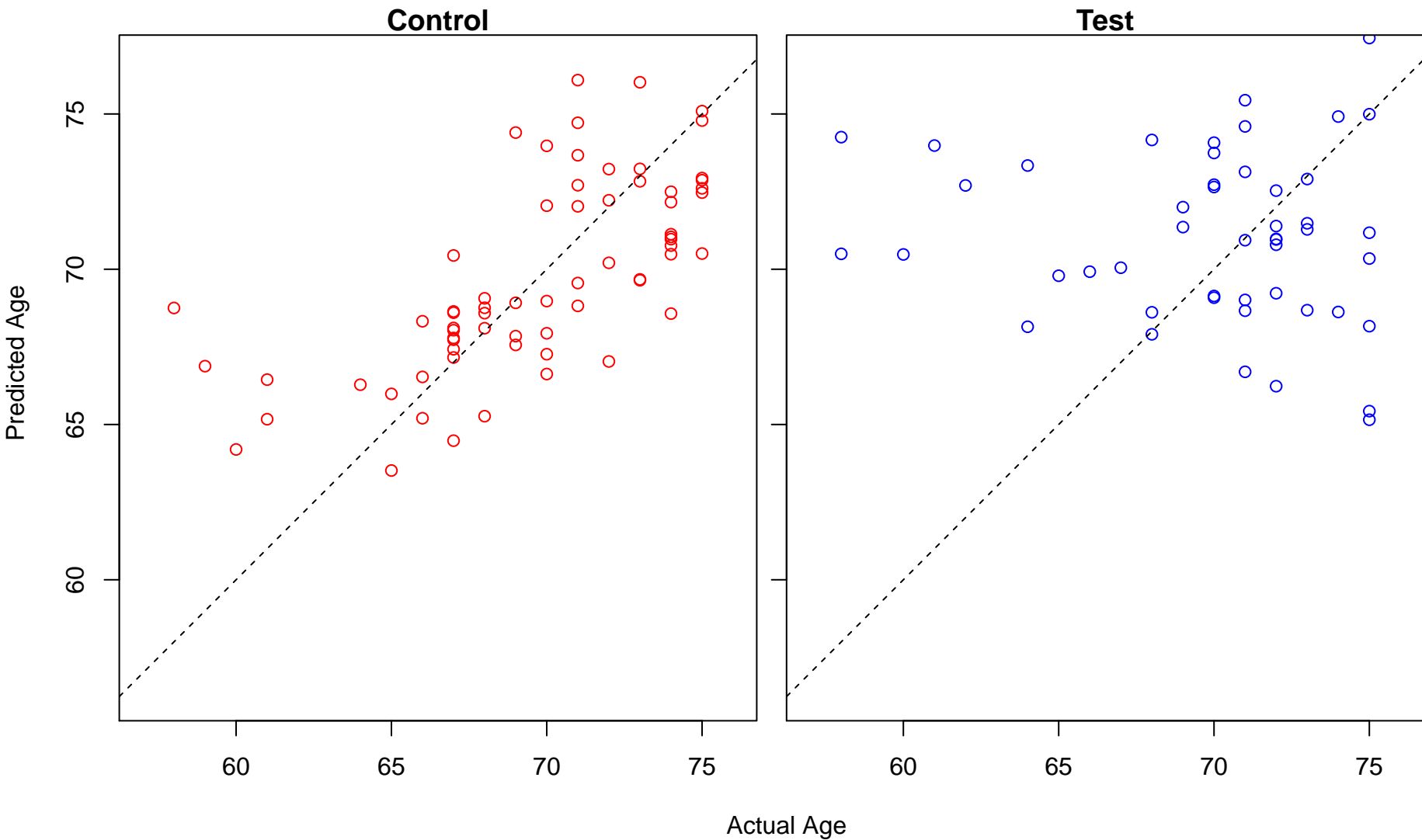
negative regulation of phosphate metabolic process (Score: 1.502541)



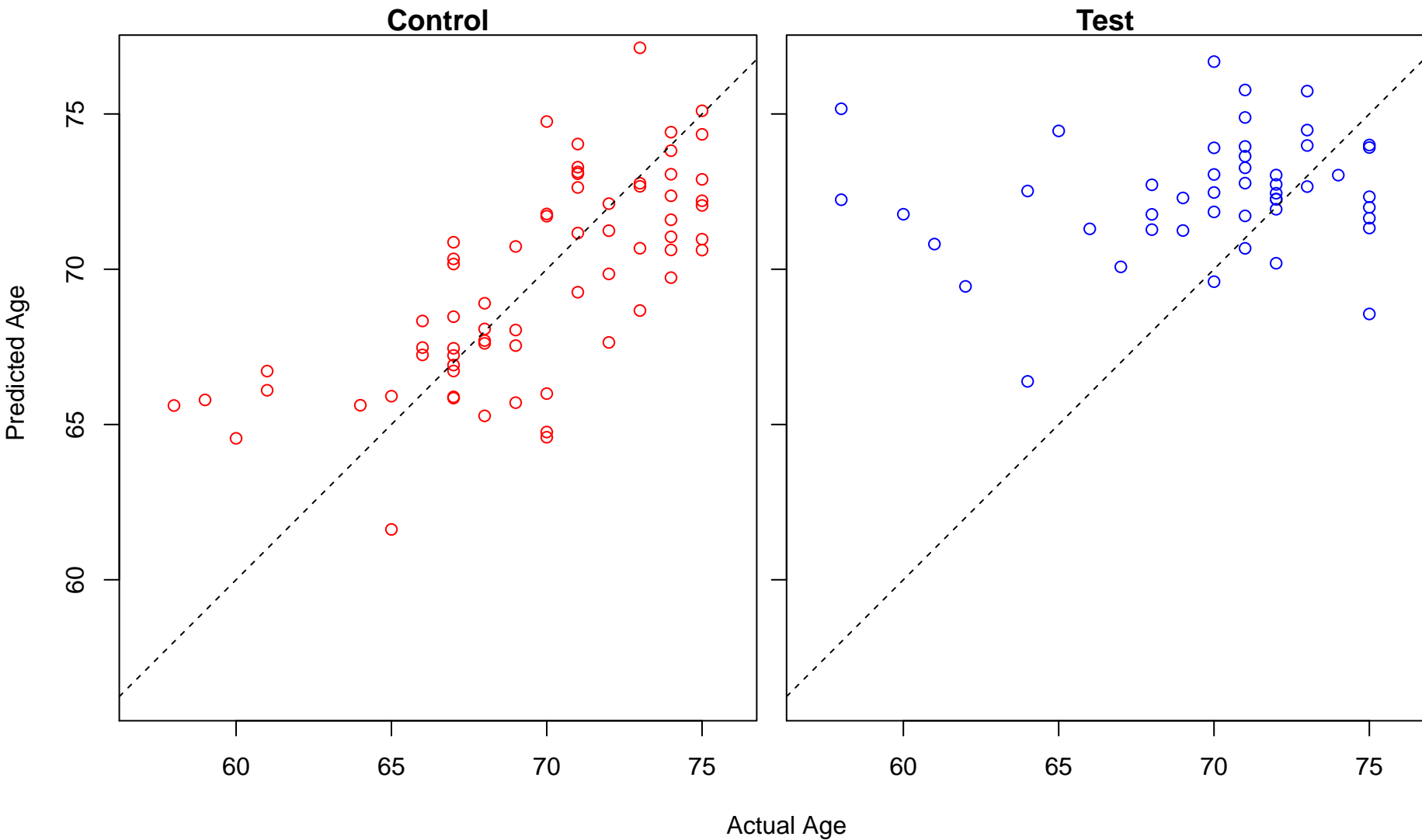
termination of RNA polymerase I transcription (Score: 1.502221)



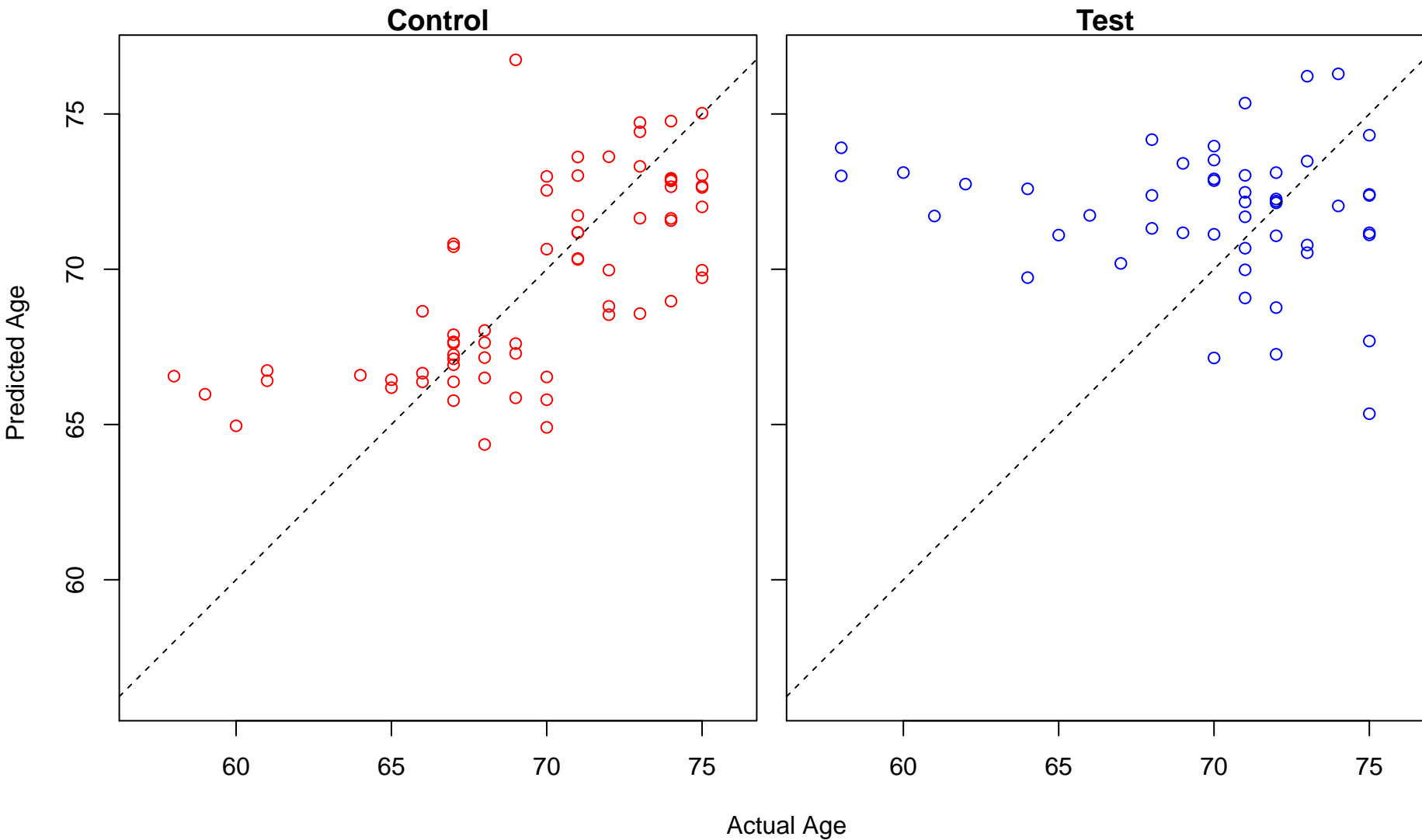
rRNA-containing ribonucleoprotein complex export from nucleus (Score: 1.502107)



response to light stimulus (Score: 1.502058)

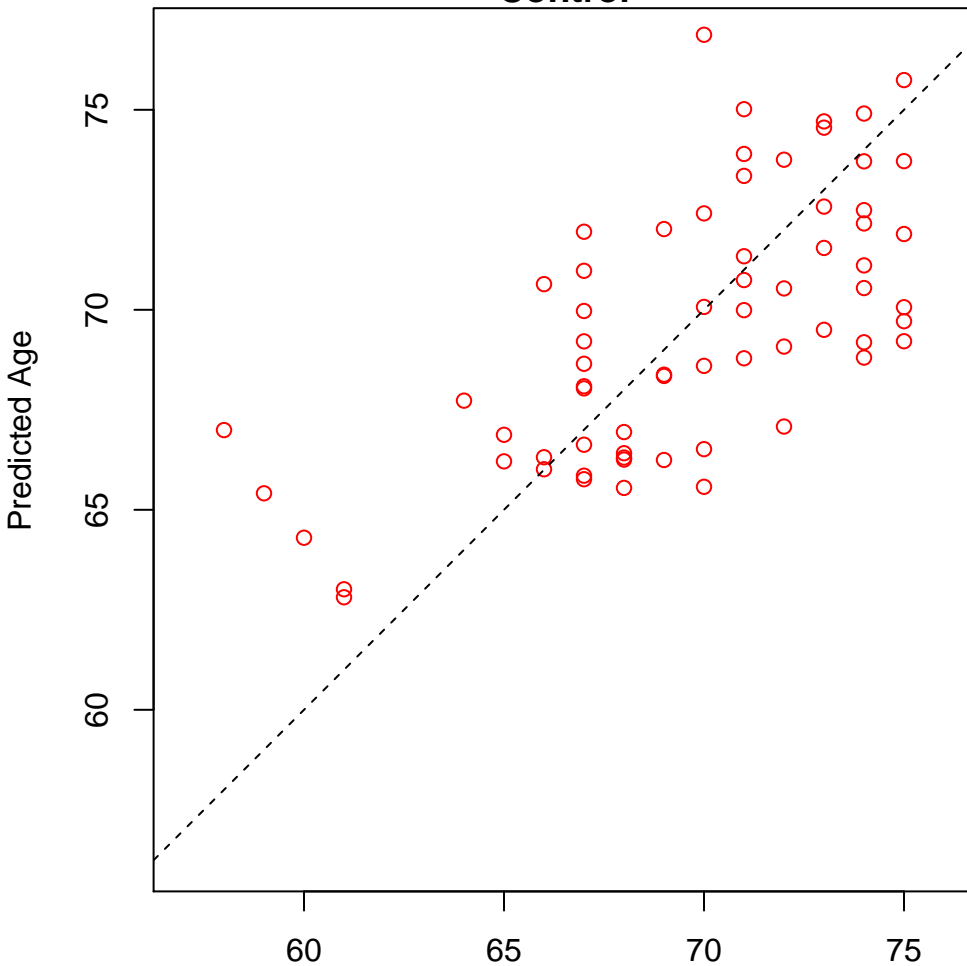


stem cell differentiation (Score: 1.501452)

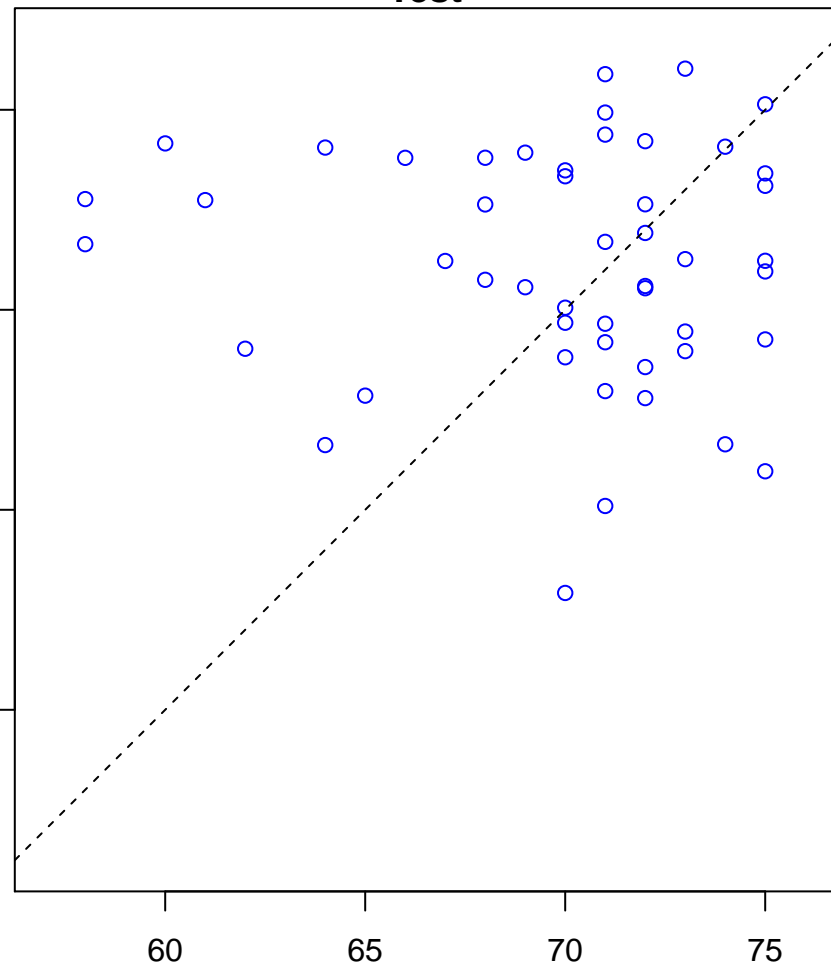


regulation of adenylate cyclase activity (Score: 1.501400)

Control

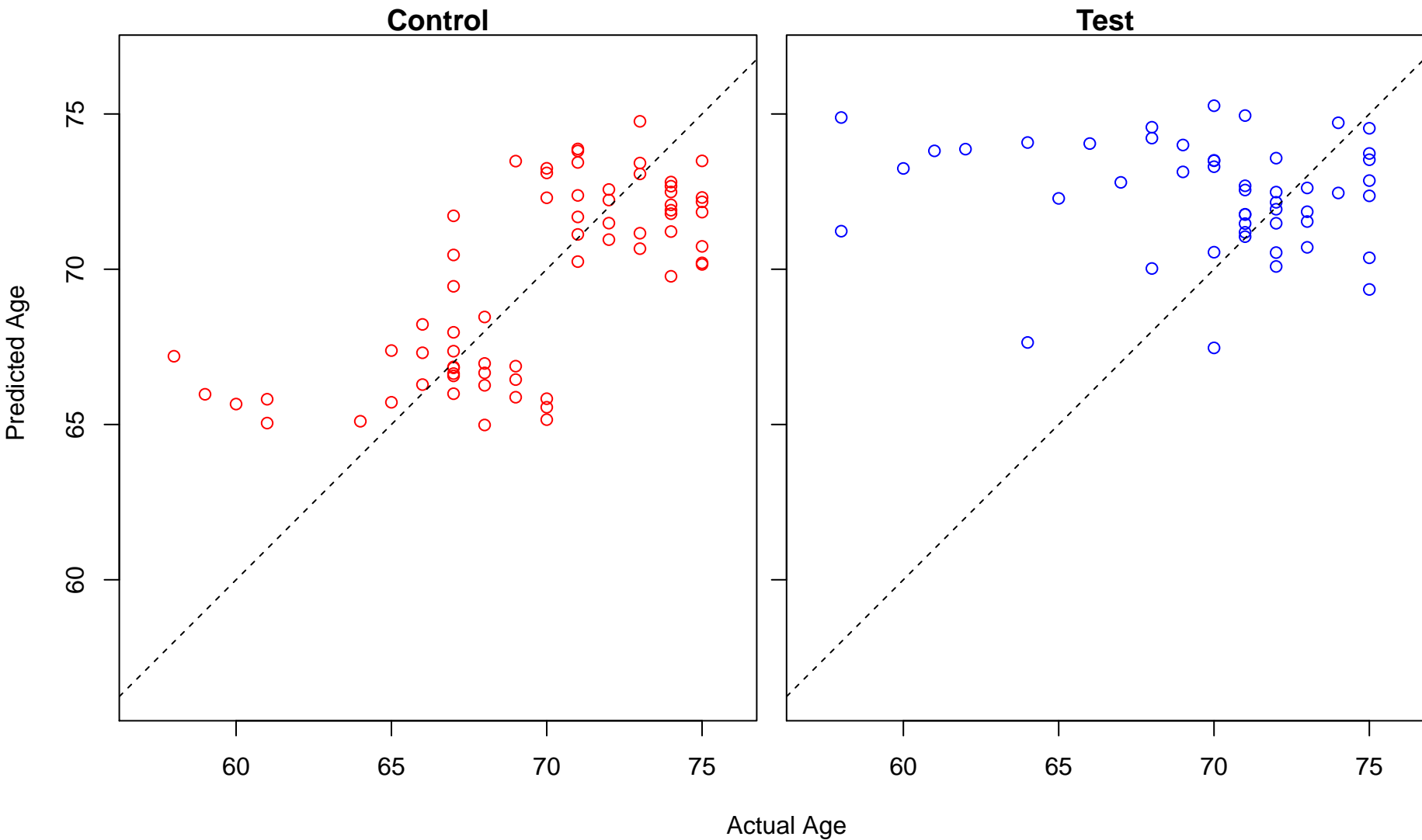


Test

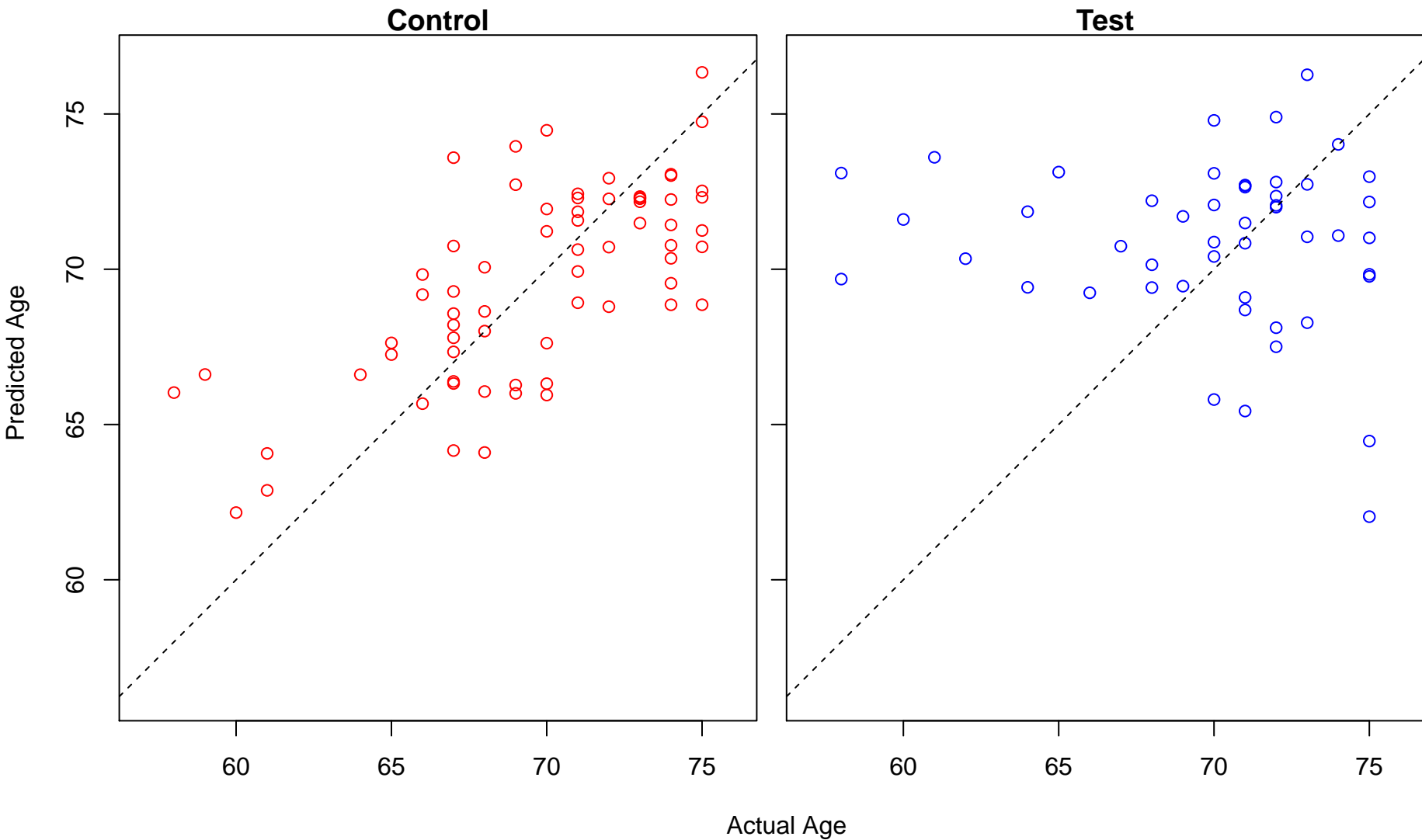


Actual Age

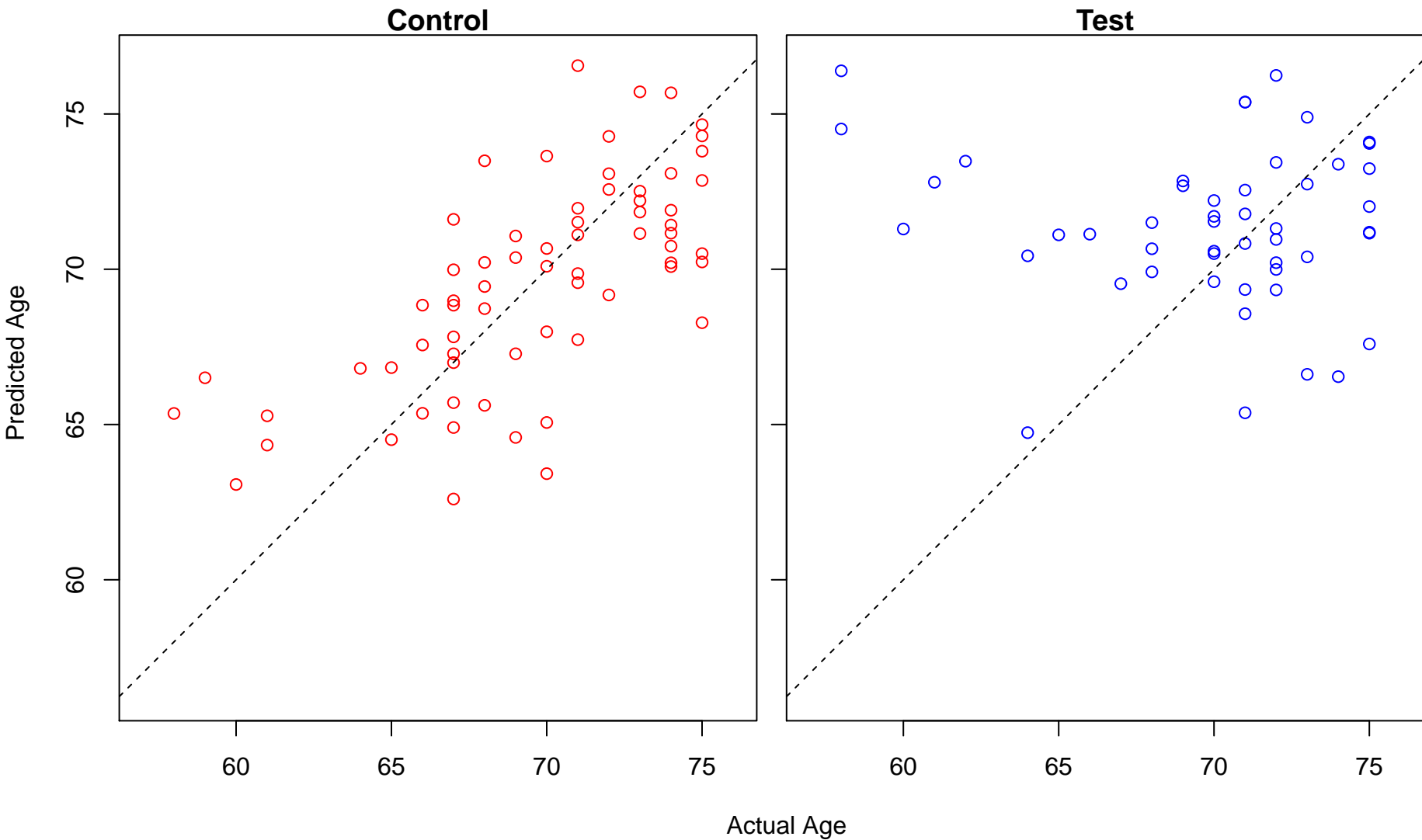
transcription elongation from RNA polymerase I promoter (Score: 1.501022)



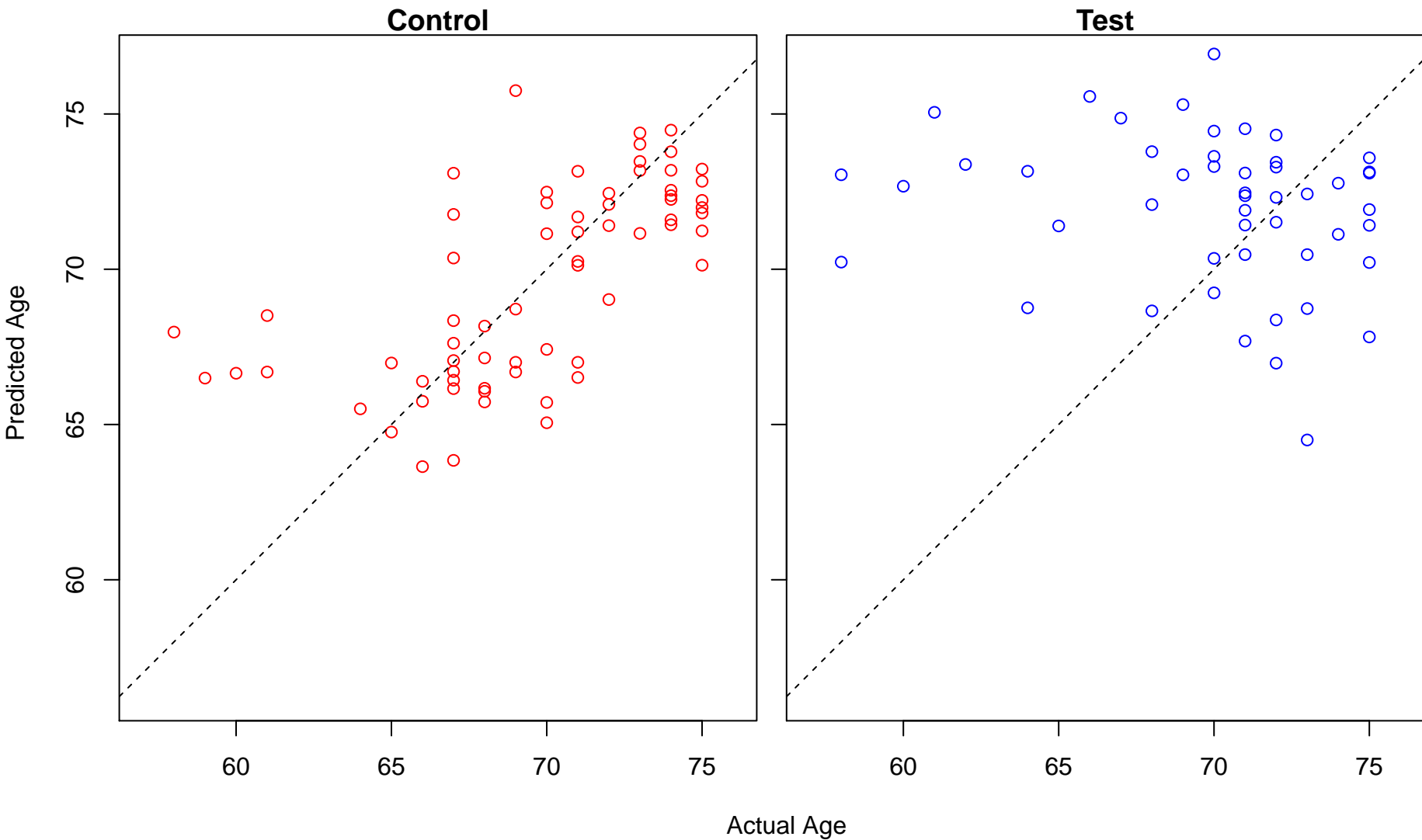
positive regulation of potassium ion transmembrane transport (Score: 1.500541)



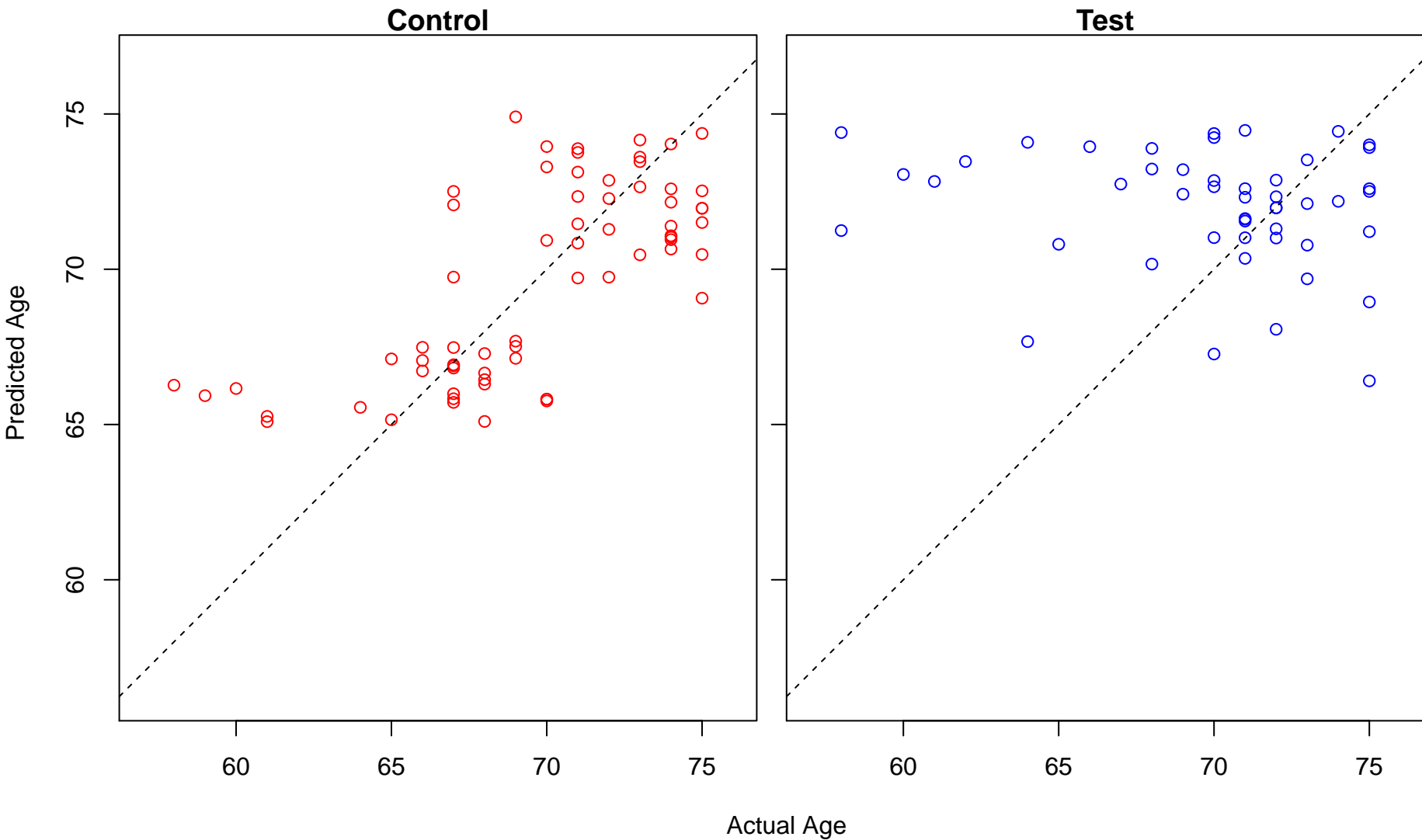
histone H4-K16 acetylation (Score: 1.500487)



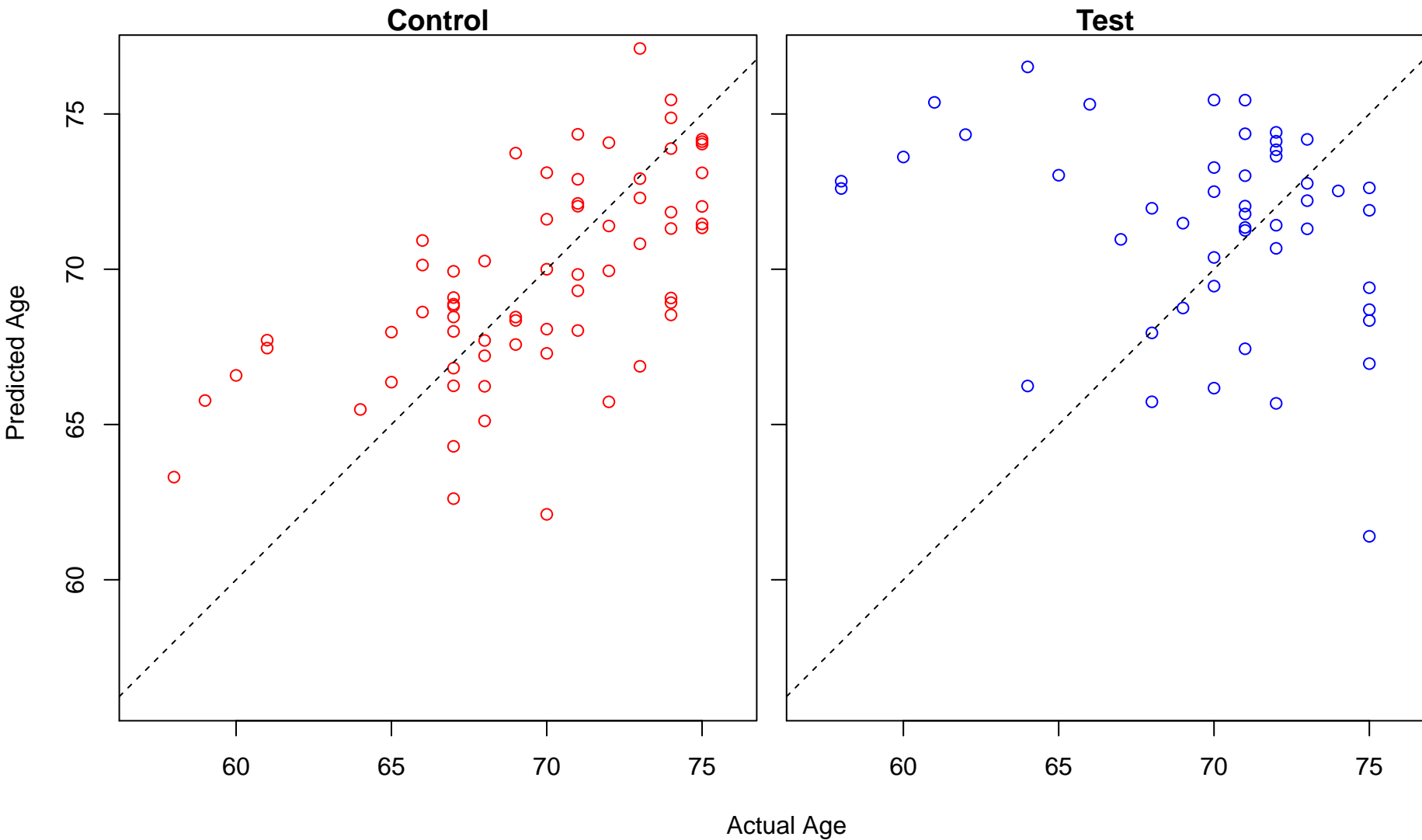
regulation of type 2 immune response (Score: 1.499315)



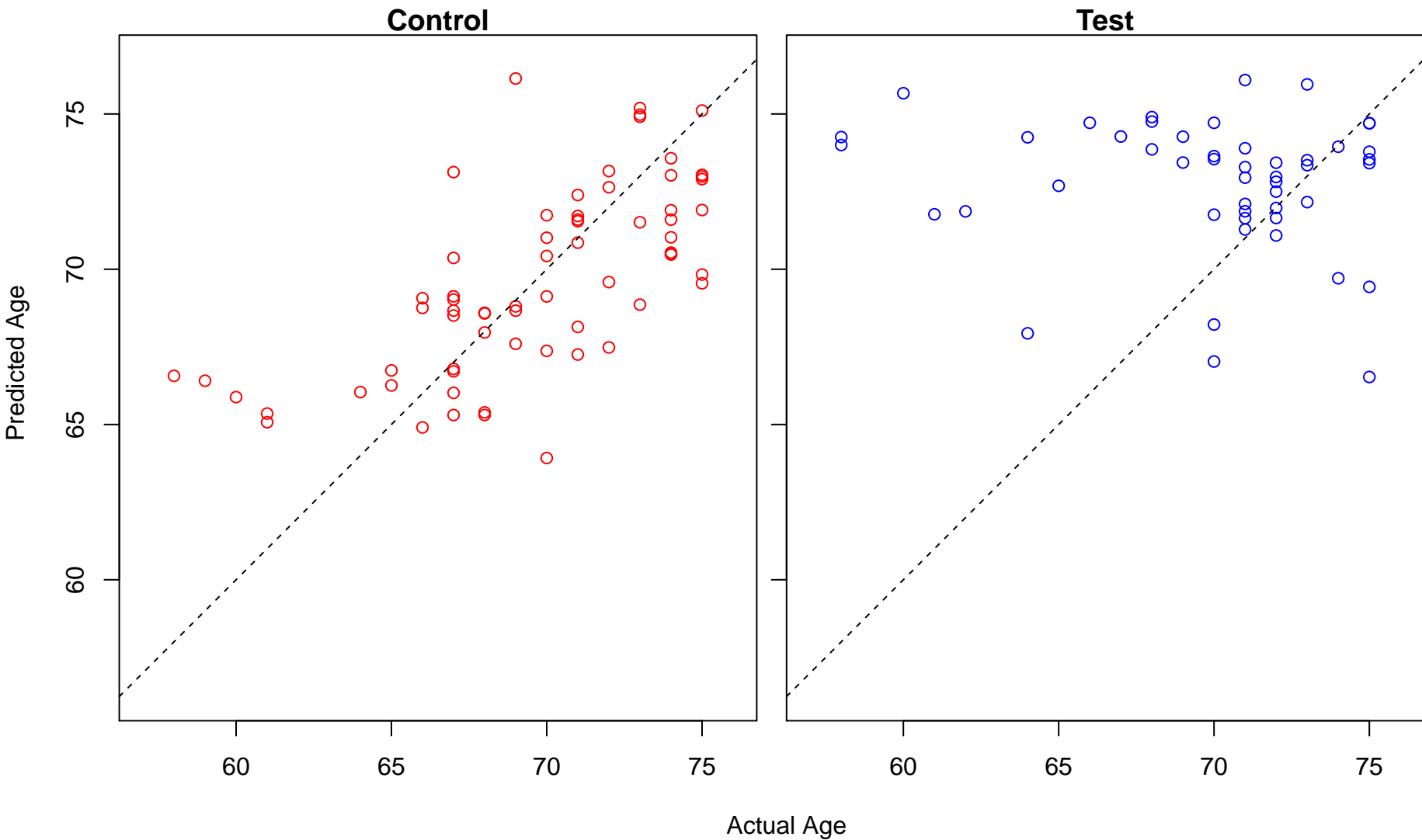
mannosylation (Score: 1.499222)



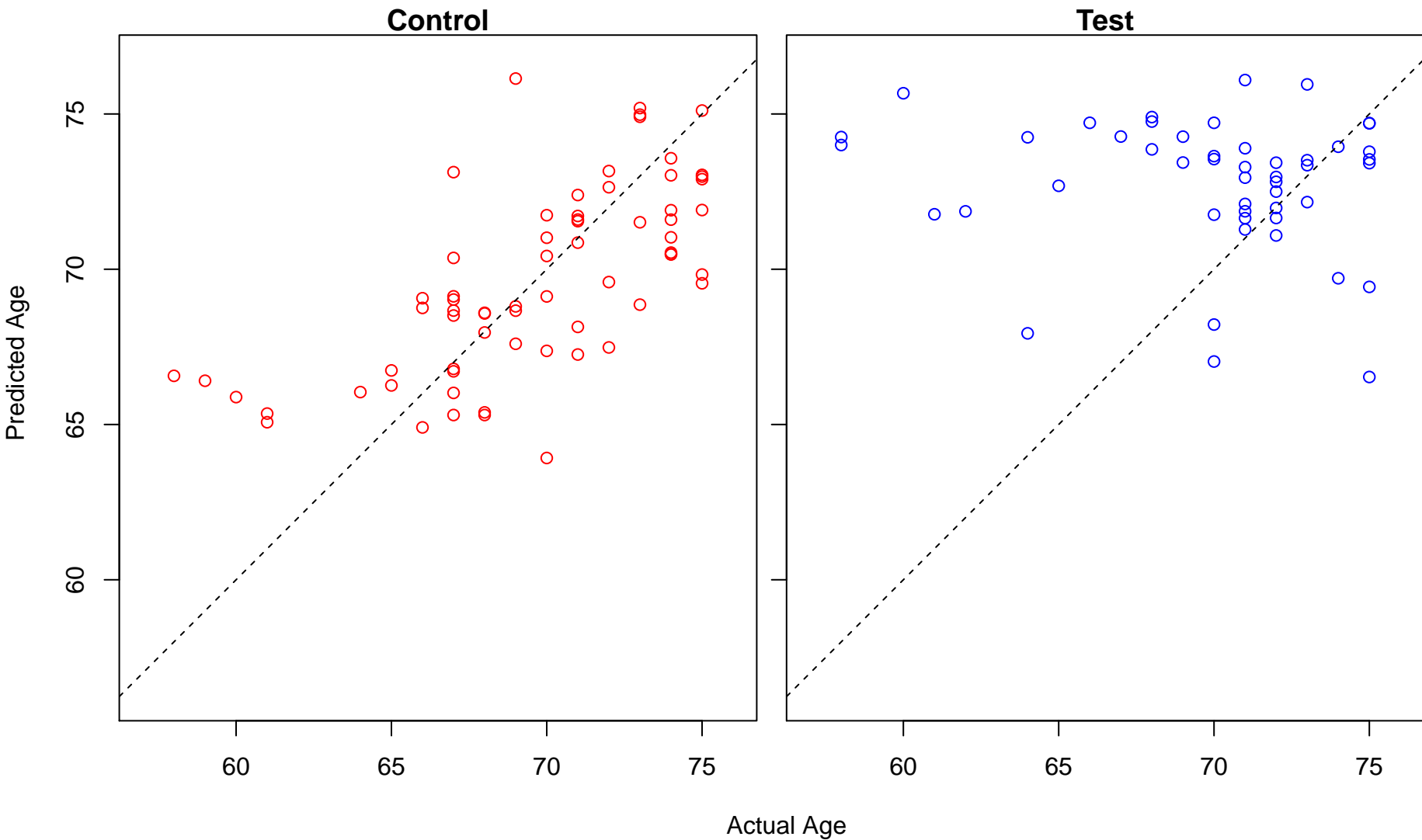
positive regulation of establishment of protein localization to telomere (Score: 1.498502)



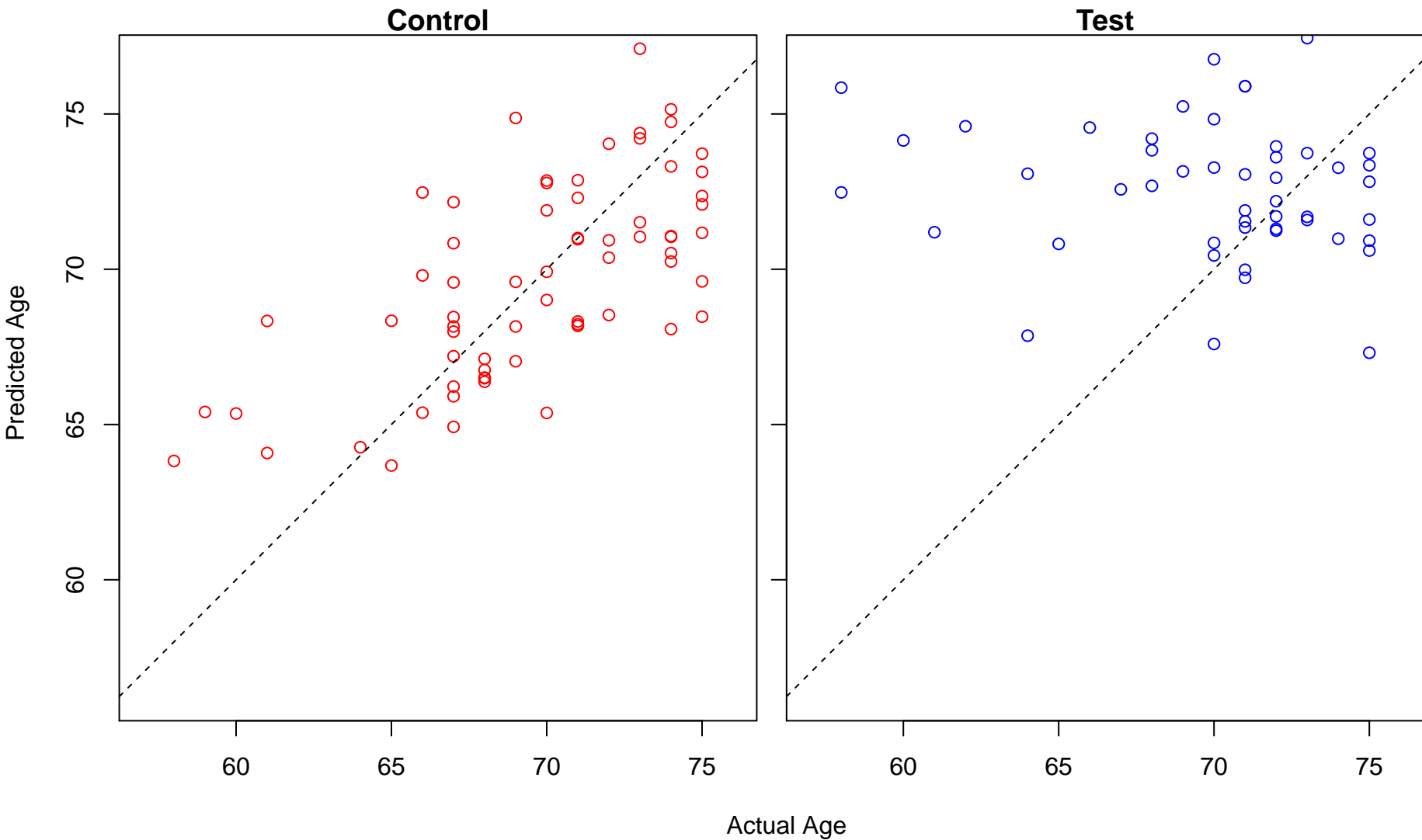
T cell differentiation in thymus (Score: 1.498431)



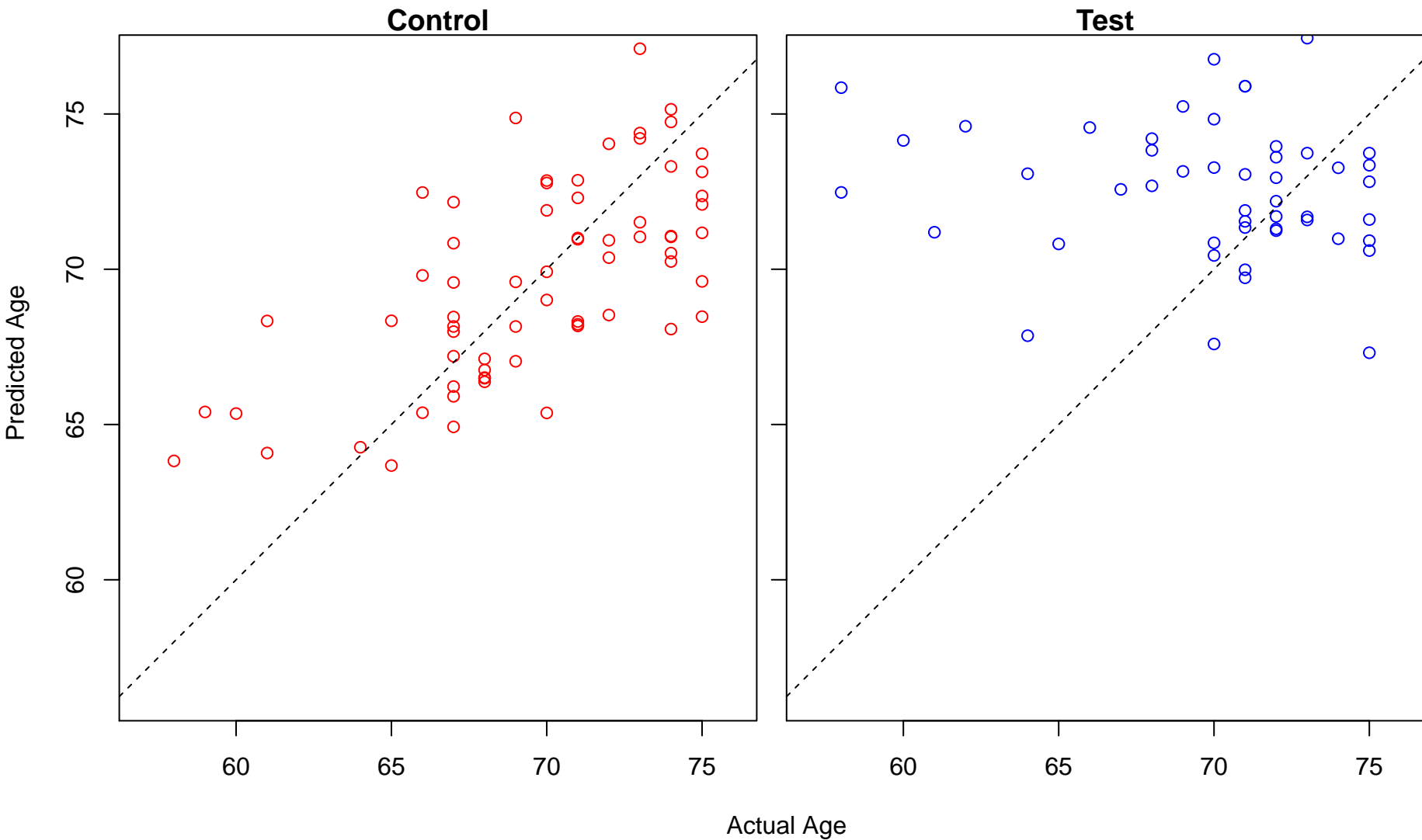
thymocyte aggregation (Score: 1.498431)



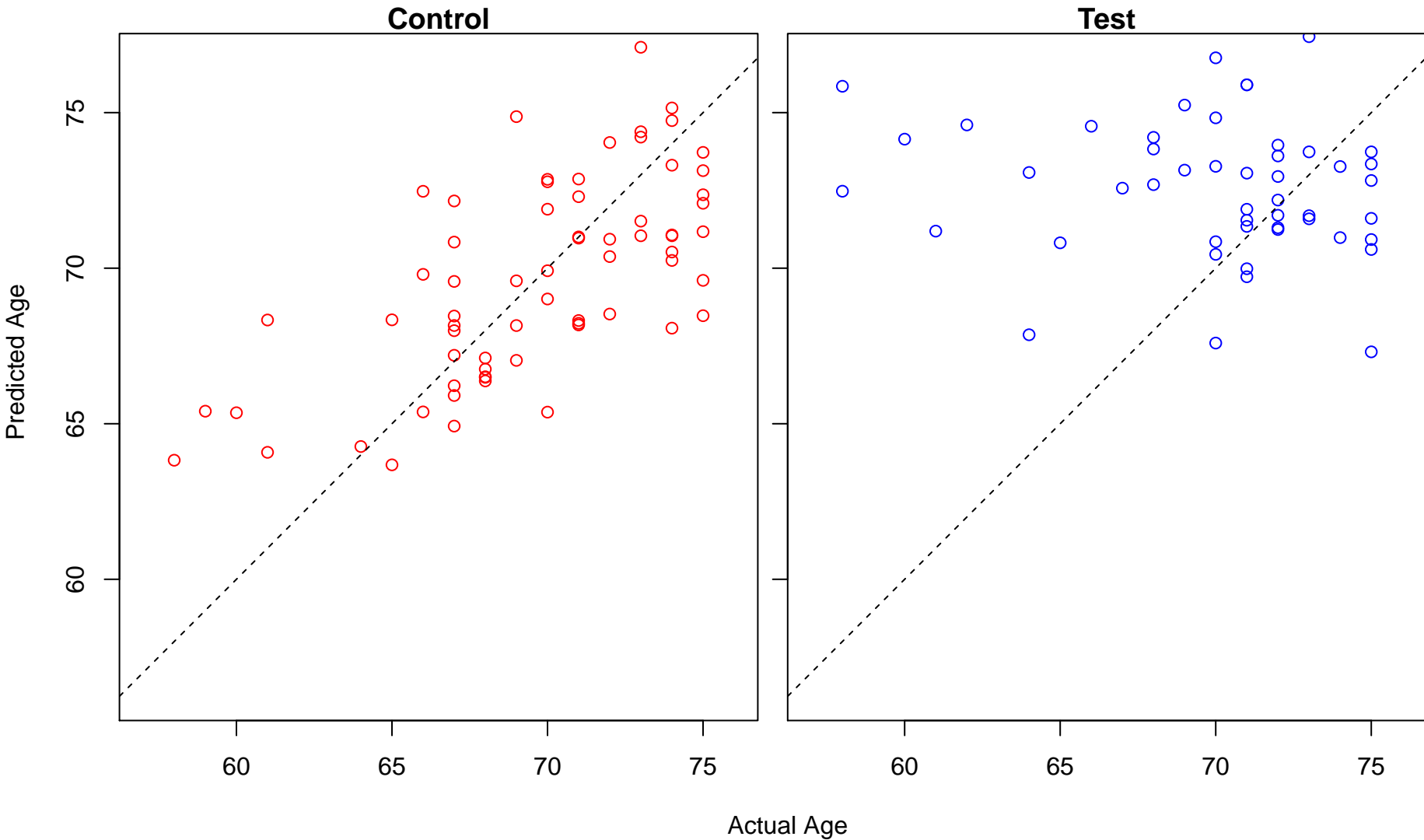
establishment of mitochondrion localization, microtubule-mediated (Score: 1.497682)



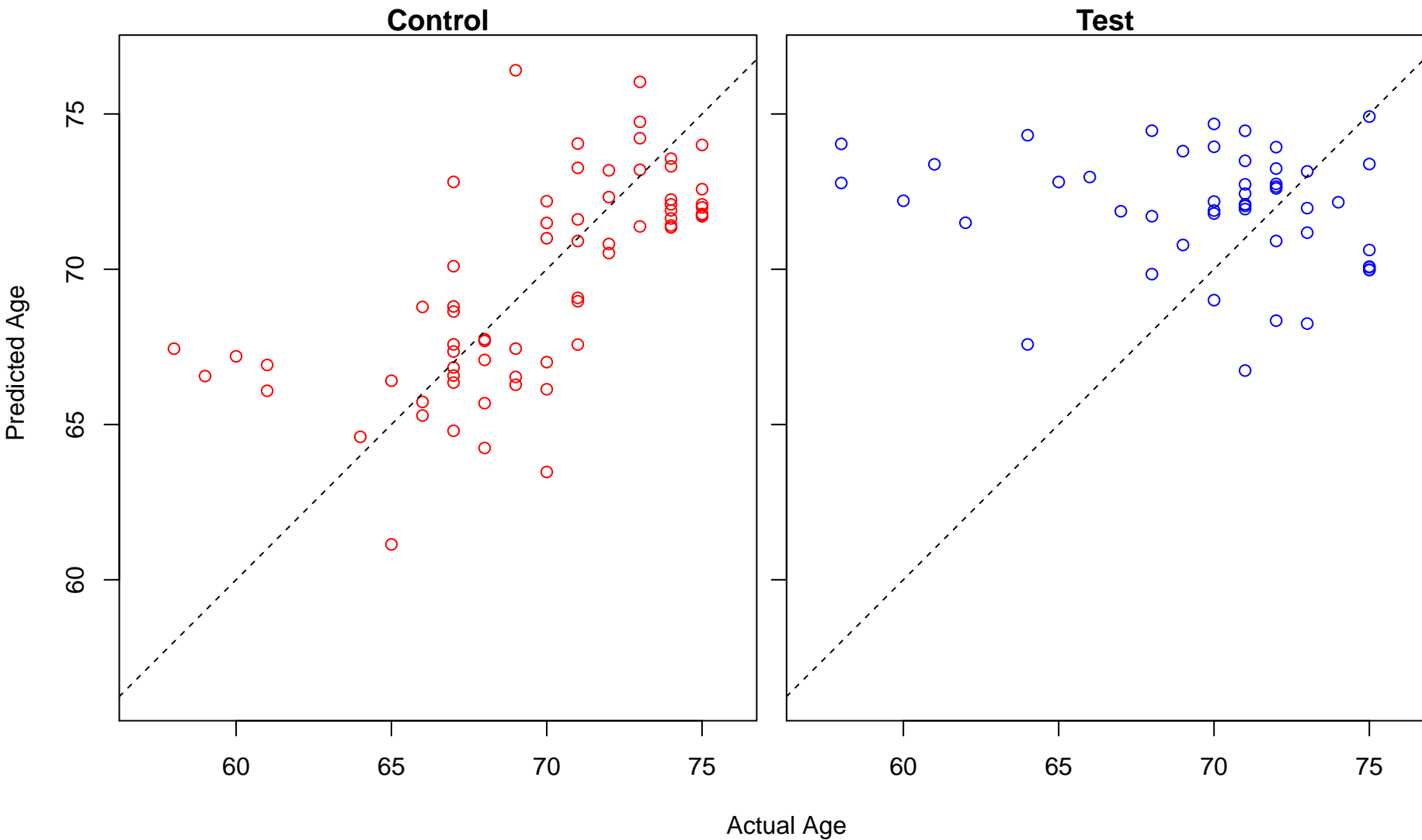
mitochondrion transport along microtubule (Score: 1.497682)



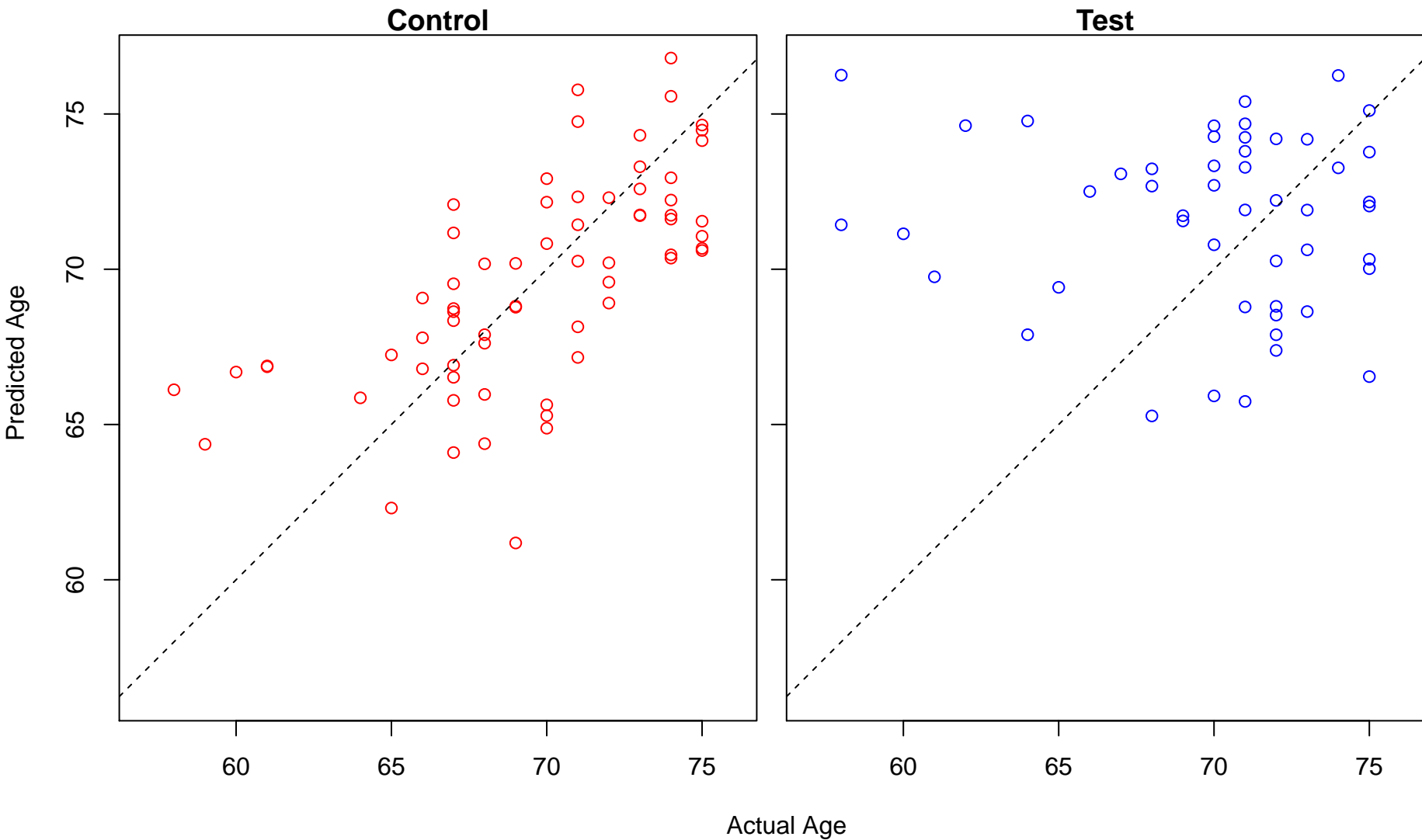
establishment of mitochondrion localization (Score: 1.497682)



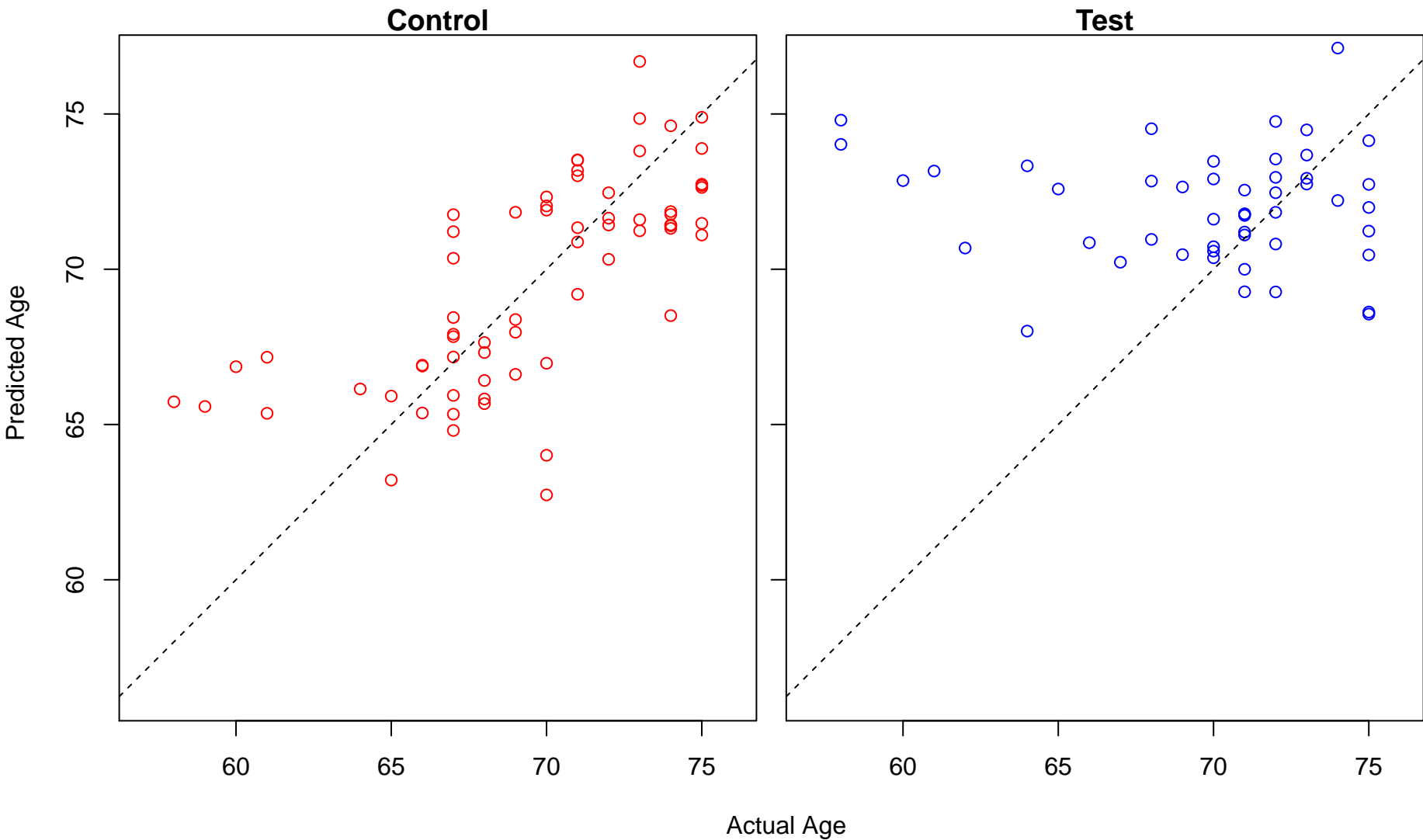
regulation of secretion by cell (Score: 1.496880)



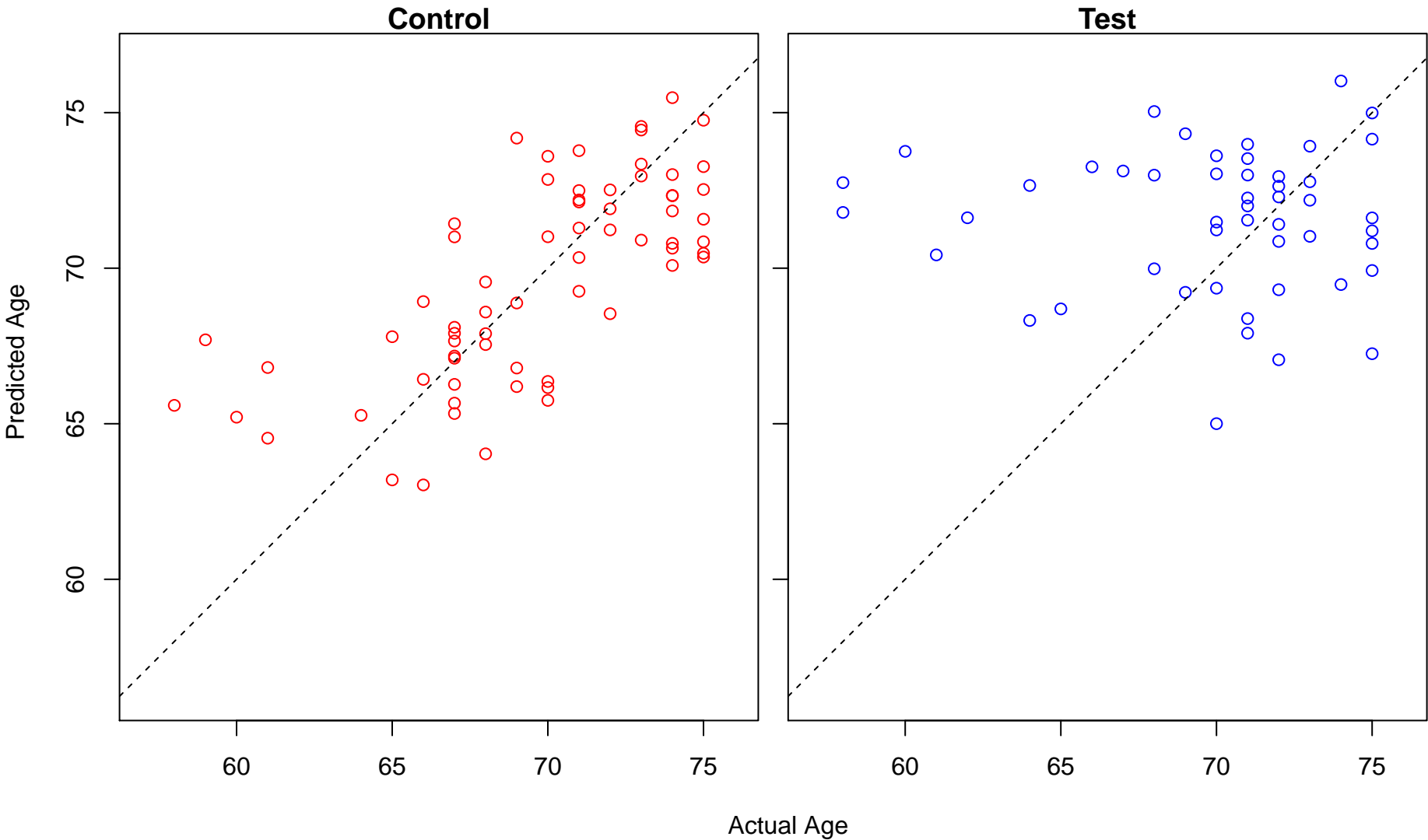
response to starvation (Score: 1.496356)



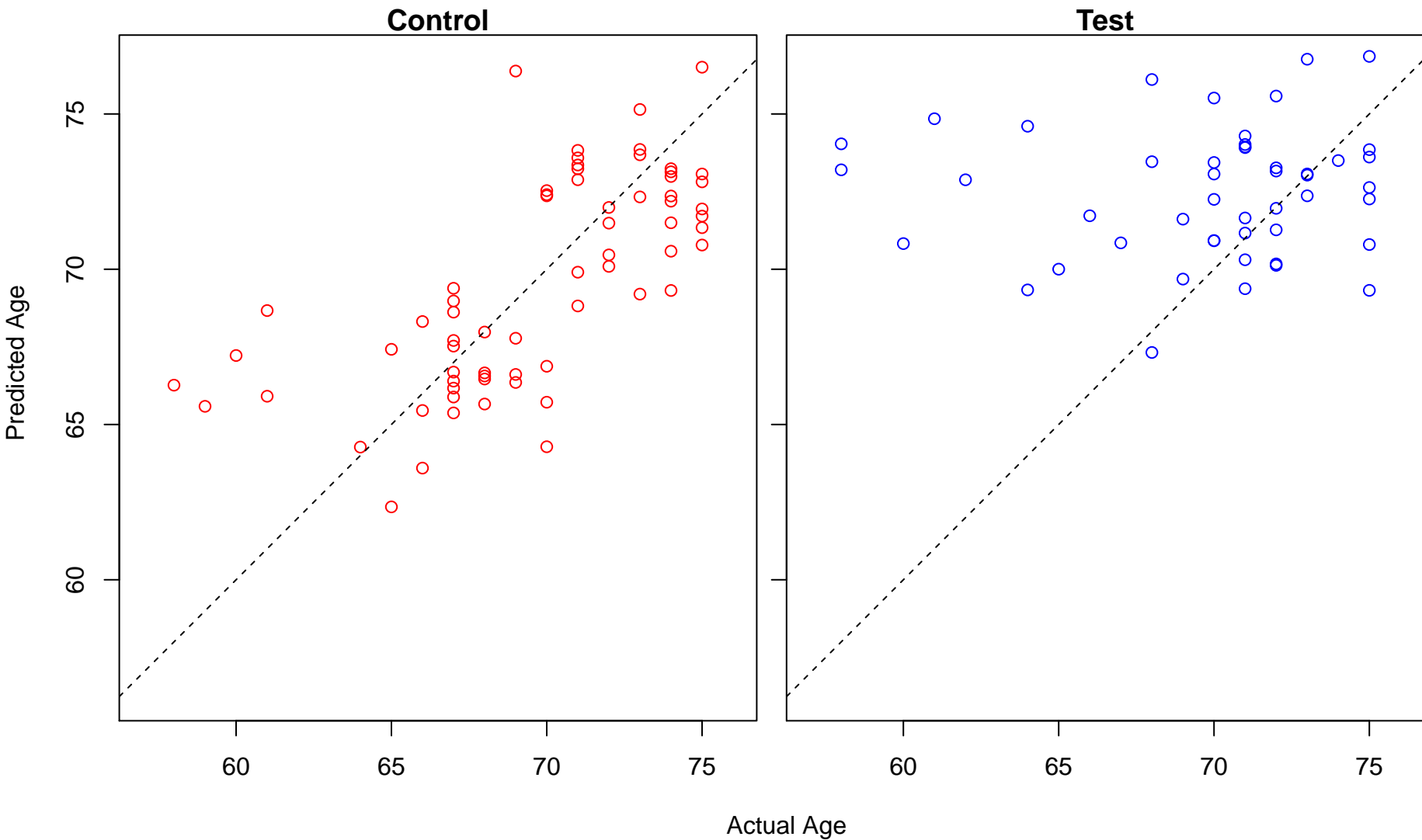
negative regulation of DNA replication (Score: 1.496342)



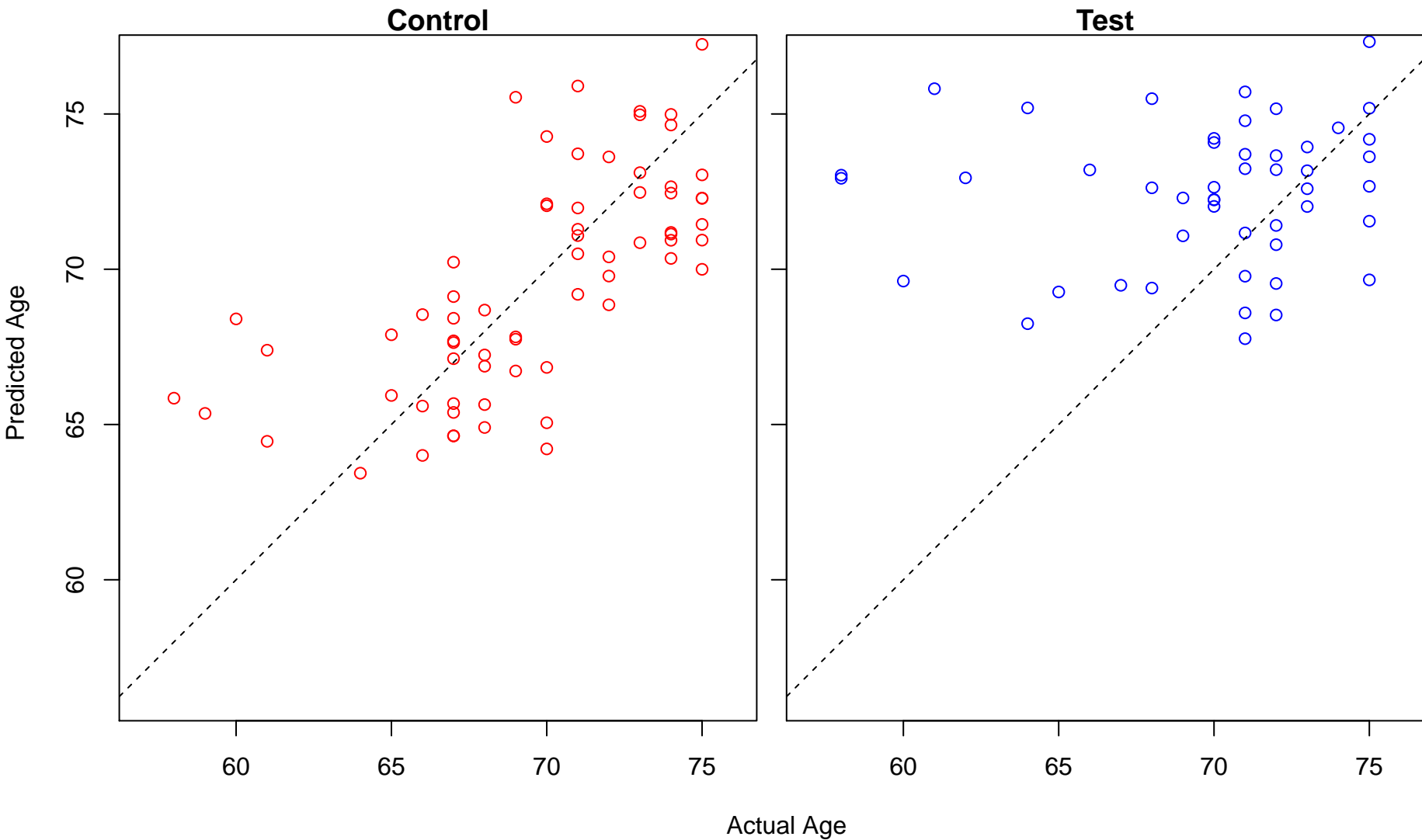
positive regulation of transcription from RNA polymerase II promoter in response to stress (Score: 1.49)



muscle organ development (Score: 1.495611)

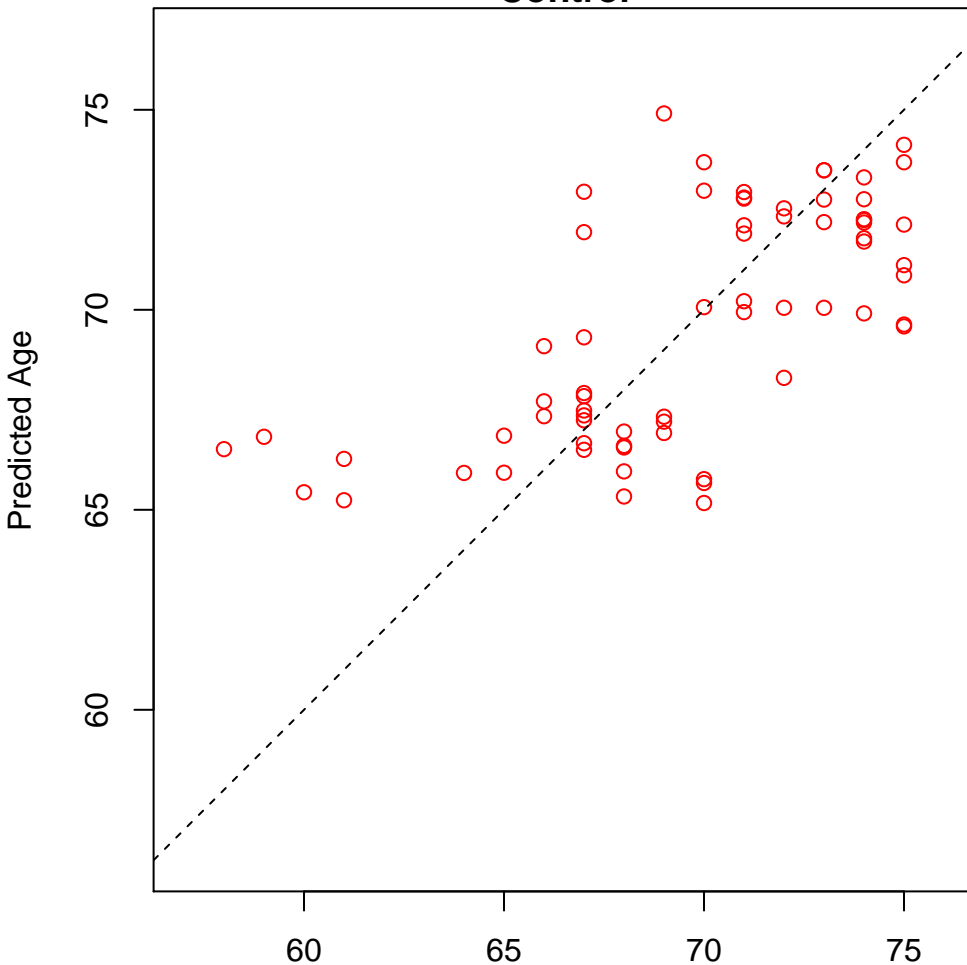


muscle tissue development (Score: 1.495317)

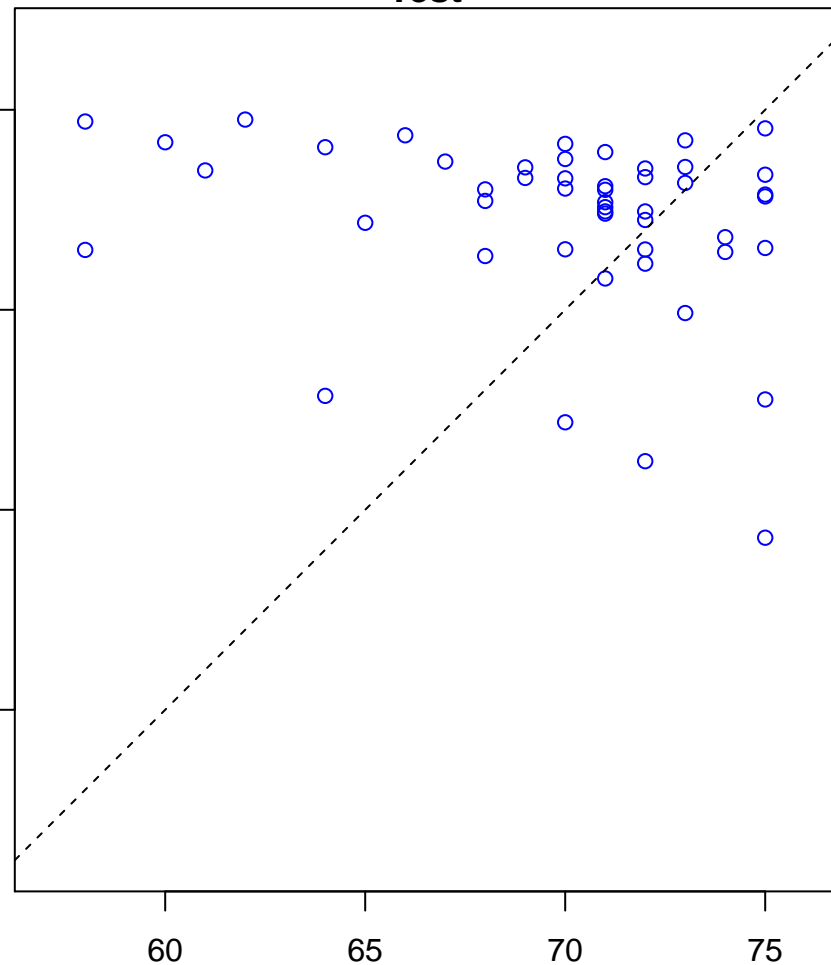


ribosomal large subunit biogenesis (Score: 1.495260)

Control

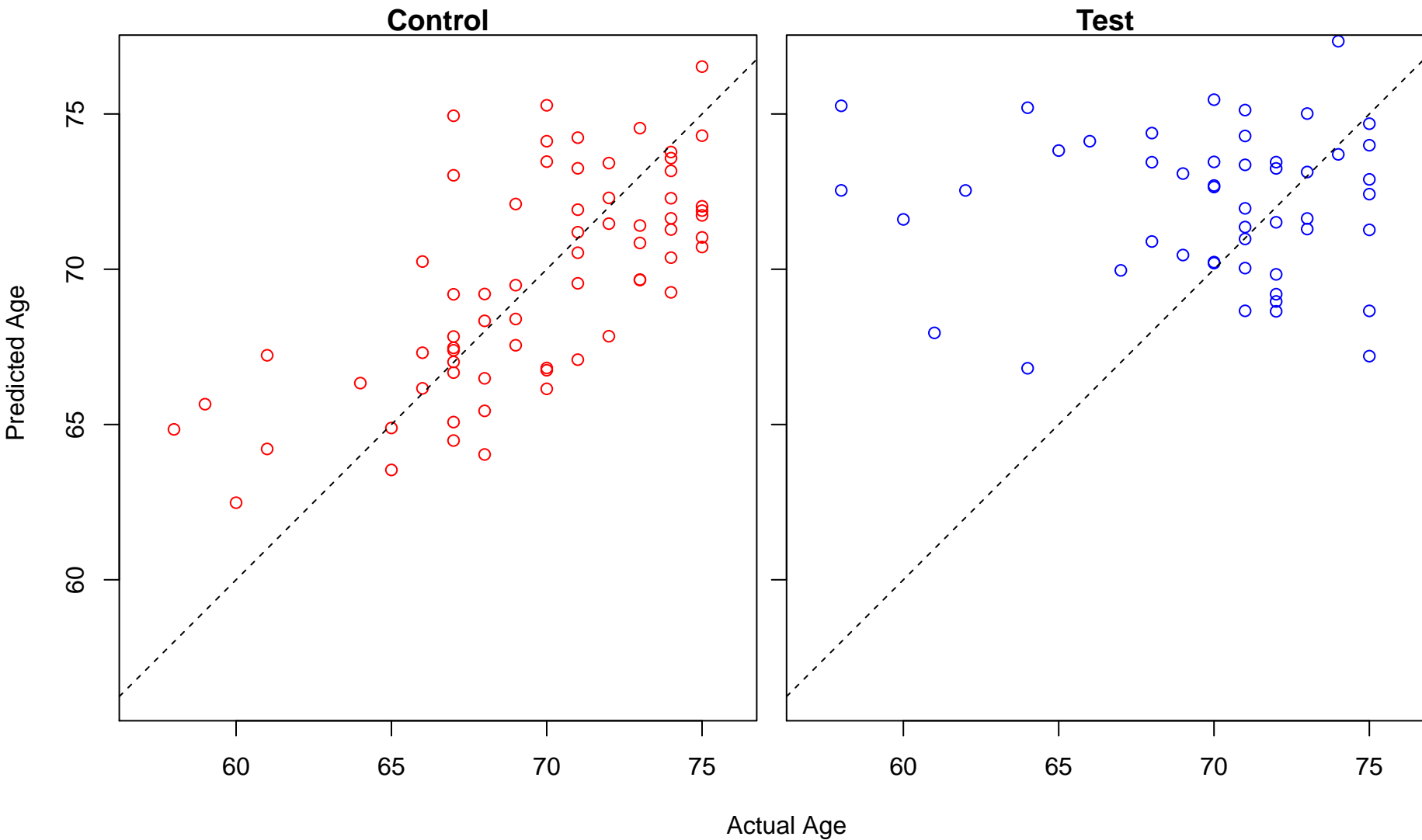


Test

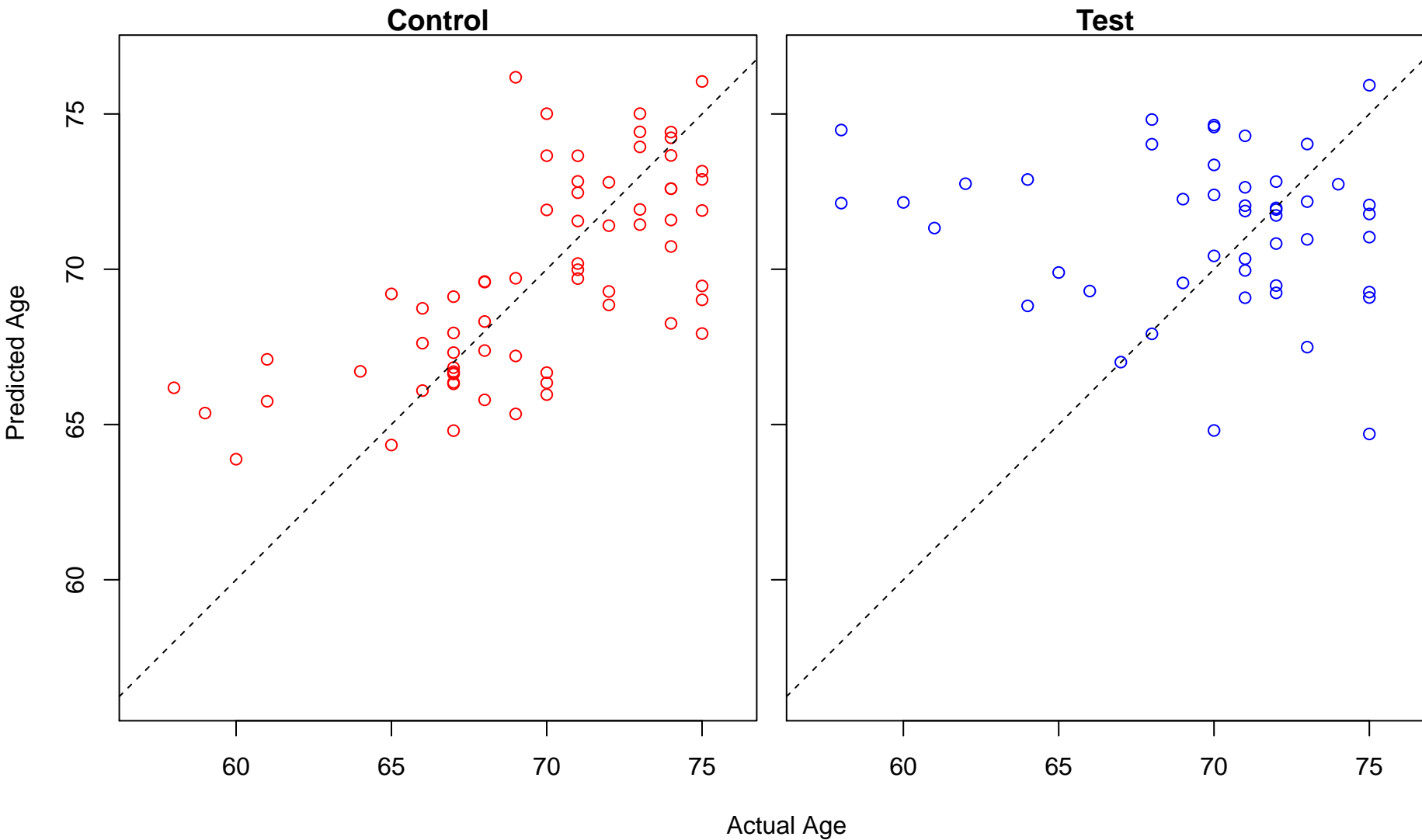


Actual Age

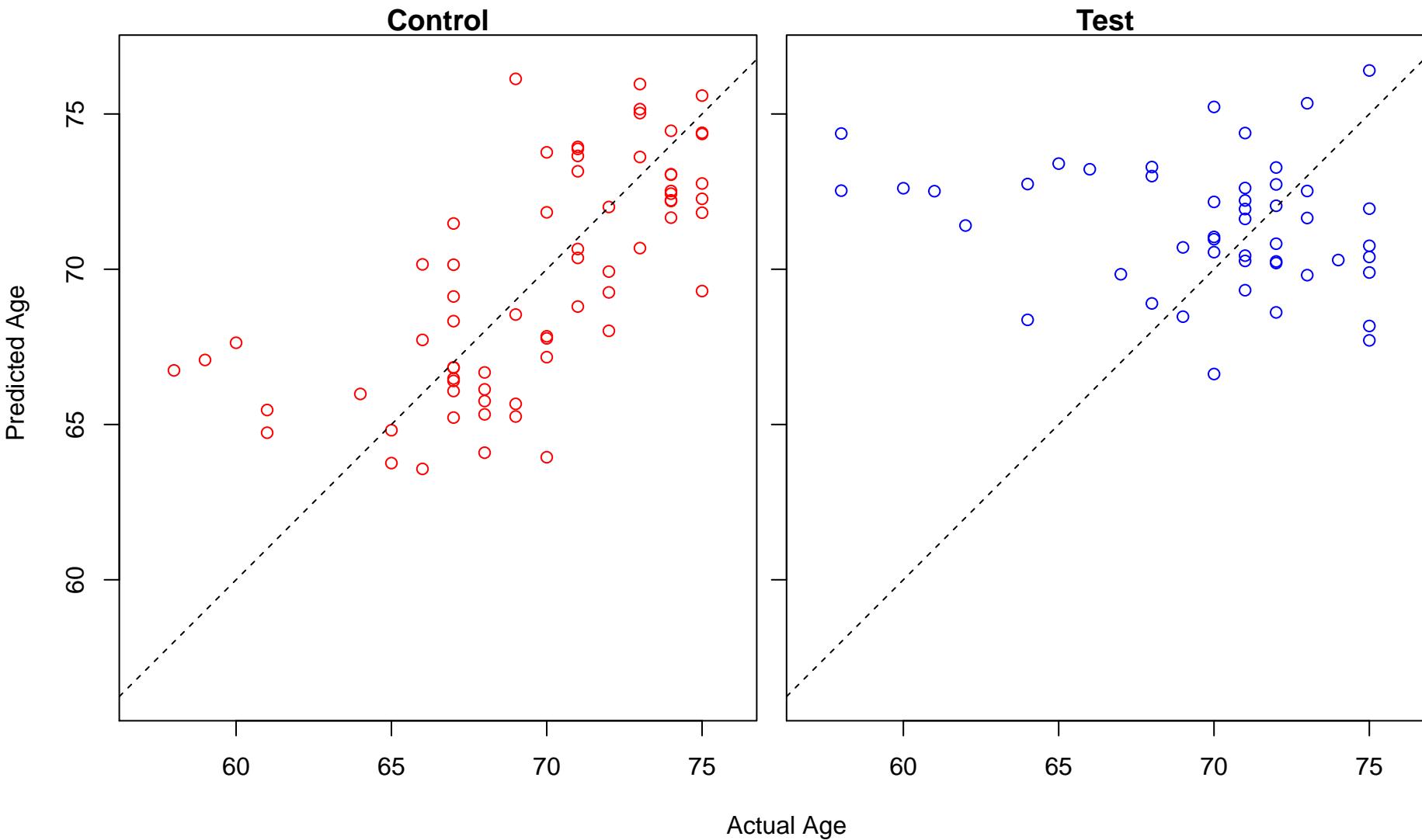
response to acid chemical (Score: 1.495232)



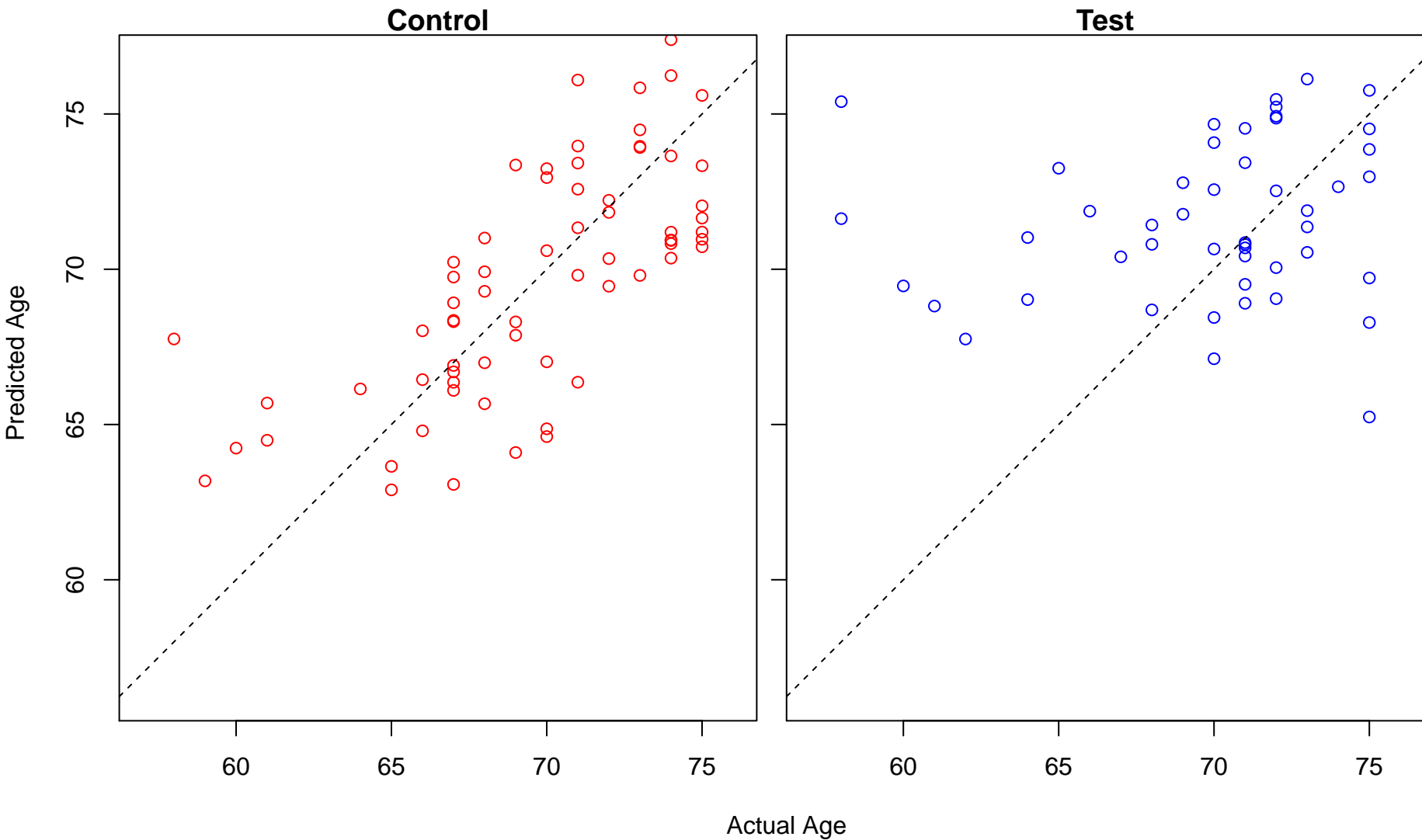
T cell activation involved in immune response (Score: 1.495145)



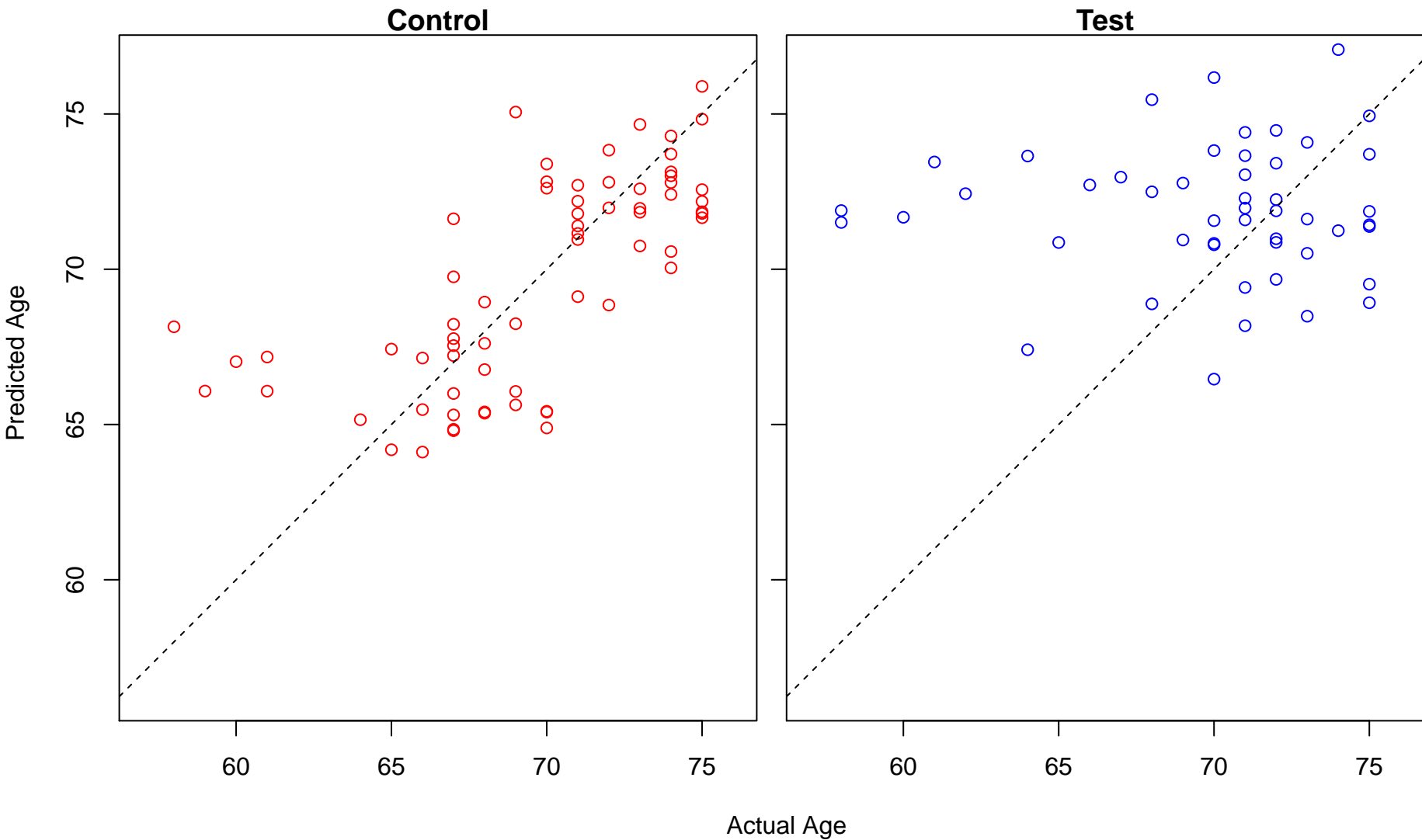
regulation of peptide secretion (Score: 1.494689)



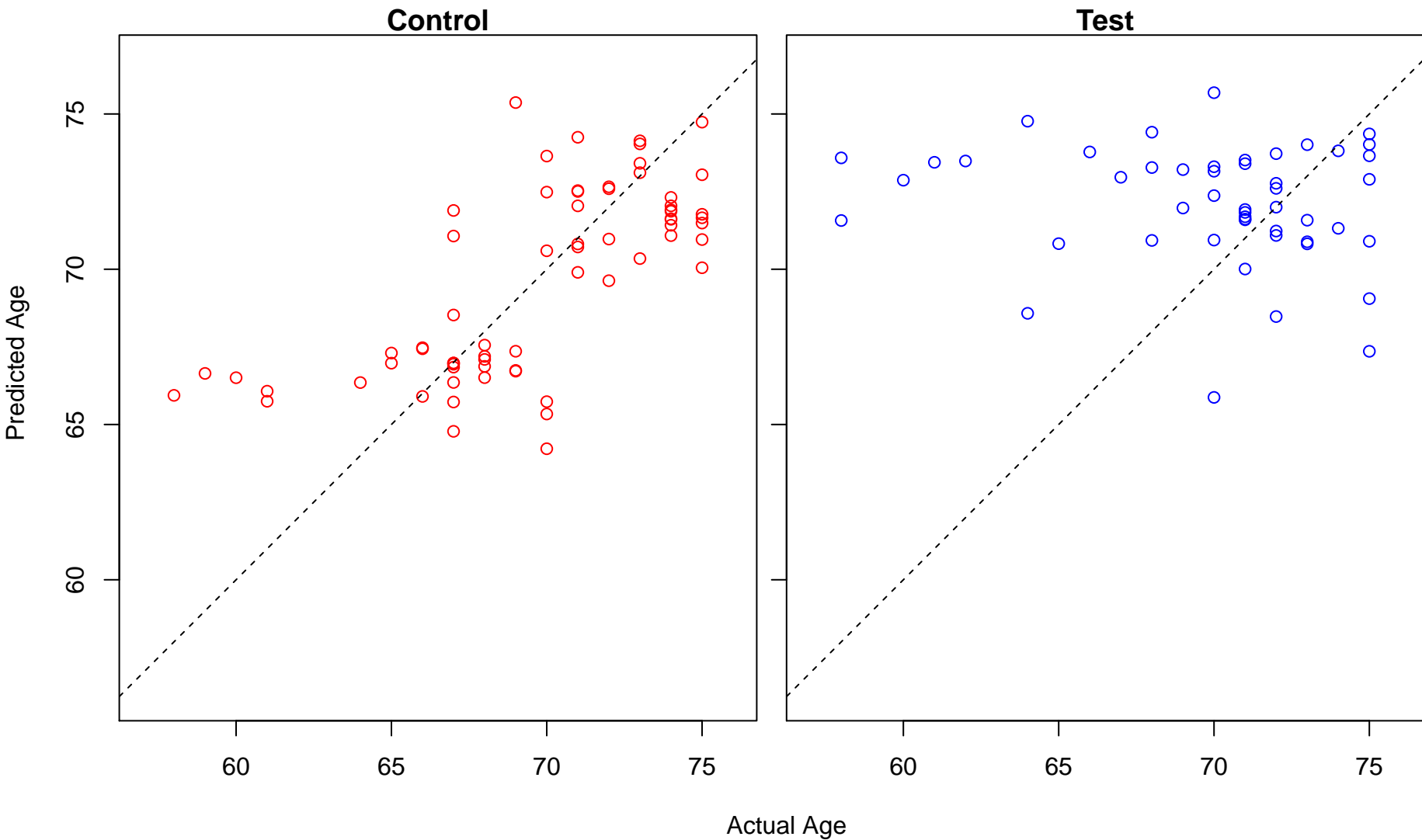
regulation of metal ion transport (Score: 1.494660)



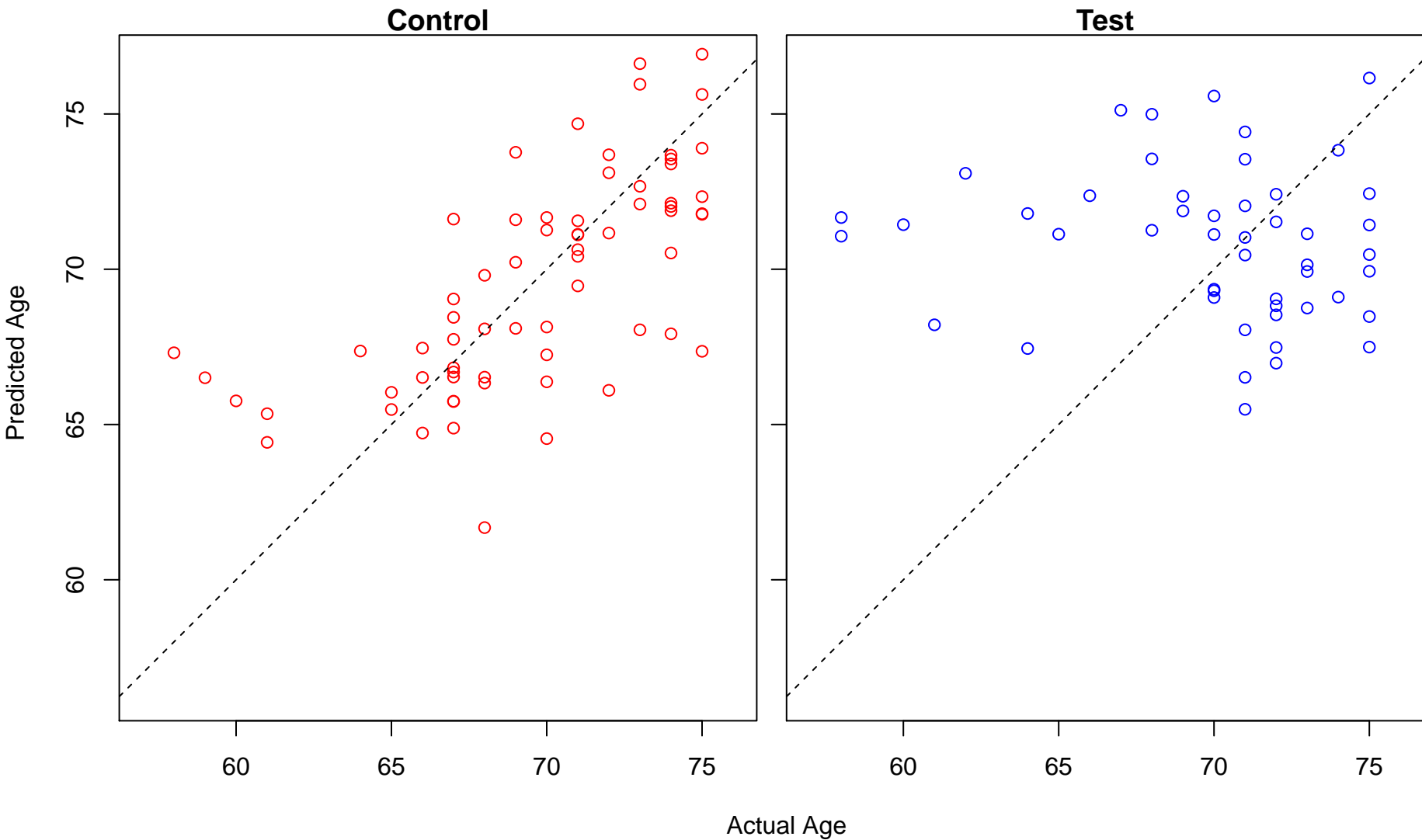
intracellular receptor signaling pathway (Score: 1.494480)



positive regulation of peptidyl-serine phosphorylation (Score: 1.494312)

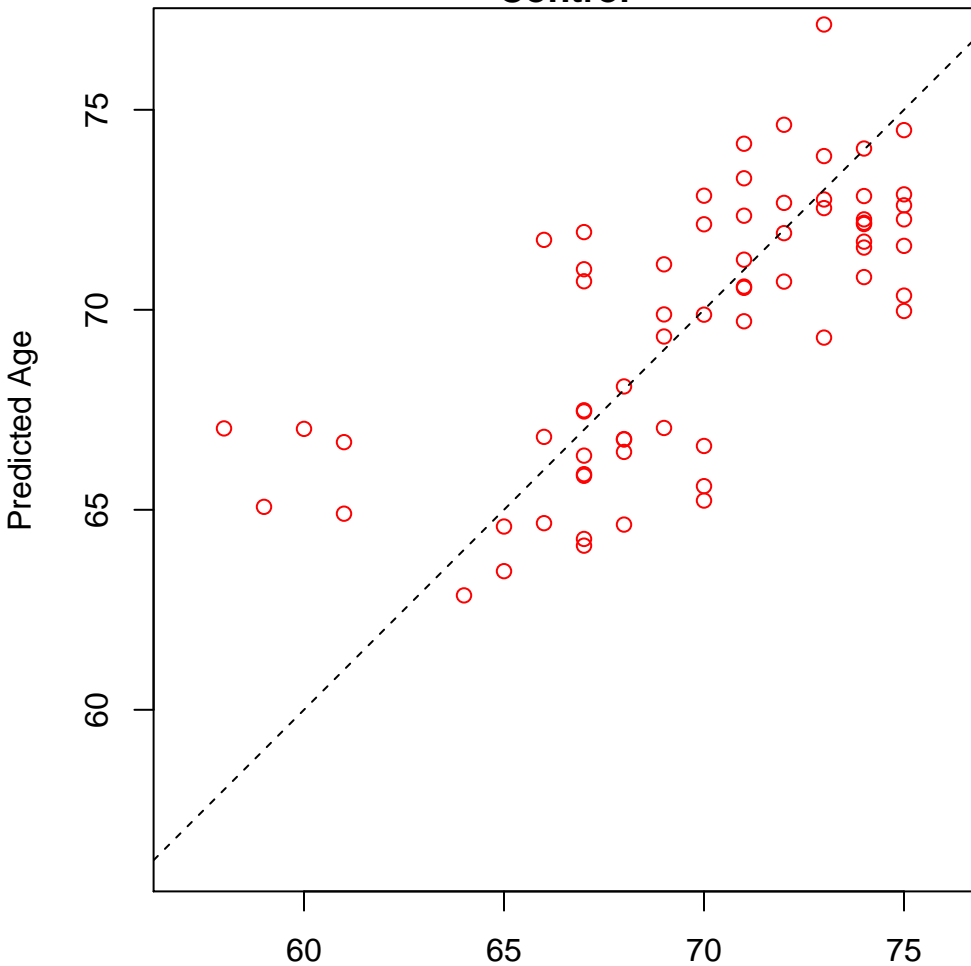


defense response to fungus (Score: 1.494077)

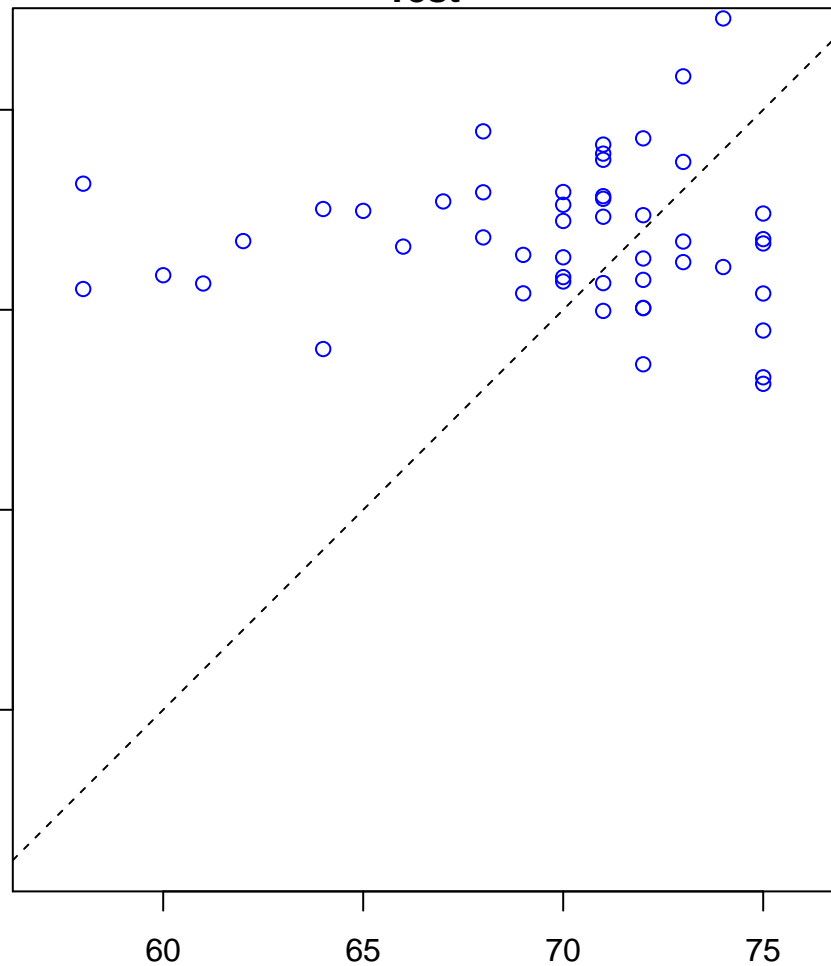


regulation of mRNA metabolic process (Score: 1.493676)

Control

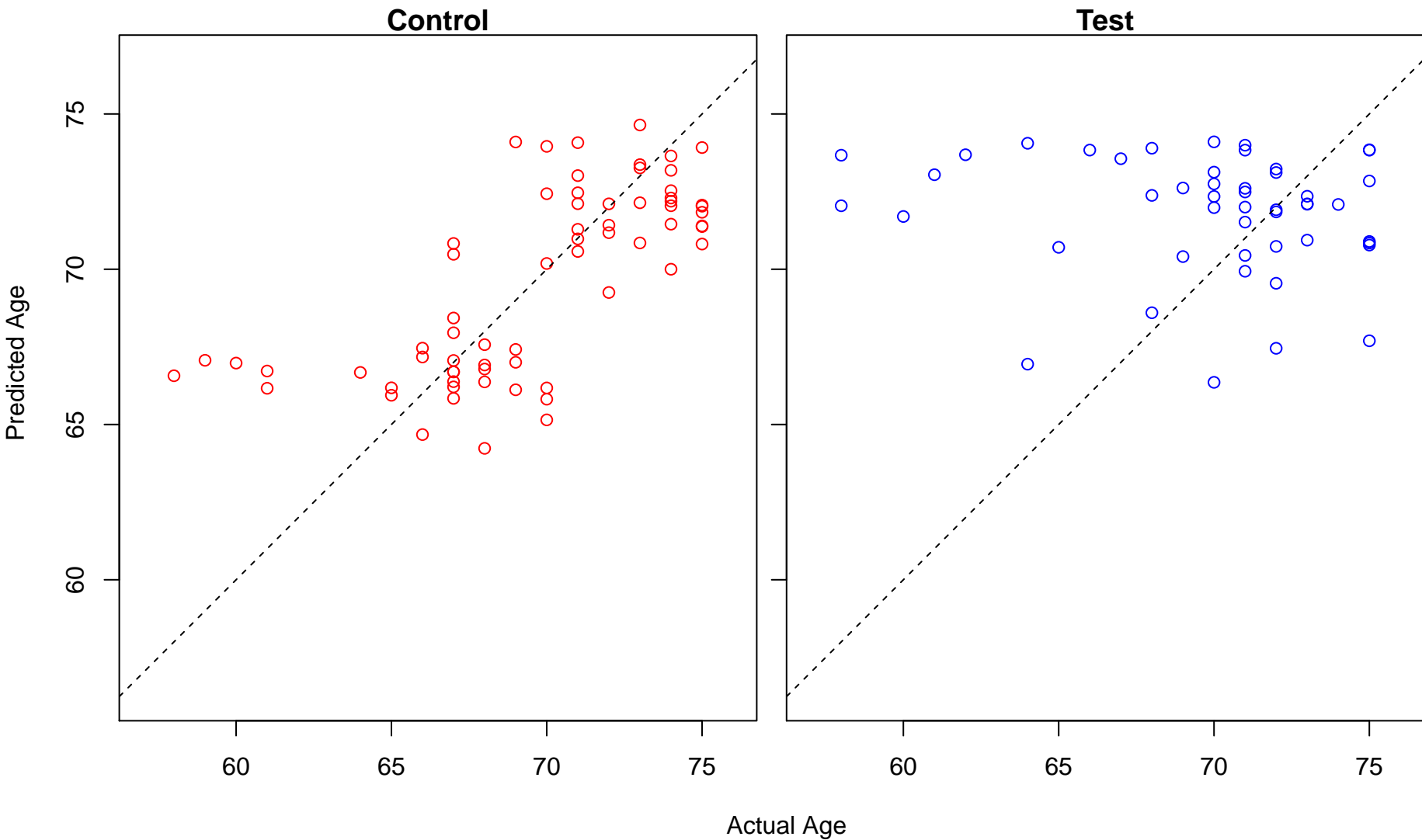


Test

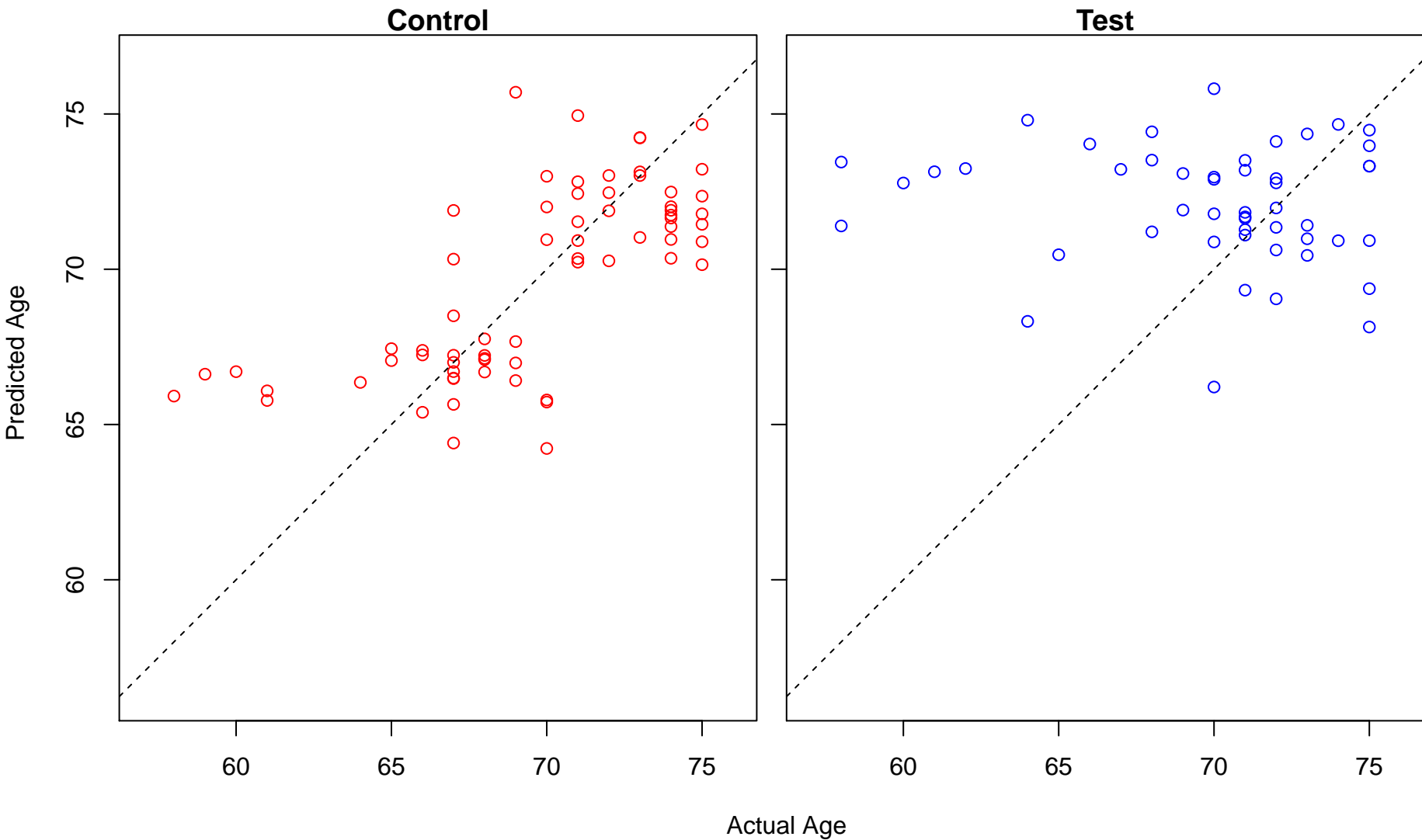


Actual Age

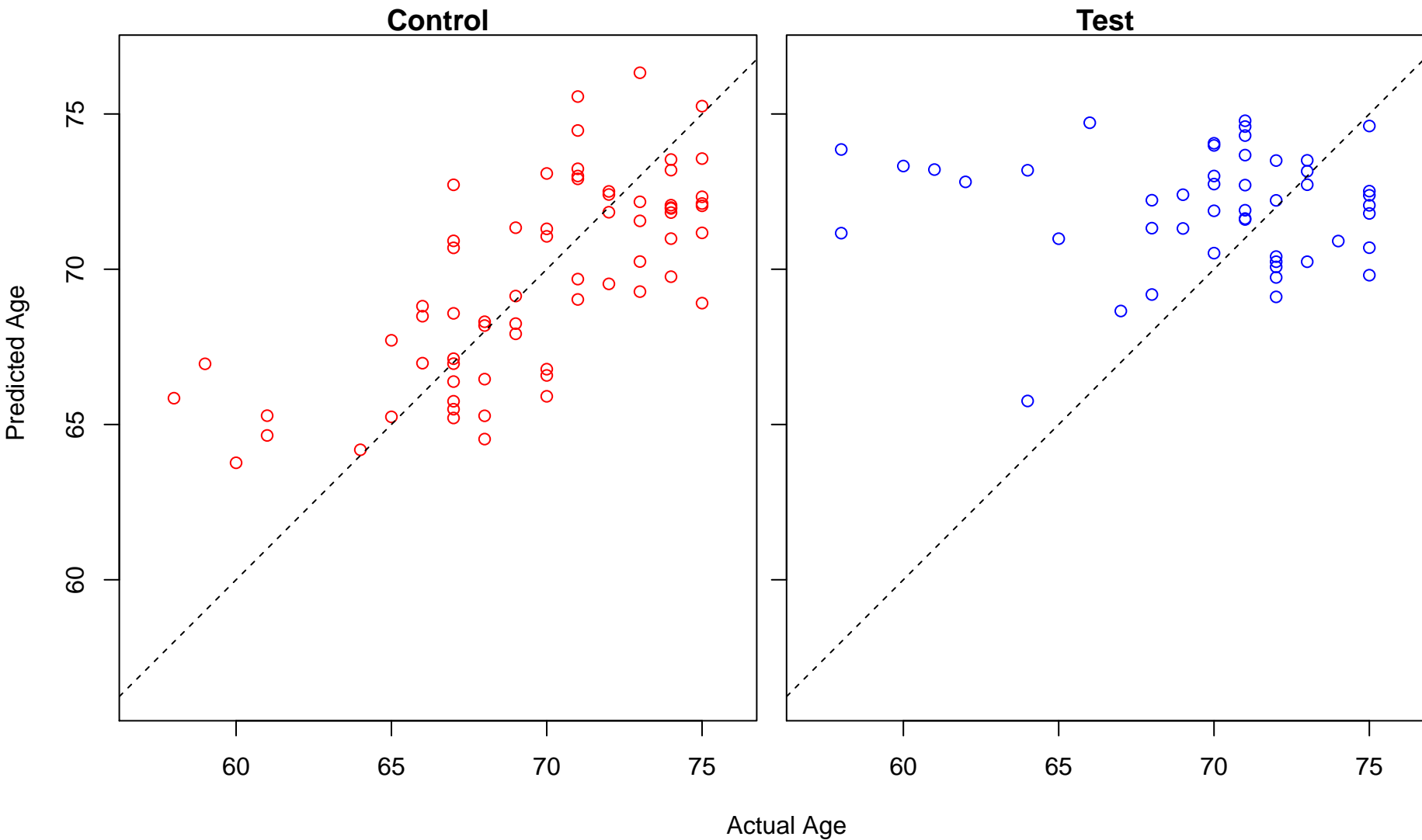
regulation of chemotaxis (Score: 1.493206)



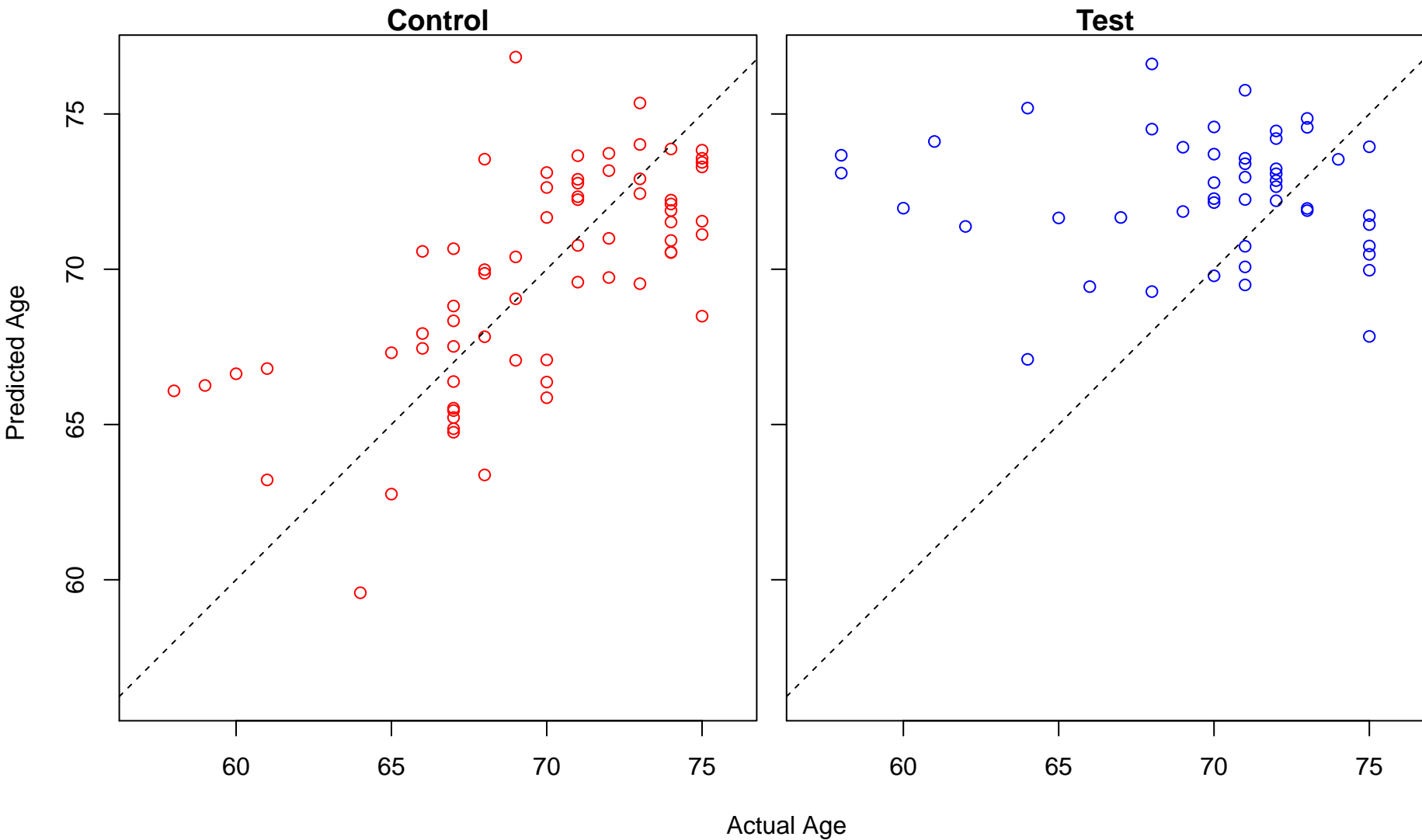
protein repair (Score: 1.491725)



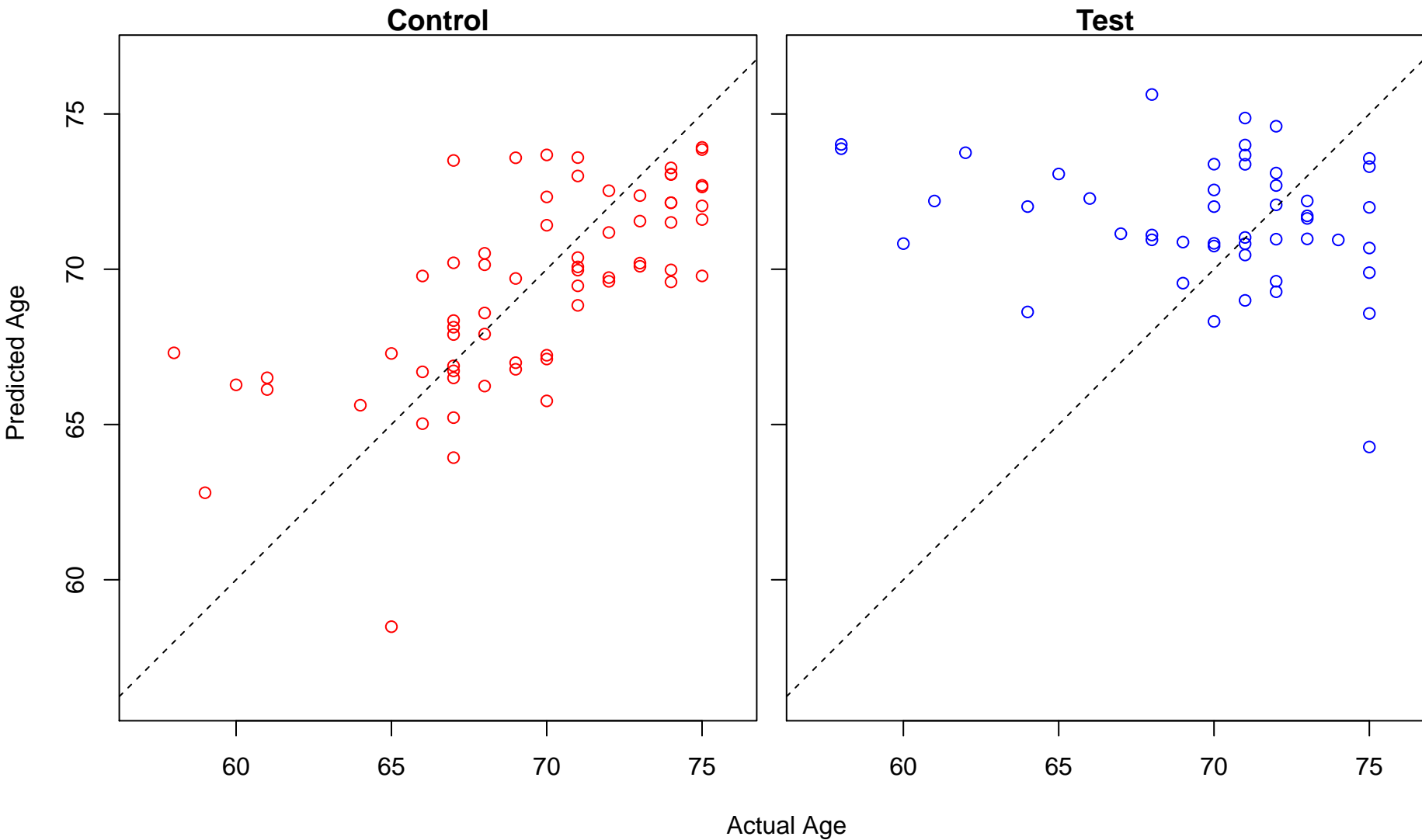
vasculogenesis (Score: 1.491535)



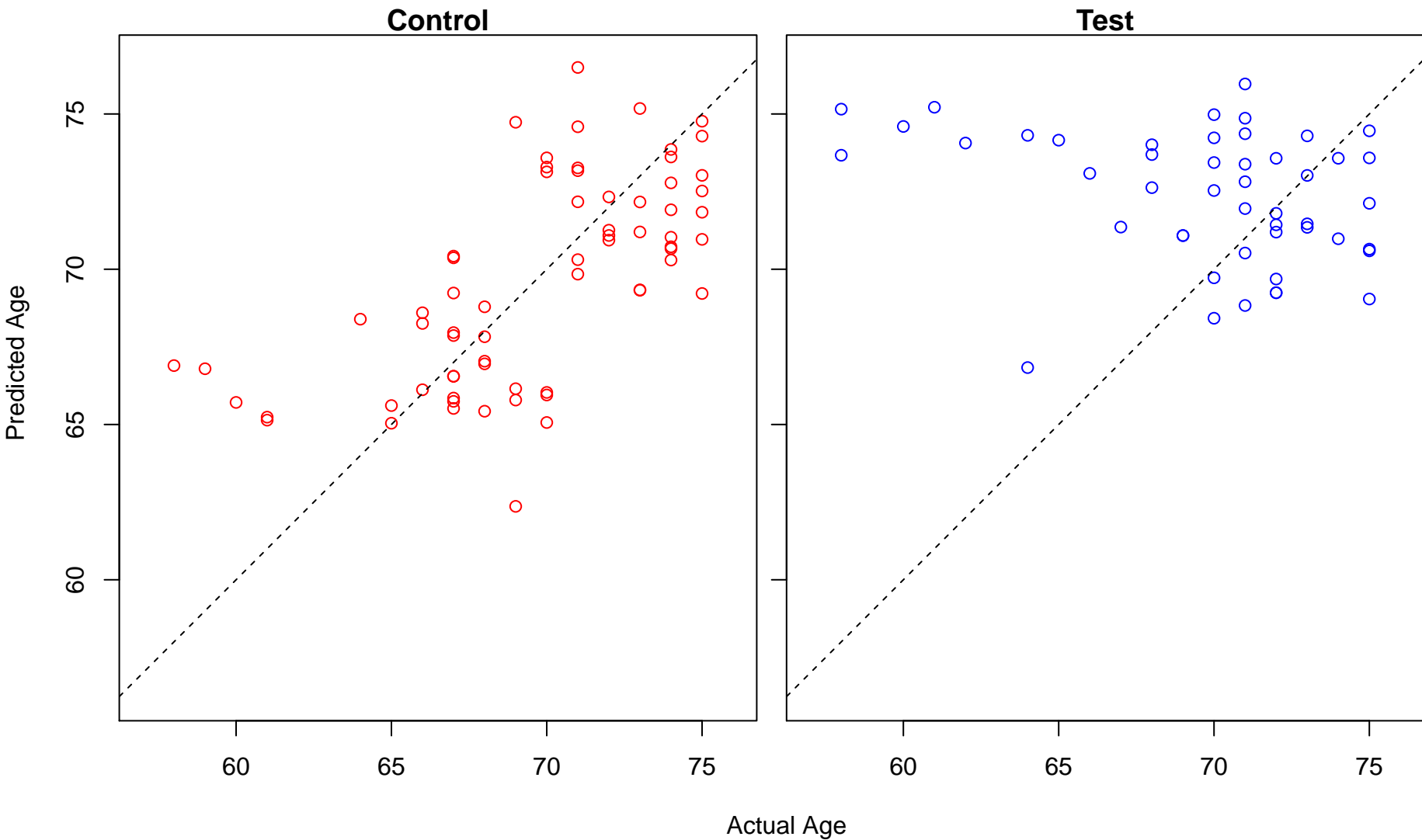
gene silencing (Score: 1.489985)



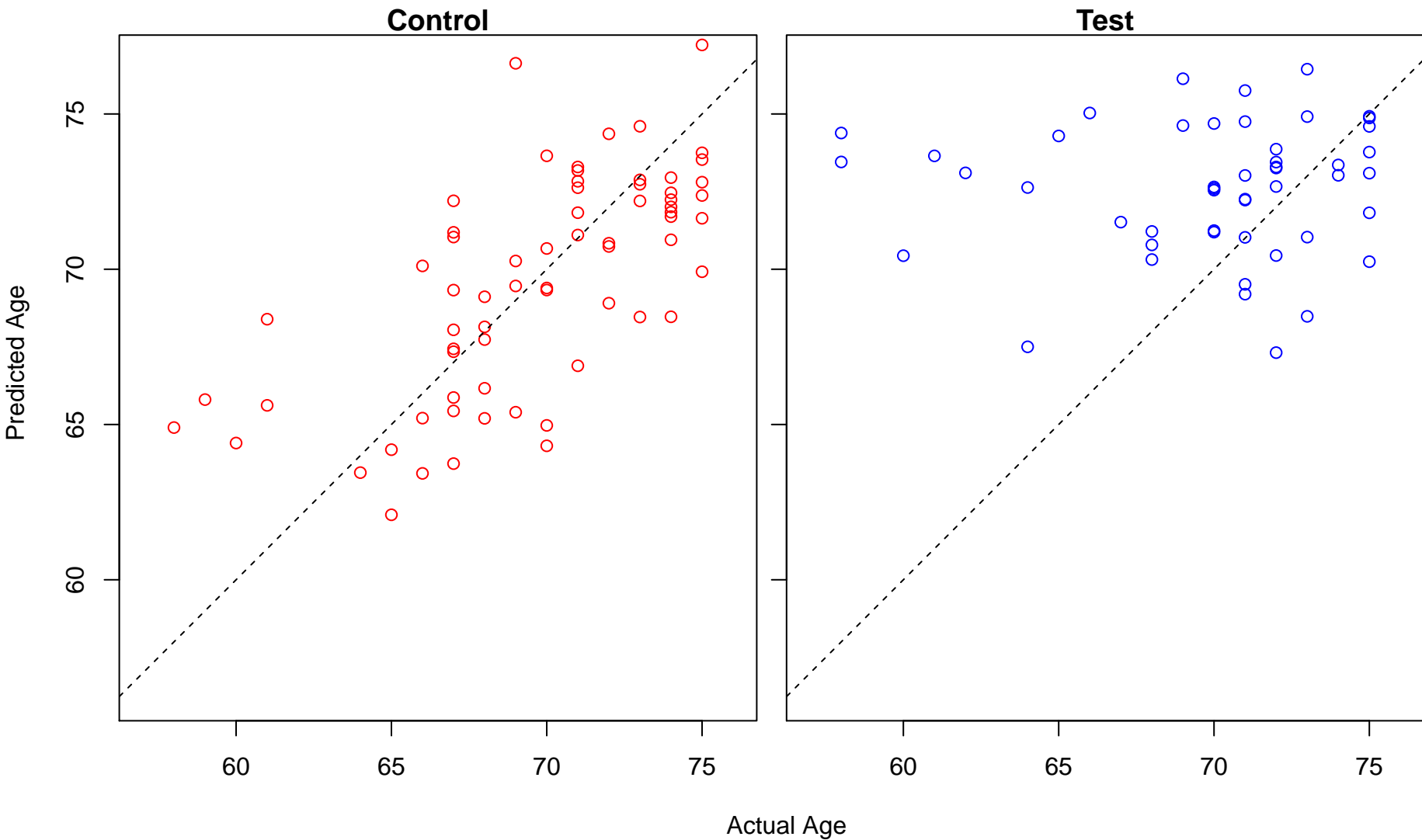
positive regulation of peptidyl-tyrosine phosphorylation (Score: 1.489836)



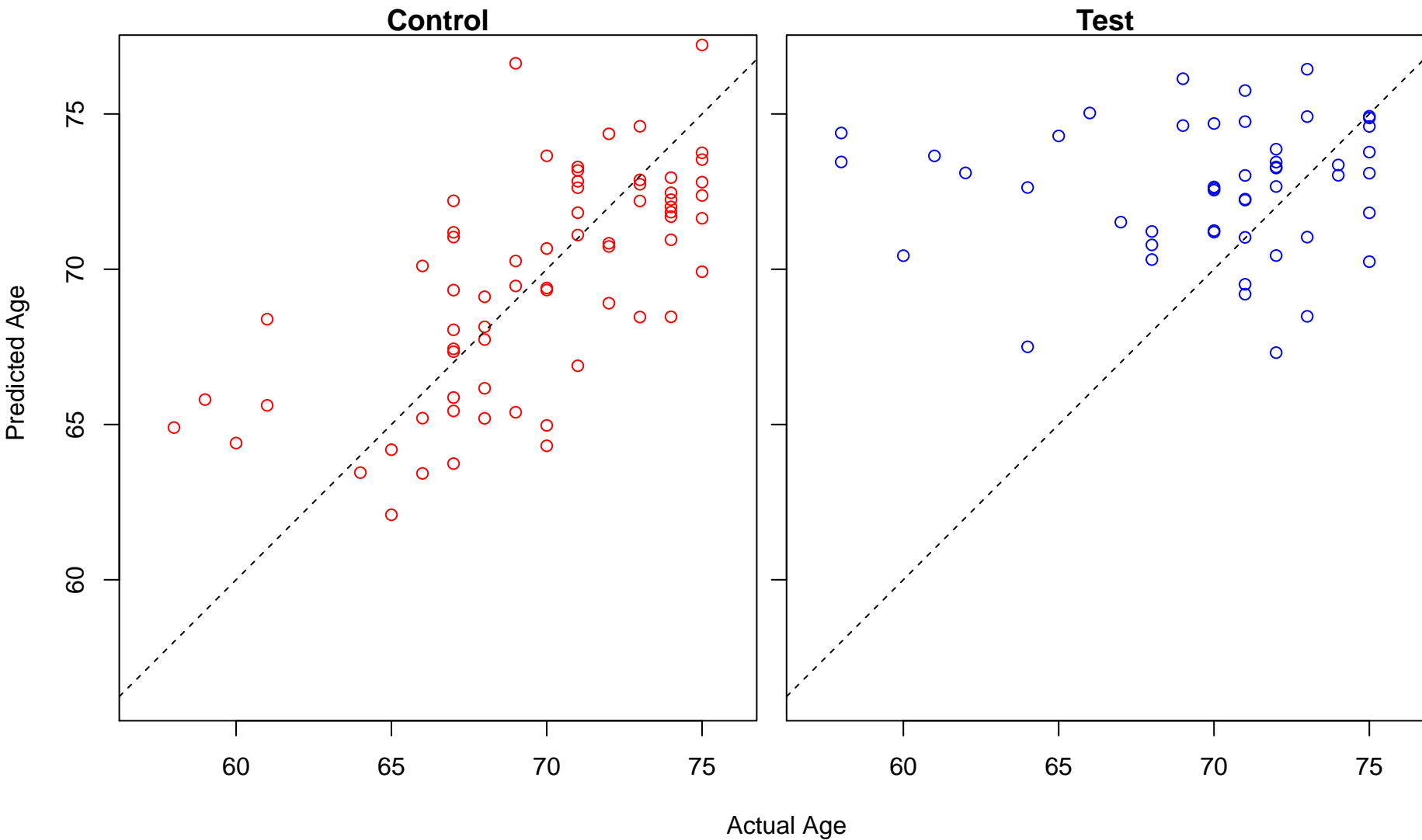
water transport (Score: 1.489454)



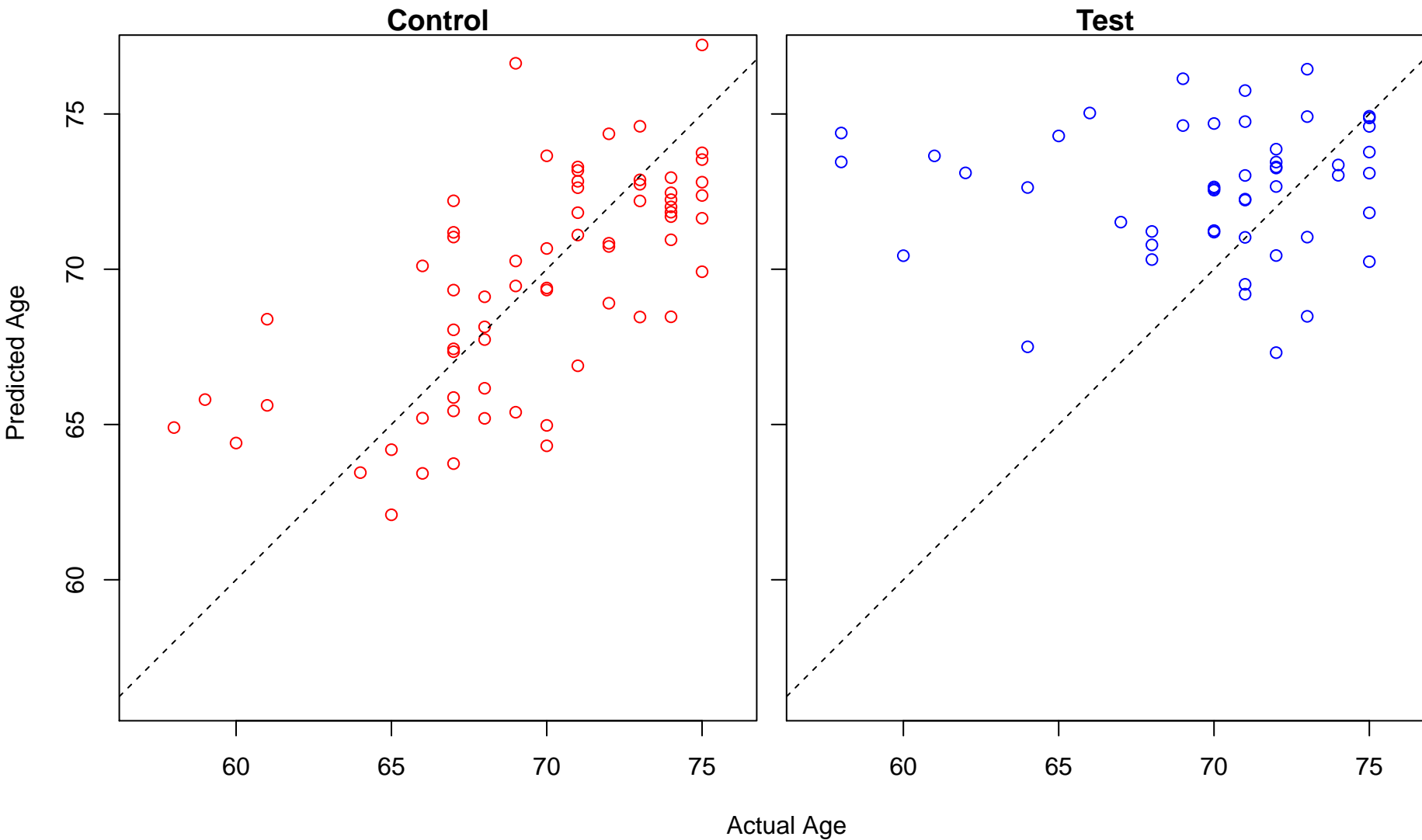
multi-organism transport (Score: 1.489334)



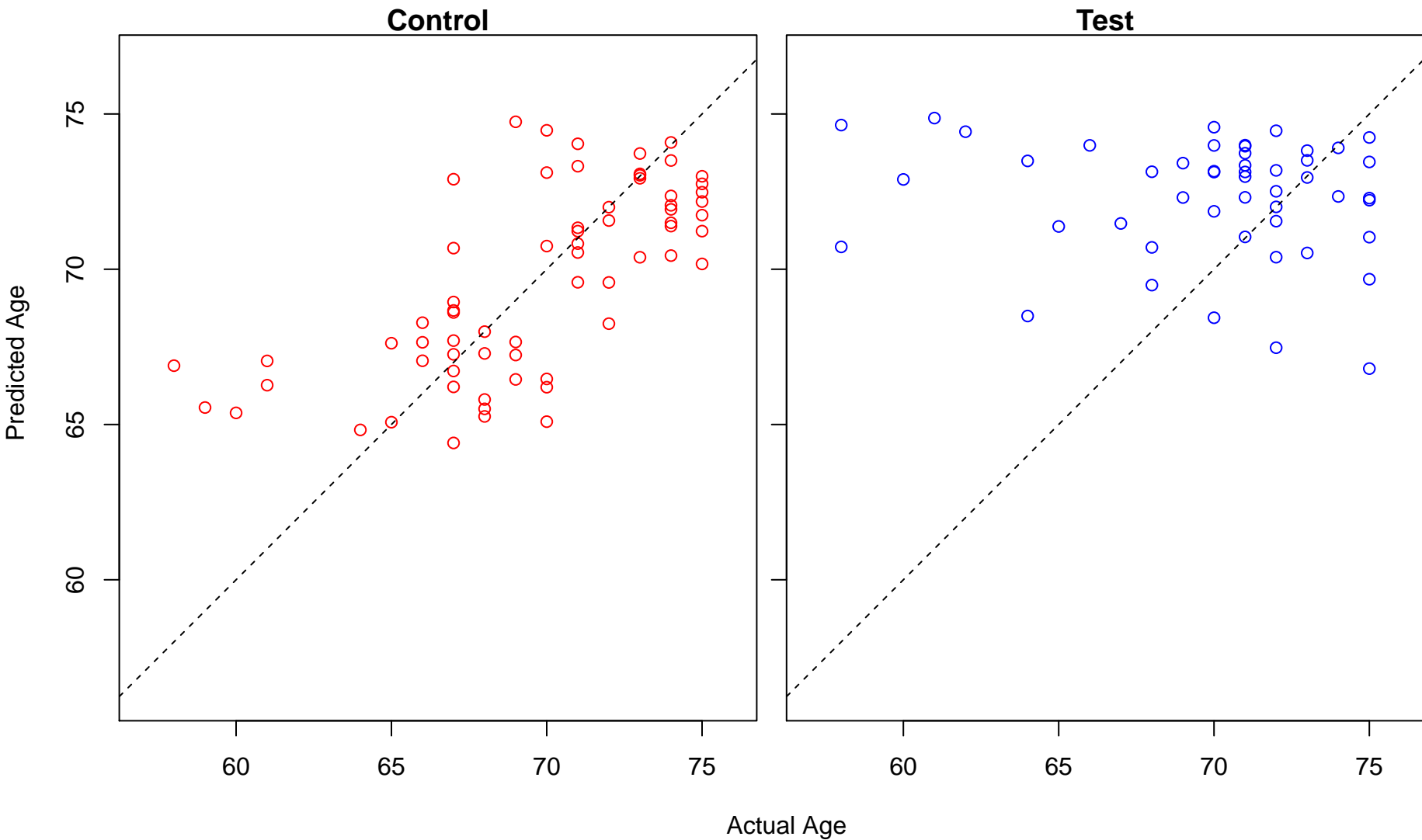
transport of virus (Score: 1.489334)



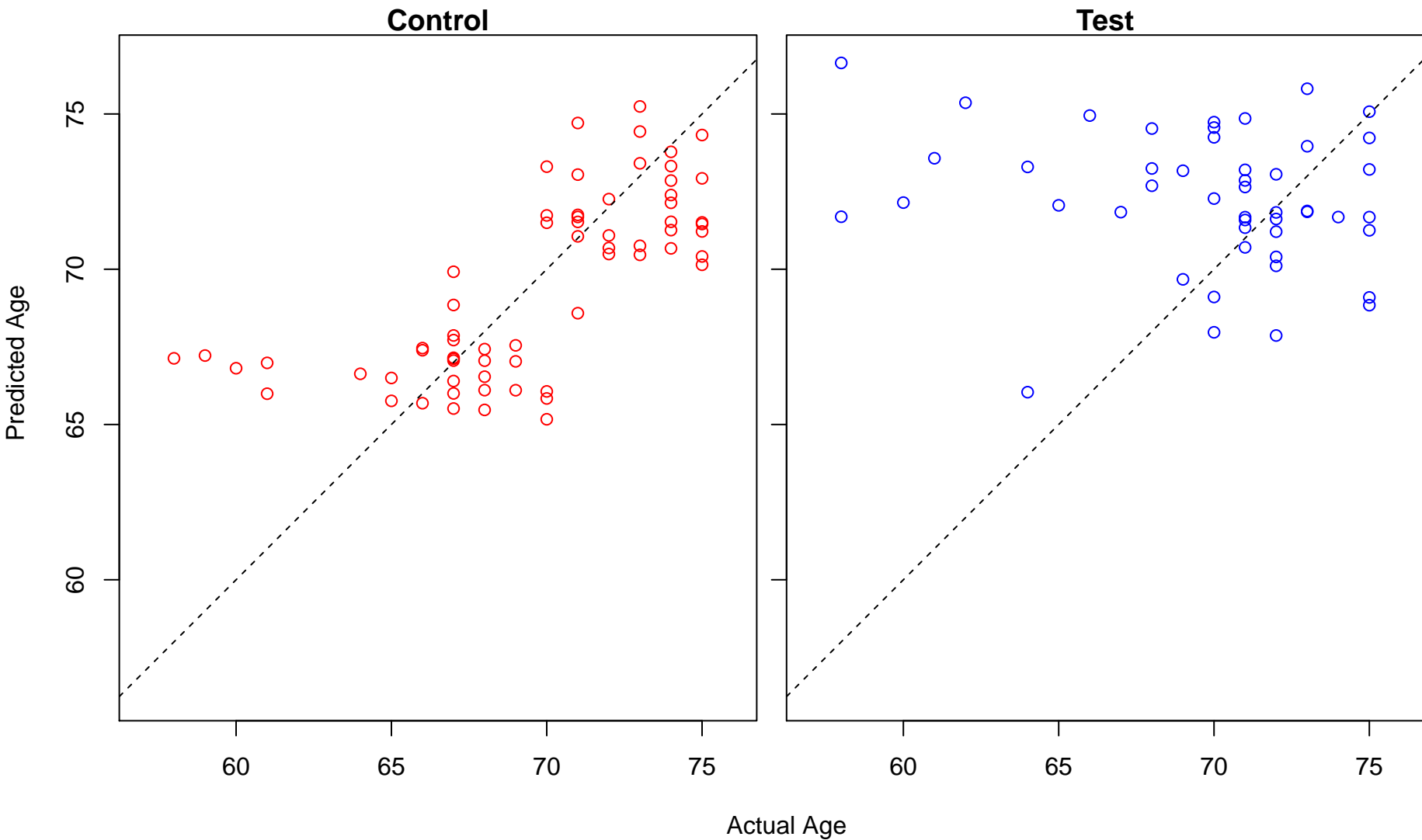
multi-organism localization (Score: 1.489334)



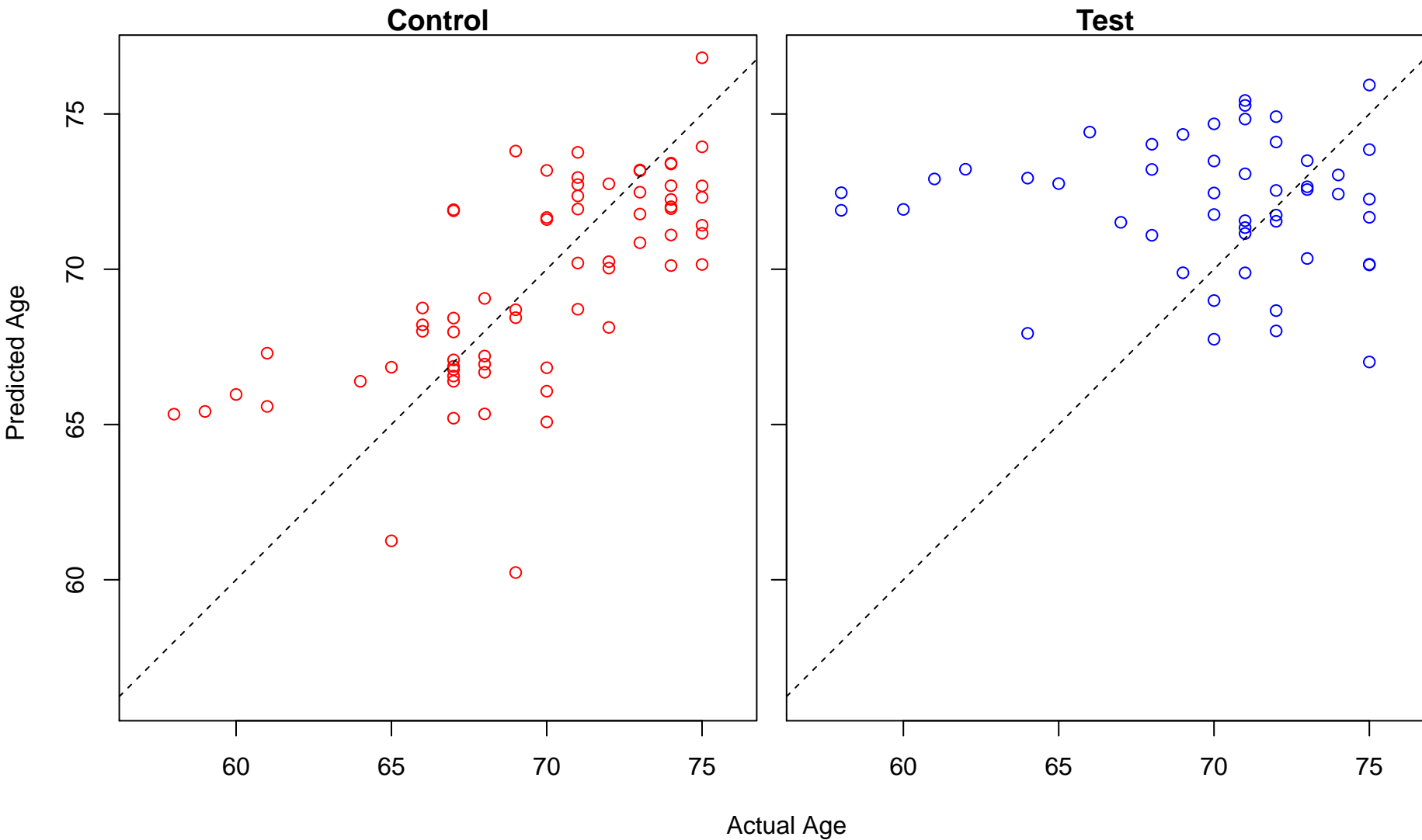
osteoblast differentiation (Score: 1.489293)



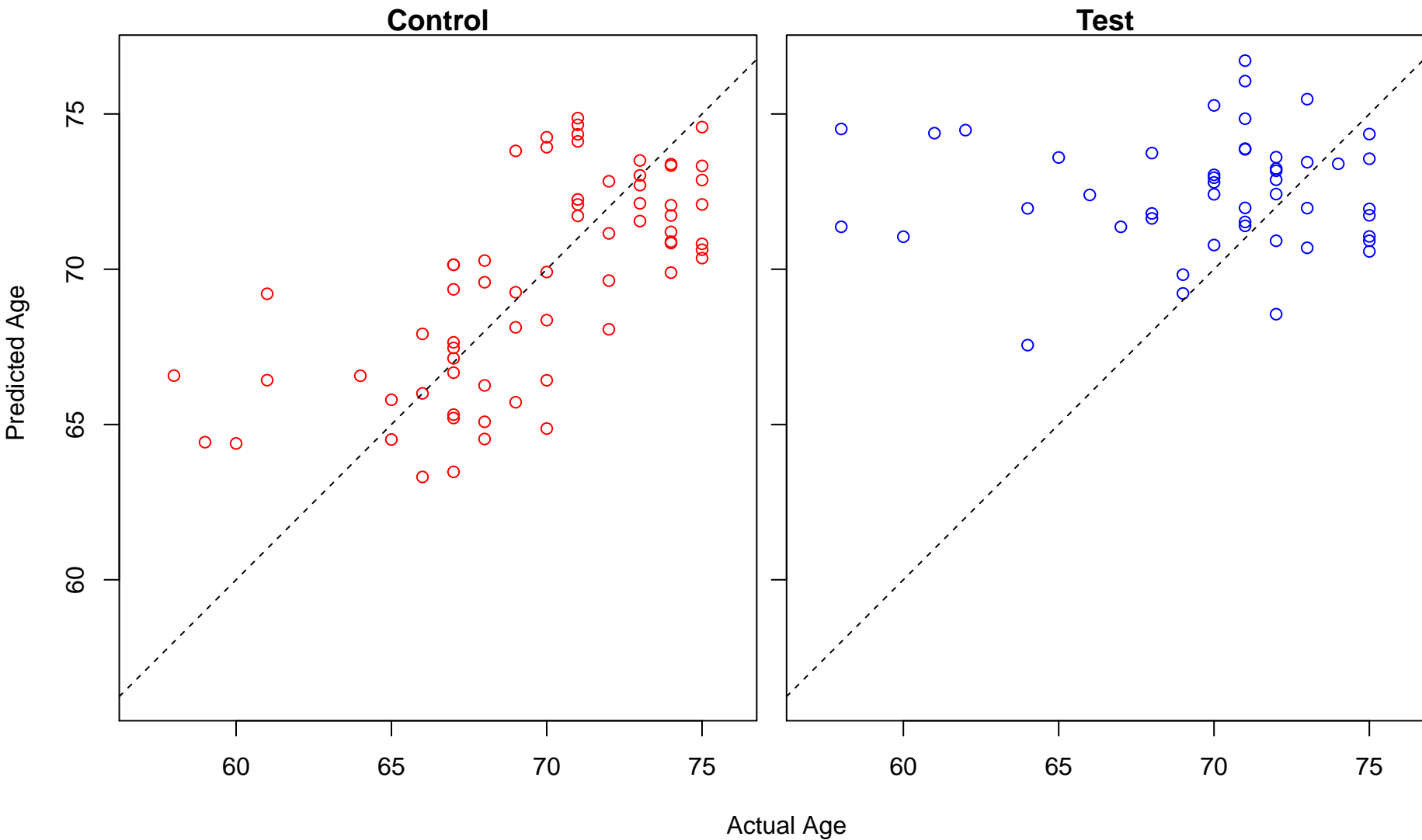
cellular detoxification (Score: 1.489041)



regulation of cellular response to insulin stimulus (Score: 1.488466)

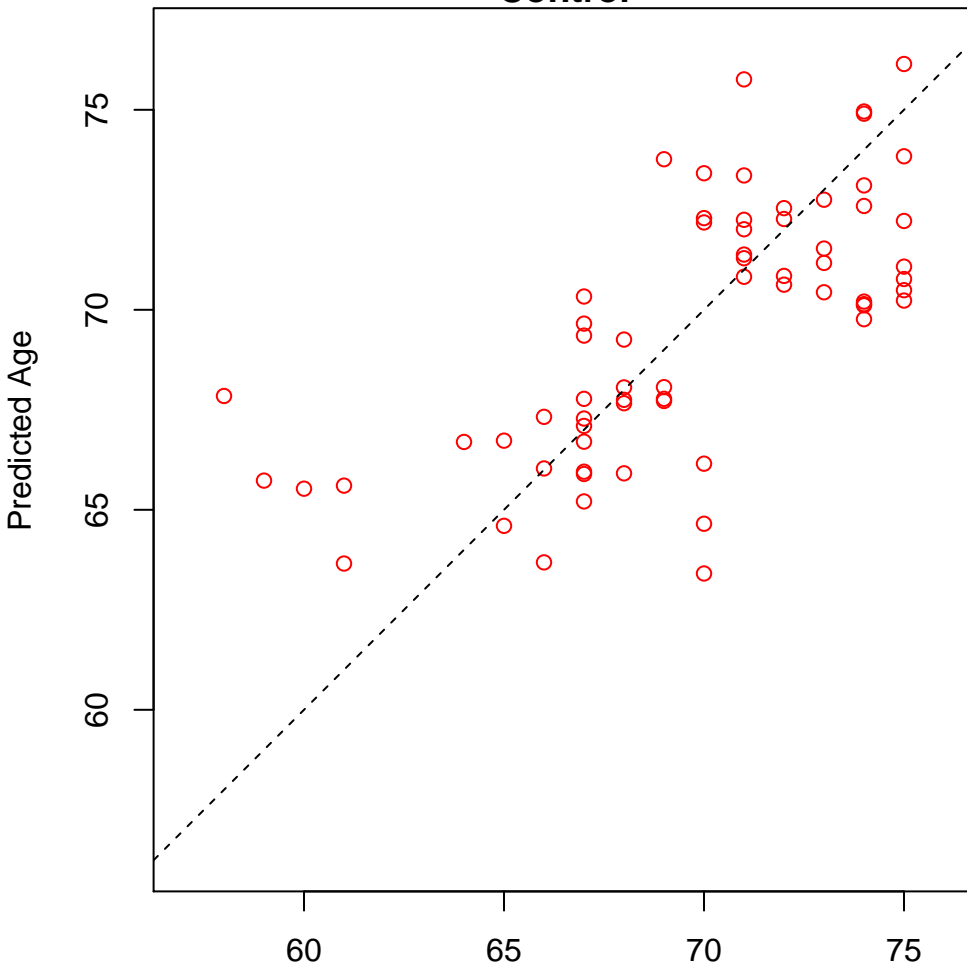


multicellular organismal homeostasis (Score: 1.488129)

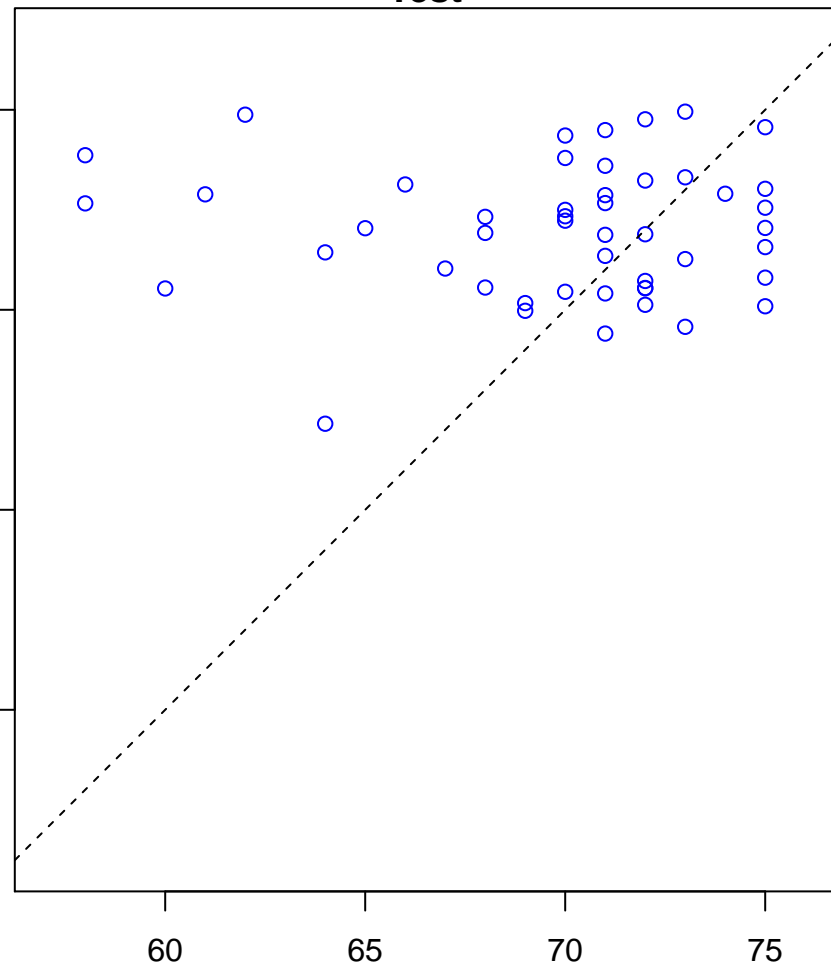


regulation of cellular component size (Score: 1.487635)

Control

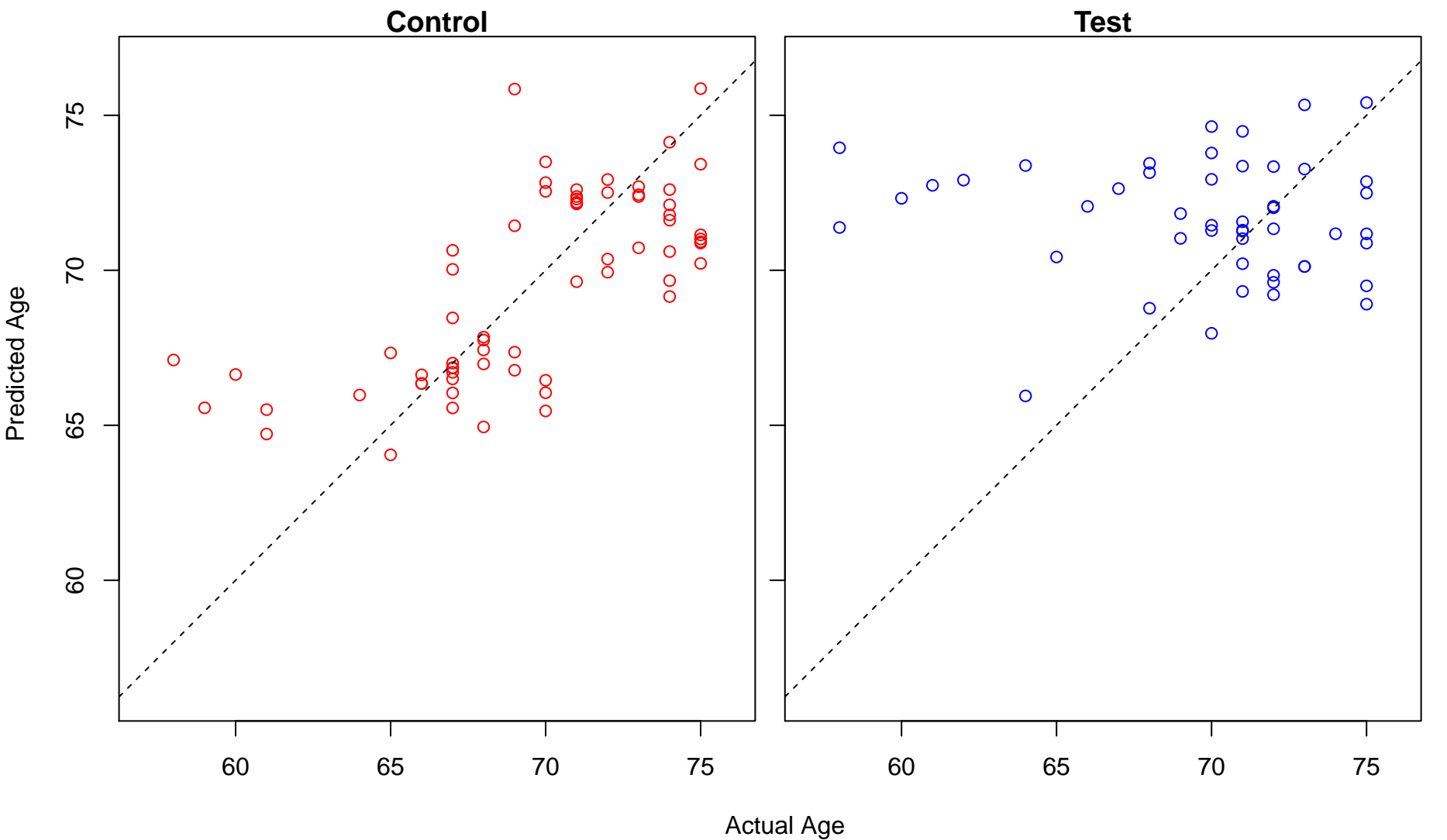


Test

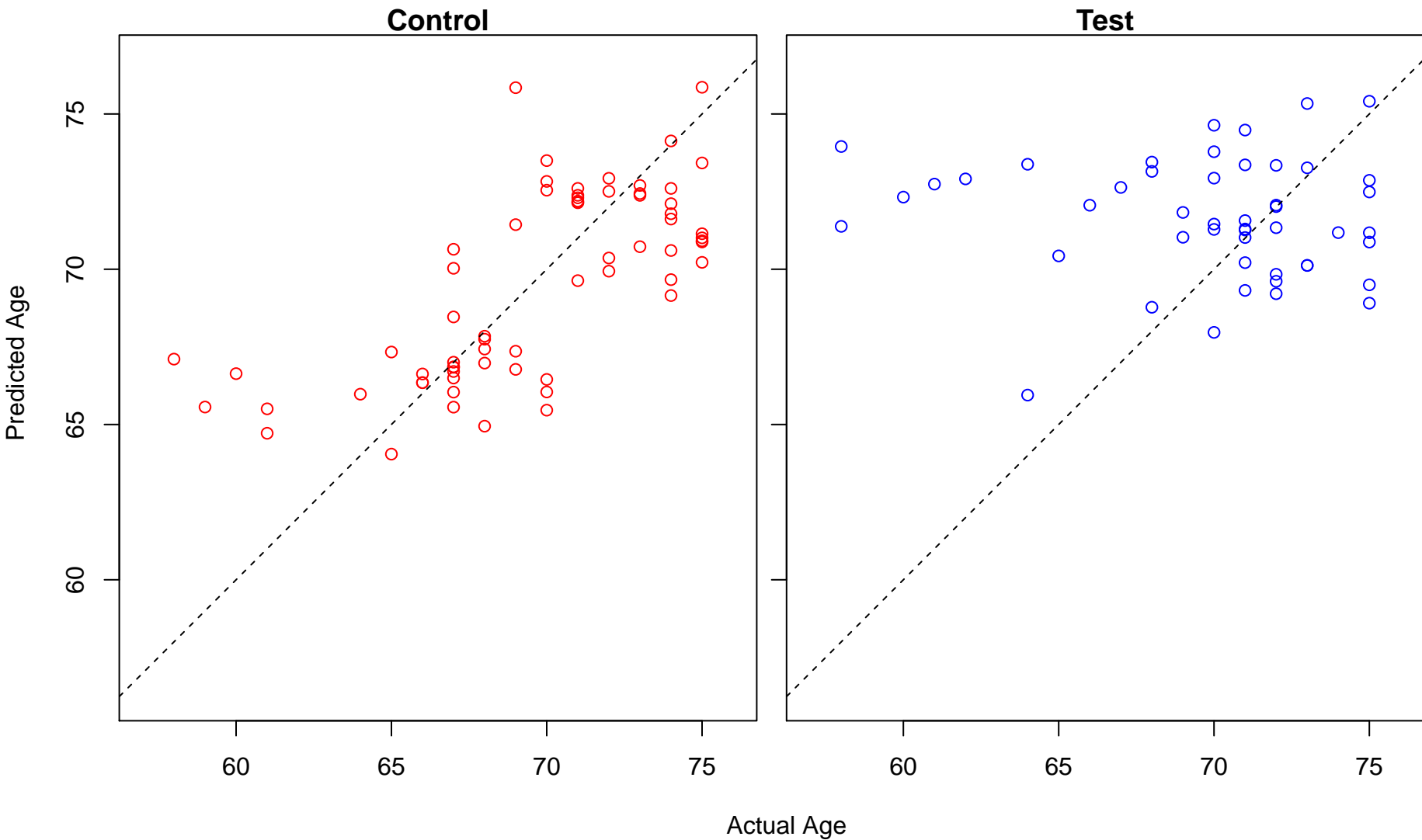


Actual Age

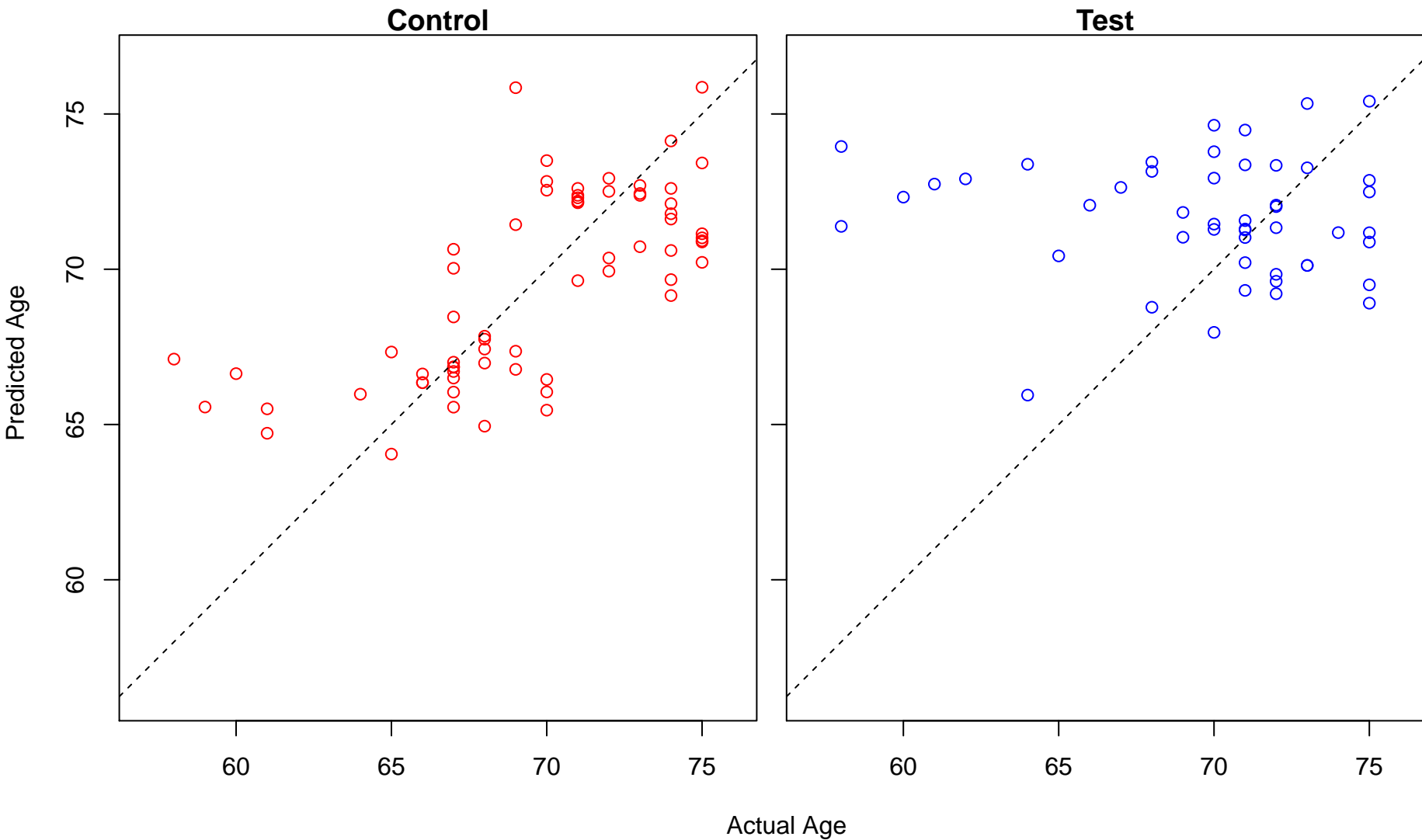
immune response–regulating cell surface receptor signaling pathway involved in phagocytosis (Score: 1.0)



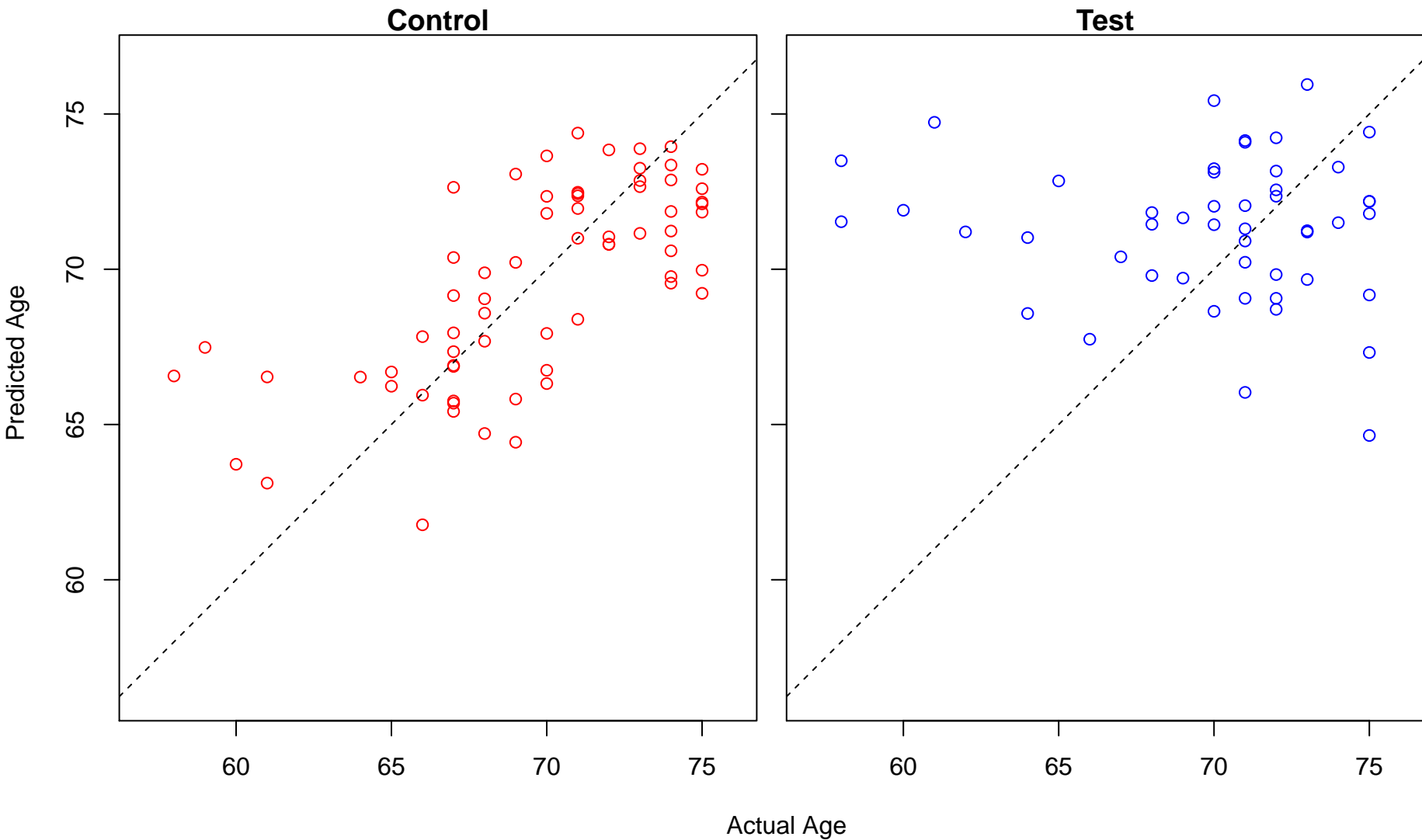
Fc-gamma receptor signaling pathway (Score: 1.486836)



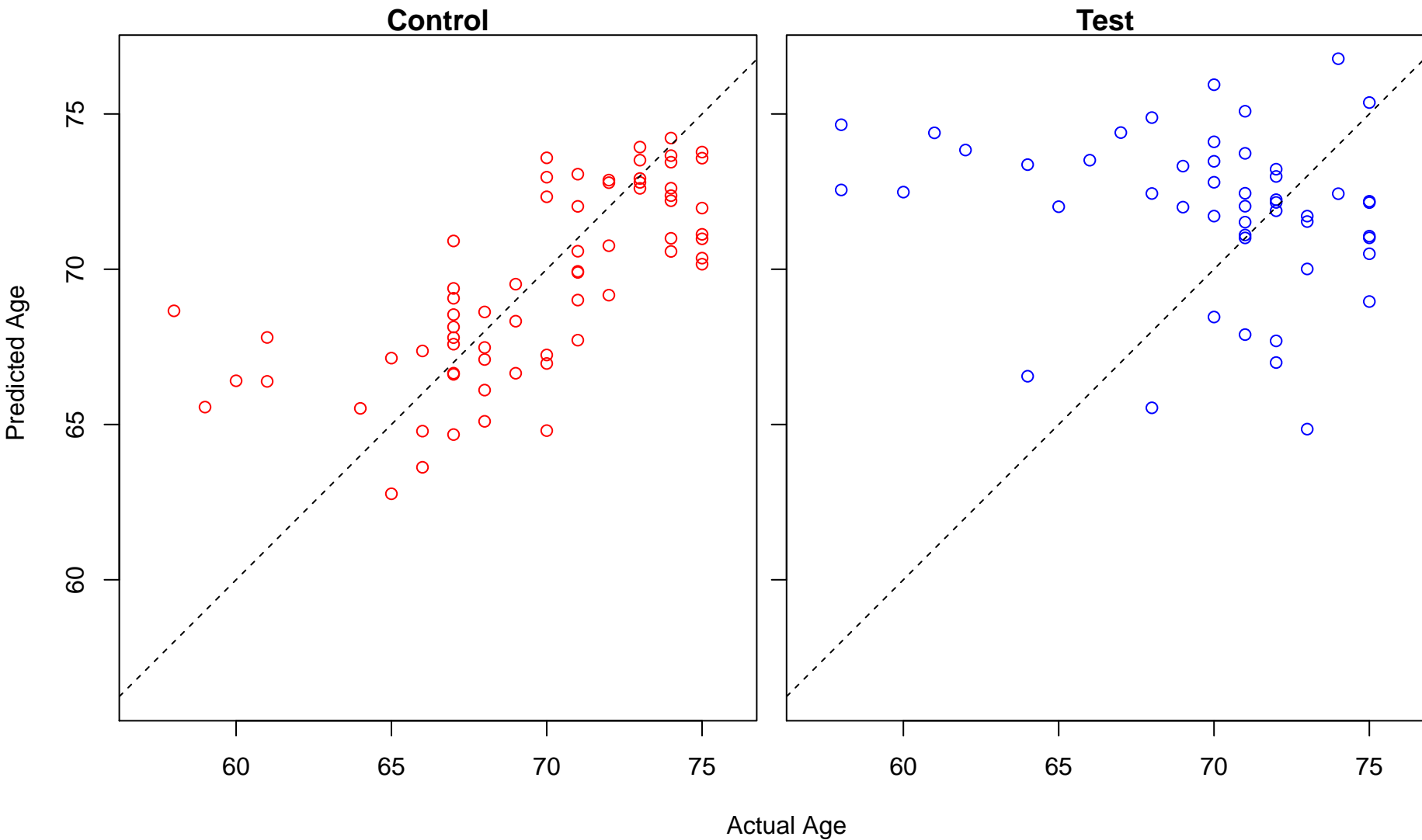
Fc-gamma receptor signaling pathway involved in phagocytosis (Score: 1.486836)



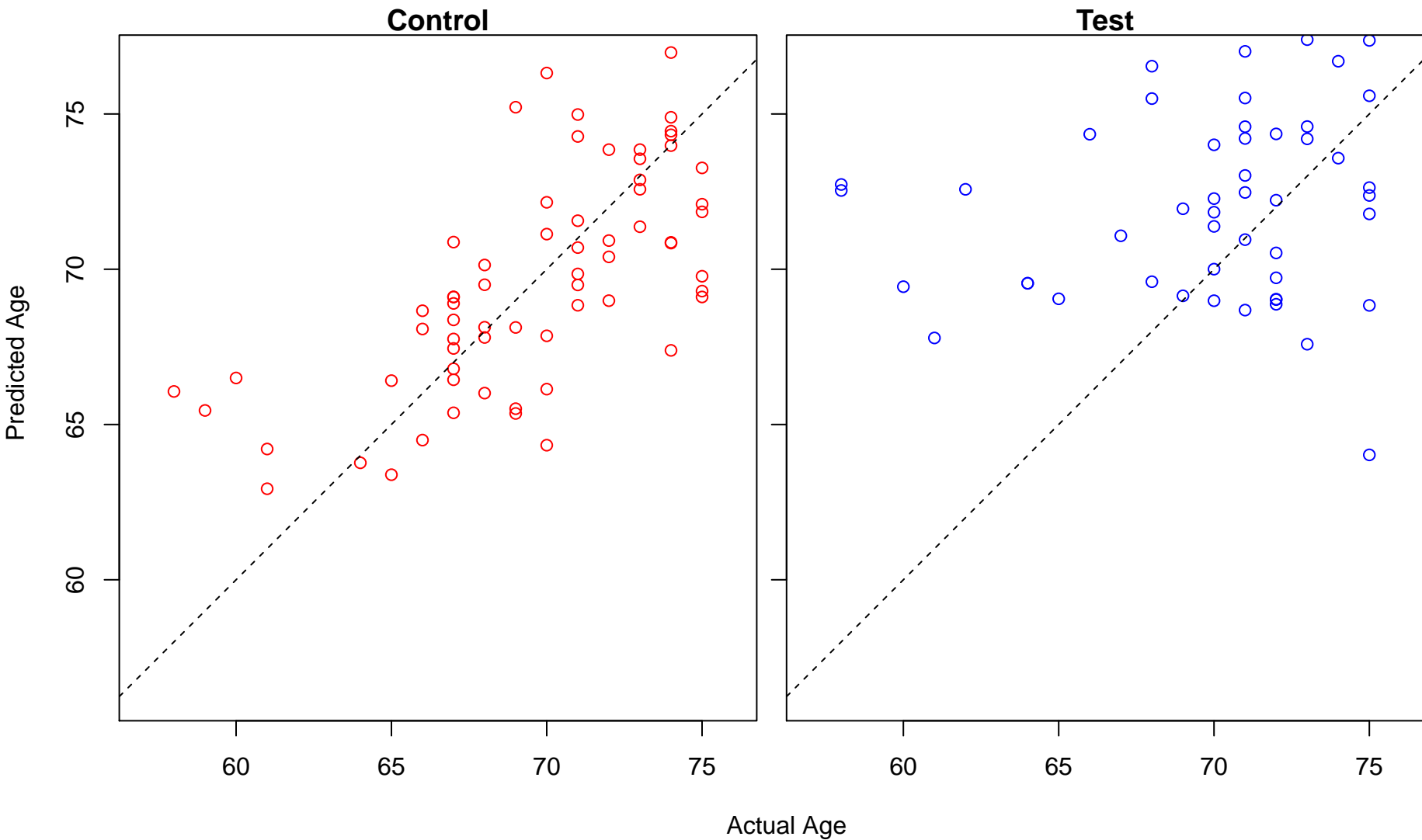
regulation of potassium ion transmembrane transport (Score: 1.486044)



positive regulation of immune effector process (Score: 1.485651)

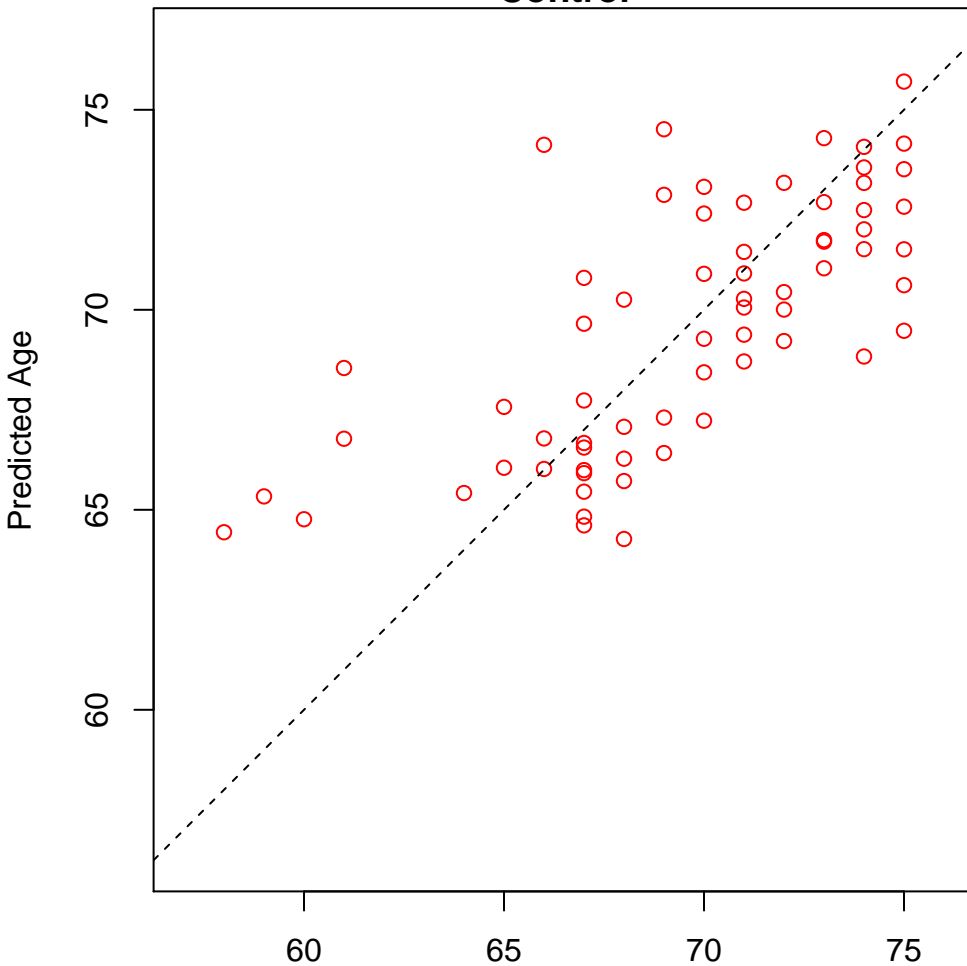


lamellipodium organization (Score: 1.485380)

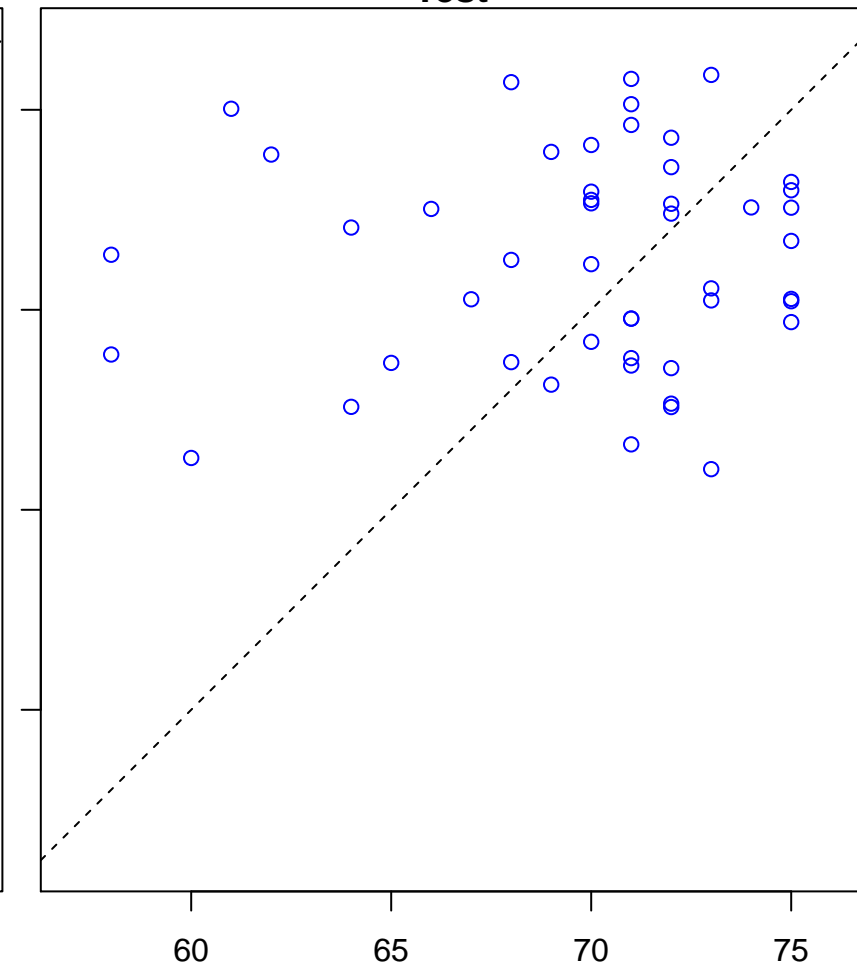


ribonucleoprotein complex disassembly (Score: 1.485240)

Control

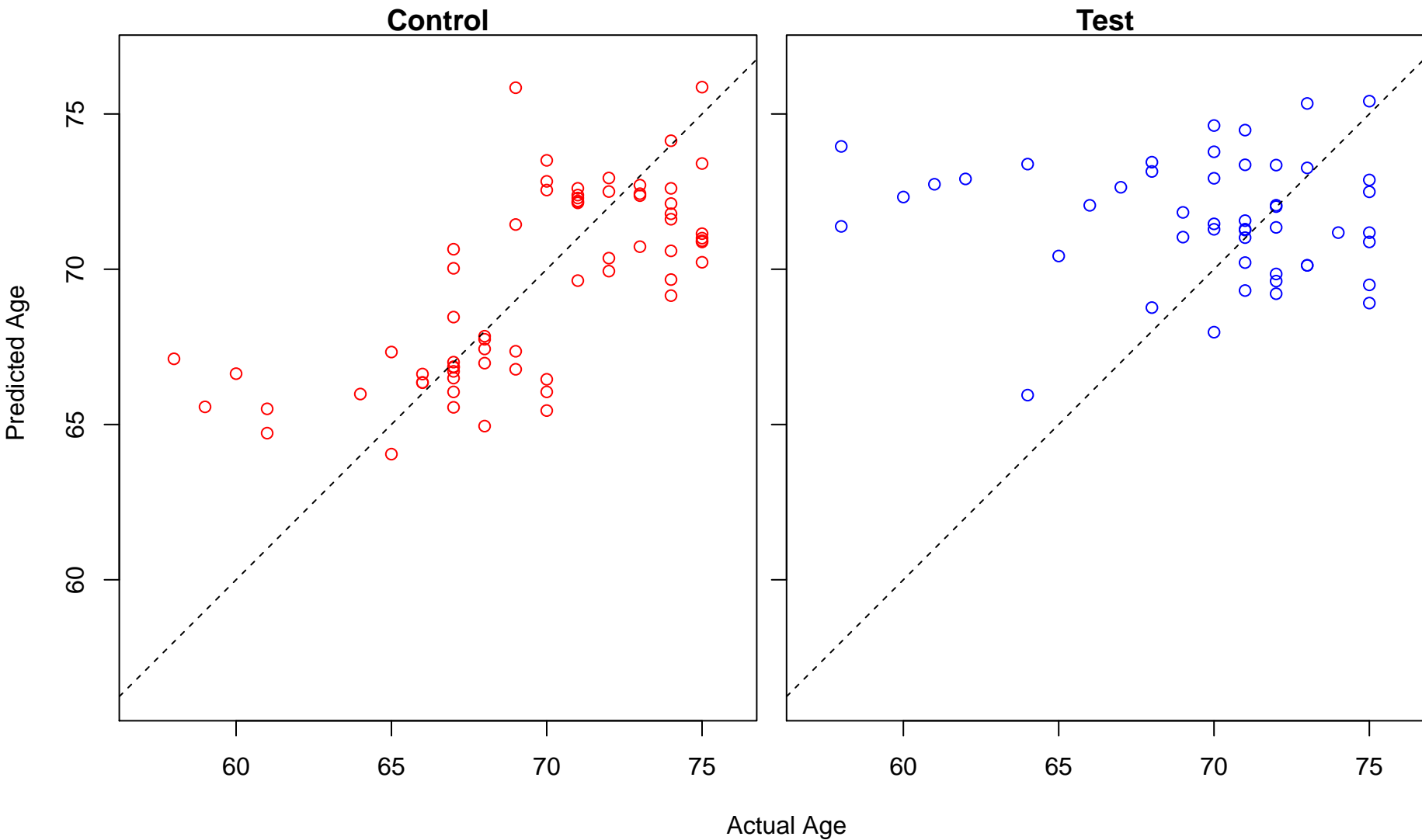


Test

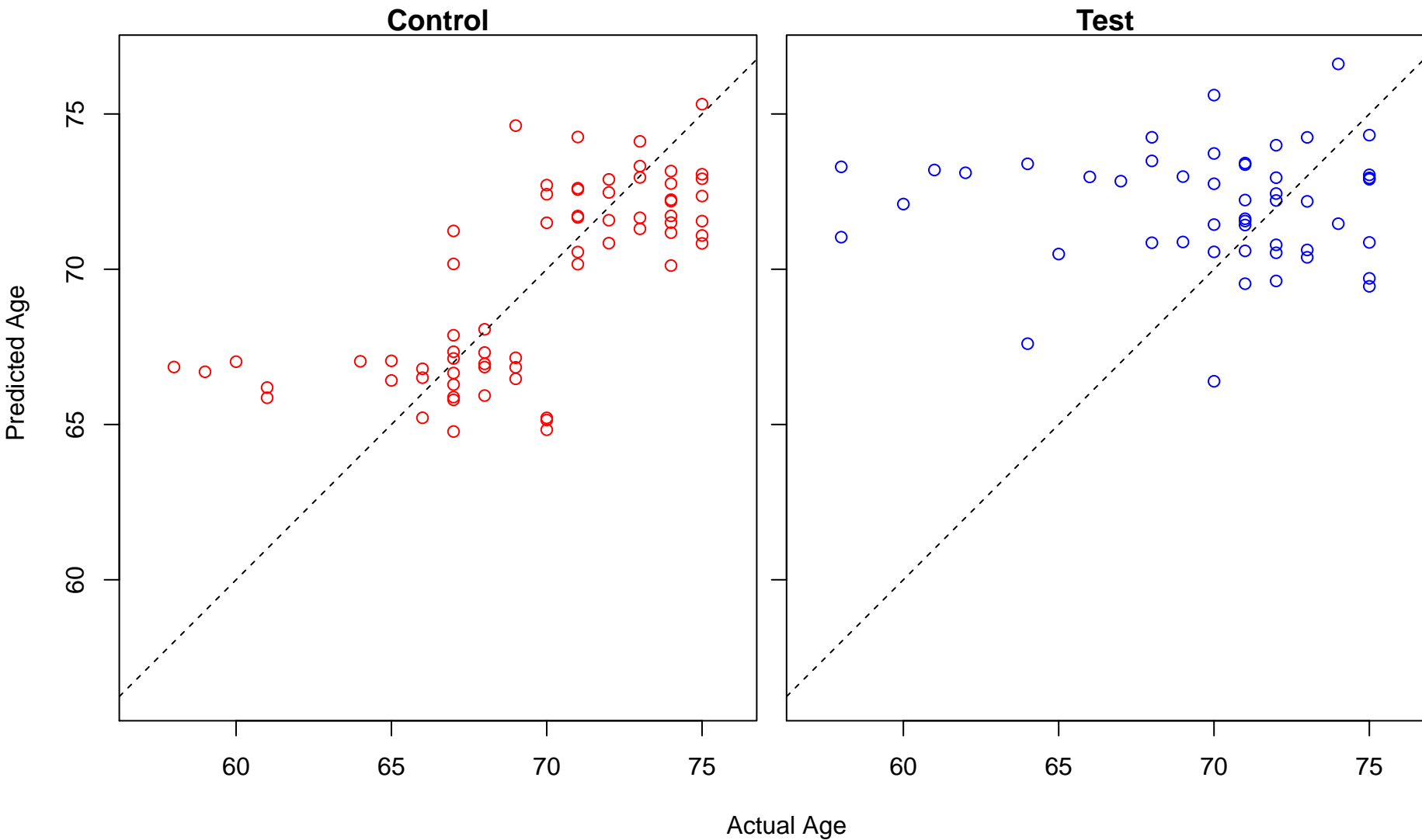


Actual Age

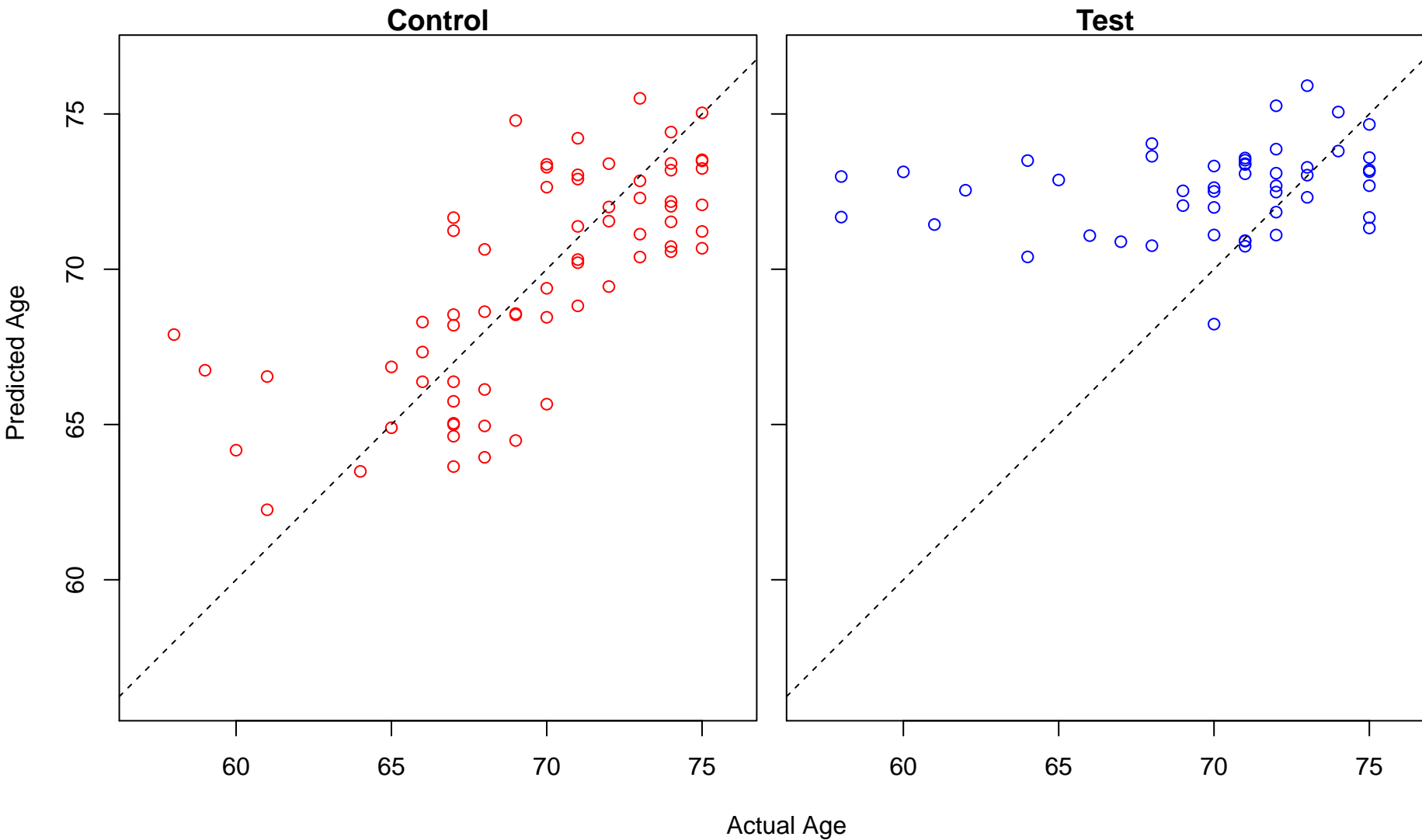
Fc receptor mediated stimulatory signaling pathway (Score: 1.484999)



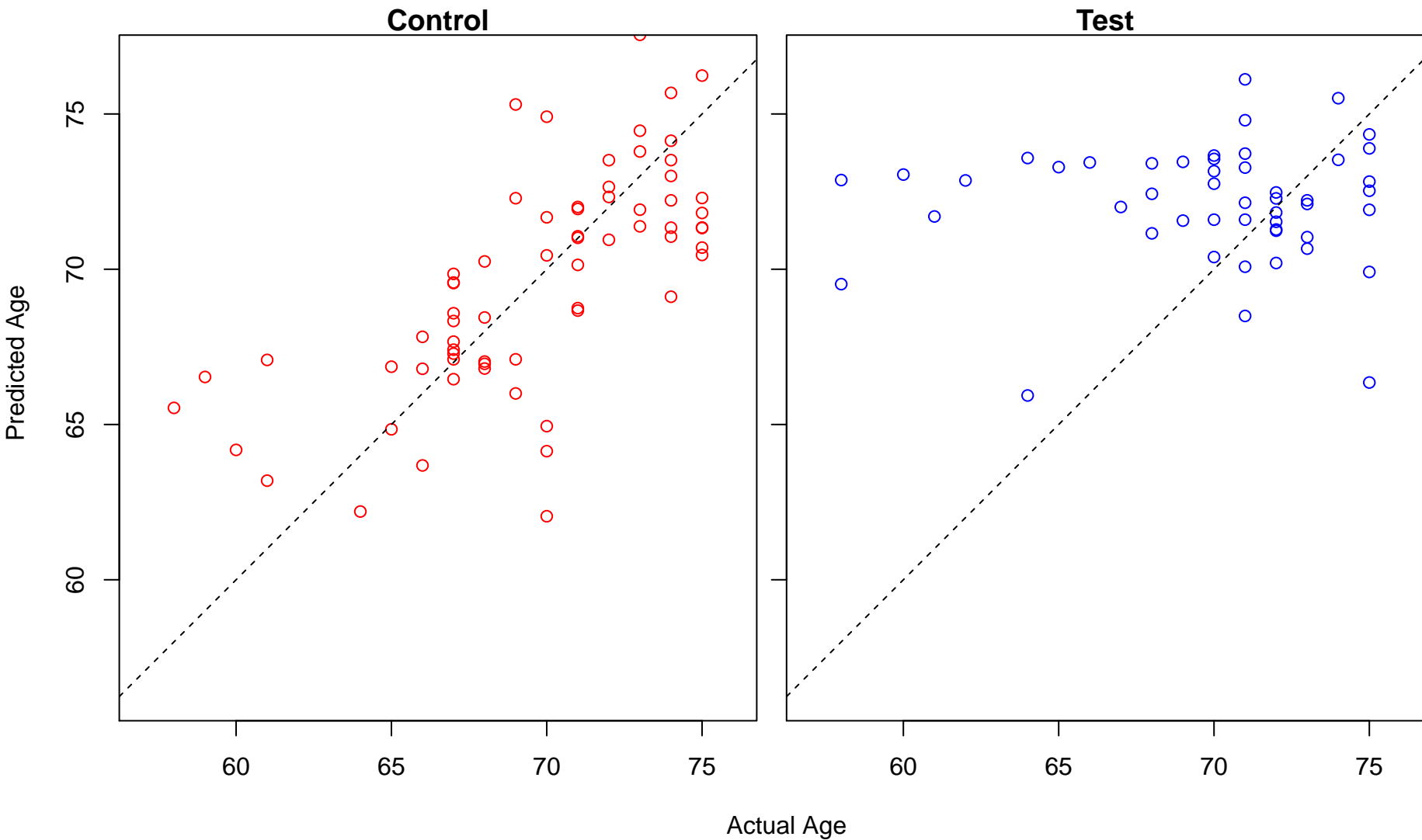
regulation of oxidative stress-induced cell death (Score: 1.484799)



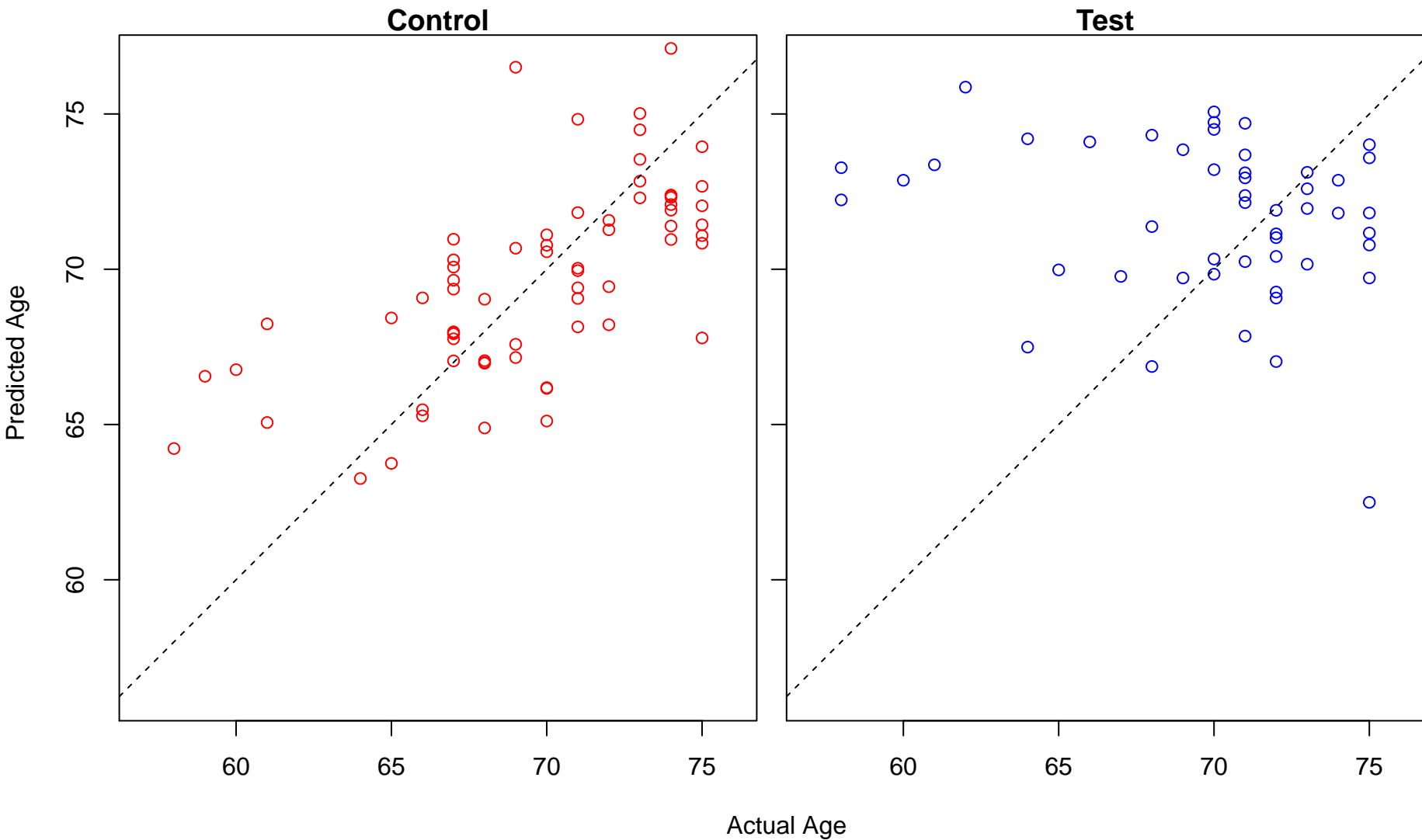
cellular response to topologically incorrect protein (Score: 1.484704)



regulation of protein kinase B signaling (Score: 1.484619)

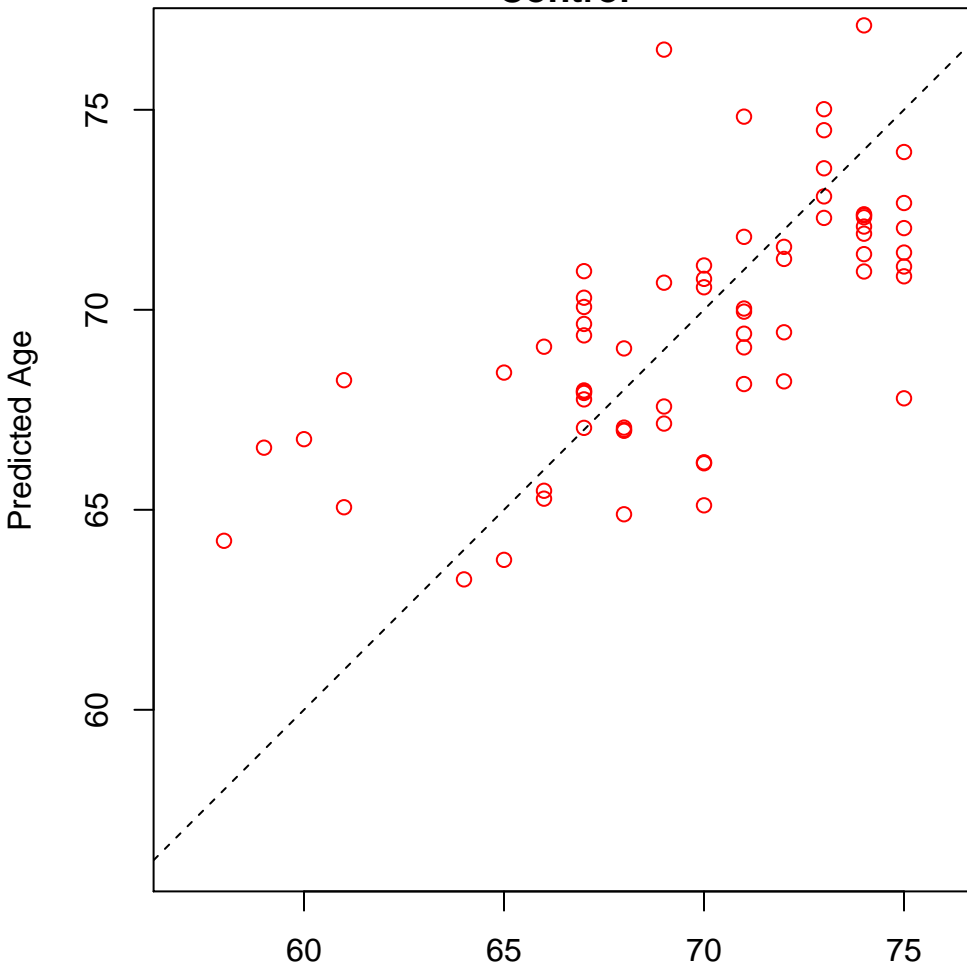


regulation of T cell differentiation in thymus (Score: 1.484445)

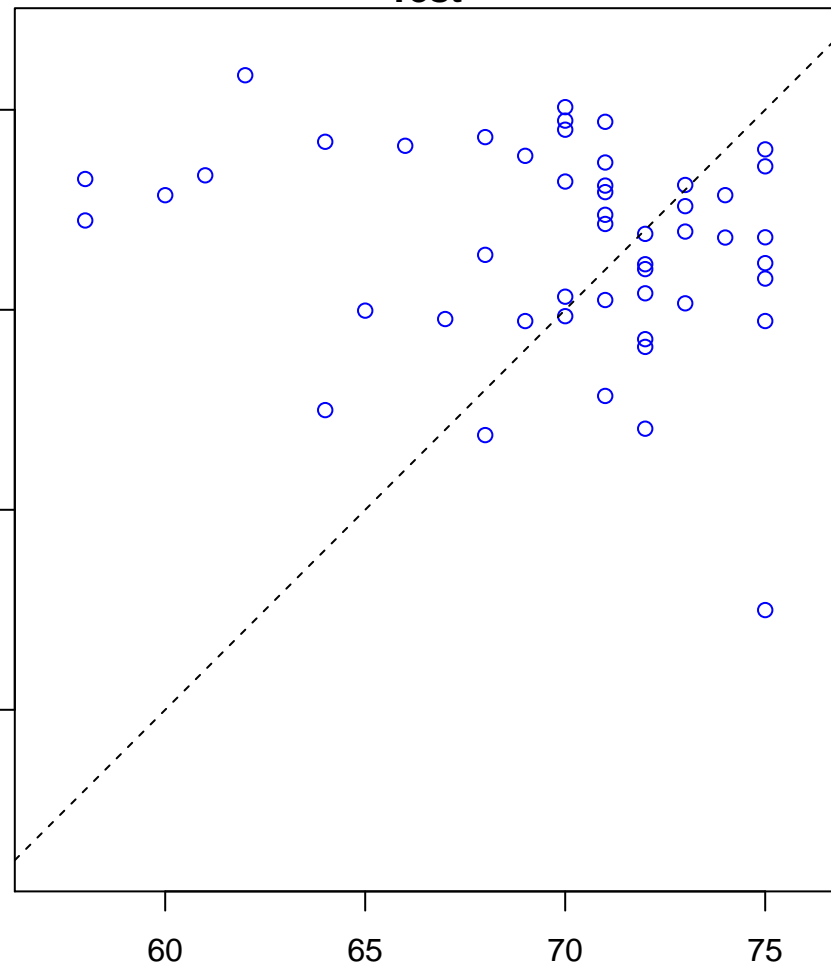


regulation of thymocyte aggregation (Score: 1.484445)

Control

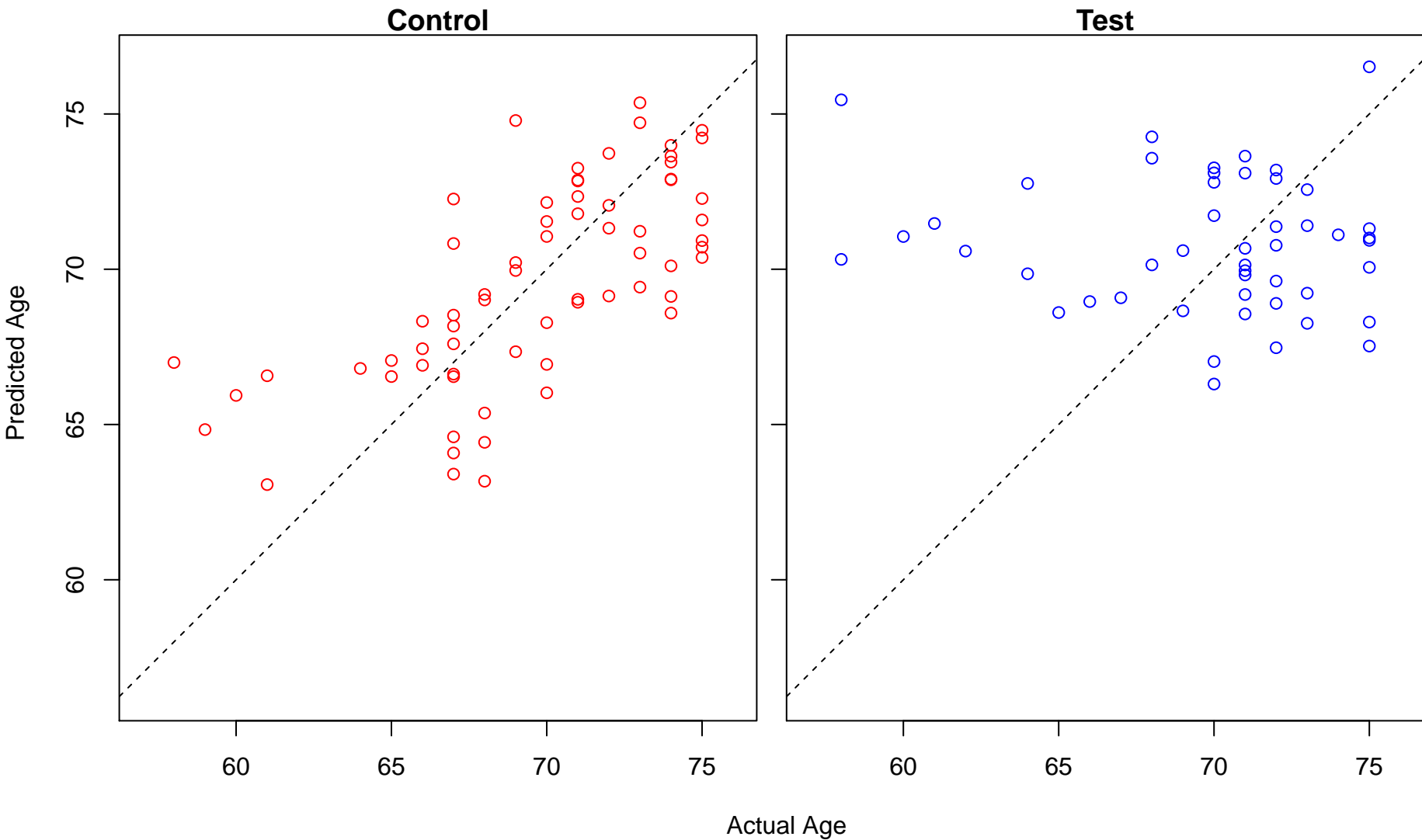


Test

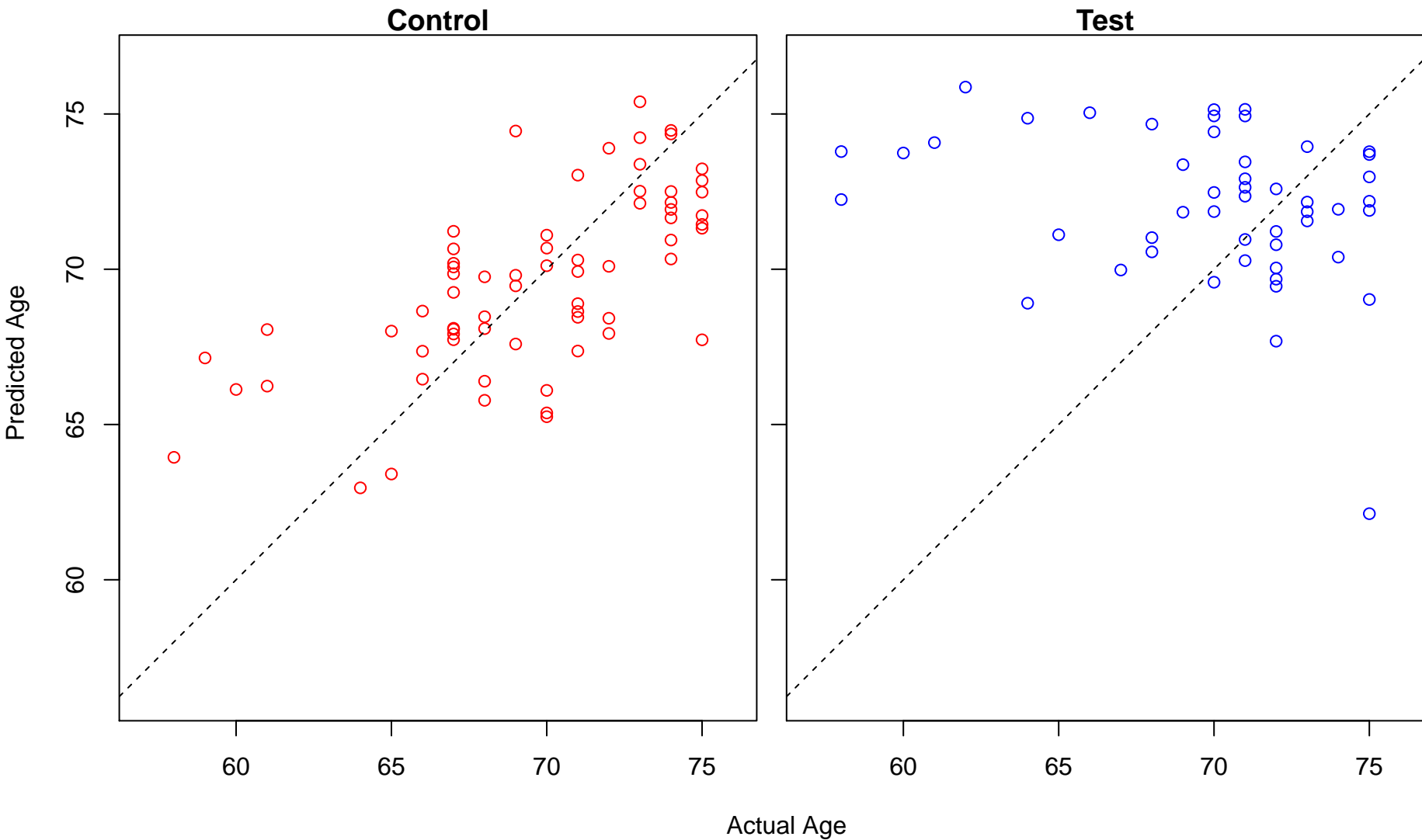


Actual Age

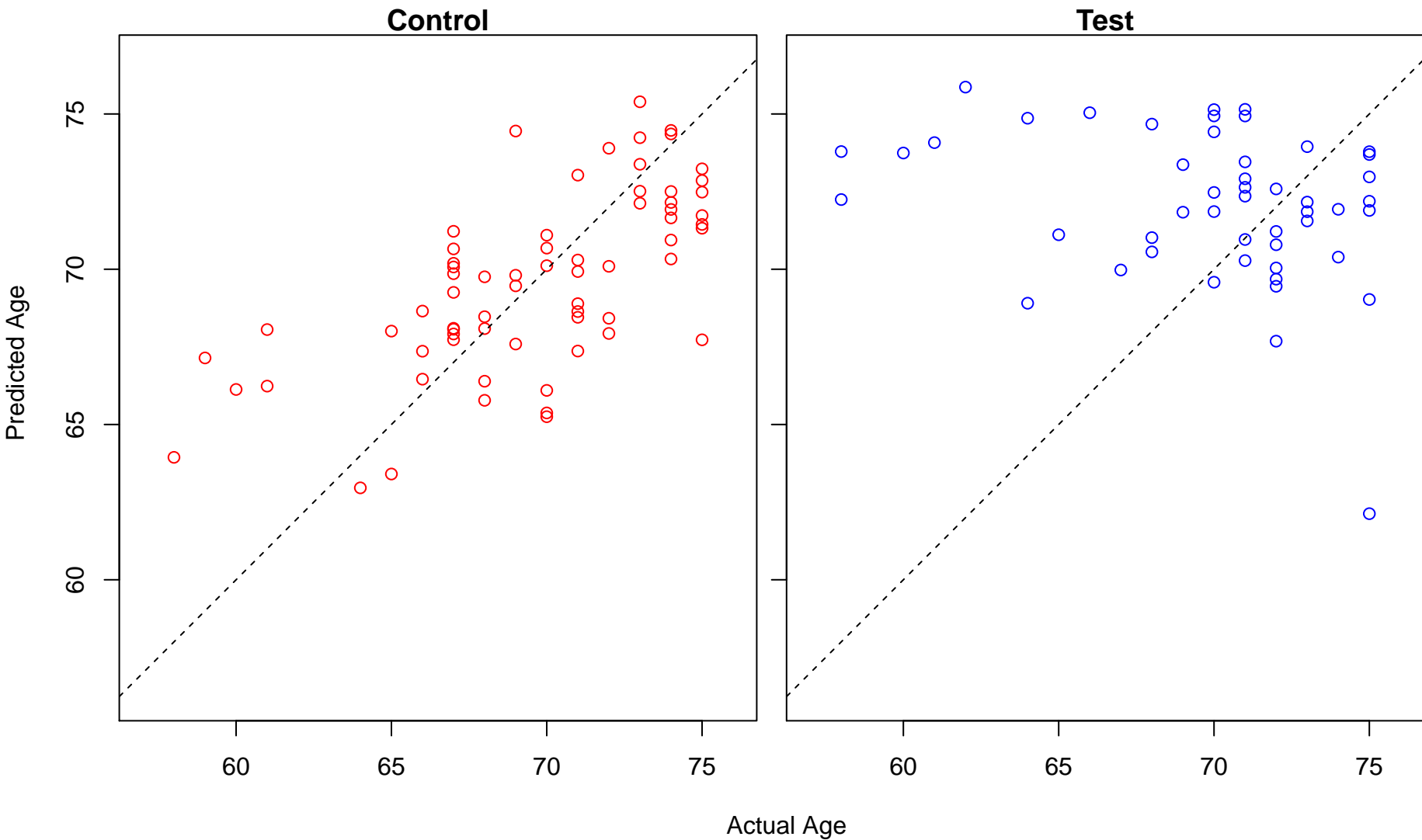
B cell receptor signaling pathway (Score: 1.484428)



positive regulation of T cell differentiation in thymus (Score: 1.483163)

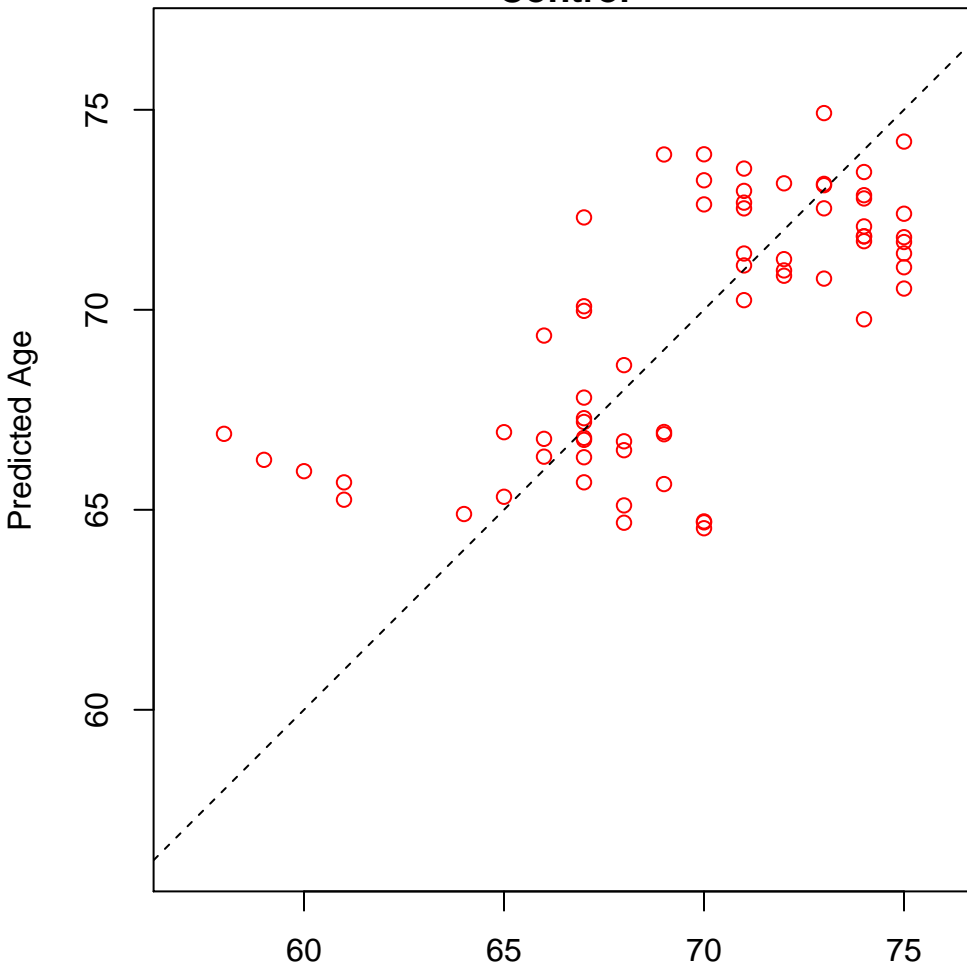


positive regulation of thymocyte aggregation (Score: 1.483163)

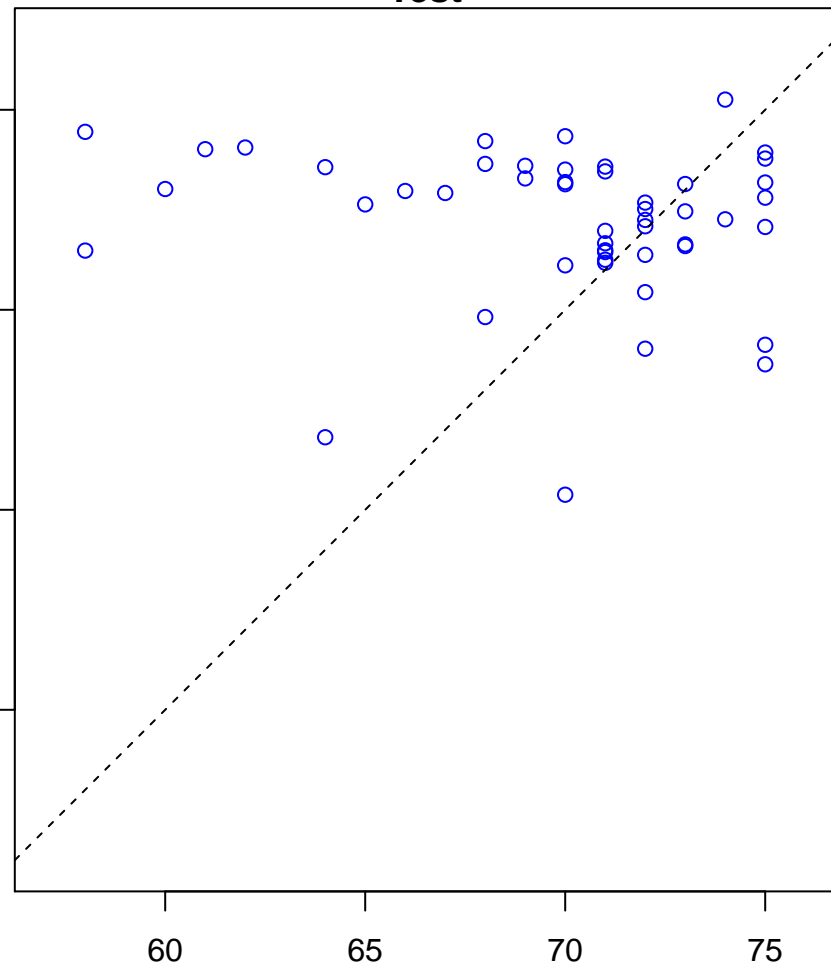


7-methylguanosine mRNA capping (Score: 1.483110)

Control

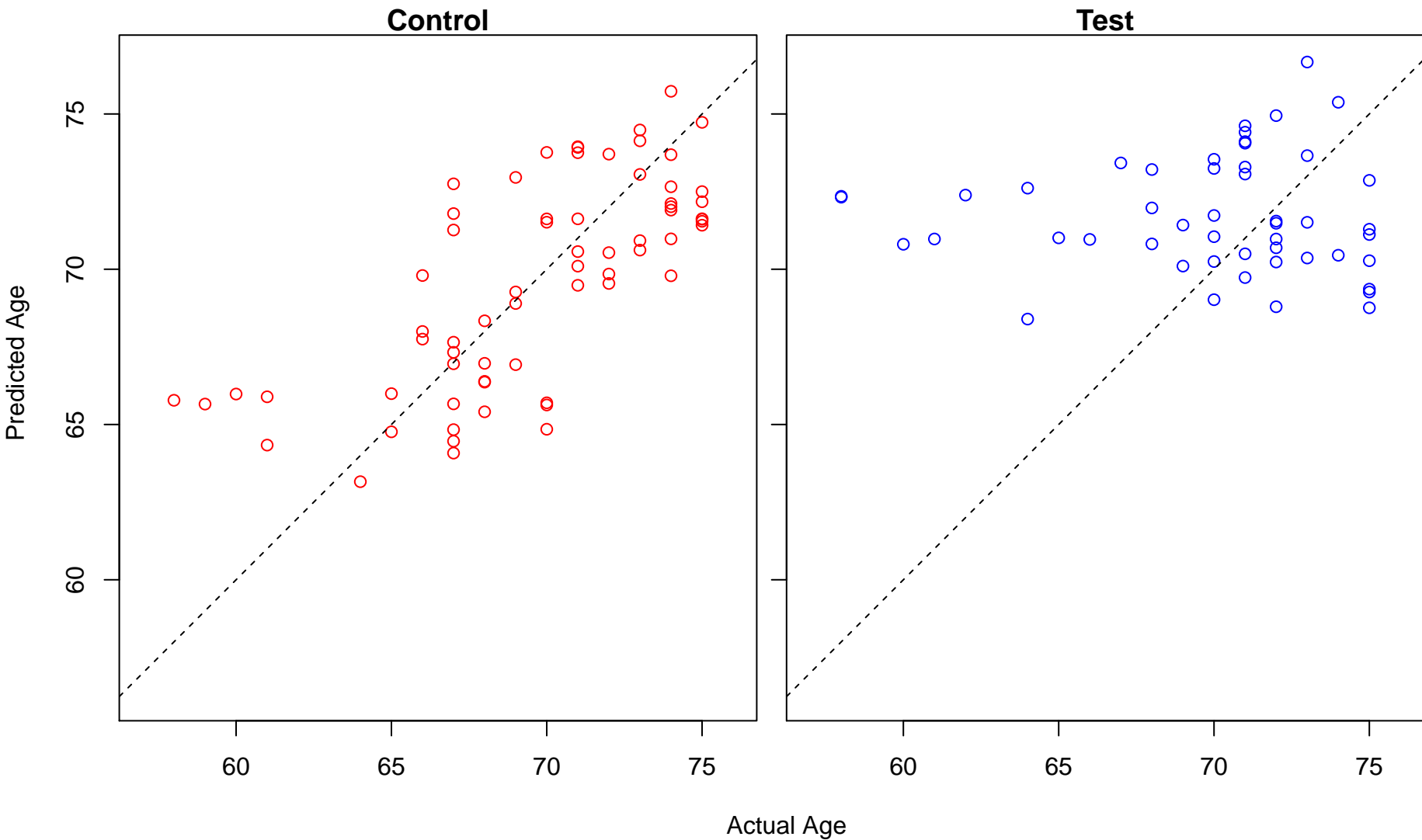


Test

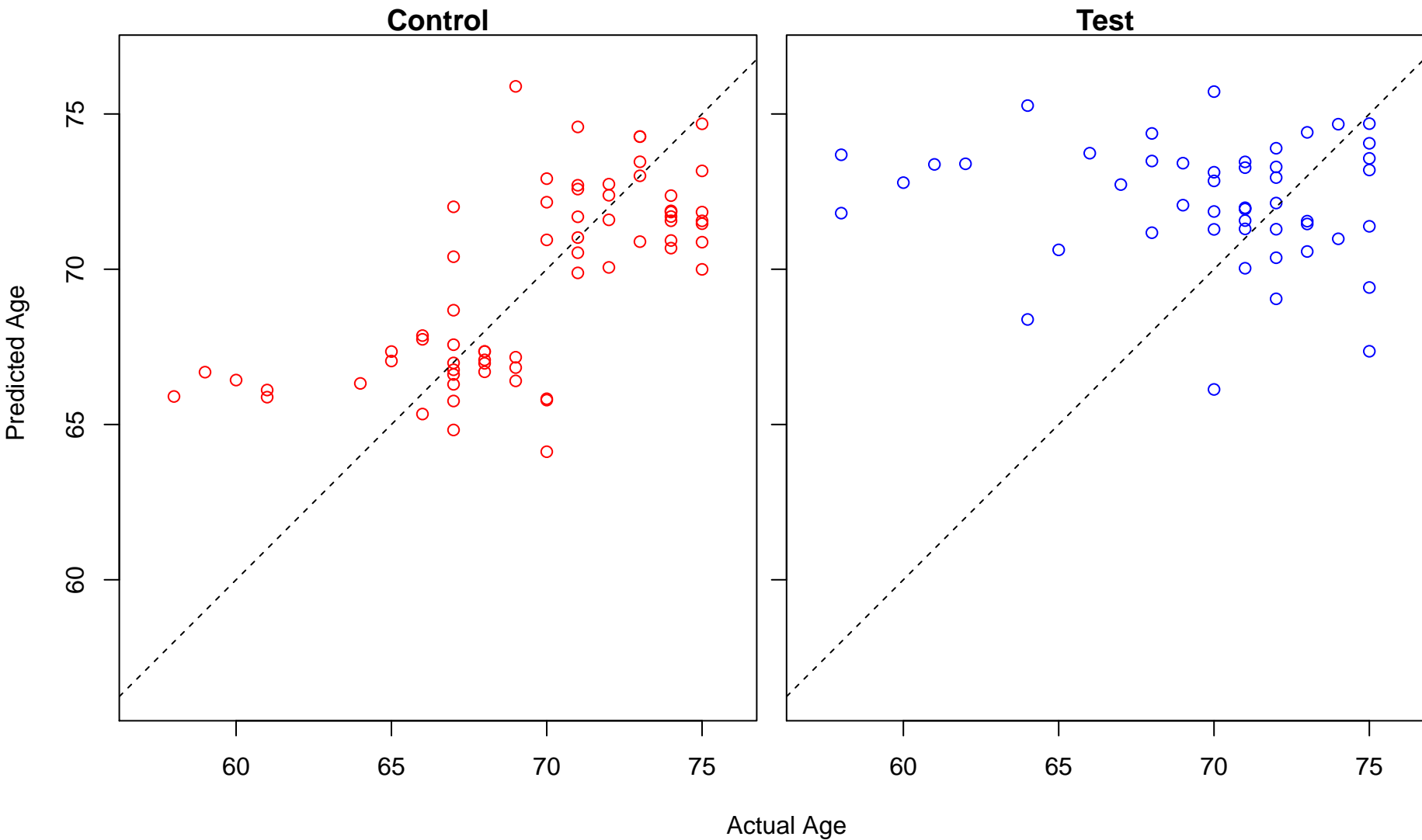


Actual Age

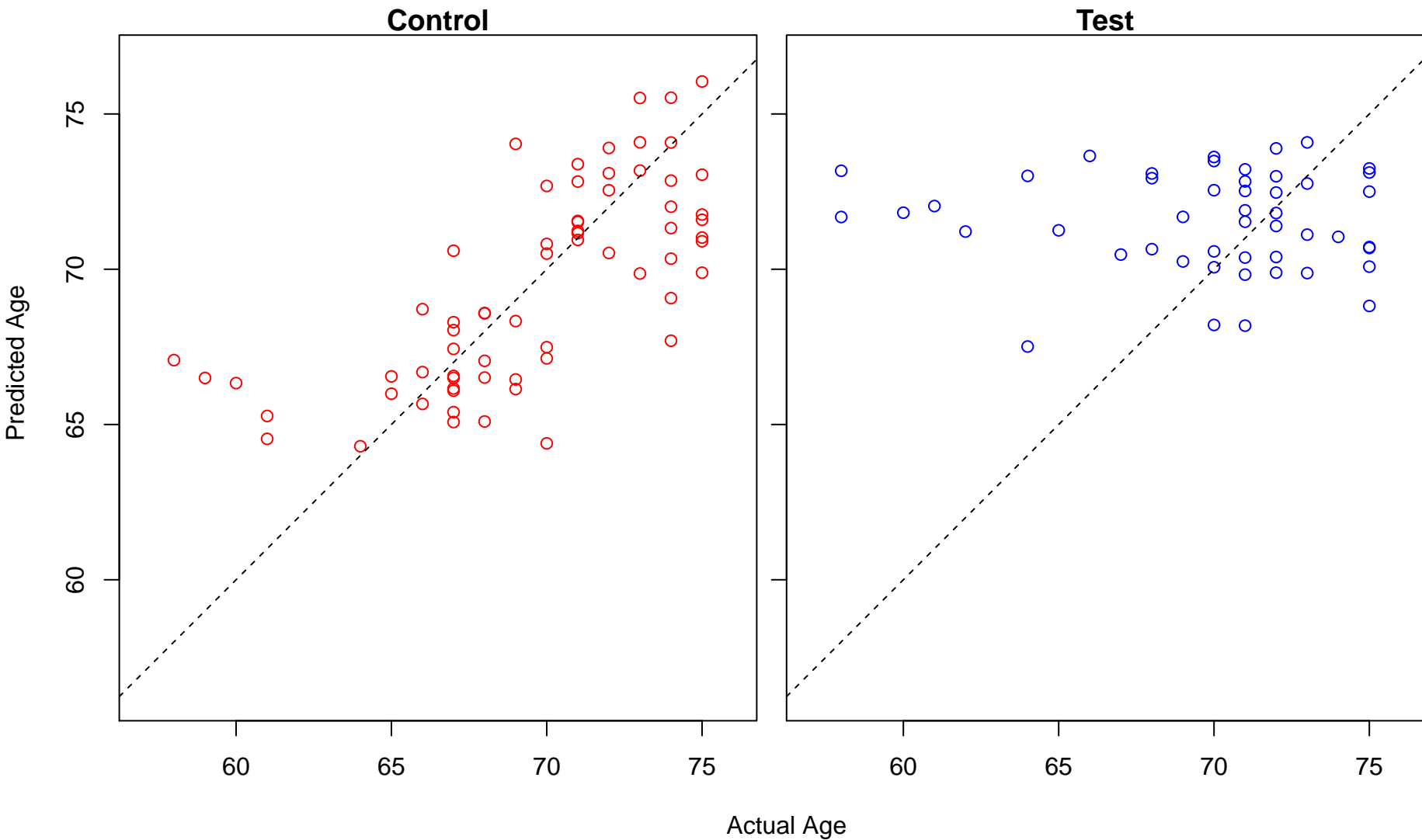
regulation of mRNA splicing, via spliceosome (Score: 1.482133)



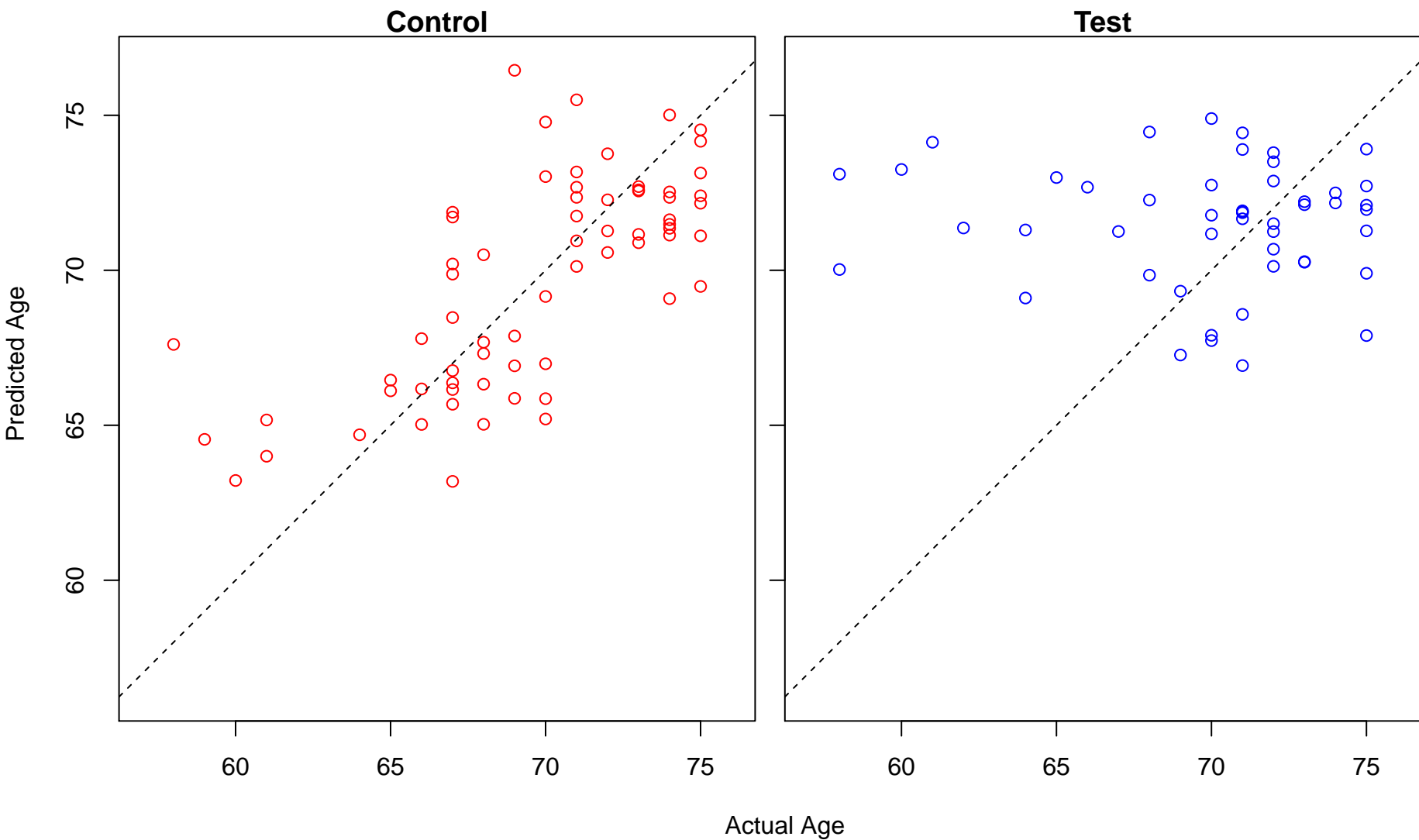
nucleobase-containing small molecule interconversion (Score: 1.480182)



cellular lipid catabolic process (Score: 1.479859)

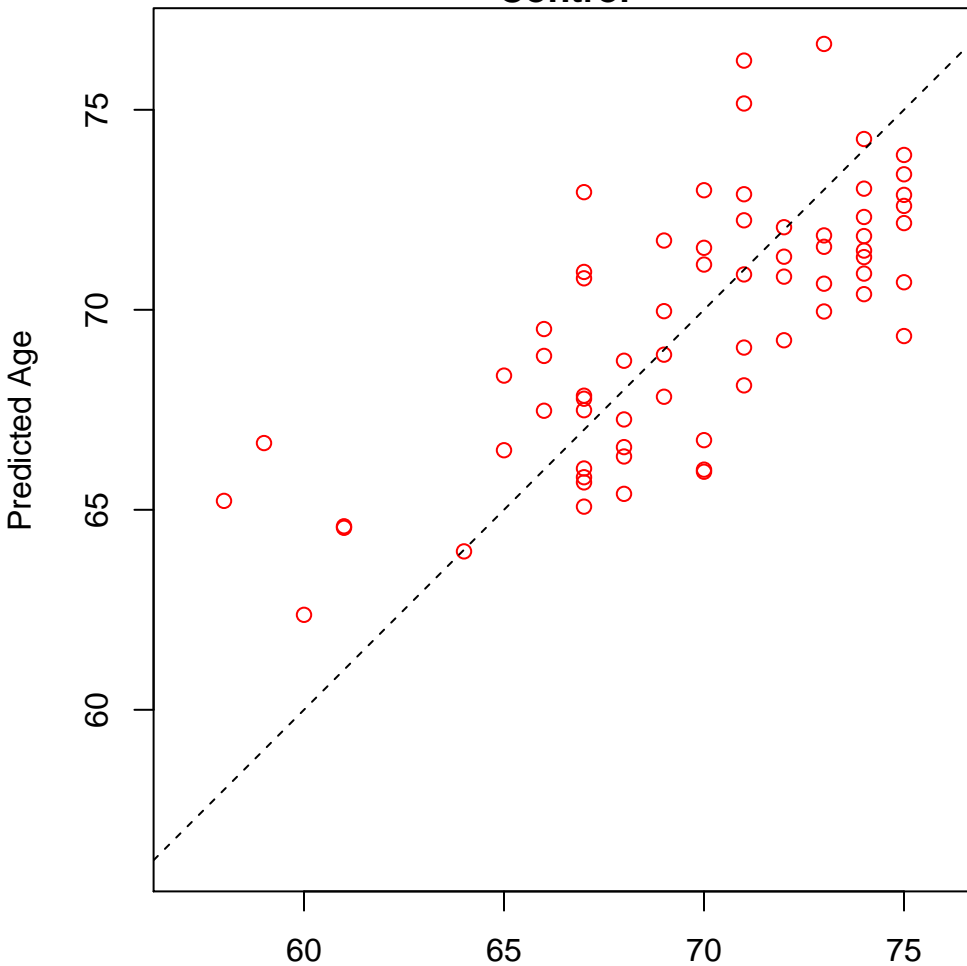


intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress (Score: 1.47941)

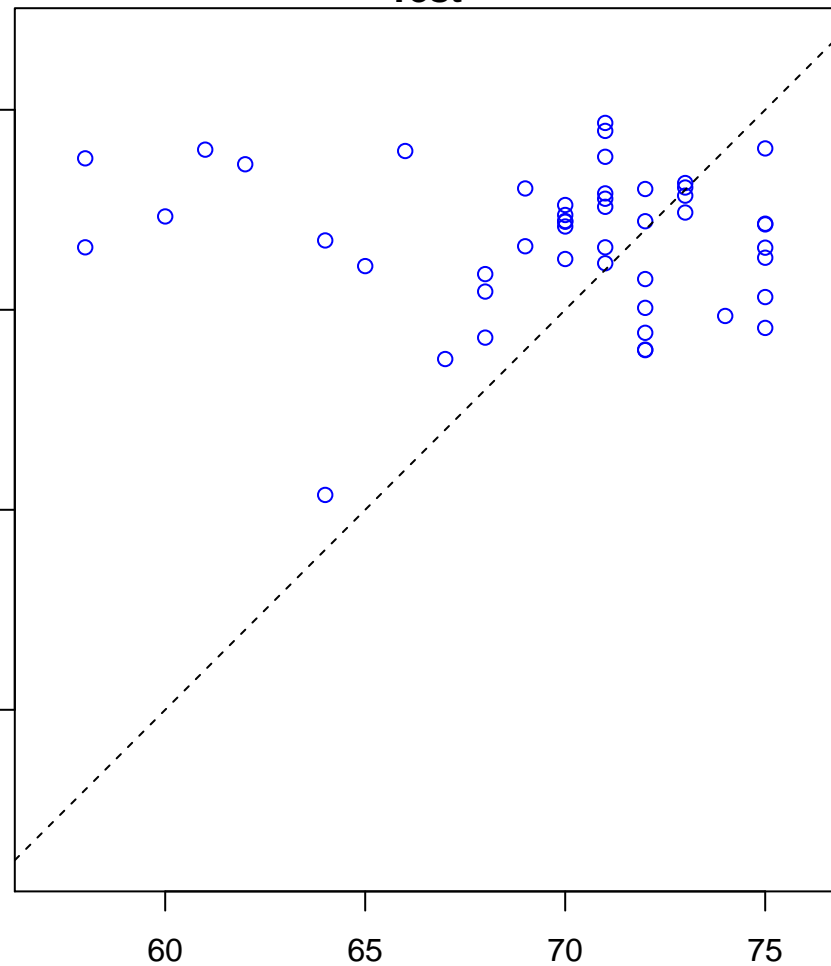


morphogenesis of an endothelium (Score: 1.478691)

Control

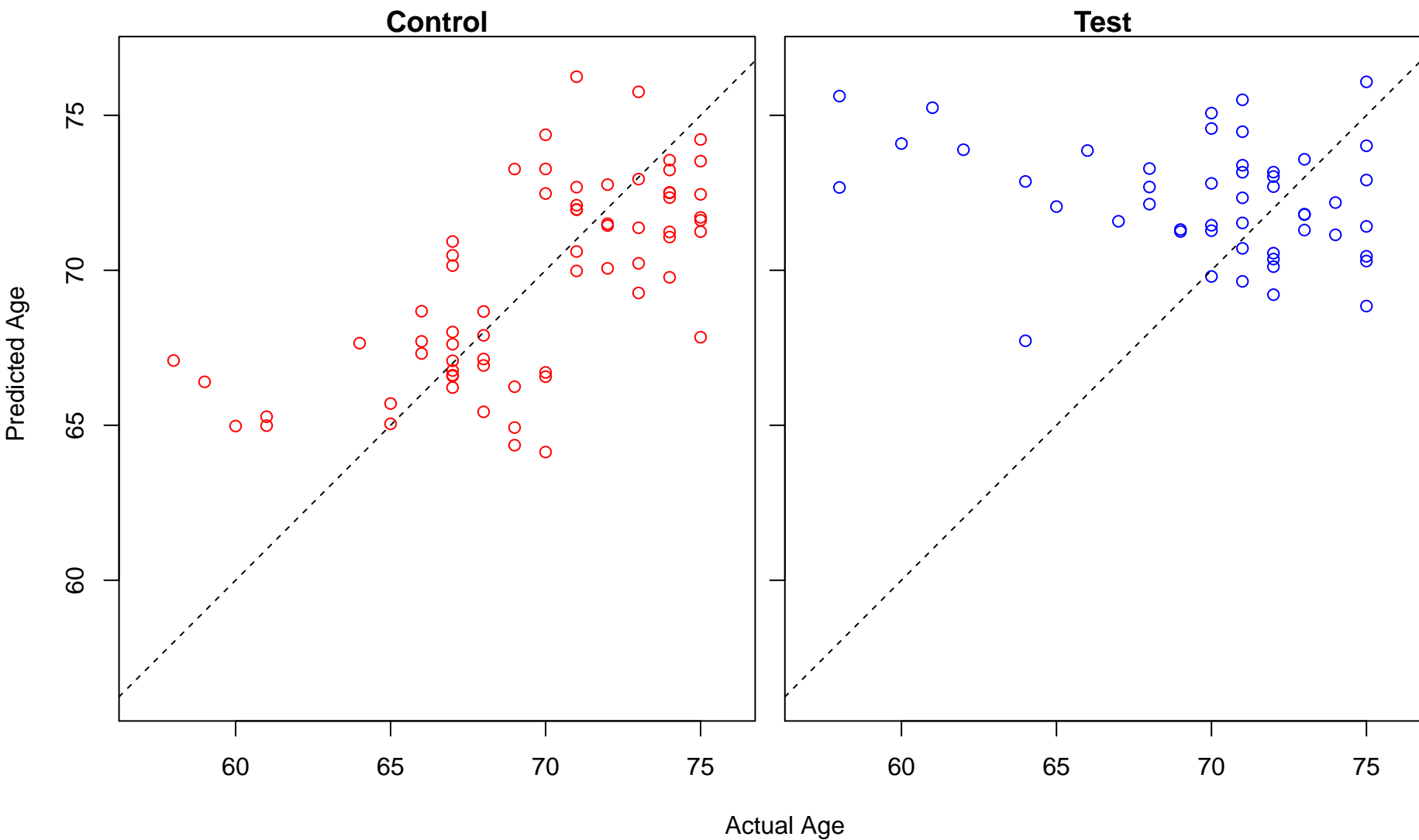


Test

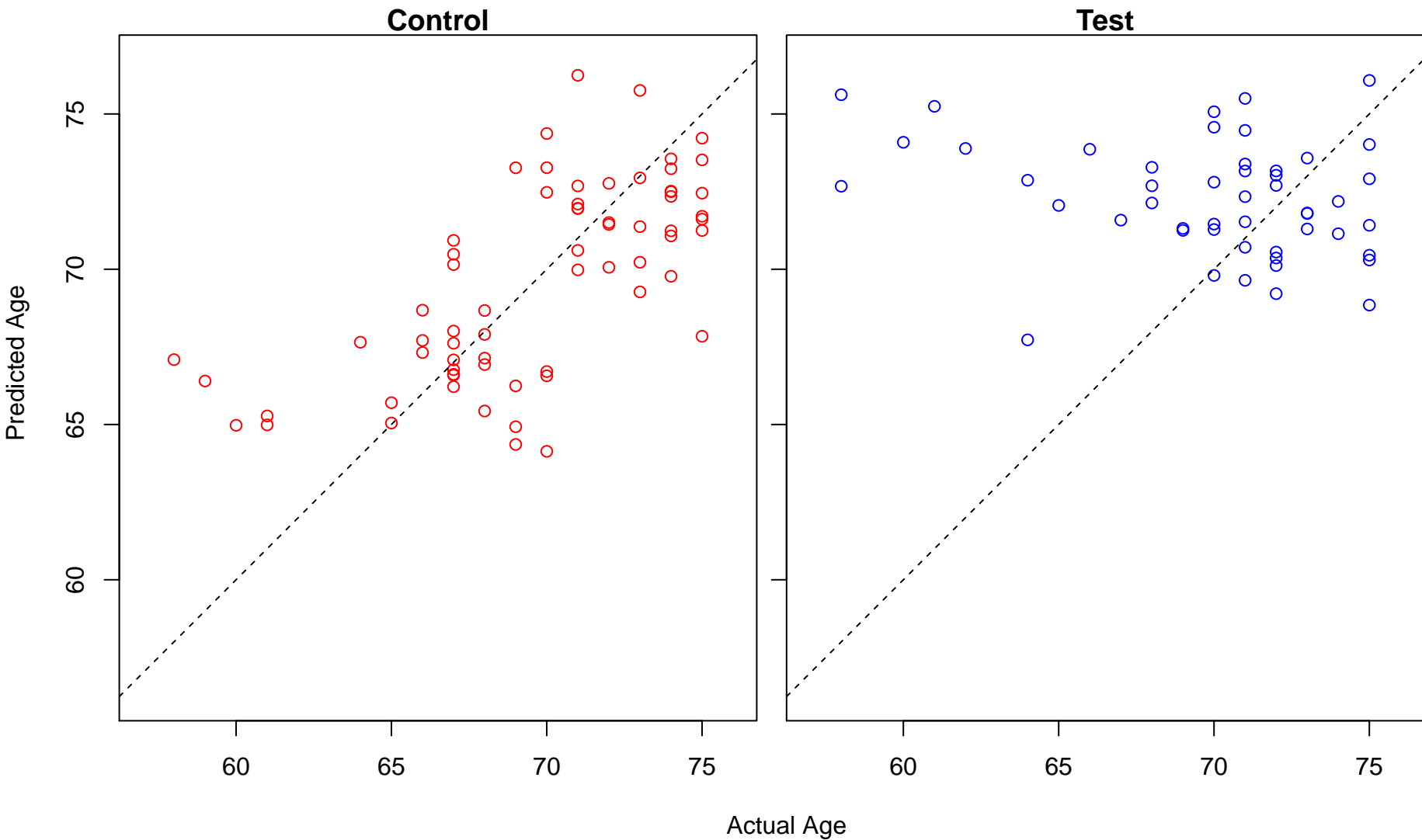


Actual Age

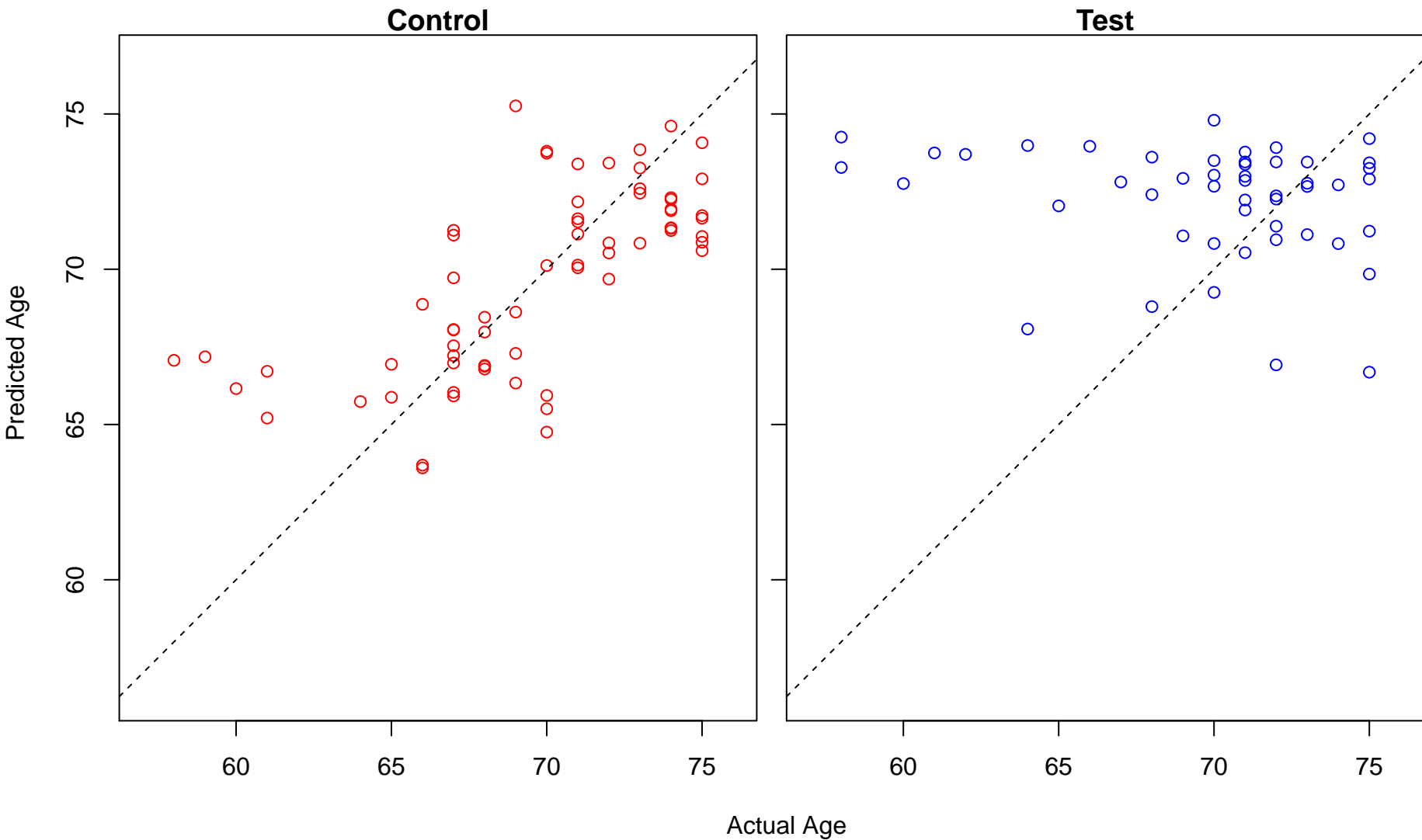
water homeostasis (Score: 1.478480)



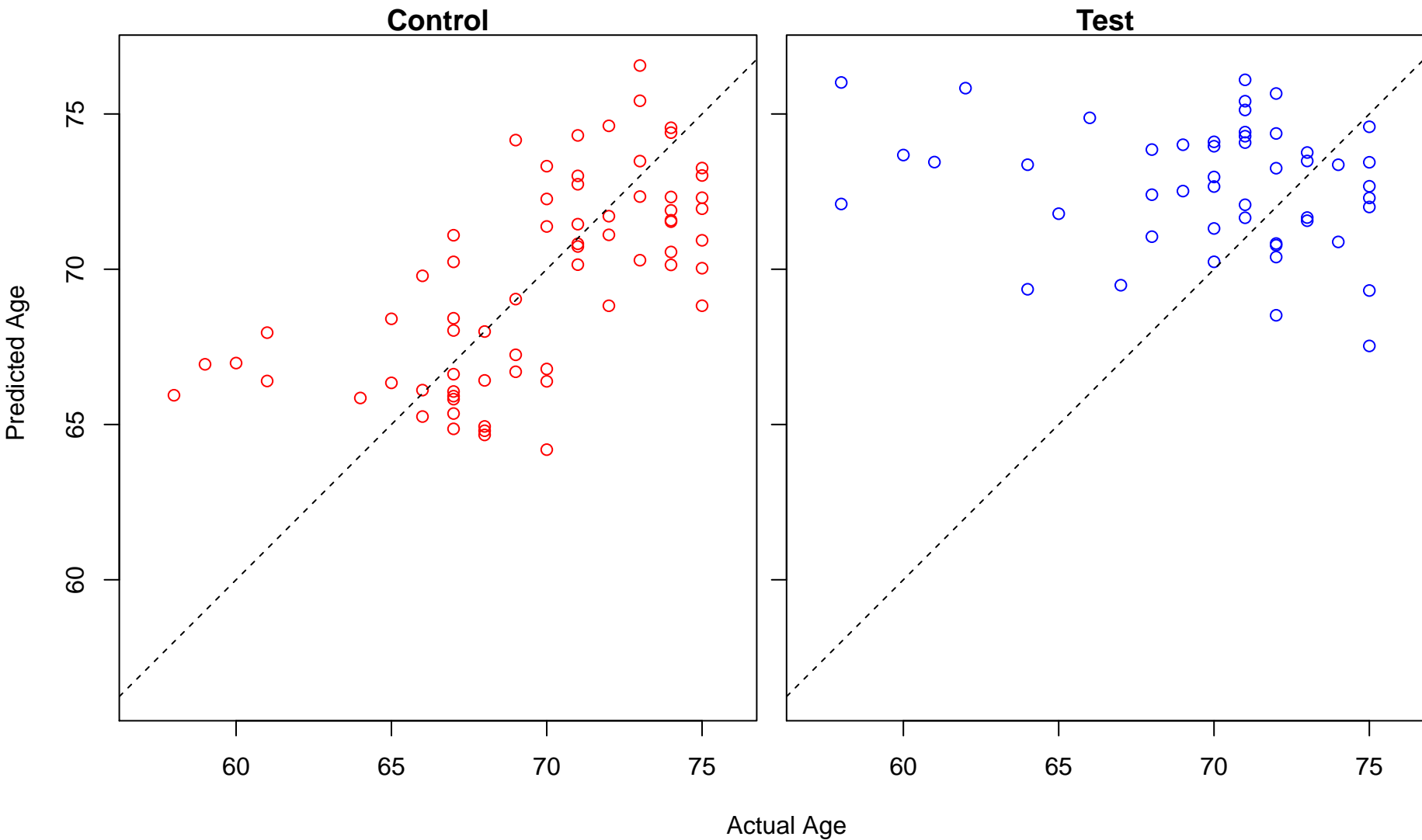
multicellular organismal water homeostasis (Score: 1.478480)



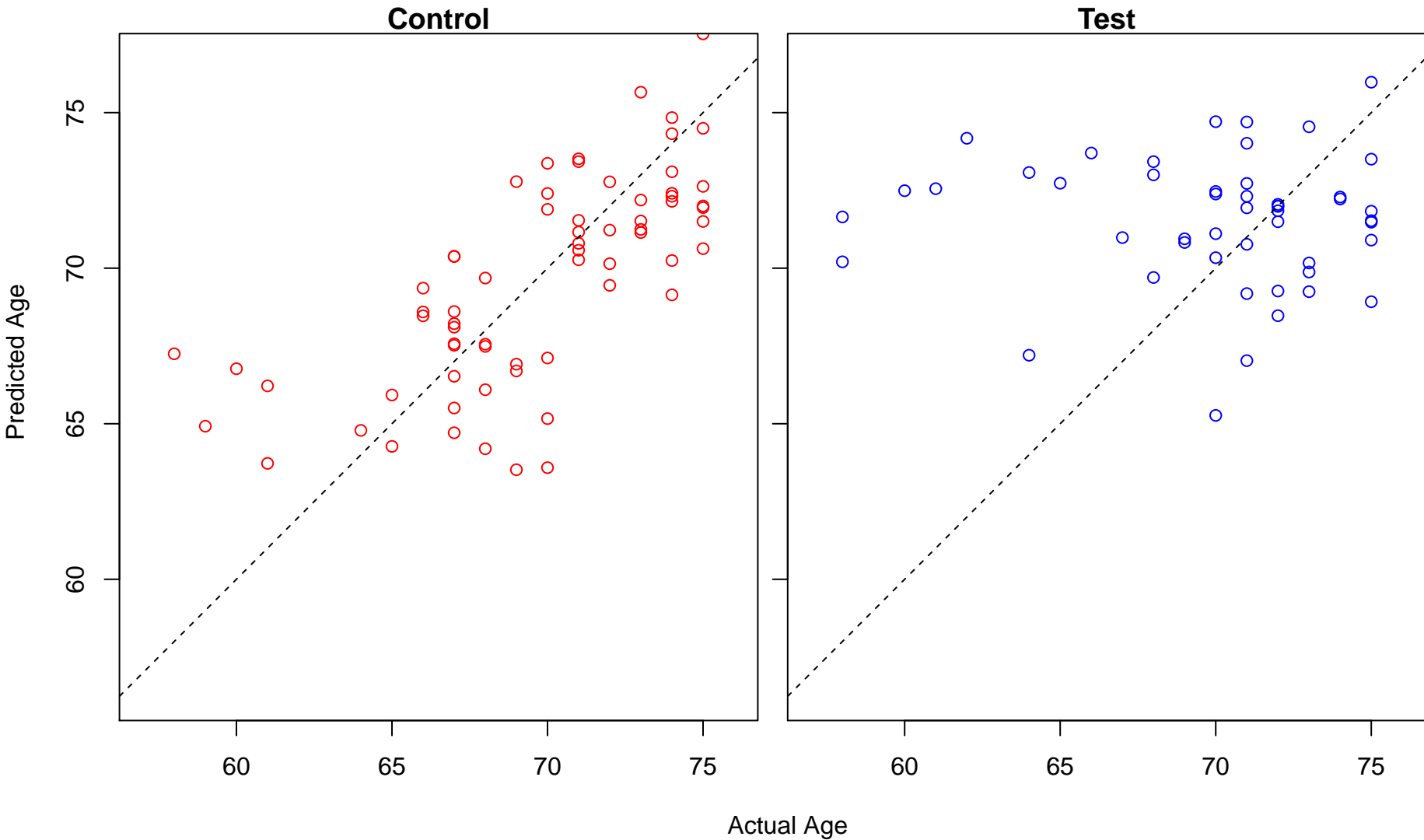
centrosome cycle (Score: 1.478465)



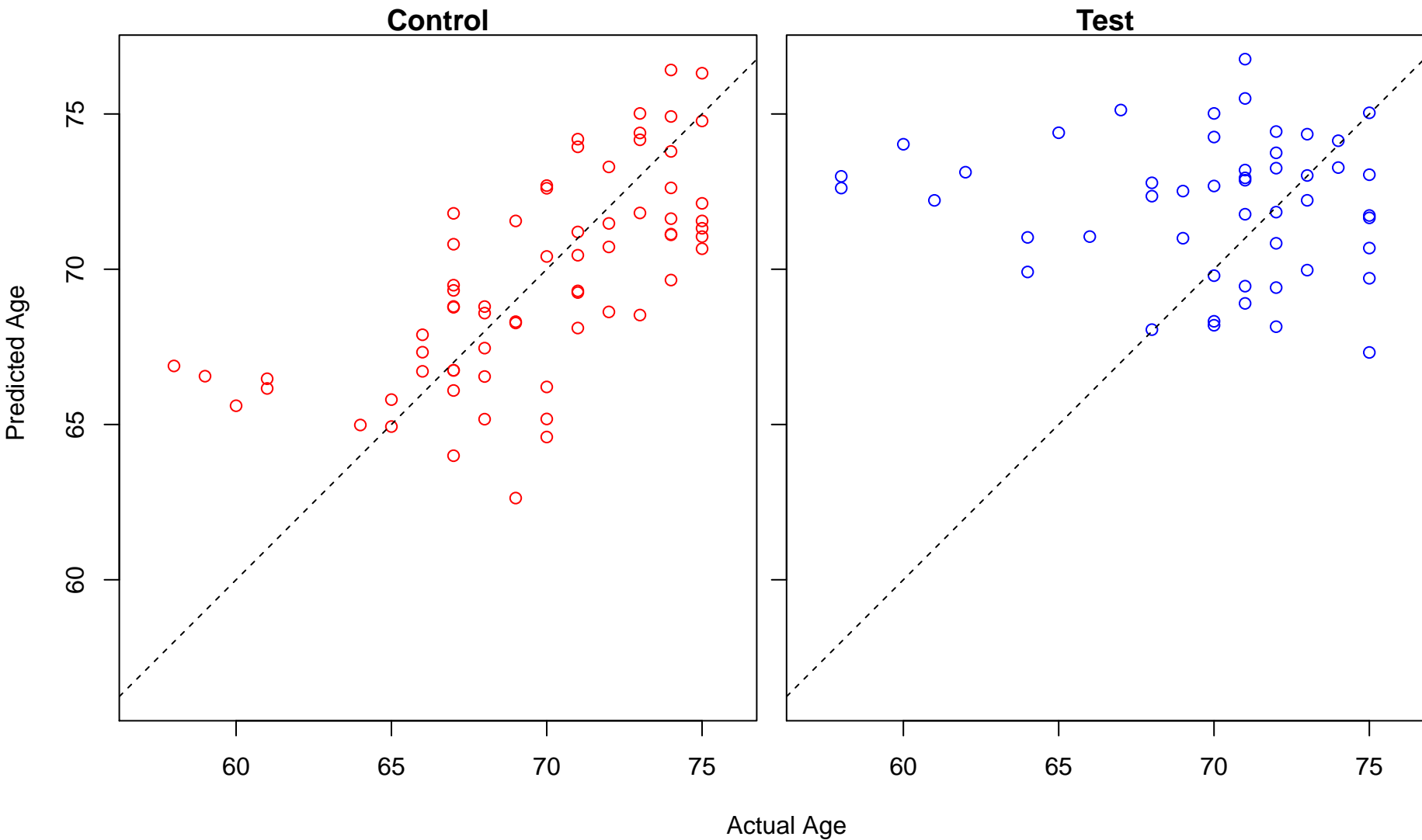
regulation of blood vessel endothelial cell migration (Score: 1.478041)



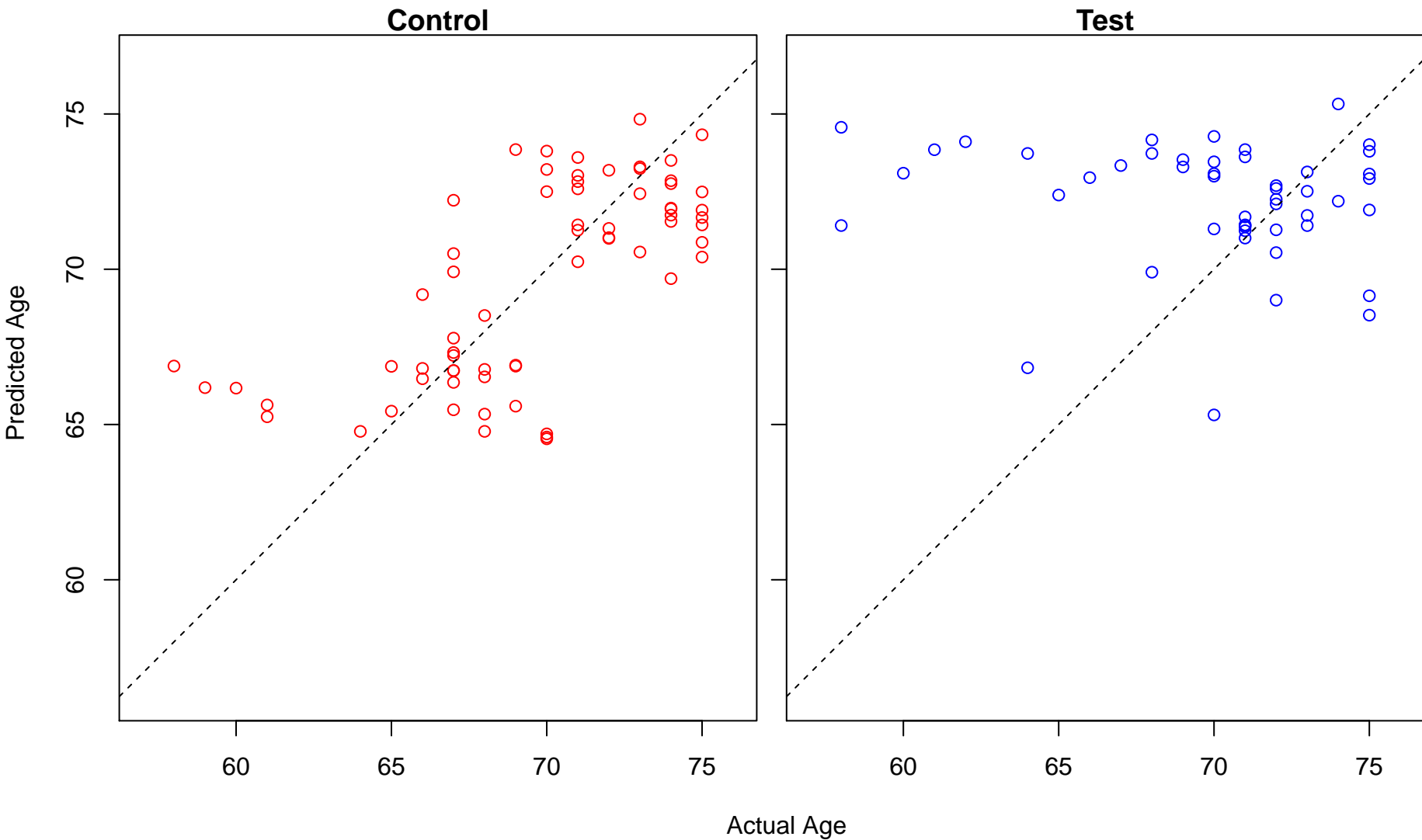
regulation of carbohydrate biosynthetic process (Score: 1.476600)



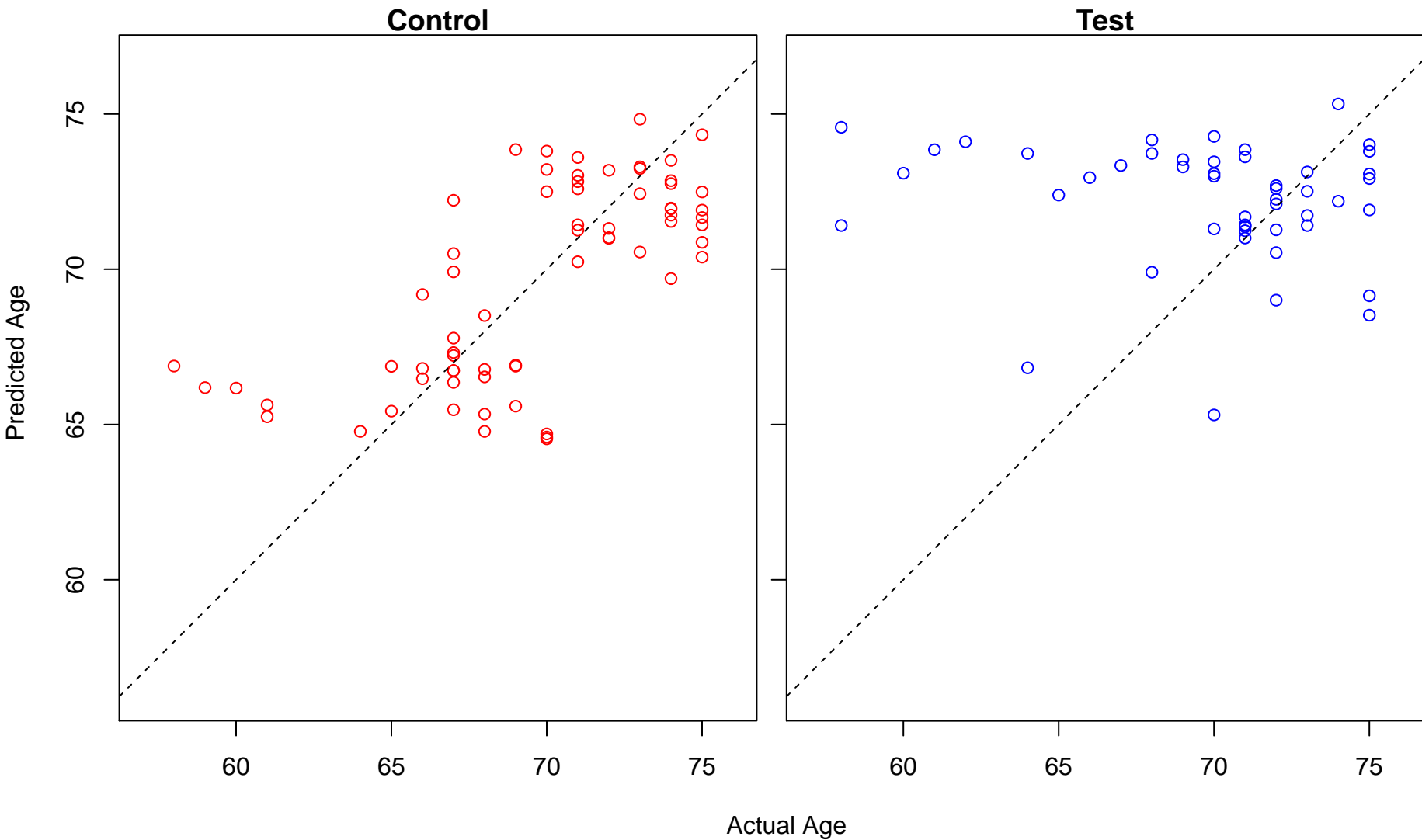
positive regulation of autophagy (Score: 1.476182)



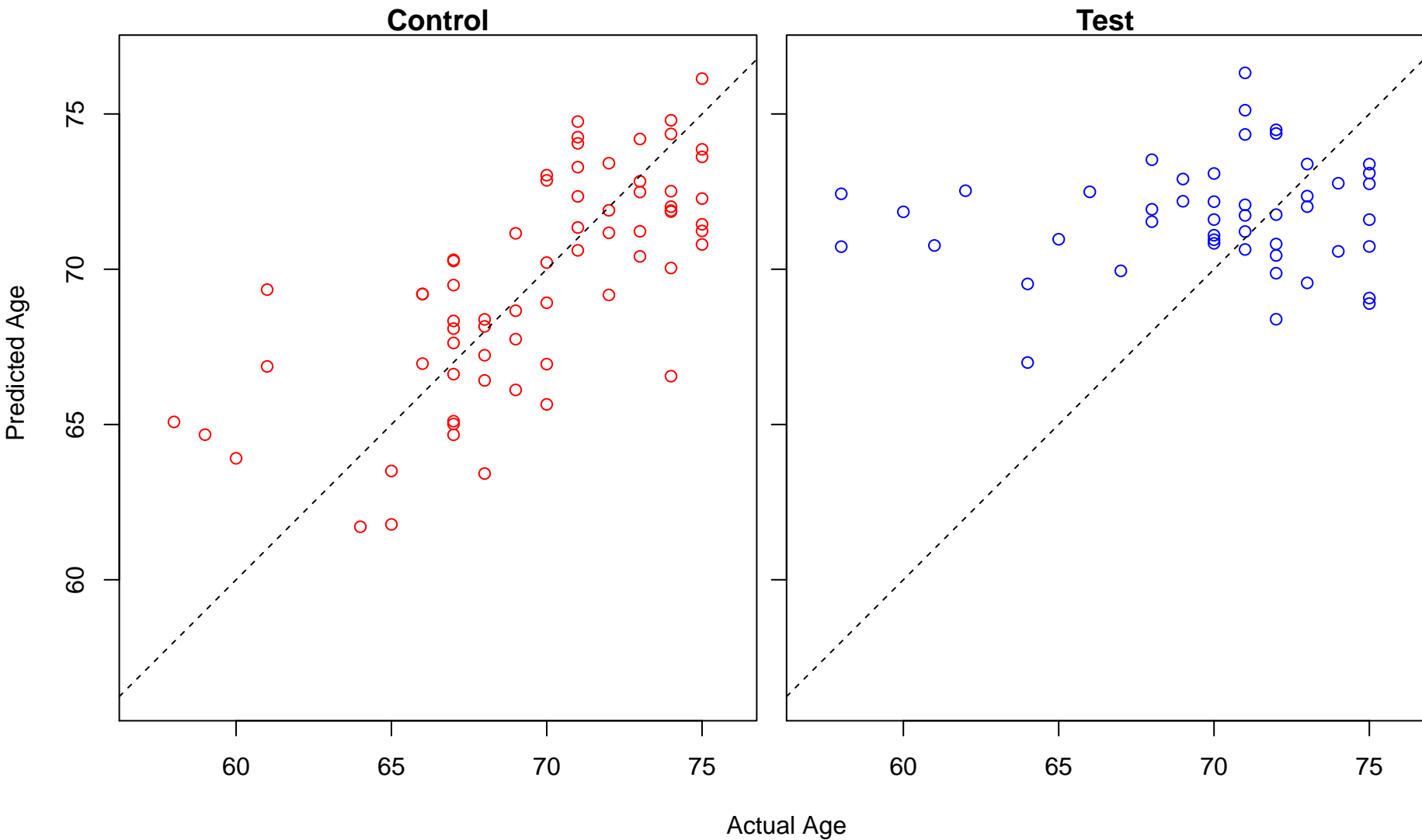
7-methylguanosine RNA capping (Score: 1.476157)



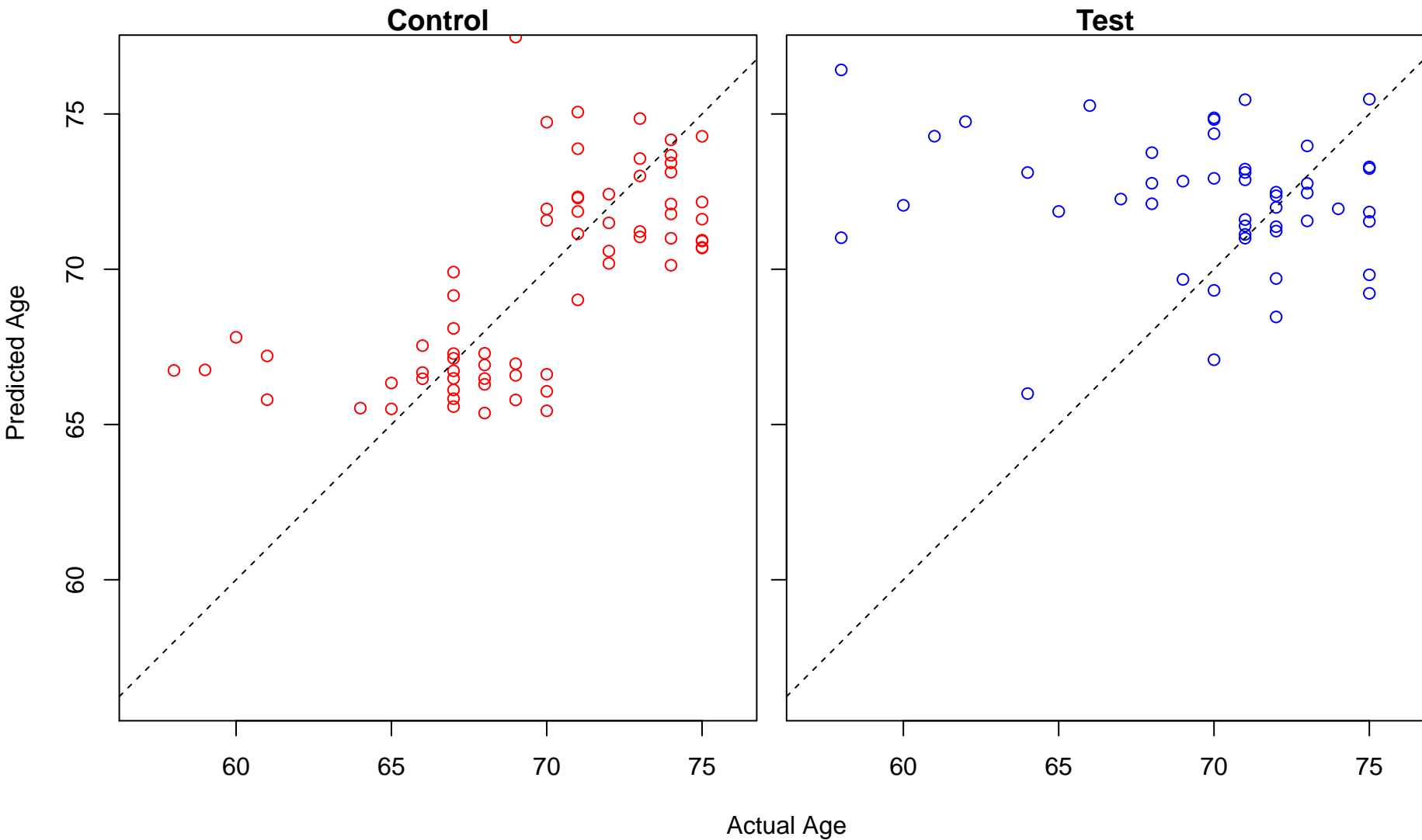
RNA capping (Score: 1.476157)



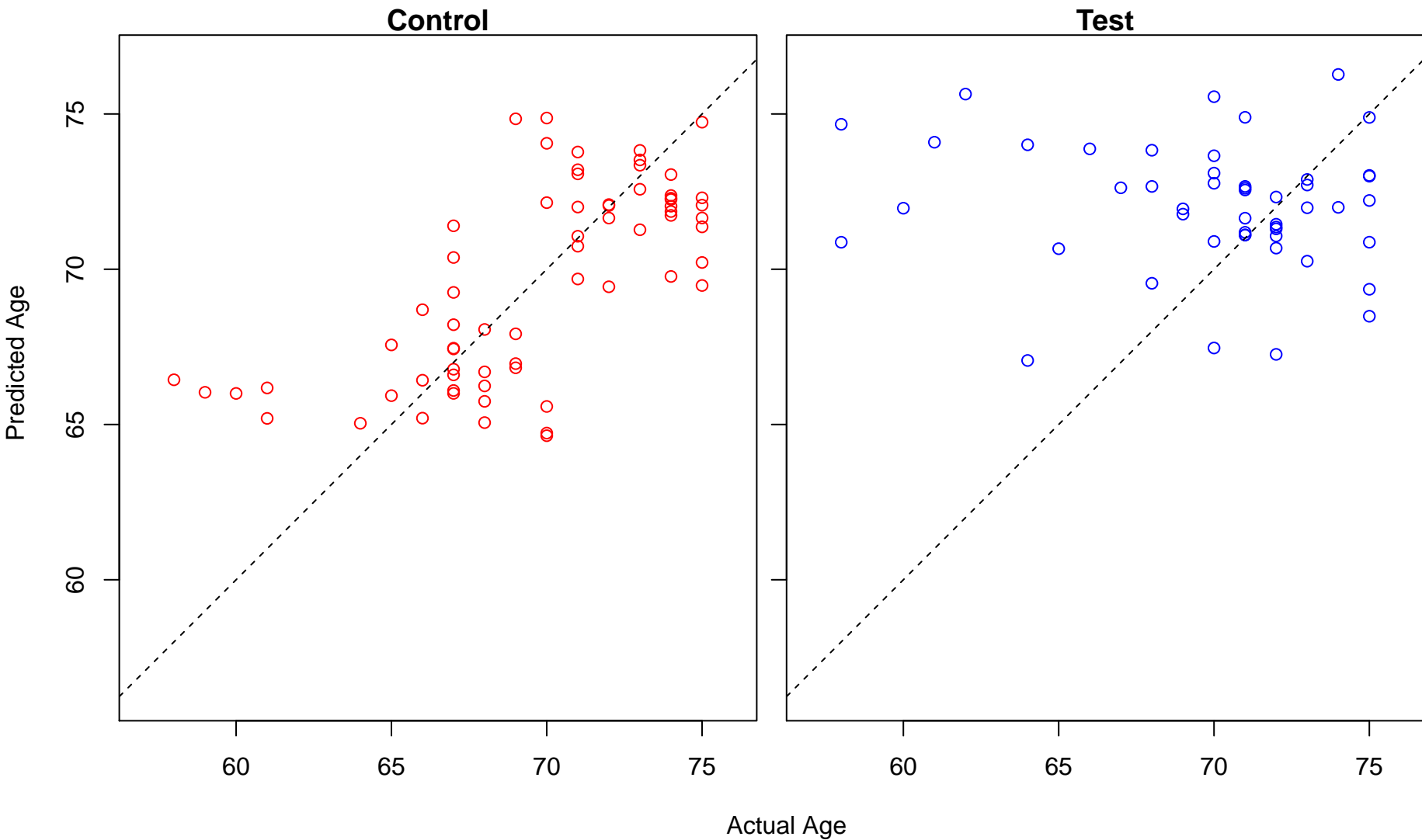
protein import into nucleus, translocation (Score: 1.476102)



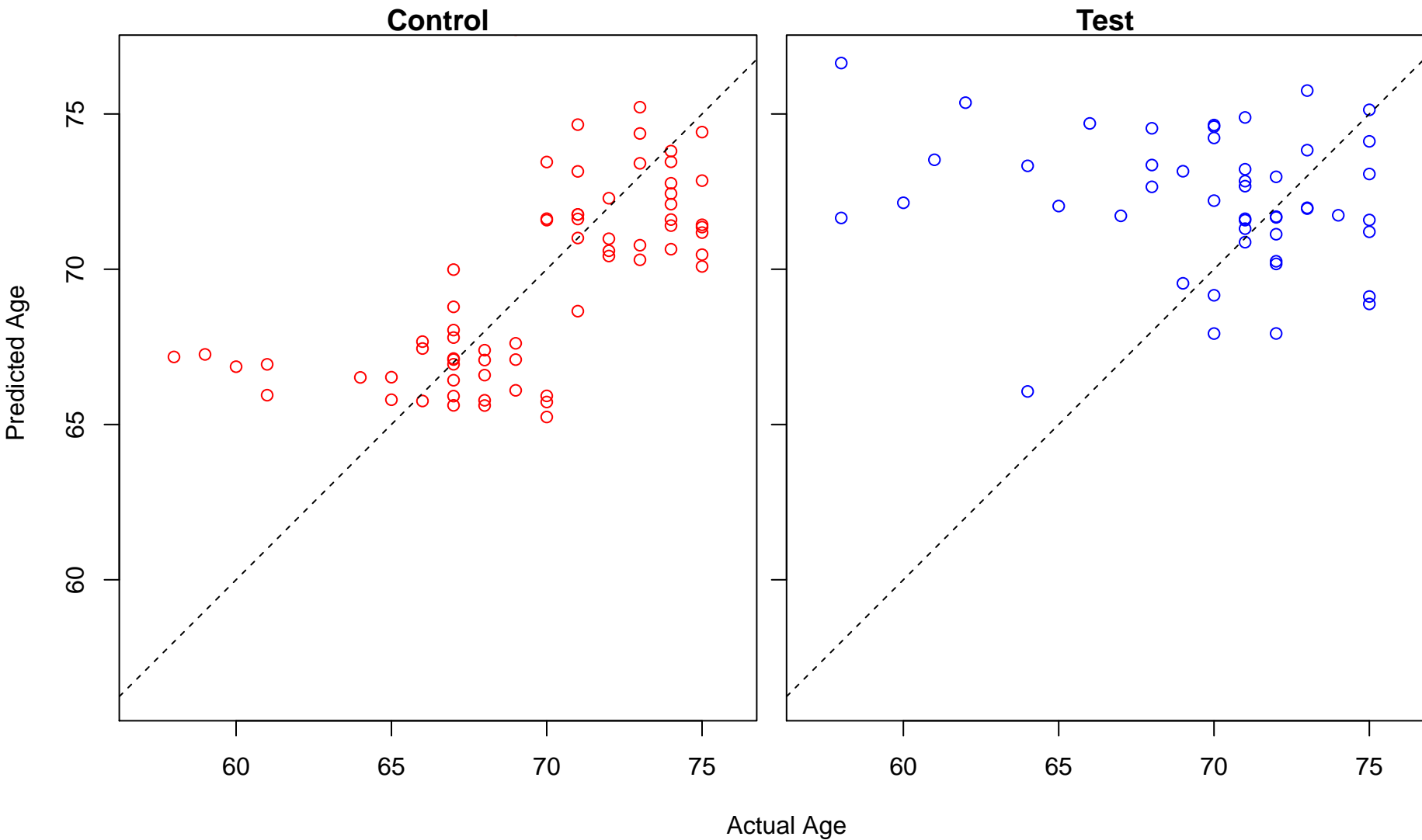
response to toxic substance (Score: 1.475275)



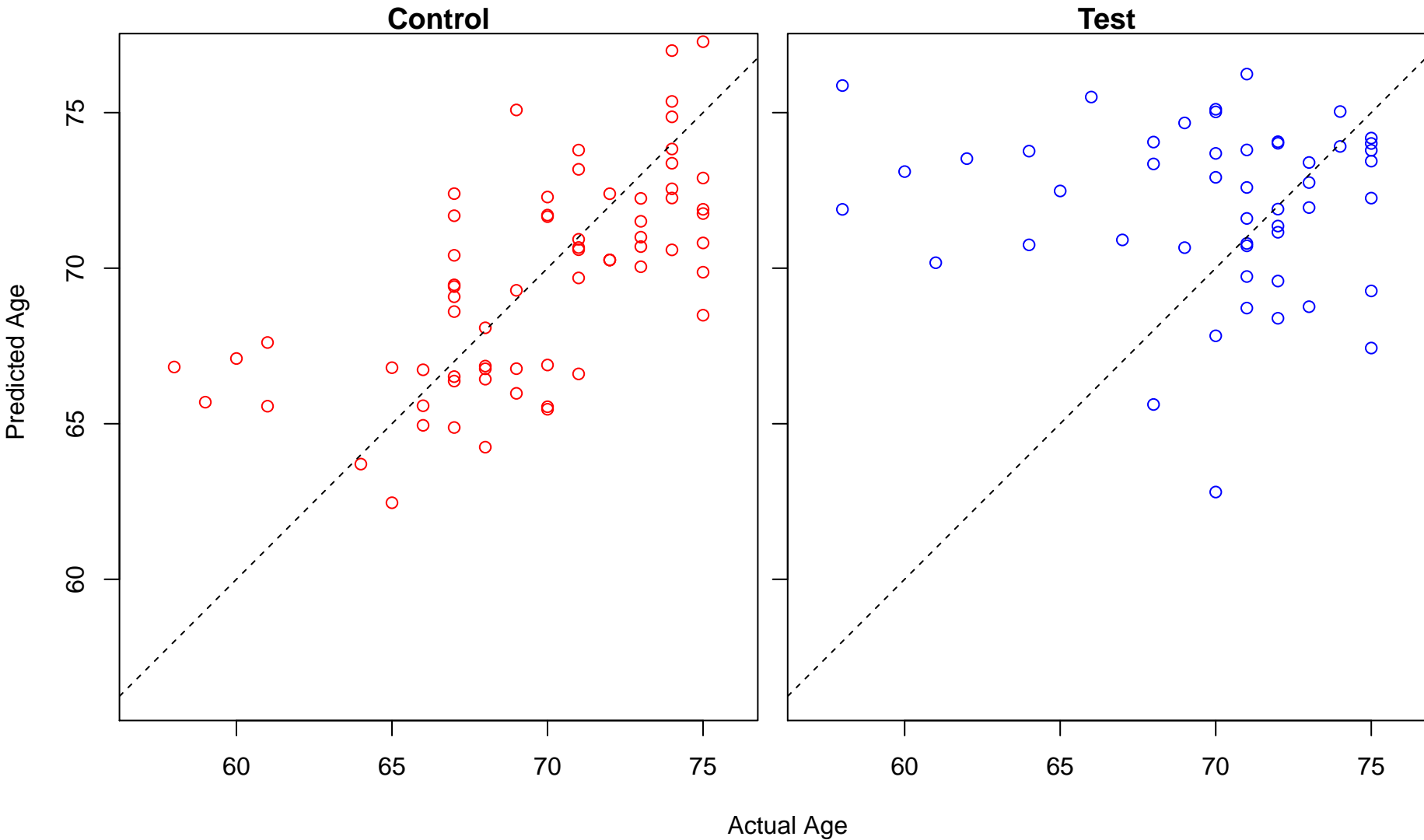
global genome nucleotide-excision repair (Score: 1.475165)



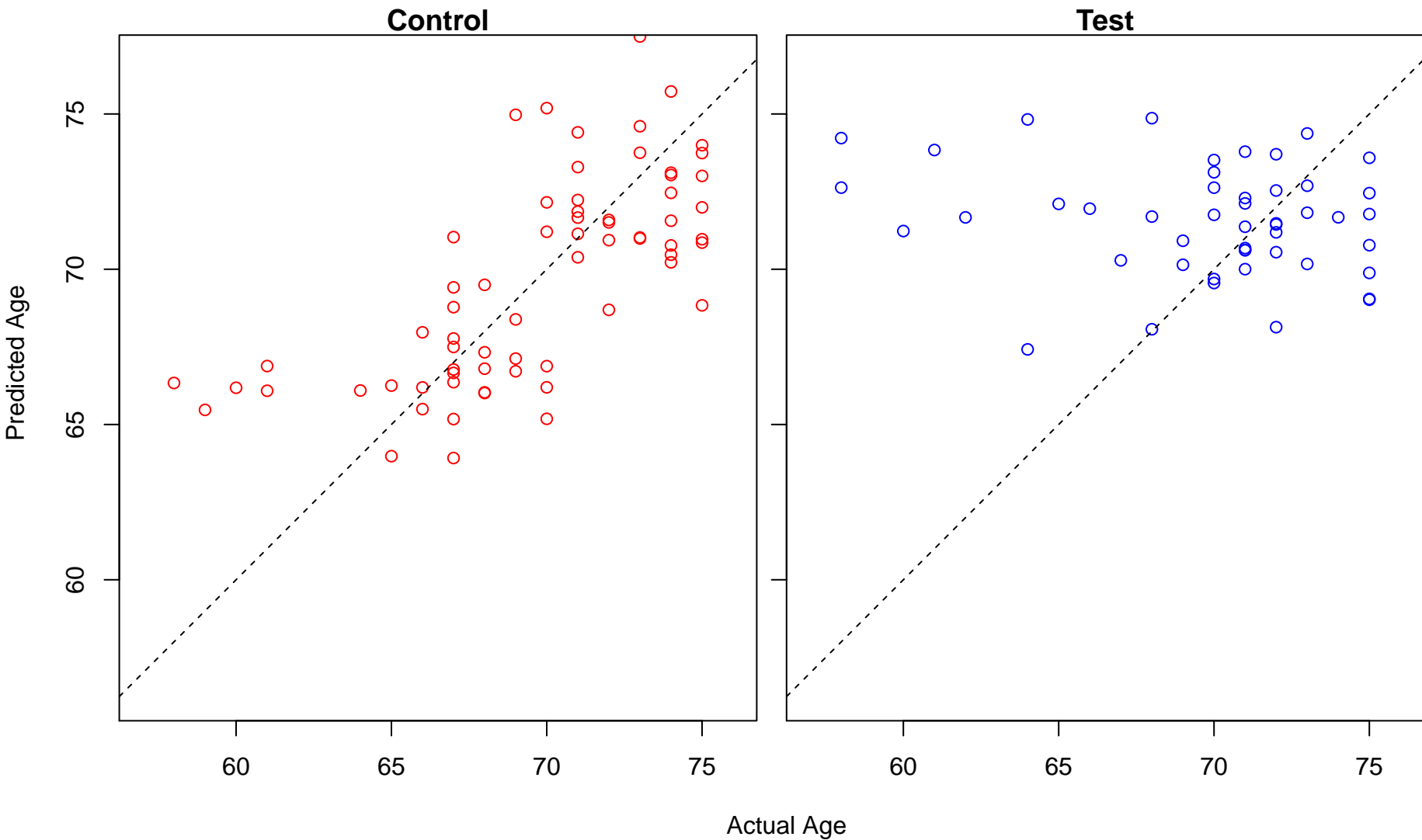
detoxification (Score: 1.473749)



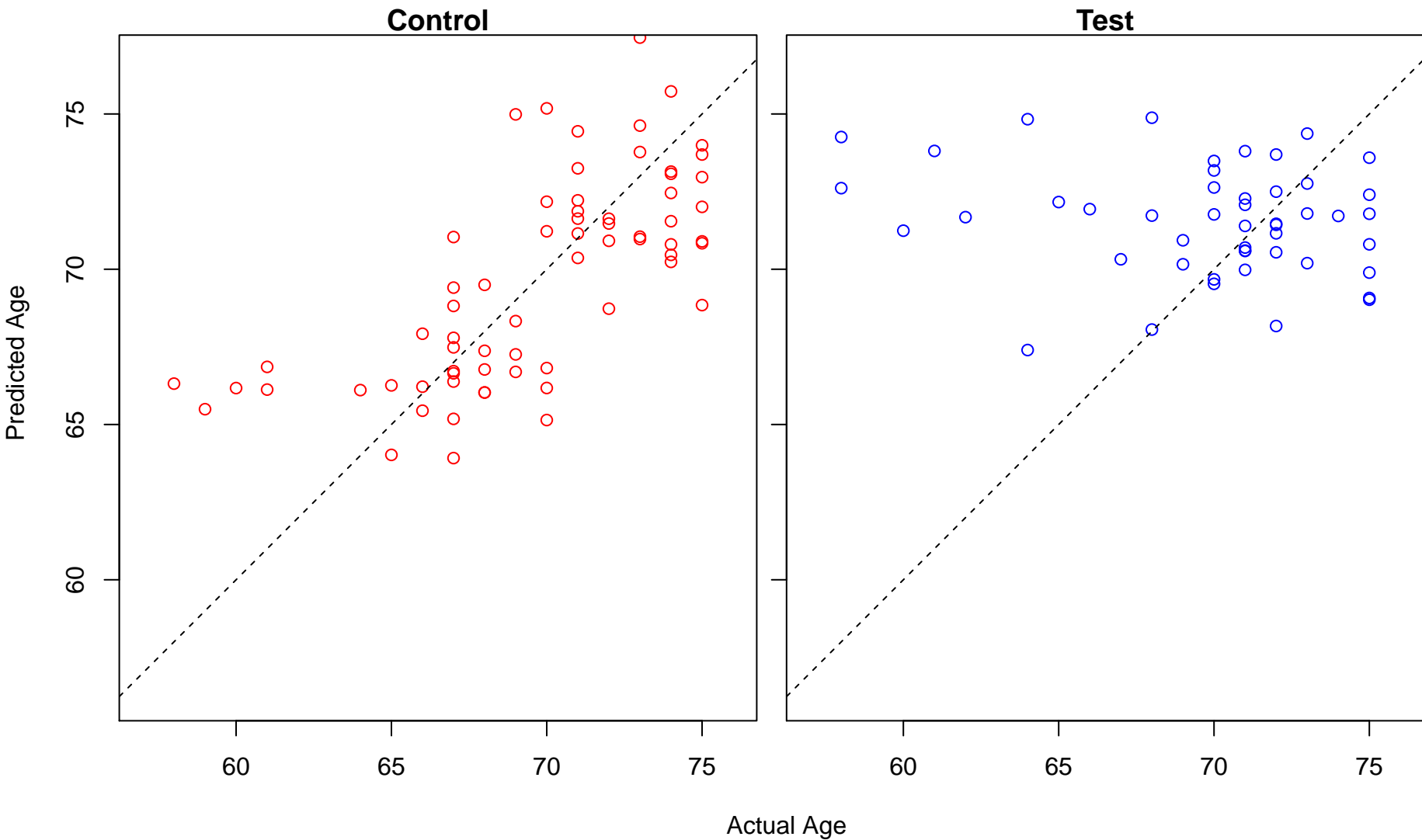
regulation of response to interferon-gamma (Score: 1.473154)



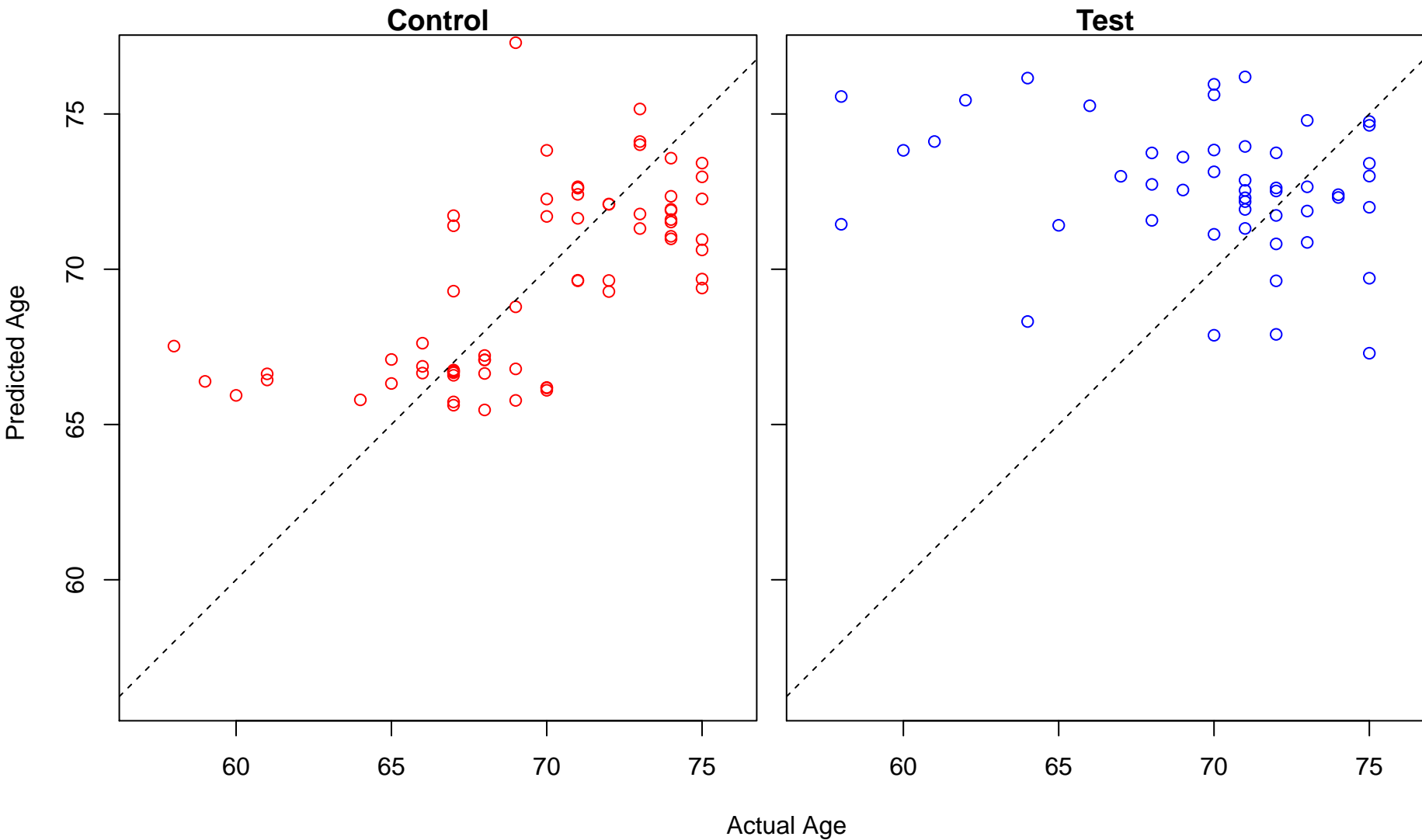
positive regulation of telomere maintenance via telomerase (Score: 1.472965)



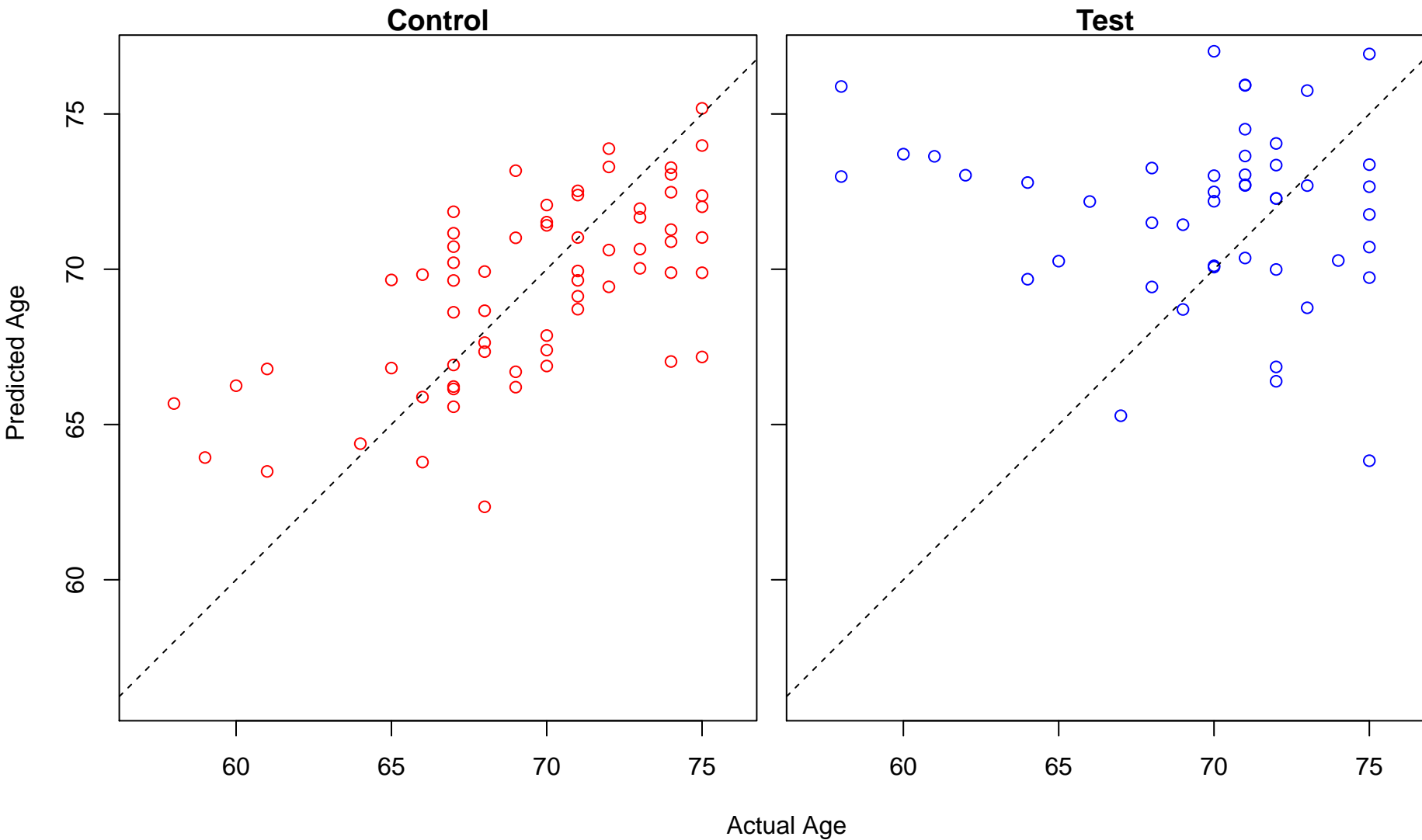
positive regulation of telomere maintenance via telomere lengthening (Score: 1.472259)



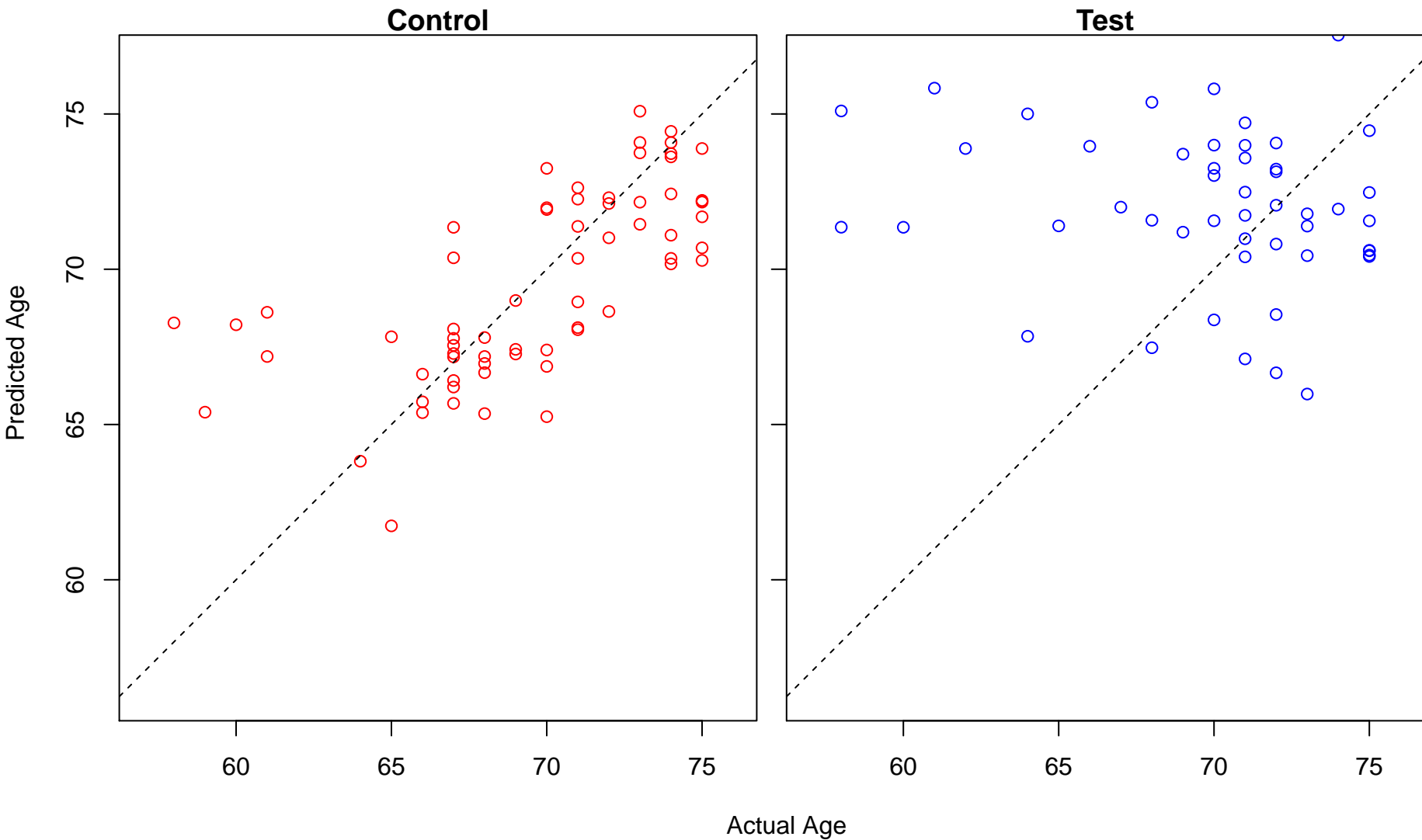
iron ion homeostasis (Score: 1.471648)



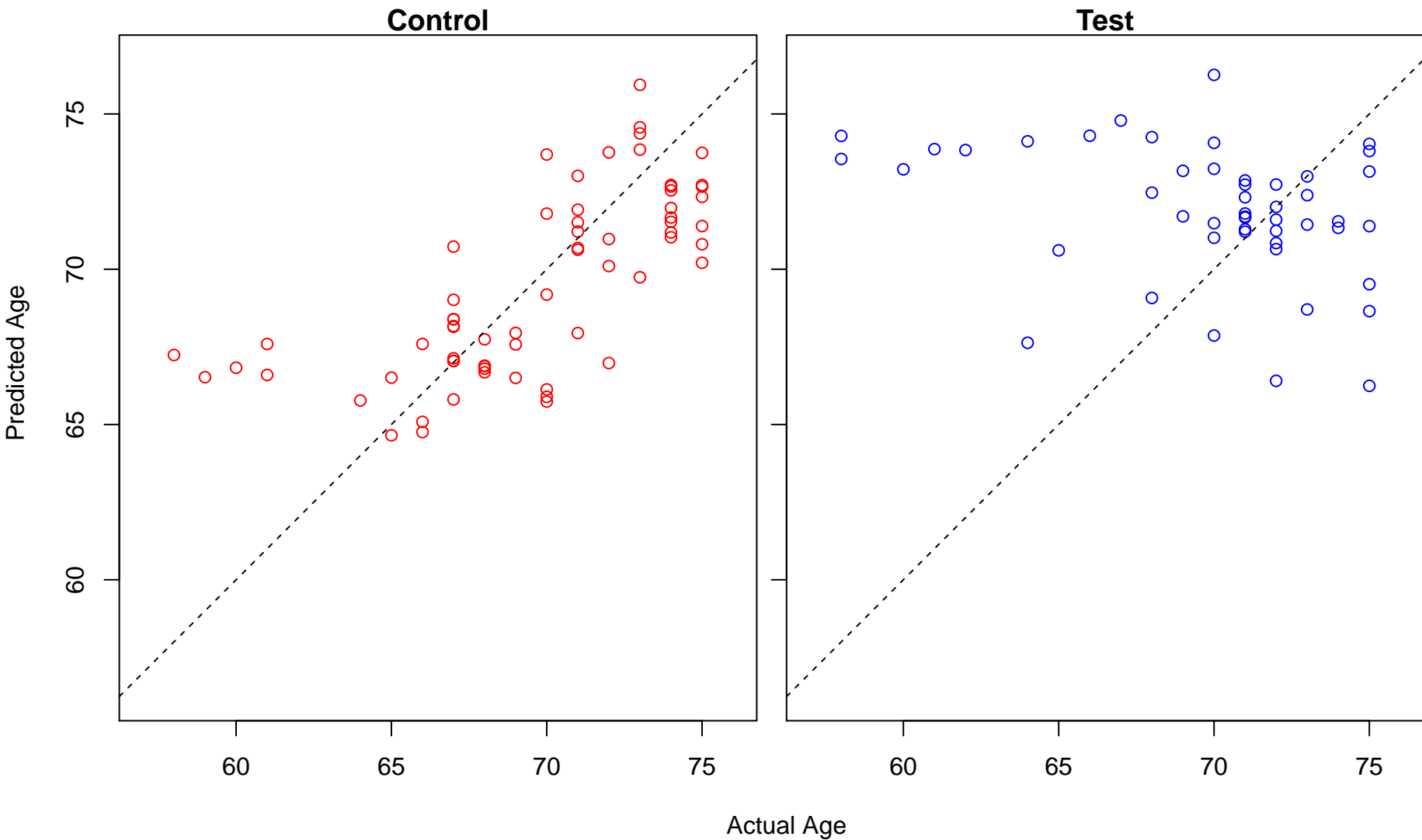
action potential (Score: 1.471147)



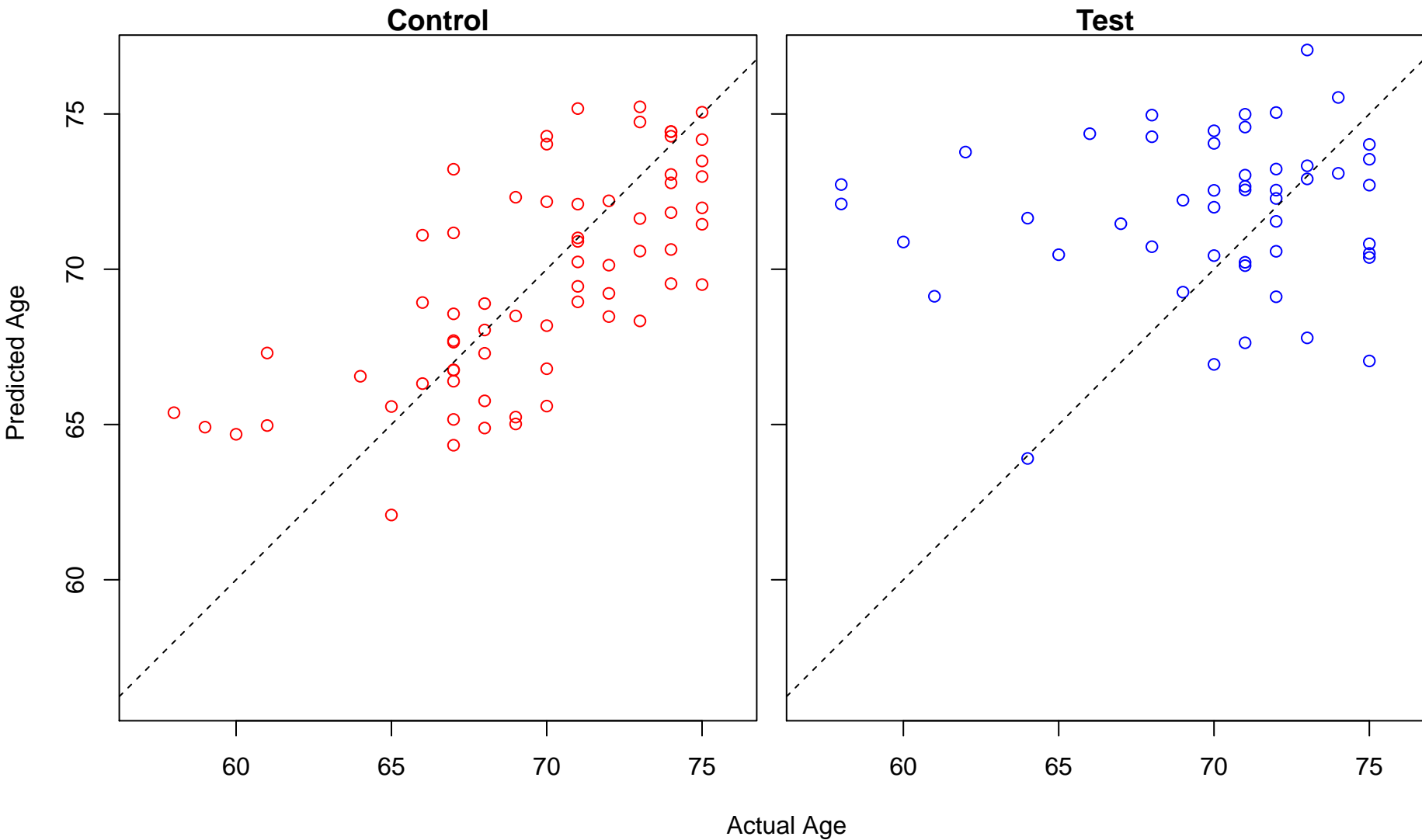
negative regulation of secretion (Score: 1.470522)



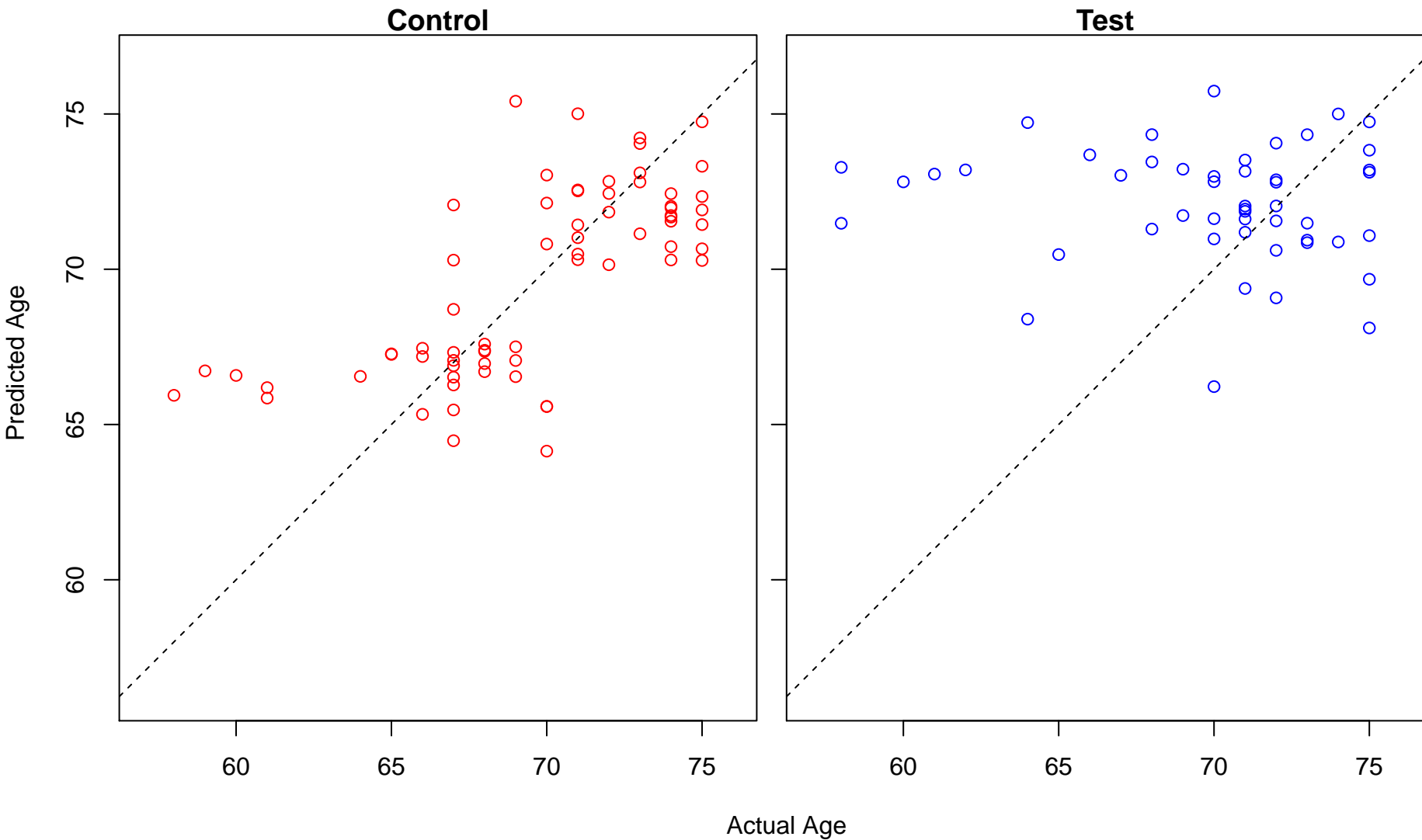
positive regulation of inflammatory response (Score: 1.468954)



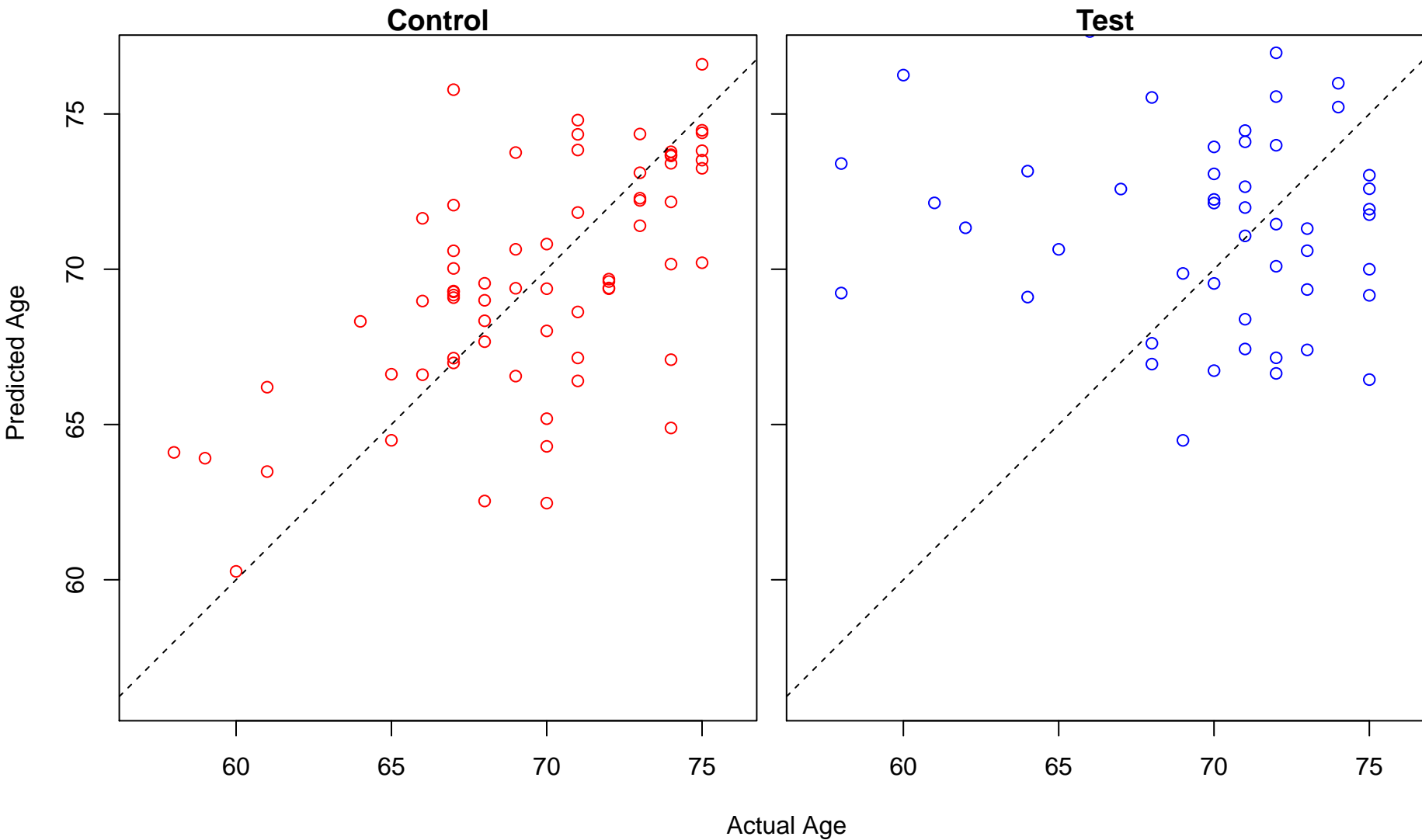
cell aging (Score: 1.467363)



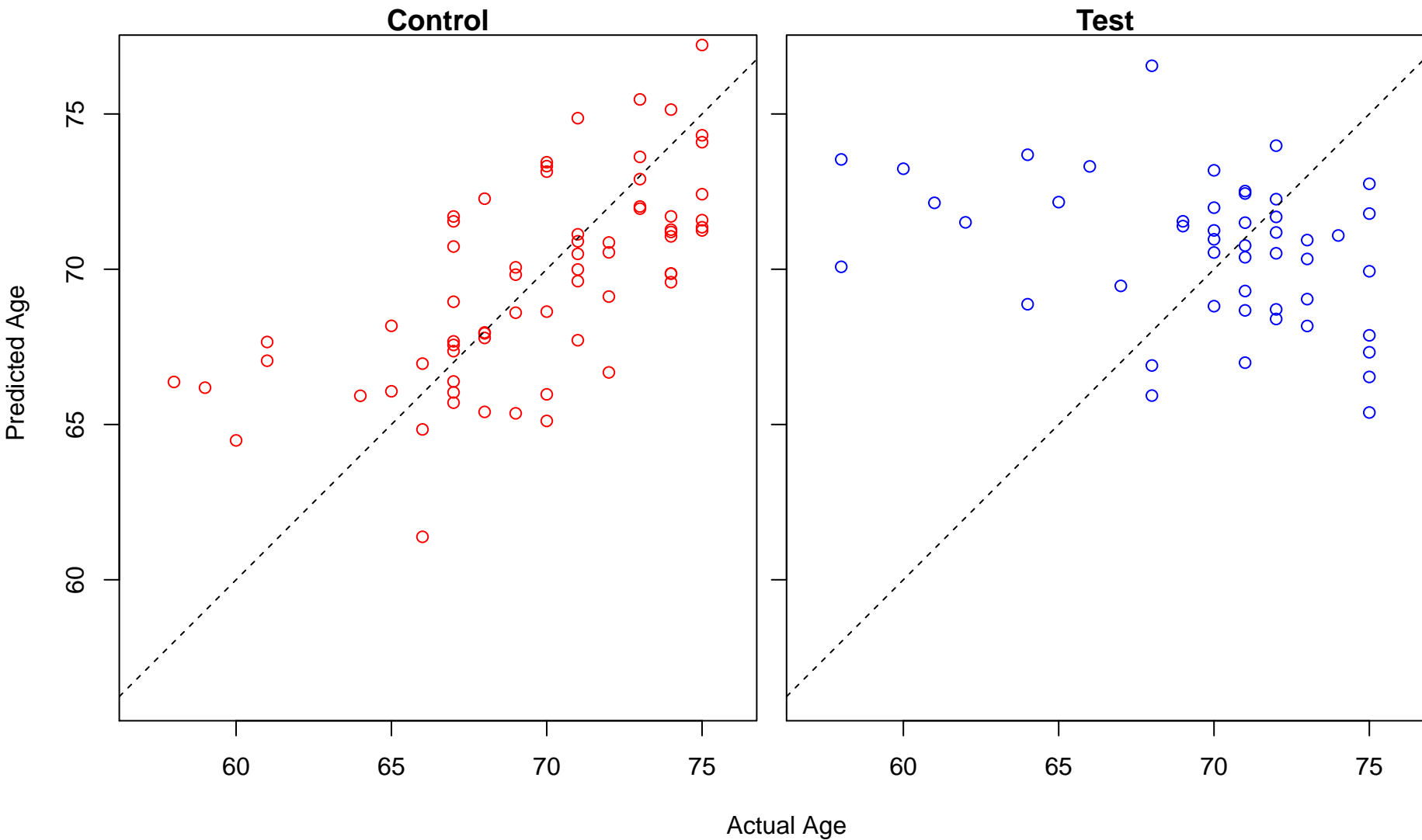
negative regulation of hydrogen peroxide-induced cell death (Score: 1.467240)



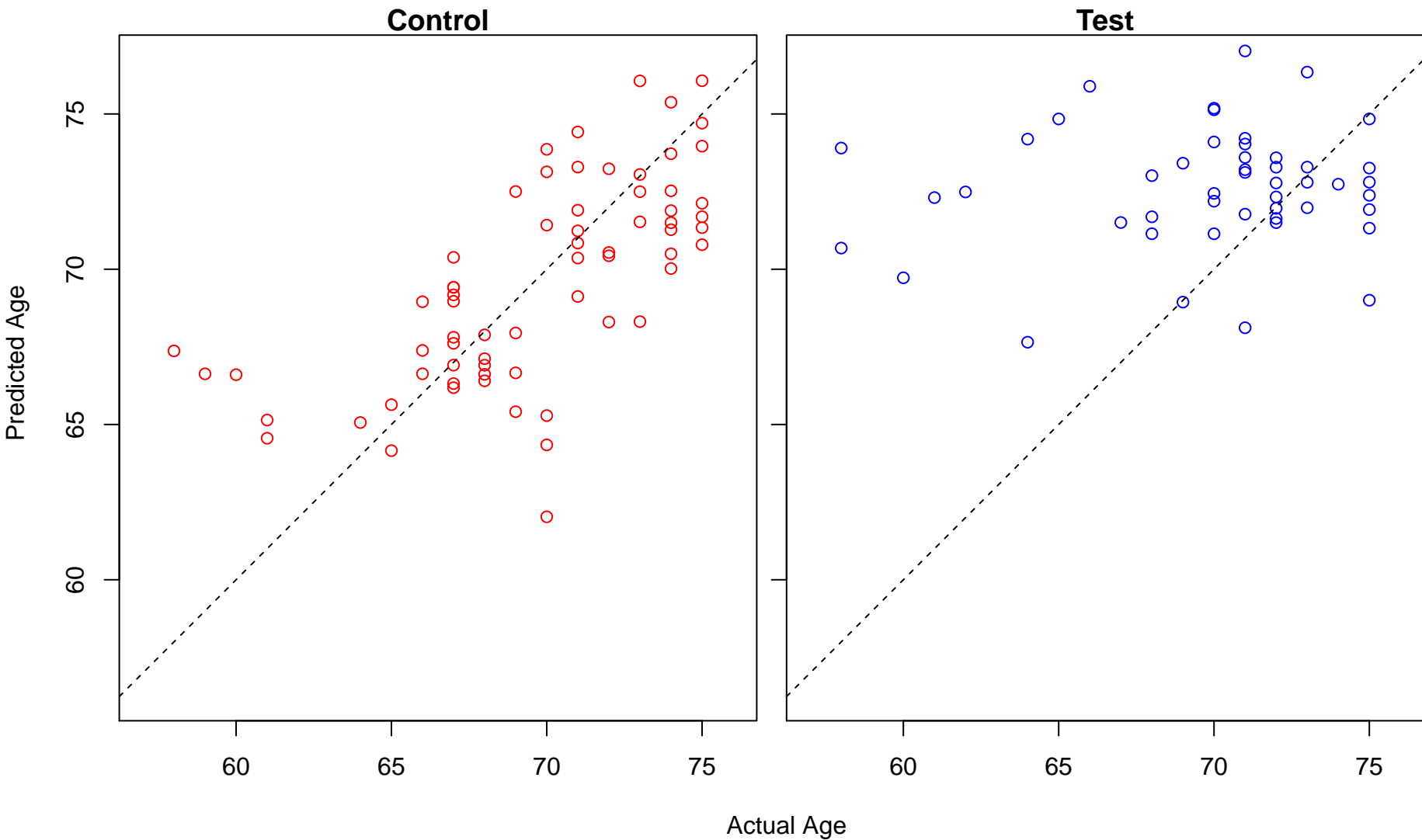
positive regulation of ossification (Score: 1.467126)



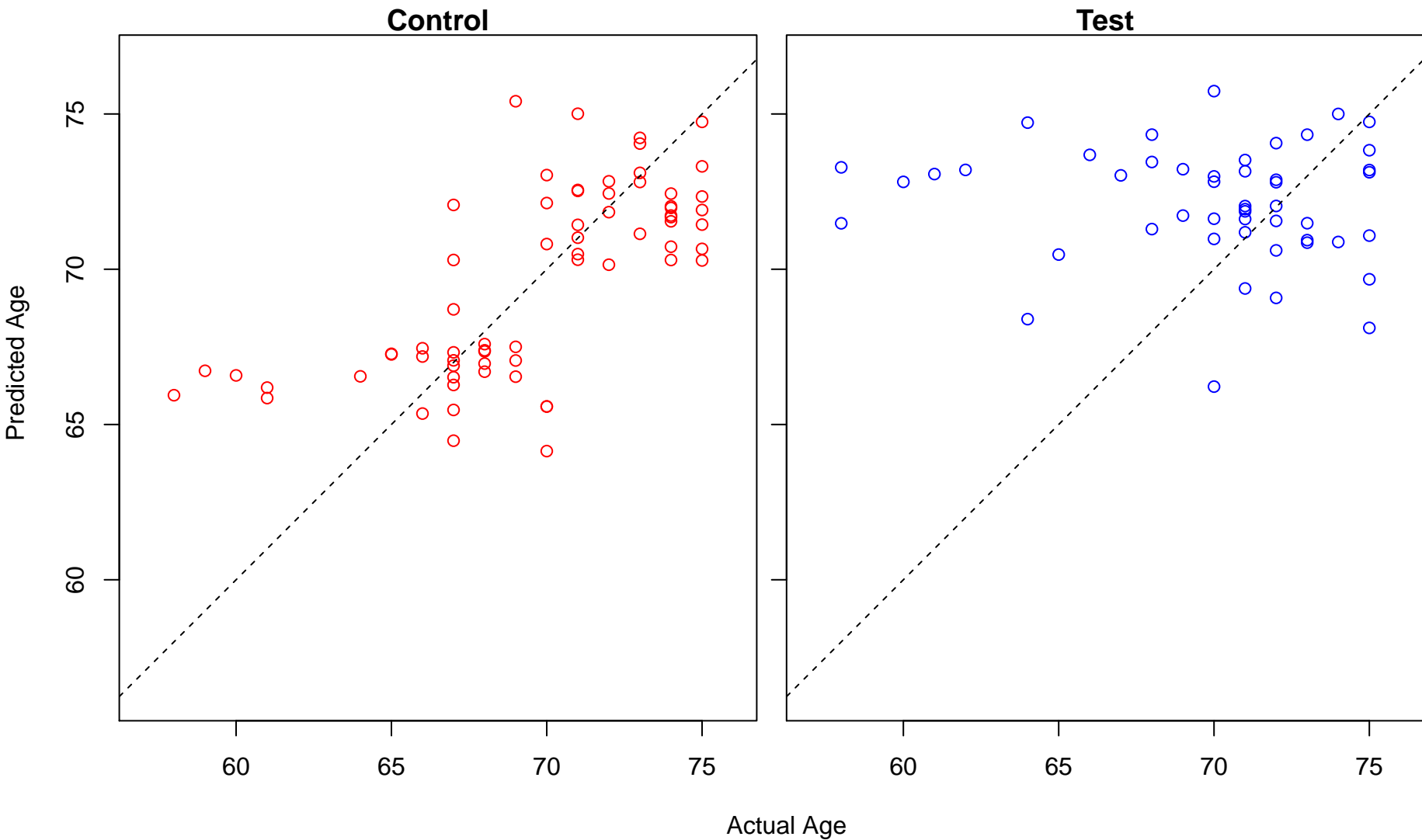
regulation of triglyceride metabolic process (Score: 1.466886)



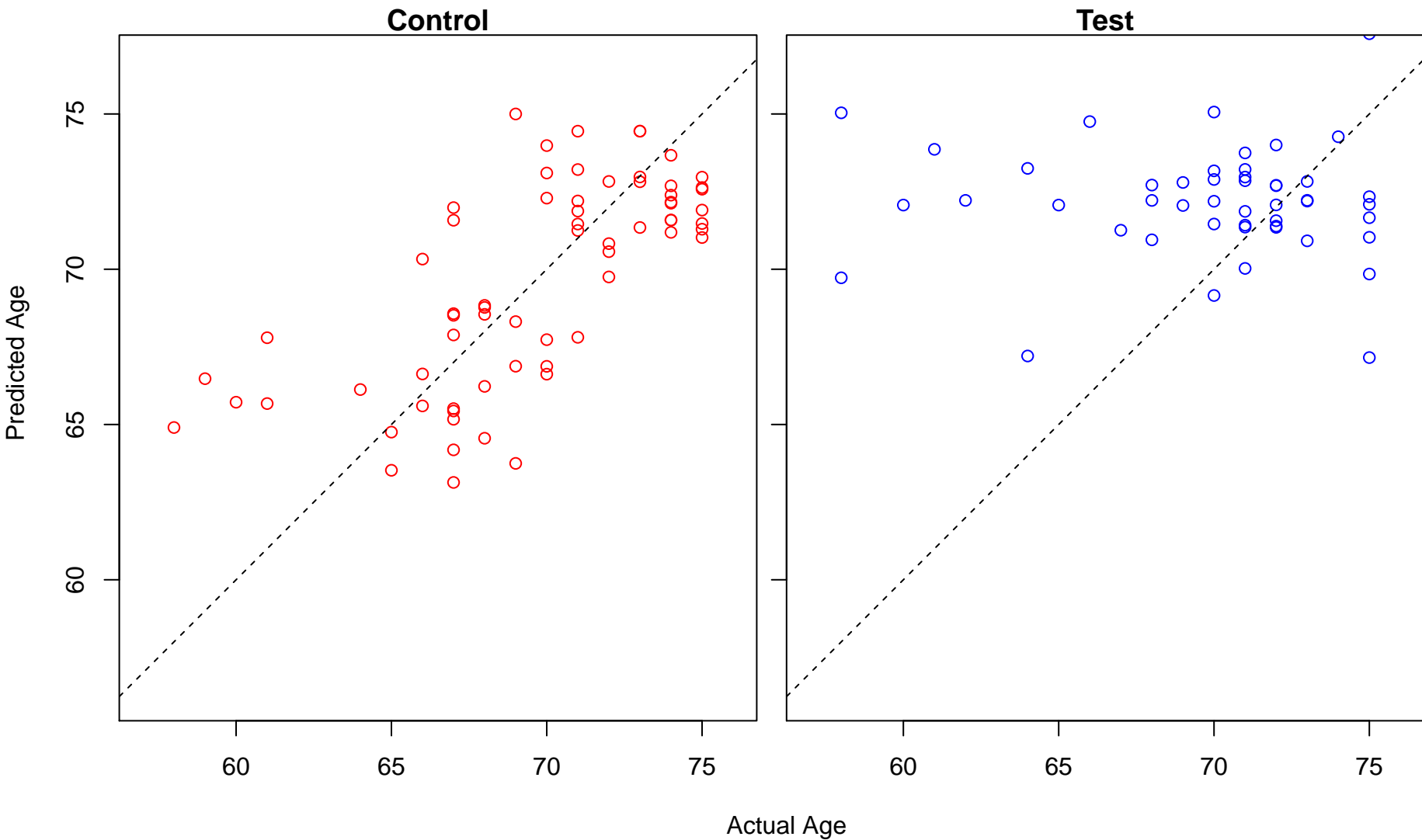
response to transforming growth factor beta (Score: 1.466776)



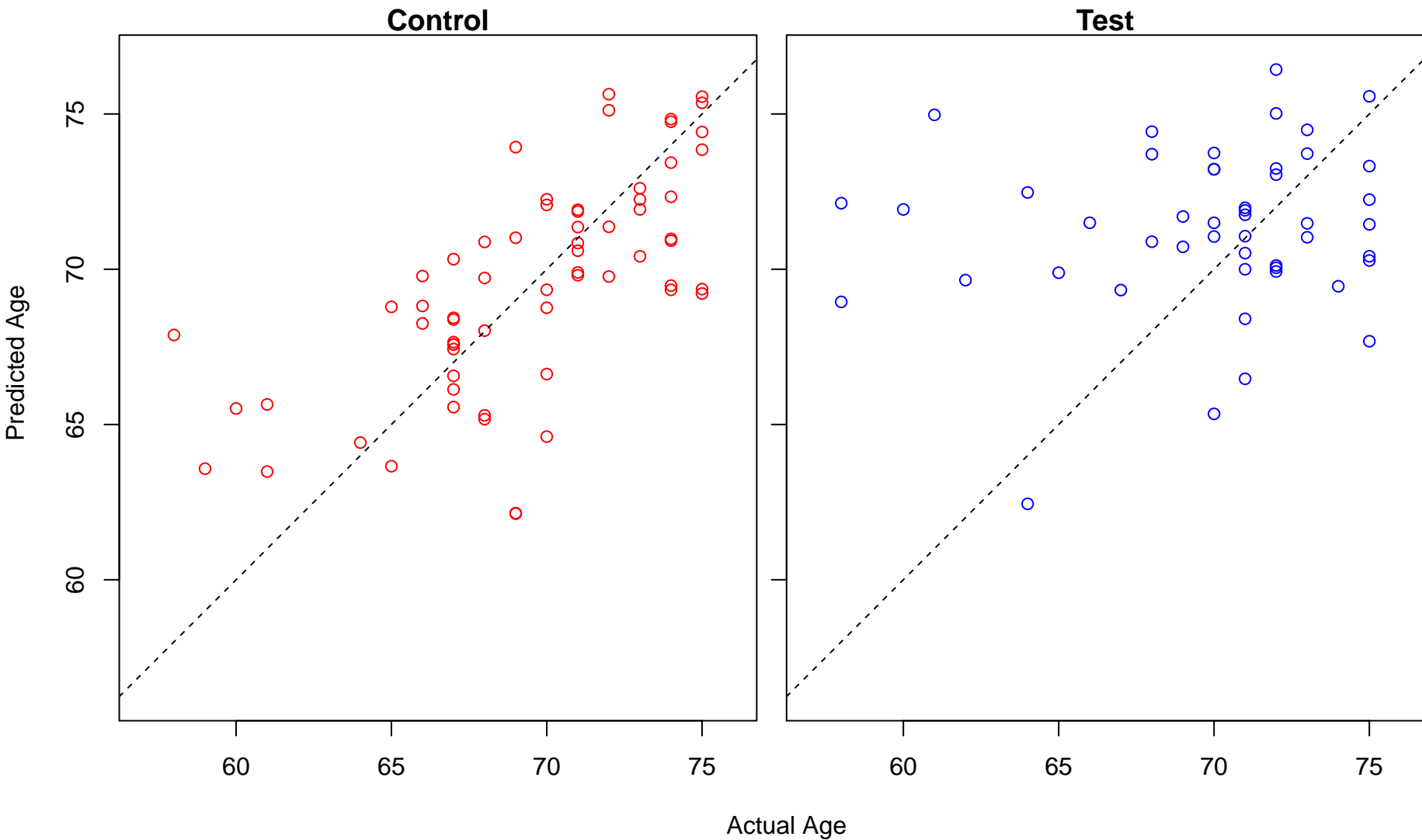
negative regulation of response to reactive oxygen species (Score: 1.466409)



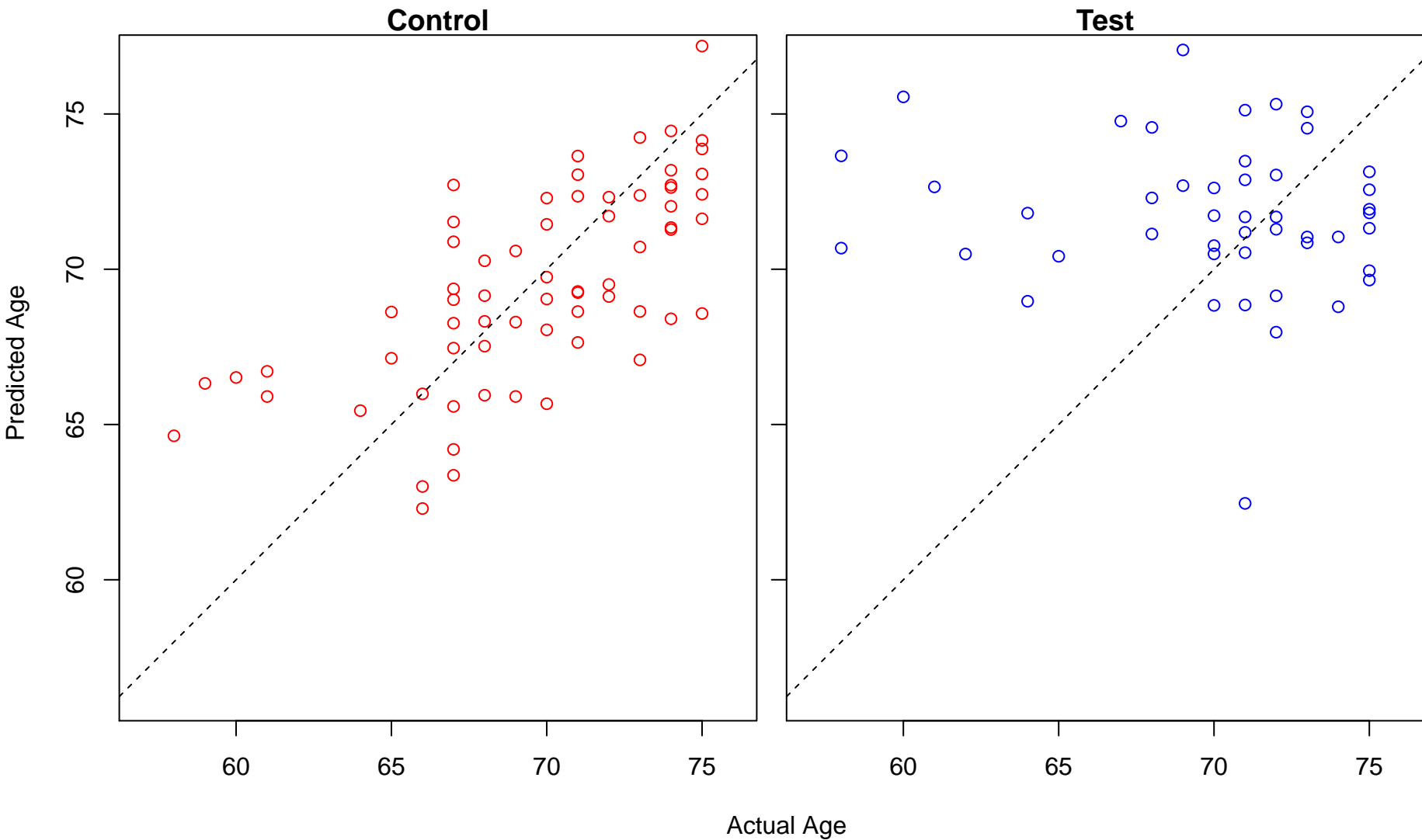
chromatin assembly (Score: 1.466265)



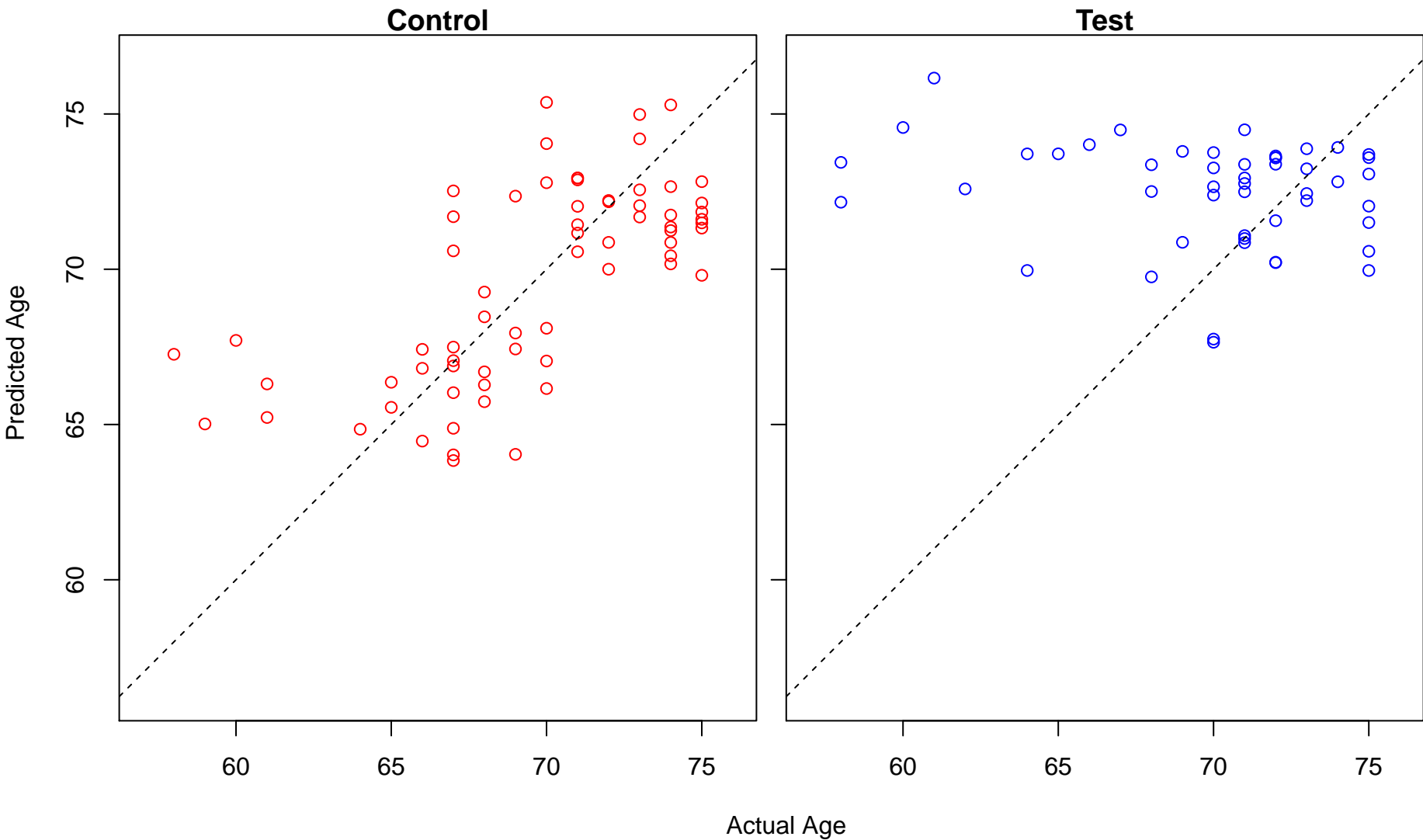
DNA modification (Score: 1.466223)



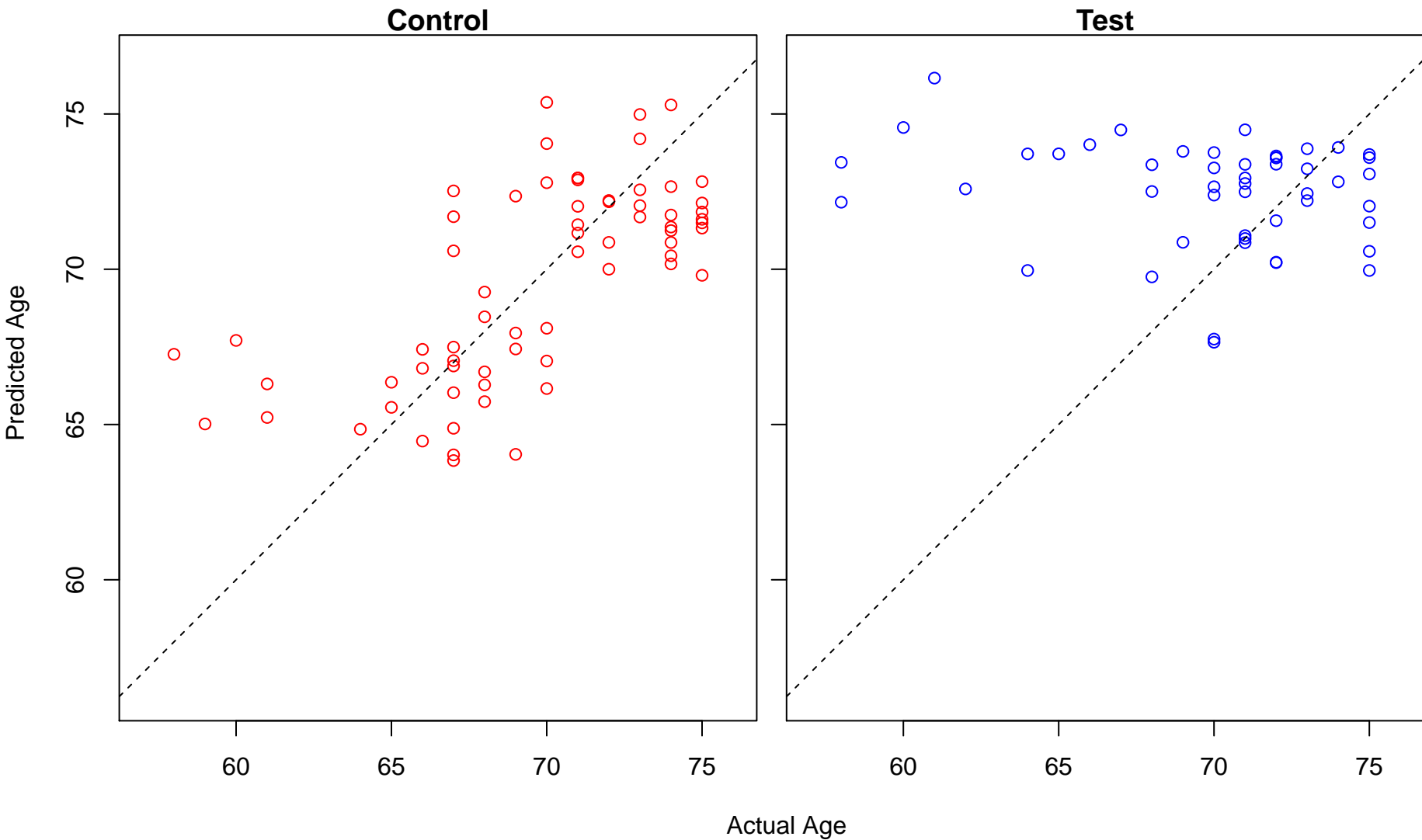
monocyte chemotaxis (Score: 1.465609)



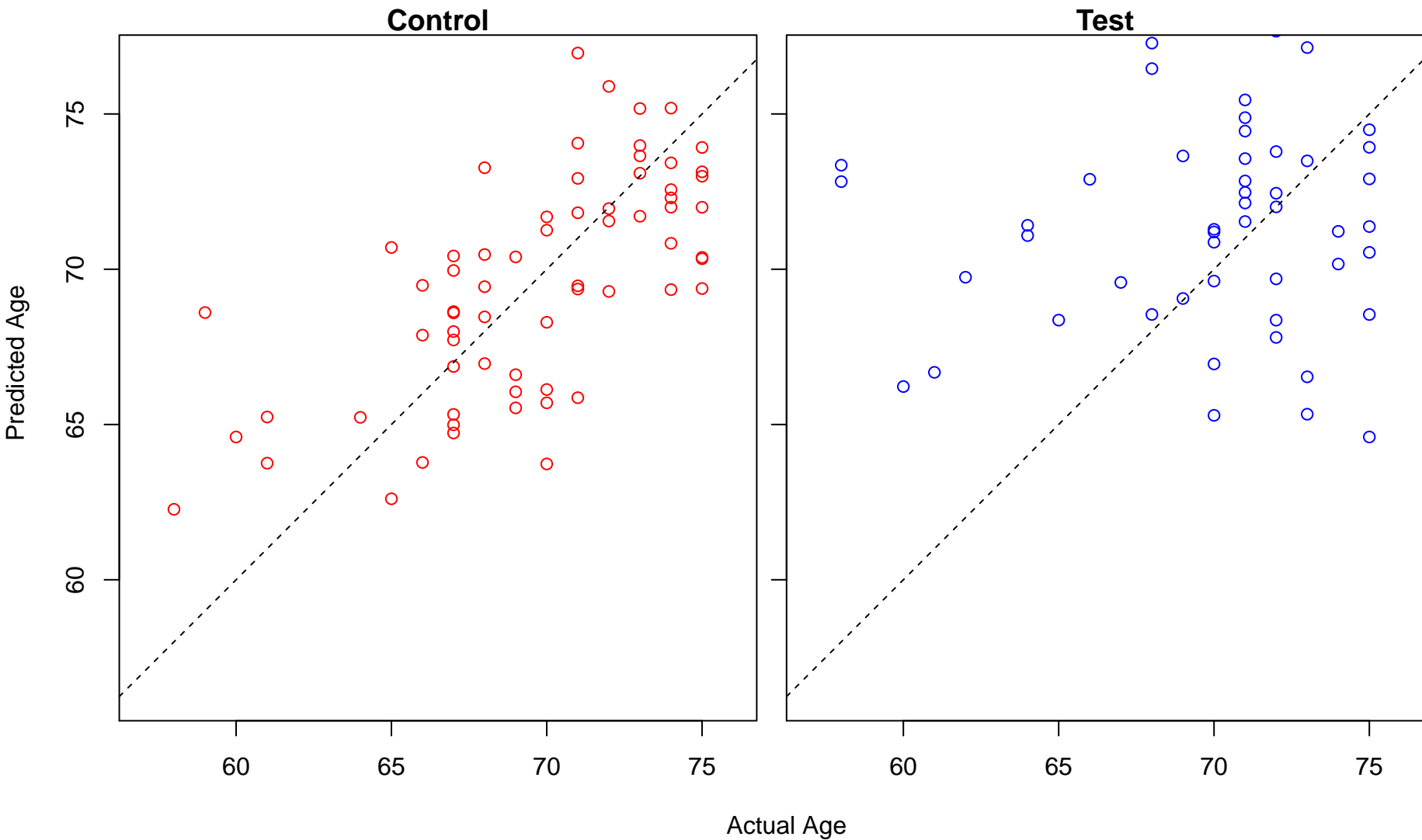
meiotic cell cycle (Score: 1.465546)



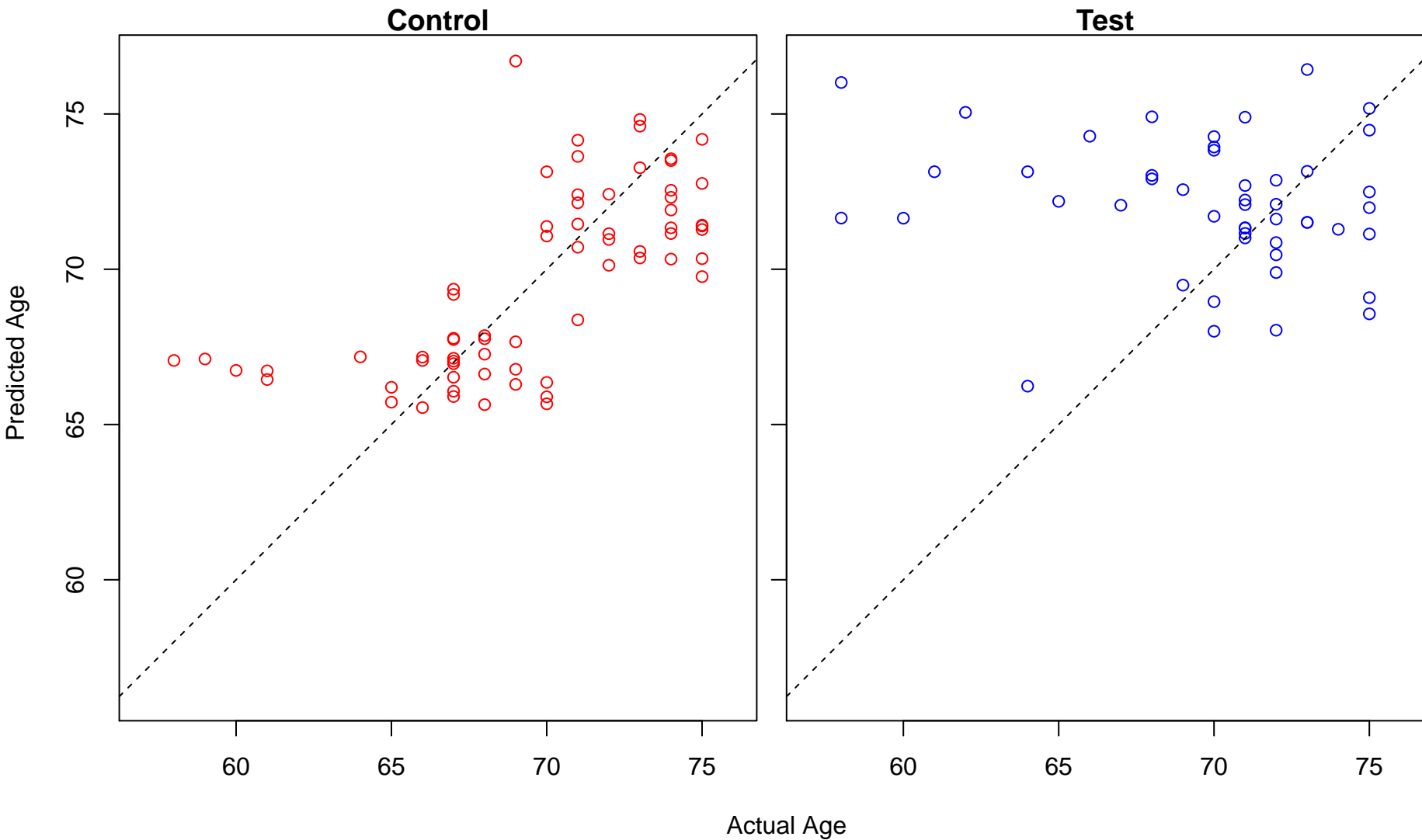
meiotic cell cycle process (Score: 1.465546)



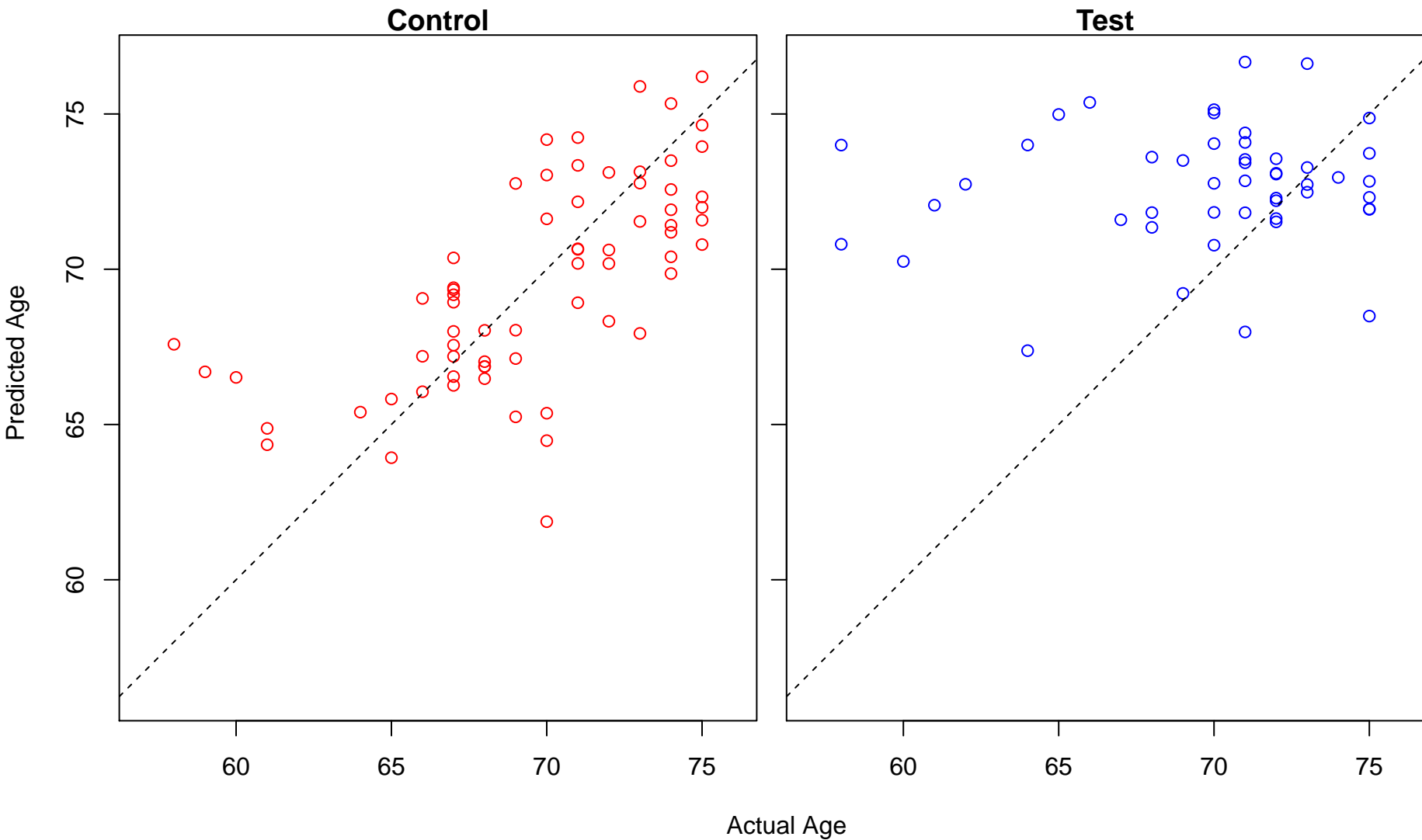
lamellipodium assembly (Score: 1.465105)



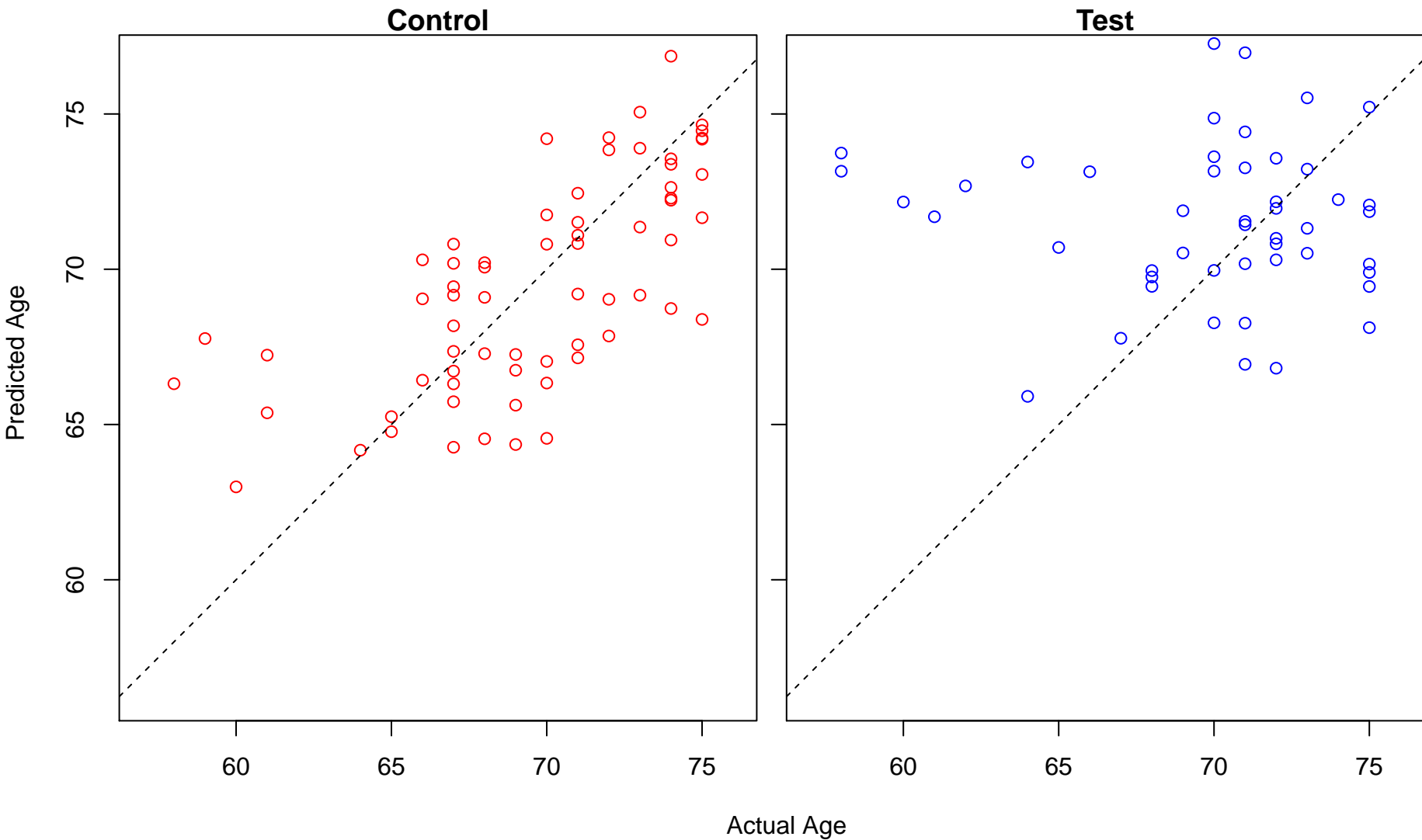
cellular oxidant detoxification (Score: 1.463729)



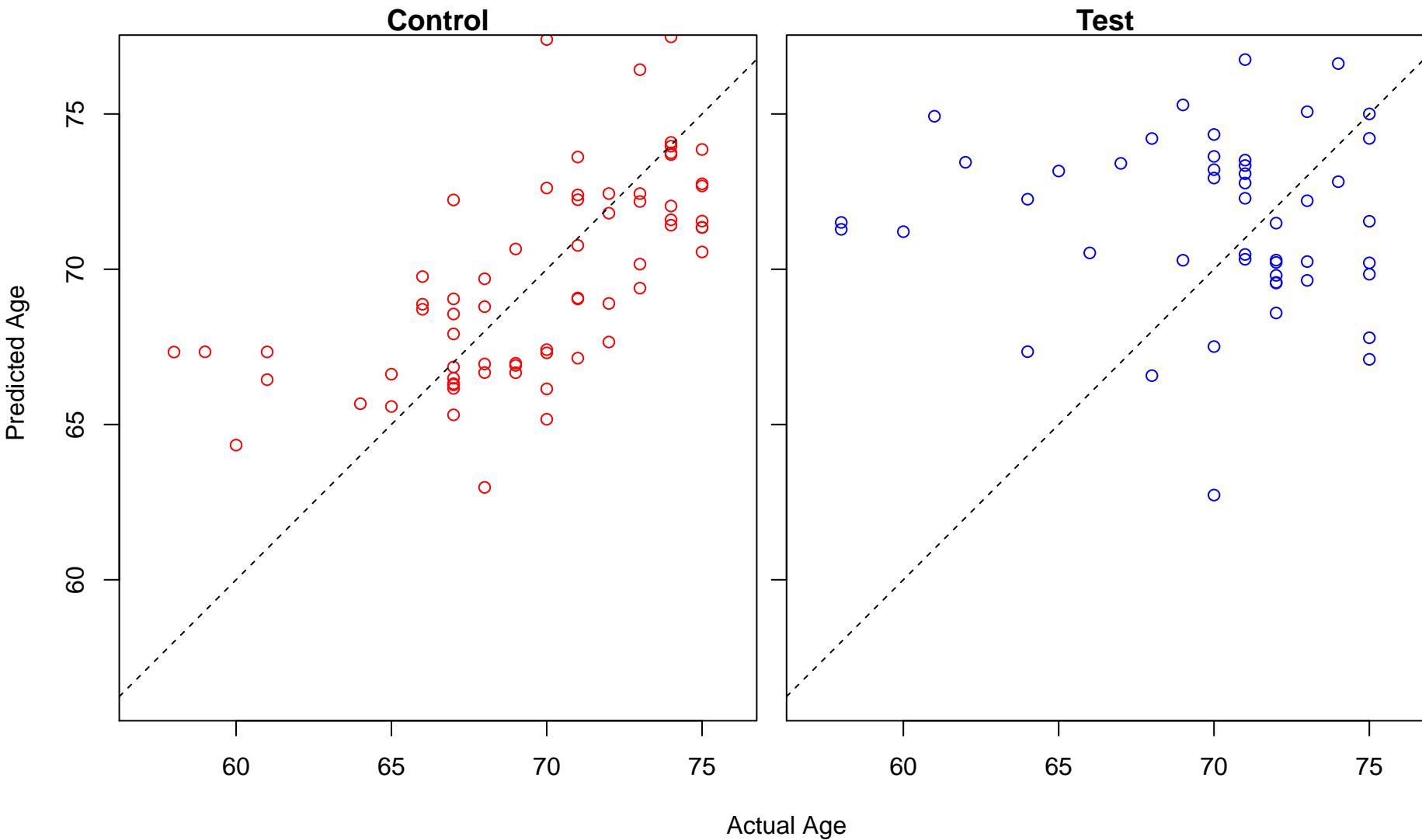
cellular response to transforming growth factor beta stimulus (Score: 1.463416)



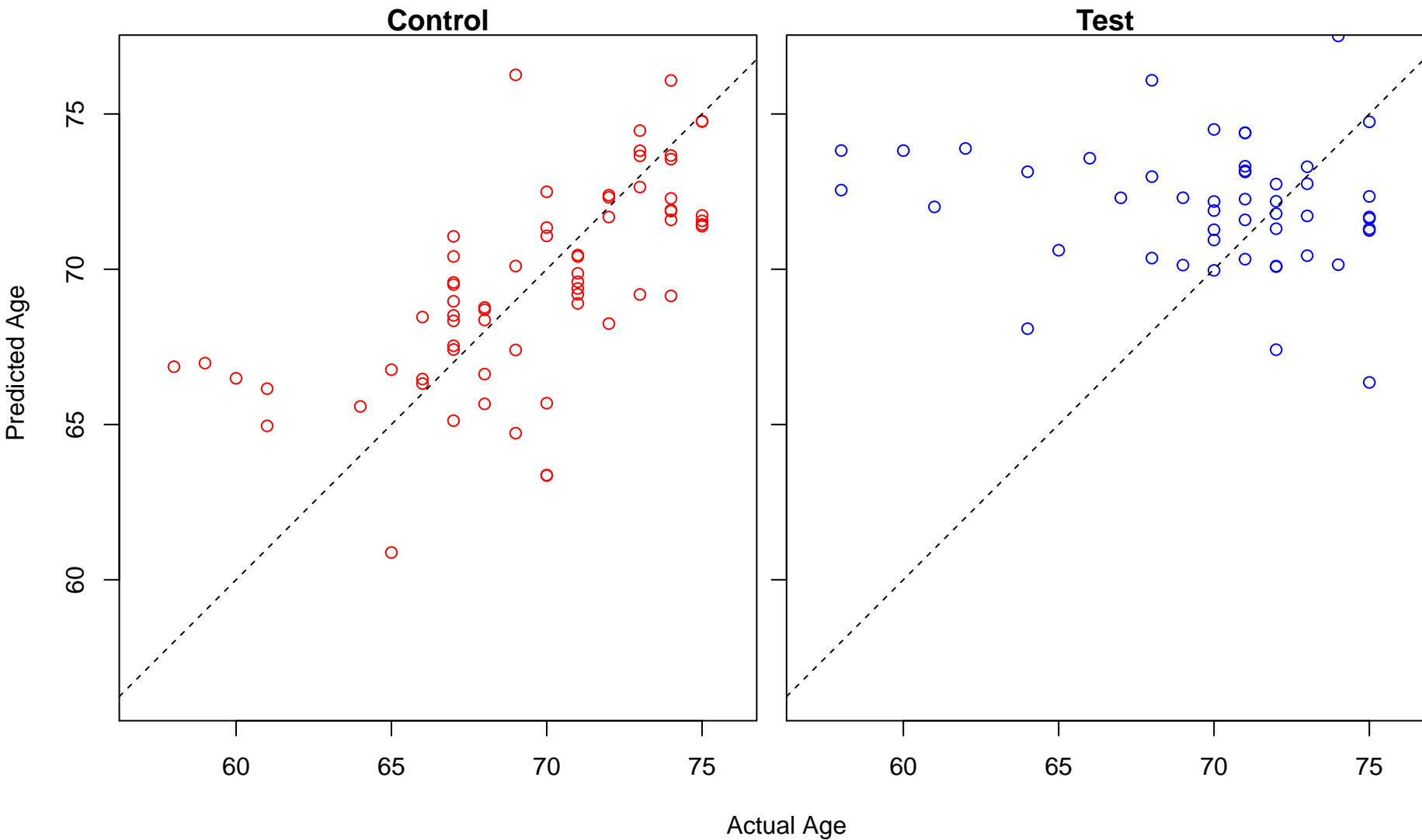
single-organism behavior (Score: 1.463406)



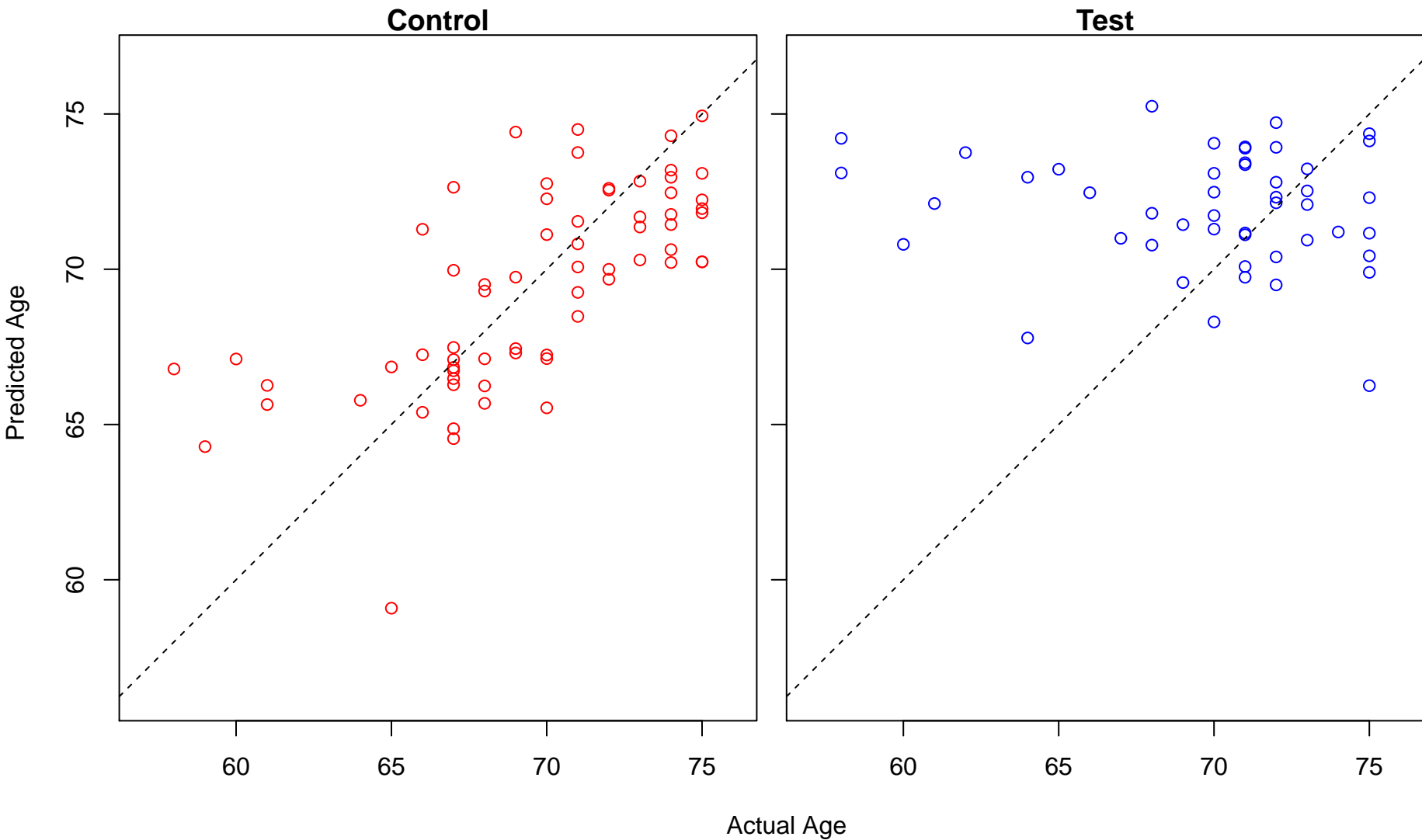
regulation of telomere capping (Score: 1.461995)



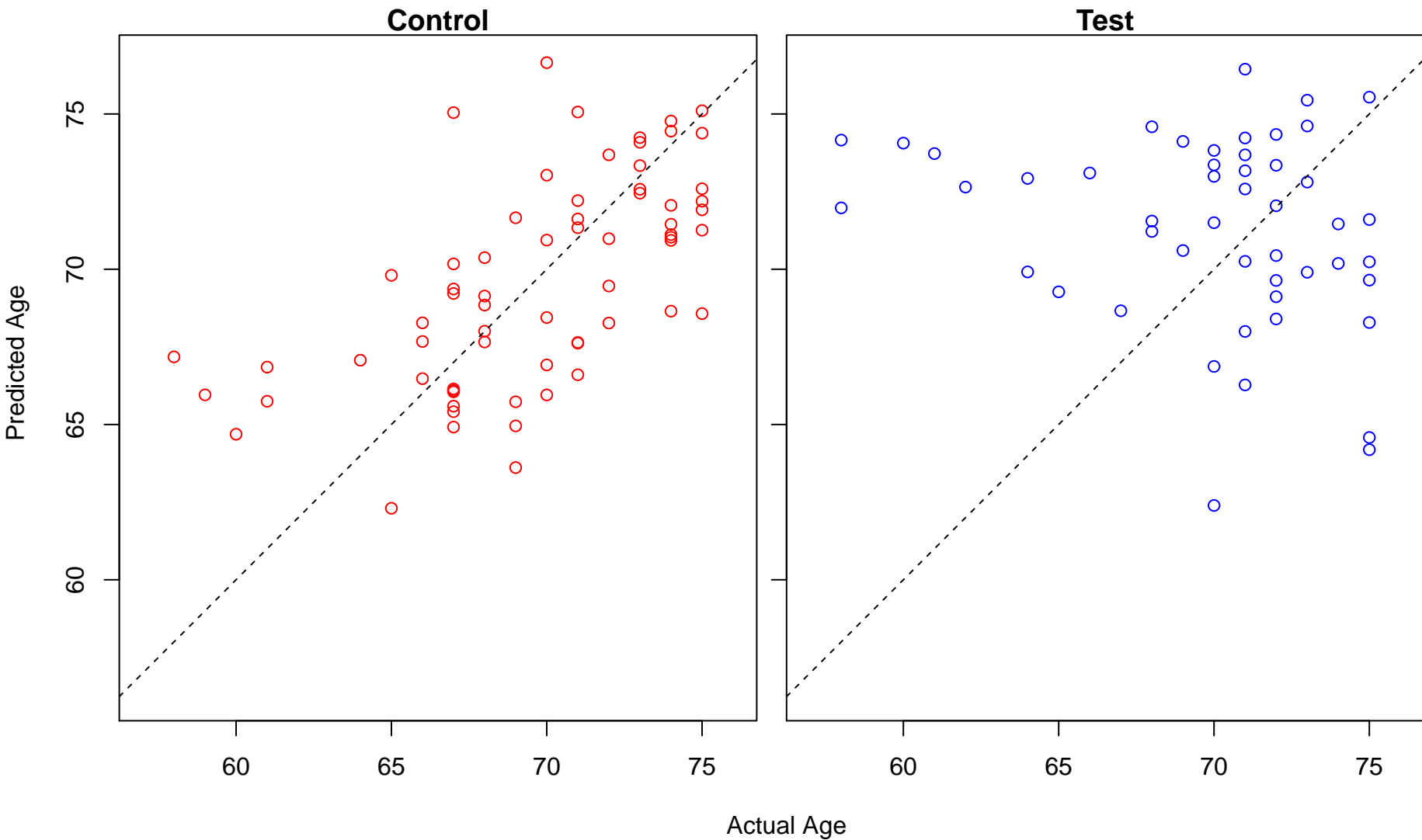
angiogenesis (Score: 1.461911)



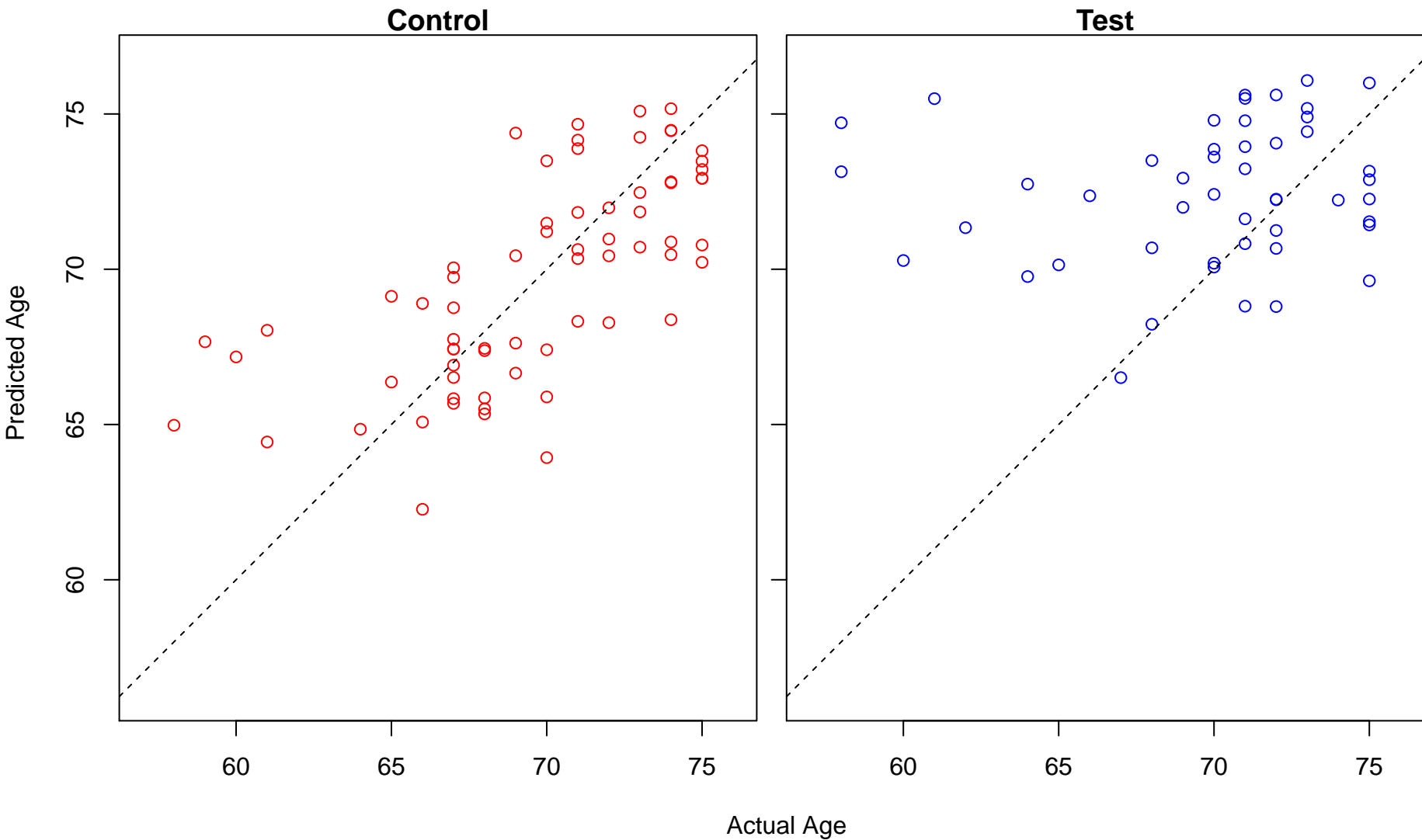
regulation of peptidyl-tyrosine phosphorylation (Score: 1.461653)



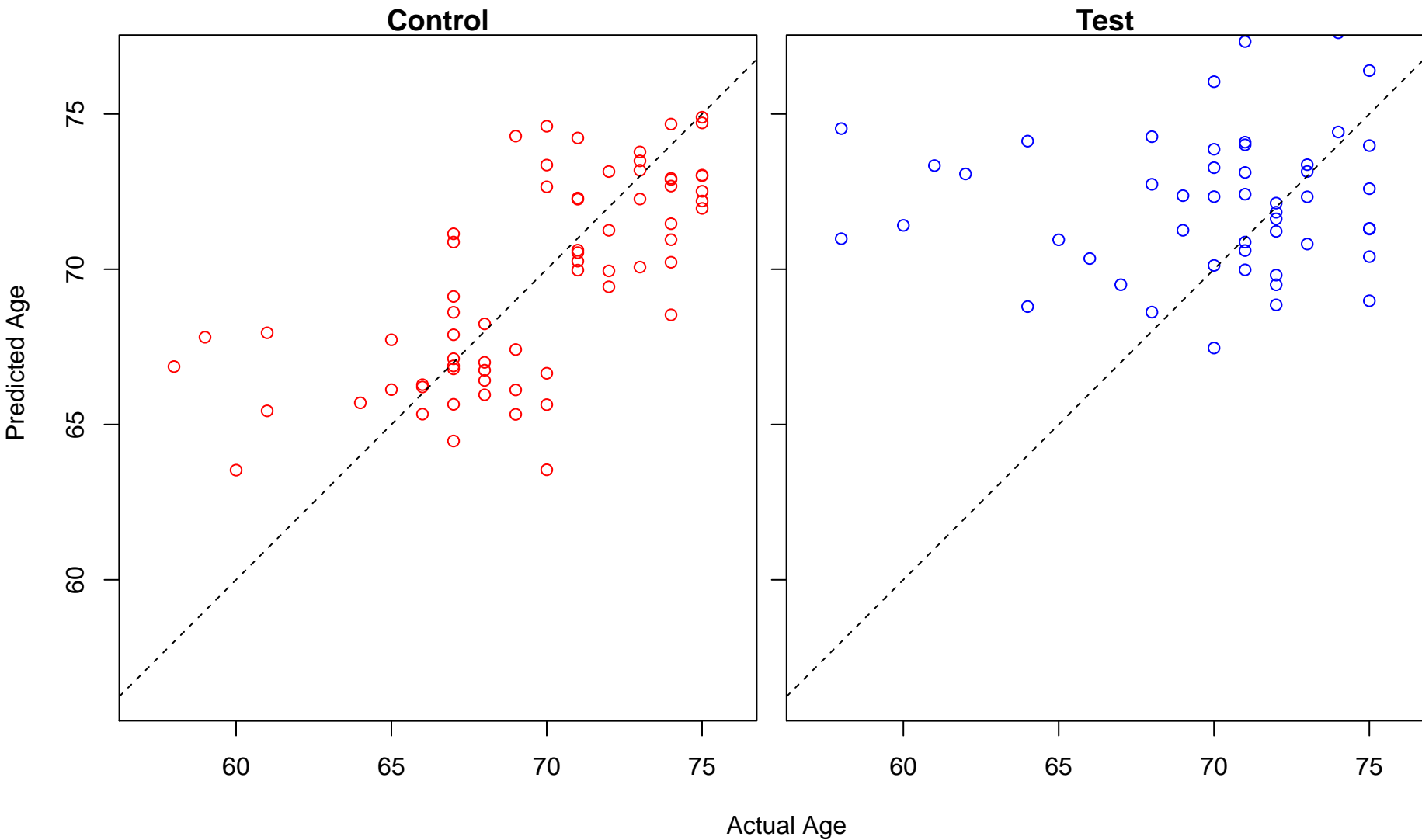
Rho protein signal transduction (Score: 1.461527)



cardiac ventricle development (Score: 1.460849)

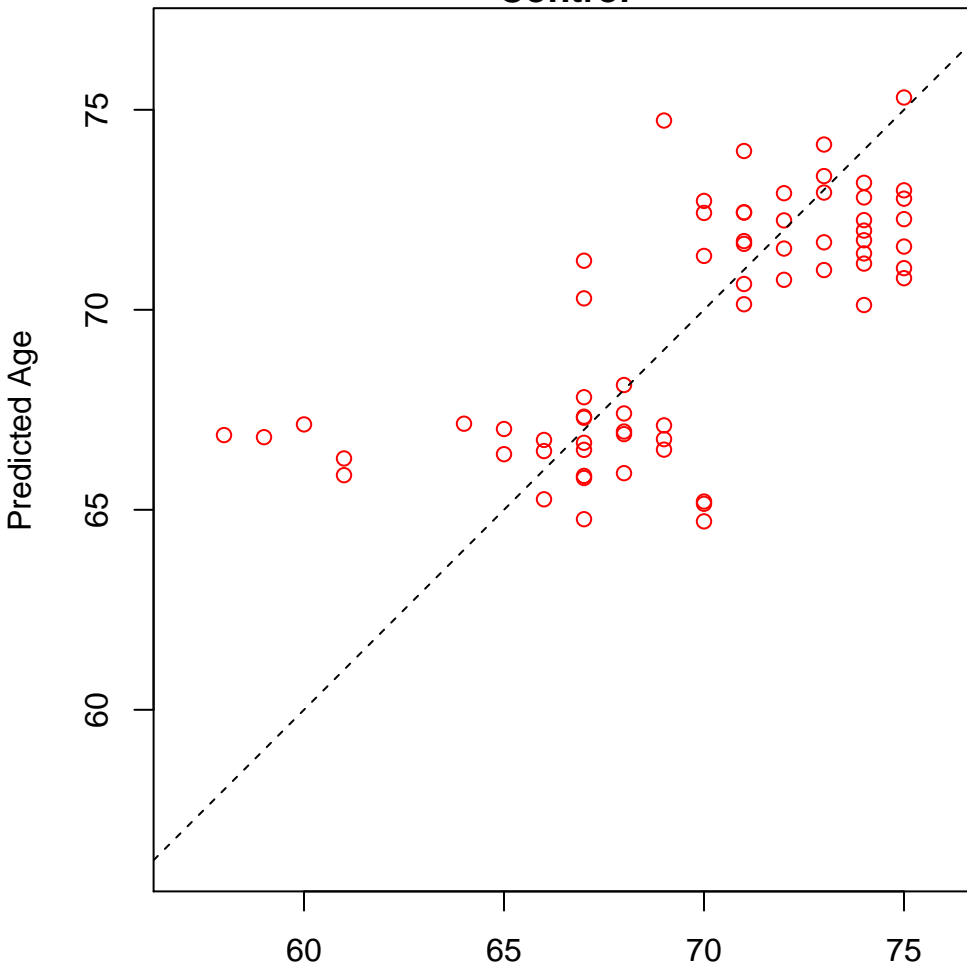


amino acid transport (Score: 1.458644)

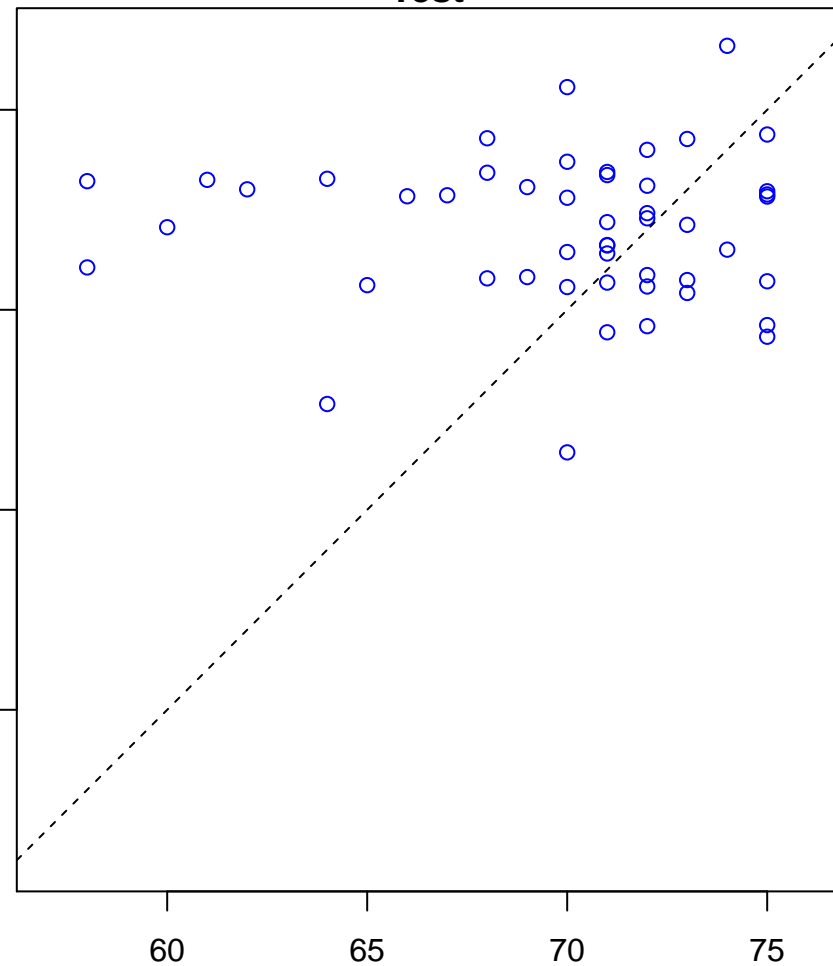


regulation of response to oxidative stress (Score: 1.458471)

Control

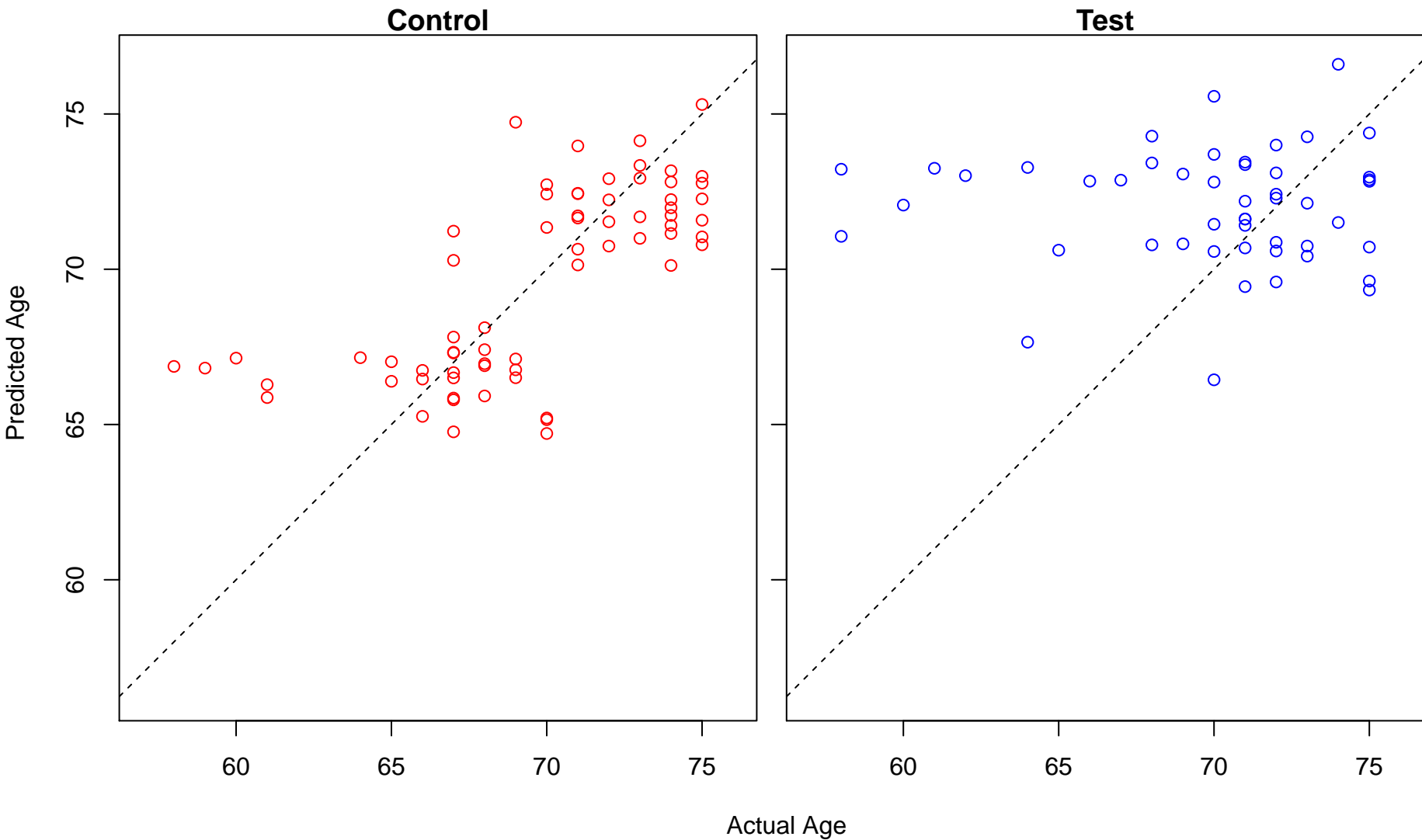


Test

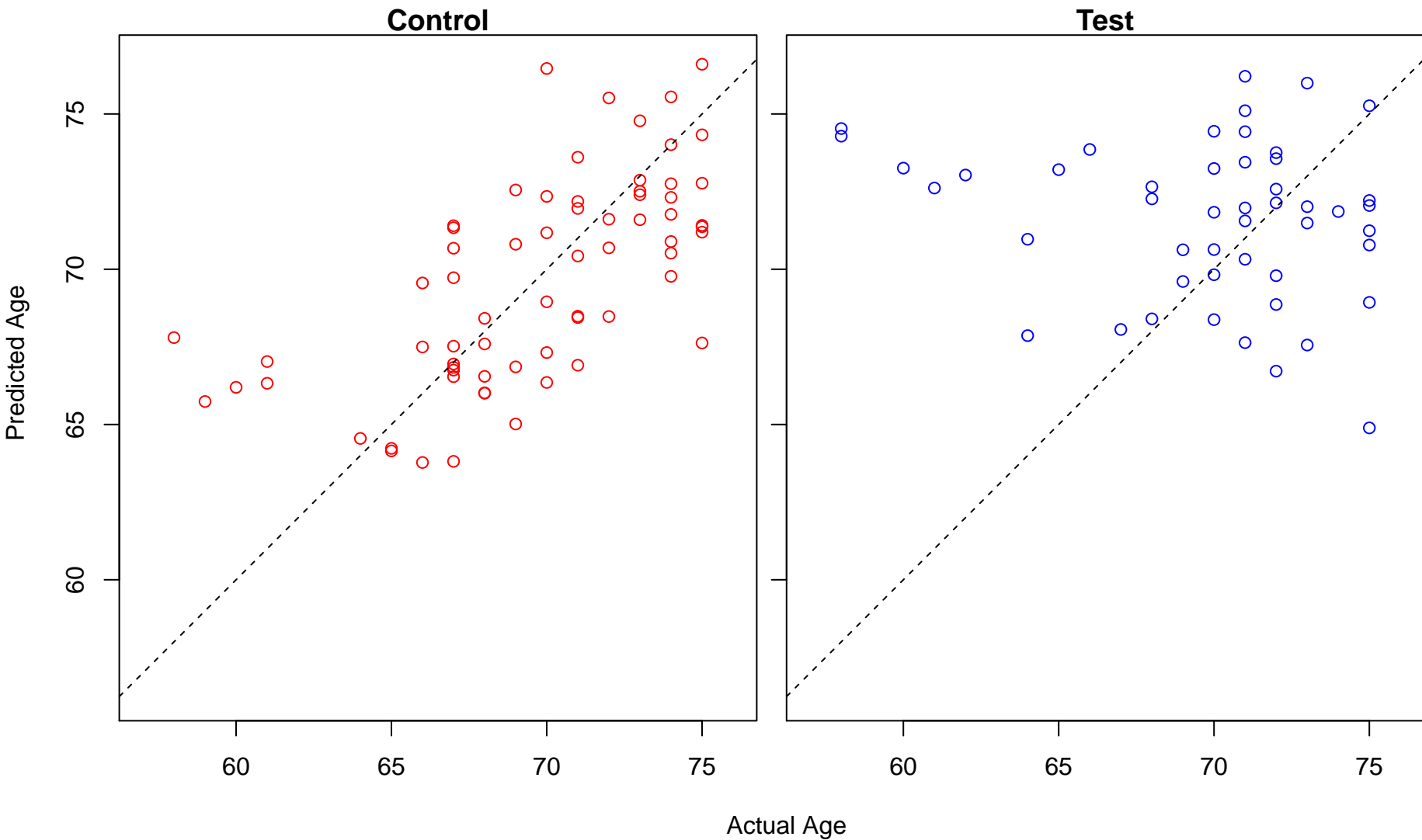


Actual Age

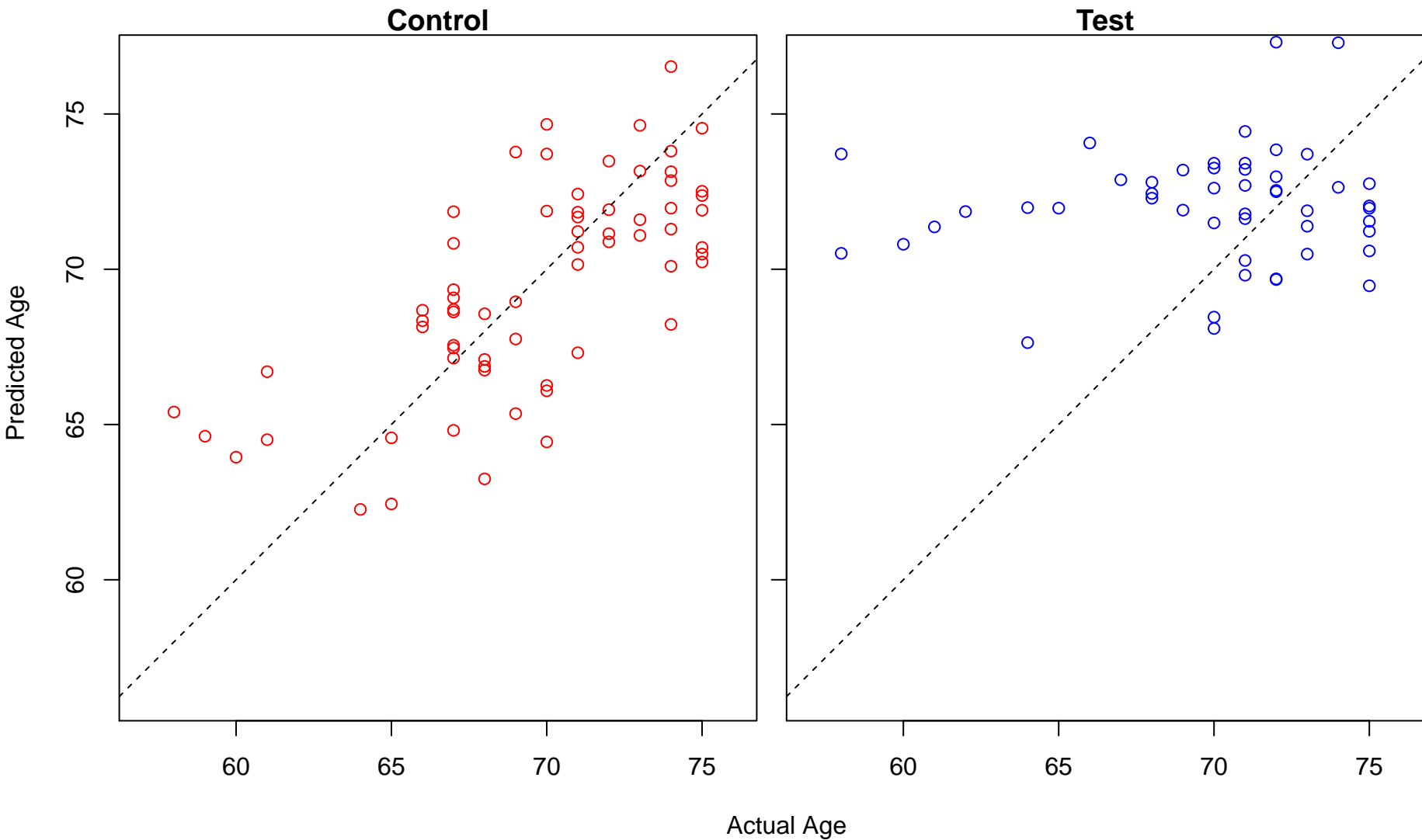
regulation of cellular response to oxidative stress (Score: 1.458194)



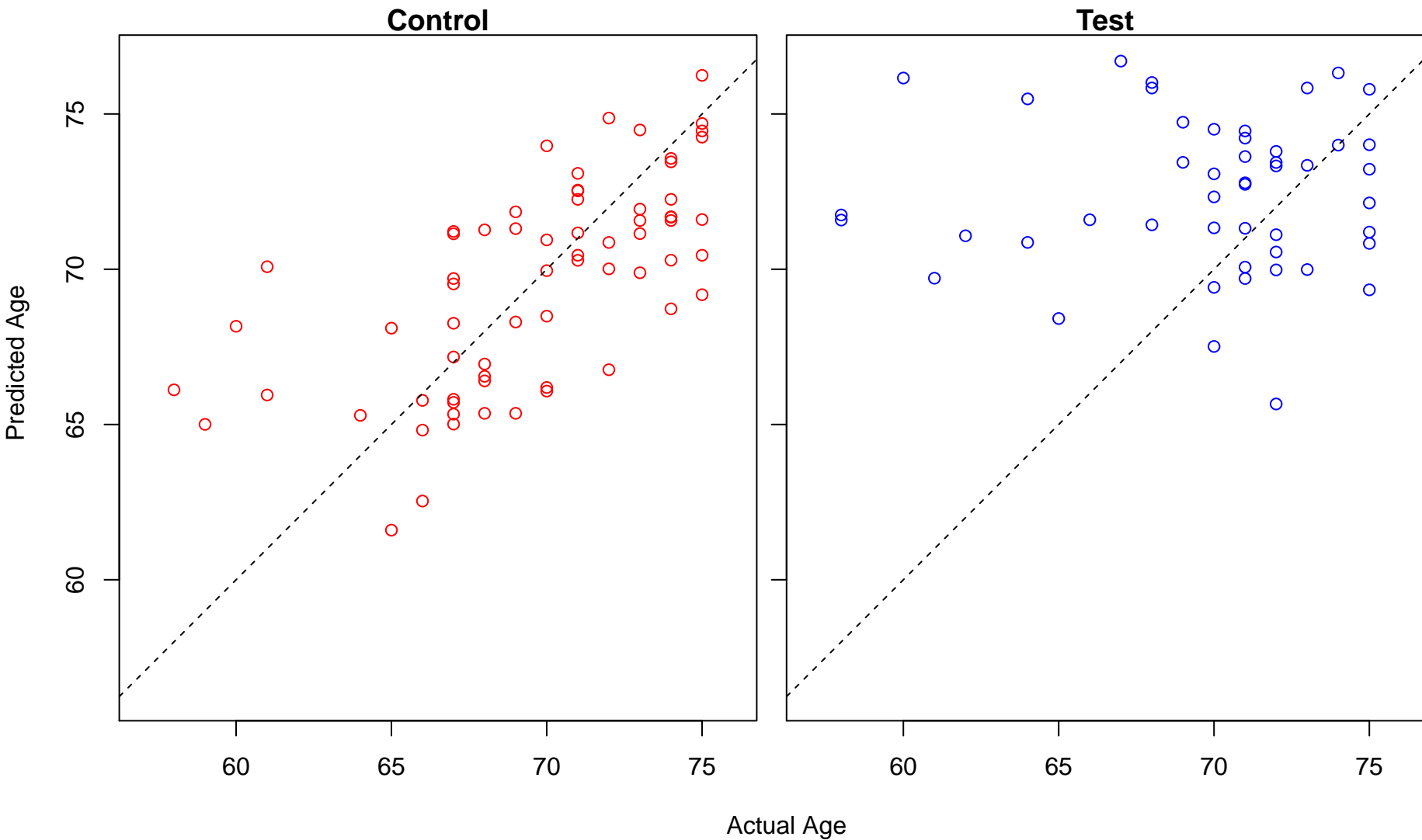
regulation of cell junction assembly (Score: 1.457847)



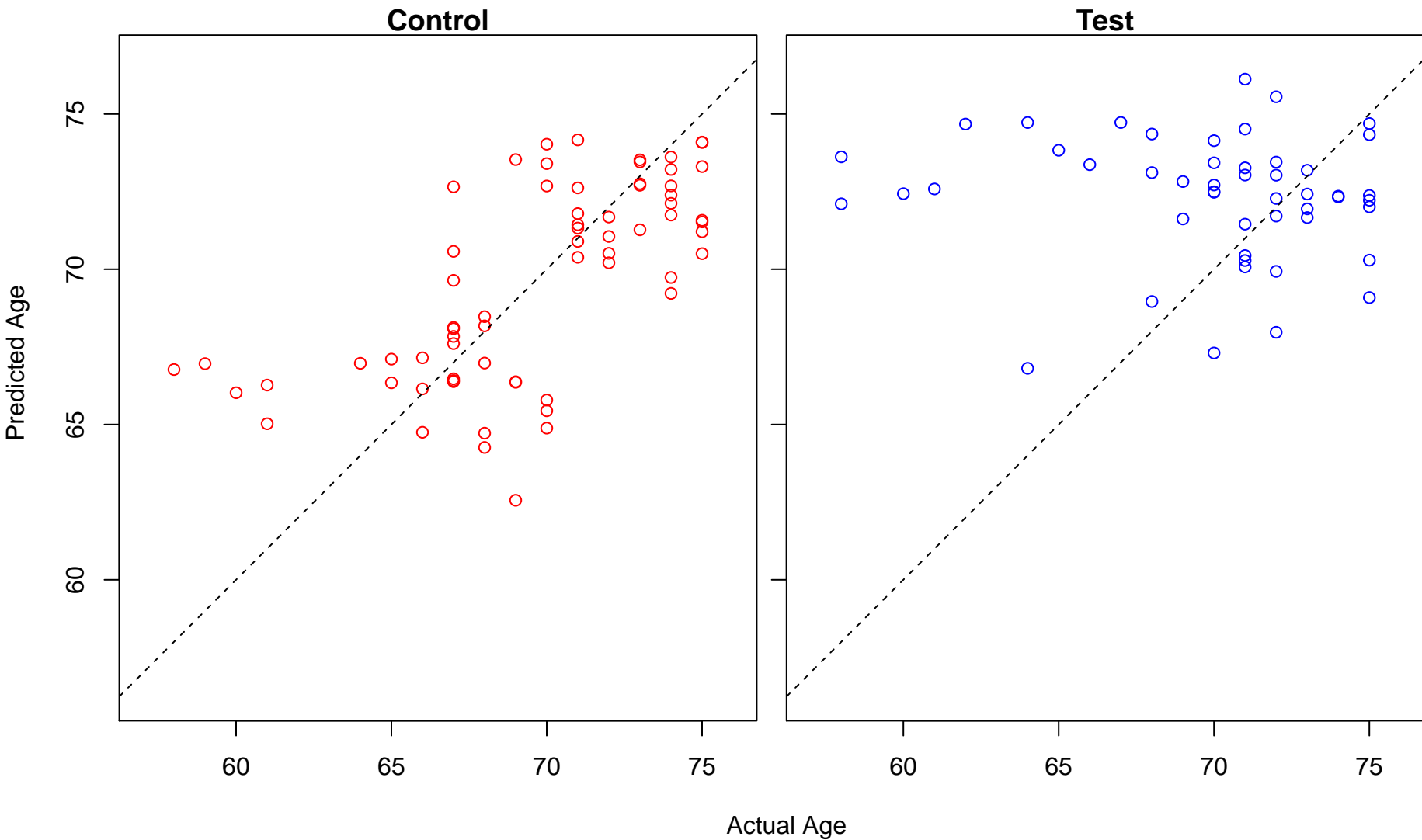
calcium ion transport (Score: 1.456851)



response to fluid shear stress (Score: 1.455631)

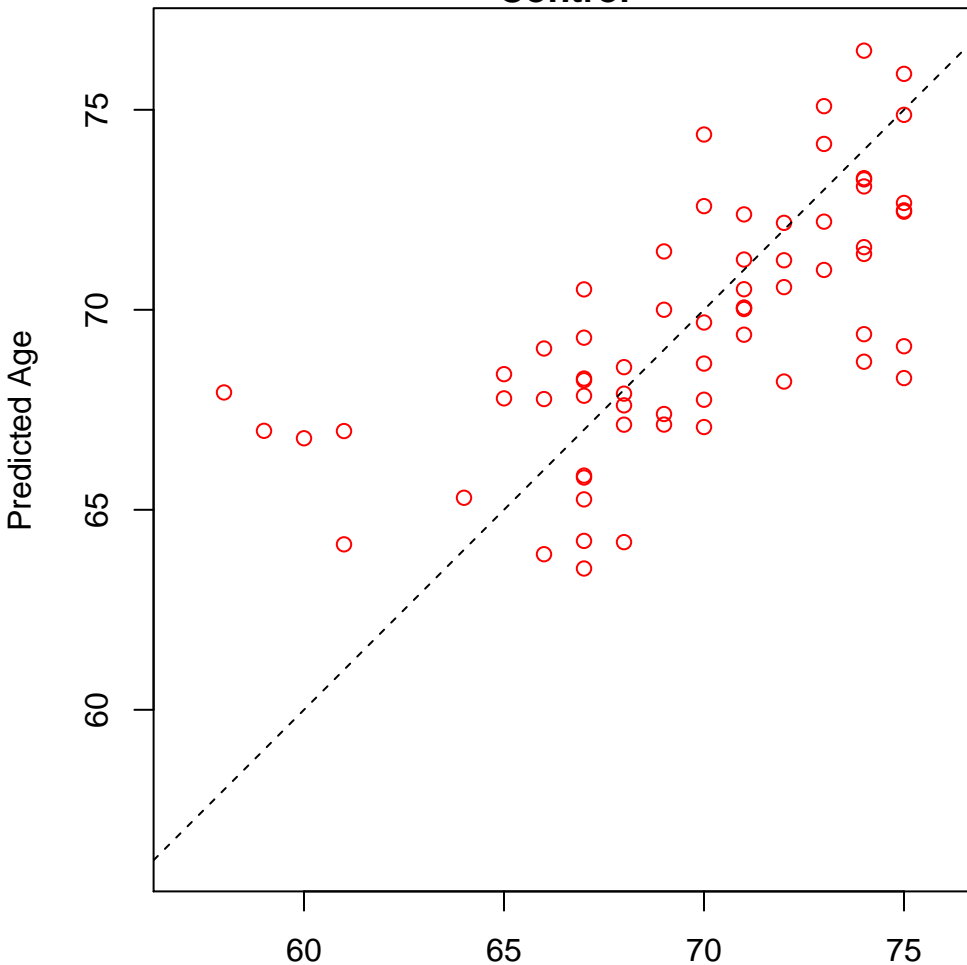


regulation of histone modification (Score: 1.455501)

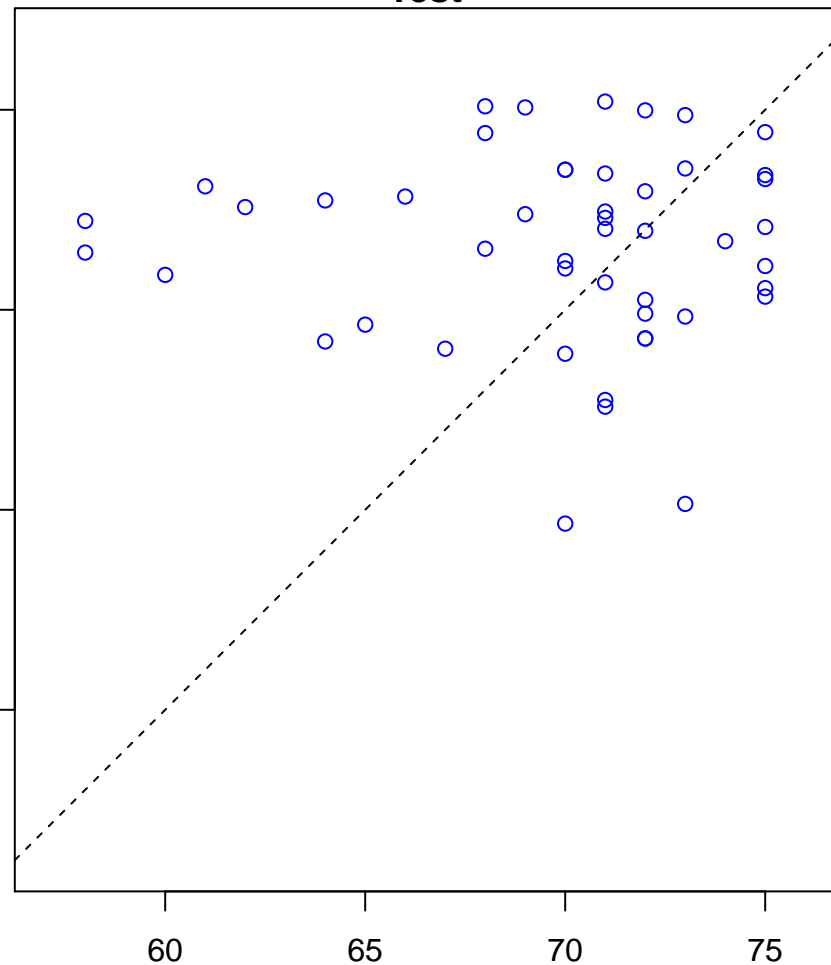


phosphatidic acid biosynthetic process (Score: 1.455081)

Control



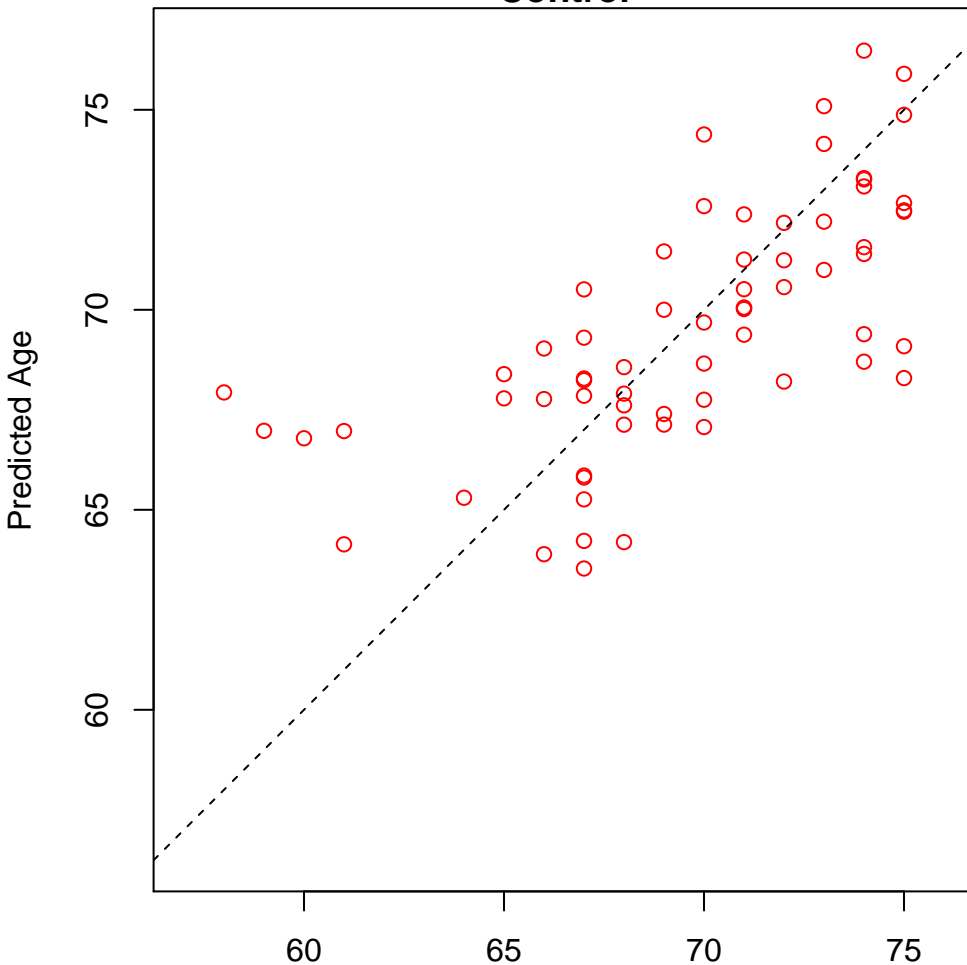
Test



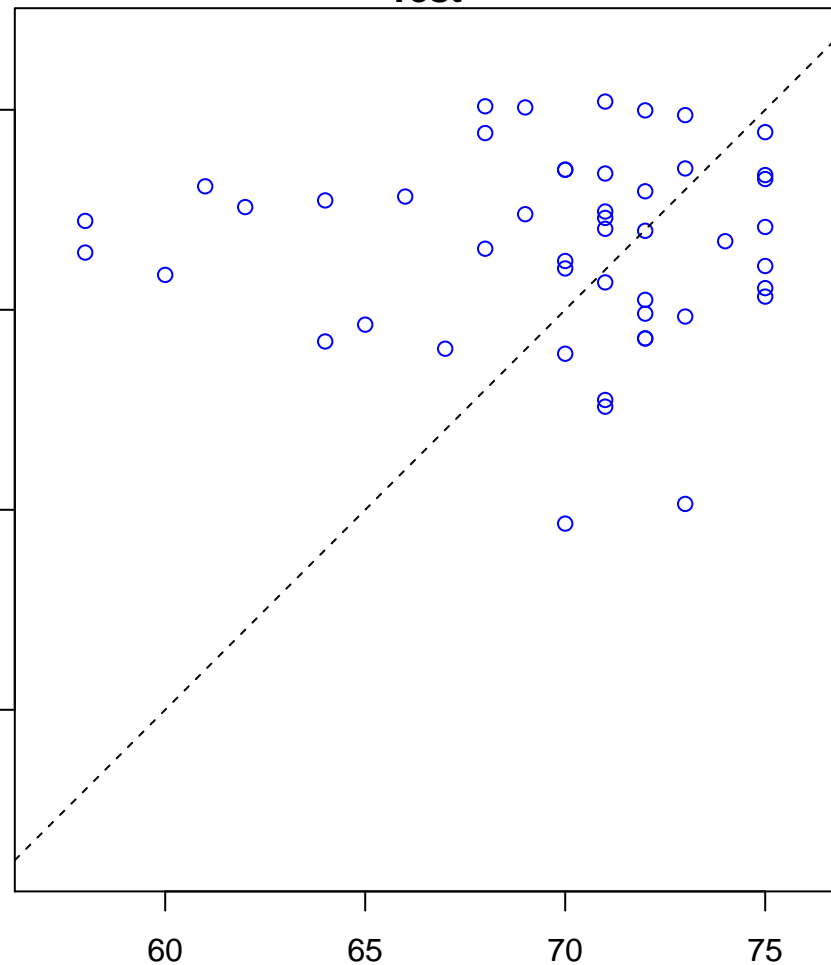
Actual Age

phosphatidic acid metabolic process (Score: 1.455081)

Control

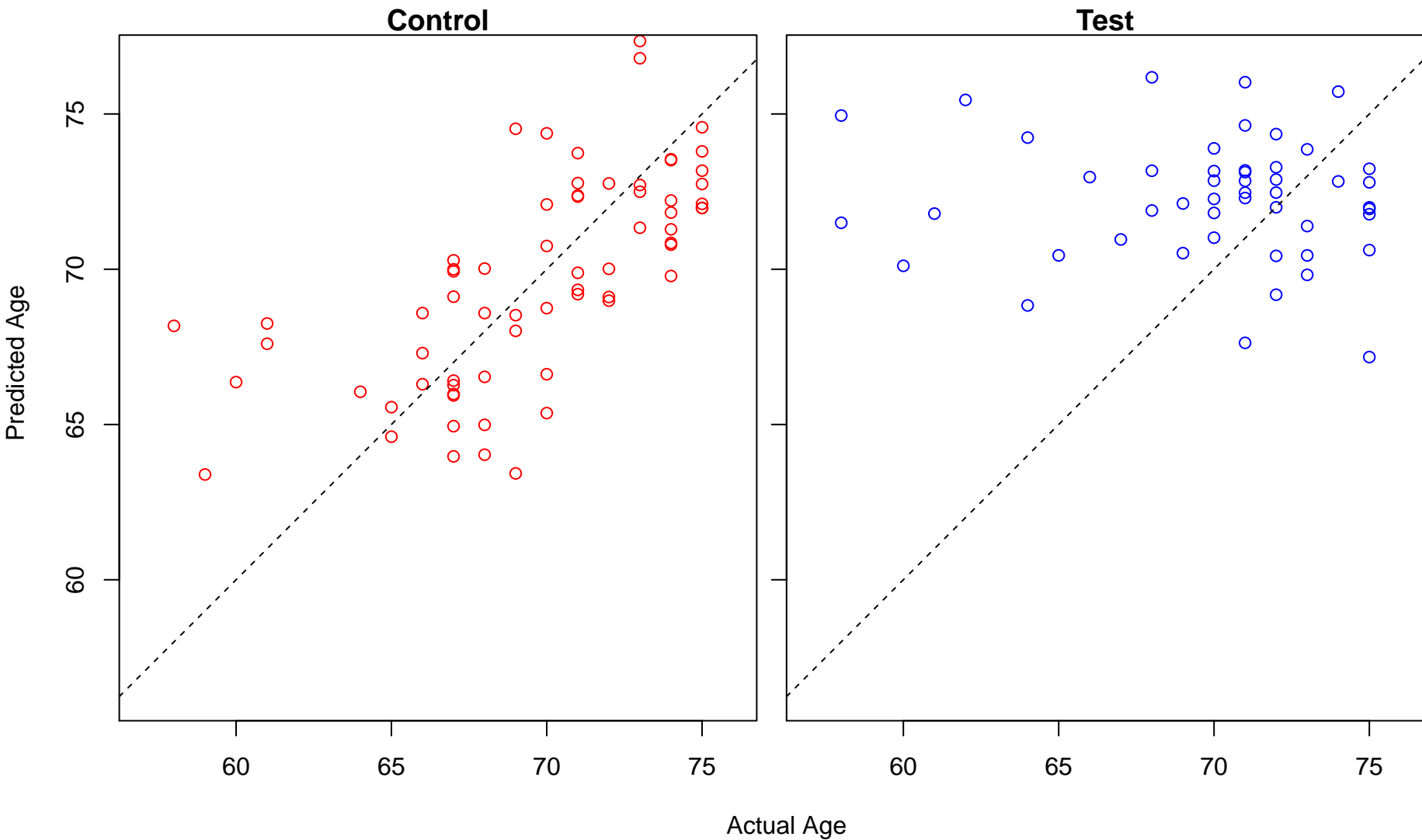


Test

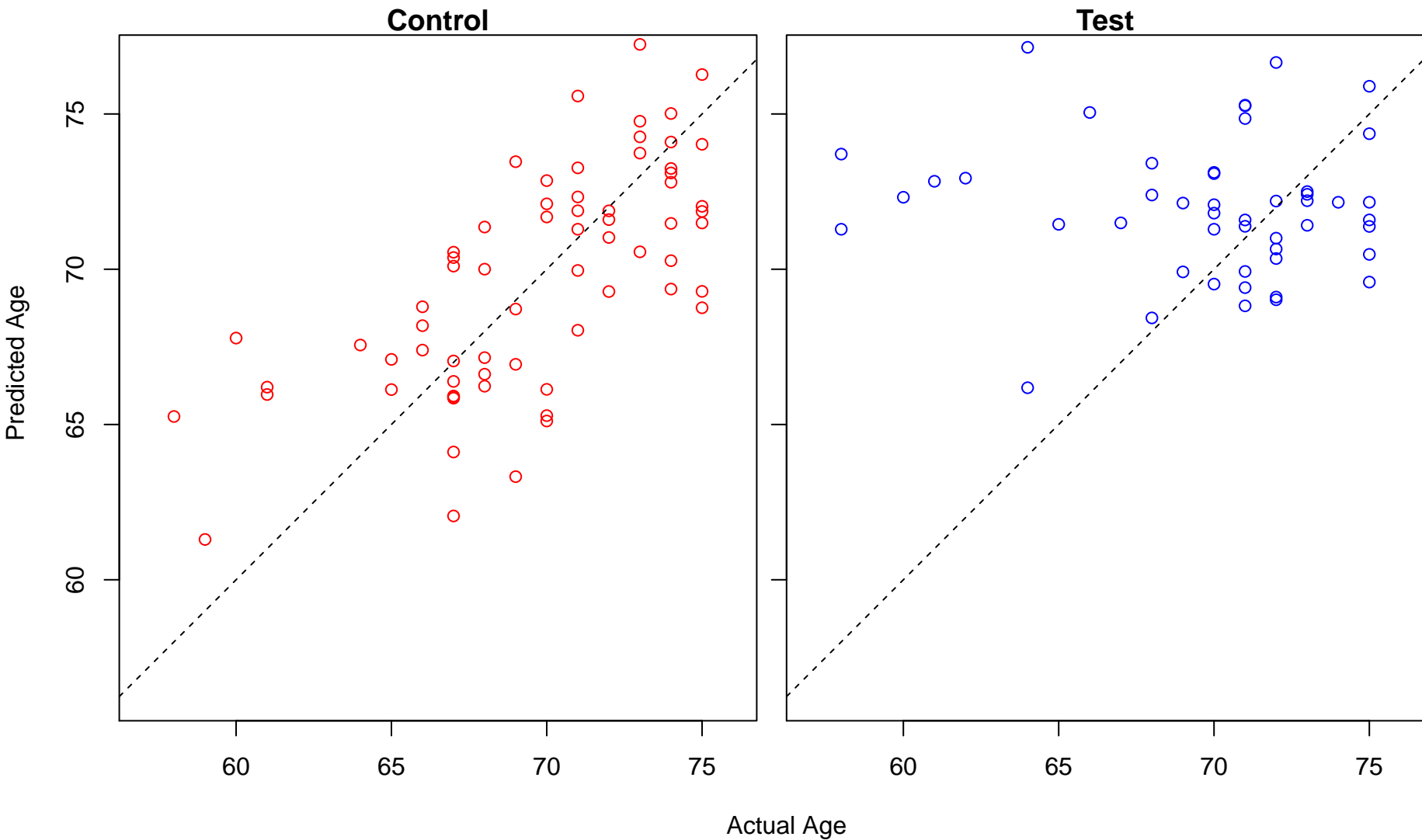


Actual Age

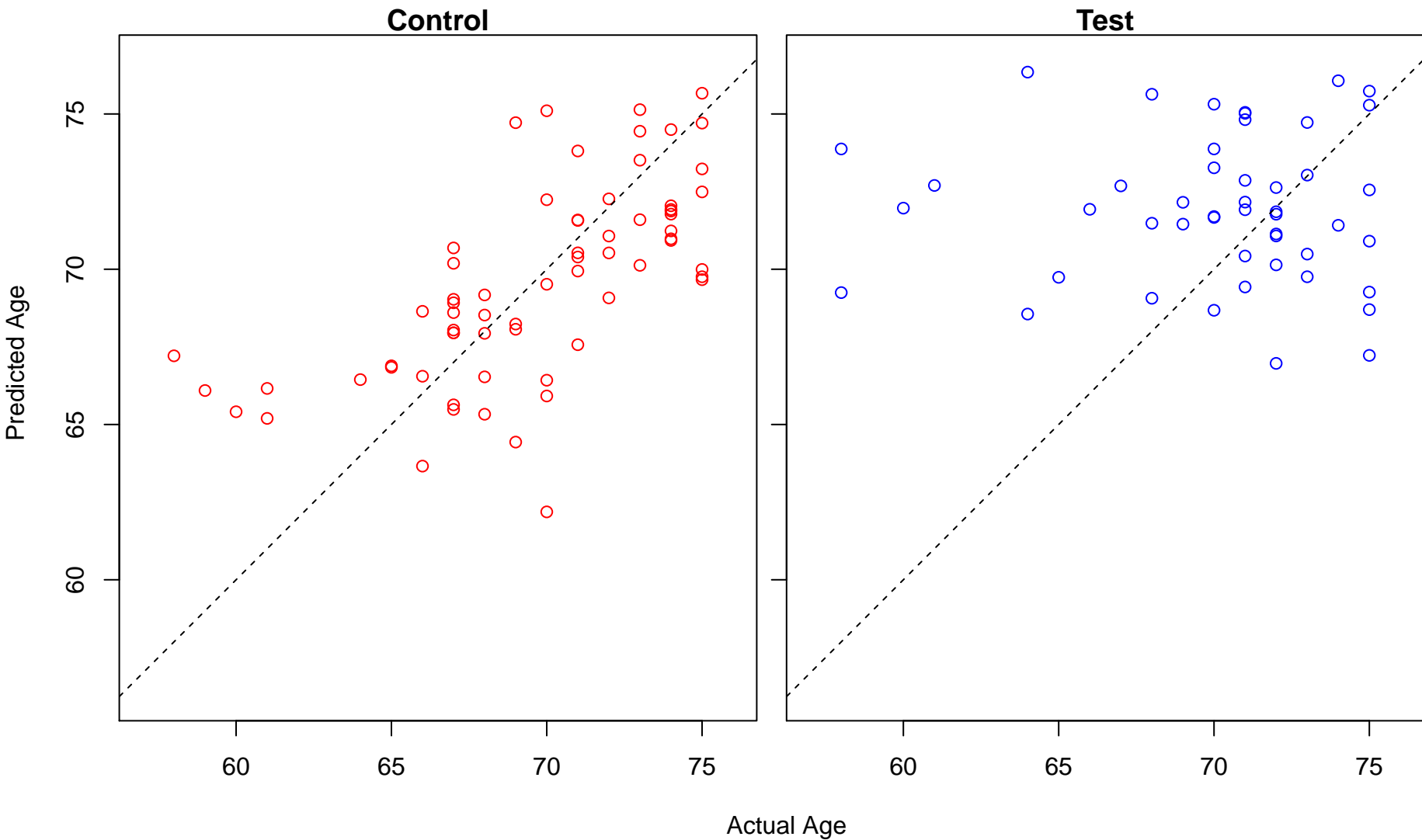
response to estrogen (Score: 1.454645)



purine-containing compound catabolic process (Score: 1.454568)

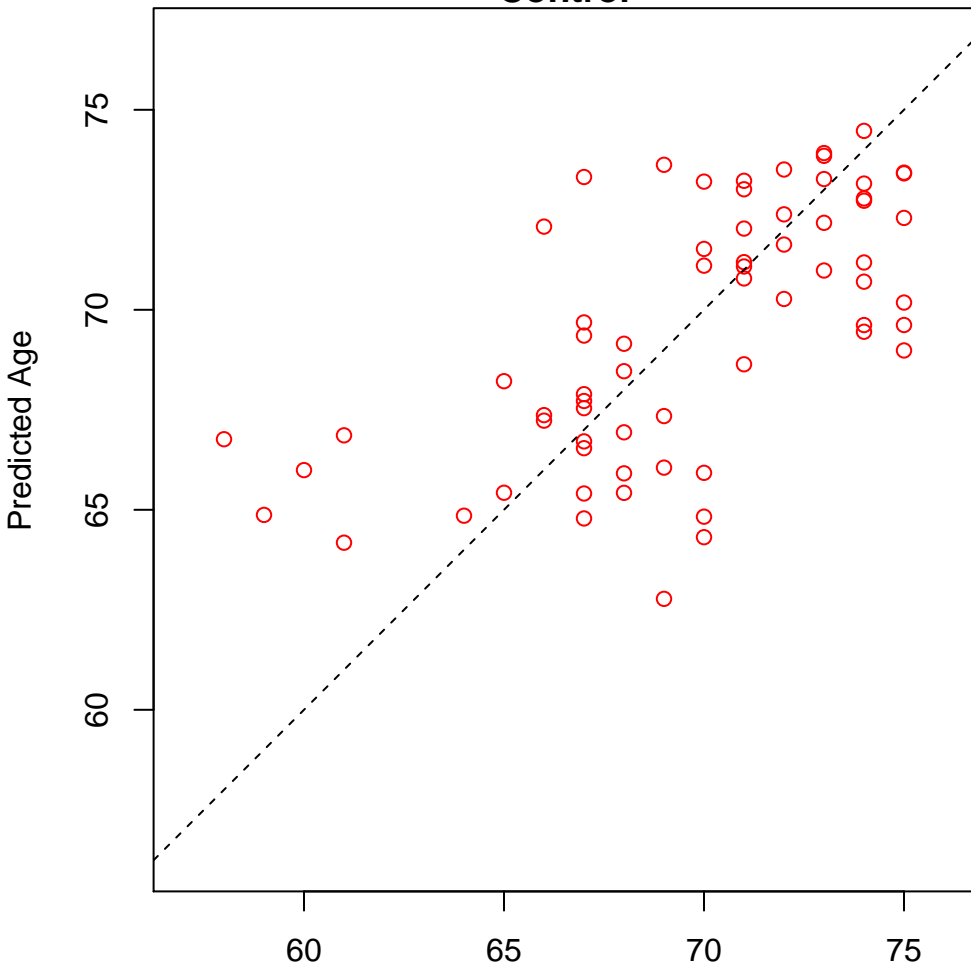


protein neddylation (Score: 1.454563)

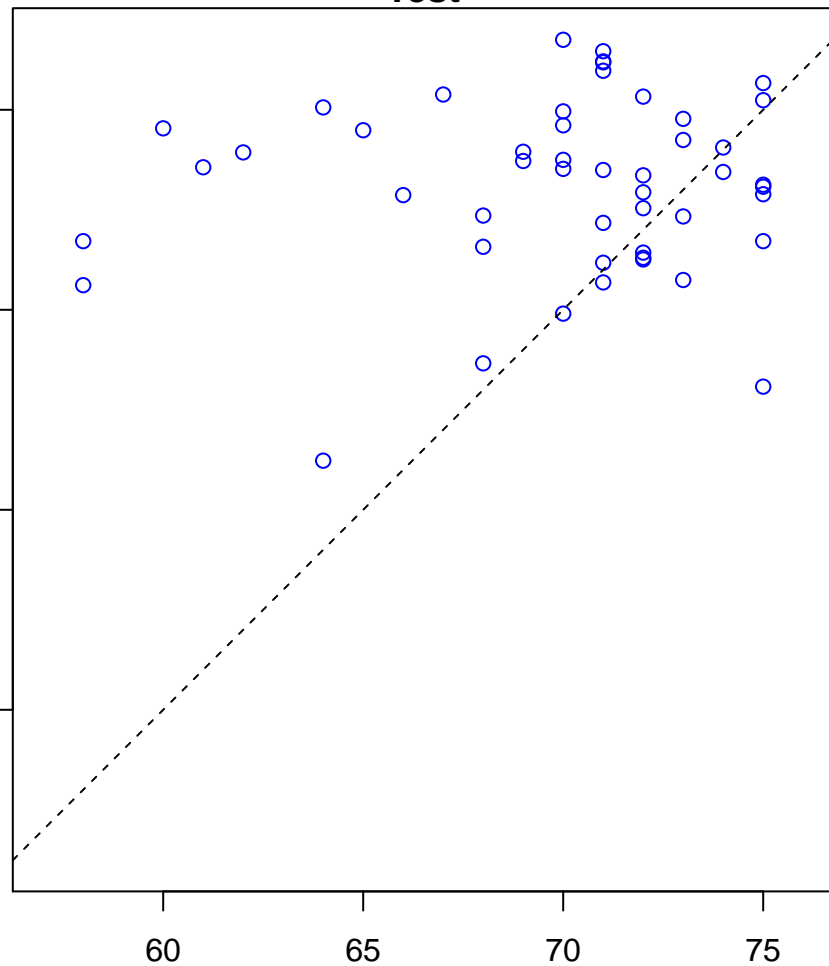


cellular carbohydrate metabolic process (Score: 1.454326)

Control

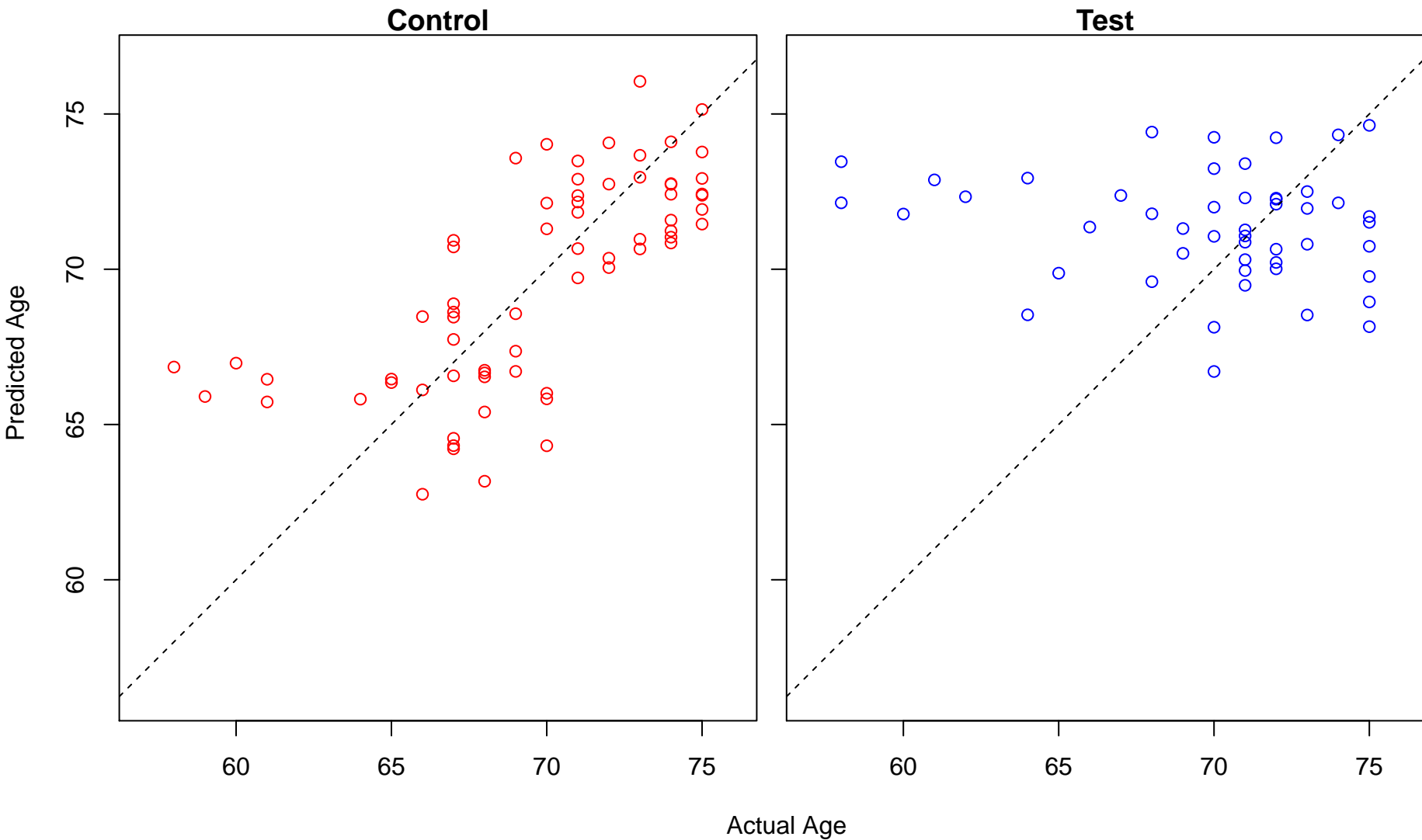


Test

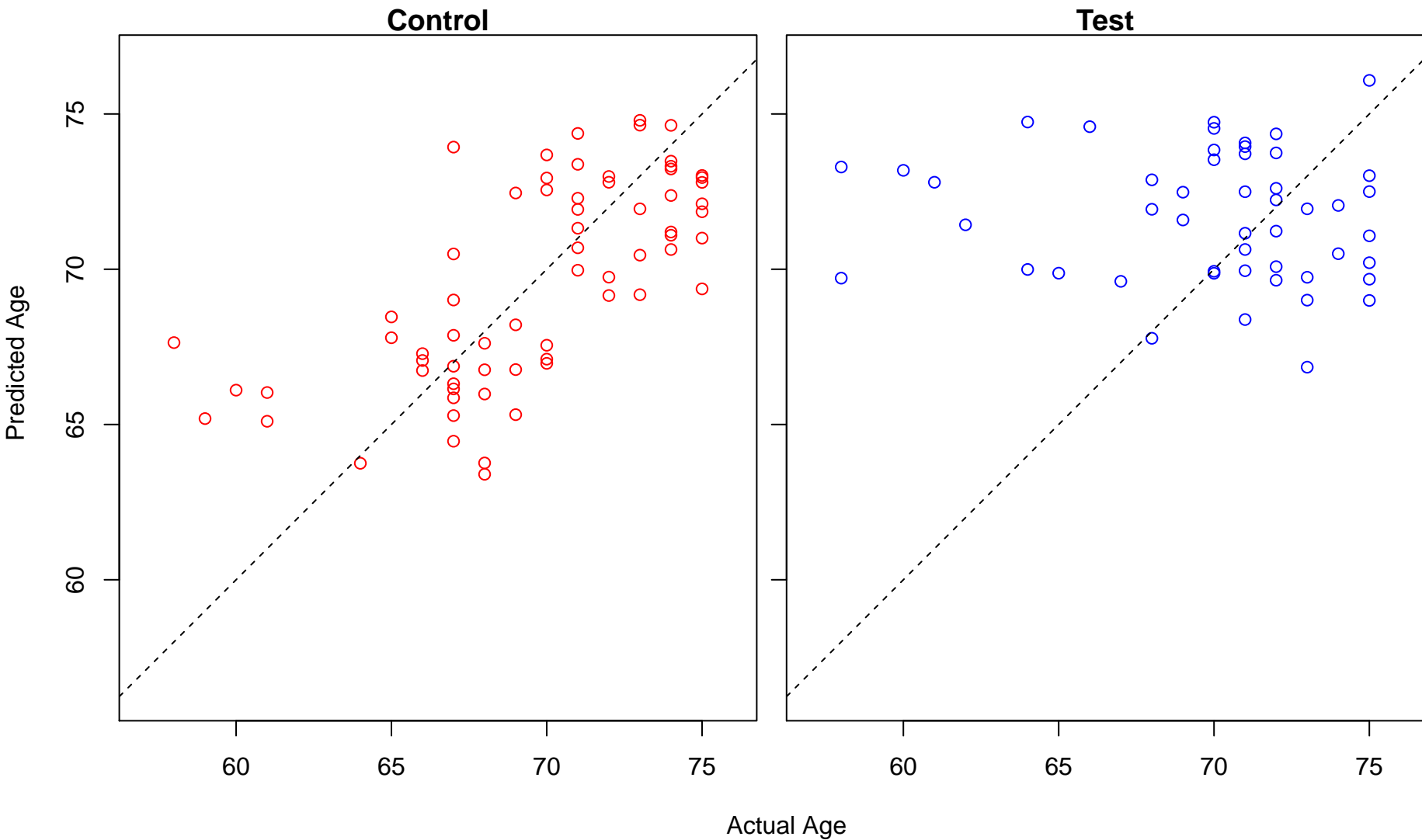


Actual Age

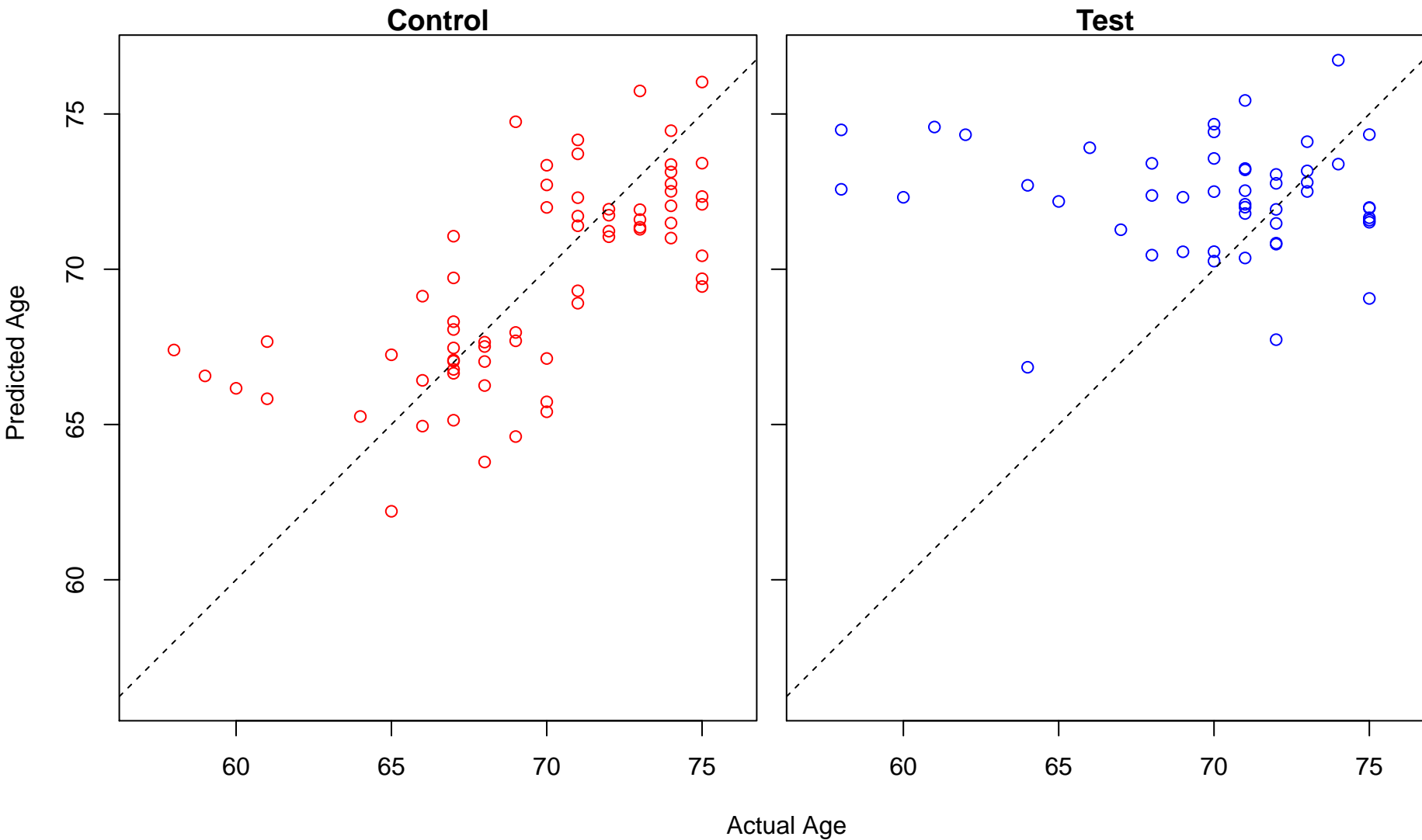
positive regulation of intrinsic apoptotic signaling pathway (Score: 1.454217)



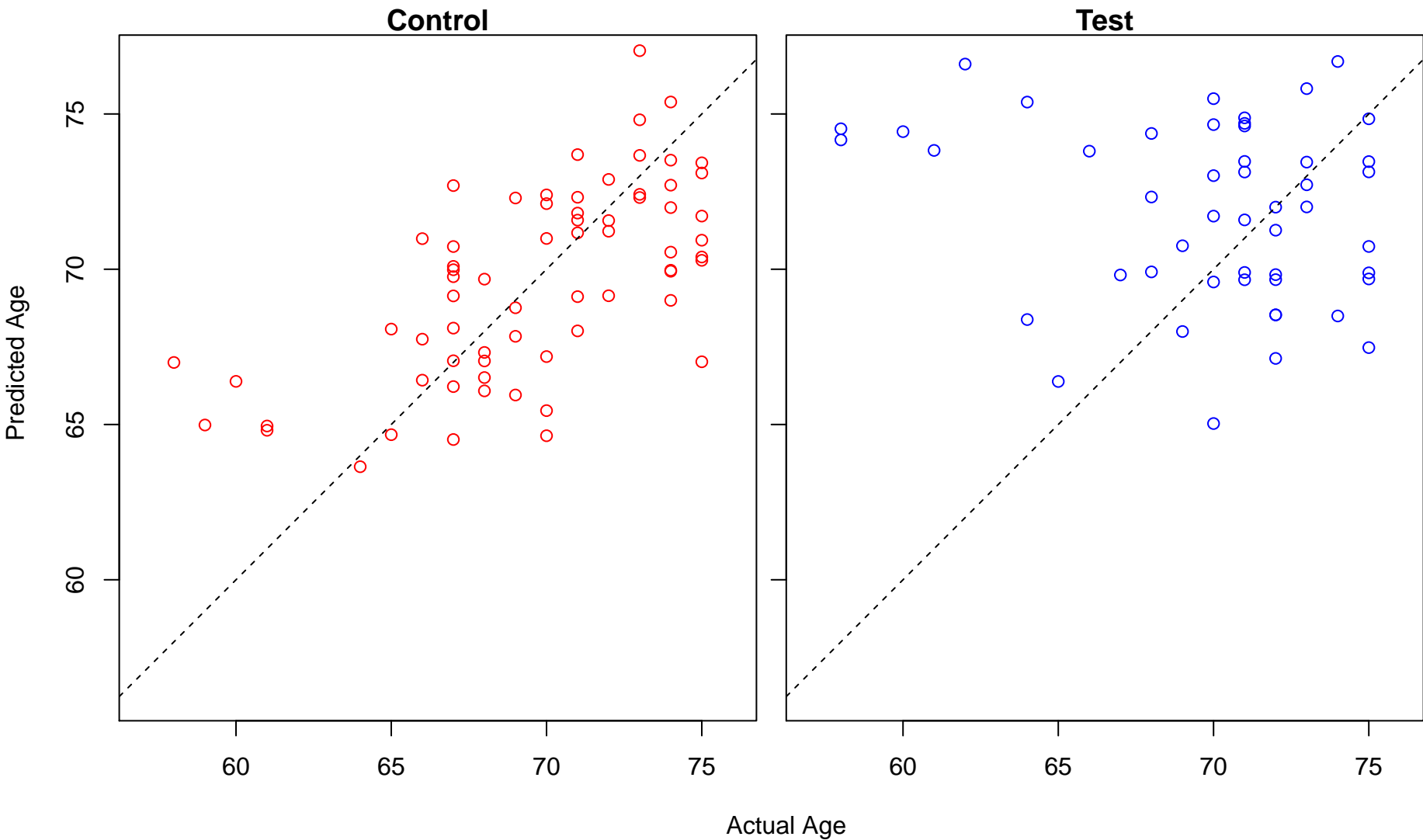
negative regulation of epithelial cell proliferation (Score: 1.452741)



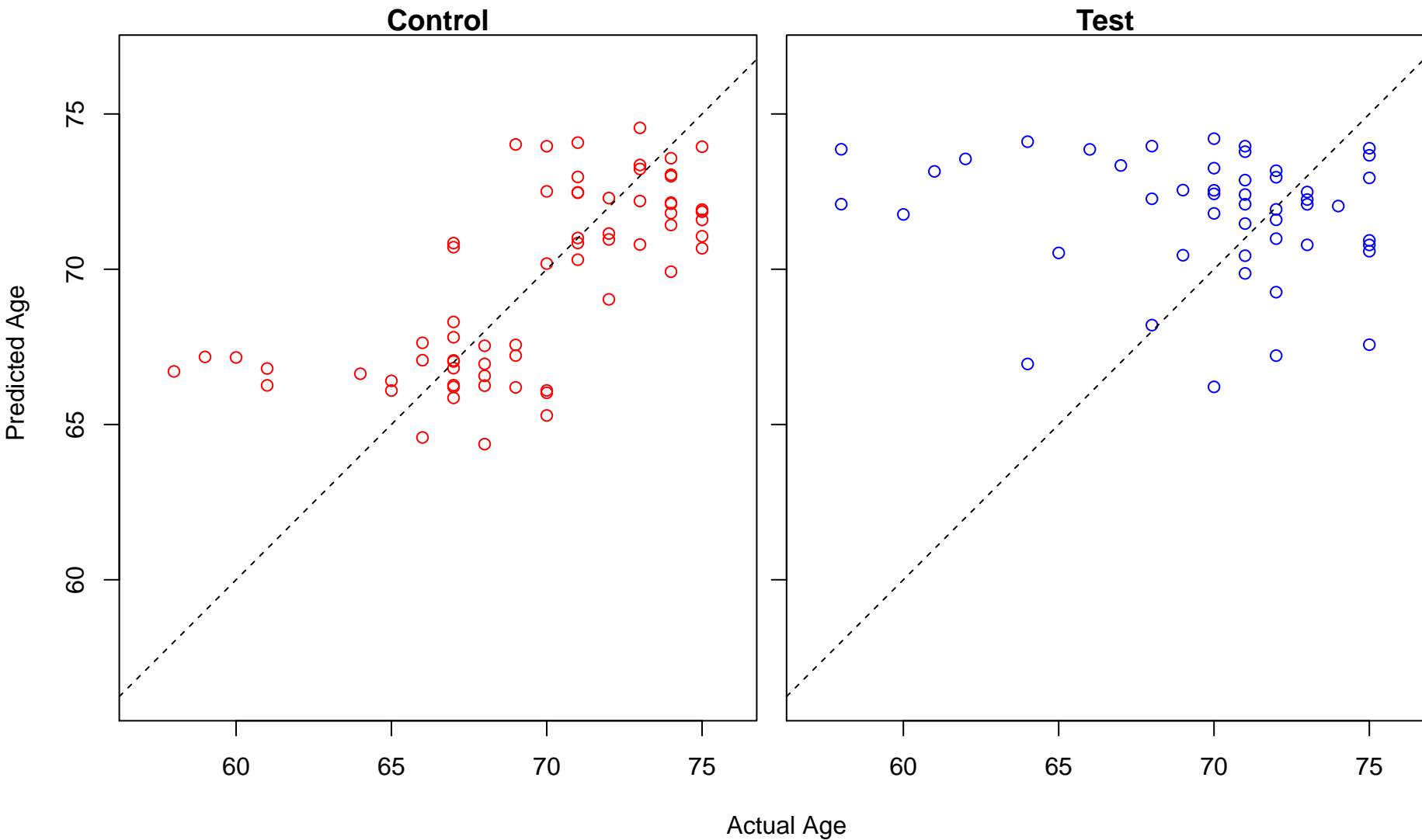
neurological system process (Score: 1.452497)



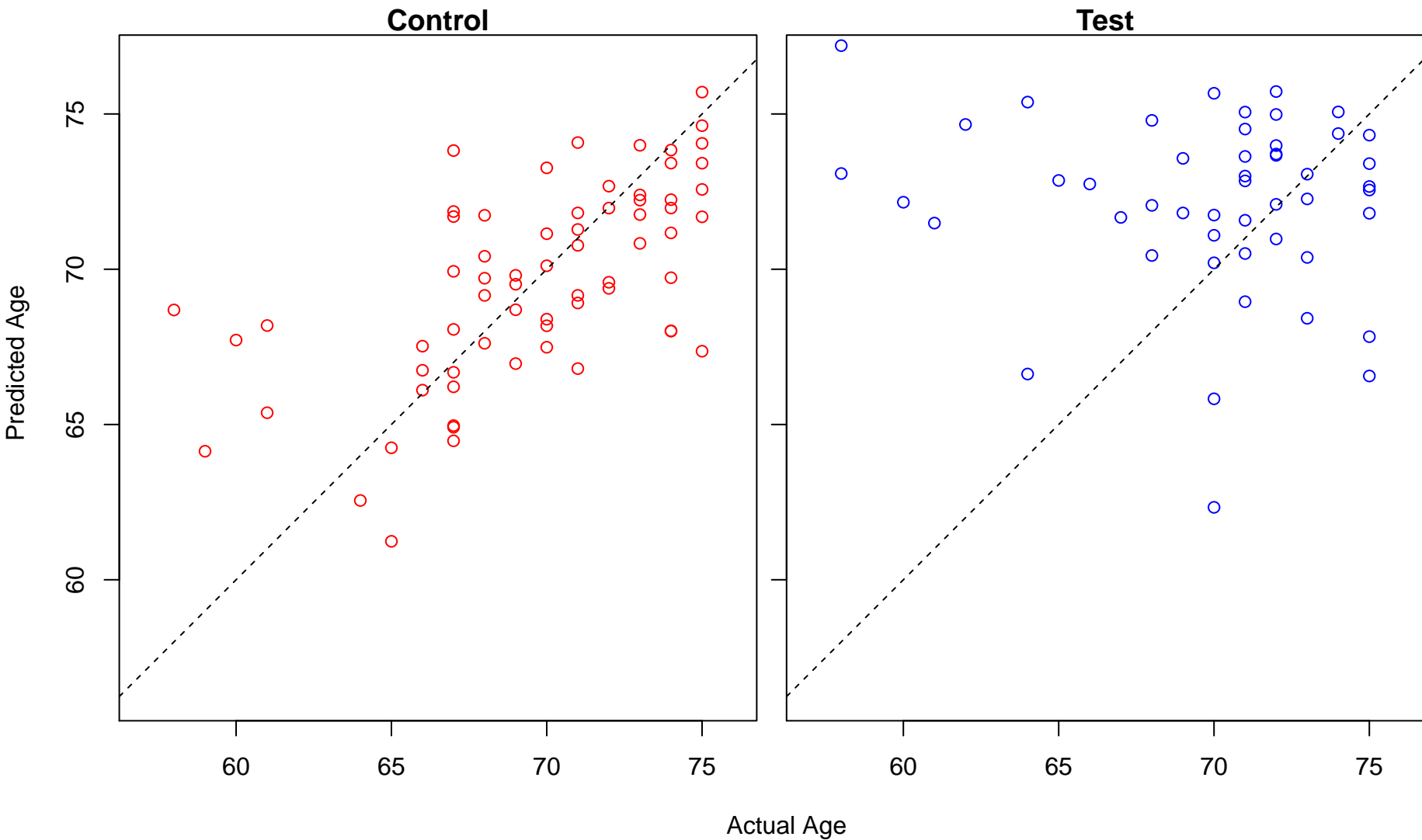
mast cell activation (Score: 1.452193)



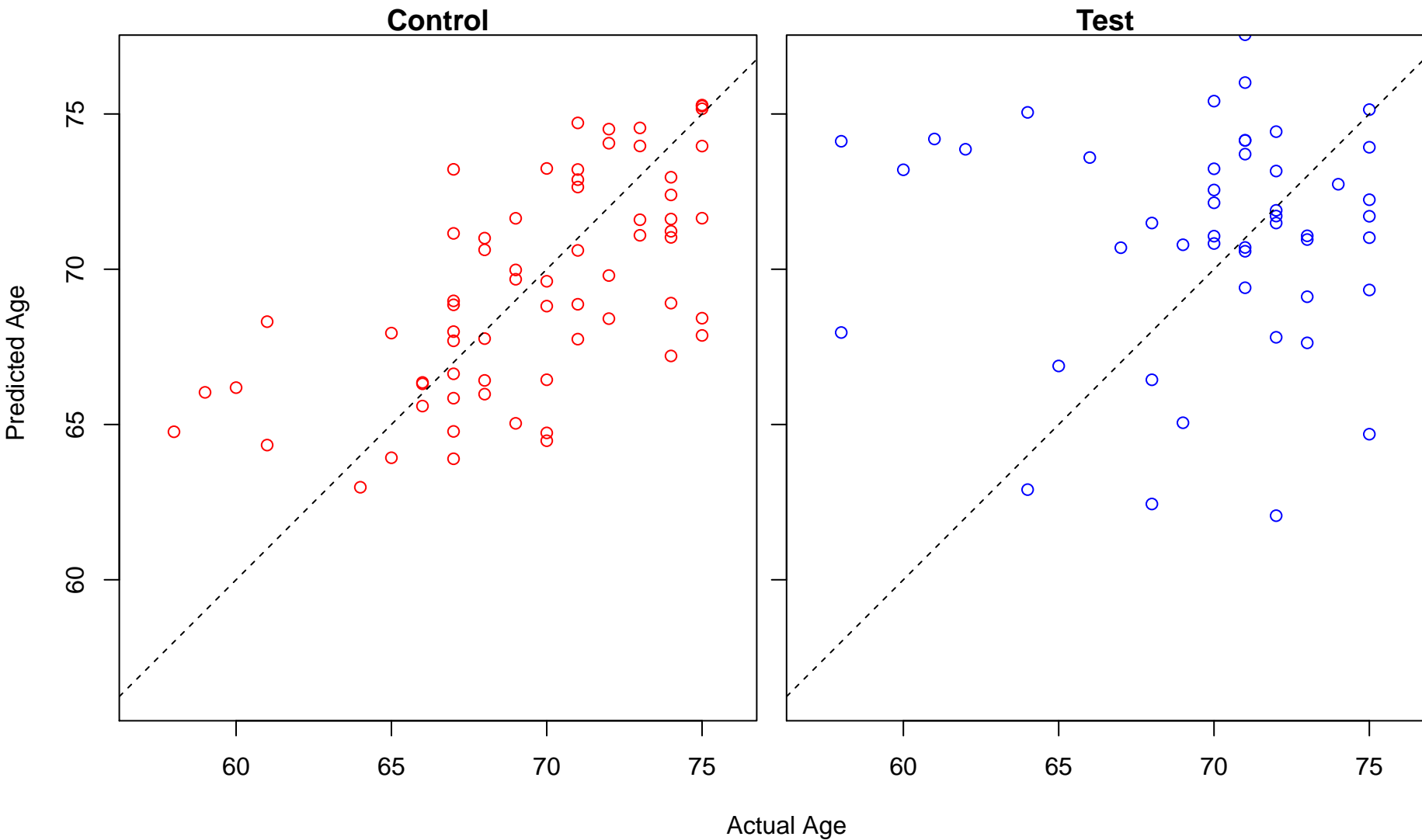
regulation of behavior (Score: 1.452162)



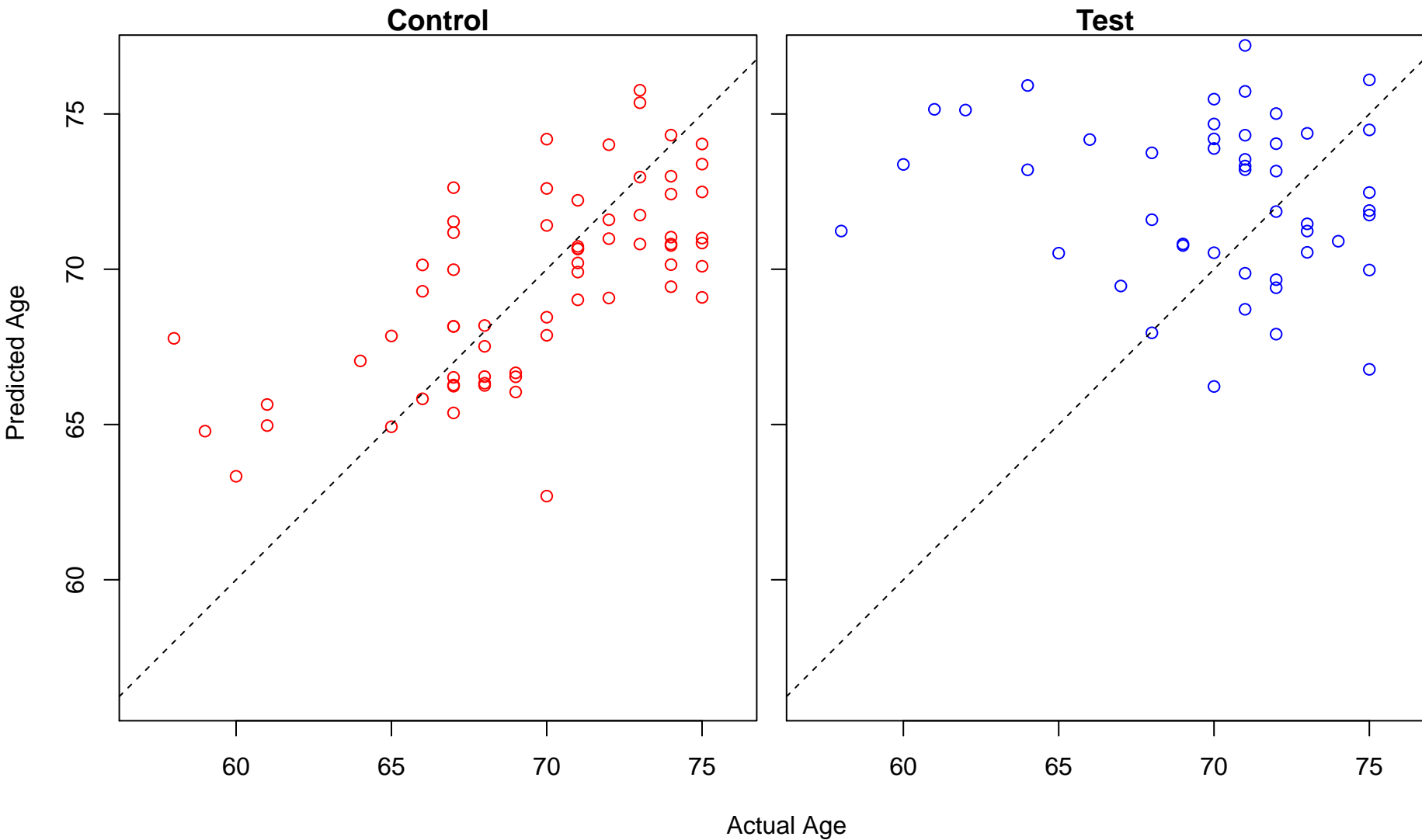
regulation of endothelial cell differentiation (Score: 1.451908)



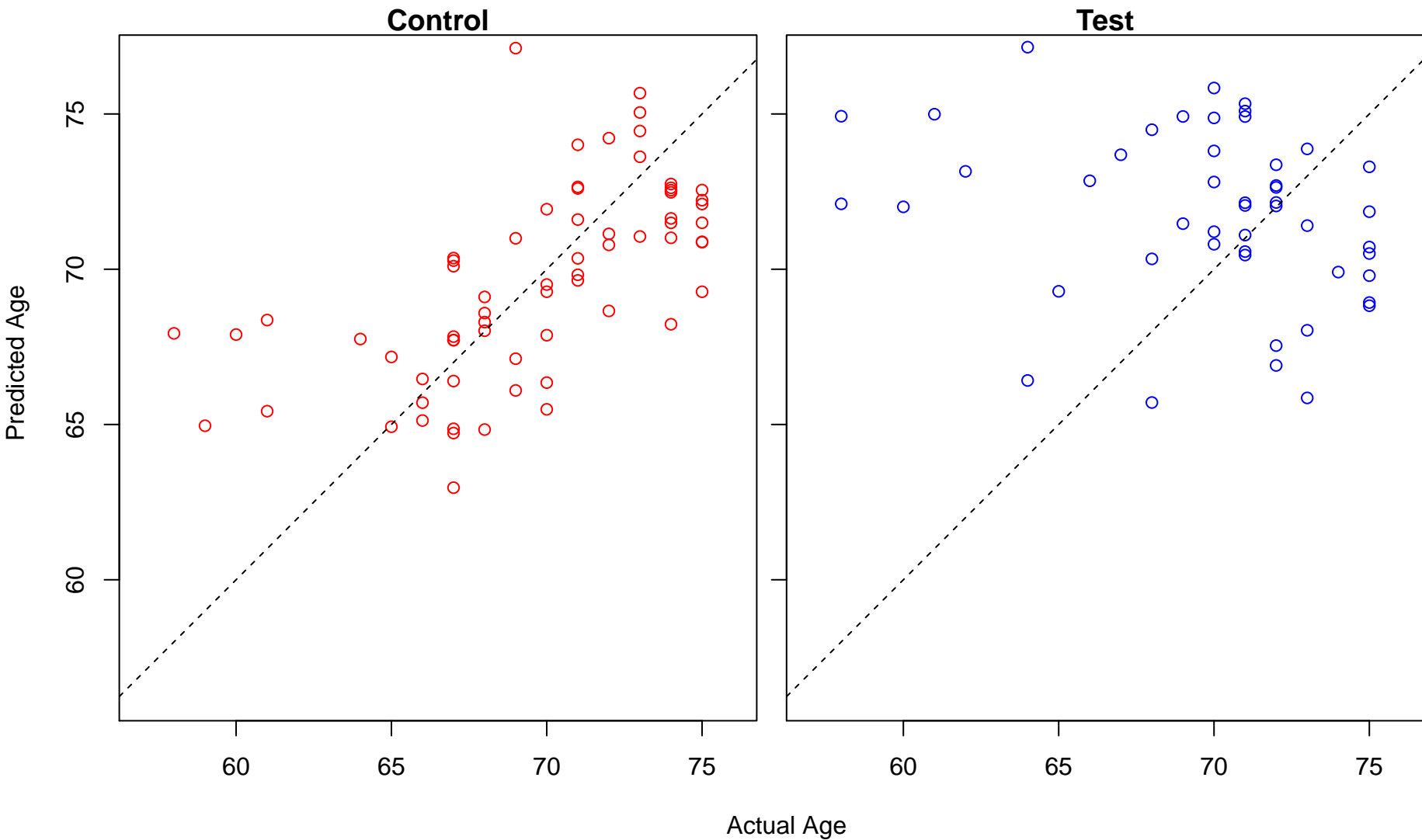
positive regulation of synaptic transmission (Score: 1.450143)



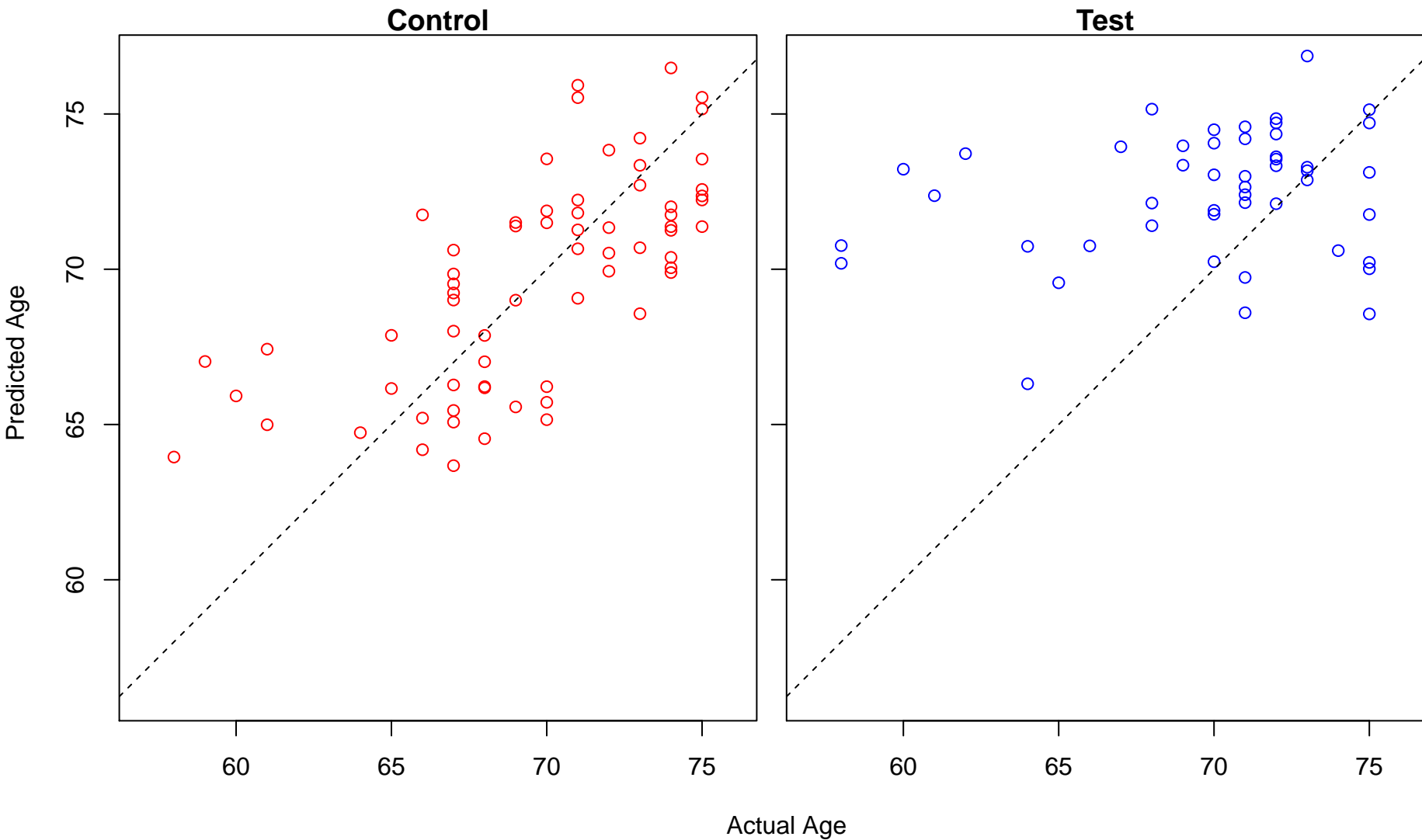
vacuolar acidification (Score: 1.449977)



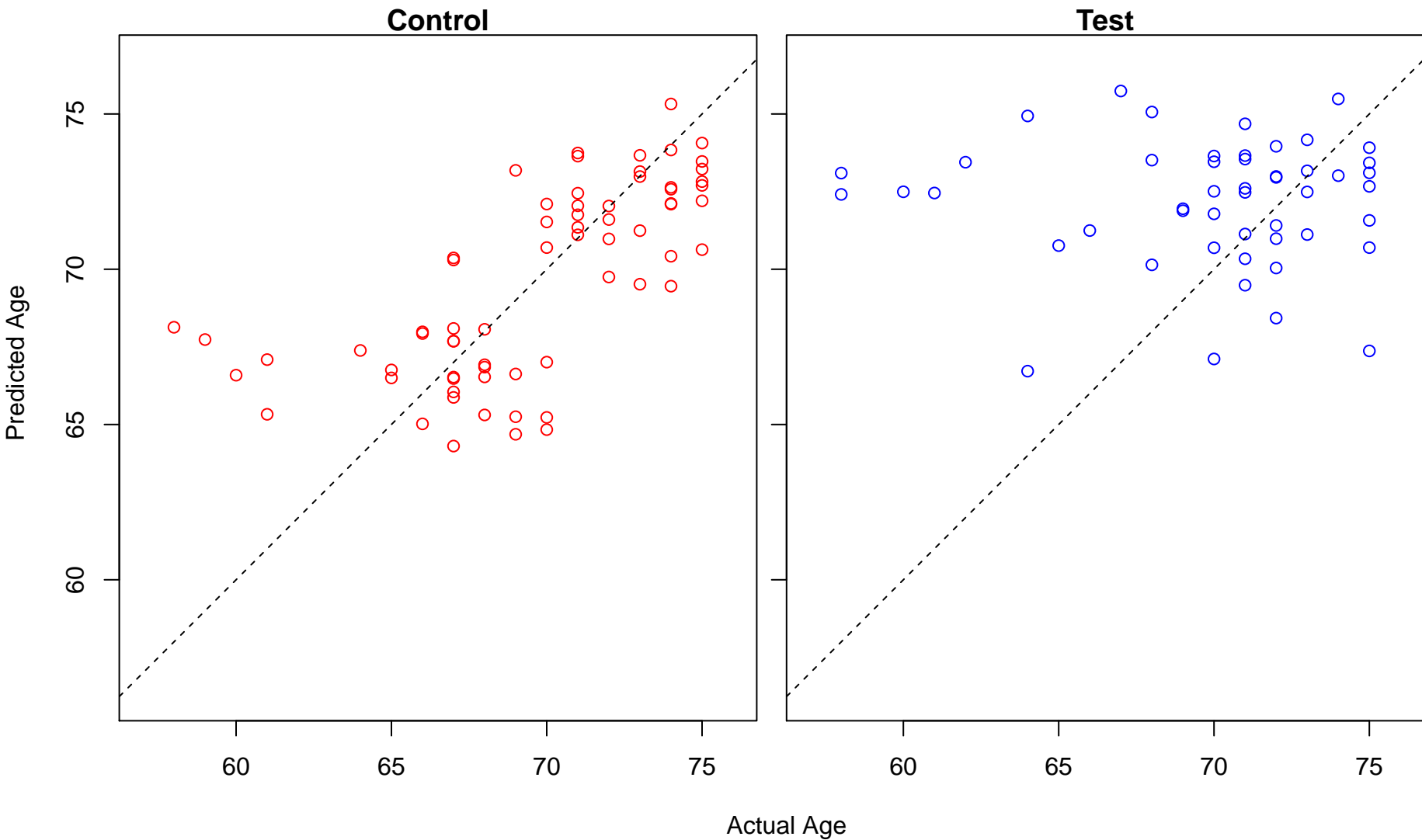
negative regulation of exocytosis (Score: 1.449788)



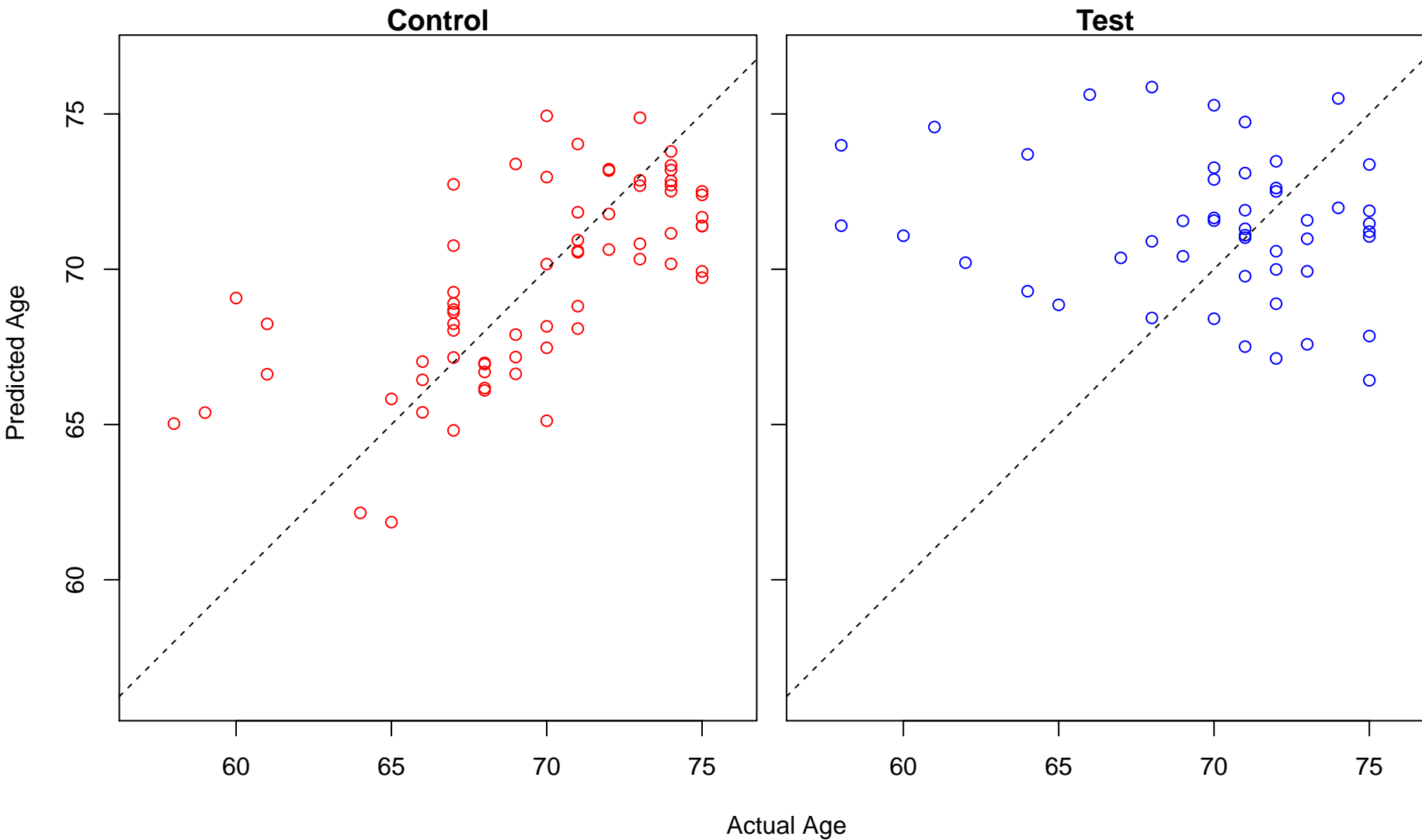
cholesterol metabolic process (Score: 1.449021)



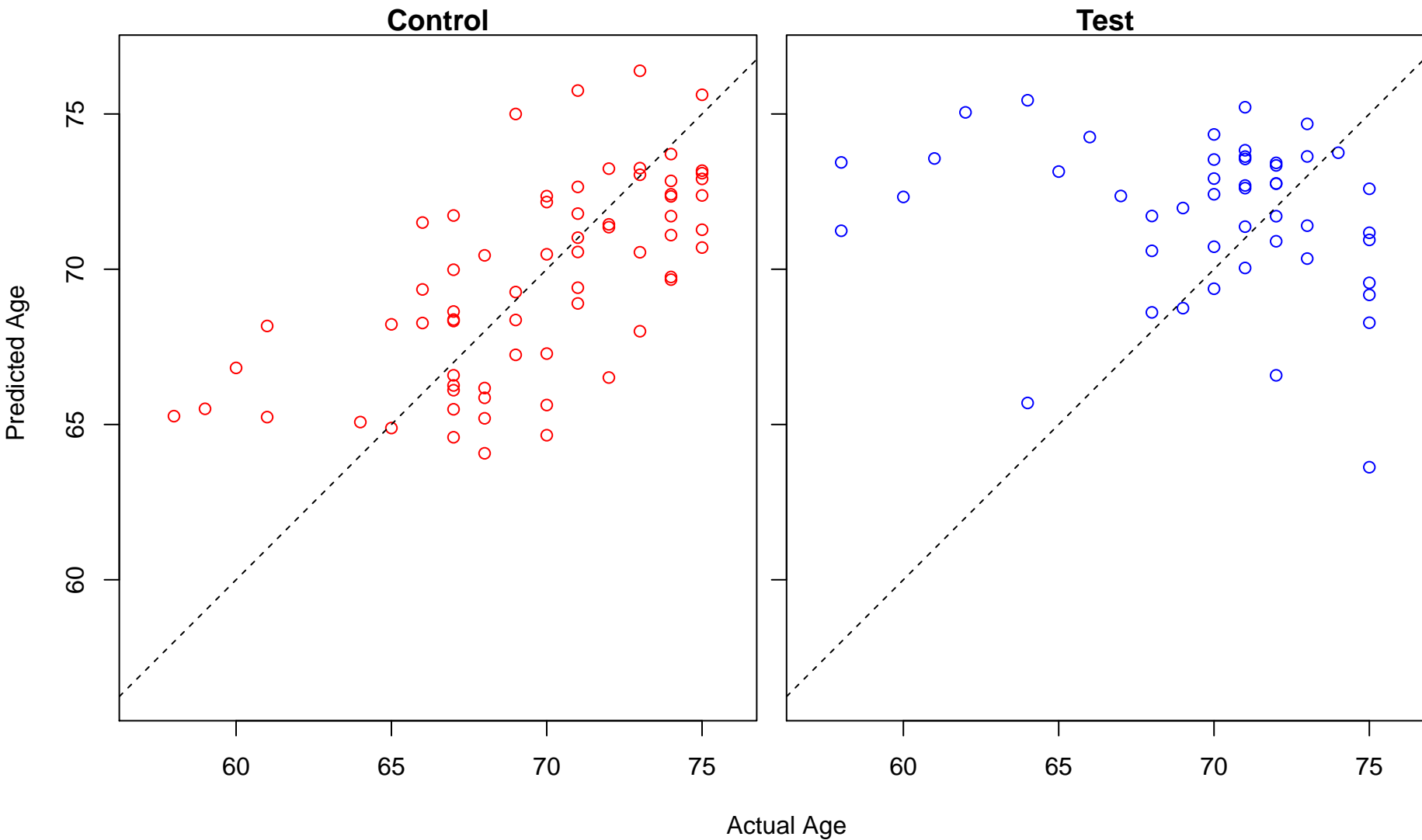
negative regulation of smooth muscle cell migration (Score: 1.448441)



cellular response to drug (Score: 1.448174)

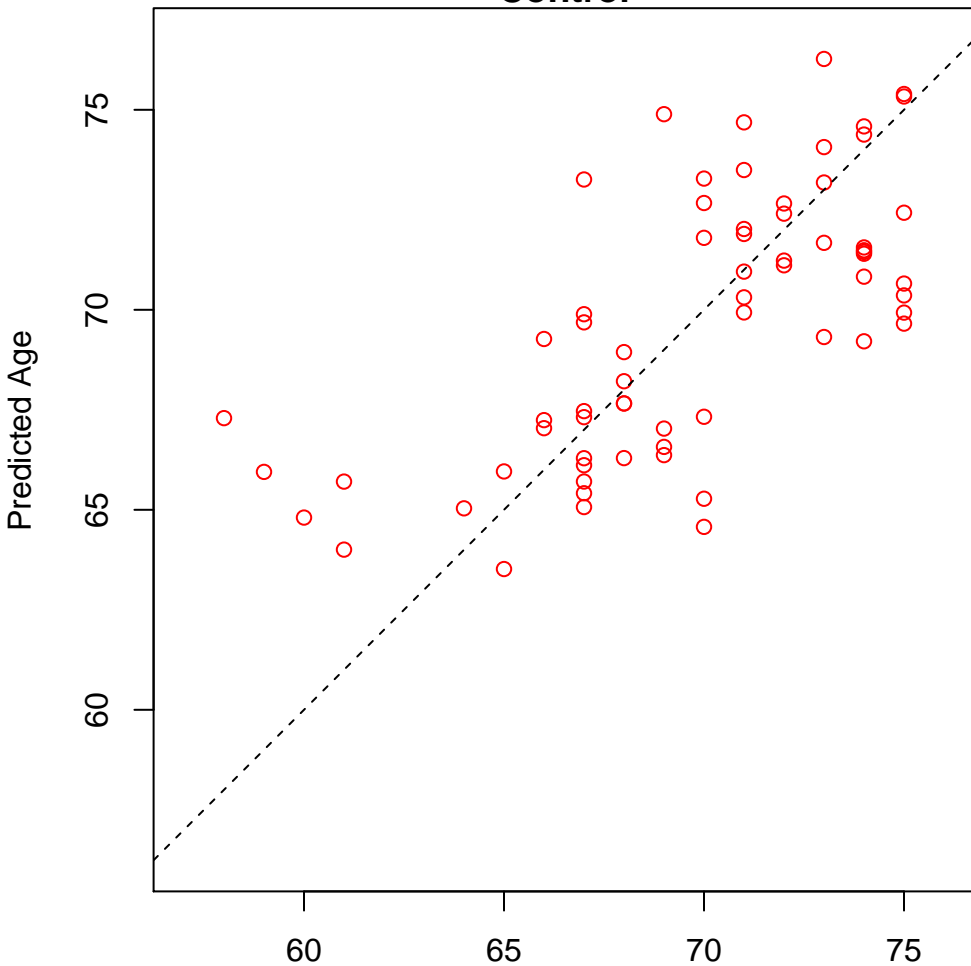


positive regulation of protein localization to chromosome, telomeric region (Score: 1.448119)

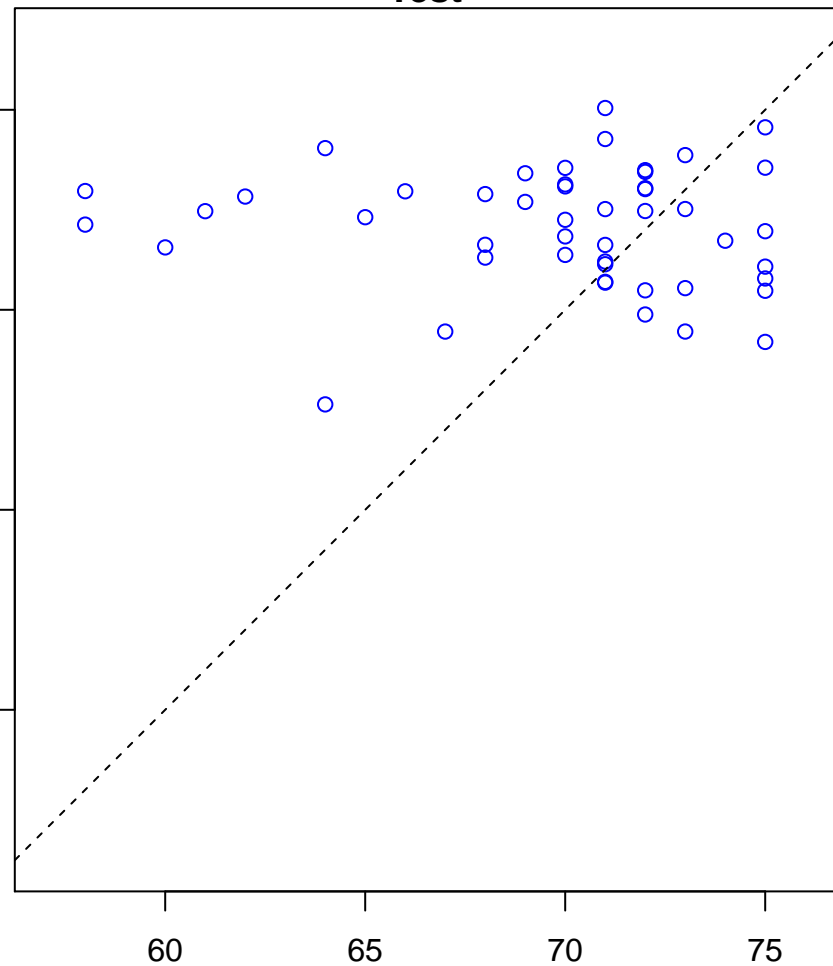


monocarboxylic acid metabolic process (Score: 1.447655)

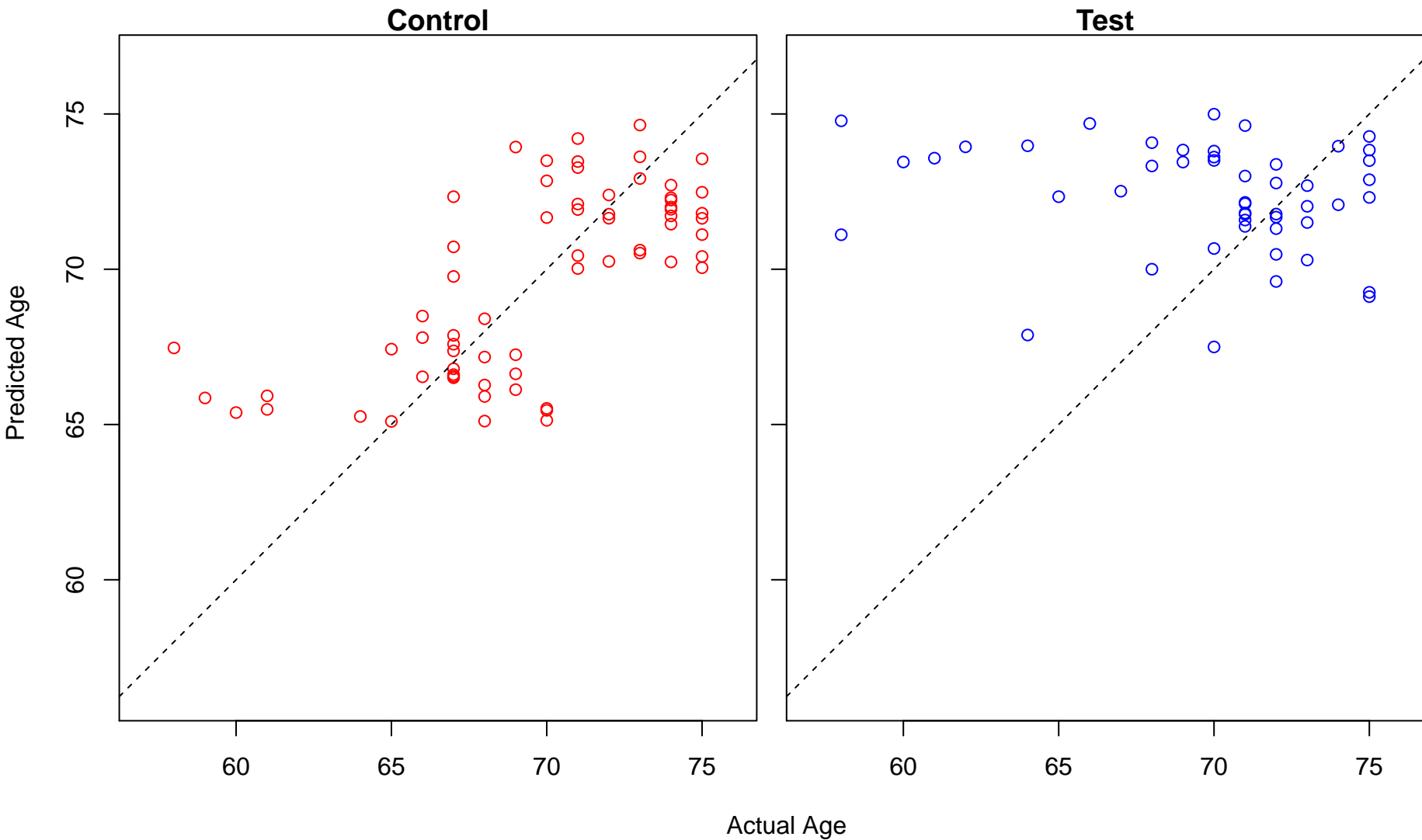
Control



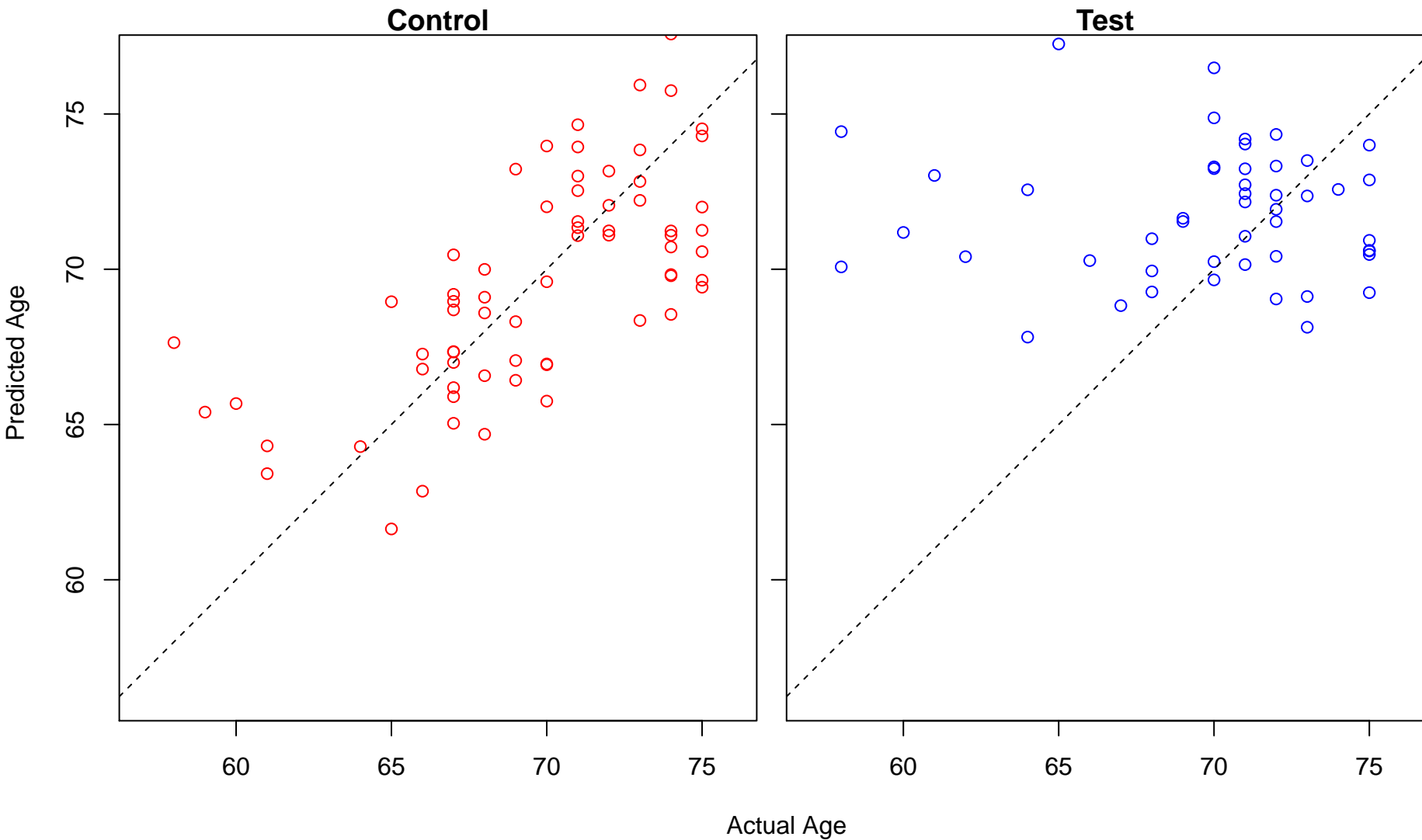
Test



transcription from RNA polymerase I promoter (Score: 1.445999)

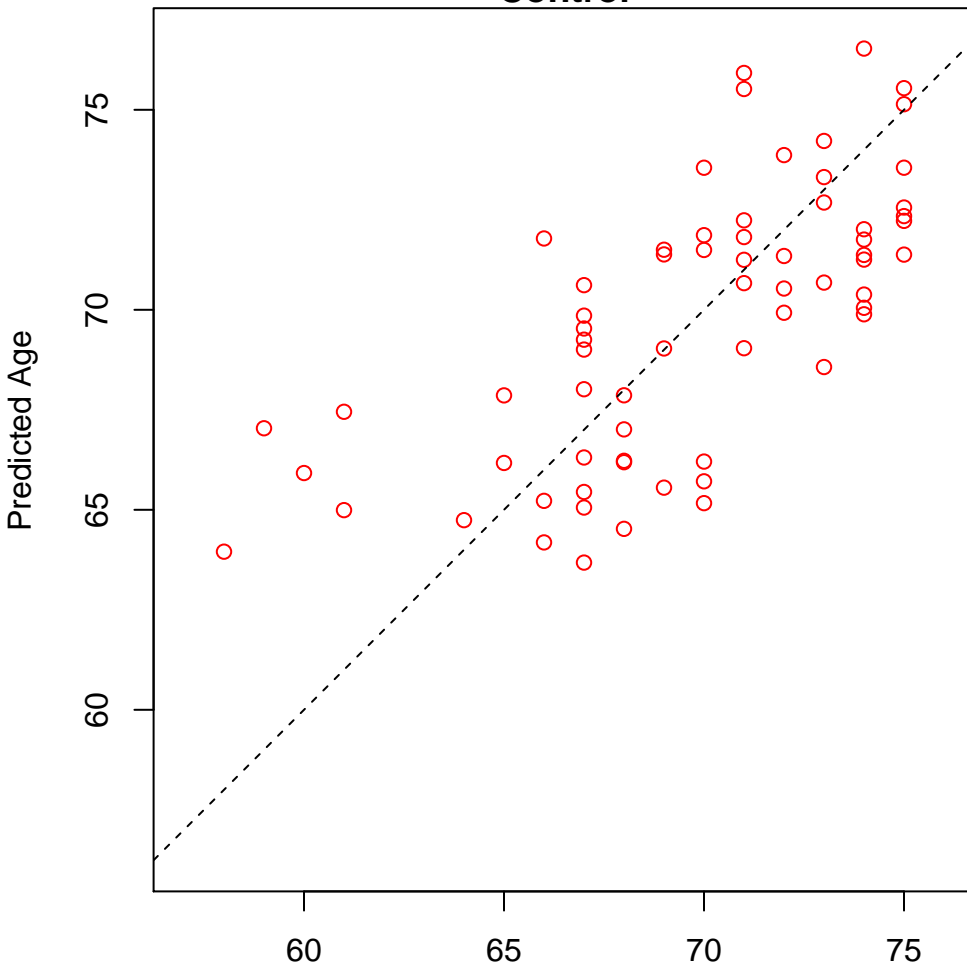


monosaccharide transport (Score: 1.445439)

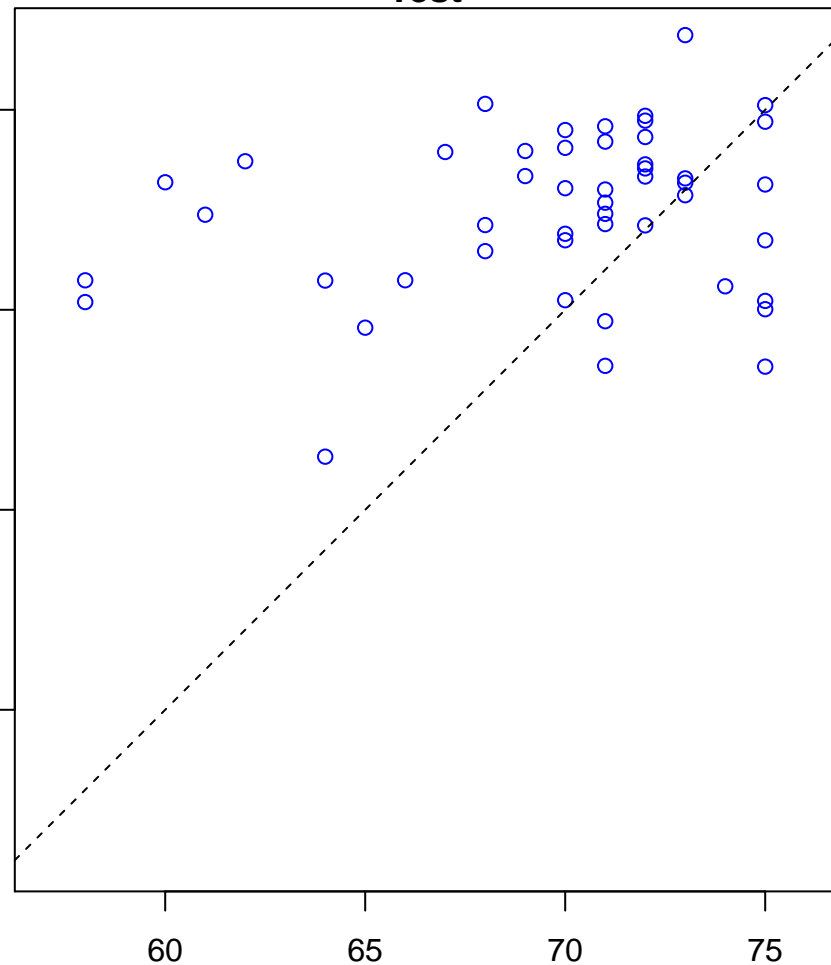


secondary alcohol metabolic process (Score: 1.445371)

Control

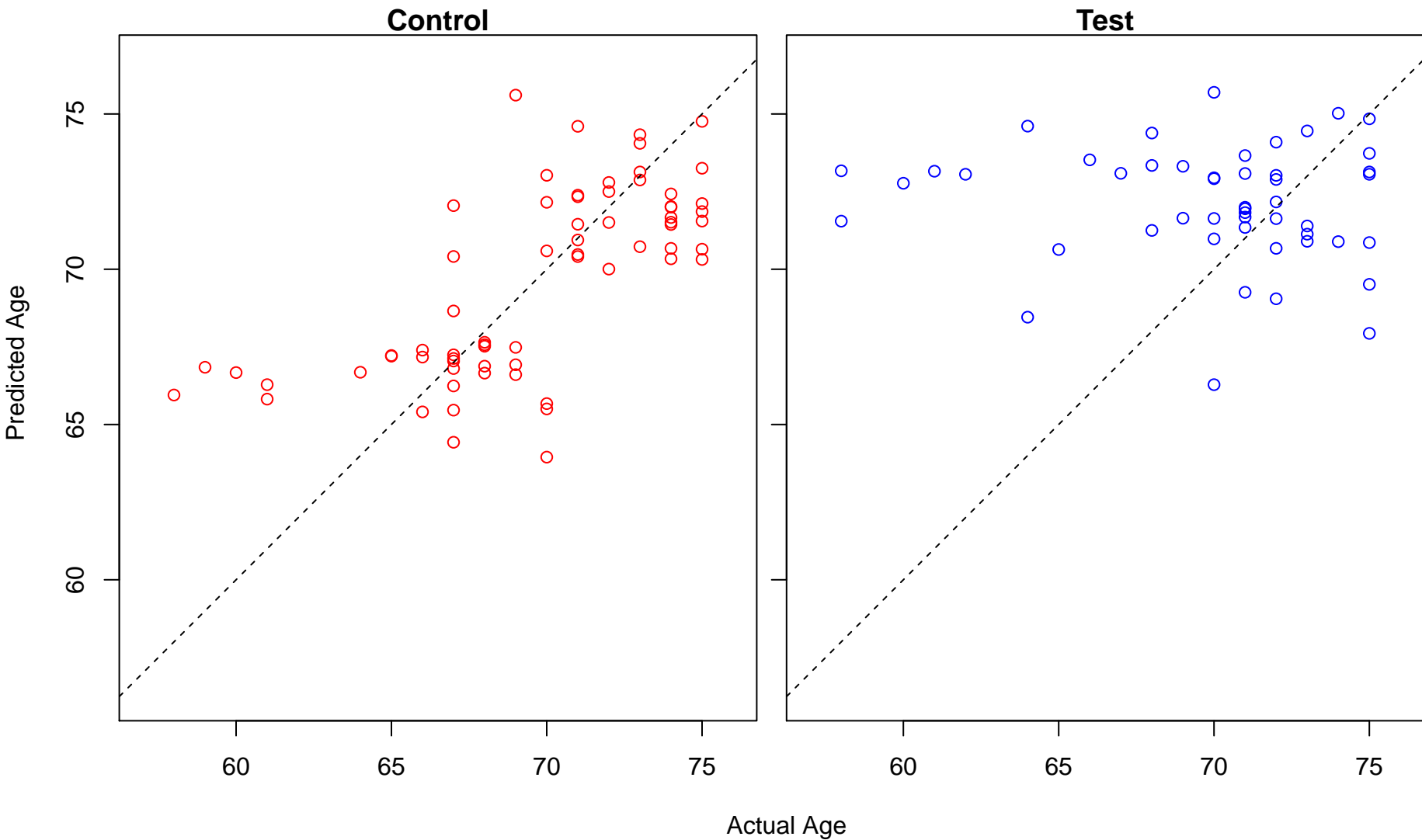


Test

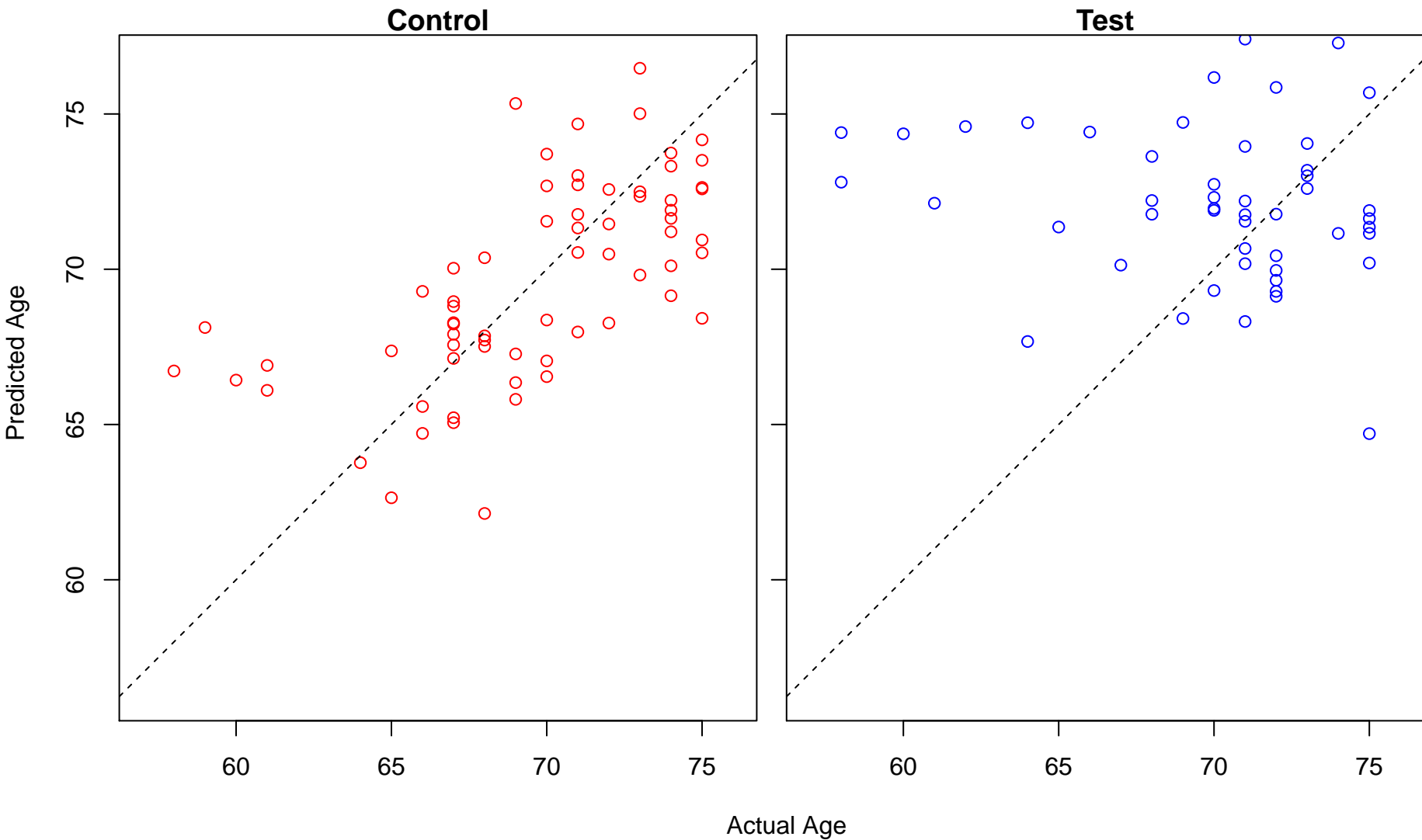


Actual Age

regulation of response to reactive oxygen species (Score: 1.444847)

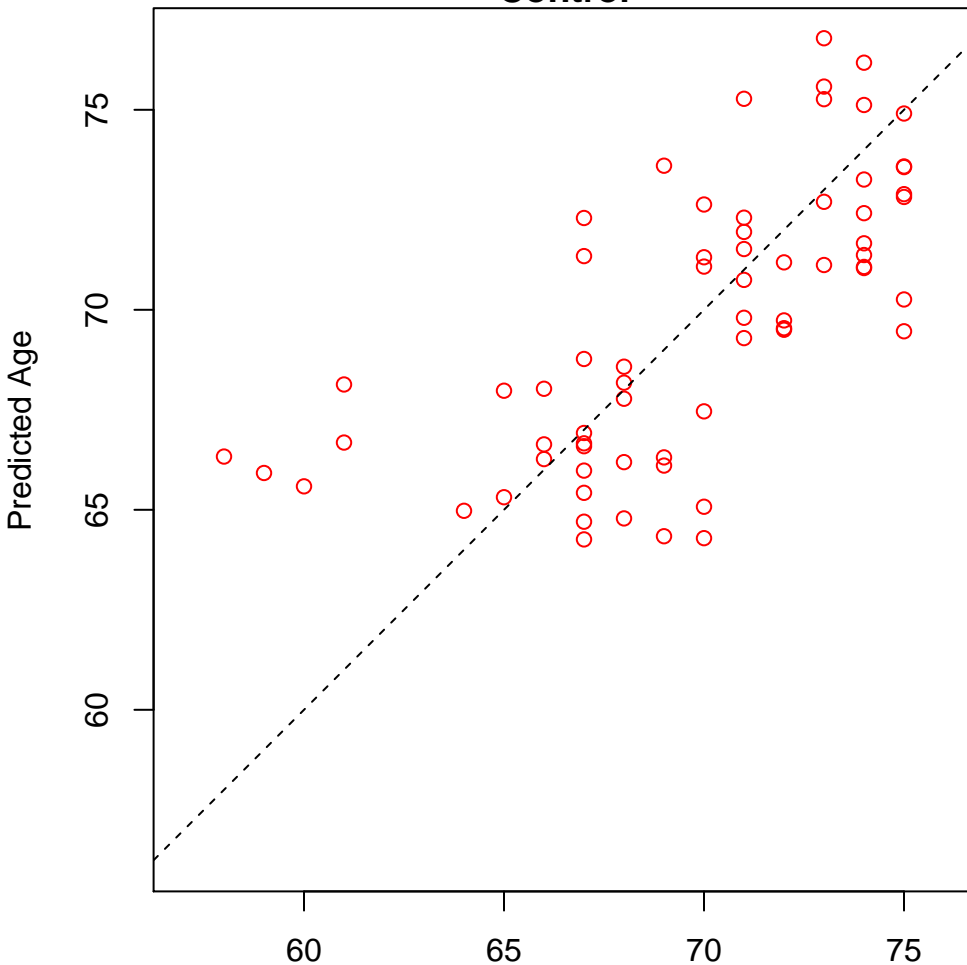


regulation of epithelial to mesenchymal transition (Score: 1.444811)

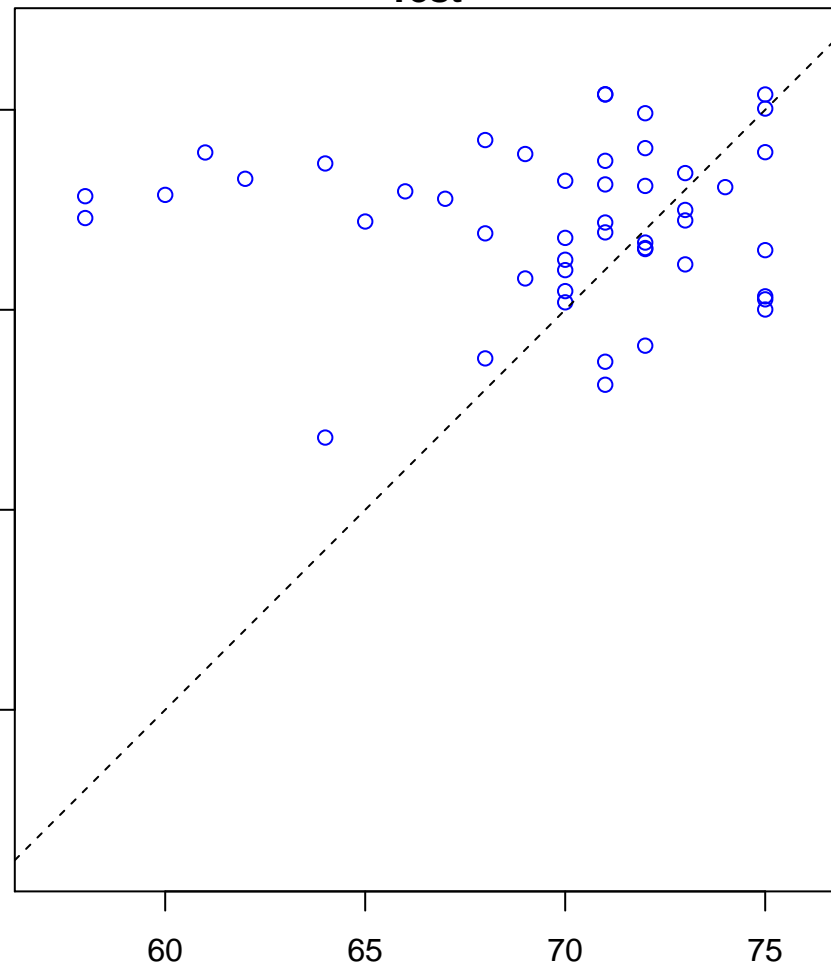


organophosphate catabolic process (Score: 1.444671)

Control

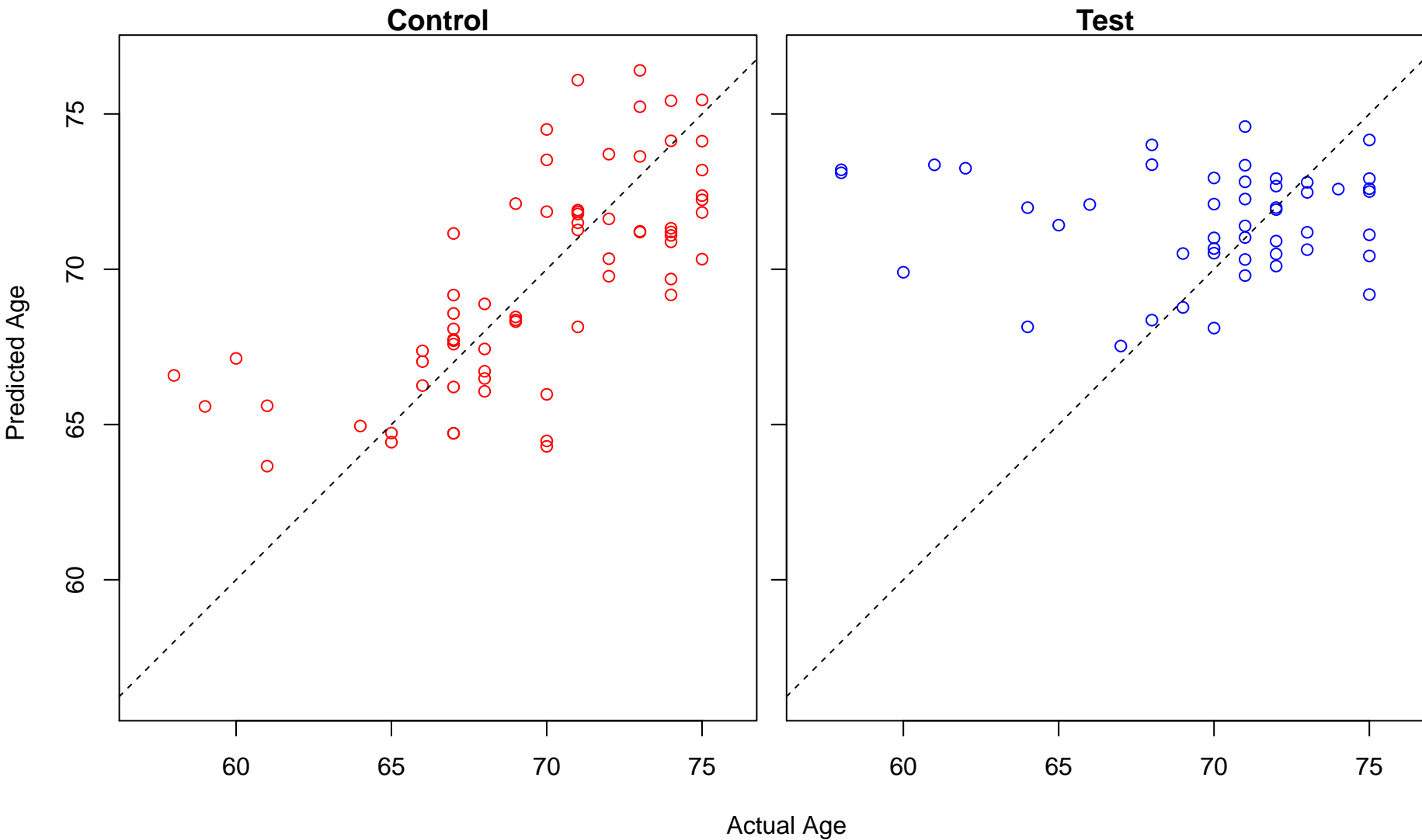


Test

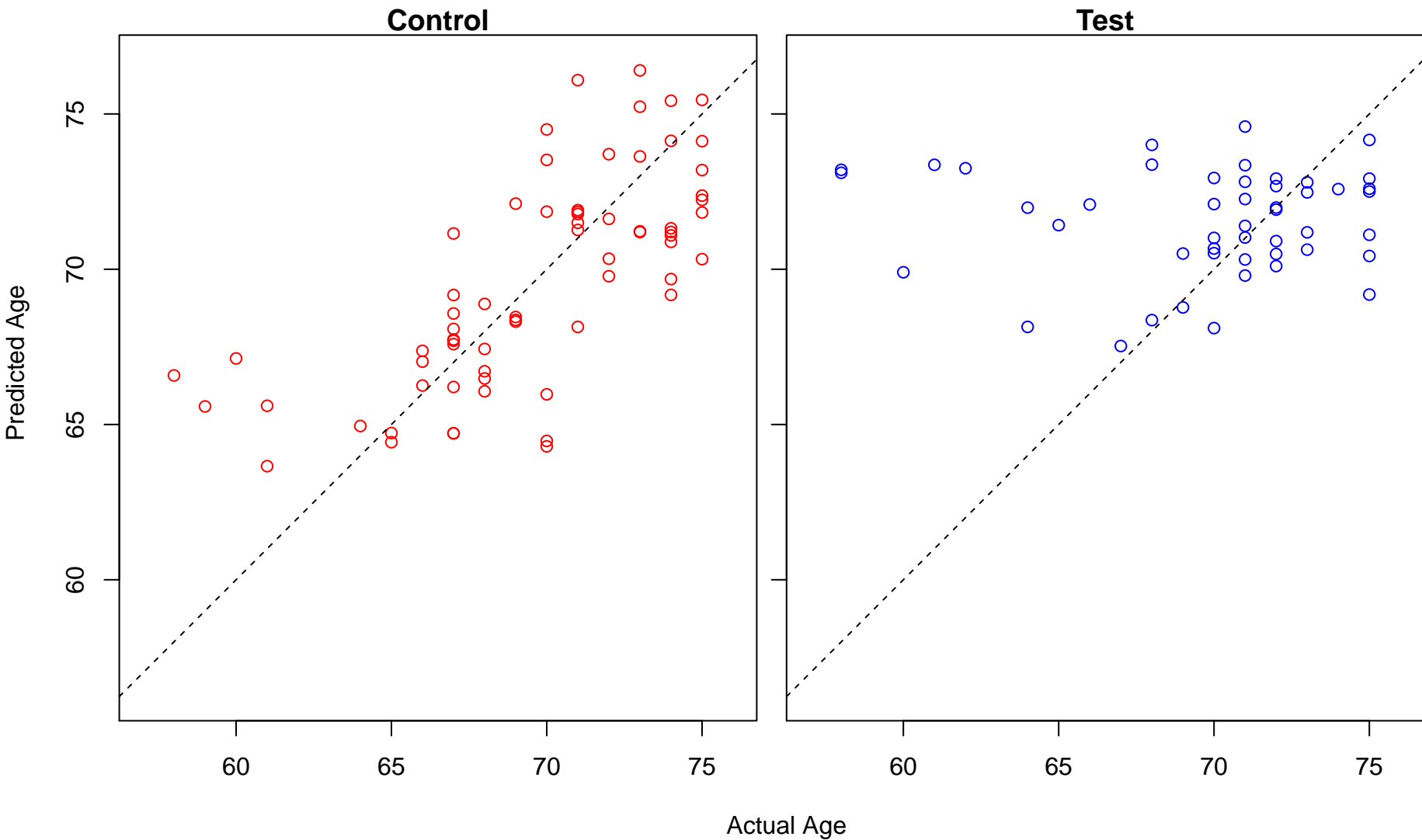


Actual Age

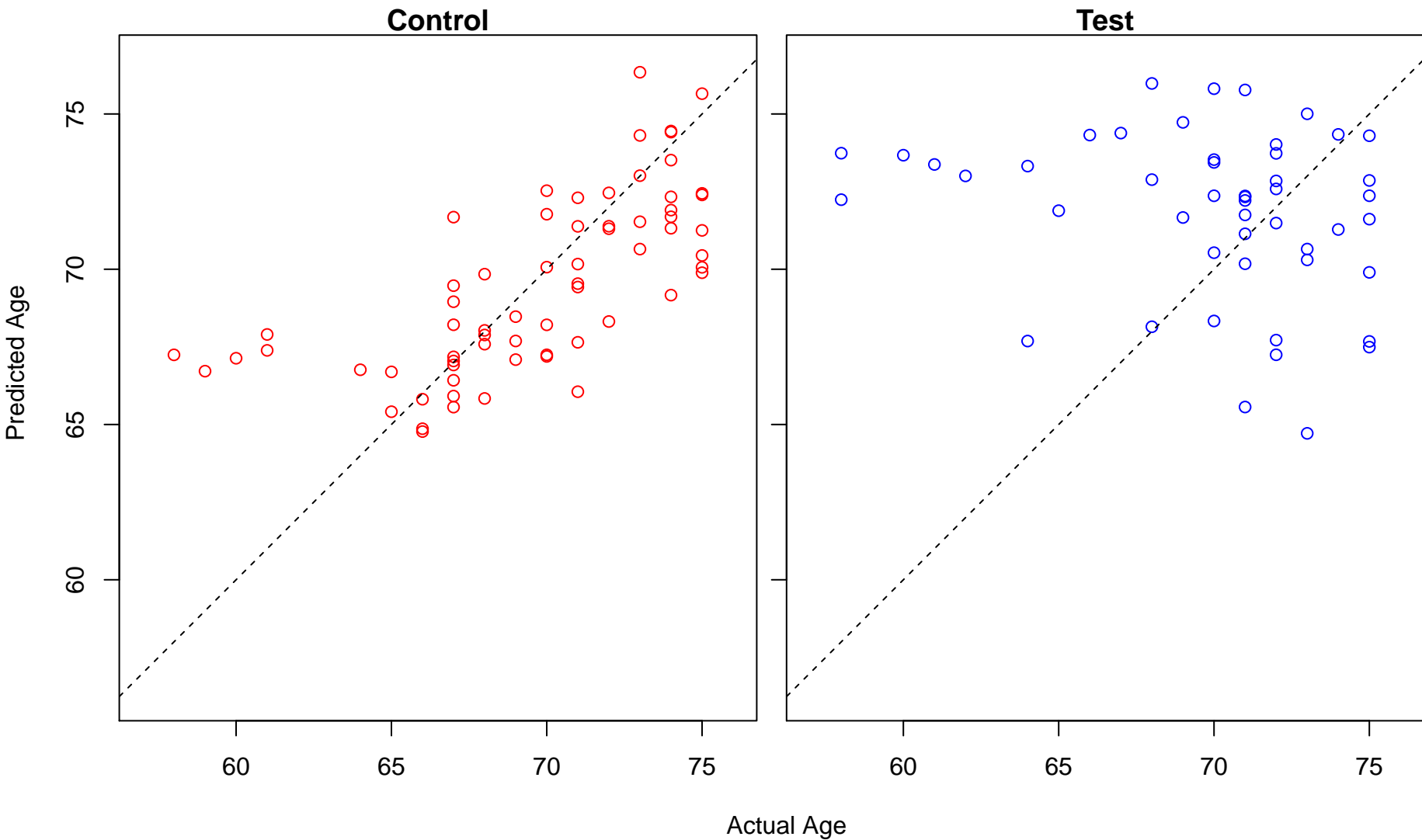
negative regulation of dephosphorylation (Score: 1.444289)



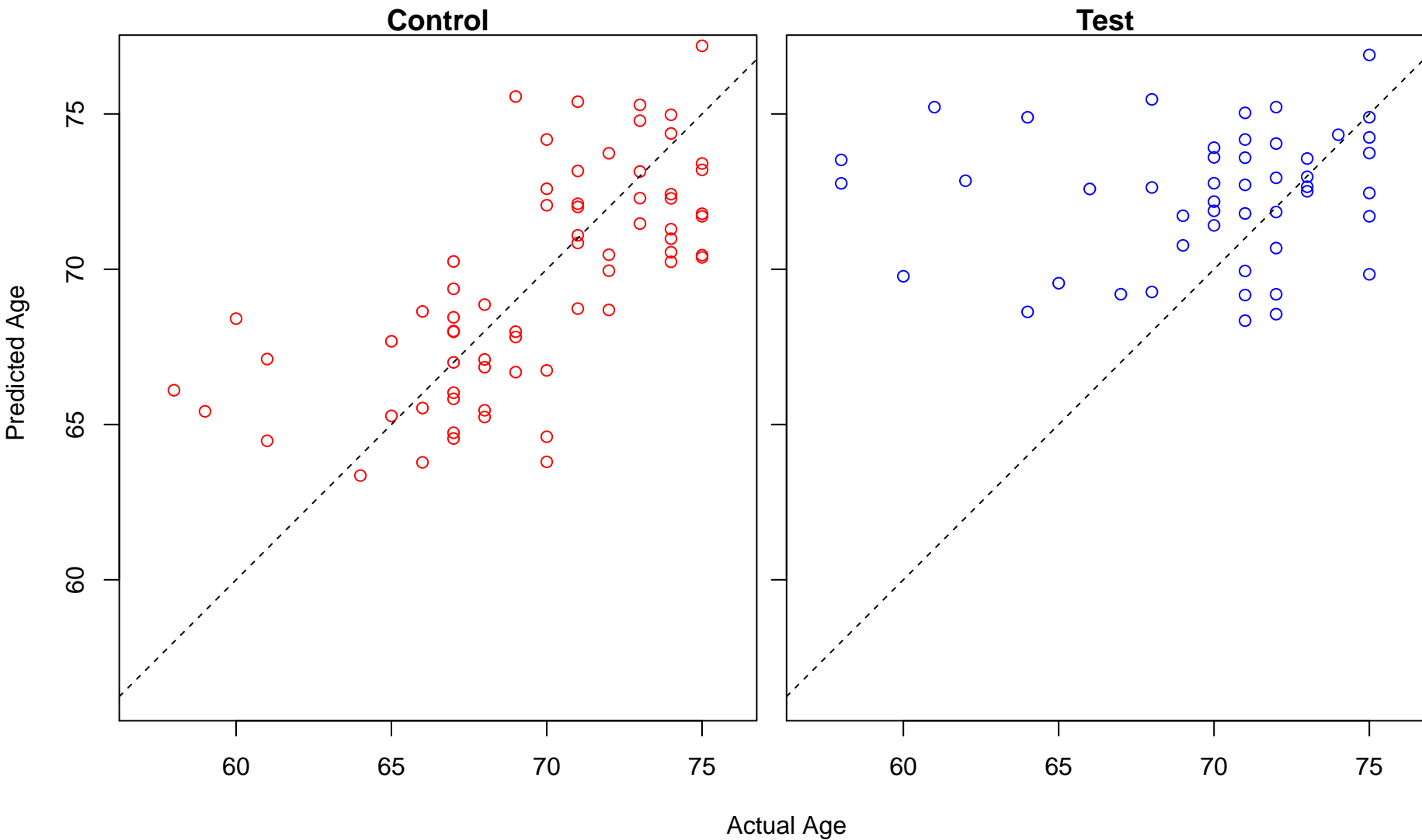
negative regulation of protein dephosphorylation (Score: 1.444289)



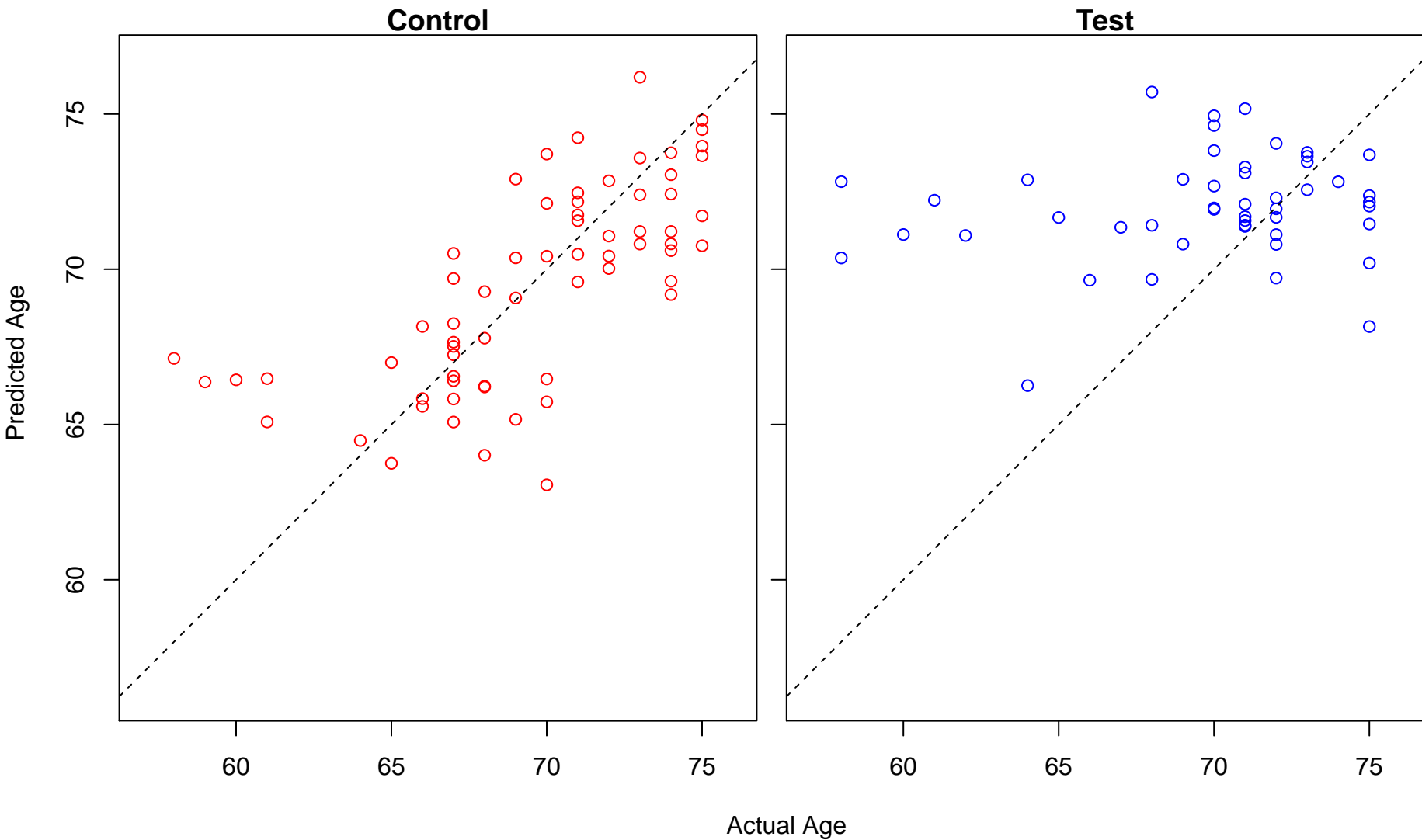
alpha-beta T cell activation (Score: 1.443924)



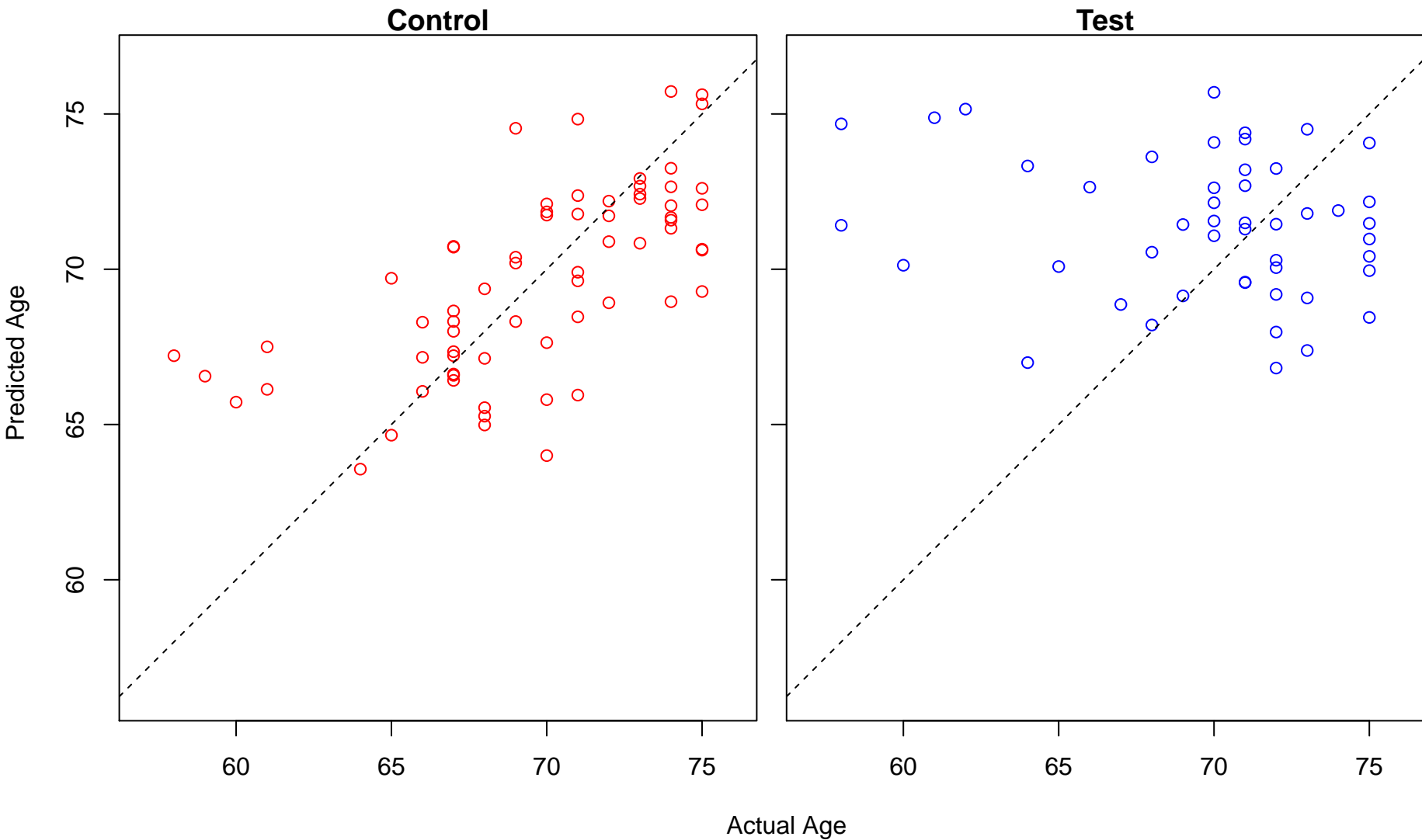
striated muscle tissue development (Score: 1.443615)



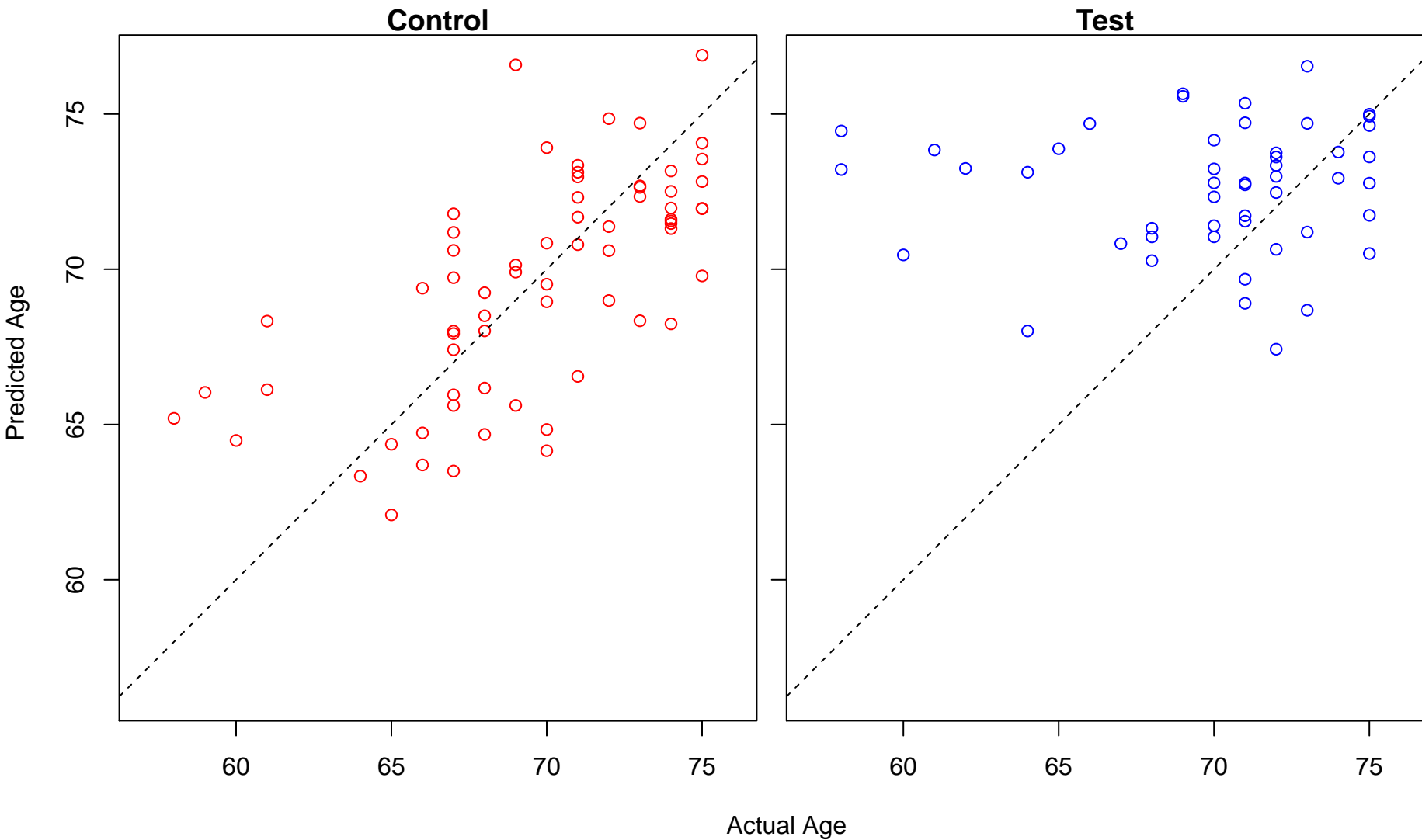
vacuole organization (Score: 1.443464)



monosaccharide metabolic process (Score: 1.442317)

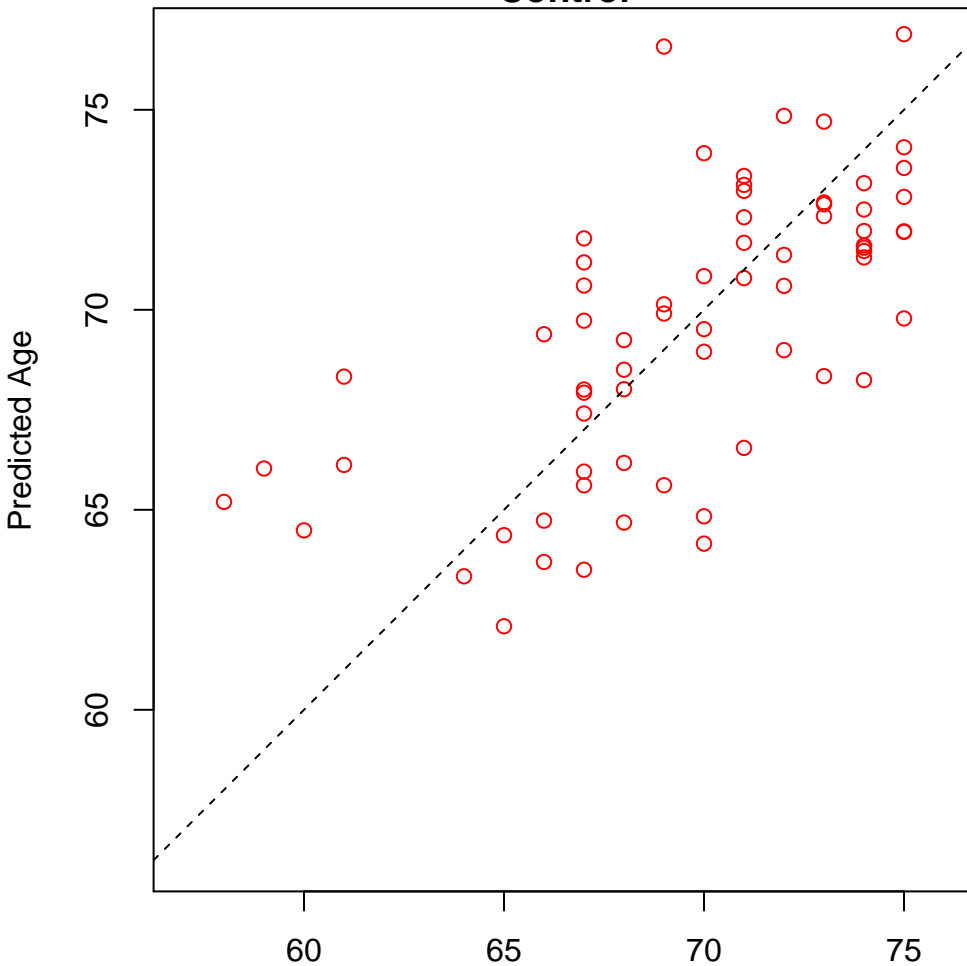


intracellular transport of virus (Score: 1.442066)

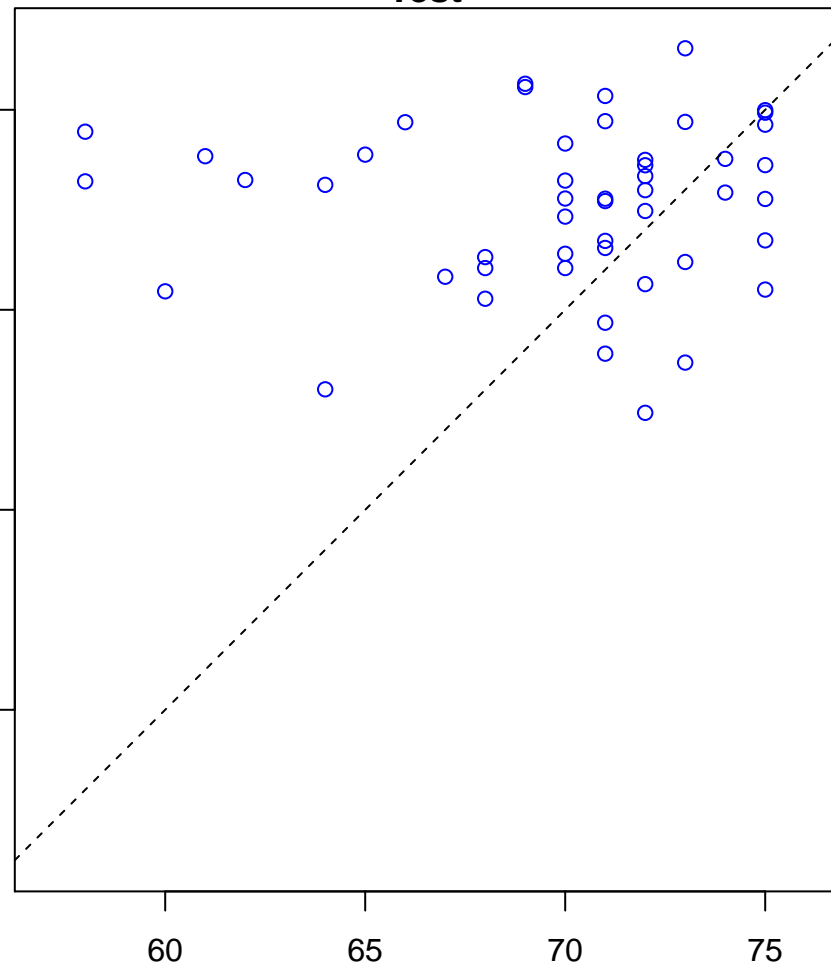


multi-organism intracellular transport (Score: 1.442066)

Control

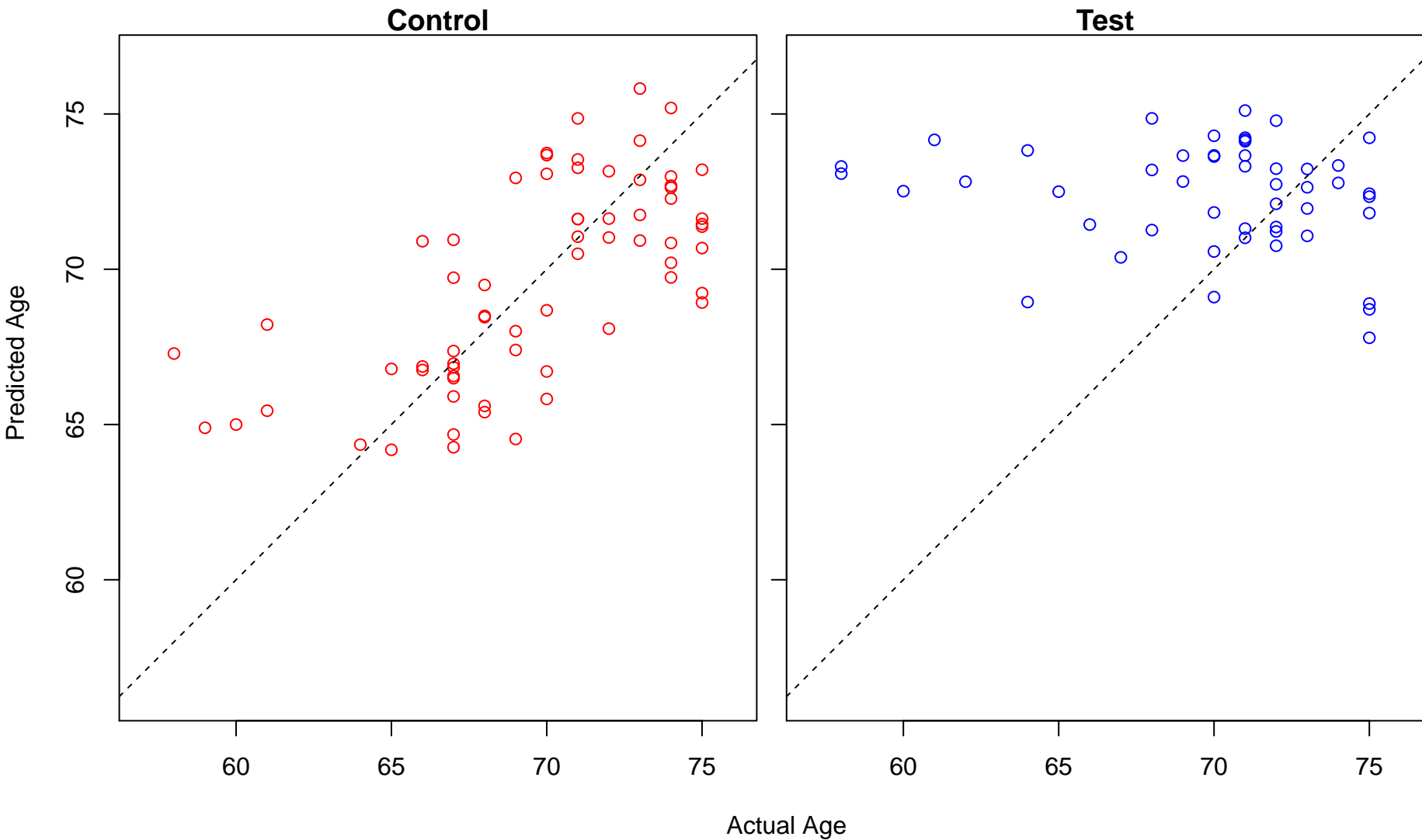


Test

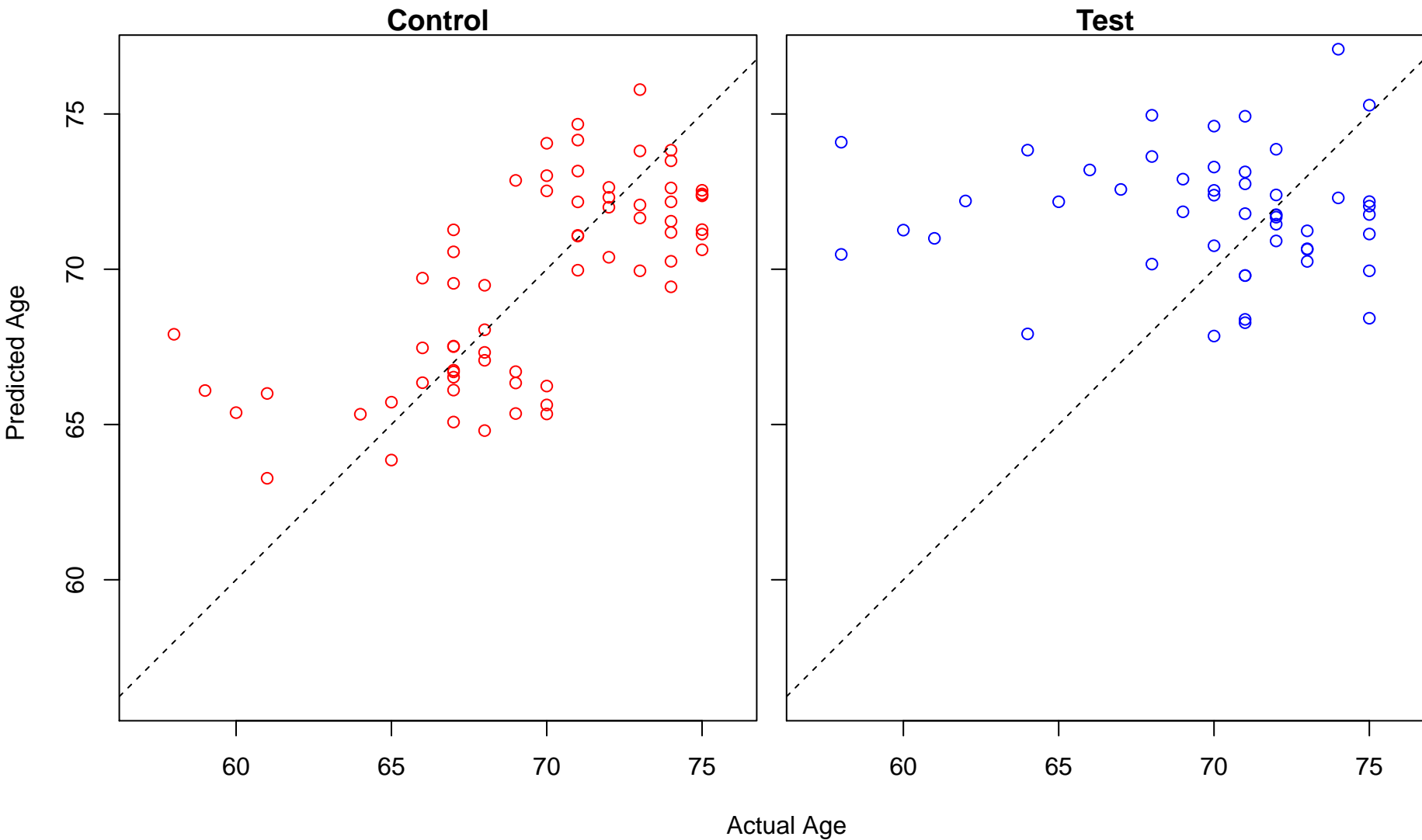


Actual Age

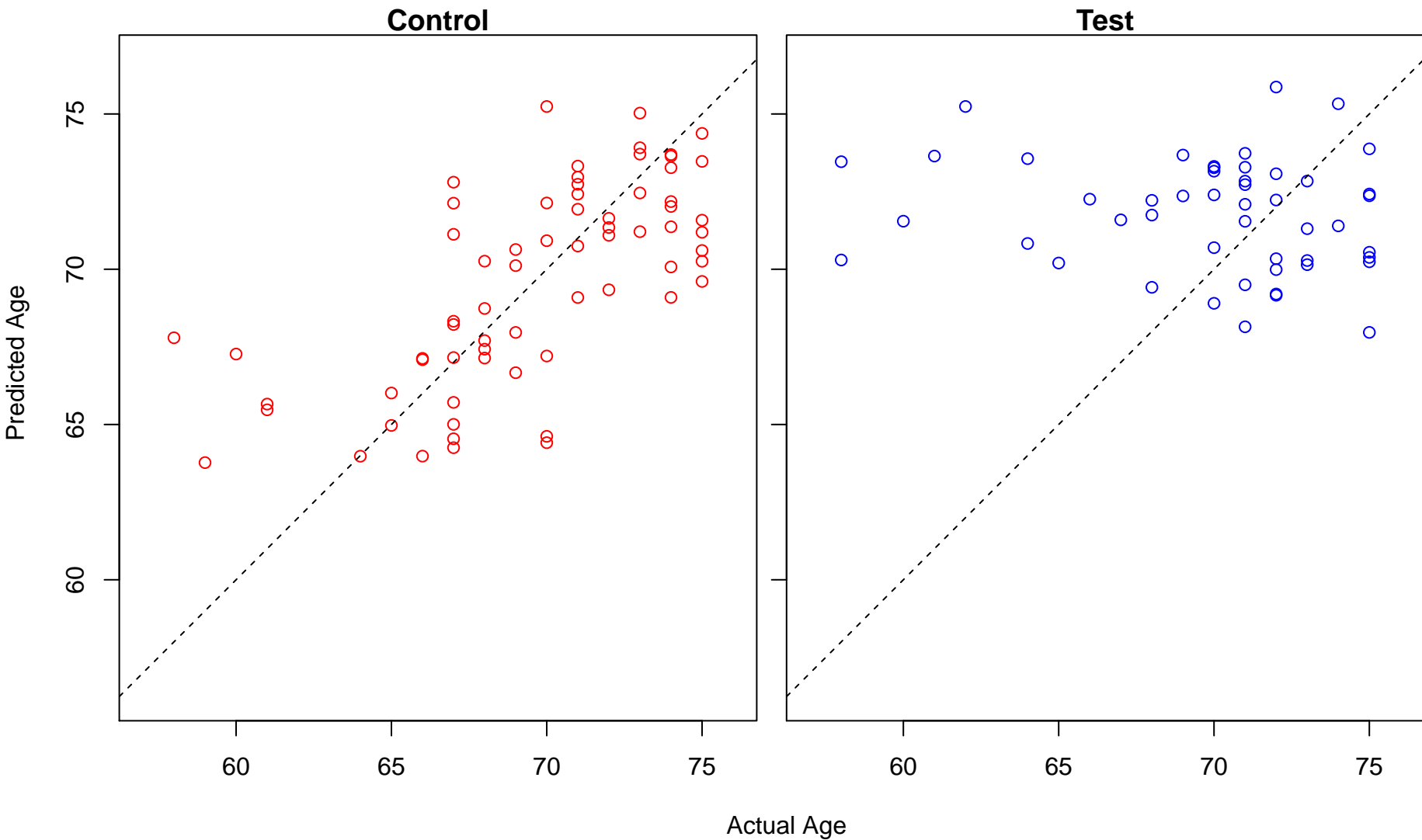
regulation of signal transduction by p53 class mediator (Score: 1.440634)



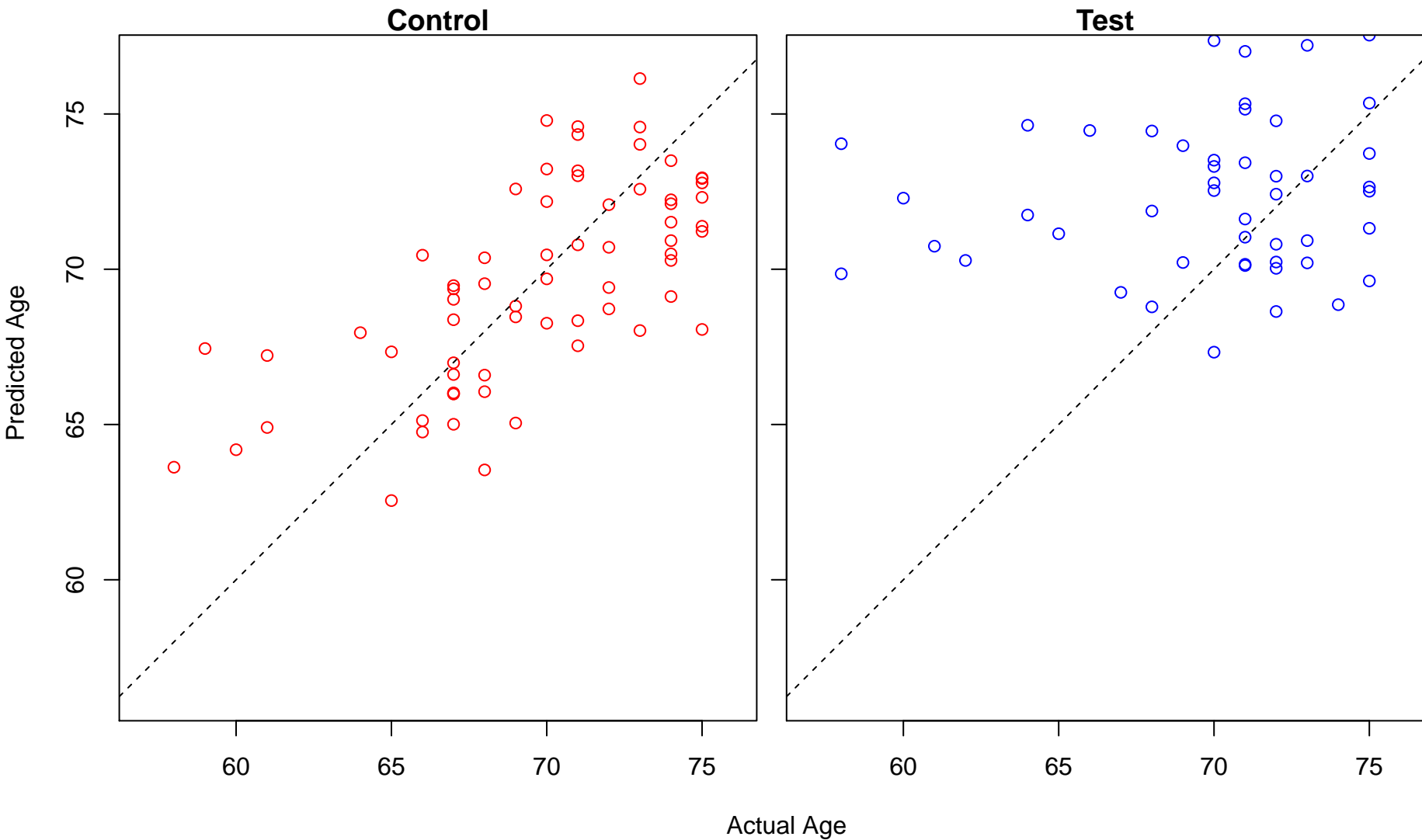
positive regulation of gene expression, epigenetic (Score: 1.440428)



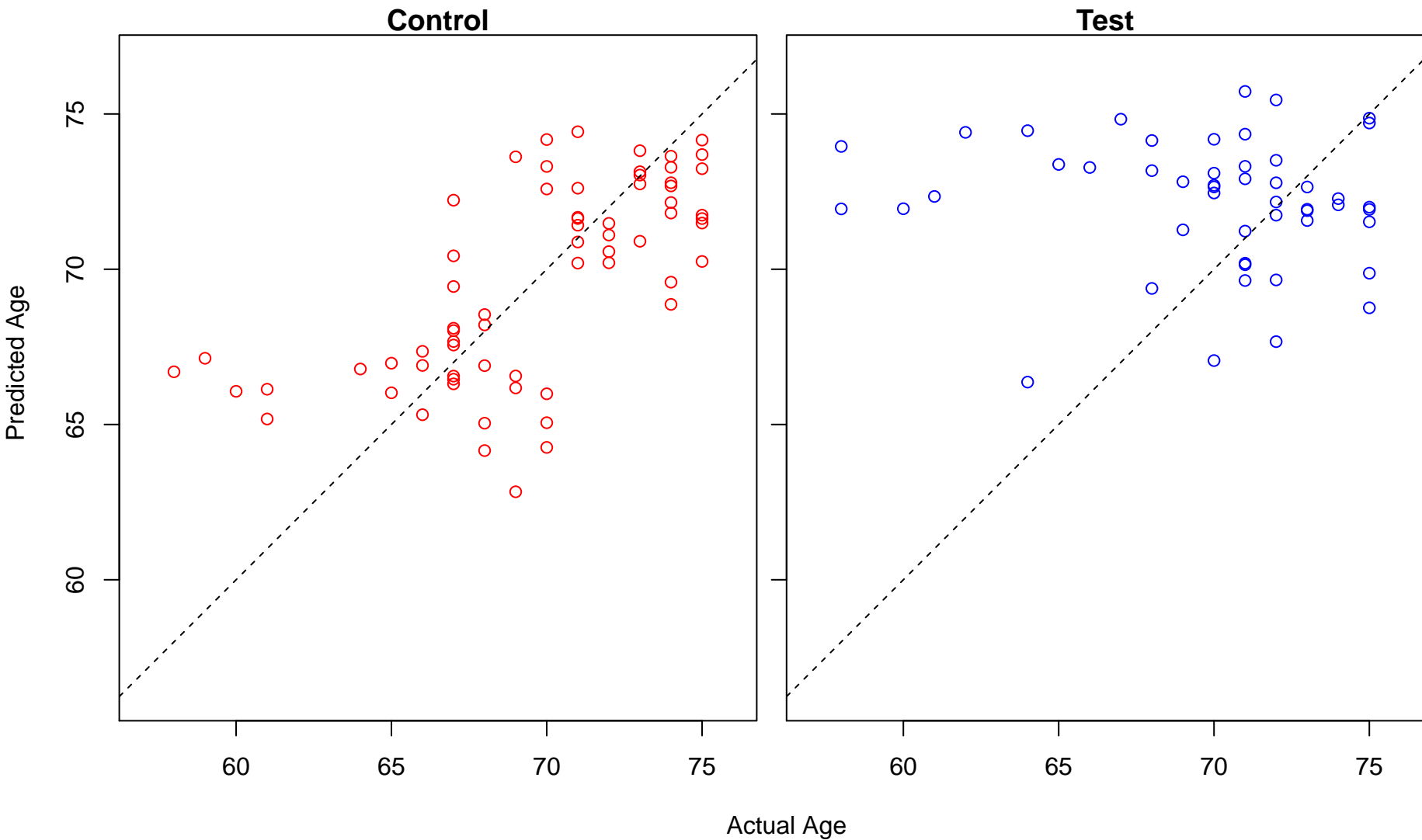
regulation of establishment of cell polarity (Score: 1.440299)



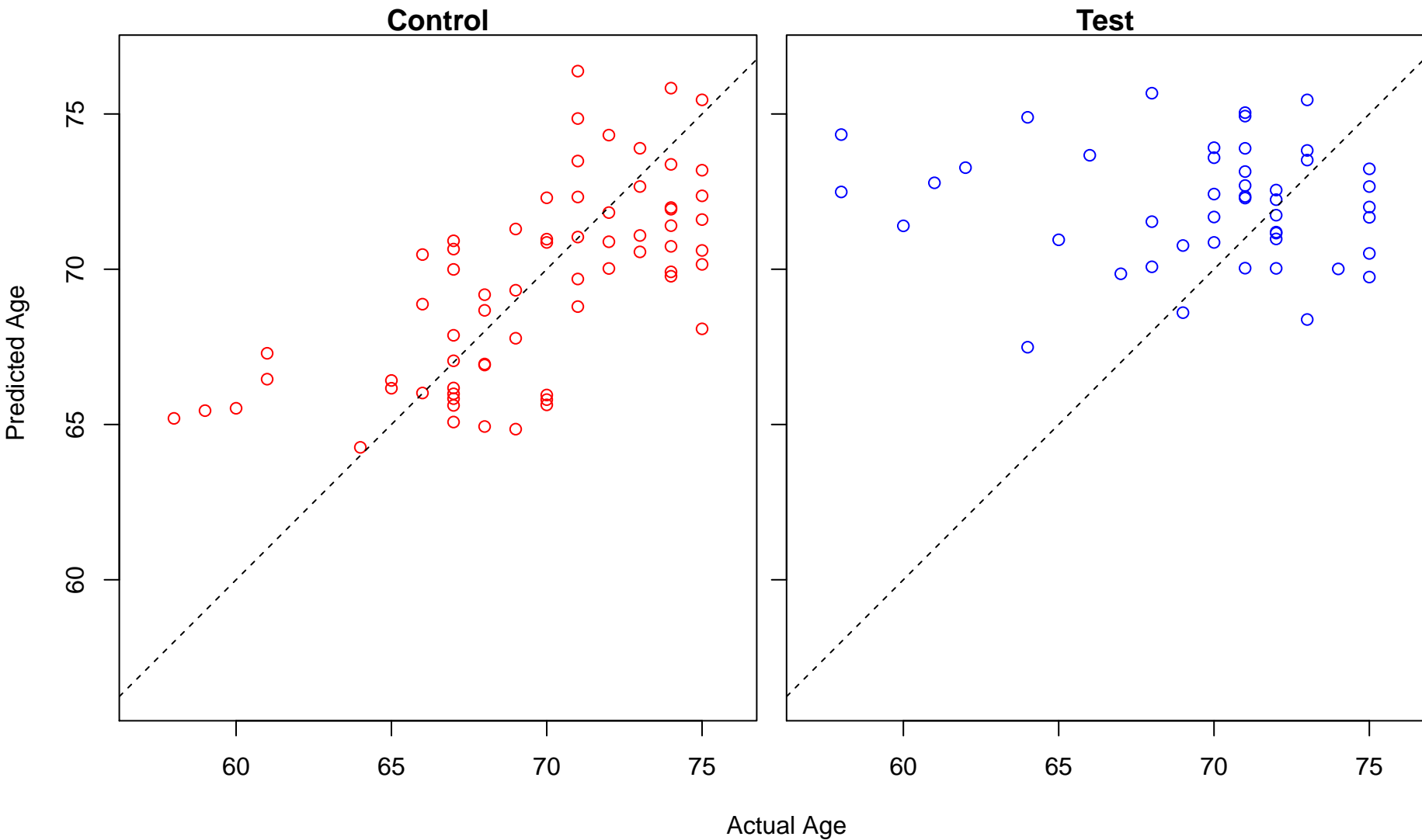
regulation of transcription from RNA polymerase I promoter (Score: 1.440217)



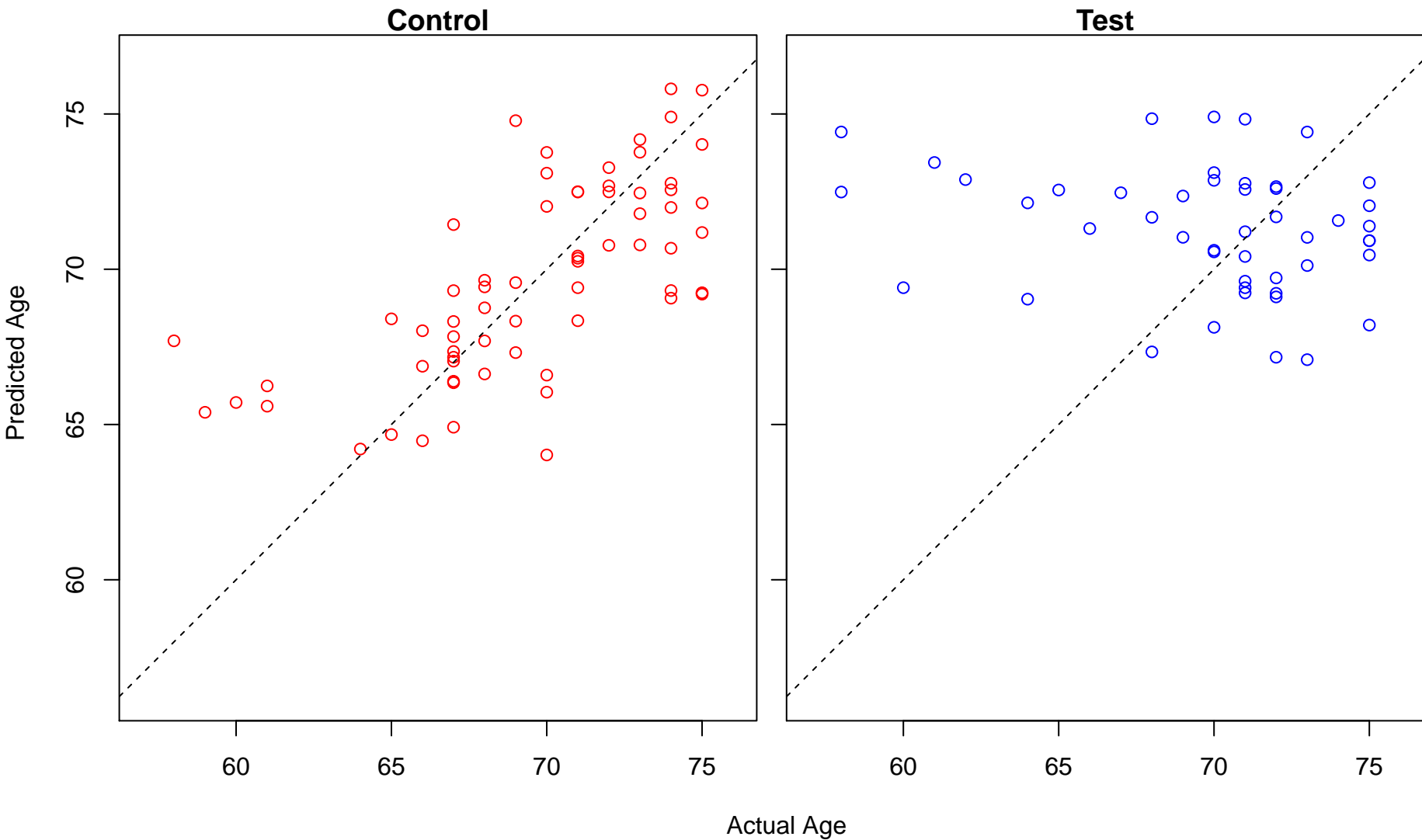
regulation of chromatin modification (Score: 1.439067)



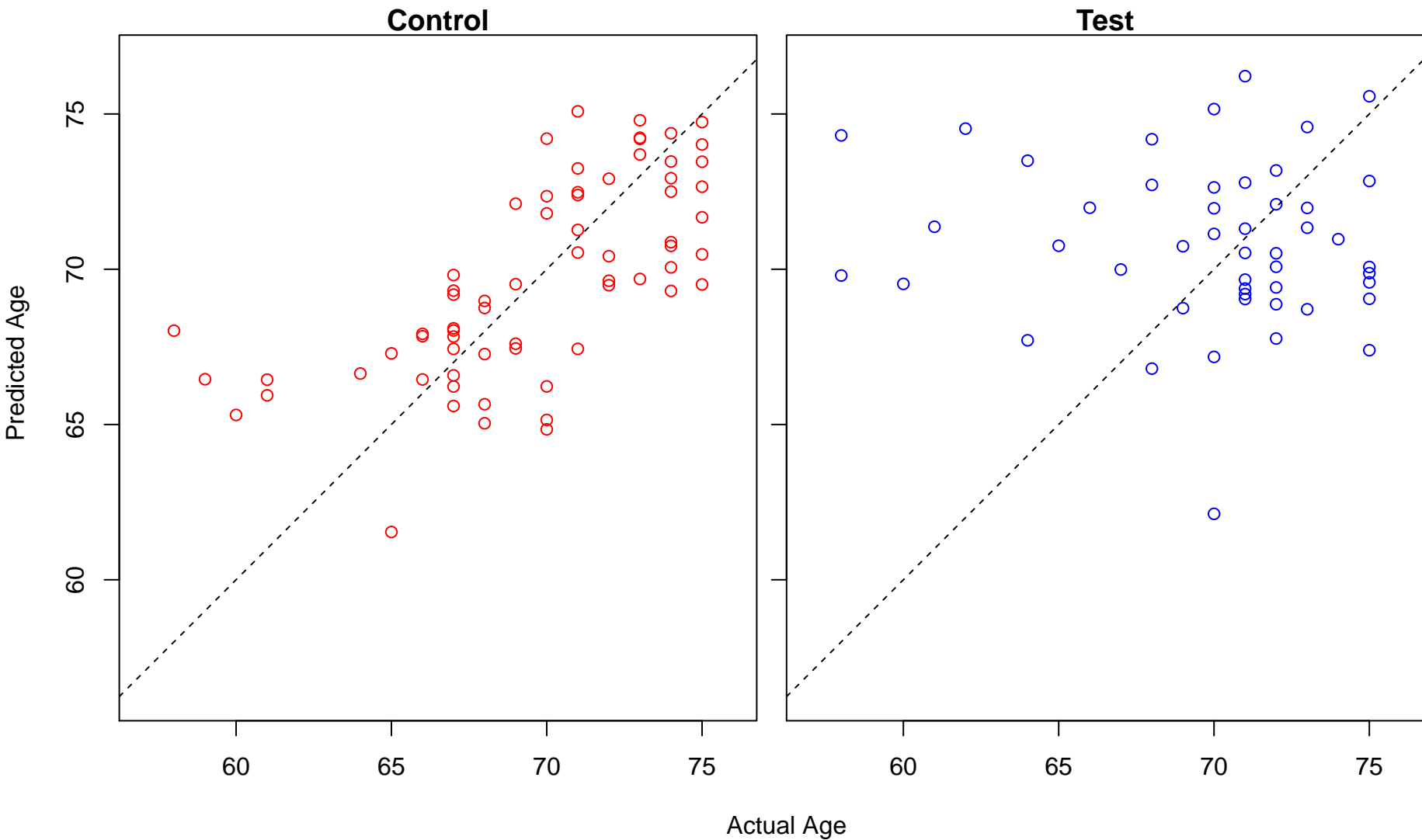
regulated exocytosis (Score: 1.438562)



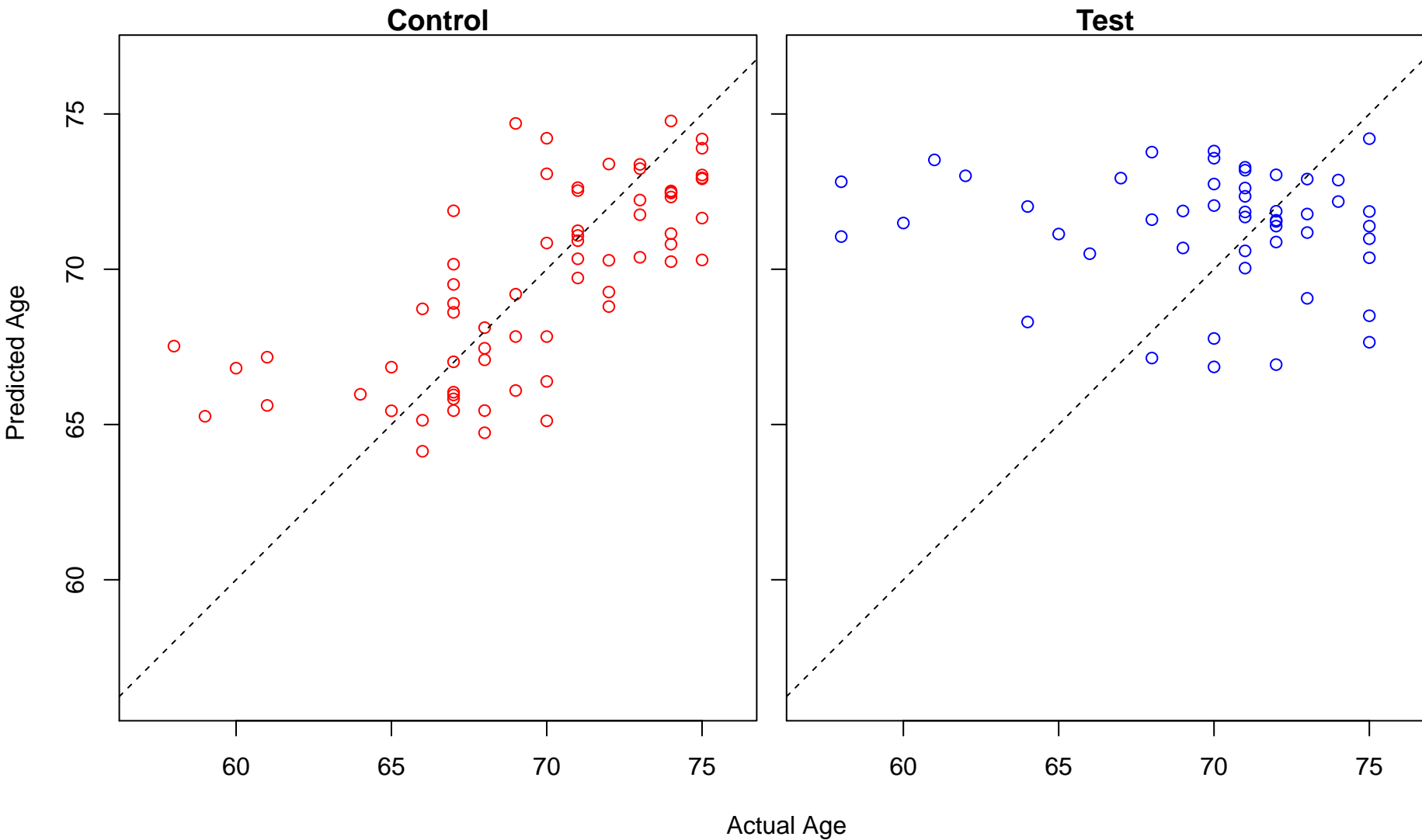
positive regulation of nucleocytoplasmic transport (Score: 1.438472)



regulation of sequestering of calcium ion (Score: 1.437567)

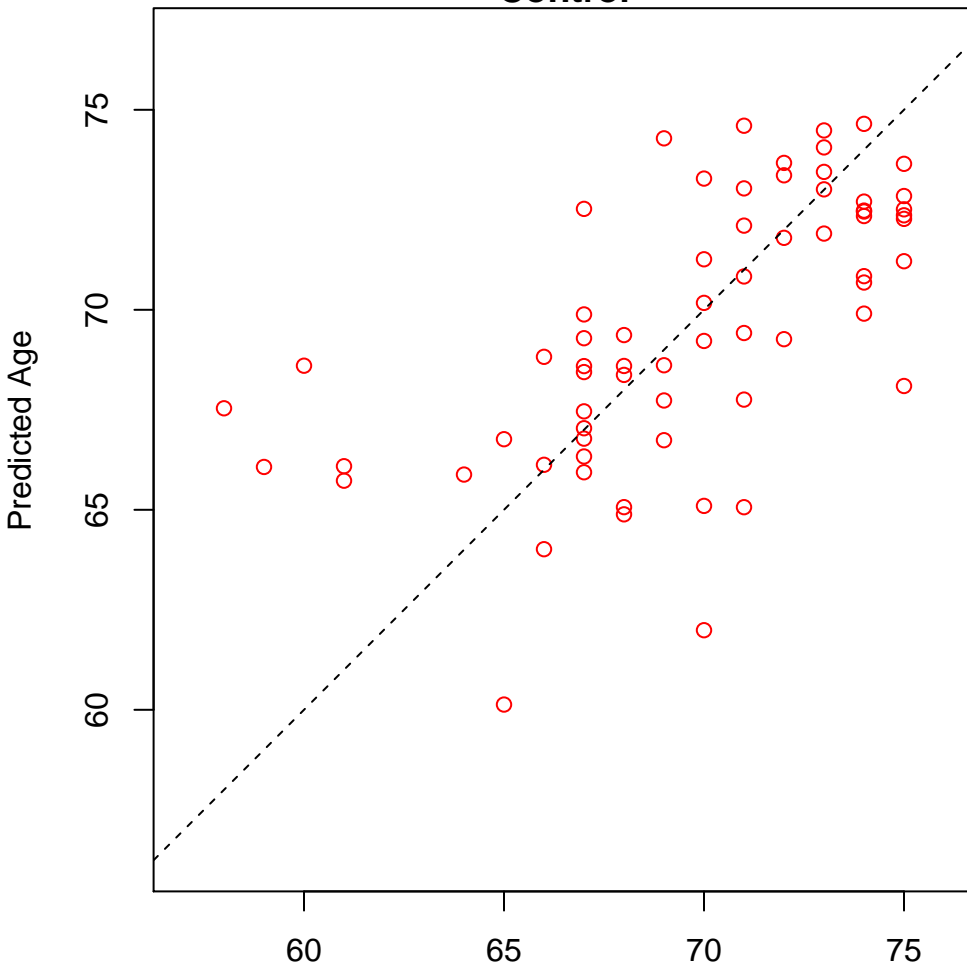


mitochondrial fission (Score: 1.436650)

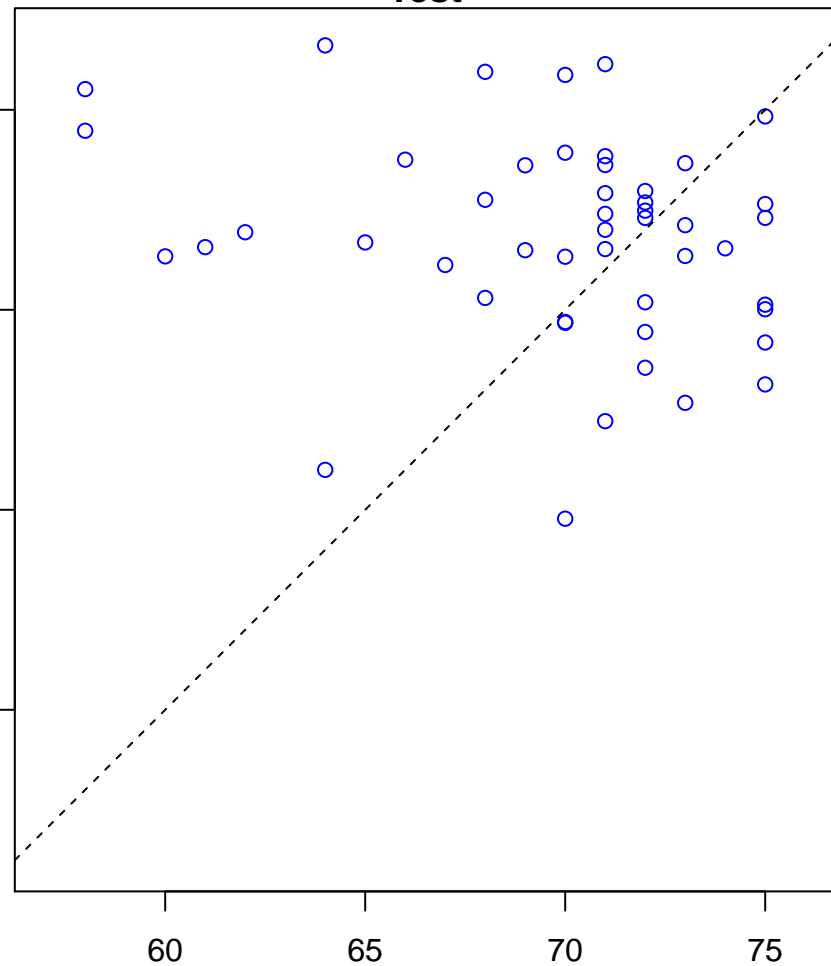


positive regulation of protein secretion (Score: 1.436294)

Control

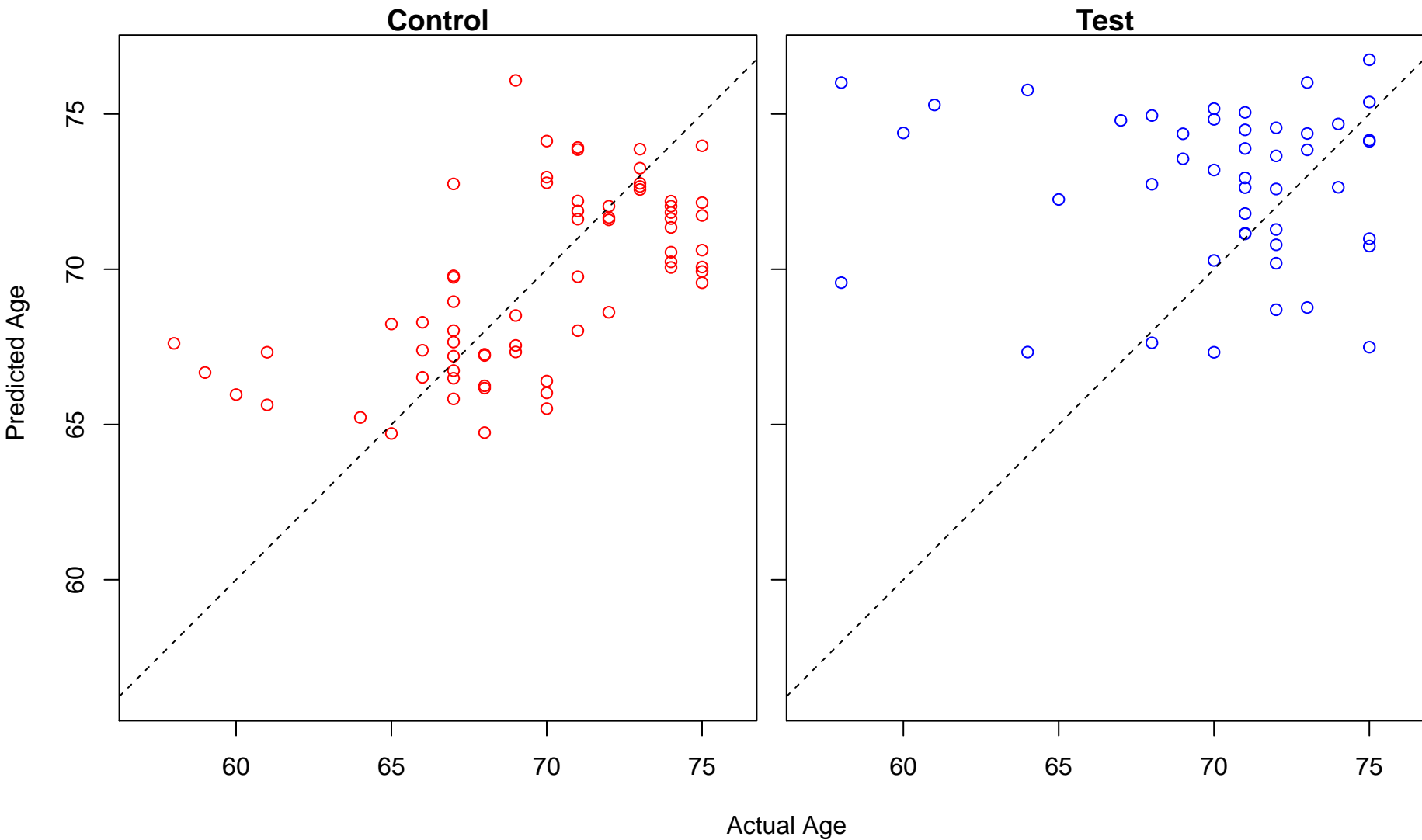


Test

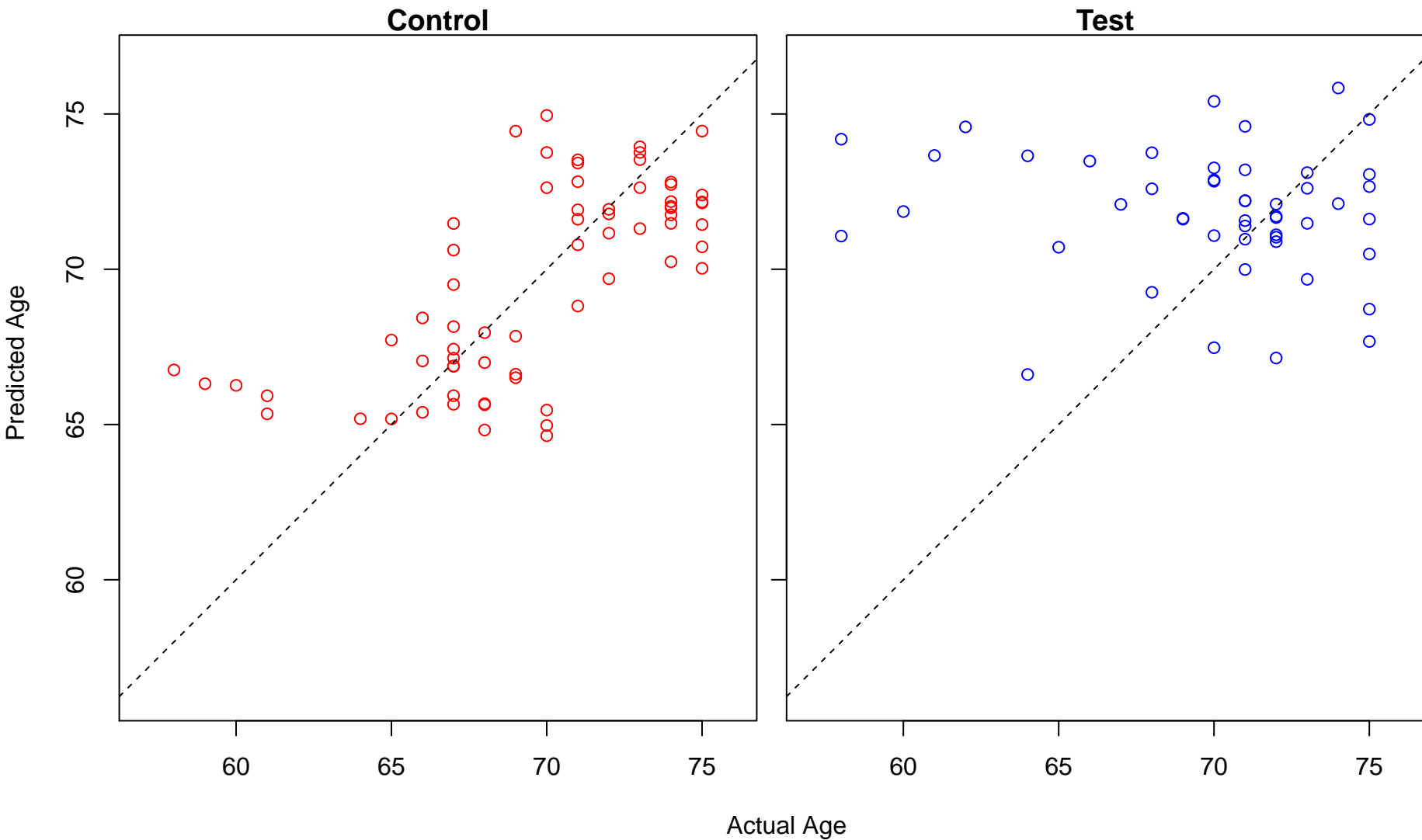


Actual Age

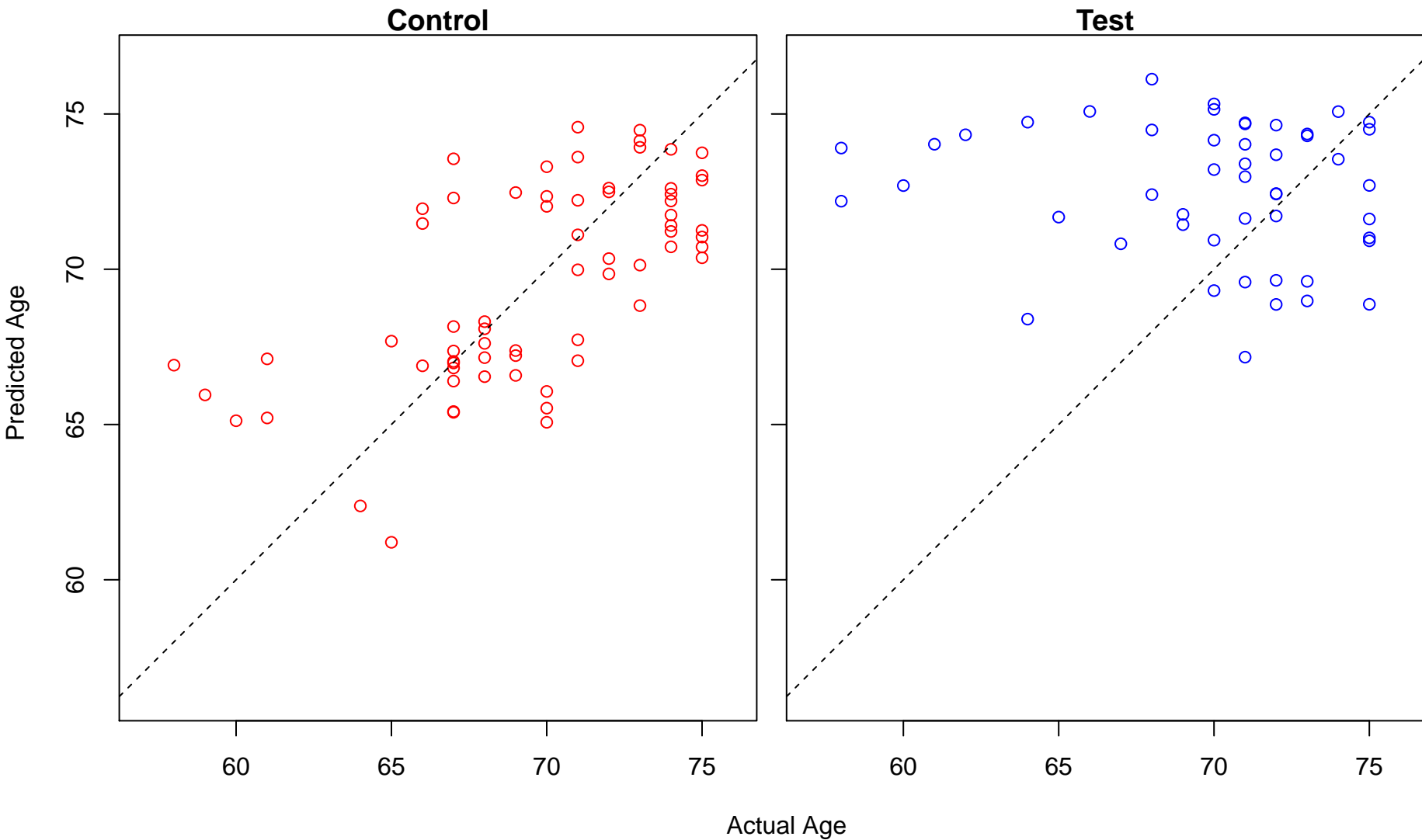
interstrand cross-link repair (Score: 1.436028)



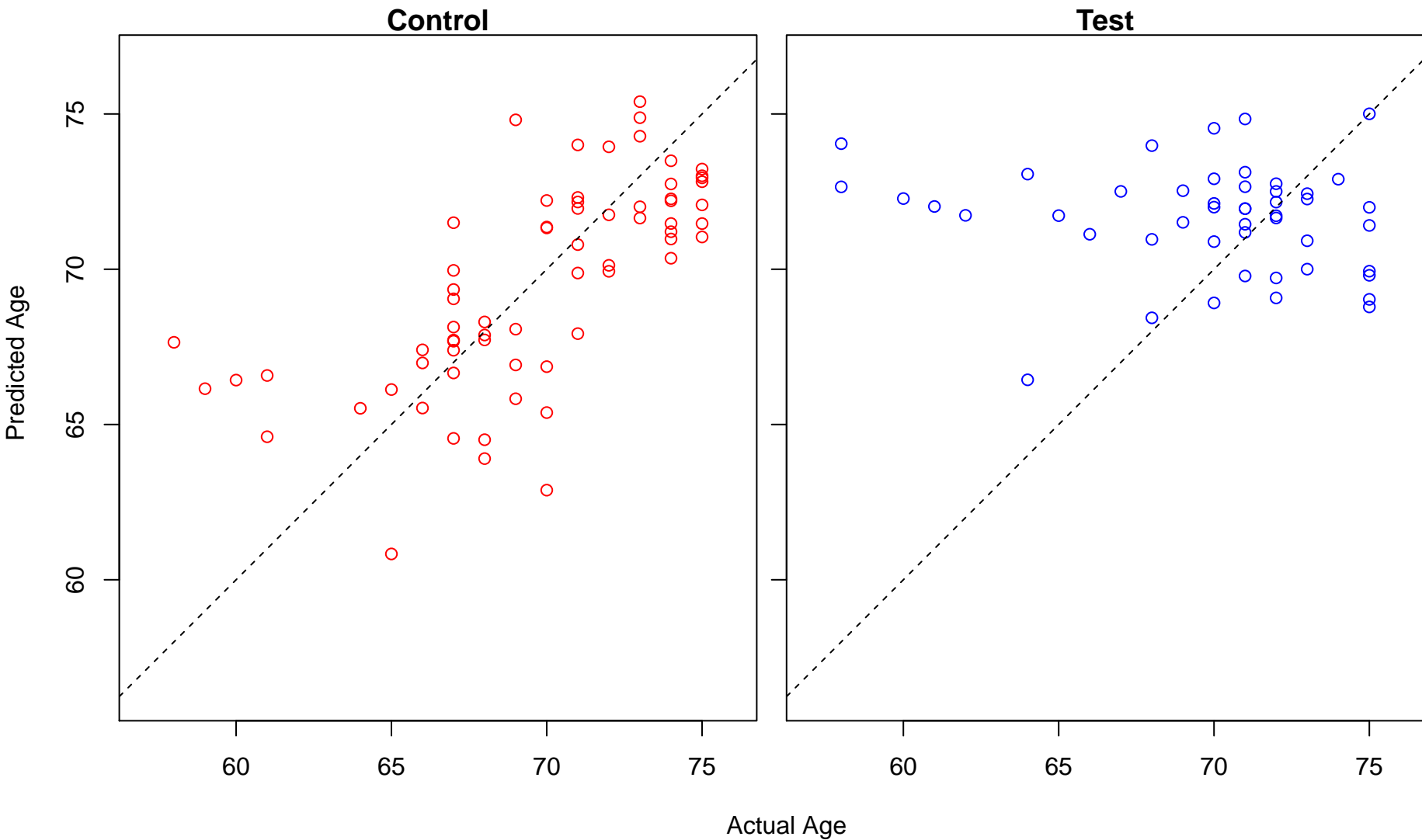
transcription-coupled nucleotide-excision repair (Score: 1.435972)



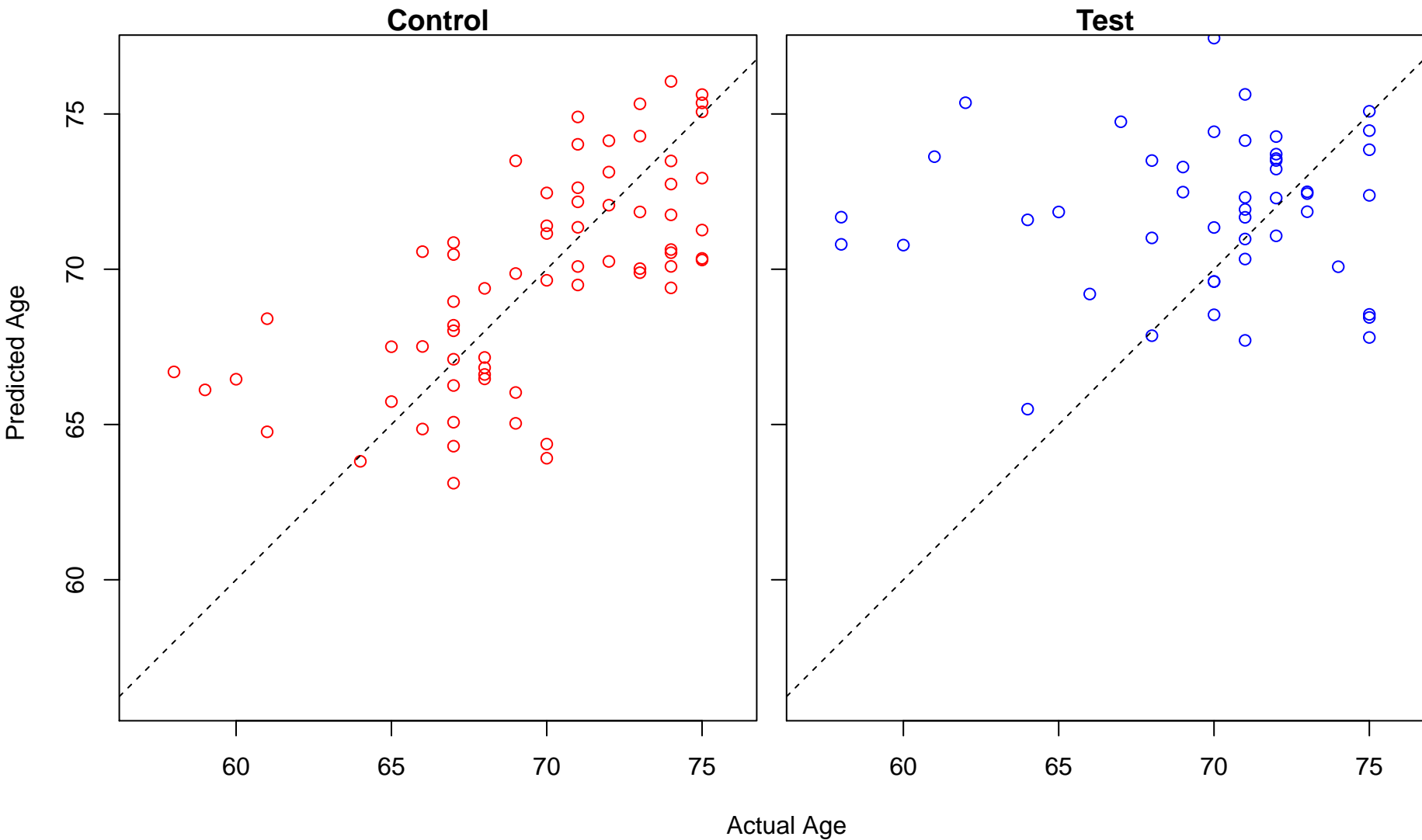
positive regulation of type I interferon production (Score: 1.435735)



positive regulation of secretion by cell (Score: 1.435640)

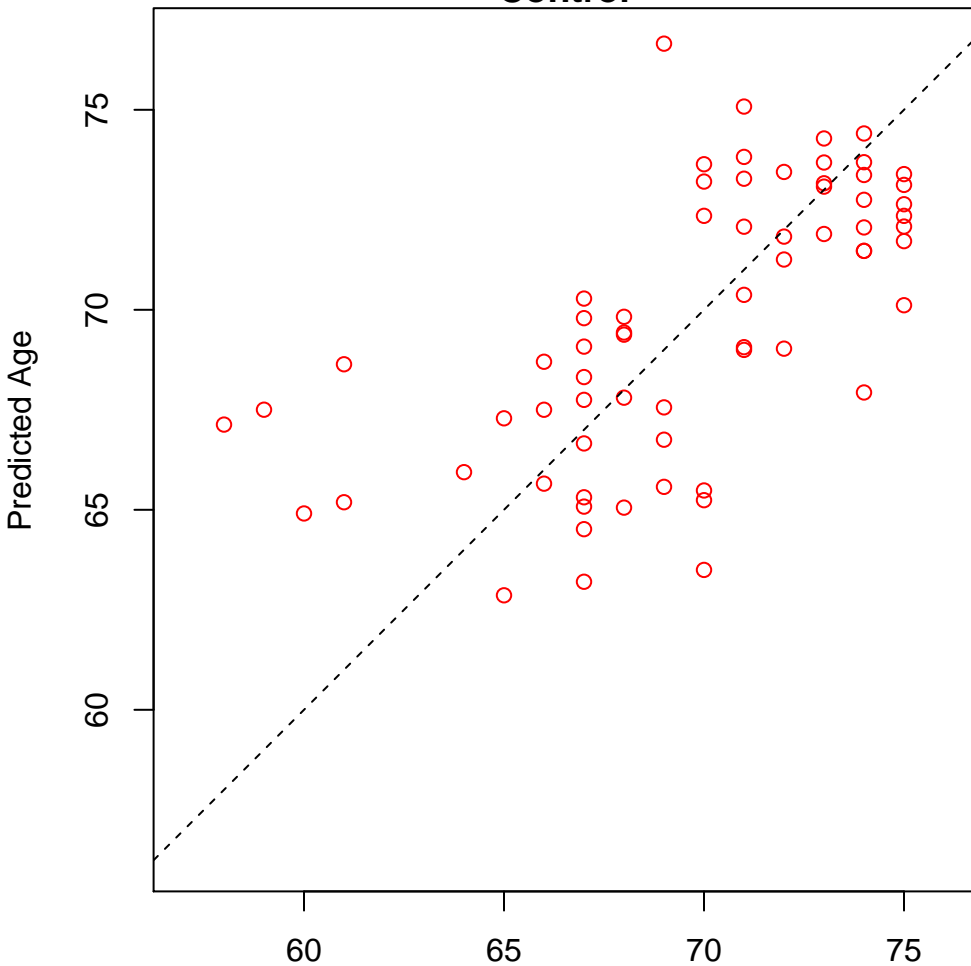


sterol biosynthetic process (Score: 1.434888)

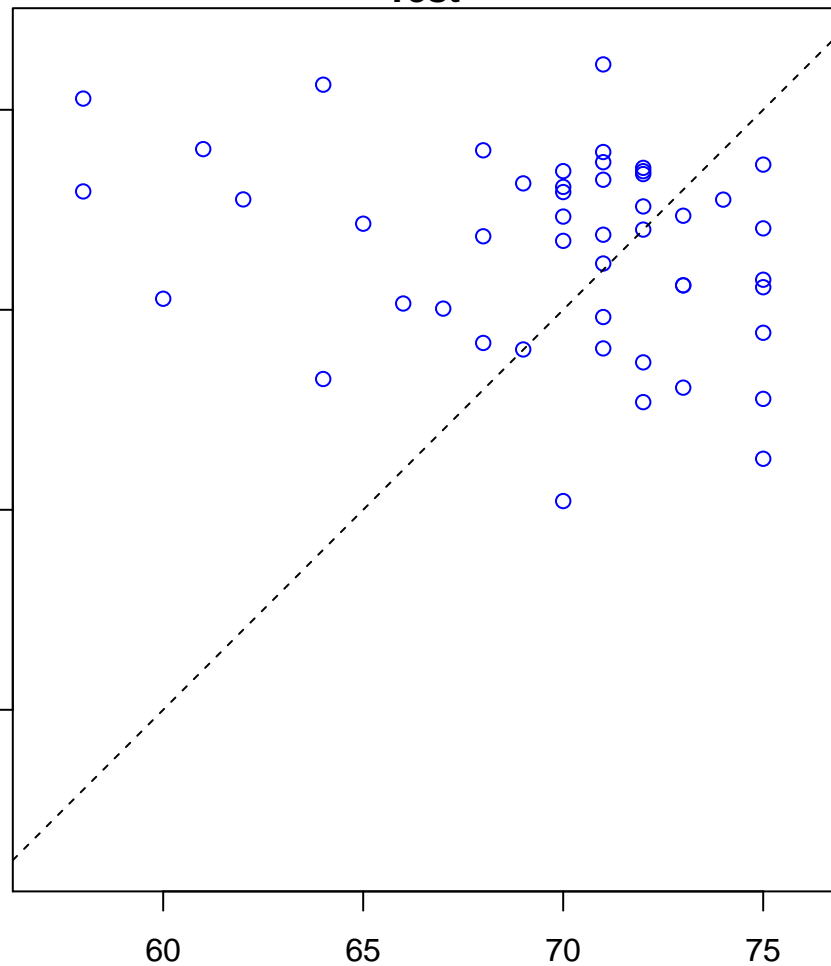


response to molecule of bacterial origin (Score: 1.434776)

Control

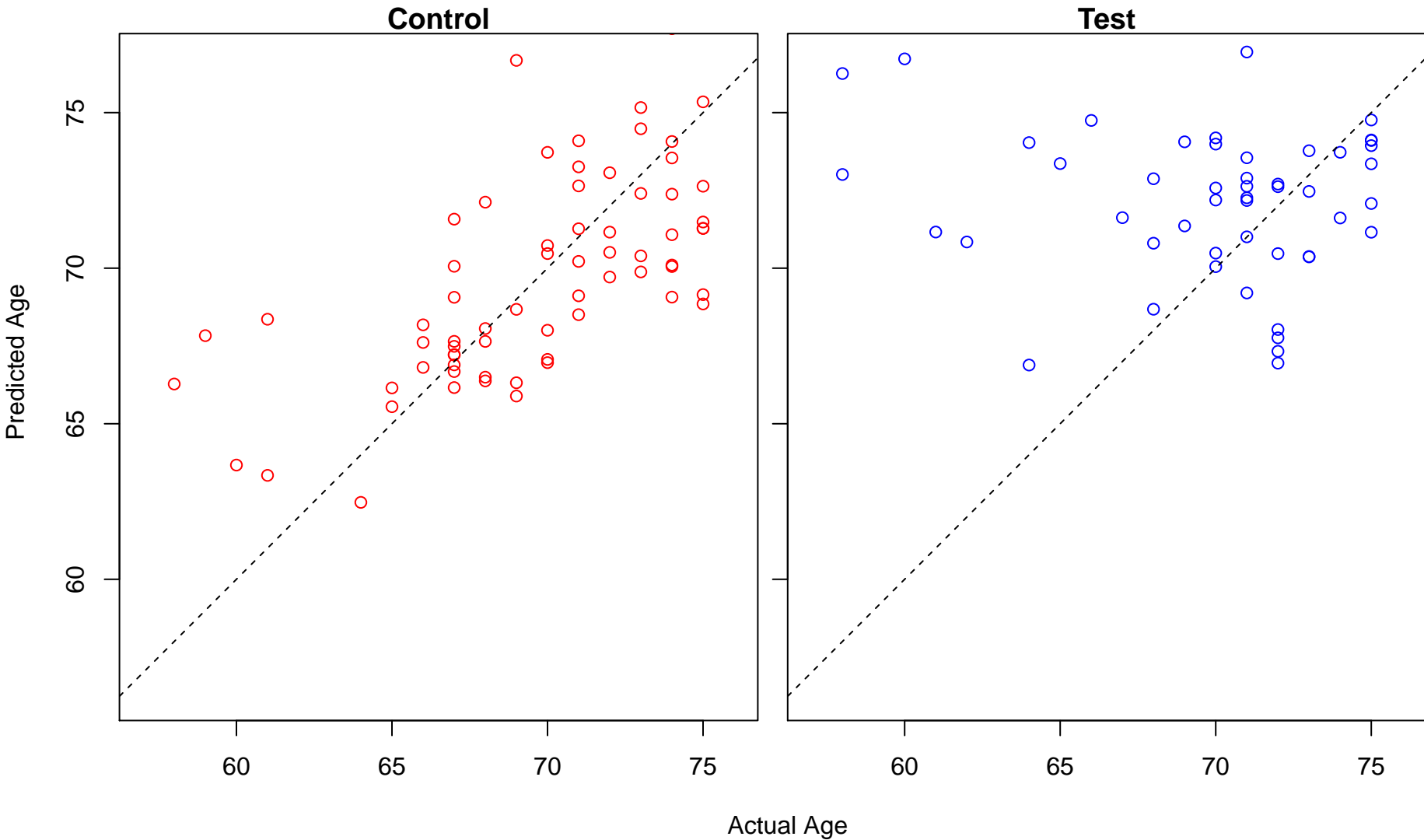


Test

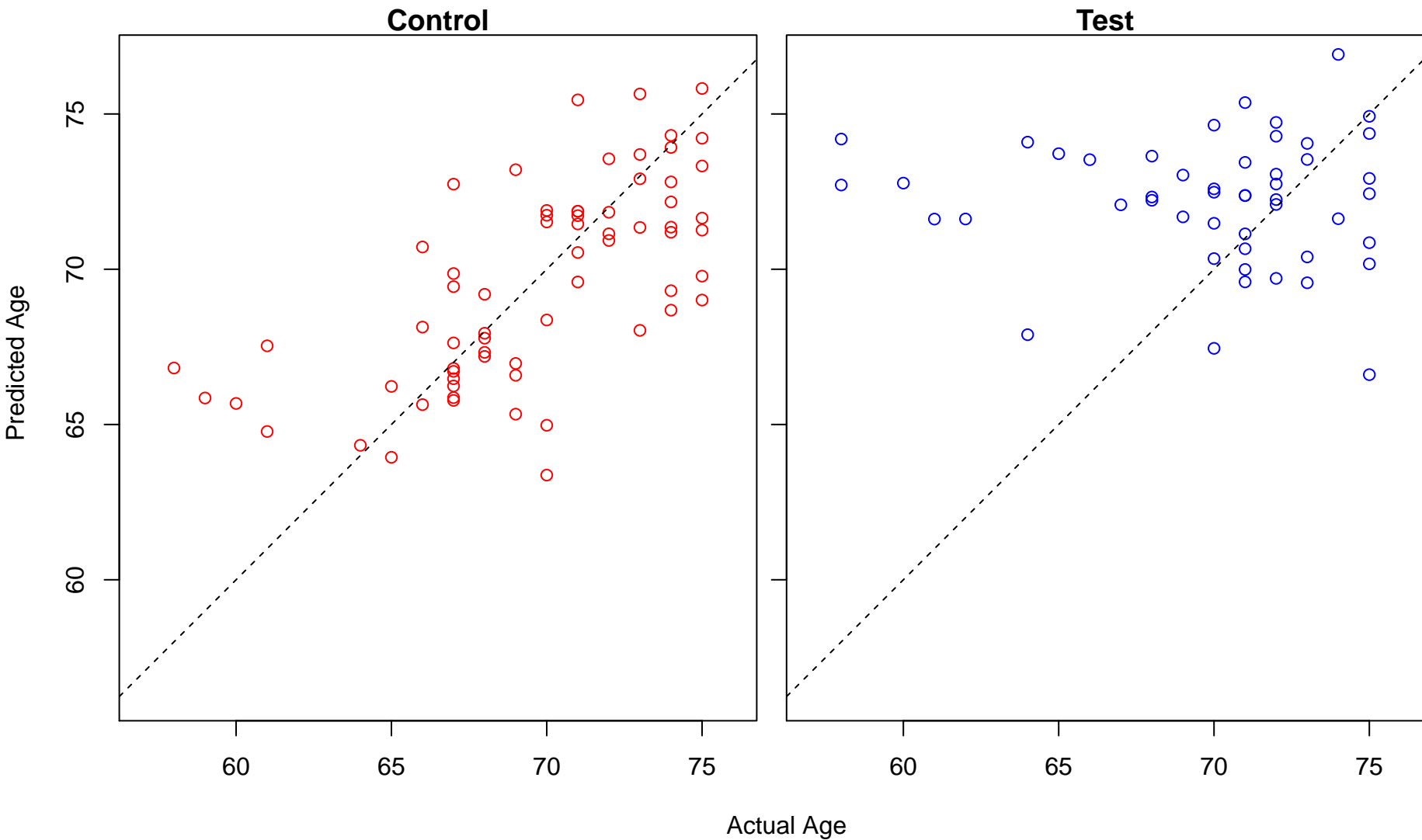


Actual Age

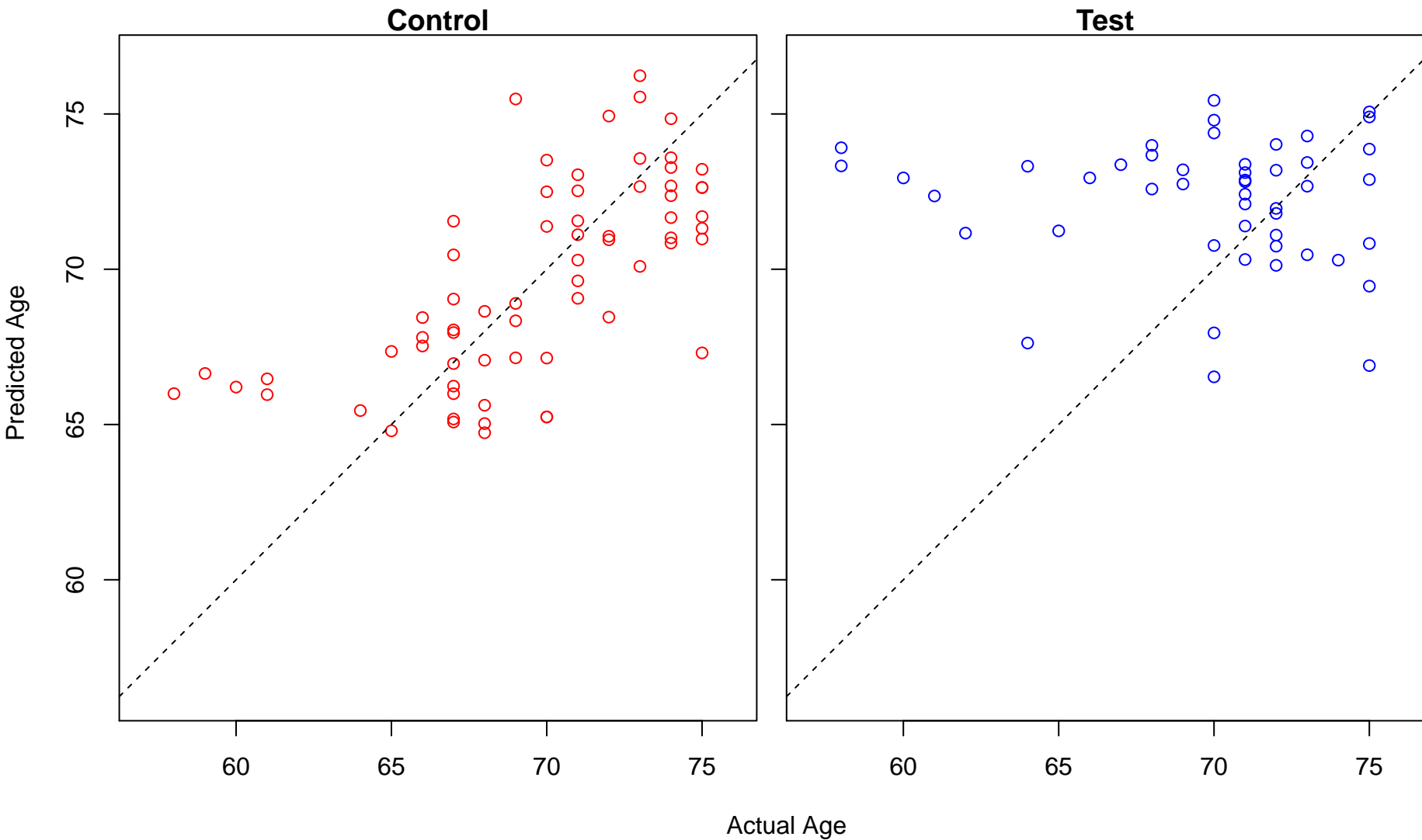
regulation of dendritic spine morphogenesis (Score: 1.434567)



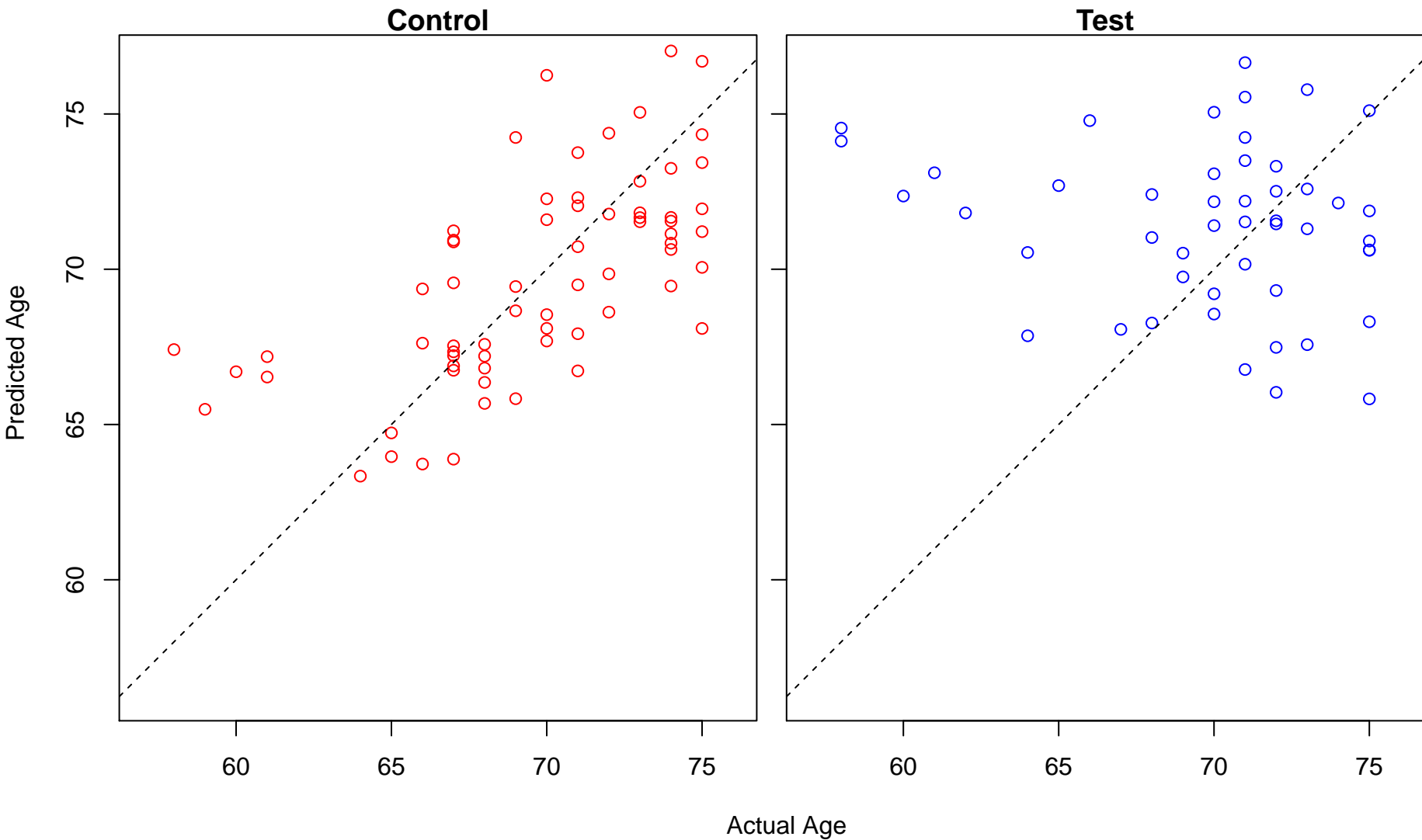
fatty acid metabolic process (Score: 1.434527)



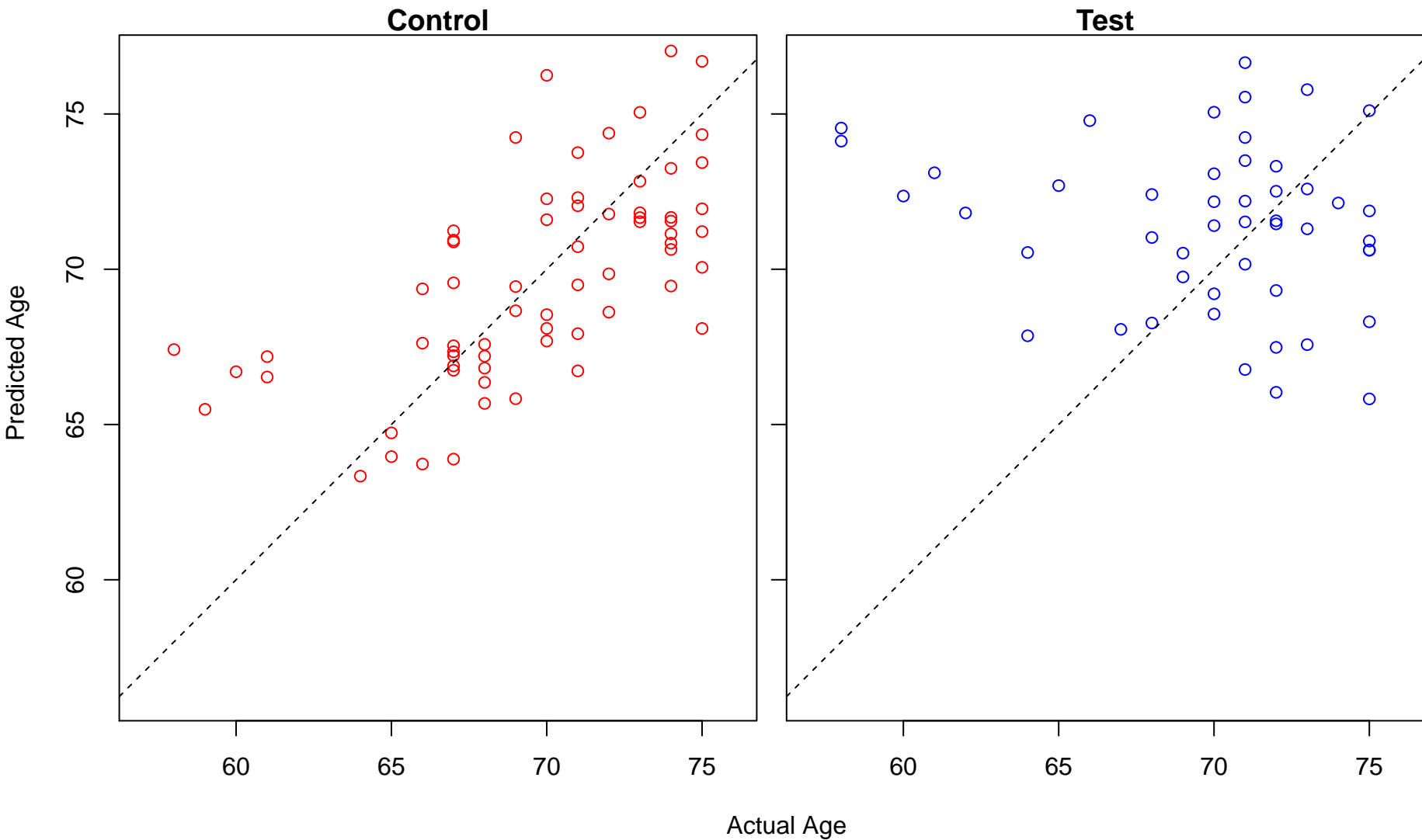
positive T cell selection (Score: 1.434083)



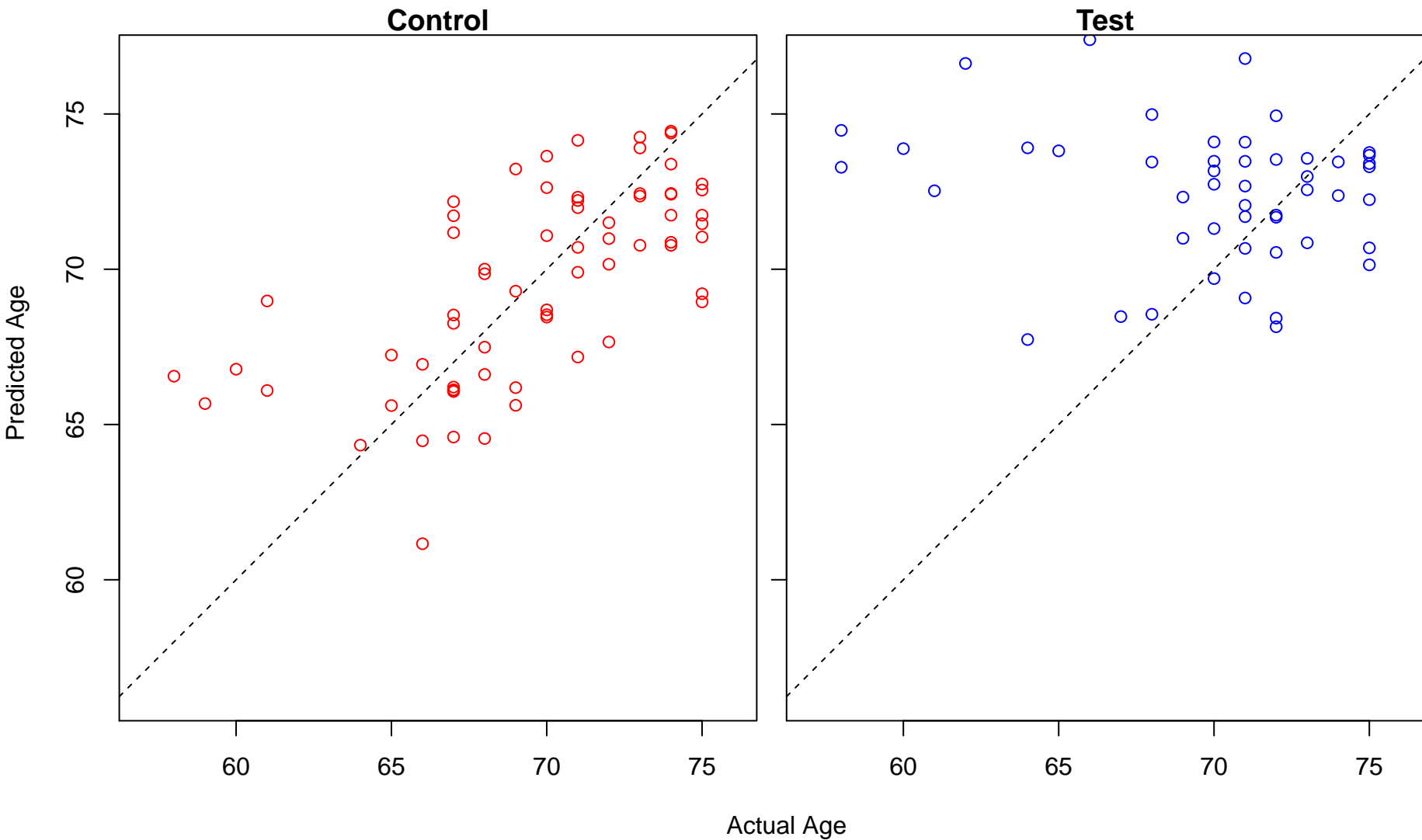
regulation of focal adhesion assembly (Score: 1.433308)



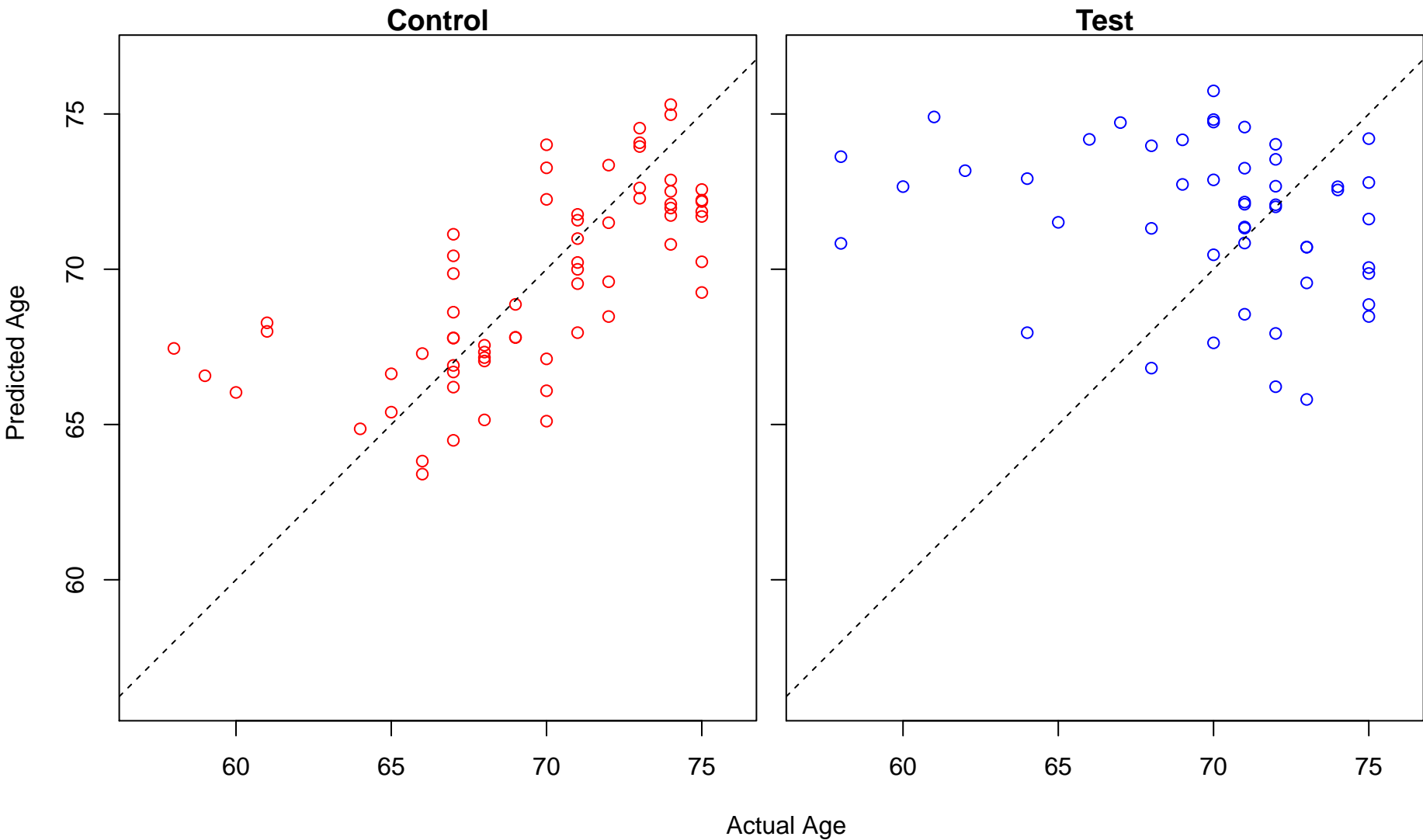
regulation of cell-substrate junction assembly (Score: 1.433308)



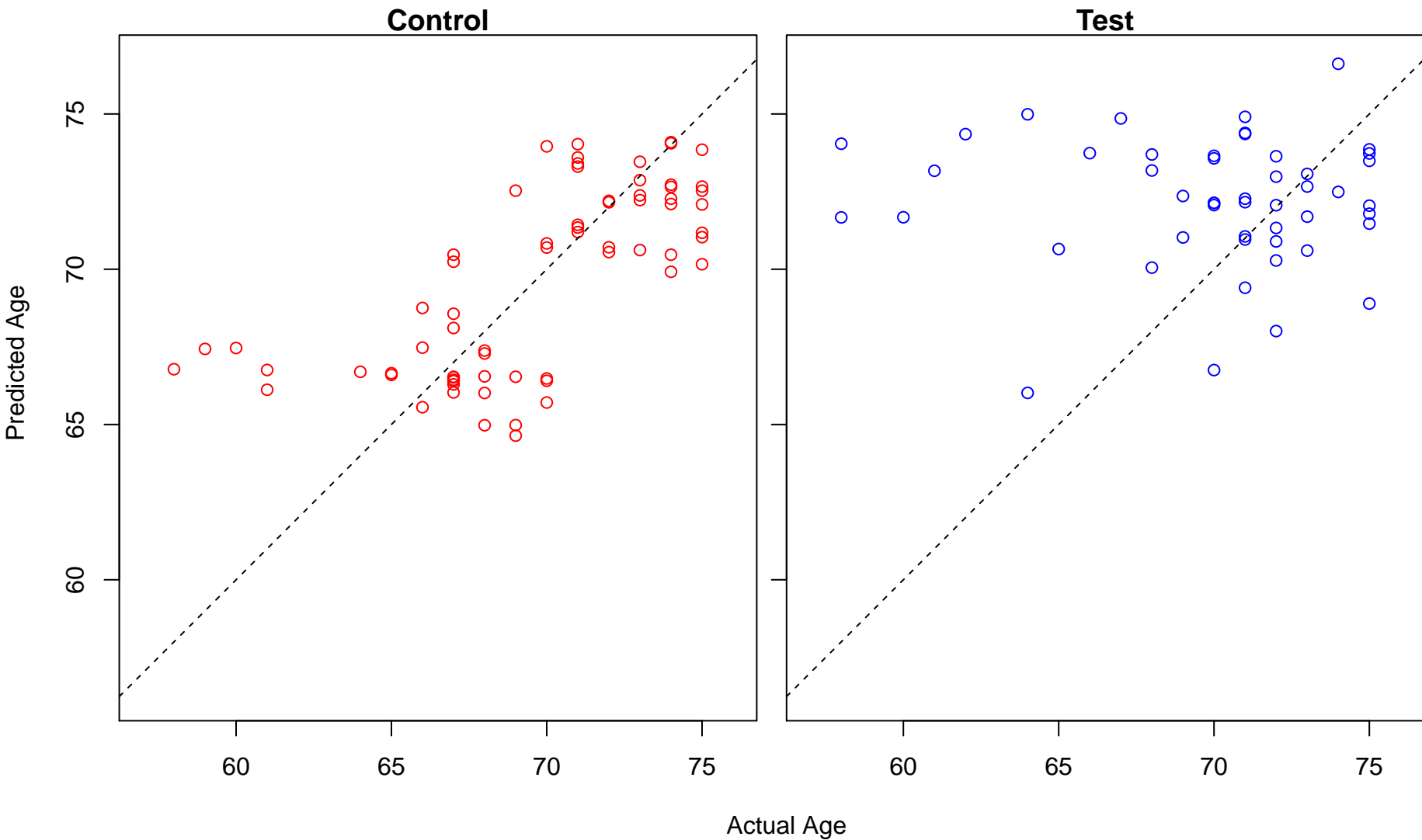
histone H3-K4 trimethylation (Score: 1.432695)



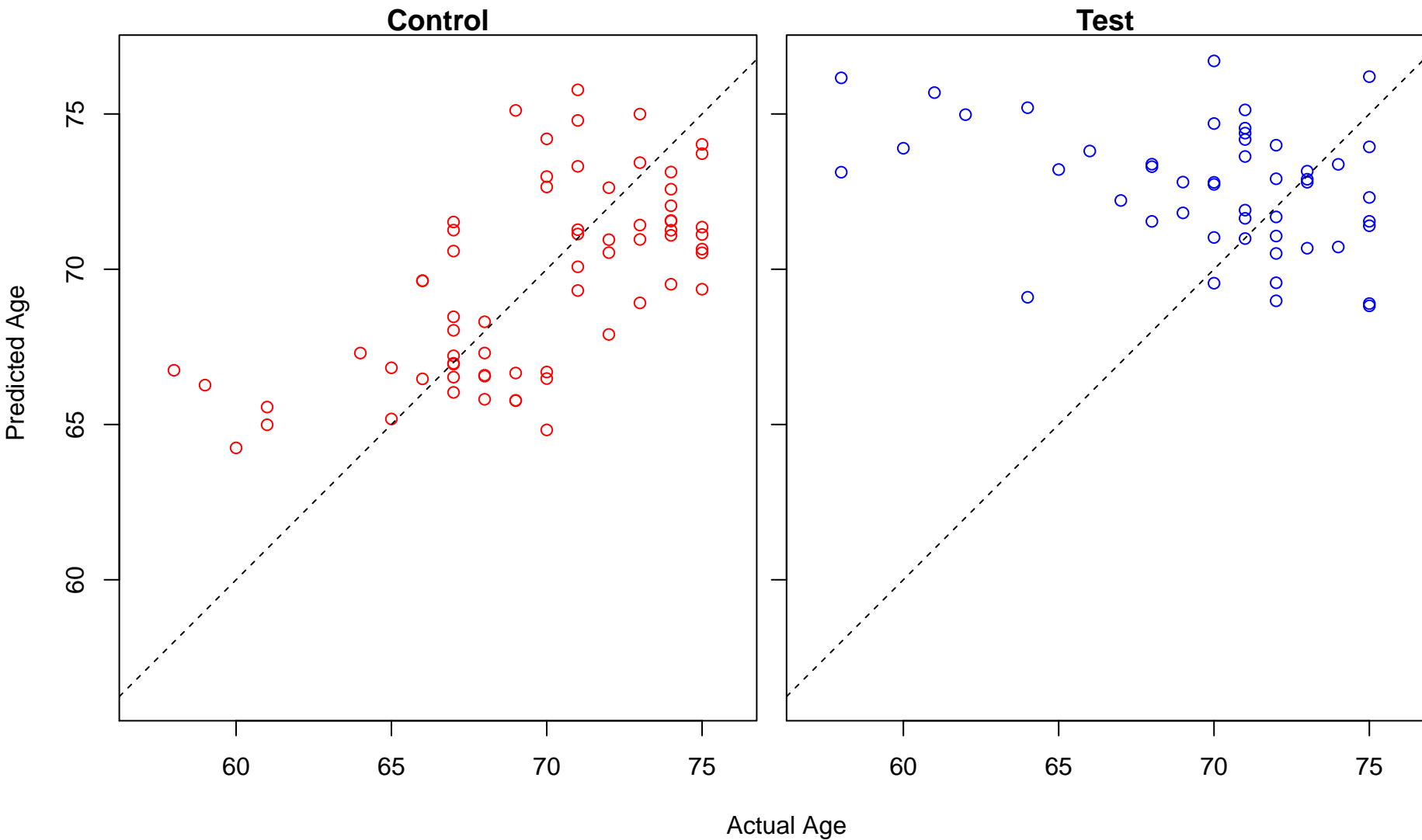
ve immune response based on somatic recombination of immune receptors built from immunoglobulin su



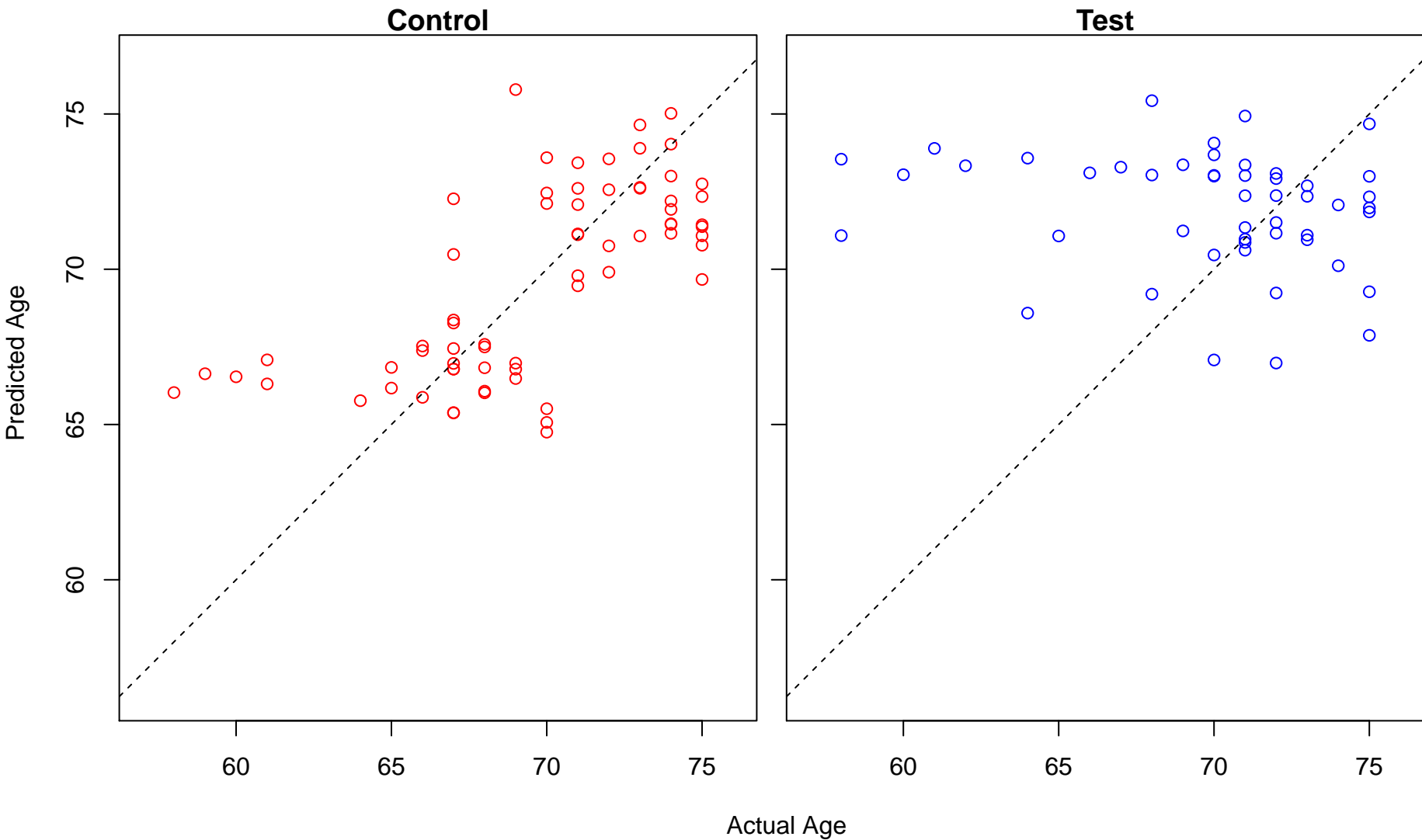
positive regulation of smooth muscle cell migration (Score: 1.431993)



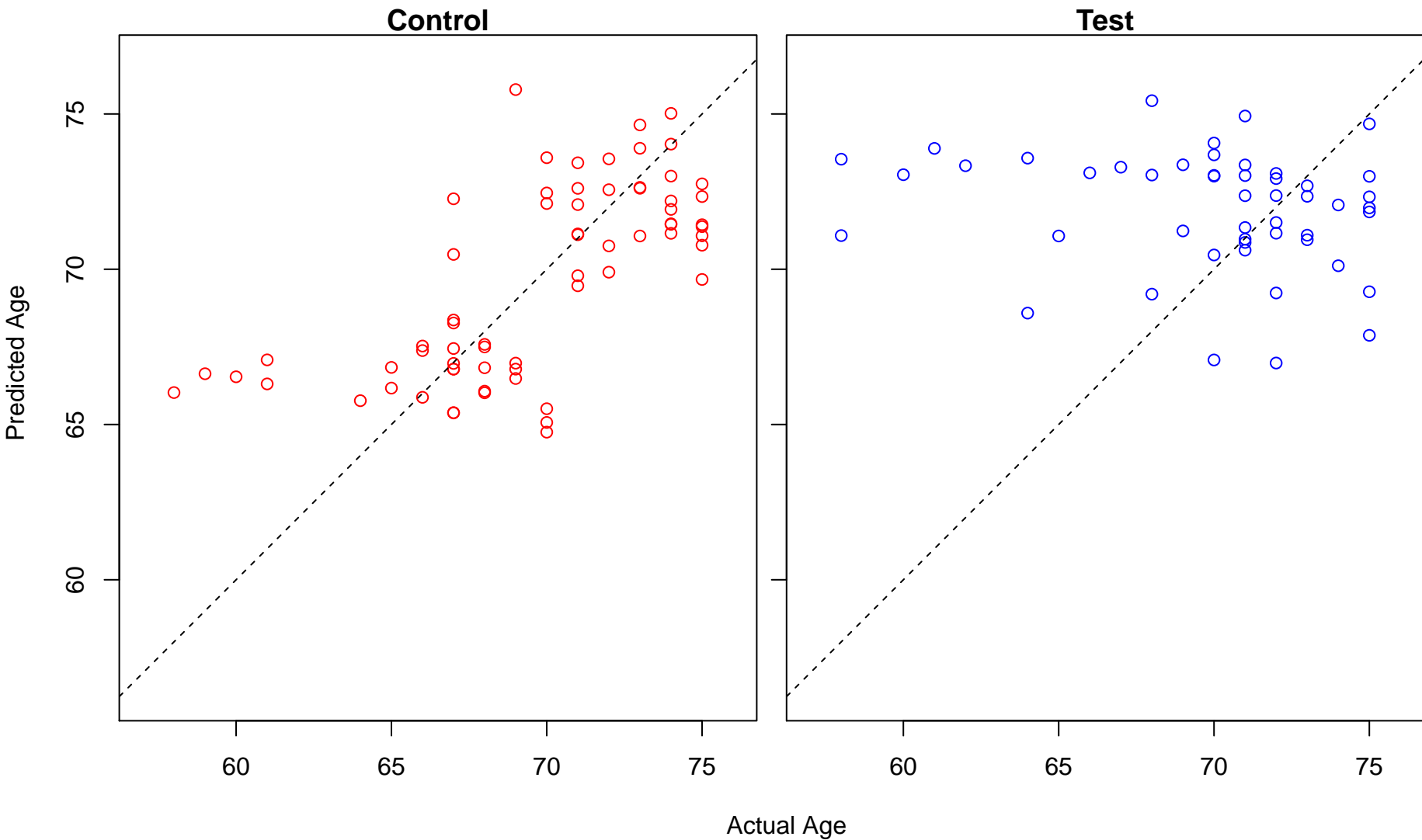
fluid transport (Score: 1.431602)



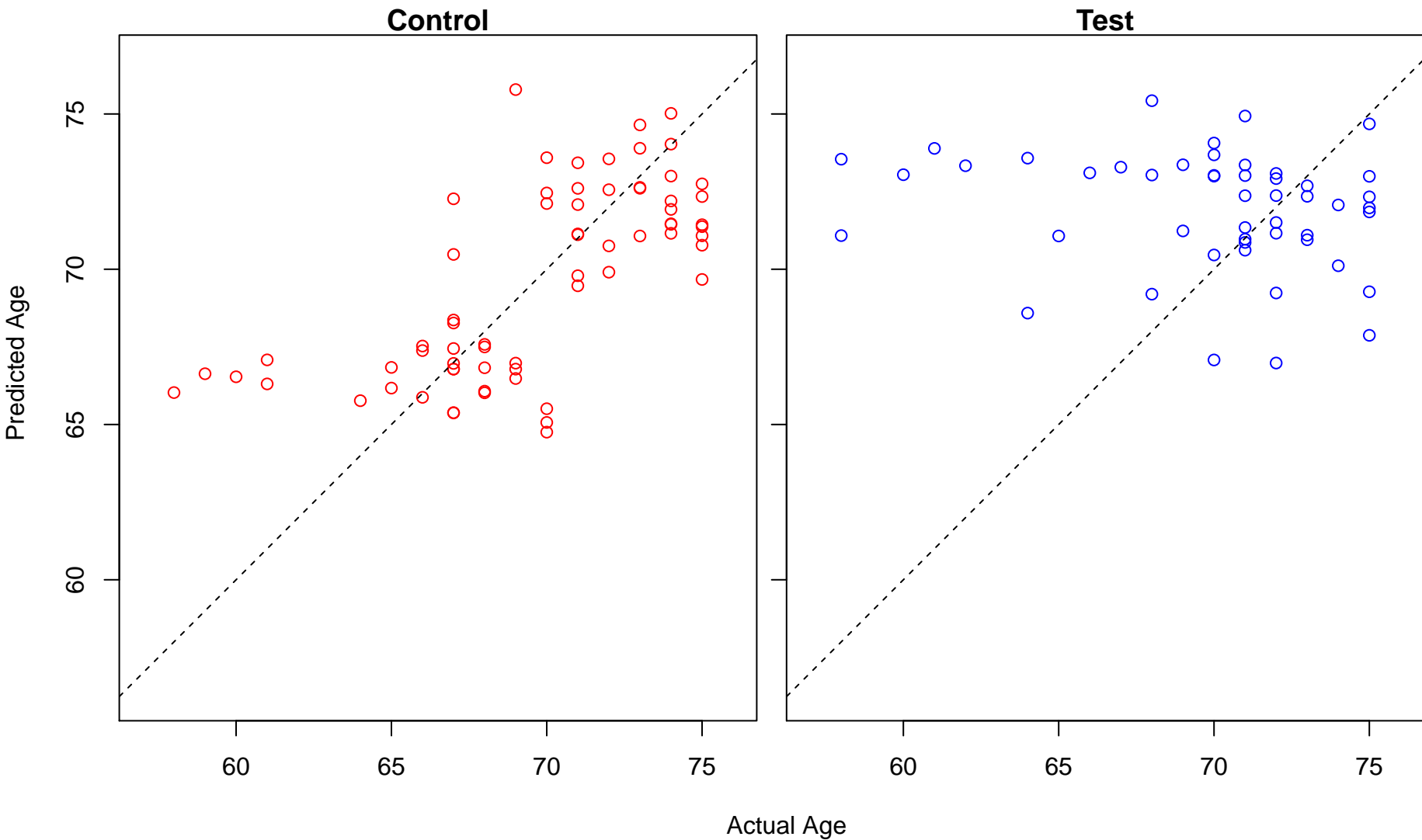
mitotic spindle assembly checkpoint (Score: 1.431157)



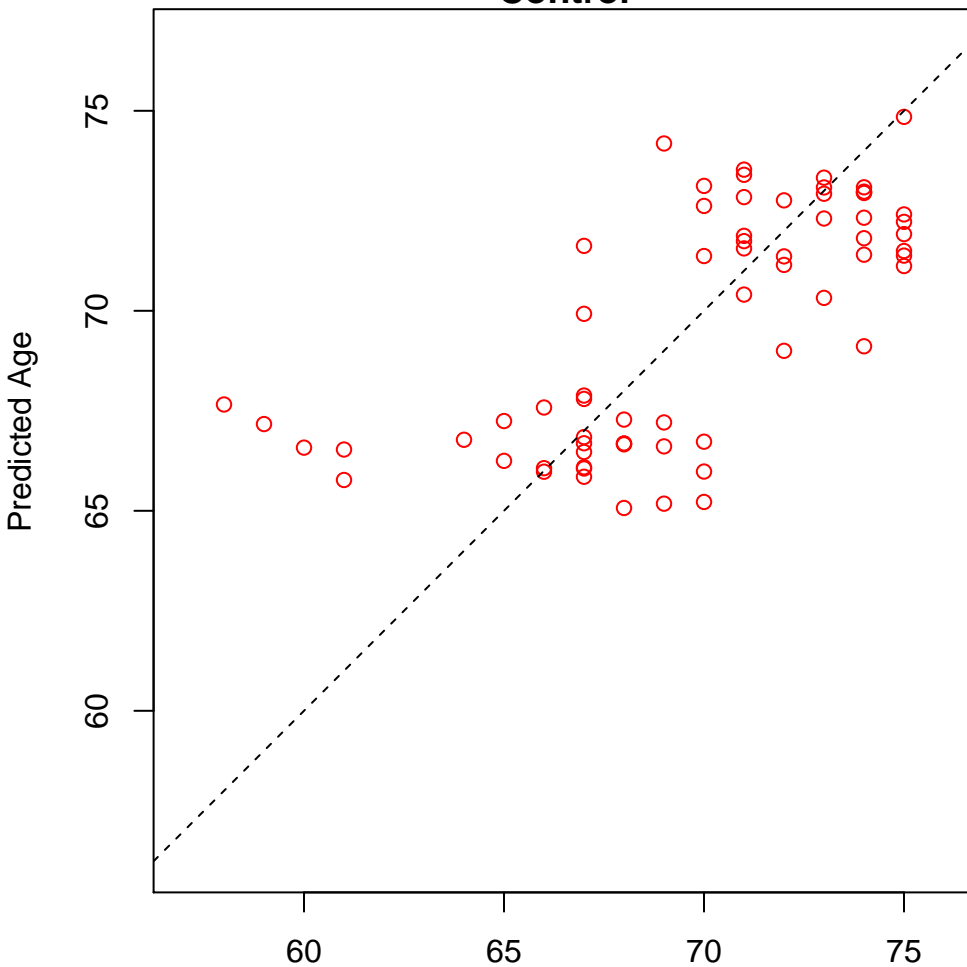
spindle assembly checkpoint (Score: 1.431157)



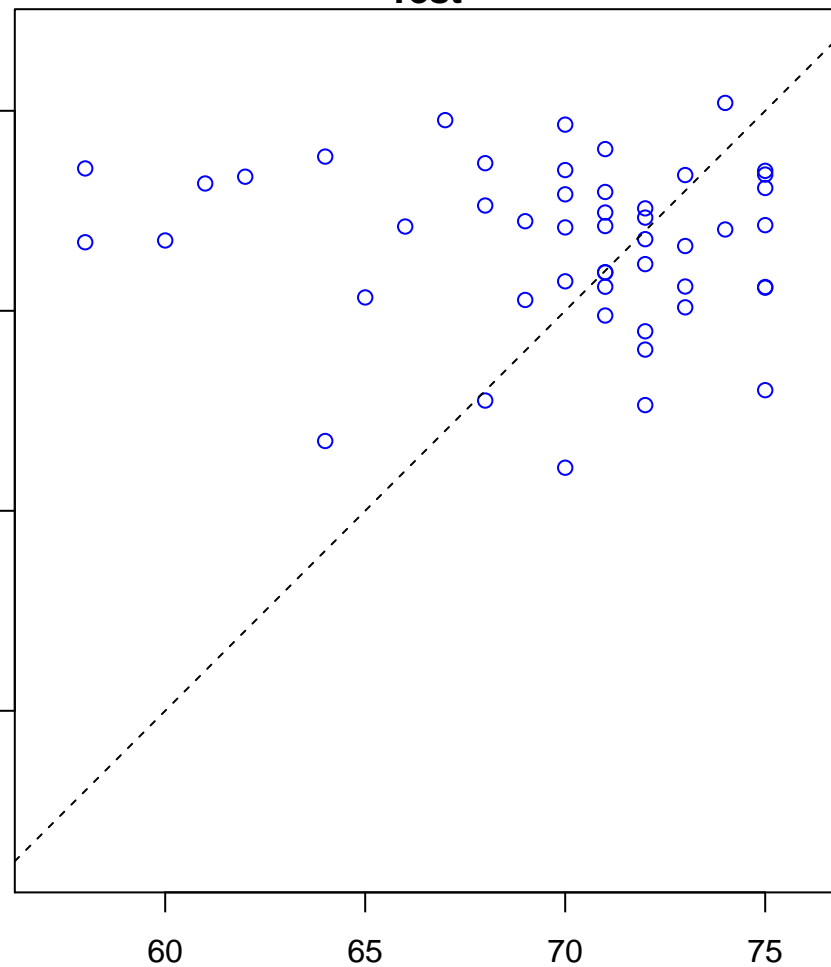
negative regulation of ubiquitin protein ligase activity (Score: 1.431157)



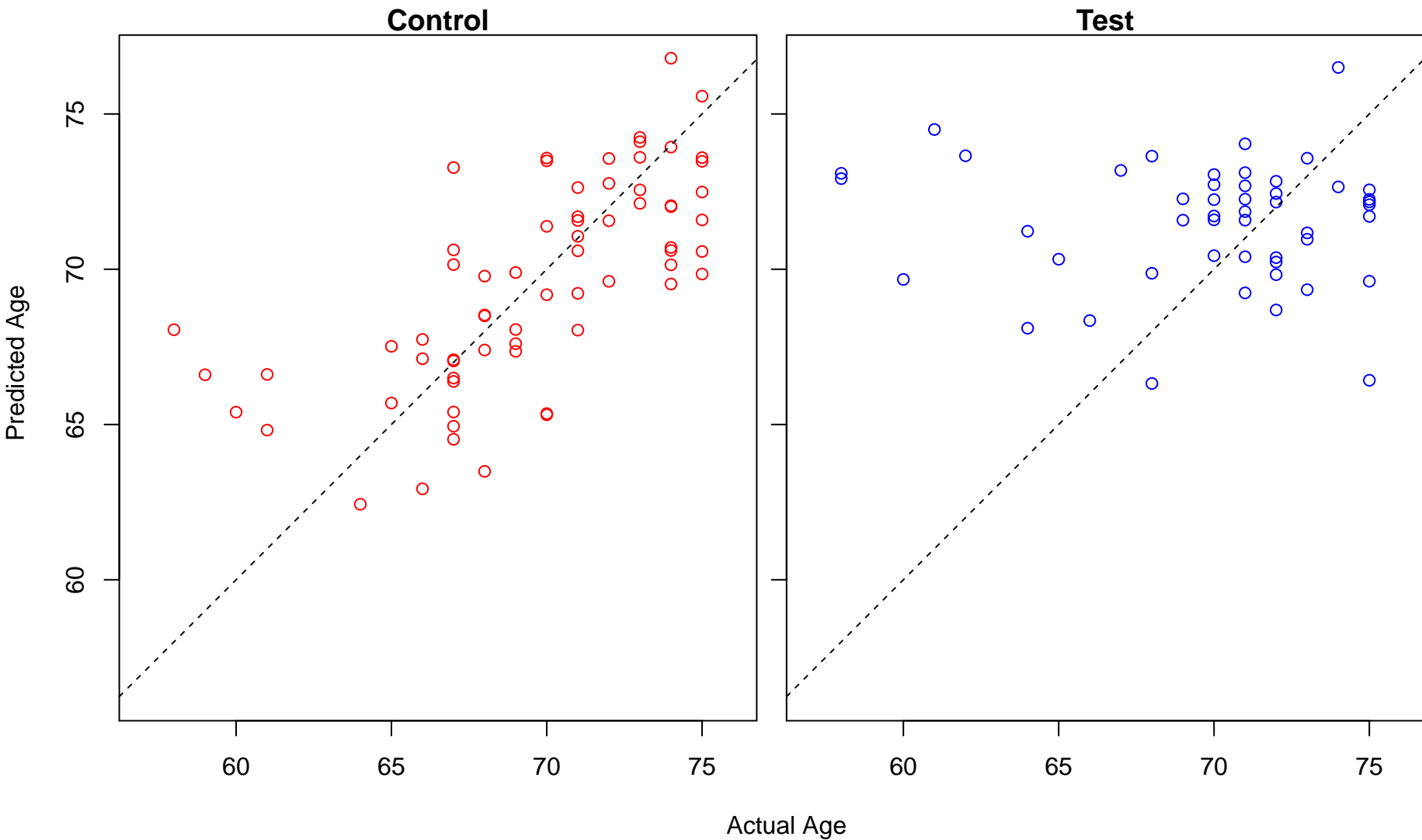
Control



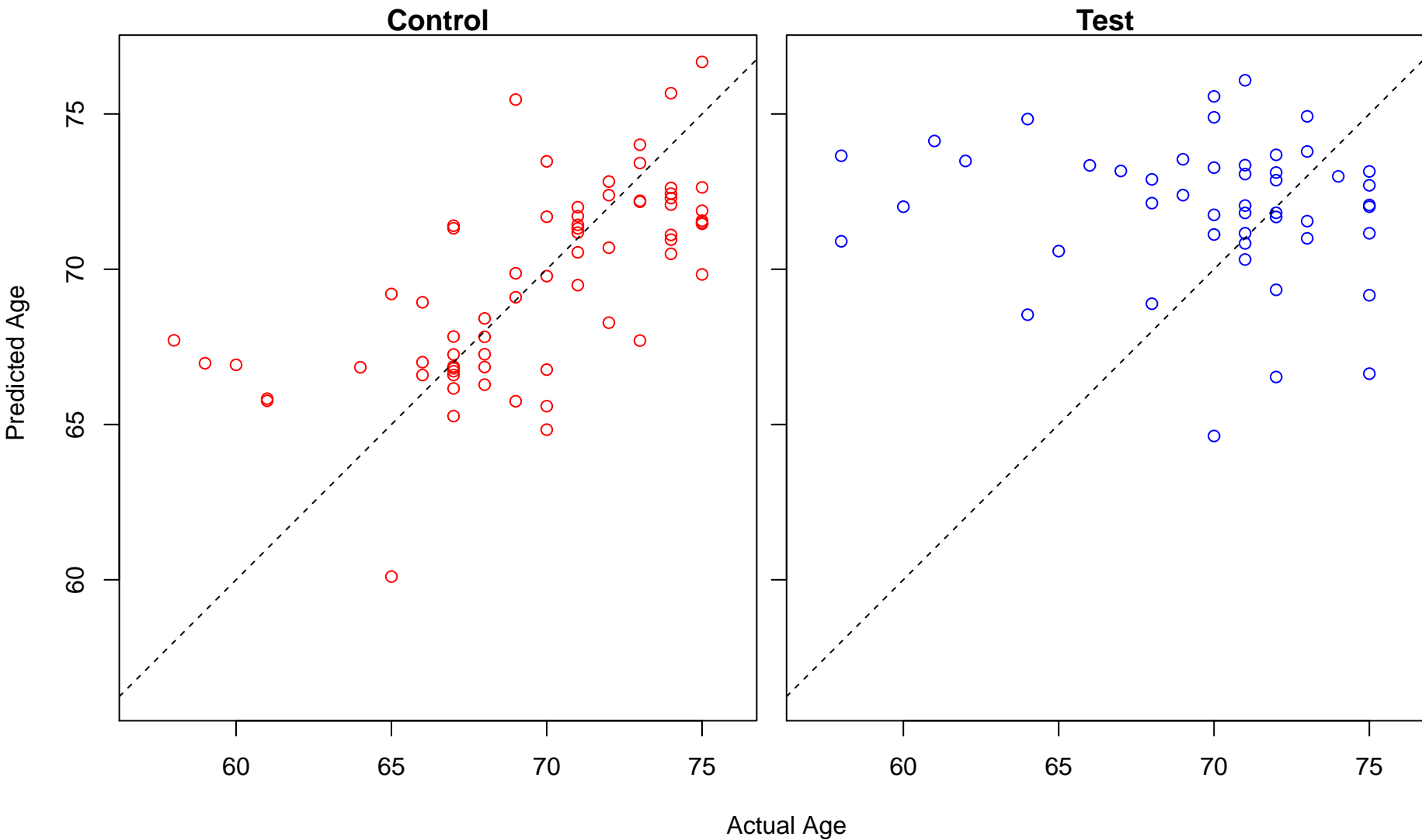
Test



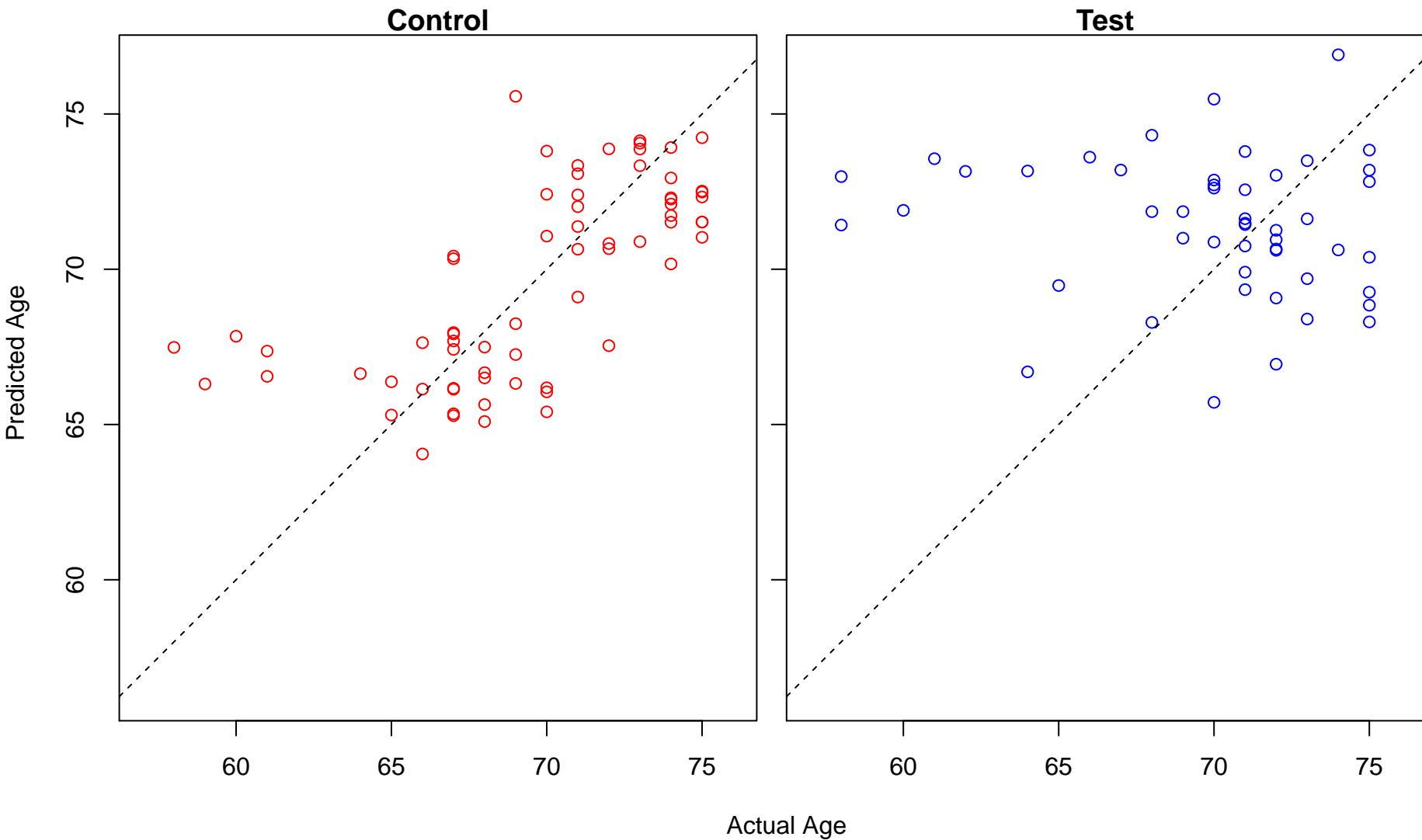
heterotypic cell-cell adhesion (Score: 1.430006)



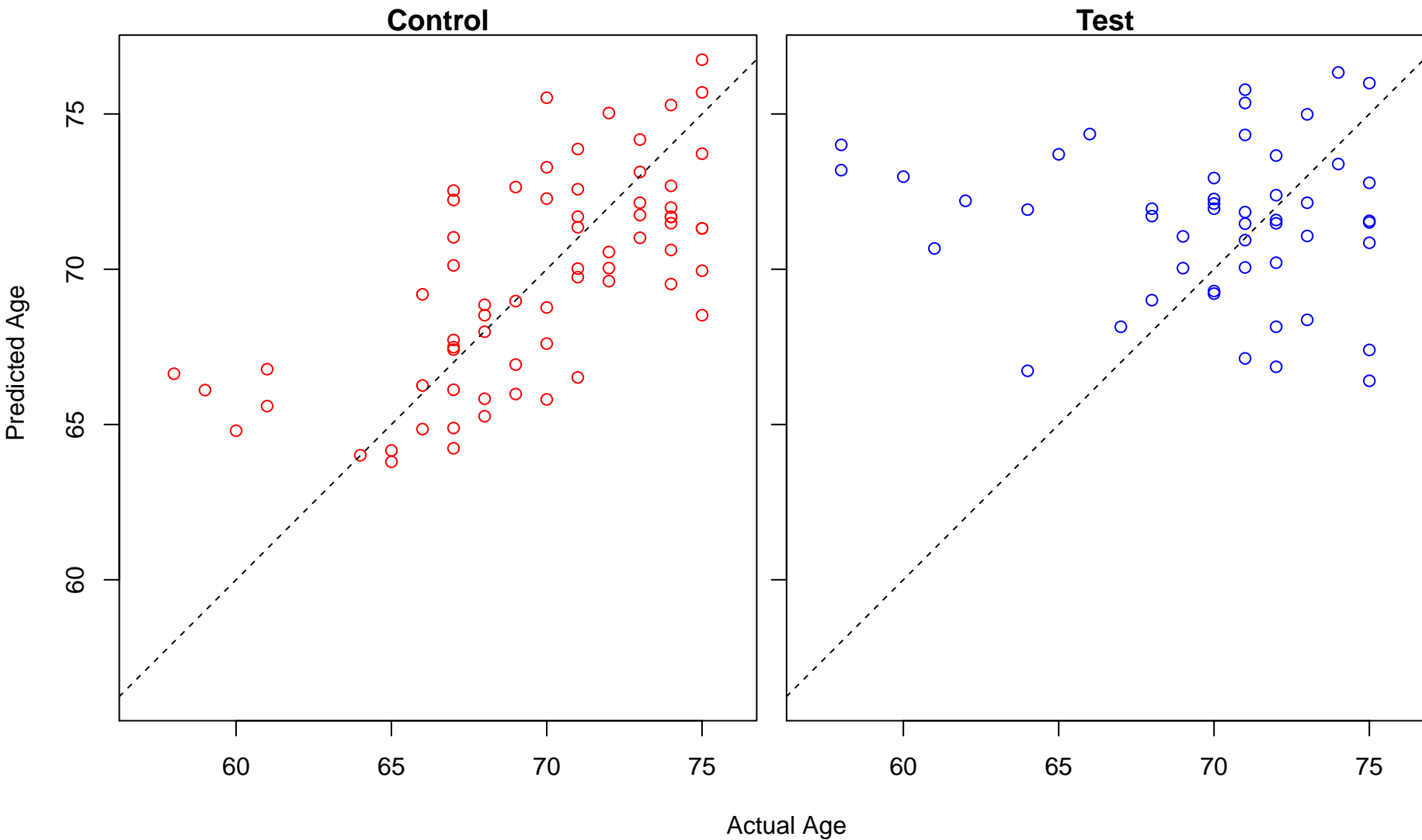
tRNA aminoacylation for protein translation (Score: 1.429374)



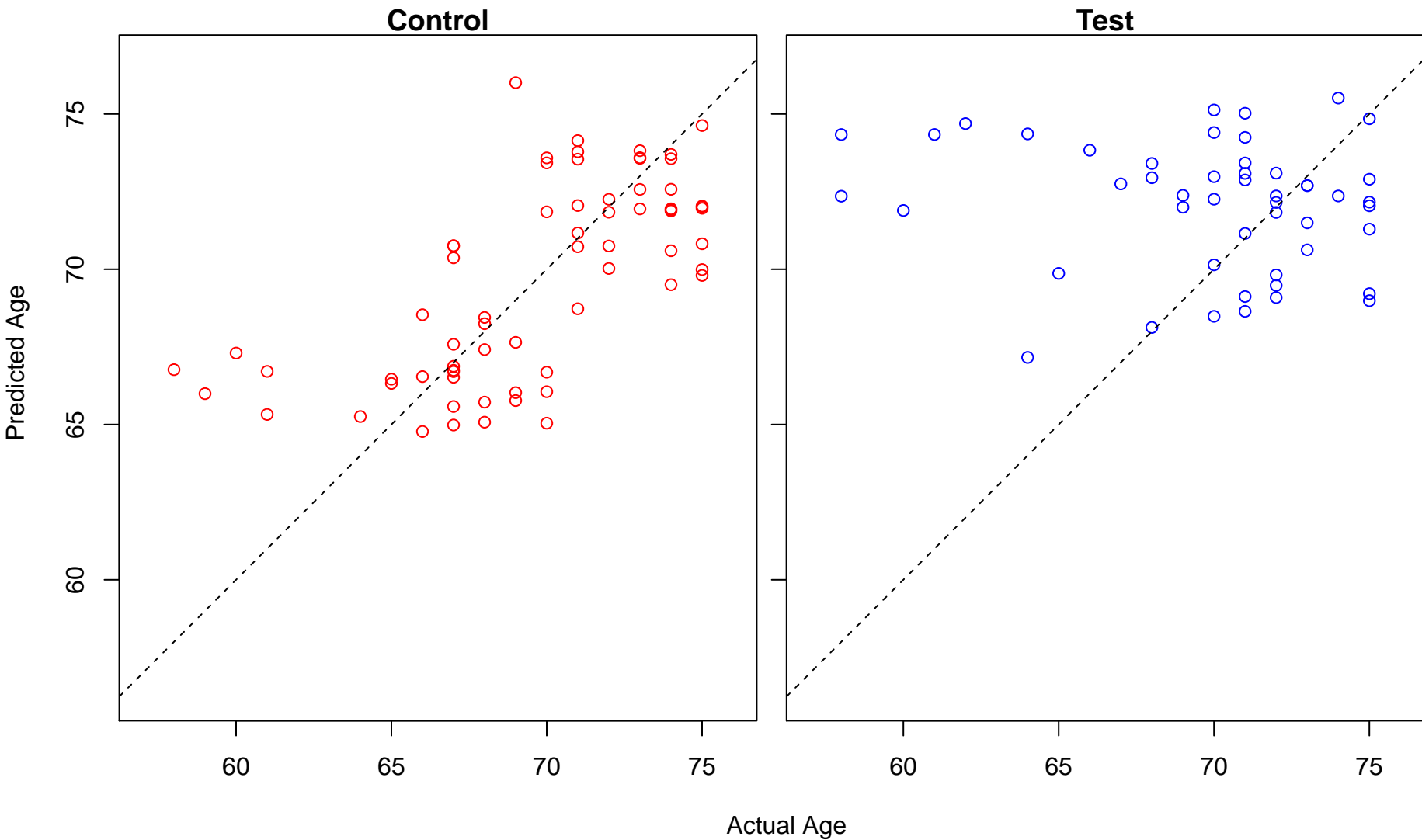
leukocyte chemotaxis (Score: 1.429259)



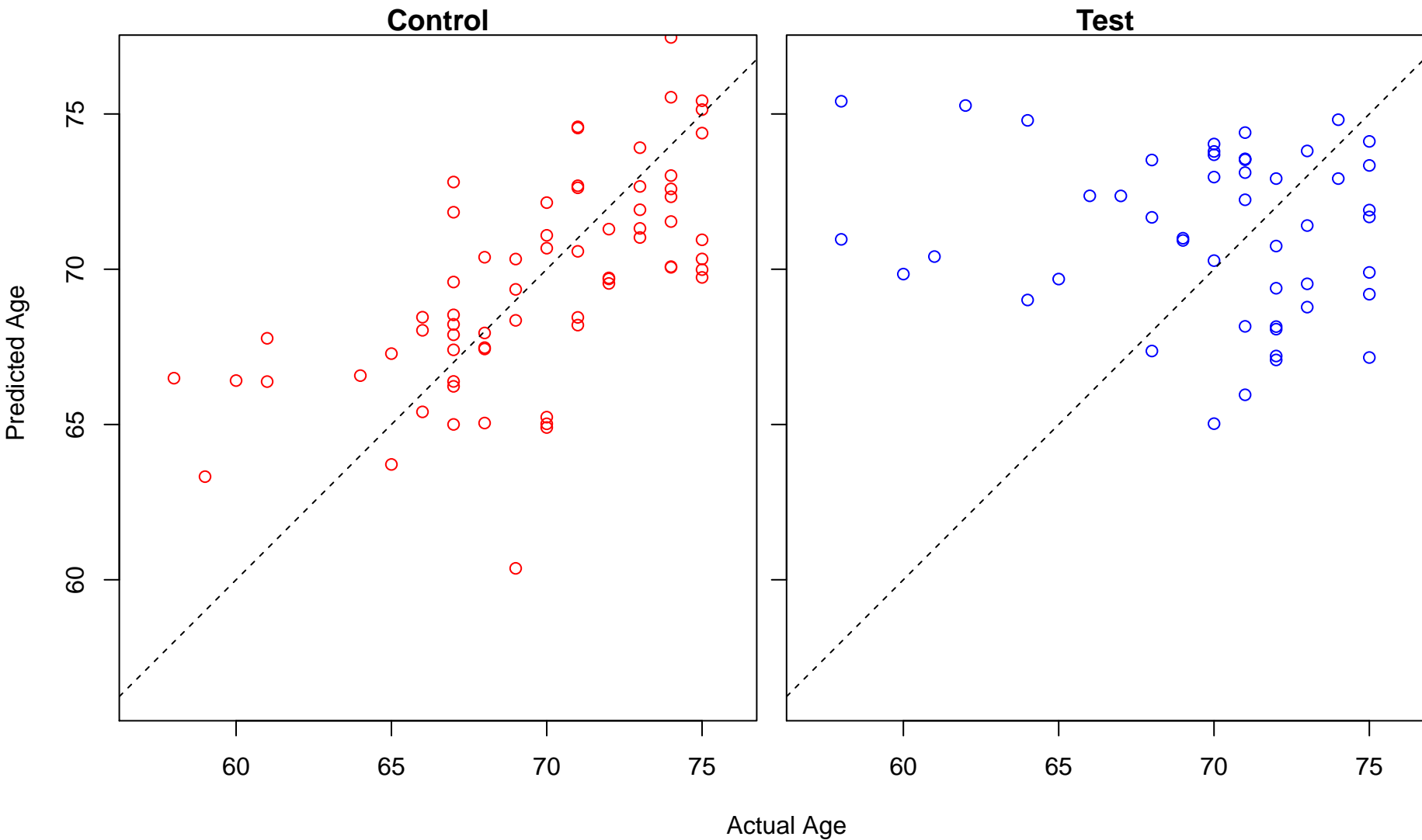
regulation of cell-matrix adhesion (Score: 1.428904)



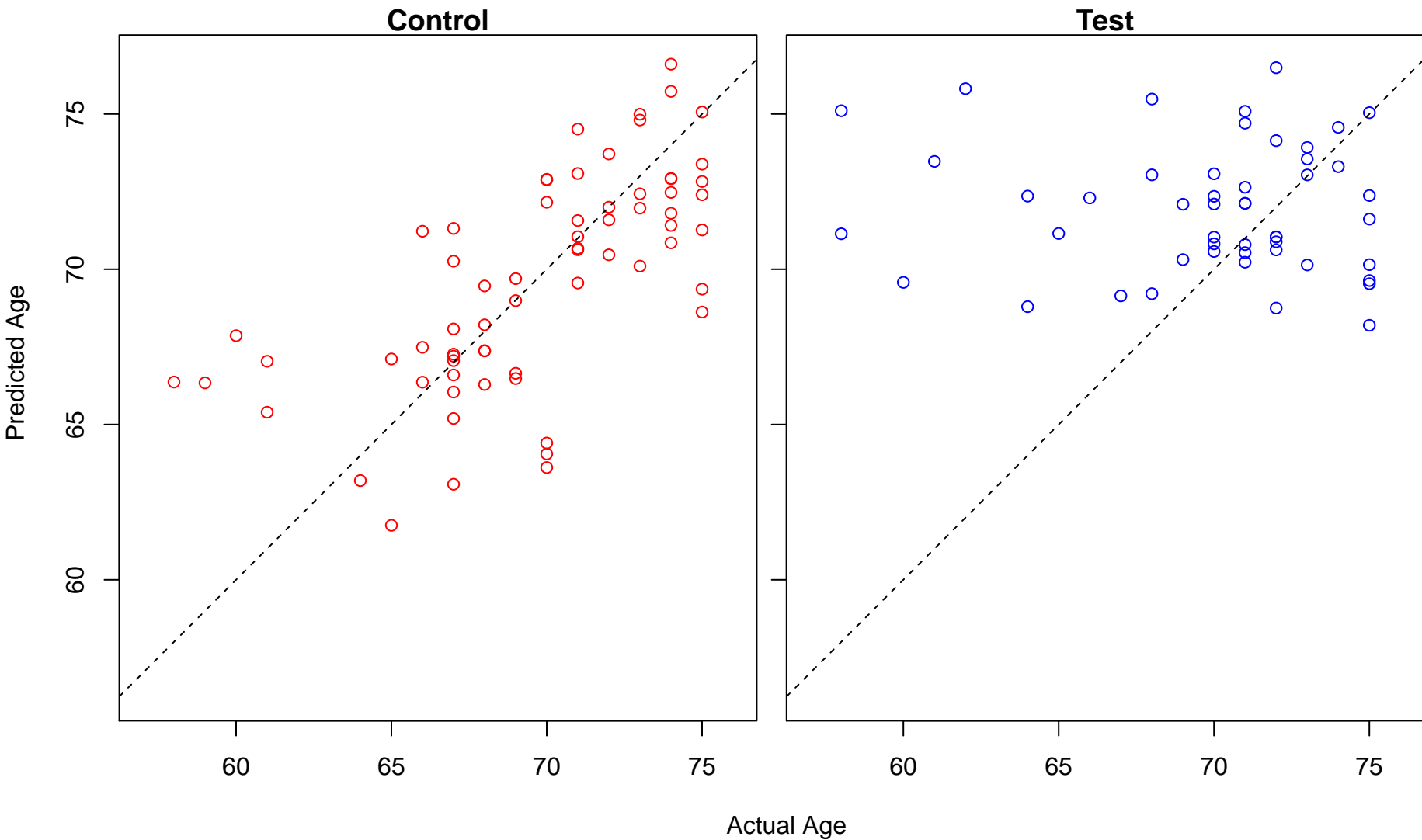
cilium assembly (Score: 1.428880)



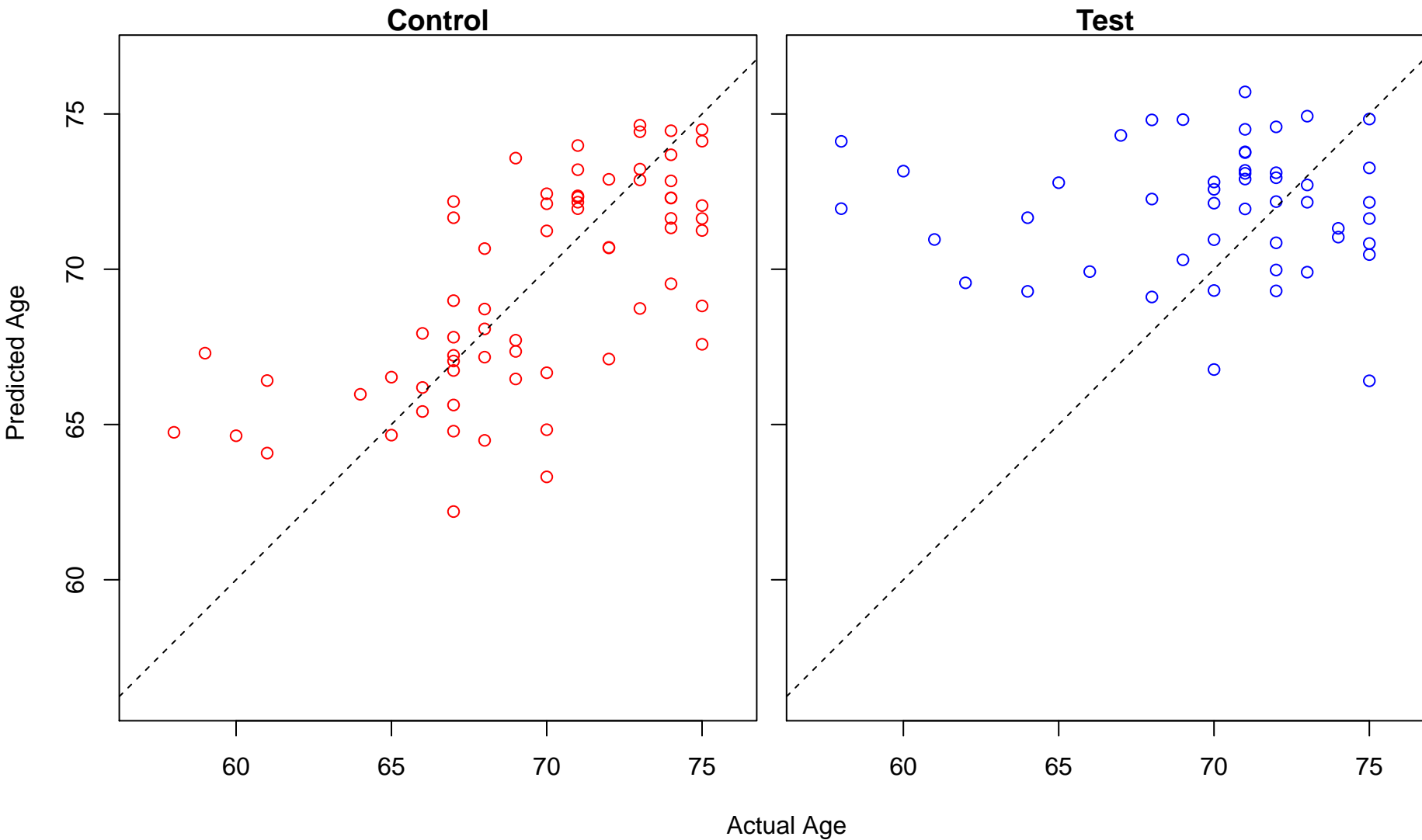
cellular response to starvation (Score: 1.428316)



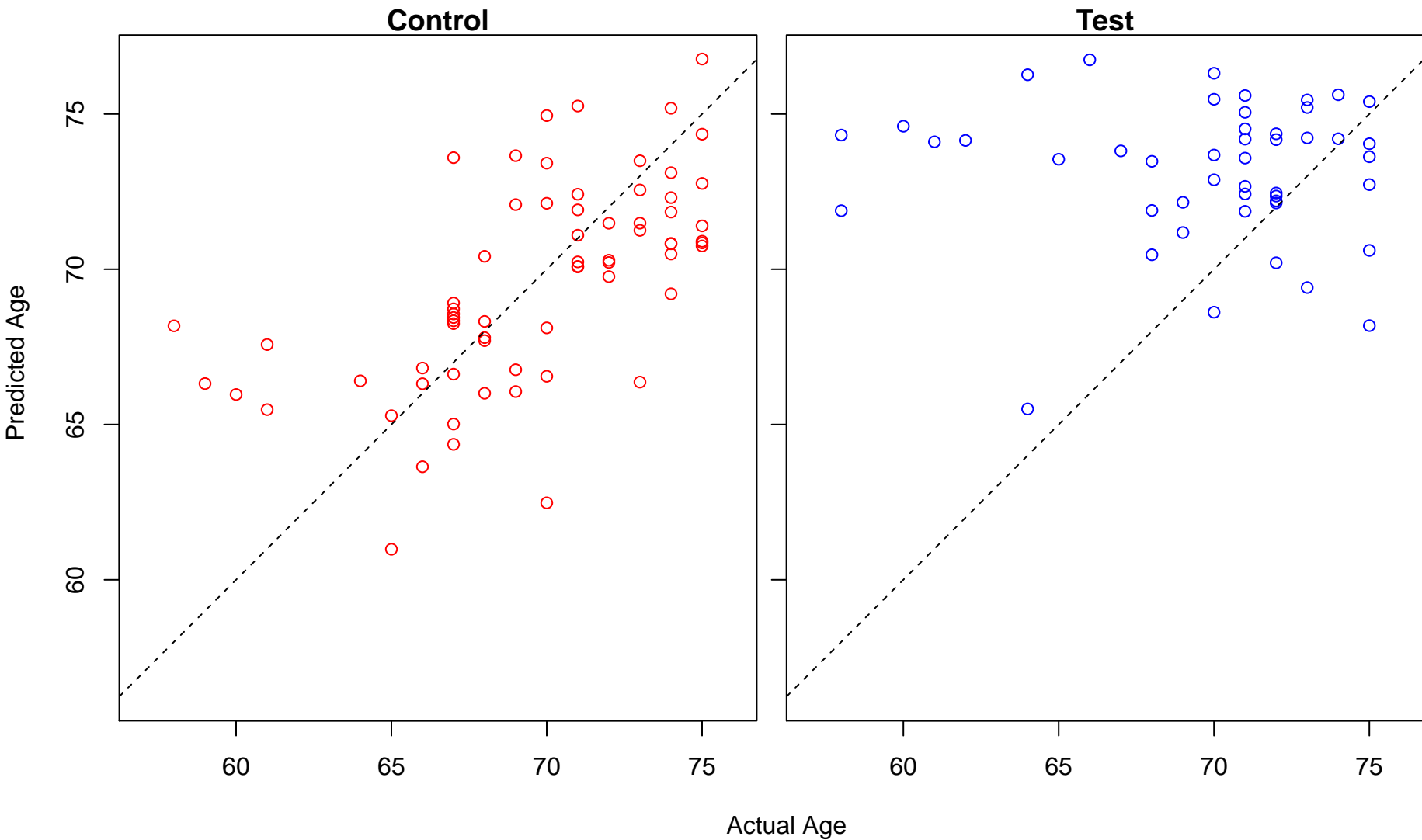
negative regulation of cellular amide metabolic process (Score: 1.427816)



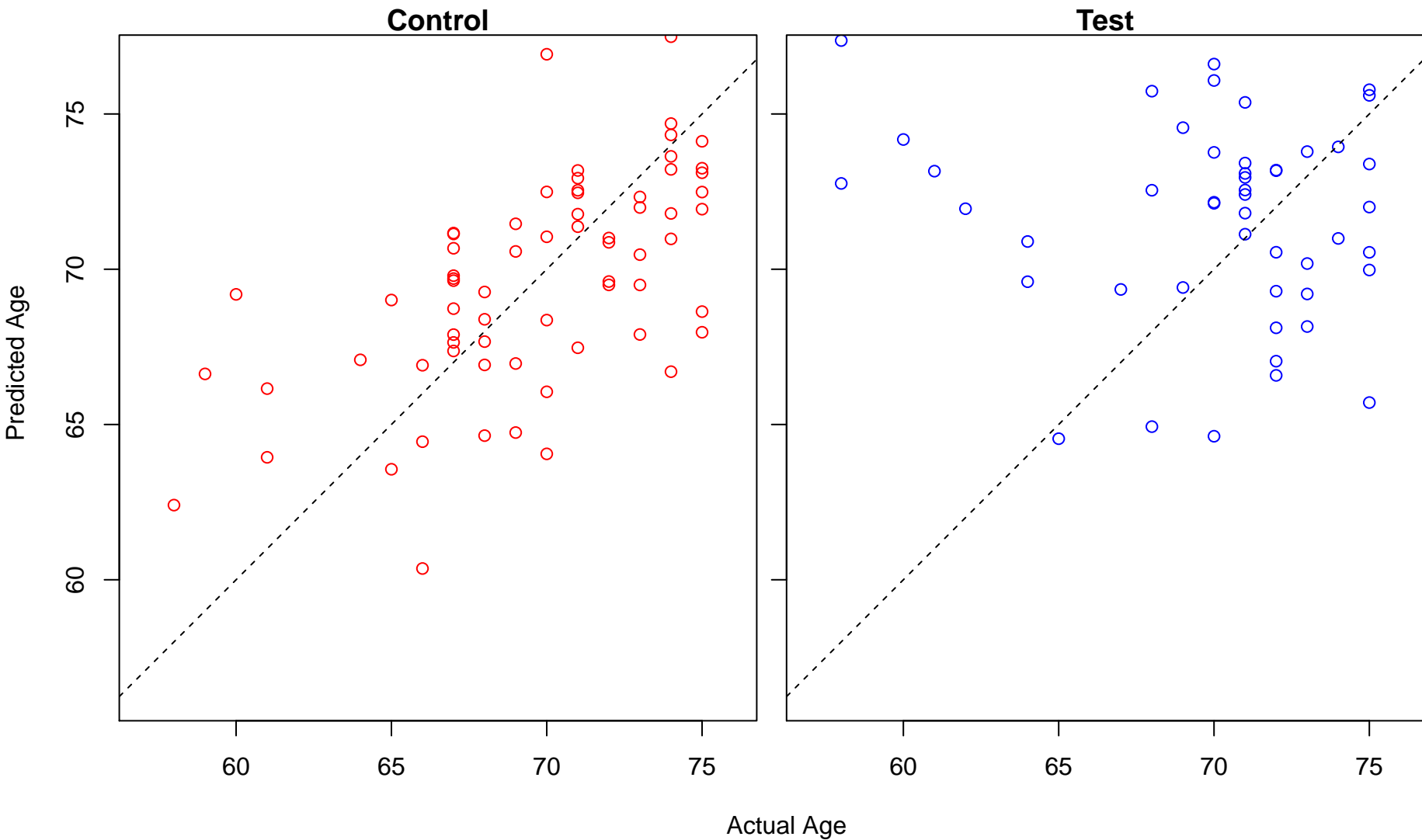
regulation of DNA-templated transcription in response to stress (Score: 1.427813)



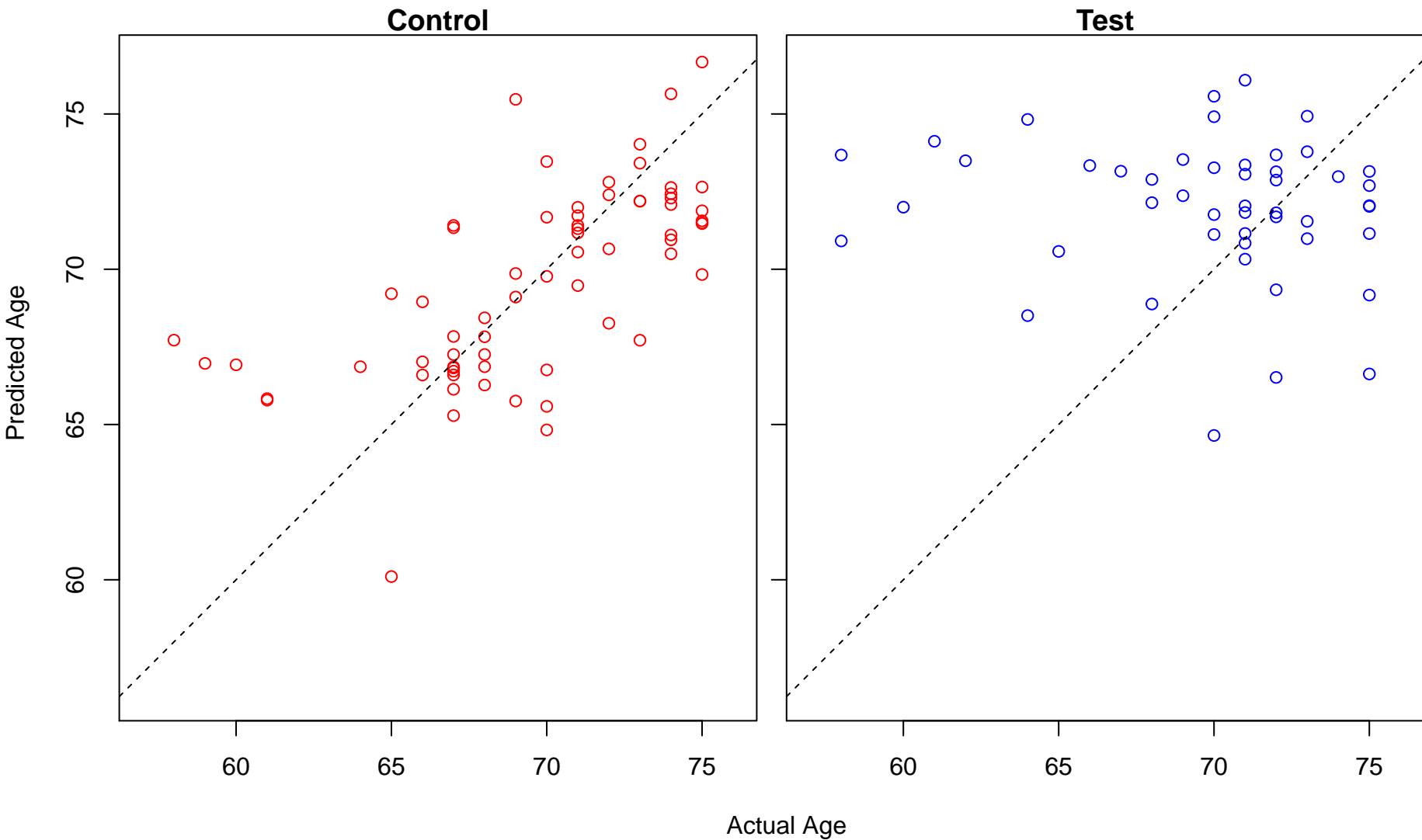
JNK cascade (Score: 1.427348)



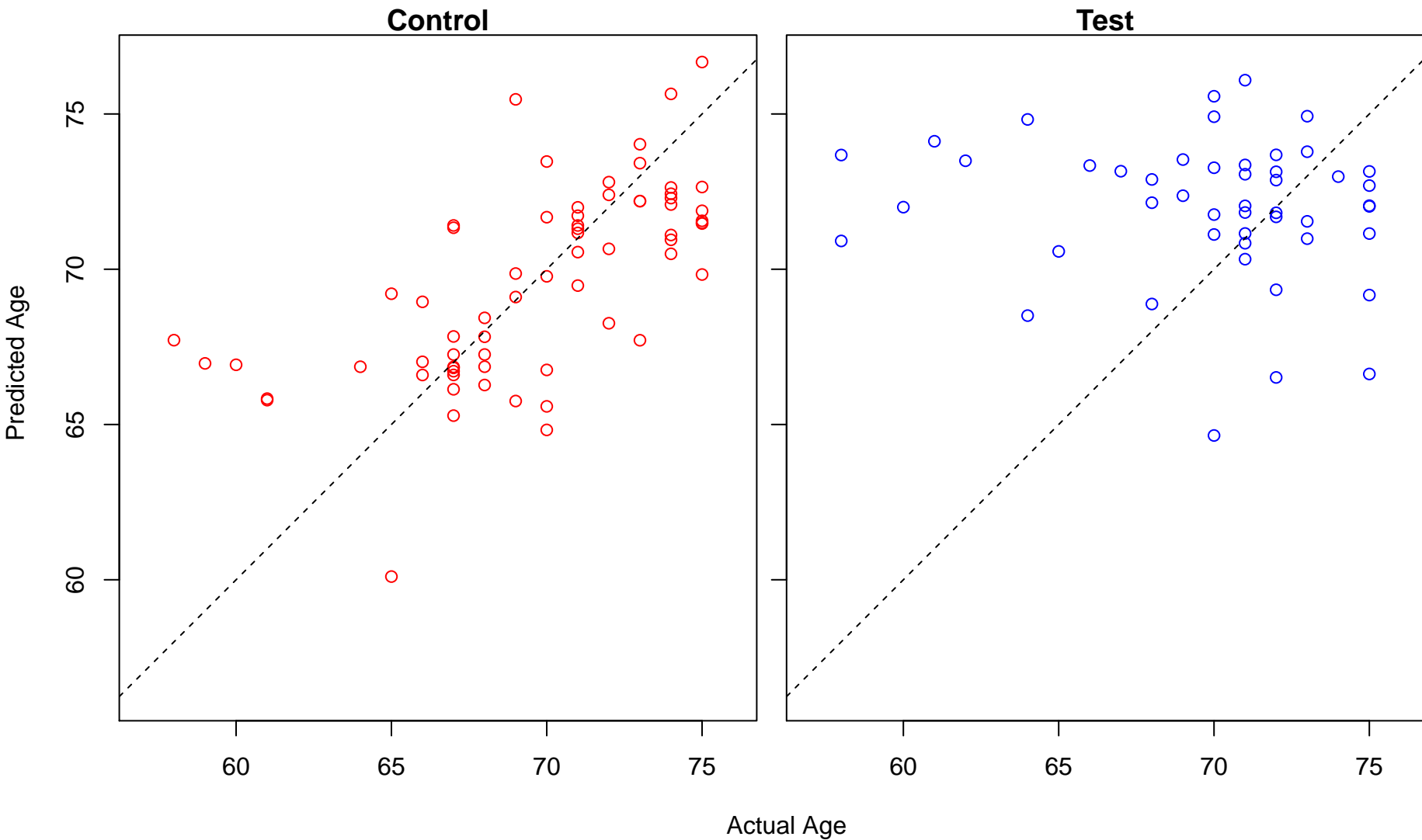
negative regulation of osteoclast differentiation (Score: 1.427140)



amino acid activation (Score: 1.427011)

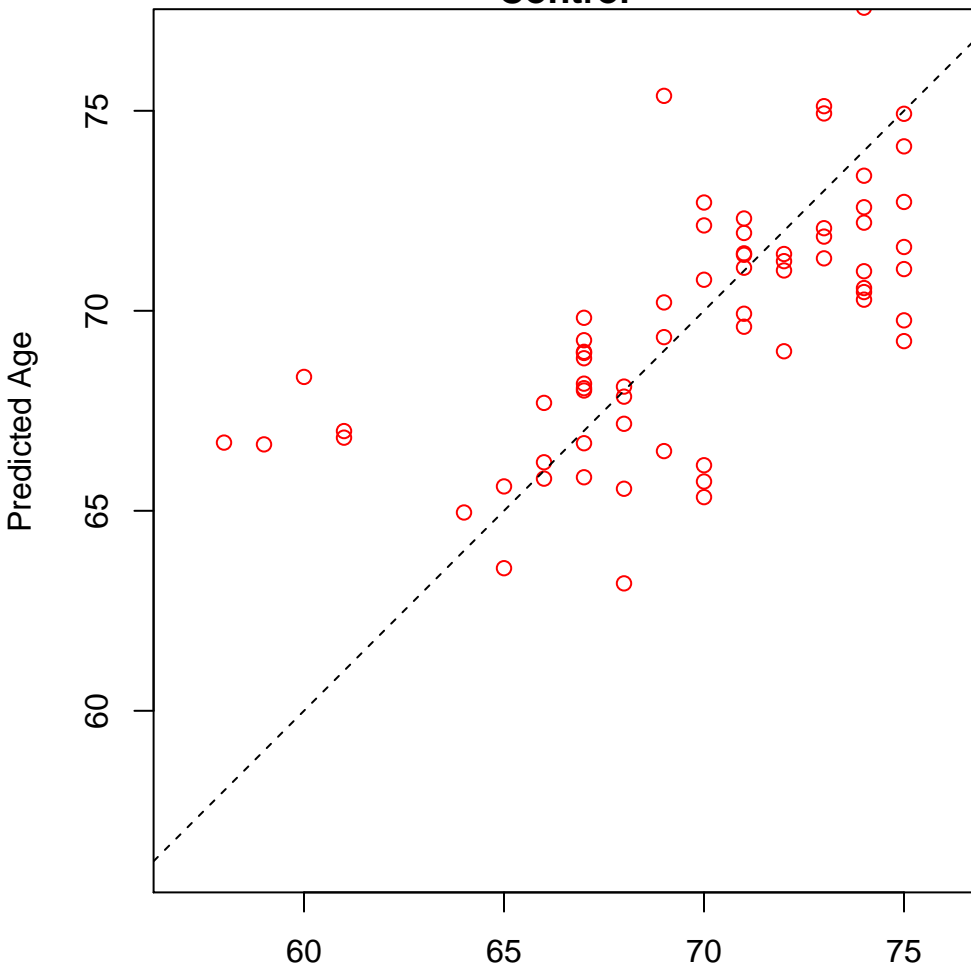


tRNA aminoacylation (Score: 1.427011)

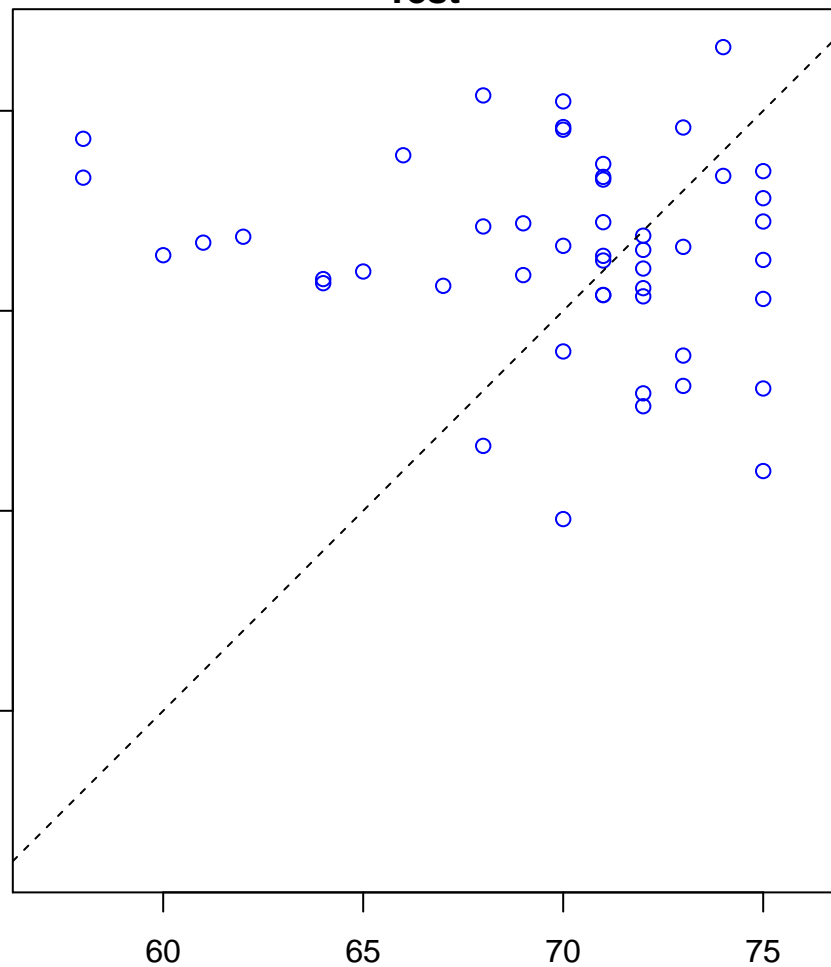


regulation of osteoclast differentiation (Score: 1.426657)

Control

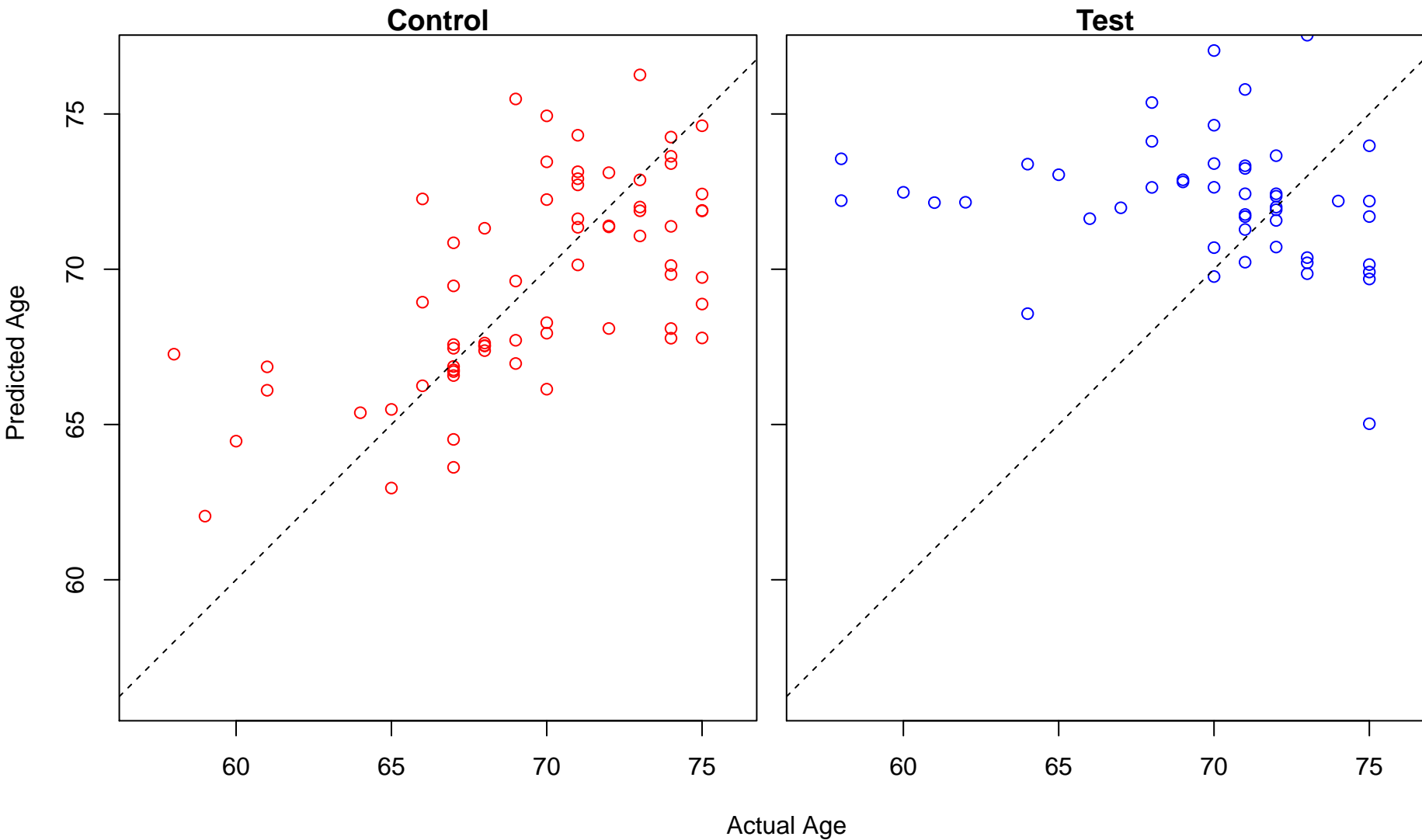


Test

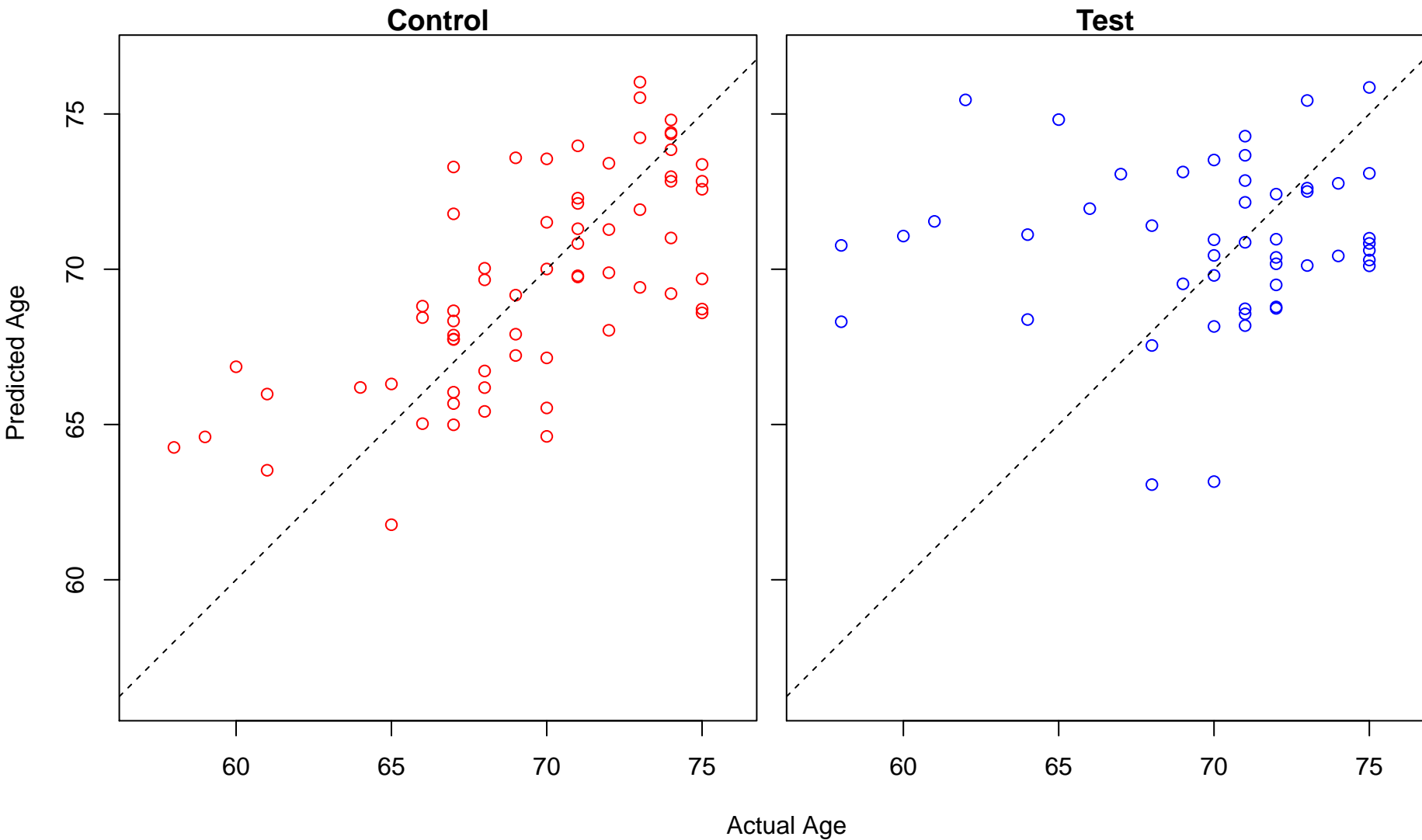


Actual Age

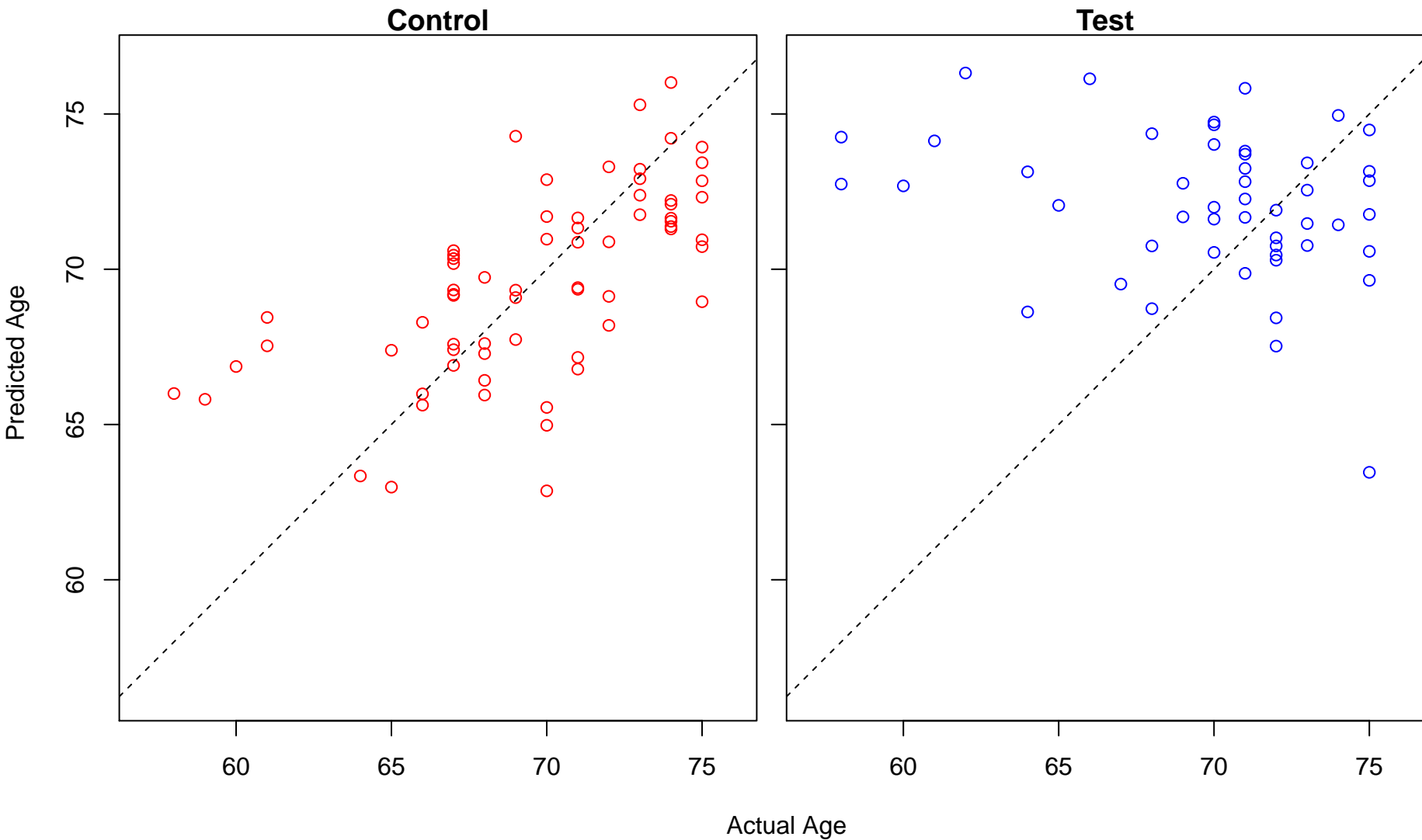
regulation of DNA damage response, signal transduction by p53 class mediator (Score: 1.426526)



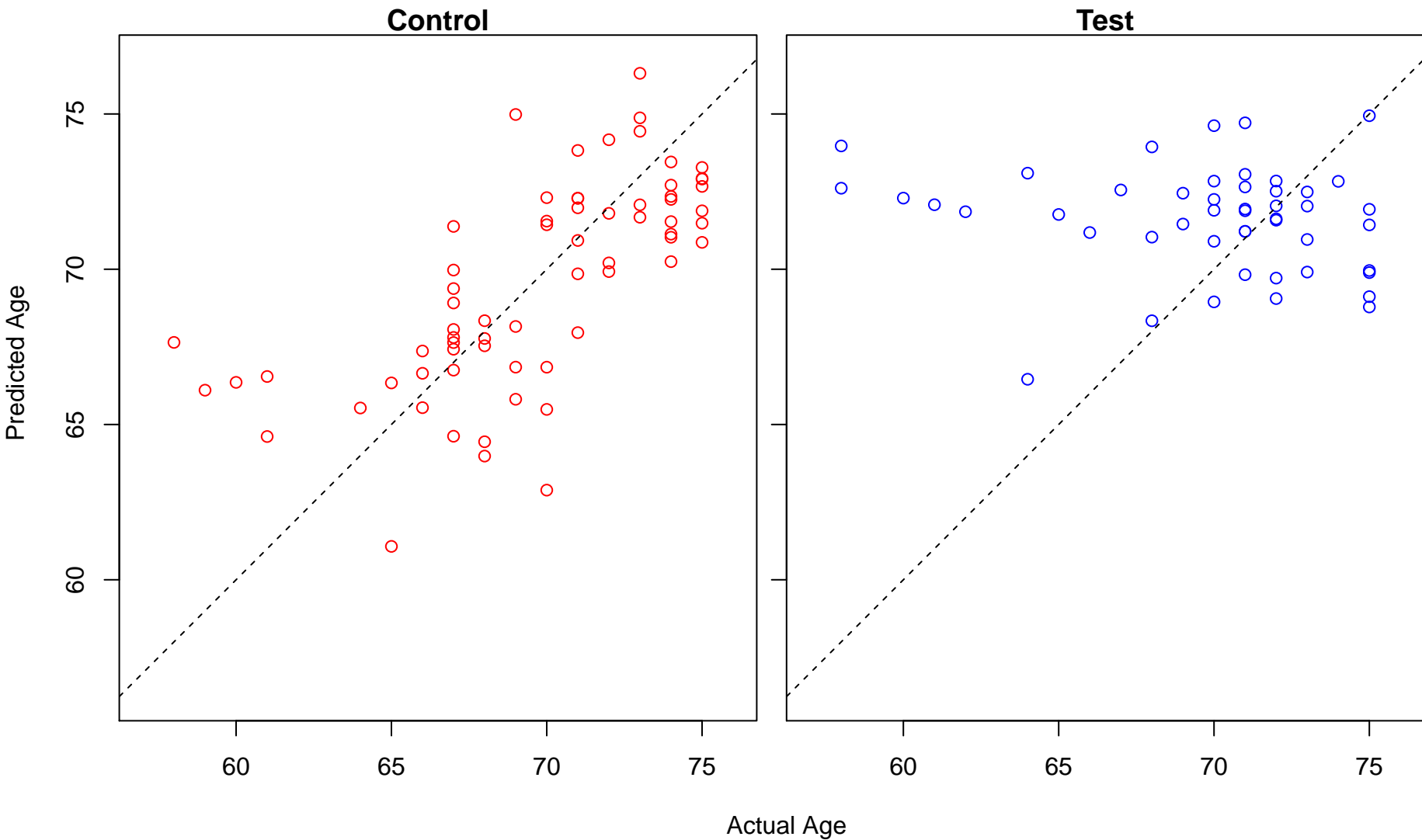
regulation of gluconeogenesis (Score: 1.426152)



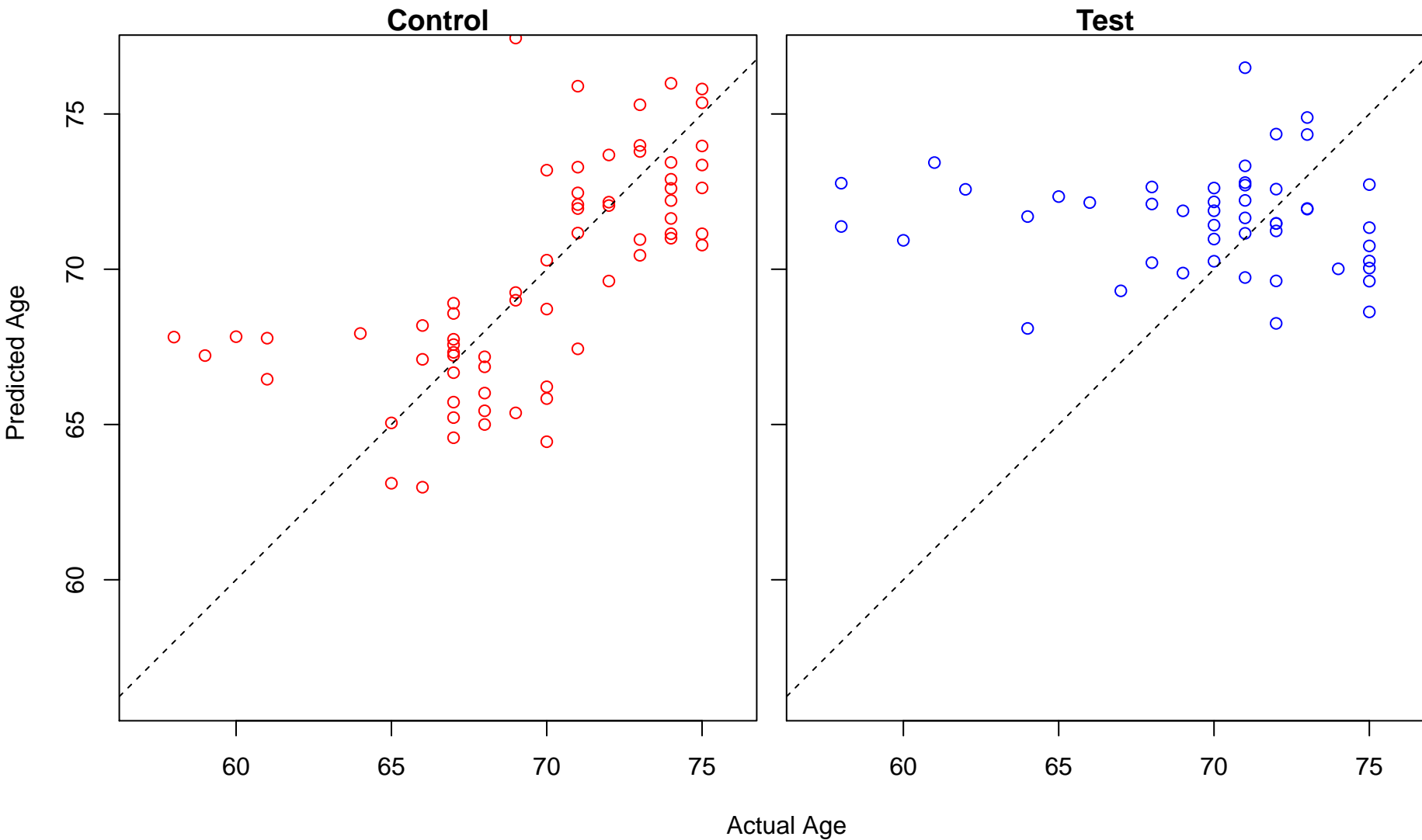
regulation of tissue remodeling (Score: 1.426135)



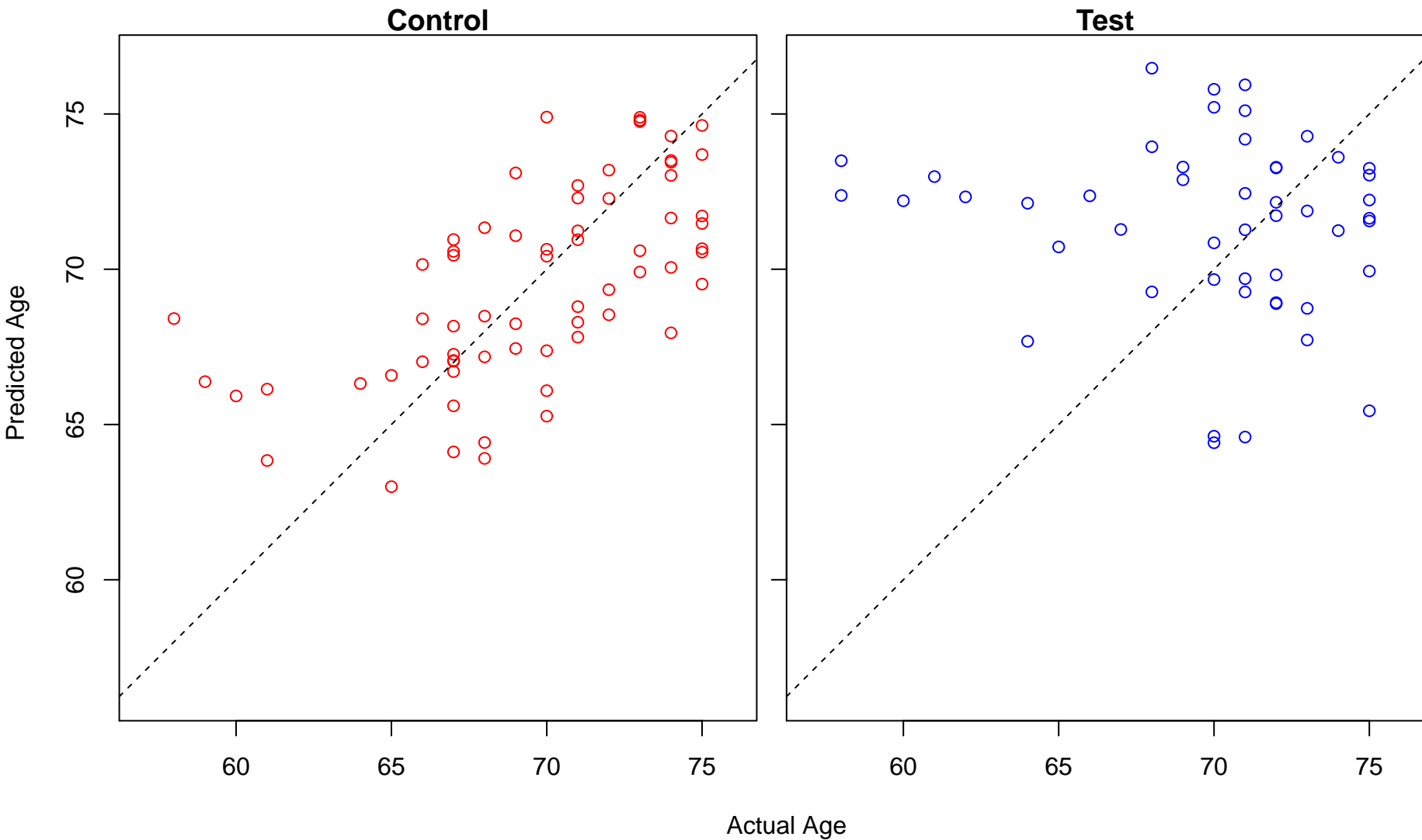
positive regulation of secretion (Score: 1.425927)



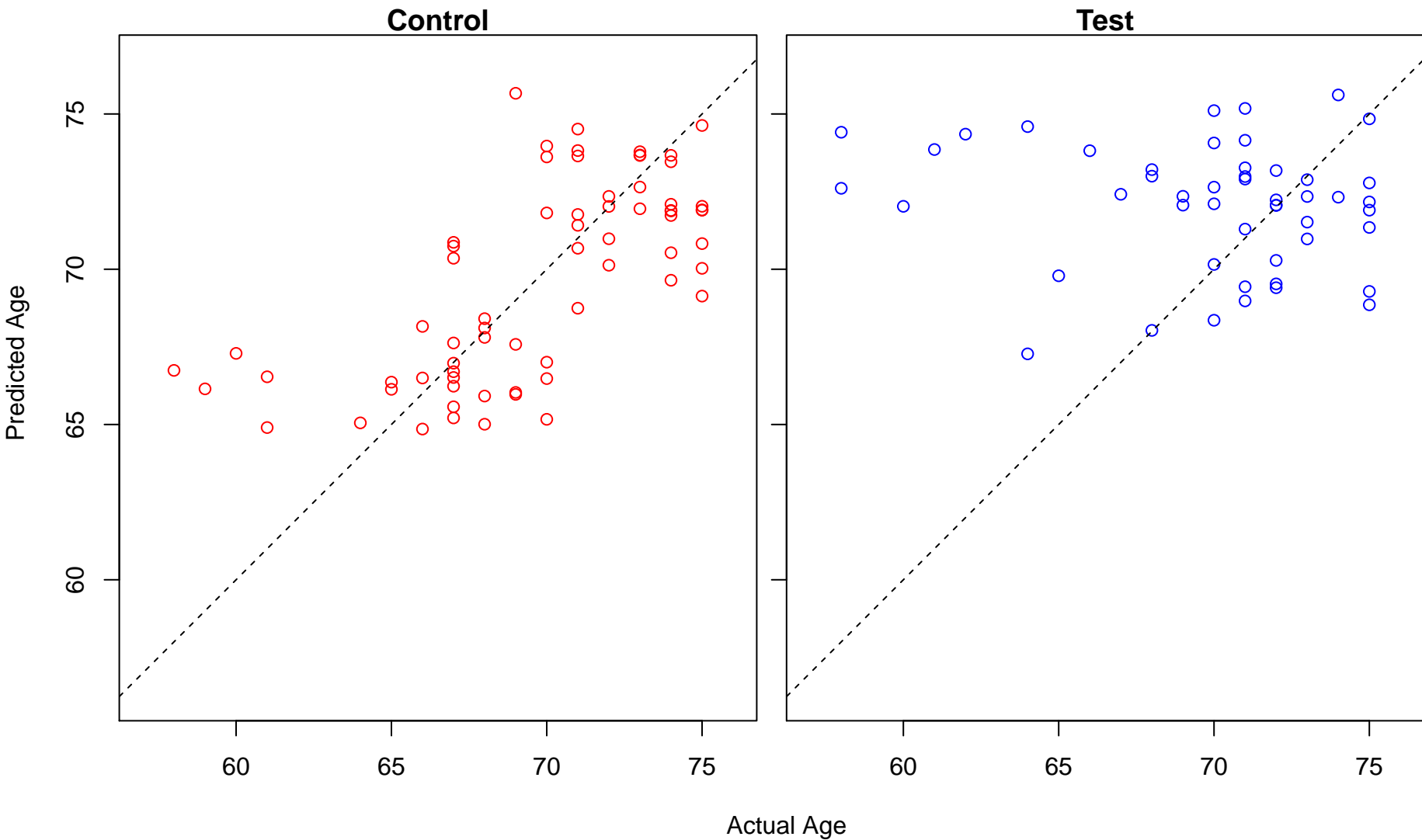
protein tetramerization (Score: 1.425865)



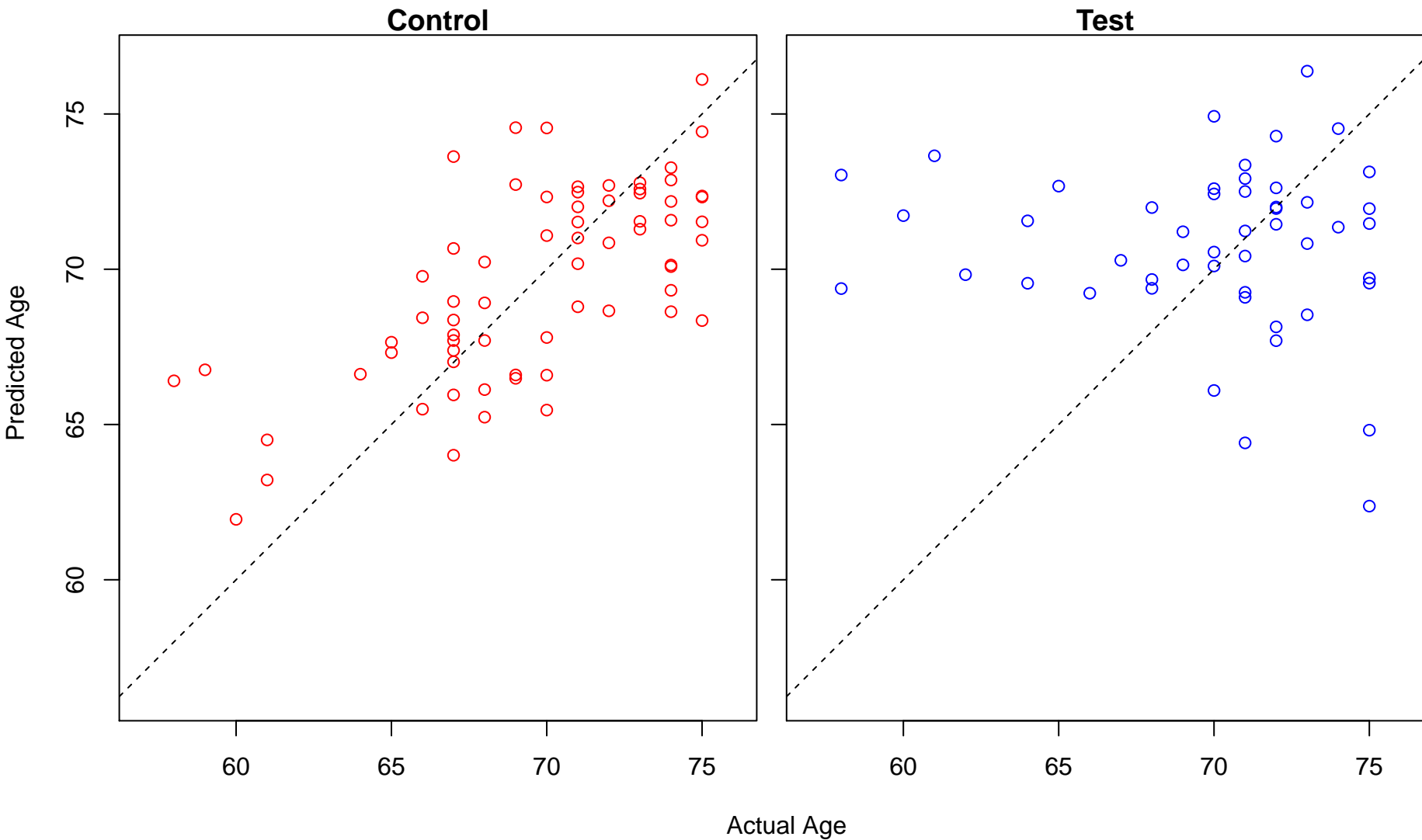
phosphatidylethanolamine biosynthetic process (Score: 1.425582)



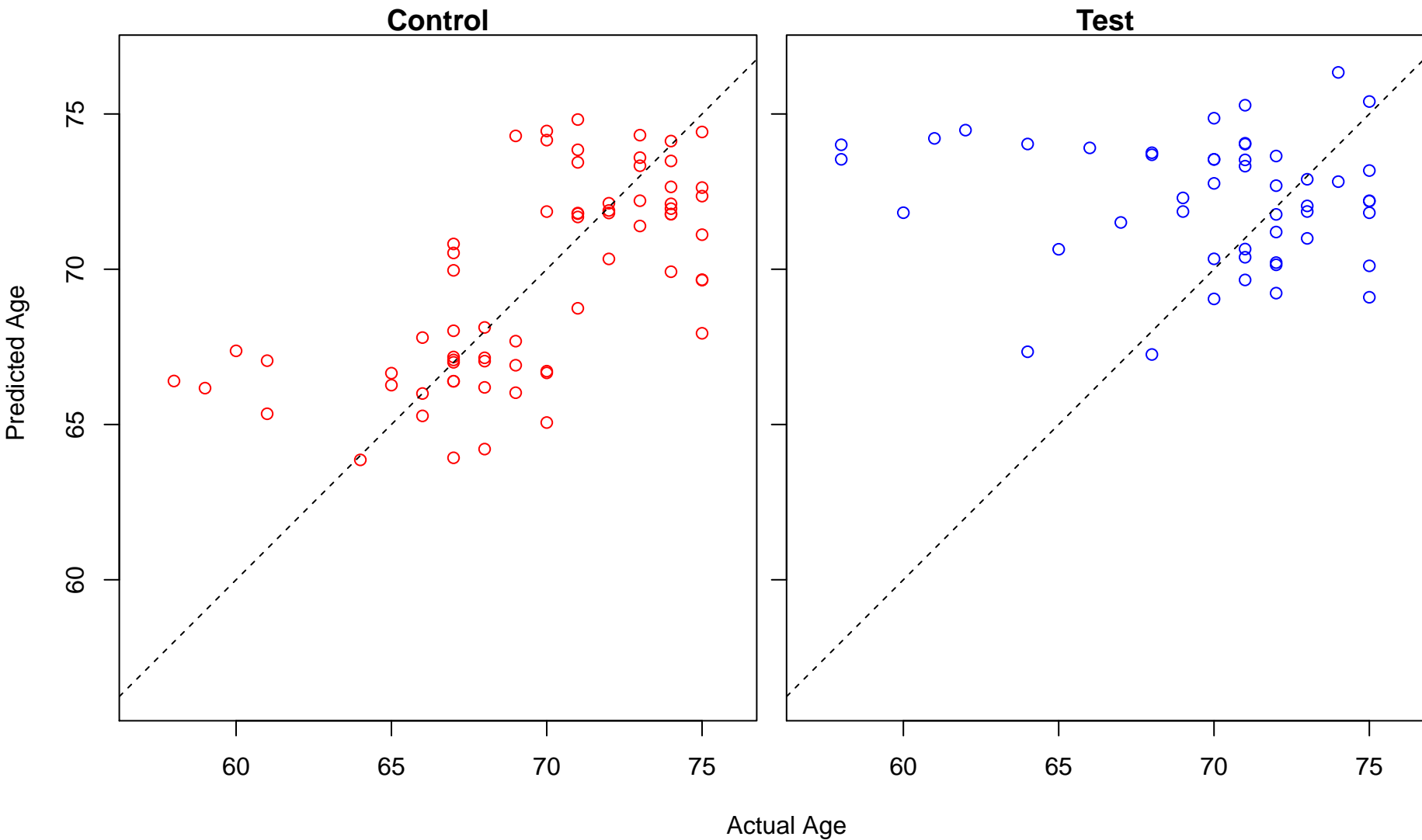
cilium organization (Score: 1.425208)



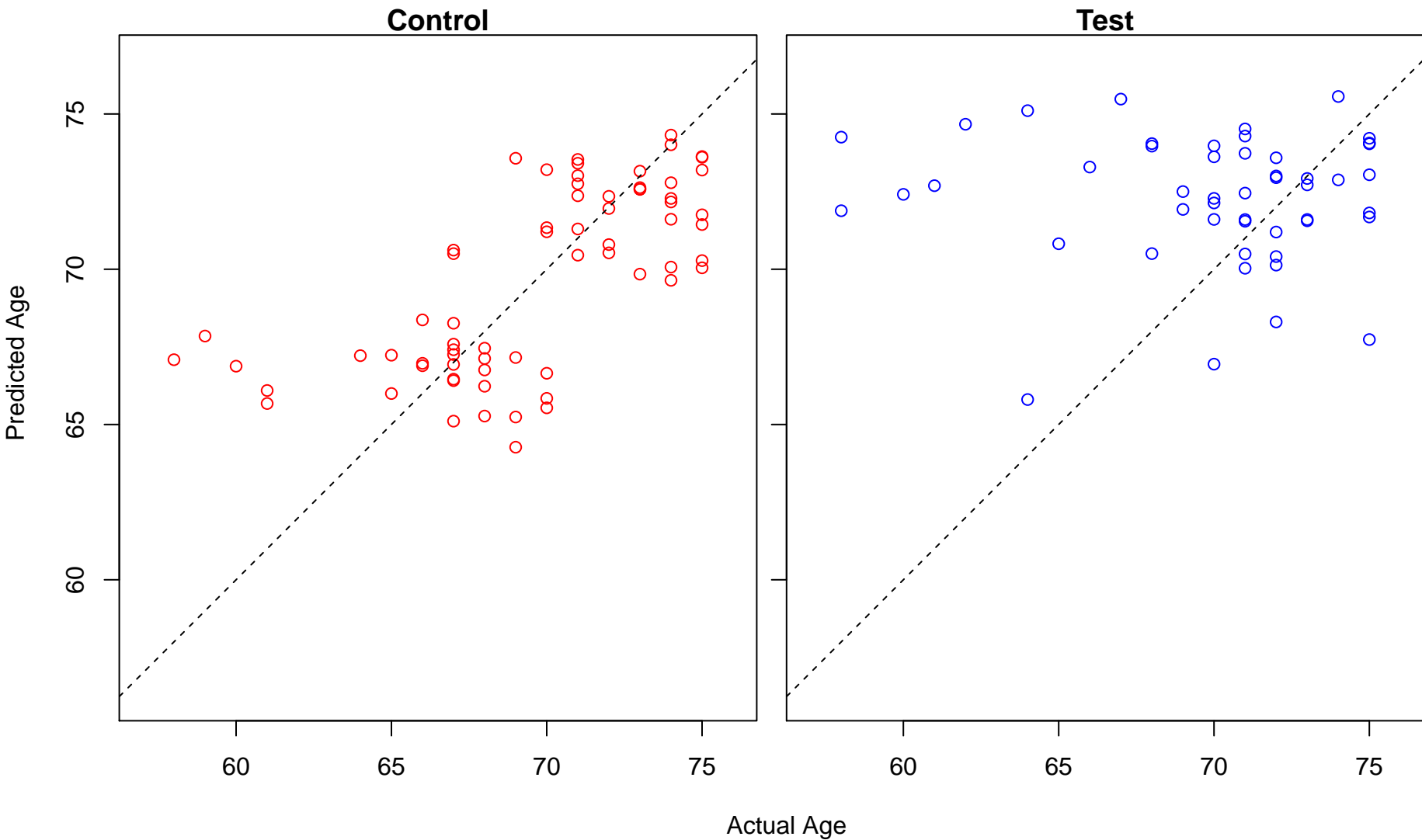
positive regulation of potassium ion transport (Score: 1.424882)



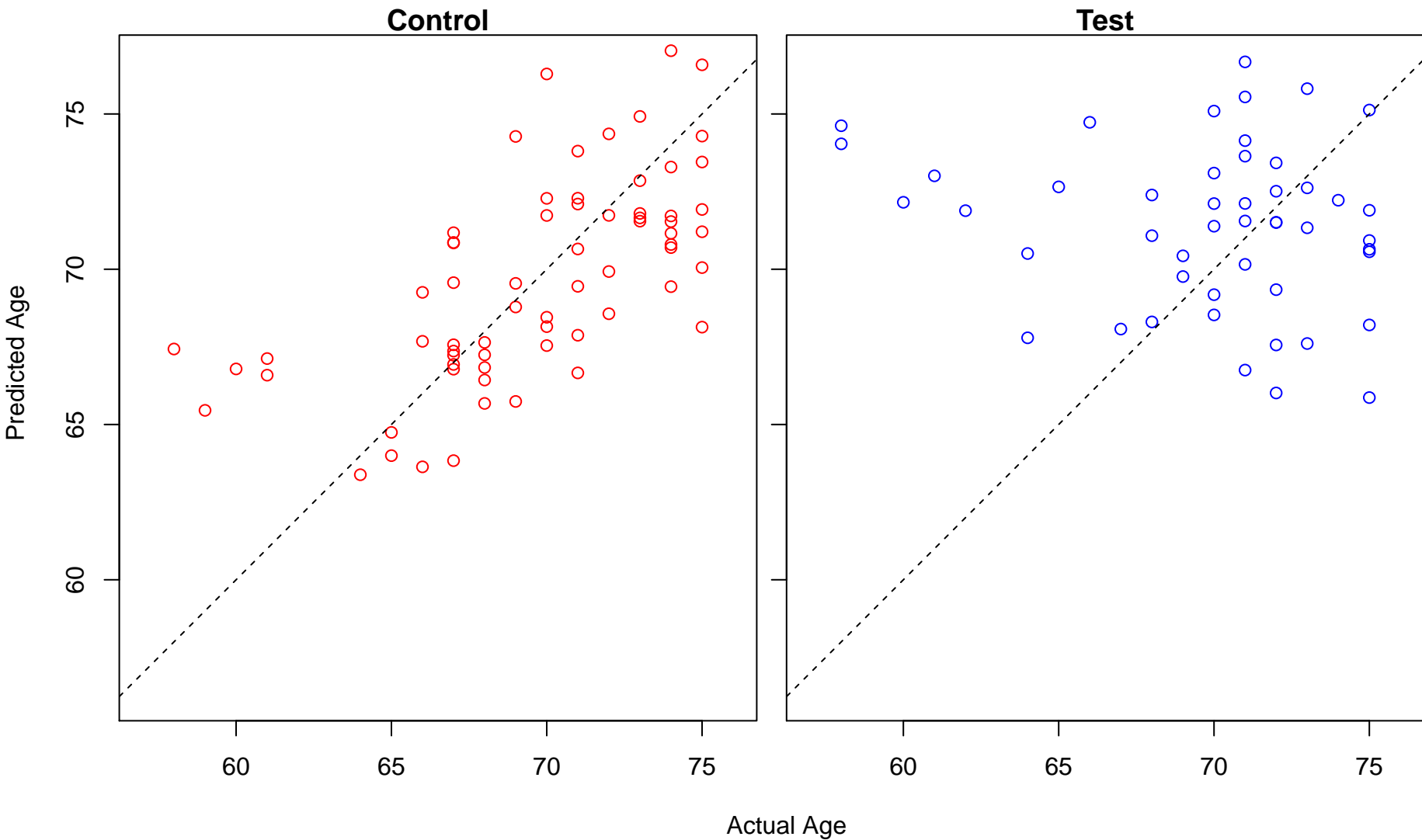
cellular component assembly involved in morphogenesis (Score: 1.424516)



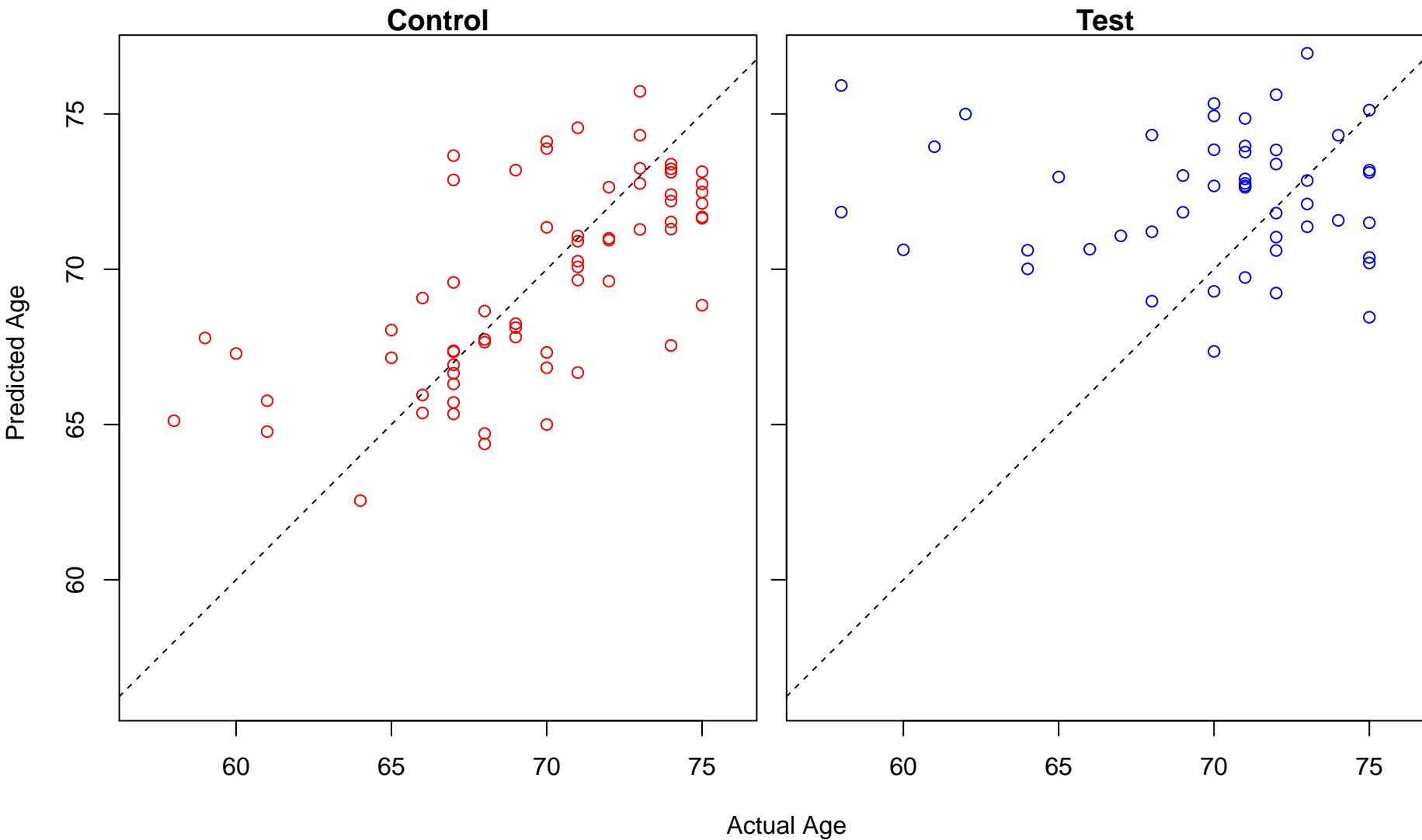
Rac protein signal transduction (Score: 1.424326)



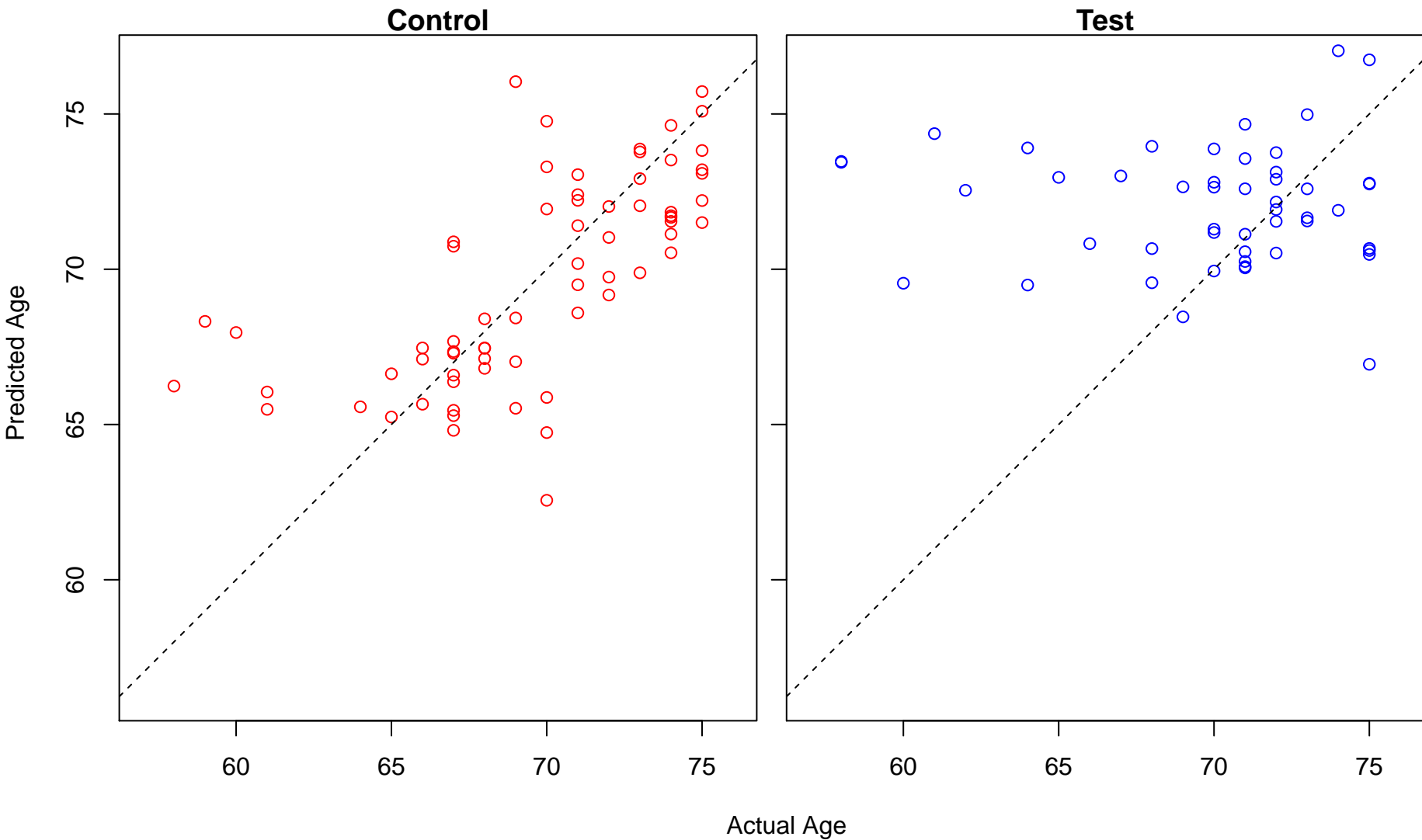
regulation of adherens junction organization (Score: 1.424099)



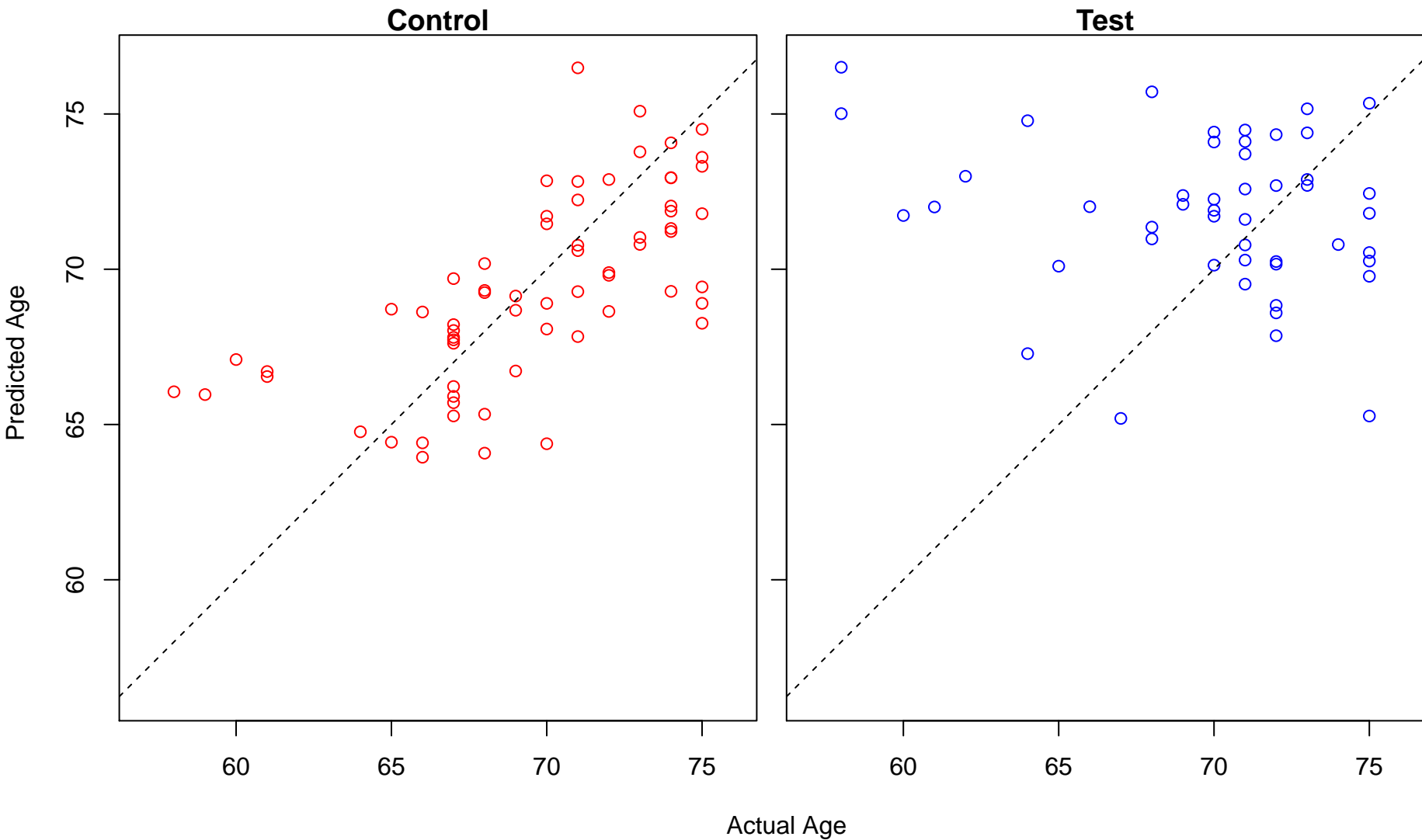
multicellular organismal signaling (Score: 1.423995)



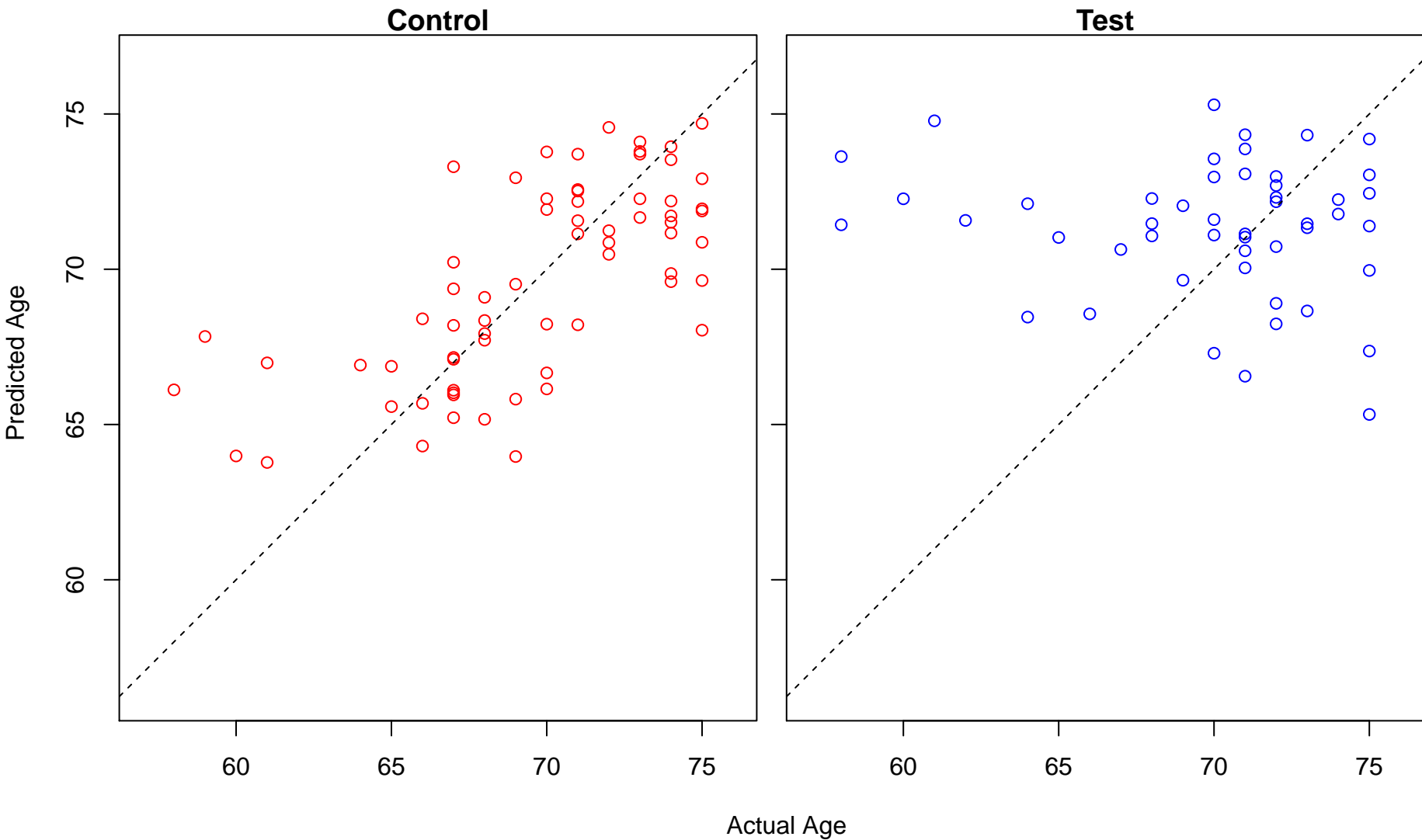
positive regulation of MAP kinase activity (Score: 1.423776)



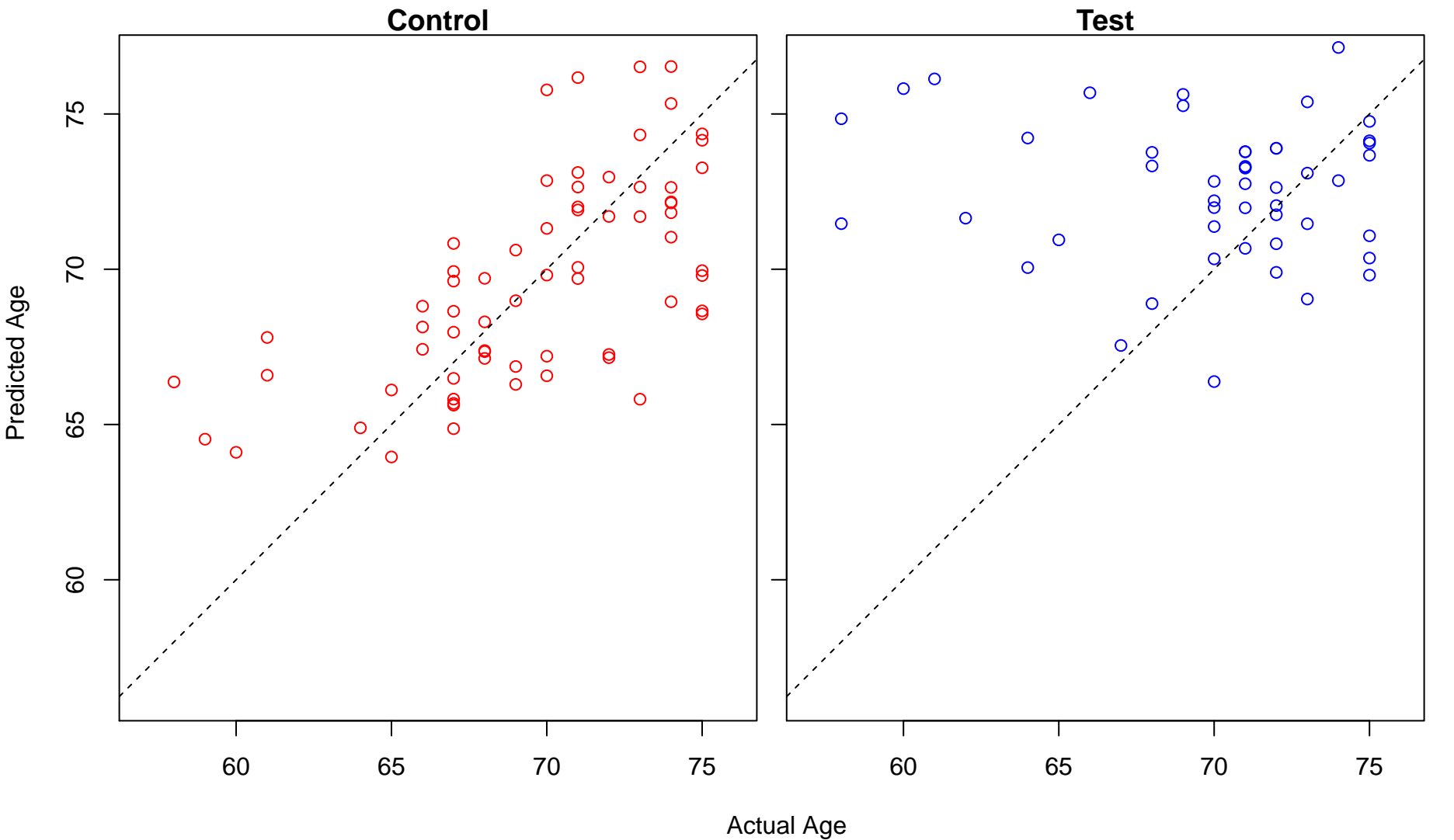
stem cell development (Score: 1.423718)



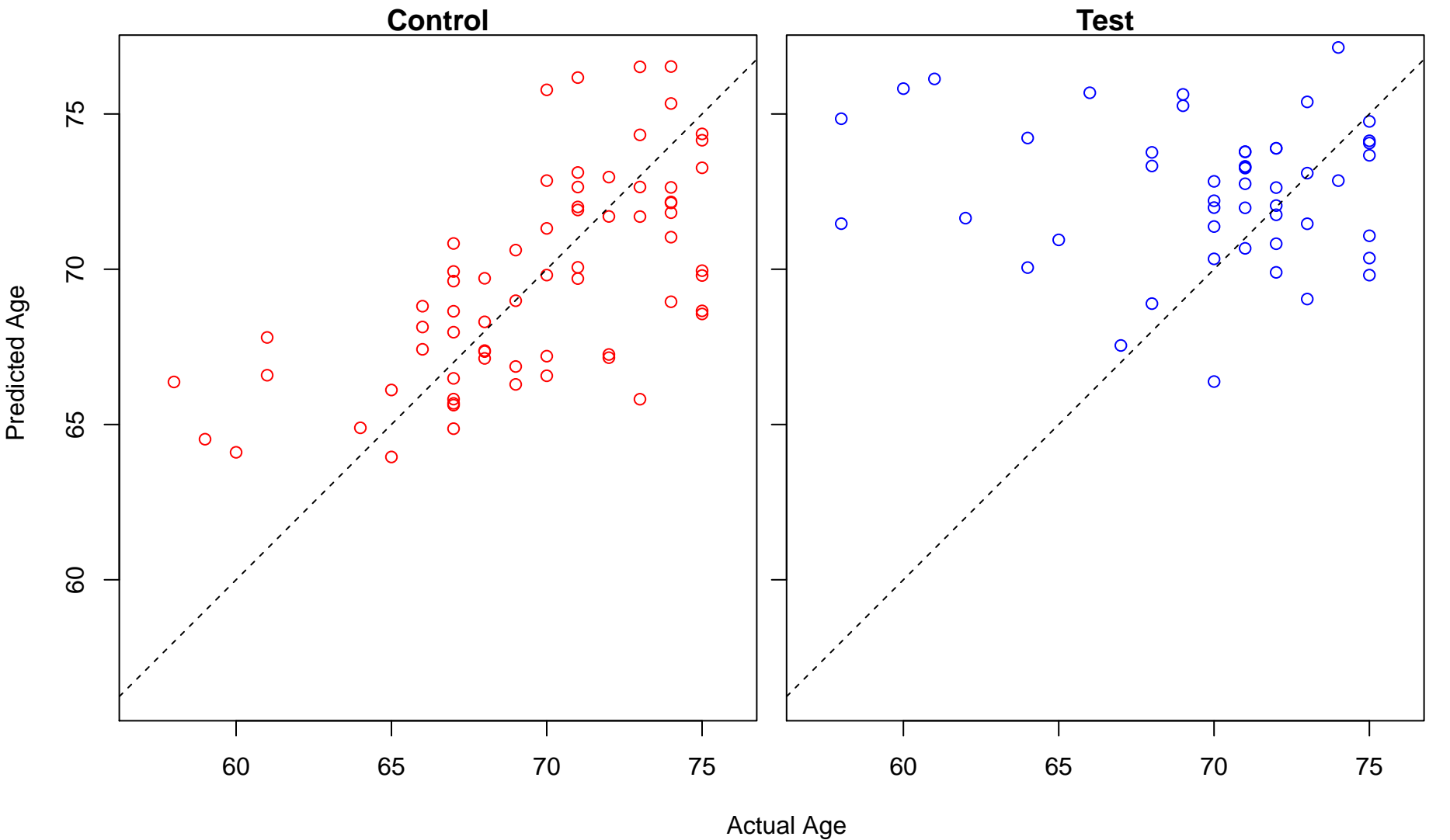
regulation of potassium ion transmembrane transporter activity (Score: 1.423395)



Regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (Score

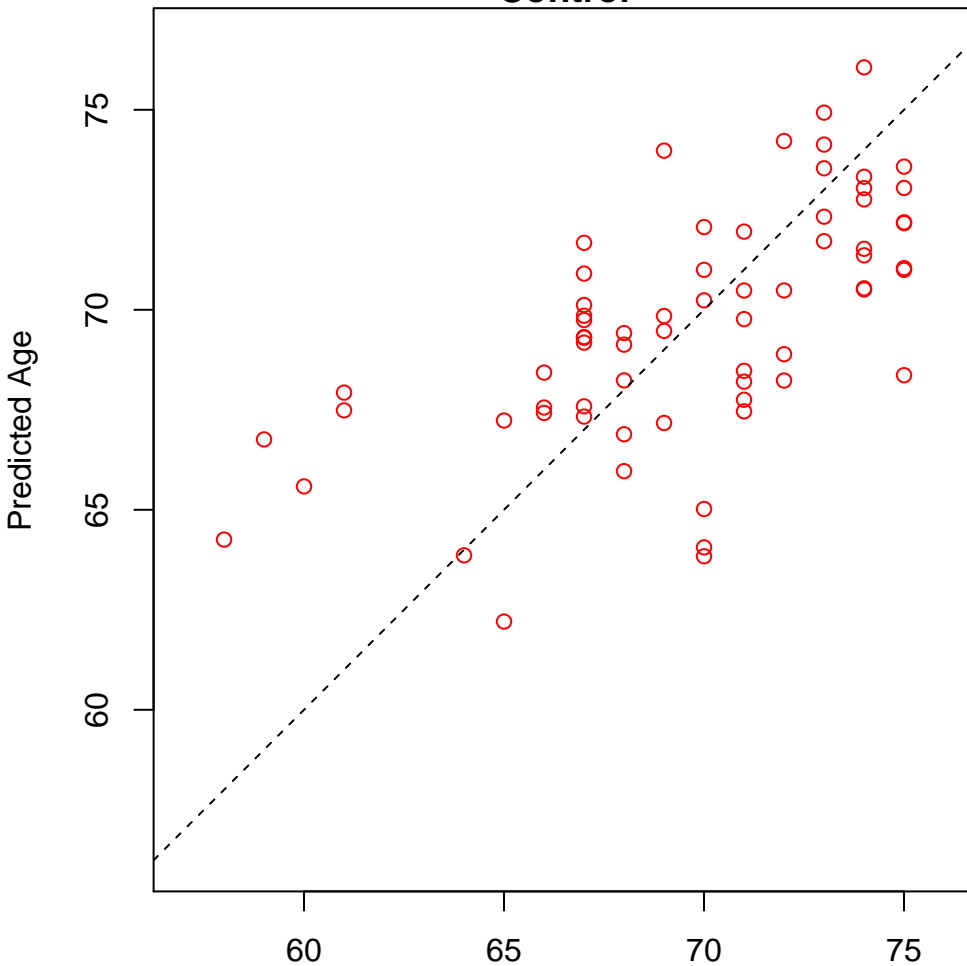


ve regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (S

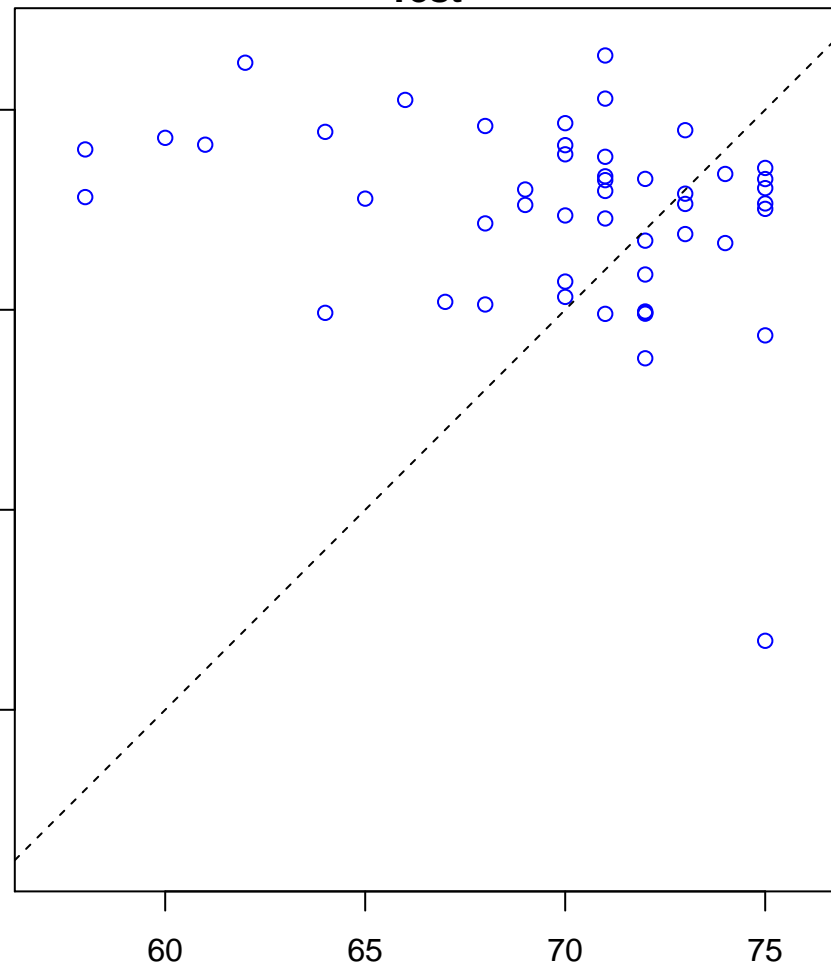


positive regulation of tissue remodeling (Score: 1.423063)

Control



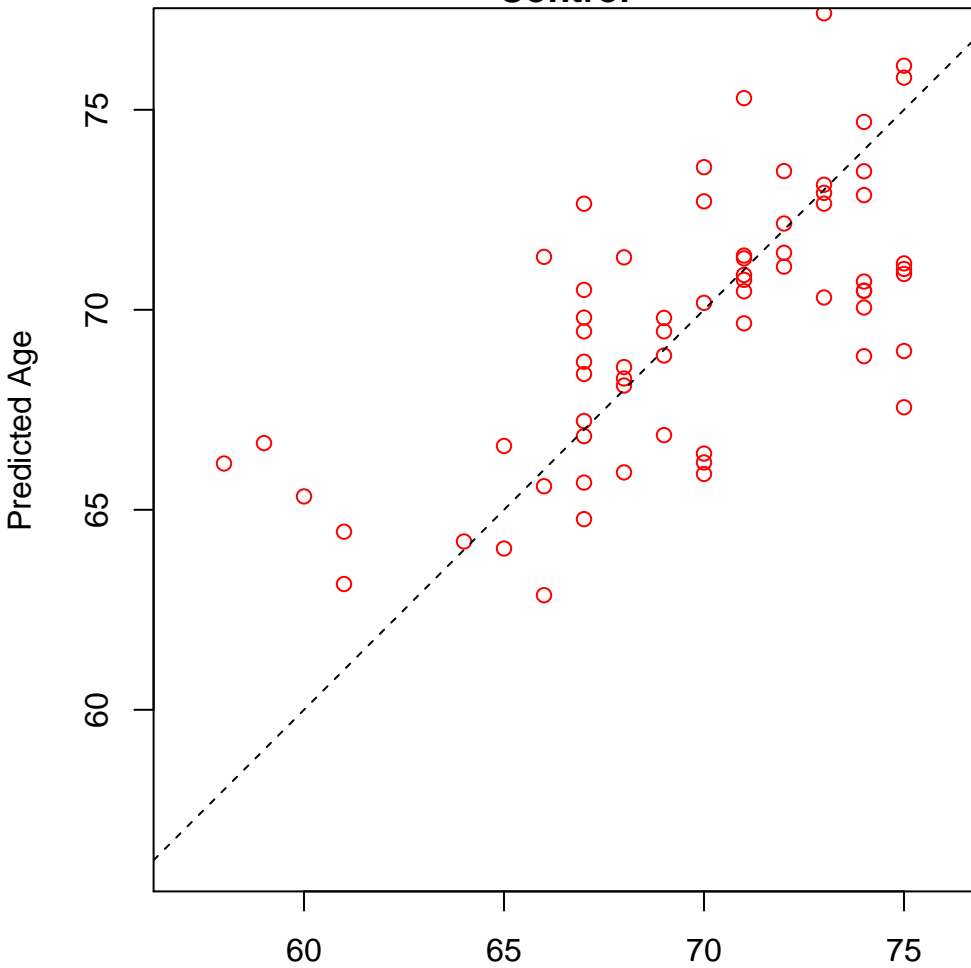
Test



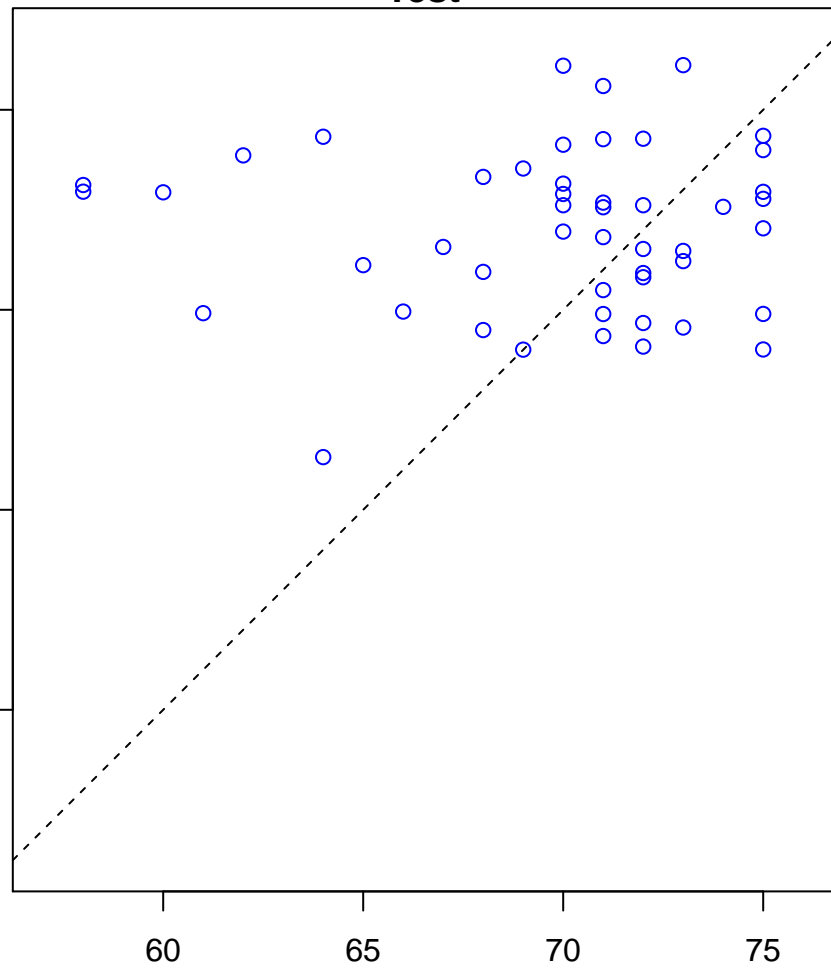
Actual Age

regulation of viral release from host cell (Score: 1.422836)

Control

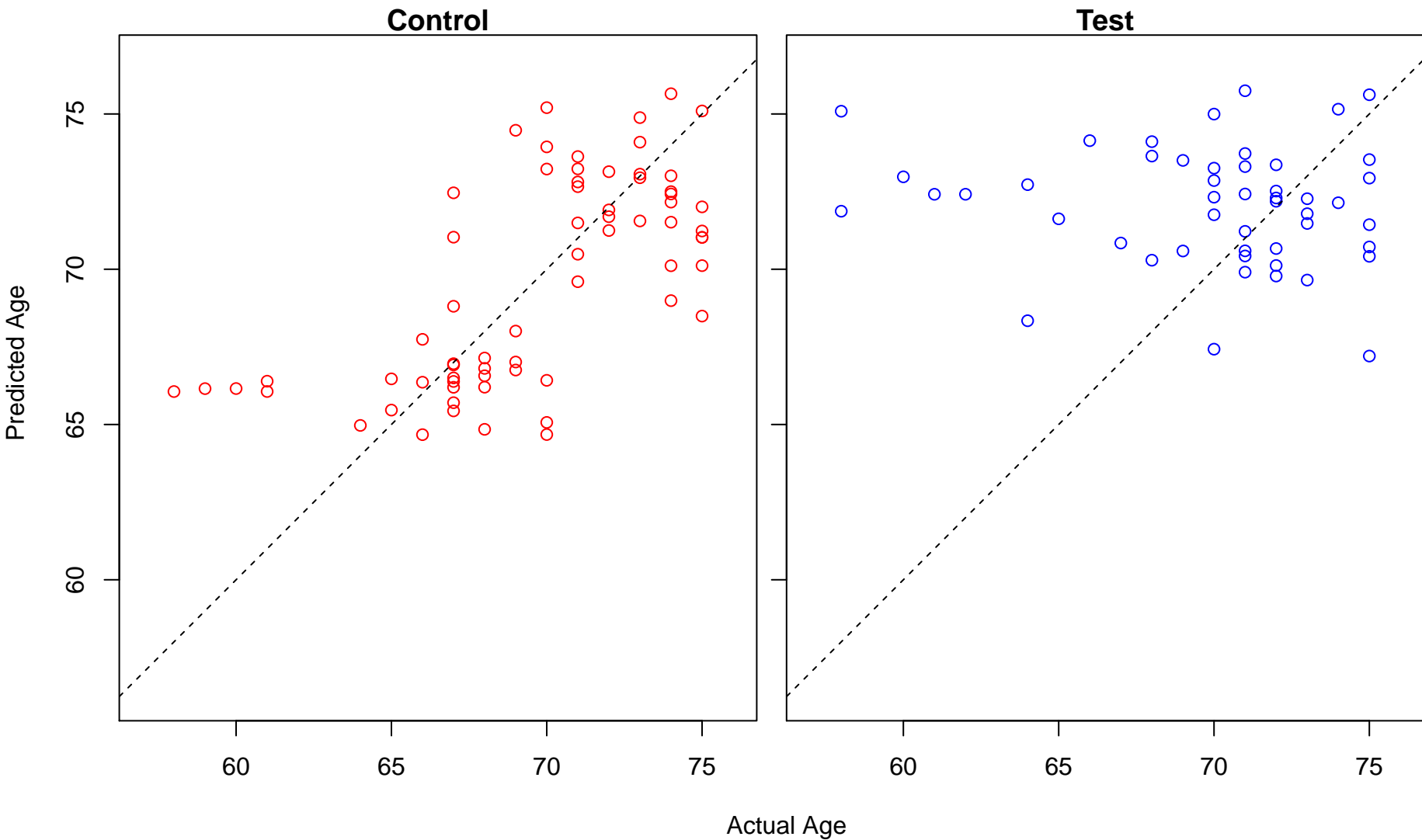


Test

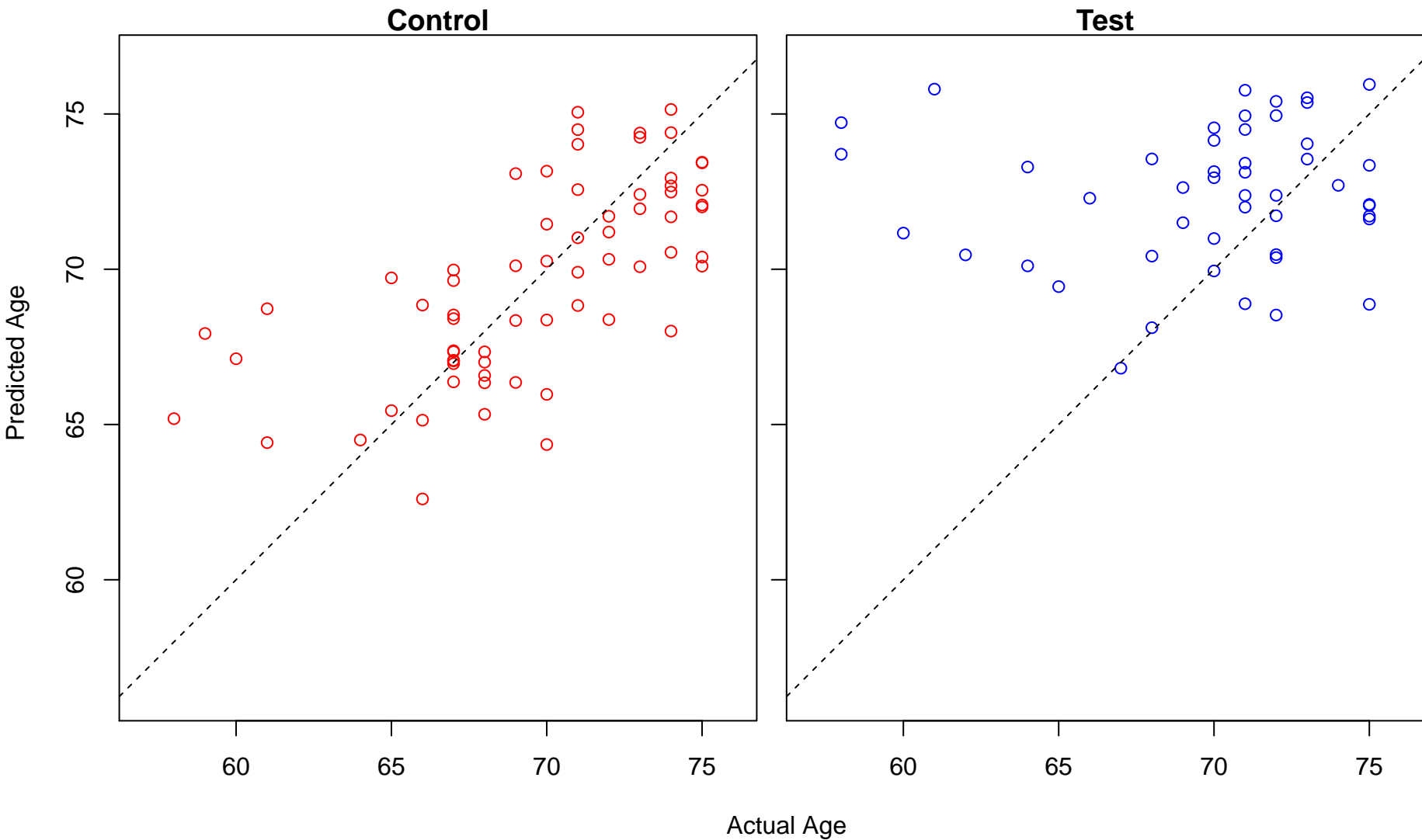


Actual Age

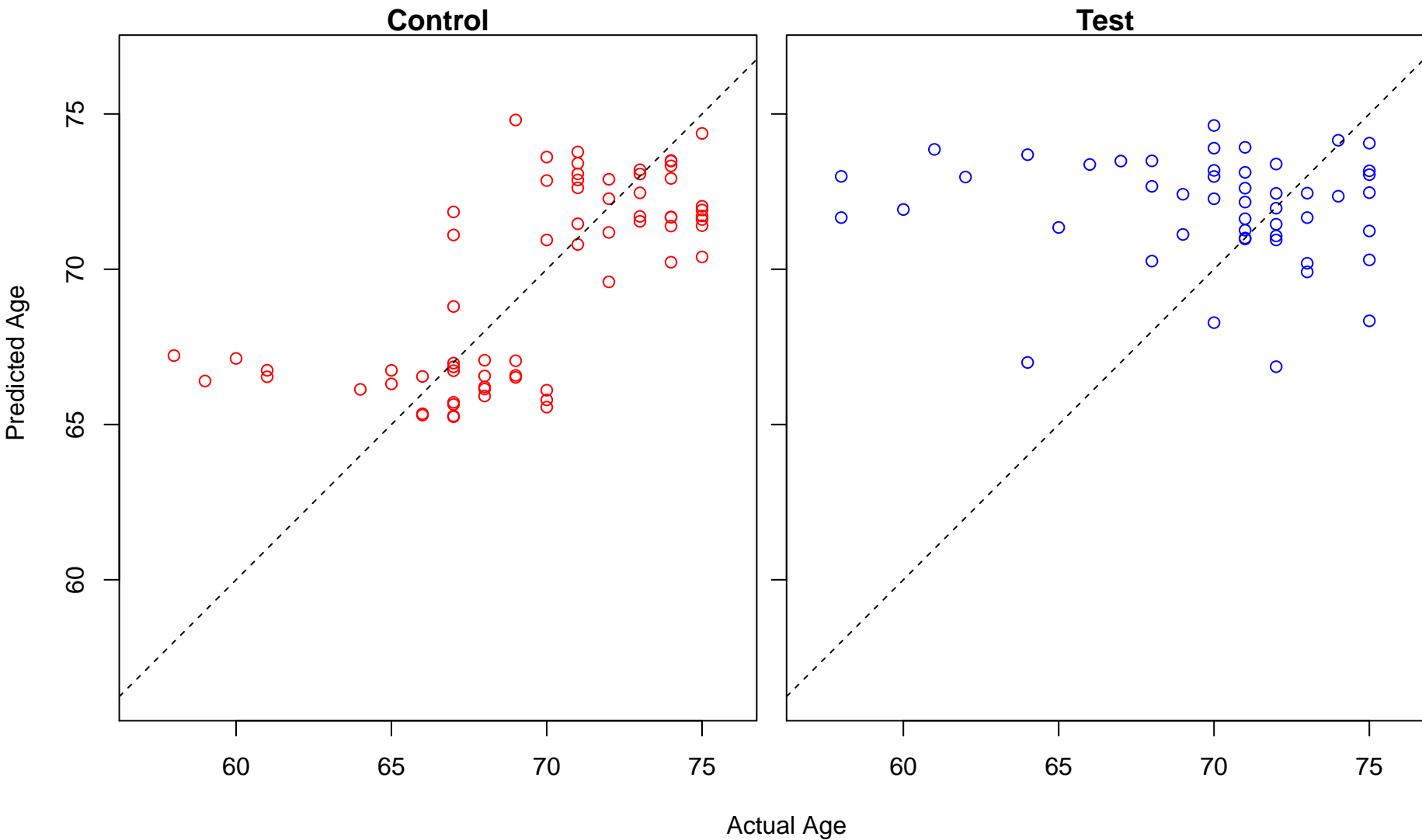
regulation of epithelial cell migration (Score: 1.422093)



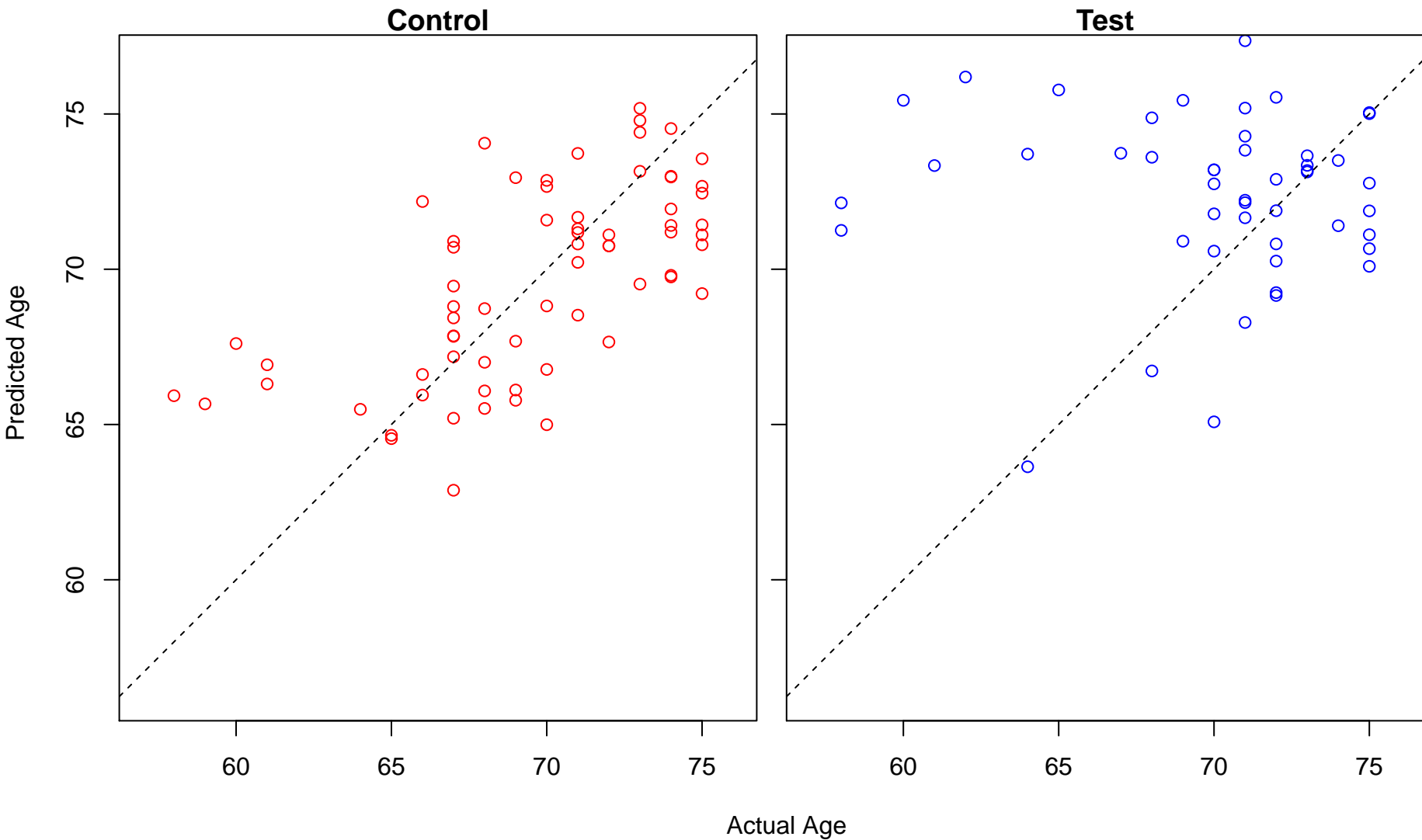
cardiac ventricle morphogenesis (Score: 1.421914)



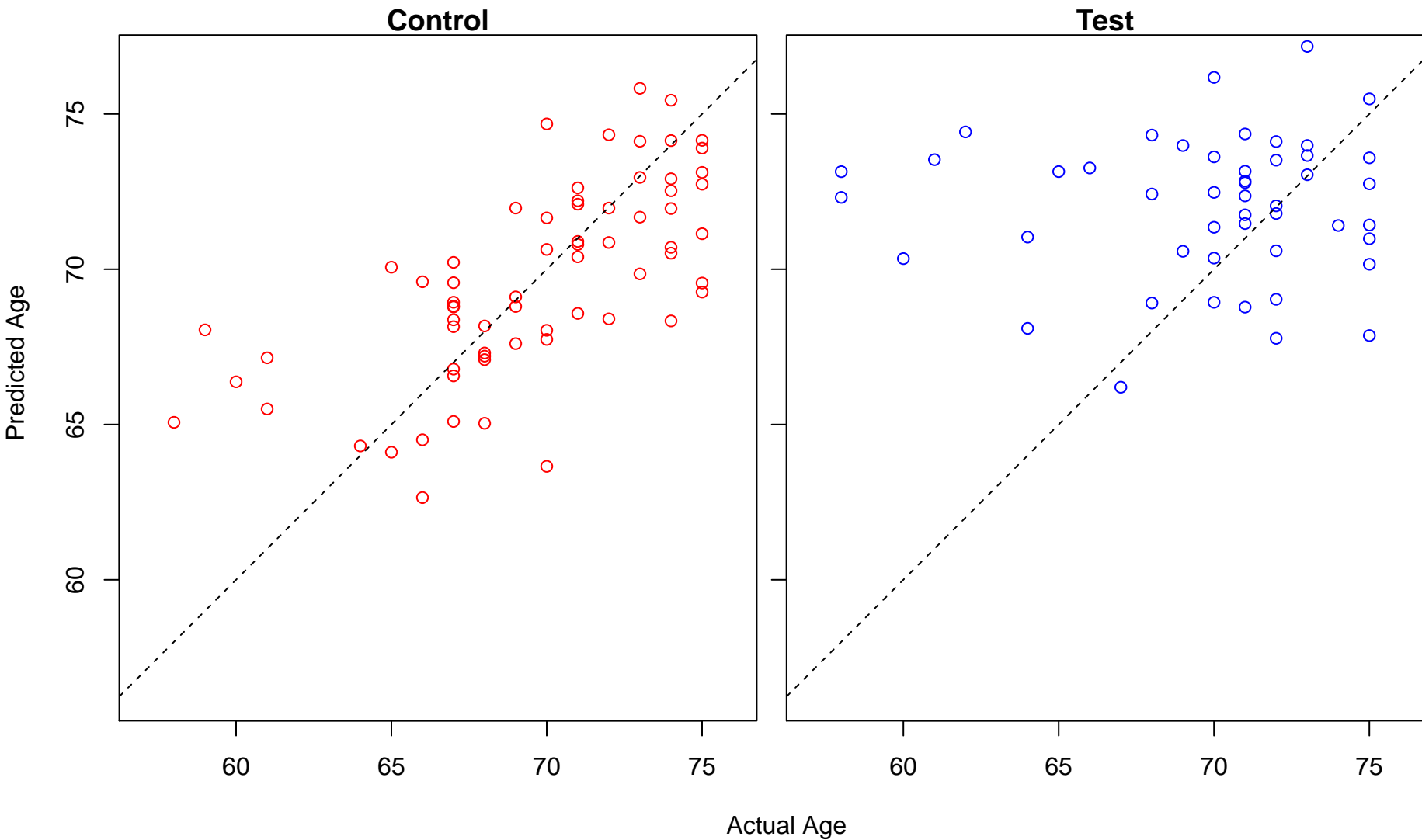
translational elongation (Score: 1.421911)



regulation of histone H3-K27 methylation (Score: 1.421721)

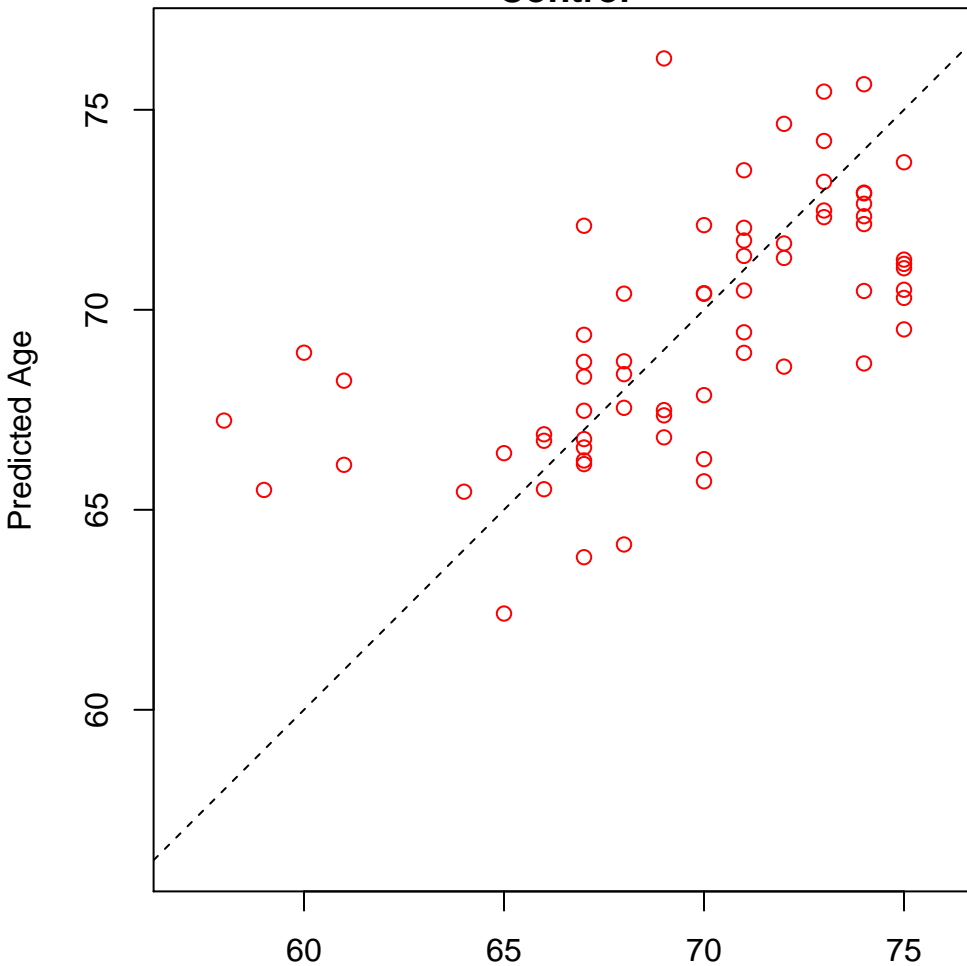


heart trabecula morphogenesis (Score: 1.421503)

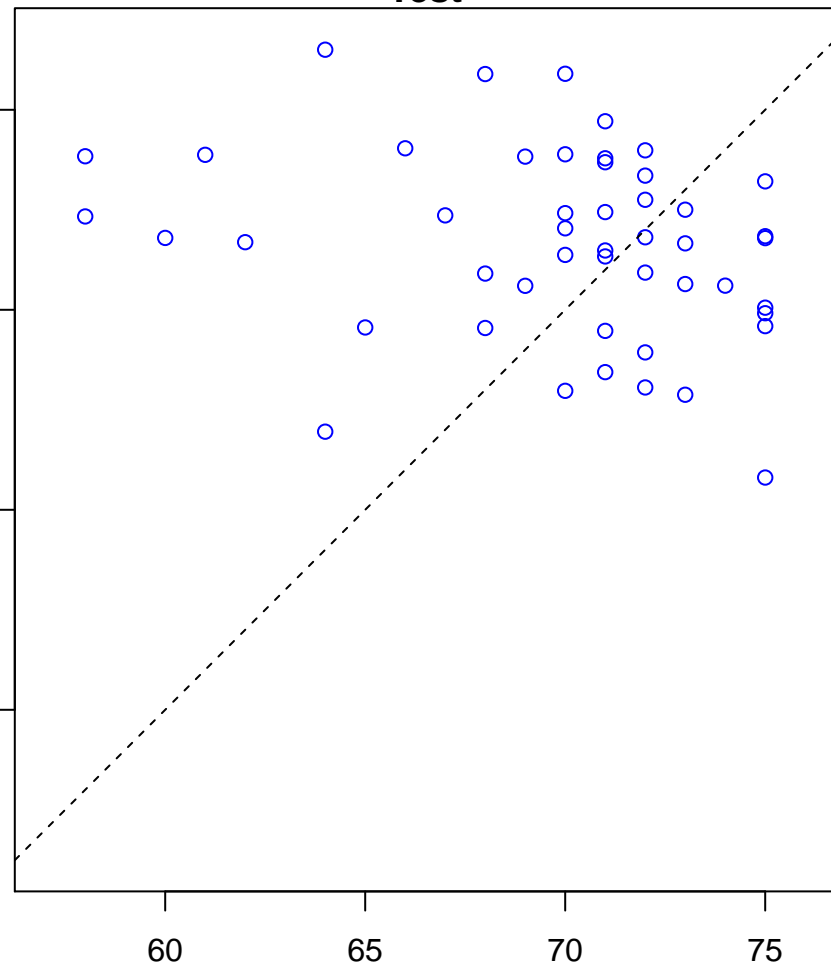


regulation of interleukin-1 production (Score: 1.421361)

Control

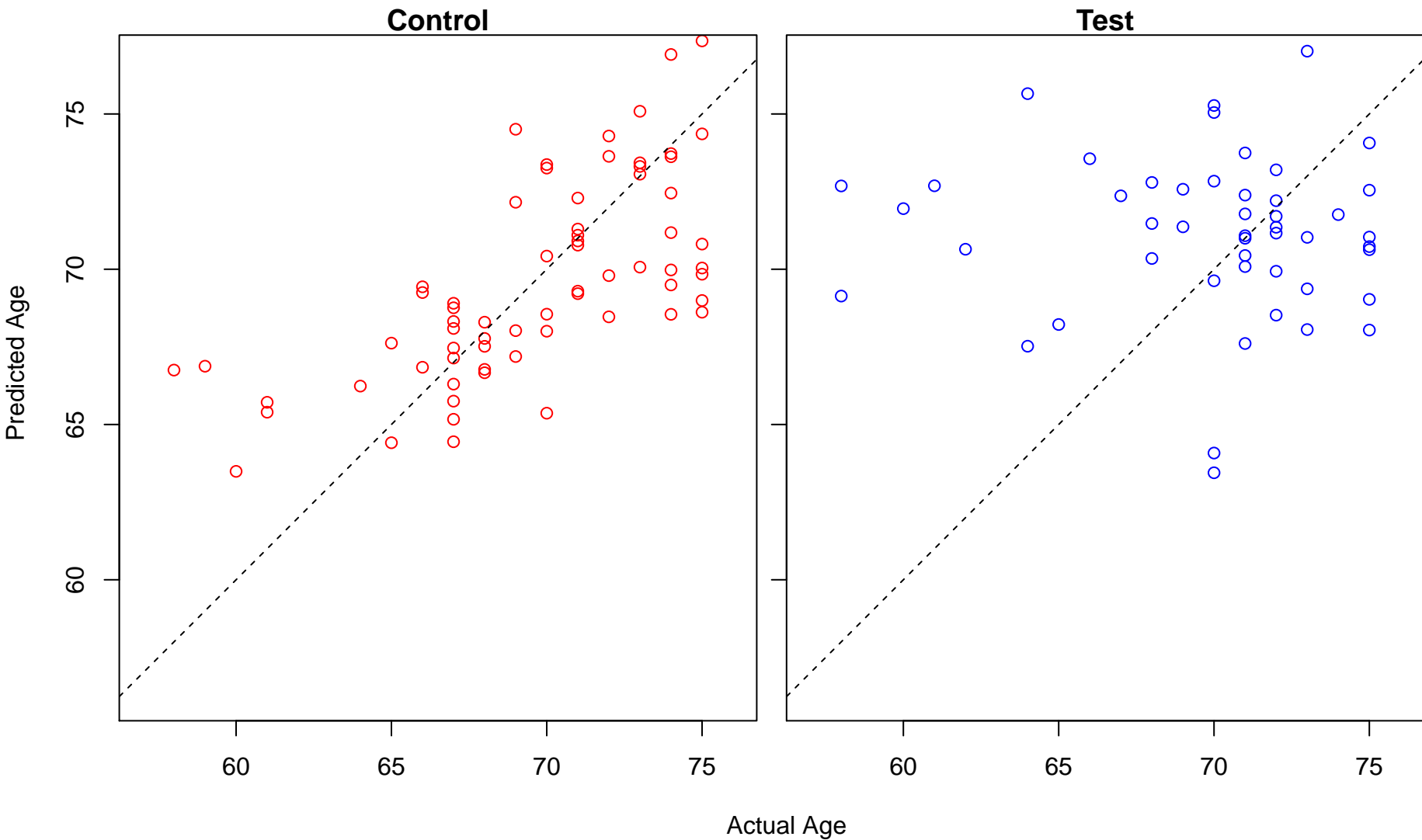


Test

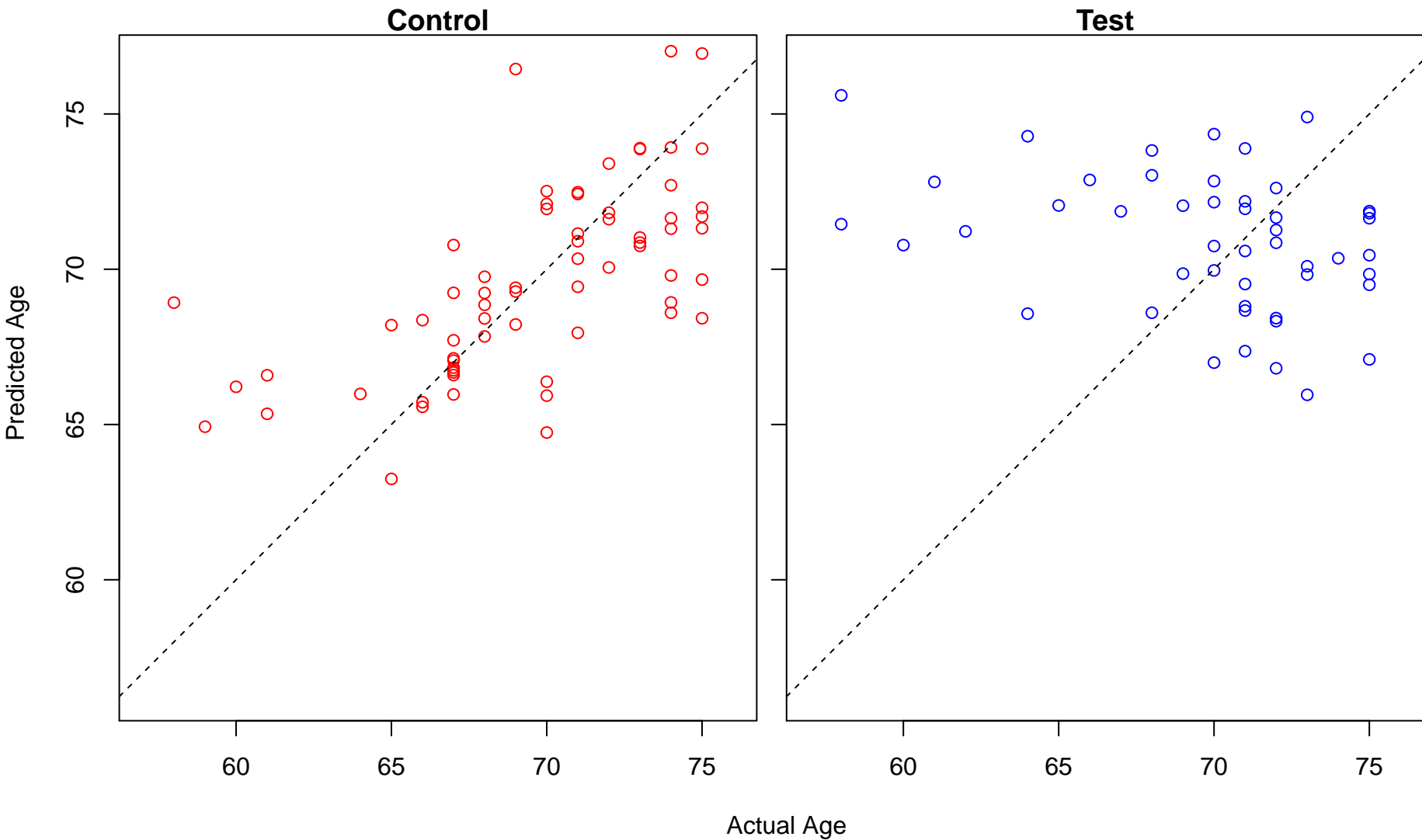


Actual Age

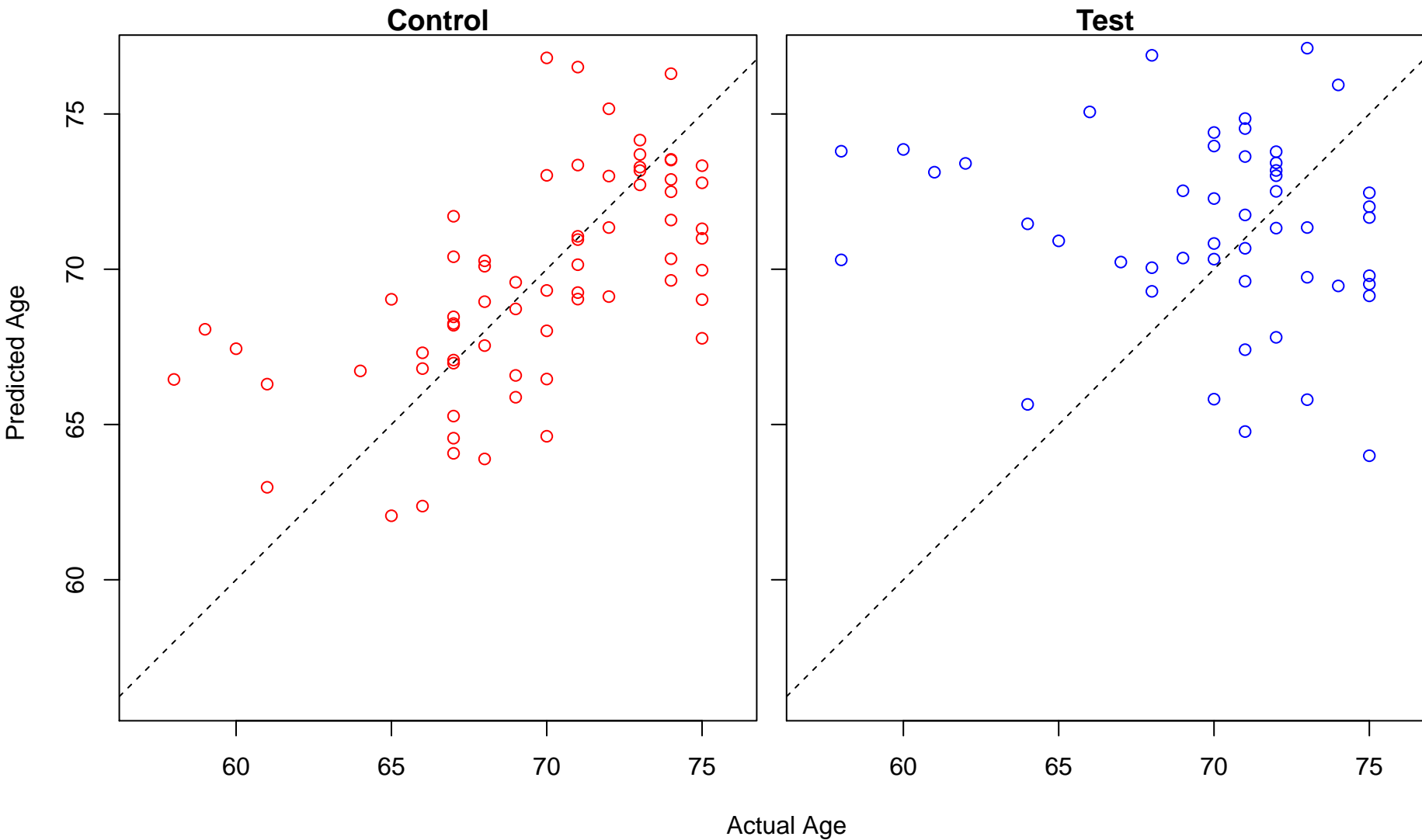
negative regulation of fatty acid oxidation (Score: 1.421002)



positive regulation of transcription factor import into nucleus (Score: 1.420727)

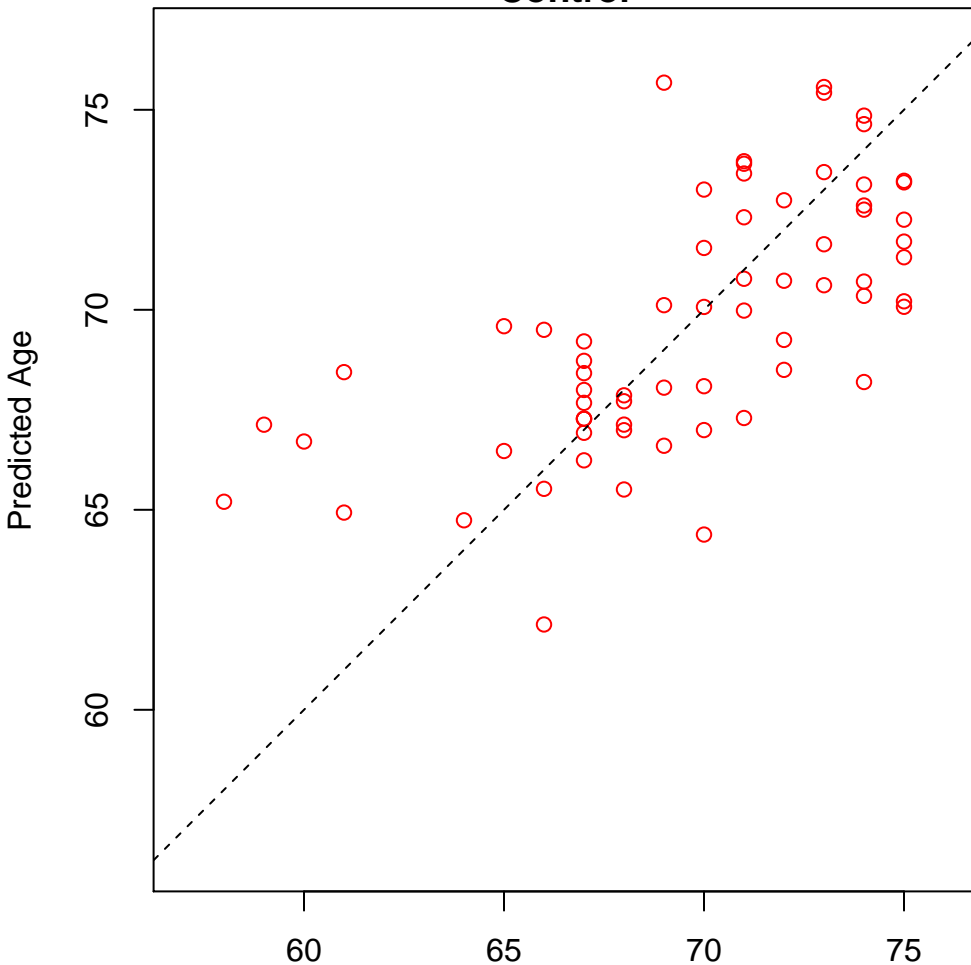


positive regulation of interleukin-1 secretion (Score: 1.420542)

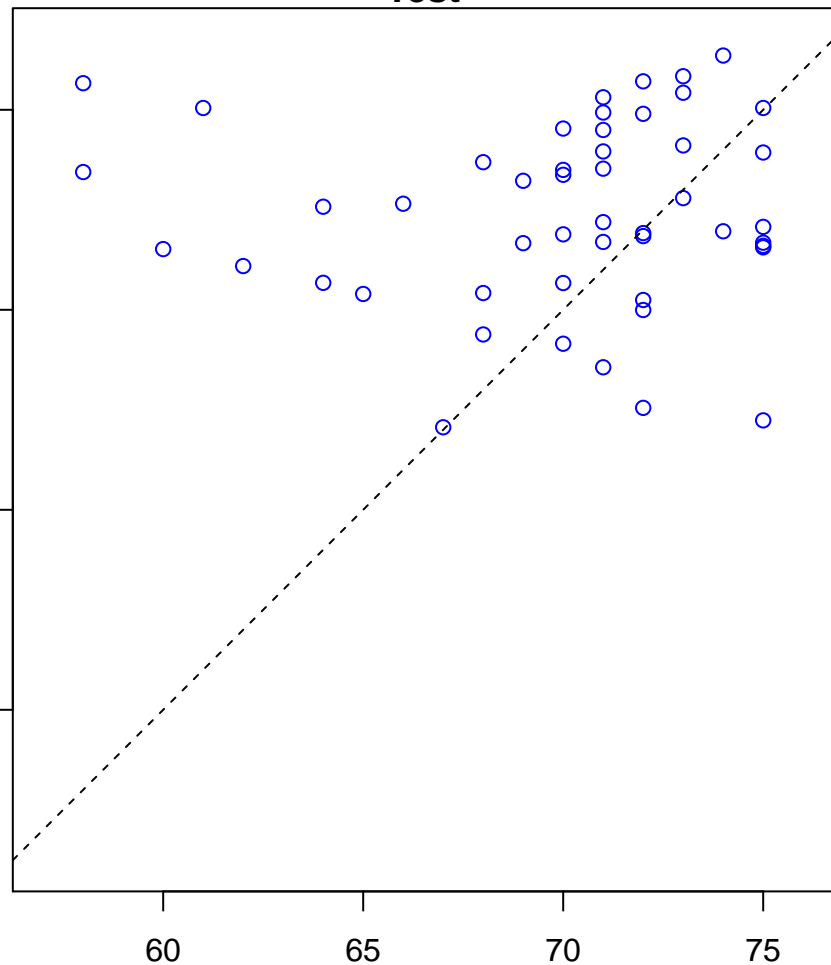


cardiac muscle tissue morphogenesis (Score: 1.420477)

Control

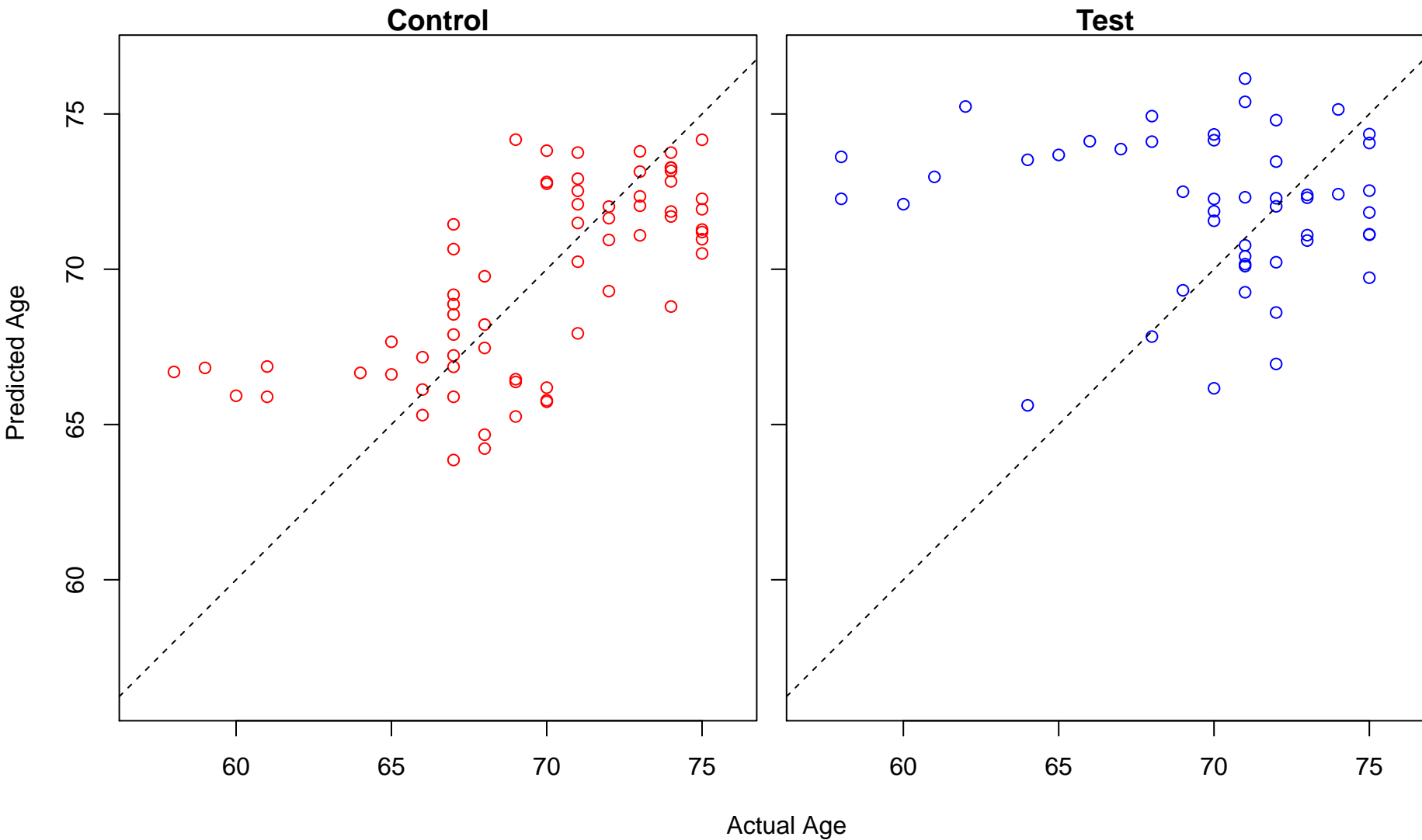


Test

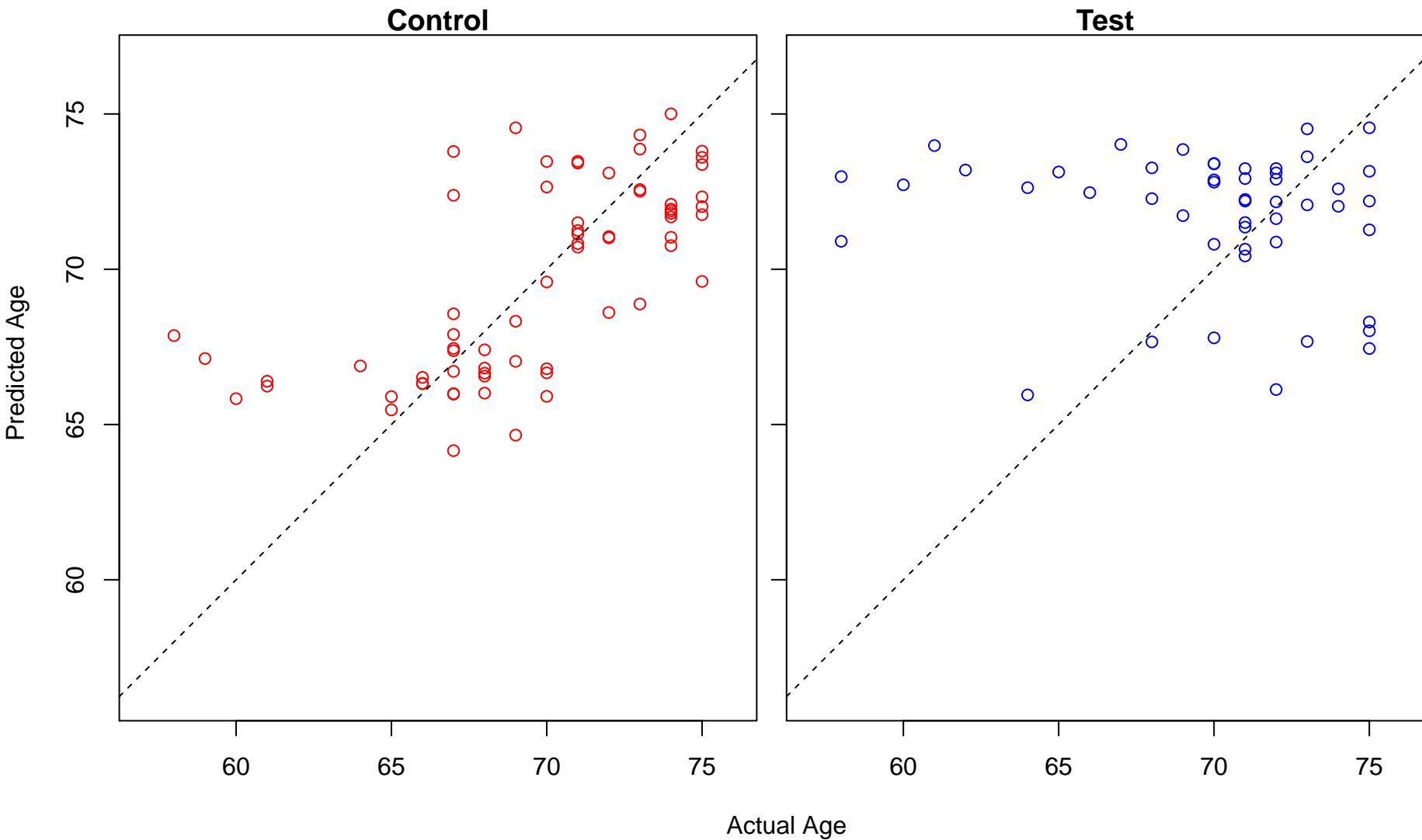


Actual Age

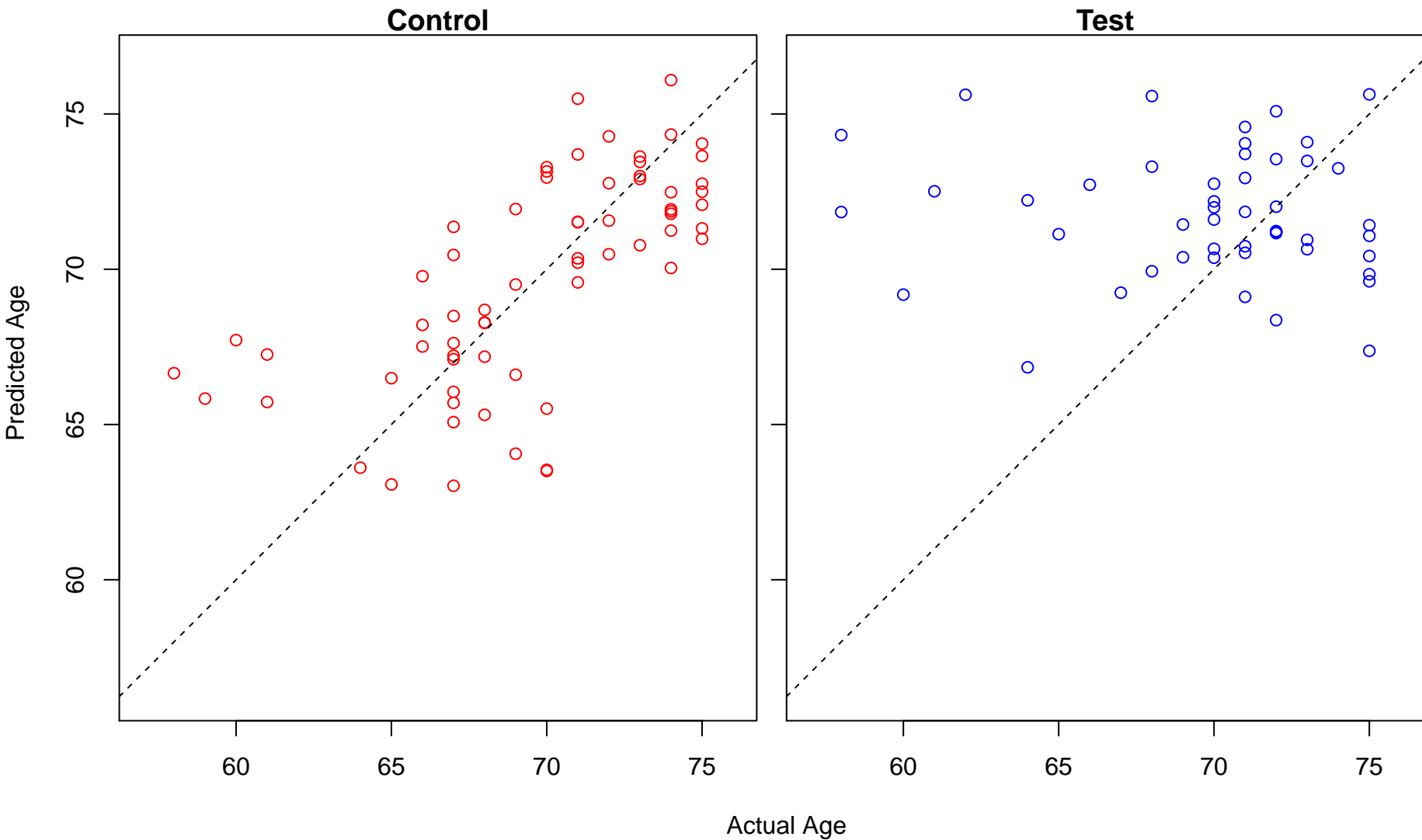
positive regulation of histone methylation (Score: 1.420458)



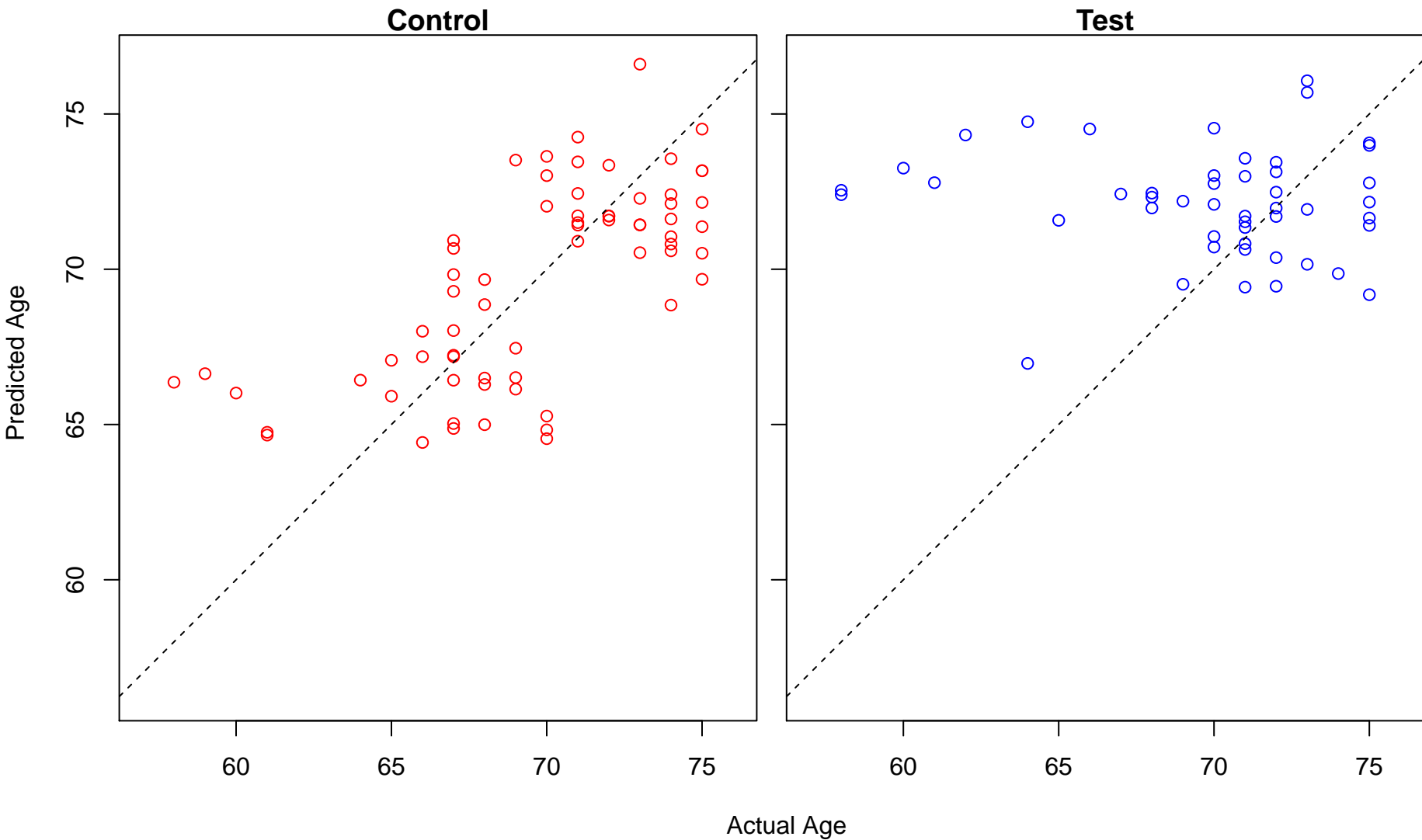
mRNA 3'-splice site recognition (Score: 1.420036)



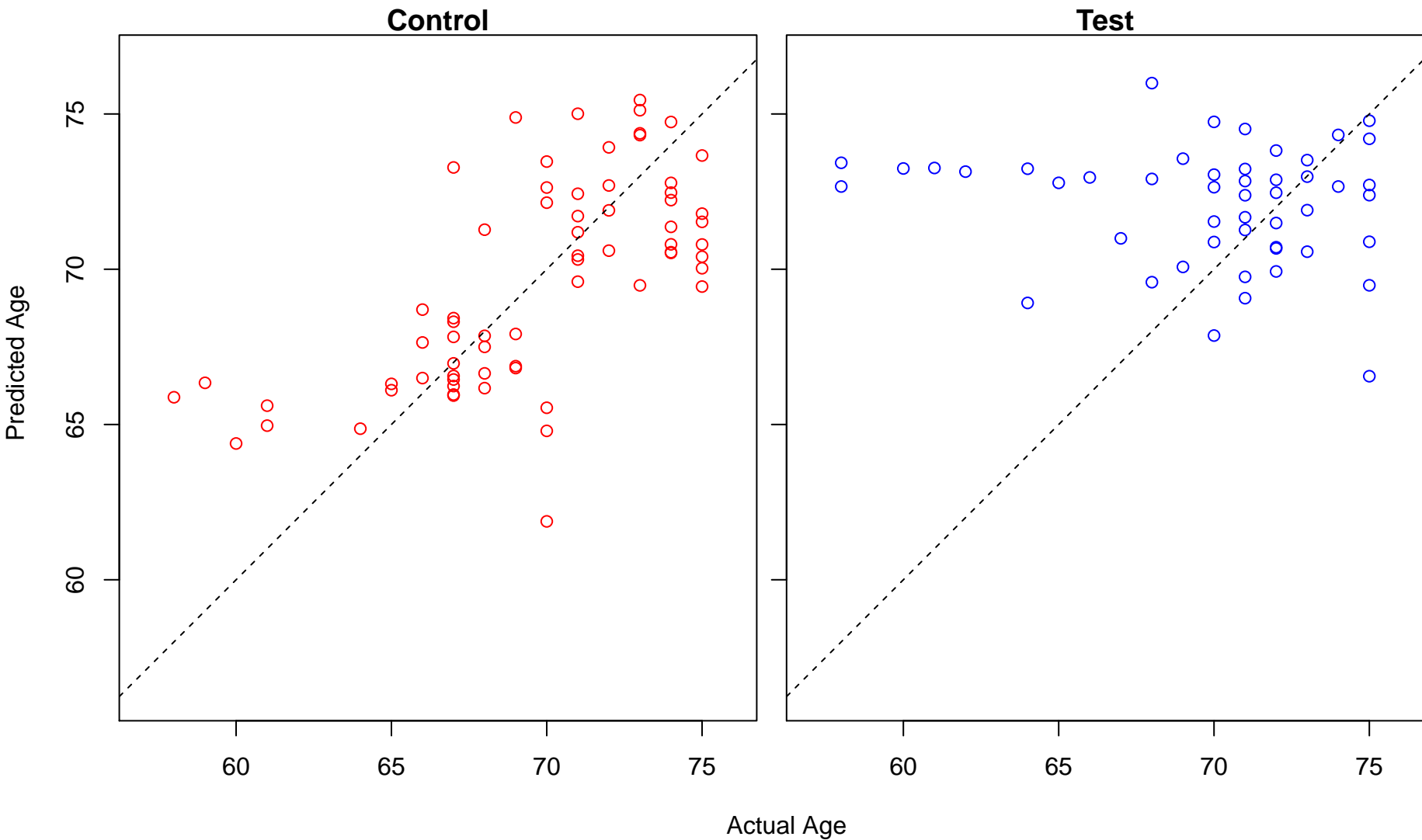
negative regulation of translation (Score: 1.418997)



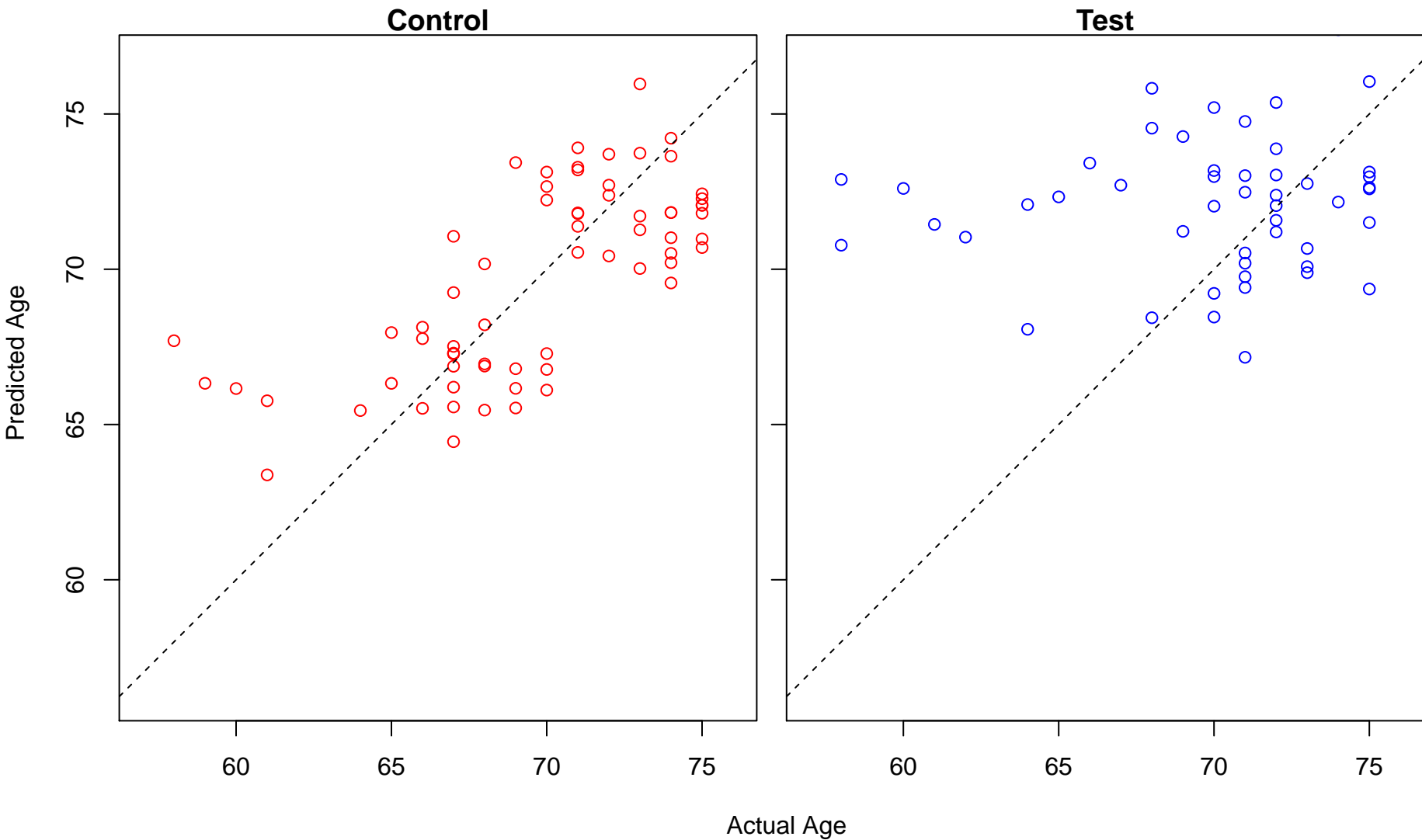
regulation of cellular response to growth factor stimulus (Score: 1.417586)



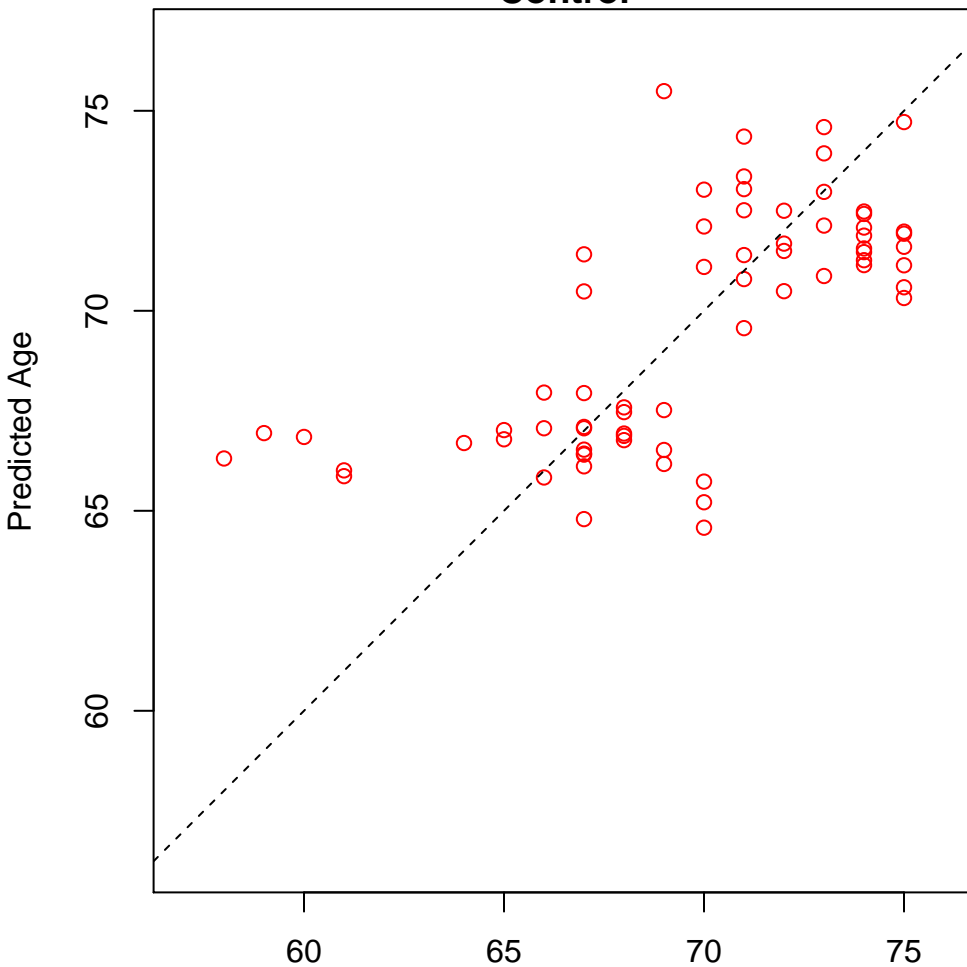
negative regulation of proteolysis involved in cellular protein catabolic process (Score: 1.416952)



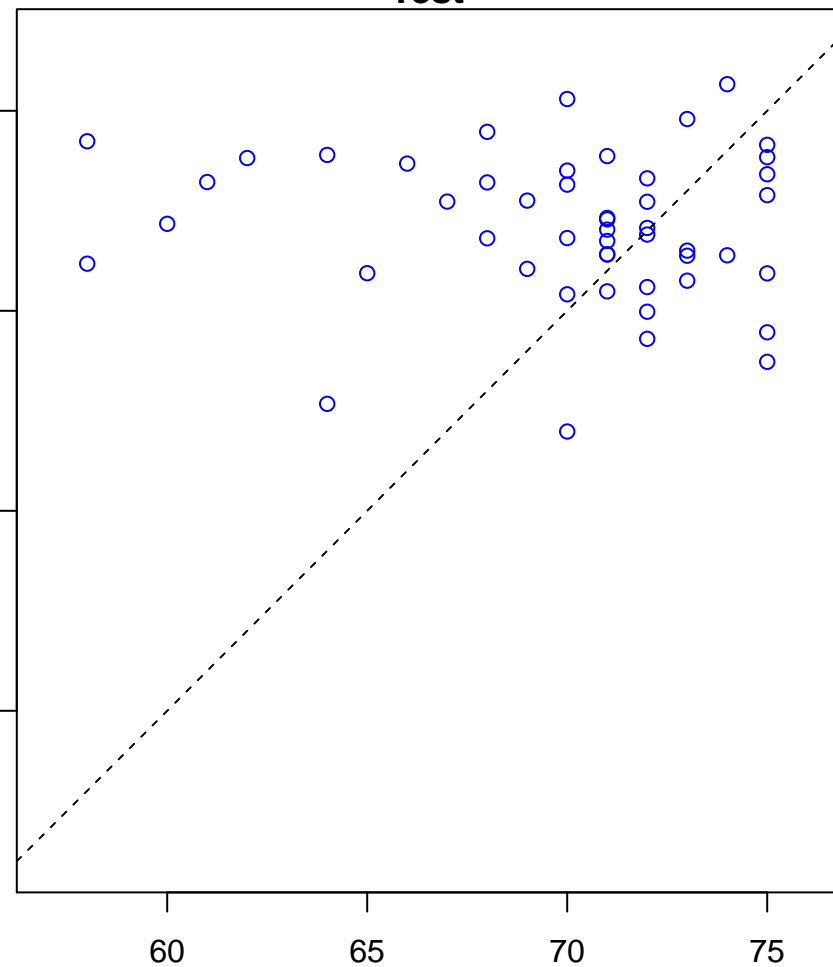
chromatin silencing at rDNA (Score: 1.416060)



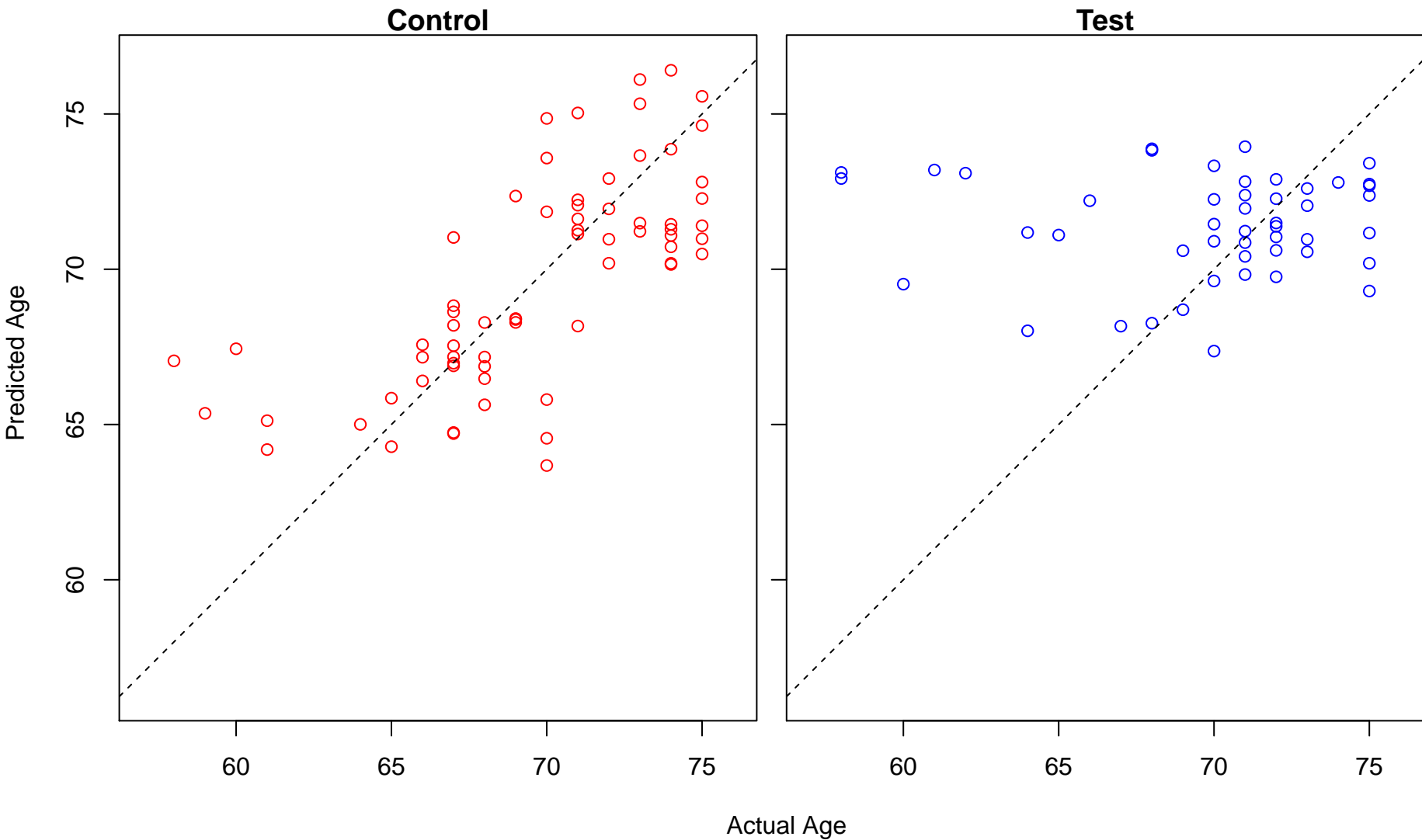
Control



Test

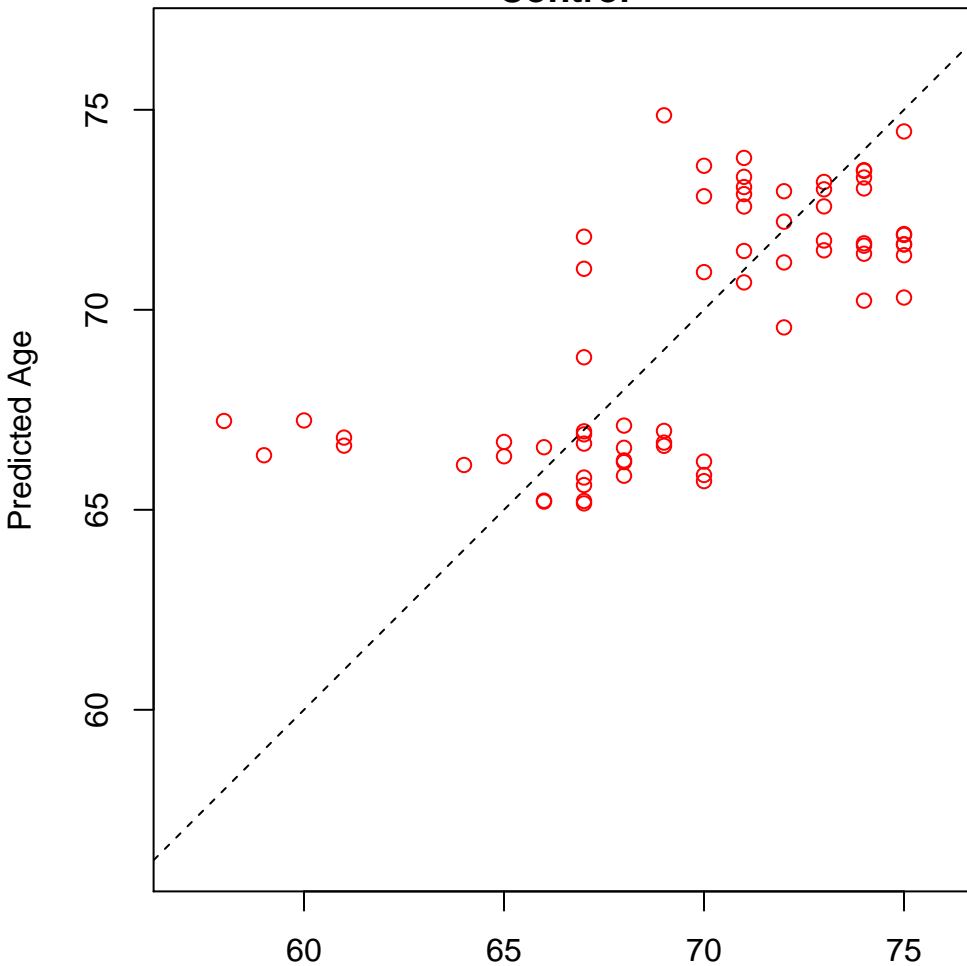


negative regulation of phosphatase activity (Score: 1.415146)

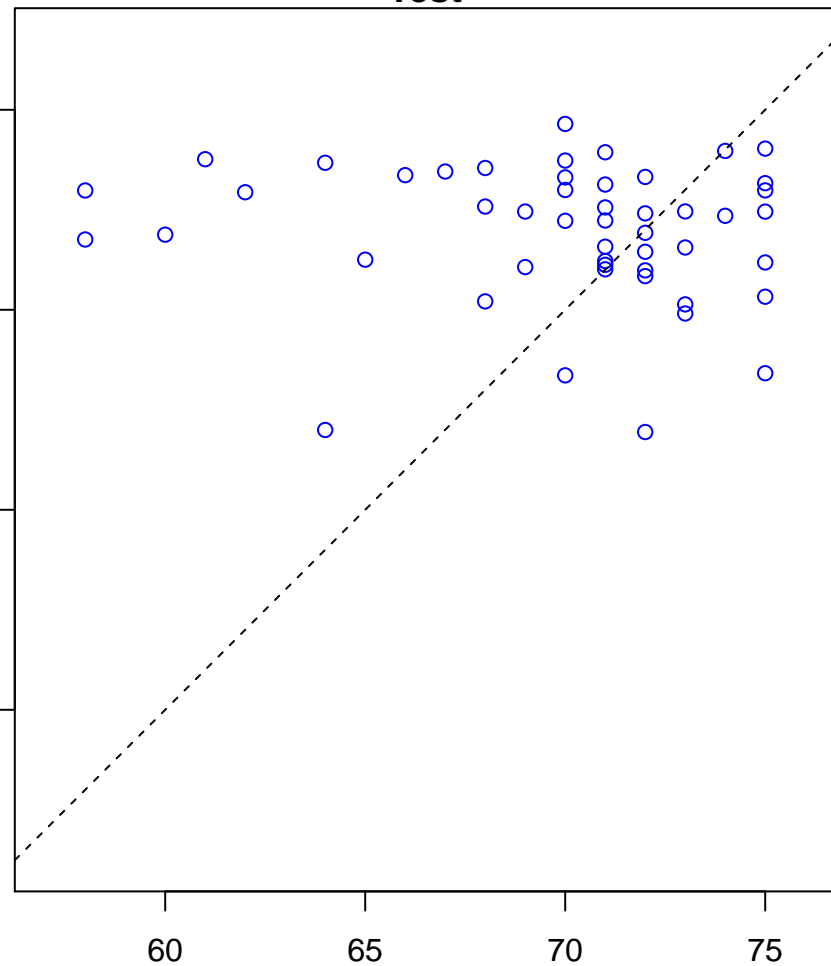


cellular protein complex disassembly (Score: 1.414297)

Control

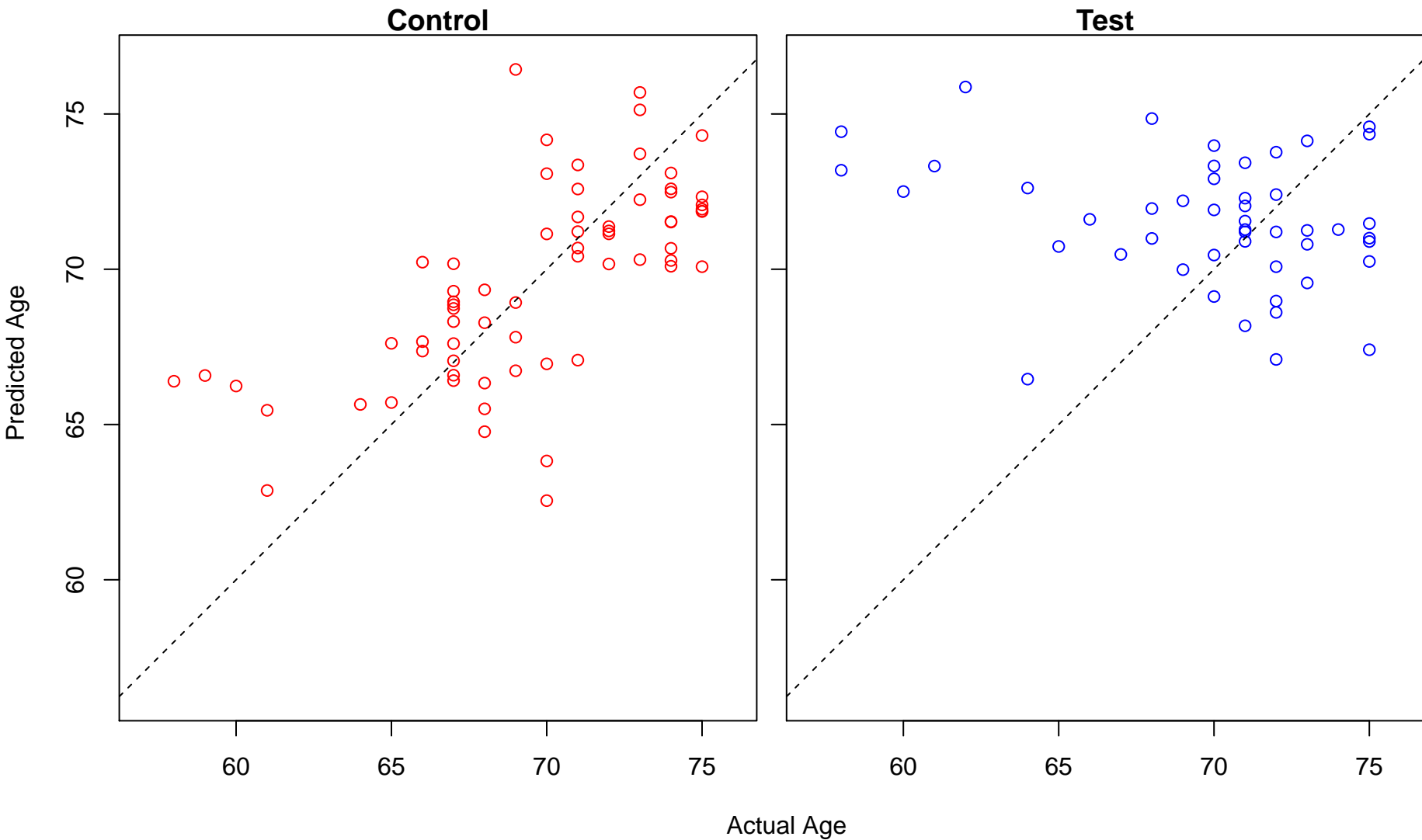


Test

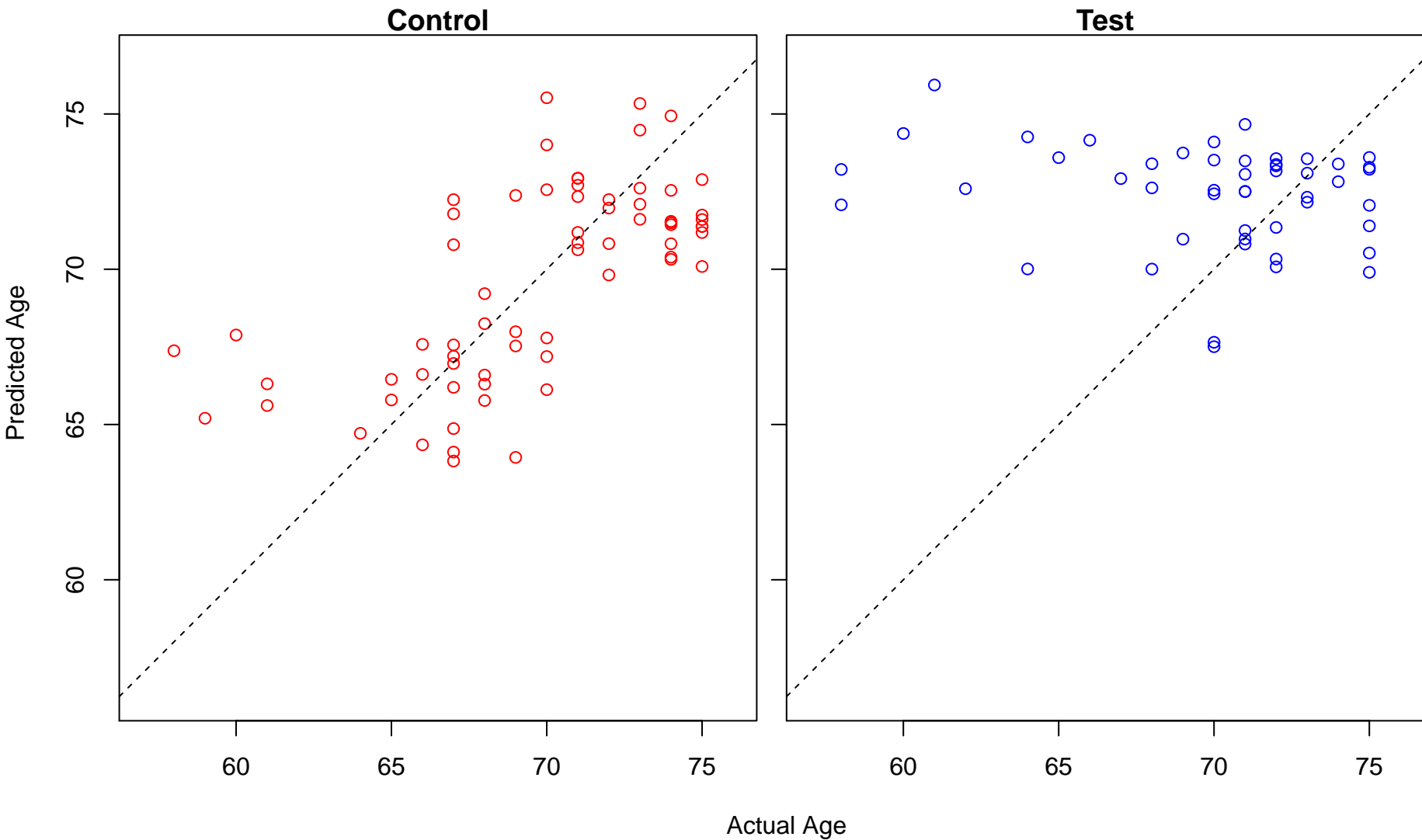


Actual Age

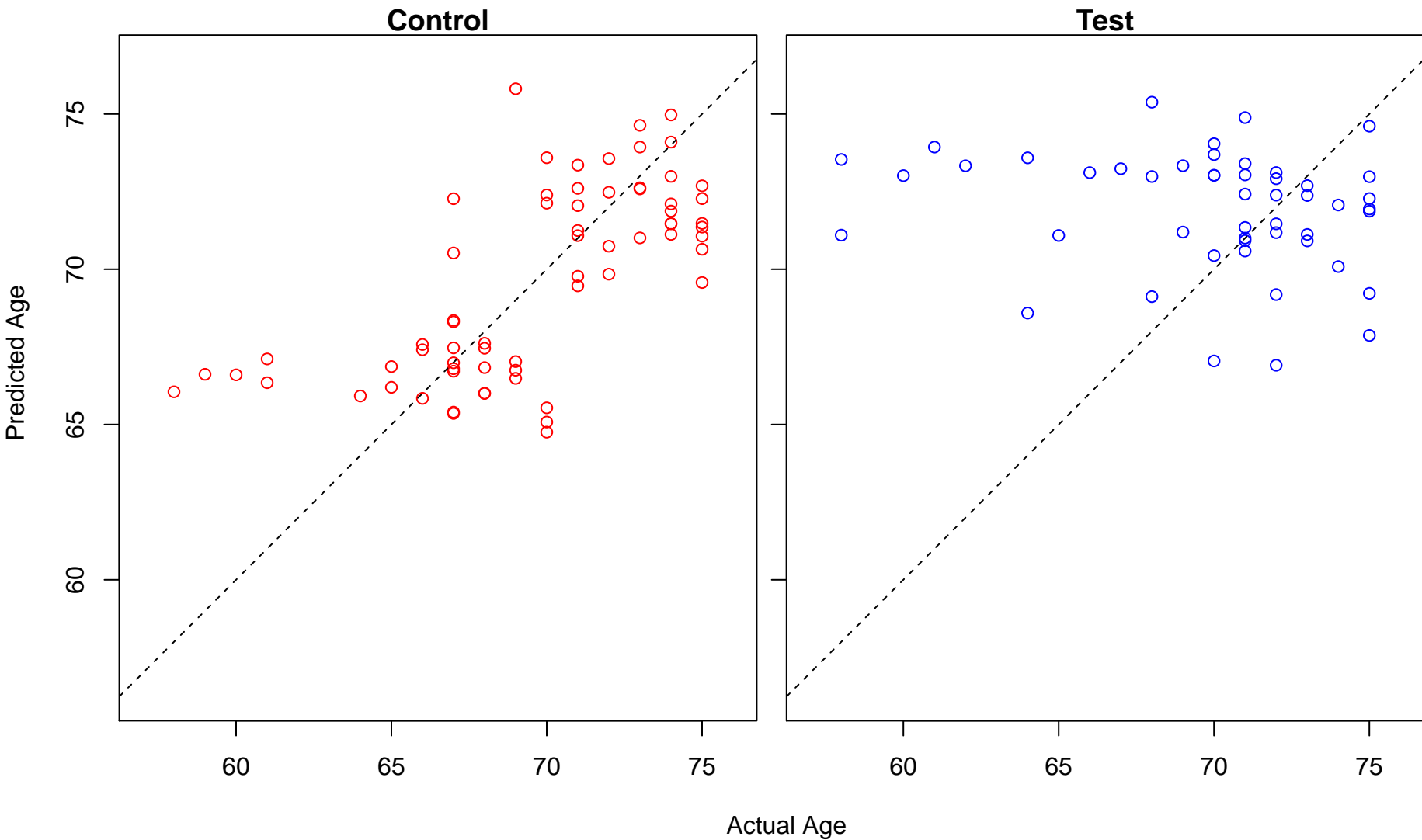
respiratory gaseous exchange (Score: 1.413735)



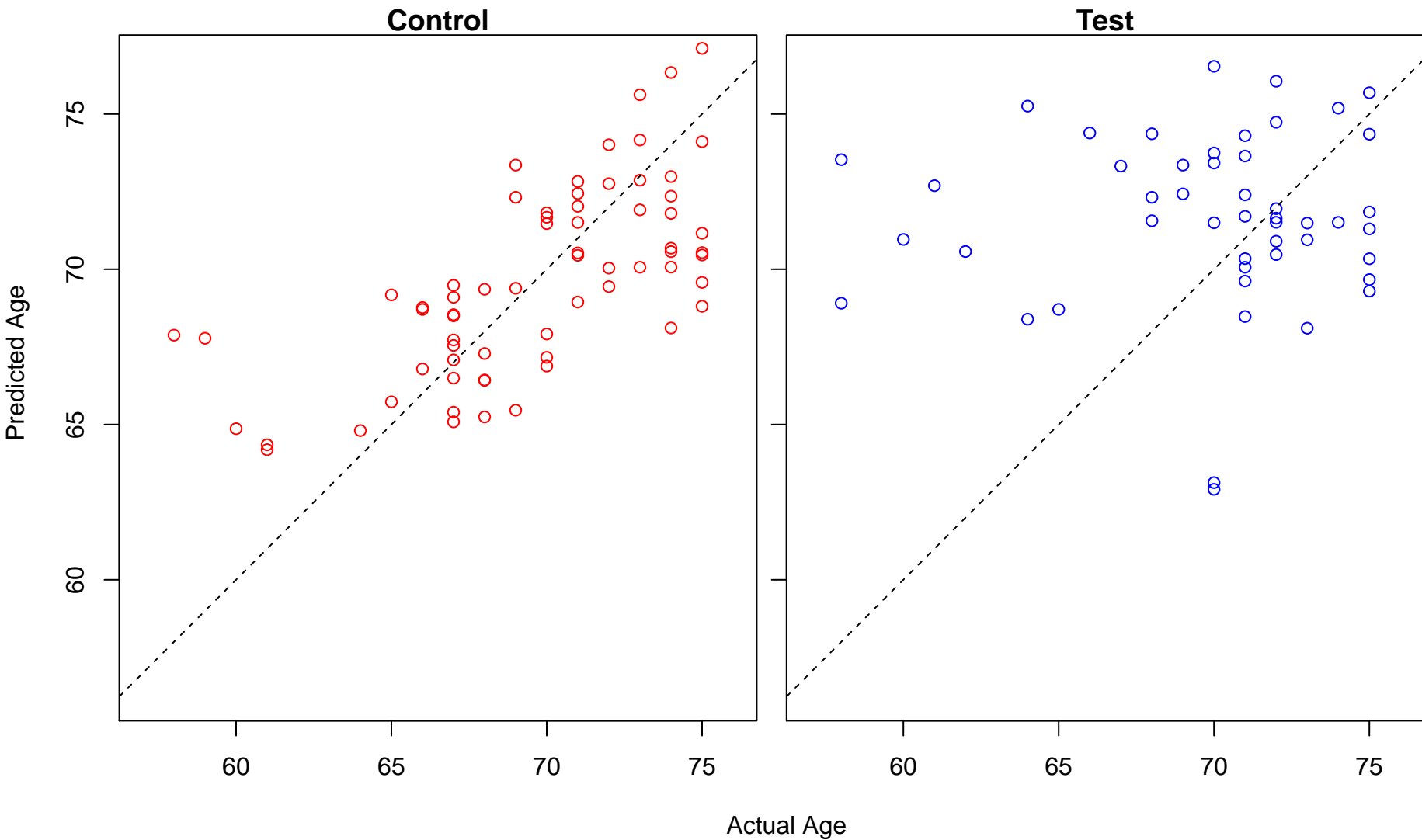
meiotic nuclear division (Score: 1.413690)



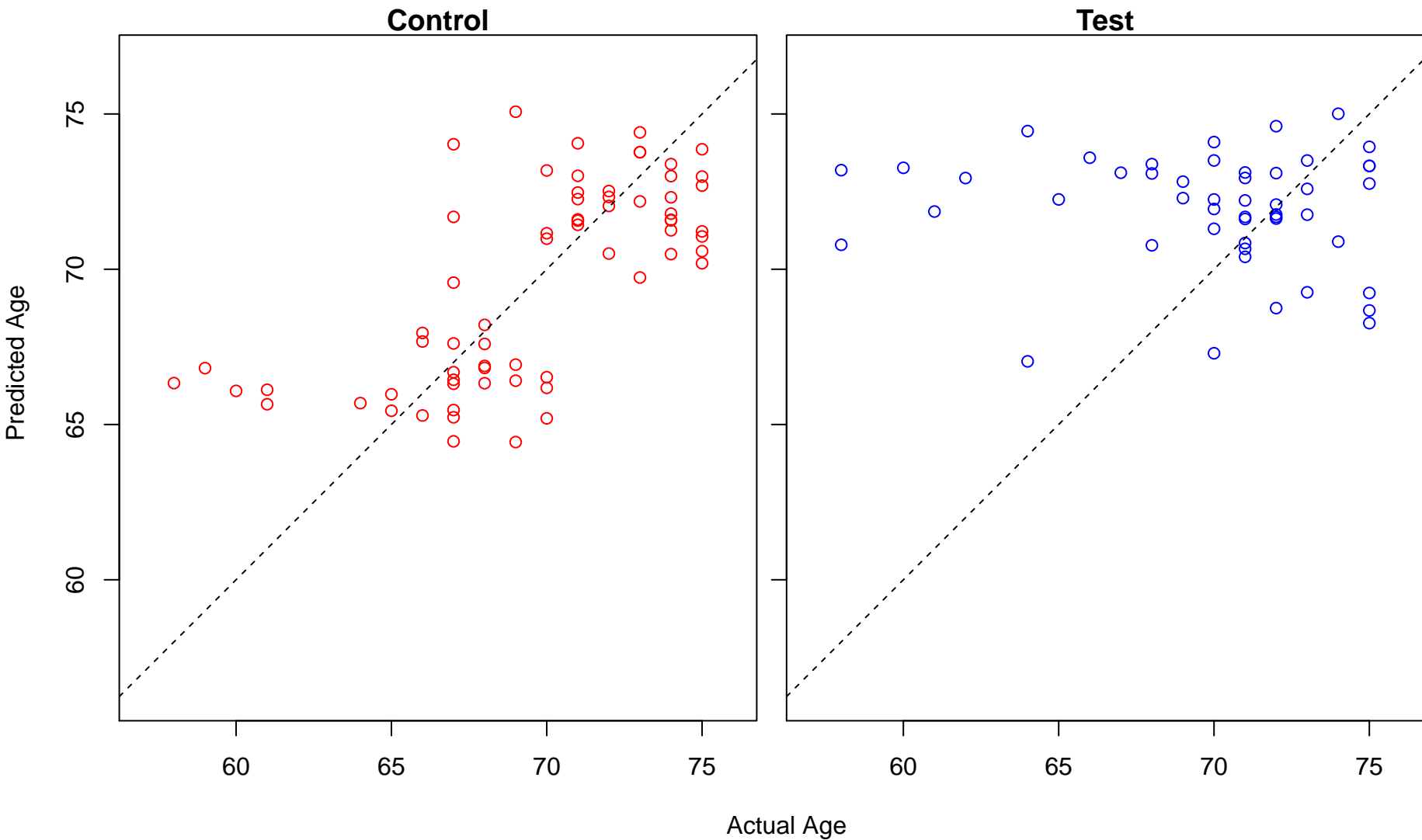
spindle checkpoint (Score: 1.413391)



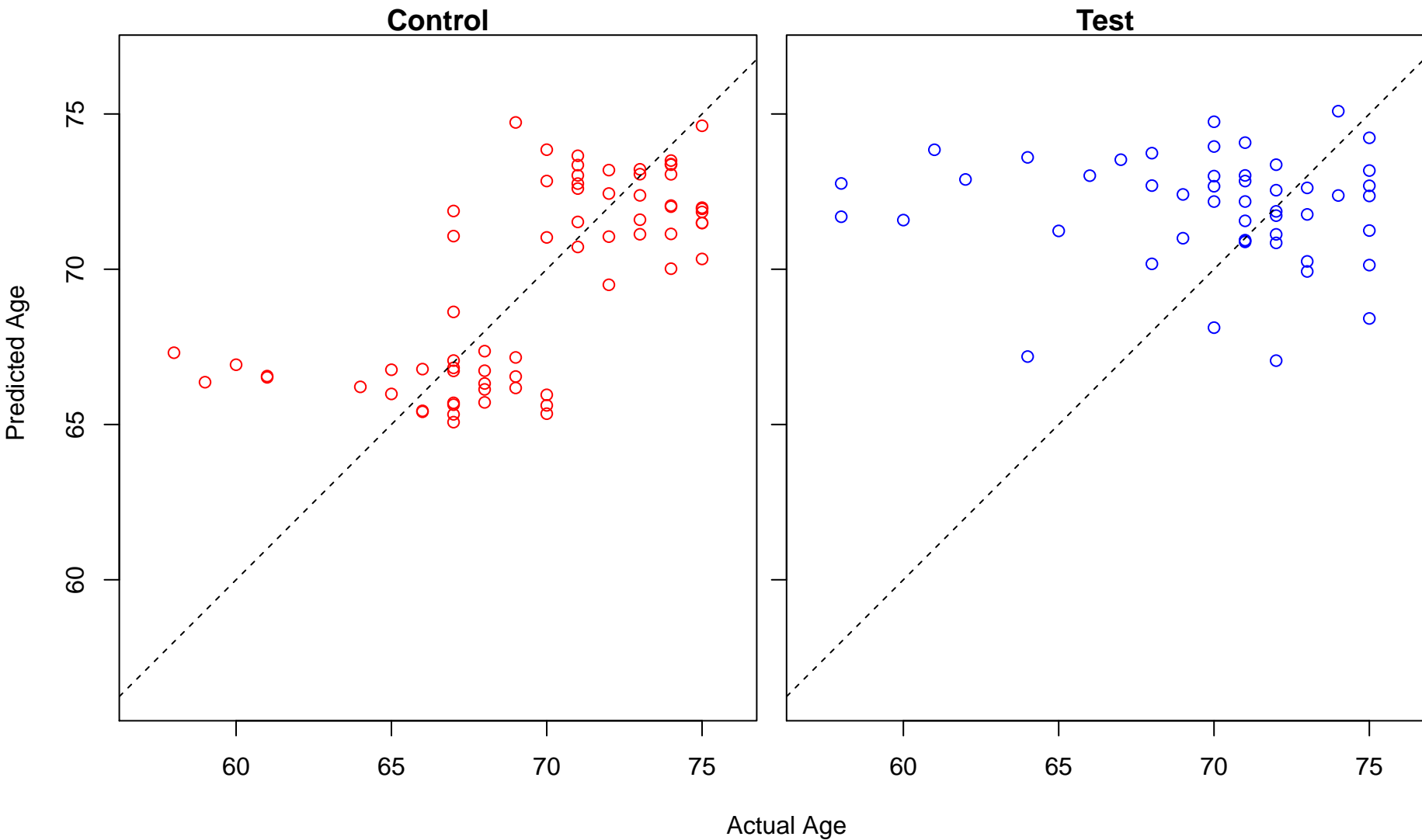
negative regulation of fatty acid biosynthetic process (Score: 1.413364)



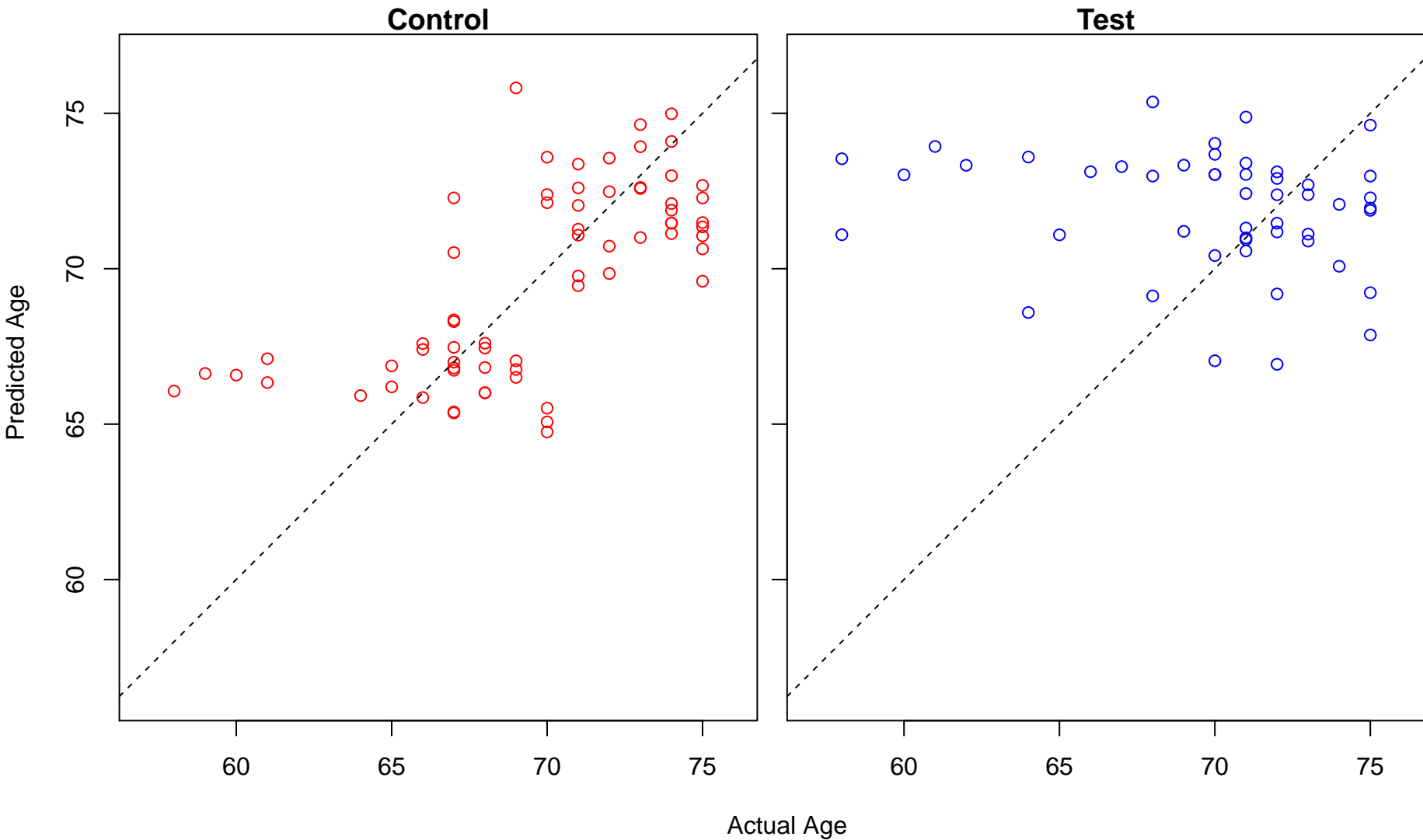
spliceosomal complex assembly (Score: 1.413354)



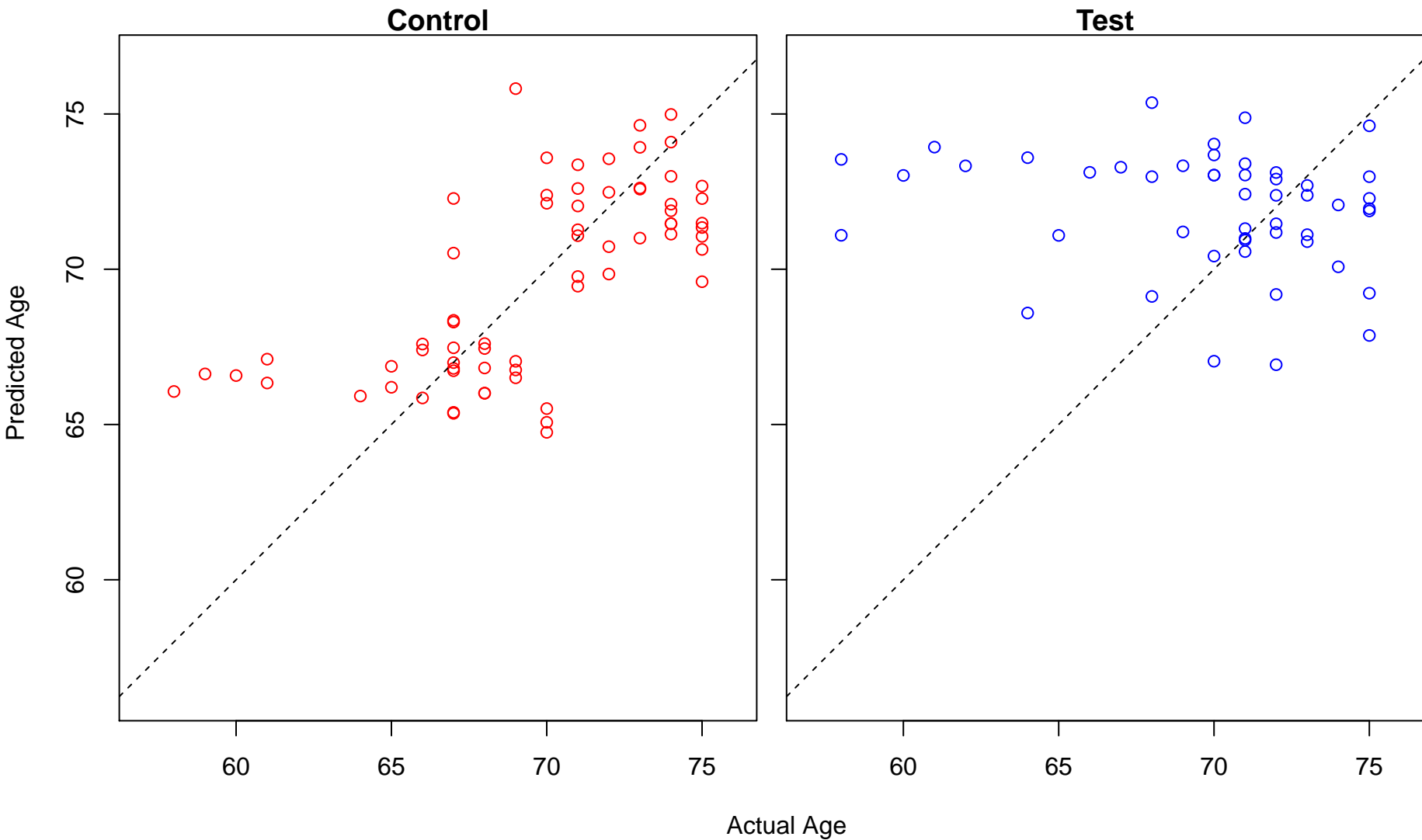
peptide metabolic process (Score: 1.413003)



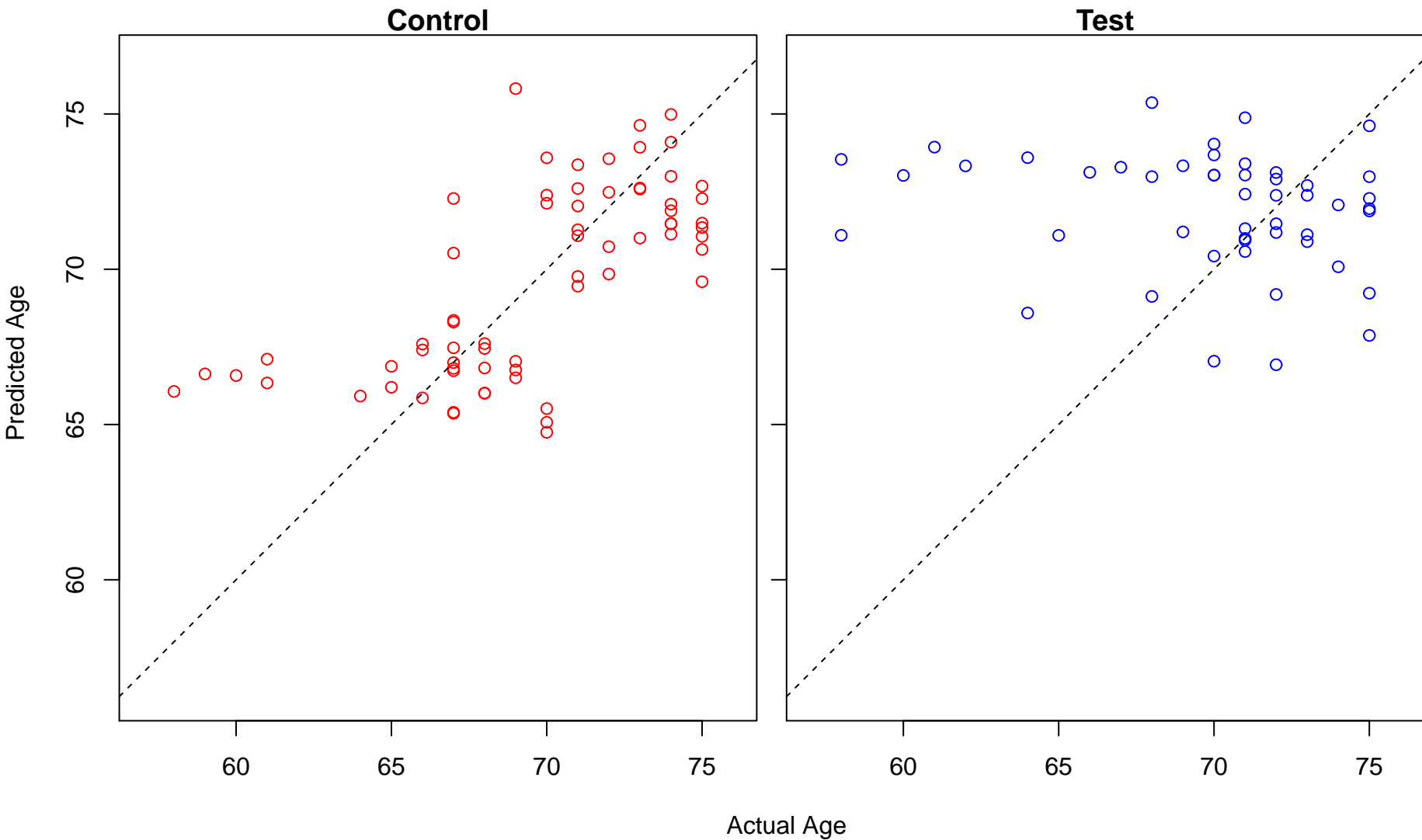
negative regulation of mitotic metaphase/anaphase transition (Score: 1.412983)



mitotic spindle checkpoint (Score: 1.412983)

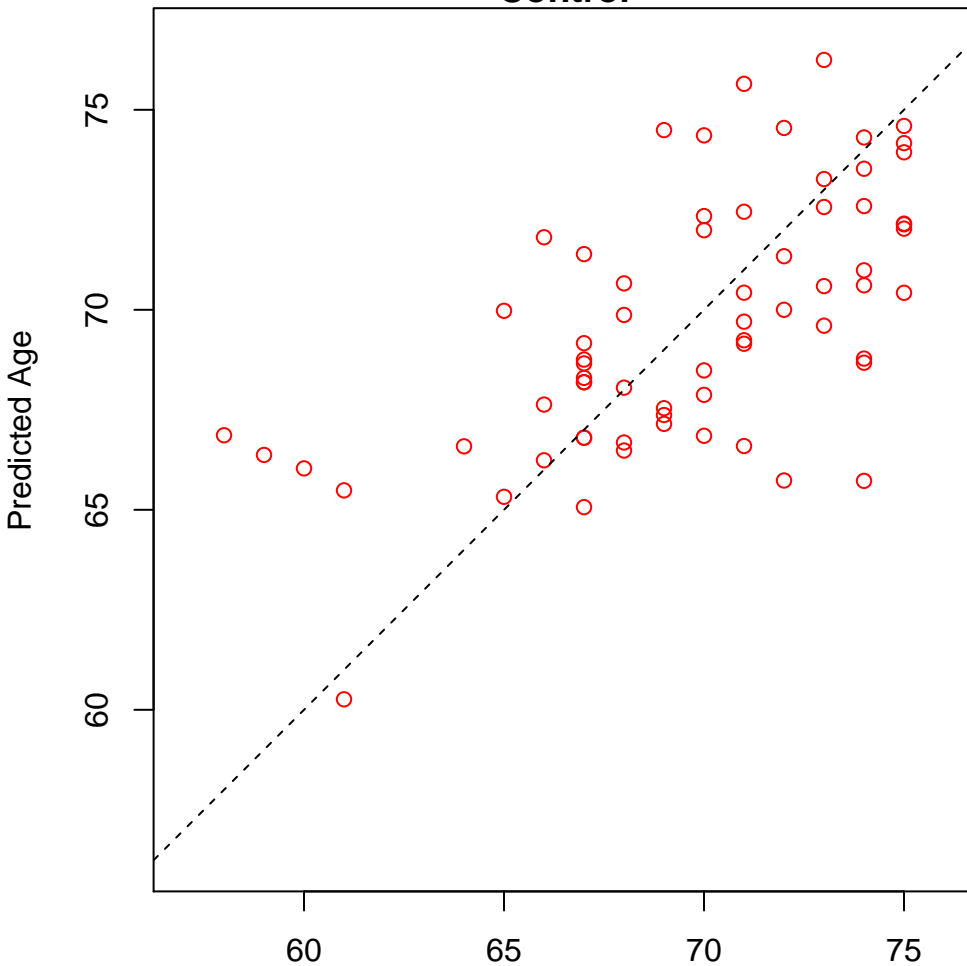


negative regulation of mitotic sister chromatid separation (Score: 1.412983)

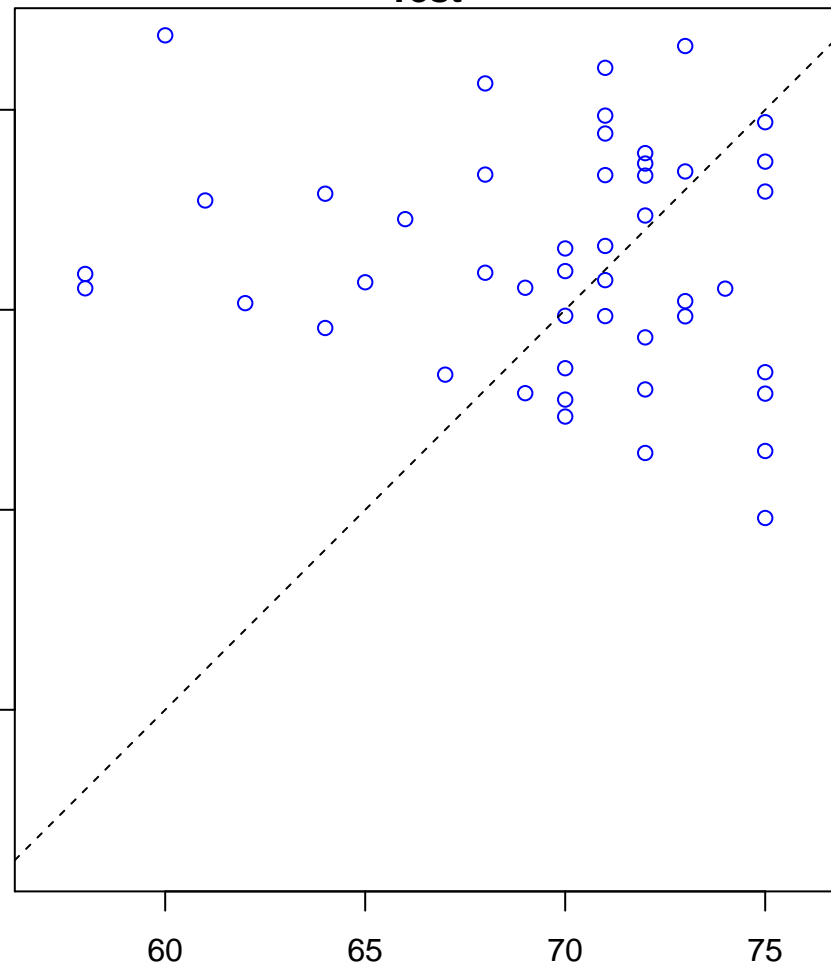


neurotransmitter metabolic process (Score: 1.412922)

Control

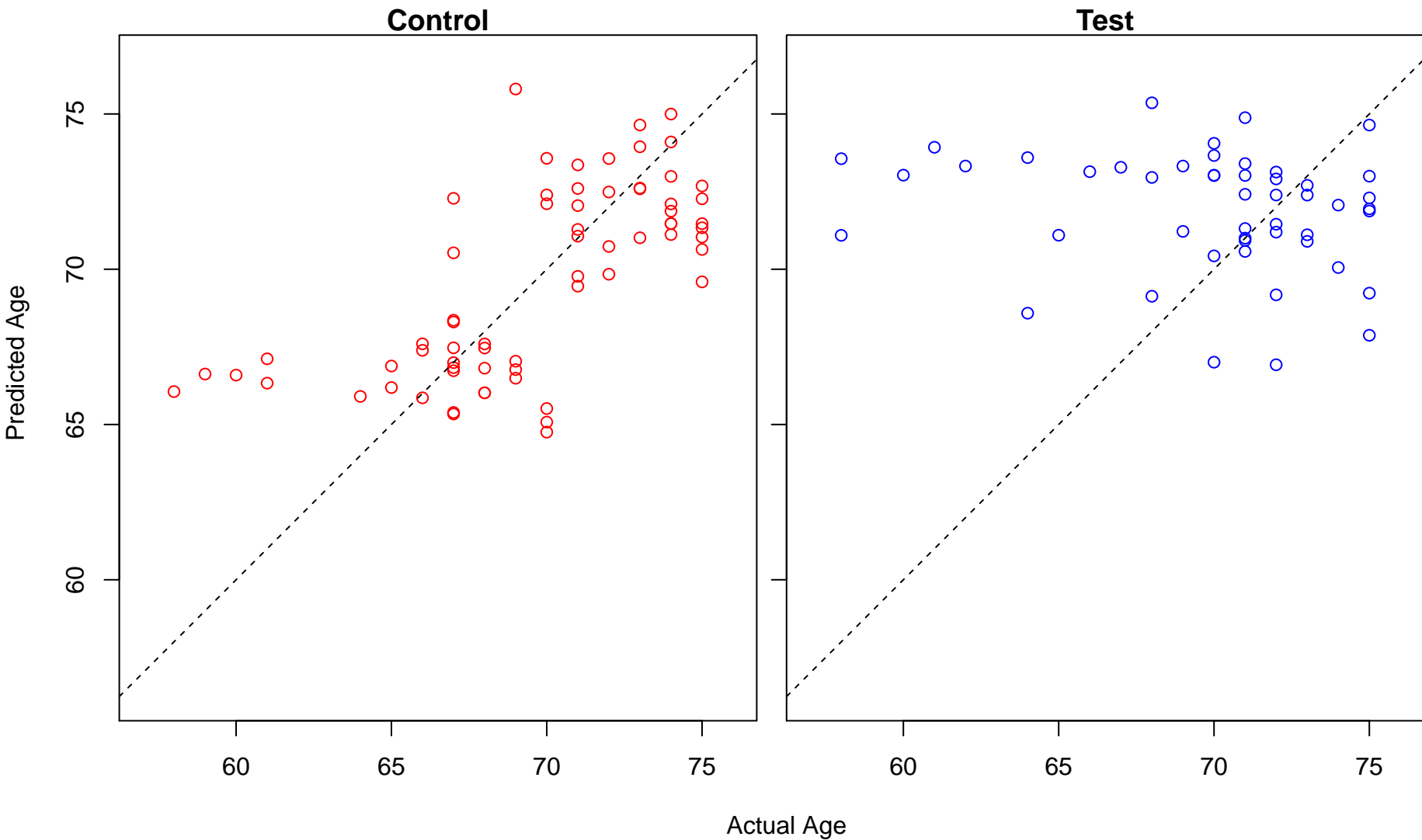


Test



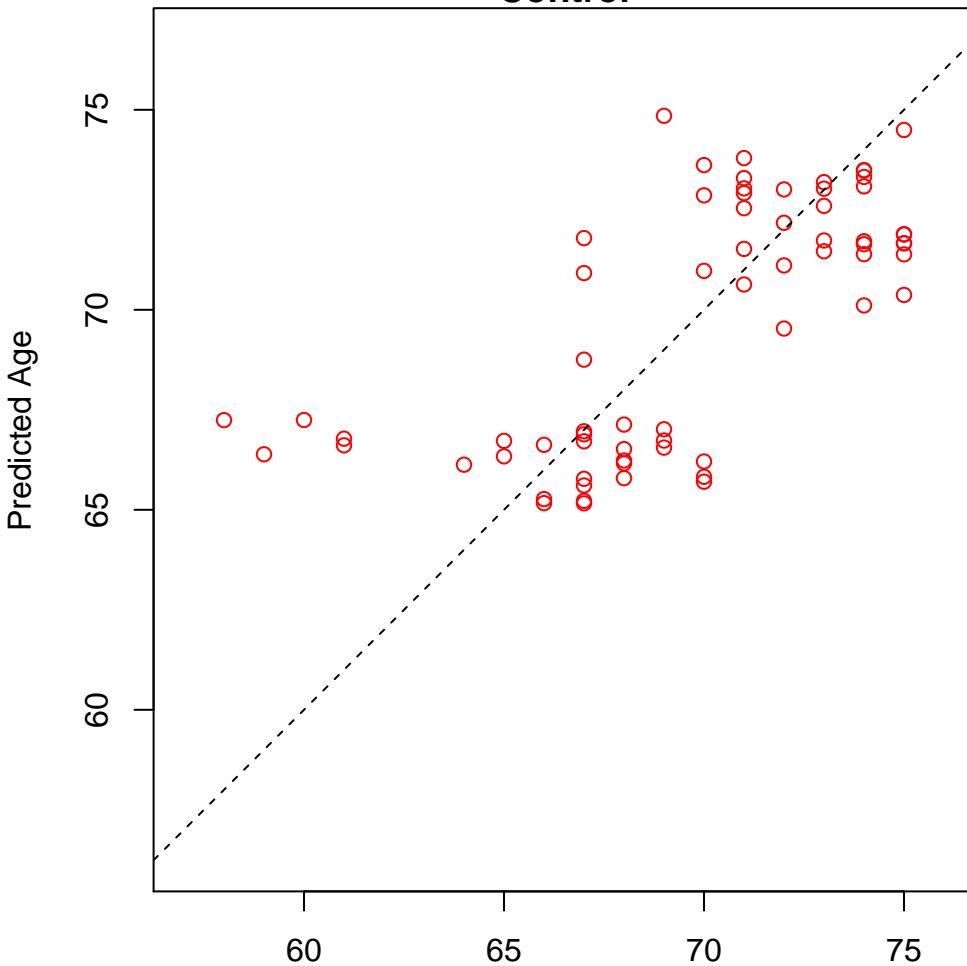
Actual Age

negative regulation of metaphase/anaphase transition of cell cycle (Score: 1.412575)

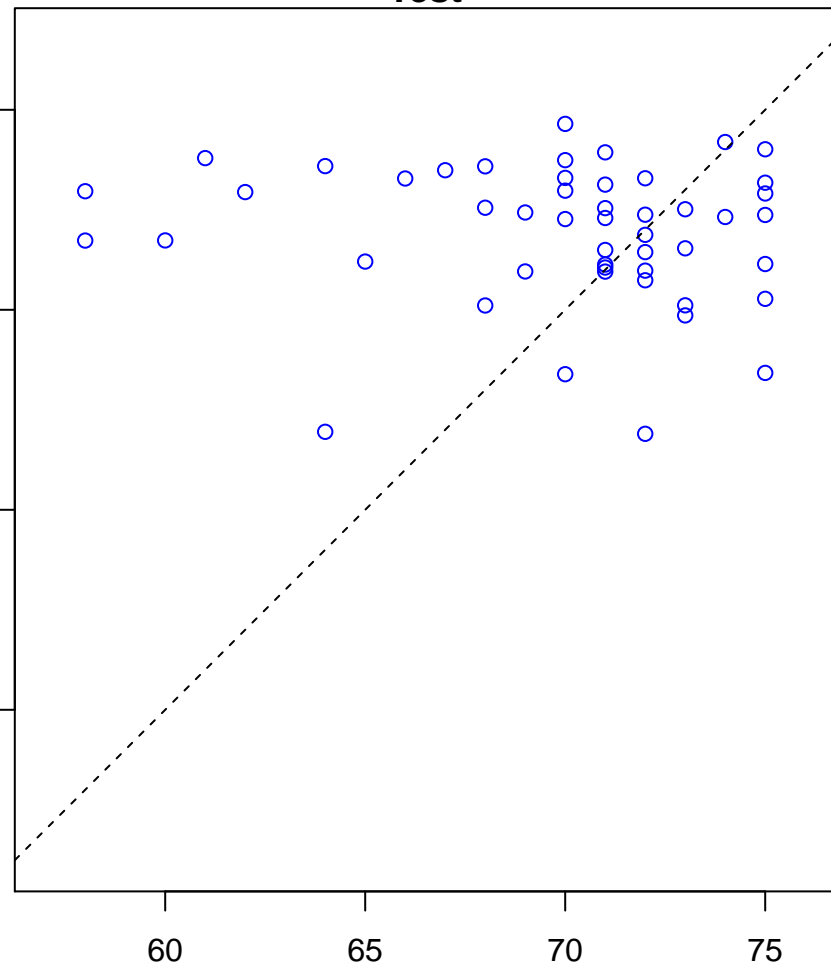


macromolecular complex disassembly (Score: 1.412408)

Control

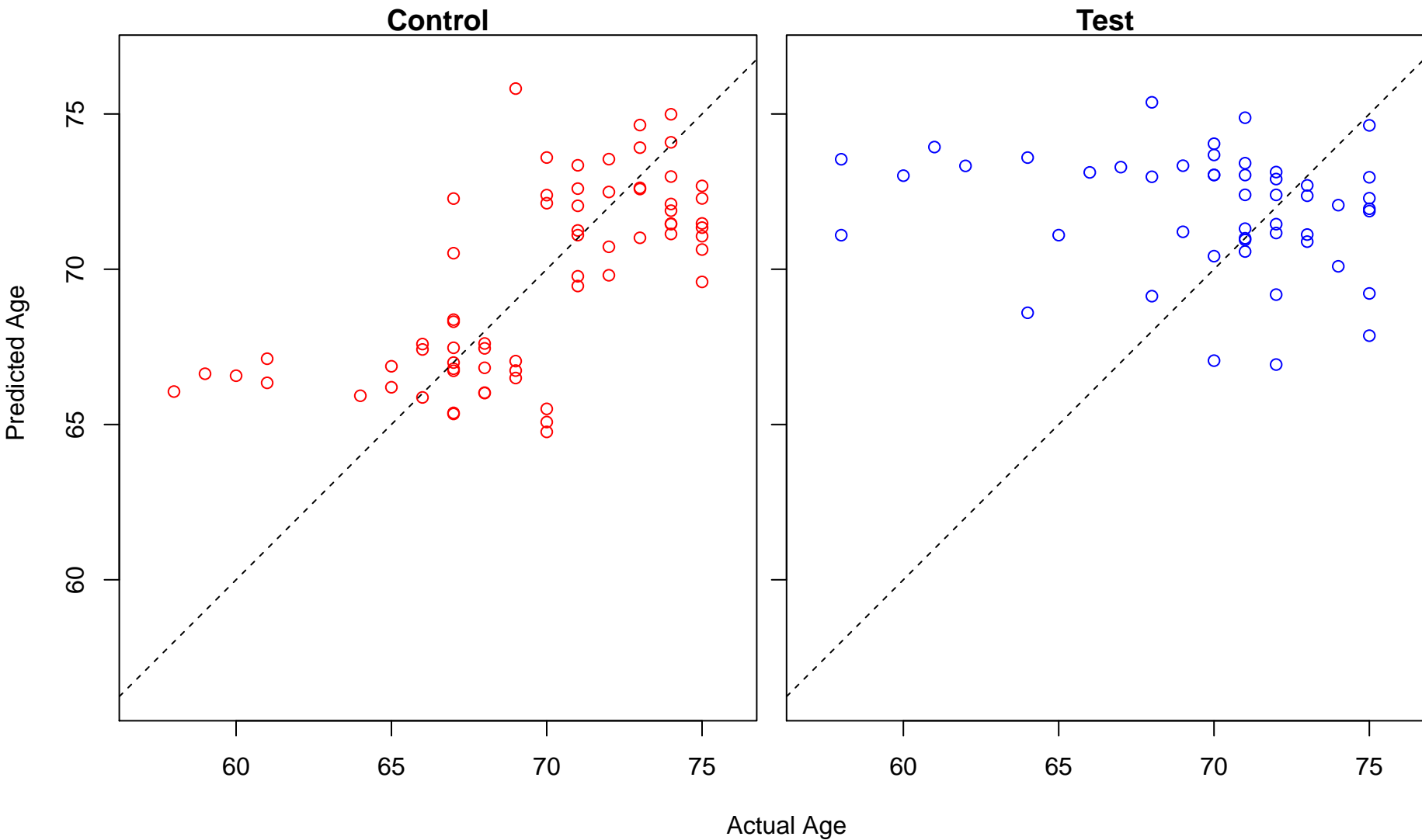


Test

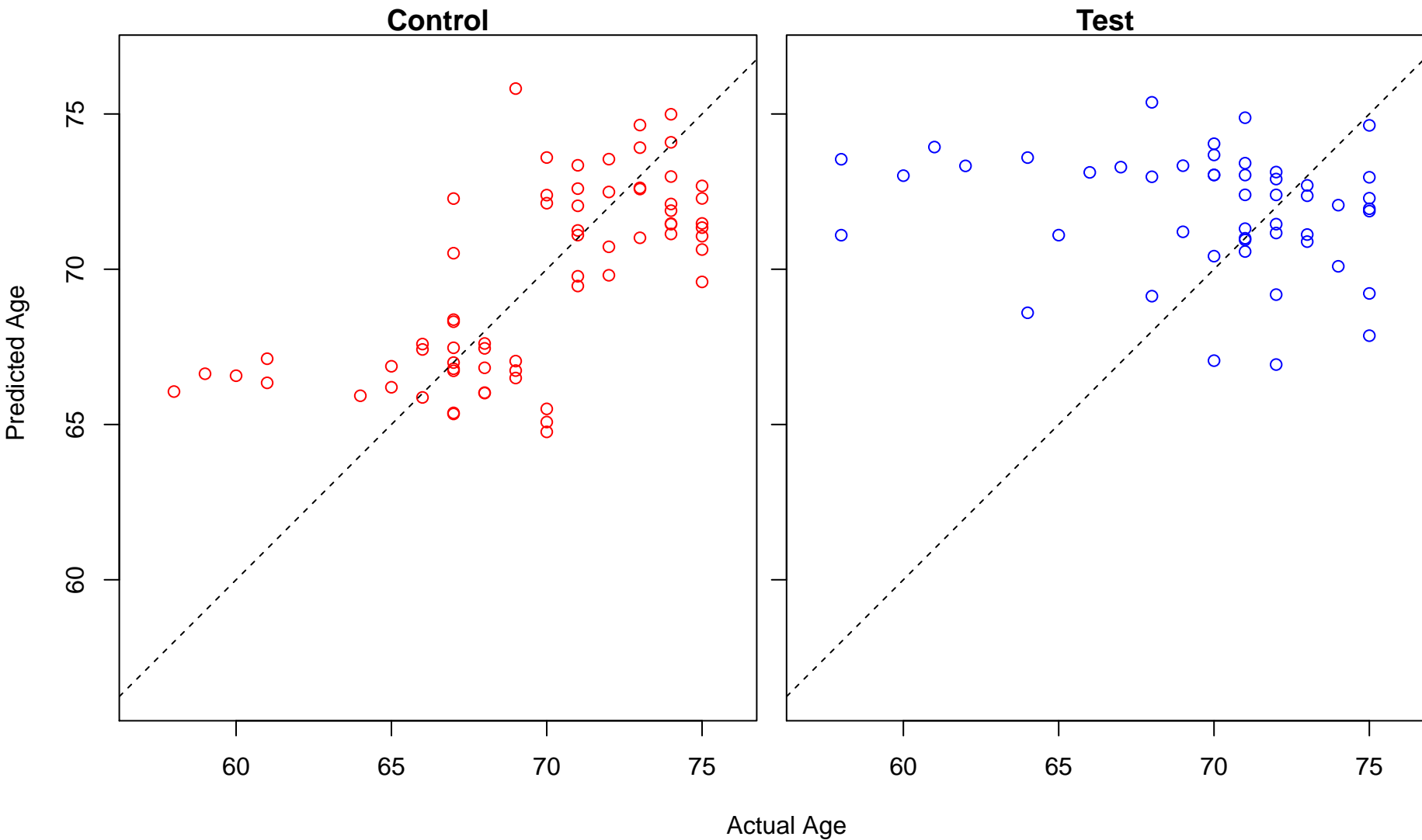


Actual Age

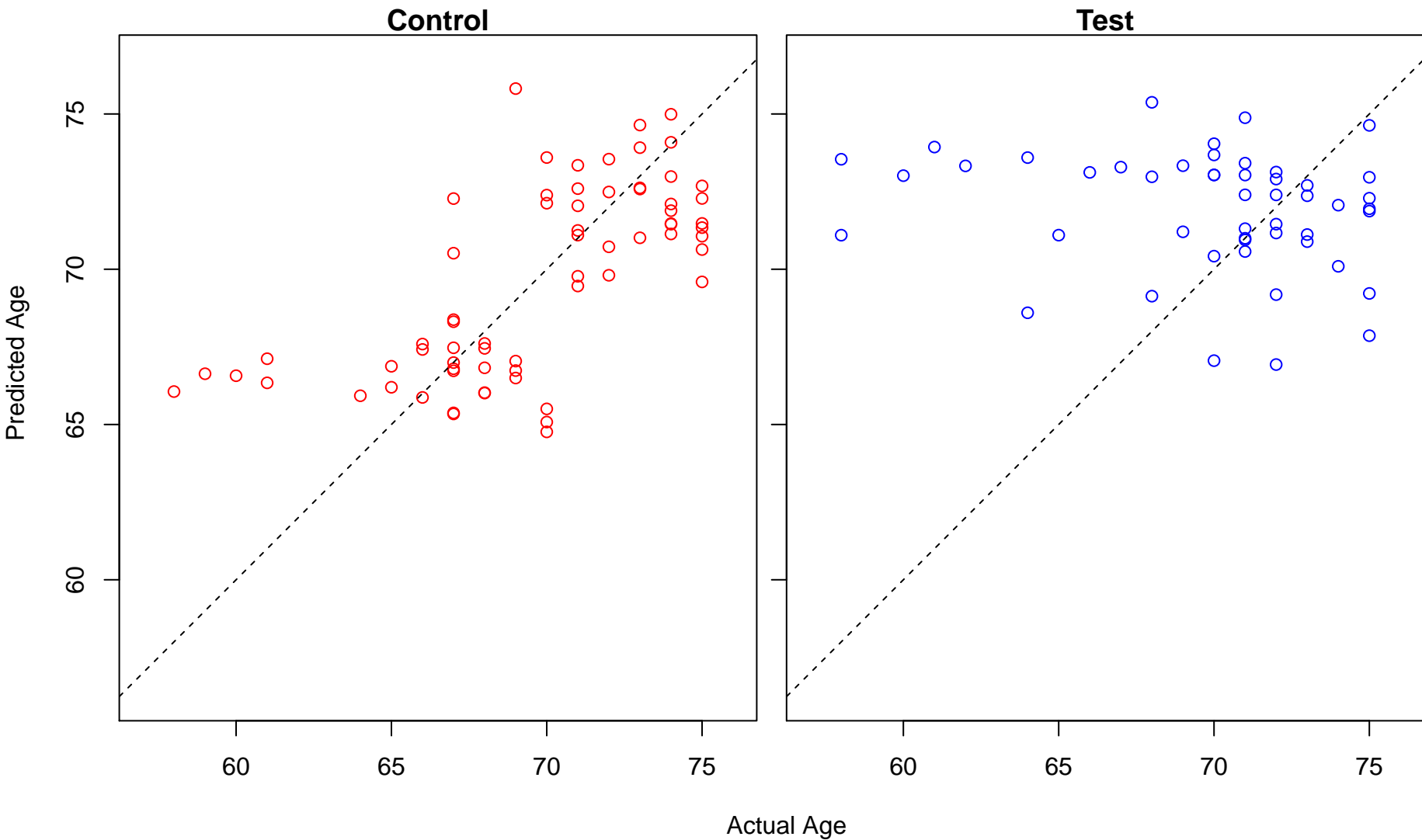
negative regulation of sister chromatid segregation (Score: 1.412036)



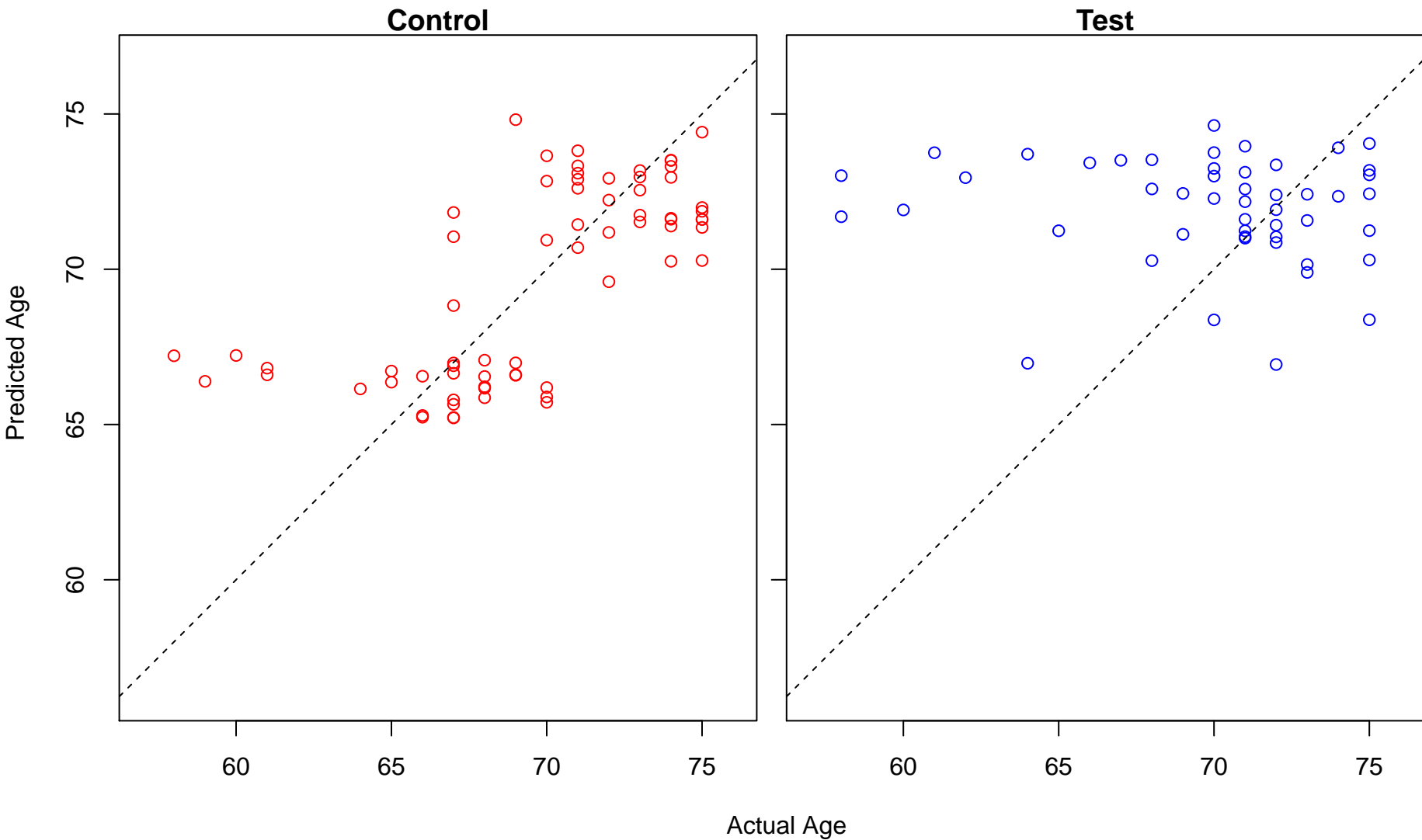
negative regulation of mitotic sister chromatid segregation (Score: 1.412036)



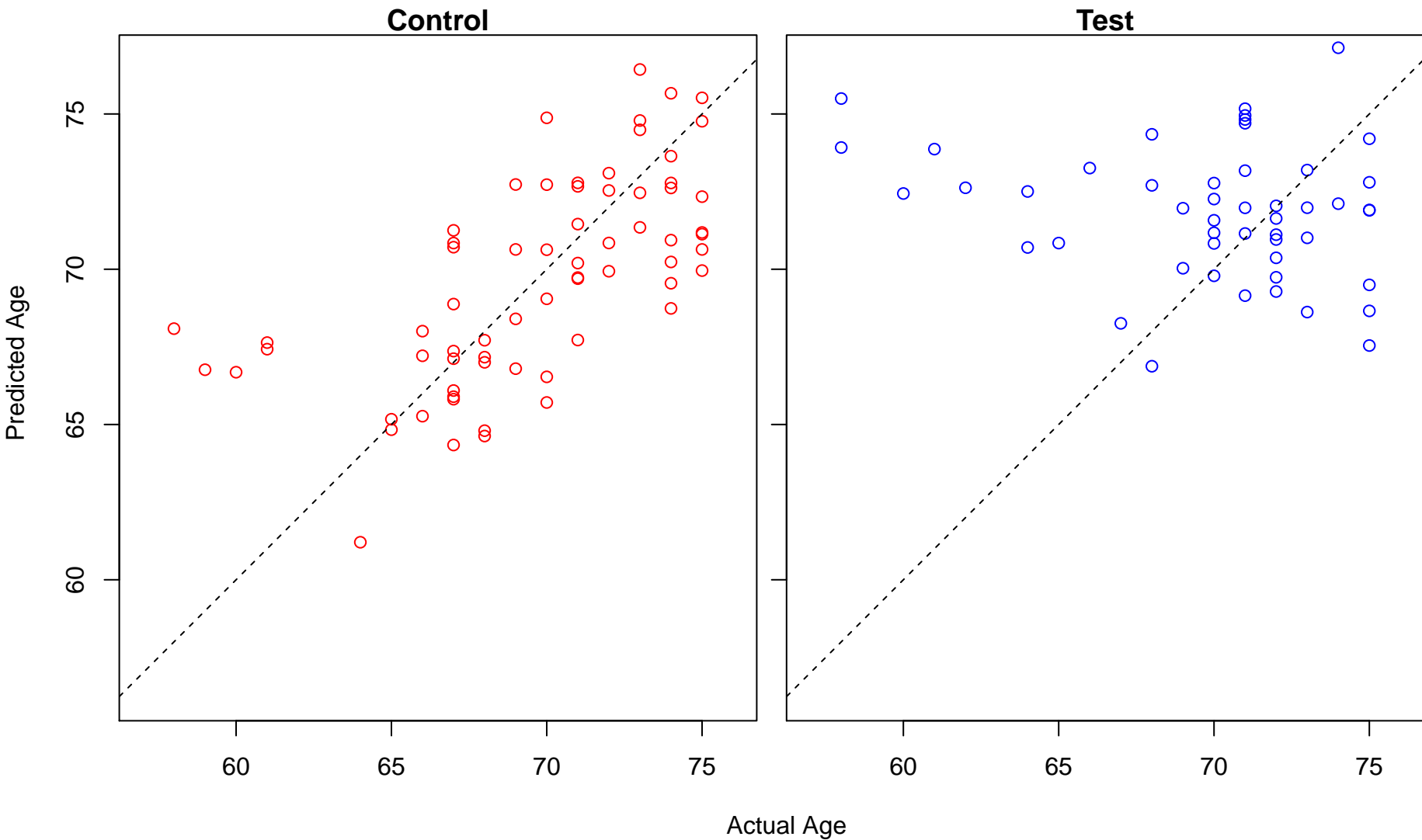
negative regulation of chromosome segregation (Score: 1.412036)



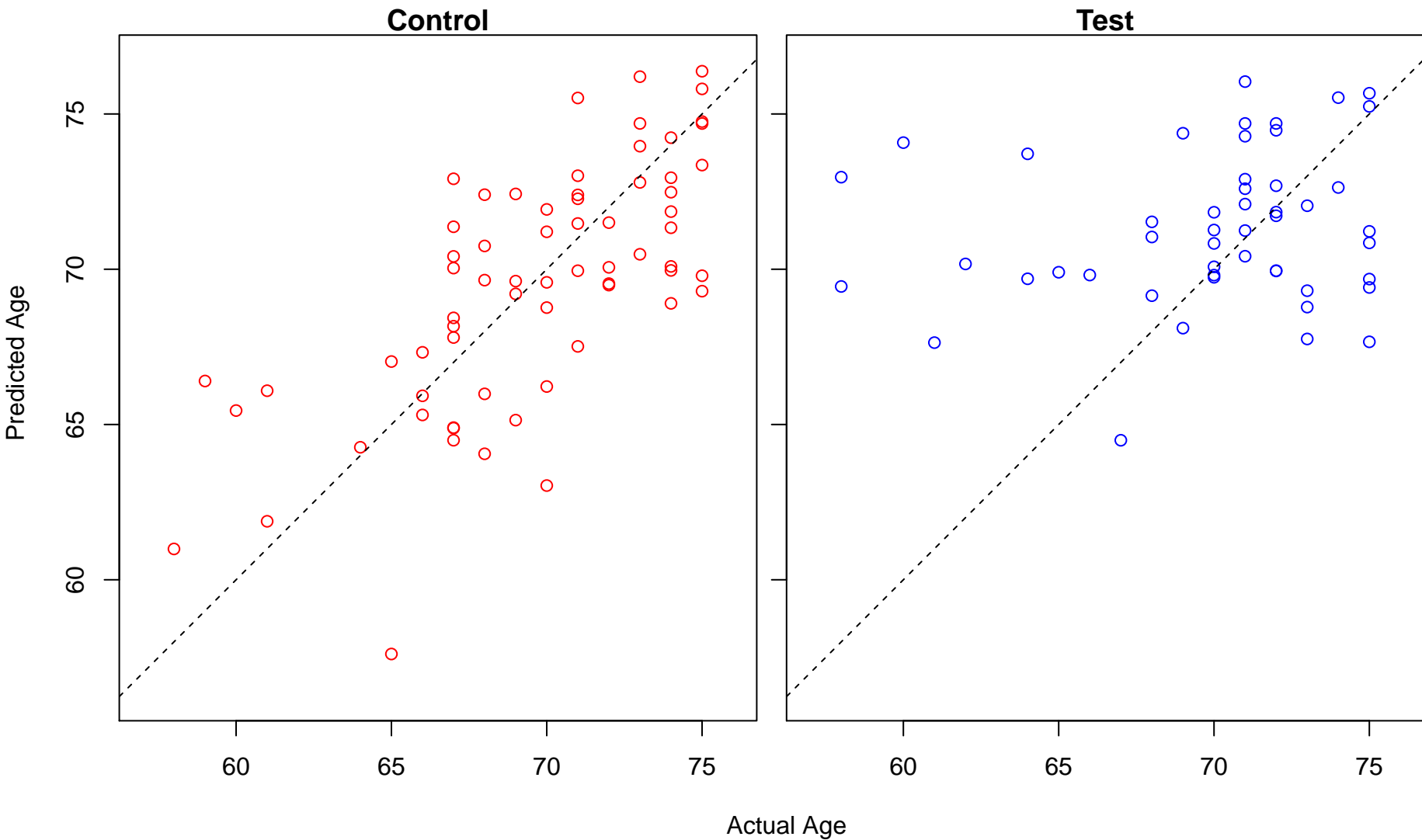
translational termination (Score: 1.411727)



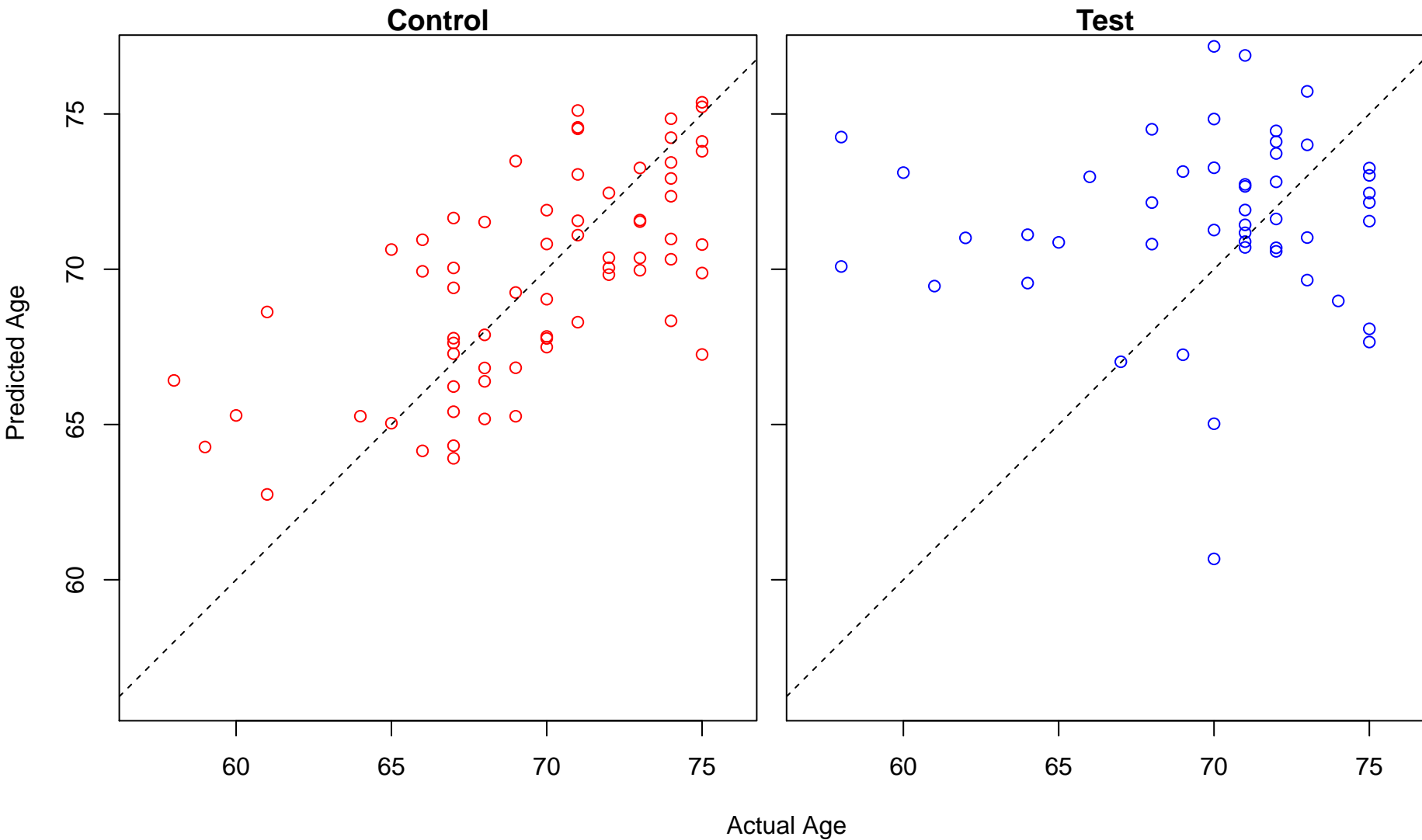
regulation of stress fiber assembly (Score: 1.411432)



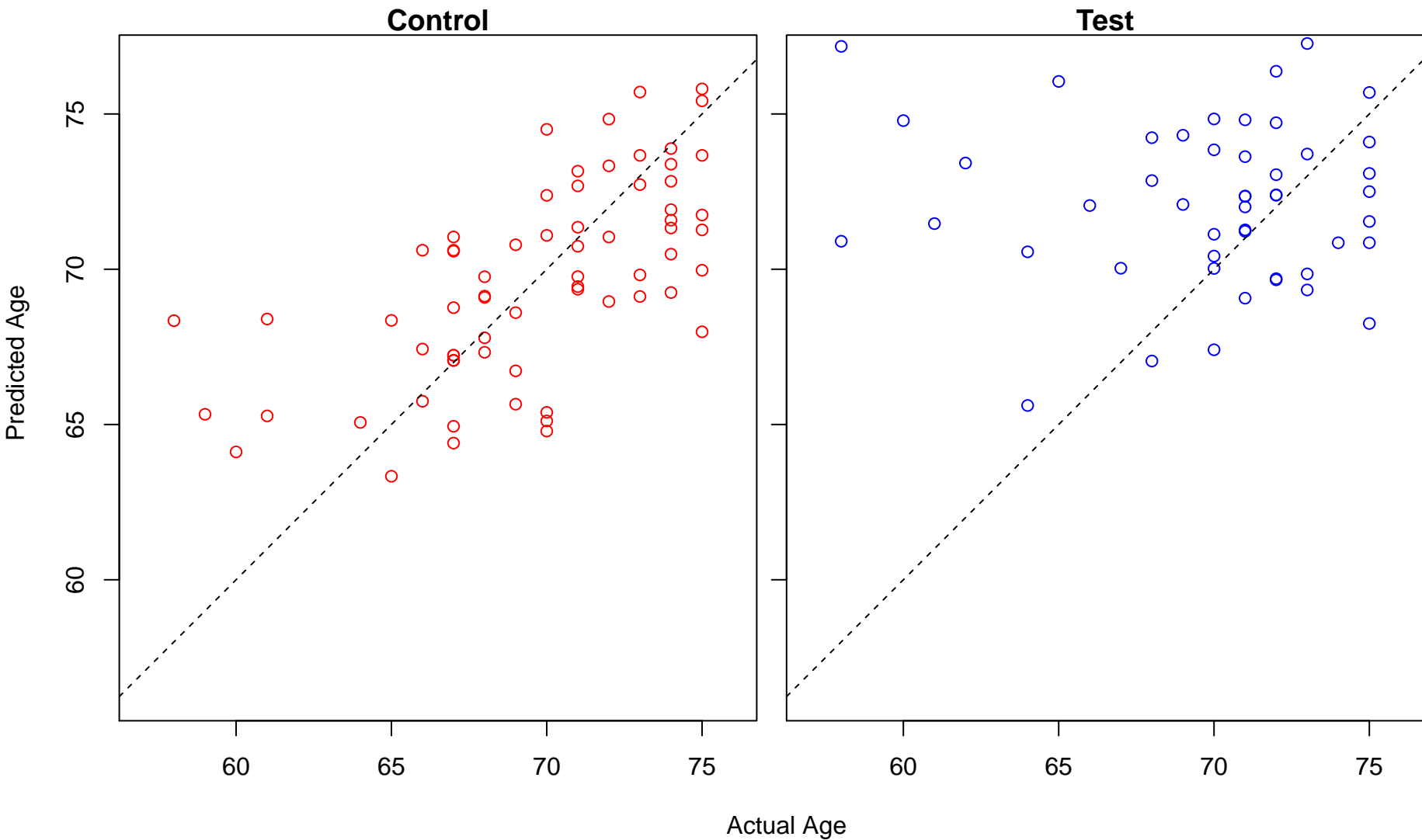
positive regulation of purine nucleotide metabolic process (Score: 1.411321)



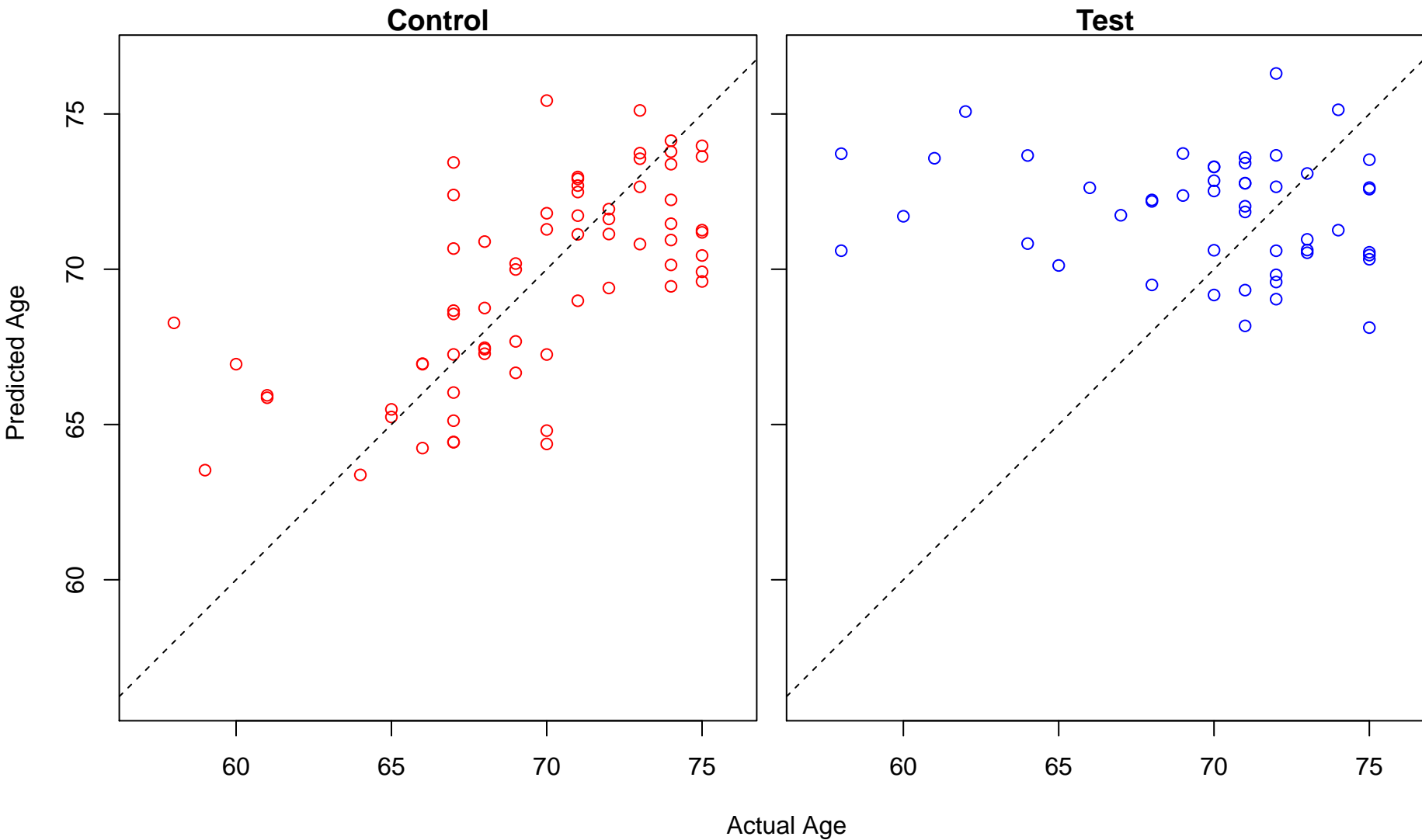
receptor clustering (Score: 1.411232)



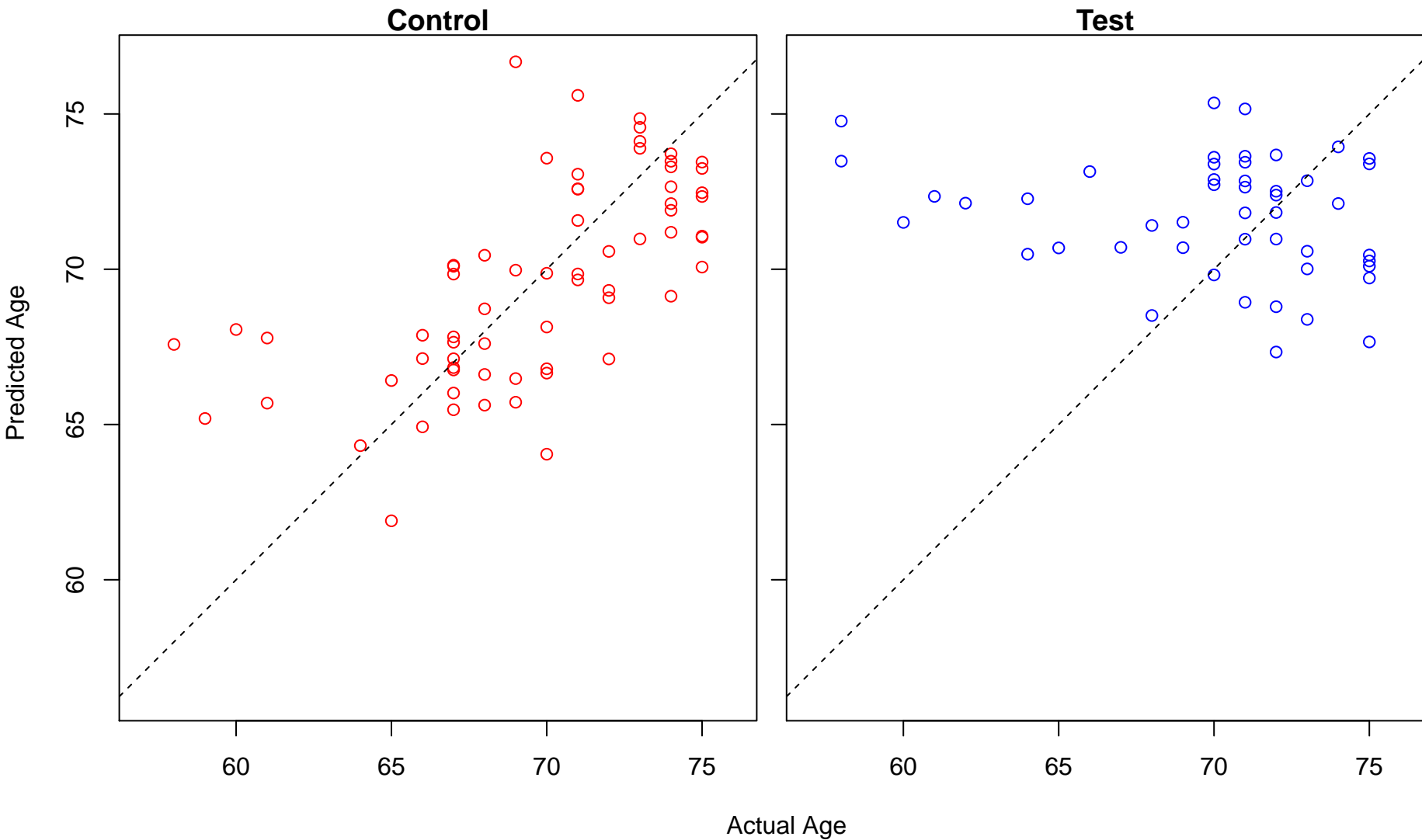
fatty-acyl-CoA metabolic process (Score: 1.410475)



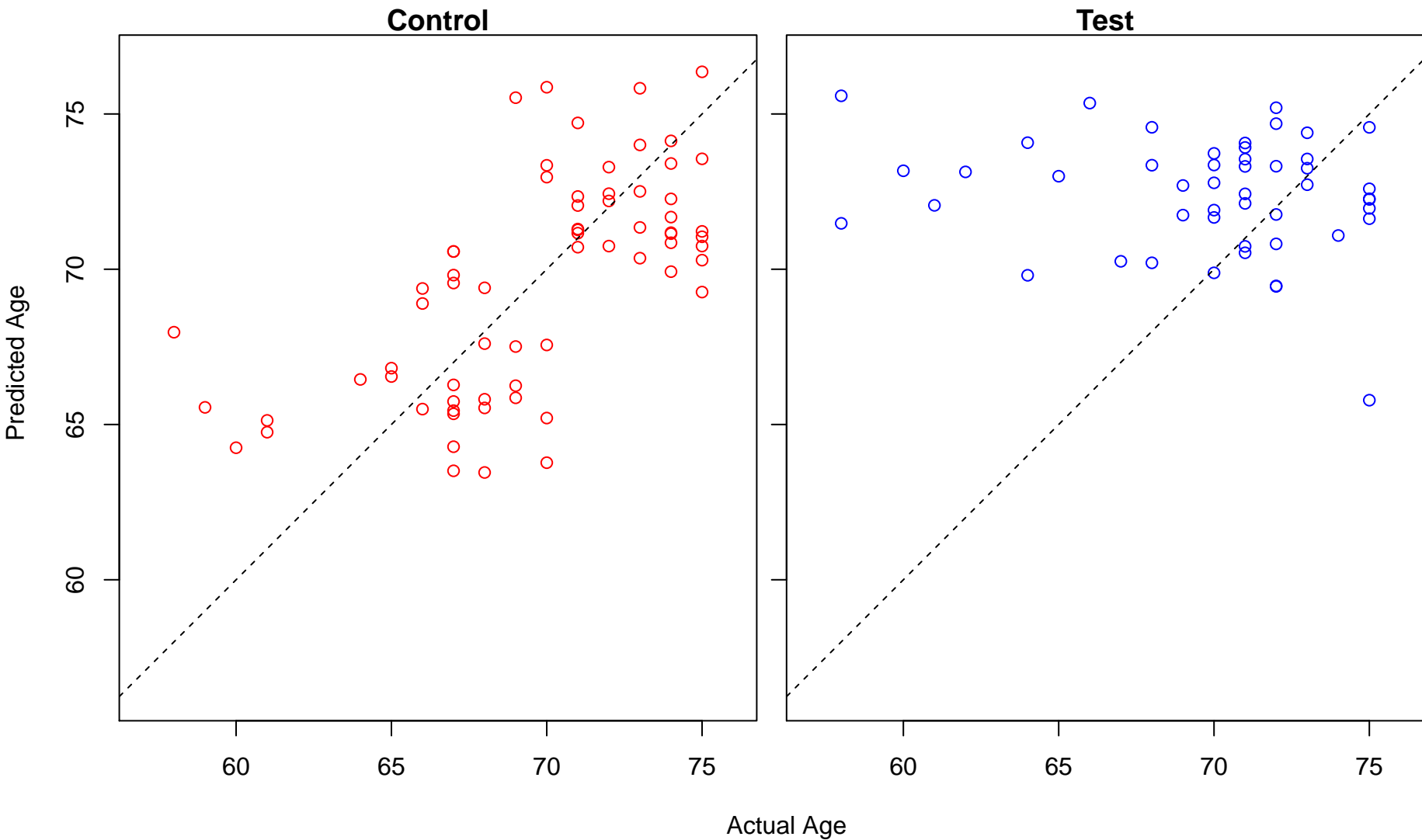
regulation of establishment or maintenance of cell polarity (Score: 1.410211)



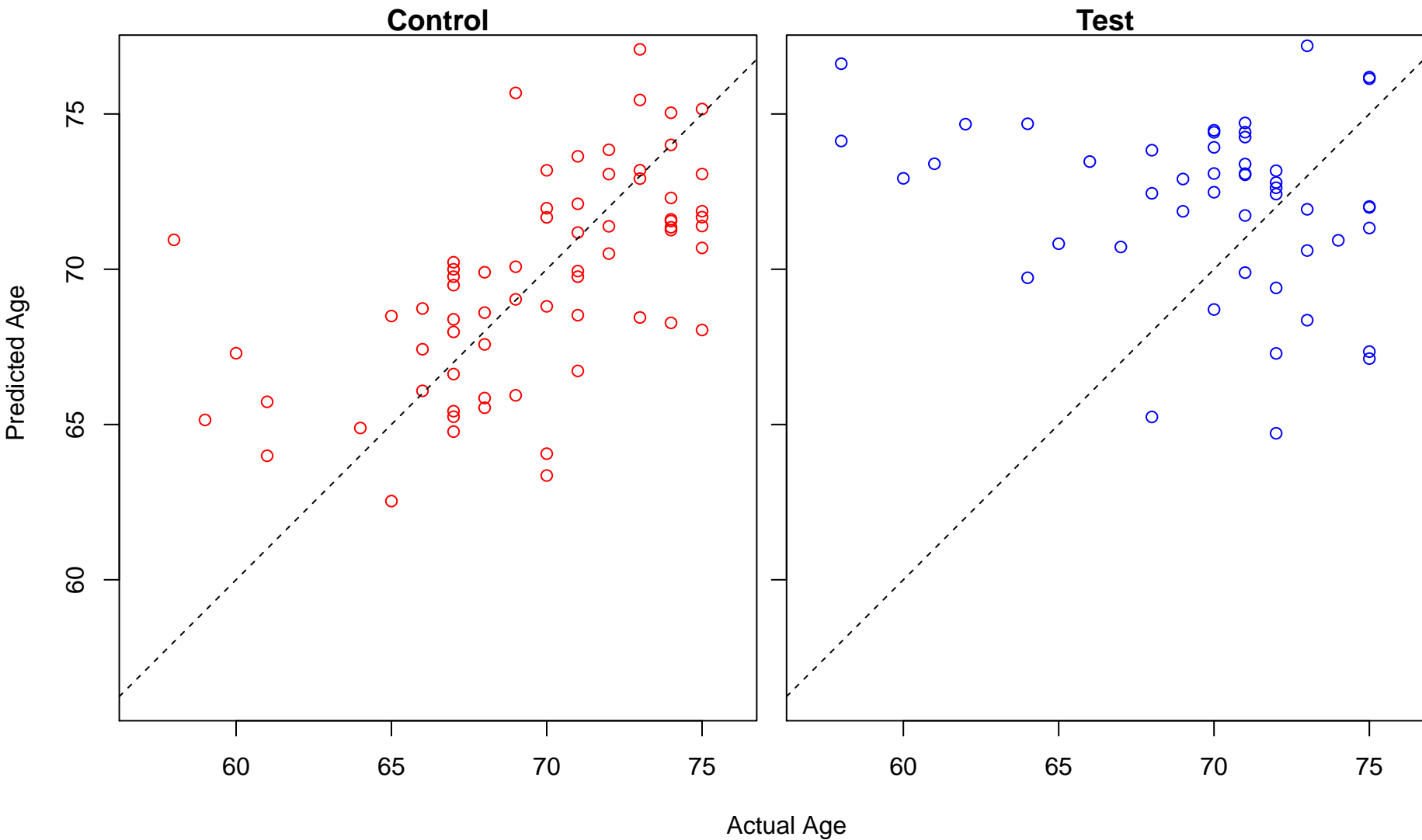
negative regulation of leukocyte differentiation (Score: 1.409559)



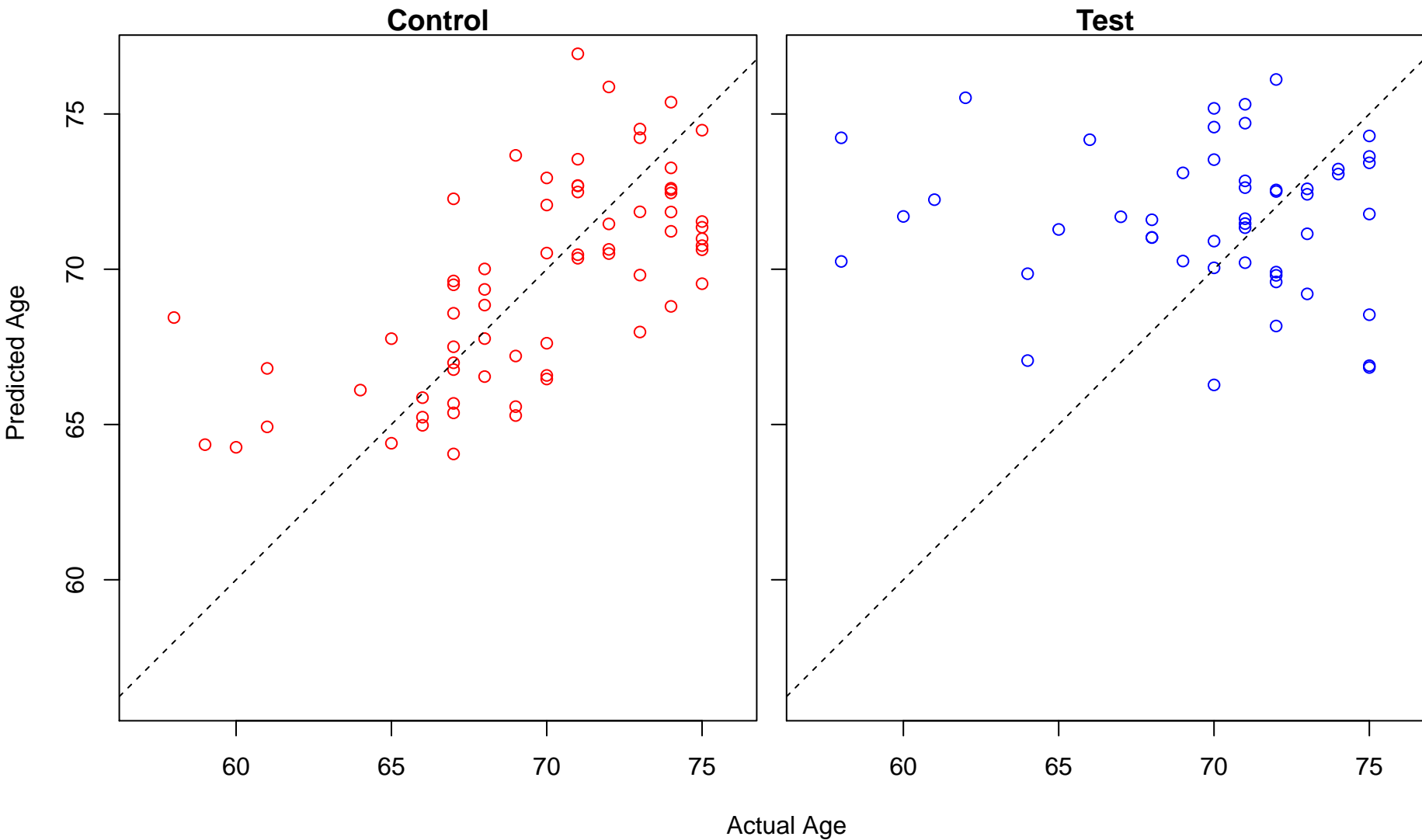
localization within membrane (Score: 1.409433)



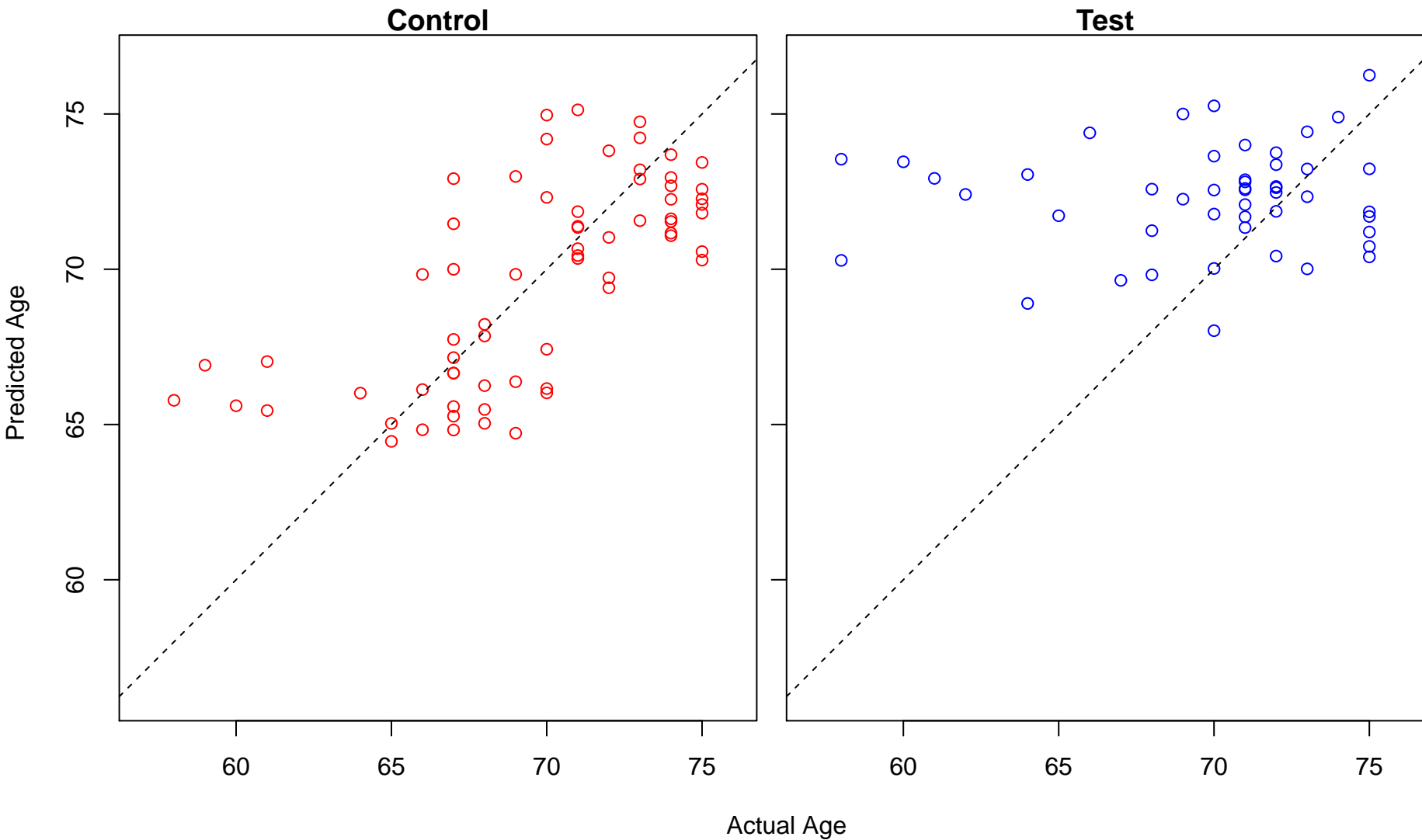
regulation of cell killing (Score: 1.409336)



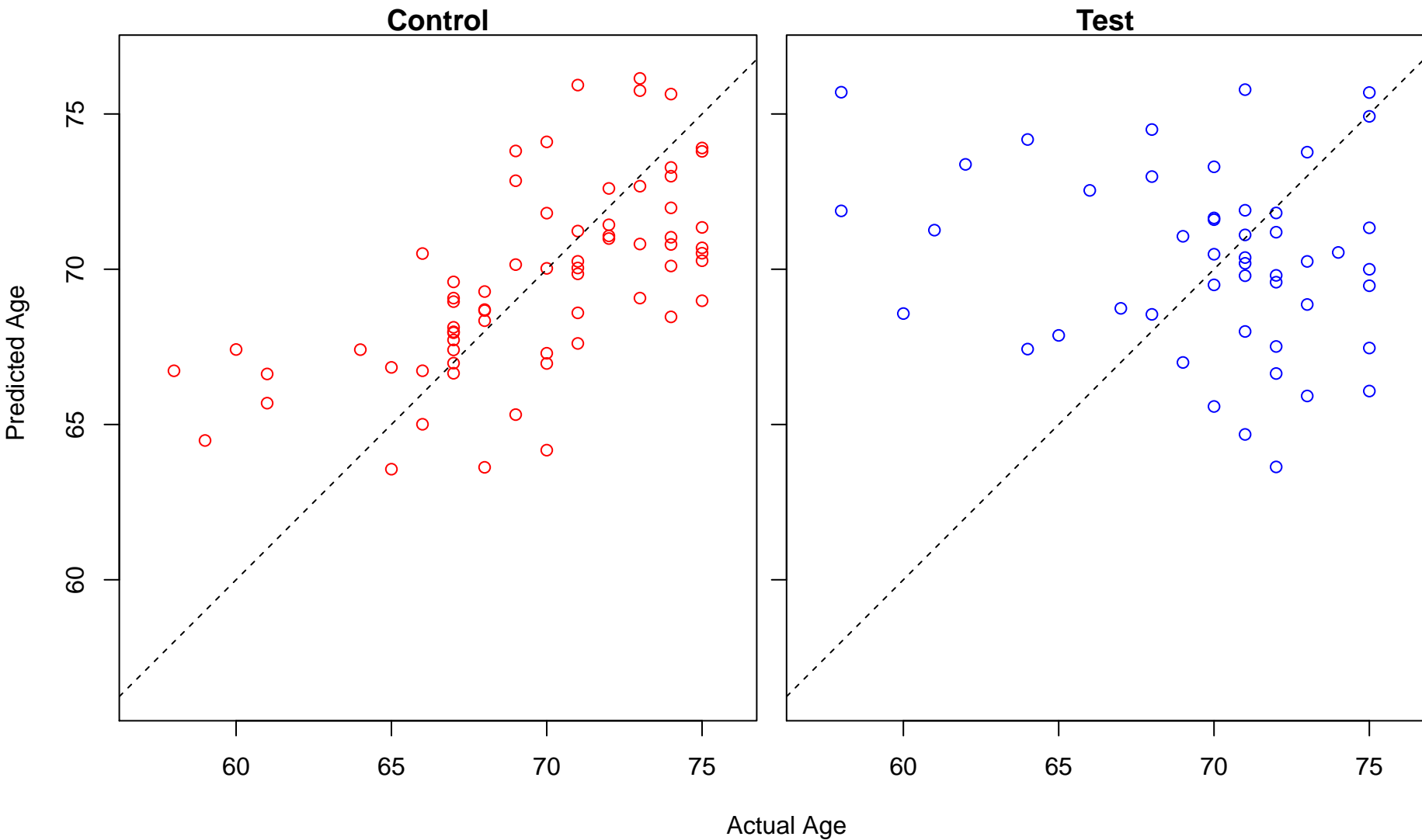
response to glucagon (Score: 1.409289)



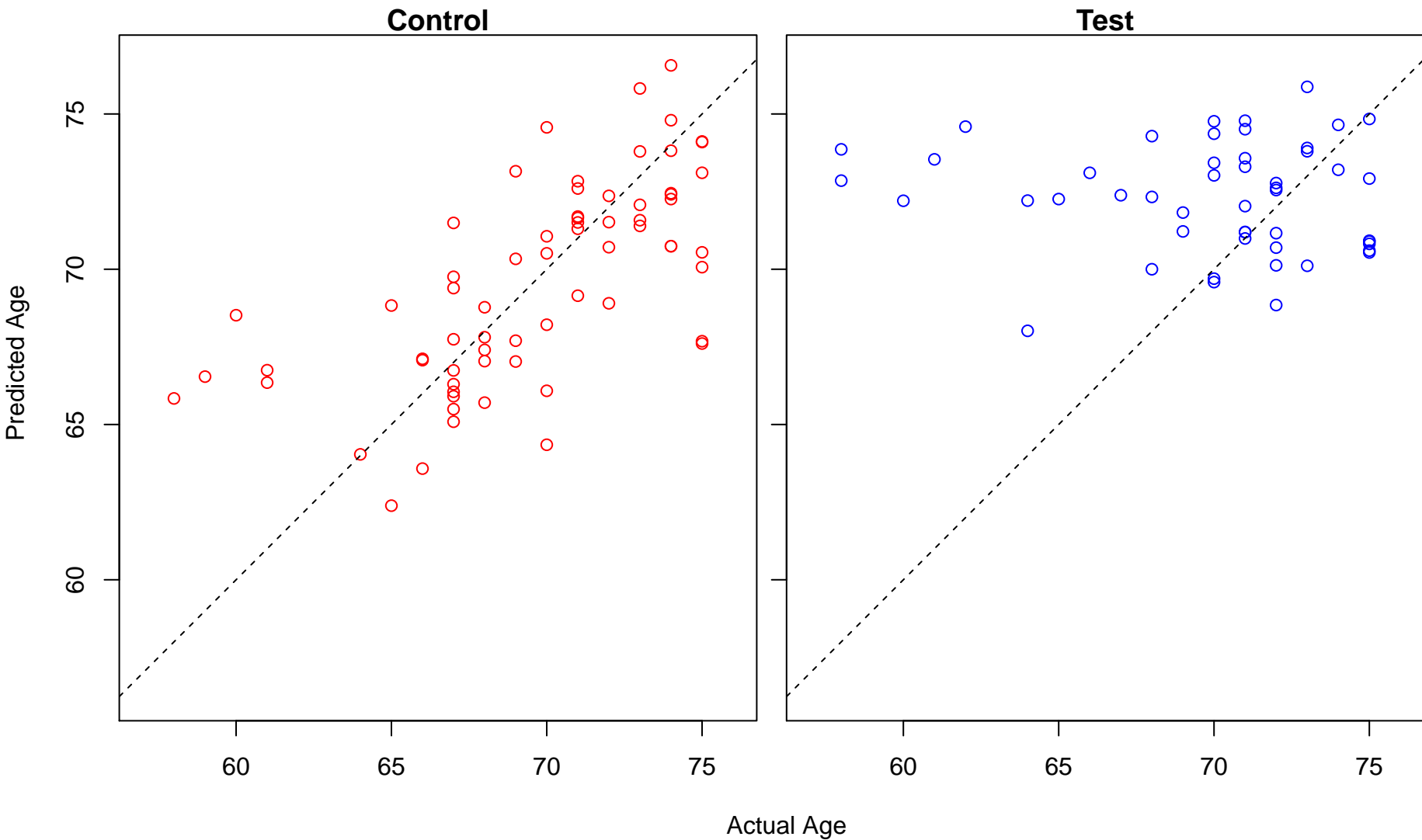
protein-DNA complex assembly (Score: 1.408813)



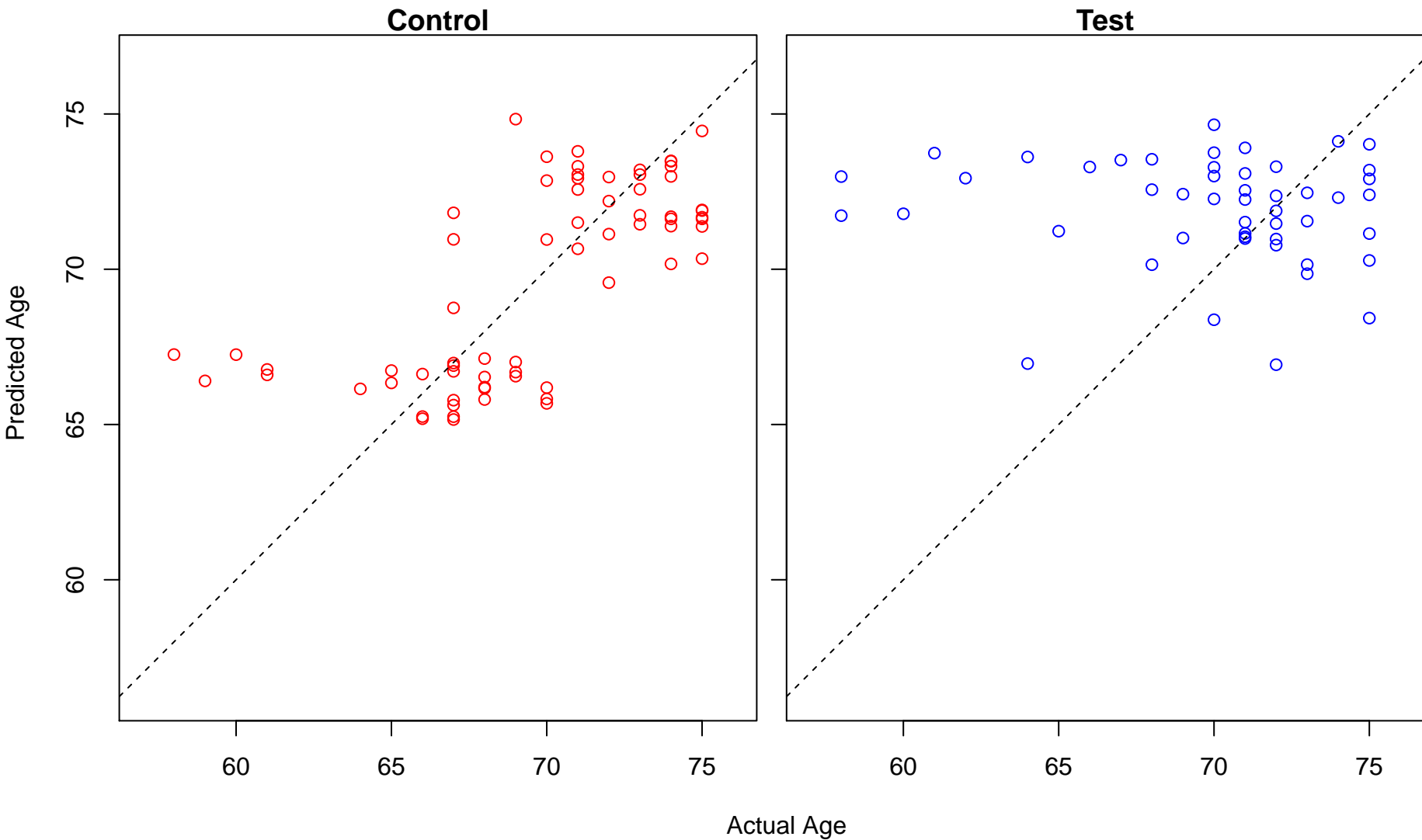
negative regulation of receptor activity (Score: 1.408203)



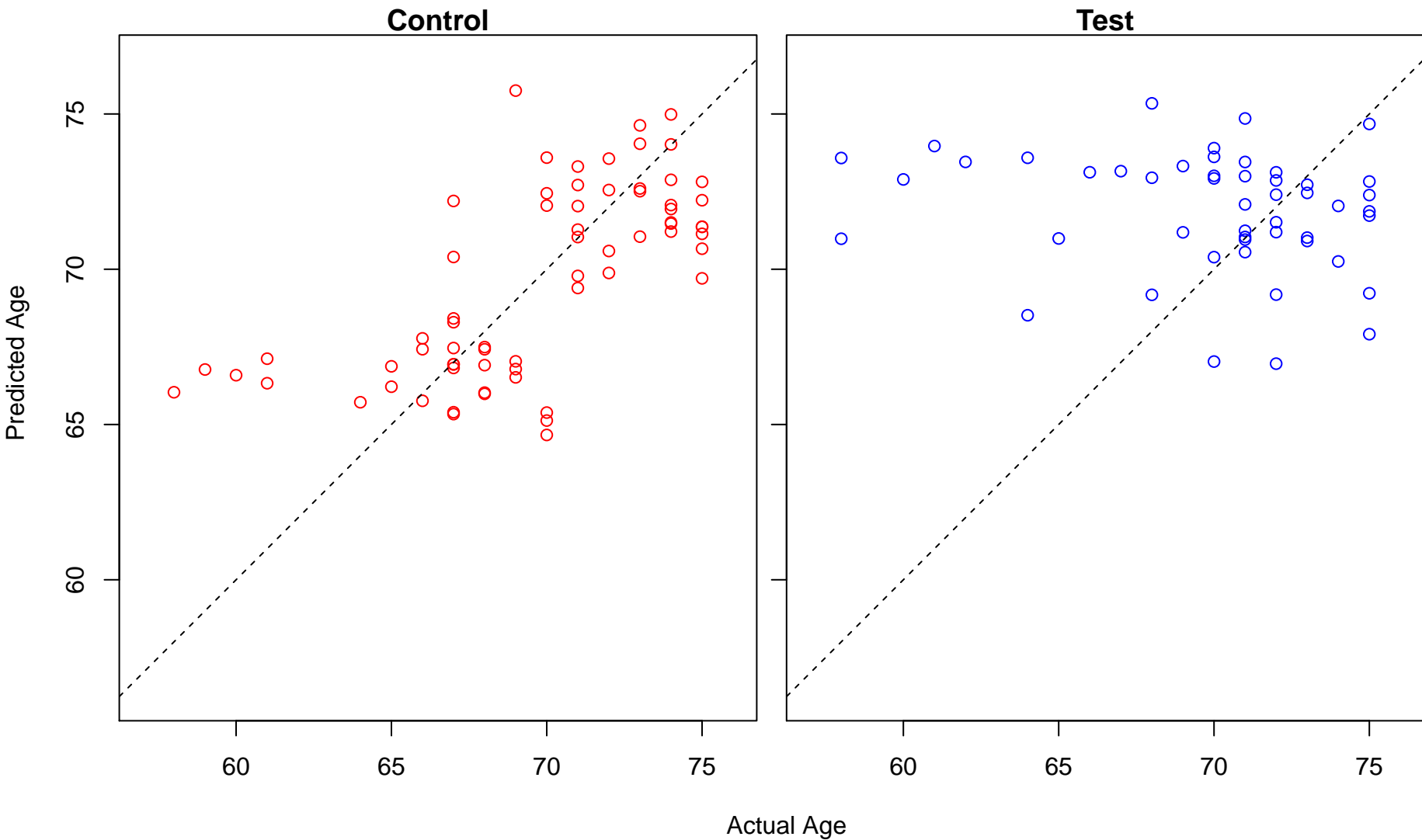
phospholipid transport (Score: 1.408067)



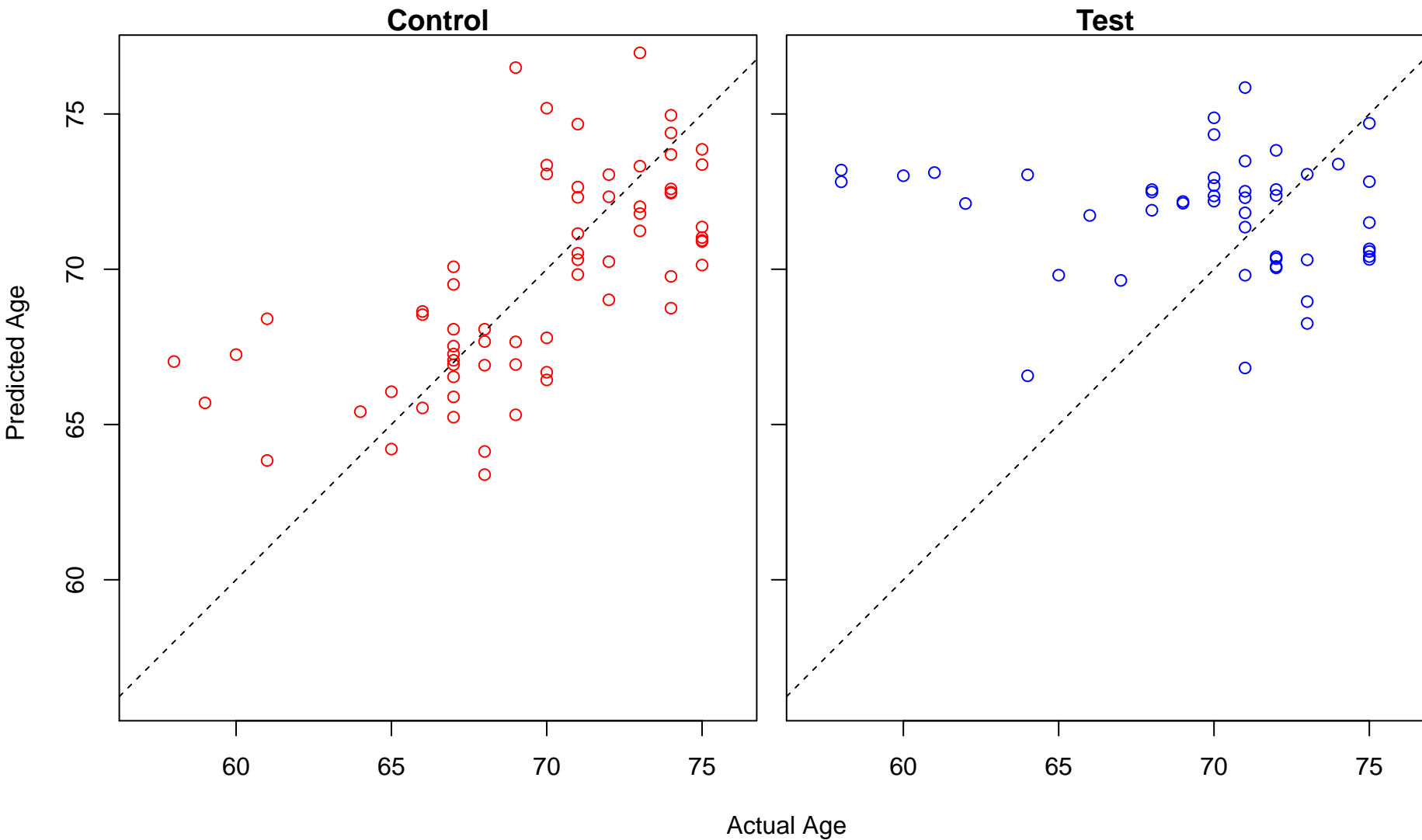
protein complex disassembly (Score: 1.407680)



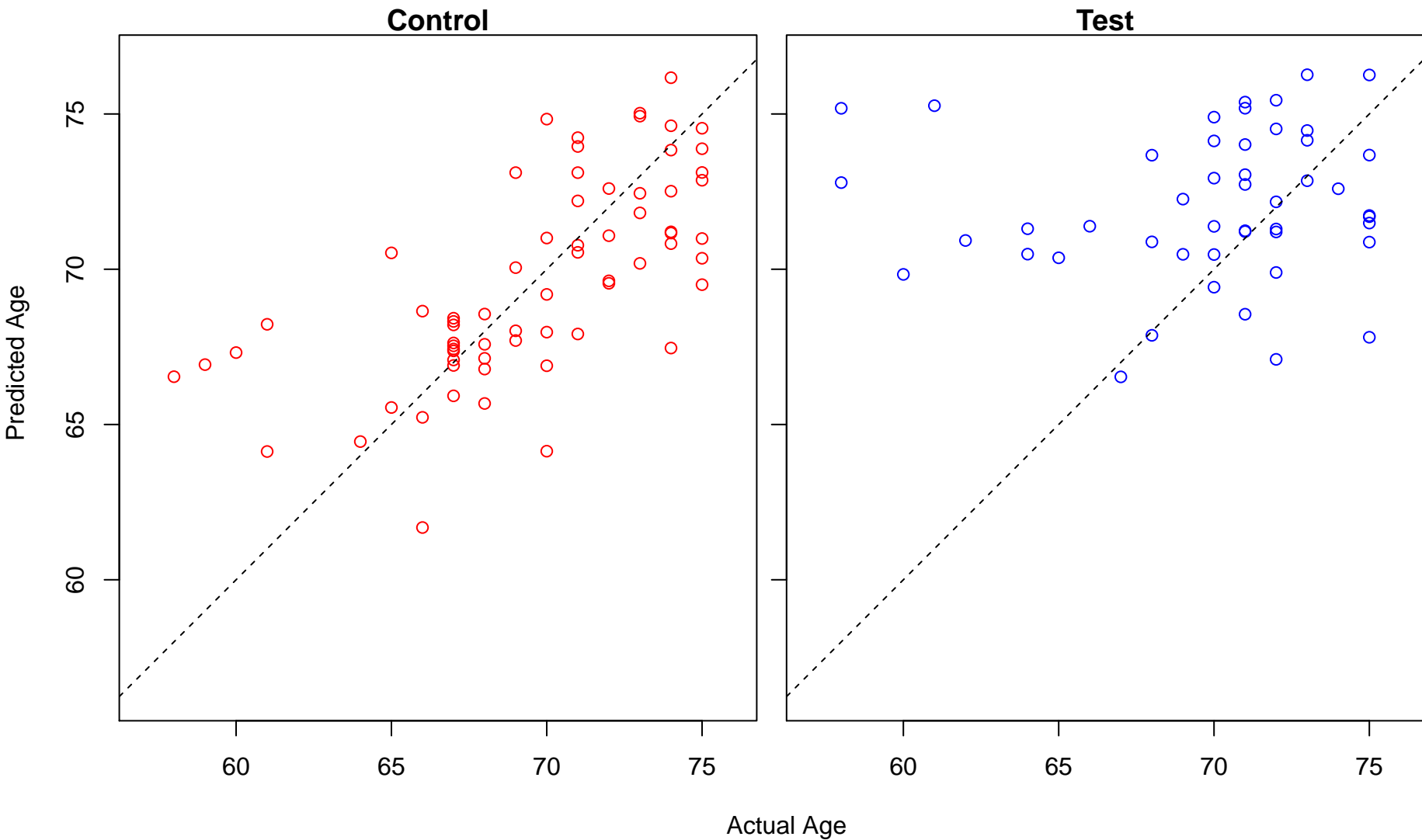
negative regulation of mitotic nuclear division (Score: 1.407352)



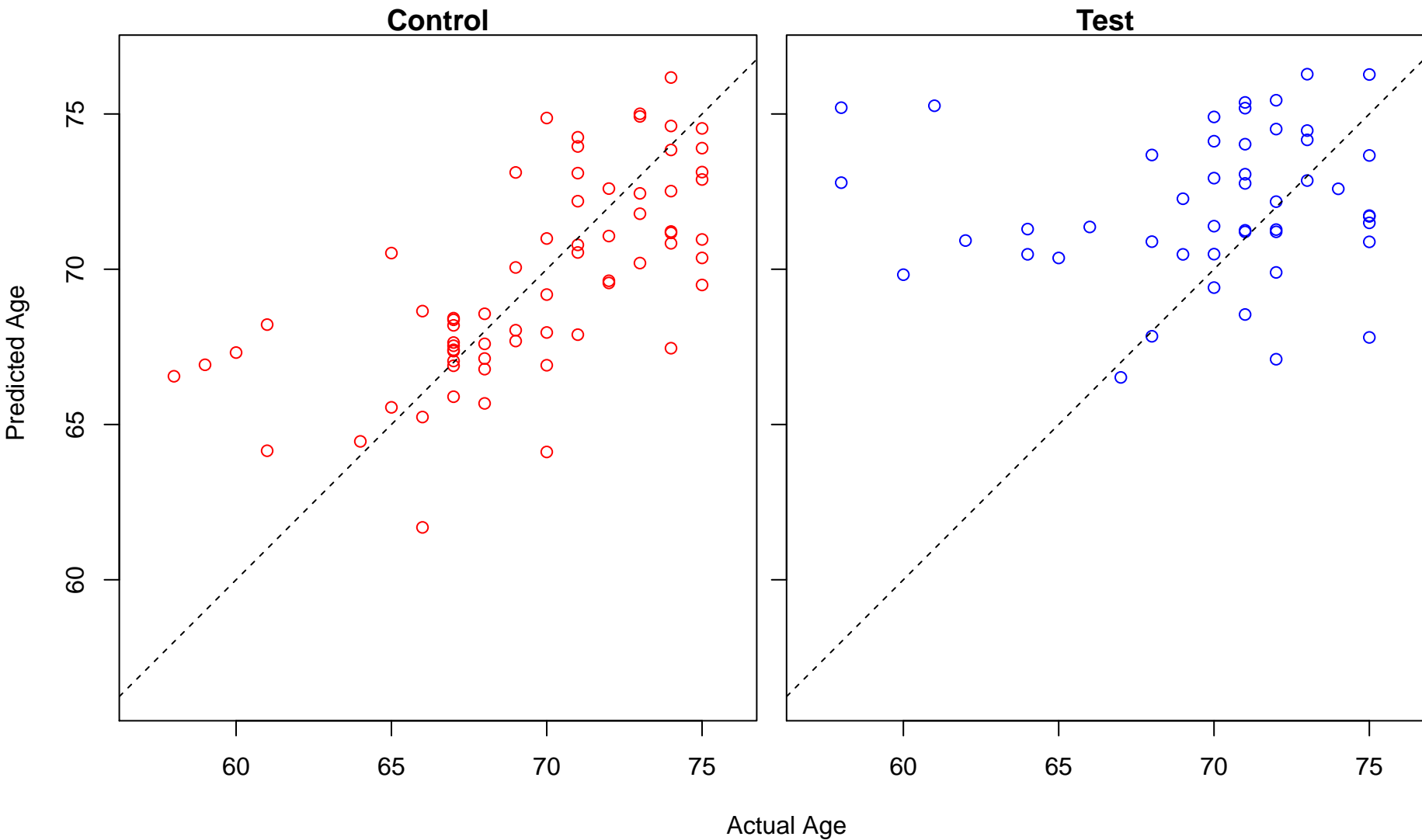
sexual reproduction (Score: 1.407150)



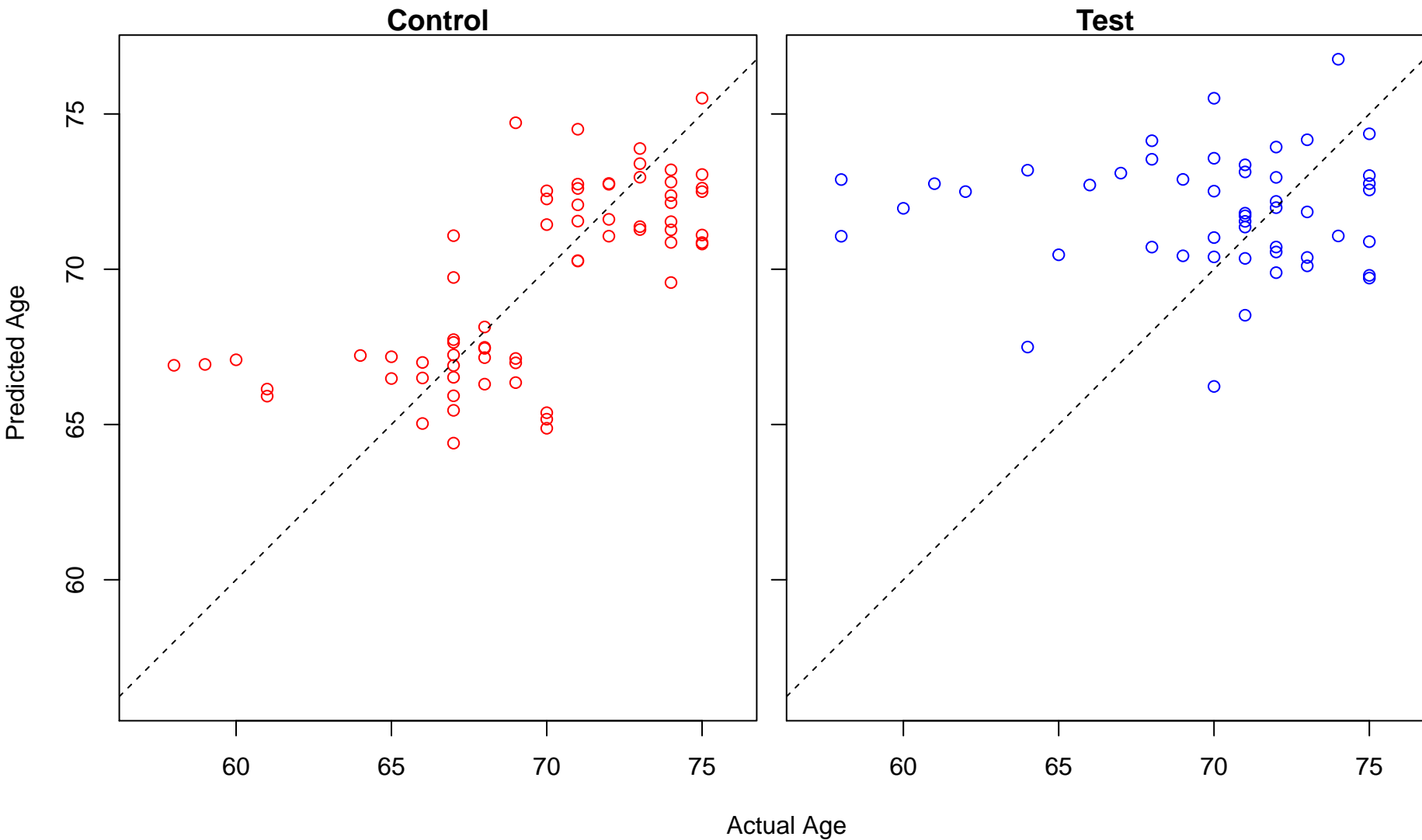
ventricular cardiac muscle tissue morphogenesis (Score: 1.406583)



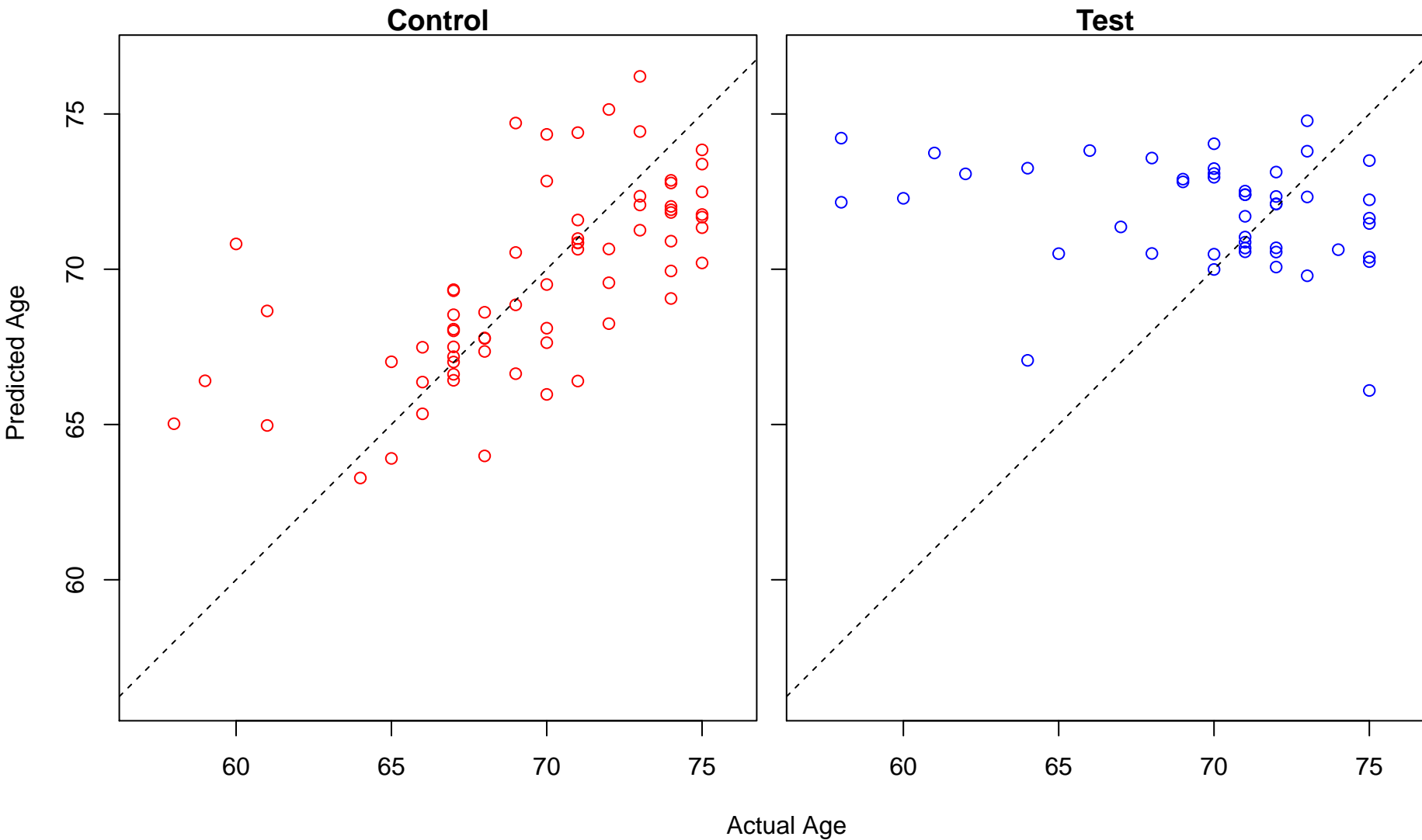
ventricular cardiac muscle tissue development (Score: 1.406488)



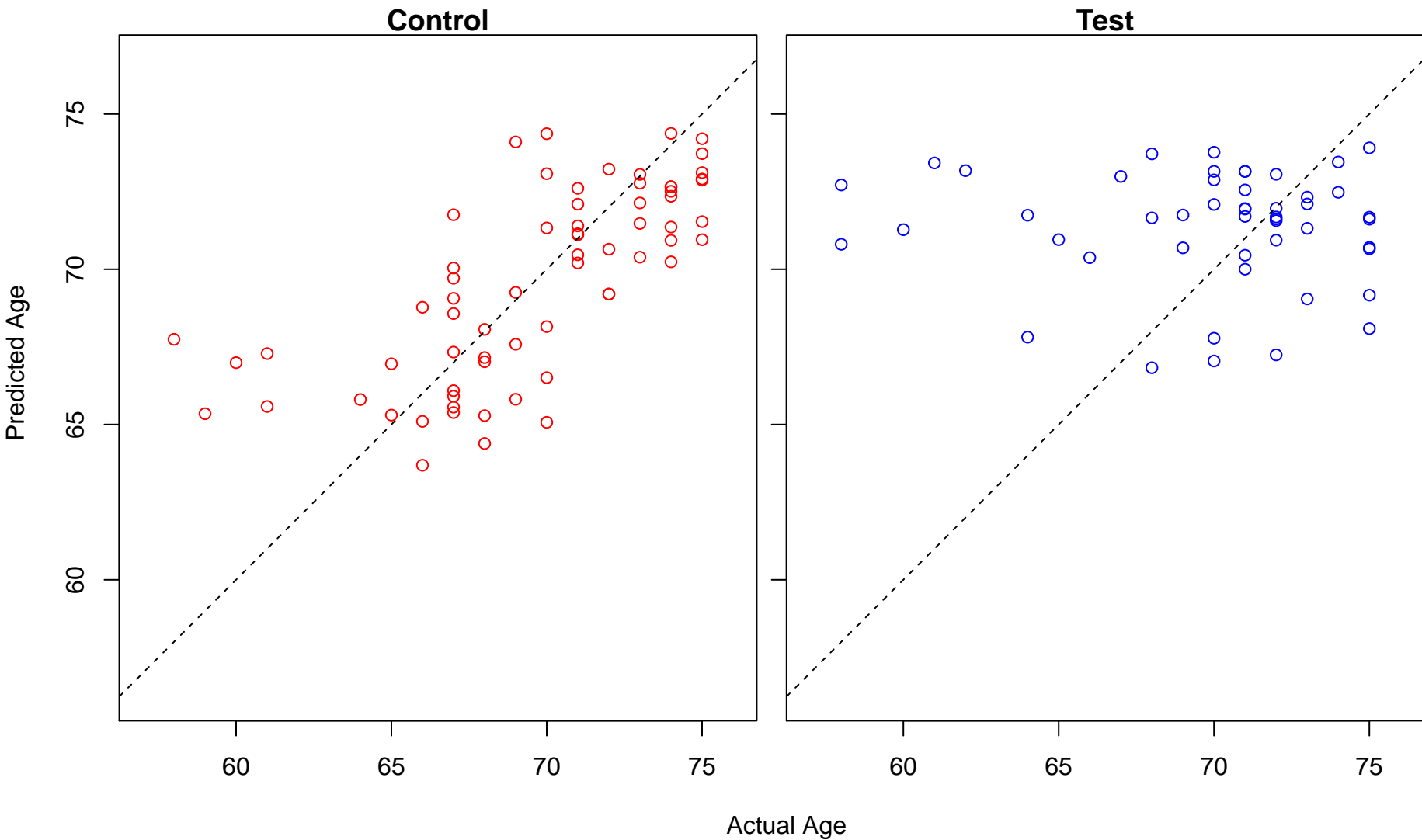
negative regulation of oxidative stress-induced cell death (Score: 1.405866)



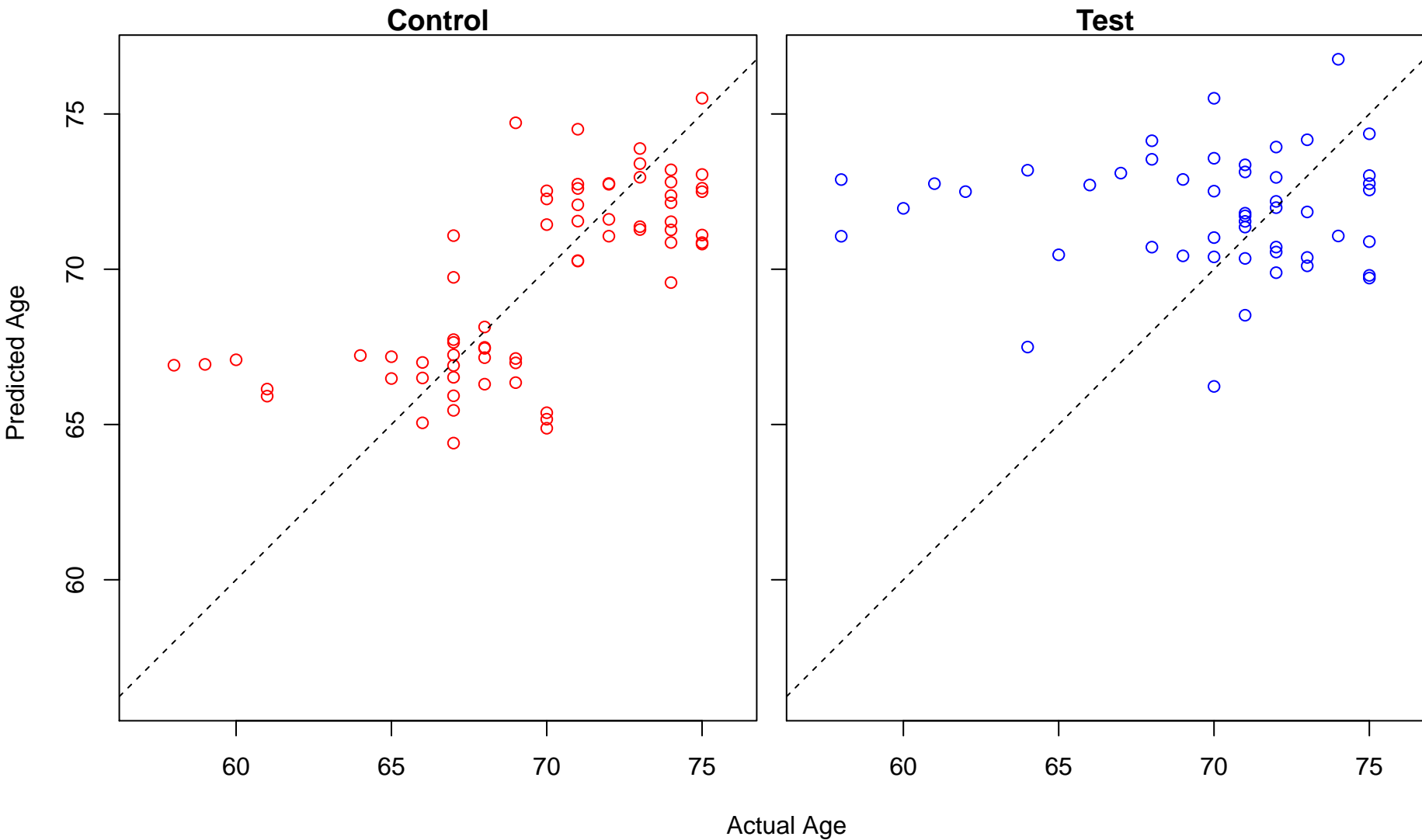
cytokine secretion (Score: 1.405554)



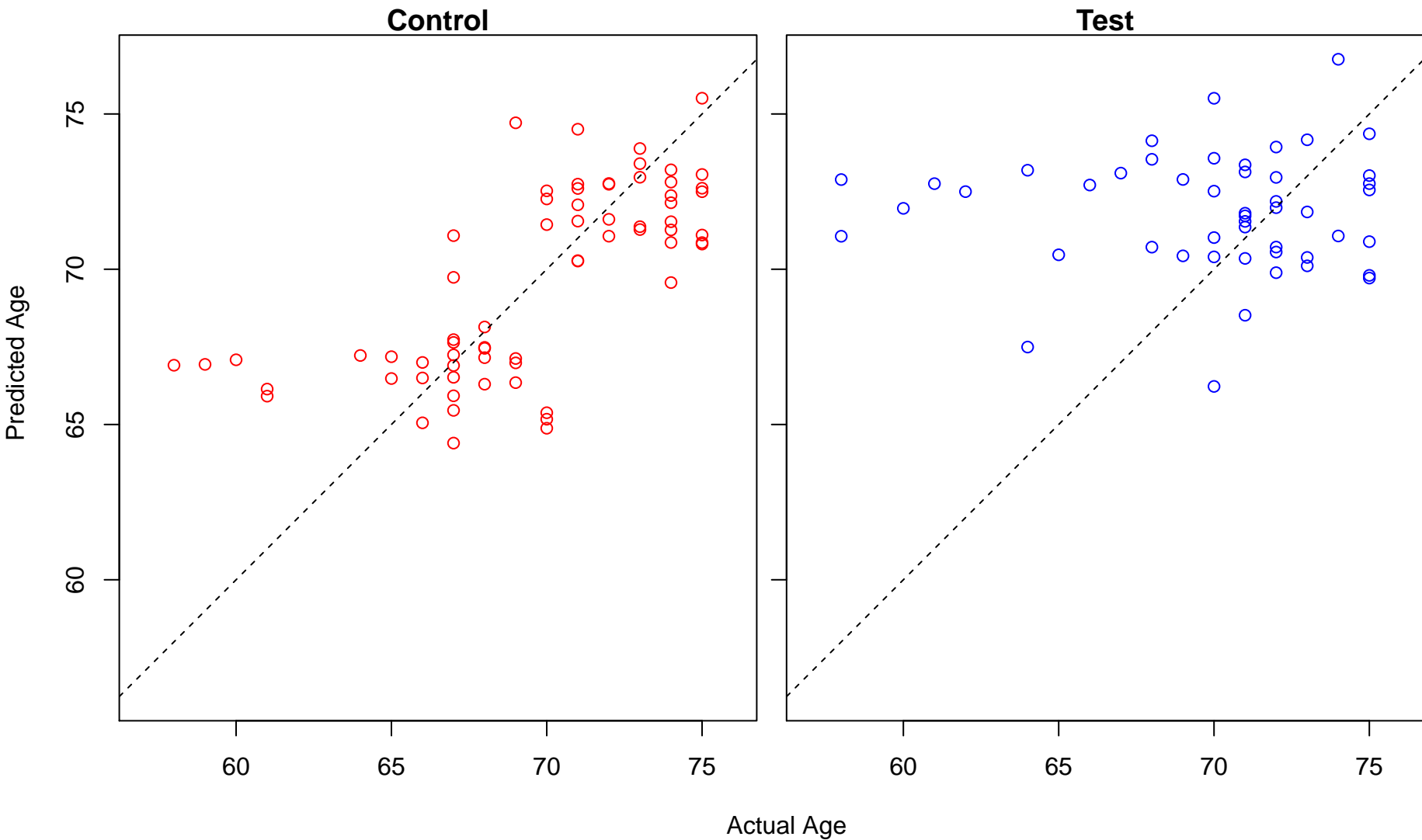
mitochondrial fragmentation involved in apoptotic process (Score: 1.405525)



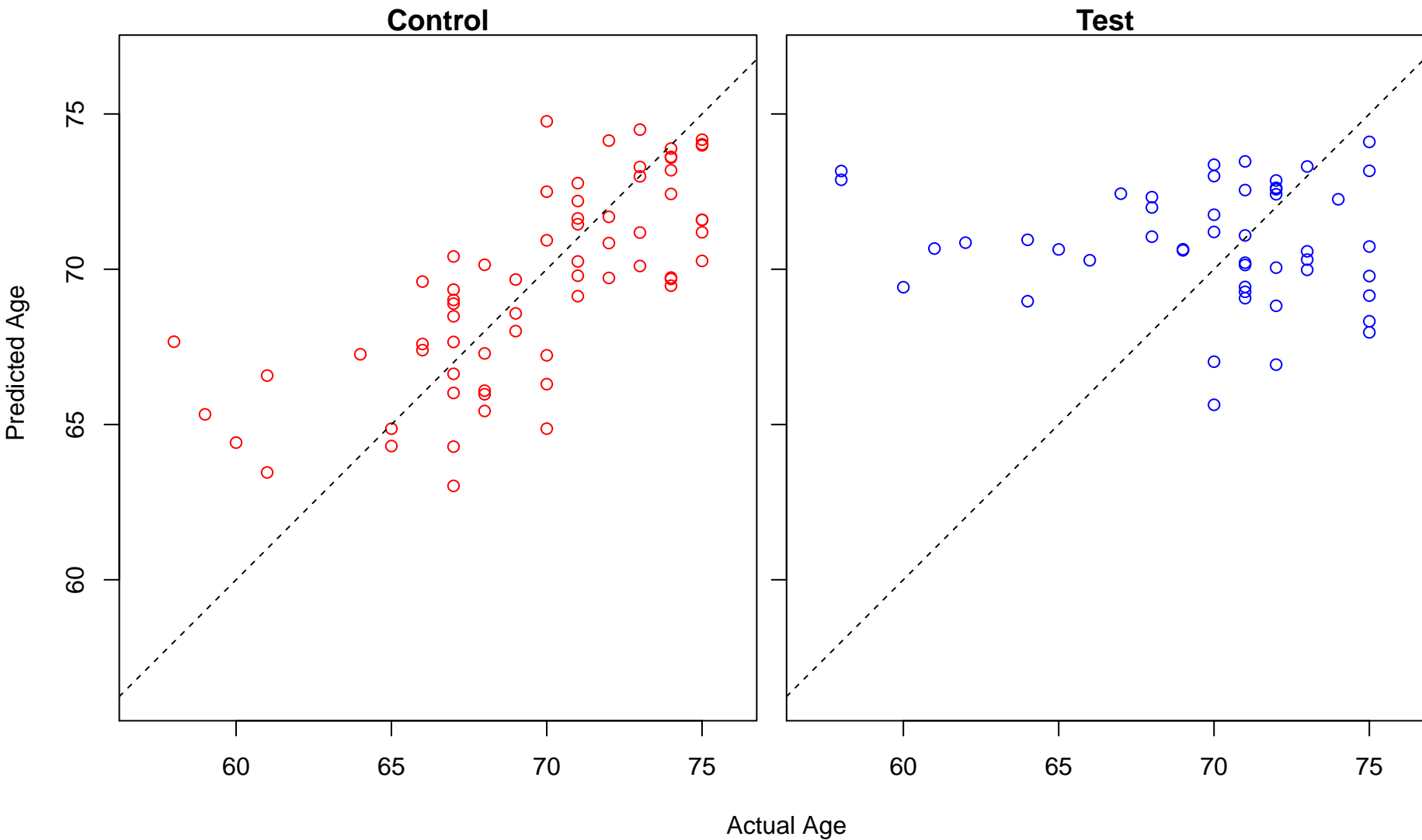
negative regulation of cellular response to oxidative stress (Score: 1.405212)



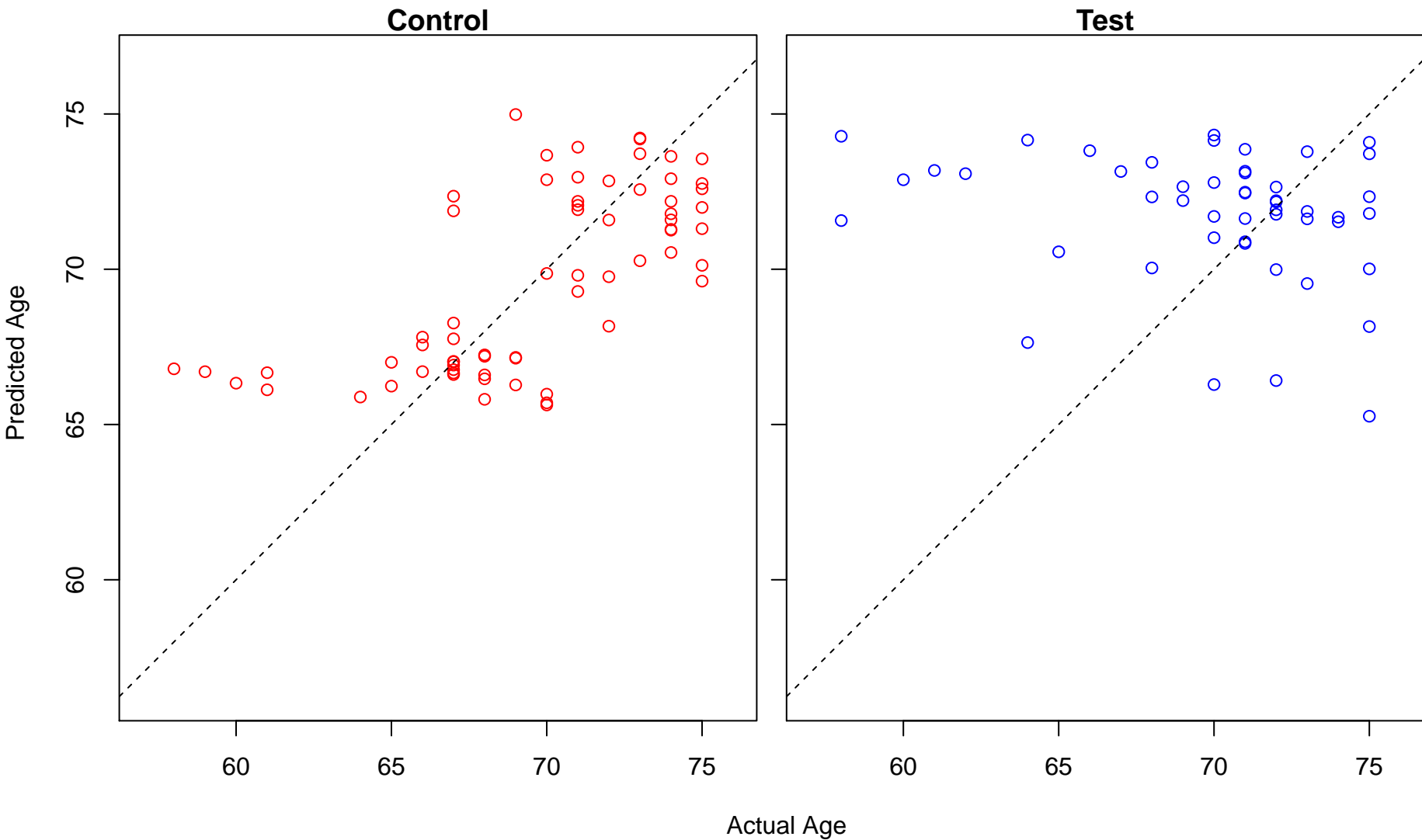
negative regulation of response to oxidative stress (Score: 1.405212)



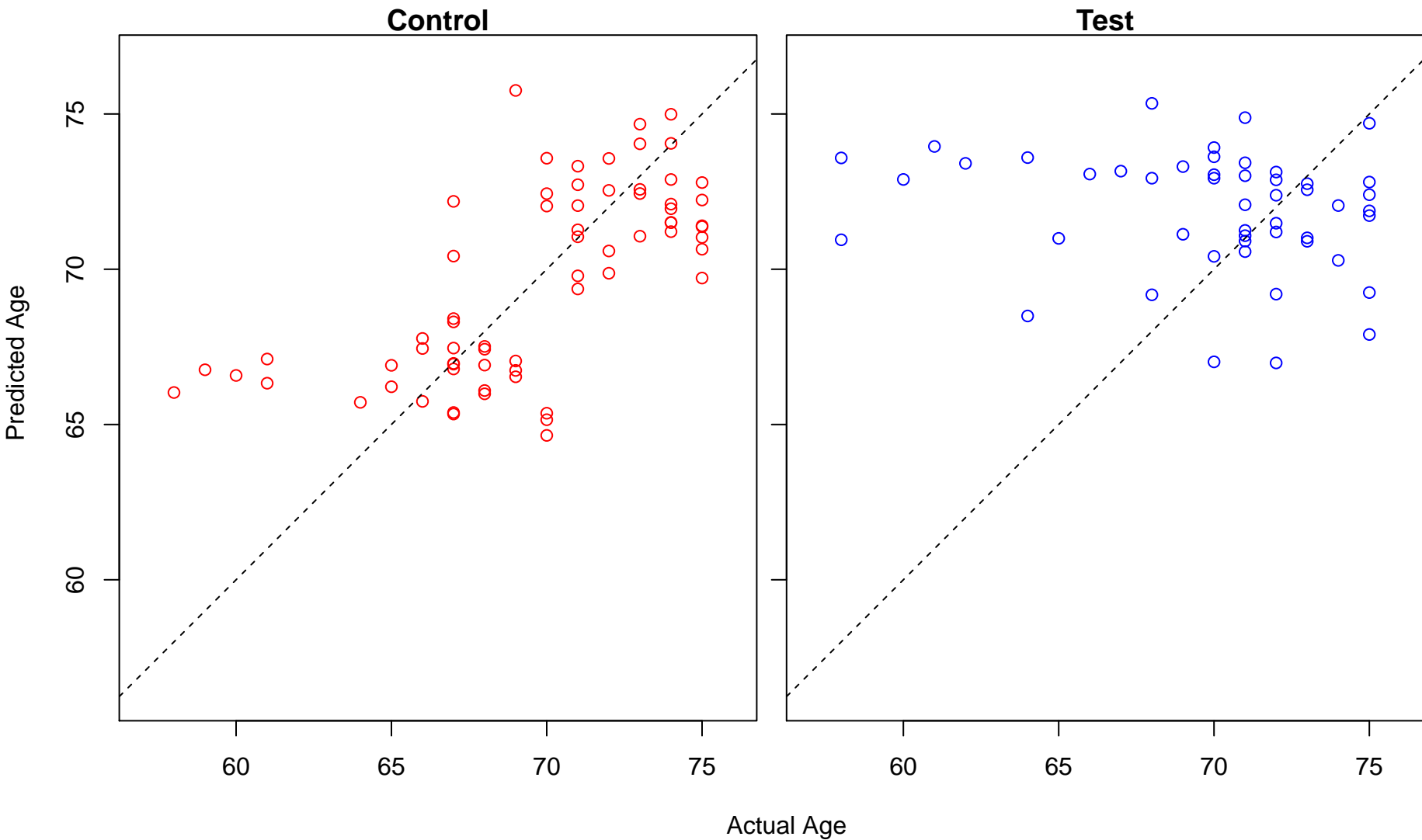
calcium ion homeostasis (Score: 1.404100)



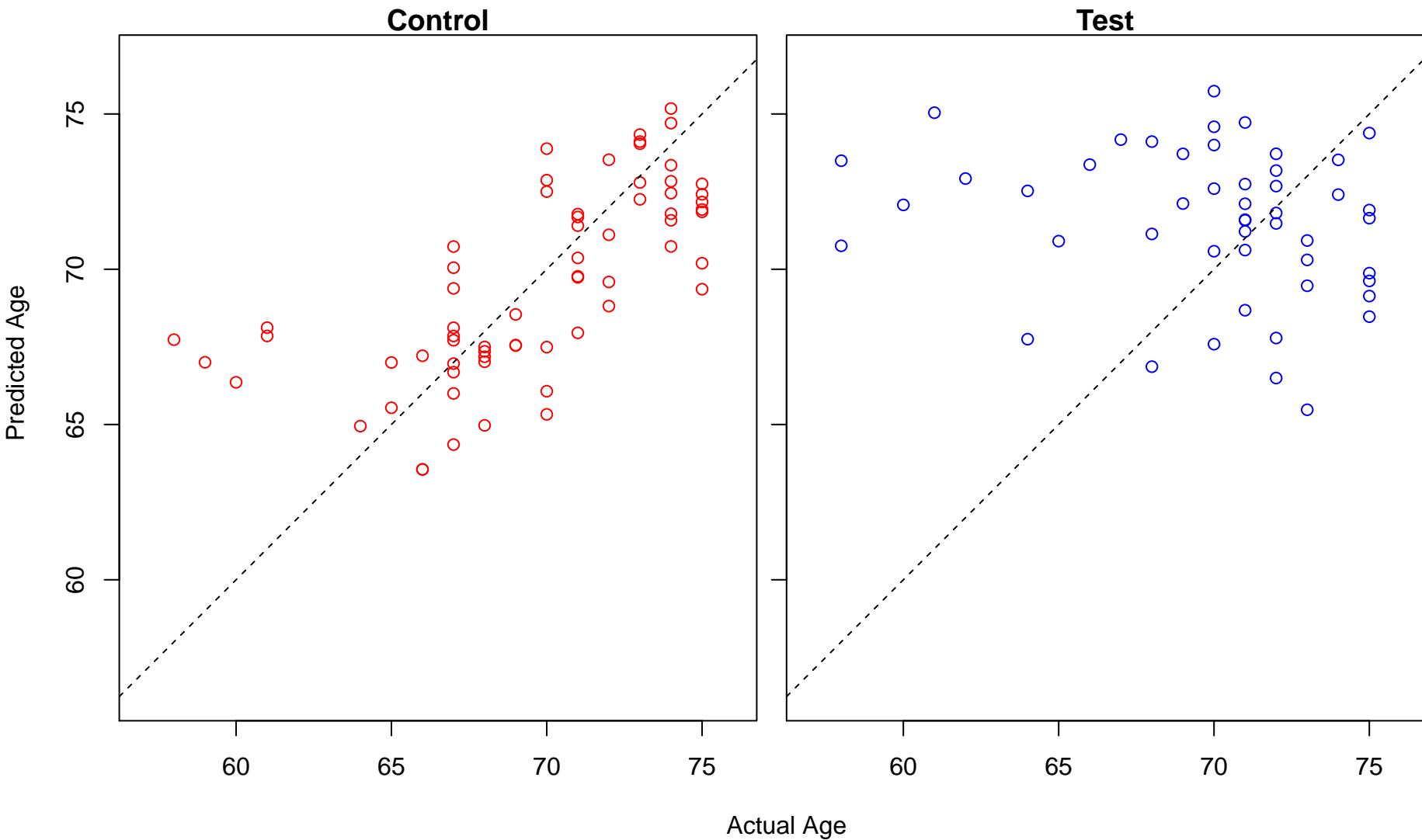
negative regulation of NF-kappaB transcription factor activity (Score: 1.403844)



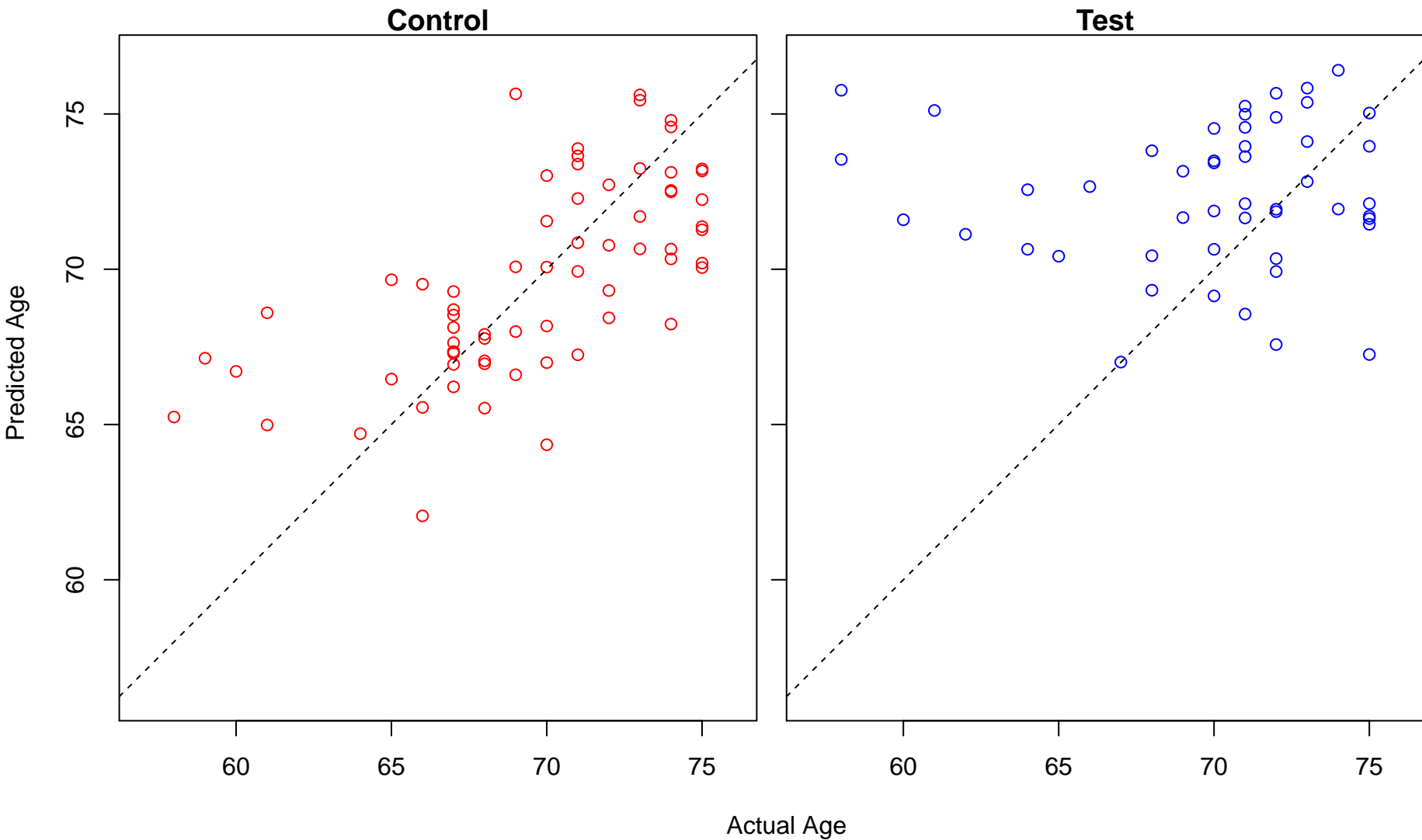
negative regulation of nuclear division (Score: 1.403778)



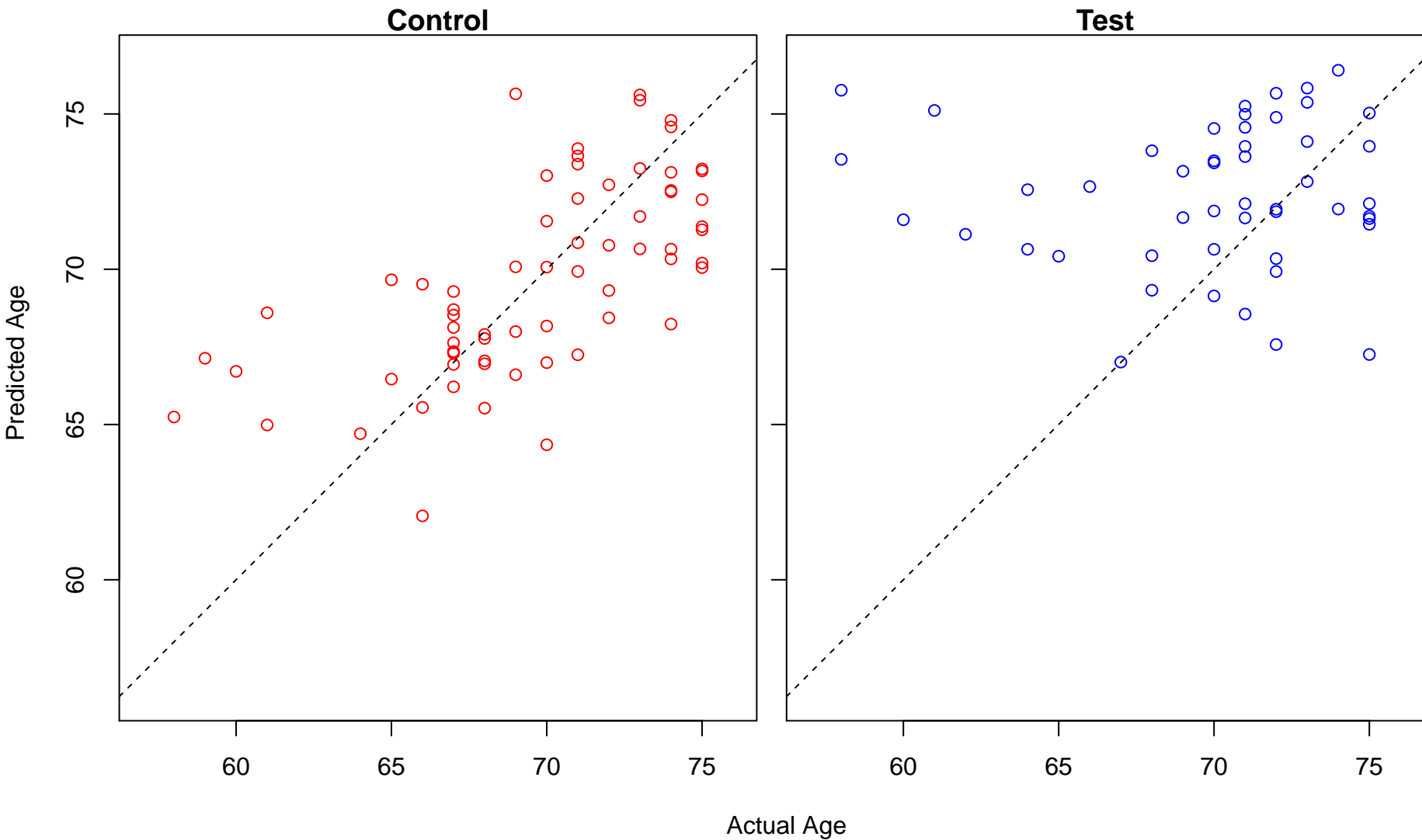
positive regulation of adaptive immune response (Score: 1.403677)



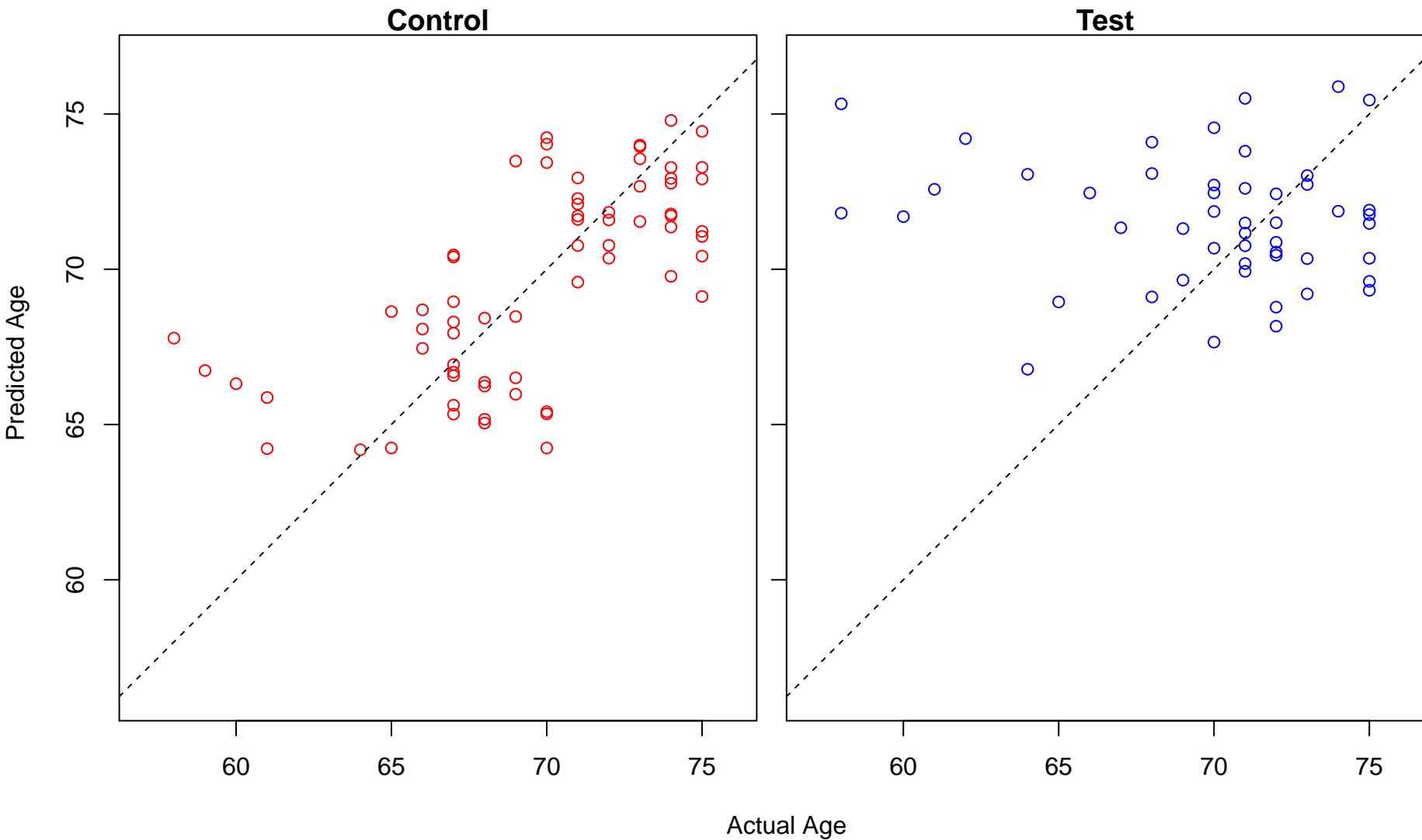
muscle organ morphogenesis (Score: 1.403531)



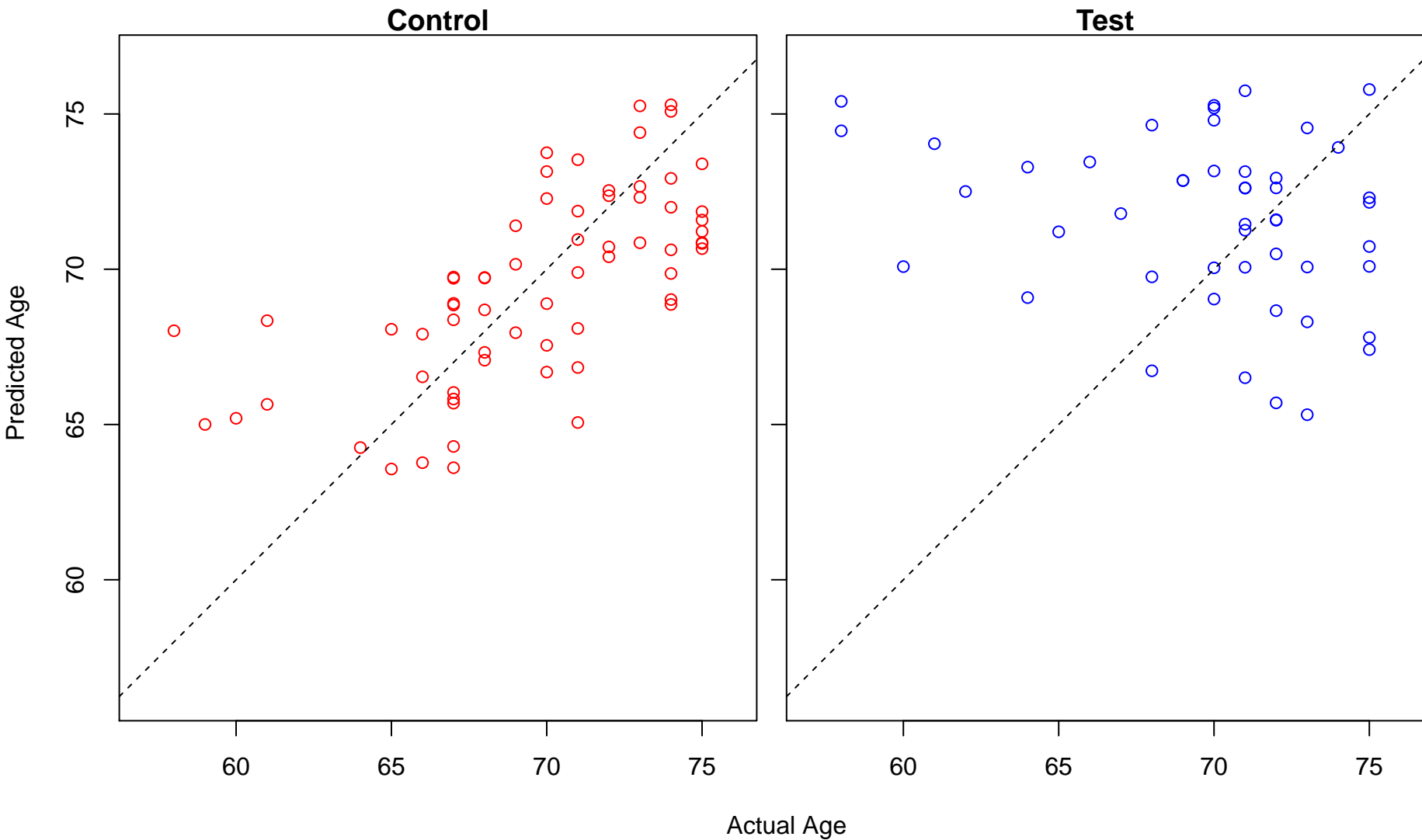
muscle tissue morphogenesis (Score: 1.403531)



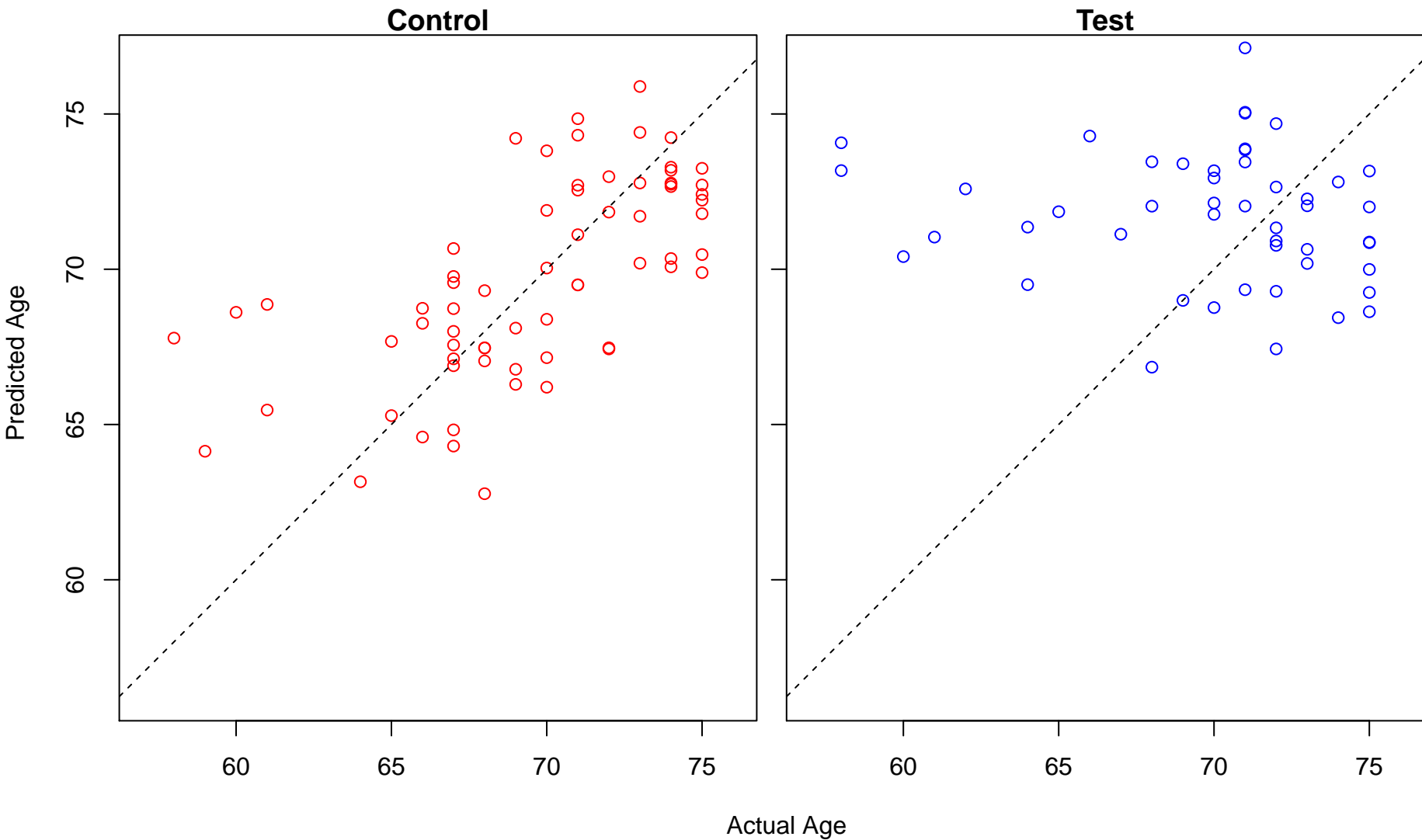
Golgi vesicle transport (Score: 1.403028)



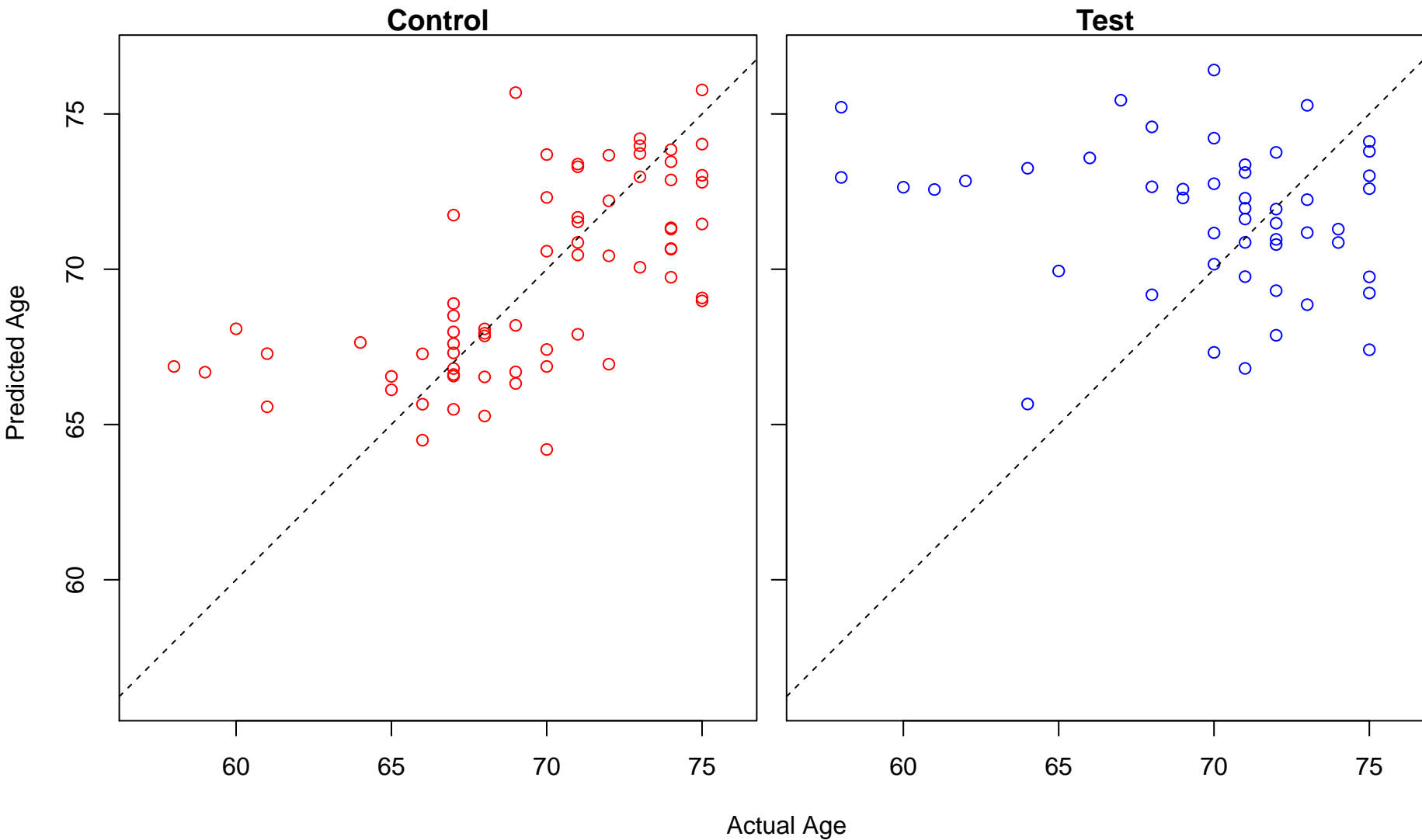
regulation of lymphocyte mediated immunity (Score: 1.402741)



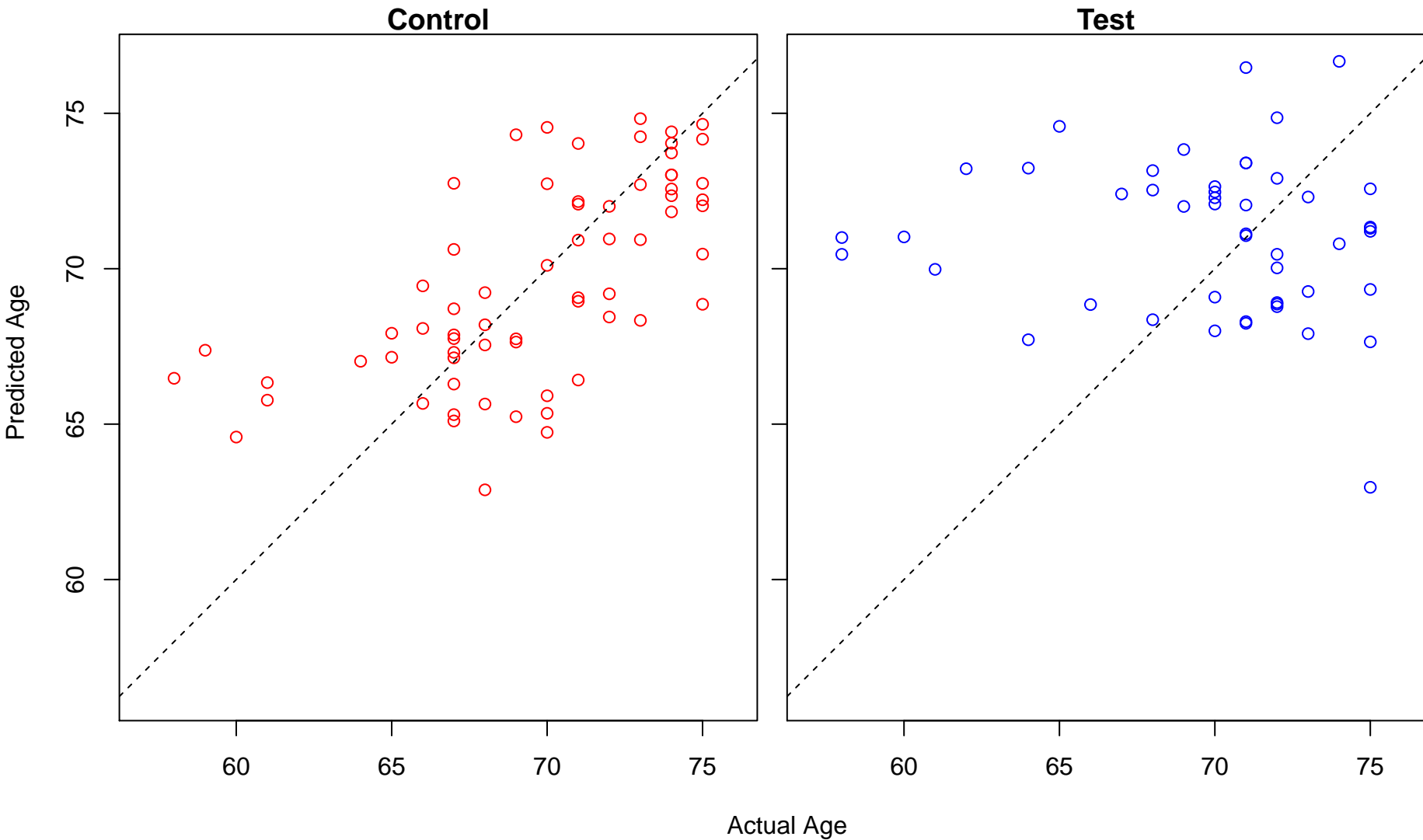
vesicle fusion (Score: 1.402609)



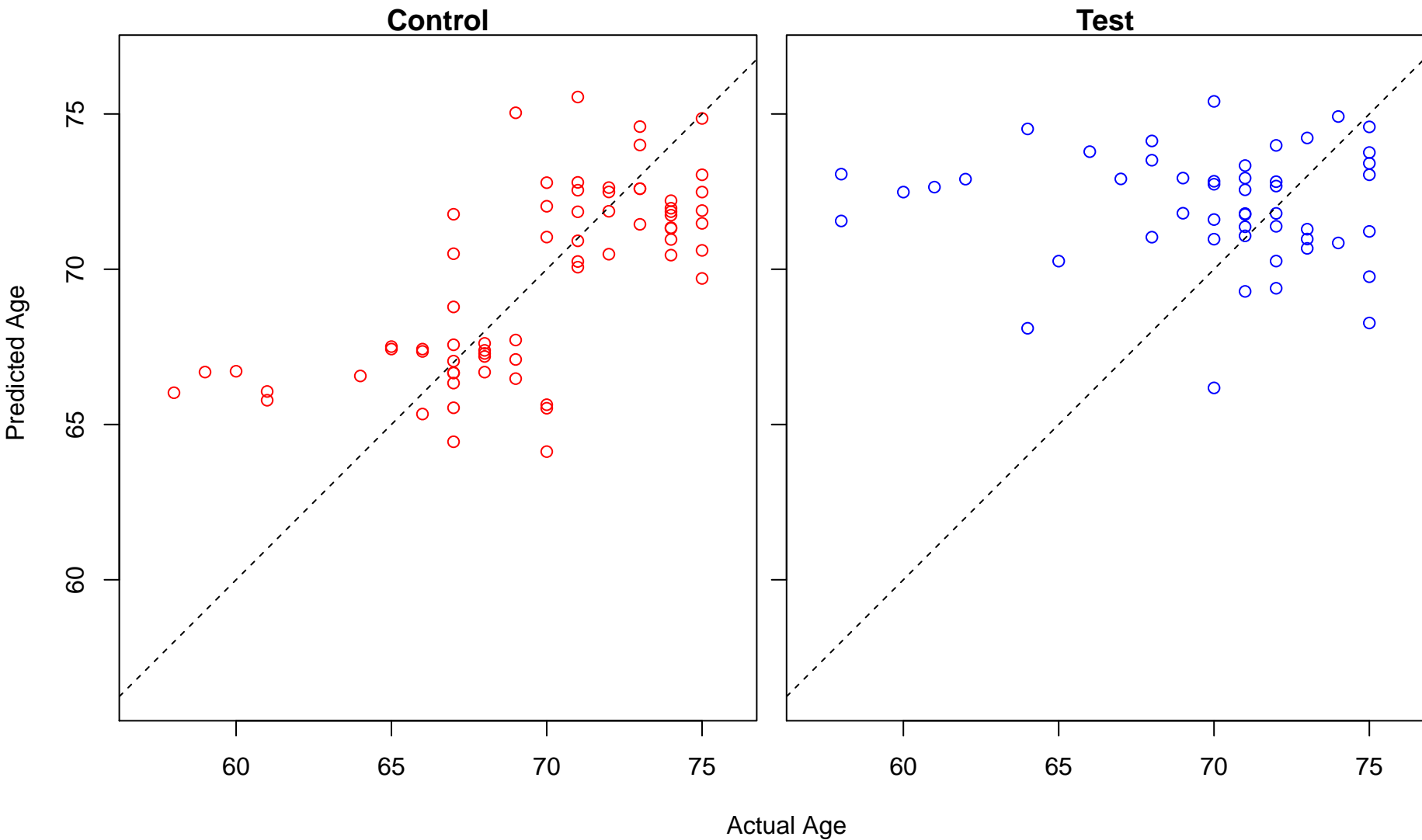
cellular zinc ion homeostasis (Score: 1.402397)



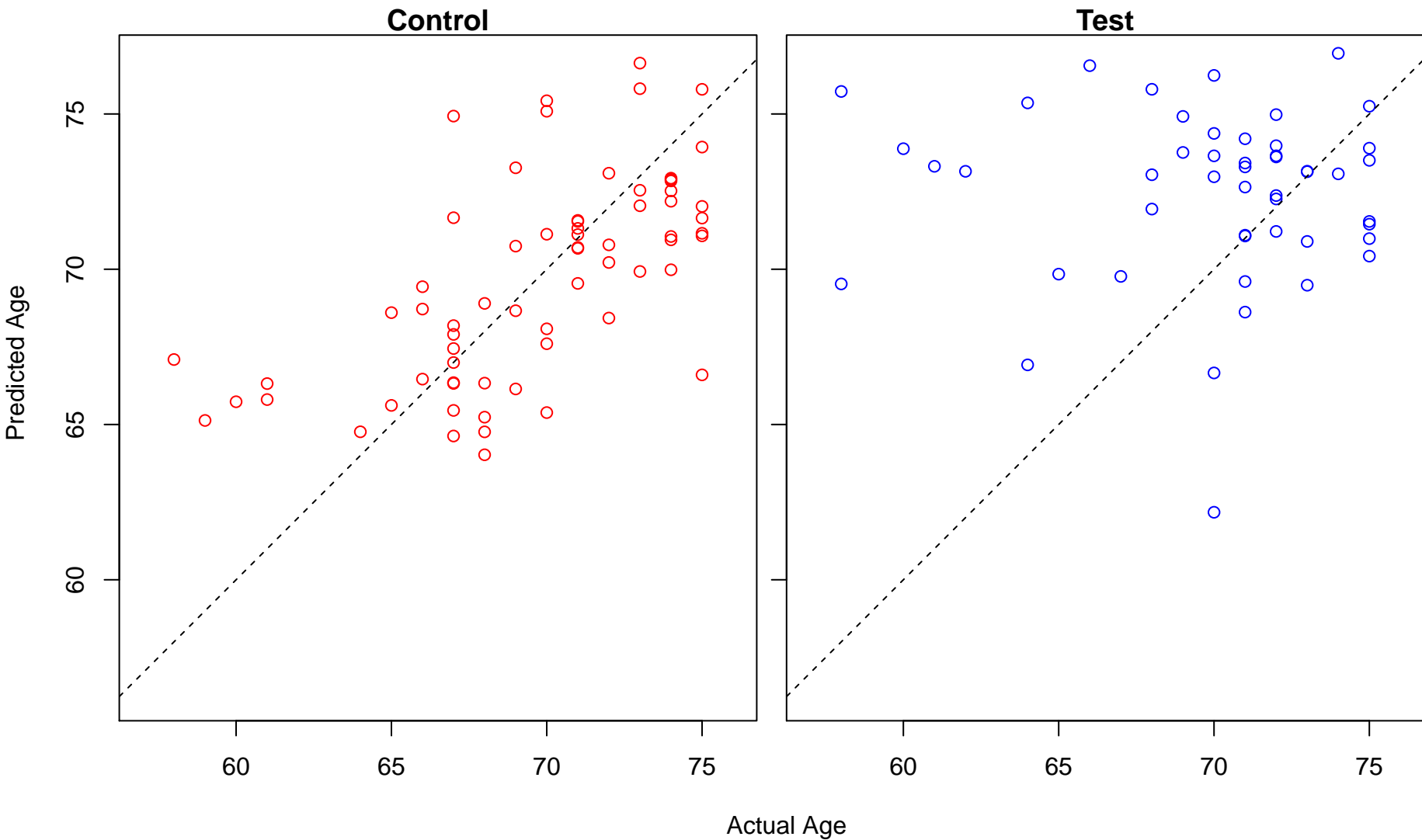
positive regulation of pri-miRNA transcription from RNA polymerase II promoter (Score: 1.402215)



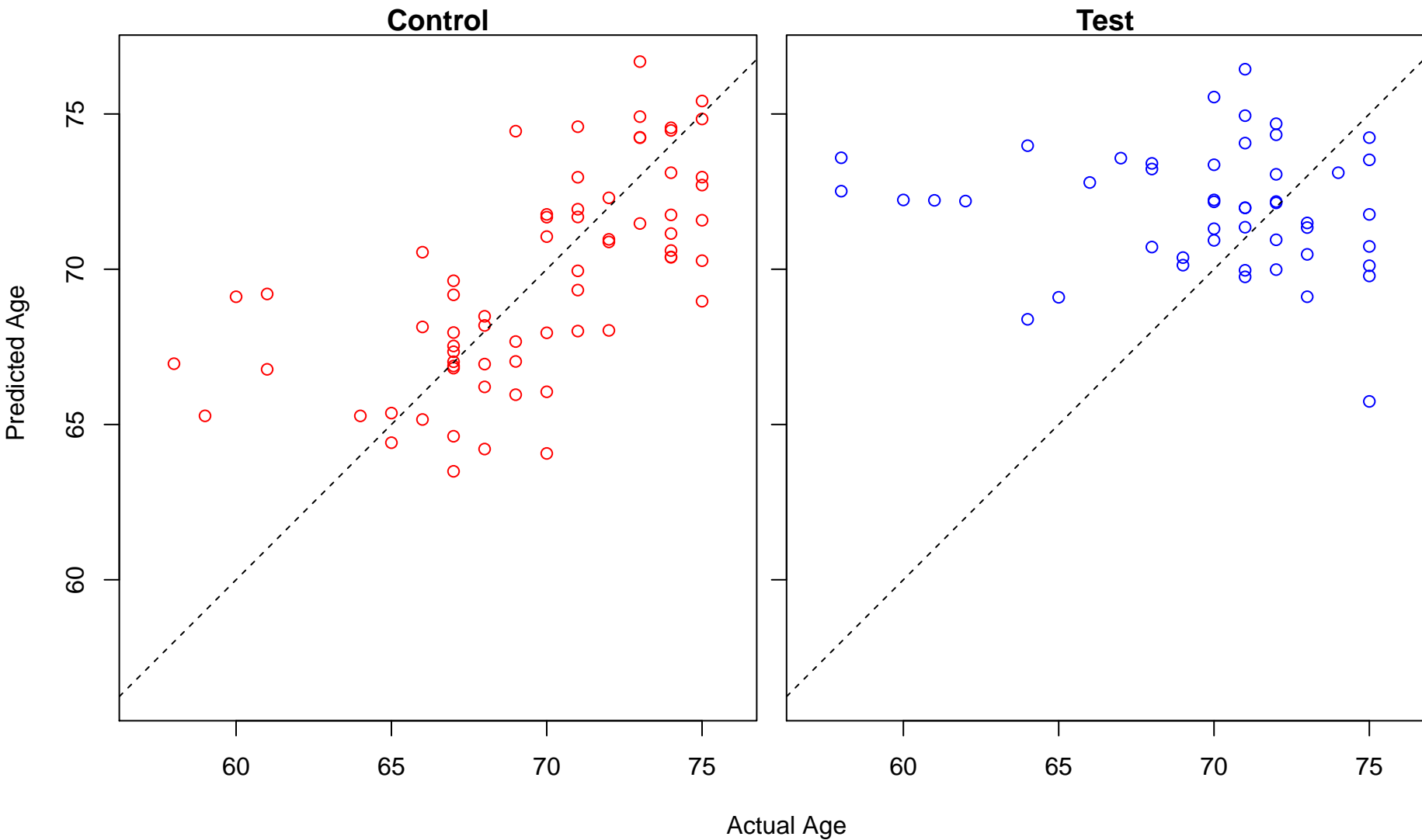
regulation of protein import into nucleus, translocation (Score: 1.402140)



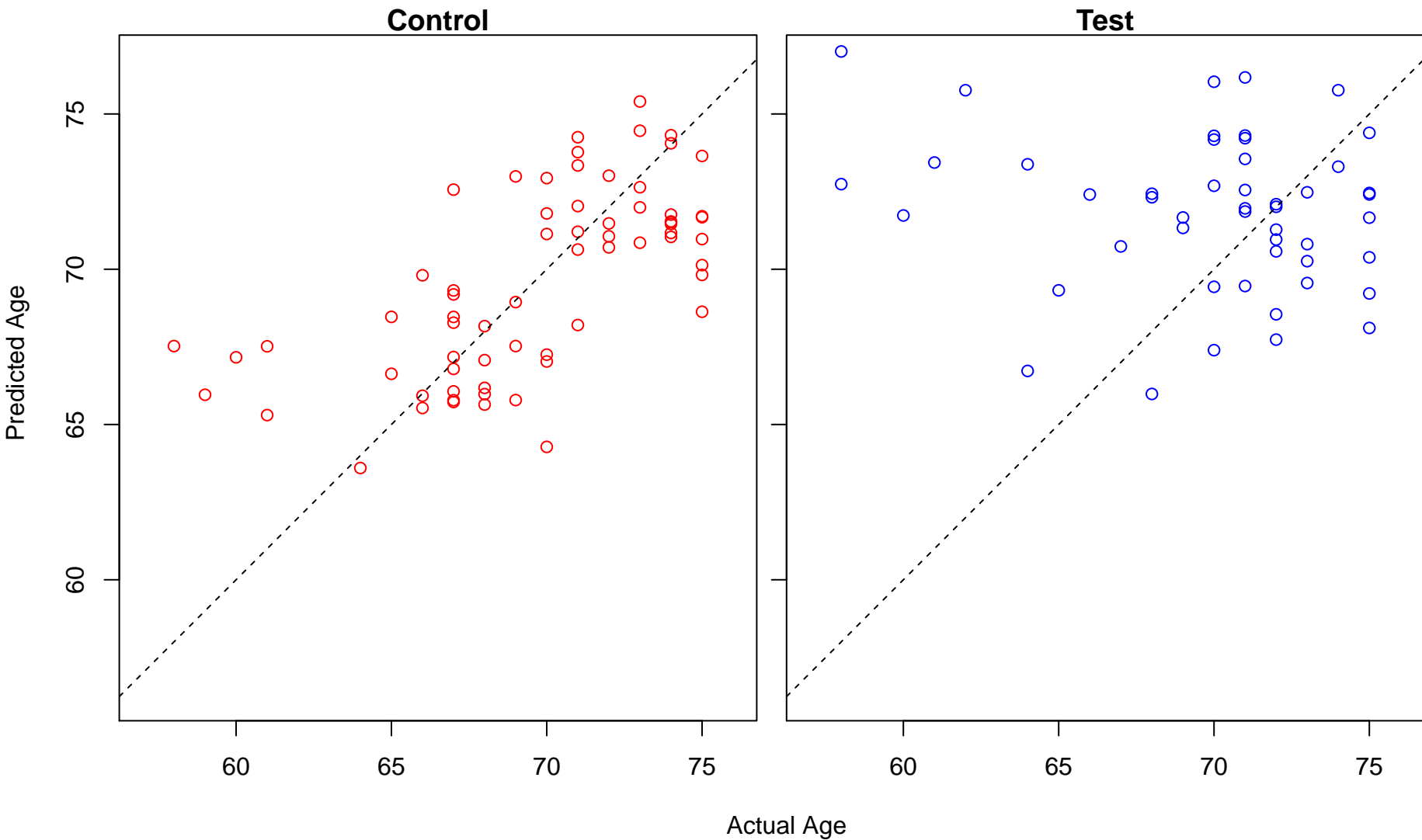
negative regulation of lipid metabolic process (Score: 1.402054)



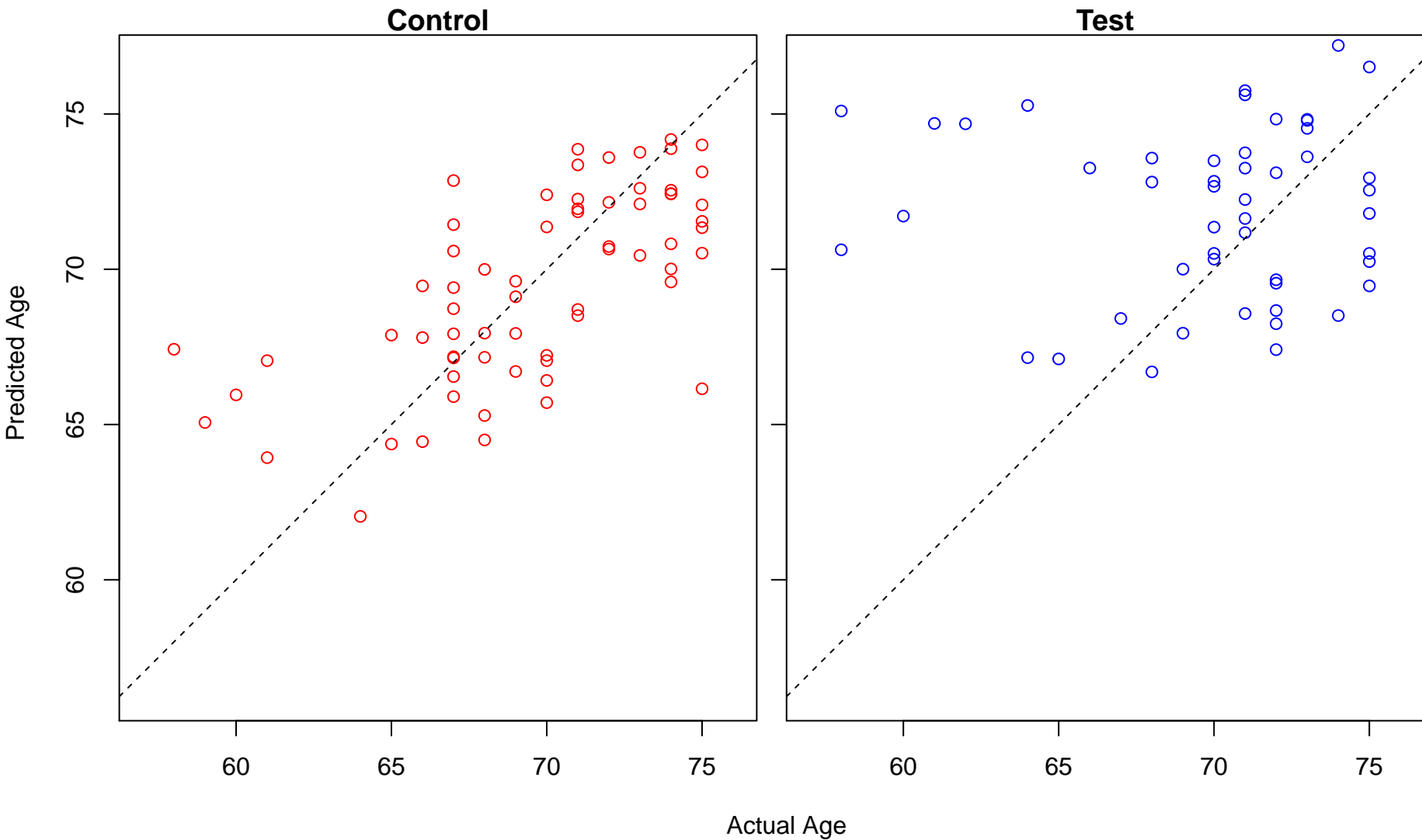
carbohydrate derivative catabolic process (Score: 1.401771)



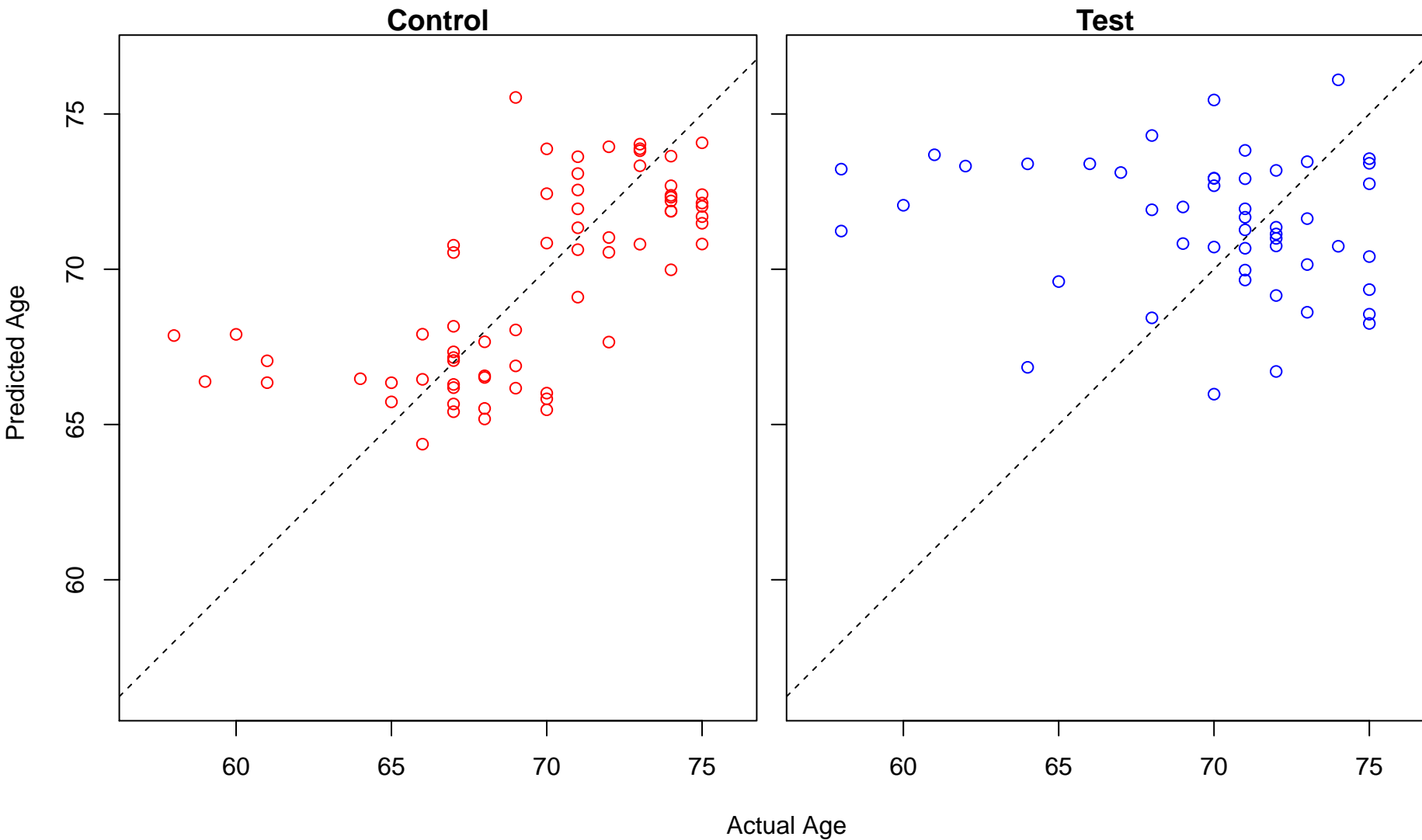
snRNA metabolic process (Score: 1.401669)



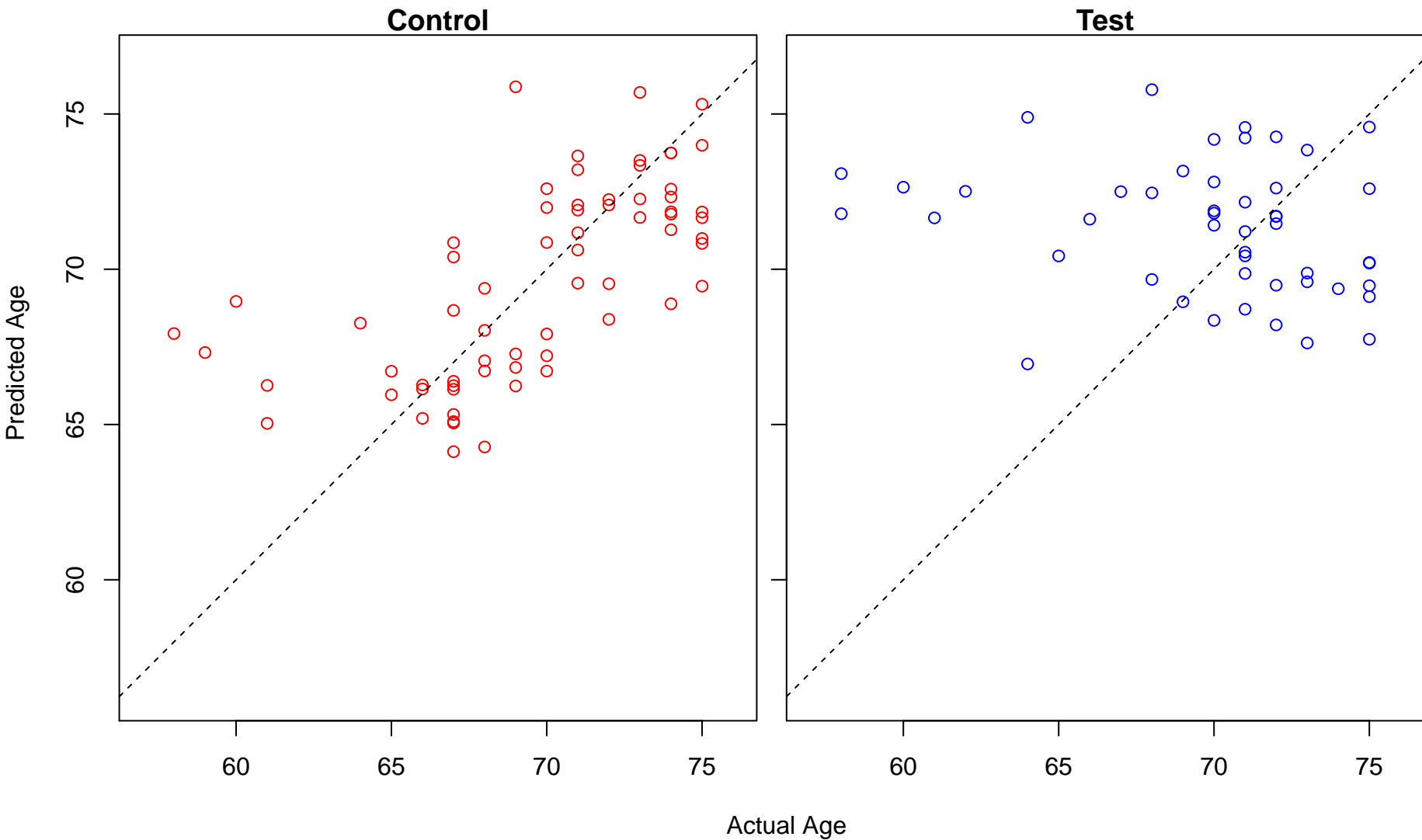
lysosome localization (Score: 1.401280)



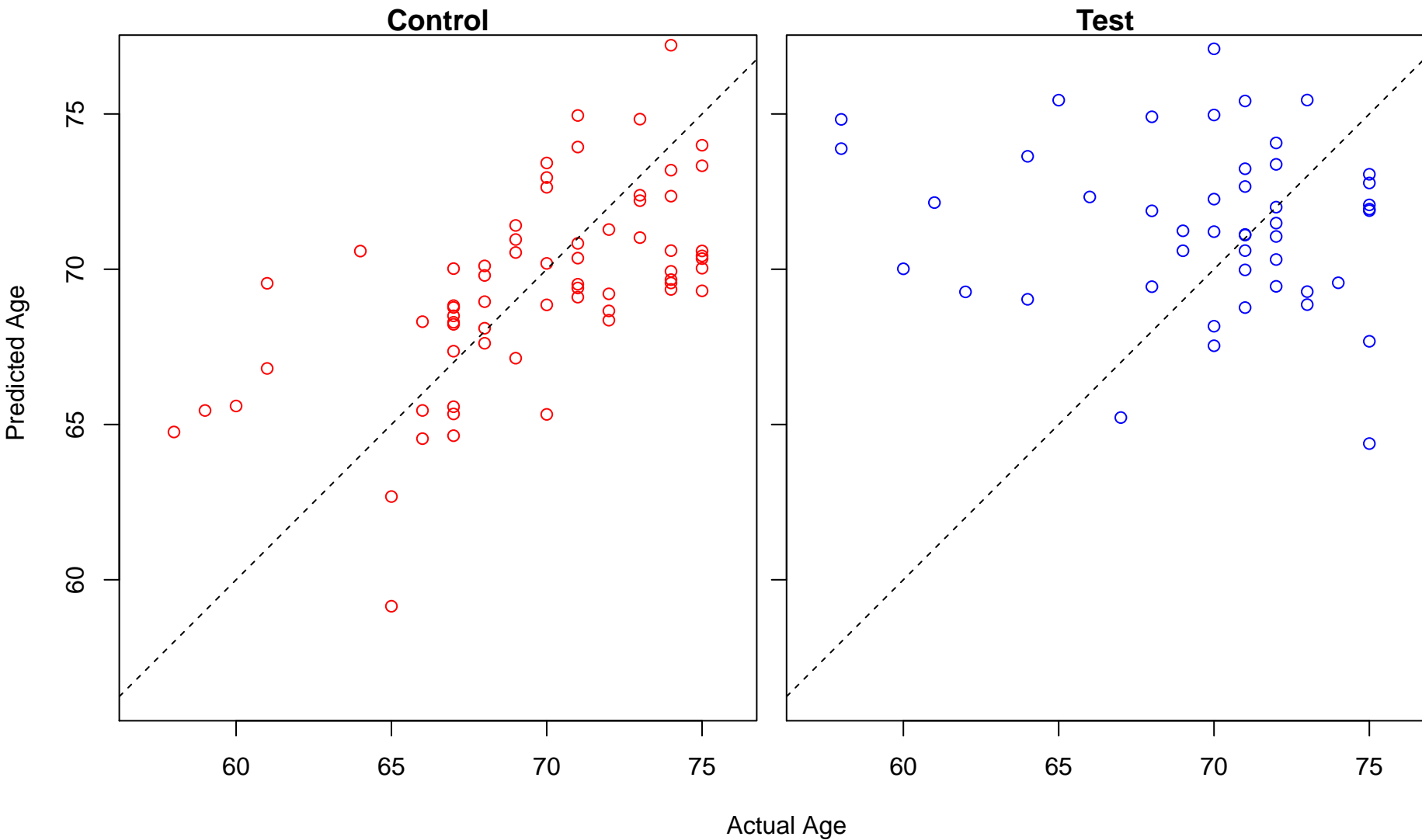
cell chemotaxis (Score: 1.401245)



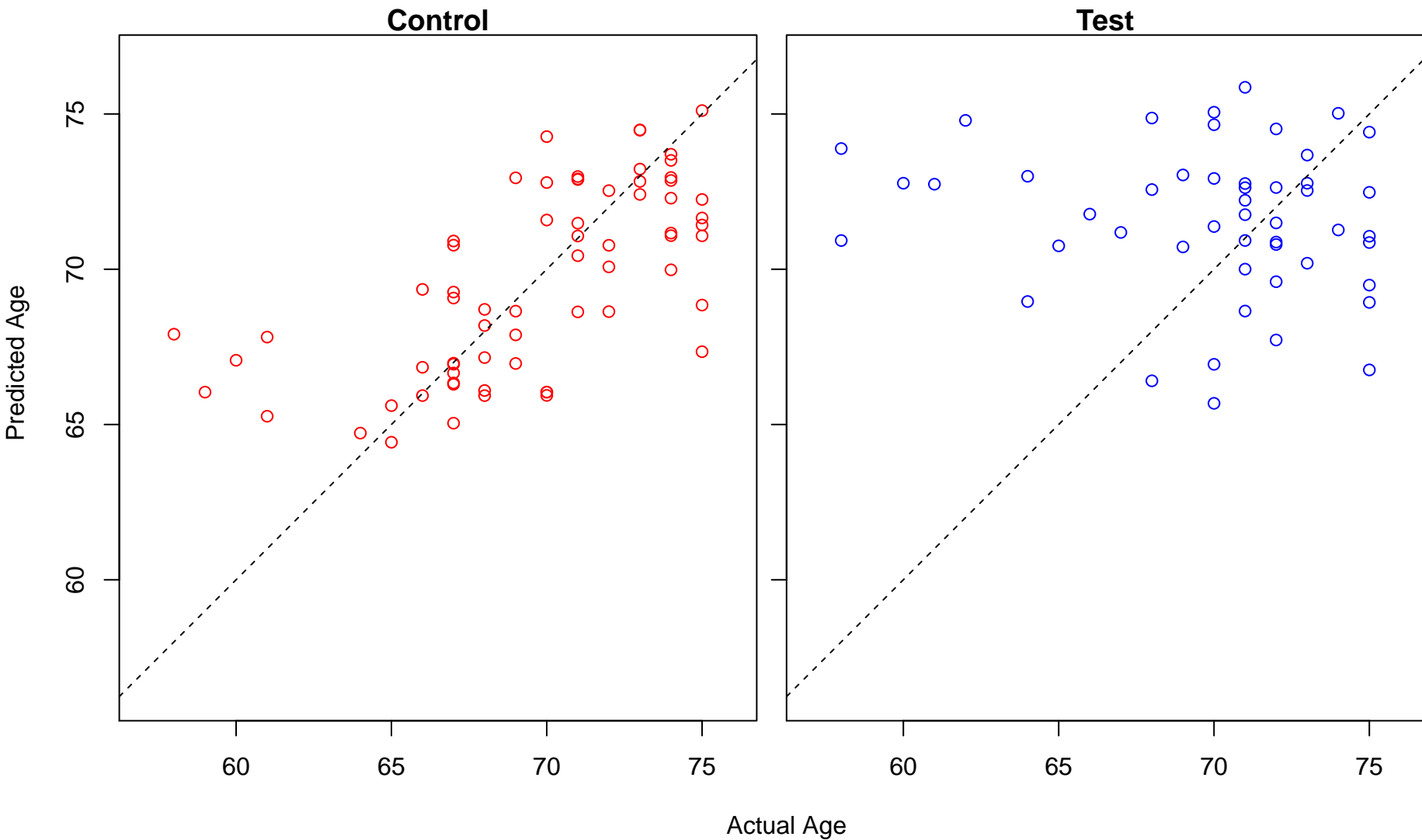
negative regulation of lymphocyte activation (Score: 1.401103)



regulation of granulocyte chemotaxis (Score: 1.400006)

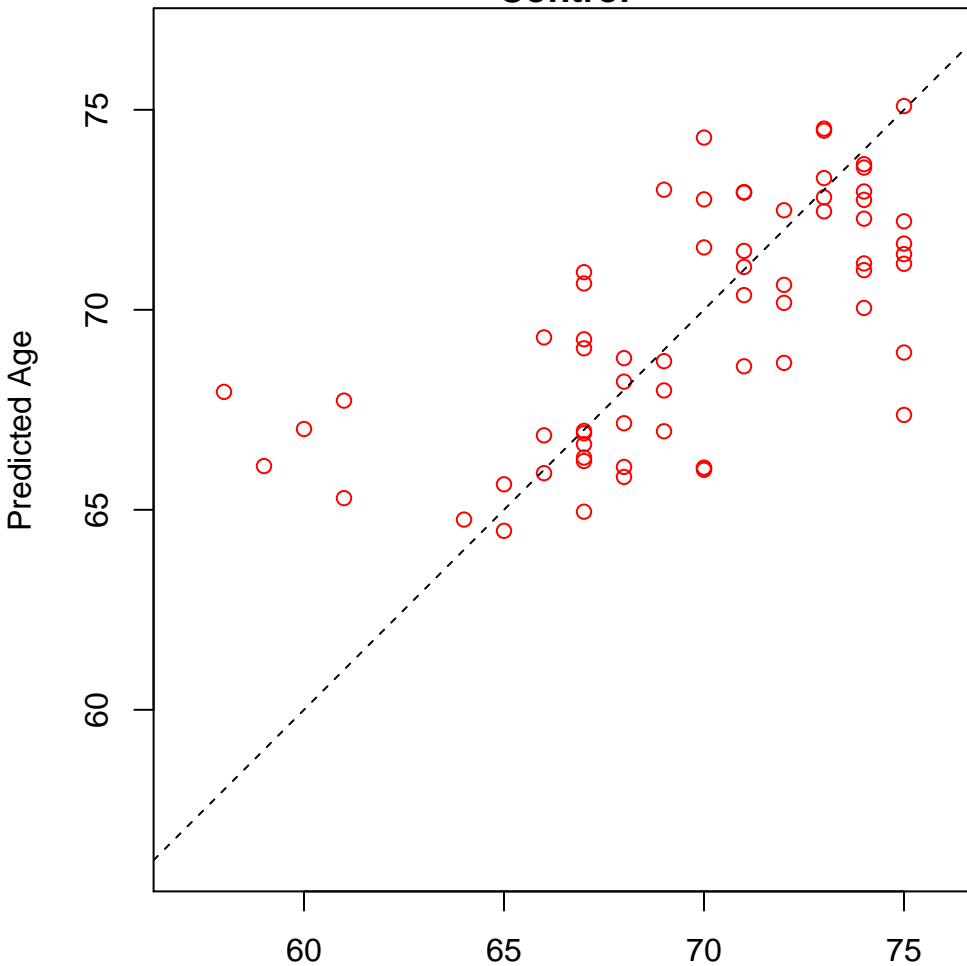


positive regulation of phospholipase C activity (Score: 1.399941)

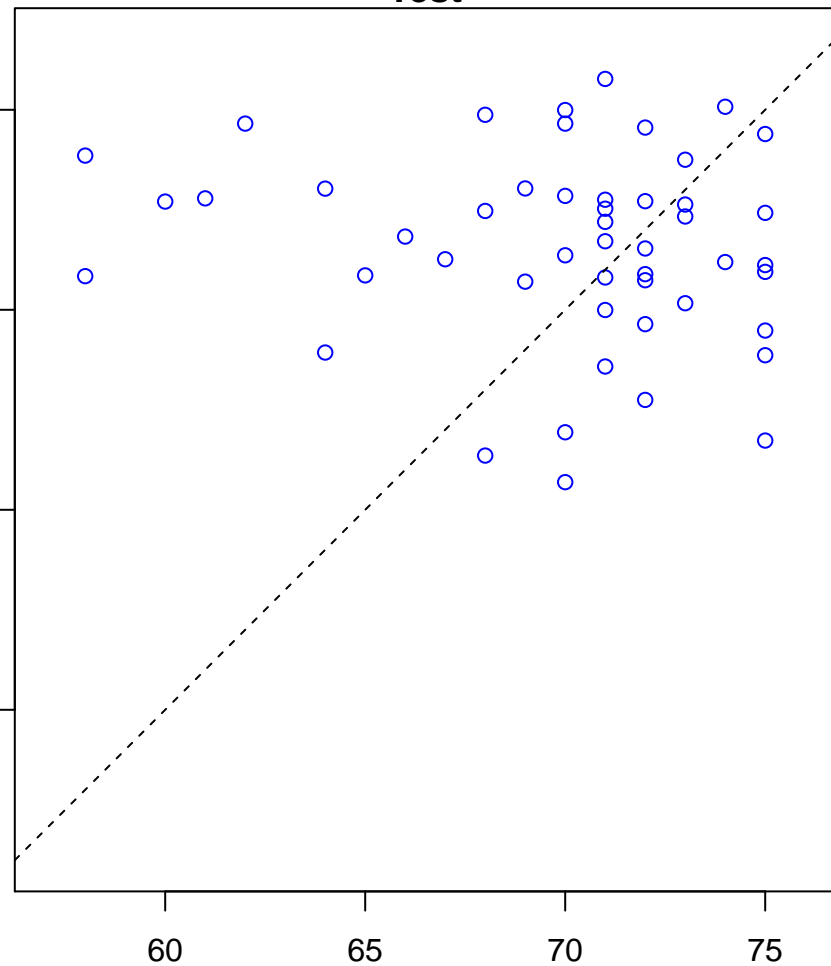


activation of phospholipase C activity (Score: 1.399844)

Control

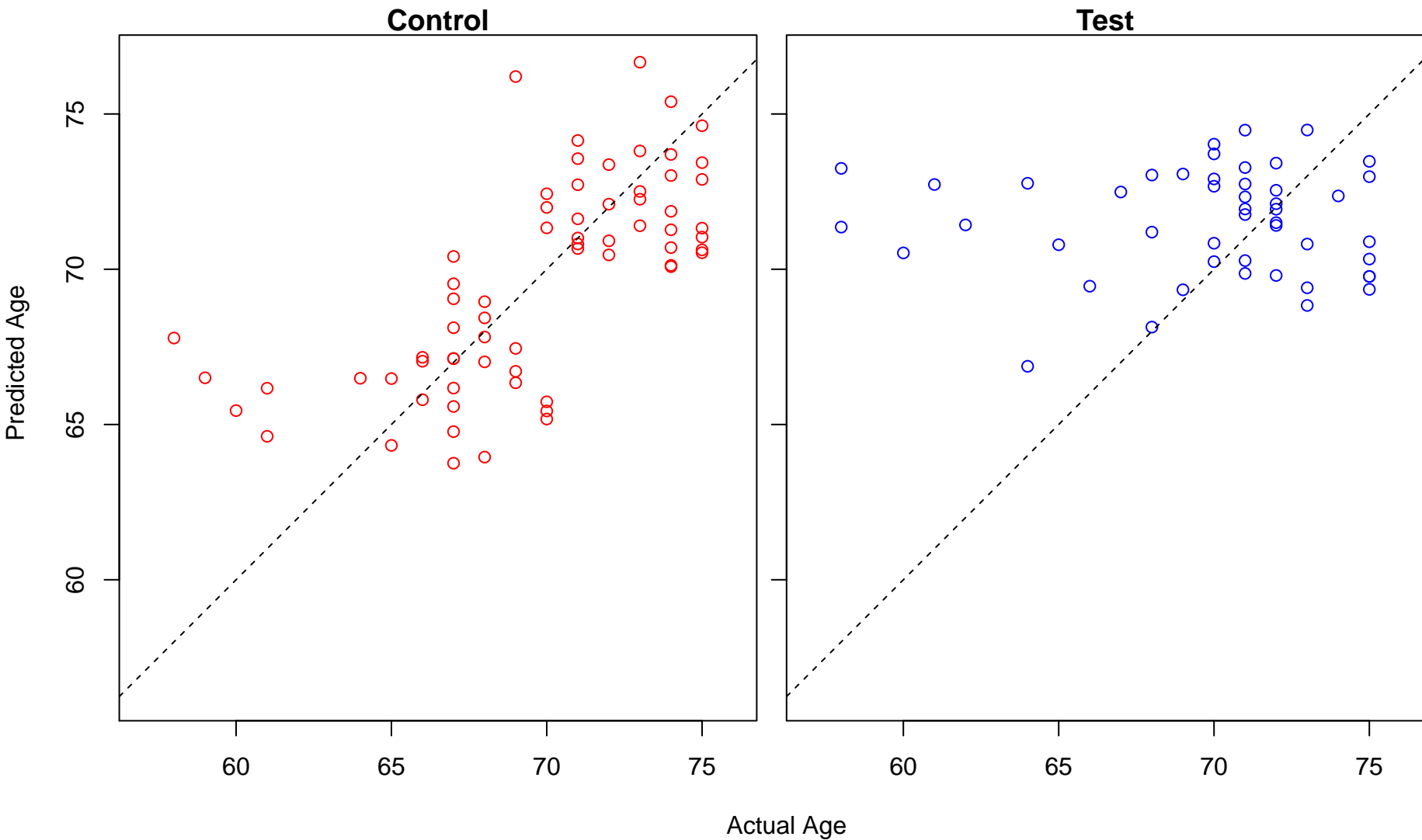


Test



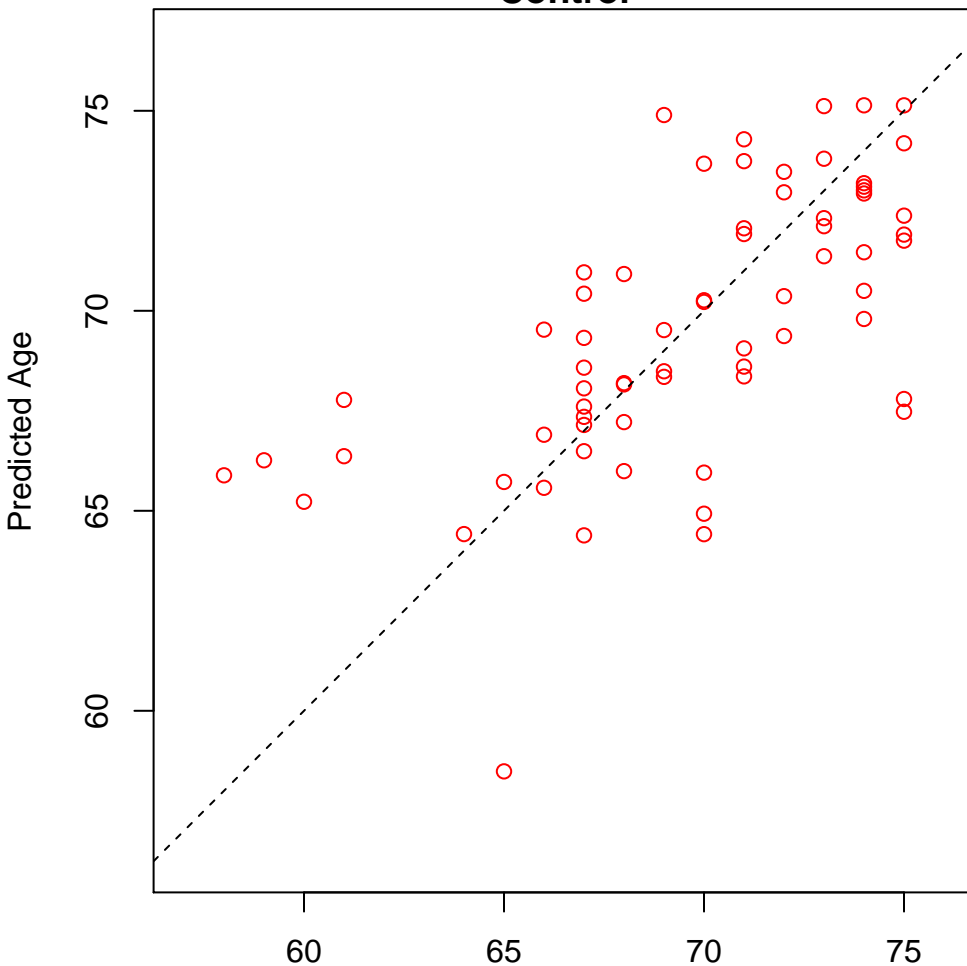
Actual Age

regulation of vesicle-mediated transport (Score: 1.399430)

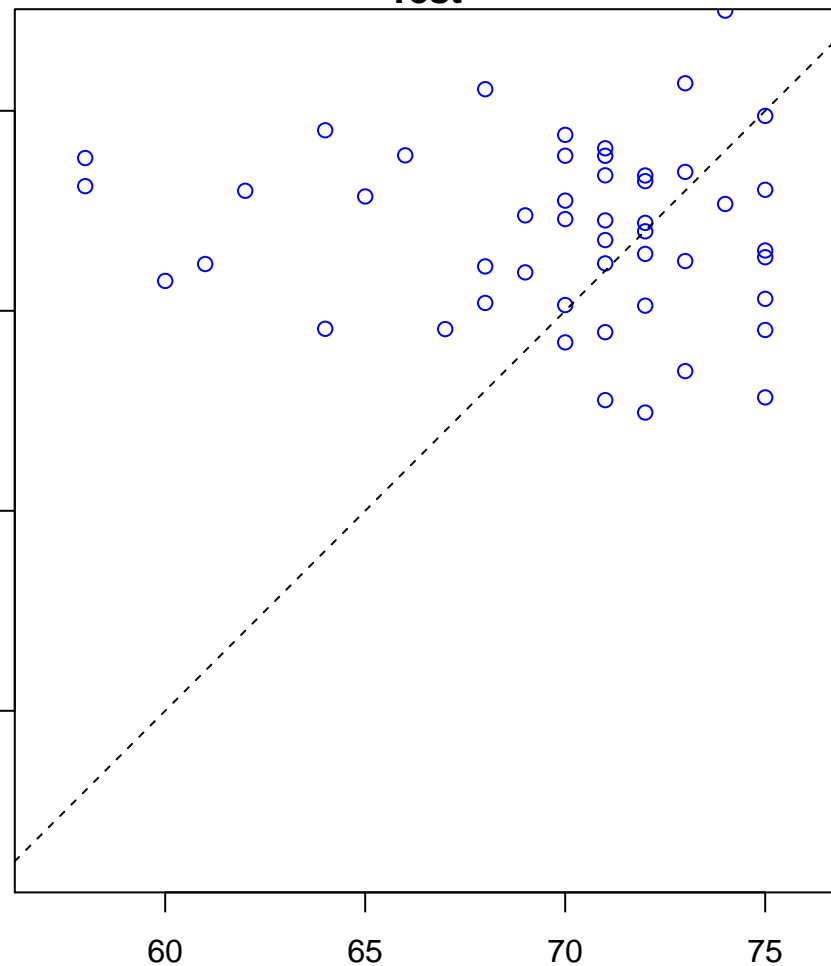


regulation of ERK1 and ERK2 cascade (Score: 1.399163)

Control

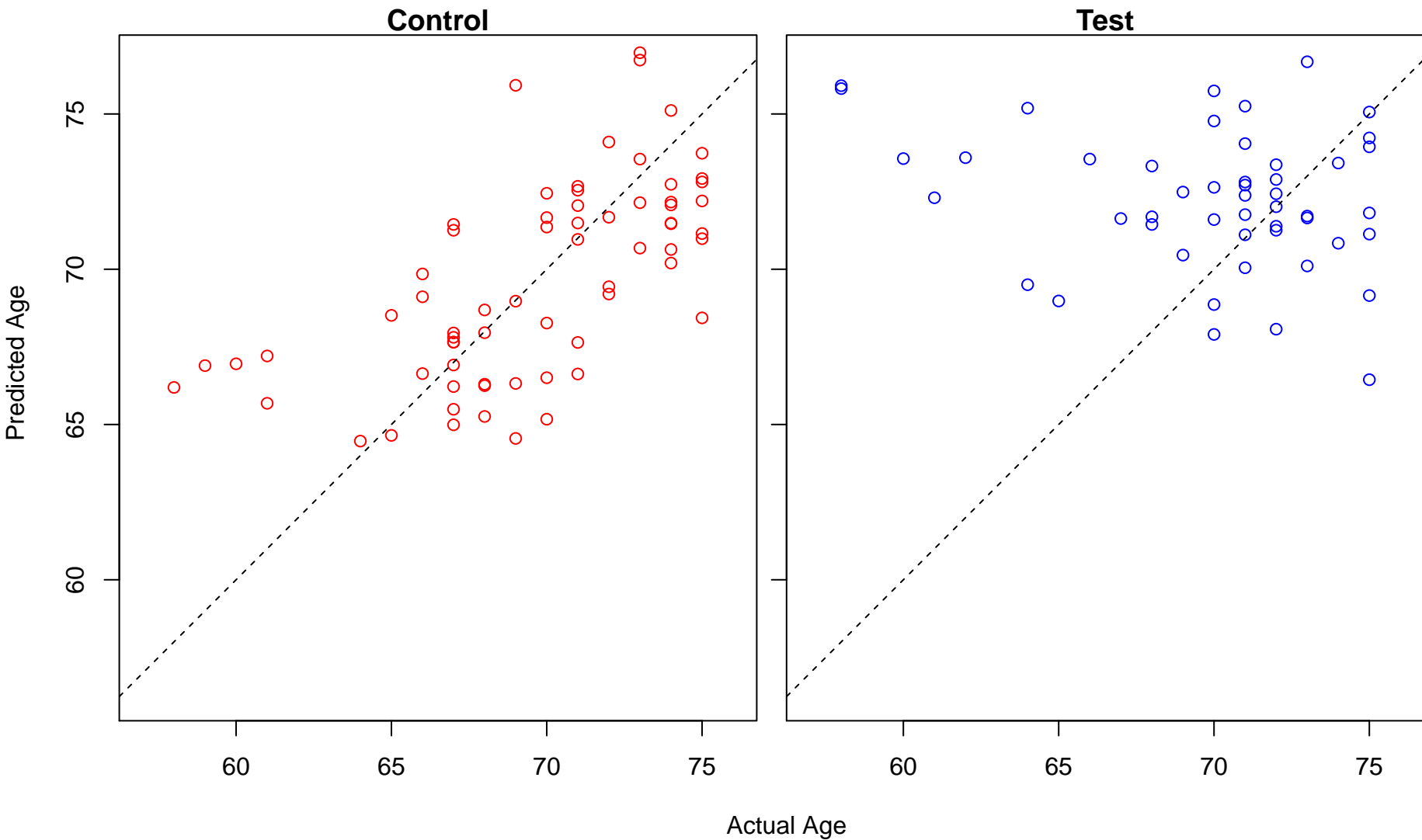


Test

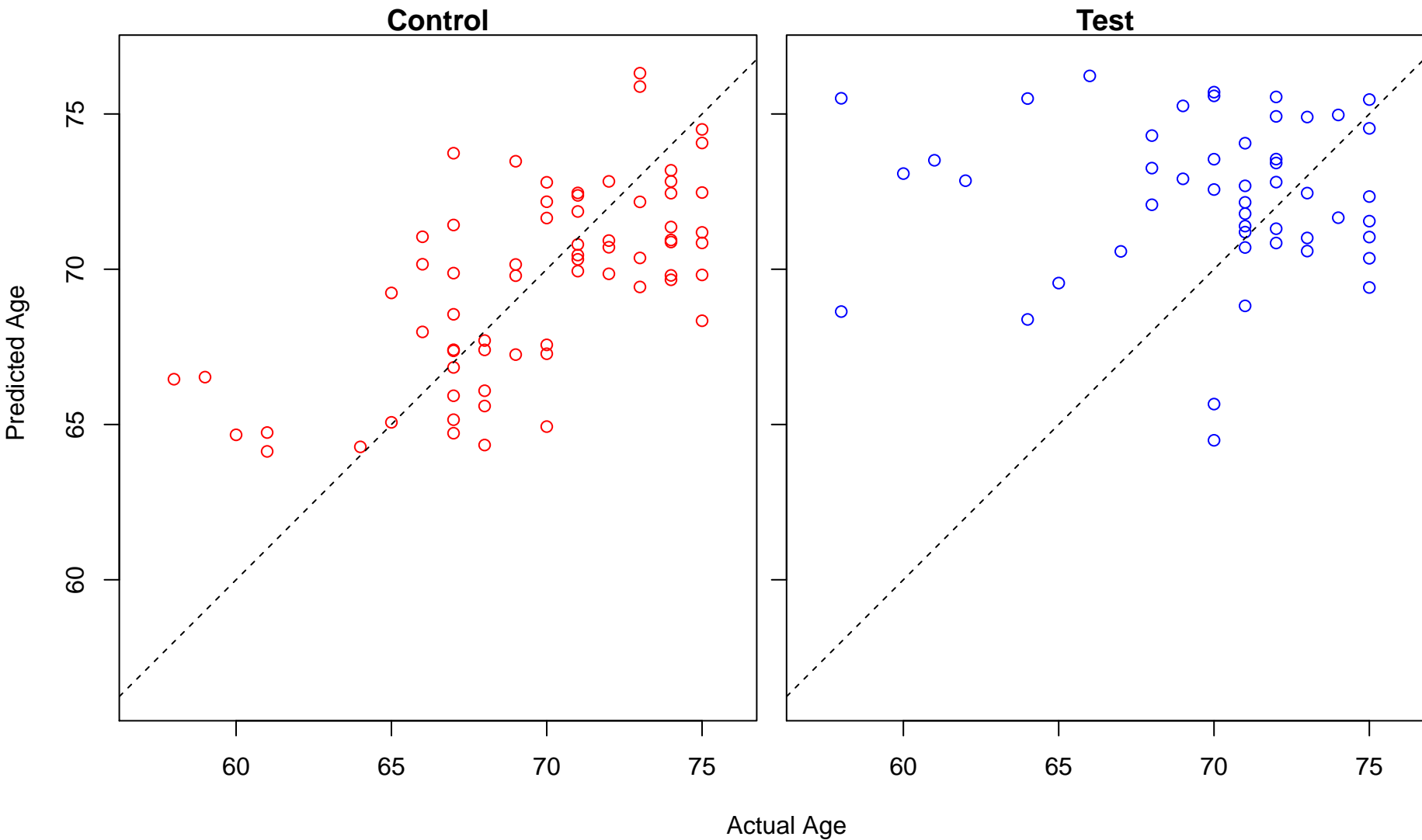


Actual Age

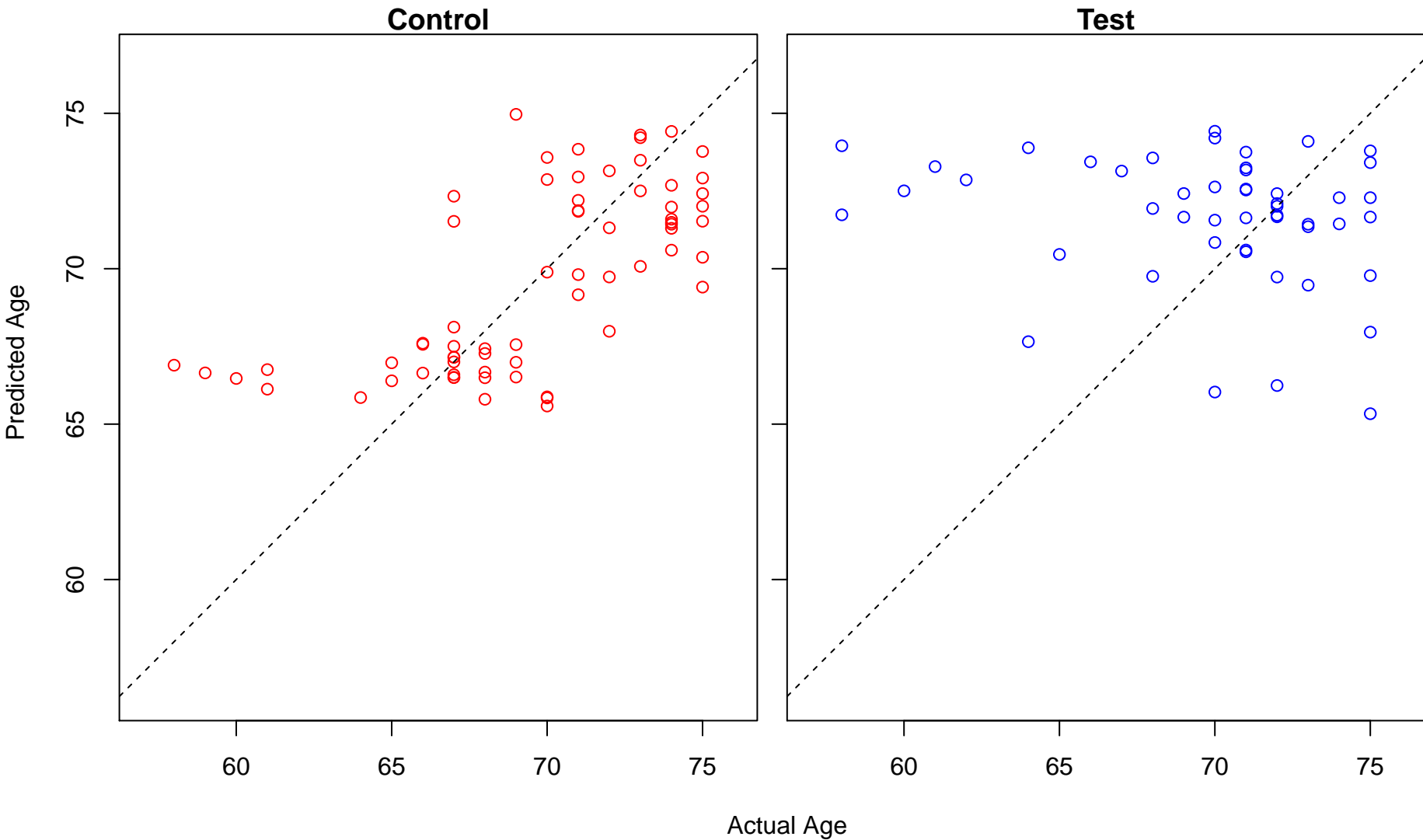
inorganic anion transport (Score: 1.398890)



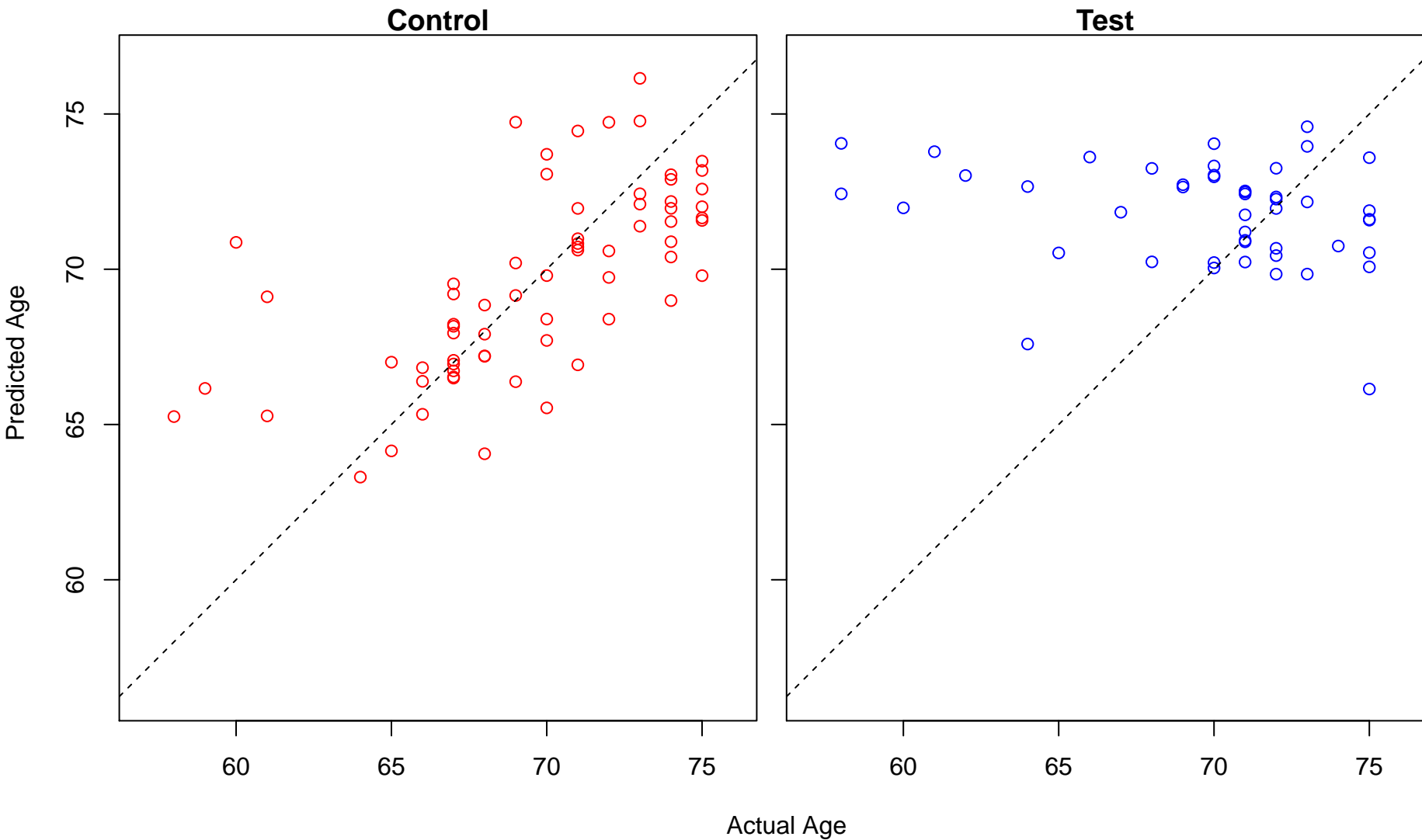
negative regulation of lipid biosynthetic process (Score: 1.398167)



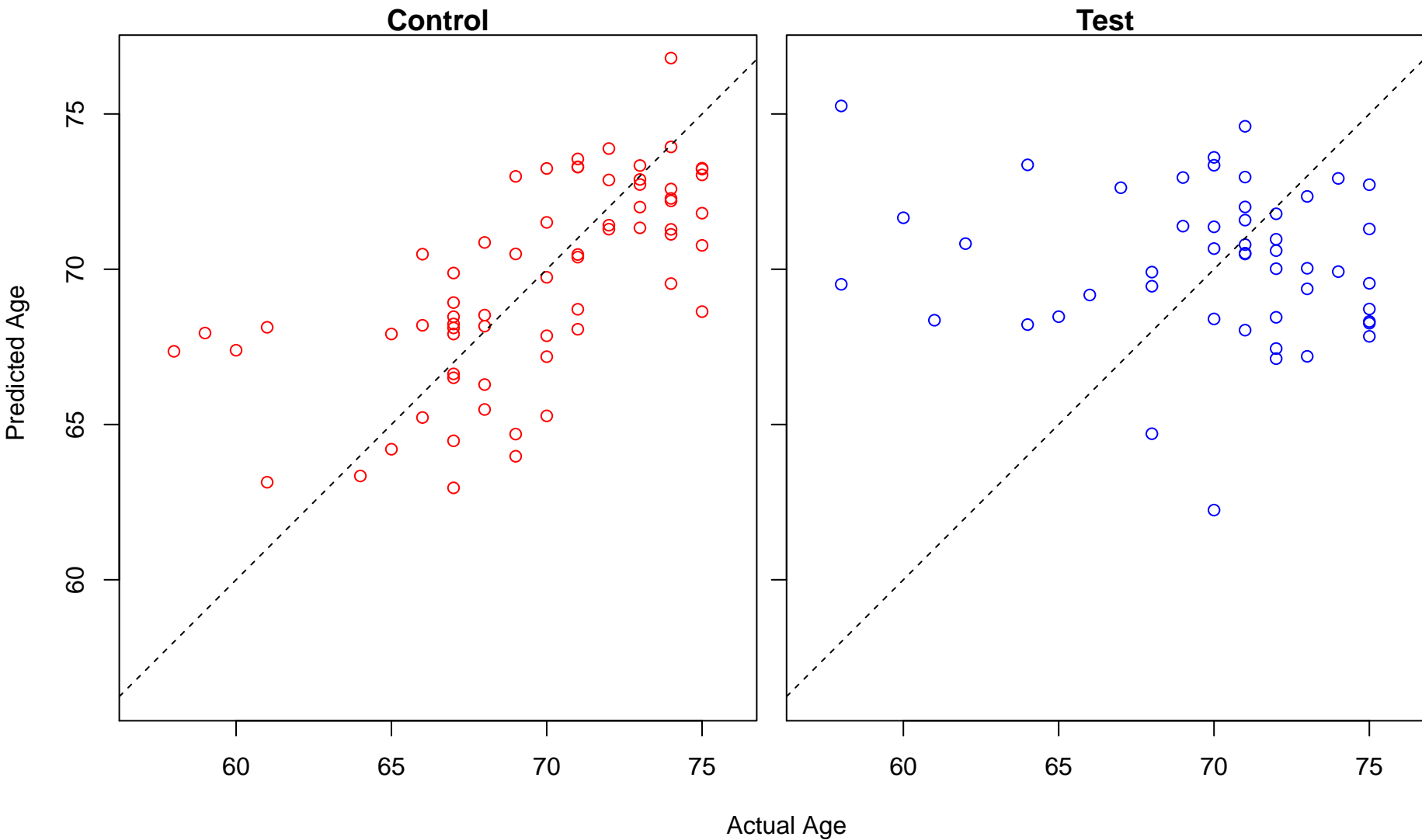
negative regulation of sequence-specific DNA binding transcription factor activity (Score: 1.39728)



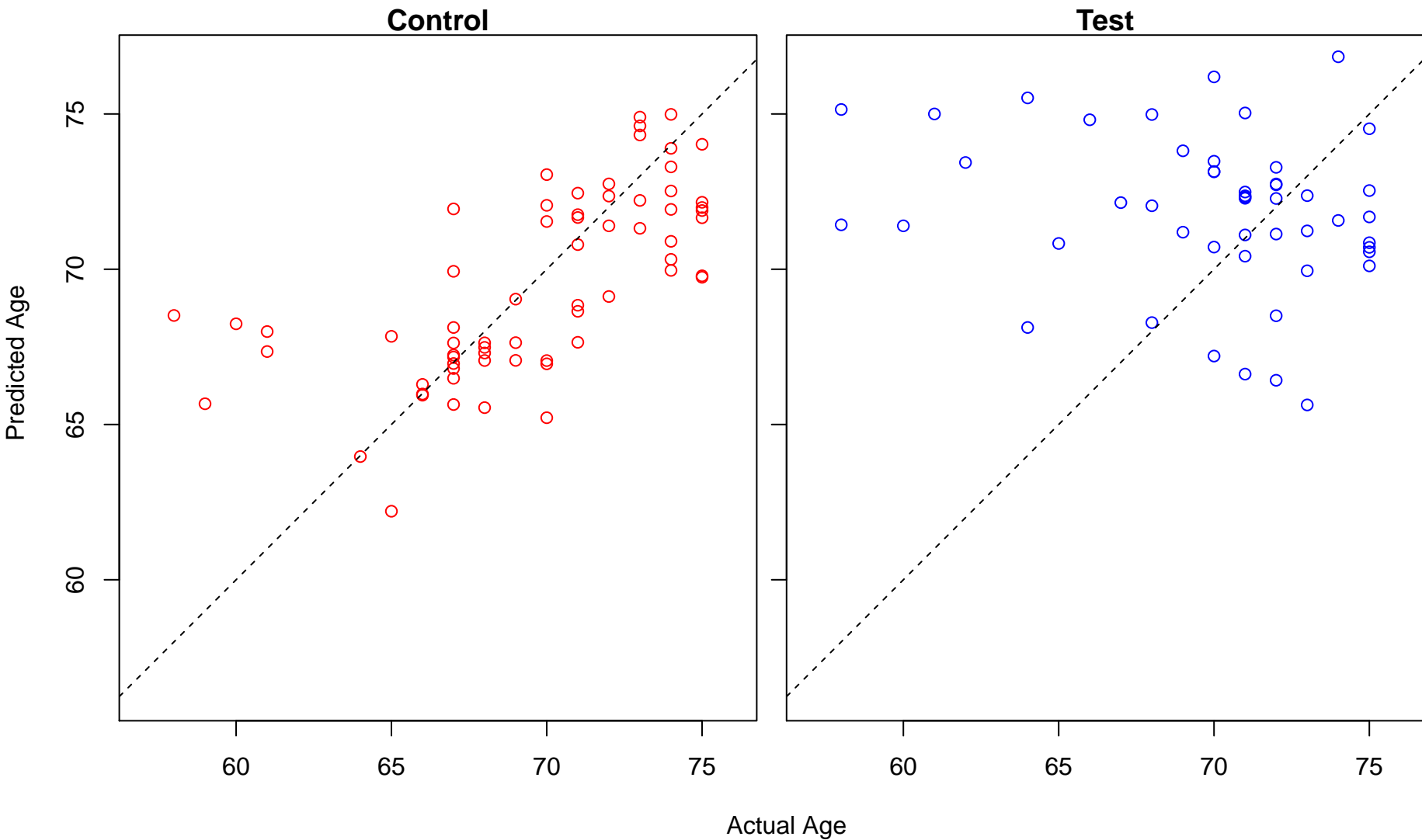
protein secretion (Score: 1.396913)



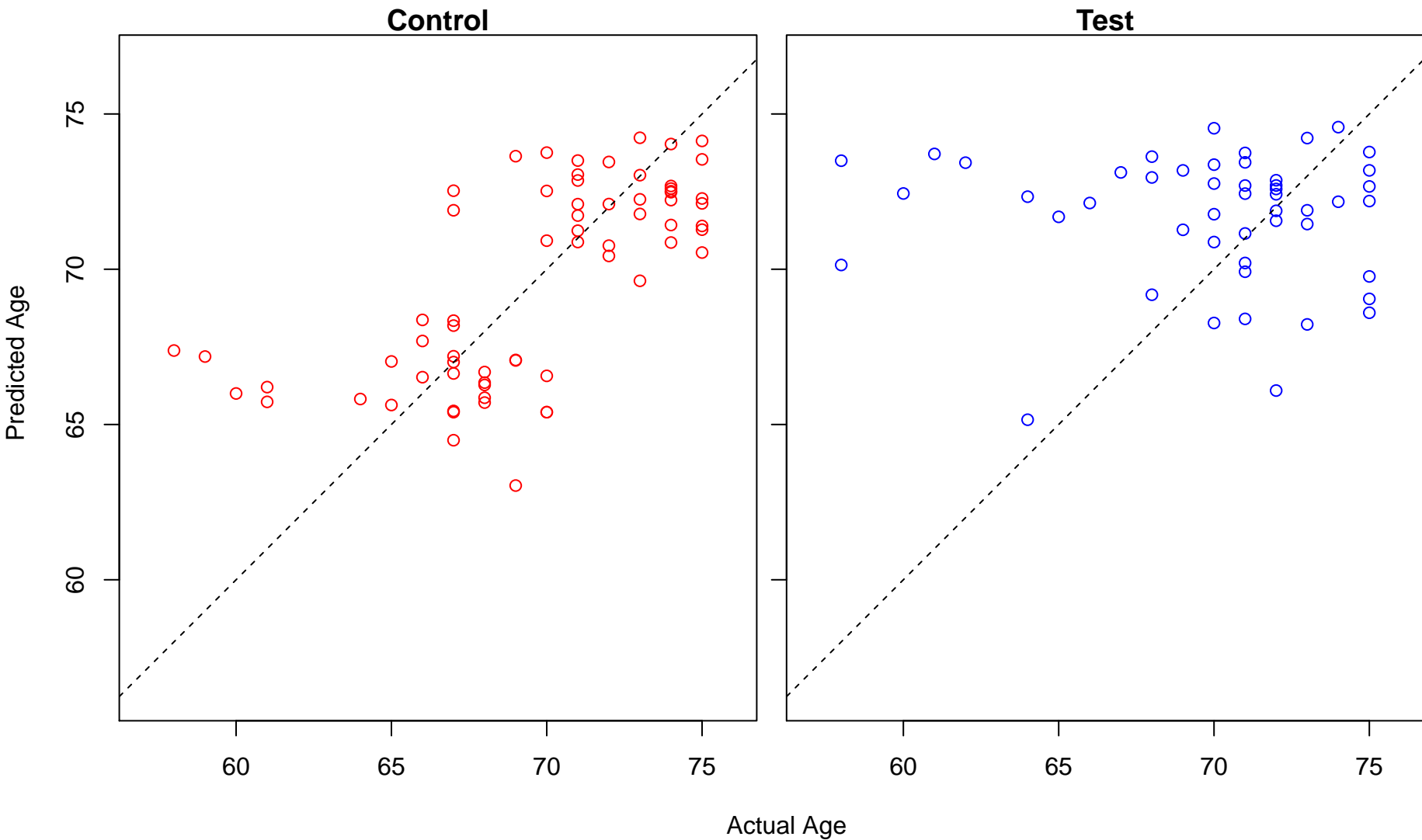
synapse organization (Score: 1.395985)



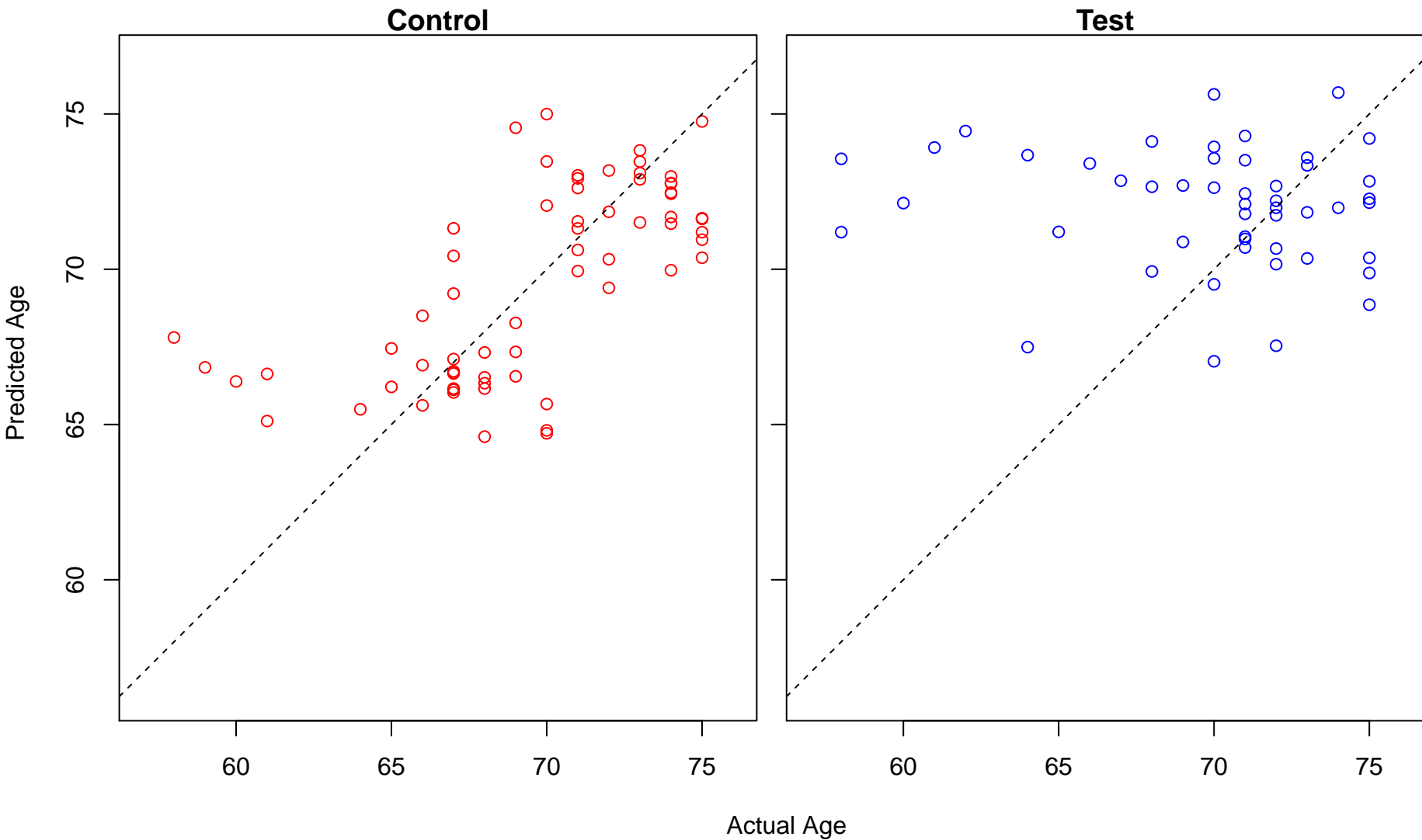
negative regulation of secretion by cell (Score: 1.394991)



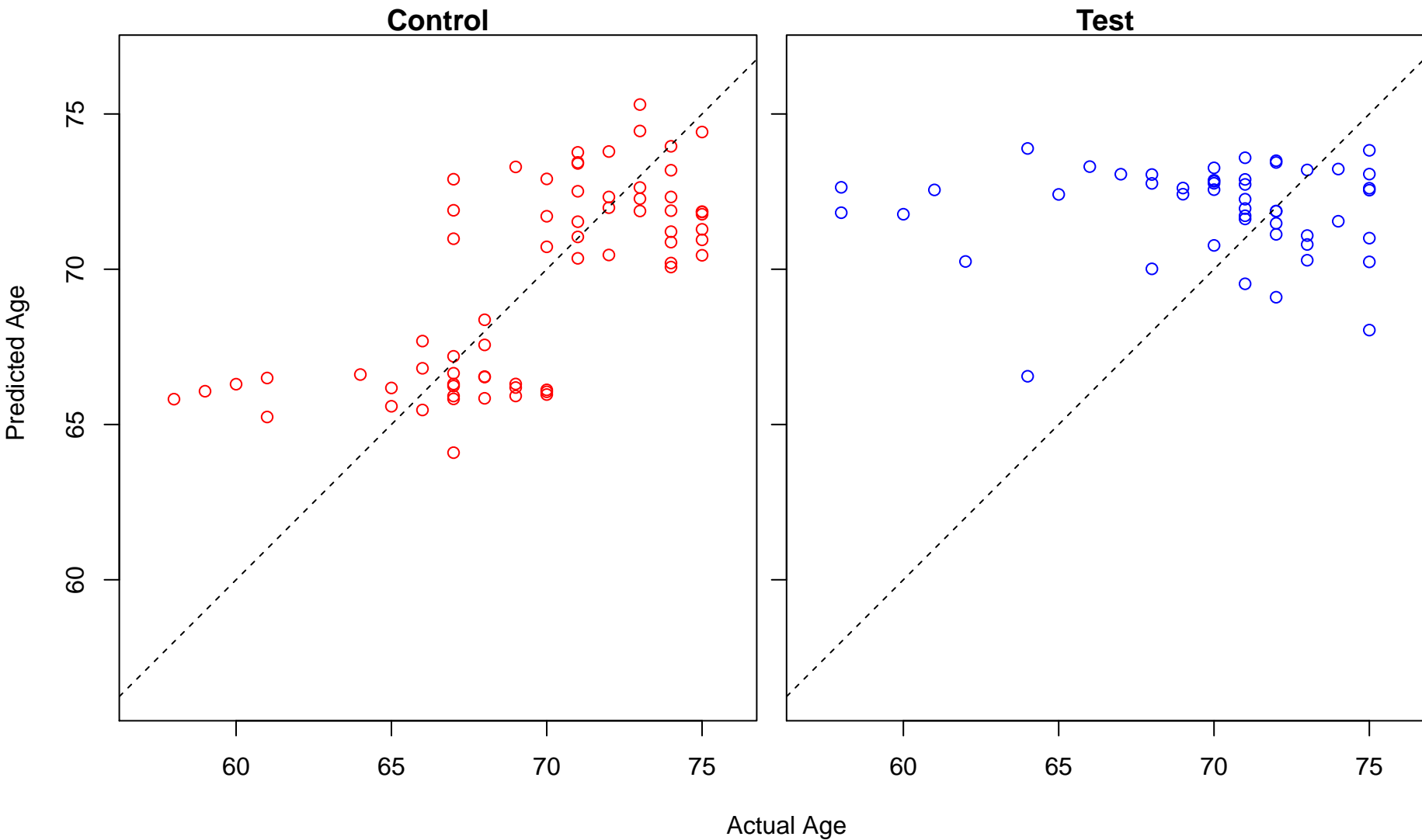
mRNA splice site selection (Score: 1.394811)



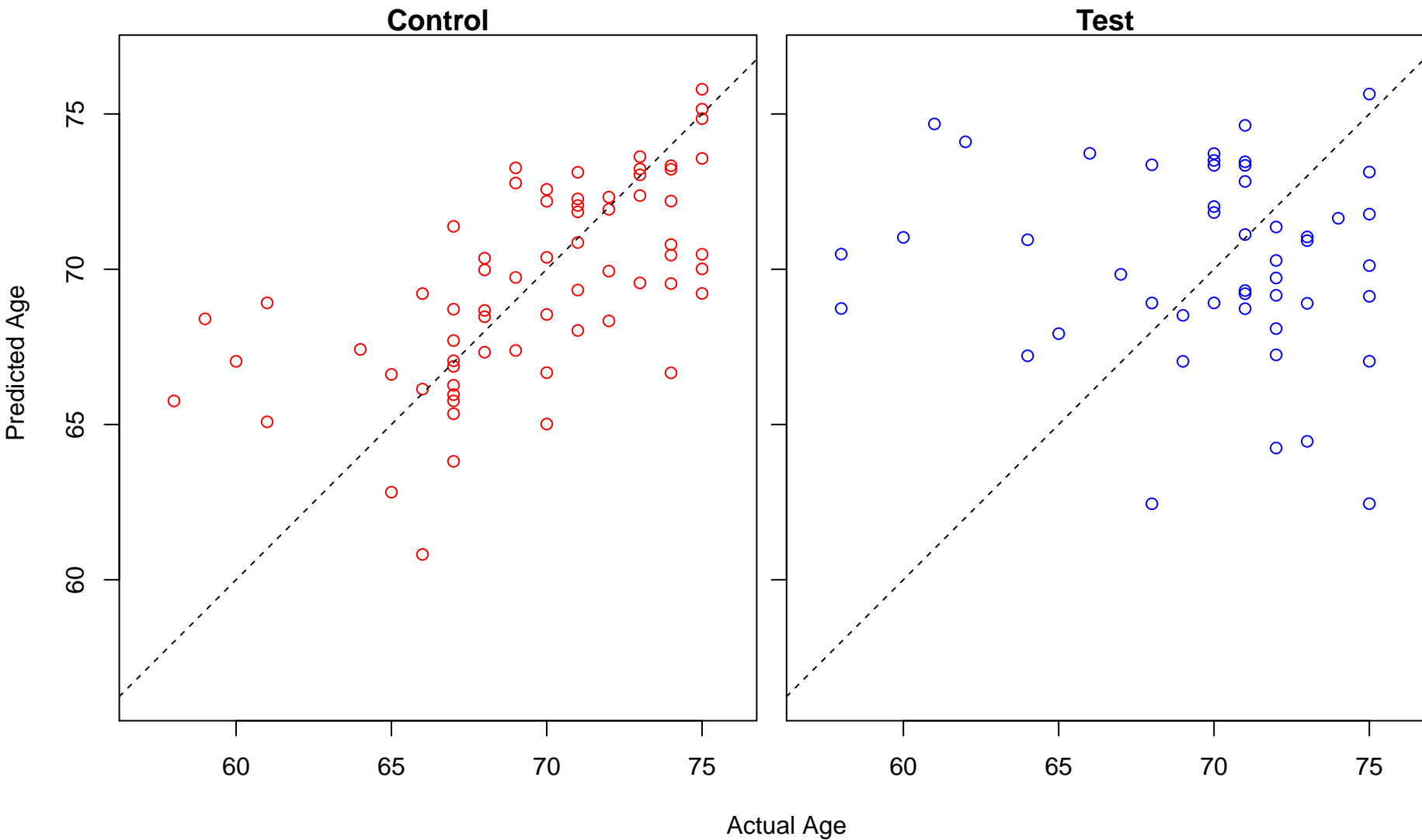
DNA recombination (Score: 1.394525)



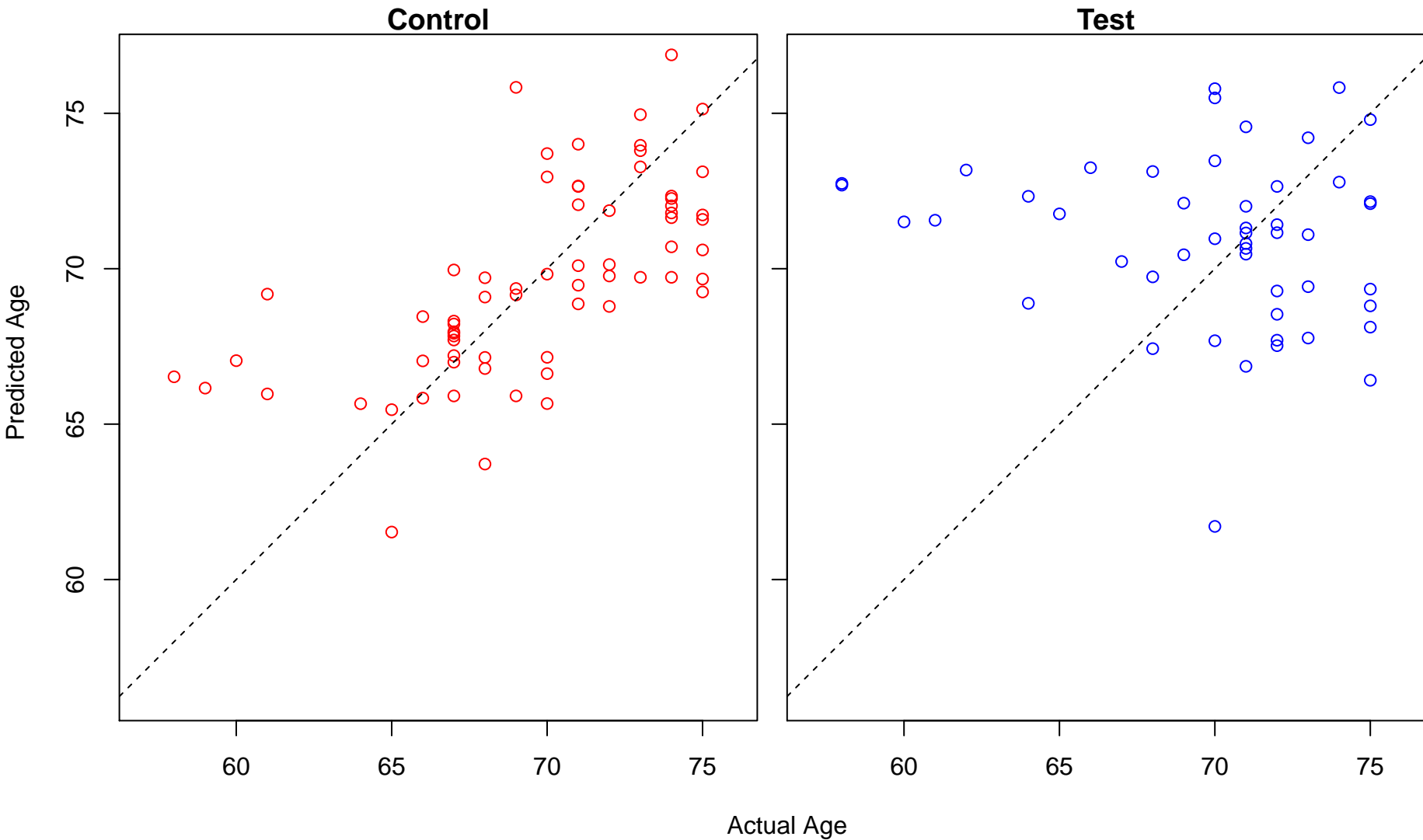
ribosomal small subunit biogenesis (Score: 1.394370)



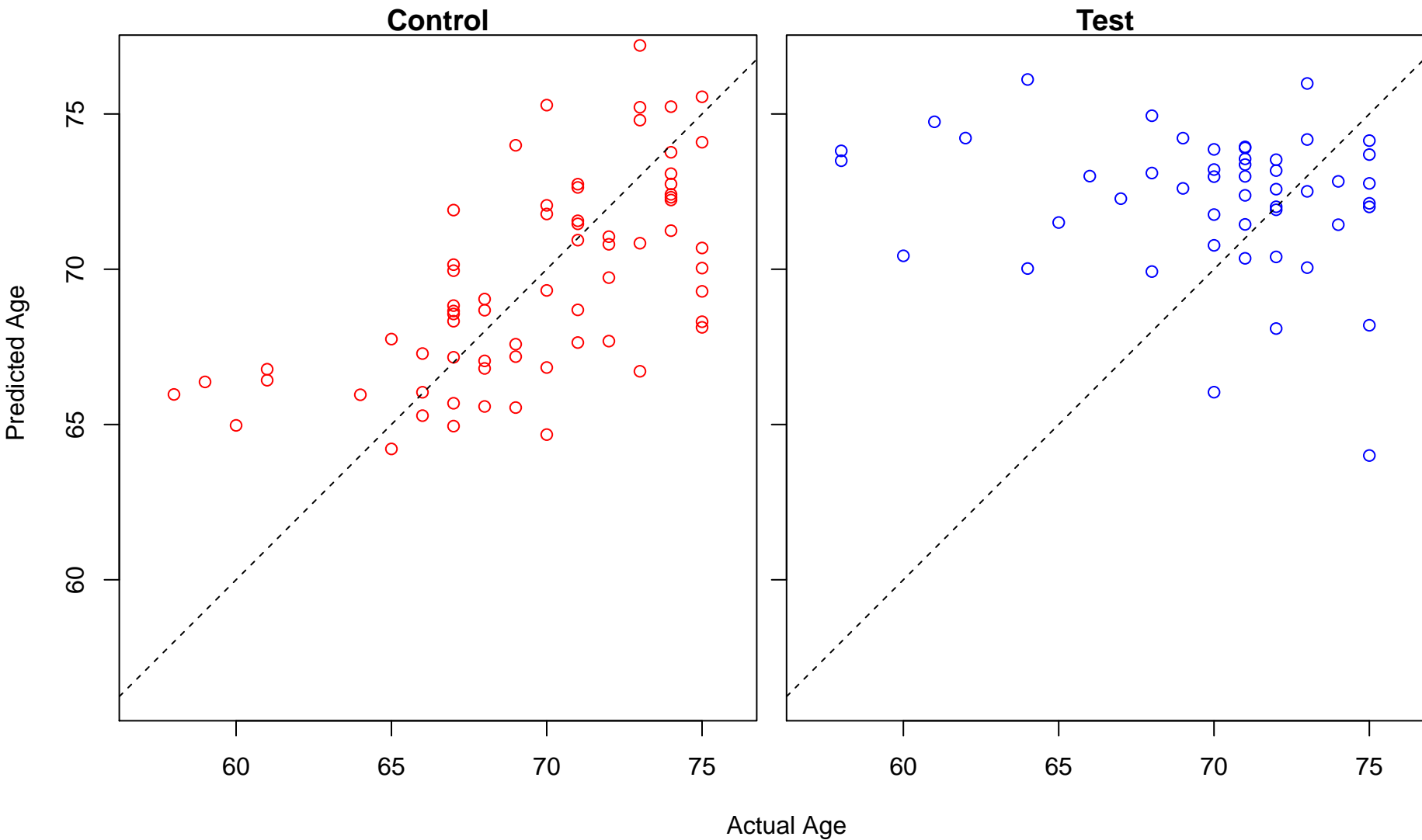
positive regulation of excitatory postsynaptic potential (Score: 1.394075)



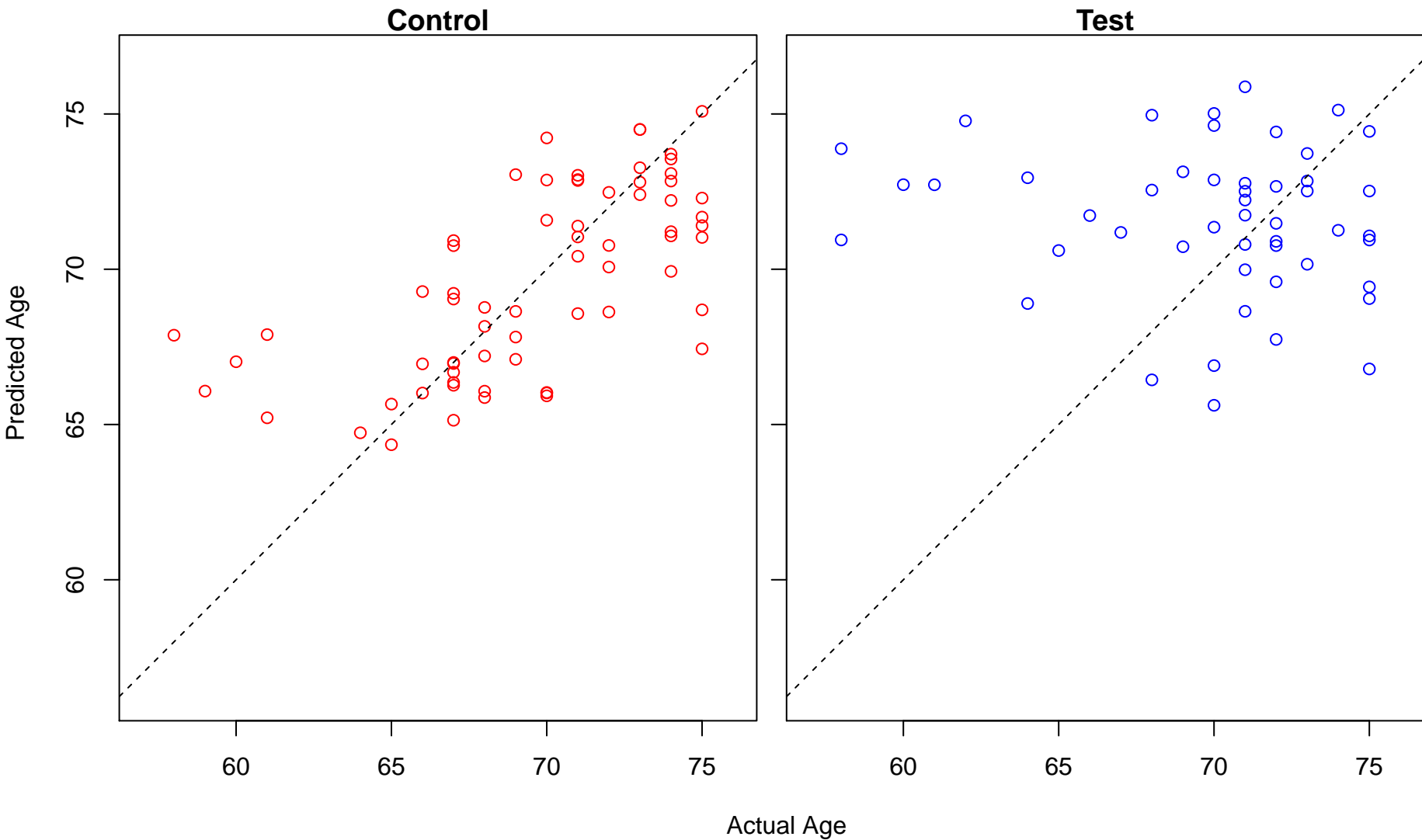
positive regulation of calcium ion transport (Score: 1.394003)



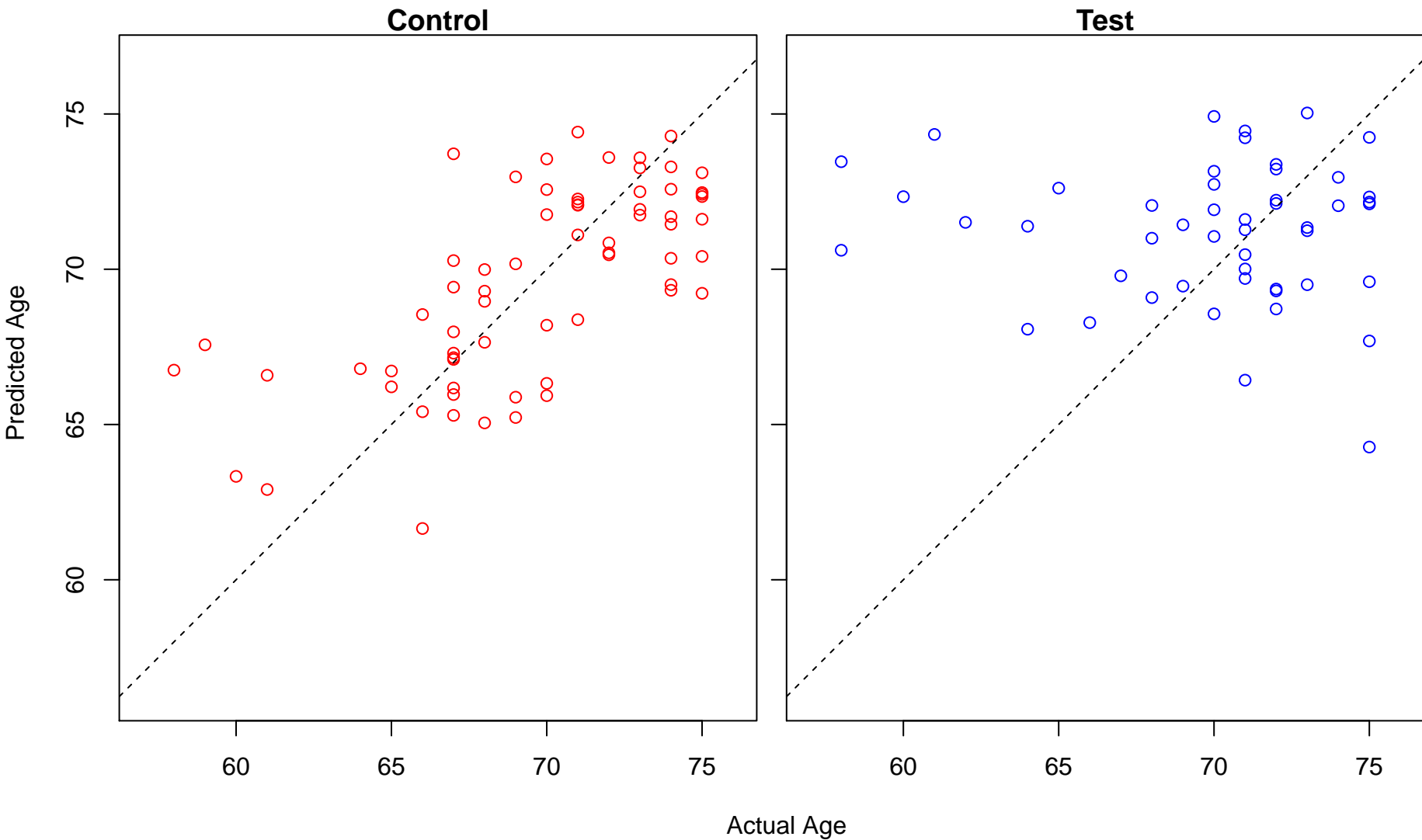
regulation of sodium ion transmembrane transport (Score: 1.393461)



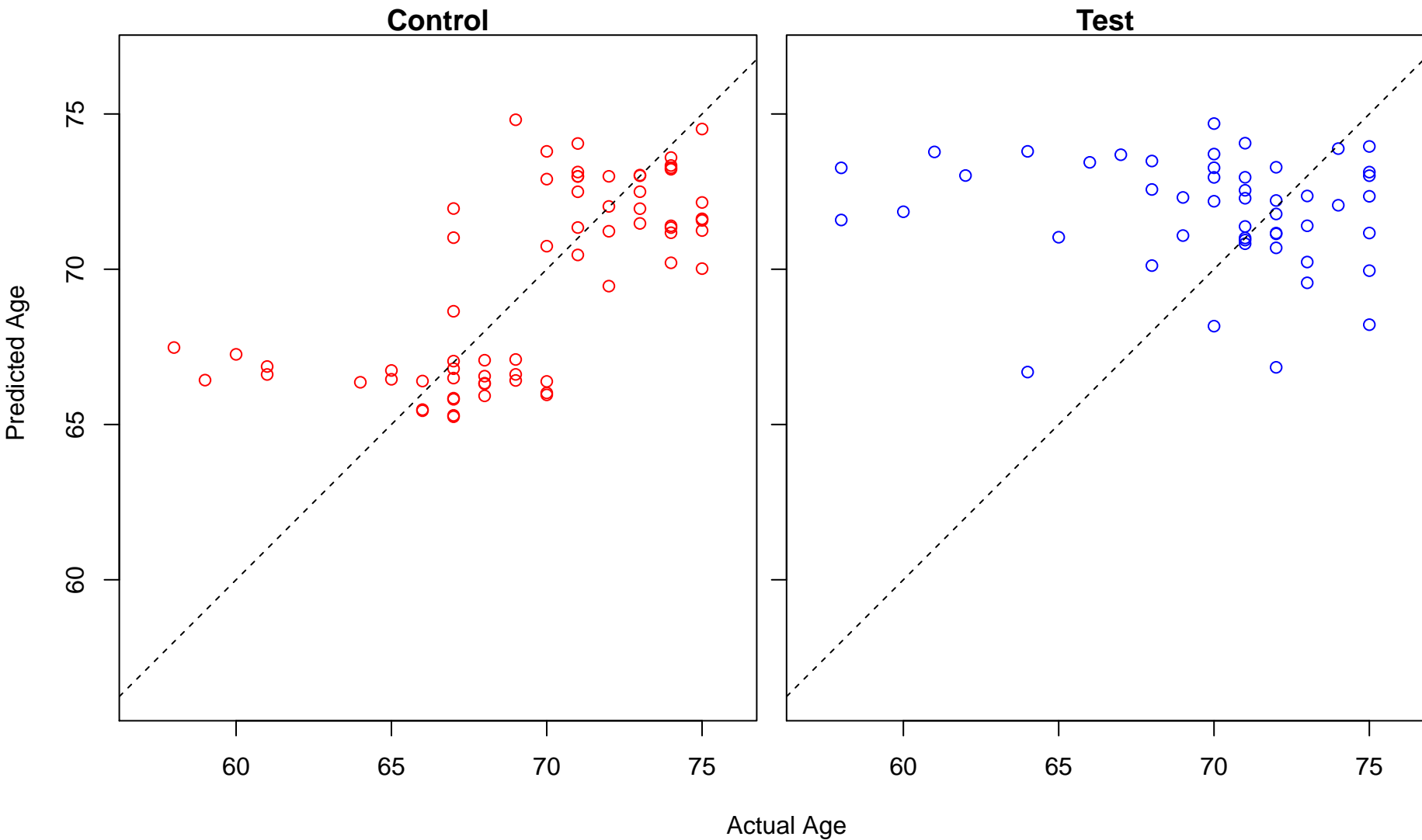
regulation of phospholipase C activity (Score: 1.393395)



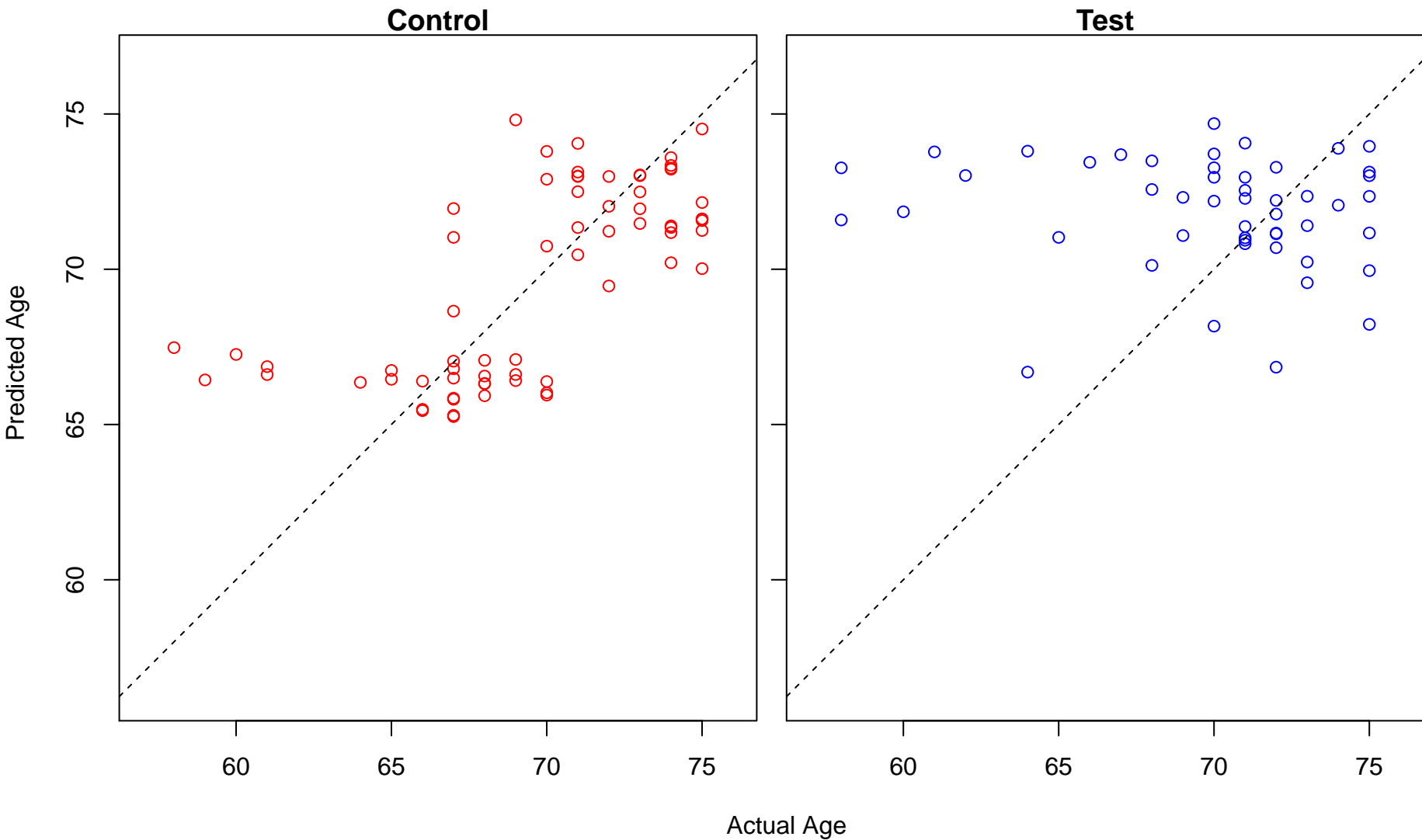
regulation of potassium ion transport (Score: 1.391428)



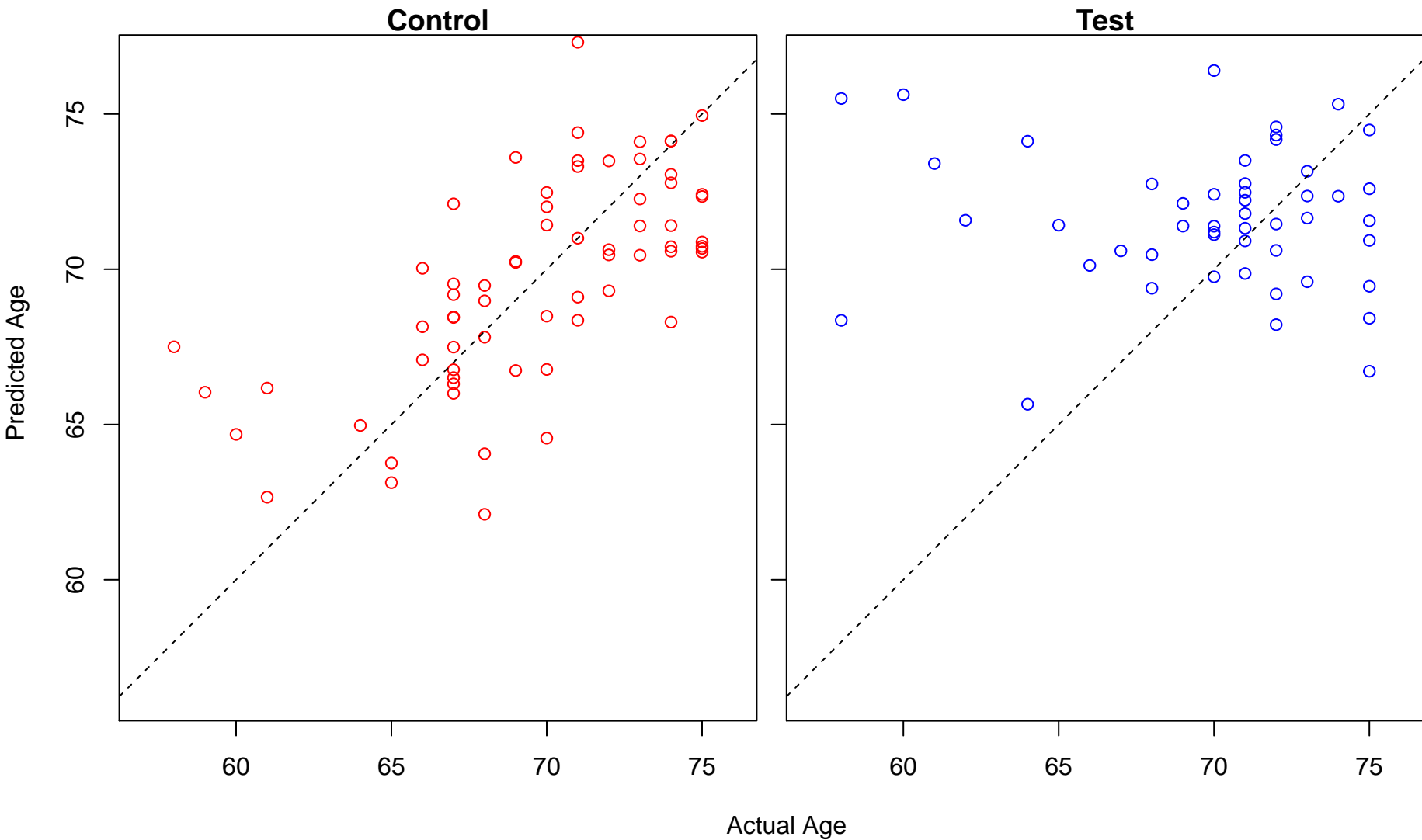
SRP-dependent cotranslational protein targeting to membrane (Score: 1.391360)



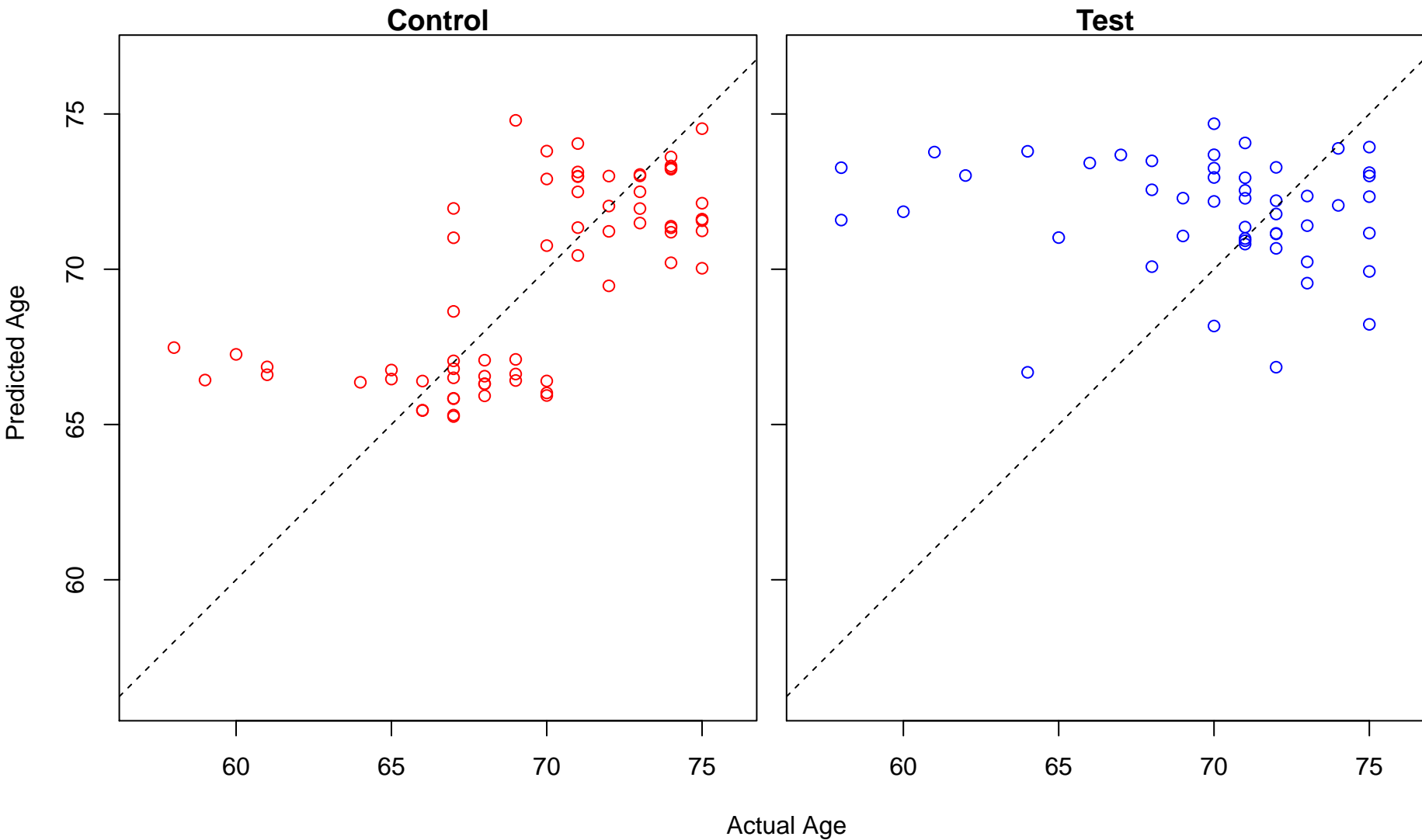
cotranslational protein targeting to membrane (Score: 1.391276)



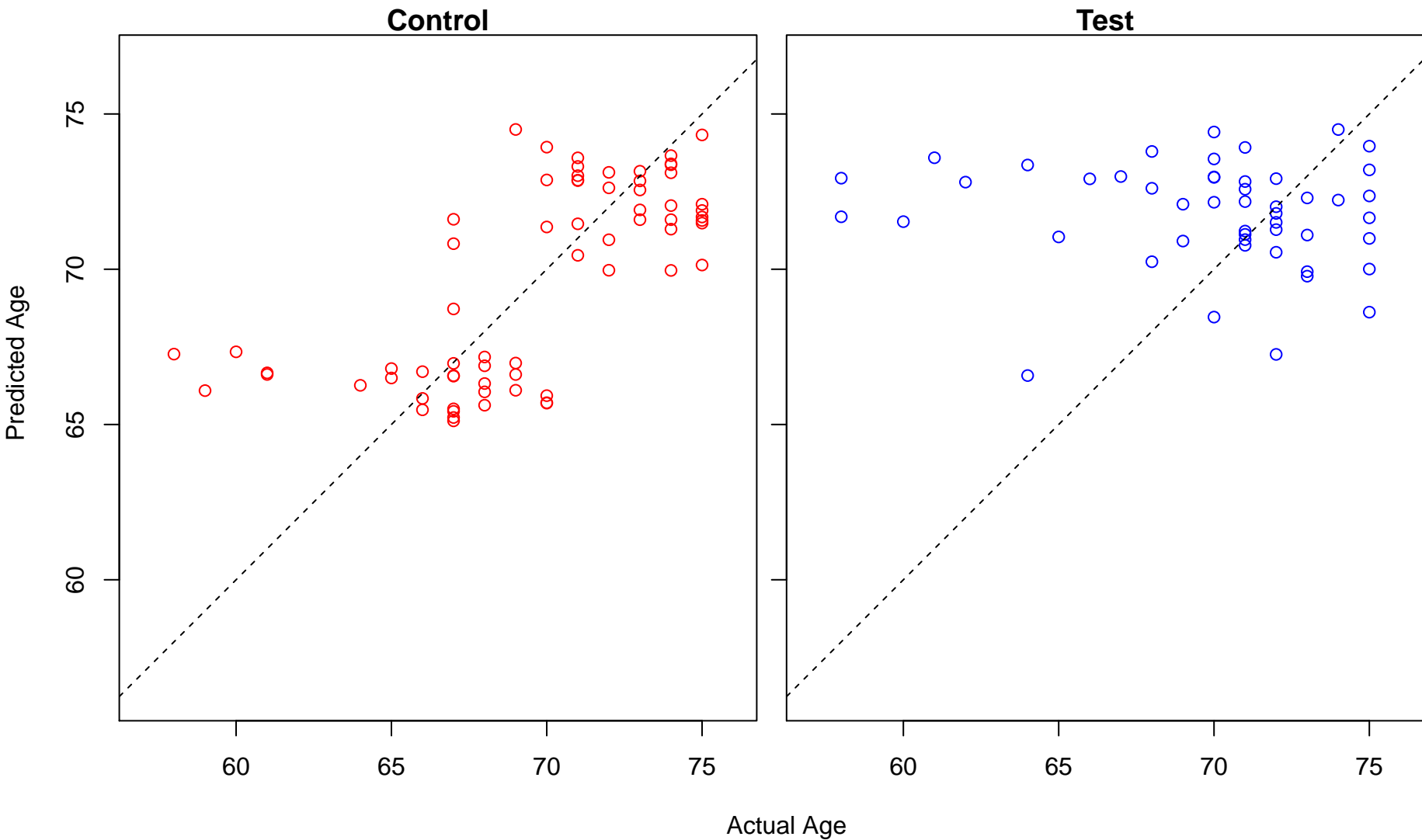
developmental process involved in reproduction (Score: 1.390960)



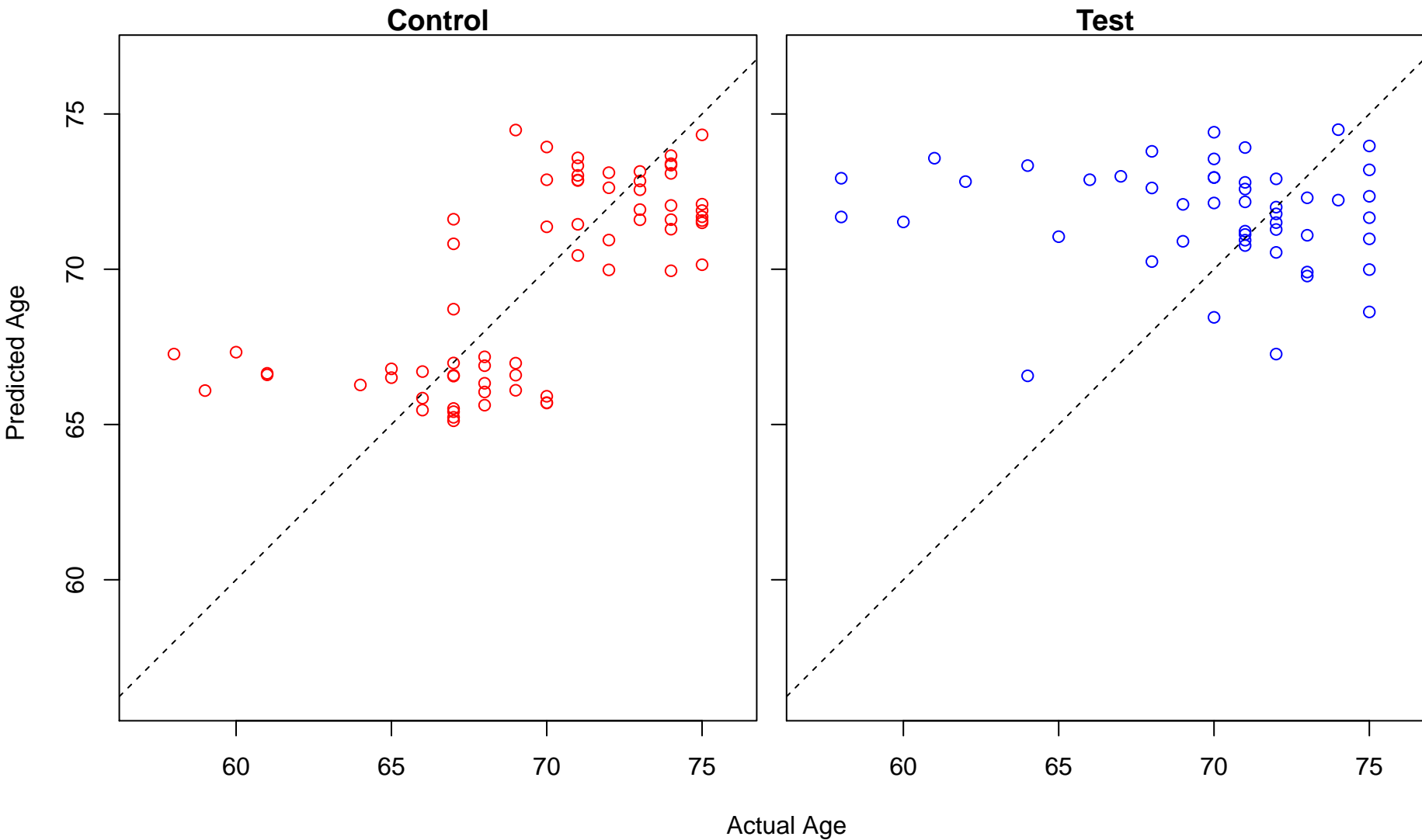
protein targeting to ER (Score: 1.390524)



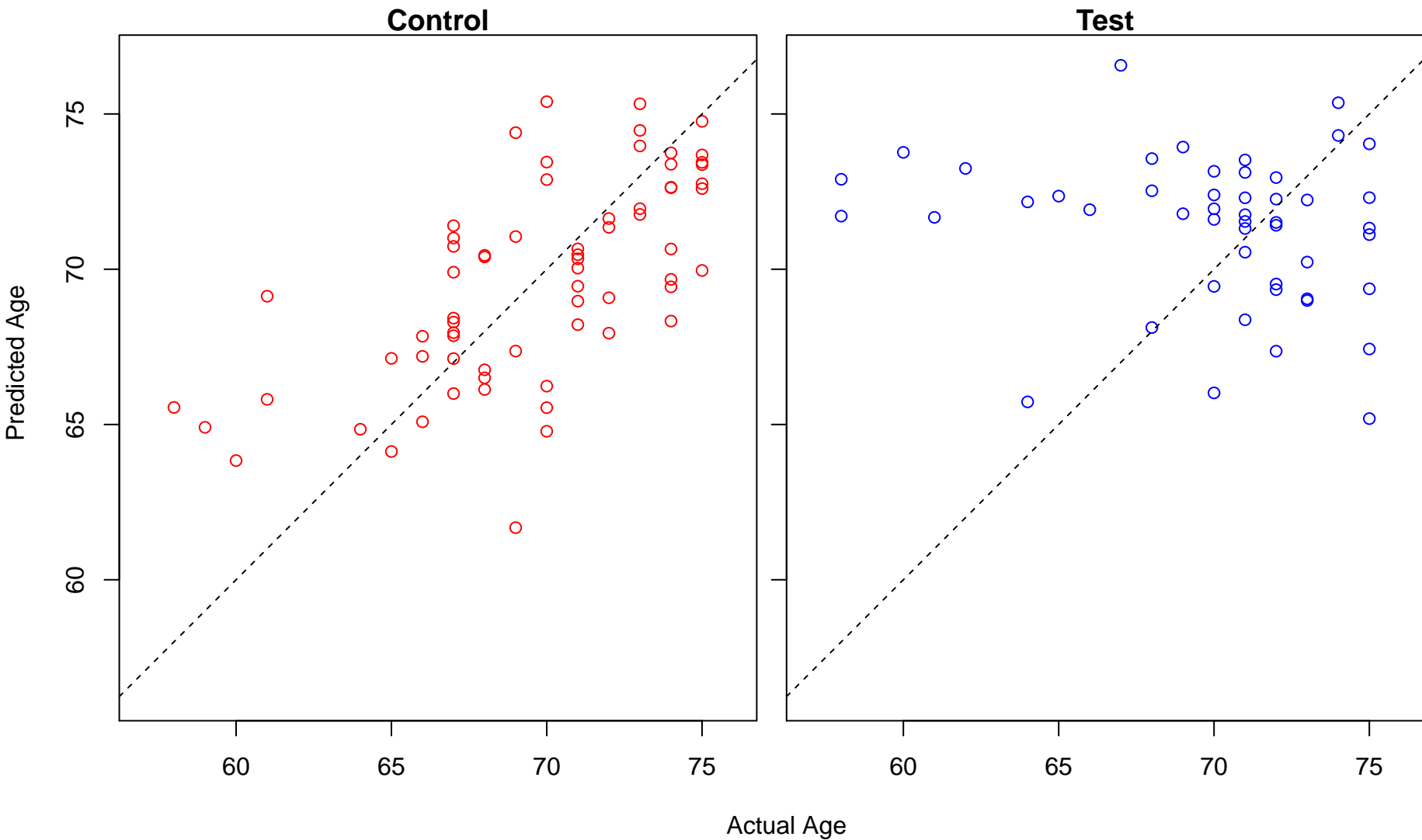
heterocycle catabolic process (Score: 1.390370)



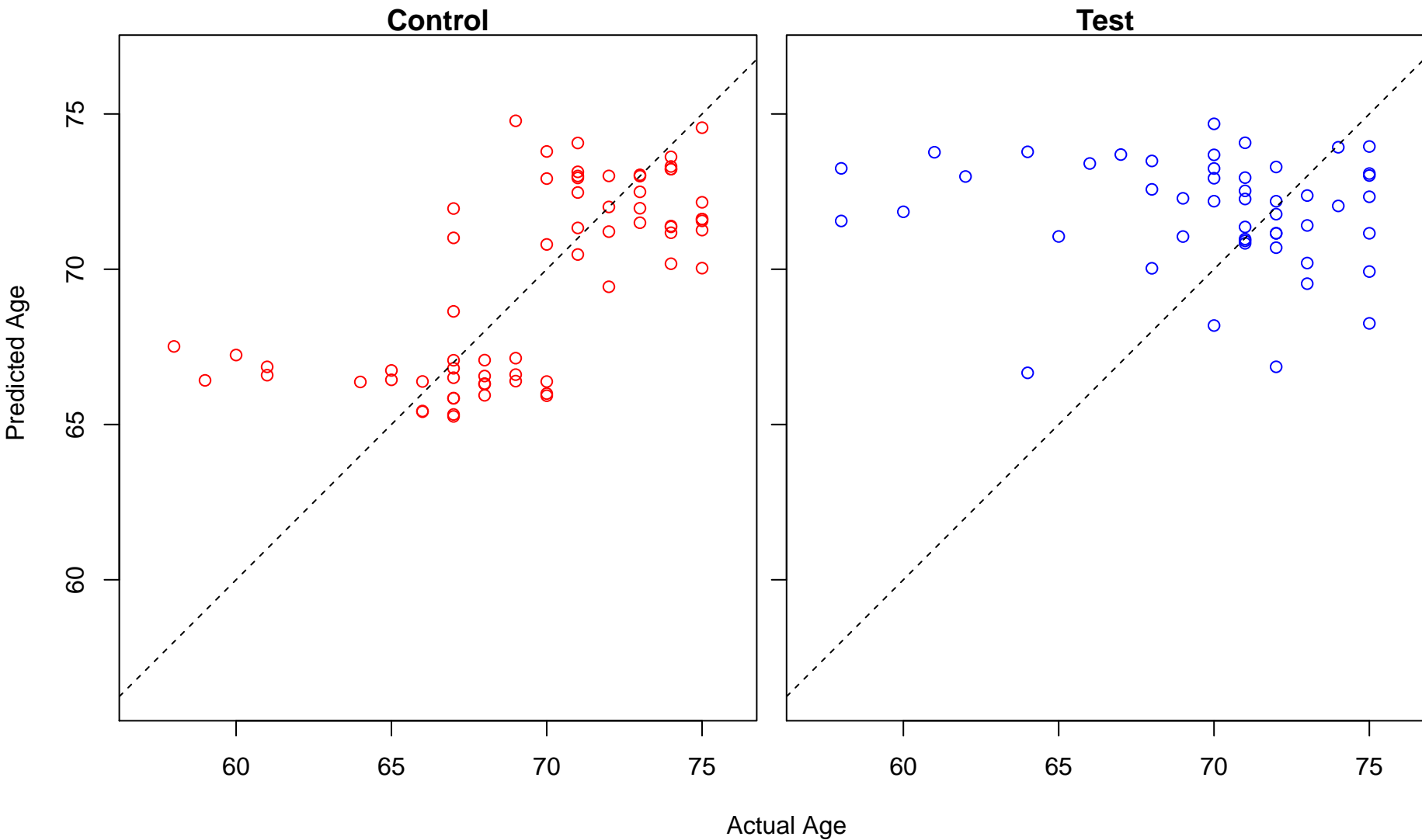
cellular nitrogen compound catabolic process (Score: 1.390364)



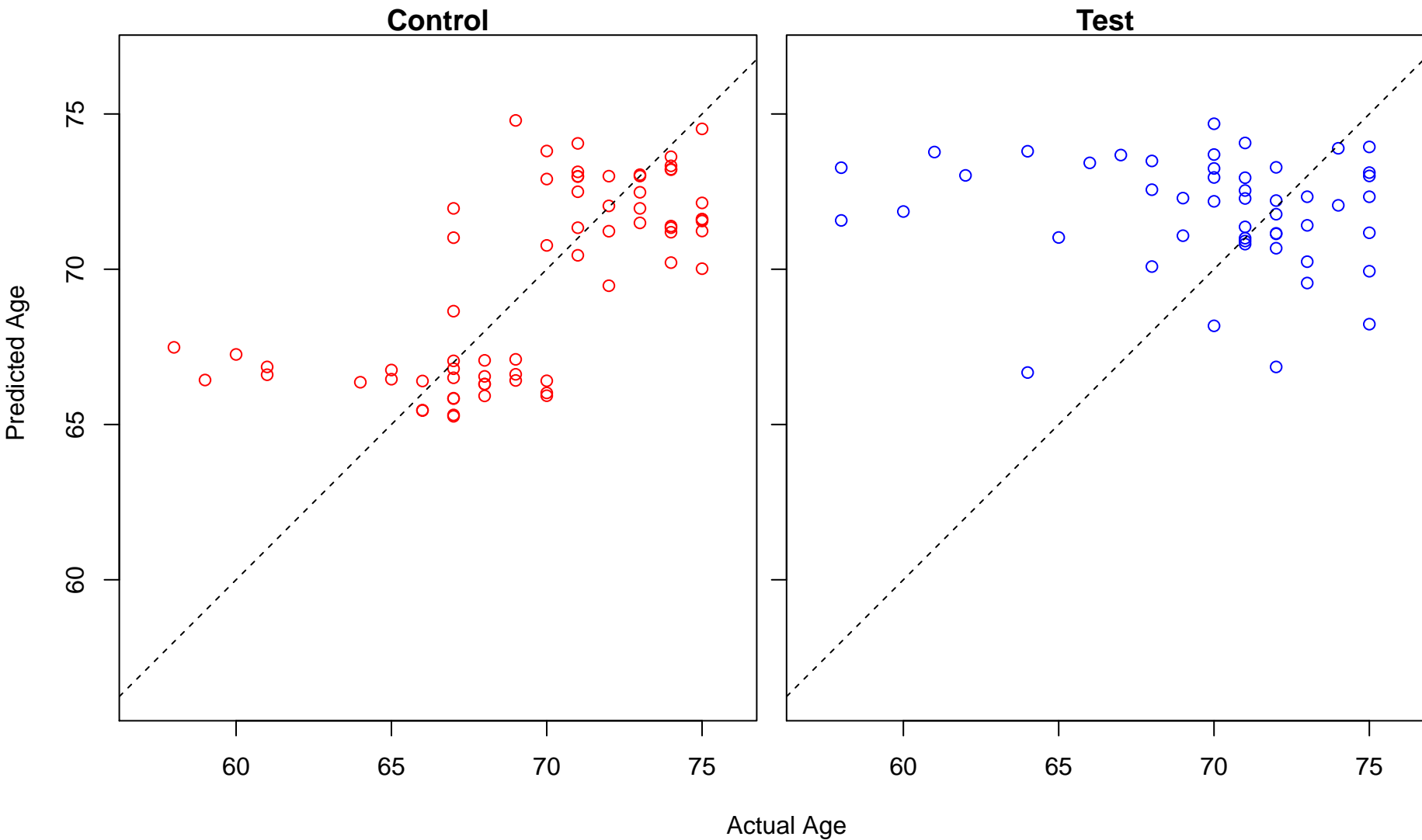
positive regulation of lipid metabolic process (Score: 1.389986)



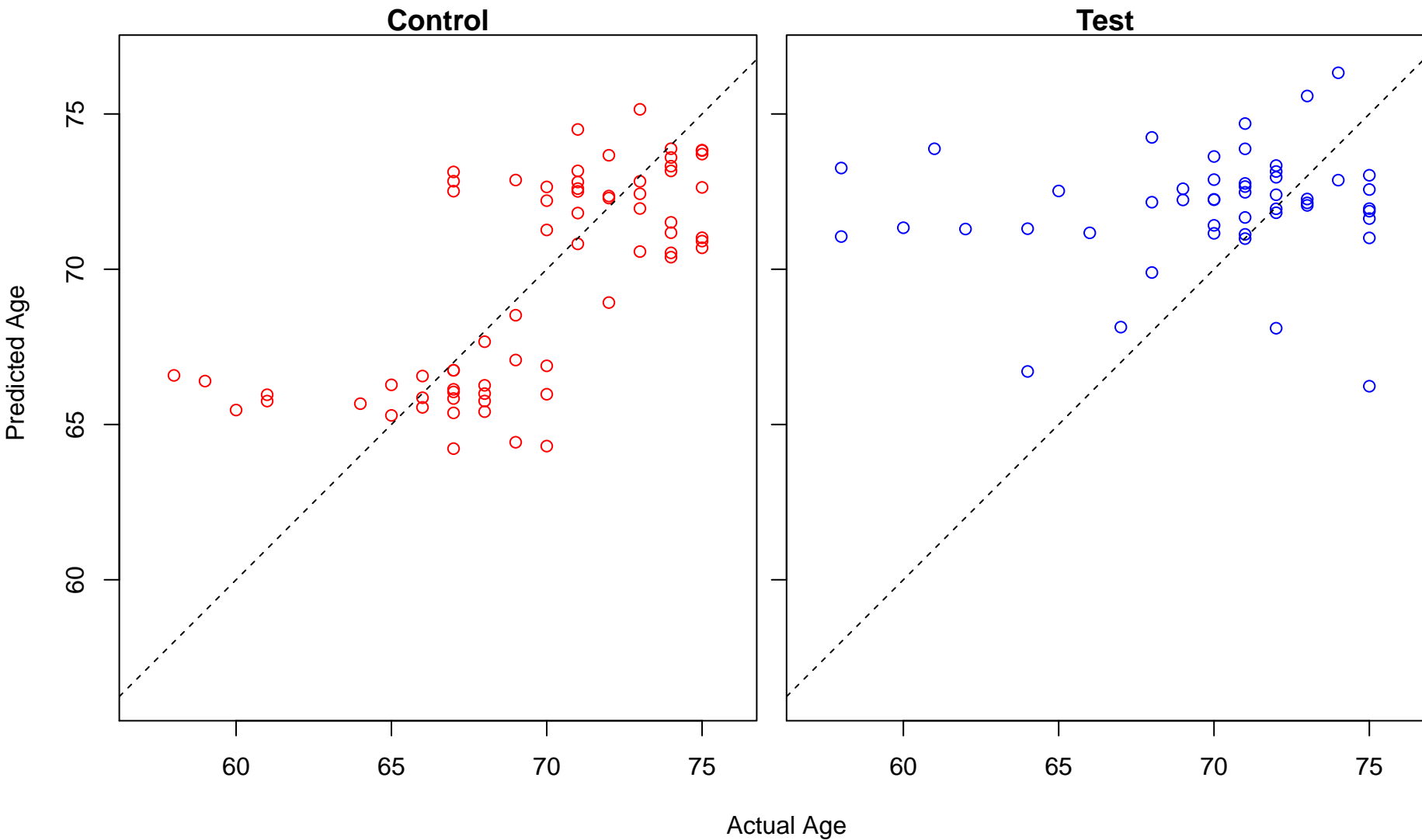
protein localization to endoplasmic reticulum (Score: 1.389371)



establishment of protein localization to endoplasmic reticulum (Score: 1.389097)

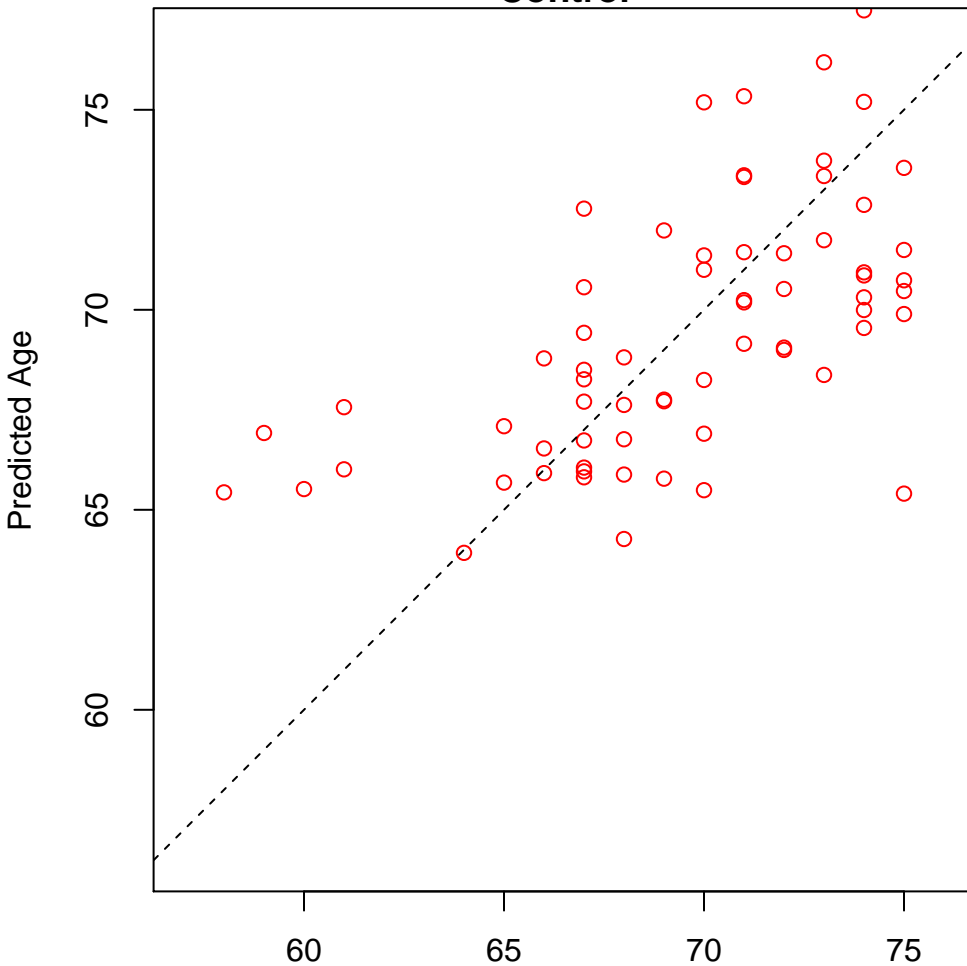


rRNA metabolic process (Score: 1.387813)

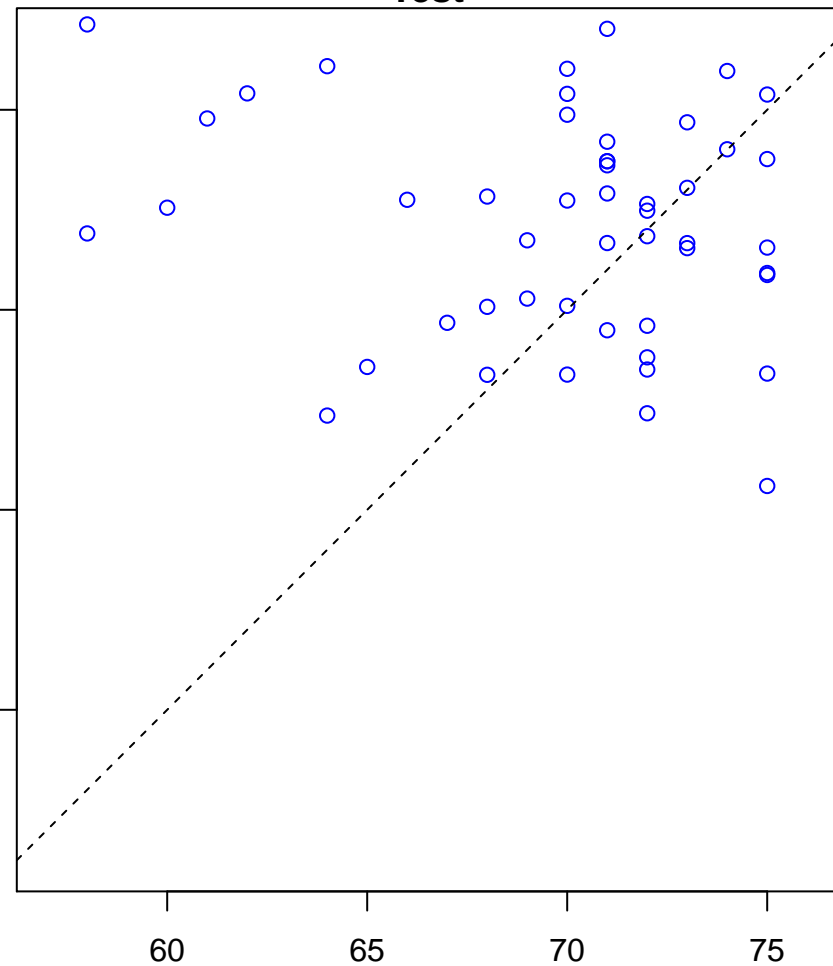


regulation of autophagosome assembly (Score: 1.386911)

Control

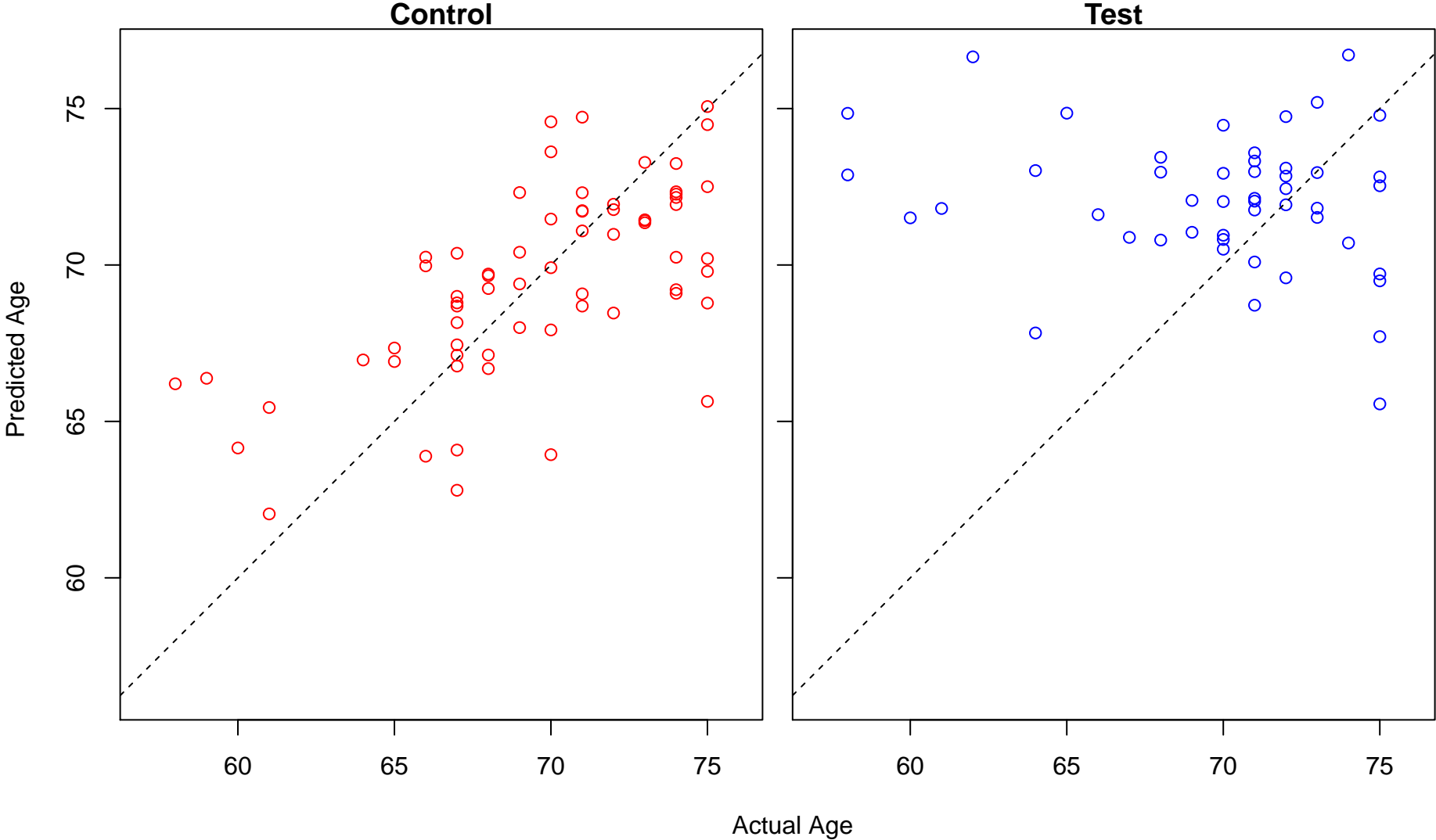


Test

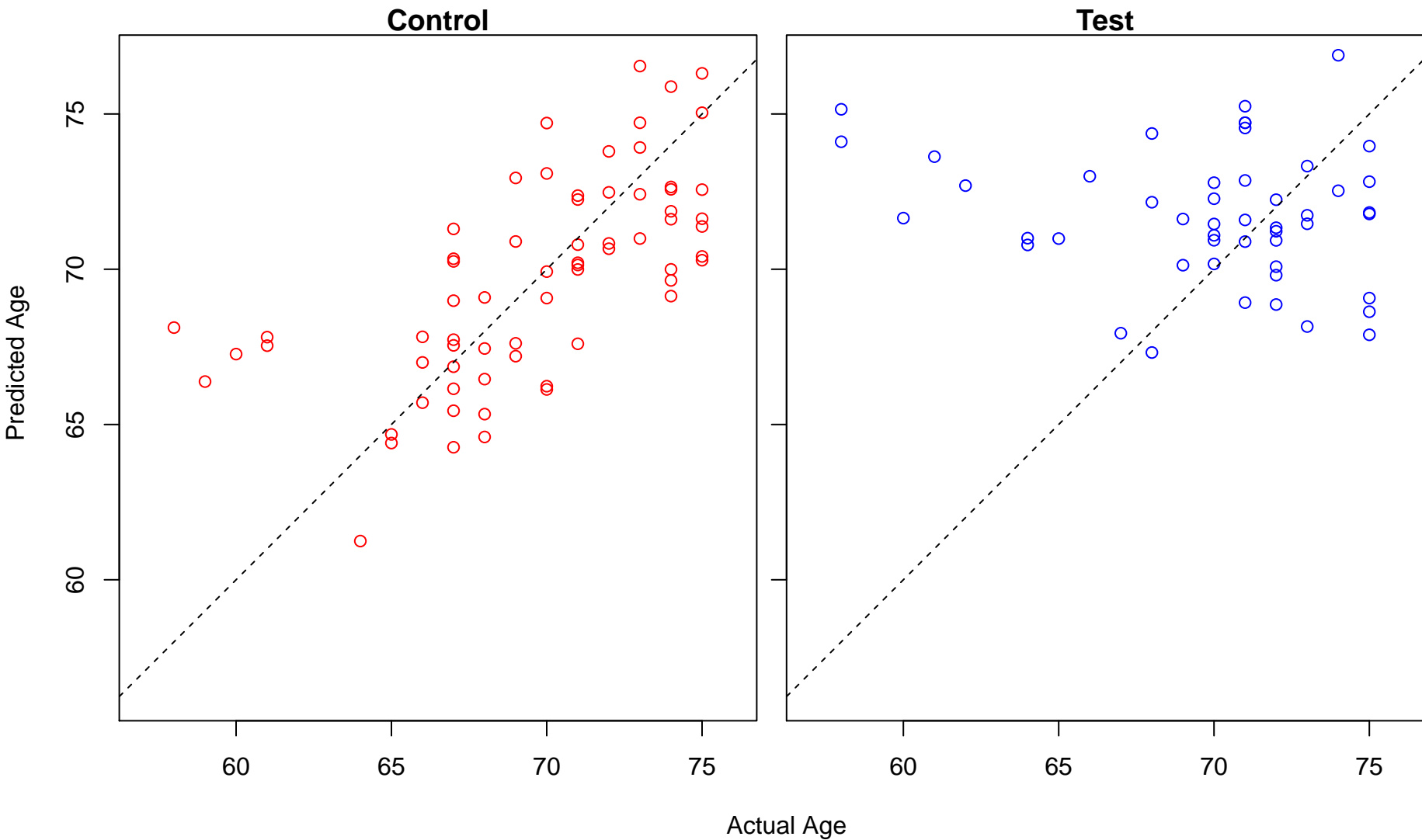


Actual Age

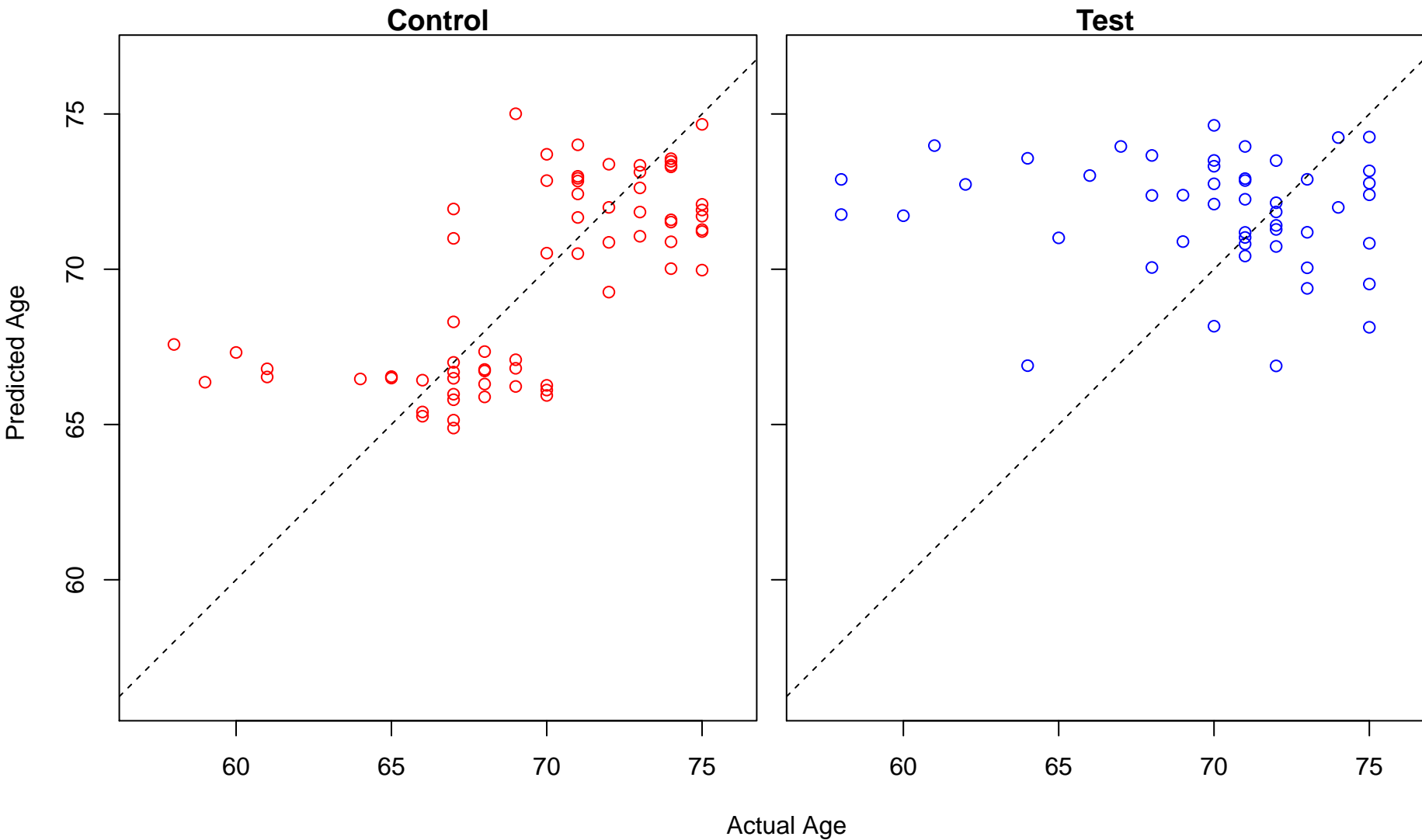
positive regulation of cytokine-mediated signaling pathway (Score: 1.386484)



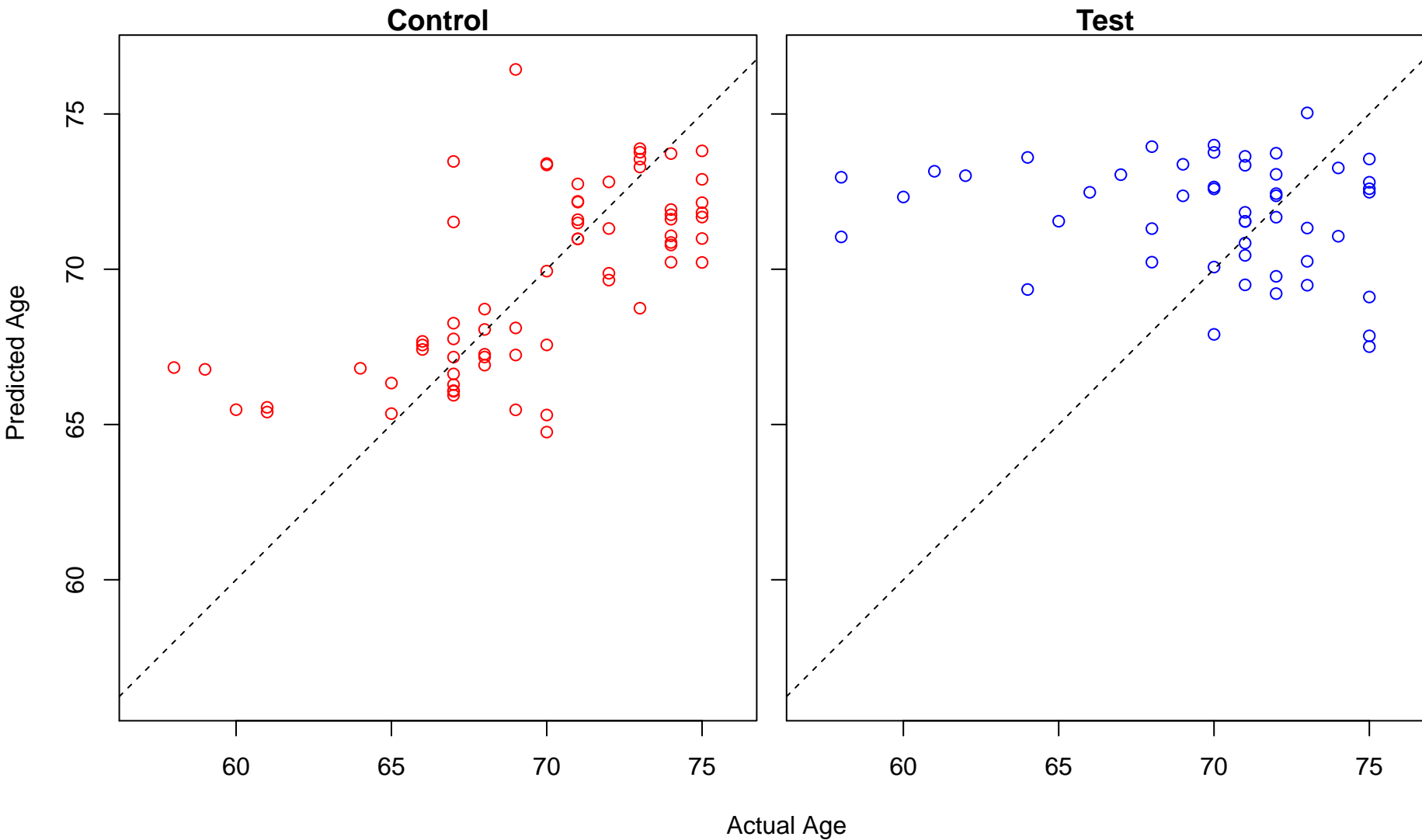
regulation of actin filament bundle assembly (Score: 1.385339)



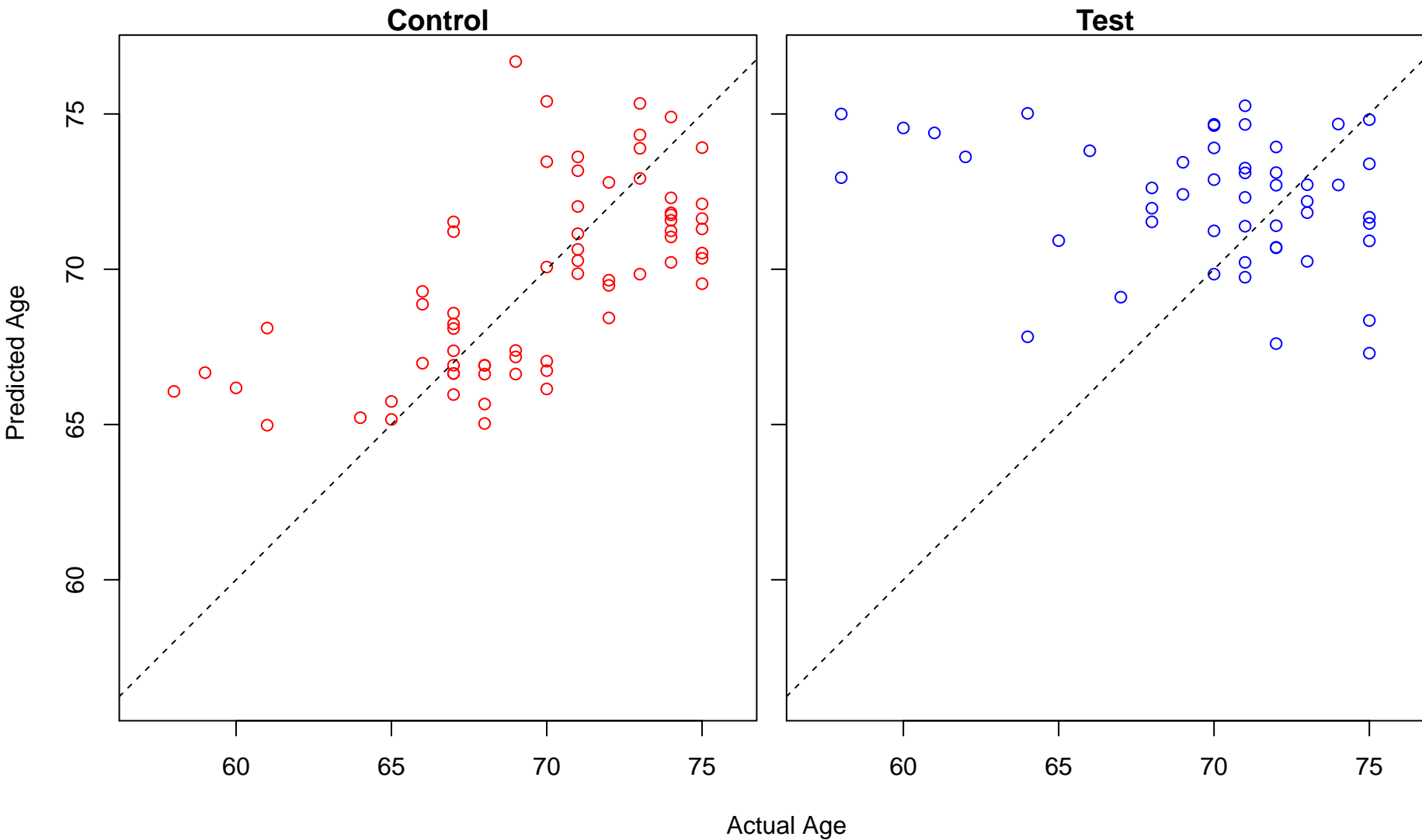
cellular modified amino acid metabolic process (Score: 1.385128)



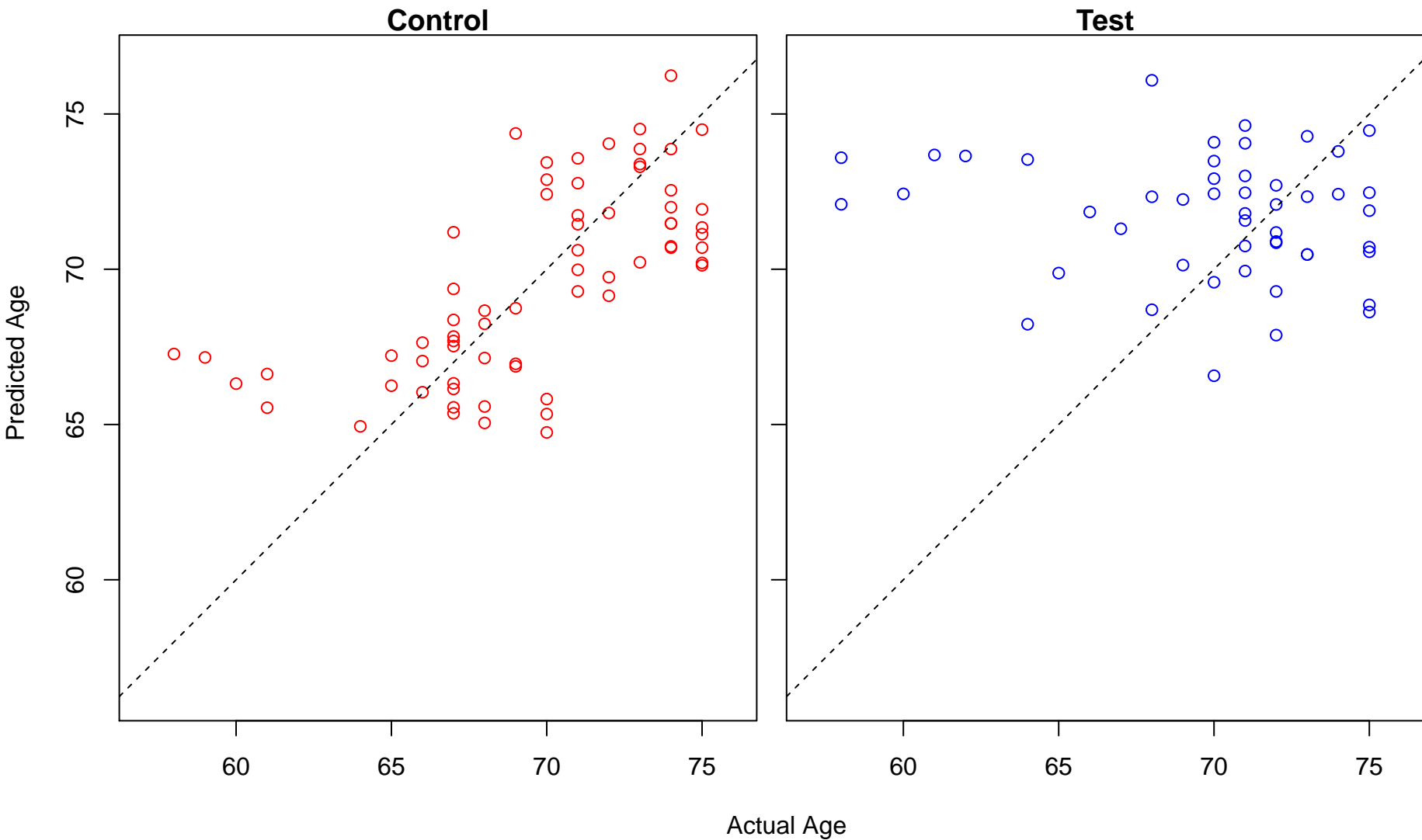
isoprenoid metabolic process (Score: 1.383825)



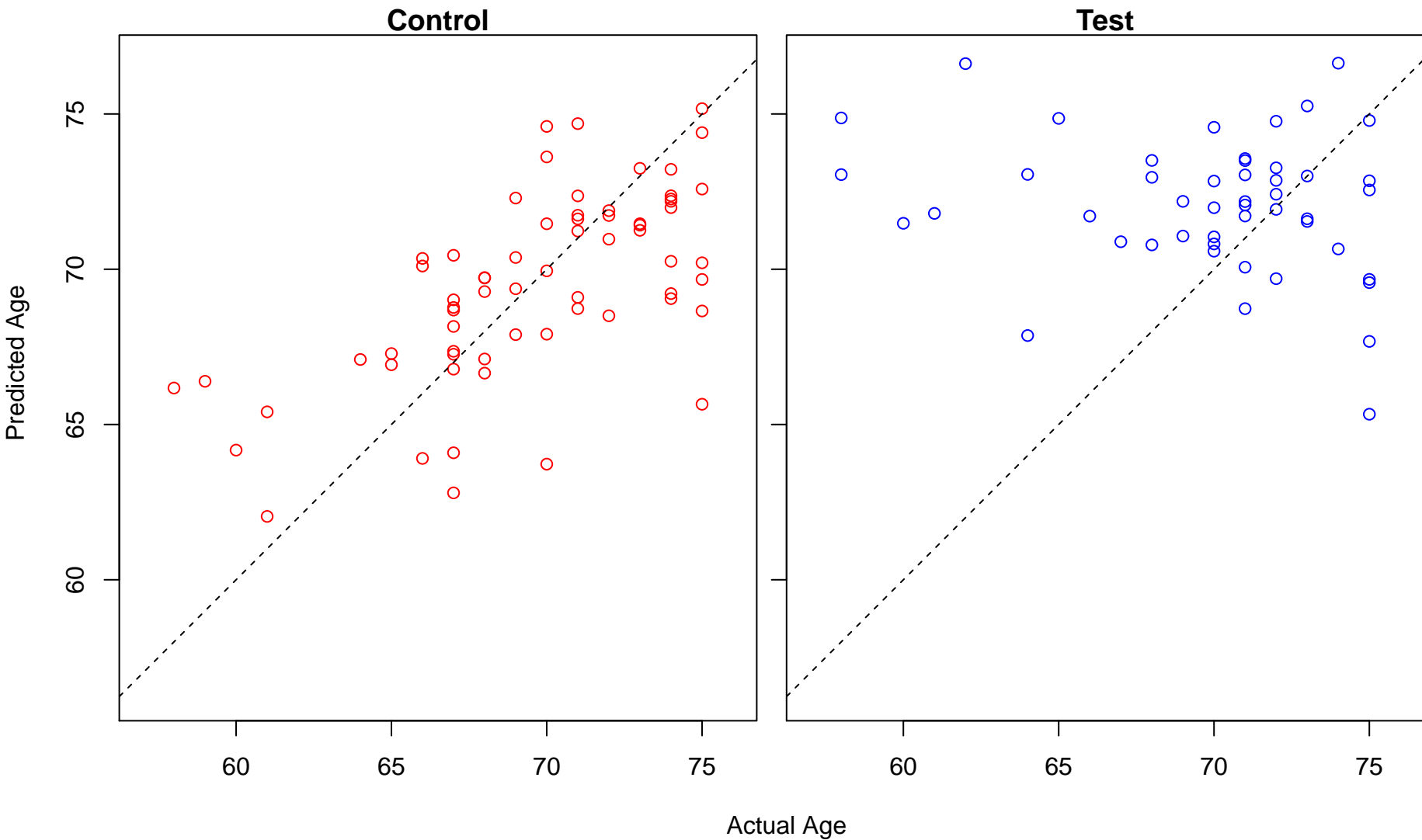
gamete generation (Score: 1.383461)



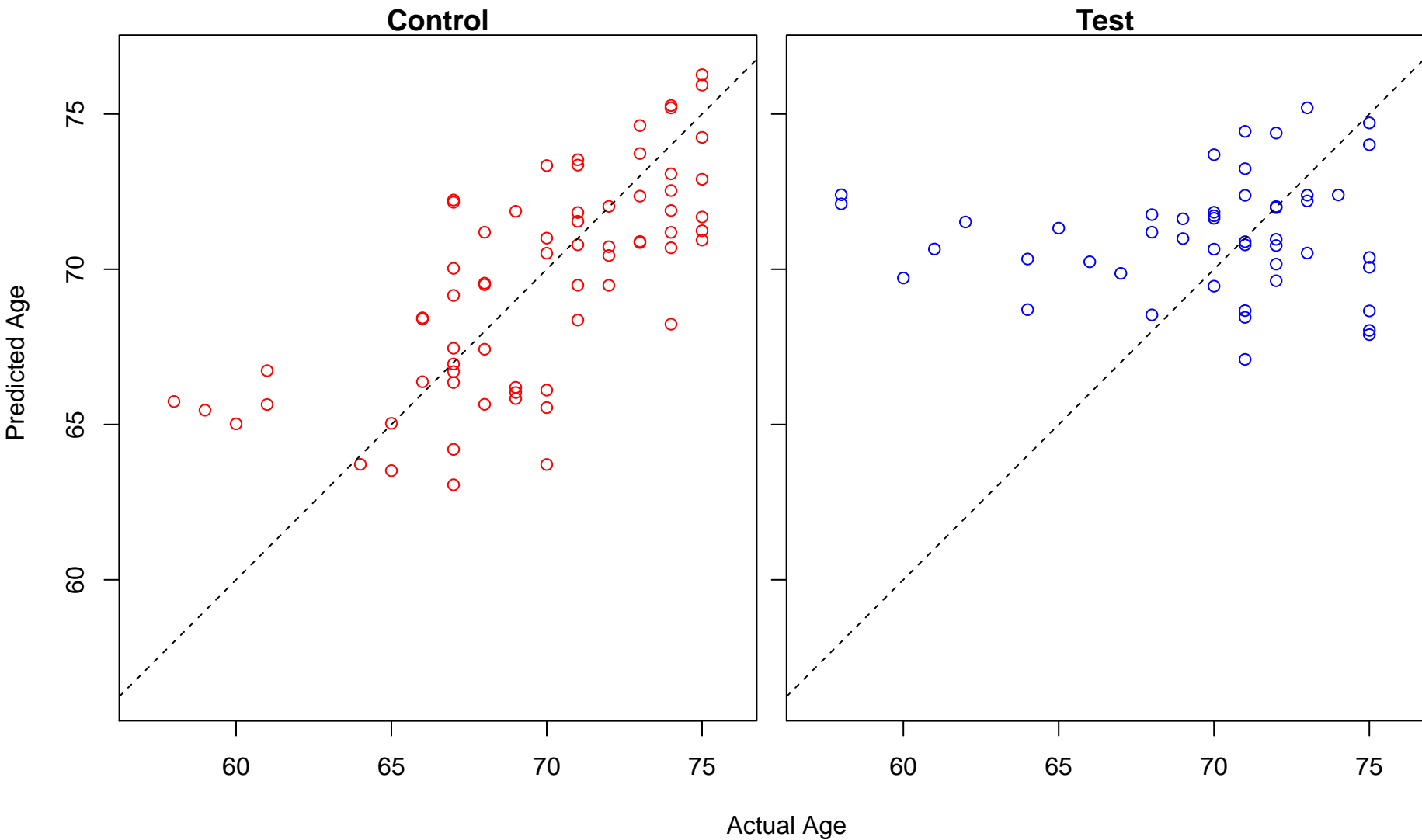
negative regulation of cellular protein catabolic process (Score: 1.383439)



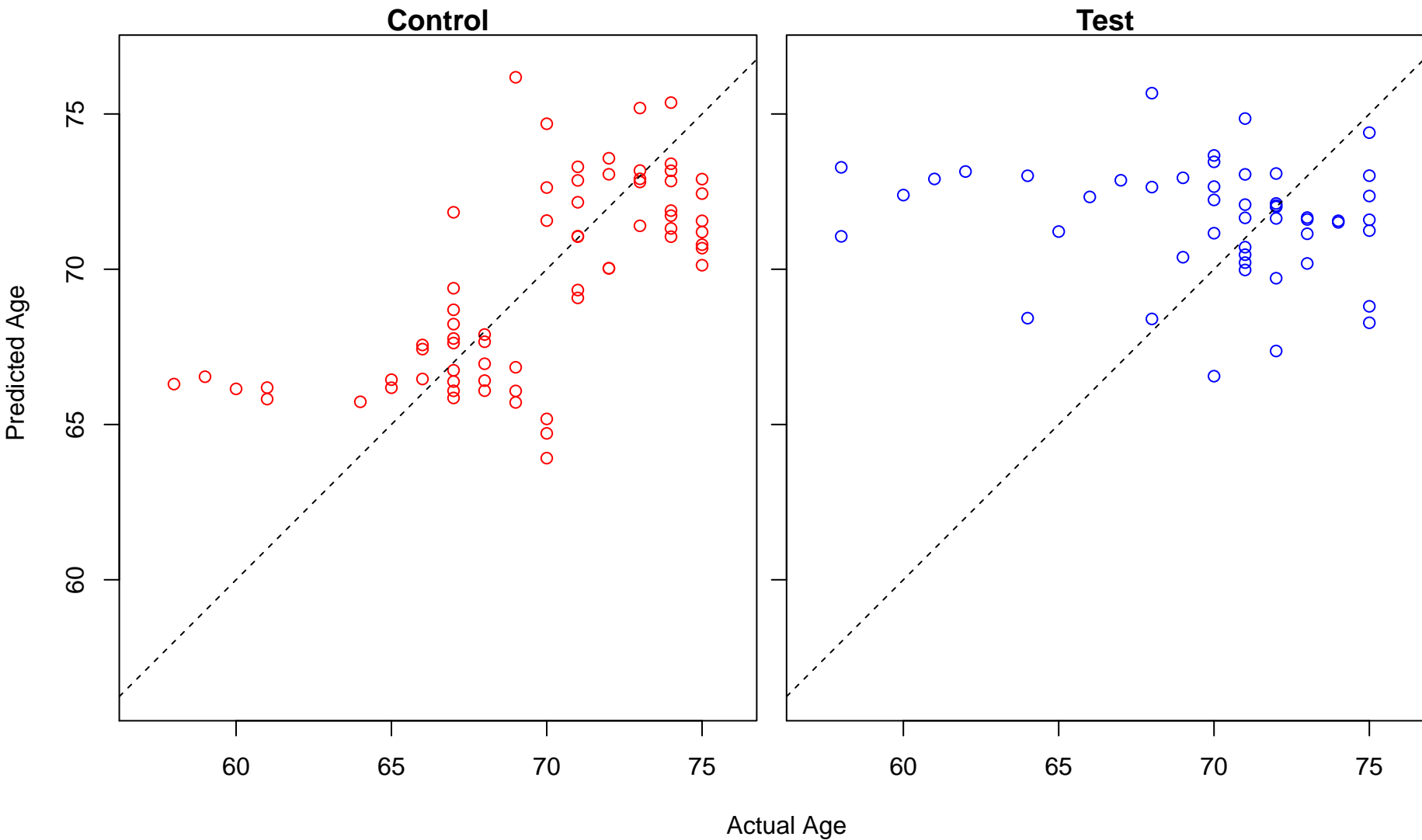
positive regulation of response to cytokine stimulus (Score: 1.382823)



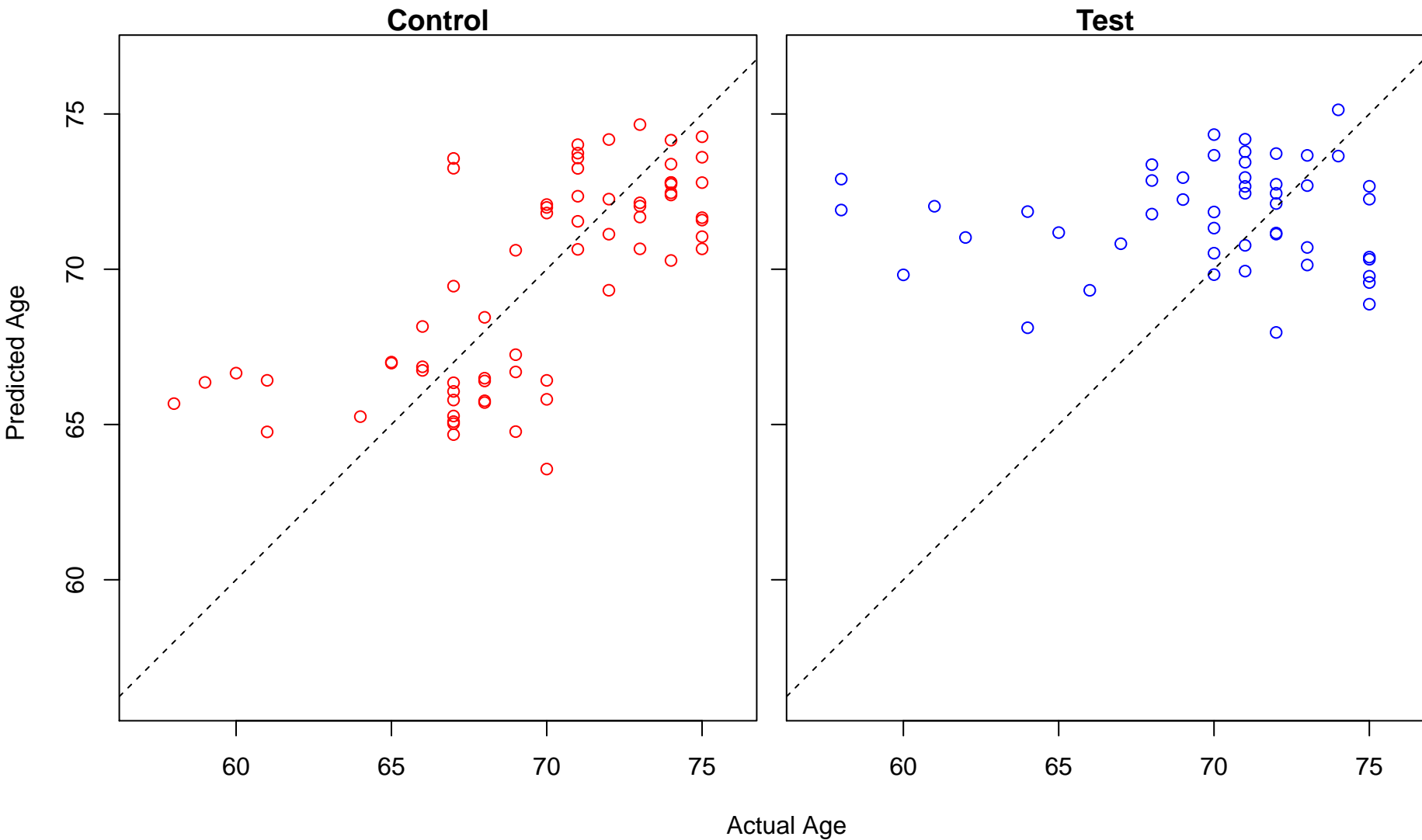
positive regulation of proteasomal protein catabolic process (Score: 1.382091)



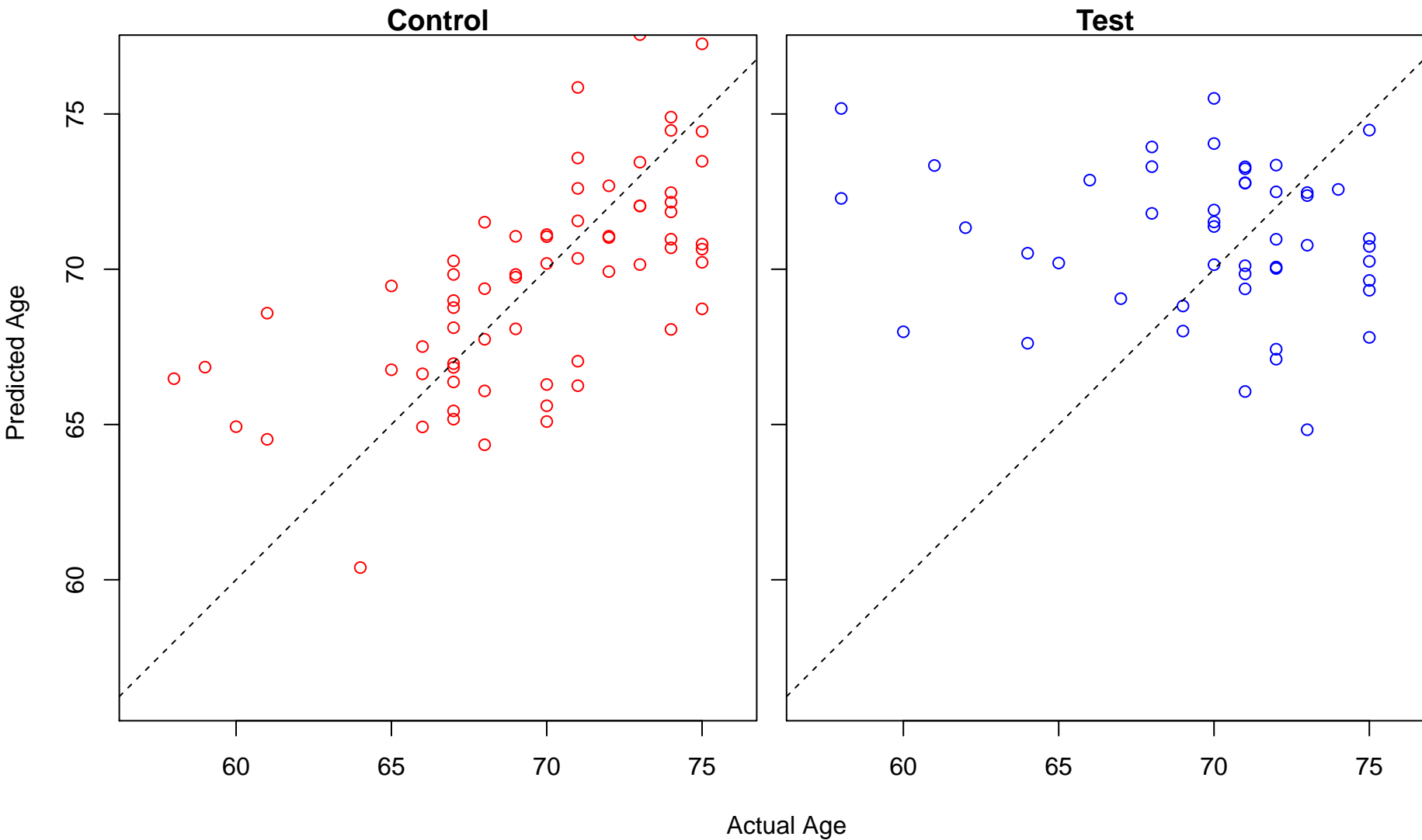
negative regulation of cell division (Score: 1.381528)



spliceosomal snRNP assembly (Score: 1.381201)

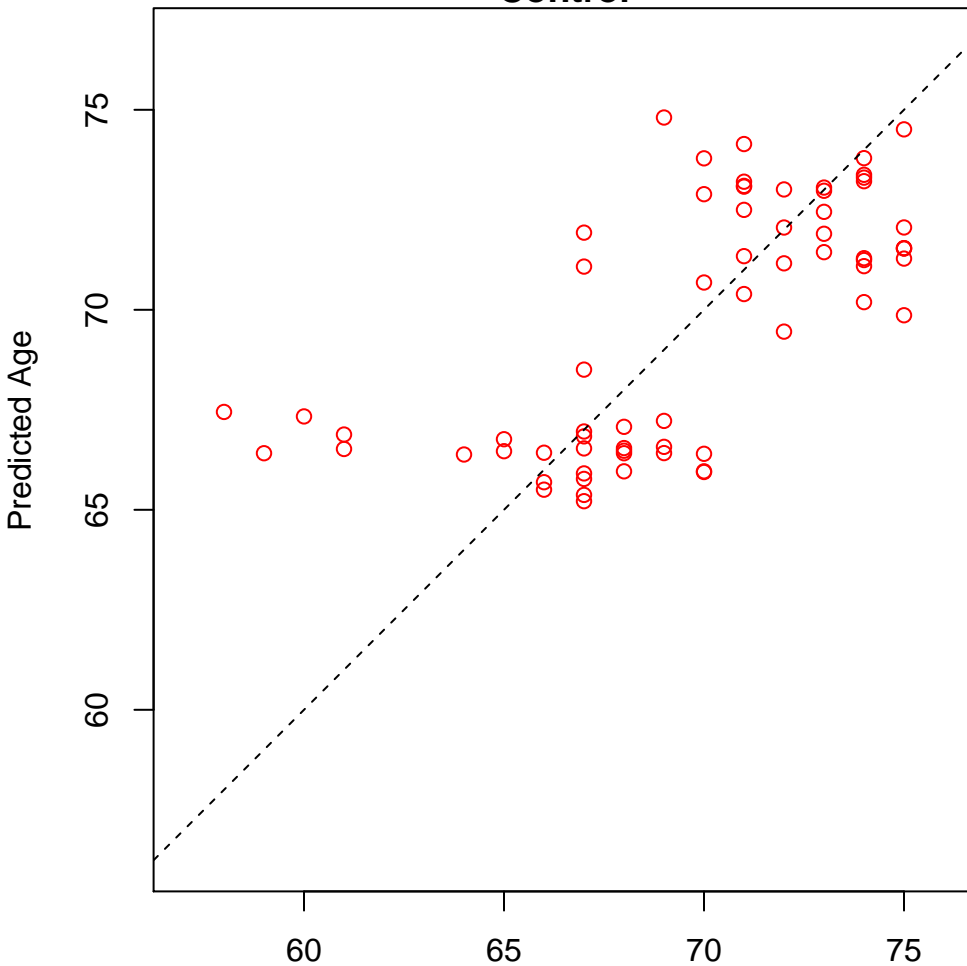


response to interferon- α (Score: 1.380922)

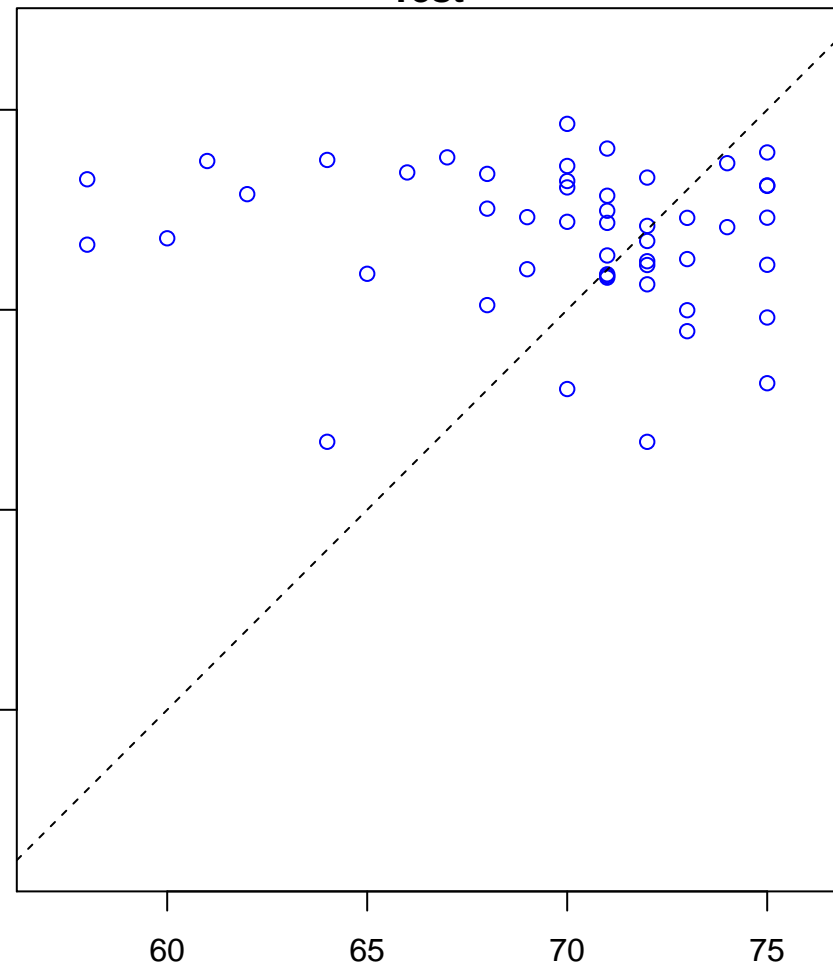


selenium compound metabolic process (Score: 1.380439)

Control

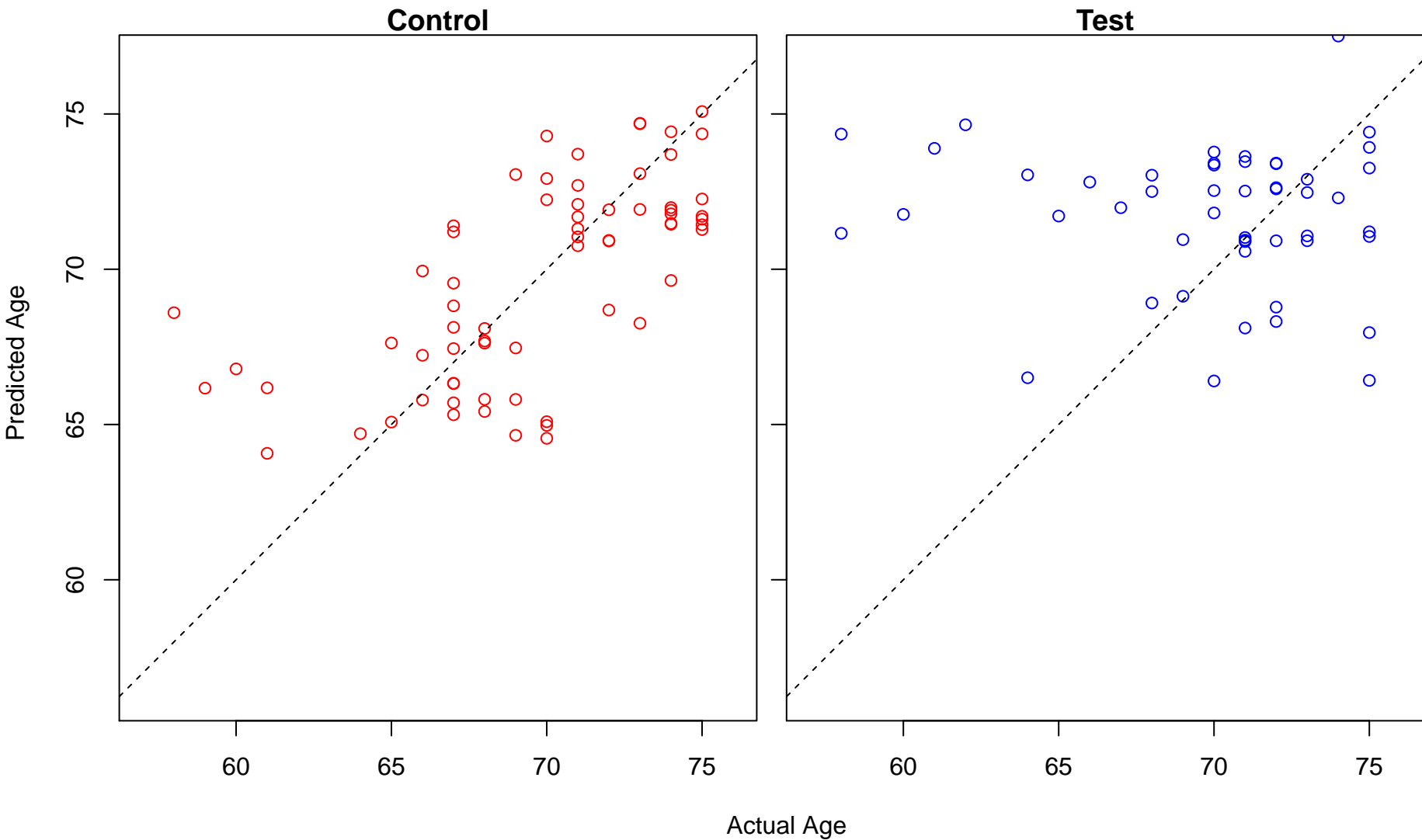


Test

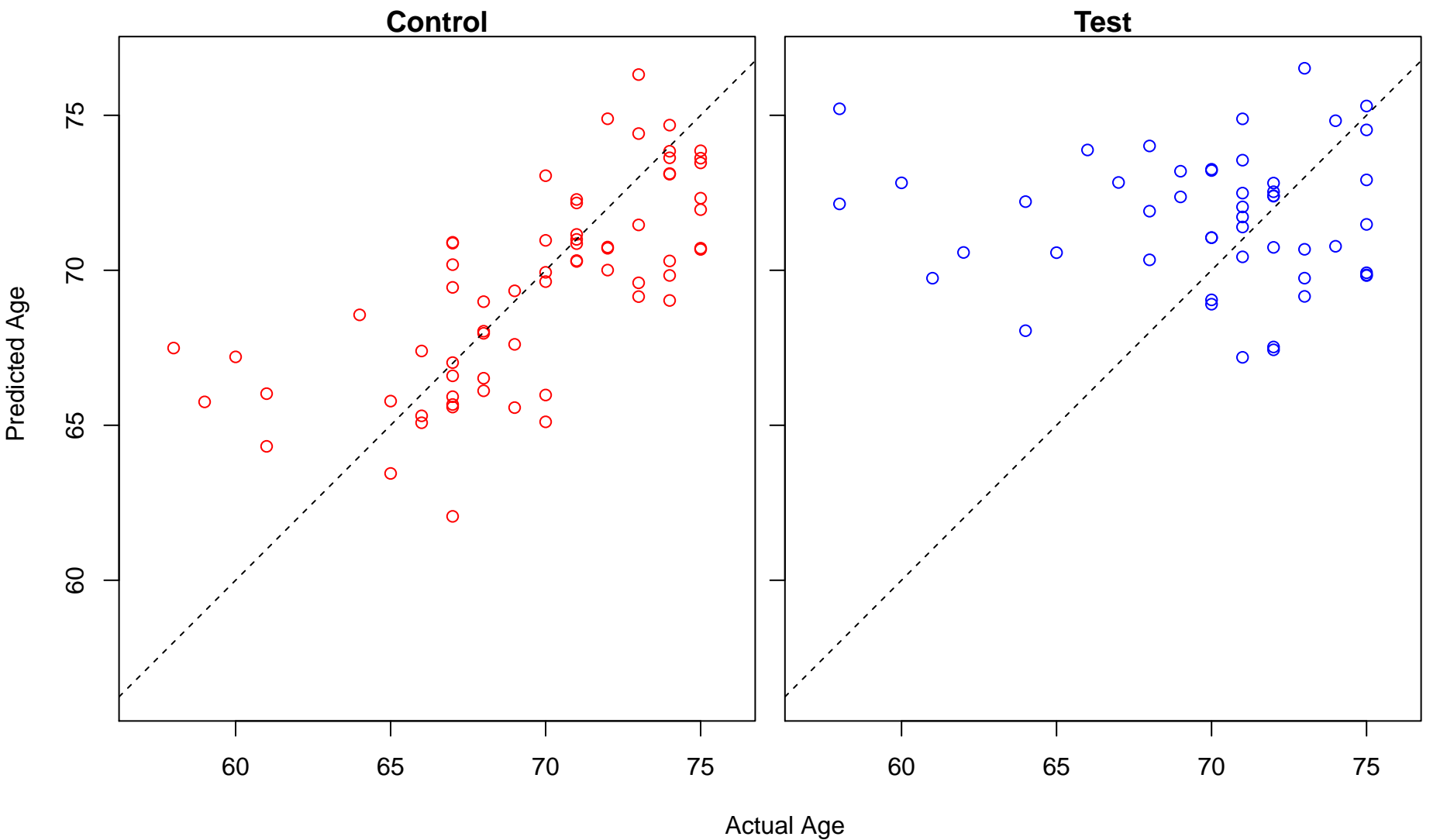


Actual Age

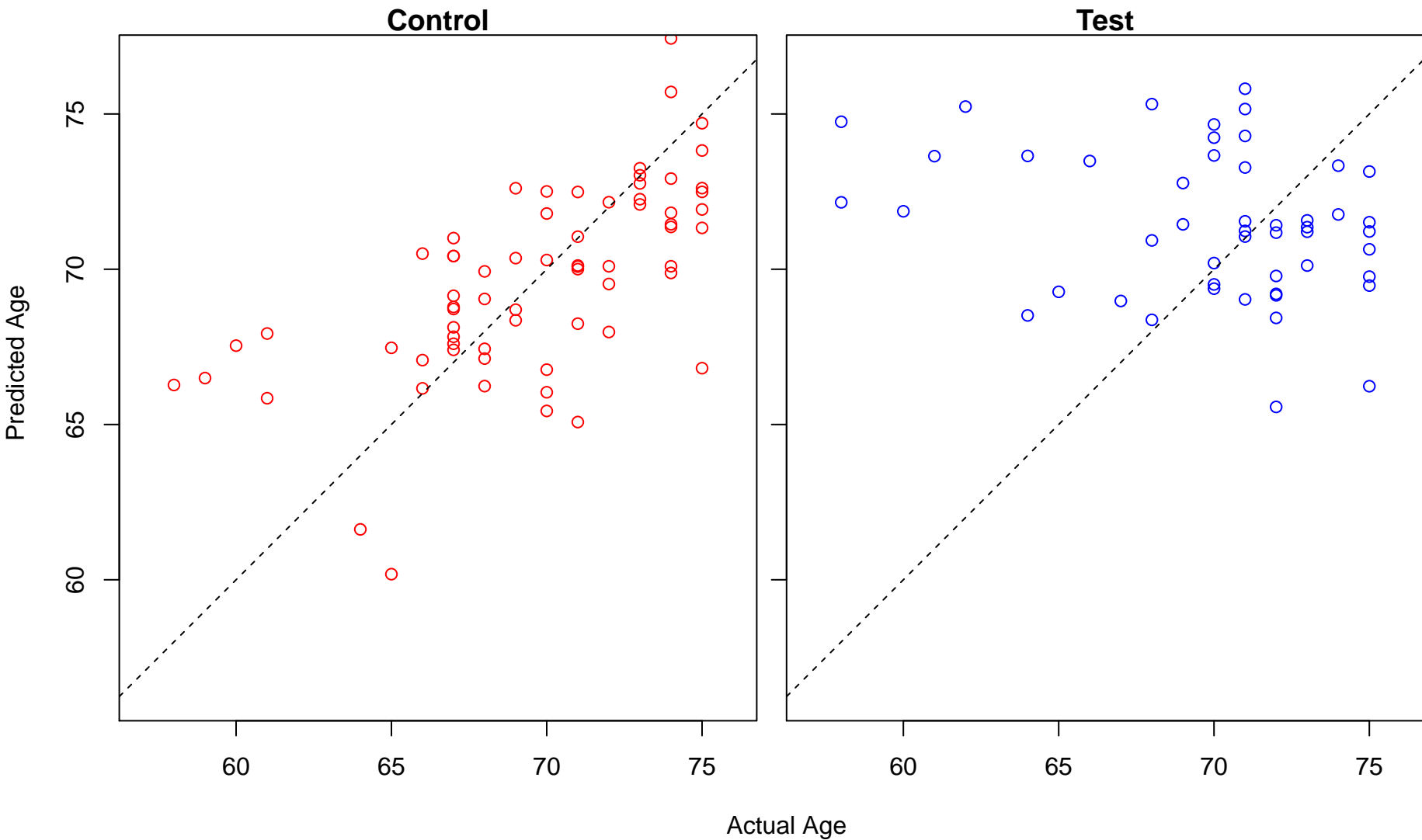
receptor-mediated endocytosis (Score: 1.380376)



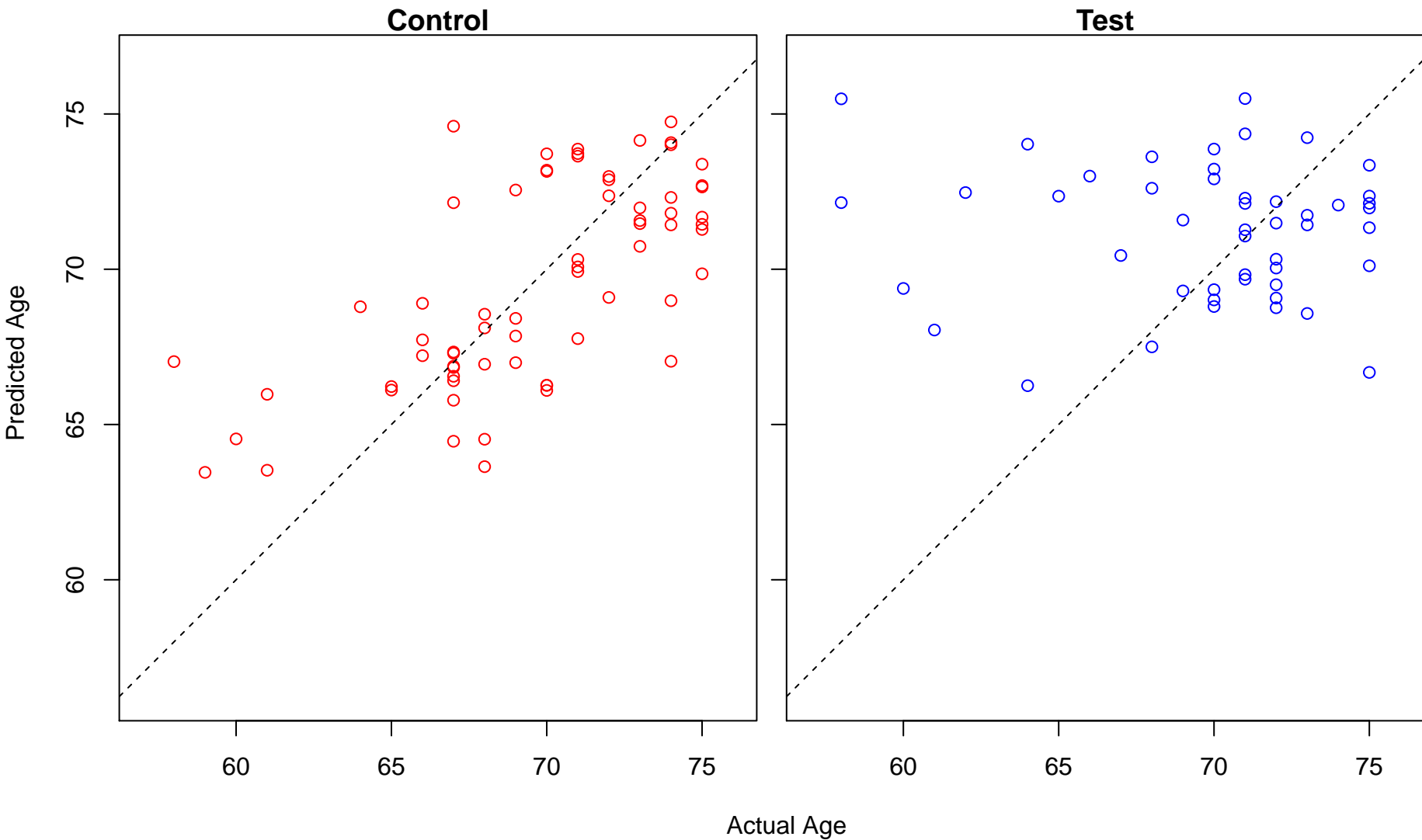
G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (Score: 1.0)



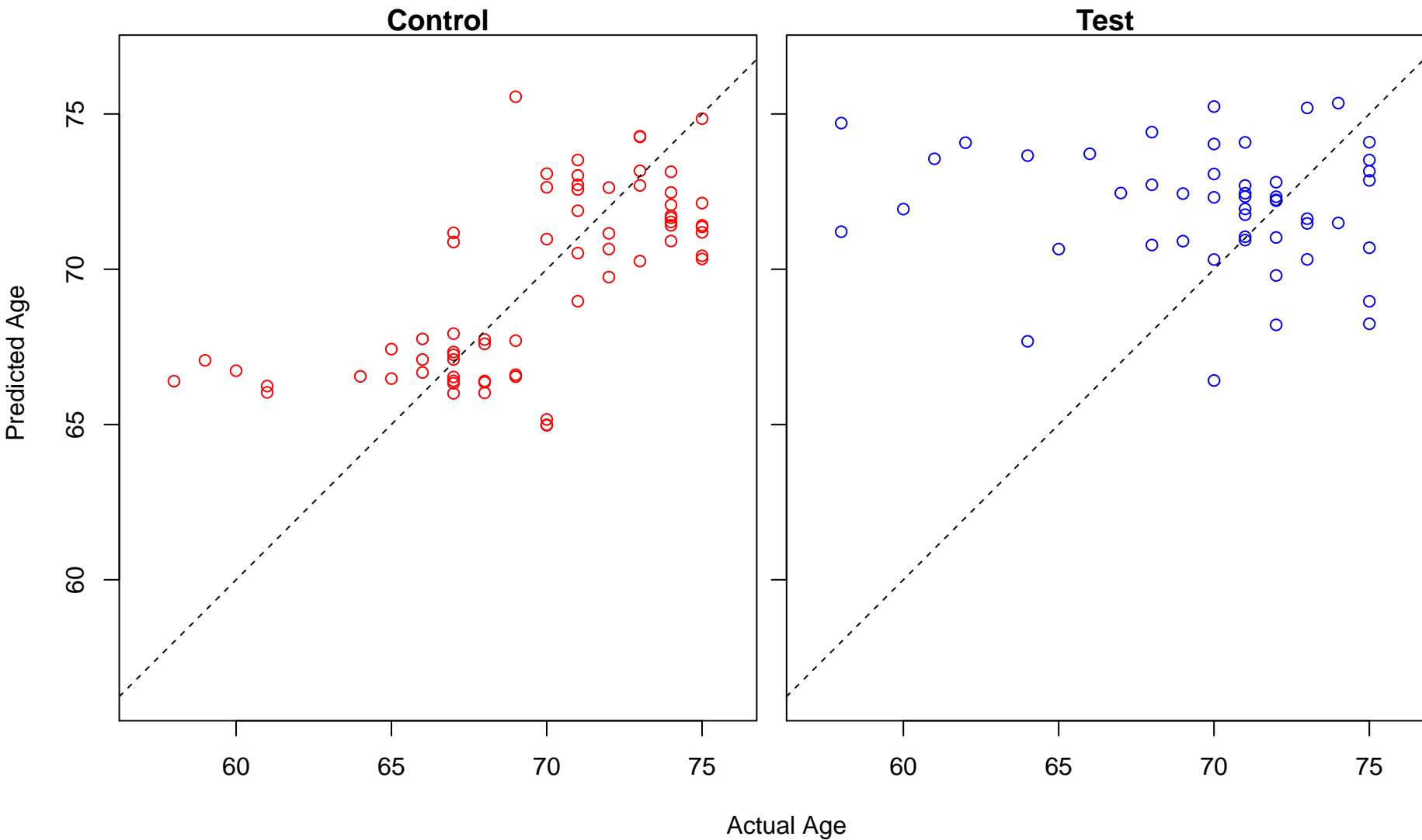
regulation of membrane protein ectodomain proteolysis (Score: 1.380184)



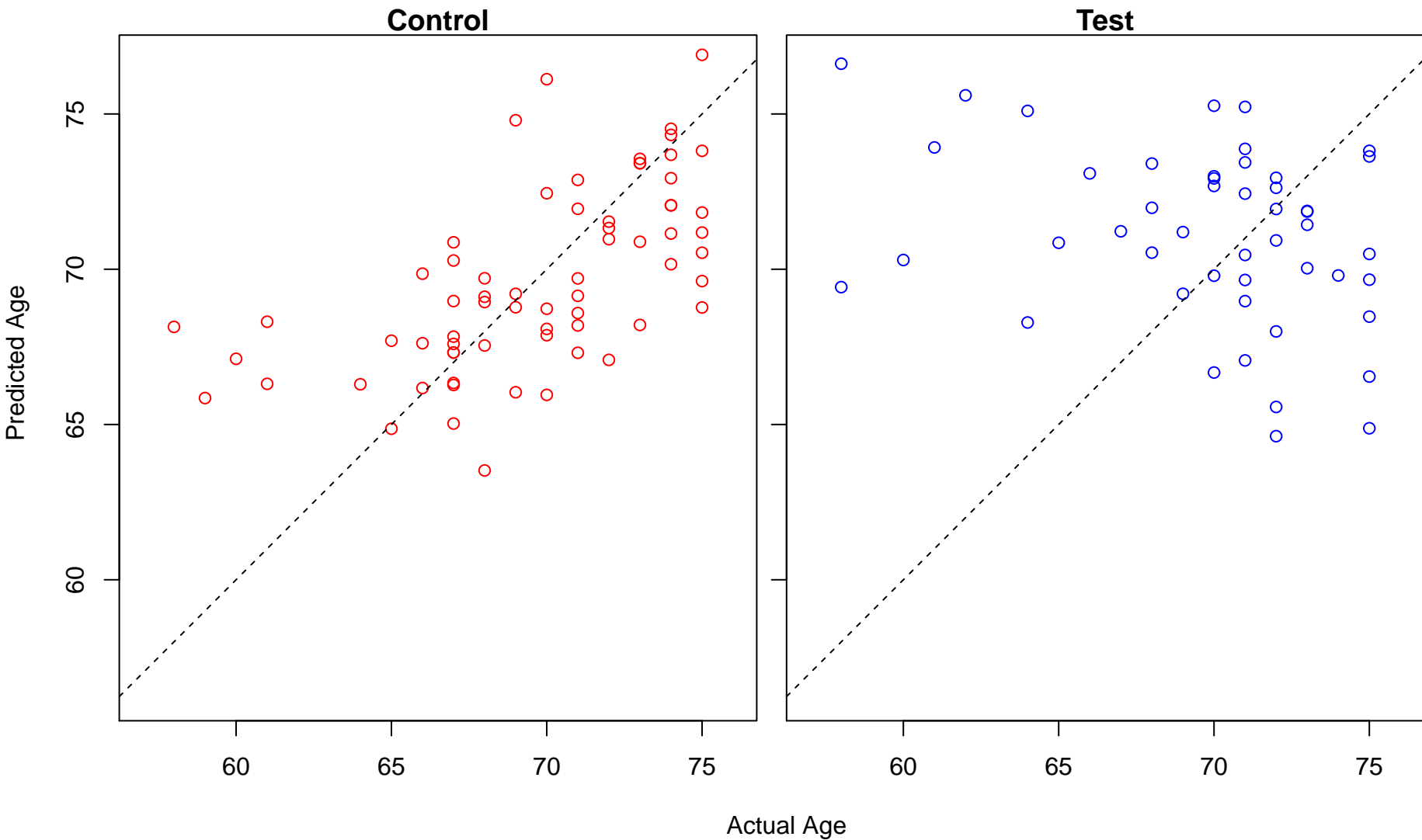
cellular response to acid chemical (Score: 1.379954)



response to oxidative stress (Score: 1.379759)

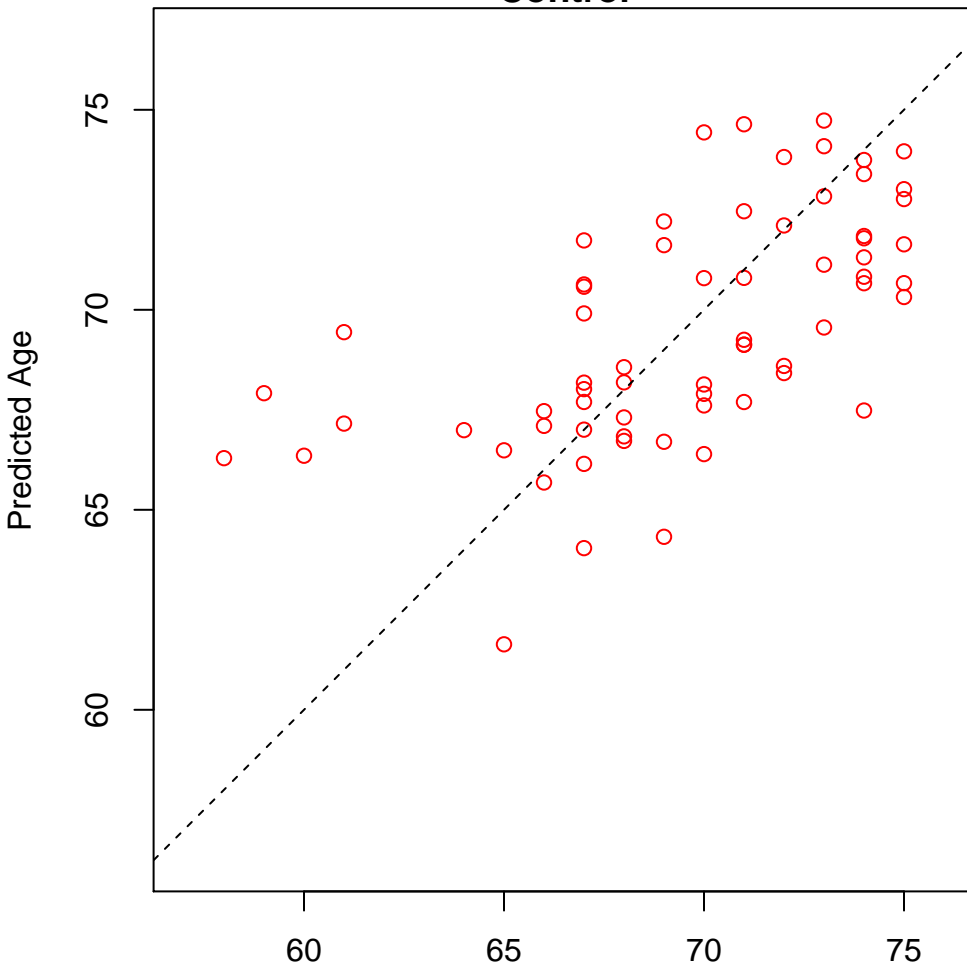


xenobiotic catabolic process (Score: 1.379641)

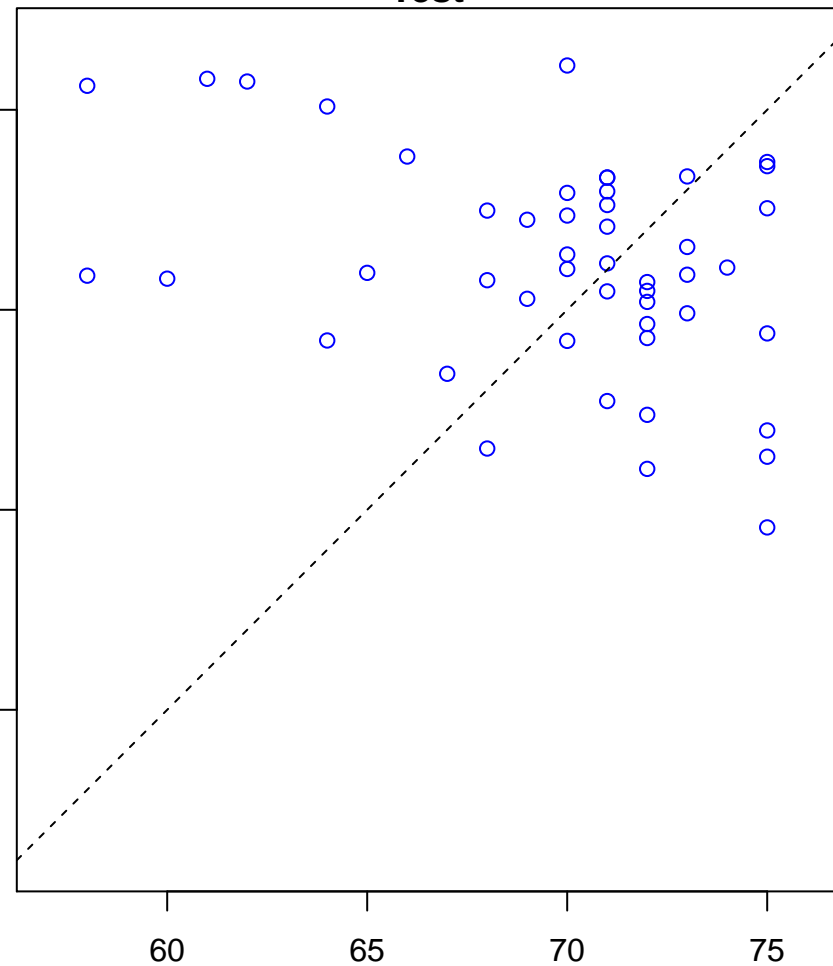


L-ascorbic acid metabolic process (Score: 1.379475)

Control

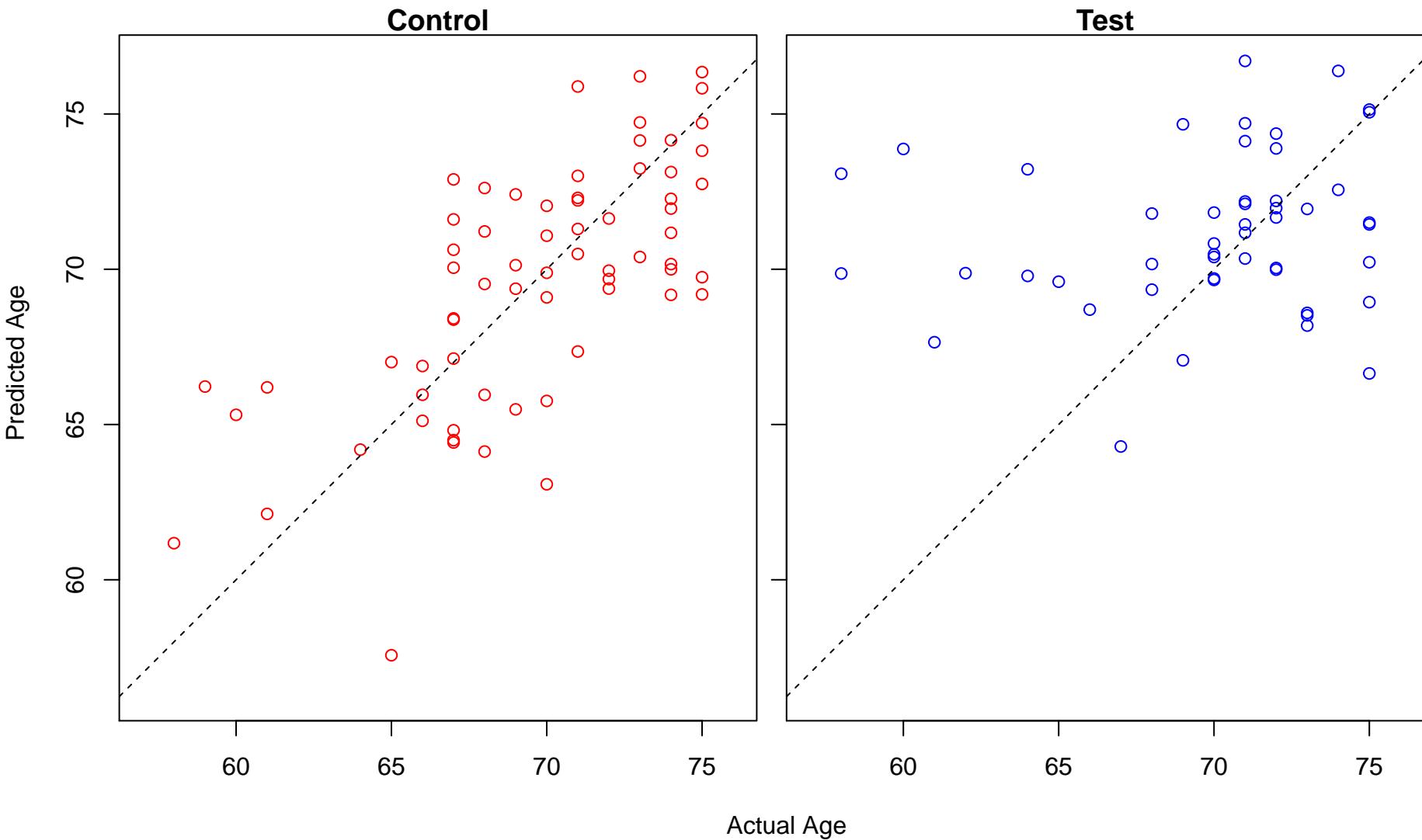


Test

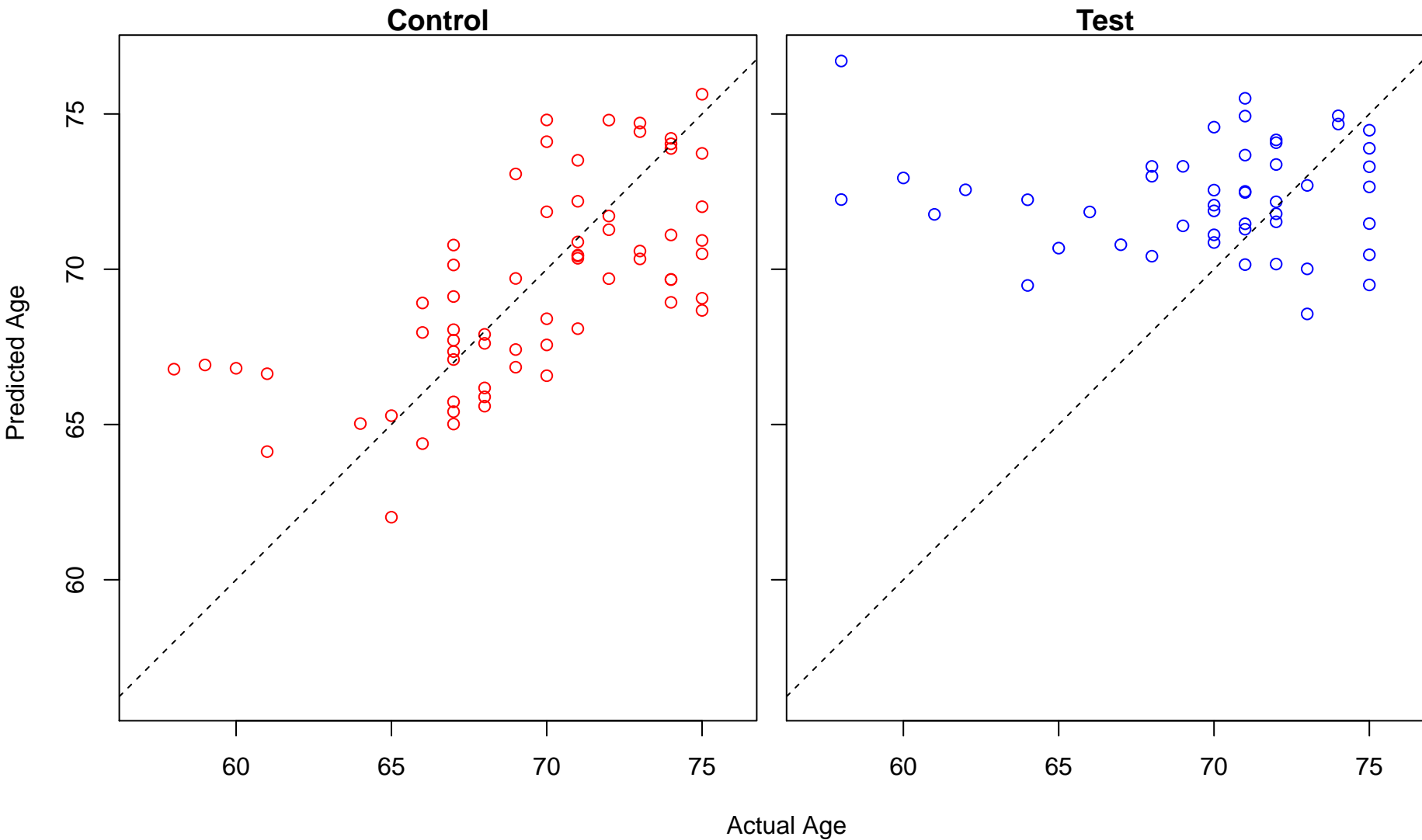


Actual Age

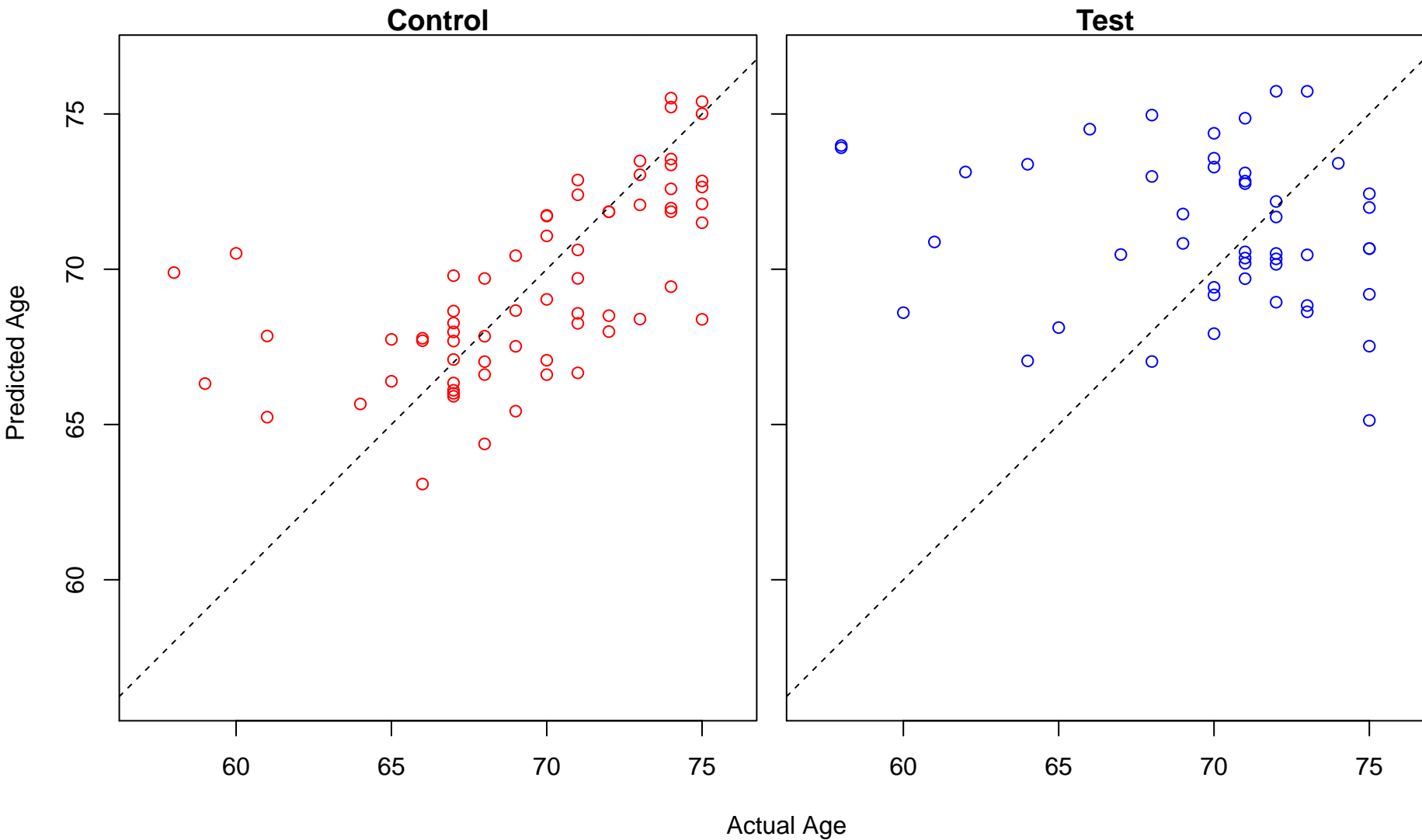
positive regulation of nucleotide metabolic process (Score: 1.379386)



microtubule-based movement (Score: 1.378674)

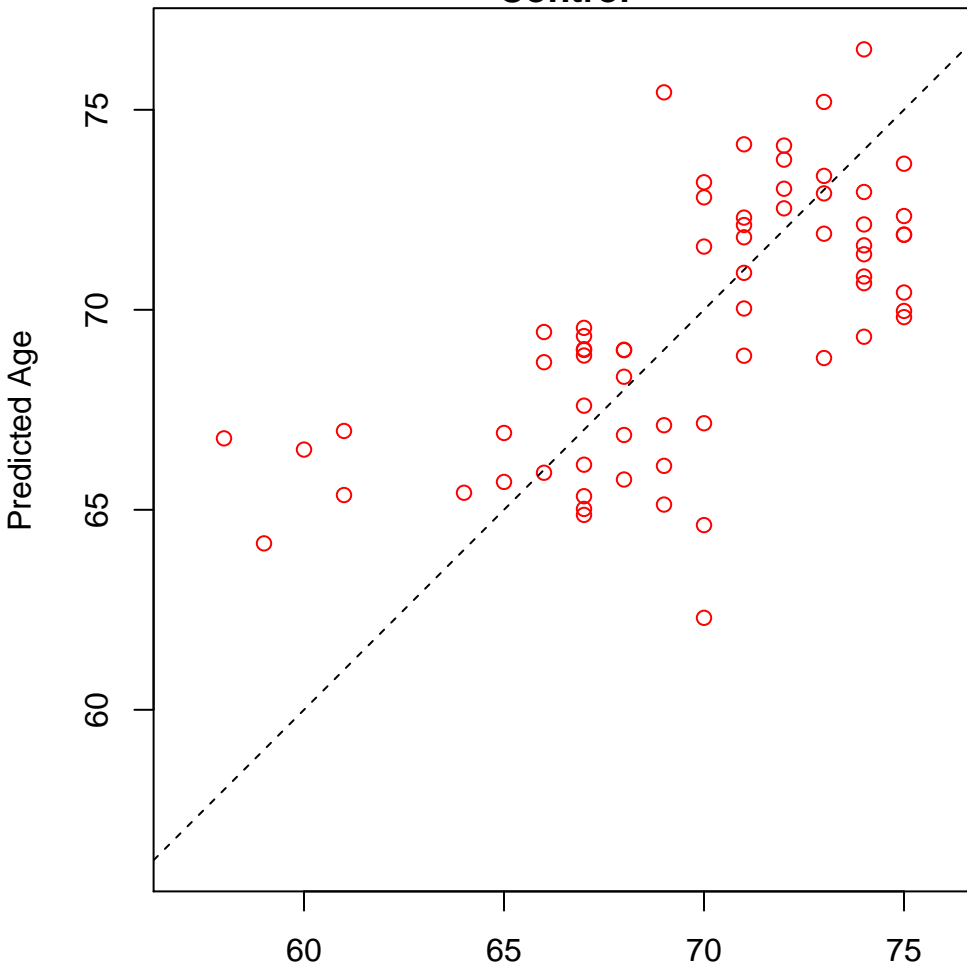


response to zinc ion (Score: 1.378076)

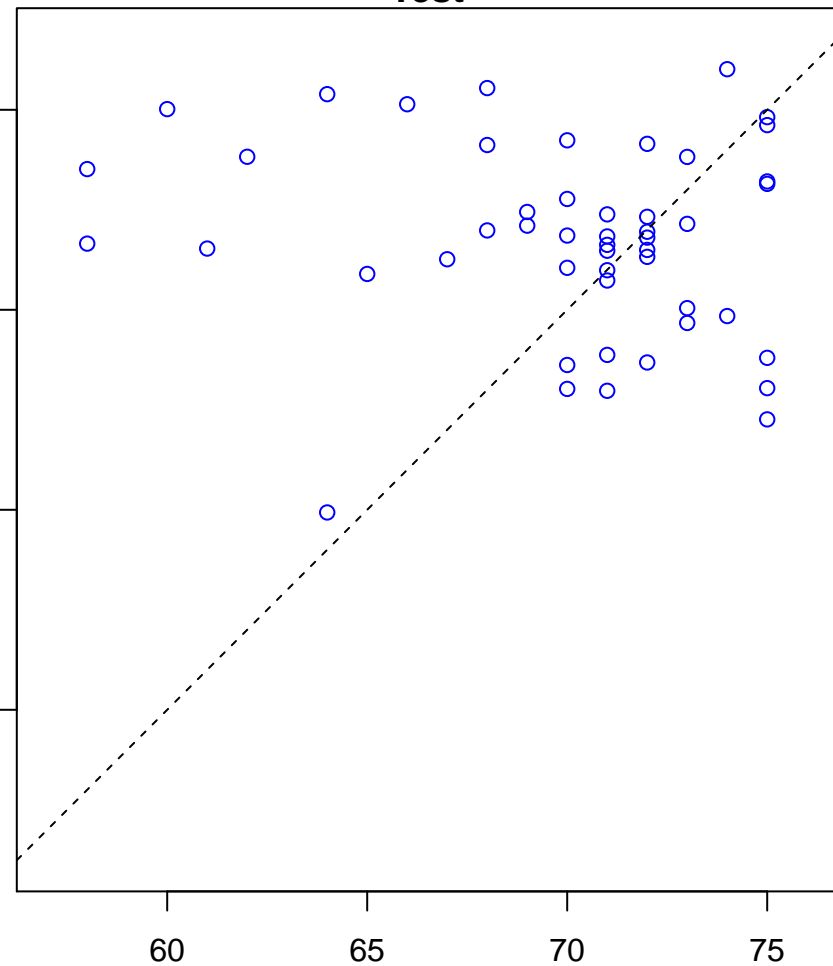


RNA phosphodiester bond hydrolysis (Score: 1.378052)

Control

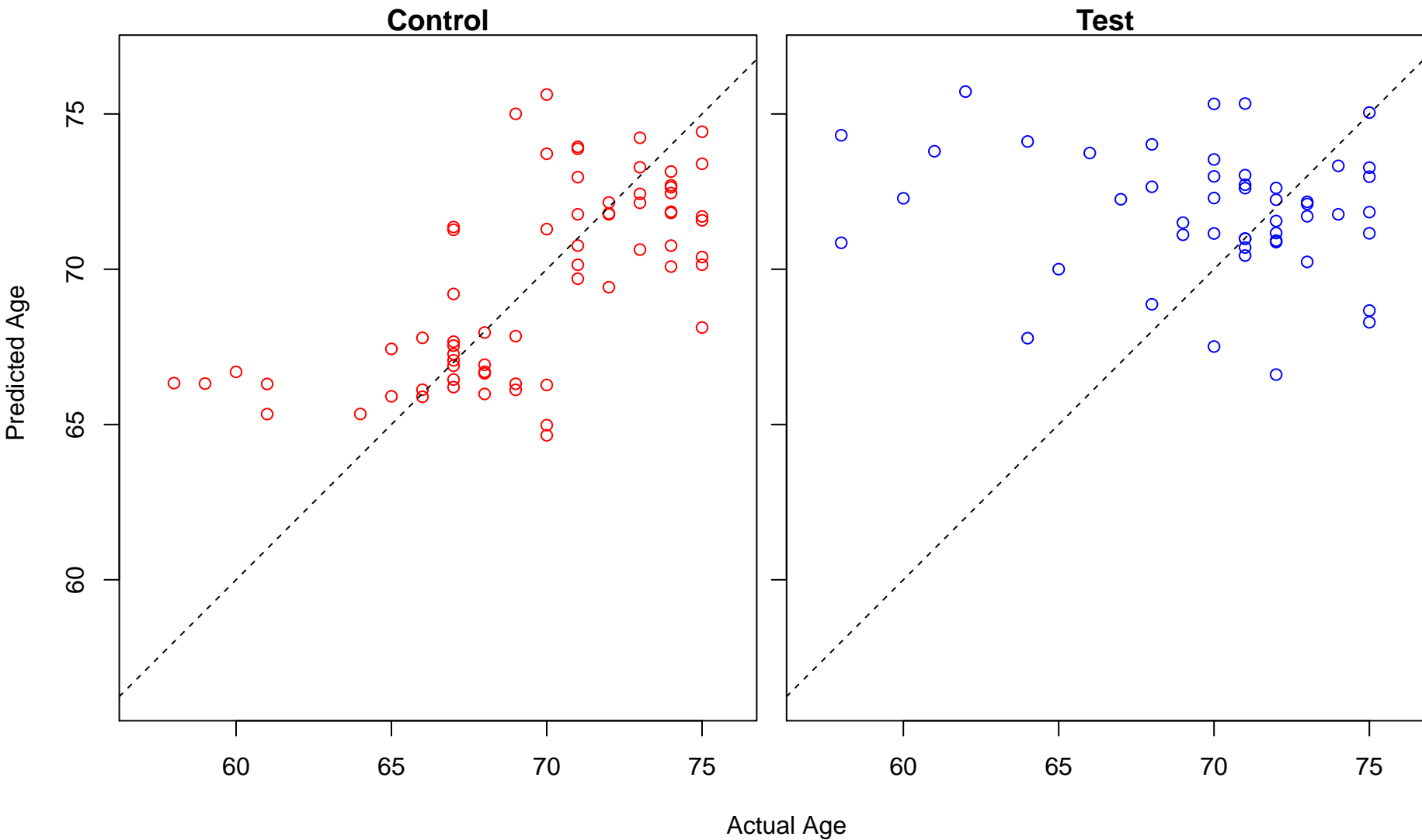


Test

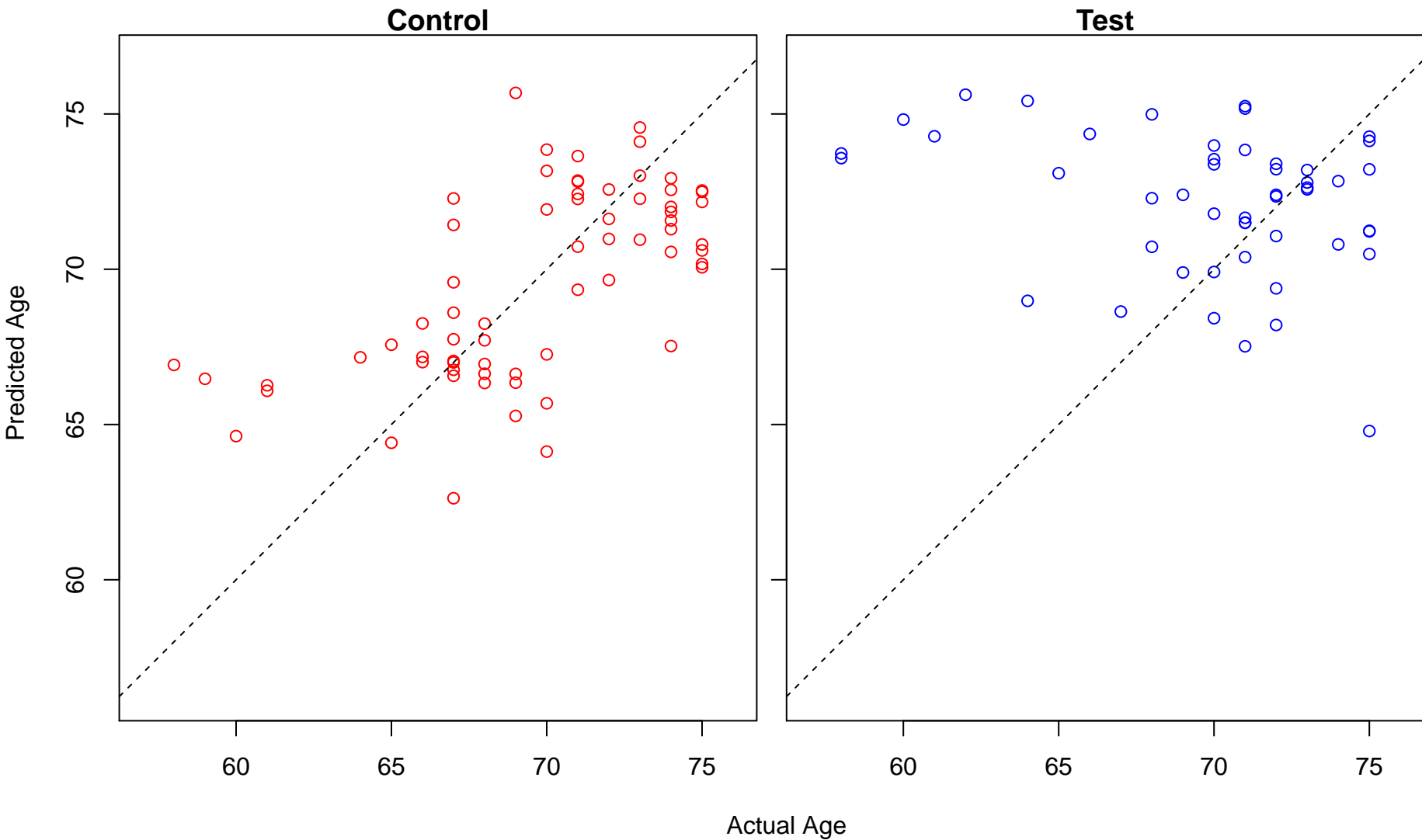


Actual Age

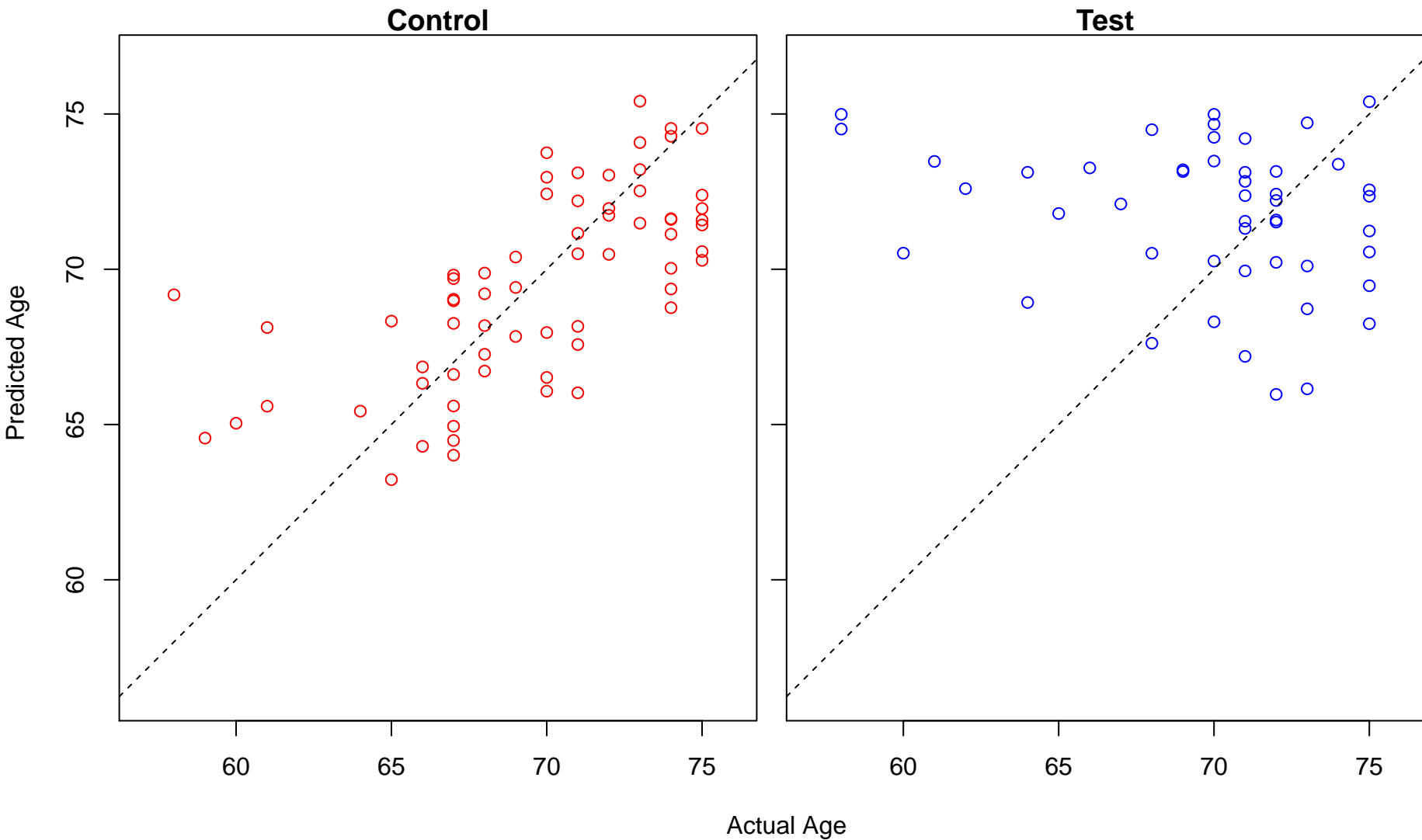
nucleotide-excision repair, DNA damage recognition (Score: 1.377518)



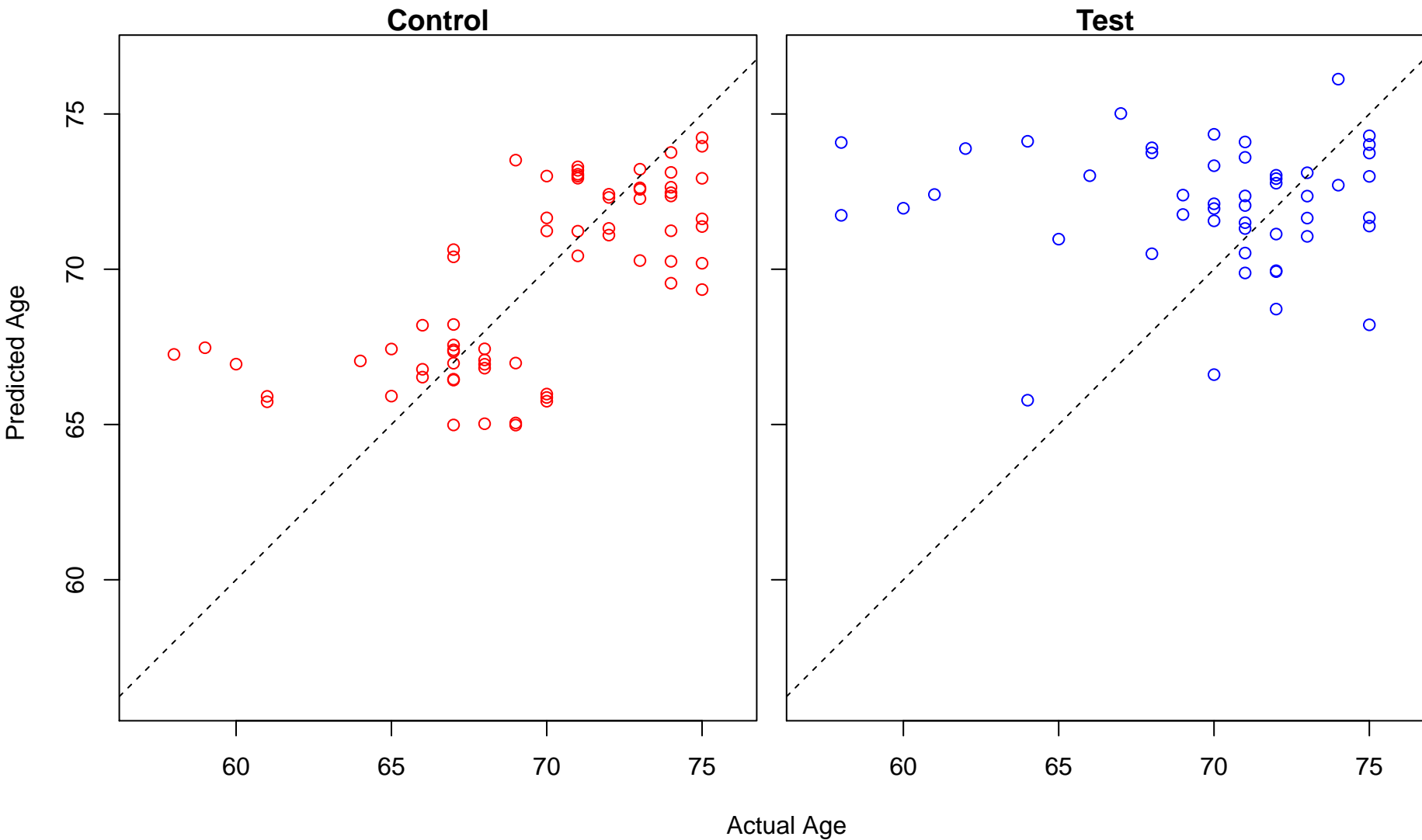
lipid phosphorylation (Score: 1.377136)



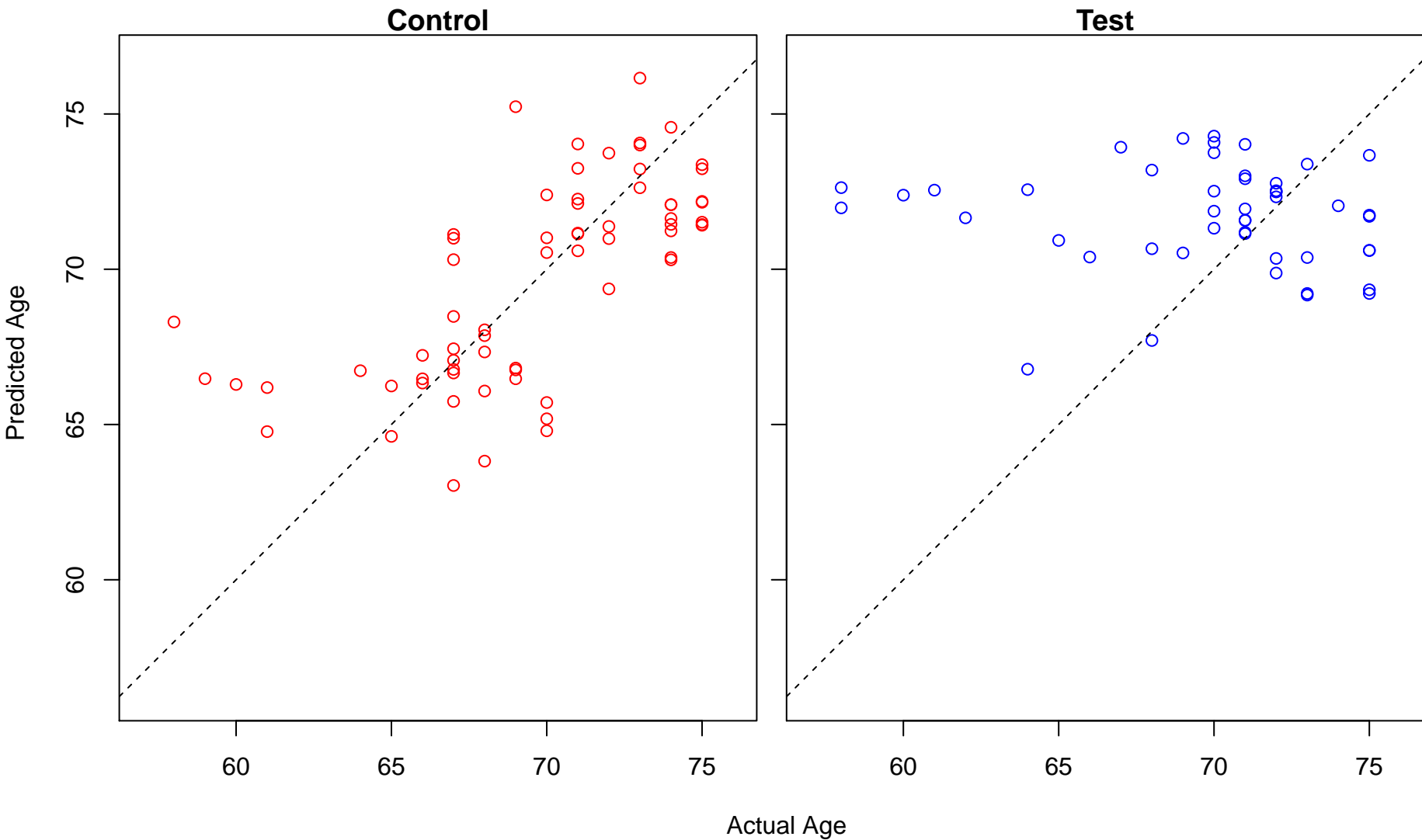
regulation of leukocyte mediated immunity (Score: 1.376902)



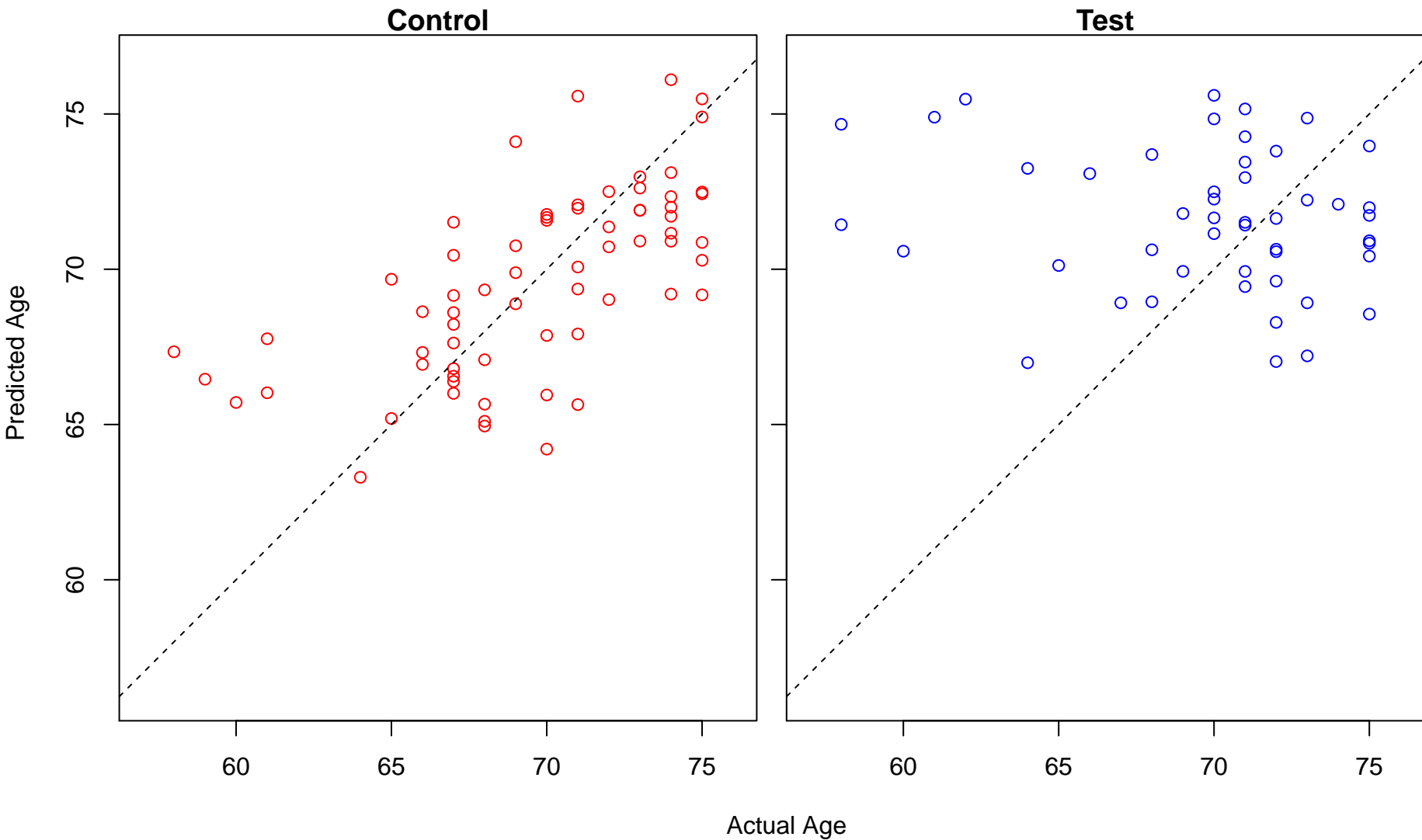
ruffle organization (Score: 1.376195)



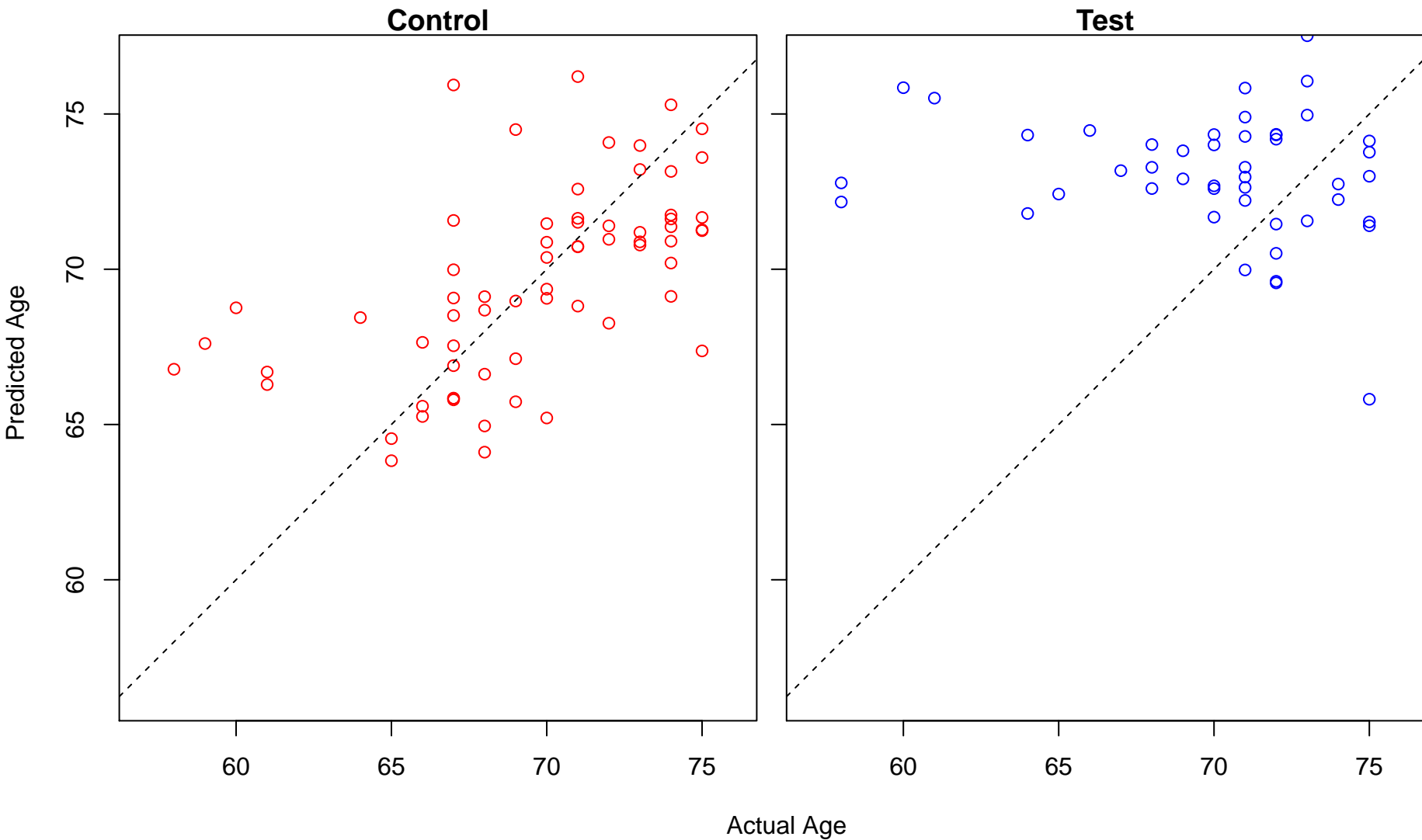
regulation of exocytosis (Score: 1.375849)



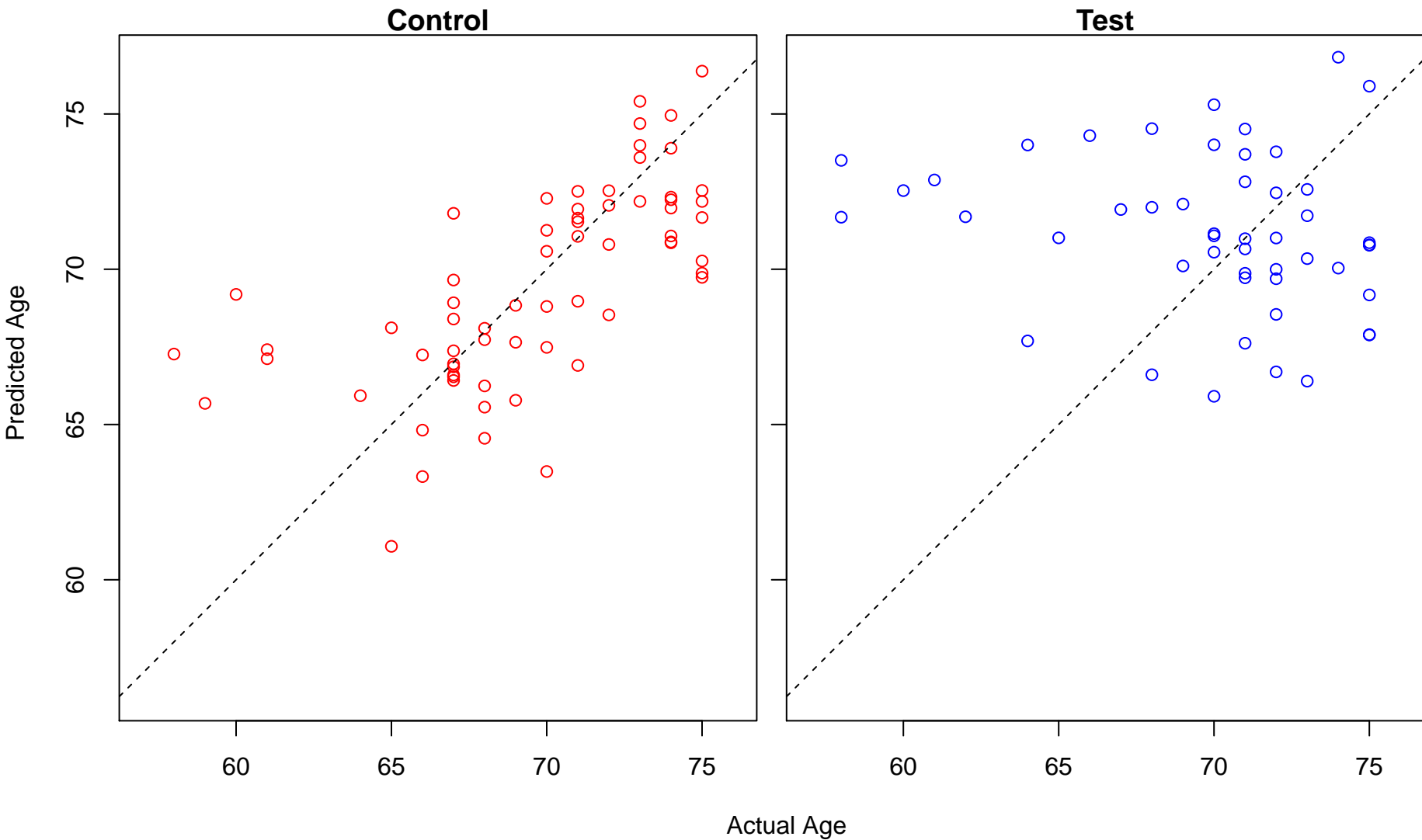
glucose metabolic process (Score: 1.375712)



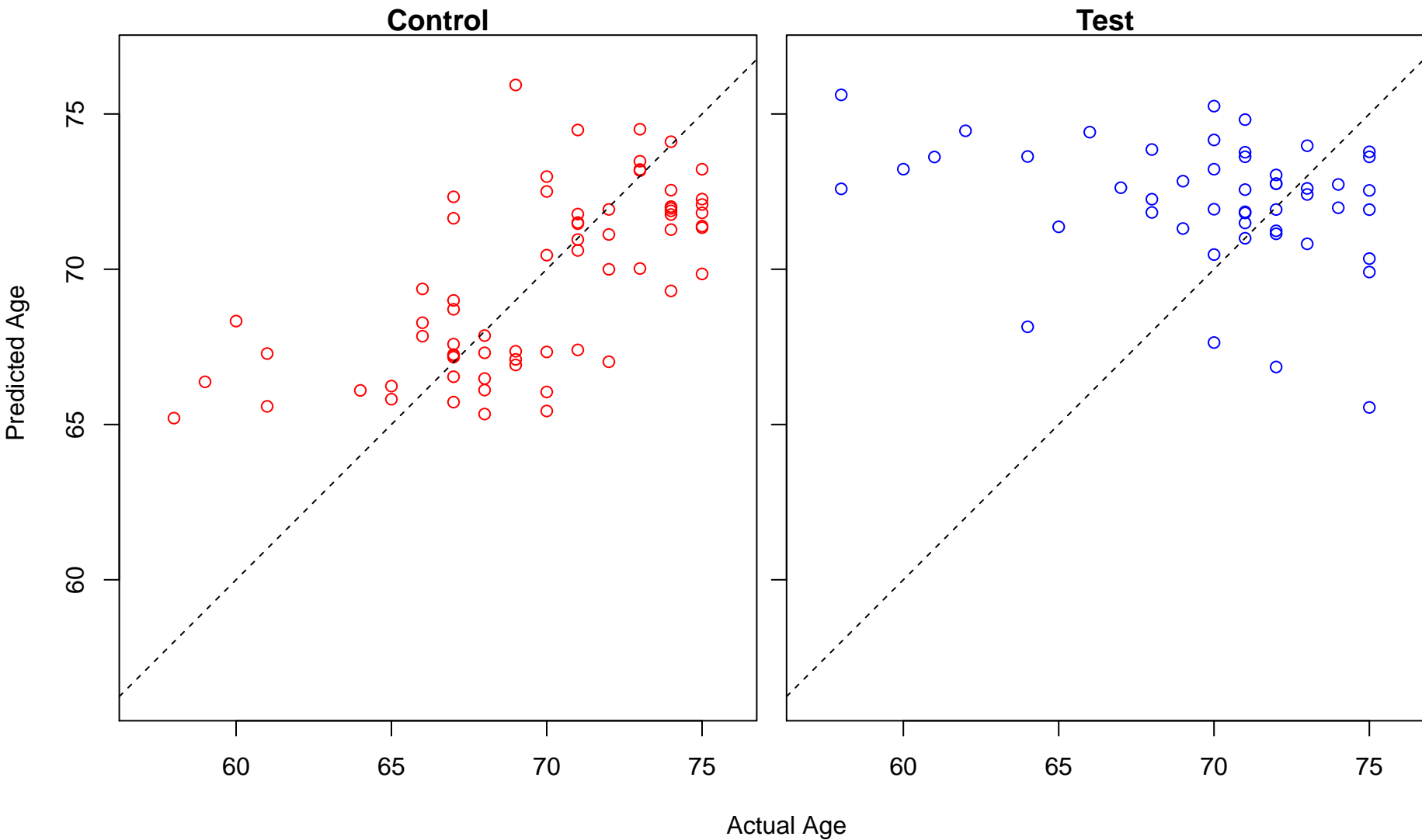
regulation of translational elongation (Score: 1.375572)



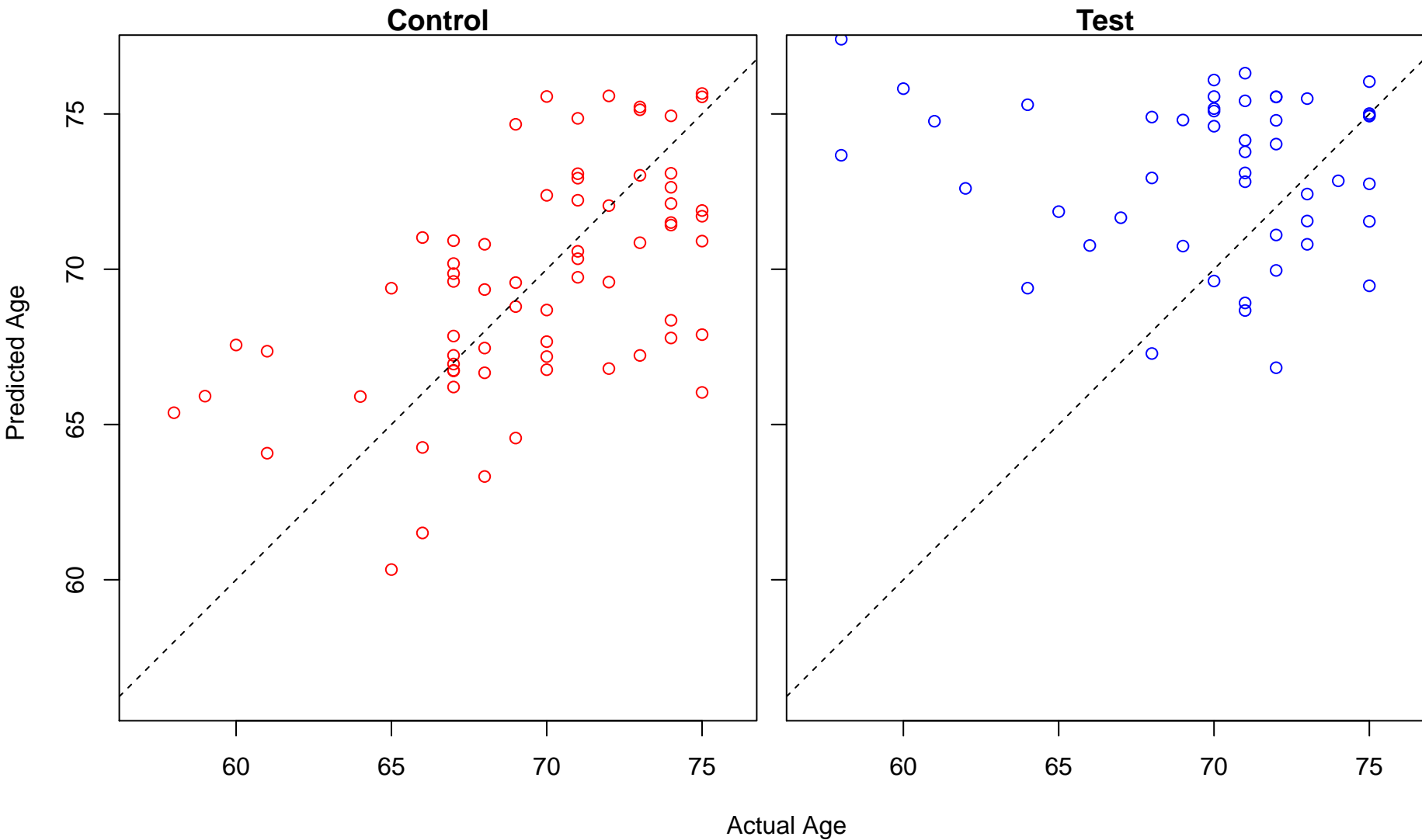
regulation of cytokine secretion (Score: 1.375276)



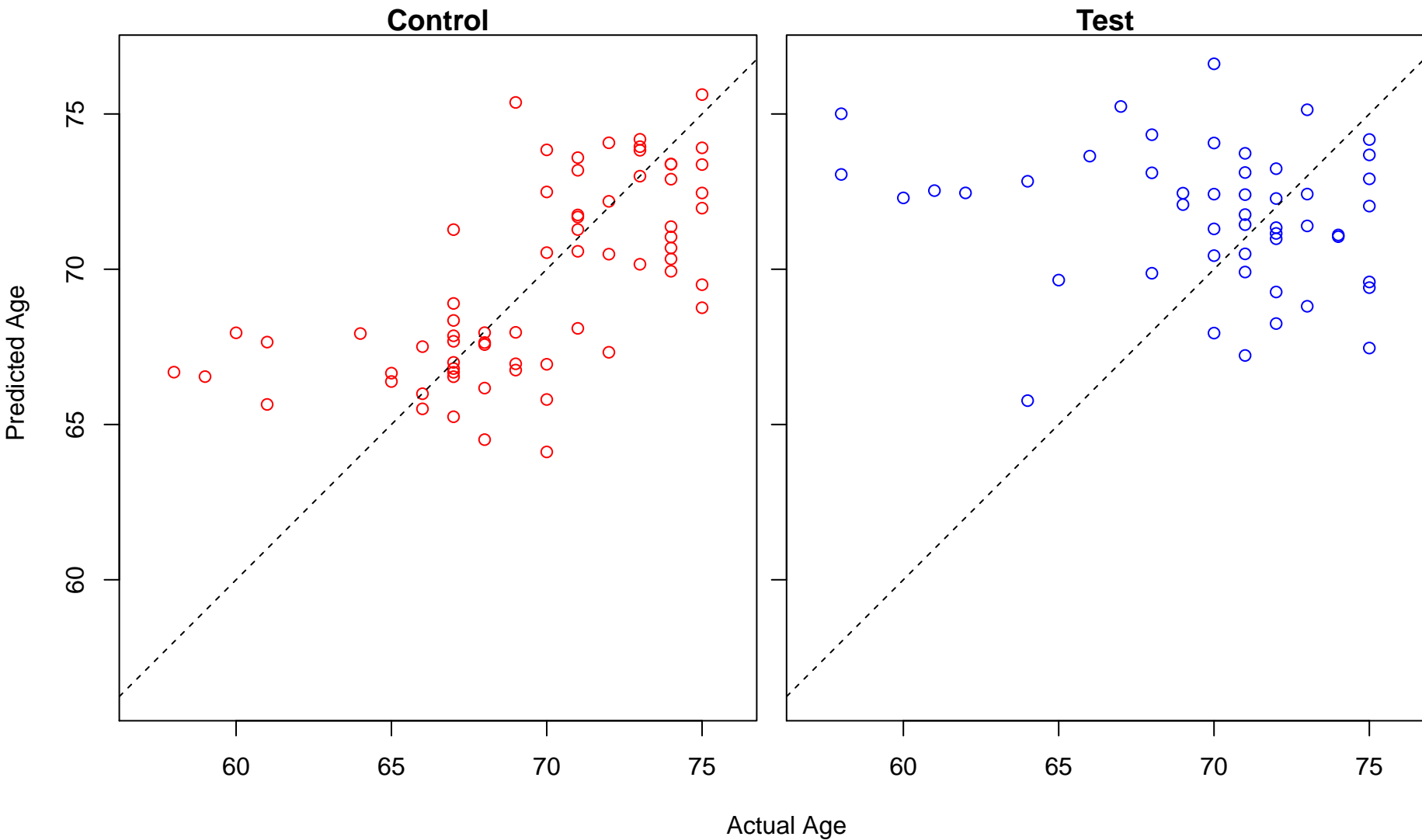
cellular amino acid catabolic process (Score: 1.375066)



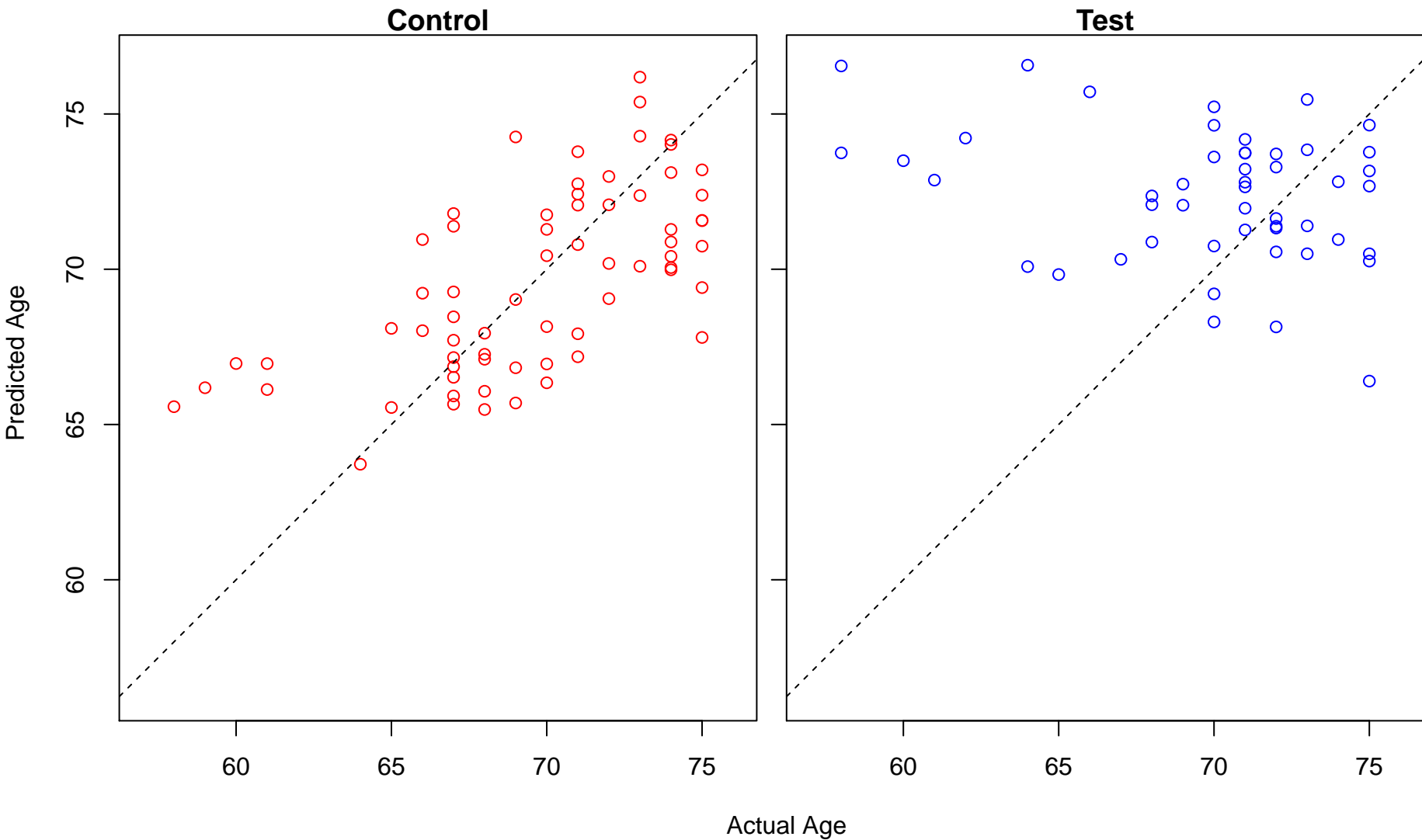
cellular aldehyde metabolic process (Score: 1.374797)



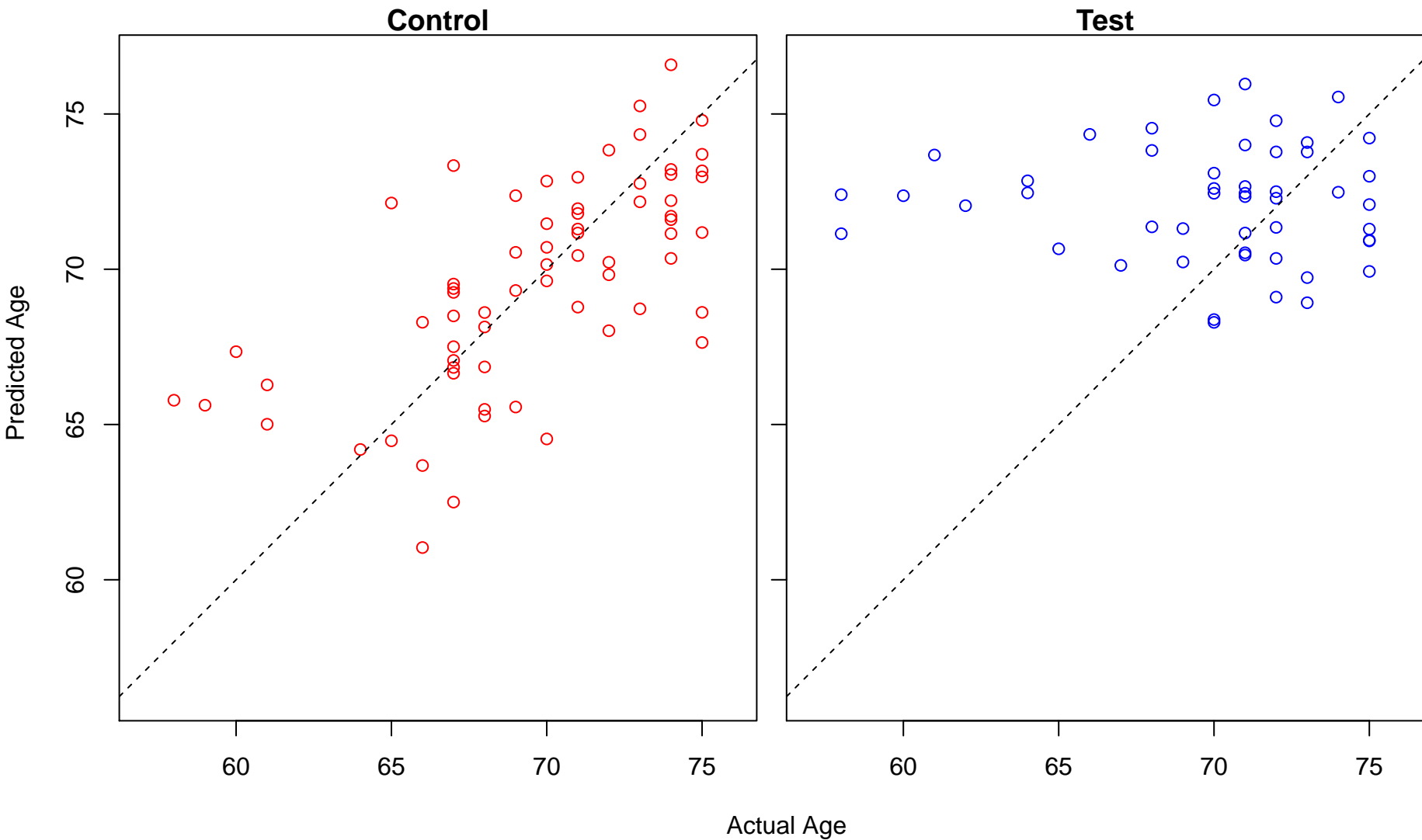
zinc ion homeostasis (Score: 1.374484)



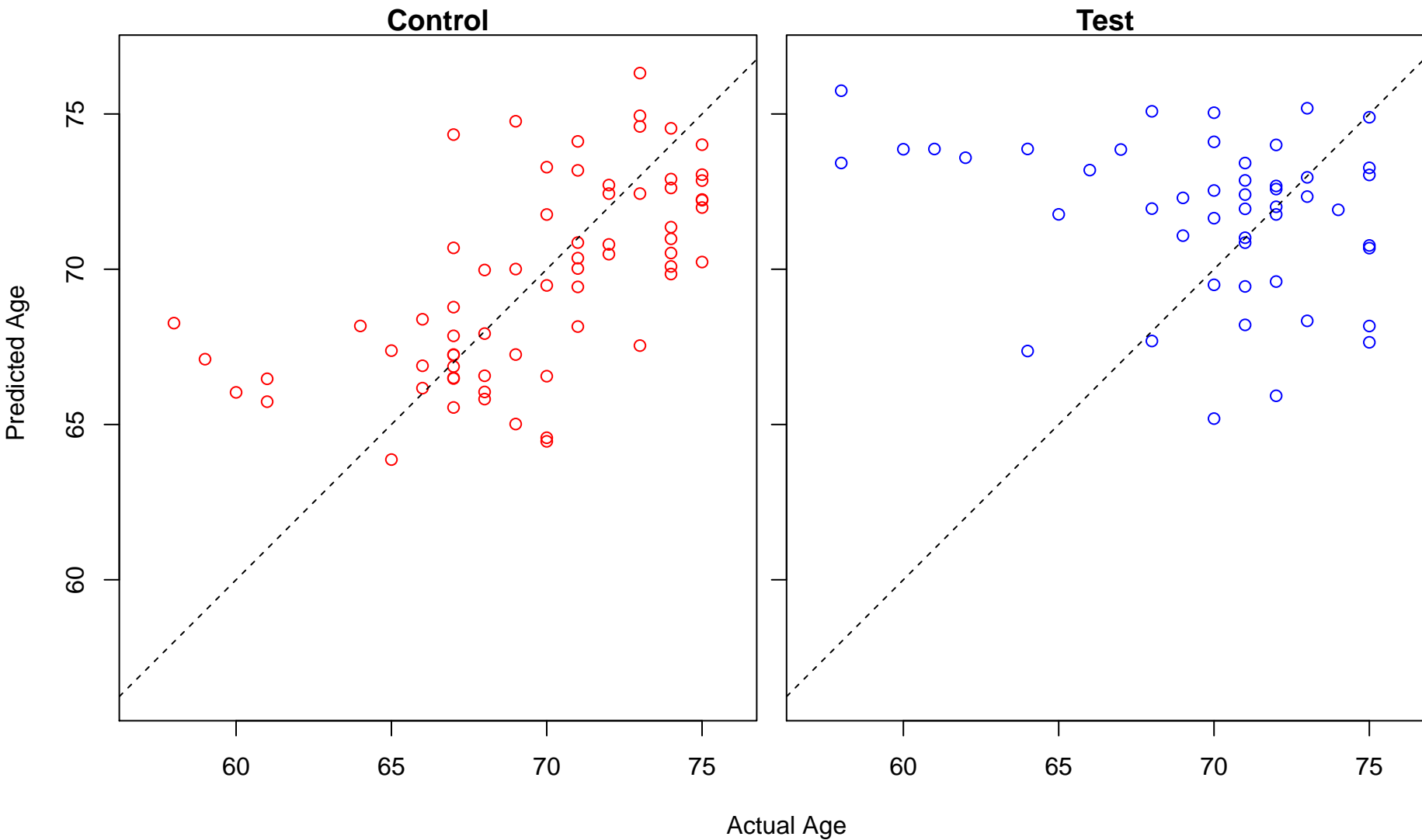
inorganic anion transmembrane transport (Score: 1.372728)



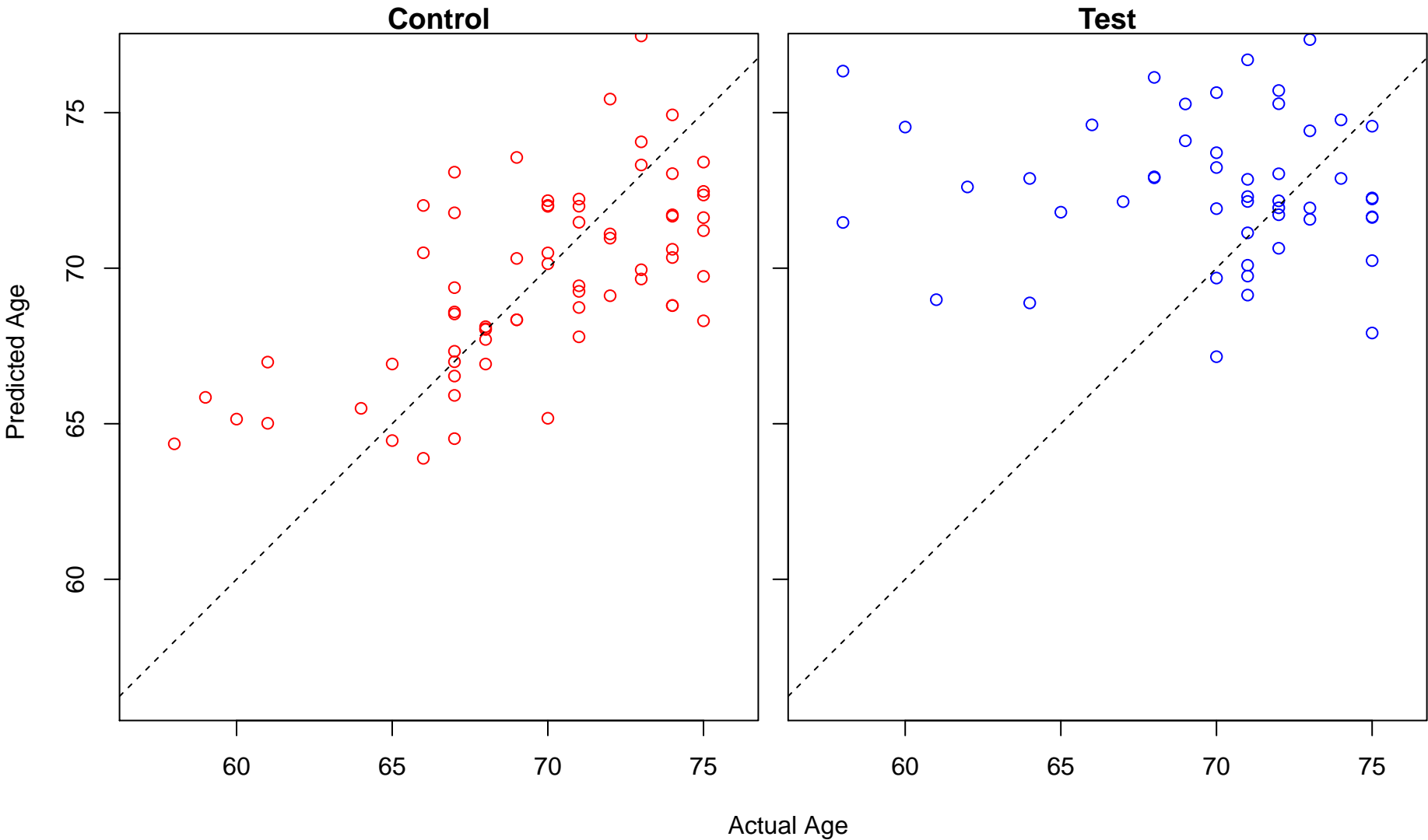
filopodium assembly (Score: 1.372296)



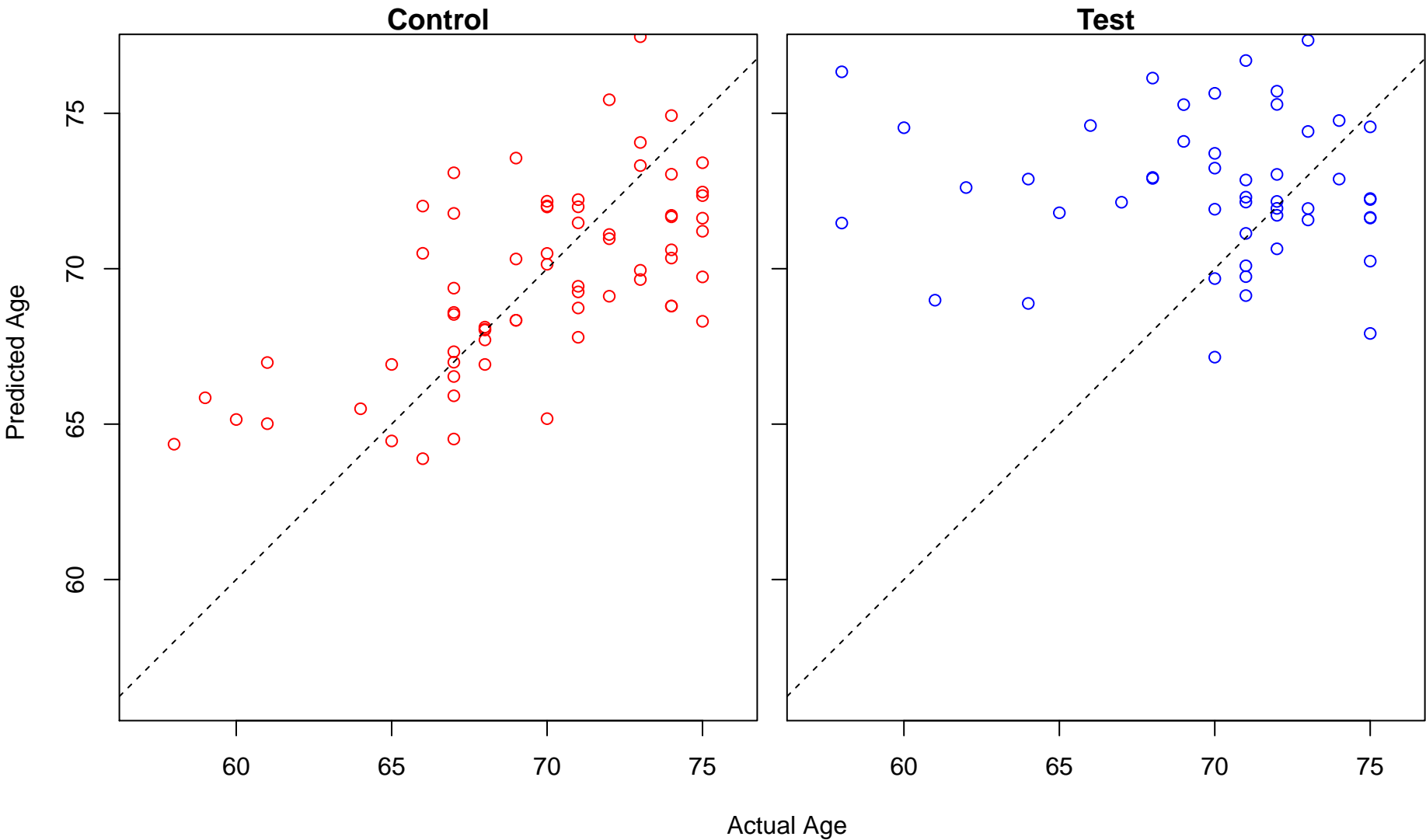
coenzyme biosynthetic process (Score: 1.371908)



positive regulation of mitochondrial membrane permeability involved in apoptotic process (Score: 1.37)

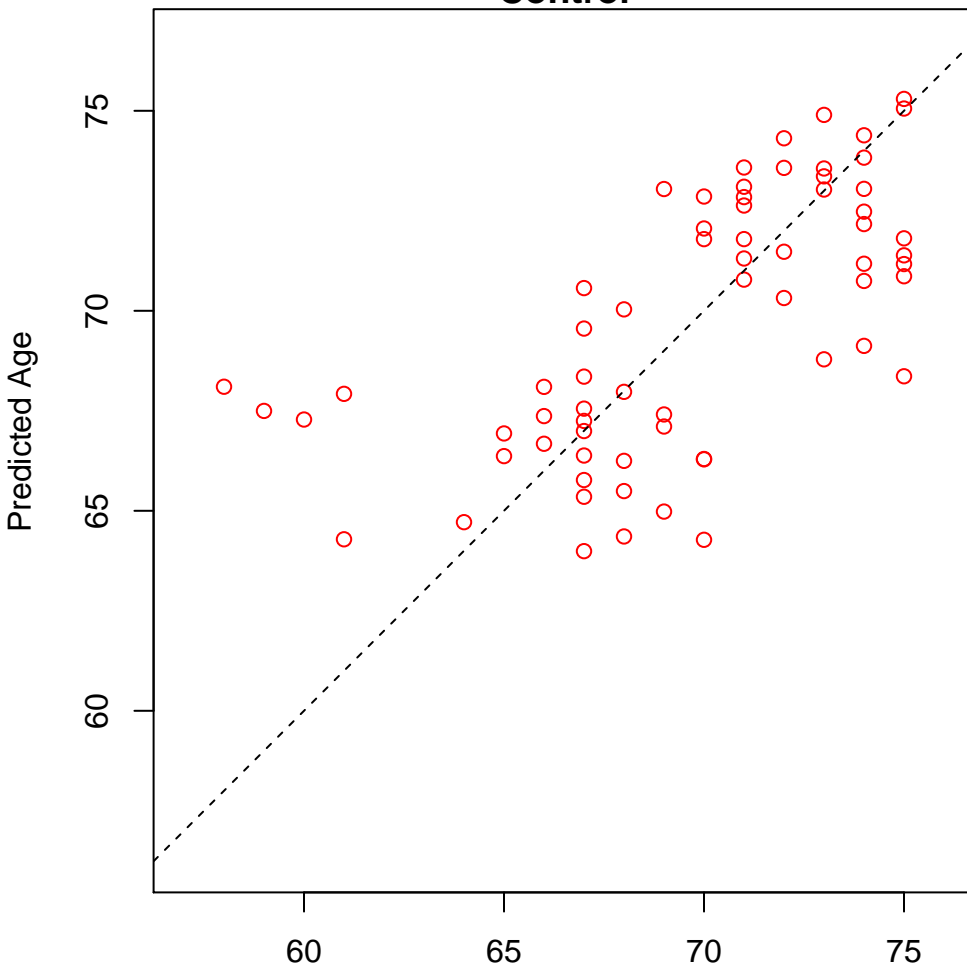


mitochondrial outer membrane permeabilization involved in programmed cell death (Score: 1.37135)

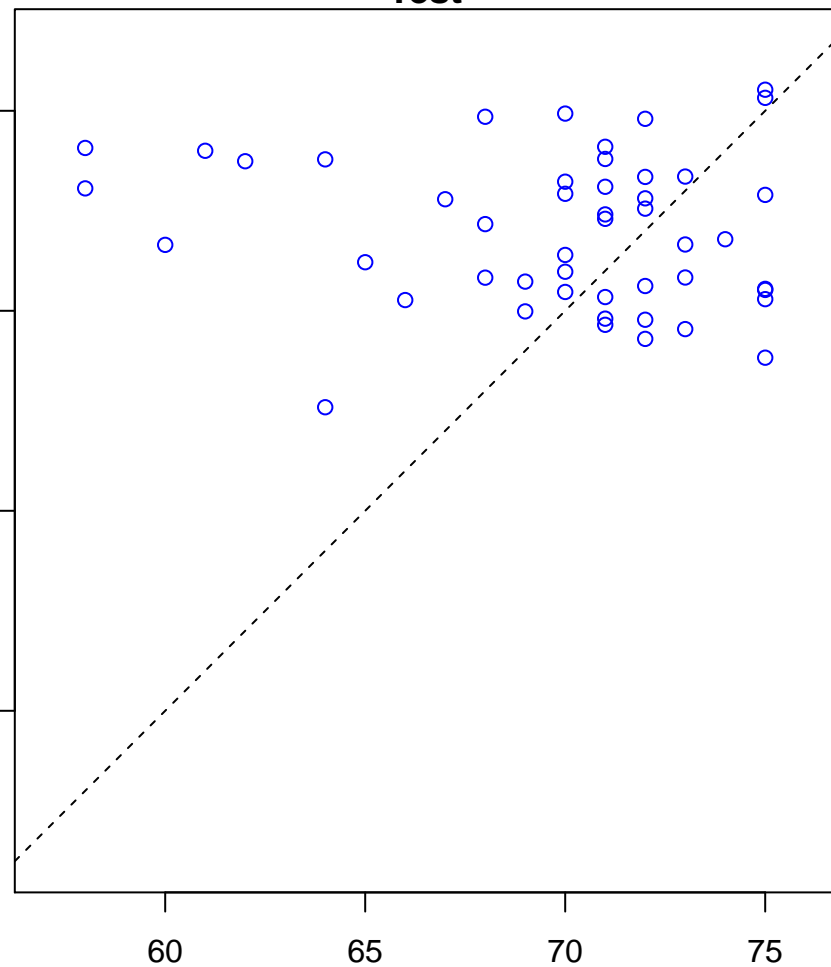


sulfur compound metabolic process (Score: 1.370997)

Control

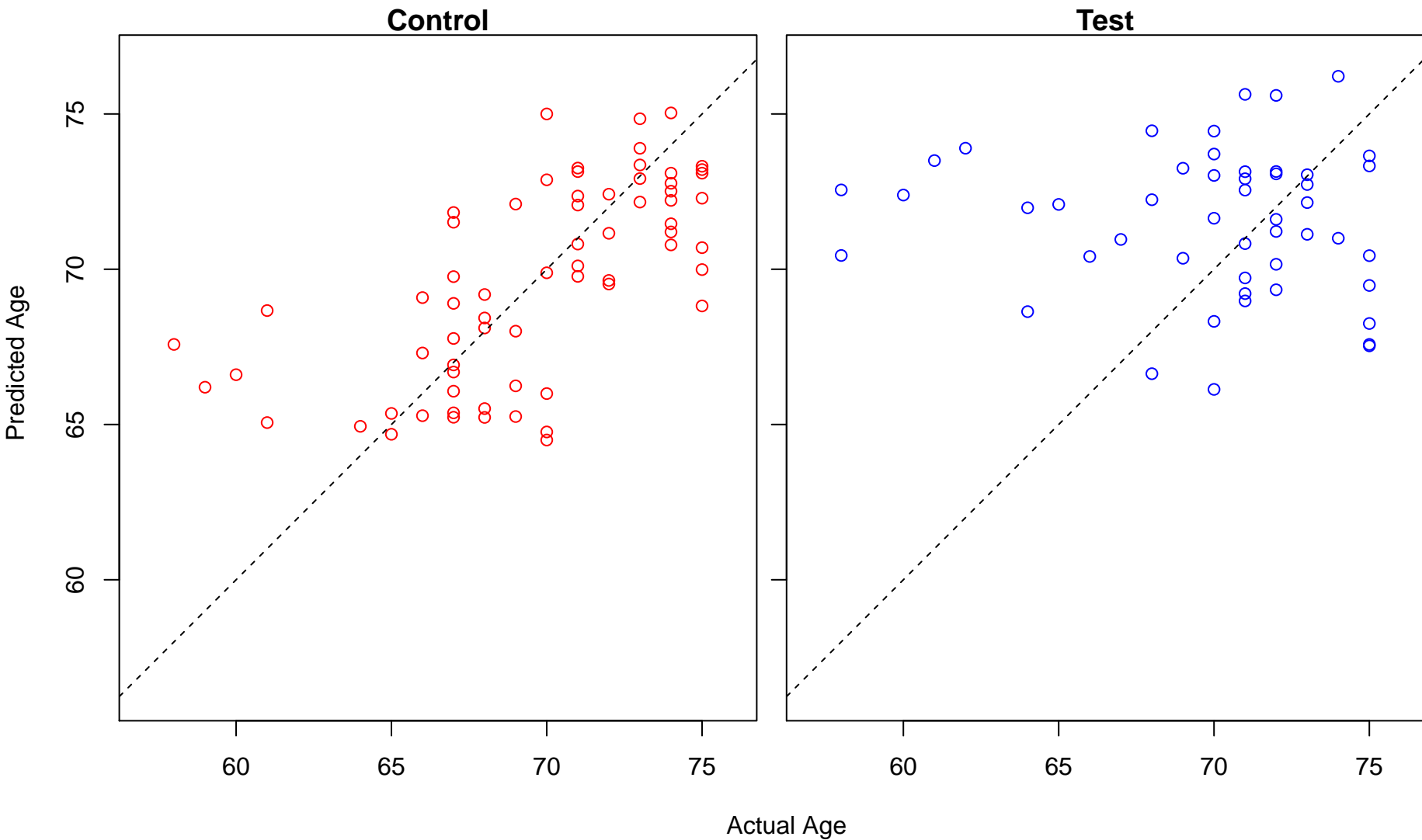


Test

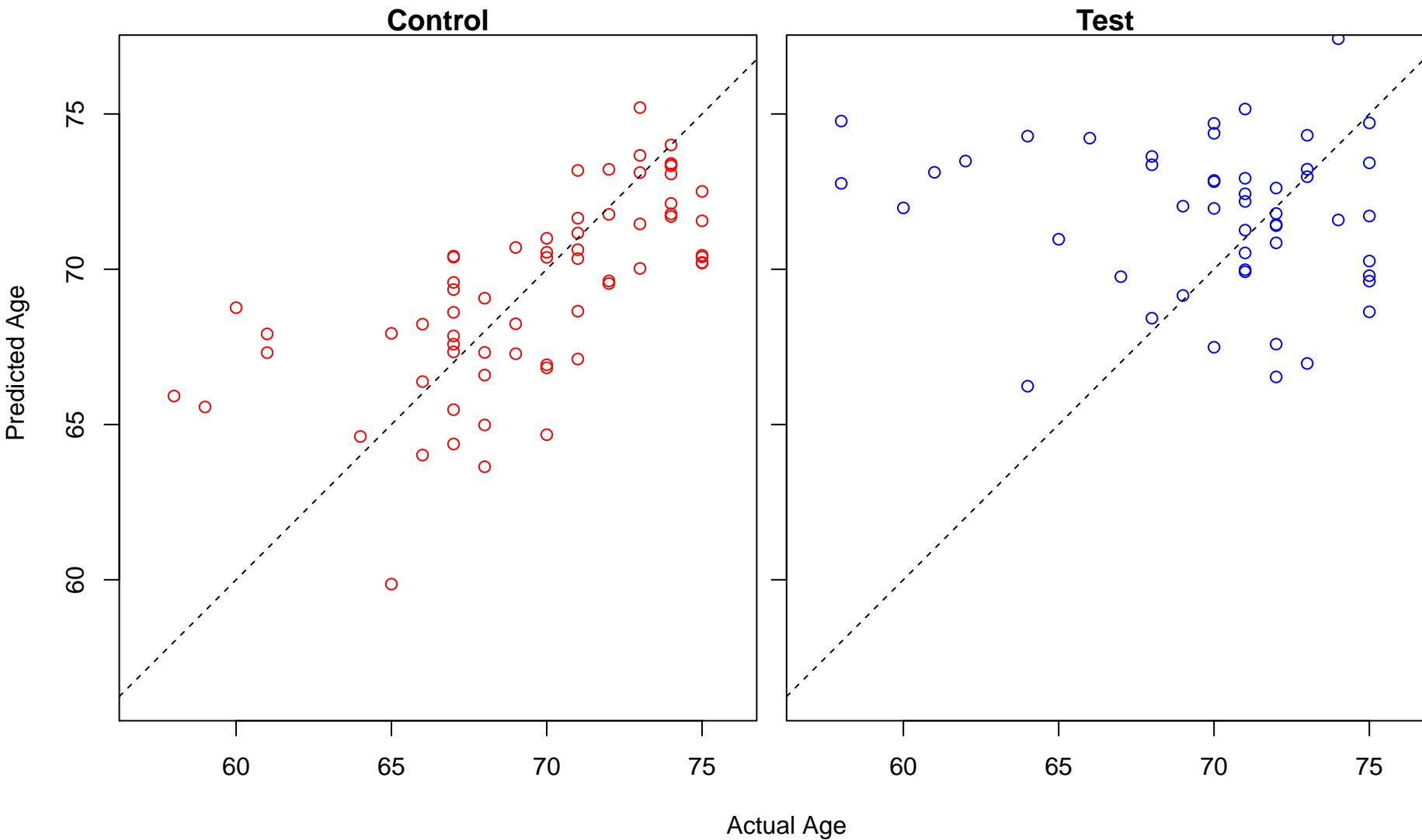


Actual Age

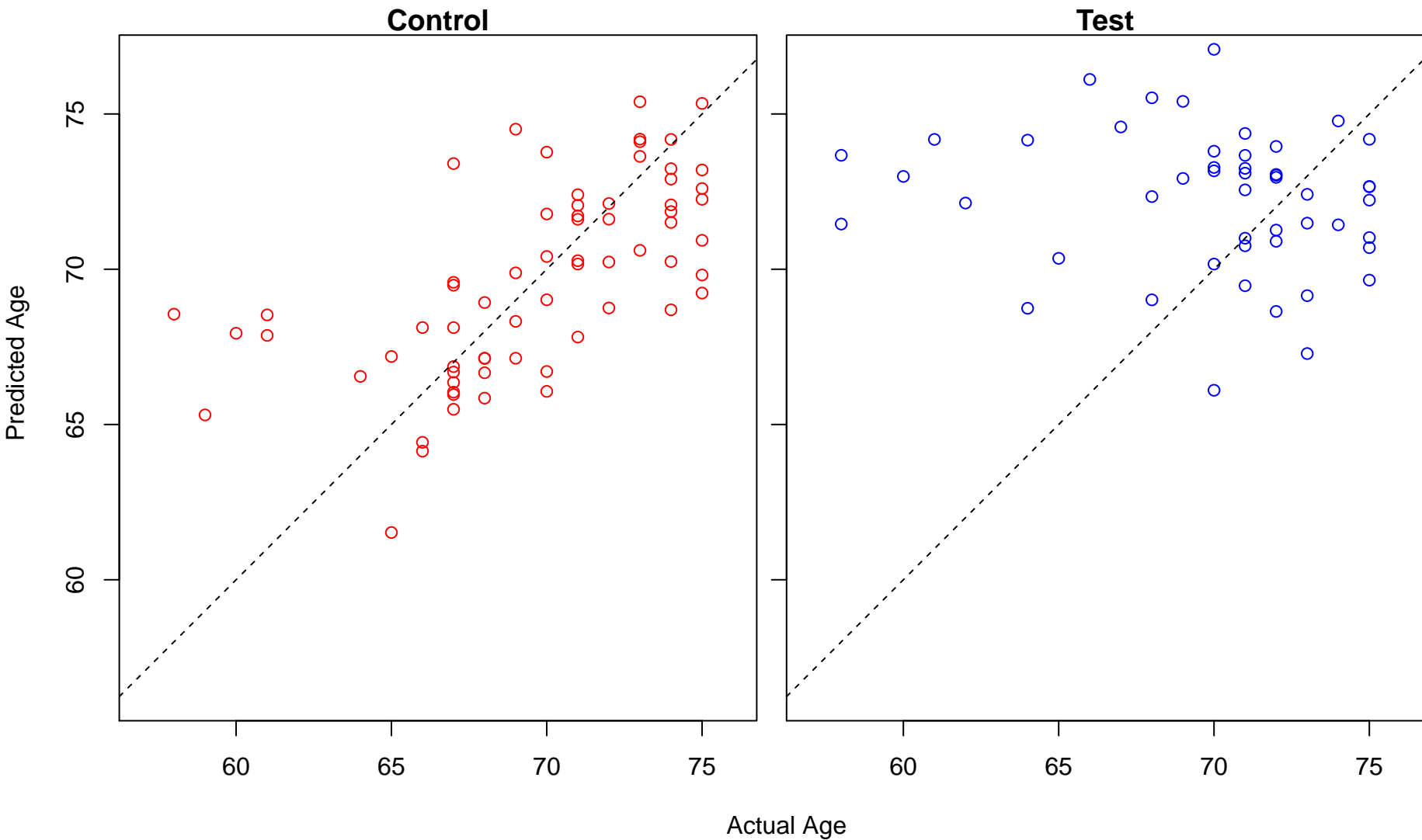
regulation of phospholipase activity (Score: 1.370908)



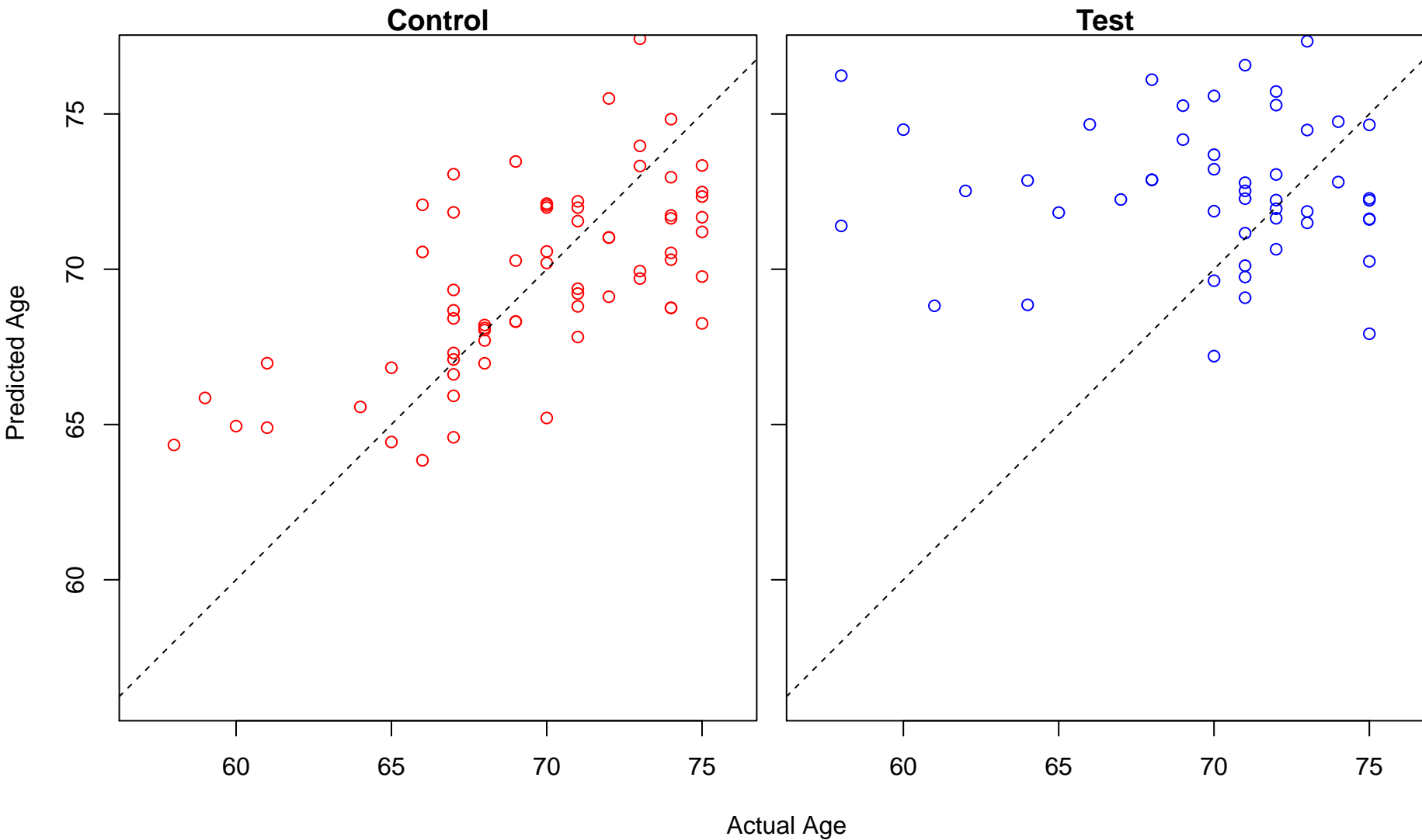
interferon- γ -mediated signaling pathway (Score: 1.370278)



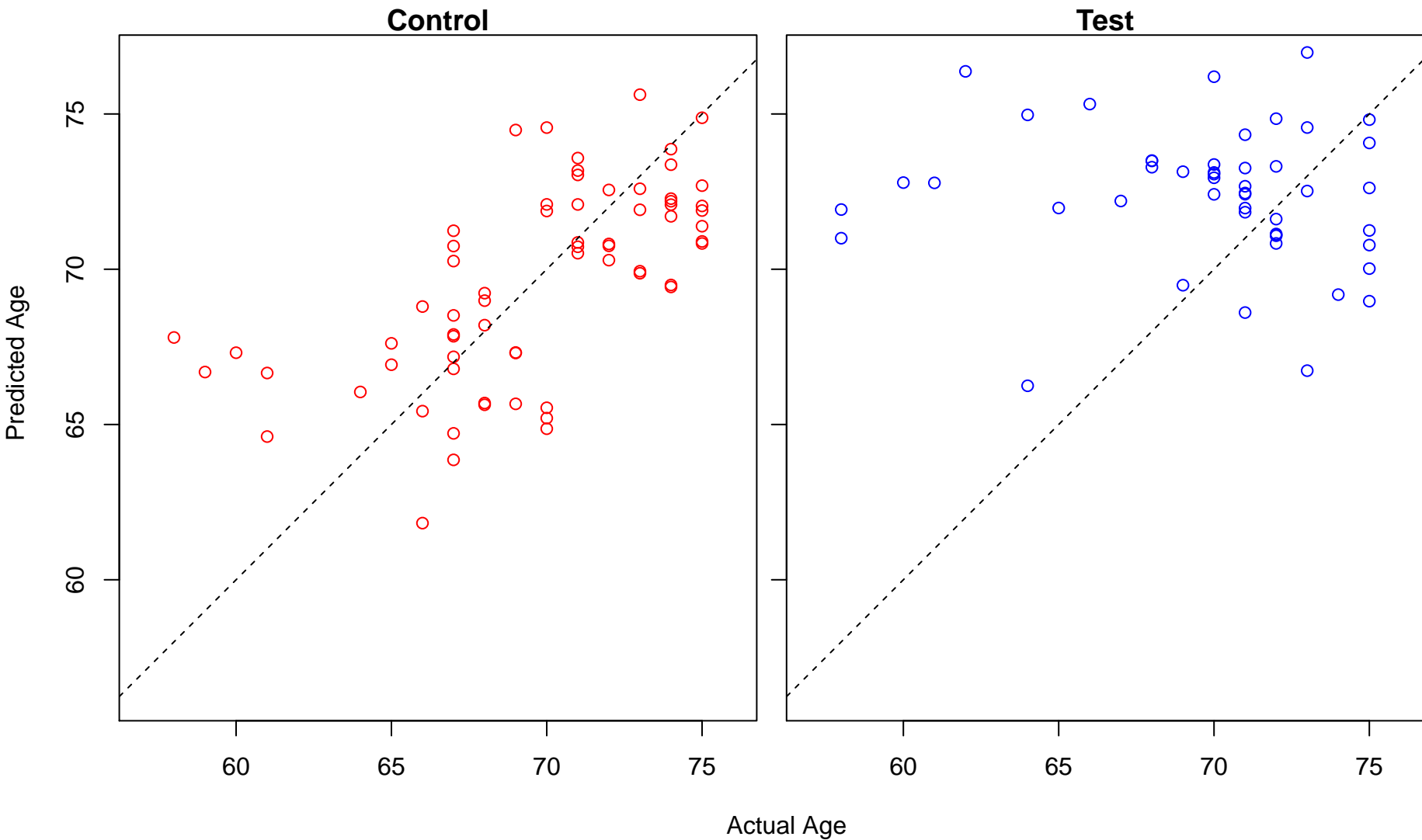
regulation of interleukin-2 production (Score: 1.370048)



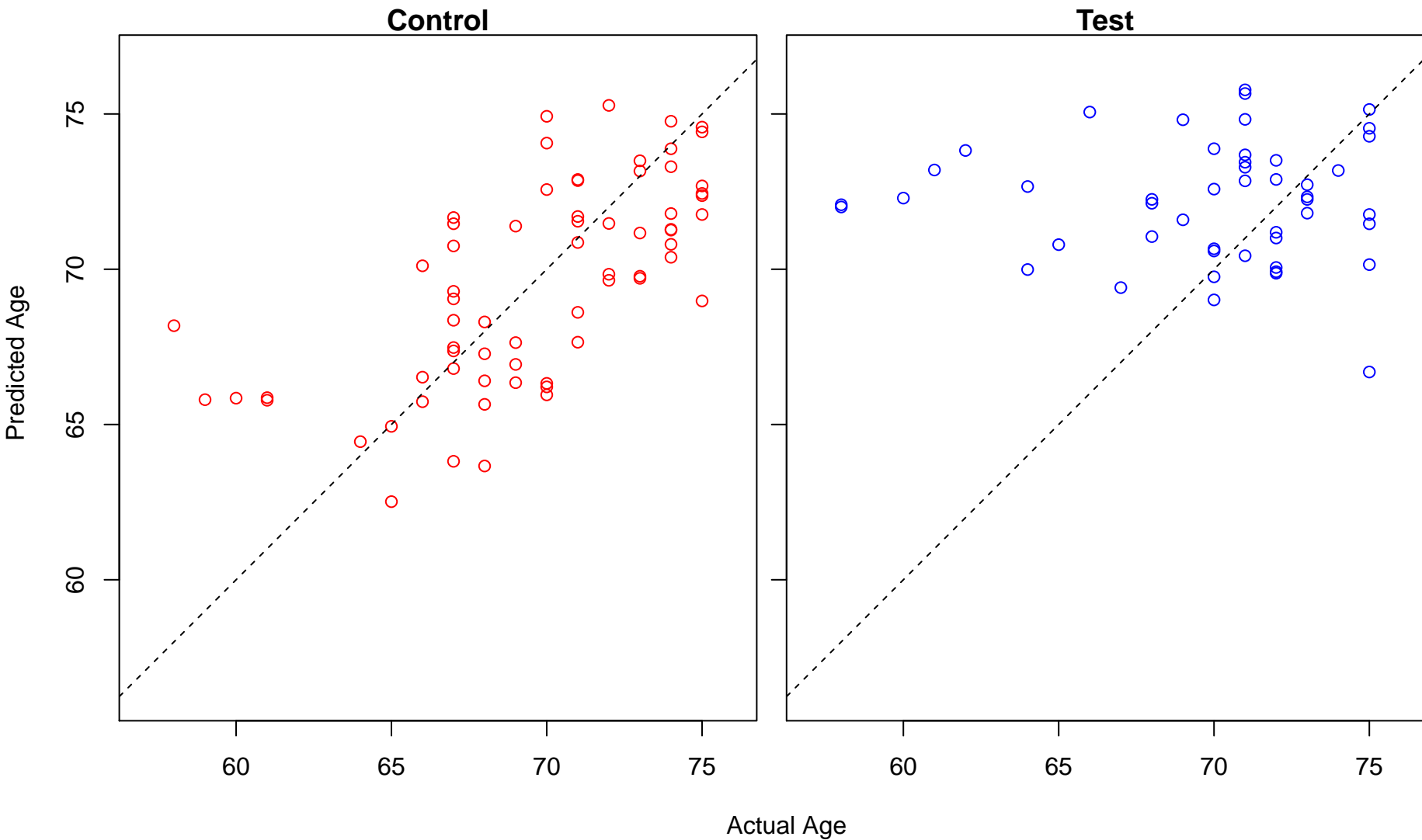
mitochondrial outer membrane permeabilization (Score: 1.369674)



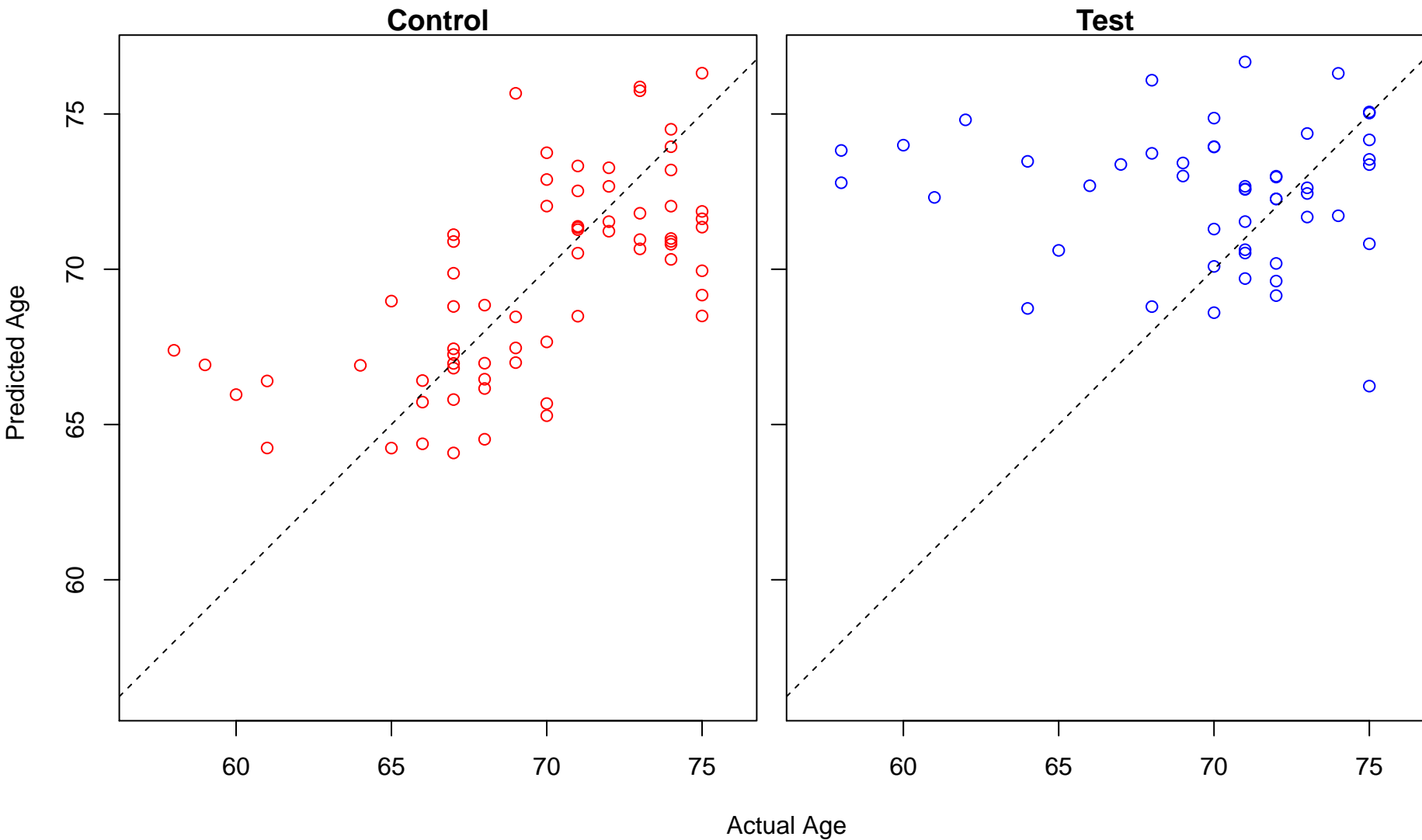
negative regulation of cellular response to growth factor stimulus (Score: 1.369607)



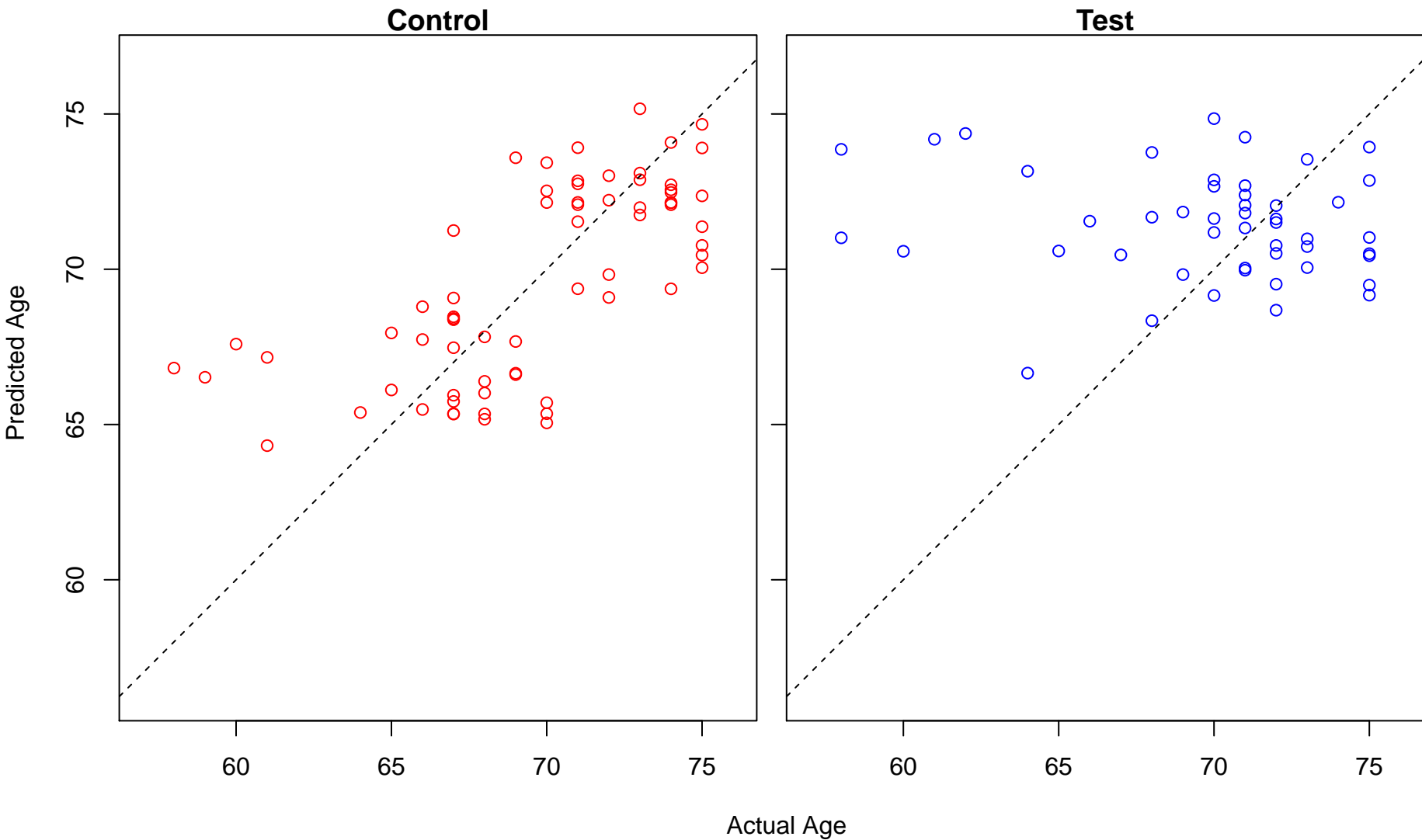
embryonic morphogenesis (Score: 1.369450)



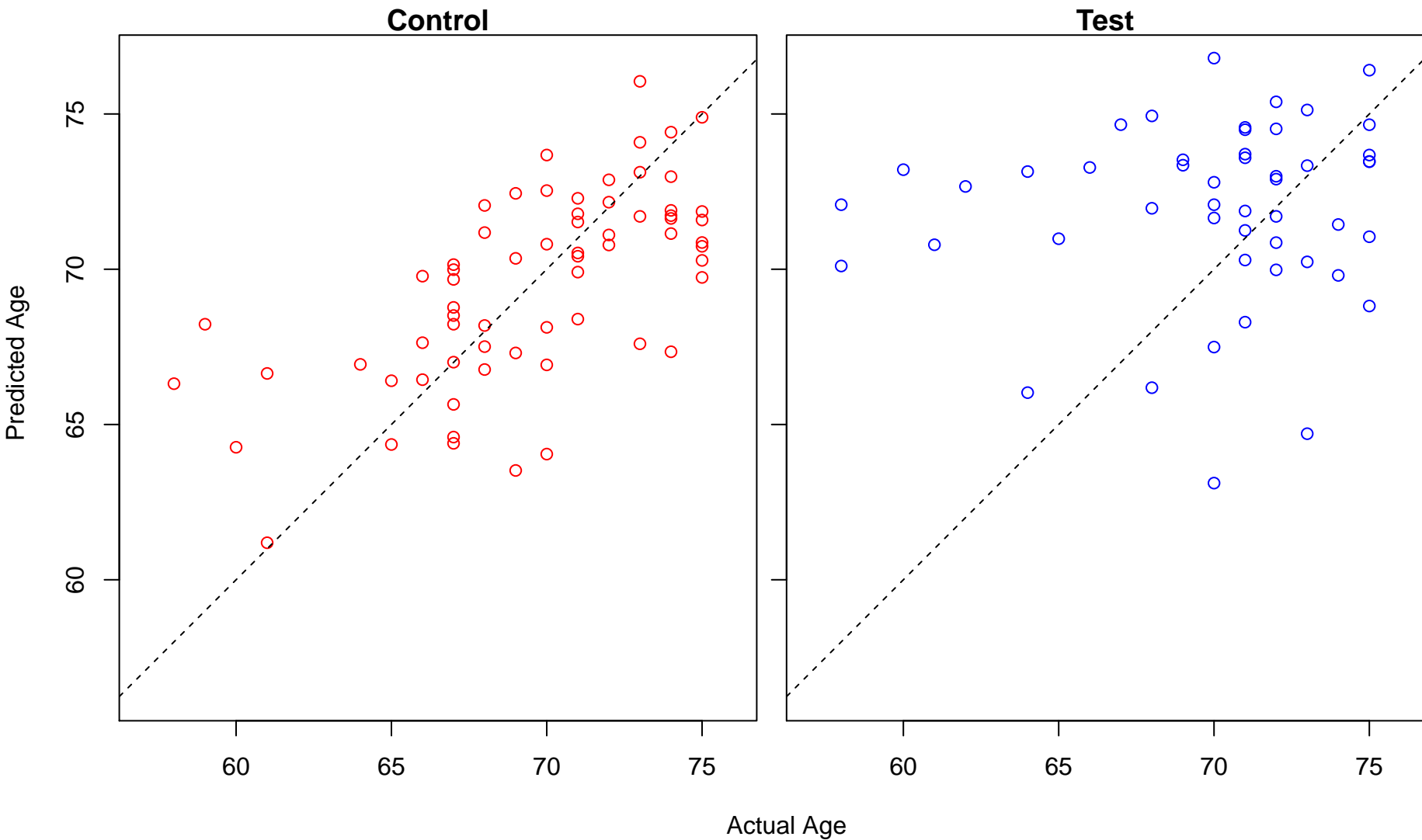
growth (Score: 1.369202)



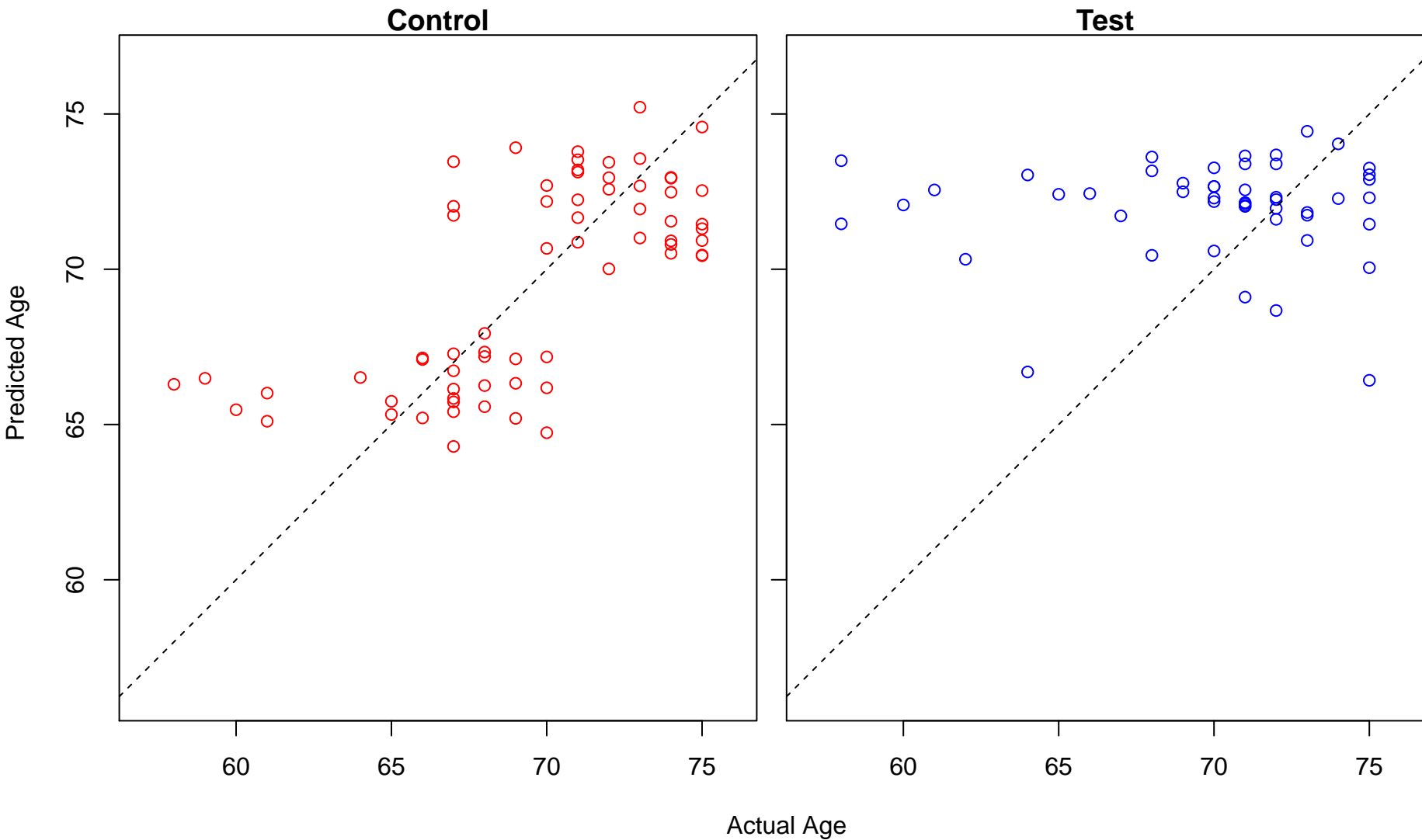
small molecule catabolic process (Score: 1.368168)



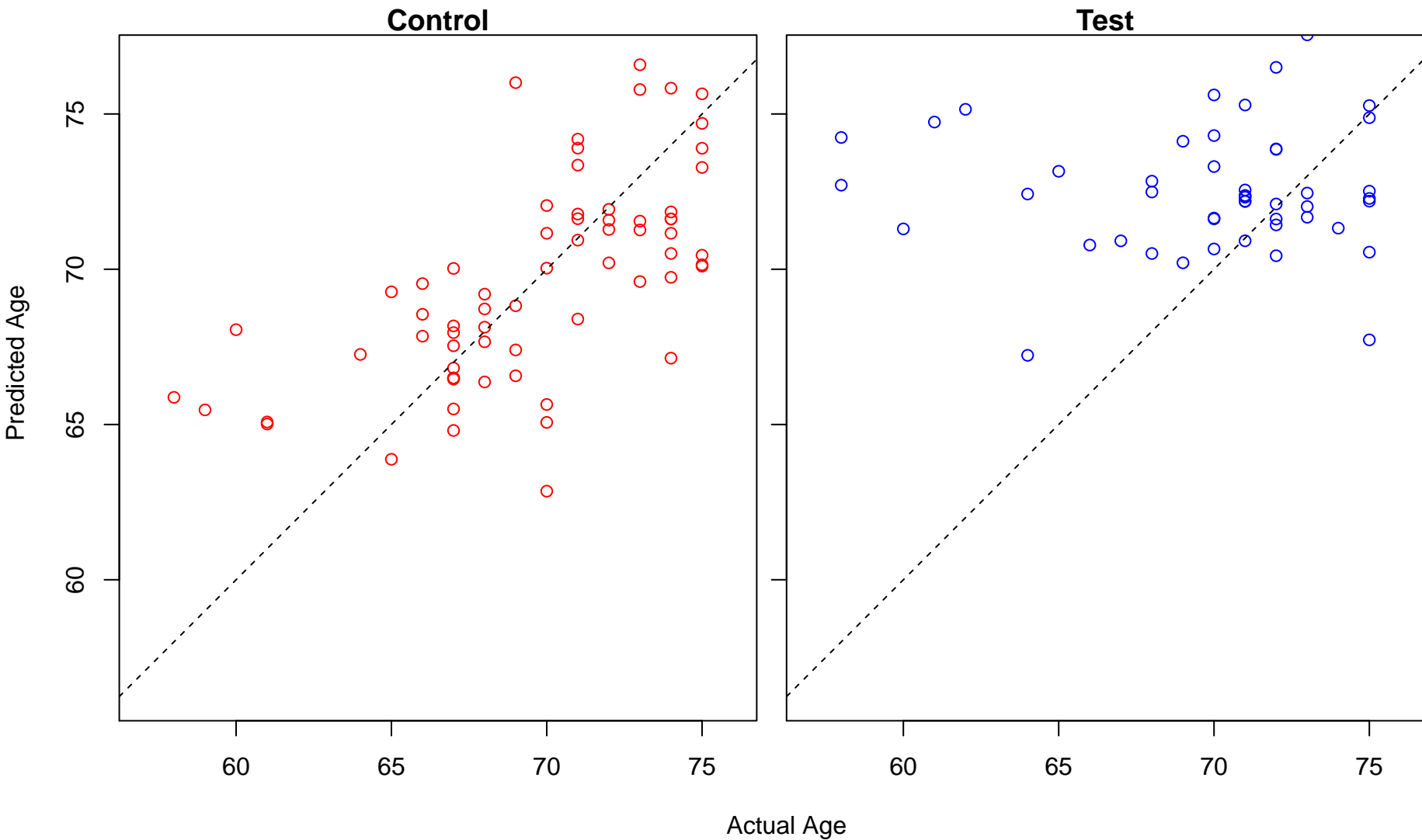
mRNA transcription from RNA polymerase II promoter (Score: 1.367652)



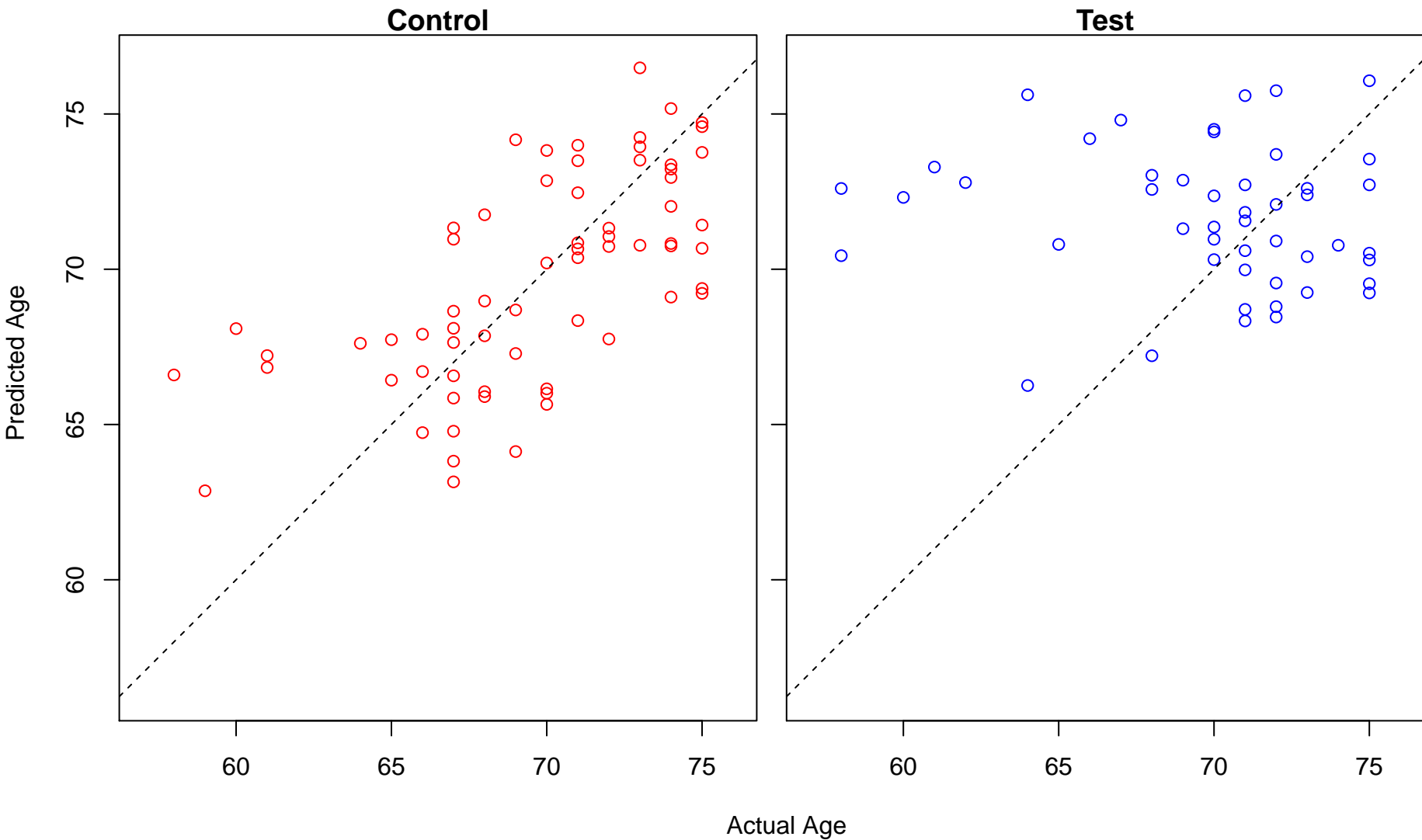
rRNA processing (Score: 1.367433)



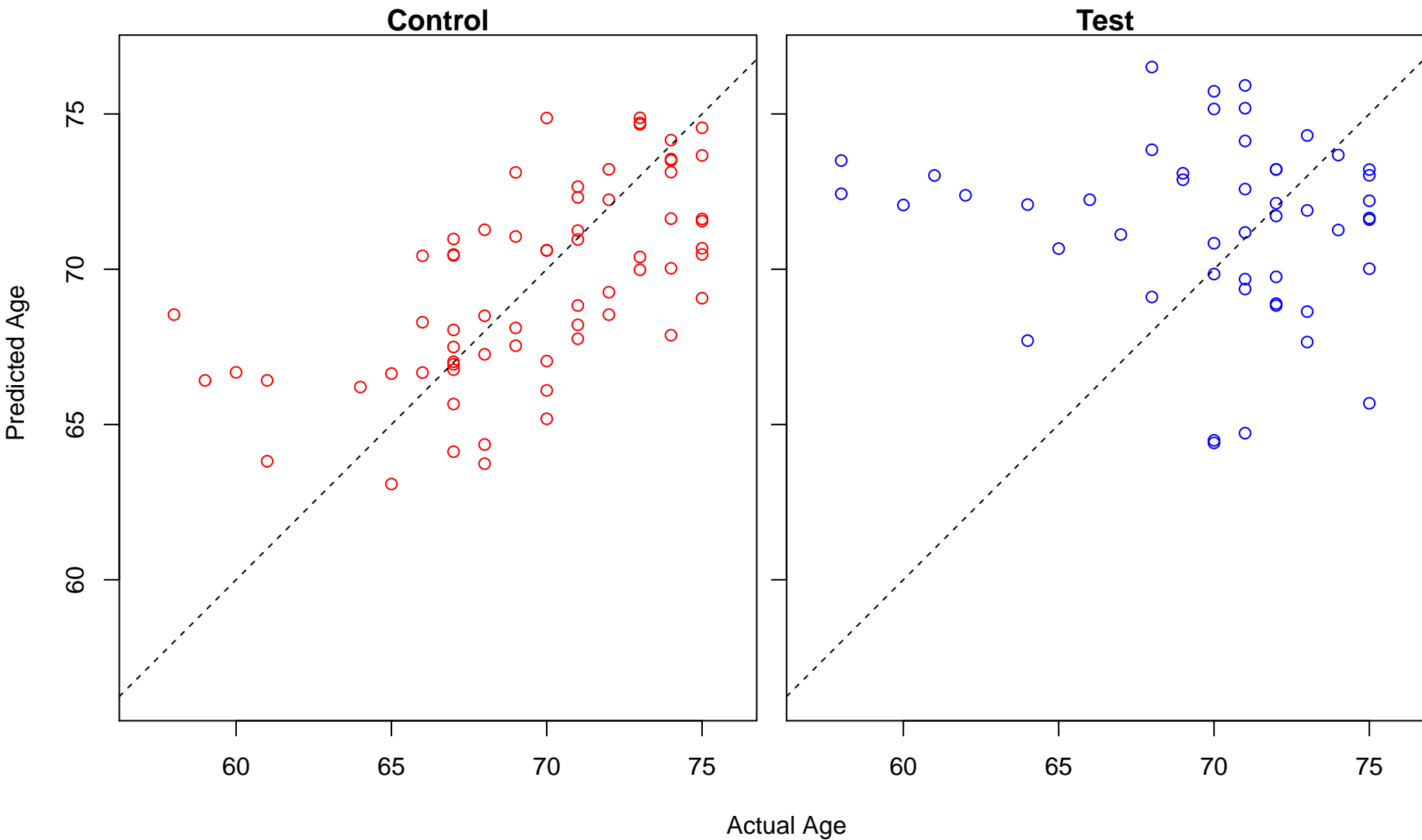
protein refolding (Score: 1.367407)



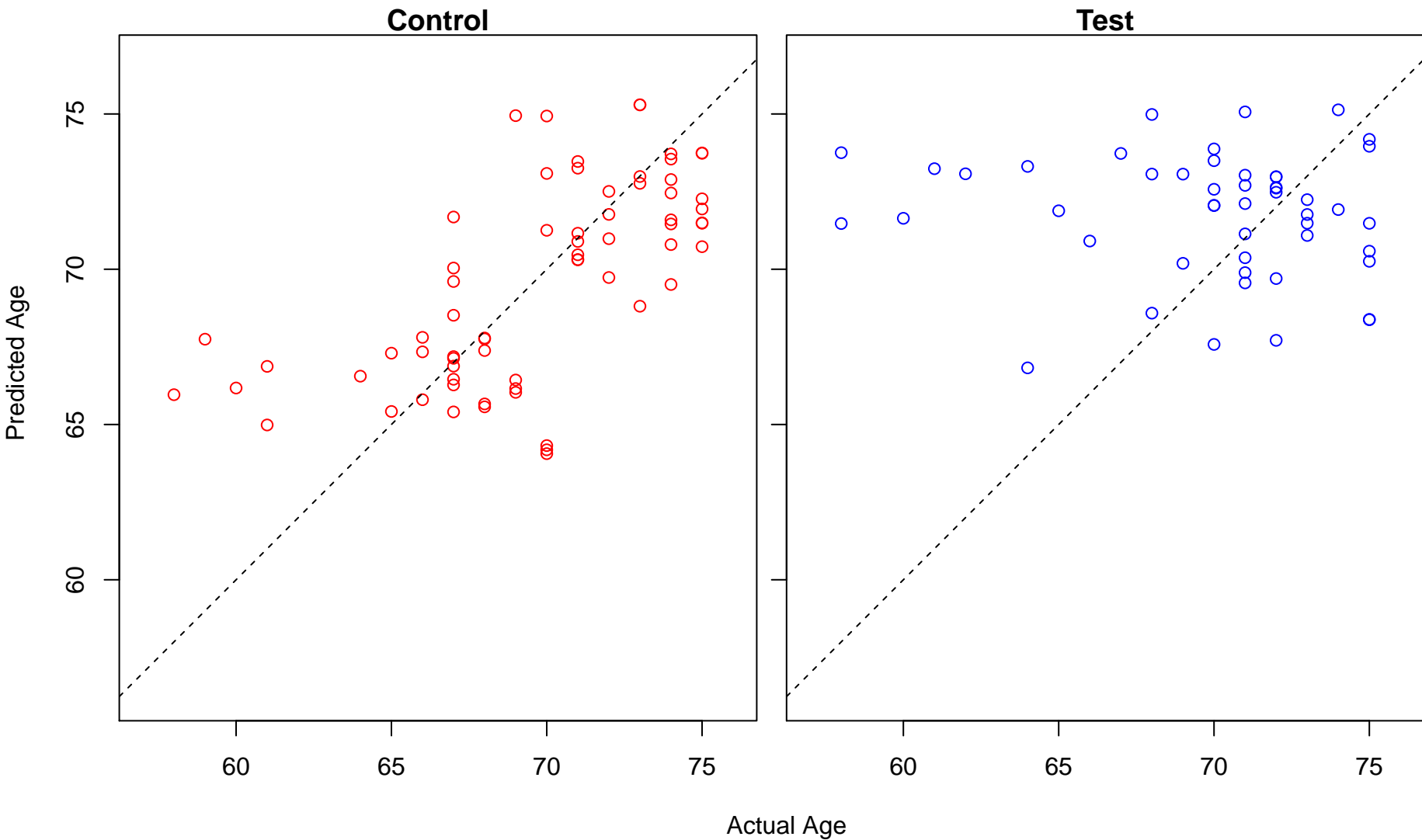
purine nucleotide catabolic process (Score: 1.366949)



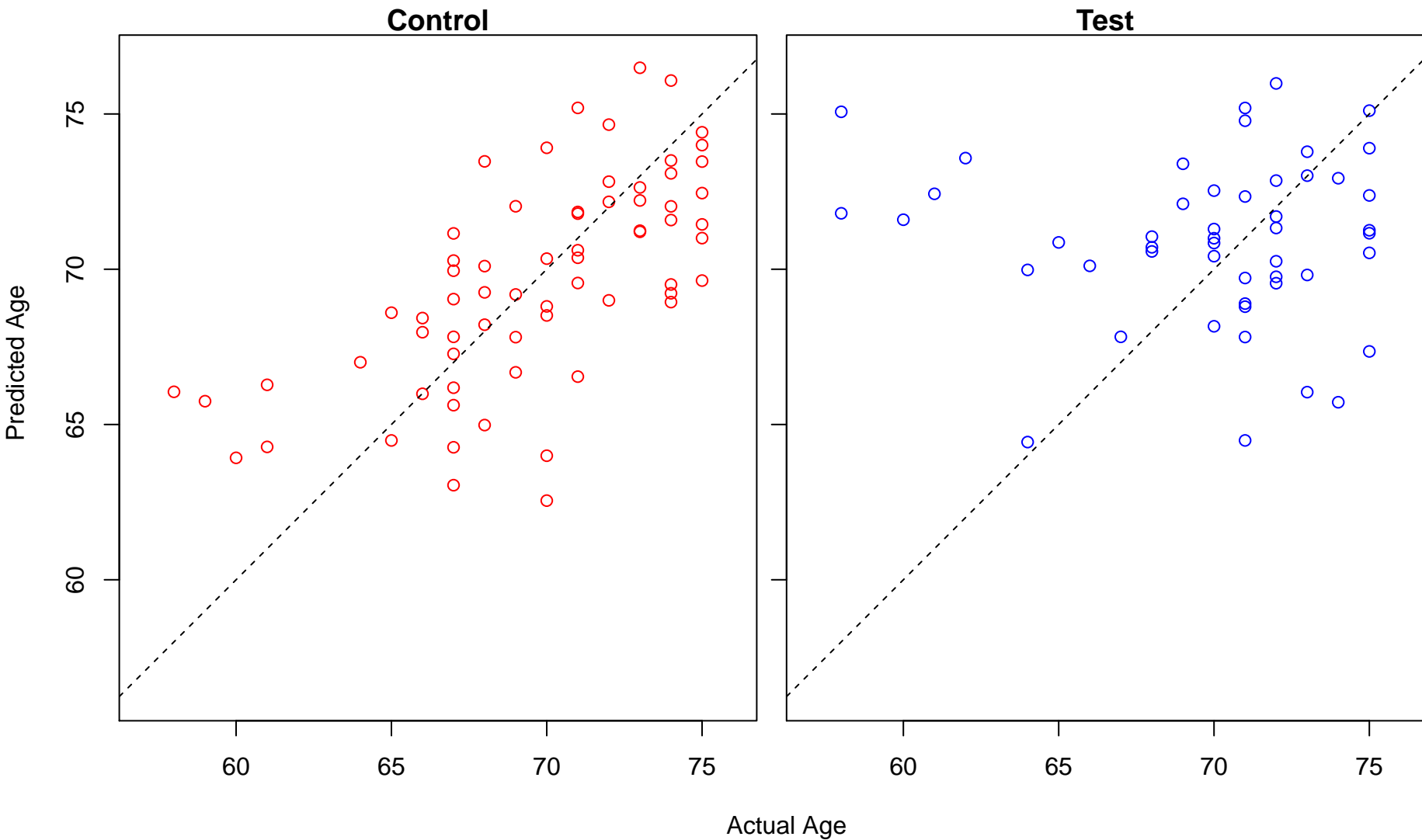
phosphatidylethanolamine metabolic process (Score: 1.366922)



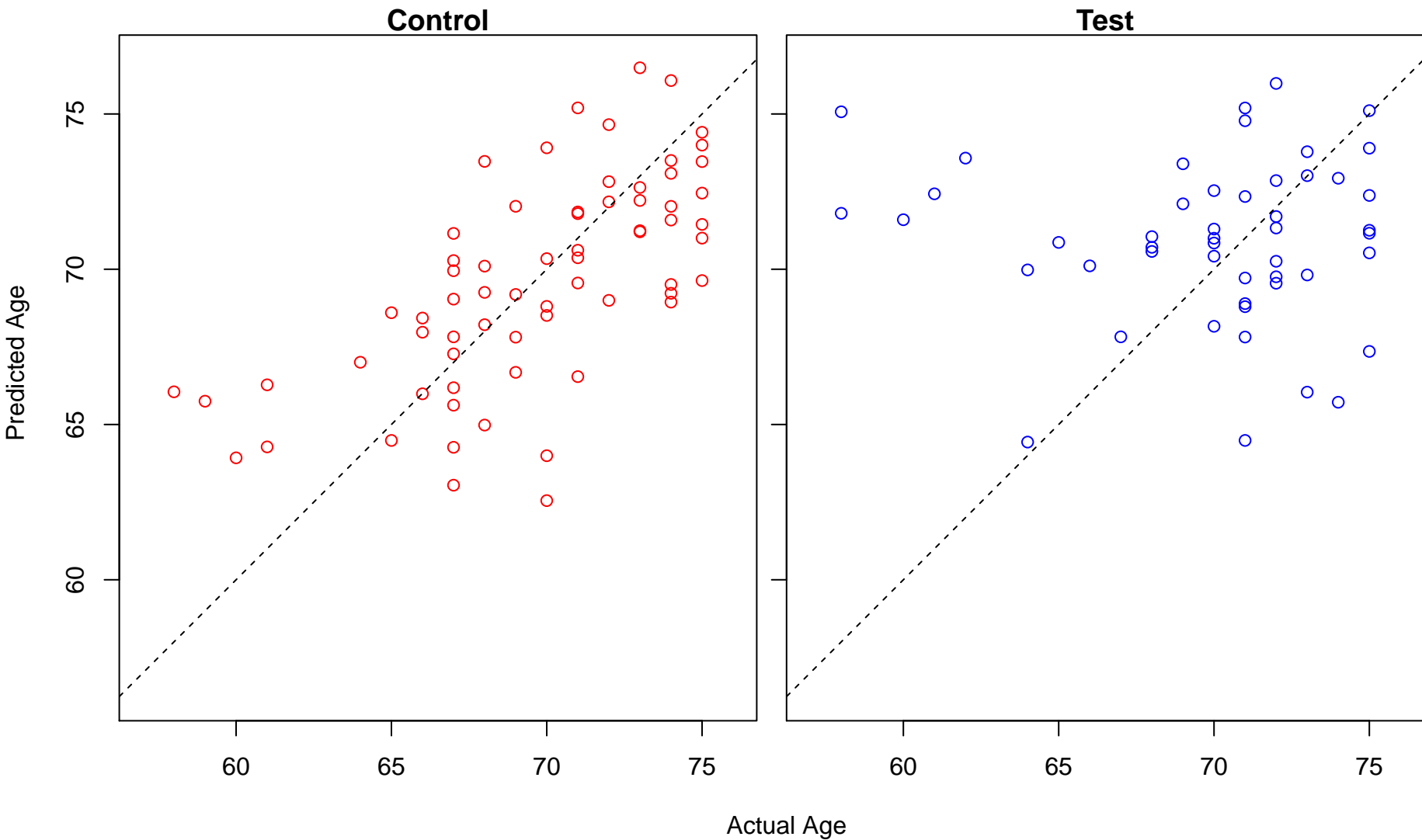
negative regulation of chromosome organization (Score: 1.366335)



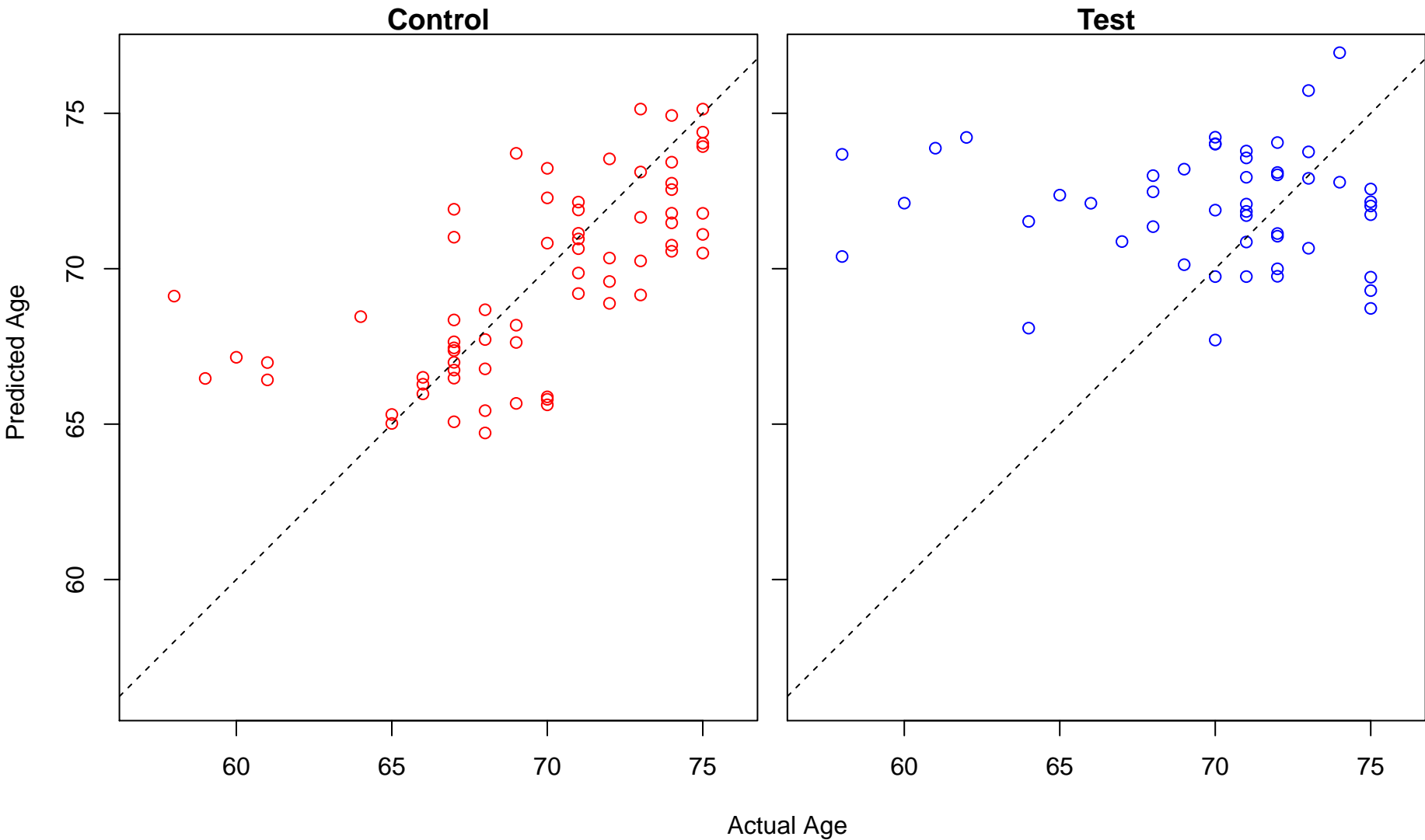
histone H4-K5 acetylation (Score: 1.366167)



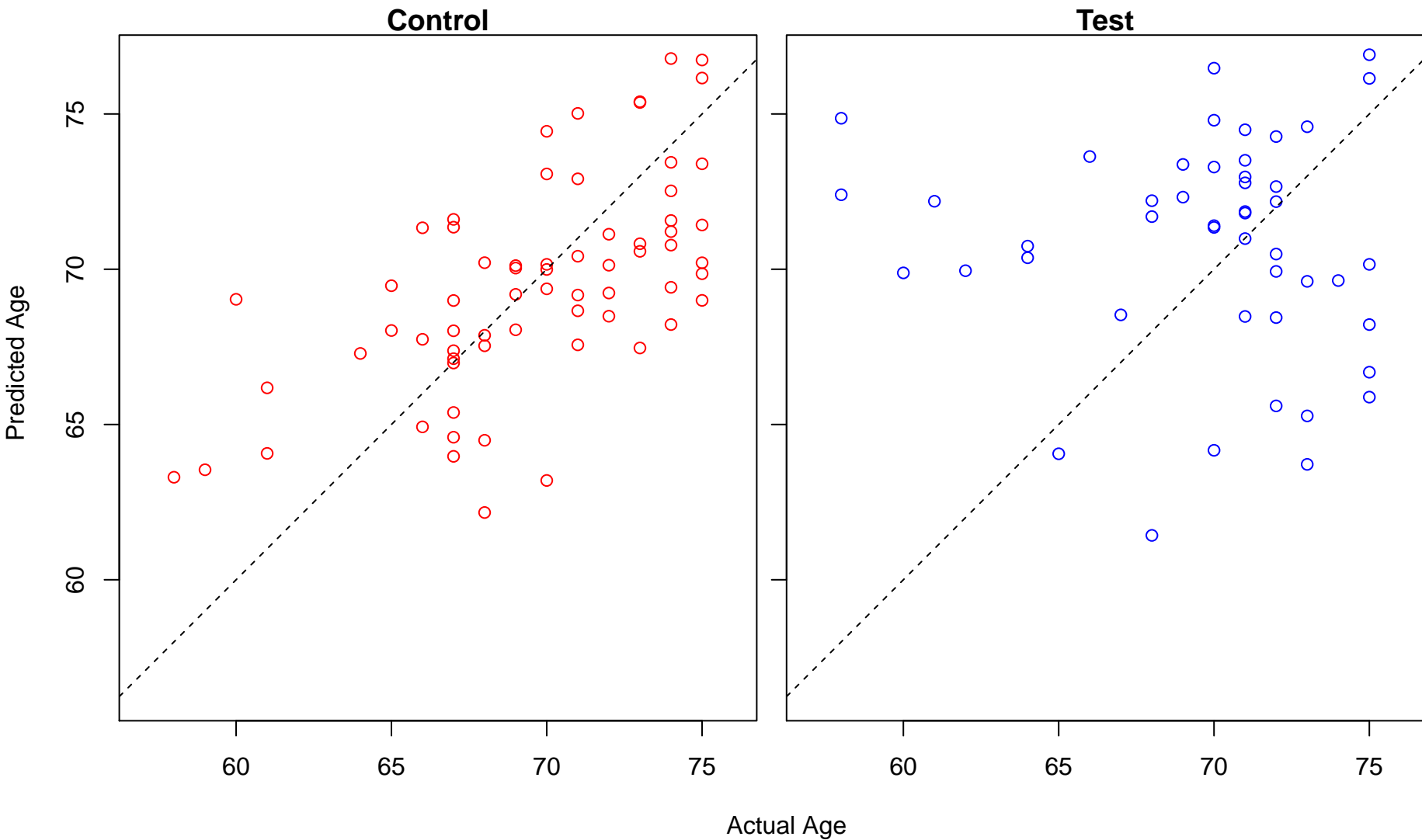
histone H4-K8 acetylation (Score: 1.366167)



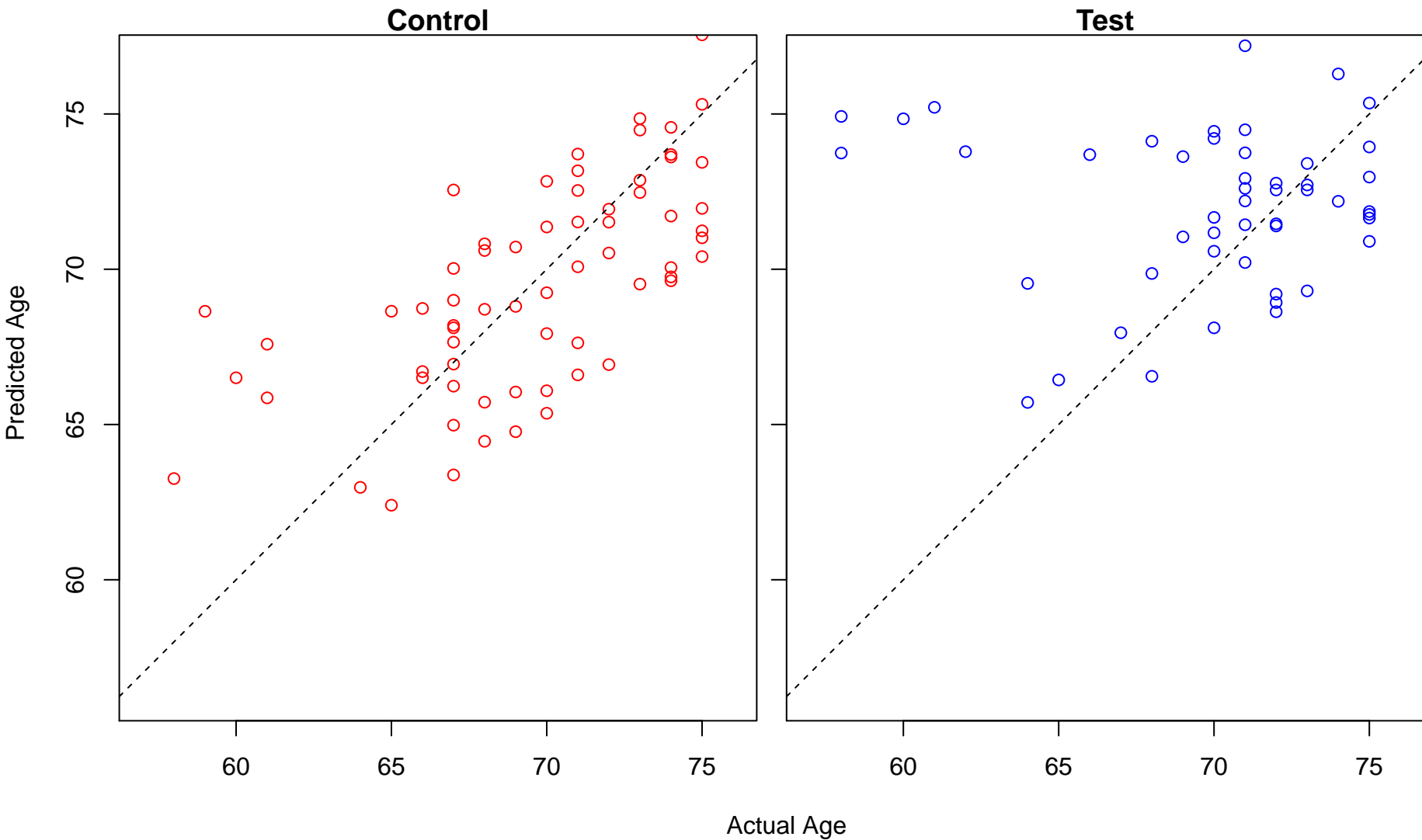
regulation of oxidative stress-induced intrinsic apoptotic signaling pathway (Score: 1.364132)



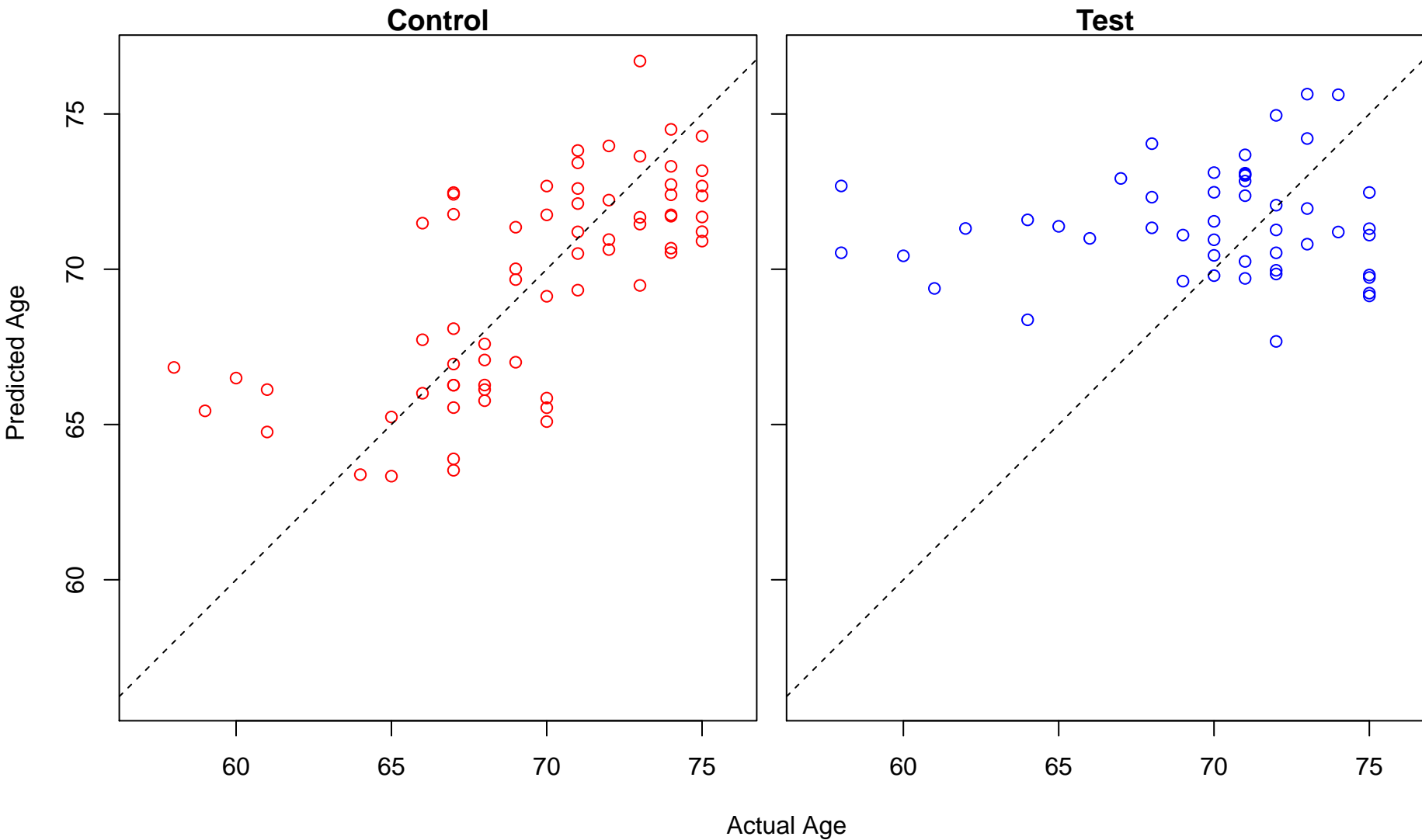
negative regulation of cell killing (Score: 1.363849)



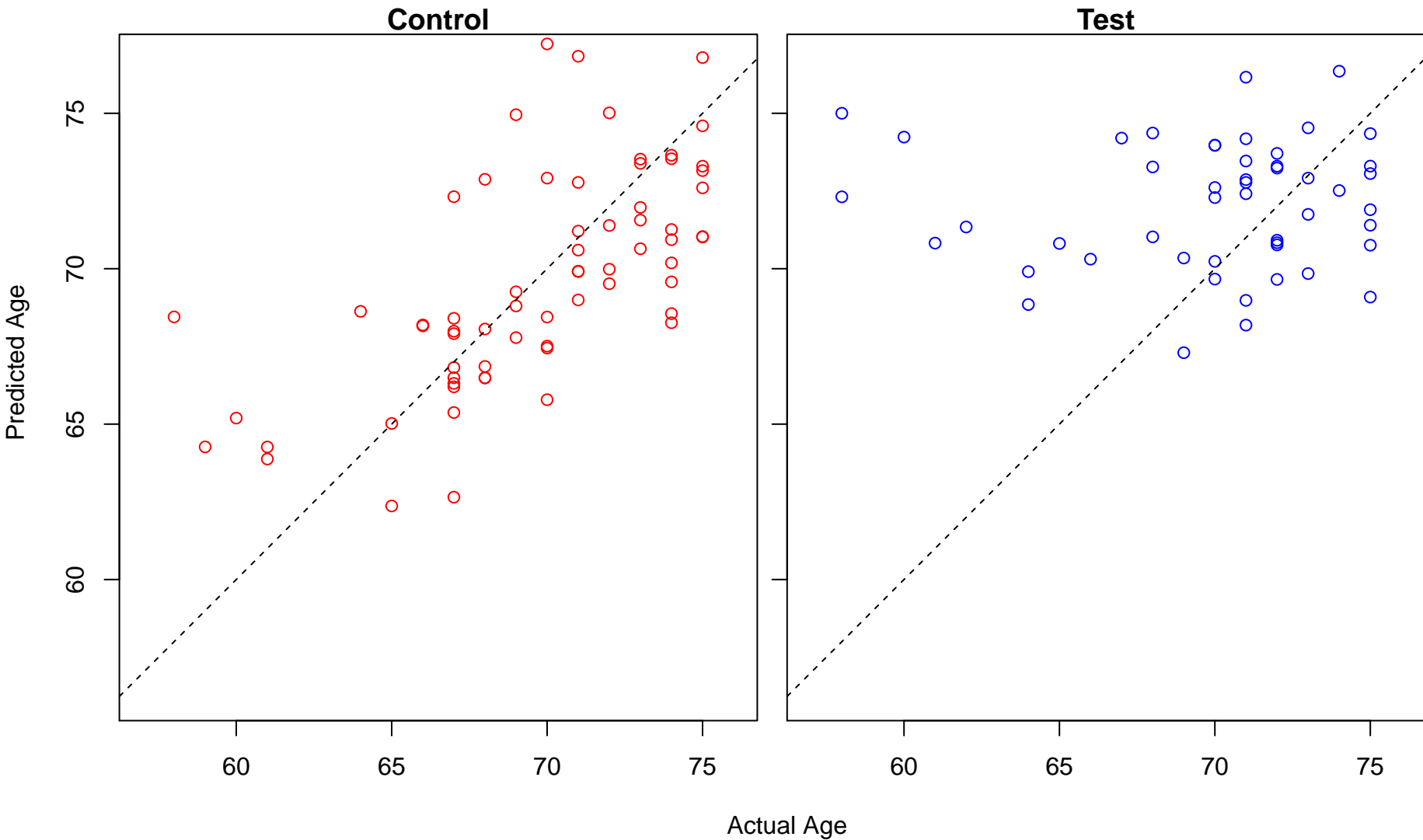
modulation of synaptic transmission (Score: 1.363847)



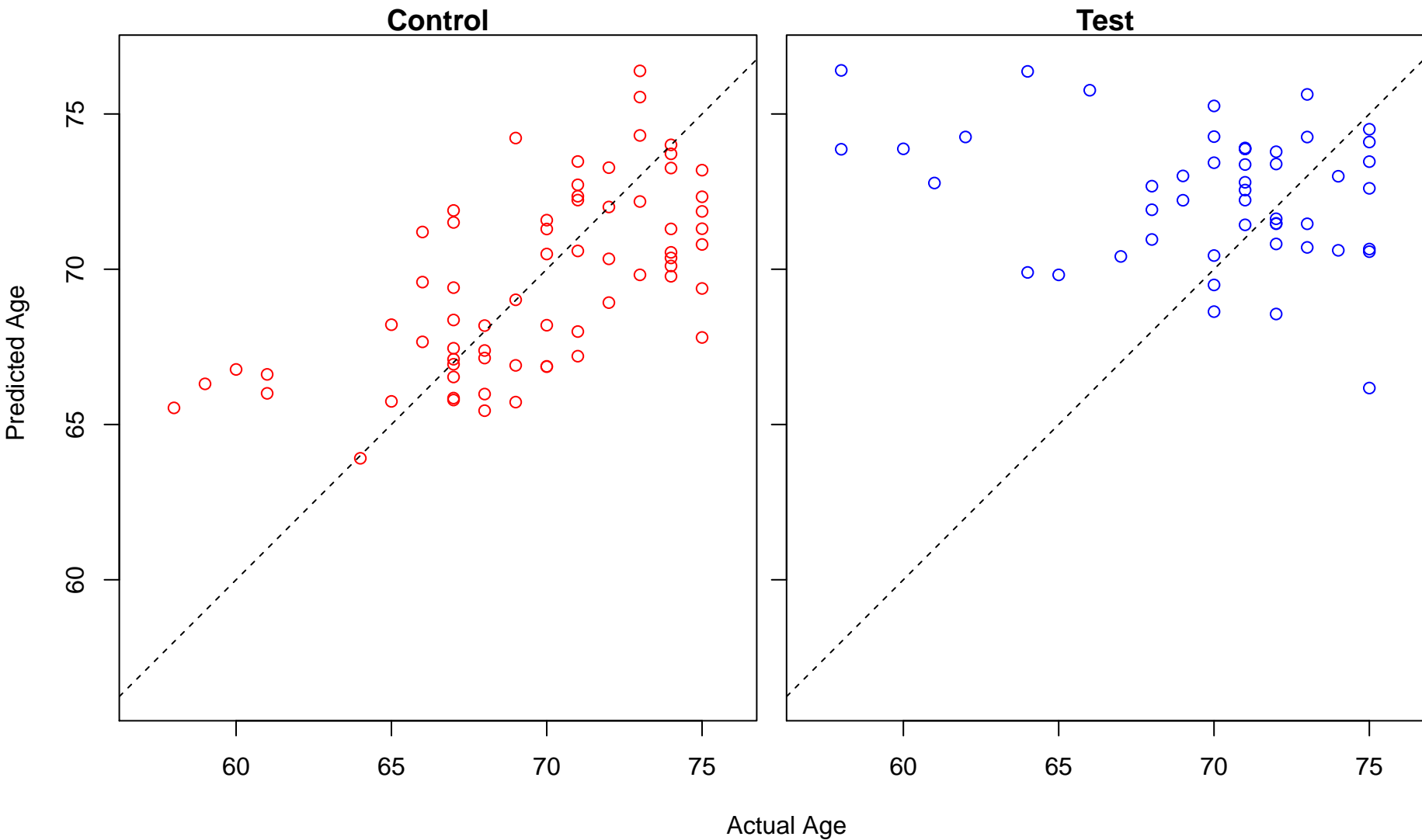
regulation of mRNA processing (Score: 1.362907)



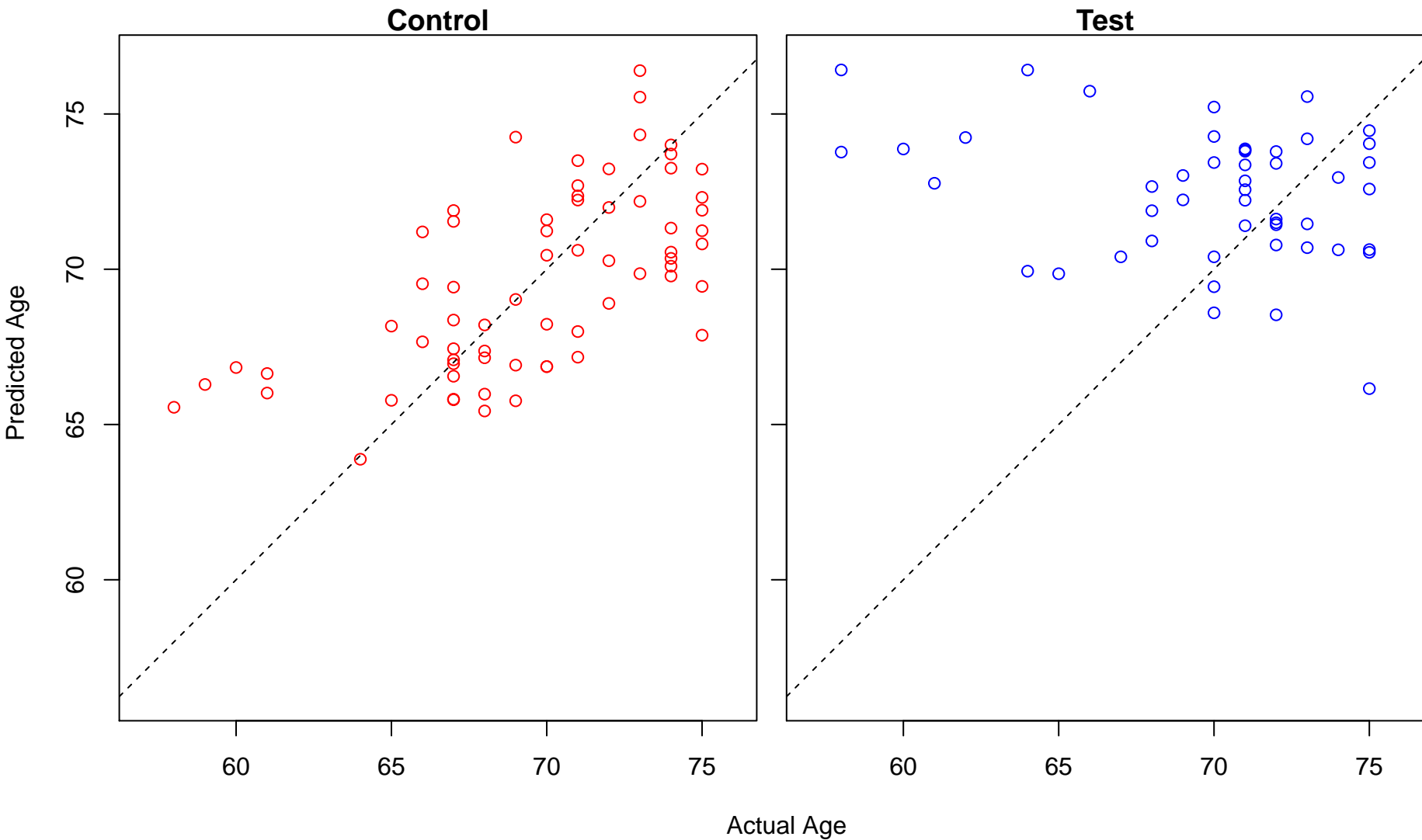
glycosphingolipid metabolic process (Score: 1.362262)



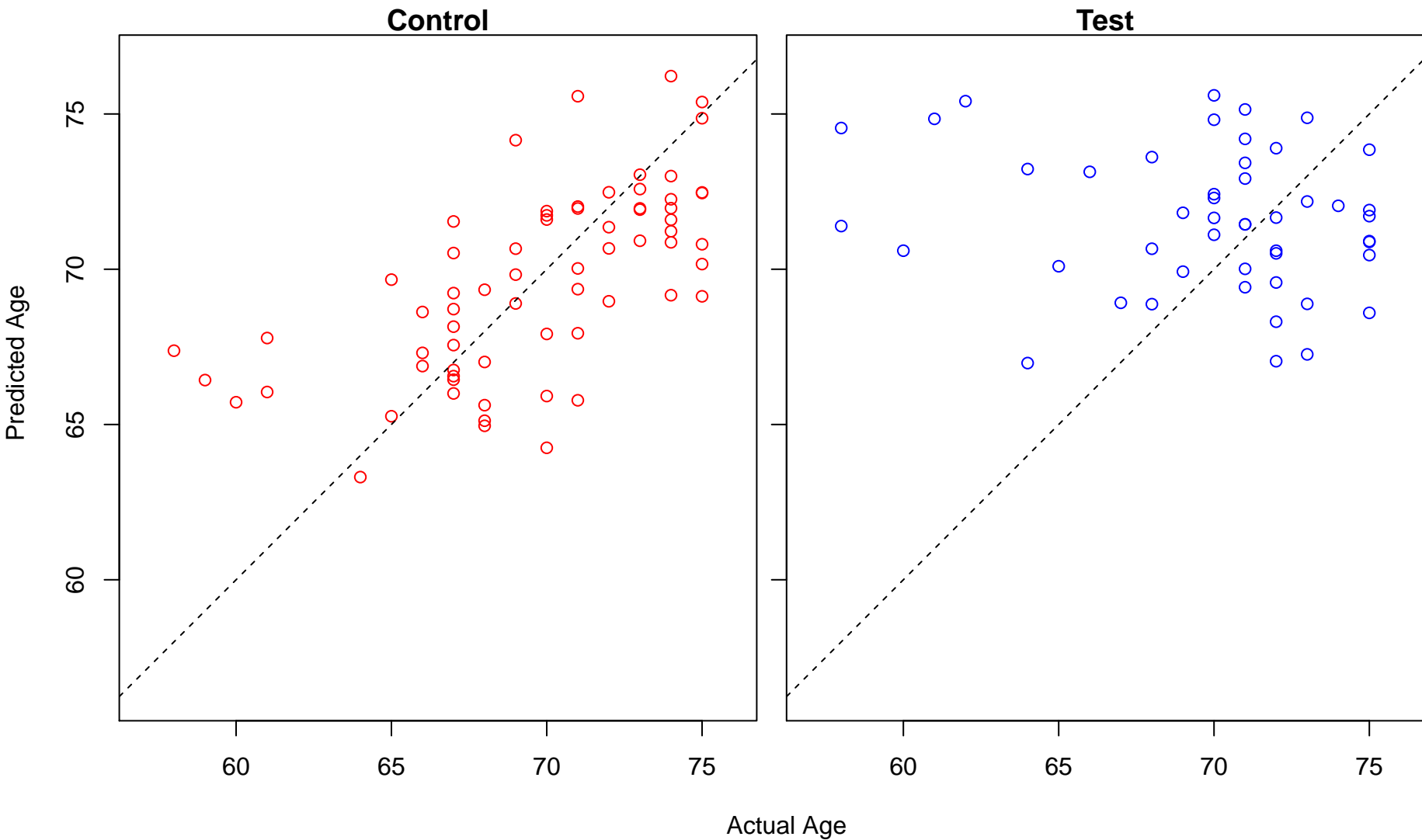
chloride transport (Score: 1.362044)



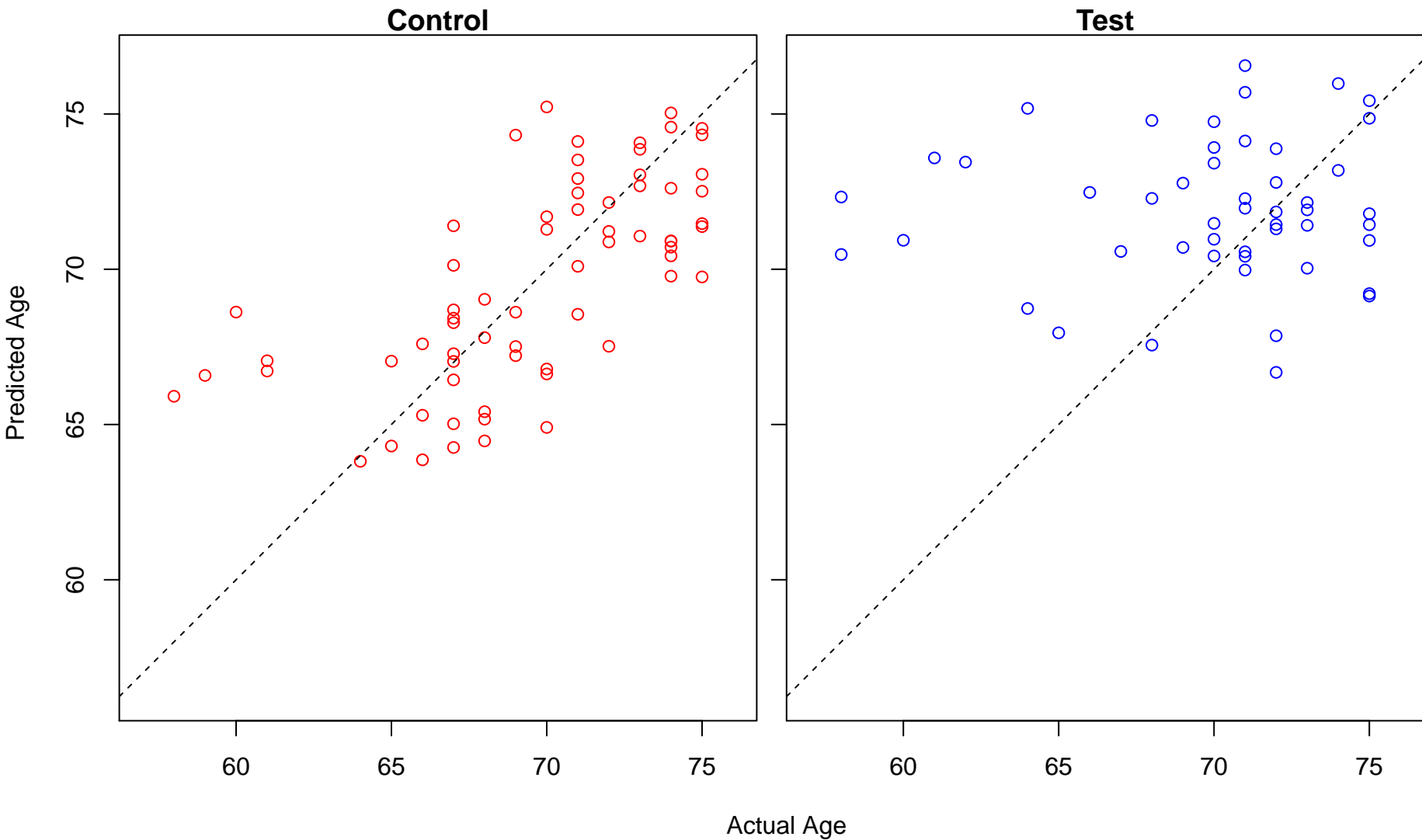
chloride transmembrane transport (Score: 1.361868)



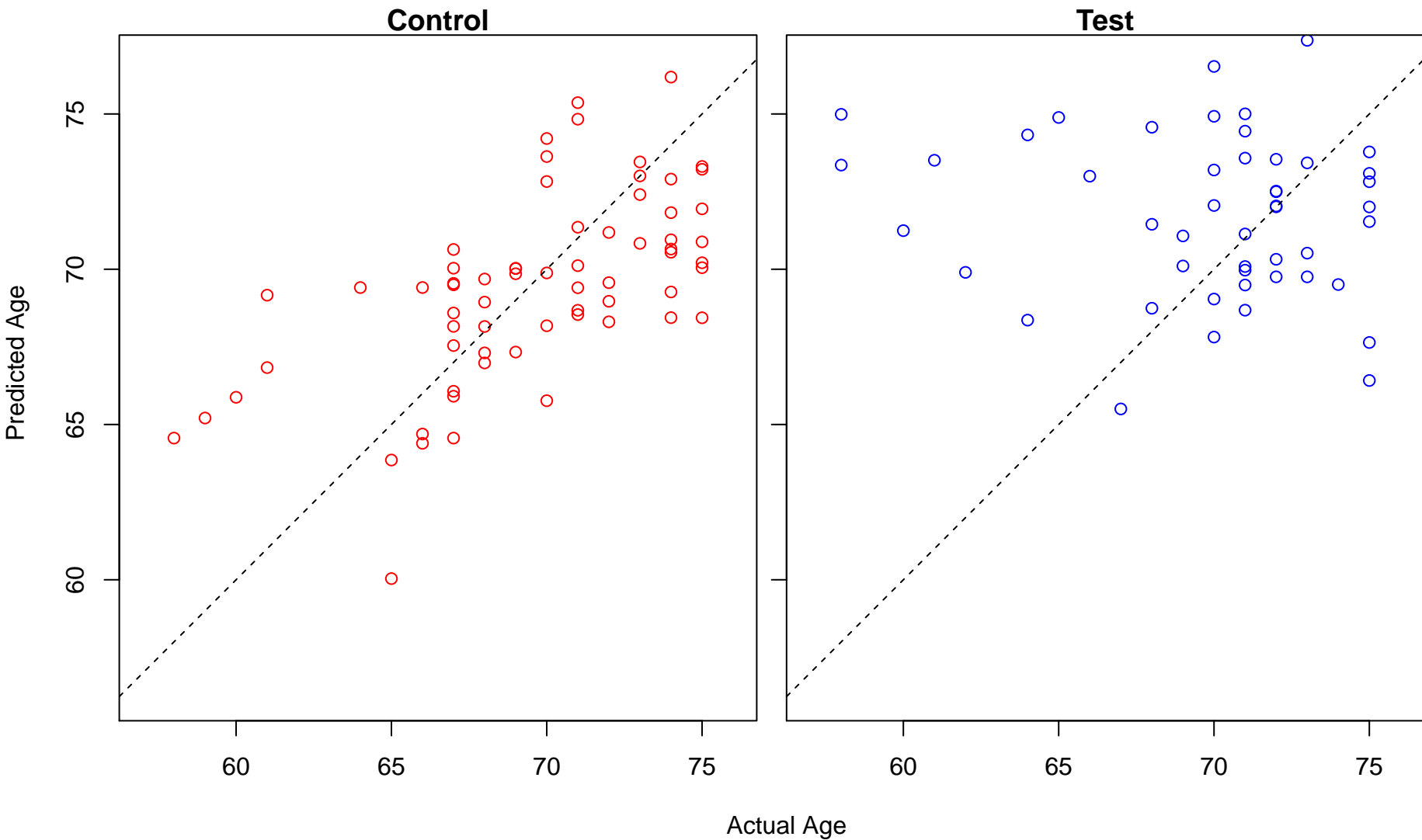
hexose metabolic process (Score: 1.360514)



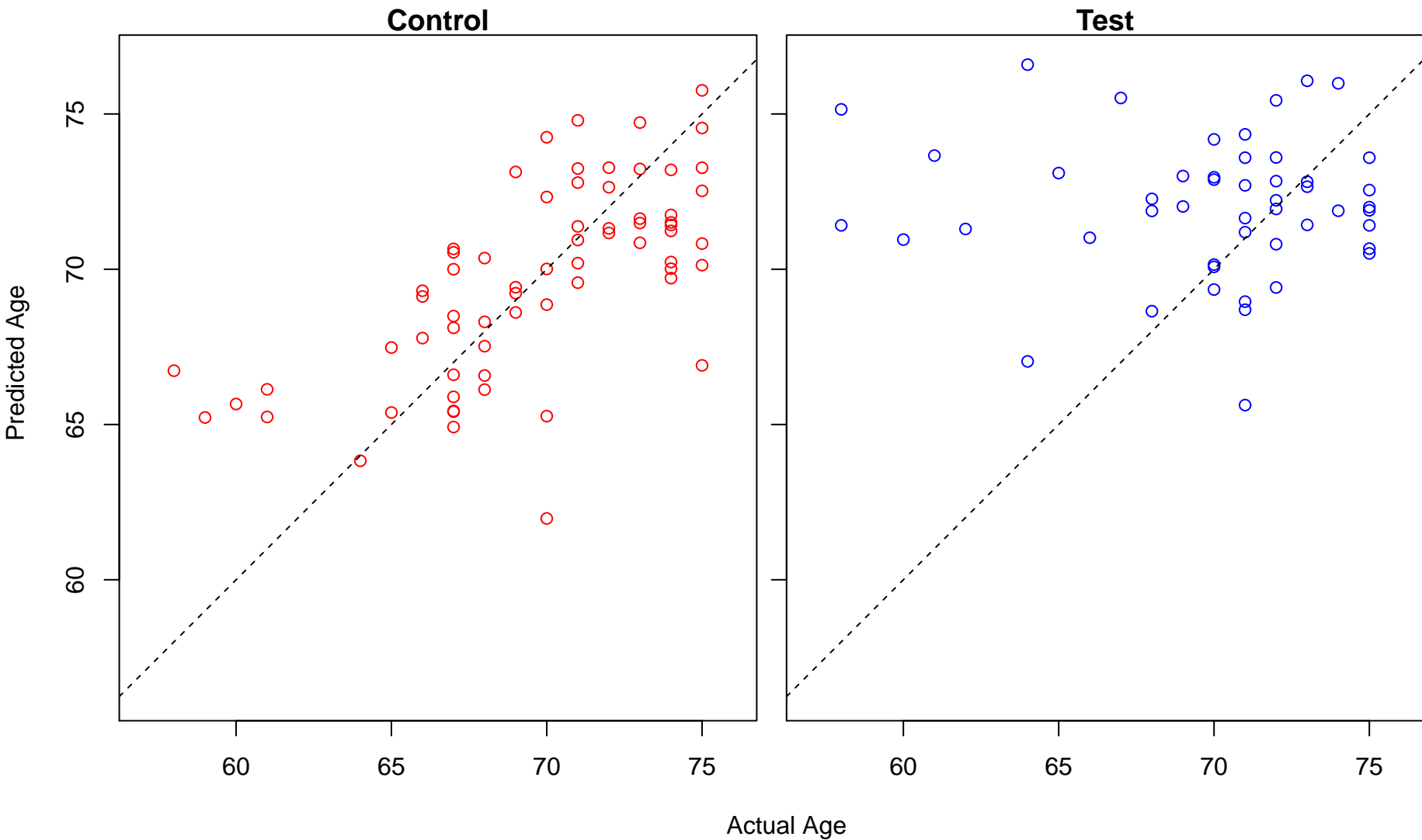
skeletal muscle organ development (Score: 1.360370)



regulation of neutrophil chemotaxis (Score: 1.359507)

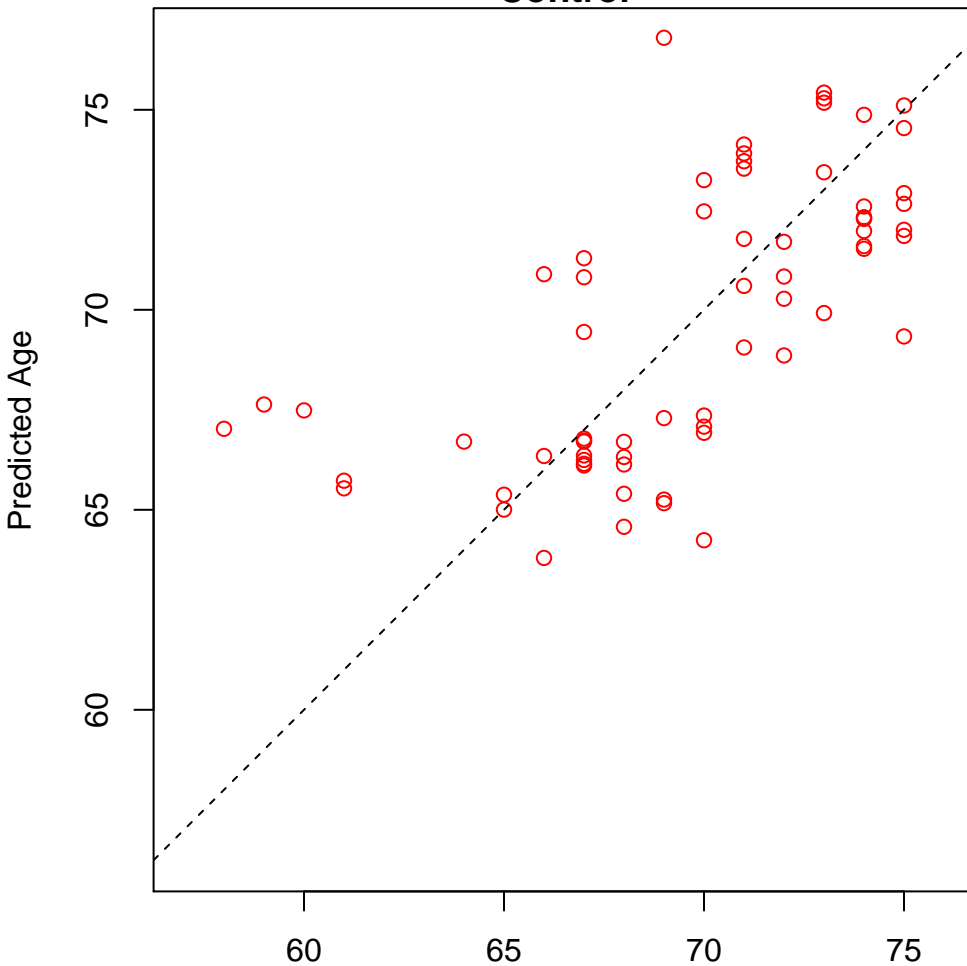


sperm motility (Score: 1.359041)

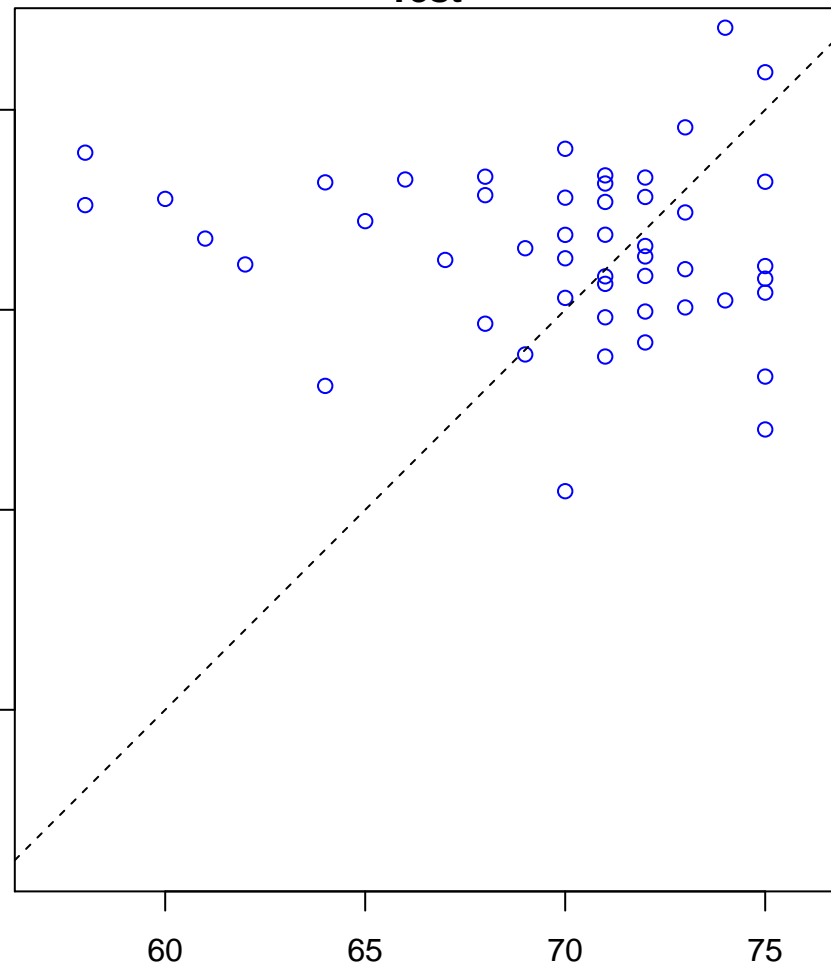


regulation of peptide hormone secretion (Score: 1.358975)

Control

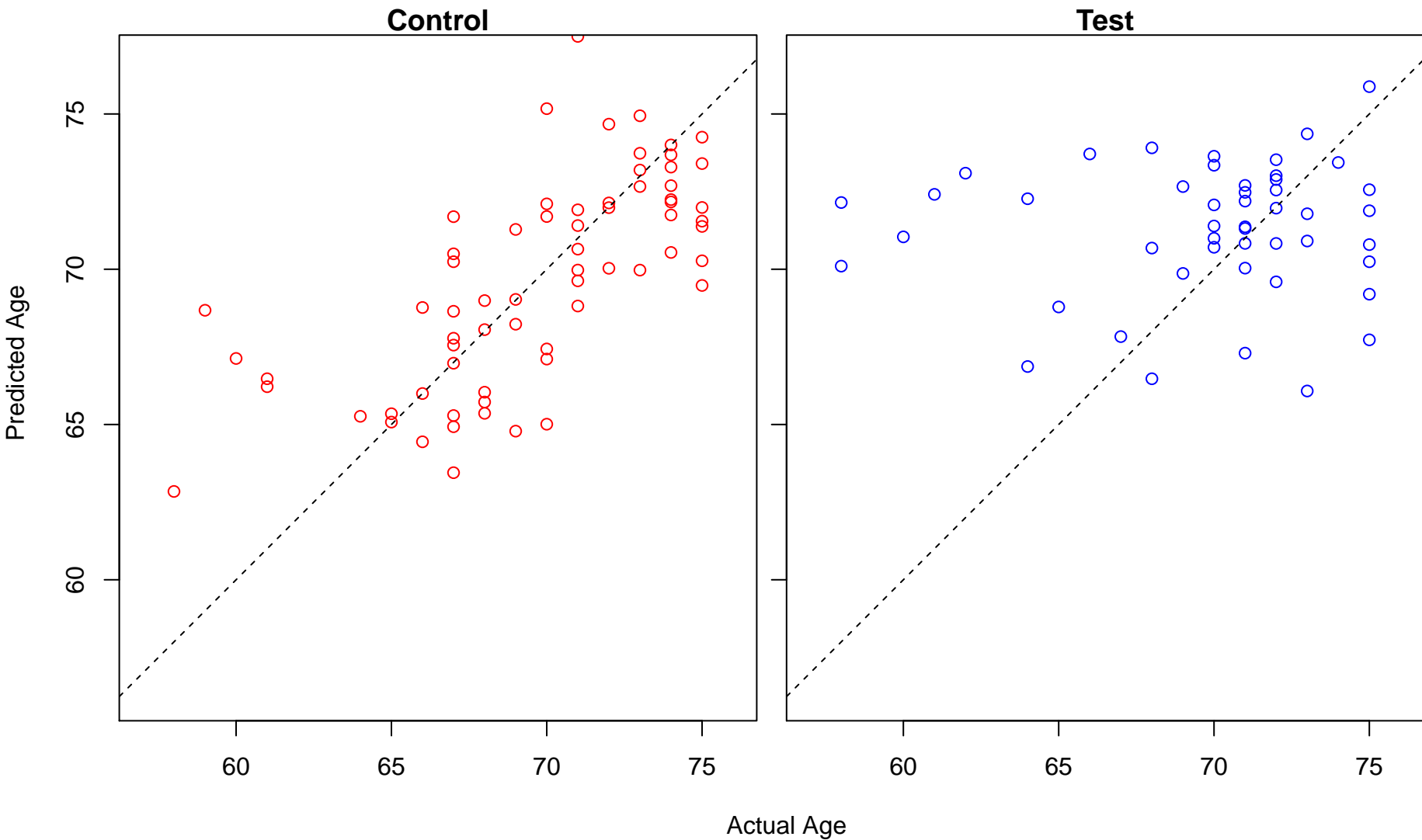


Test

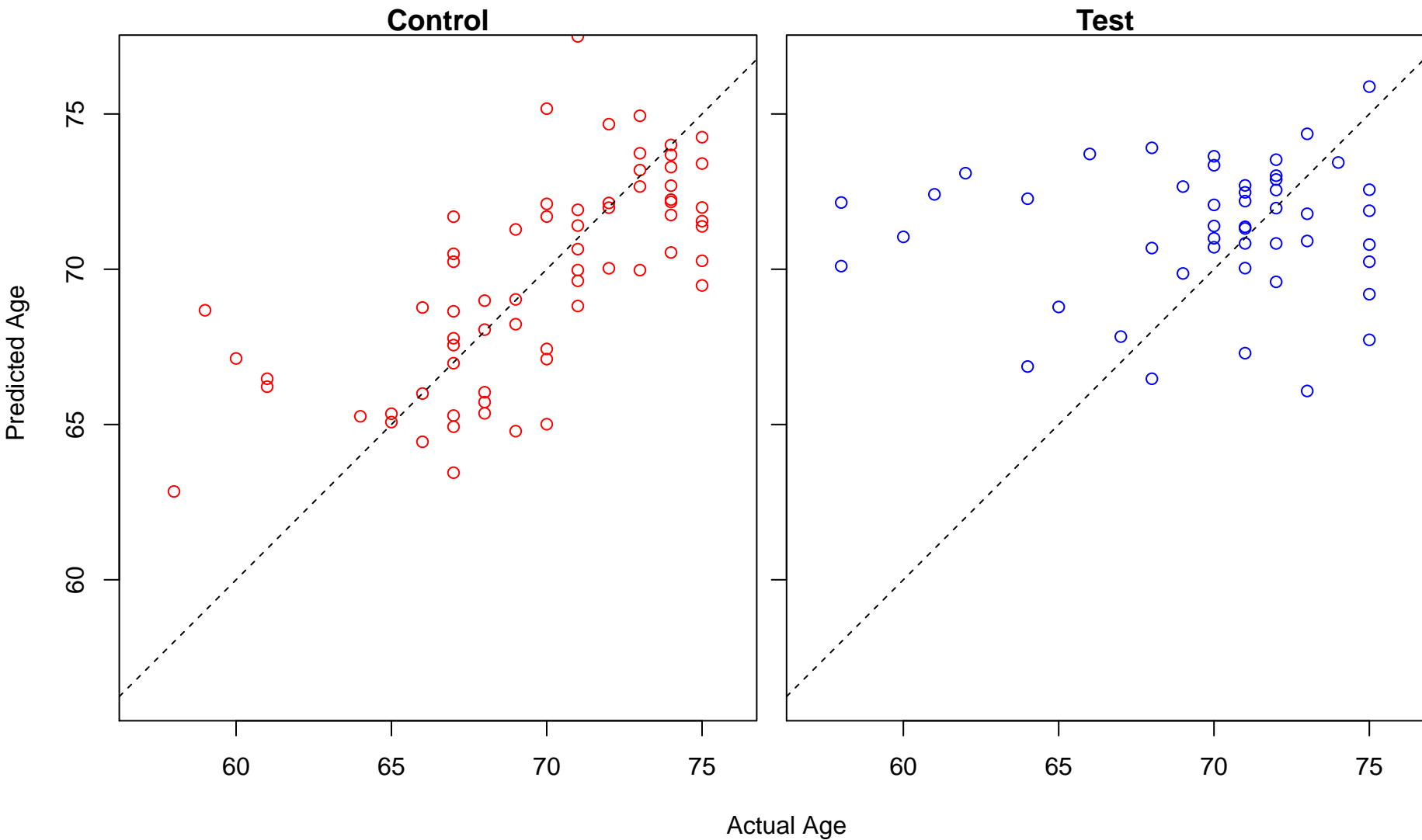


Actual Age

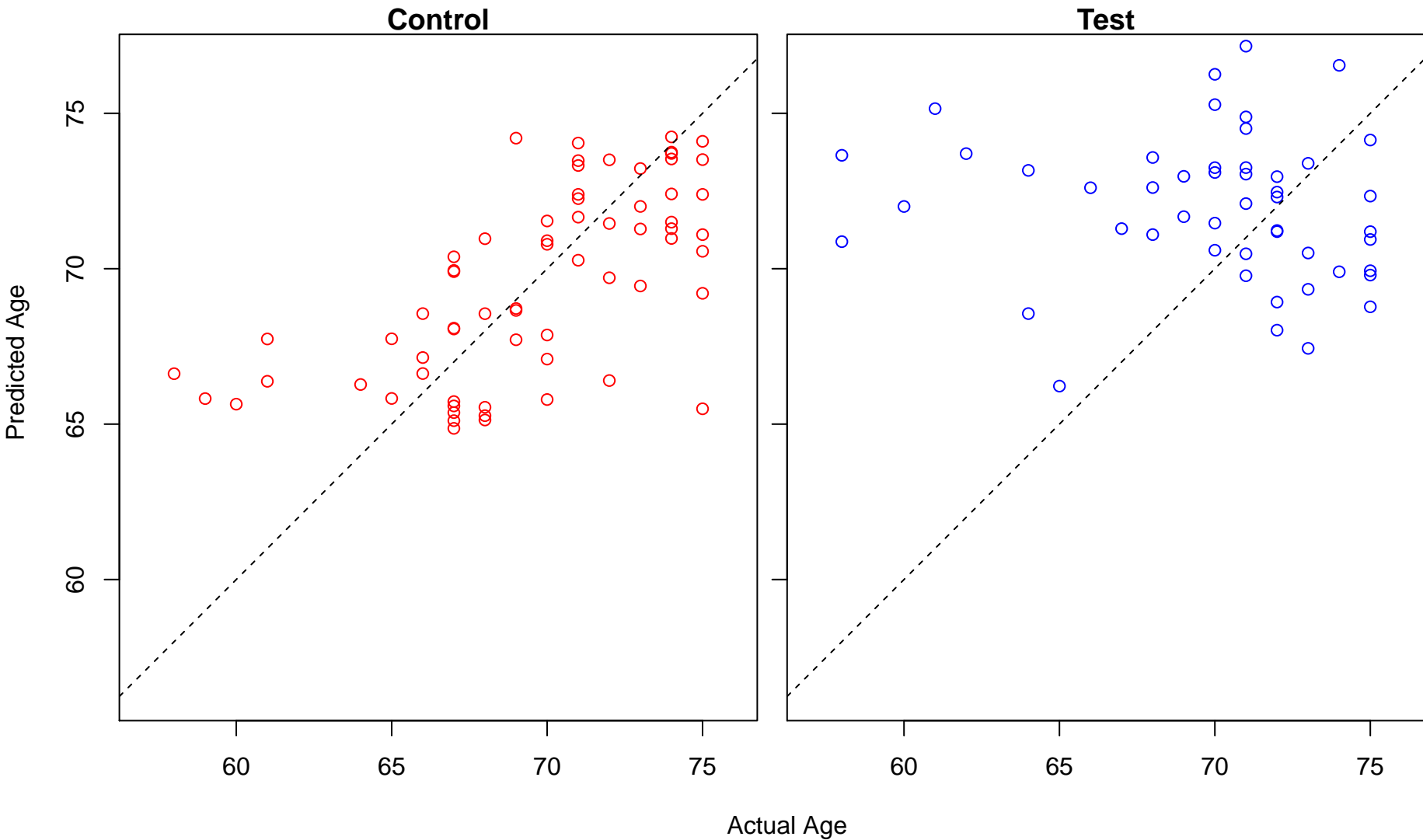
DNA replication-independent nucleosome assembly (Score: 1.358895)



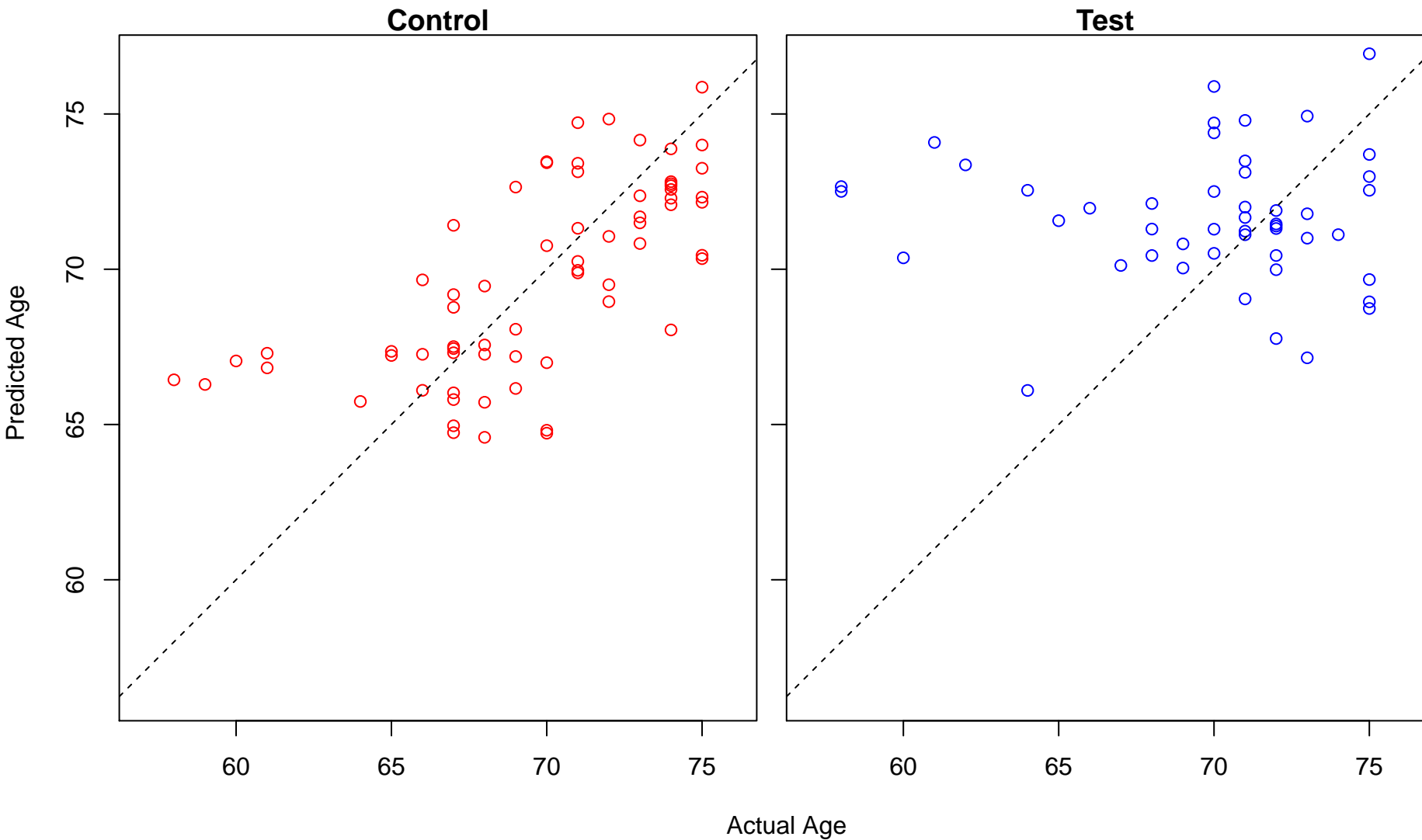
DNA replication-independent nucleosome organization (Score: 1.358895)



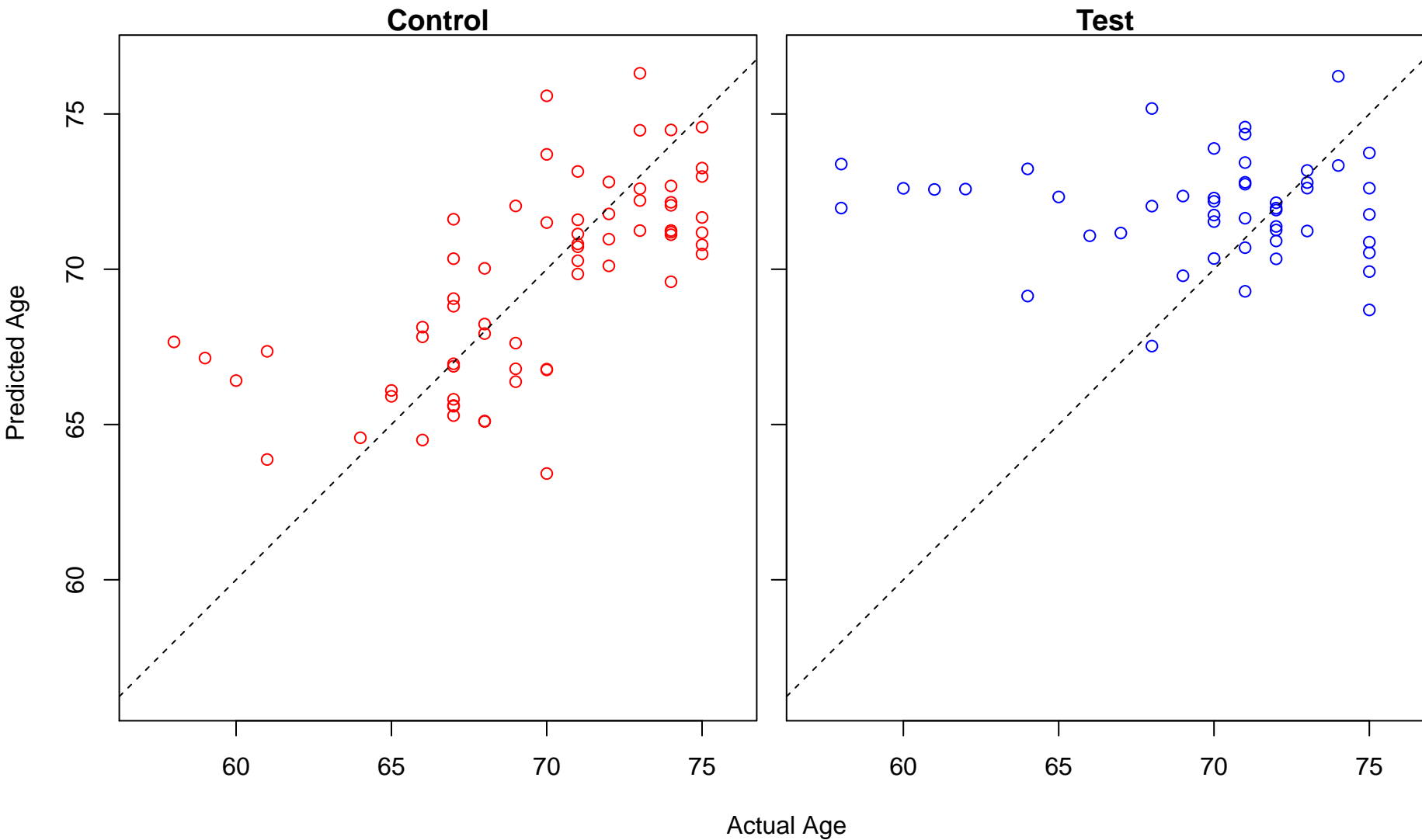
positive regulation of T-helper 1 type immune response (Score: 1.358636)



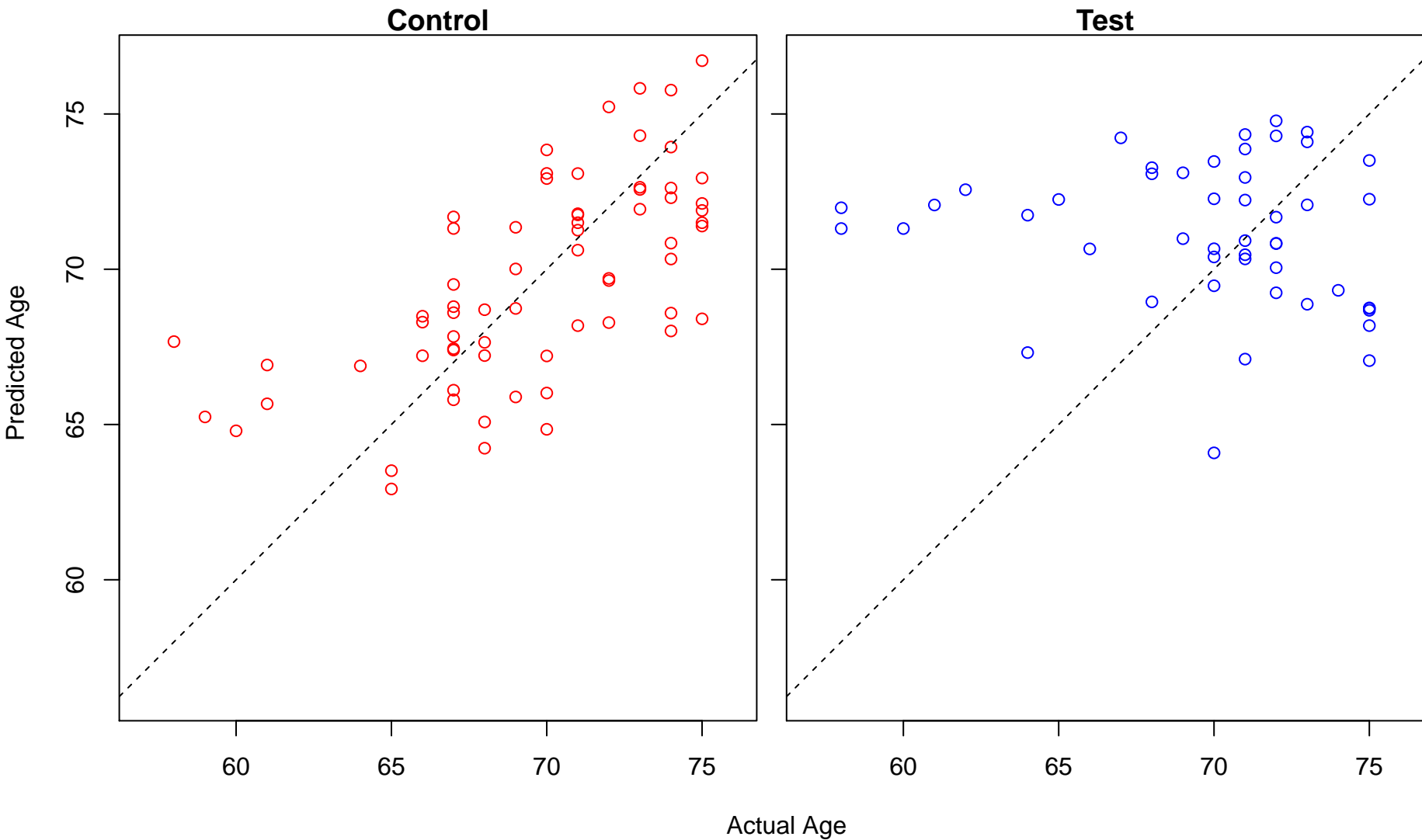
calcium ion regulated exocytosis (Score: 1.358098)



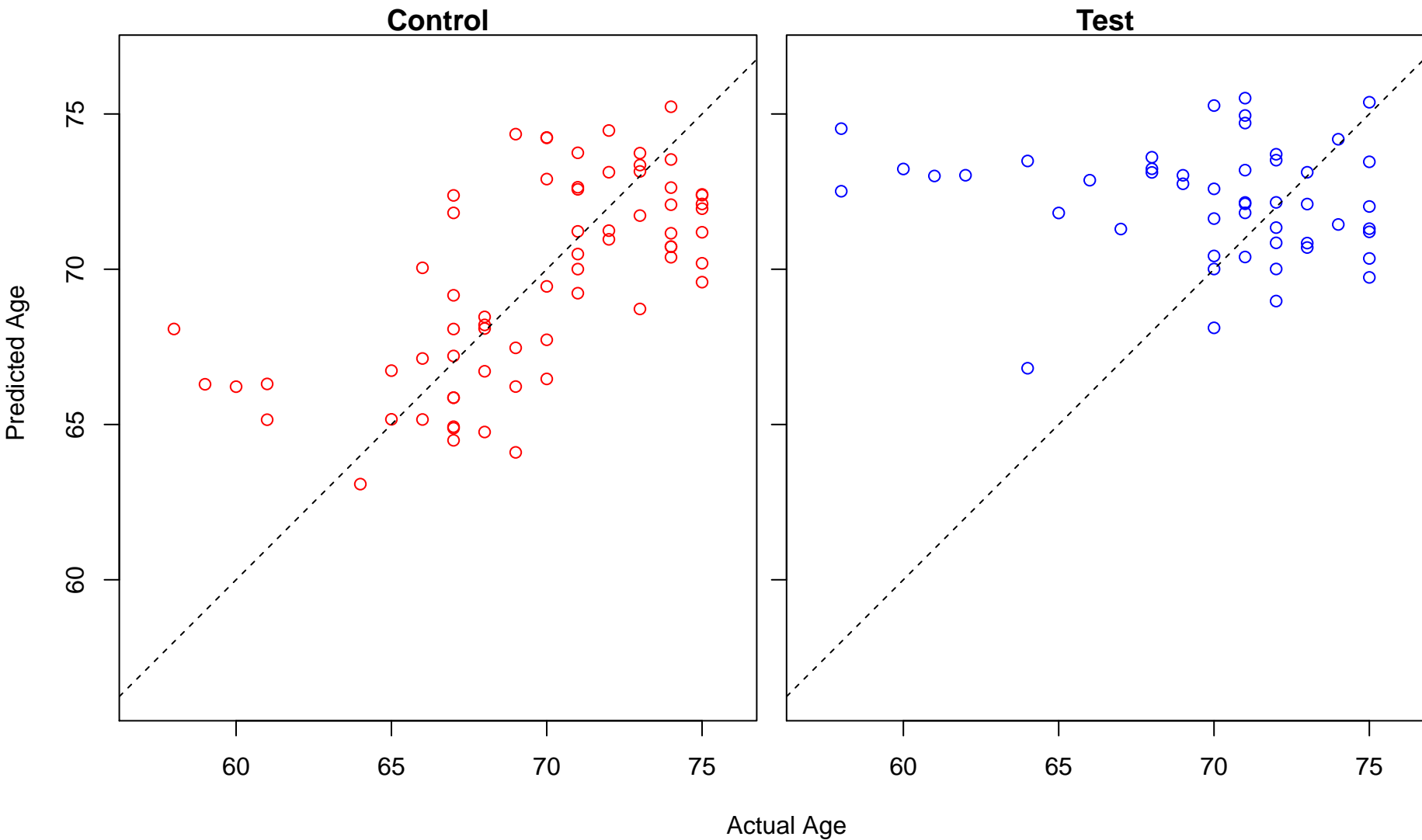
negative regulation of organelle organization (Score: 1.357952)



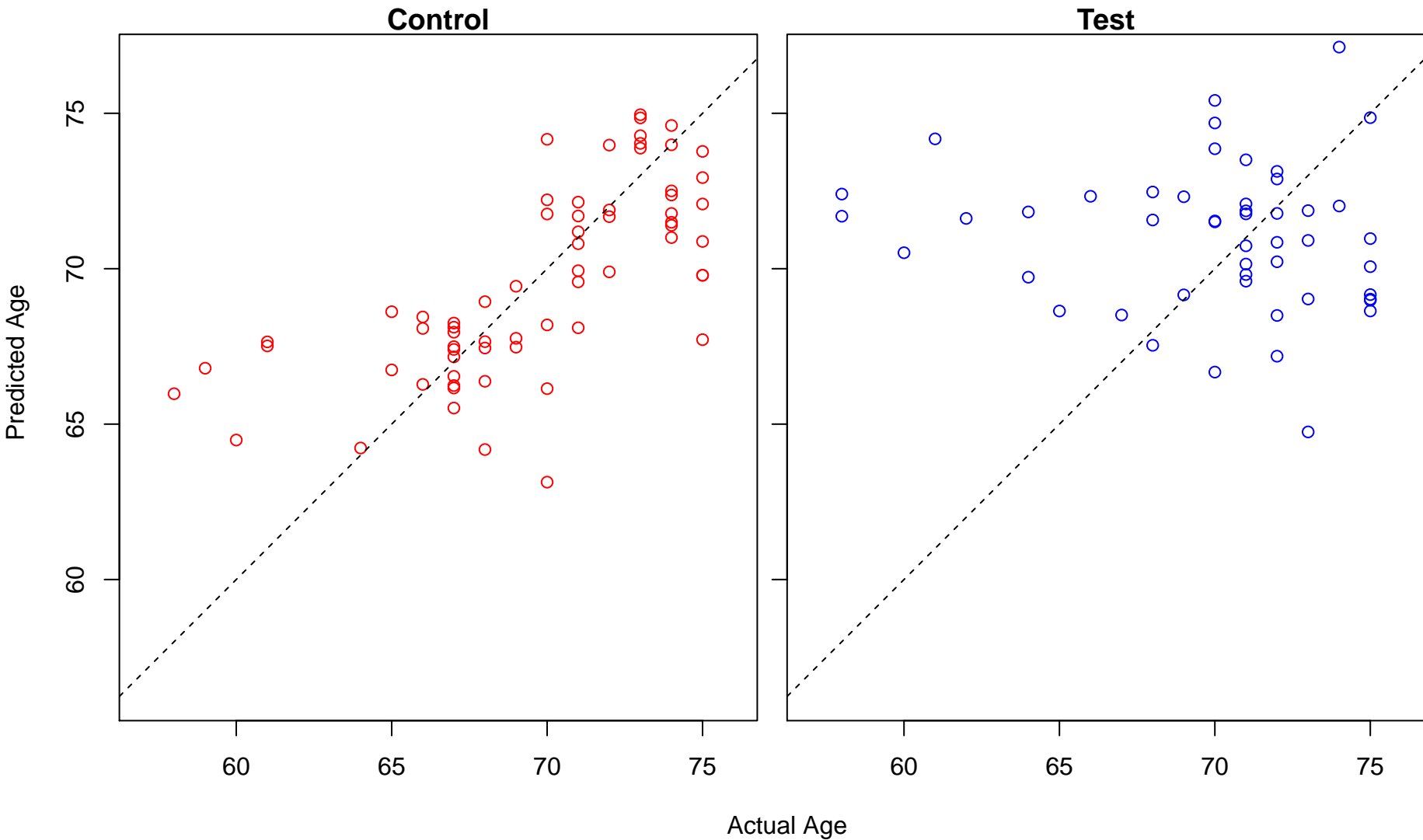
calcium ion import (Score: 1.357643)



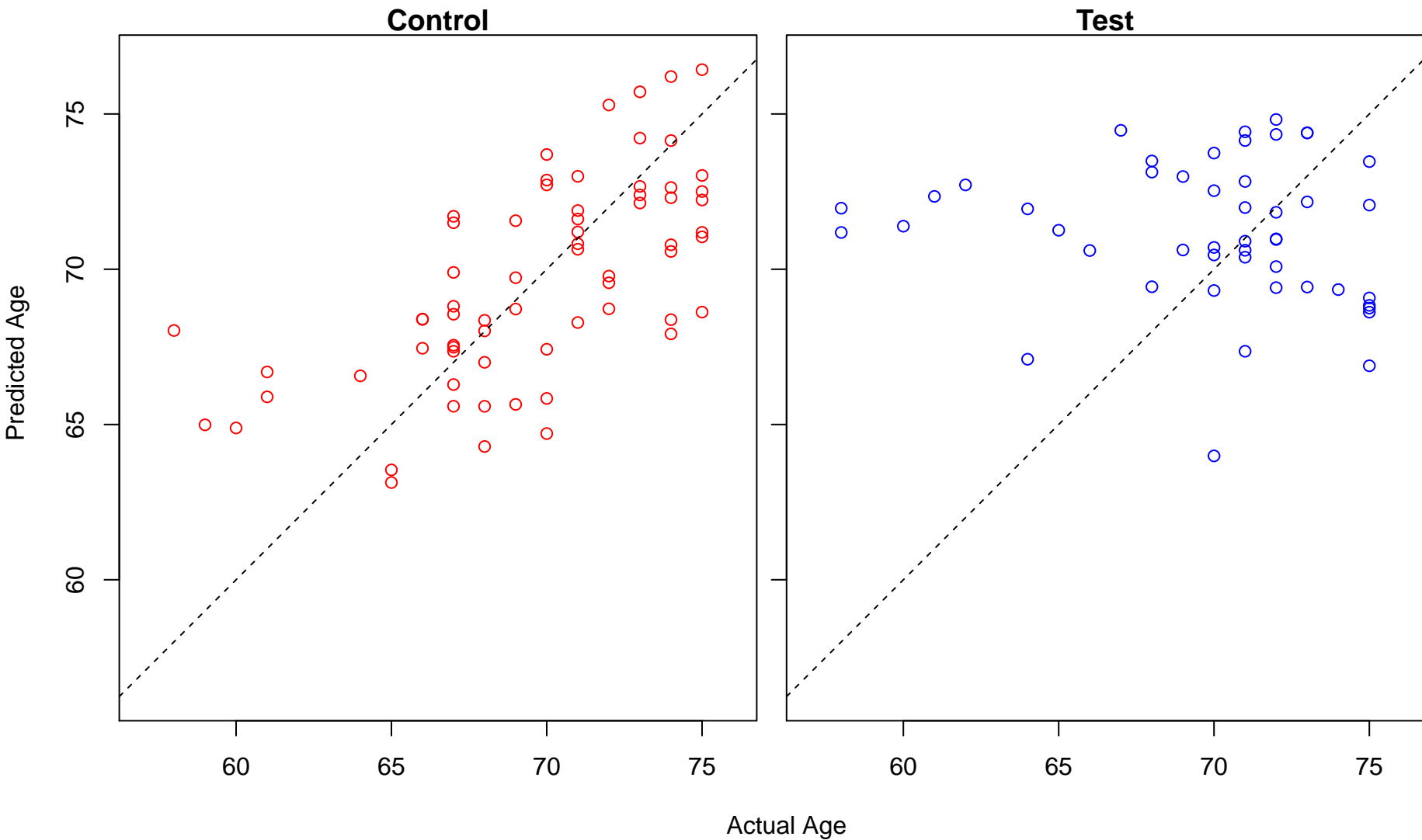
apoptotic nuclear changes (Score: 1.357372)



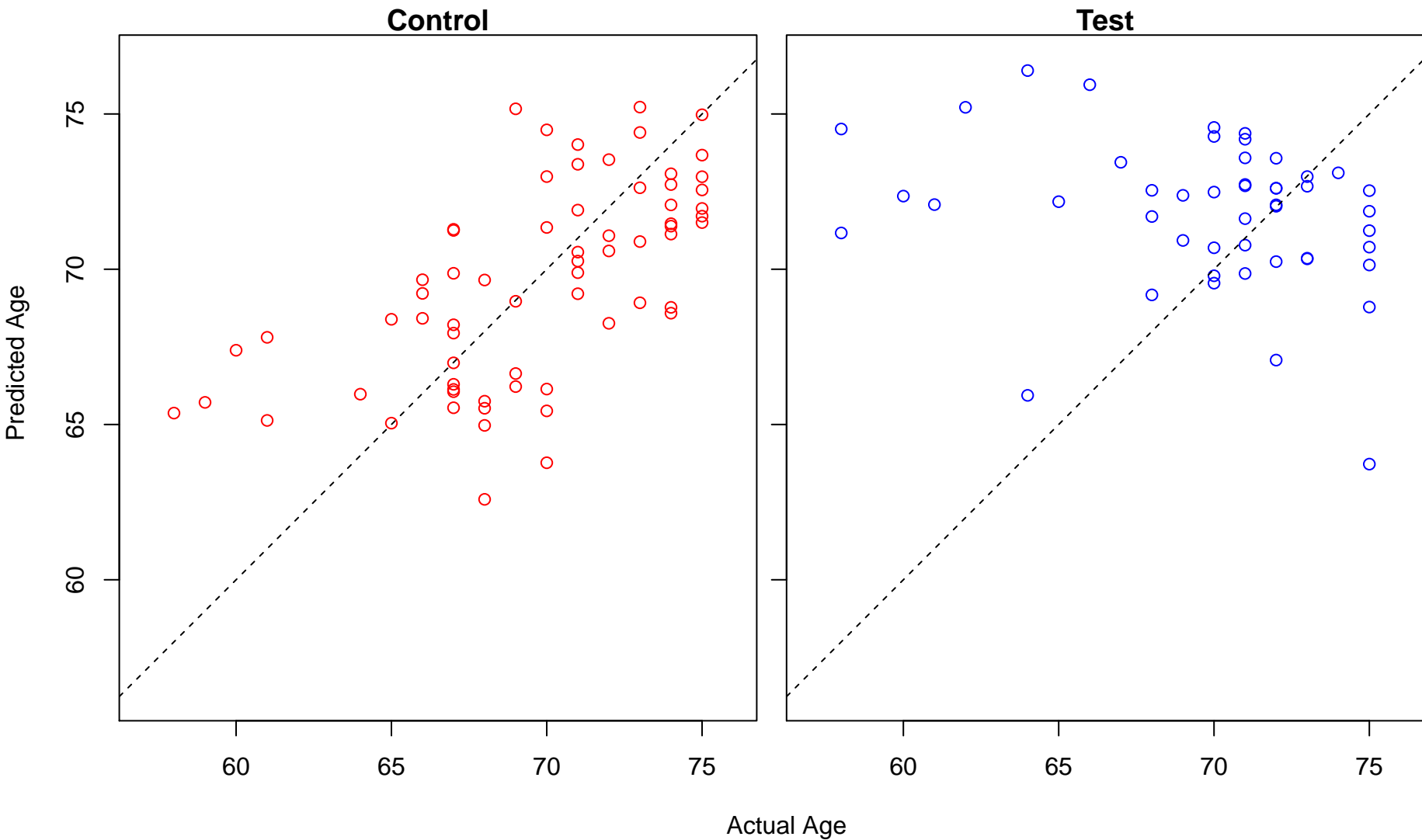
regulation of interferon- γ production (Score: 1.356751)



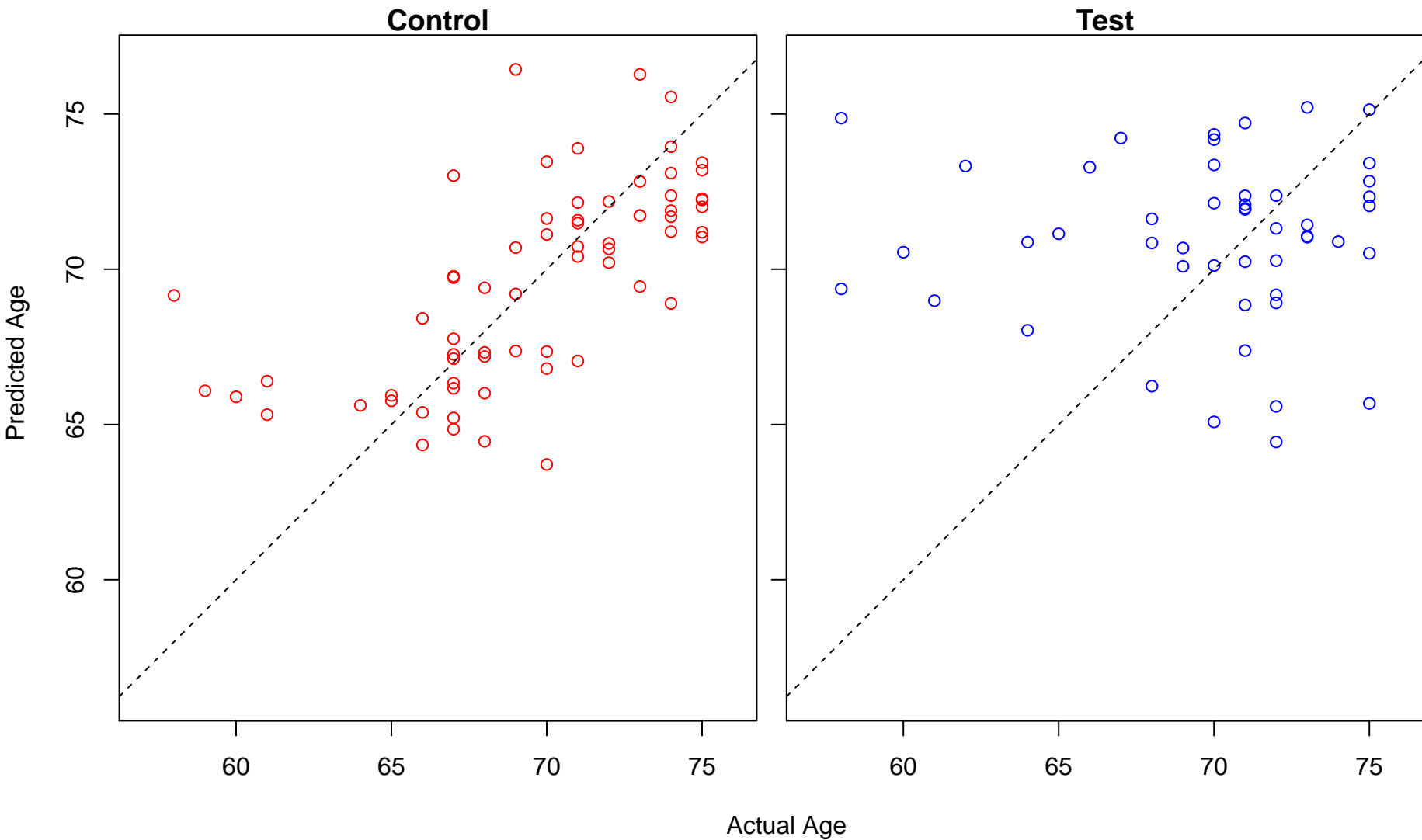
cytosolic calcium ion transport (Score: 1.356736)



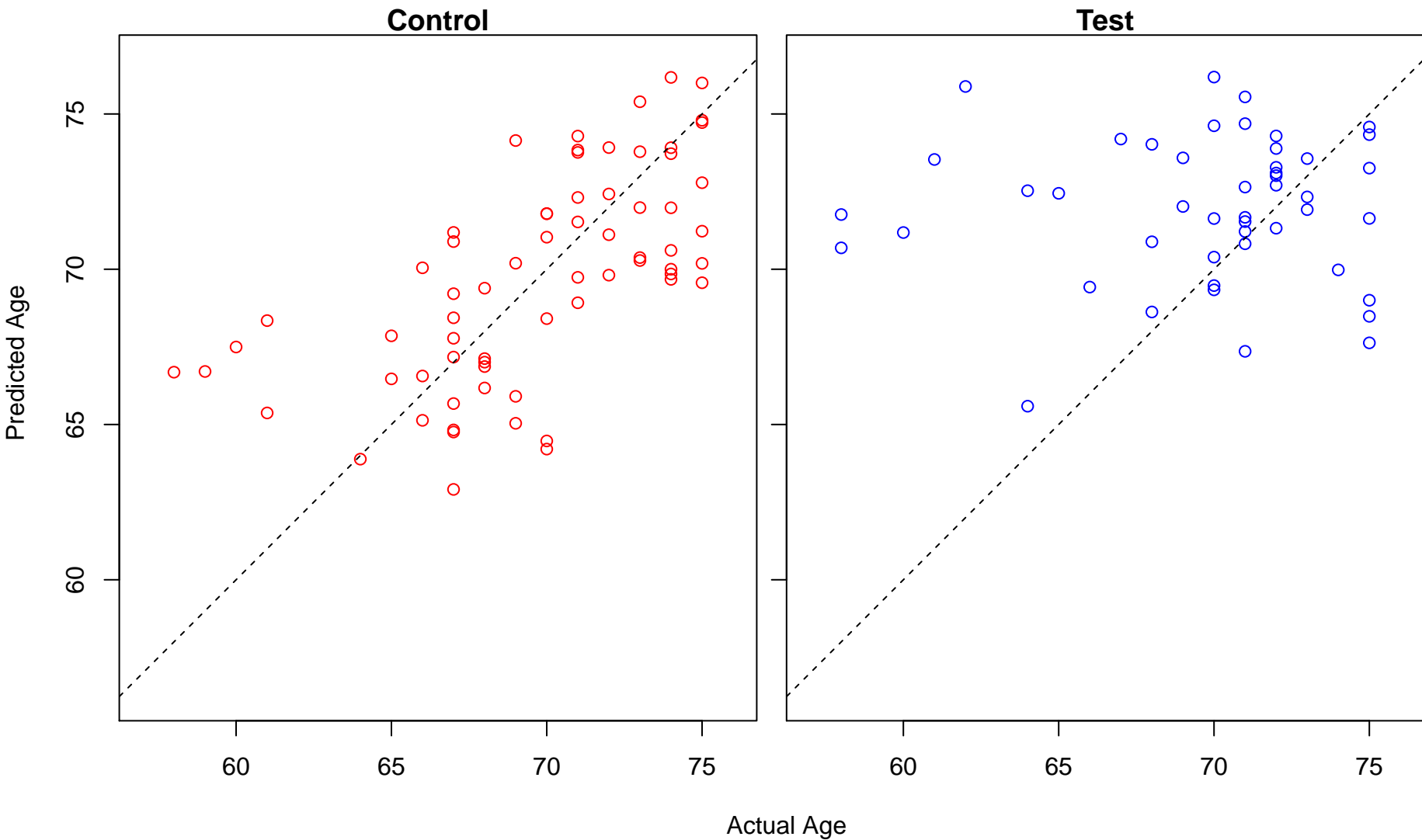
regulation of protein localization to chromosome, telomeric region (Score: 1.356734)



positive regulation of natural killer cell mediated cytotoxicity (Score: 1.356539)

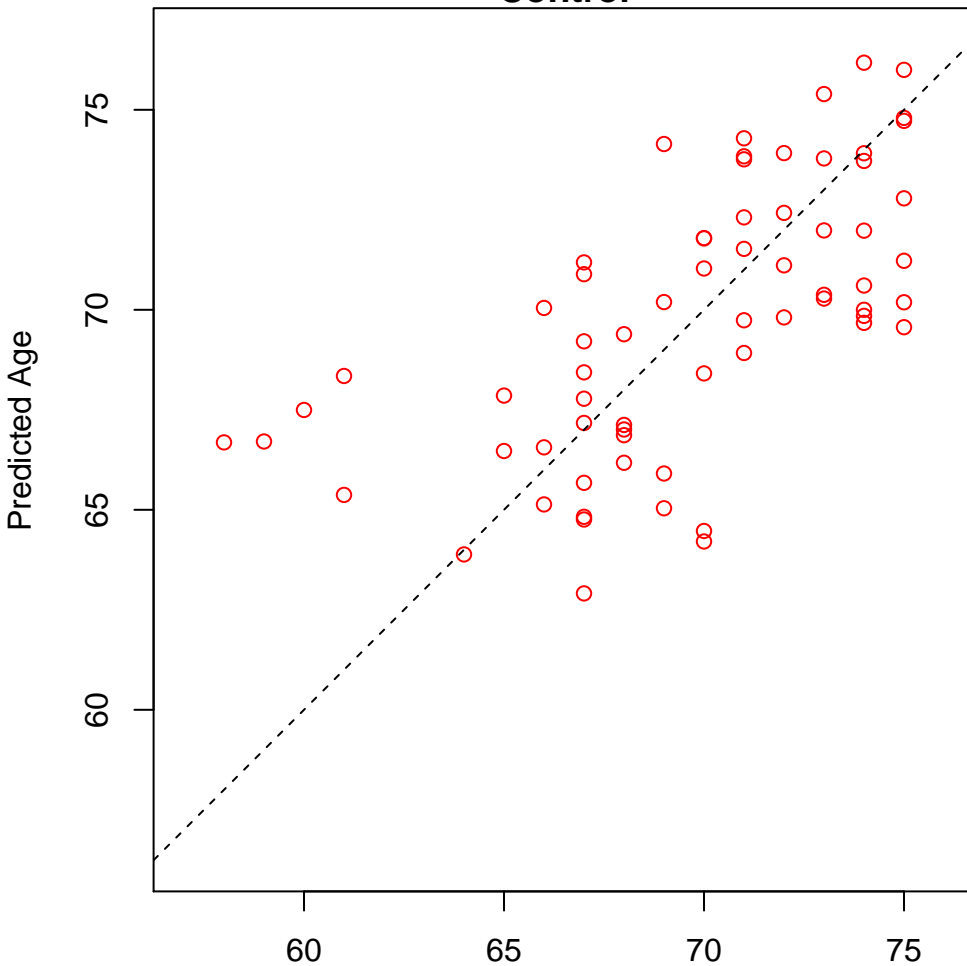


cholesterol biosynthetic process (Score: 1.356459)

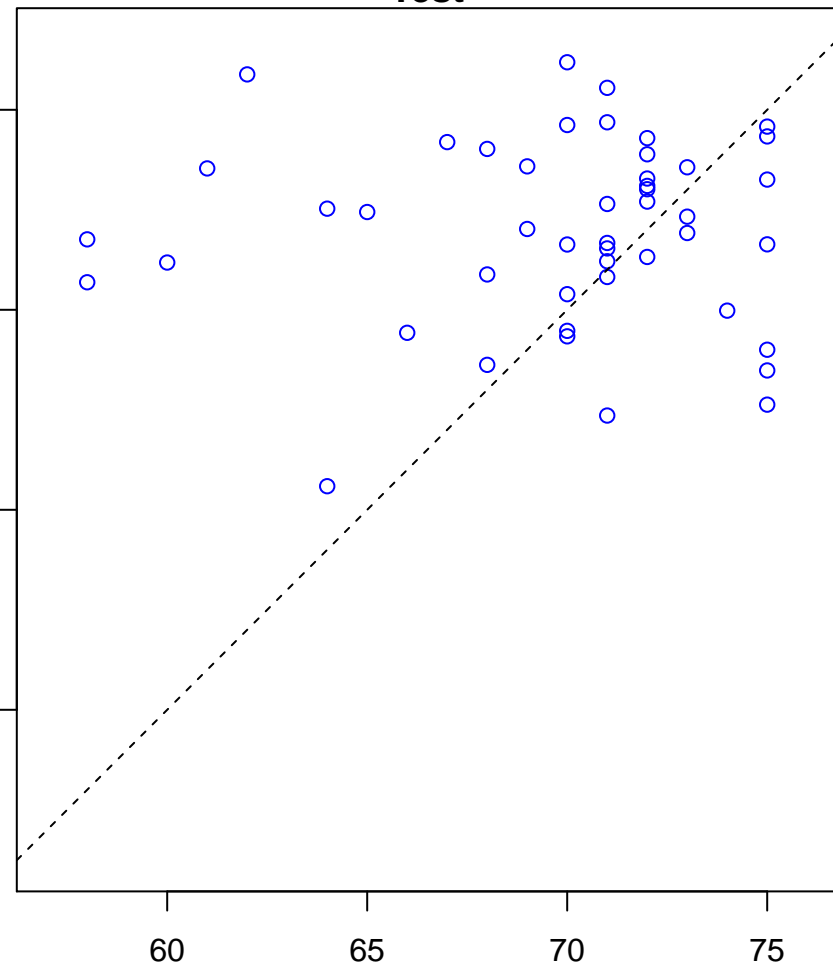


secondary alcohol biosynthetic process (Score: 1.356459)

Control

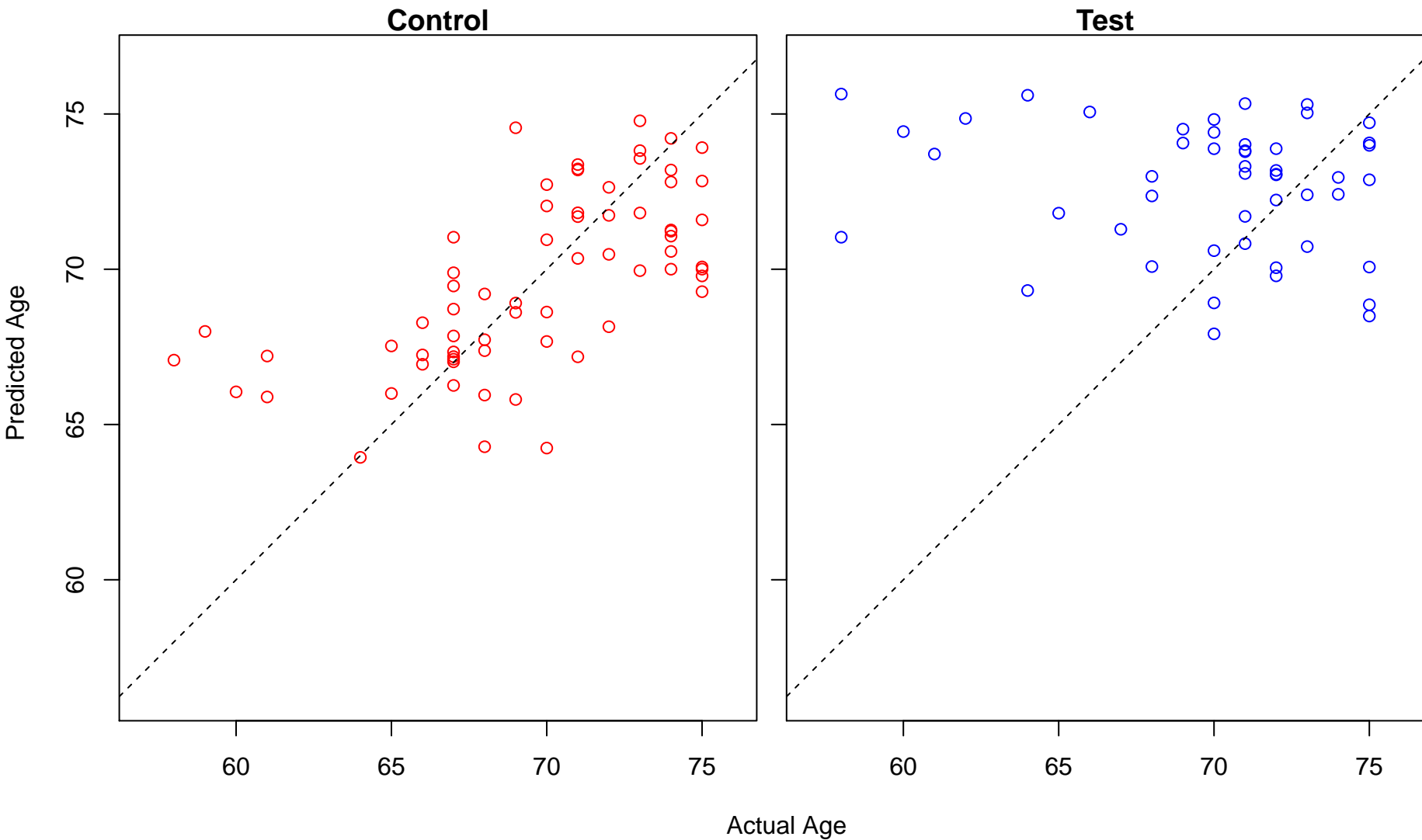


Test

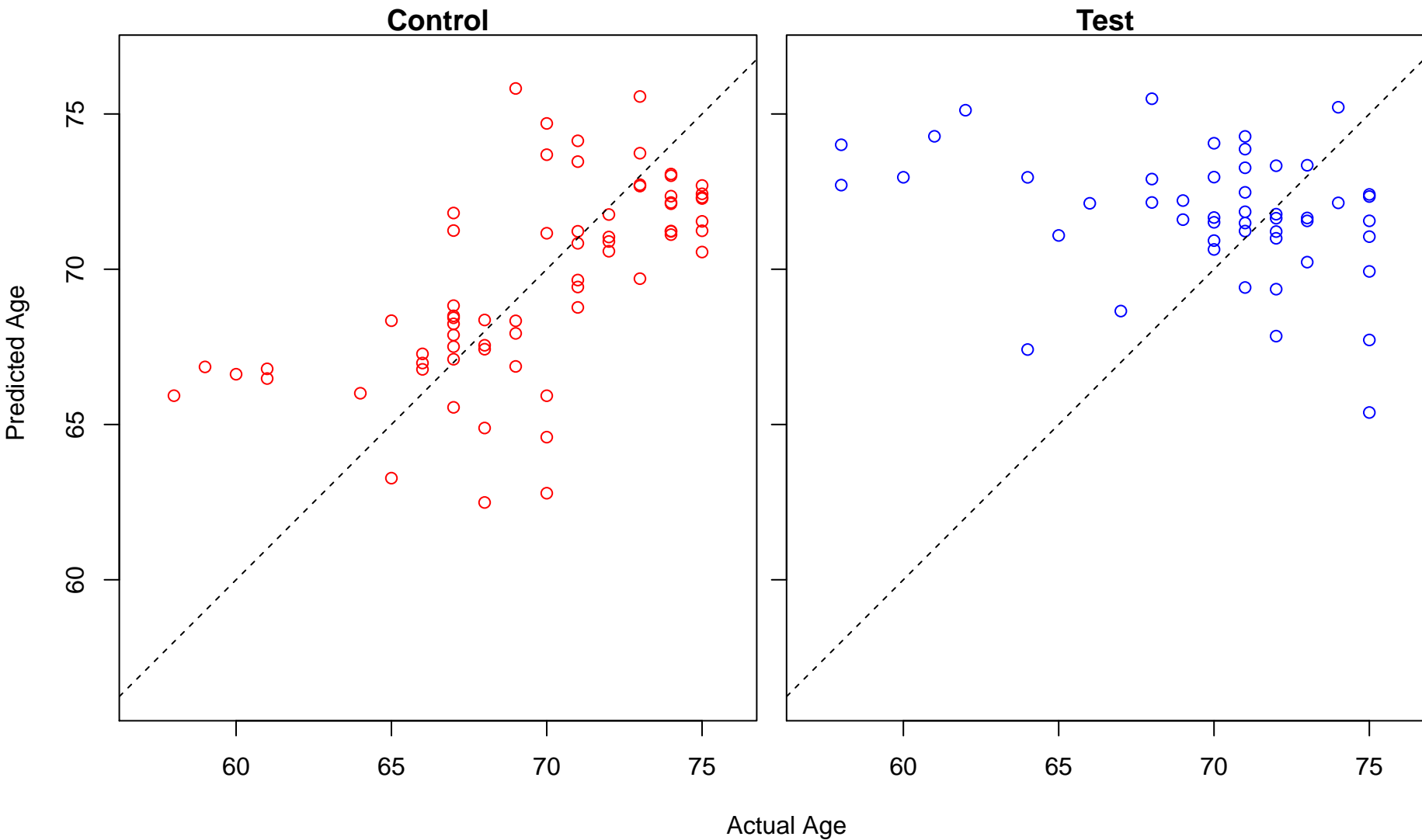


Actual Age

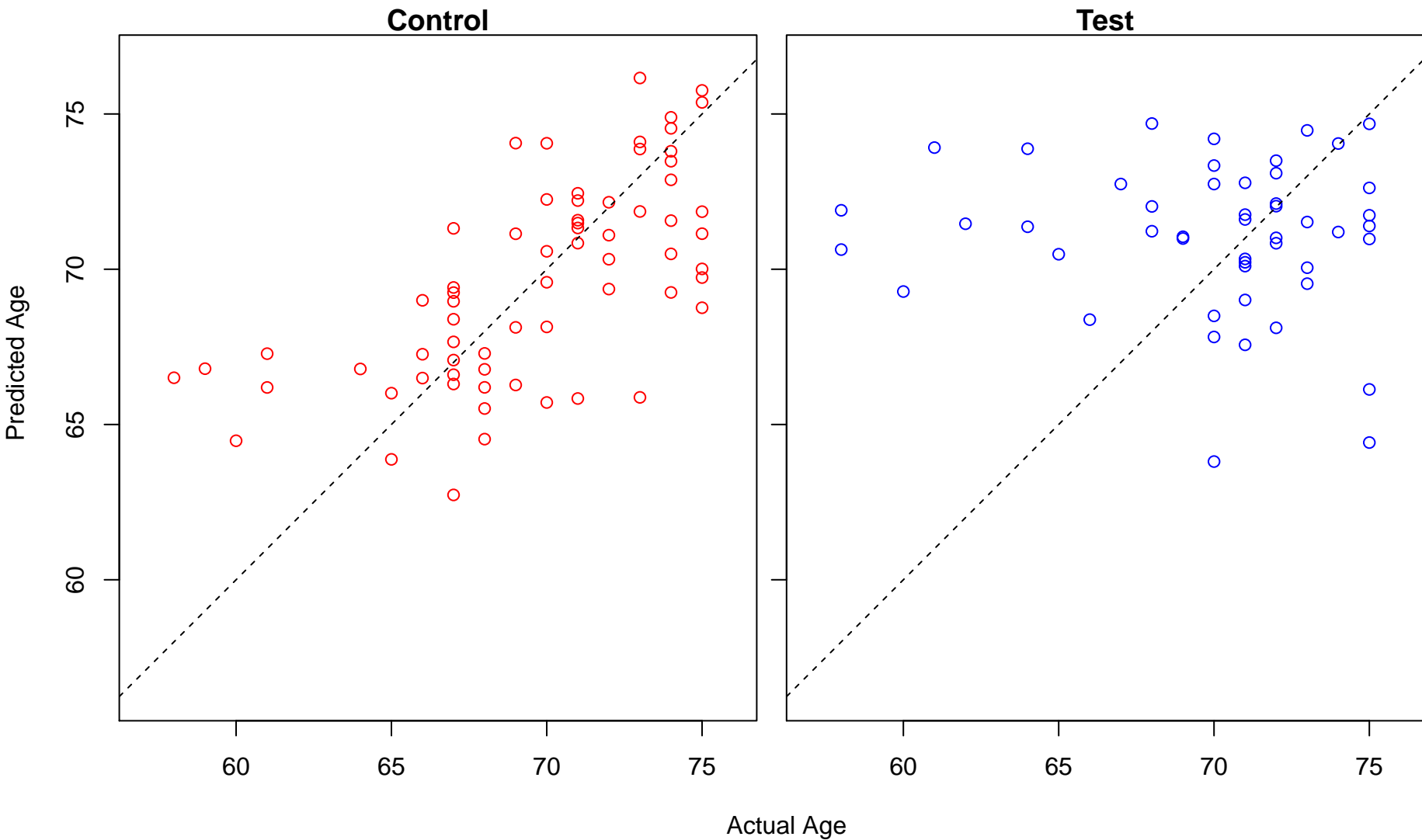
protein ufmylation (Score: 1.355868)



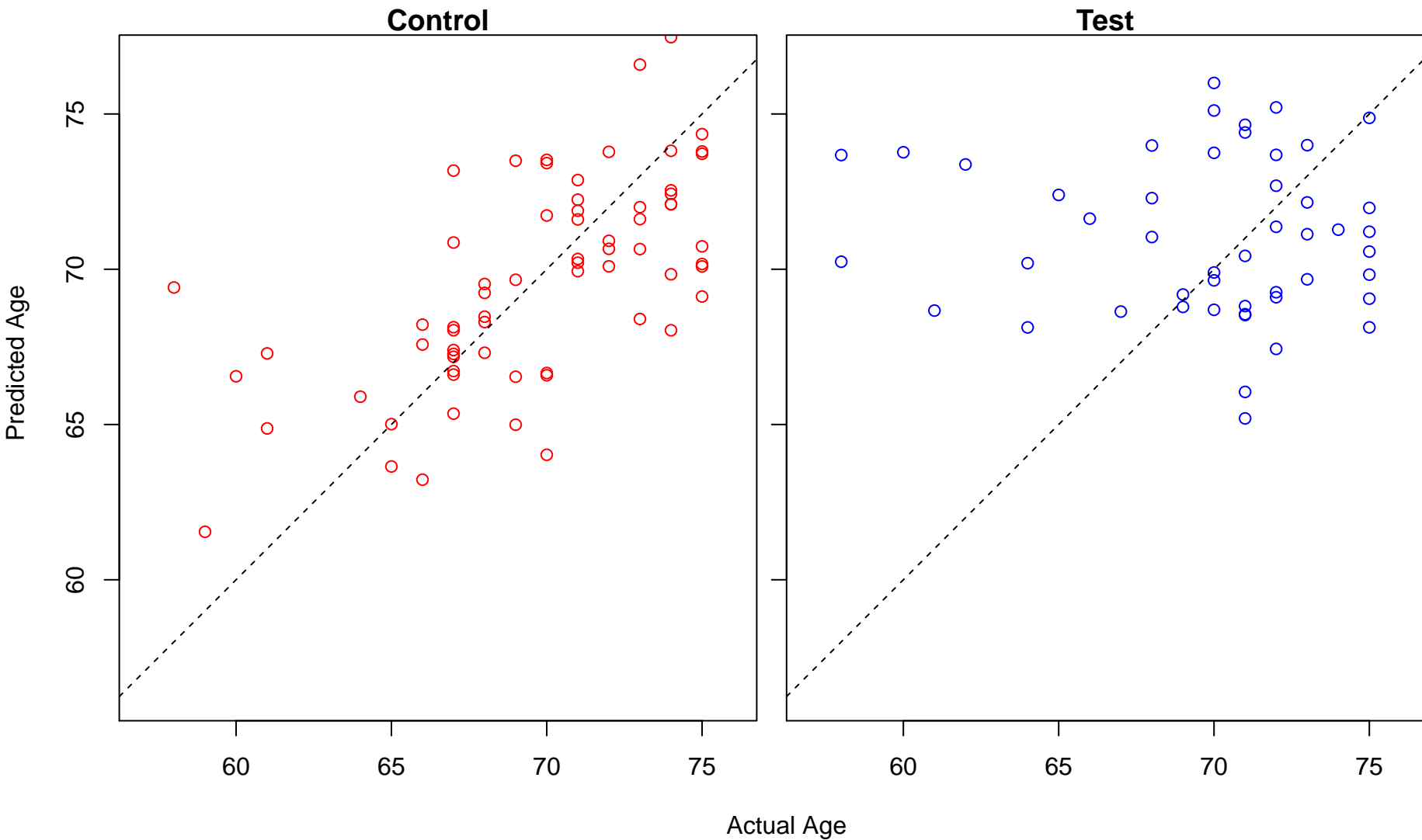
negative regulation of anoikis (Score: 1.354780)



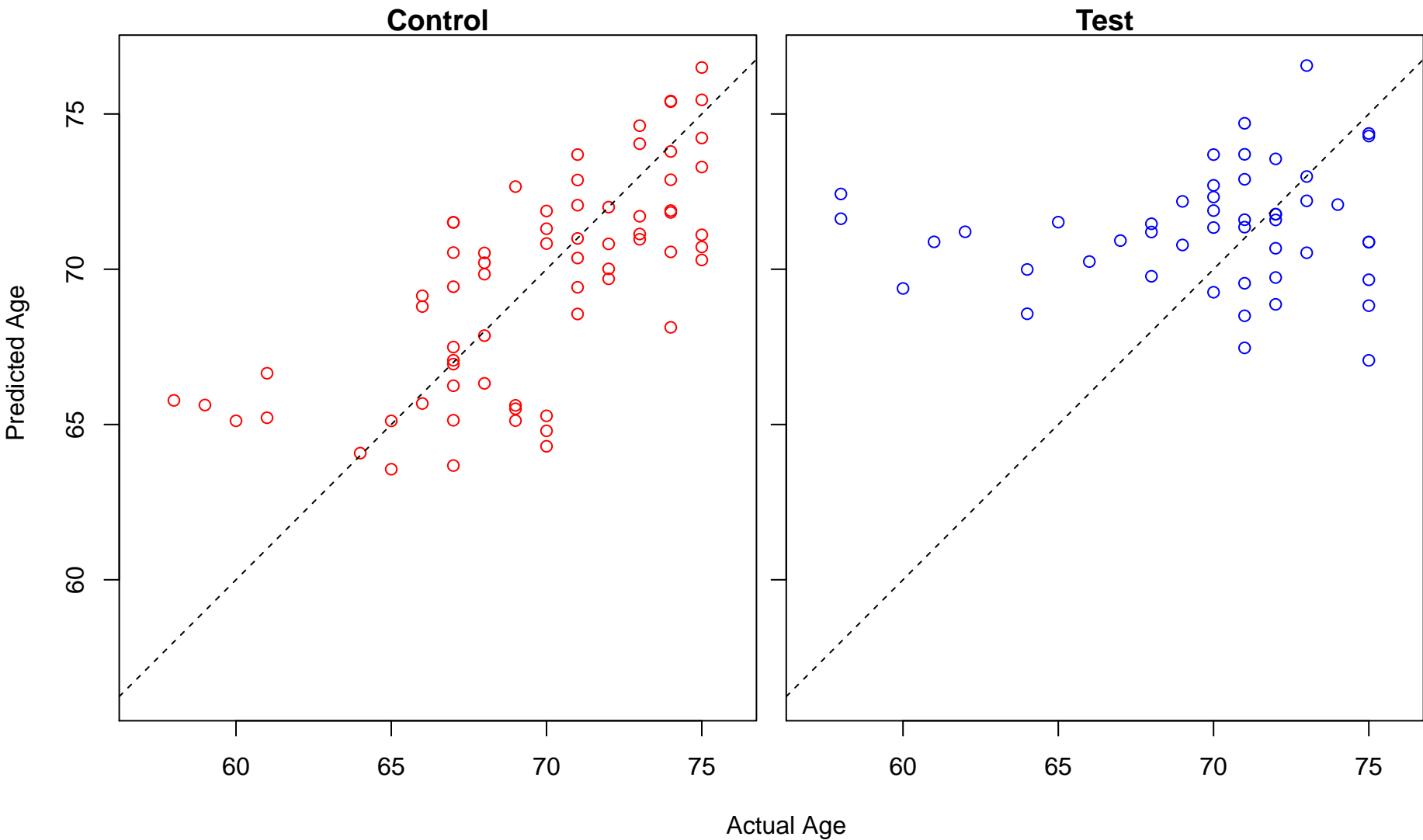
positive regulation of sodium ion transmembrane transport (Score: 1.354364)



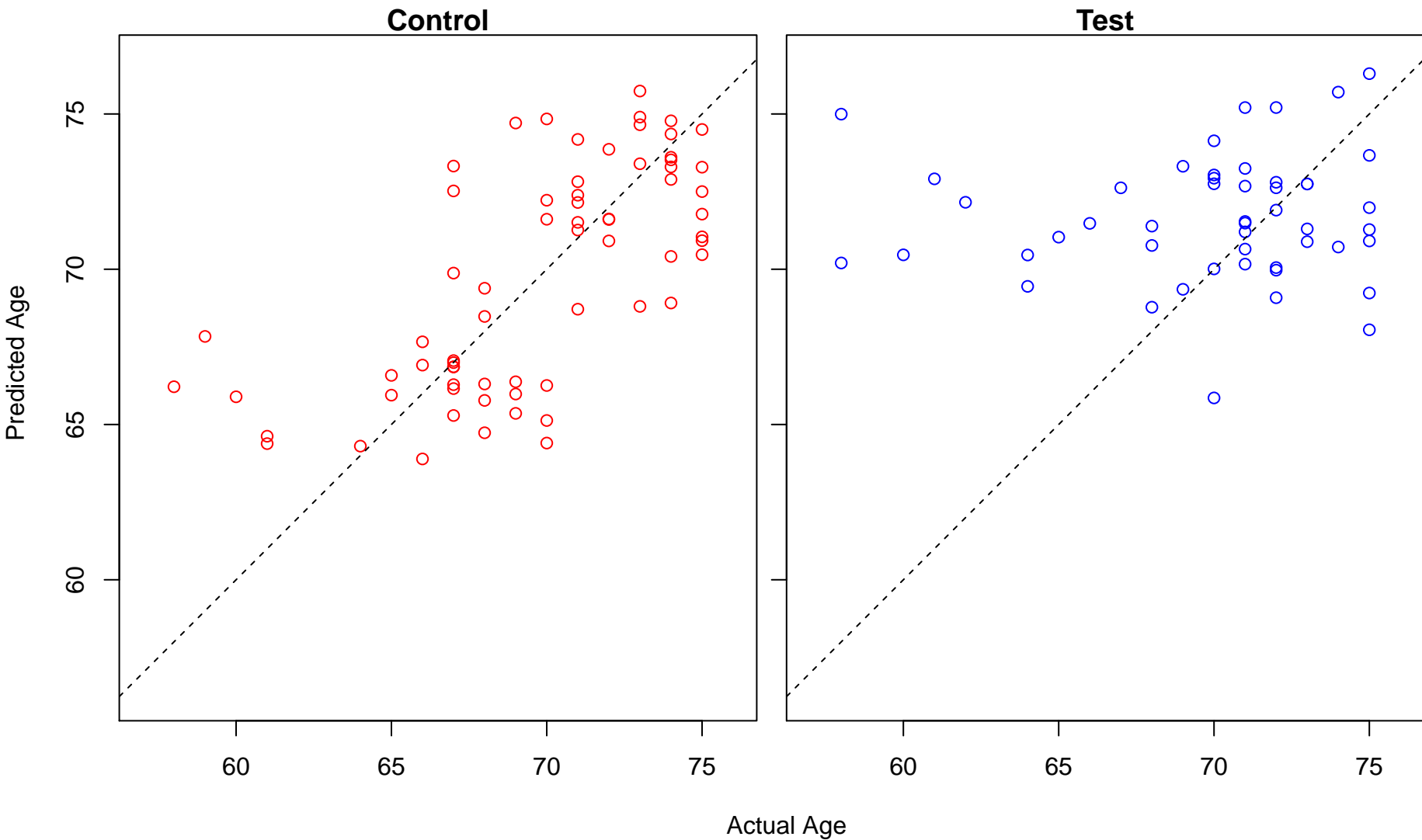
calcium-mediated signaling (Score: 1.353816)



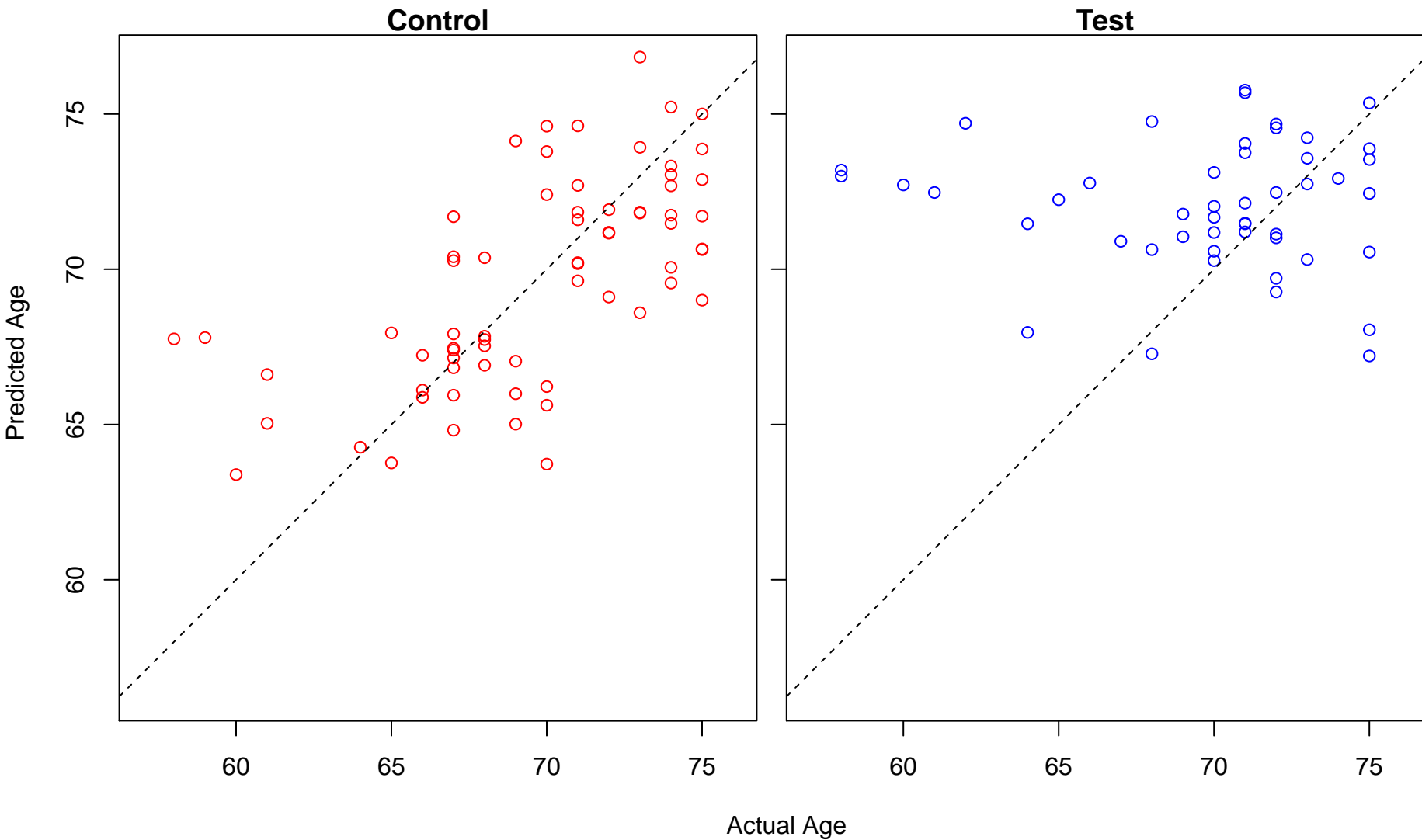
positive regulation of proteasomal ubiquitin-dependent protein catabolic process (Score: 1.353632)



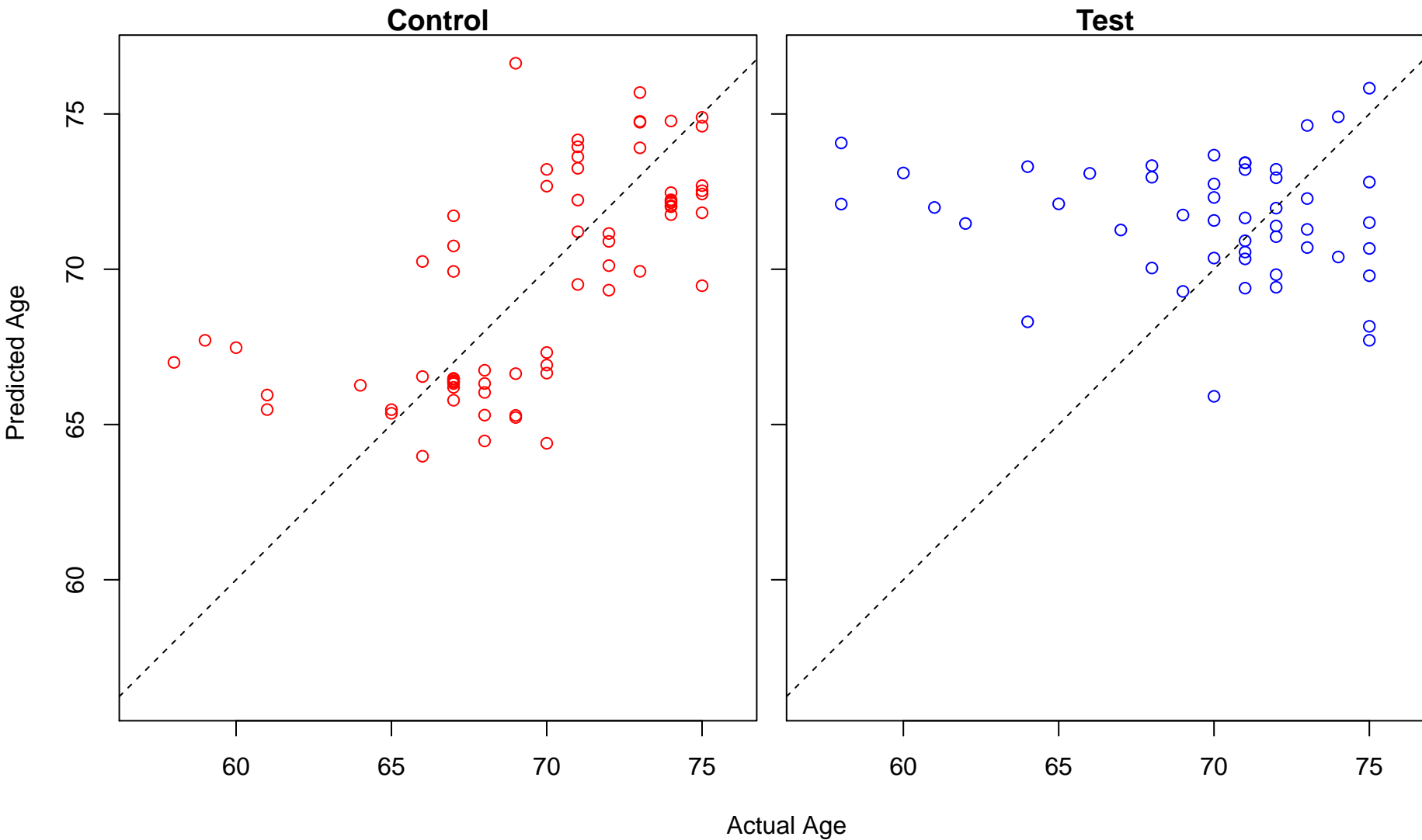
regulation of system process (Score: 1.353320)



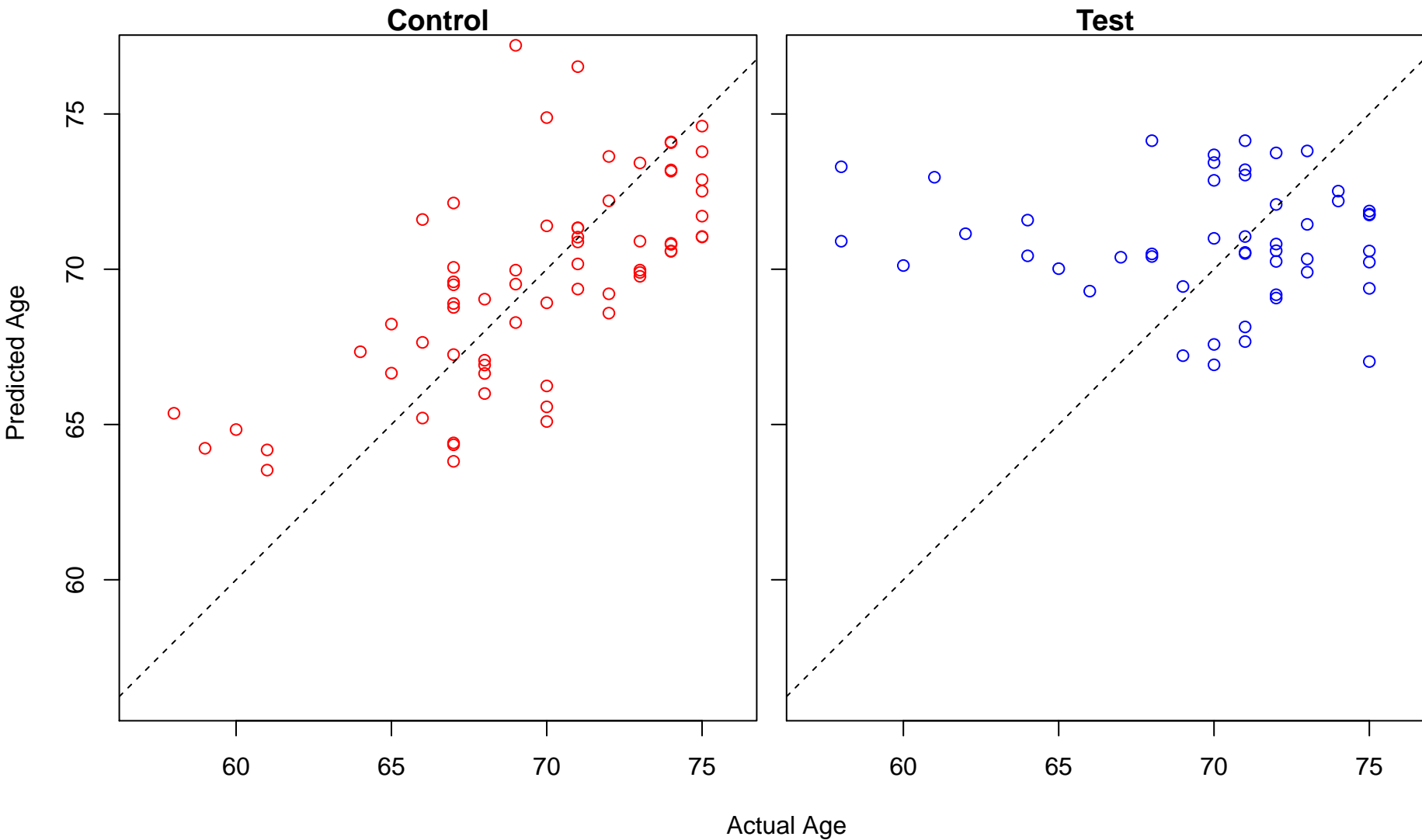
regulation of nervous system development (Score: 1.352715)



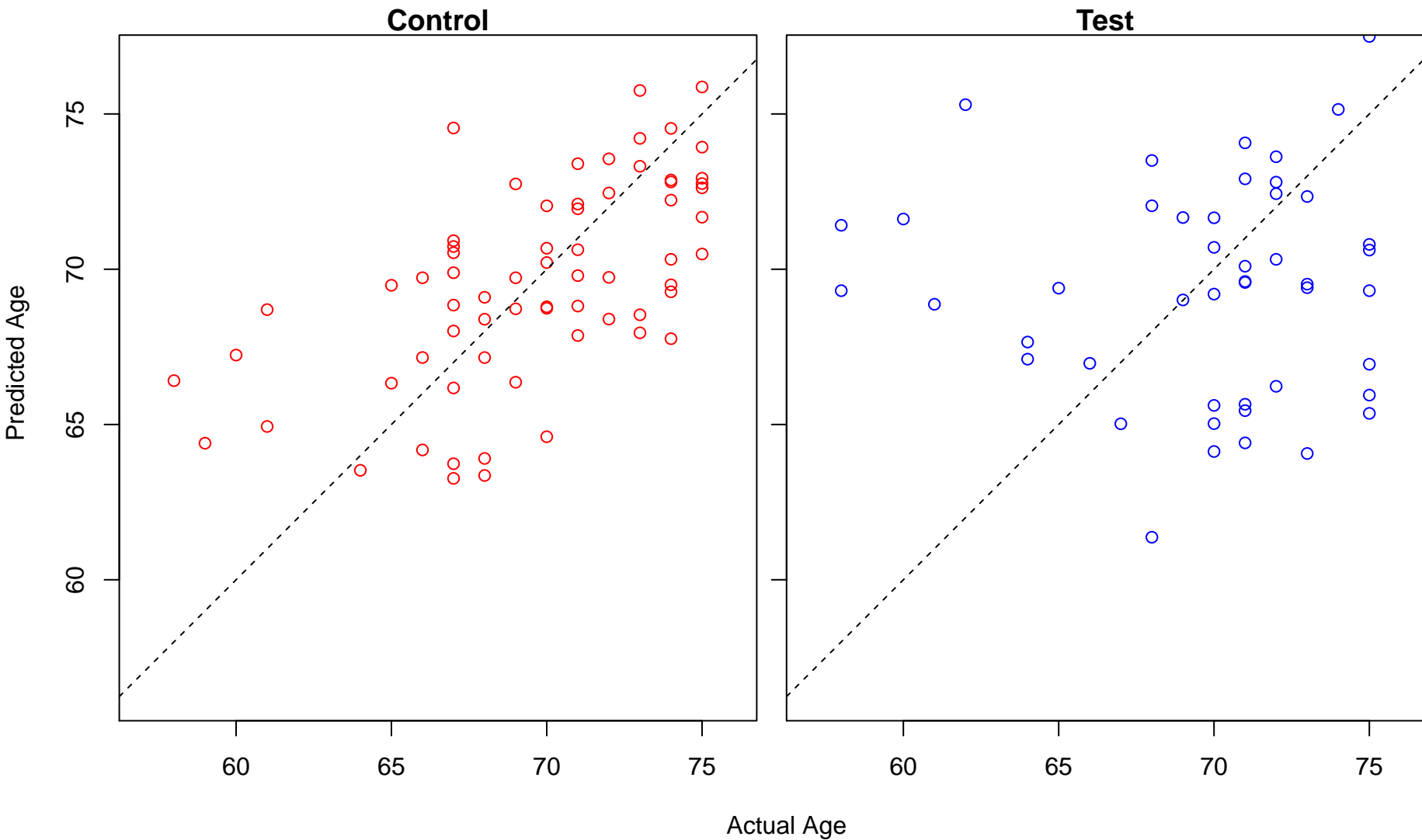
regulation of insulin secretion (Score: 1.352633)



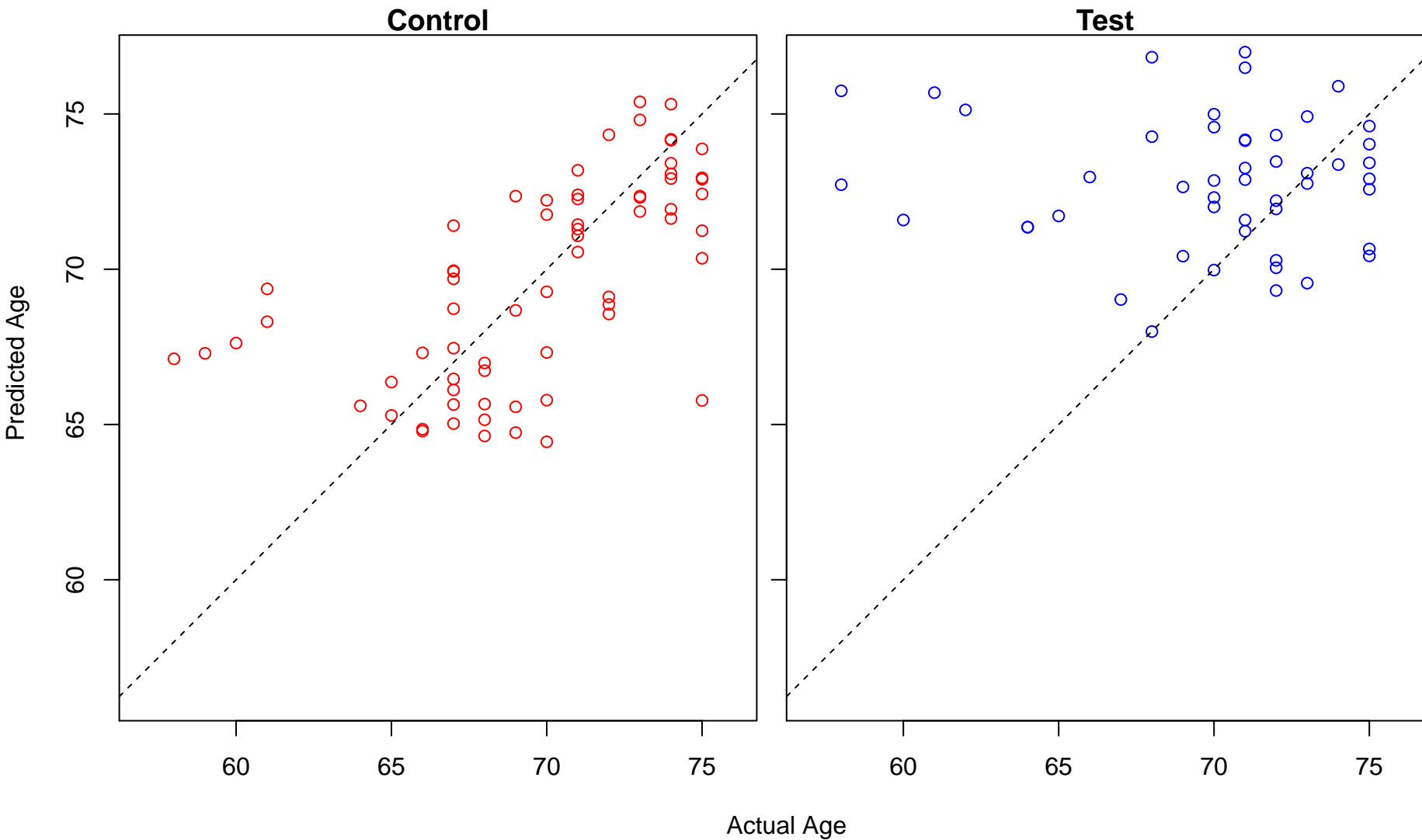
endoplasmic reticulum calcium ion homeostasis (Score: 1.352406)



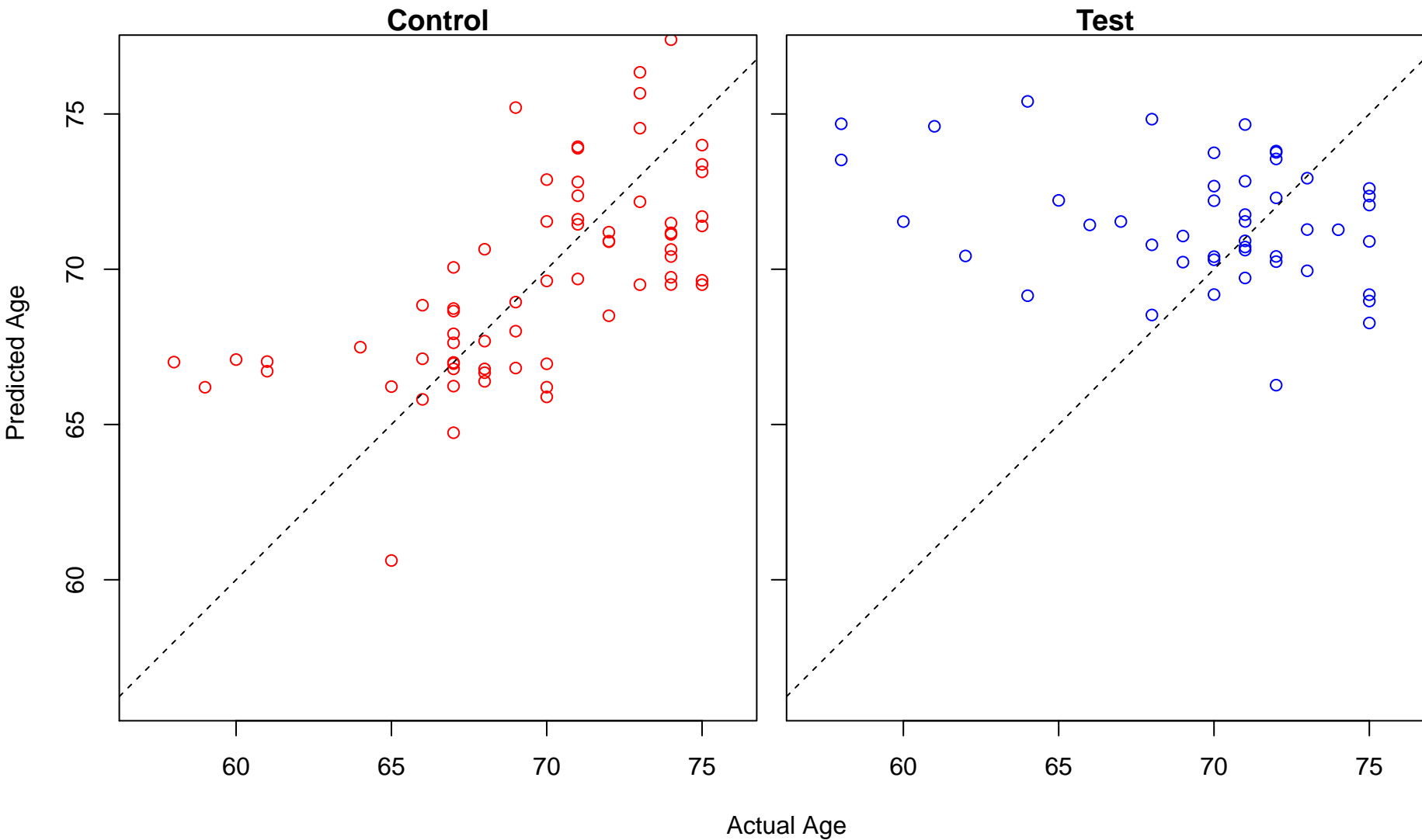
regulation of epidermal growth factor-activated receptor activity (Score: 1.352272)



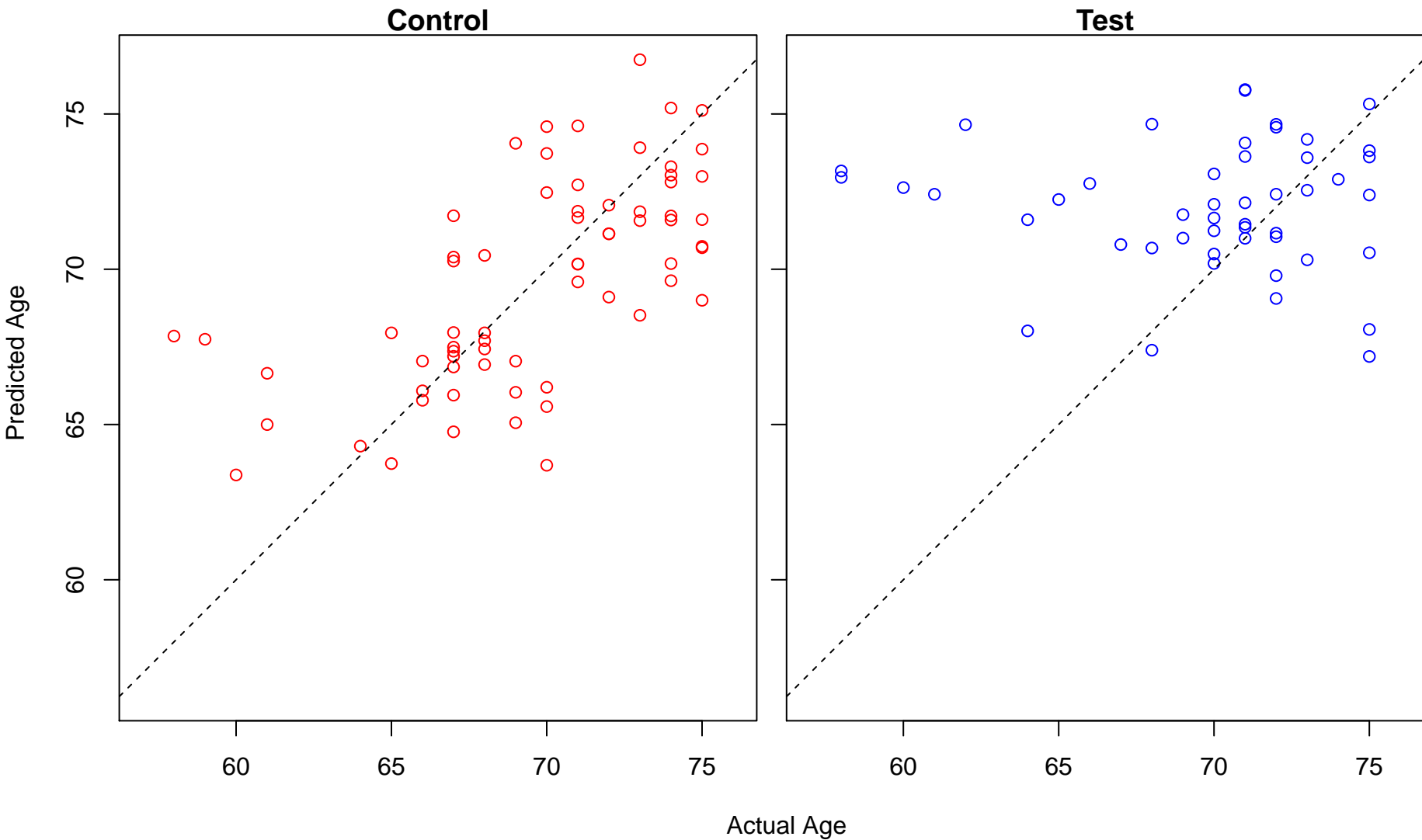
regulation of ATPase activity (Score: 1.352241)



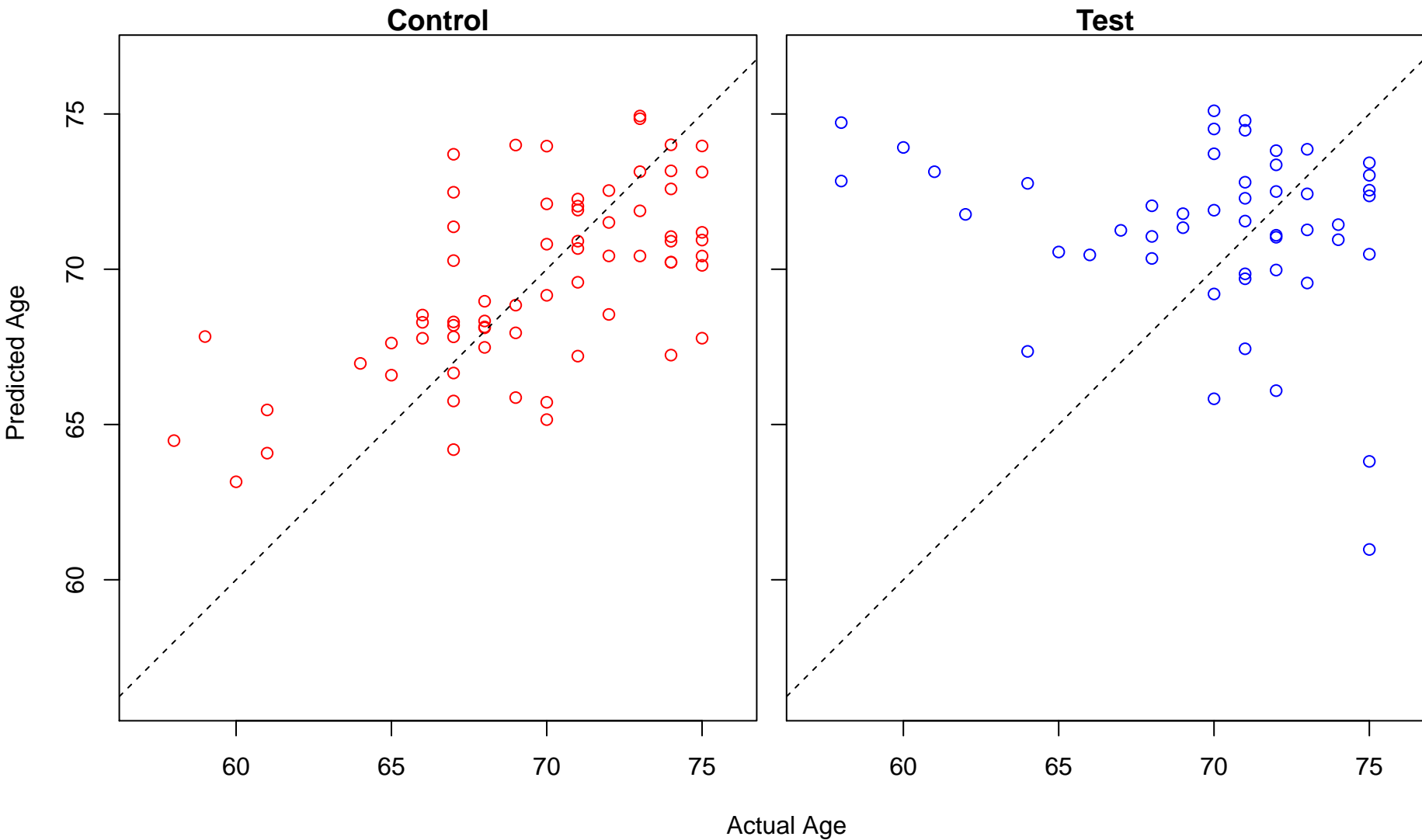
positive regulation of telomerase activity (Score: 1.351527)



regulation of neurogenesis (Score: 1.351109)

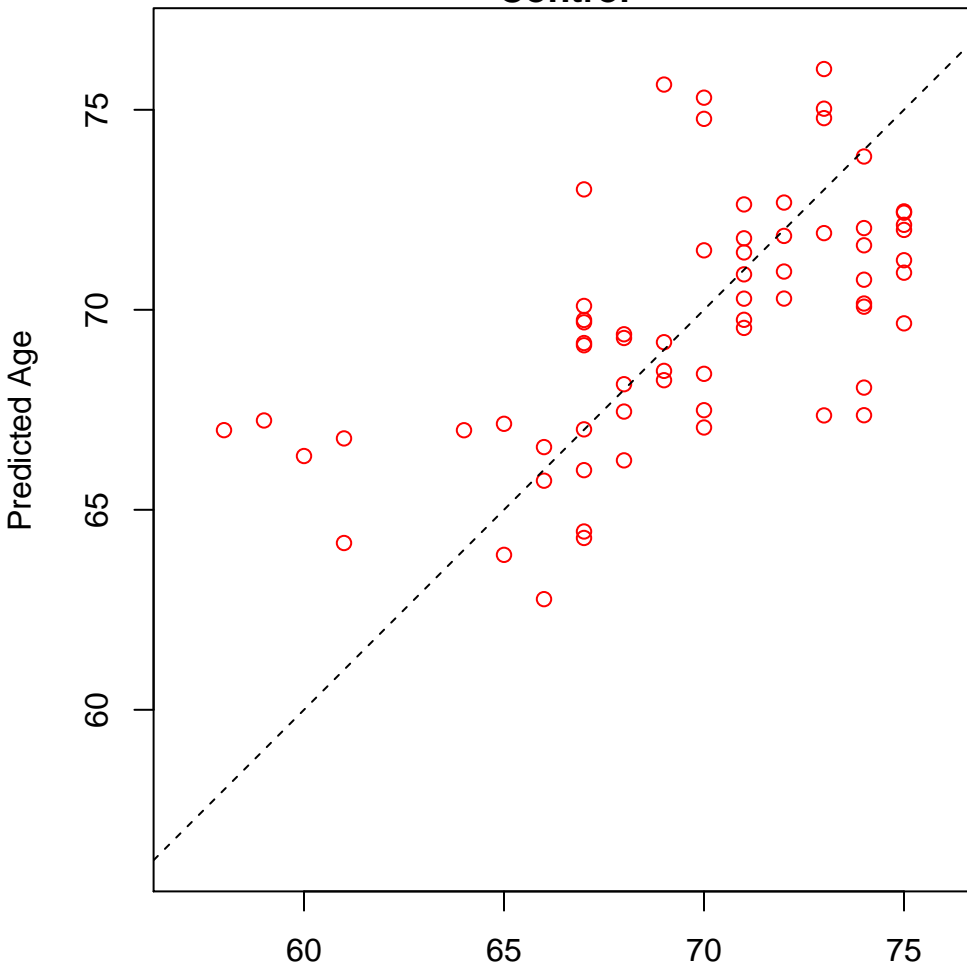


regulation of delayed rectifier potassium channel activity (Score: 1.350587)

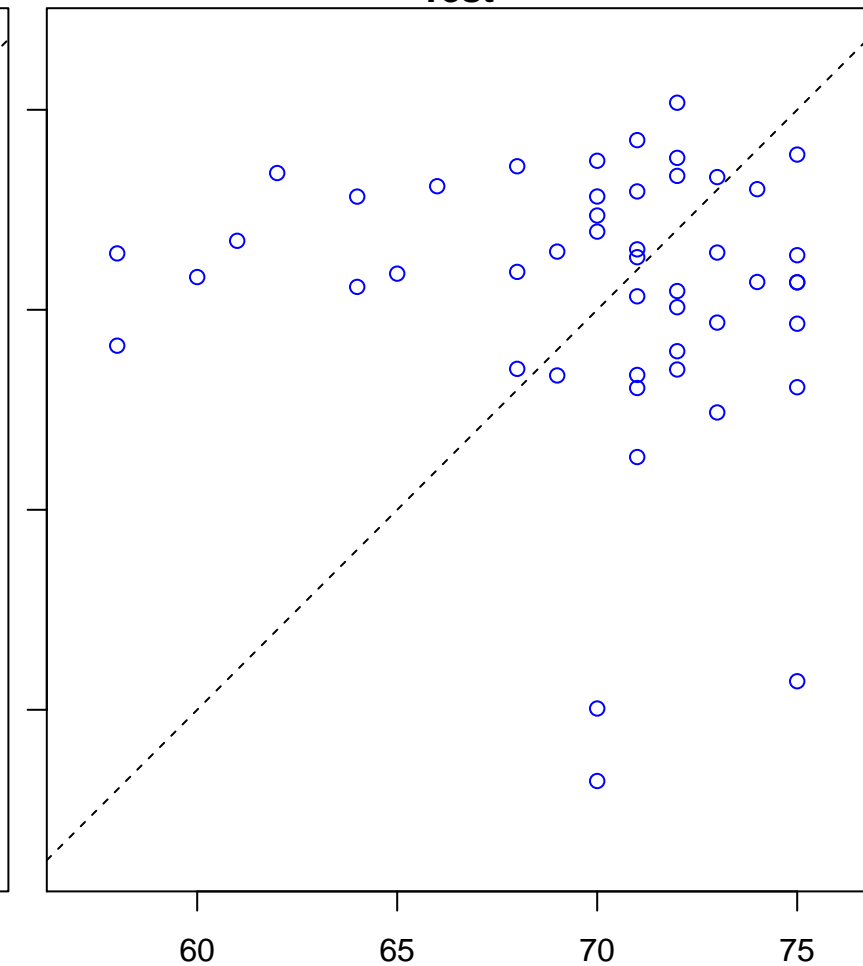


mitochondrial genome maintenance (Score: 1.350310)

Control

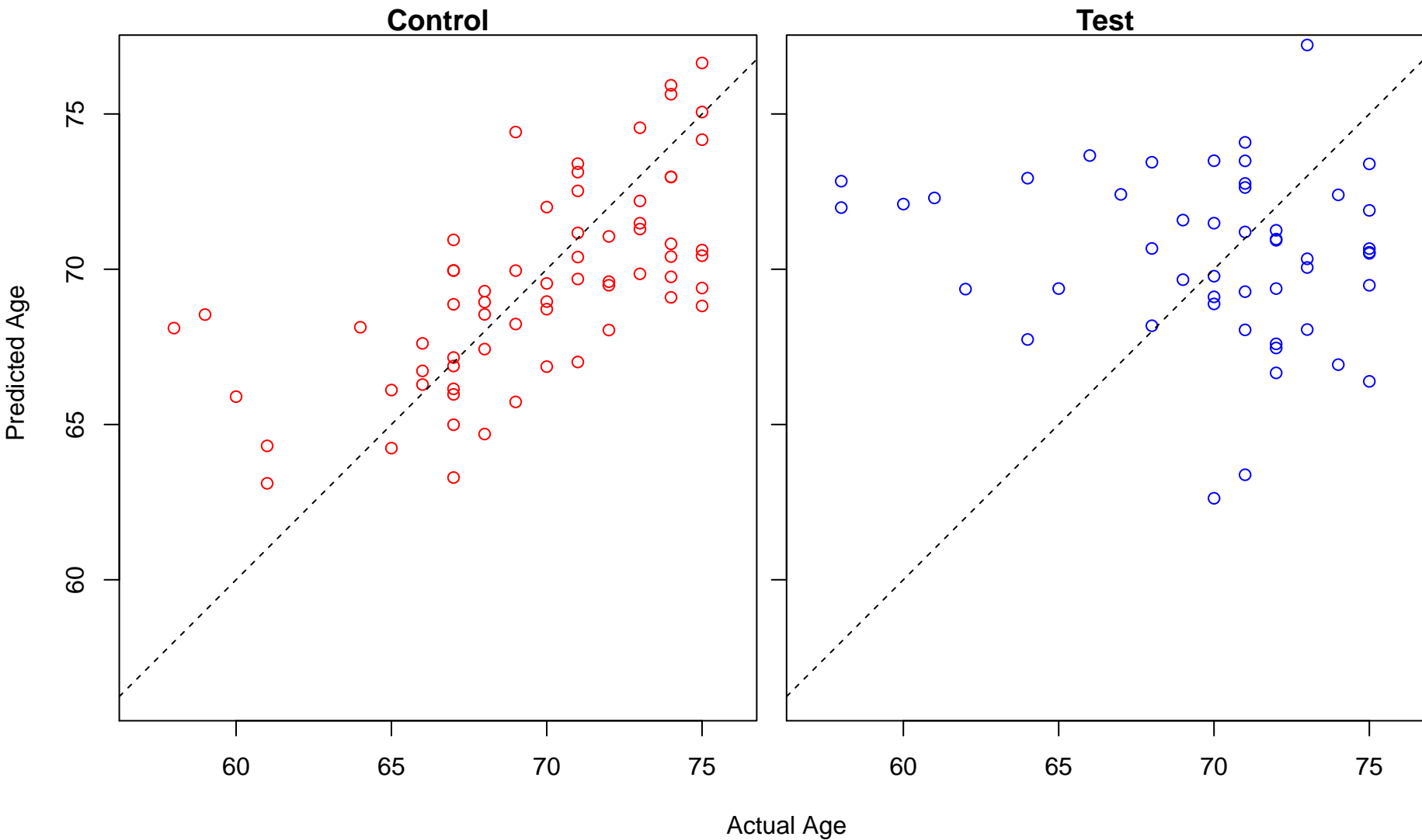


Test

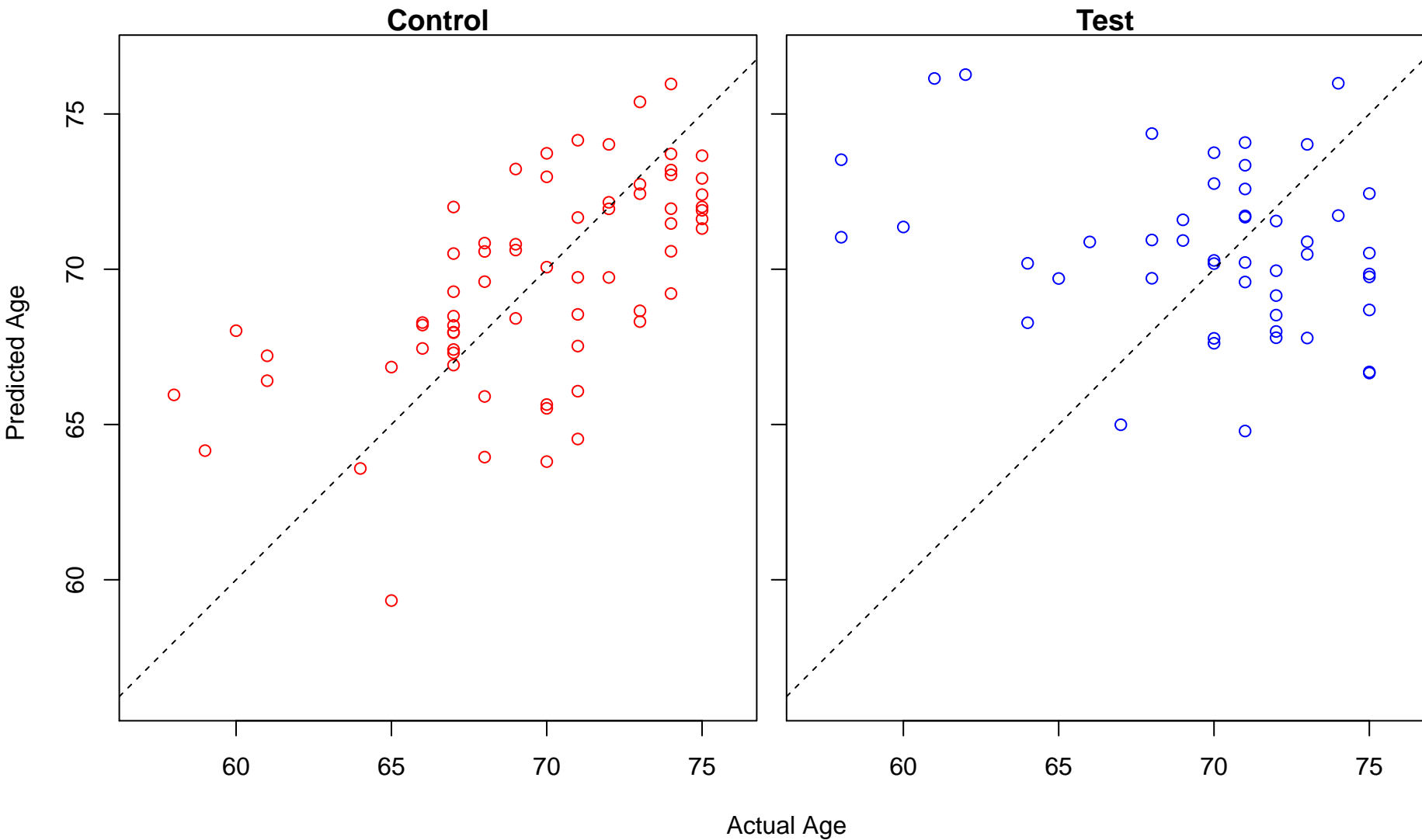


Actual Age

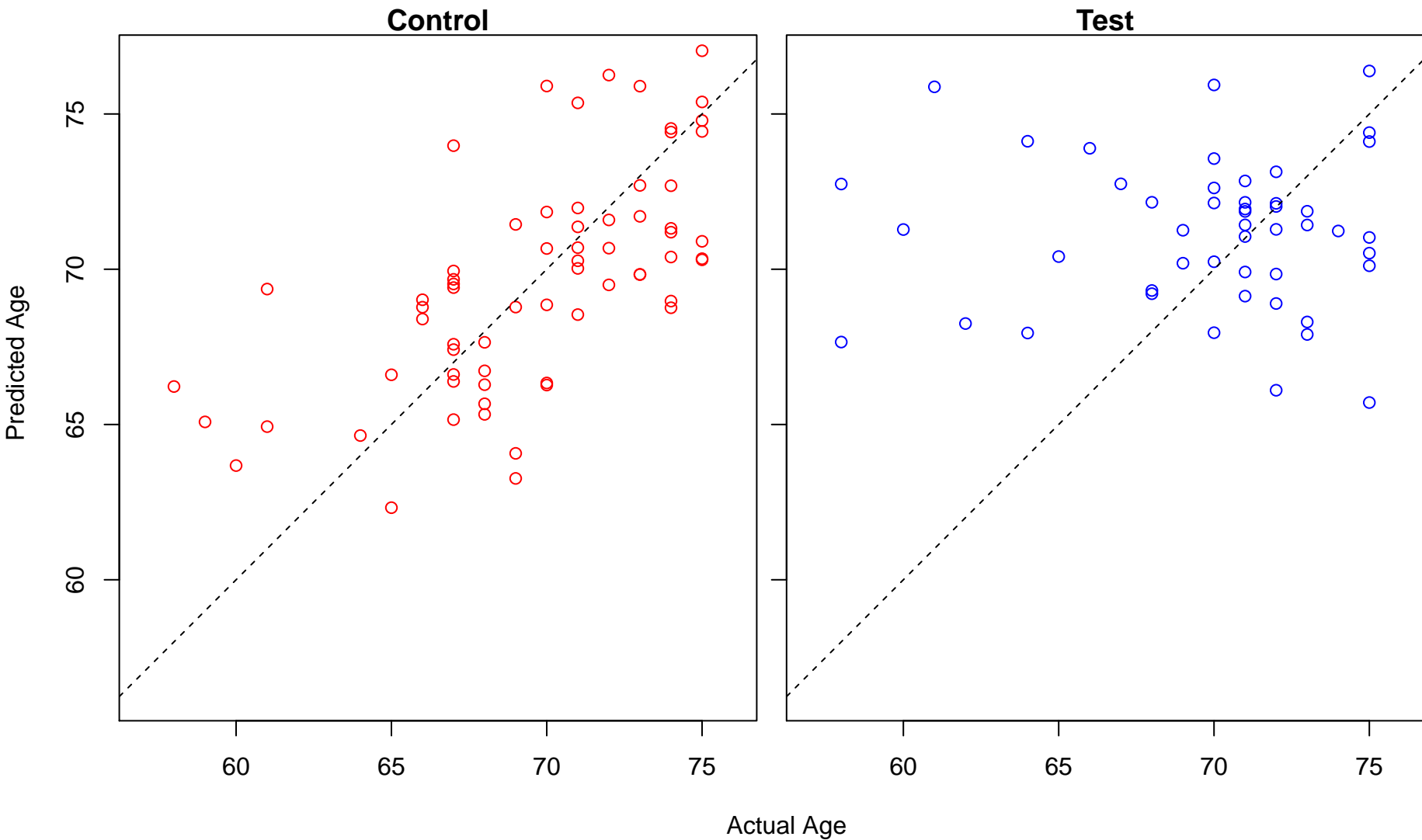
negative regulation of purine nucleotide metabolic process (Score: 1.350280)



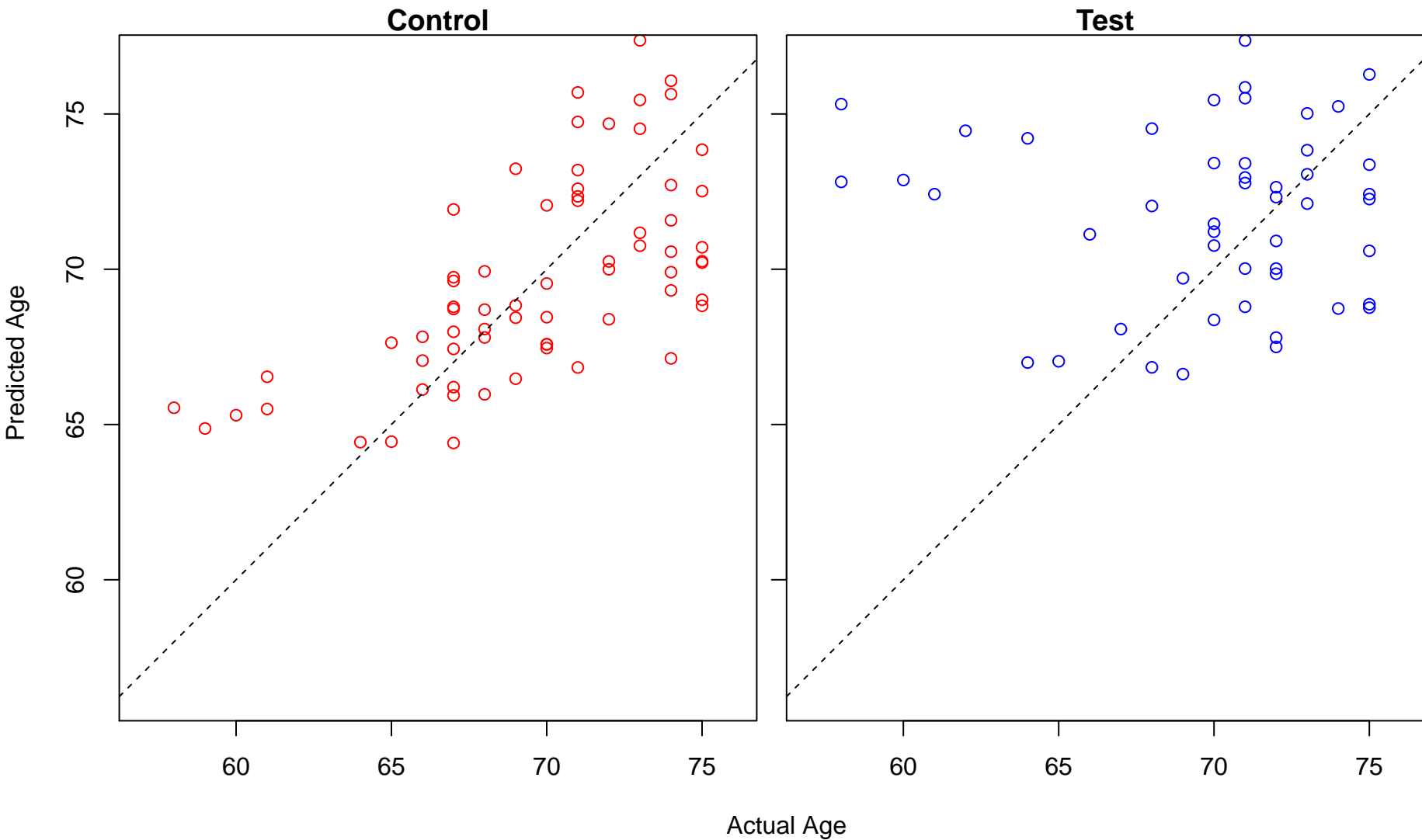
regulation of extrinsic apoptotic signaling pathway in absence of ligand (Score: 1.350193)



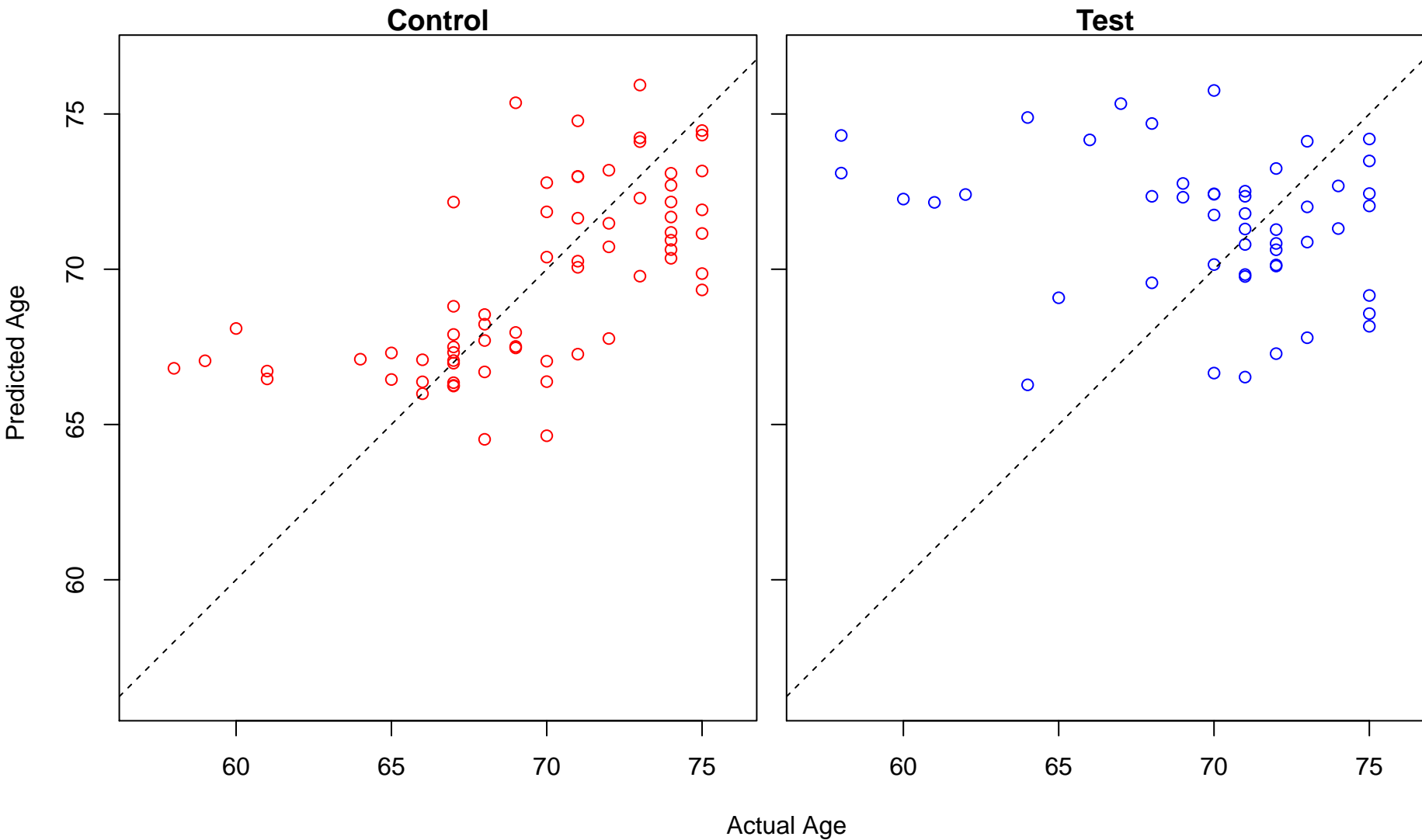
demethylation (Score: 1.350191)



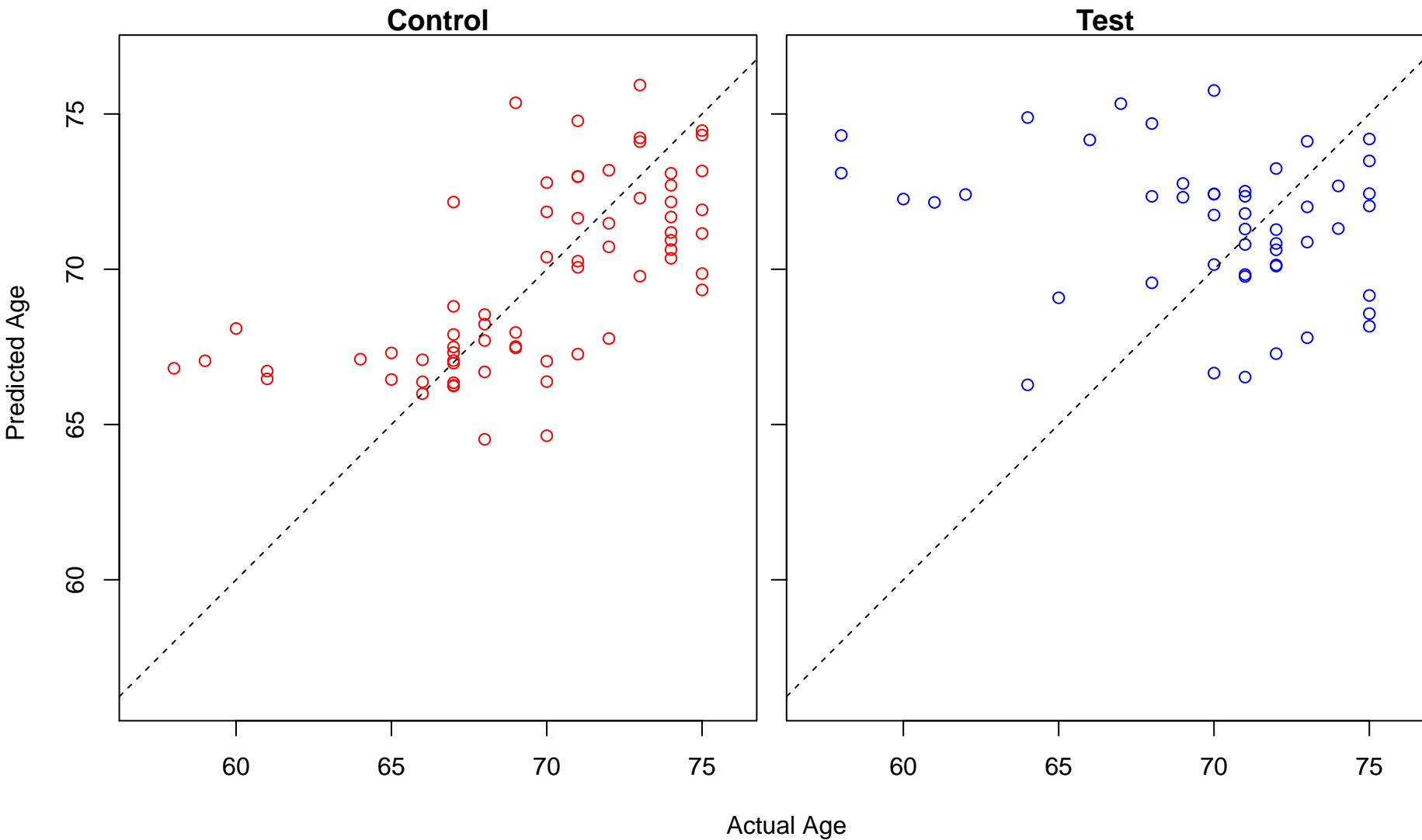
leukocyte degranulation (Score: 1.350029)



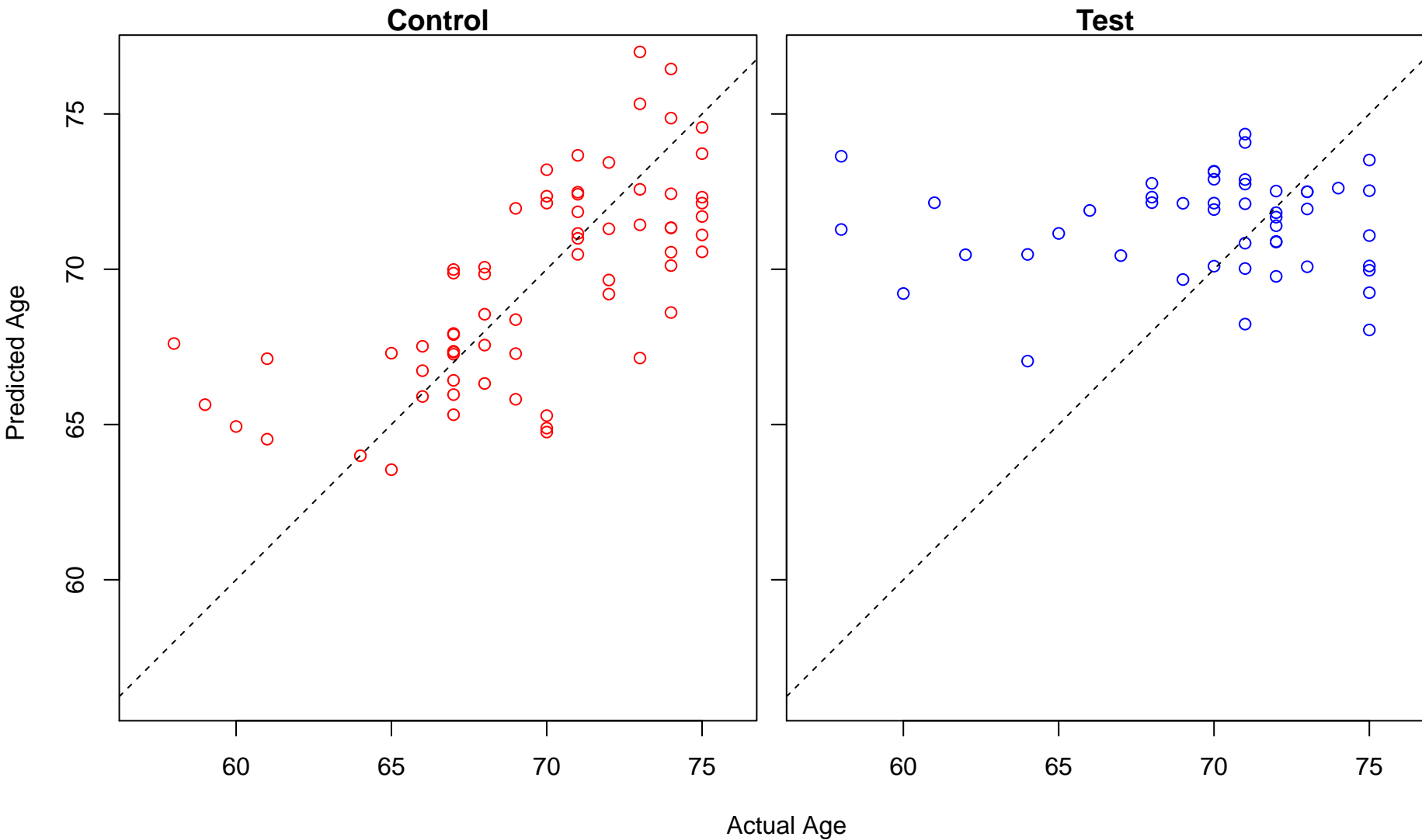
protein nitrosylation (Score: 1.349993)



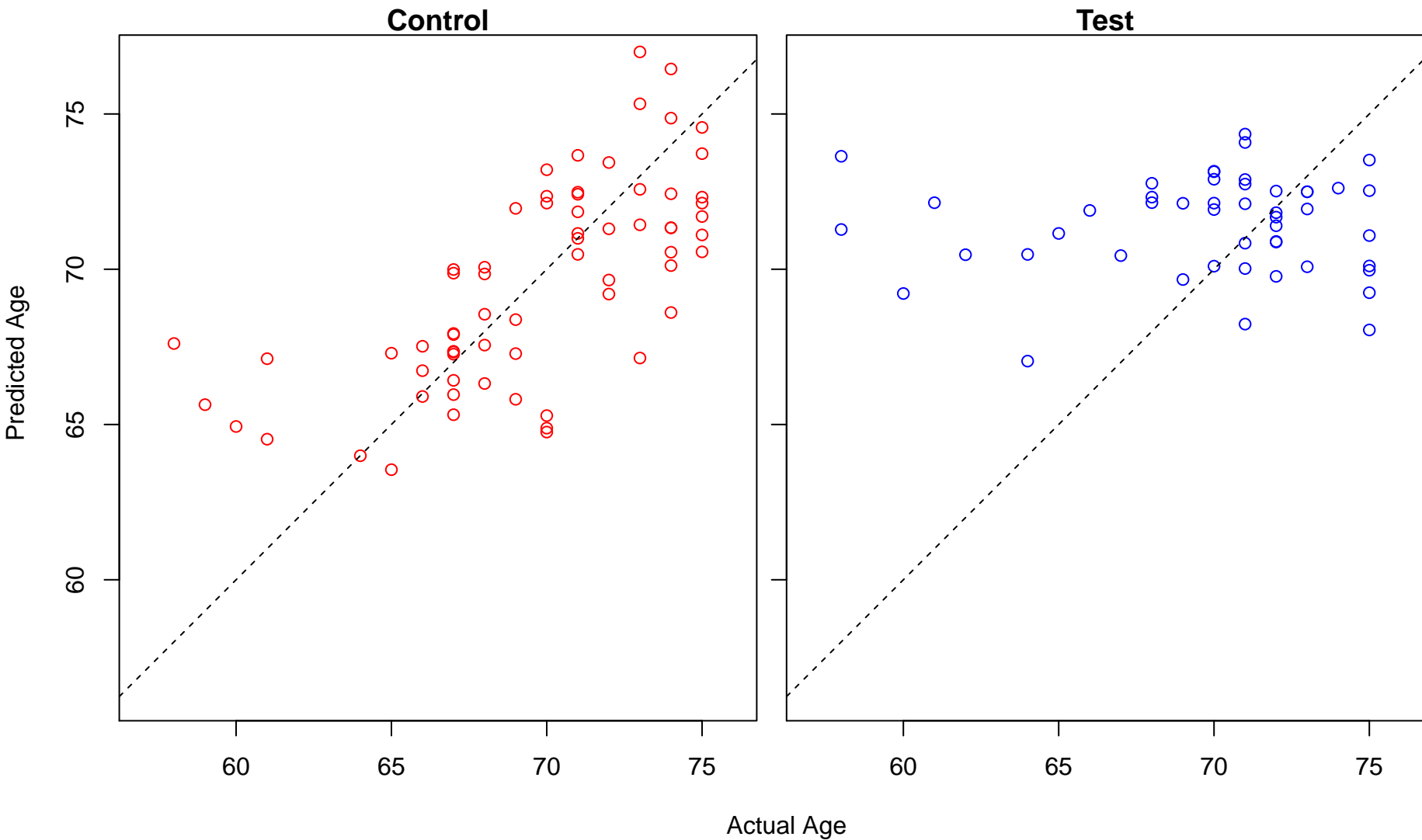
peptidyl-cysteine S-nitrosylation (Score: 1.349993)



extracellular matrix organization (Score: 1.349946)

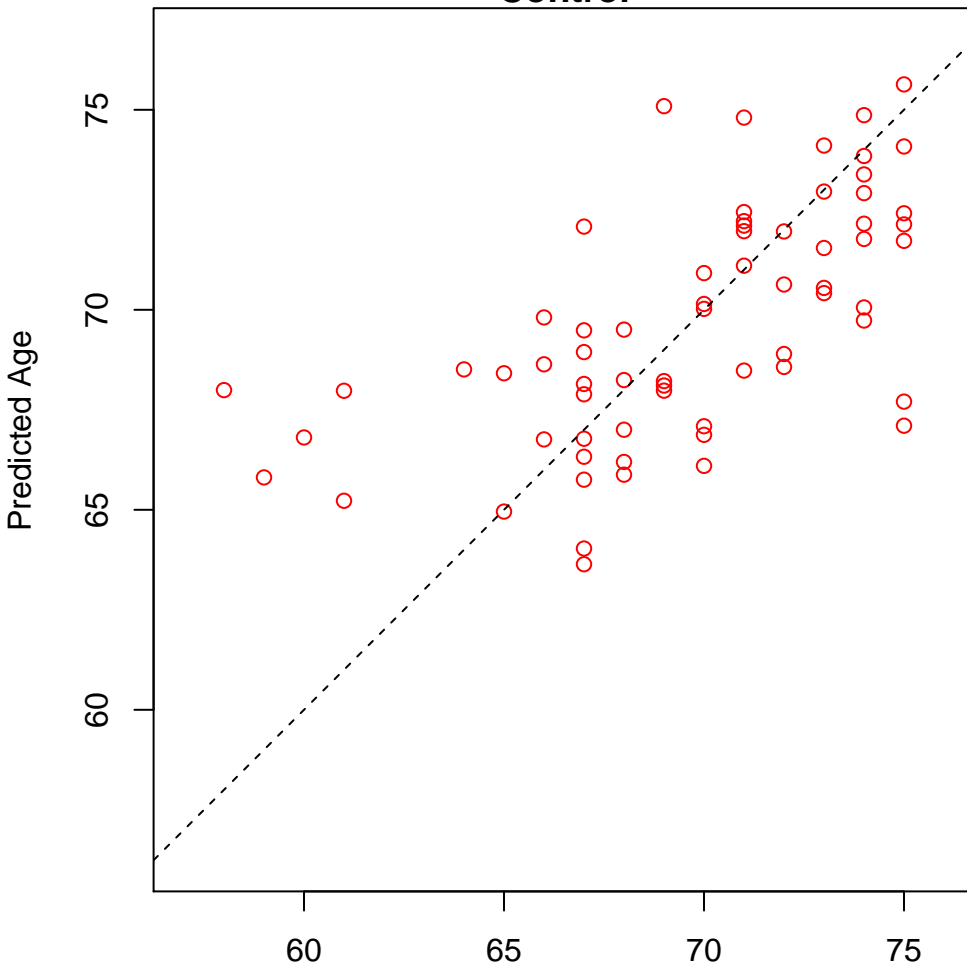


extracellular structure organization (Score: 1.349946)

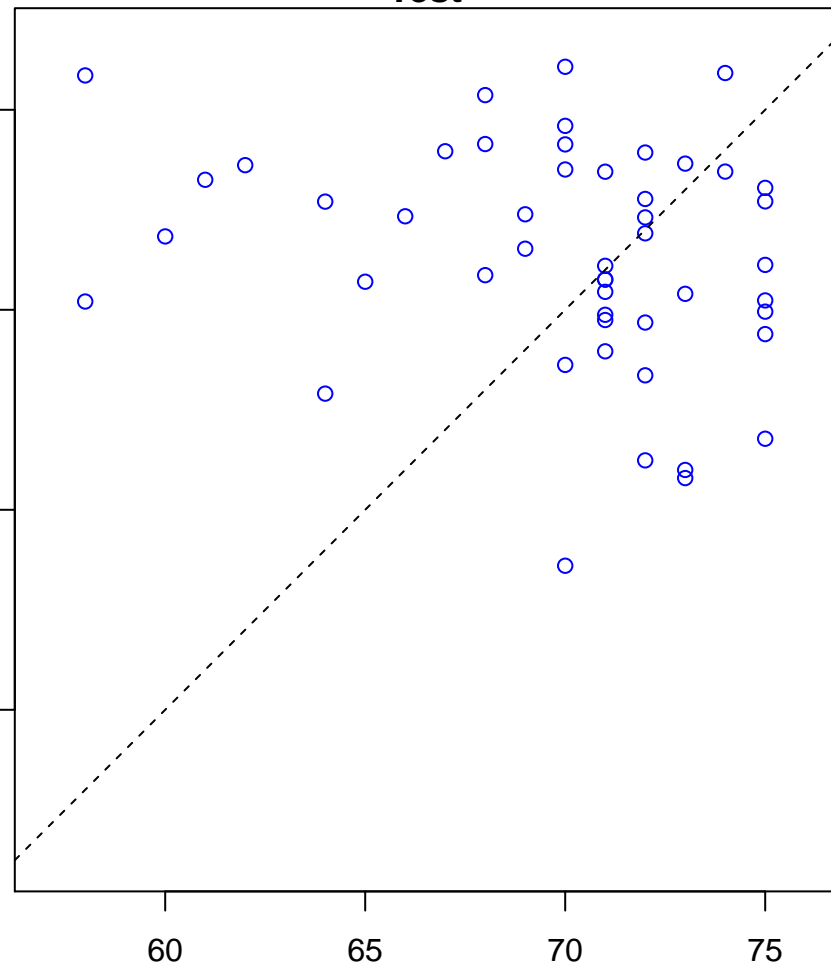


telomere maintenance via telomerase (Score: 1.349505)

Control

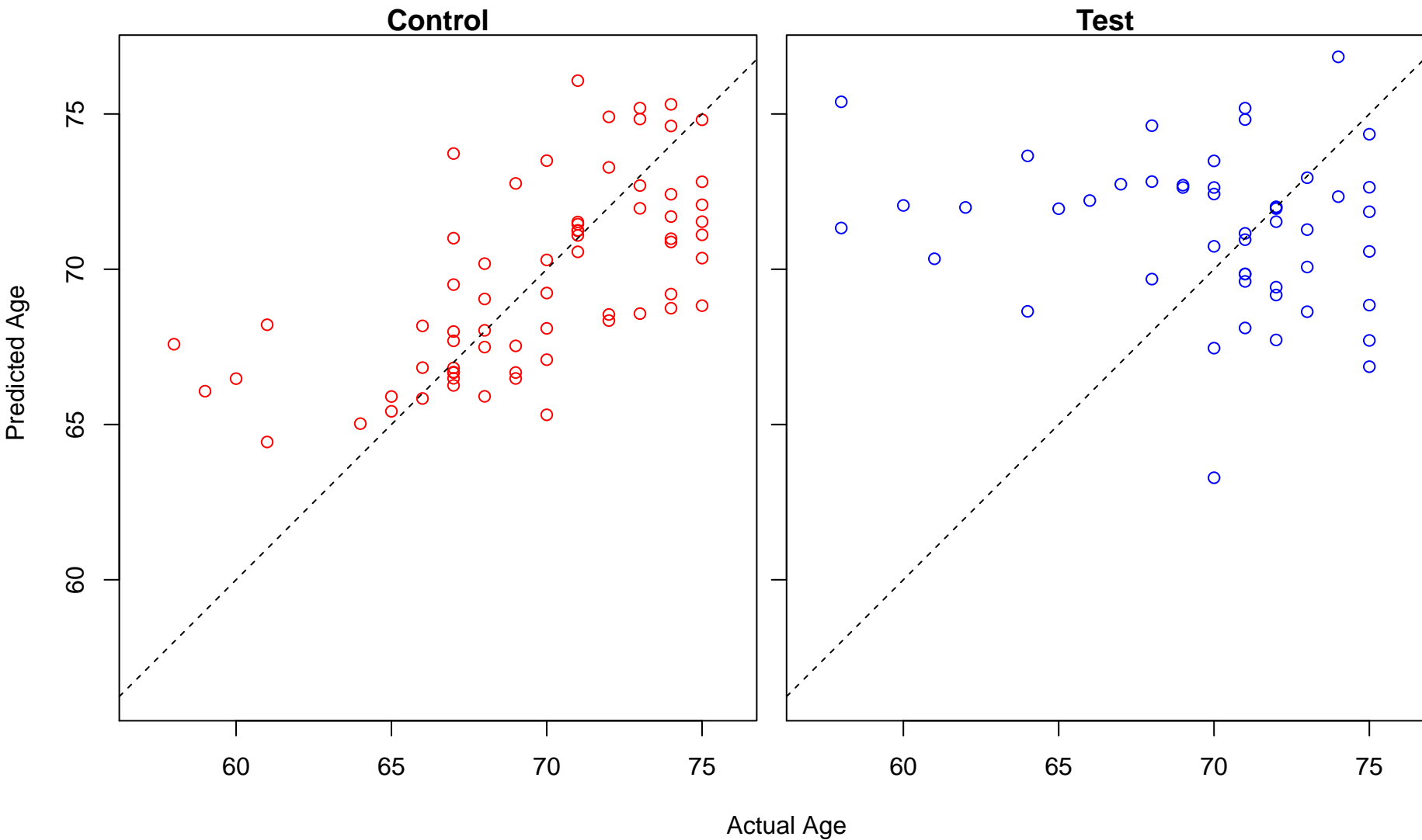


Test

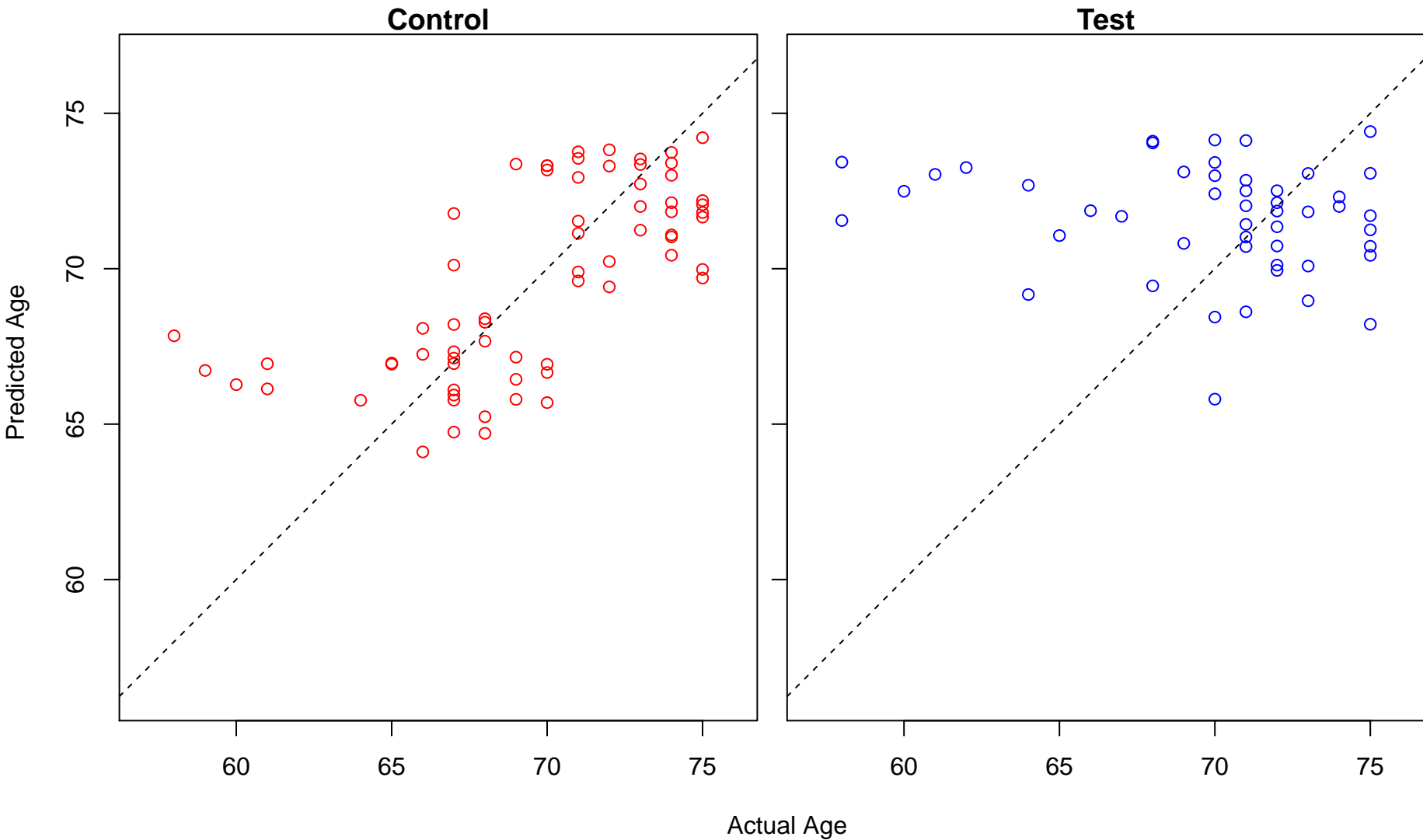


Actual Age

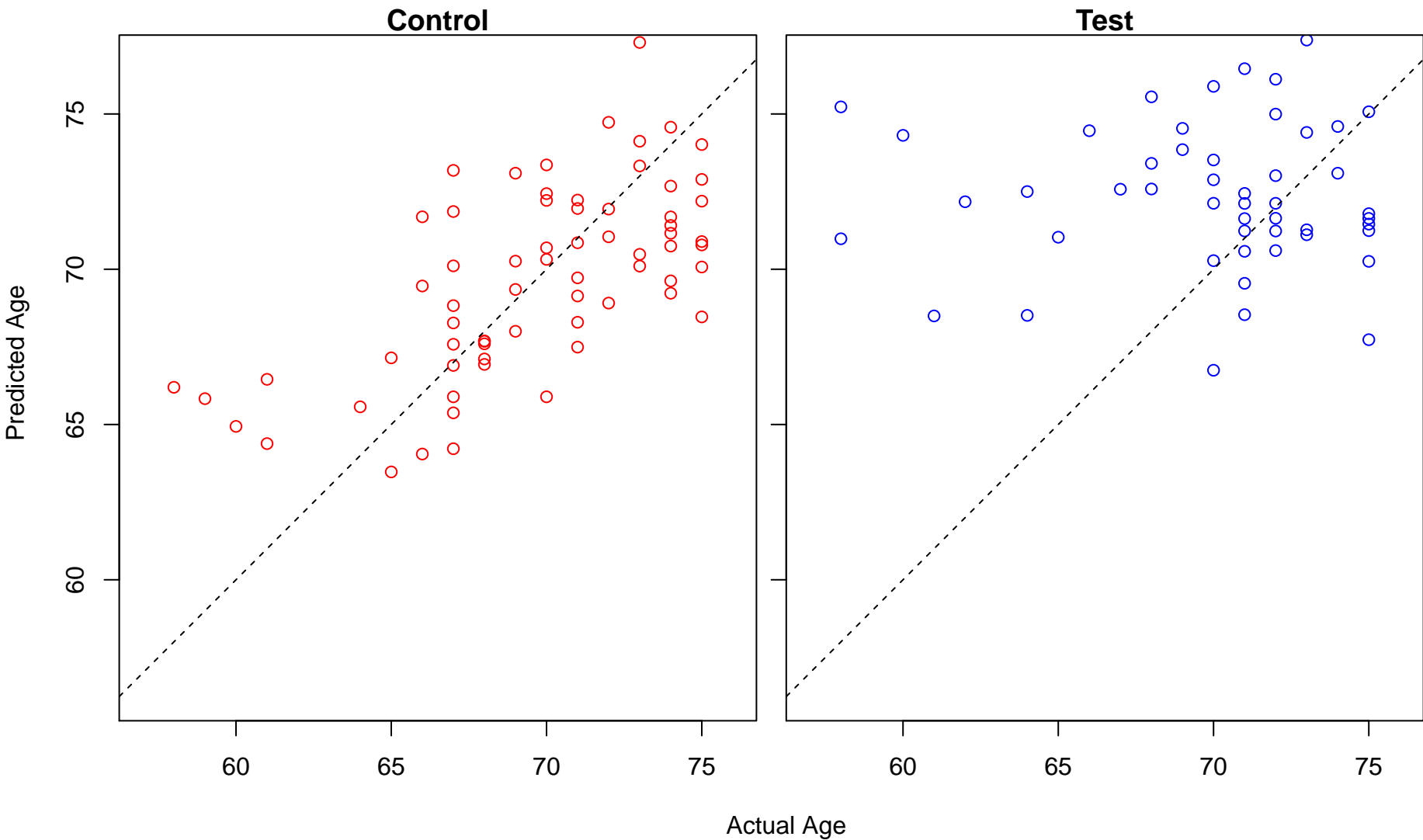
spliceosomal tri-snRNP complex assembly (Score: 1.349209)



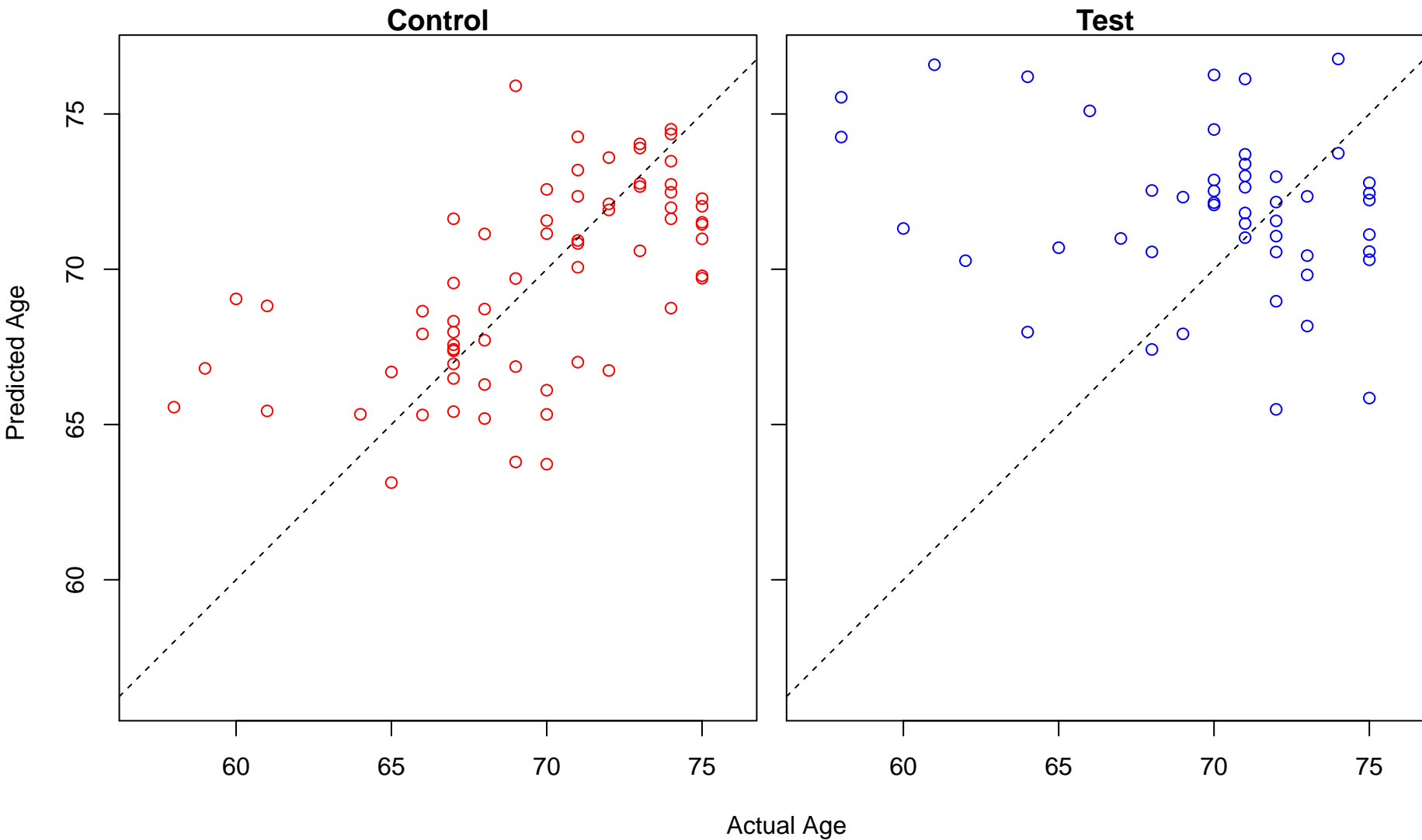
regulation of G2/M transition of mitotic cell cycle (Score: 1.348315)



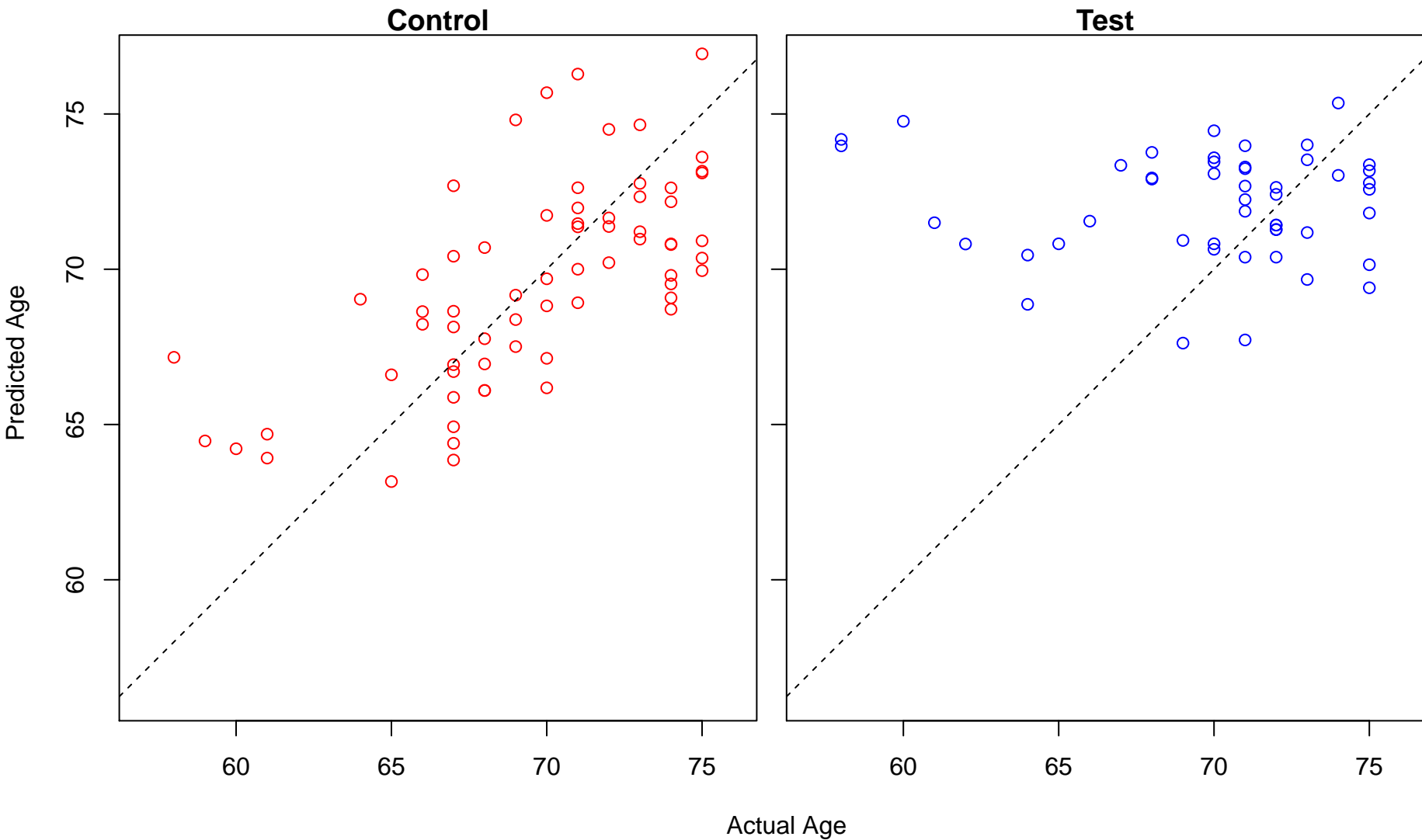
regulation of mitochondrial membrane permeability involved in apoptotic process (Score: 1.347417)



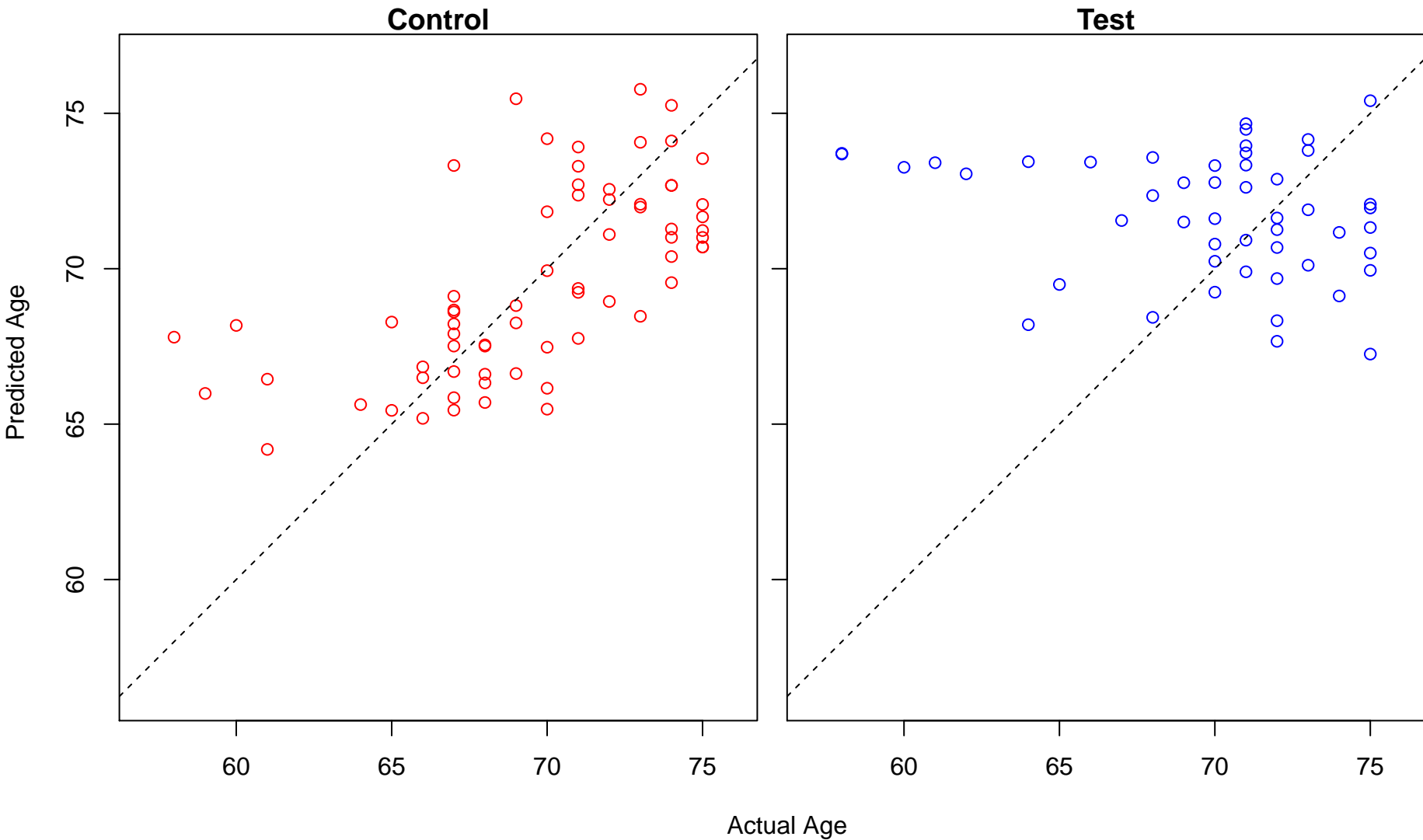
regulation of NF-kappaB import into nucleus (Score: 1.347113)



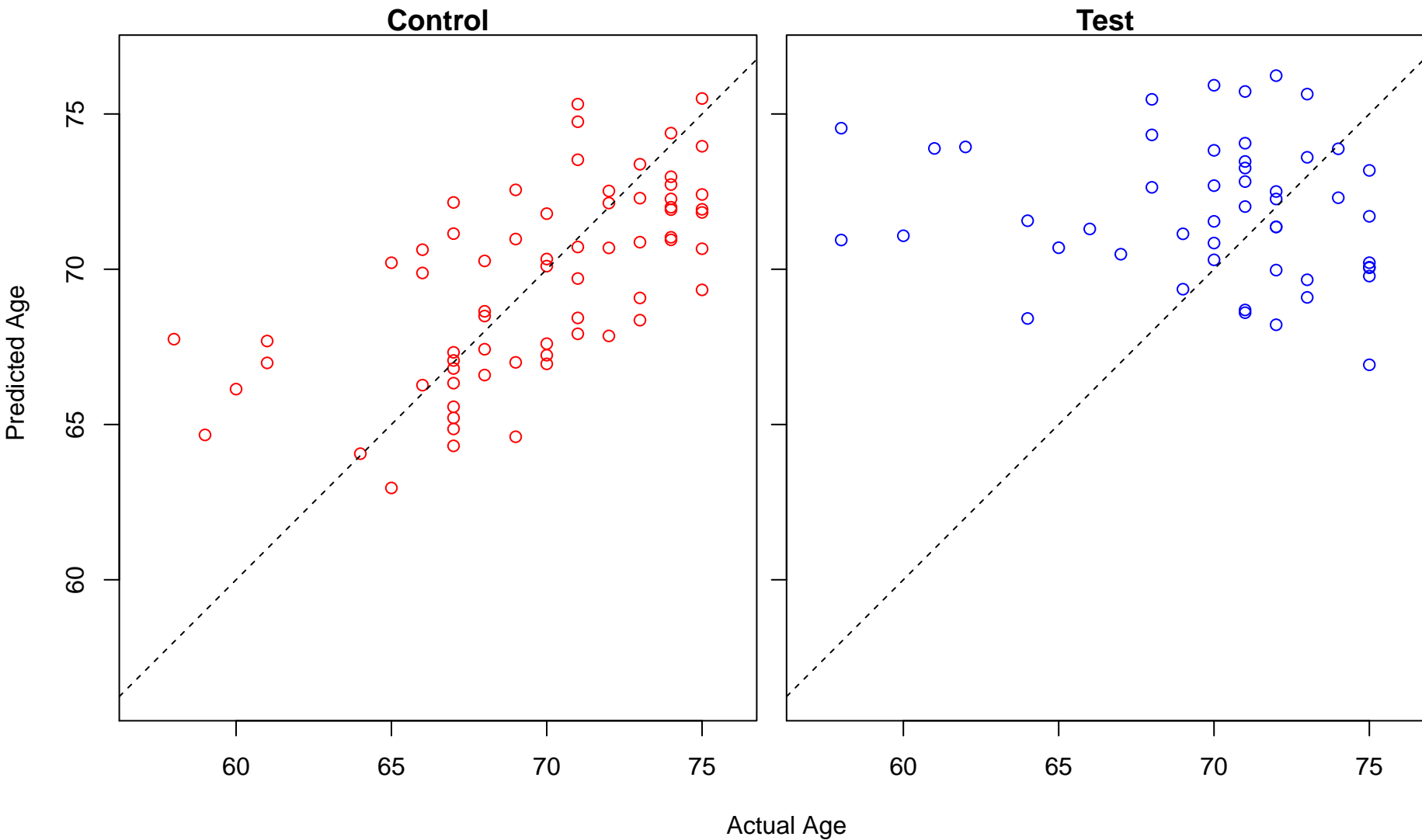
ceramide metabolic process (Score: 1.346167)



adenylate cyclase–modulating G–protein coupled receptor signaling pathway (Score: 1.345654)

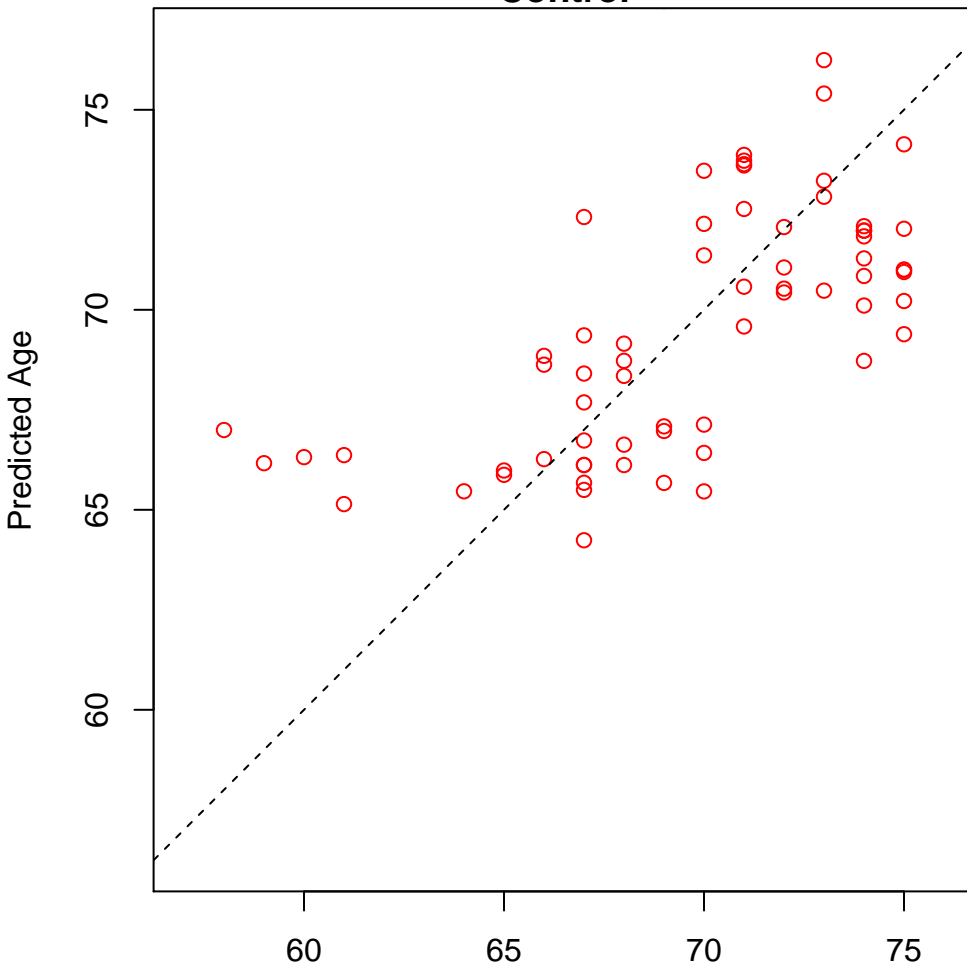


positive regulation of interferon-beta production (Score: 1.345552)

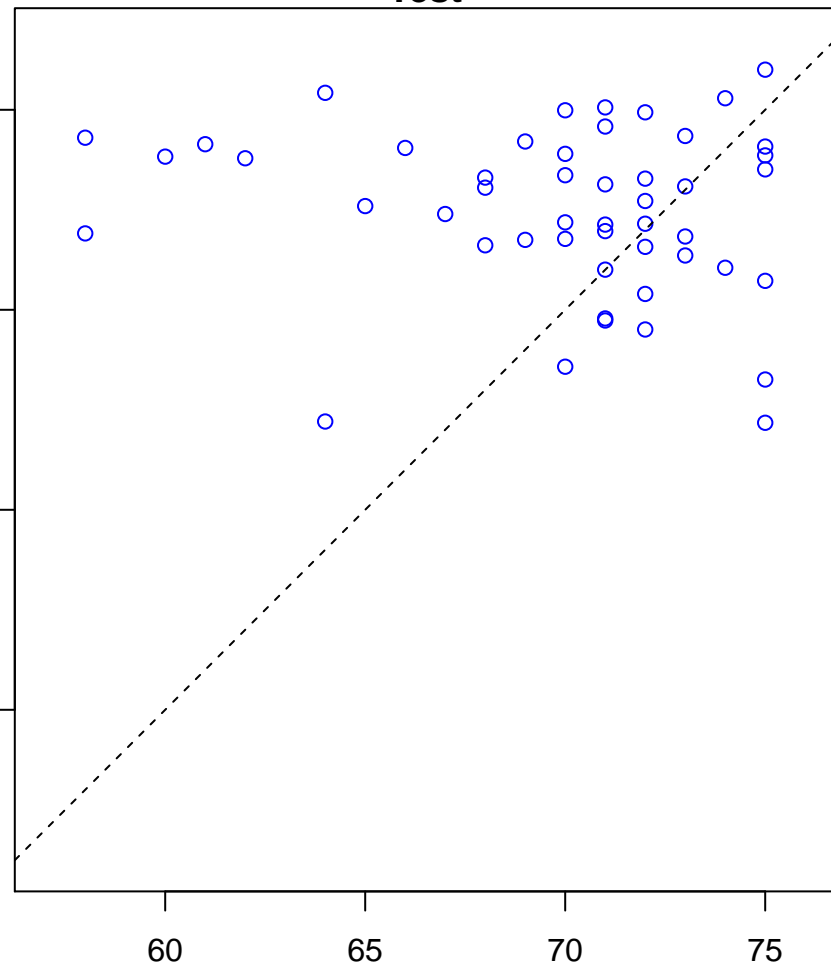


regulation of cellular response to heat (Score: 1.344833)

Control

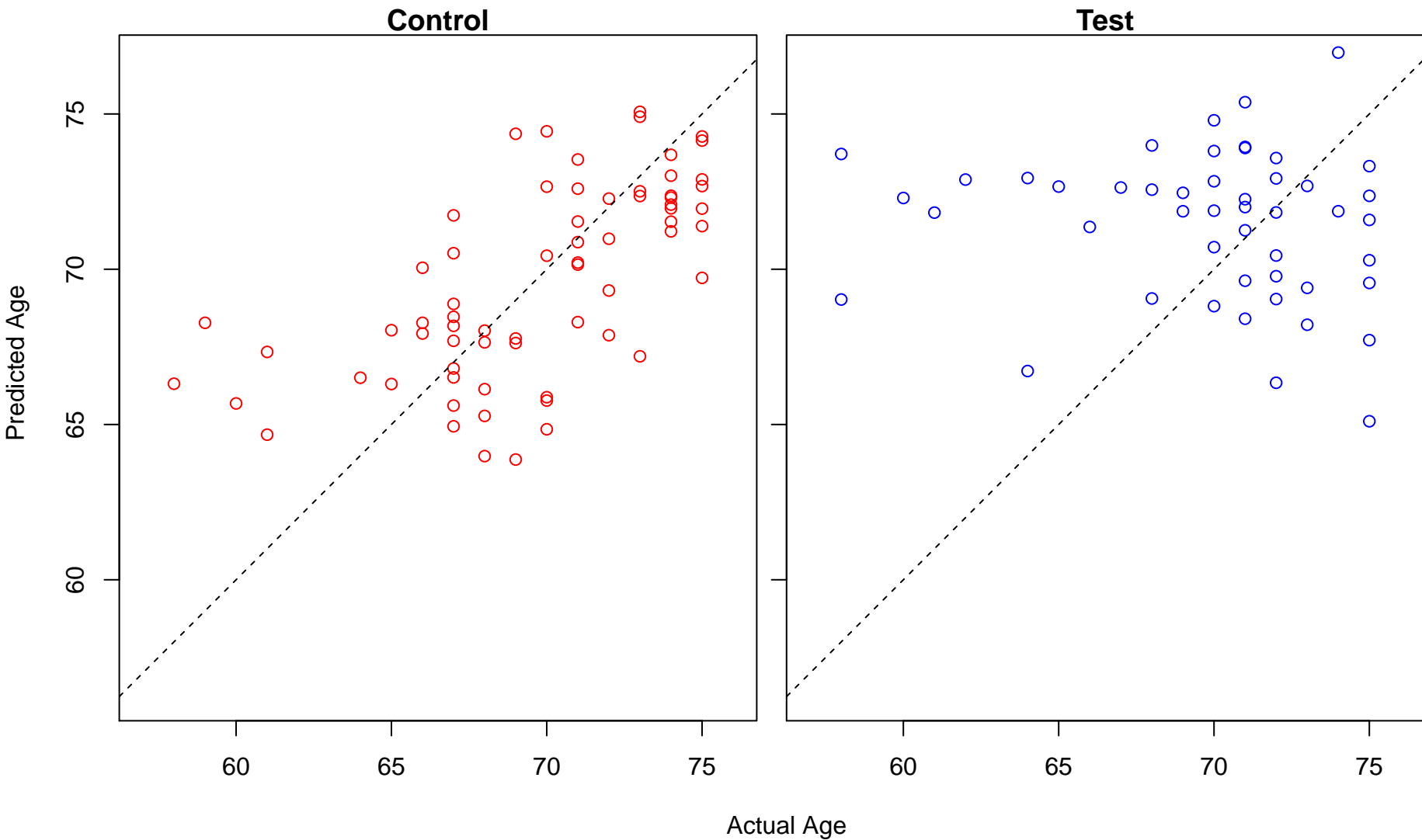


Test

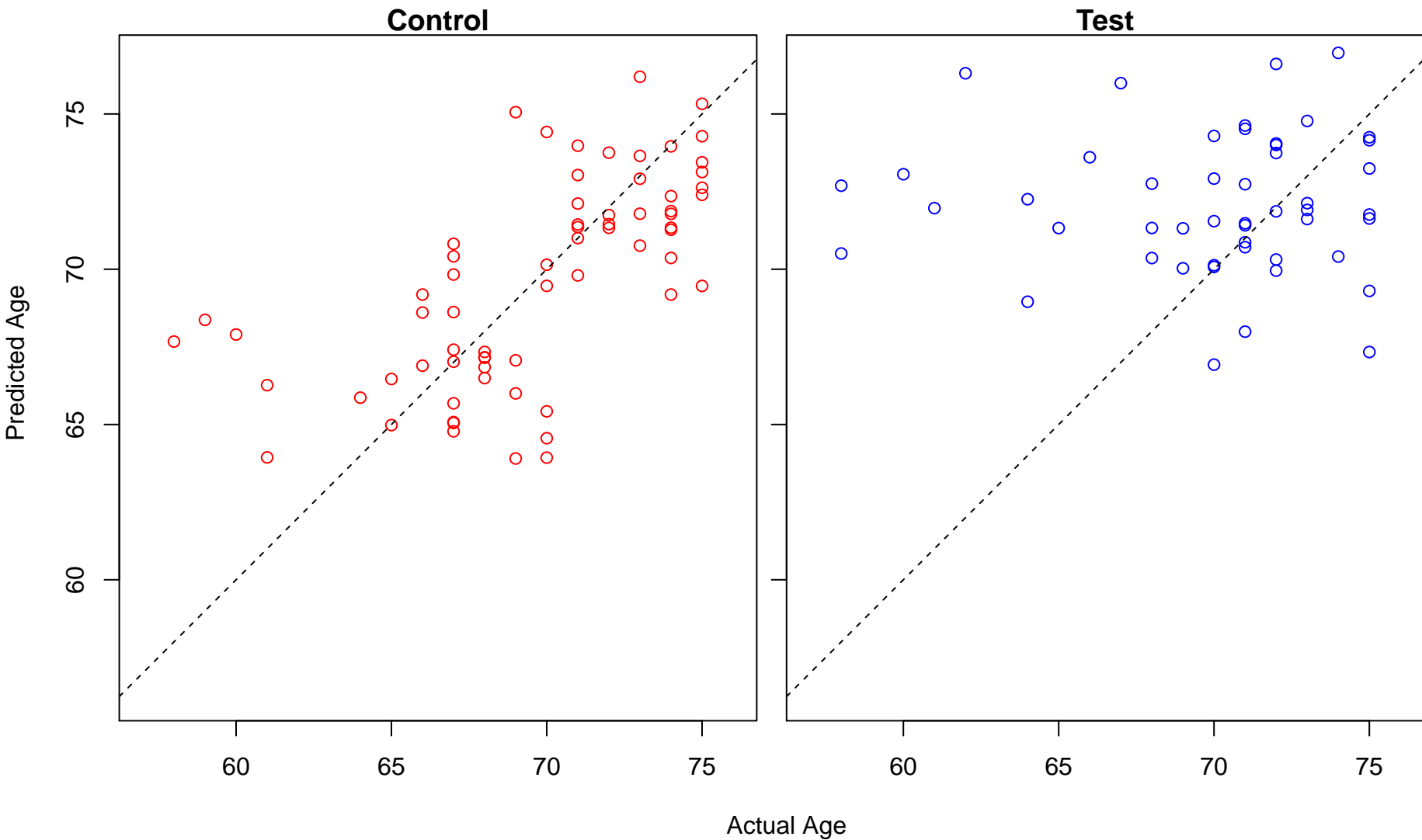


Actual Age

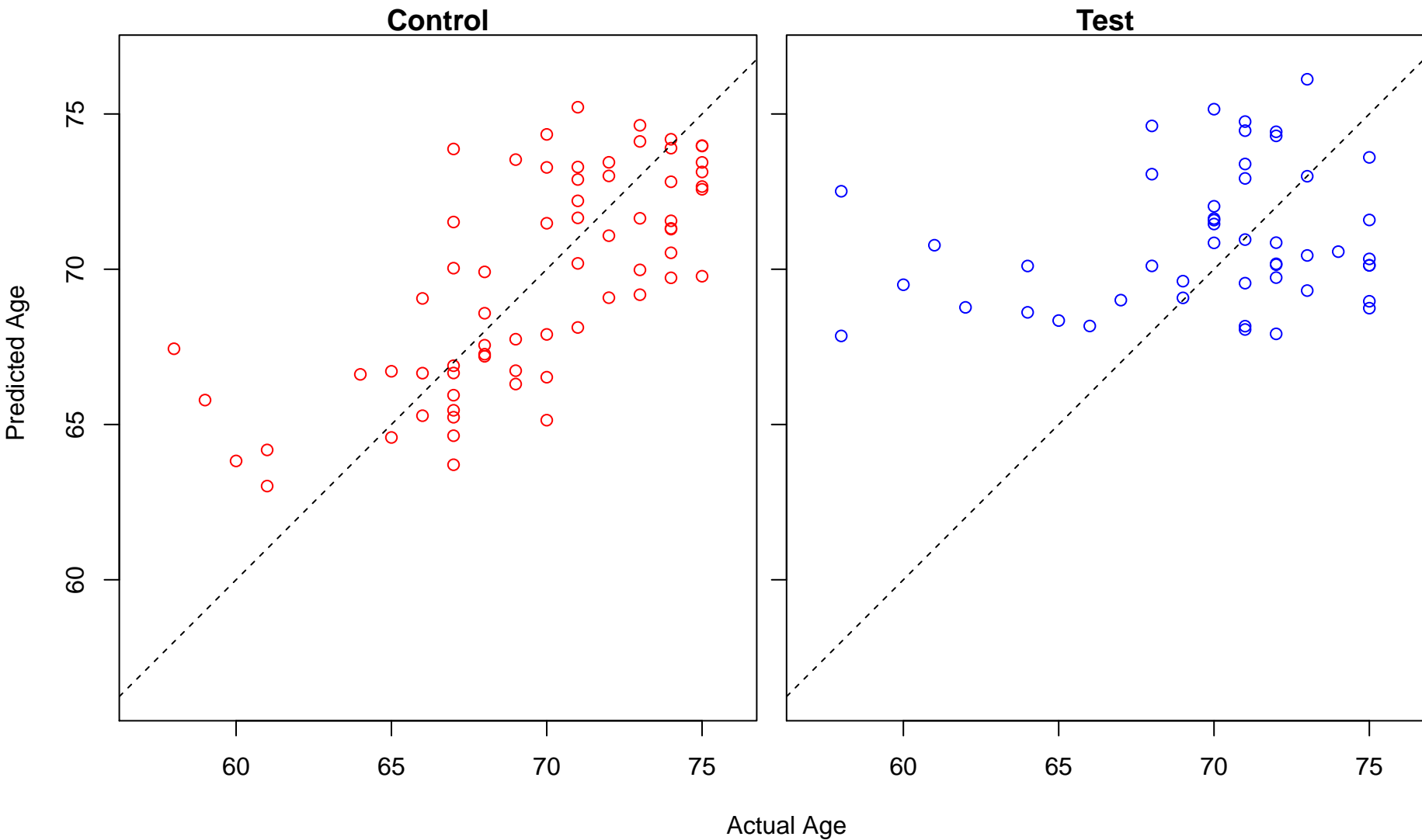
regulation of pri-miRNA transcription from RNA polymerase II promoter (Score: 1.344622)



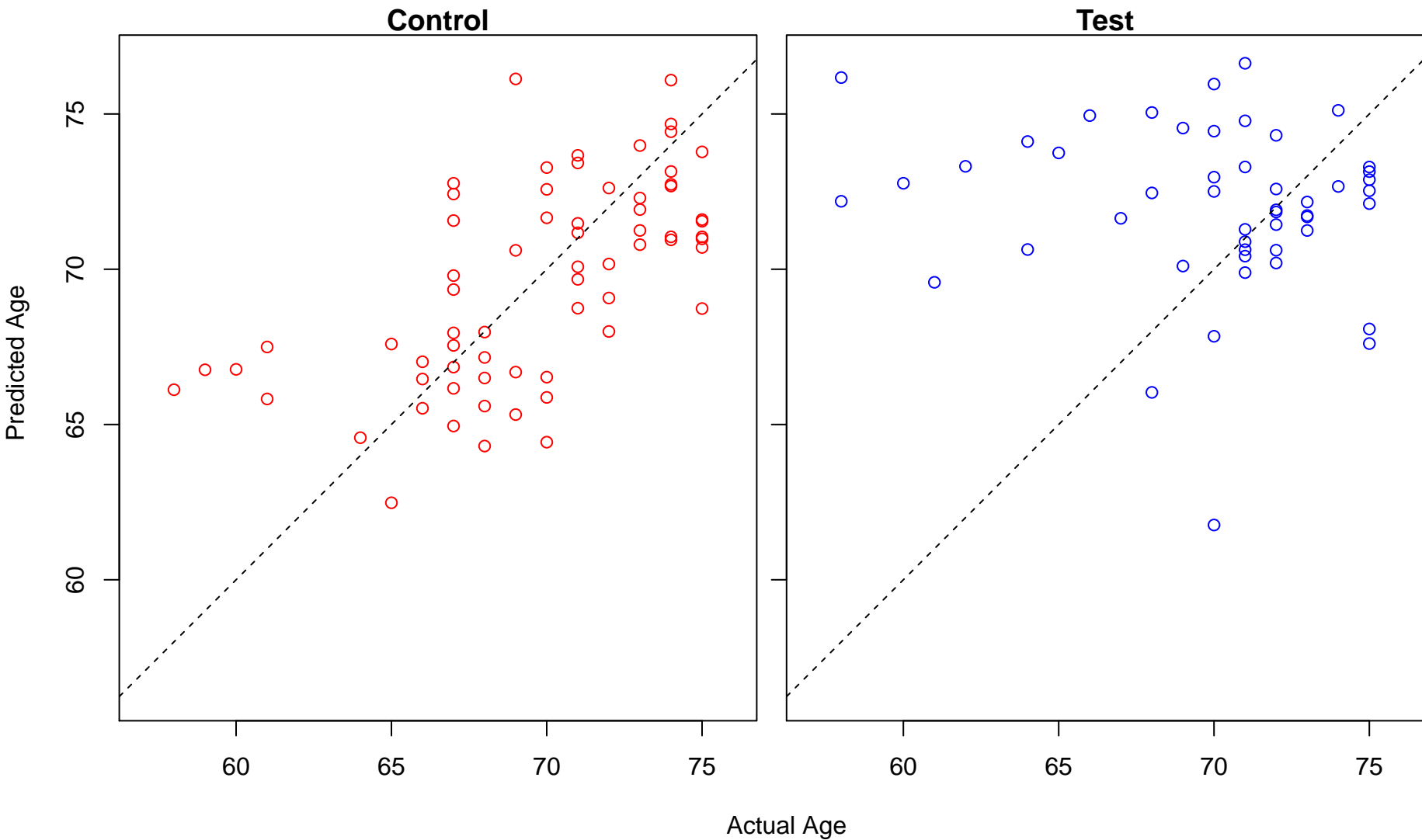
regulation of tumor necrosis factor–mediated signaling pathway (Score: 1.344500)



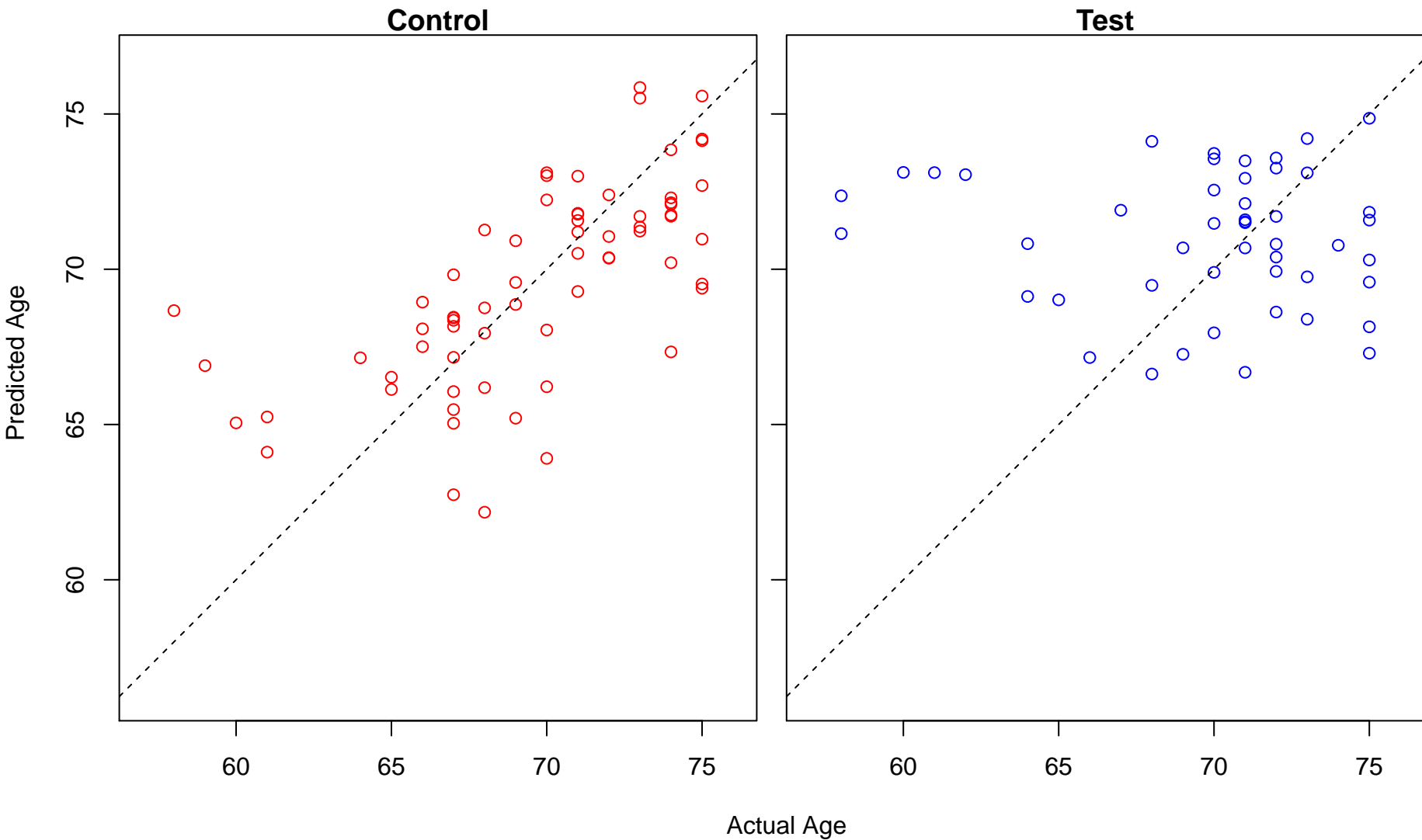
erythrocyte differentiation (Score: 1.344118)



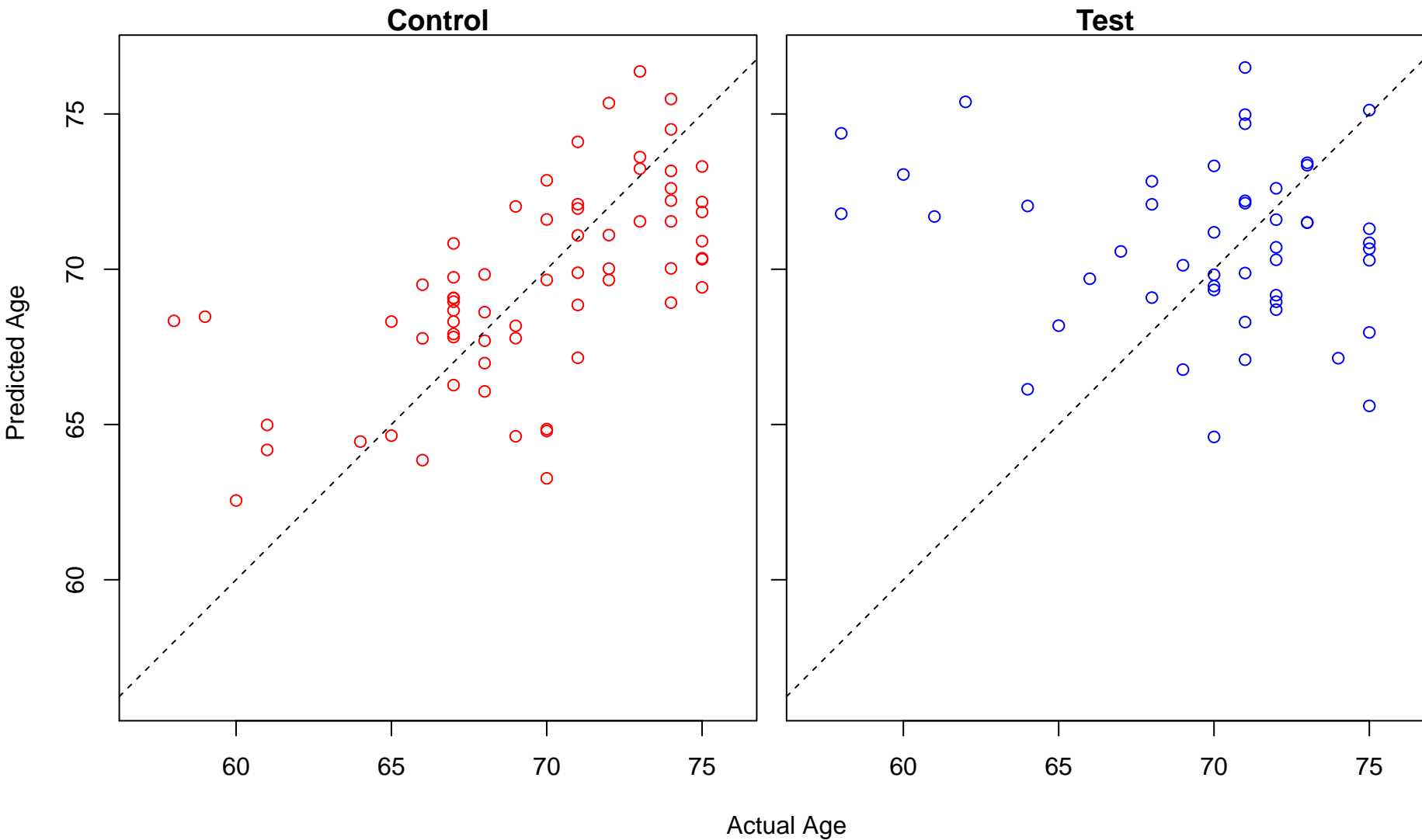
regulation of interferon-gamma-mediated signaling pathway (Score: 1.343946)



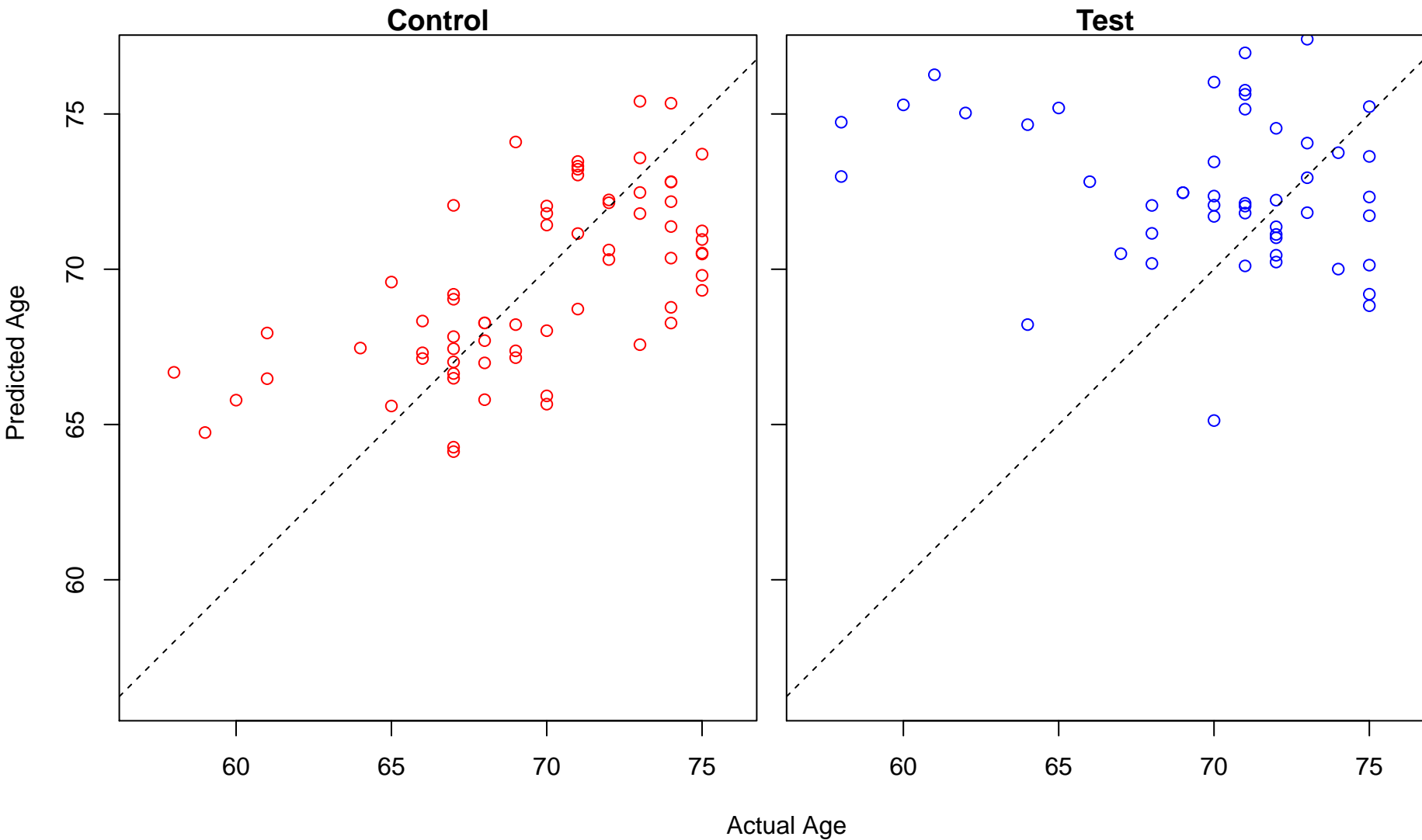
negative regulation of organelle assembly (Score: 1.342836)



myeloid cell activation involved in immune response (Score: 1.342463)

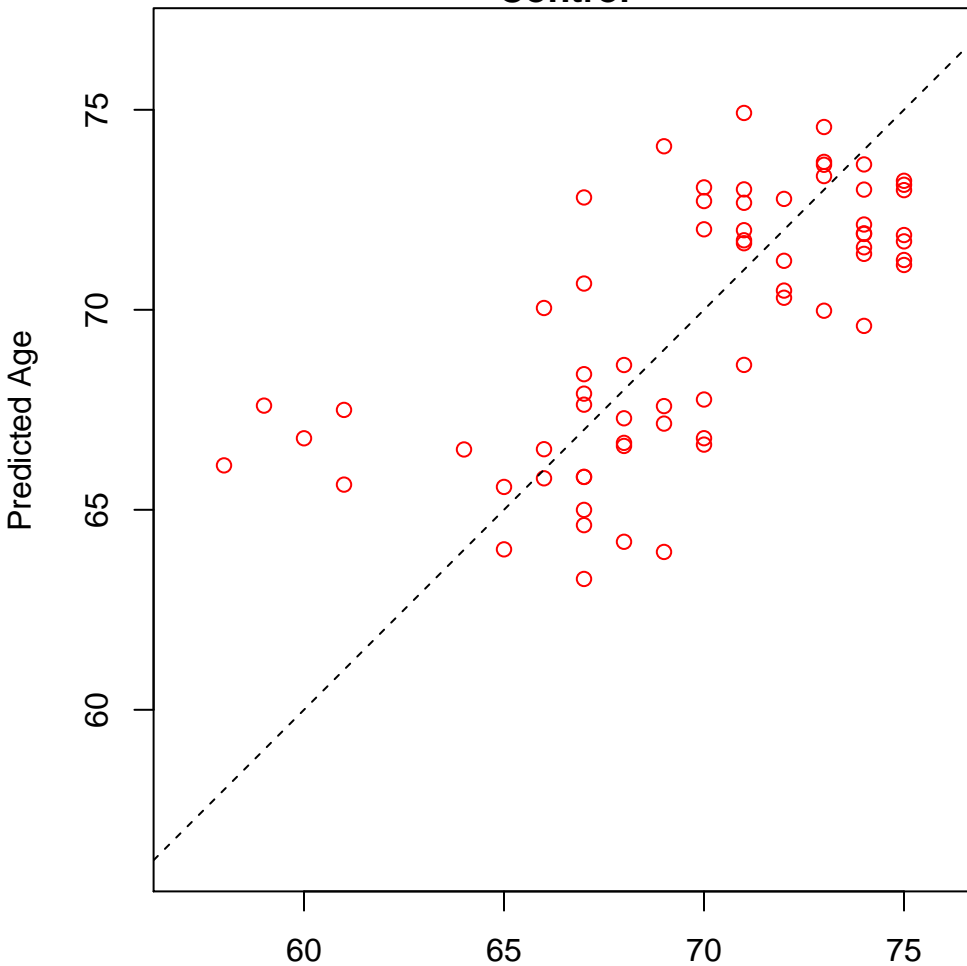


activation of protein kinase A activity (Score: 1.342044)

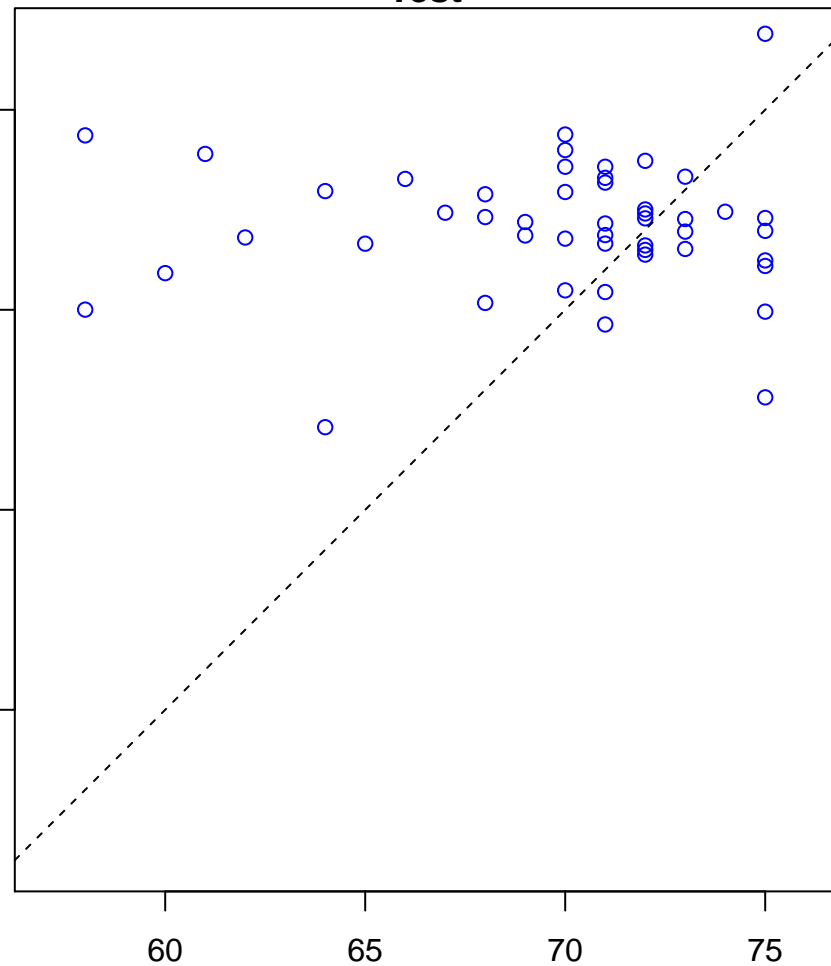


chromatin assembly or disassembly (Score: 1.341889)

Control

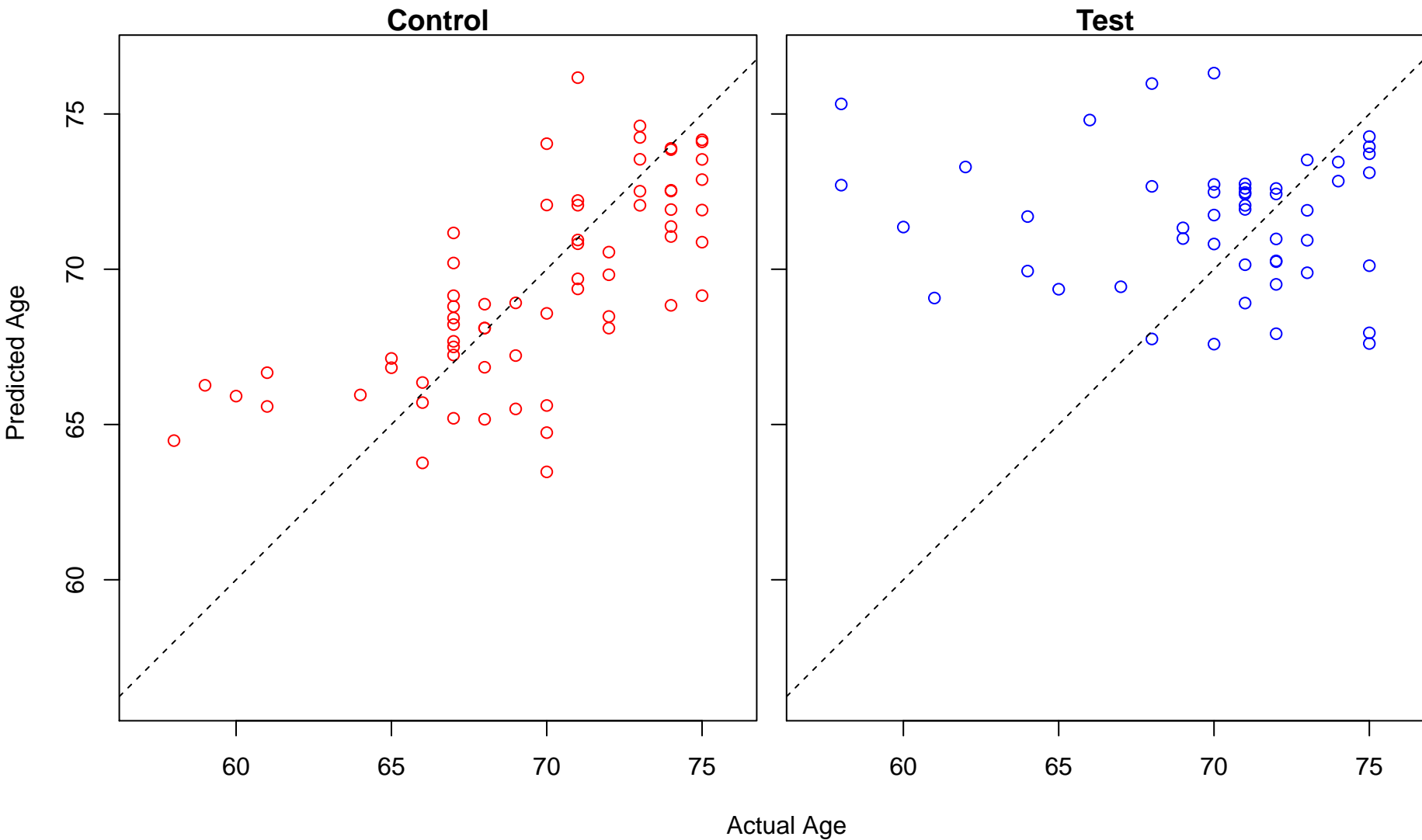


Test

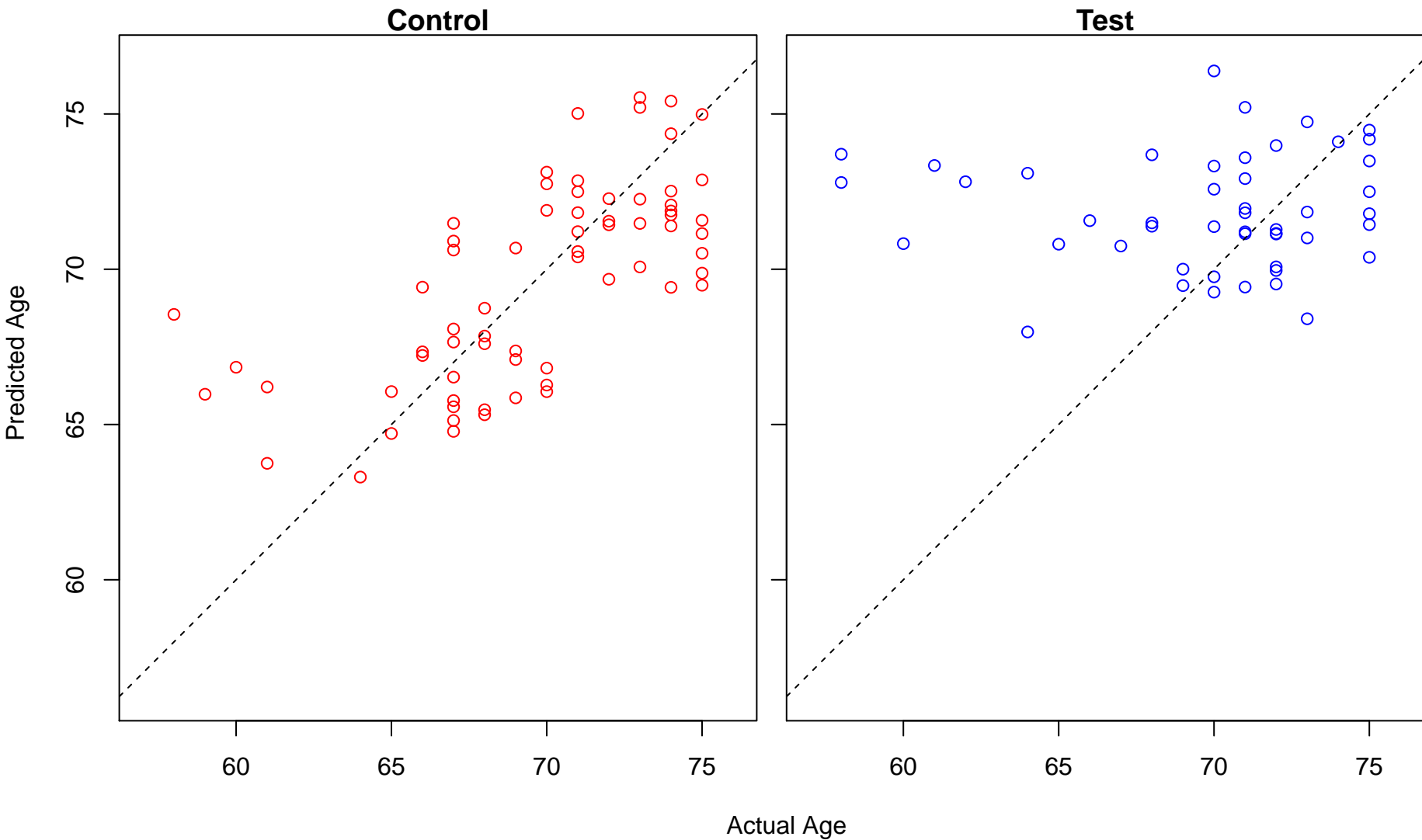


Actual Age

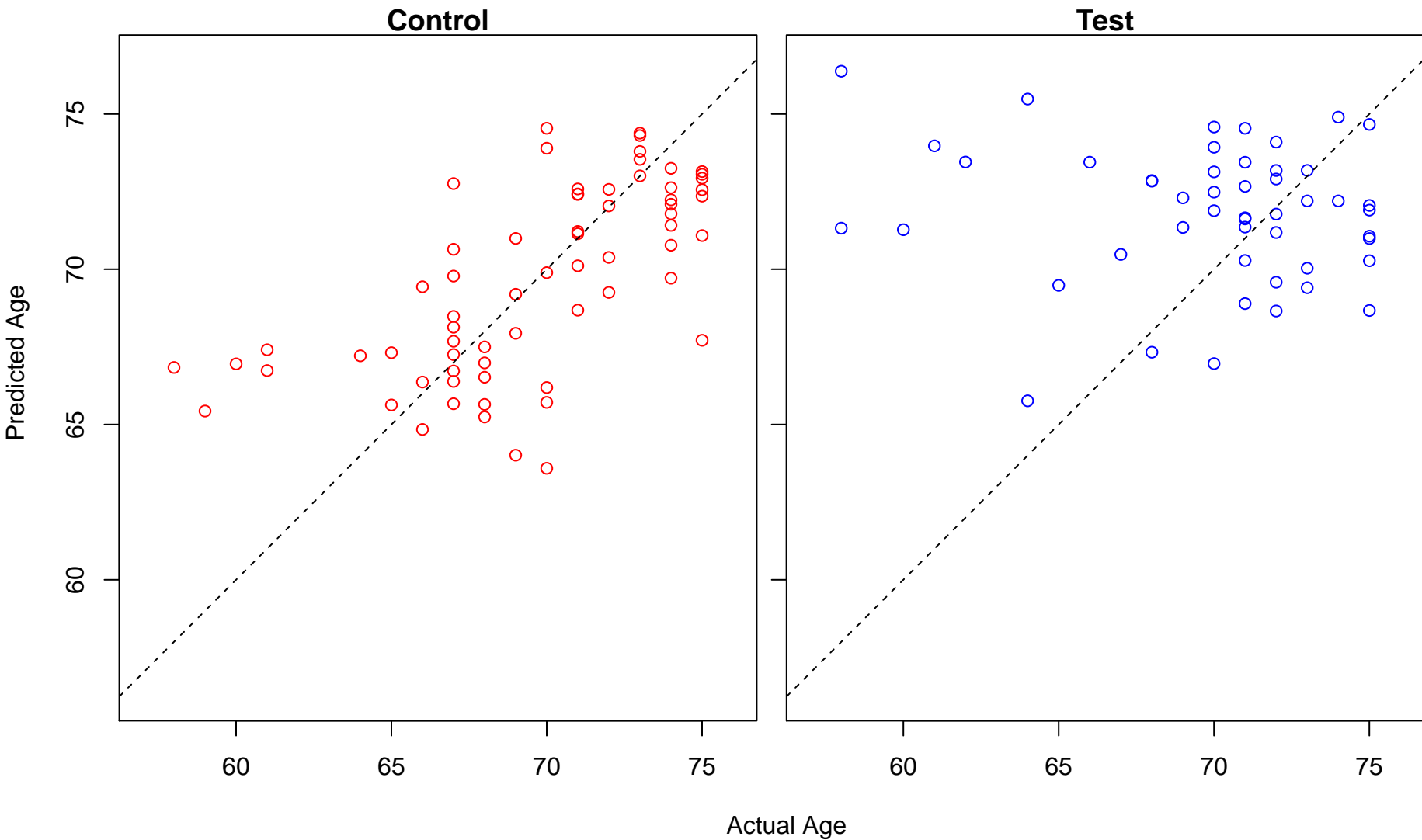
negative regulation of myeloid leukocyte differentiation (Score: 1.341883)



transcription from RNA polymerase III promoter (Score: 1.341494)

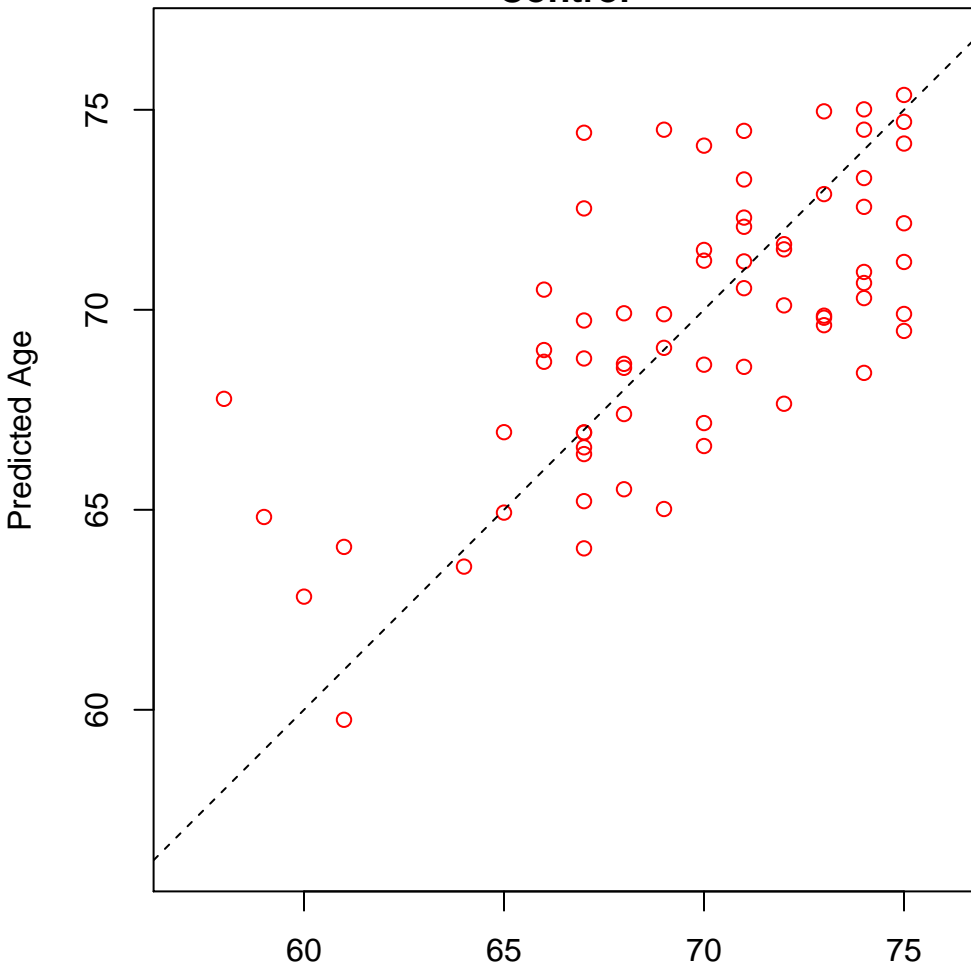


skeletal system morphogenesis (Score: 1.341429)

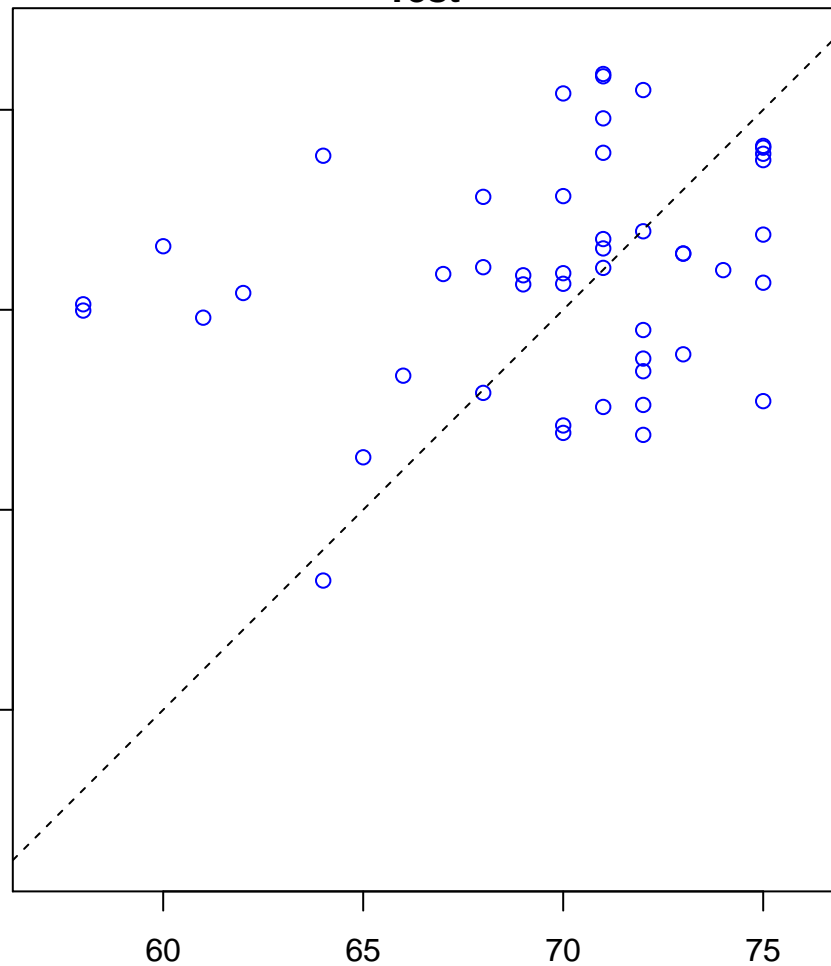


anterior/posterior pattern specification (Score: 1.341283)

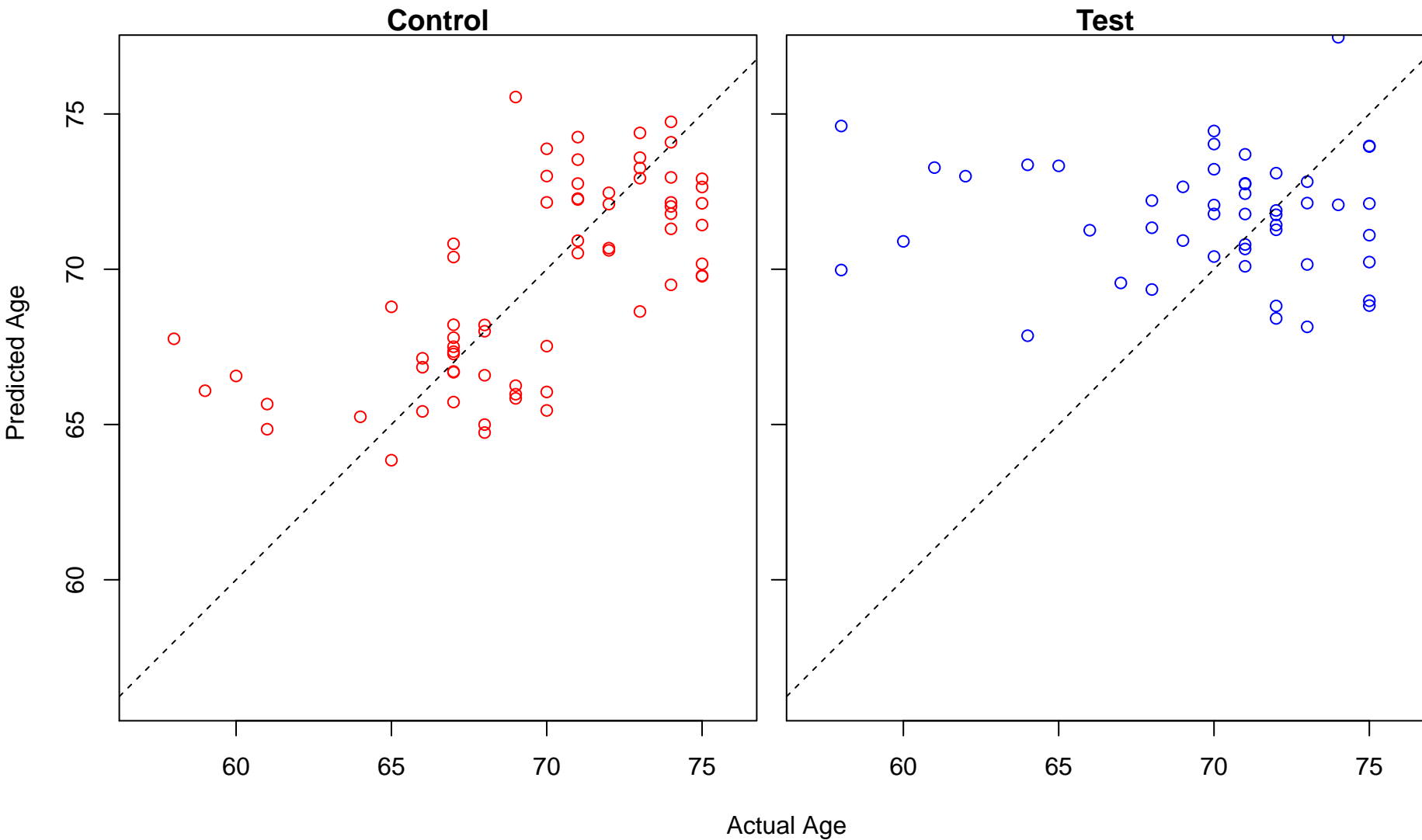
Control



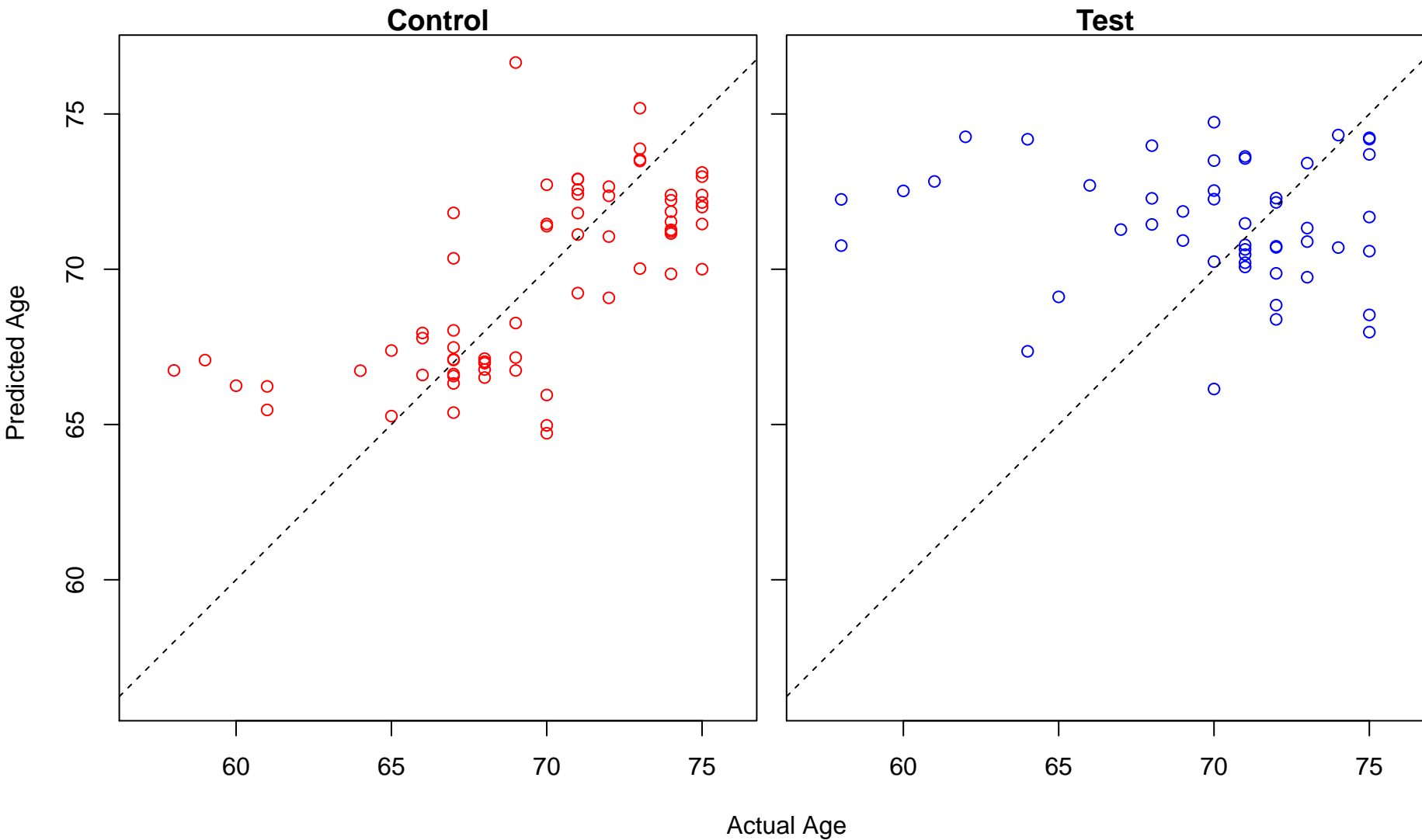
Test



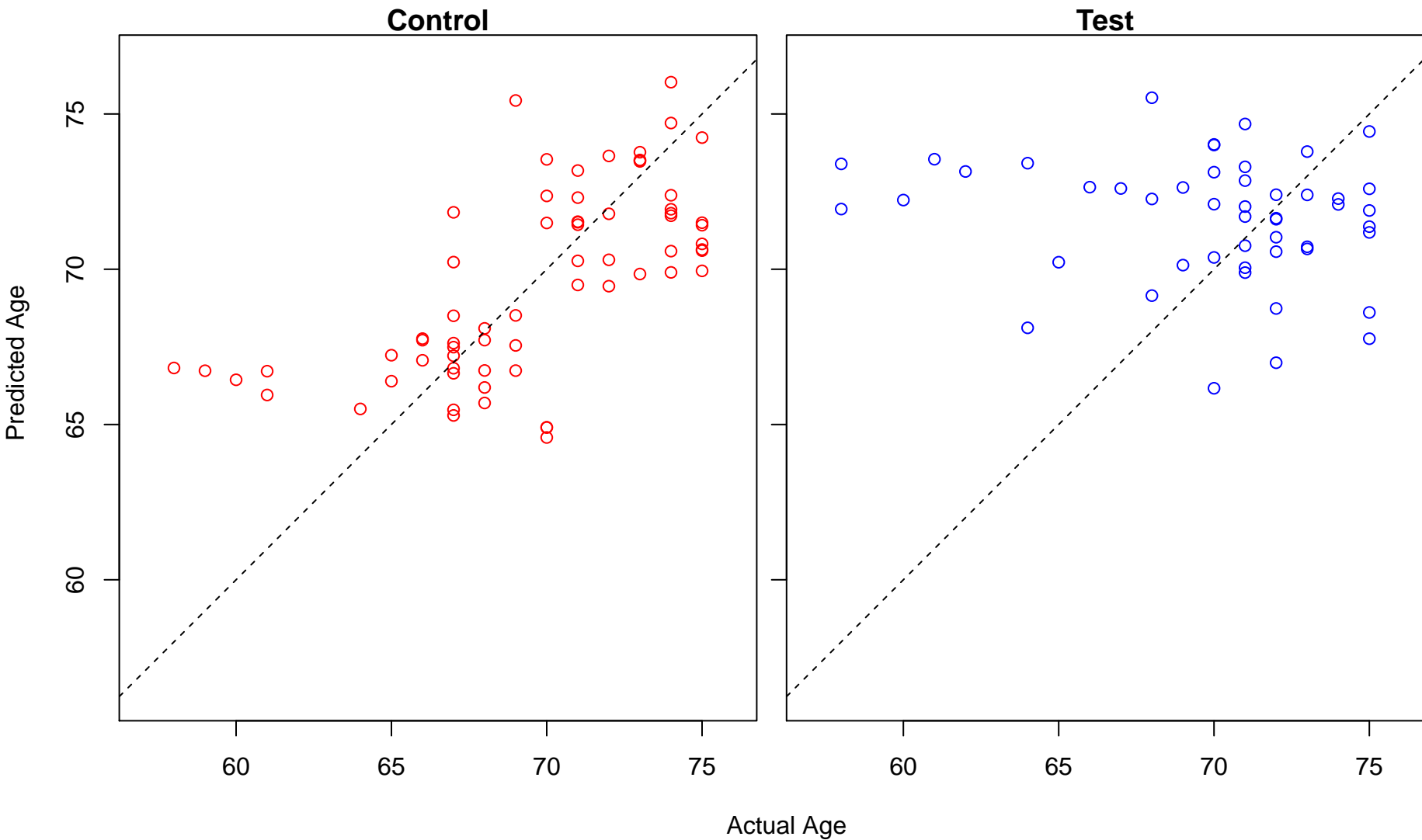
carbohydrate transport (Score: 1.341243)



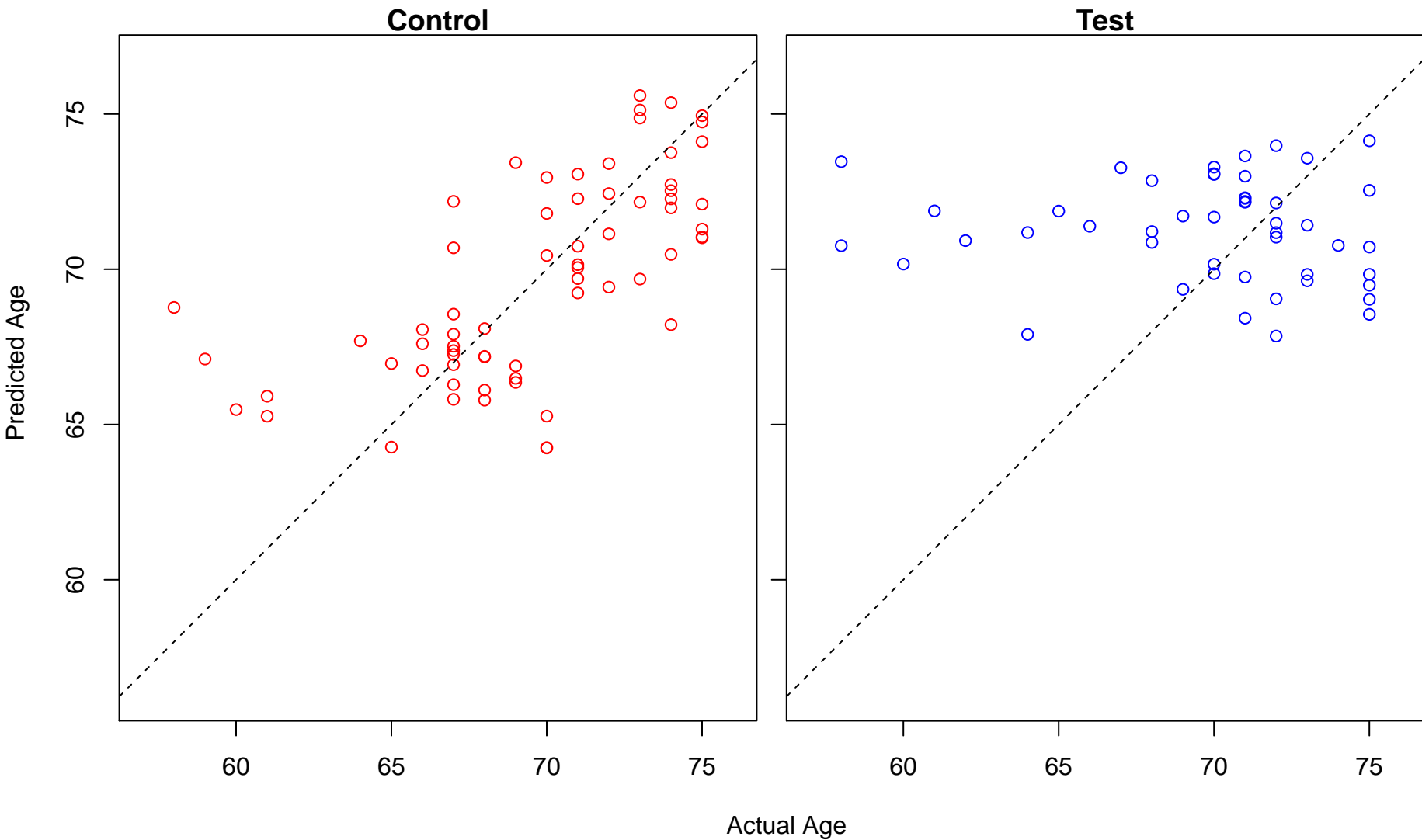
lymphocyte chemotaxis (Score: 1.339572)



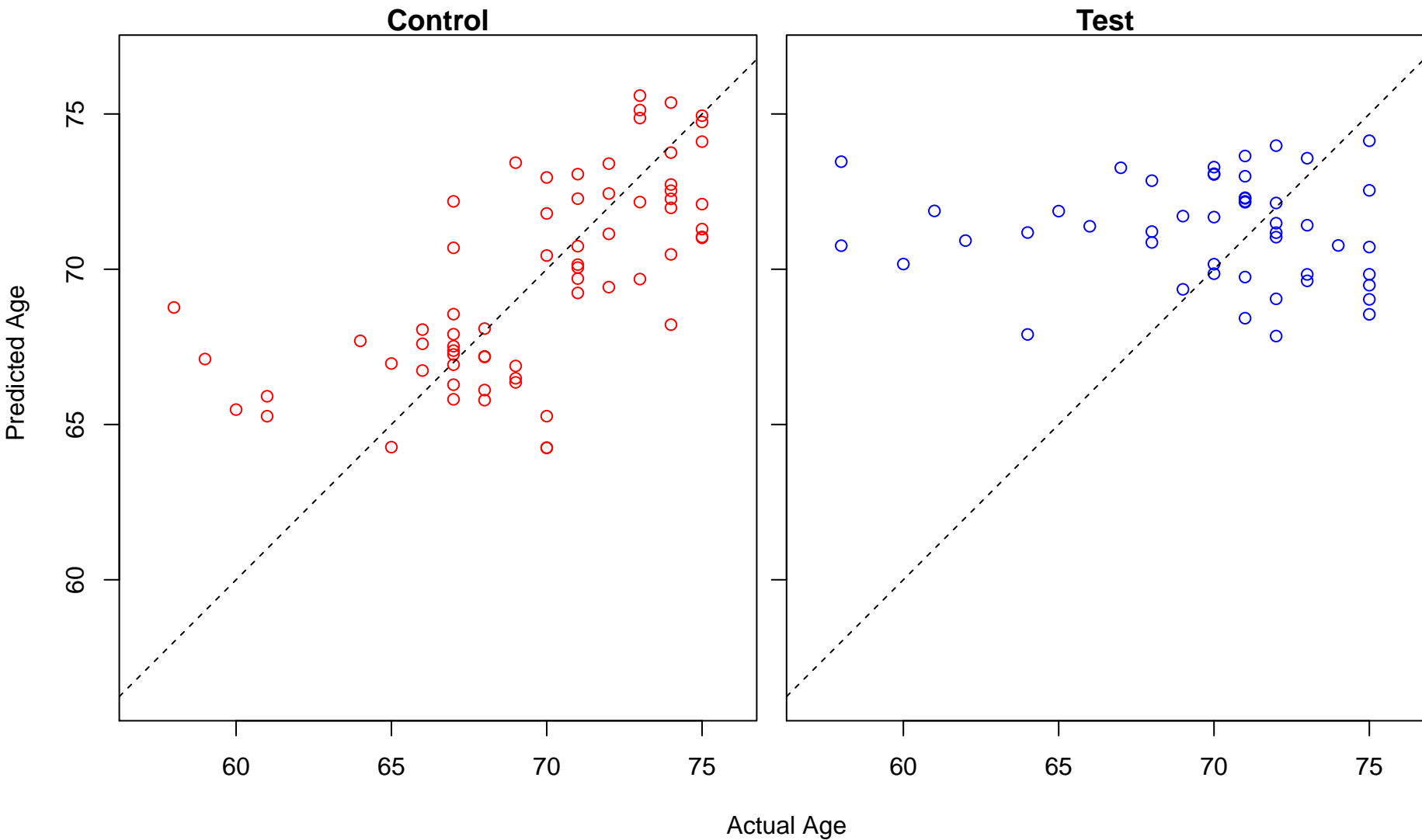
negative regulation of proteasomal ubiquitin-dependent protein catabolic process (Score: 1.33953)



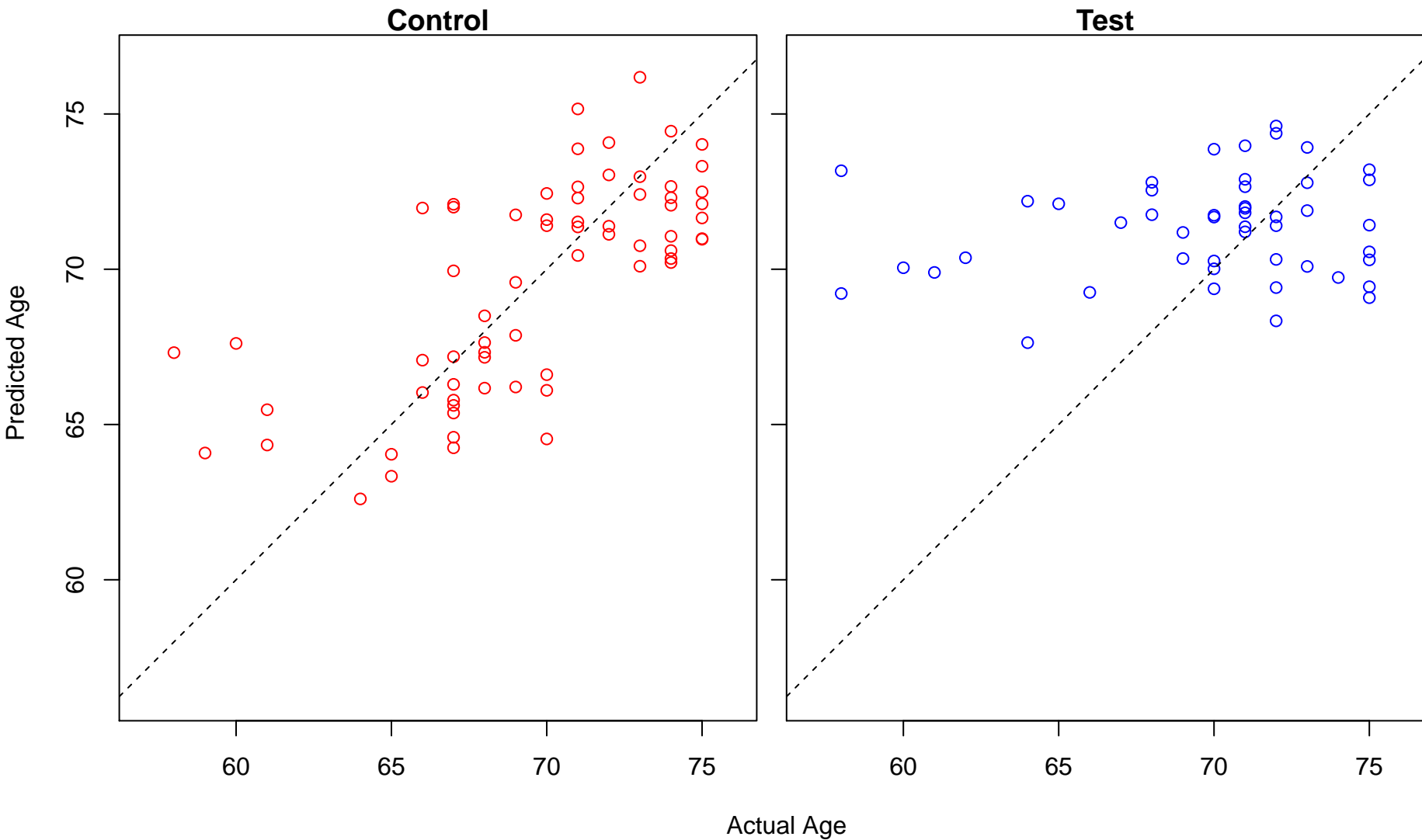
neutral lipid metabolic process (Score: 1.338544)



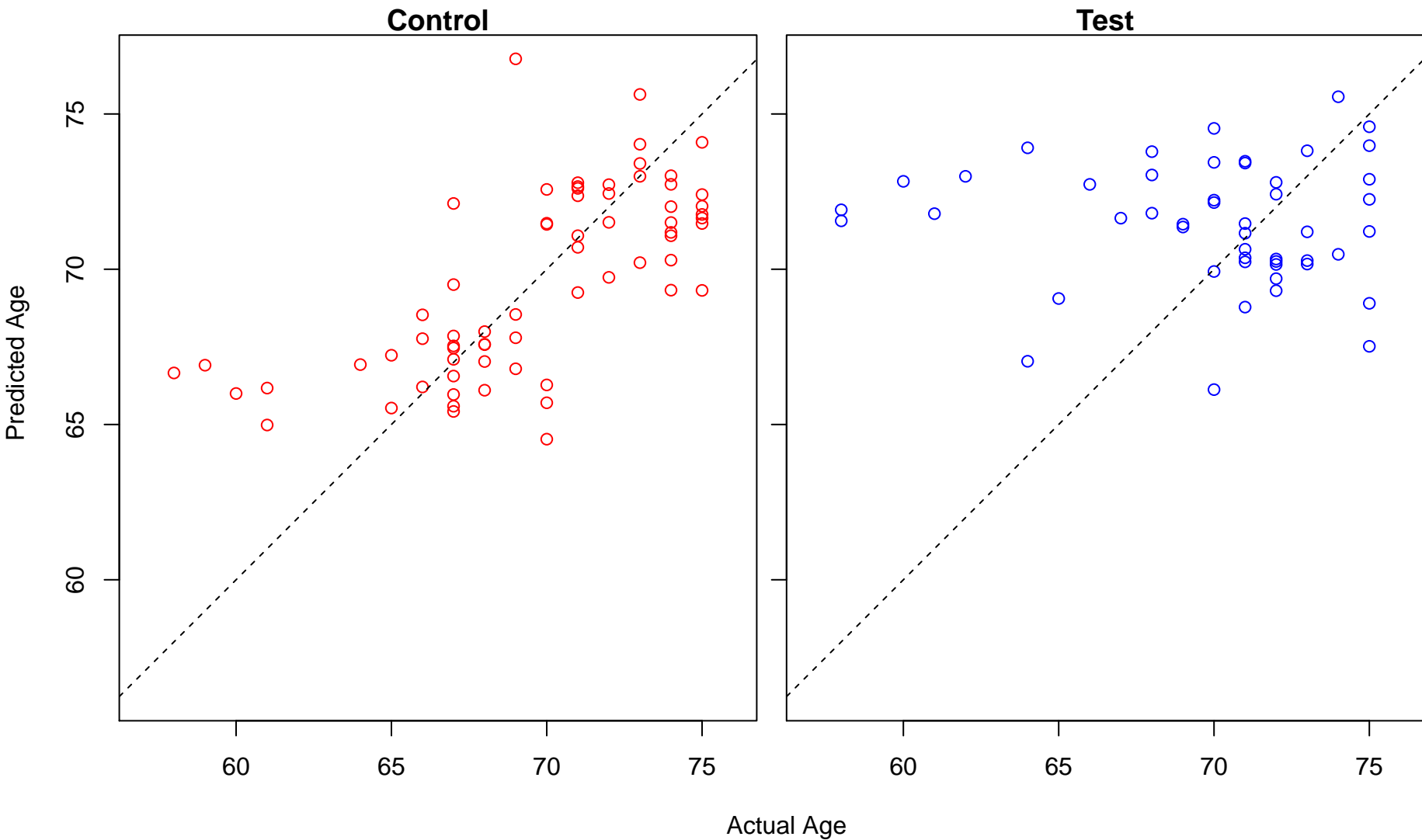
acylglycerol metabolic process (Score: 1.338544)



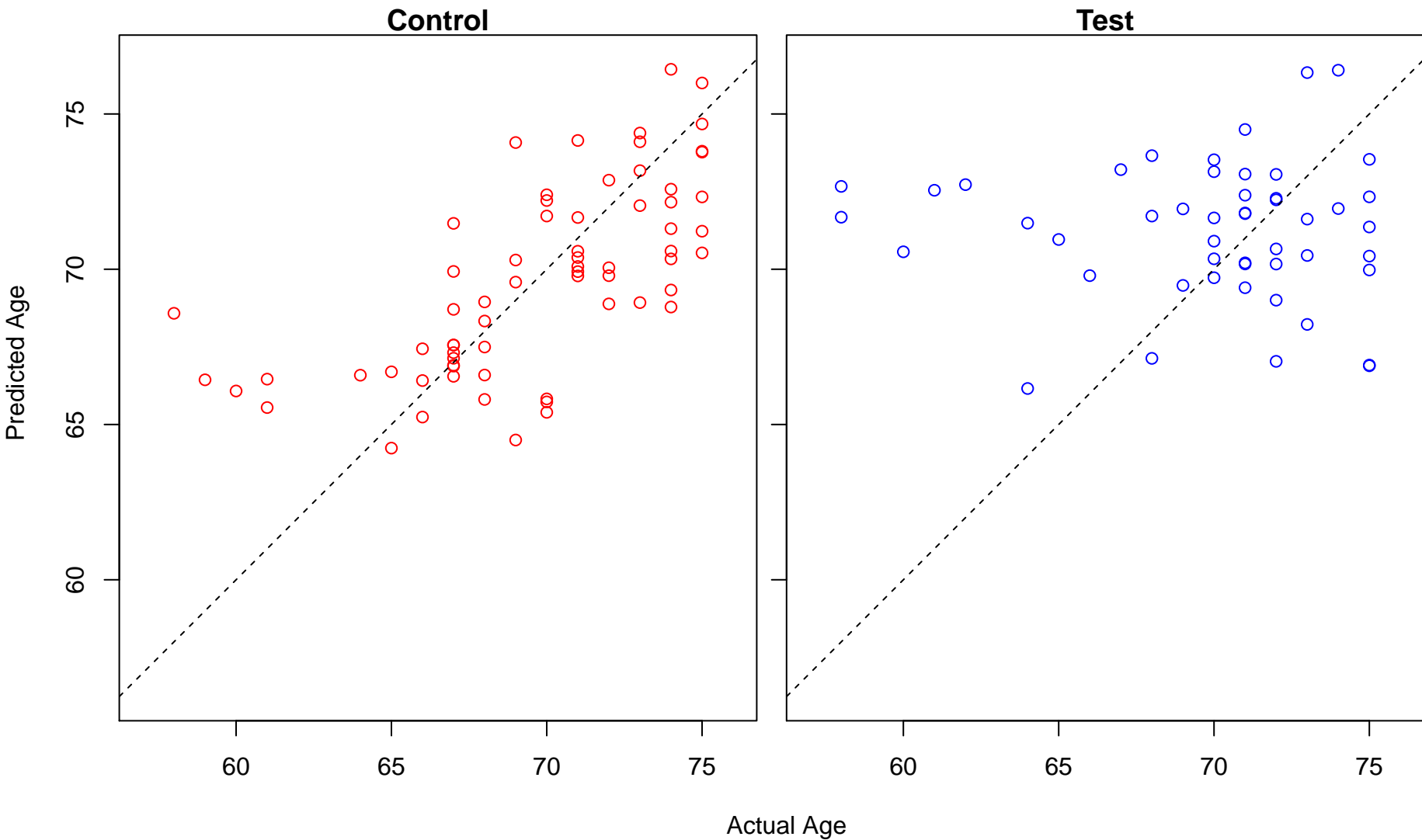
regulation of RNA splicing (Score: 1.338203)



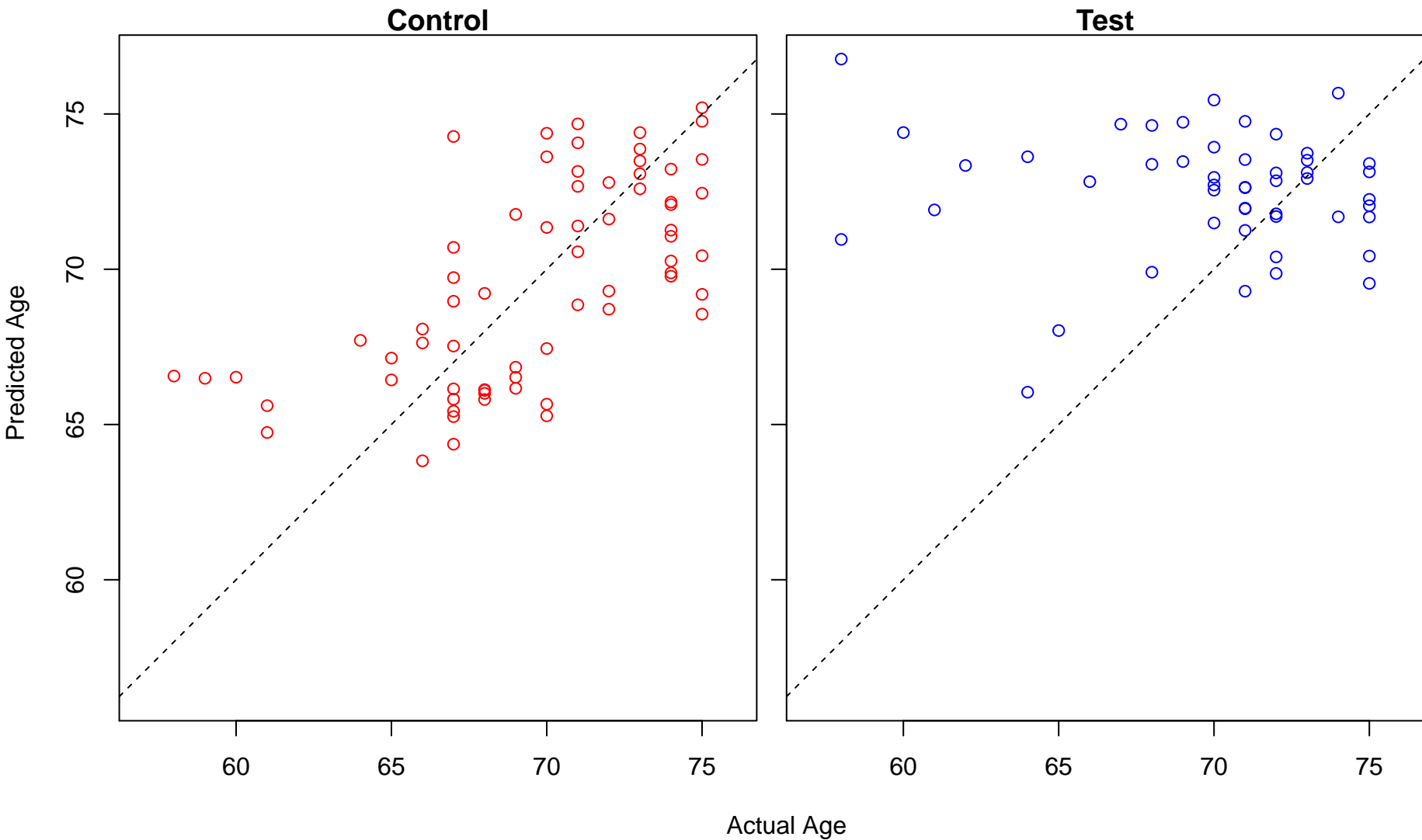
lymphocyte migration (Score: 1.338199)



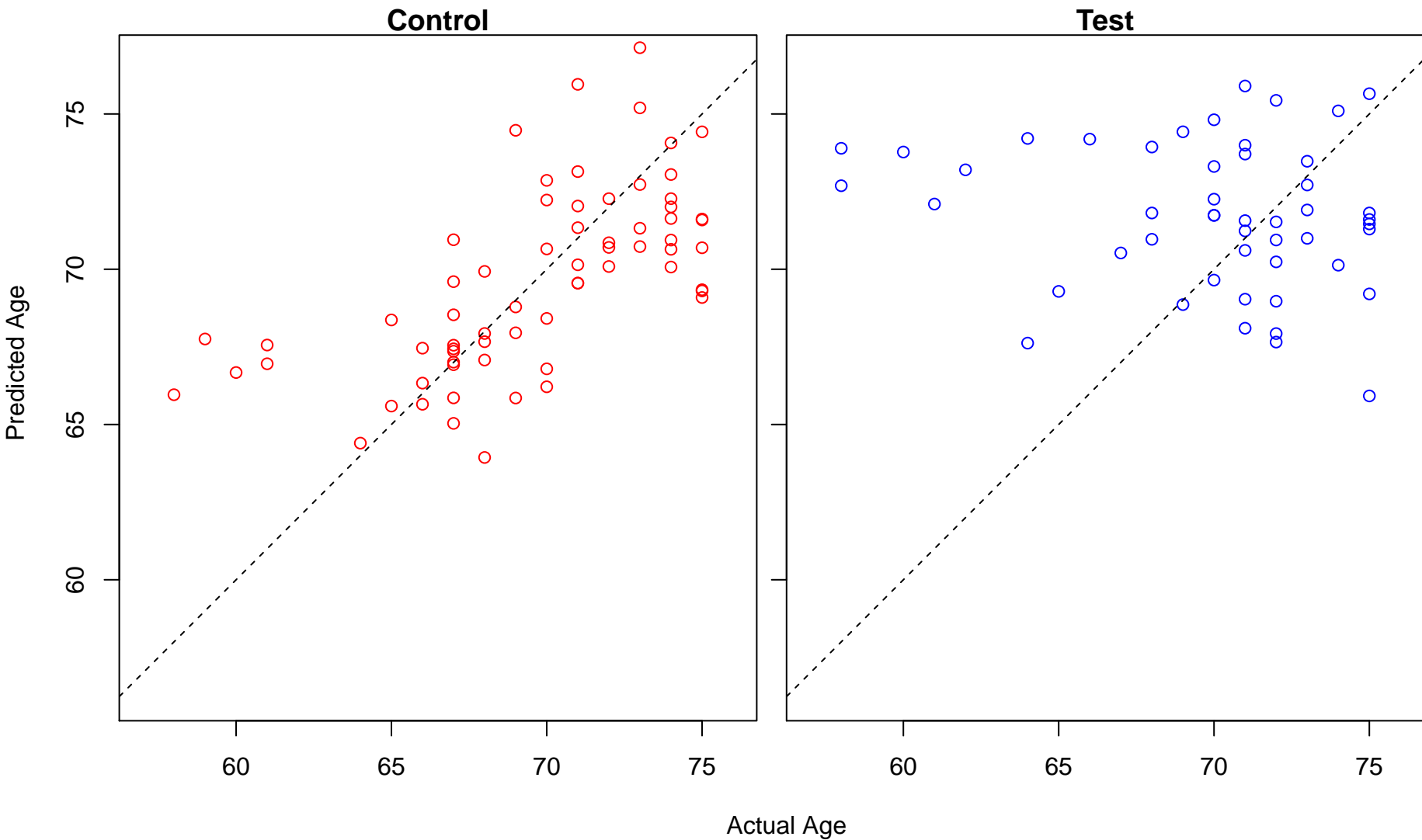
autophagosome assembly (Score: 1.338130)



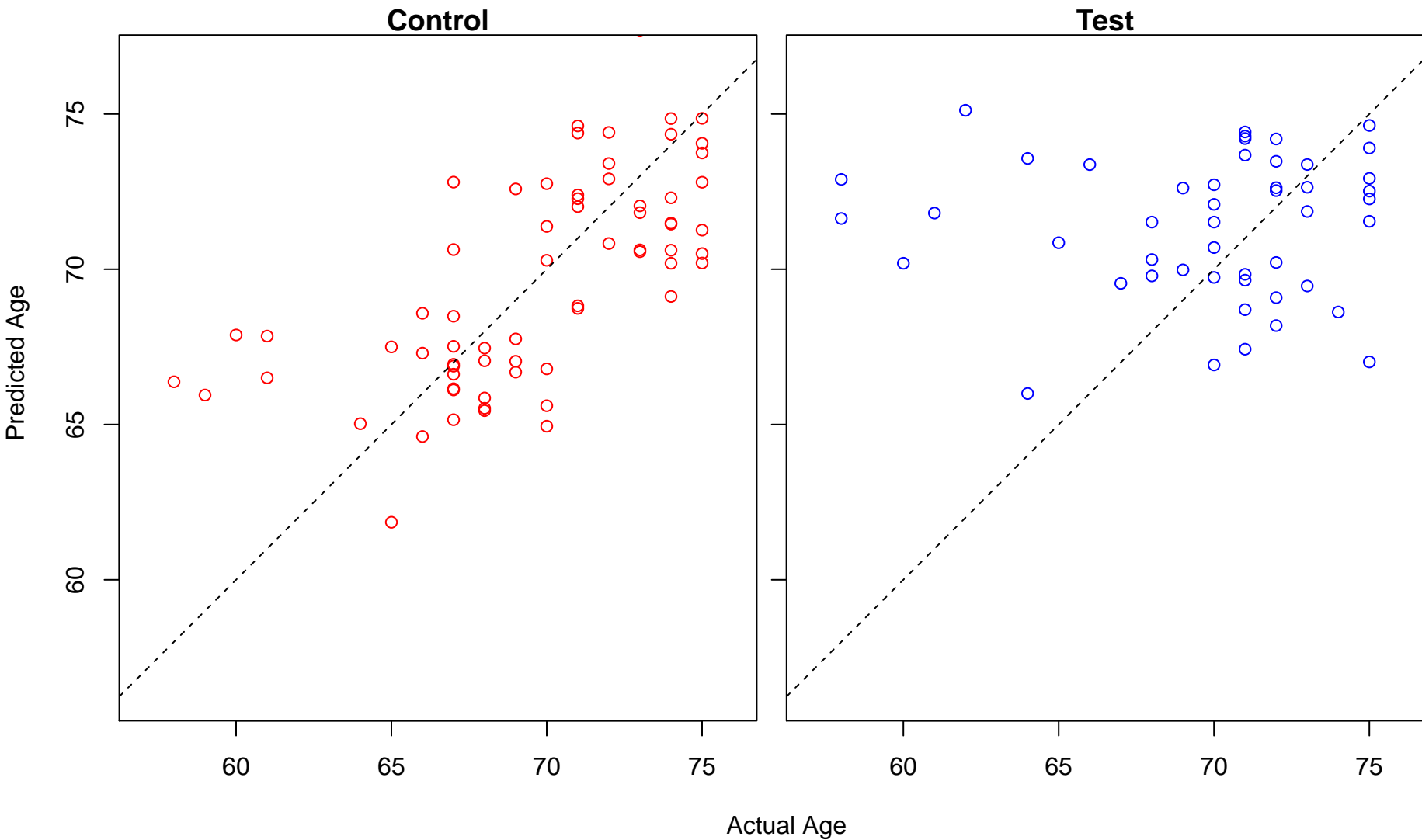
epidermis development (Score: 1.337881)



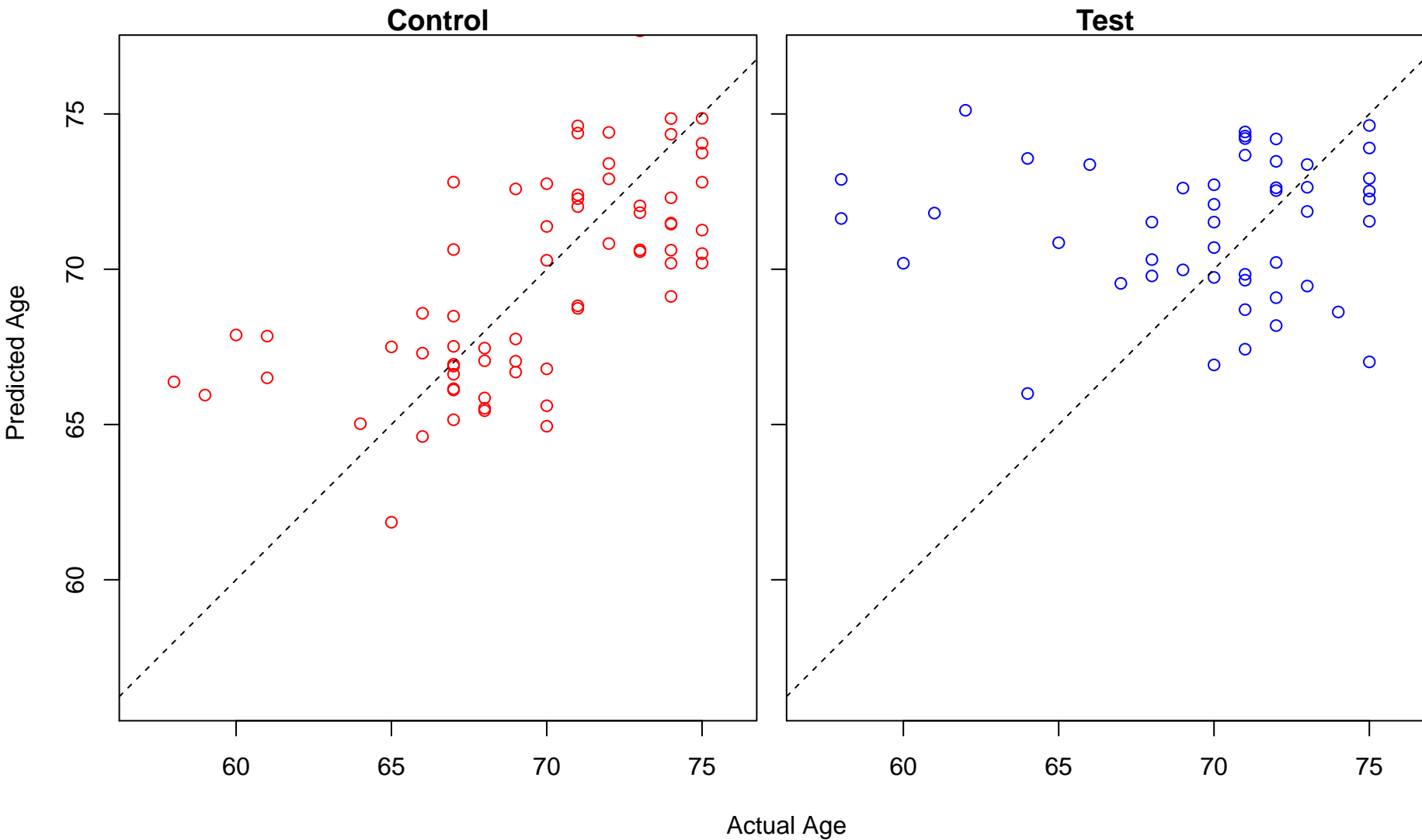
positive regulation of stem cell differentiation (Score: 1.337486)



regulation of JAK-STAT cascade (Score: 1.337458)

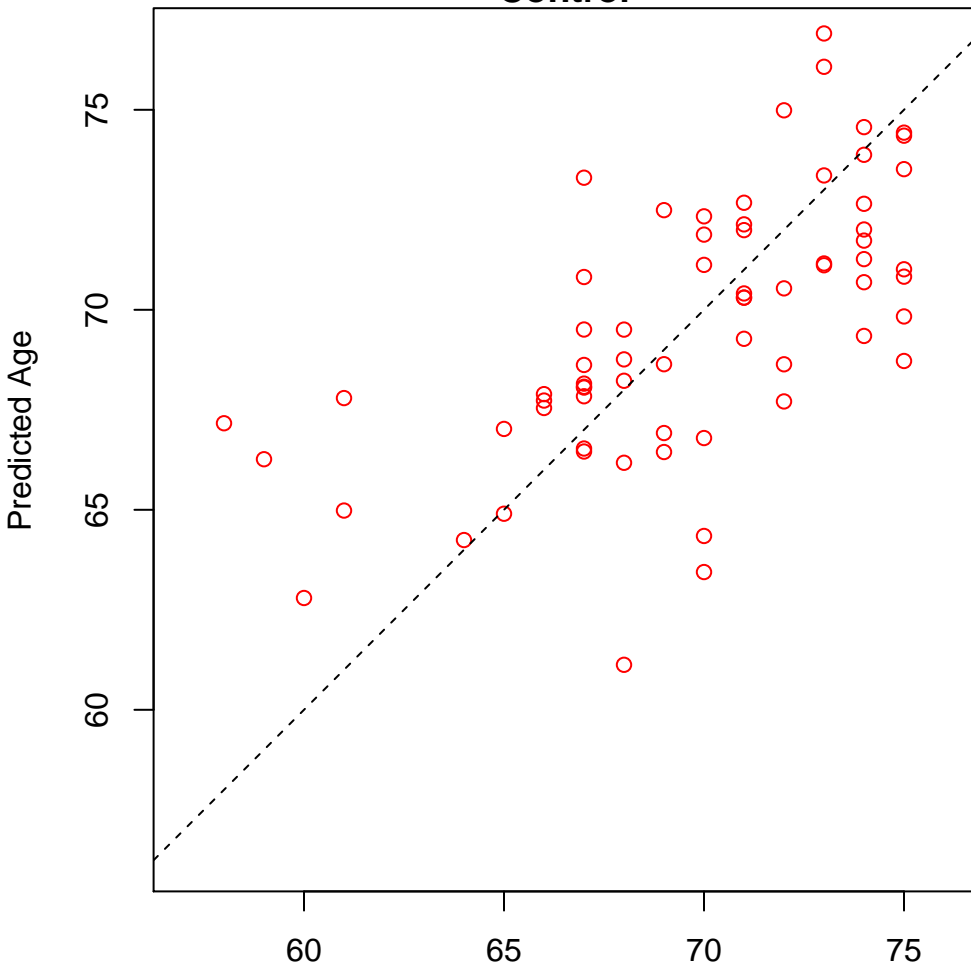


regulation of STAT cascade (Score: 1.337458)

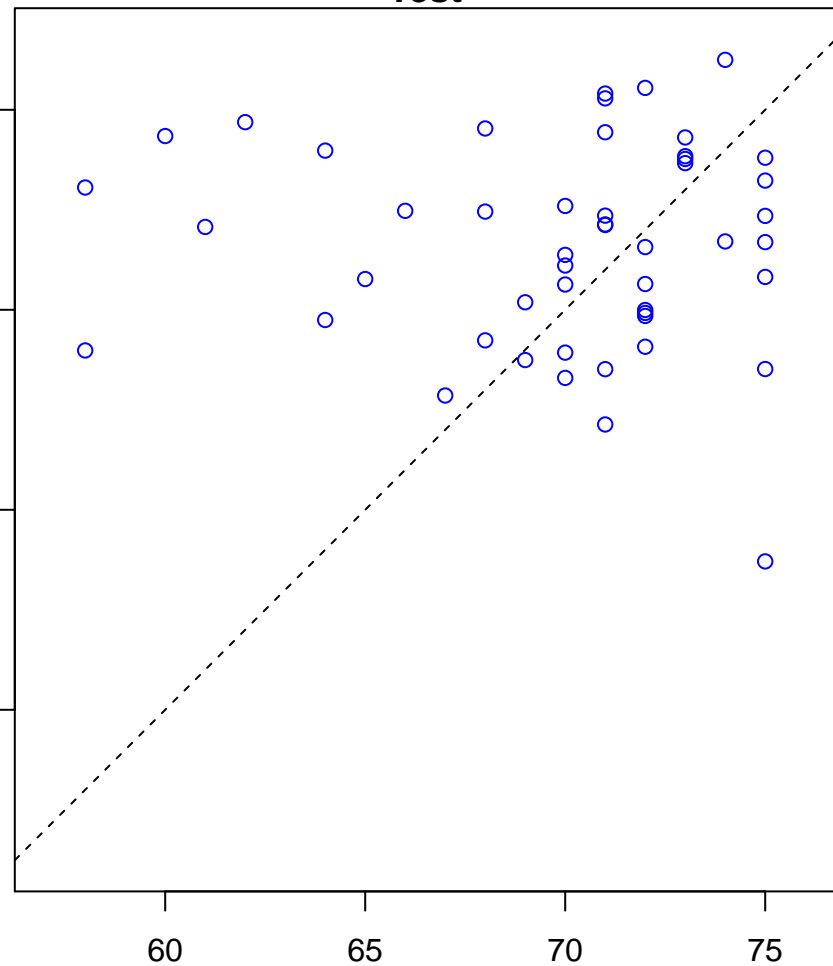


phosphatidylinositol 3-kinase signaling (Score: 1.336230)

Control

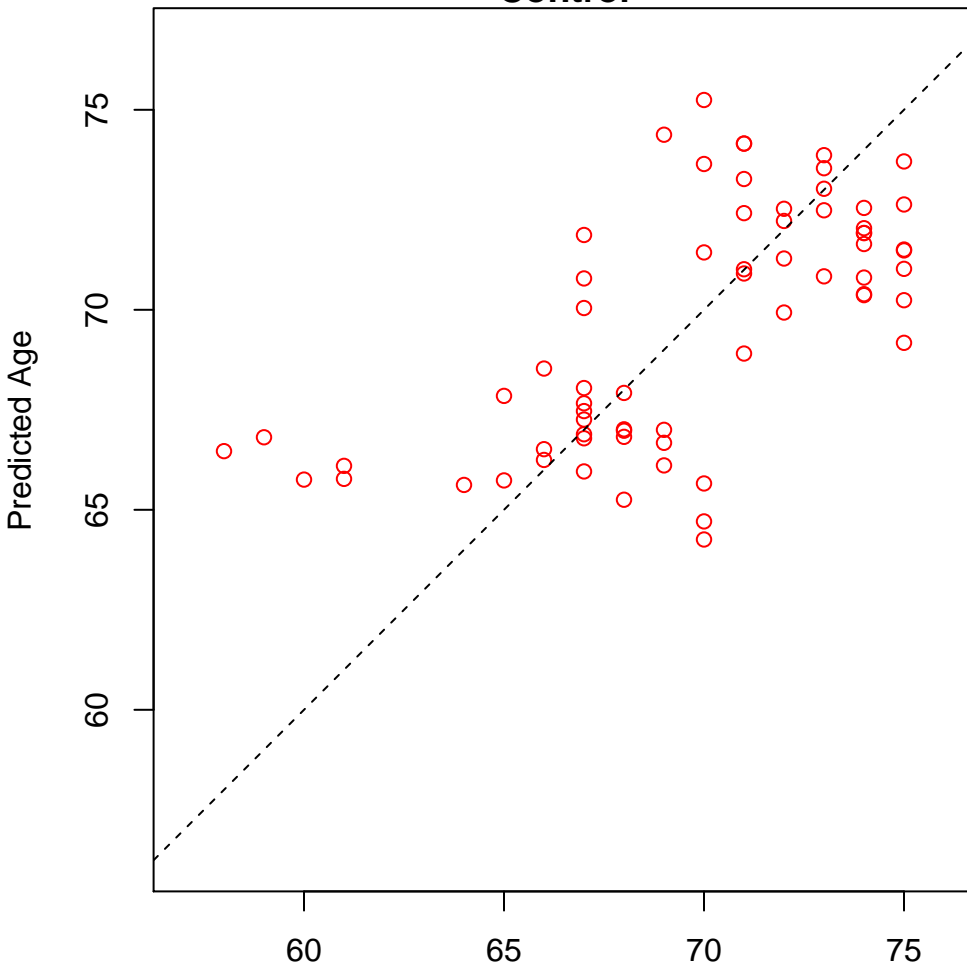


Test

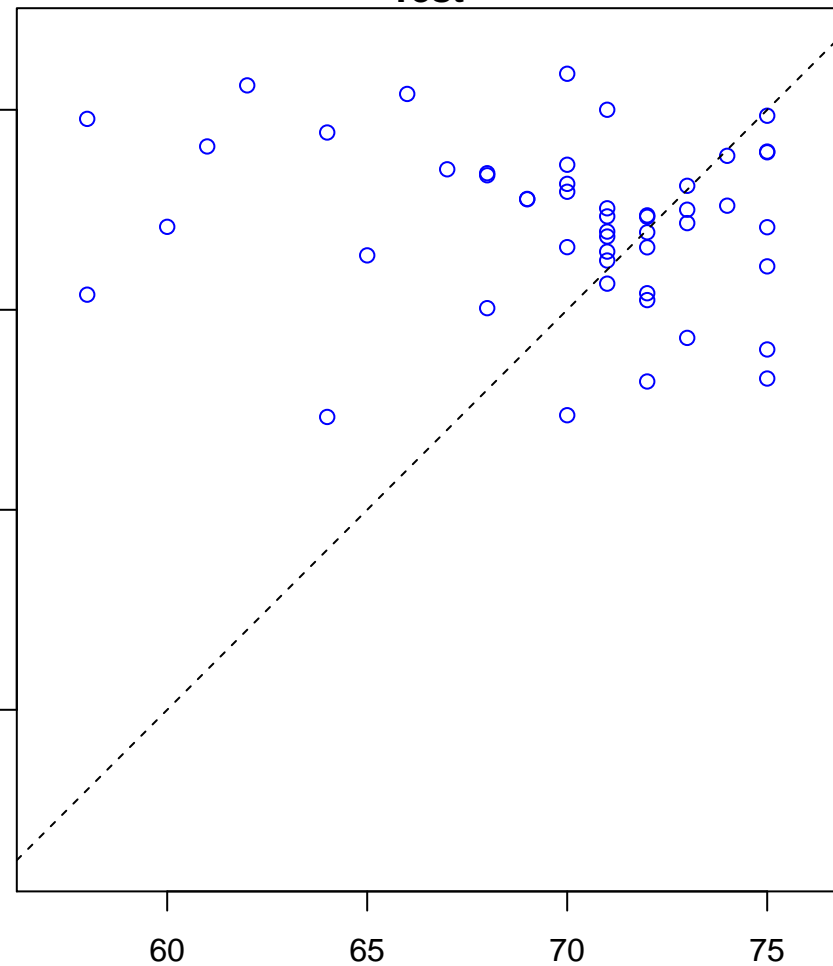


nucleotide-excision repair, DNA incision (Score: 1.335450)

Control



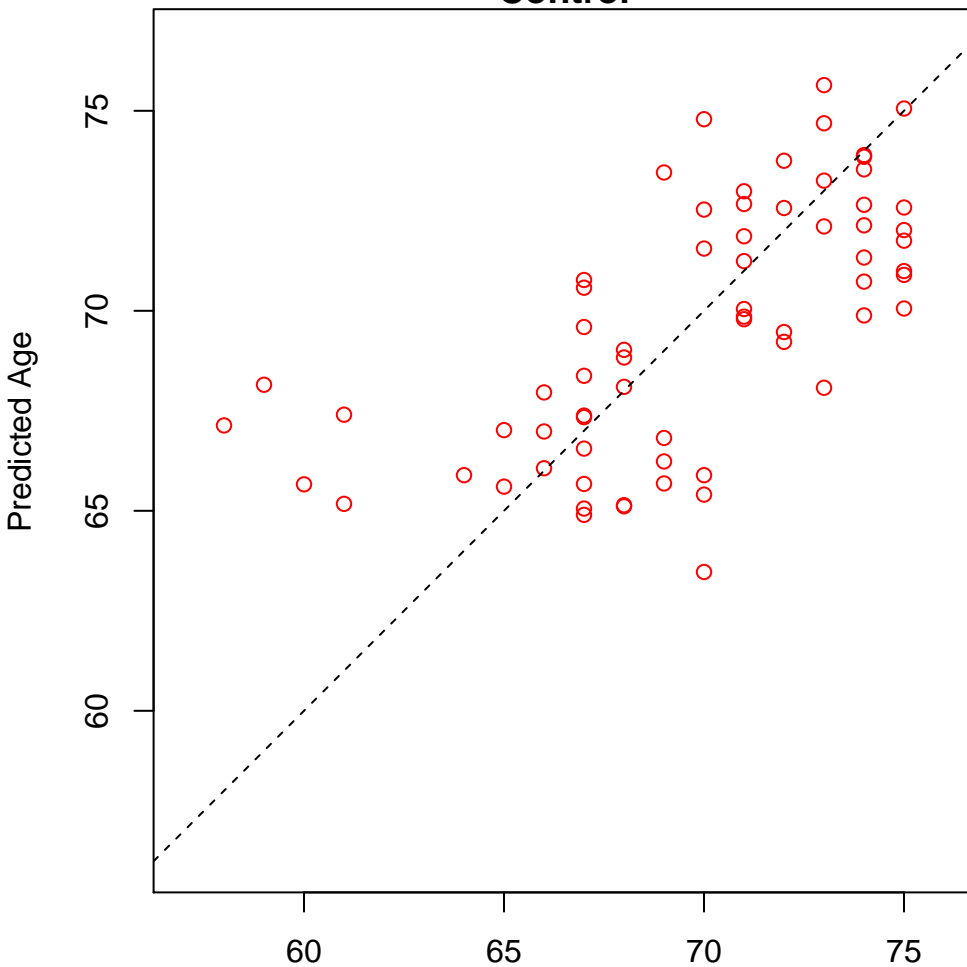
Test



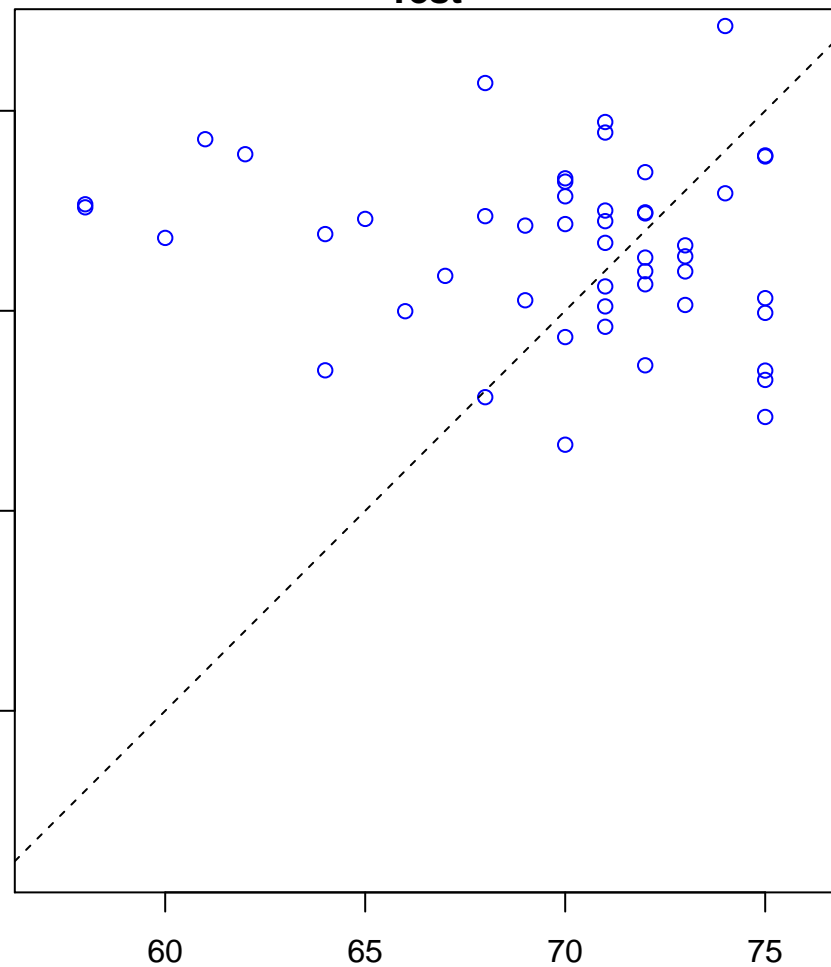
Actual Age

negative regulation of catabolic process (Score: 1.334714)

Control

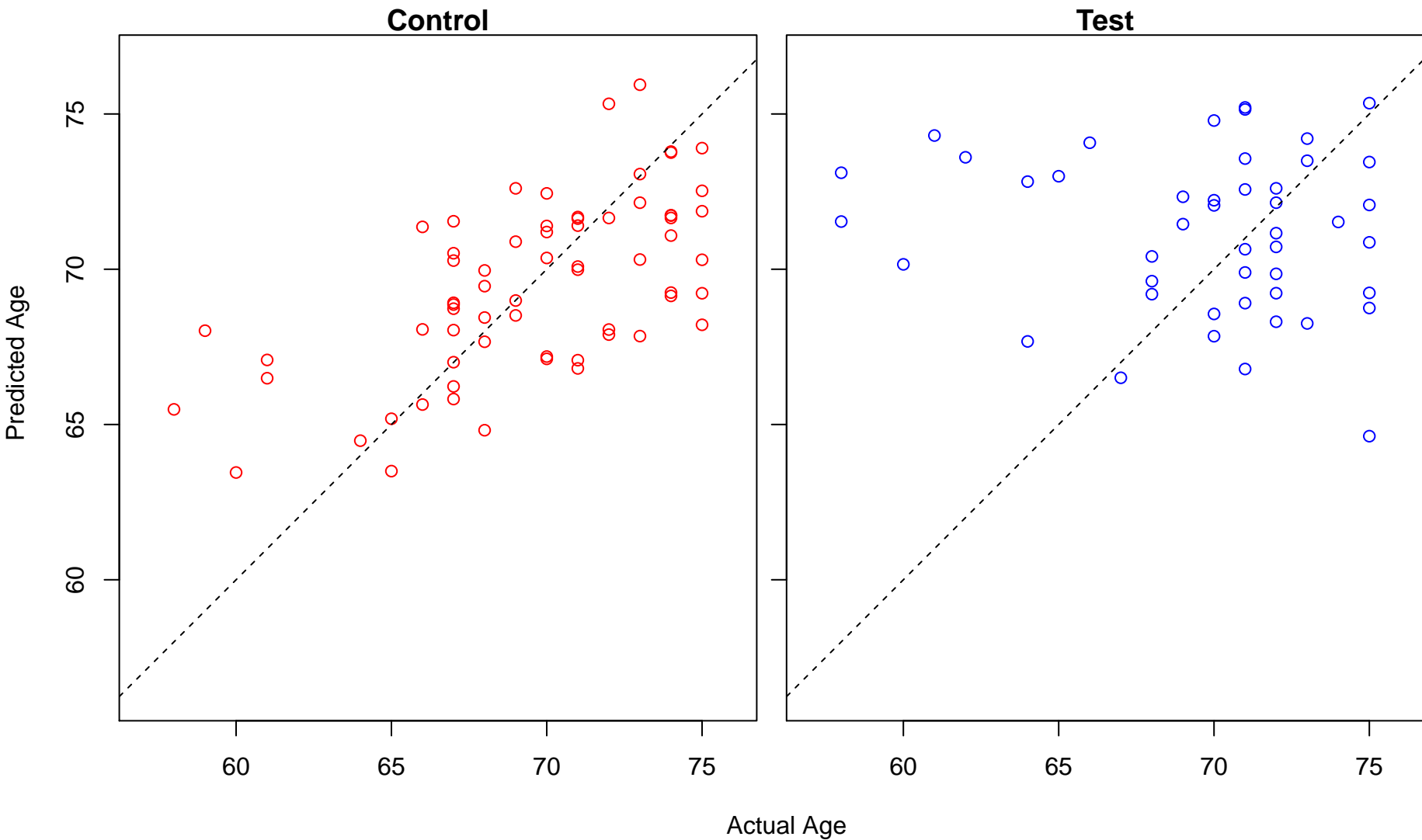


Test

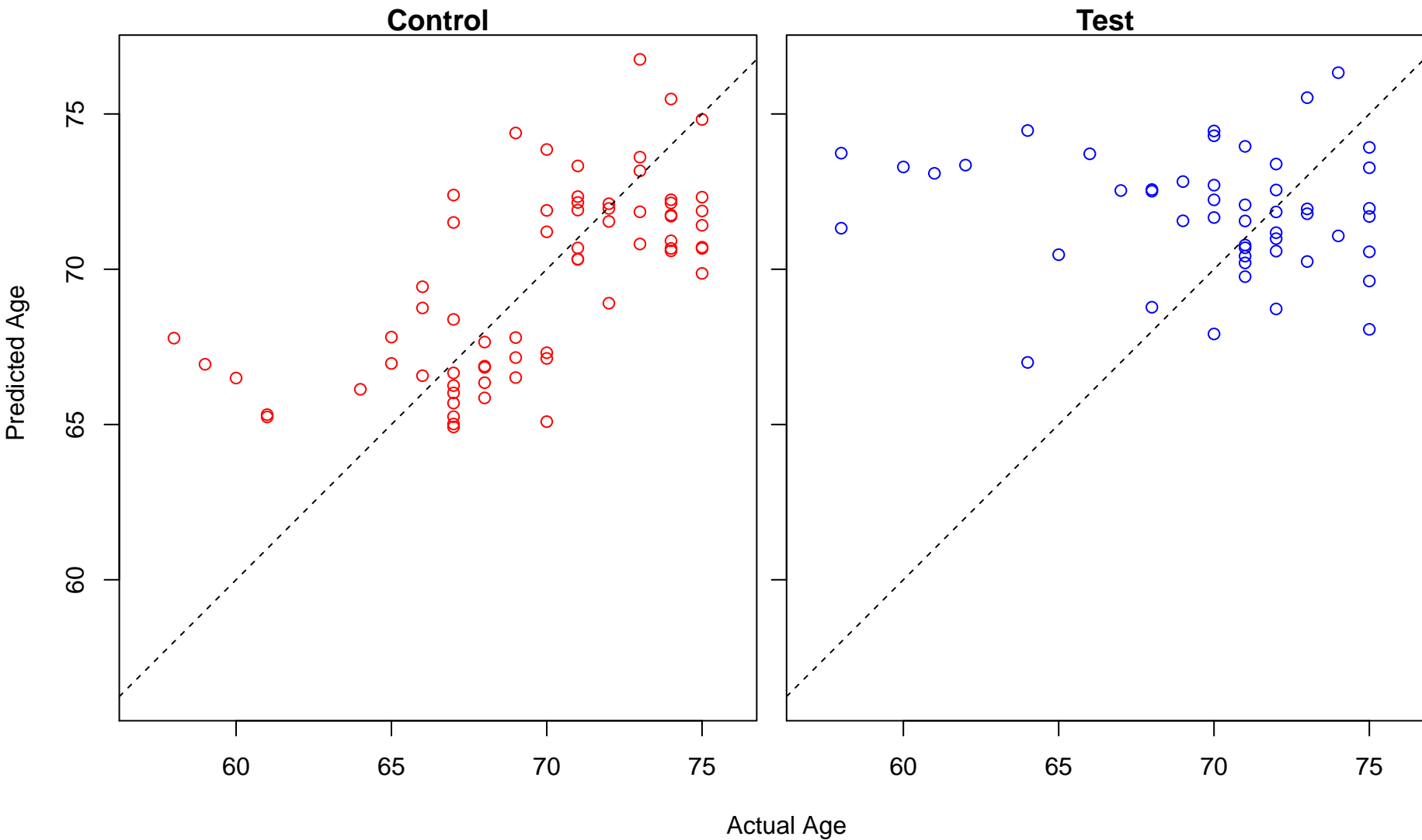


Actual Age

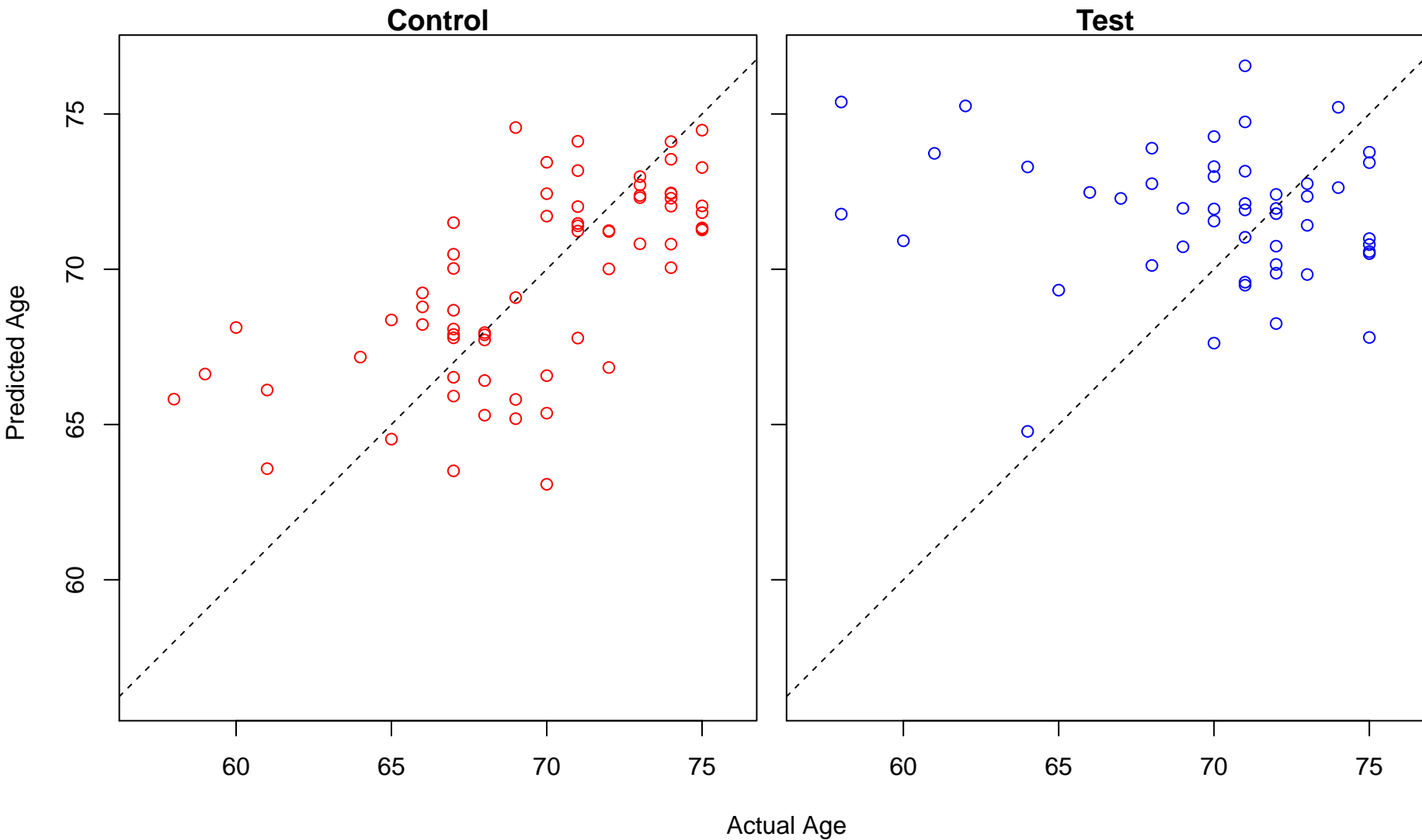
visual behavior (Score: 1.334481)



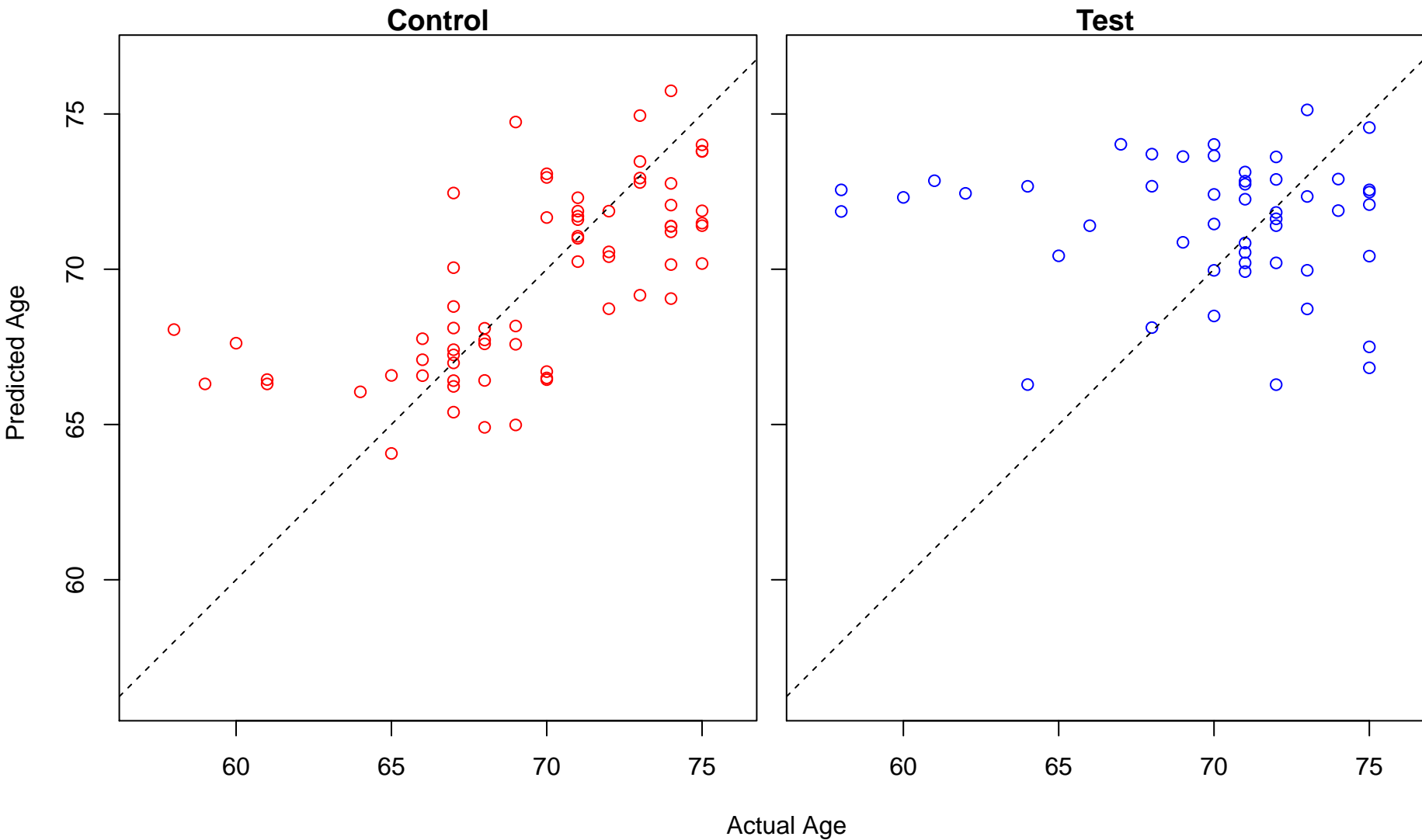
myelination (Score: 1.334214)



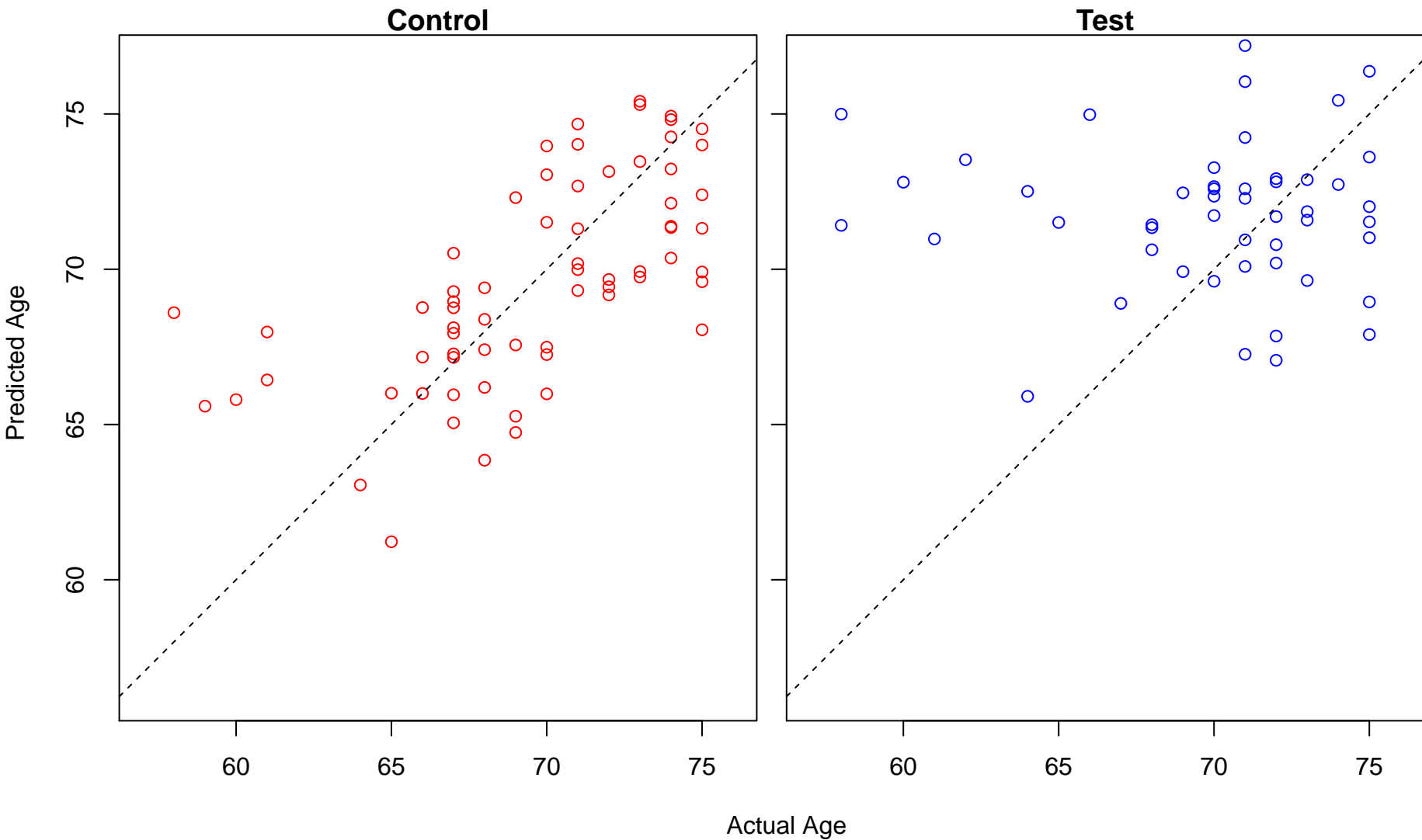
alpha-amino acid catabolic process (Score: 1.332495)



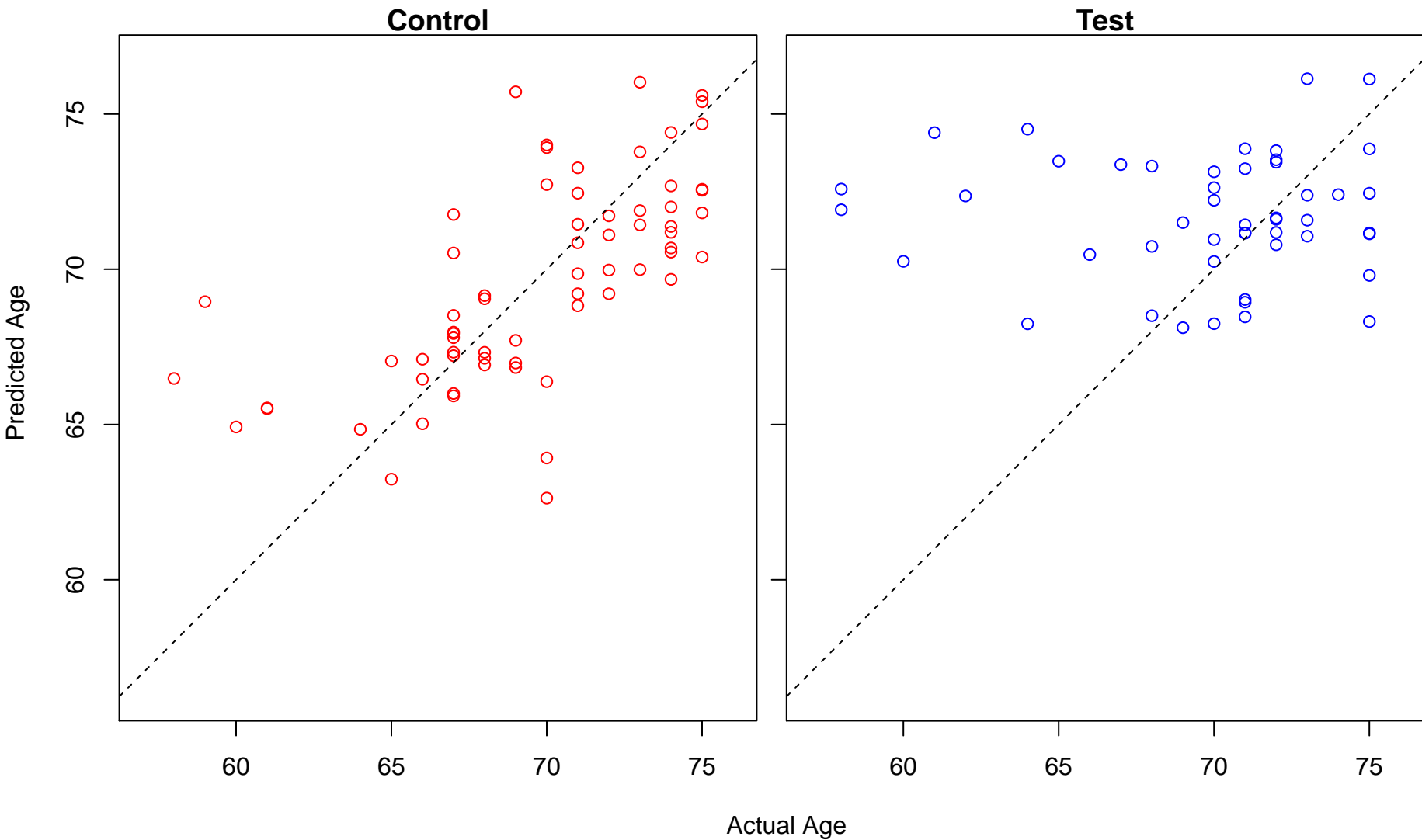
regulation of cilium assembly (Score: 1.332373)



regulation of cell morphogenesis involved in differentiation (Score: 1.332056)

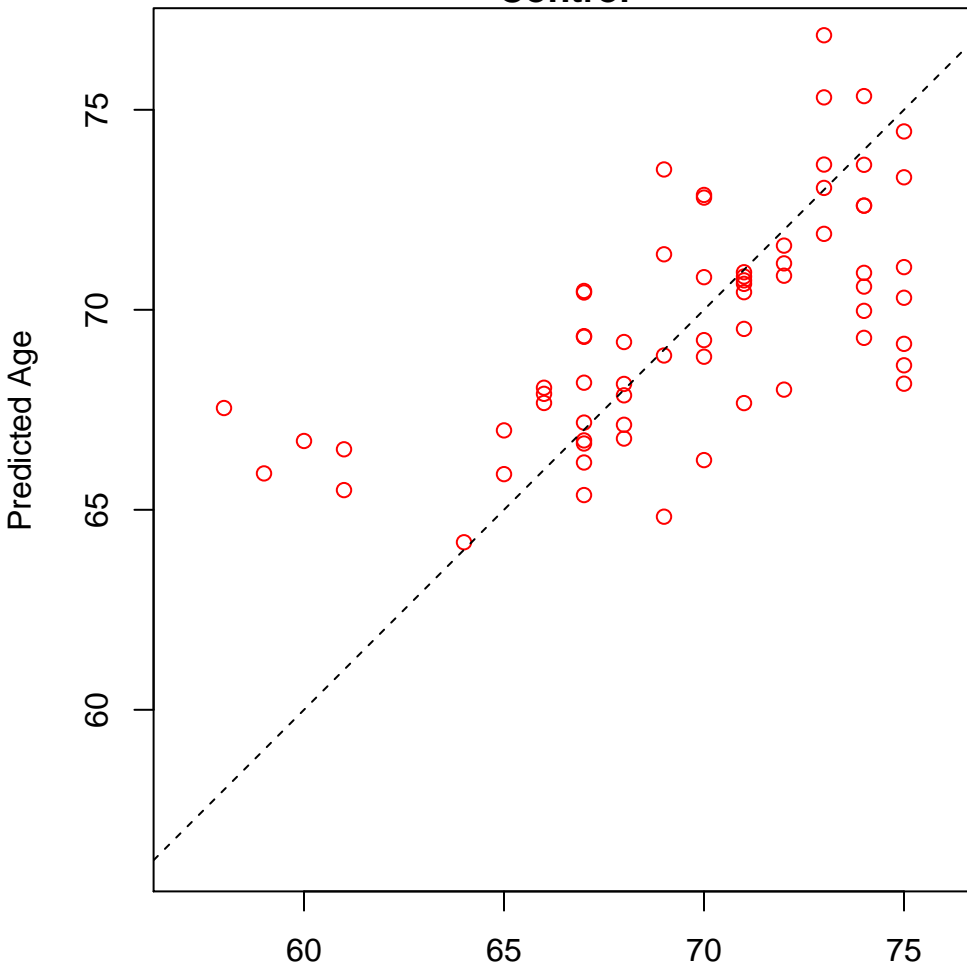


activation of MAPK activity (Score: 1.331834)

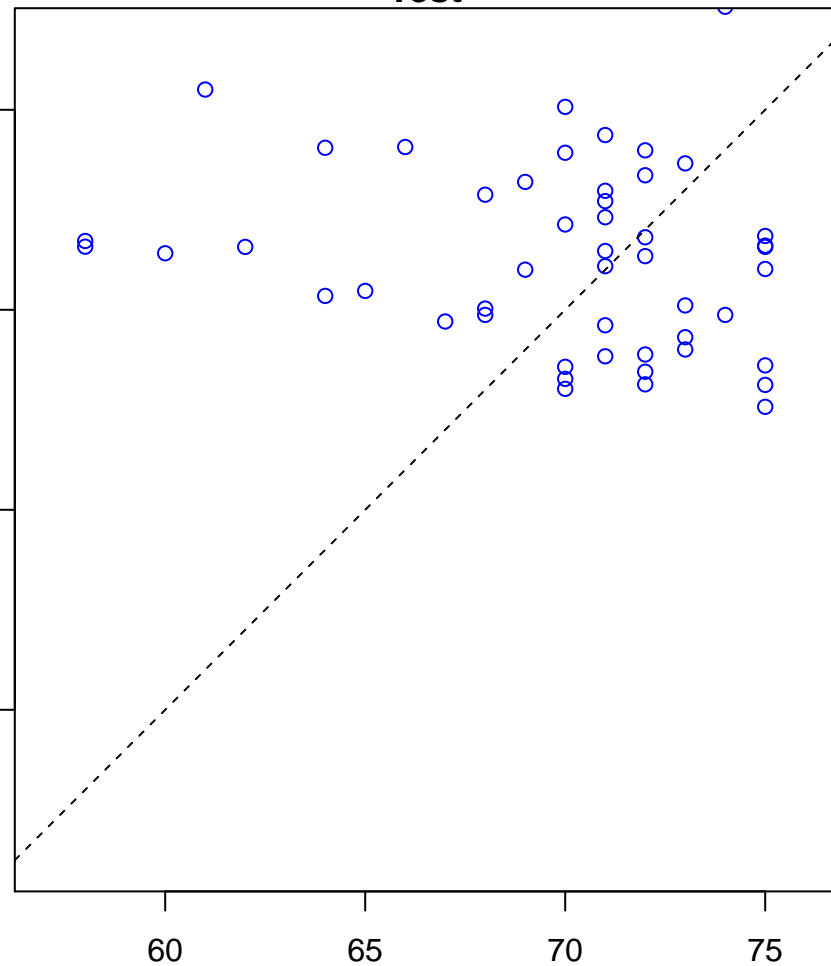


phosphatidylglycerol metabolic process (Score: 1.331764)

Control

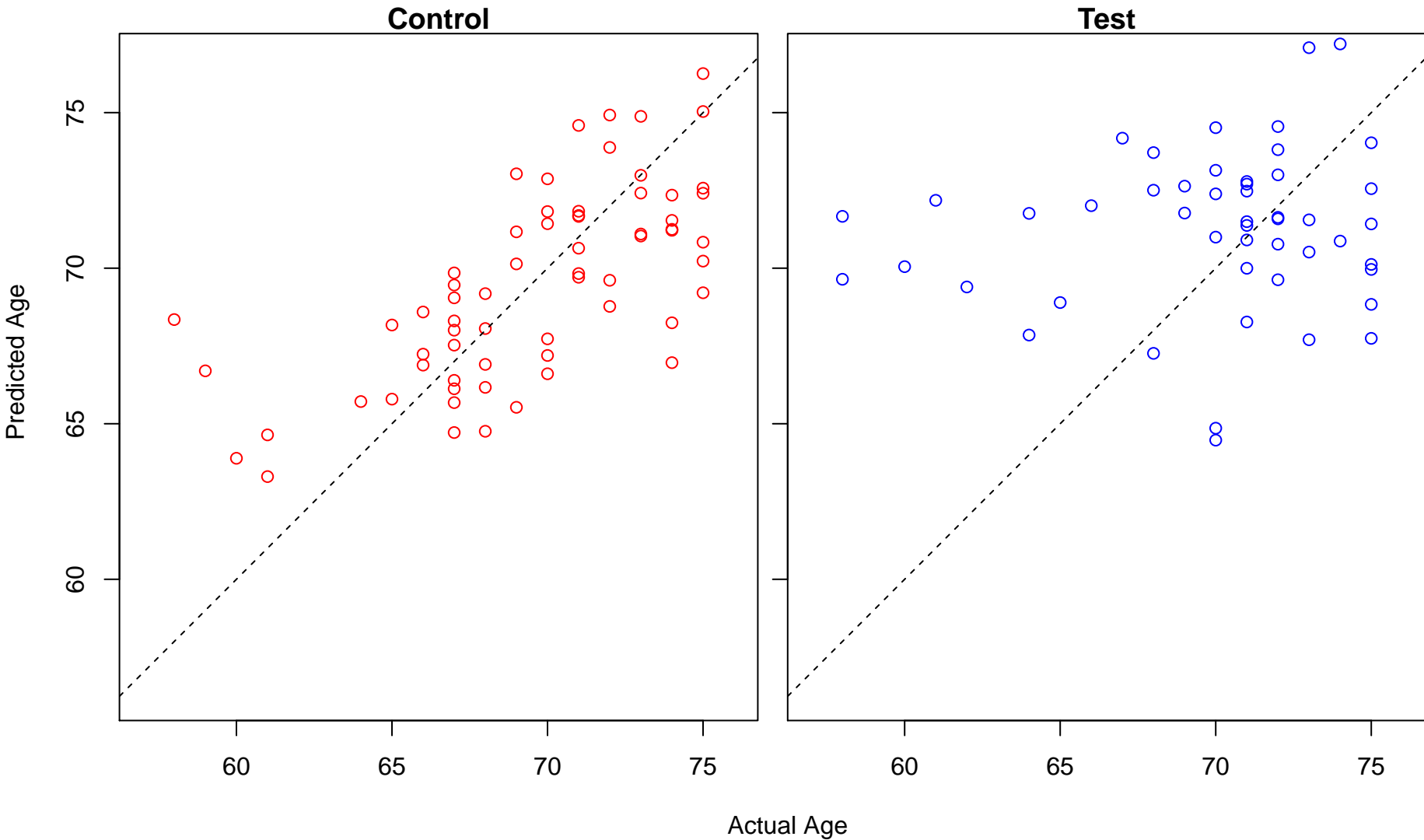


Test

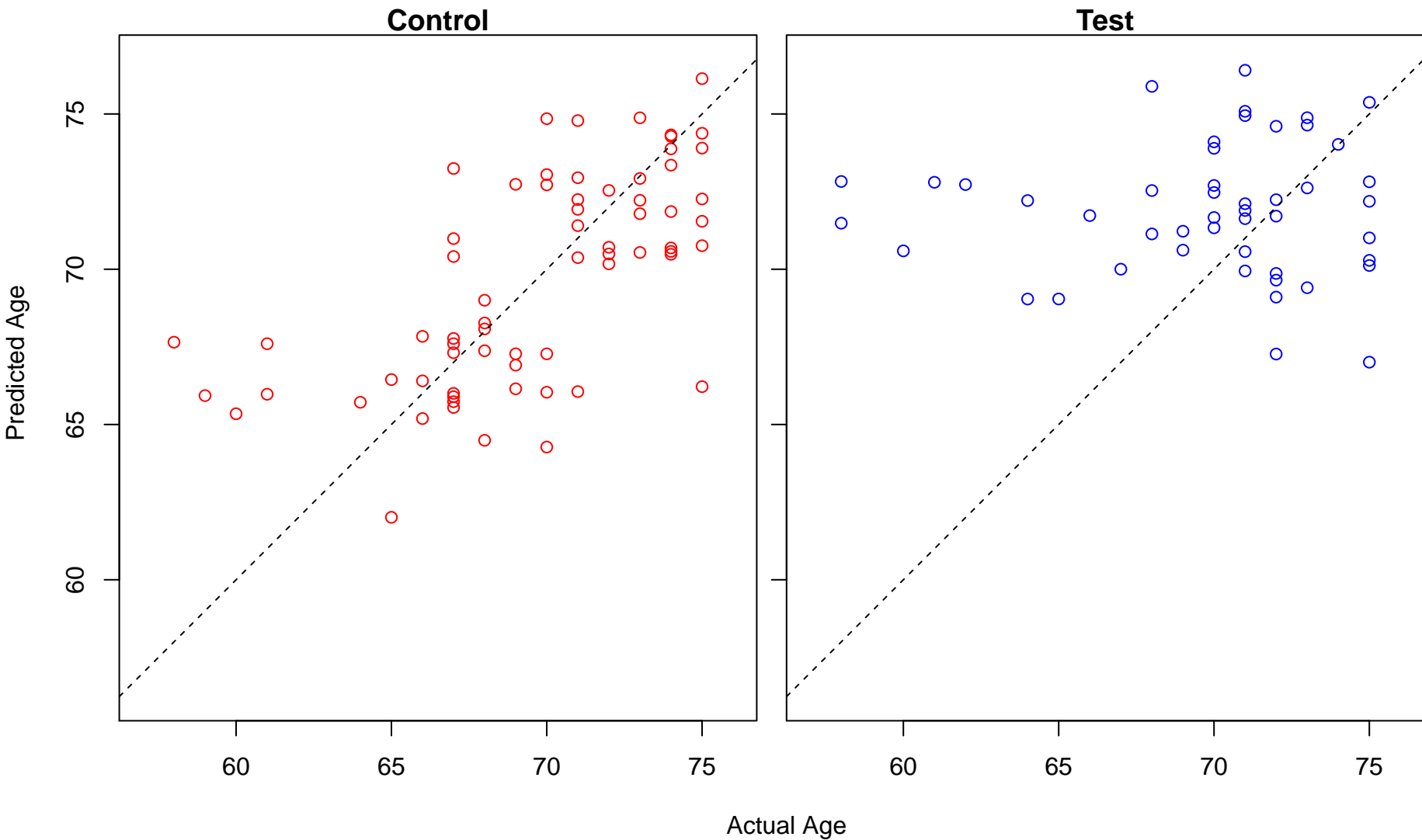


Actual Age

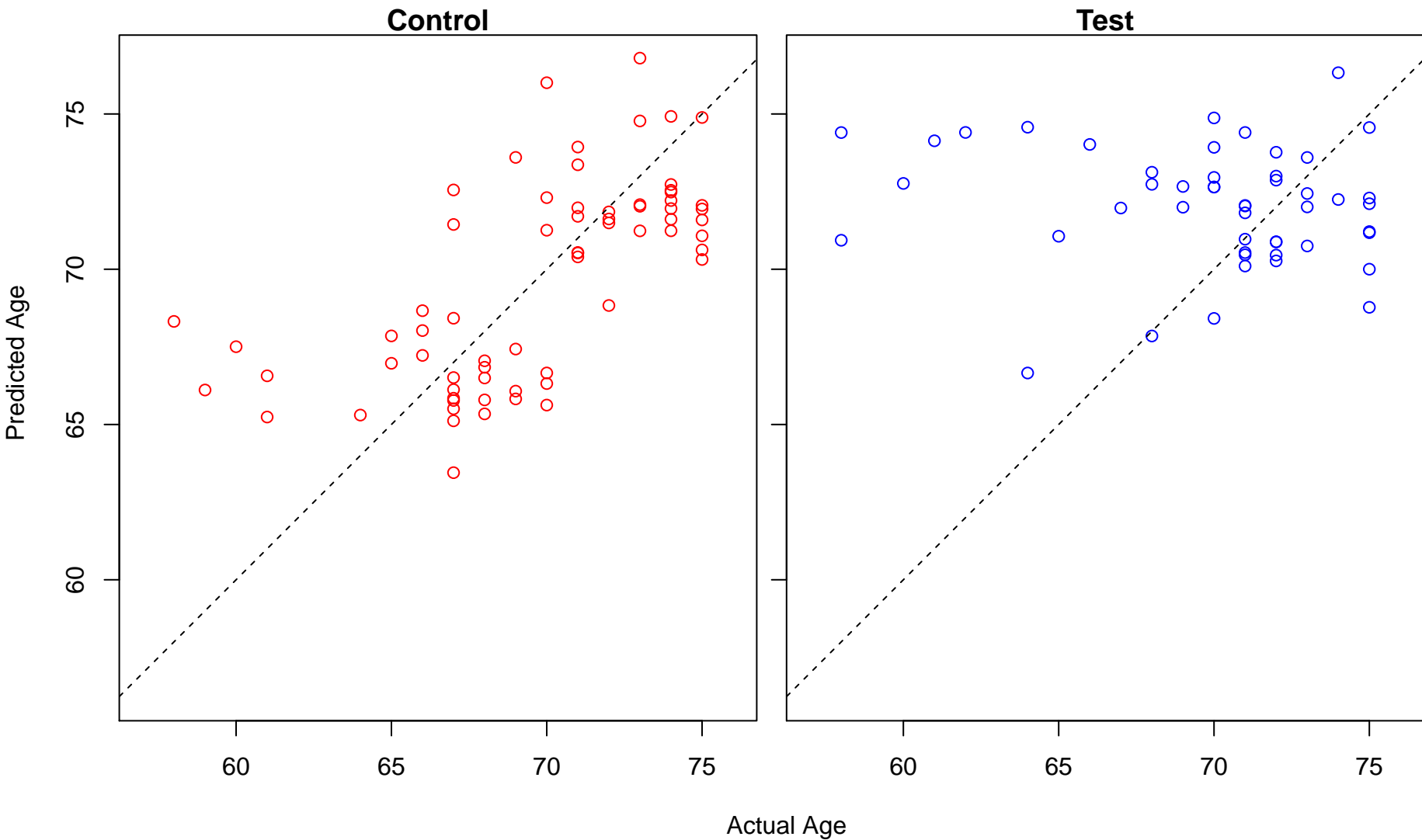
regulation of fatty acid biosynthetic process (Score: 1.331526)



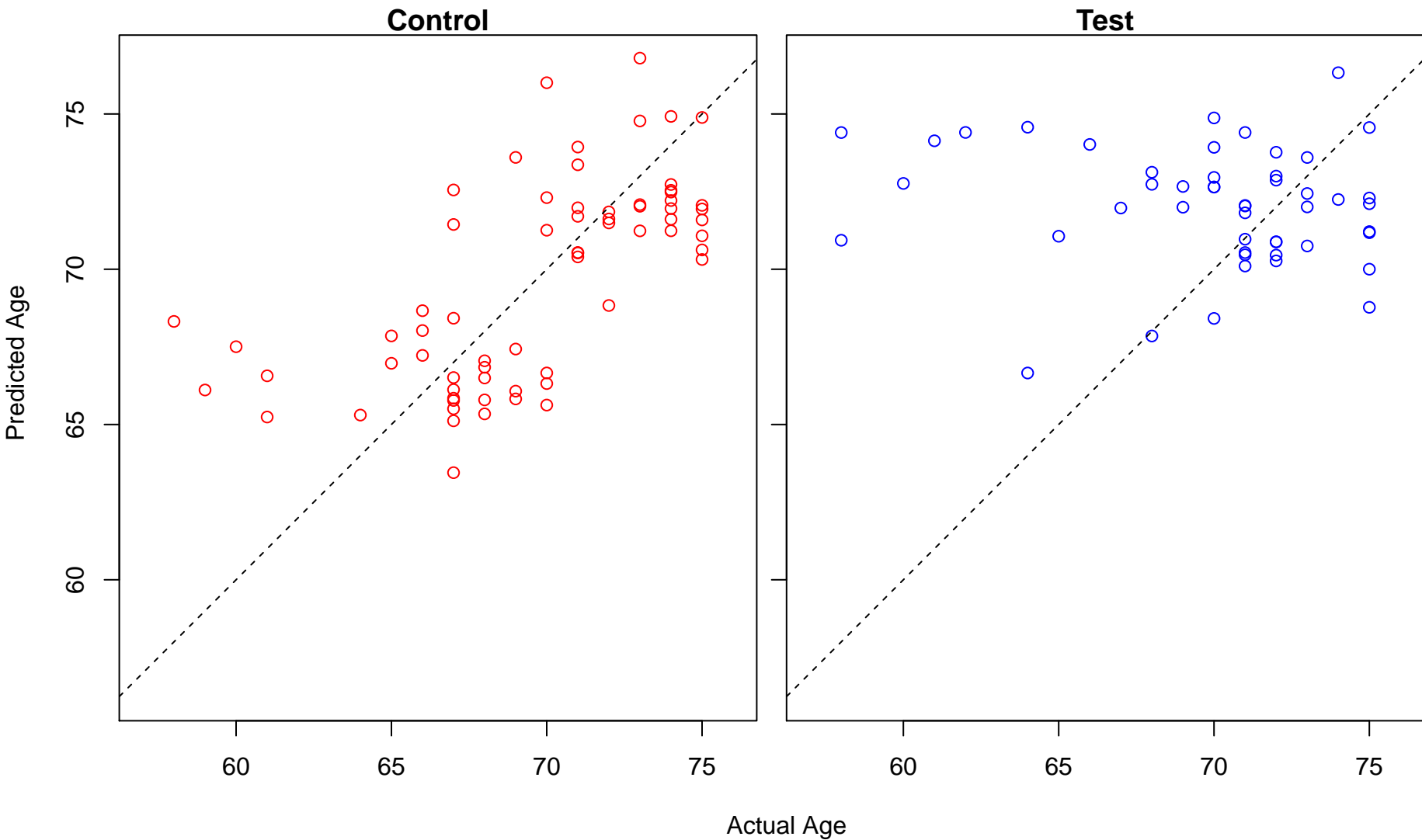
myeloid cell differentiation (Score: 1.331419)



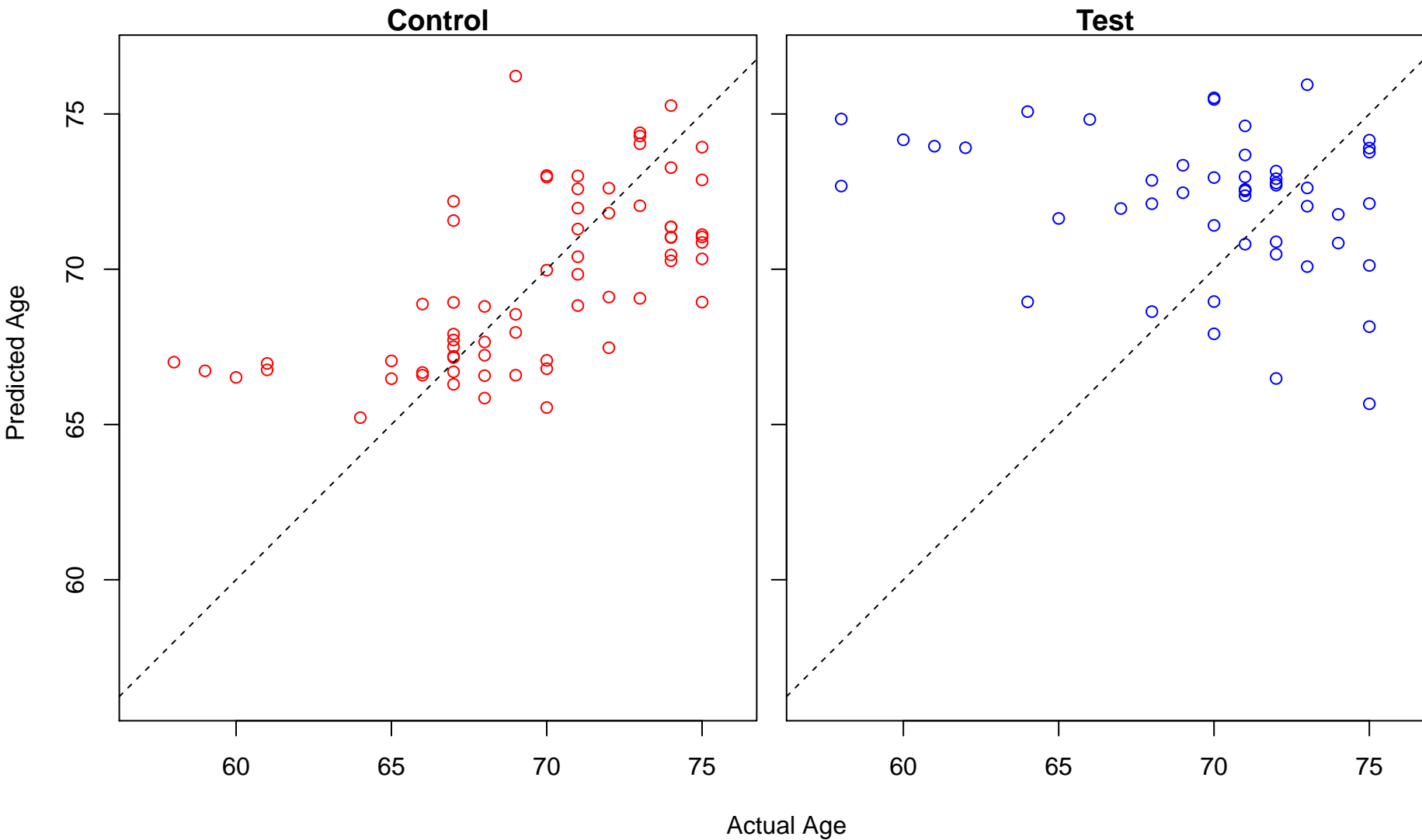
ensheathment of neurons (Score: 1.330556)



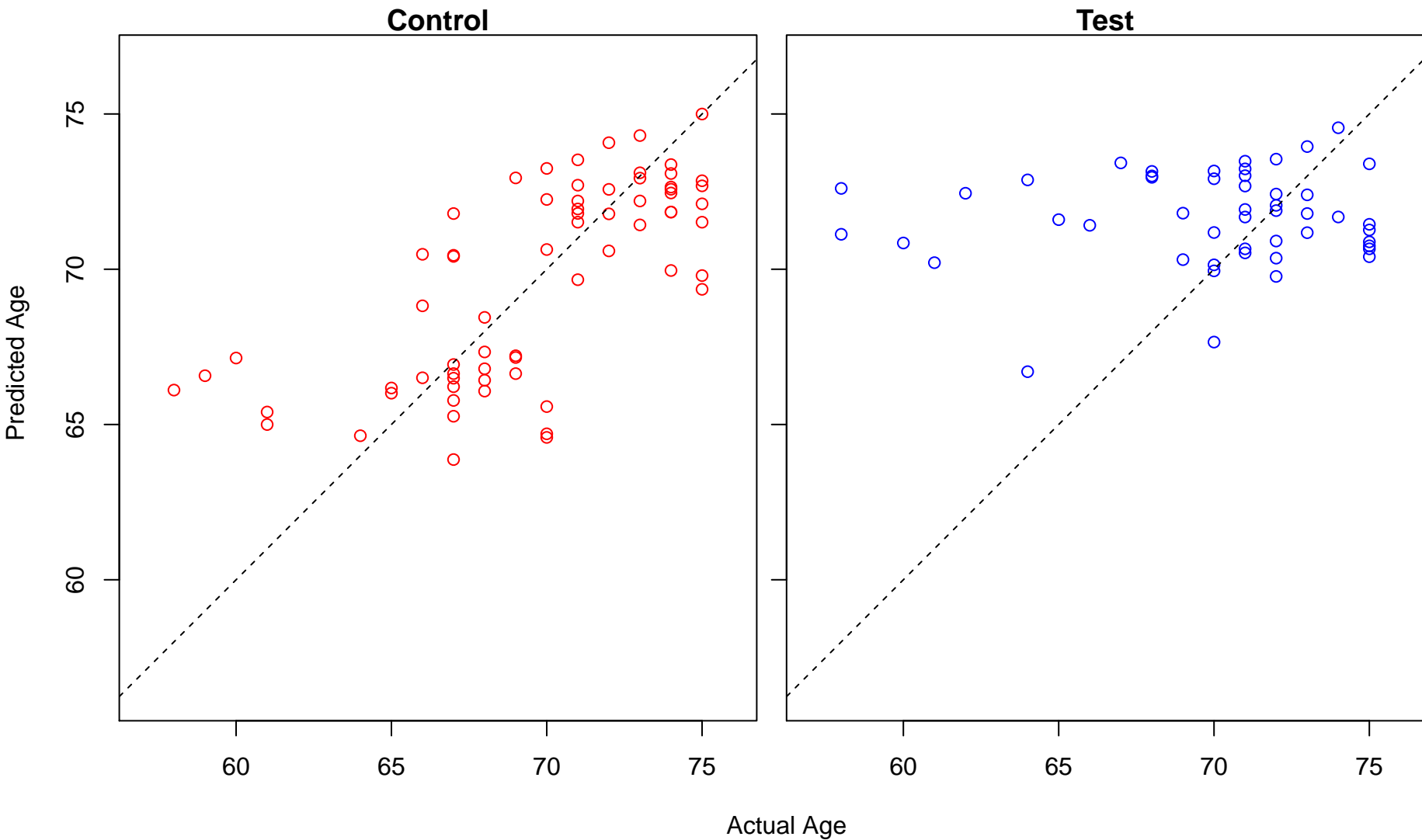
axon ensheathment (Score: 1.330556)



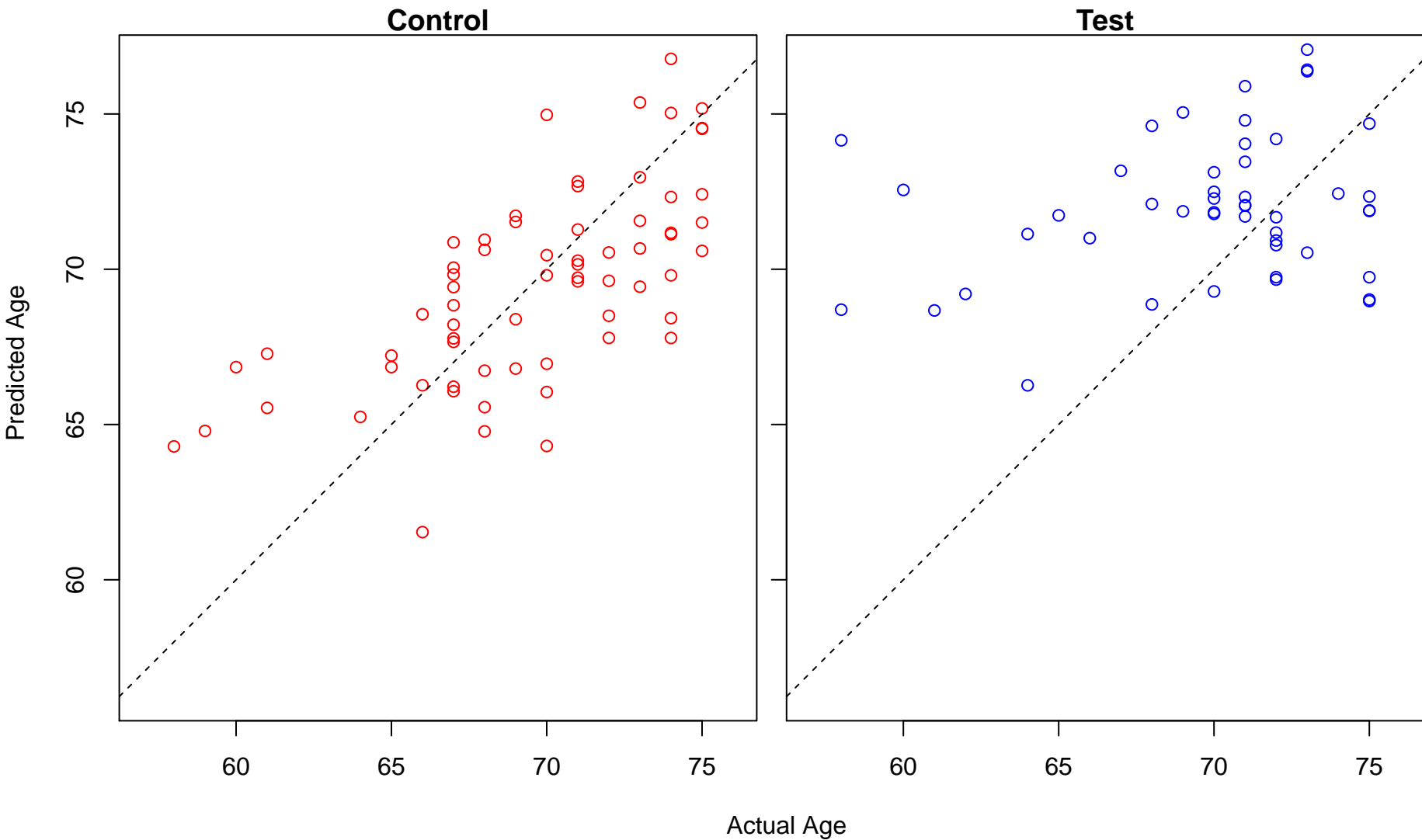
negative regulation of MAP kinase activity (Score: 1.330312)



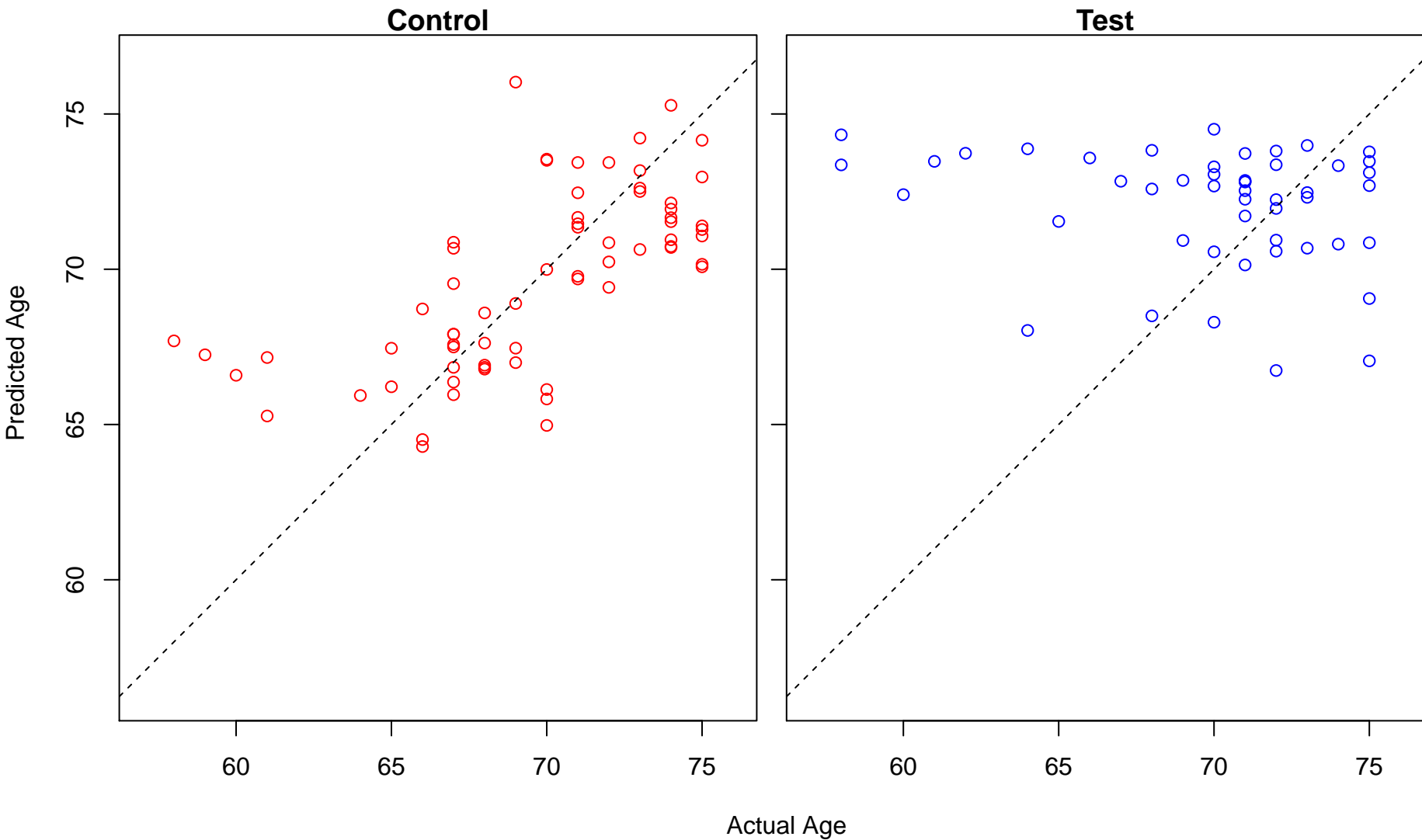
regulation of alternative mRNA splicing, via spliceosome (Score: 1.329946)



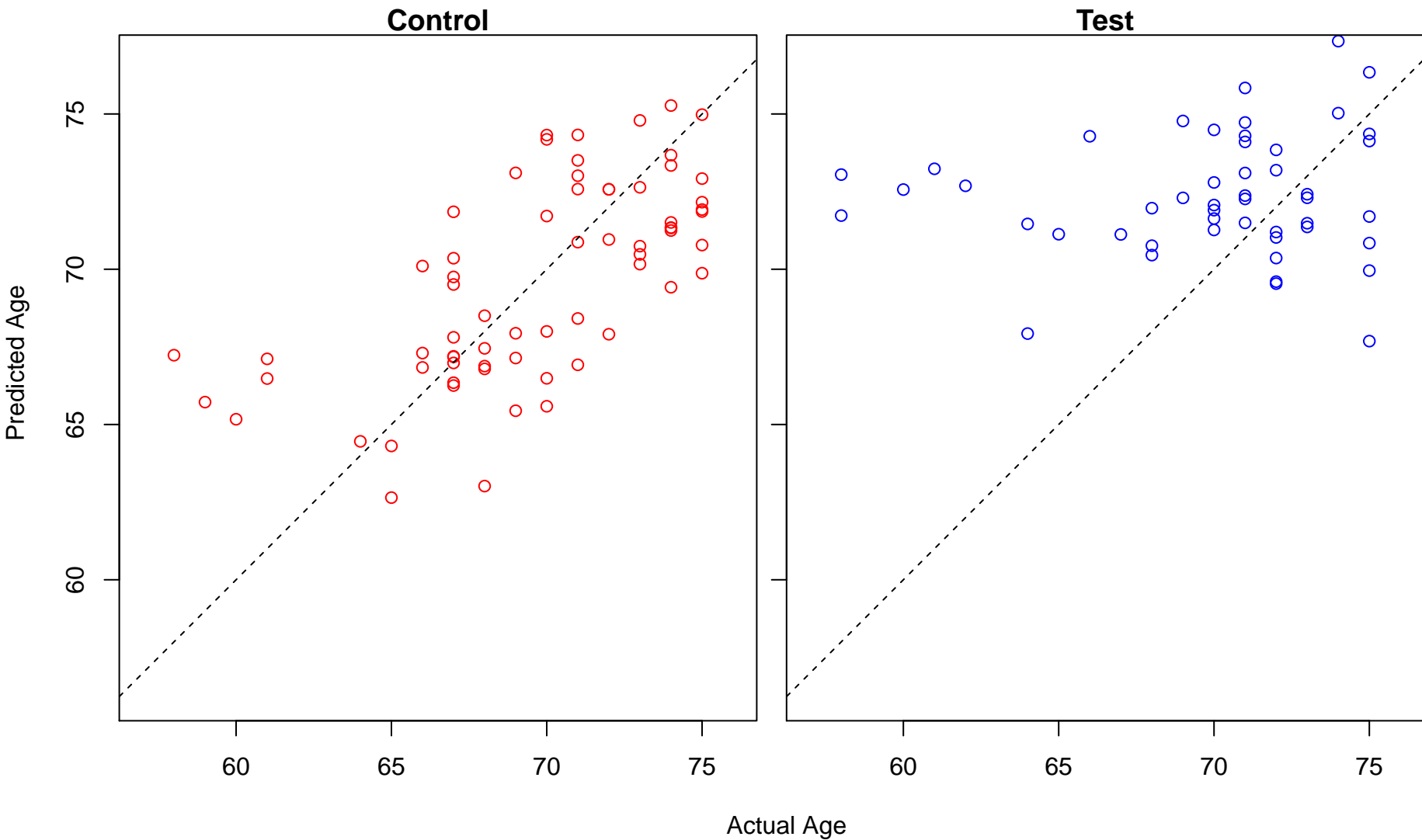
negative regulation of lipid storage (Score: 1.329573)



centrosome organization (Score: 1.328947)

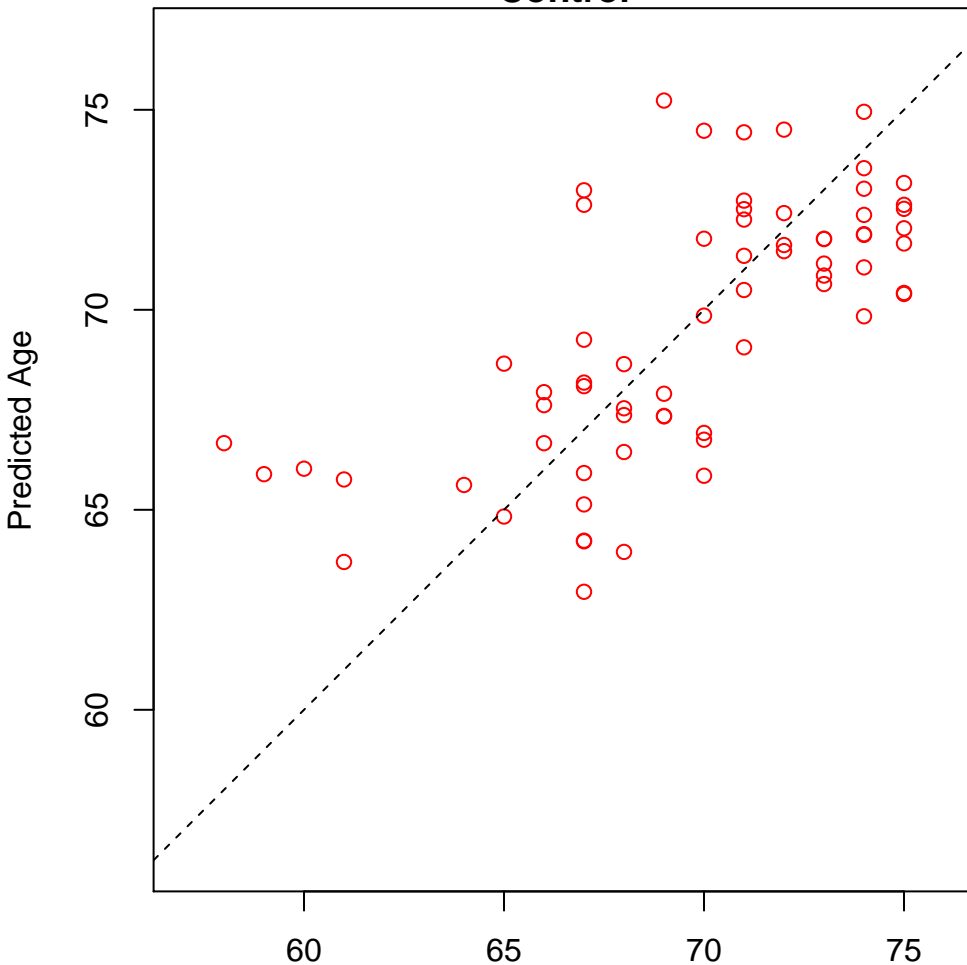


embryo development (Score: 1.328881)

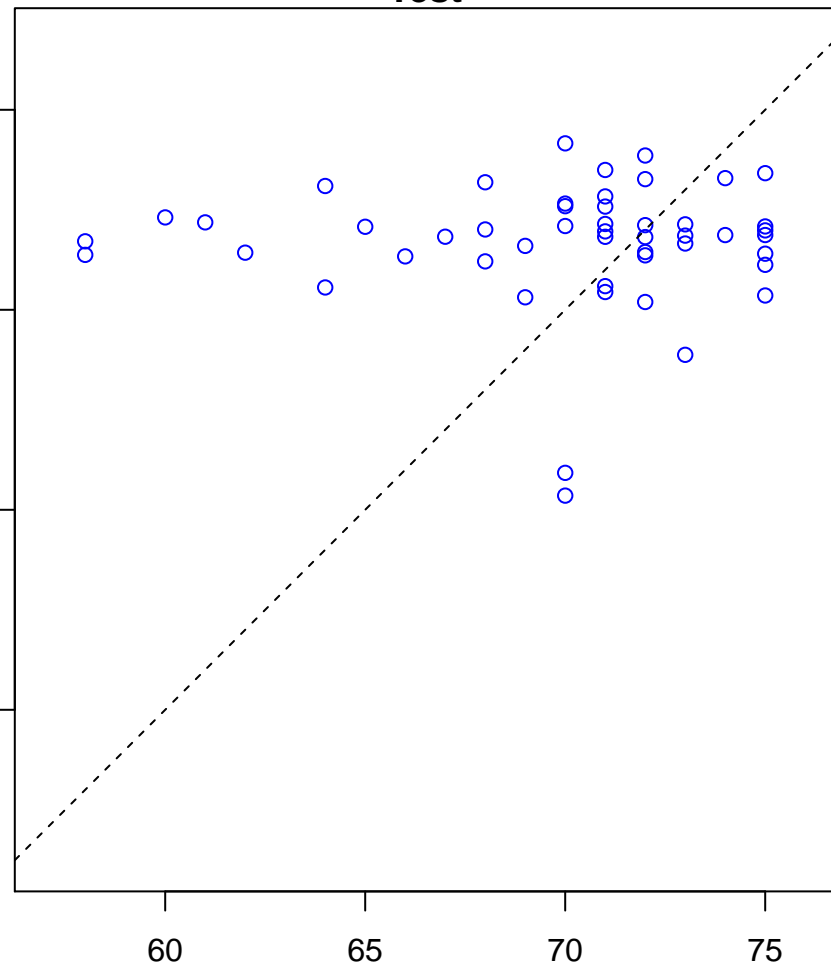


positive regulation of nuclease activity (Score: 1.328666)

Control

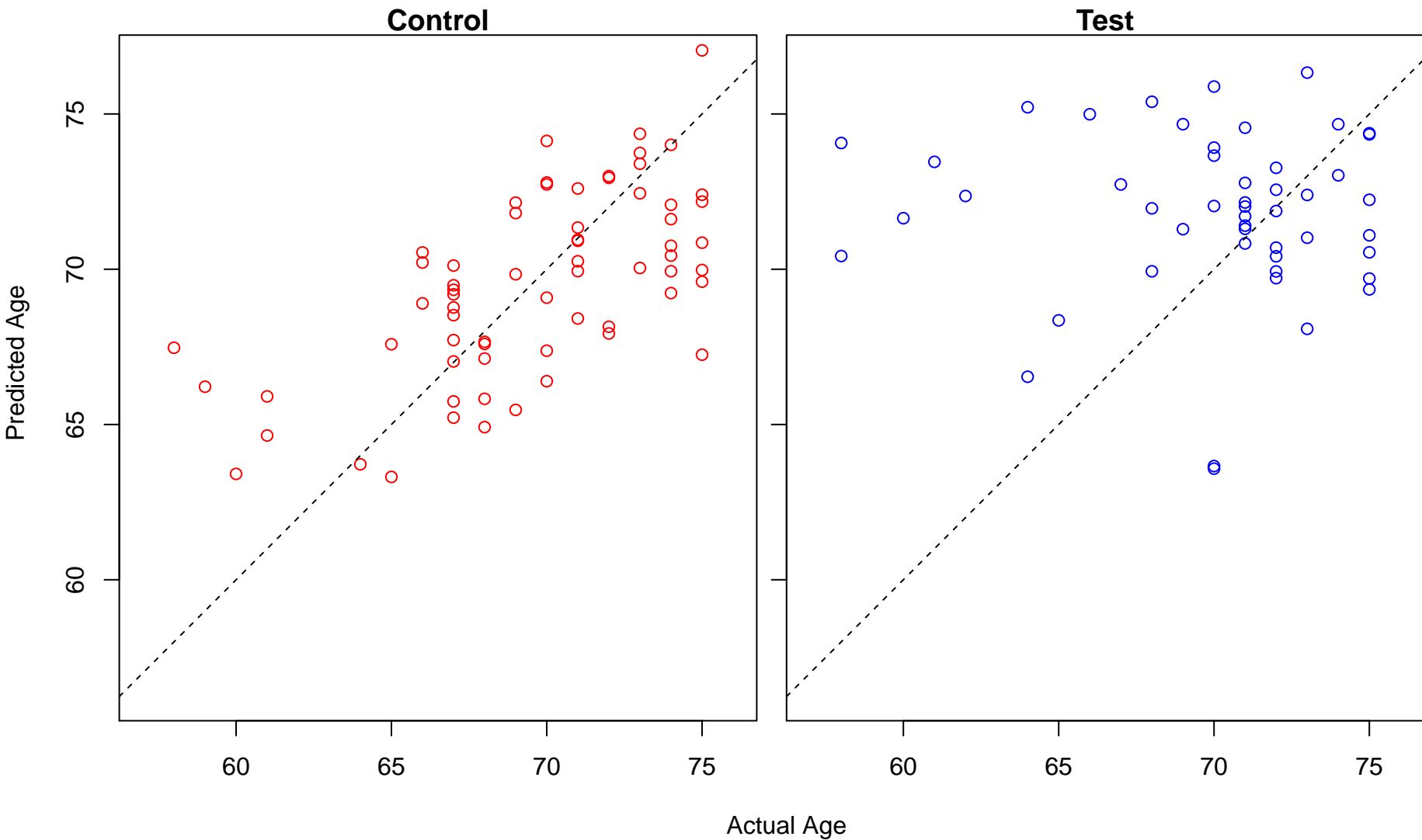


Test

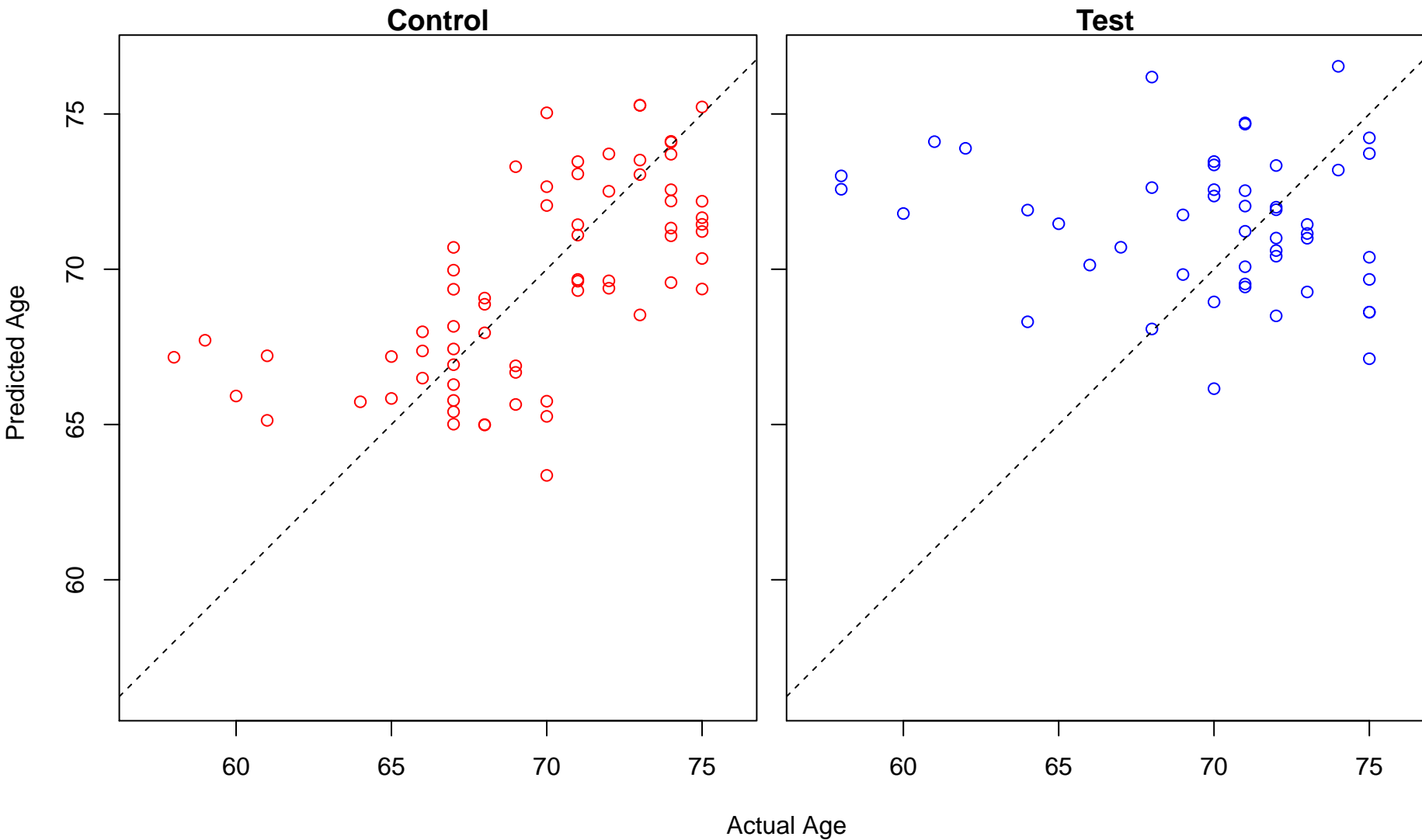


Actual Age

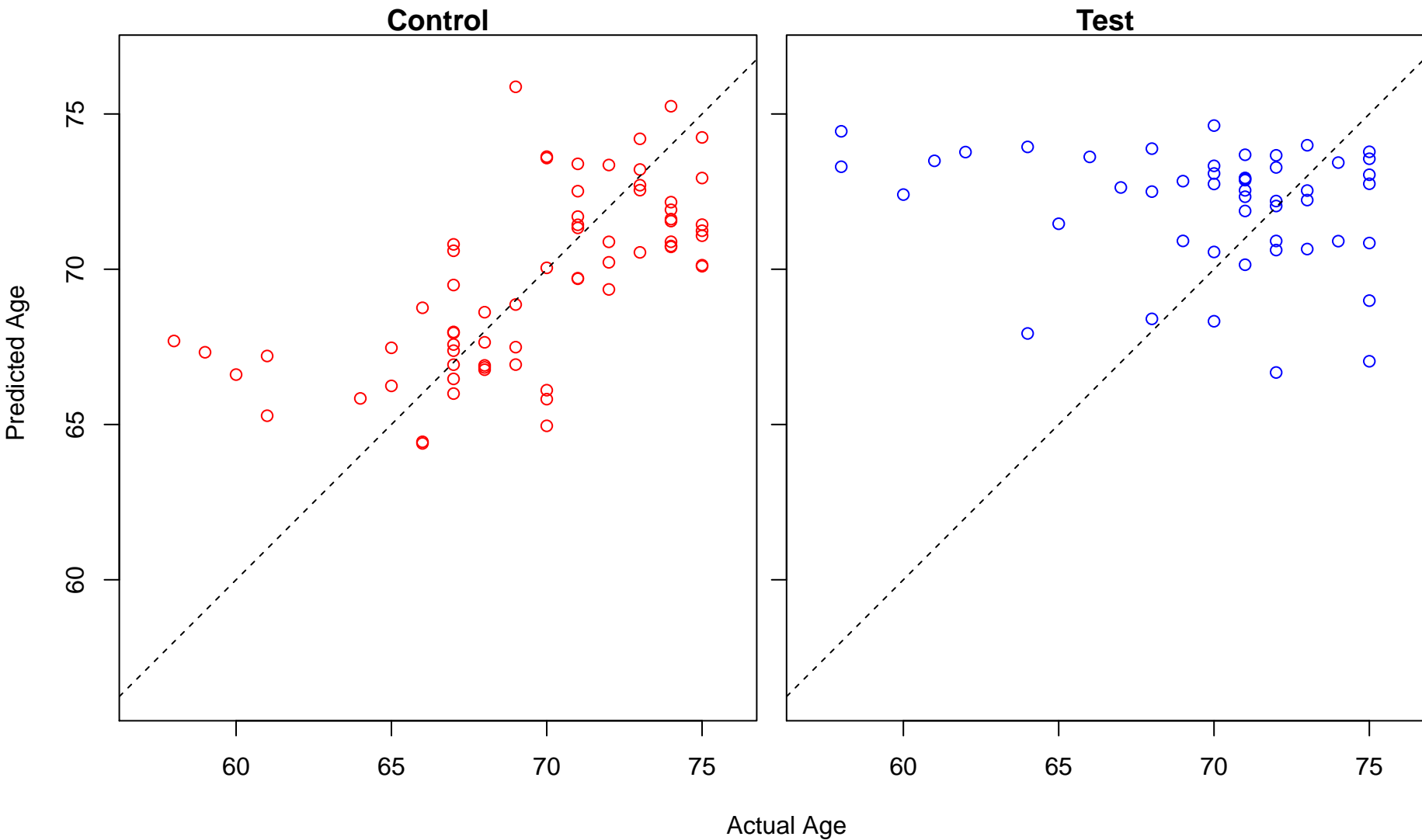
regulation of fatty acid oxidation (Score: 1.328608)



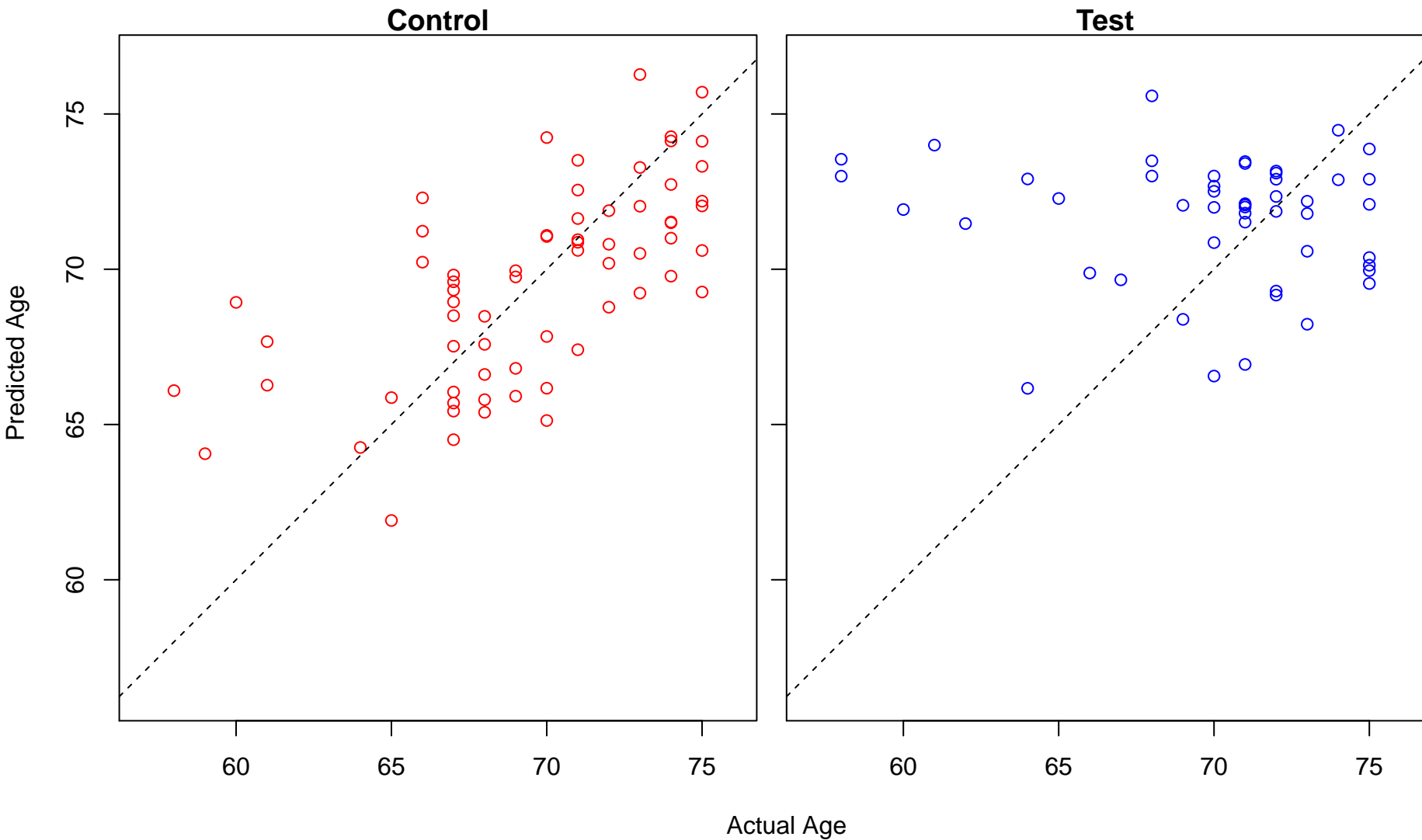
negative regulation of cellular catabolic process (Score: 1.328396)



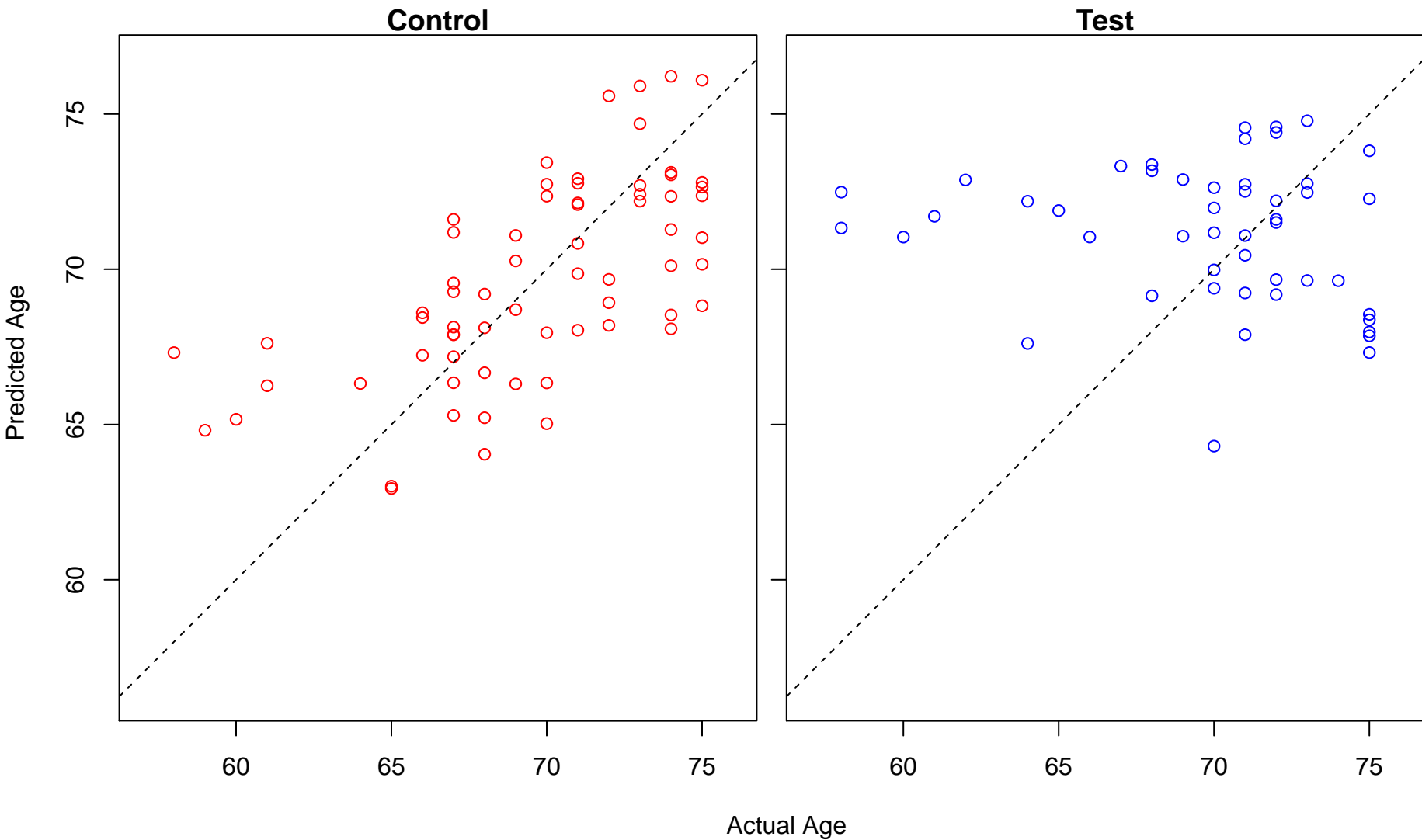
microtubule organizing center organization (Score: 1.327238)



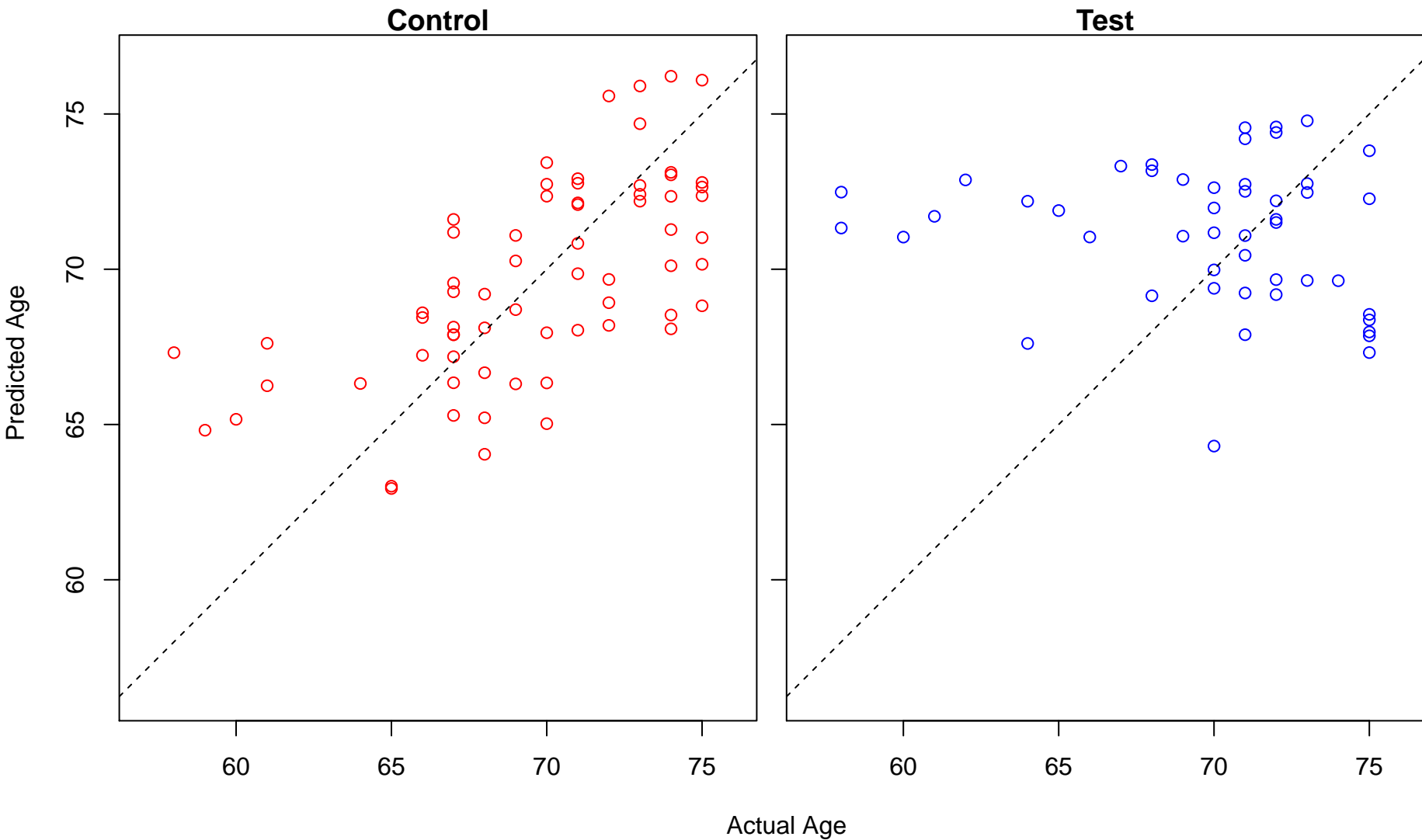
response to growth hormone (Score: 1.327079)



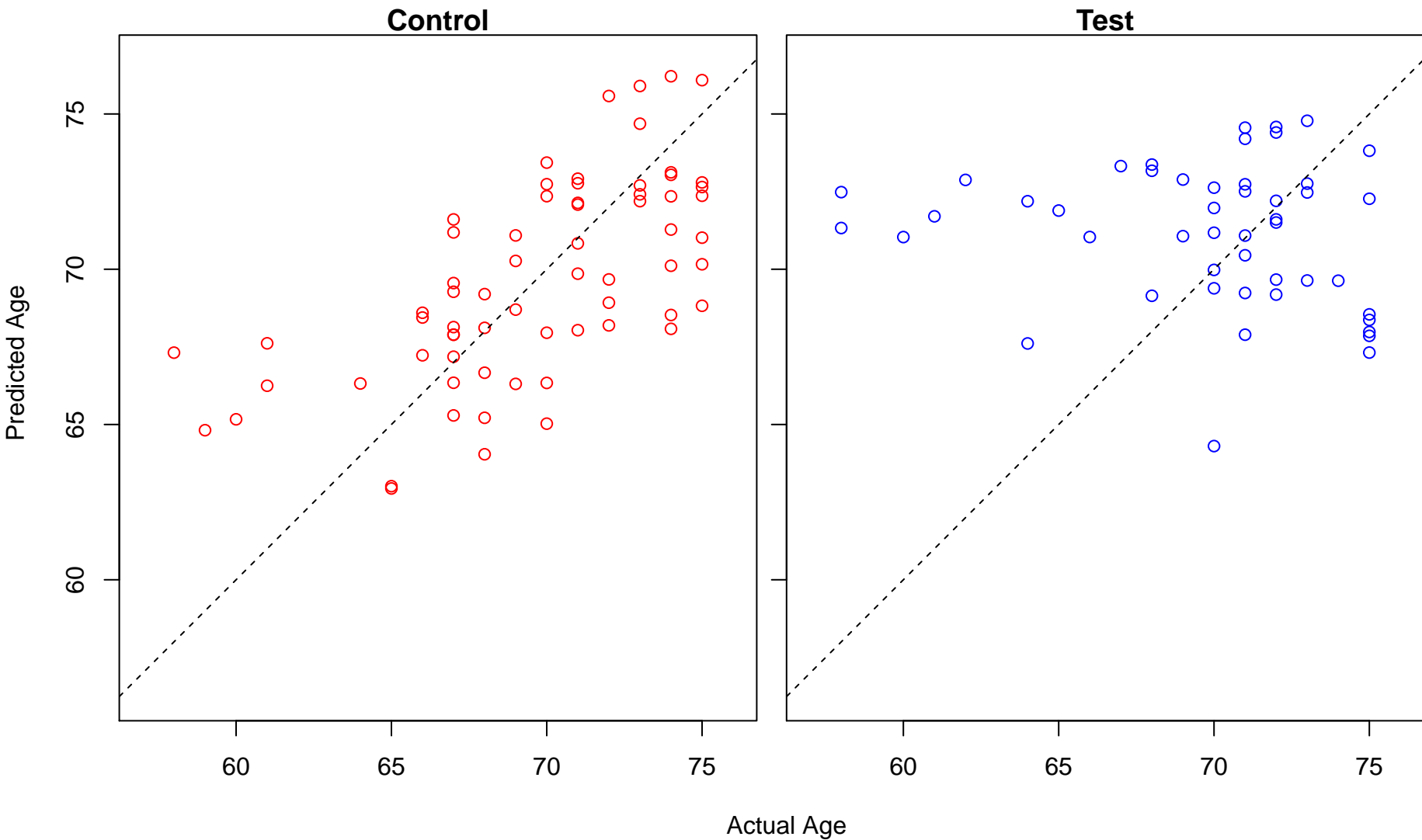
release of sequestered calcium ion into cytosol (Score: 1.327072)



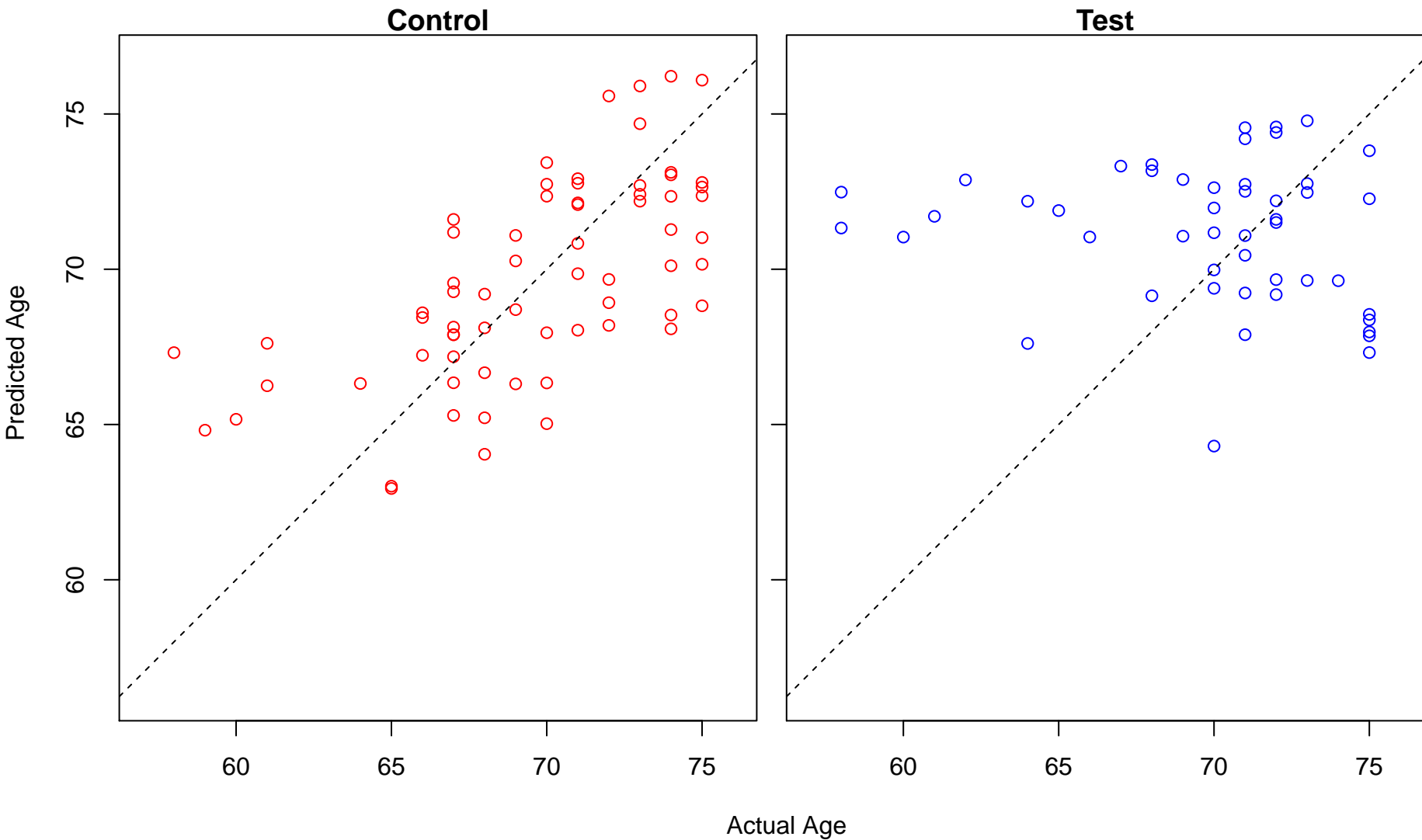
negative regulation of sequestering of calcium ion (Score: 1.327072)



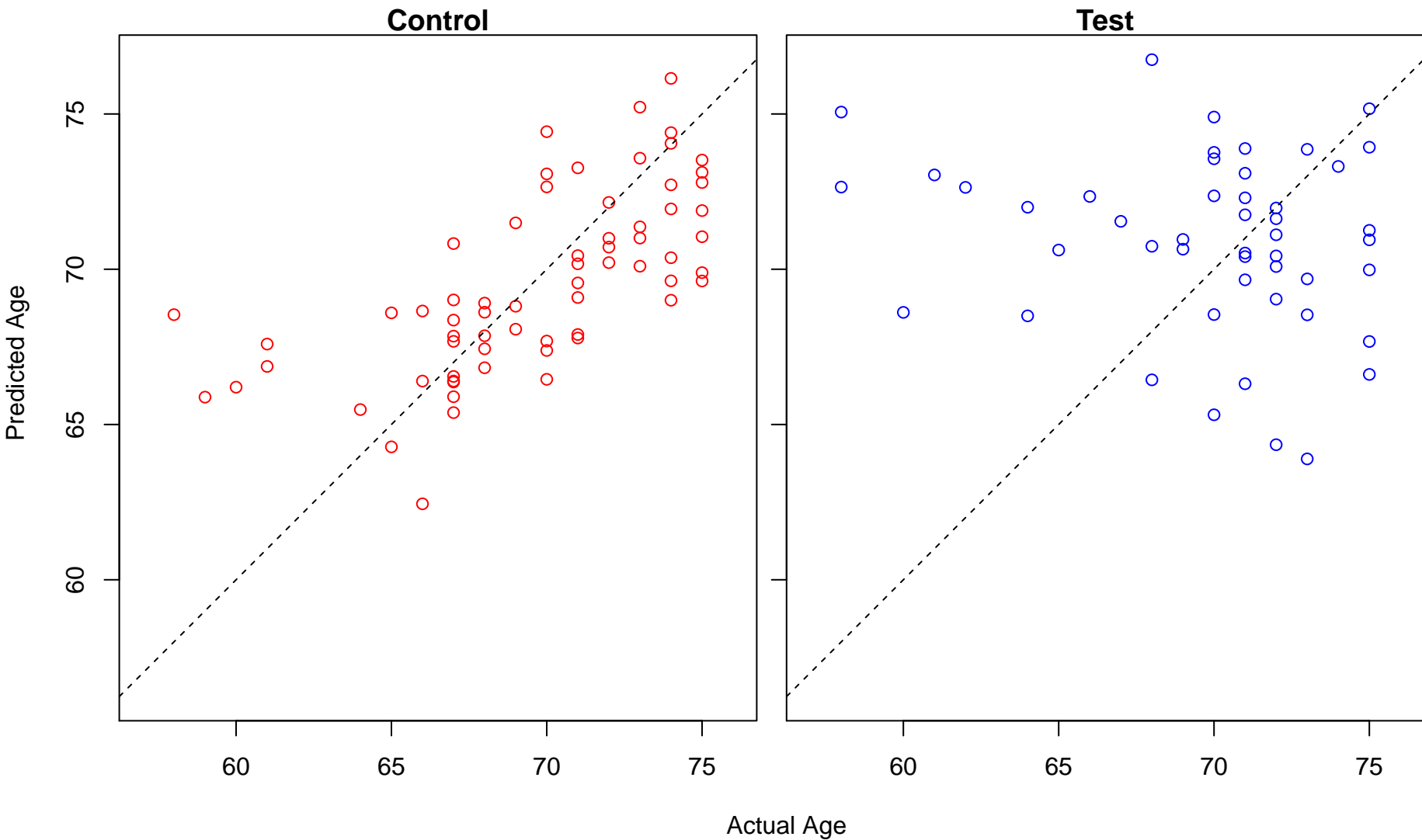
calcium ion transmembrane import into cytosol (Score: 1.327072)



calcium ion import into cytosol (Score: 1.327072)

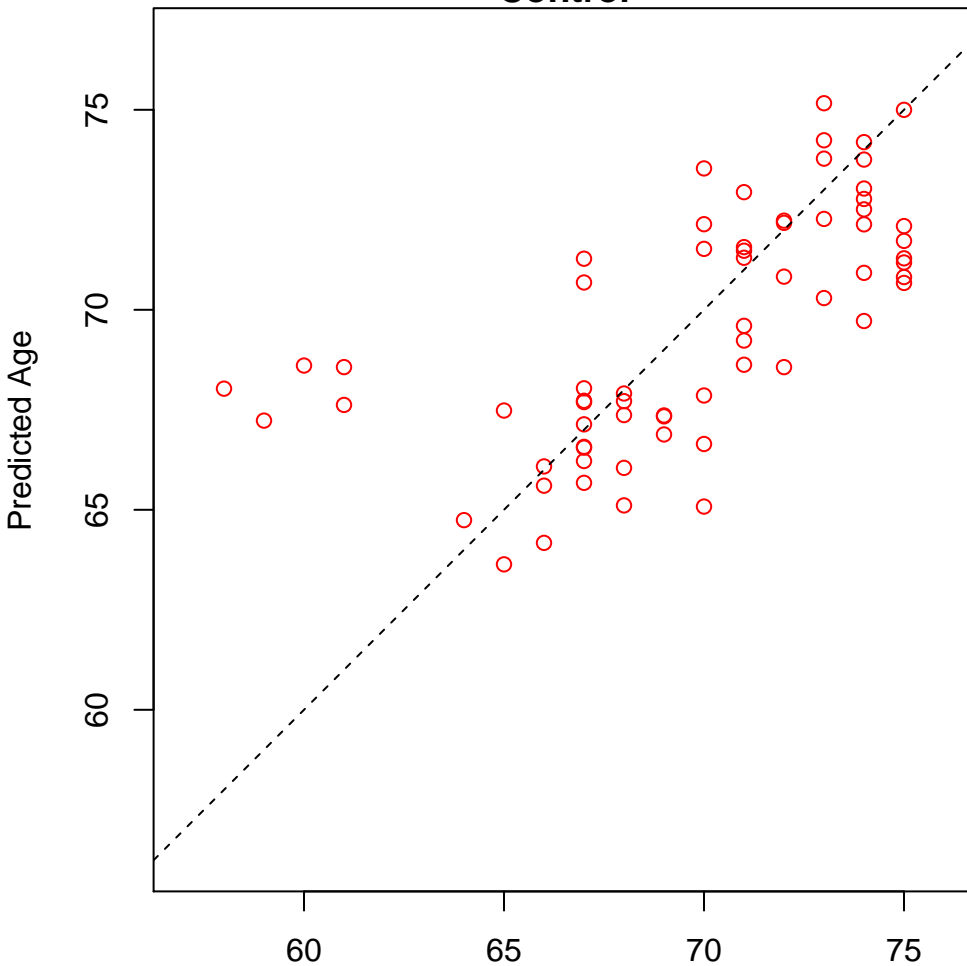


regulation of production of molecular mediator of immune response (Score: 1.327057)

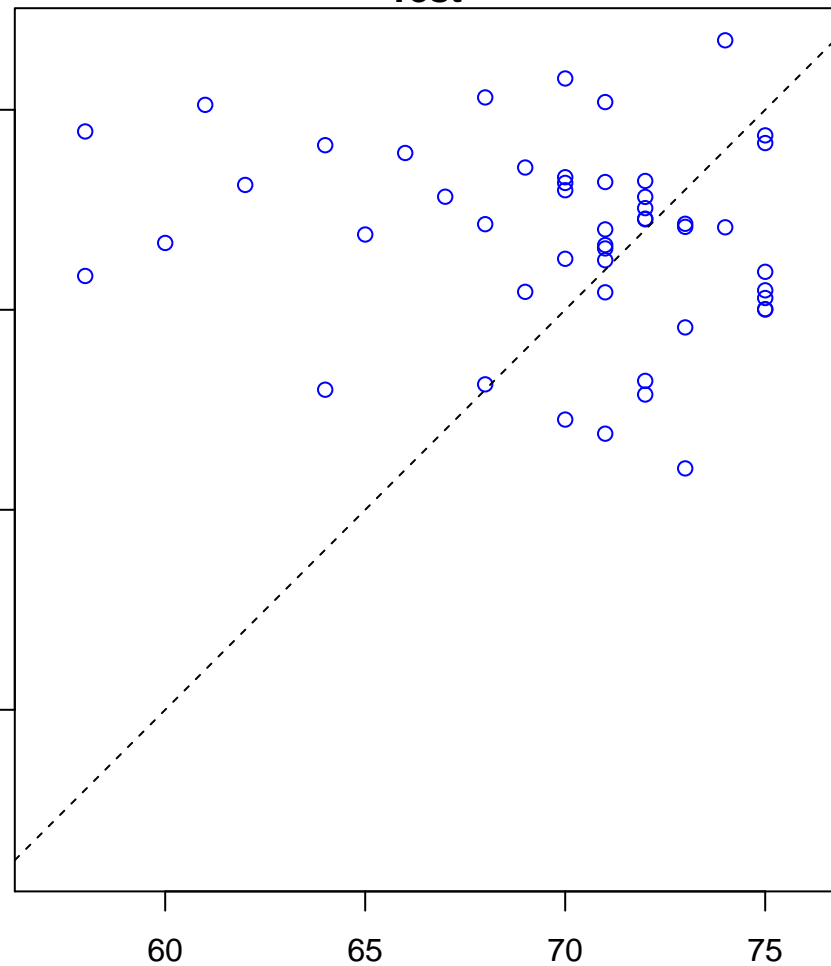


negative regulation of protein transport (Score: 1.326905)

Control

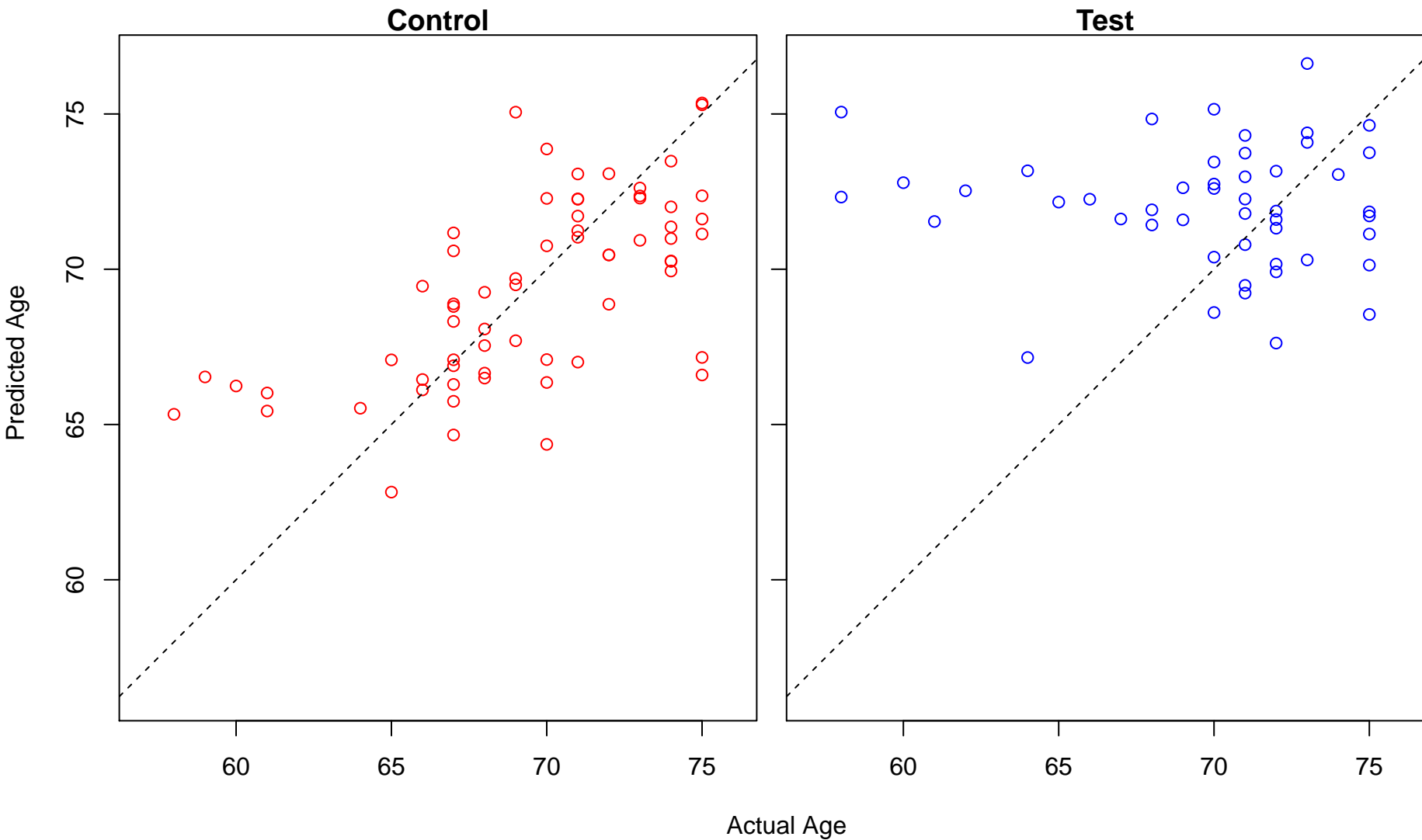


Test

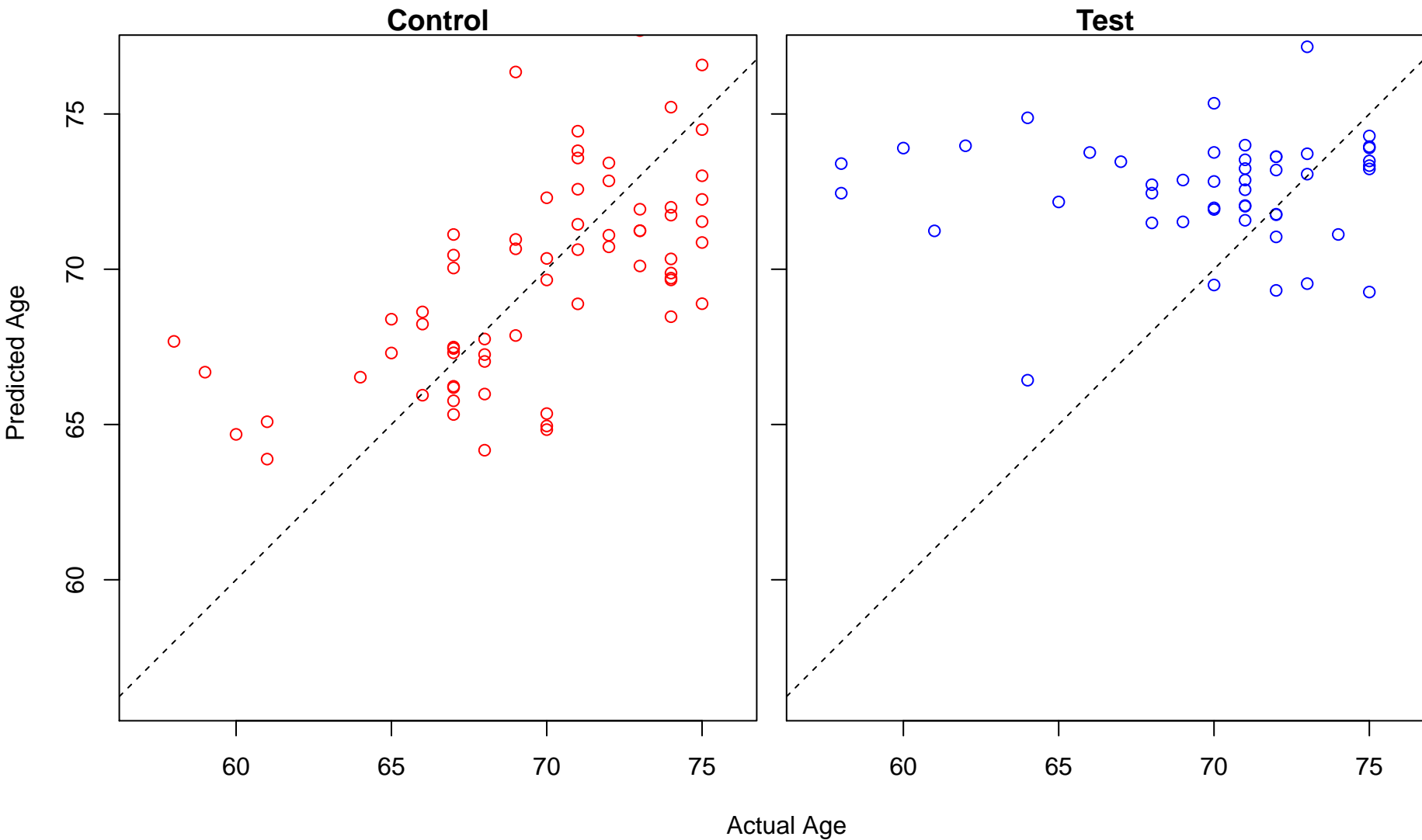


Actual Age

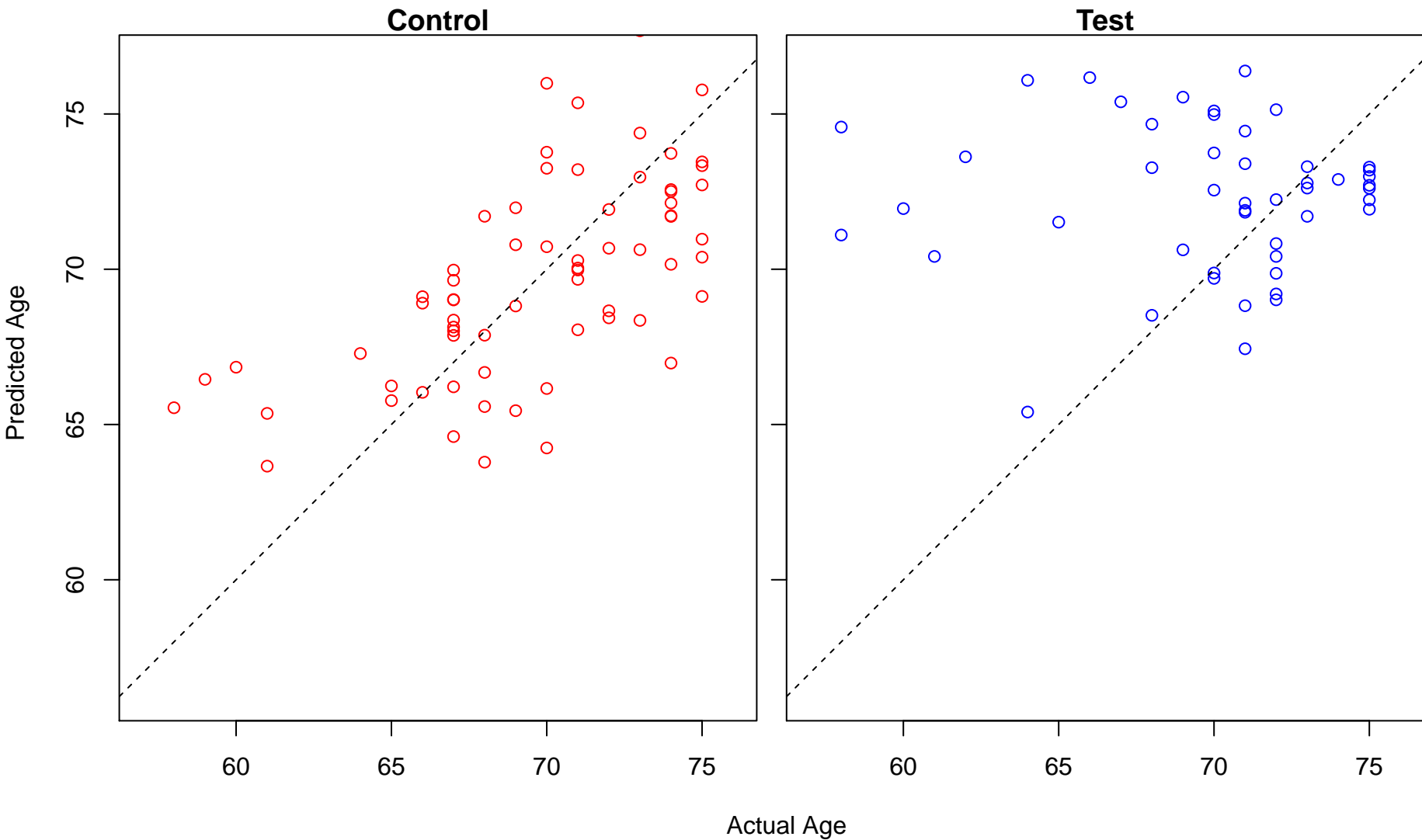
lipid localization (Score: 1.326328)



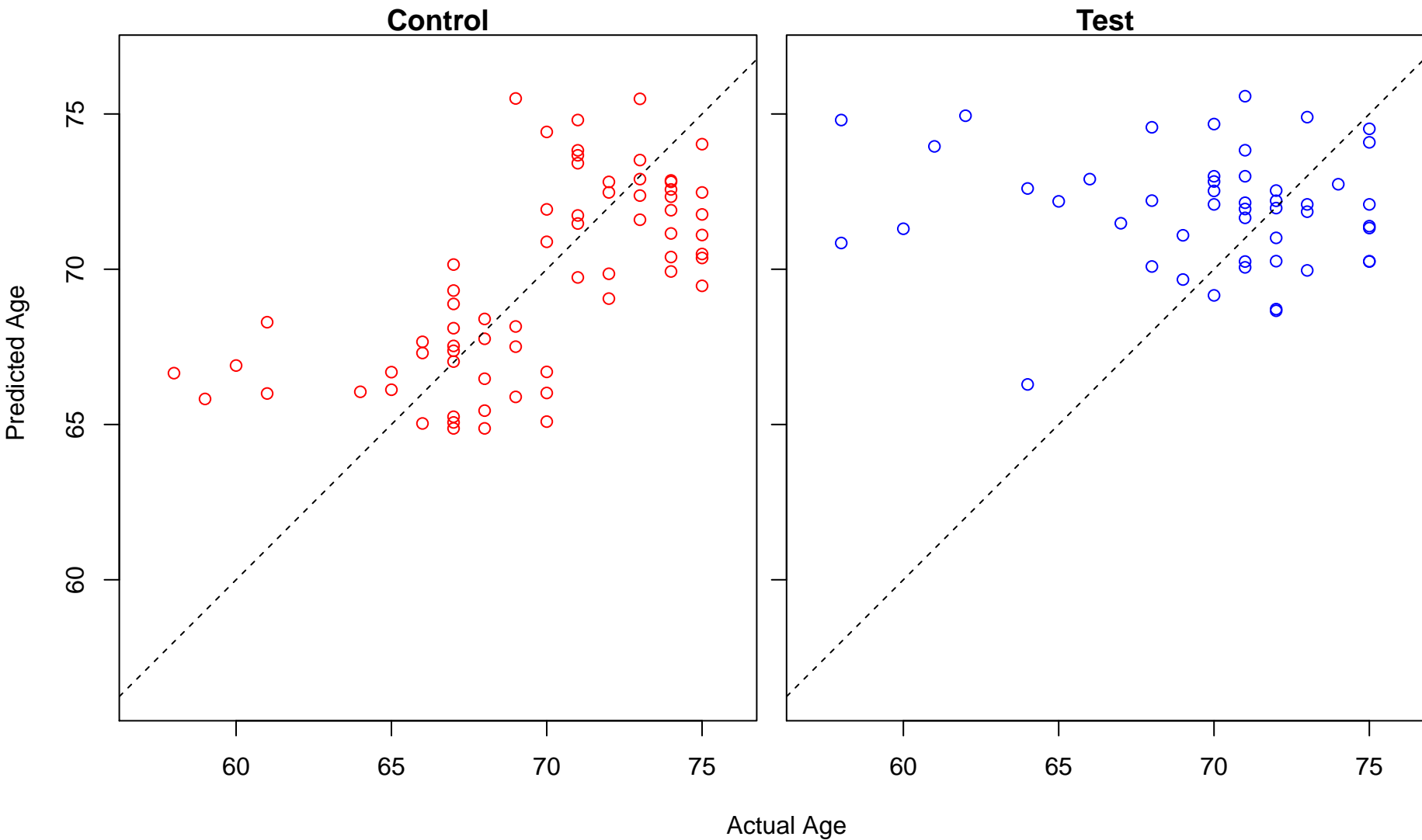
carbohydrate biosynthetic process (Score: 1.325293)



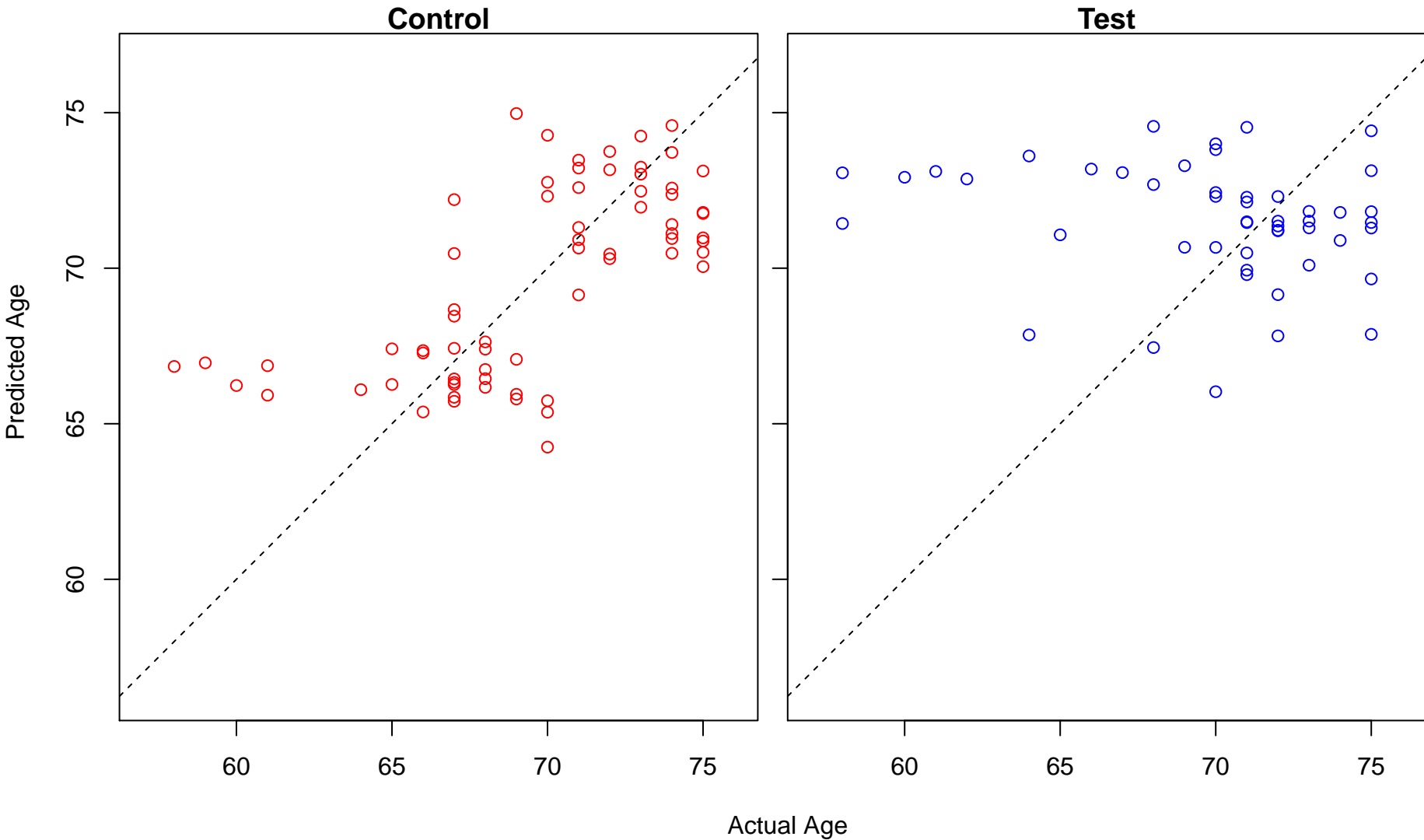
negative regulation of histone methylation (Score: 1.325267)



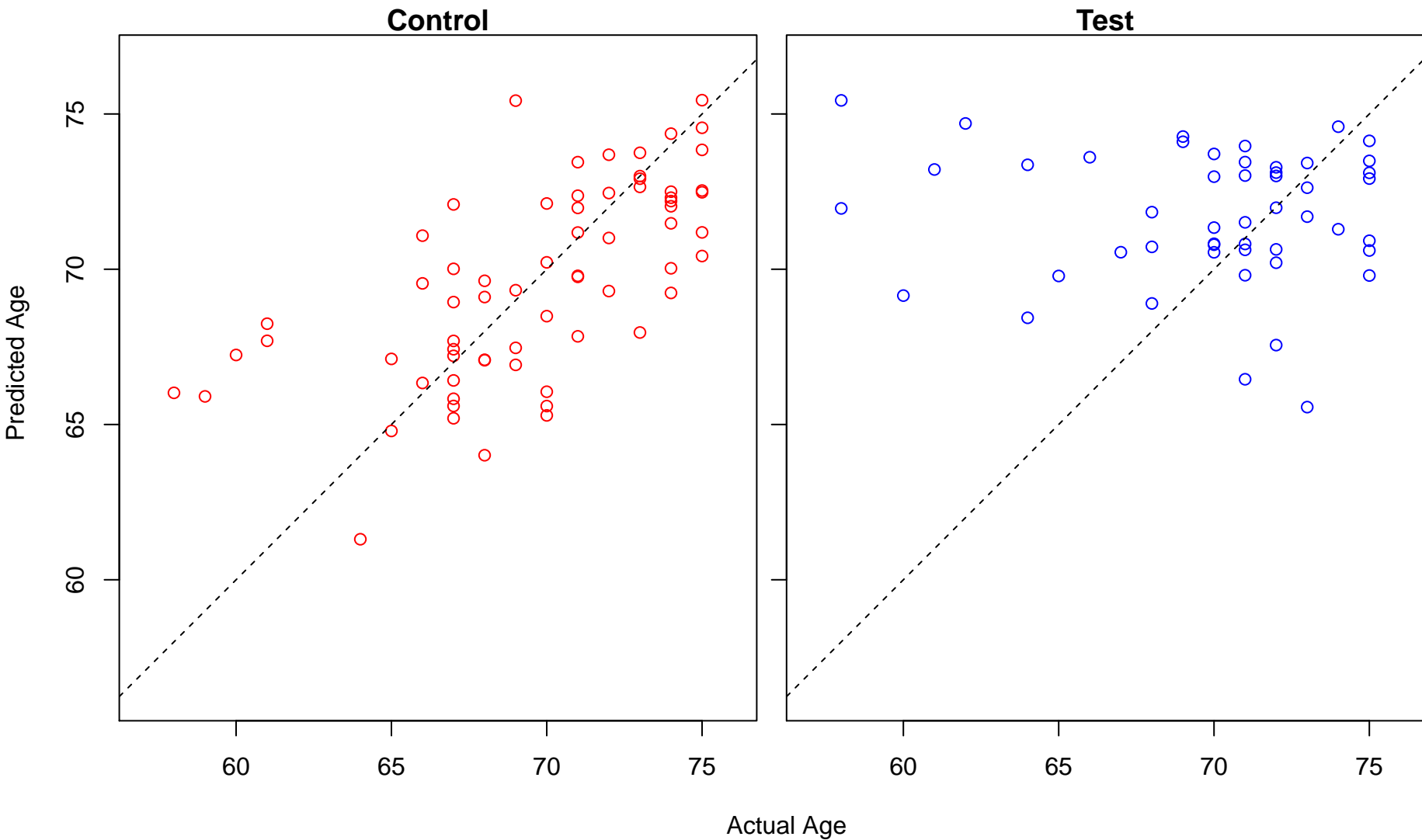
anatomical structure homeostasis (Score: 1.325222)



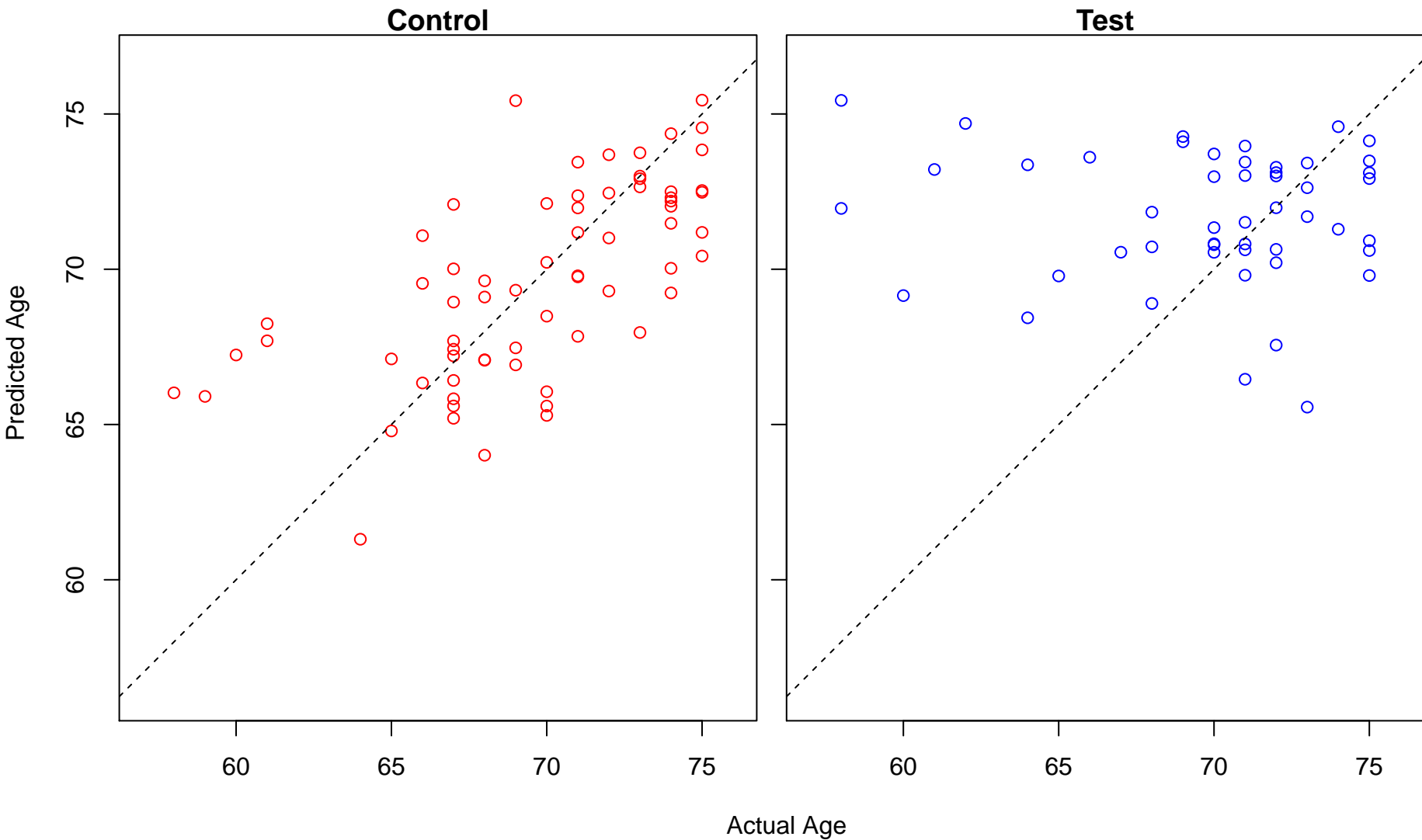
regulation of mitotic sister chromatid segregation (Score: 1.325194)



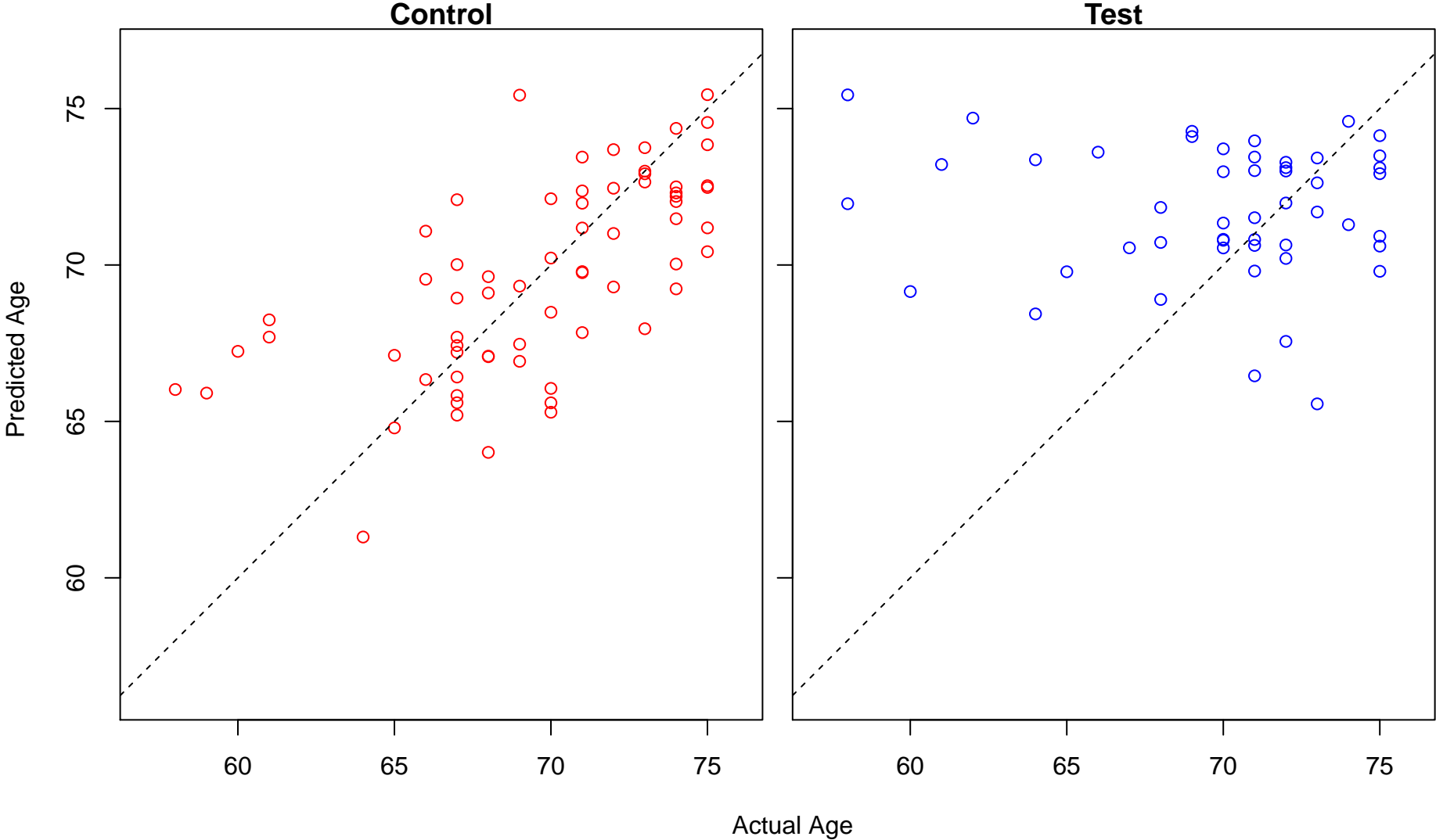
intracellular transport of viral protein in host cell (Score: 1.324653)



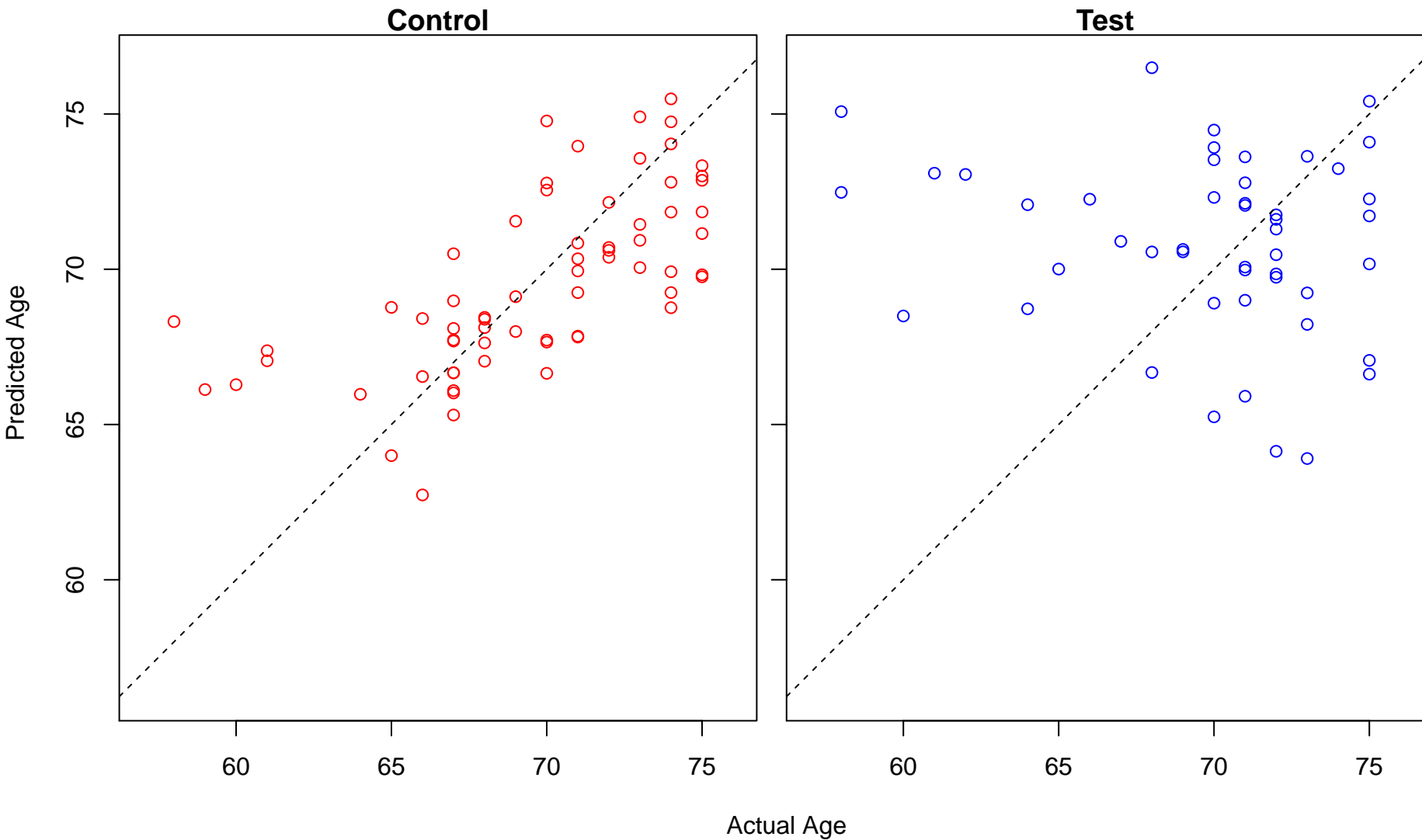
sybiont intracellular protein transport in host (Score: 1.324653)



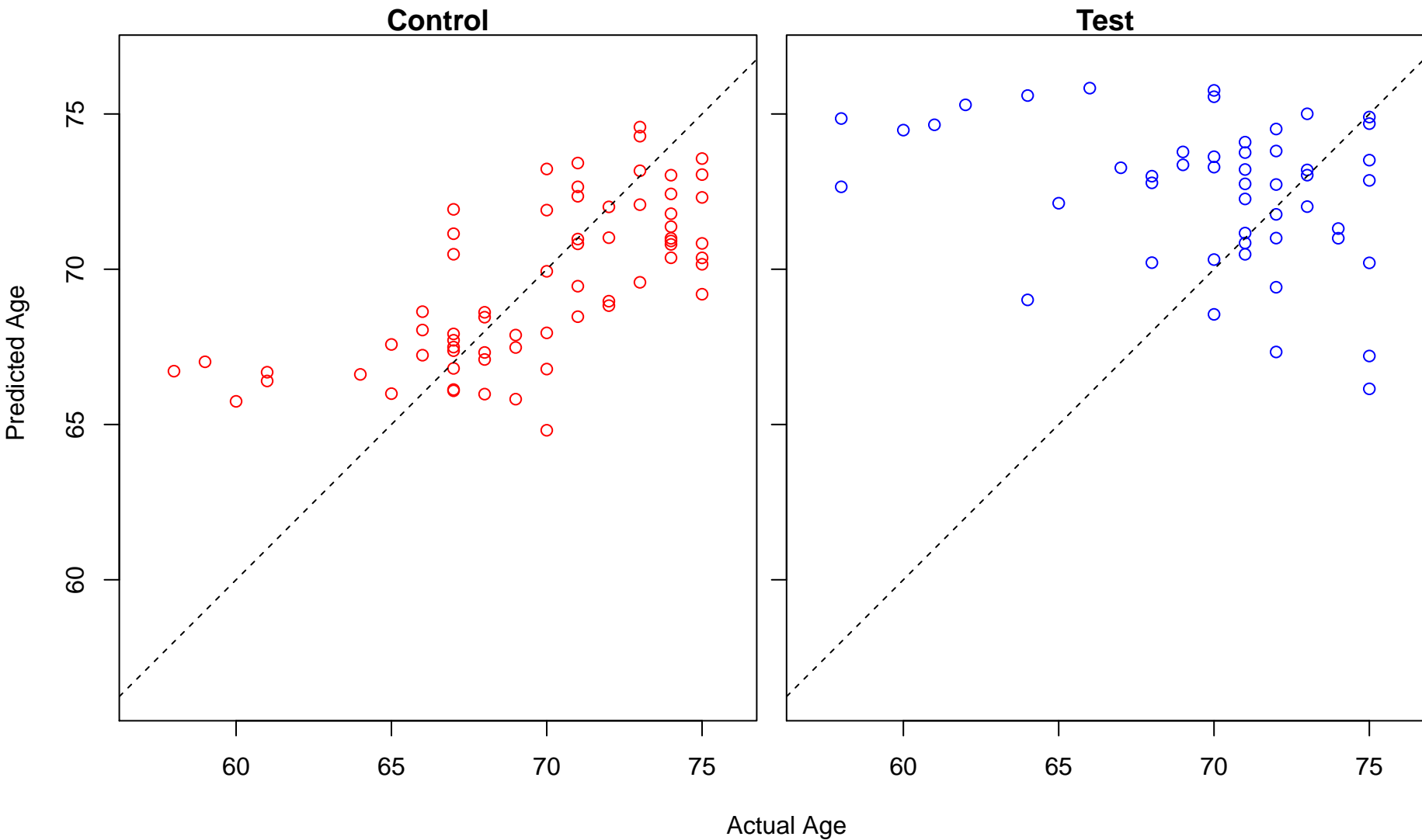
intracellular protein transport in other organism involved in symbiotic interaction (Score: 1.324653)



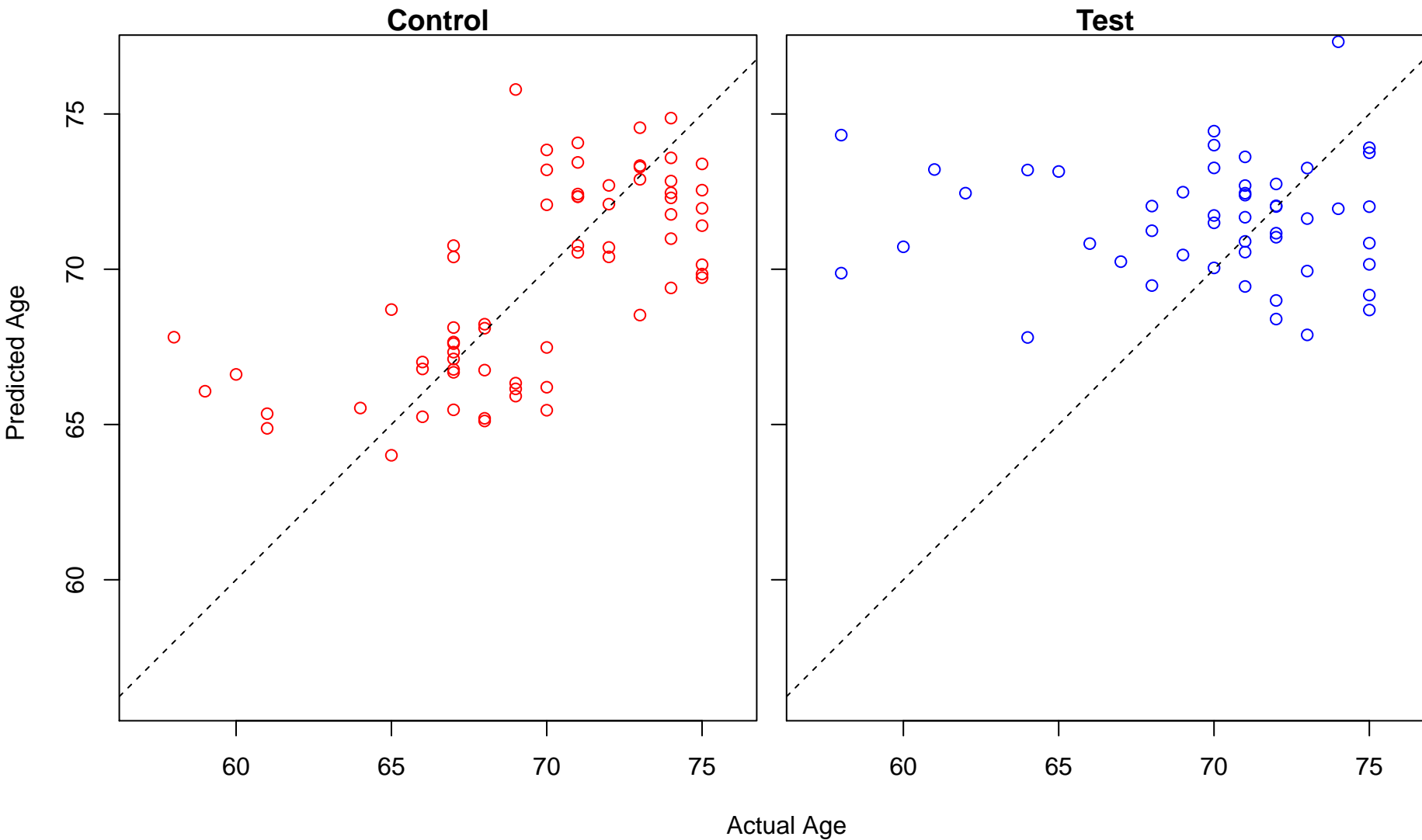
regulation of cytokine production involved in immune response (Score: 1.324440)



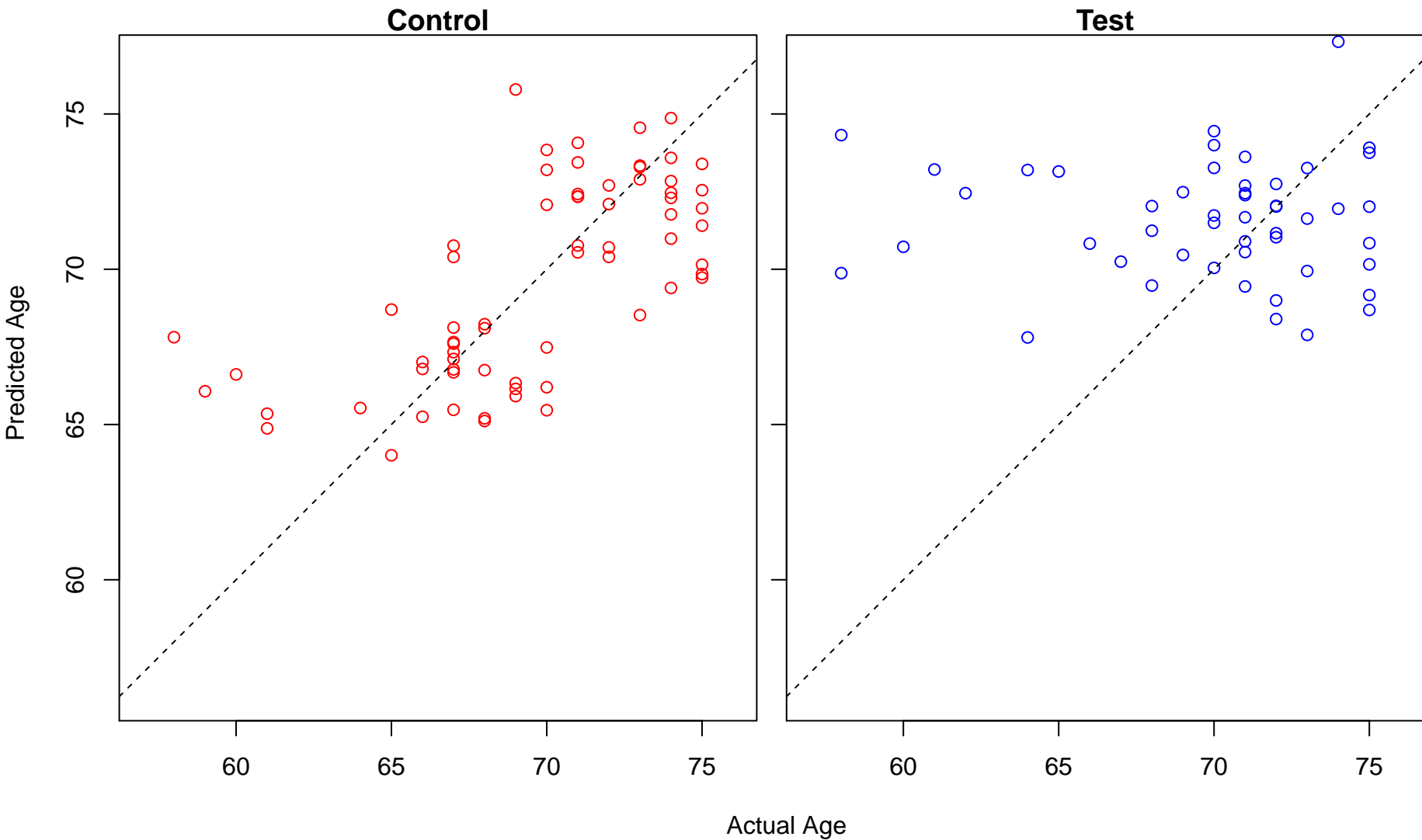
protein localization to cilium (Score: 1.324381)



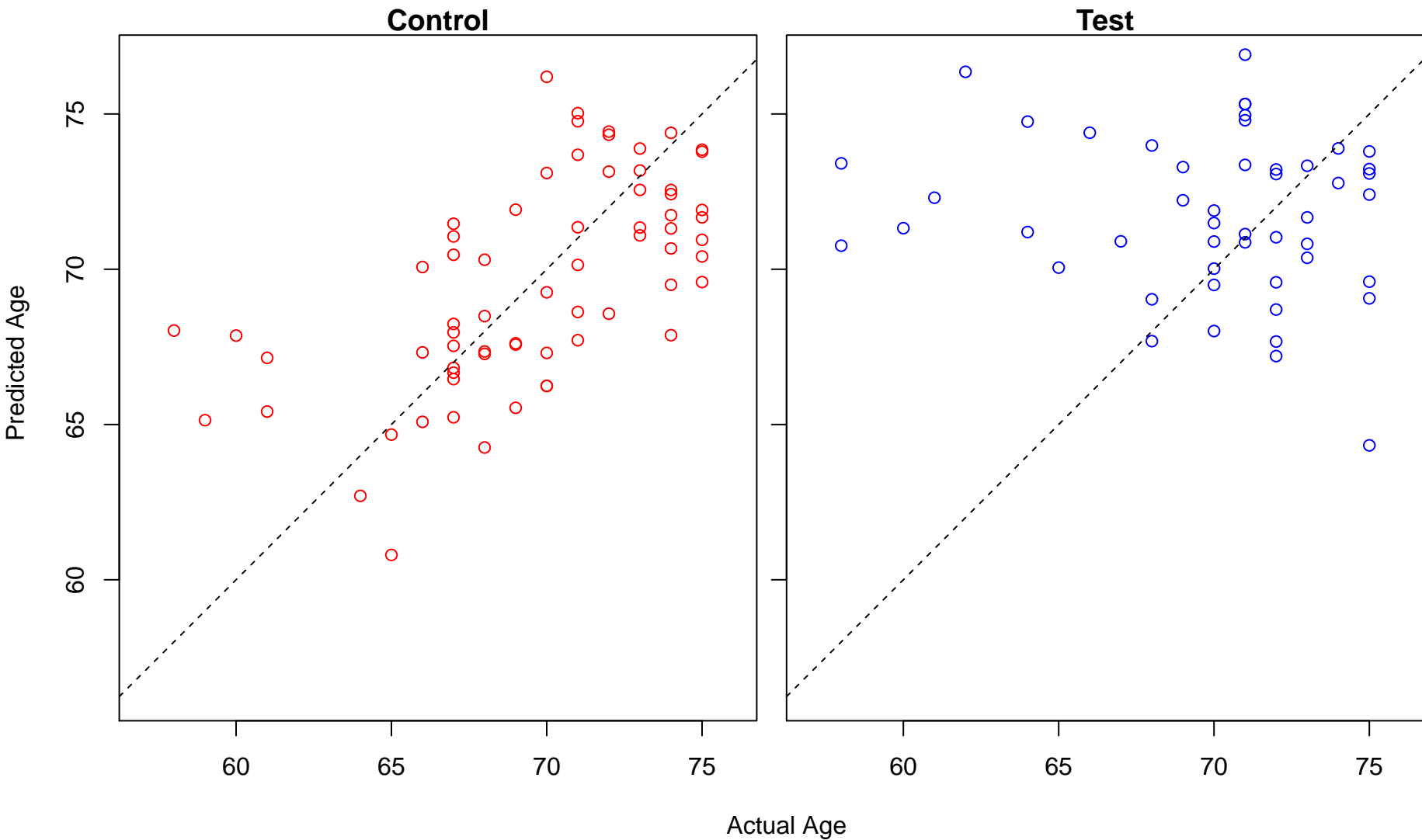
hexose transport (Score: 1.323882)



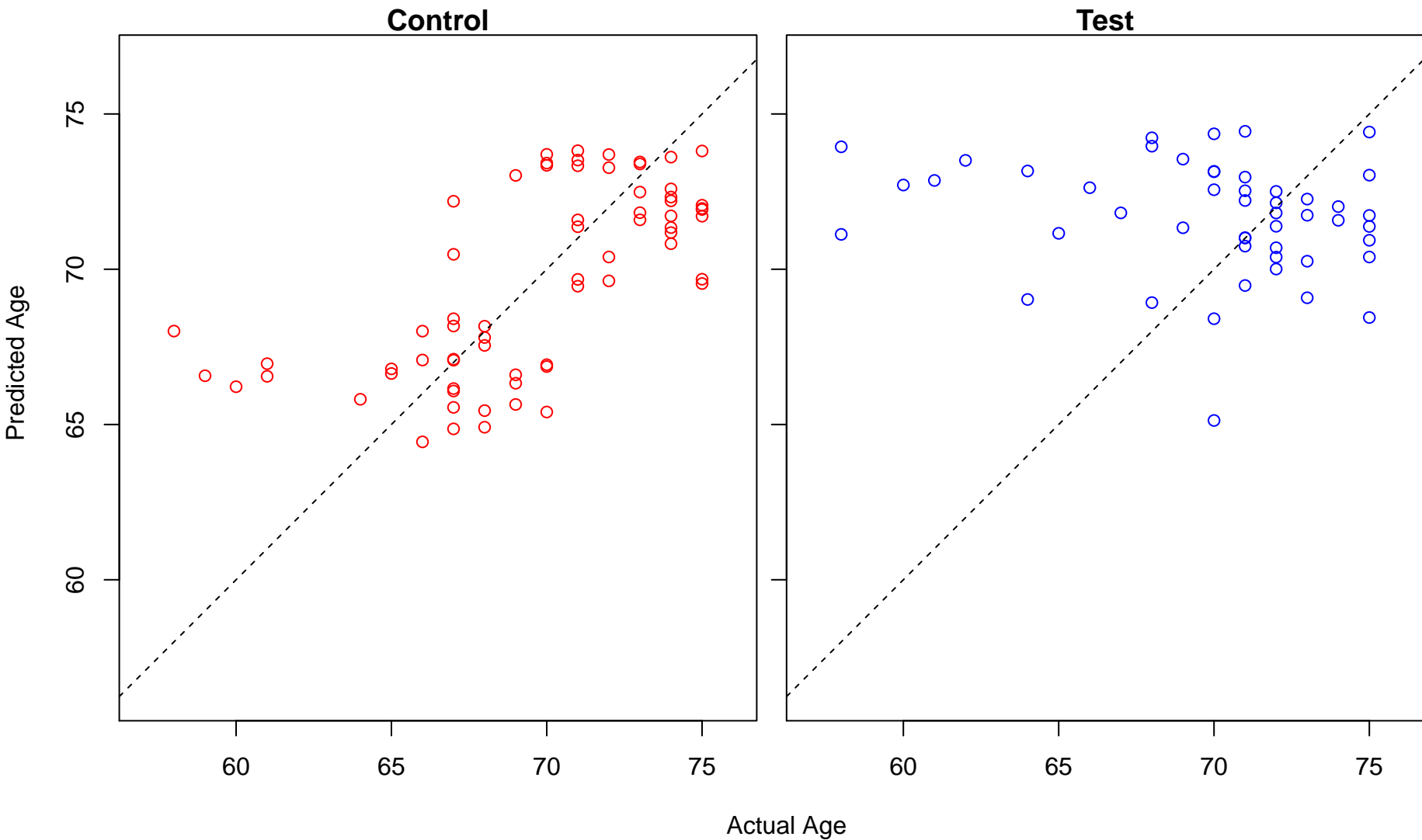
glucose transport (Score: 1.323882)



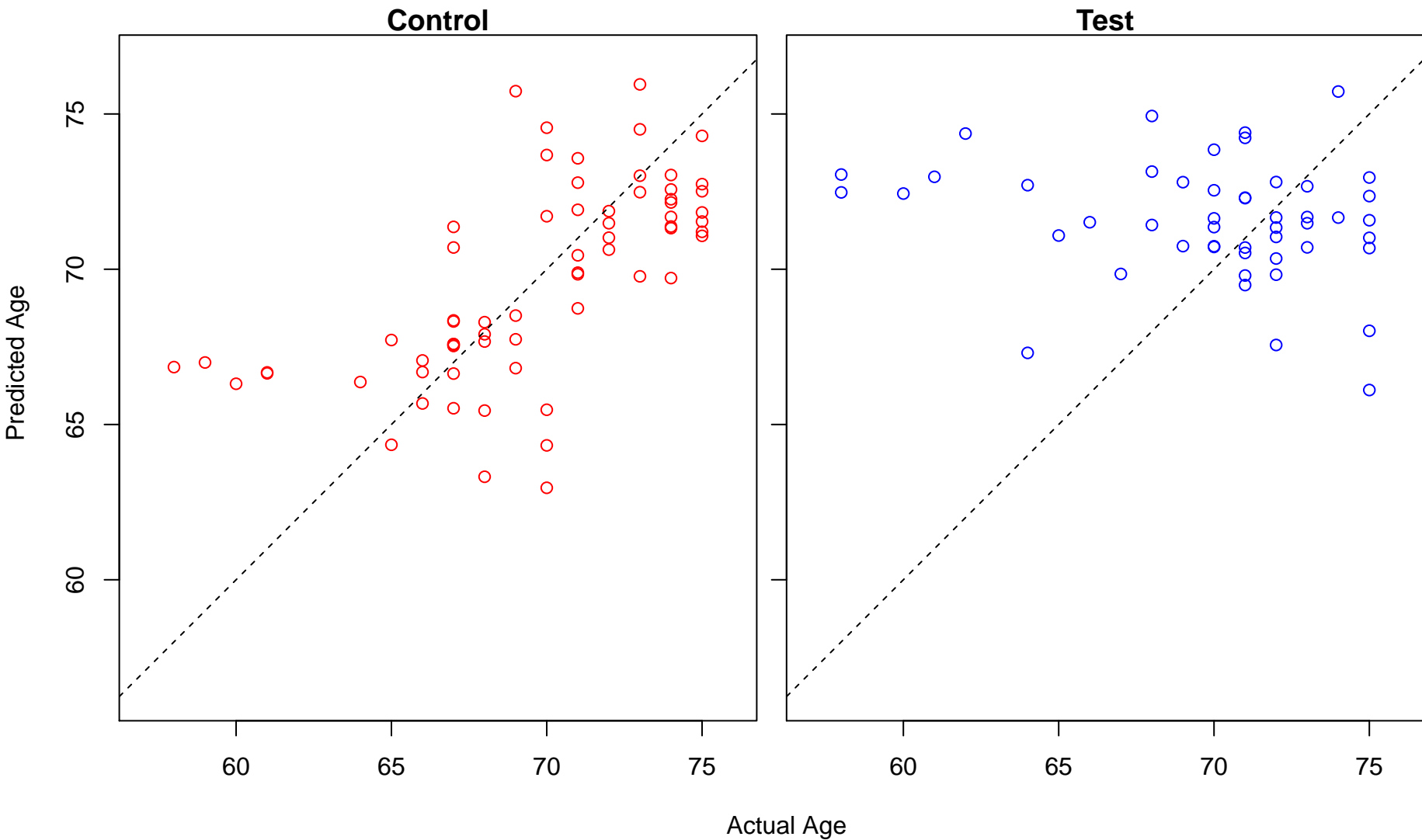
gastrulation (Score: 1.322435)



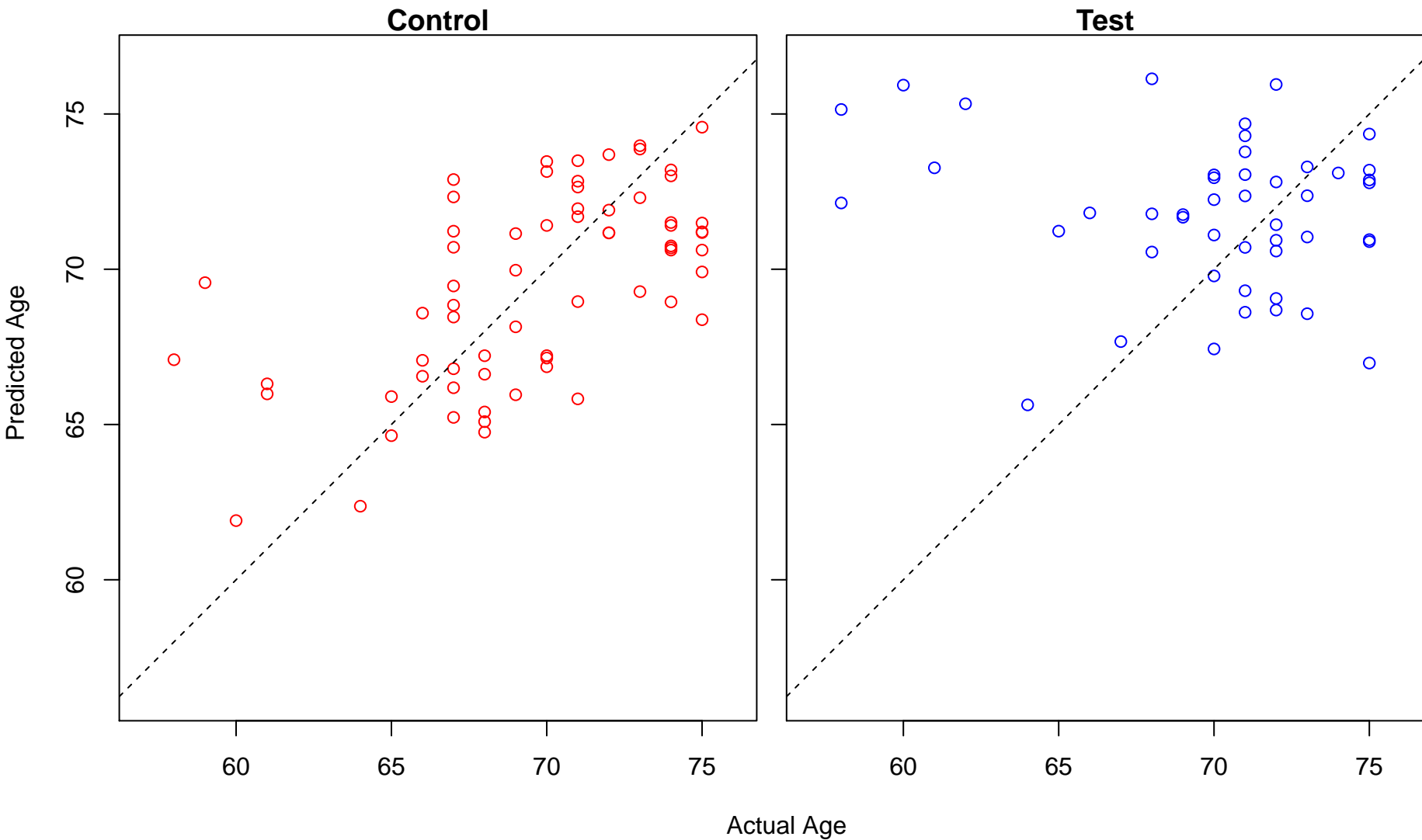
regulation of cell cycle G2/M phase transition (Score: 1.321299)



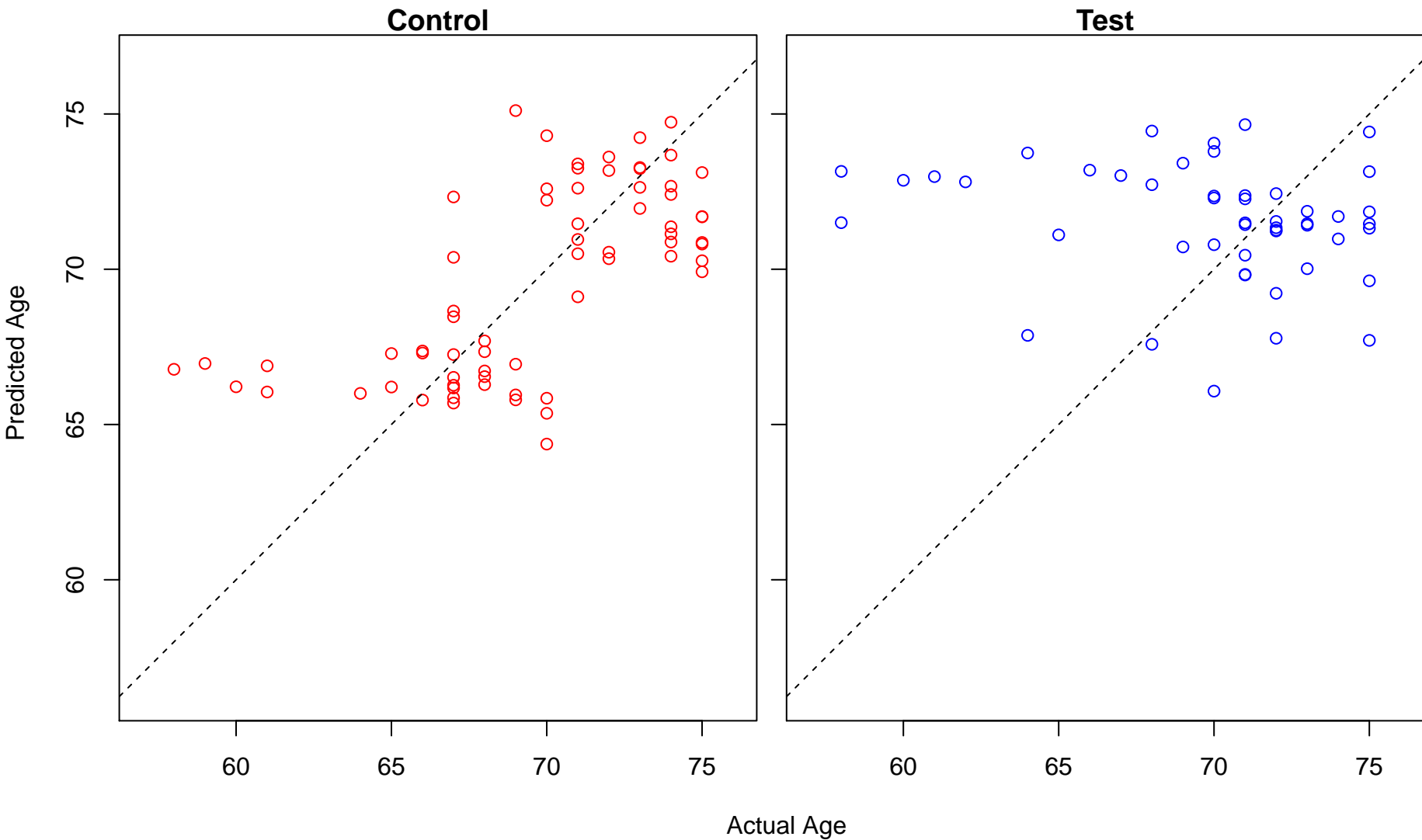
regulation of anoikis (Score: 1.321083)



cellular response to interleukin-1 (Score: 1.320844)

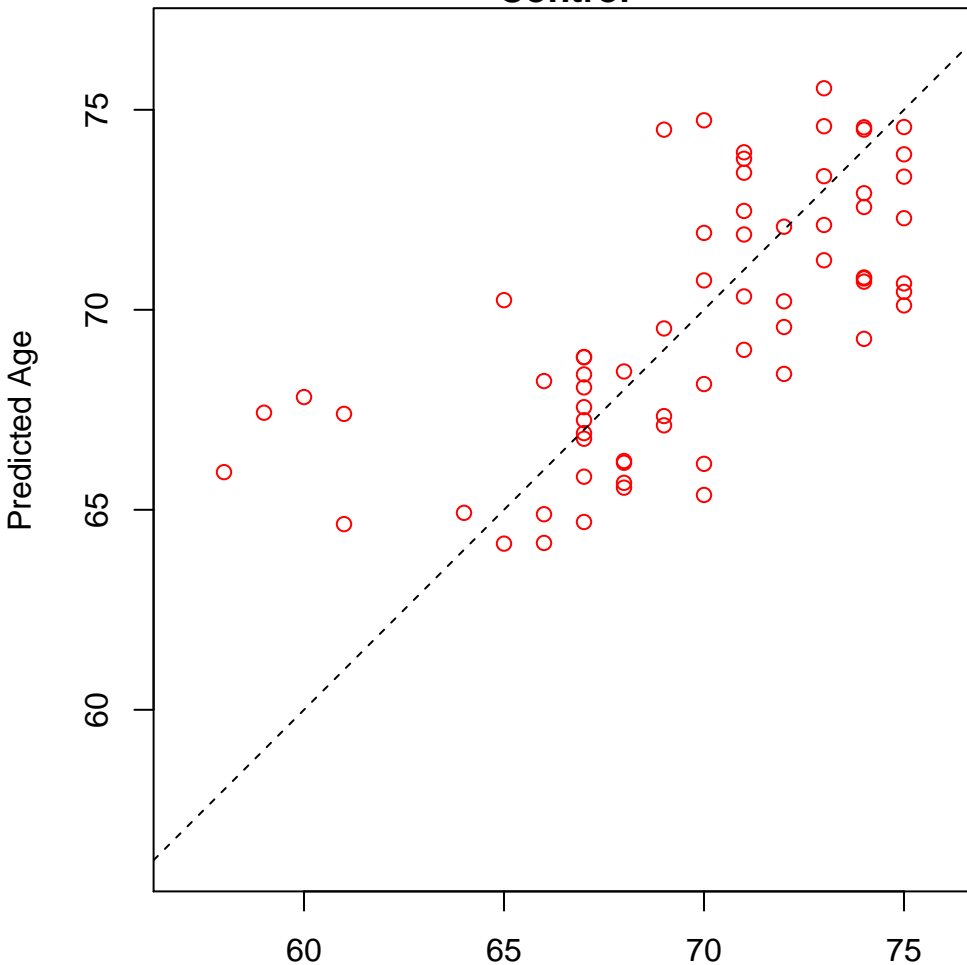


regulation of sister chromatid segregation (Score: 1.320625)

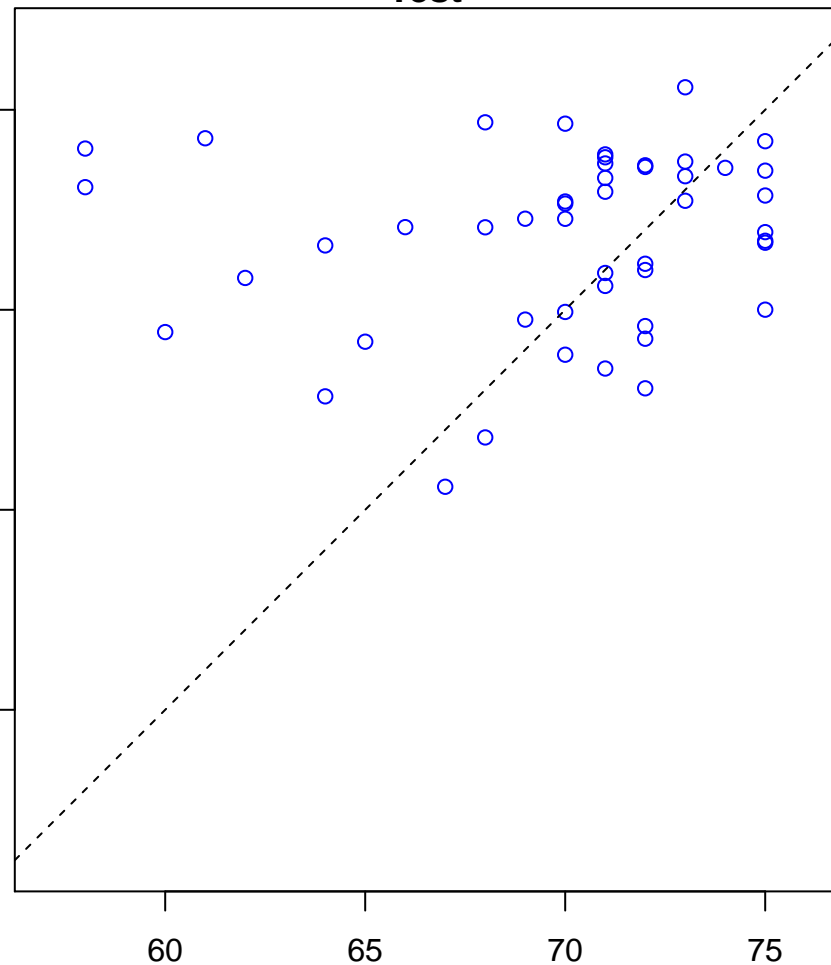


cardiac muscle tissue development (Score: 1.320594)

Control

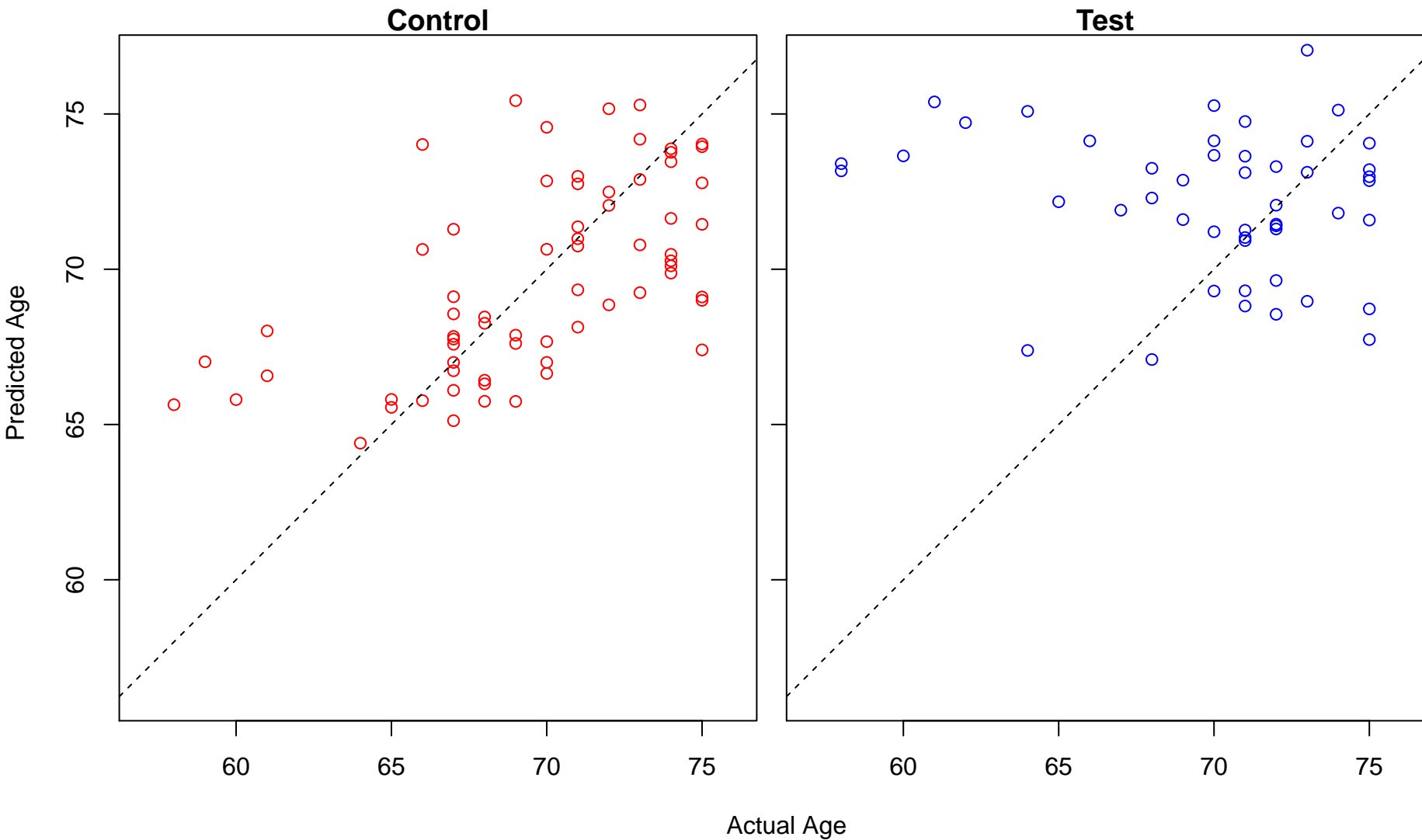


Test

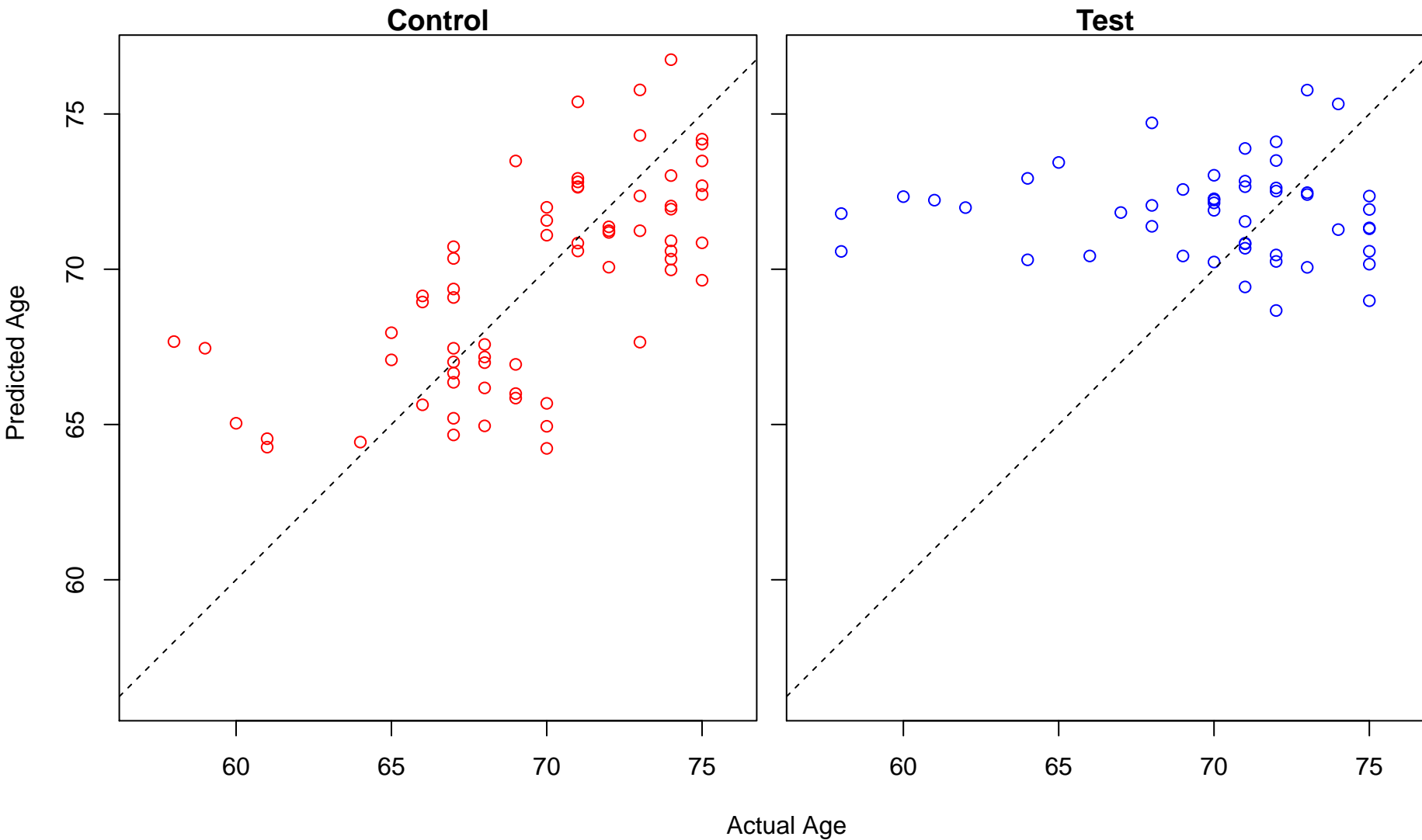


Actual Age

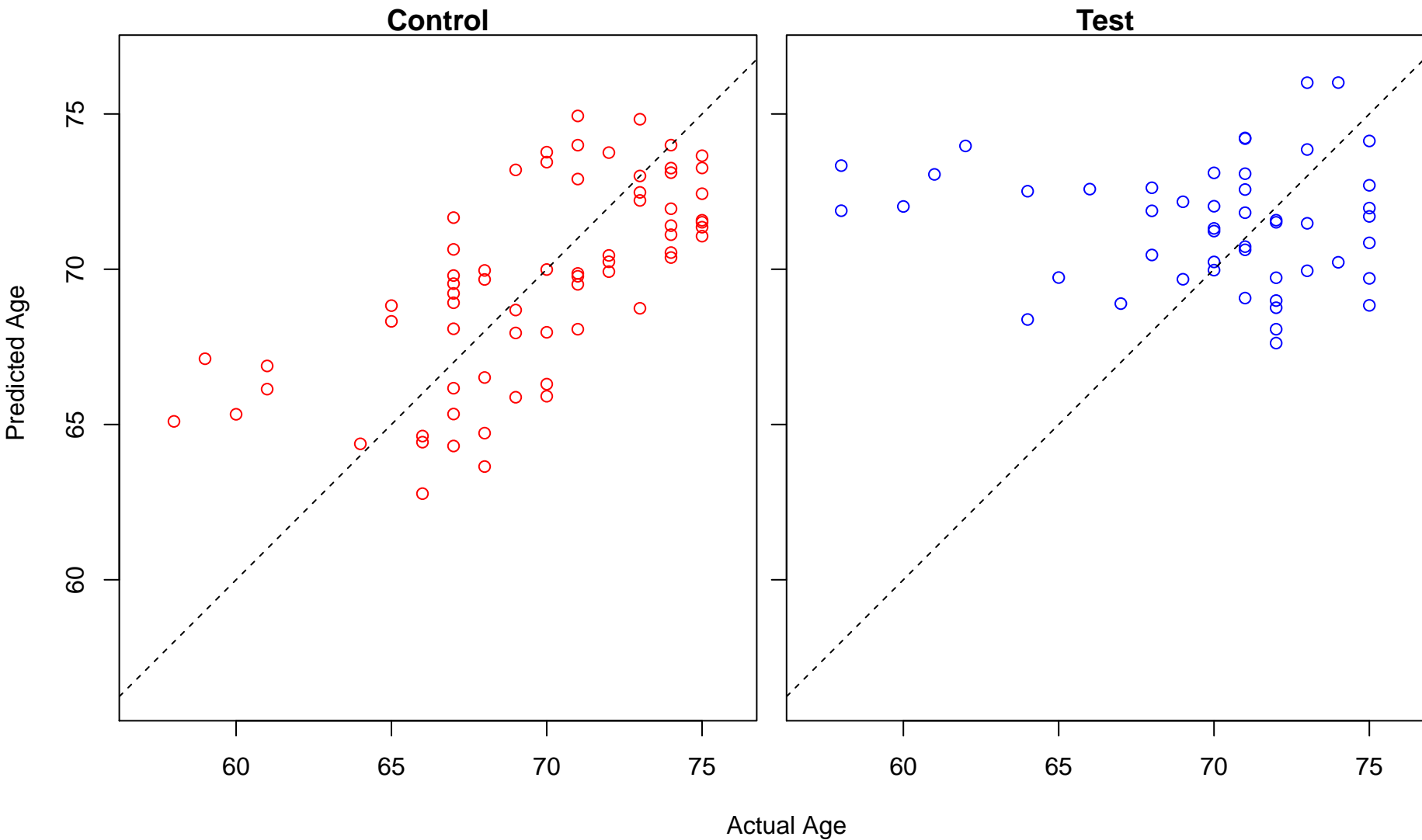
associative learning (Score: 1.320579)



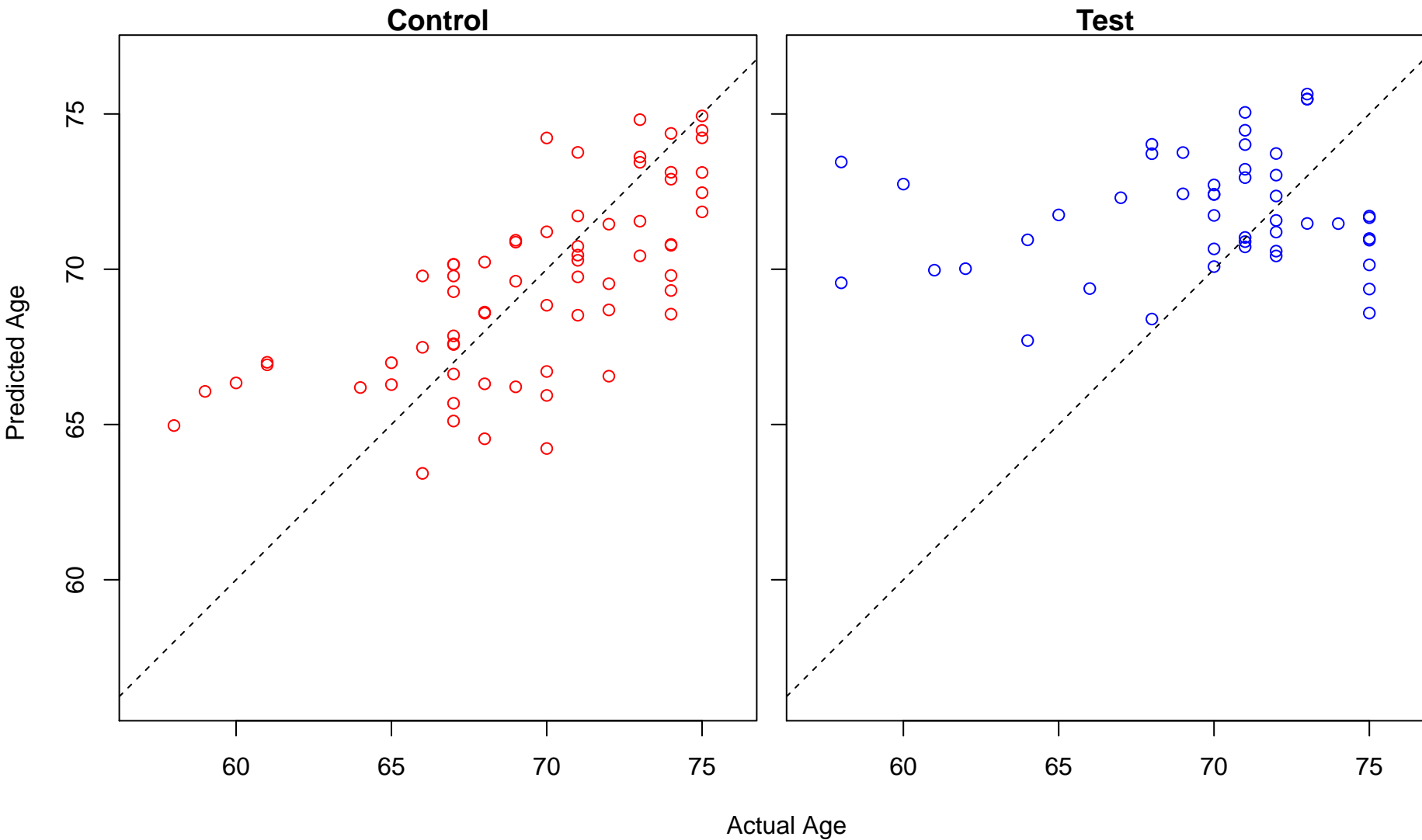
negative regulation of cell growth (Score: 1.320309)



regulation of BMP signaling pathway (Score: 1.319953)



regulation of lipid storage (Score: 1.319766)

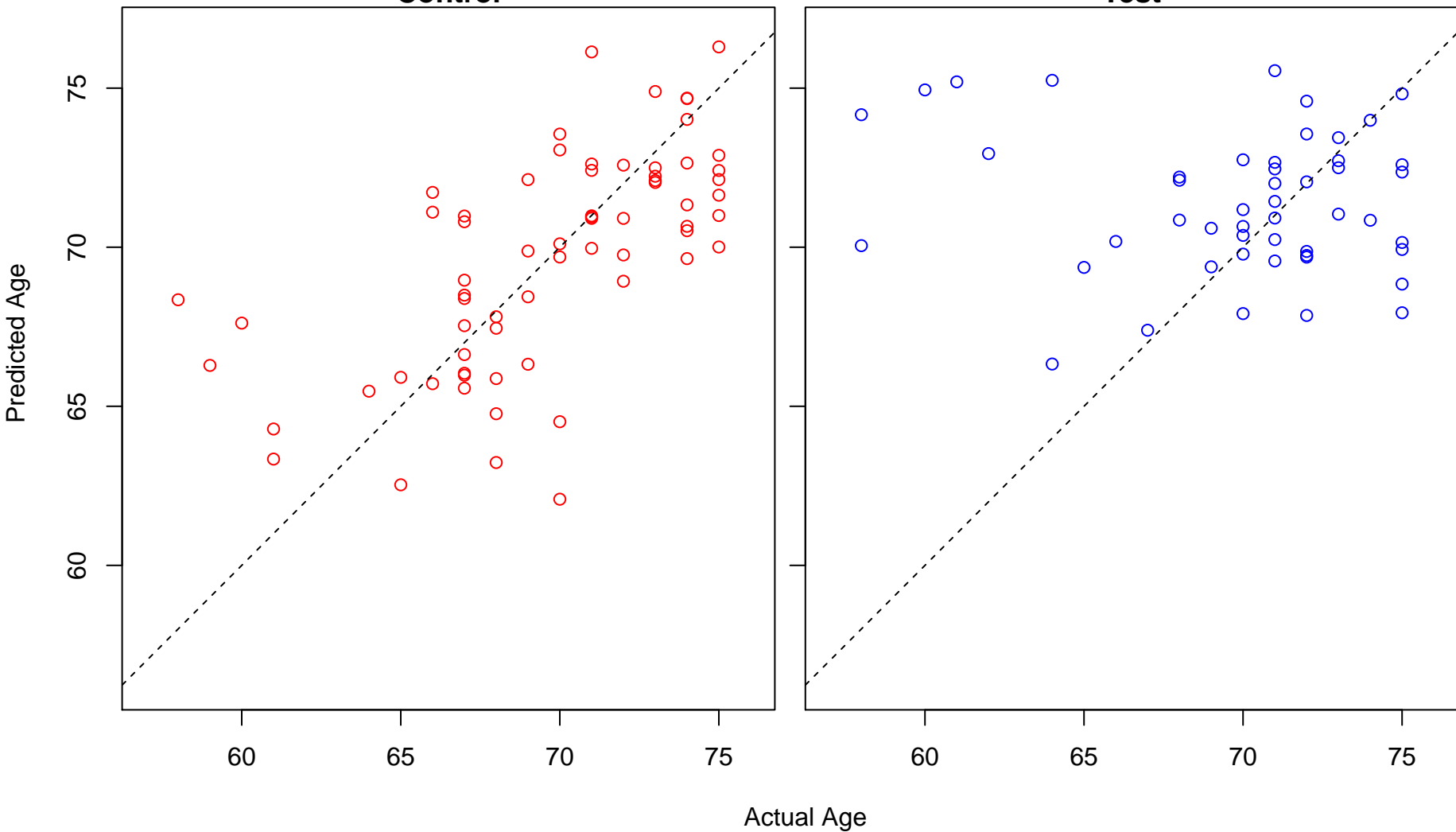


Control

Control

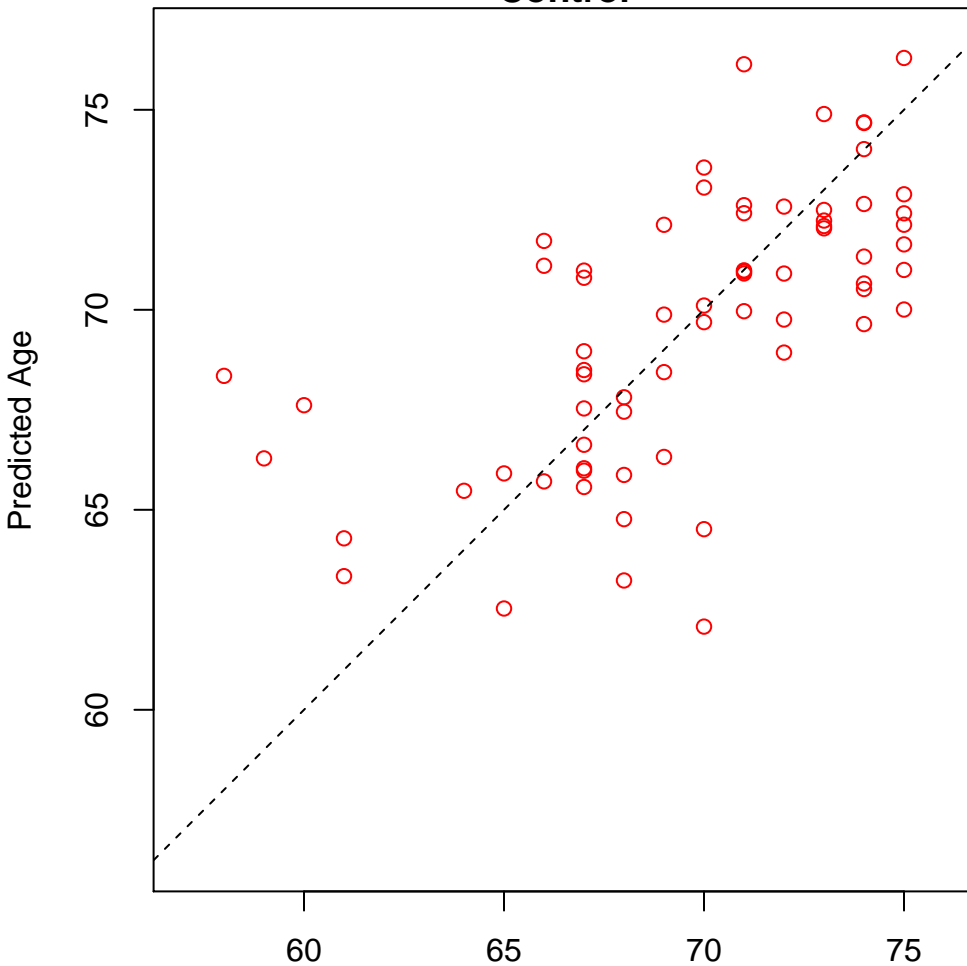
Test

Test

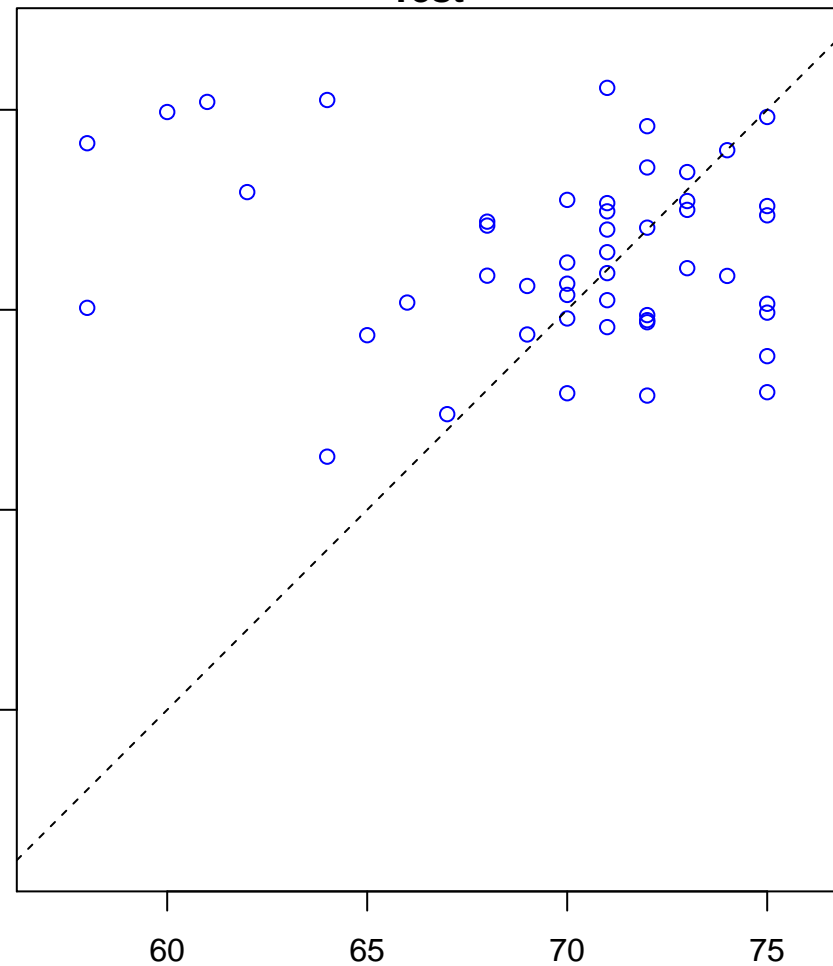


reproductive system development (Score: 1.319757)

Control

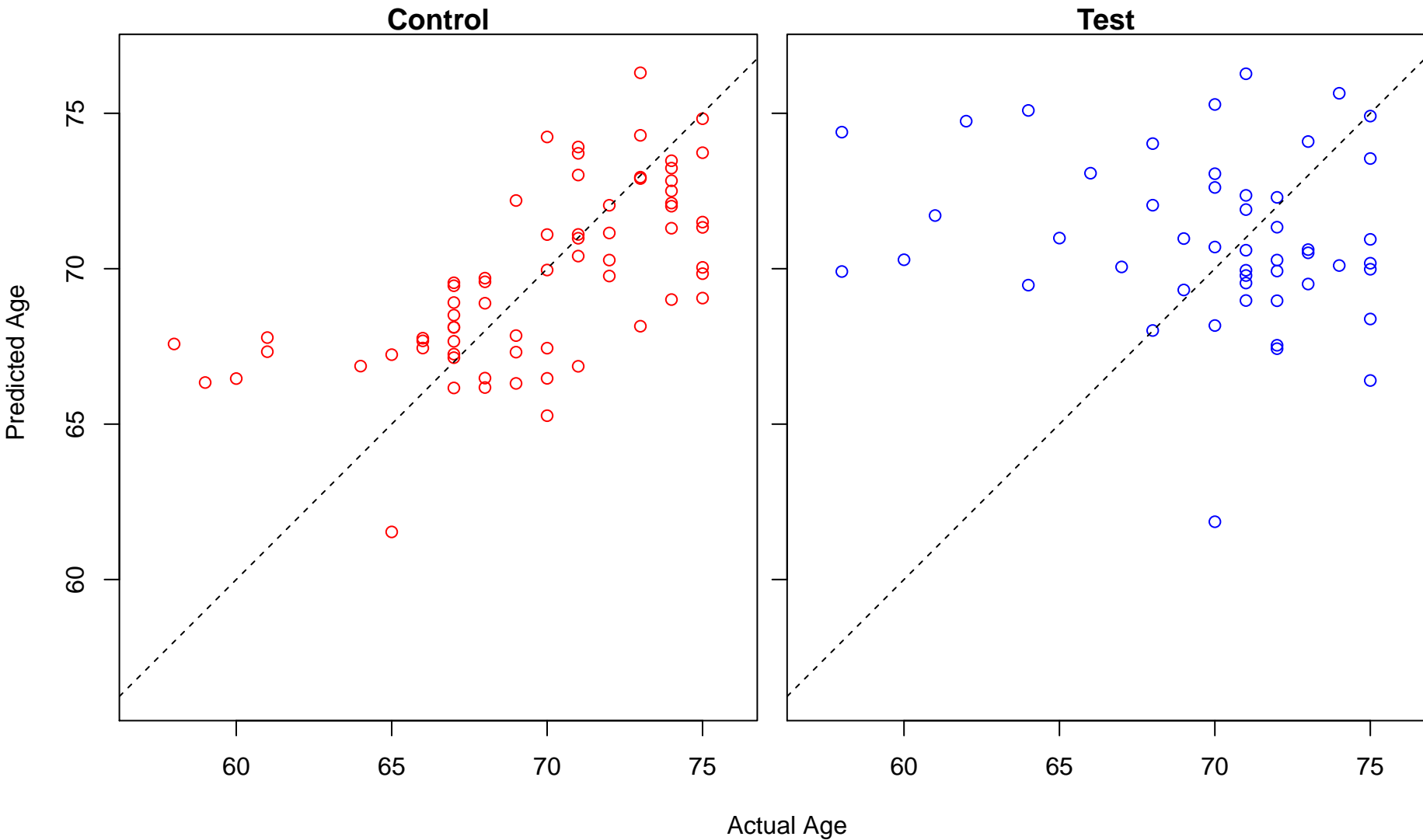


Test

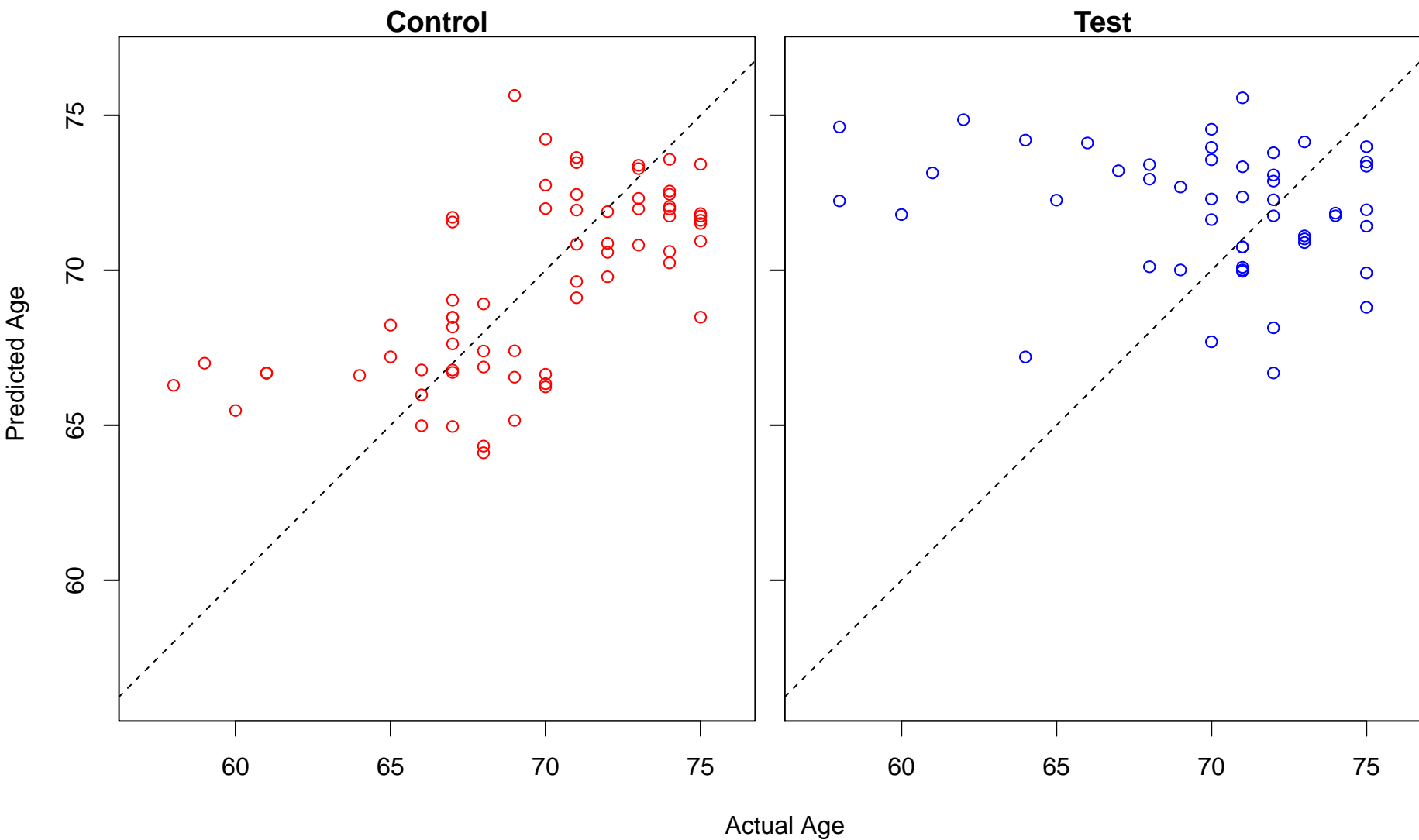


Actual Age

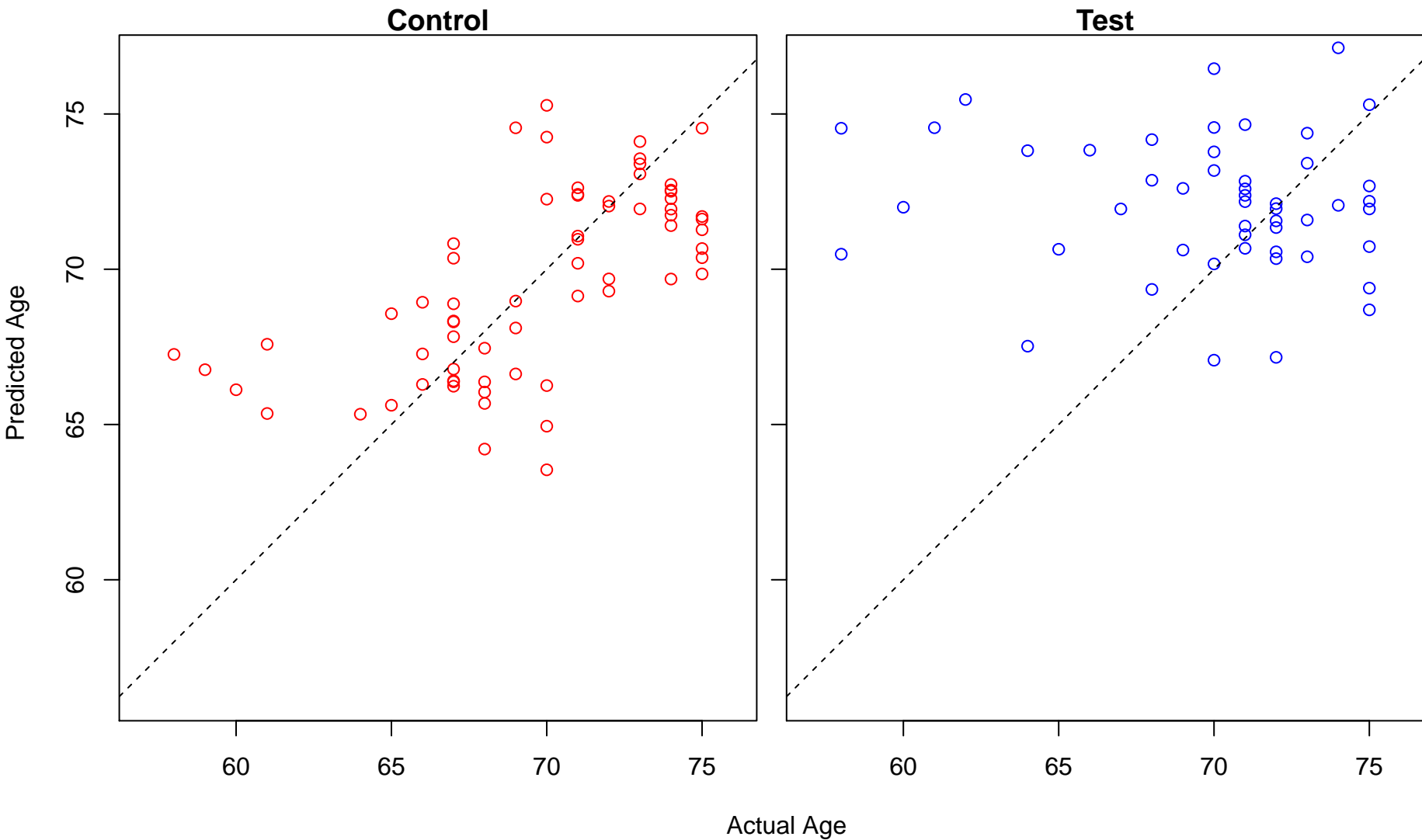
positive regulation of release of sequestered calcium ion into cytosol (Score: 1.318396)



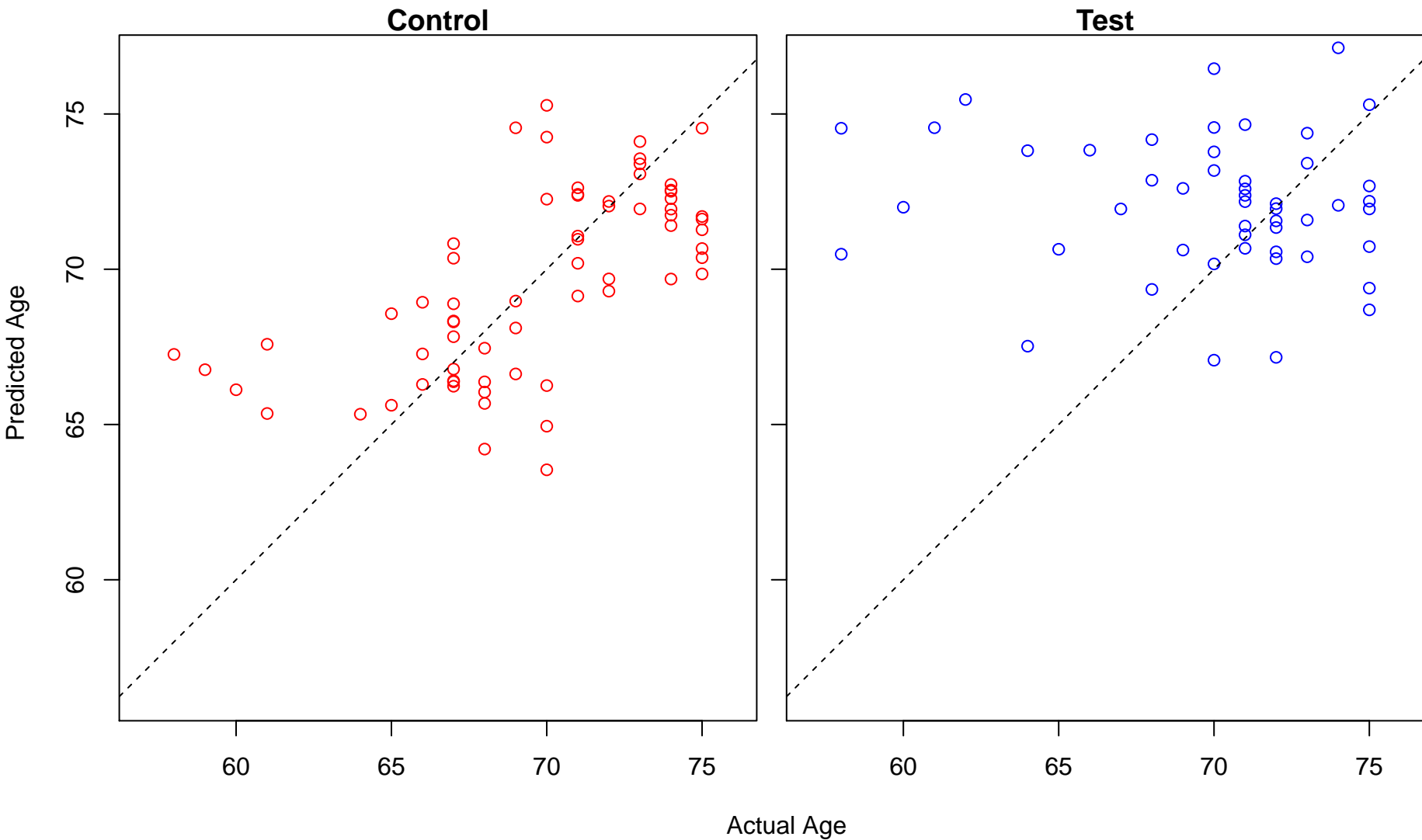
positive regulation of histone H3-K4 methylation (Score: 1.318115)



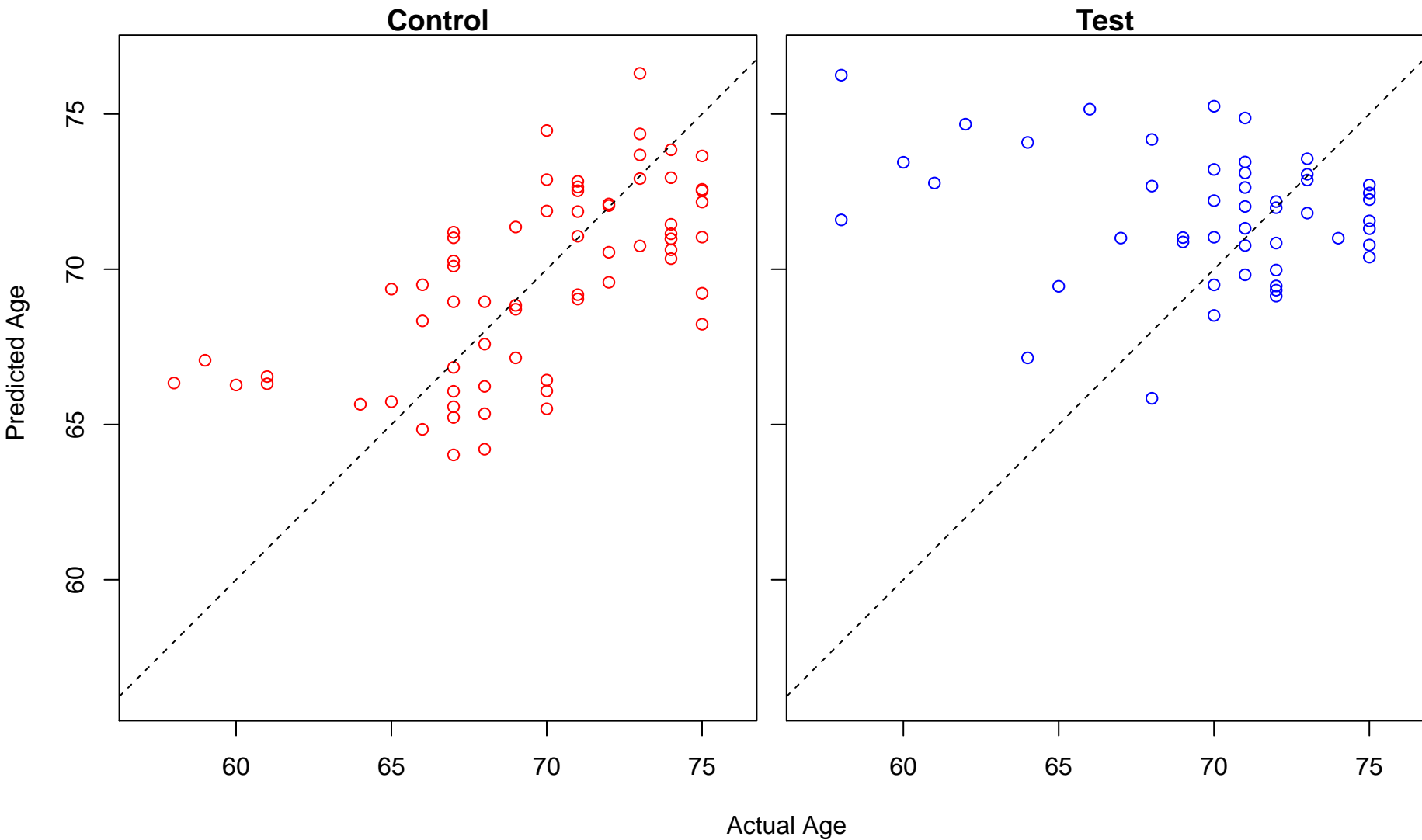
double-strand break repair via homologous recombination (Score: 1.317732)



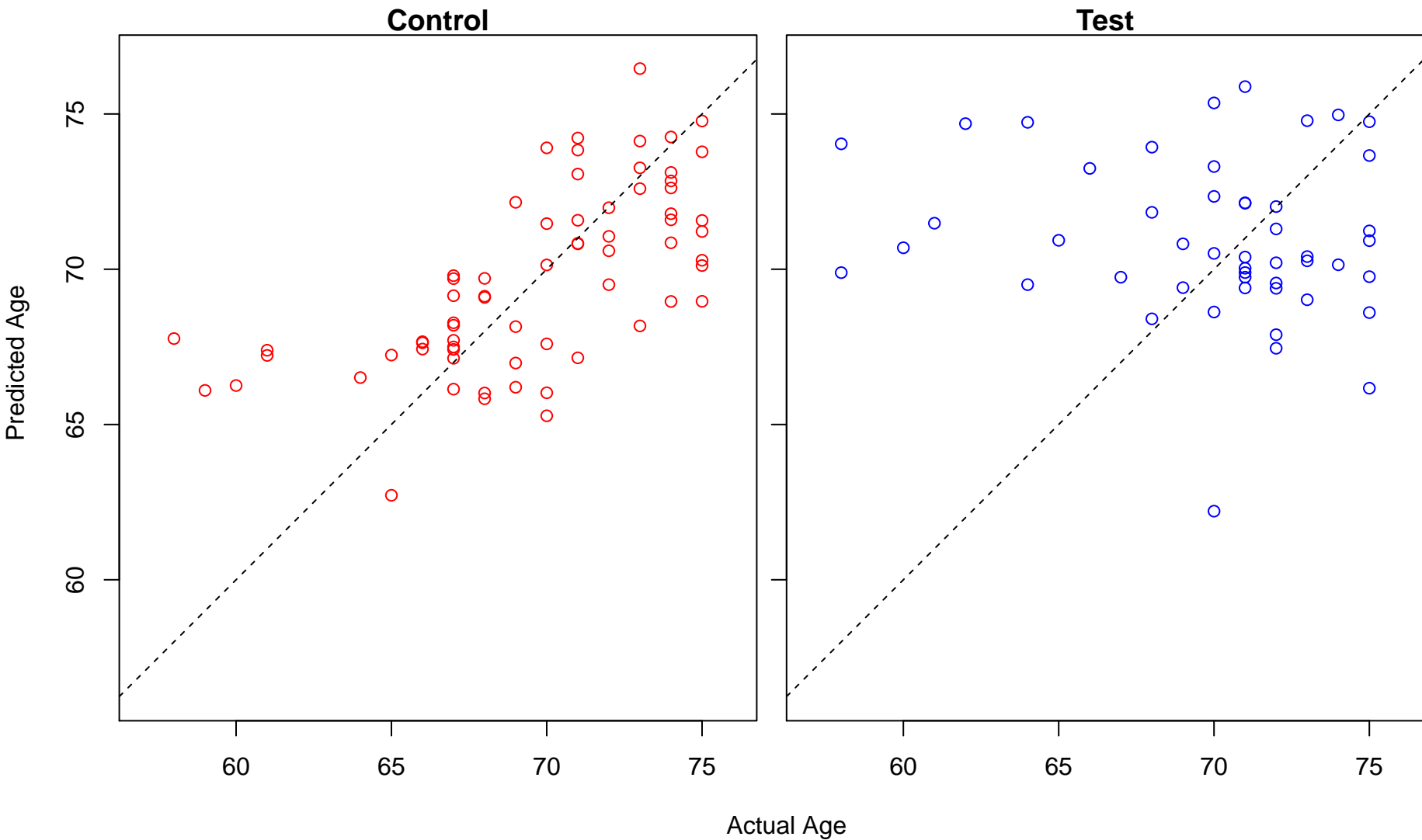
recombinational repair (Score: 1.317732)



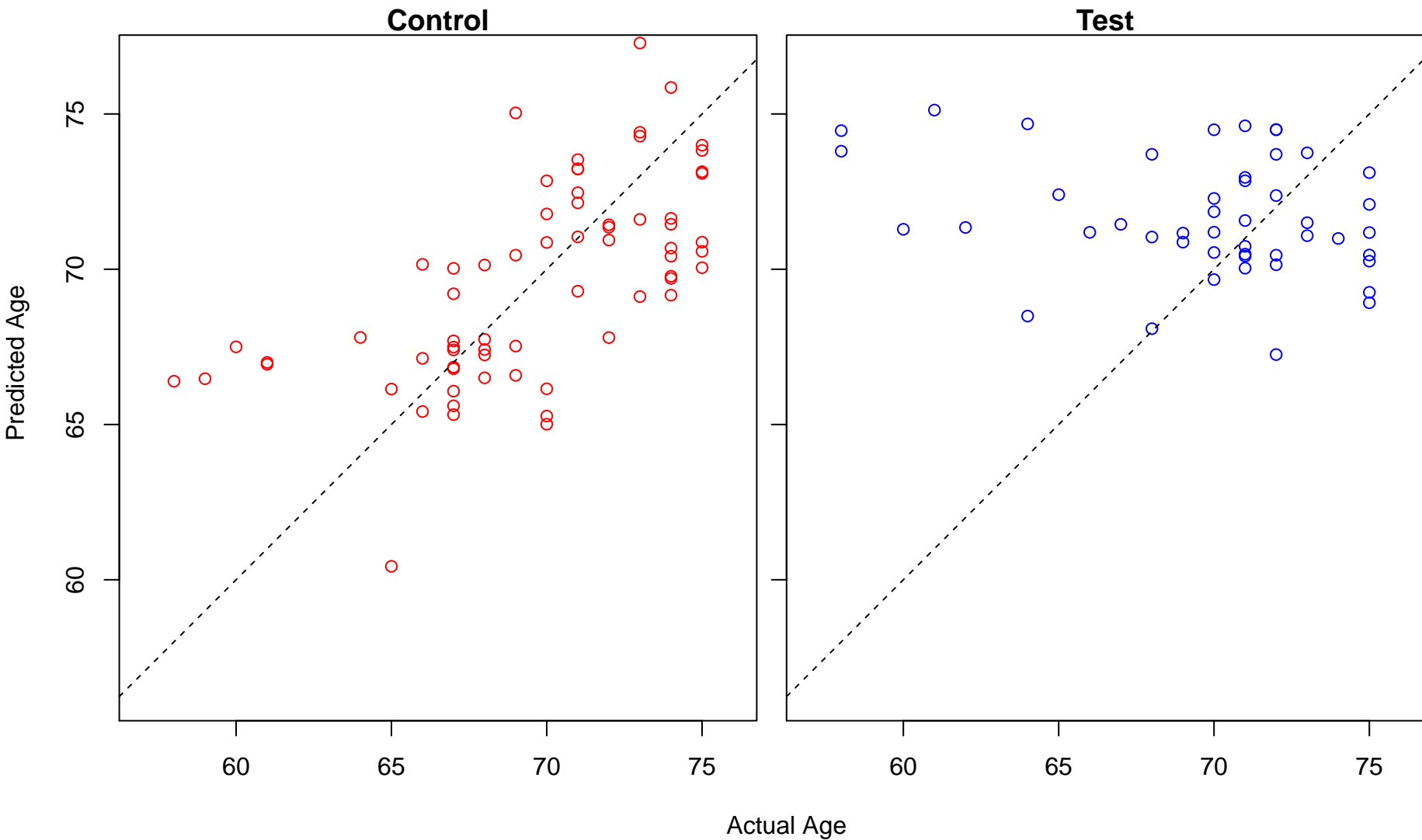
retrograde vesicle-mediated transport, Golgi to ER (Score: 1.317688)



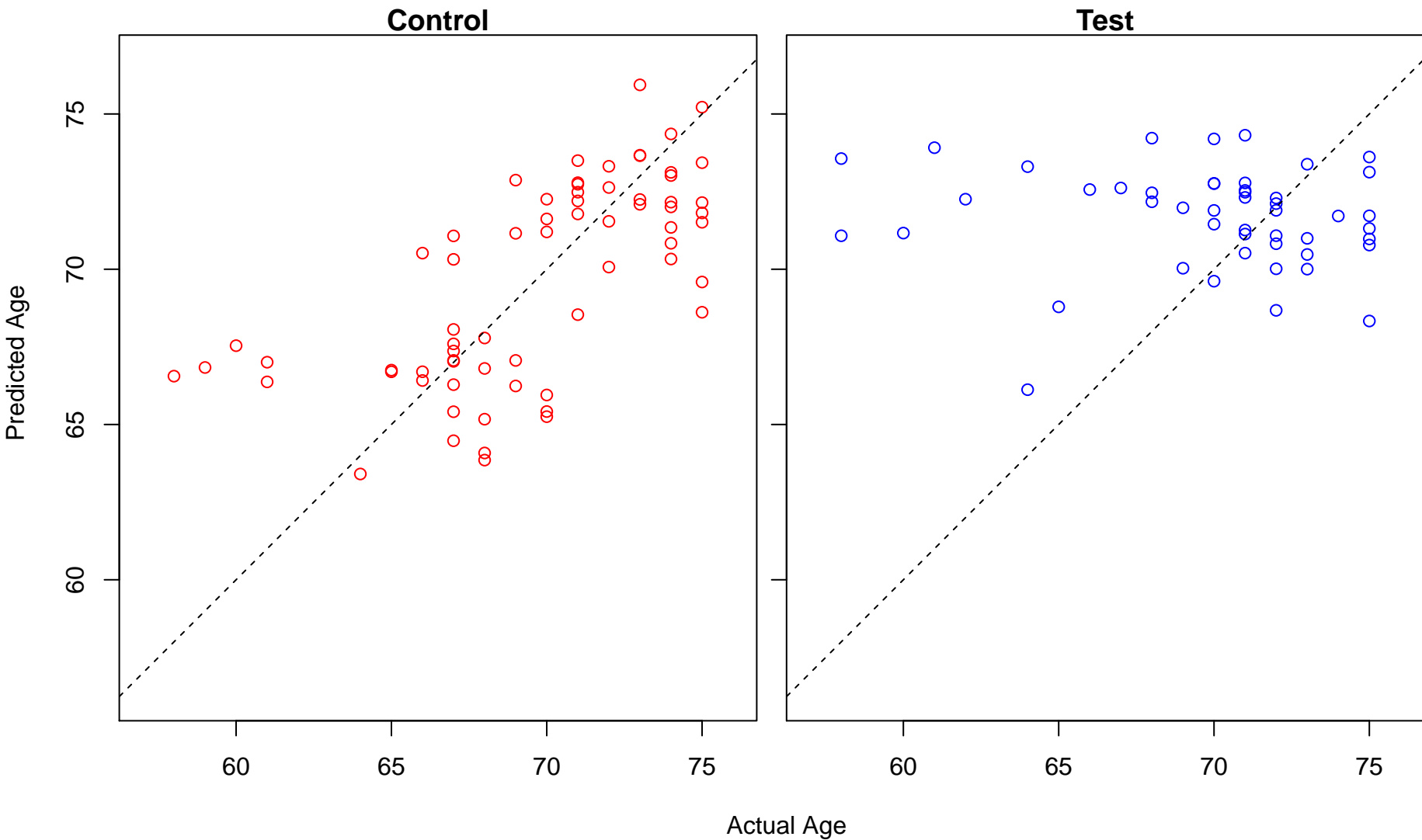
positive regulation of calcium ion transport into cytosol (Score: 1.317418)



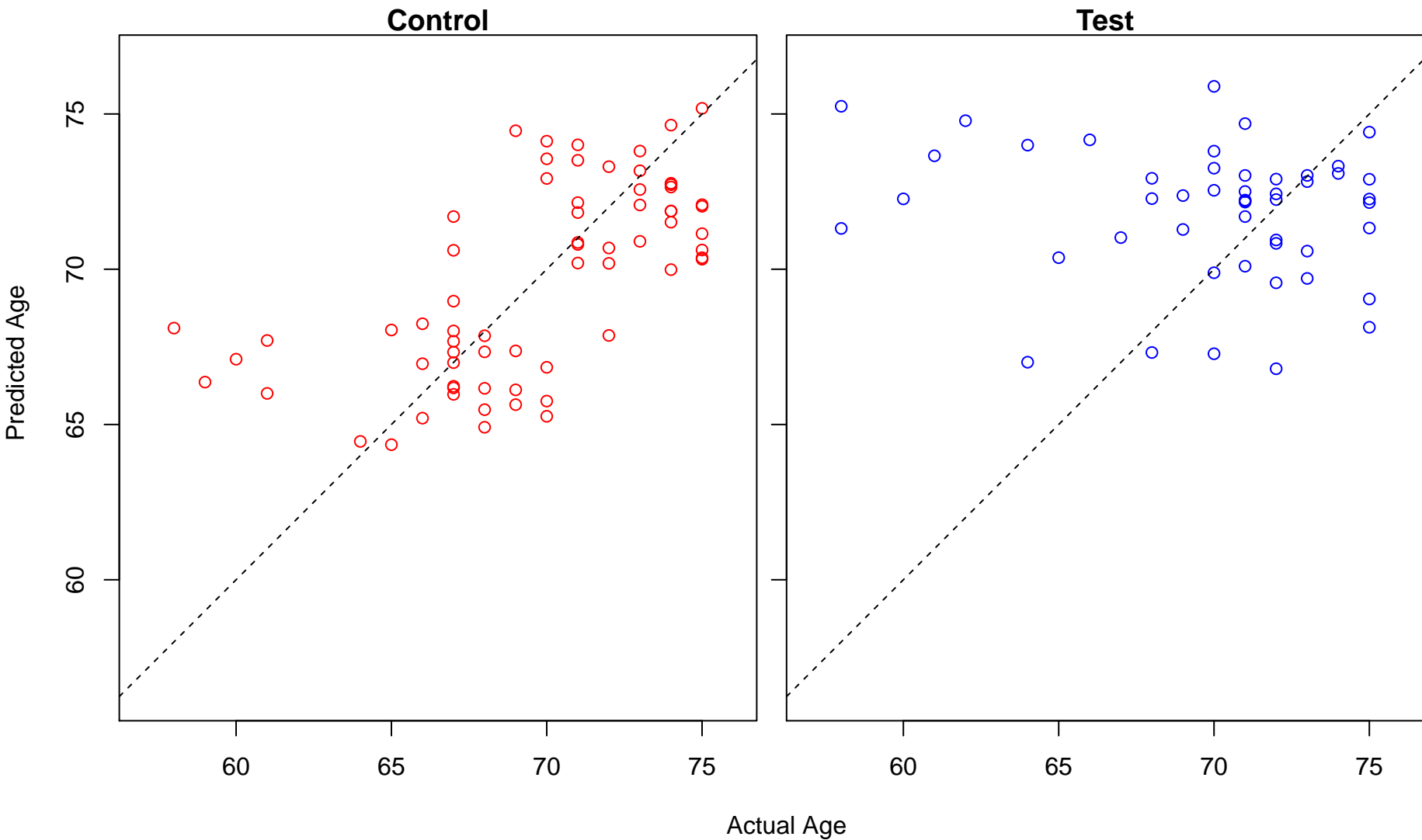
regulation of telomerase activity (Score: 1.317301)



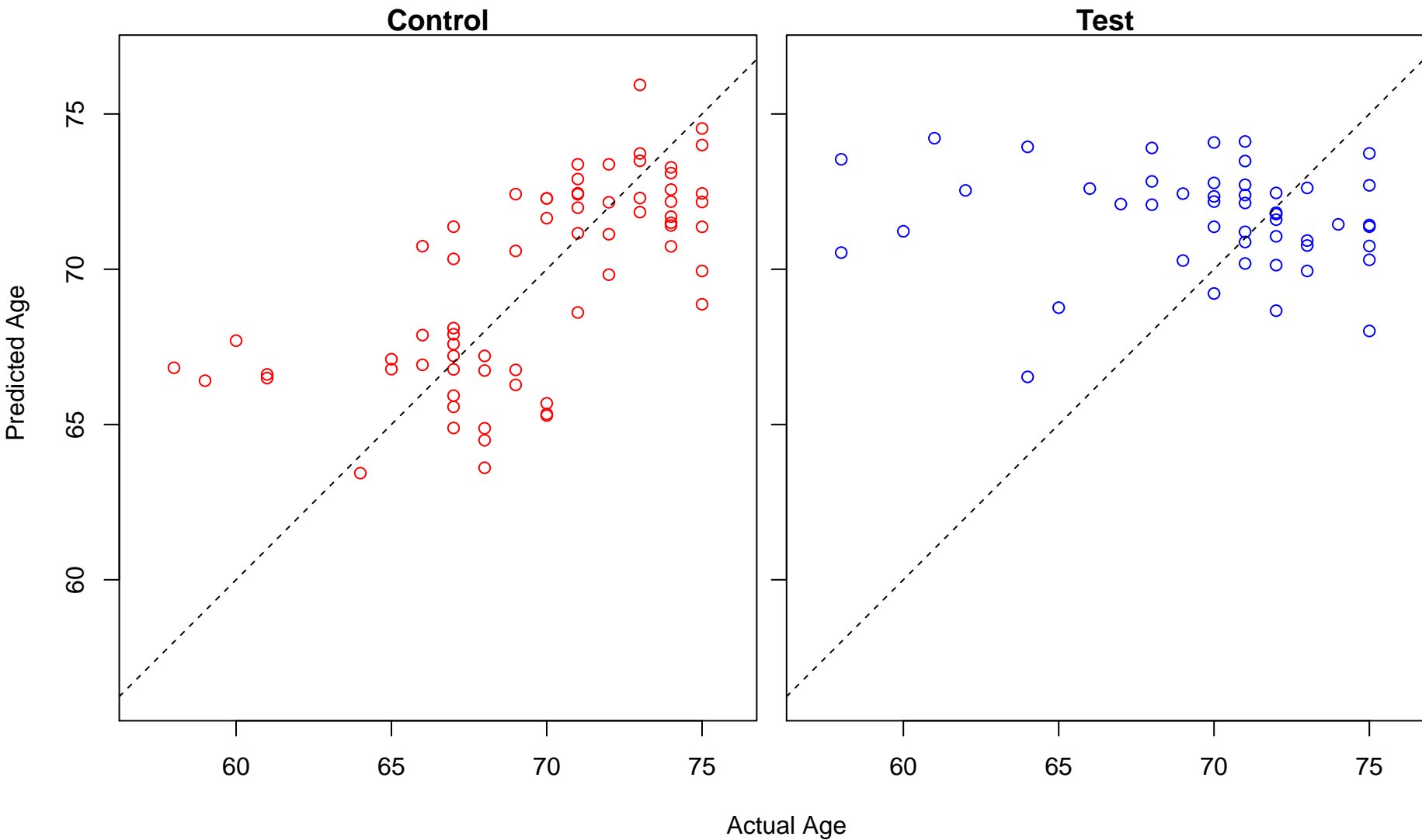
pyrimidine-containing compound metabolic process (Score: 1.316834)



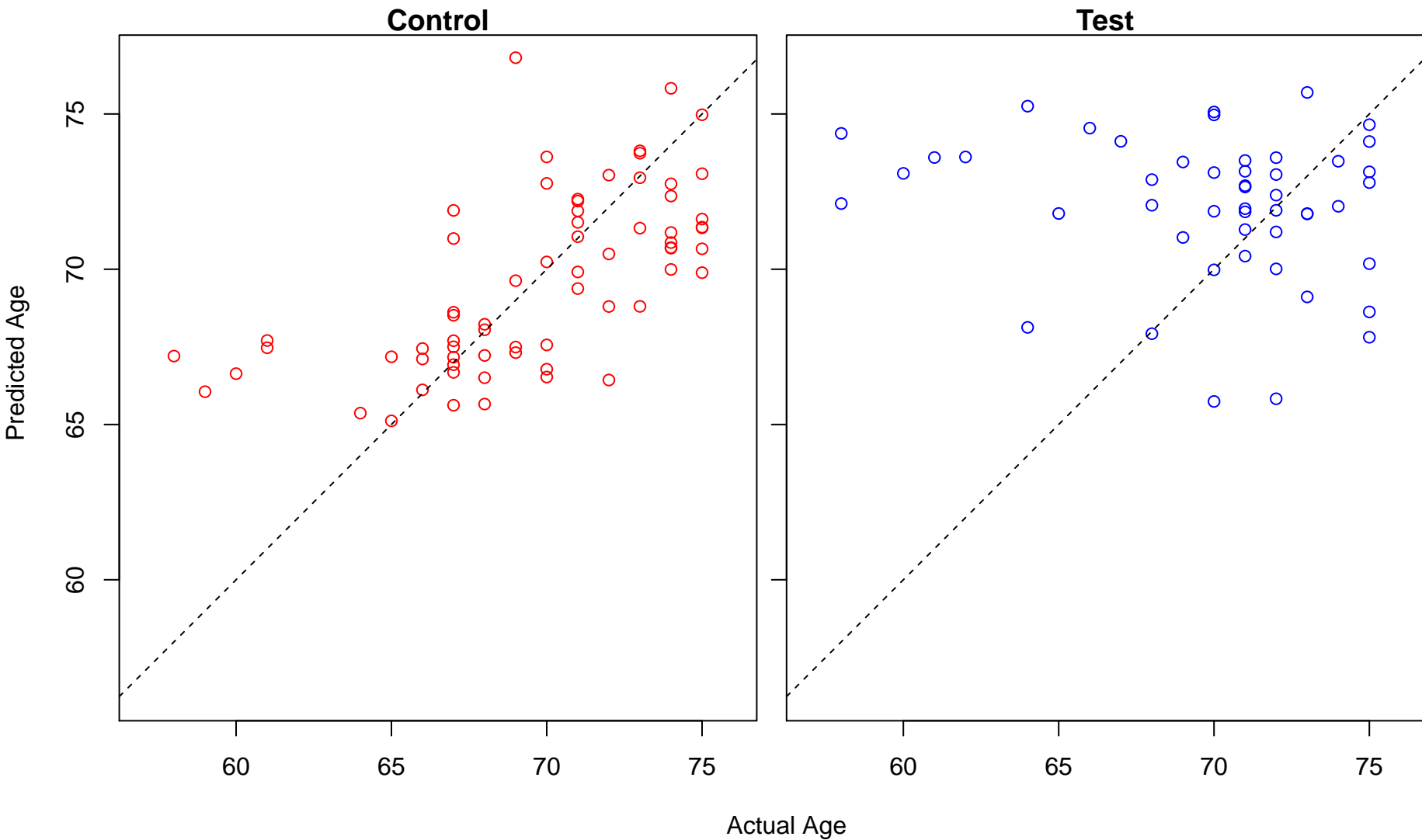
negative regulation of protein serine/threonine kinase activity (Score: 1.316450)



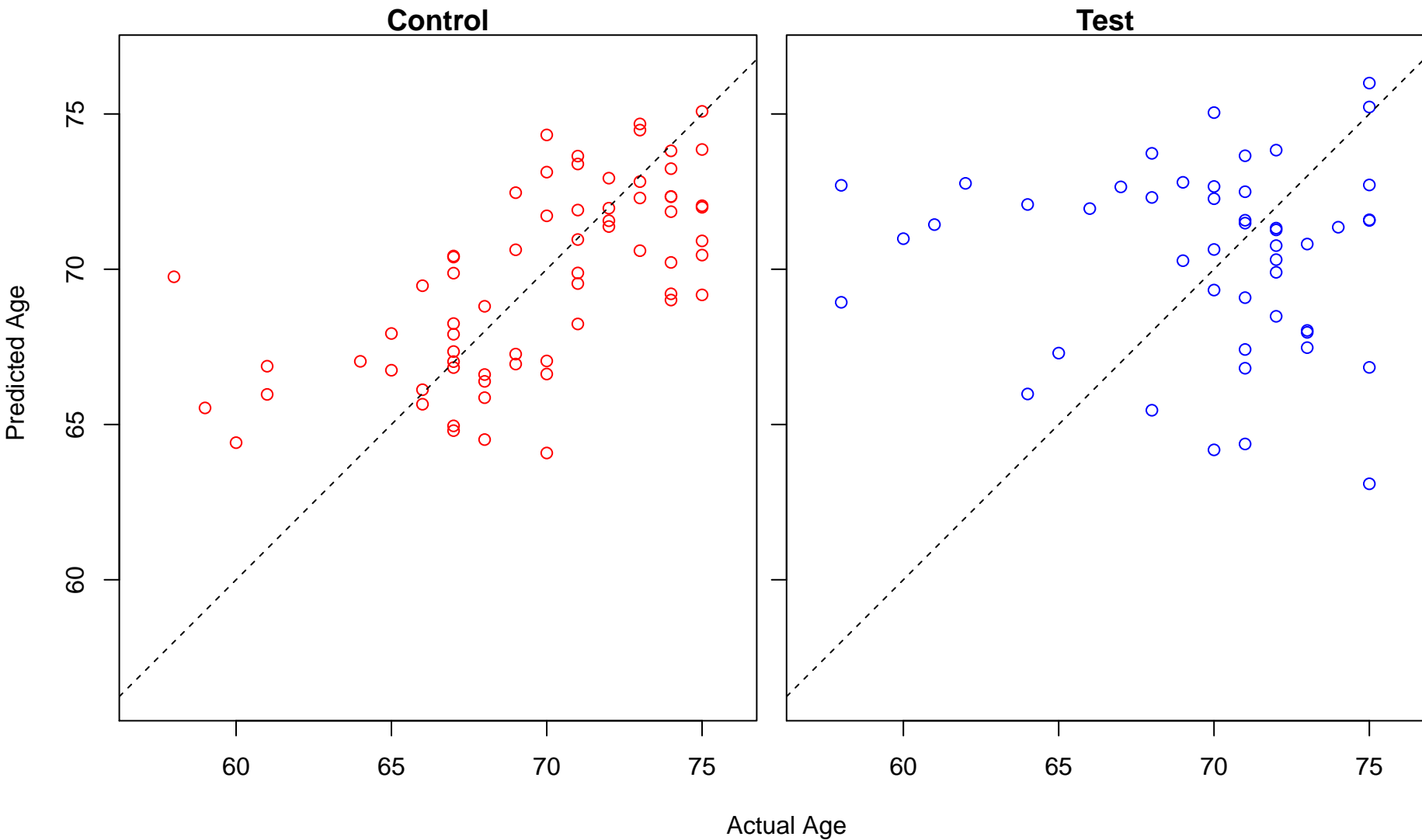
pyrimidine nucleoside metabolic process (Score: 1.315408)



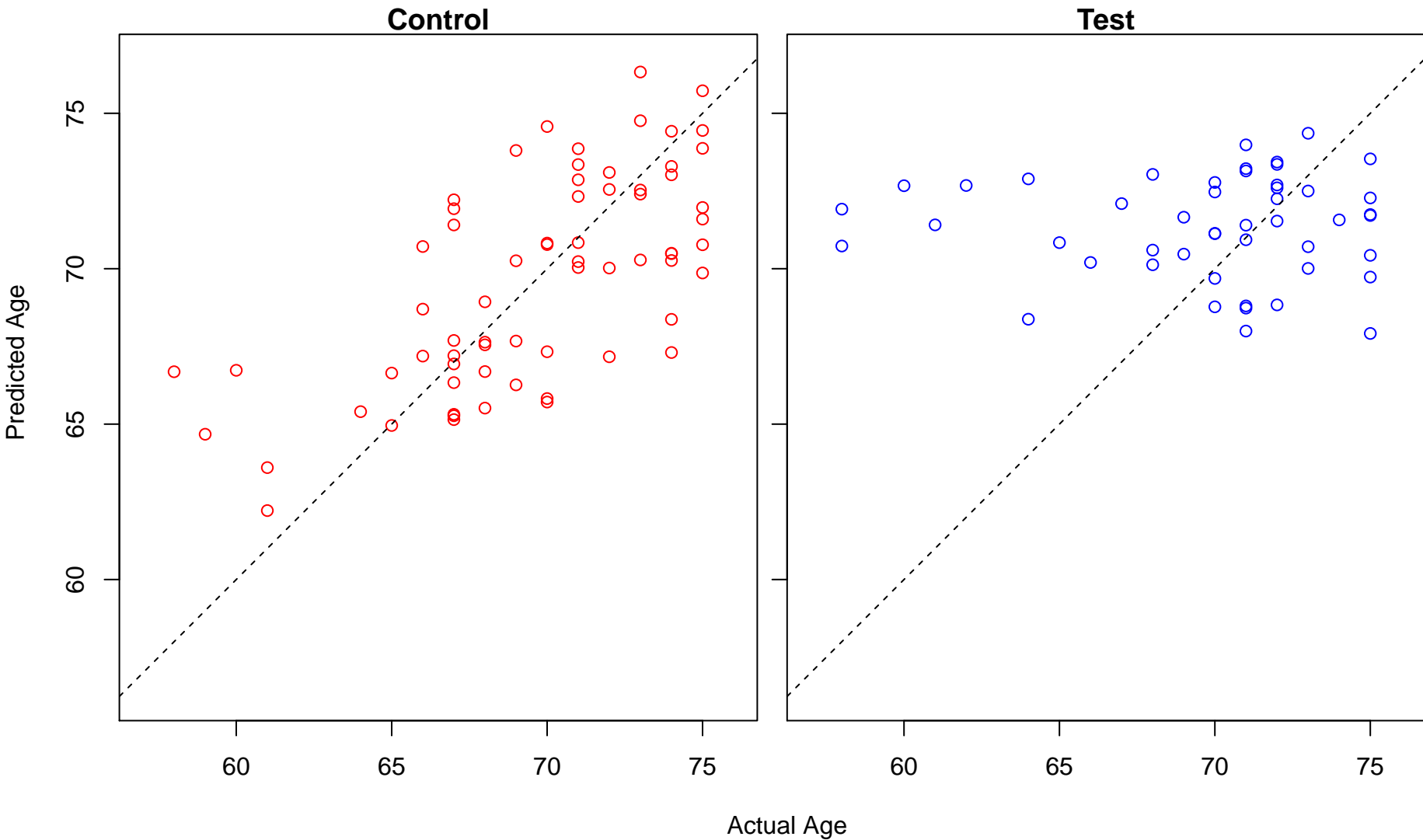
regulation of JUN kinase activity (Score: 1.315131)



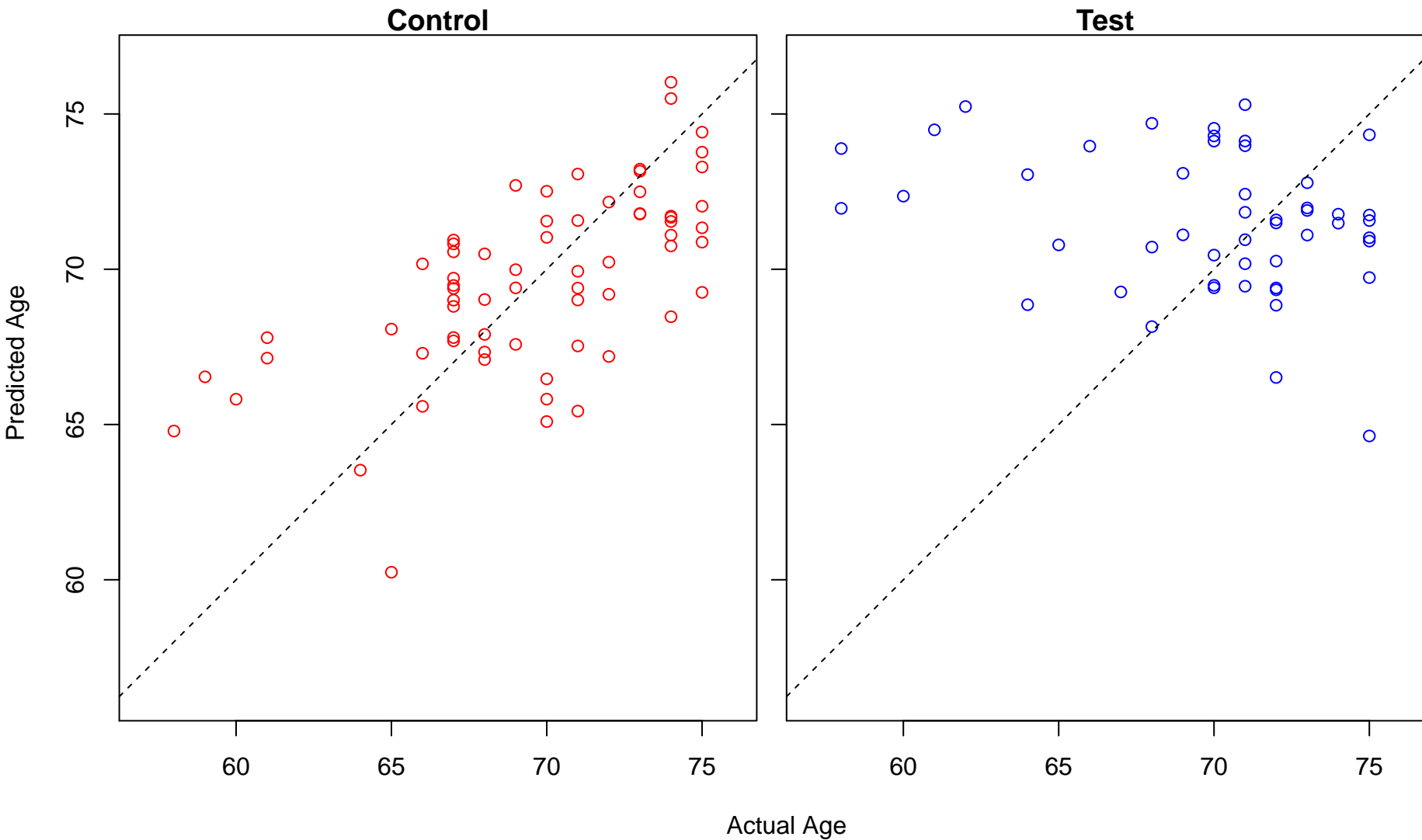
mucosal immune response (Score: 1.315036)



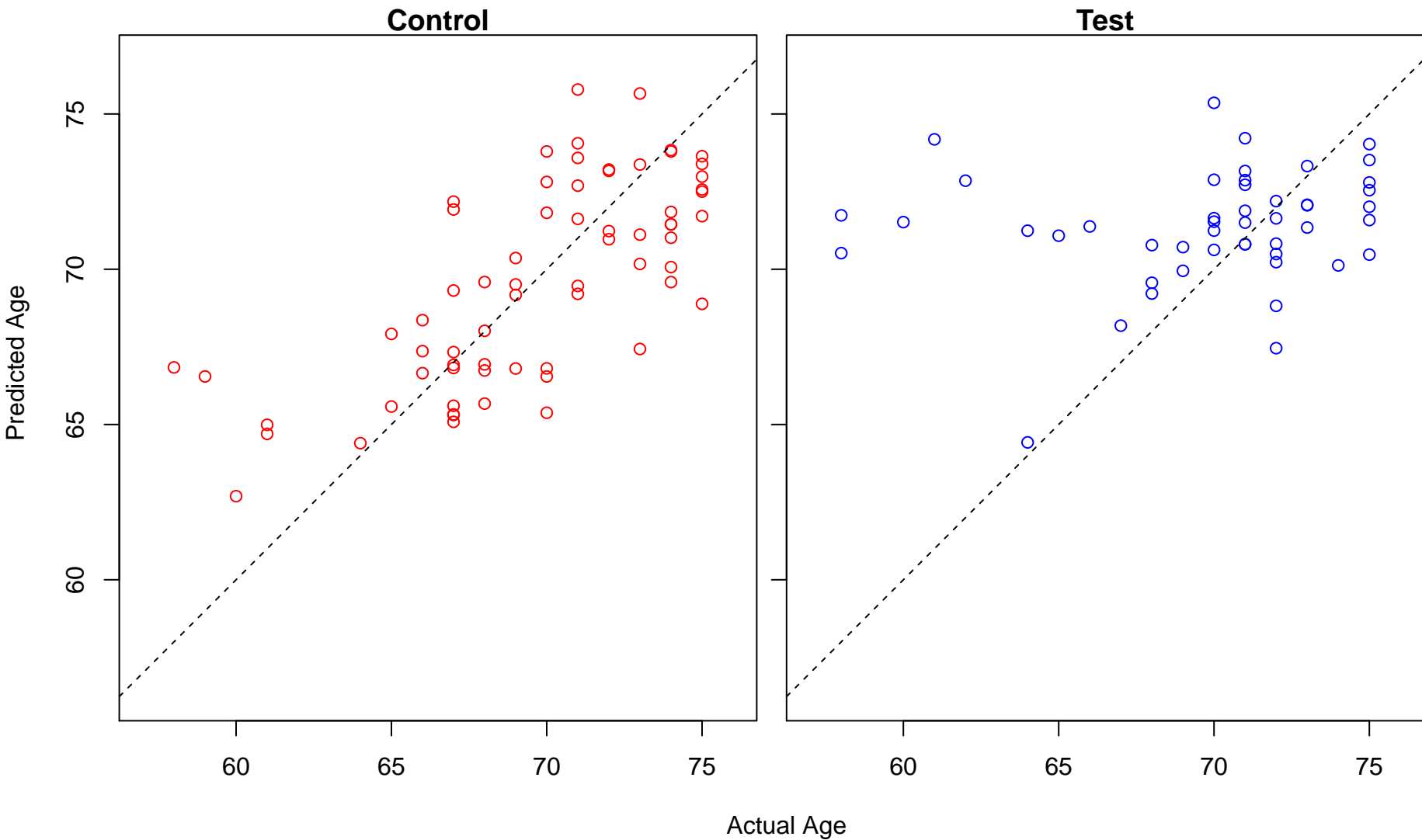
negative regulation of epidermal growth factor receptor signaling pathway (Score: 1.314869)



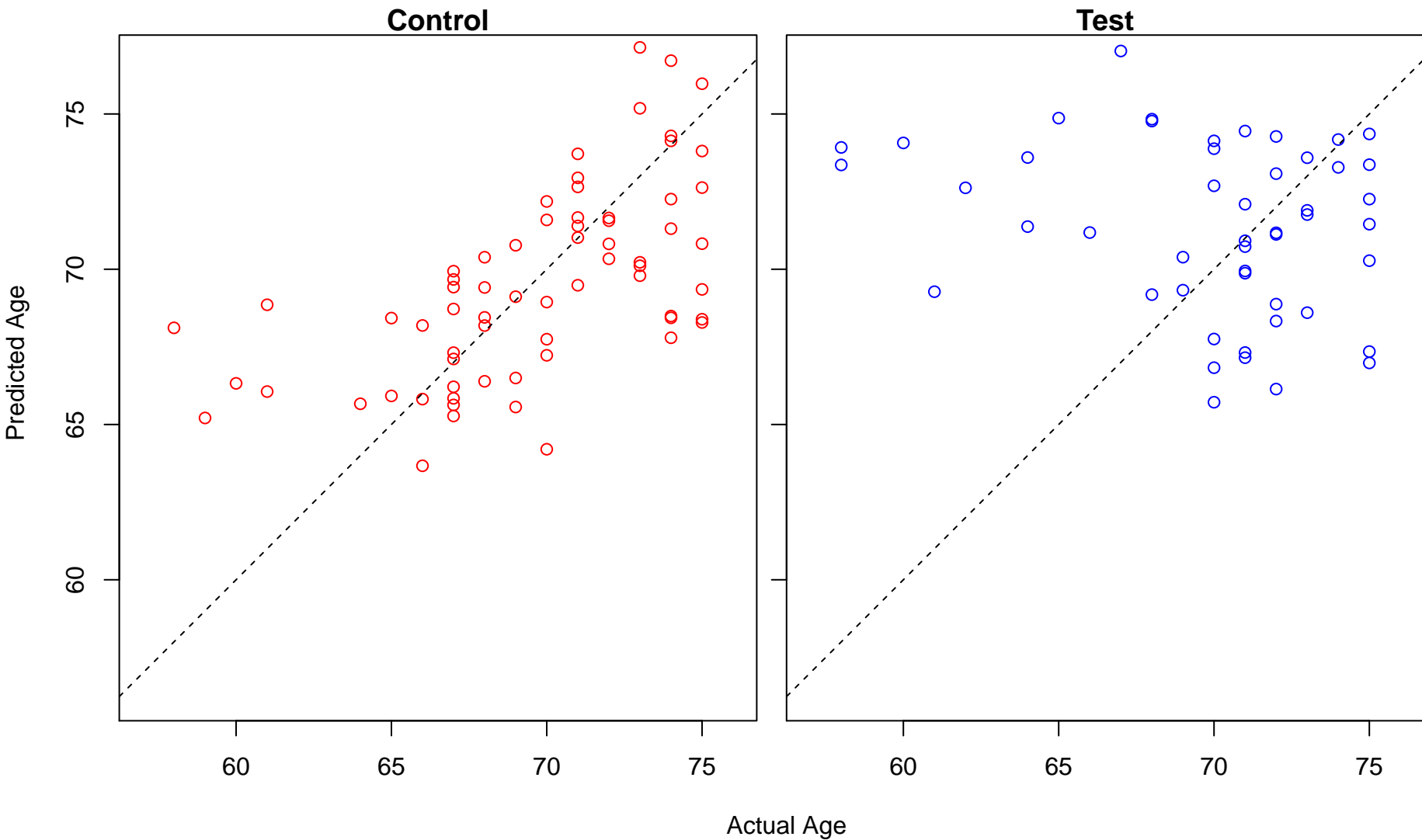
positive regulation of membrane protein ectodomain proteolysis (Score: 1.314862)



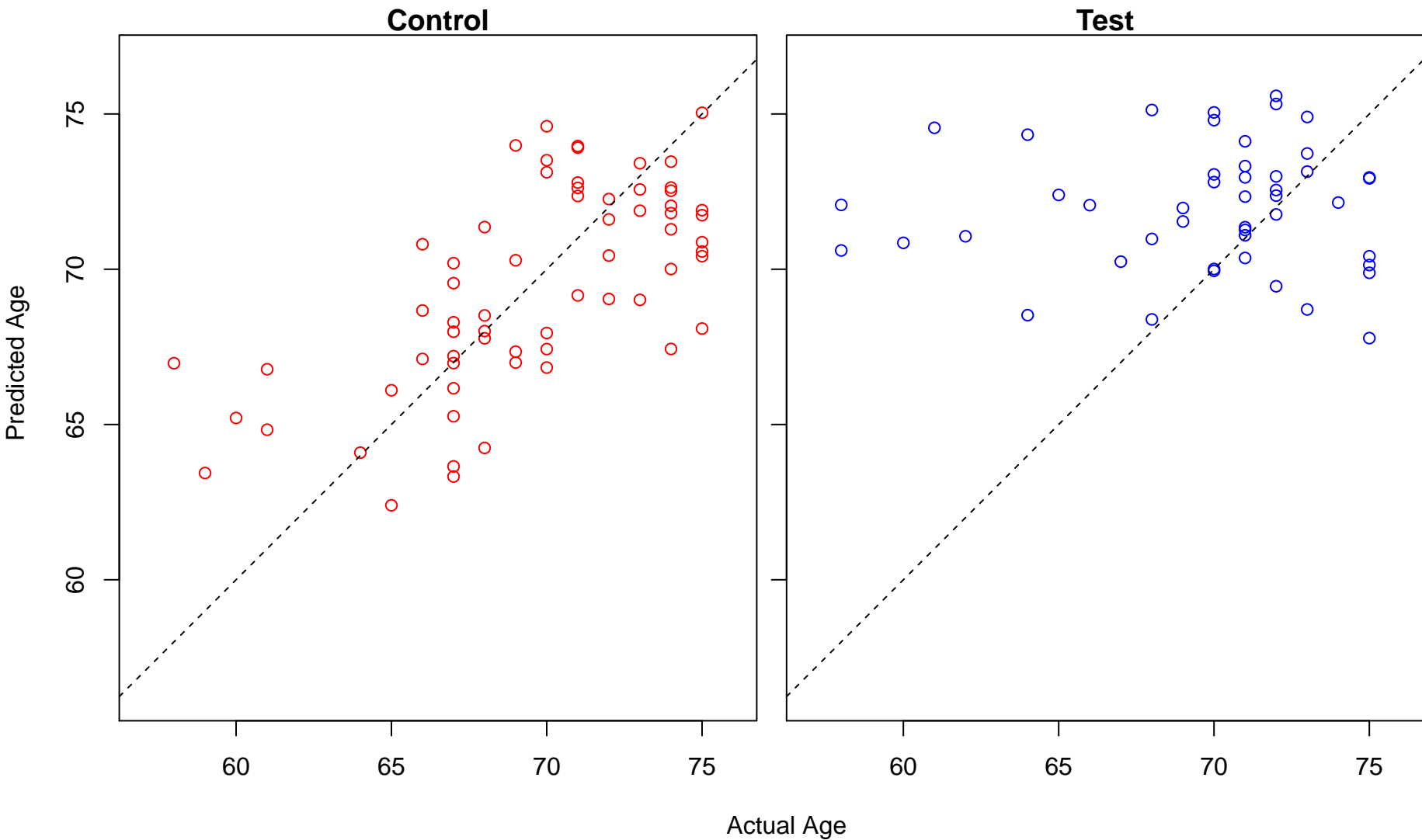
endothelium development (Score: 1.314700)



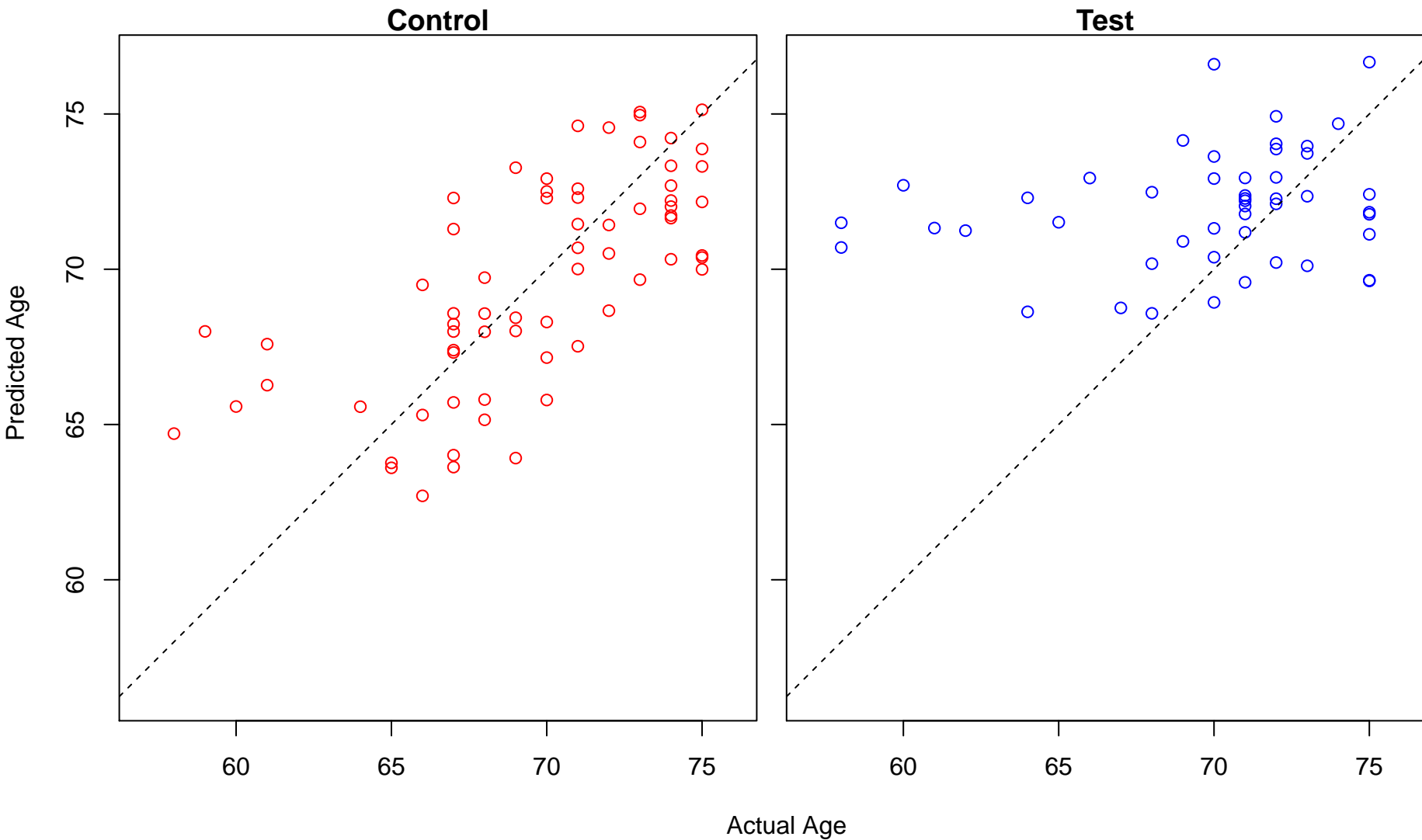
positive regulation of TOR signaling (Score: 1.314359)



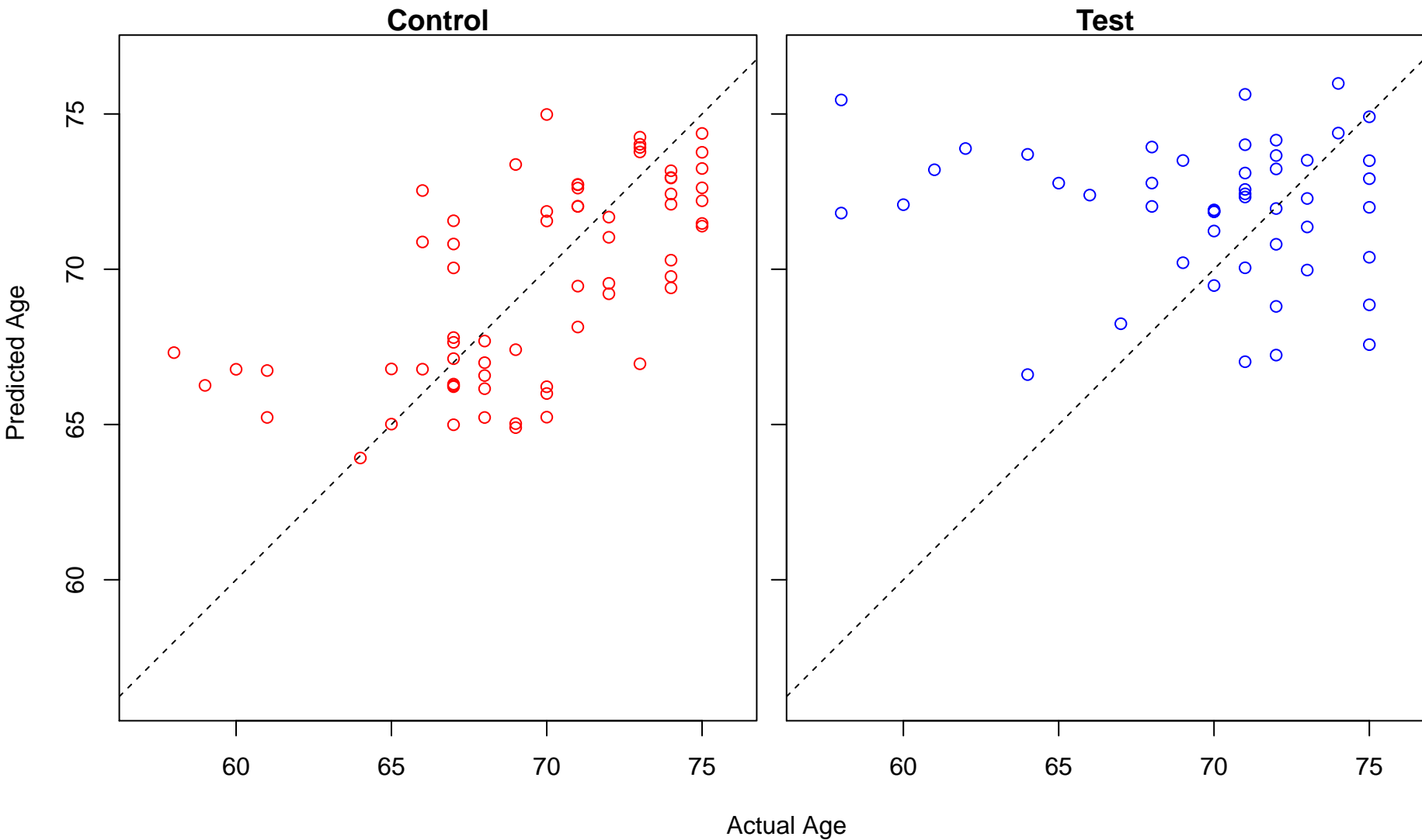
negative regulation of signal transduction by p53 class mediator (Score: 1.314127)



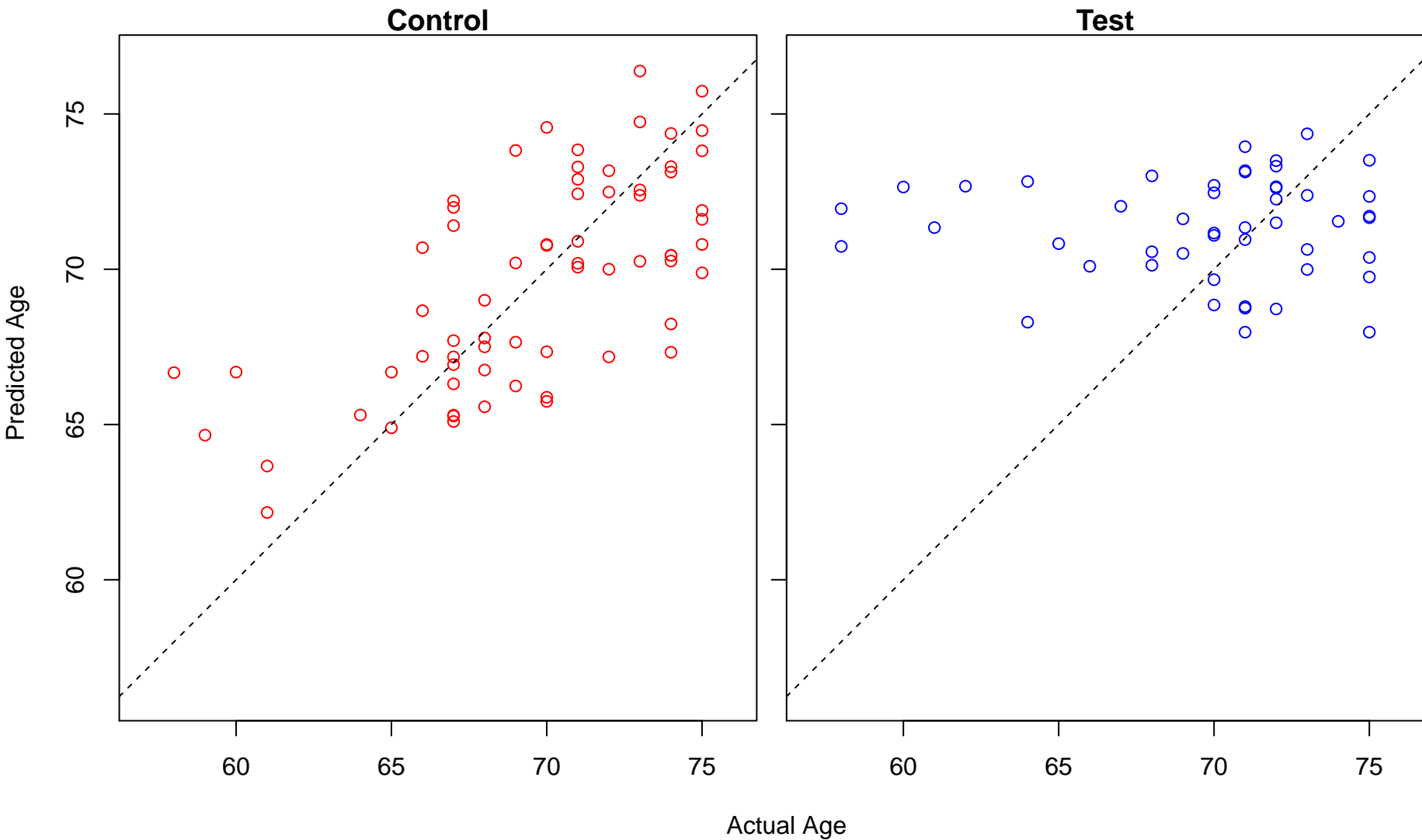
nucleosome assembly (Score: 1.313287)



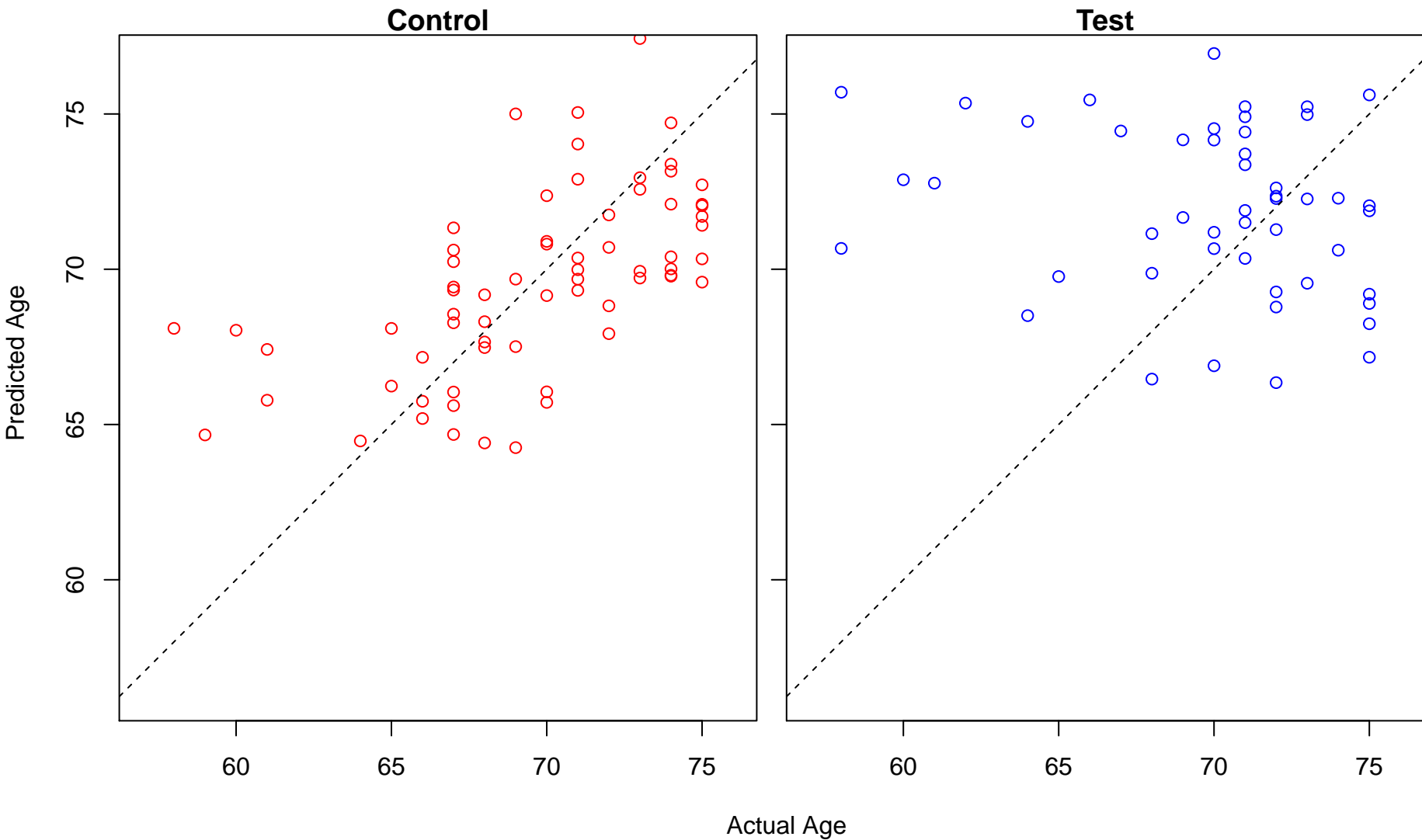
regulation of glucose transport (Score: 1.313192)



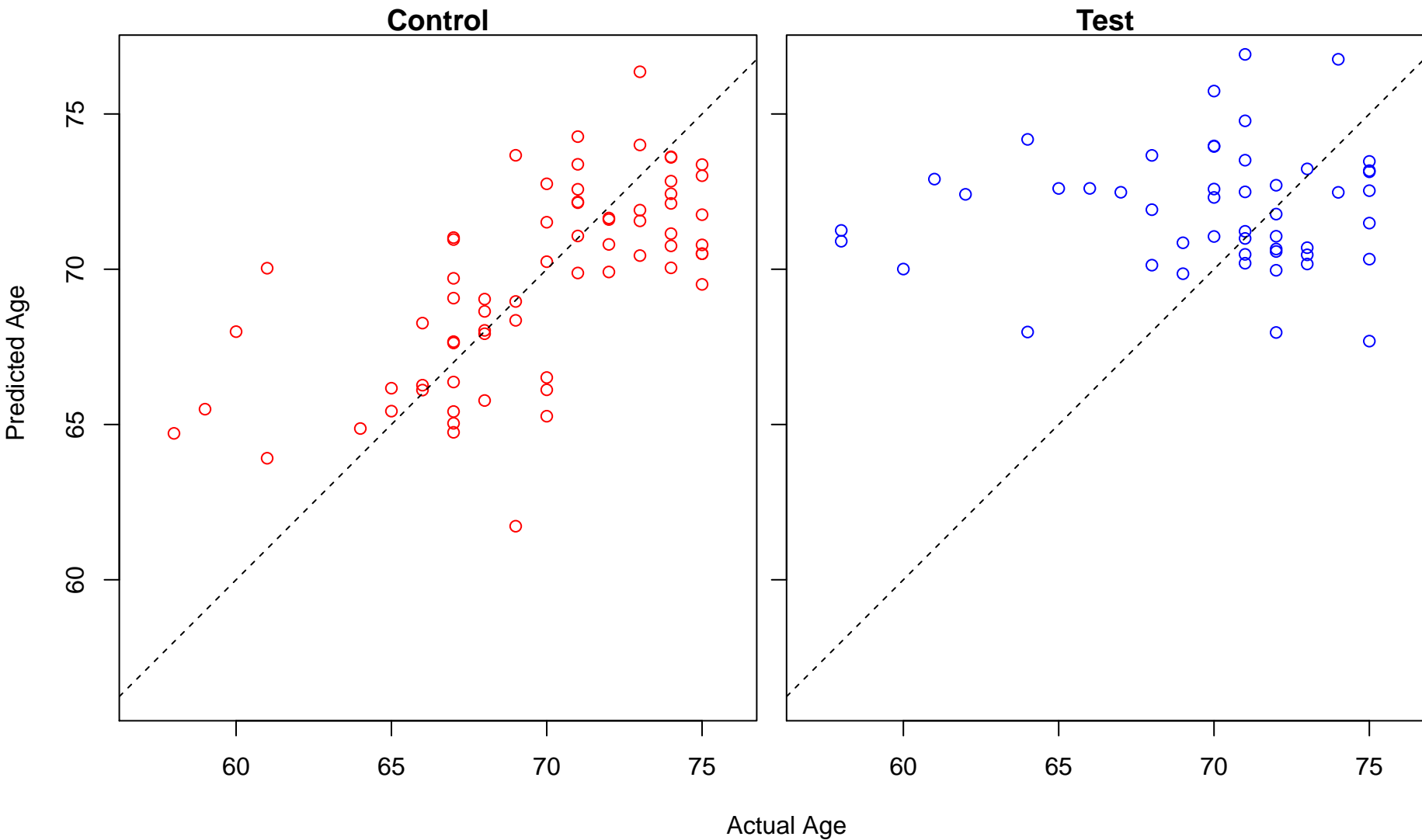
negative regulation of ERBB signaling pathway (Score: 1.312997)



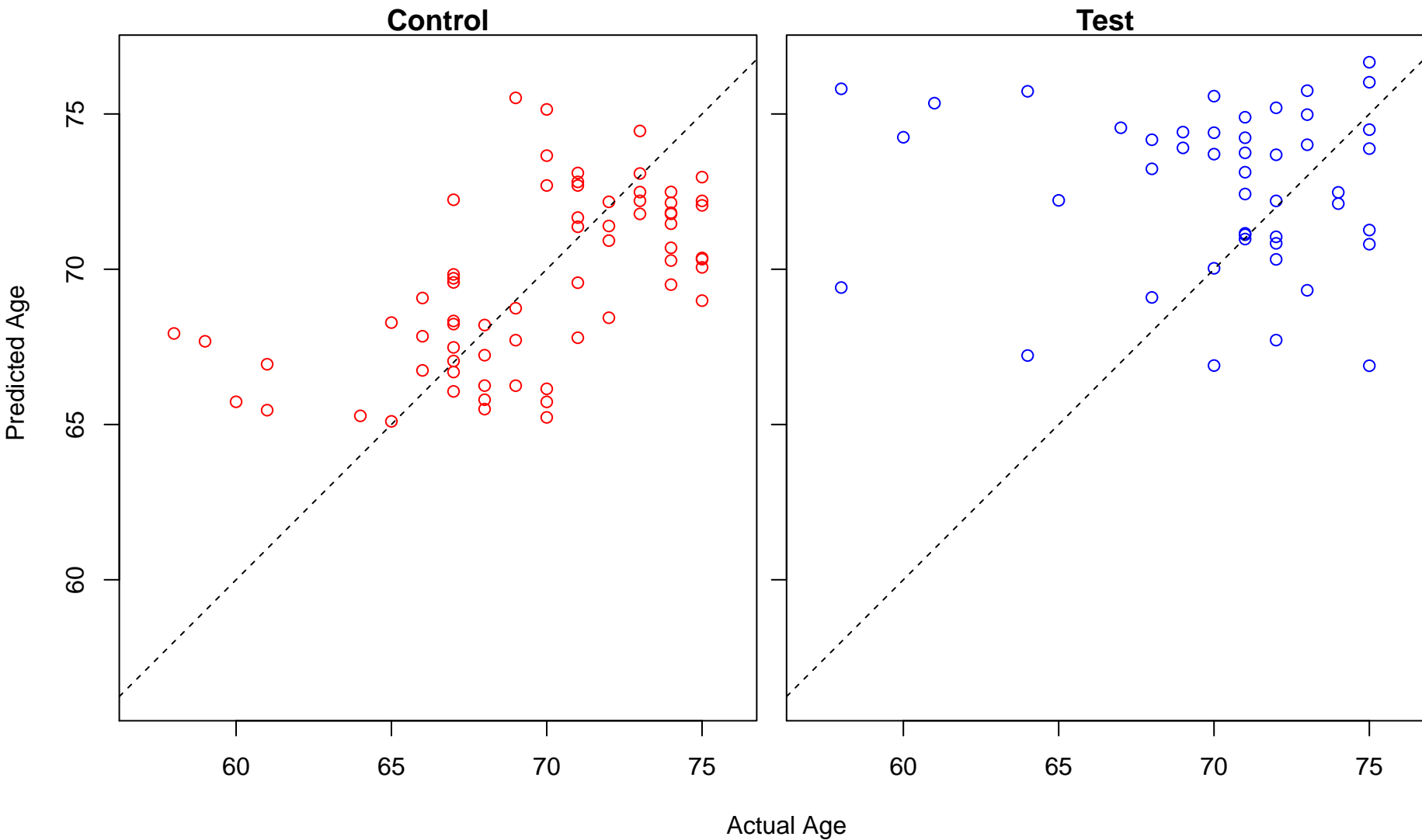
regulation of immunoglobulin mediated immune response (Score: 1.312750)



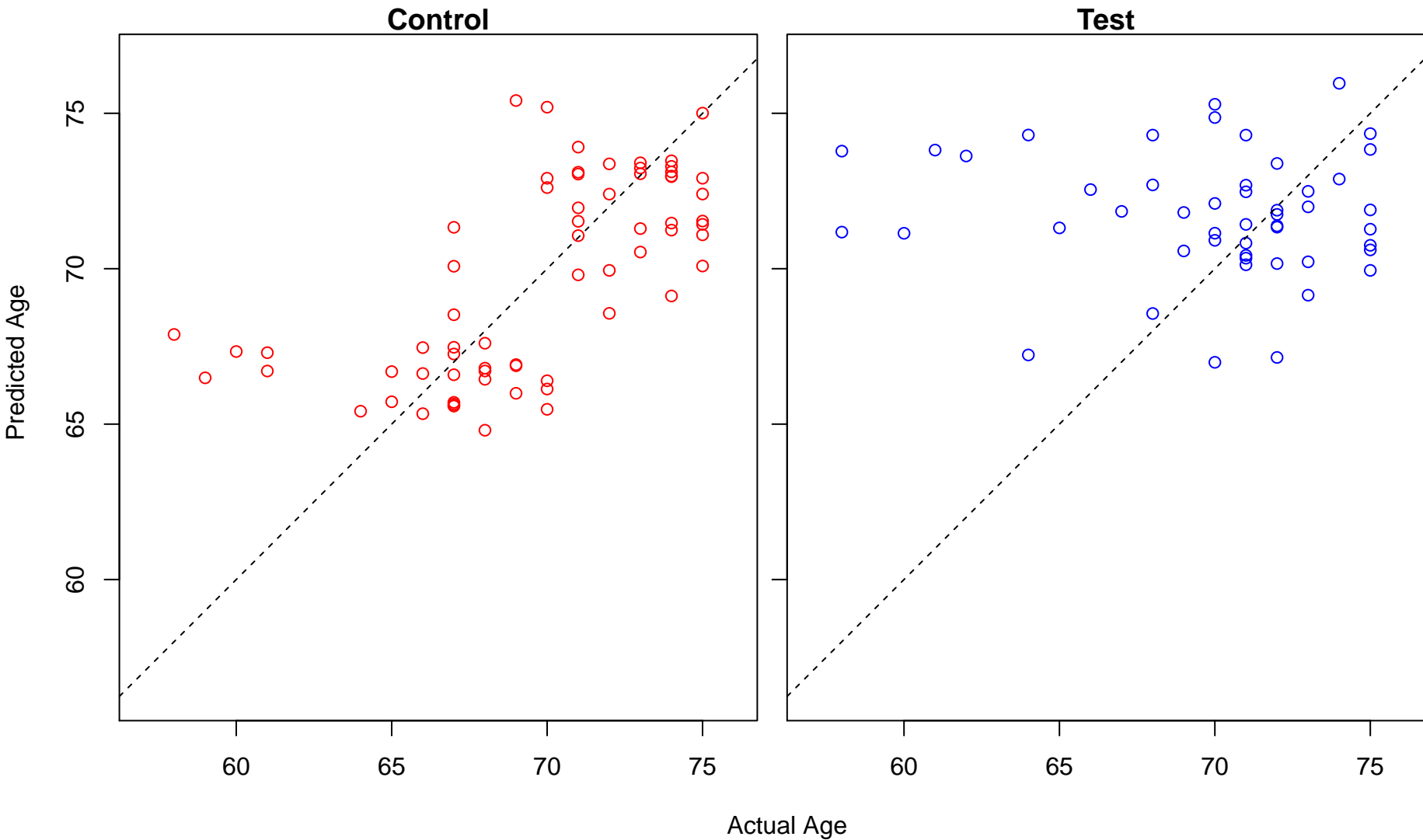
early endosome to late endosome transport (Score: 1.312272)



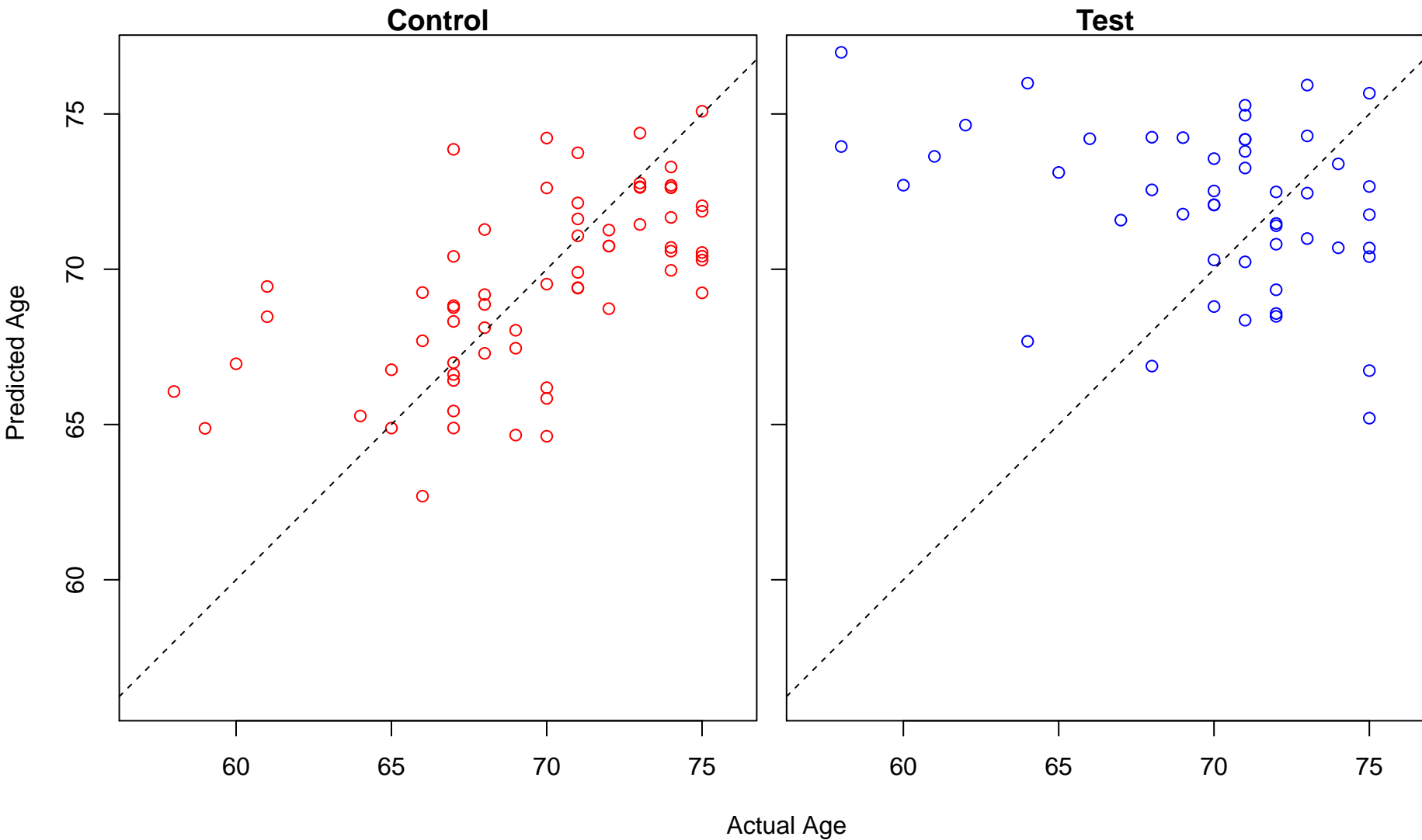
nucleotide-excision repair, DNA gap filling (Score: 1.311967)



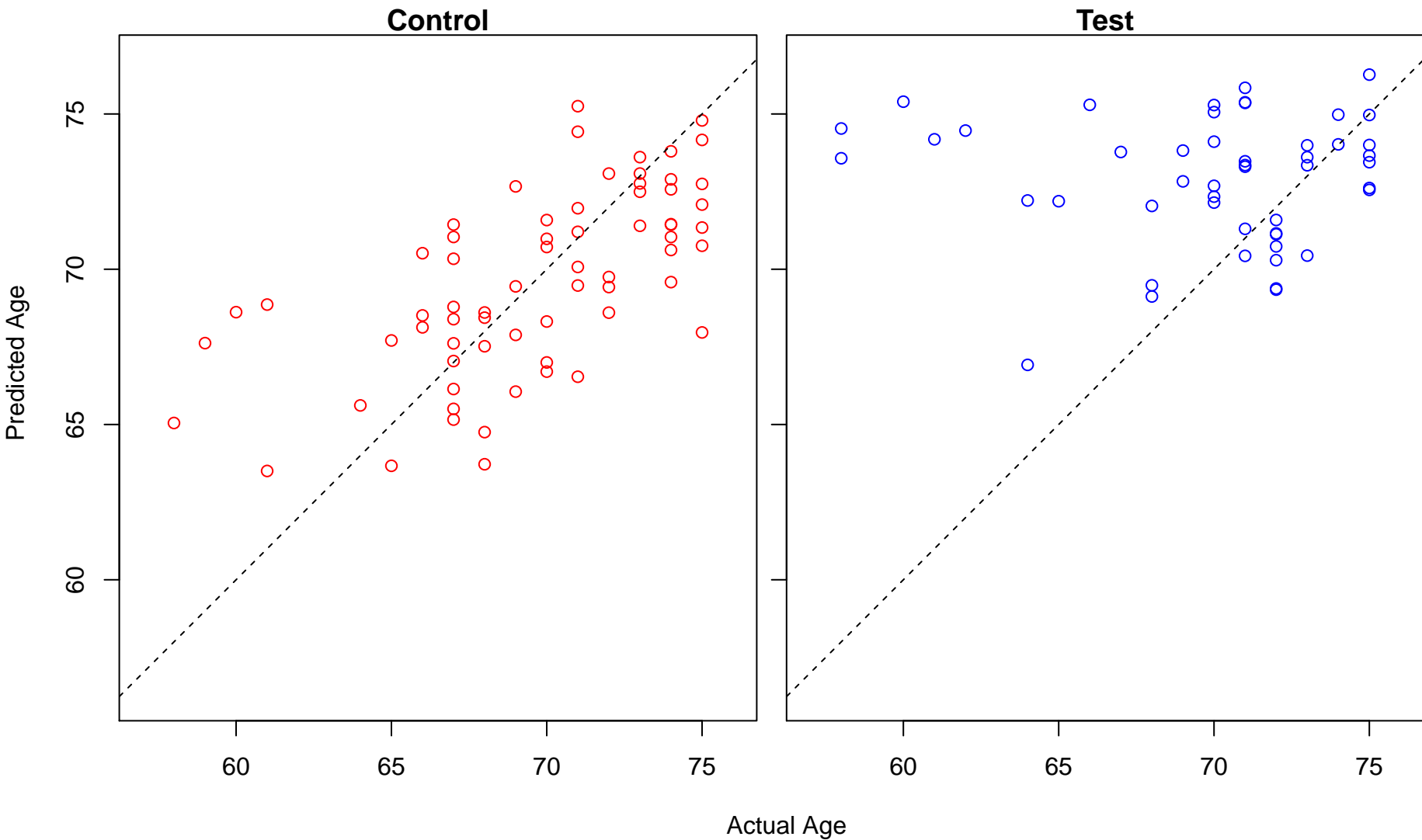
regulation of stress-activated MAPK cascade (Score: 1.310494)



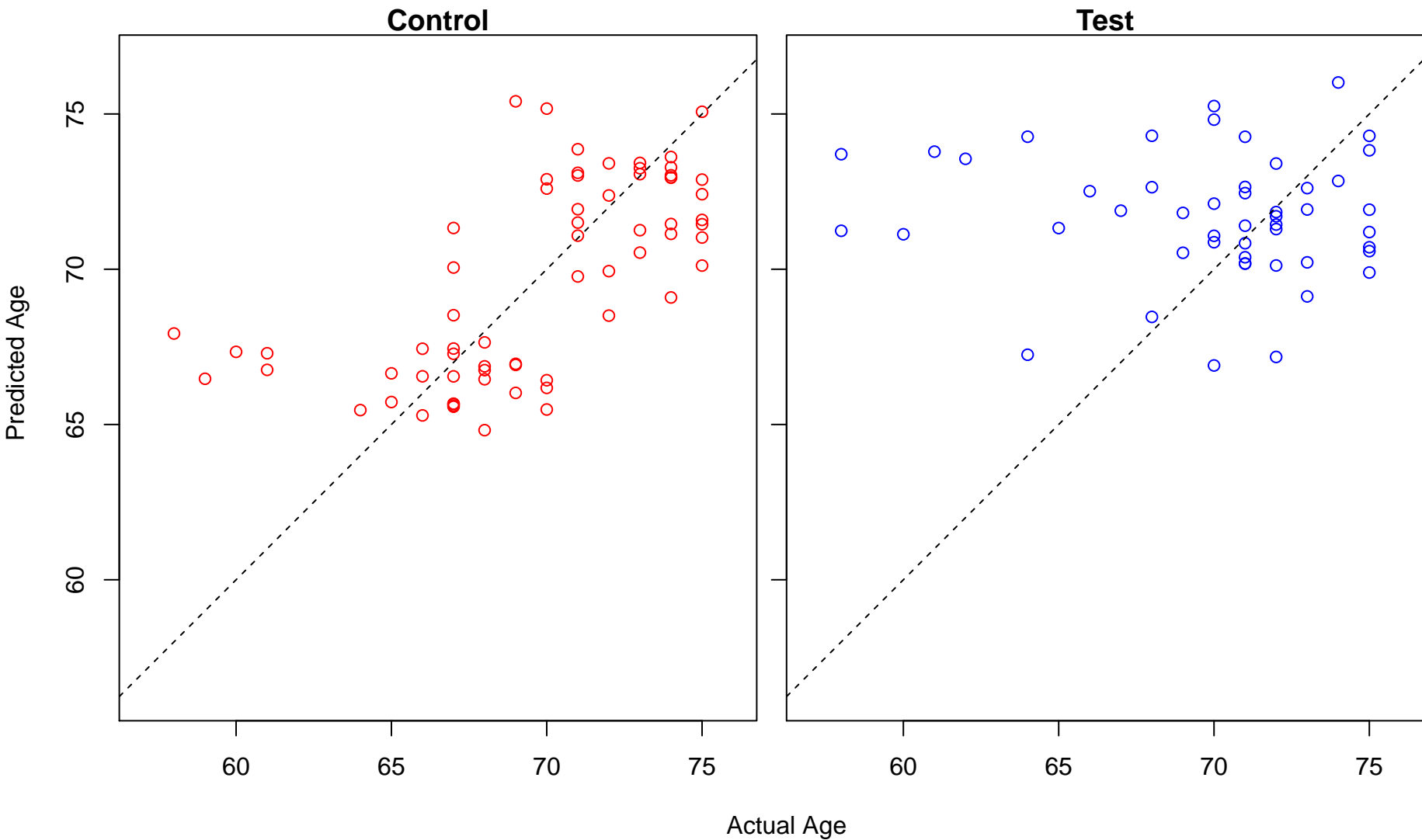
odontogenesis (Score: 1.308824)



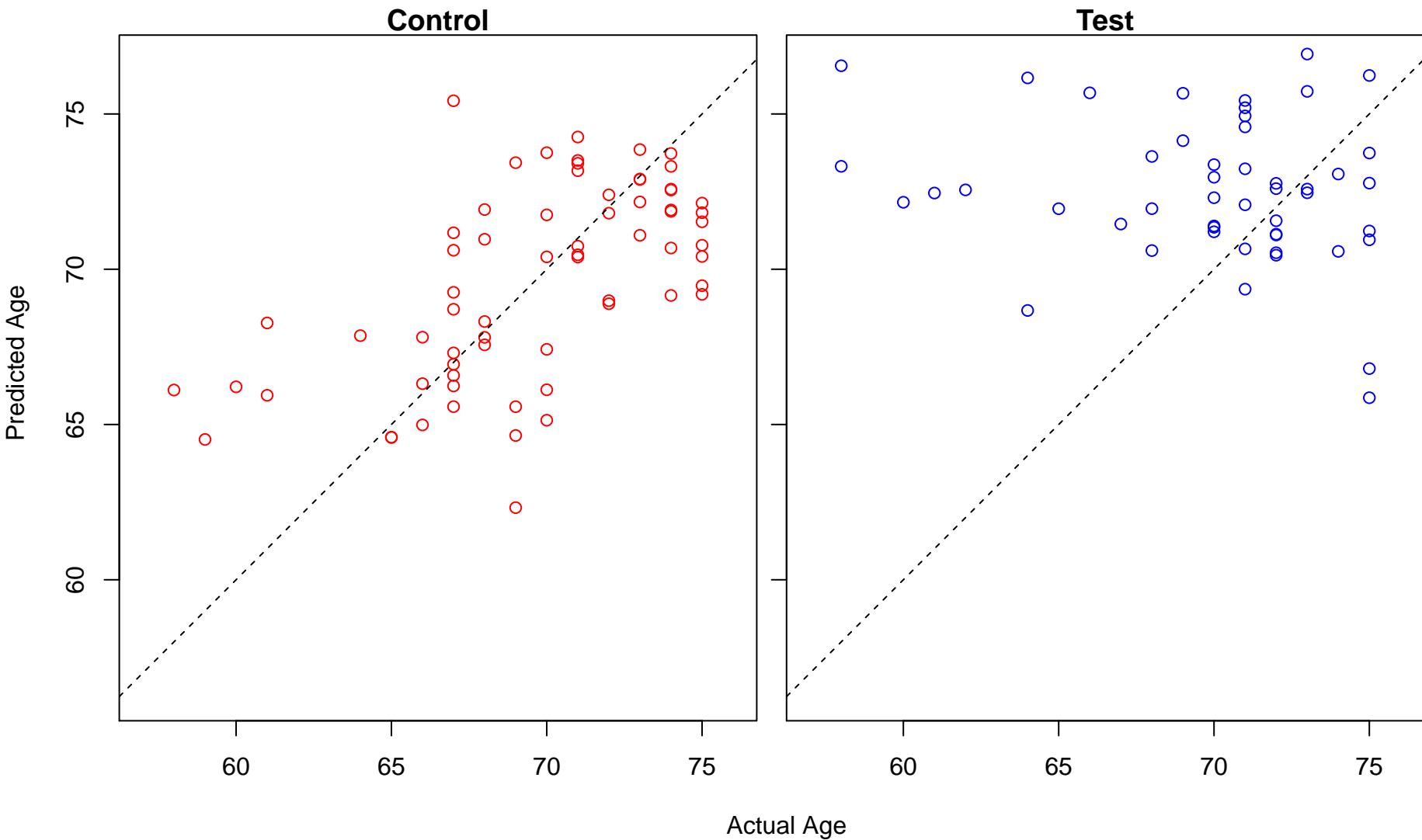
DNA replication initiation (Score: 1.308093)



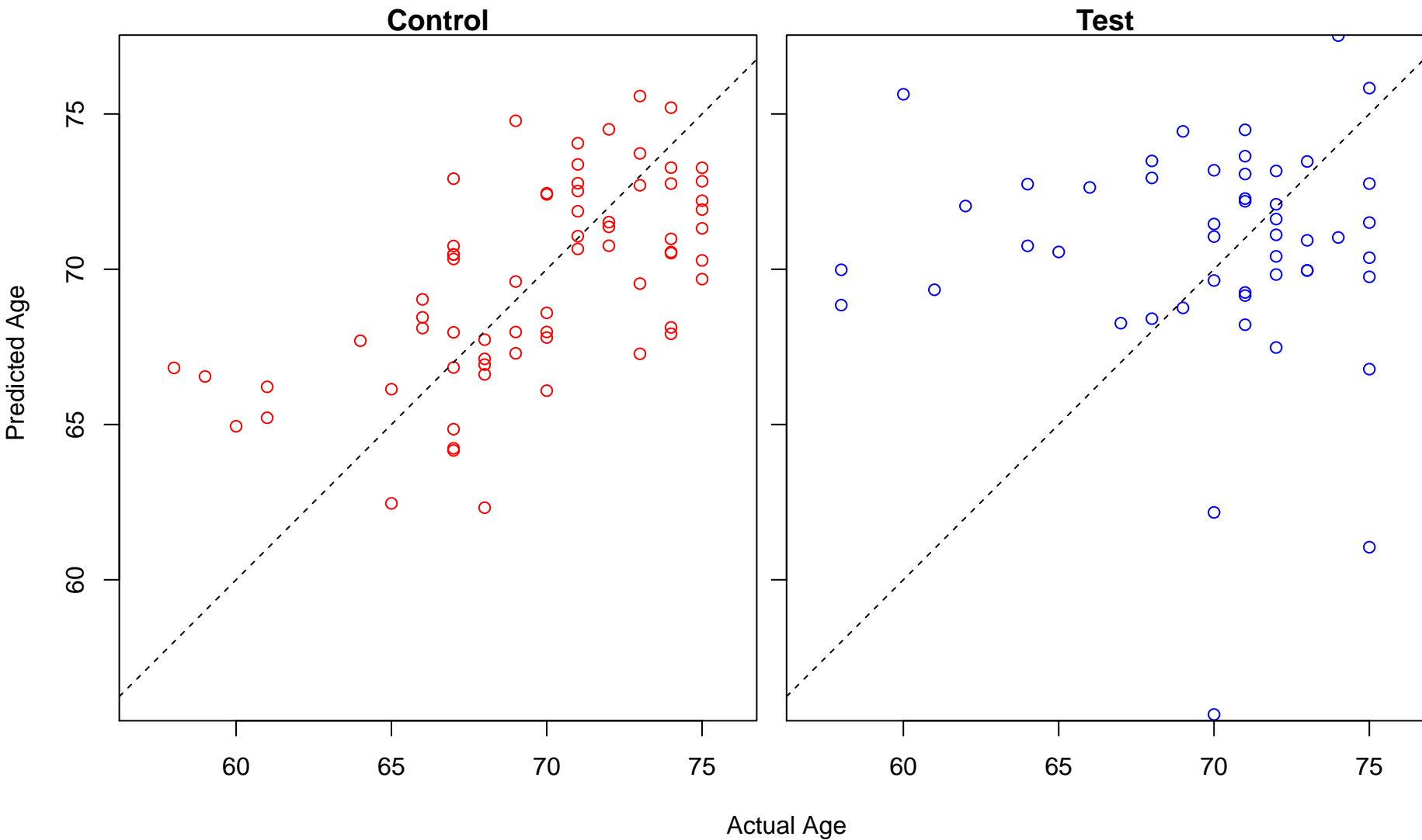
regulation of stress-activated protein kinase signaling cascade (Score: 1.307968)



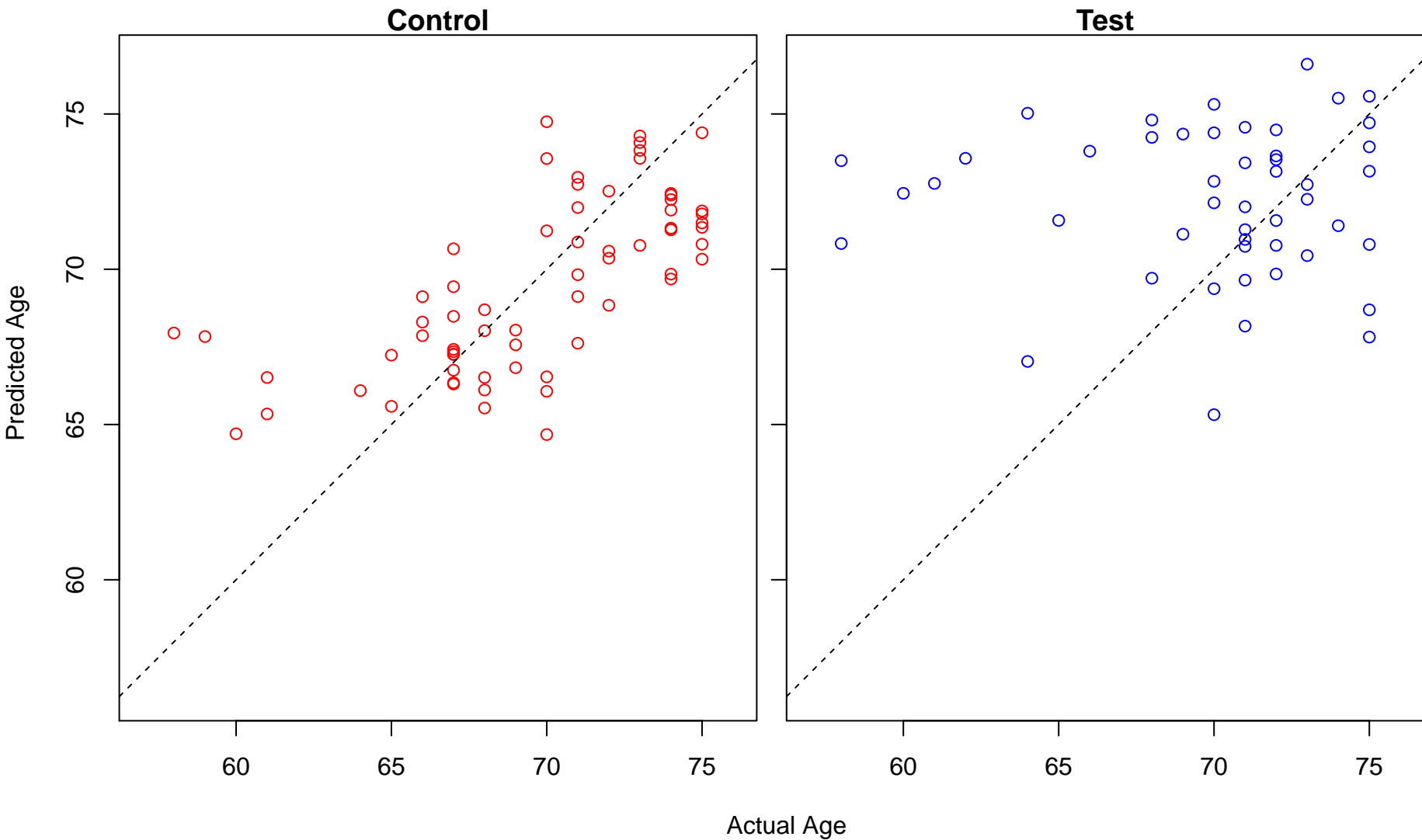
head morphogenesis (Score: 1.307790)



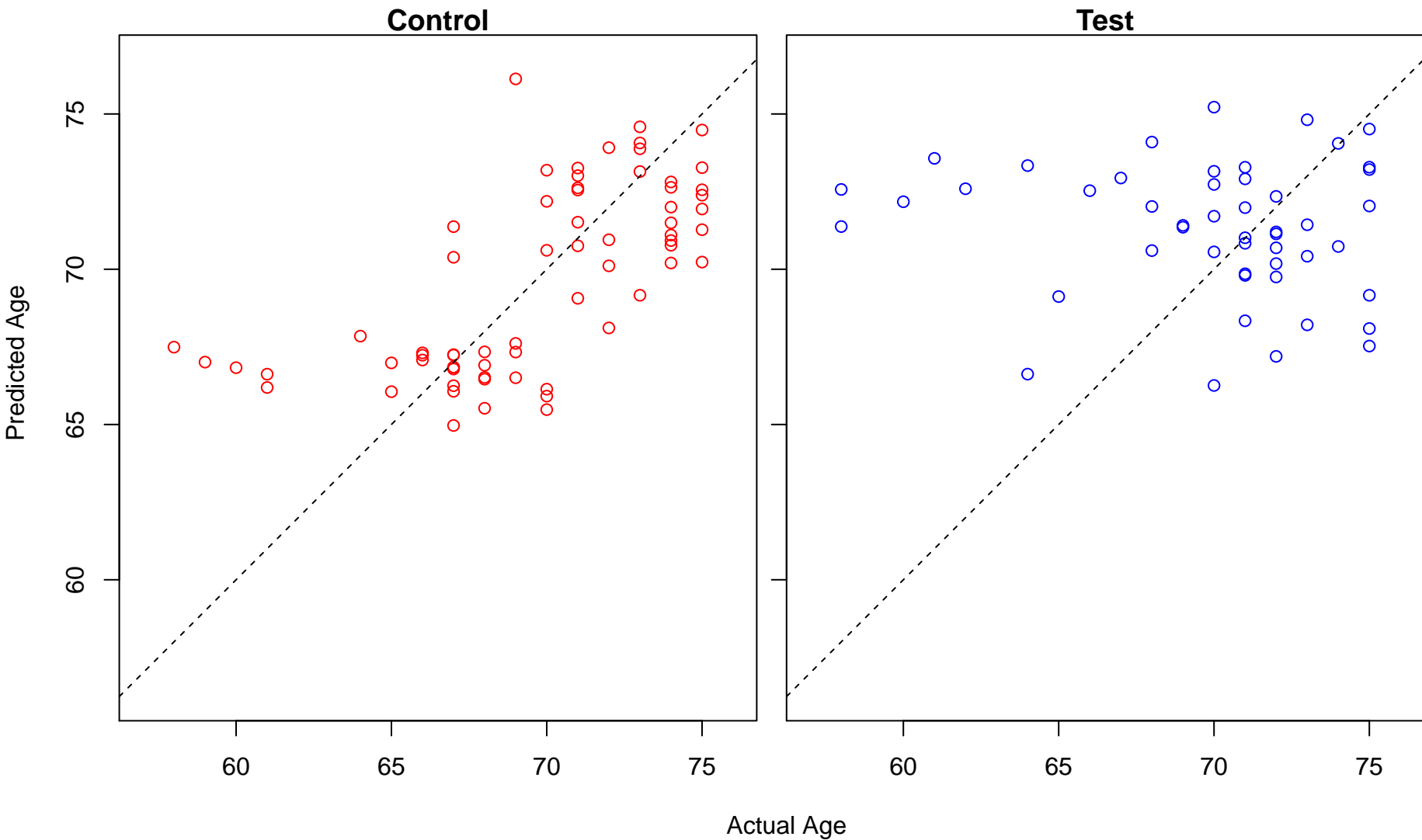
nucleotide transmembrane transport (Score: 1.307108)



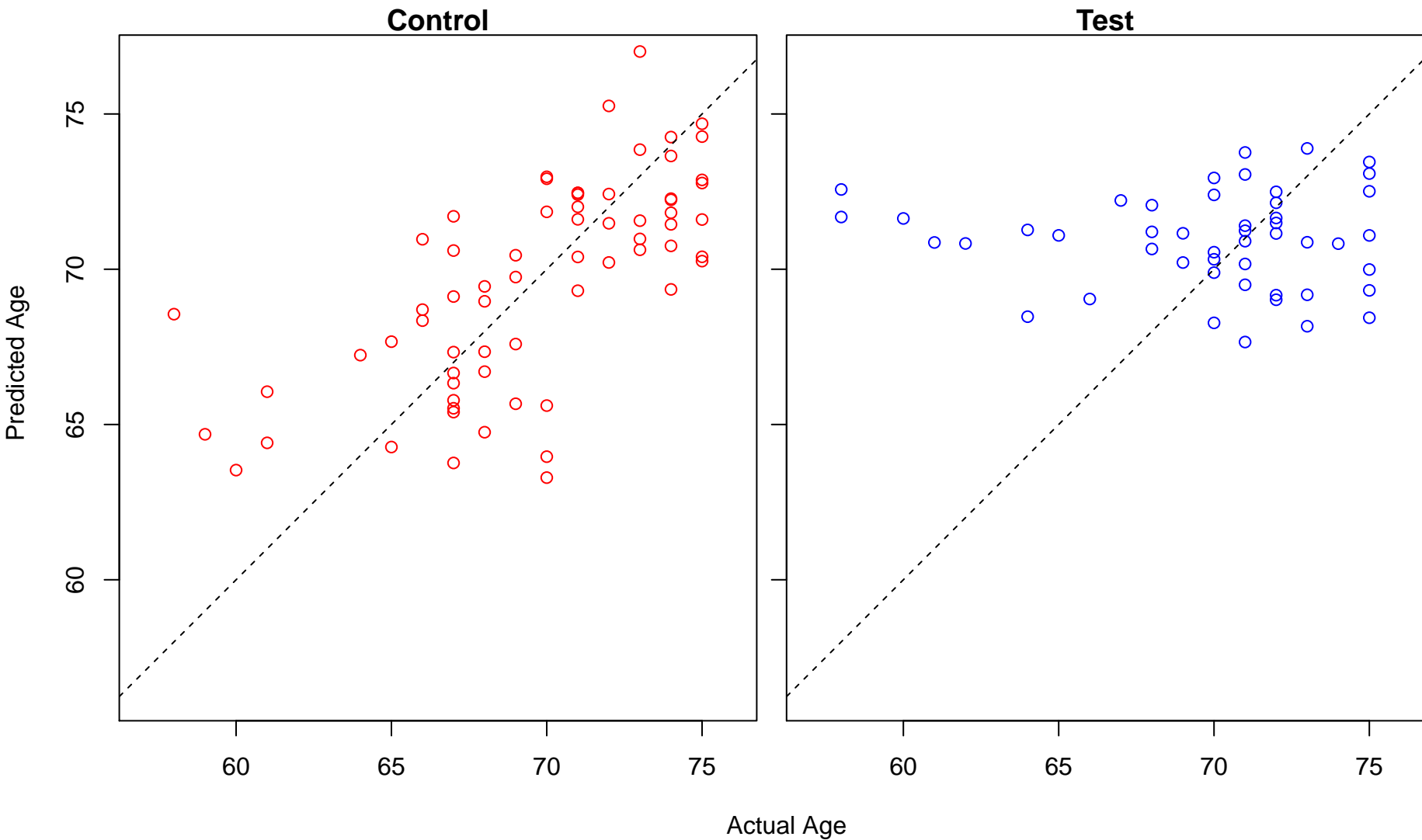
DNA strand elongation involved in DNA replication (Score: 1.306952)



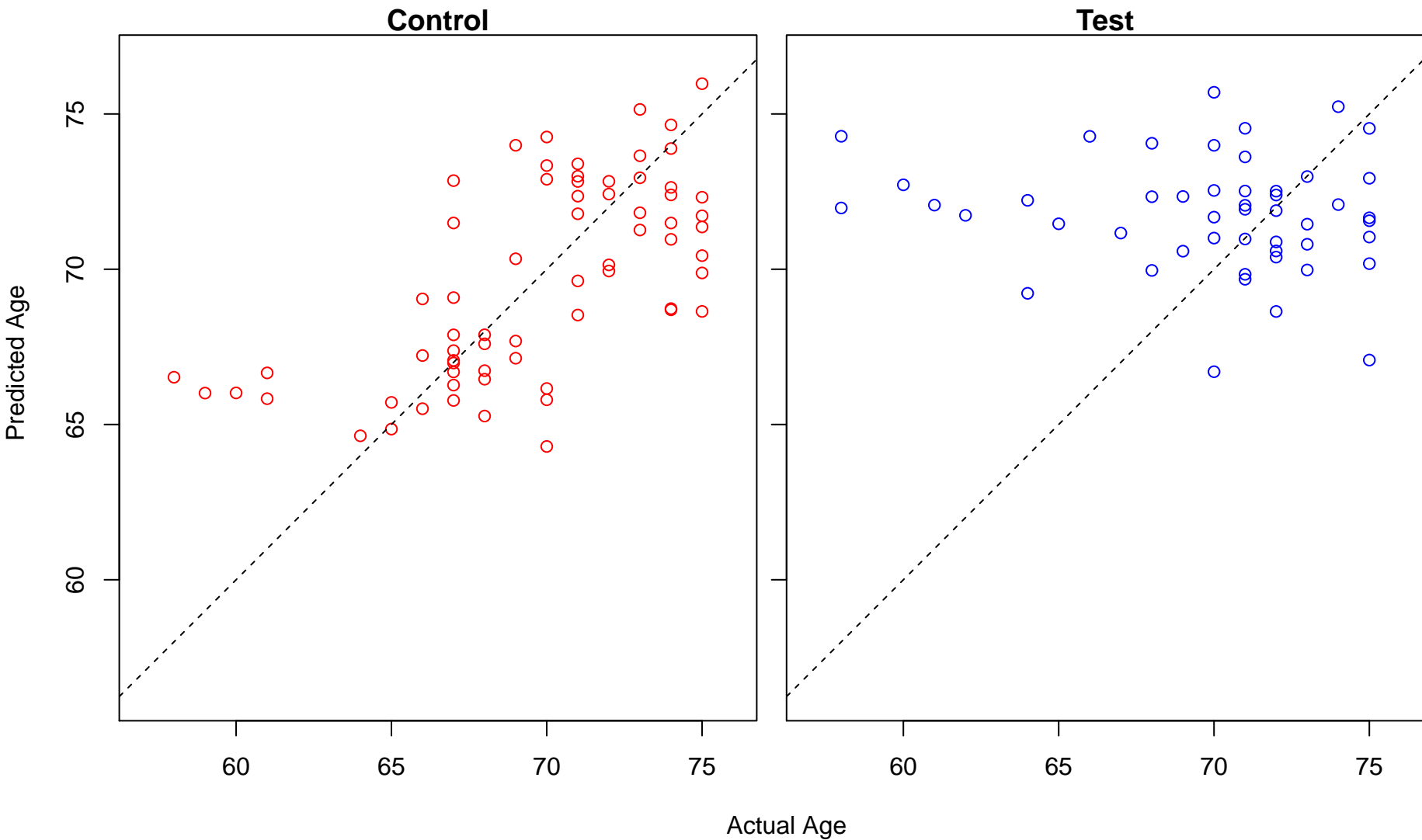
neutrophil chemotaxis (Score: 1.306854)



cellular defense response (Score: 1.306733)

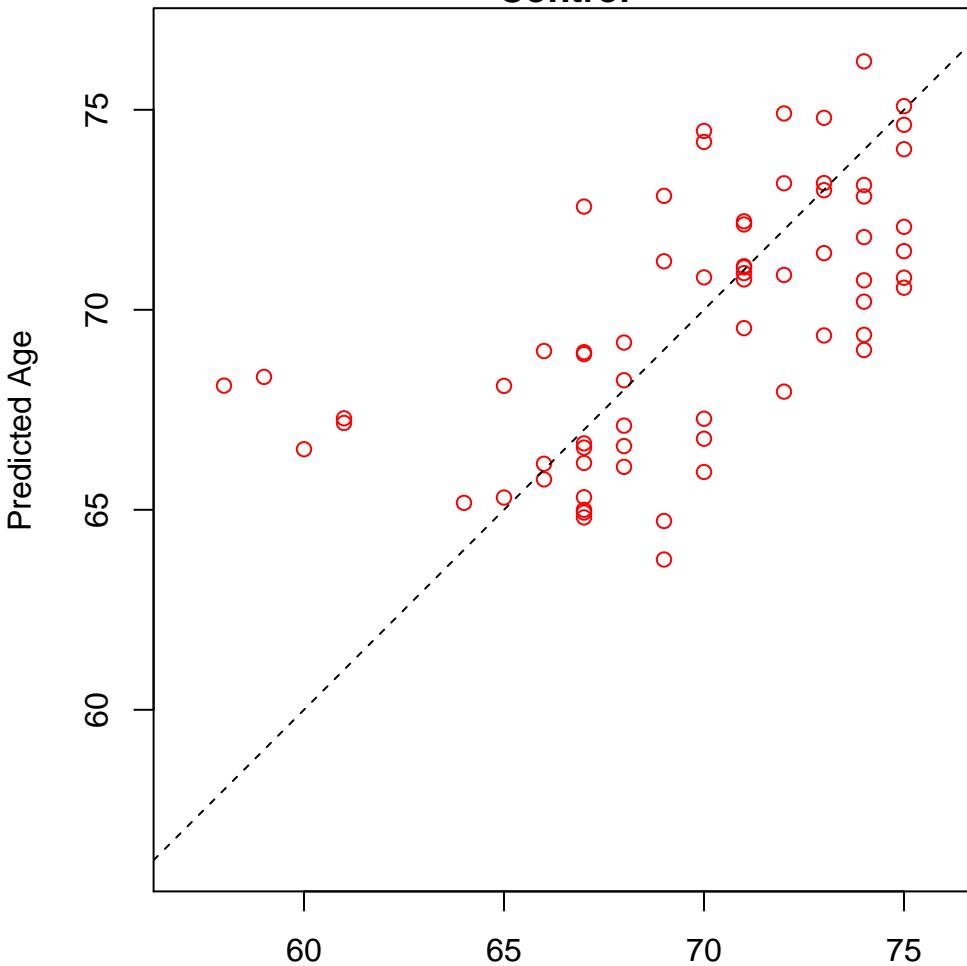


positive regulation of epithelial cell migration (Score: 1.306474)

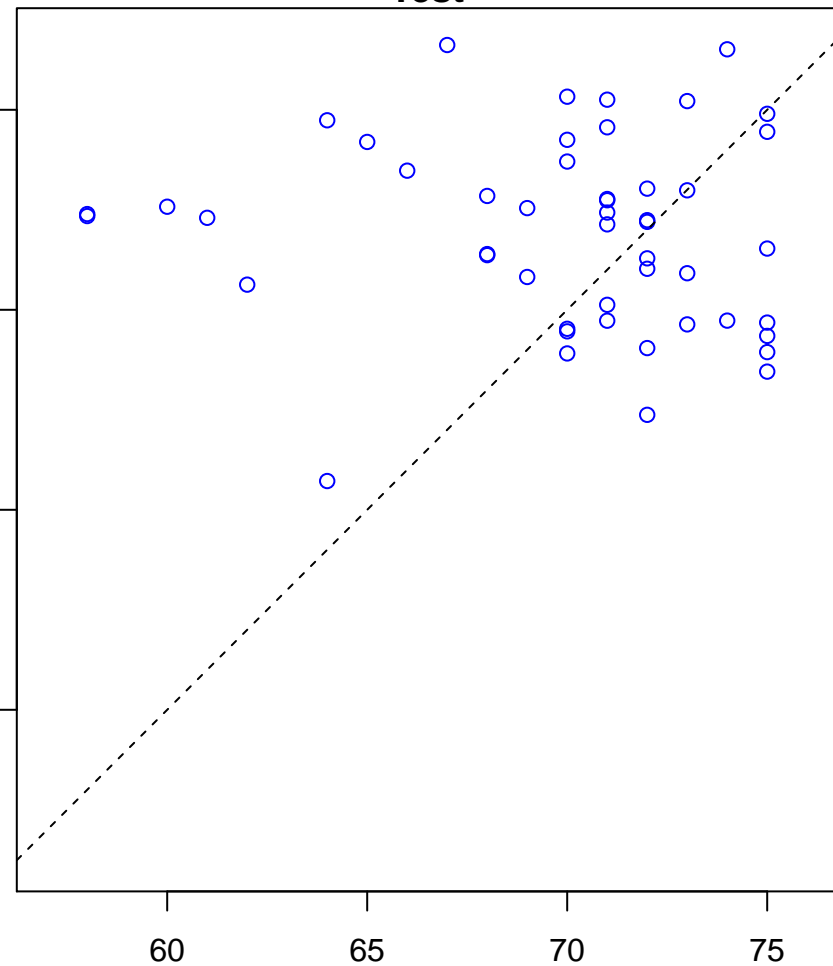


DNA catabolic process, endonucleolytic (Score: 1.306129)

Control

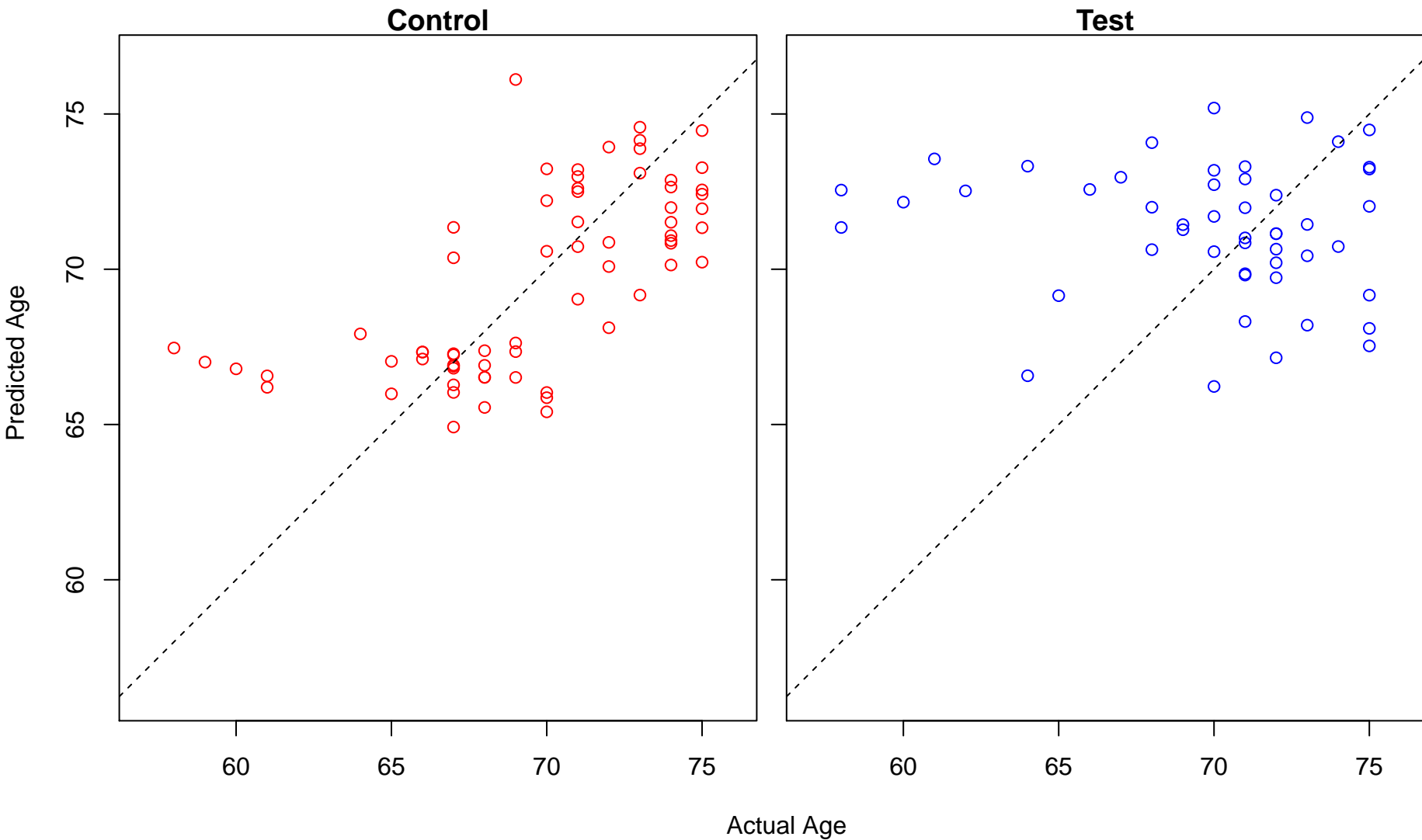


Test

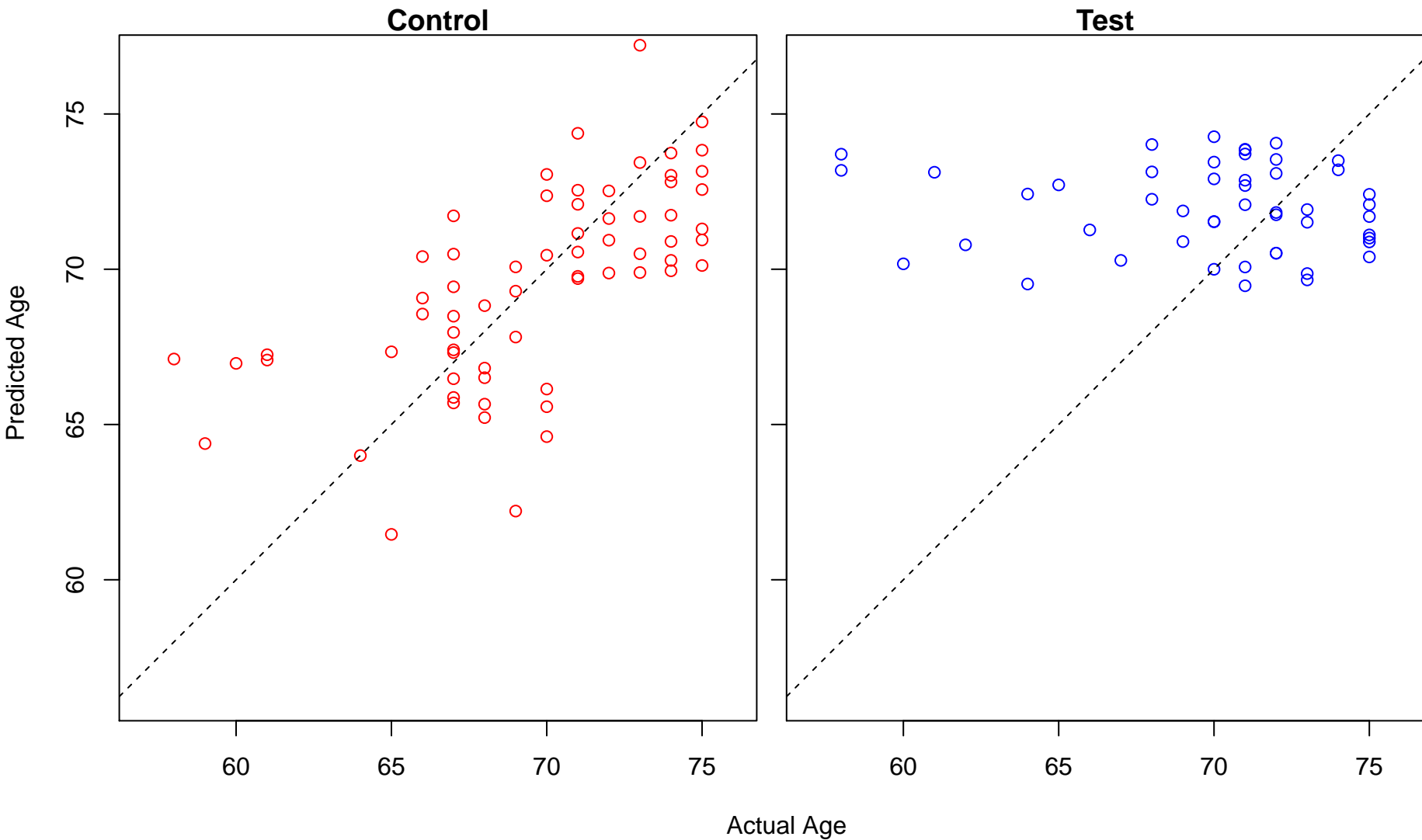


Actual Age

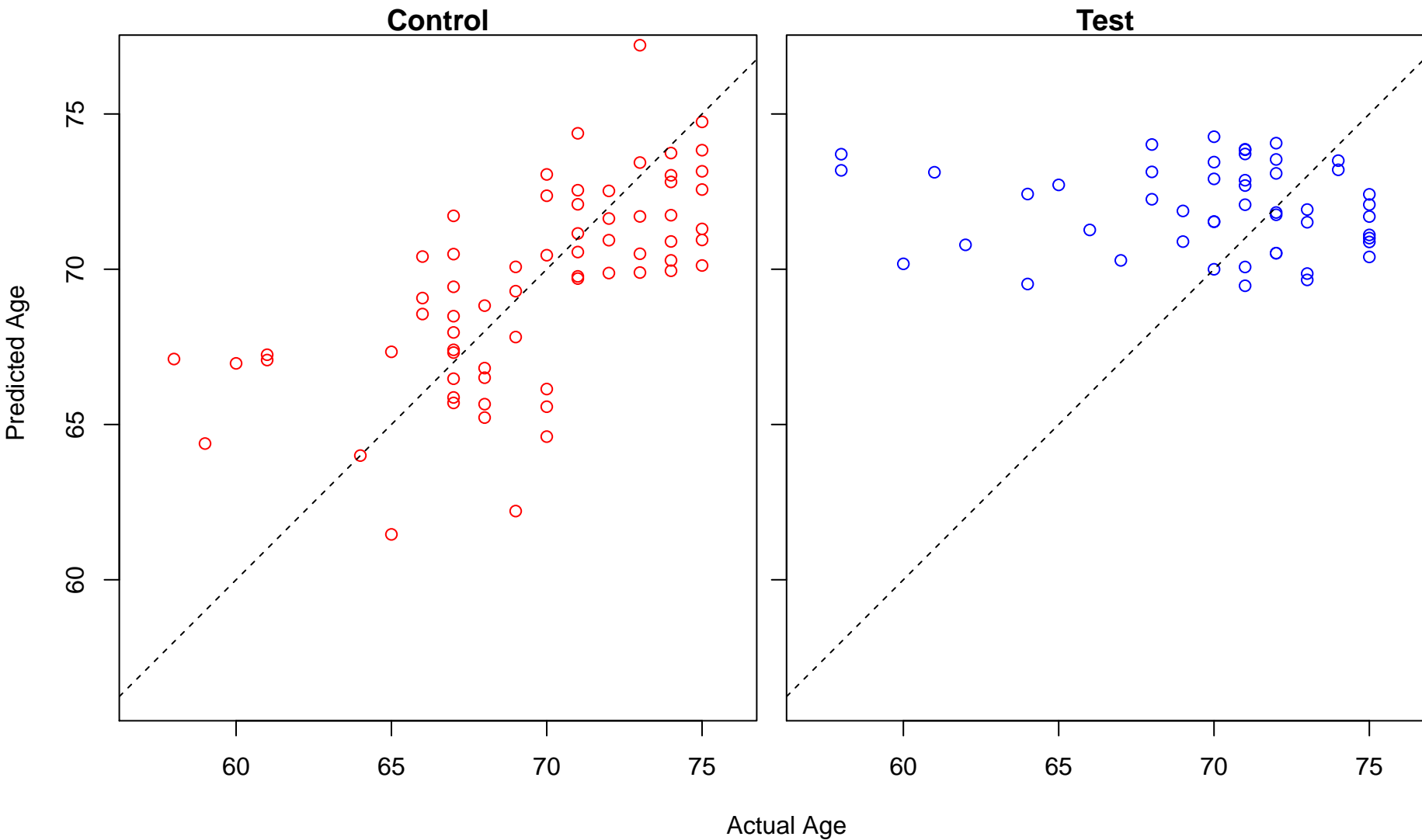
neutrophil migration (Score: 1.305870)



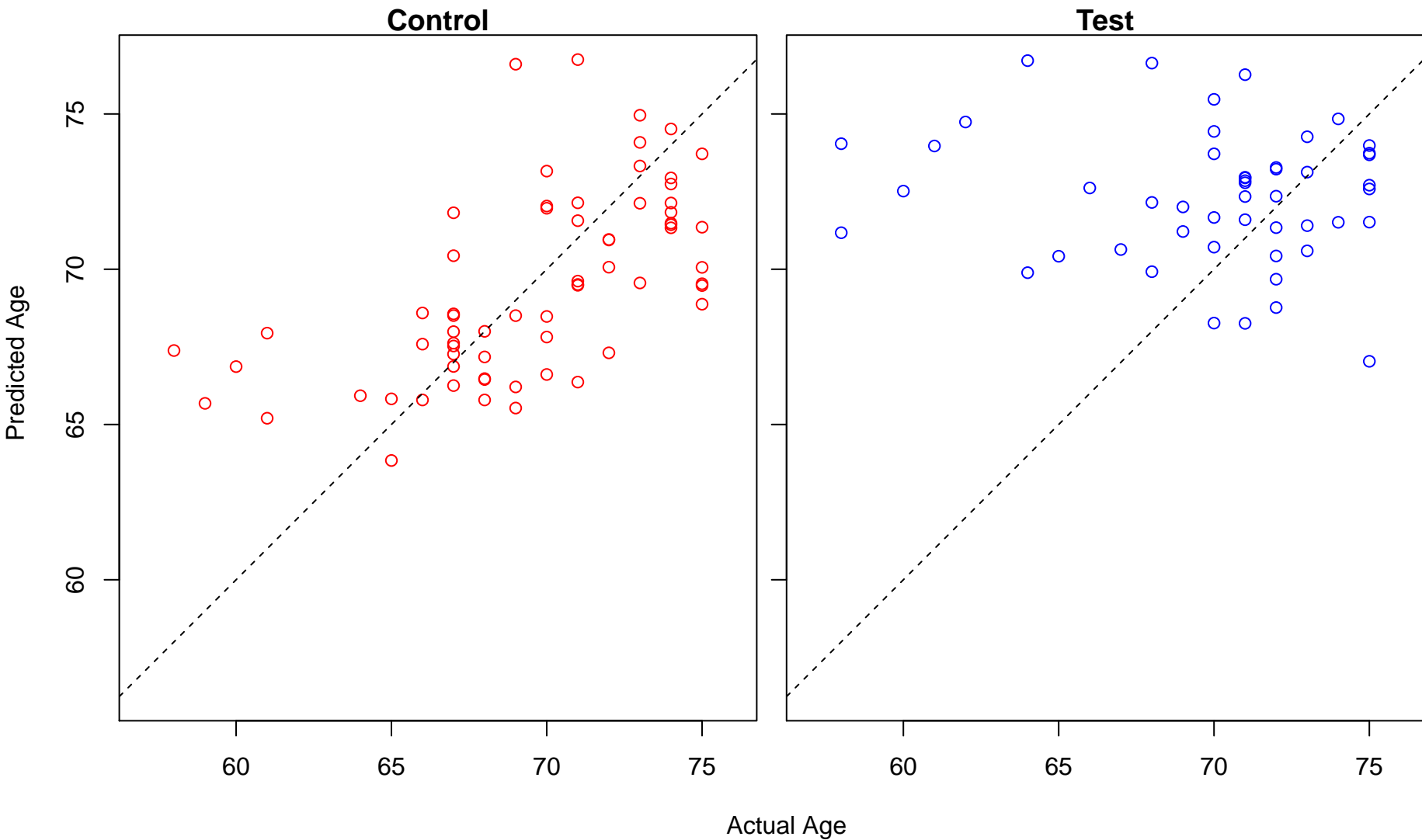
JAK-STAT cascade (Score: 1.305339)



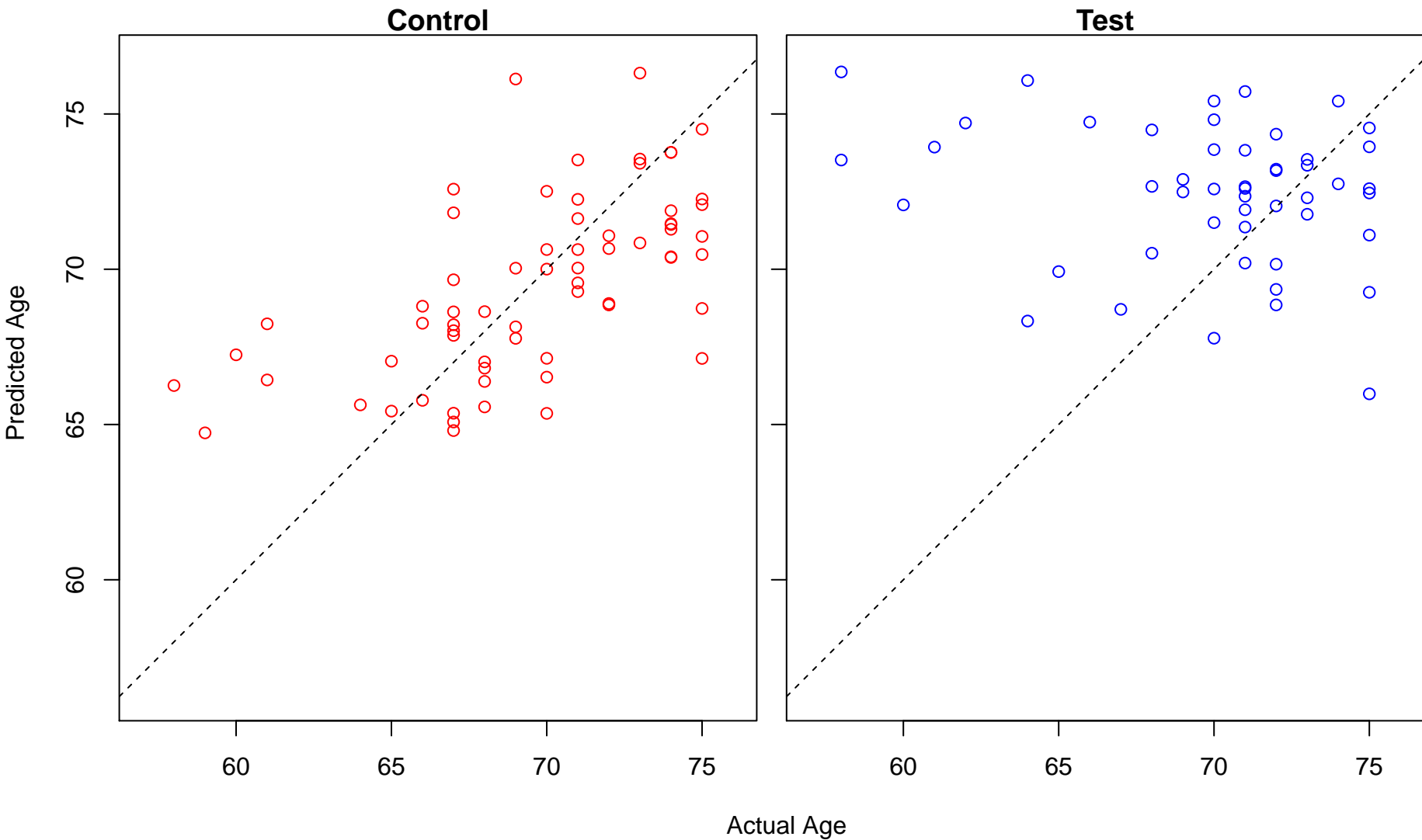
STAT cascade (Score: 1.305339)



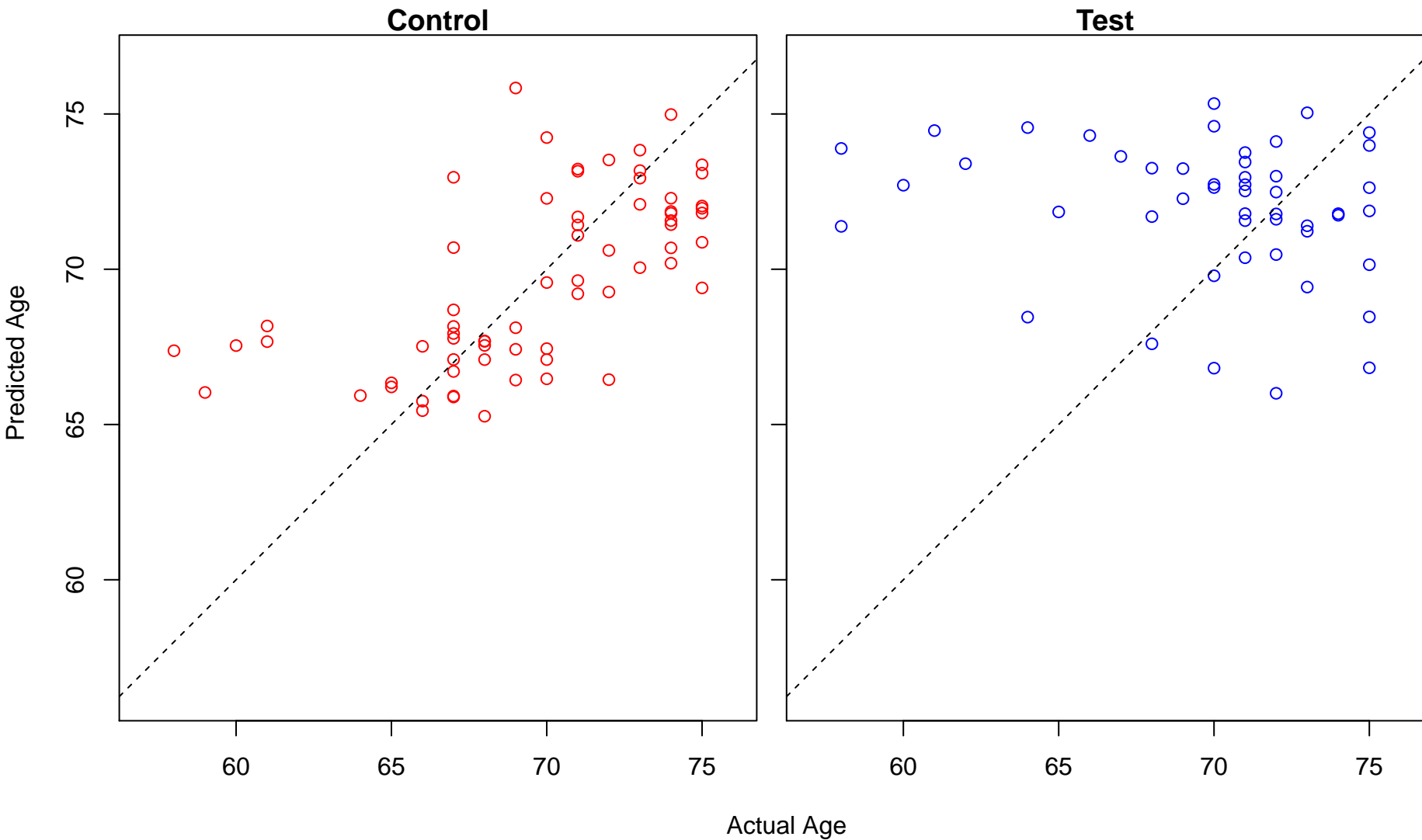
intracellular protein transmembrane import (Score: 1.304043)



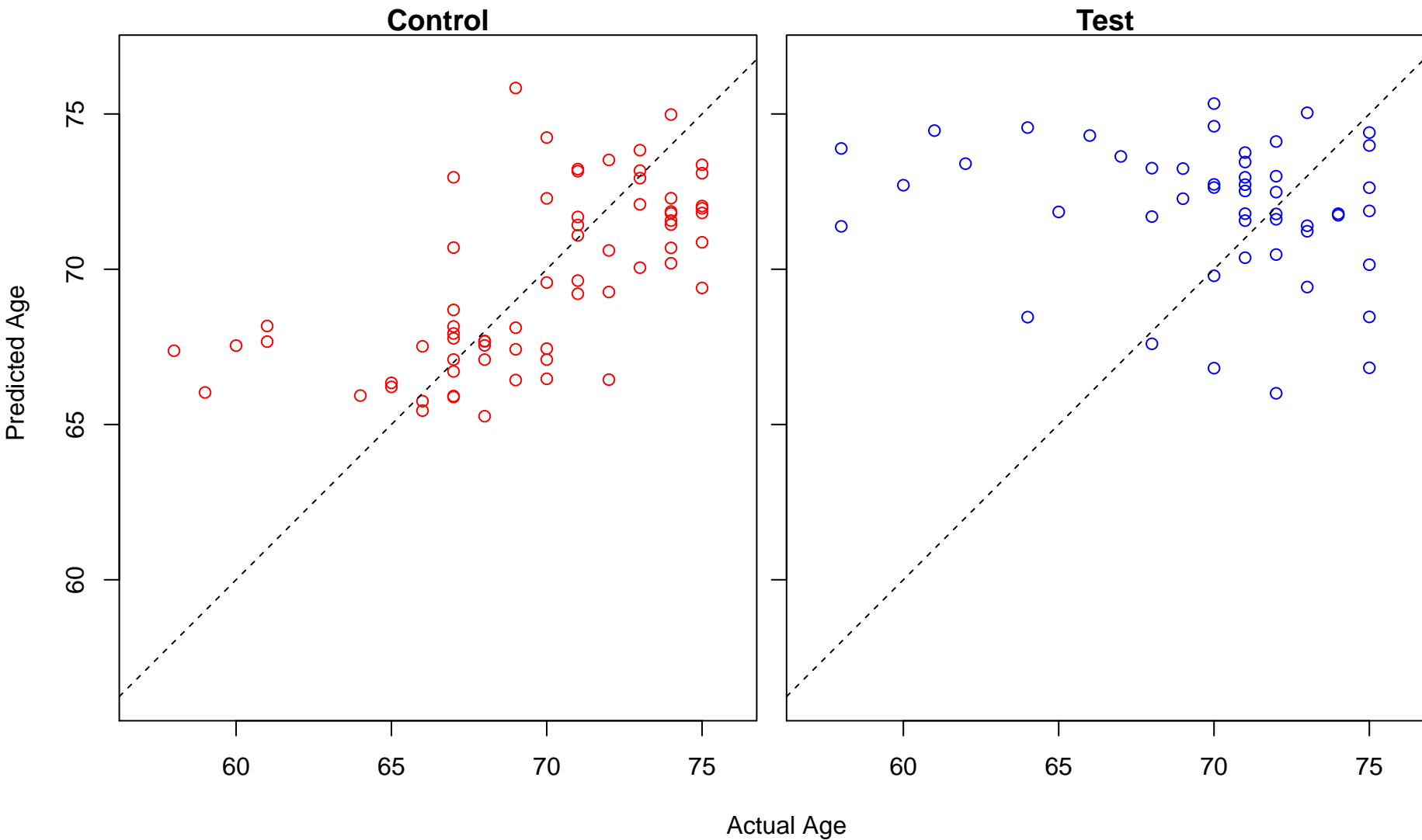
skeletal system development (Score: 1.303517)



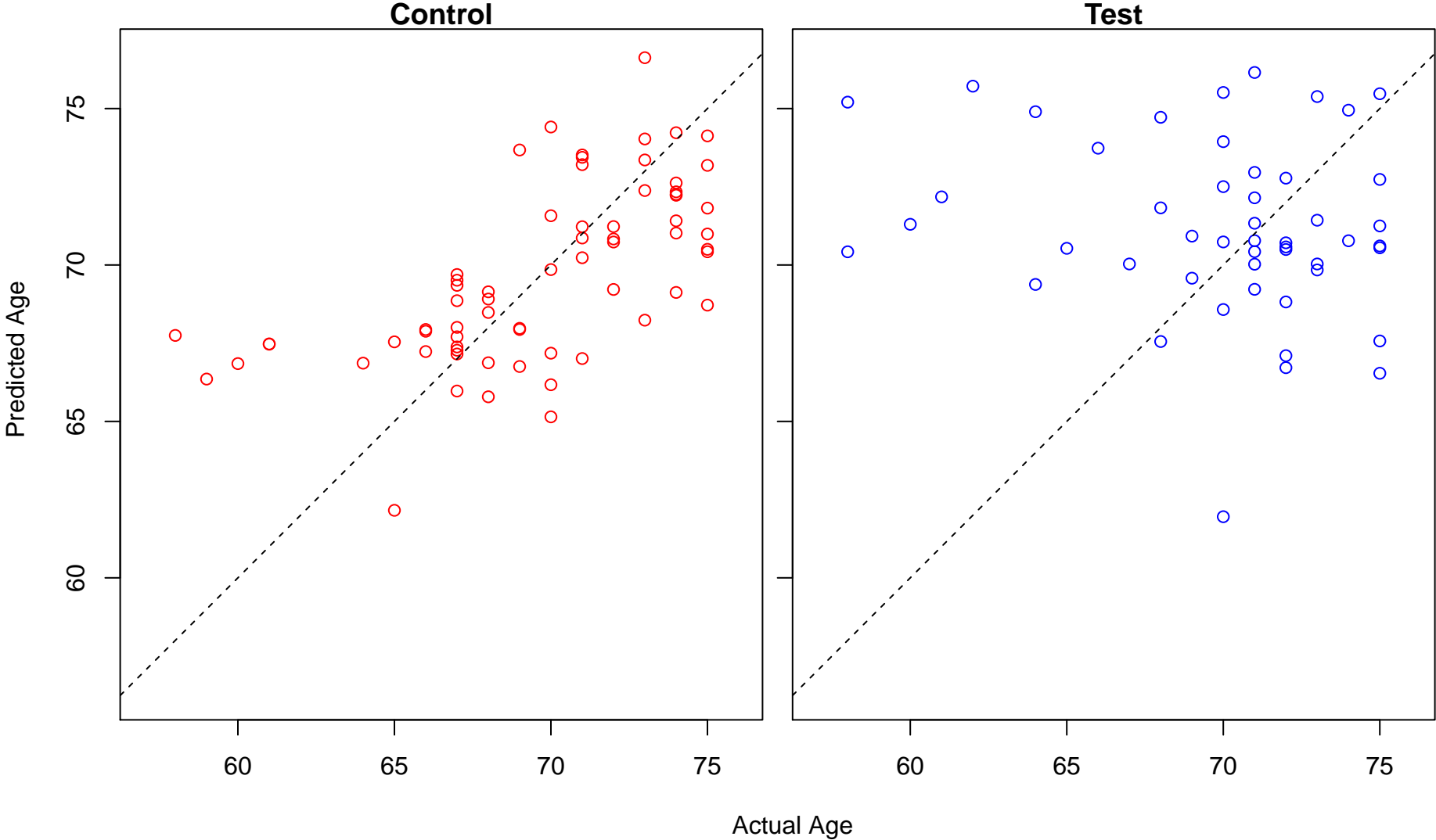
negative regulation of stress-activated MAPK cascade (Score: 1.303190)



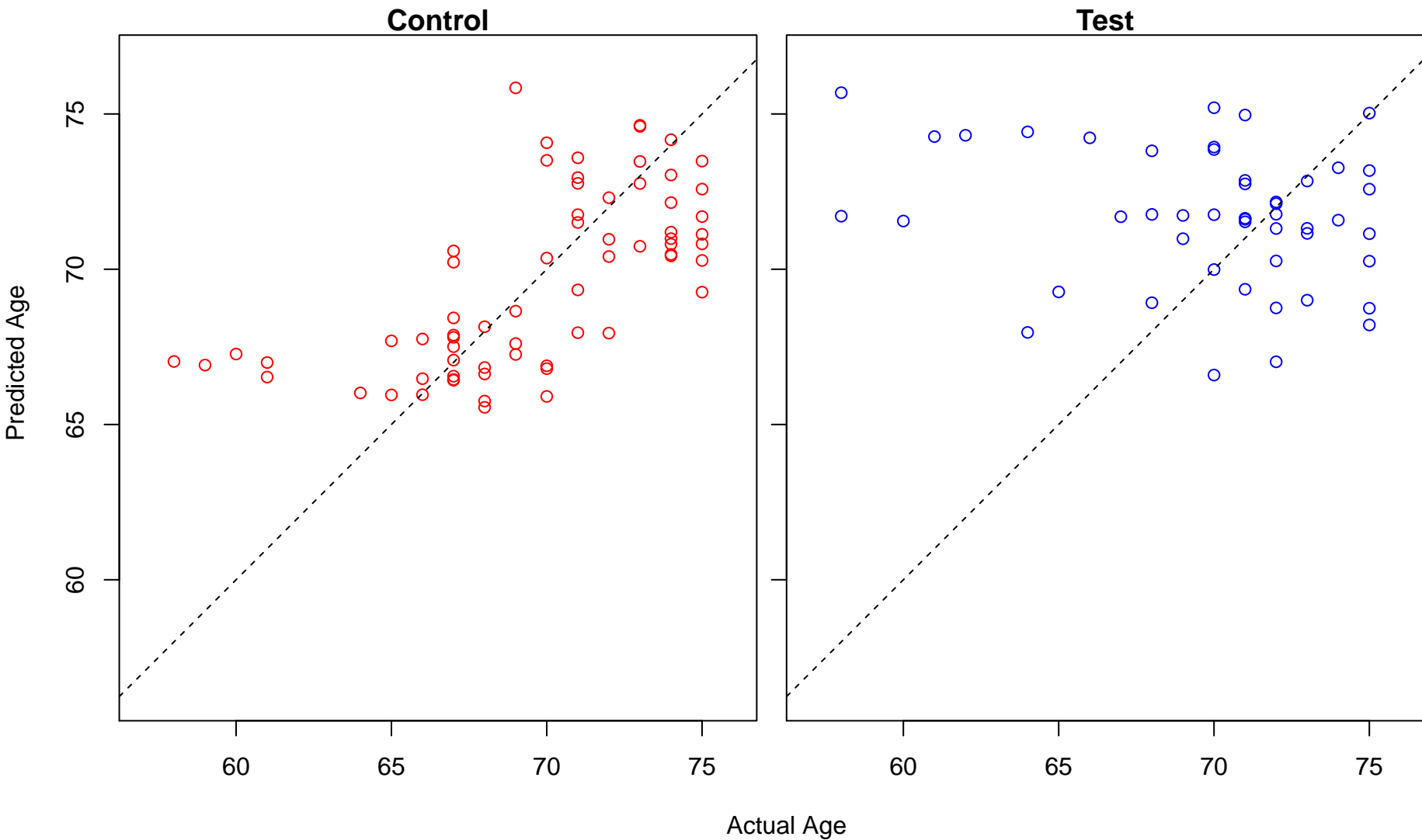
negative regulation of stress-activated protein kinase signaling cascade (Score: 1.303190)



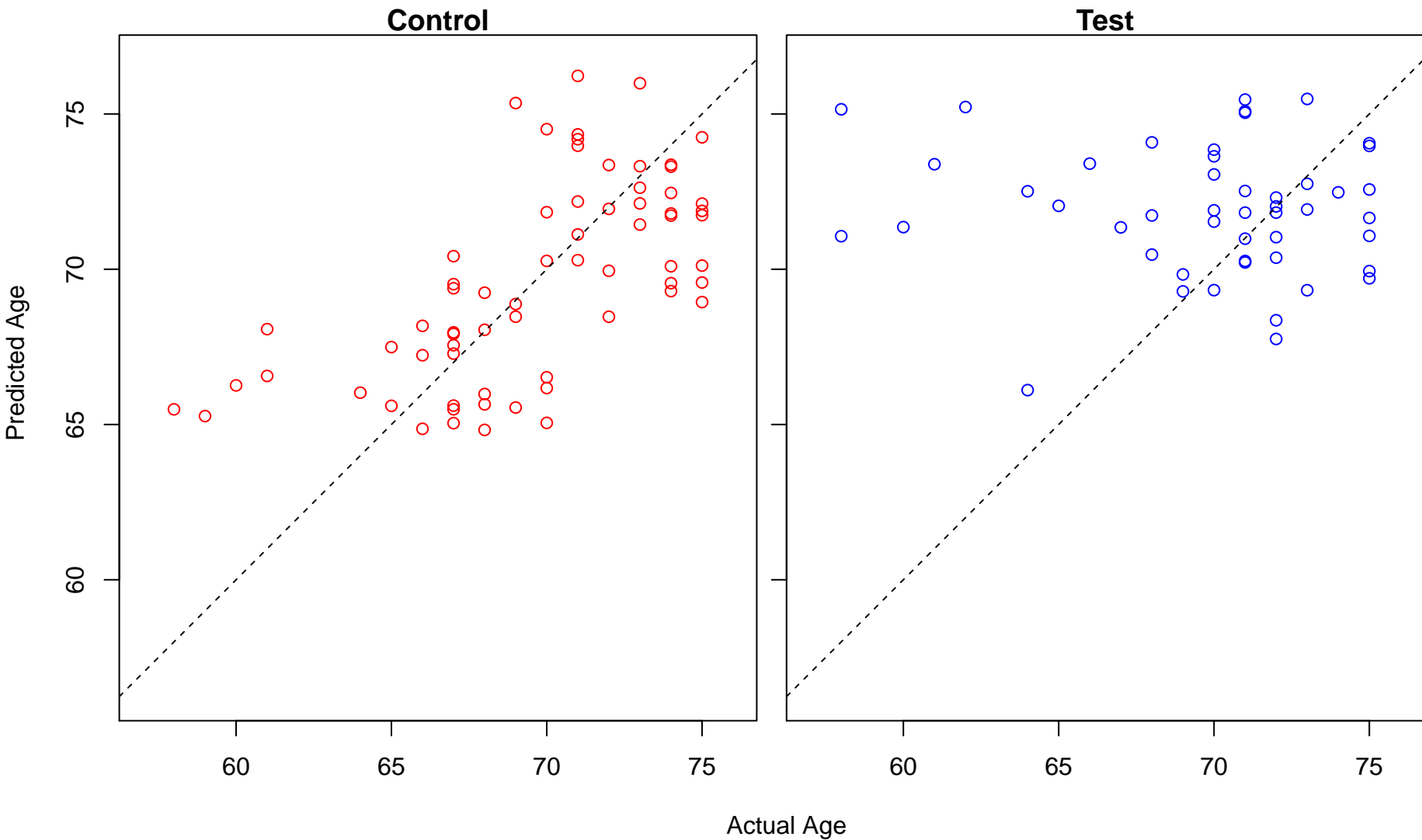
positive regulation of calcium ion transmembrane transport (Score: 1.302190)



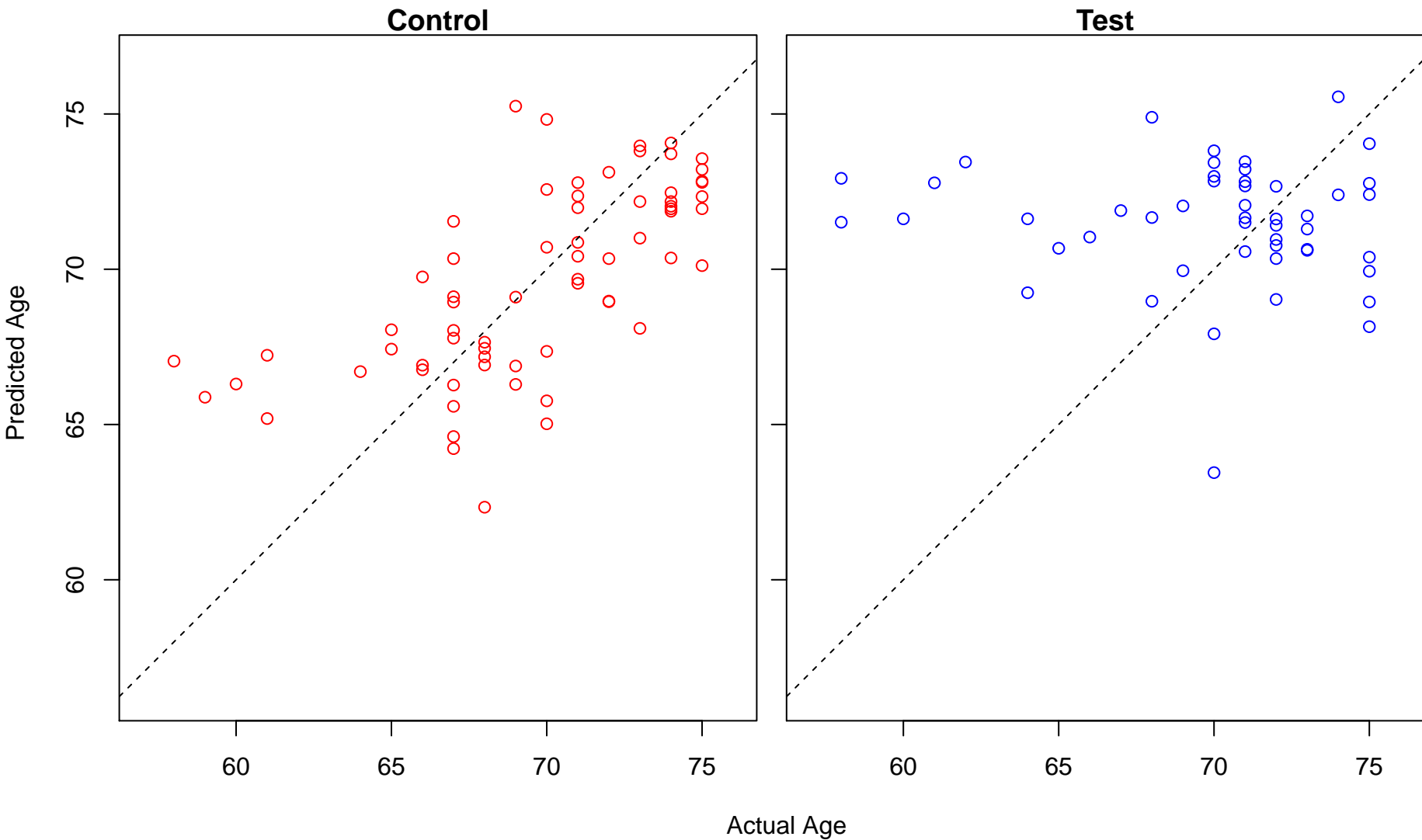
muscle structure development (Score: 1.301221)



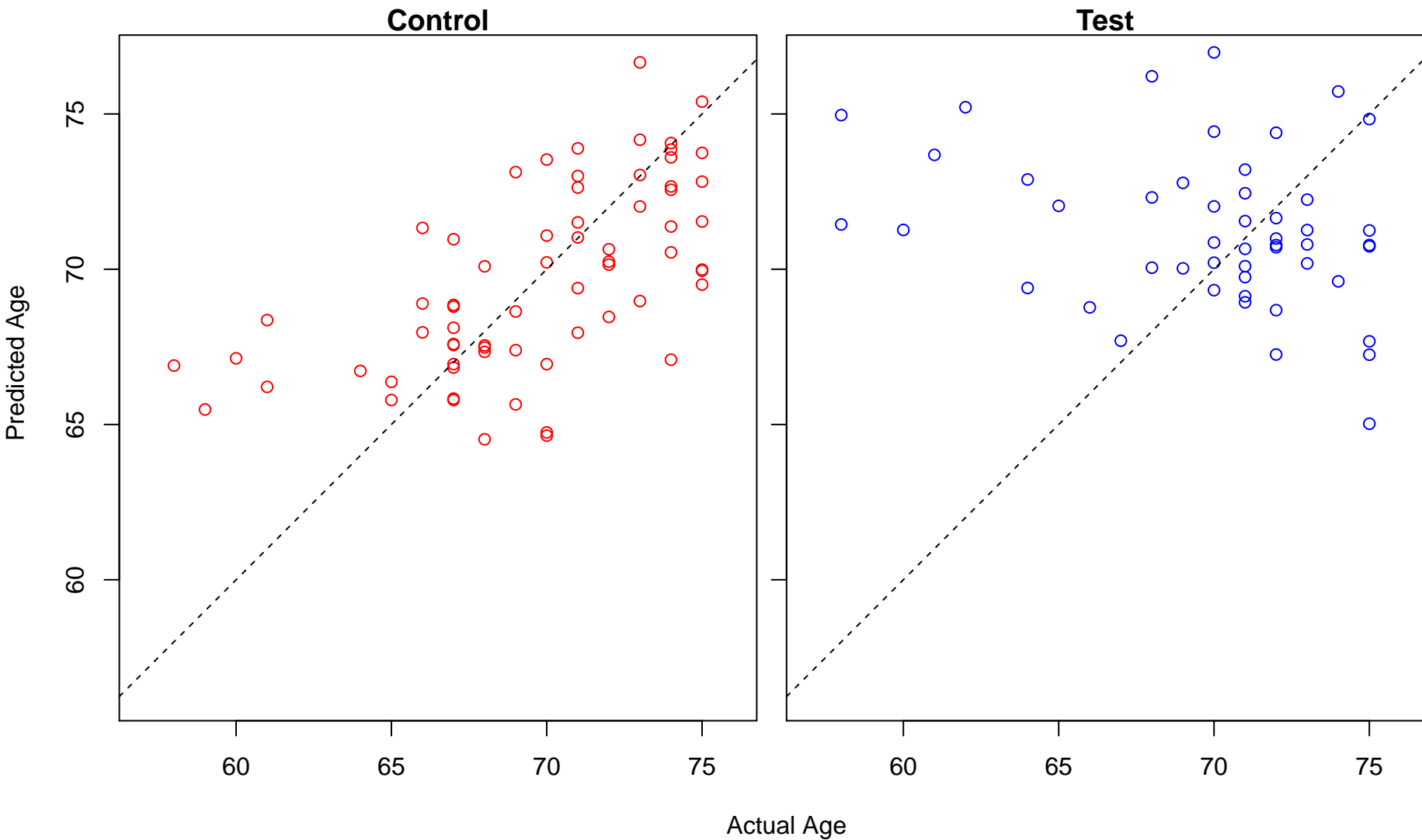
tissue homeostasis (Score: 1.300715)



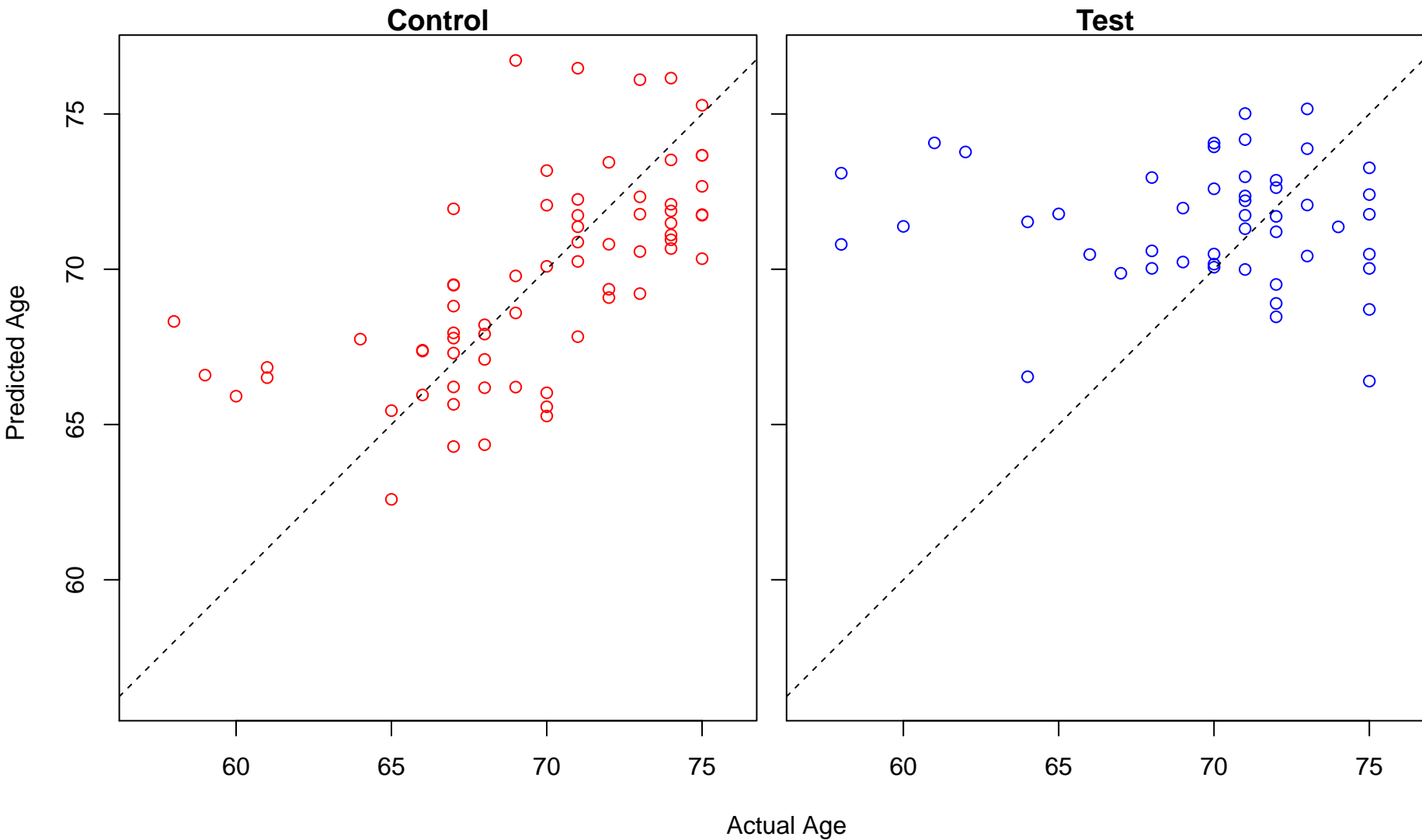
leukocyte apoptotic process (Score: 1.300584)



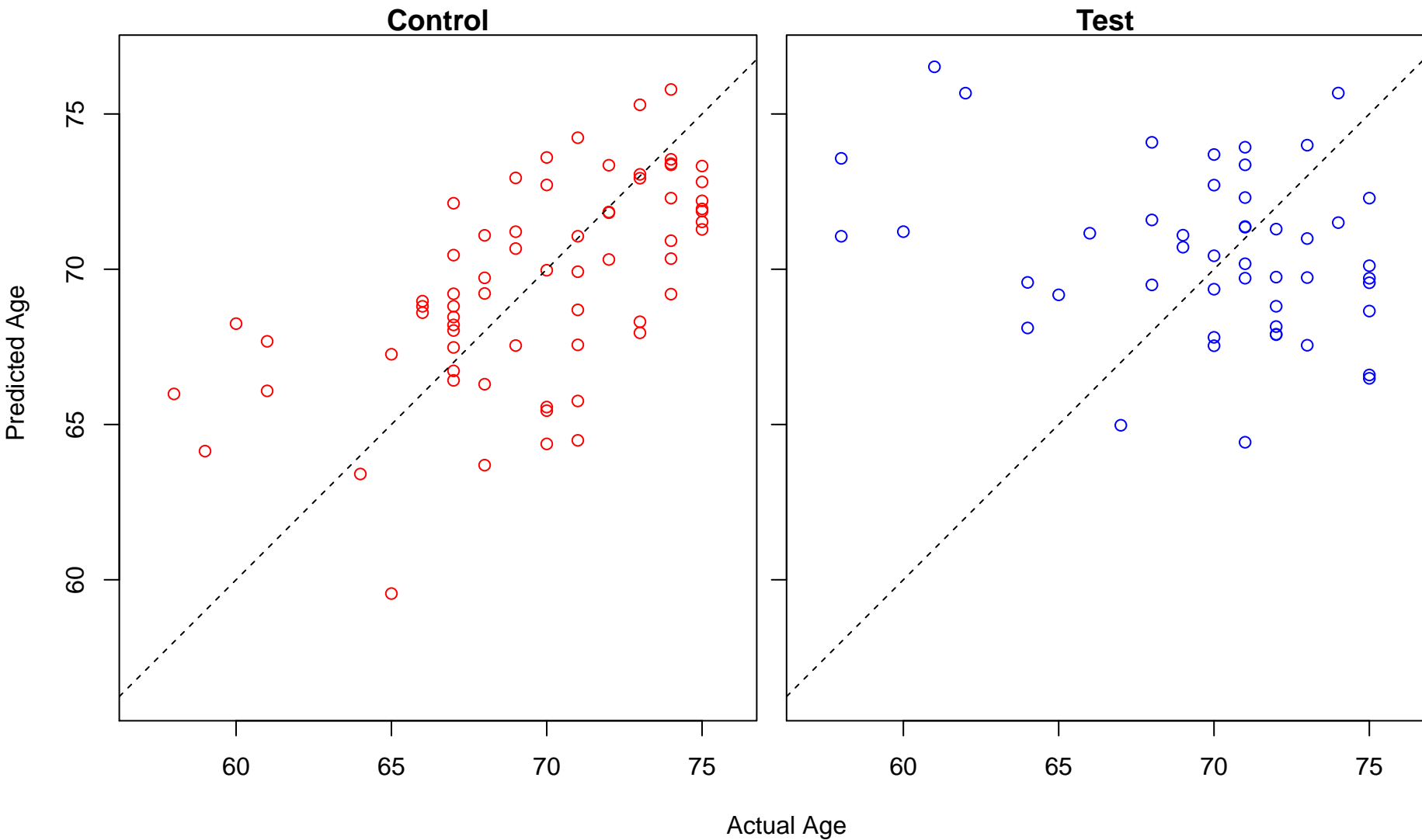
cellular response to epidermal growth factor stimulus (Score: 1.300480)



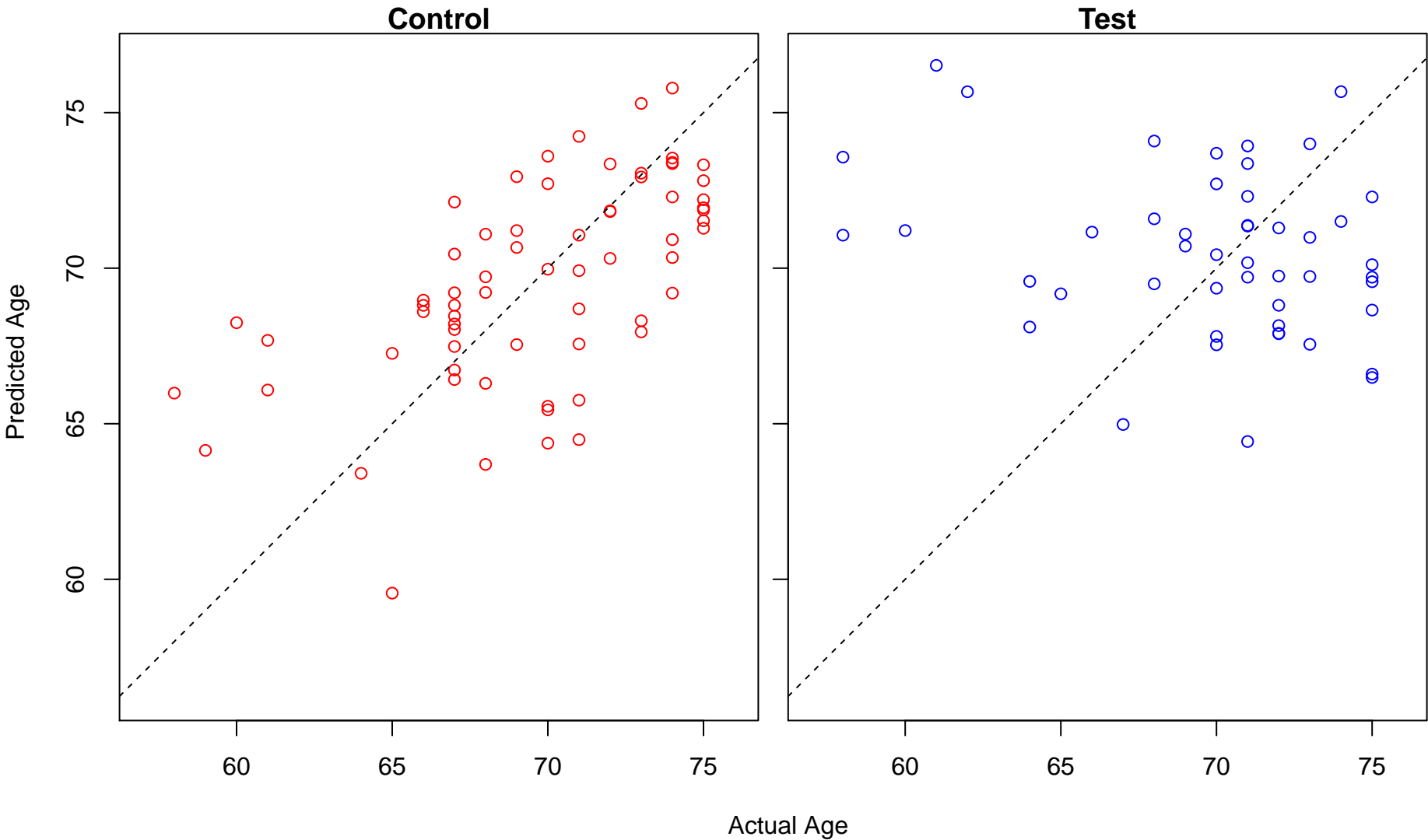
protein homotetramerization (Score: 1.299811)



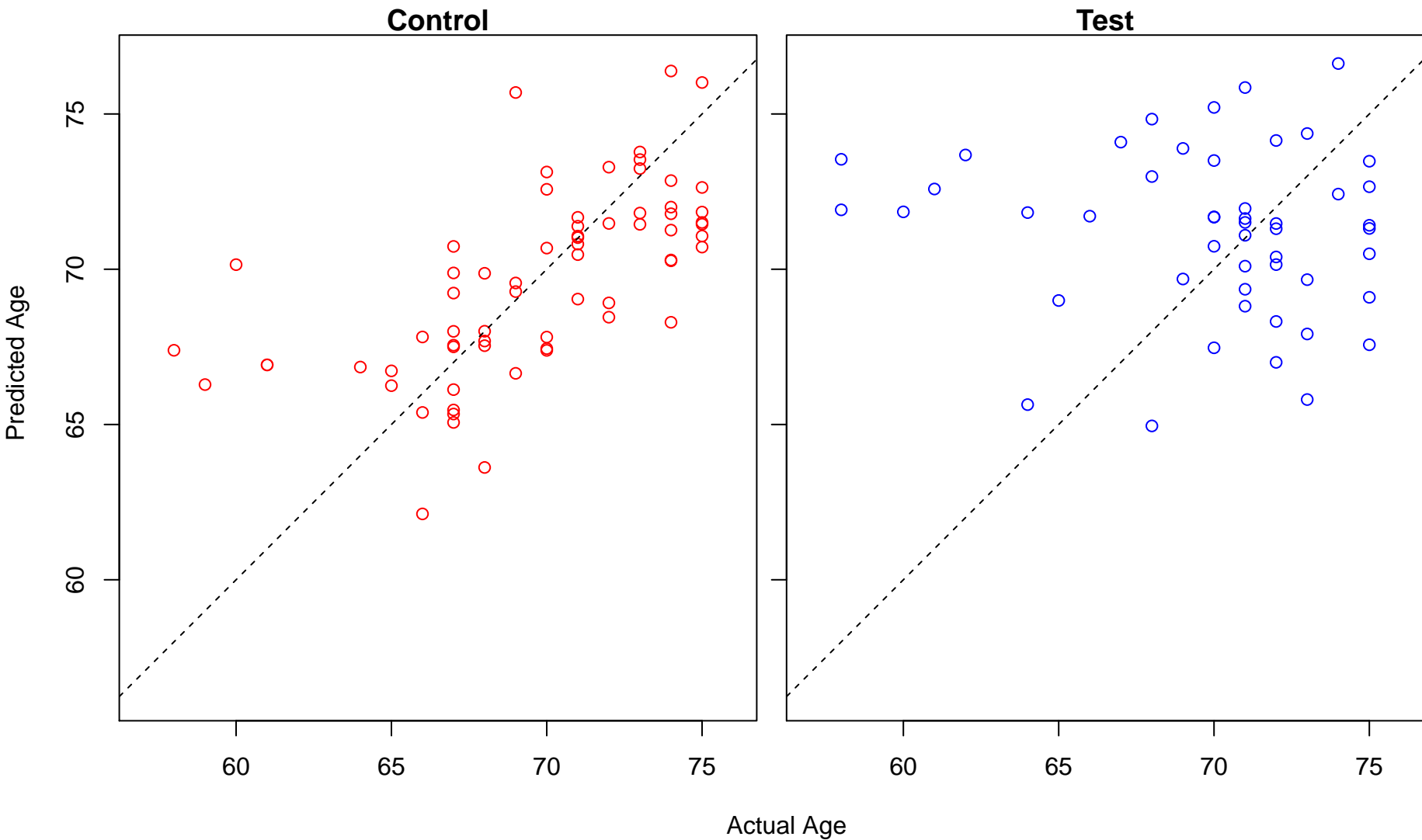
negative regulation of signal transduction in absence of ligand (Score: 1.299531)



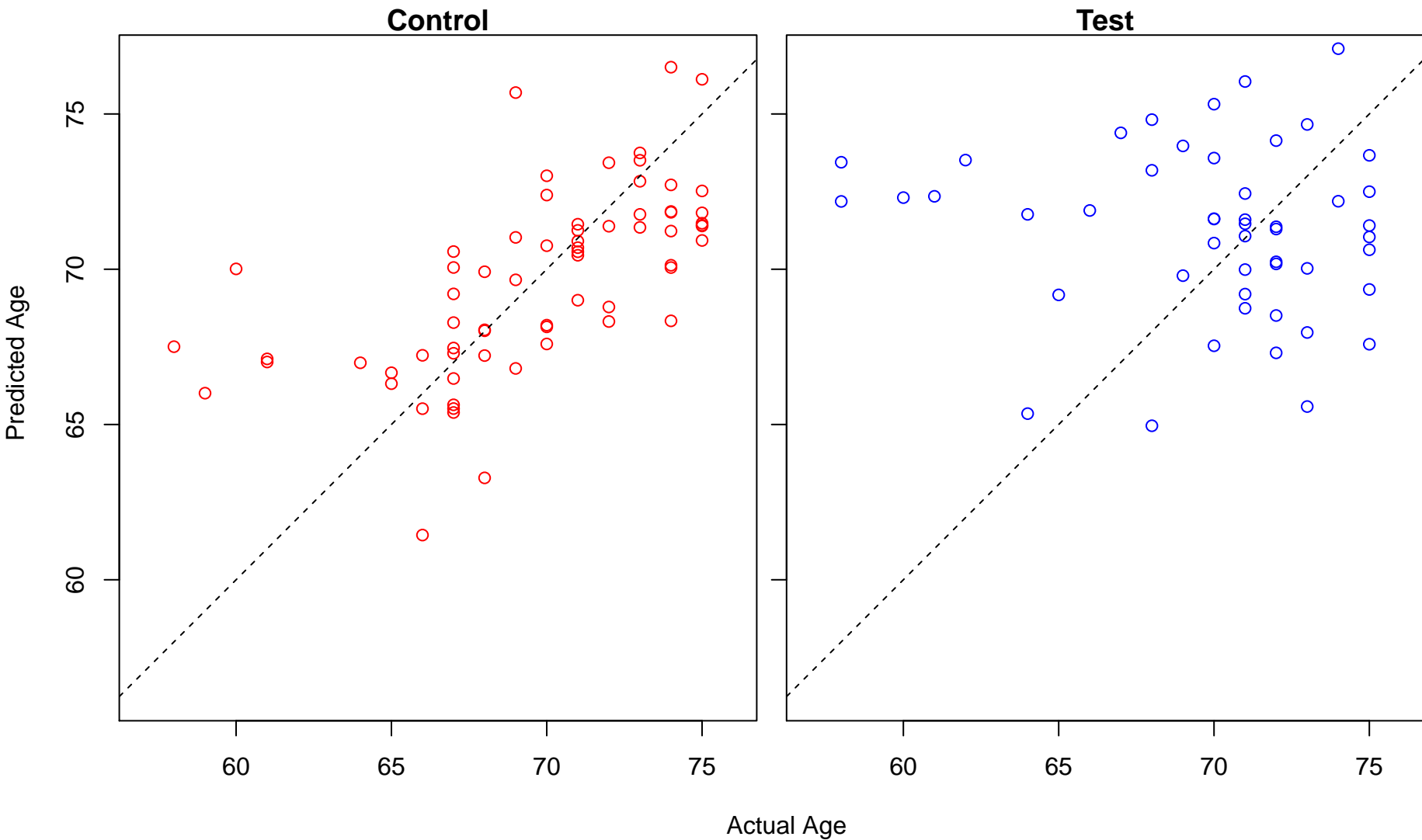
negative regulation of extrinsic apoptotic signaling pathway in absence of ligand (Score: 1.299531



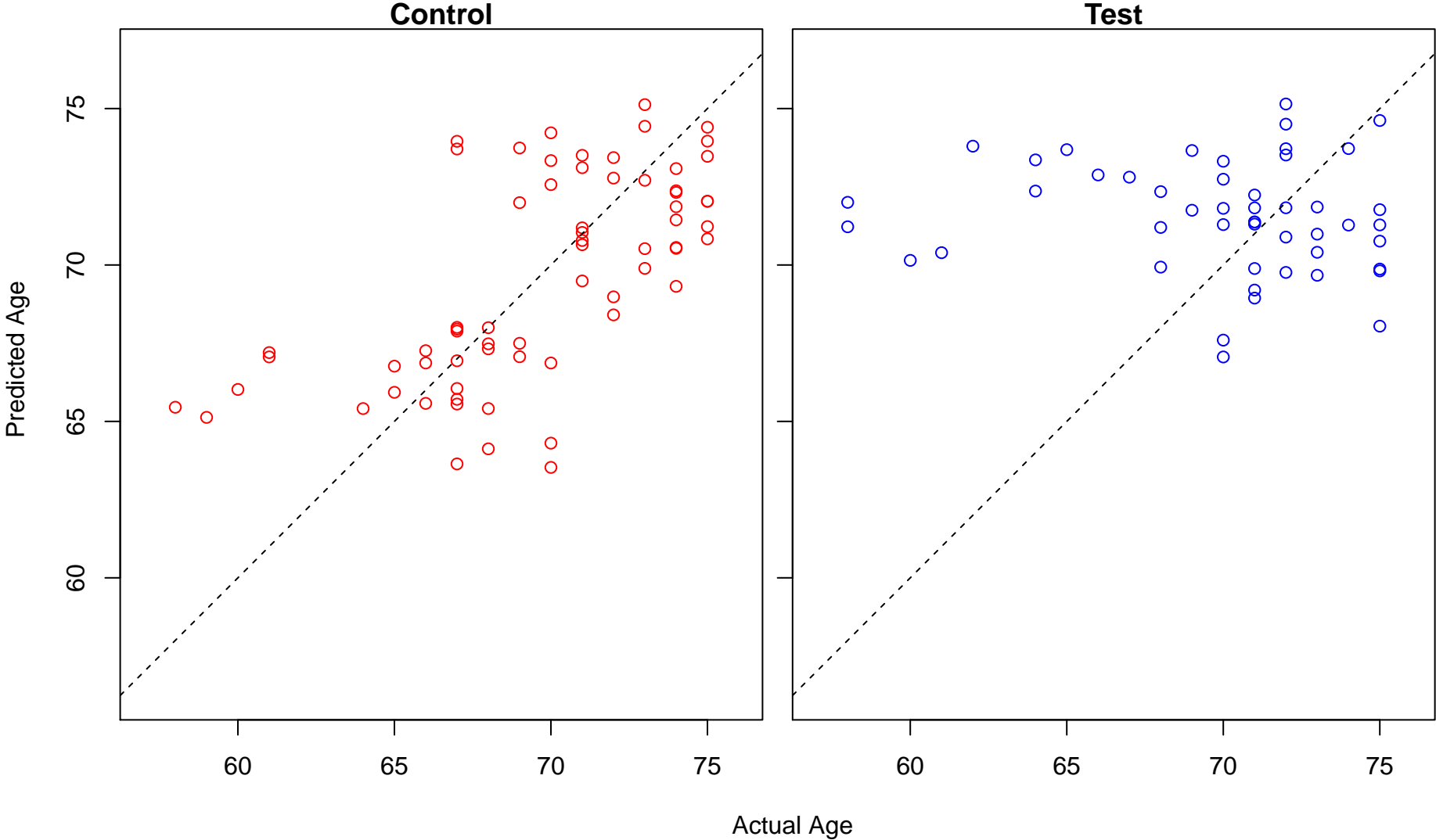
response to corticosteroid (Score: 1.298357)



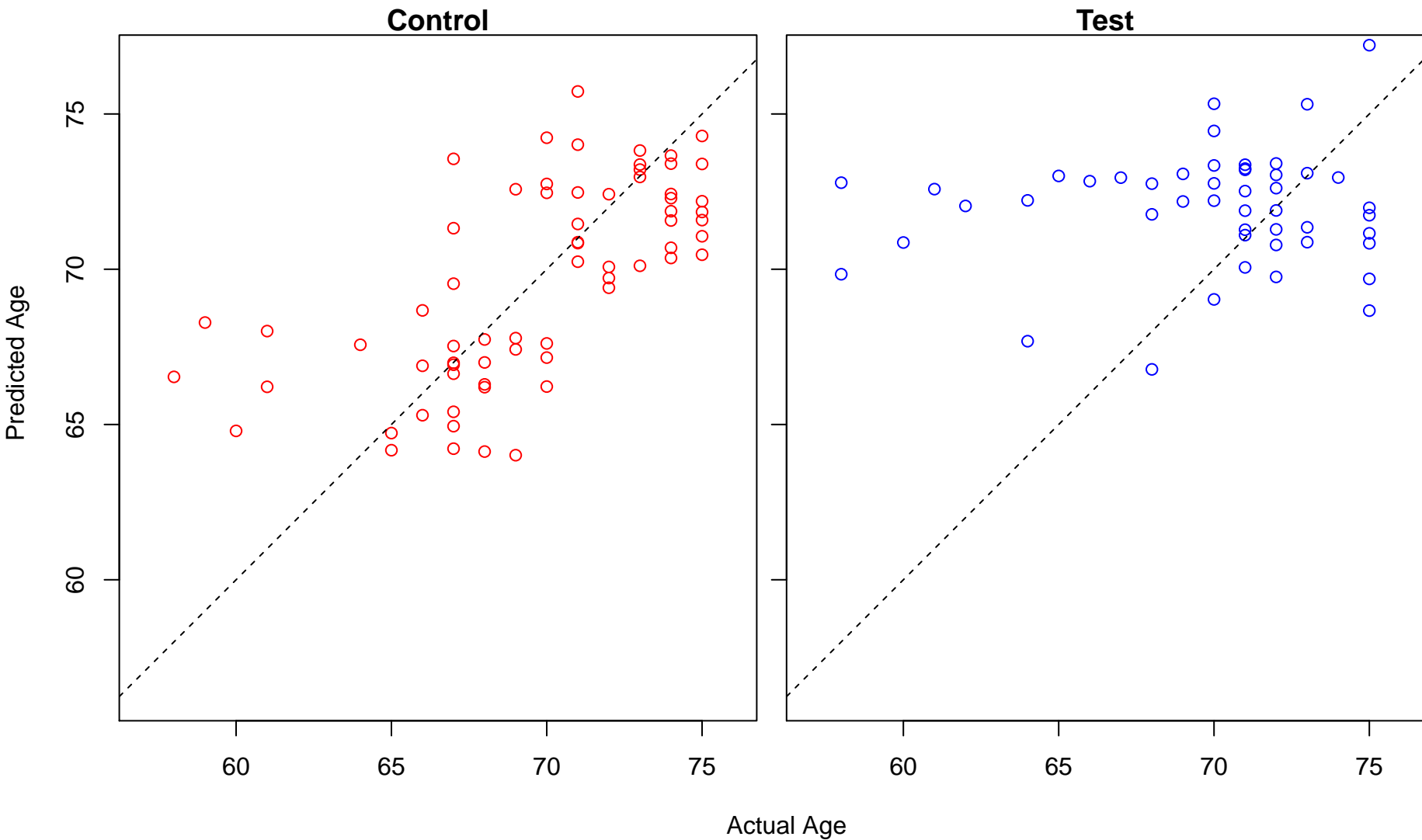
response to glucocorticoid (Score: 1.298321)



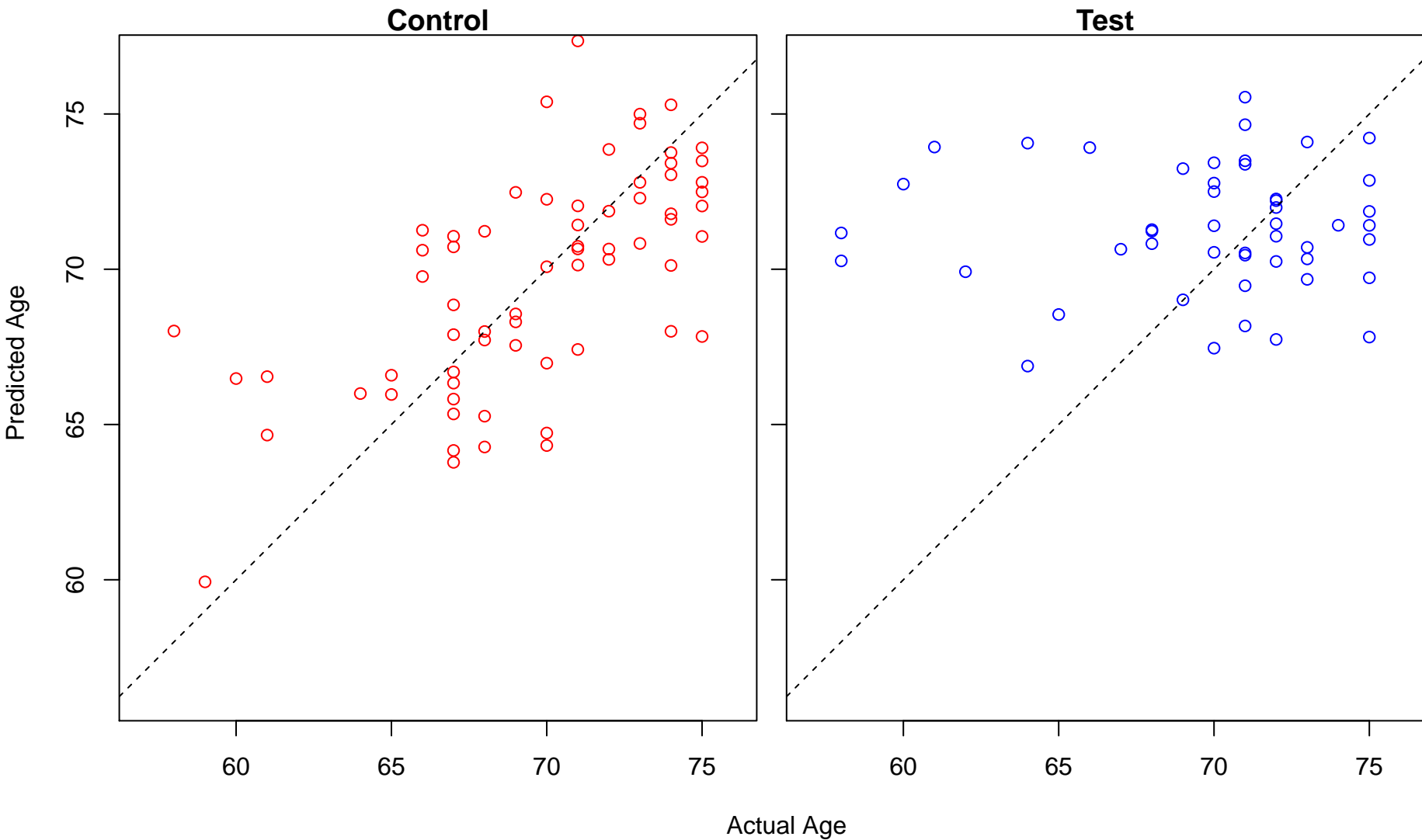
SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (Score: 1.298065)



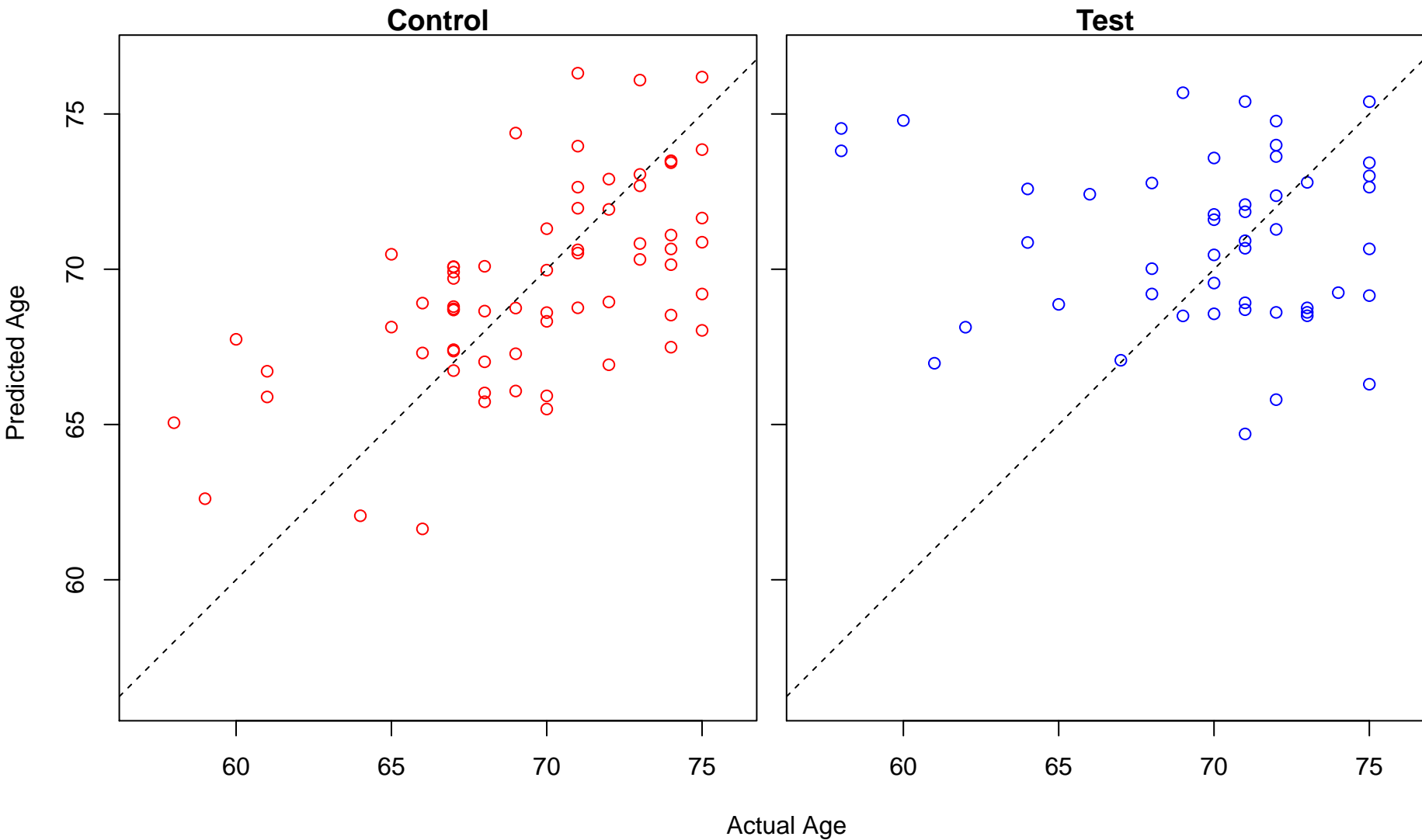
nucleosome organization (Score: 1.297941)



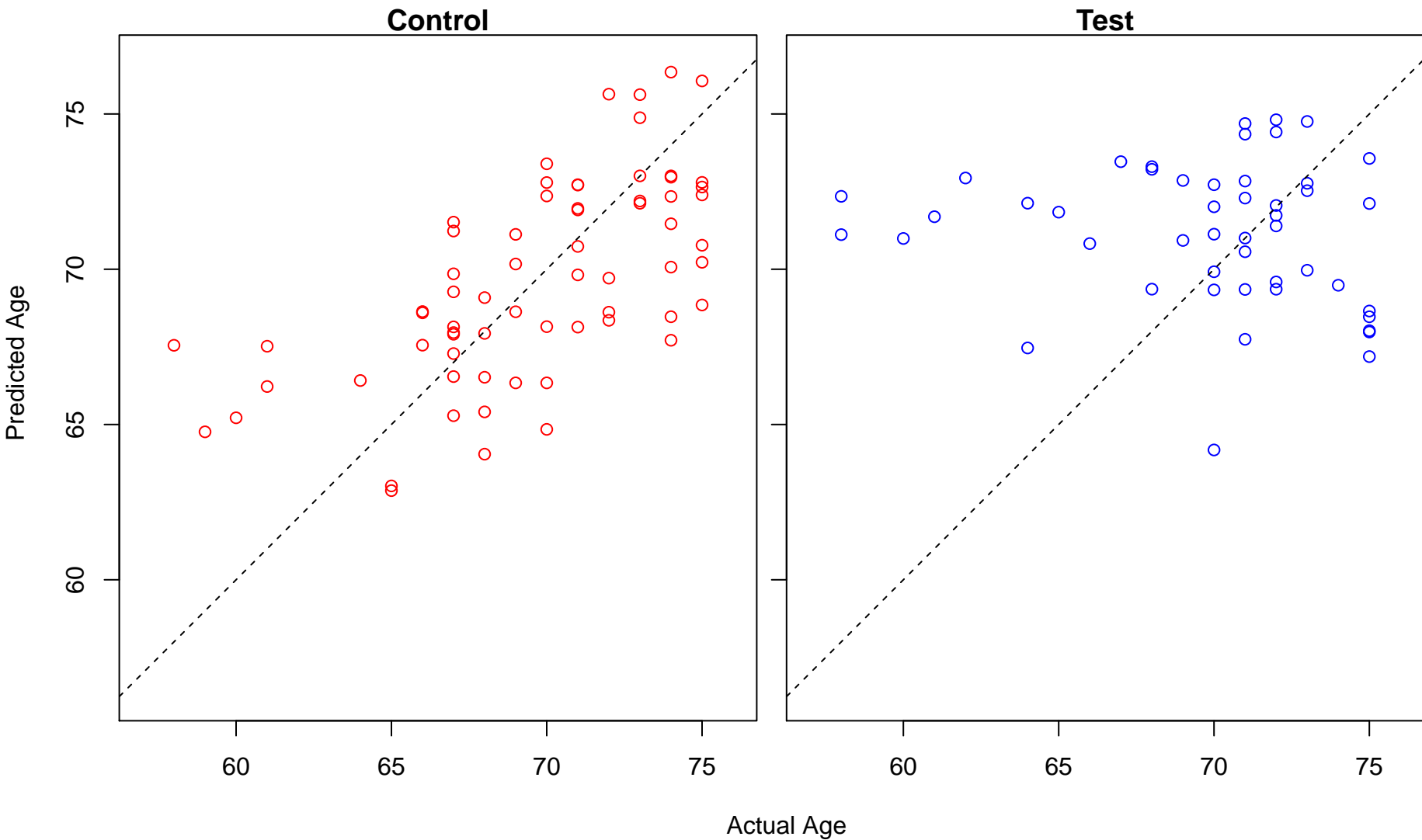
nucleoside catabolic process (Score: 1.297912)



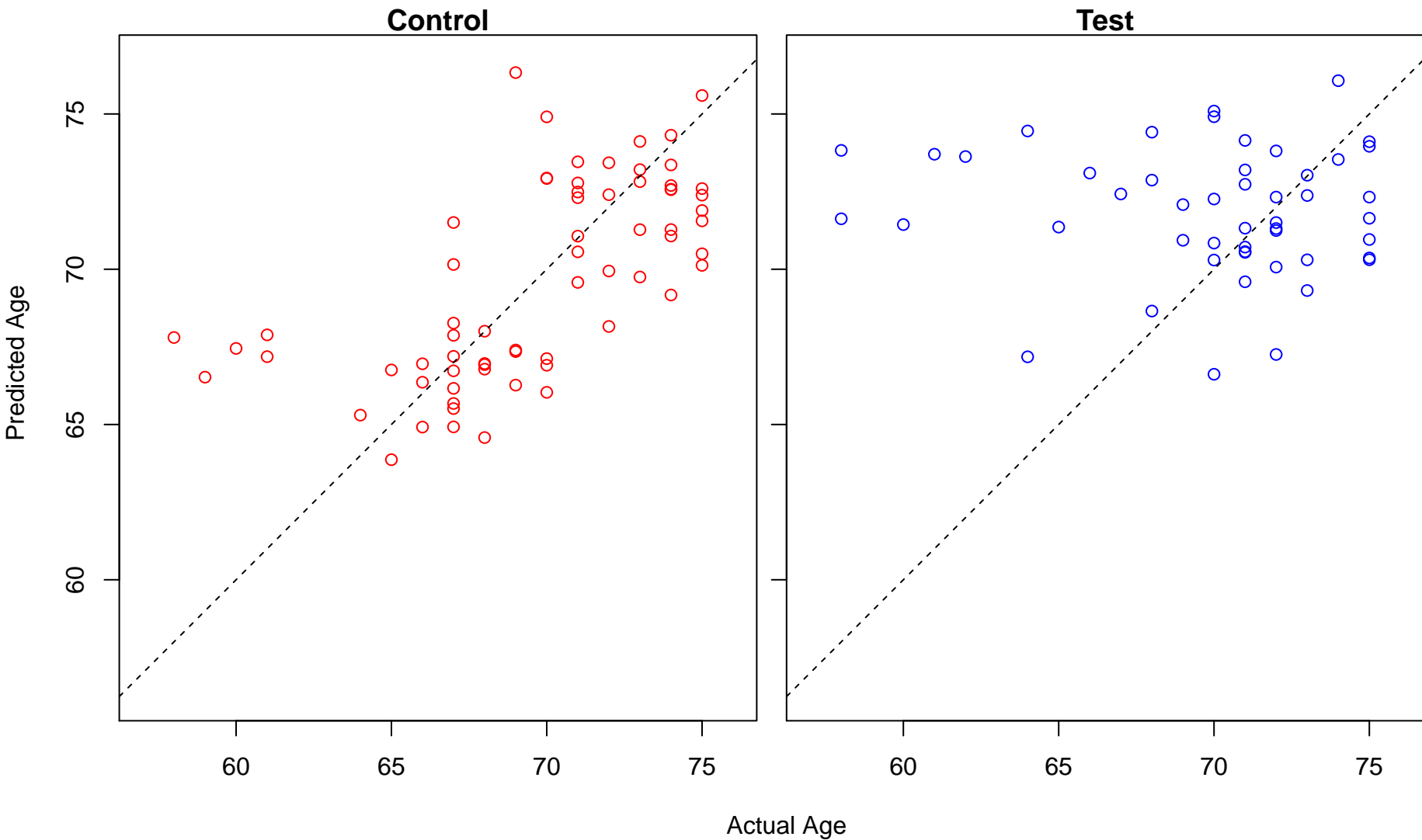
positive regulation of lyase activity (Score: 1.297435)



calcium ion transport into cytosol (Score: 1.297431)

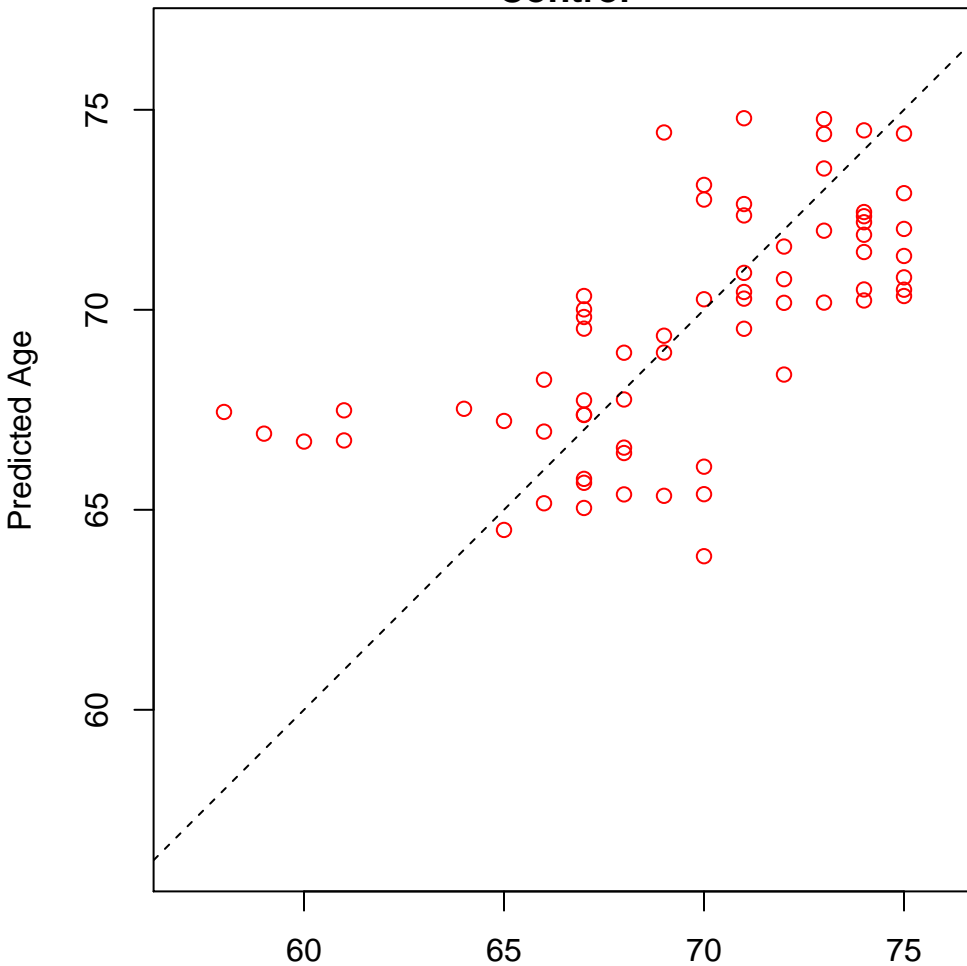


regulation of JNK cascade (Score: 1.296746)

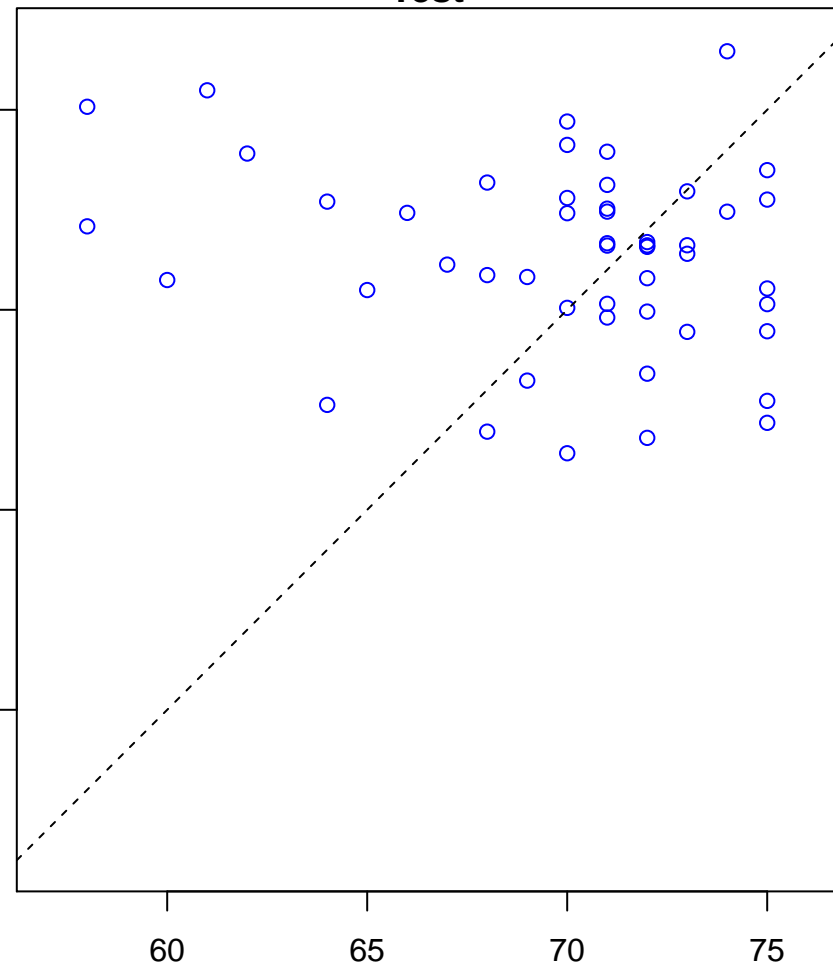


water-soluble vitamin metabolic process (Score: 1.296422)

Control

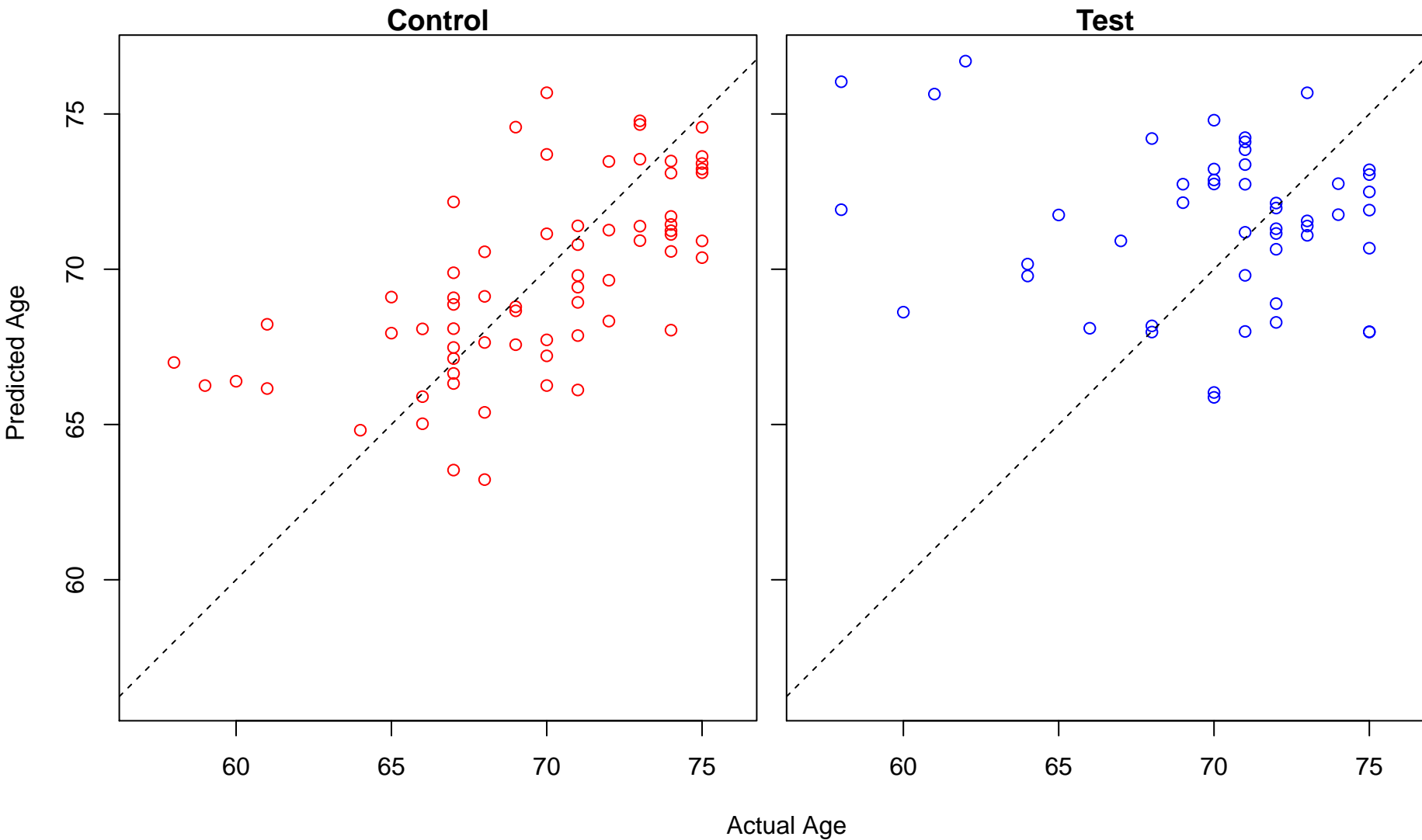


Test



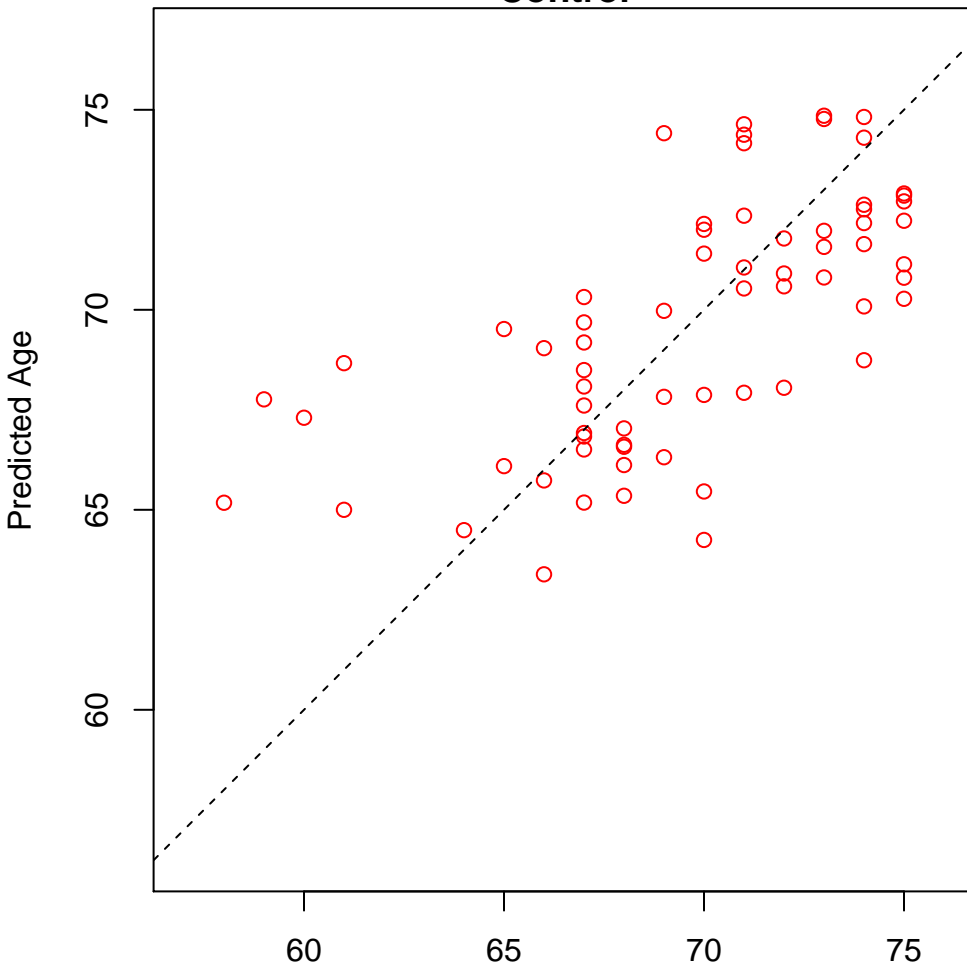
Actual Age

cellular response to alcohol (Score: 1.296297)

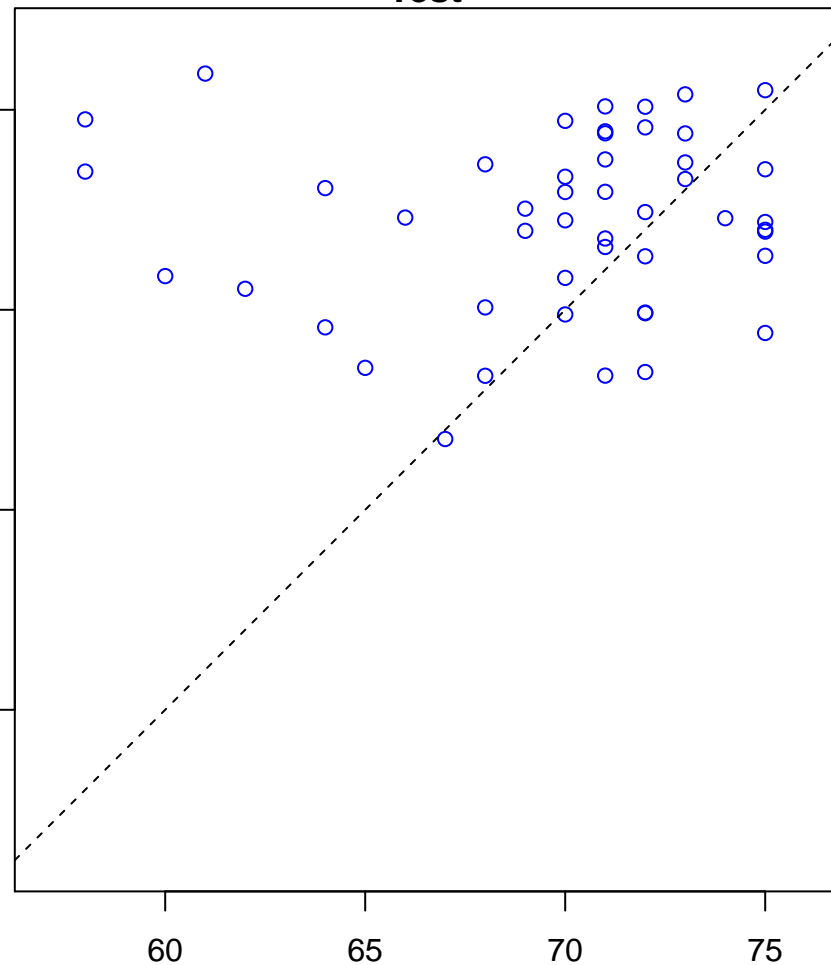


cardiac chamber morphogenesis (Score: 1.295555)

Control

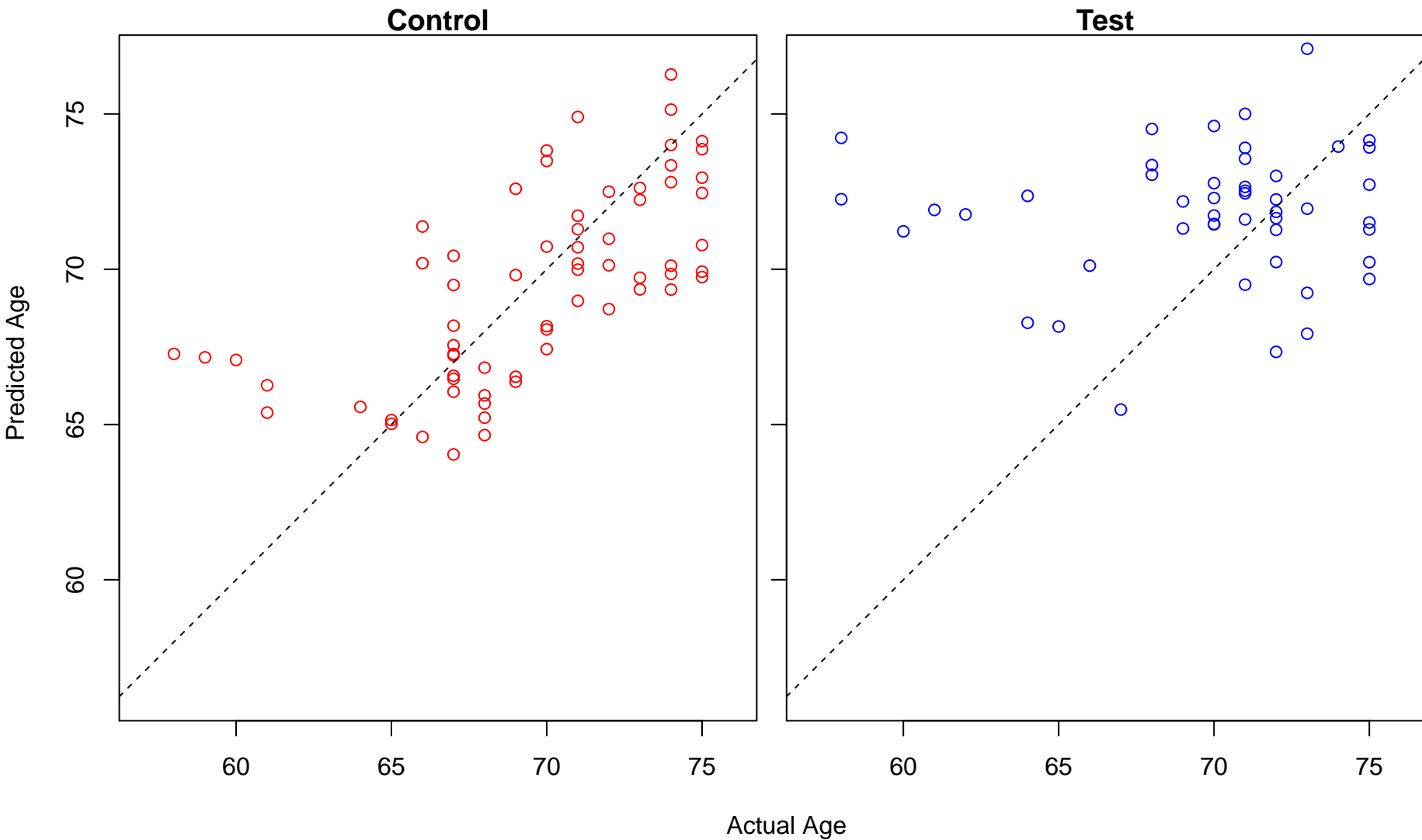


Test

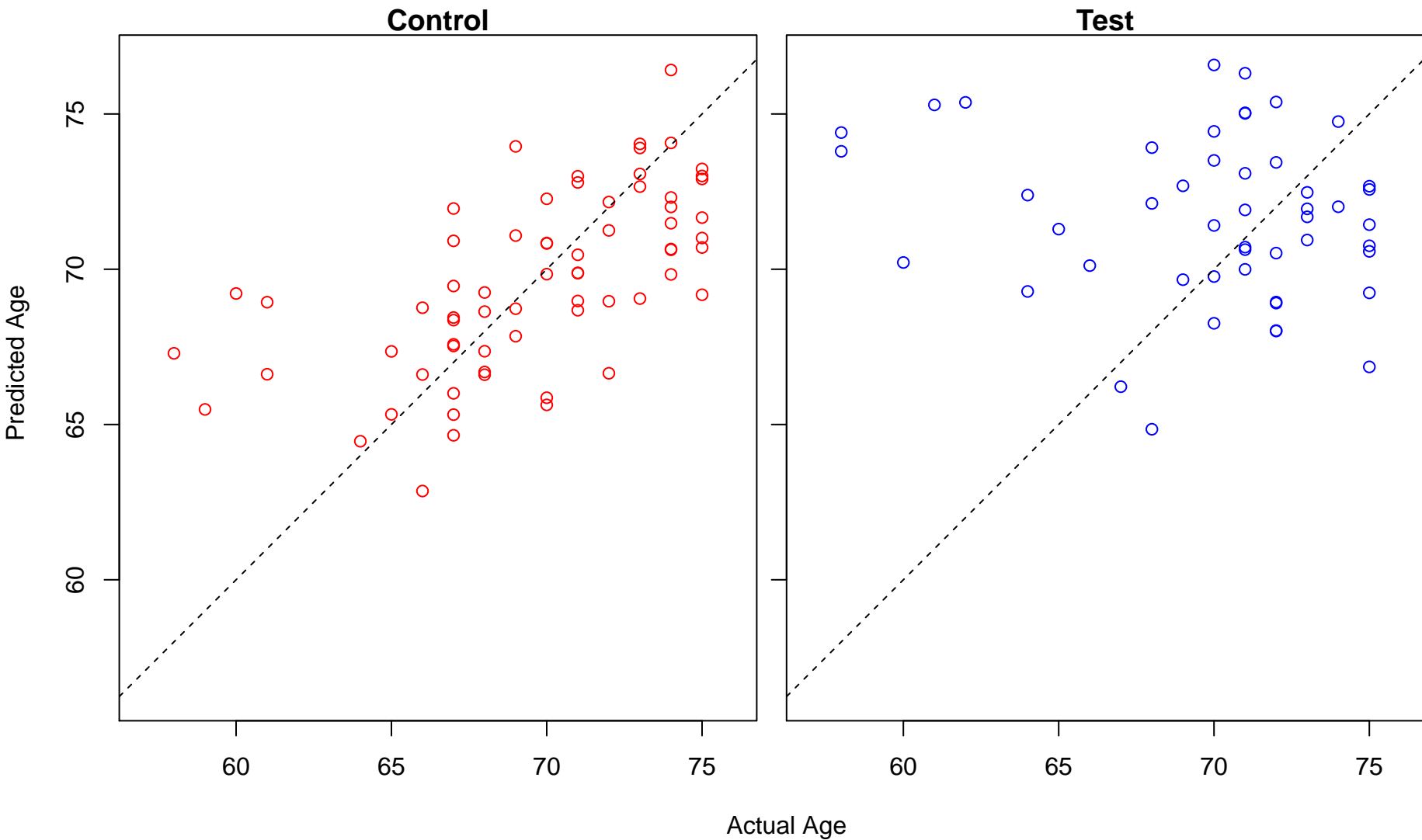


Actual Age

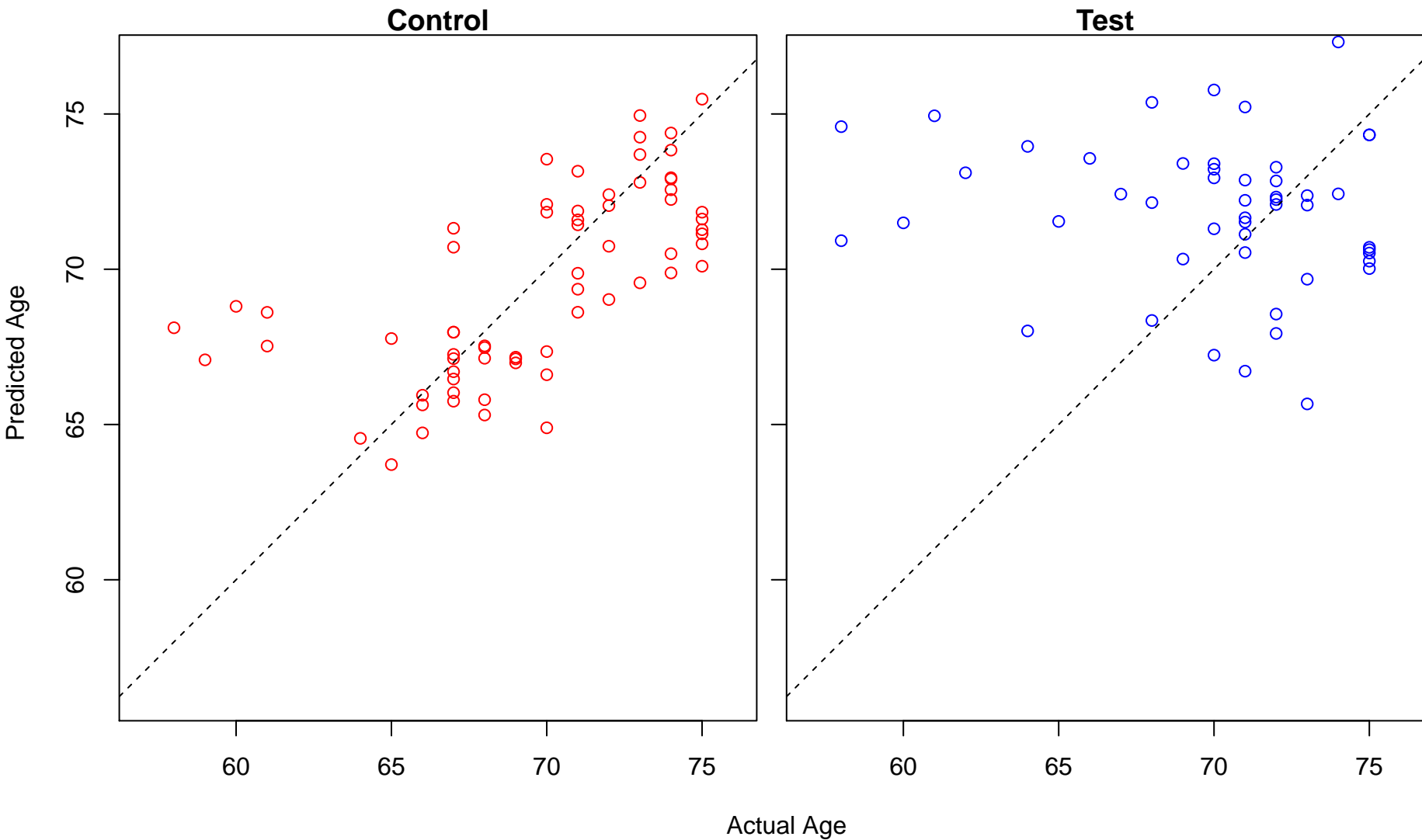
cytoskeleton-dependent intracellular transport (Score: 1.295182)



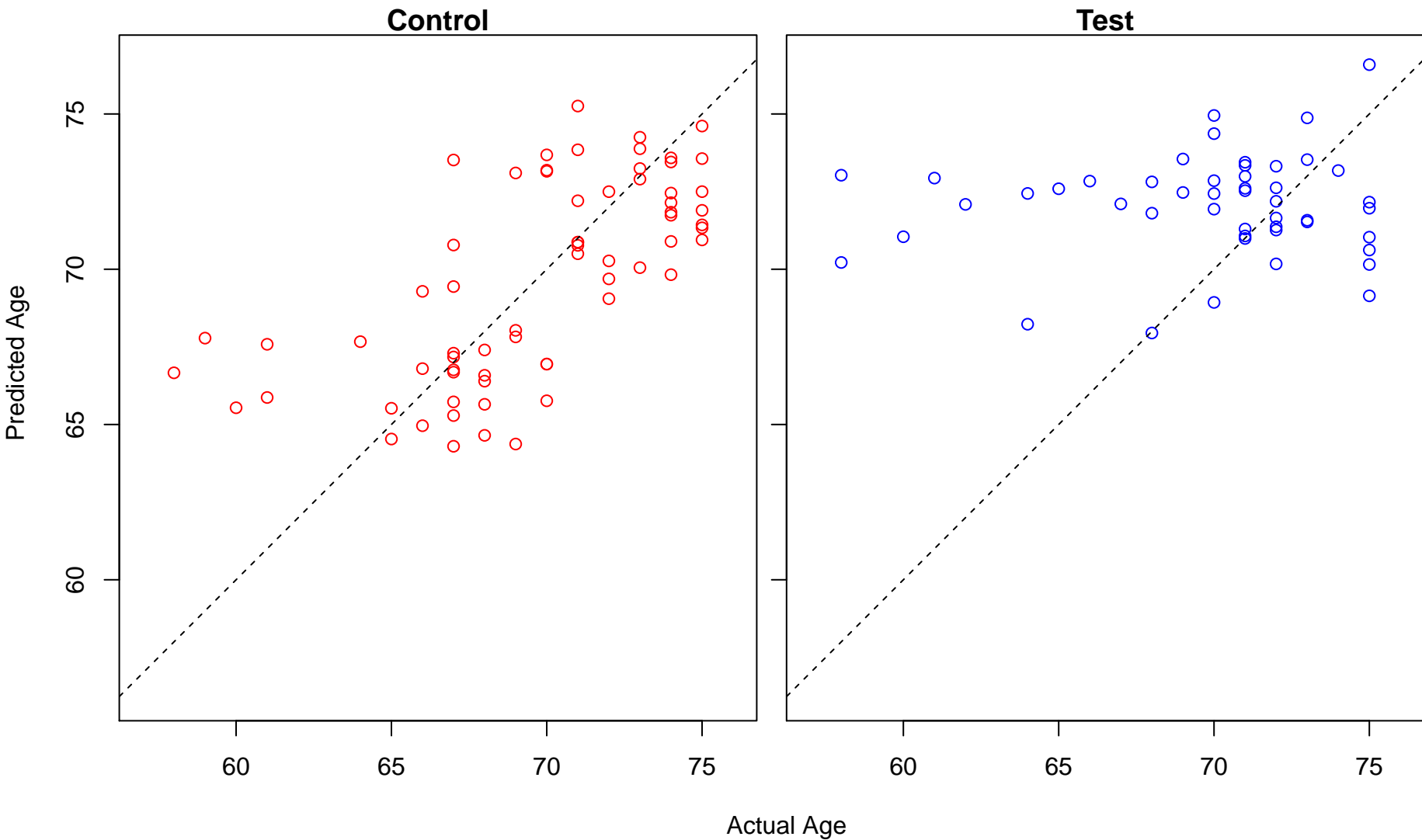
protein depolymerization (Score: 1.295136)



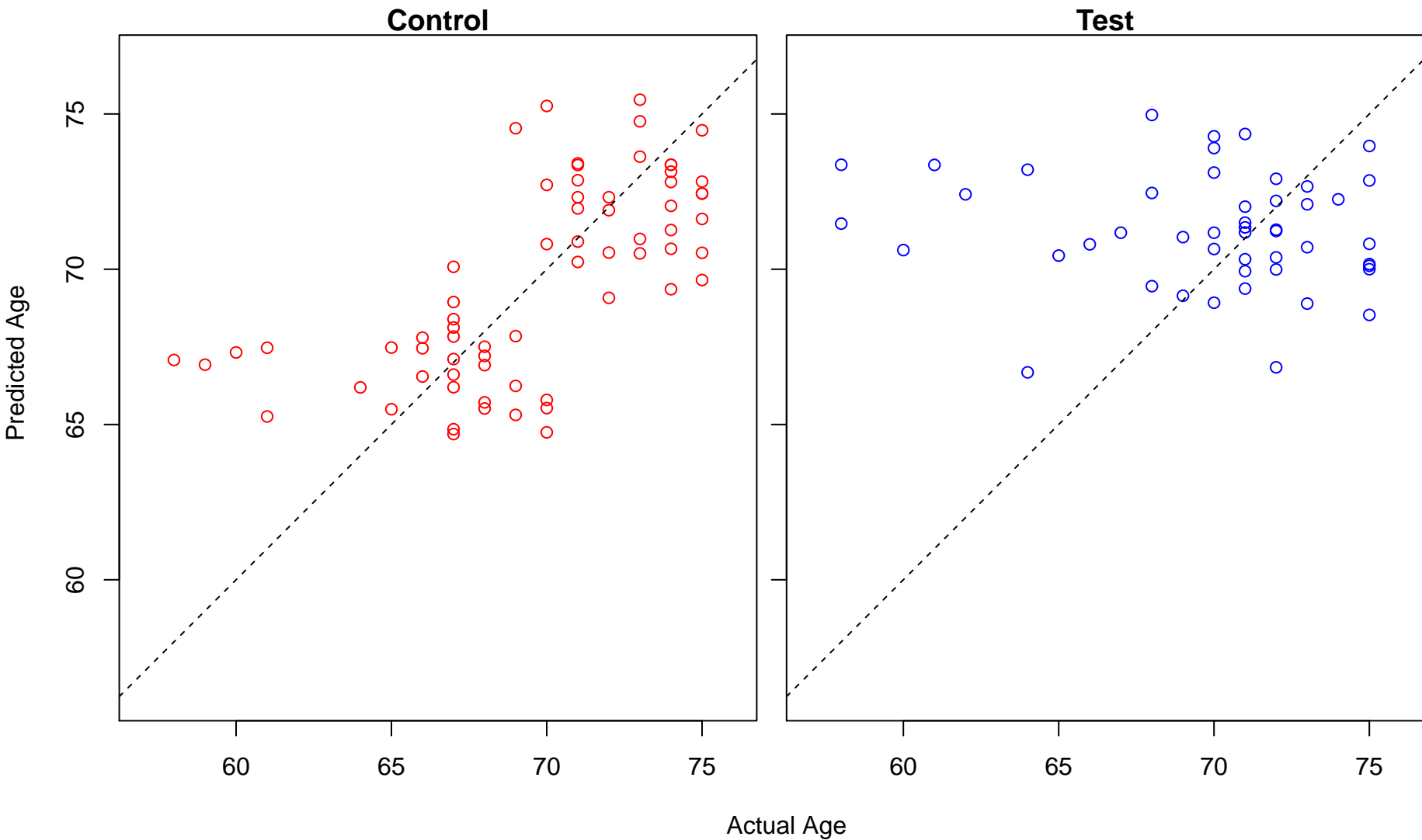
negative regulation of establishment of protein localization (Score: 1.294732)



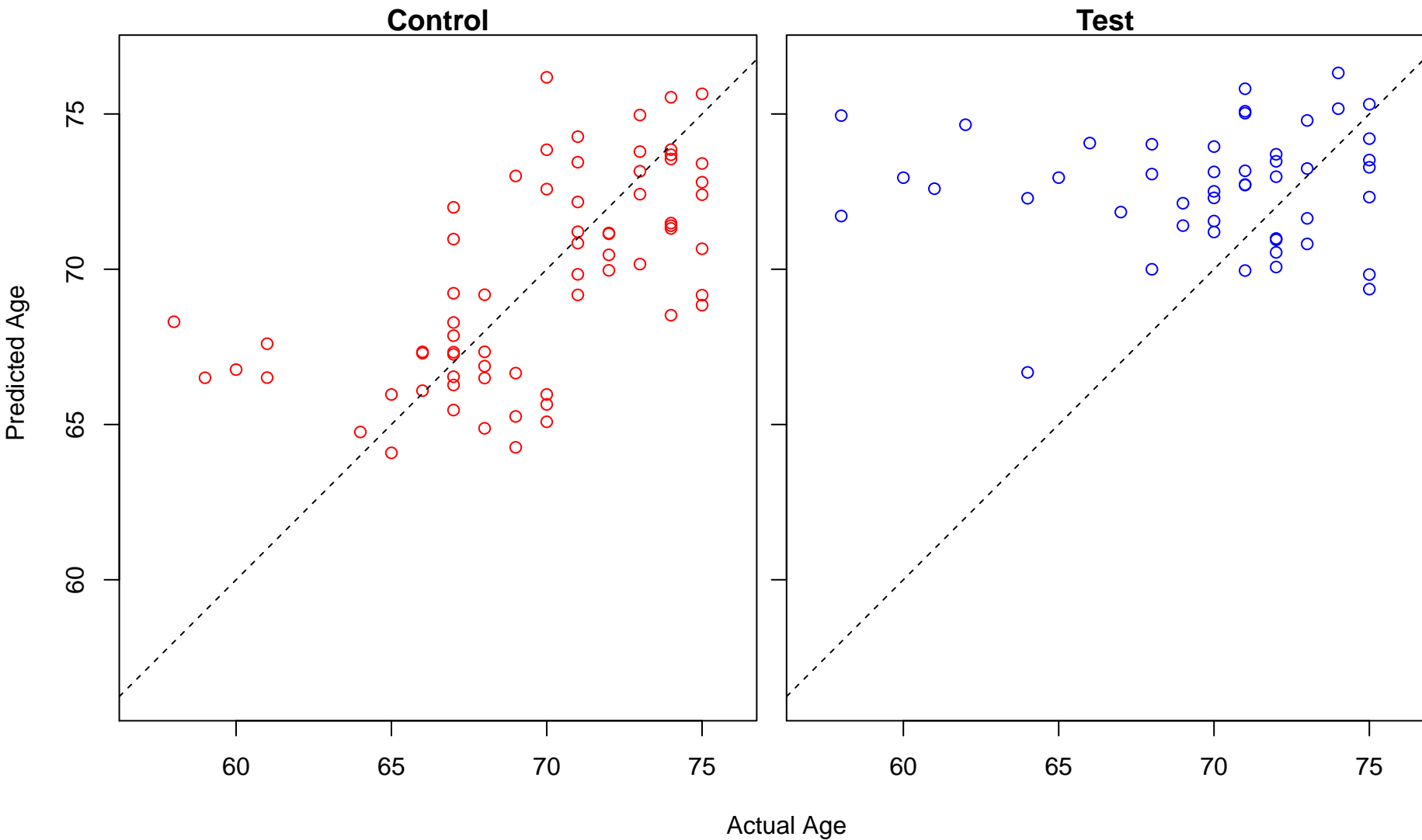
protein-DNA complex subunit organization (Score: 1.294391)



regulation of telomere maintenance (Score: 1.294289)

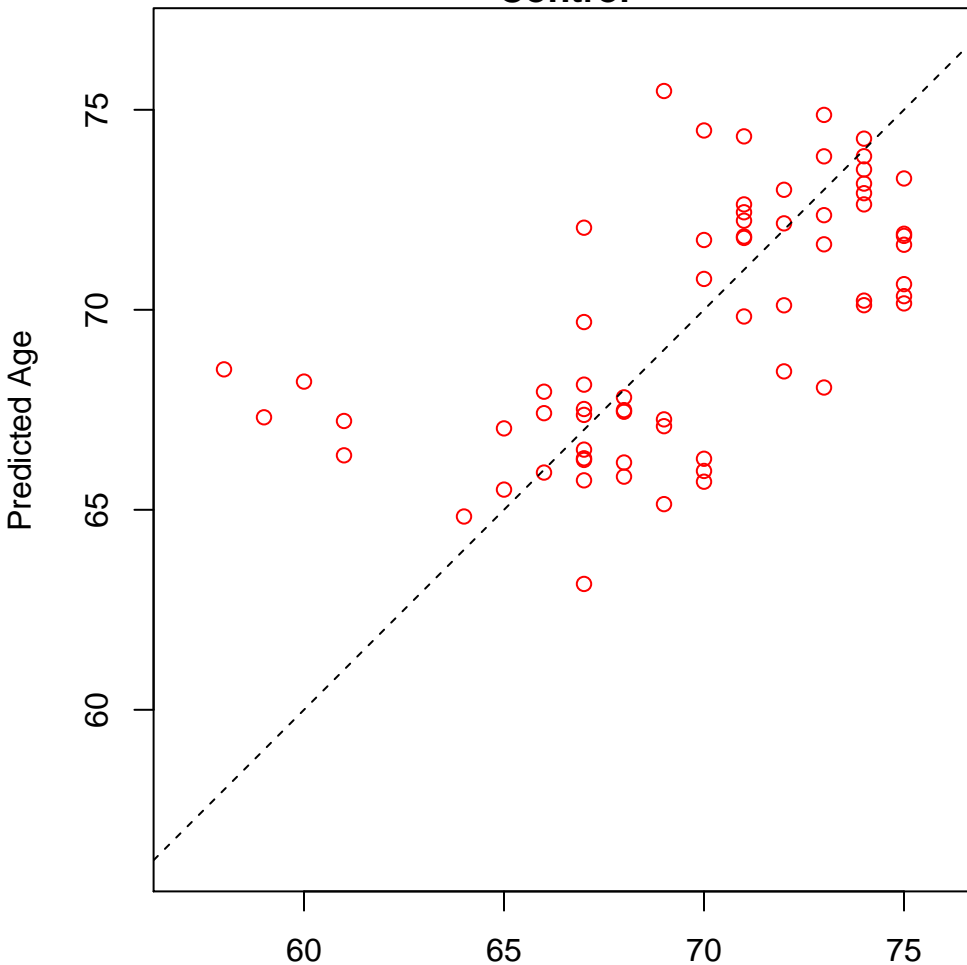


regulation of cell projection organization (Score: 1.294033)

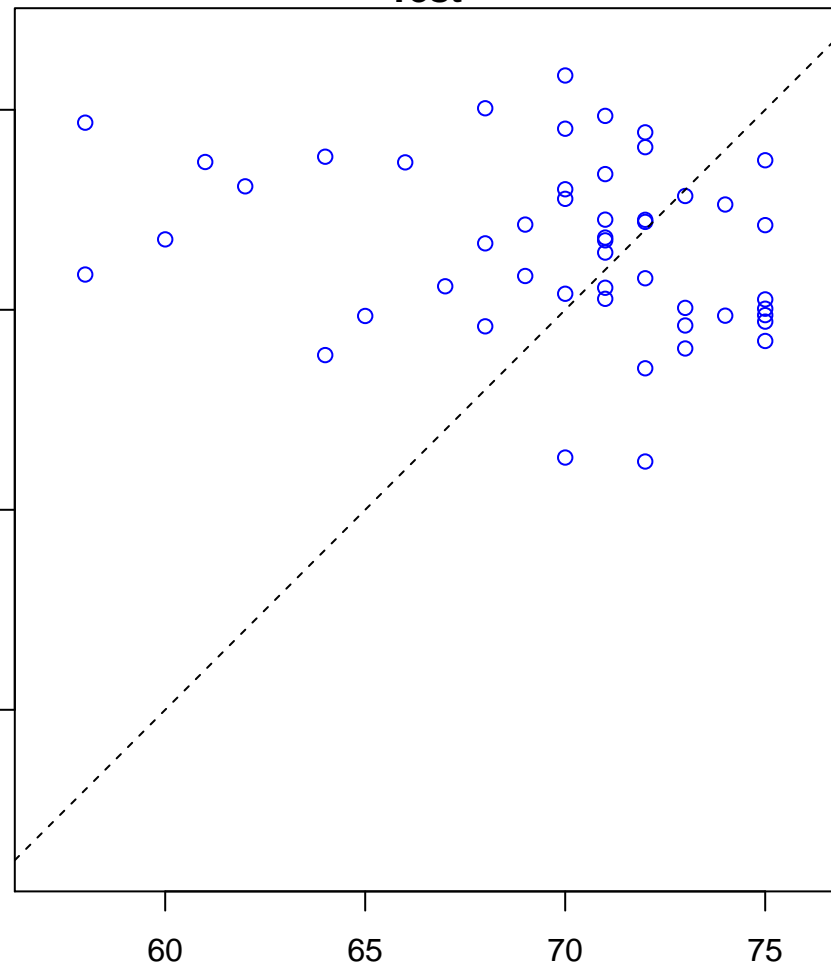


regulation of stem cell proliferation (Score: 1.293964)

Control

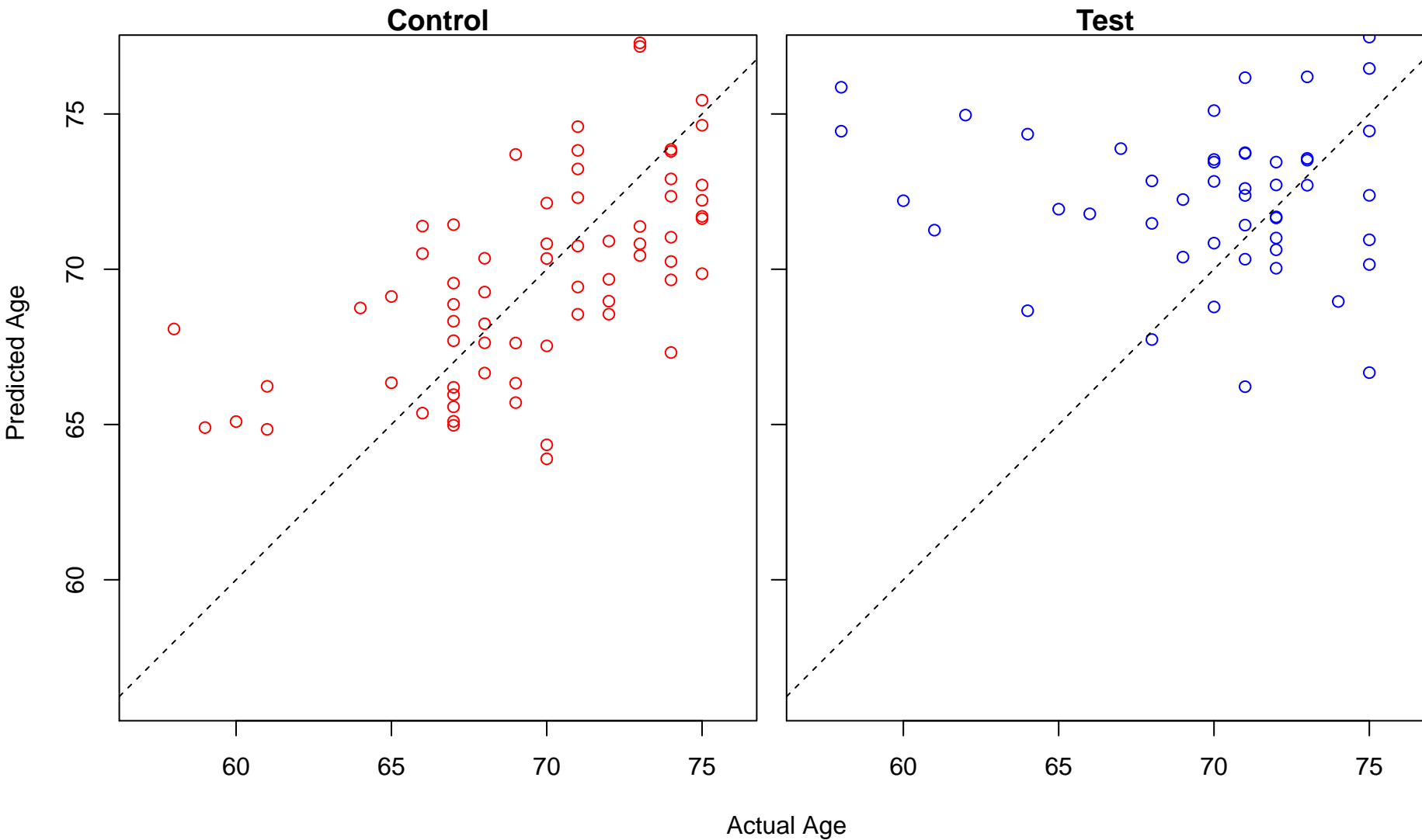


Test

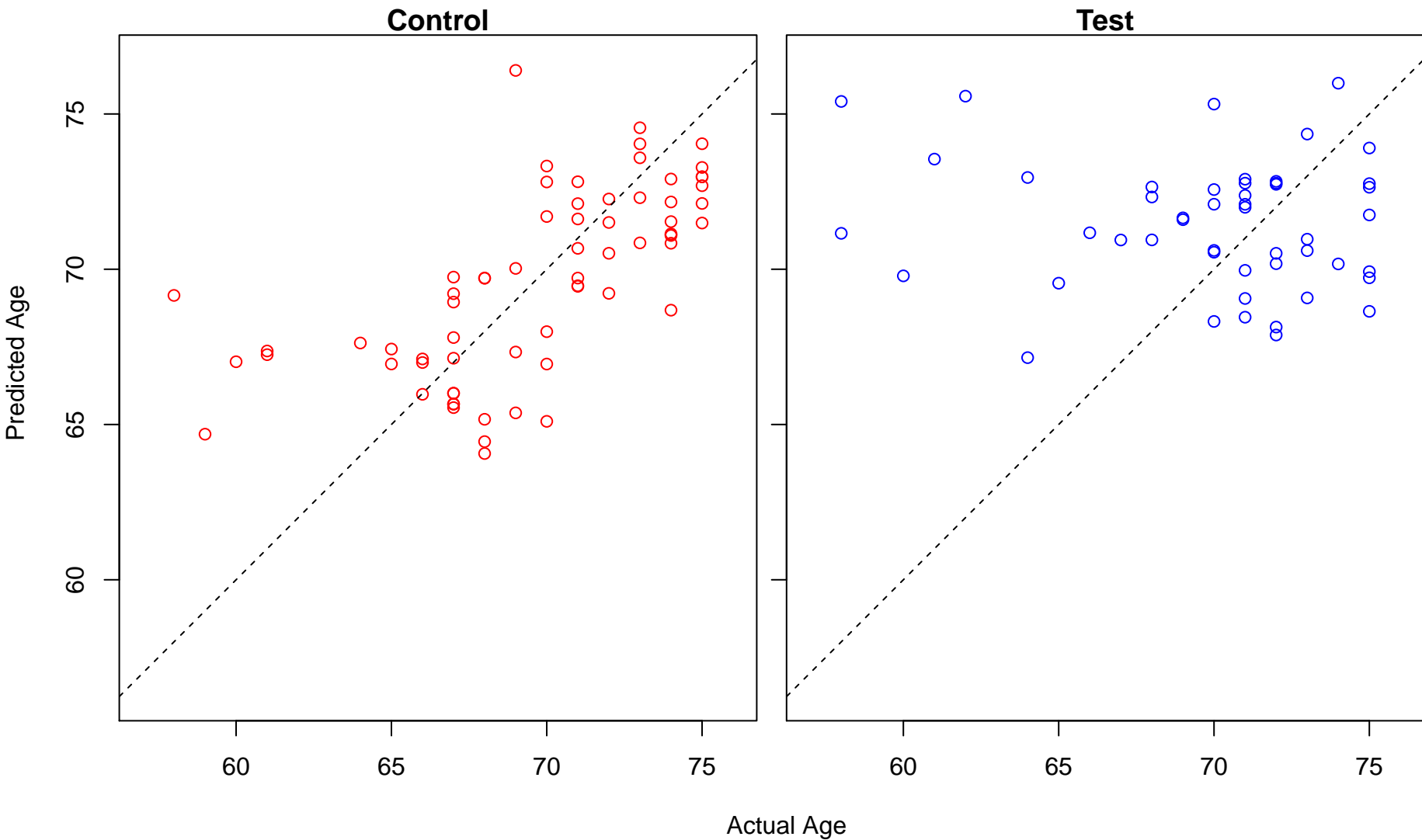


Actual Age

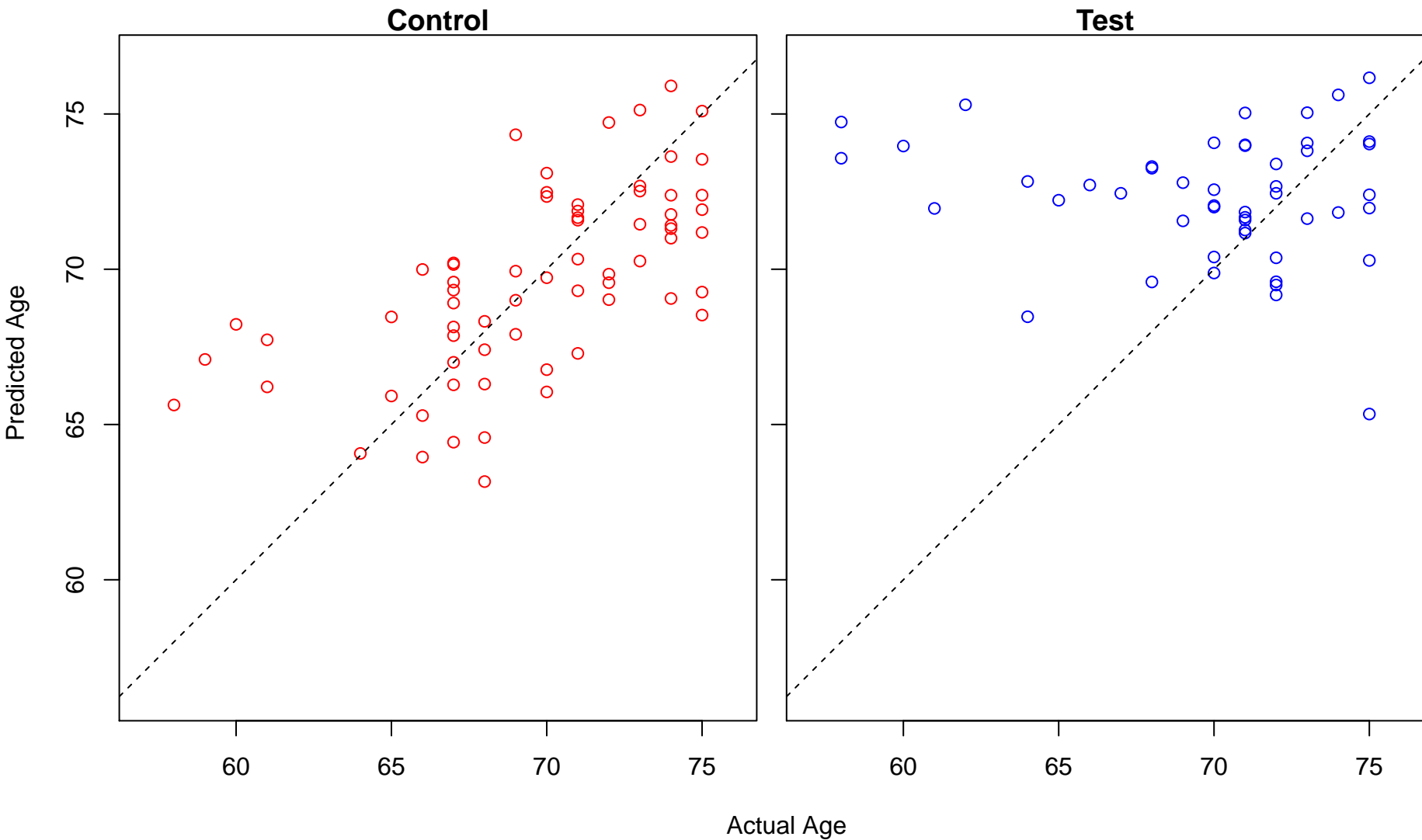
developmental maturation (Score: 1.293922)



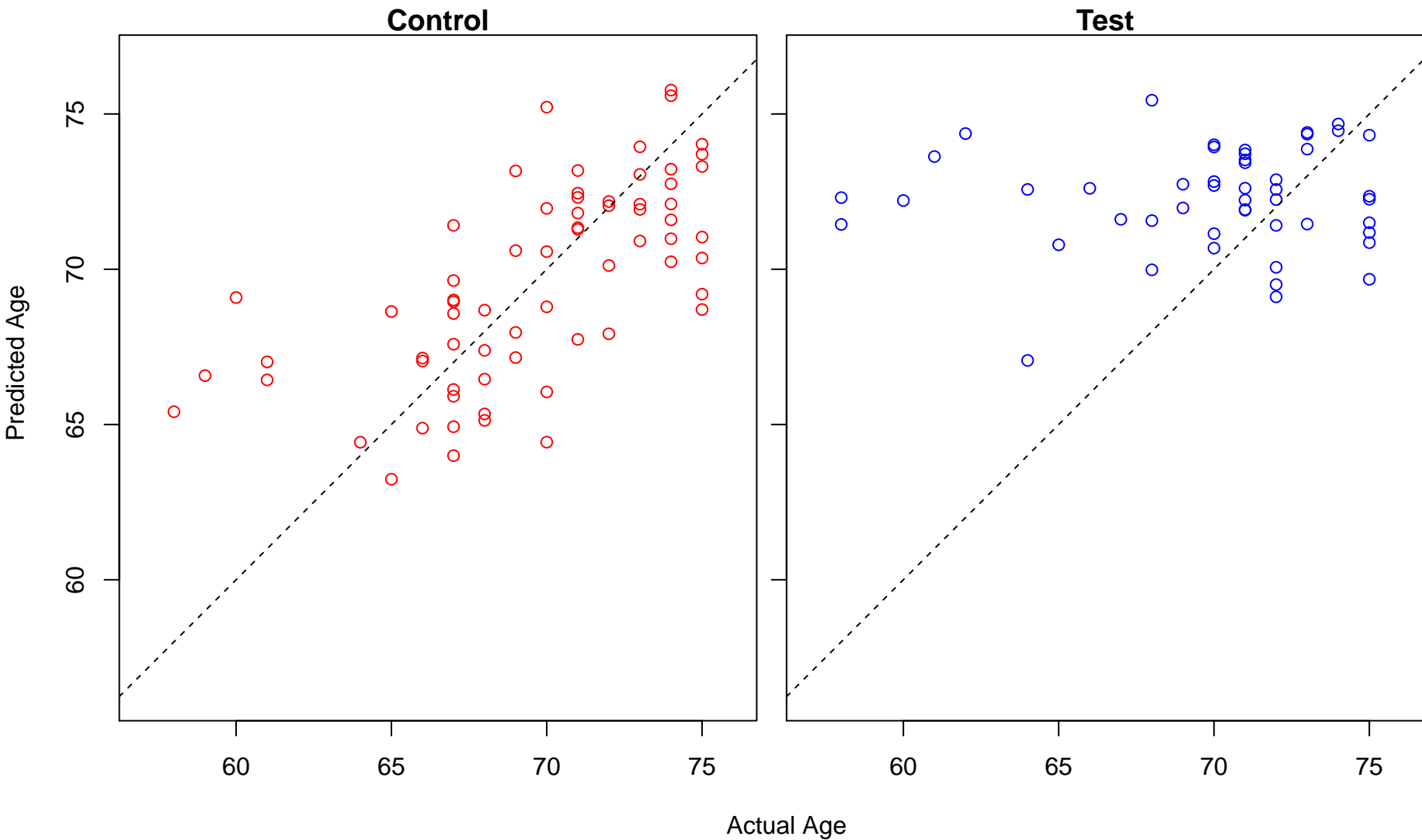
response to estradiol (Score: 1.293487)



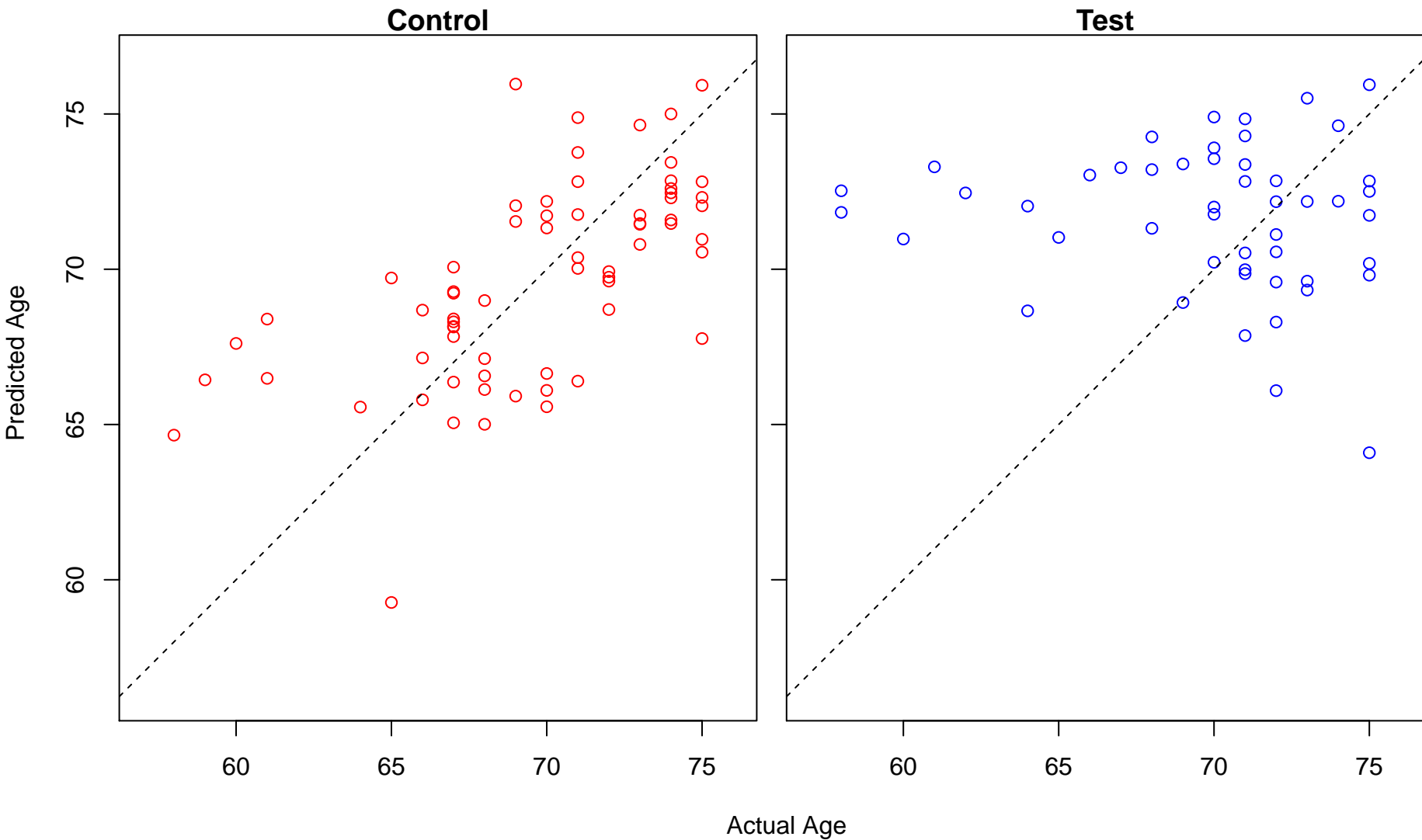
regulation of myotube differentiation (Score: 1.292862)



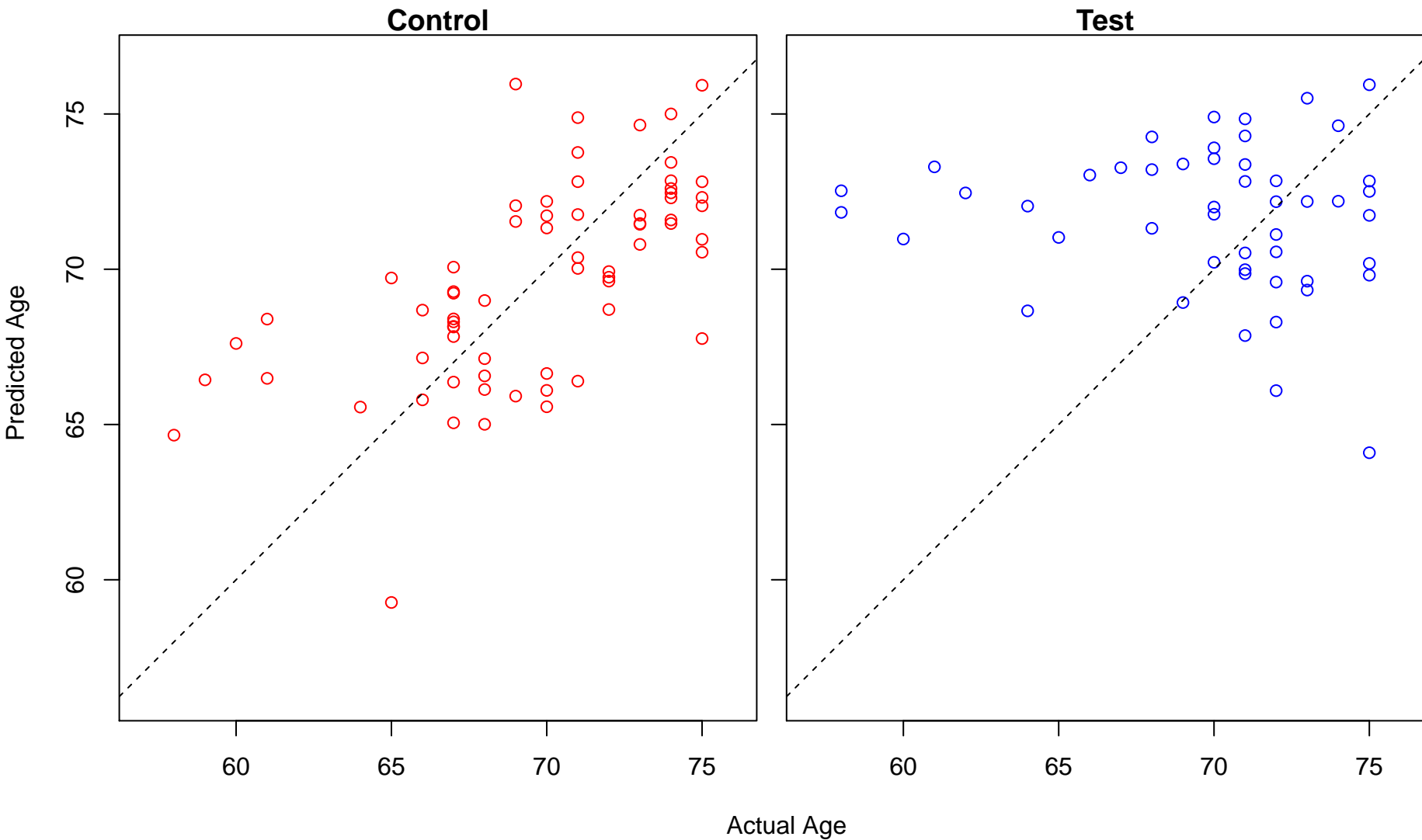
organophosphate ester transport (Score: 1.292834)



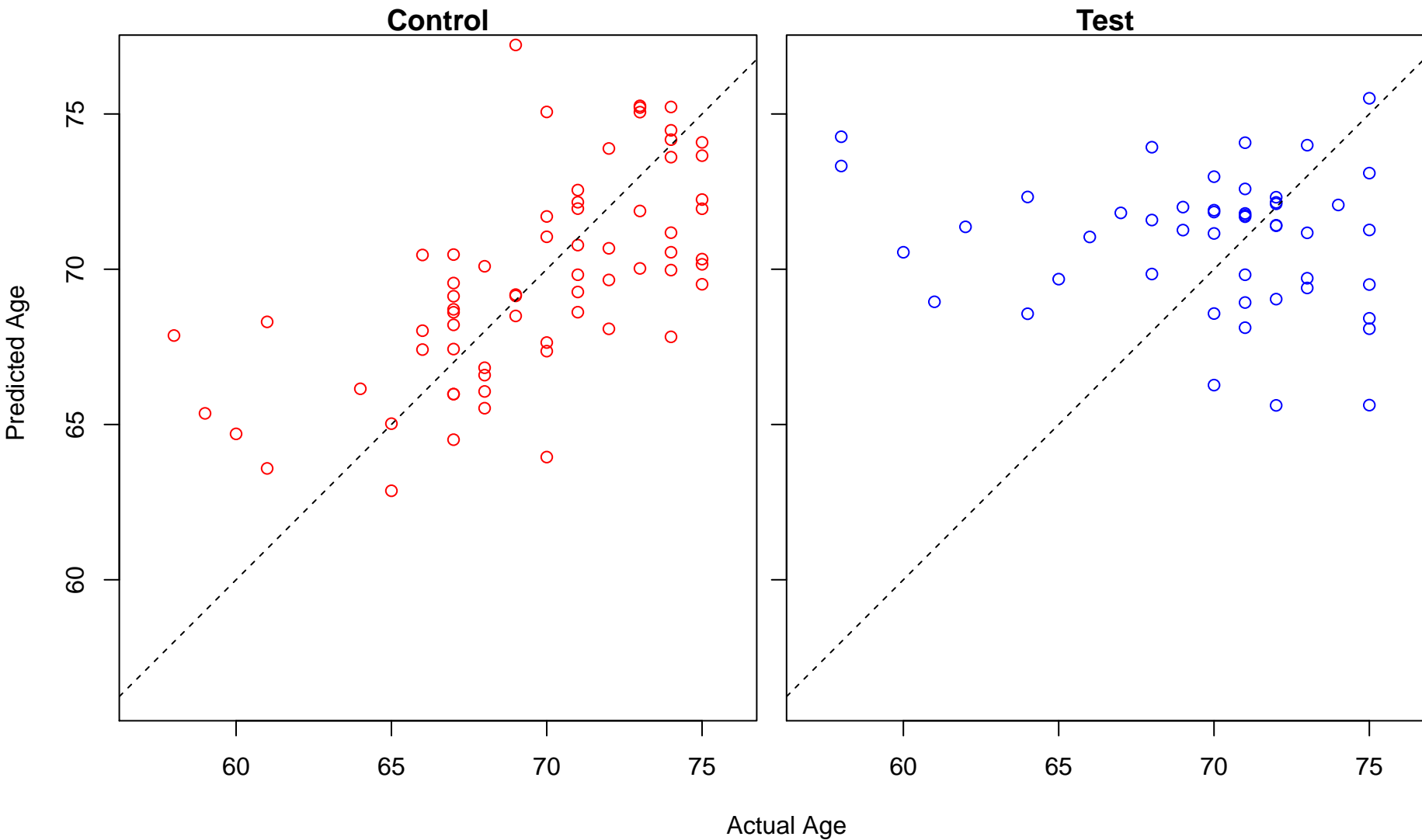
negative regulation of insulin receptor signaling pathway (Score: 1.292759)



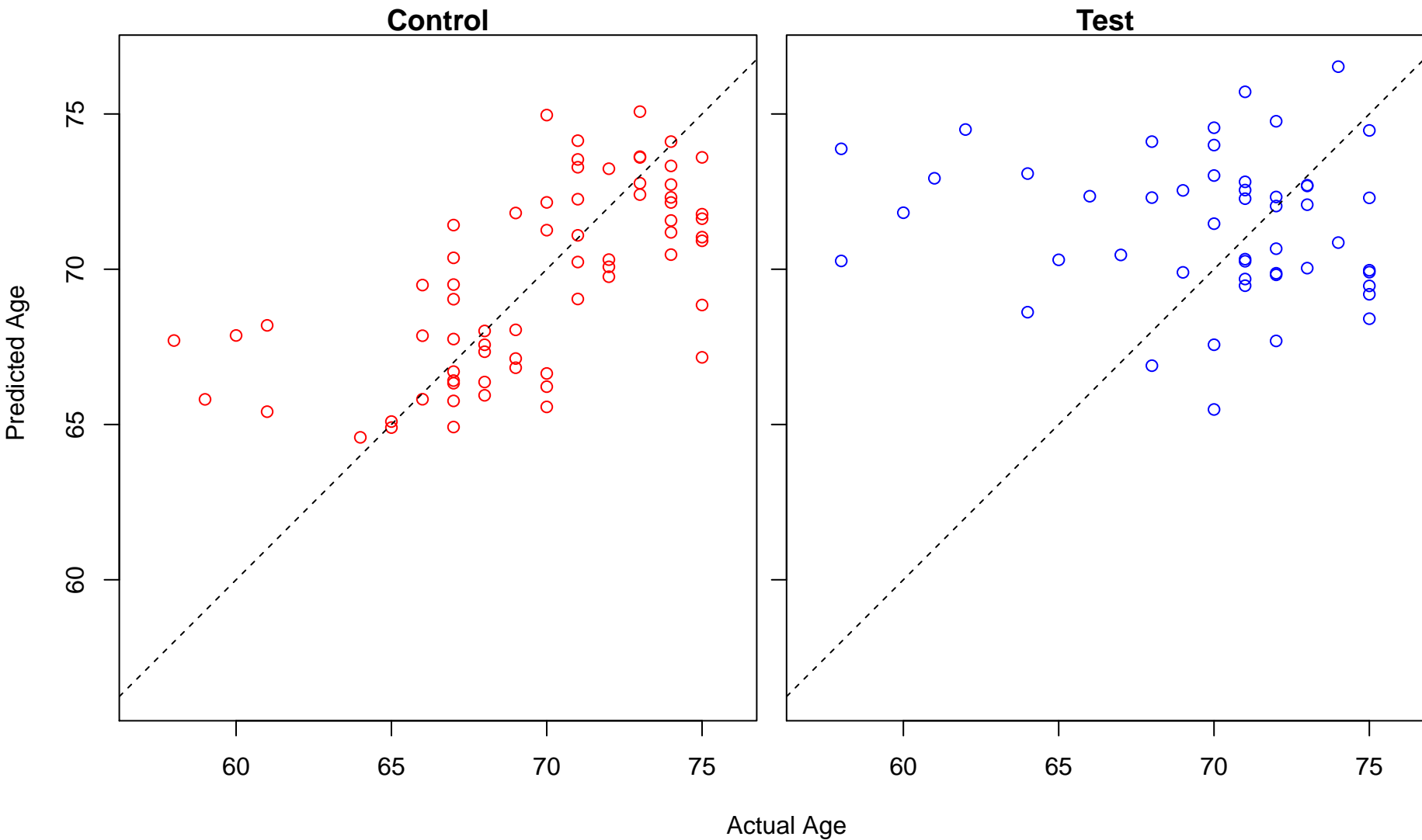
negative regulation of cellular response to insulin stimulus (Score: 1.292759)



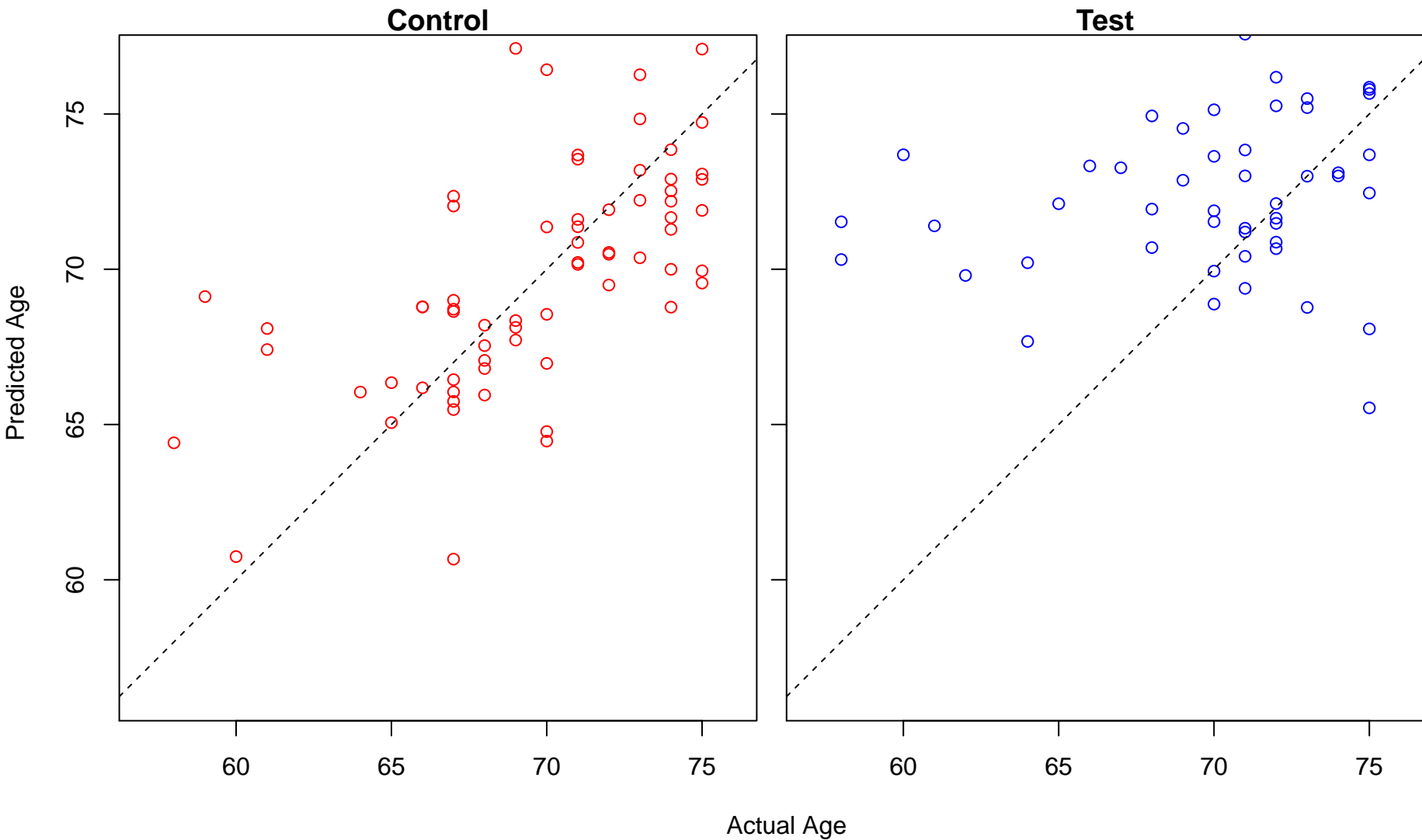
regulation of cytosolic calcium ion concentration (Score: 1.292140)



positive regulation of phospholipase activity (Score: 1.292015)

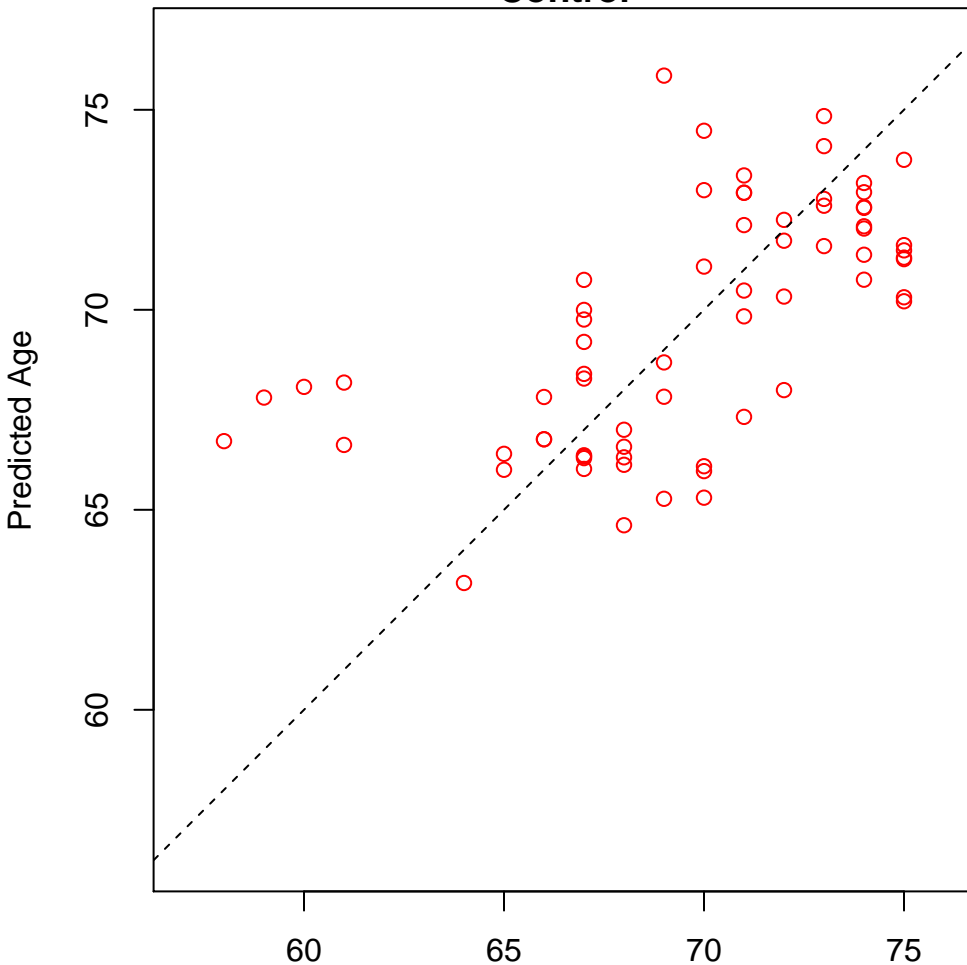


error-free translesion synthesis (Score: 1.291692)

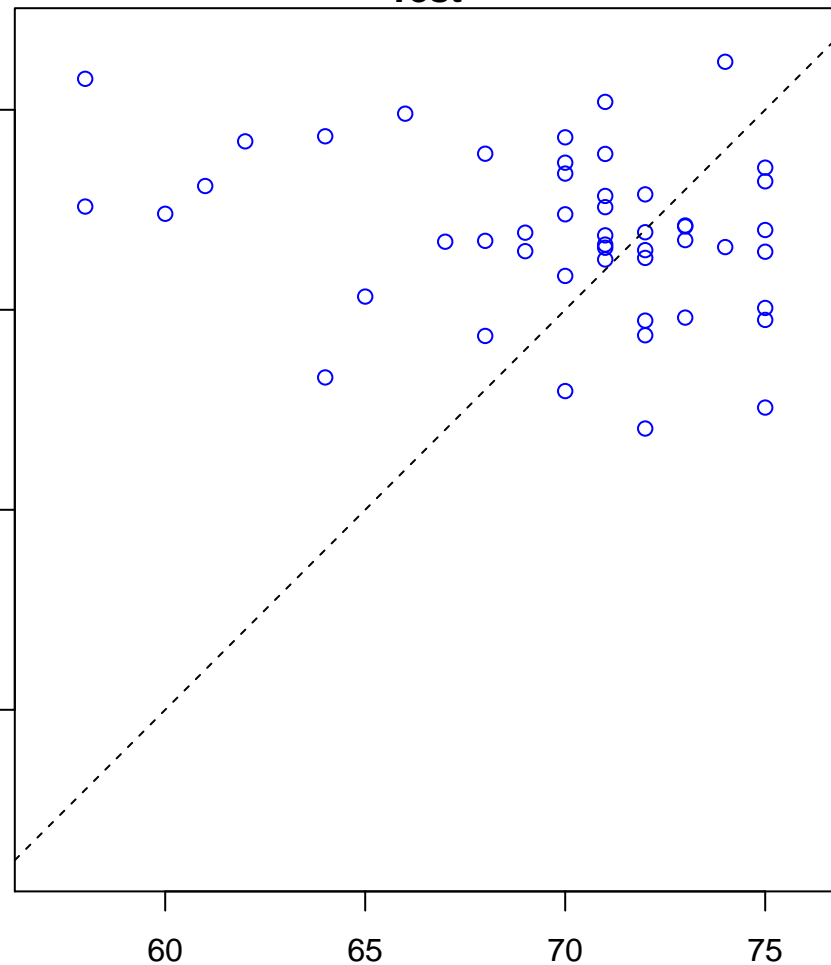


response to xenobiotic stimulus (Score: 1.291590)

Control

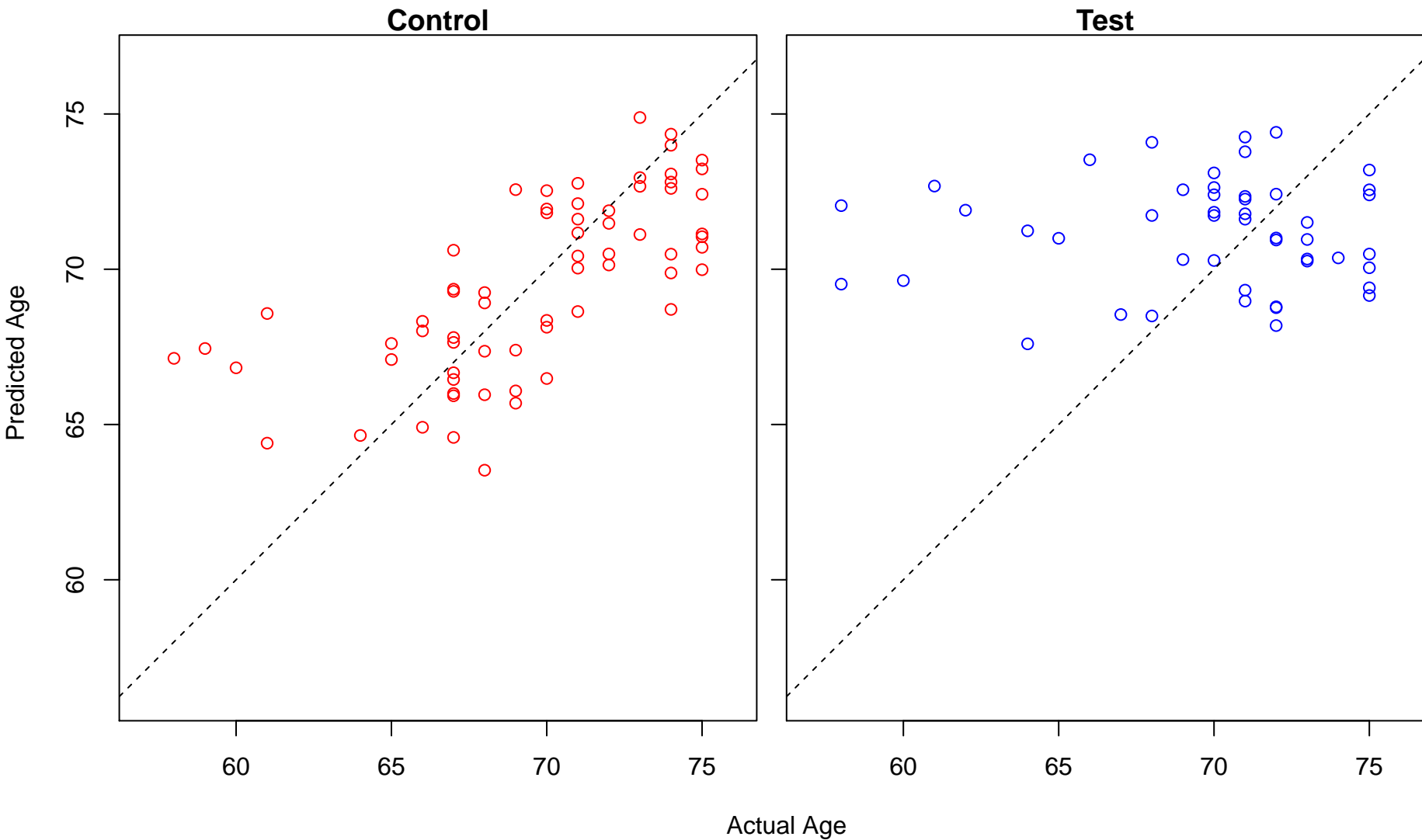


Test



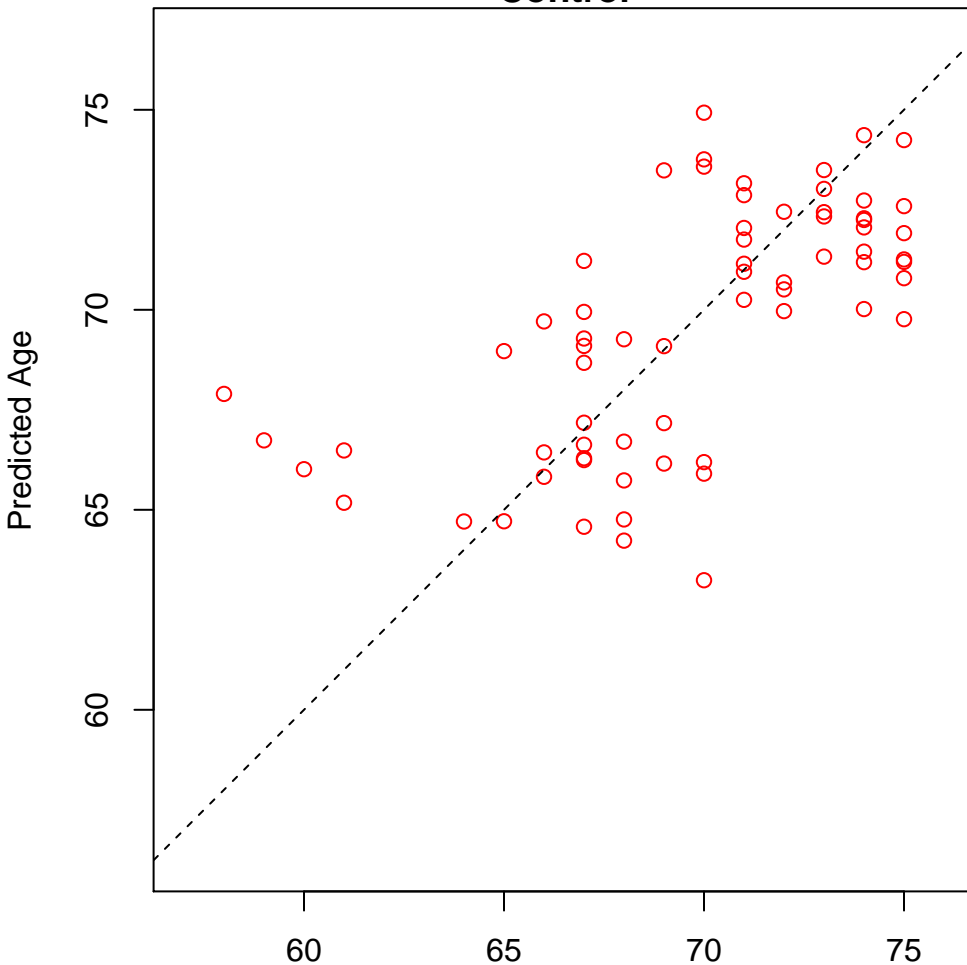
Actual Age

glycerolipid catabolic process (Score: 1.291126)

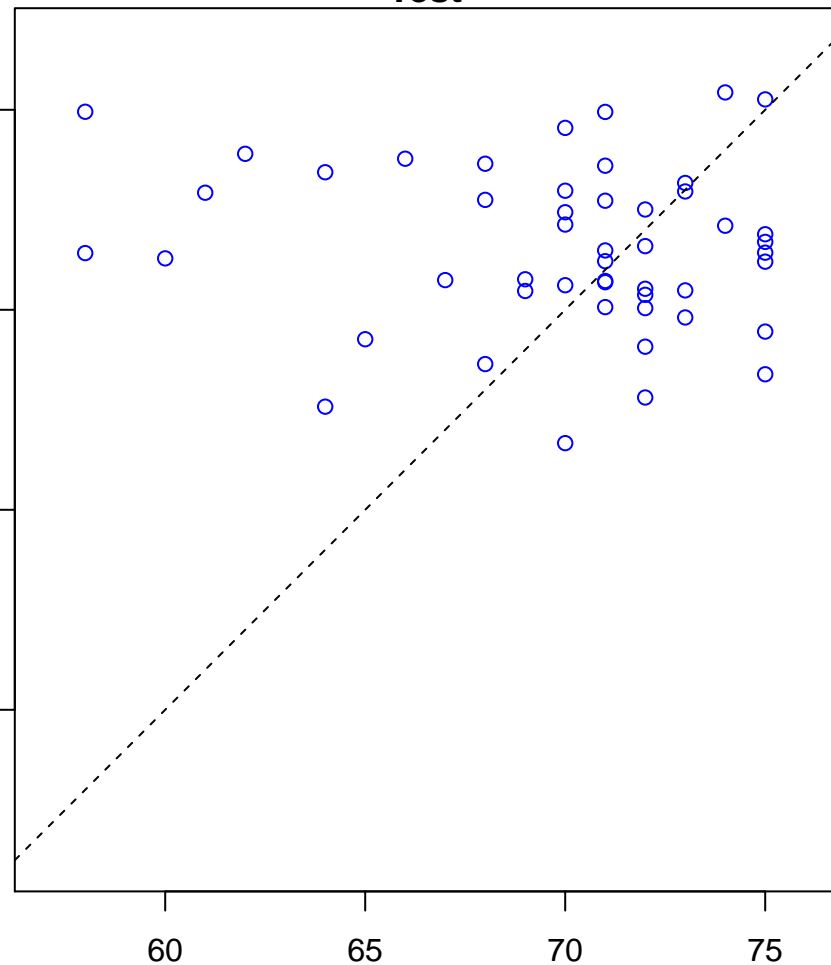


ER to Golgi vesicle-mediated transport (Score: 1.290698)

Control

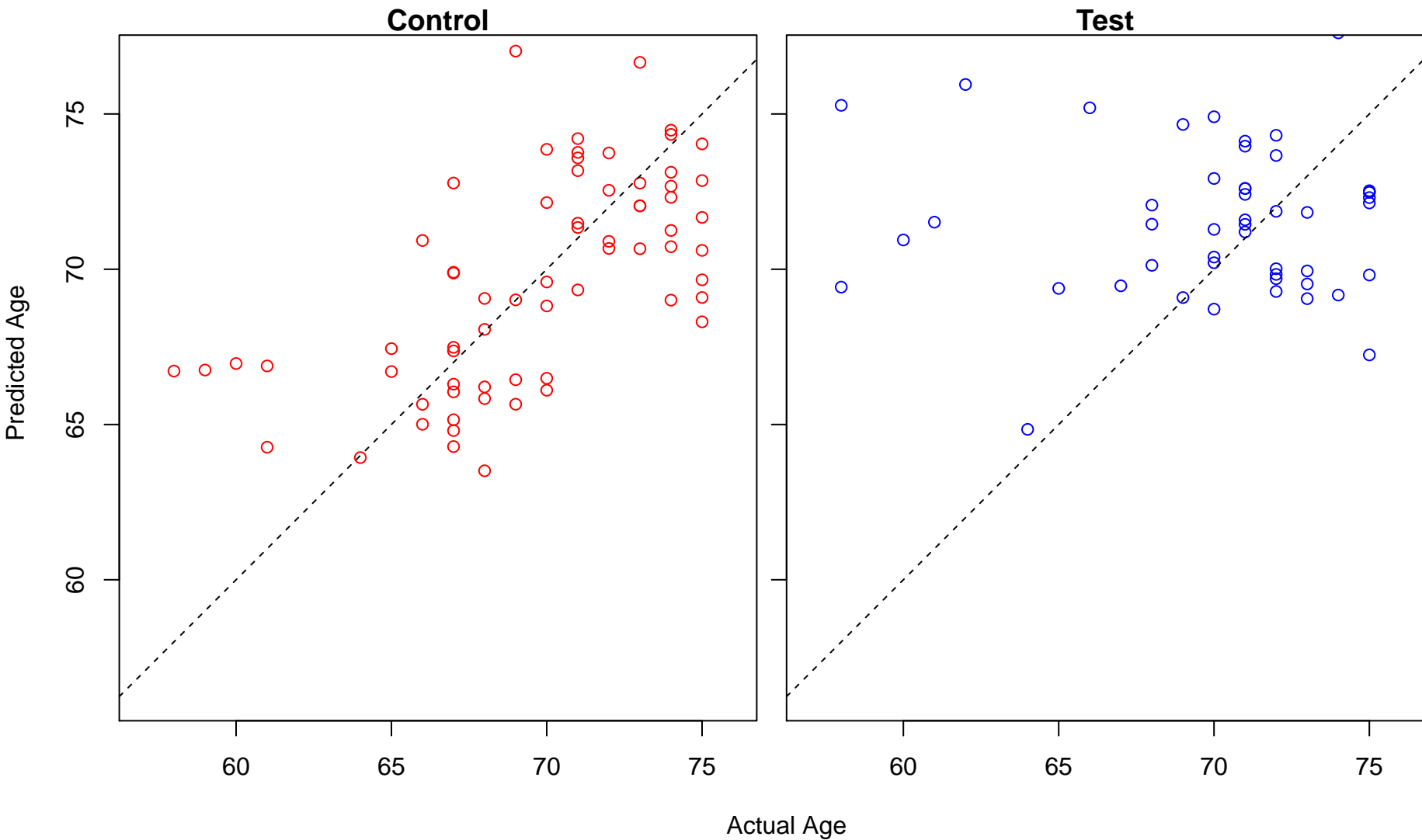


Test



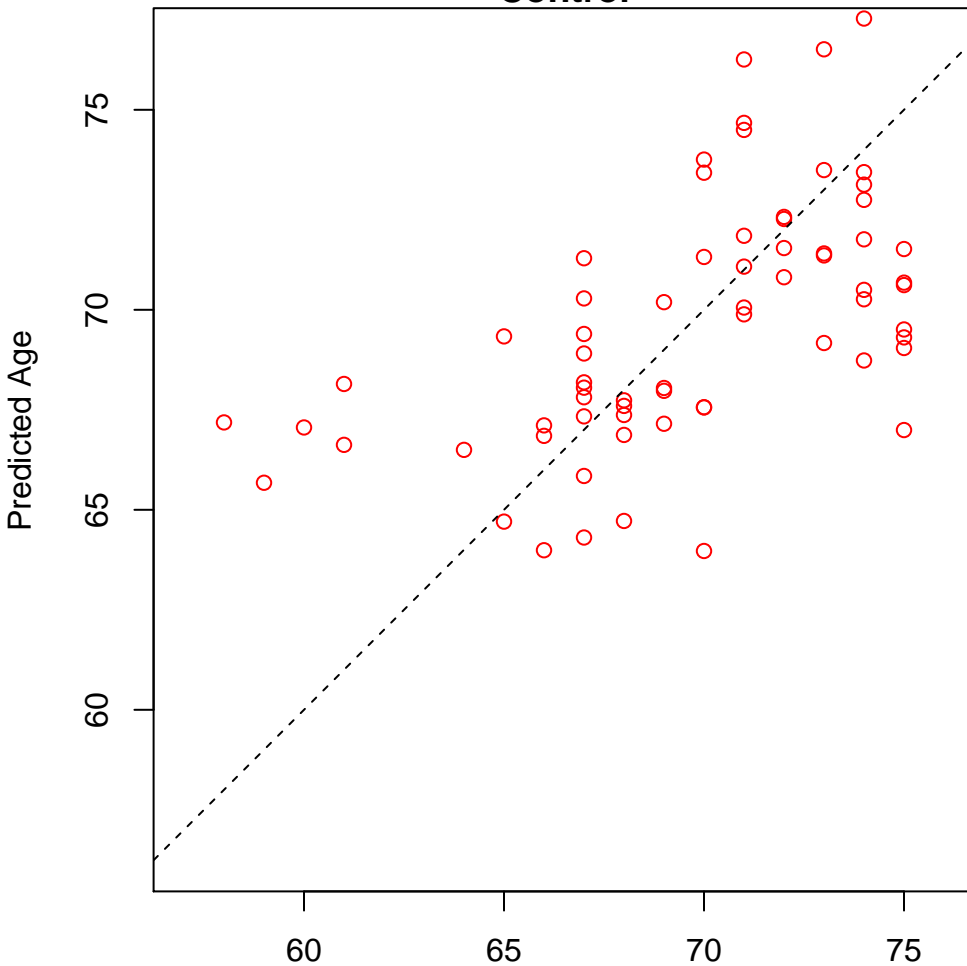
Actual Age

regulation of receptor-mediated endocytosis (Score: 1.290131)

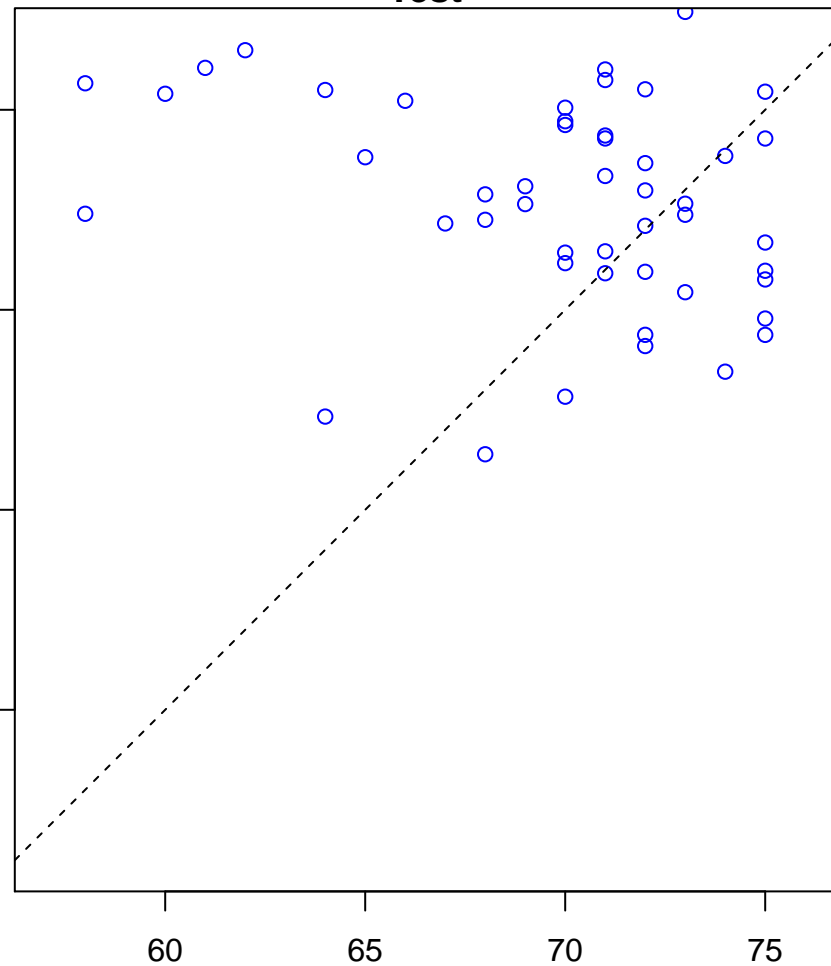


cyclic nucleotide biosynthetic process (Score: 1.290039)

Control

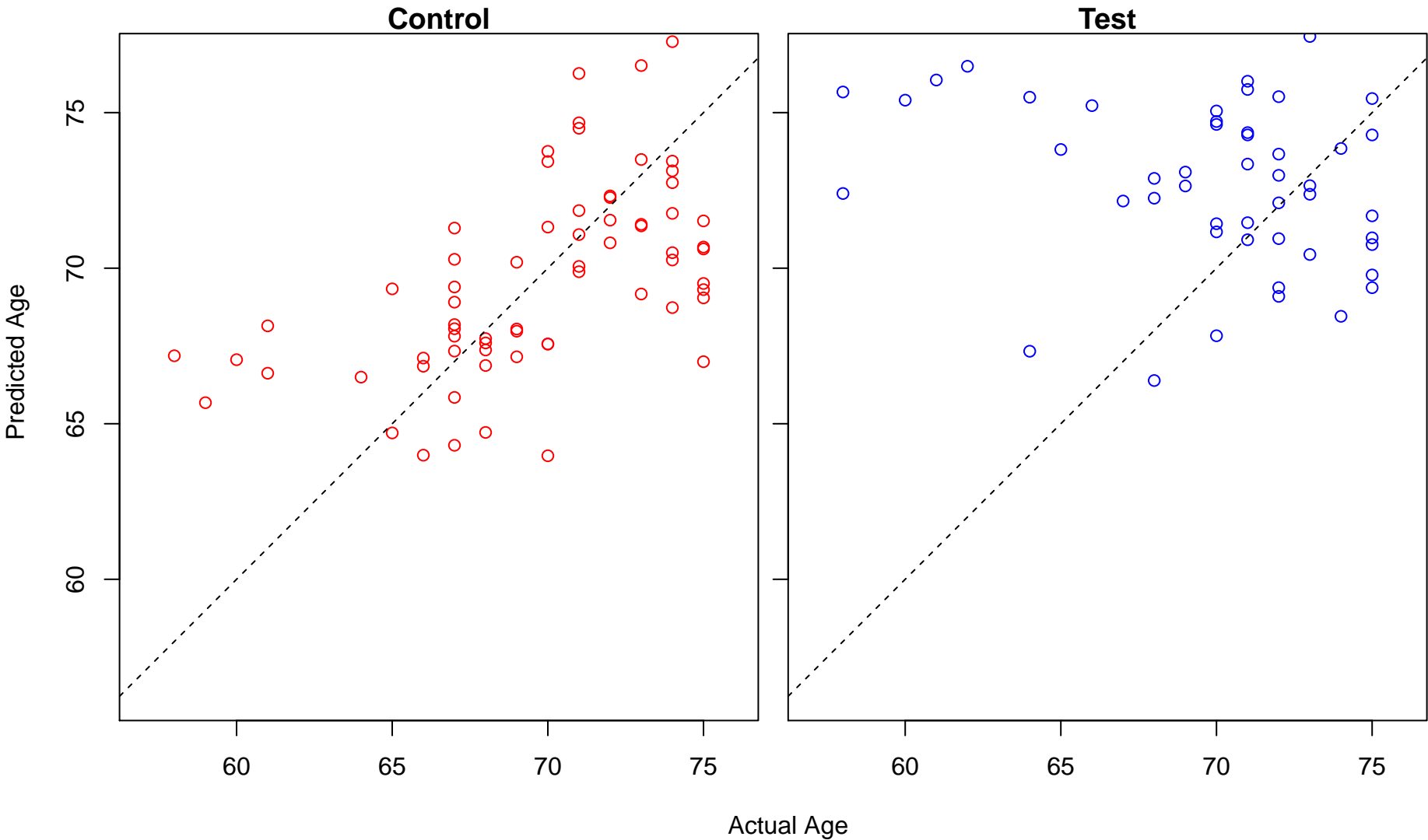


Test

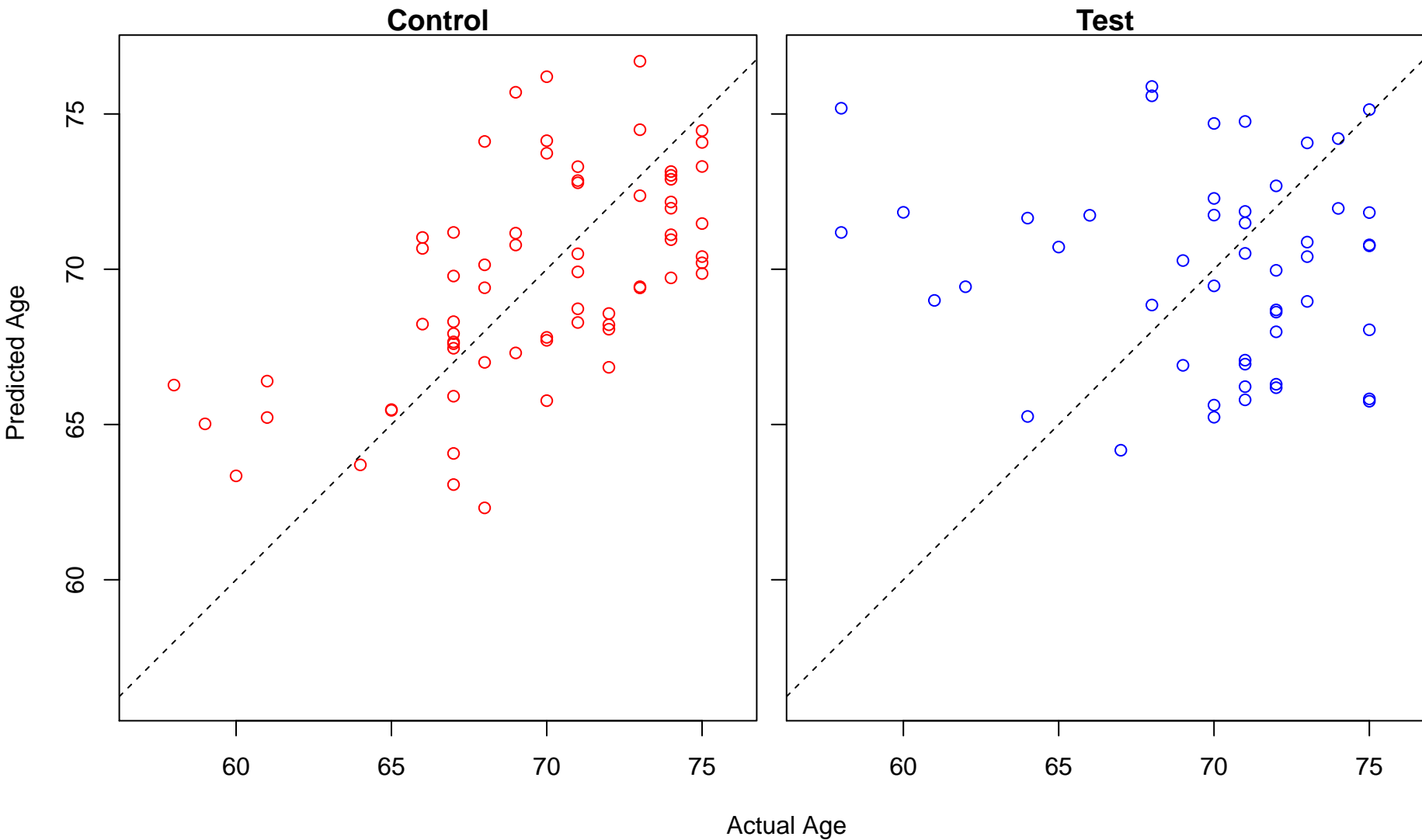


Actual Age

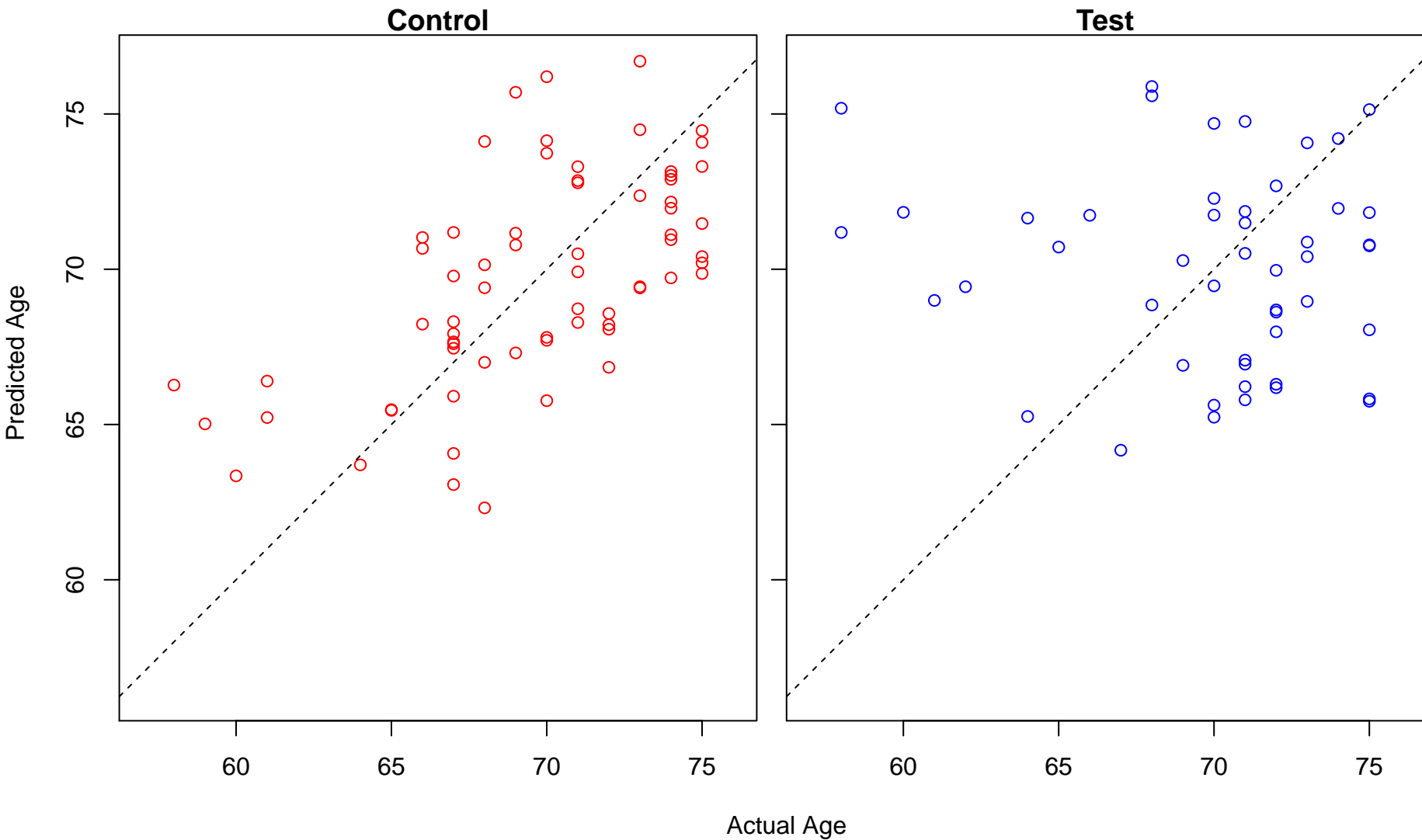
cyclic purine nucleotide metabolic process (Score: 1.290039)



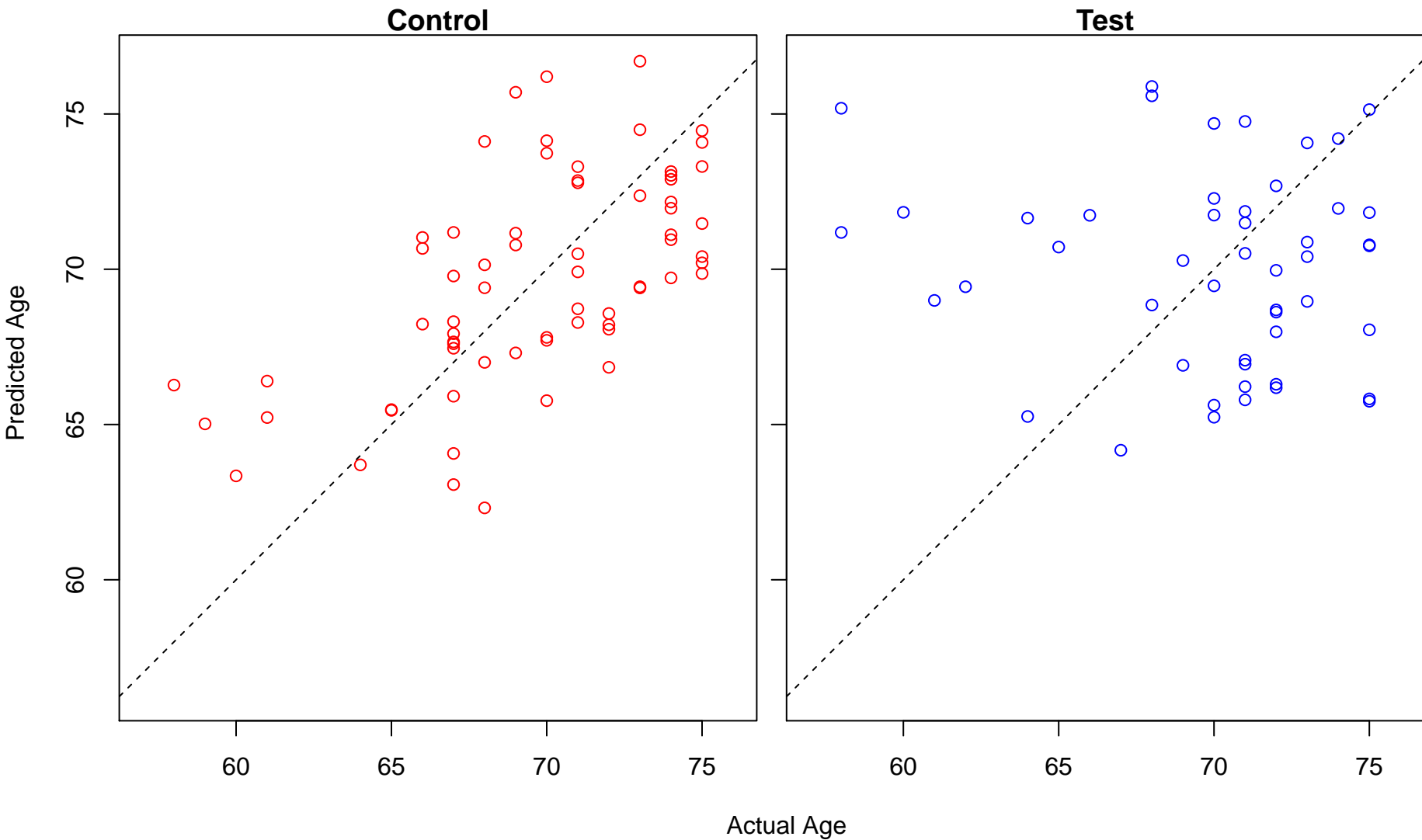
somatic recombination of immunoglobulin genes involved in immune response (Score: 1.289768)



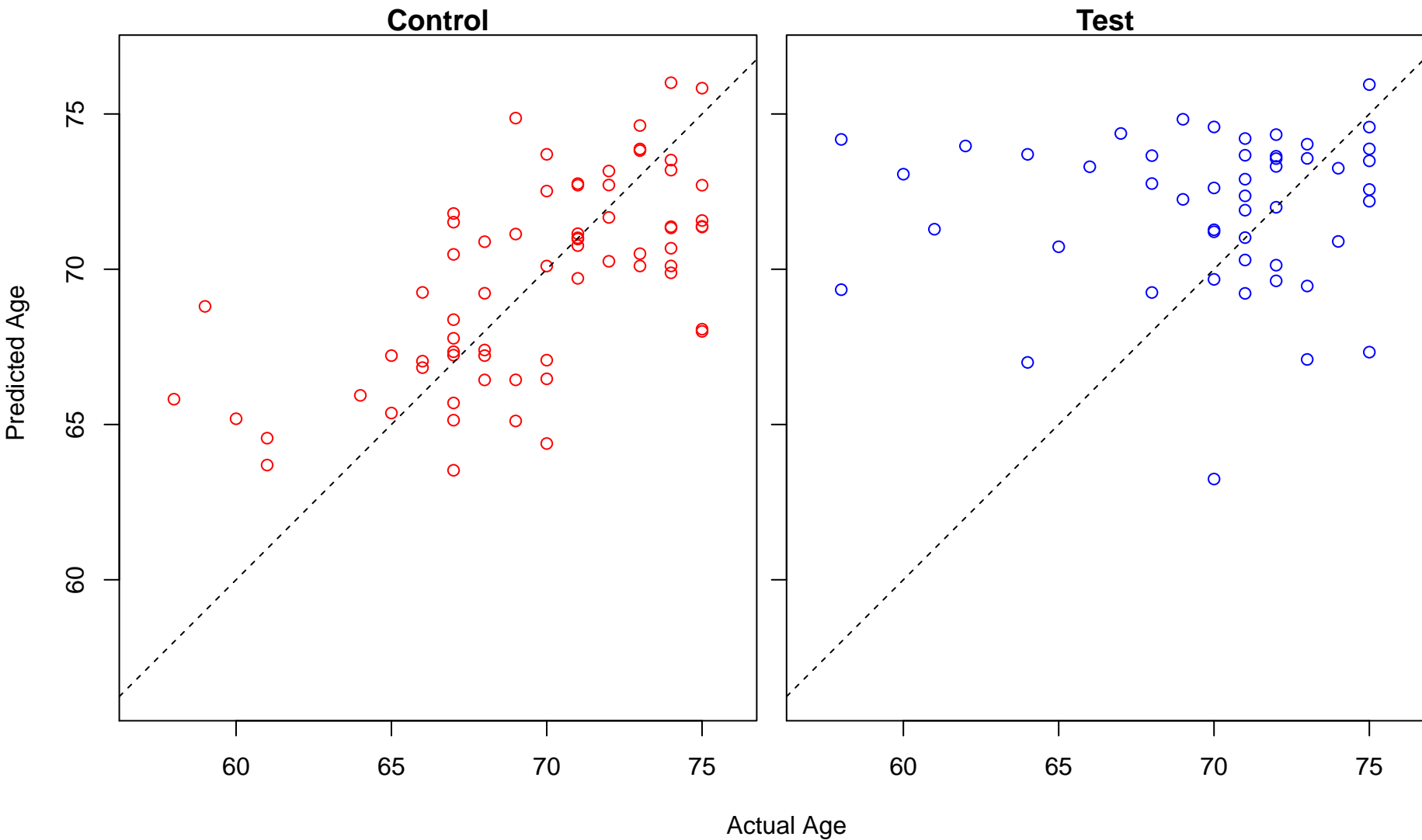
somatic diversification of immunoglobulins involved in immune response (Score: 1.289768)



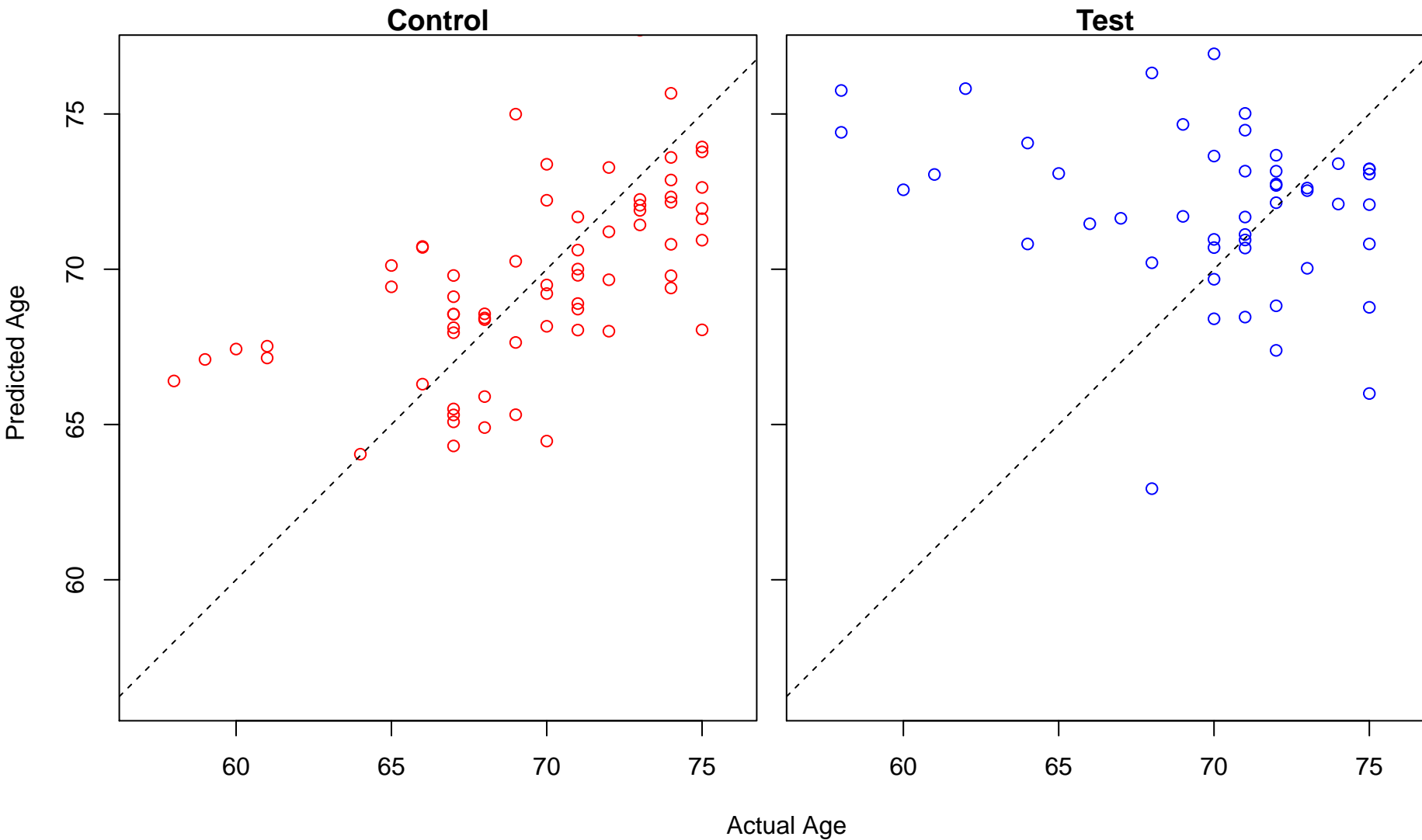
isotype switching (Score: 1.289768)



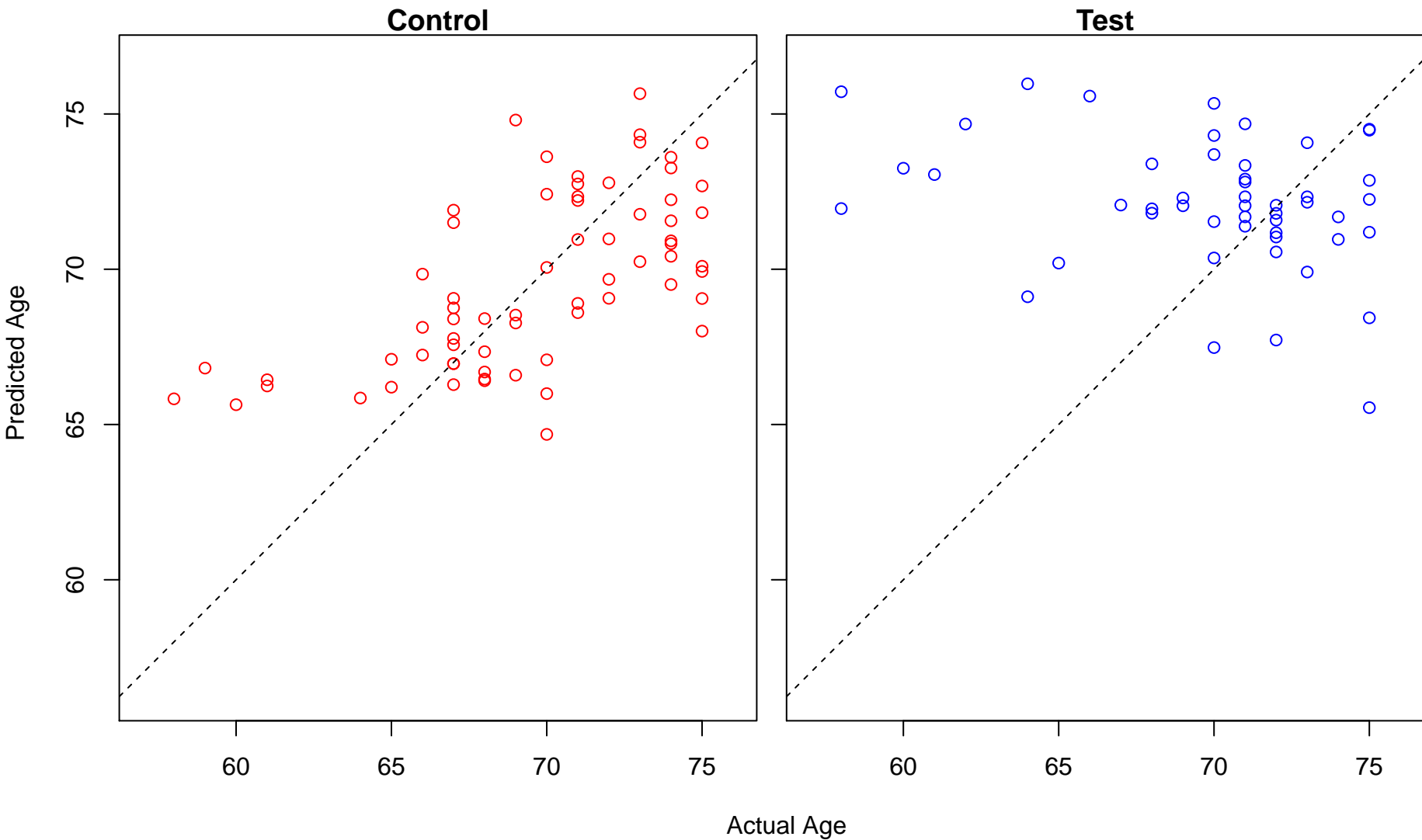
mRNA transcription (Score: 1.289721)



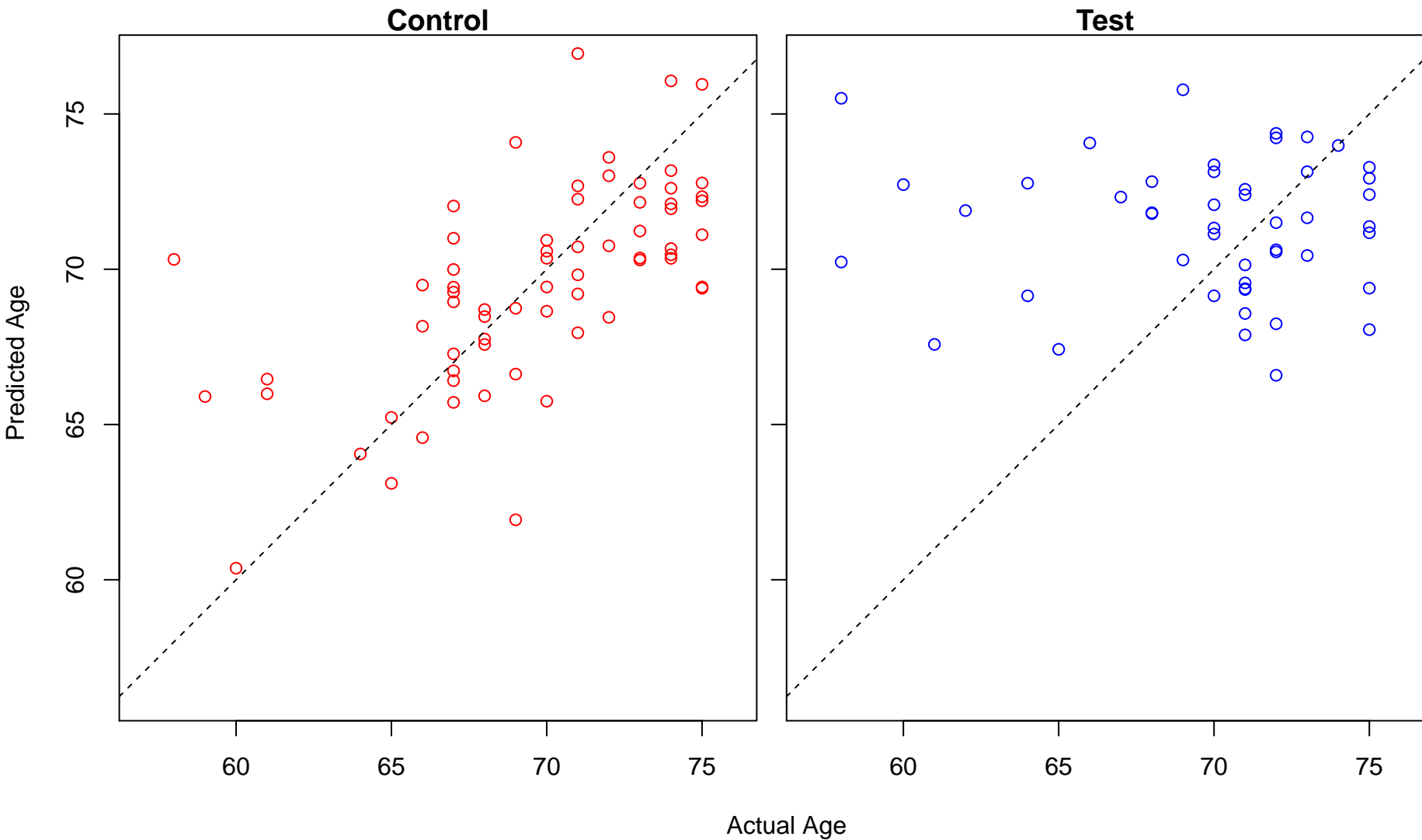
tRNA splicing, via endonucleolytic cleavage and ligation (Score: 1.289670)



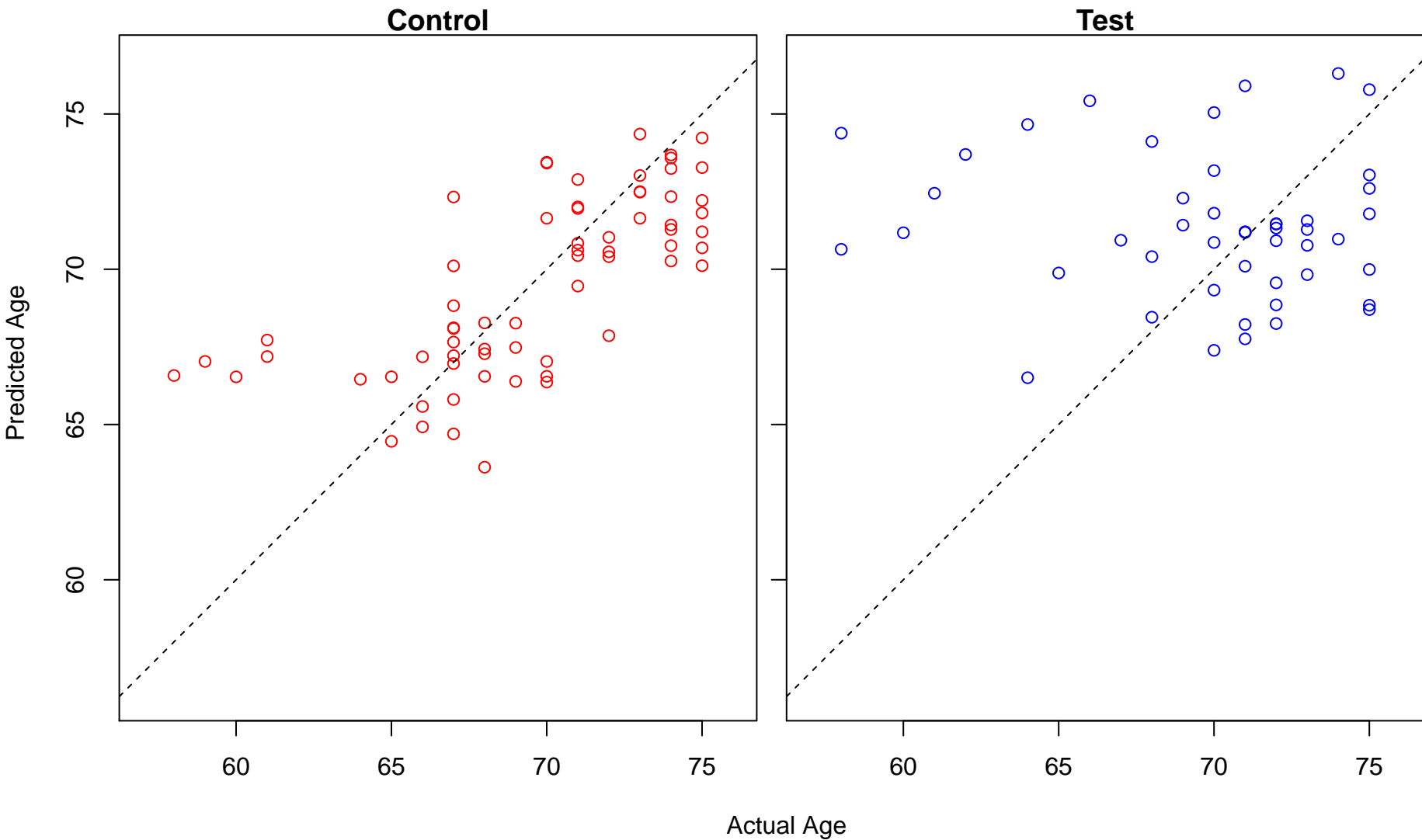
regulation of transcription from RNA polymerase II promoter in response to hypoxia (Score: 1.28964)



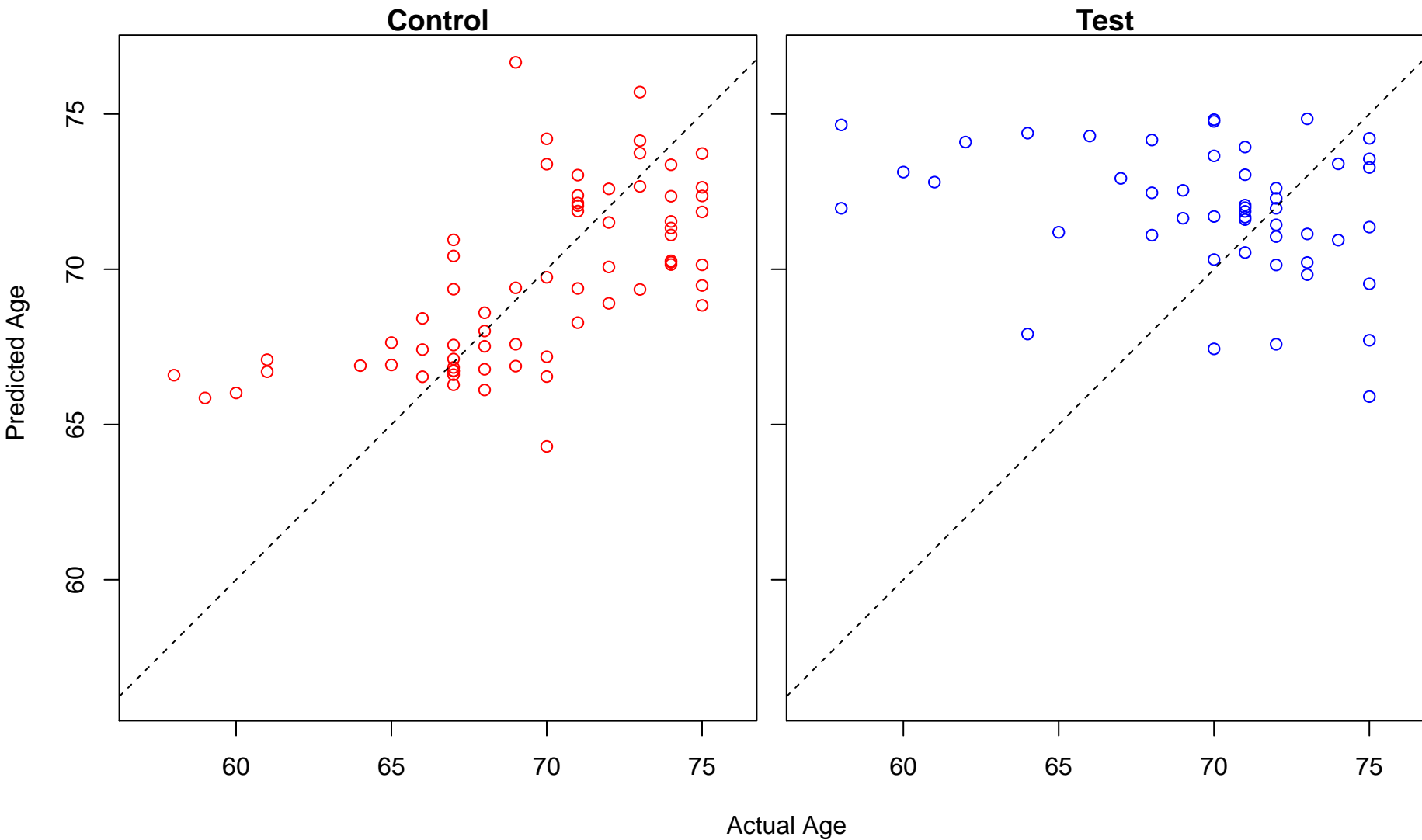
protein localization to microtubule cytoskeleton (Score: 1.289604)



negative regulation of ossification (Score: 1.289506)

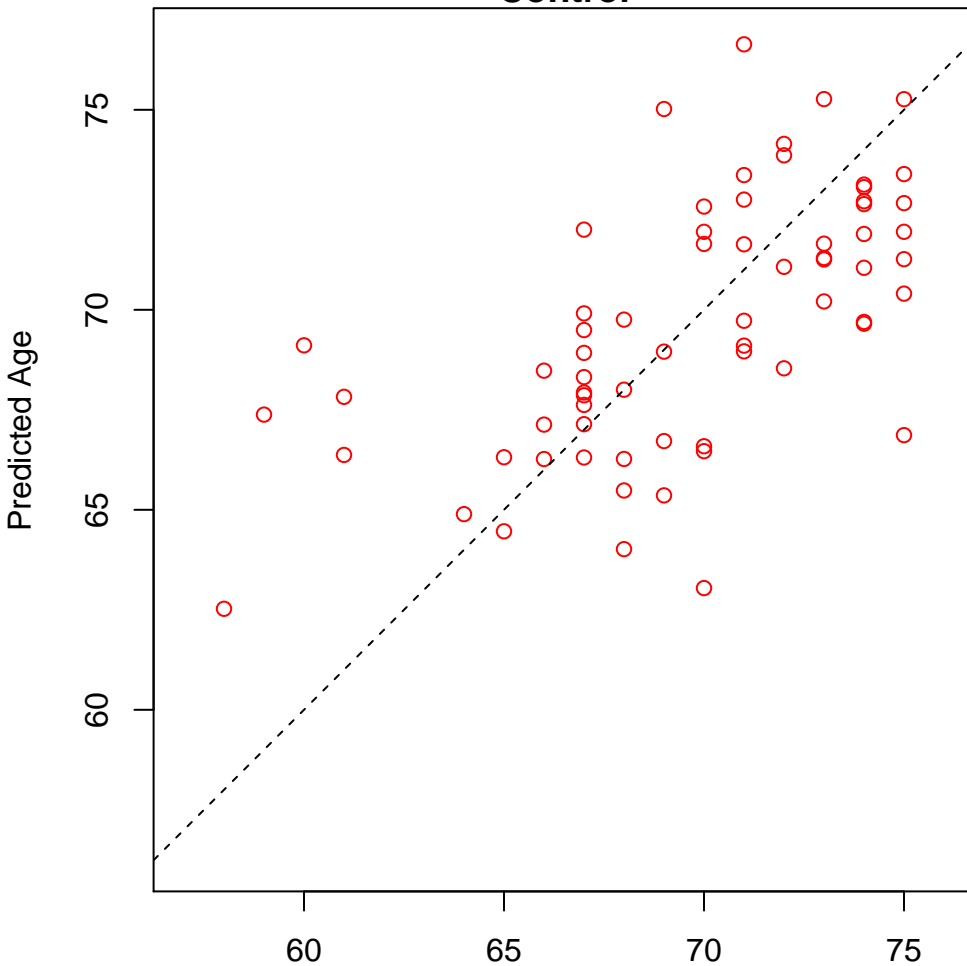


nucleic acid phosphodiester bond hydrolysis (Score: 1.288740)

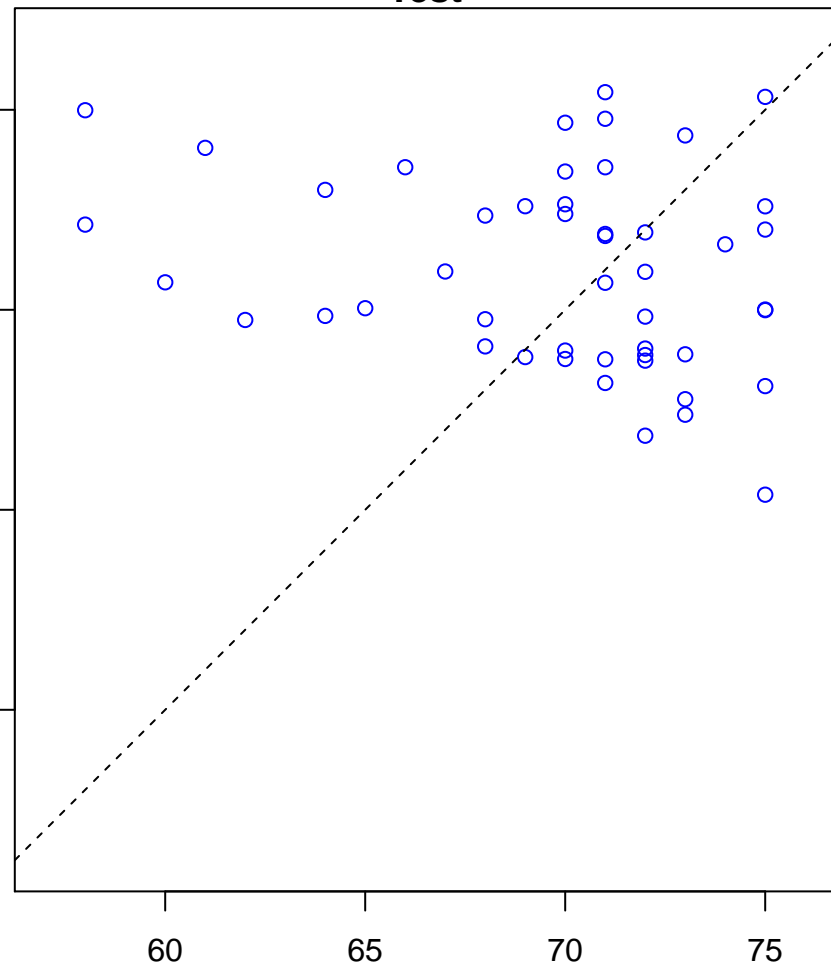


peptidyl-threonine dephosphorylation (Score: 1.288541)

Control

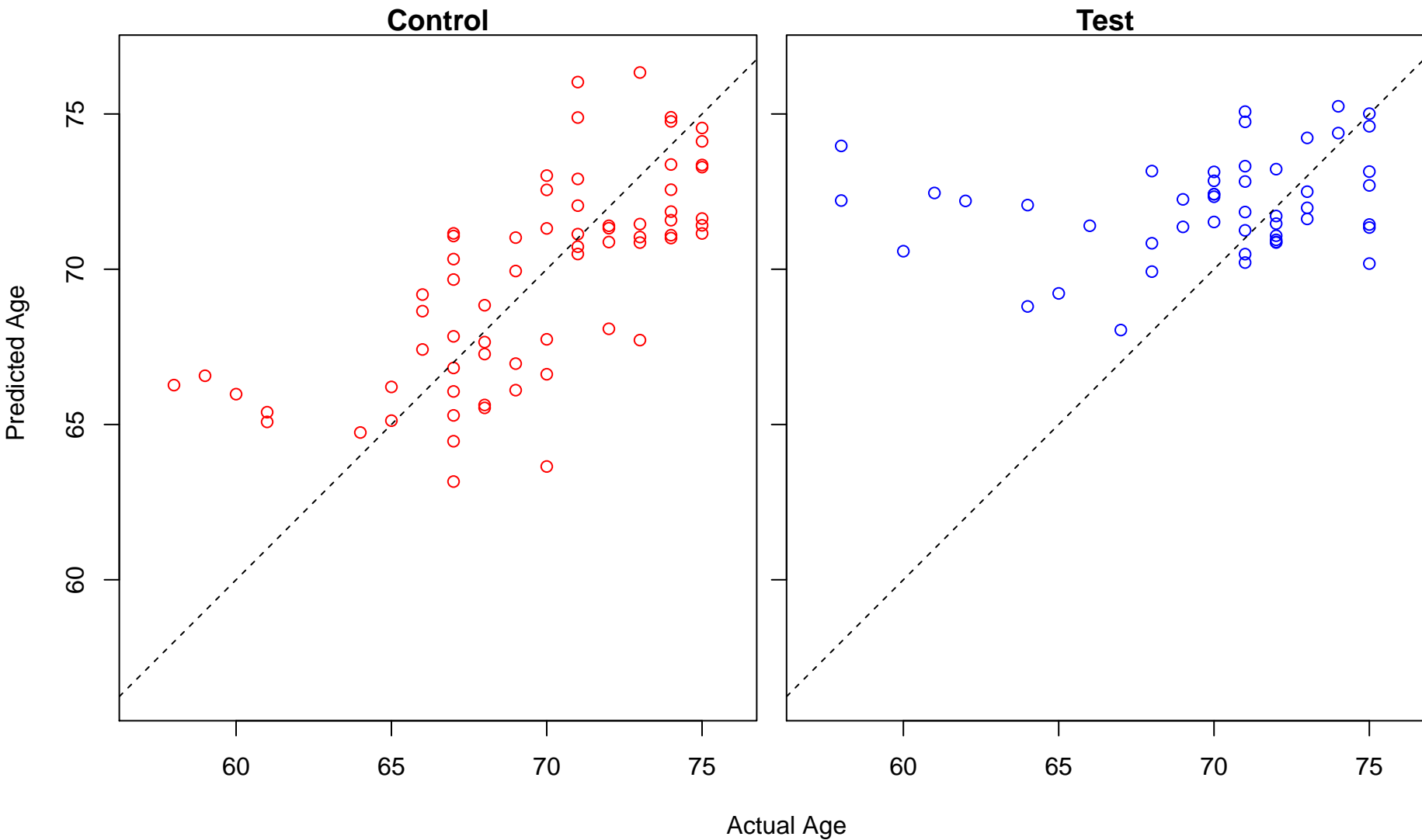


Test

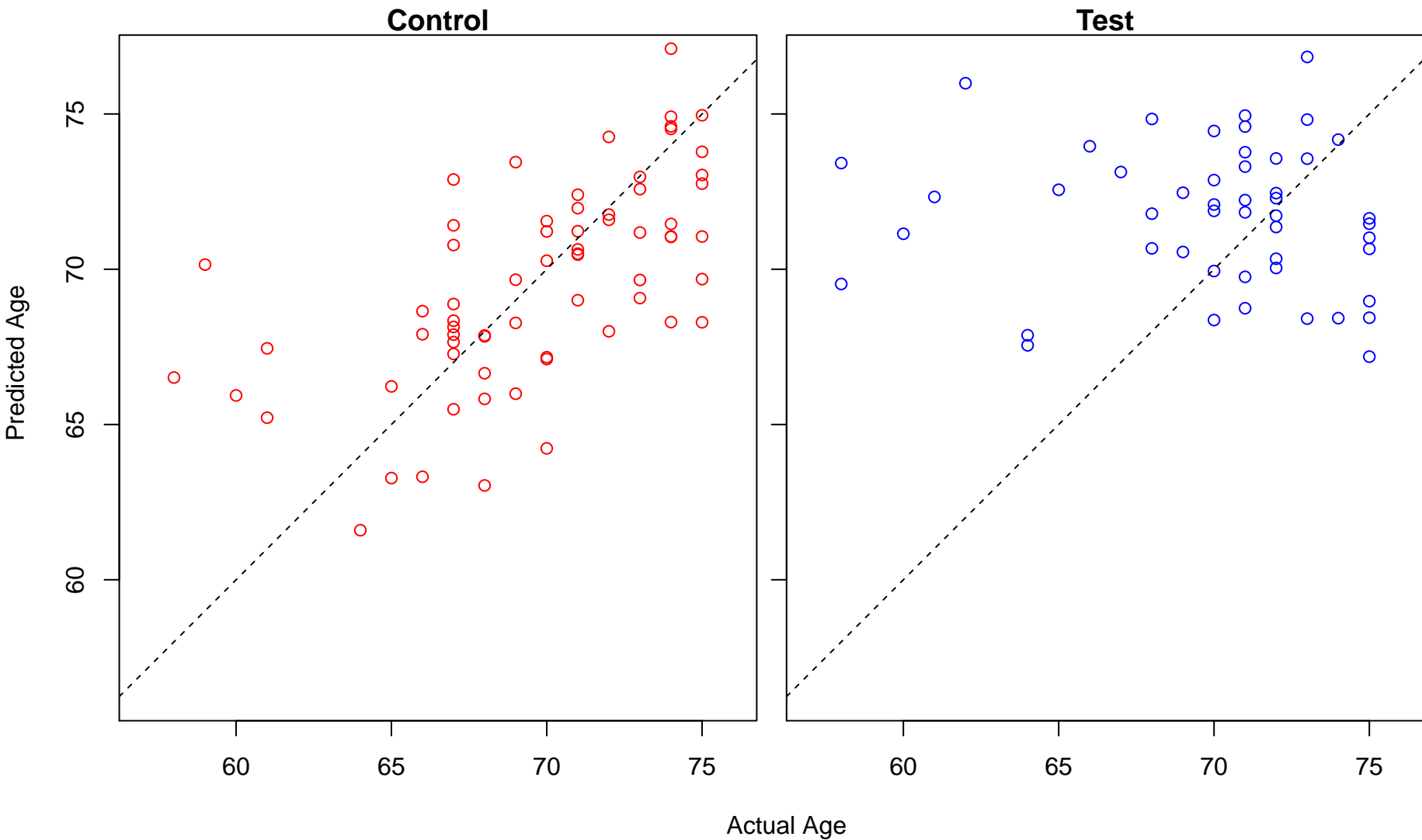


Actual Age

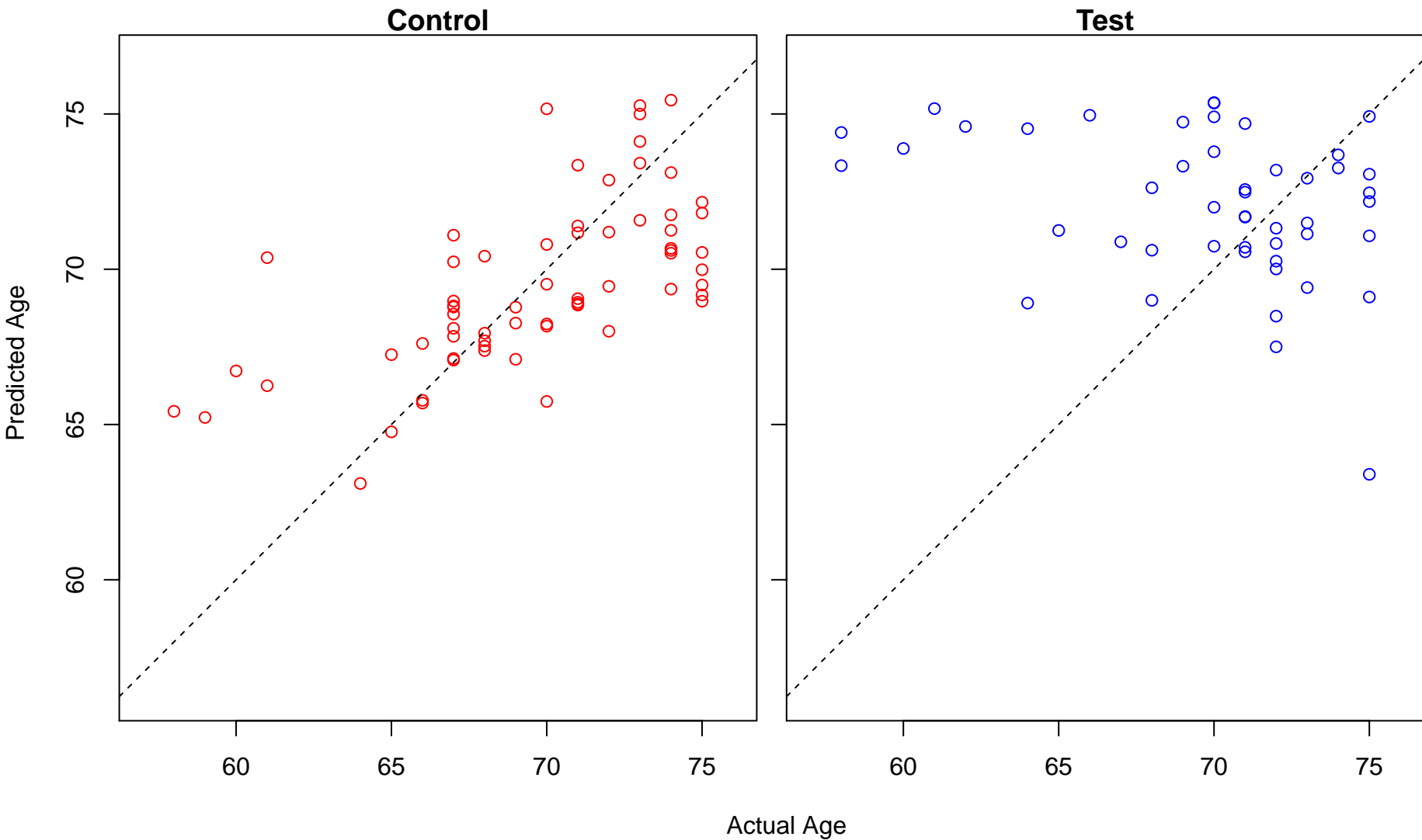
ERAD pathway (Score: 1.288470)



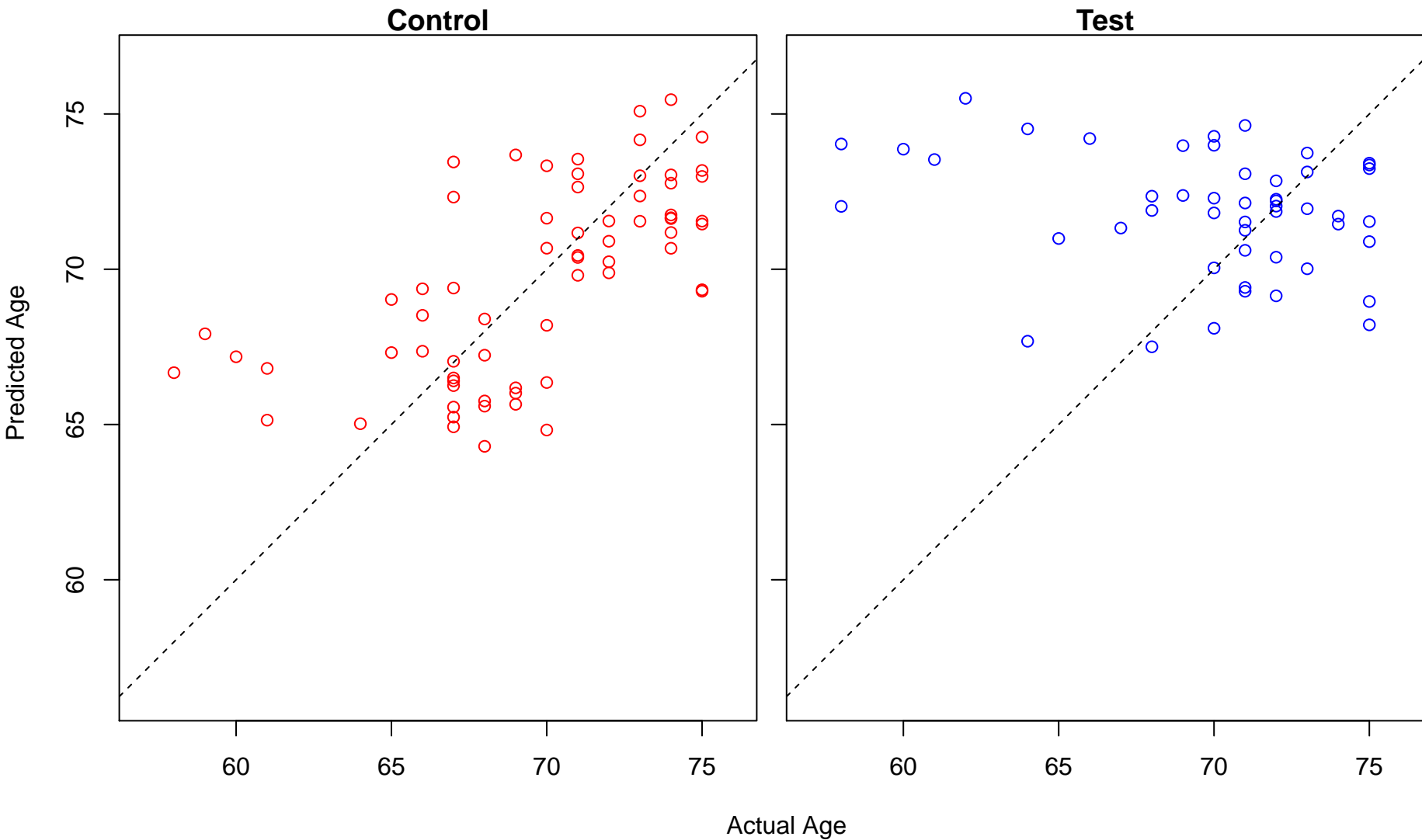
regulation of membrane lipid distribution (Score: 1.288288)



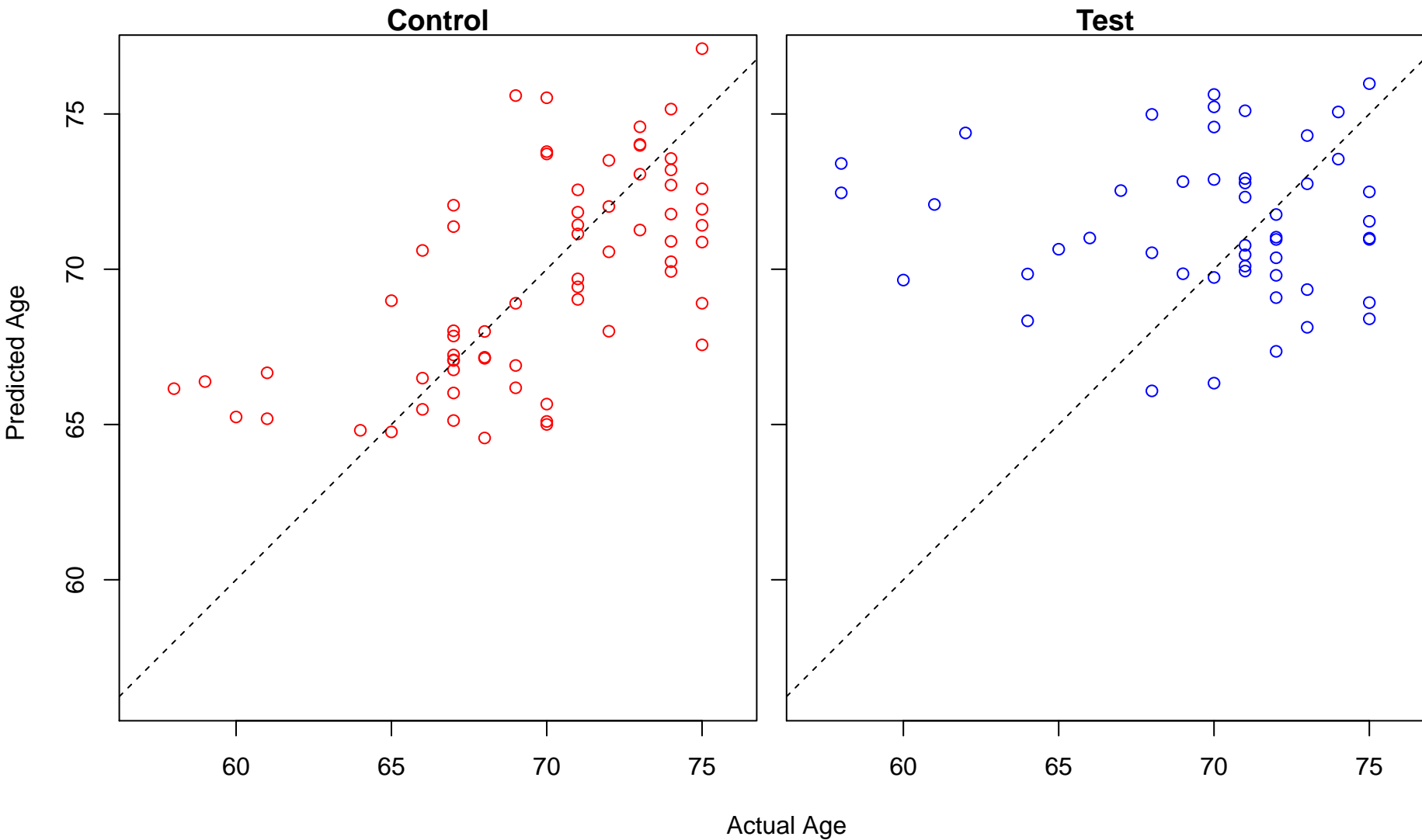
regulation of acute inflammatory response (Score: 1.288061)



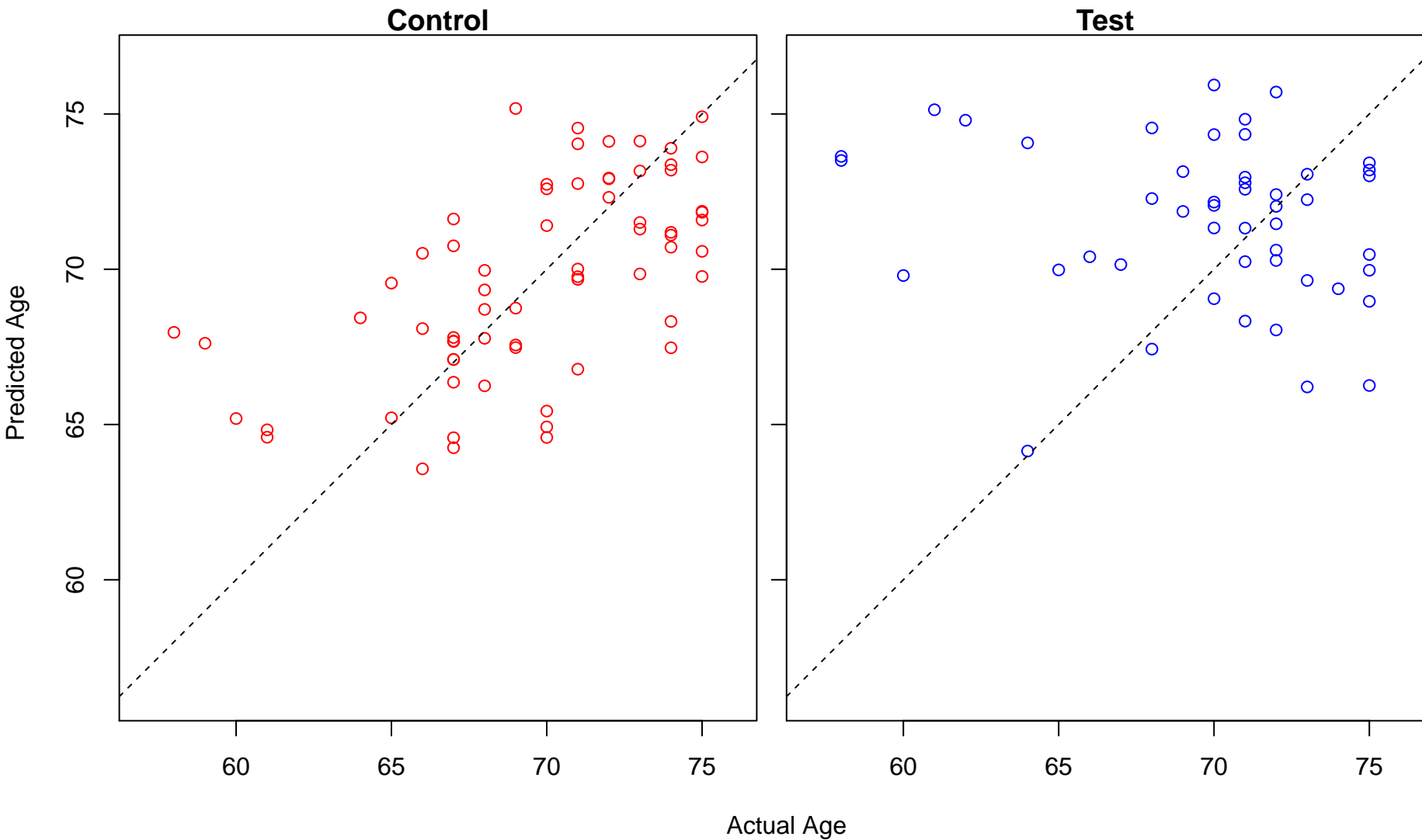
glial cell development (Score: 1.287974)



detection of stimulus (Score: 1.287456)

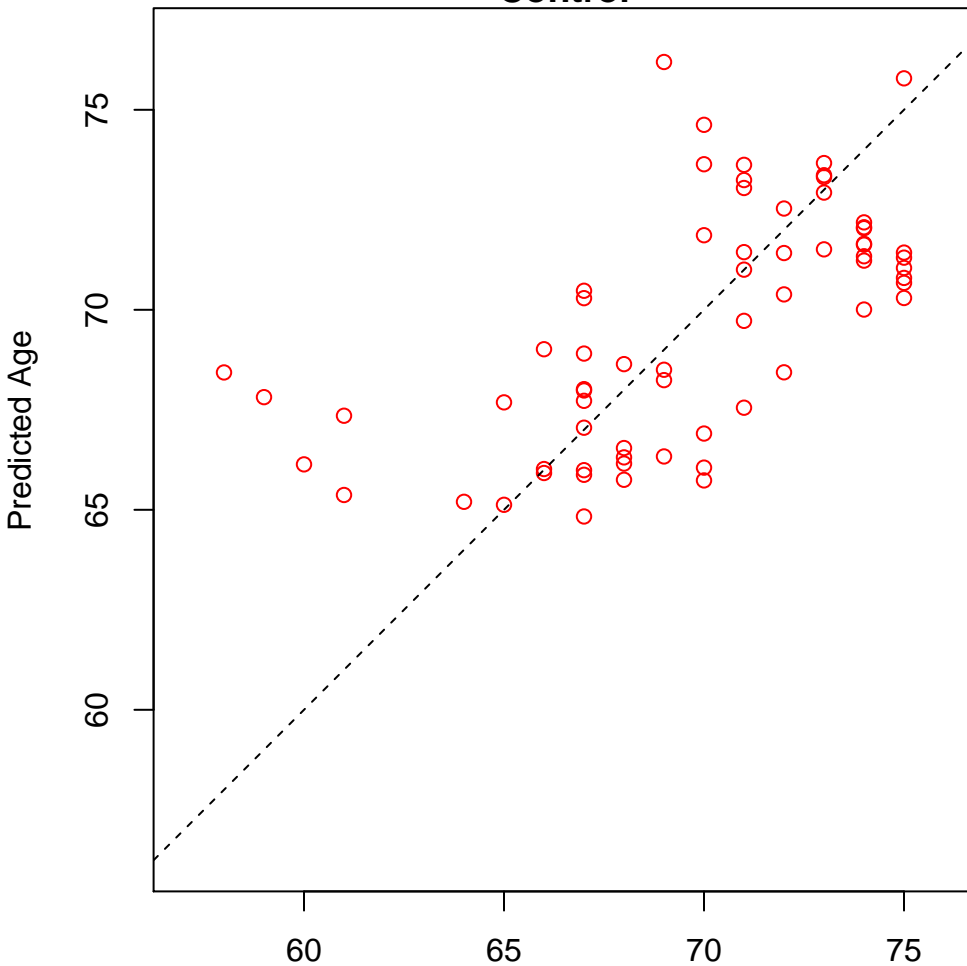


positive regulation of interleukin-8 production (Score: 1.286521)

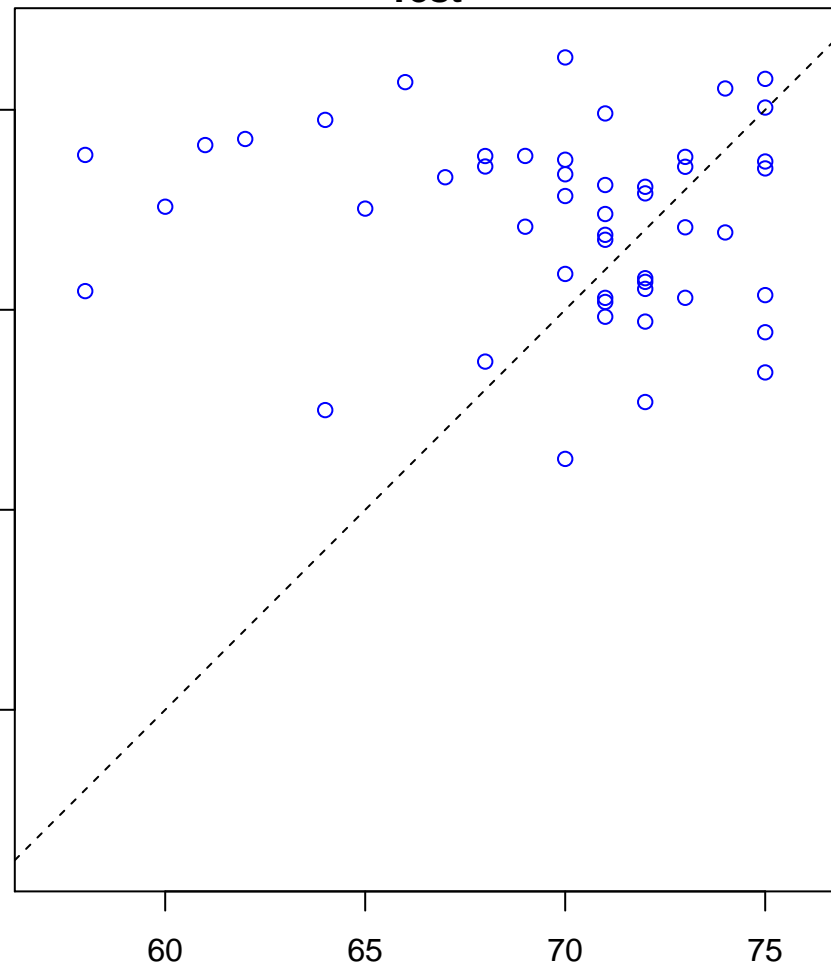


telomere maintenance via recombination (Score: 1.286140)

Control

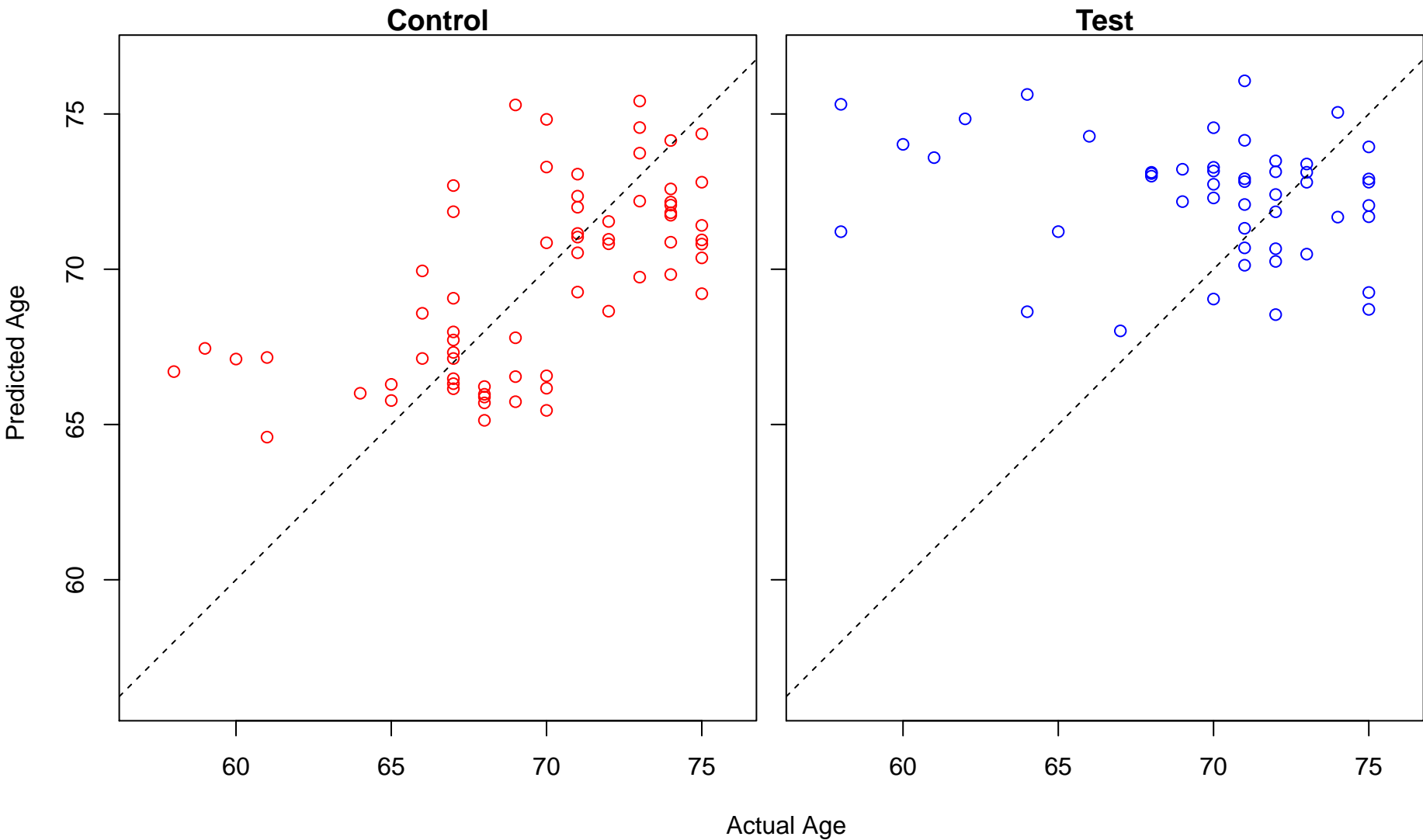


Test



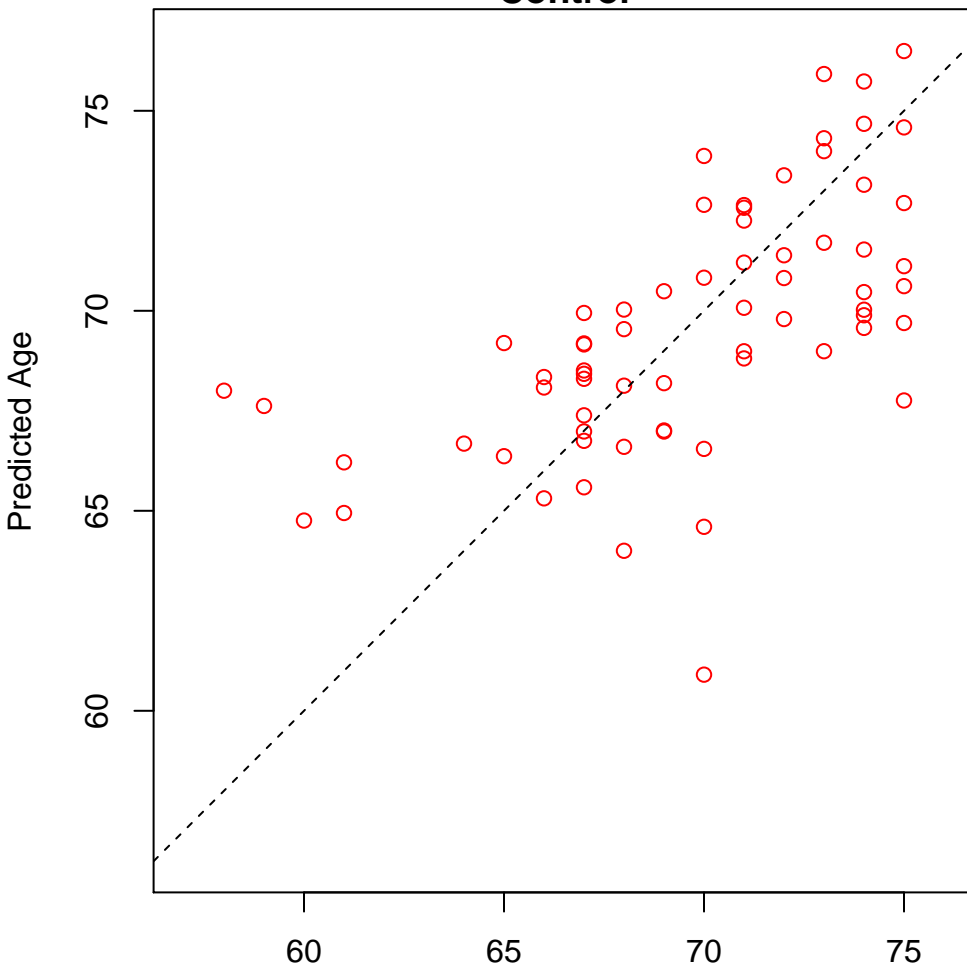
Actual Age

spermatogenesis (Score: 1.285461)

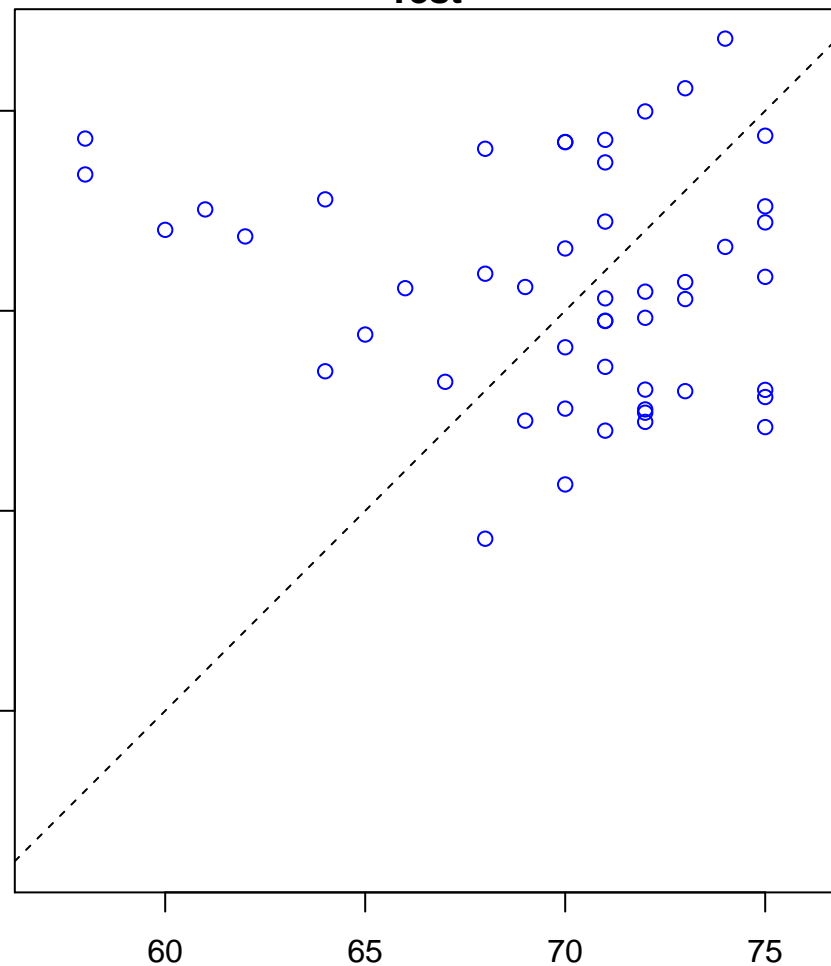


intra-Golgi vesicle-mediated transport (Score: 1.285230)

Control

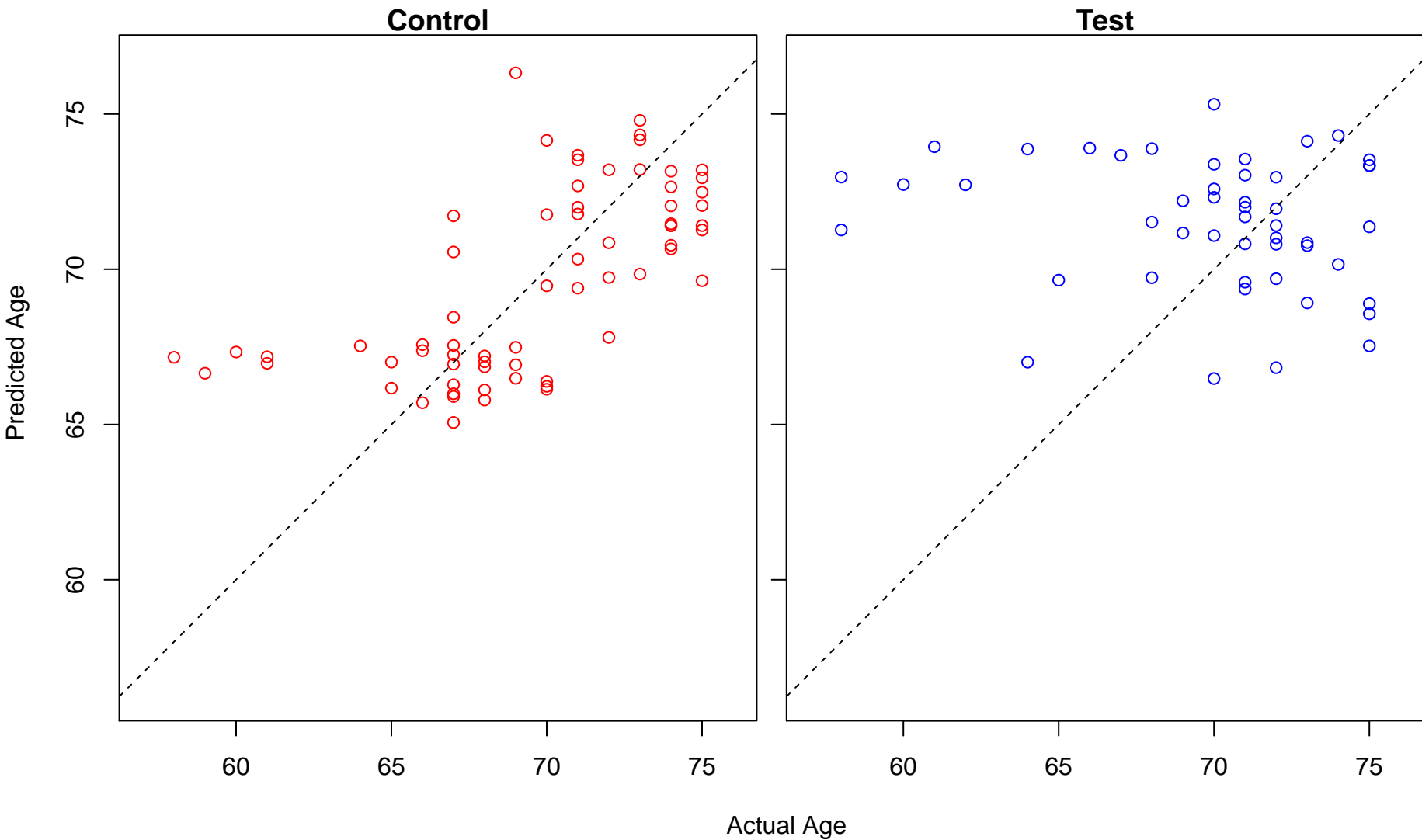


Test

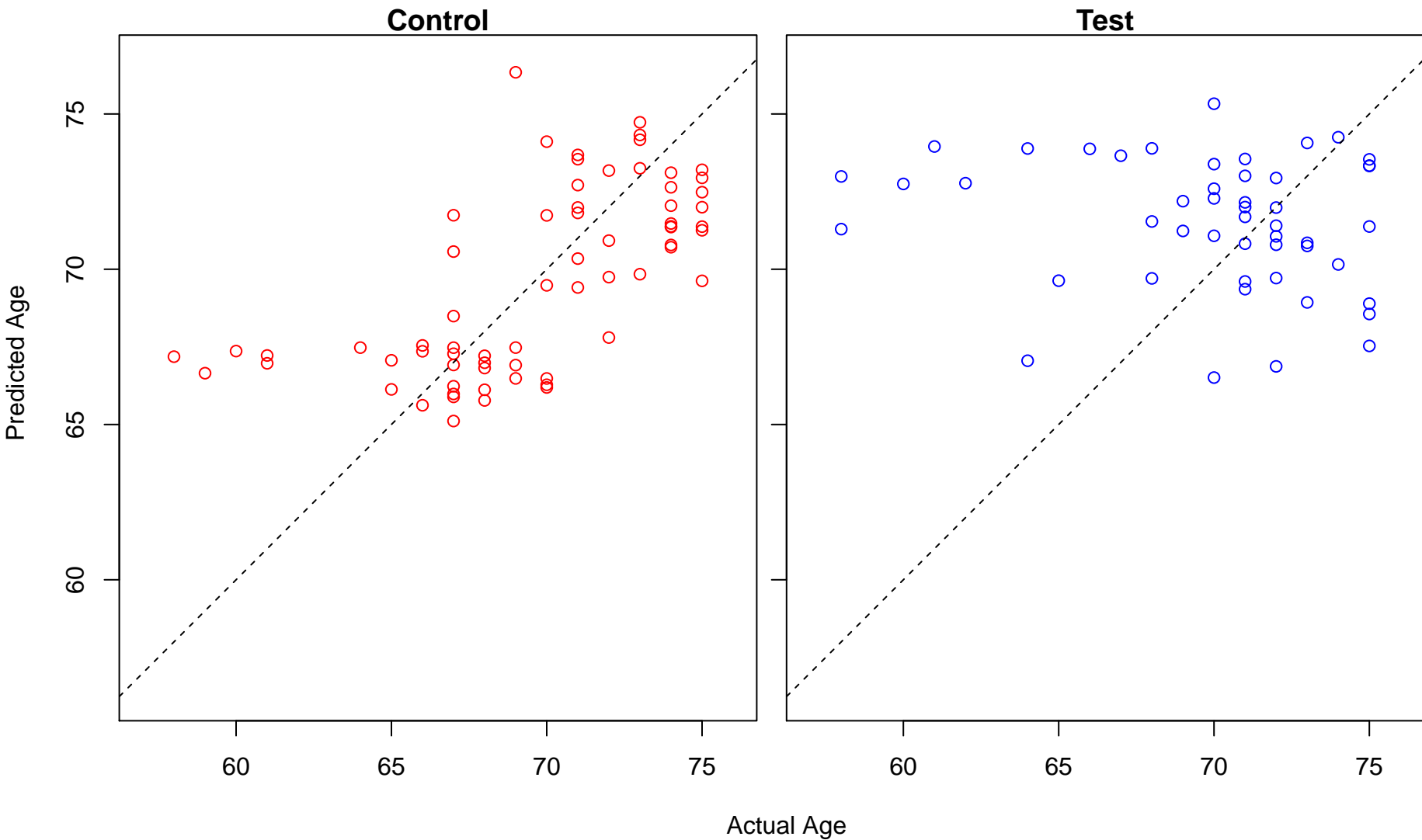


Actual Age

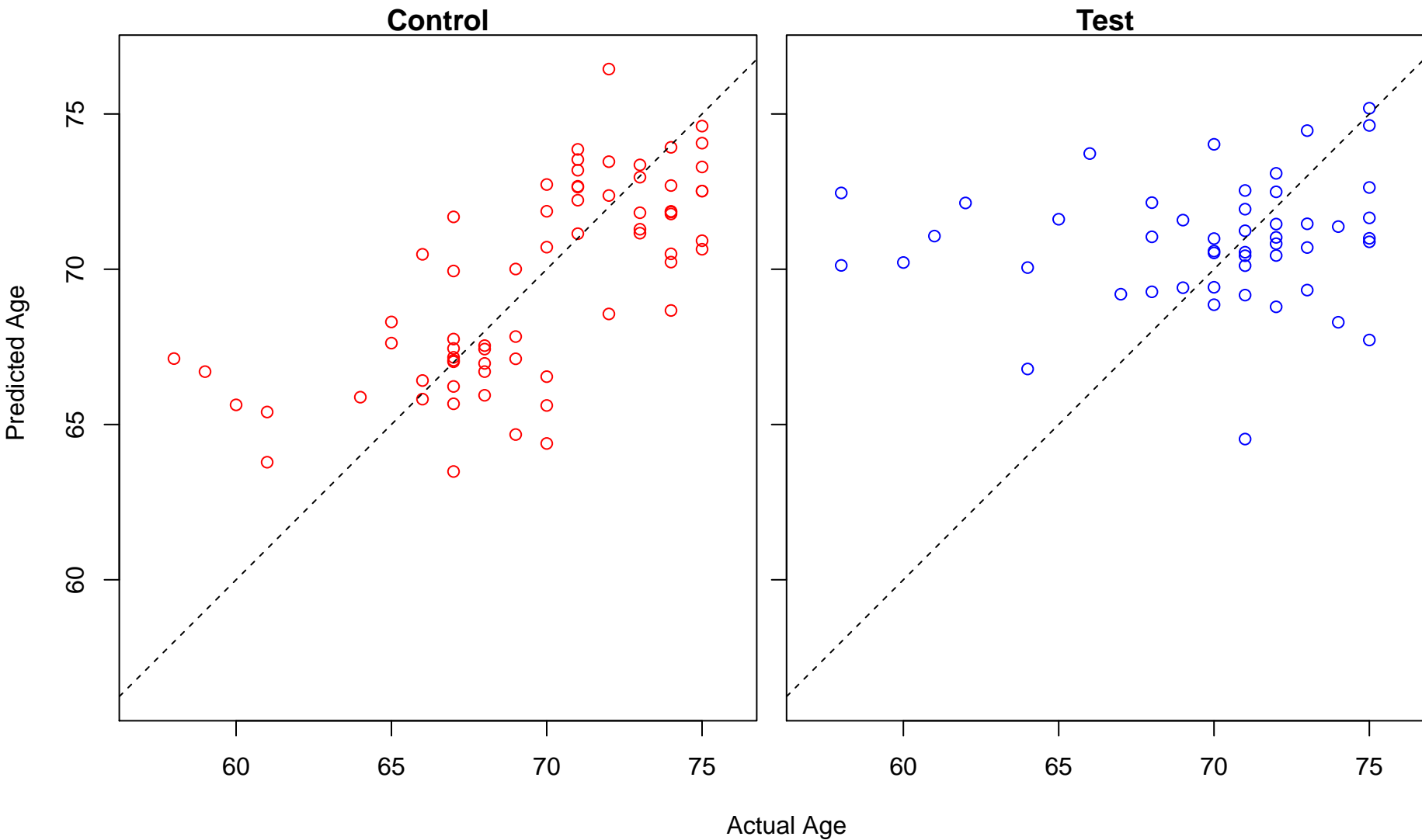
granulocyte migration (Score: 1.284217)



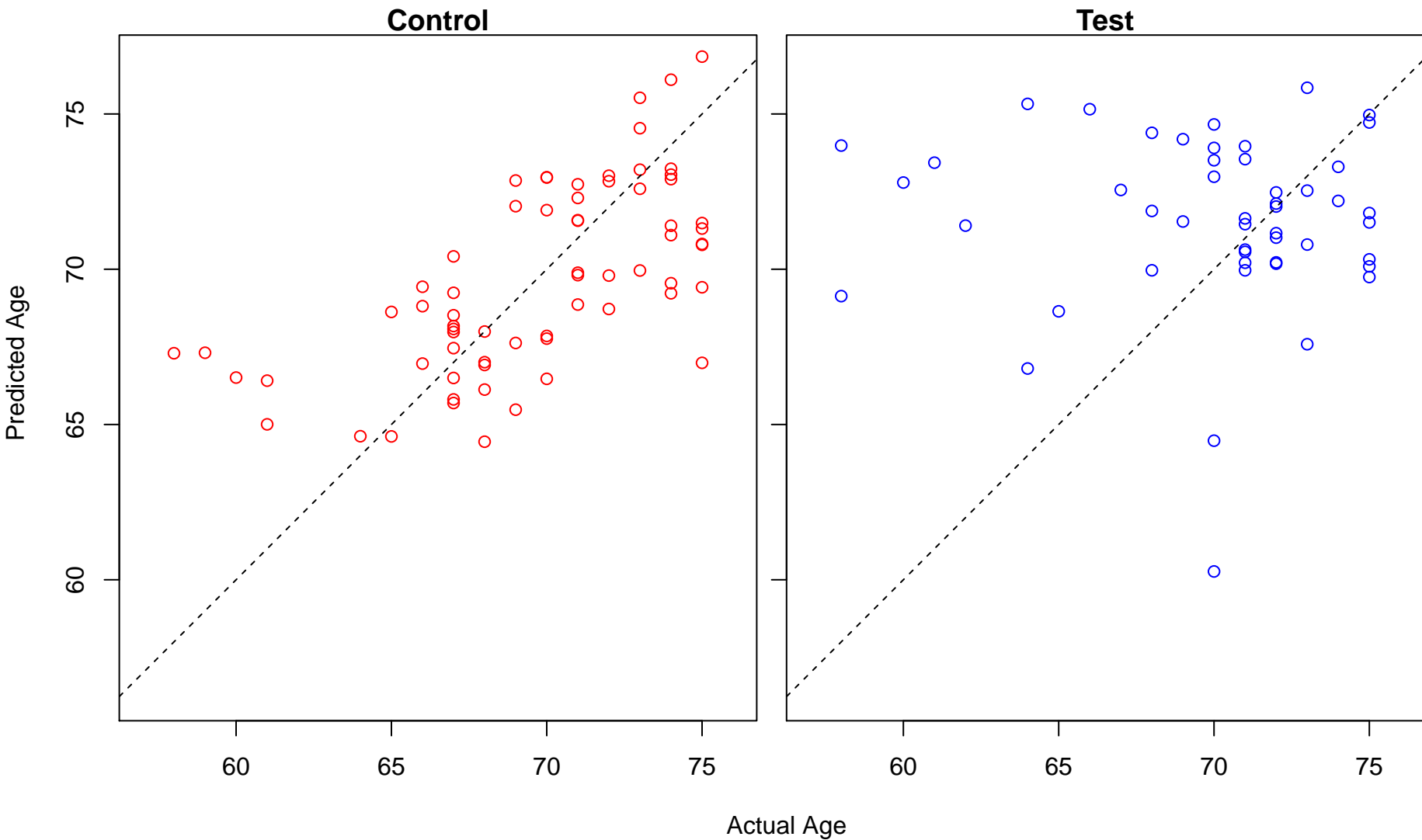
granulocyte chemotaxis (Score: 1.283414)



regulation of glycolytic process (Score: 1.283325)

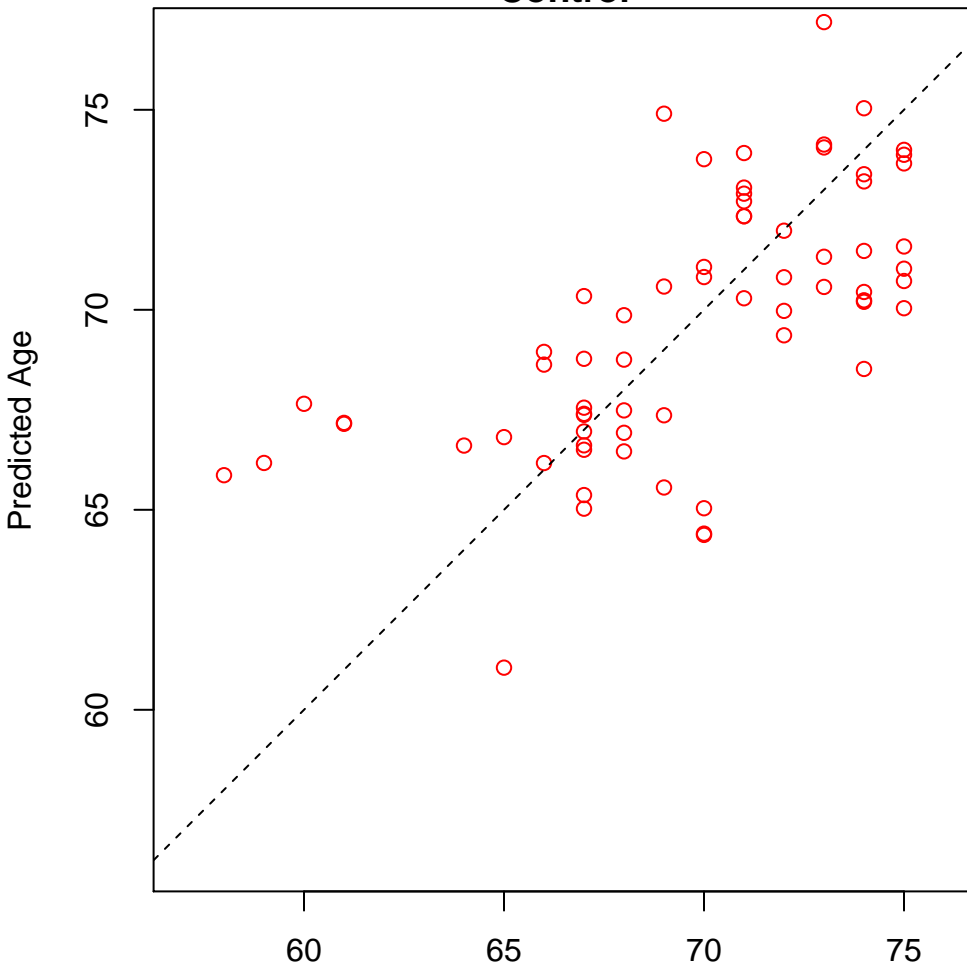


negative regulation of fatty acid metabolic process (Score: 1.283231)

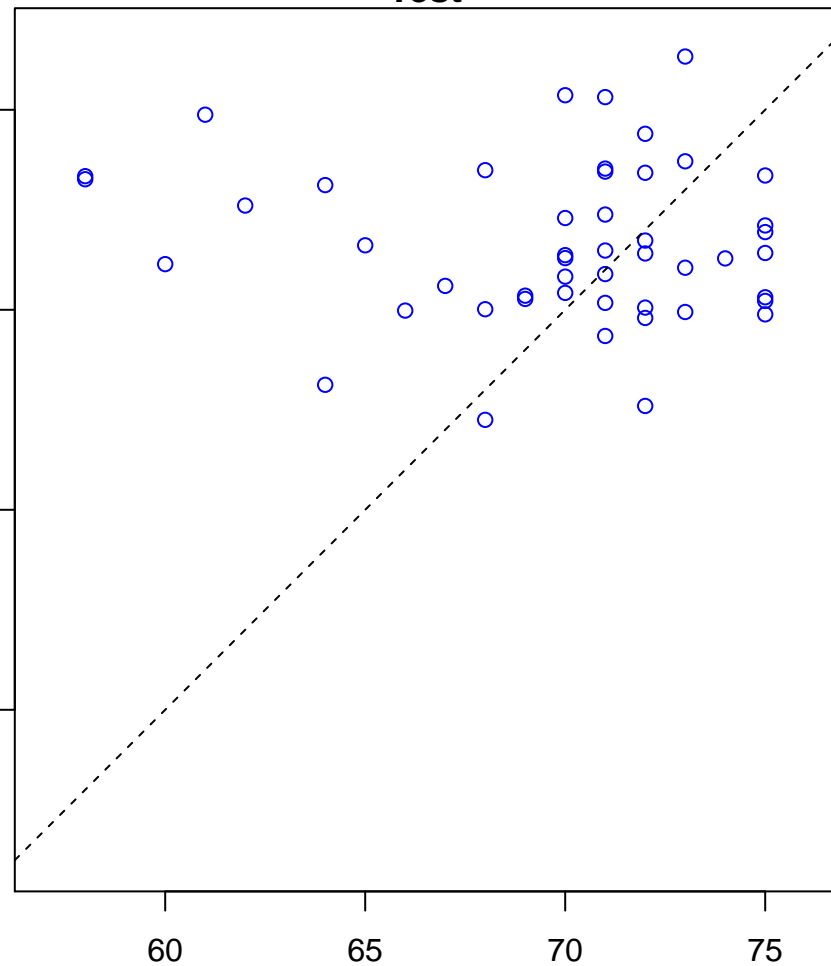


regulation of DNA biosynthetic process (Score: 1.282222)

Control

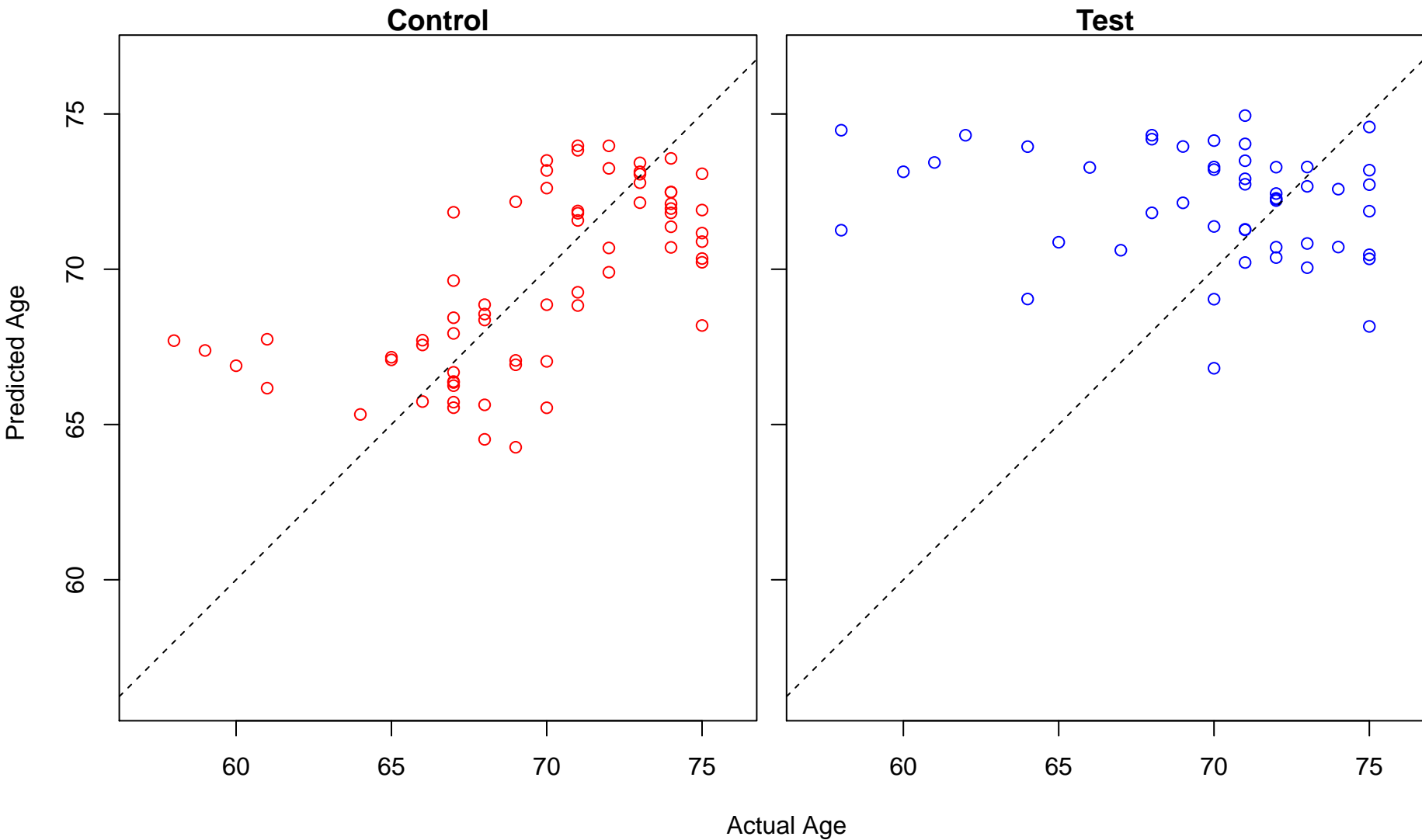


Test

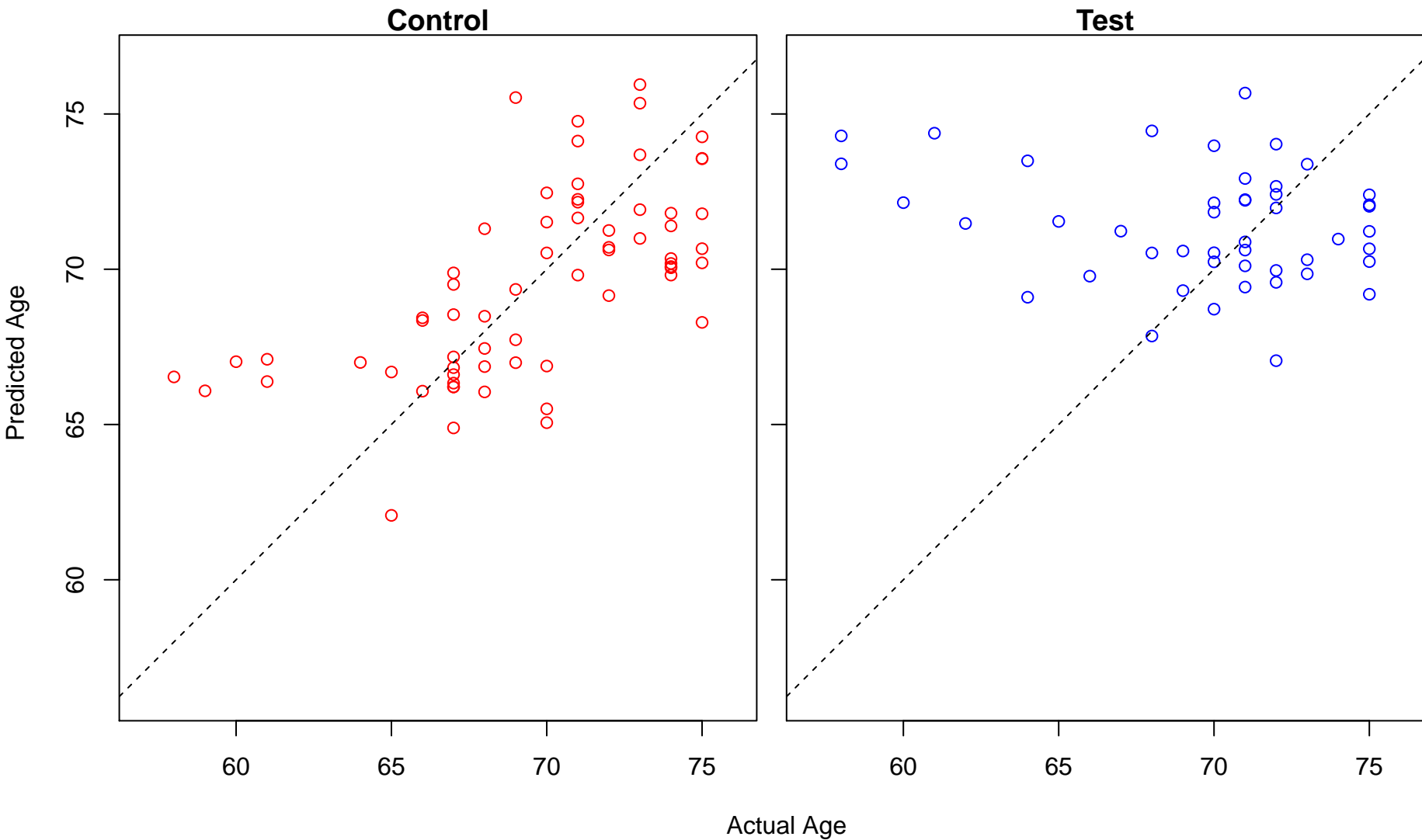


Actual Age

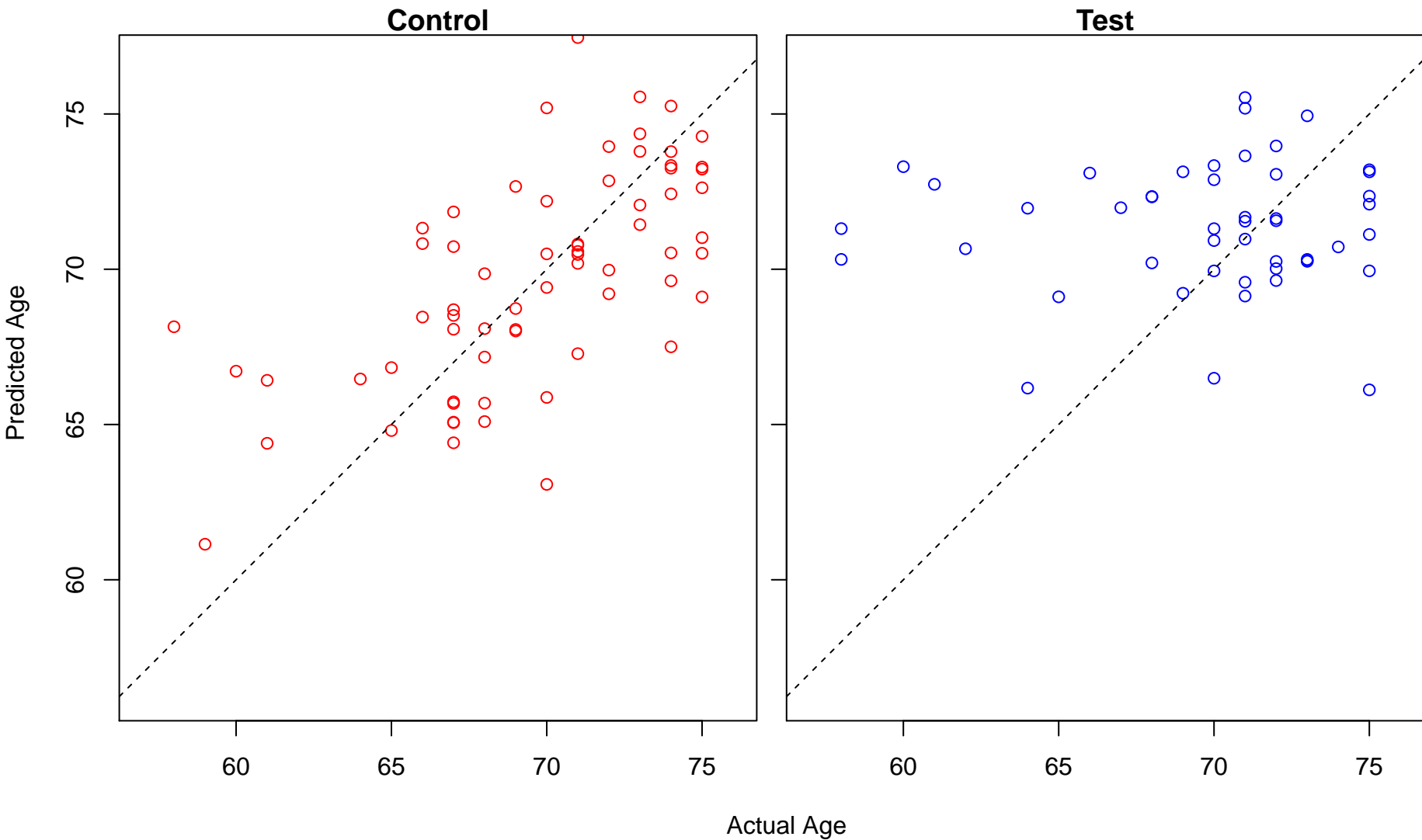
mitotic G2/M transition checkpoint (Score: 1.282183)



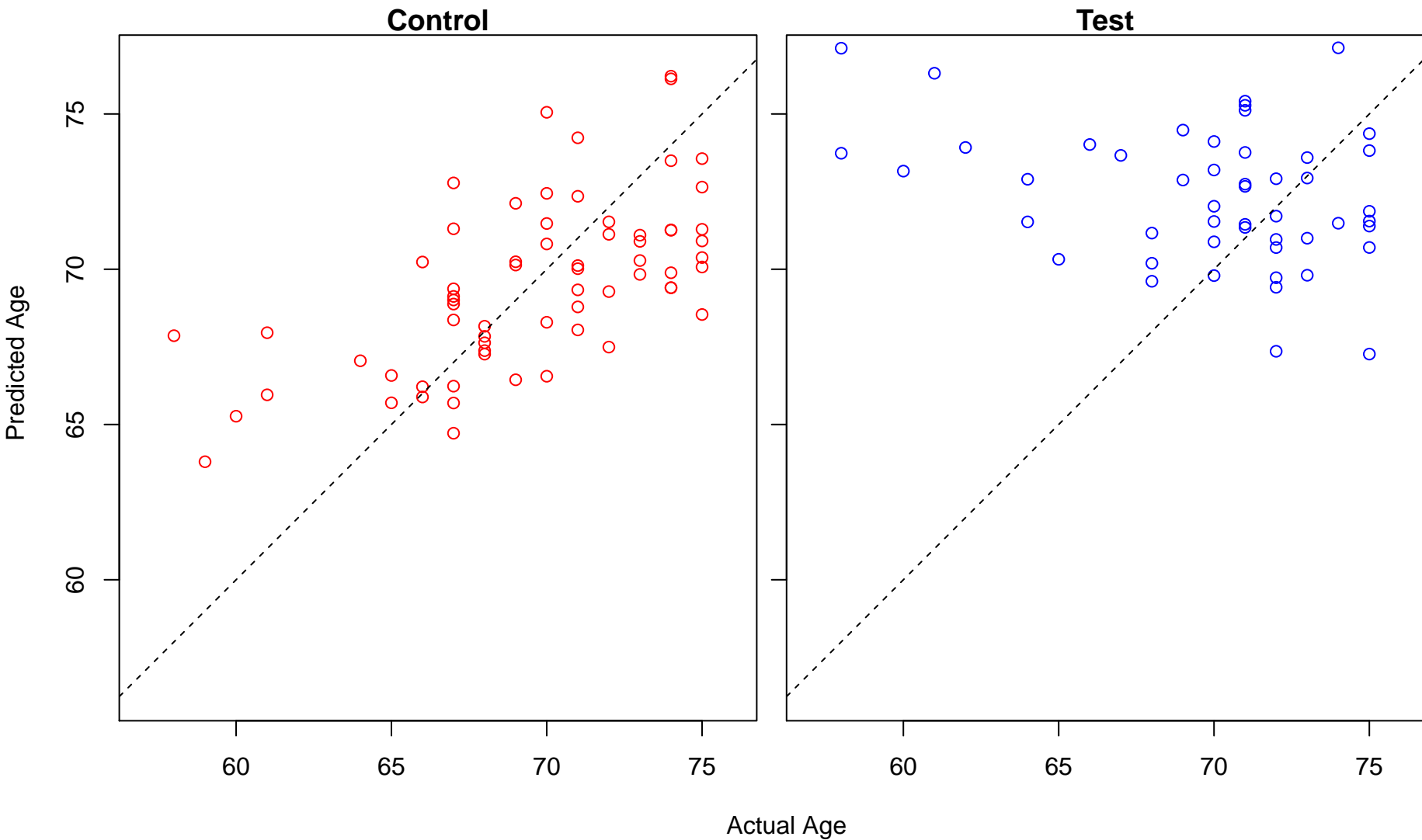
positive regulation of DNA biosynthetic process (Score: 1.282113)



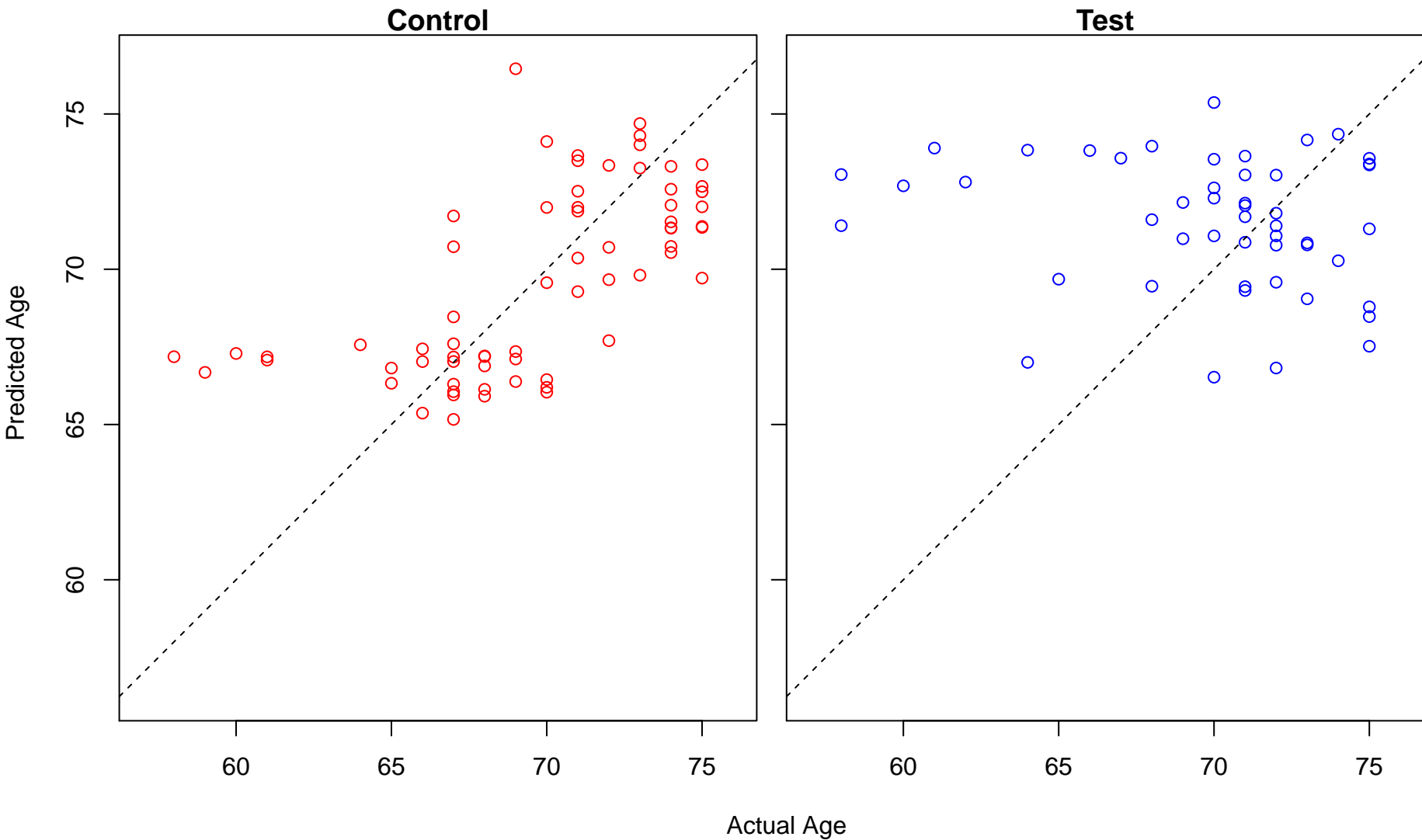
glycosyl compound catabolic process (Score: 1.281802)



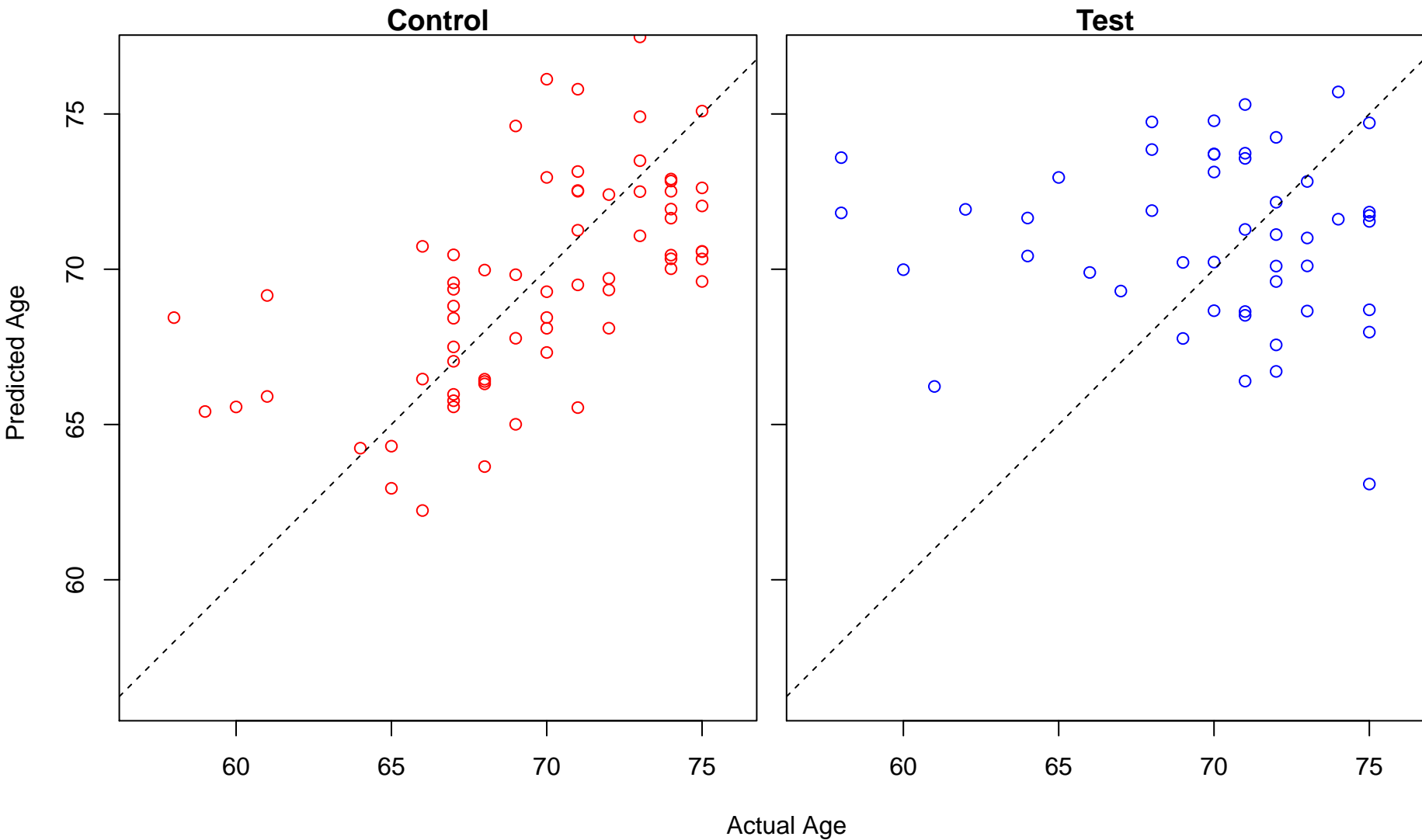
response to pH (Score: 1.281330)



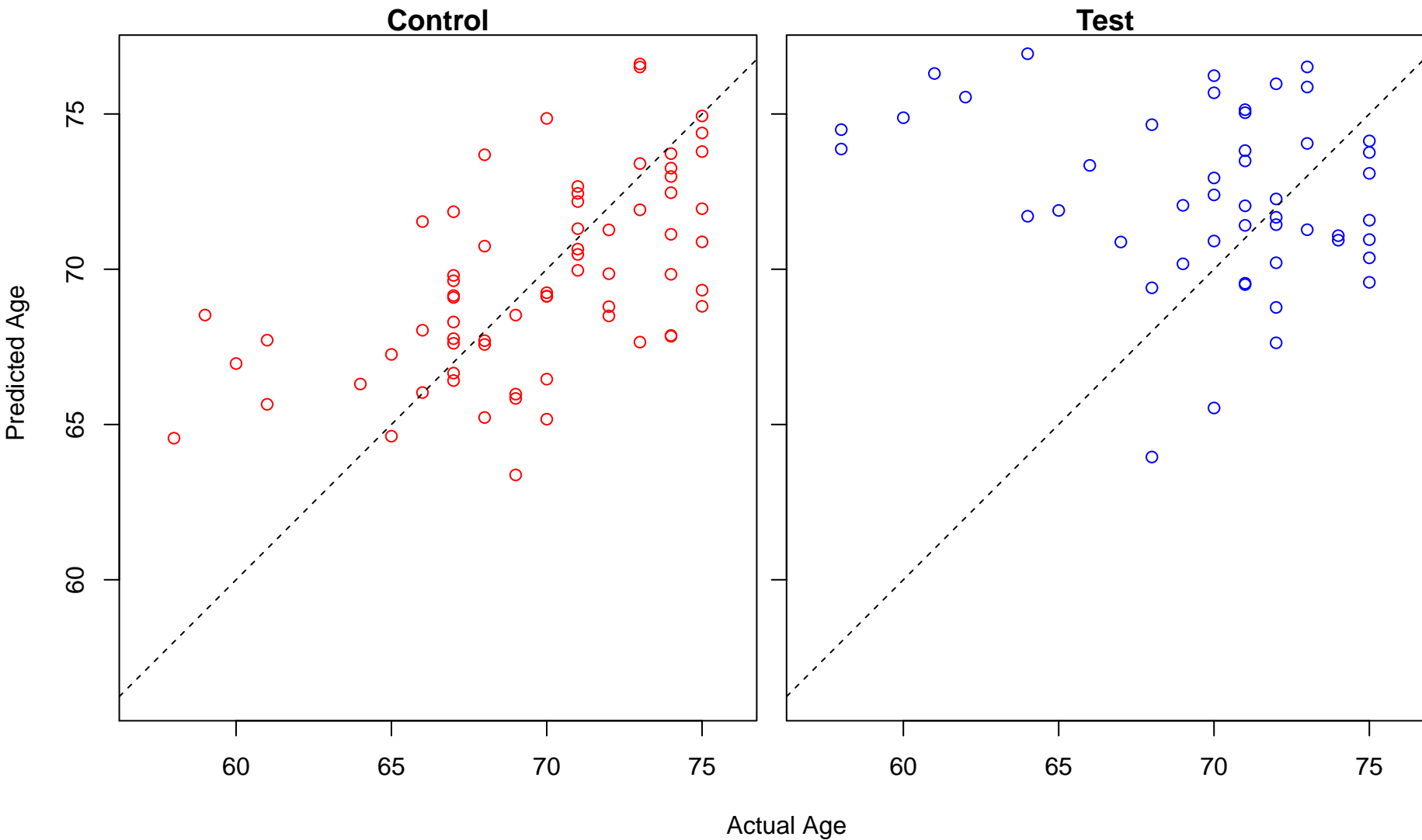
myeloid leukocyte migration (Score: 1.280327)



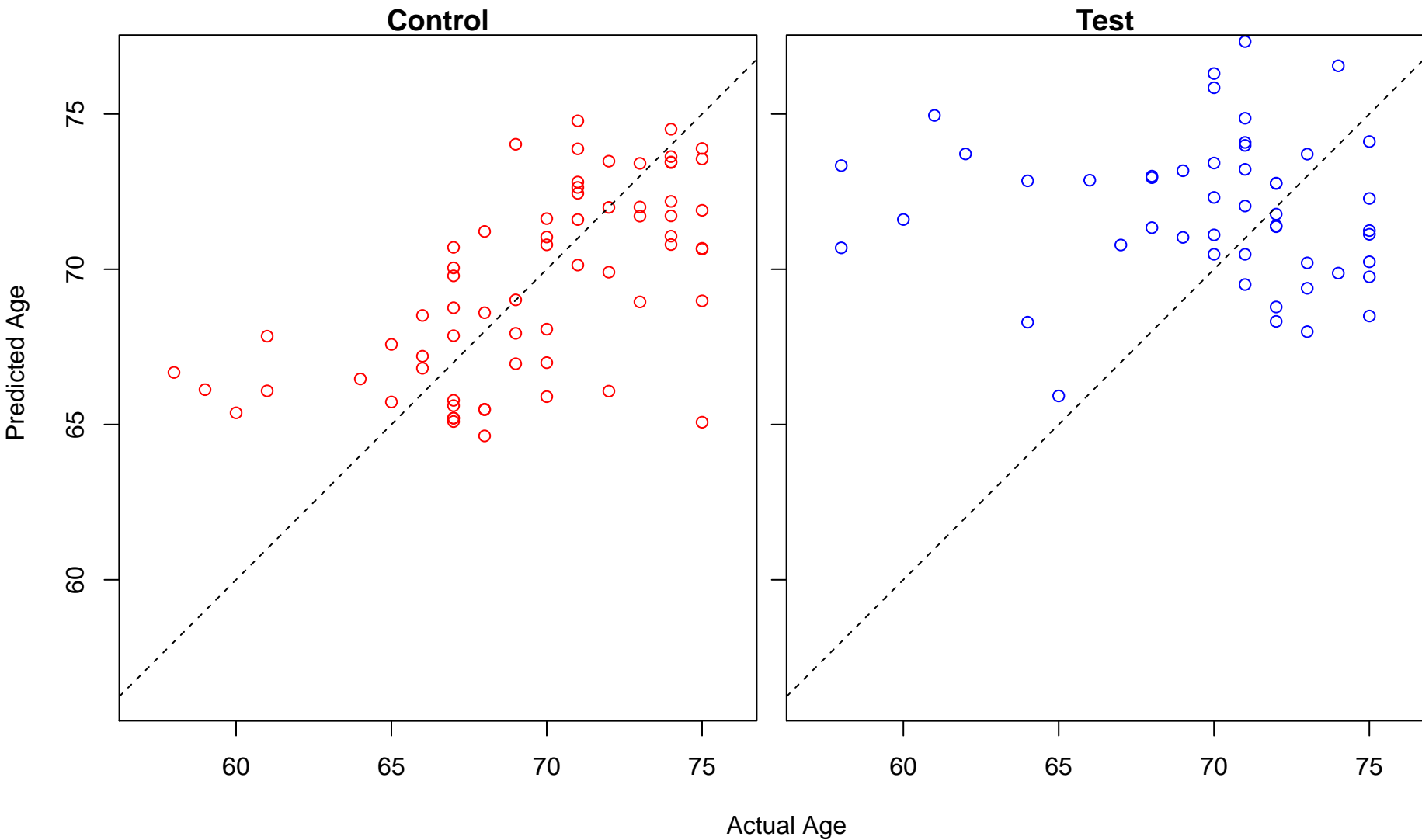
modification by host of symbiont morphology or physiology (Score: 1.280022)



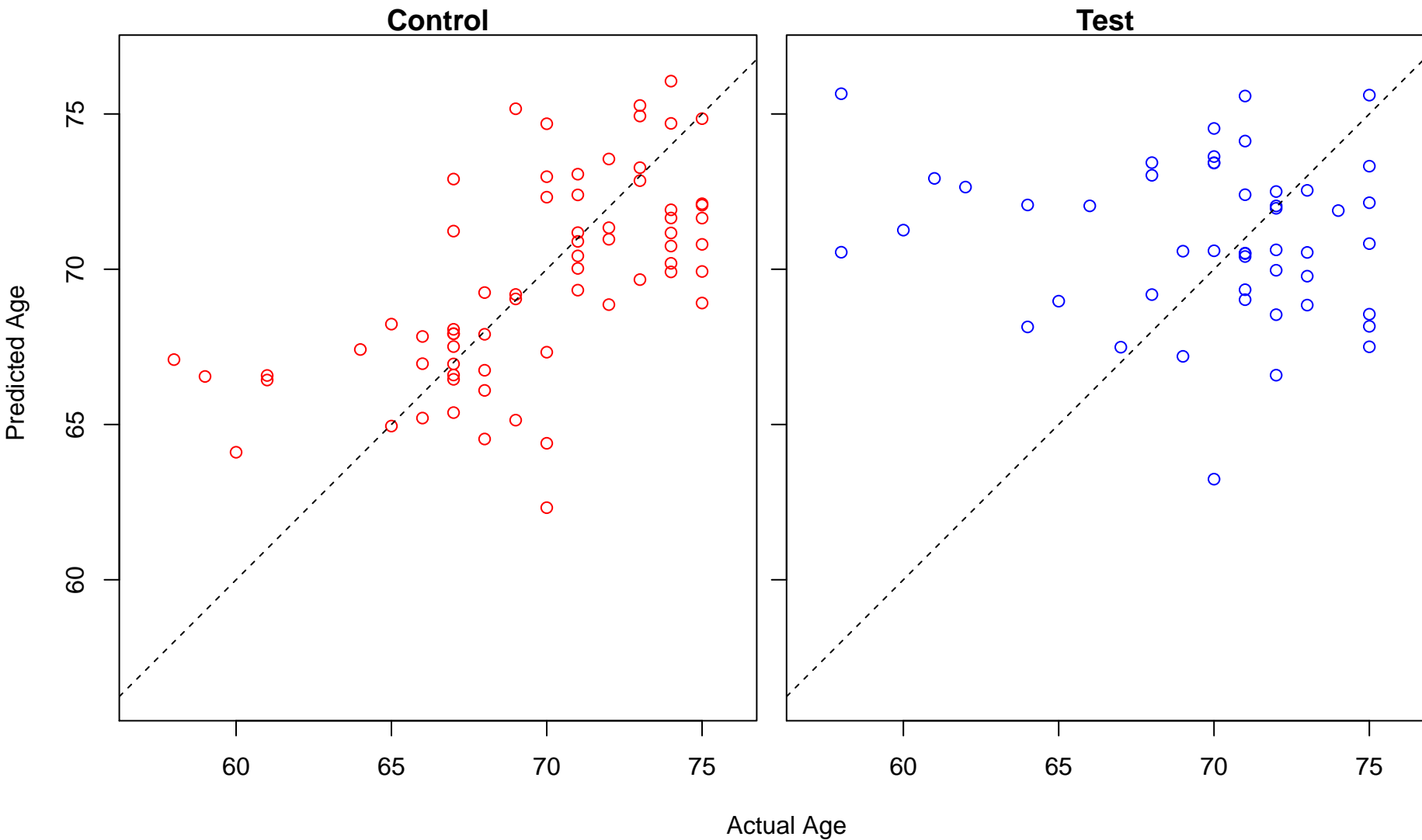
acetyl-CoA metabolic process (Score: 1.280007)



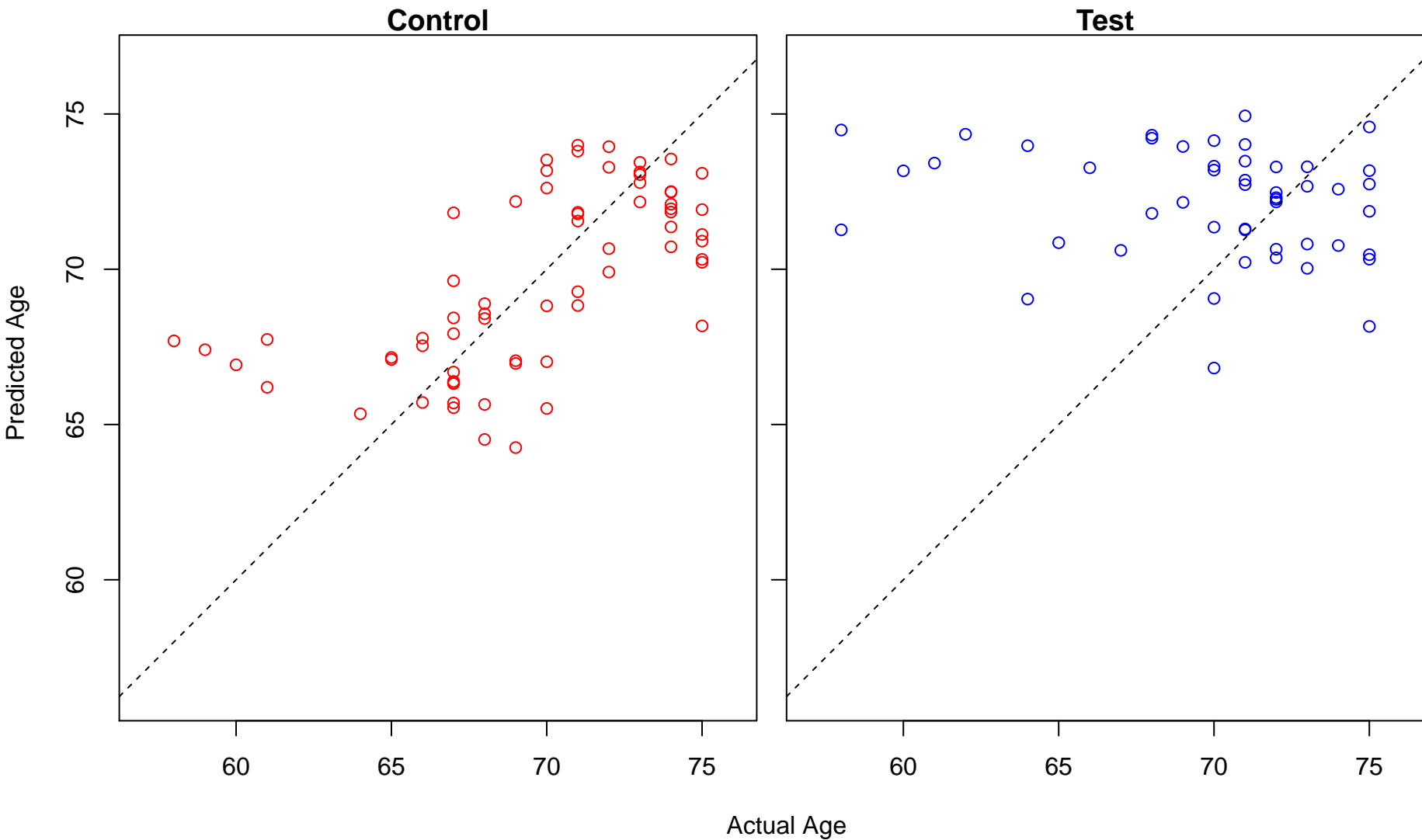
regulation of T-helper 1 type immune response (Score: 1.280003)



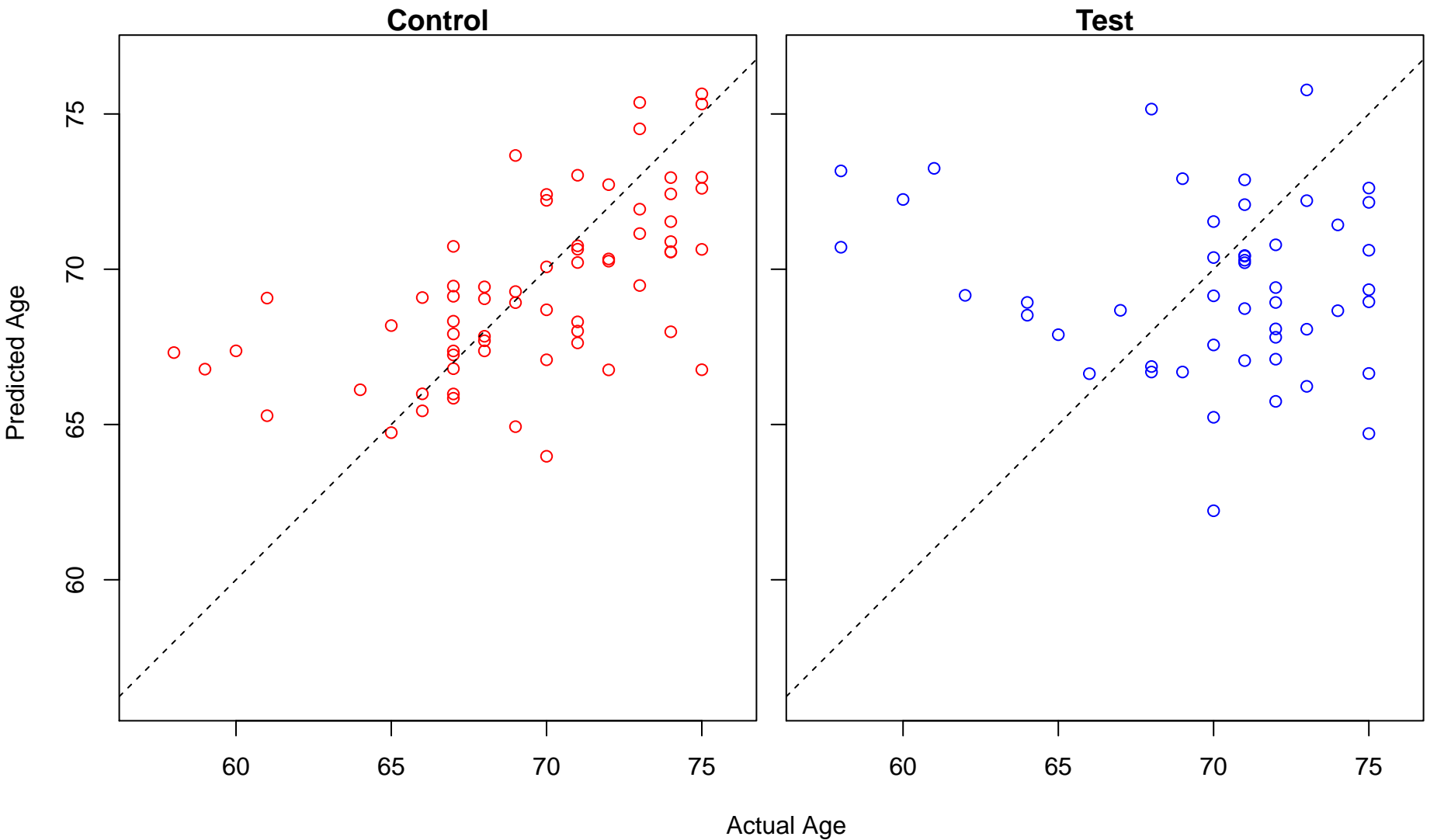
monovalent inorganic cation homeostasis (Score: 1.279192)



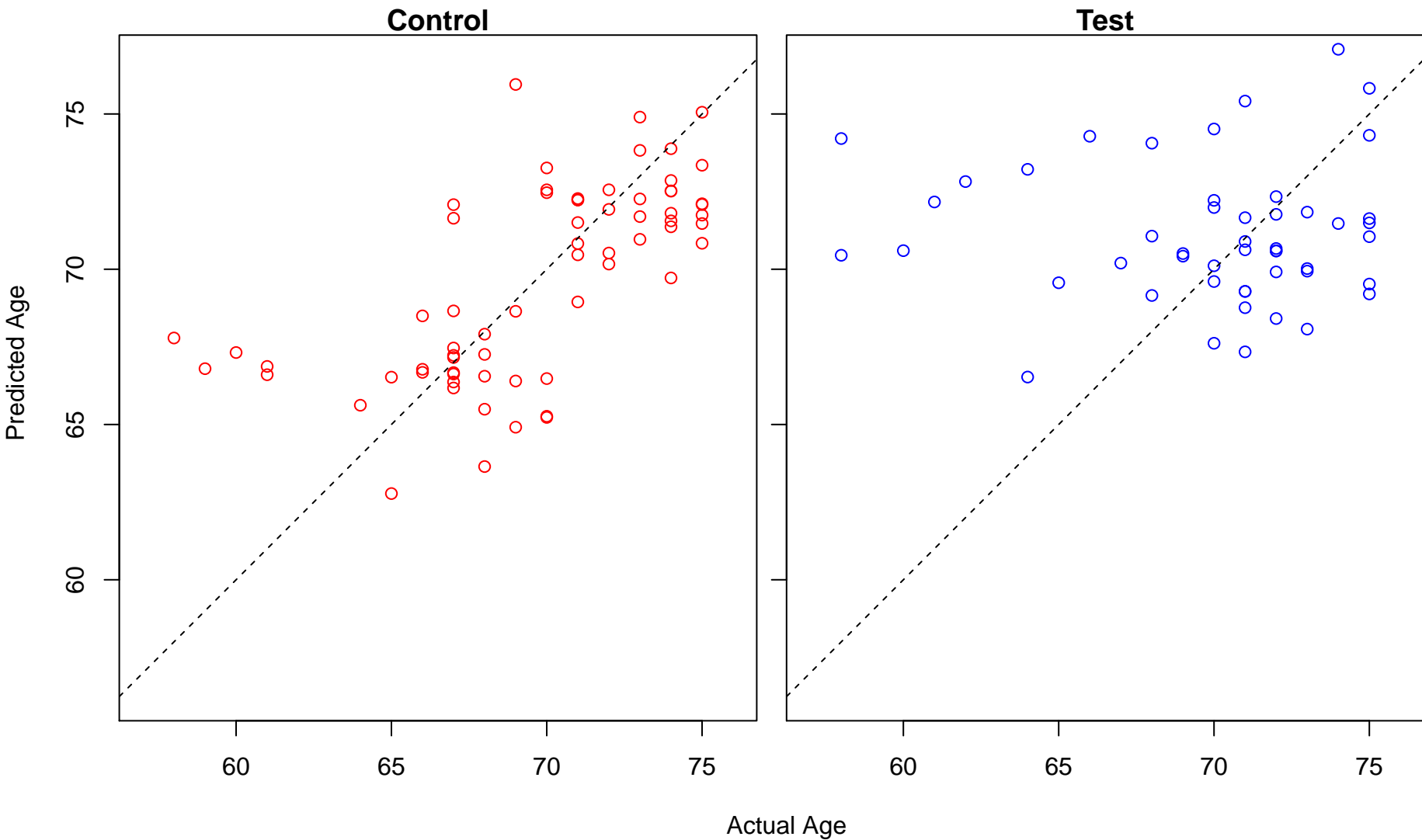
negative regulation of G2/M transition of mitotic cell cycle (Score: 1.279058)



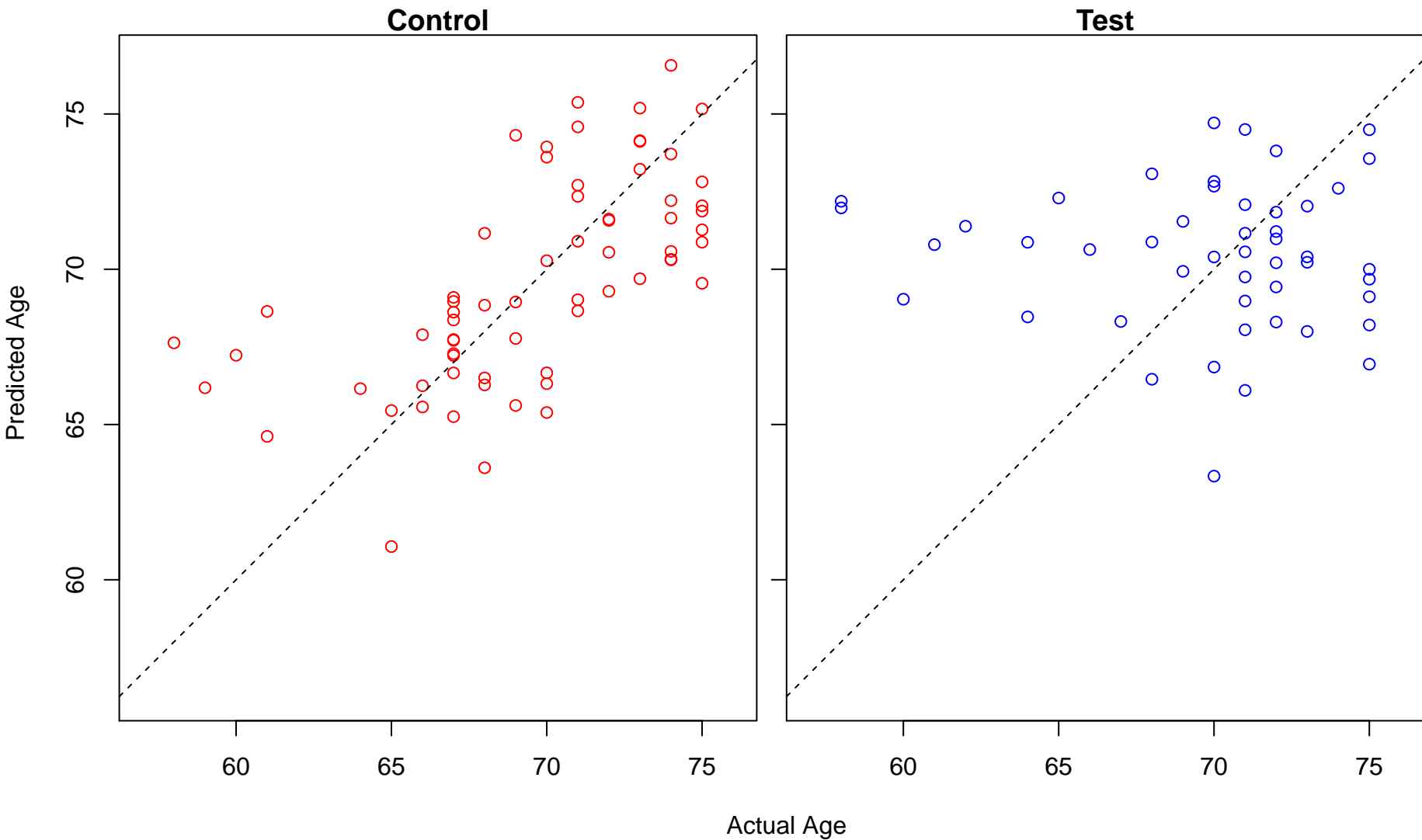
of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell cycle



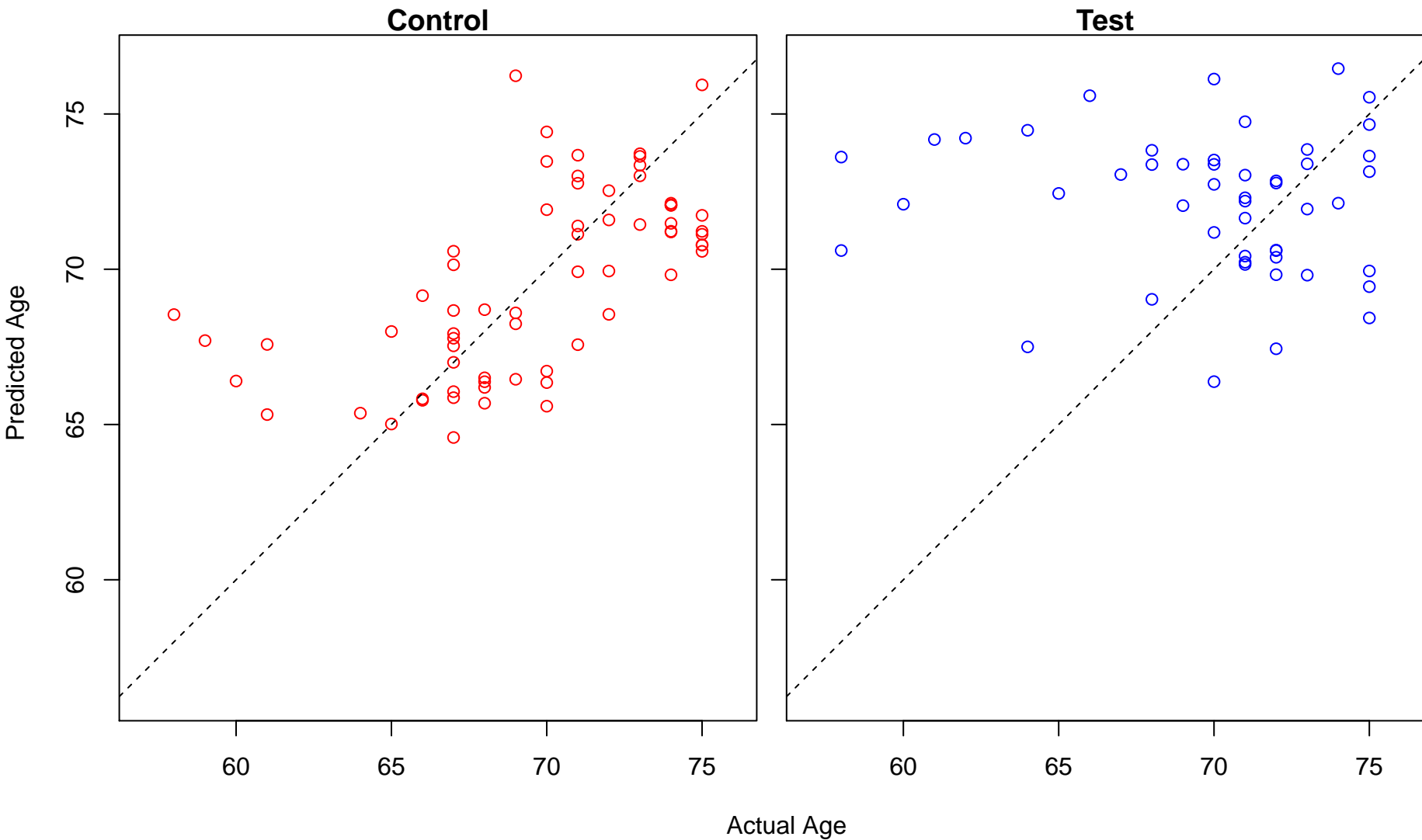
regulation of ossification (Score: 1.278433)



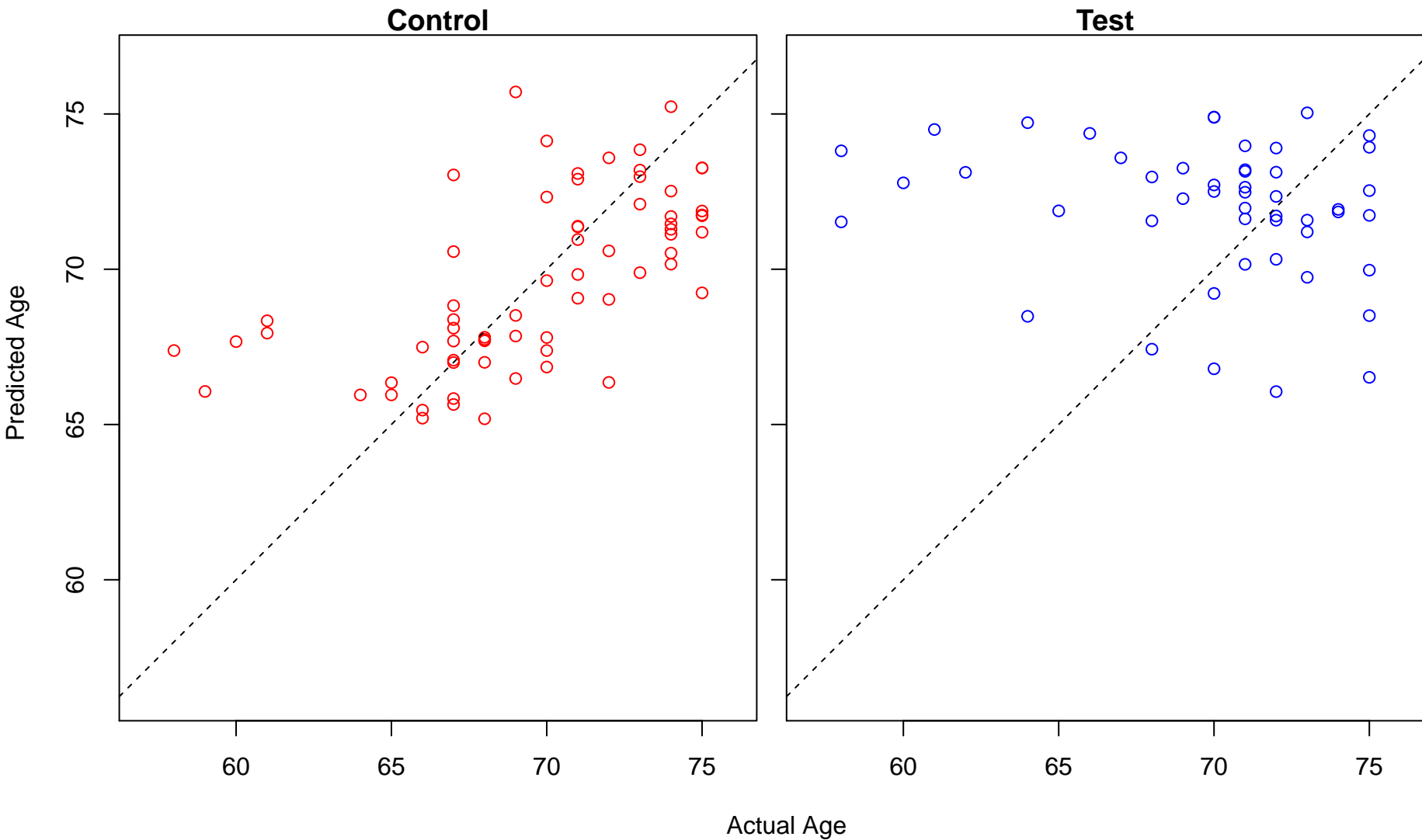
regulation of calcium ion transport (Score: 1.277763)



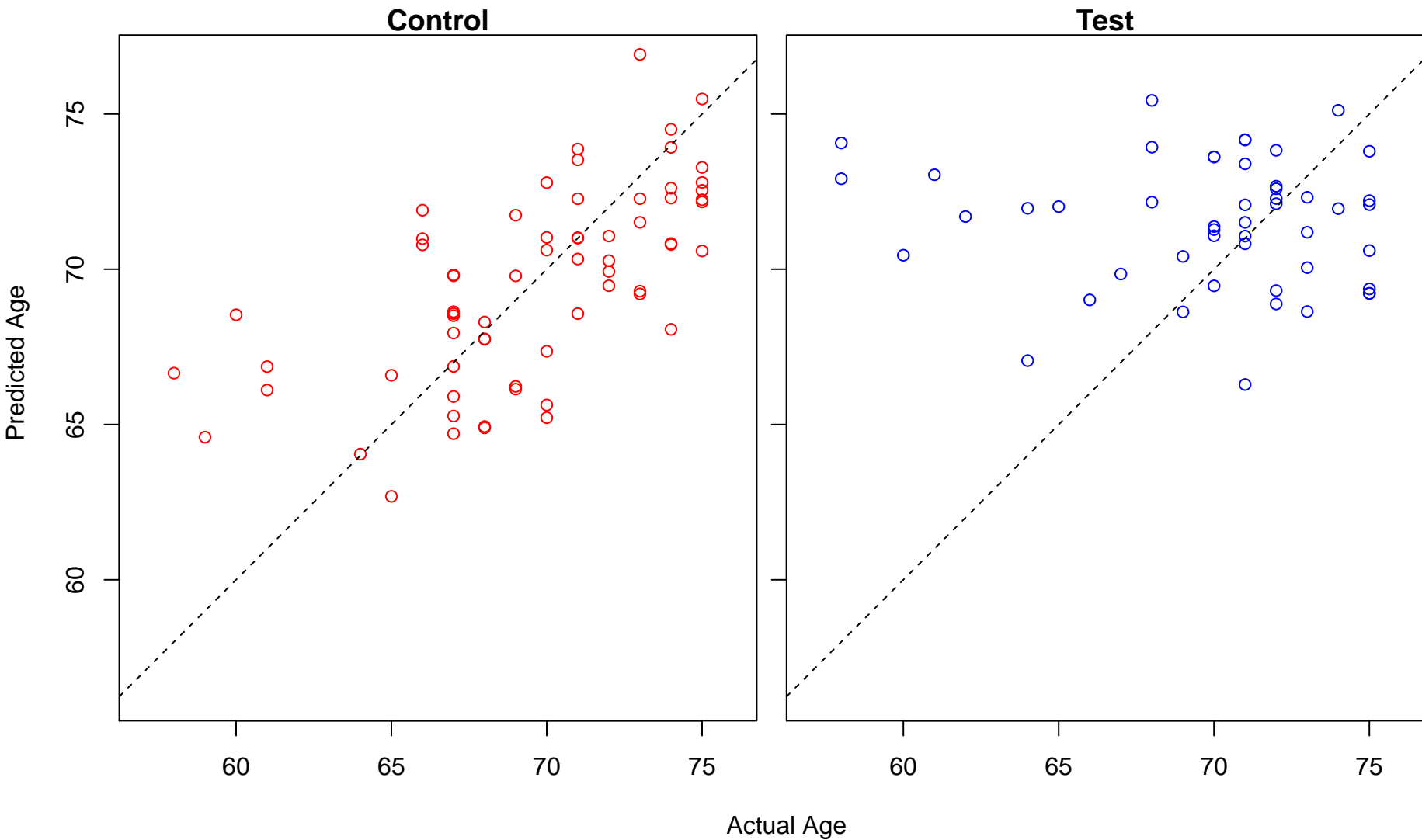
mitotic recombination (Score: 1.277030)



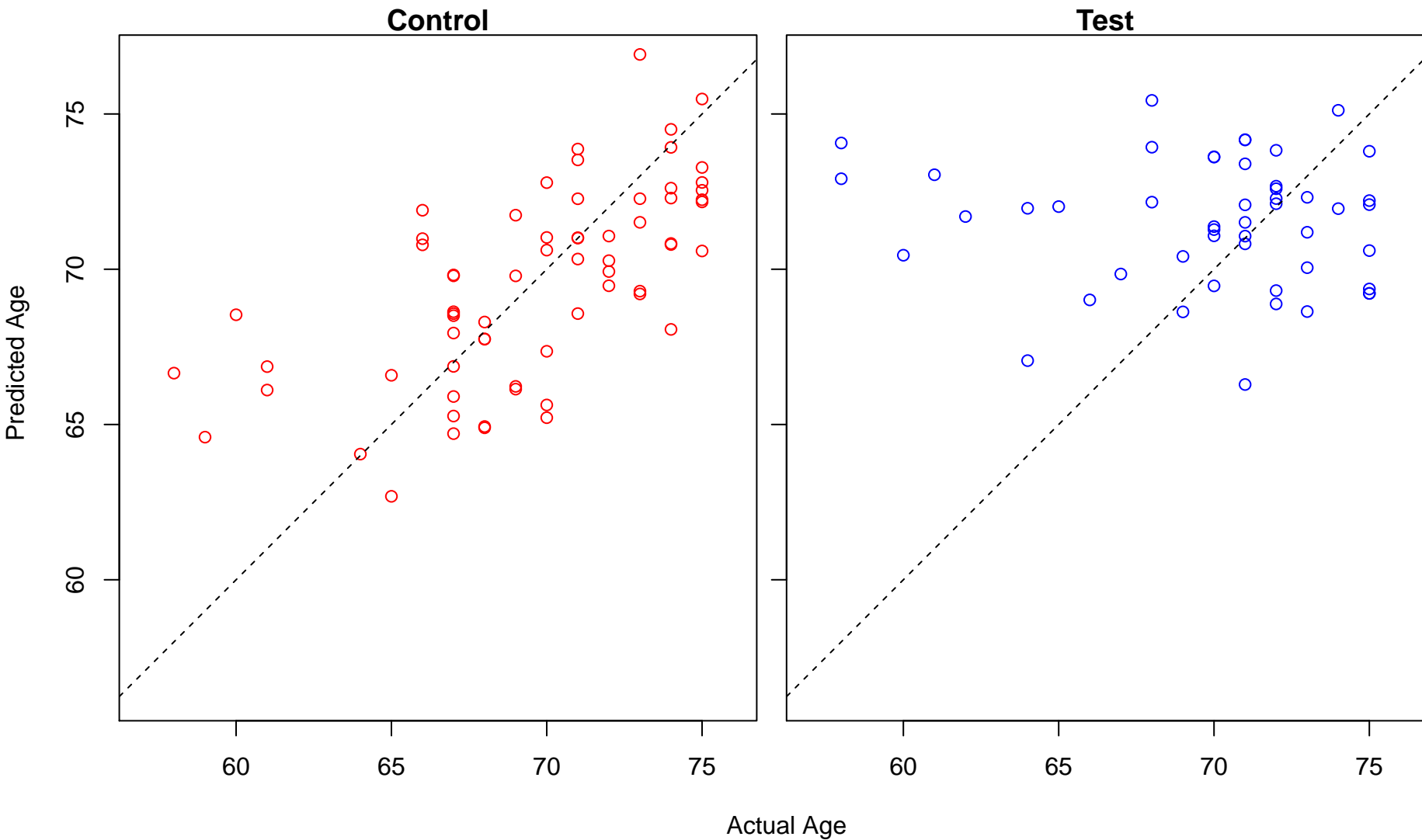
negative regulation of JNK cascade (Score: 1.276791)



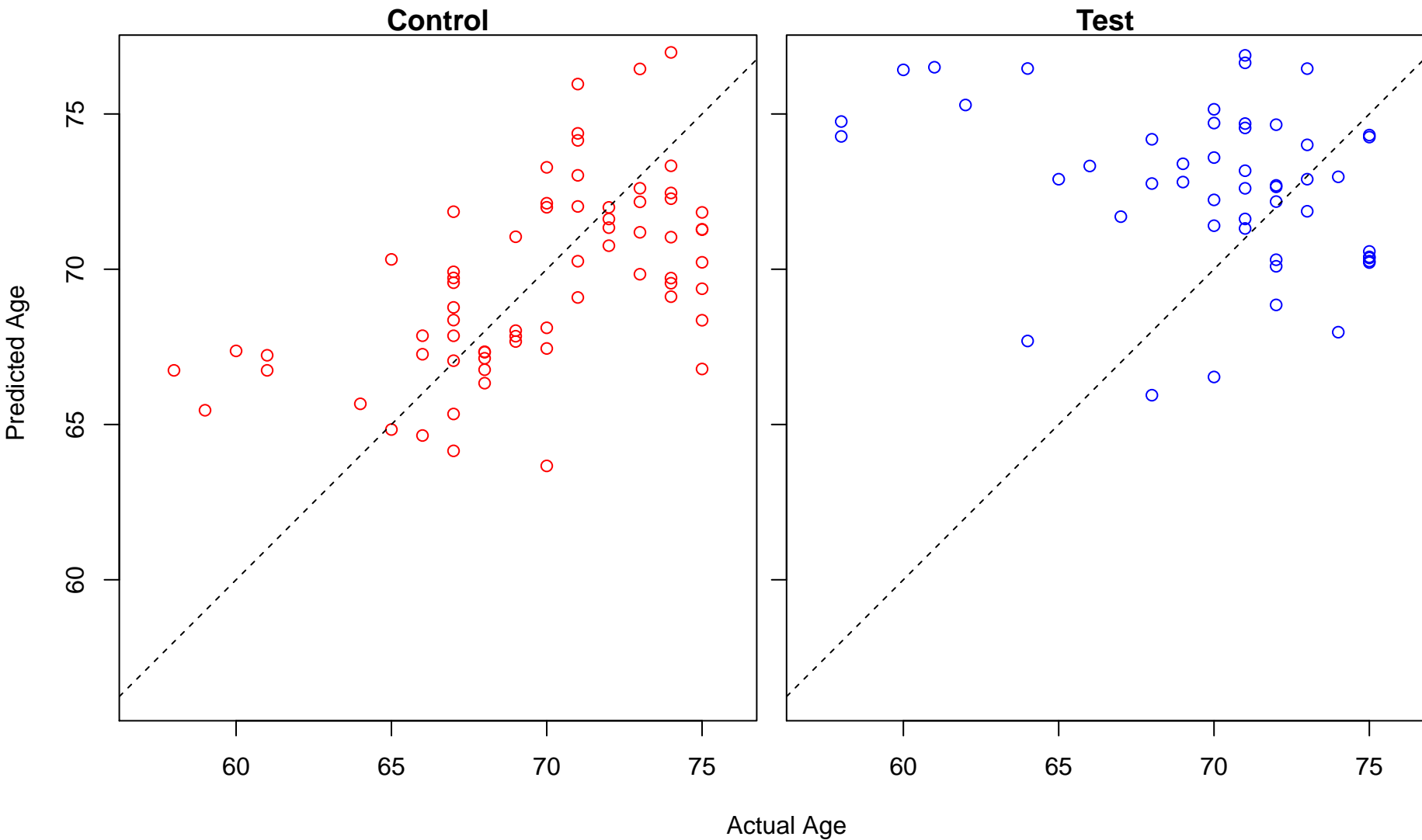
growth hormone receptor signaling pathway (Score: 1.276316)



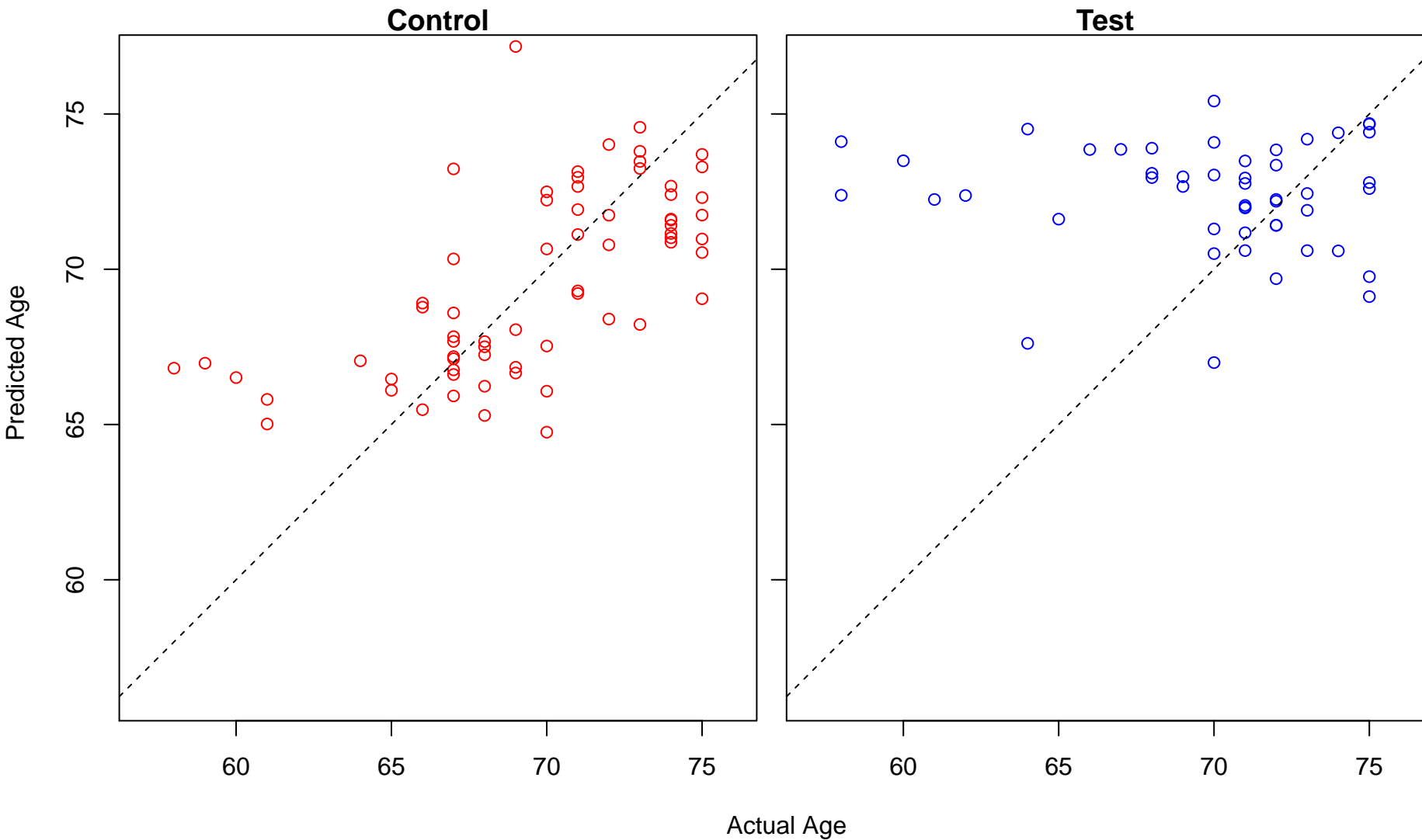
cellular response to growth hormone stimulus (Score: 1.276316)



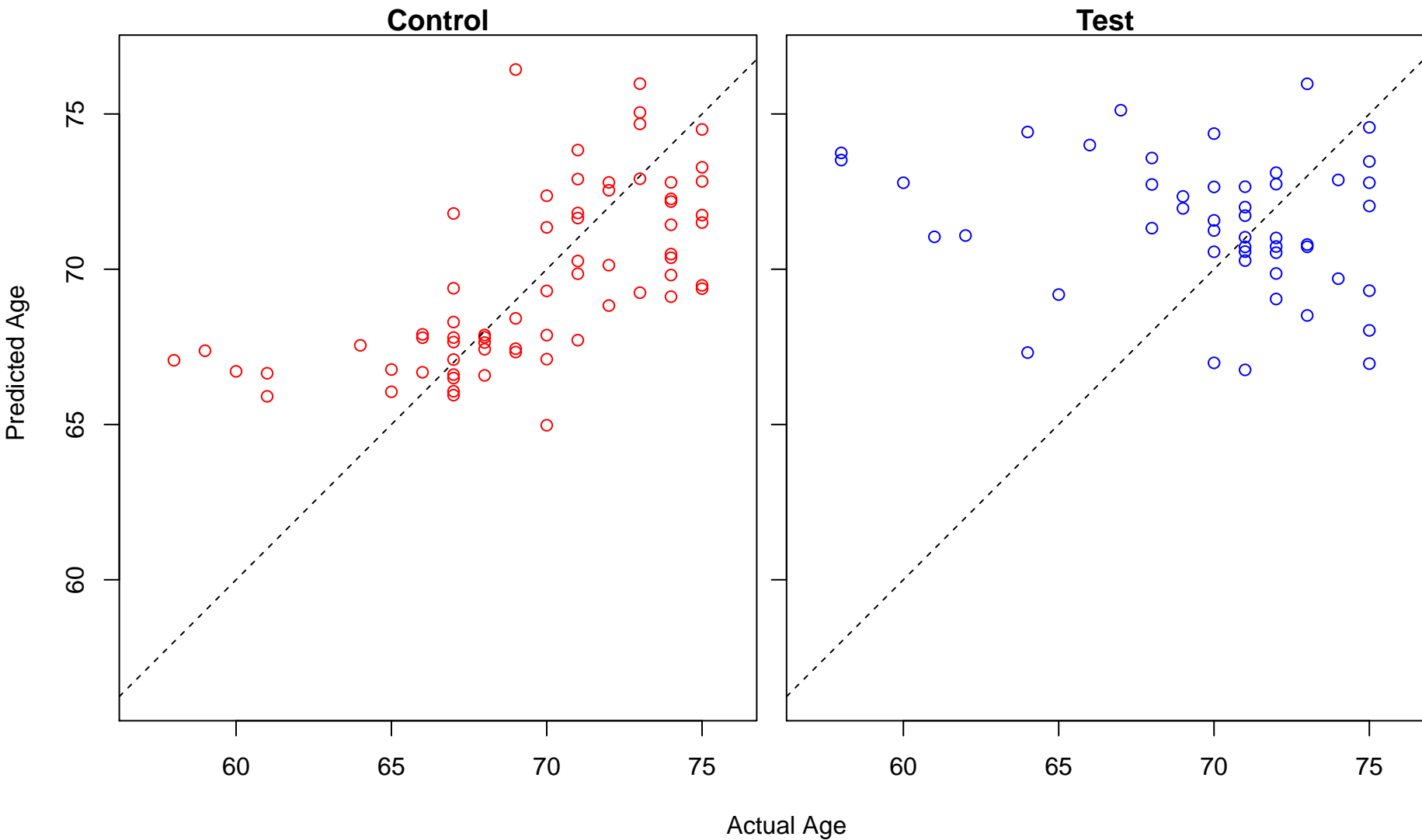
cAMP biosynthetic process (Score: 1.275402)



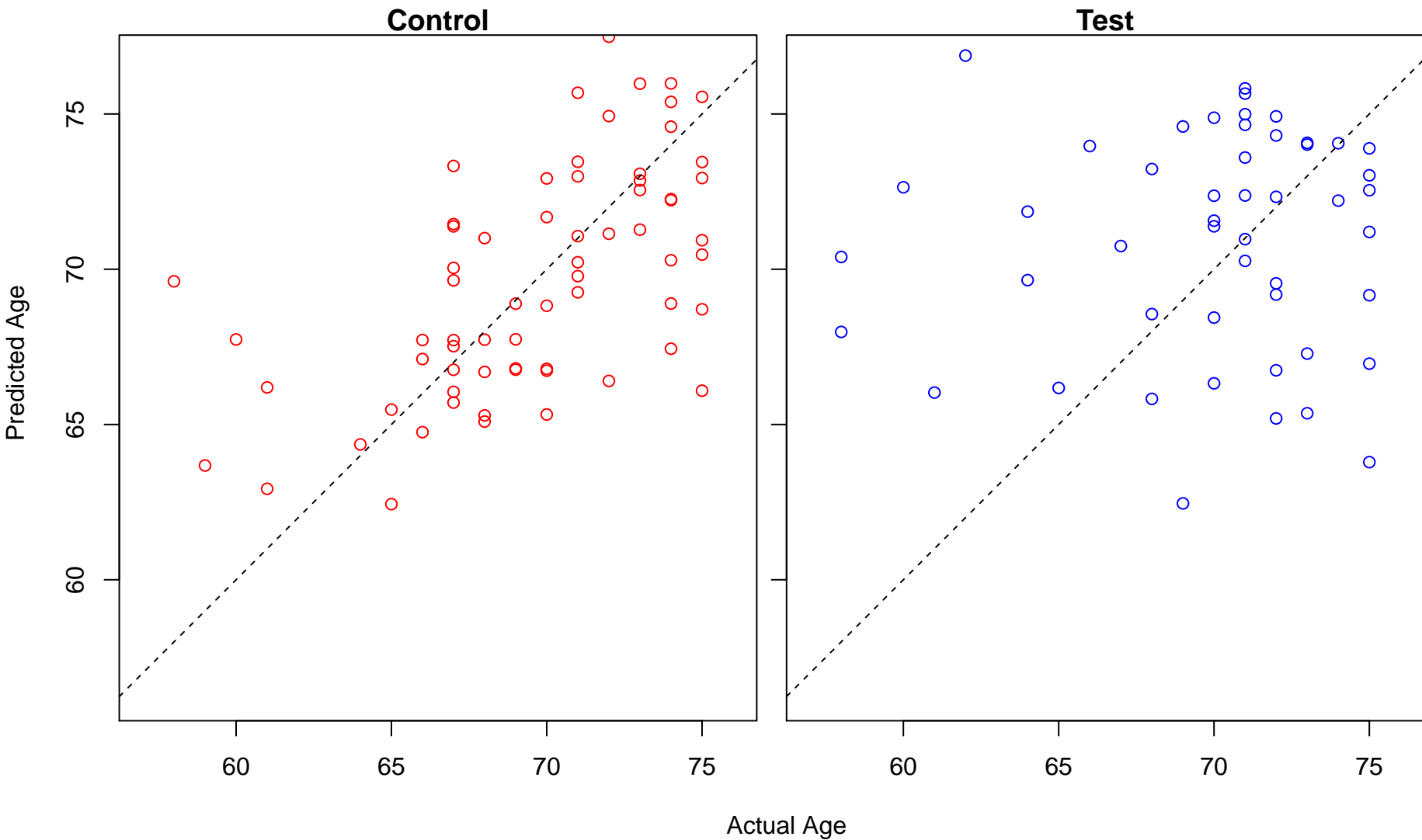
T cell selection (Score: 1.275311)



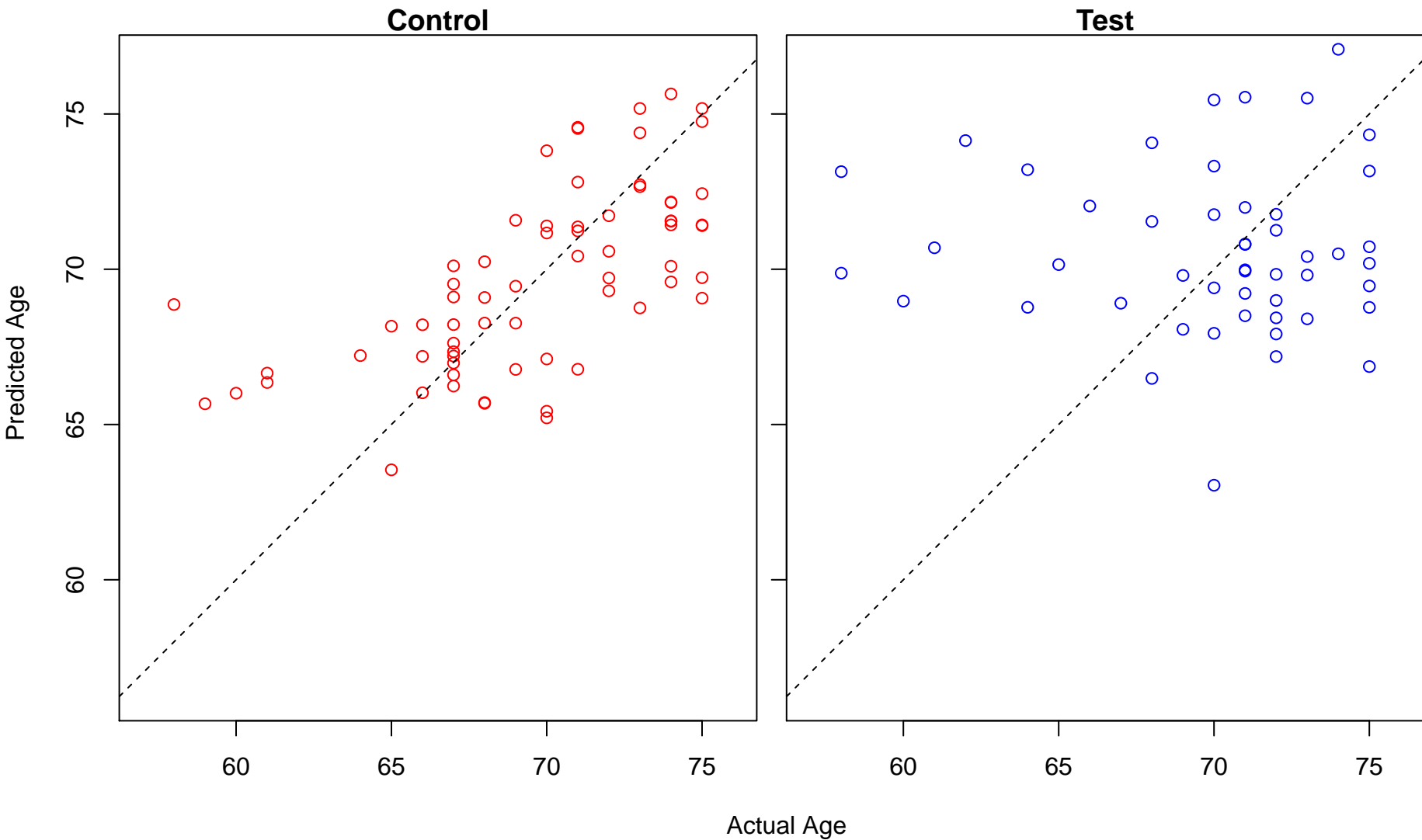
peptidyl-cysteine modification (Score: 1.275274)



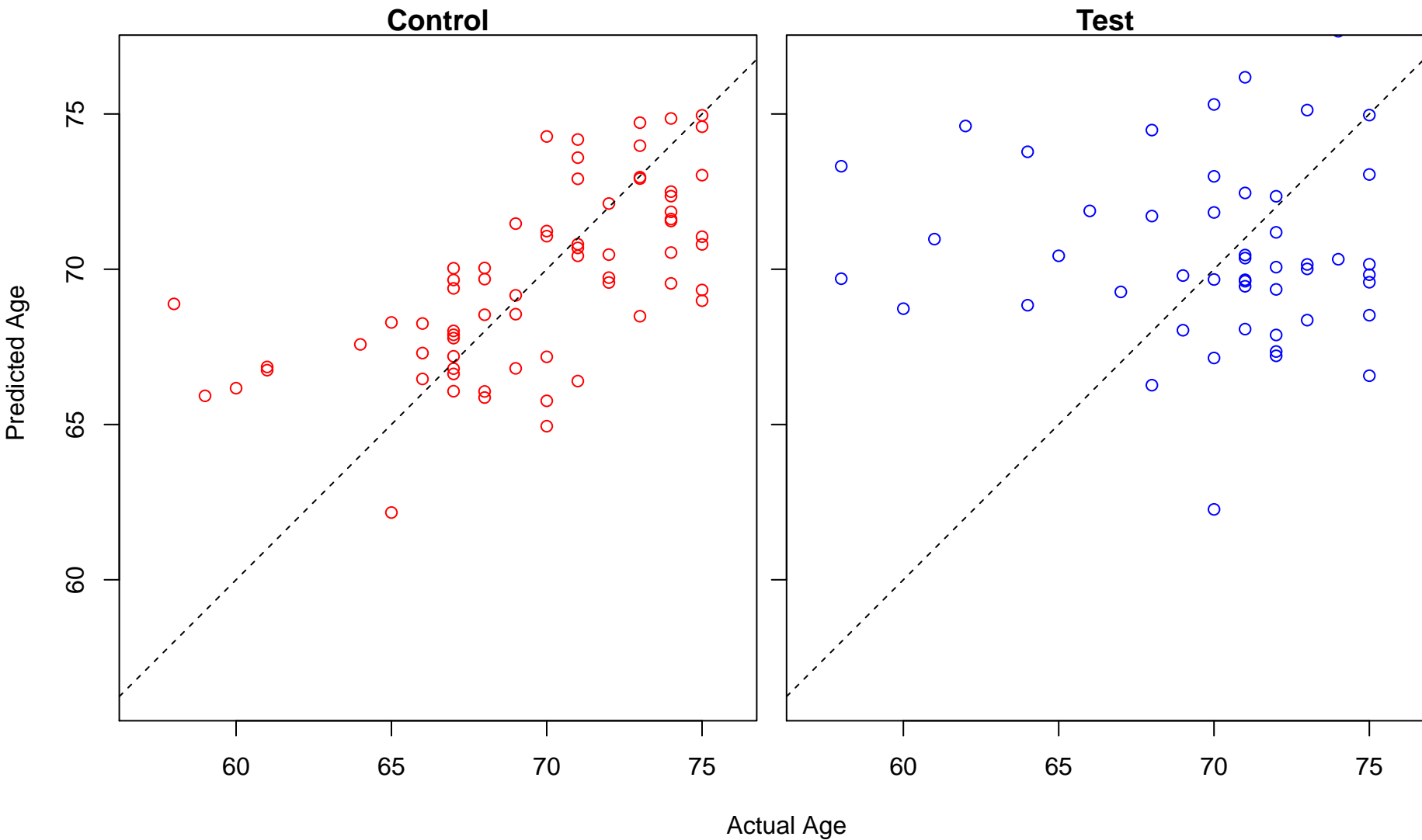
formation of primary germ layer (Score: 1.275013)



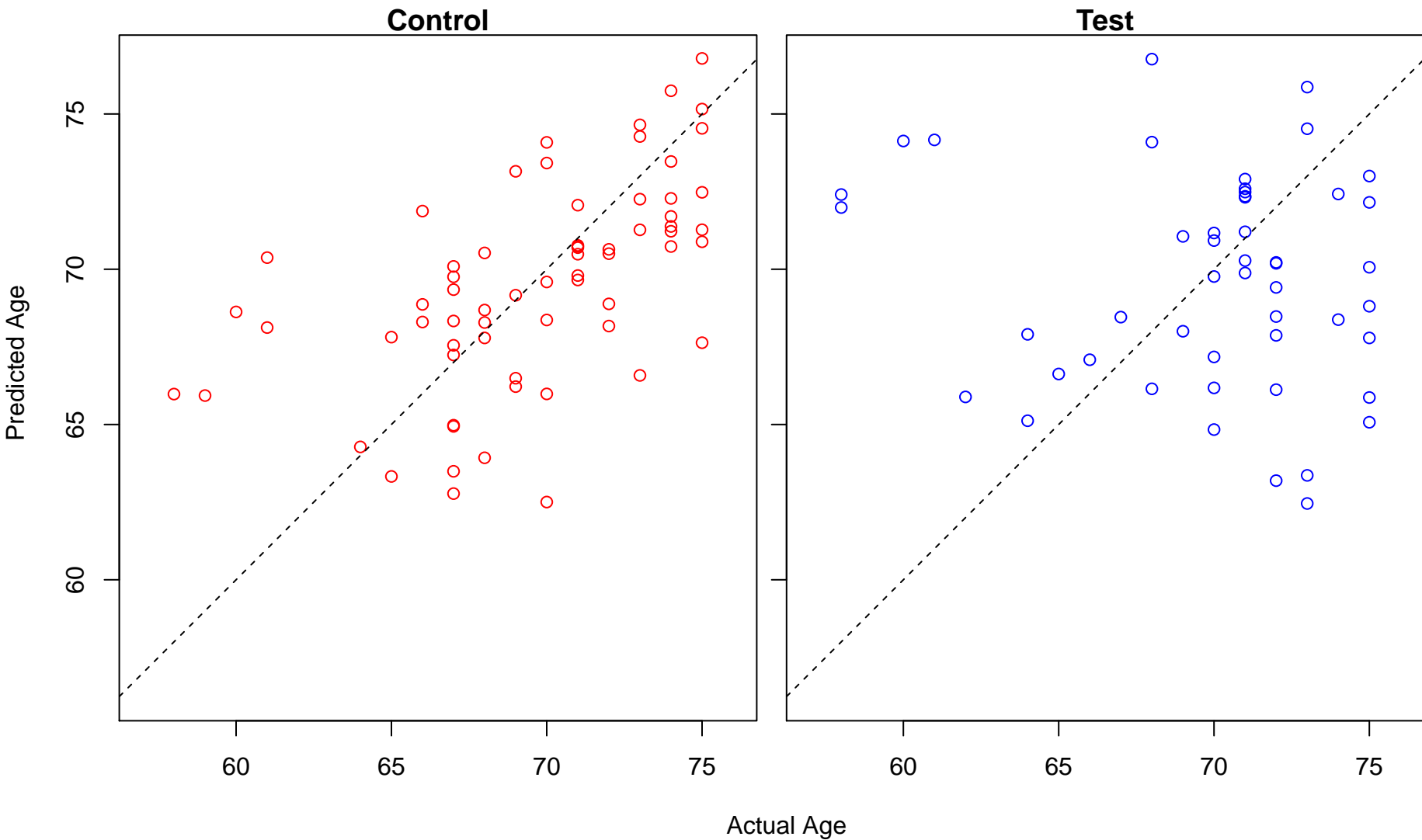
regulation of calcium ion transport into cytosol (Score: 1.274624)



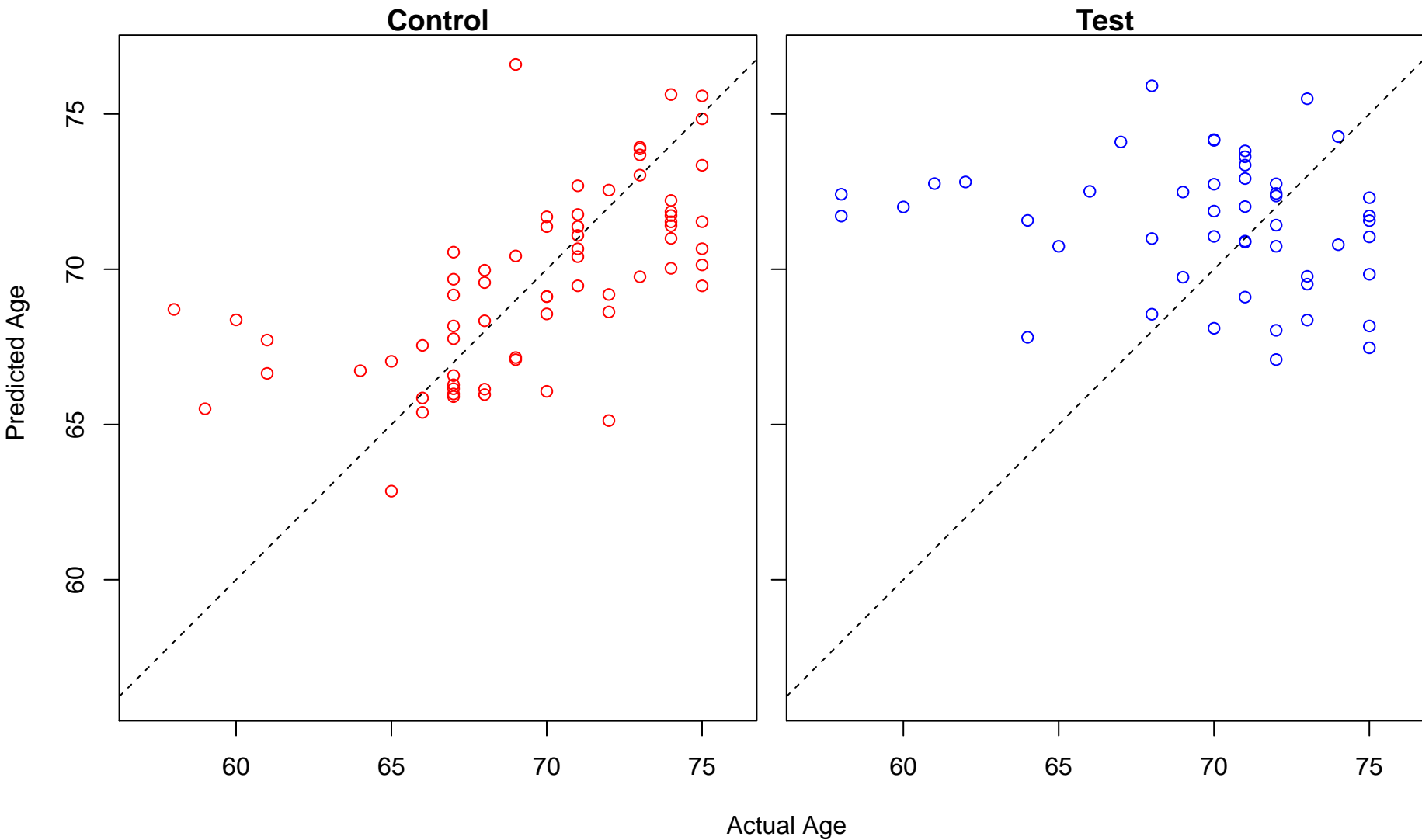
regulation of release of sequestered calcium ion into cytosol (Score: 1.273623)



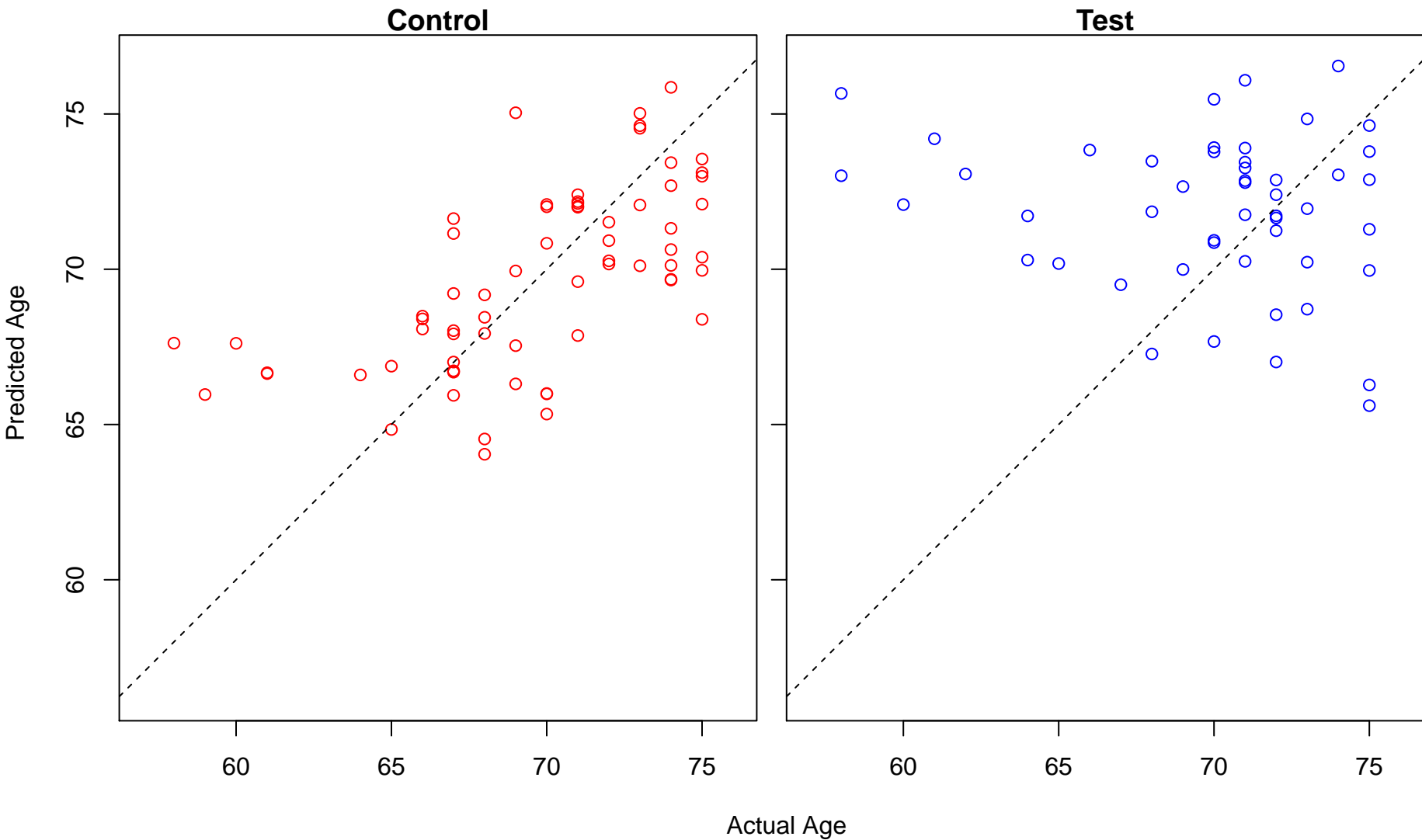
positive regulation of cyclin–dependent protein serine/threonine kinase activity (Score: 1.271749)



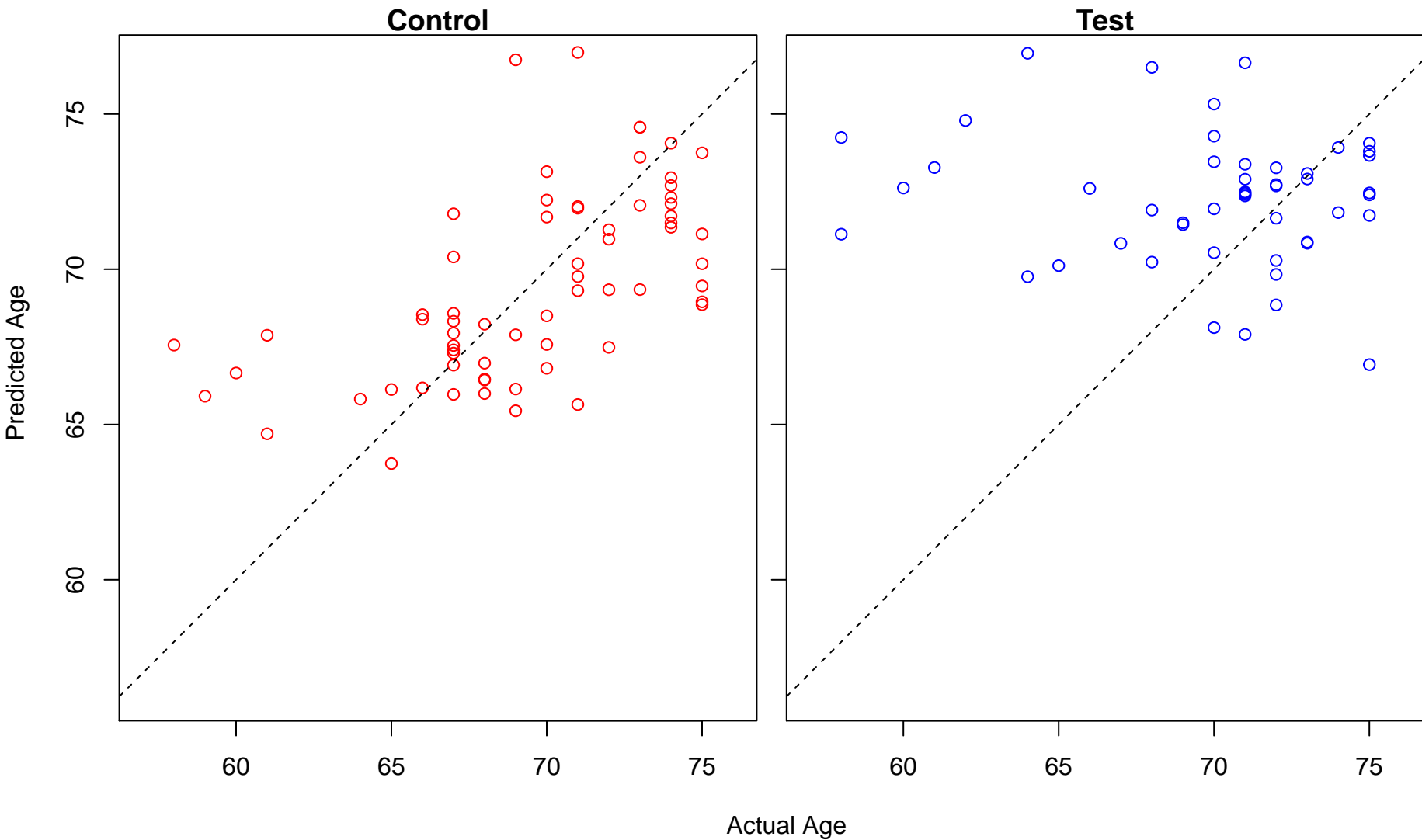
negative regulation of lymphocyte differentiation (Score: 1.271485)



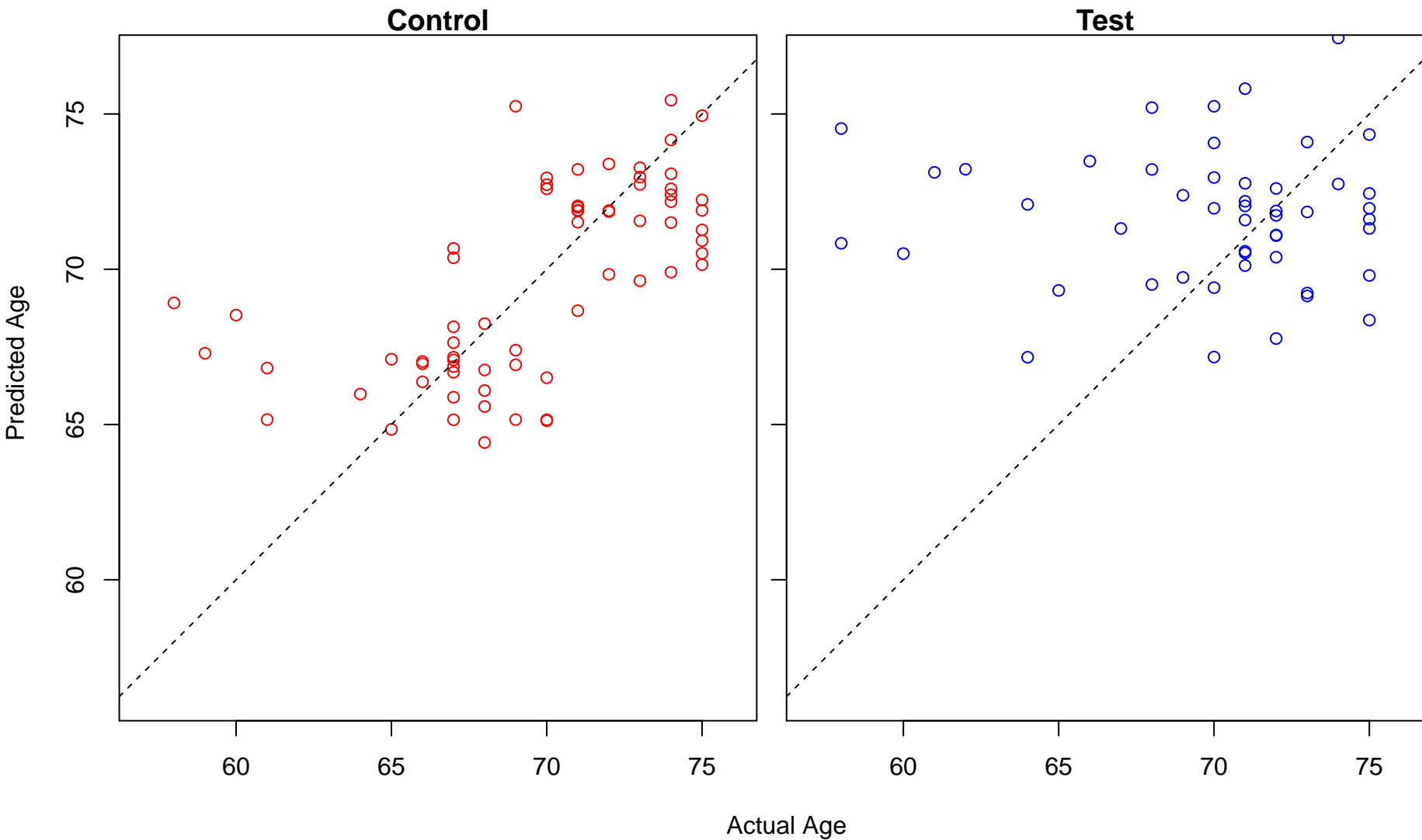
regulation of bone development (Score: 1.270998)



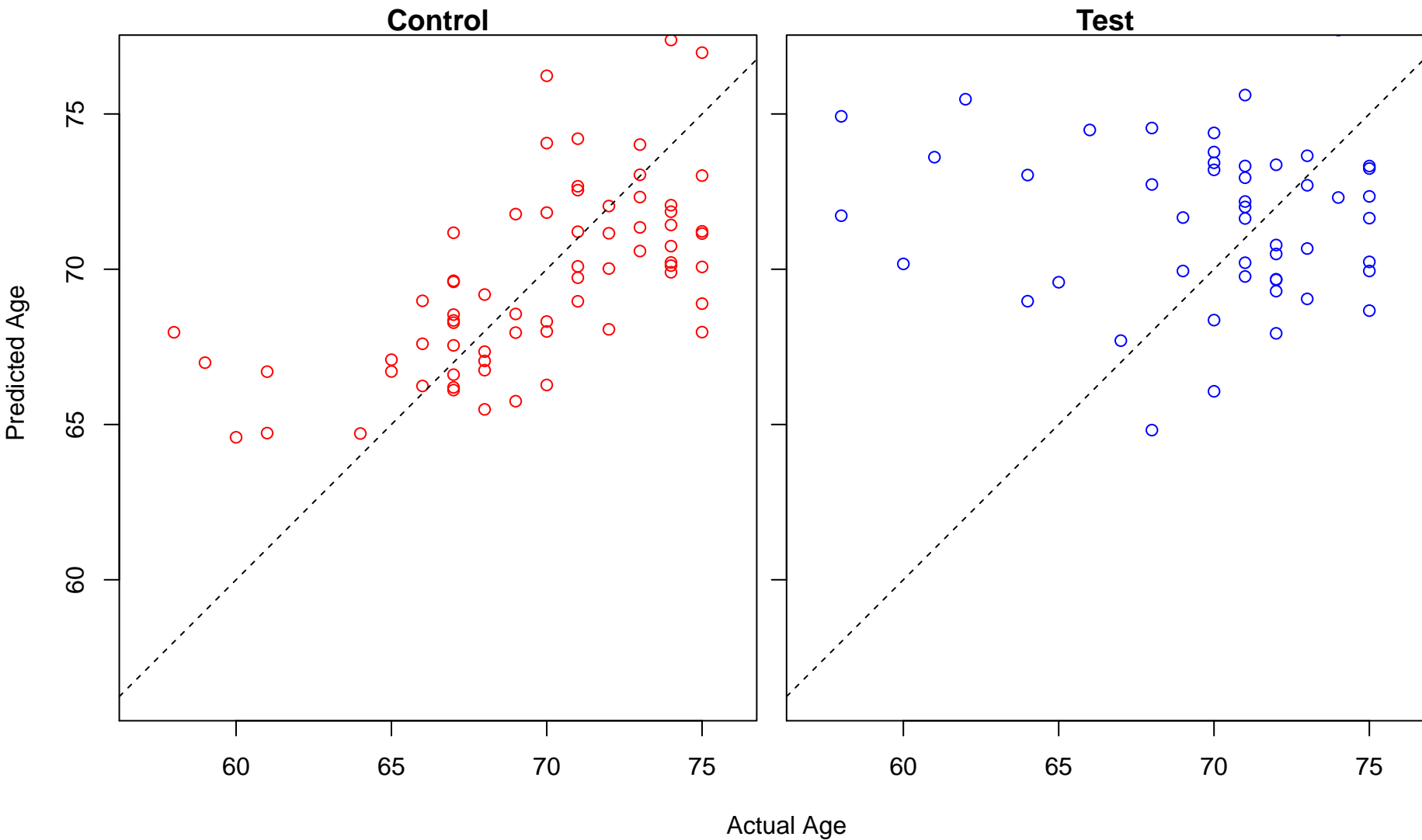
intracellular protein transmembrane transport (Score: 1.270994)



response to inorganic substance (Score: 1.270869)

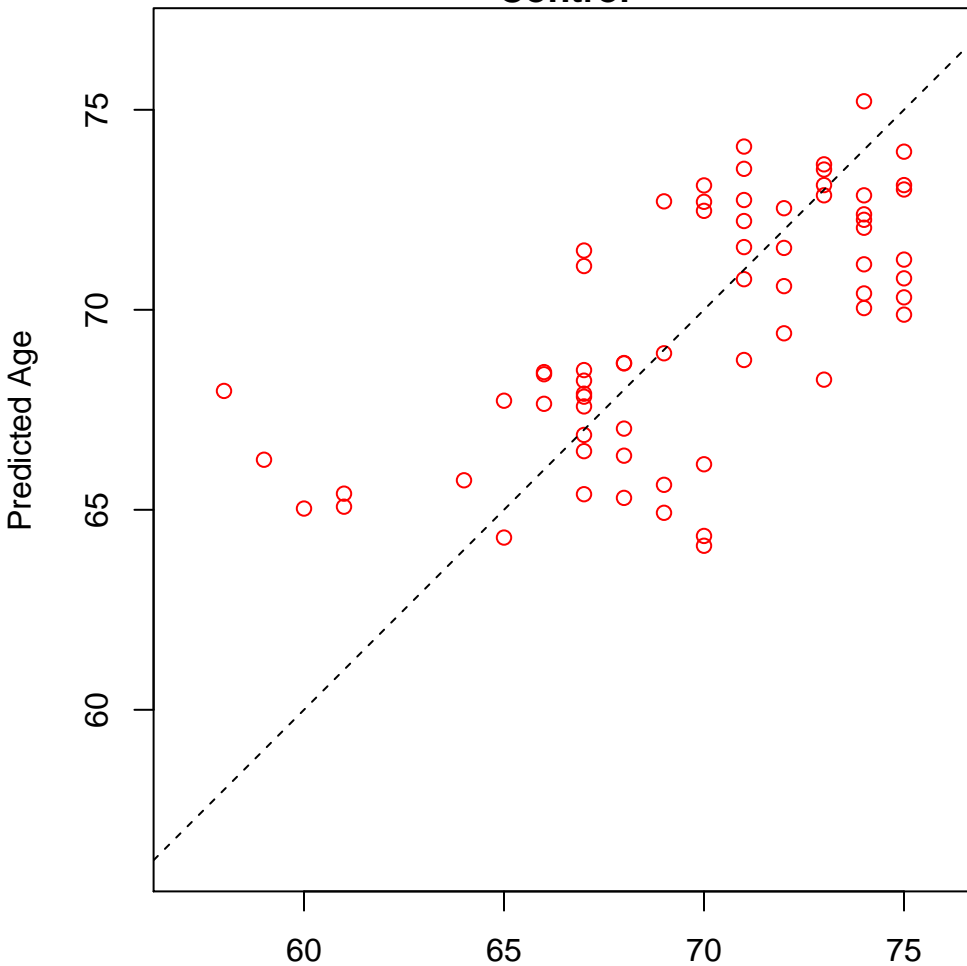


microtubule nucleation (Score: 1.270718)

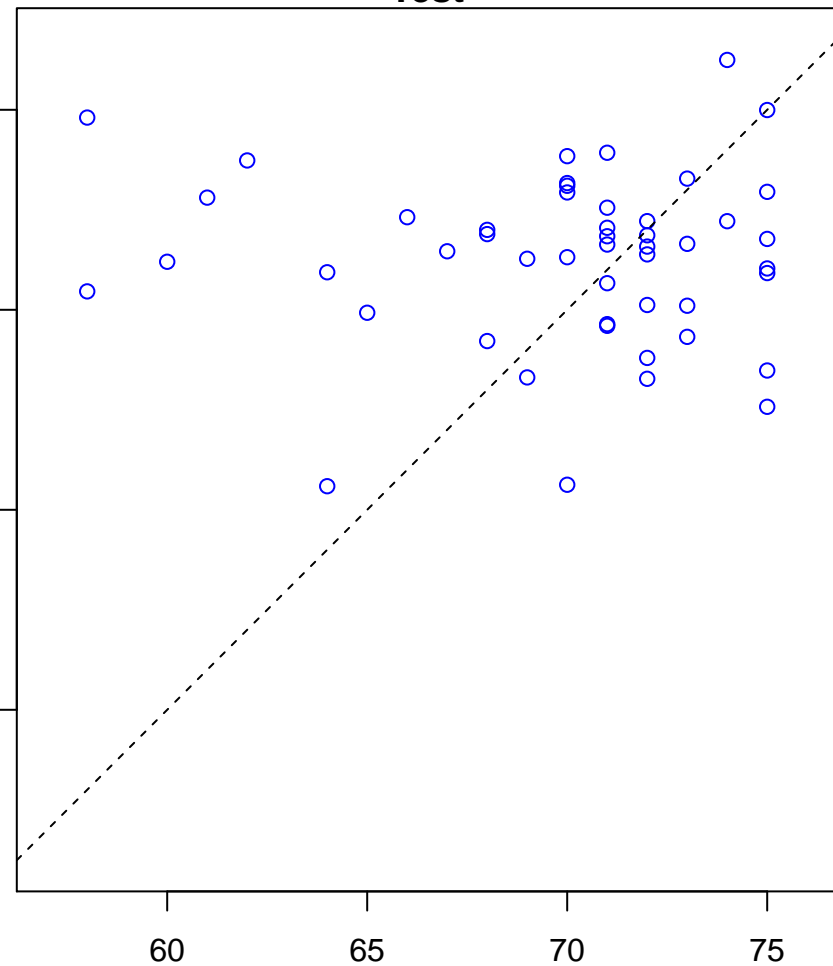


energy reserve metabolic process (Score: 1.270138)

Control

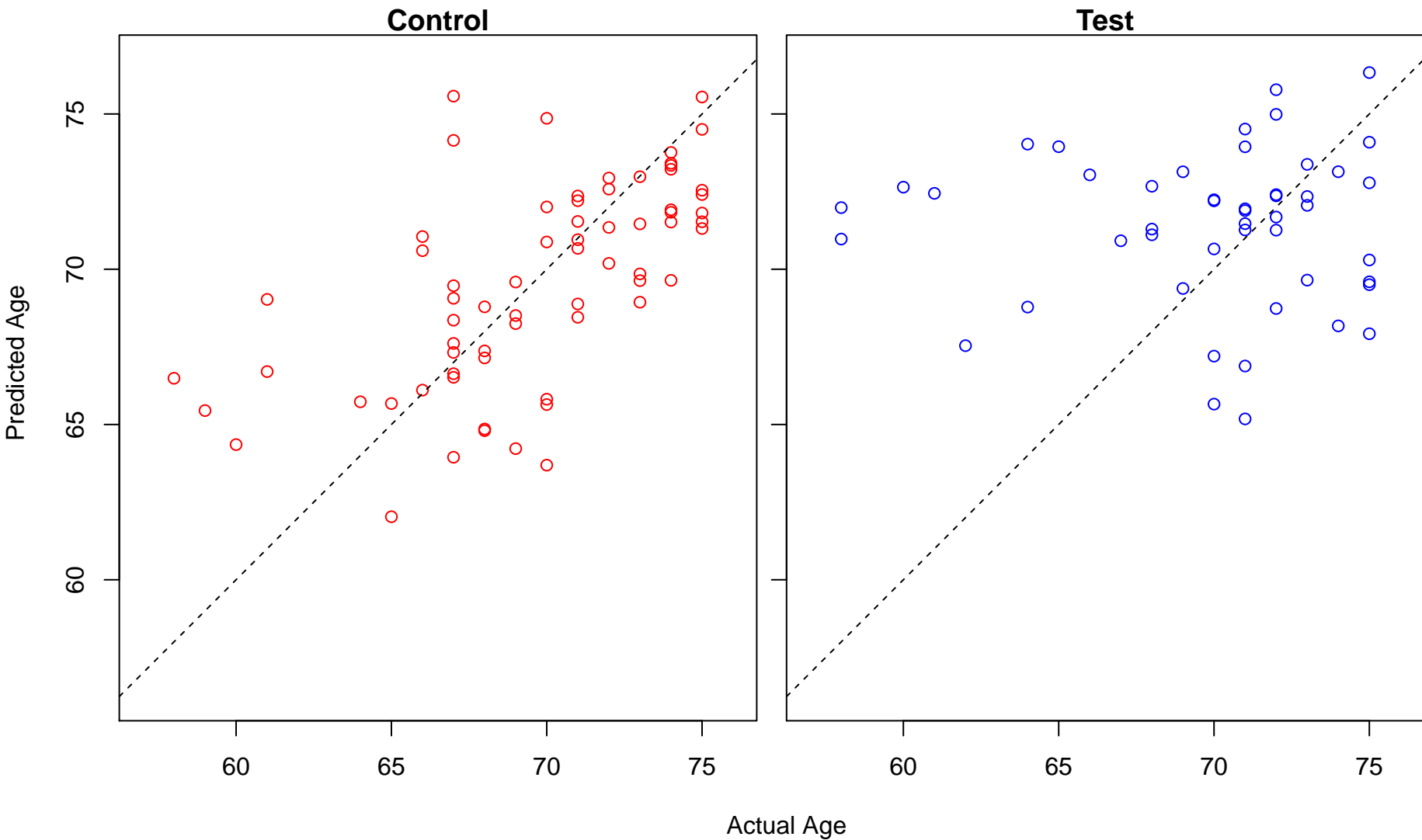


Test

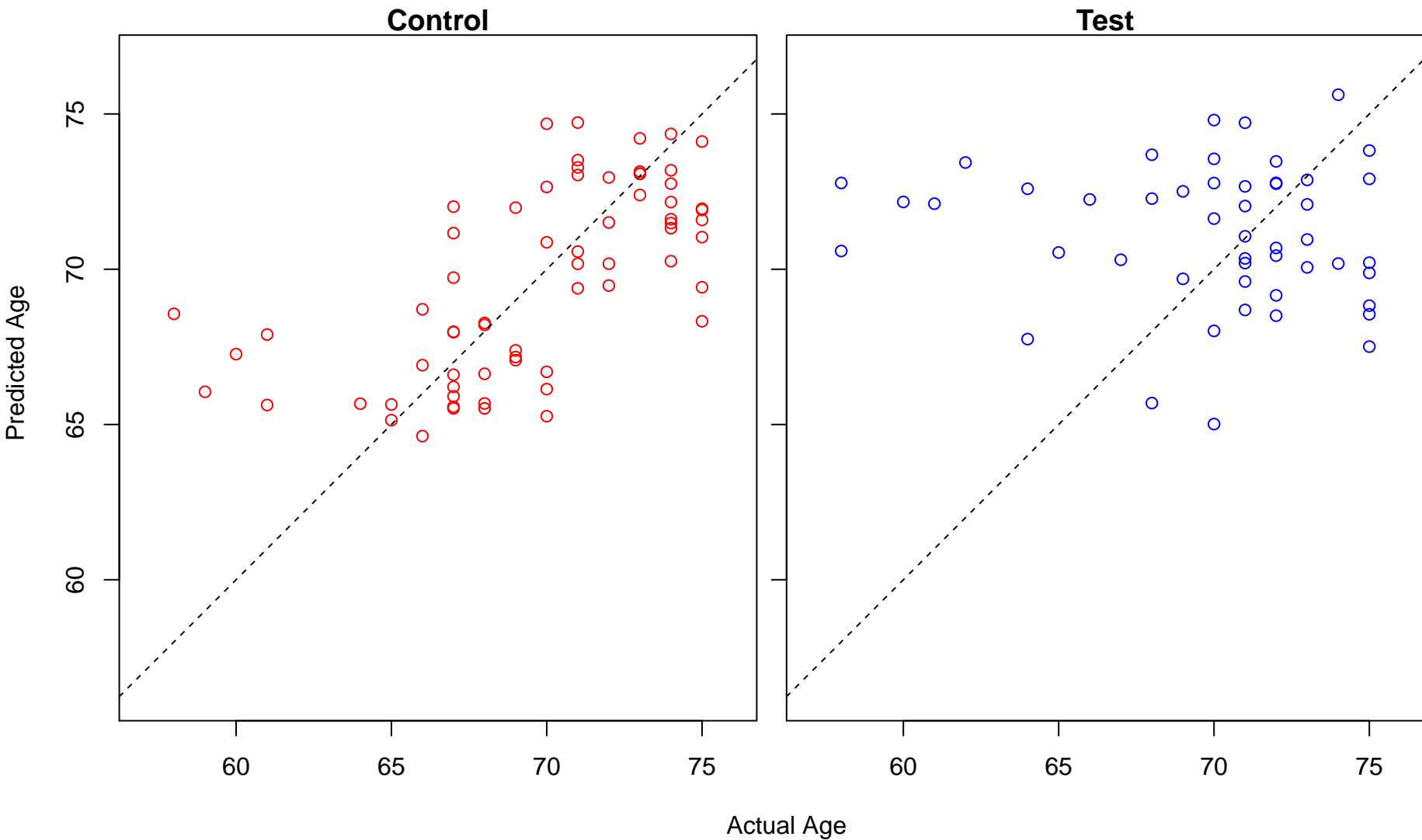


Actual Age

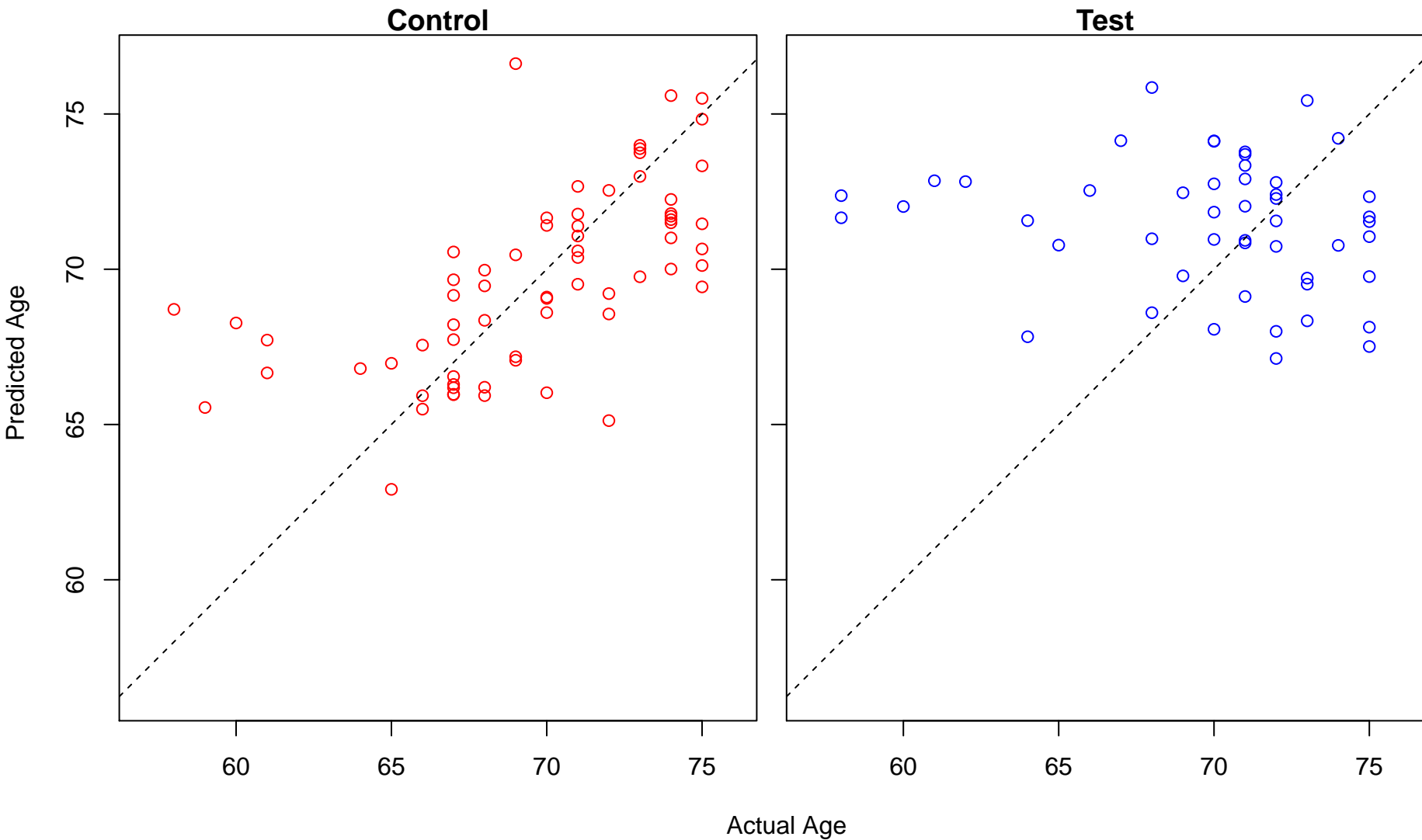
response to retinoic acid (Score: 1.269678)



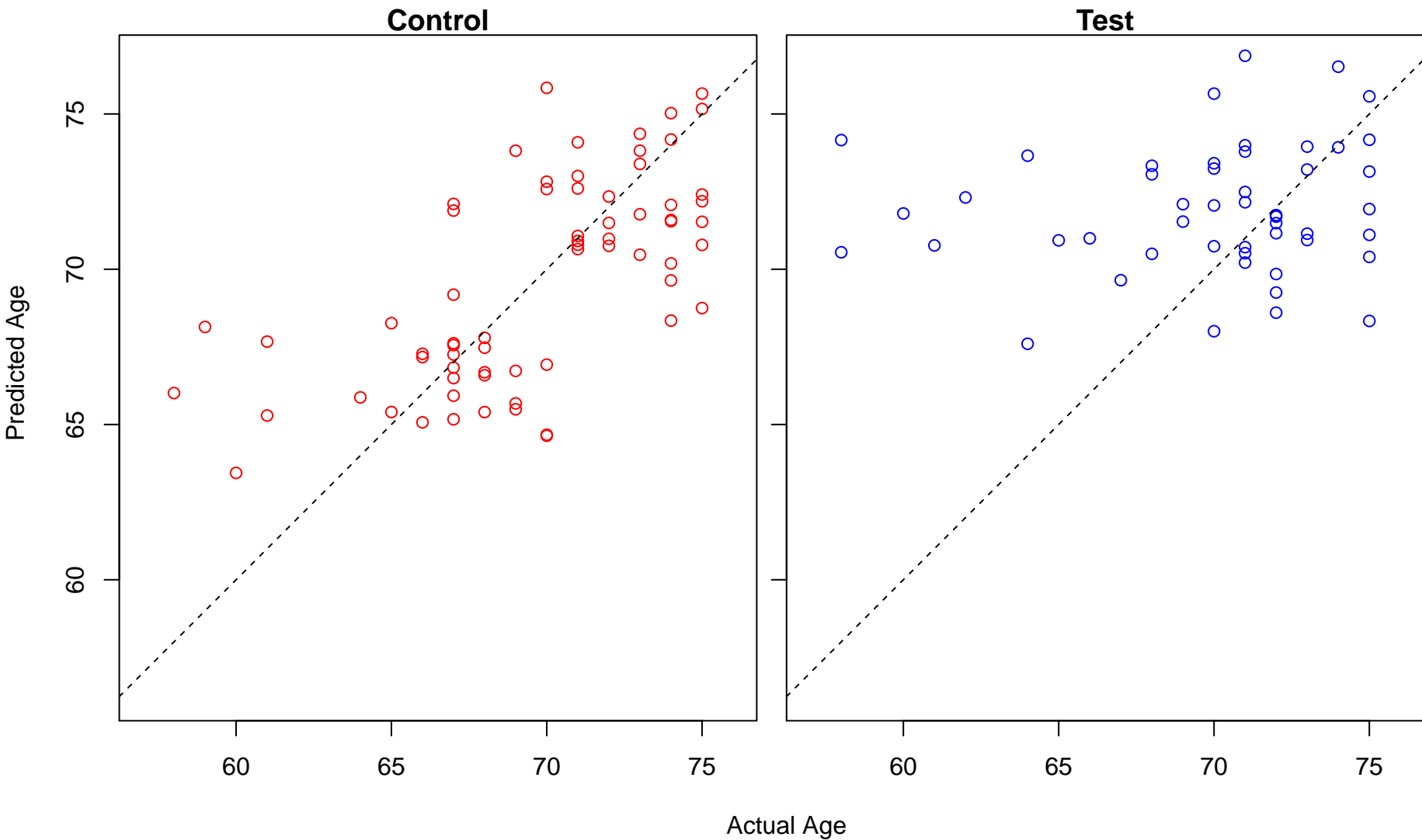
regulation of lipase activity (Score: 1.269465)



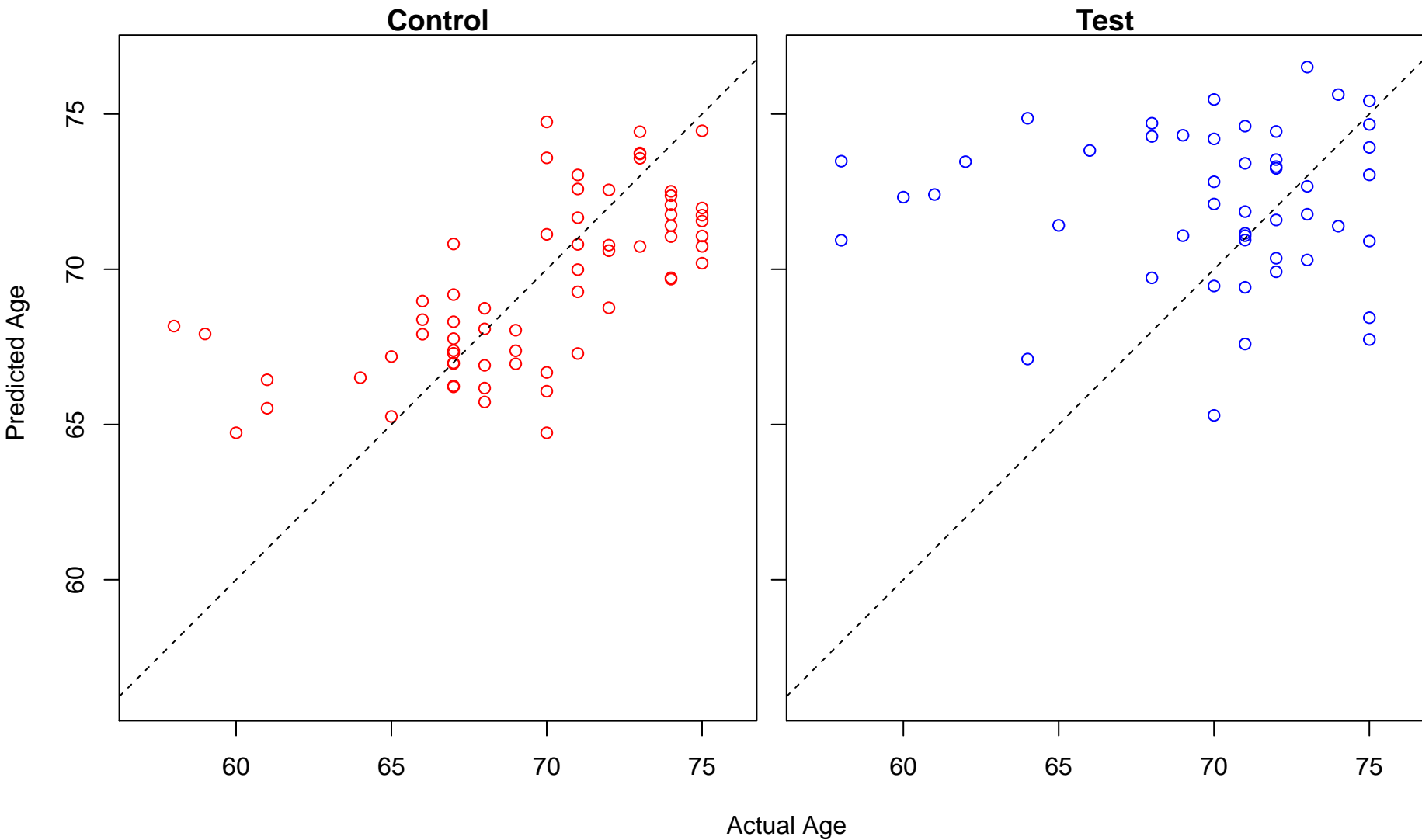
negative regulation of T cell differentiation (Score: 1.269409)



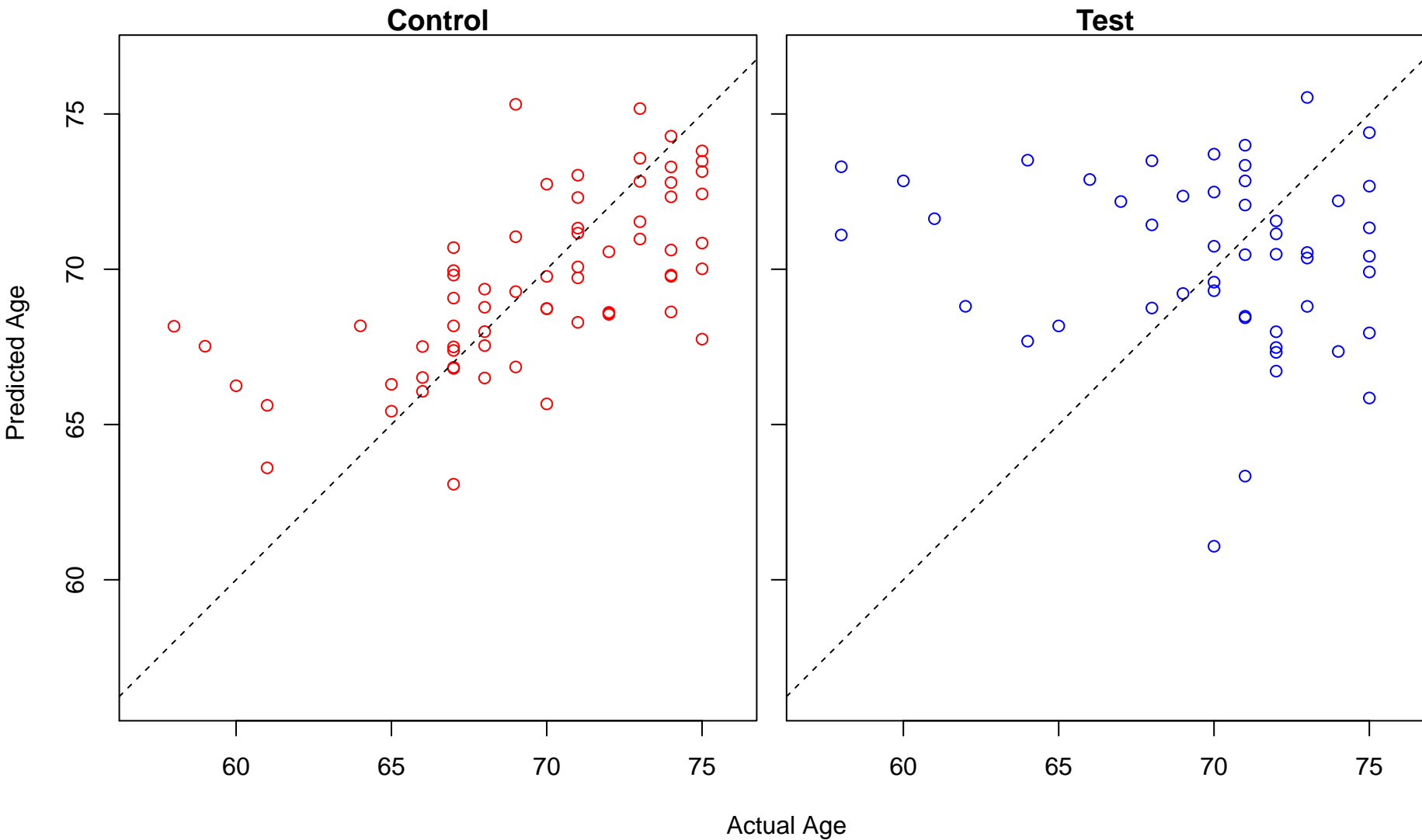
organic acid transport (Score: 1.268769)



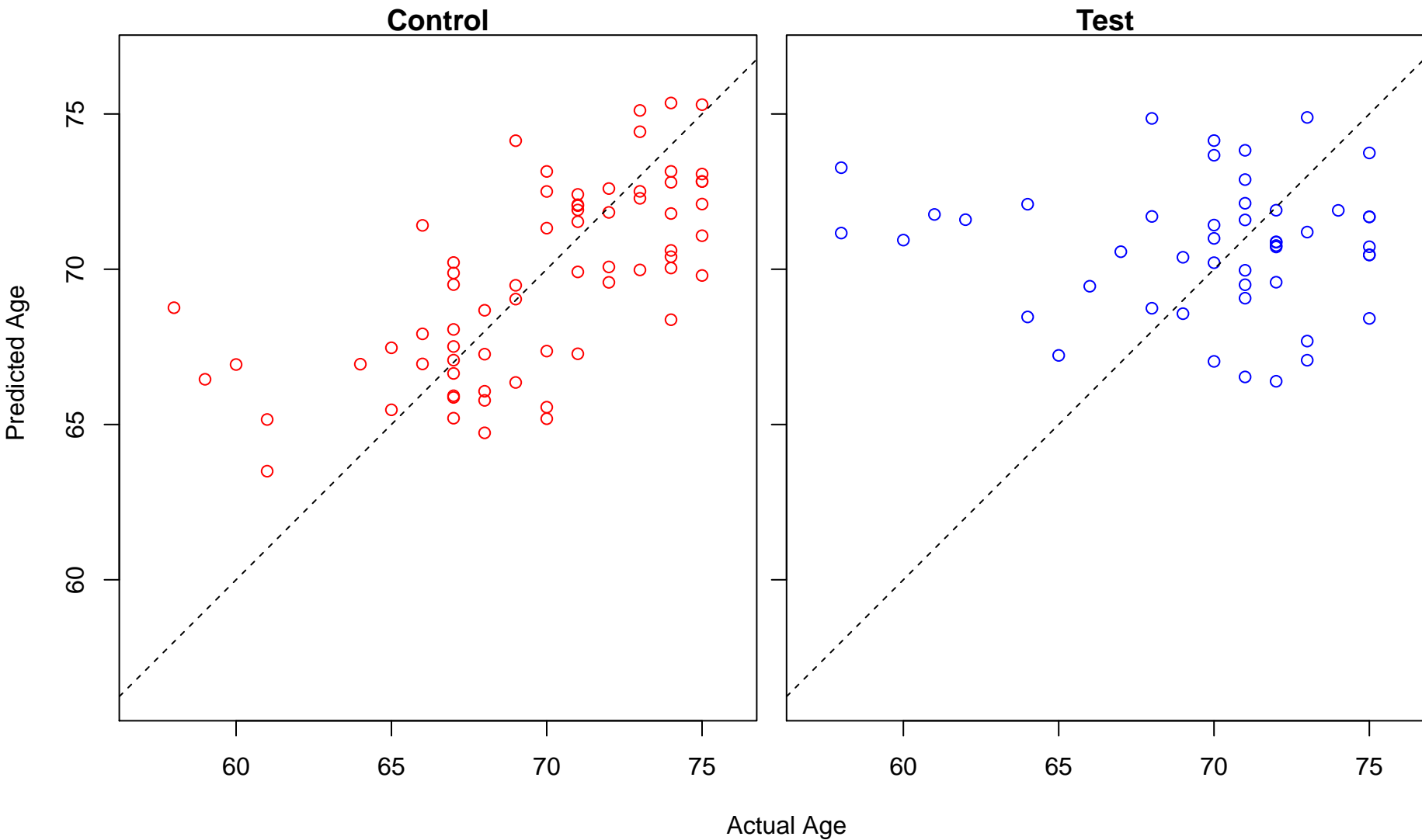
DNA strand elongation (Score: 1.267614)



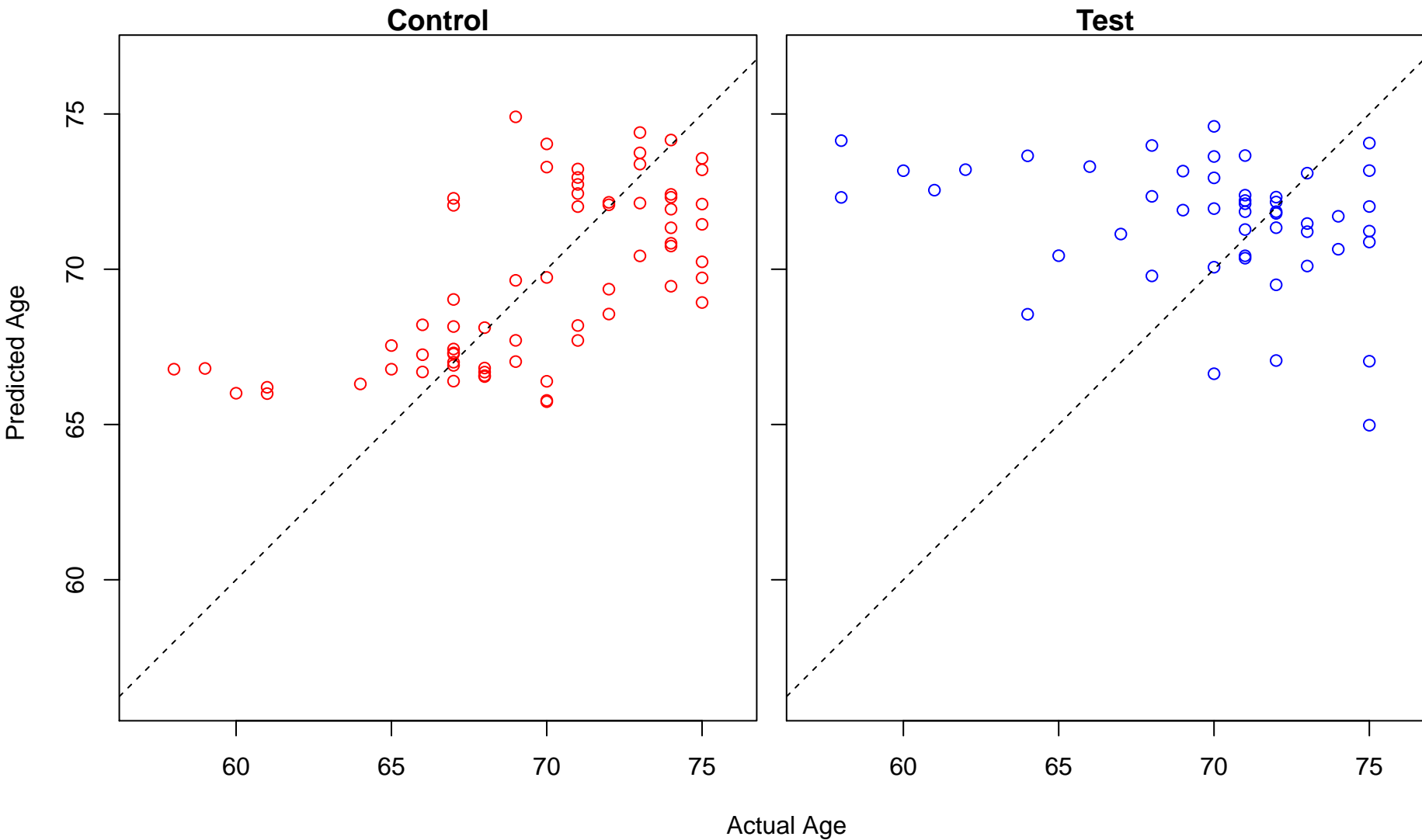
negative regulation of cyclic nucleotide biosynthetic process (Score: 1.267464)



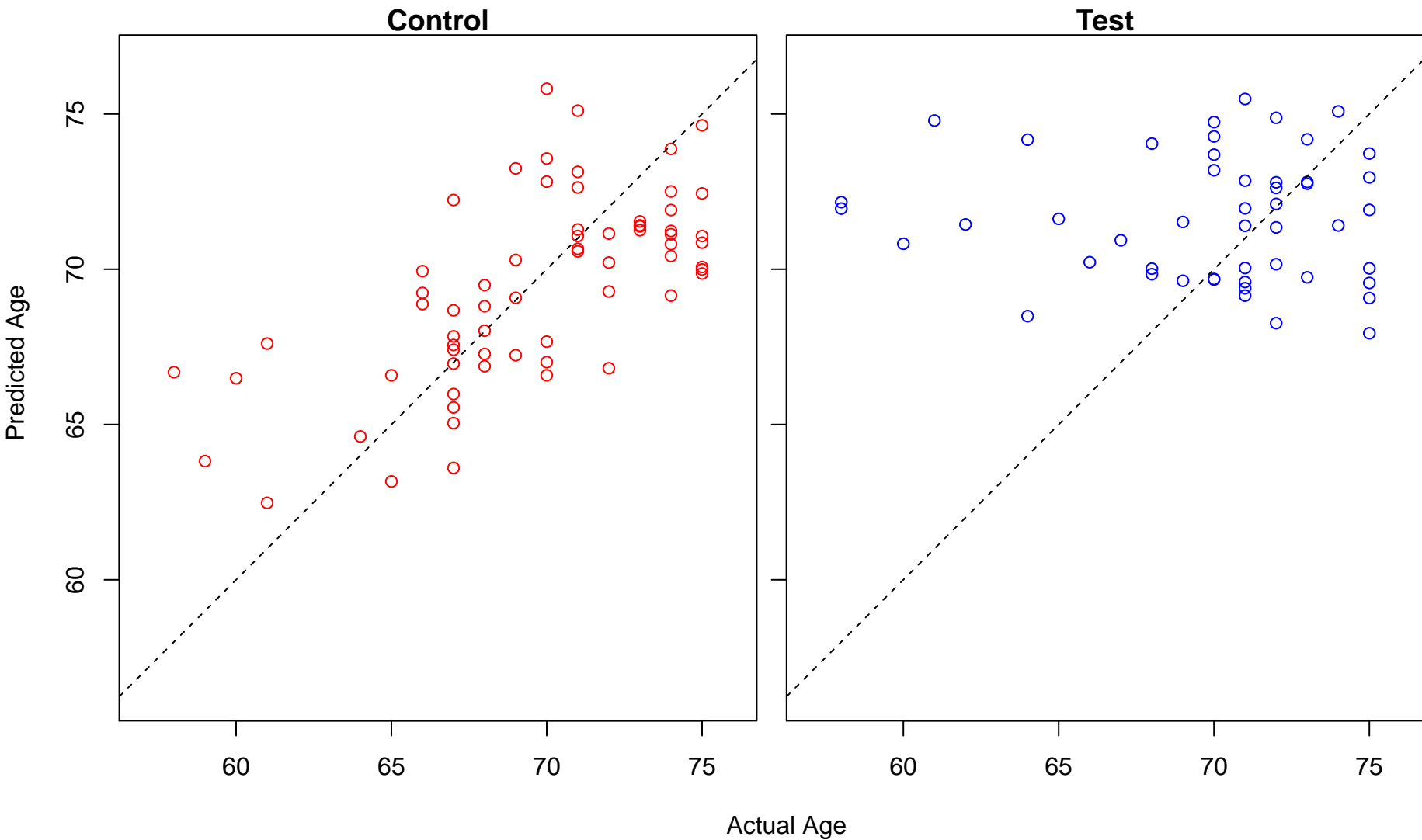
multivesicular body assembly (Score: 1.266623)



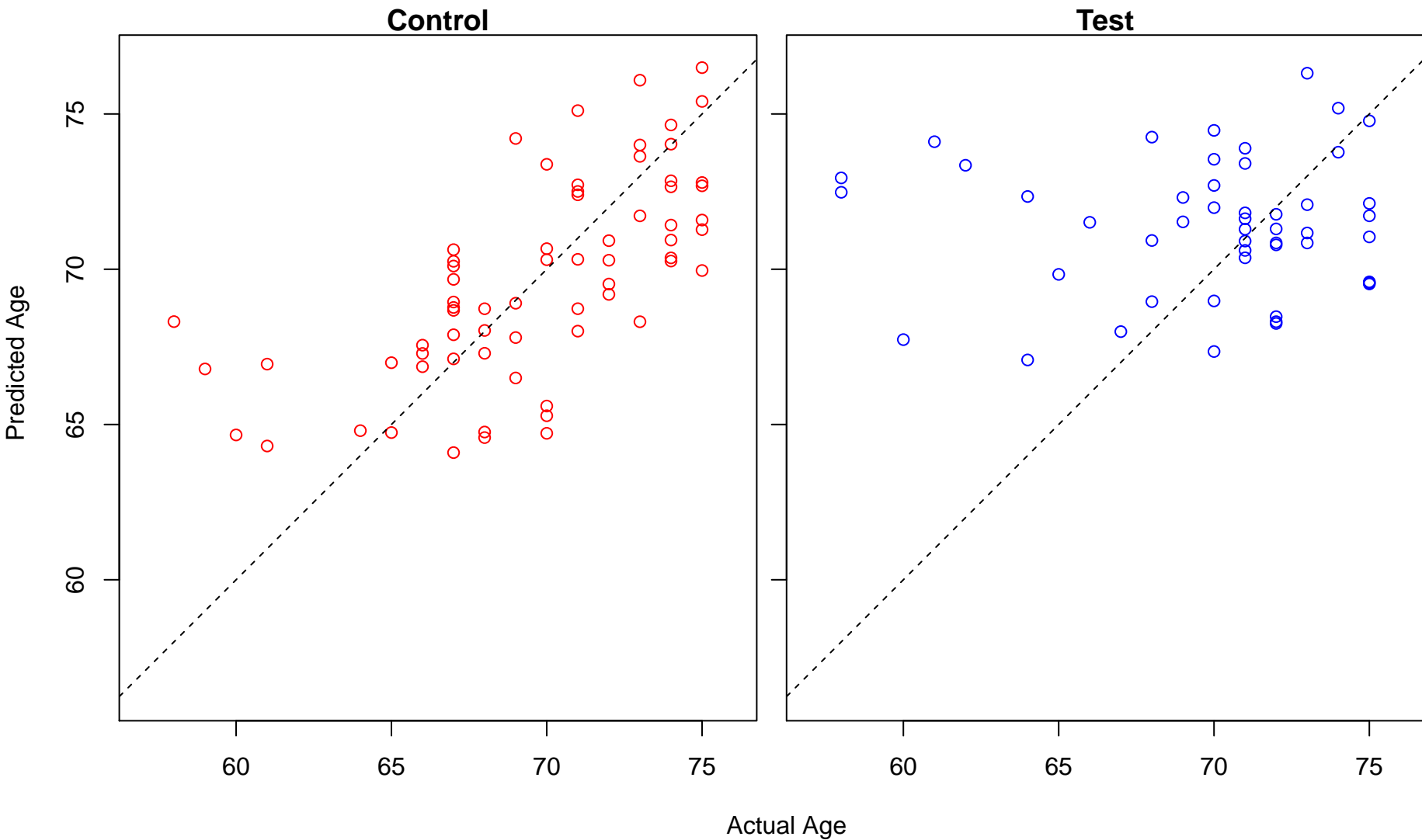
morphogenesis of an epithelial sheet (Score: 1.266352)



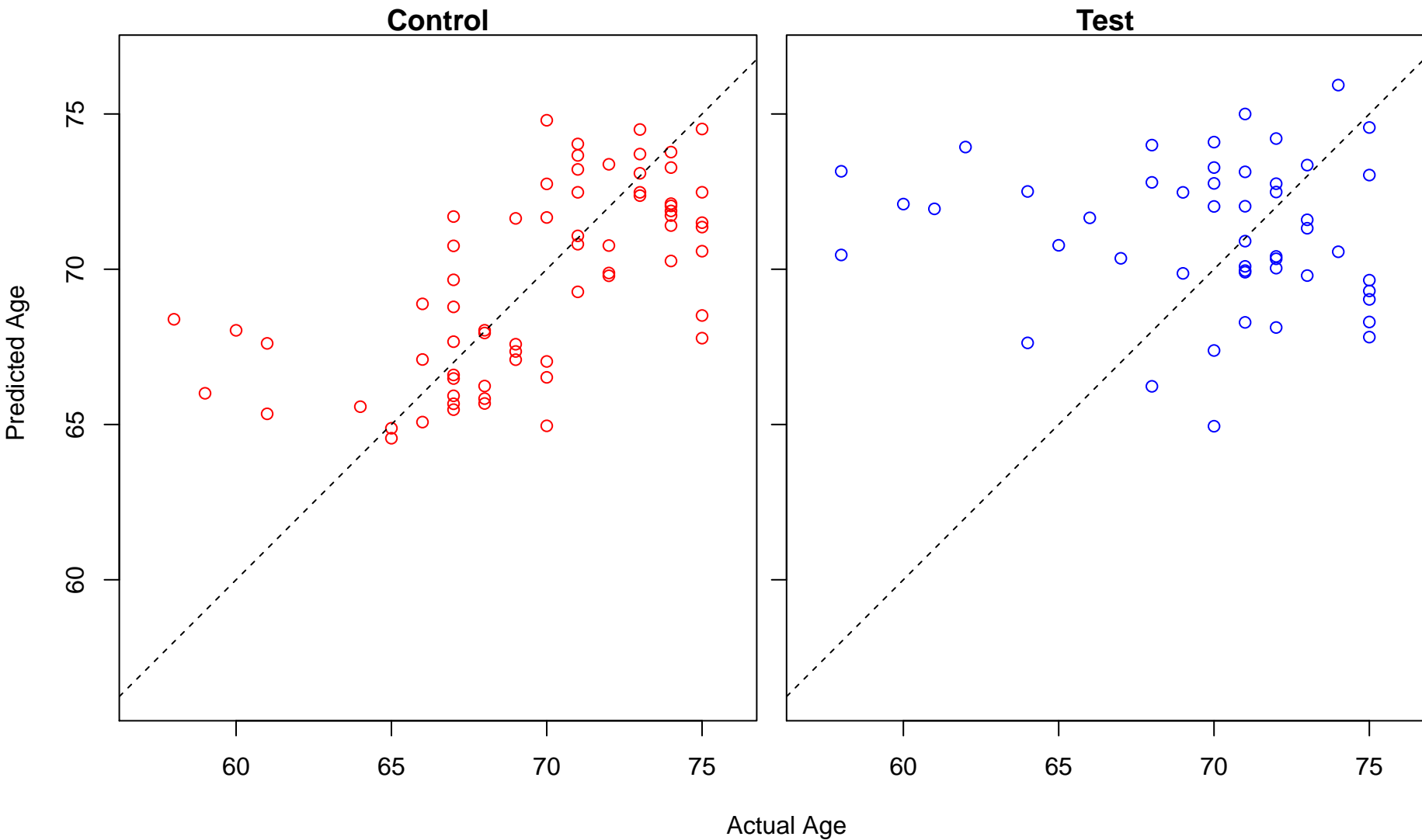
regulation of intrinsic apoptotic signaling pathway by p53 class mediator (Score: 1.266336)



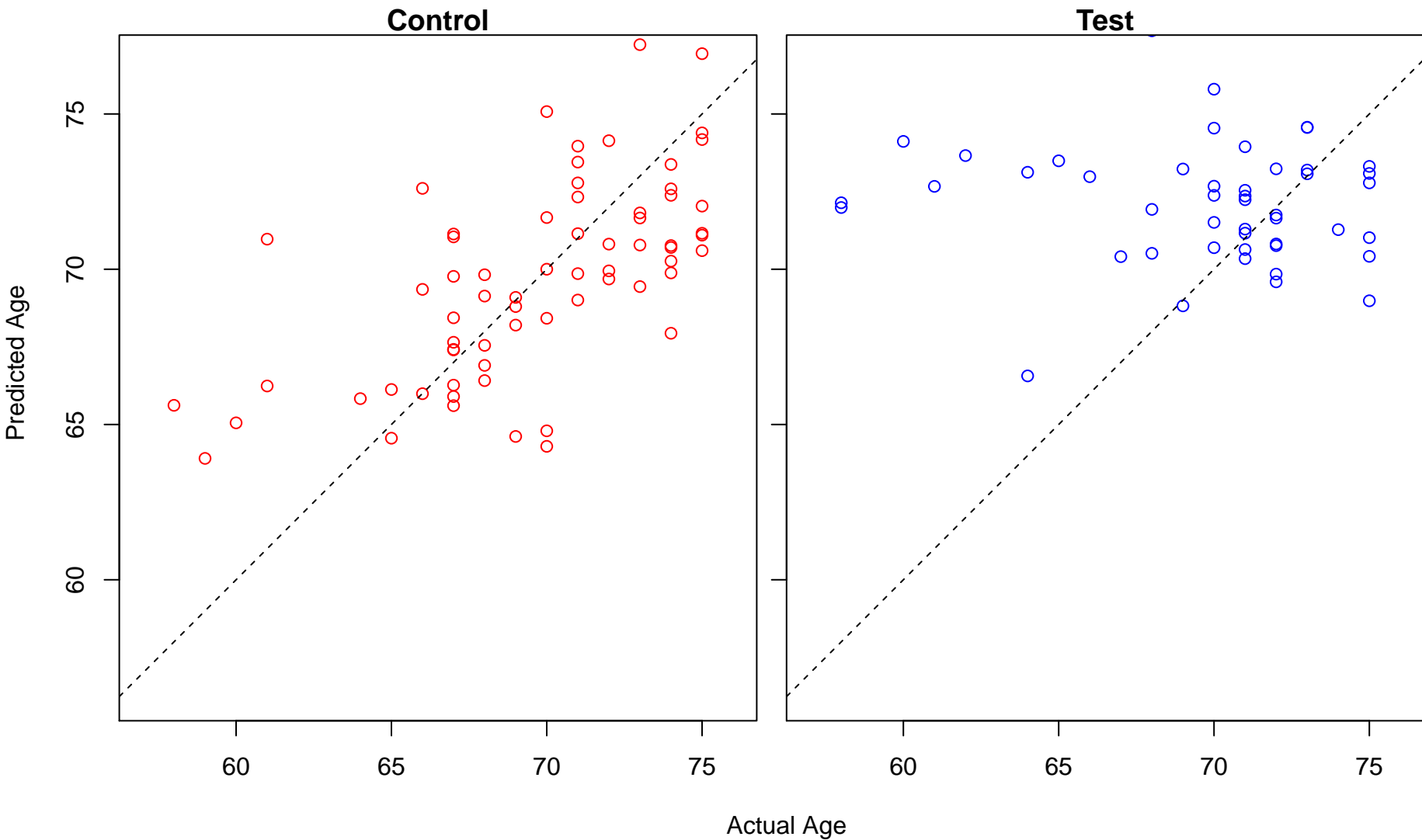
positive regulation of protein binding (Score: 1.266314)



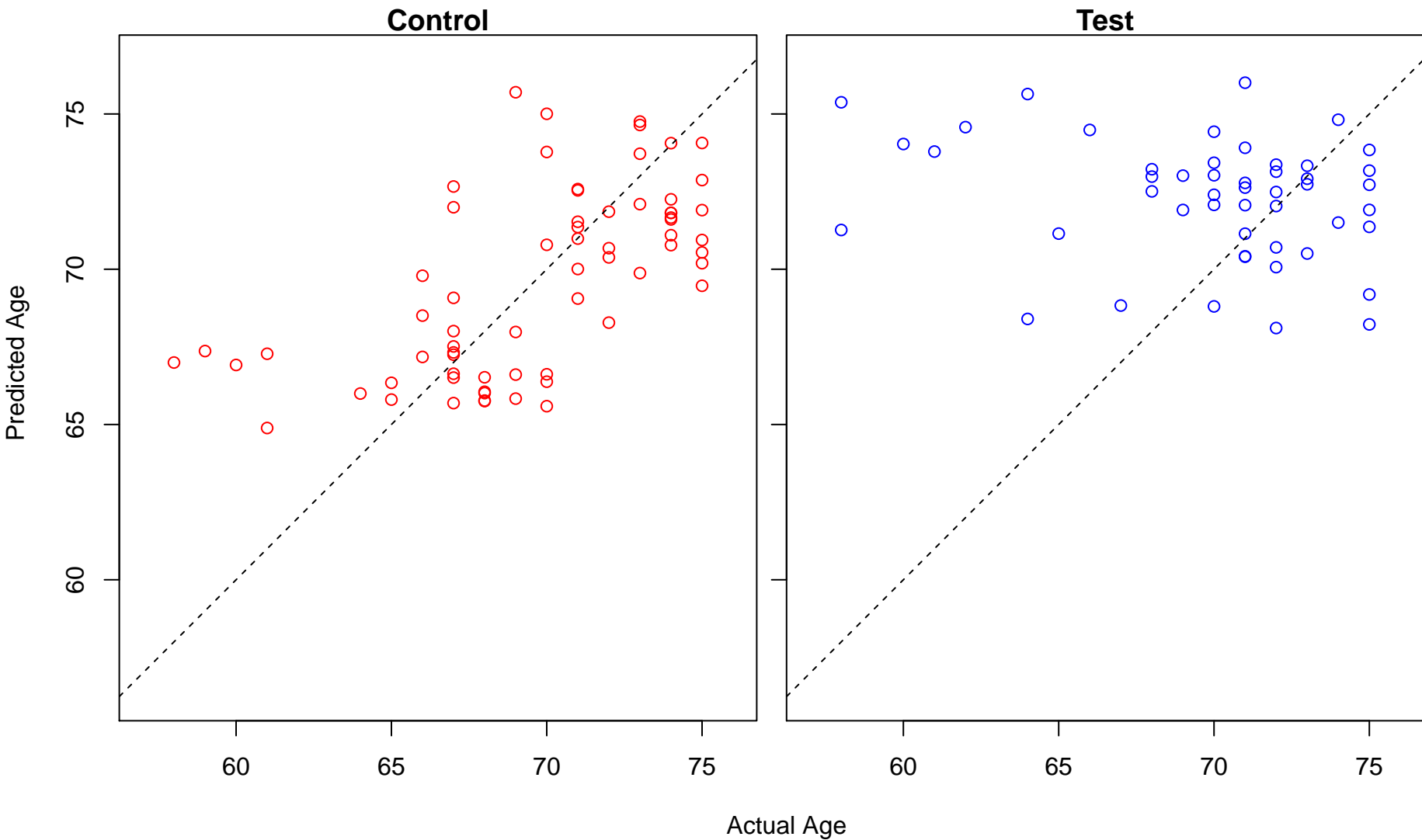
positive regulation of lipase activity (Score: 1.266160)



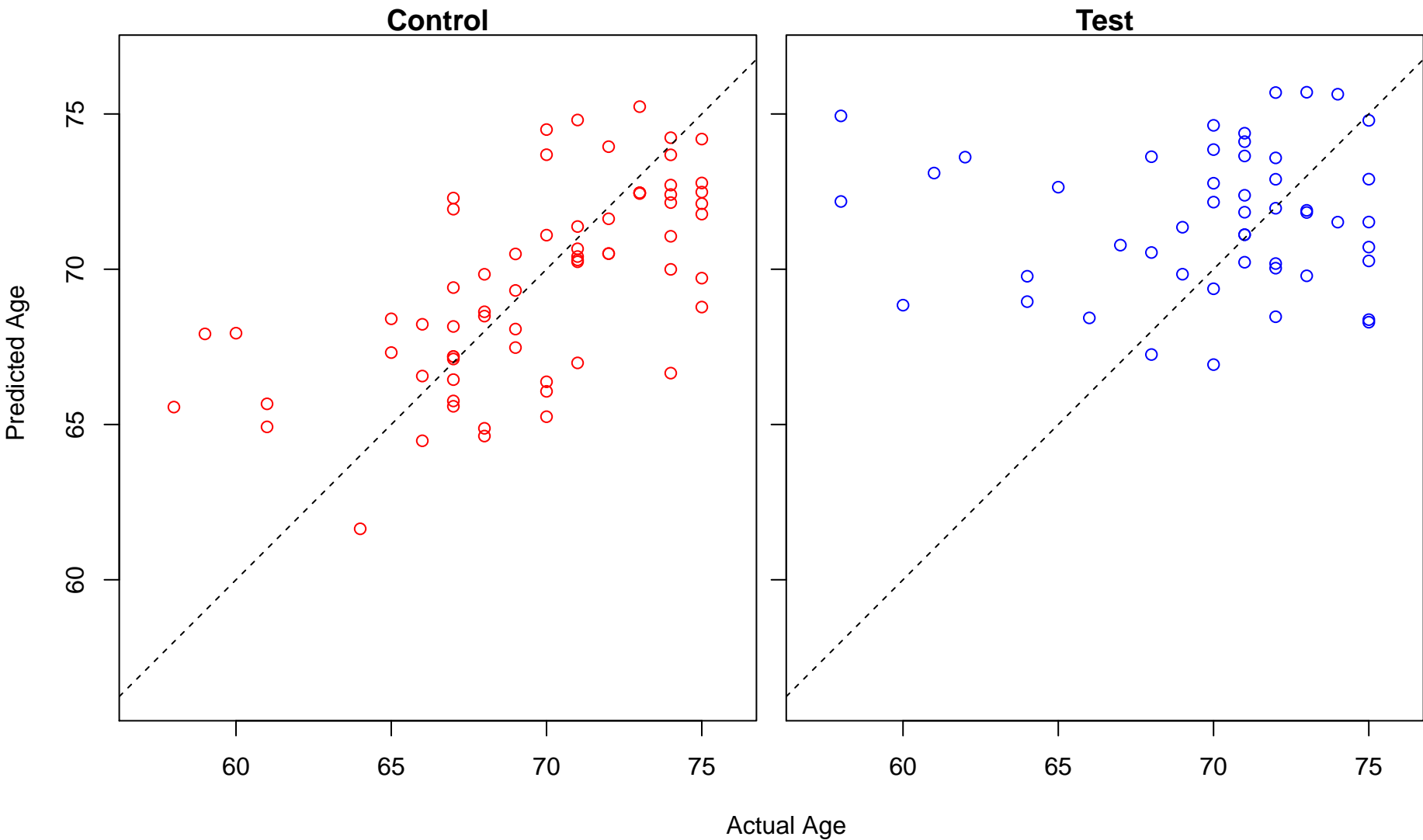
response to ethanol (Score: 1.265966)



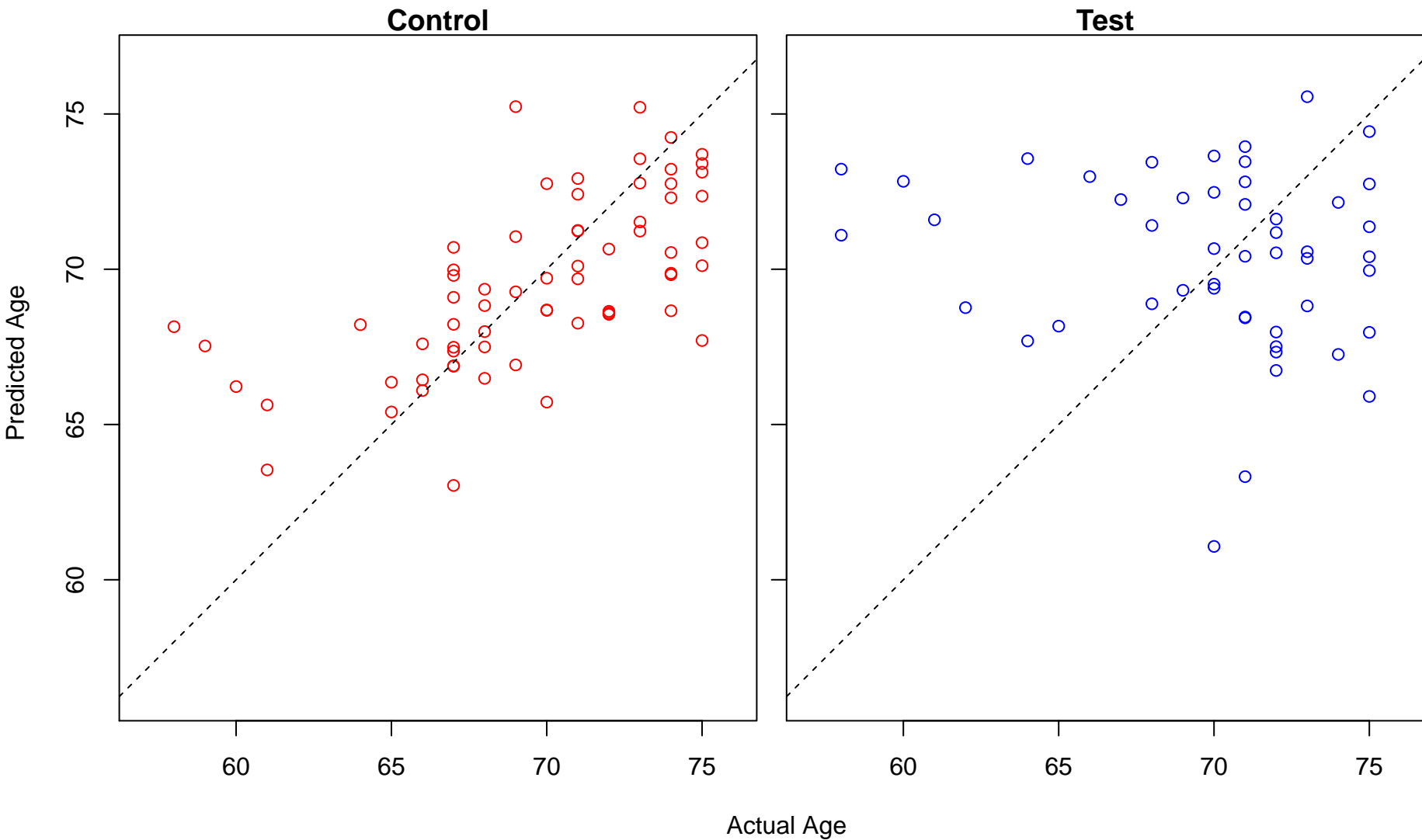
male gamete generation (Score: 1.265903)



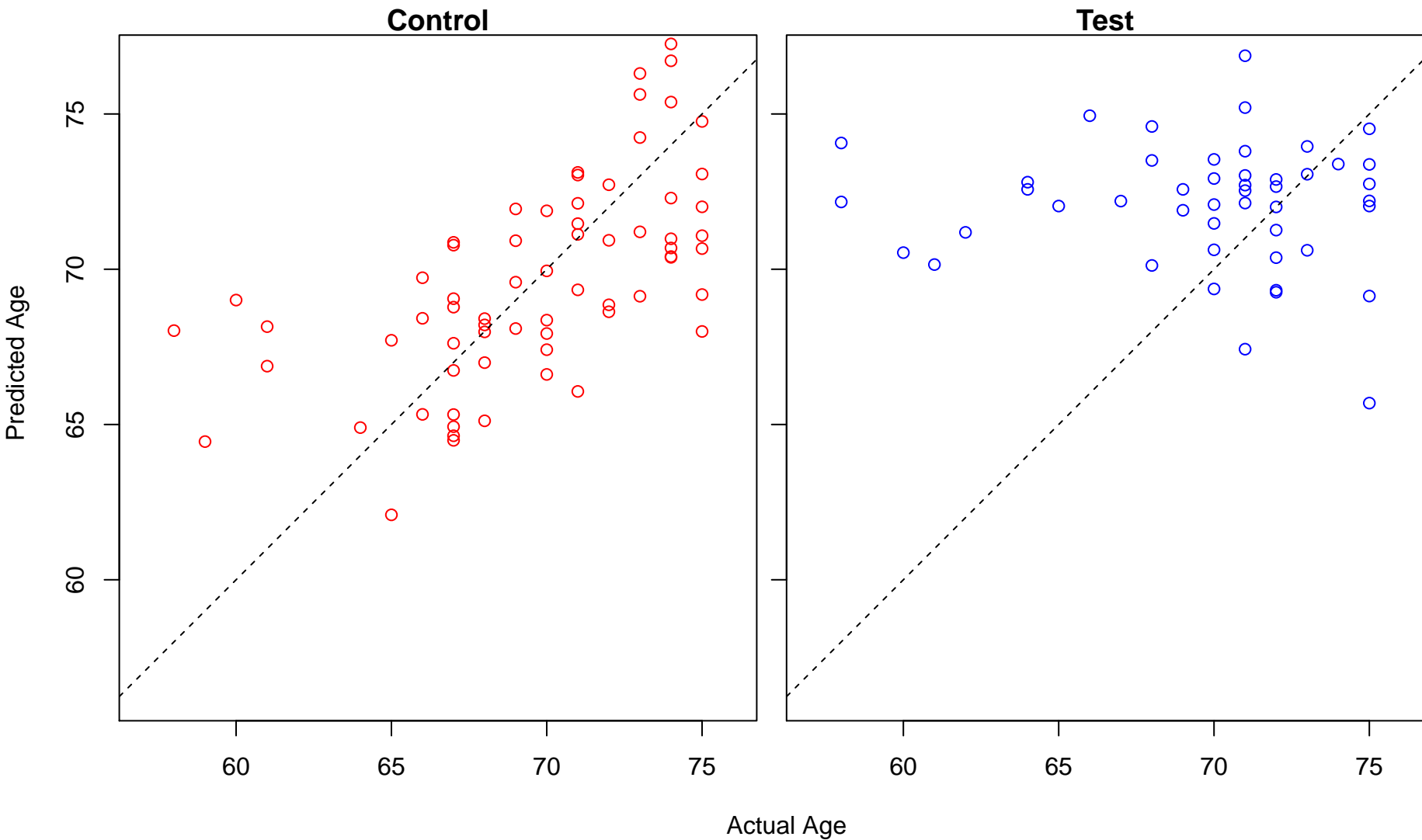
cardiac conduction (Score: 1.265756)



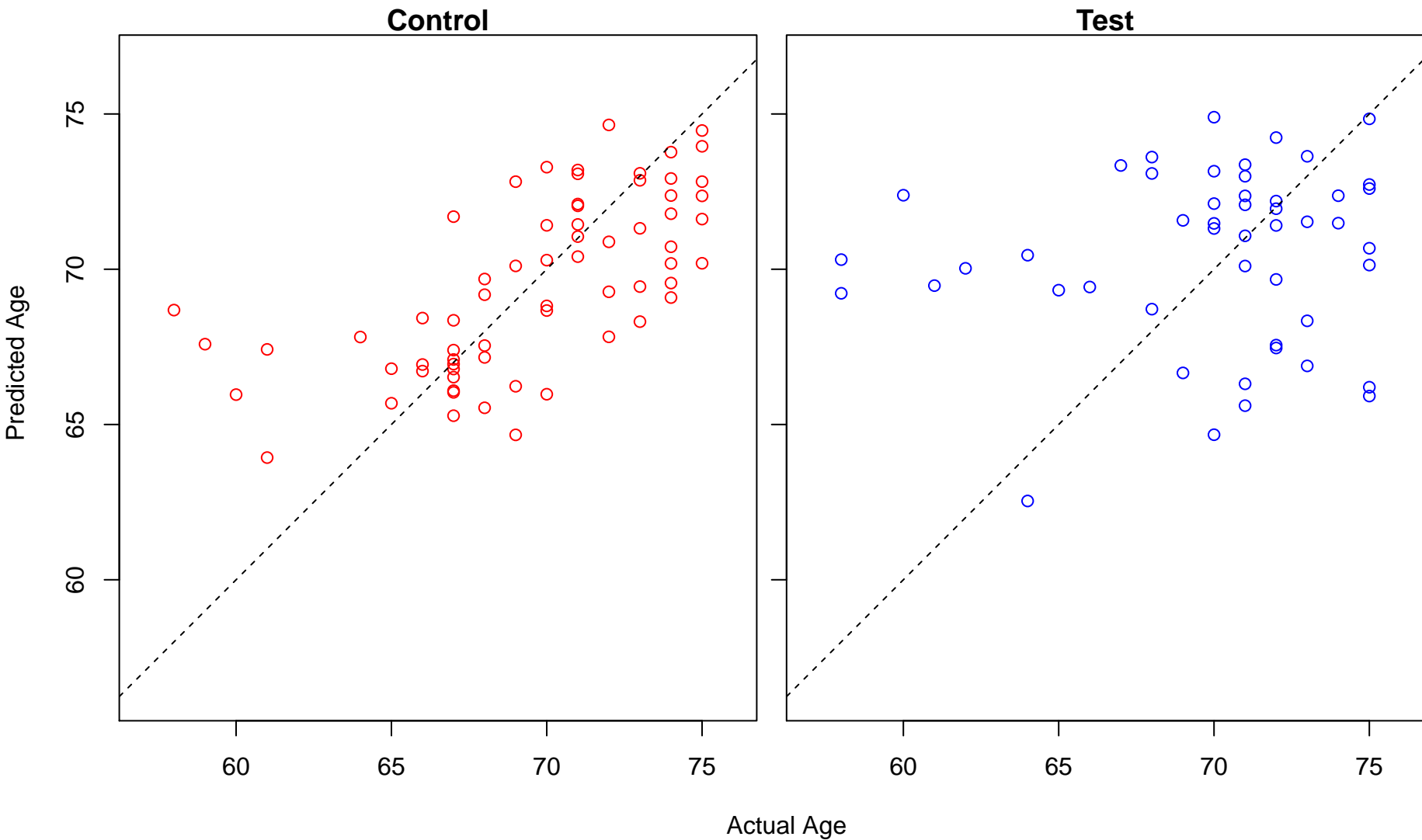
negative regulation of cyclase activity (Score: 1.265326)



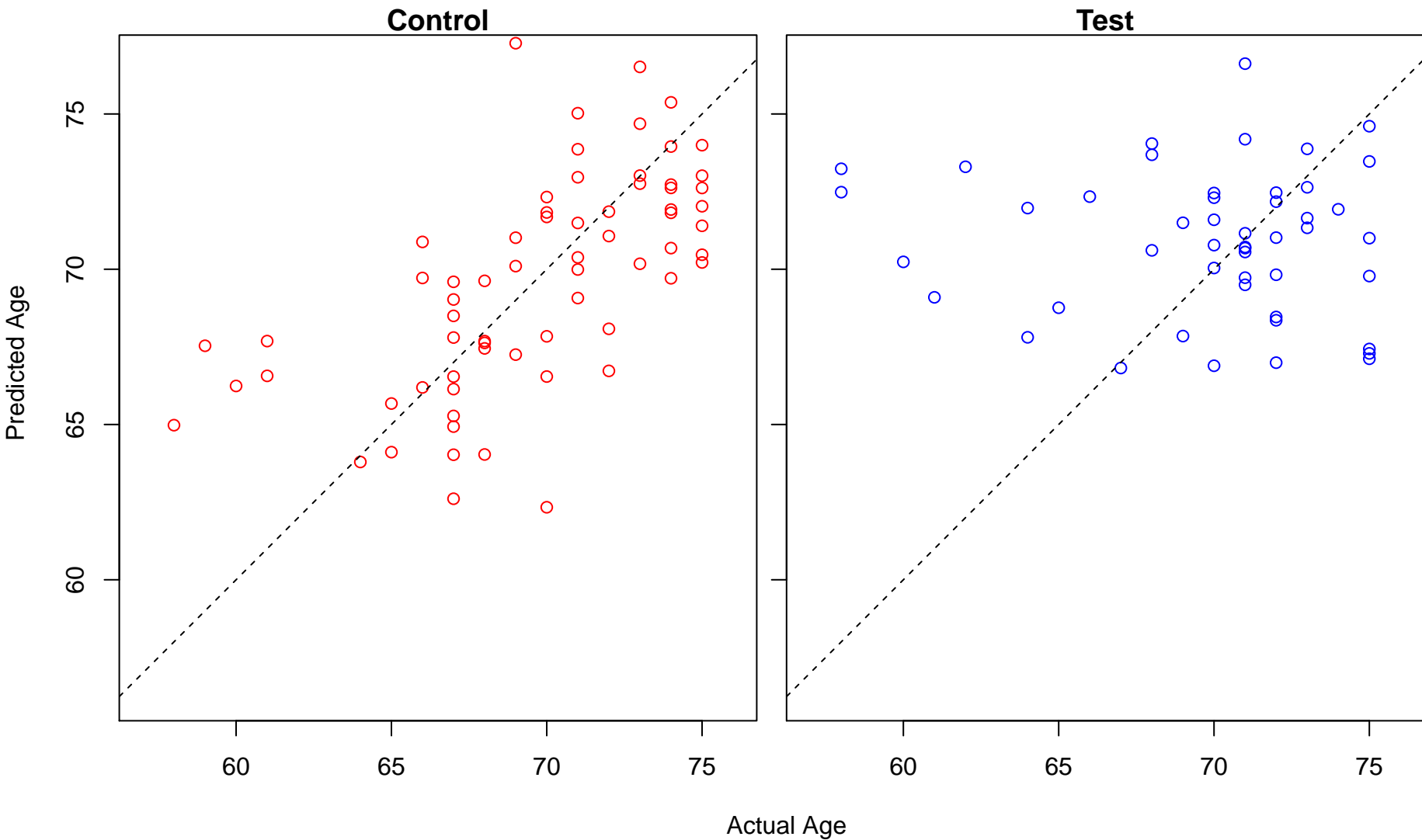
regulation of Rho protein signal transduction (Score: 1.263766)



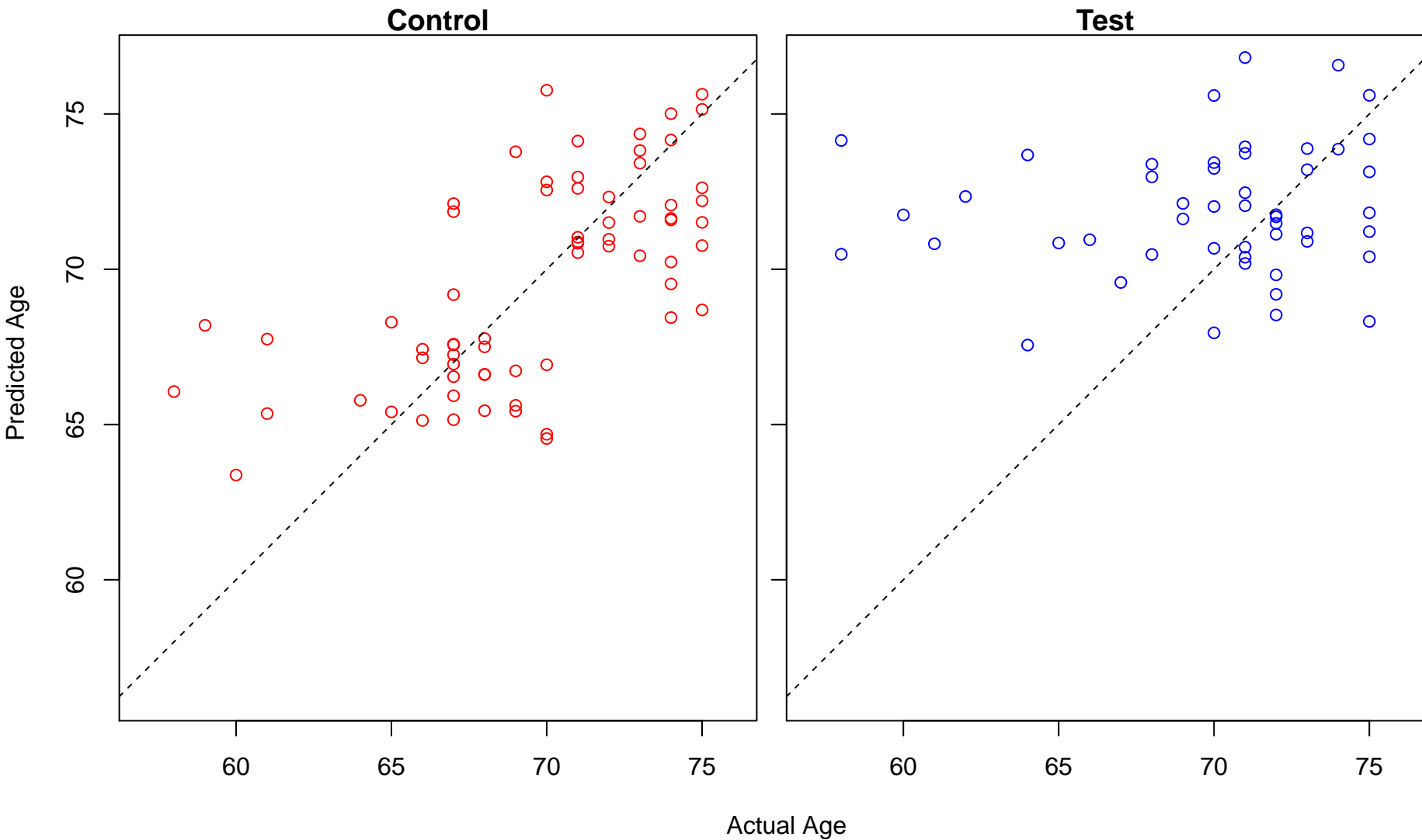
ATF6-mediated unfolded protein response (Score: 1.263714)



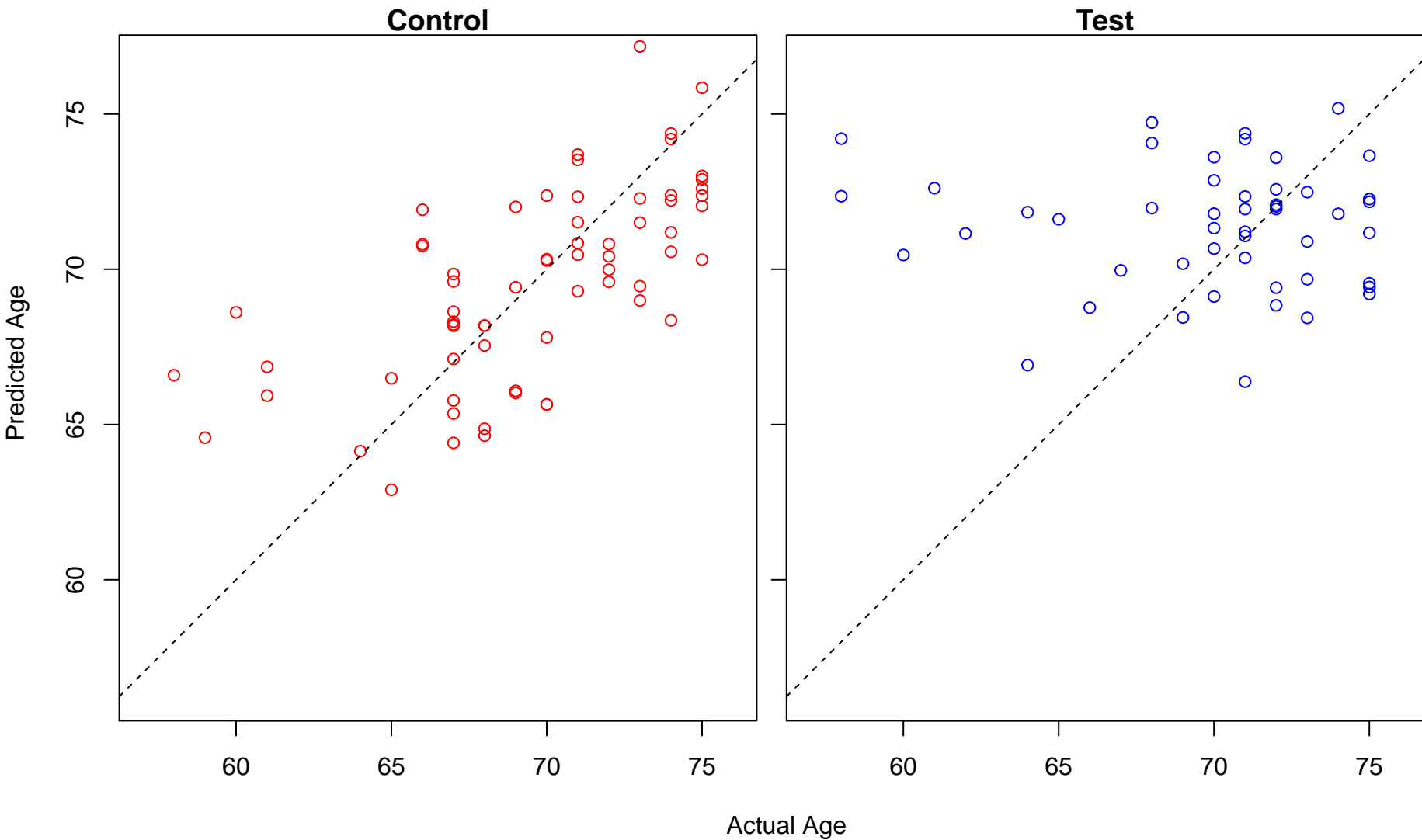
production of molecular mediator of immune response (Score: 1.263566)



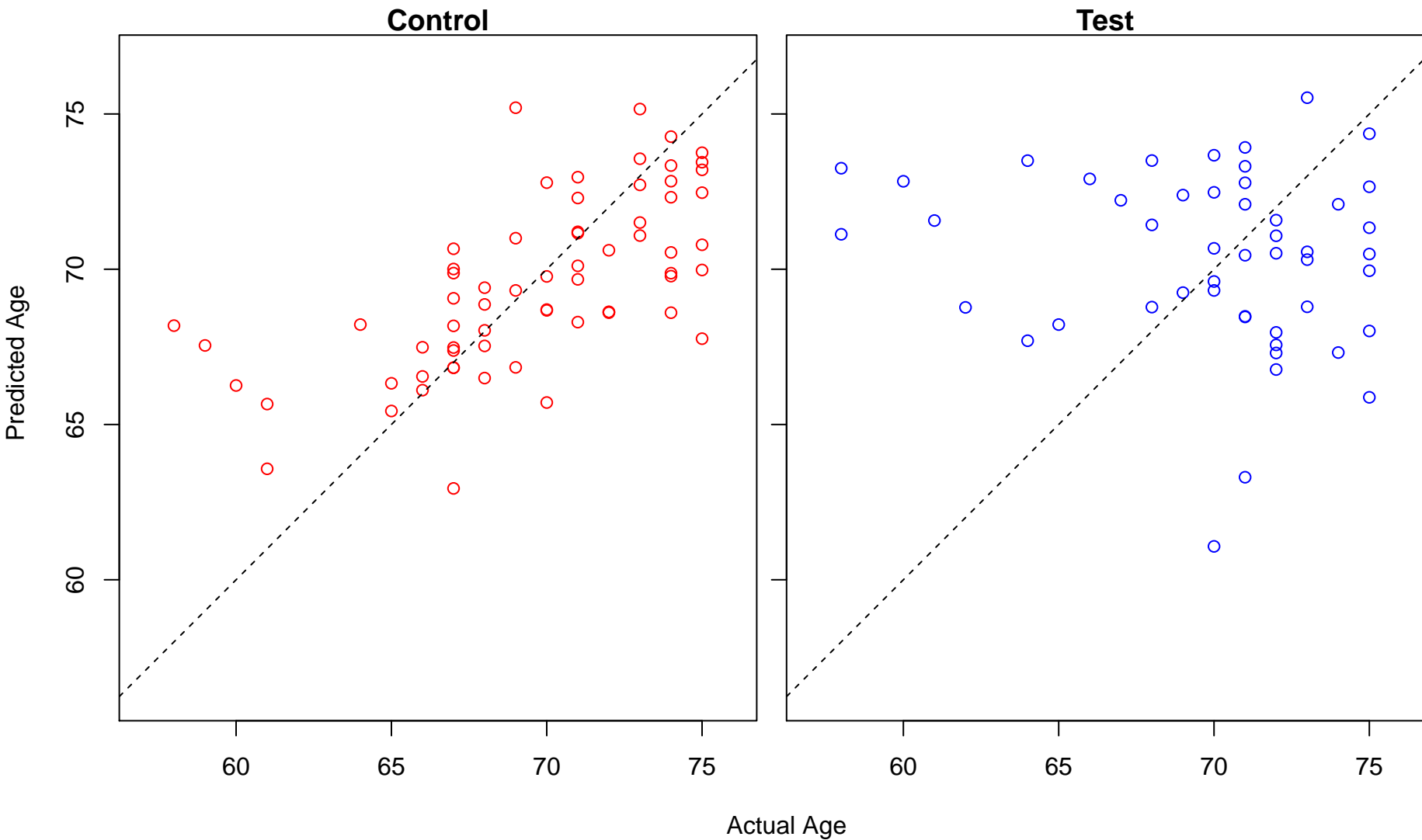
carboxylic acid transport (Score: 1.263099)



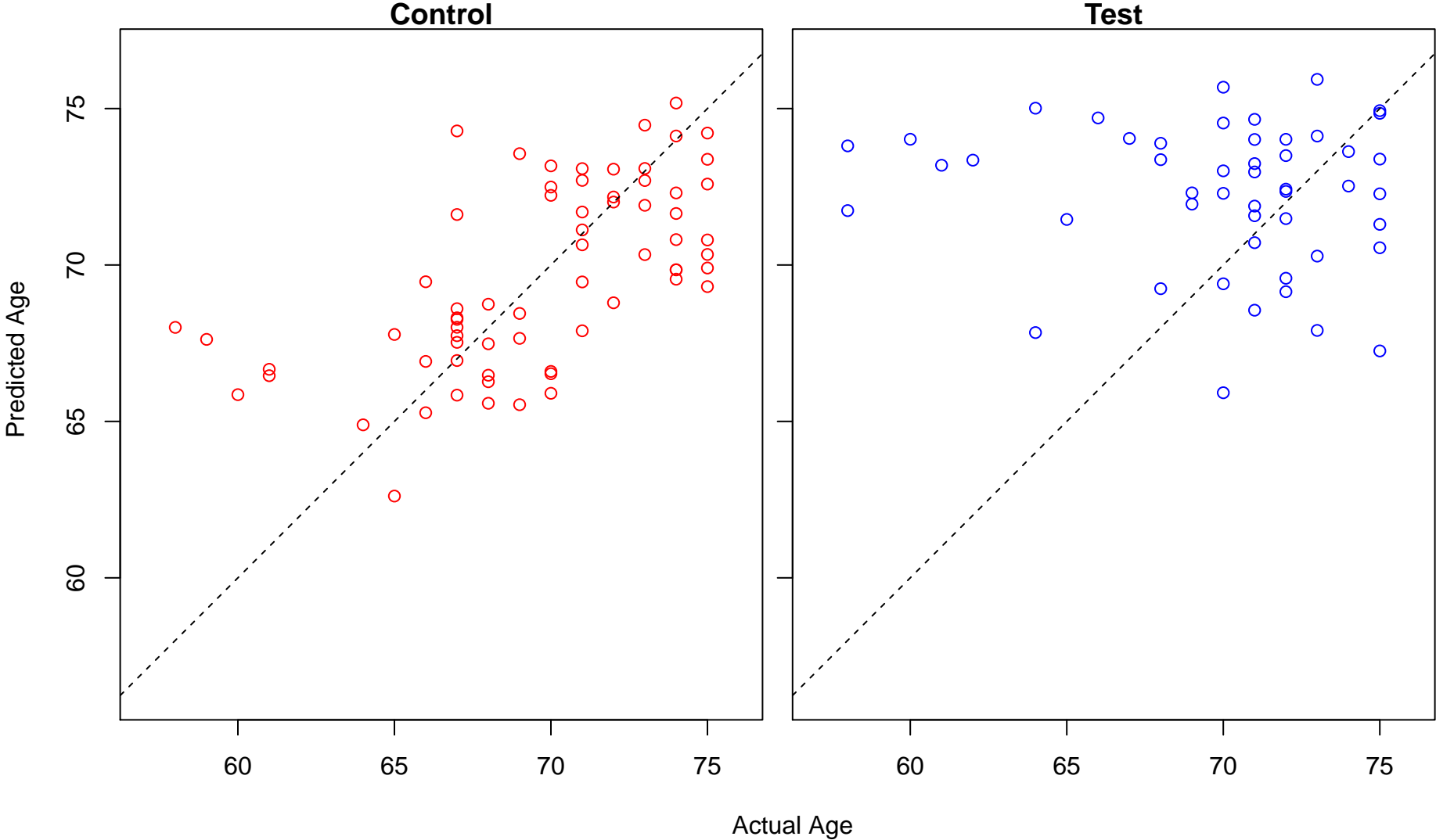
JAK-STAT cascade involved in growth hormone signaling pathway (Score: 1.263054)



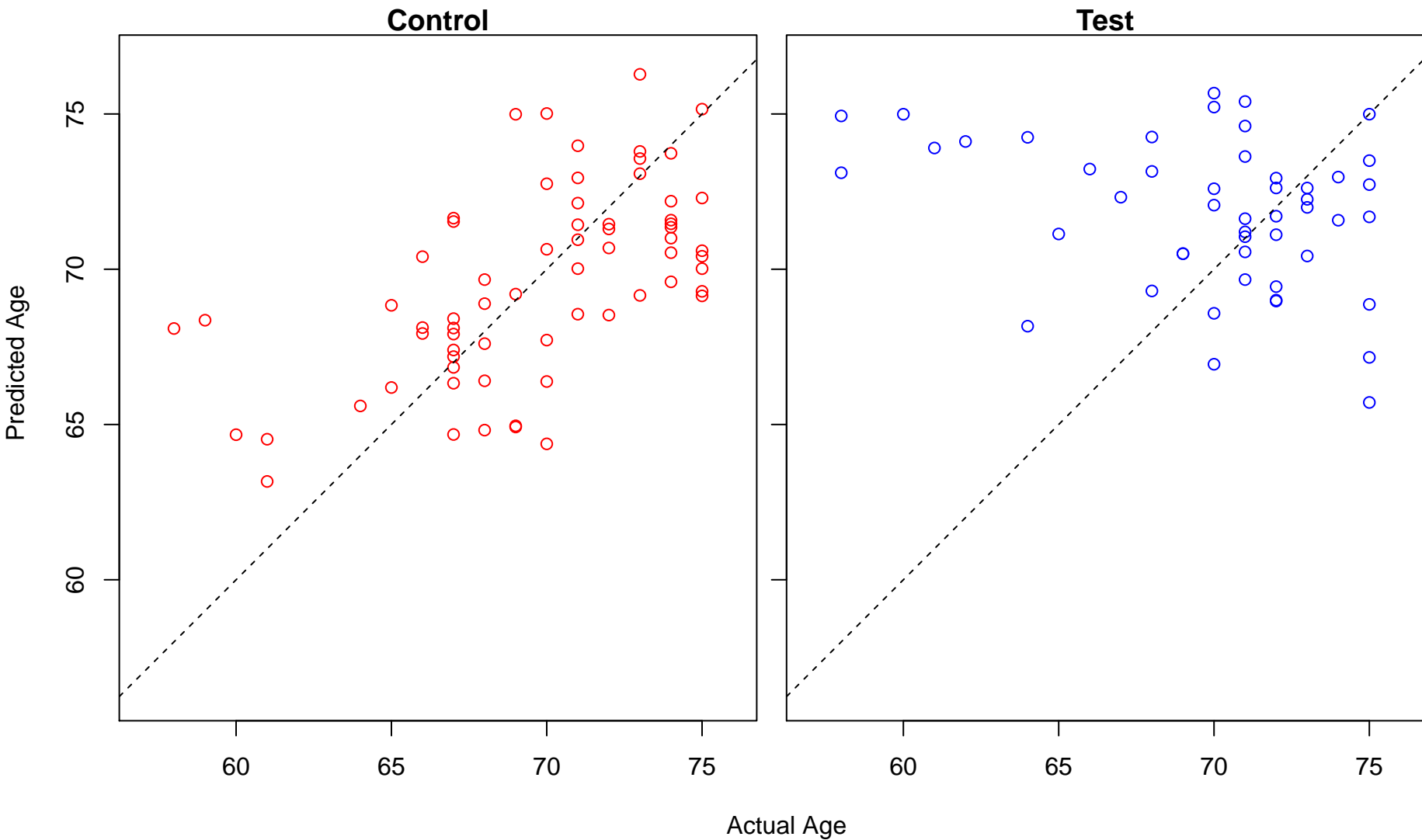
negative regulation of cAMP biosynthetic process (Score: 1.262011)



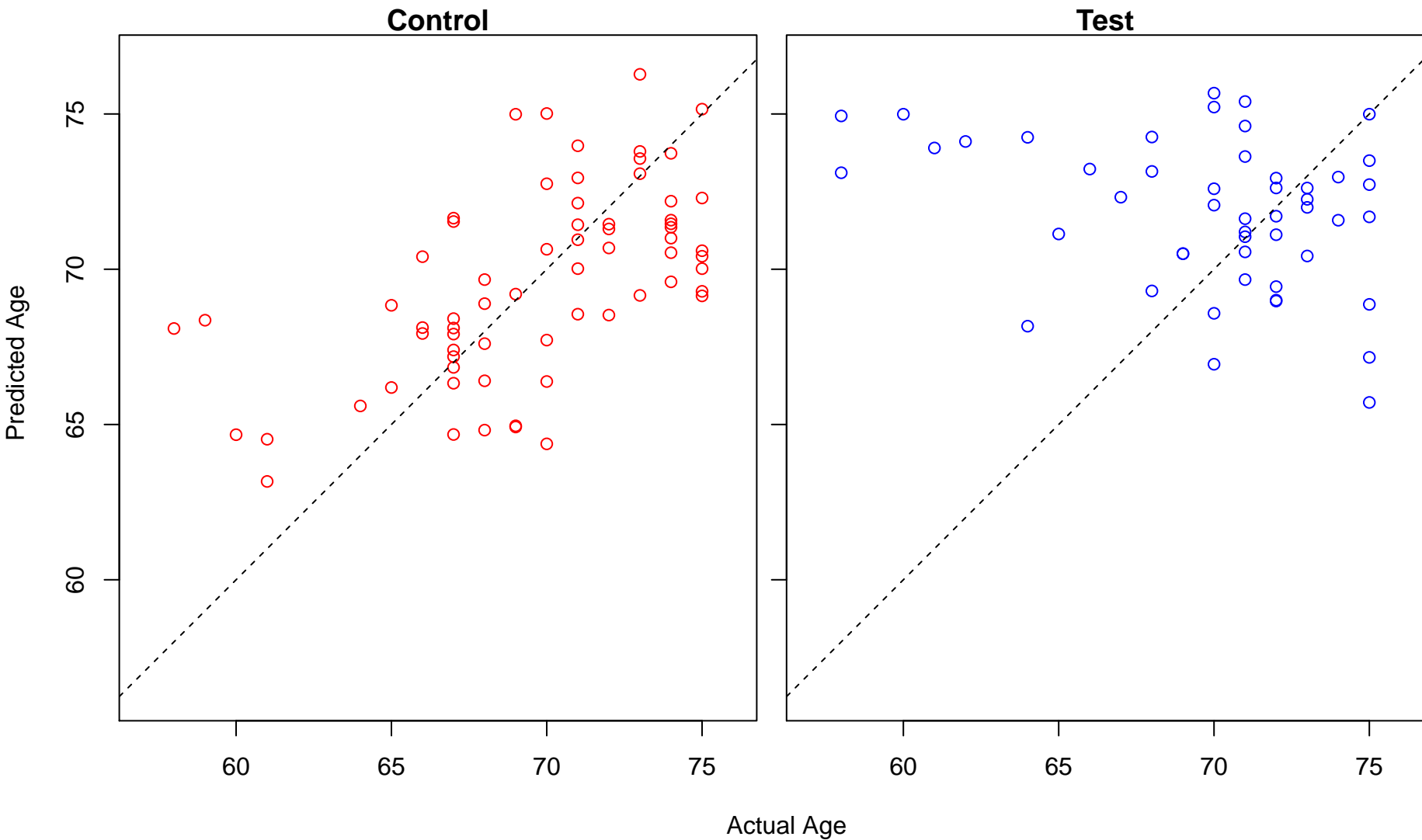
cytoplasmic pattern recognition receptor signaling pathway (Score: 1.261545)



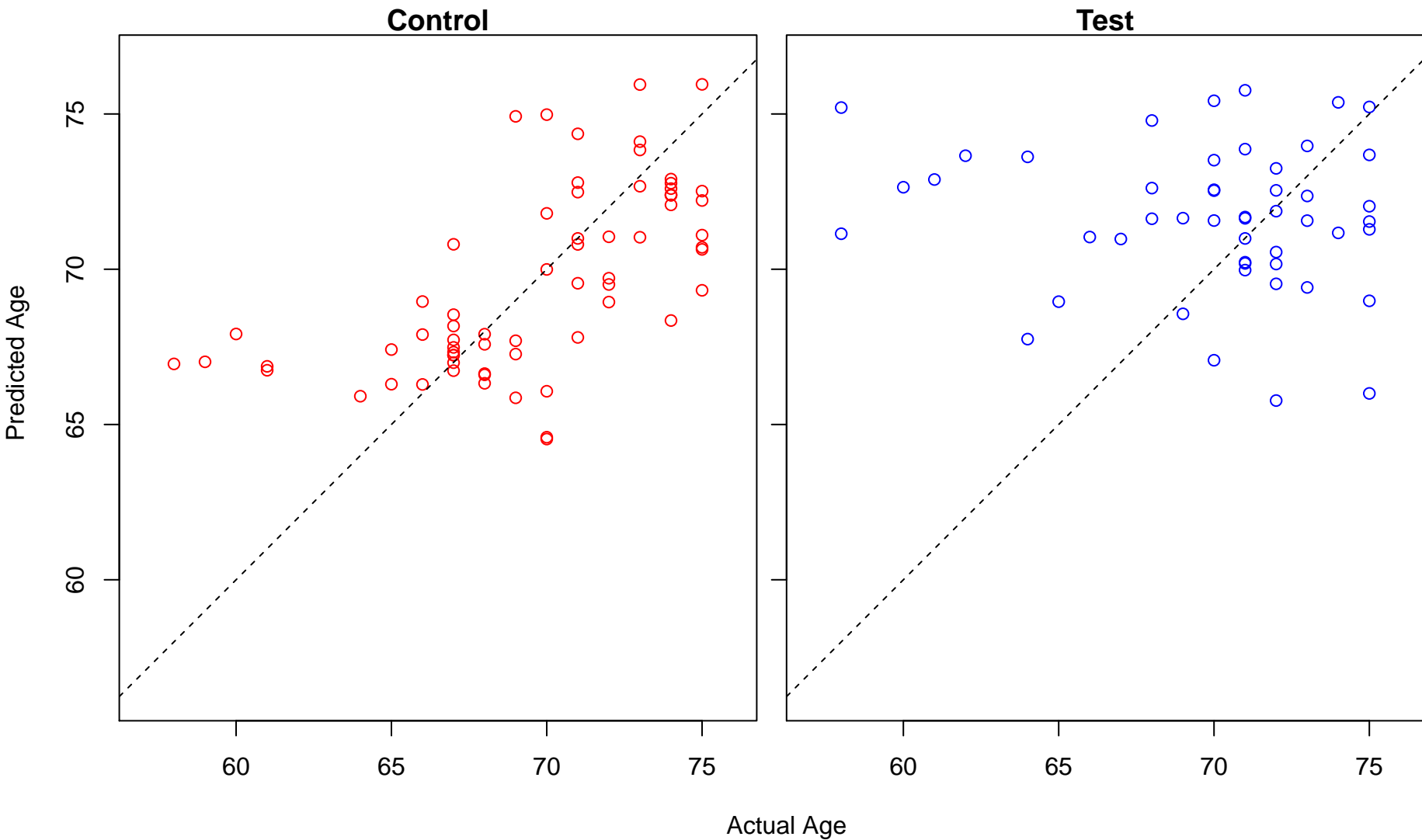
negative regulation of response to extracellular stimulus (Score: 1.261305)



negative regulation of response to nutrient levels (Score: 1.261305)

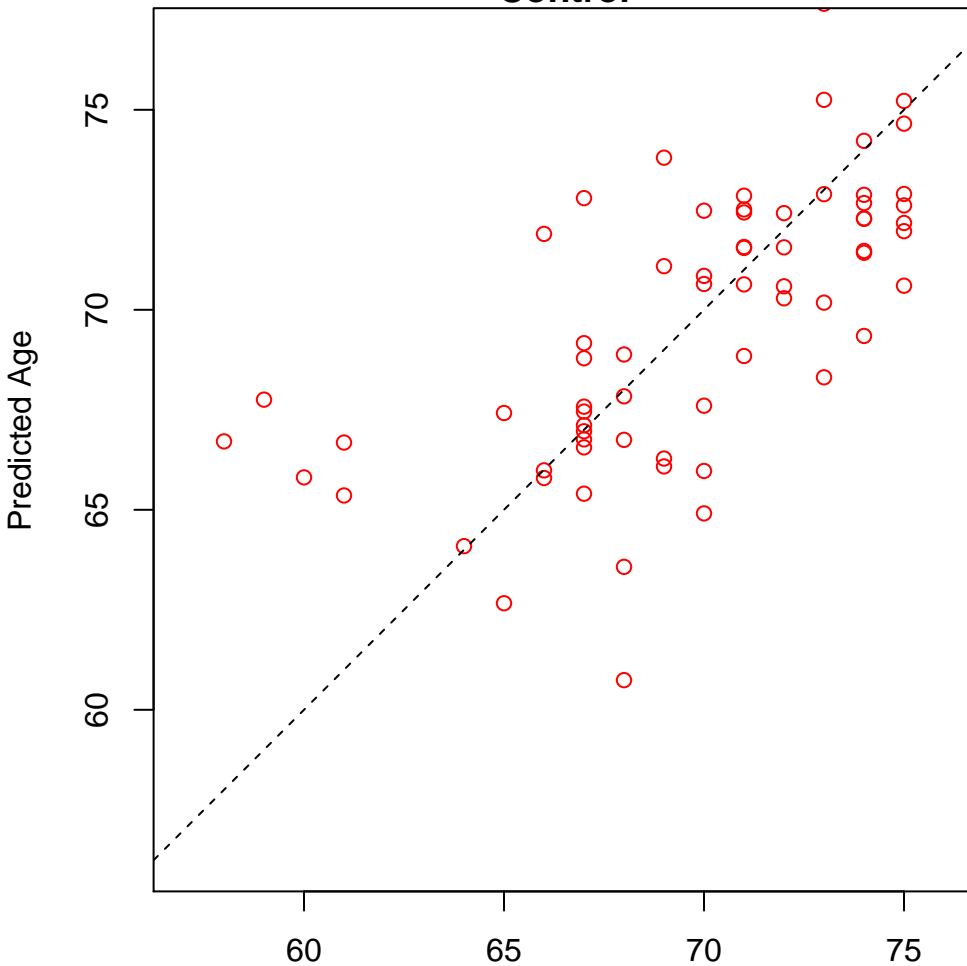


histone H3 acetylation (Score: 1.261303)

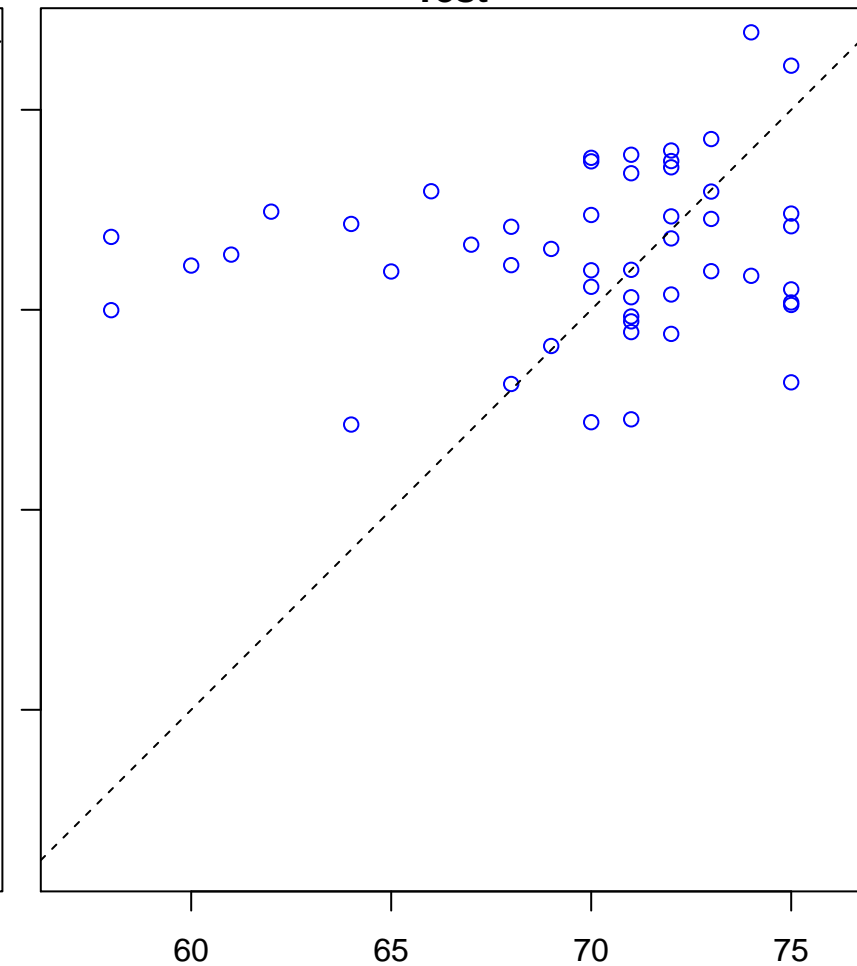


regulation of osteoblast differentiation (Score: 1.261093)

Control

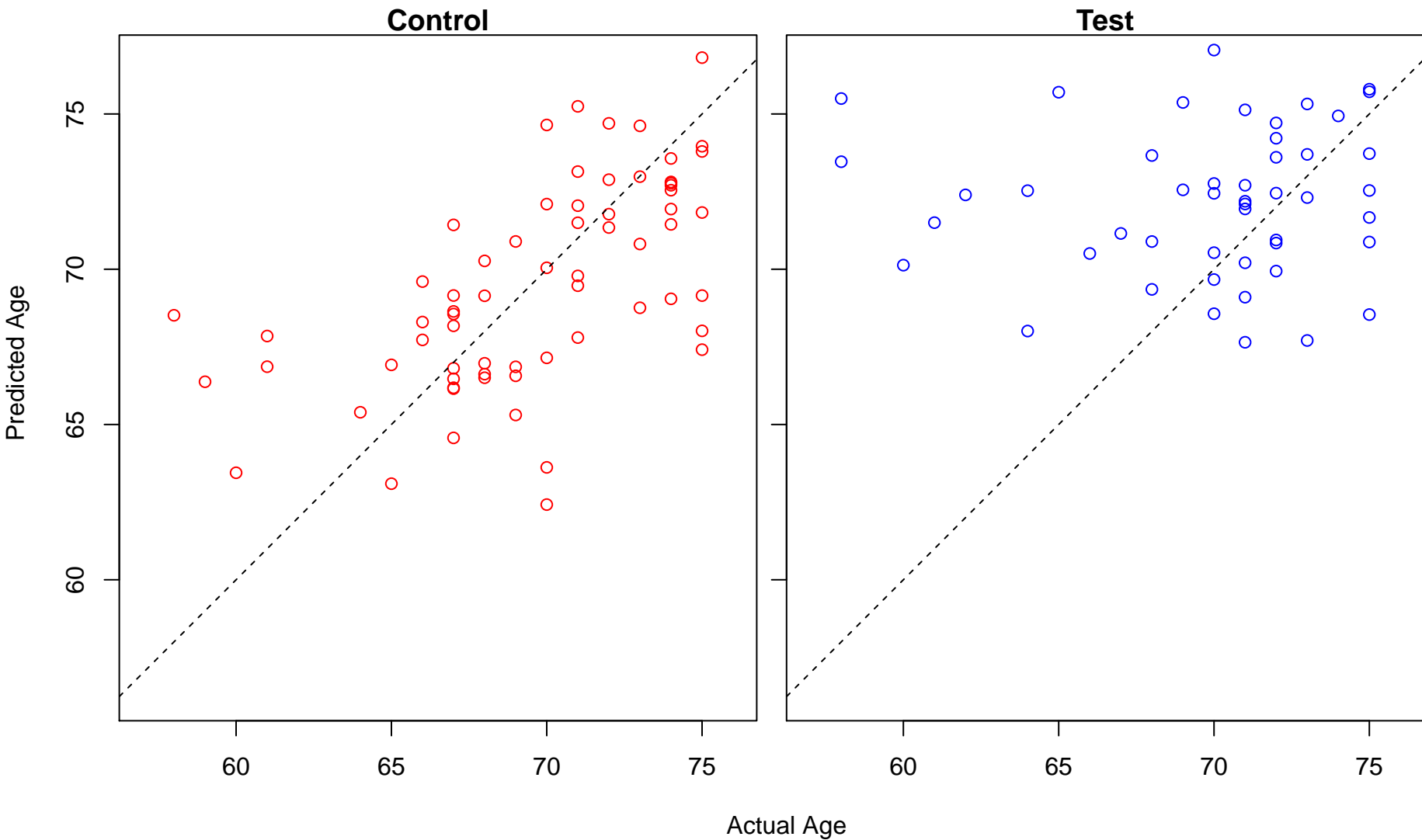


Test

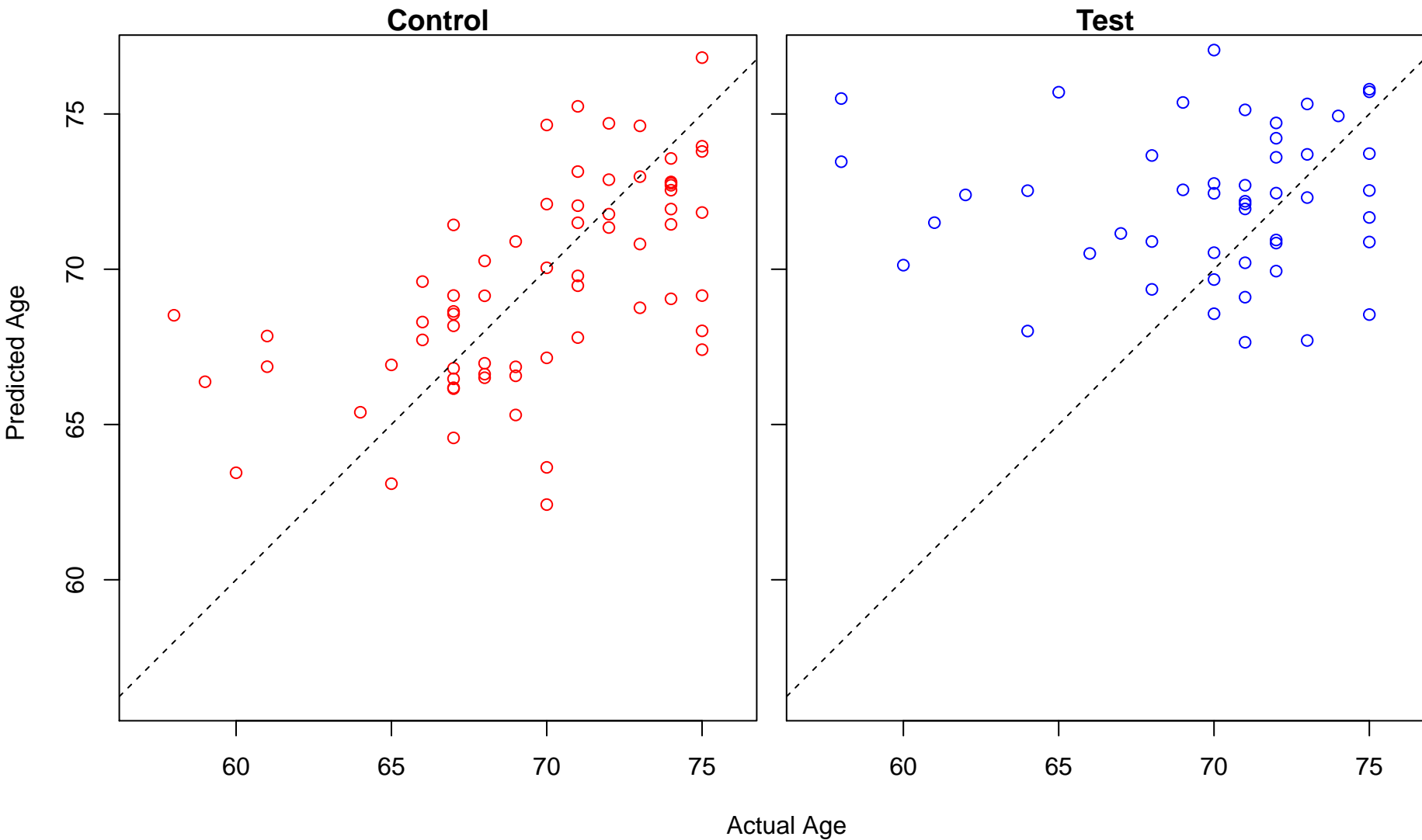


Actual Age

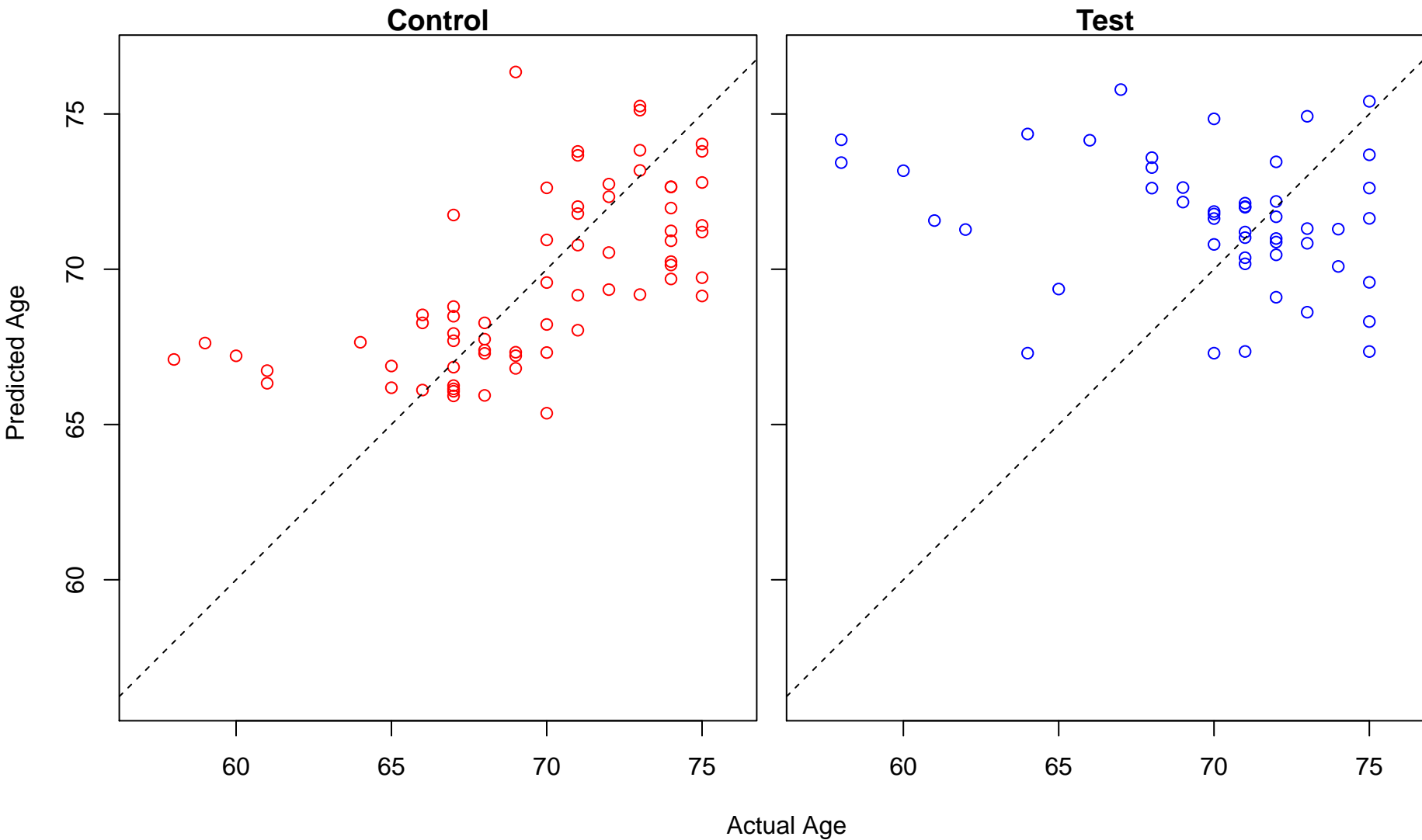
neutral lipid biosynthetic process (Score: 1.260964)



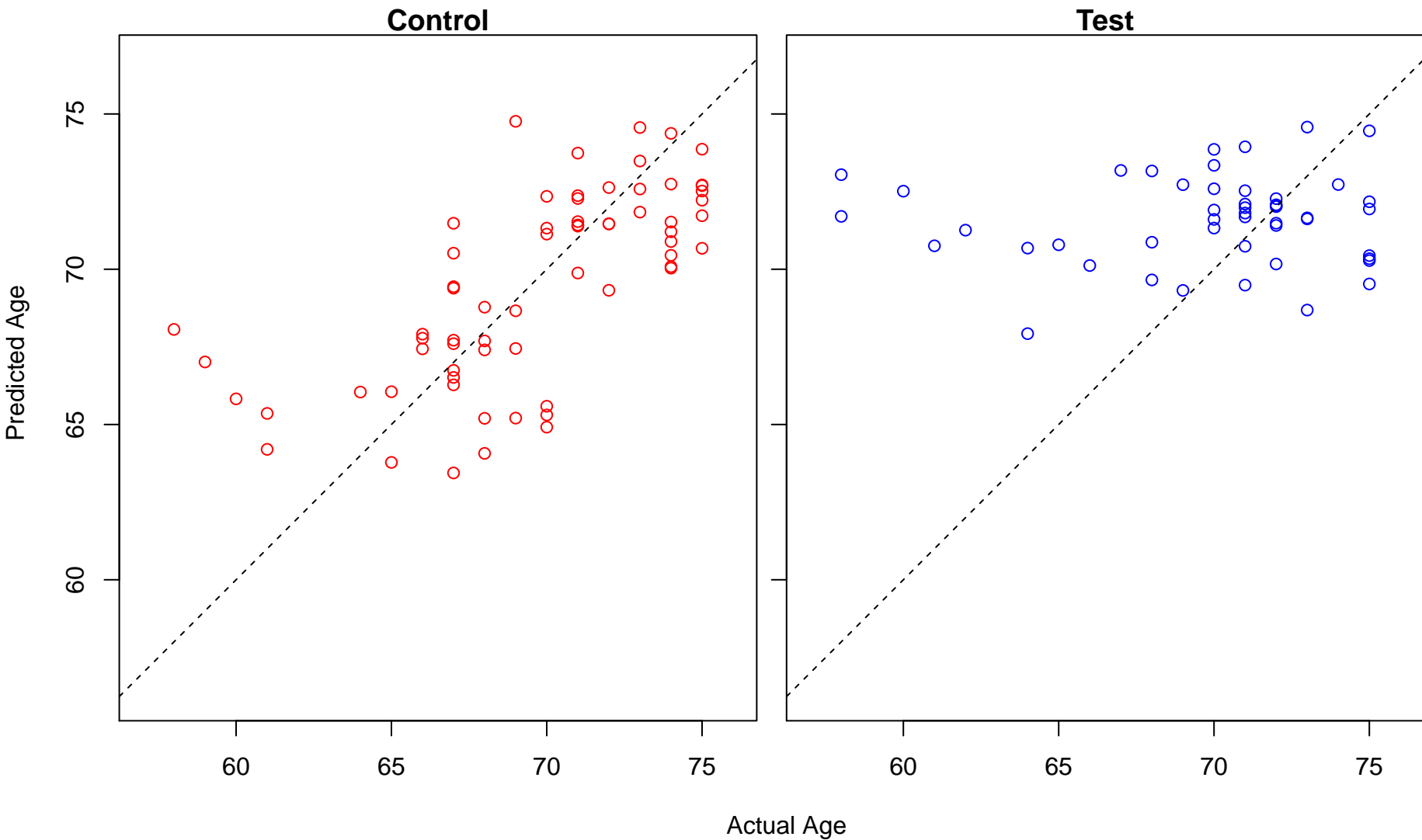
acylglycerol biosynthetic process (Score: 1.260964)



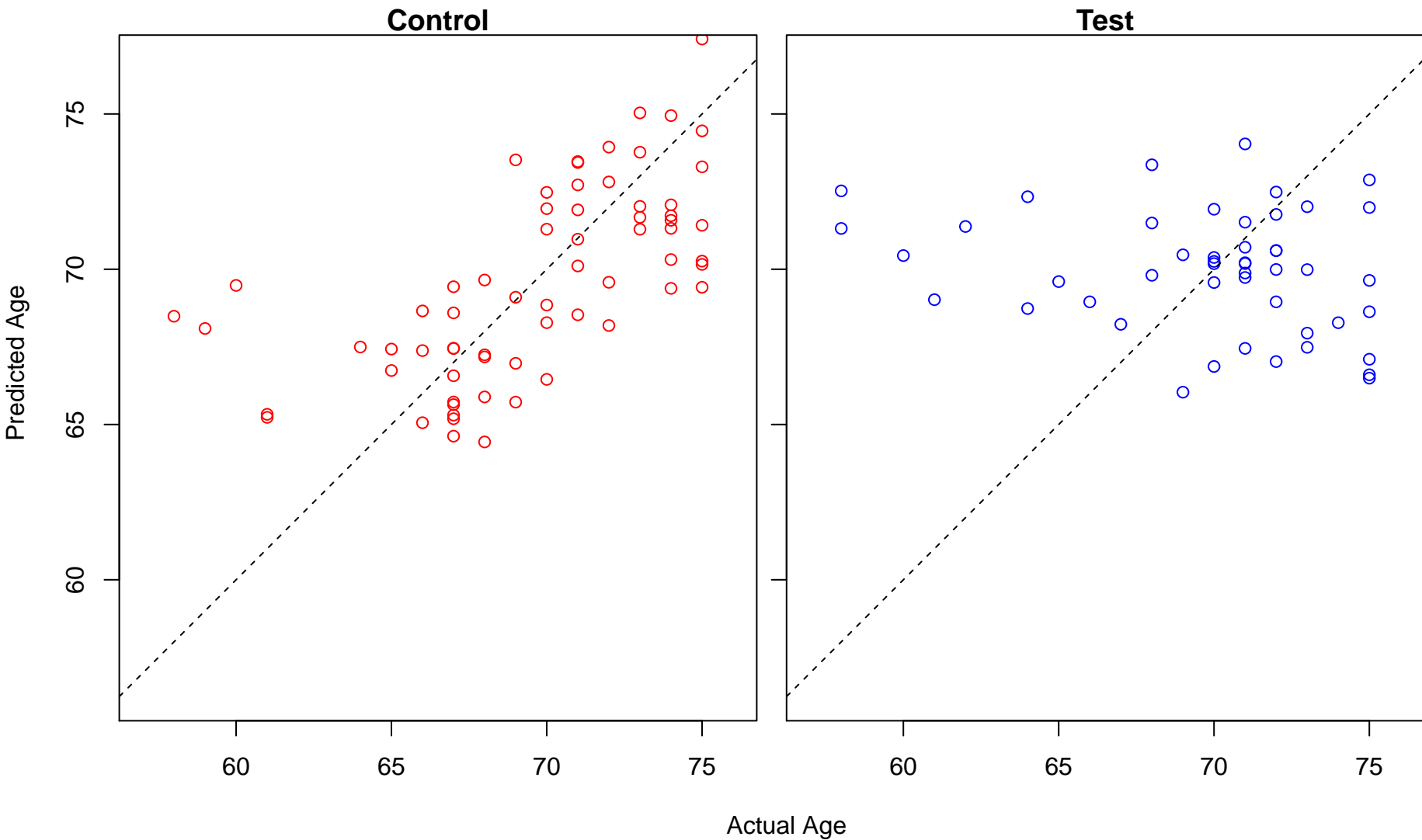
chemokine production (Score: 1.260754)



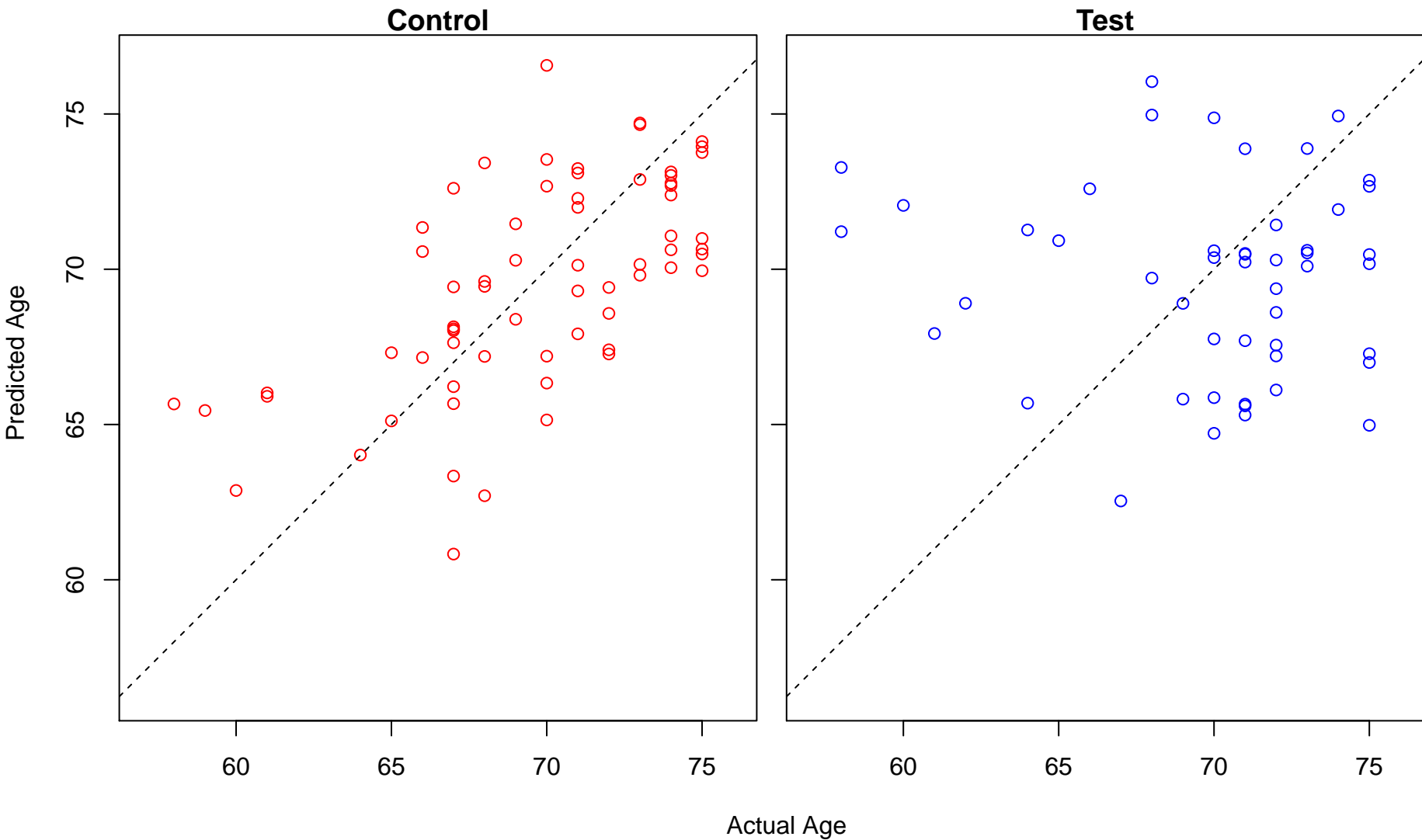
positive regulation of exocytosis (Score: 1.260513)



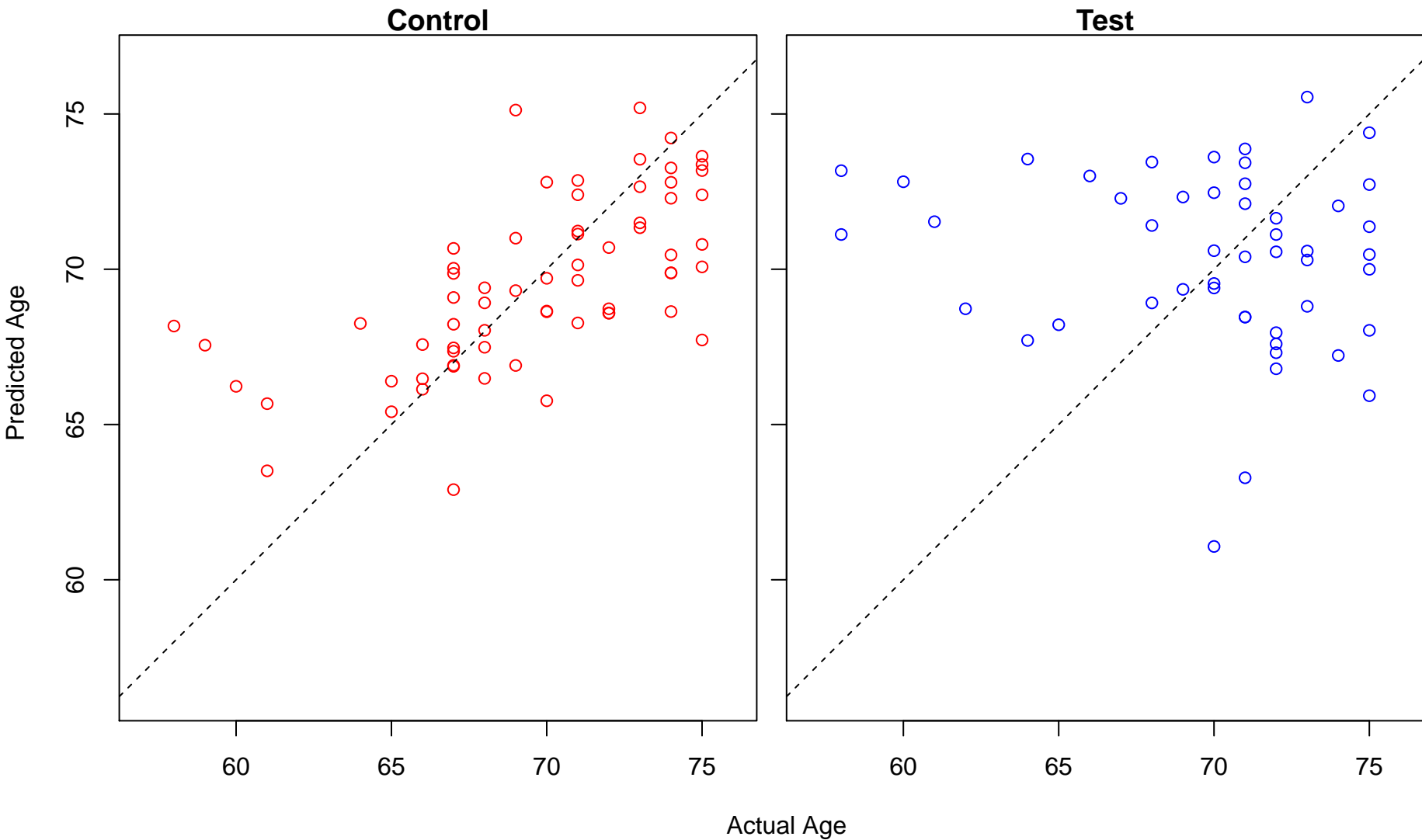
negative regulation of leukocyte proliferation (Score: 1.259989)



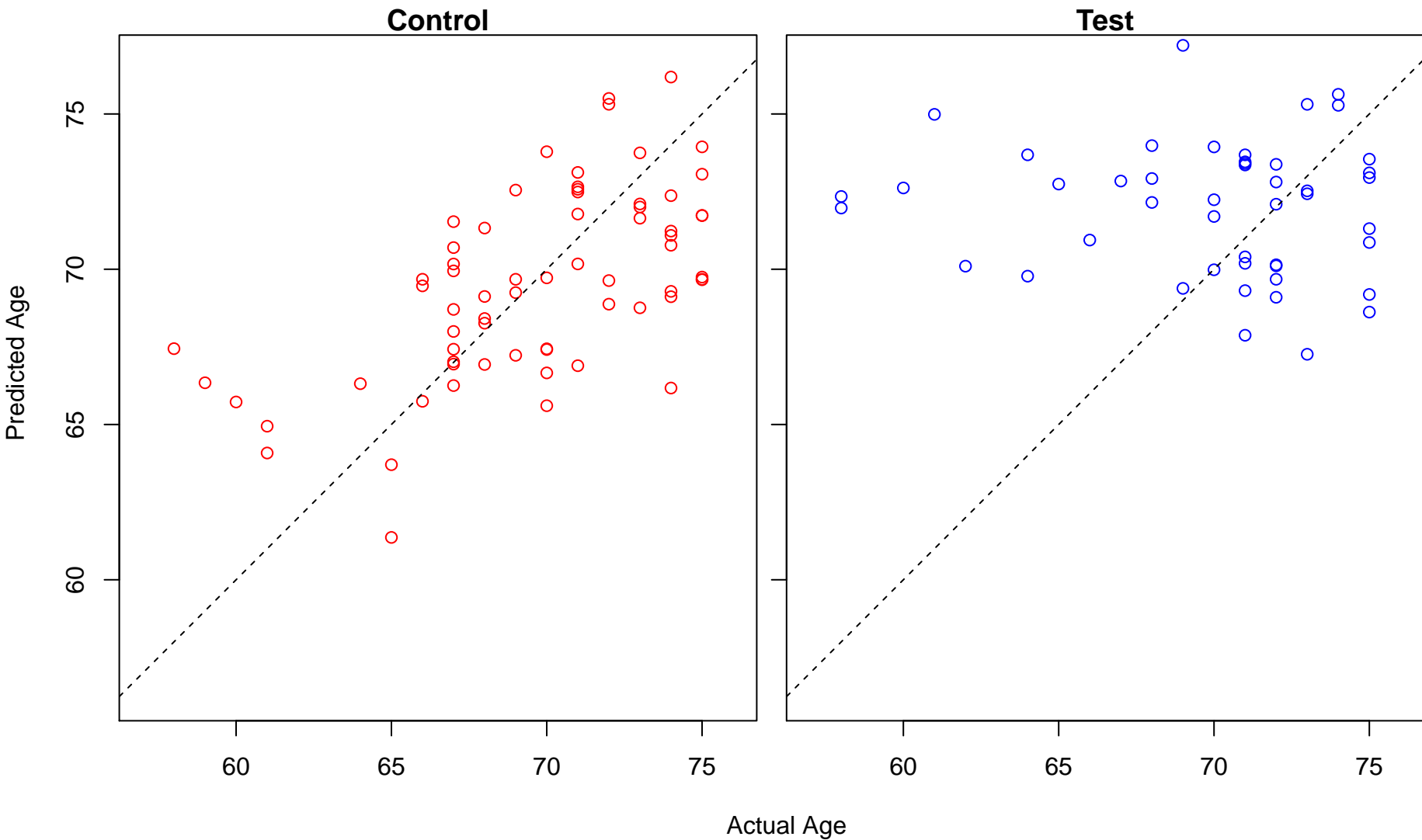
immunoglobulin production involved in immunoglobulin mediated immune response (Score: 1.2597)



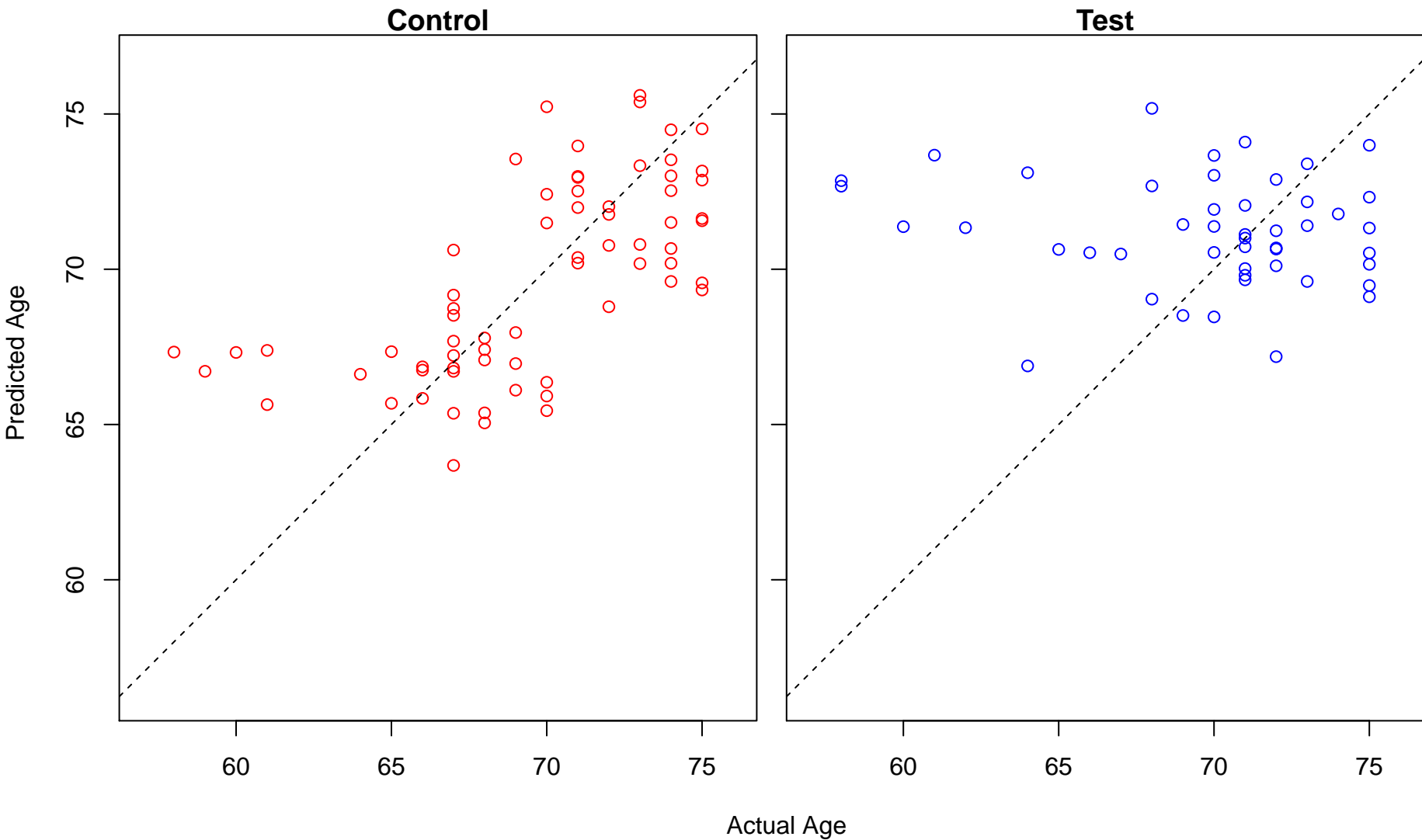
negative regulation of adenylate cyclase activity (Score: 1.259348)



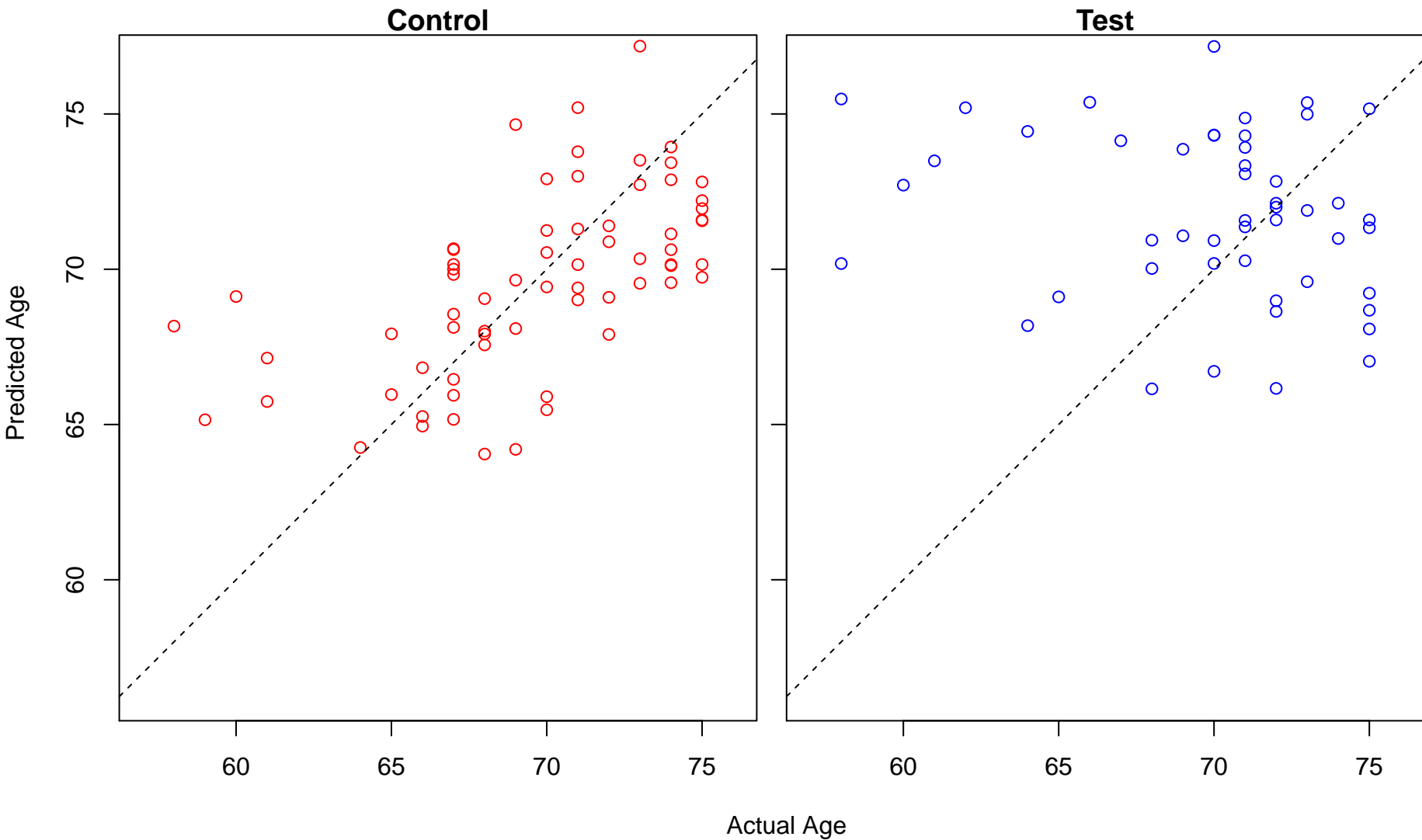
protein kinase C signaling (Score: 1.258363)



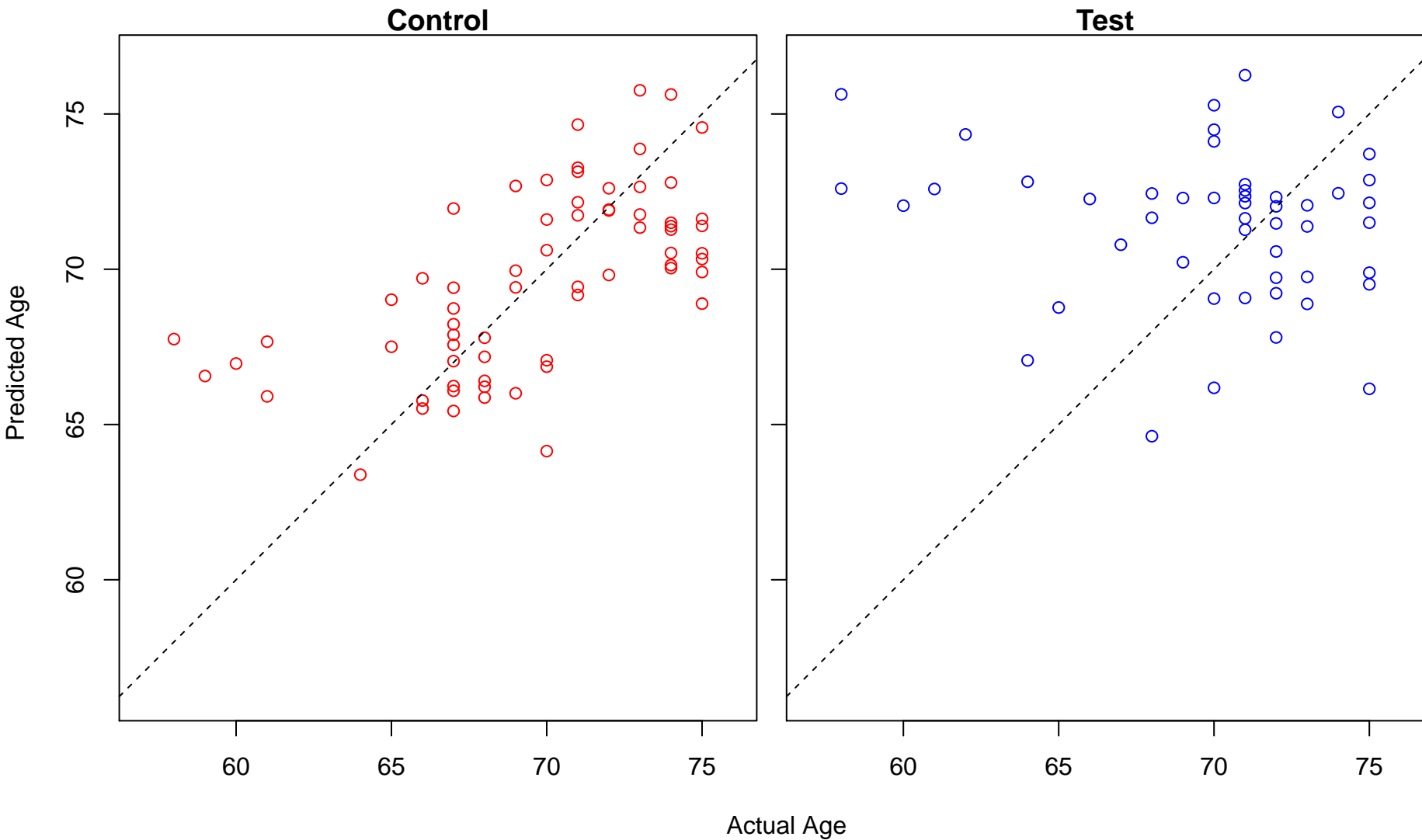
regulation of telomere maintenance via telomerase (Score: 1.258018)



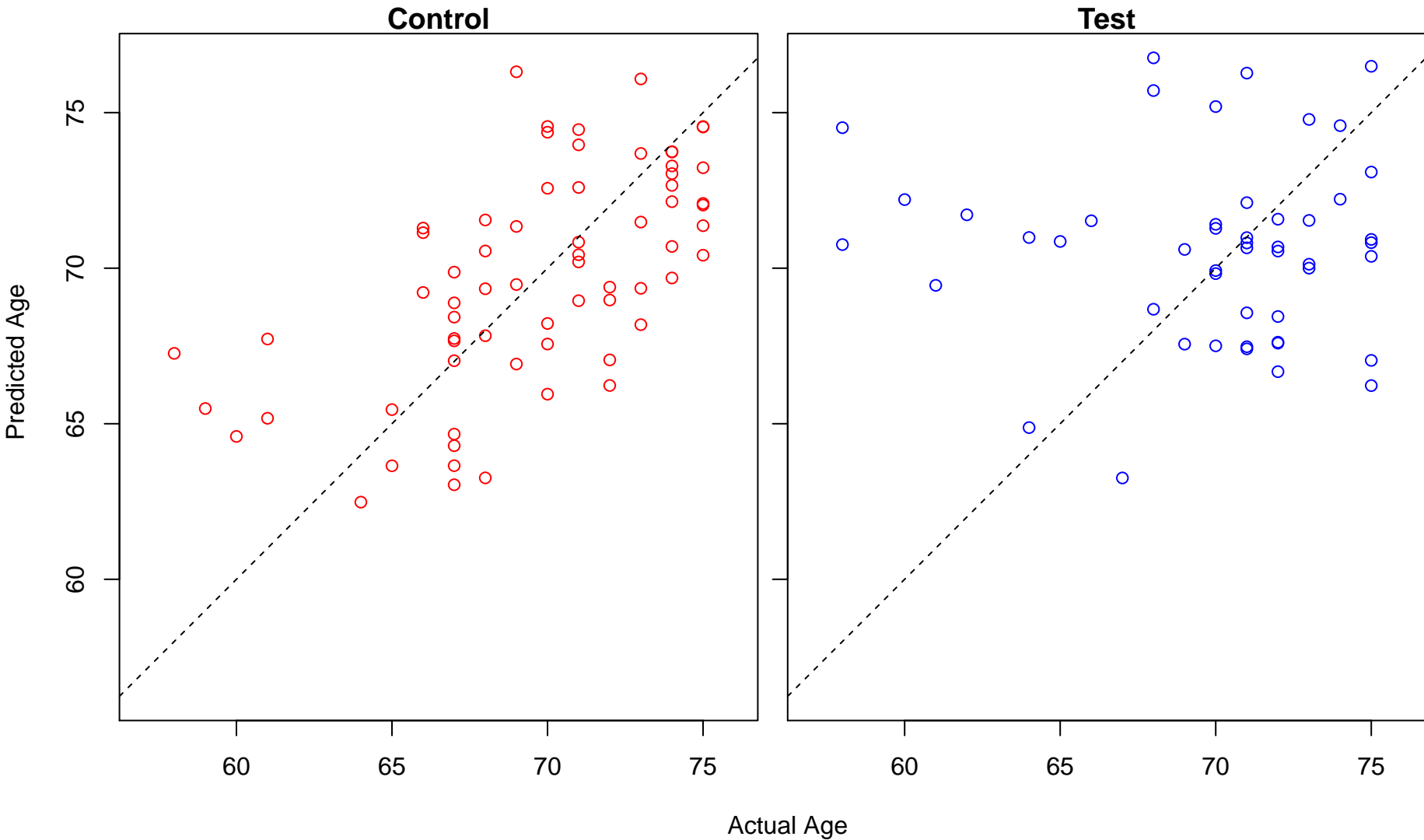
regulation of B cell mediated immunity (Score: 1.257372)



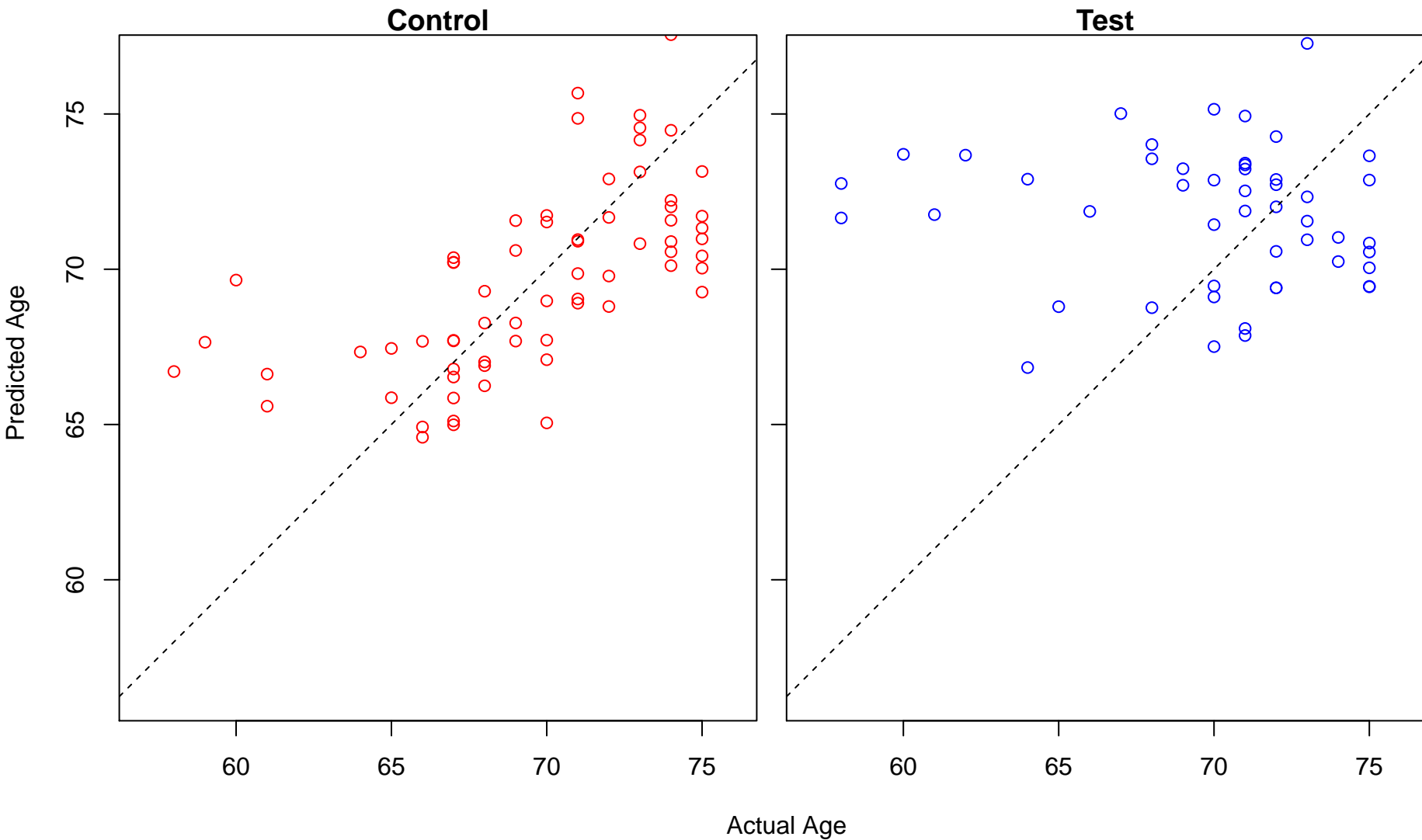
snRNA processing (Score: 1.257153)



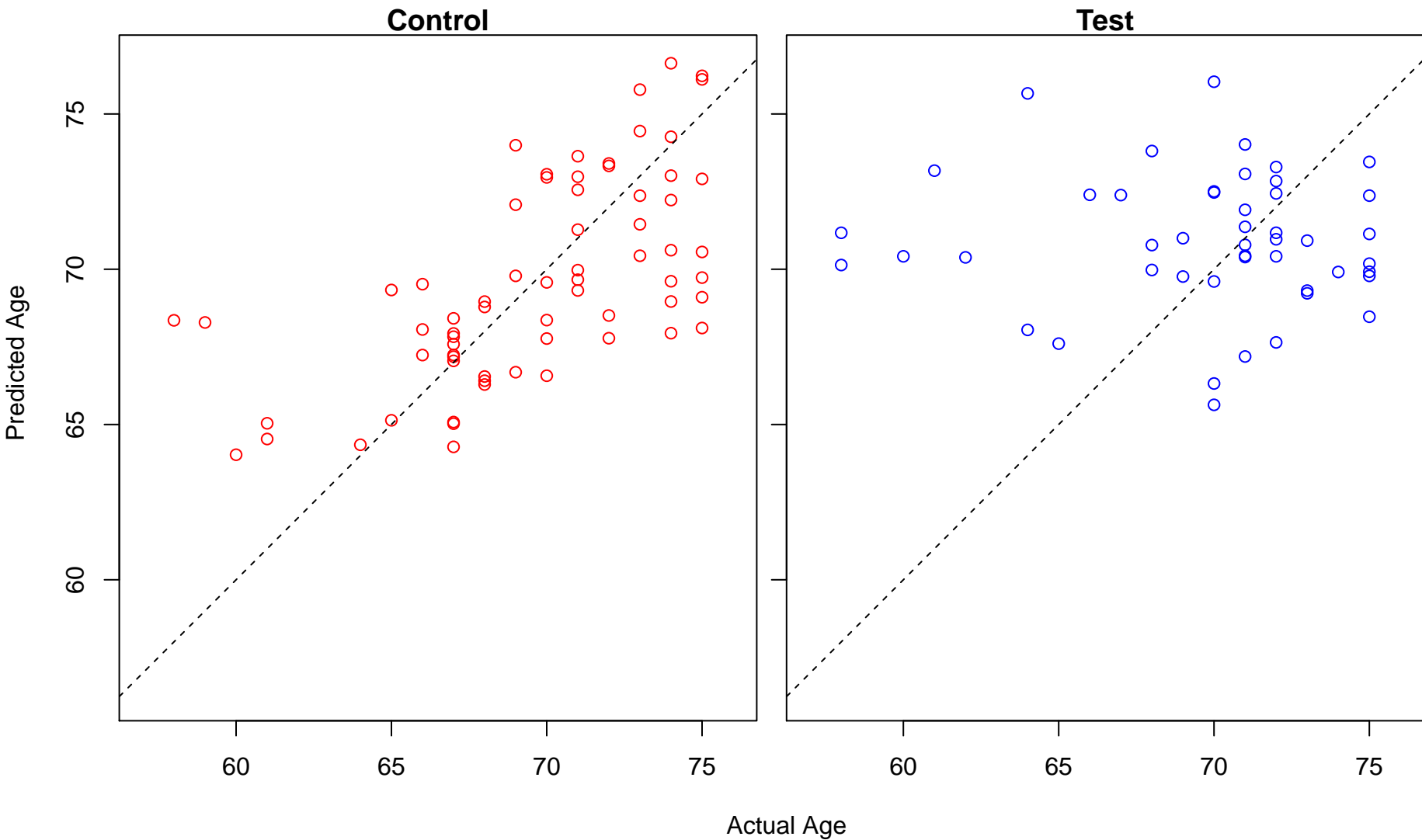
somatic diversification of immunoglobulins (Score: 1.256994)



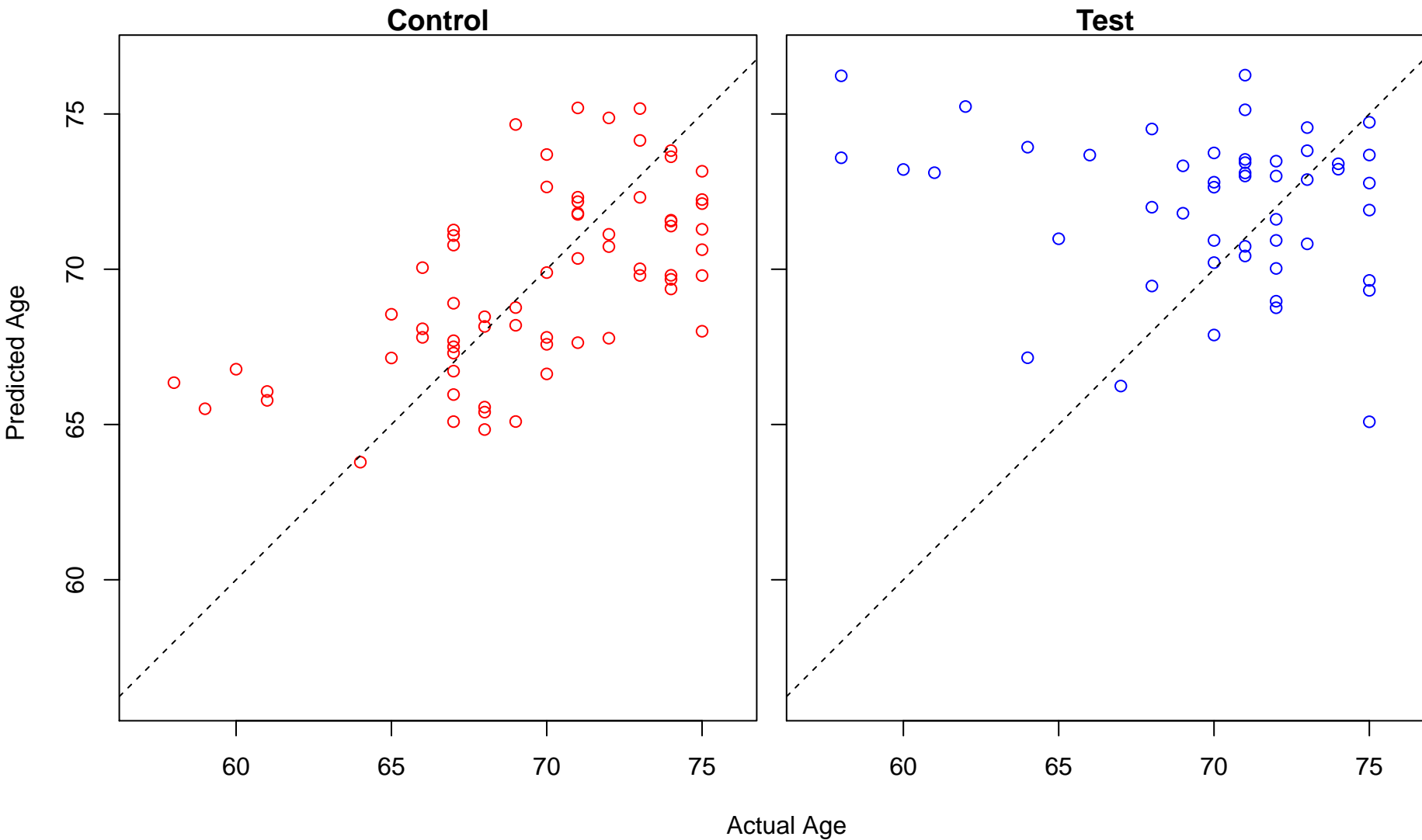
peptide cross-linking (Score: 1.256550)



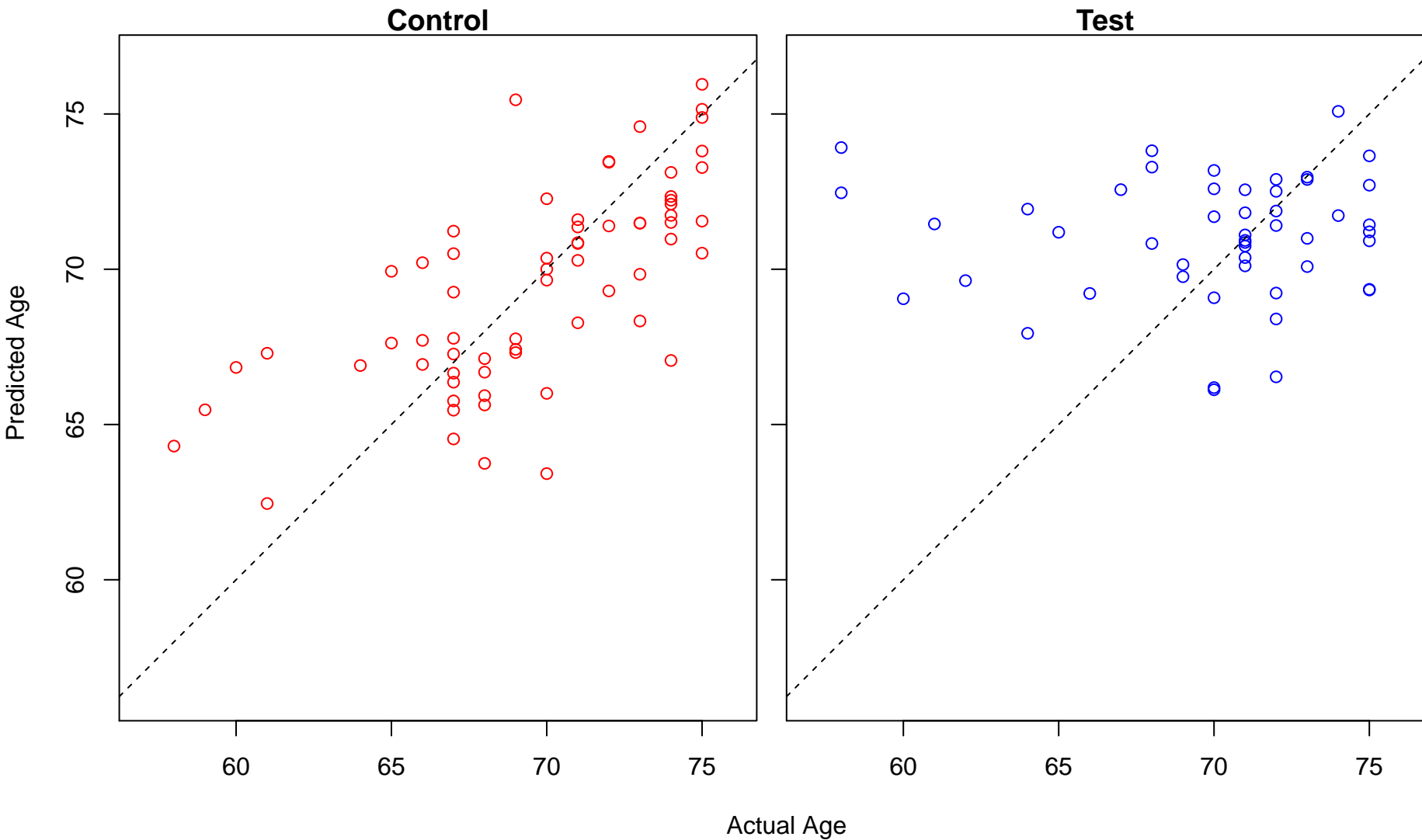
temperature homeostasis (Score: 1.256164)



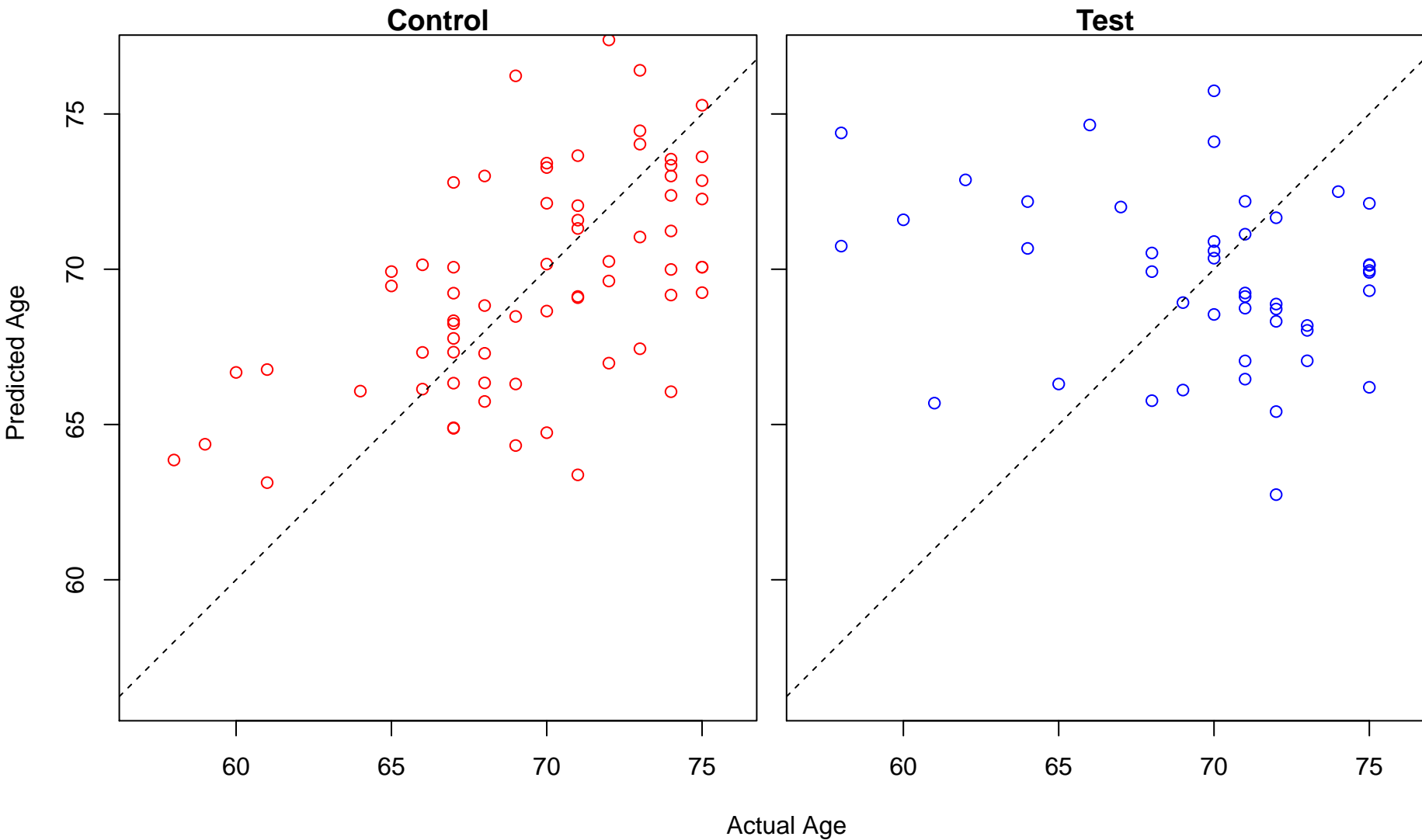
RNA phosphodiester bond hydrolysis, endonucleolytic (Score: 1.256117)



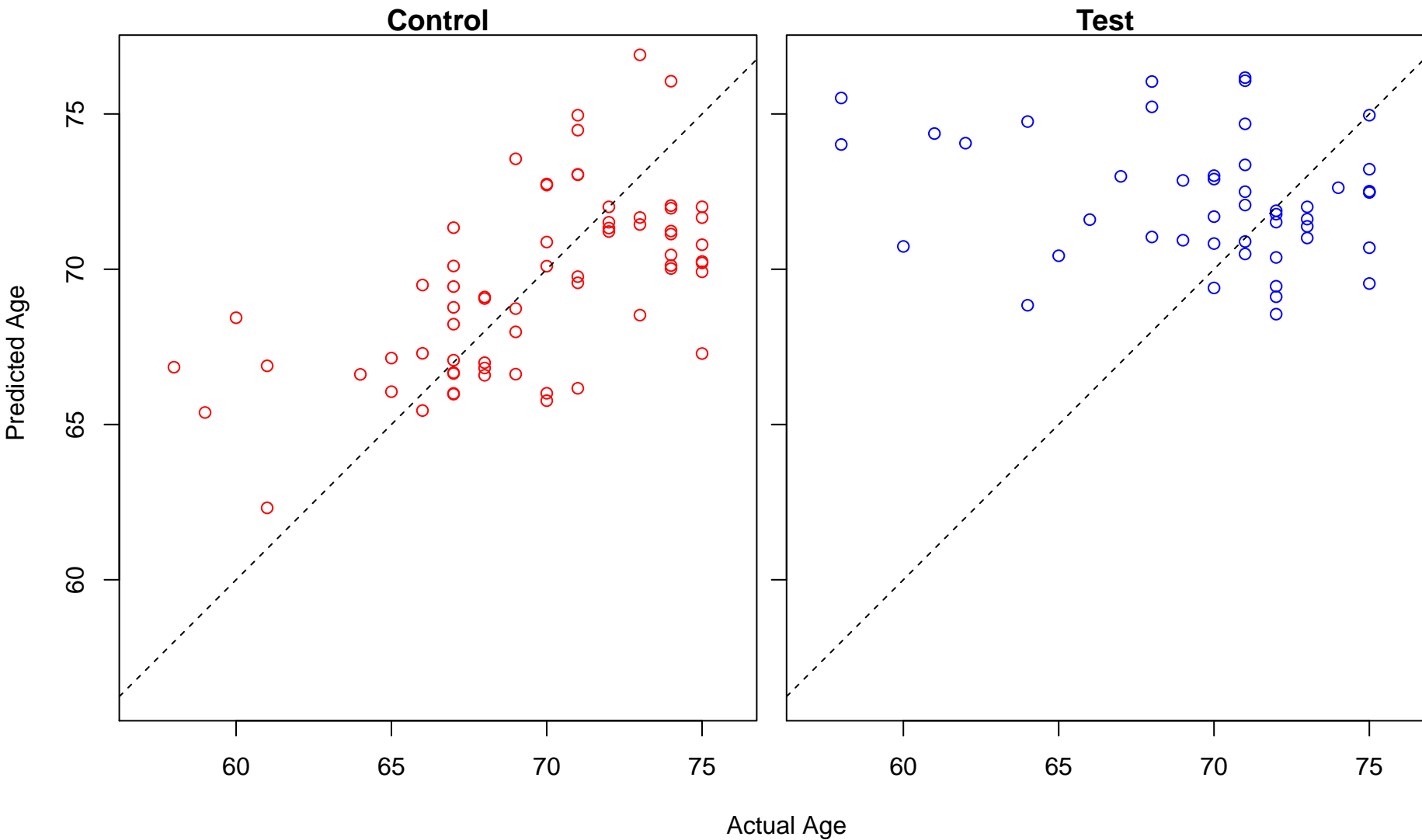
regulation of protein homodimerization activity (Score: 1.256000)



secondary metabolic process (Score: 1.254653)

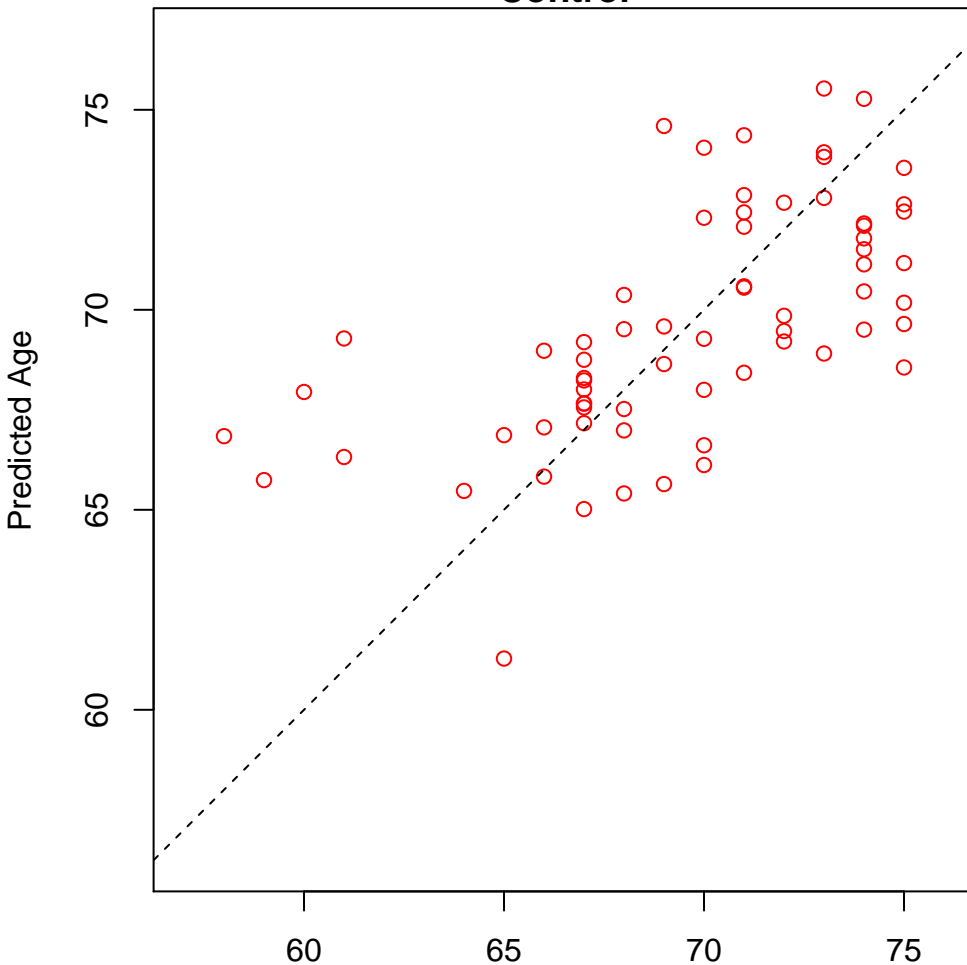


ncRNA transcription (Score: 1.254421)

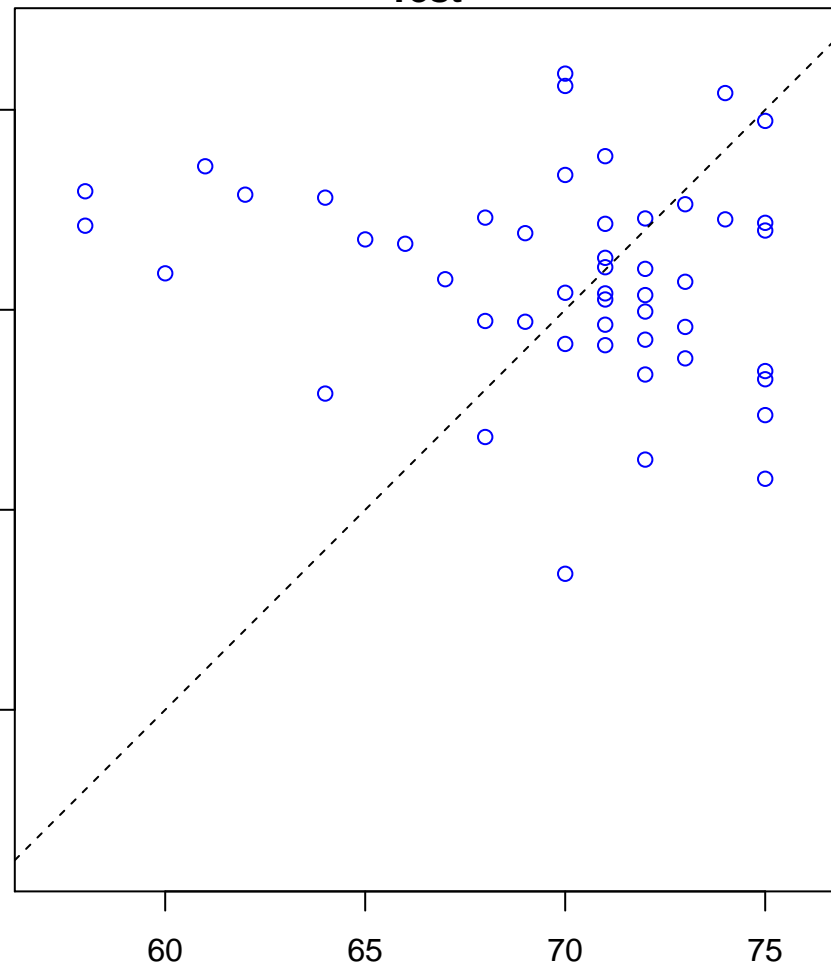


positive regulation of calcium ion import (Score: 1.254349)

Control

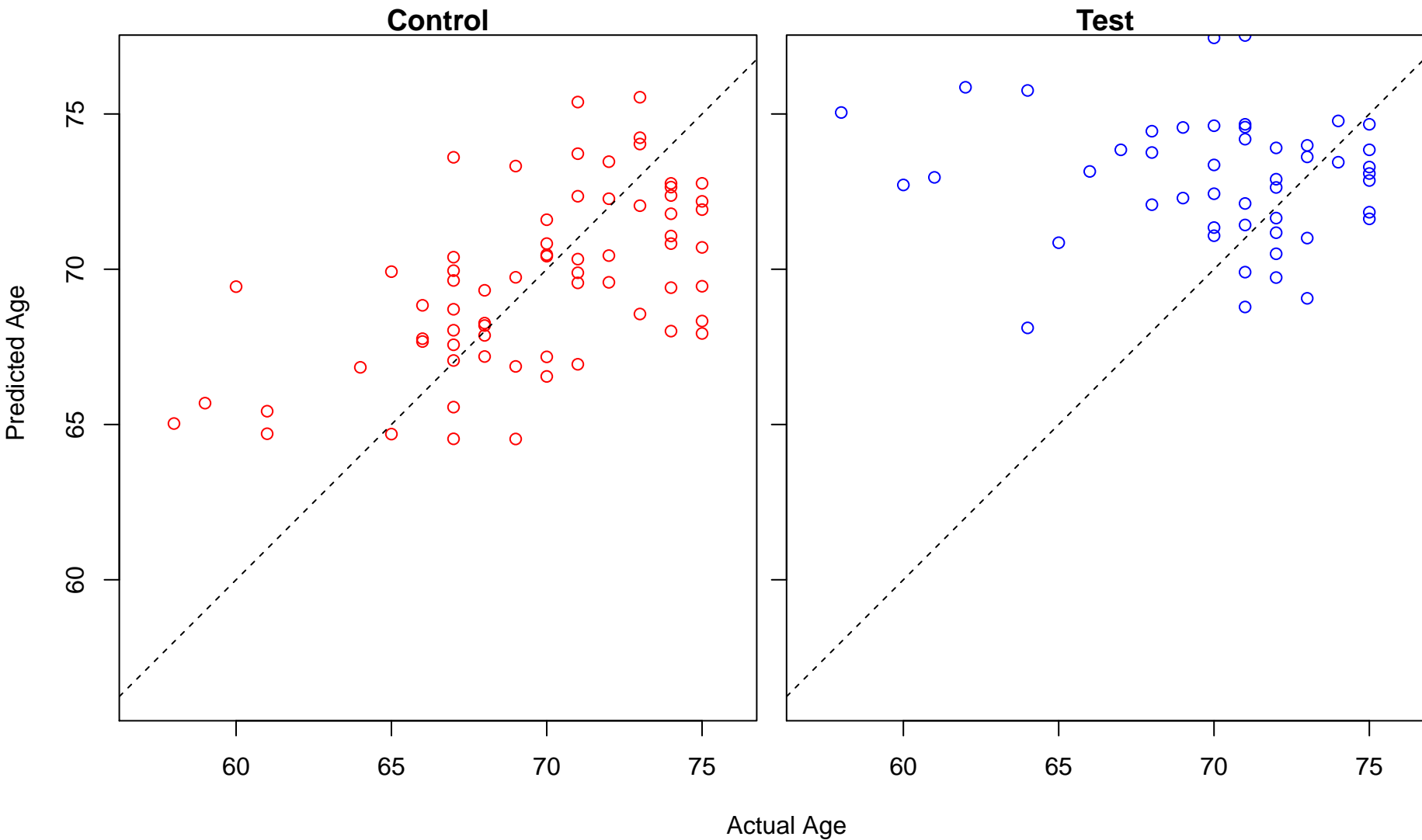


Test



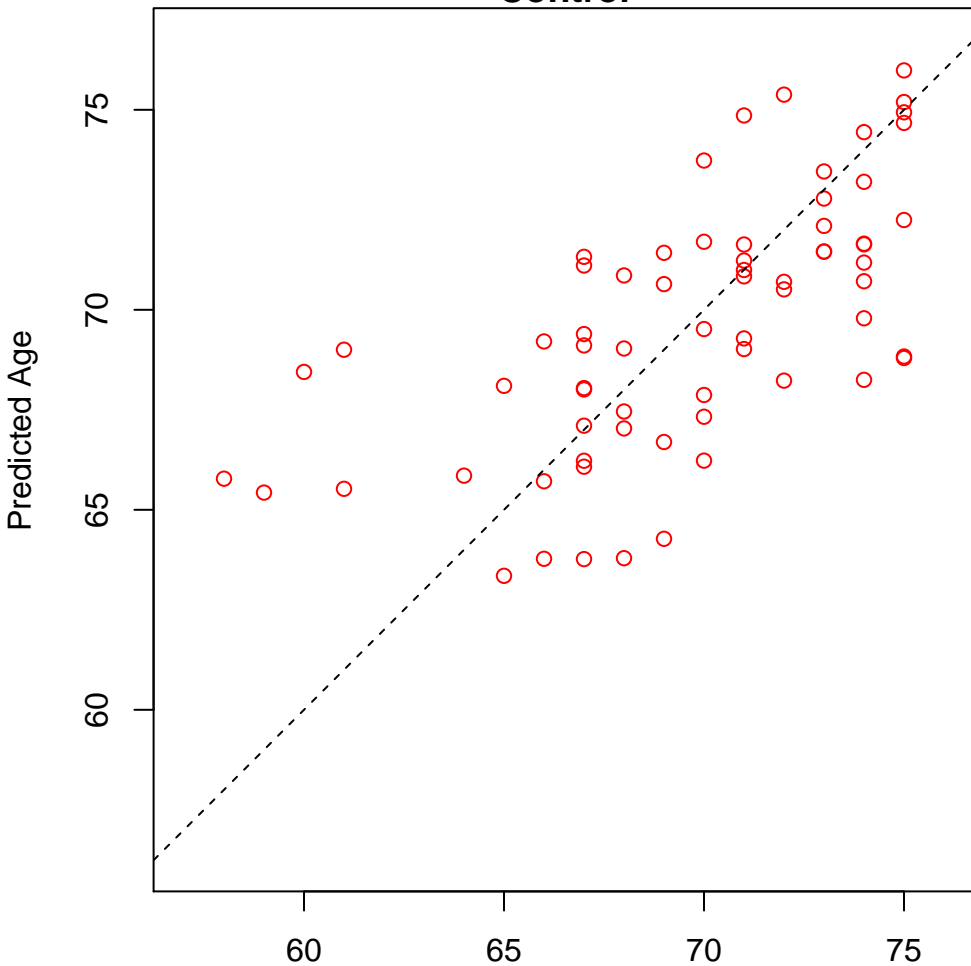
Actual Age

snRNA transcription from RNA polymerase II promoter (Score: 1.253623)

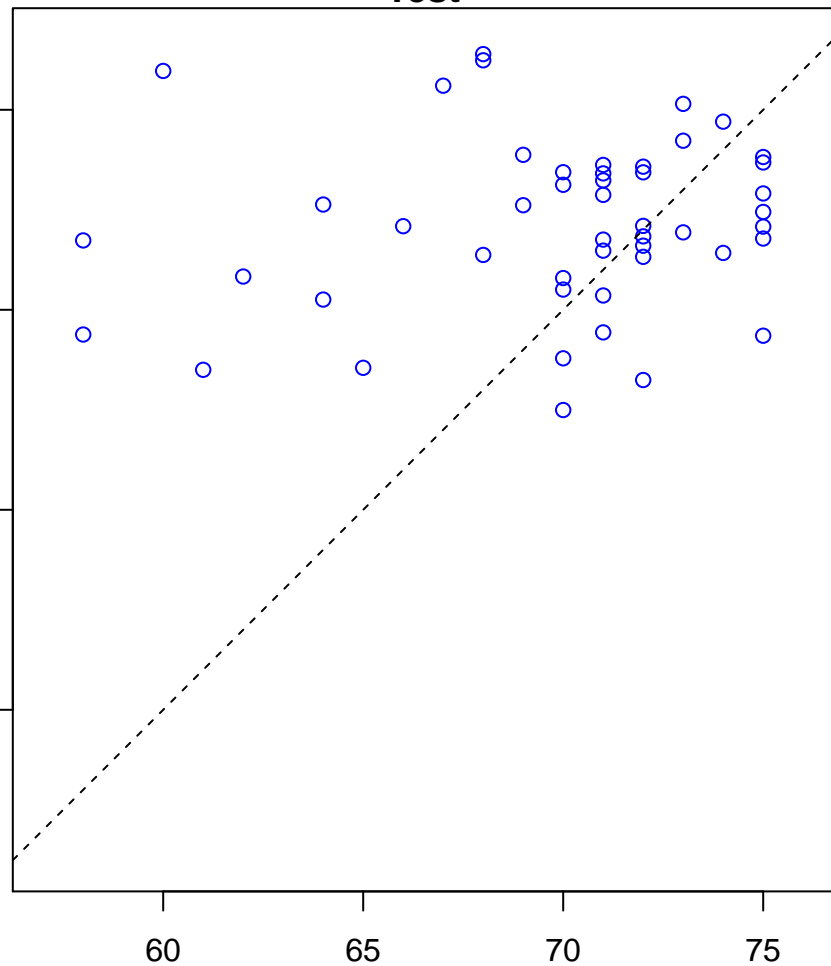


response to laminar fluid shear stress (Score: 1.253616)

Control

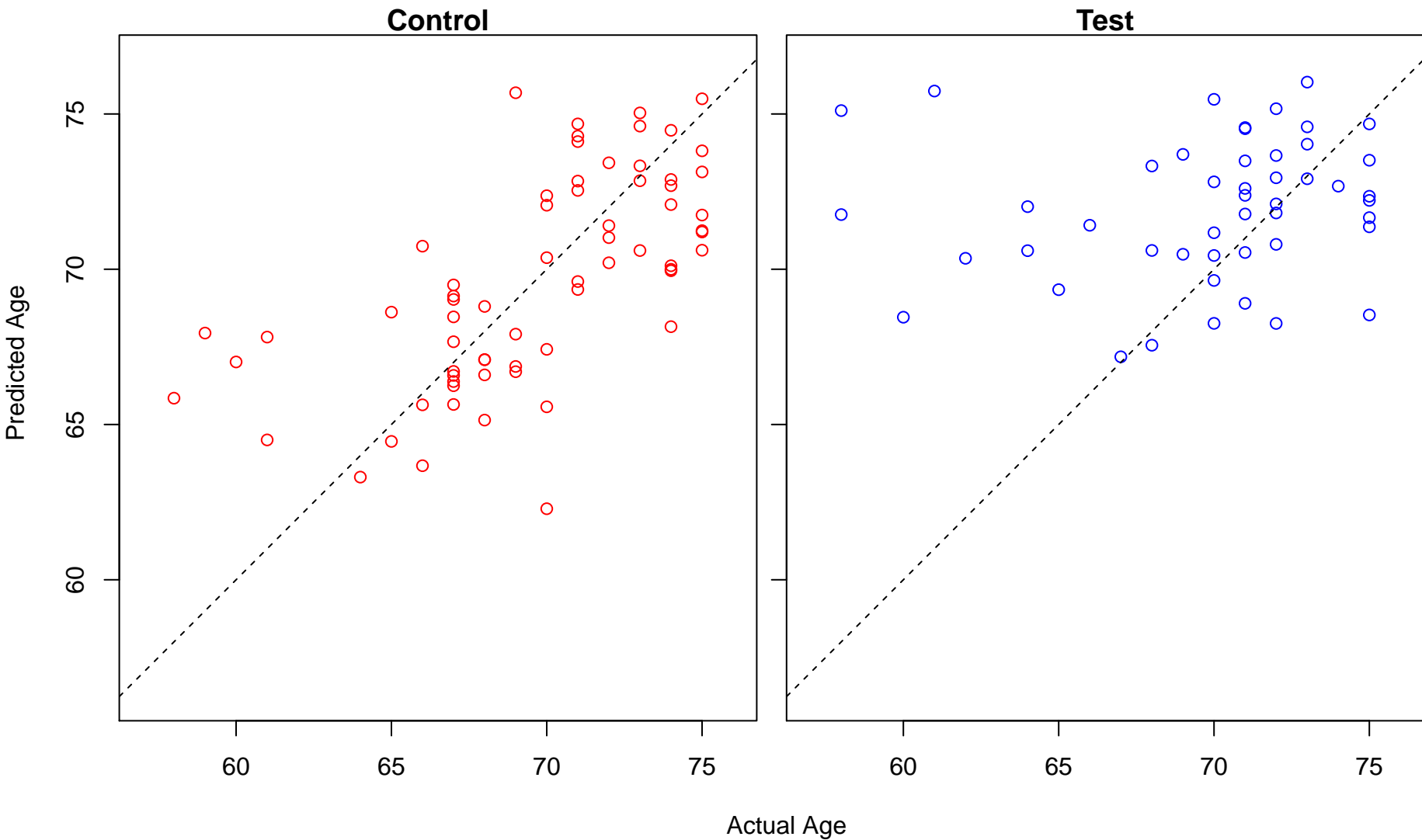


Test



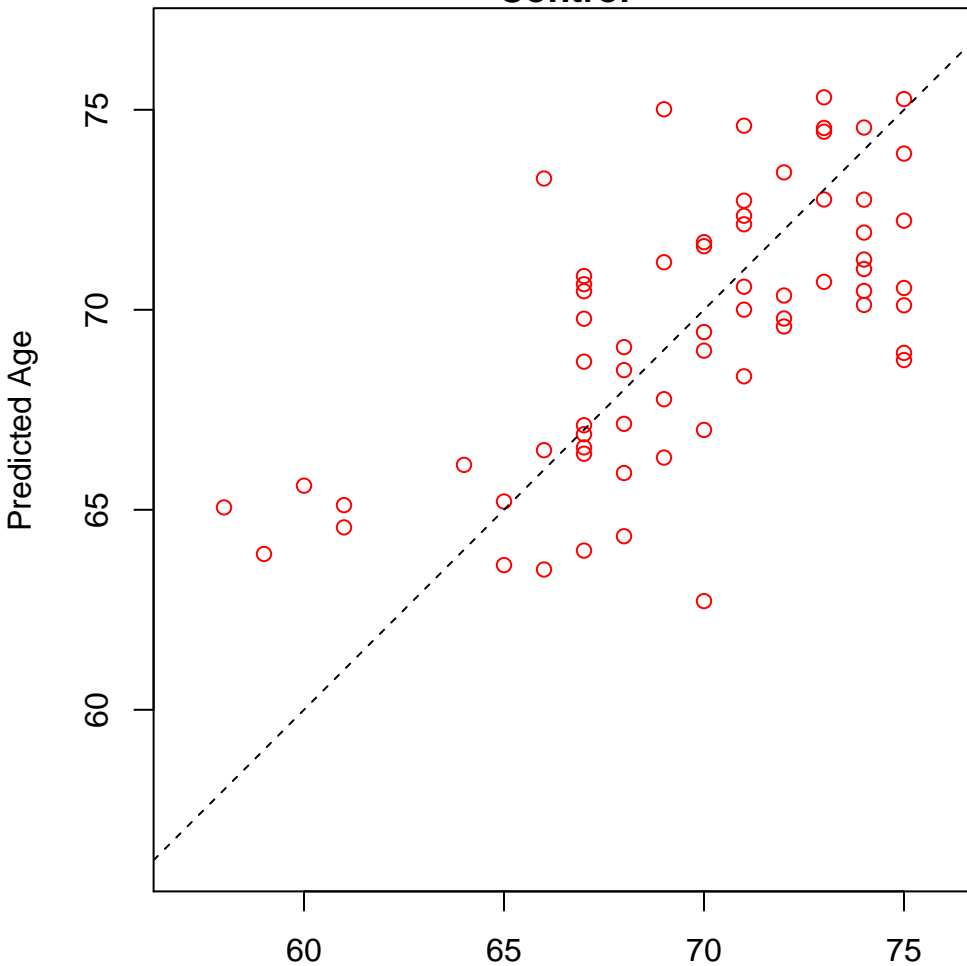
Actual Age

heart morphogenesis (Score: 1.253320)

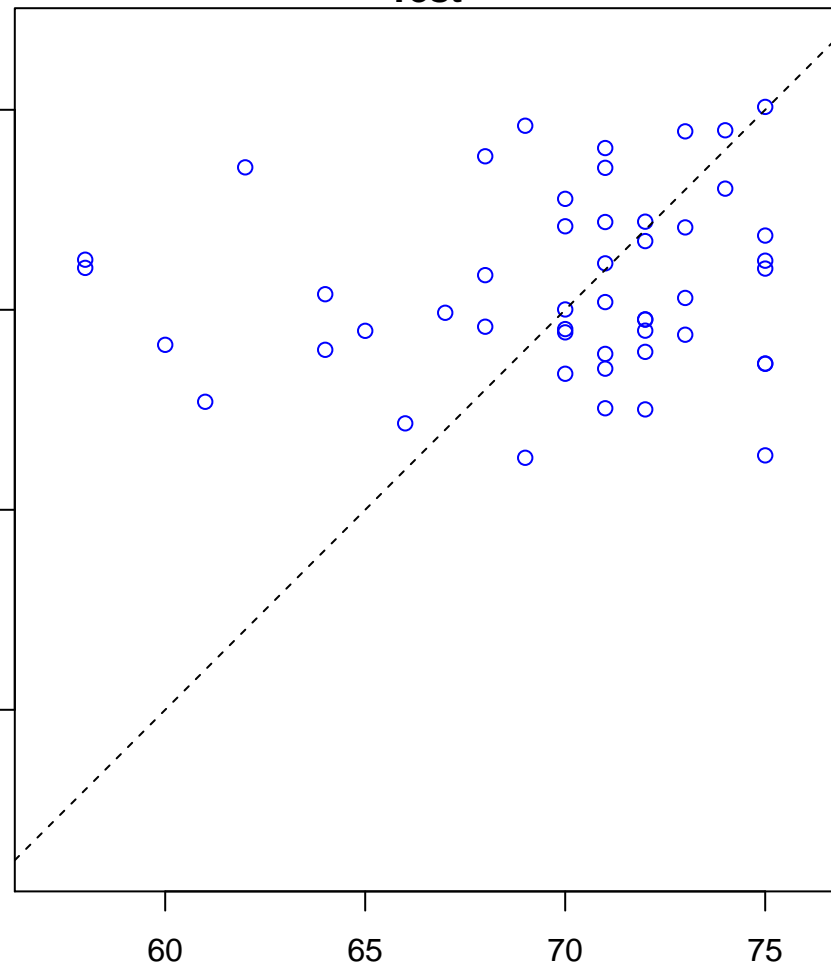


viral budding via host ESCRT complex (Score: 1.253217)

Control



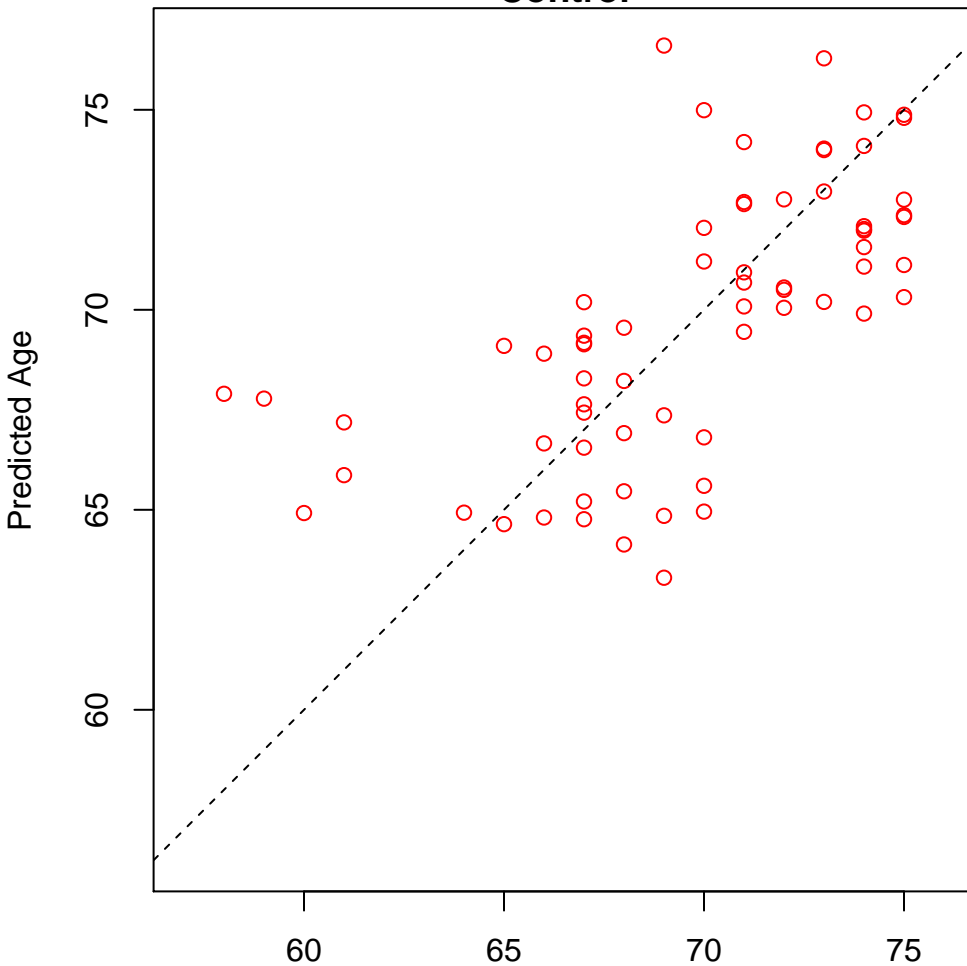
Test



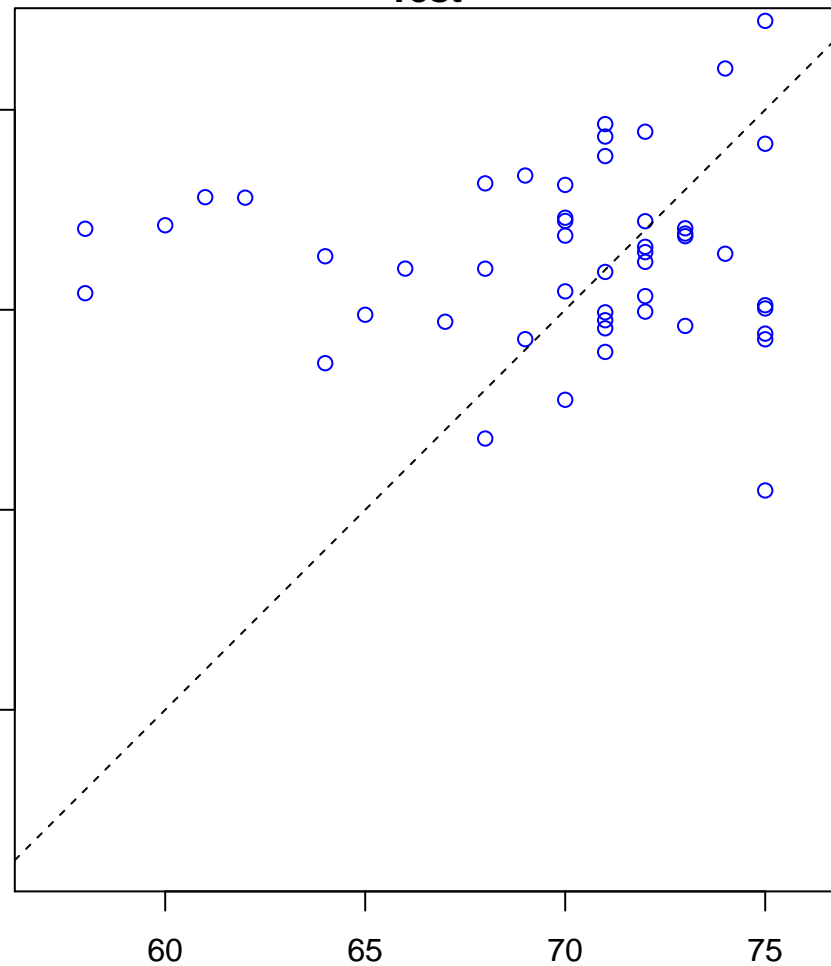
Actual Age

negative regulation of cell development (Score: 1.252793)

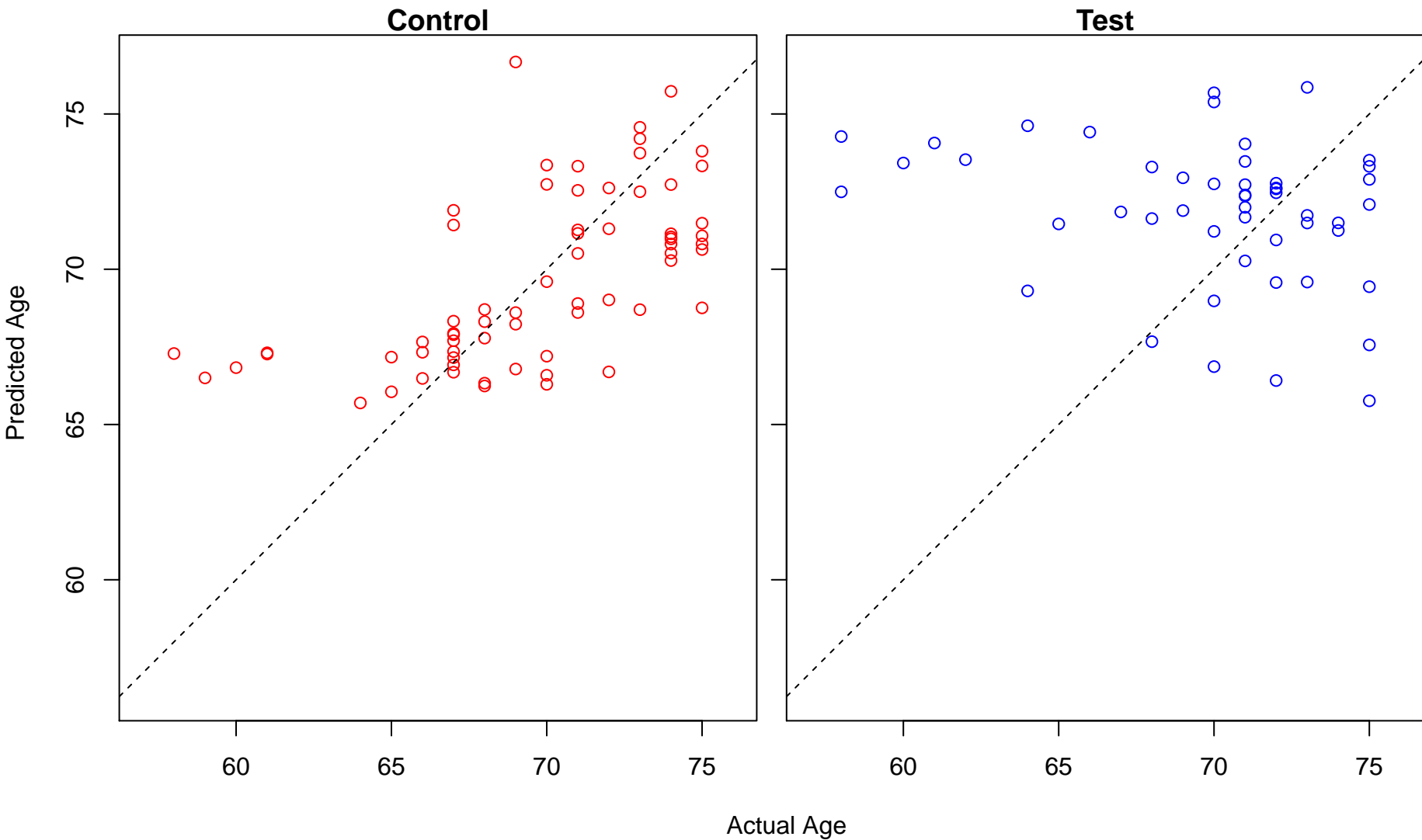
Control



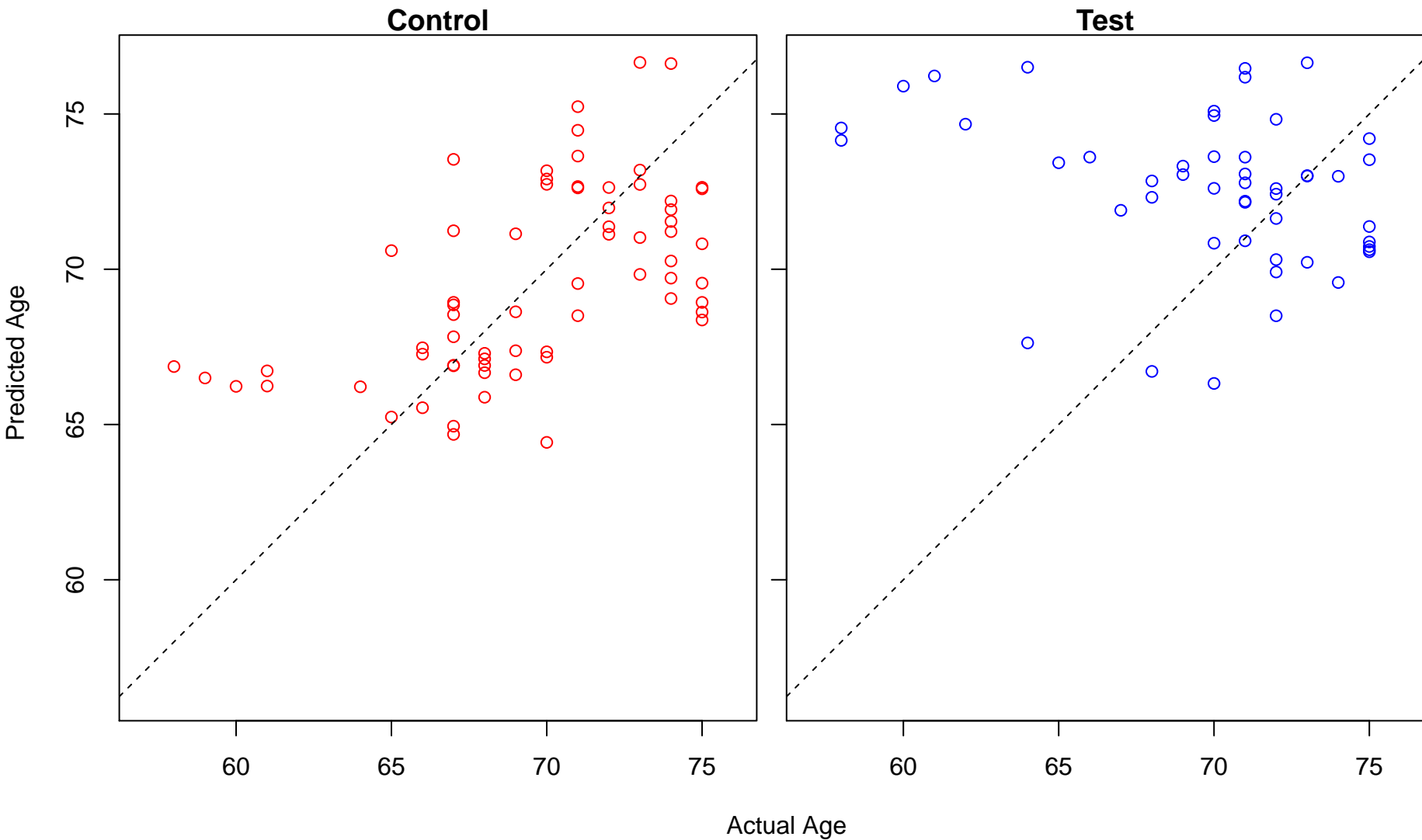
Test



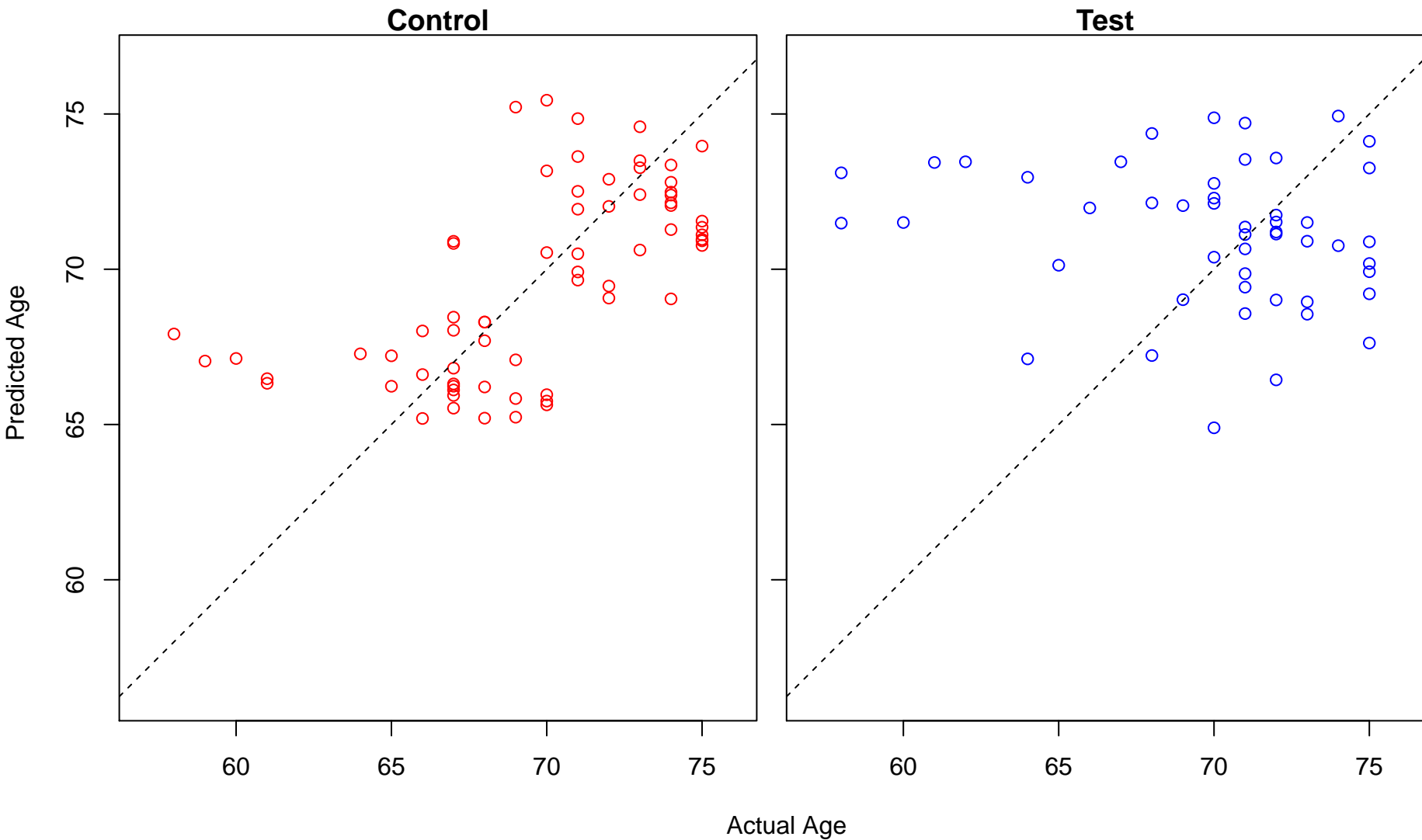
negative regulation of MAPK cascade (Score: 1.252538)



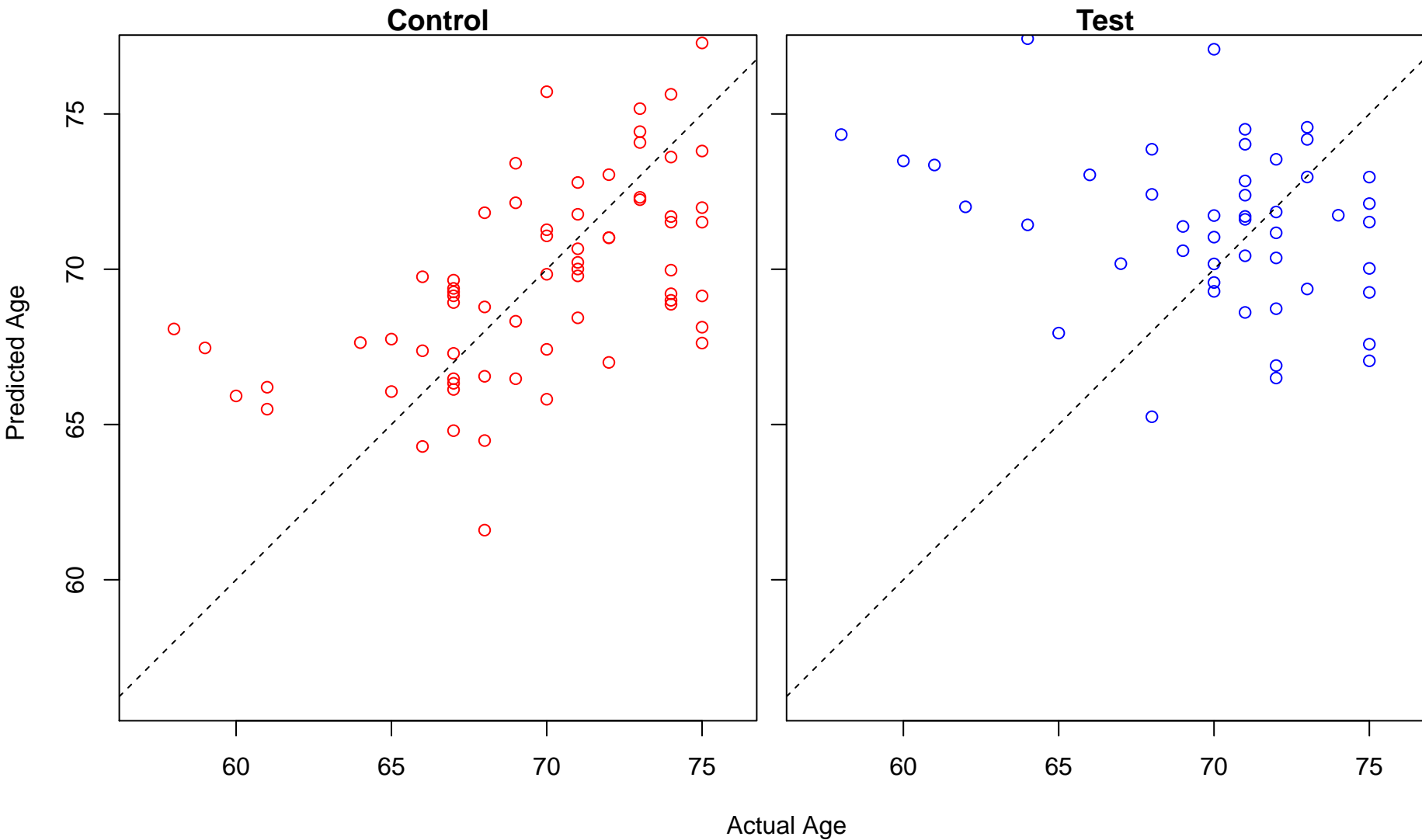
cAMP metabolic process (Score: 1.252258)



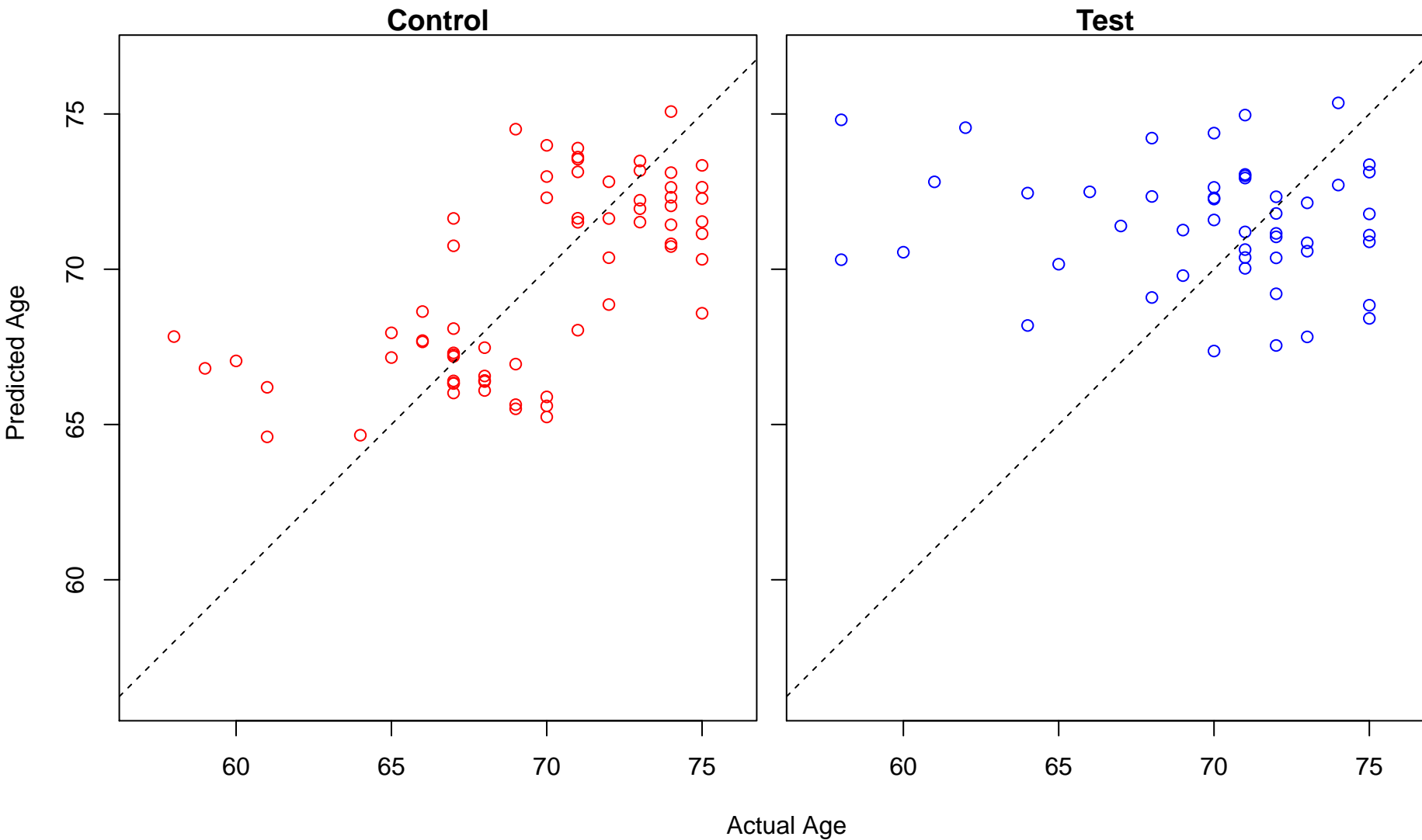
cellular response to lipid (Score: 1.252139)



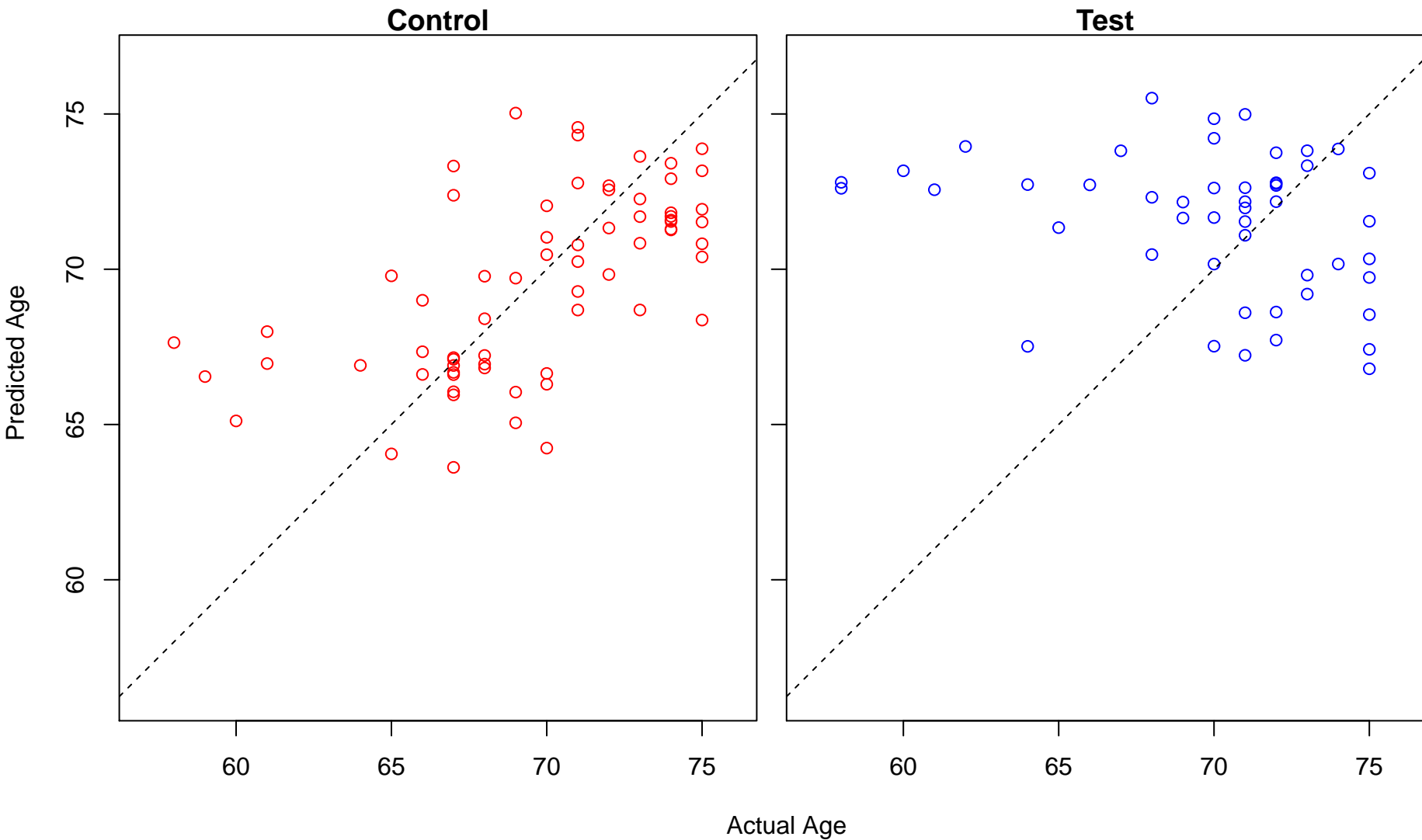
negative regulation of autophagosome assembly (Score: 1.251499)



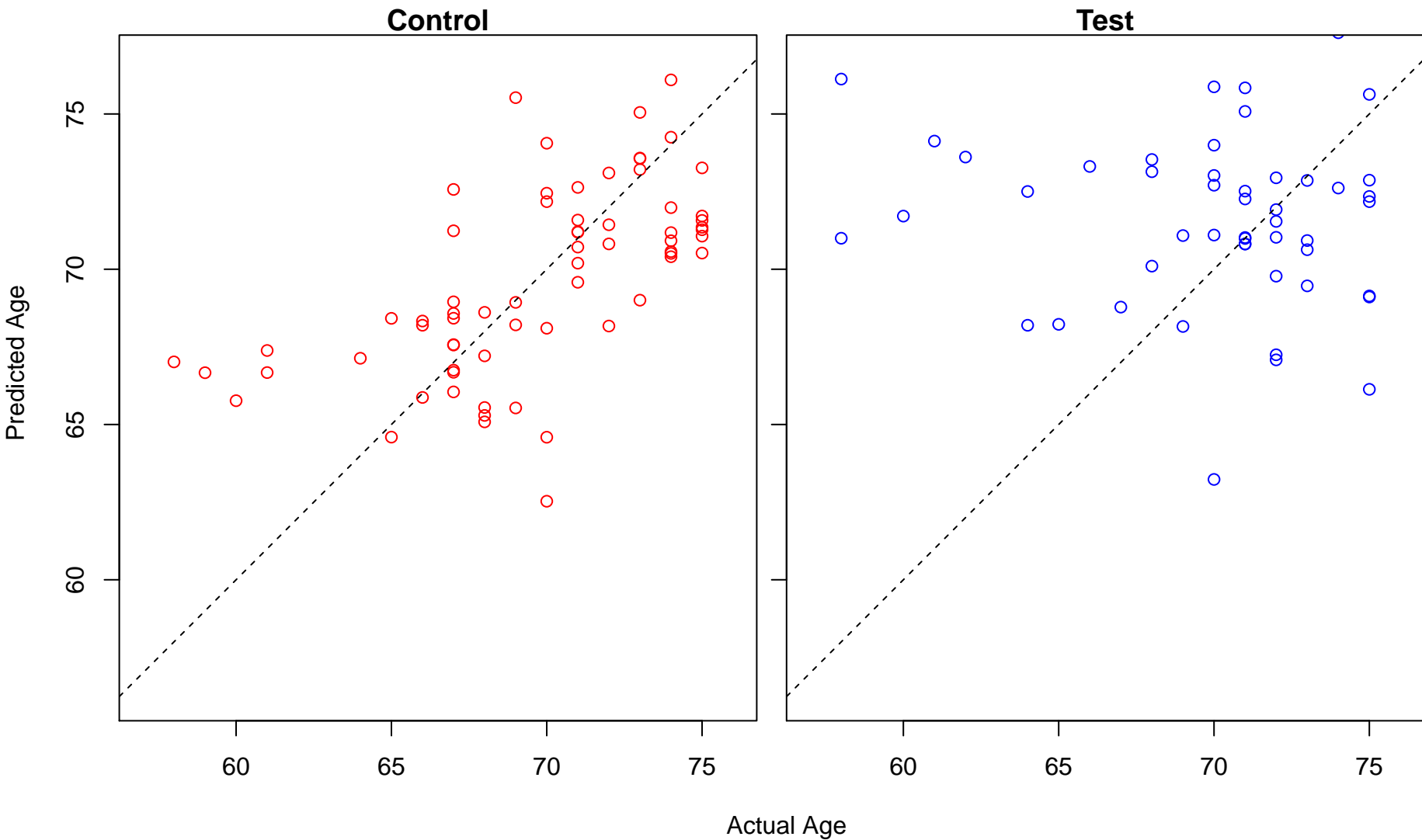
Golgi organization (Score: 1.250764)



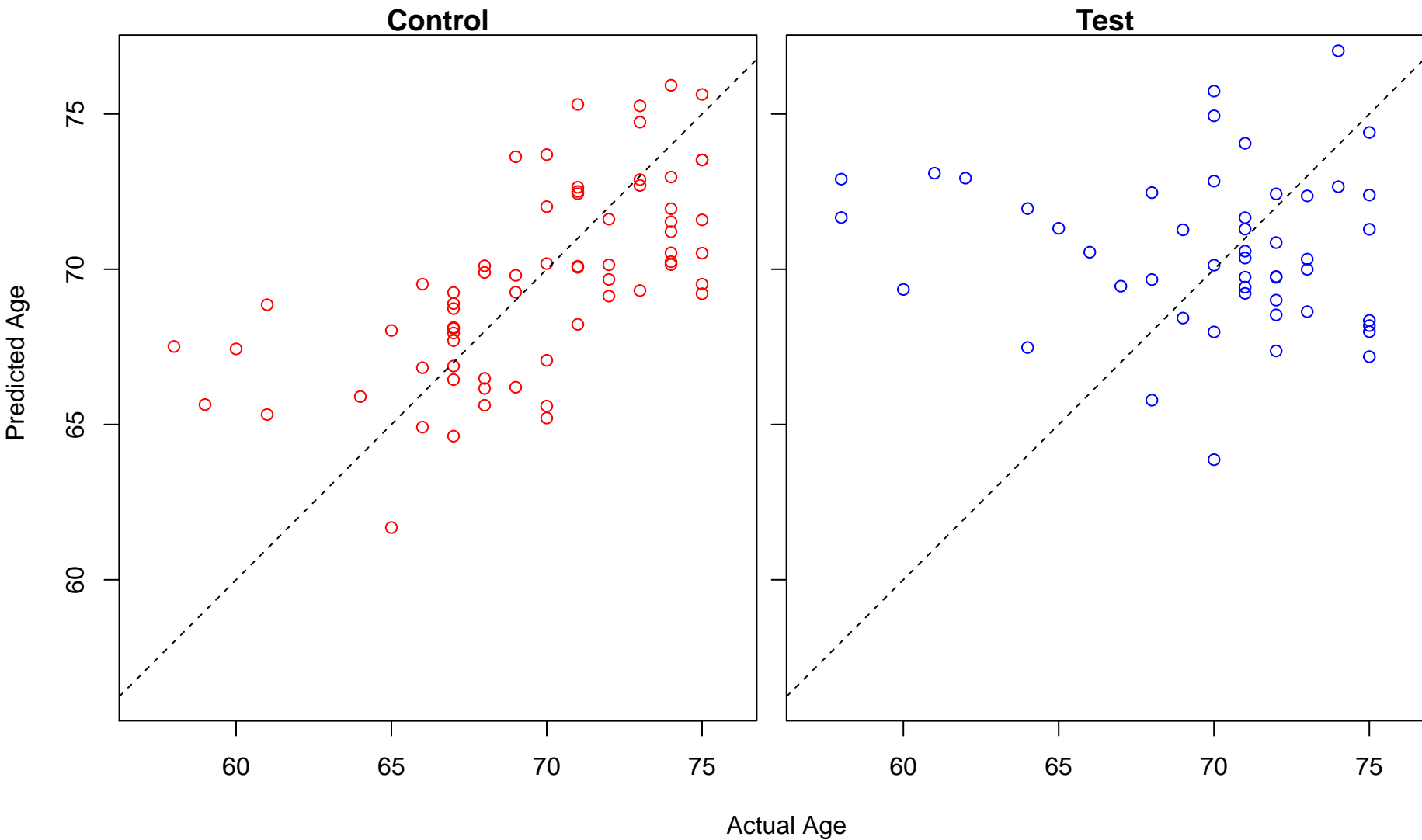
positive regulation of interferon- α production (Score: 1.249985)



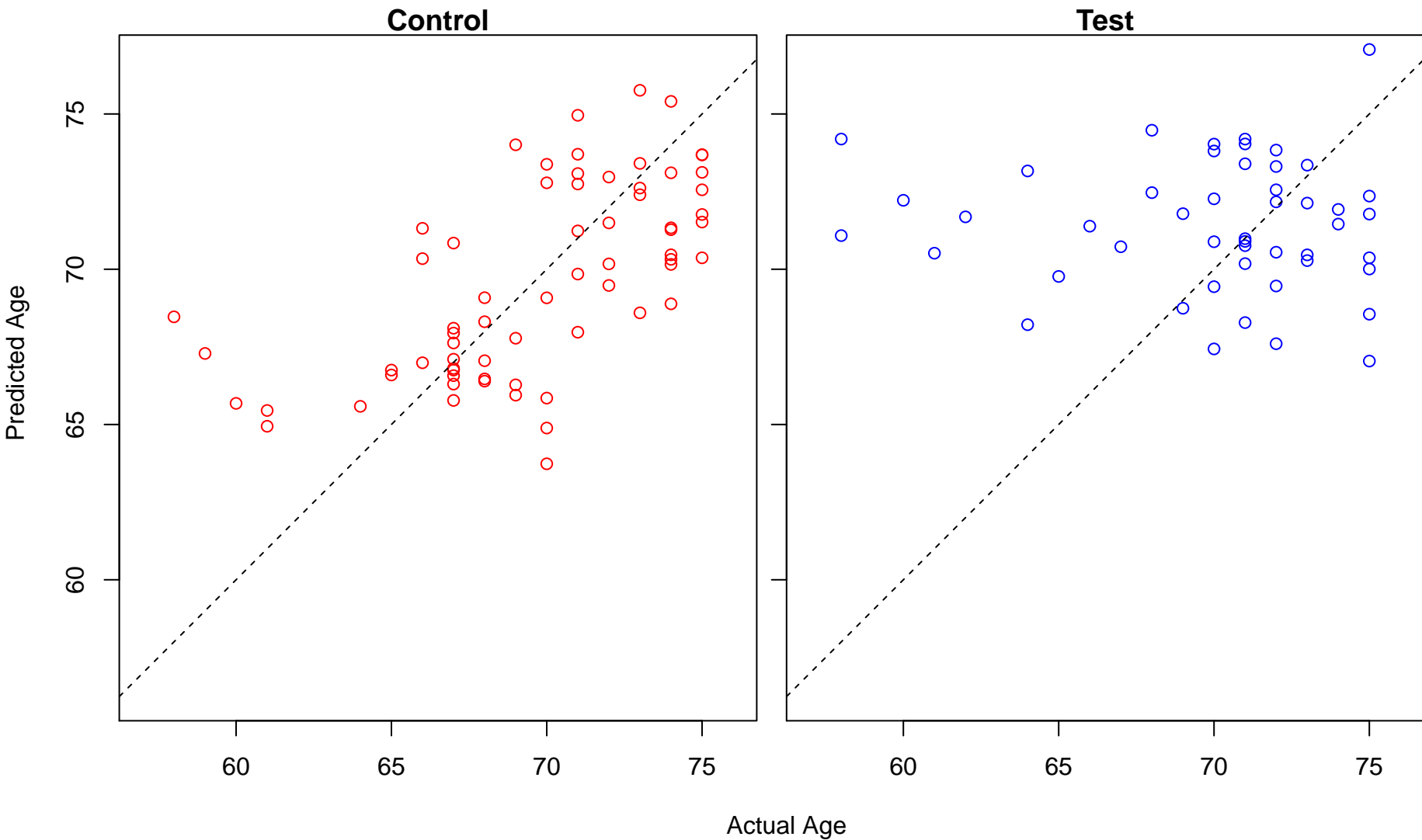
regulation of pH (Score: 1.249349)



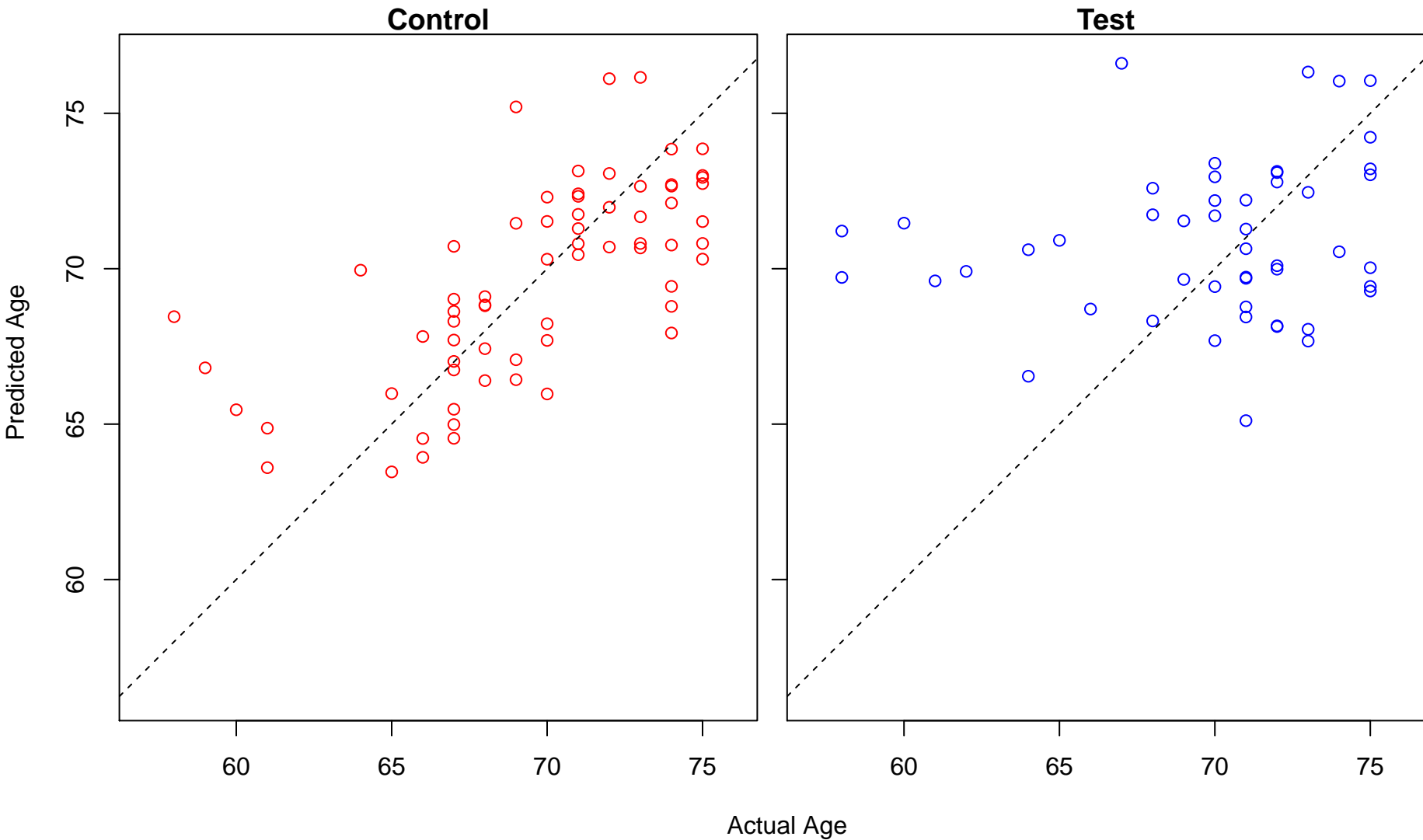
regulation of calcium ion import (Score: 1.248988)



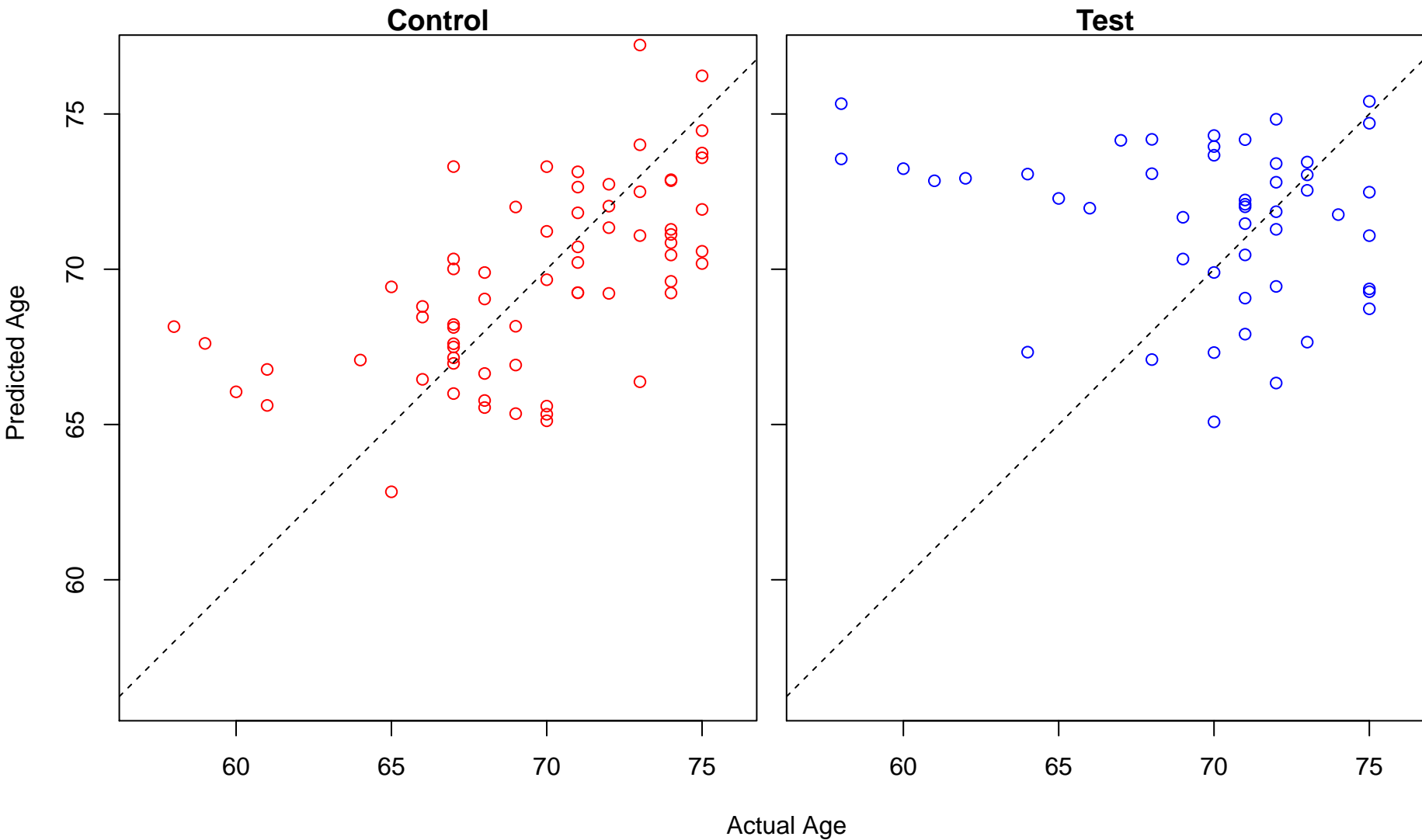
regulation of intracellular steroid hormone receptor signaling pathway (Score: 1.248652)



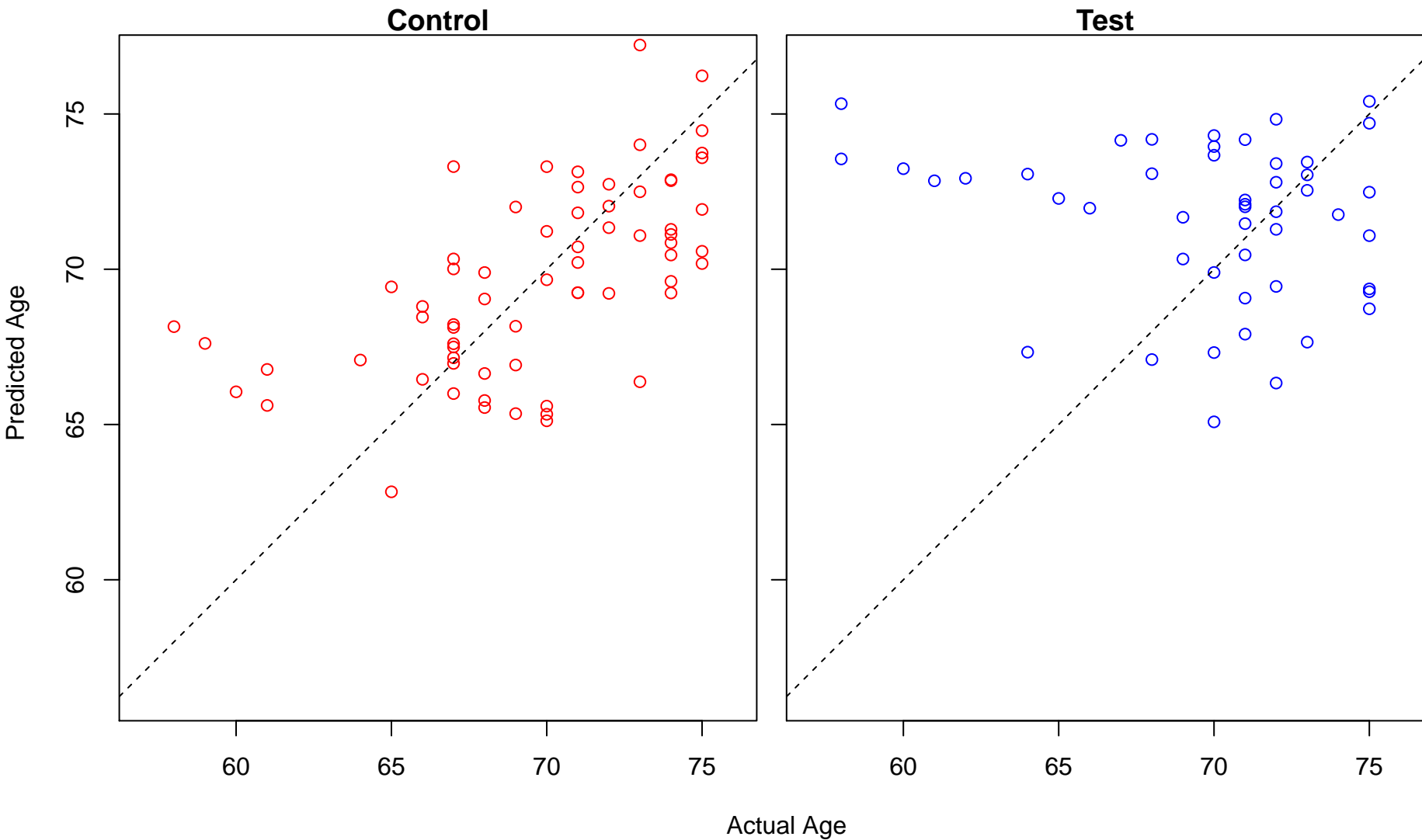
oligosaccharide metabolic process (Score: 1.248580)



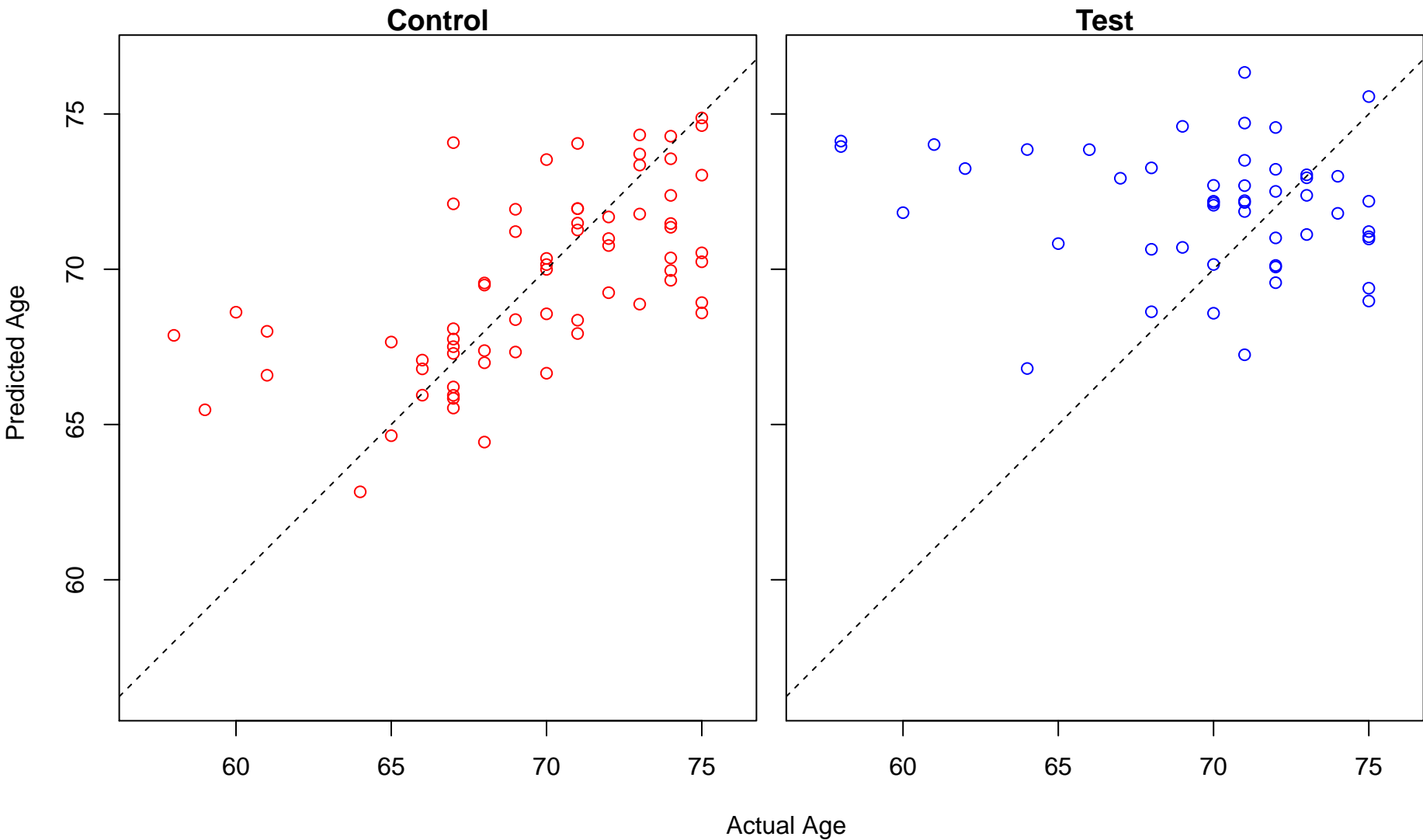
thioester biosynthetic process (Score: 1.248563)



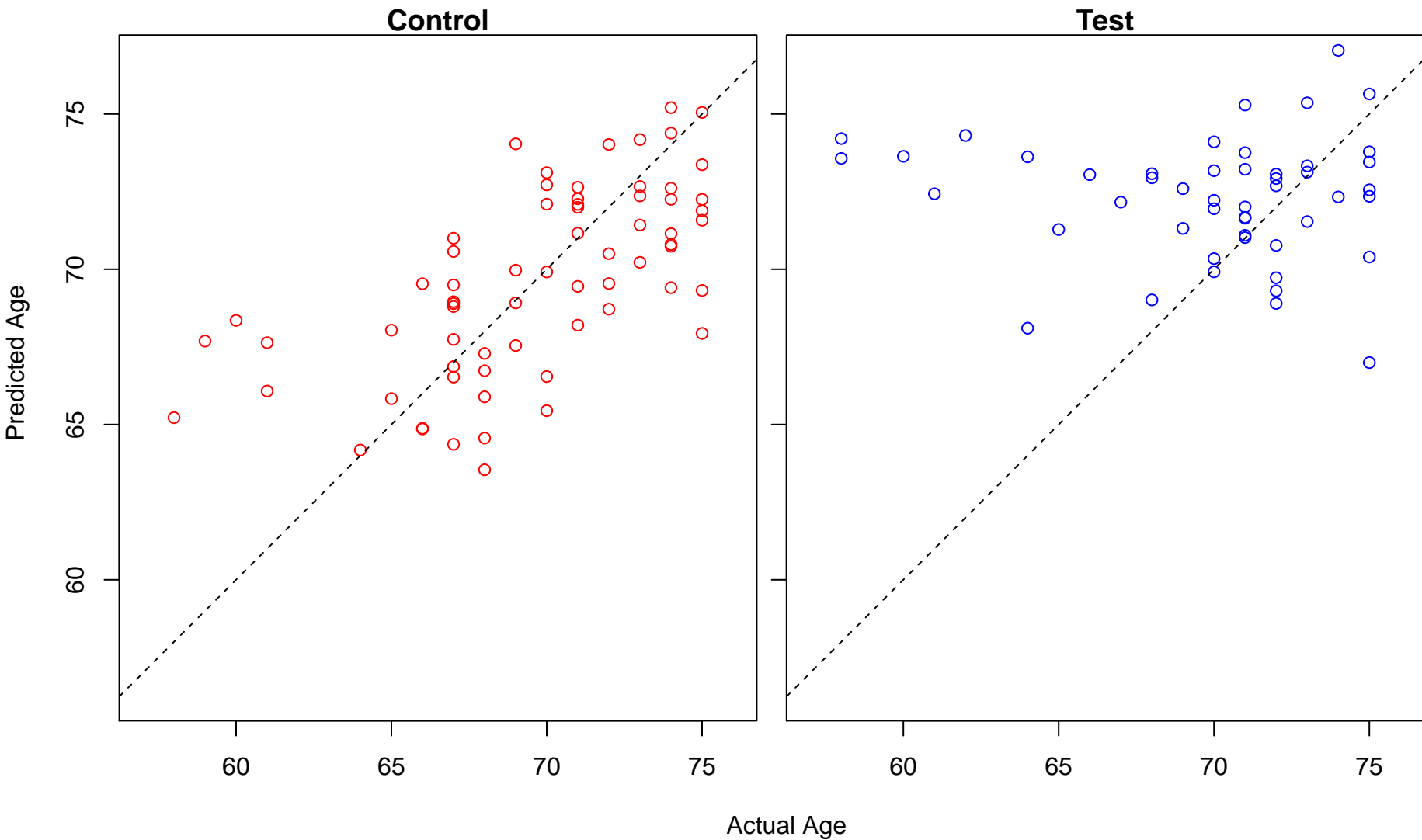
acyl-CoA biosynthetic process (Score: 1.248563)



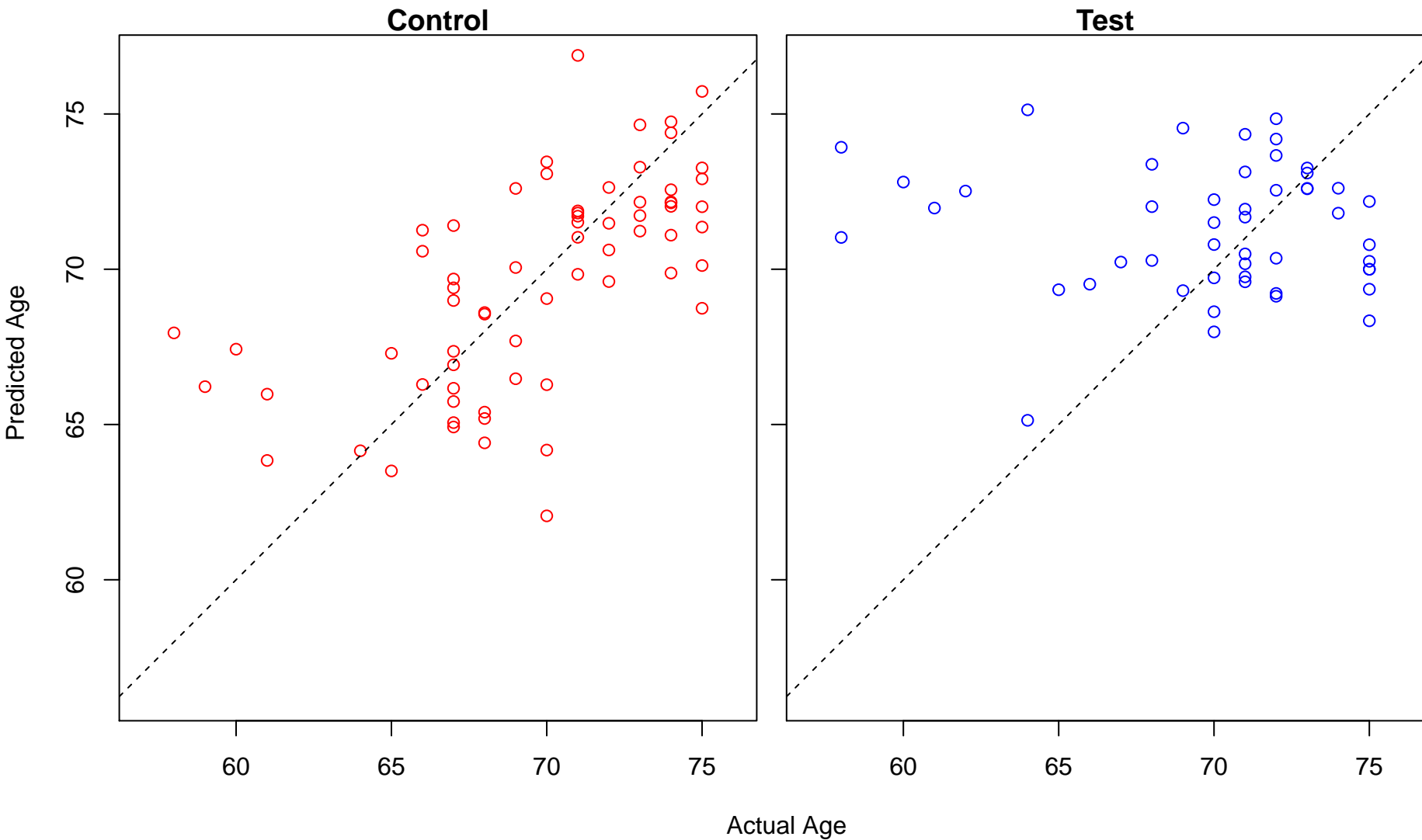
axoneme assembly (Score: 1.247893)



regulation of striated muscle cell differentiation (Score: 1.247607)

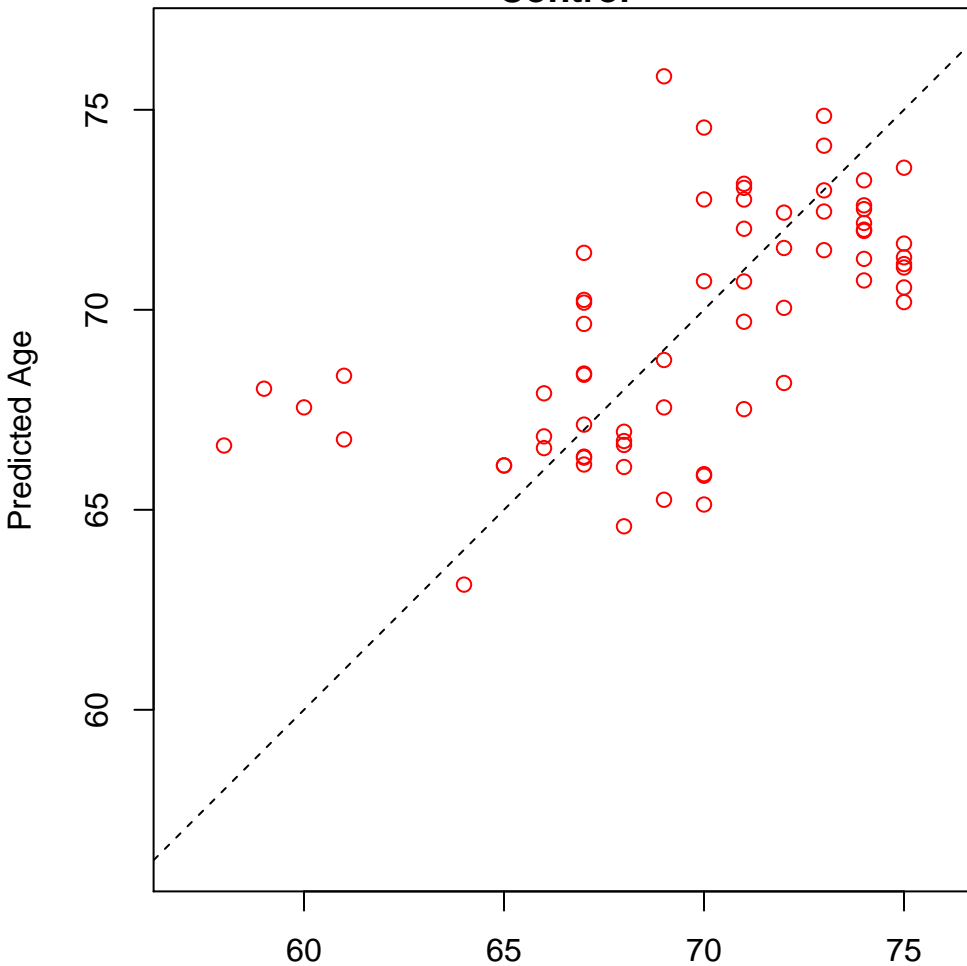


development of primary sexual characteristics (Score: 1.247602)

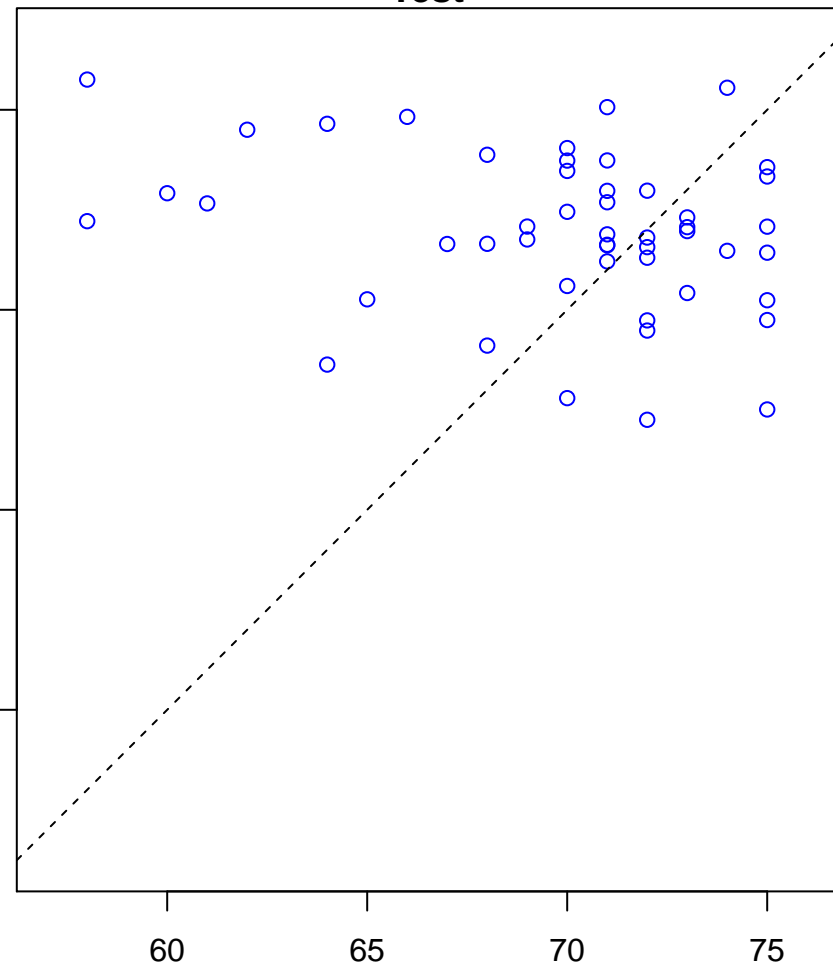


cellular response to xenobiotic stimulus (Score: 1.247523)

Control

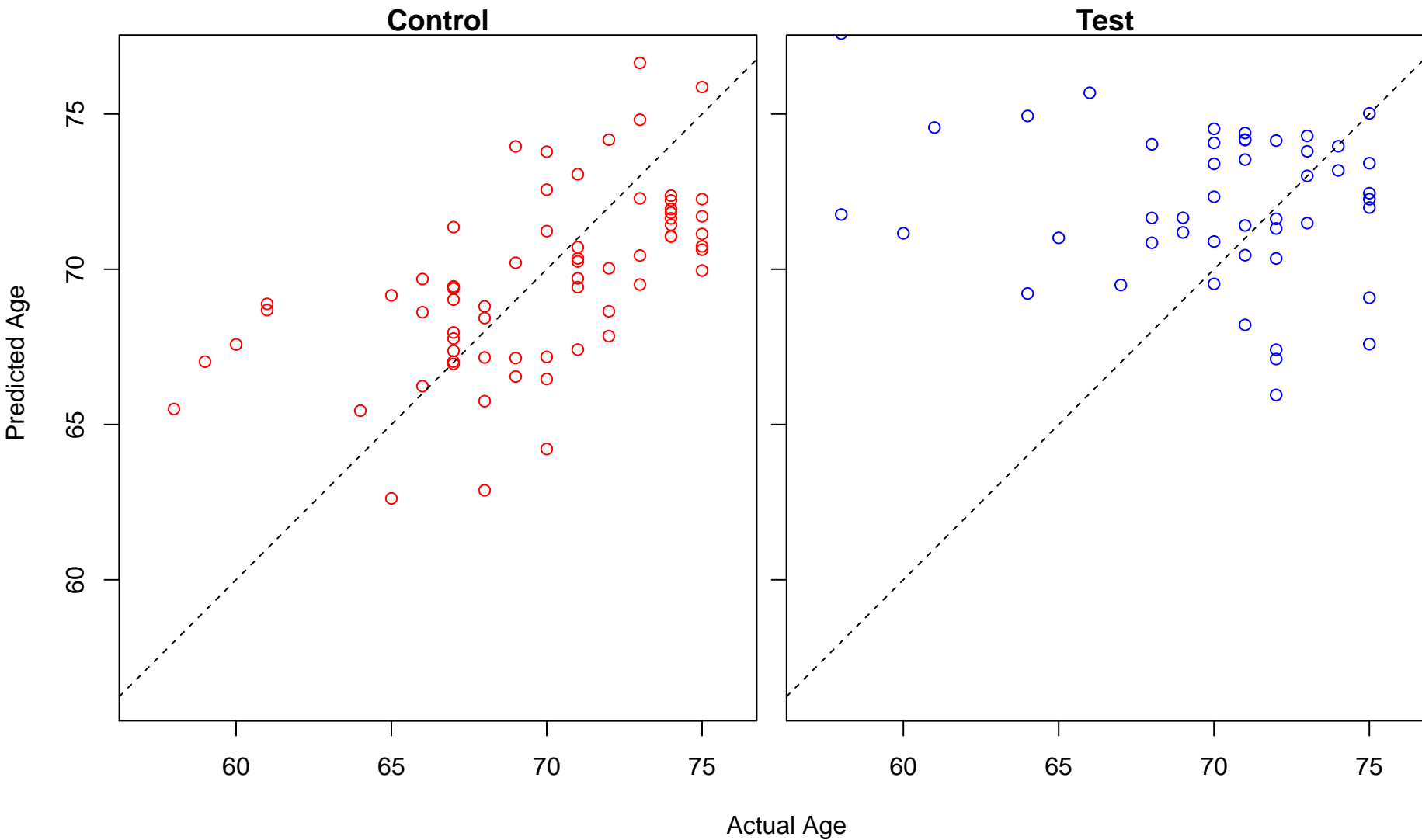


Test



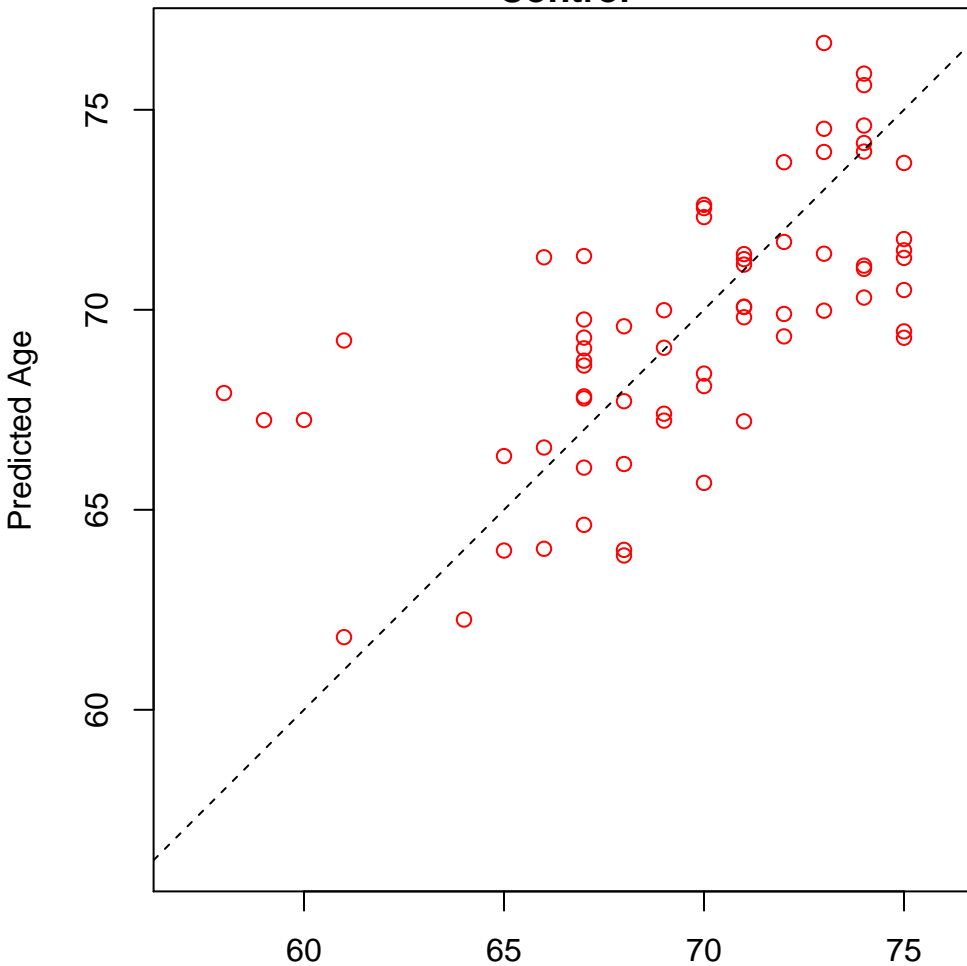
Actual Age

cellular response to arsenic-containing substance (Score: 1.246859)

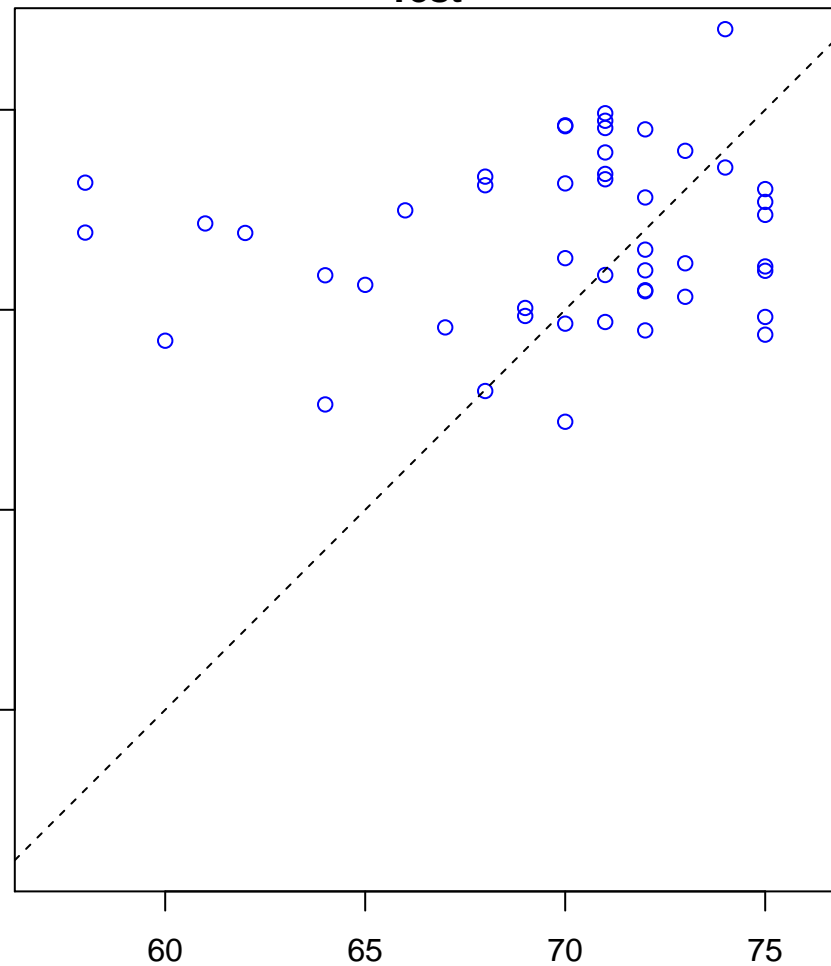


actomyosin structure organization (Score: 1.245828)

Control

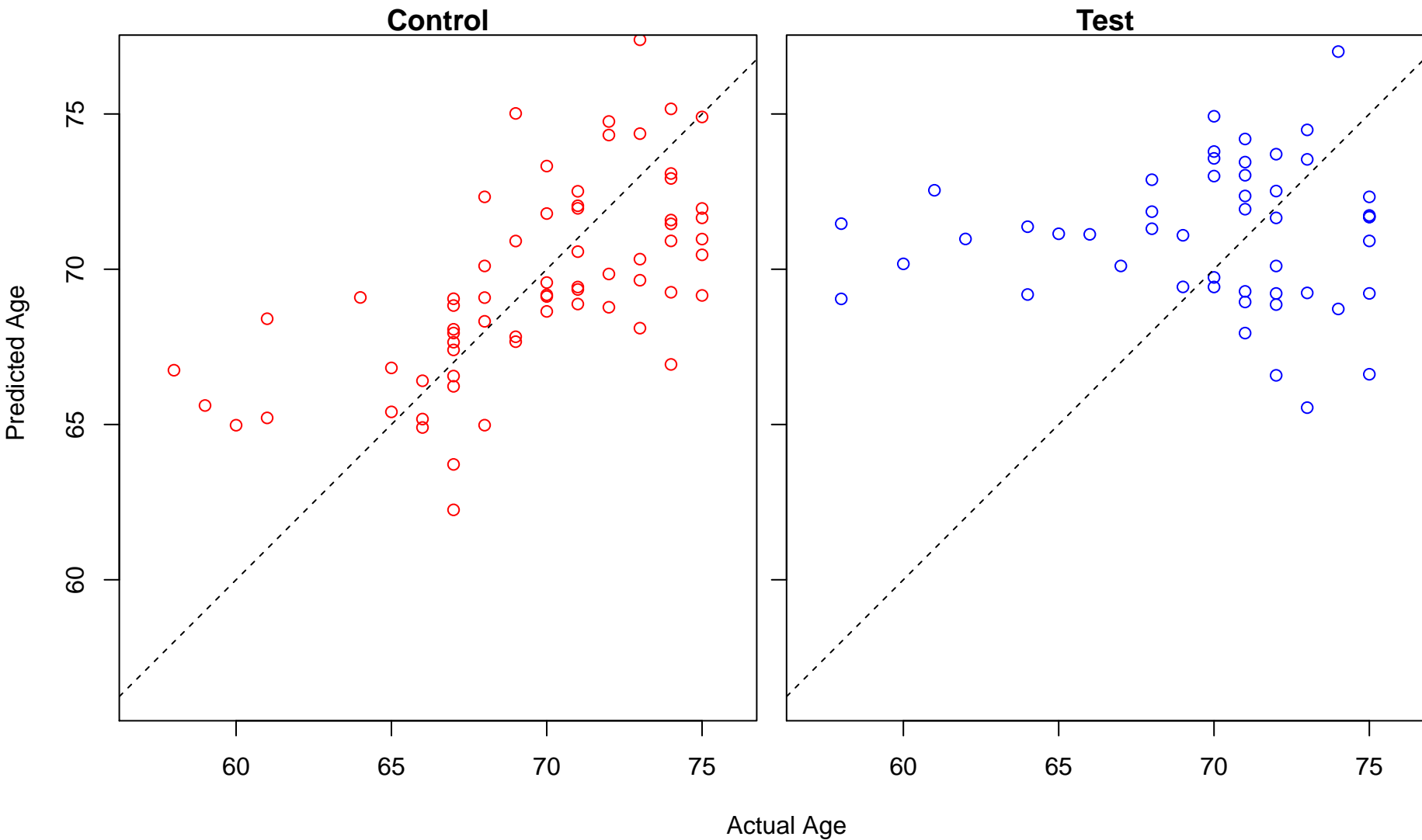


Test

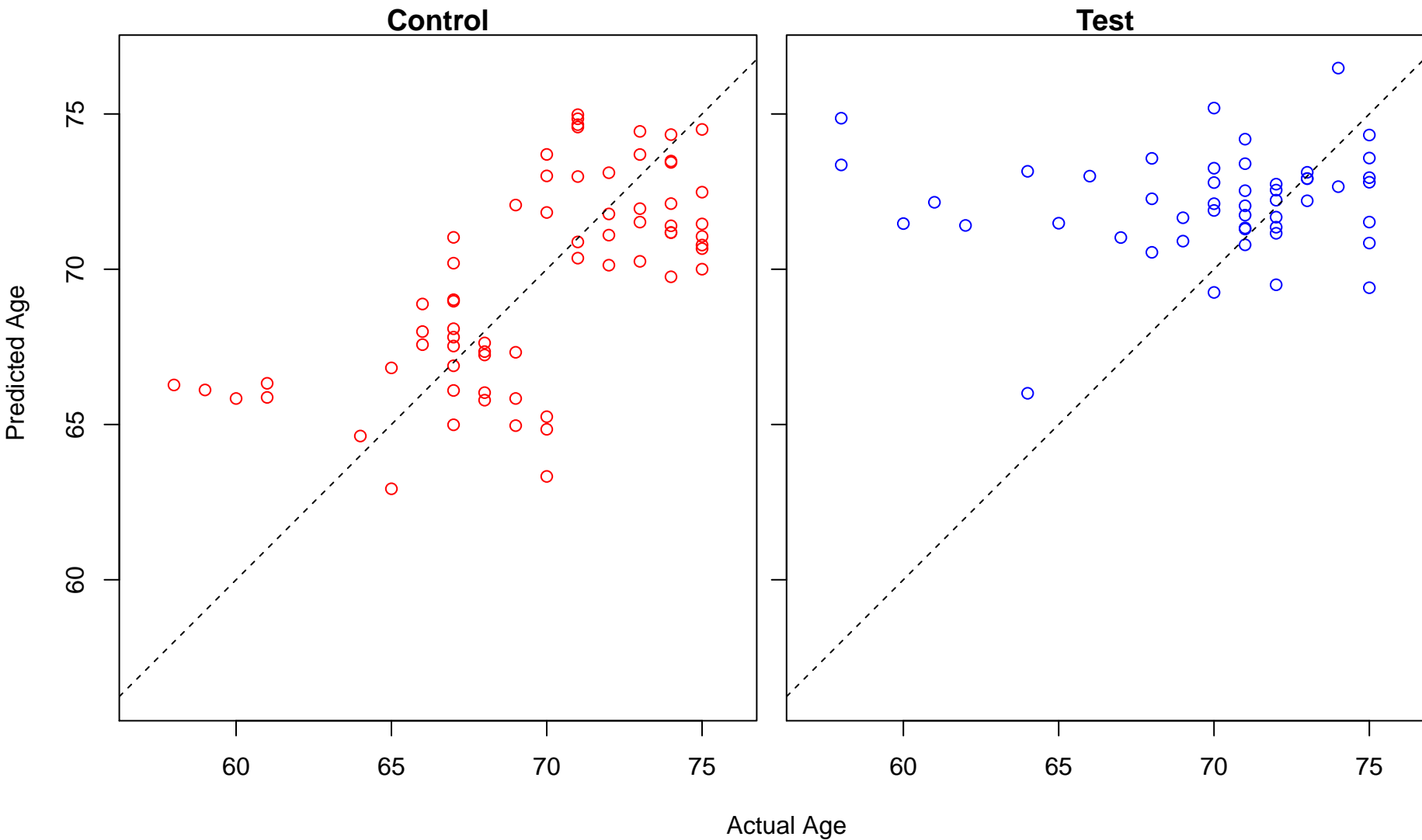


Actual Age

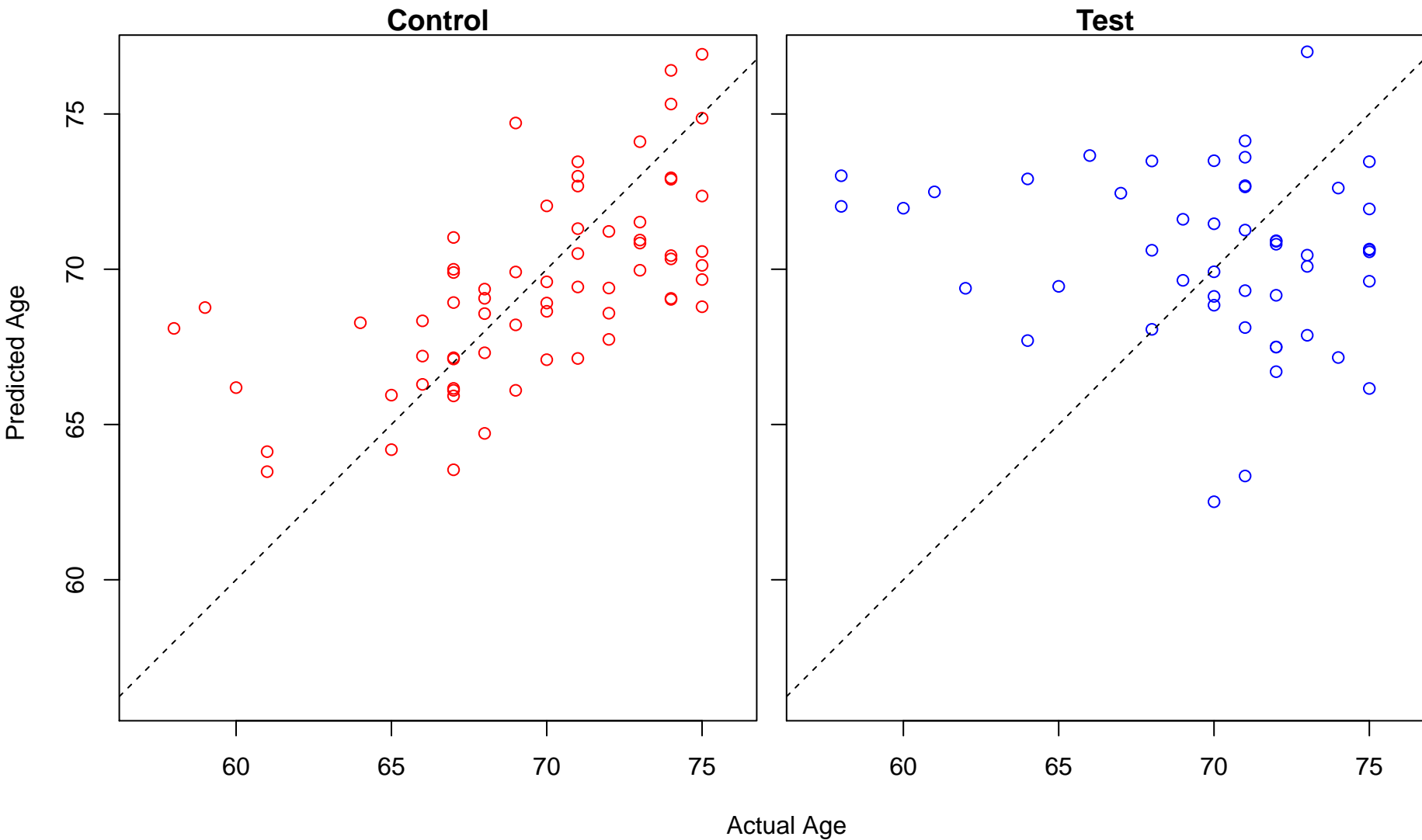
sialylation (Score: 1.245769)



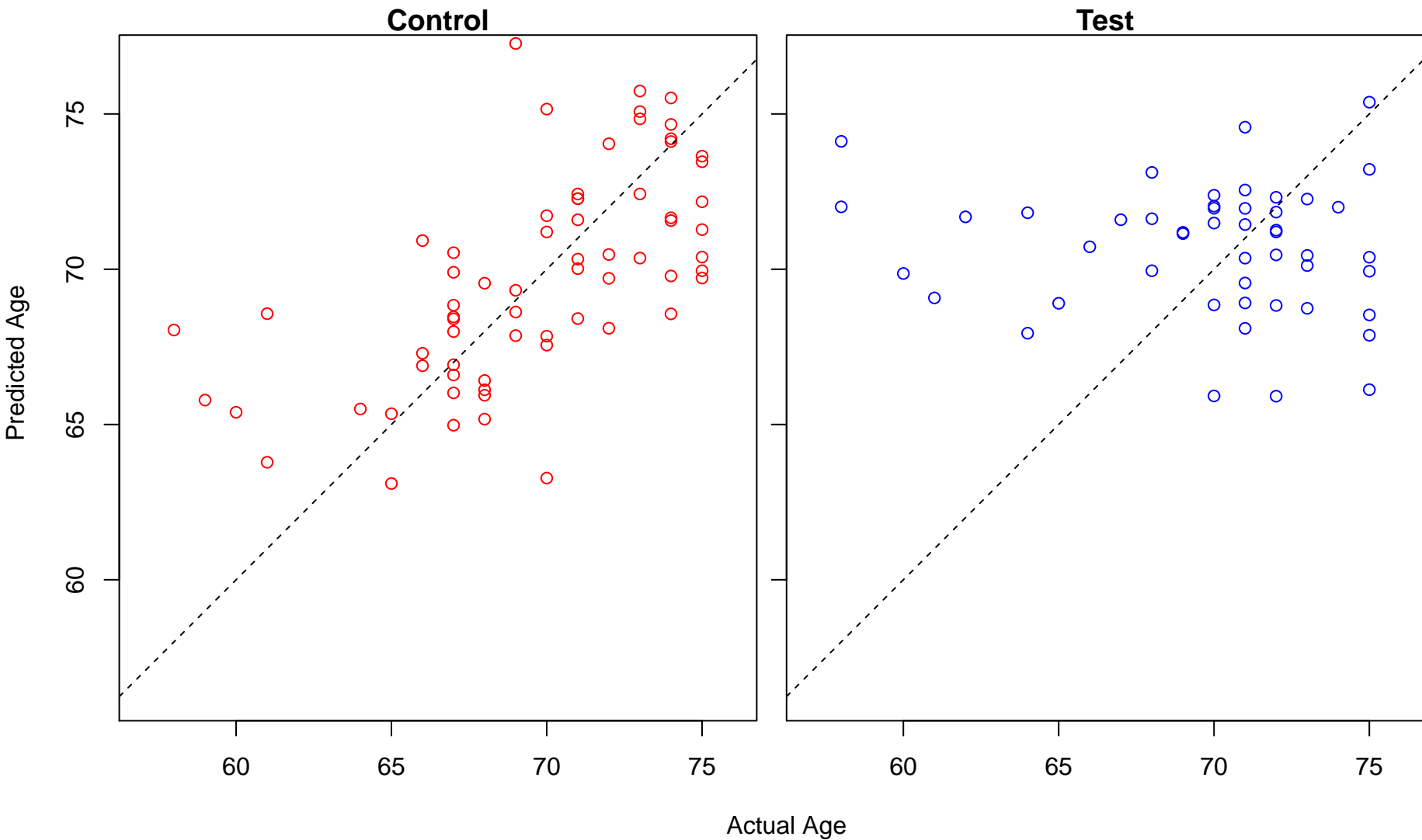
response to UV (Score: 1.245717)



negative regulation of nucleotide metabolic process (Score: 1.245155)

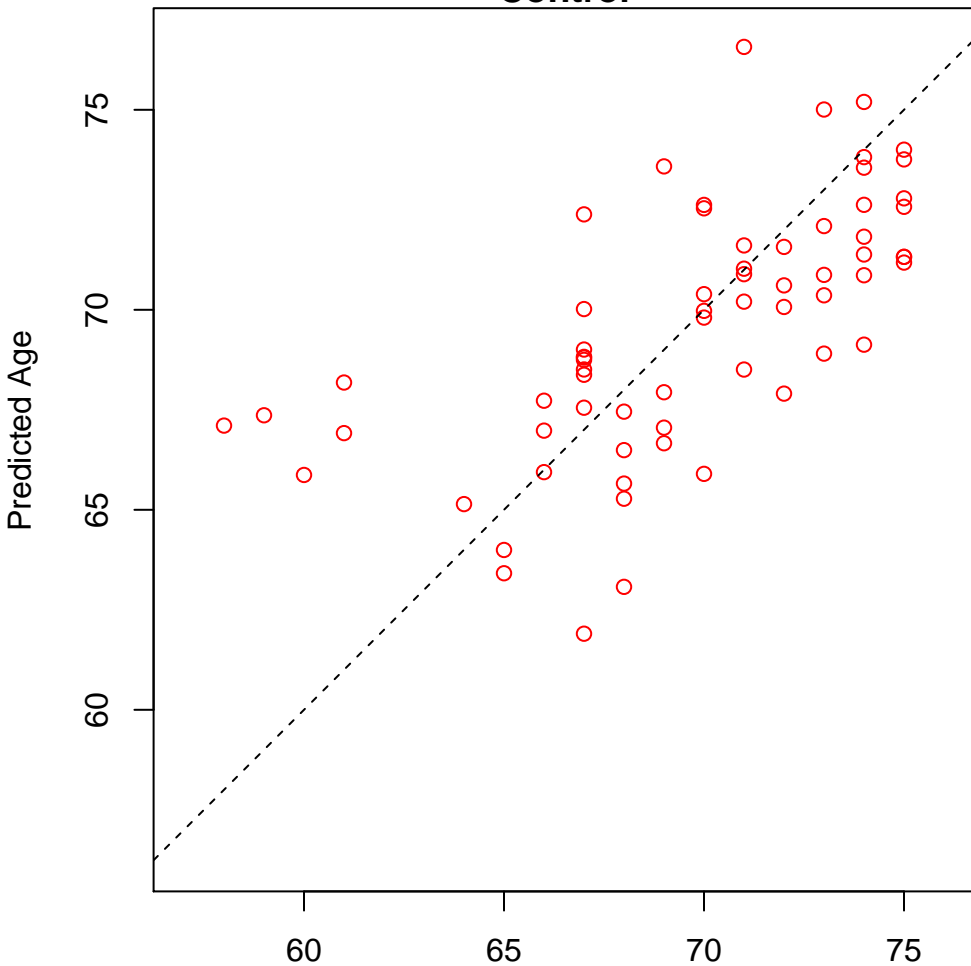


positive regulation of cytosolic calcium ion concentration (Score: 1.245038)

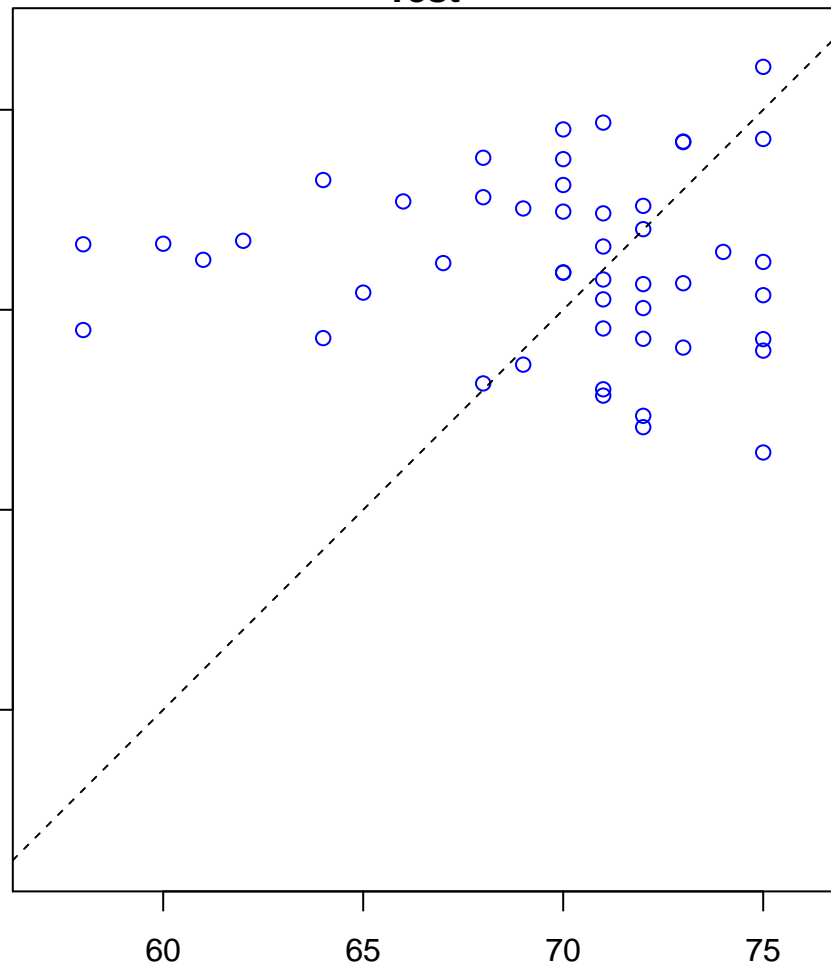


ATP-dependent chromatin remodeling (Score: 1.244944)

Control



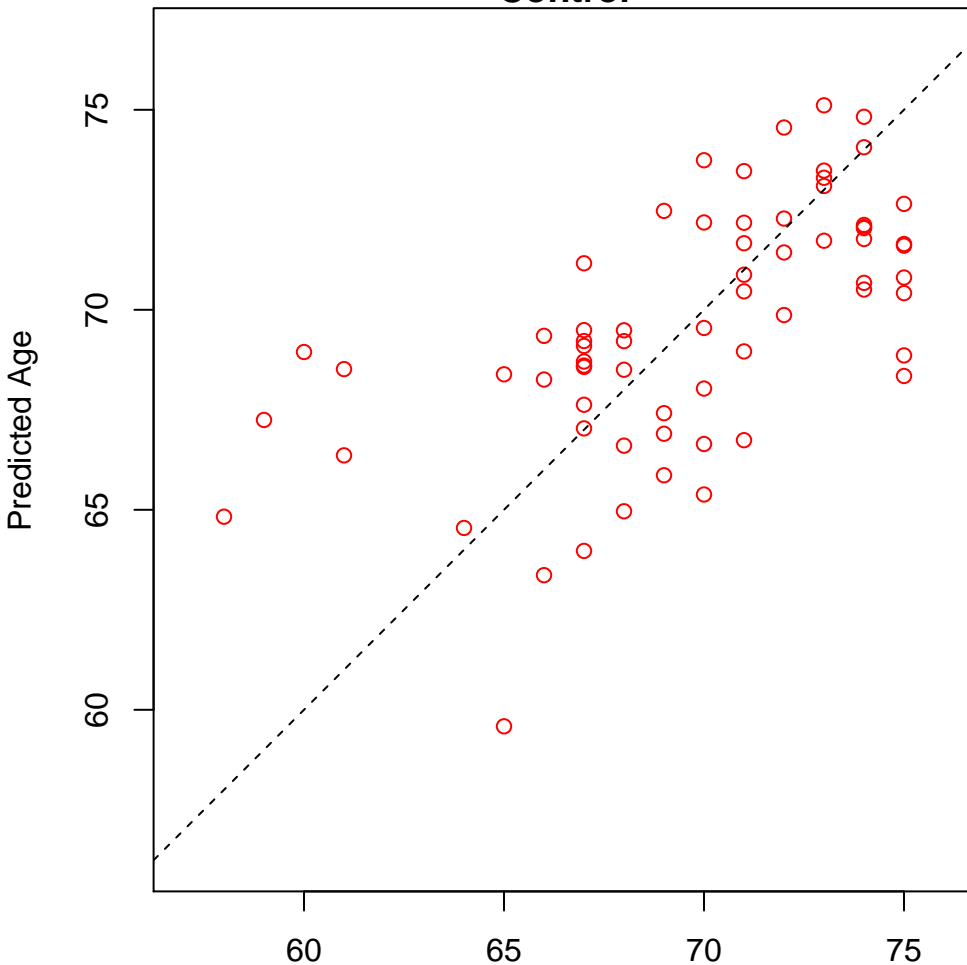
Test



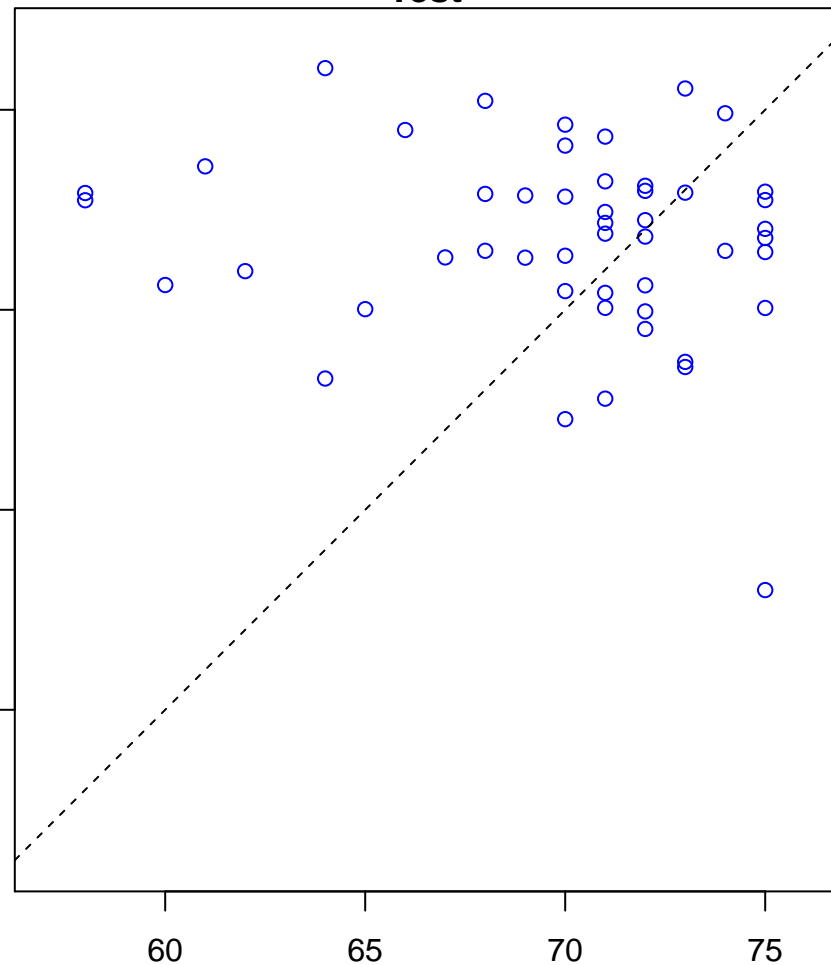
Actual Age

regulation of interleukin-1 secretion (Score: 1.244871)

Control



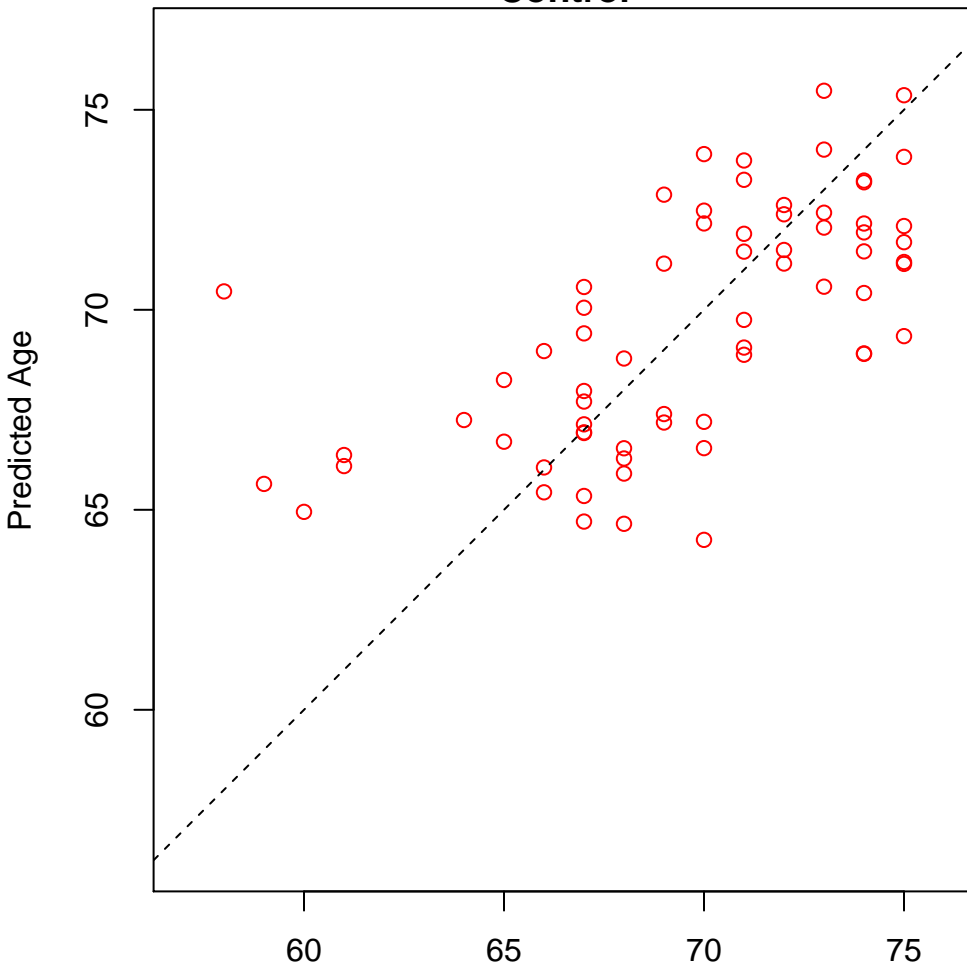
Test



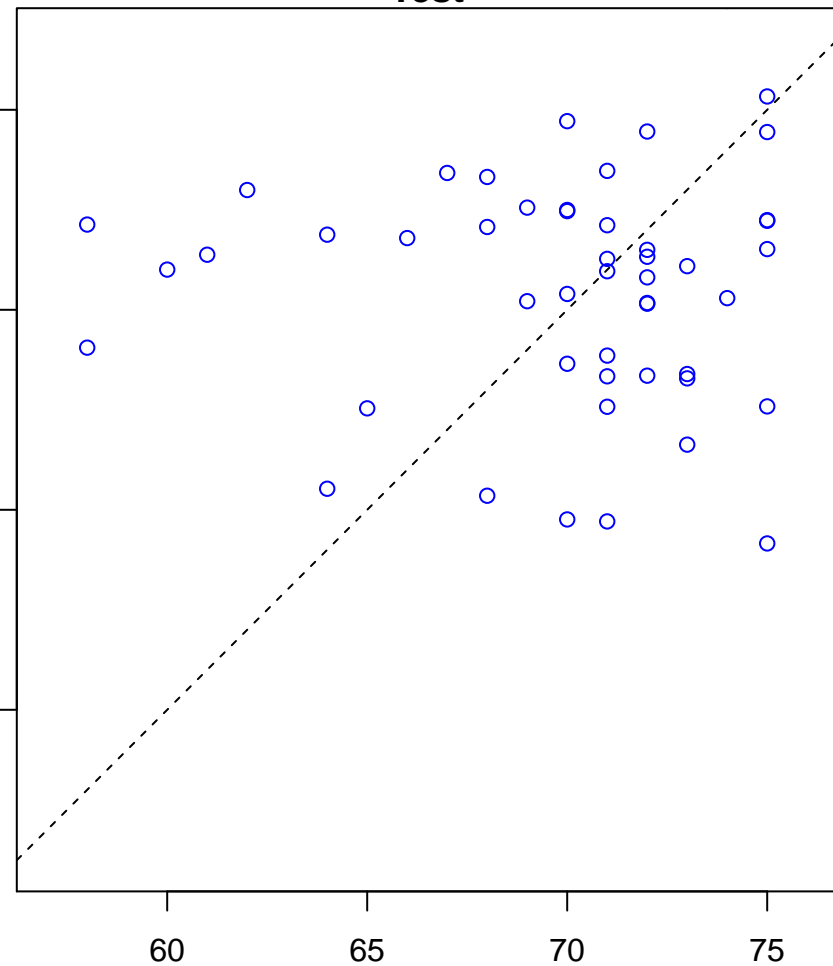
Actual Age

organ or tissue specific immune response (Score: 1.244766)

Control

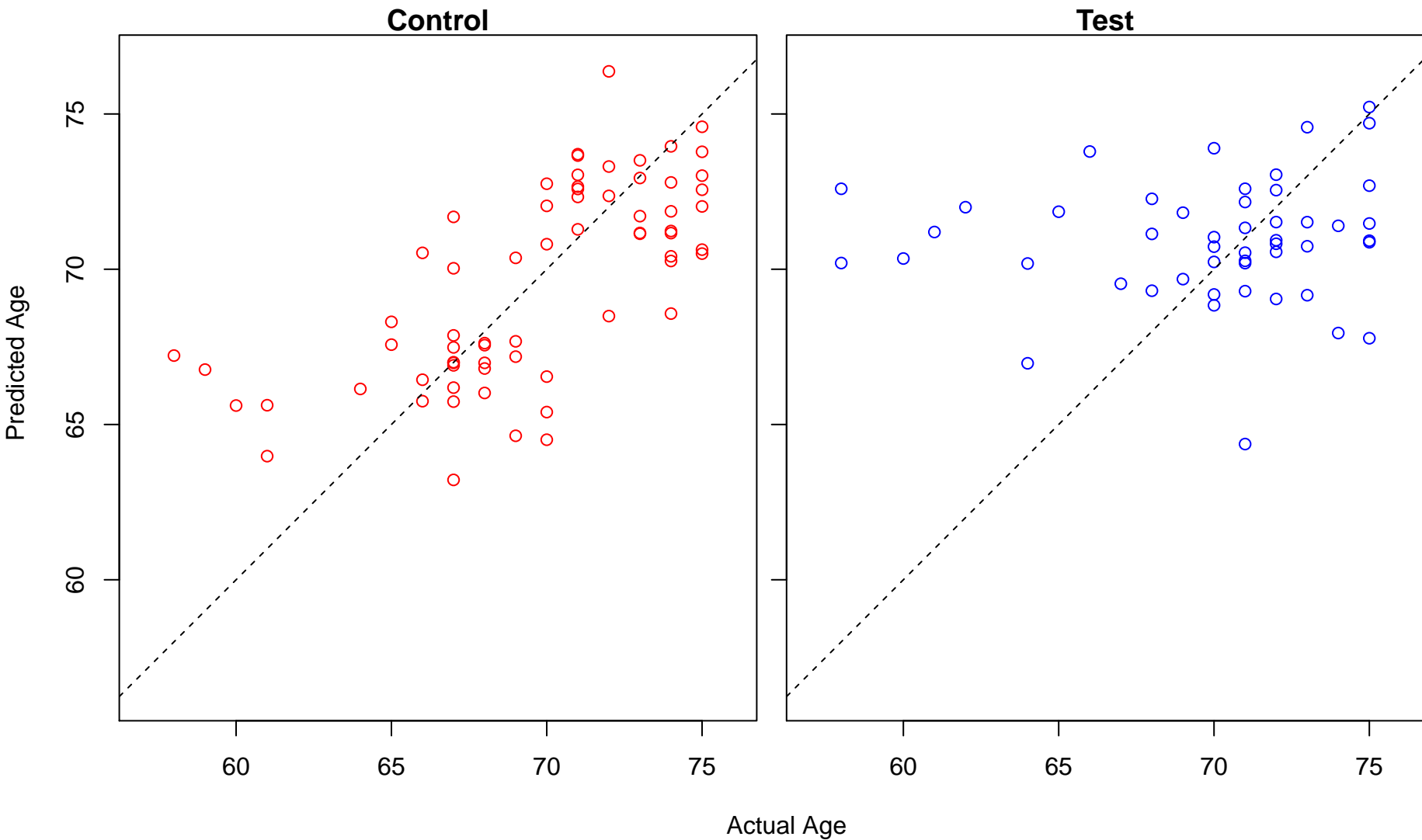


Test

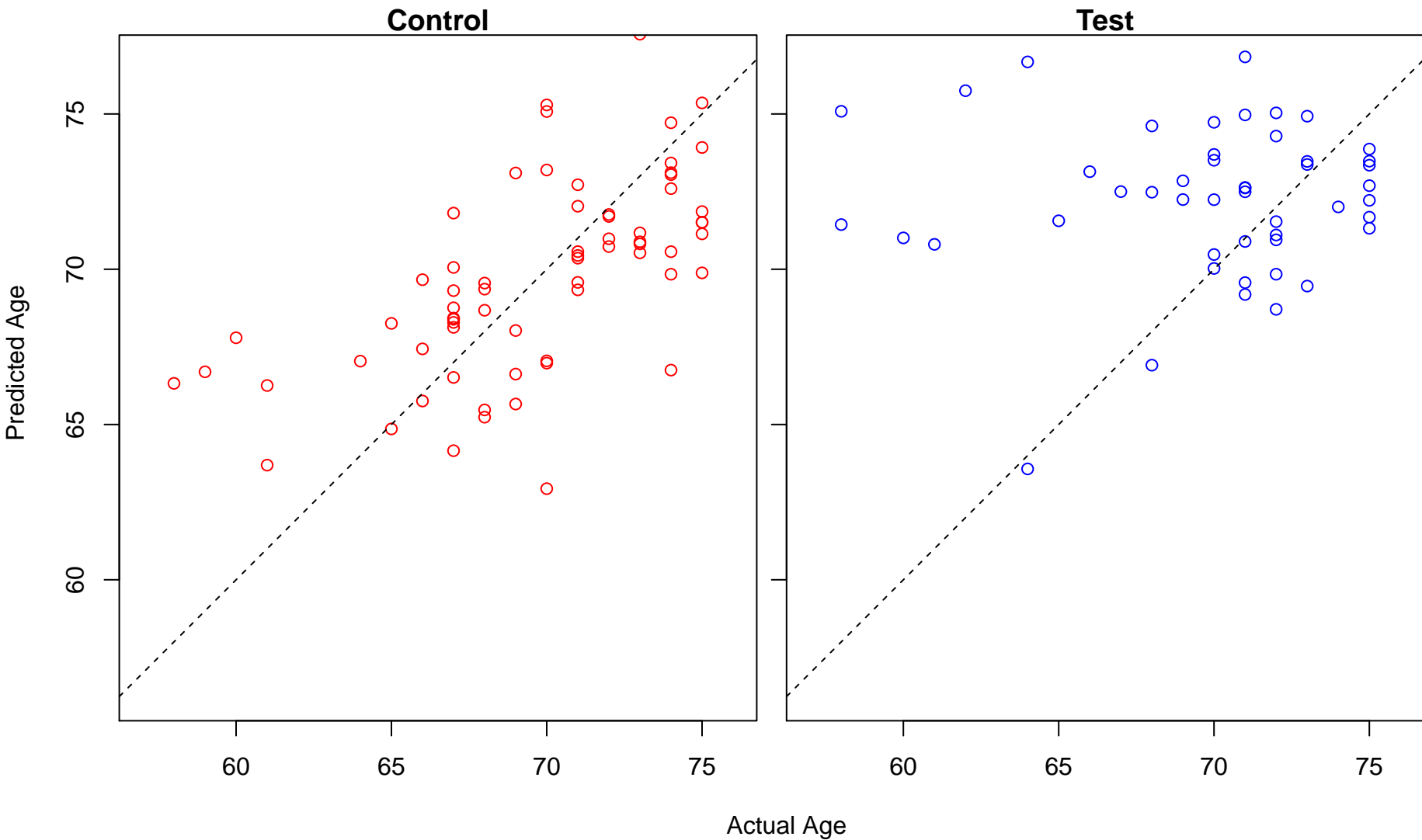


Actual Age

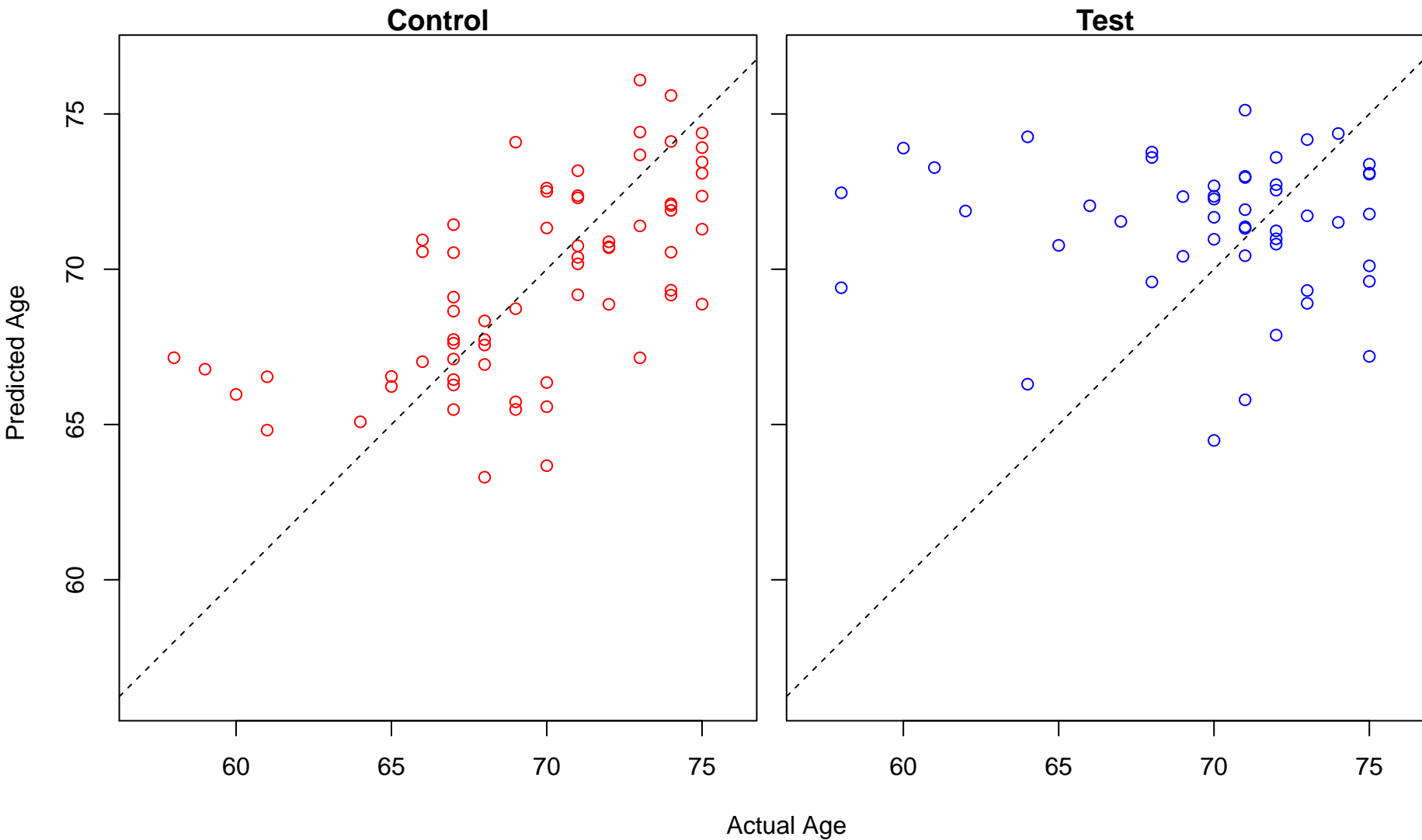
regulation of nucleotide catabolic process (Score: 1.244766)



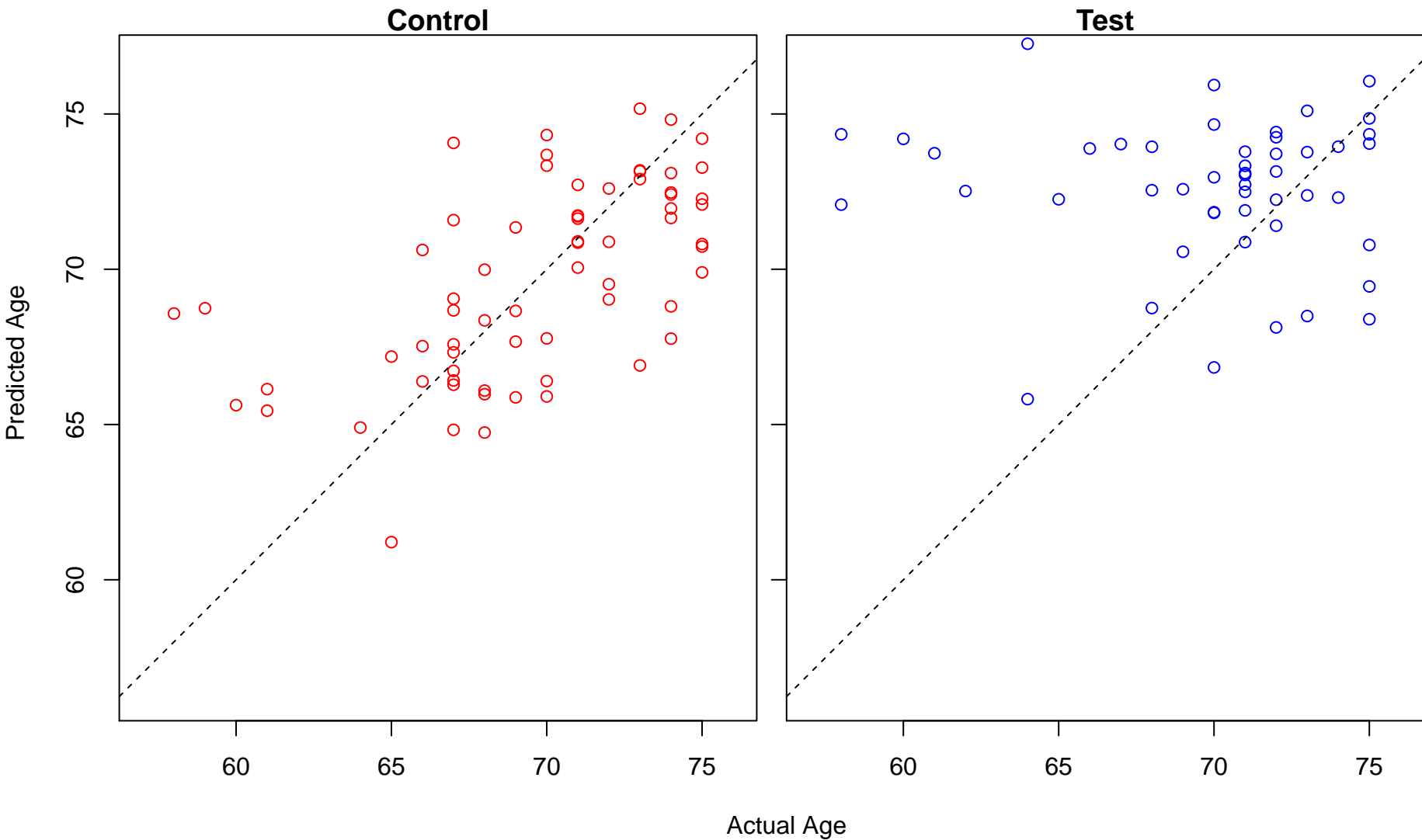
negative regulation of chromatin modification (Score: 1.244682)



regulation of polysaccharide metabolic process (Score: 1.244105)

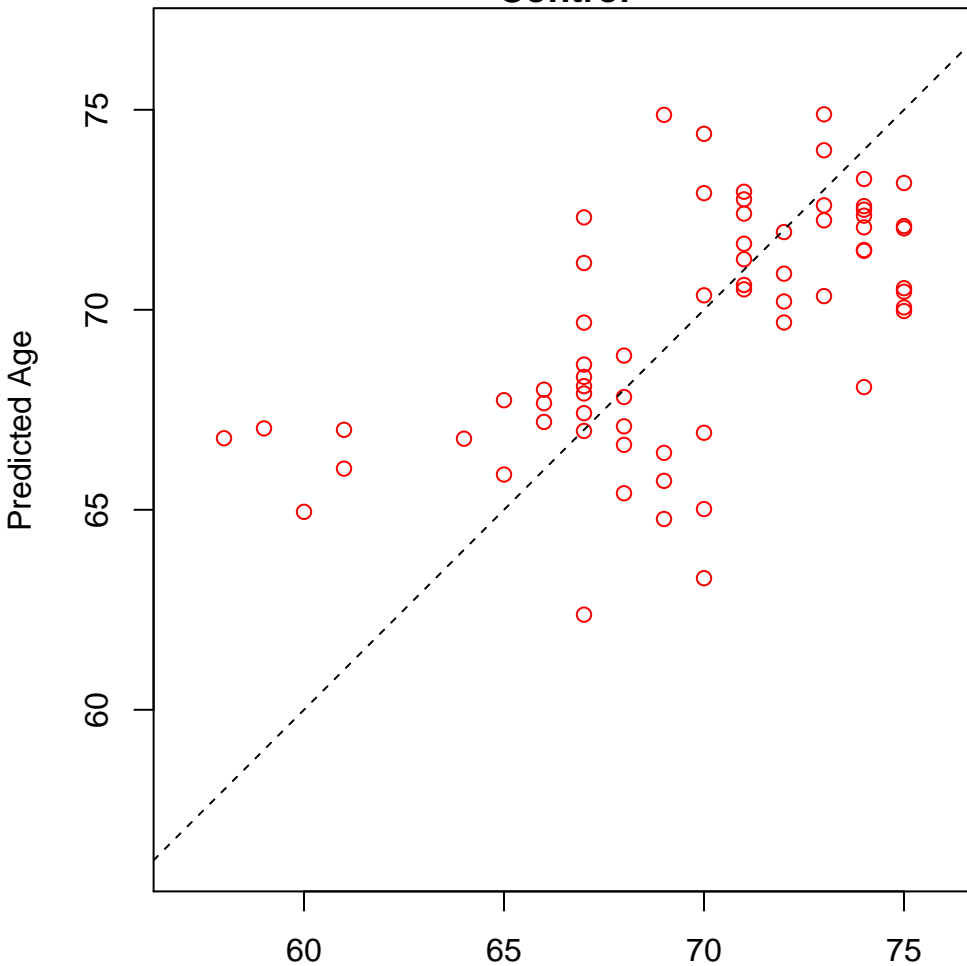


nucleotide-binding oligomerization domain containing signaling pathway (Score: 1.244010)

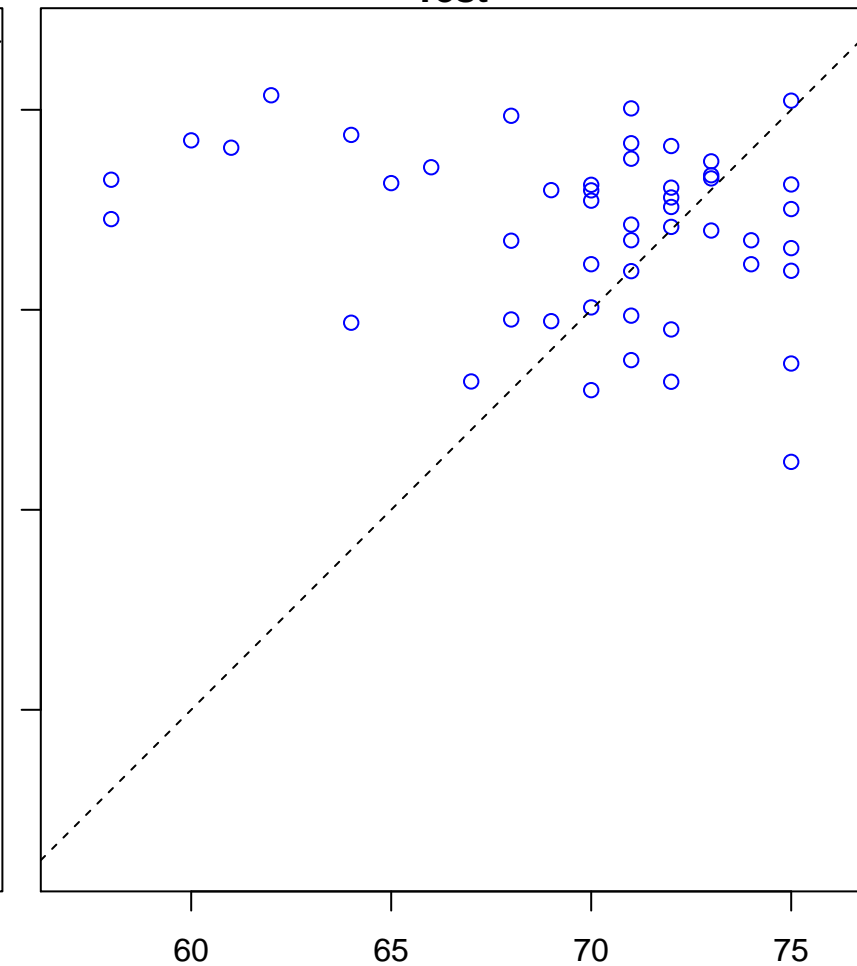


phosphatidylinositol phosphorylation (Score: 1.244006)

Control

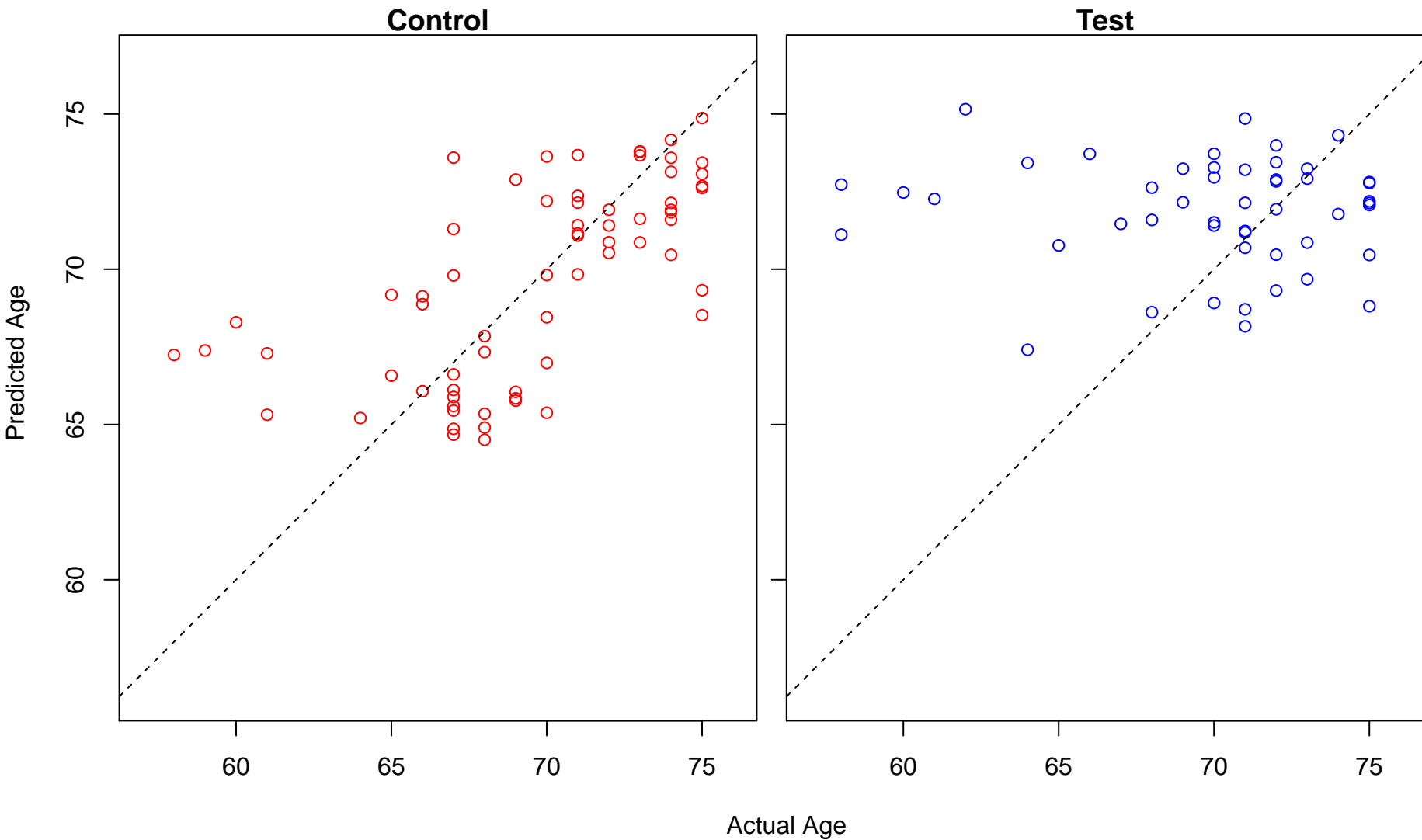


Test



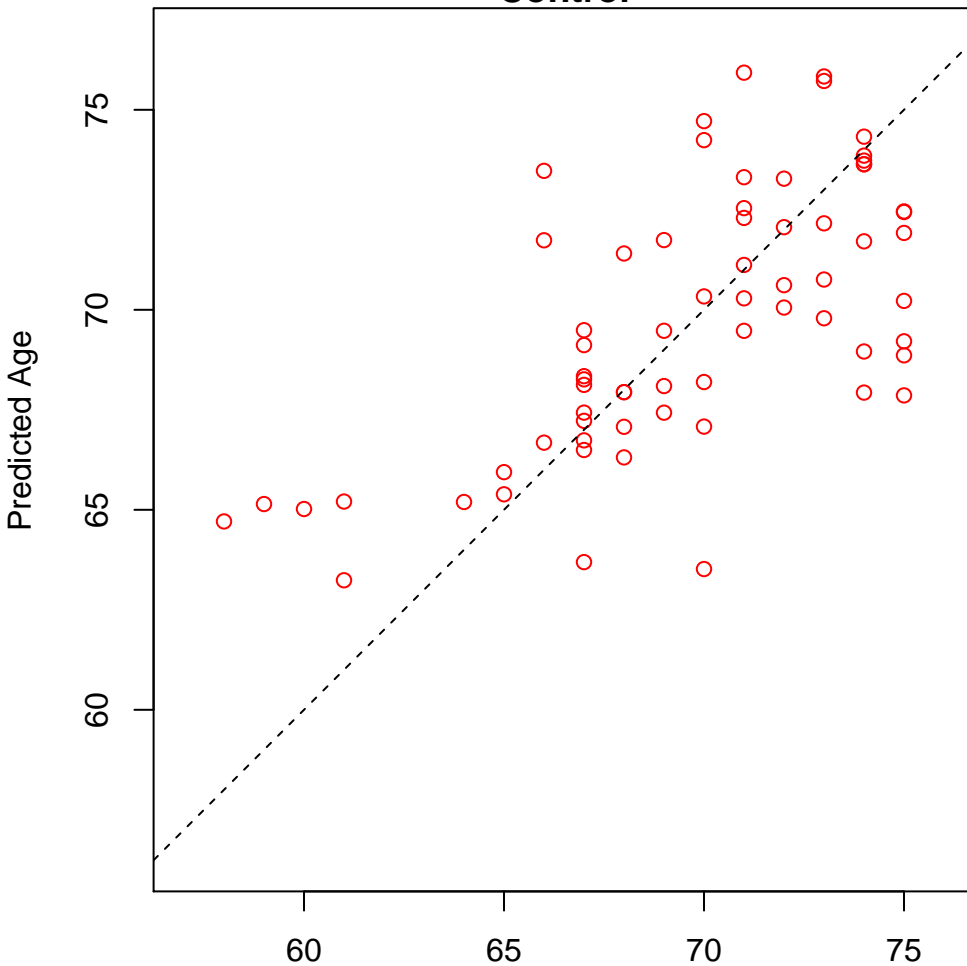
Actual Age

glial cell differentiation (Score: 1.243522)

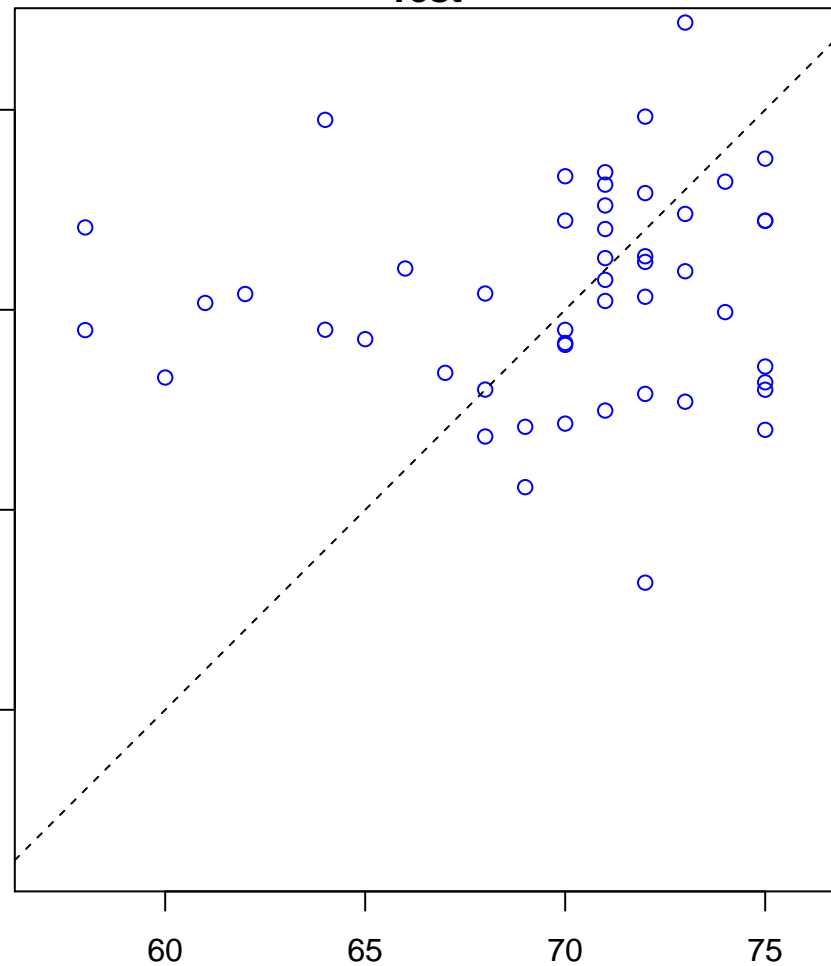


purine nucleoside catabolic process (Score: 1.243406)

Control



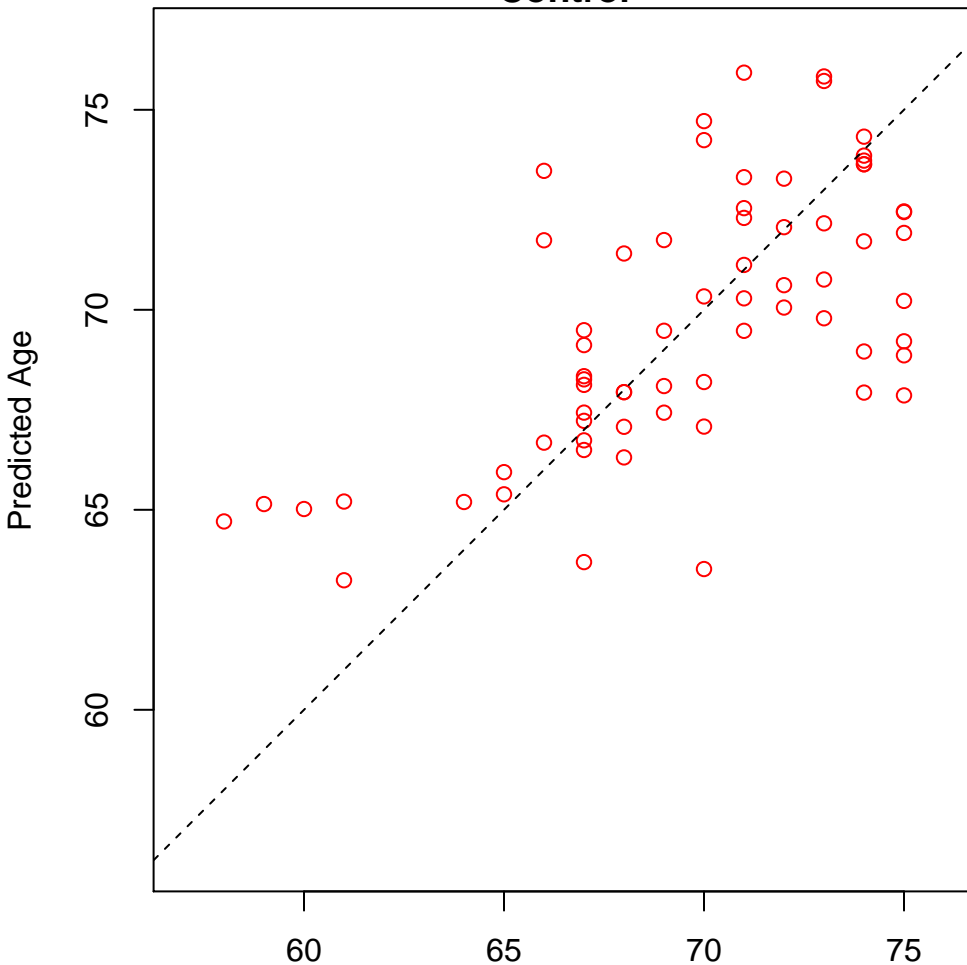
Test



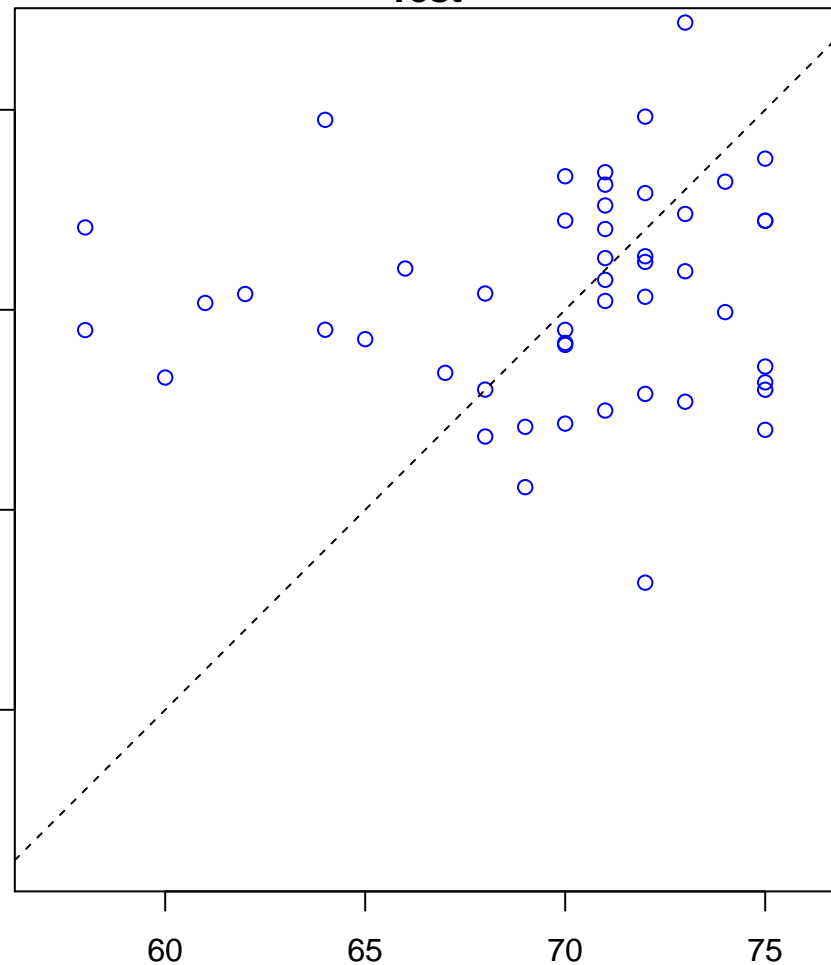
Actual Age

purine ribonucleoside catabolic process (Score: 1.243406)

Control

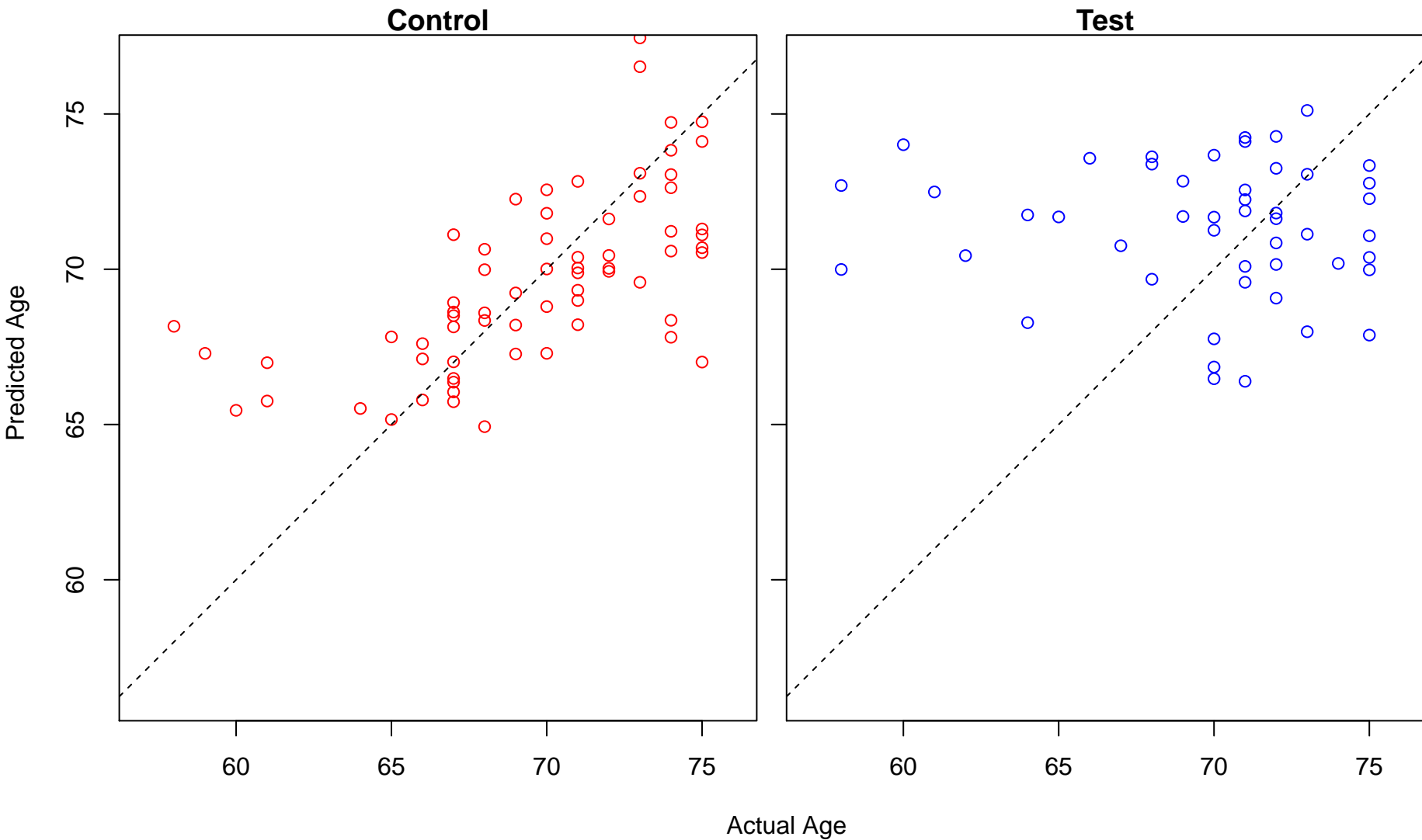


Test

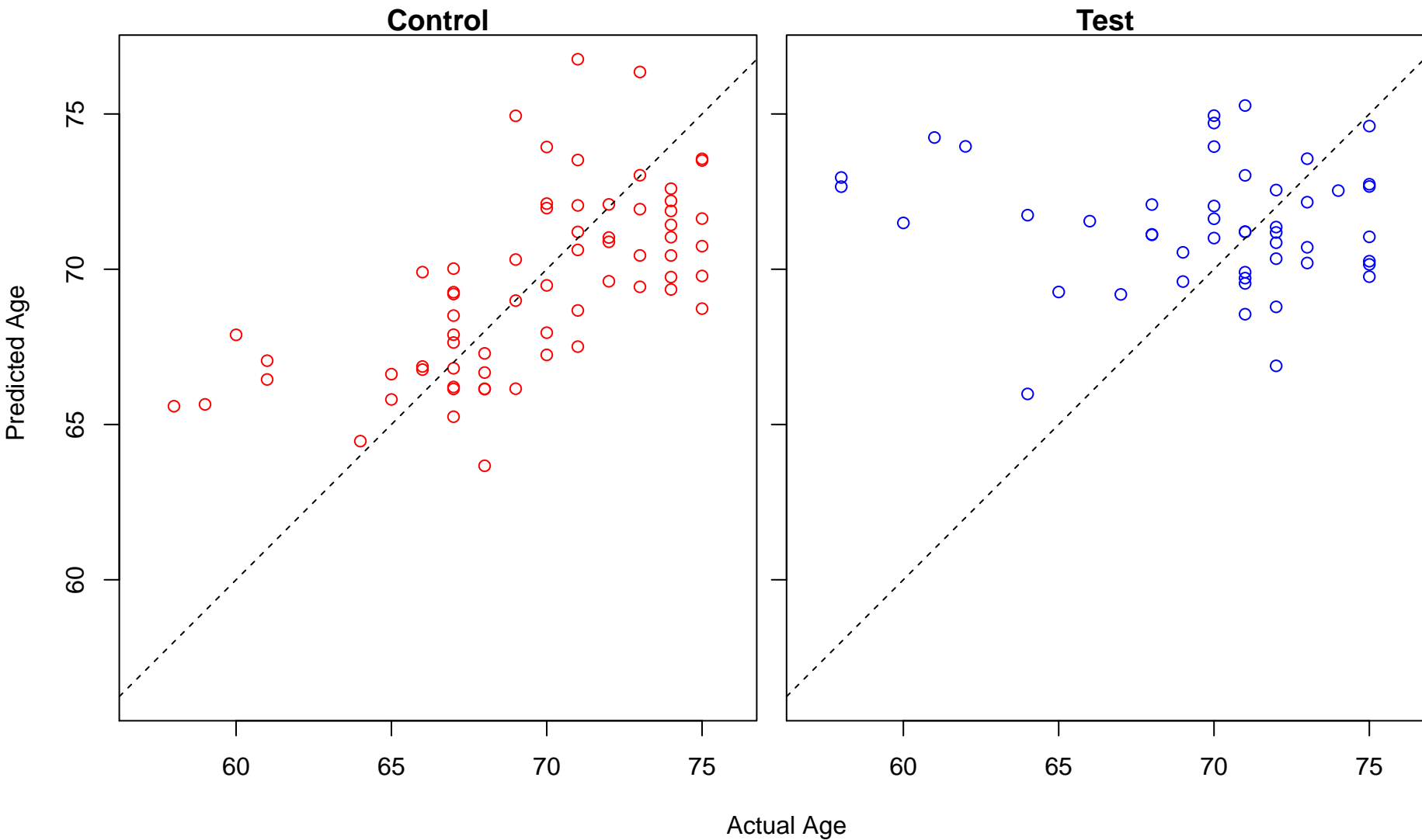


Actual Age

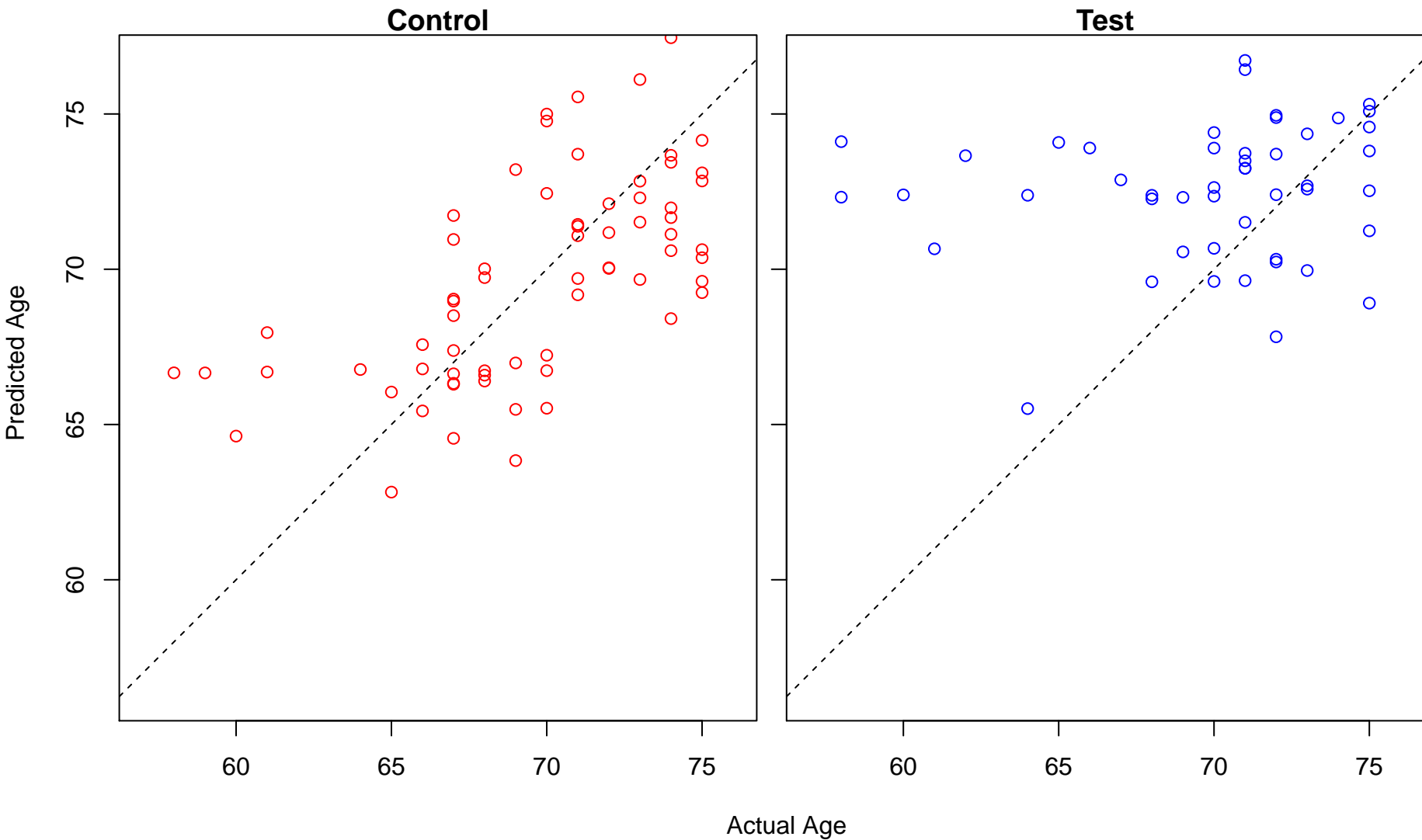
phospholipid catabolic process (Score: 1.243369)



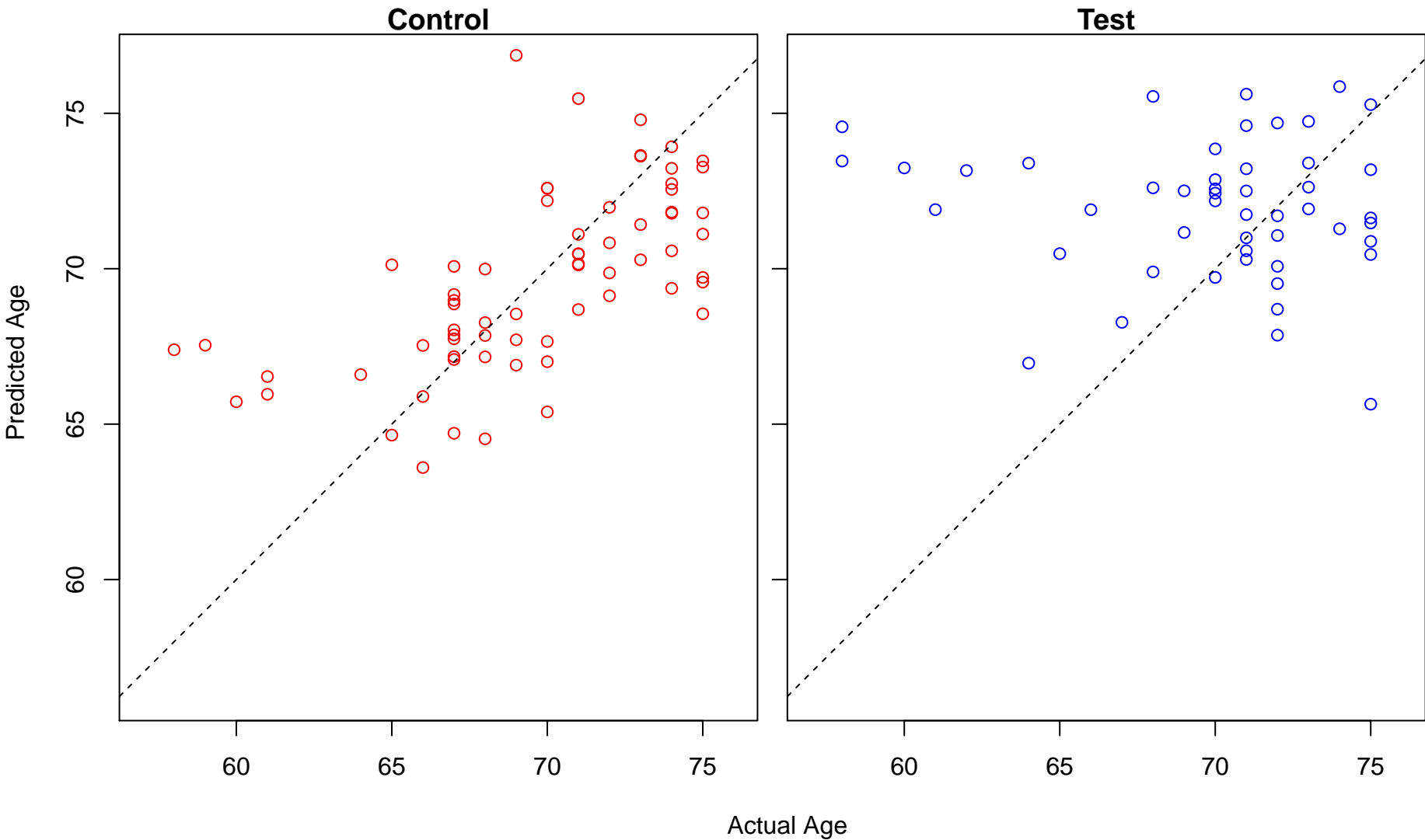
sensory perception of sound (Score: 1.242835)



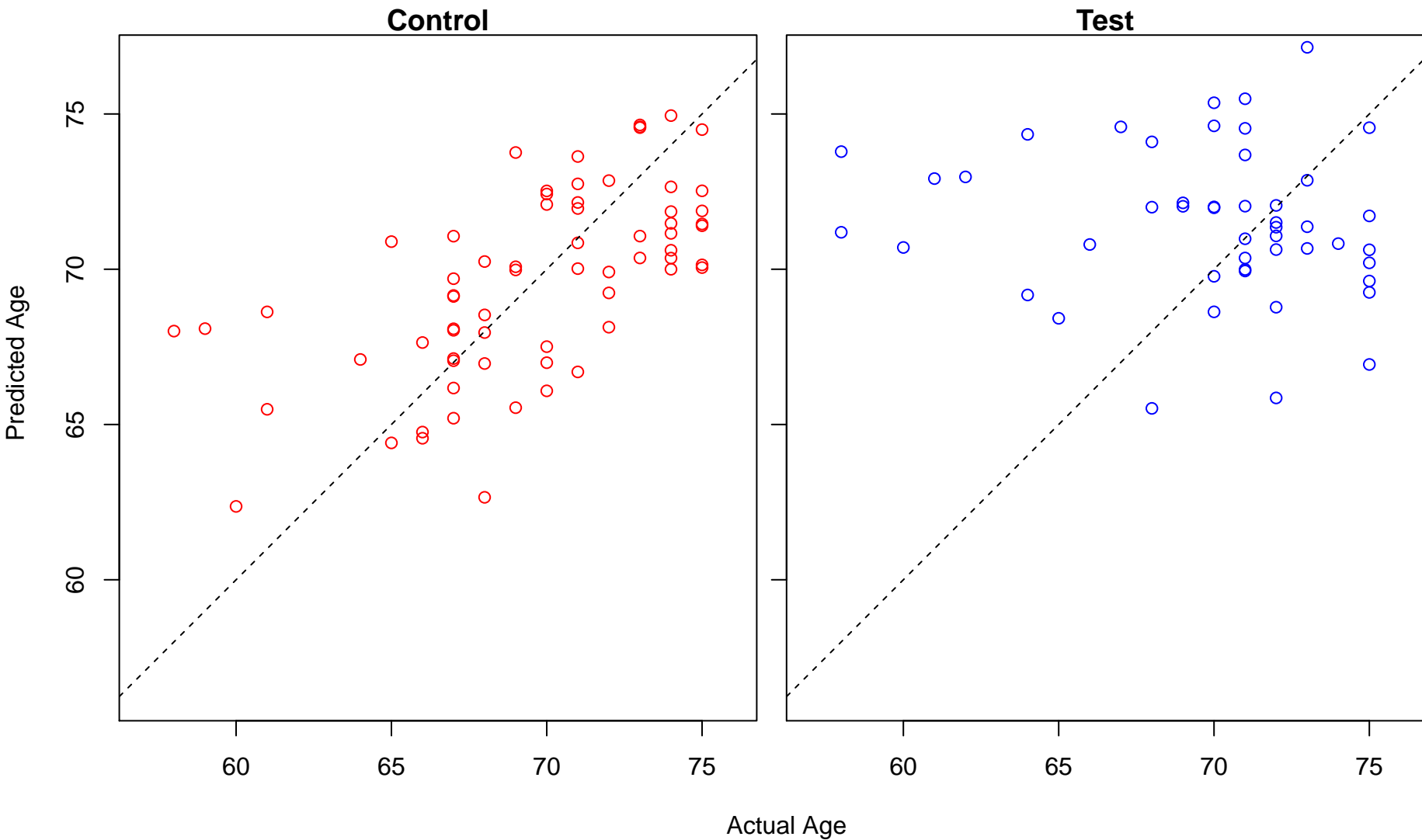
regulation of neuron projection development (Score: 1.242724)



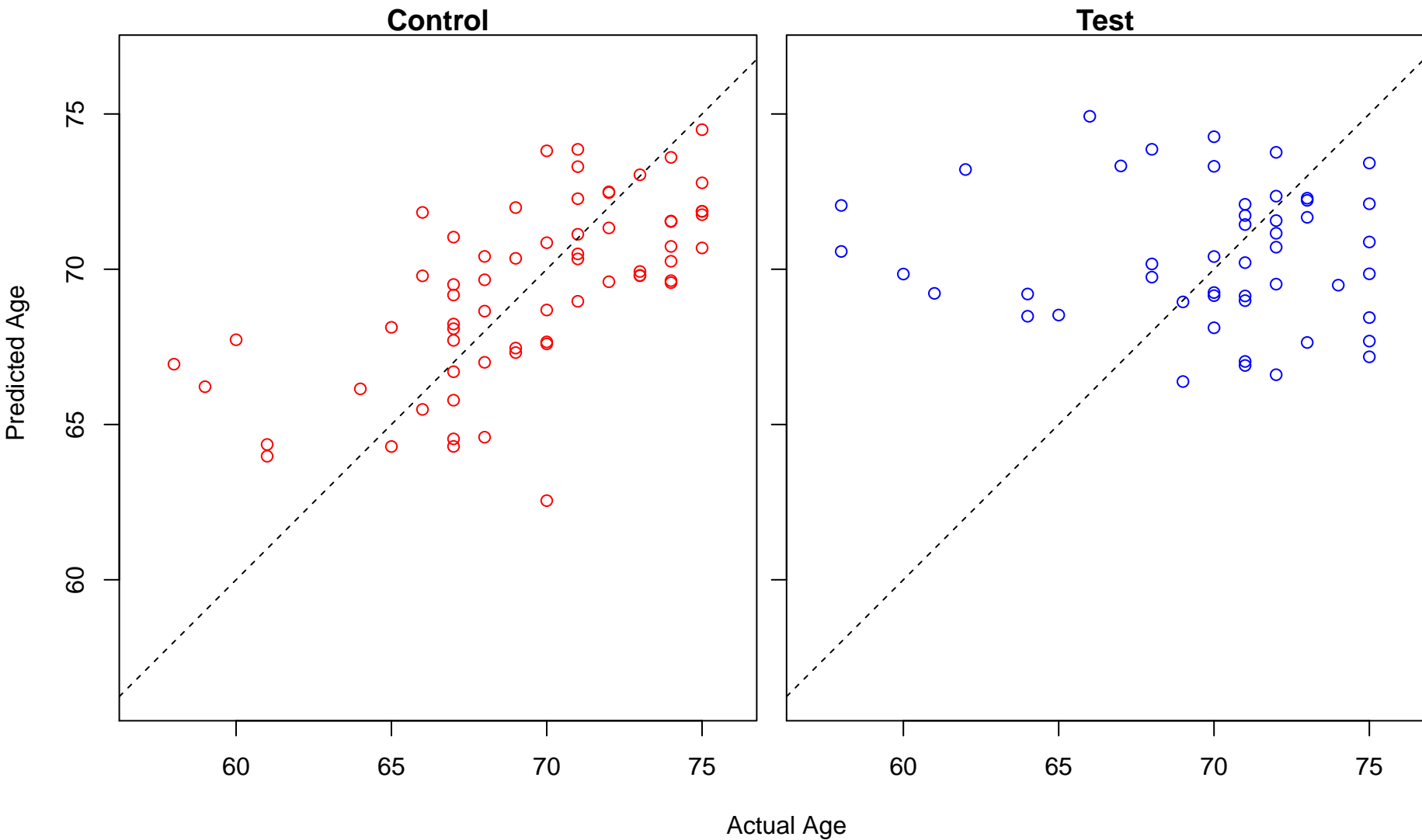
epithelial to mesenchymal transition (Score: 1.242248)



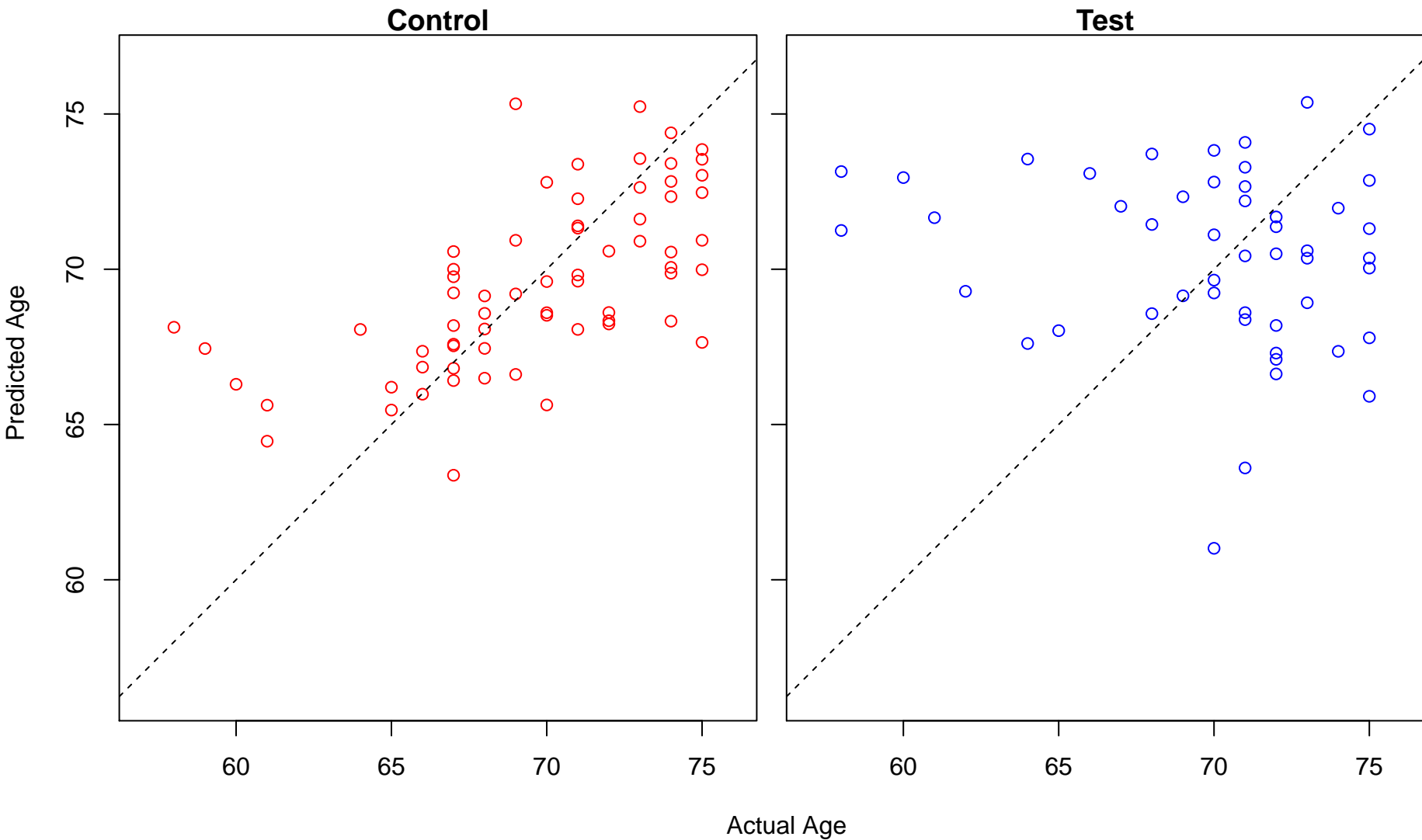
aspartate family amino acid metabolic process (Score: 1.241948)



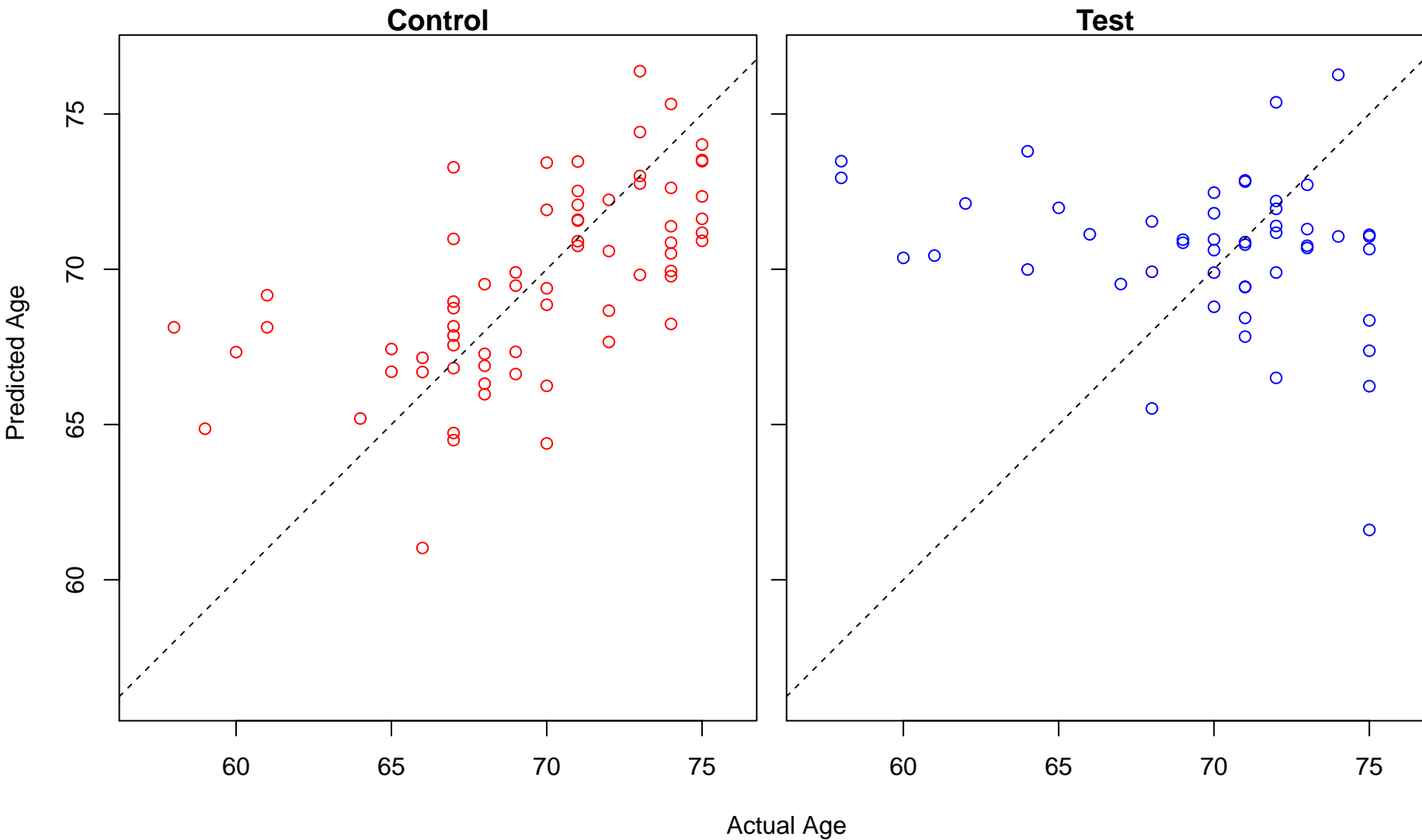
death-inducing signaling complex assembly (Score: 1.241058)



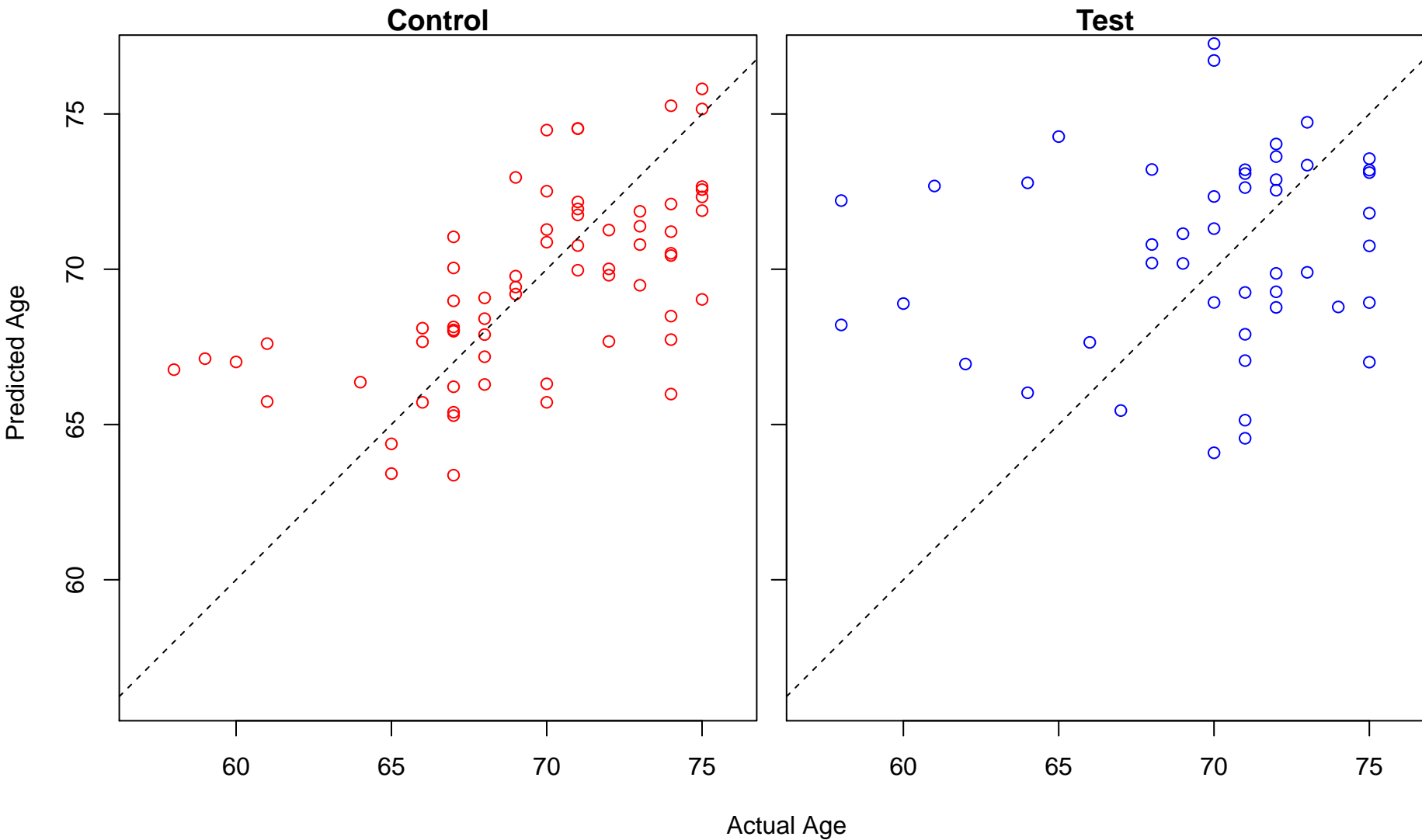
negative regulation of cyclic nucleotide metabolic process (Score: 1.240739)



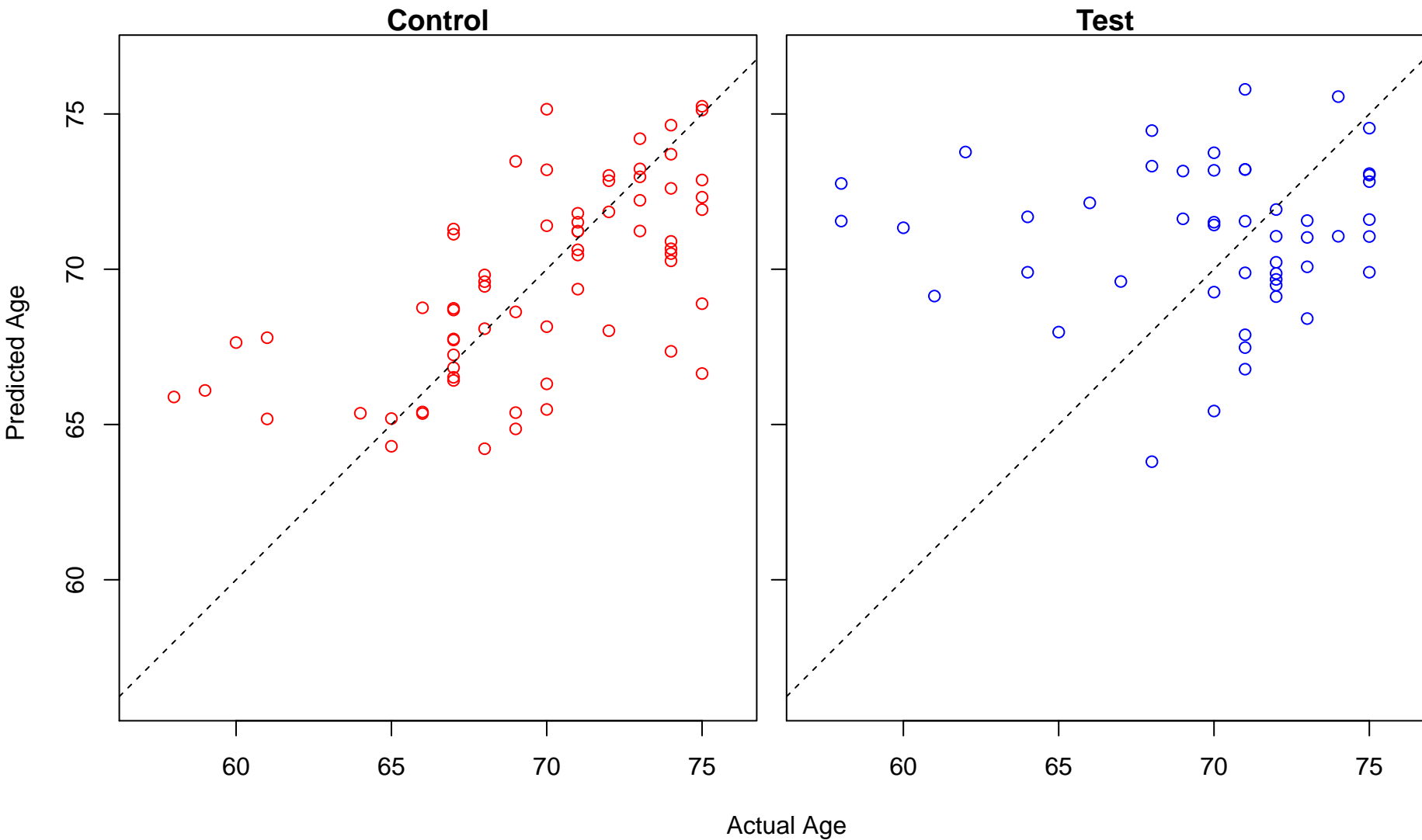
negative regulation of DNA-dependent DNA replication (Score: 1.239700)



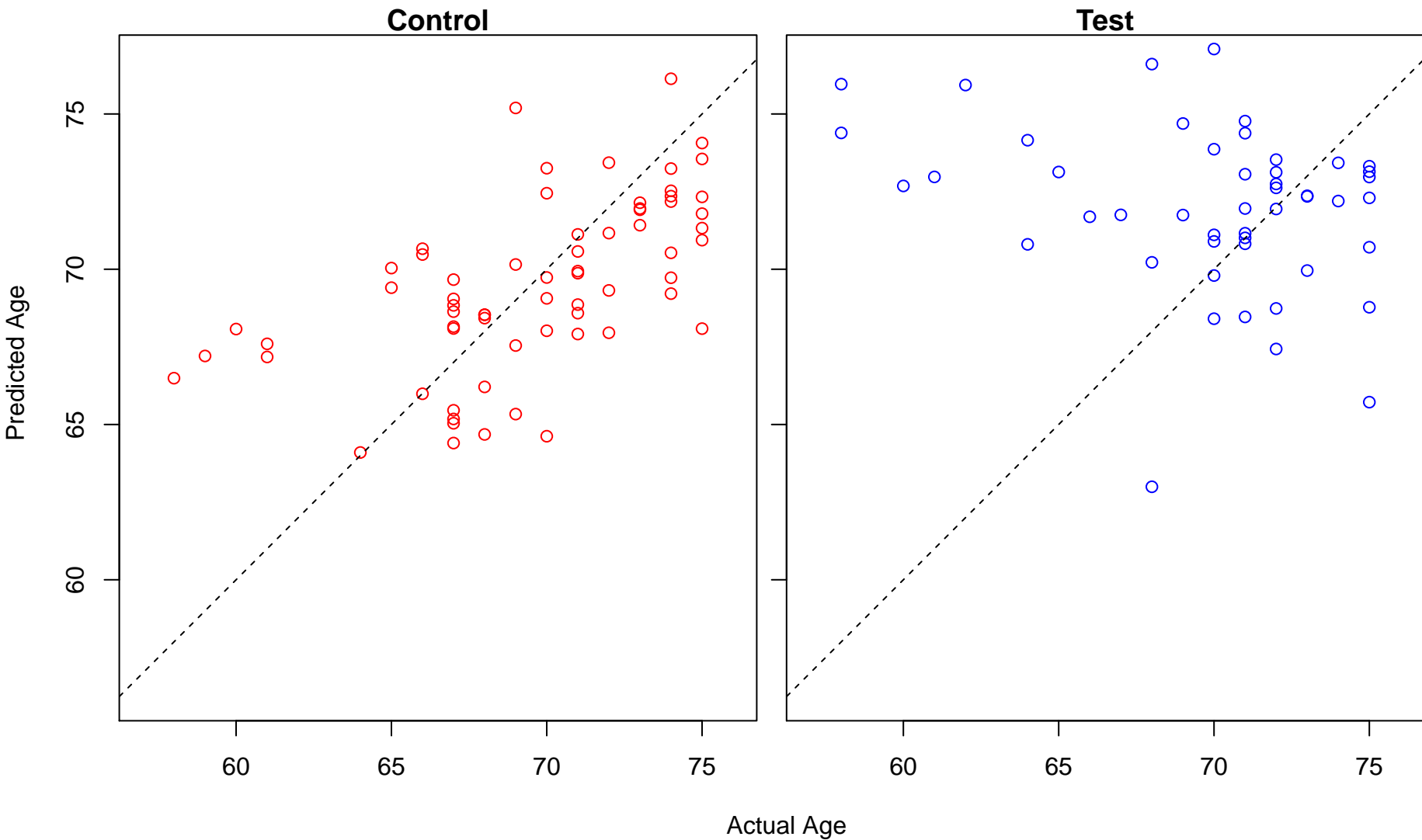
regulation of chemokine (C-X-C motif) ligand 2 production (Score: 1.239615)



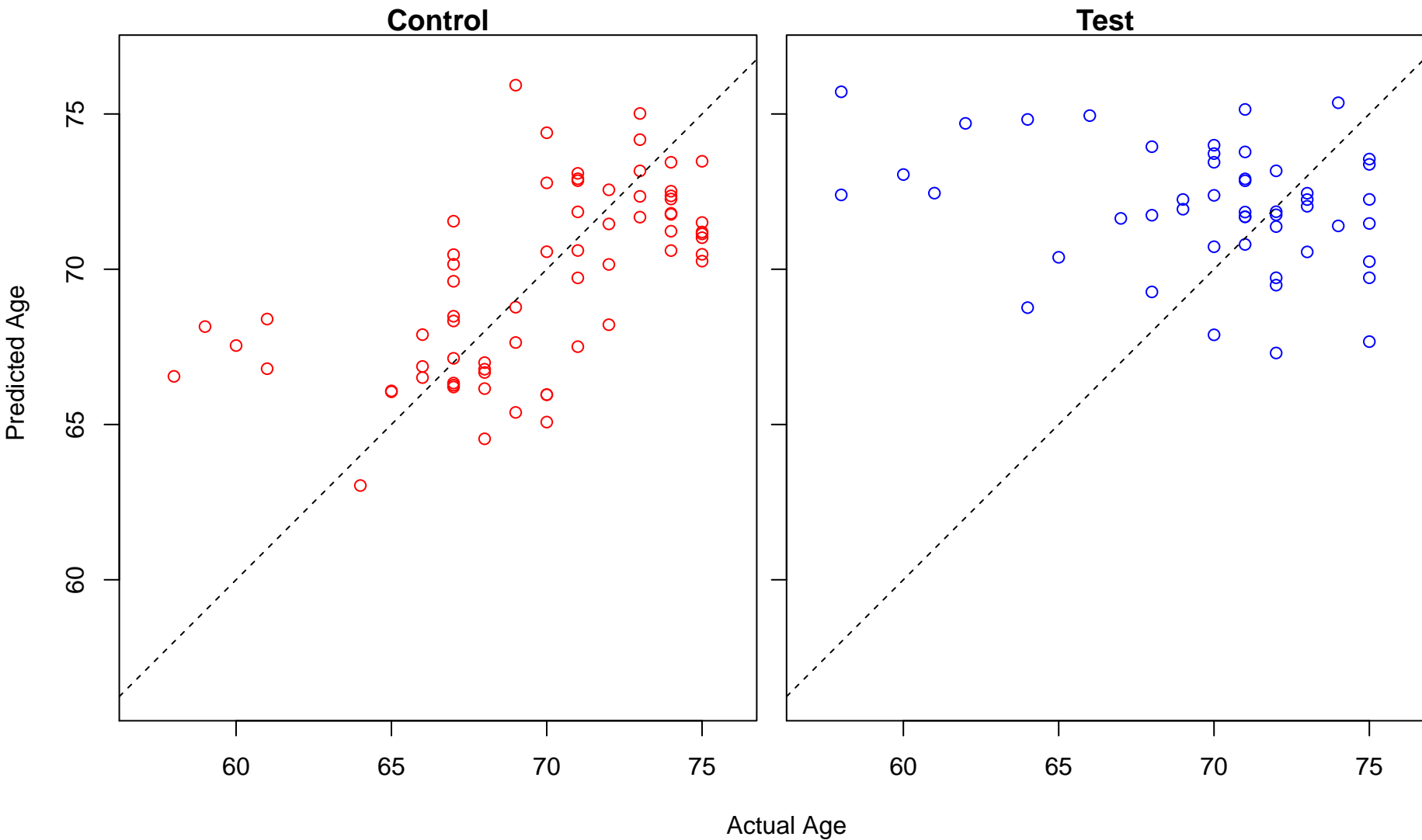
protein palmitoylation (Score: 1.239335)



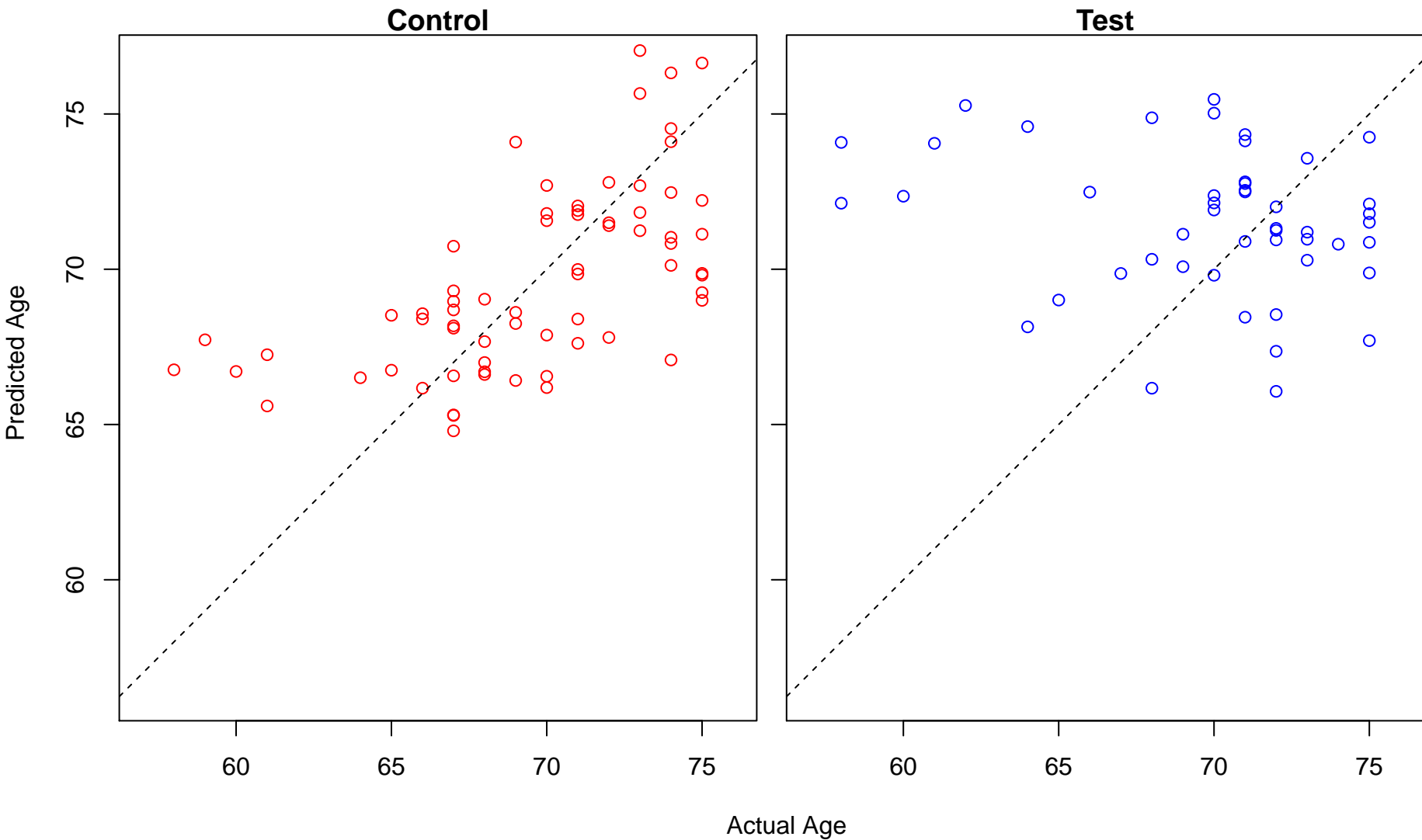
RNA splicing, via endonucleolytic cleavage and ligation (Score: 1.238957)



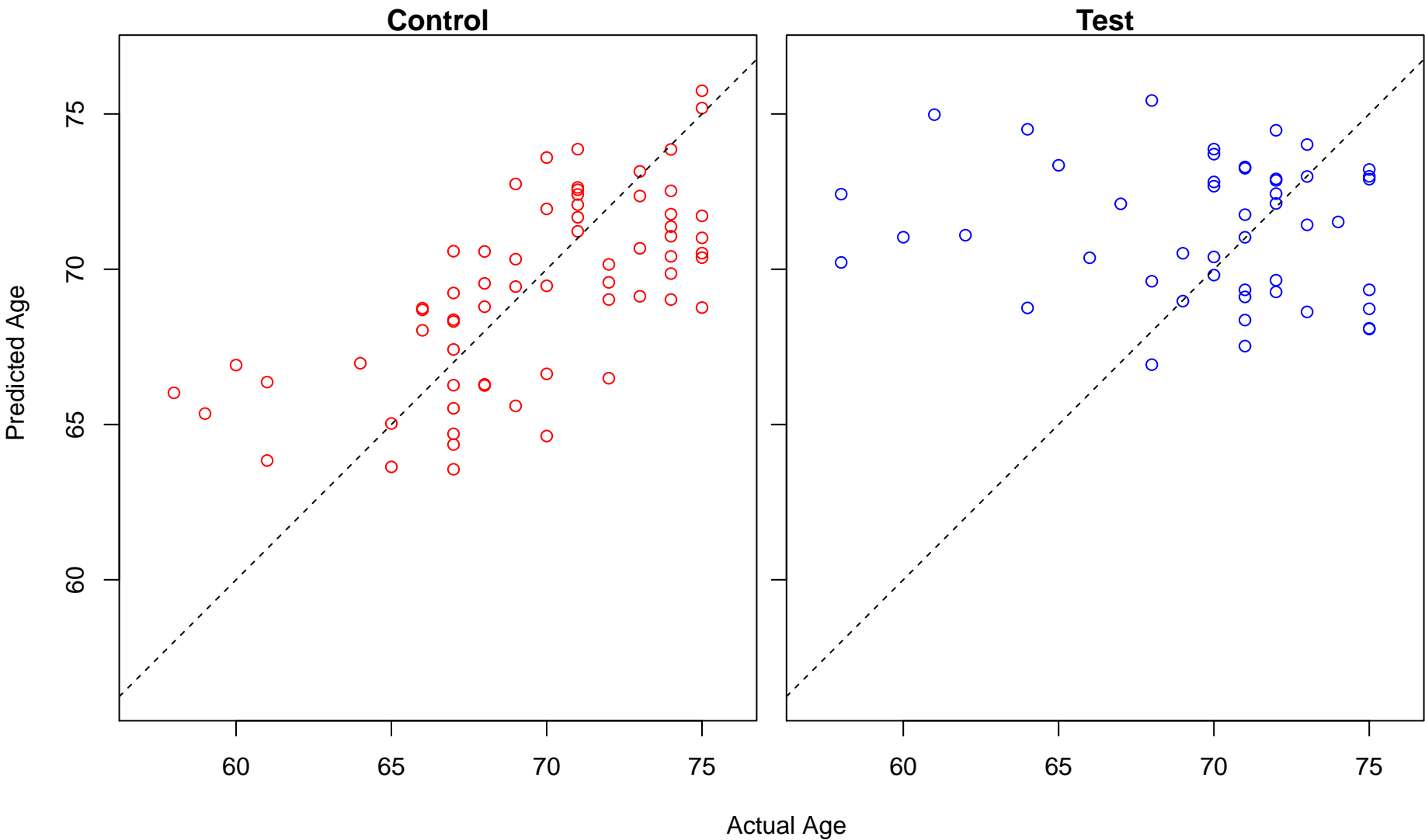
xenobiotic metabolic process (Score: 1.238607)



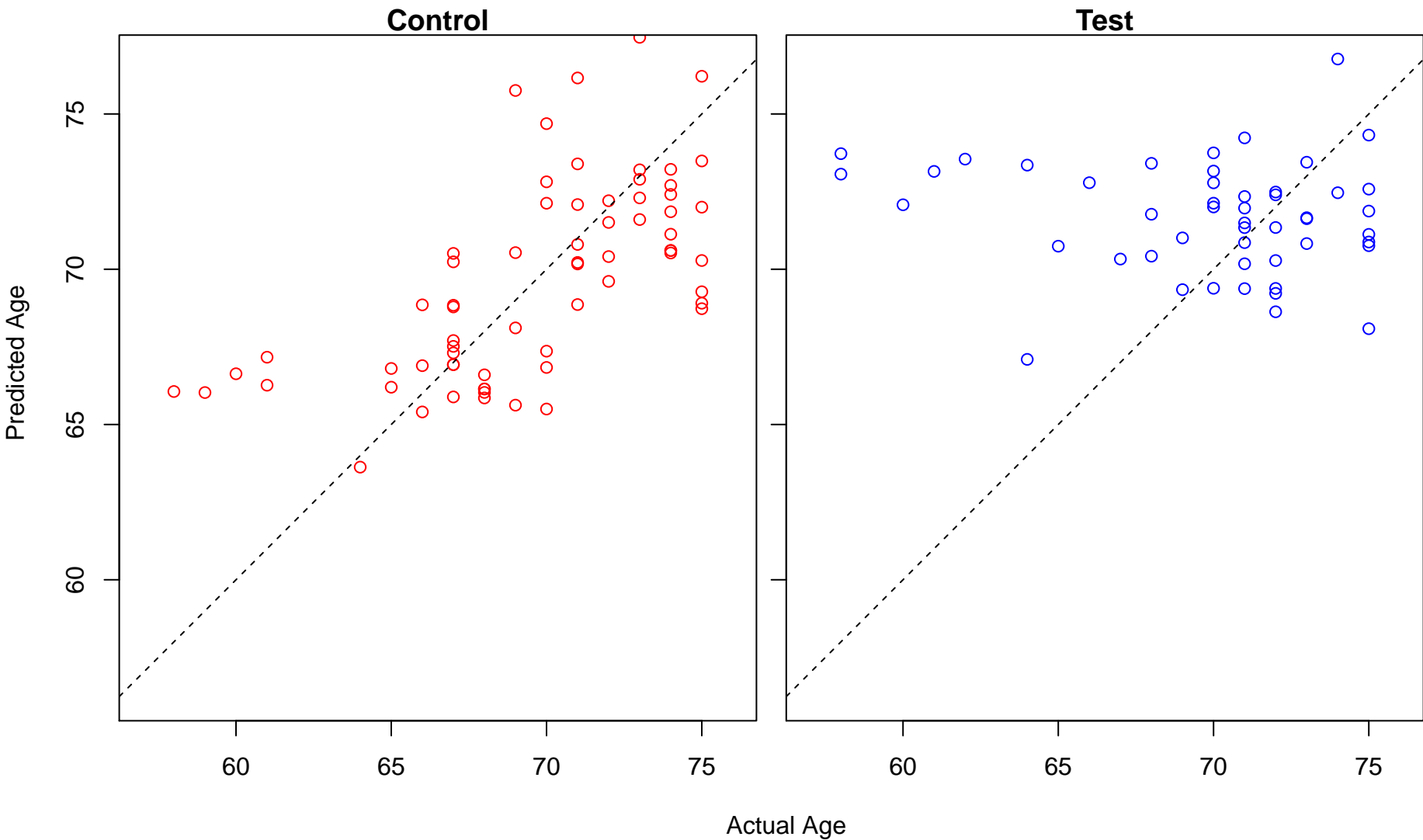
membrane assembly (Score: 1.238029)



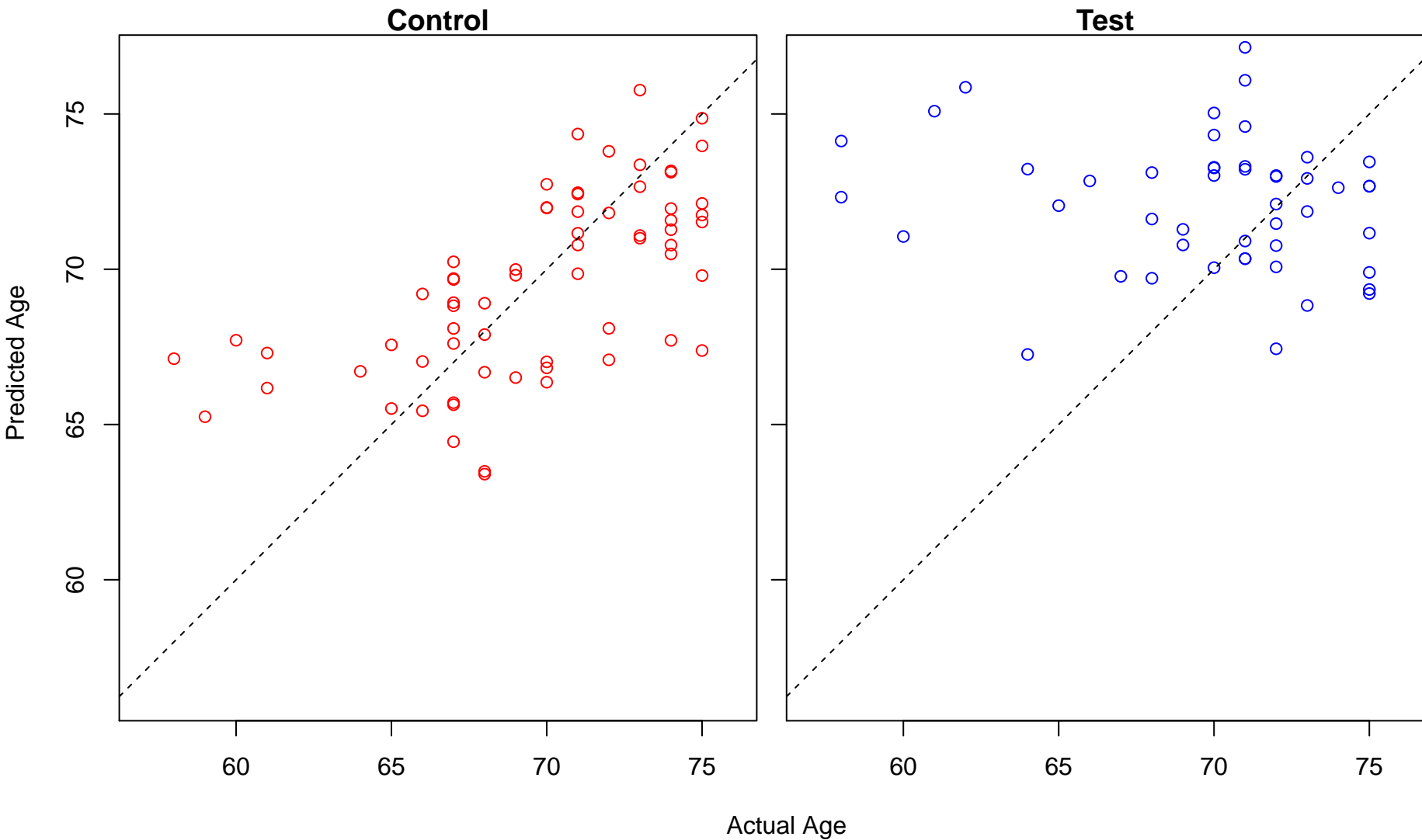
negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage (Score: 1.237)



sensory perception (Score: 1.237786)

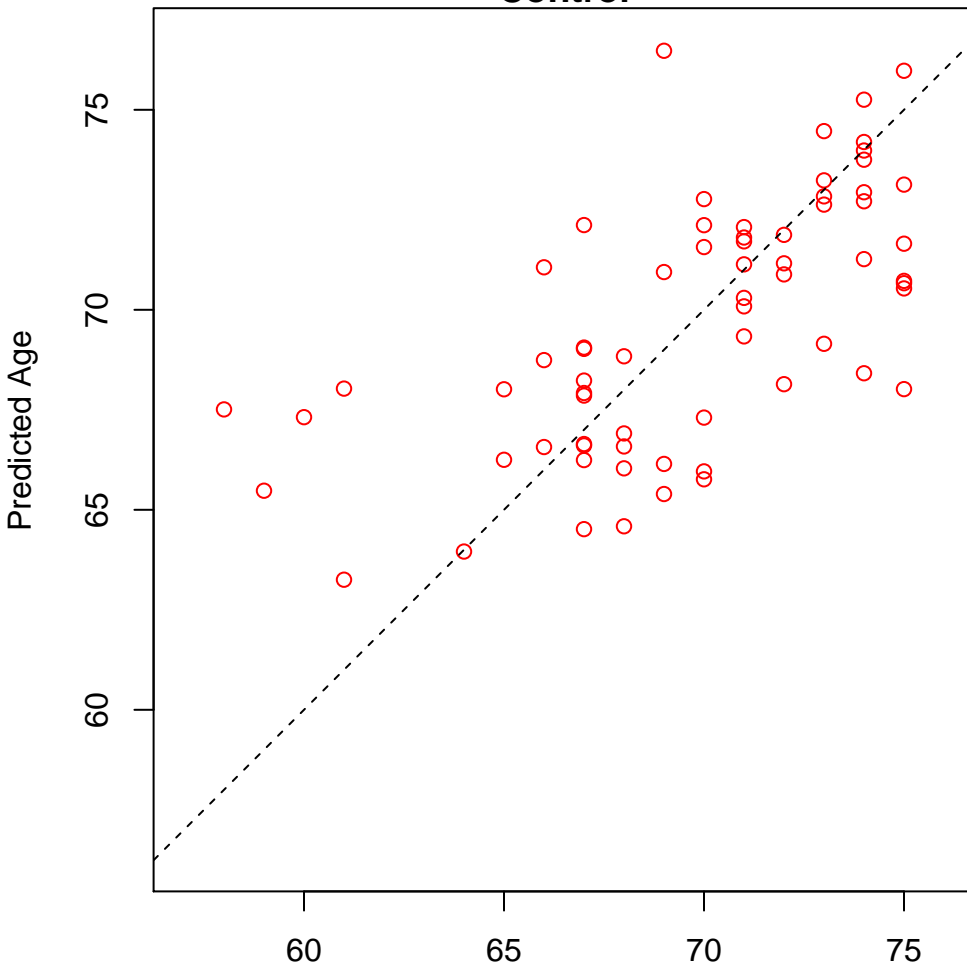


retina homeostasis (Score: 1.237169)

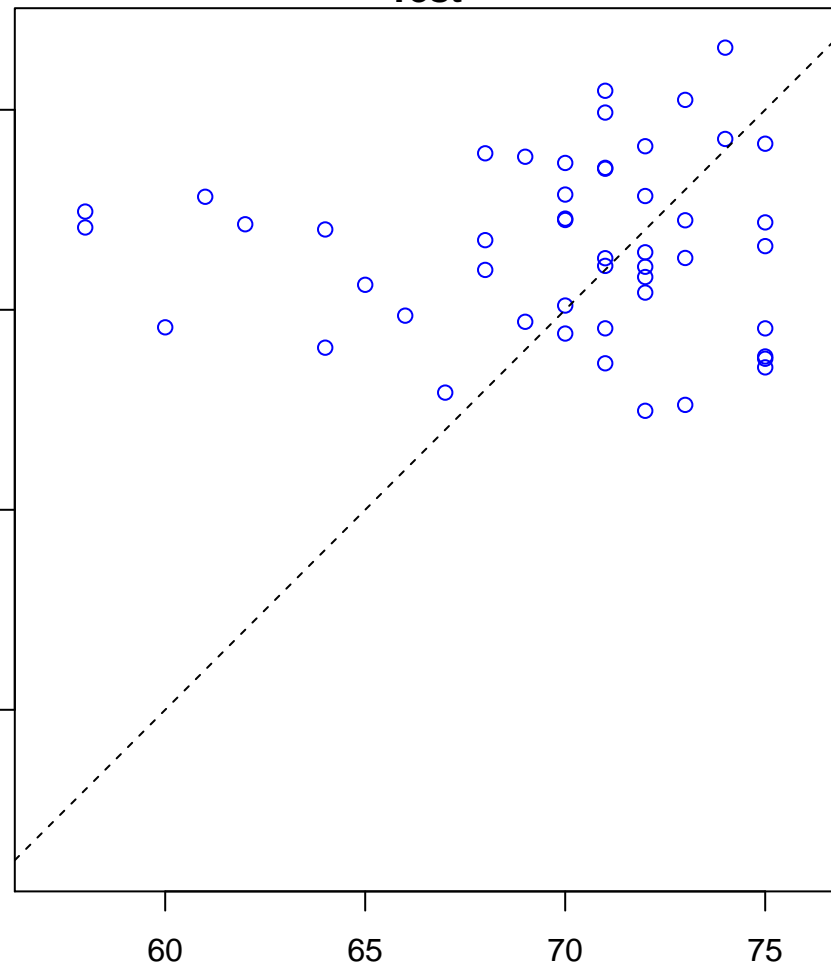


mitochondrial RNA metabolic process (Score: 1.236634)

Control

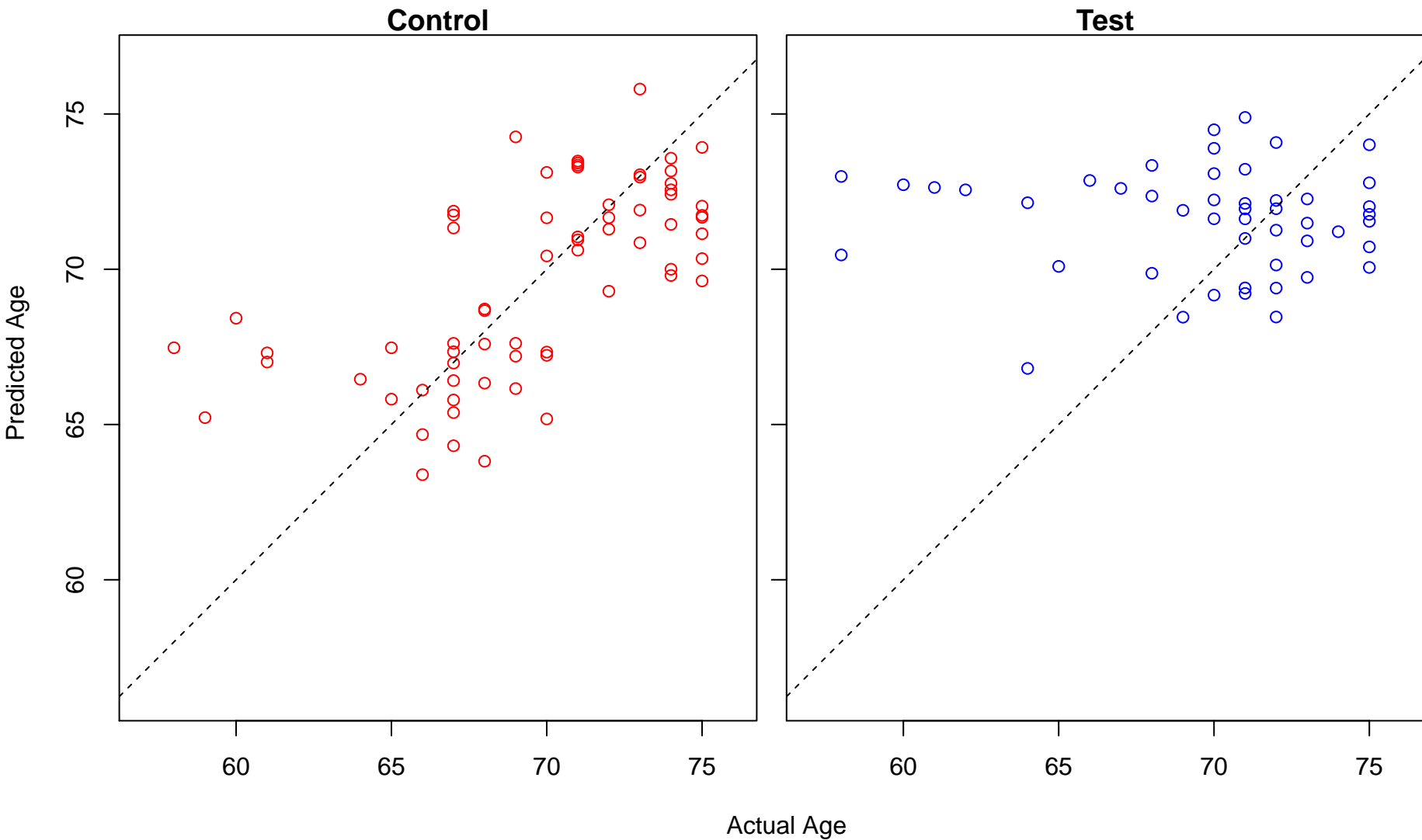


Test

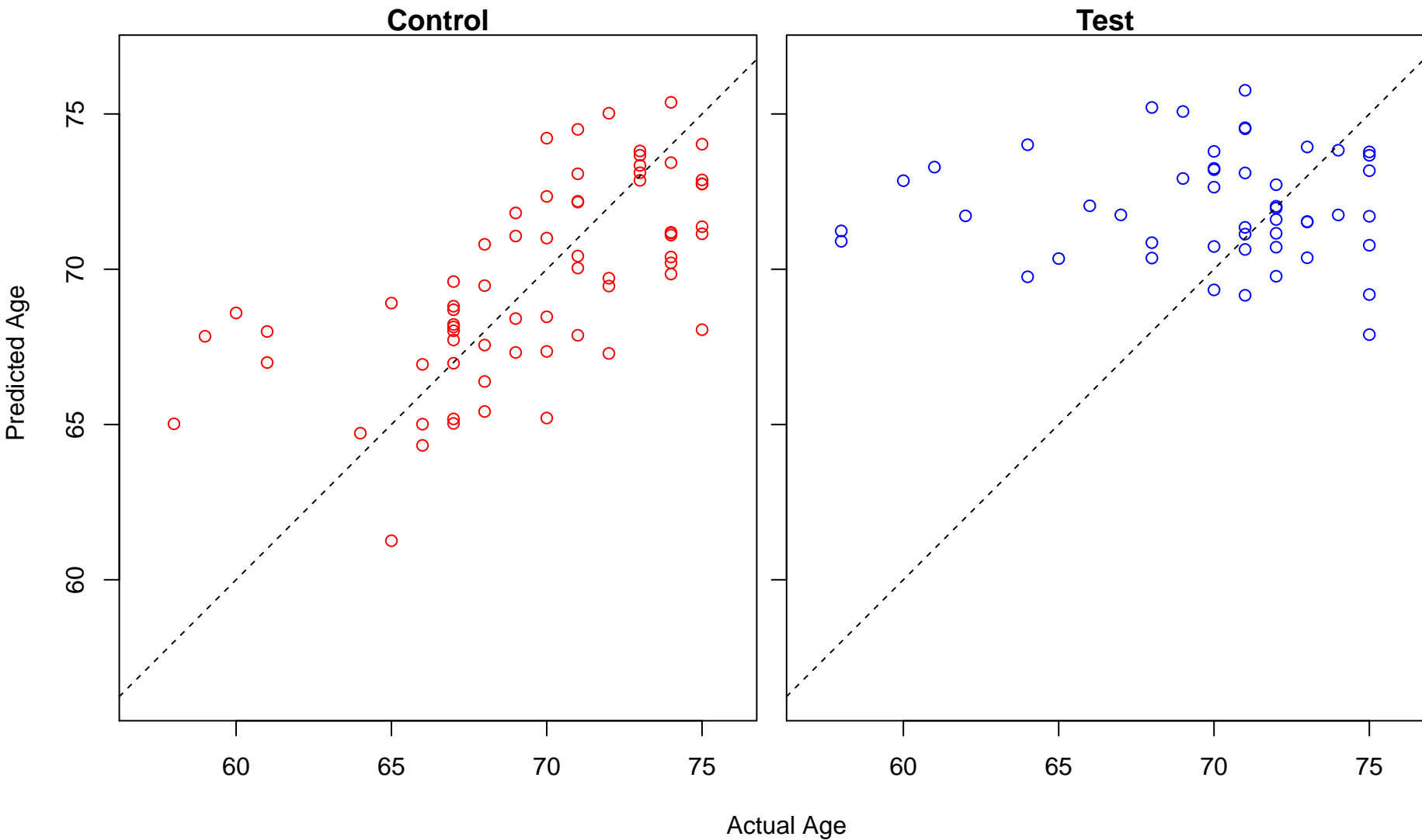


Actual Age

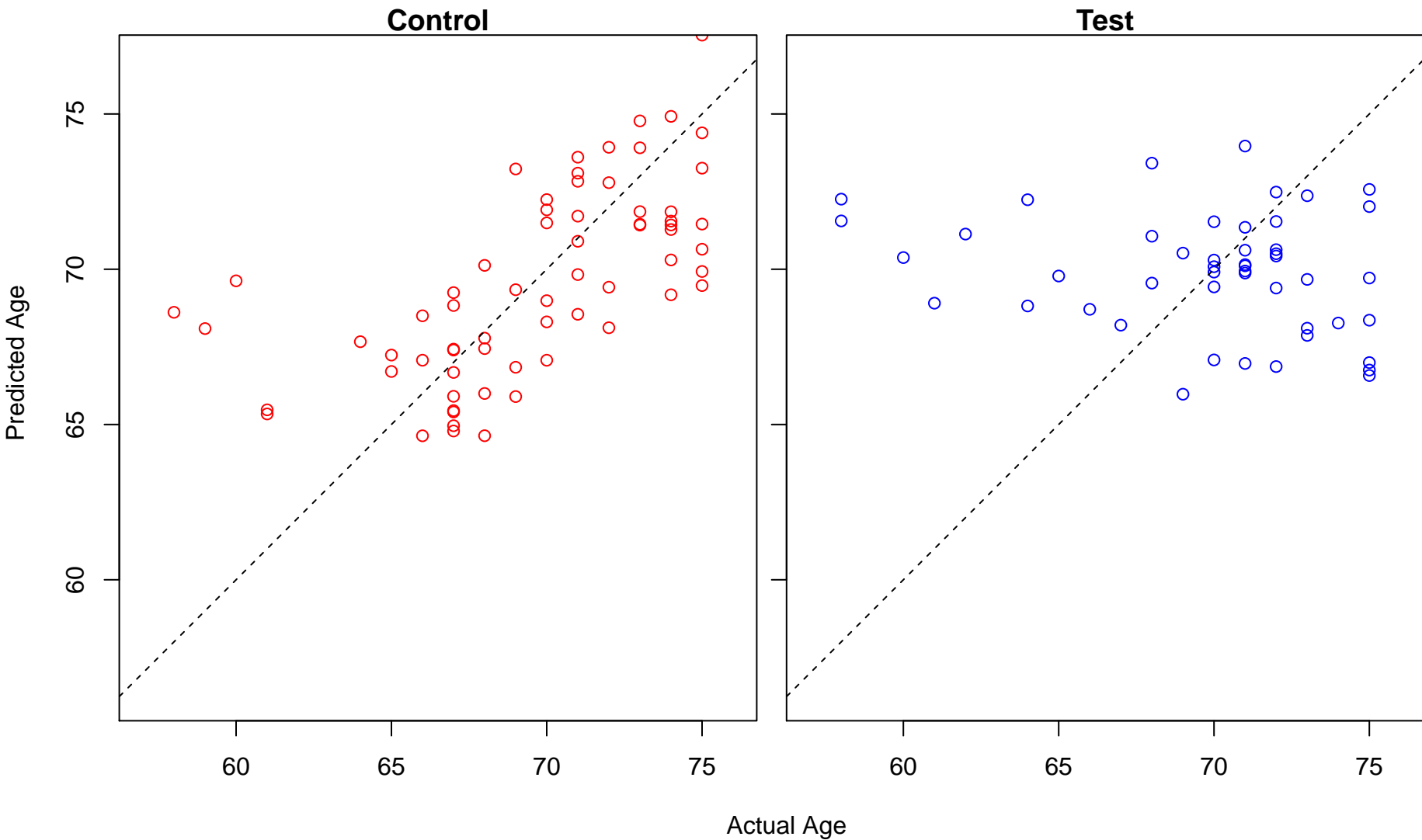
regulation of cell shape (Score: 1.236294)



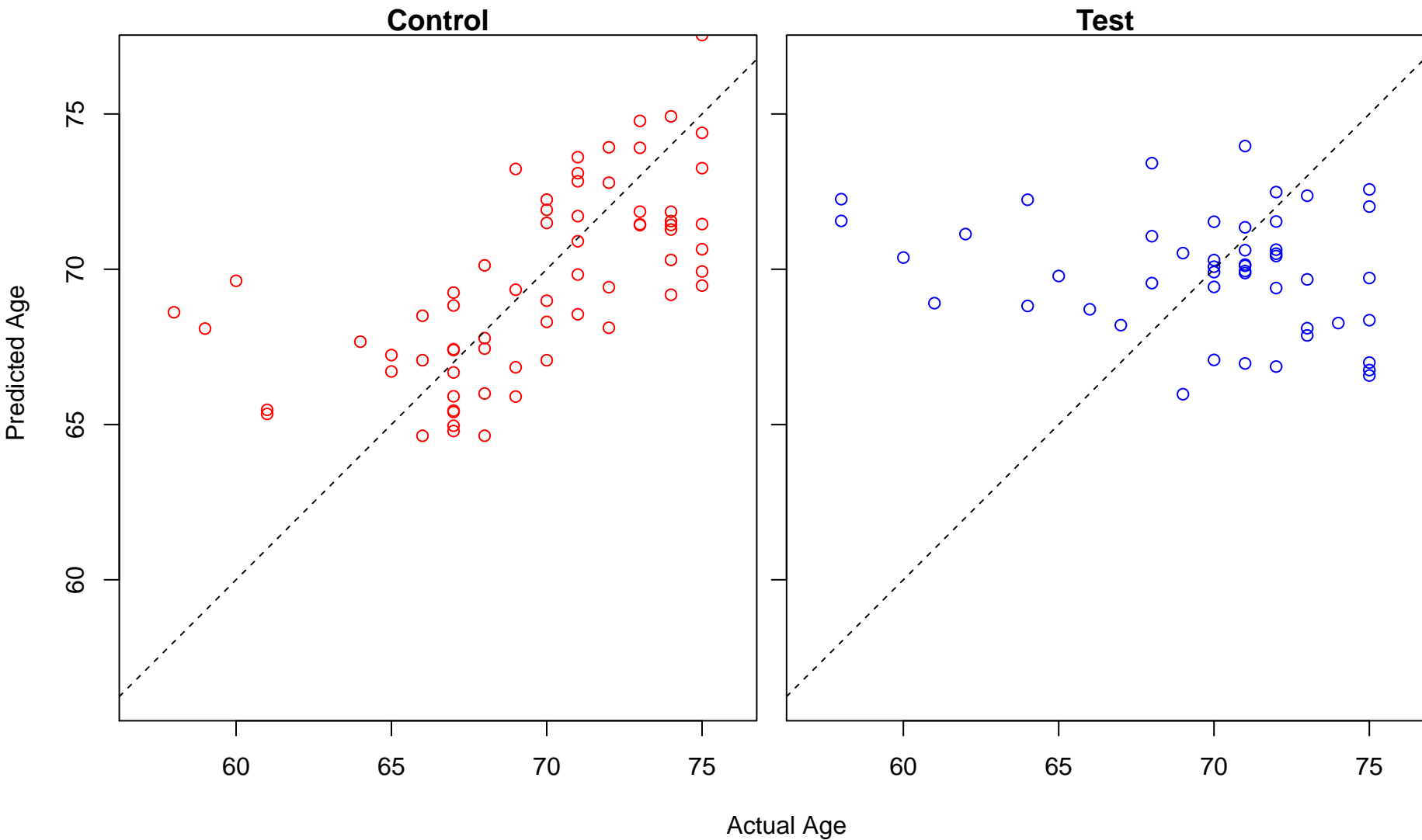
positive regulation of cyclic nucleotide metabolic process (Score: 1.236198)



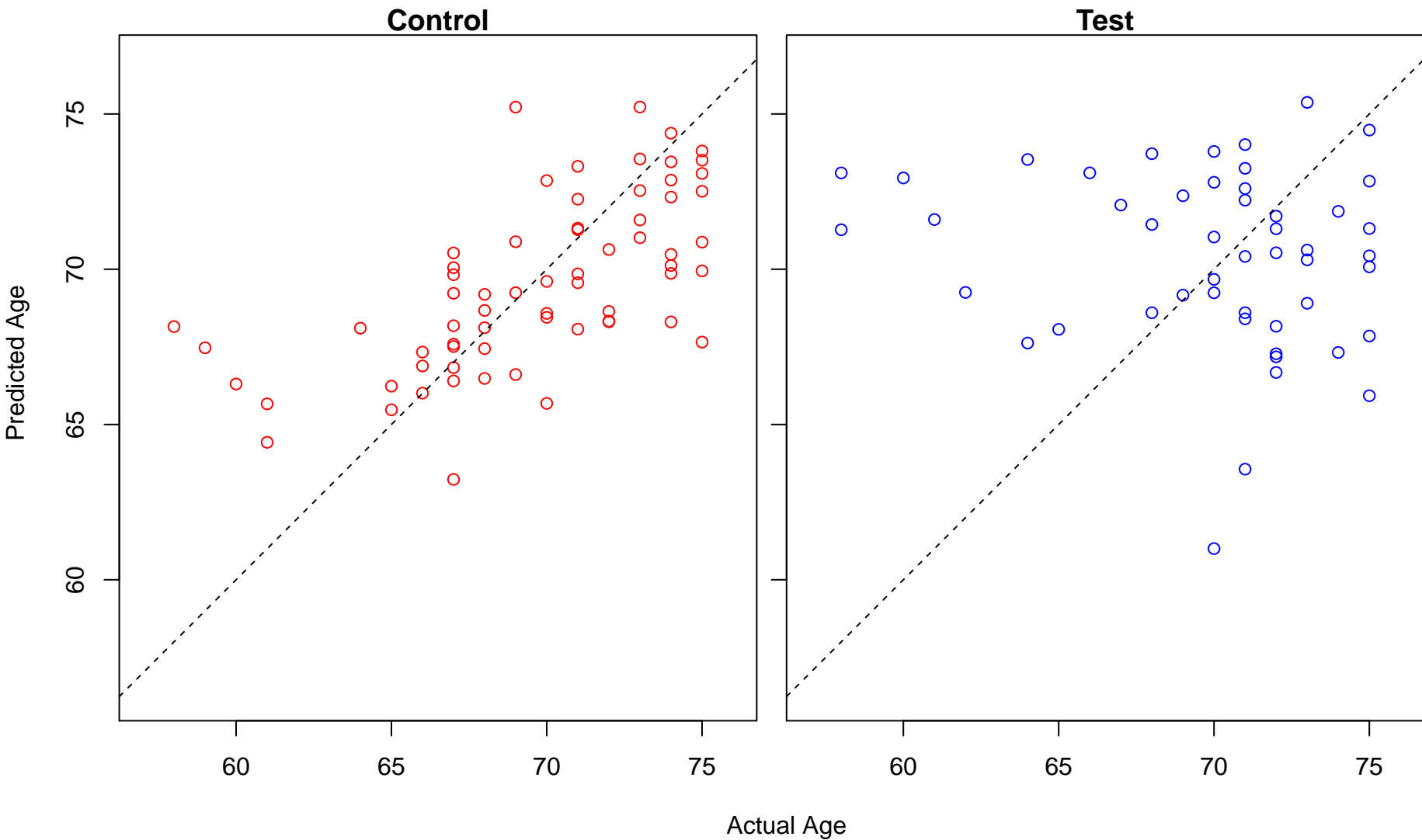
negative regulation of mononuclear cell proliferation (Score: 1.236131)



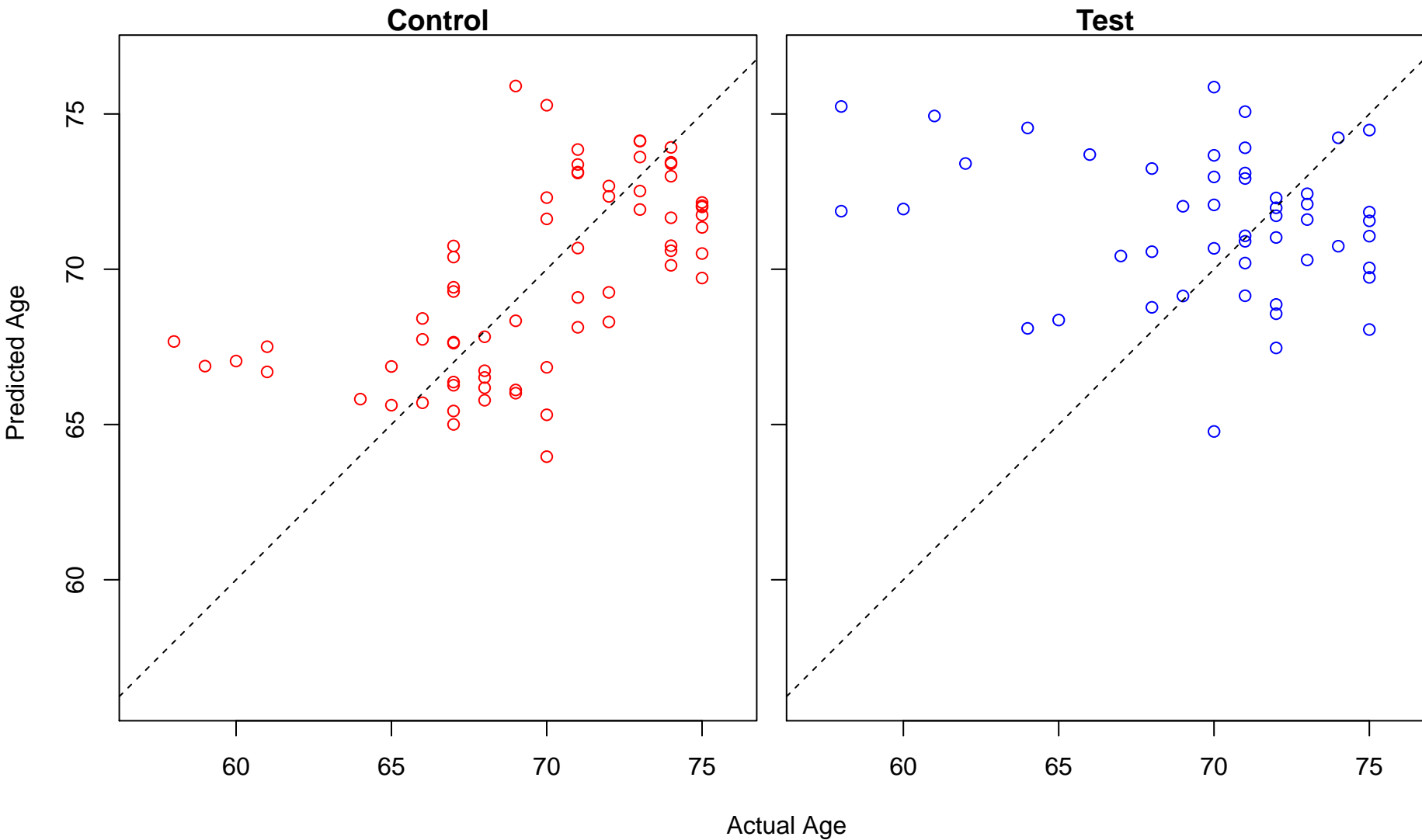
negative regulation of lymphocyte proliferation (Score: 1.236131)



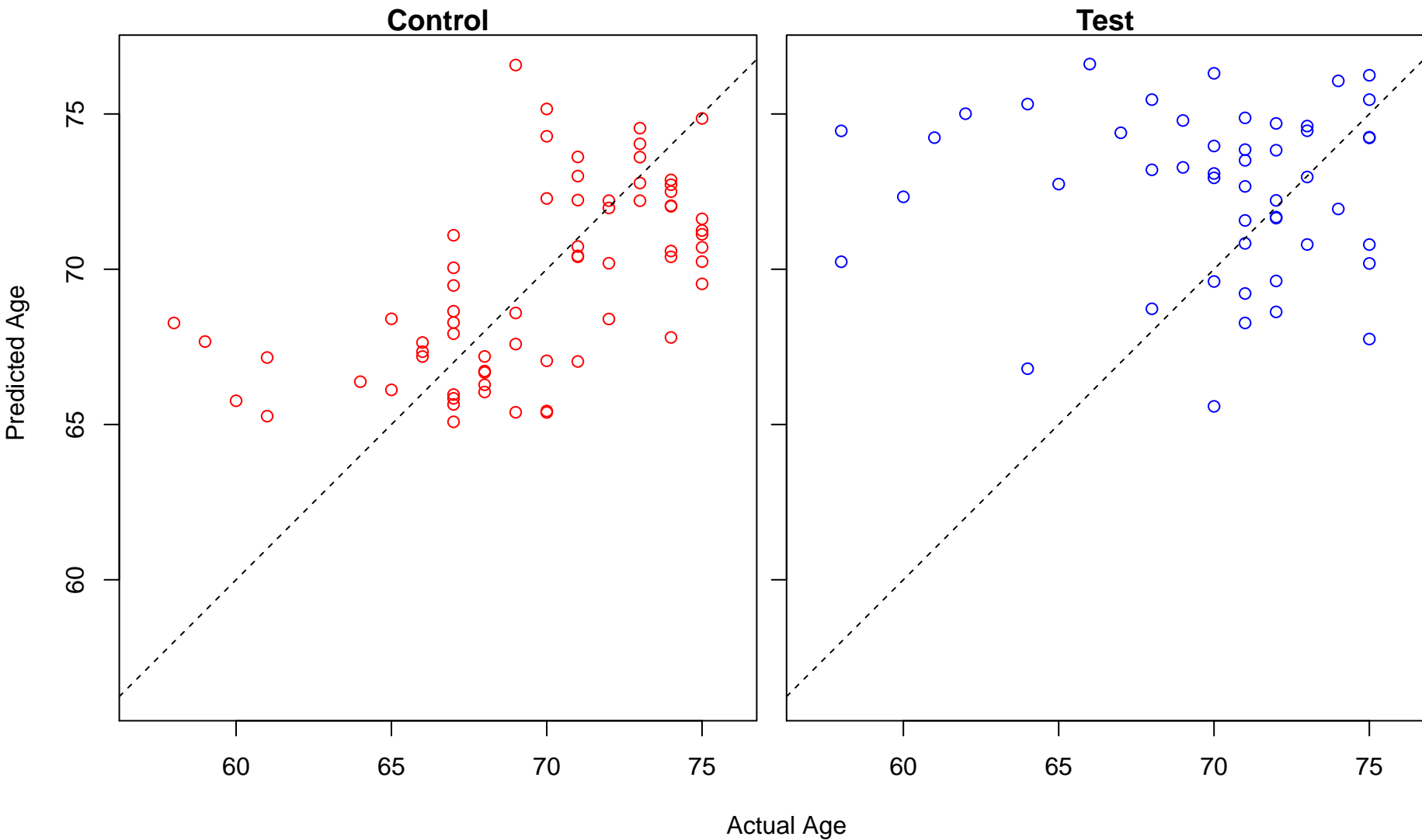
negative regulation of cAMP metabolic process (Score: 1.235681)



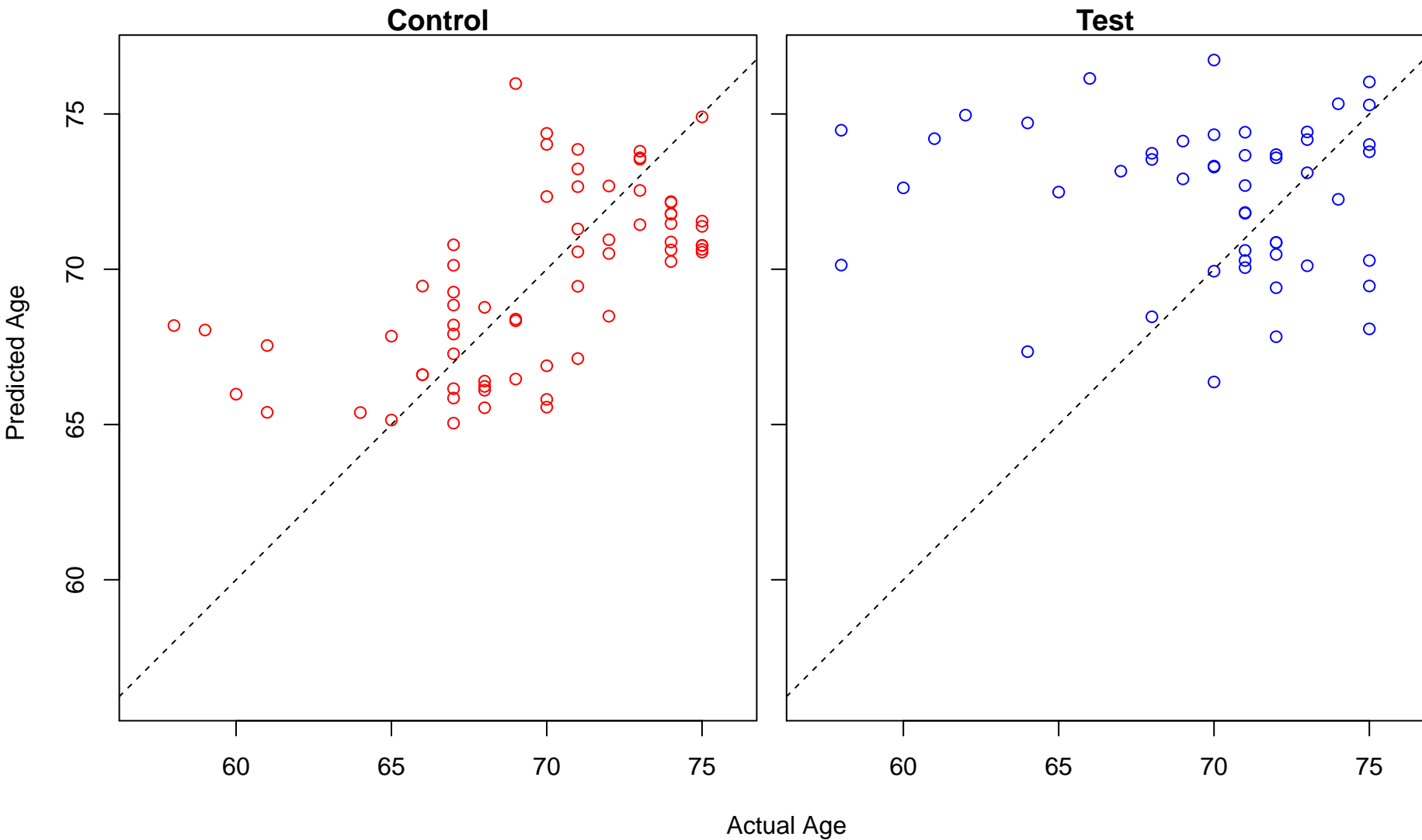
myeloid leukocyte activation (Score: 1.235029)



mismatch repair (Score: 1.234854)

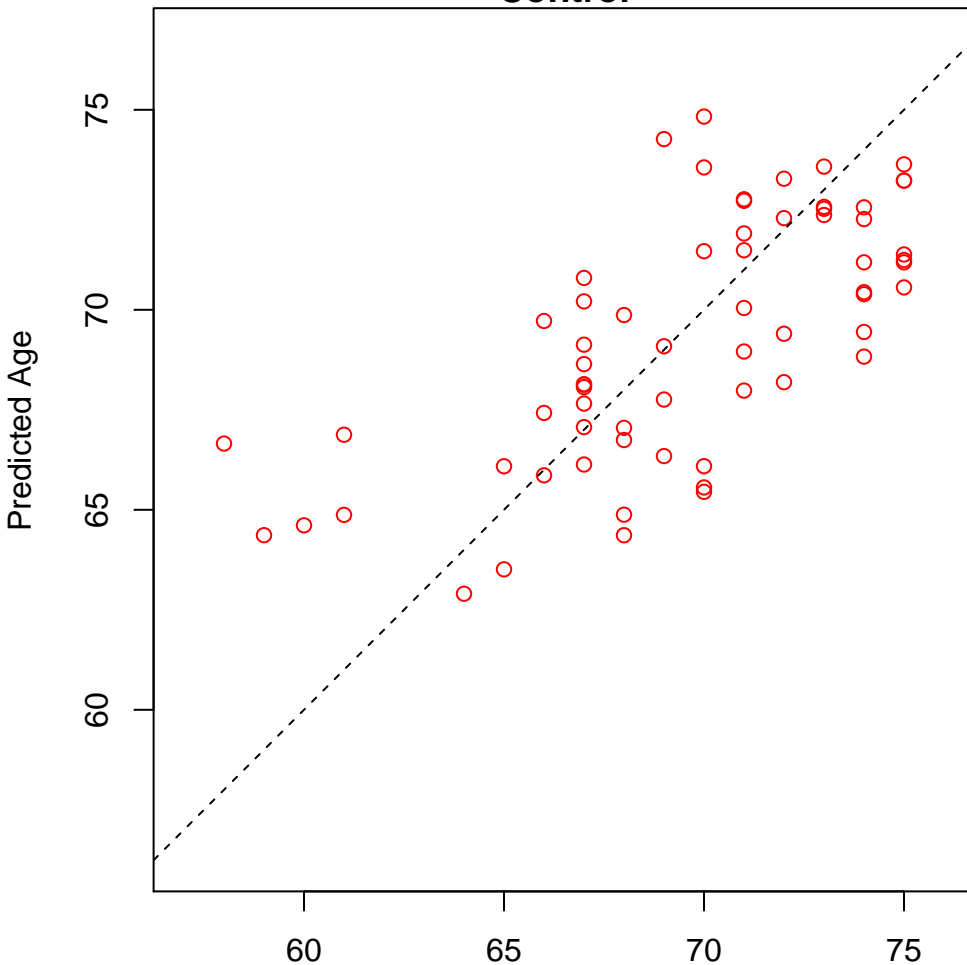


telomere maintenance via semi-conservative replication (Score: 1.234779)

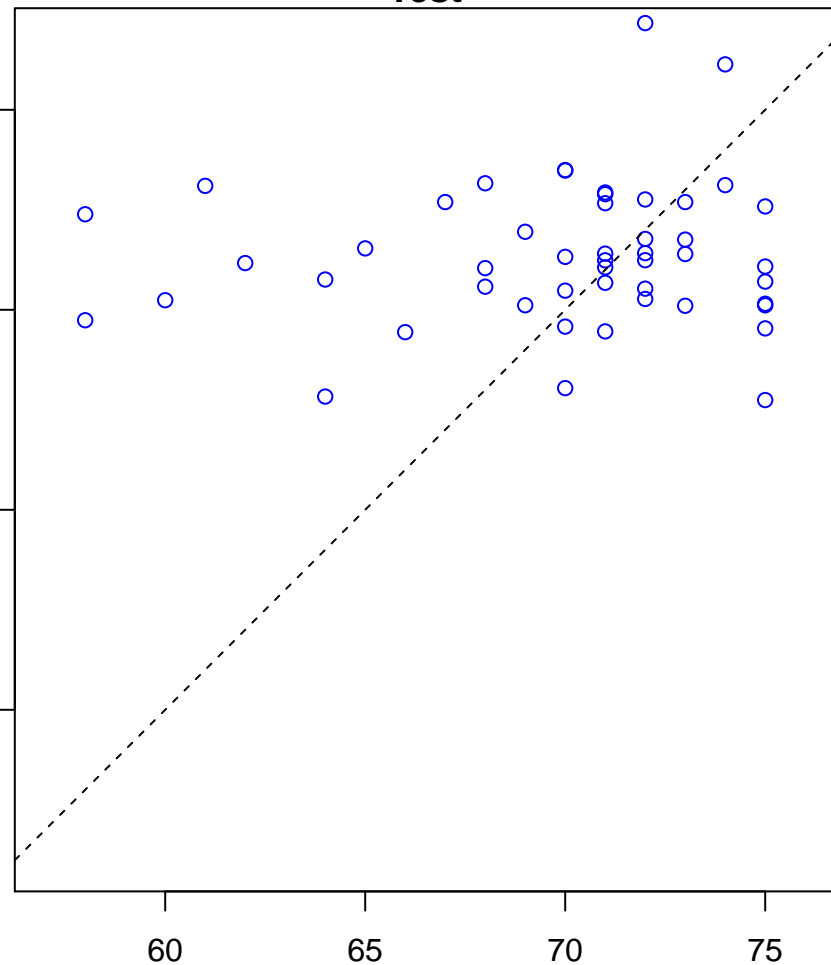


calcium ion transmembrane transport (Score: 1.234552)

Control



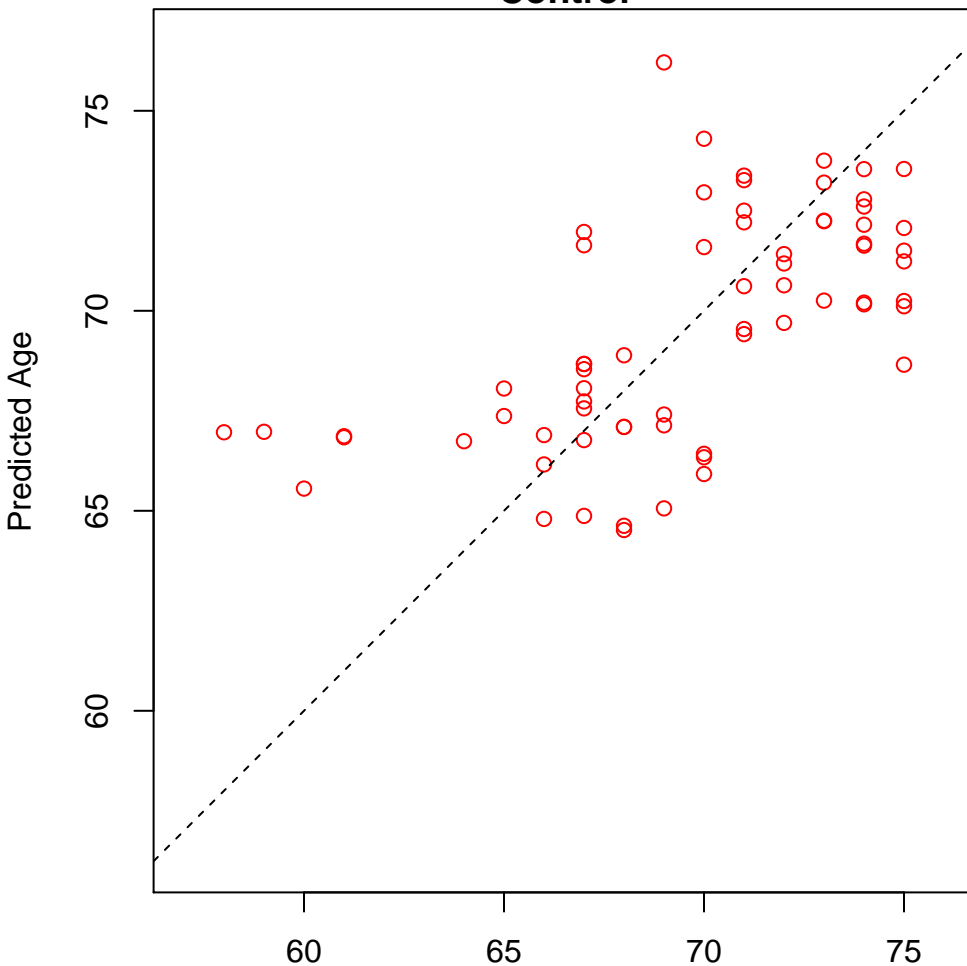
Test



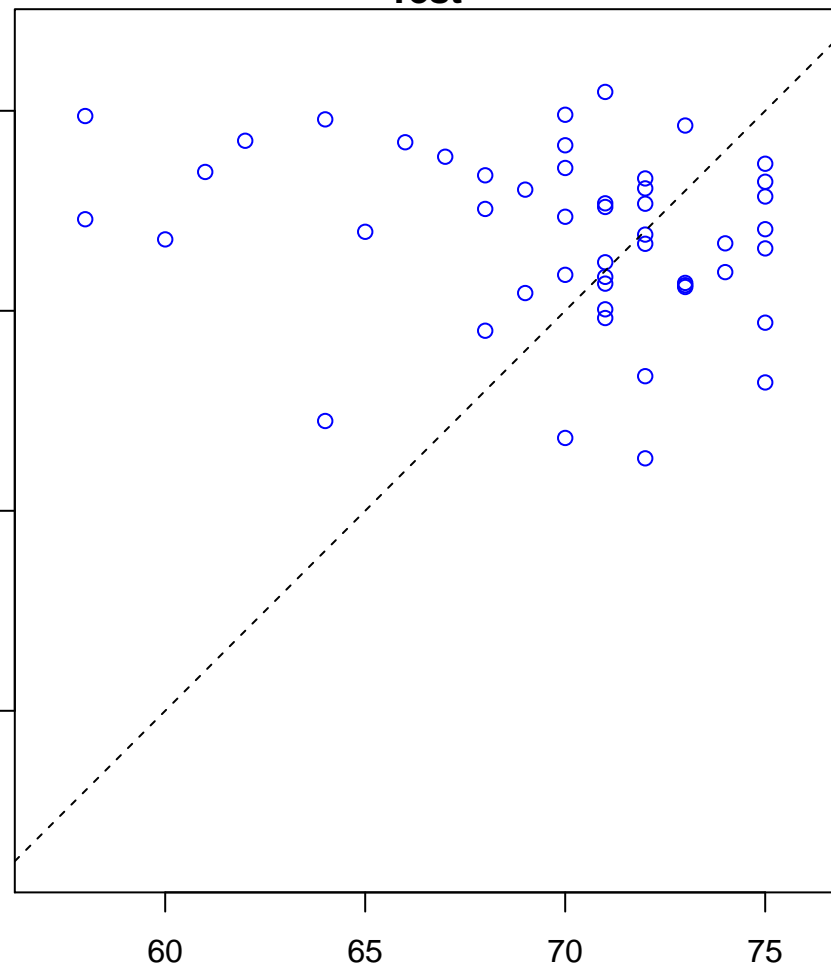
Actual Age

regulation of histone H3-K4 methylation (Score: 1.234275)

Control

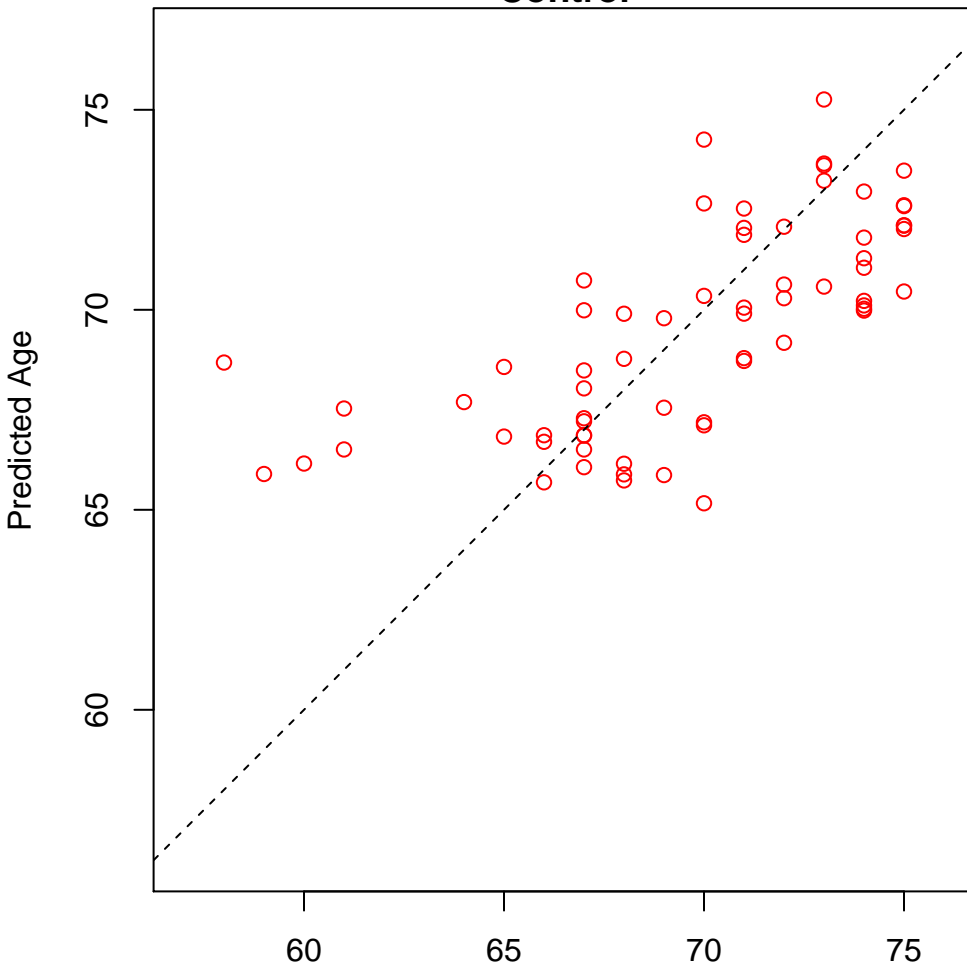


Test

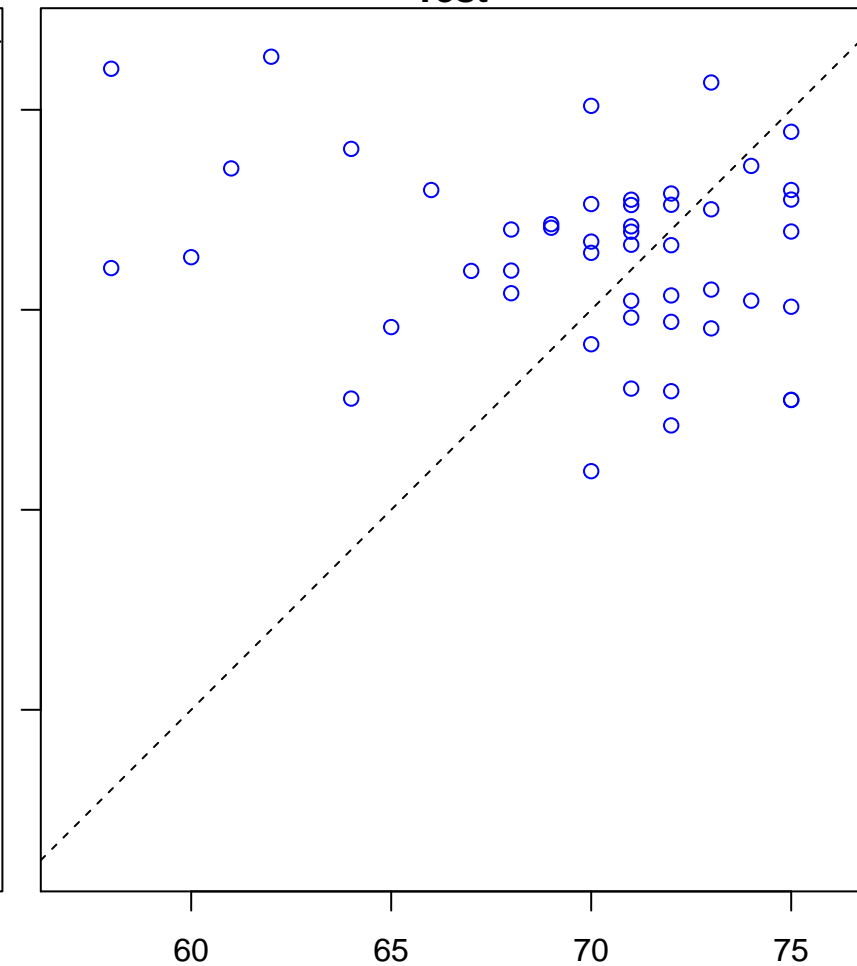


cellular response to estradiol stimulus (Score: 1.233945)

Control

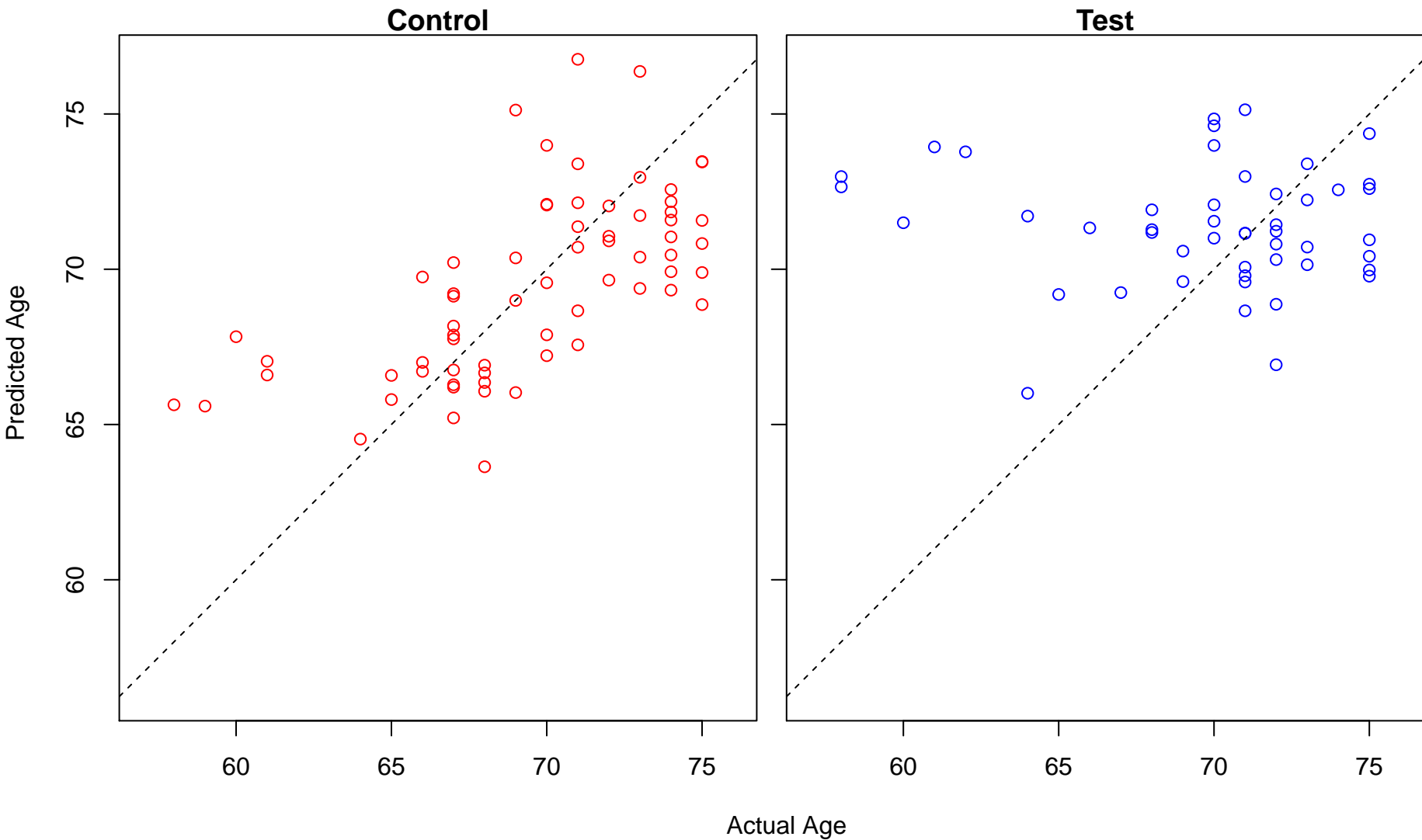


Test

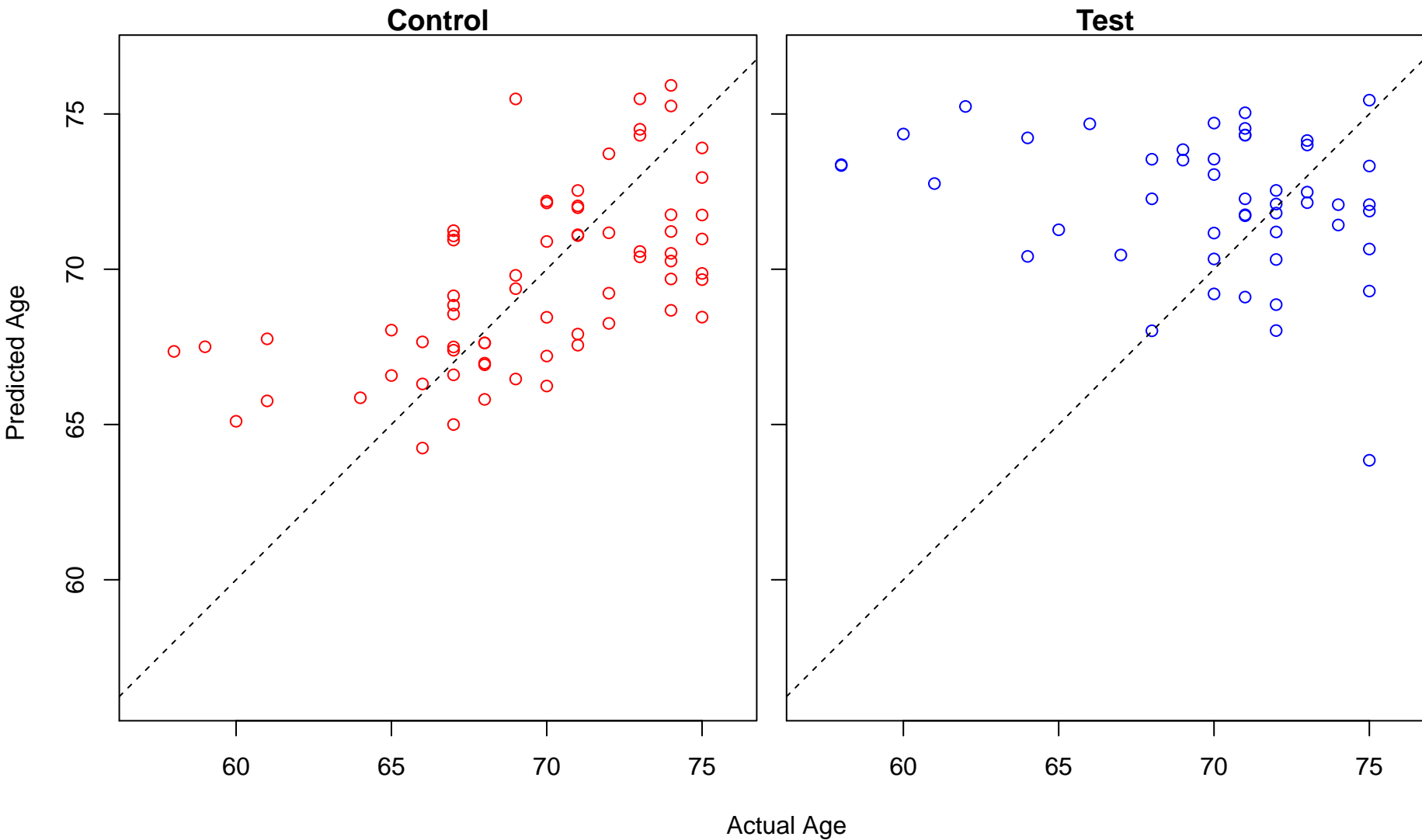


Actual Age

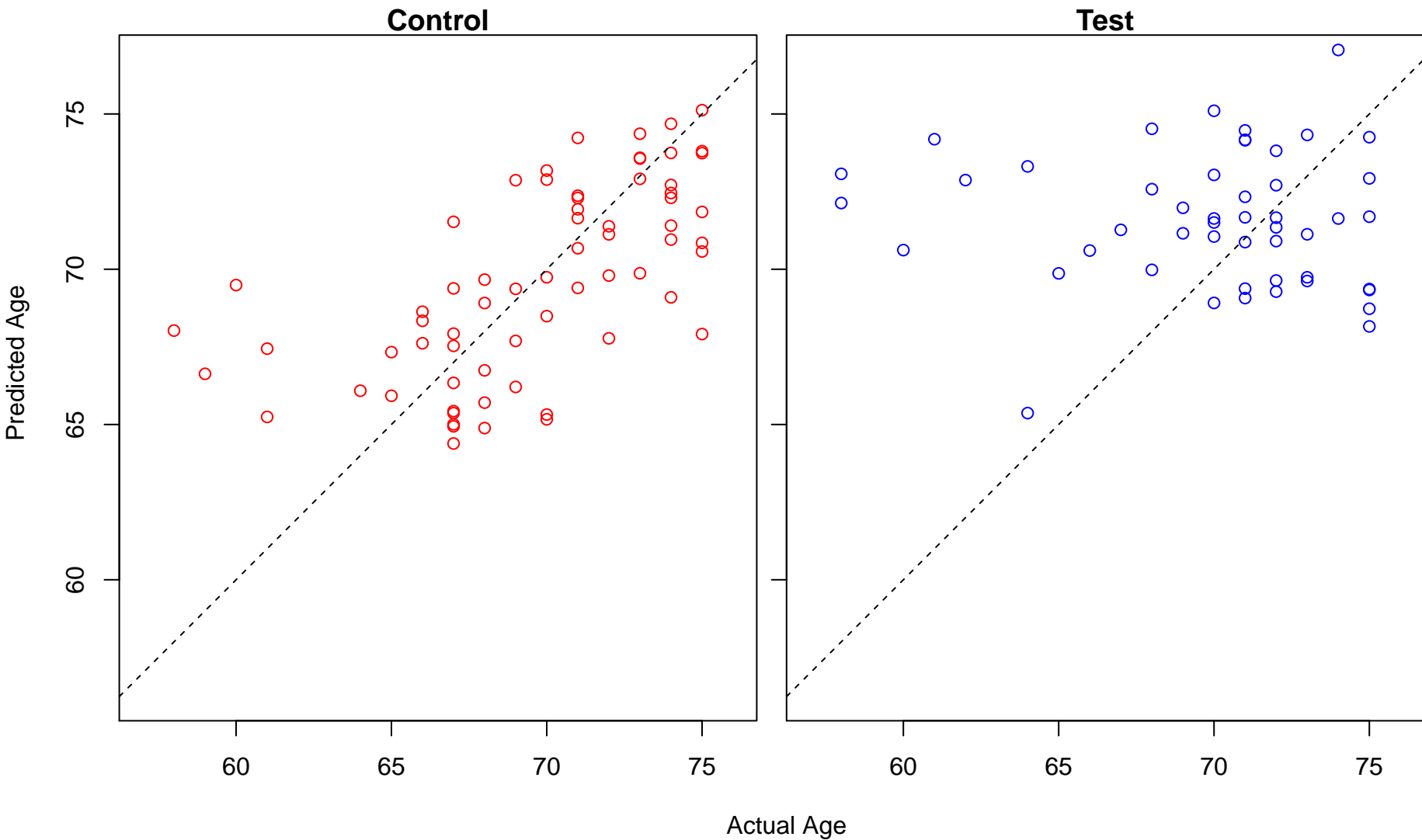
sensory perception of mechanical stimulus (Score: 1.233714)



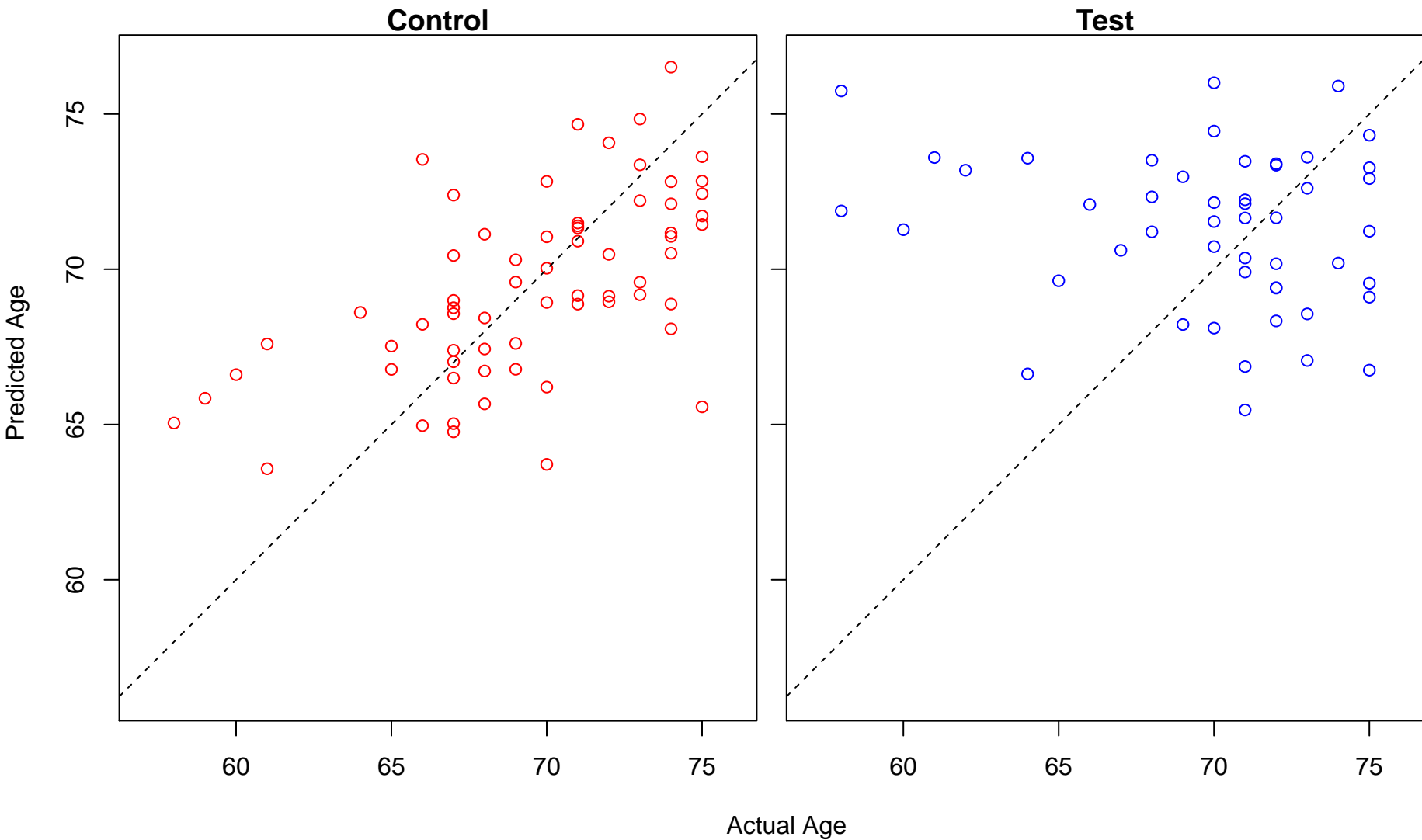
developmental growth (Score: 1.233535)



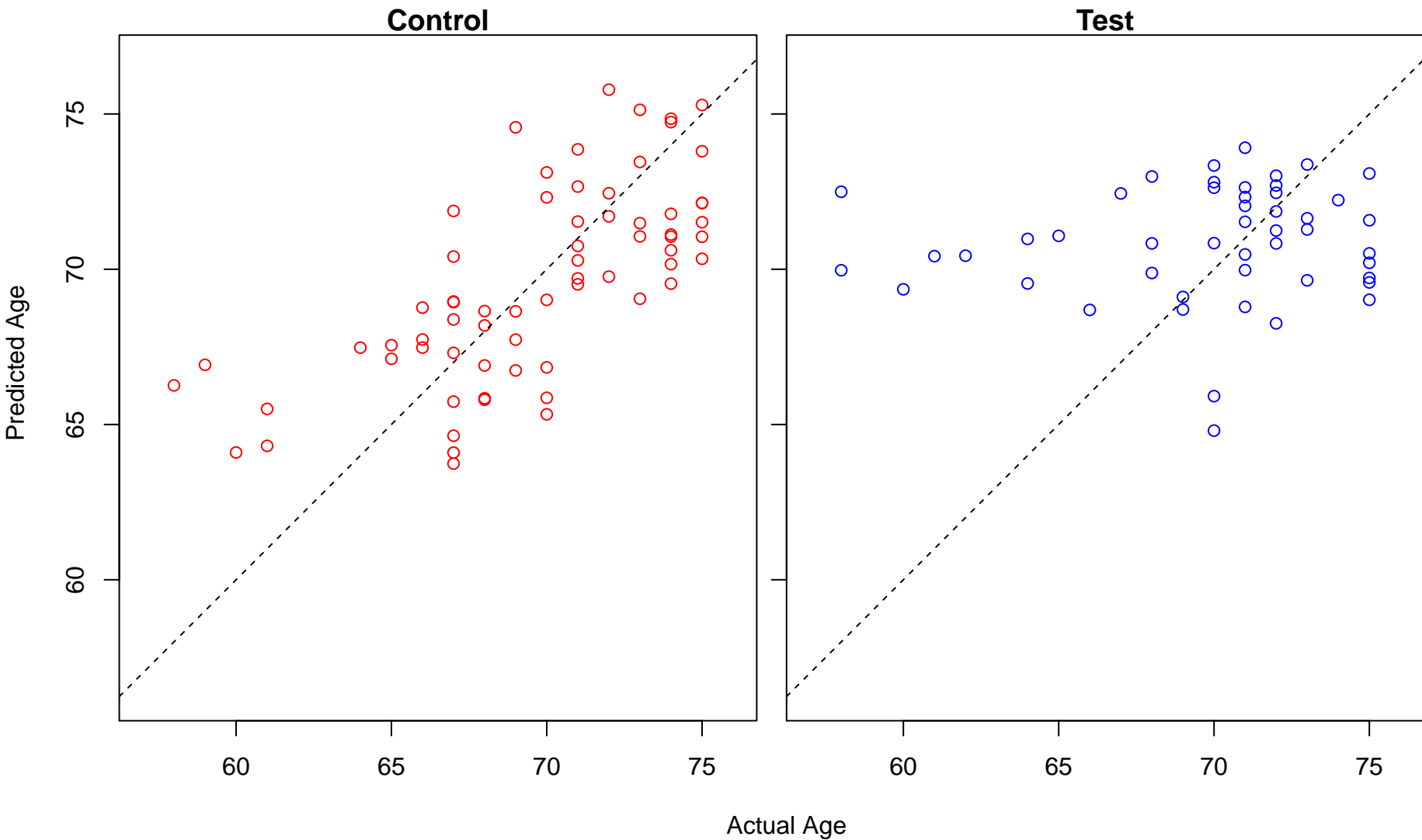
dicarboxylic acid metabolic process (Score: 1.233219)



keratan sulfate metabolic process (Score: 1.233193)

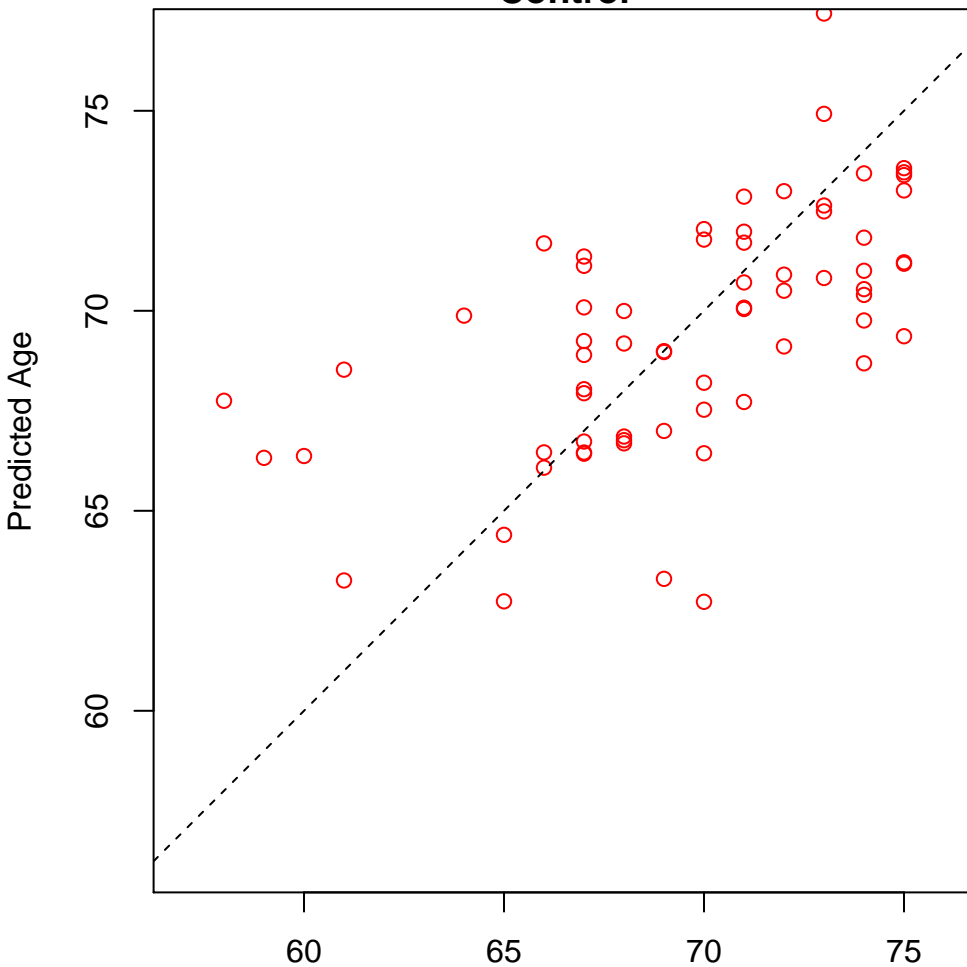


regulation of execution phase of apoptosis (Score: 1.232817)

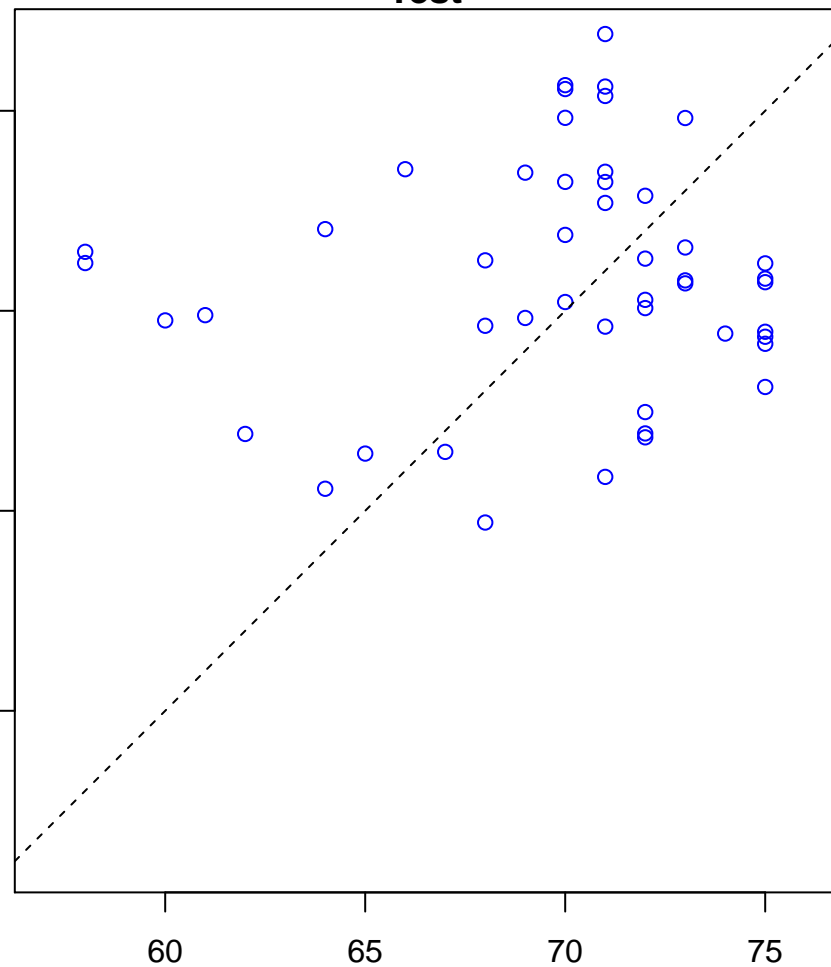


negative regulation of blood coagulation (Score: 1.231809)

Control

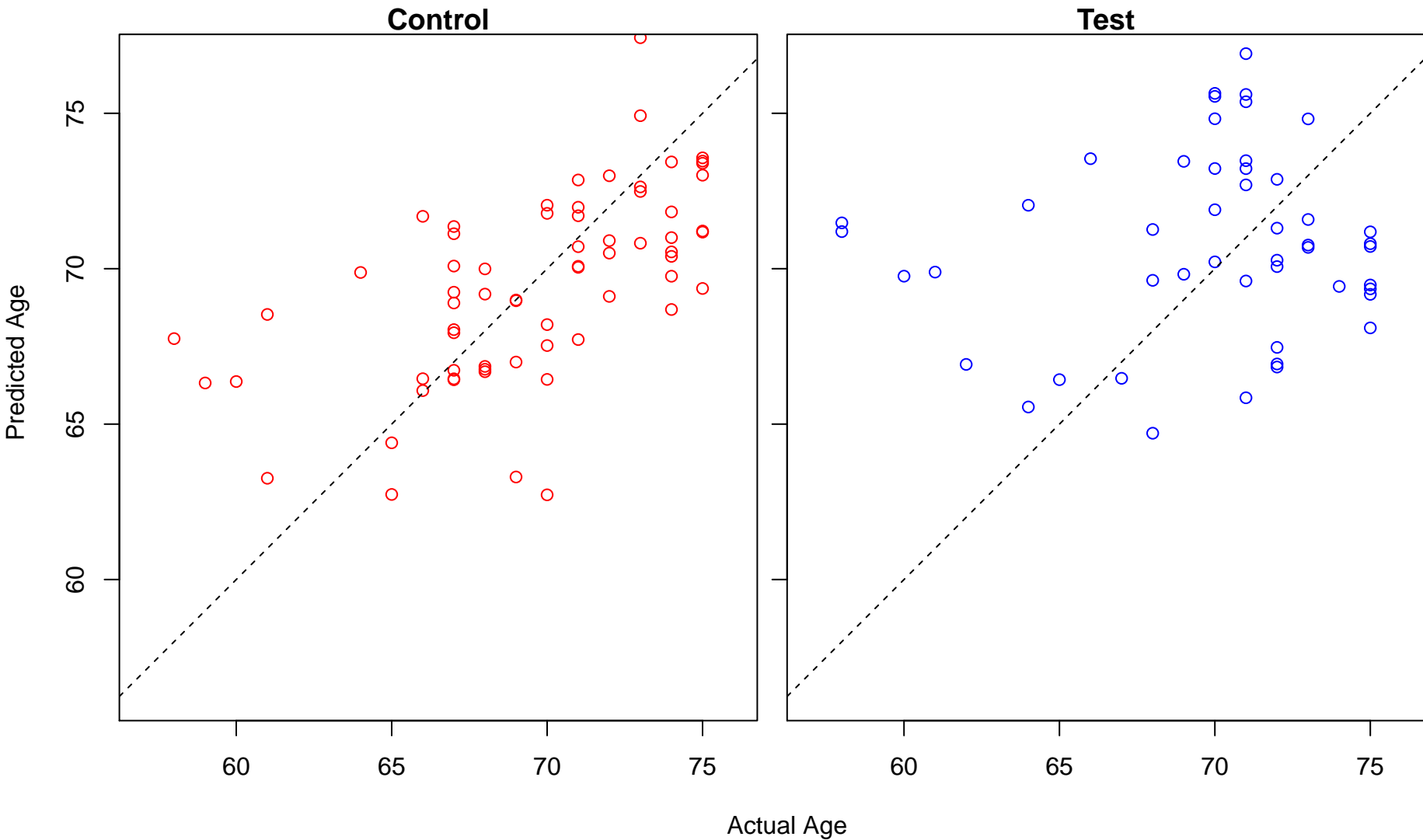


Test

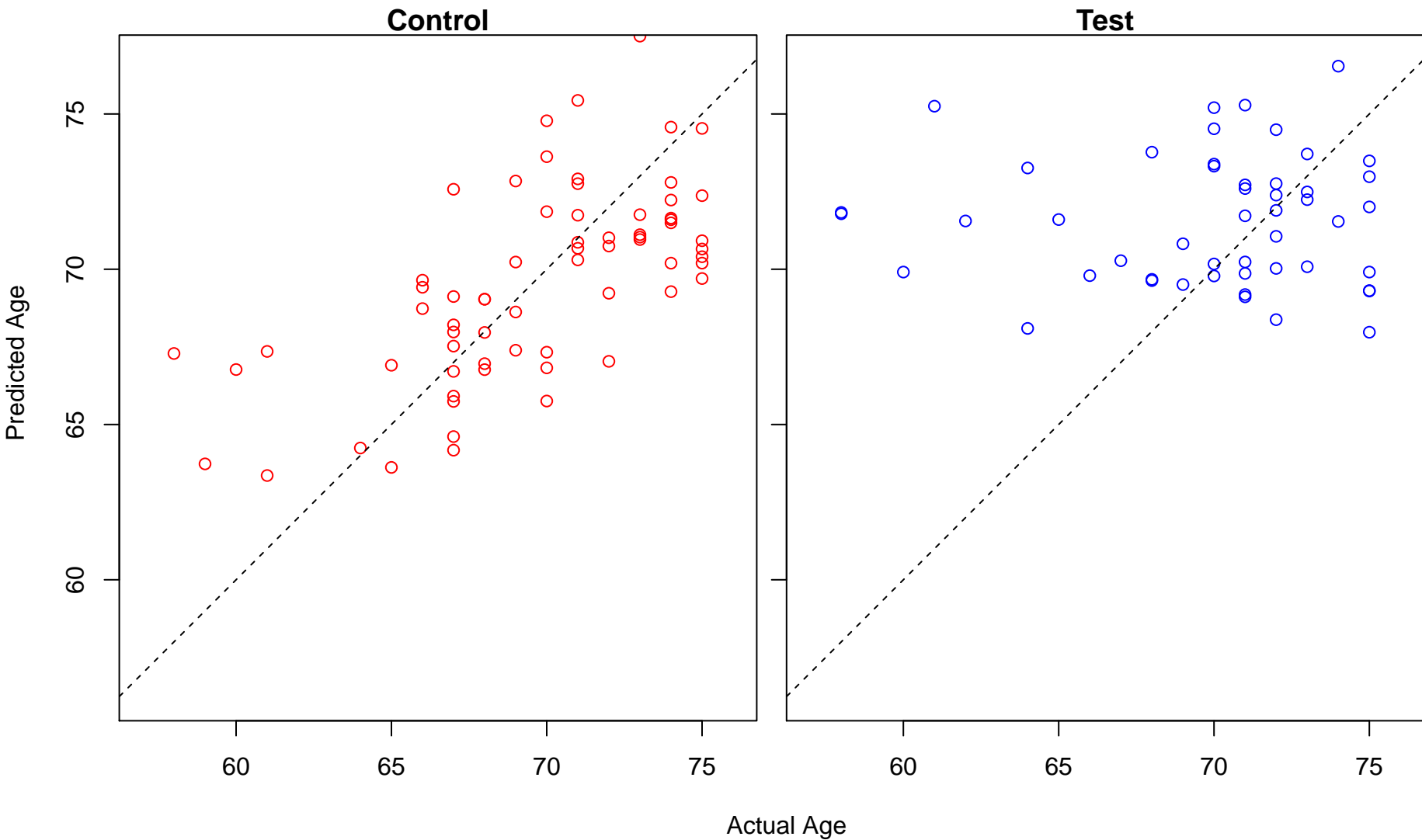


Actual Age

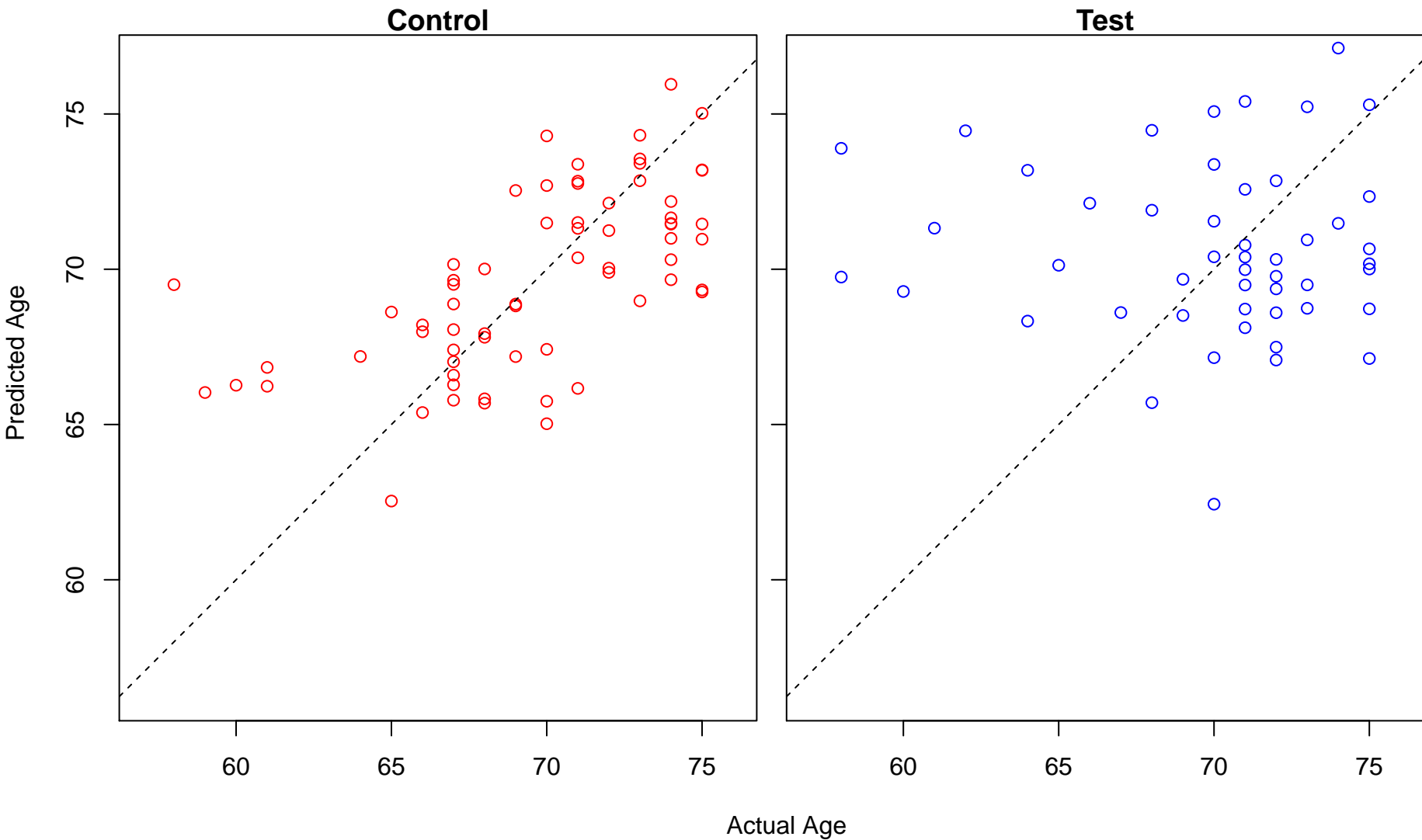
negative regulation of hemostasis (Score: 1.231809)



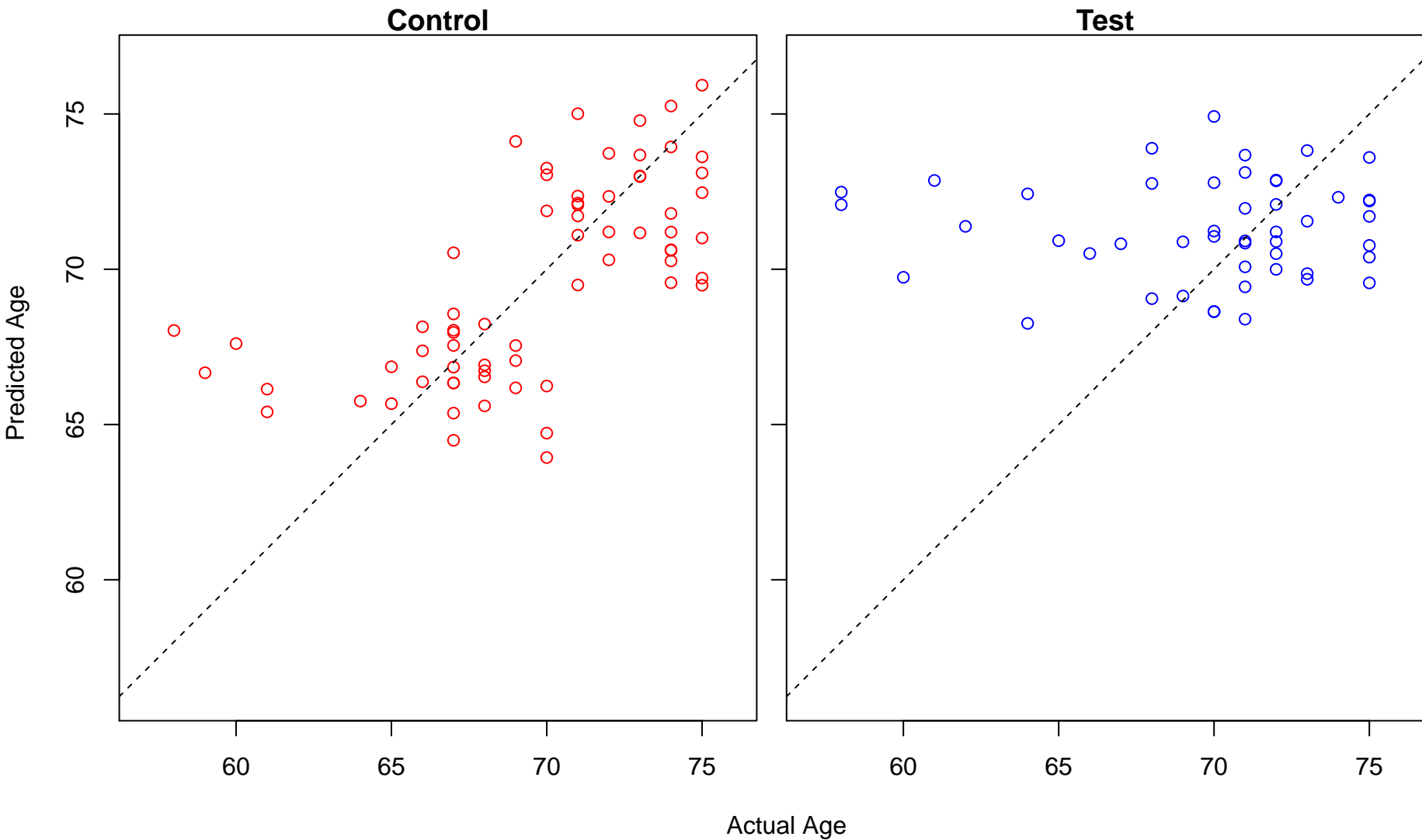
negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator (Score: 1.231710)



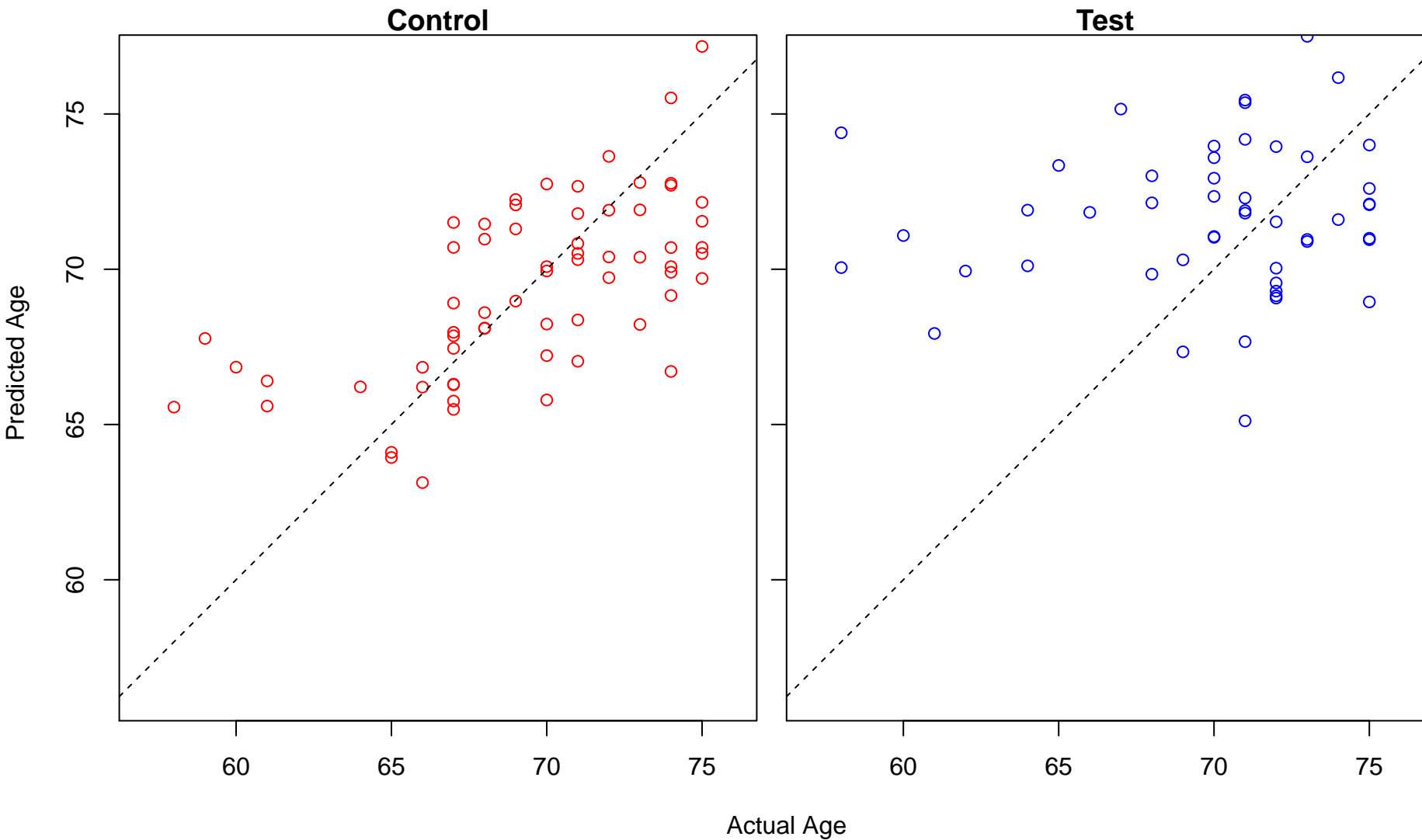
regulation of calcium ion transmembrane transport (Score: 1.231326)



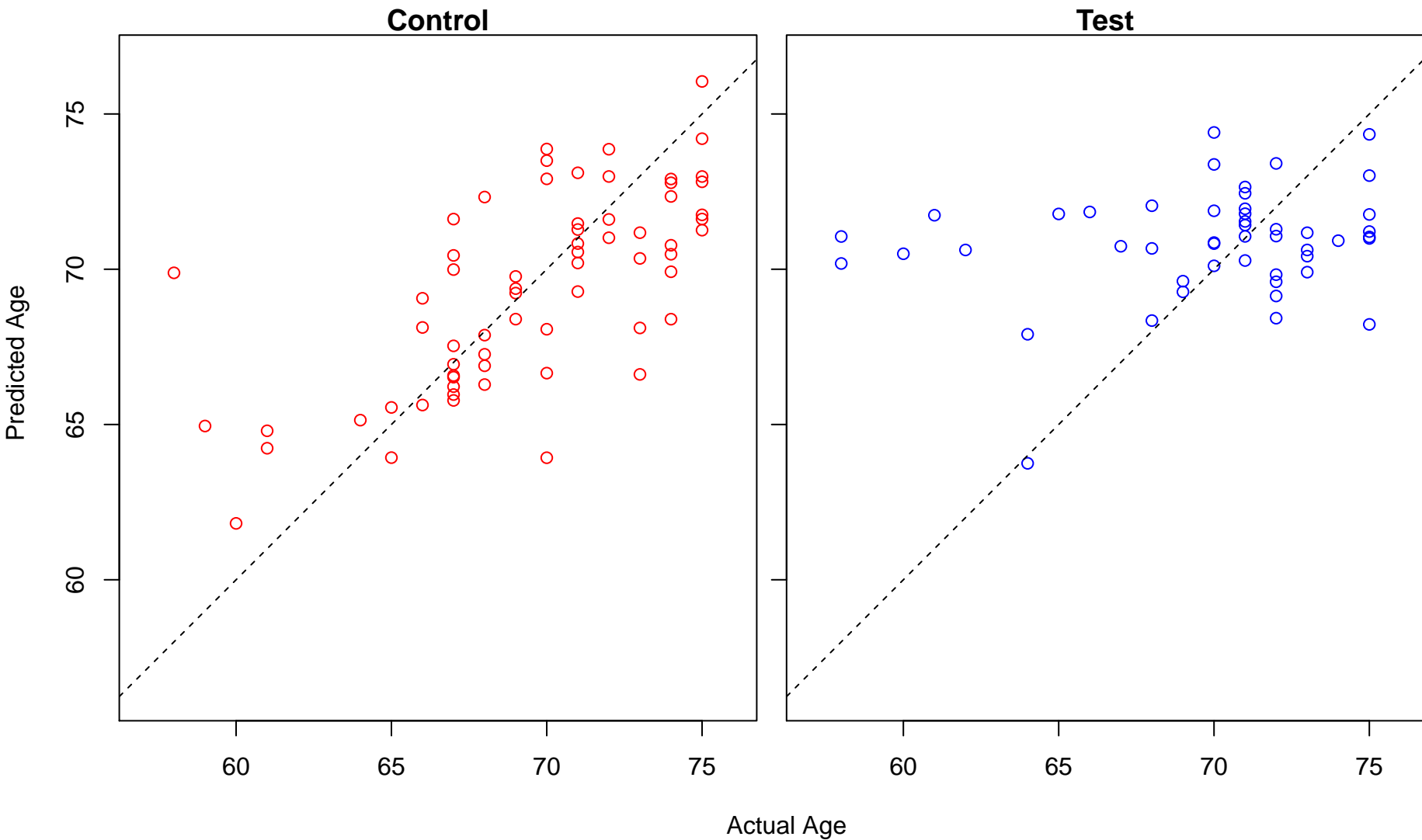
regulation of dephosphorylation (Score: 1.231264)



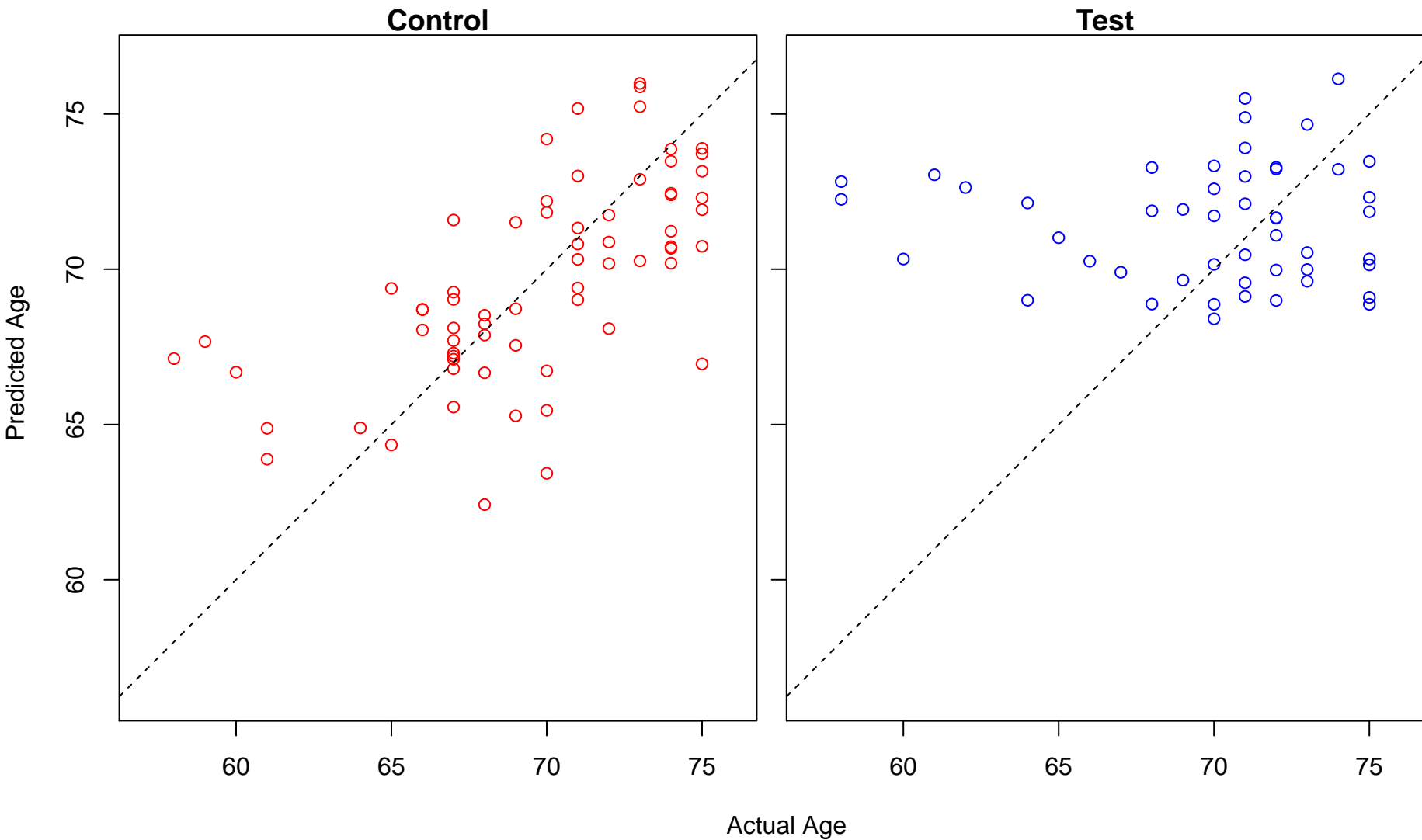
negative regulation of viral release from host cell (Score: 1.231107)



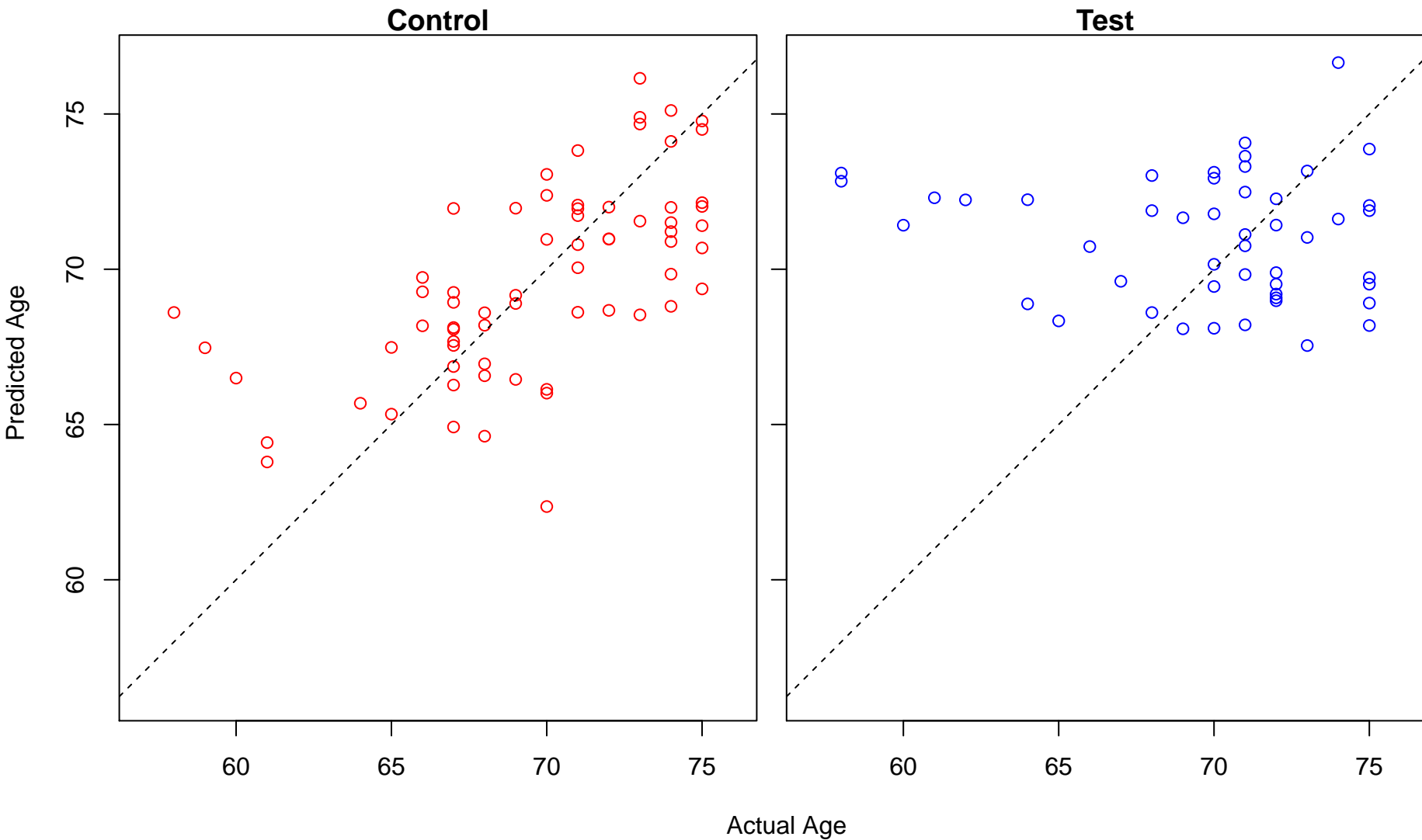
integrin-mediated signaling pathway (Score: 1.230590)



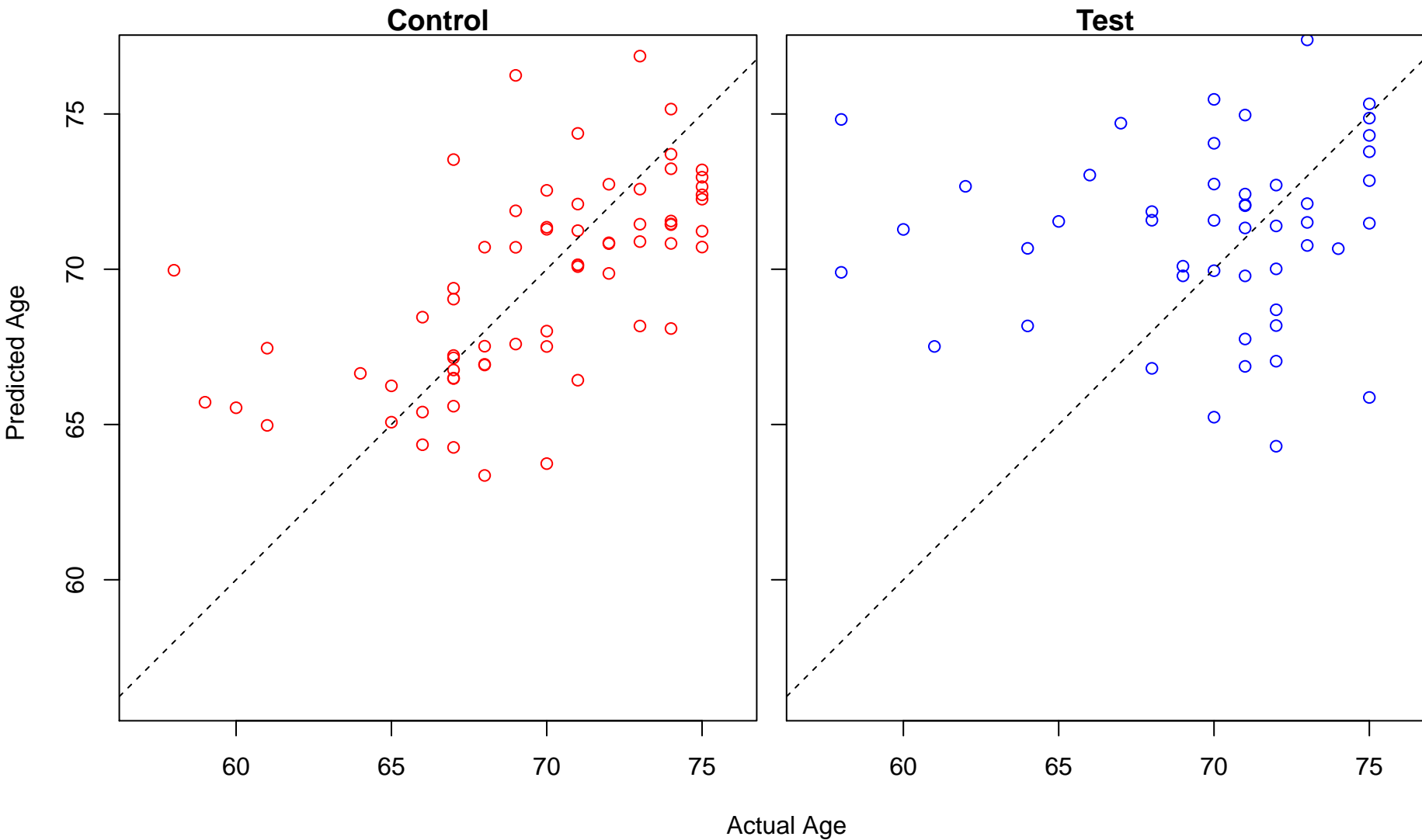
negative regulation of protein complex assembly (Score: 1.230366)



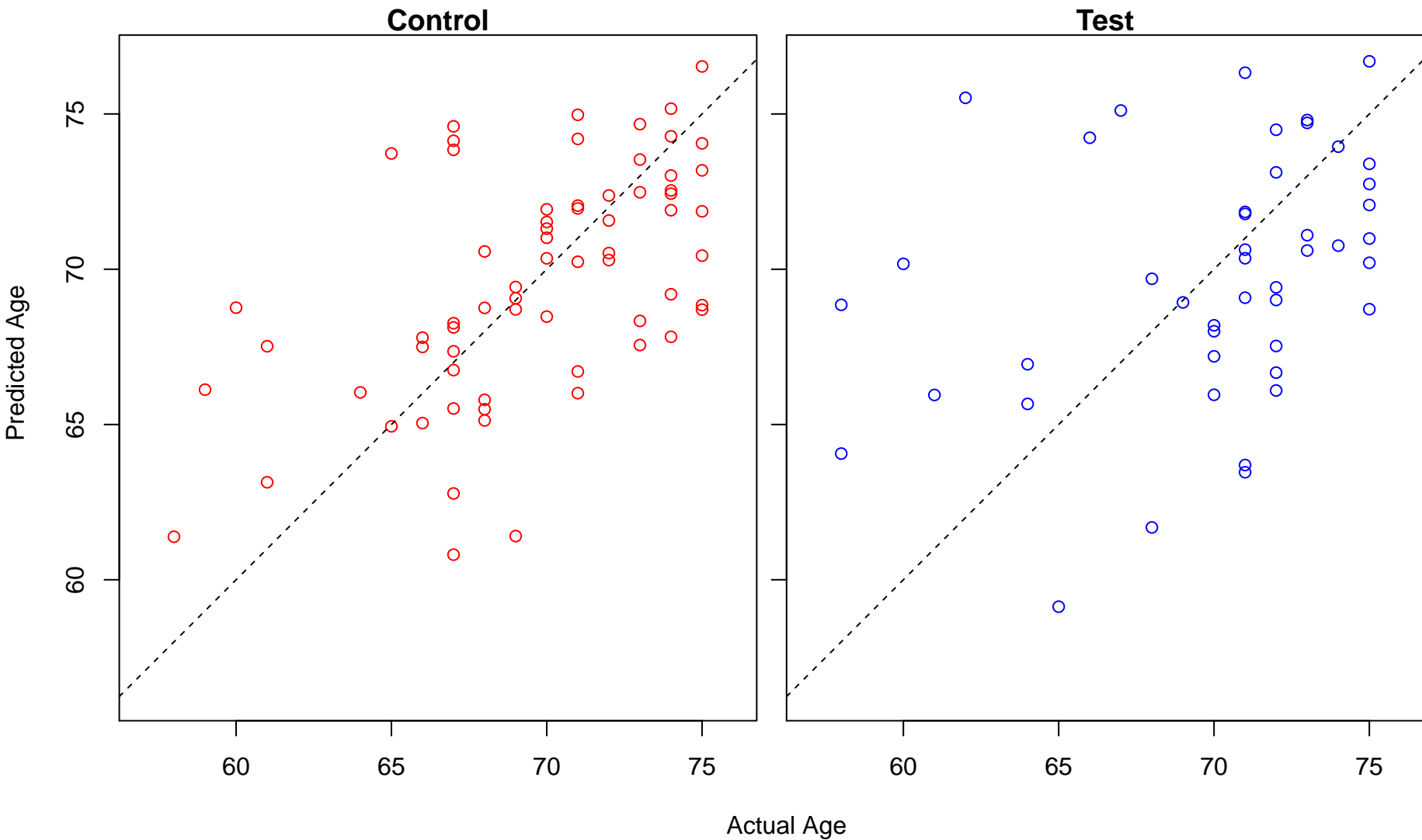
negative regulation of cytoskeleton organization (Score: 1.229762)



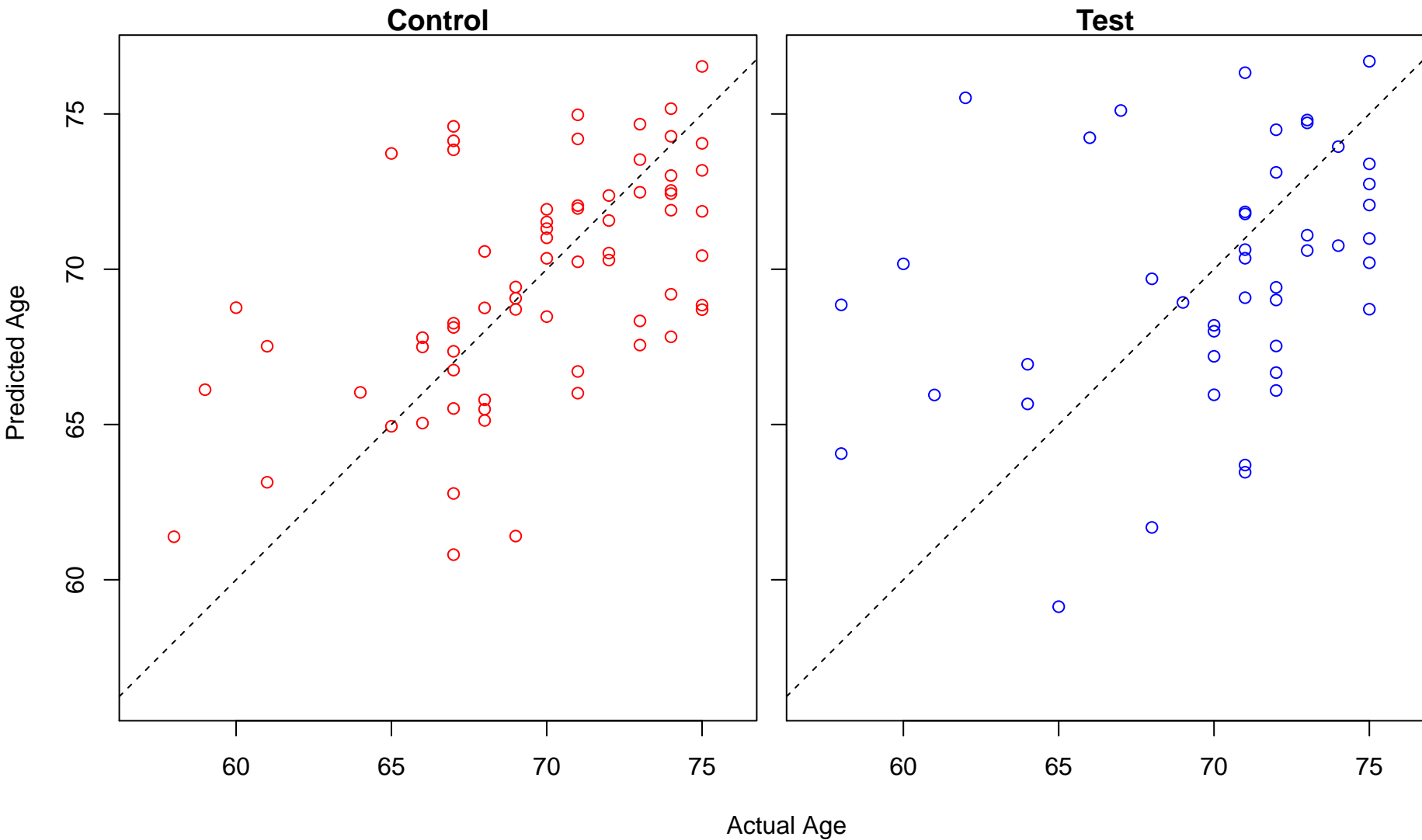
positive regulation of natural killer cell mediated immunity (Score: 1.229230)



macromolecular complex remodeling (Score: 1.228936)

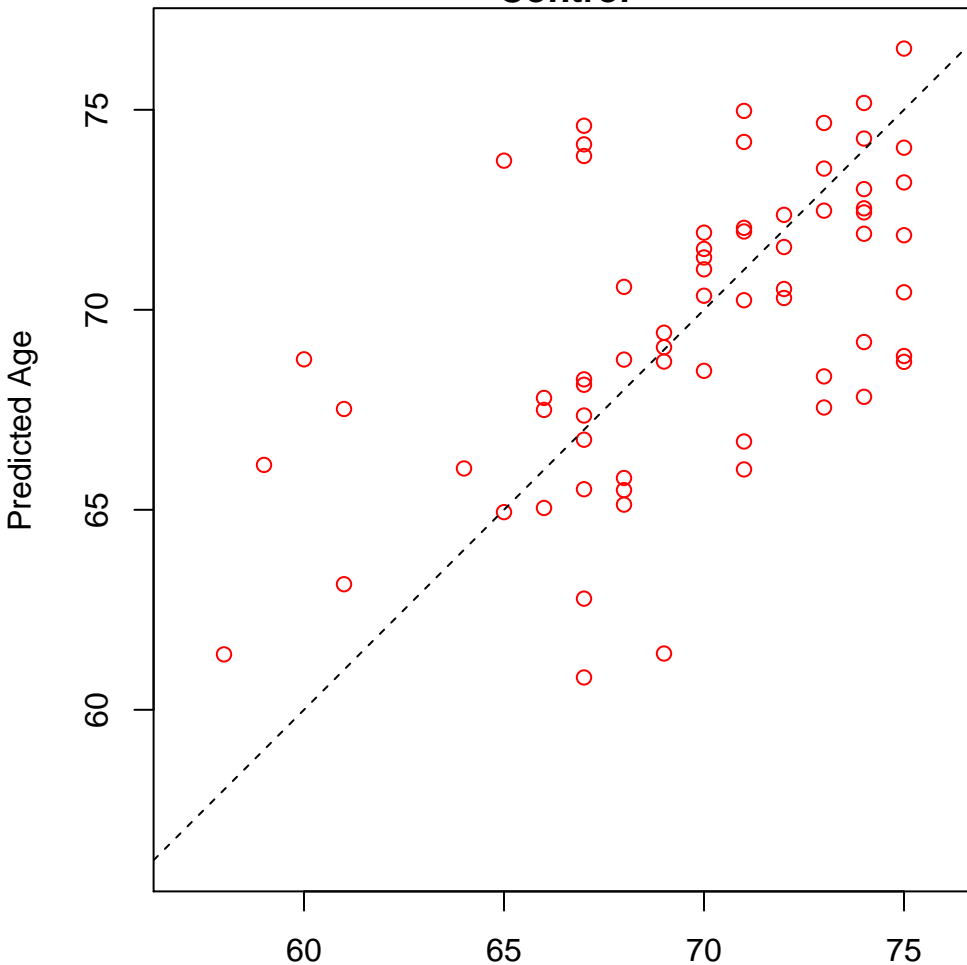


protein-lipid complex remodeling (Score: 1.228936)

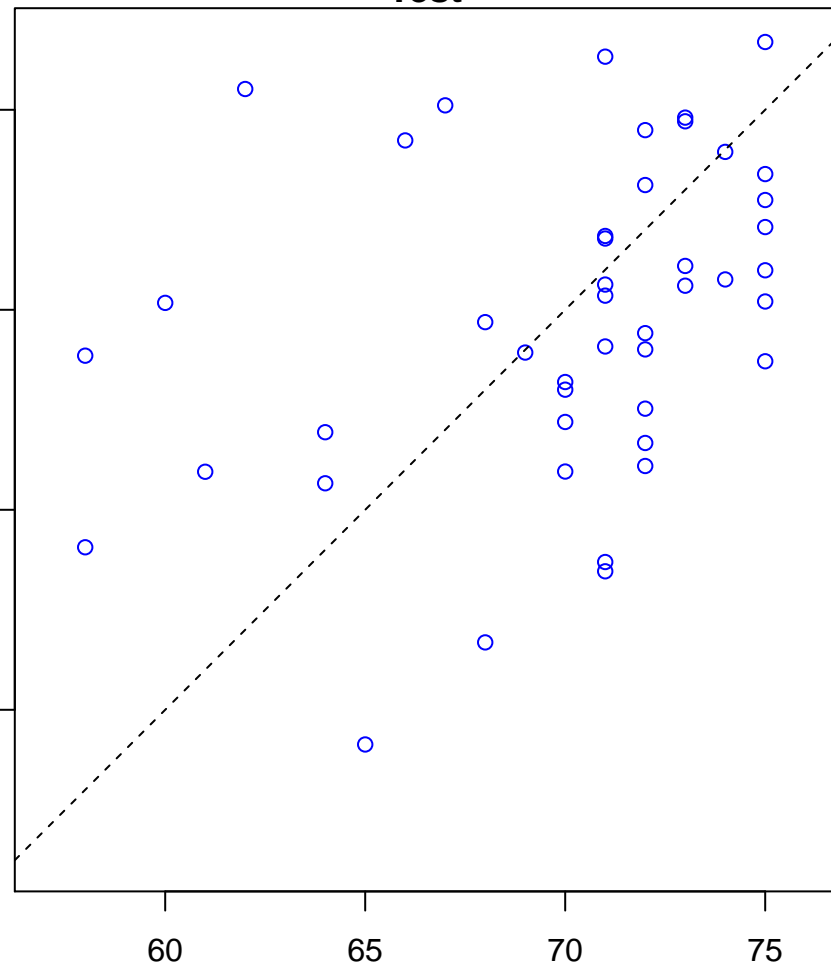


plasma lipoprotein particle remodeling (Score: 1.228936)

Control



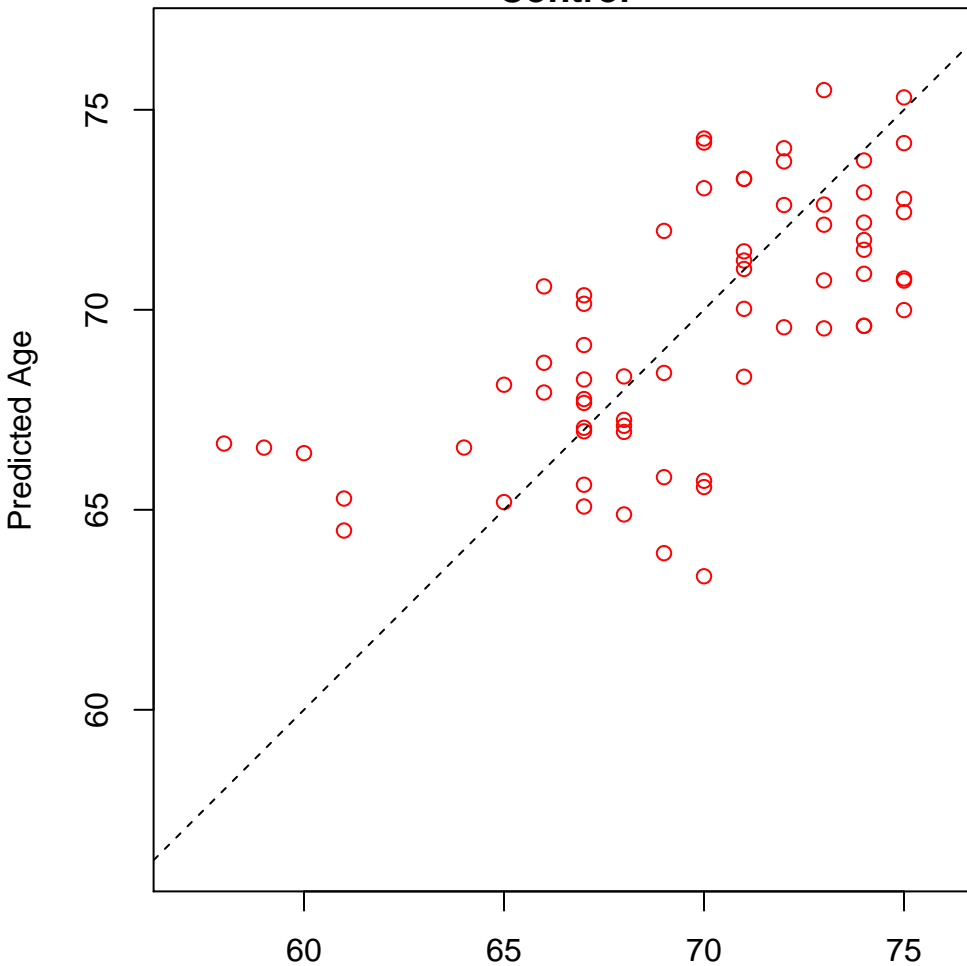
Test



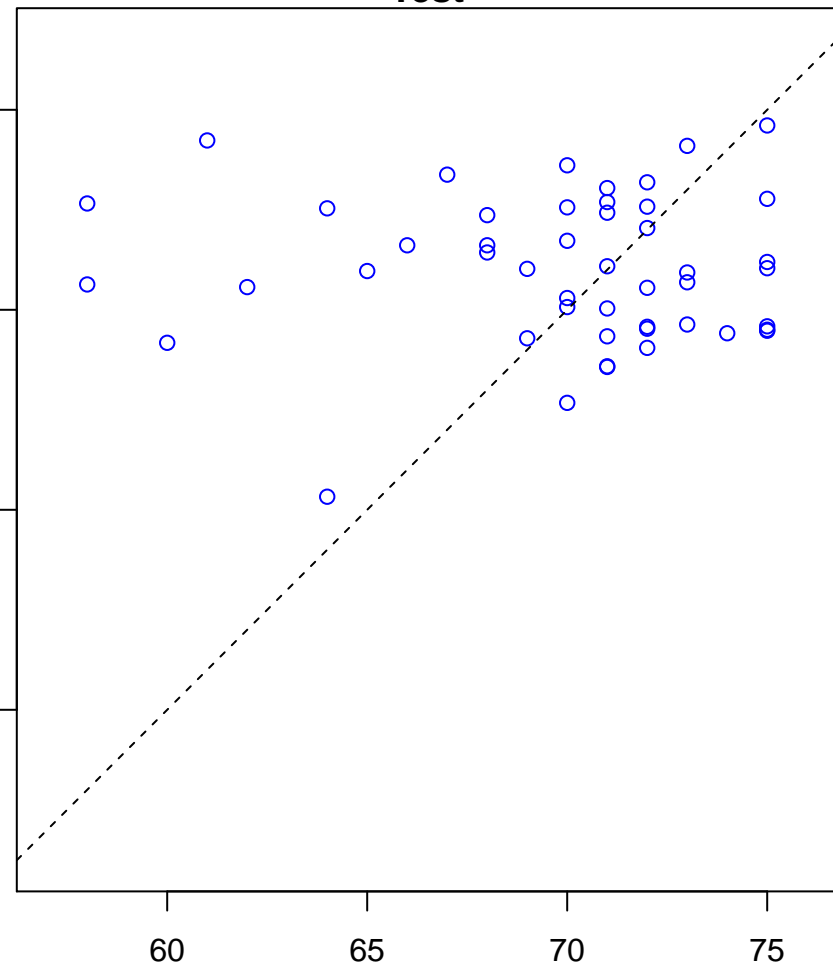
Actual Age

DNA methylation or demethylation (Score: 1.228704)

Control

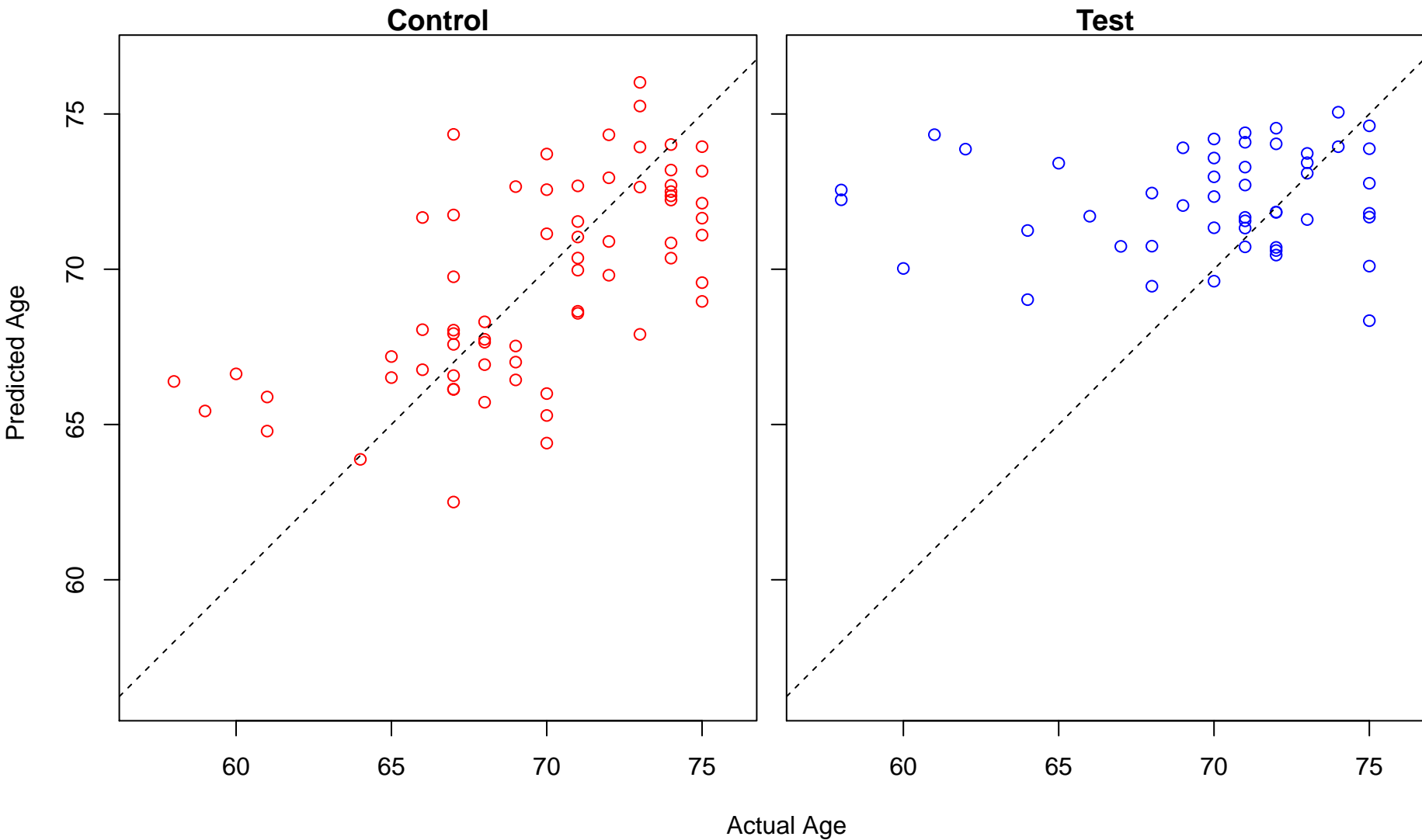


Test

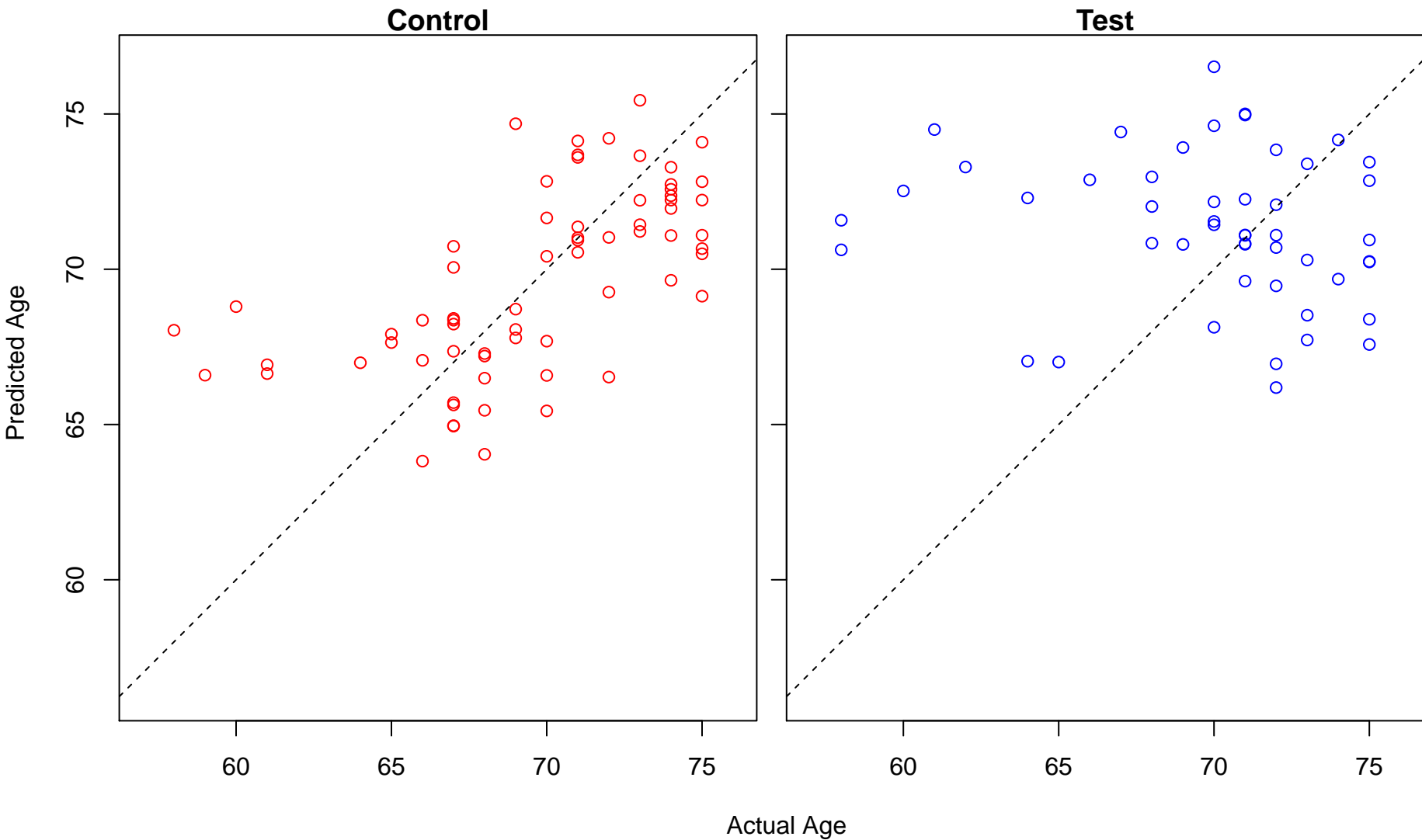


Actual Age

plasma membrane organization (Score: 1.228666)

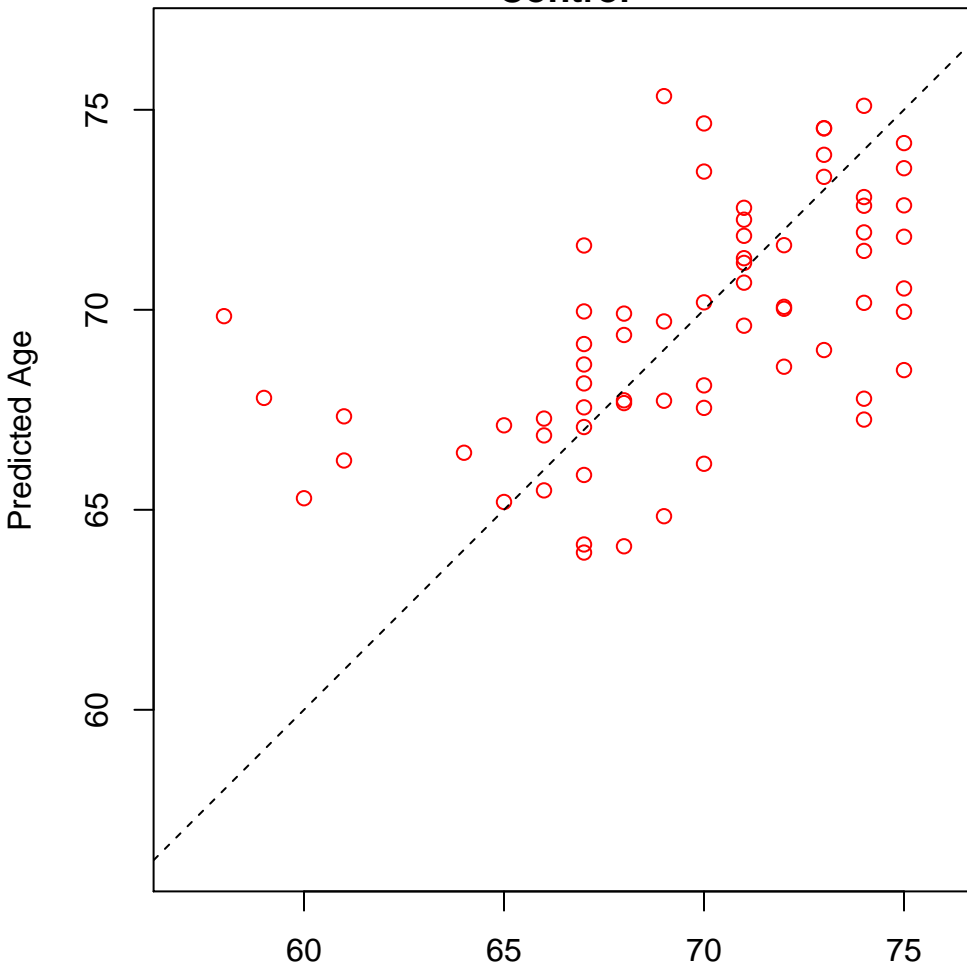


negative regulation of type 2 immune response (Score: 1.228544)

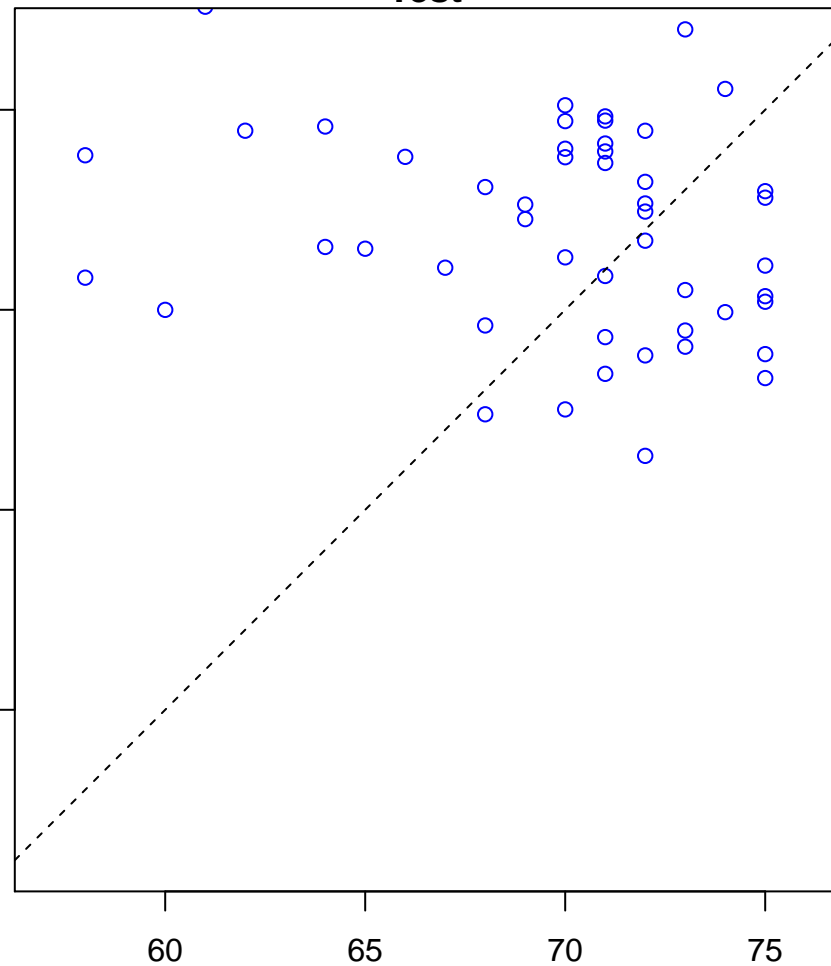


C21-steroid hormone metabolic process (Score: 1.228312)

Control

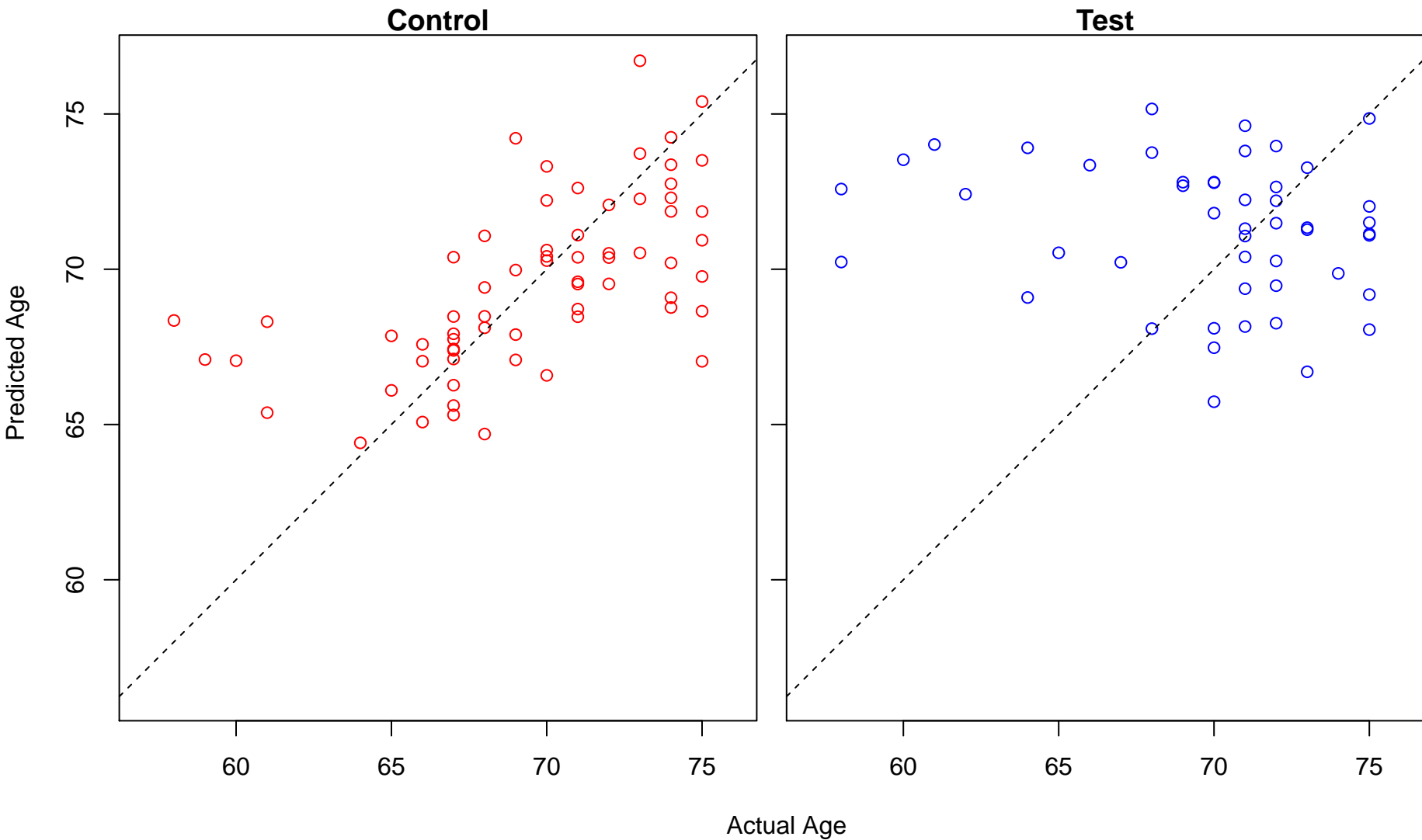


Test

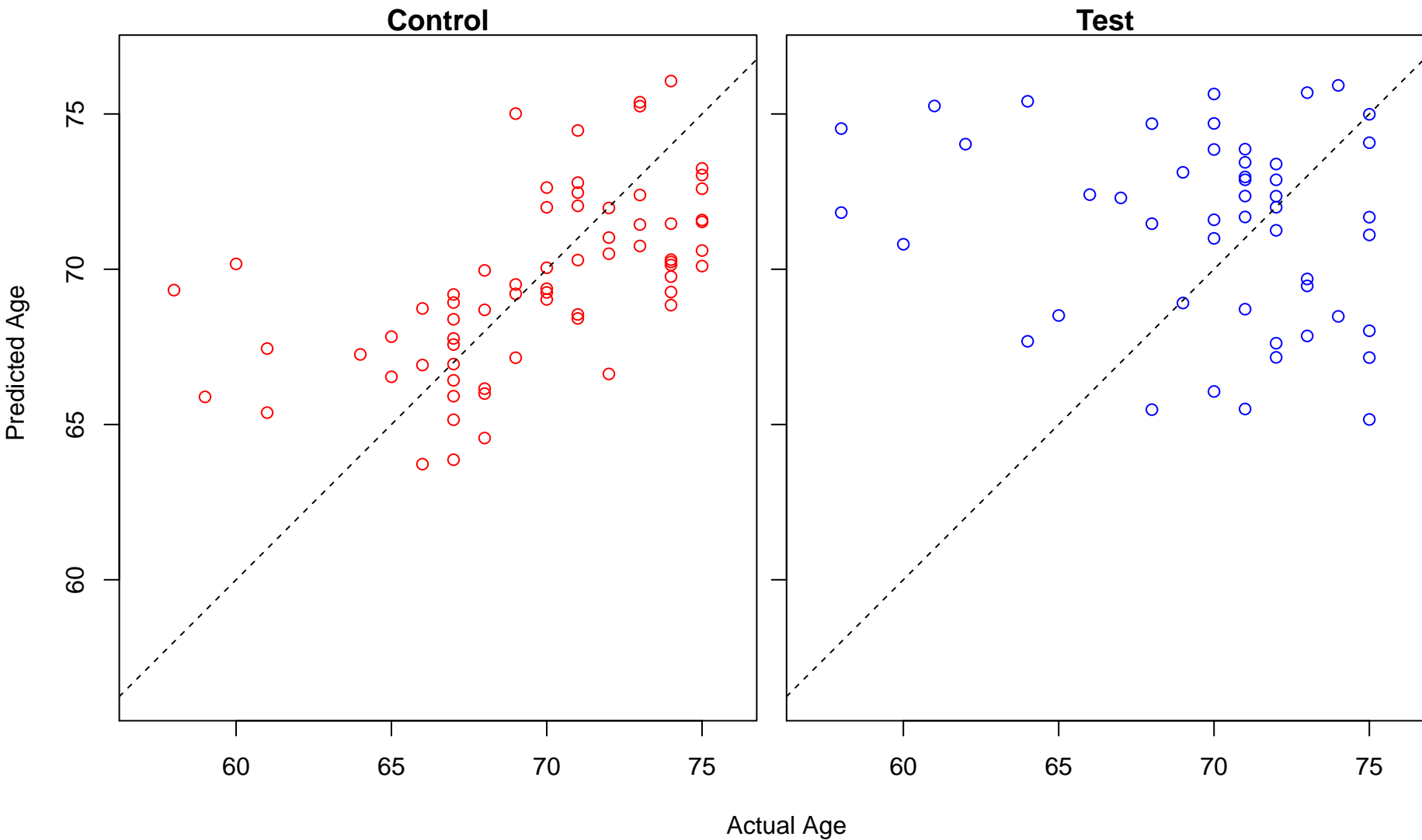


Actual Age

phosphatidylglycerol acyl-chain remodeling (Score: 1.228175)

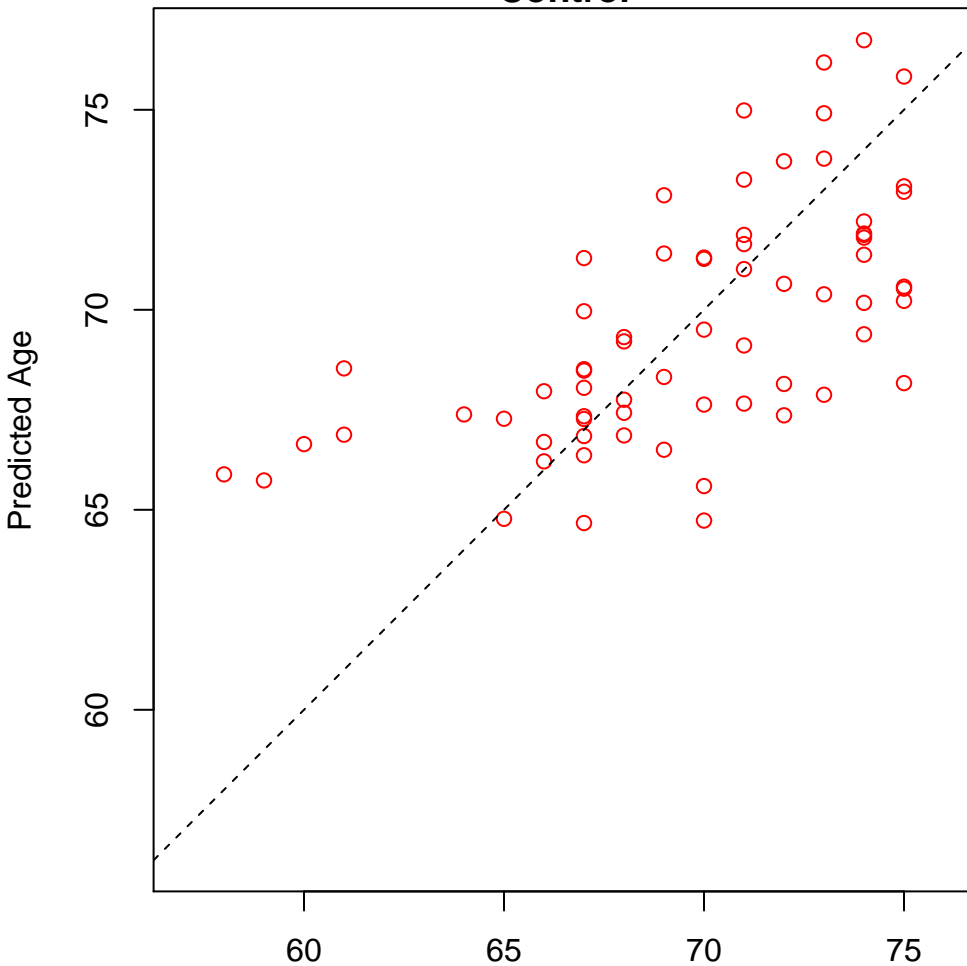


negative regulation of adaptive immune response (Score: 1.227994)

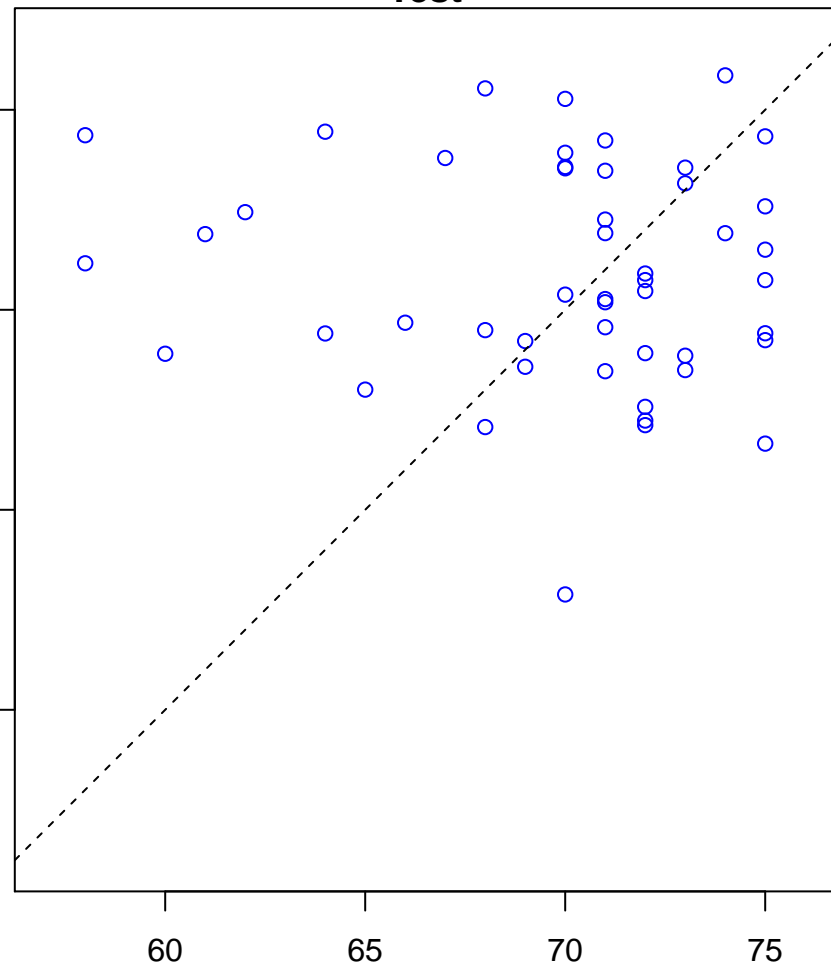


cellular response to glucose starvation (Score: 1.227581)

Control

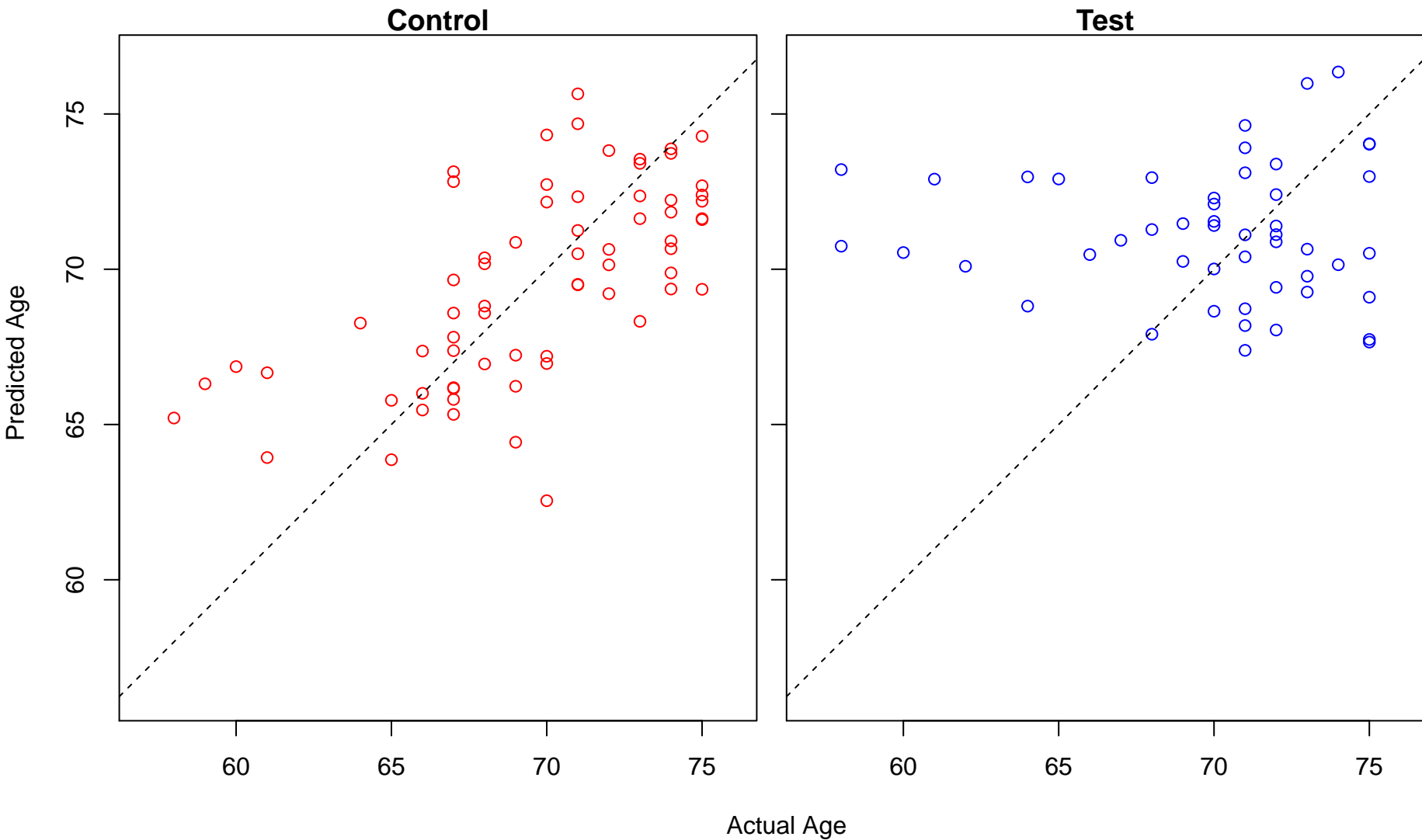


Test

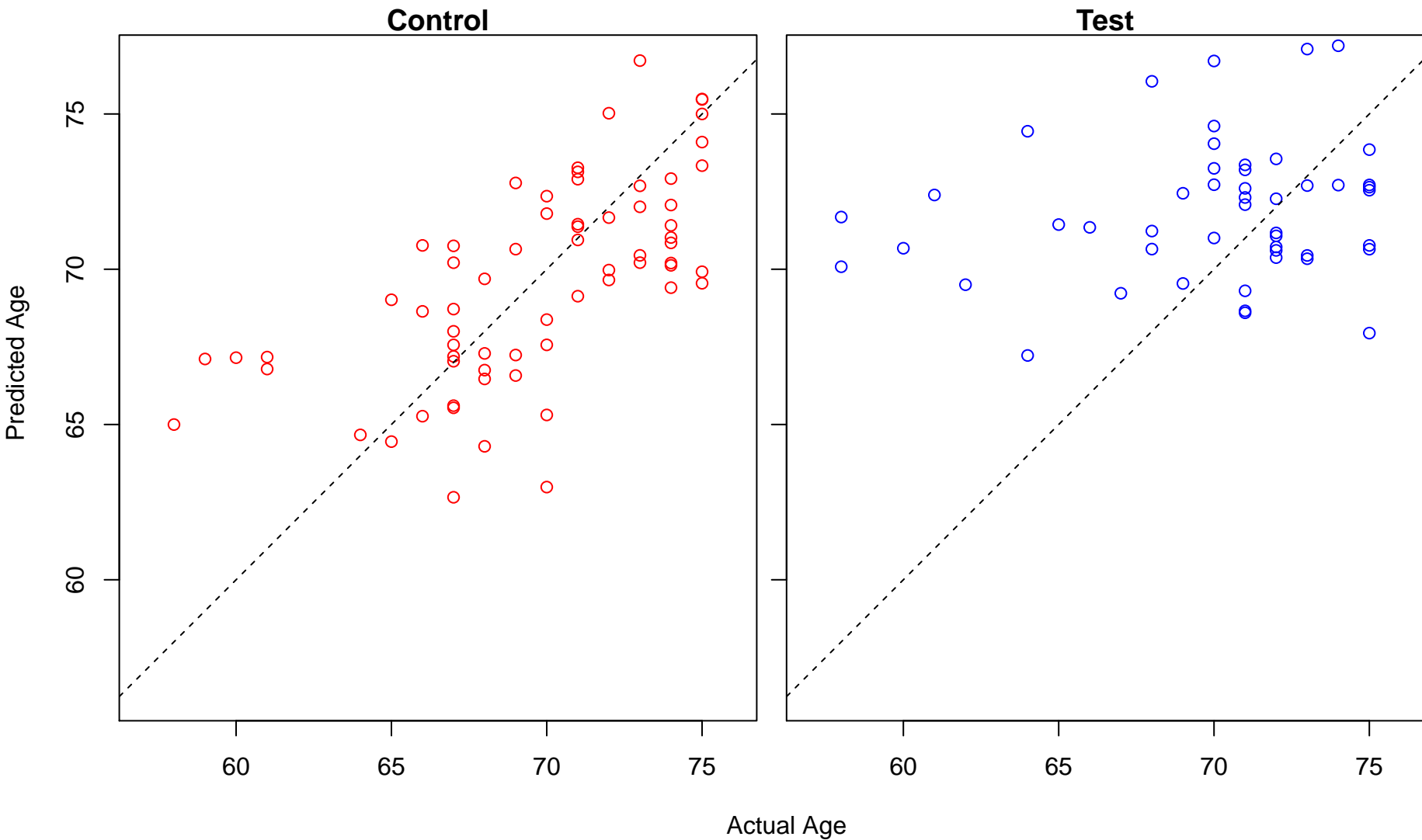


Actual Age

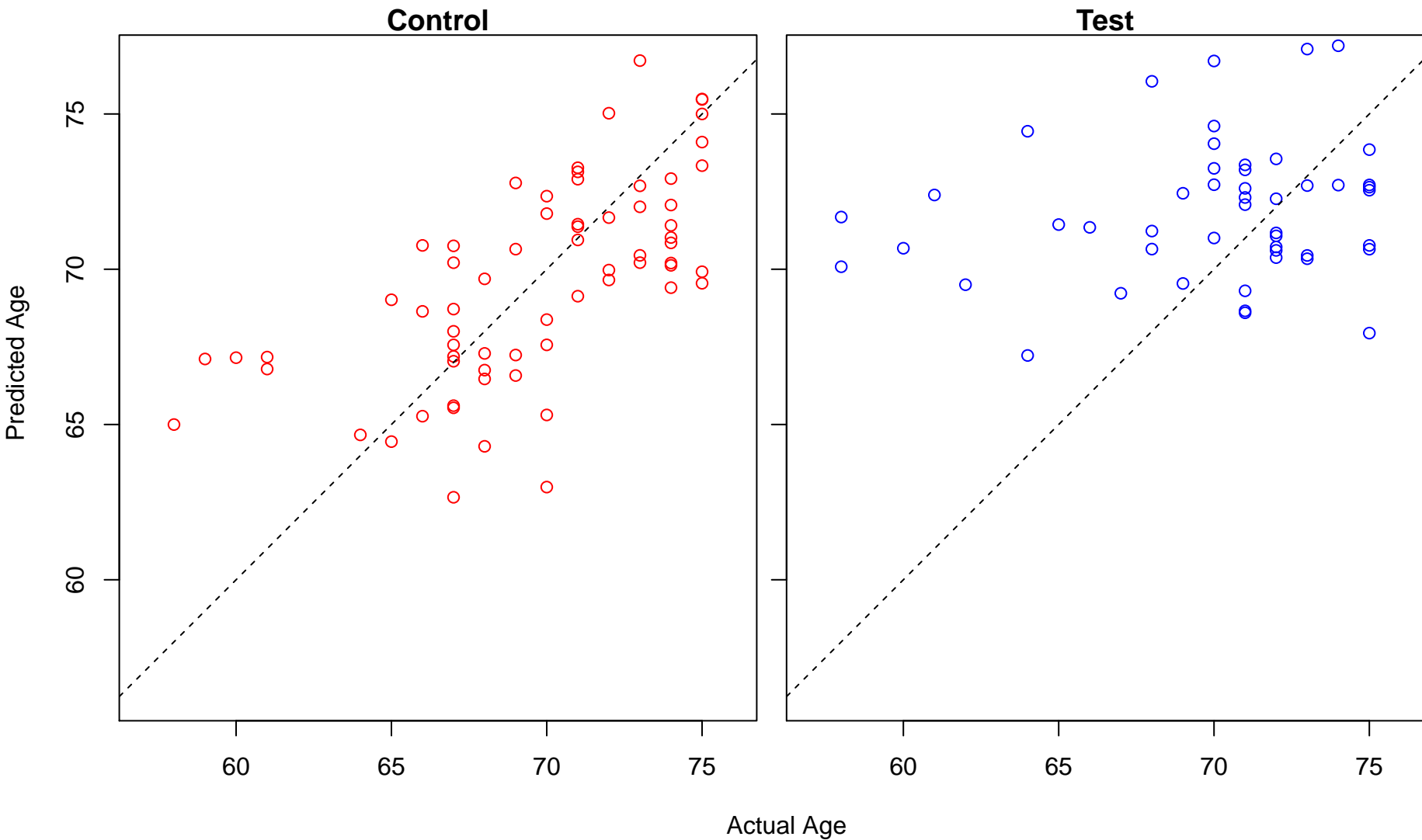
protein K63-linked ubiquitination (Score: 1.227491)



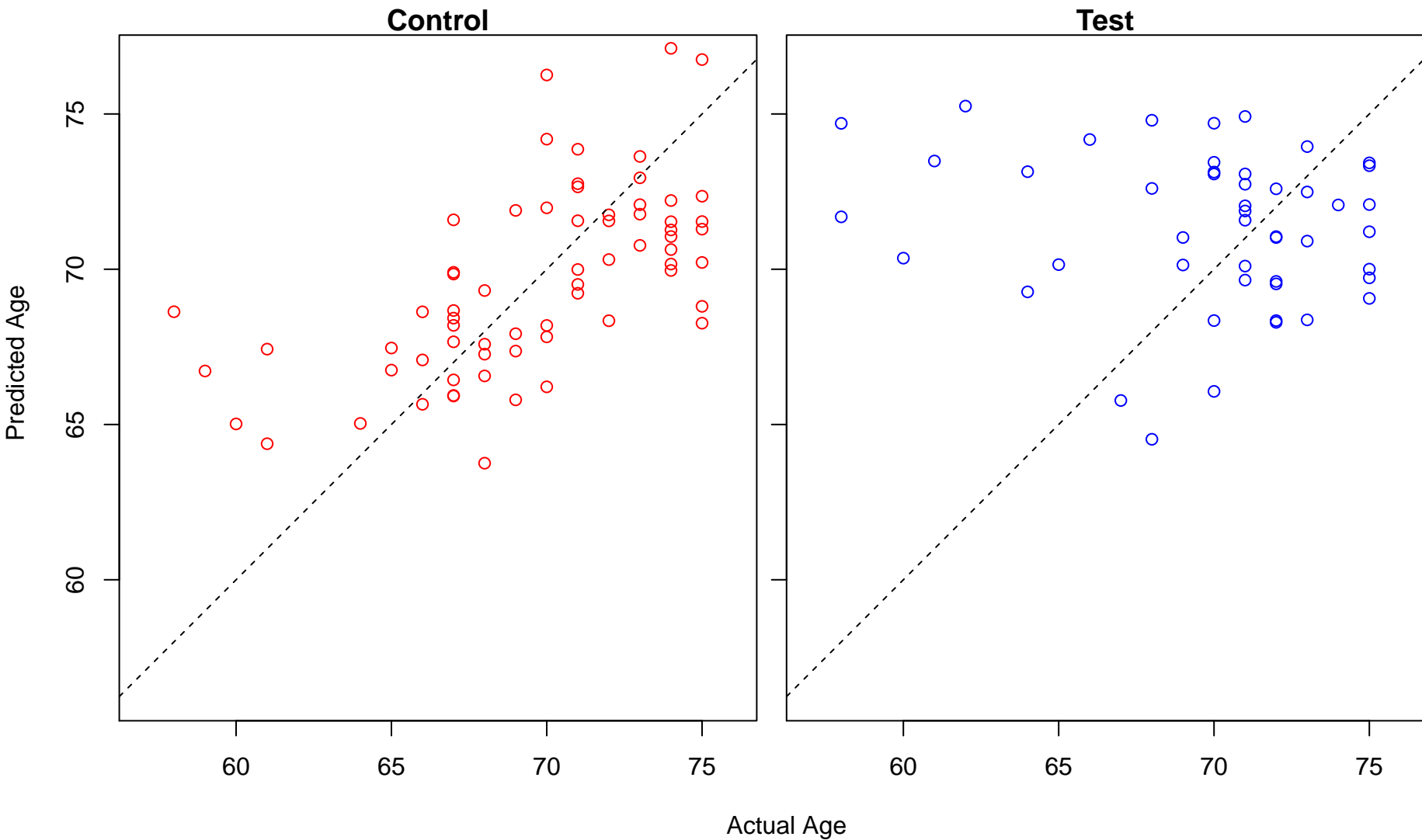
lysosome organization (Score: 1.227226)



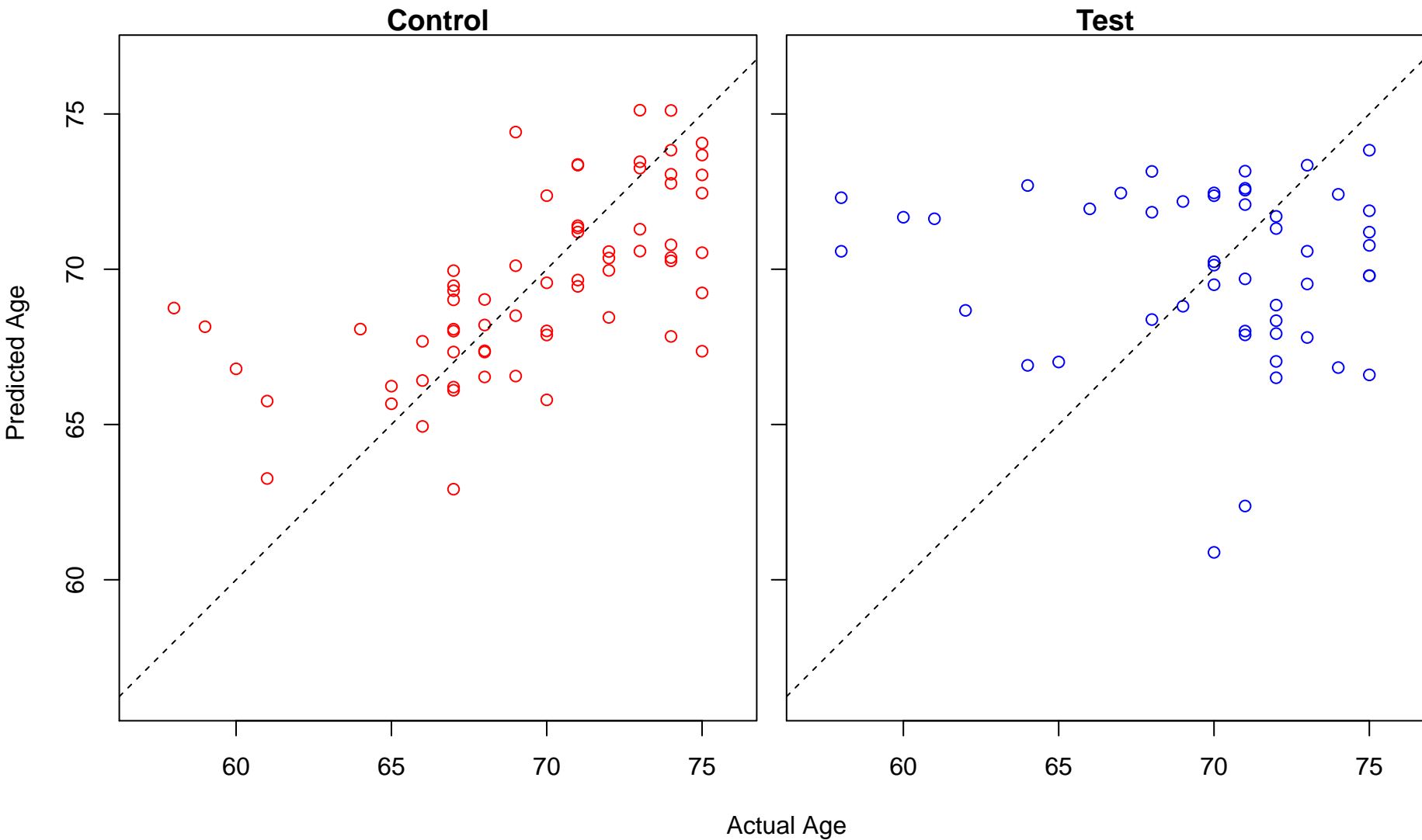
lytic vacuole organization (Score: 1.227226)



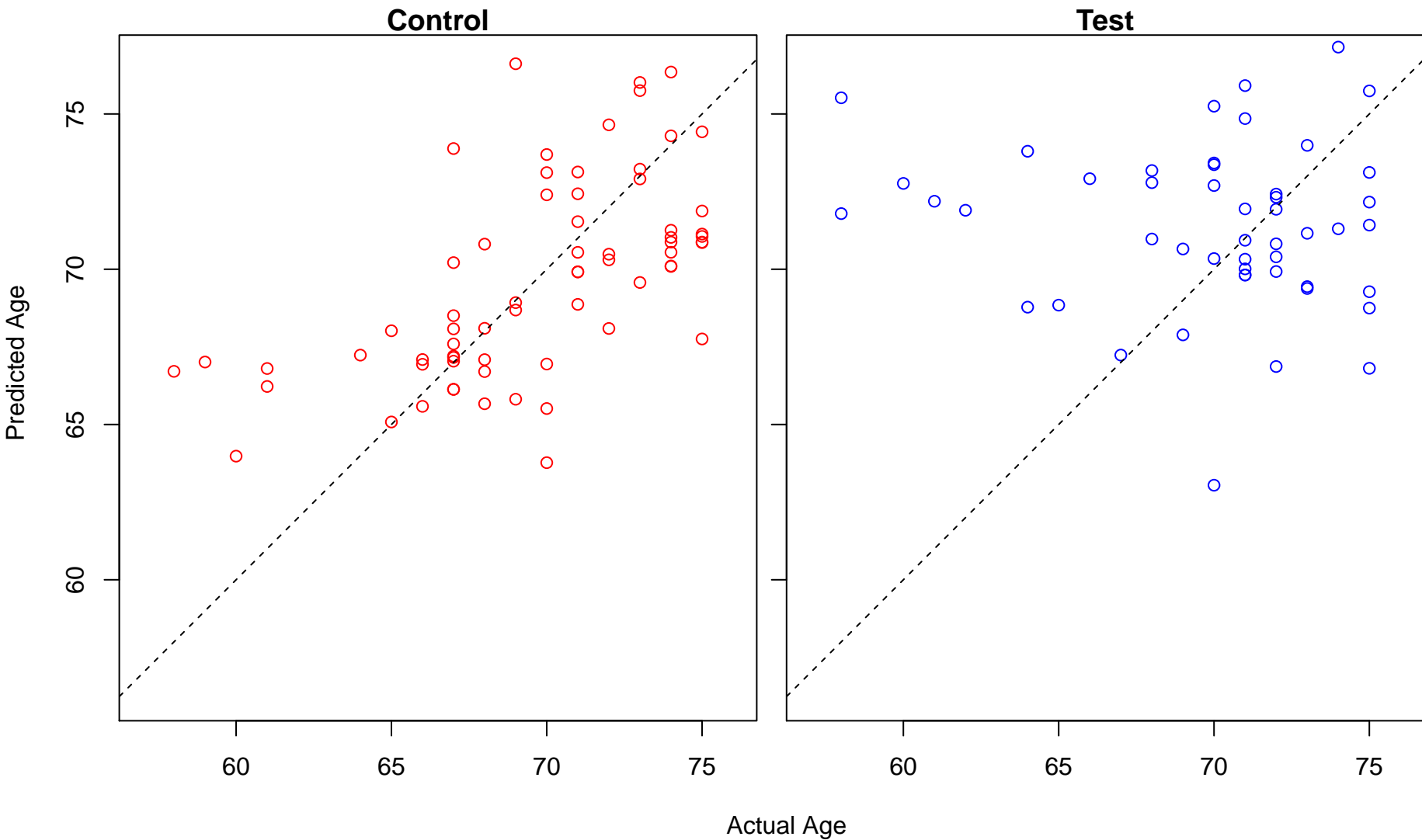
microtubule polymerization or depolymerization (Score: 1.225872)



negative regulation of lyase activity (Score: 1.225430)

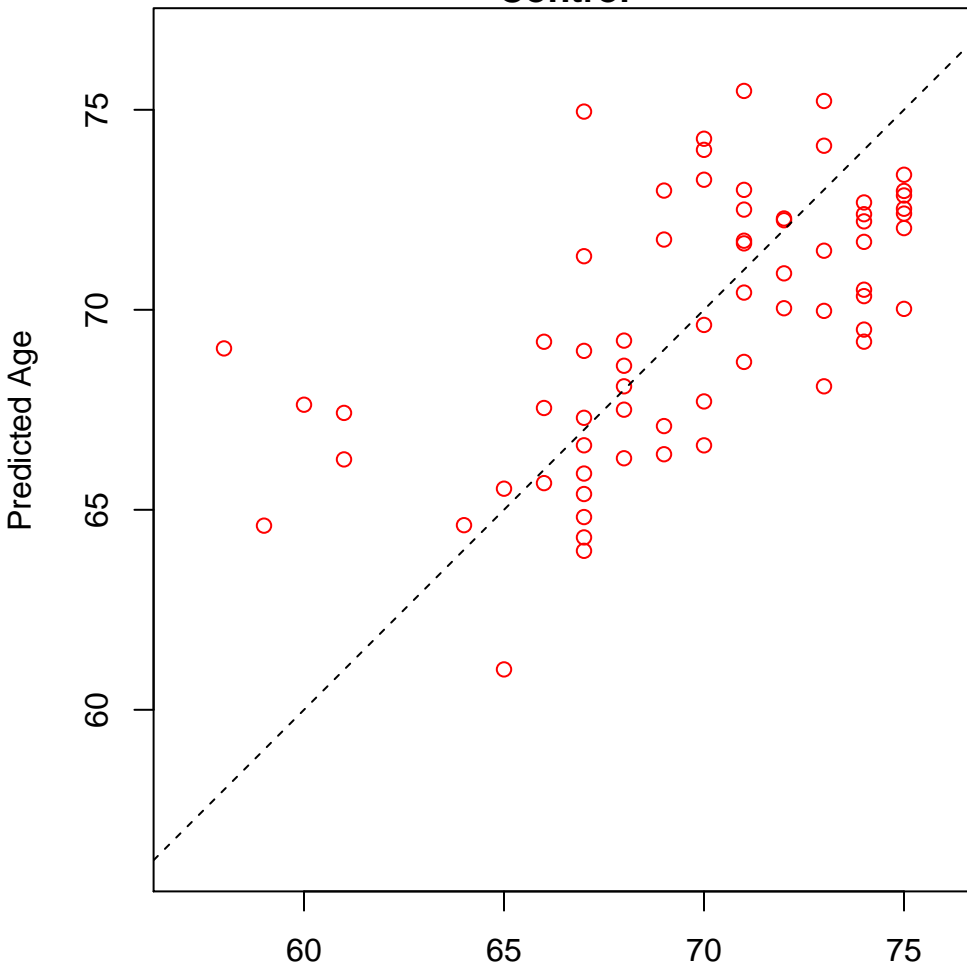


cellular monovalent inorganic cation homeostasis (Score: 1.225412)

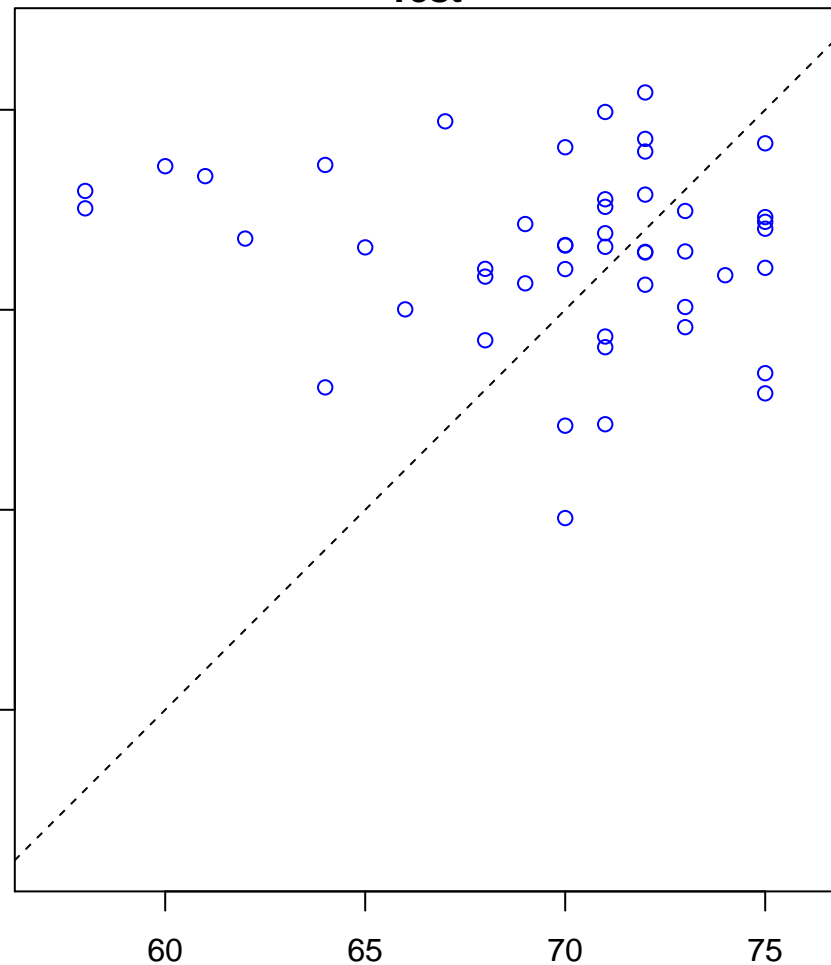


regulation of epidermis development (Score: 1.225404)

Control

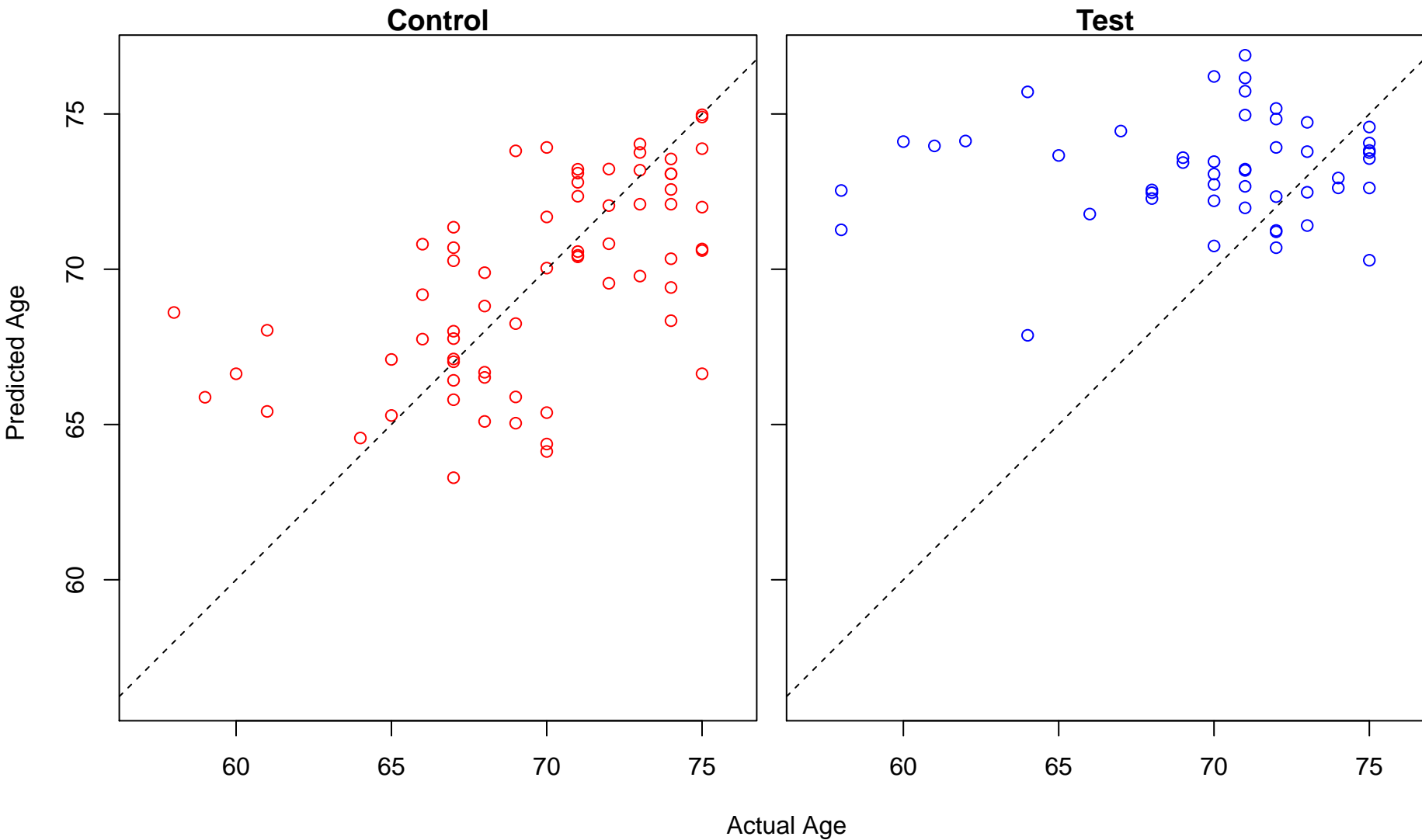


Test

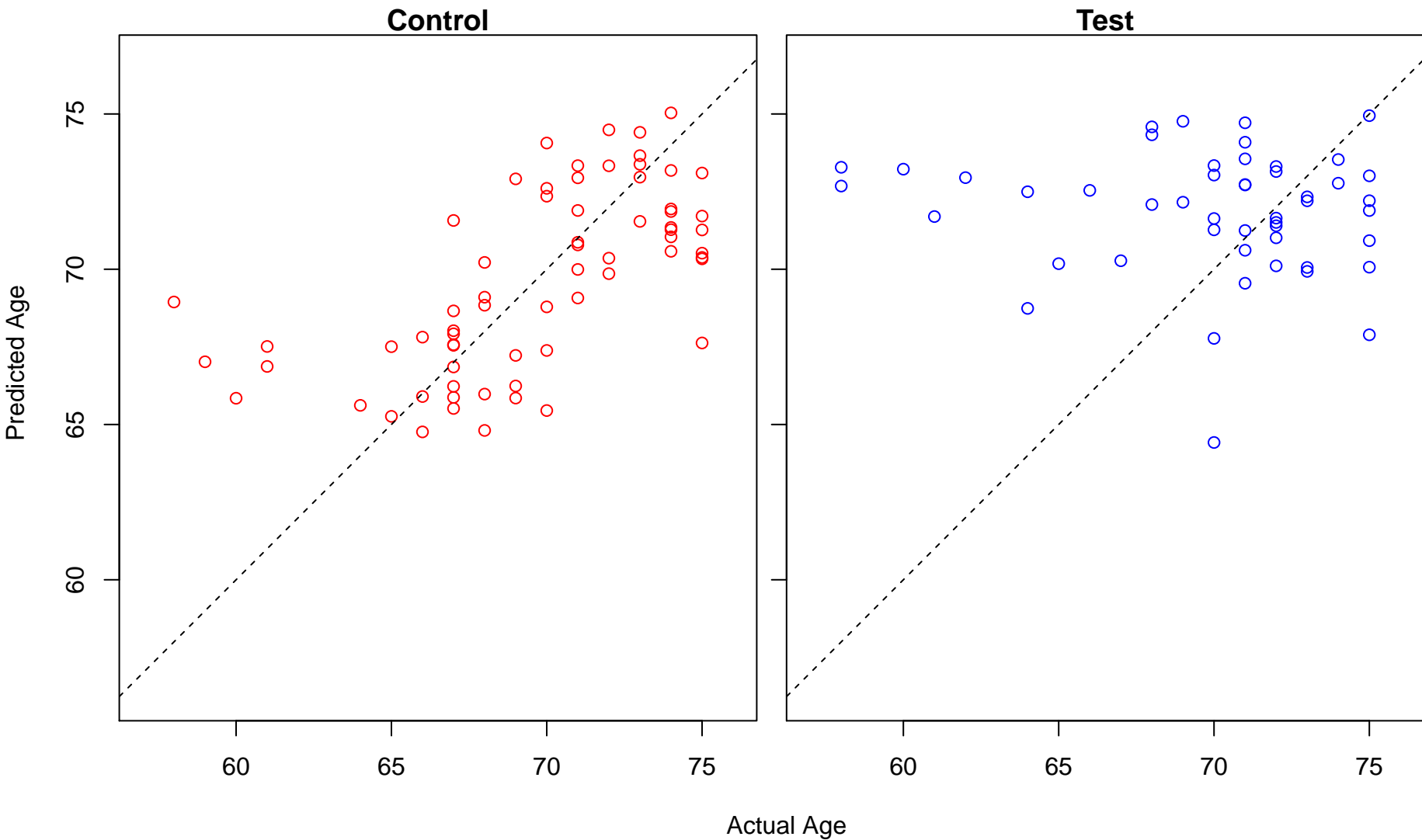


Actual Age

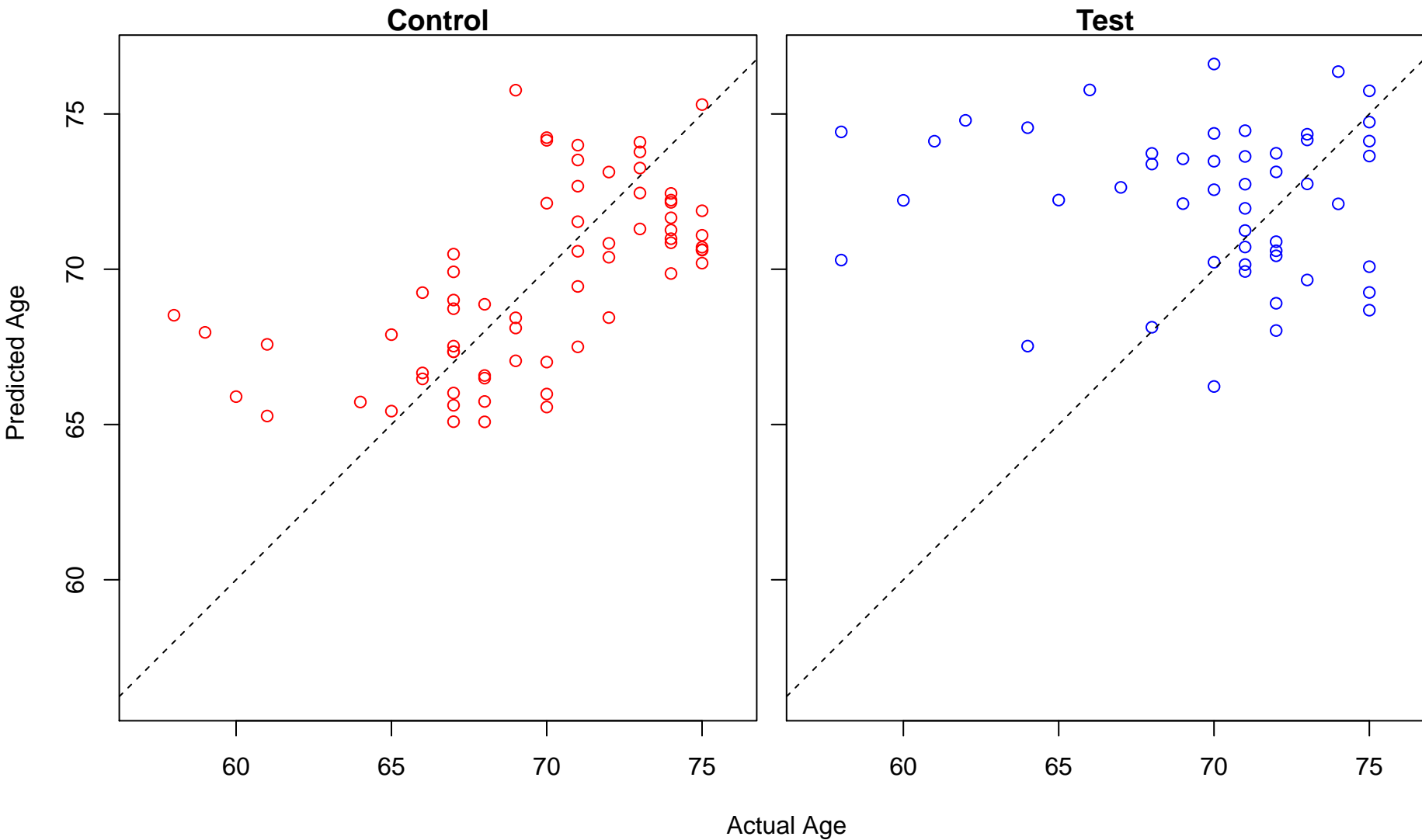
cellular polysaccharide metabolic process (Score: 1.225192)



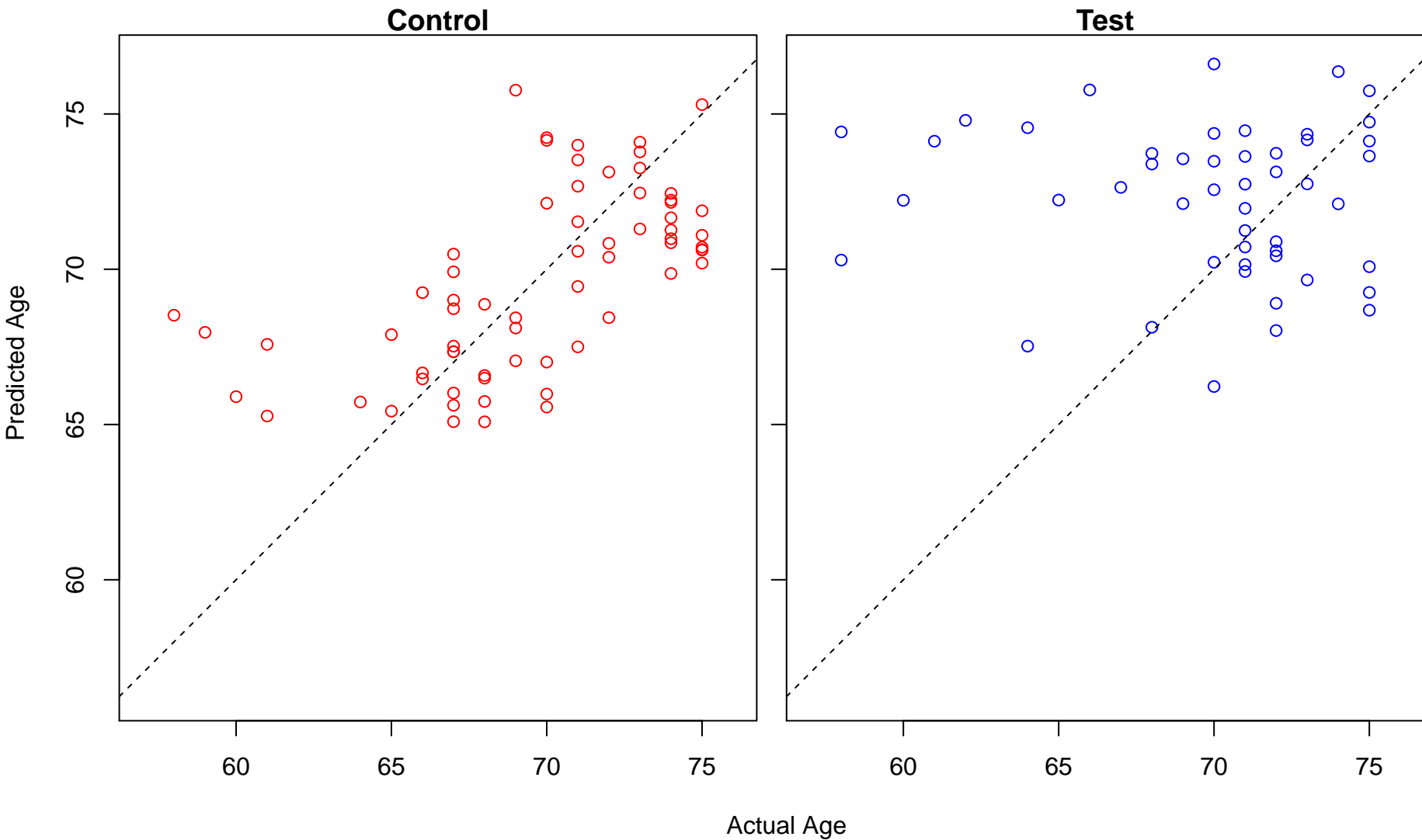
G2 DNA damage checkpoint (Score: 1.224478)



nuclear DNA replication (Score: 1.224244)

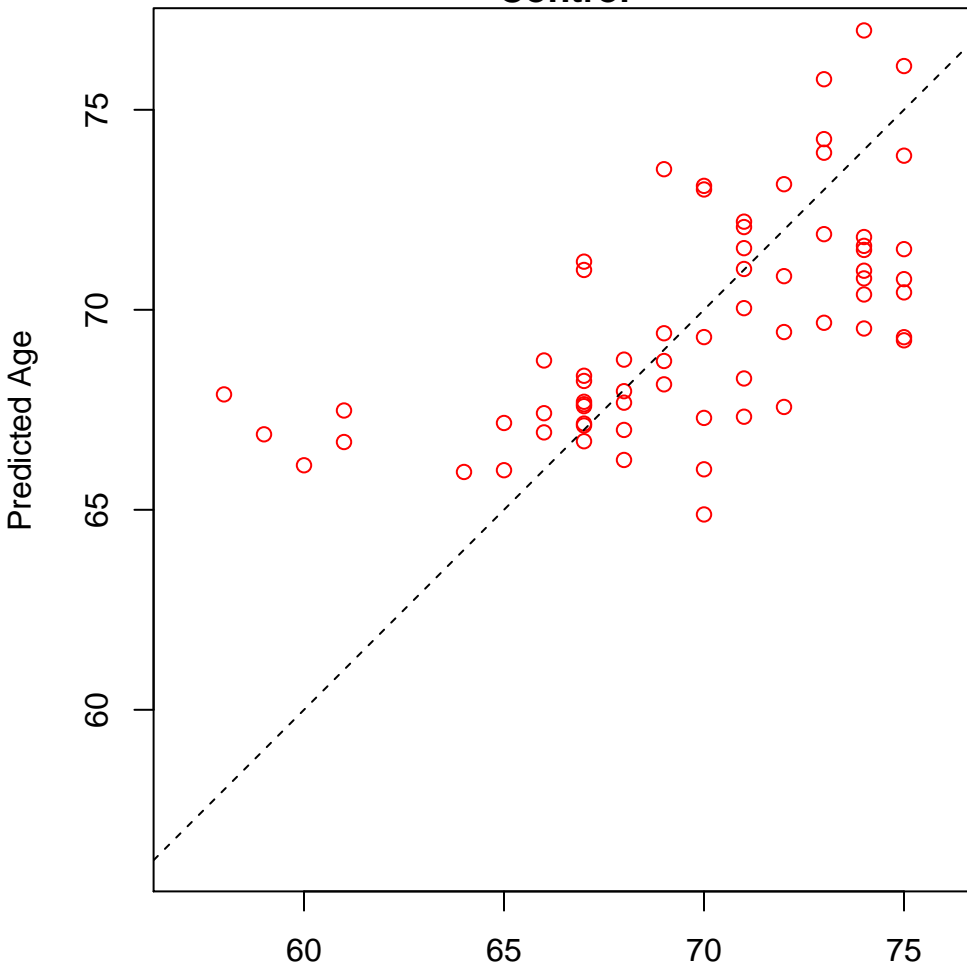


cell cycle DNA replication (Score: 1.224244)

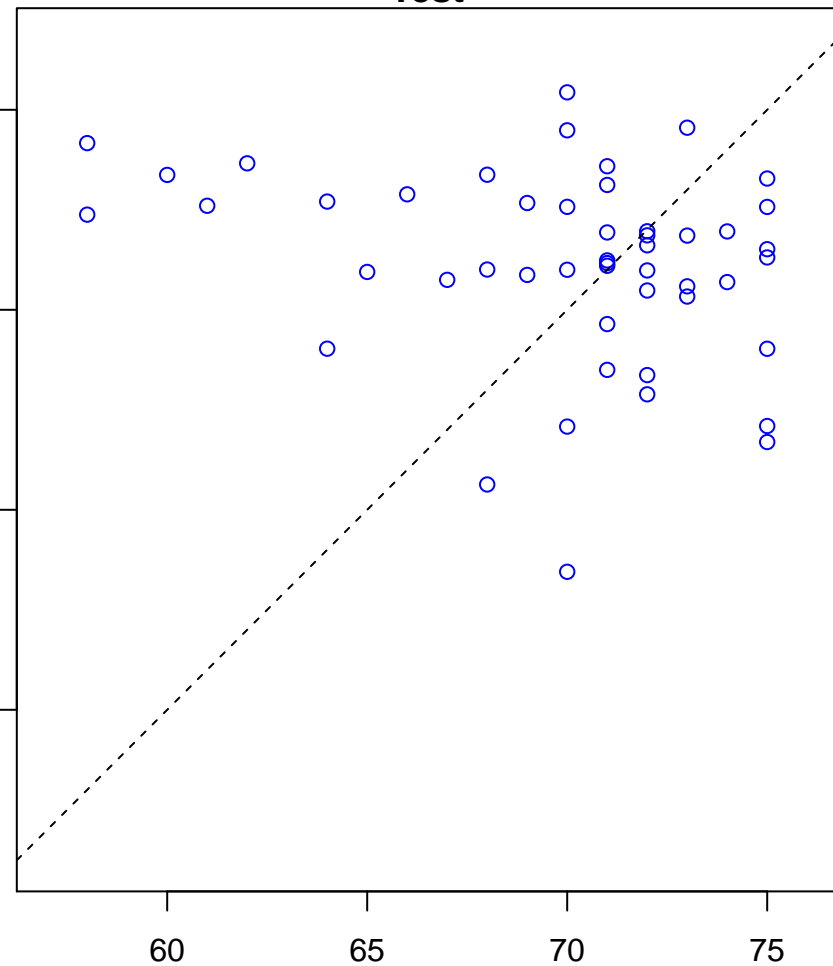


inositol phosphate metabolic process (Score: 1.223316)

Control



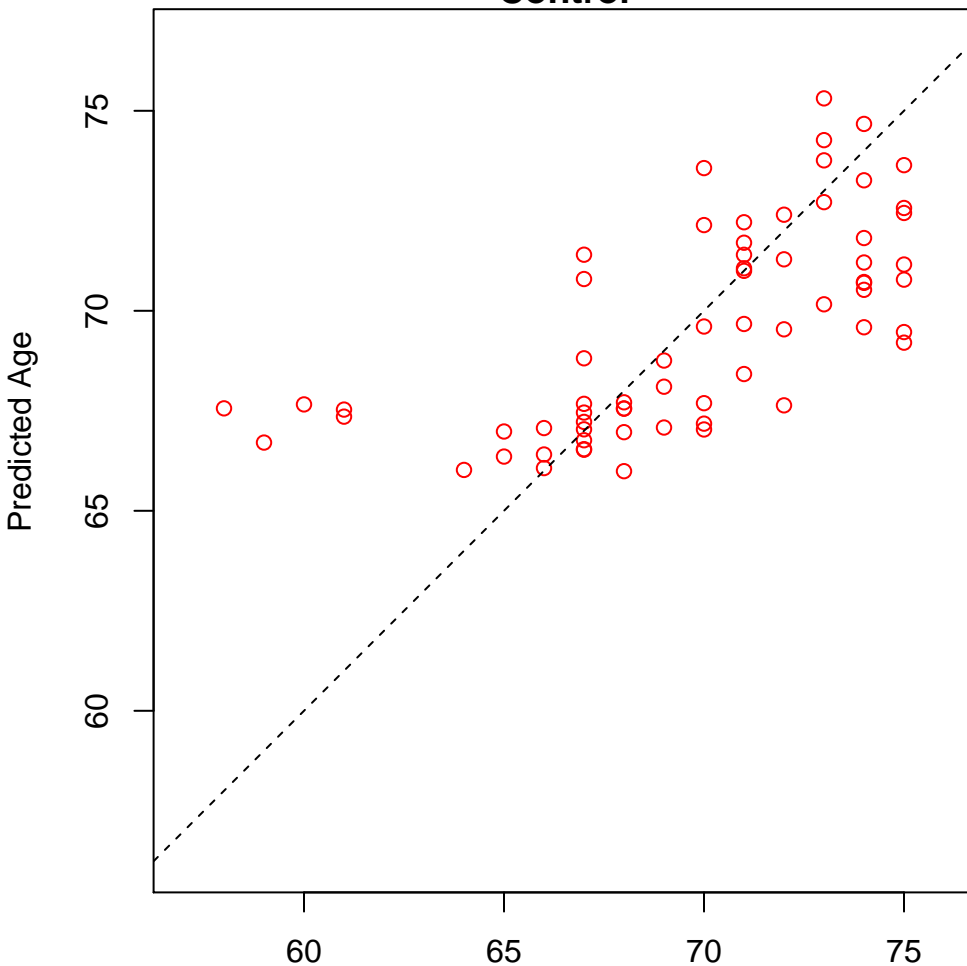
Test



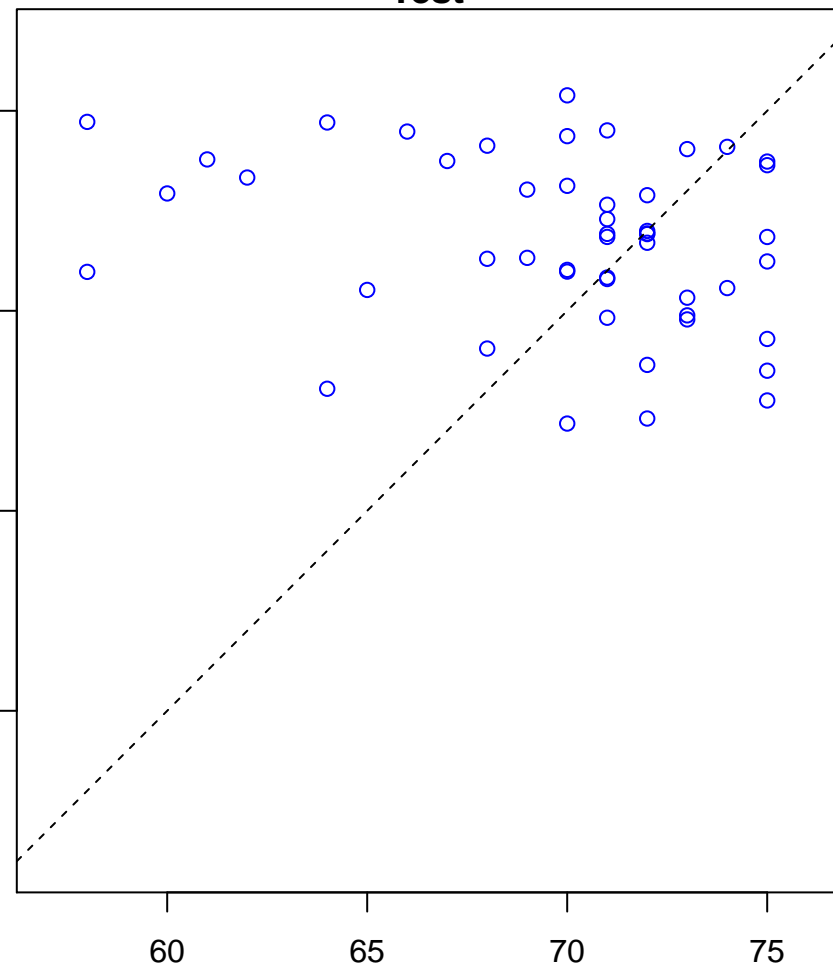
Actual Age

negative regulation of protein secretion (Score: 1.223195)

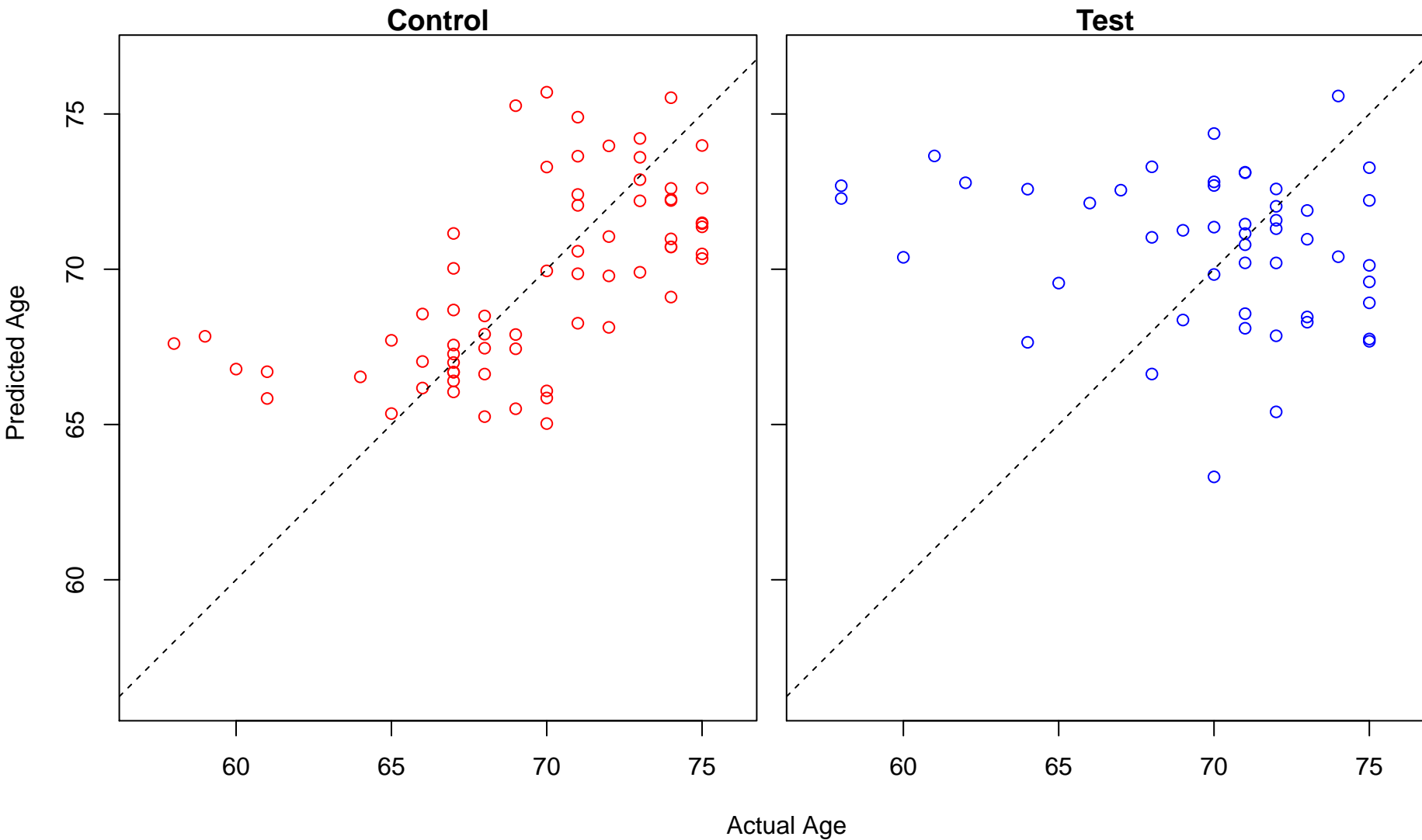
Control



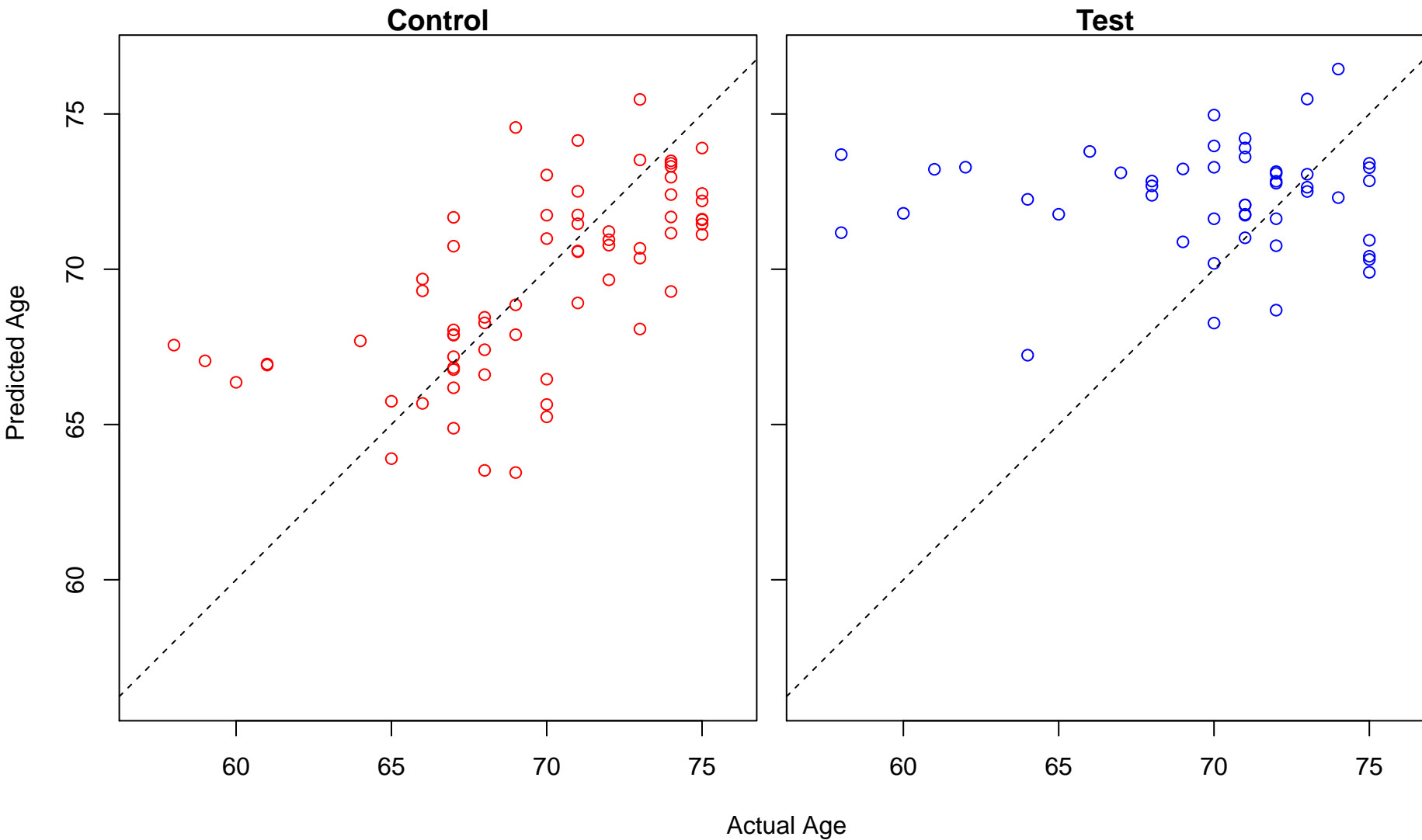
Test



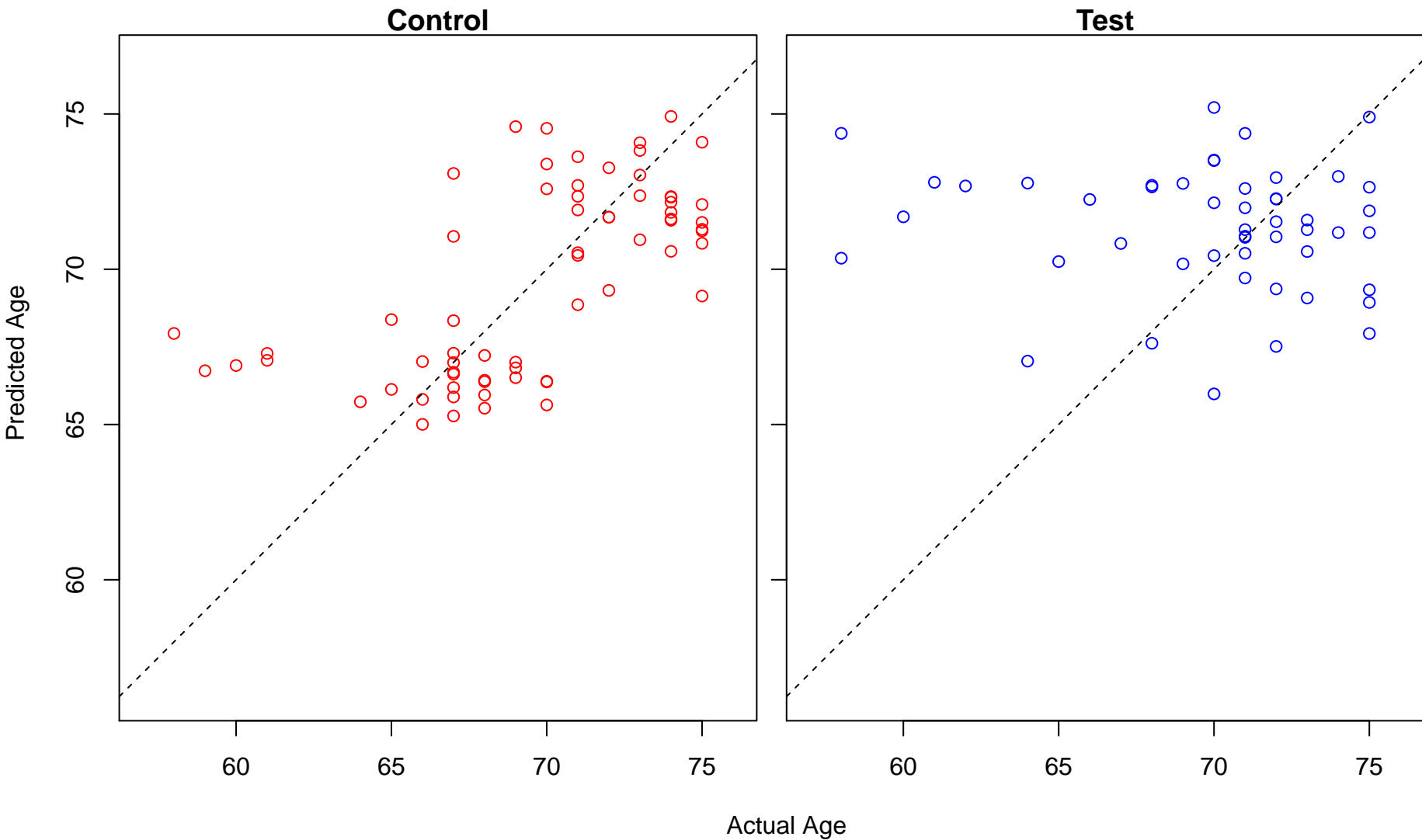
cellular response to molecule of bacterial origin (Score: 1.222686)



aging (Score: 1.222519)

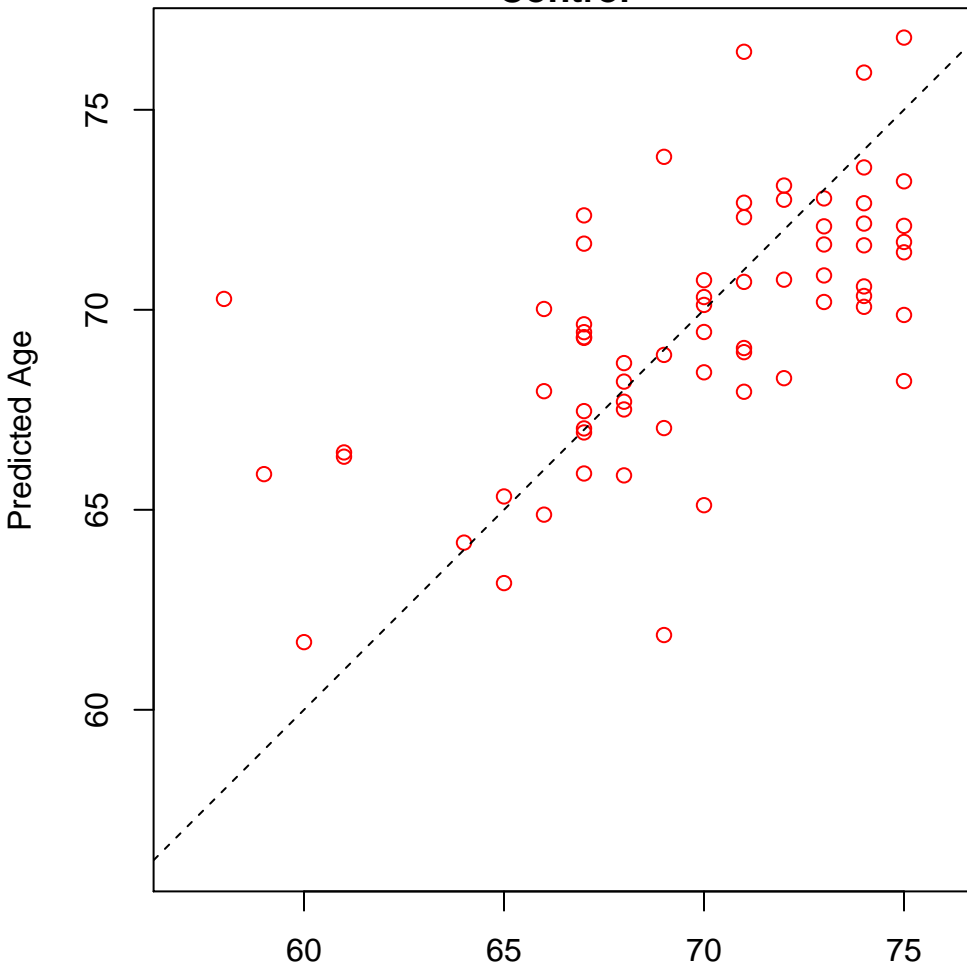


negative regulation of epithelial cell migration (Score: 1.221930)

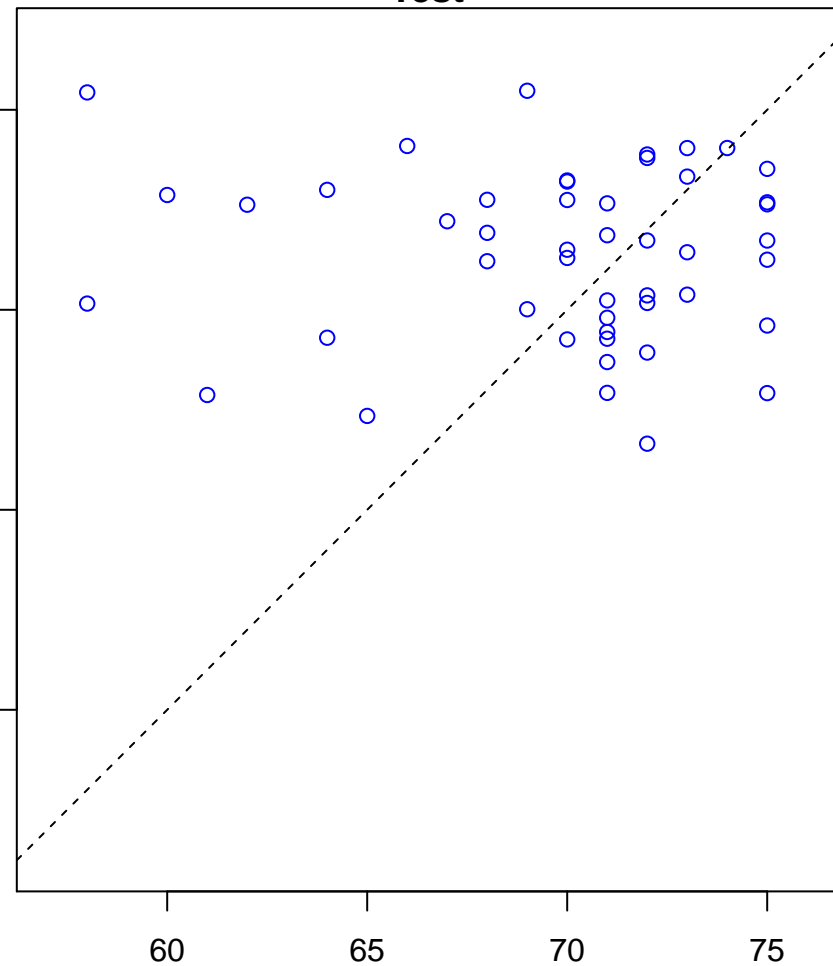


protein localization to cytoskeleton (Score: 1.221838)

Control

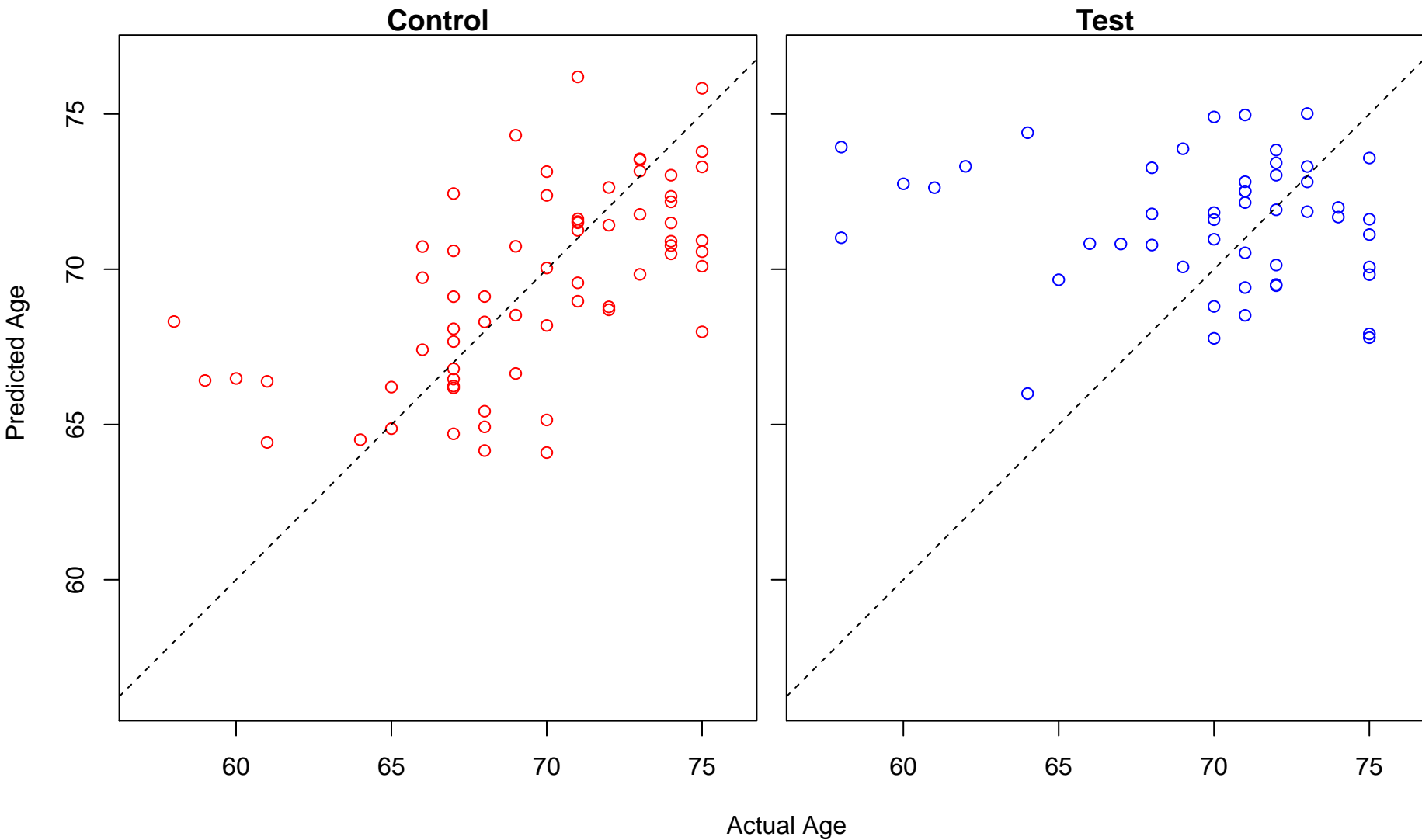


Test

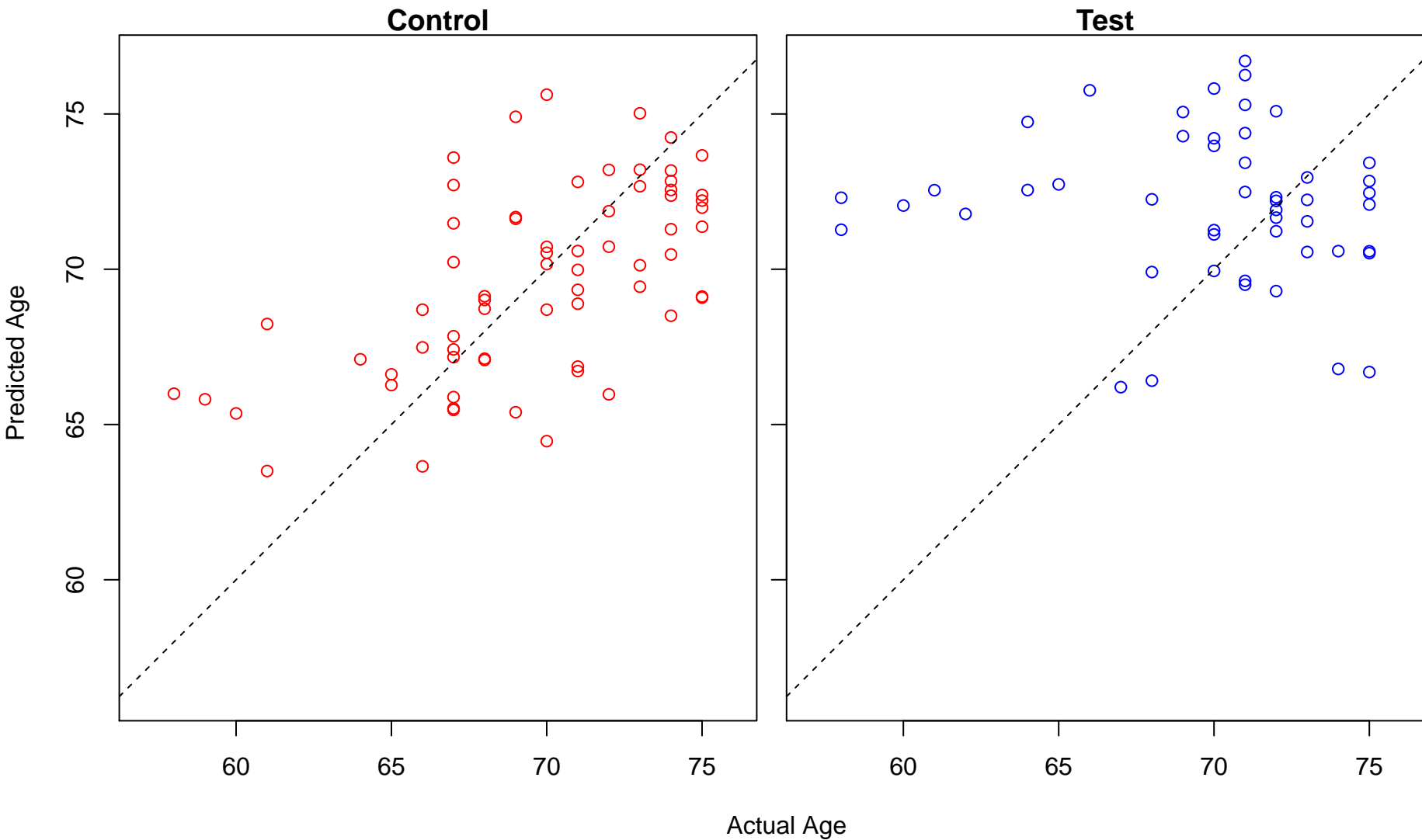


Actual Age

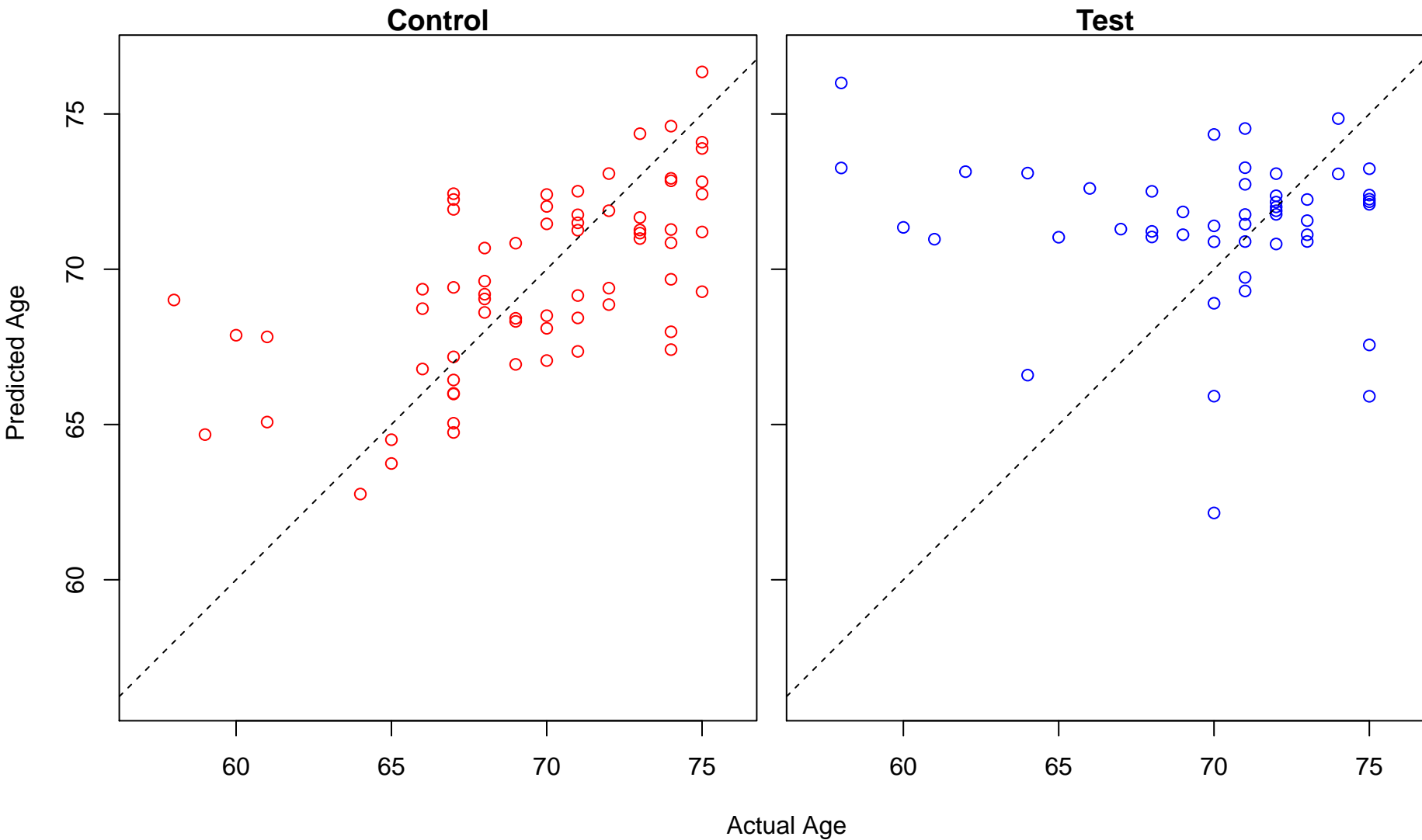
gonad development (Score: 1.221169)



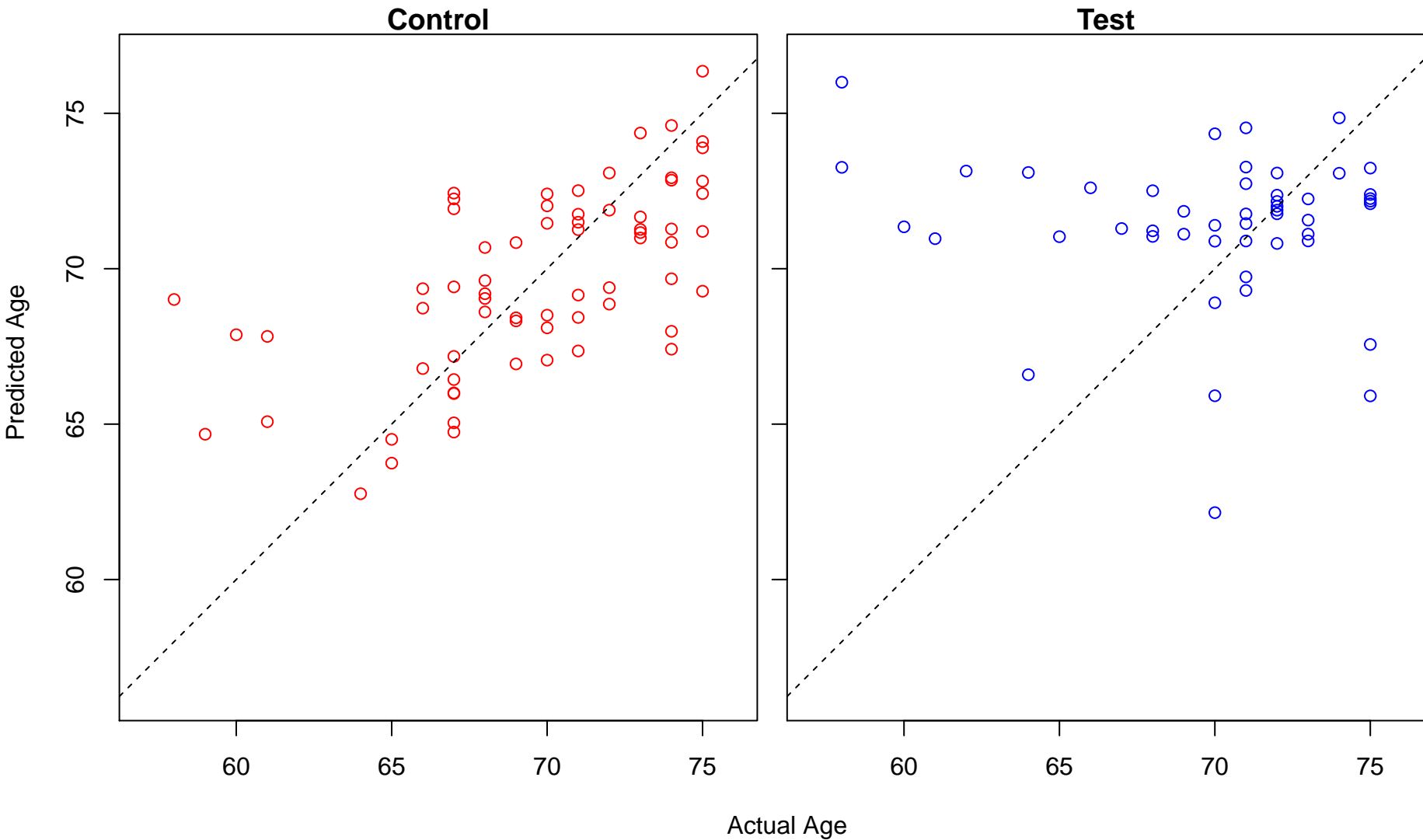
cardiolipin metabolic process (Score: 1.220982)



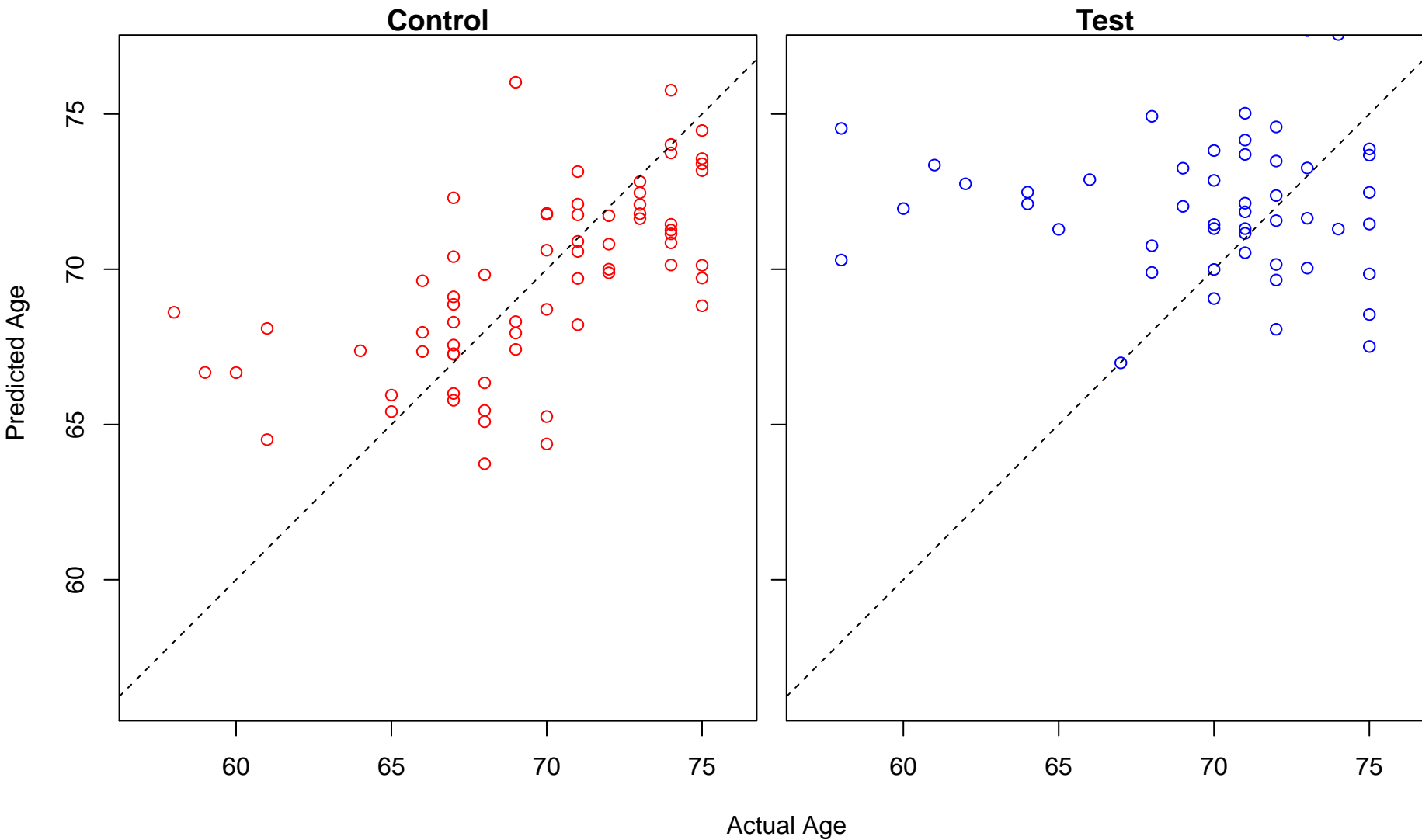
regulation of endothelial cell development (Score: 1.220902)



regulation of establishment of endothelial barrier (Score: 1.220902)

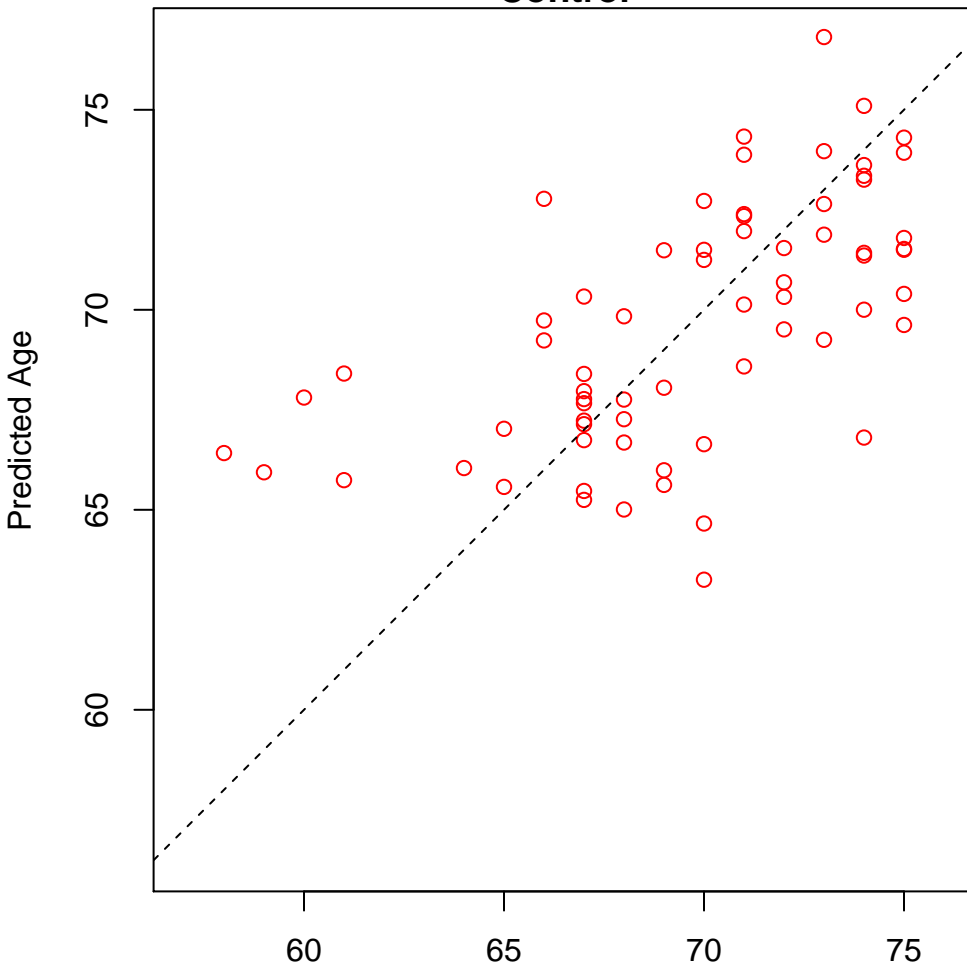


mitotic cytokinesis (Score: 1.220779)

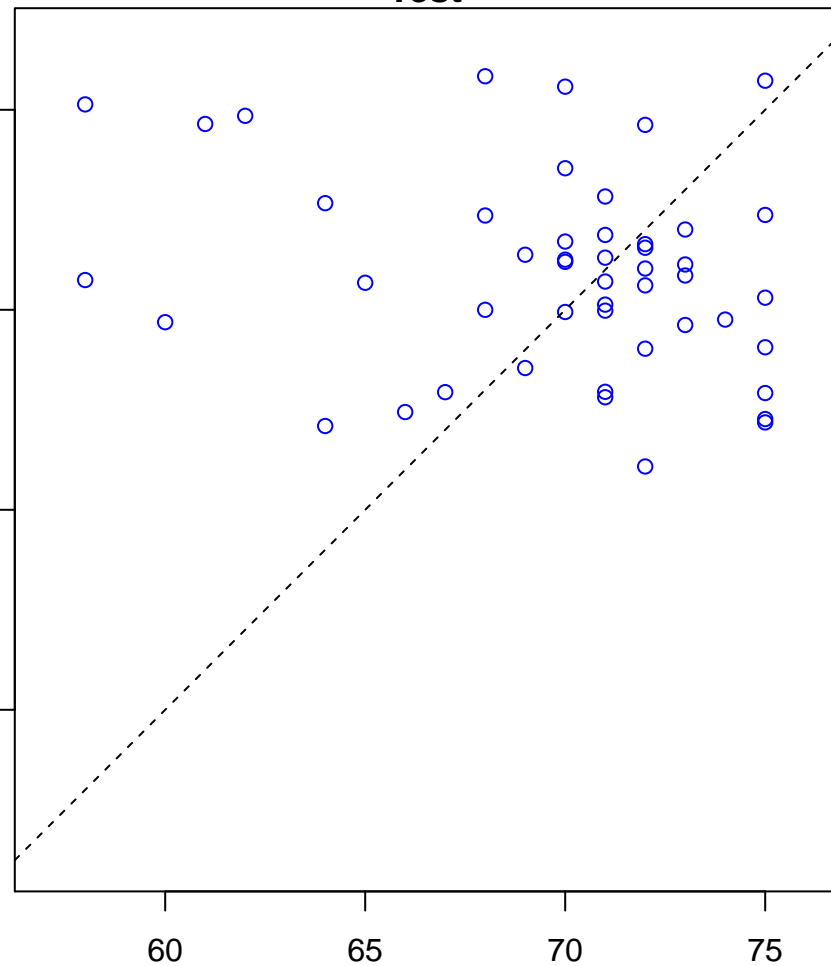


response to epidermal growth factor (Score: 1.220363)

Control

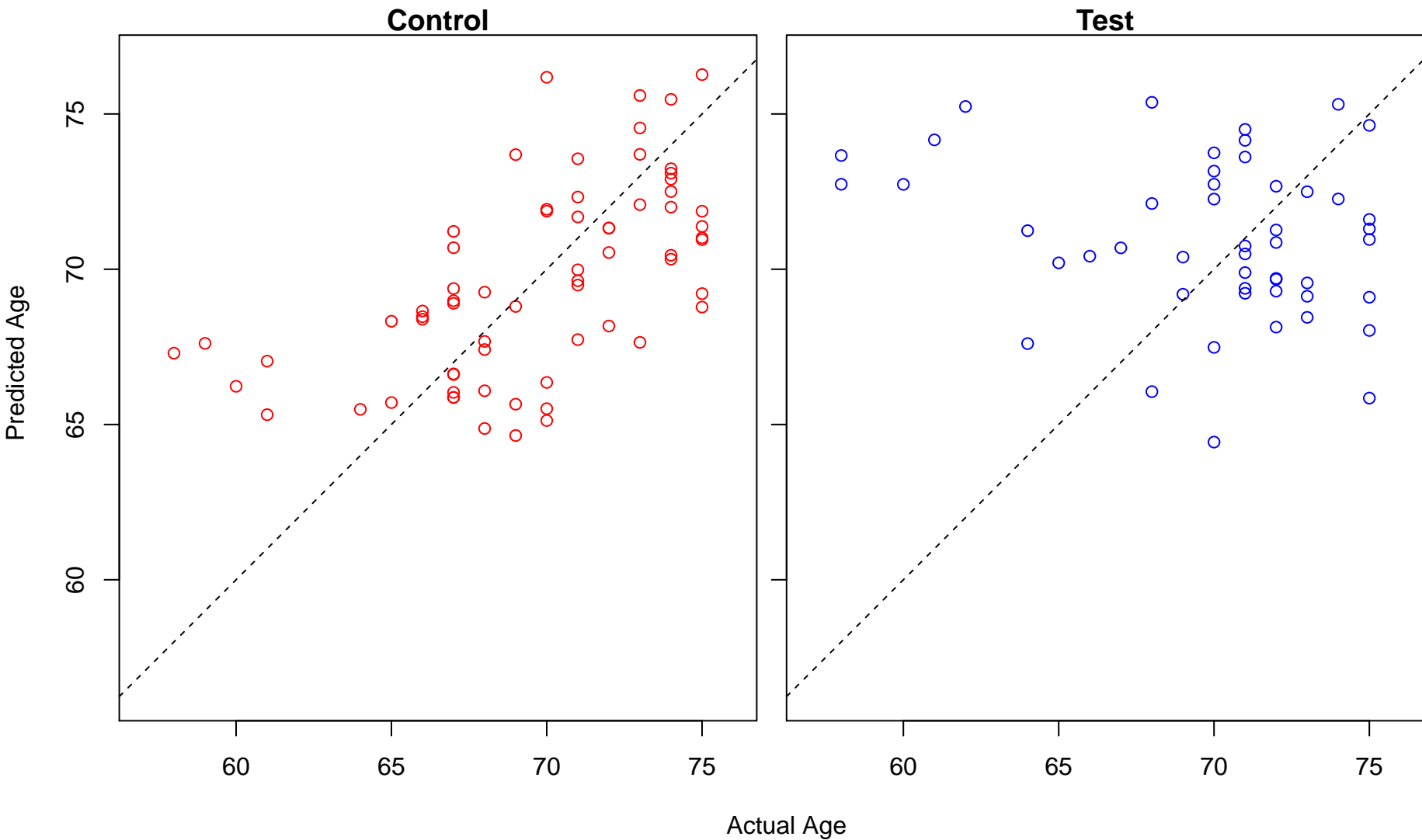


Test

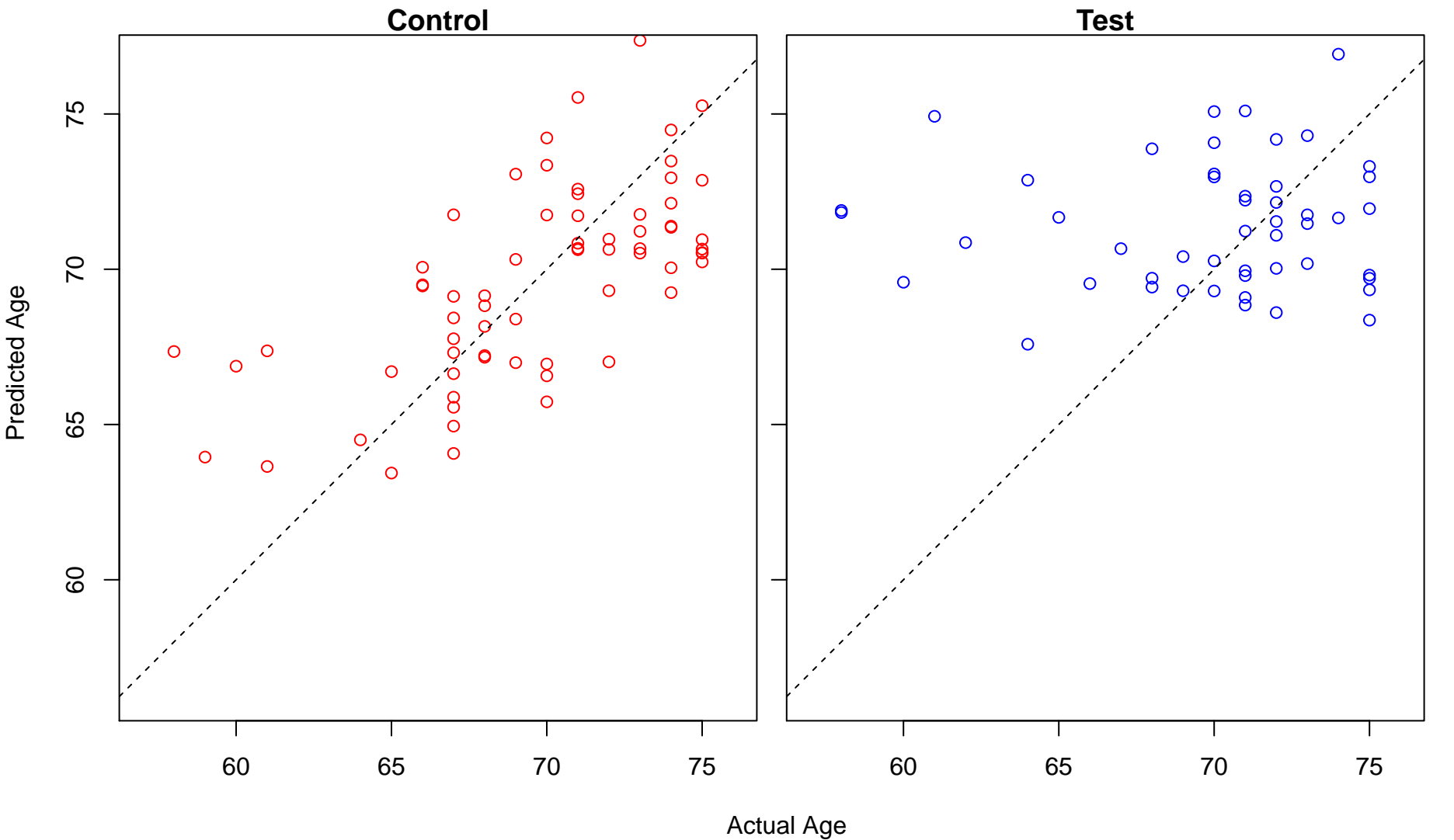


Actual Age

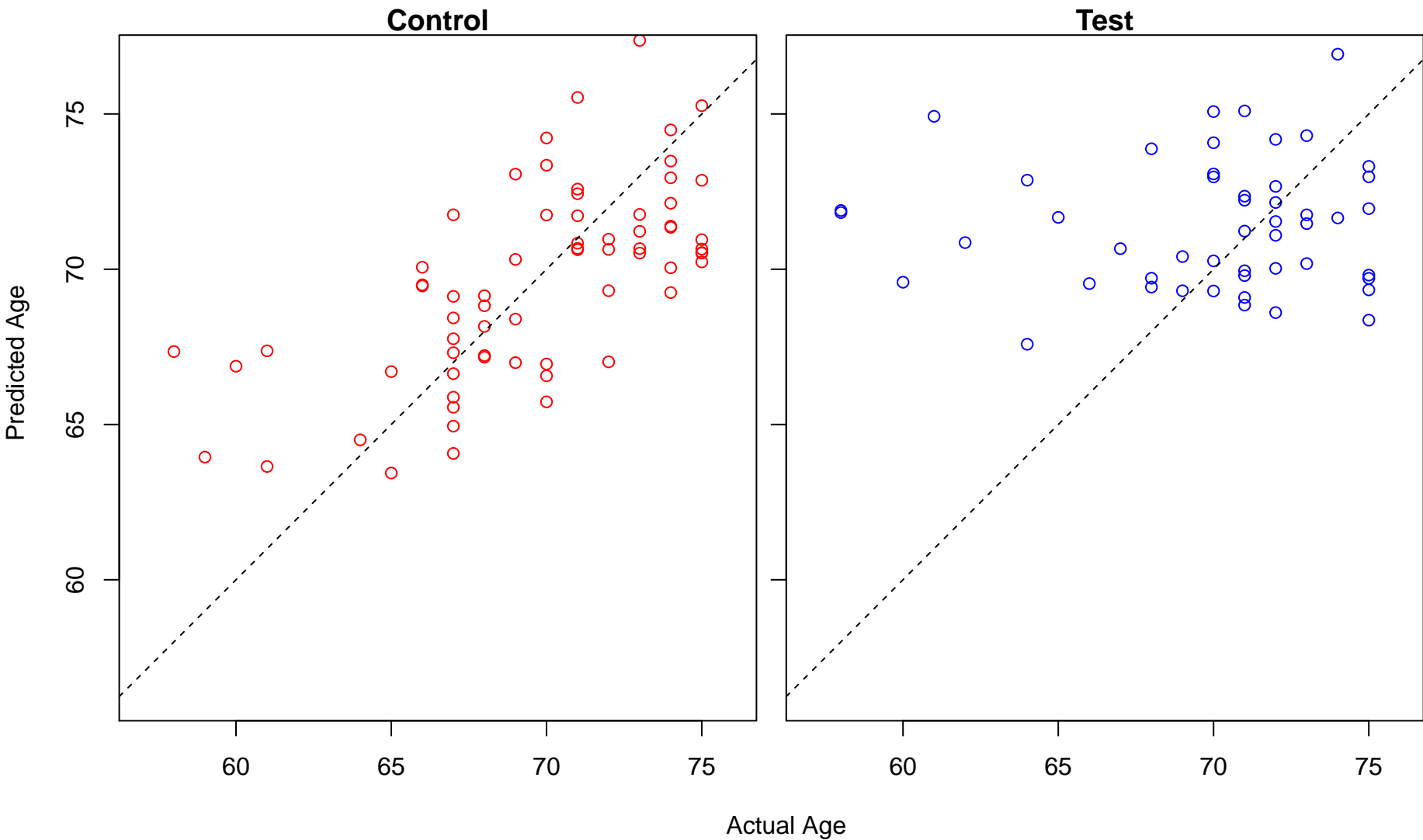
negative regulation of autophagy (Score: 1.220104)



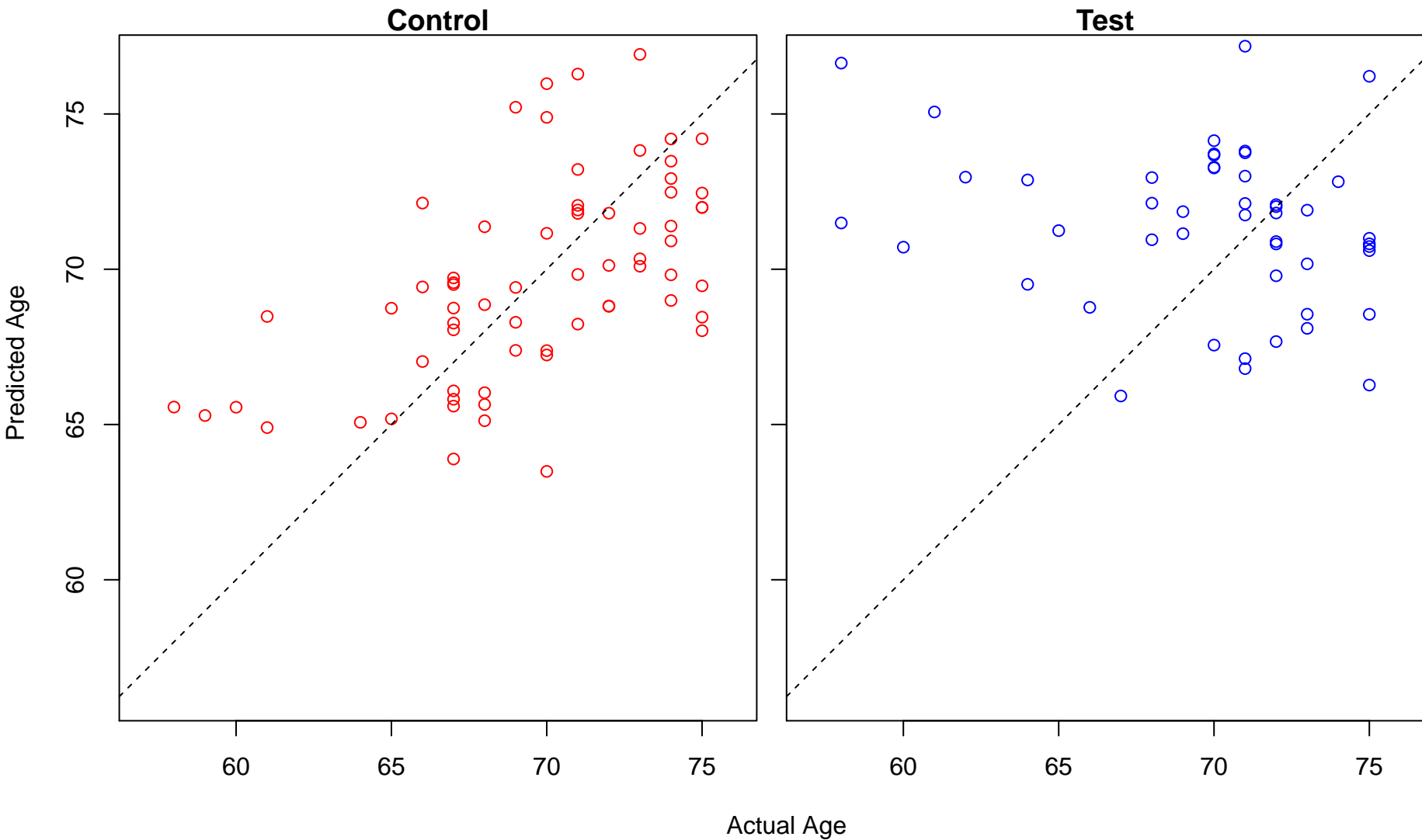
Regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (Score



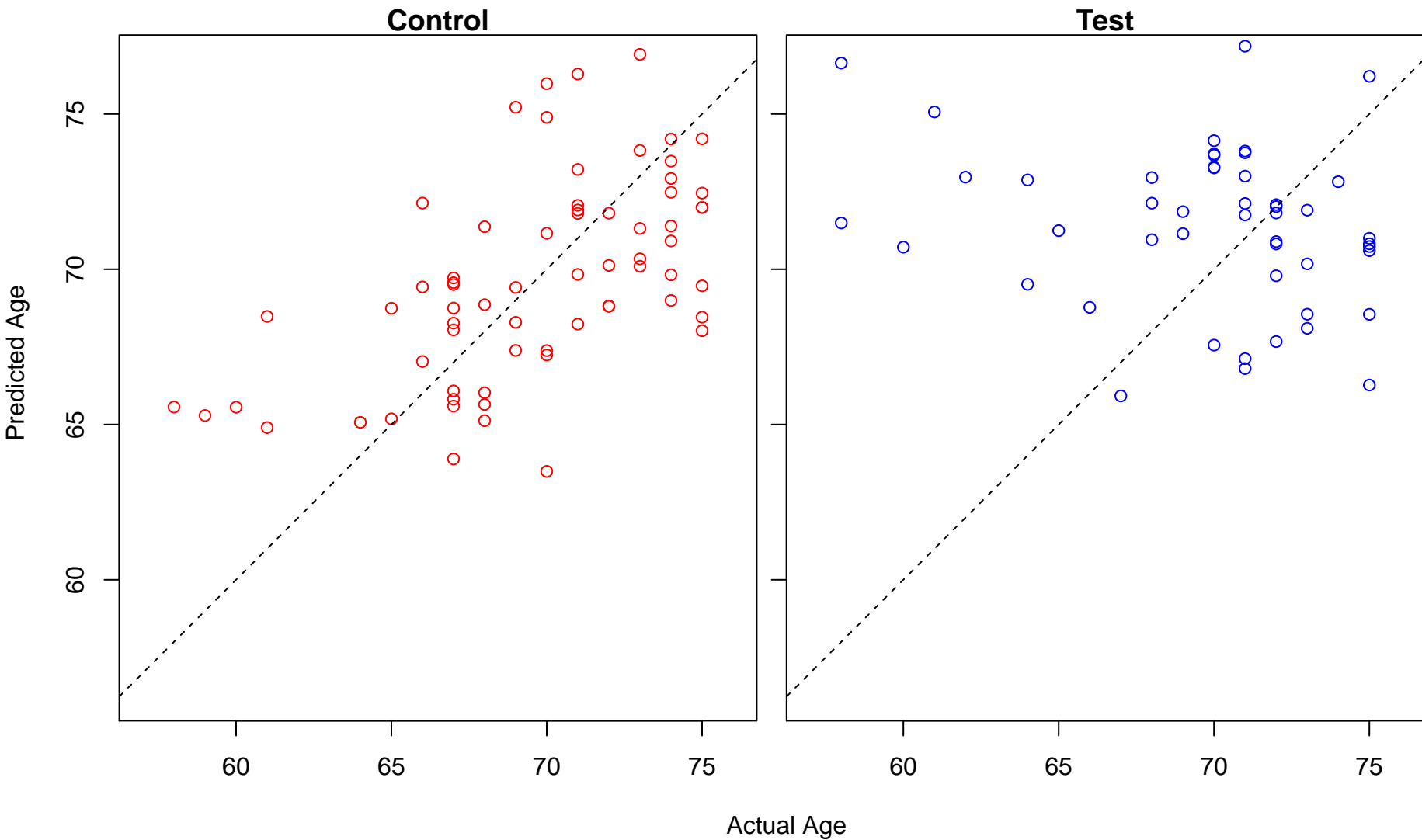
e regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (S



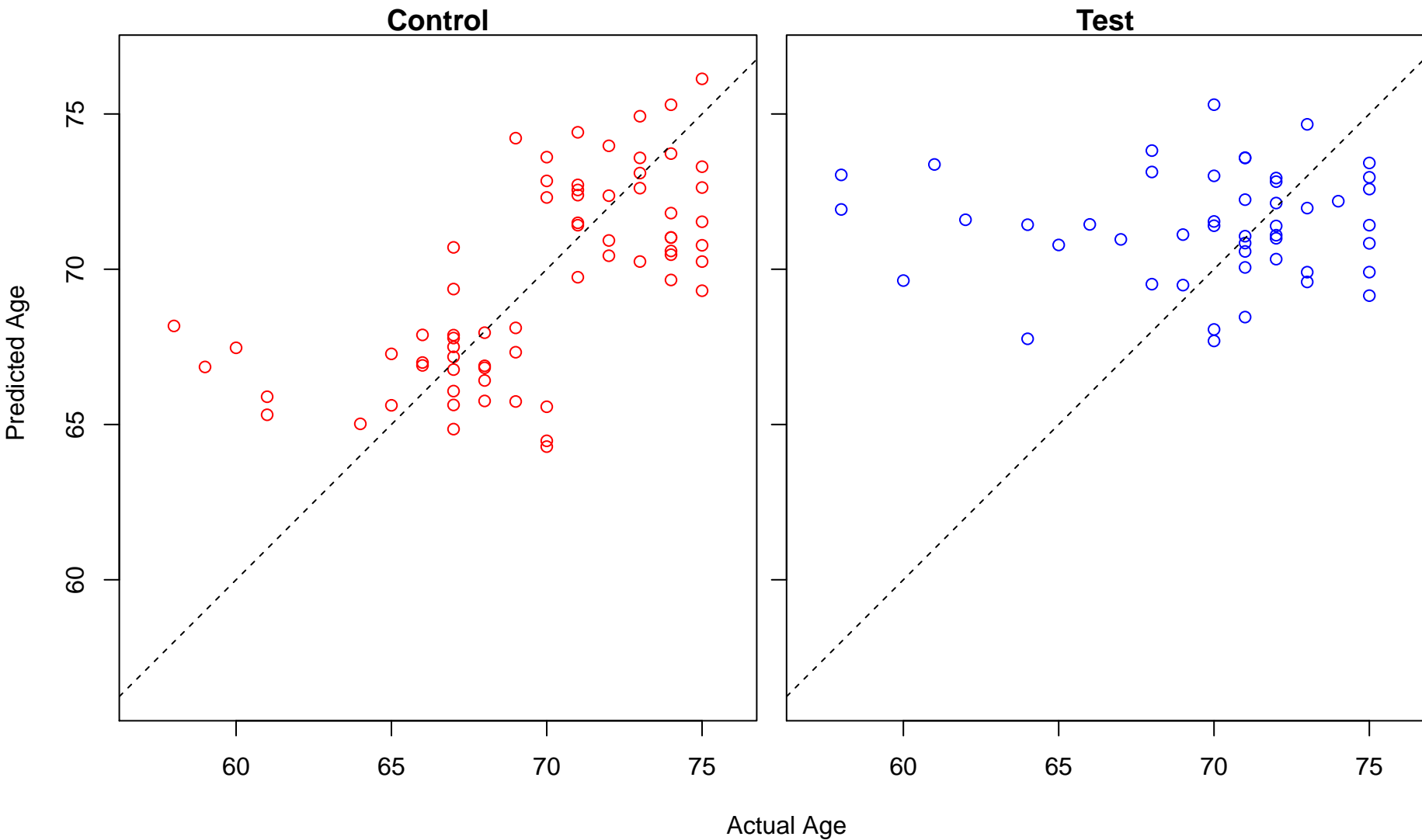
mononuclear cell proliferation (Score: 1.218564)



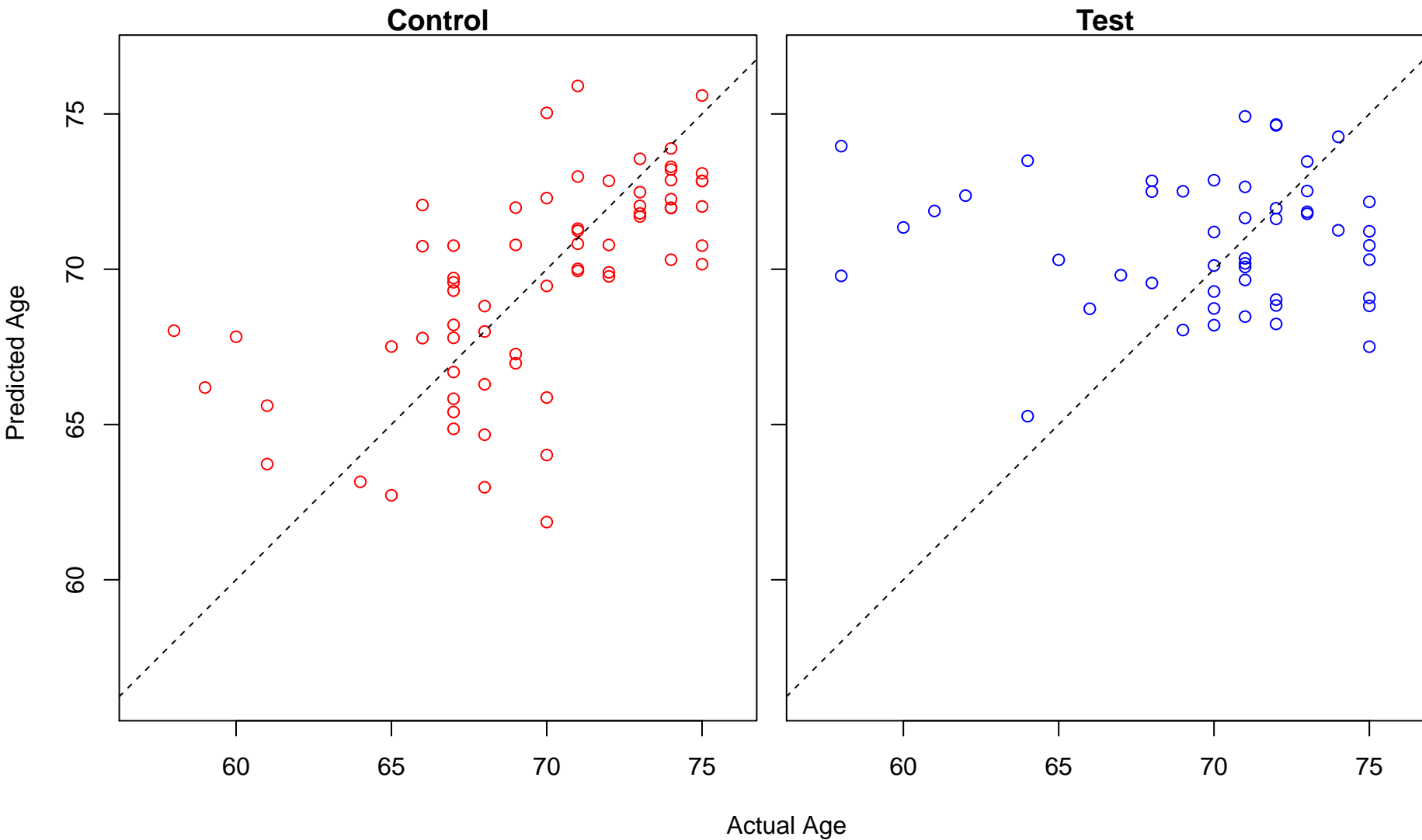
lymphocyte proliferation (Score: 1.218564)



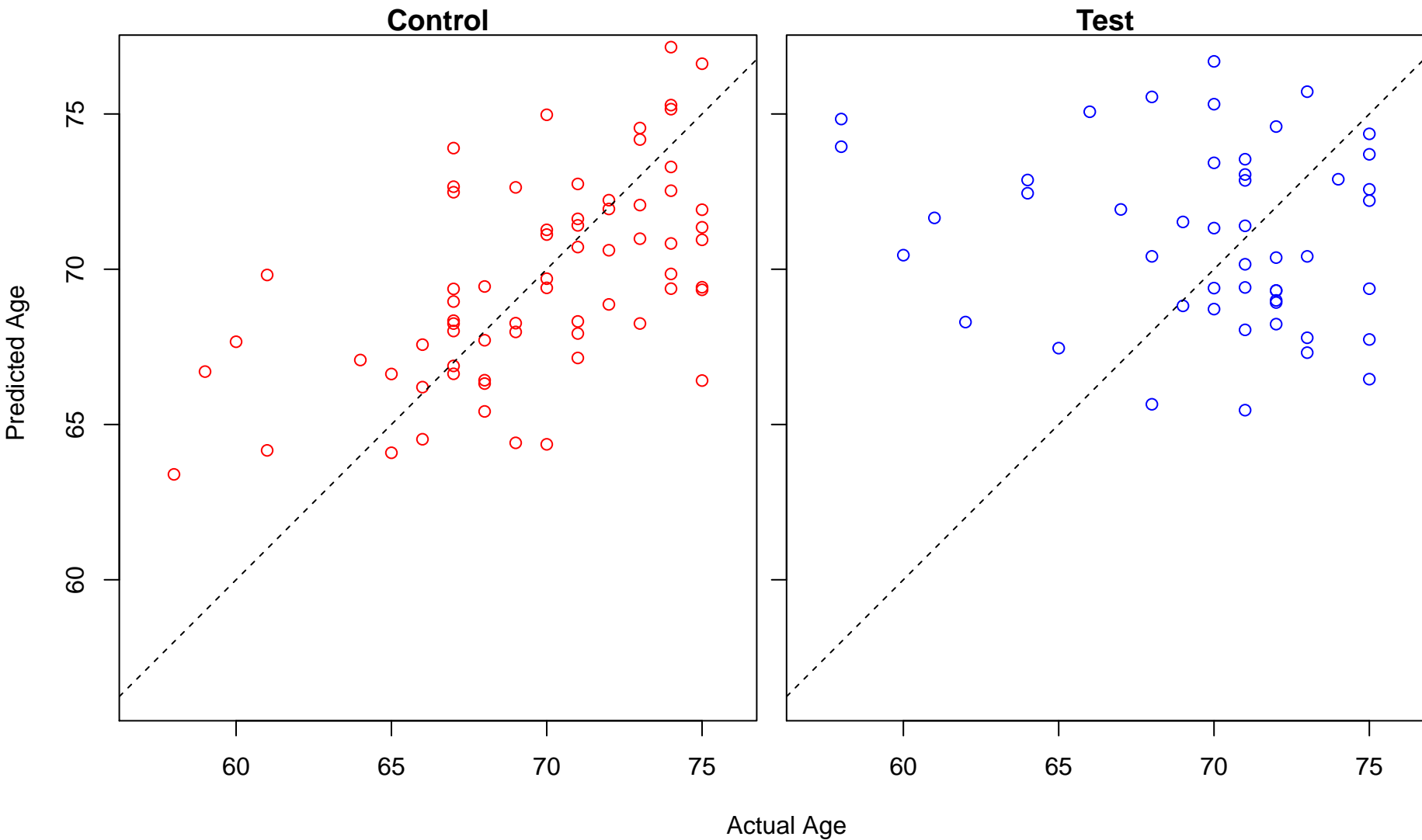
regulation of phosphatase activity (Score: 1.218233)



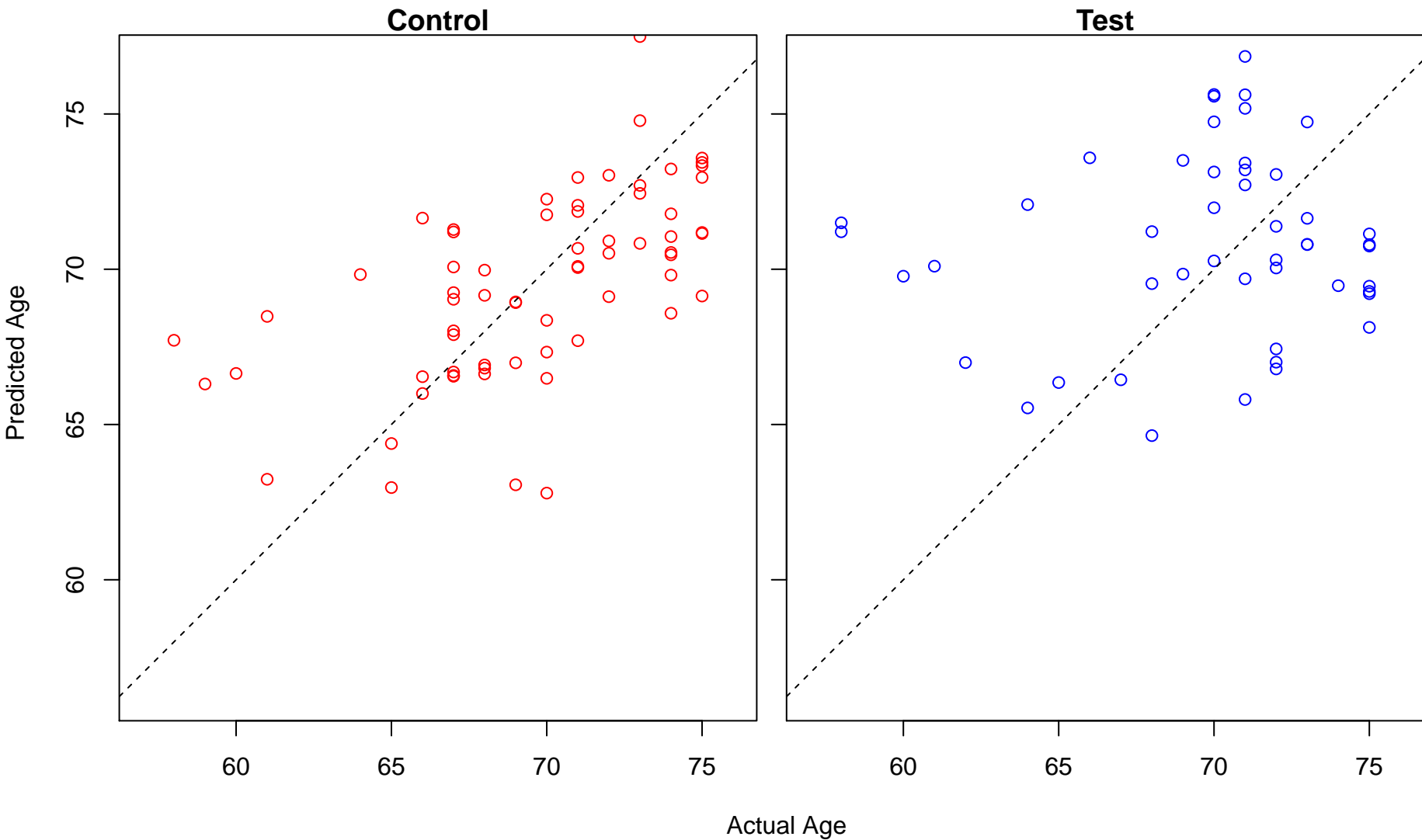
sex differentiation (Score: 1.217168)



protein myristoylation (Score: 1.217153)

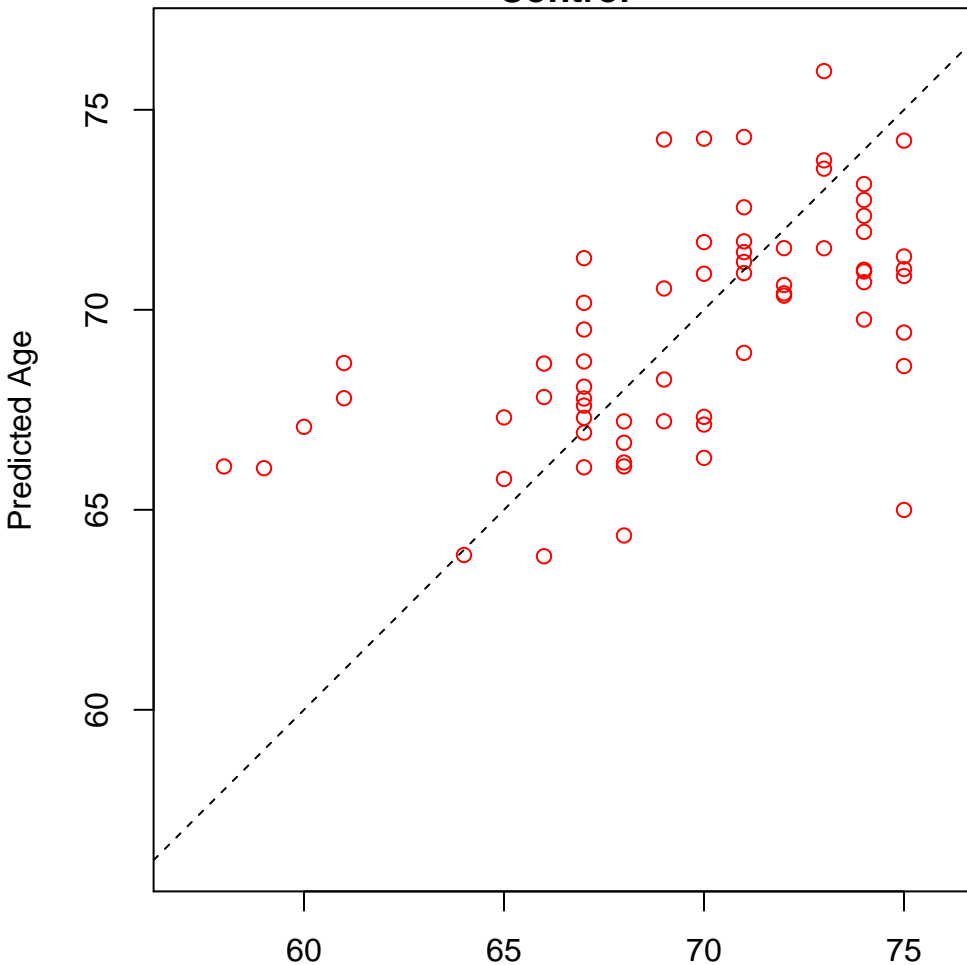


negative regulation of coagulation (Score: 1.216832)

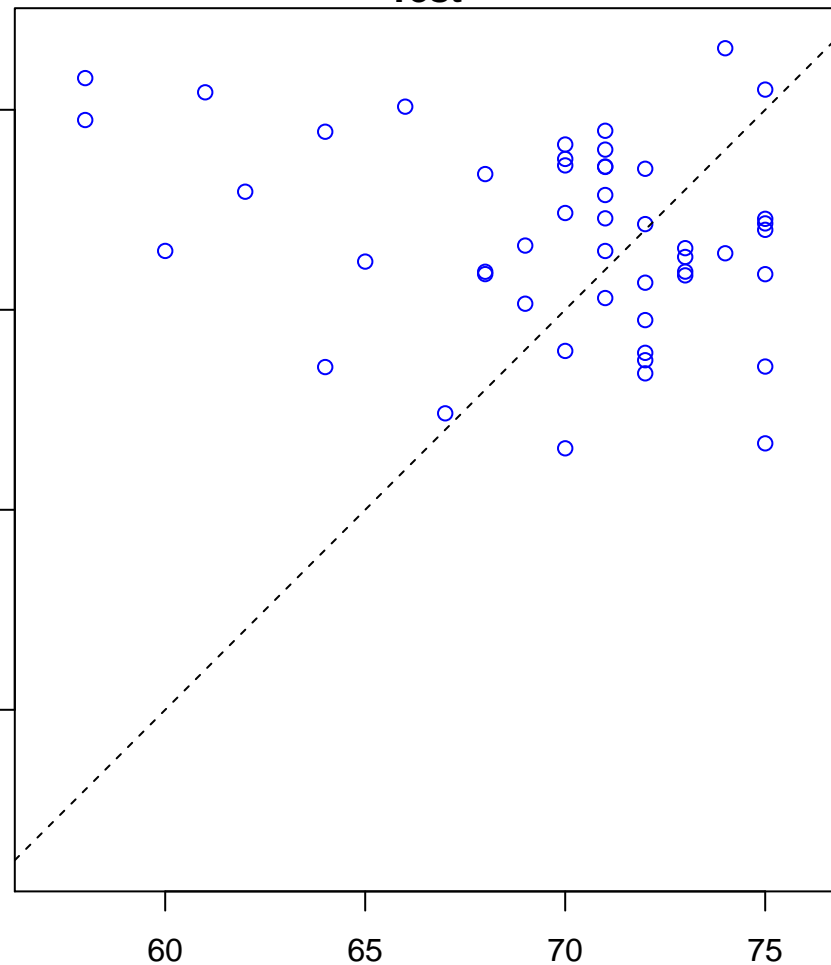


sensory perception of light stimulus (Score: 1.216794)

Control

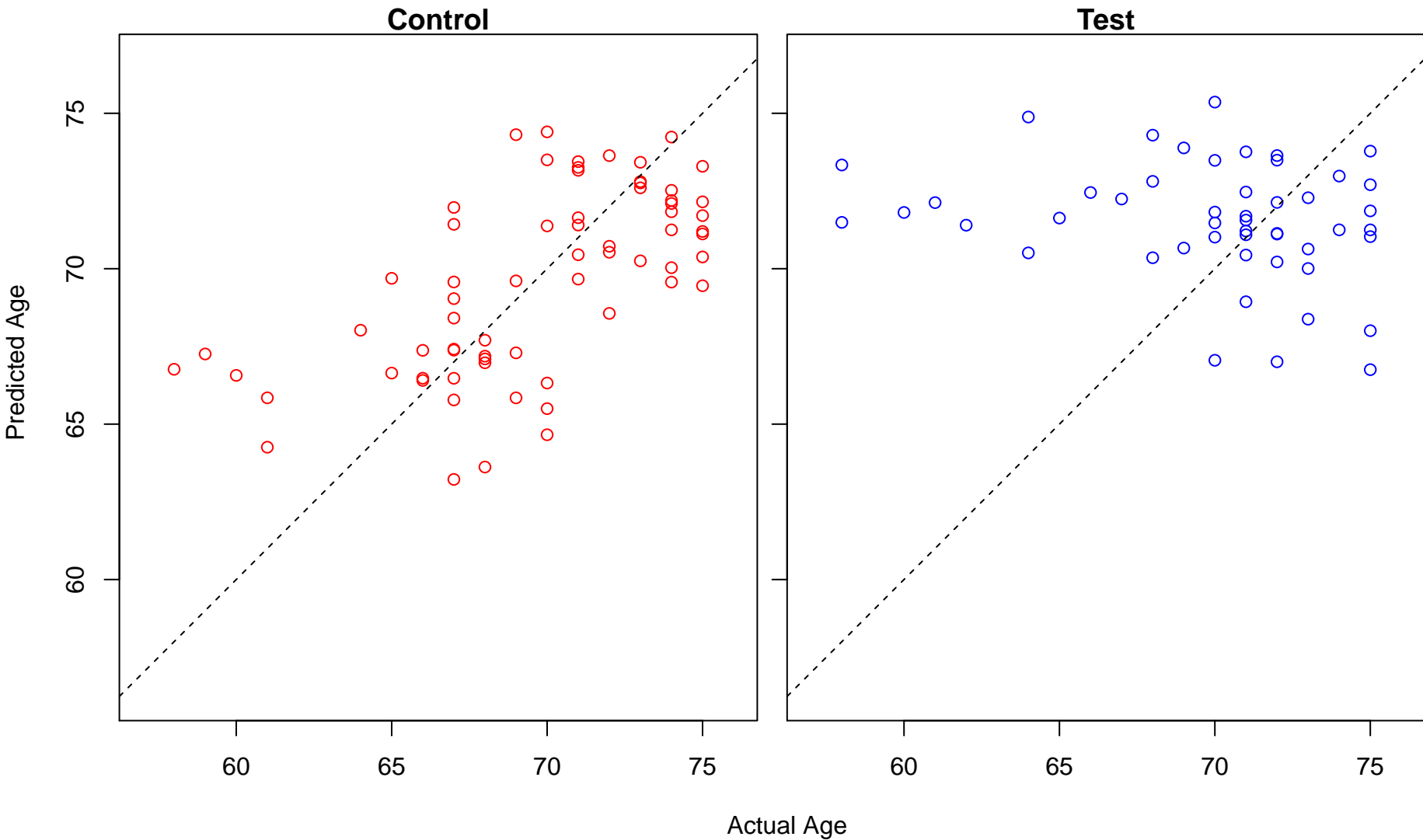


Test



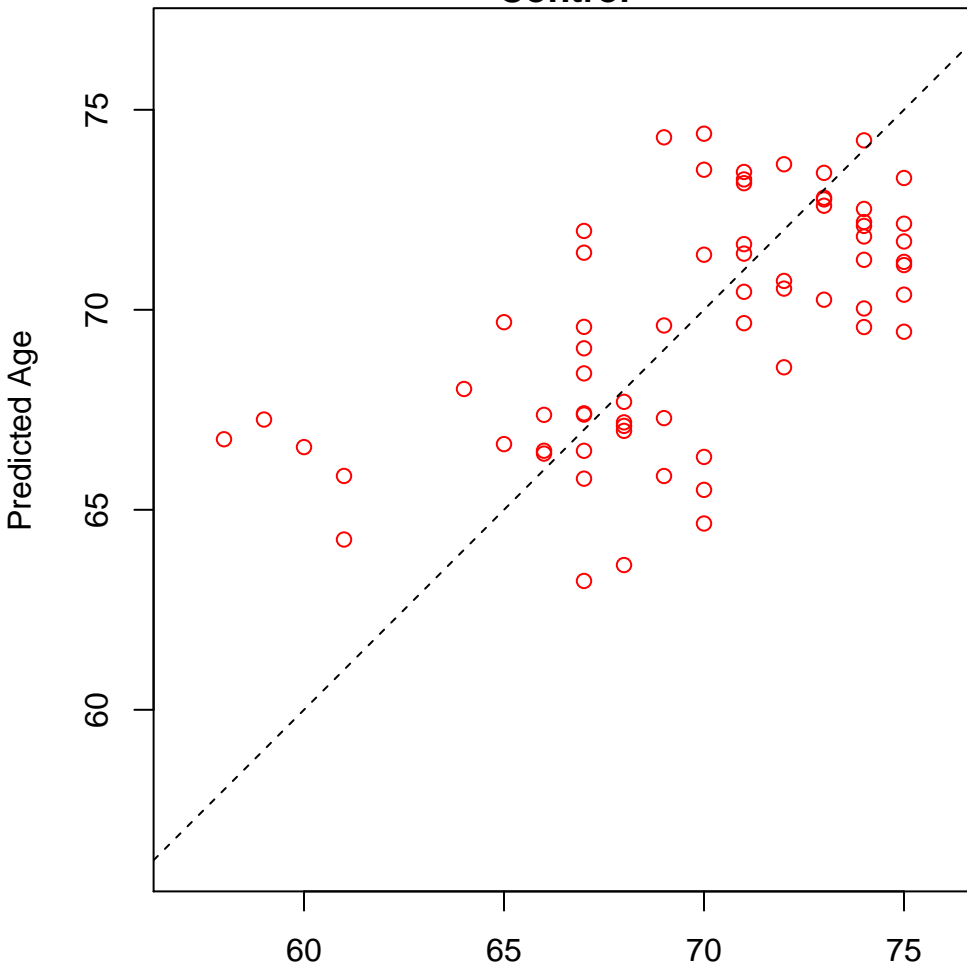
Actual Age

intrinsic apoptotic signaling pathway in response to oxidative stress (Score: 1.216603)

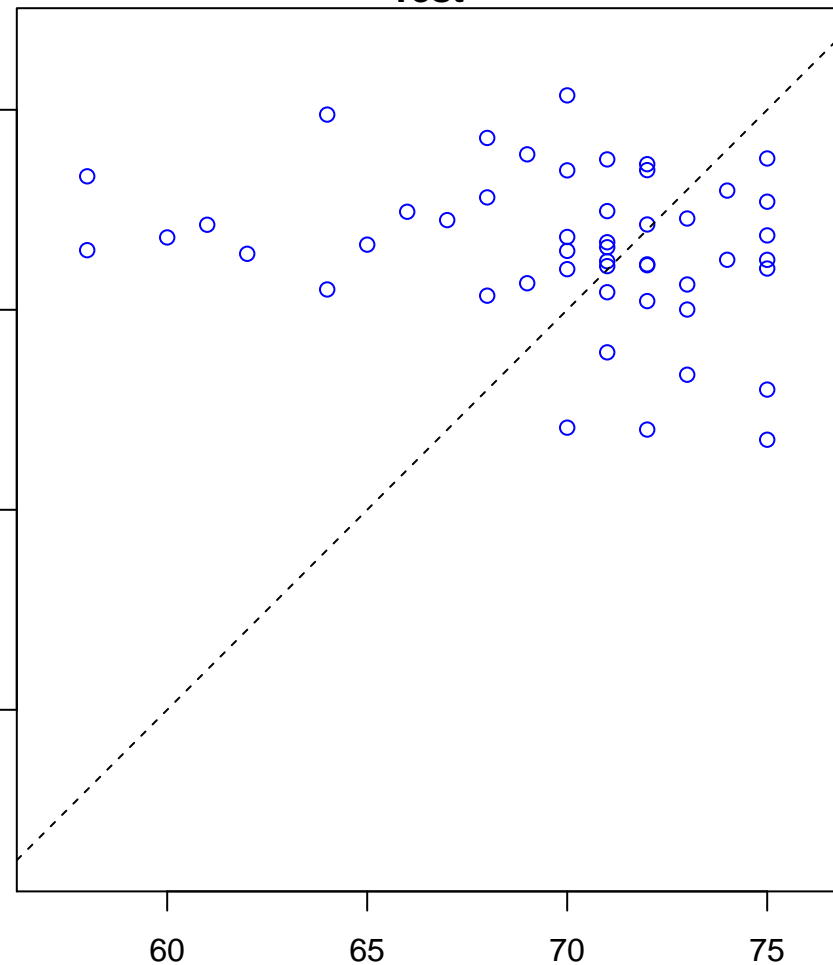


cell death in response to oxidative stress (Score: 1.216603)

Control

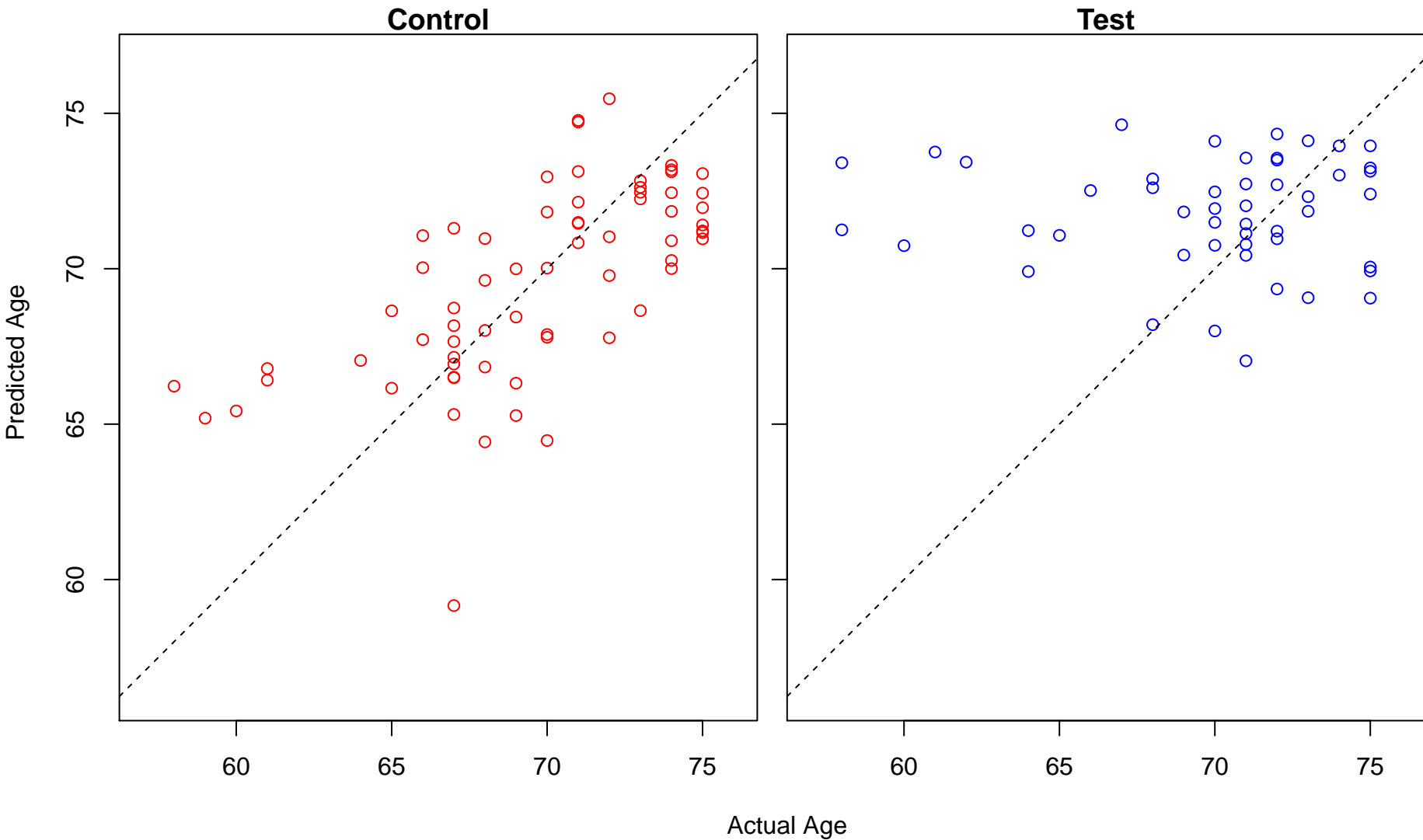


Test

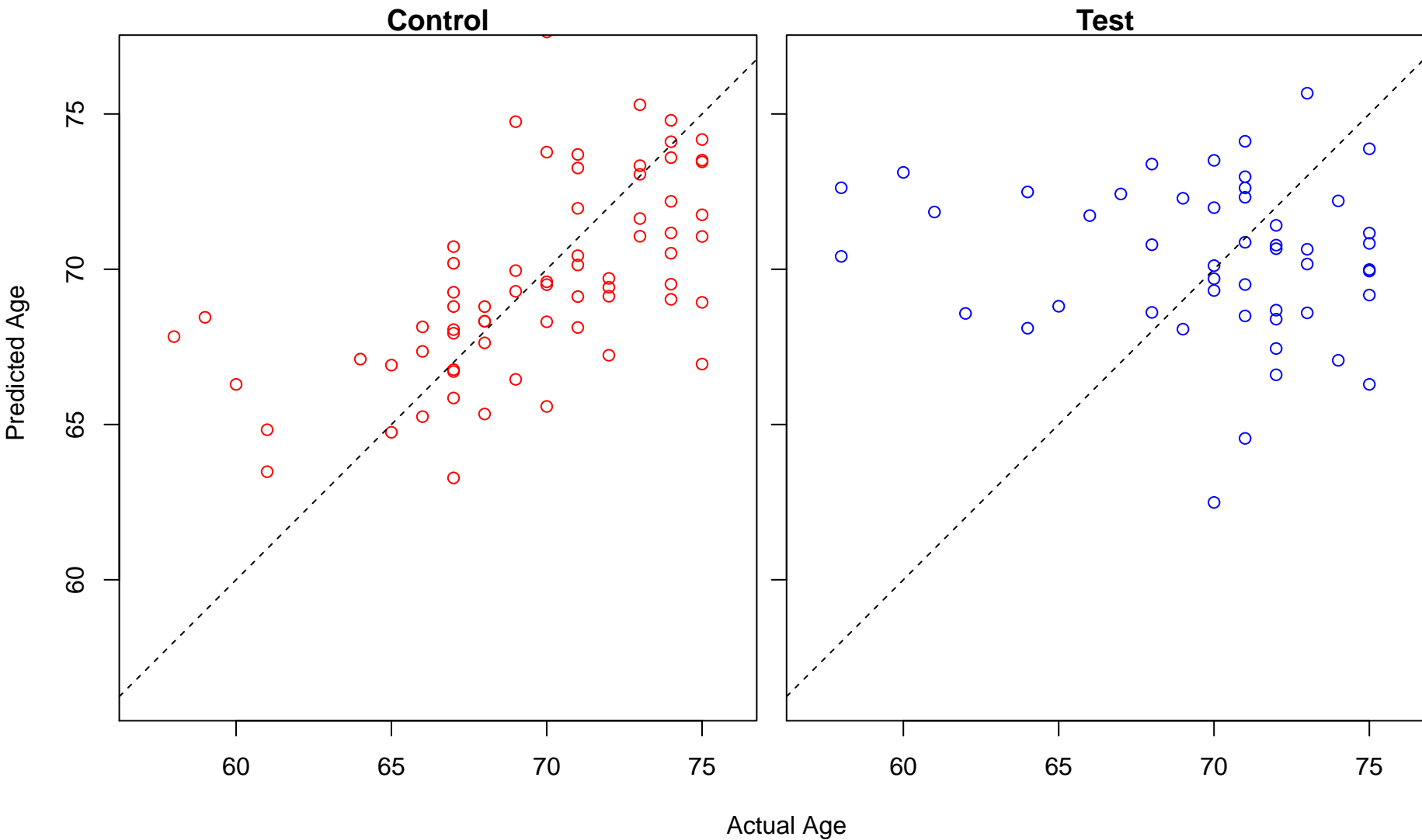


Actual Age

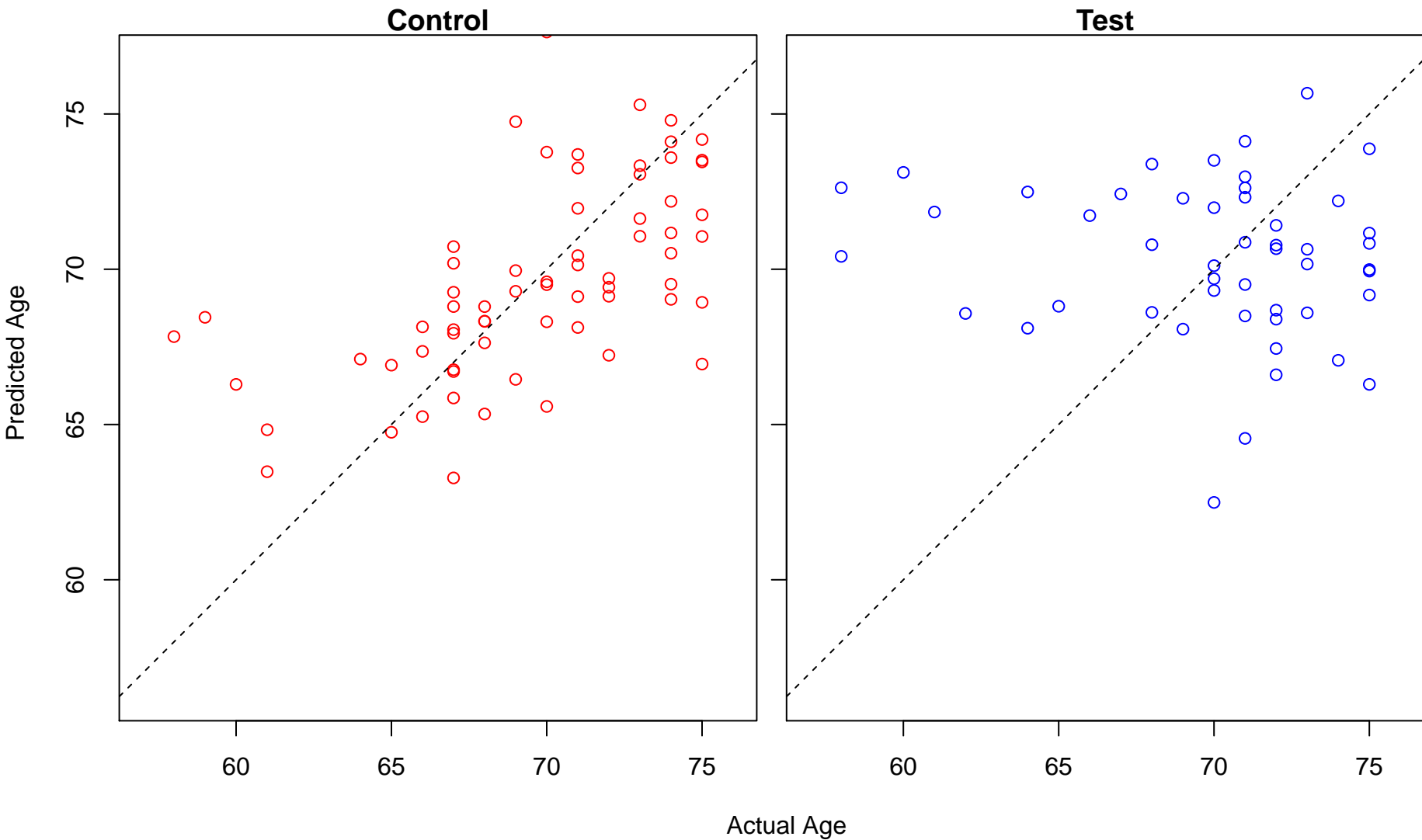
positive regulation of translational initiation (Score: 1.216260)



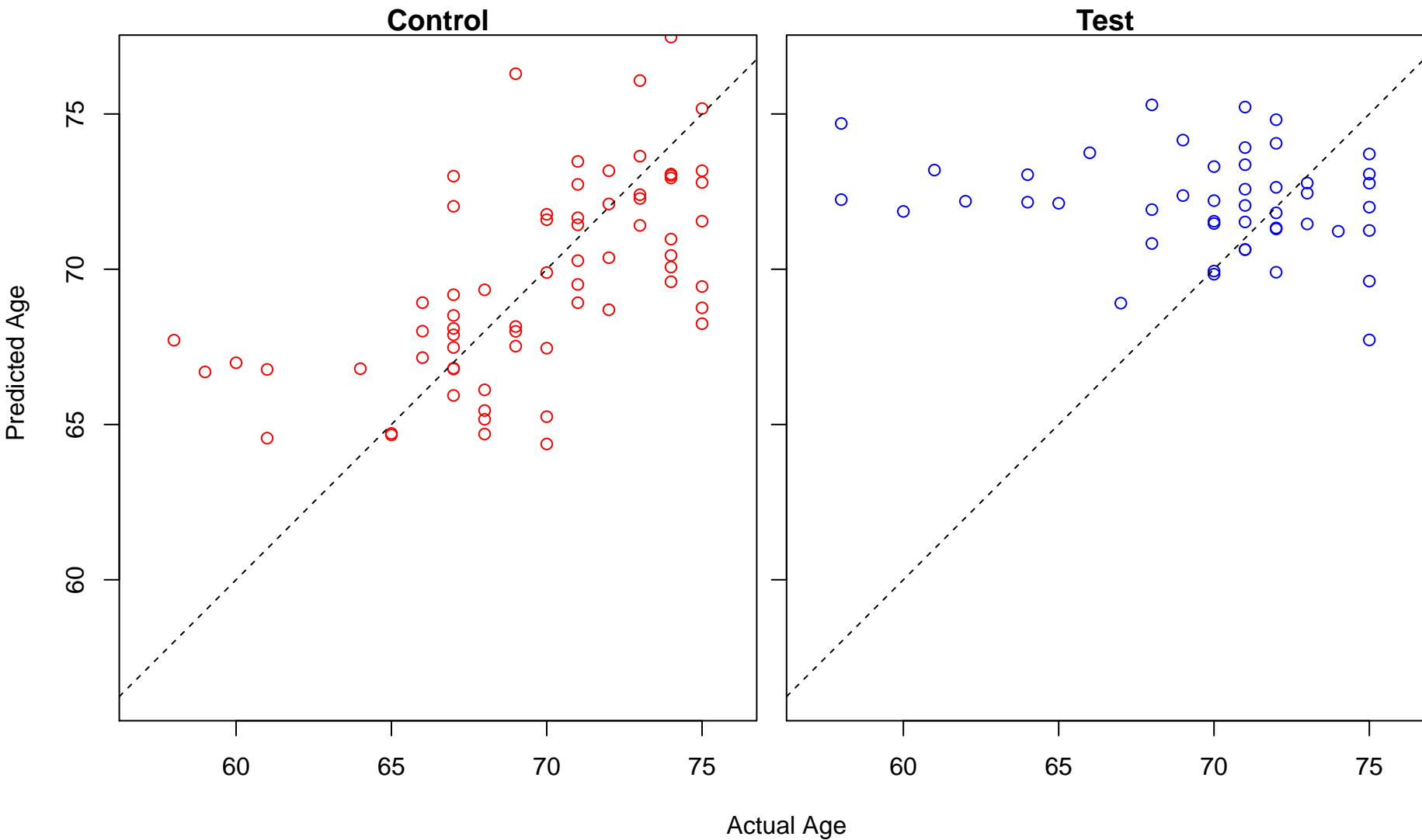
negative regulation of nucleotide biosynthetic process (Score: 1.216173)



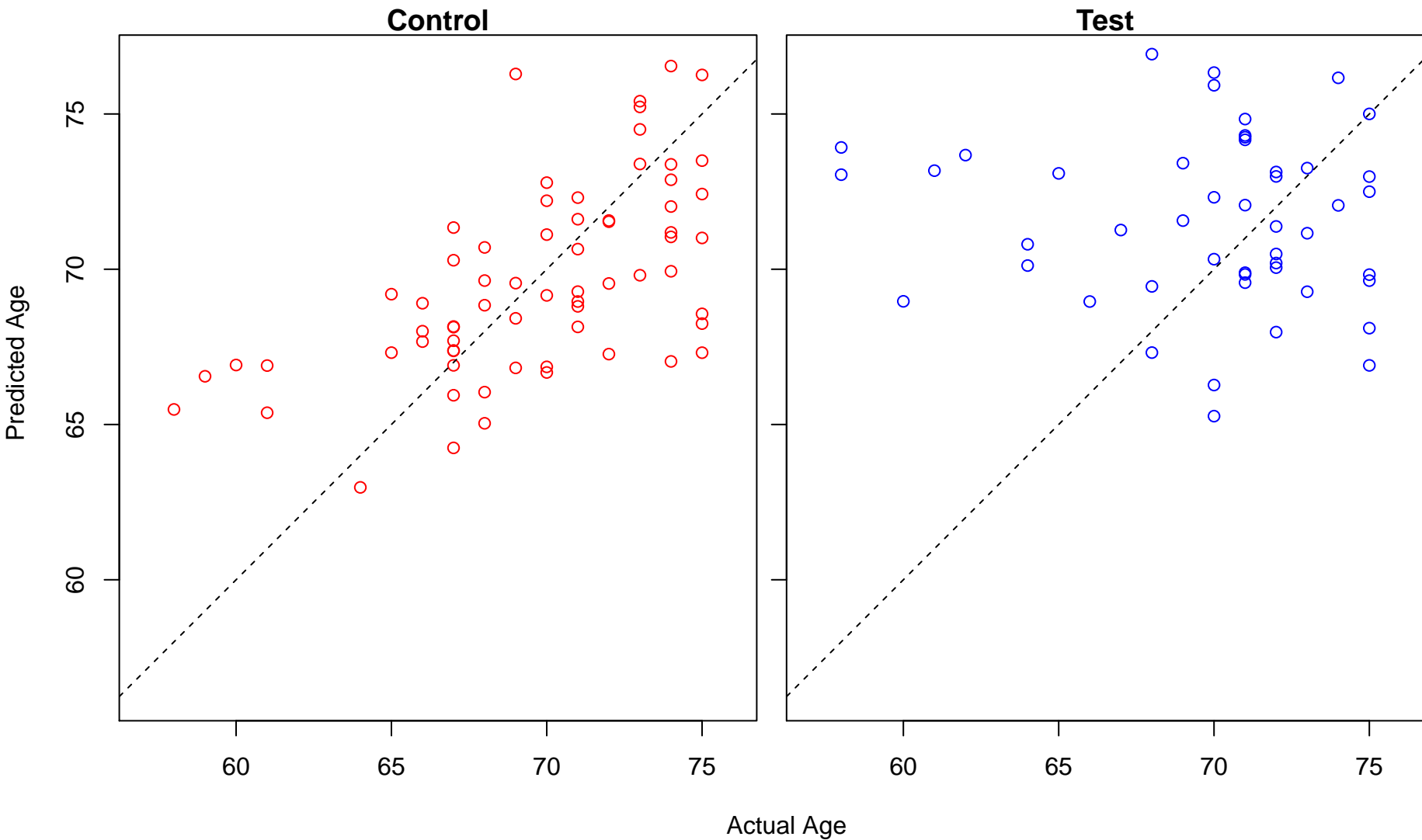
negative regulation of purine nucleotide biosynthetic process (Score: 1.216173)



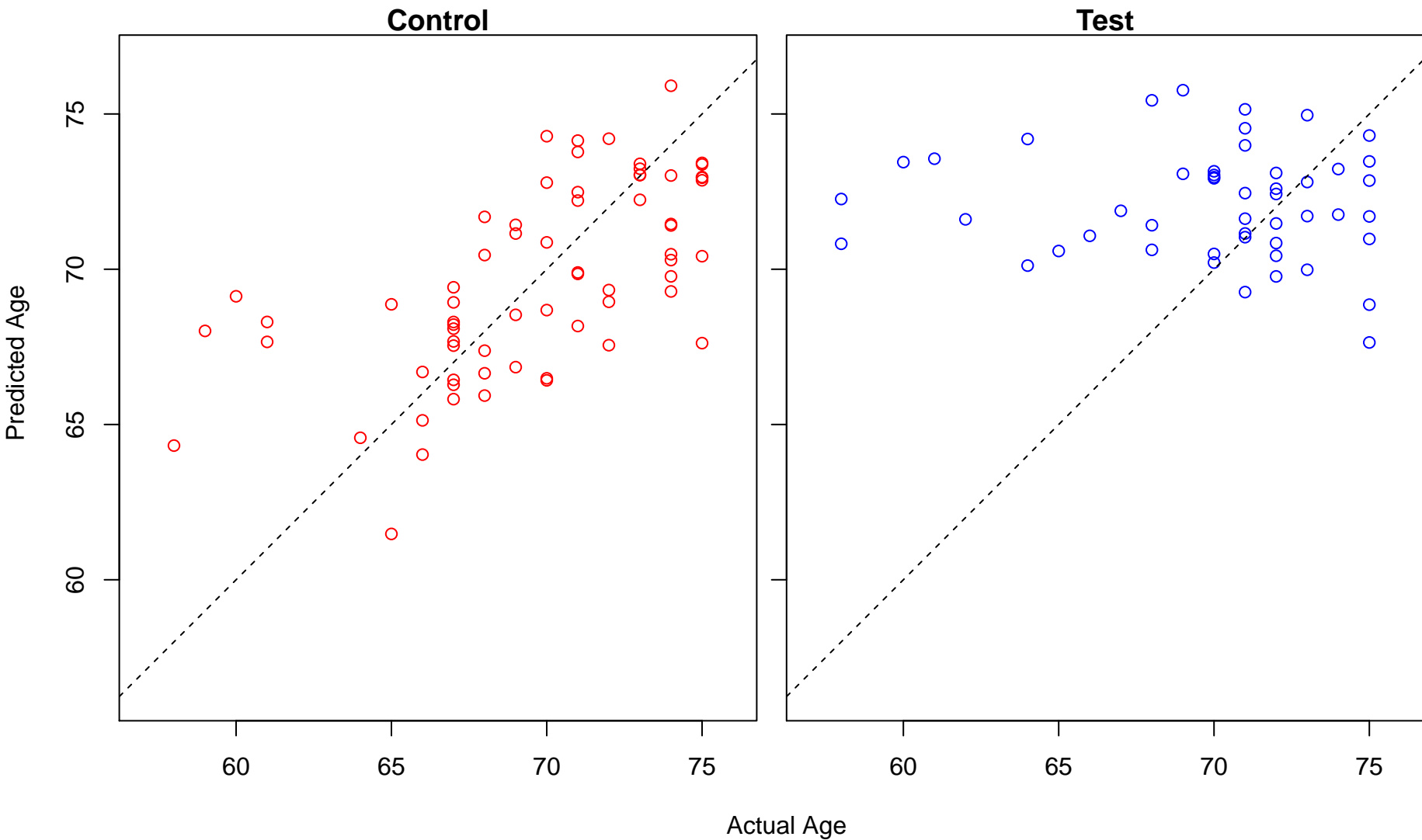
cytoskeleton-dependent cytokinesis (Score: 1.215721)



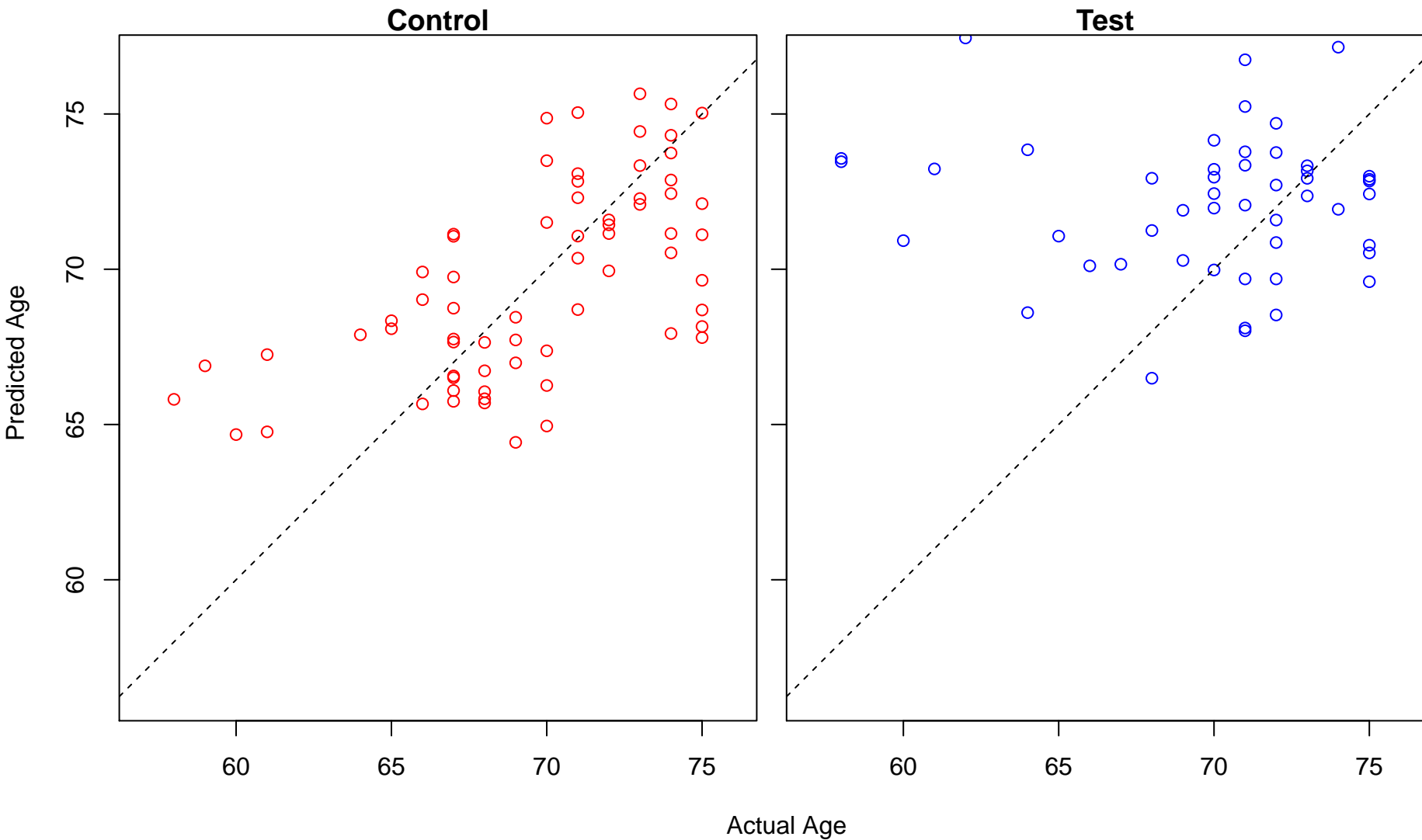
cell-cell junction assembly (Score: 1.215708)



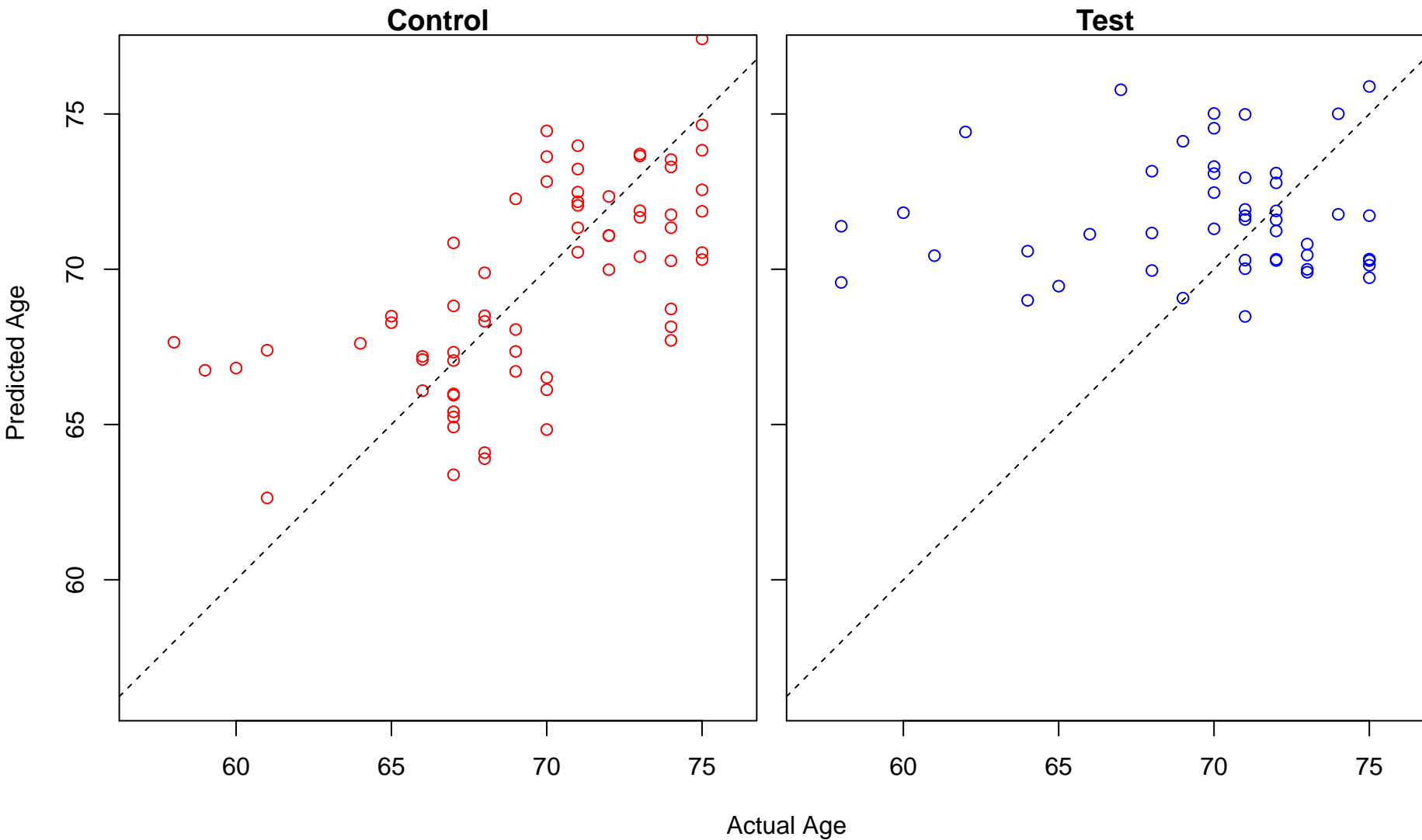
positive regulation of cAMP metabolic process (Score: 1.215315)



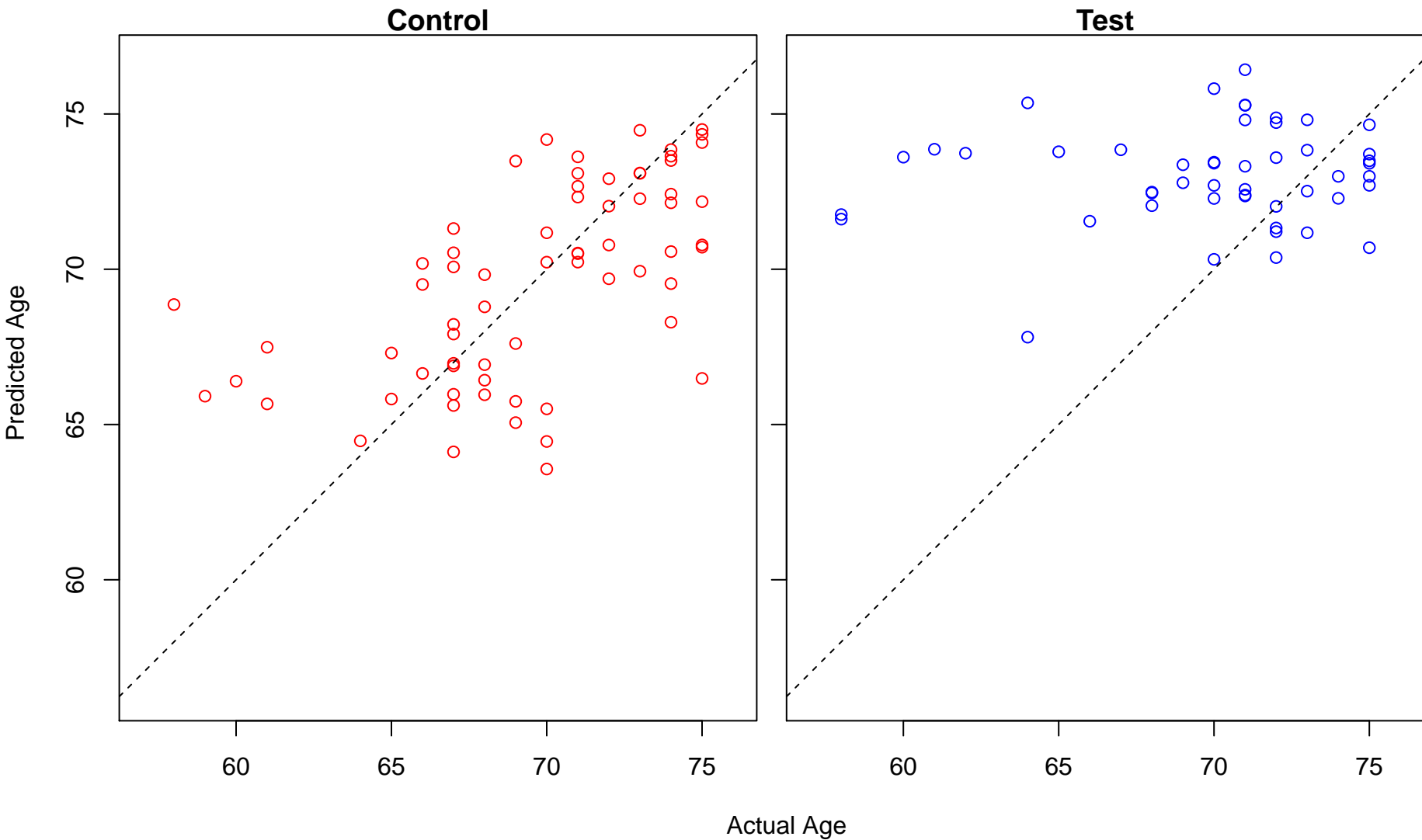
ammonium transmembrane transport (Score: 1.215228)



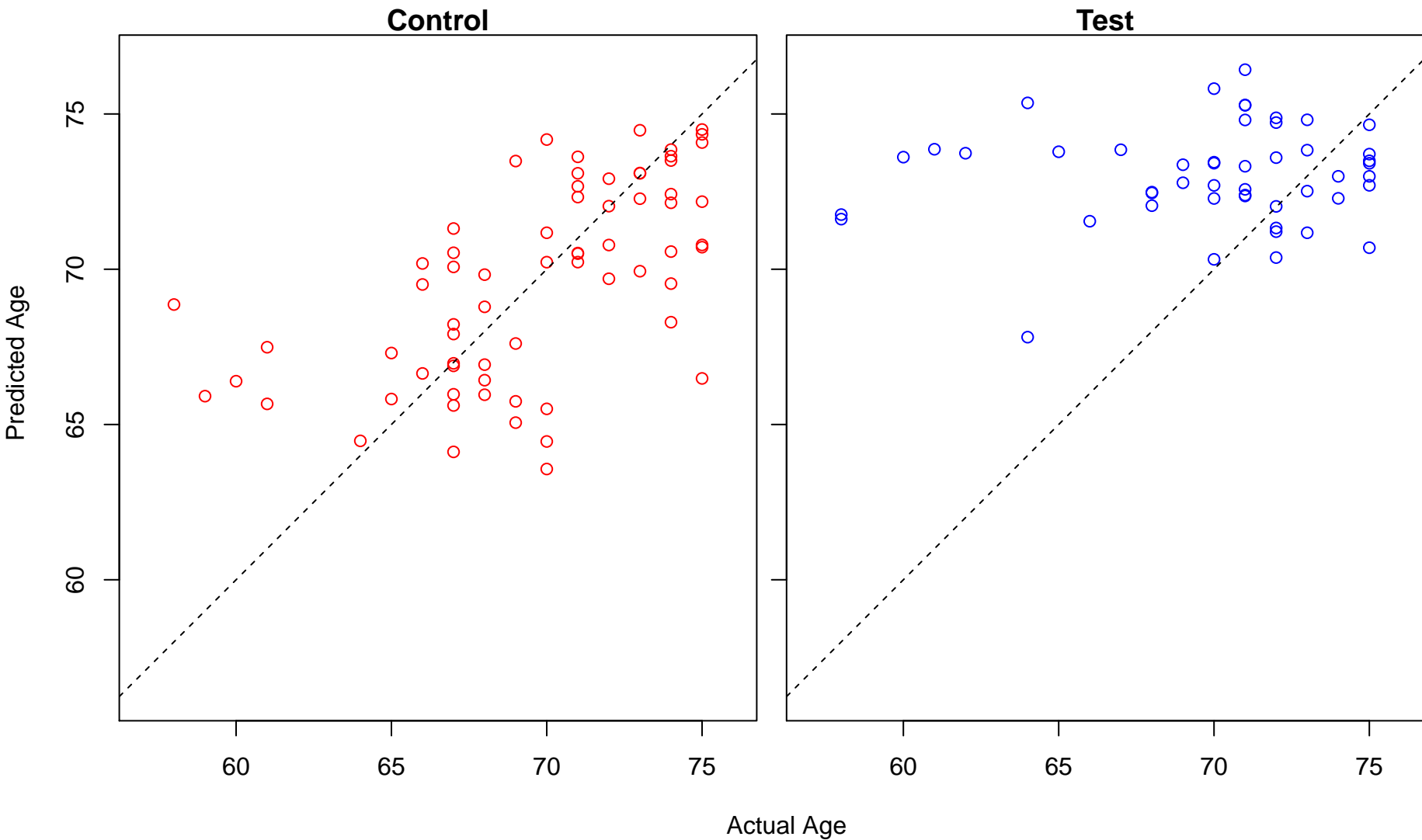
positive regulation of nuclear division (Score: 1.215083)



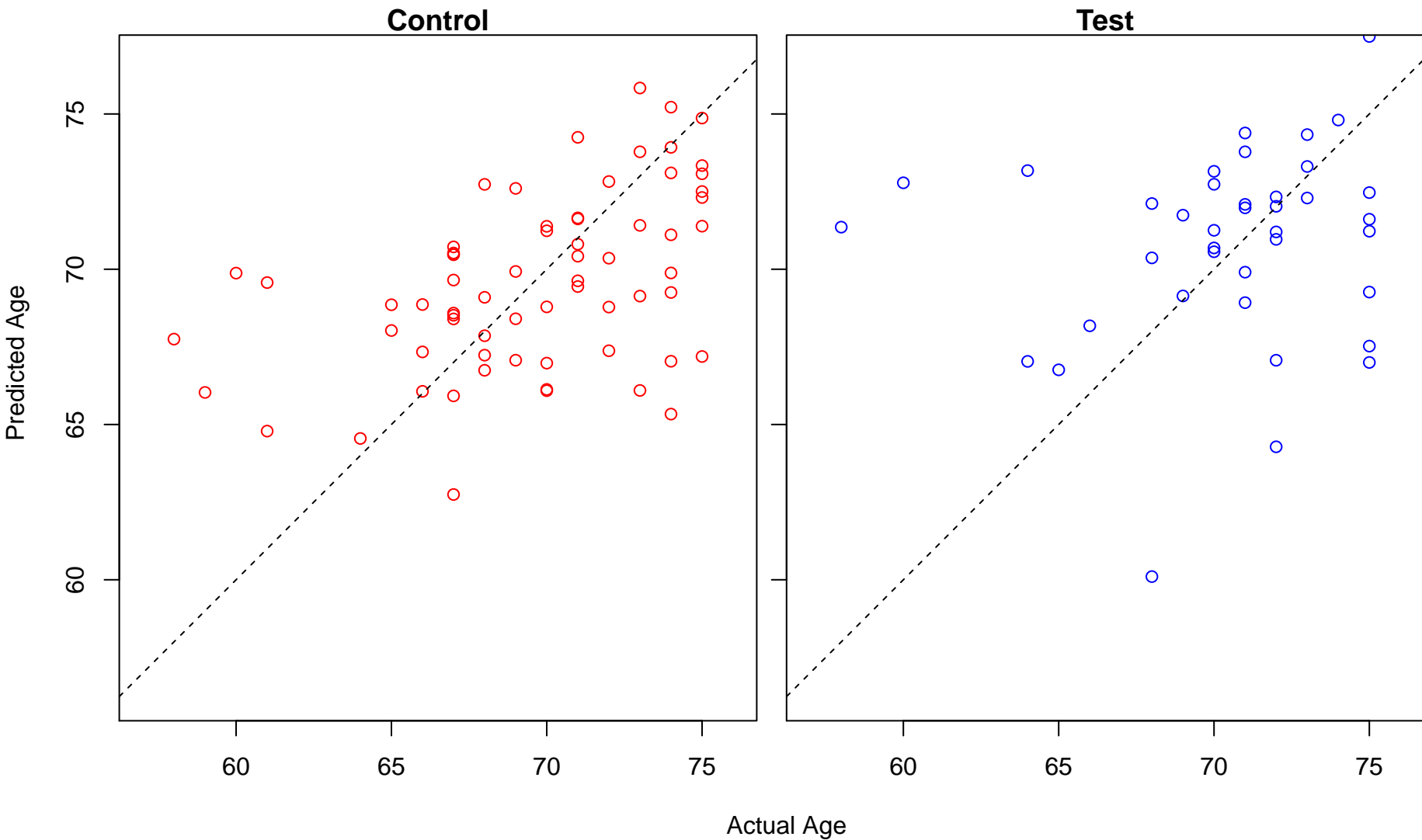
cellular glucan metabolic process (Score: 1.214768)



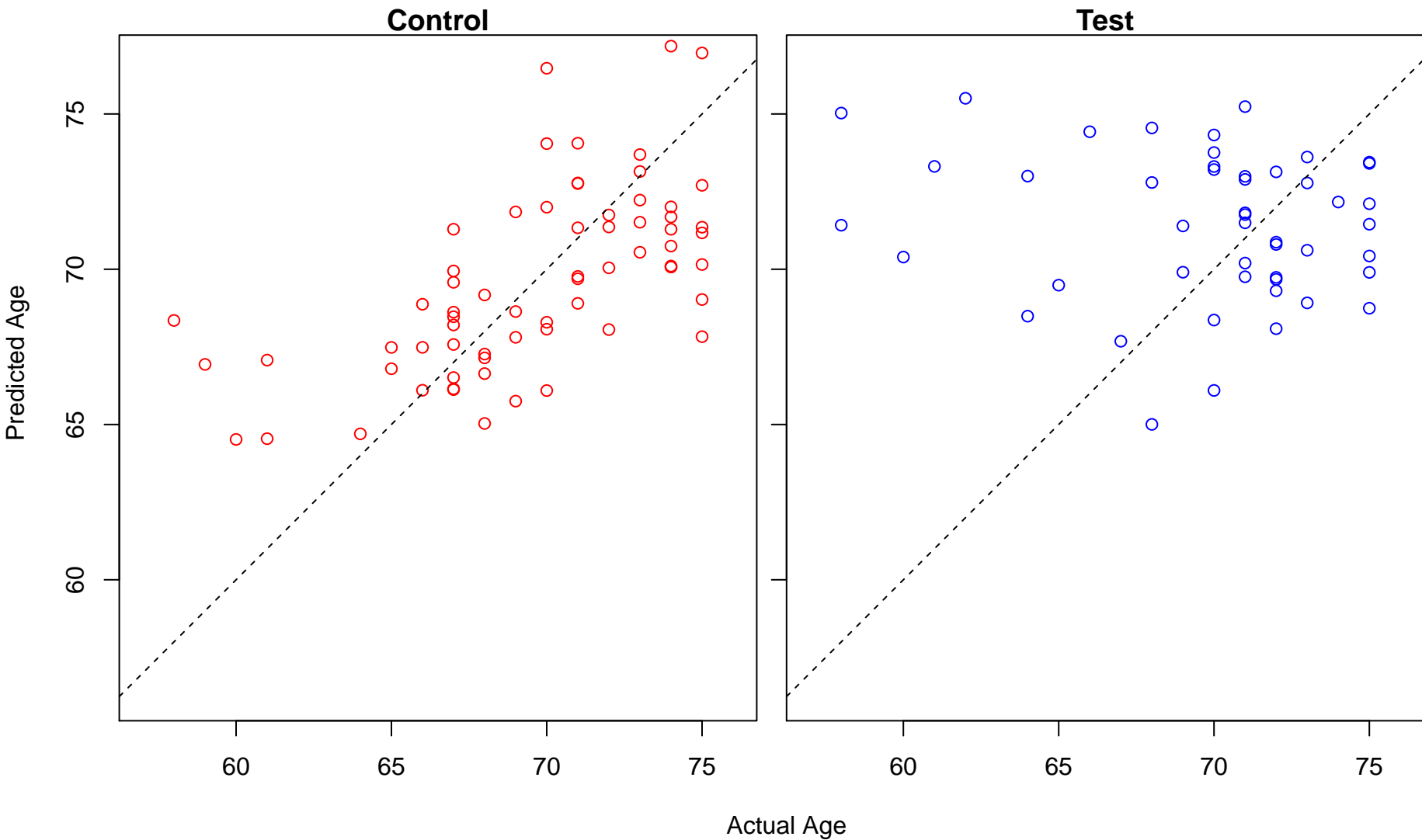
glucan metabolic process (Score: 1.214768)



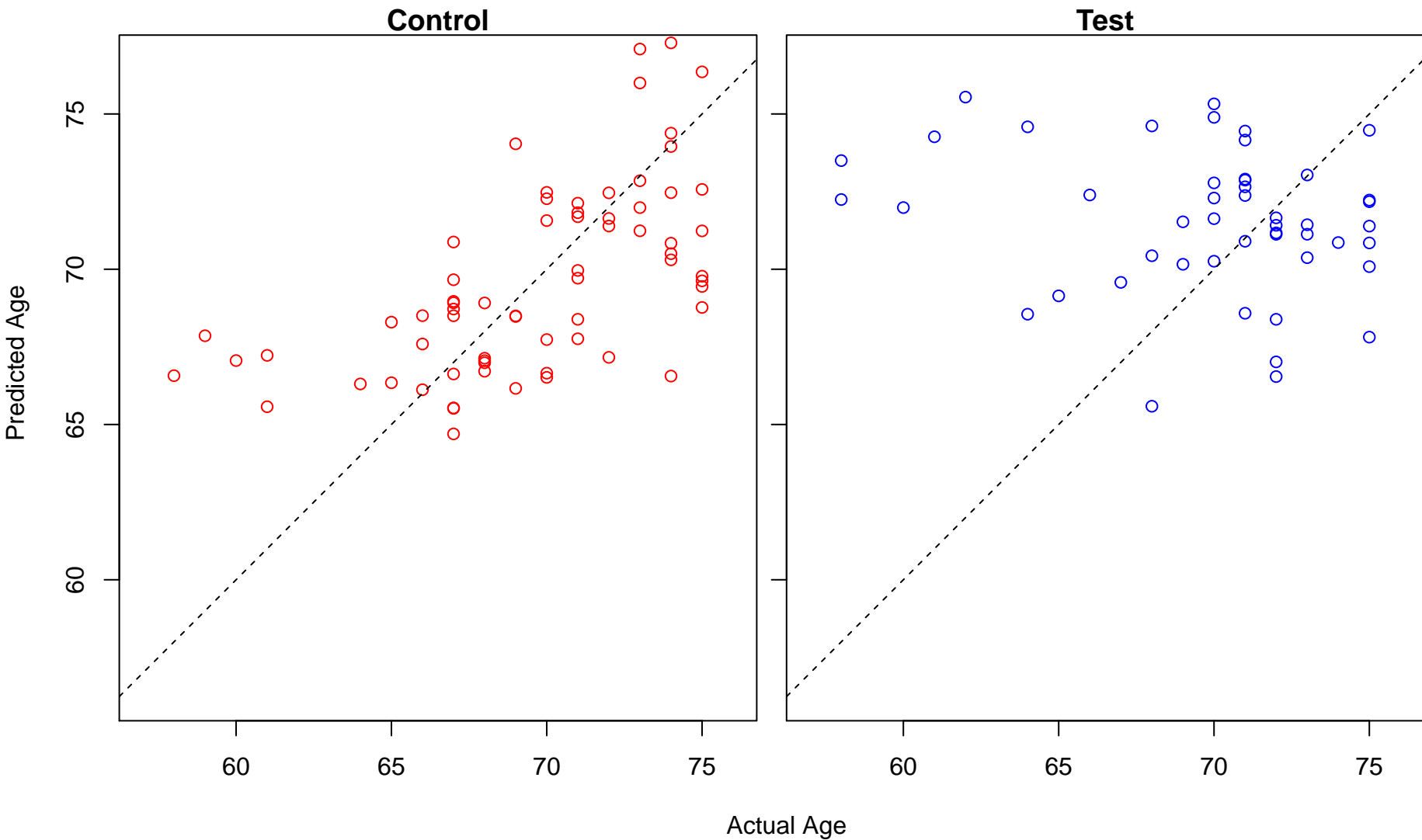
exit from mitosis (Score: 1.214741)



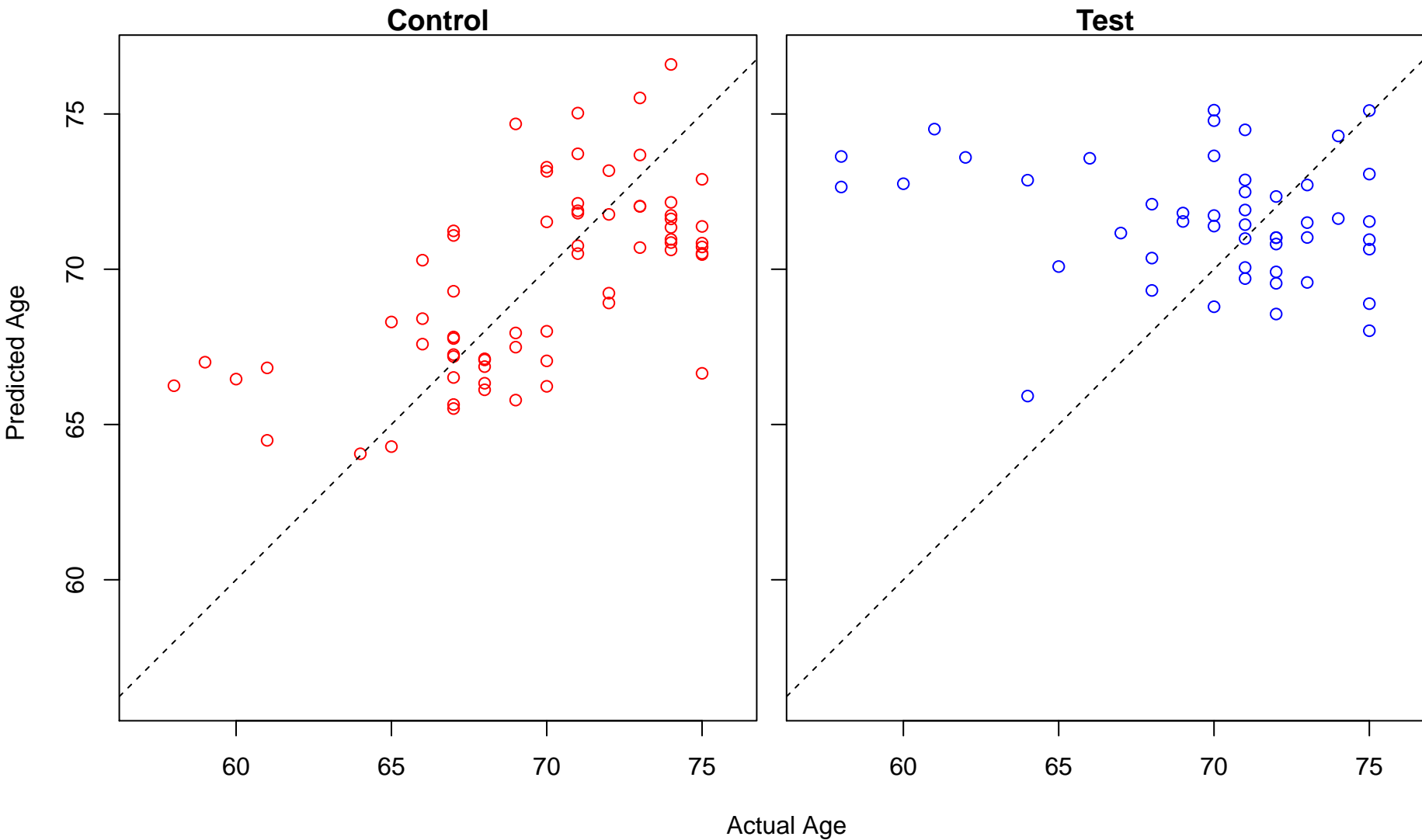
microtubule polymerization (Score: 1.214576)



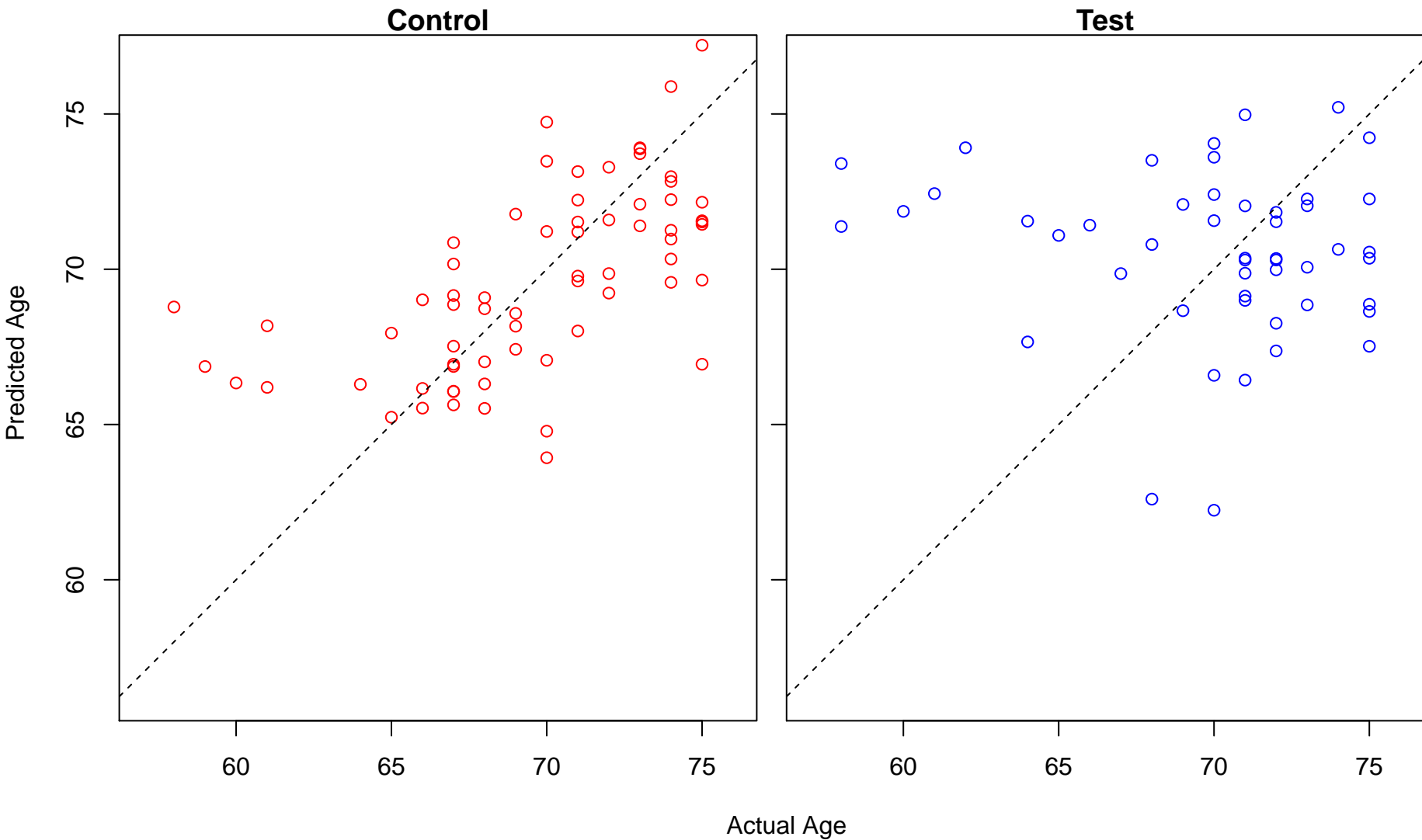
membrane biogenesis (Score: 1.213208)



regulation of developmental growth (Score: 1.213196)

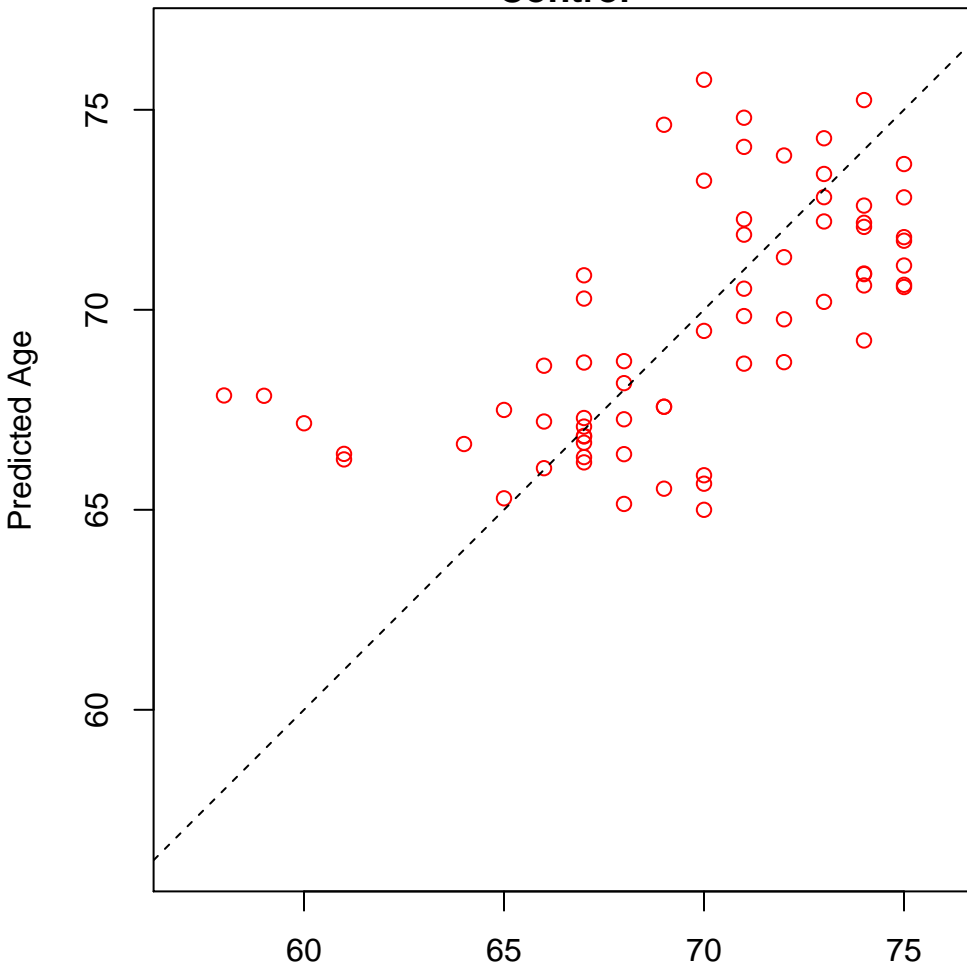


polyol metabolic process (Score: 1.213040)

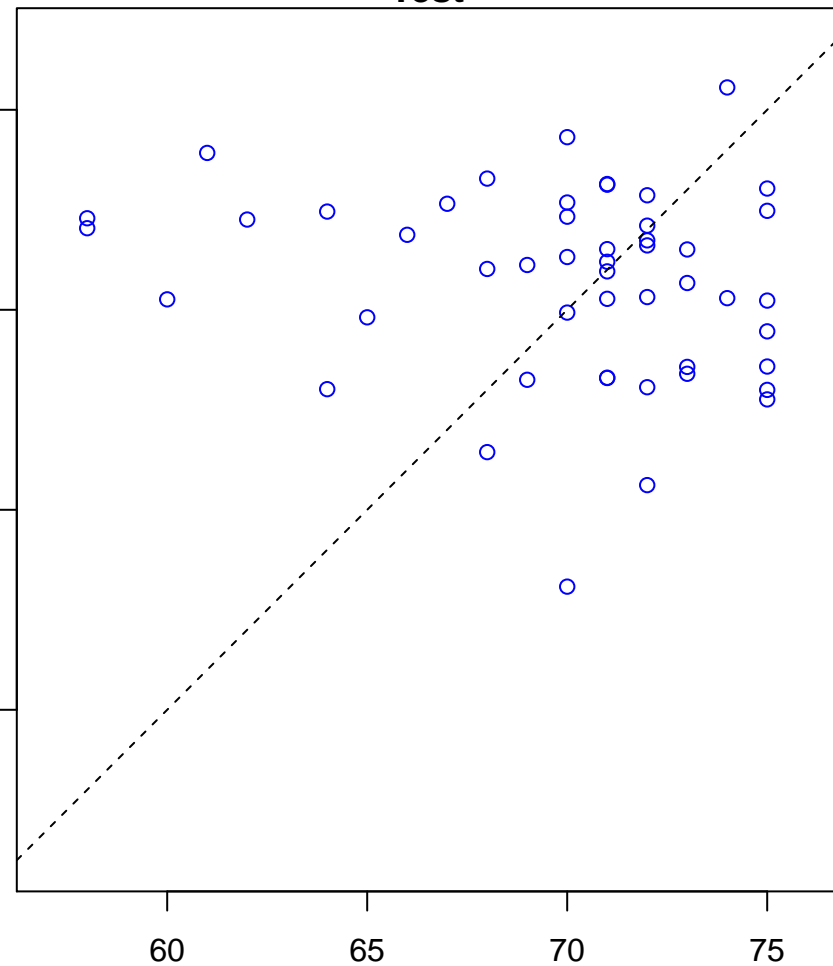


cellular response to lipopolysaccharide (Score: 1.212824)

Control

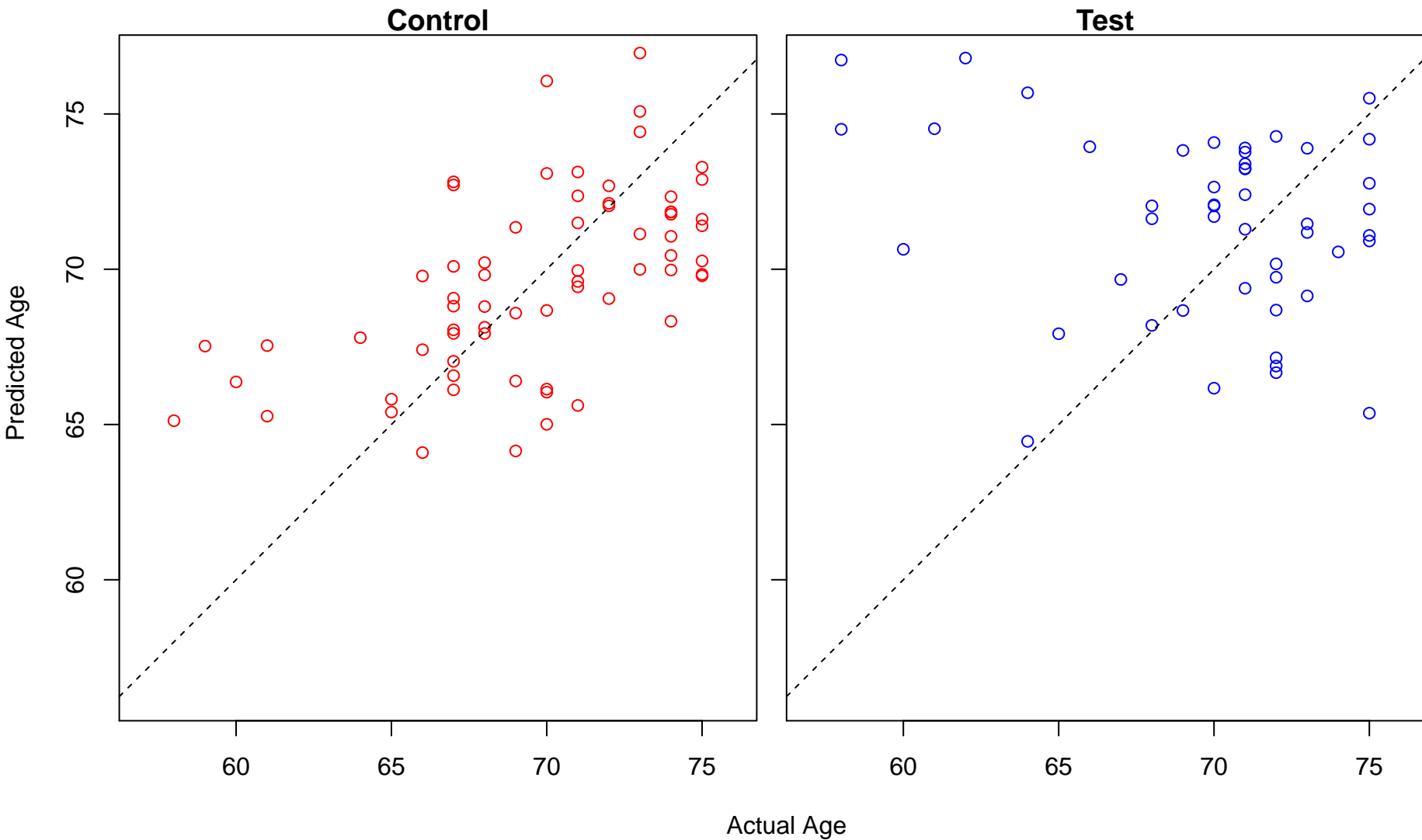


Test

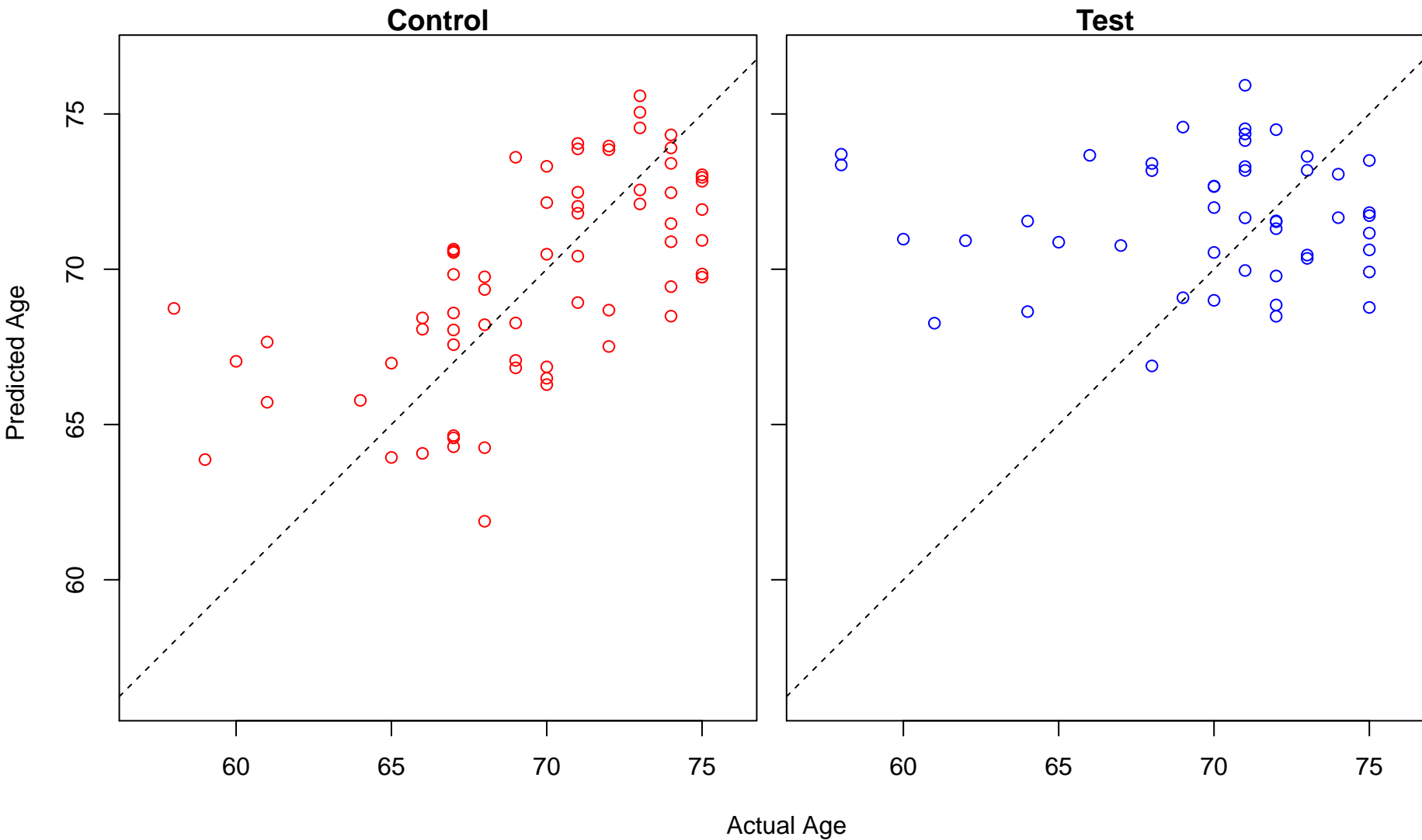


Actual Age

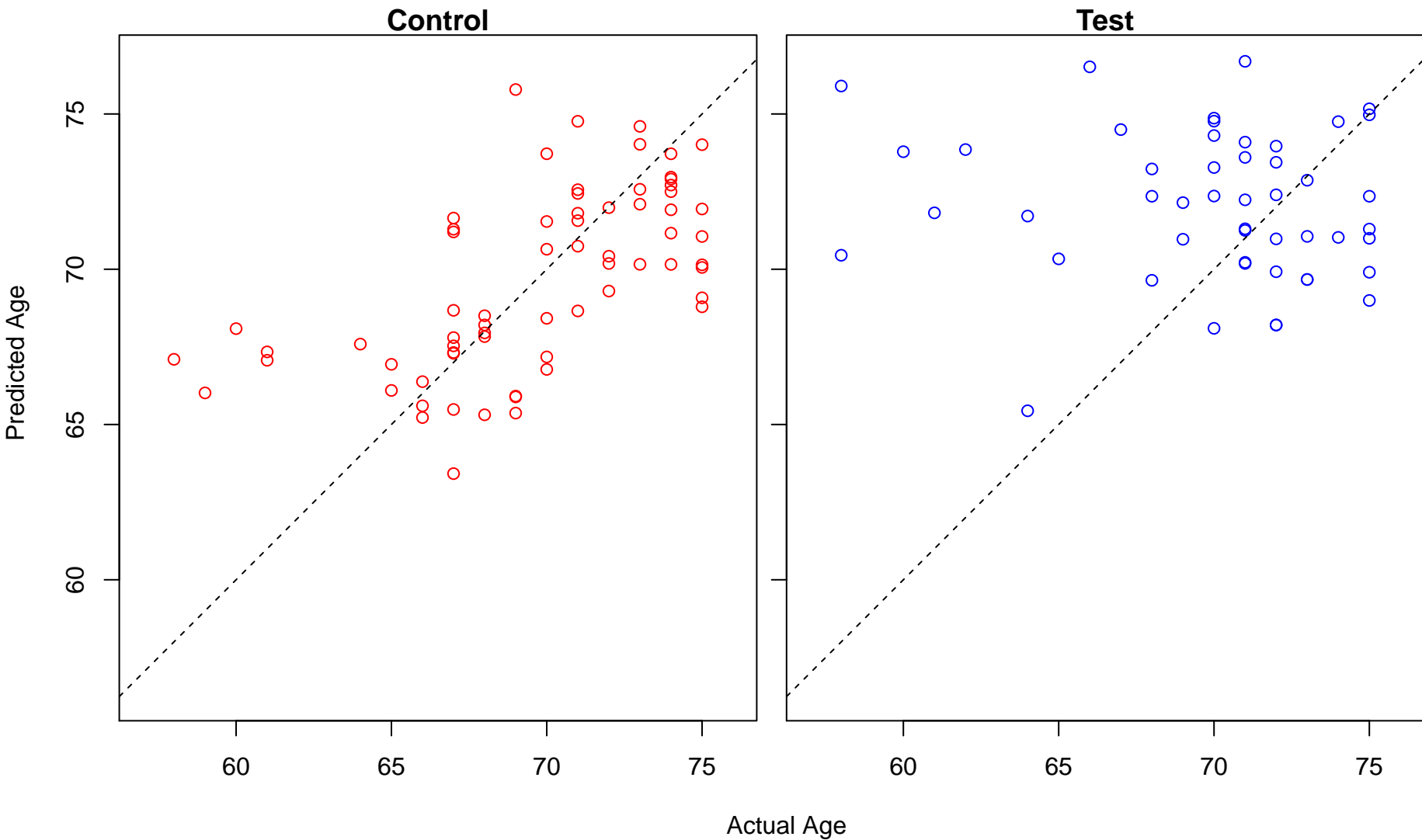
positive regulation of viral entry into host cell (Score: 1.212741)



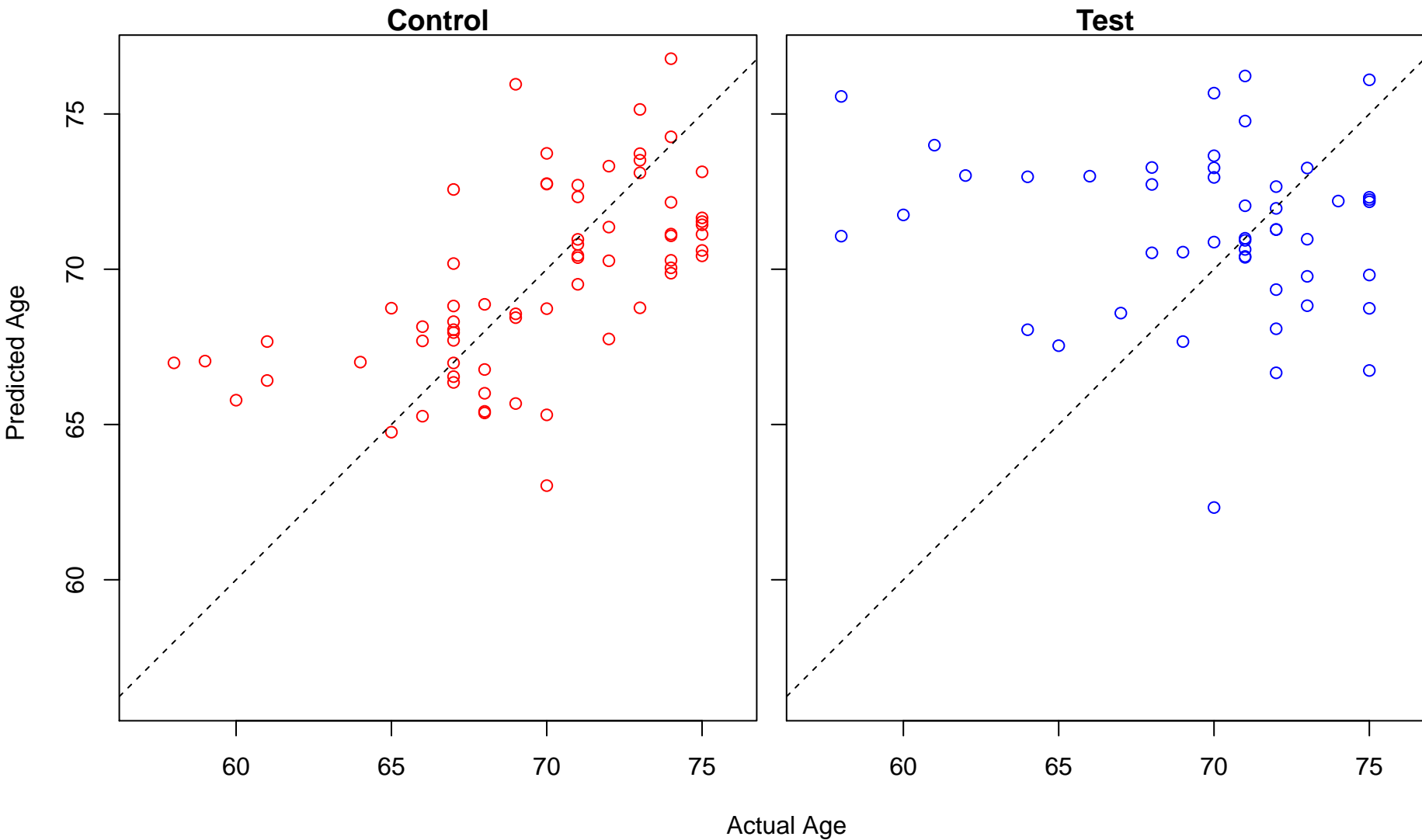
organelle membrane fusion (Score: 1.212620)



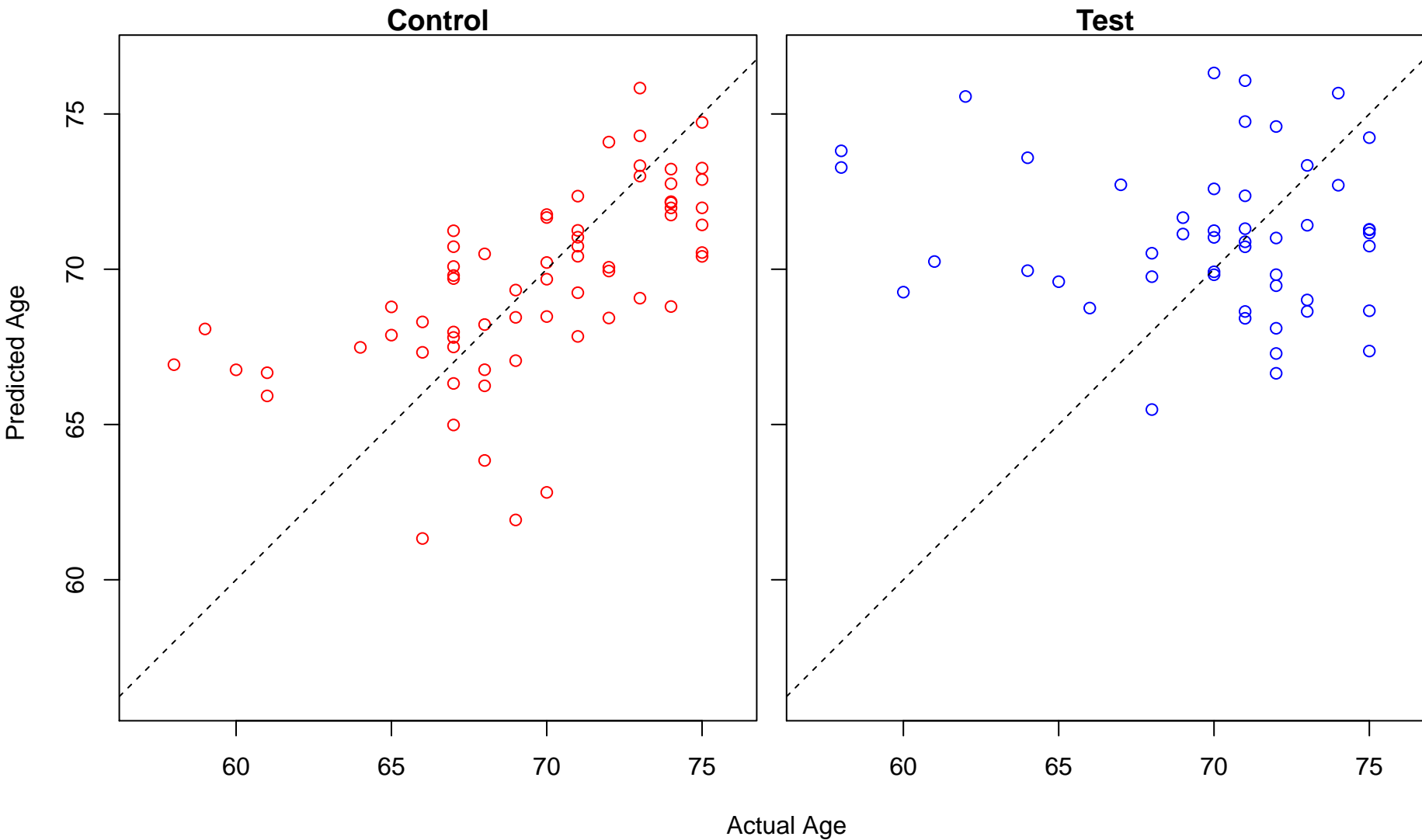
actin cytoskeleton reorganization (Score: 1.212603)



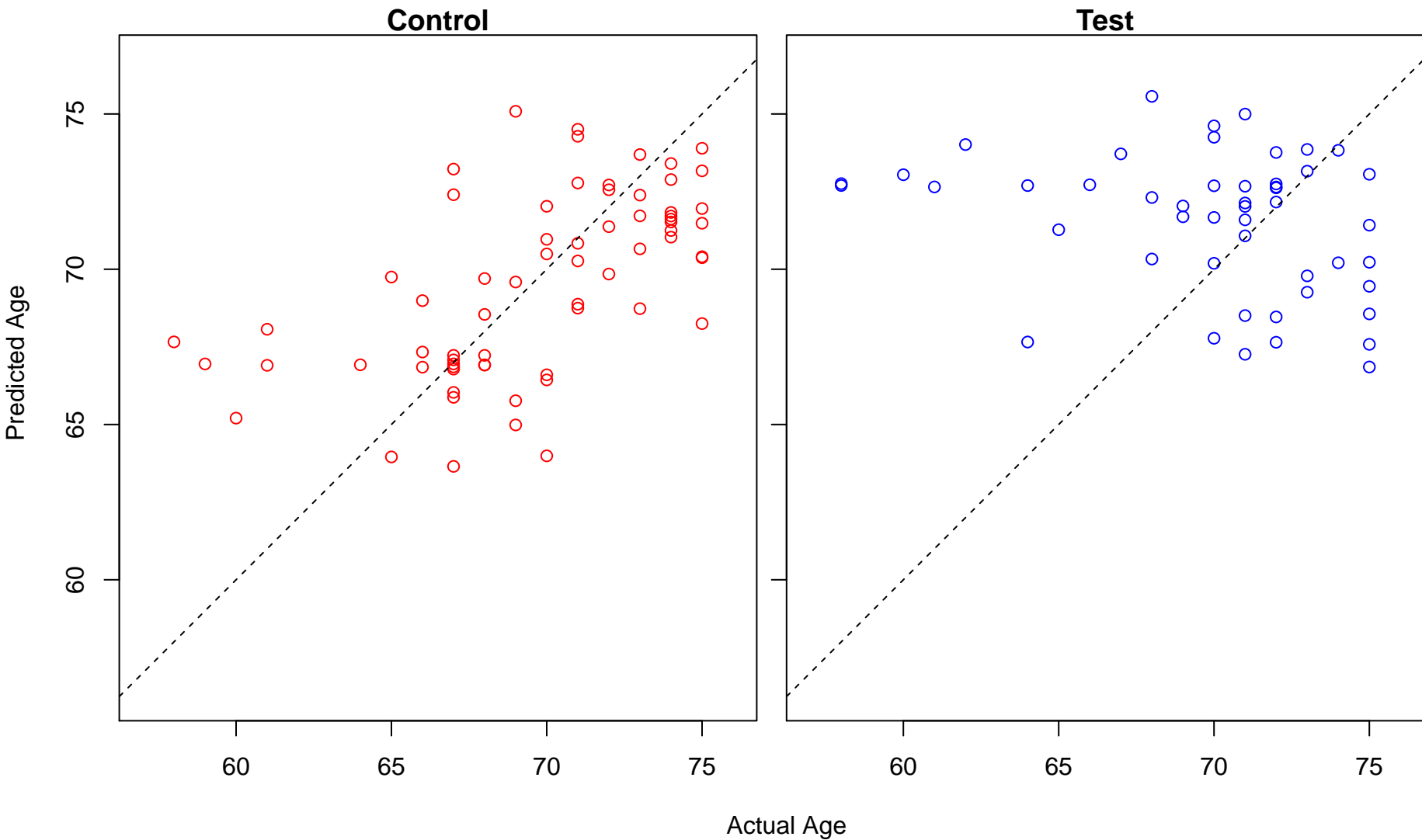
regulation of cellular pH (Score: 1.212588)



choline transport (Score: 1.212086)

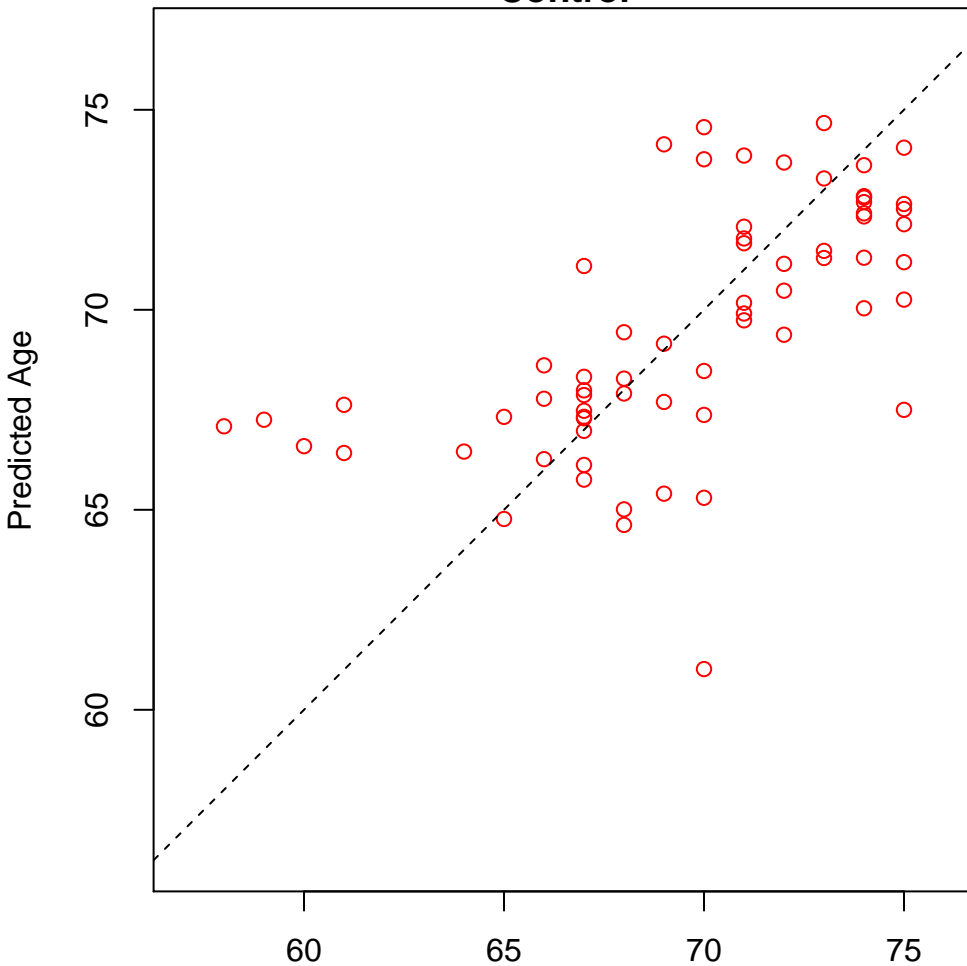


regulation of interferon- α production (Score: 1.211999)

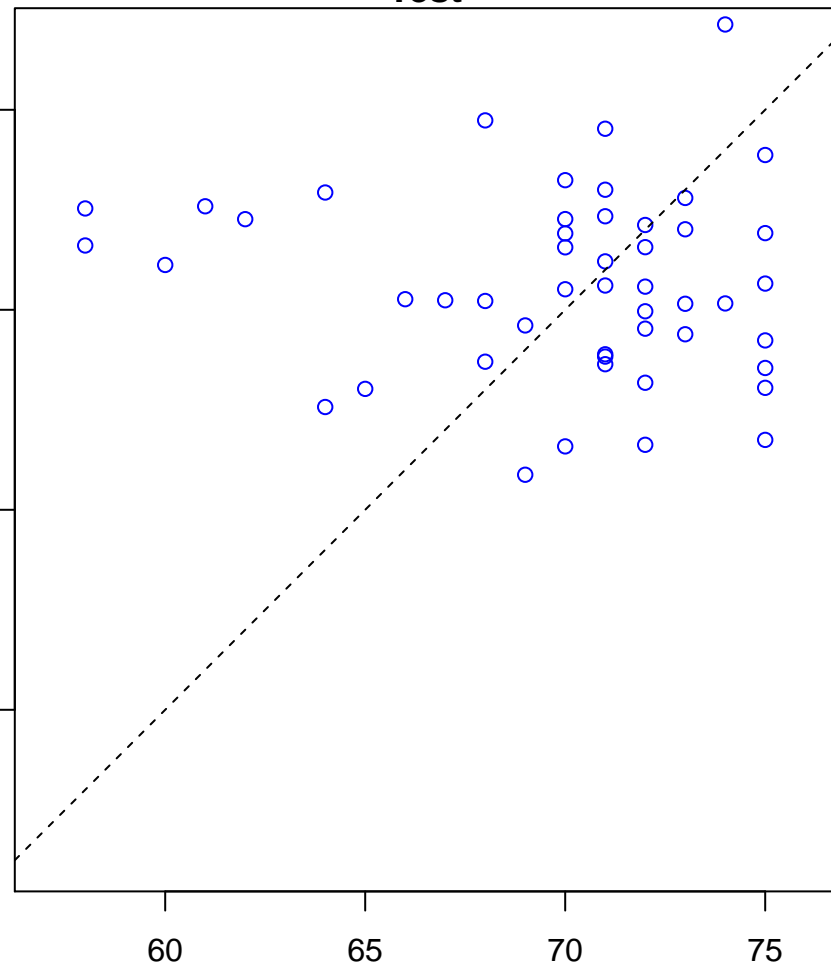


myeloid leukocyte differentiation (Score: 1.211863)

Control

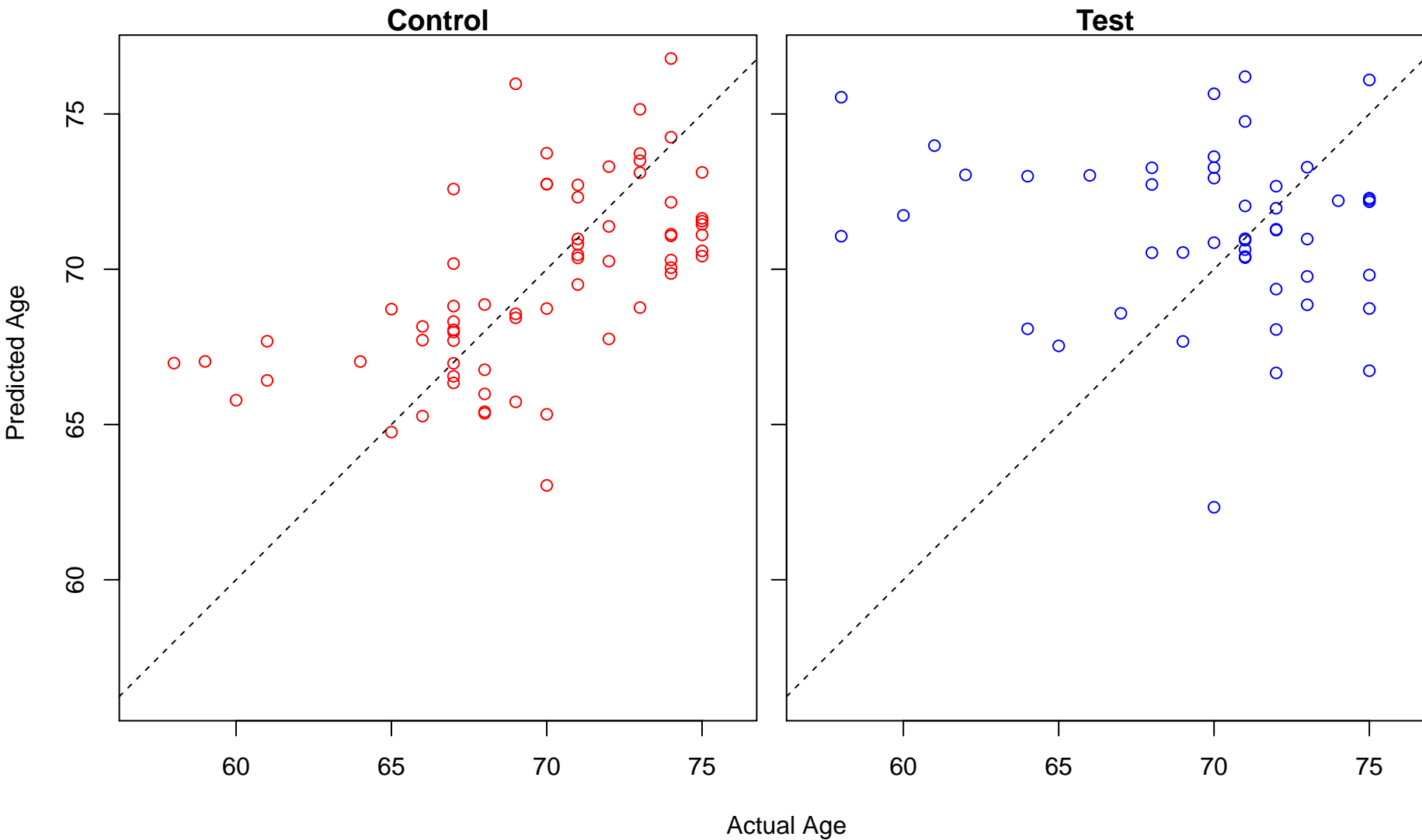


Test

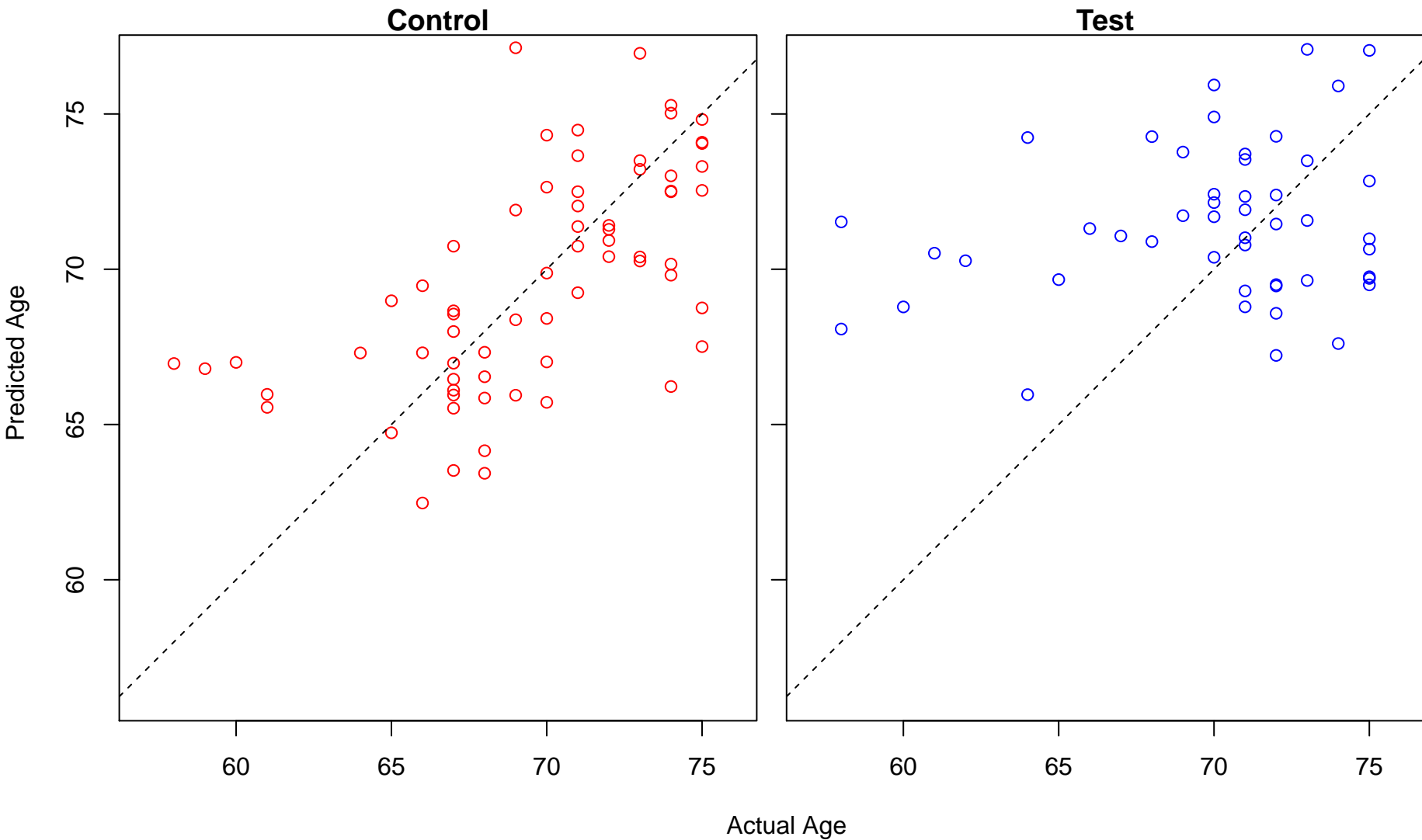


Actual Age

regulation of intracellular pH (Score: 1.211694)

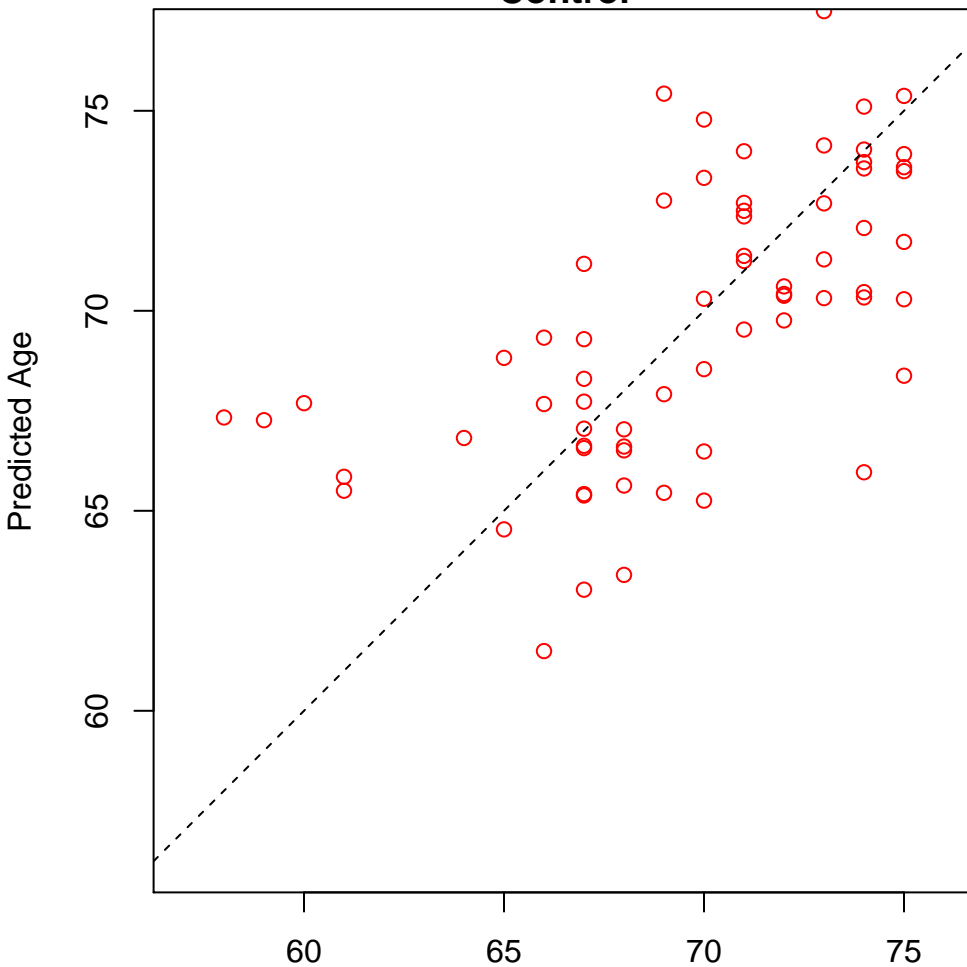


branching morphogenesis of an epithelial tube (Score: 1.210880)

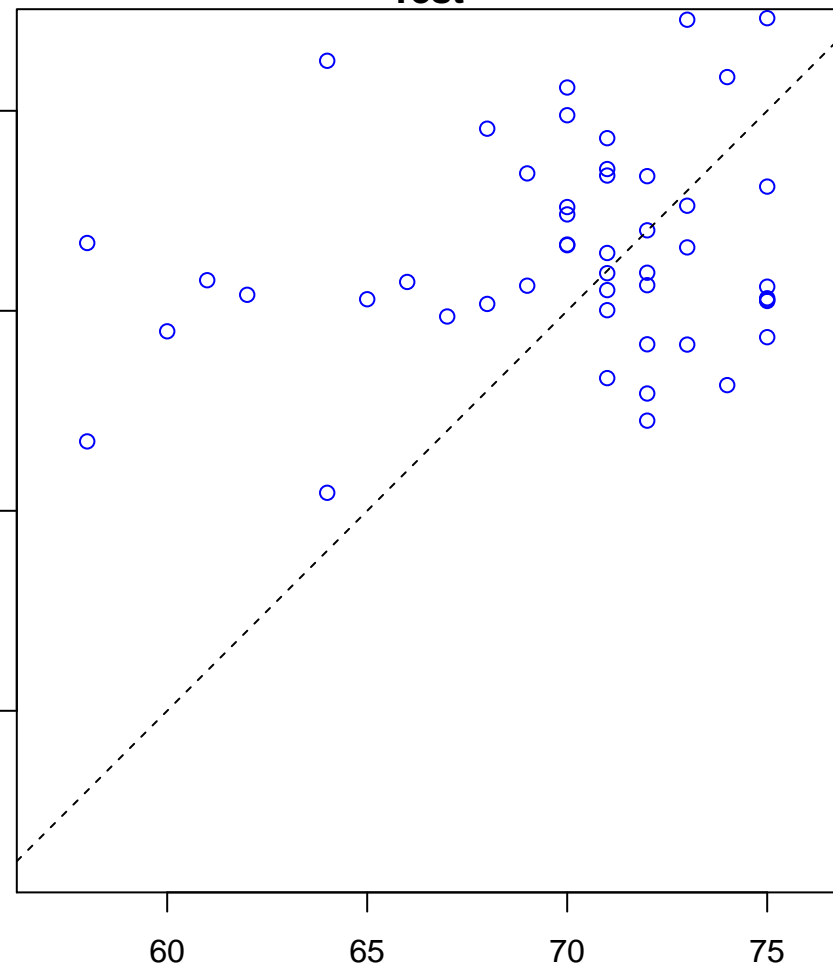


morphogenesis of a branching structure (Score: 1.210707)

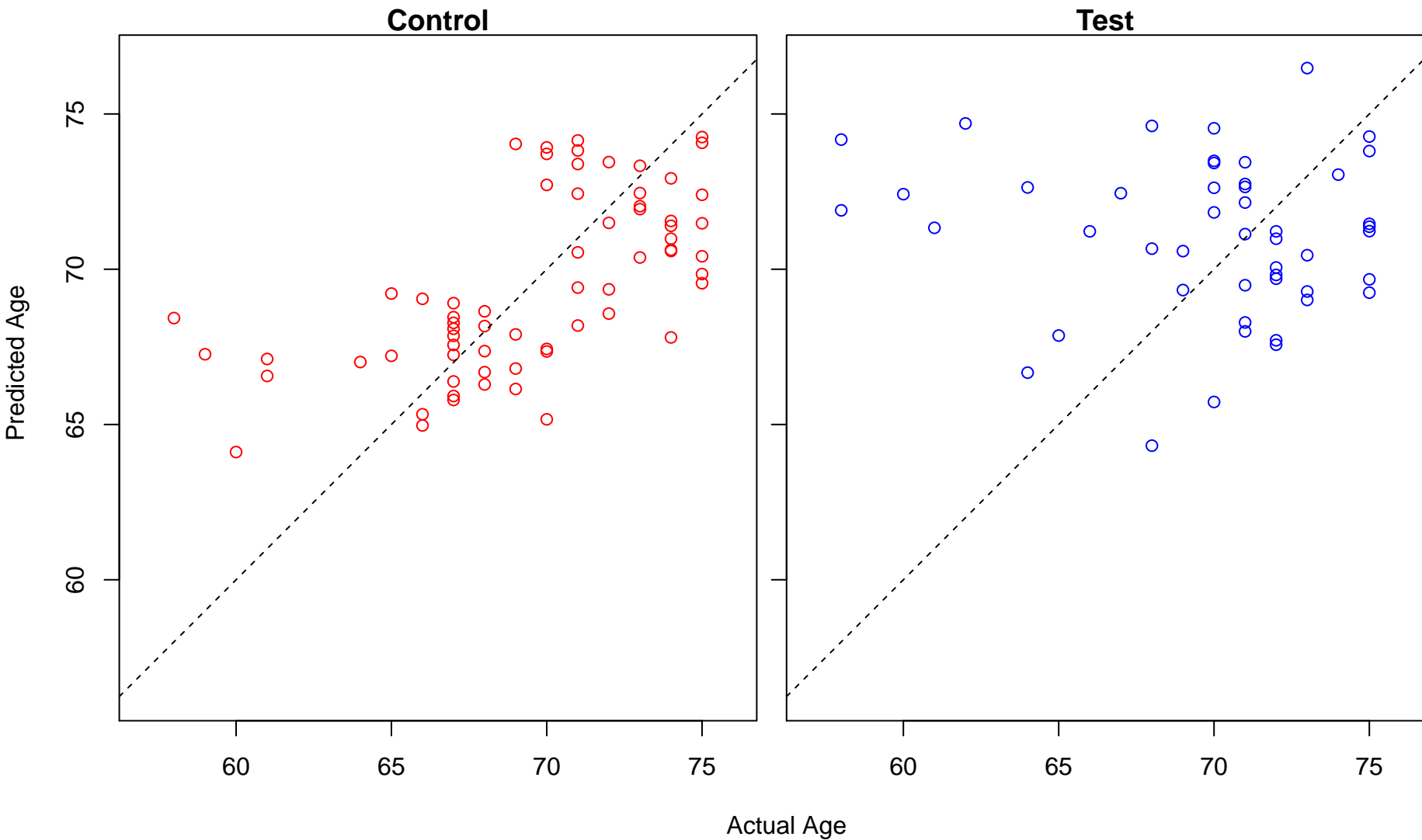
Control



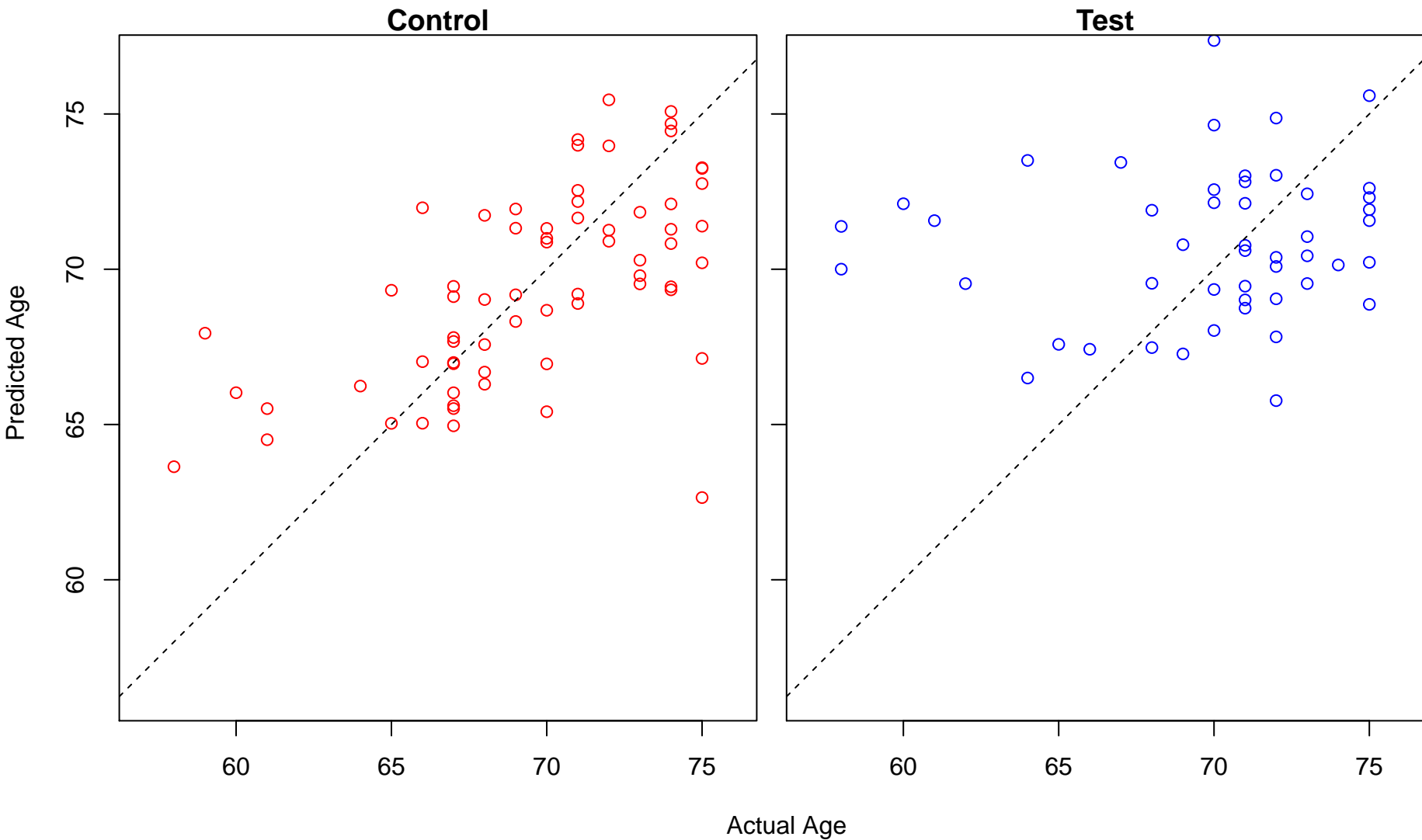
Test



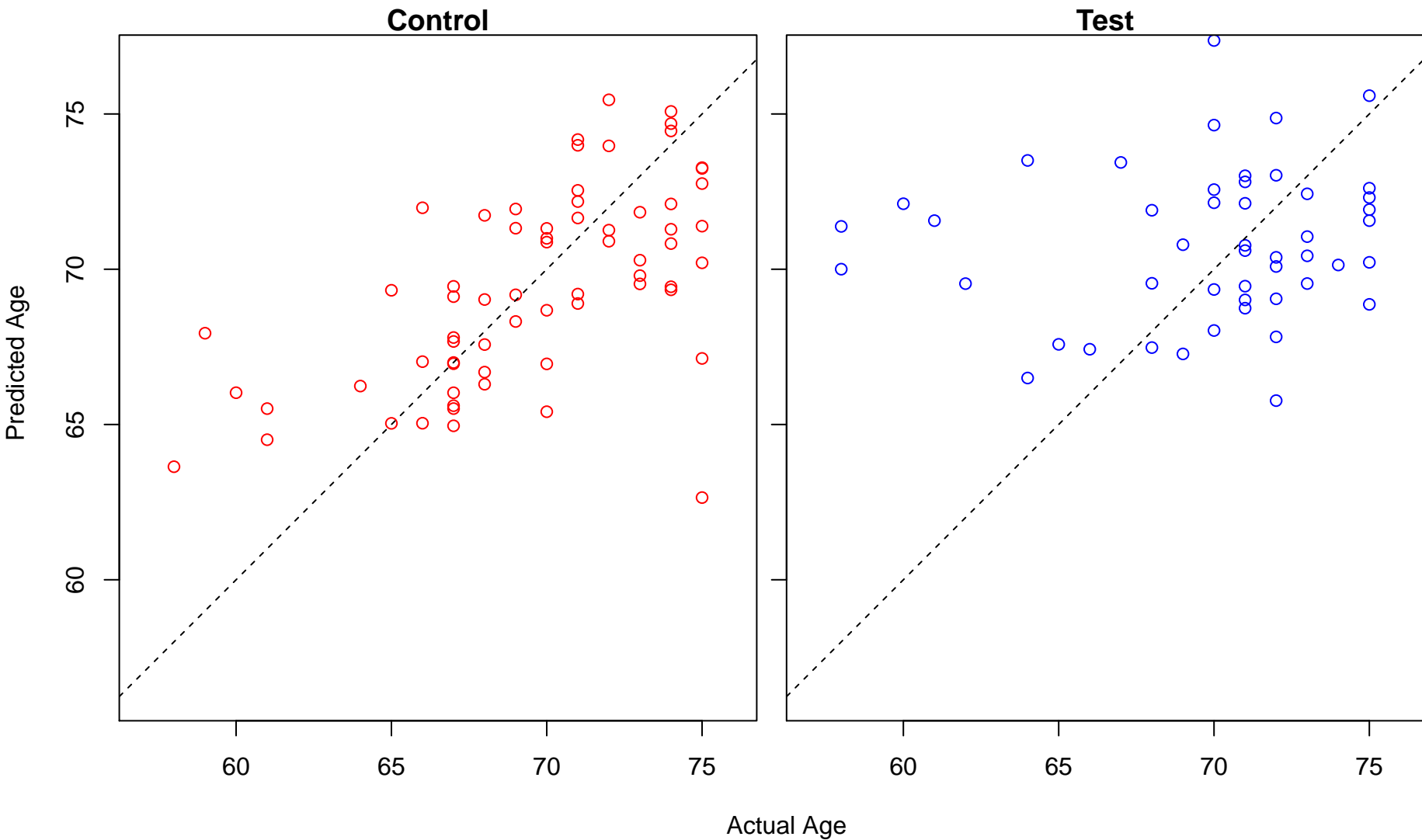
regulation of synapse organization (Score: 1.210020)



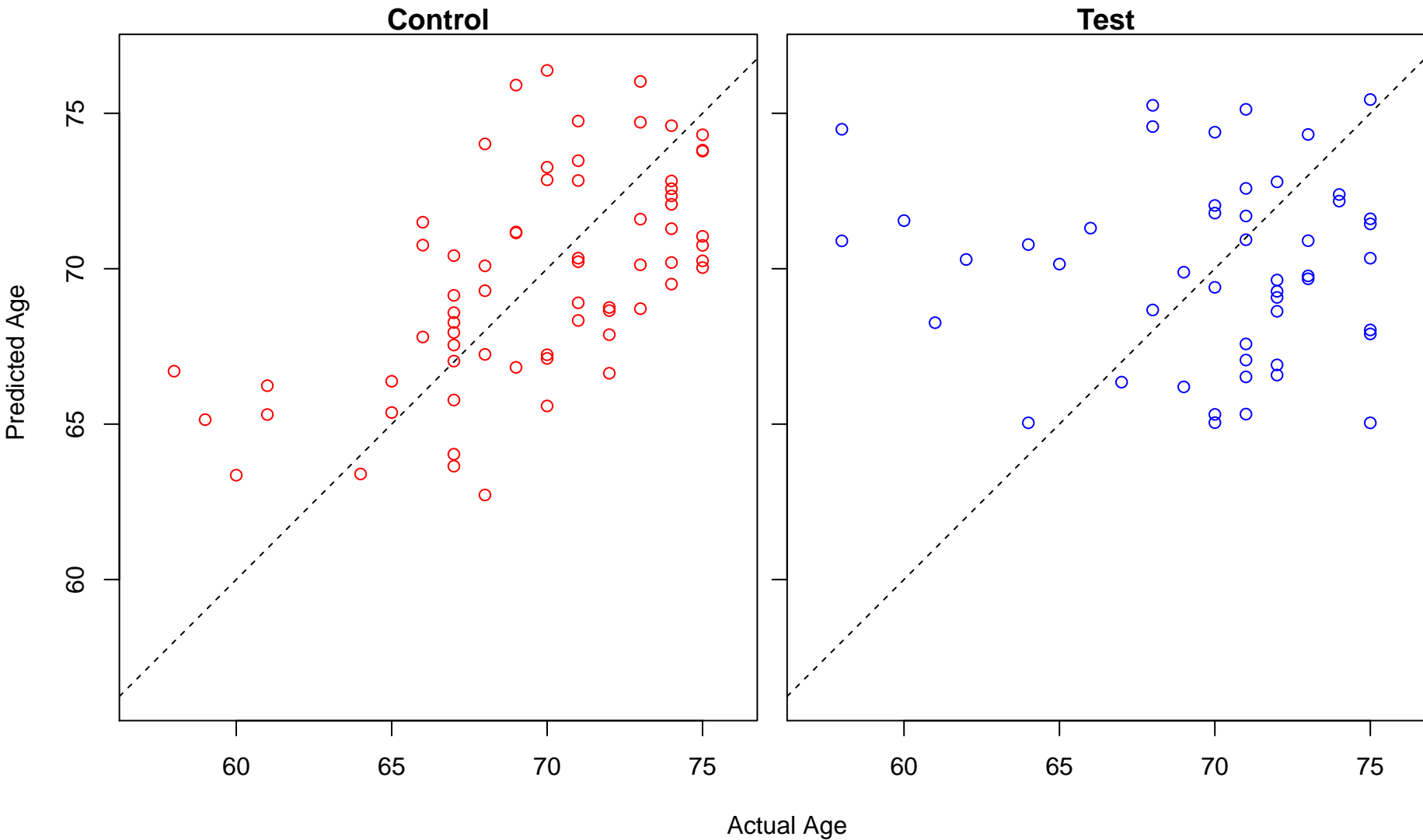
regulation of sterol transport (Score: 1.209669)



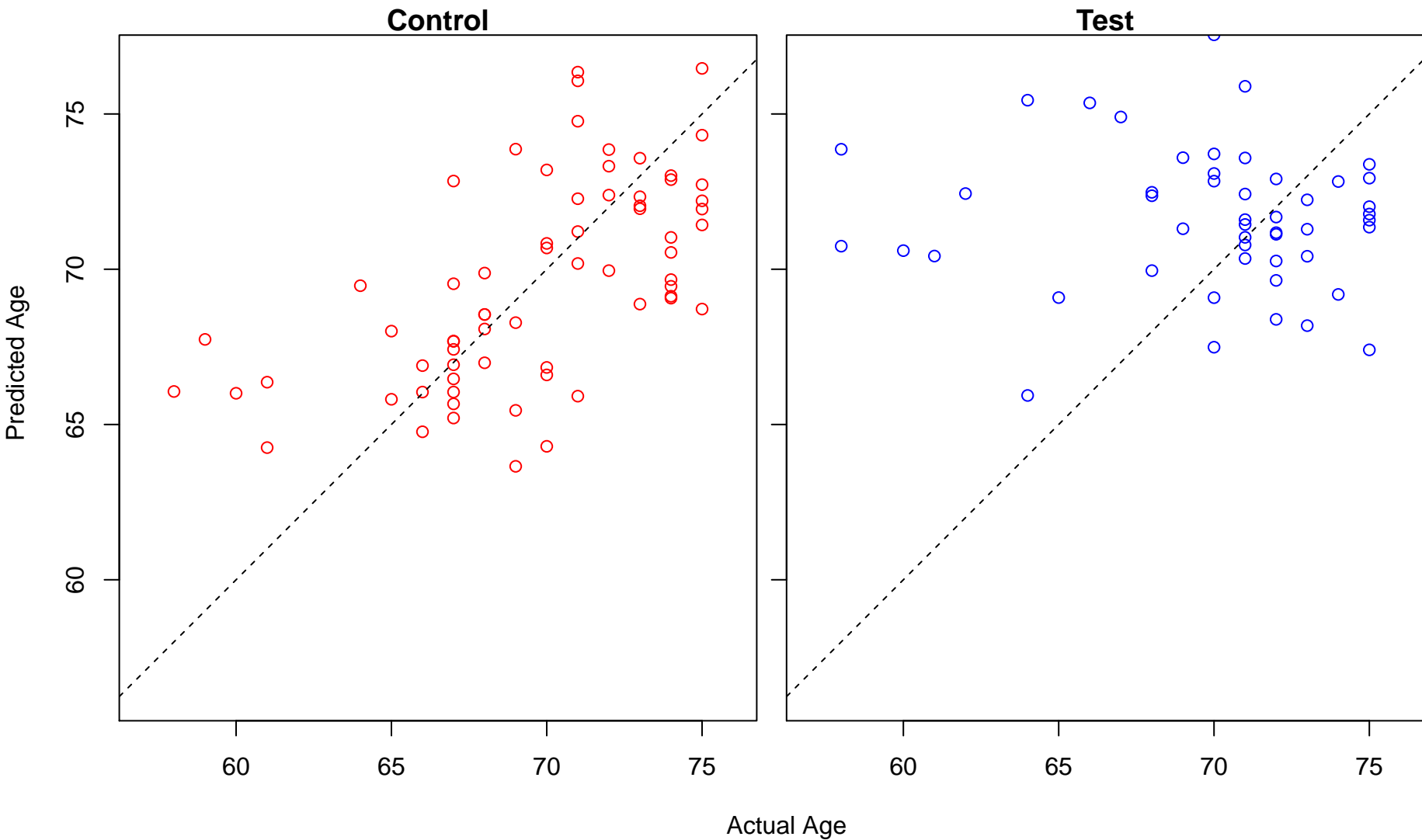
regulation of cholesterol transport (Score: 1.209669)



somatic recombination of immunoglobulin gene segments (Score: 1.209128)

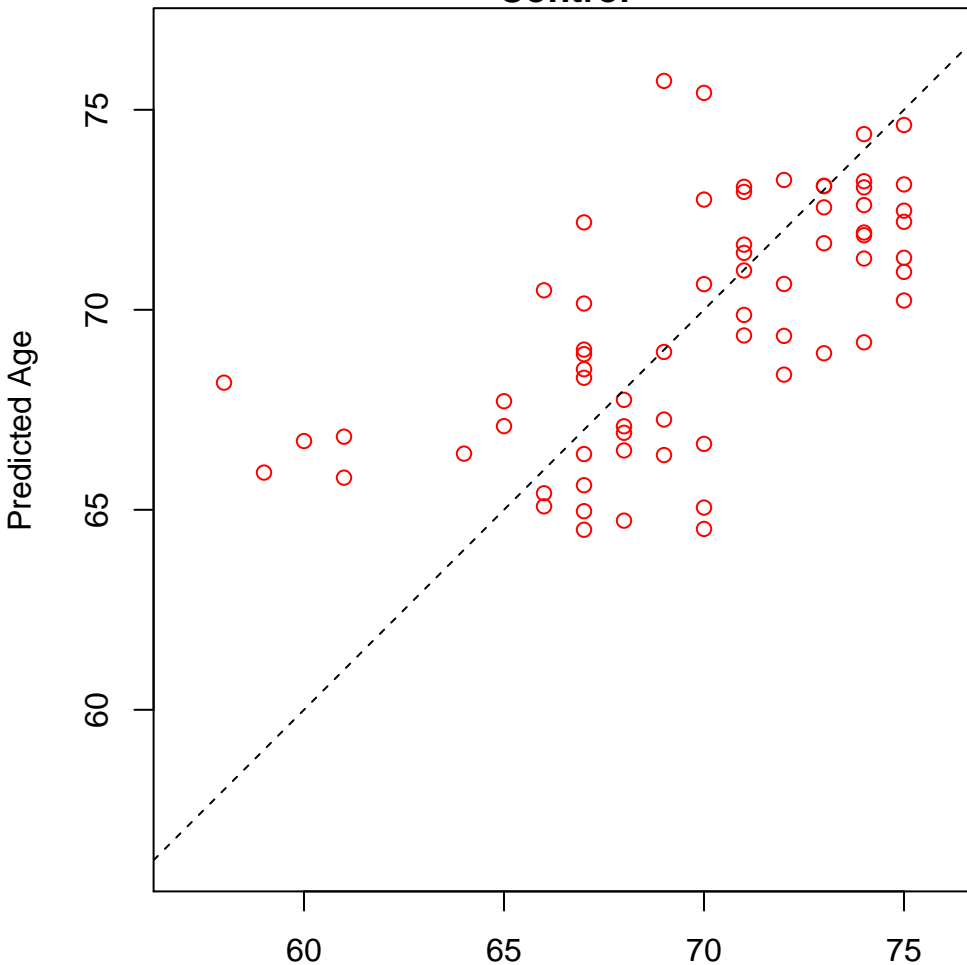


positive regulation of chromosome segregation (Score: 1.209119)

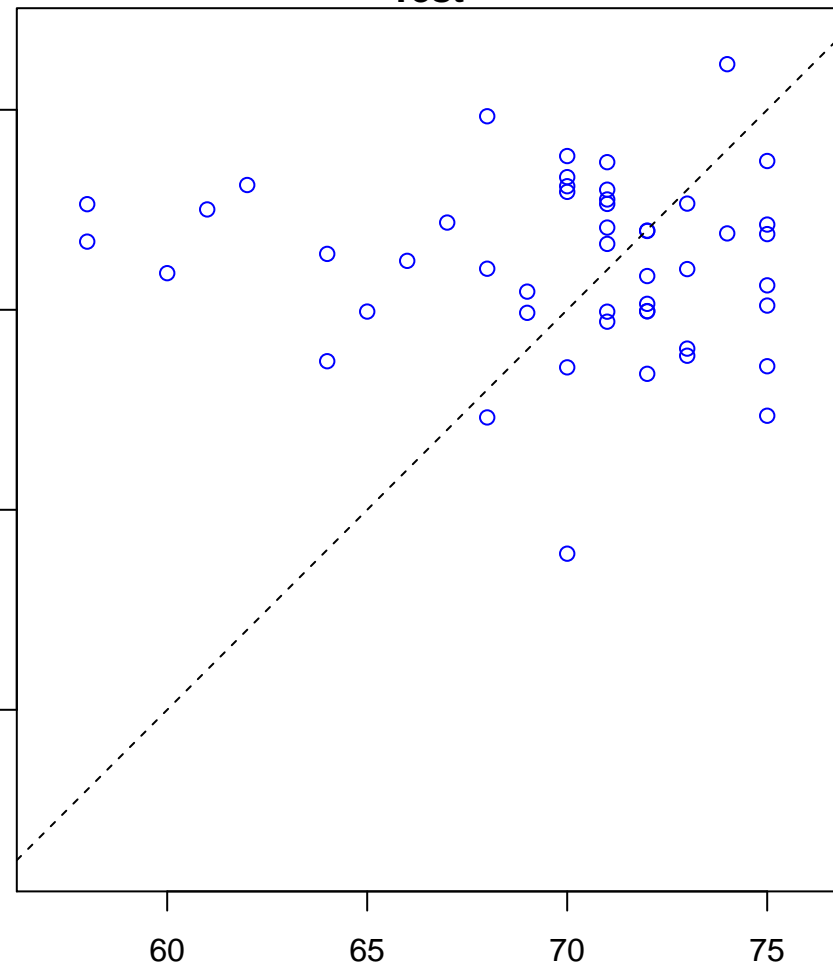


cell-type specific apoptotic process (Score: 1.209067)

Control

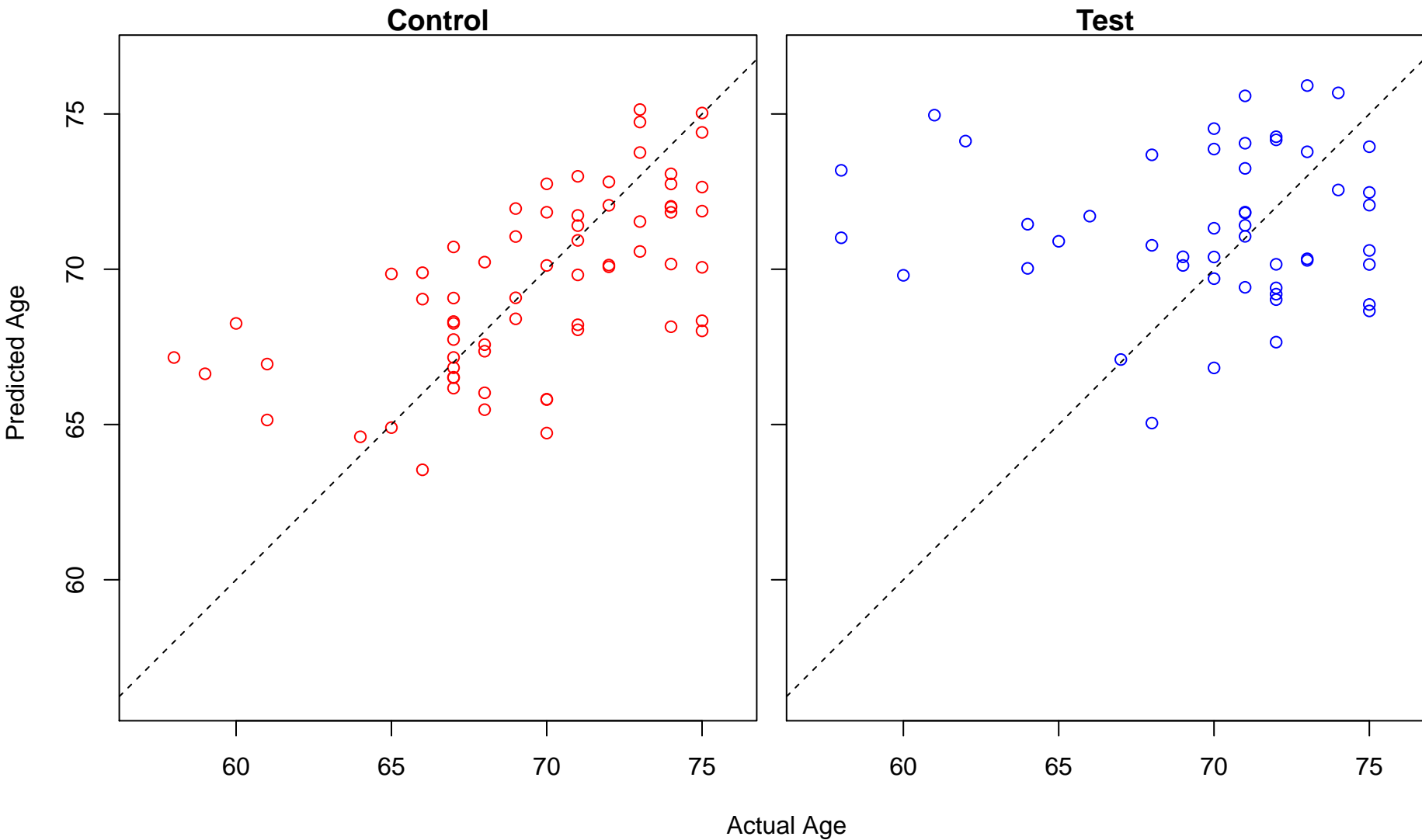


Test

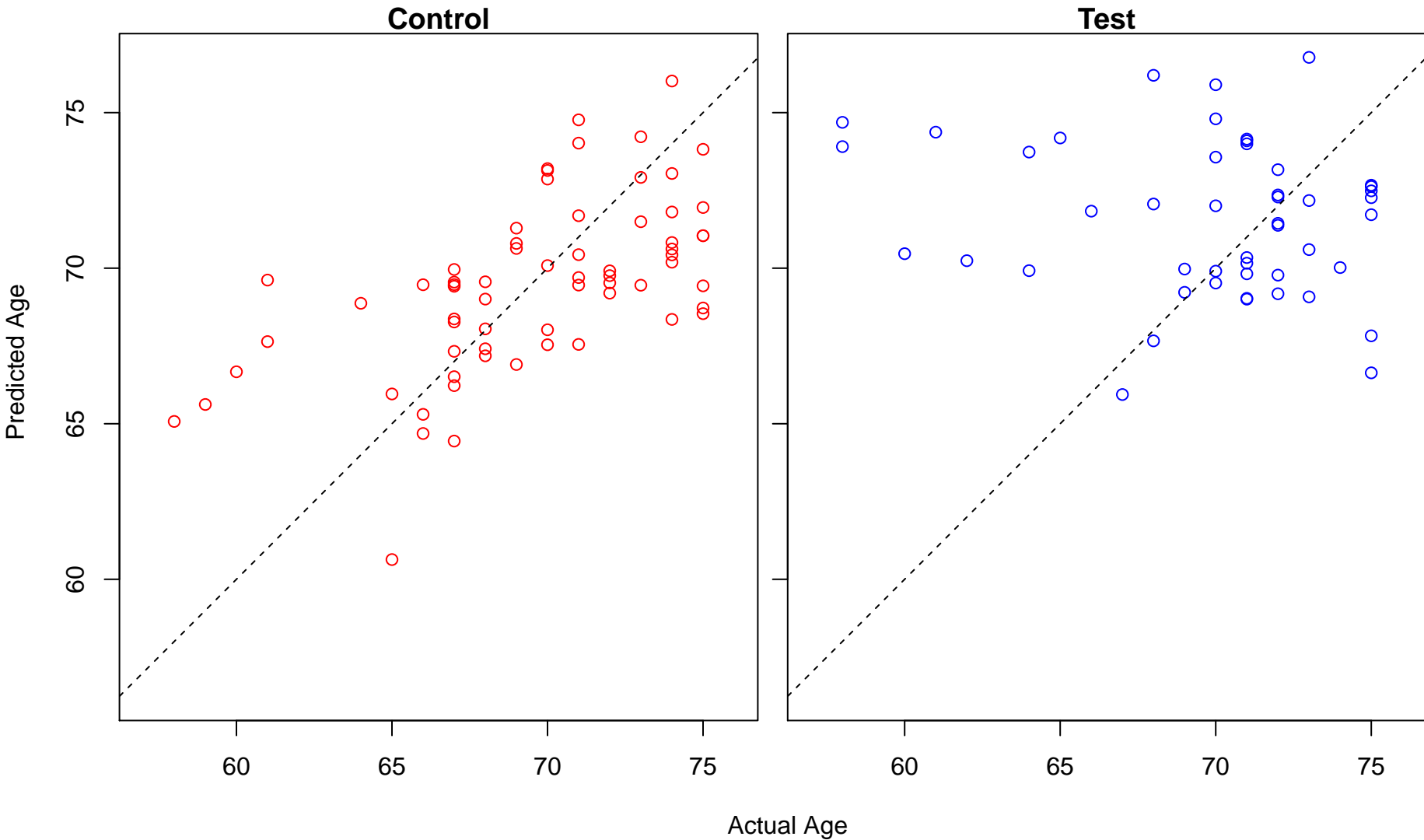


Actual Age

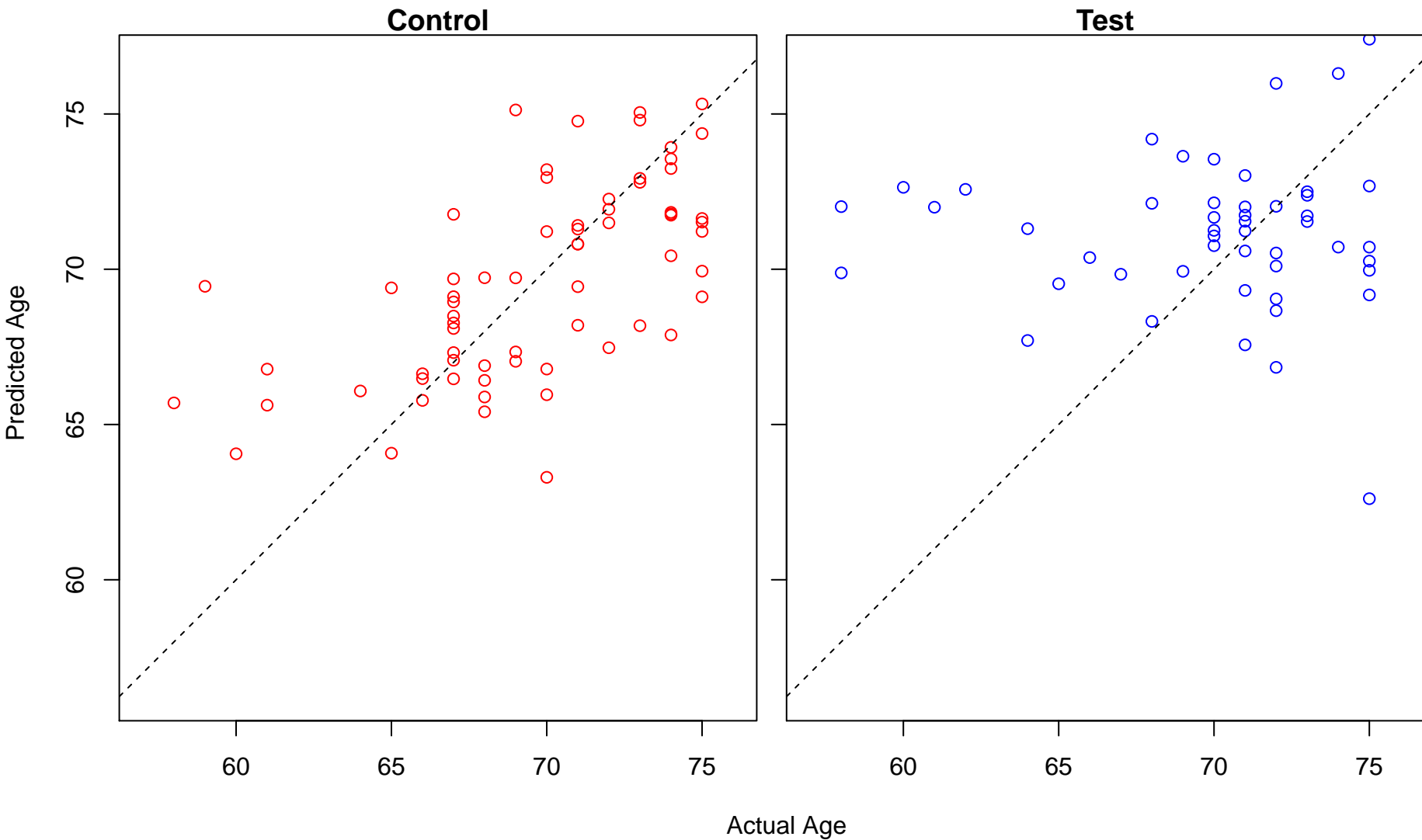
regulation of amyloid precursor protein catabolic process (Score: 1.208947)



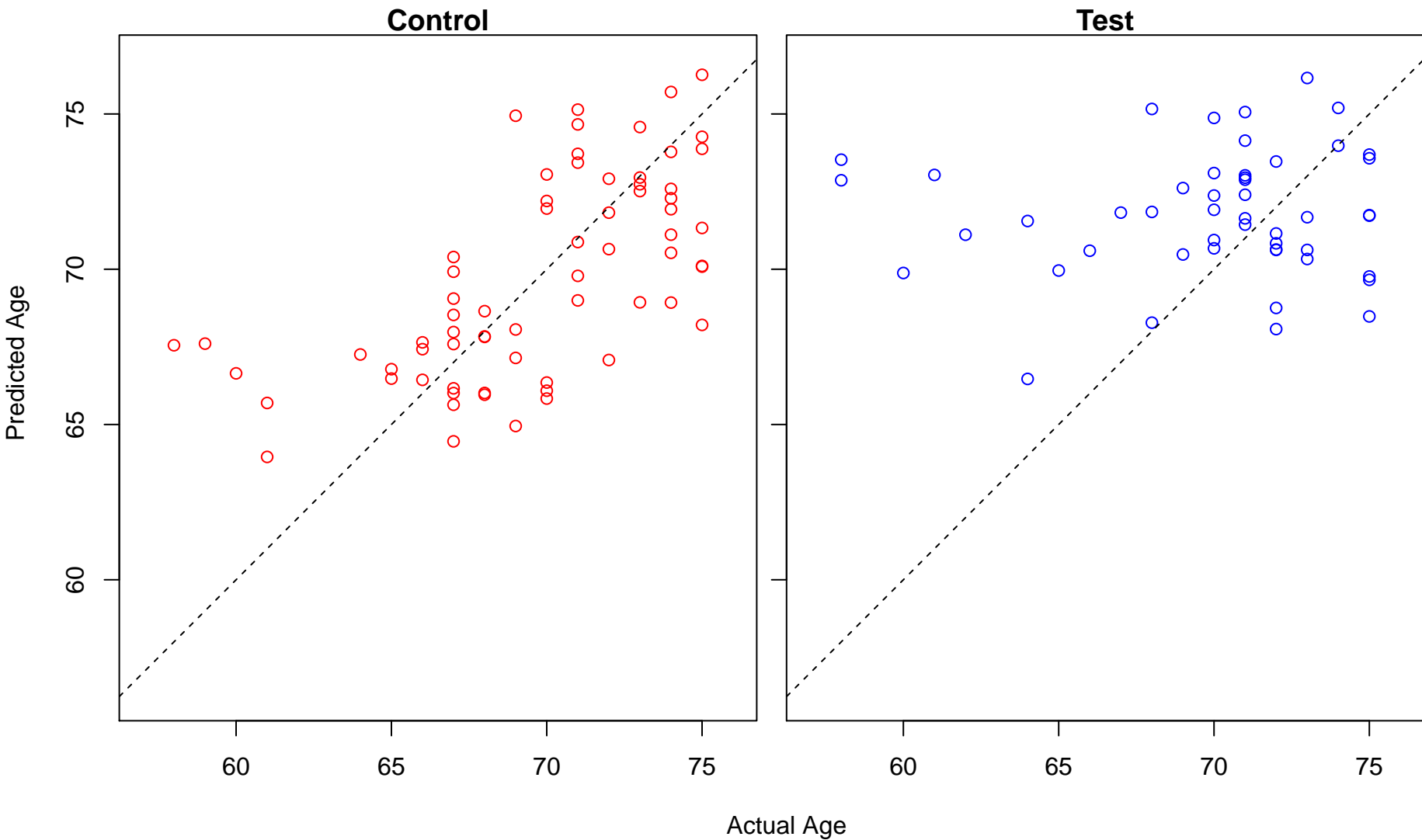
positive regulation of neutrophil chemotaxis (Score: 1.208886)



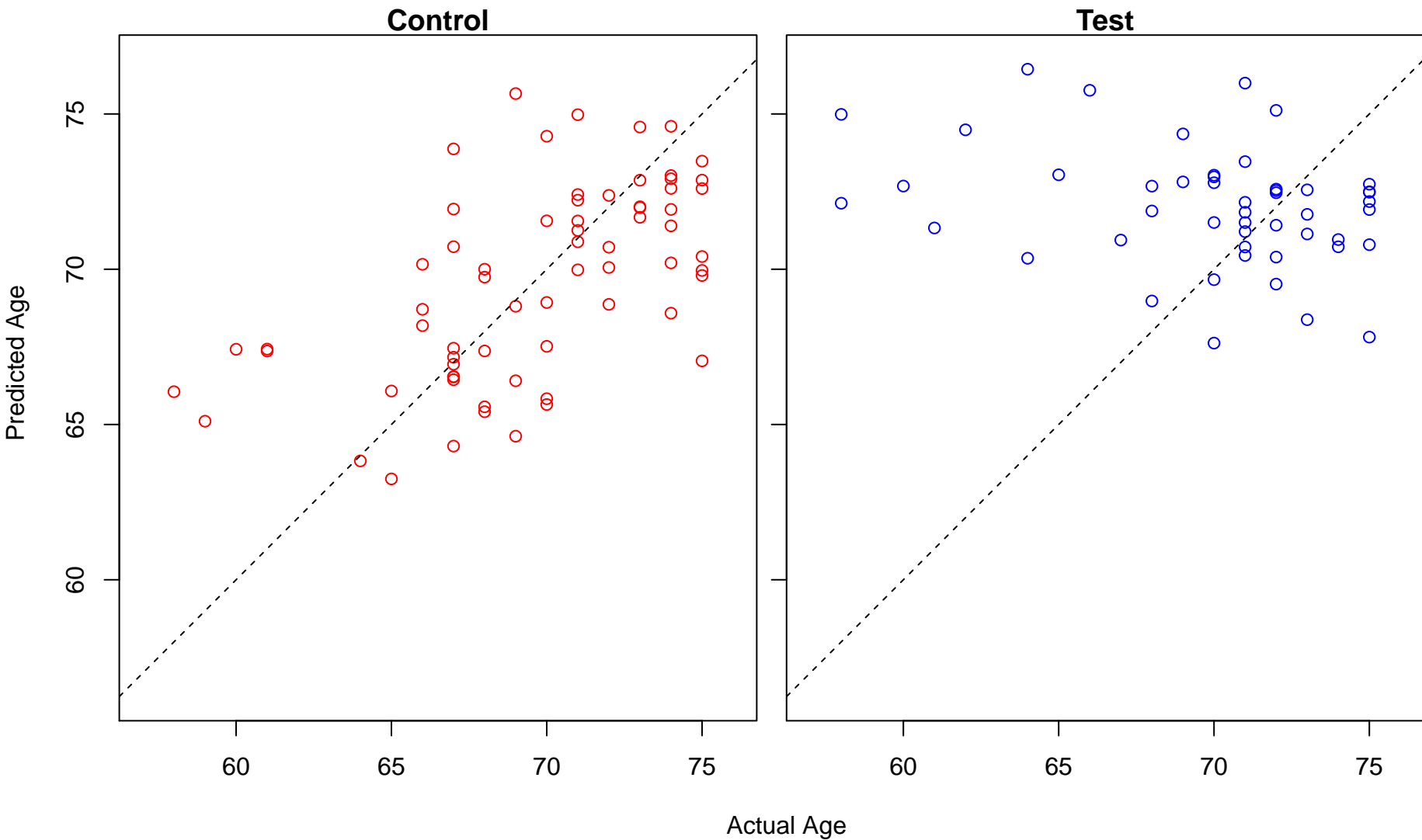
regulation of gliogenesis (Score: 1.208638)



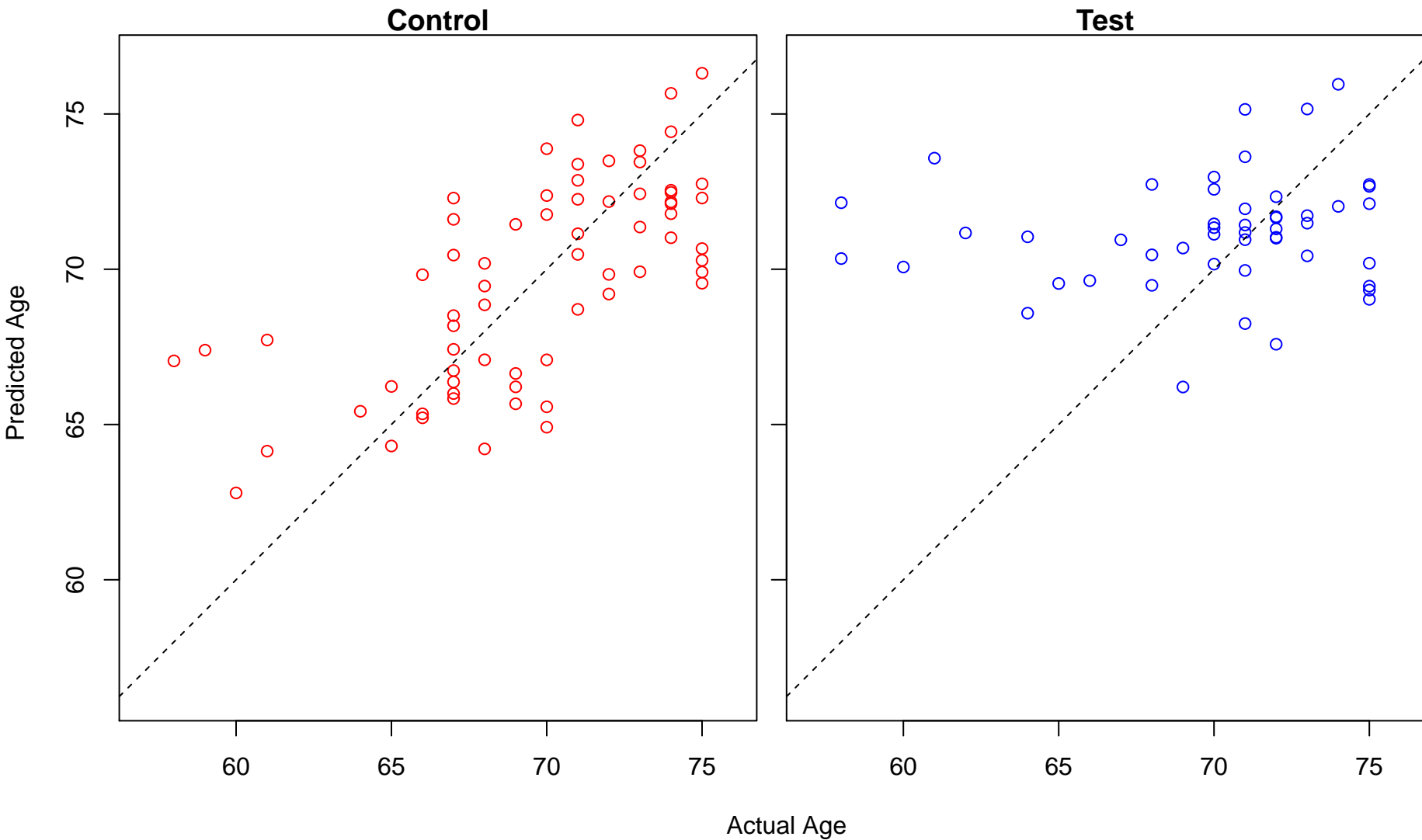
protein K48-linked ubiquitination (Score: 1.208504)



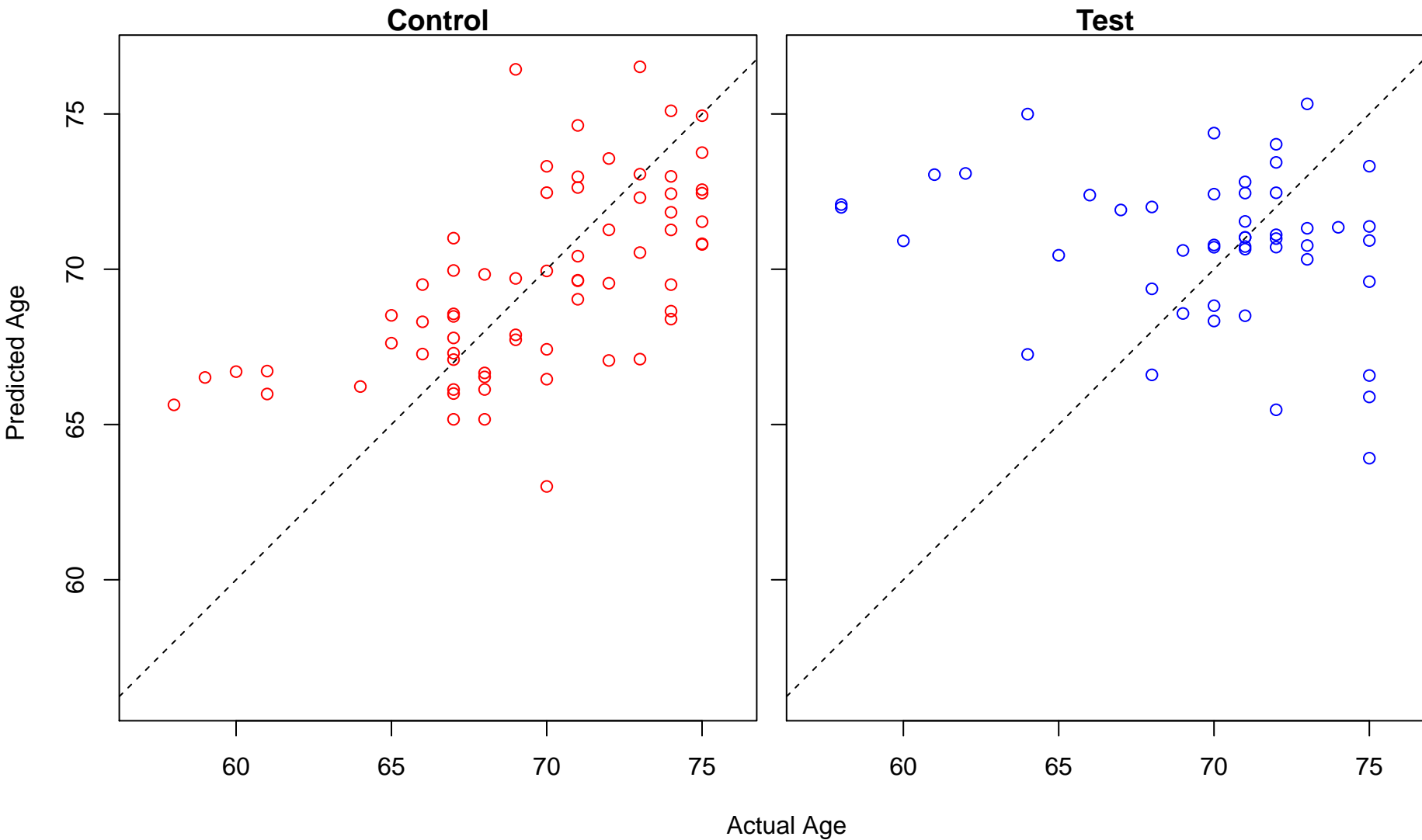
regulation of organ morphogenesis (Score: 1.208486)



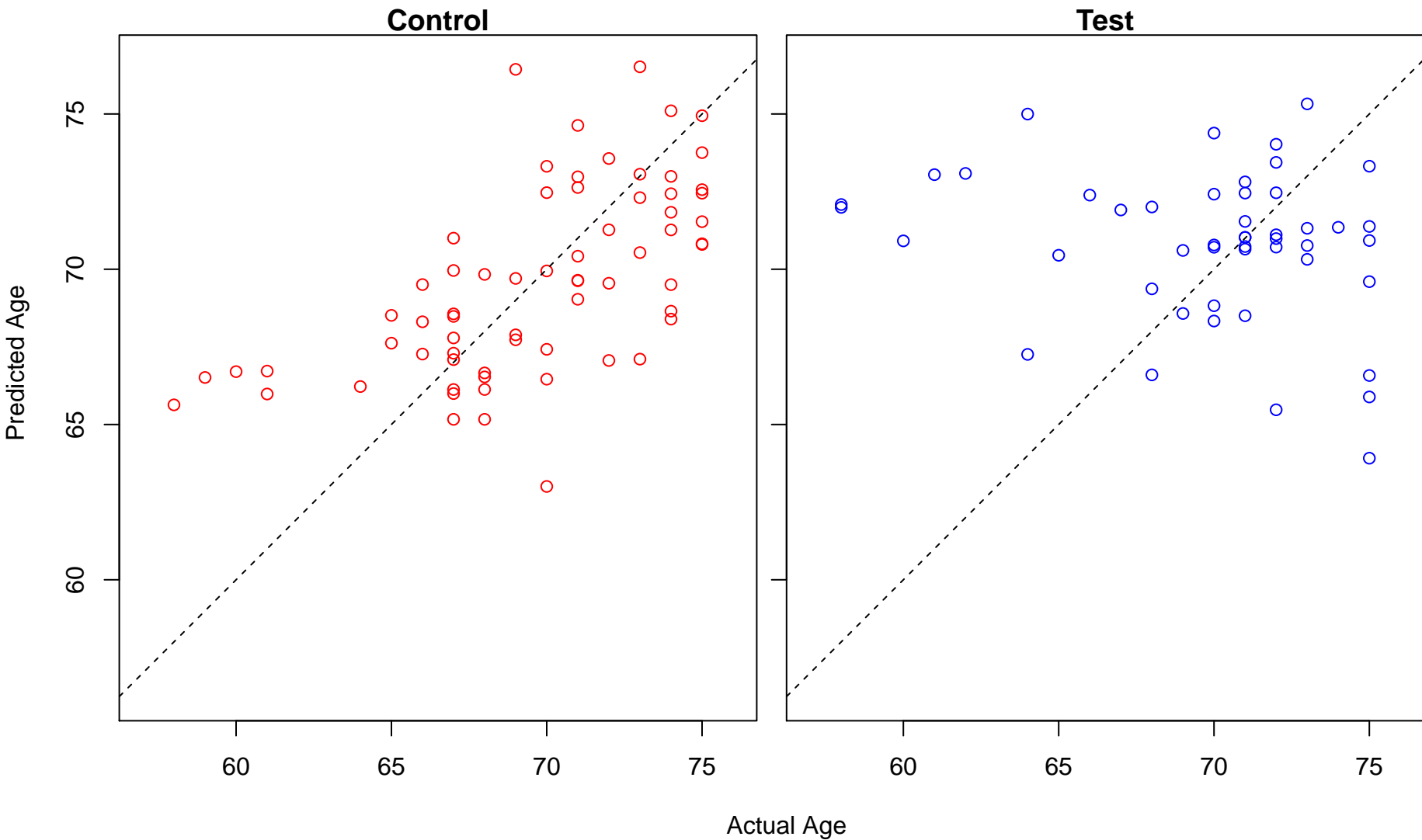
protein autoubiquitination (Score: 1.207596)



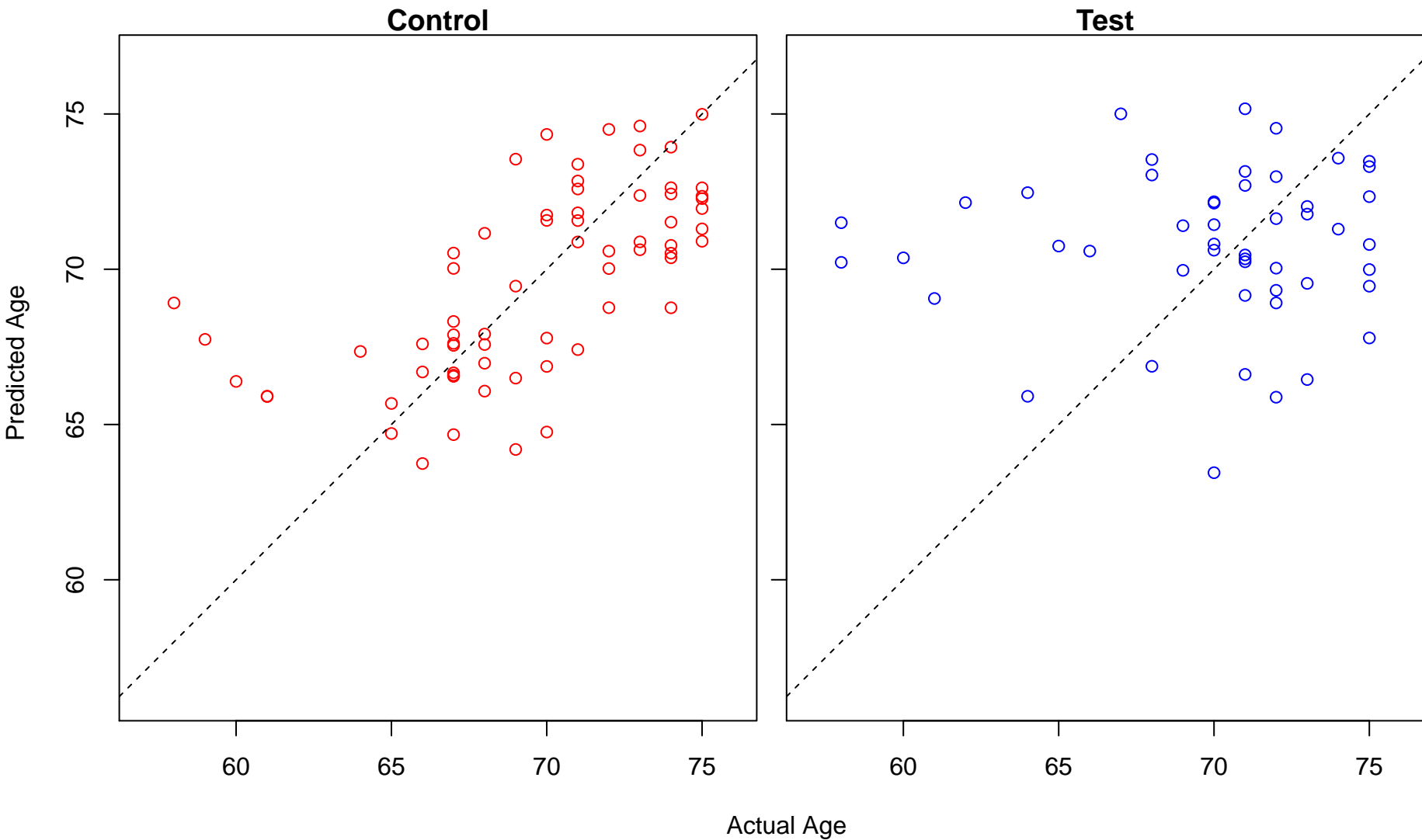
regulation of establishment of protein localization to chromosome (Score: 1.207197)



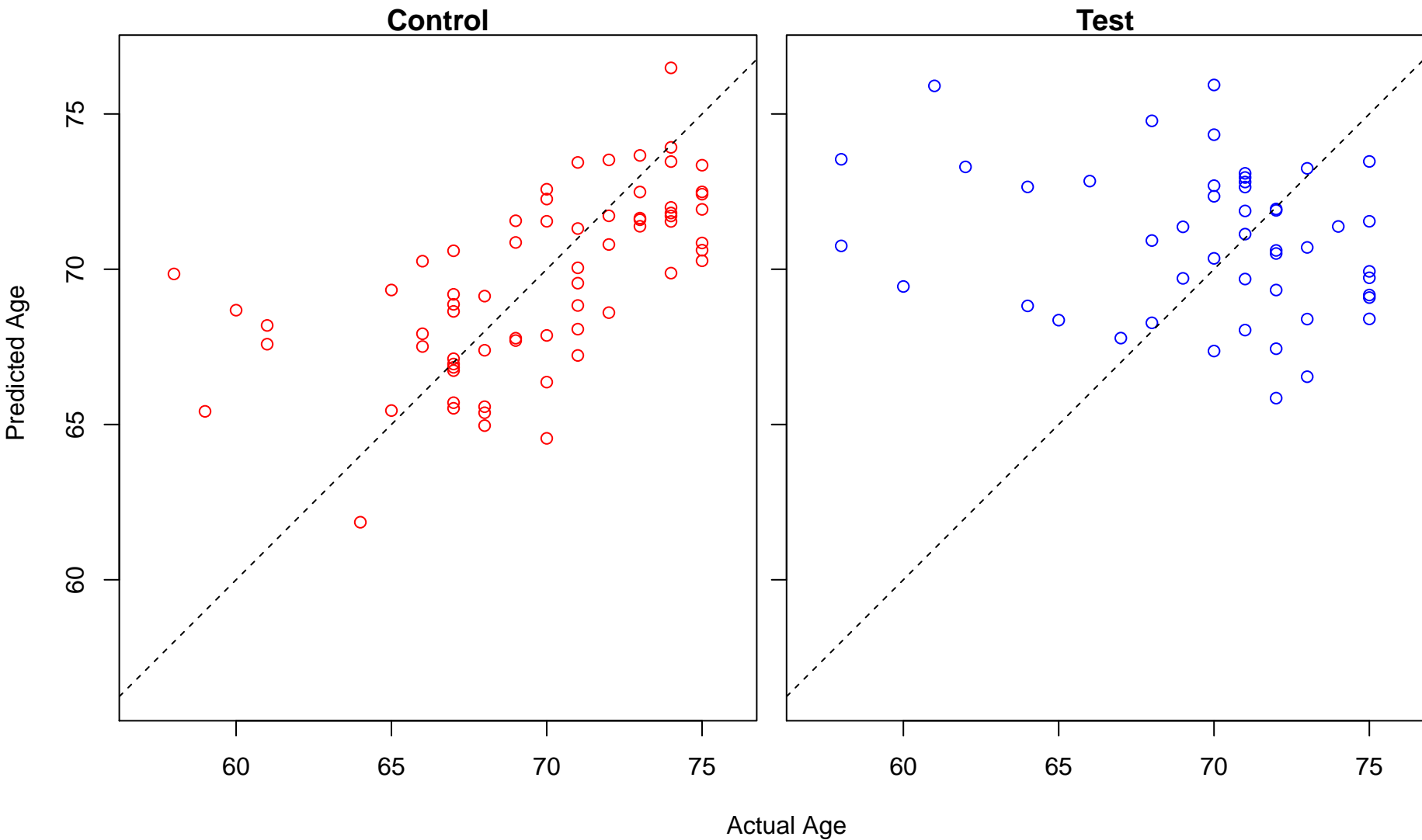
regulation of establishment of protein localization to telomere (Score: 1.207197)



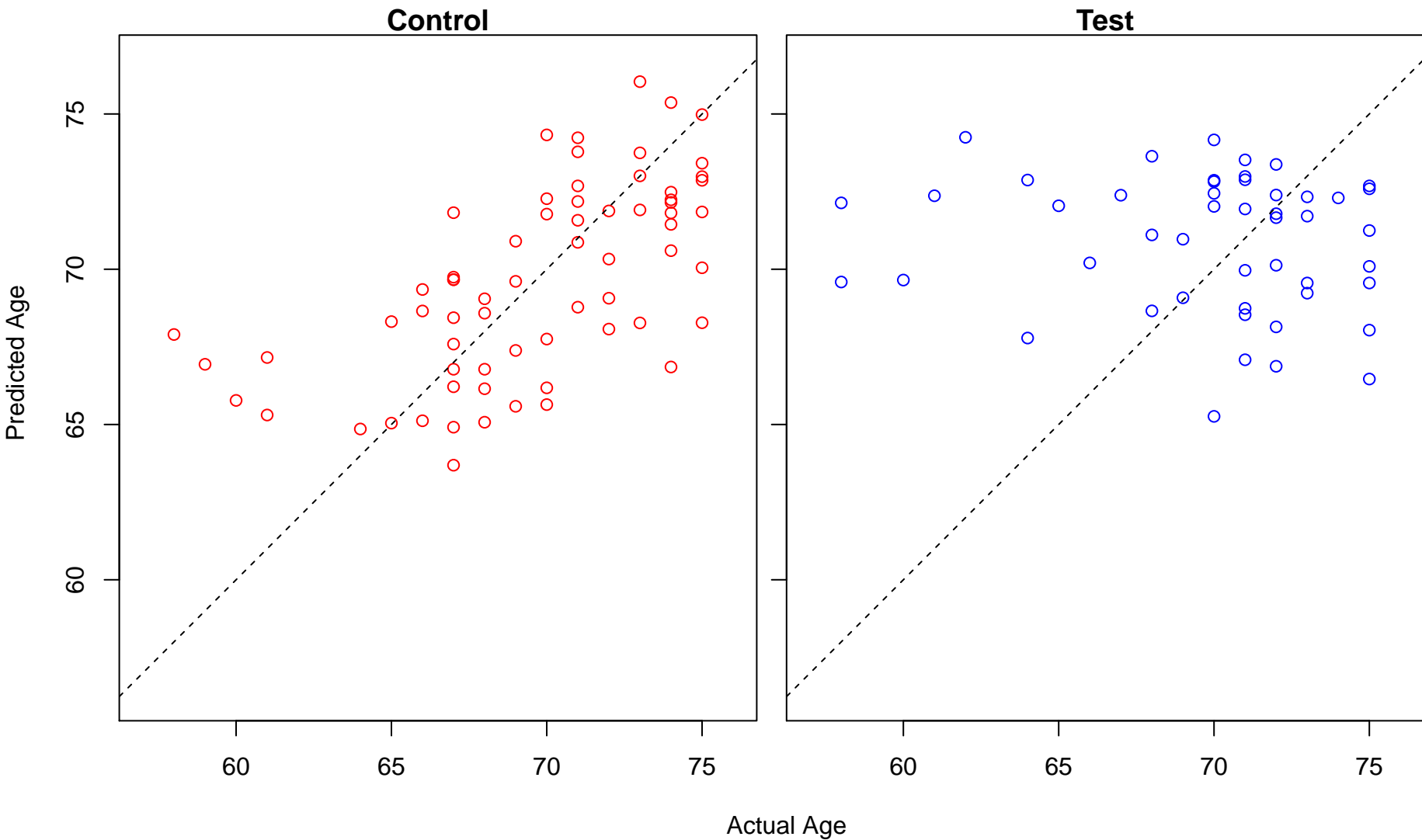
ER-nucleus signaling pathway (Score: 1.207192)



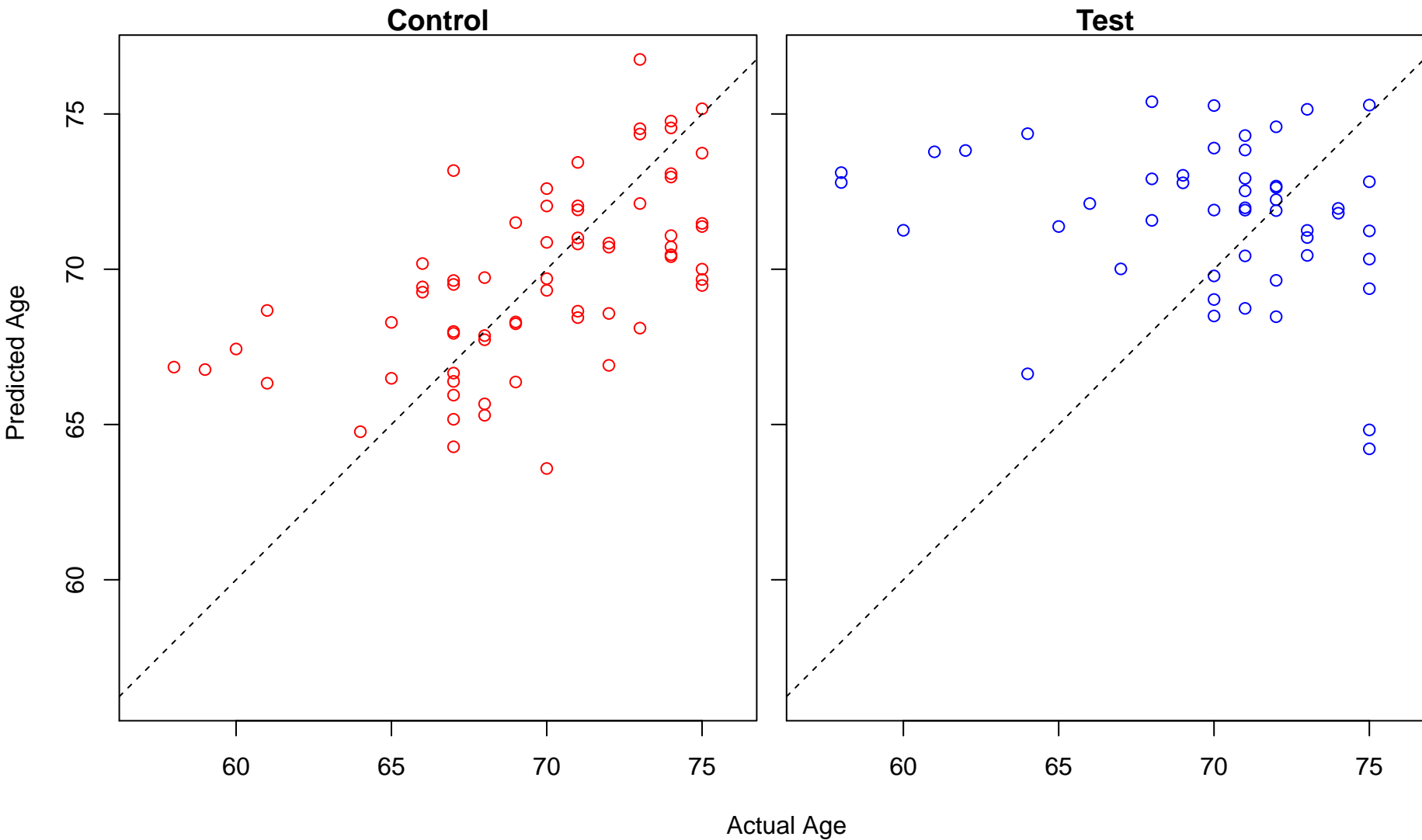
defense response to virus (Score: 1.207144)



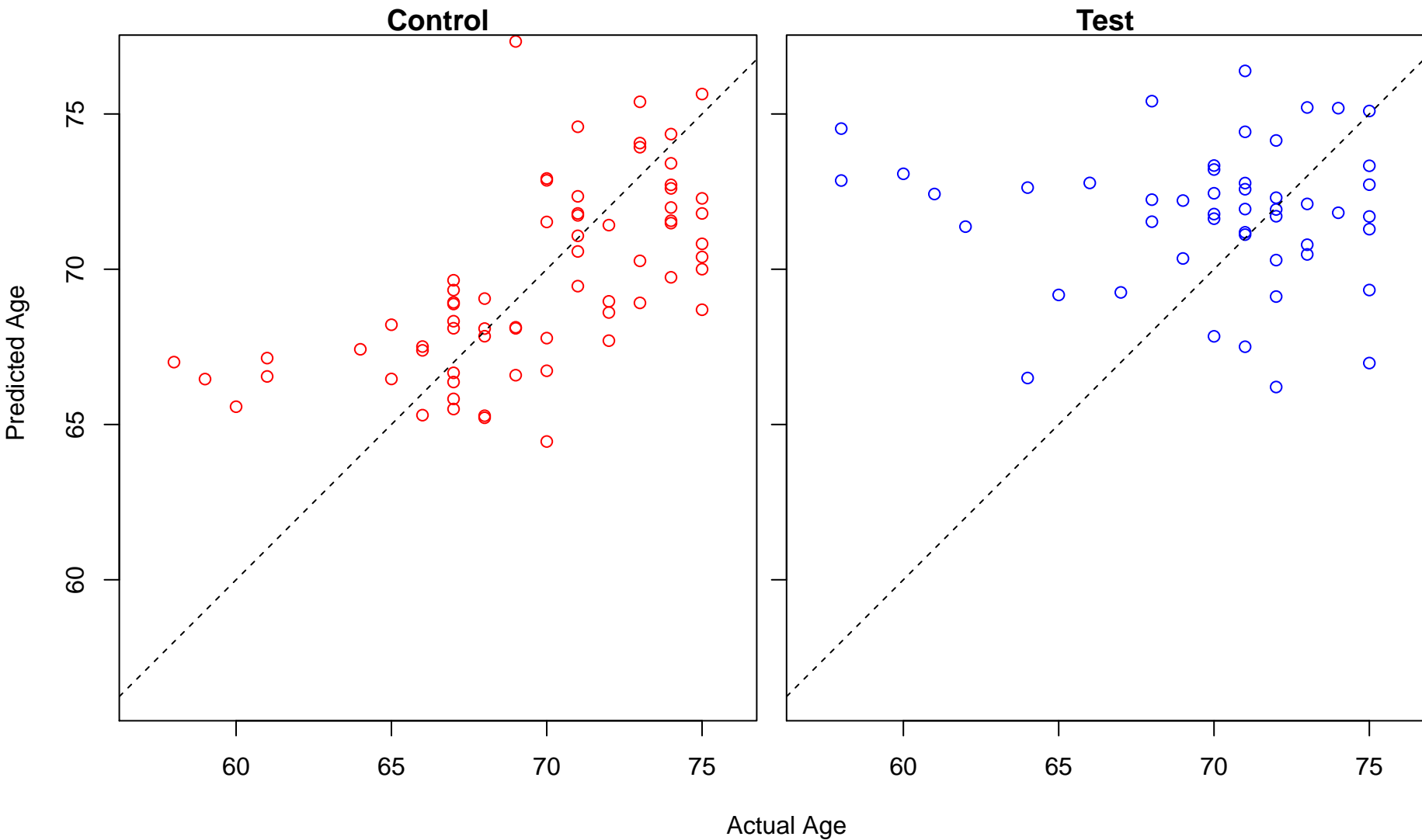
receptor metabolic process (Score: 1.206944)



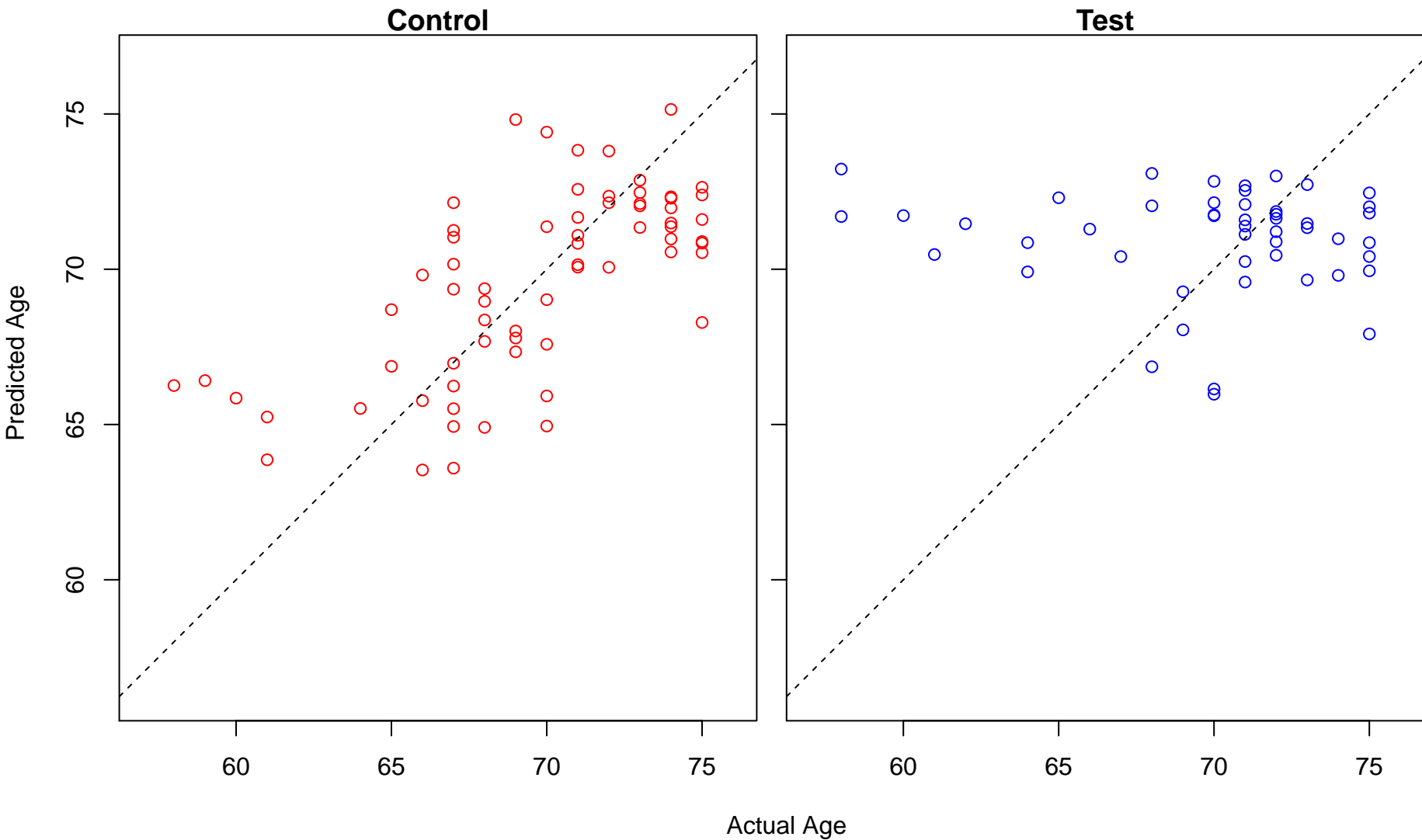
2-oxoglutarate metabolic process (Score: 1.206885)



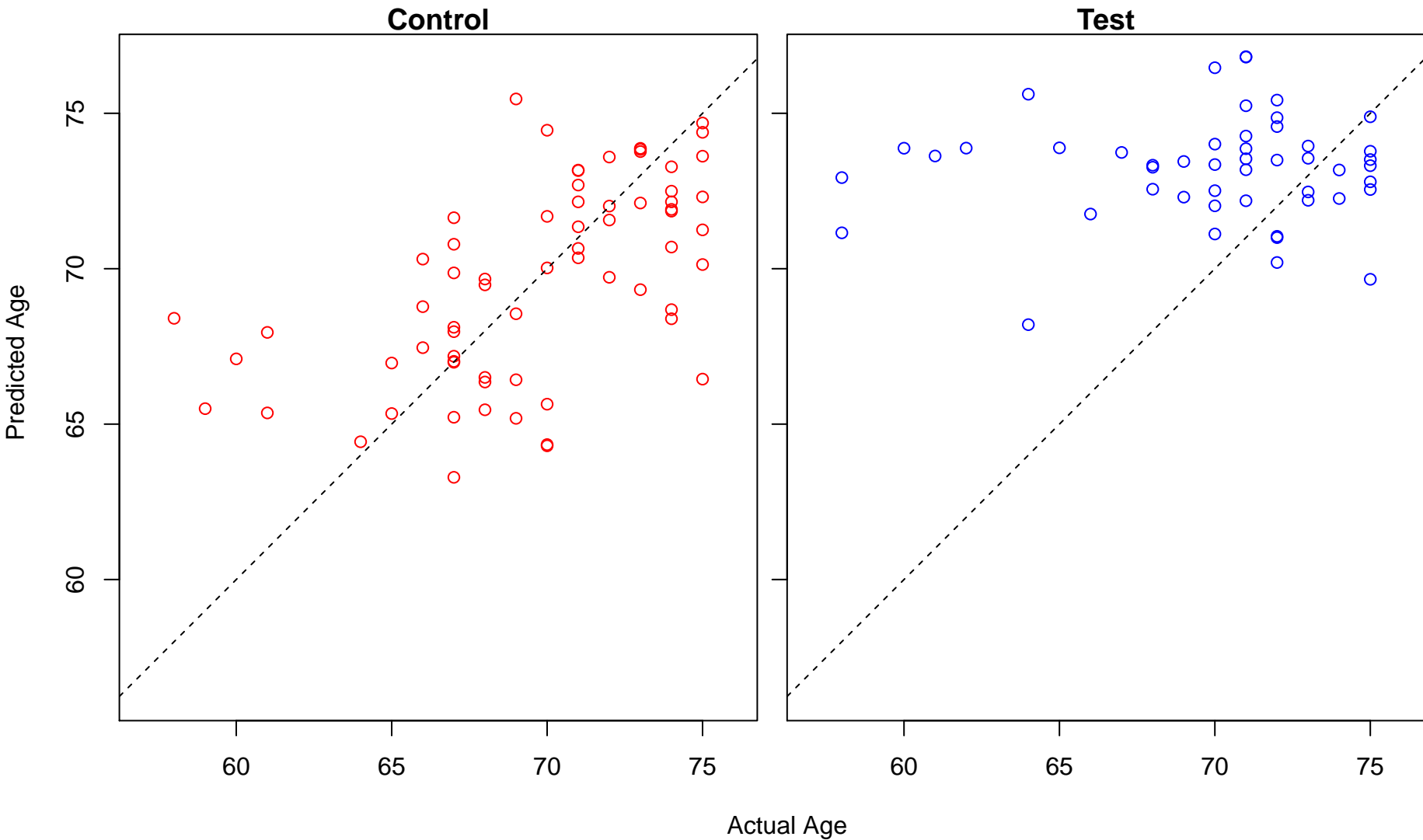
mesenchyme development (Score: 1.206461)



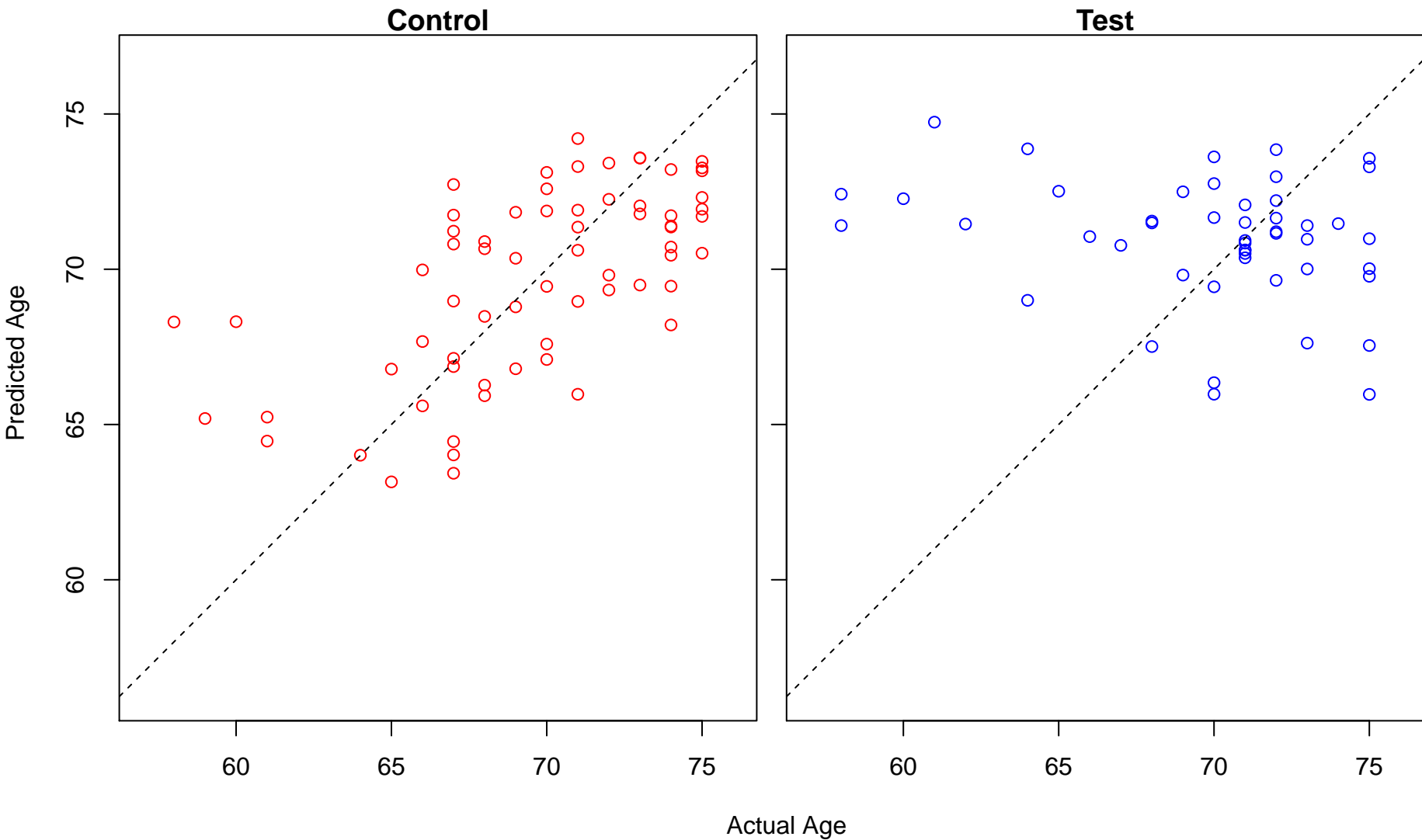
establishment or maintenance of transmembrane electrochemical gradient (Score: 1.206025)



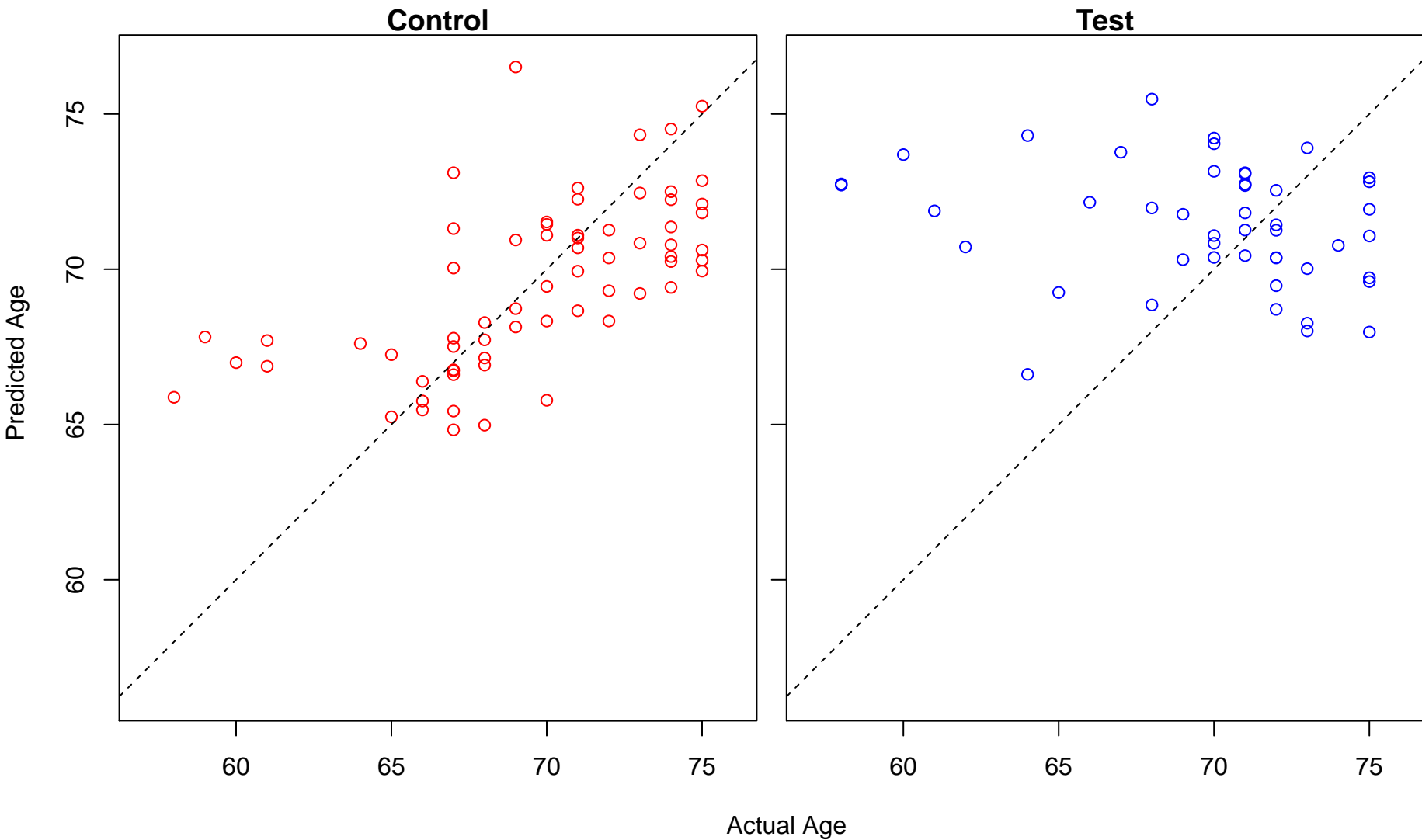
polysaccharide metabolic process (Score: 1.205723)



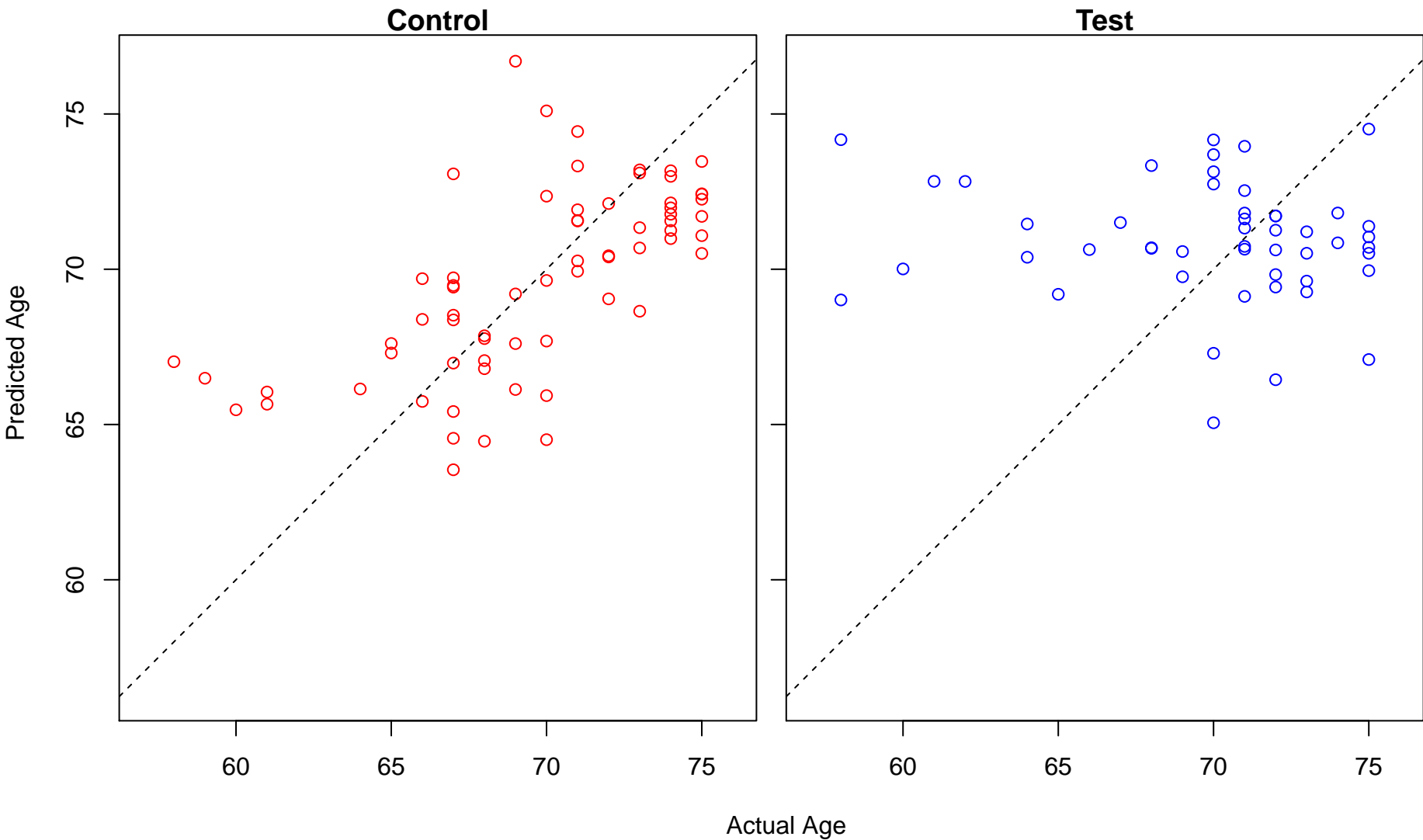
regulation of myosin-light-chain-phosphatase activity (Score: 1.205098)



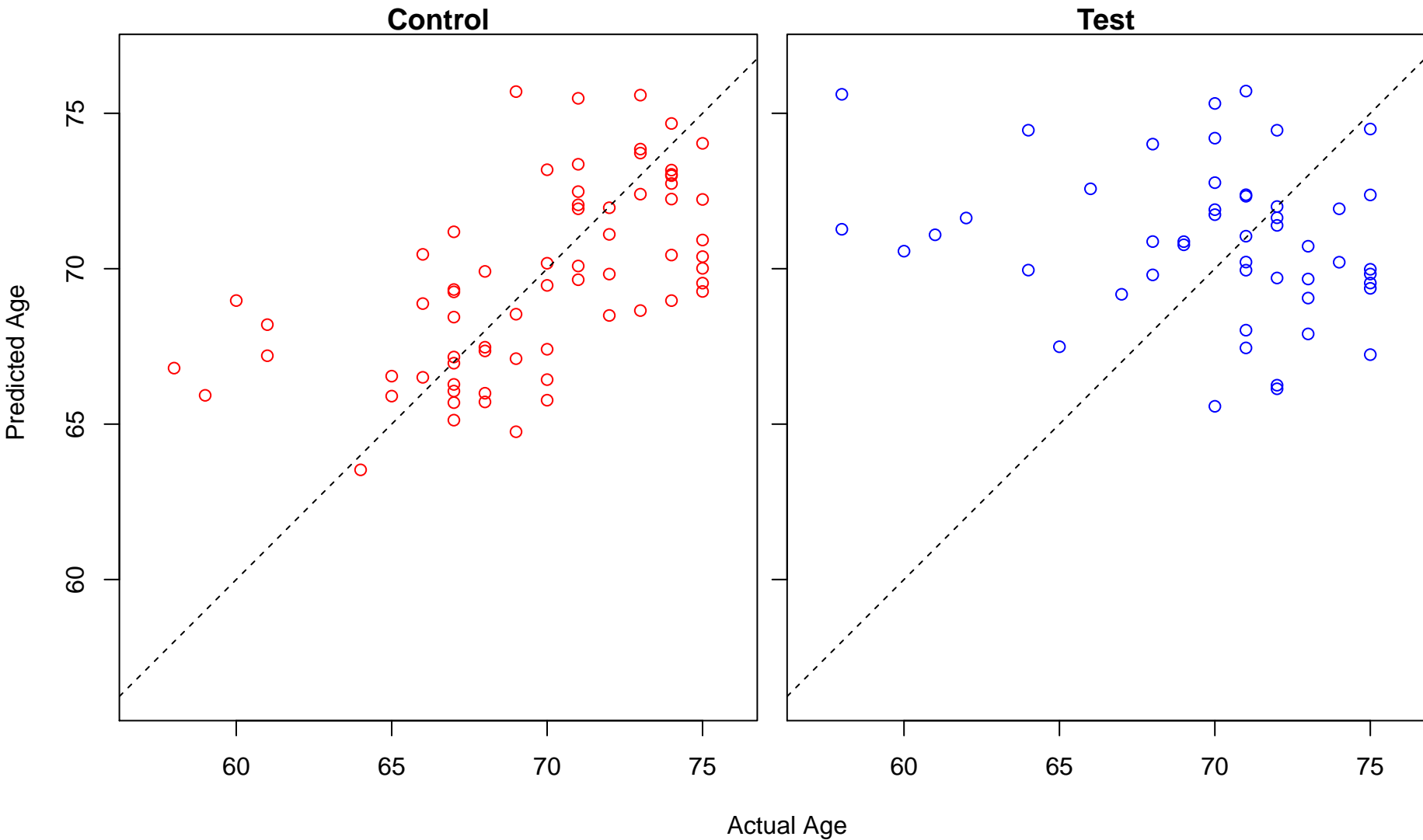
positive regulation of vesicle fusion (Score: 1.205034)



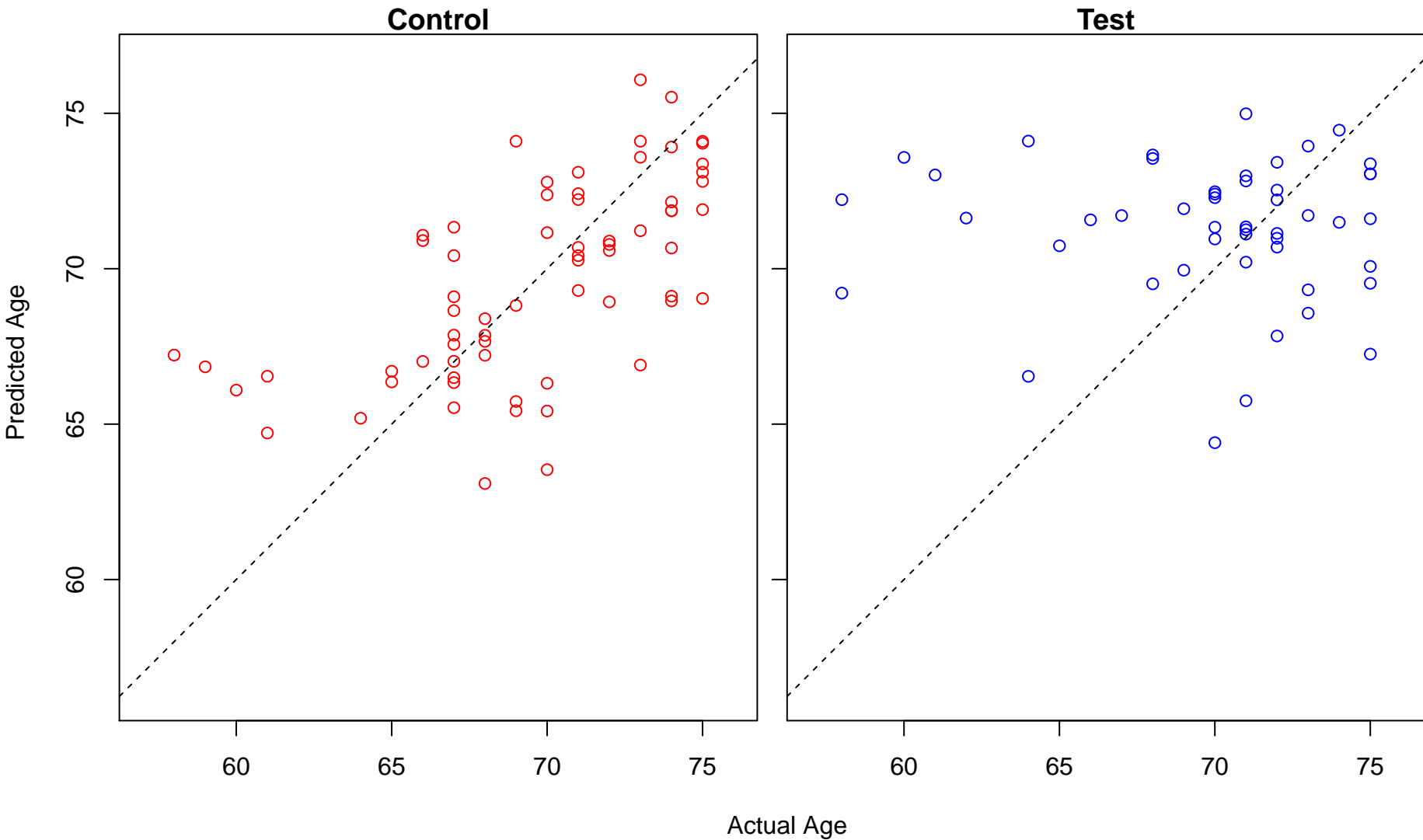
activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c (Score: 1)



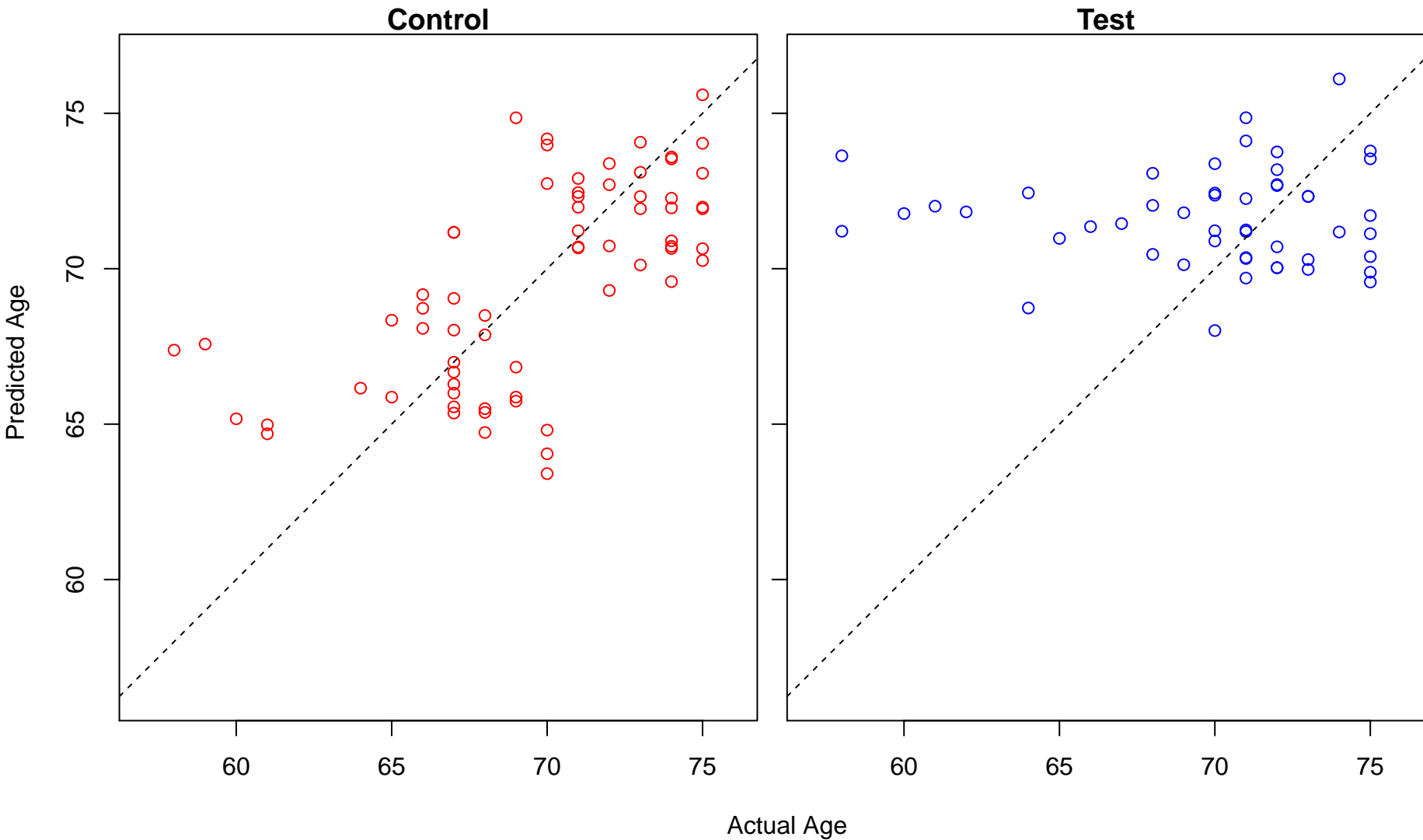
positive regulation of stem cell proliferation (Score: 1.204524)



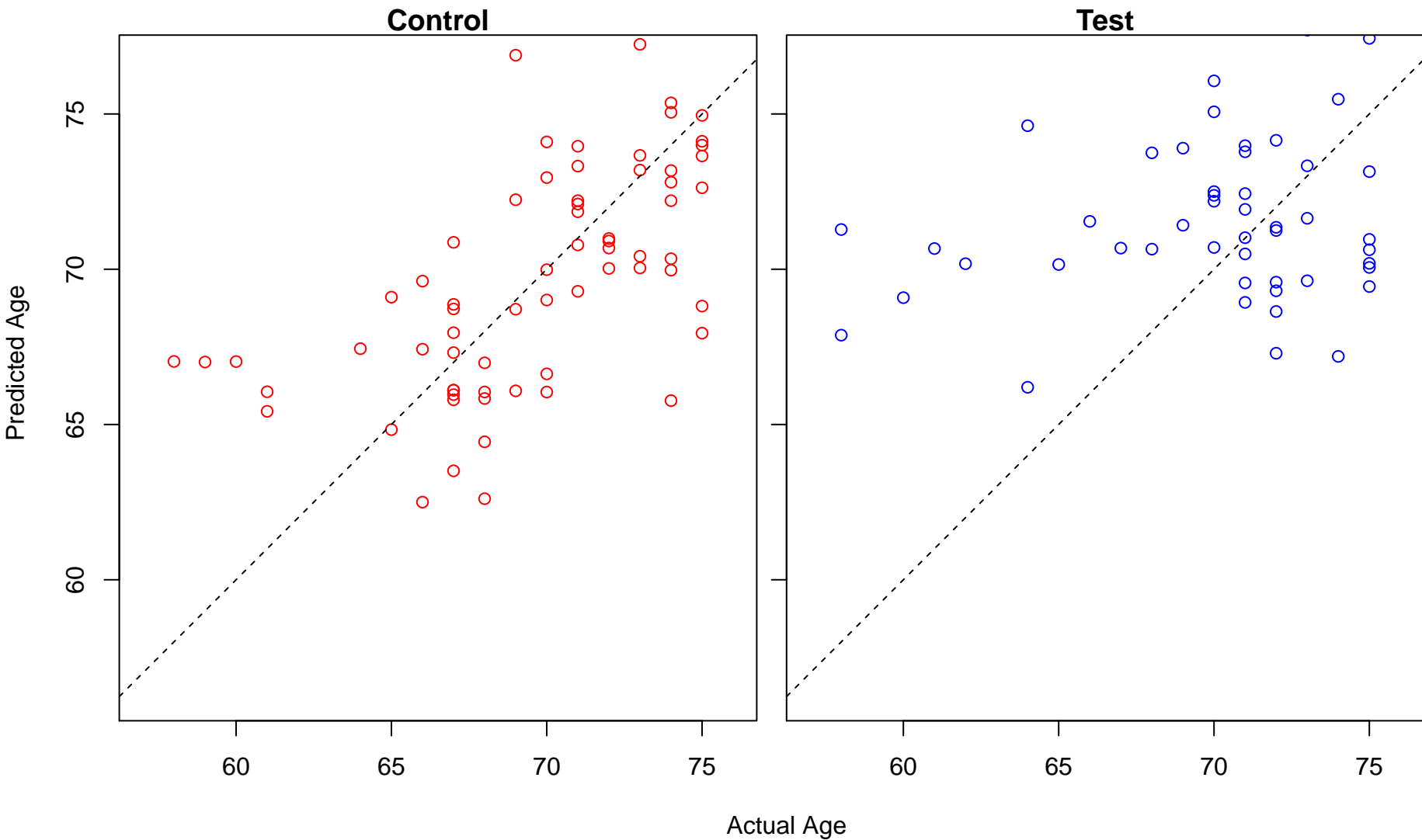
regulation of polysaccharide biosynthetic process (Score: 1.203748)



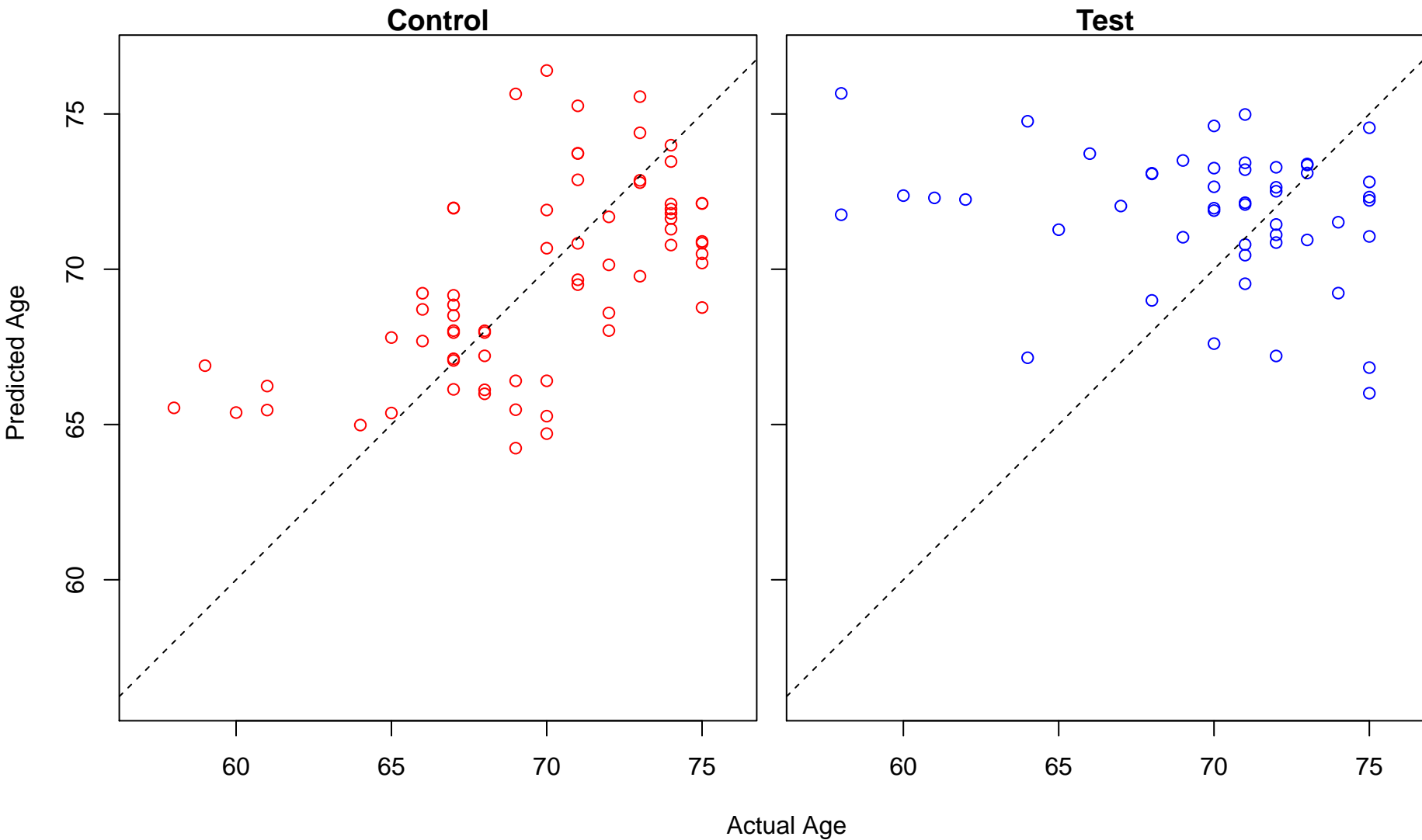
establishment of vesicle localization (Score: 1.203599)



morphogenesis of a branching epithelium (Score: 1.202973)

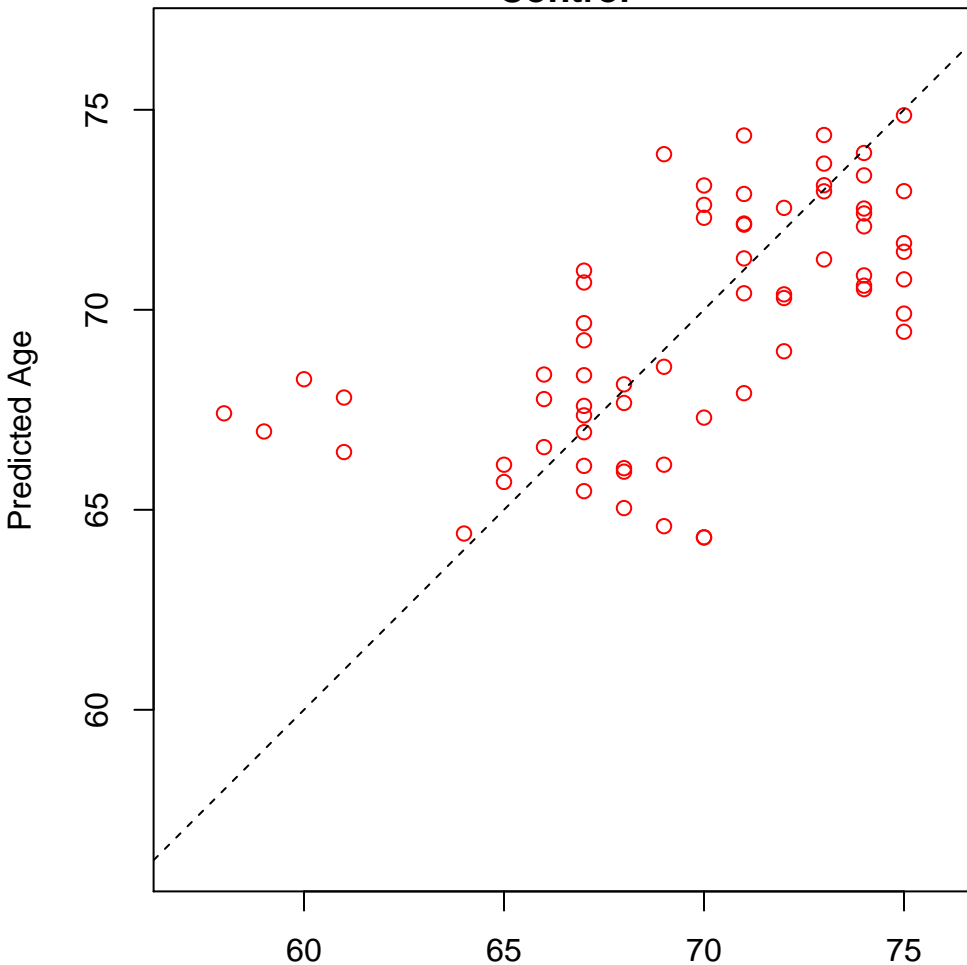


cellular response to light stimulus (Score: 1.202971)

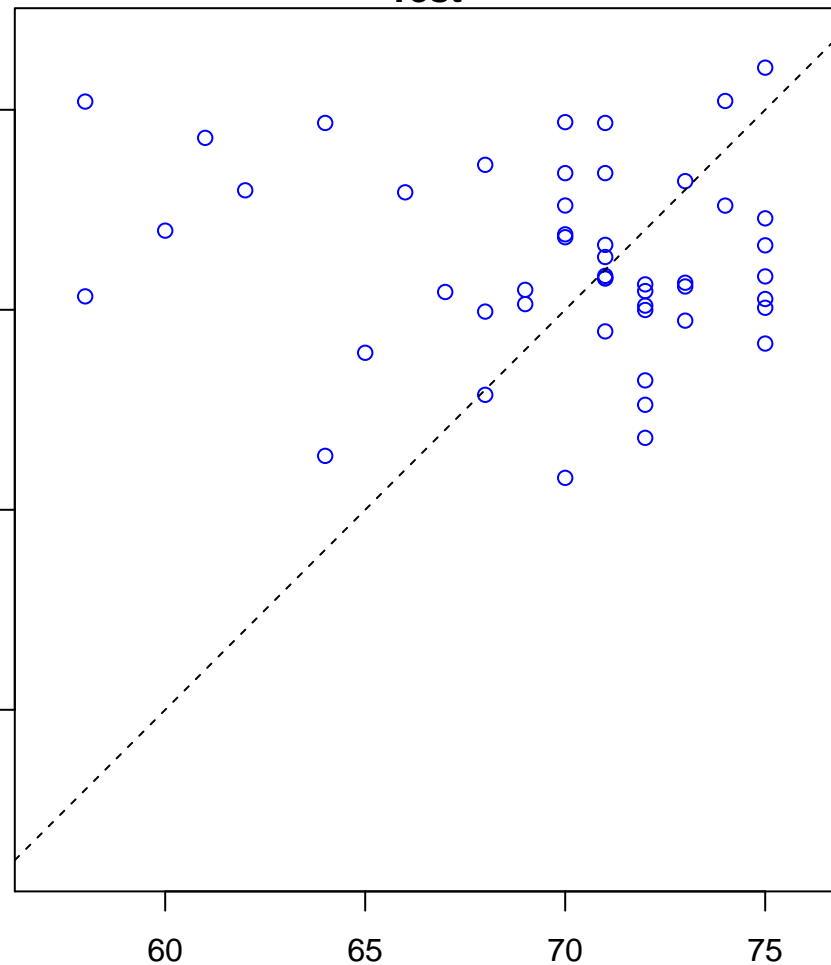


peptidyl–threonine phosphorylation (Score: 1.202797)

Control

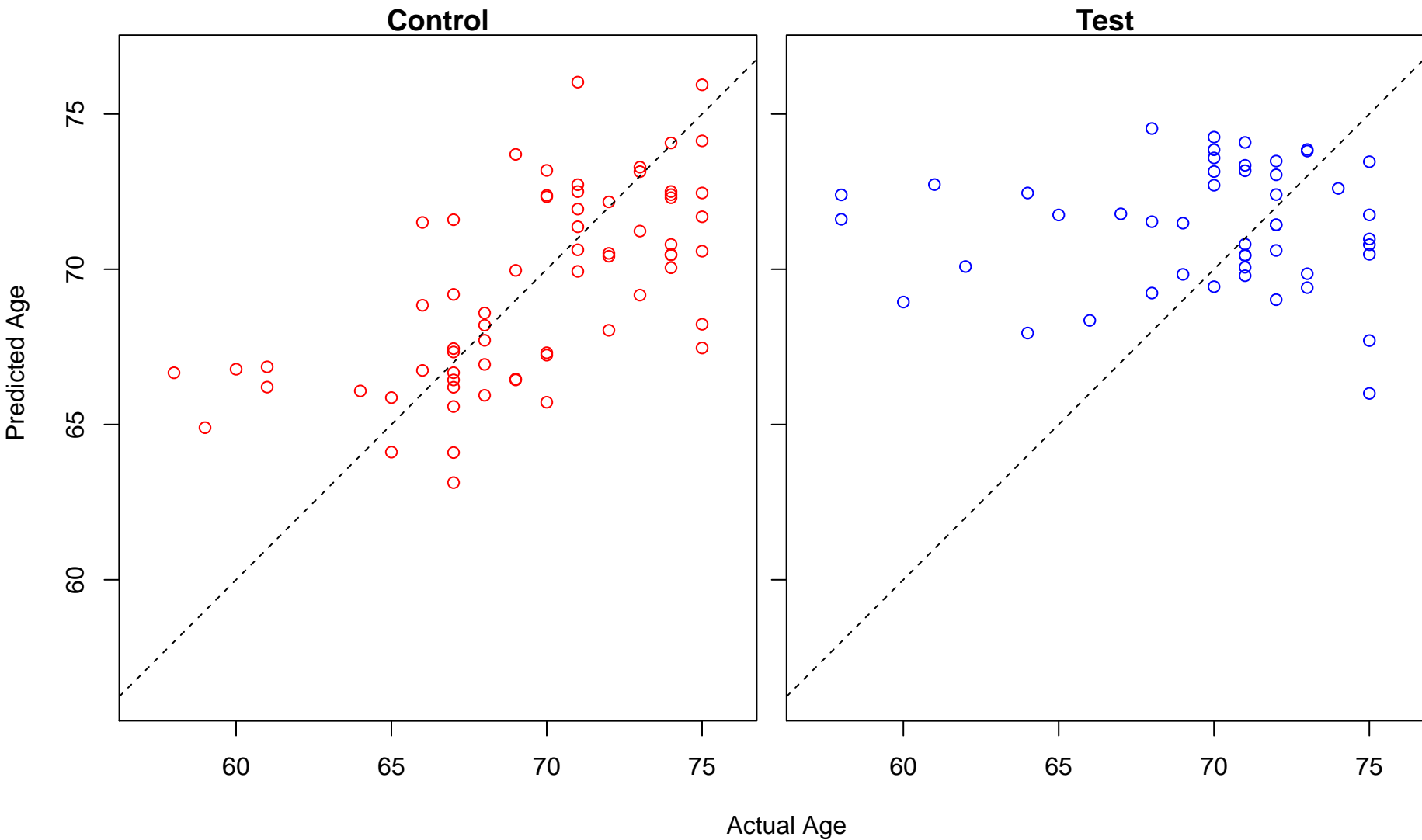


Test

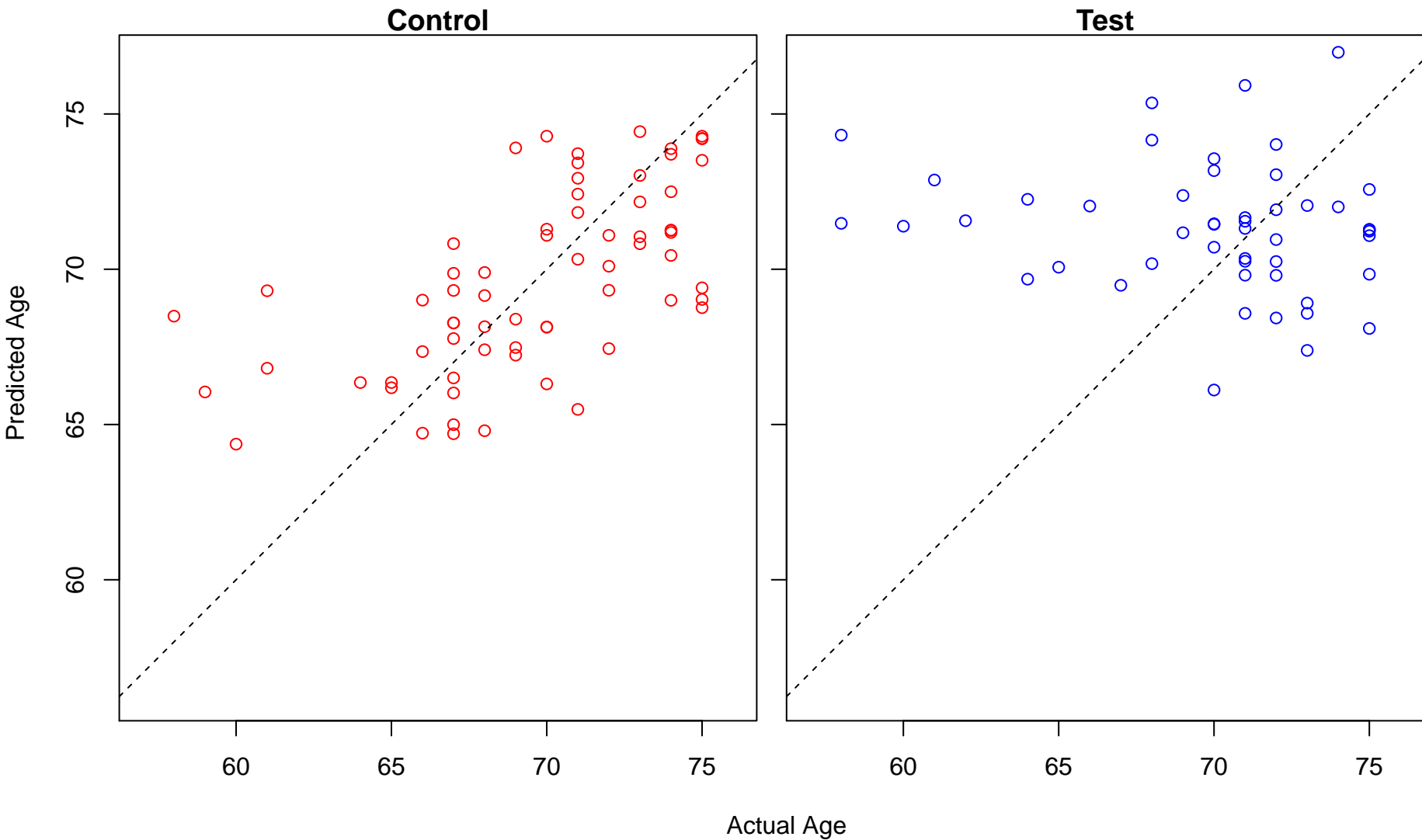


Actual Age

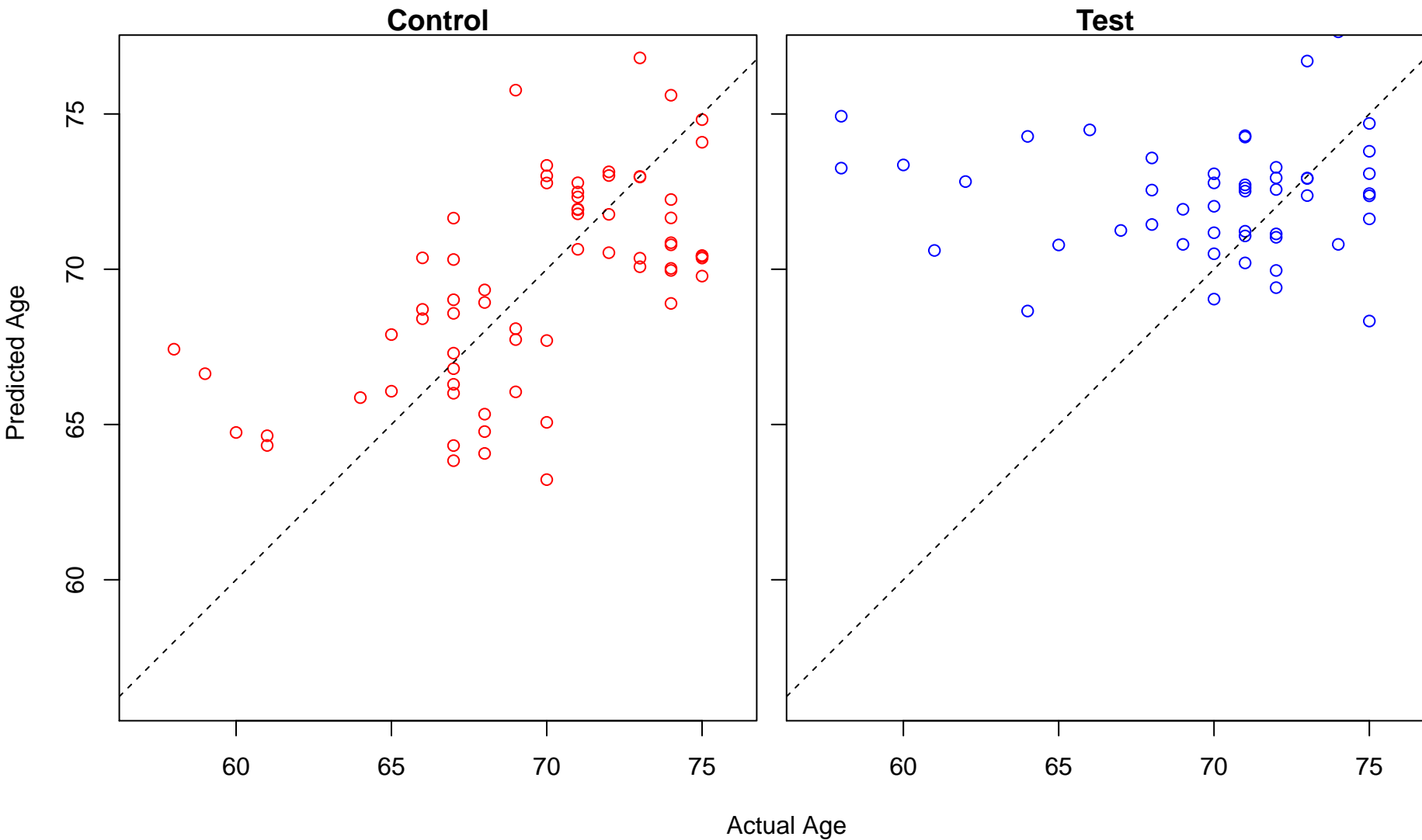
negative regulation of response to DNA damage stimulus (Score: 1.202587)



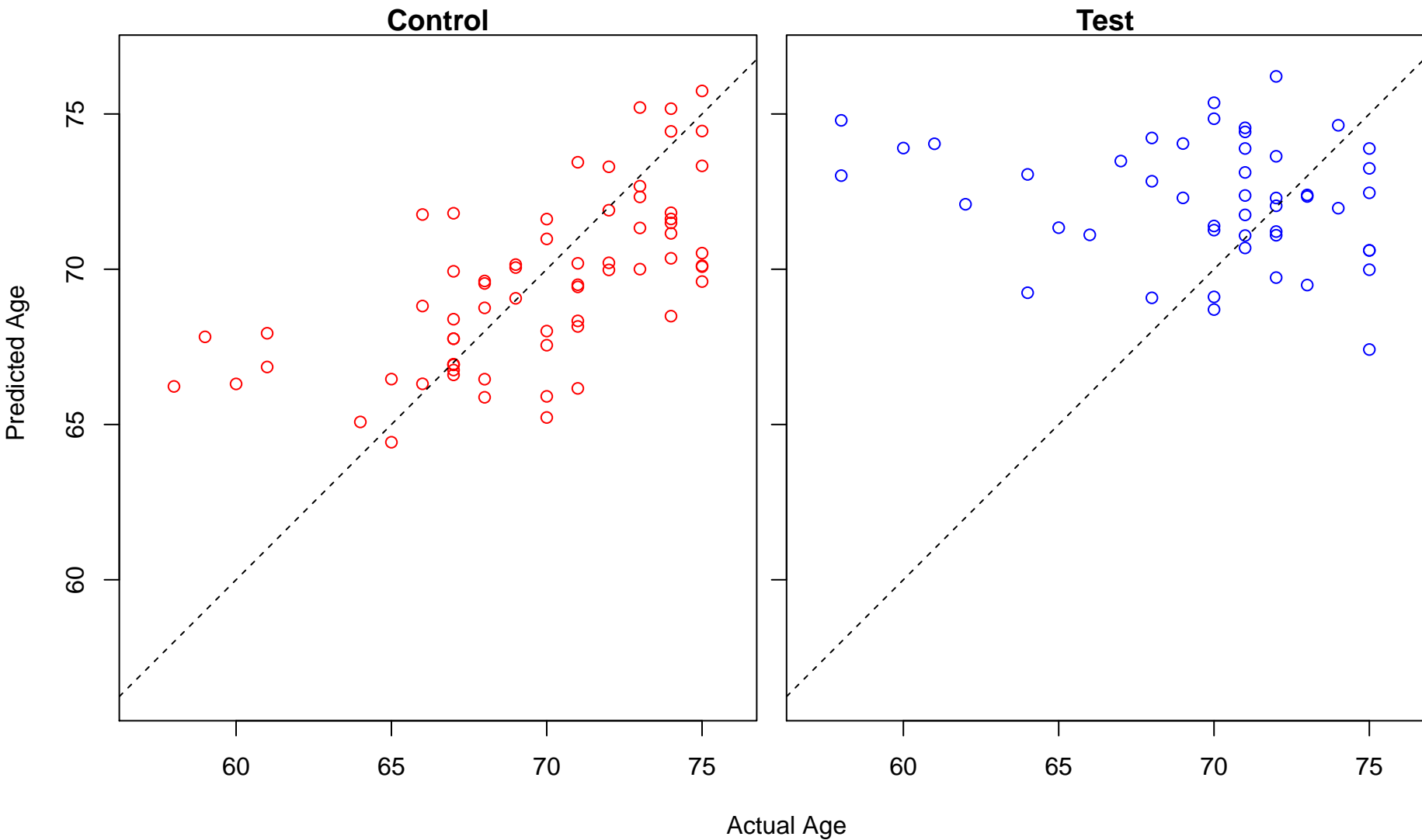
RNA-dependent DNA replication (Score: 1.202220)



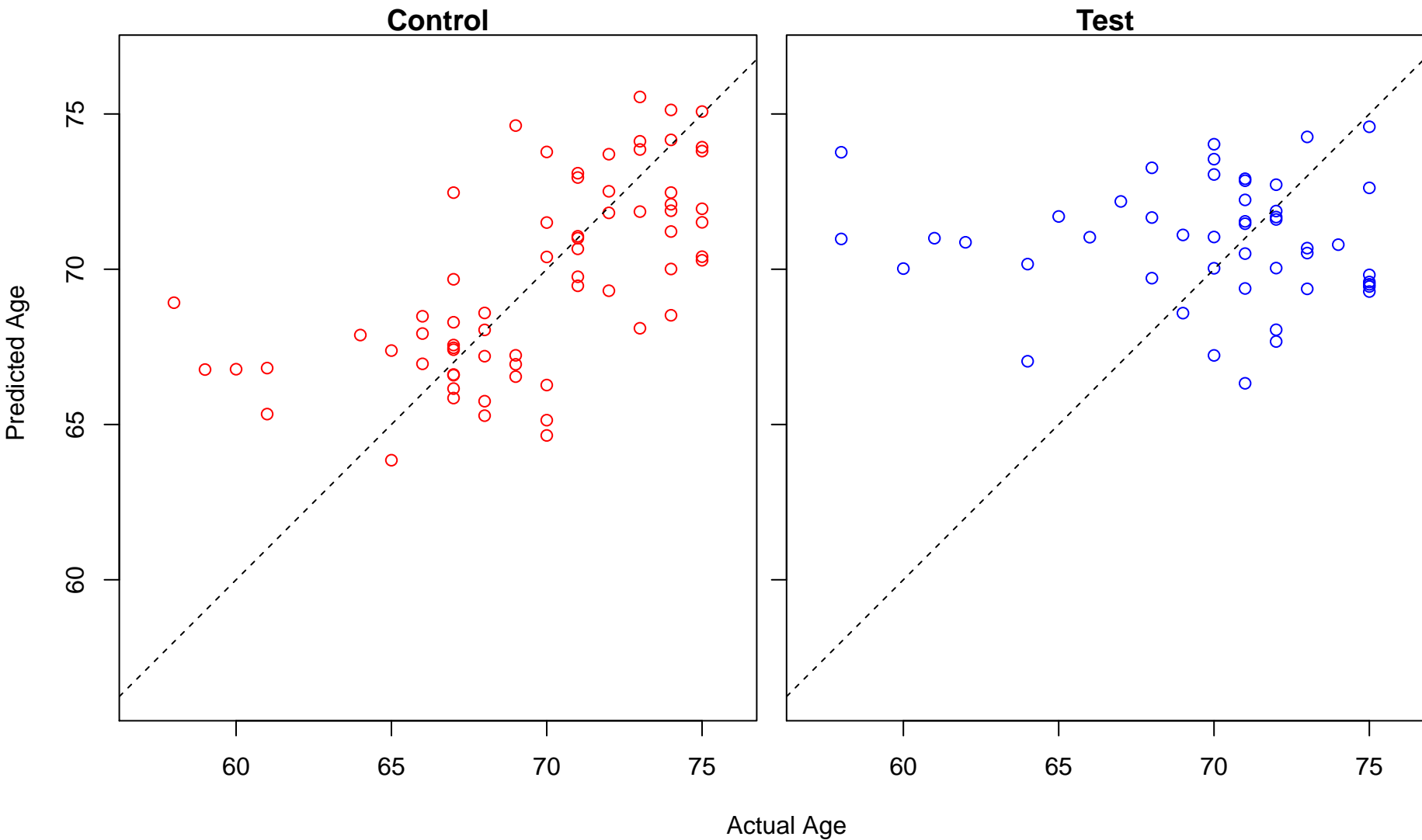
vesicle targeting (Score: 1.201884)



ISG15-protein conjugation (Score: 1.201836)

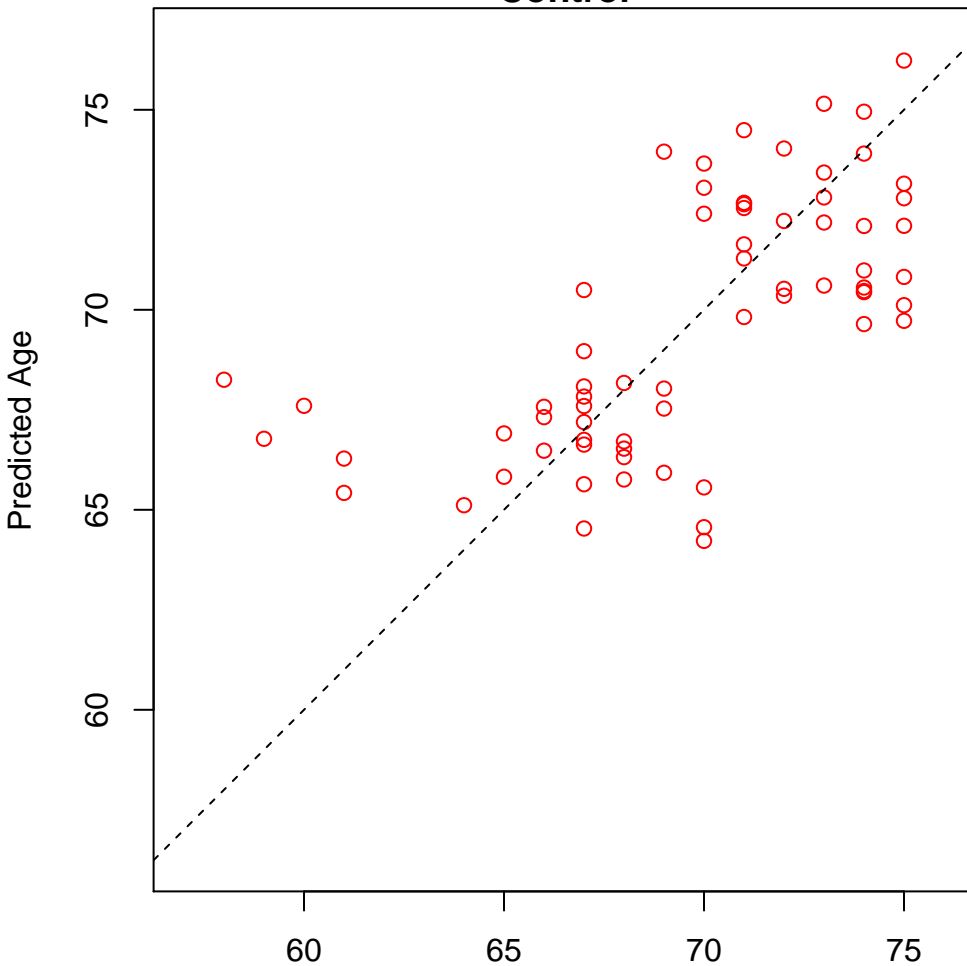


triglyceride metabolic process (Score: 1.201642)

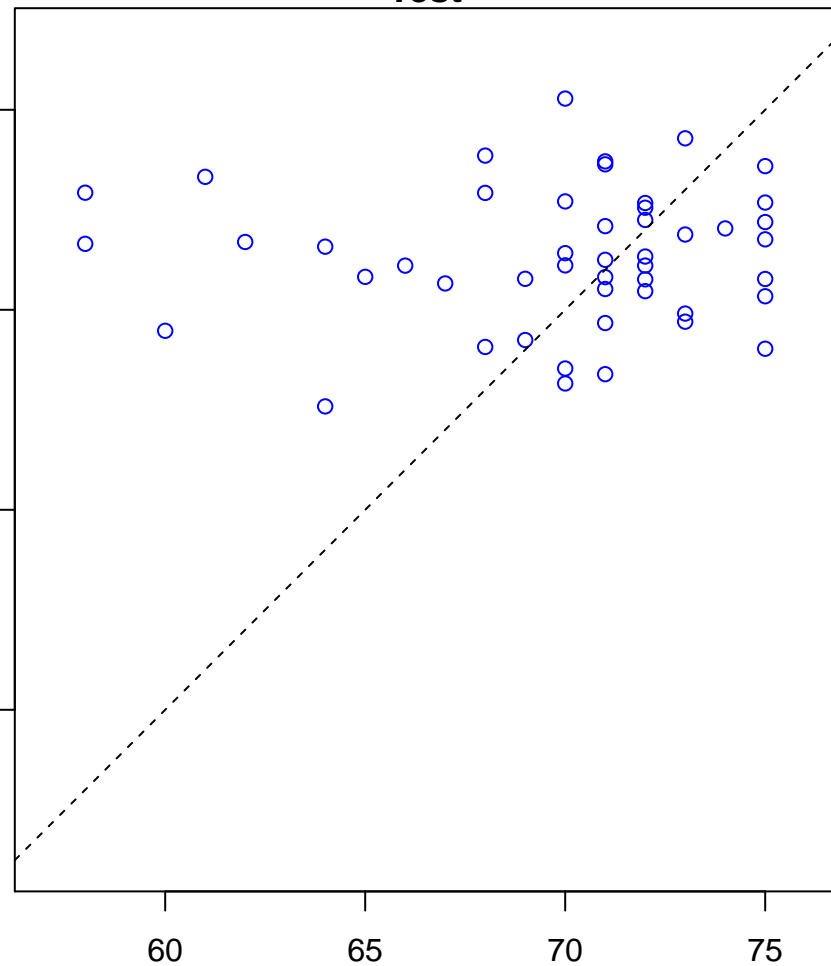


regulation of protein dephosphorylation (Score: 1.201513)

Control

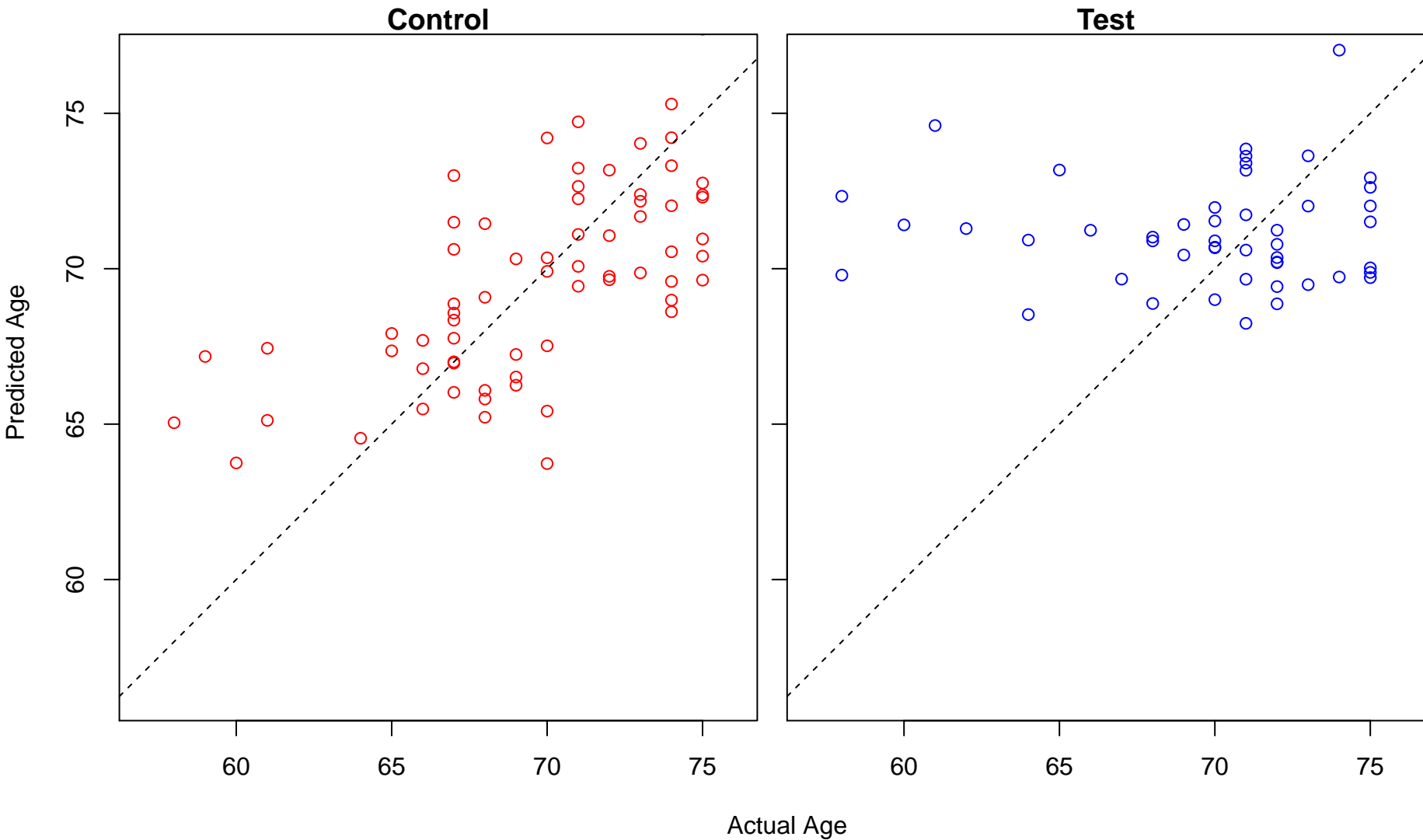


Test

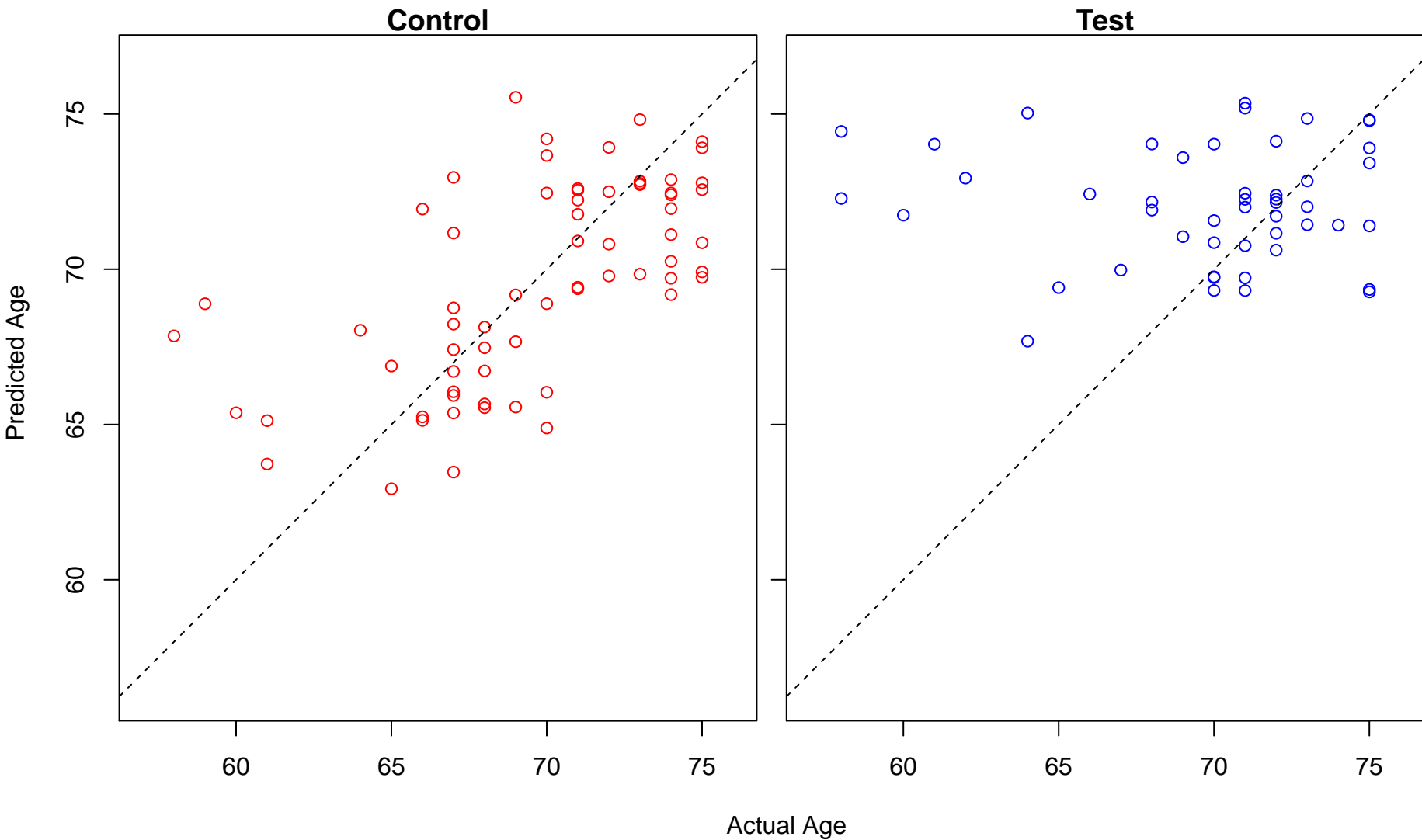


Actual Age

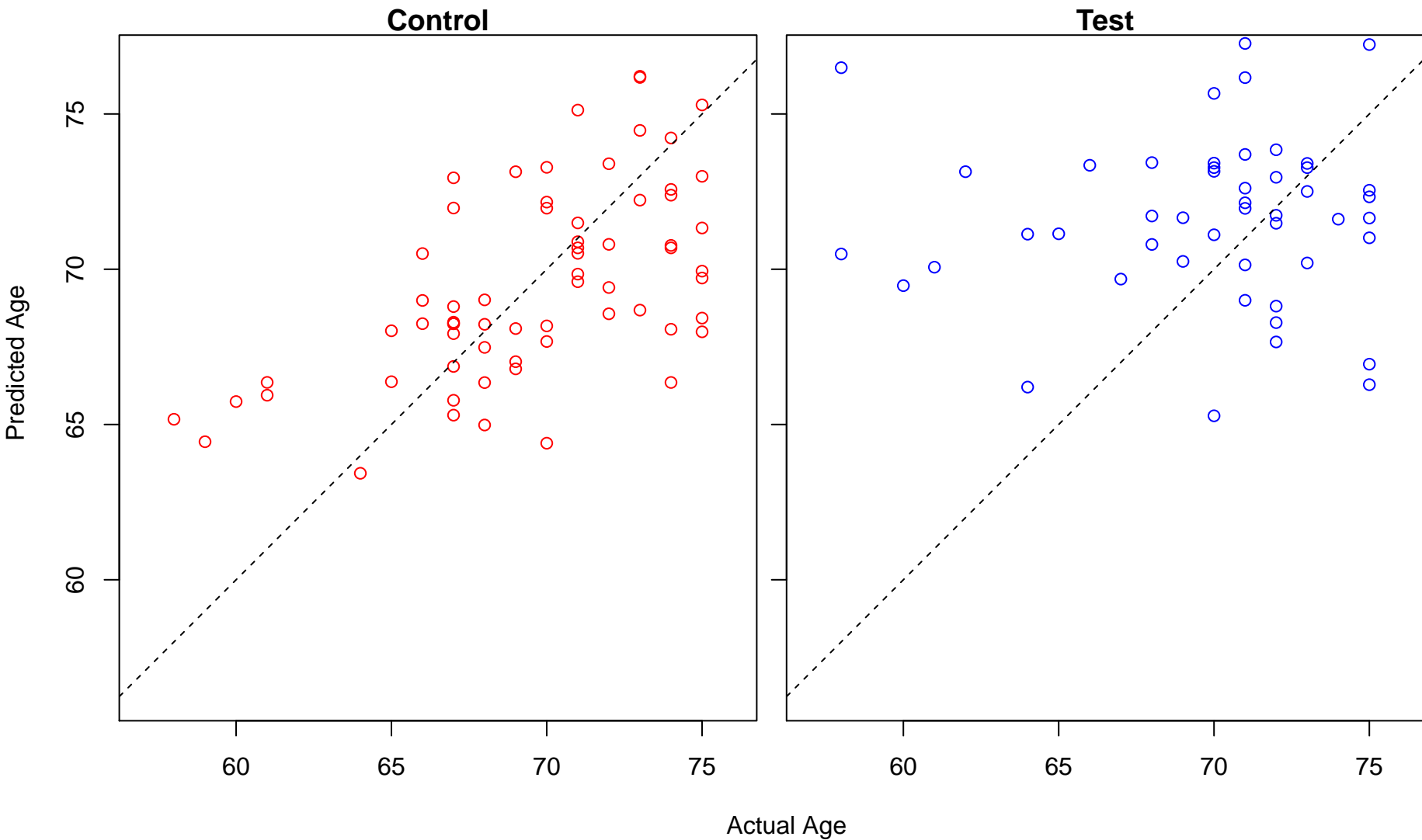
positive regulation of BMP signaling pathway (Score: 1.201300)



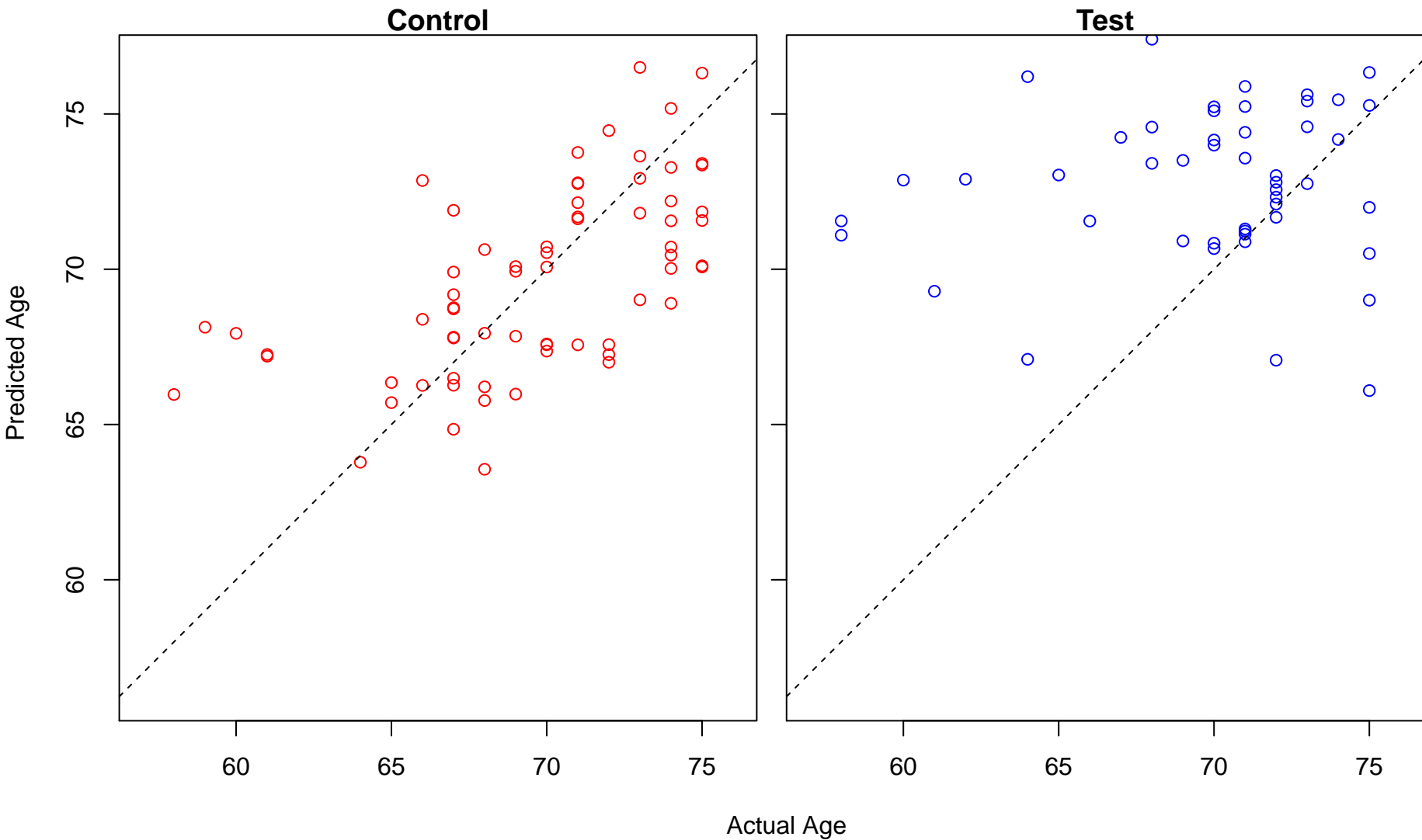
embryonic organ development (Score: 1.201154)



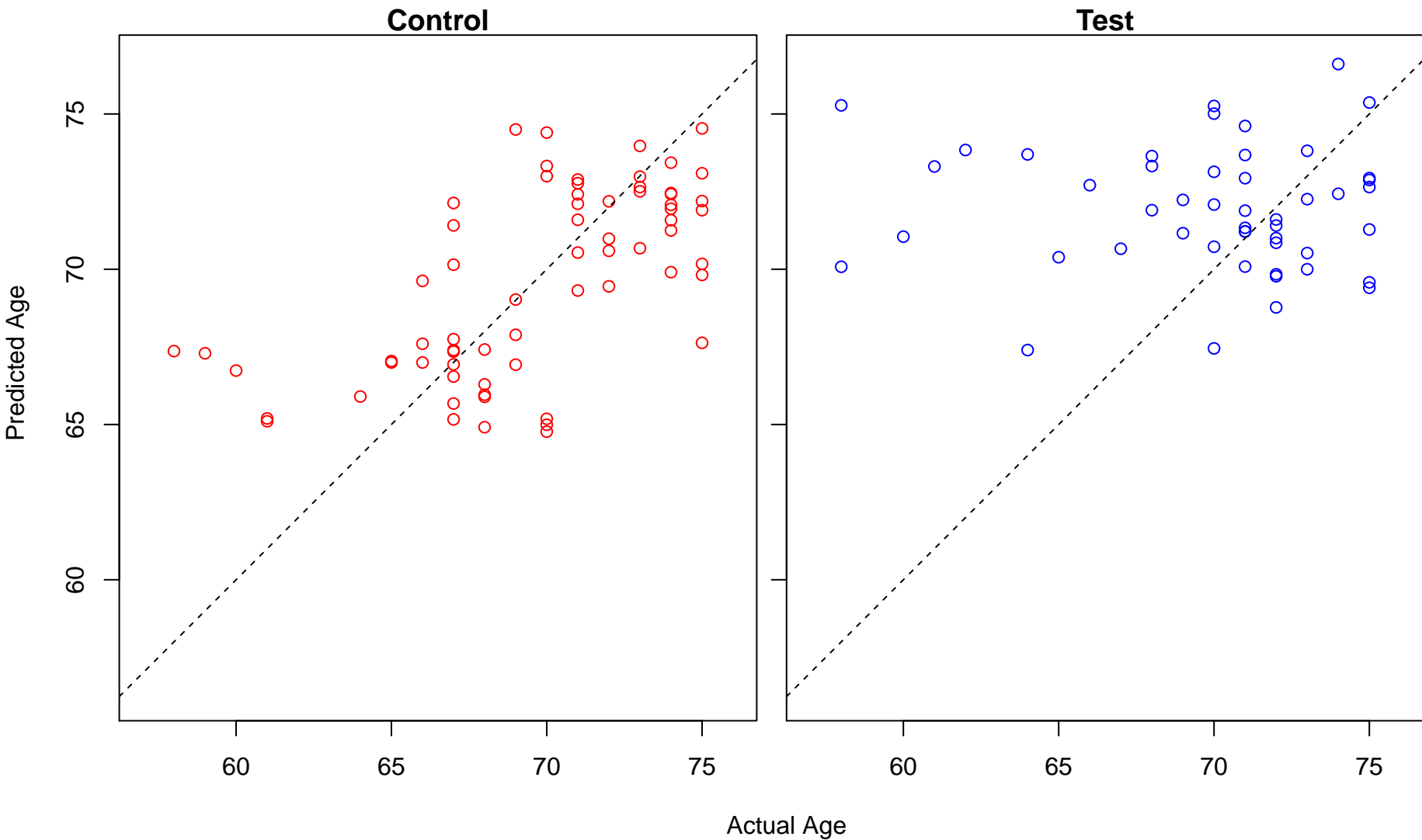
cell junction assembly (Score: 1.200976)



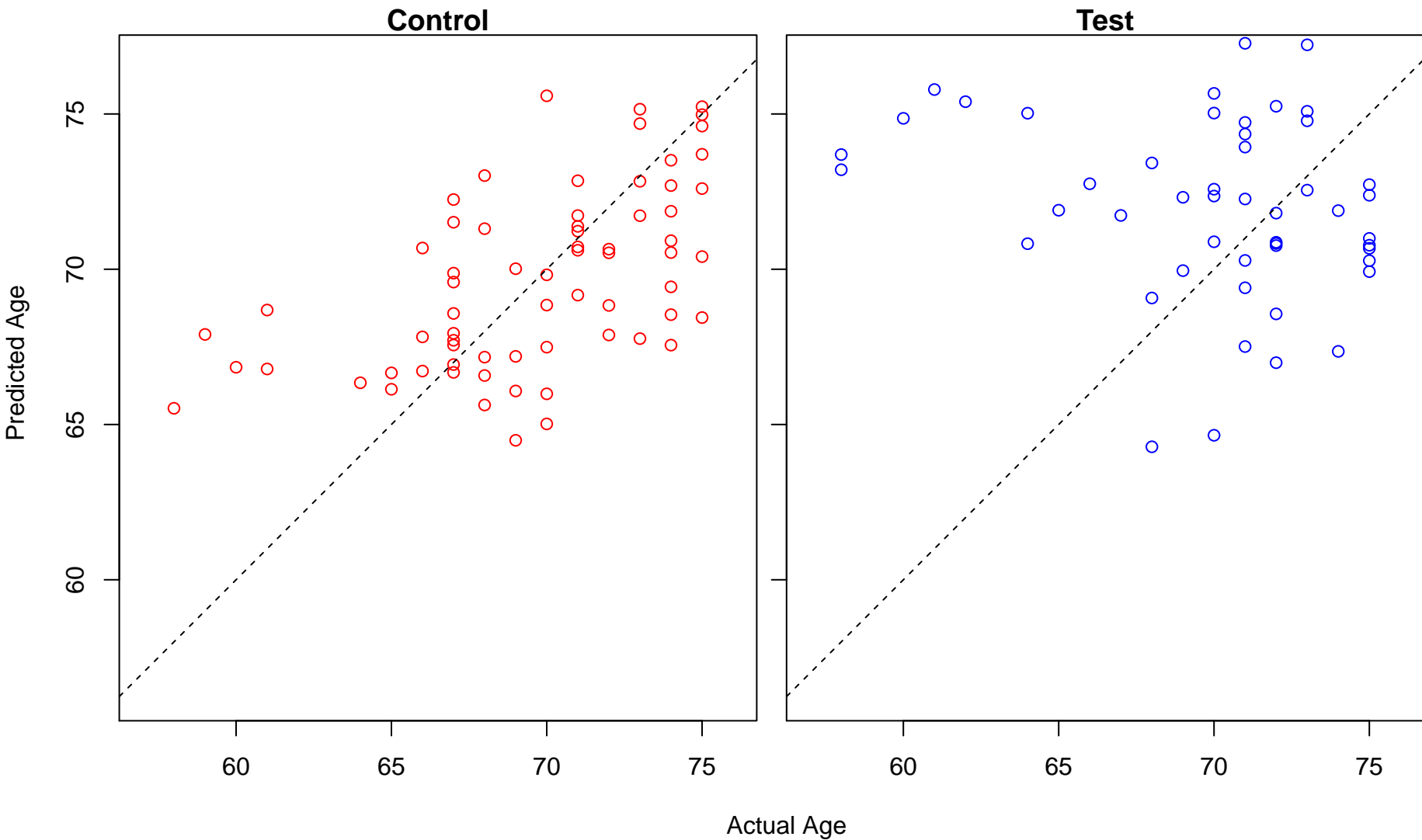
response to low-density lipoprotein particle (Score: 1.200672)



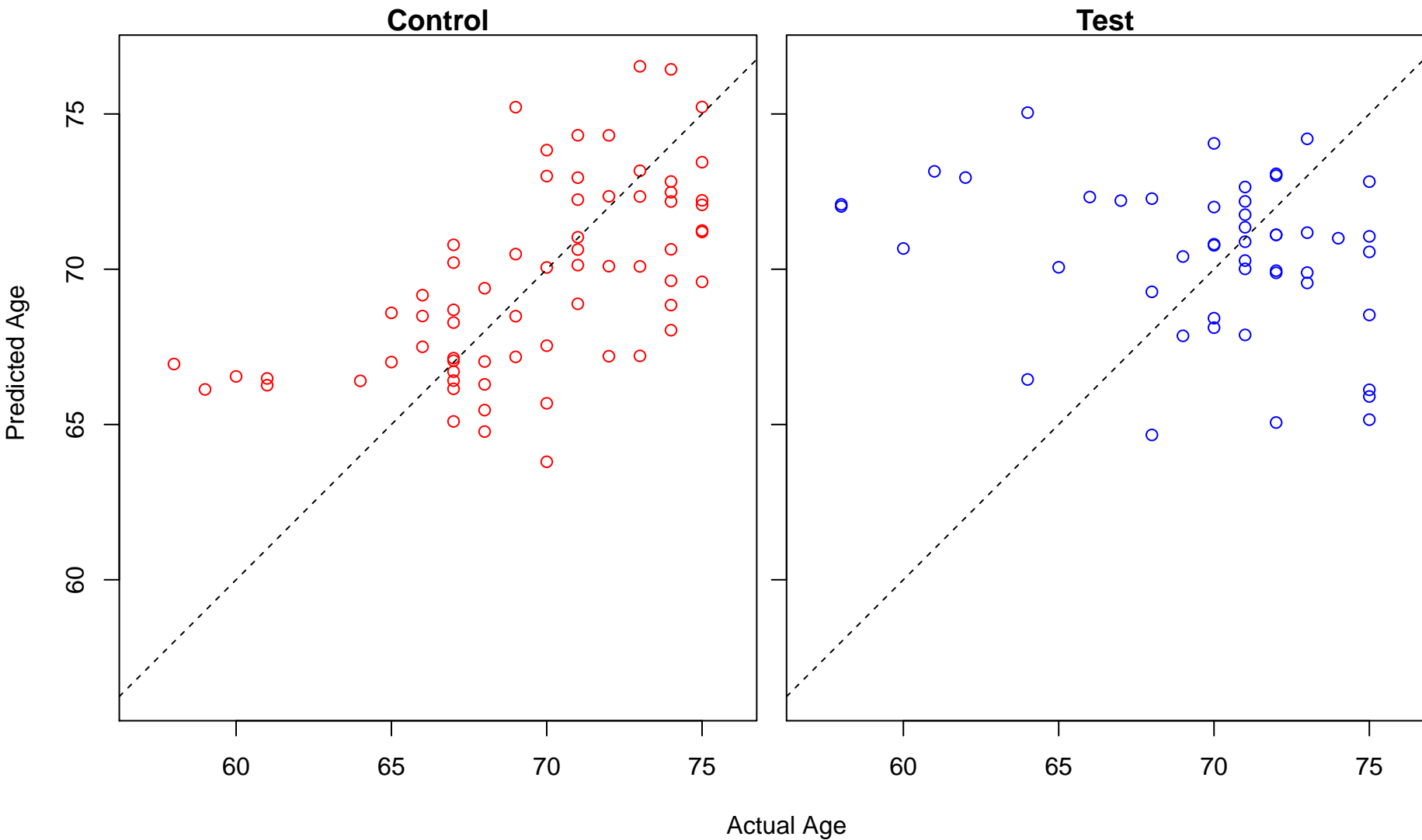
response to hydrogen peroxide (Score: 1.200422)



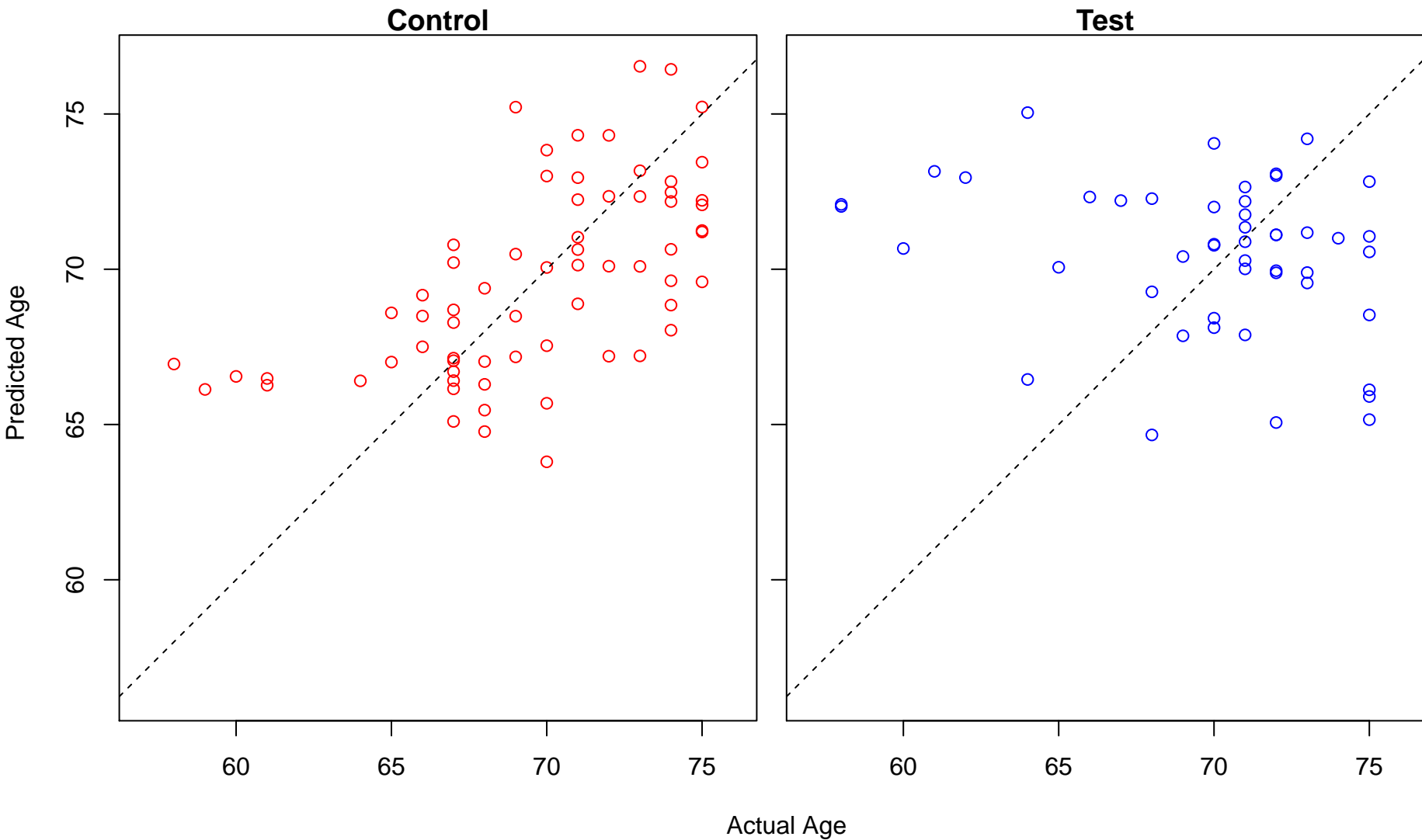
acetyl-CoA biosynthetic process (Score: 1.200330)



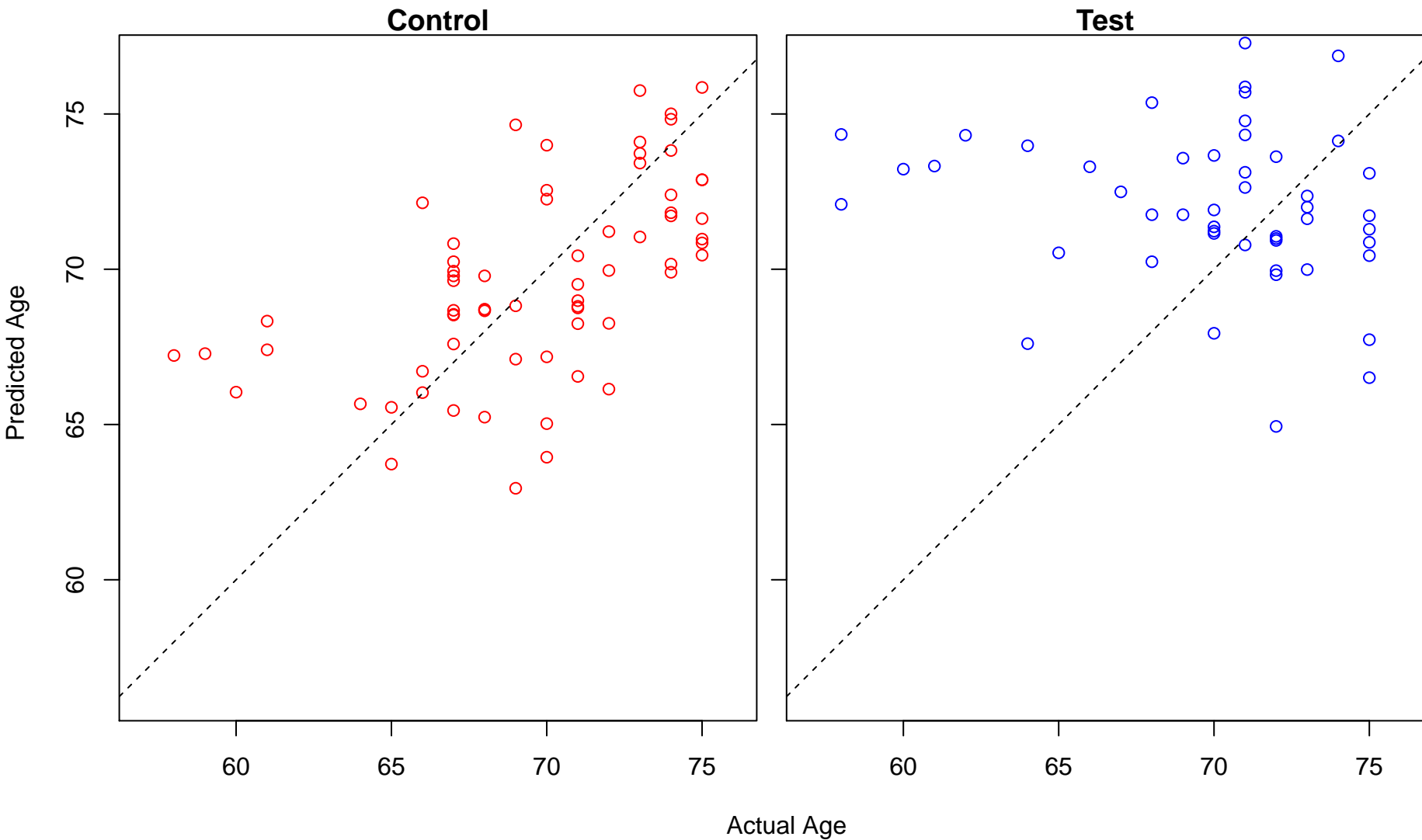
regulation of telomerase RNA localization to Cajal body (Score: 1.200160)



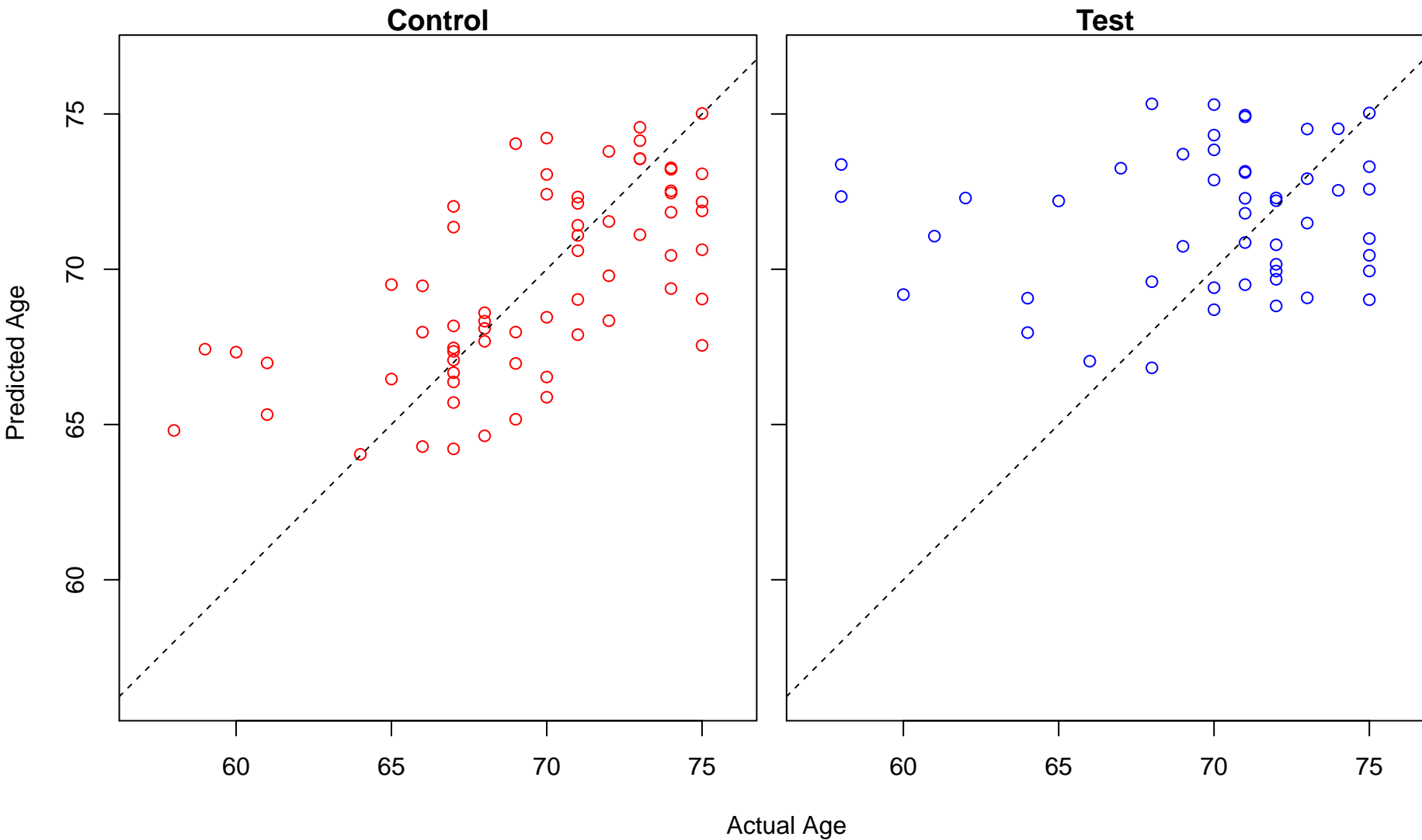
positive regulation of telomerase RNA localization to Cajal body (Score: 1.200160)



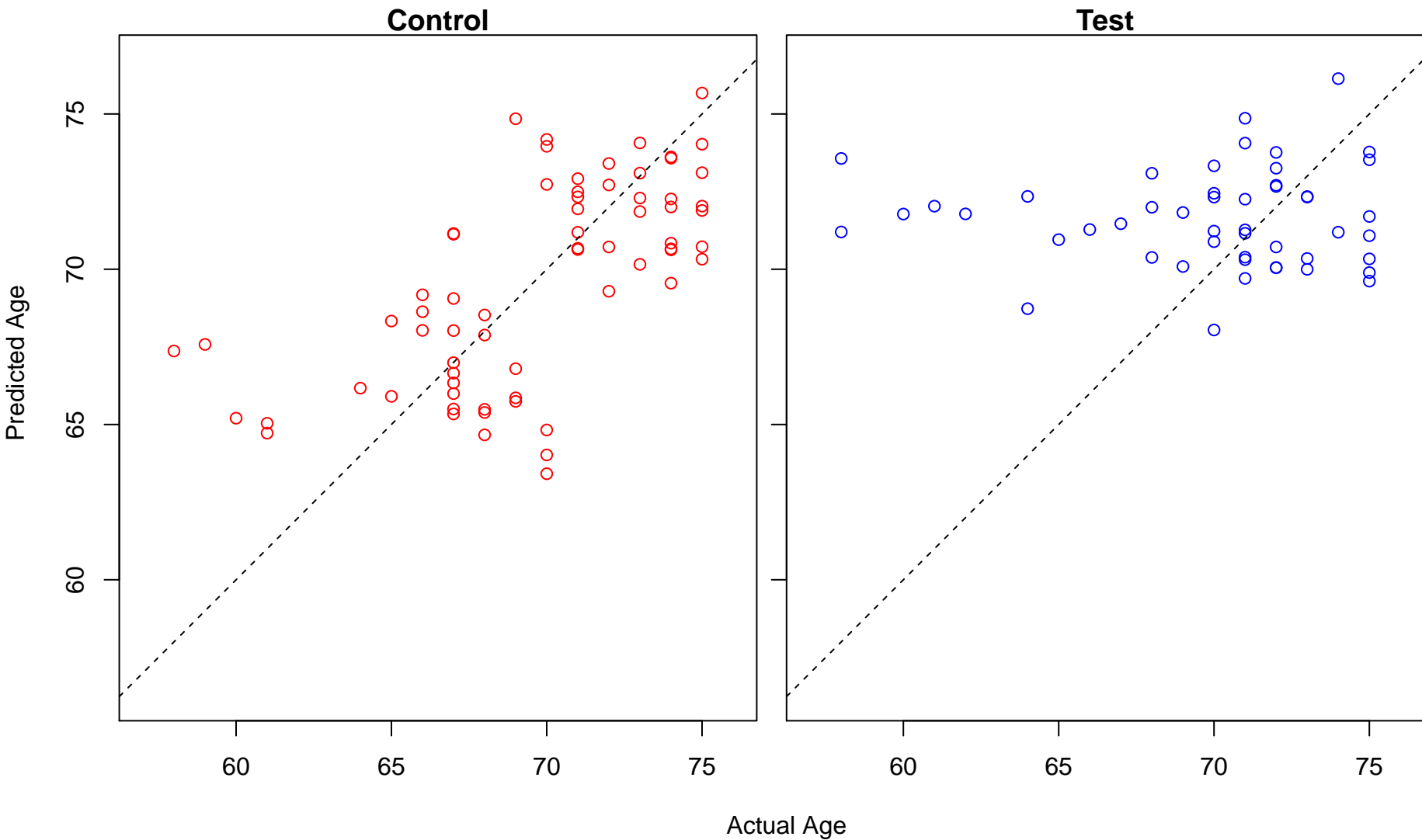
regulation of lipid catabolic process (Score: 1.200146)



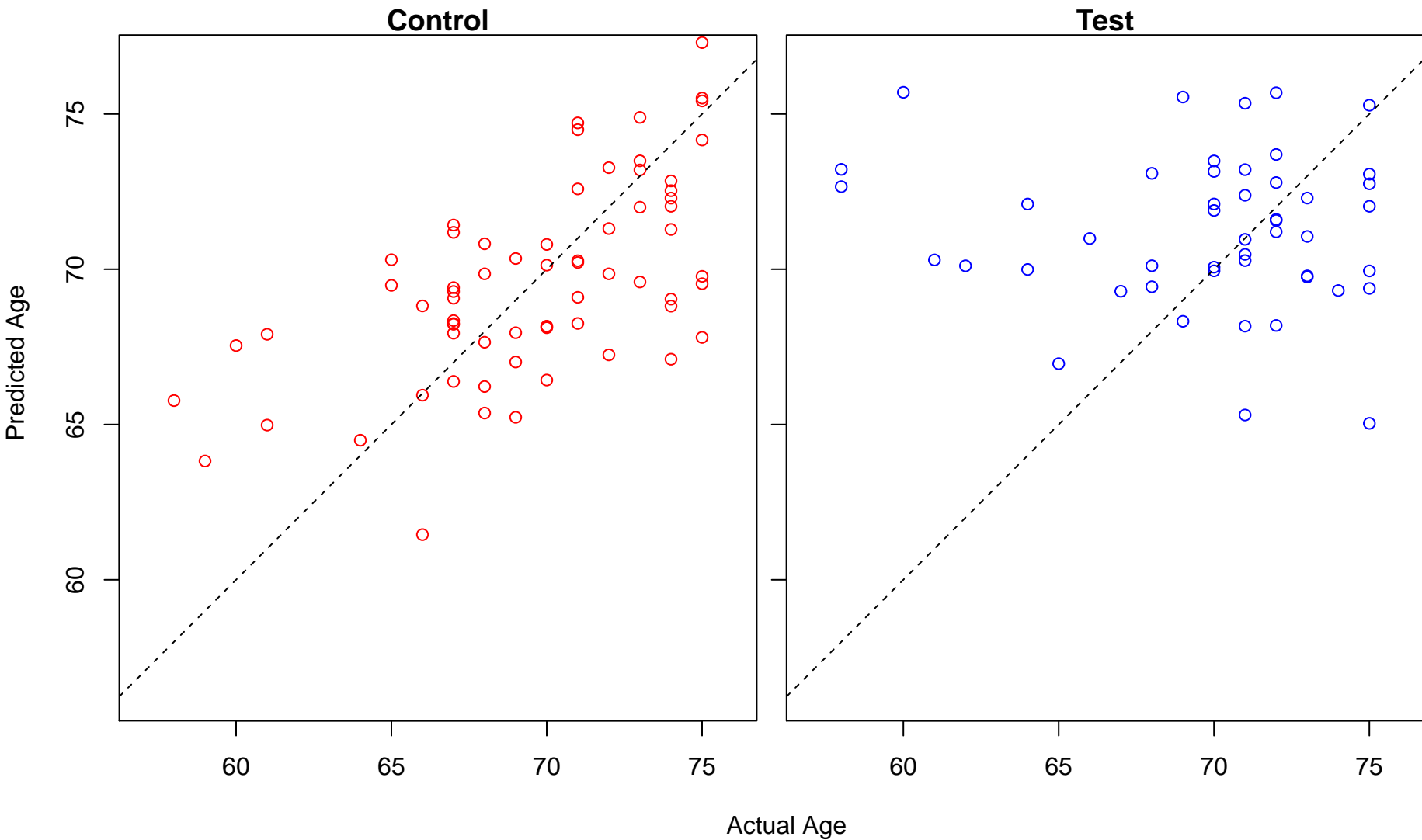
detection of abiotic stimulus (Score: 1.199601)



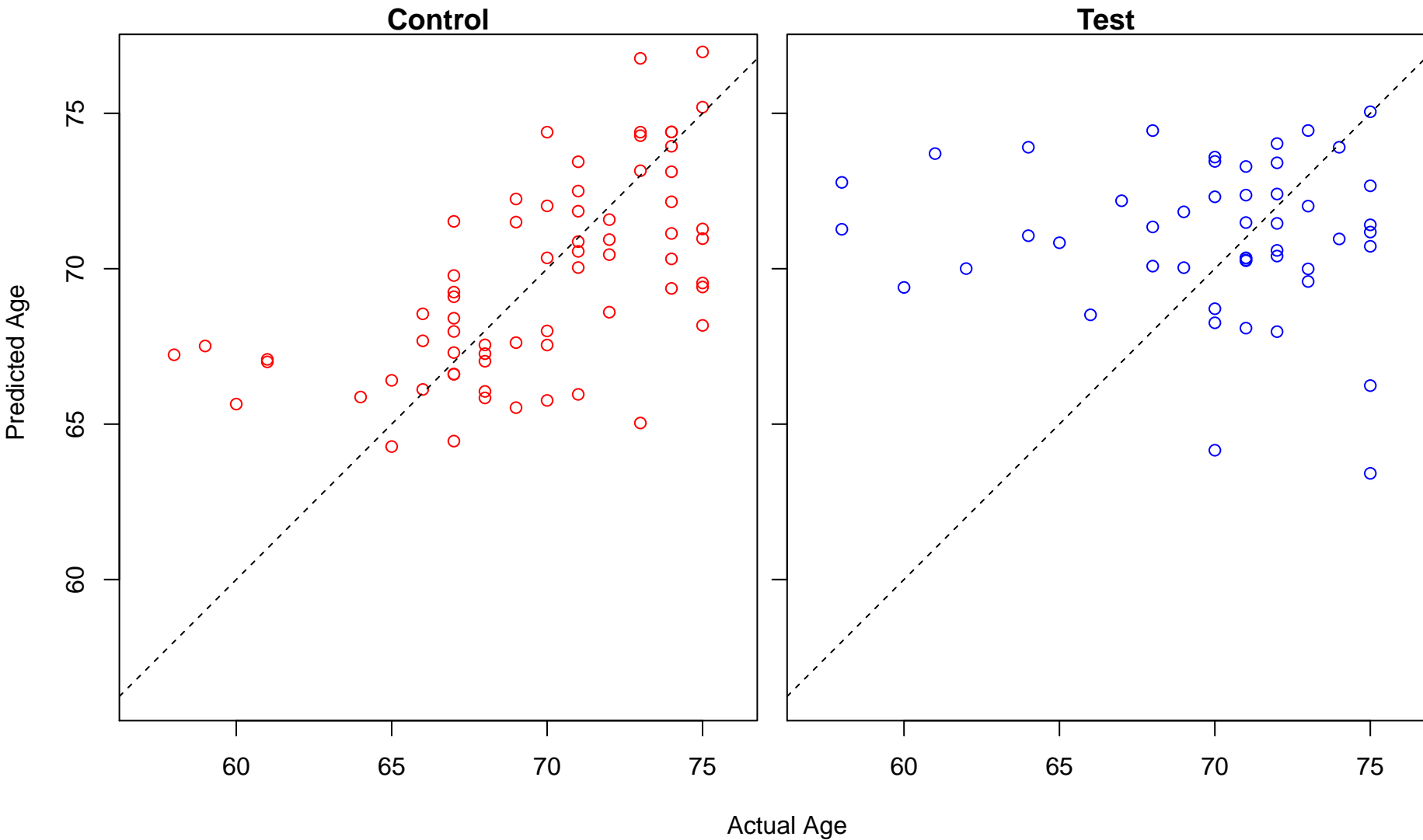
vesicle localization (Score: 1.199570)



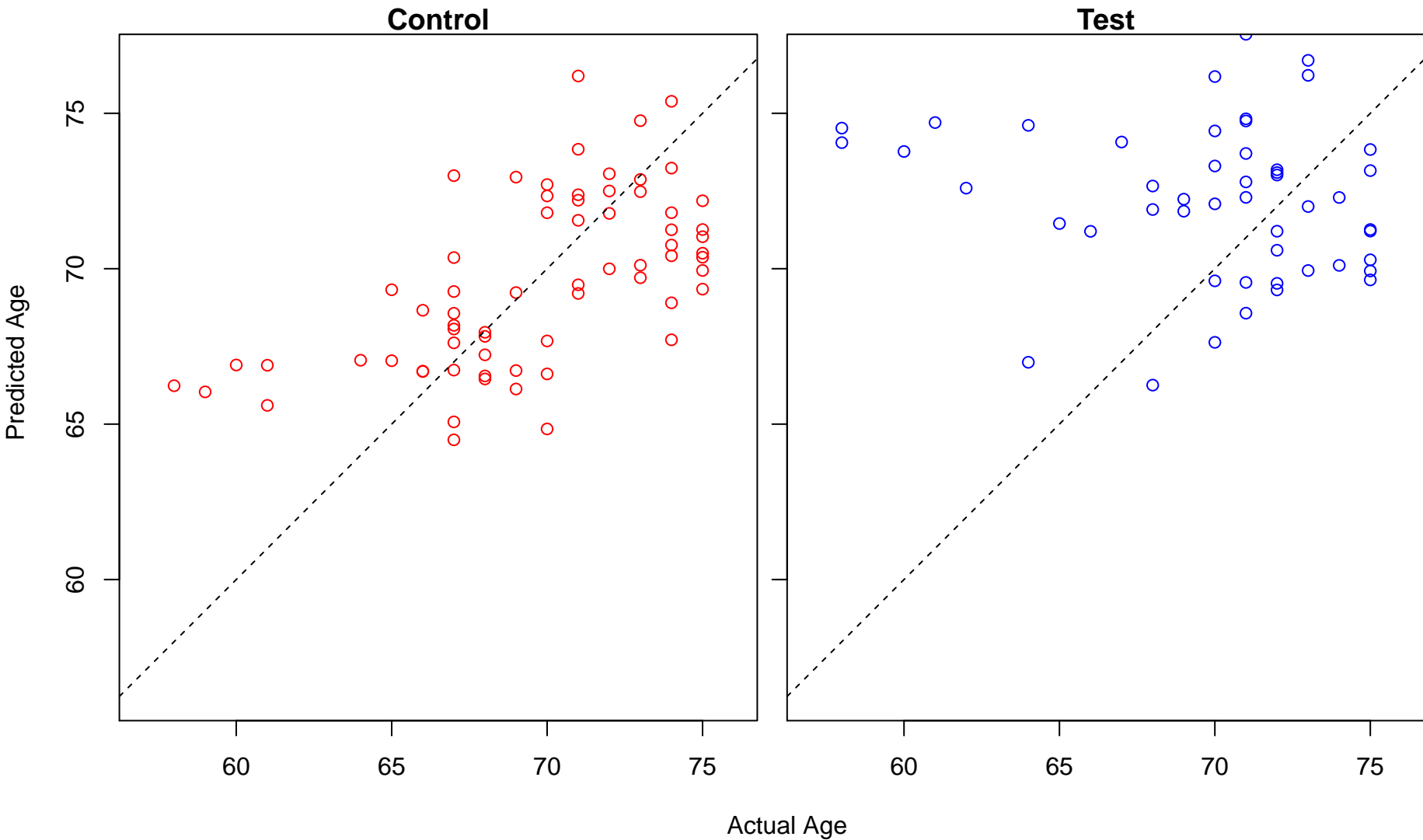
positive regulation of adenylate cyclase activity (Score: 1.199569)



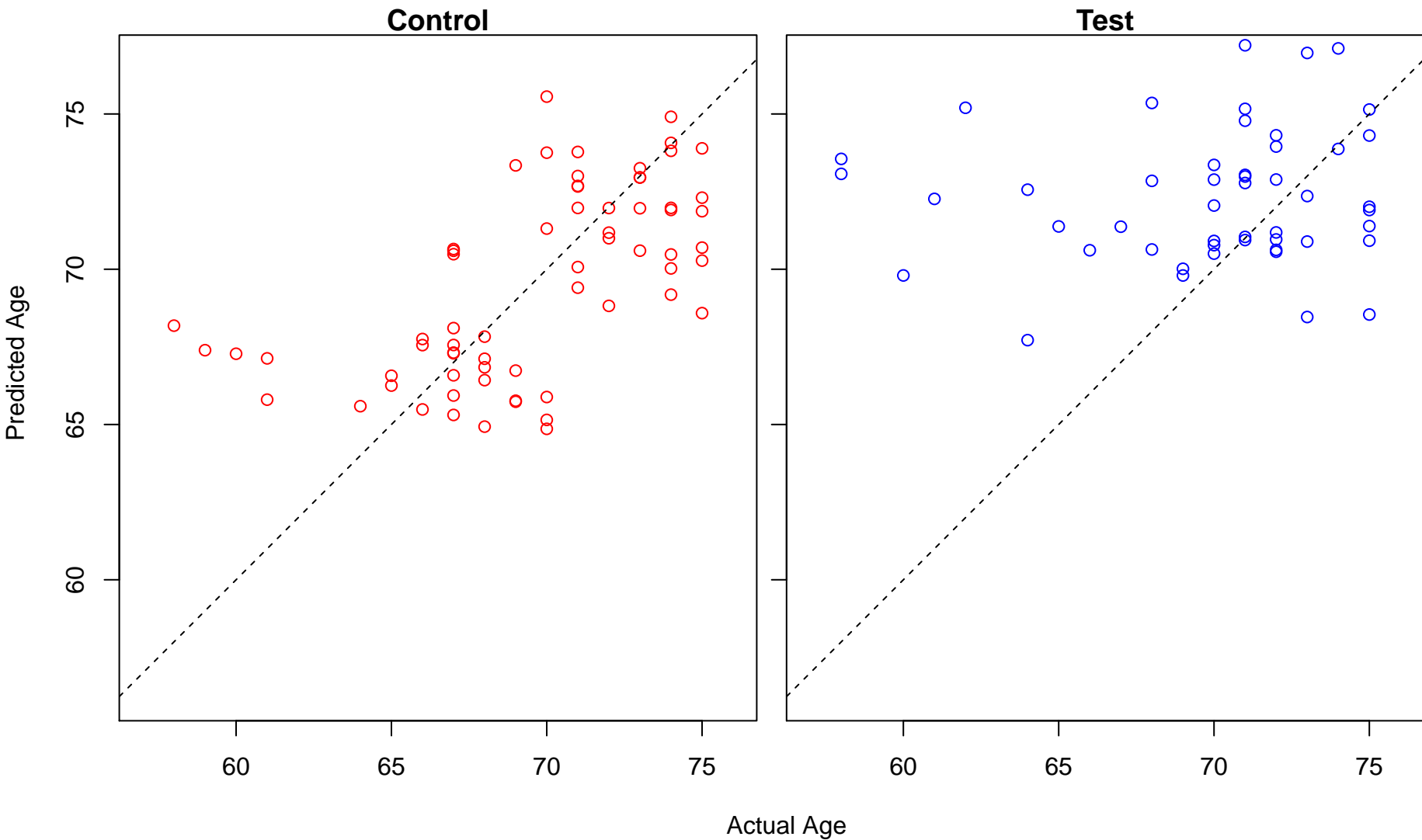
positive regulation of sodium ion transport (Score: 1.199448)



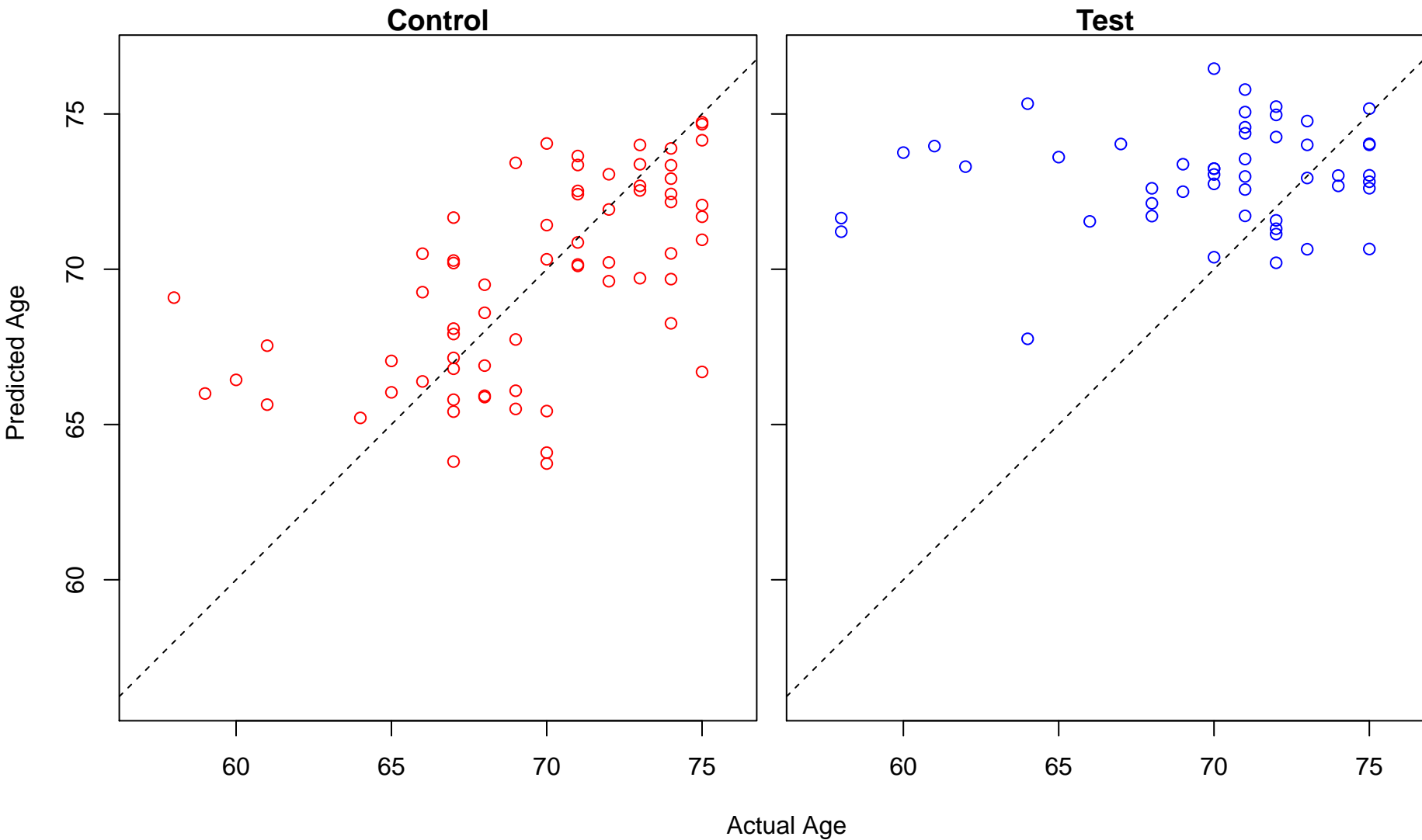
adenylate cyclase-activating G-protein coupled receptor signaling pathway (Score: 1.199243)



positive regulation of cell projection organization (Score: 1.198711)

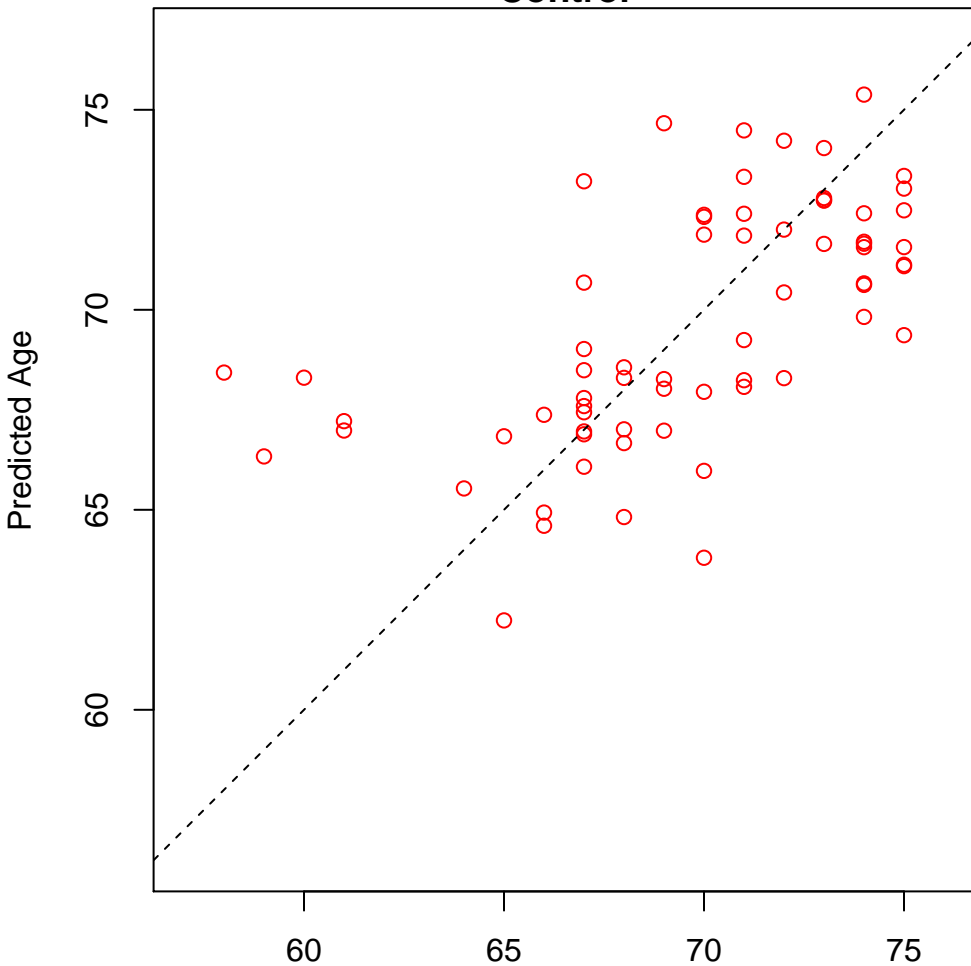


glycogen metabolic process (Score: 1.198049)

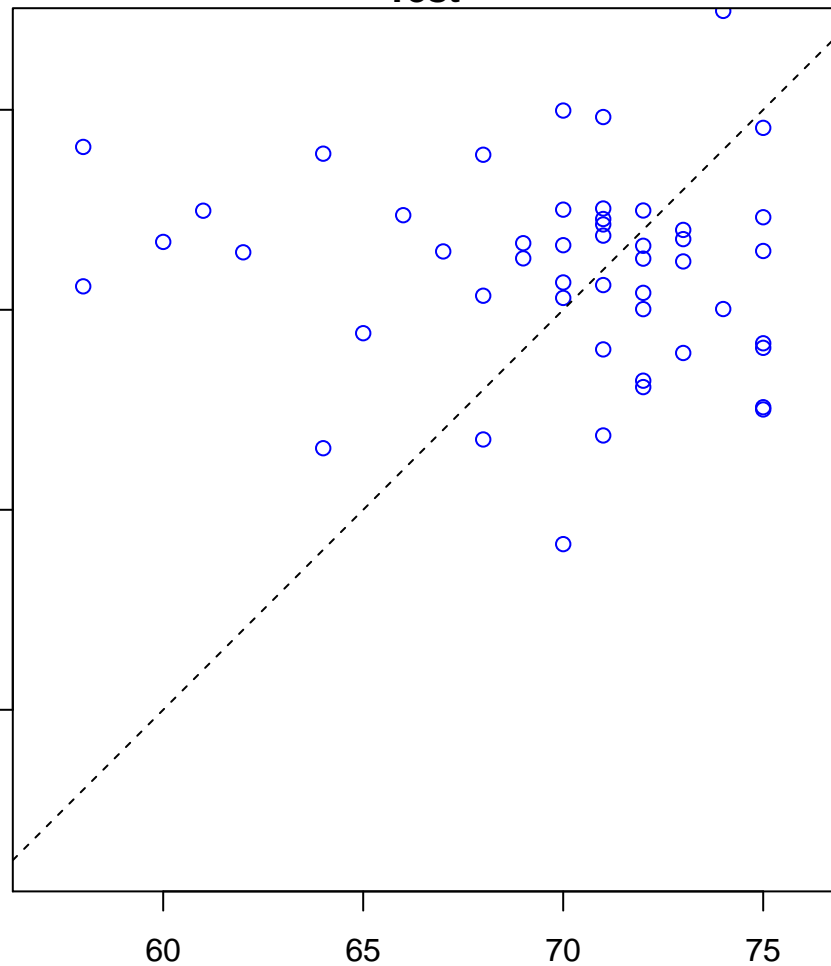


positive regulation of cytokine secretion (Score: 1.197789)

Control

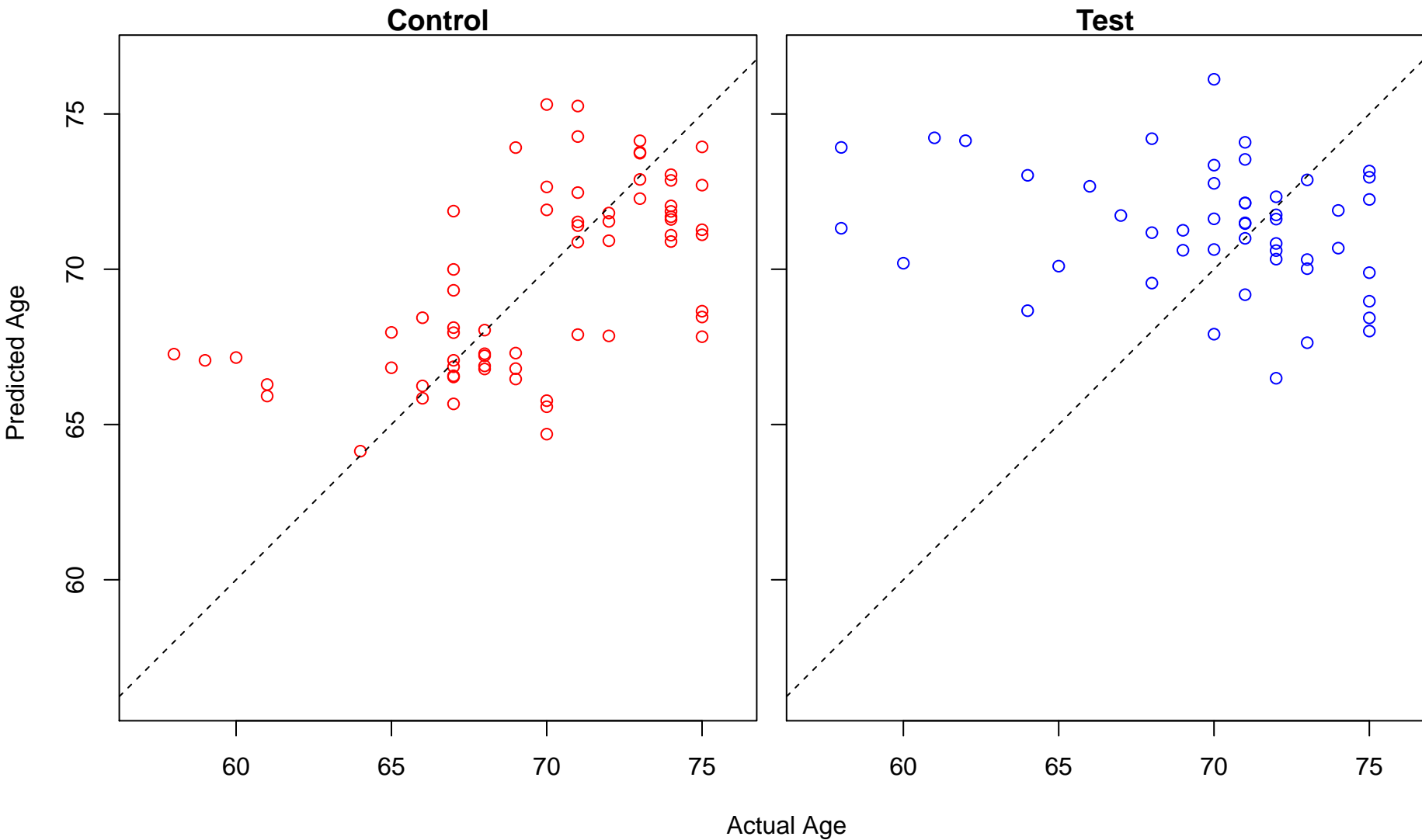


Test

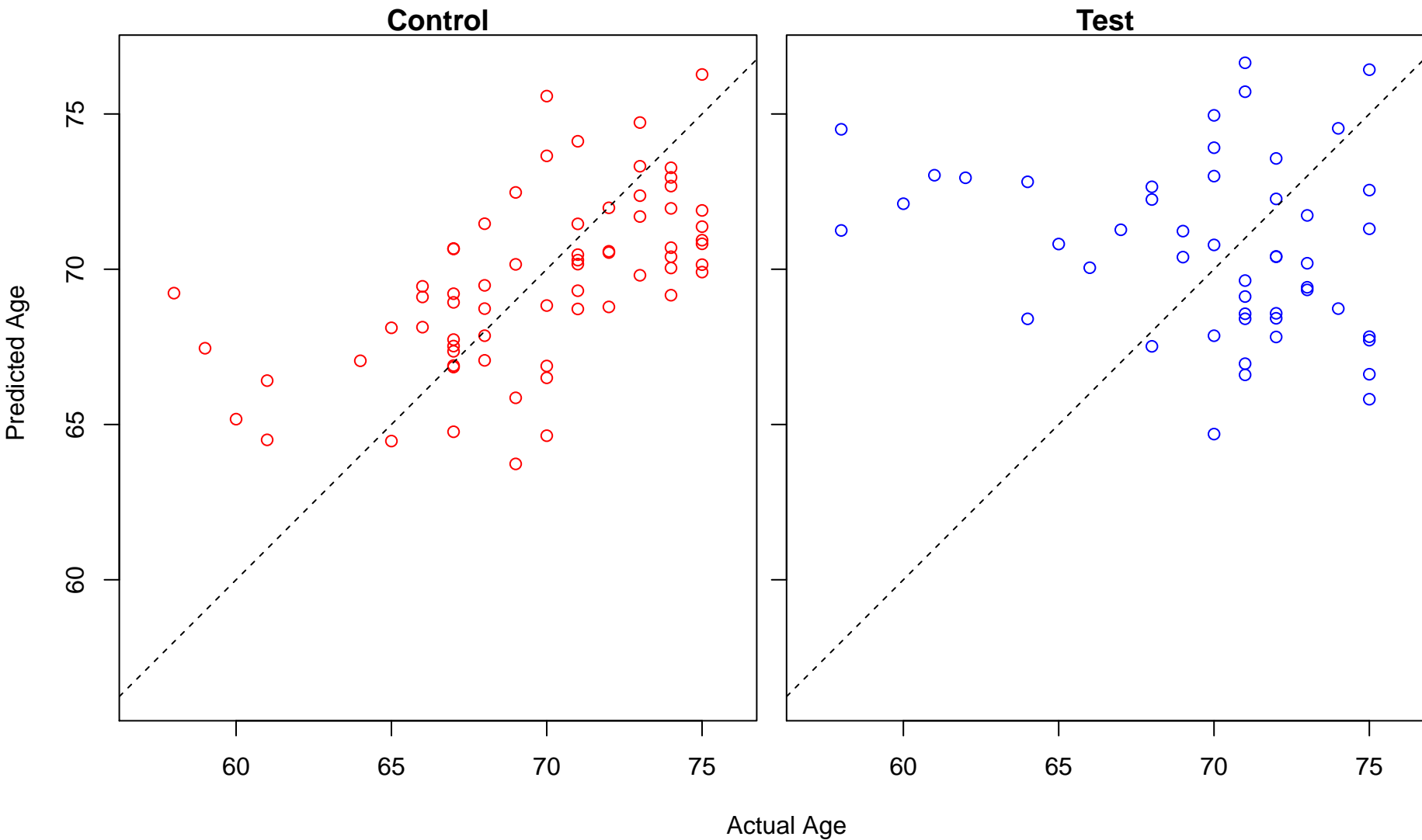


Actual Age

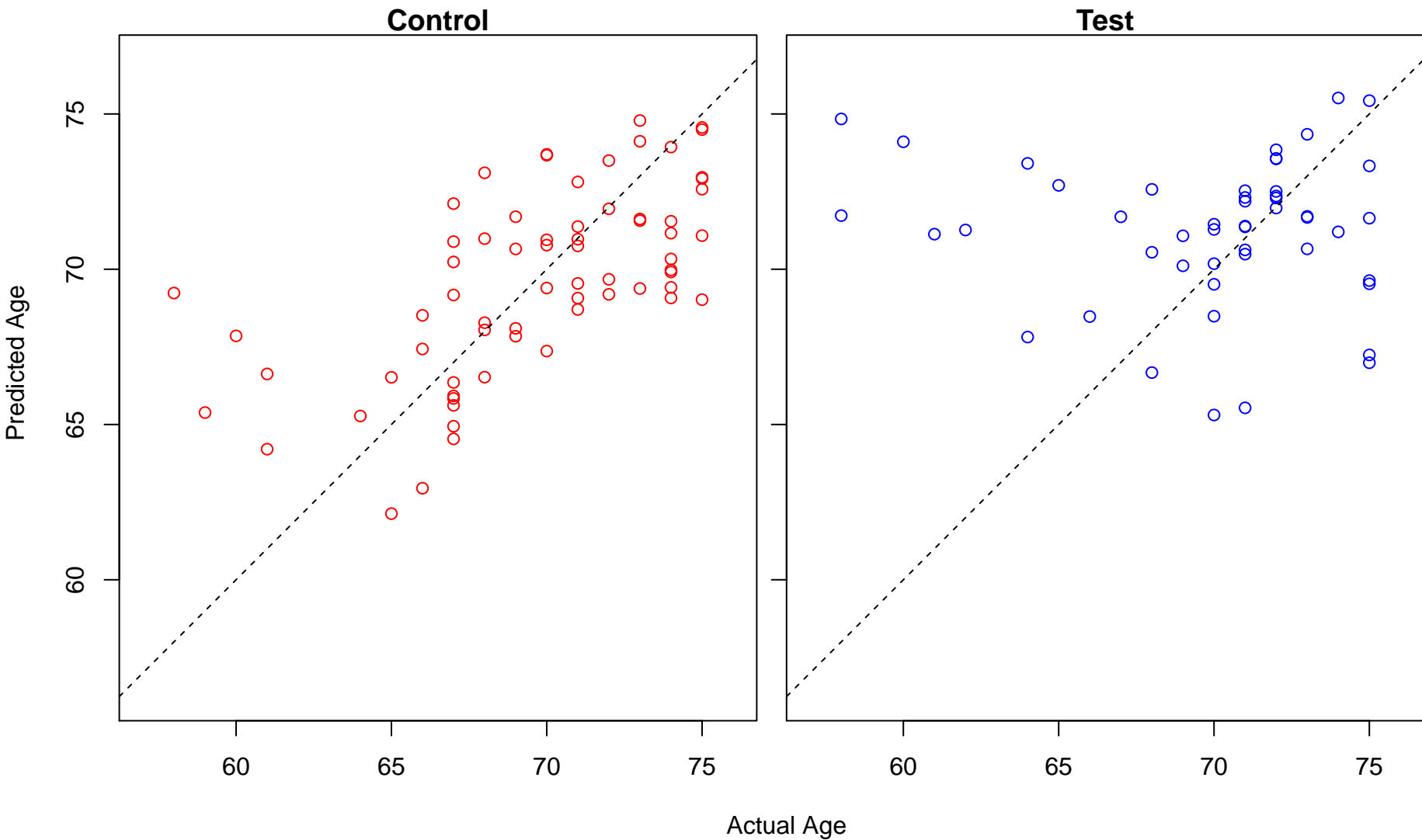
Notch signaling pathway (Score: 1.197659)



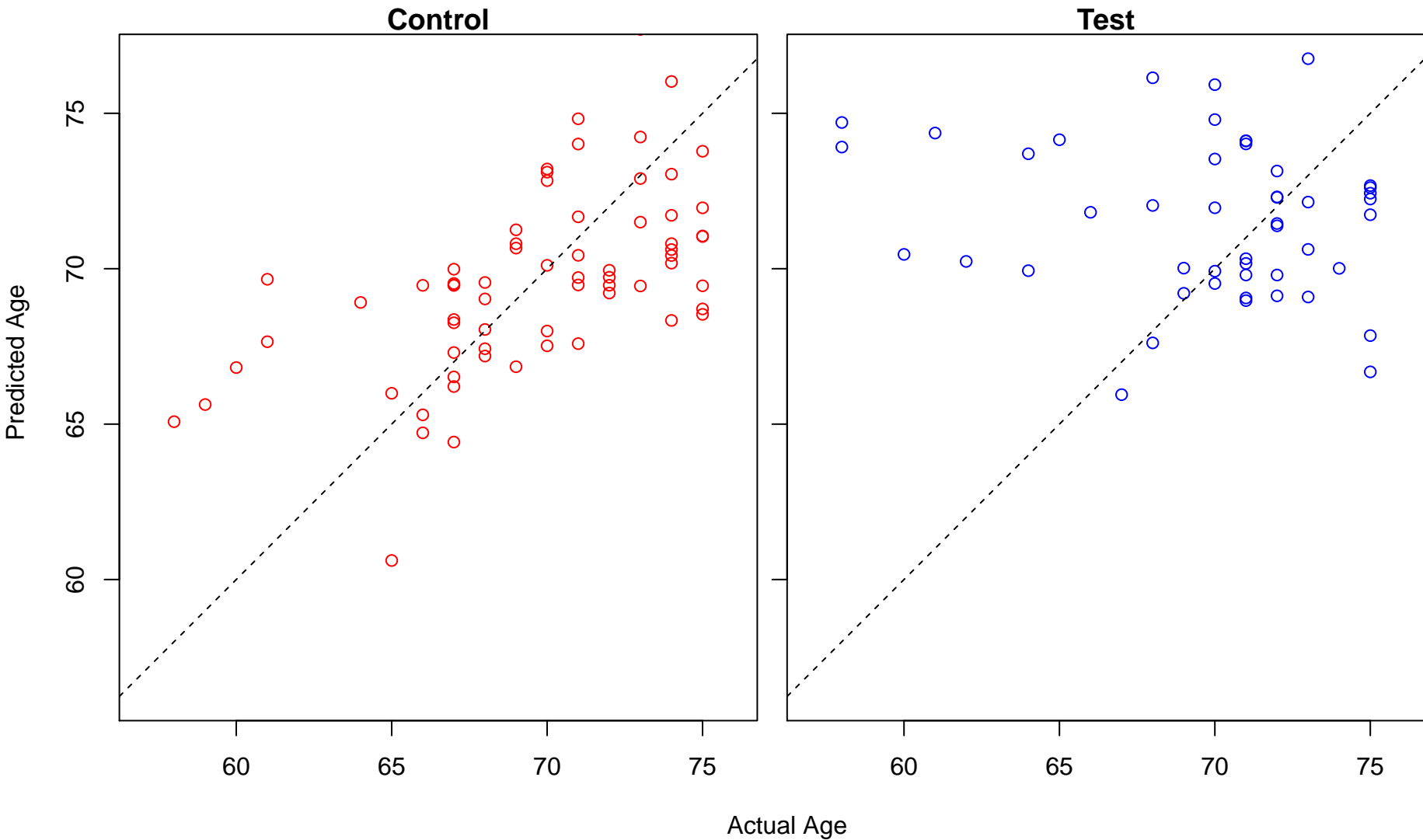
activation of GTPase activity (Score: 1.196202)



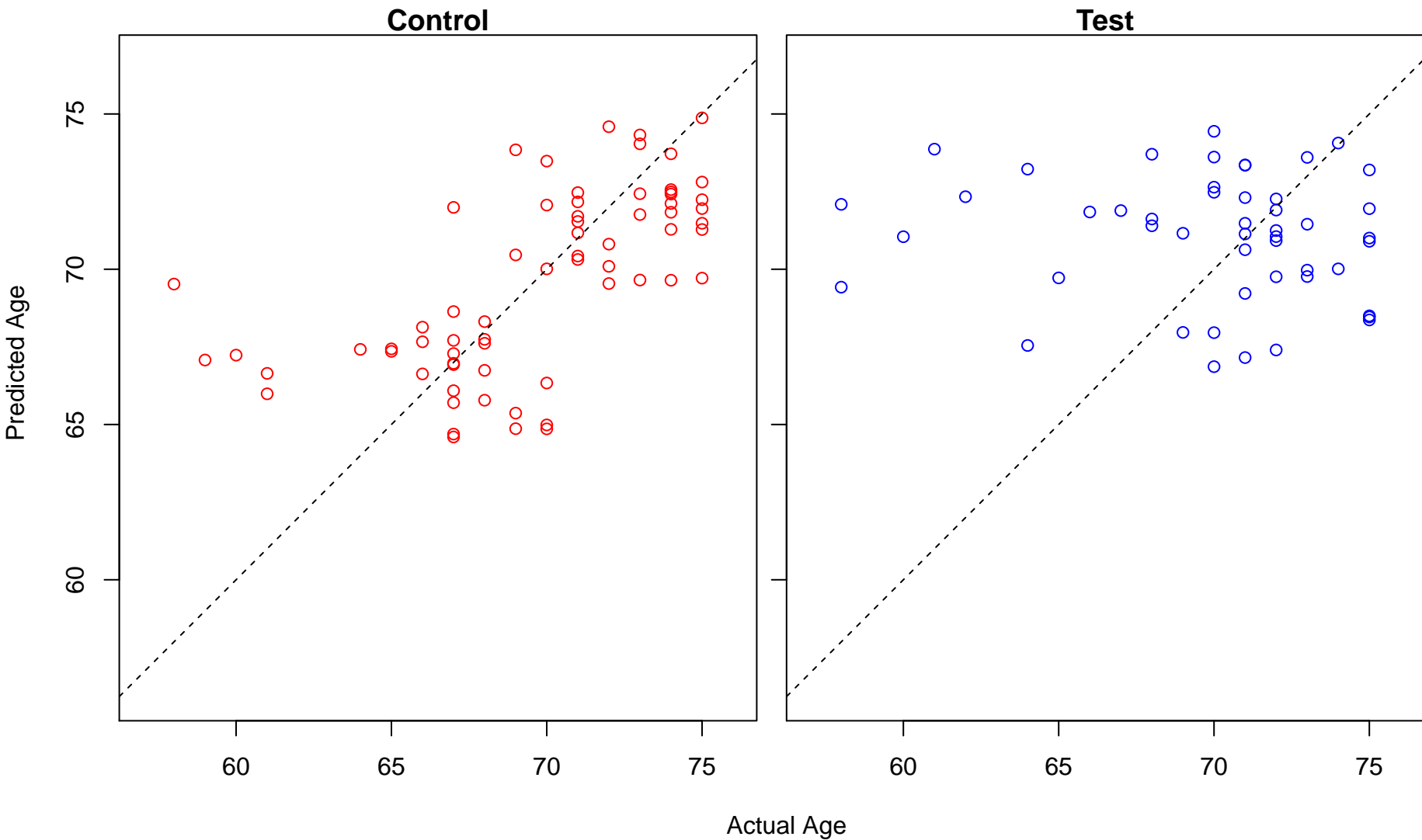
regulation of bicellular tight junction assembly (Score: 1.196108)



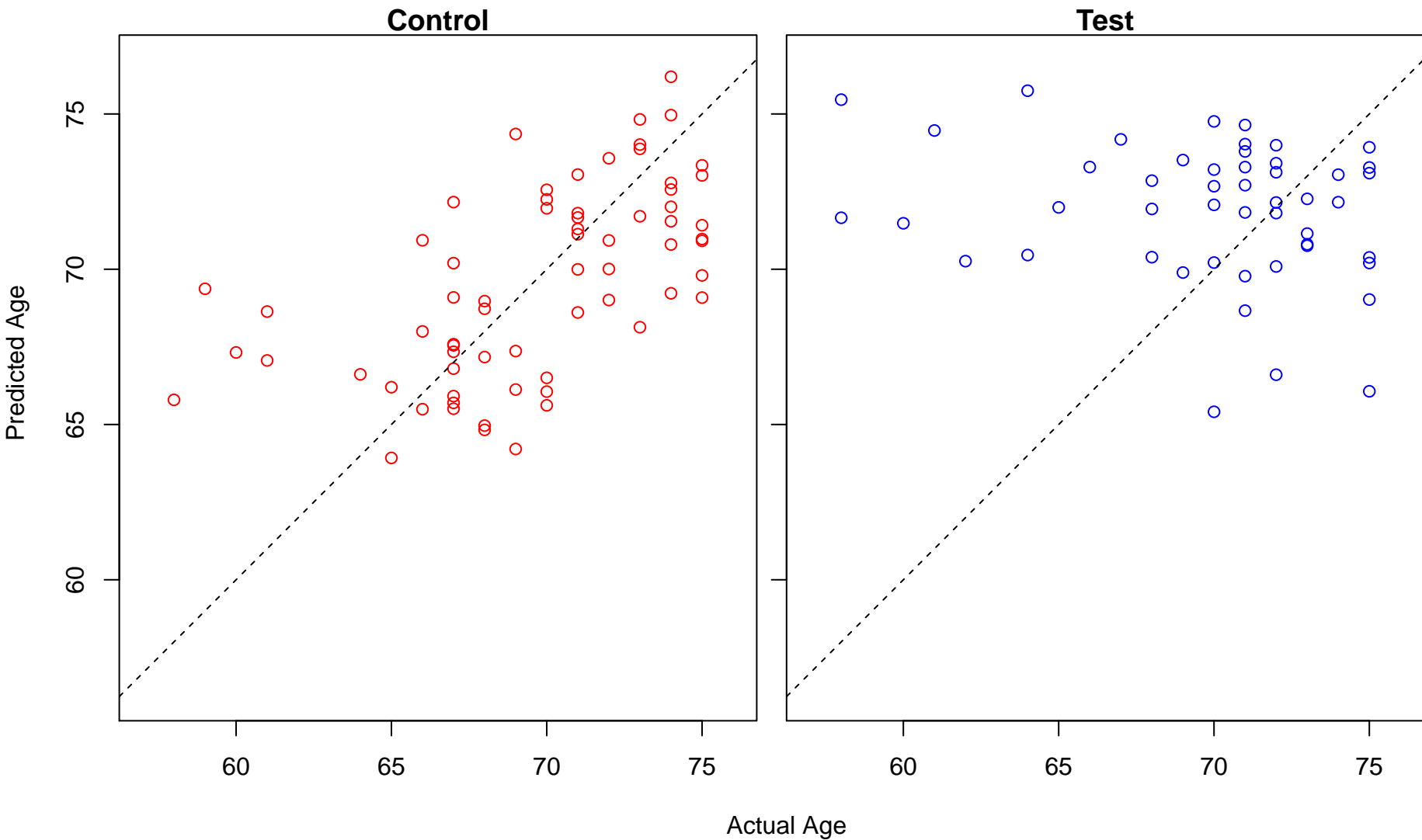
positive regulation of granulocyte chemotaxis (Score: 1.196092)



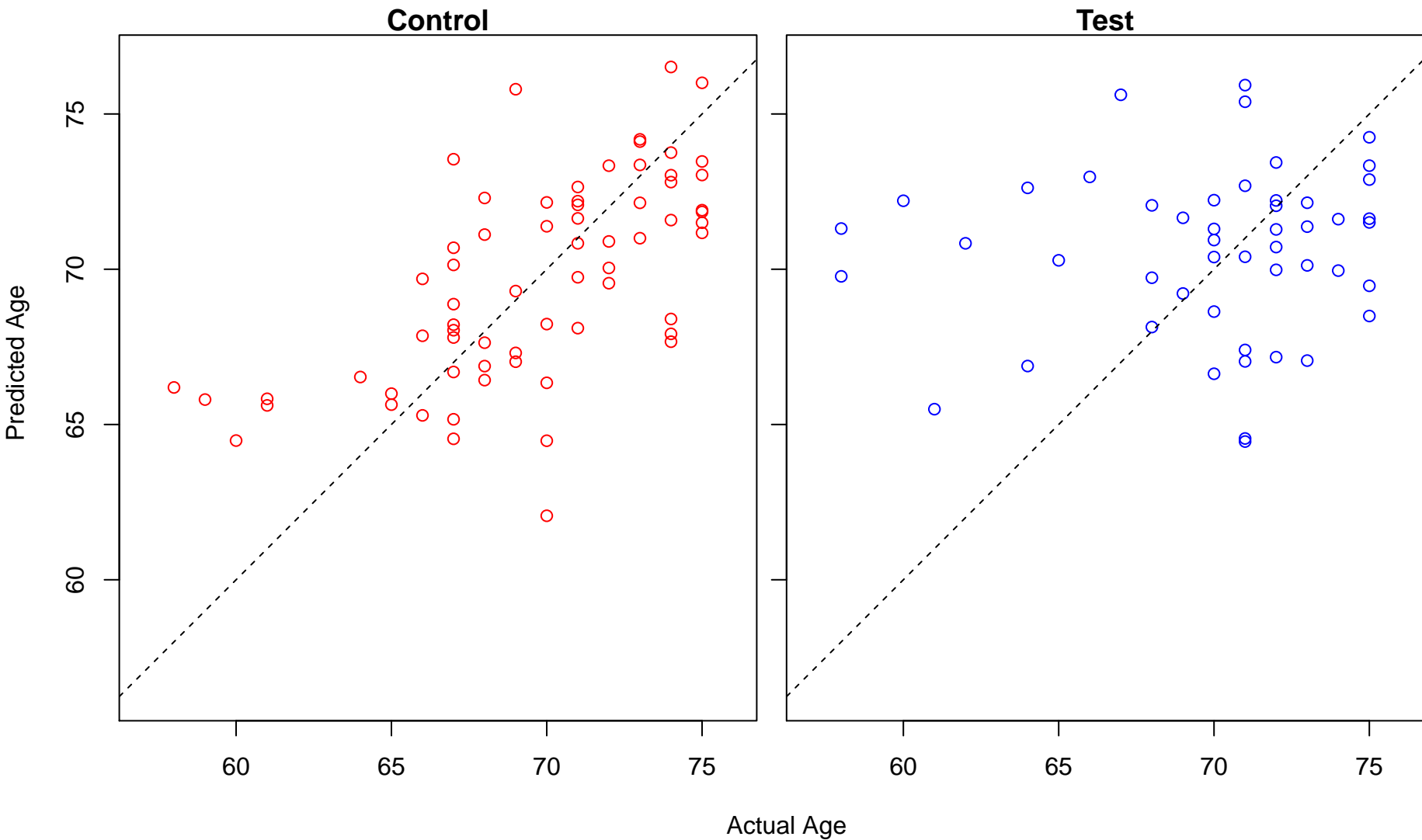
DNA catabolic process (Score: 1.196091)



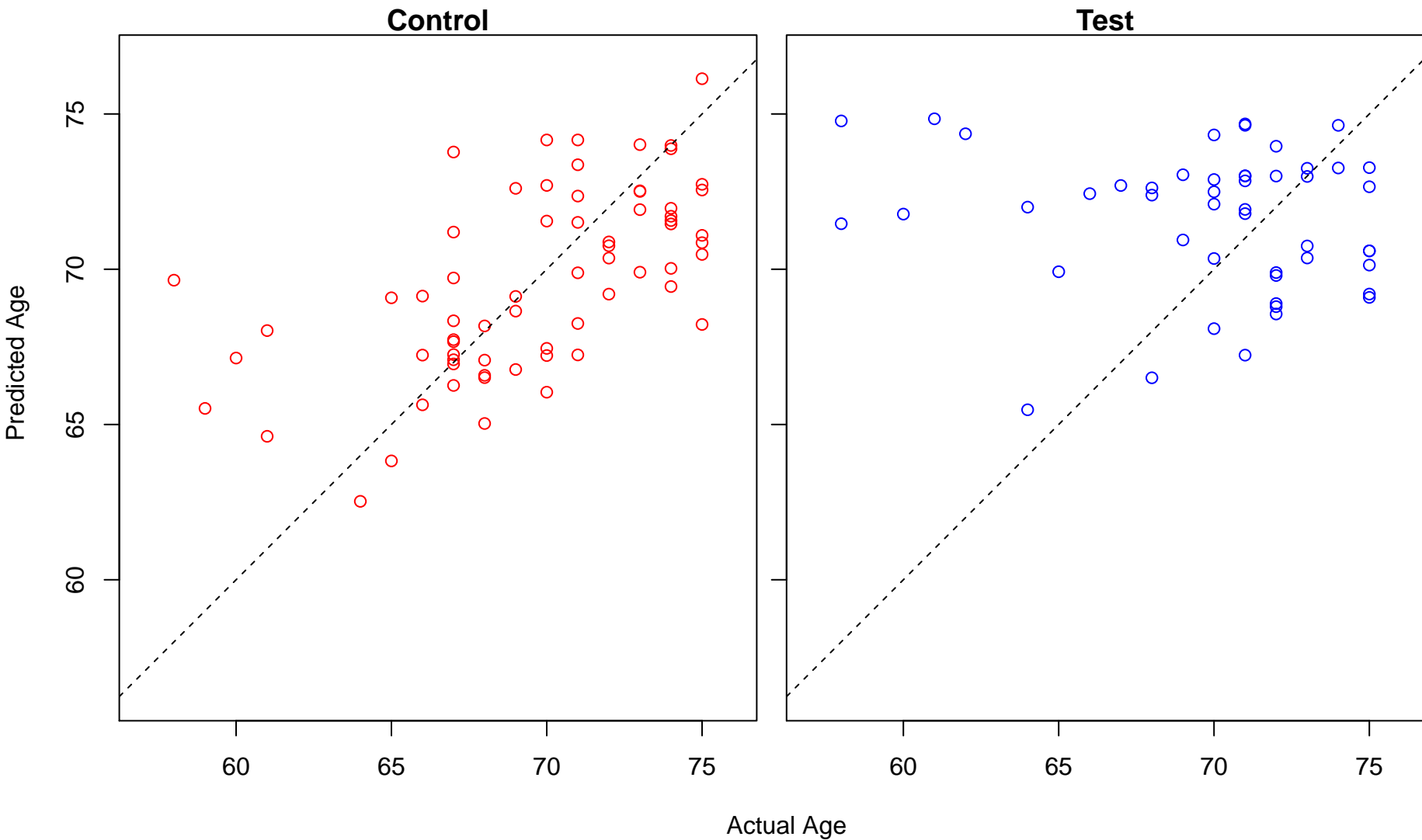
negative regulation of I-kappaB kinase/NF-kappaB signaling (Score: 1.196029)



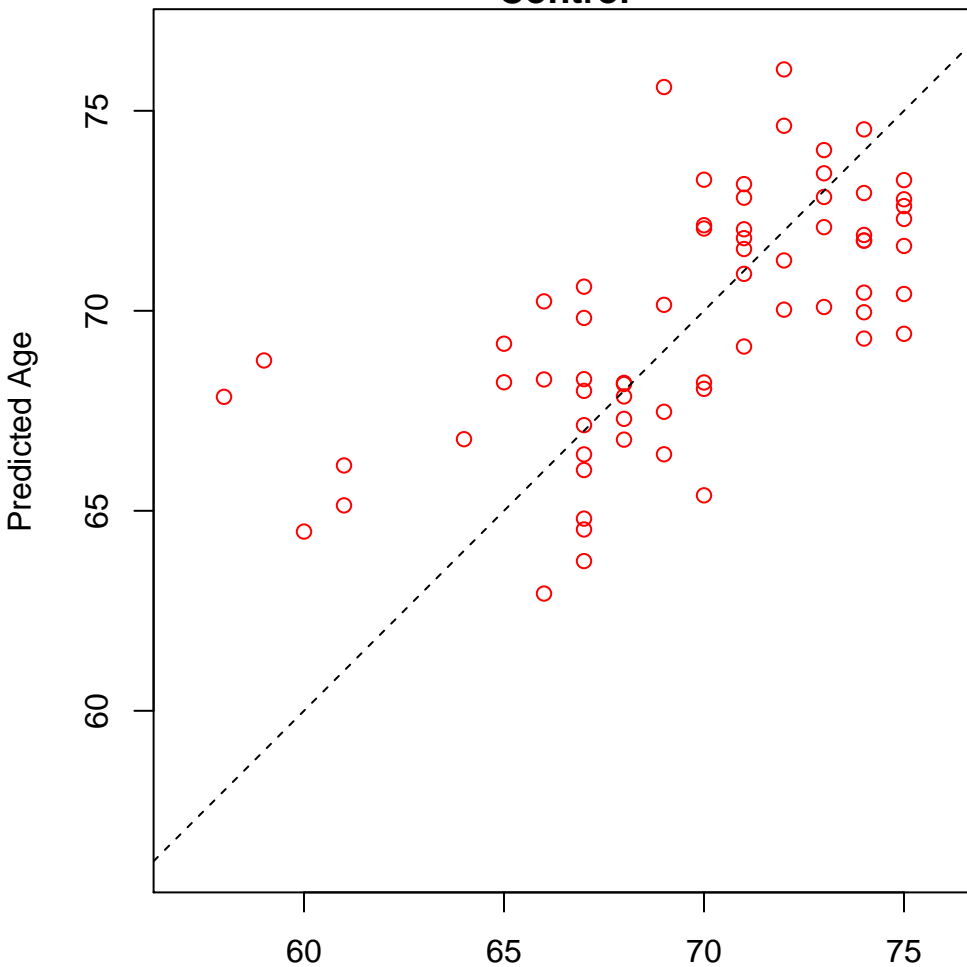
negative regulation of biomineral tissue development (Score: 1.196019)



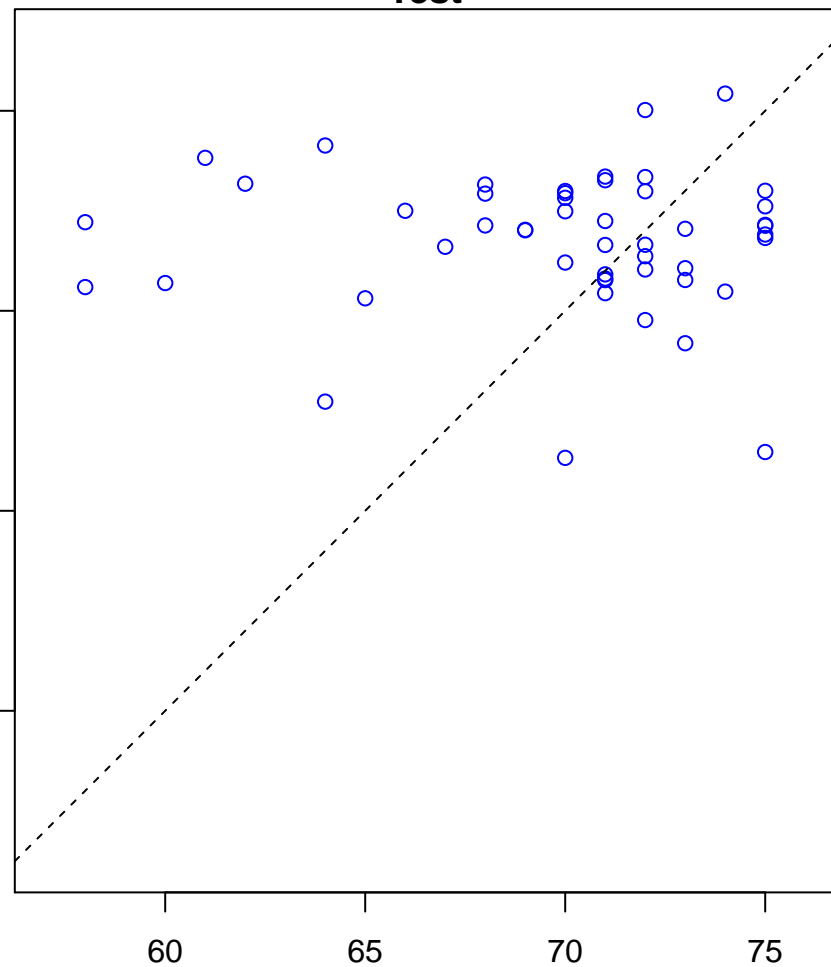
microtubule bundle formation (Score: 1.195286)



Control

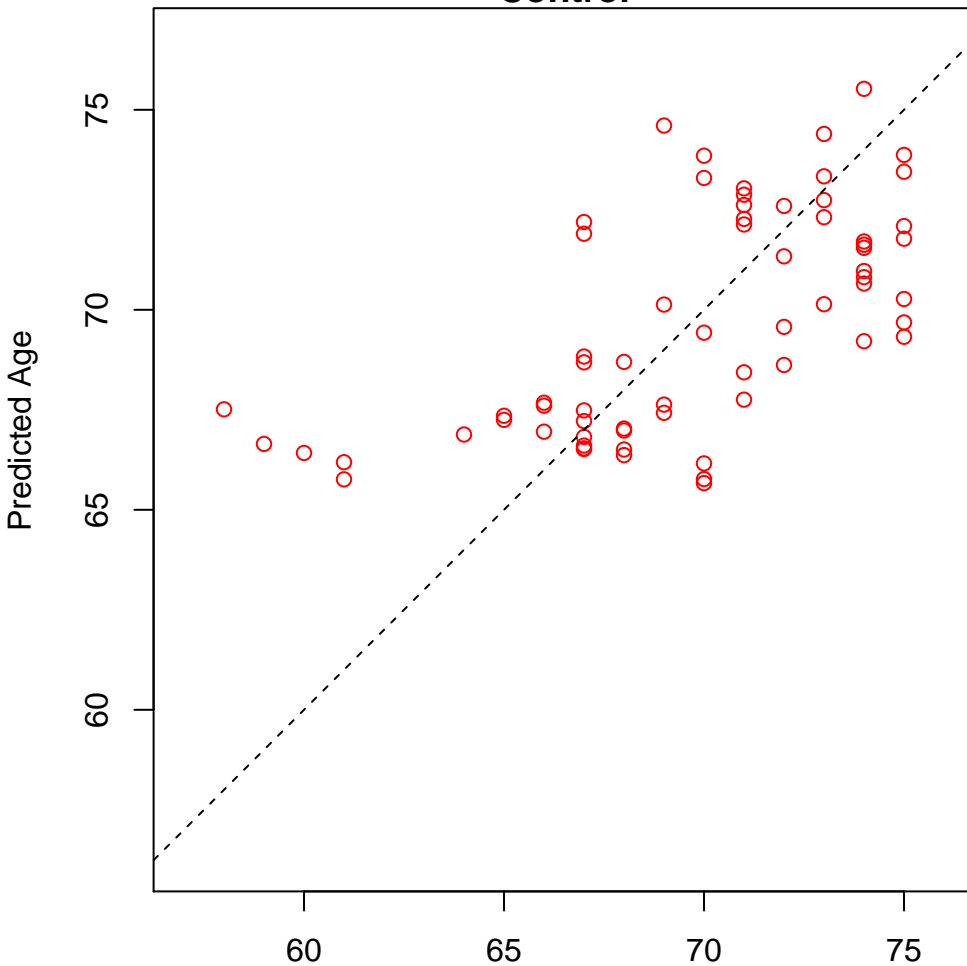


Test

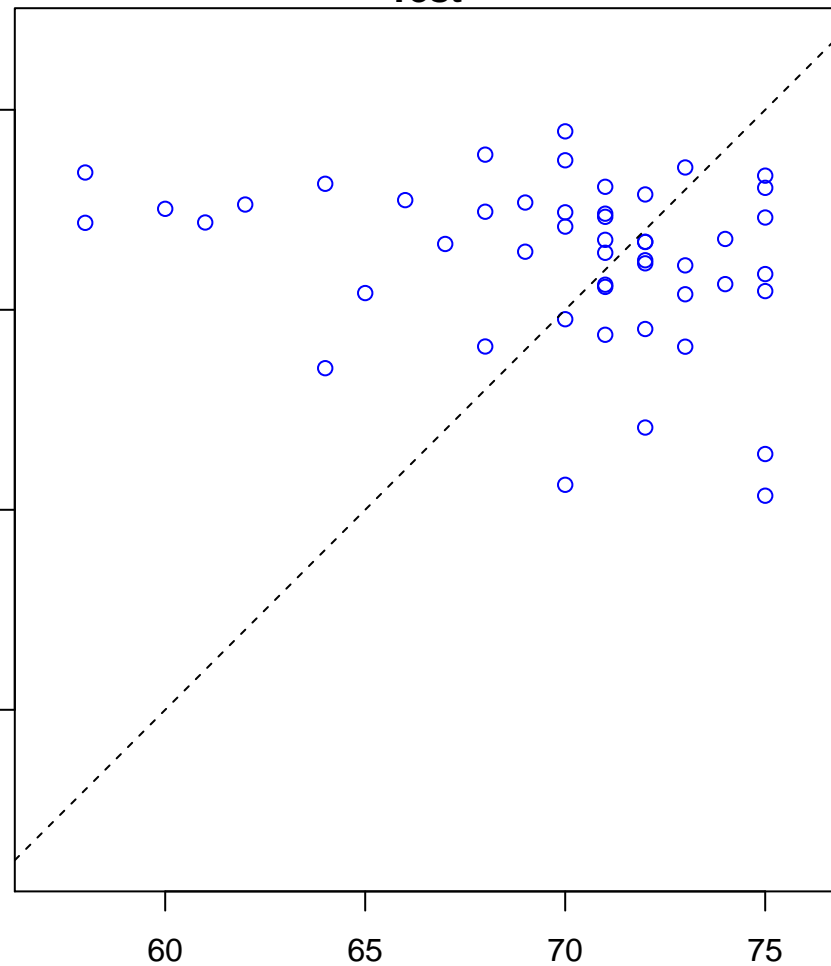


wound healing, spreading of cells (Score: 1.194919)

Control

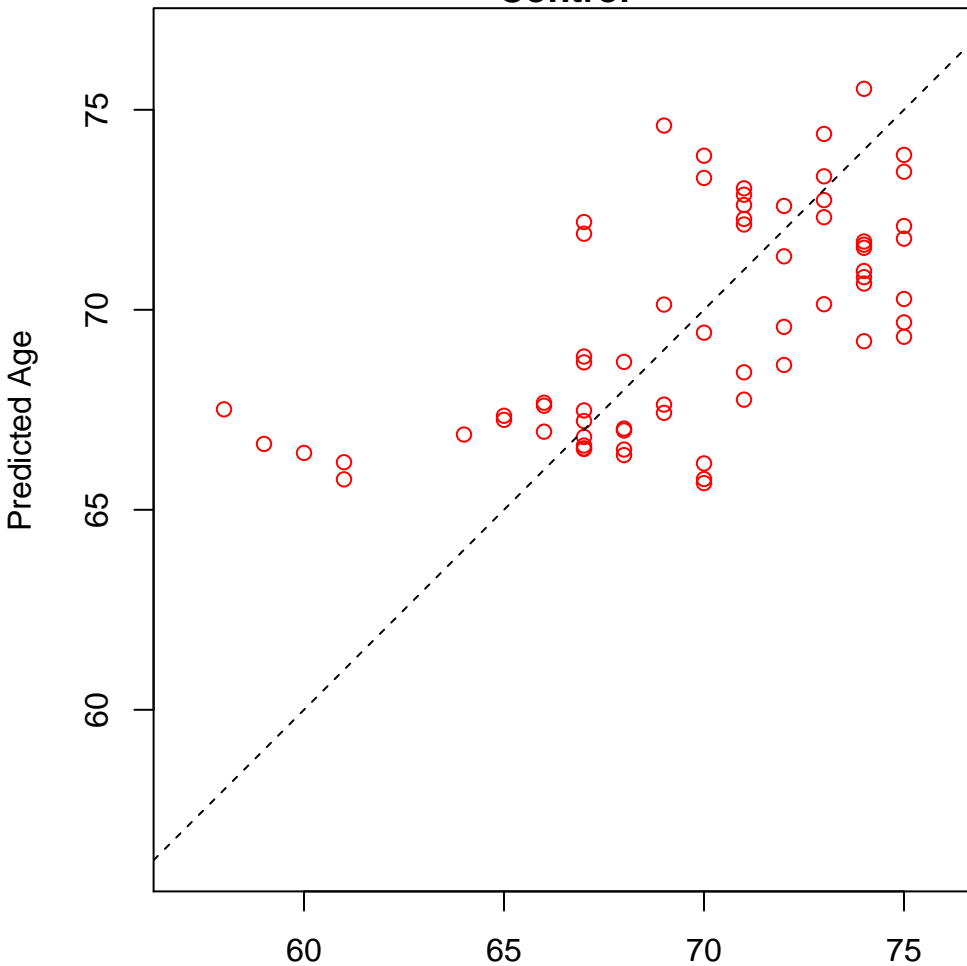


Test

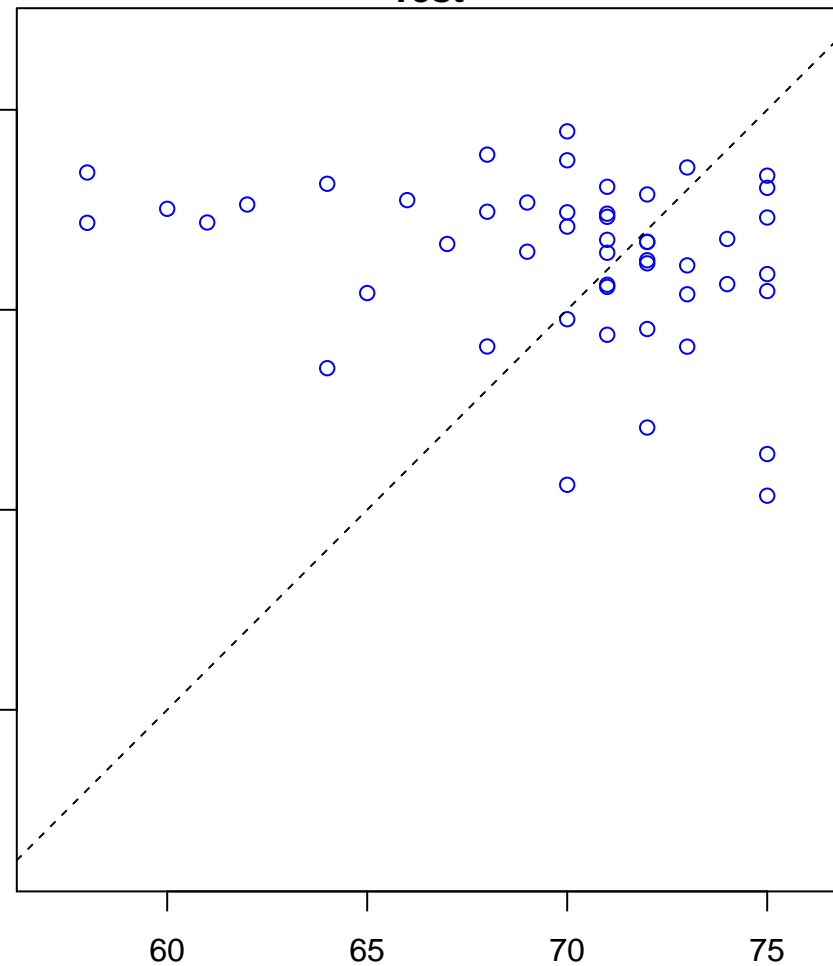


Actual Age

Control

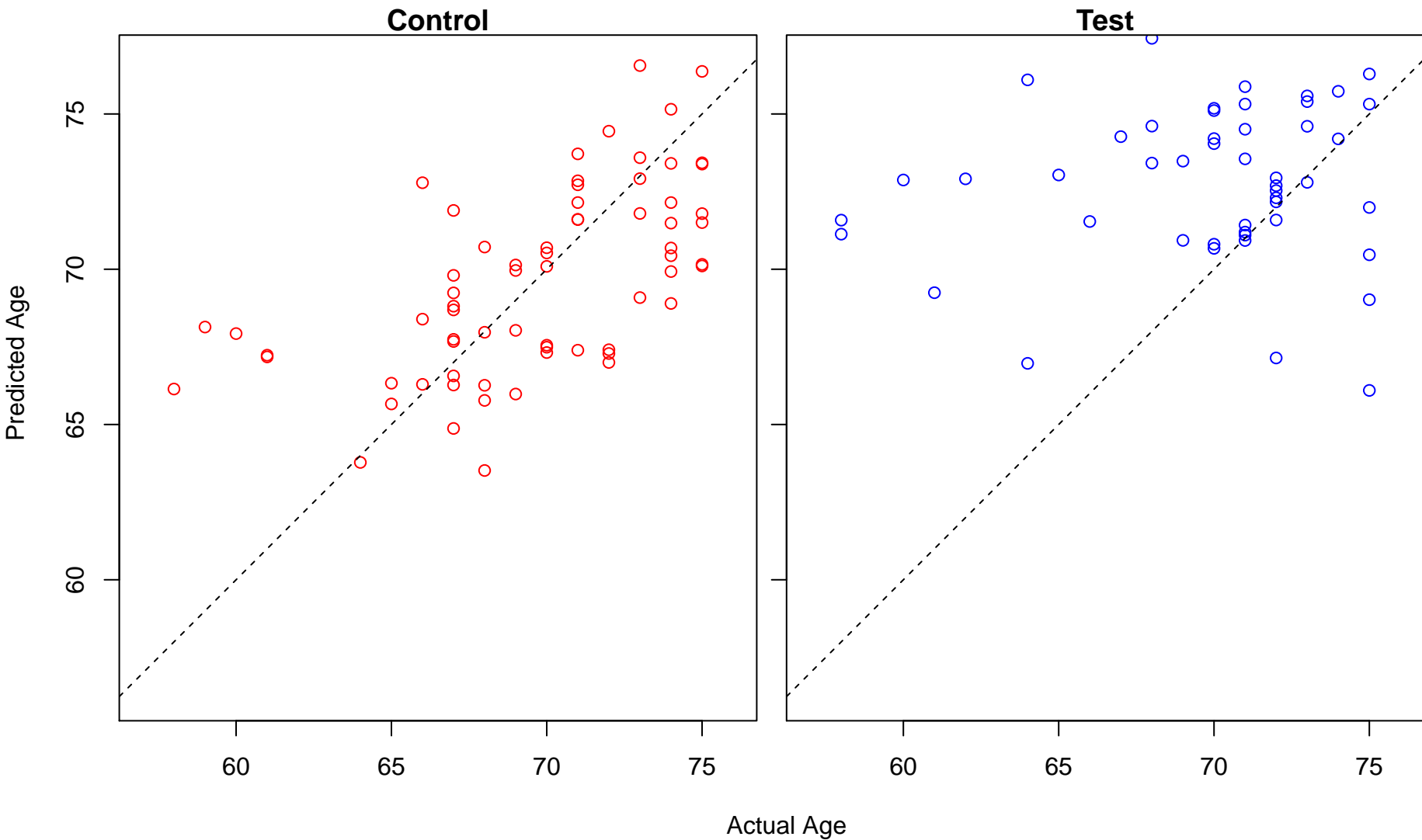


Test

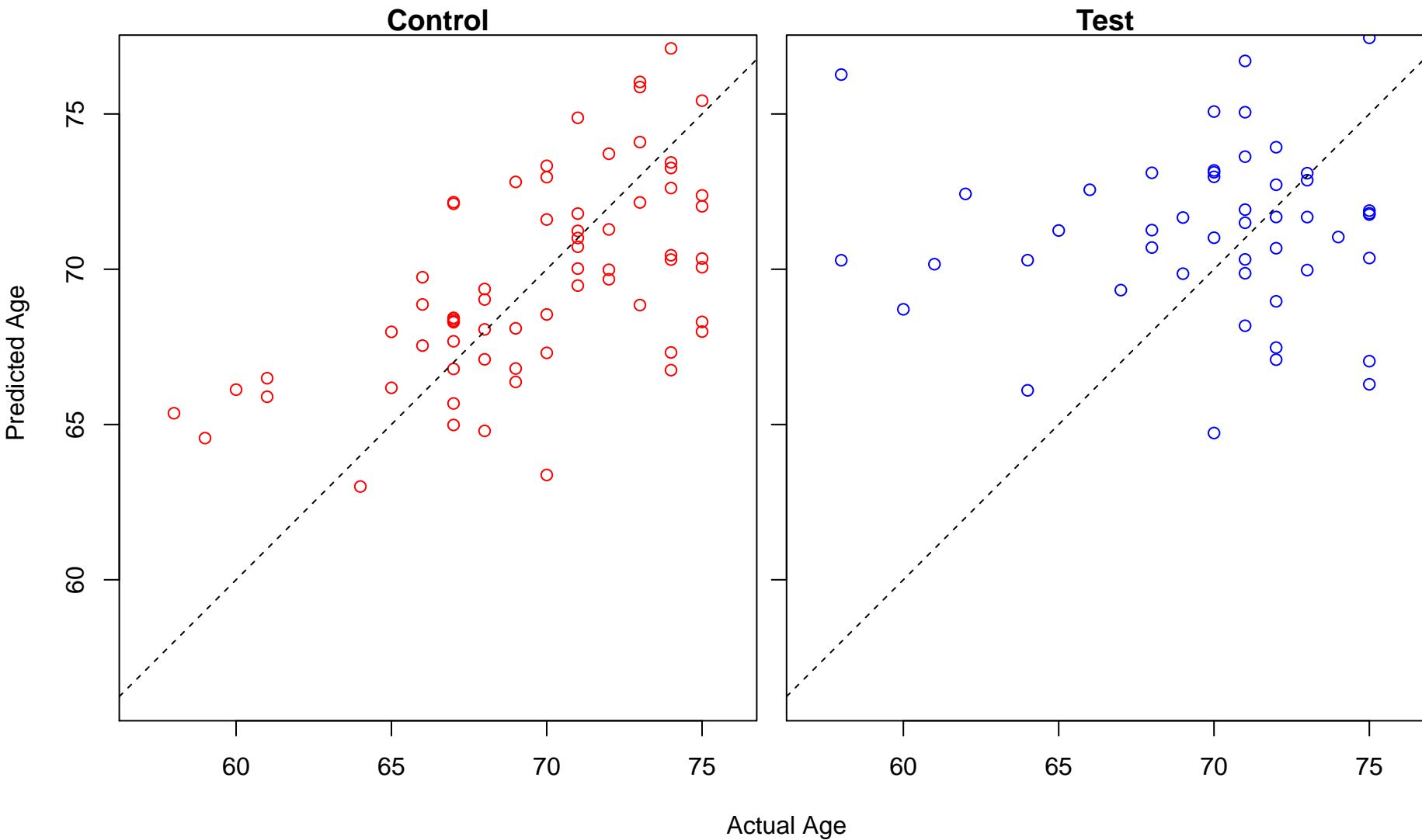


Actual Age

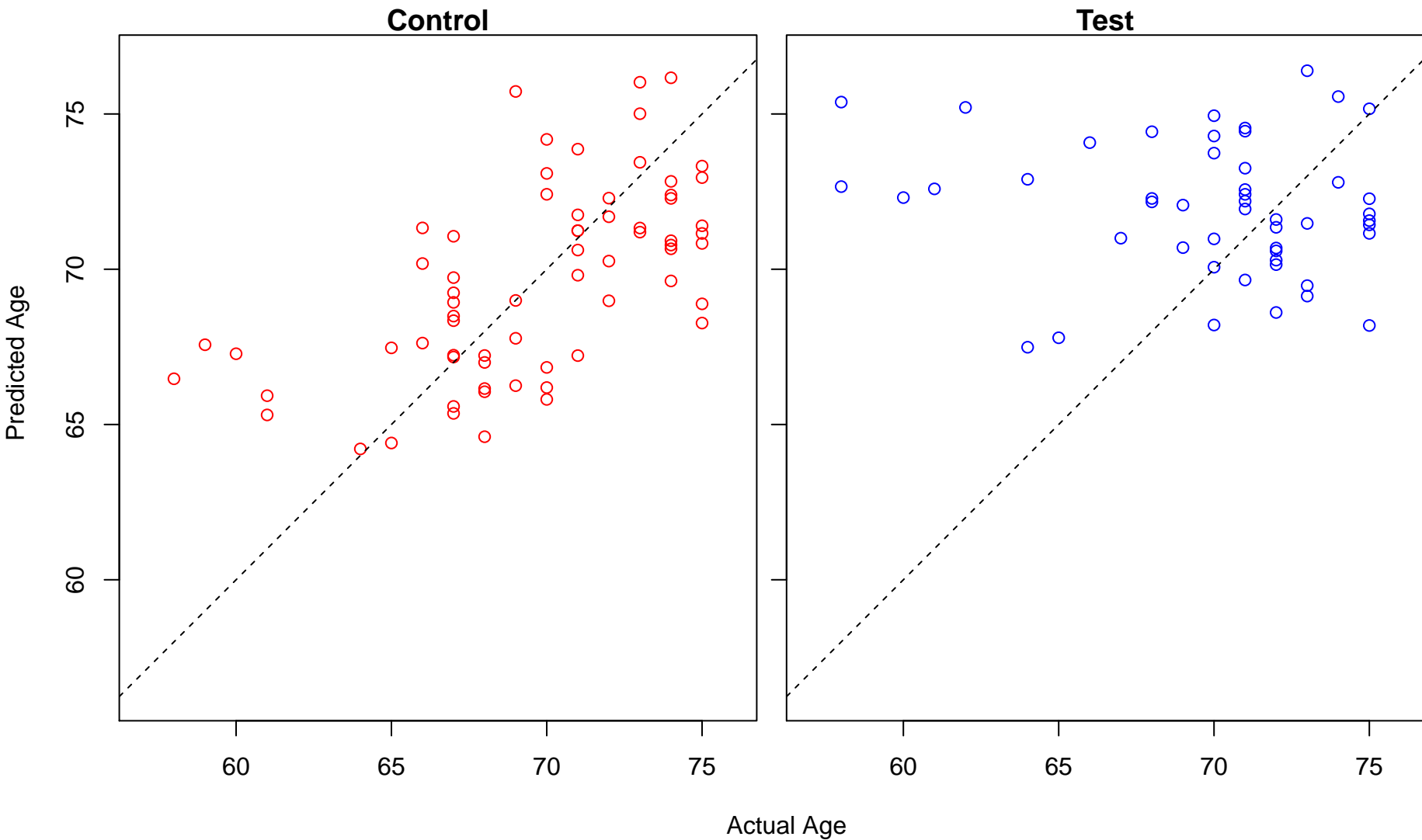
response to lipoprotein particle (Score: 1.194732)



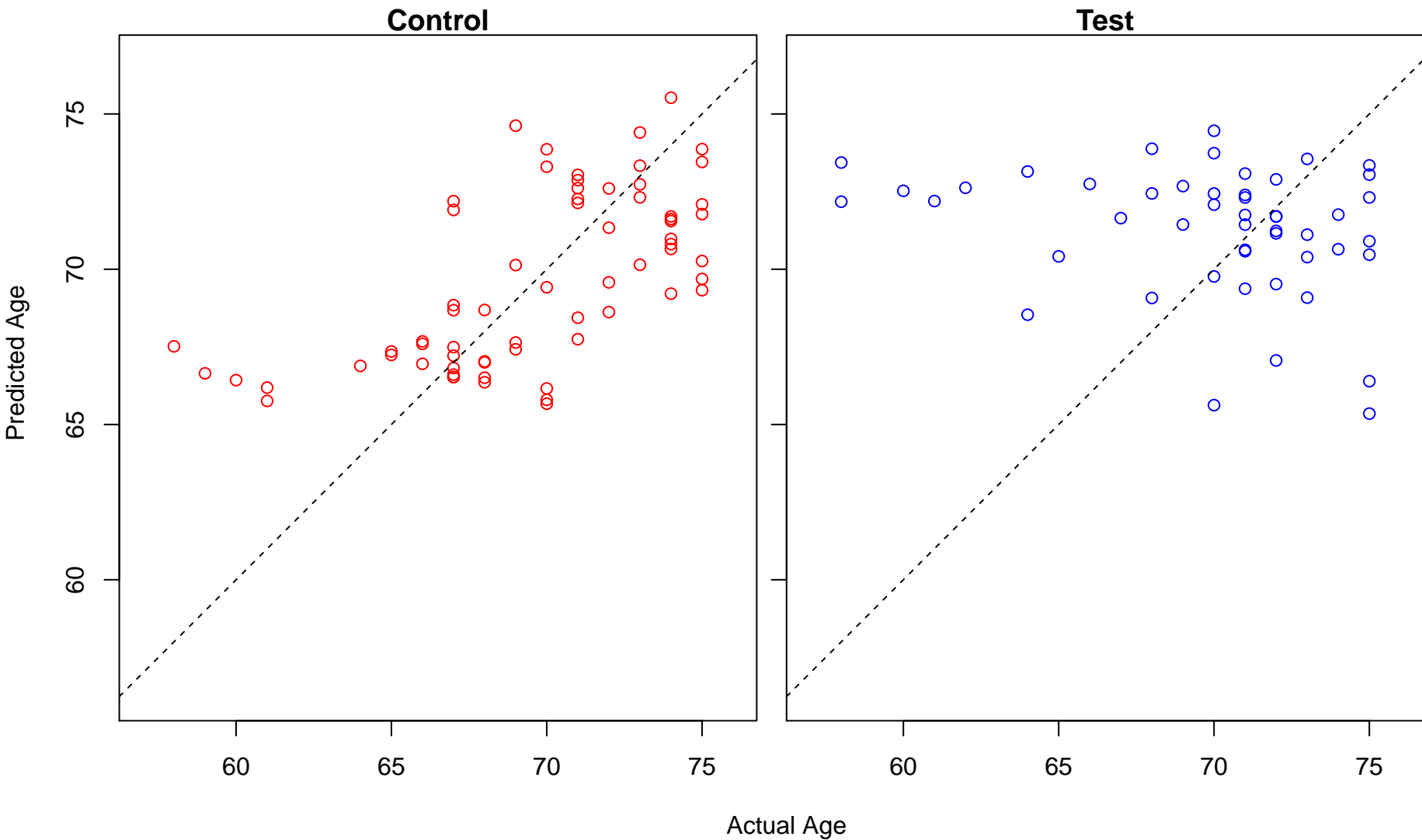
cell junction organization (Score: 1.193974)



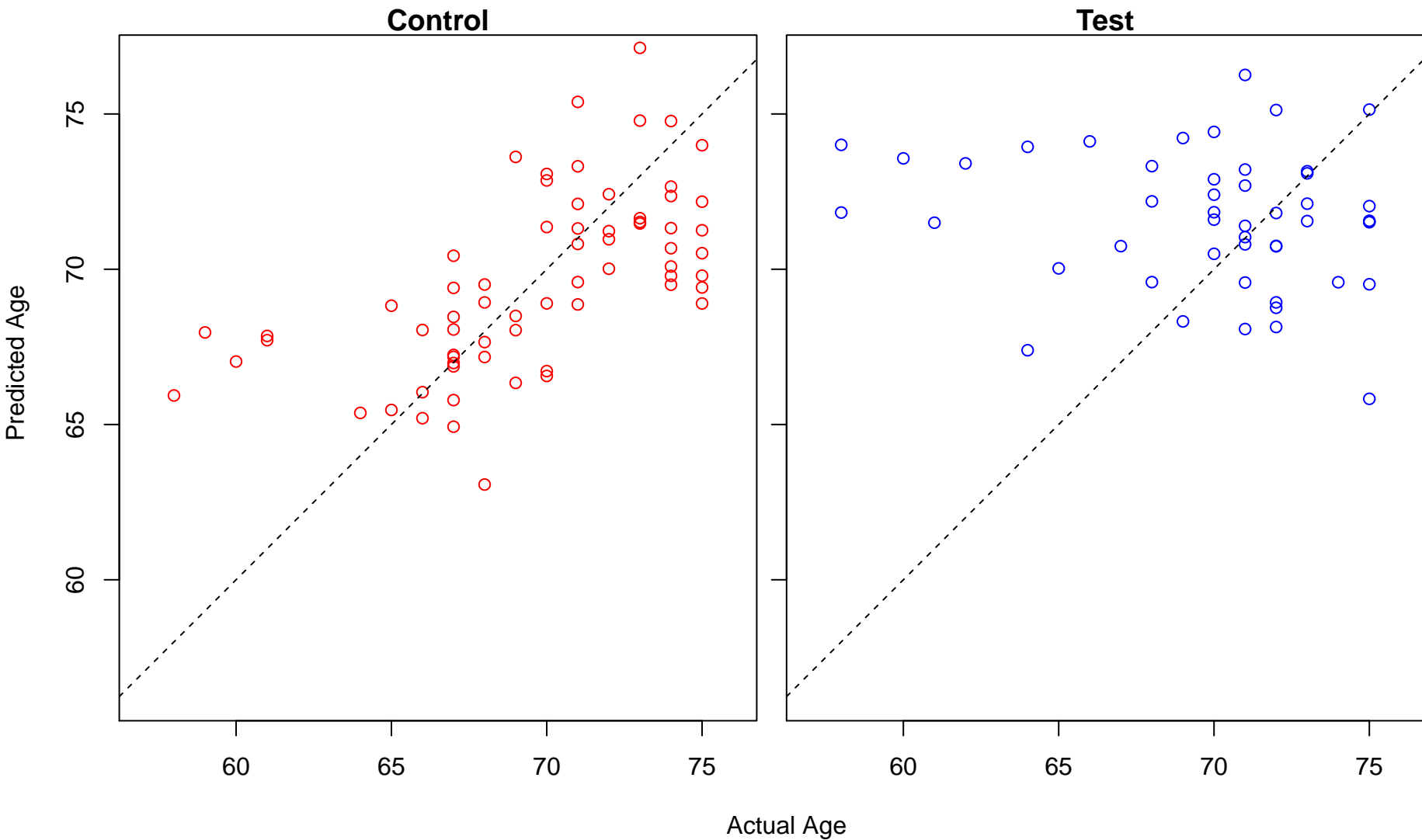
establishment of localization by movement along microtubule (Score: 1.193935)



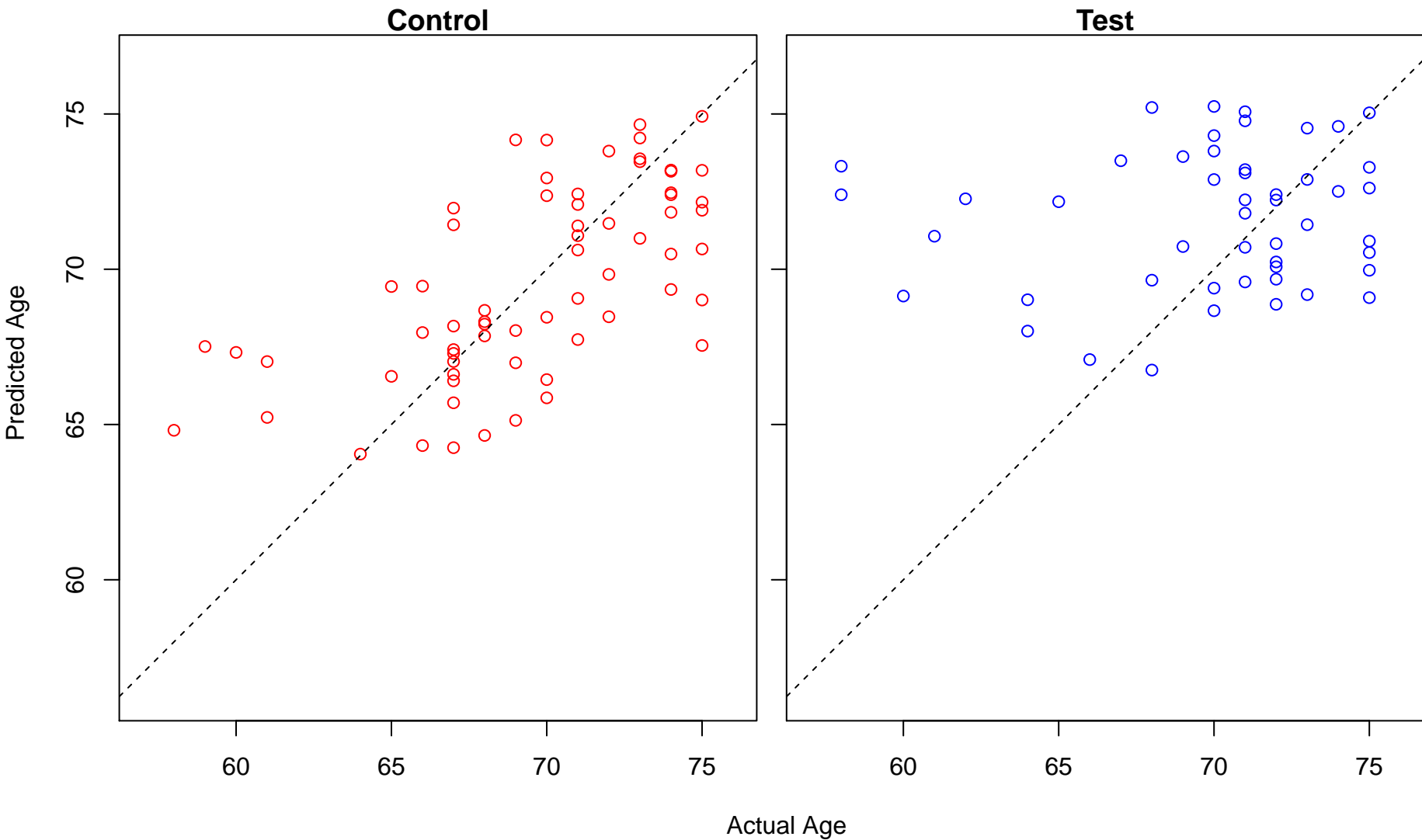
epiboly (Score: 1.193909)



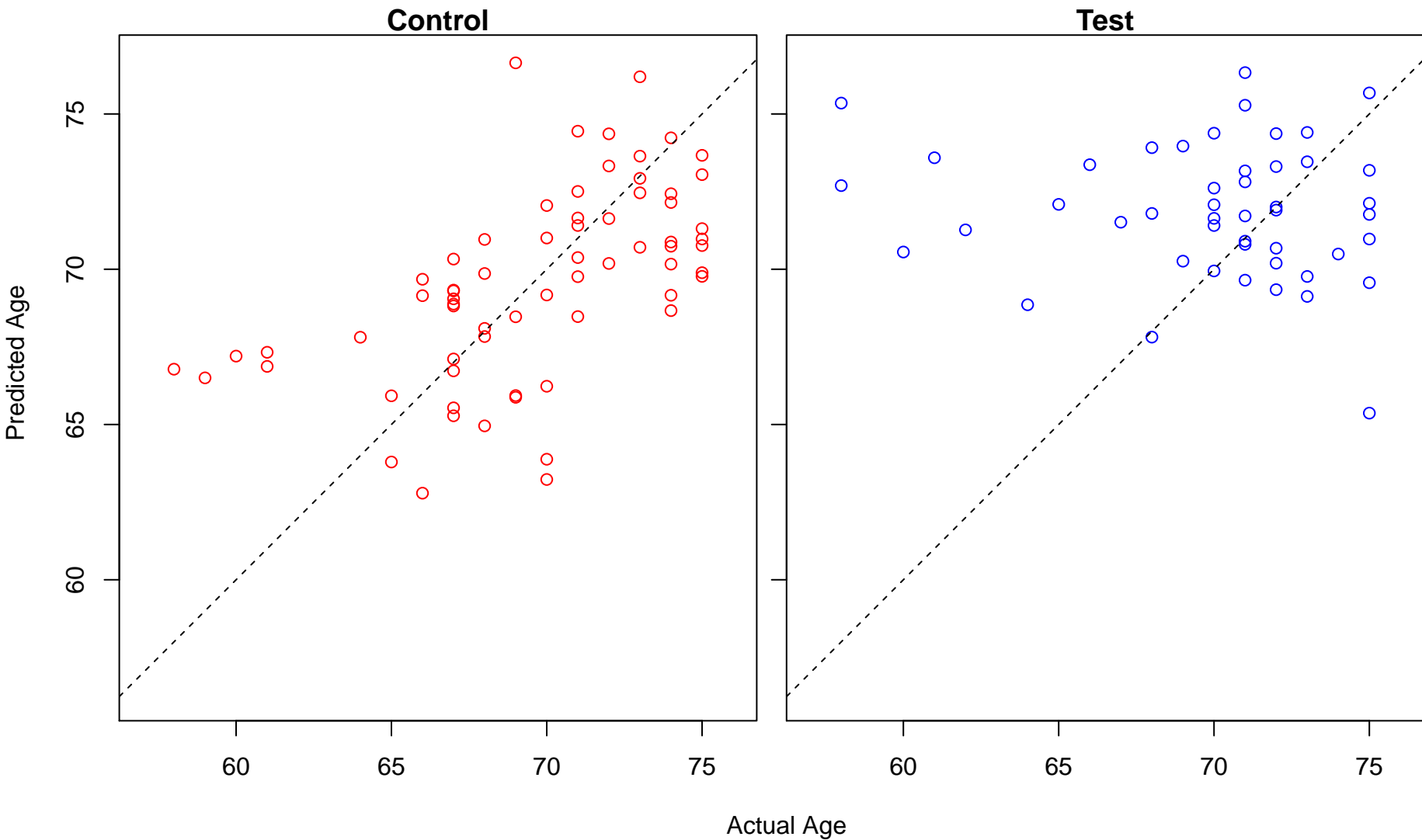
positive regulation of epithelial to mesenchymal transition (Score: 1.193308)



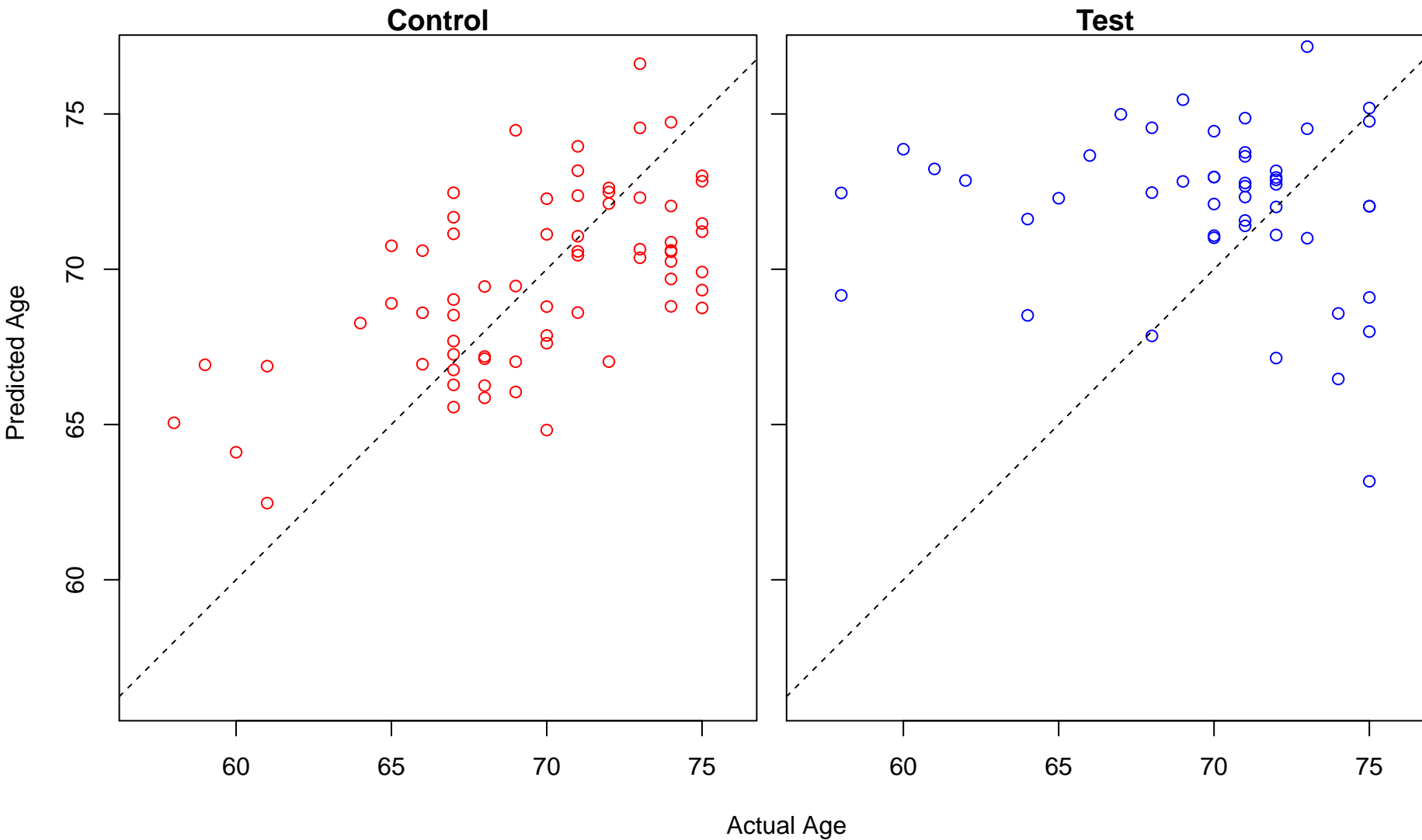
detection of external stimulus (Score: 1.192538)



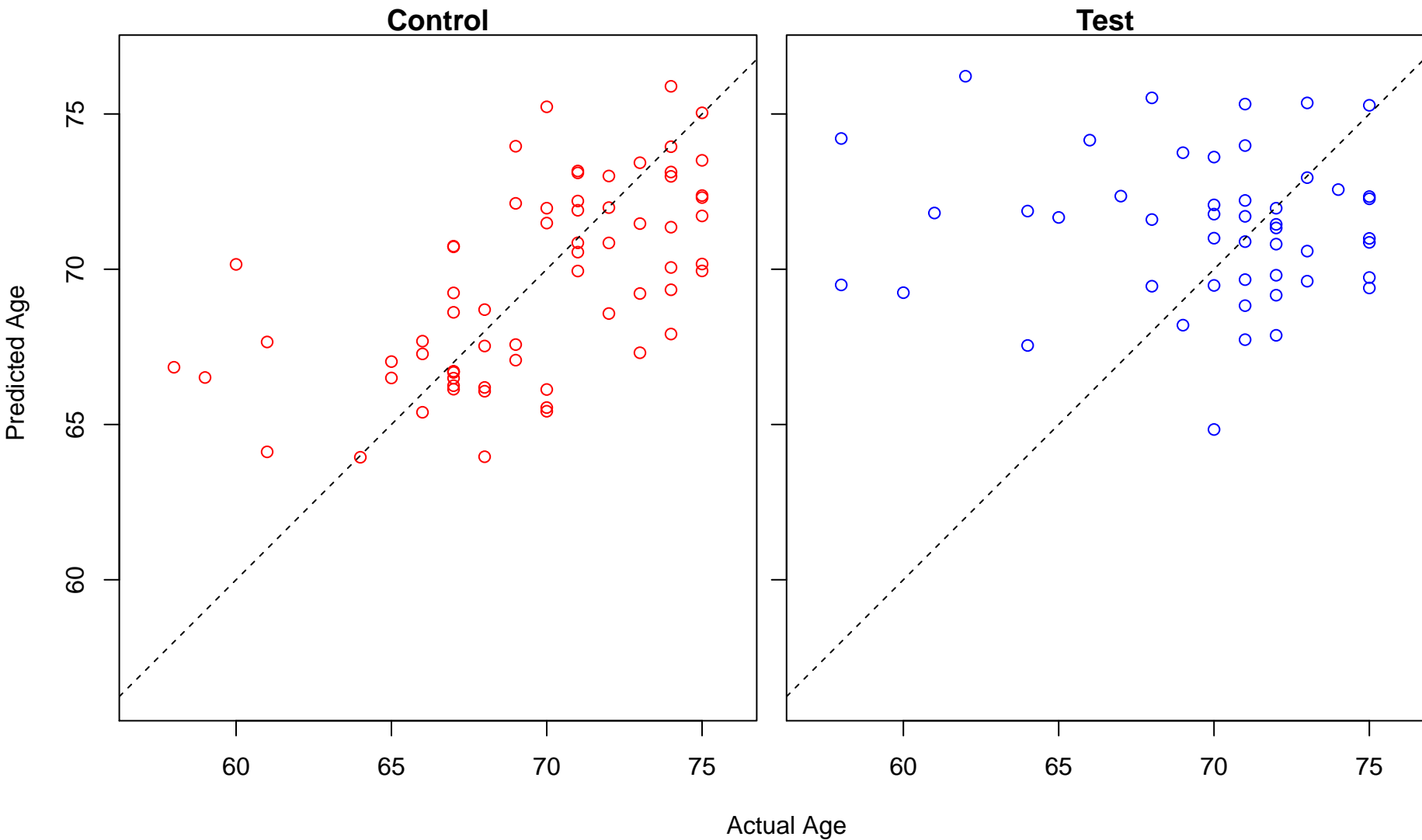
negative regulation of intracellular transport (Score: 1.192483)



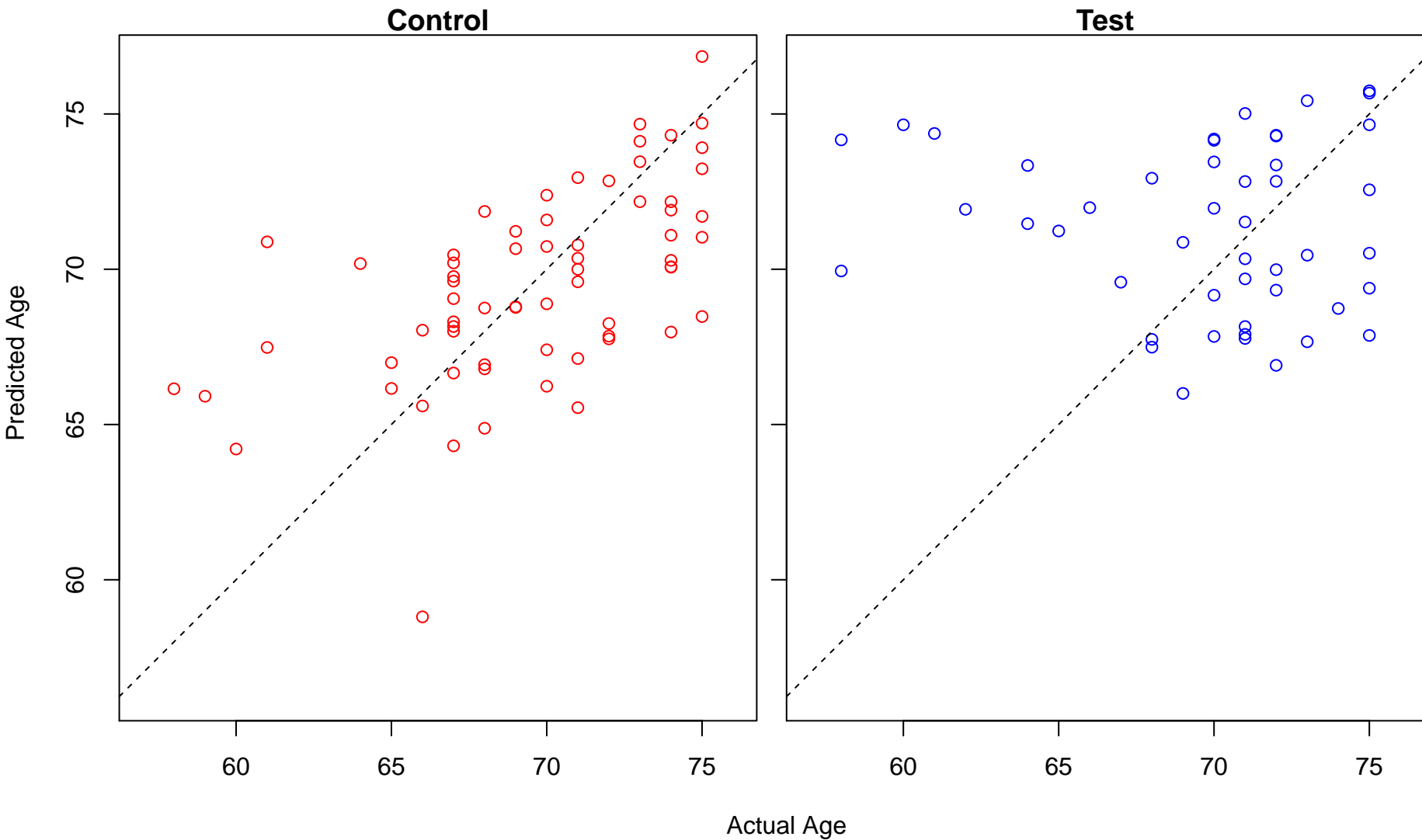
peptidyl-methionine modification (Score: 1.192054)



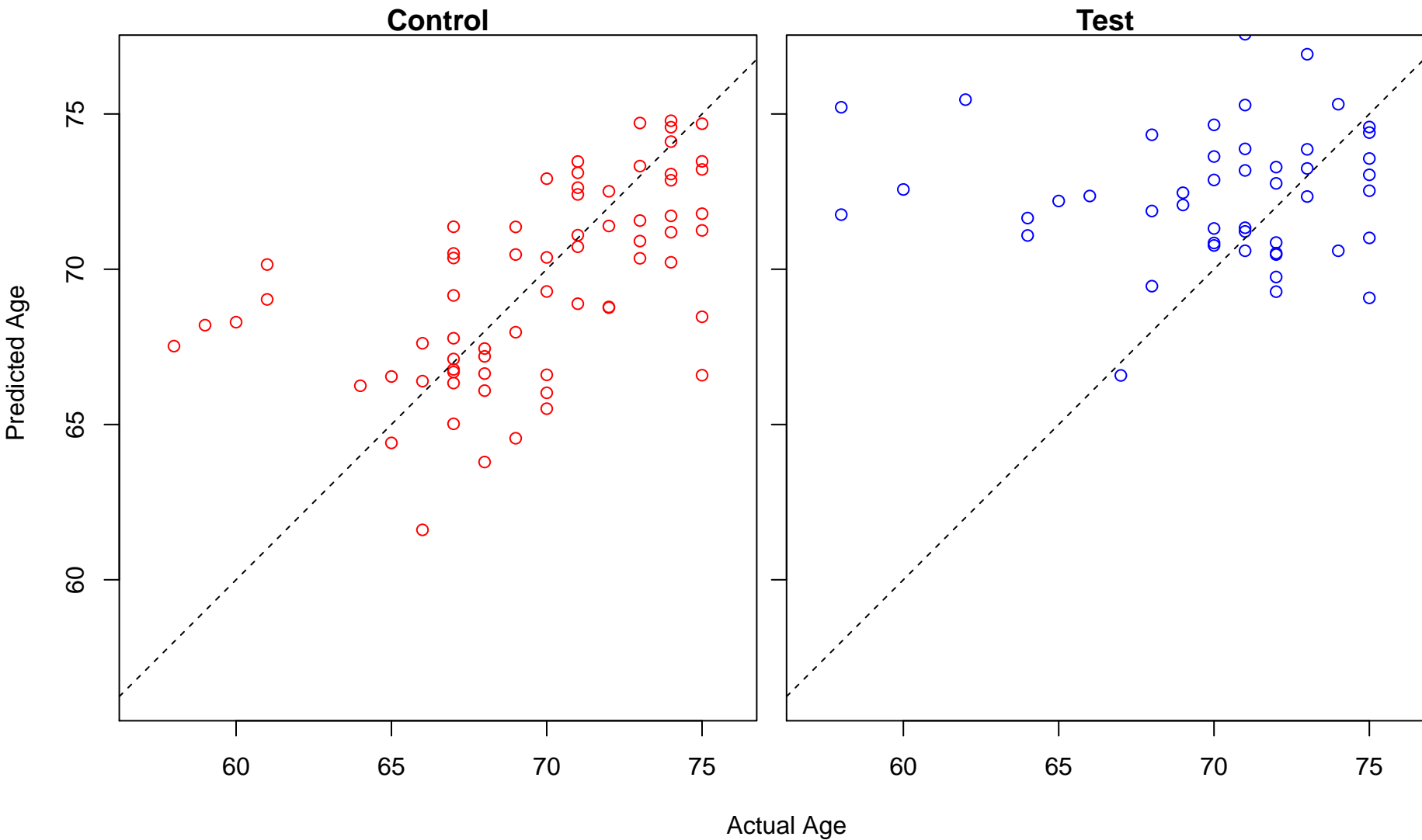
negative regulation of response to cytokine stimulus (Score: 1.191342)



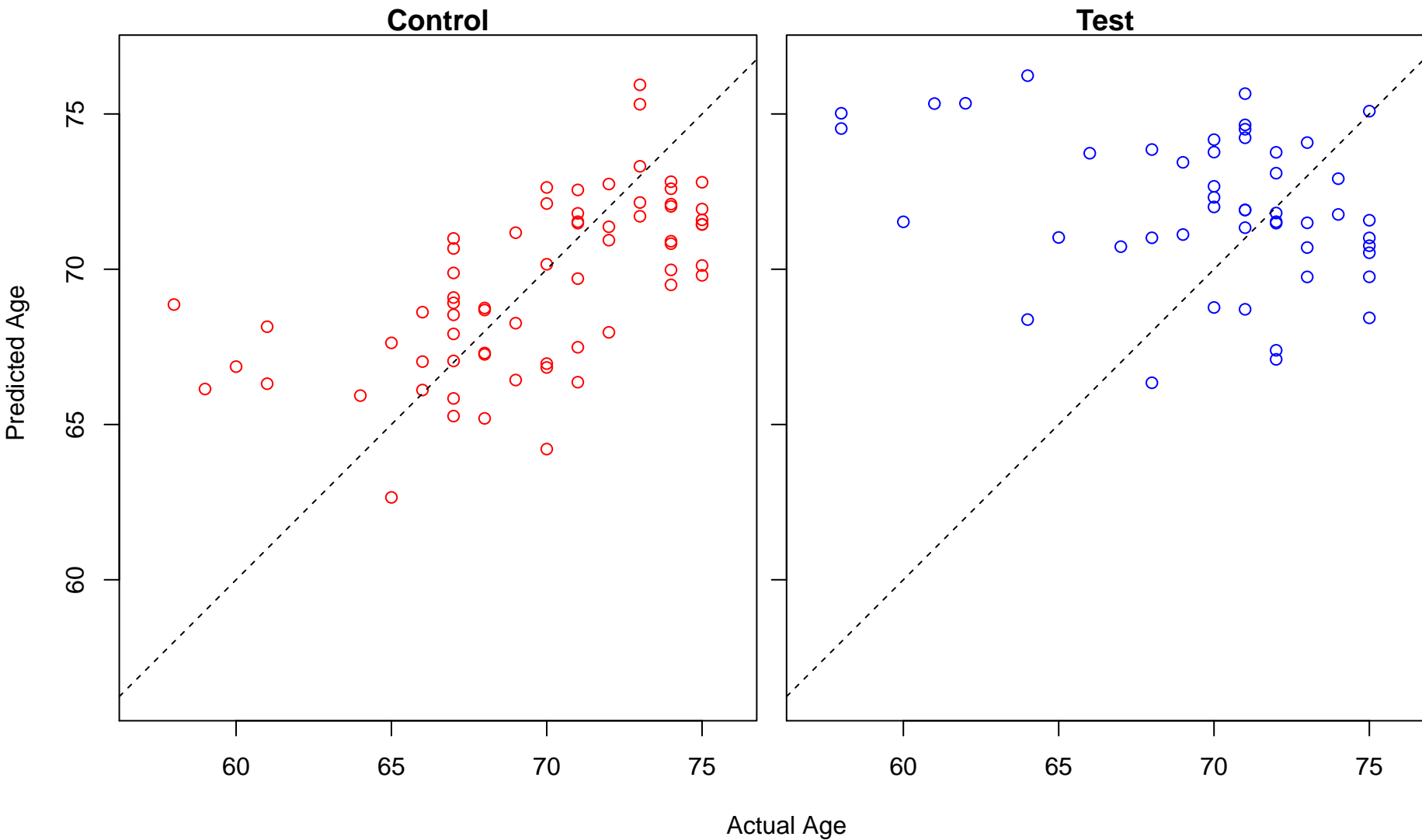
gland morphogenesis (Score: 1.190905)



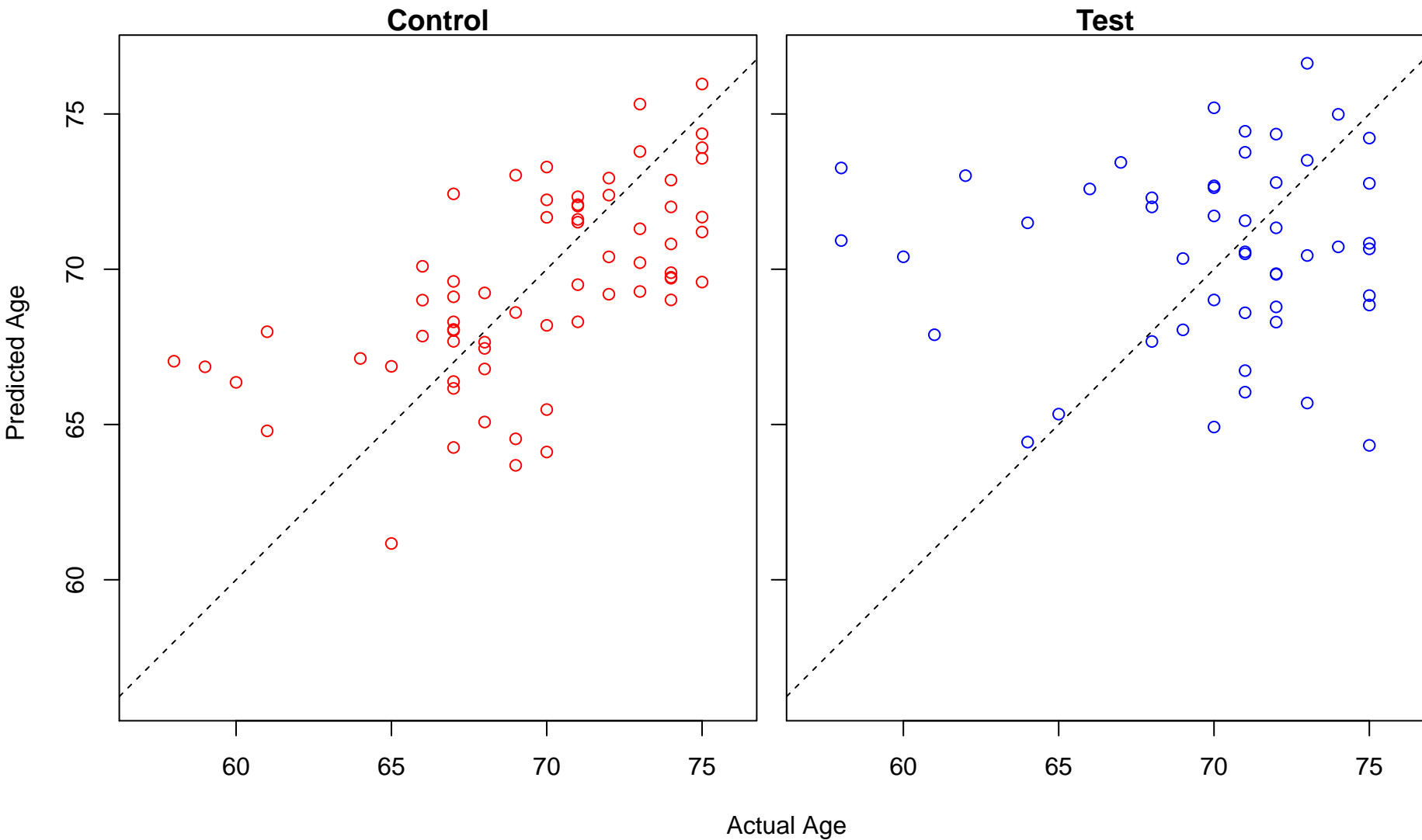
positive regulation of ATPase activity (Score: 1.190848)



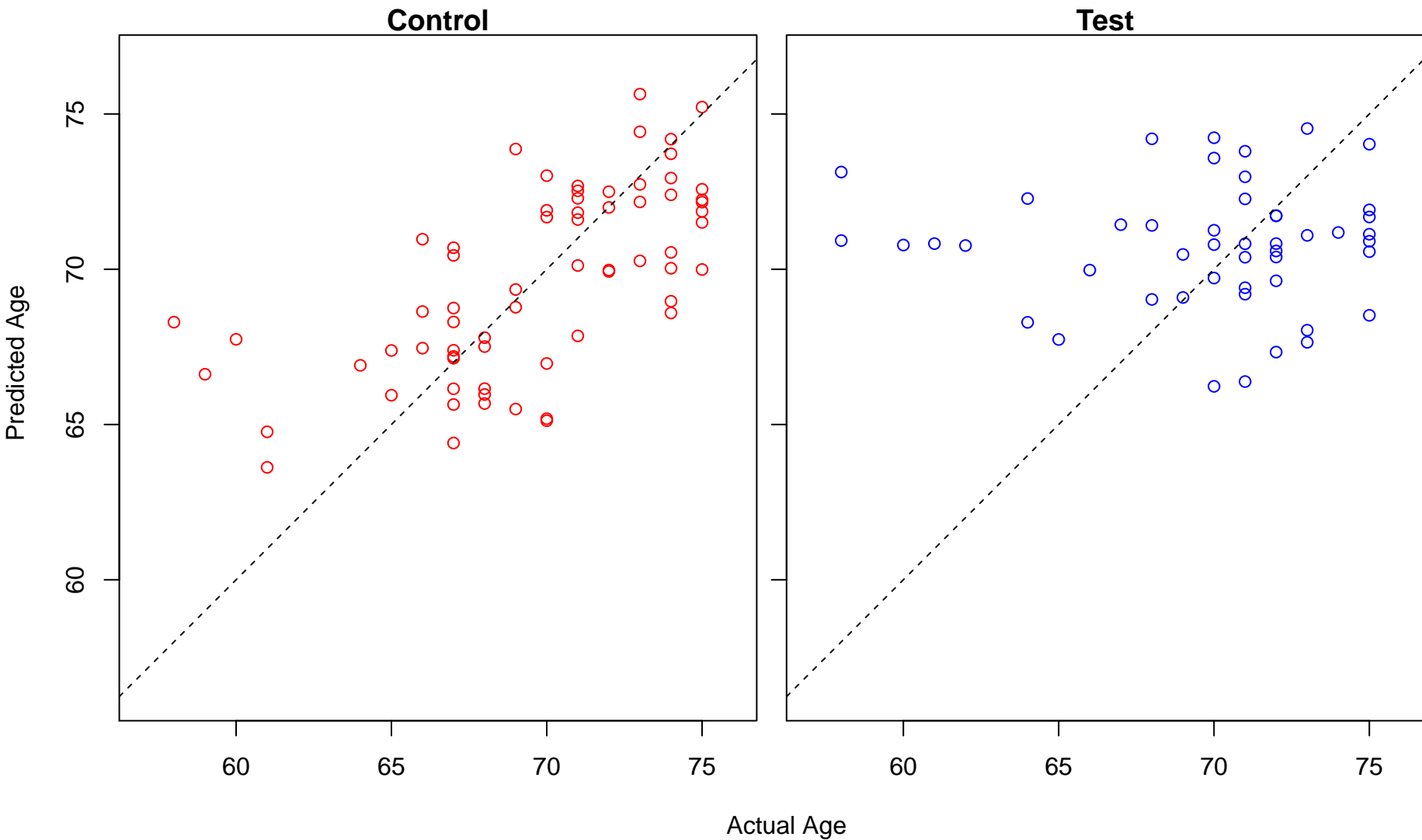
regulation of mast cell activation (Score: 1.190636)



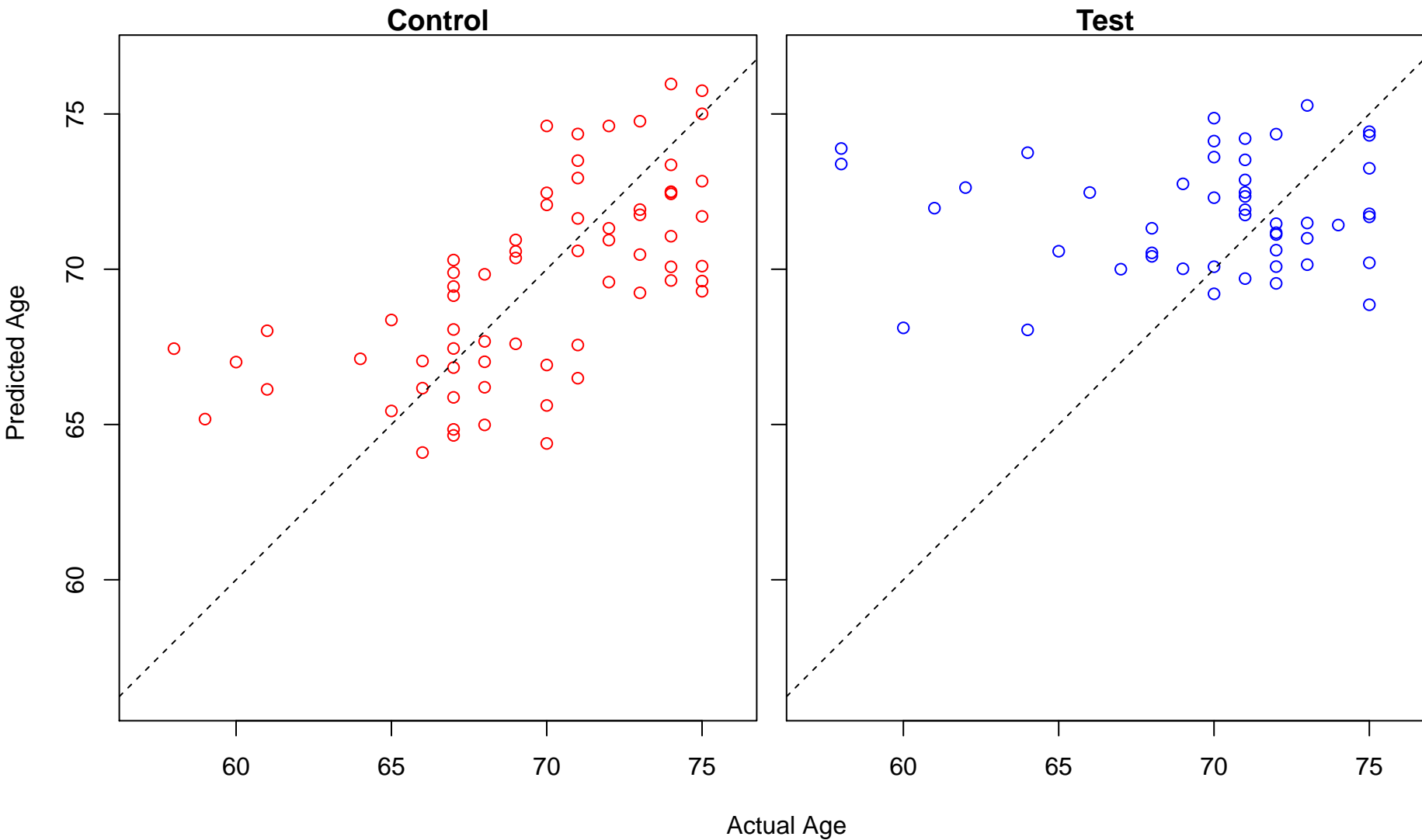
cellular senescence (Score: 1.190336)



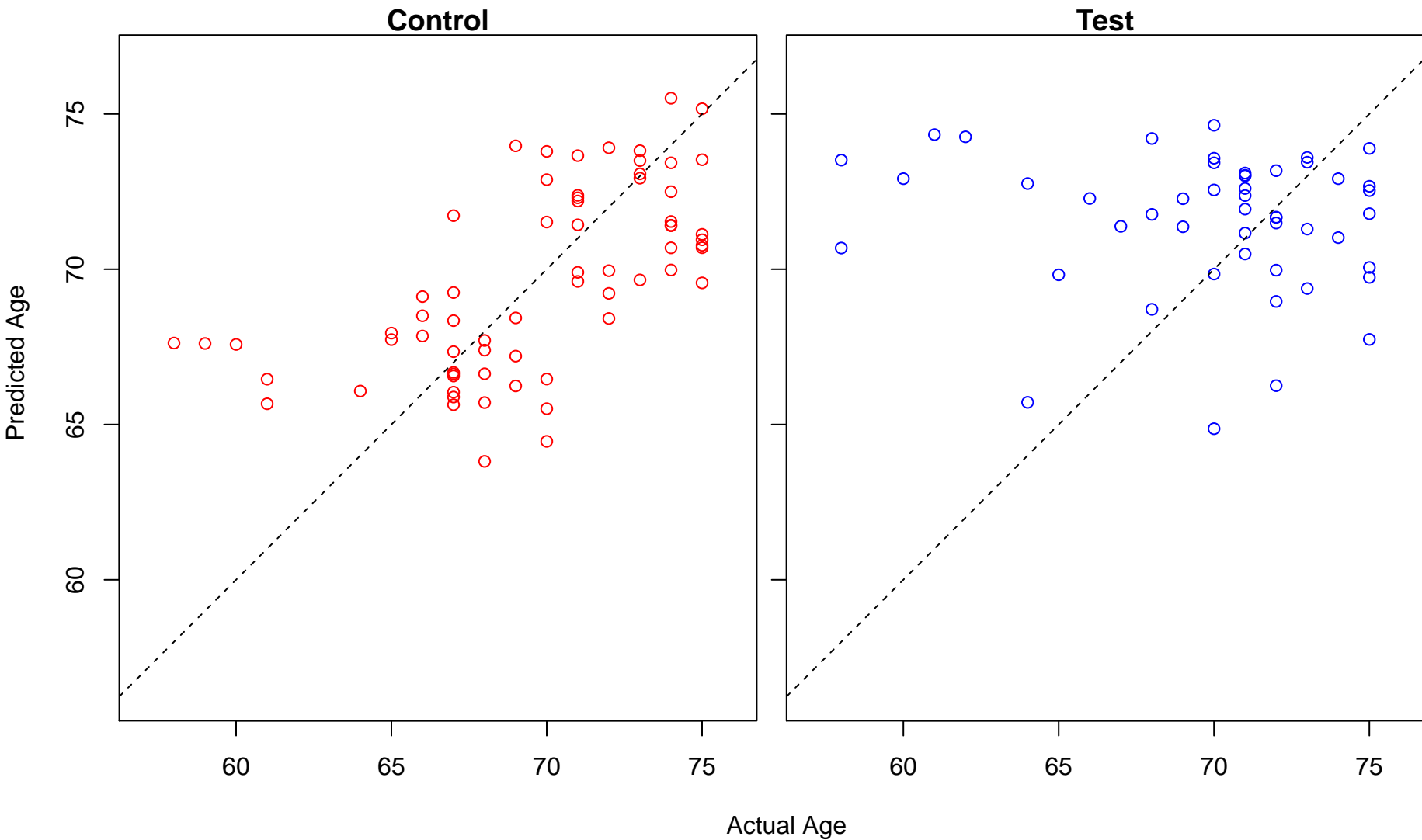
multivesicular body organization (Score: 1.190267)



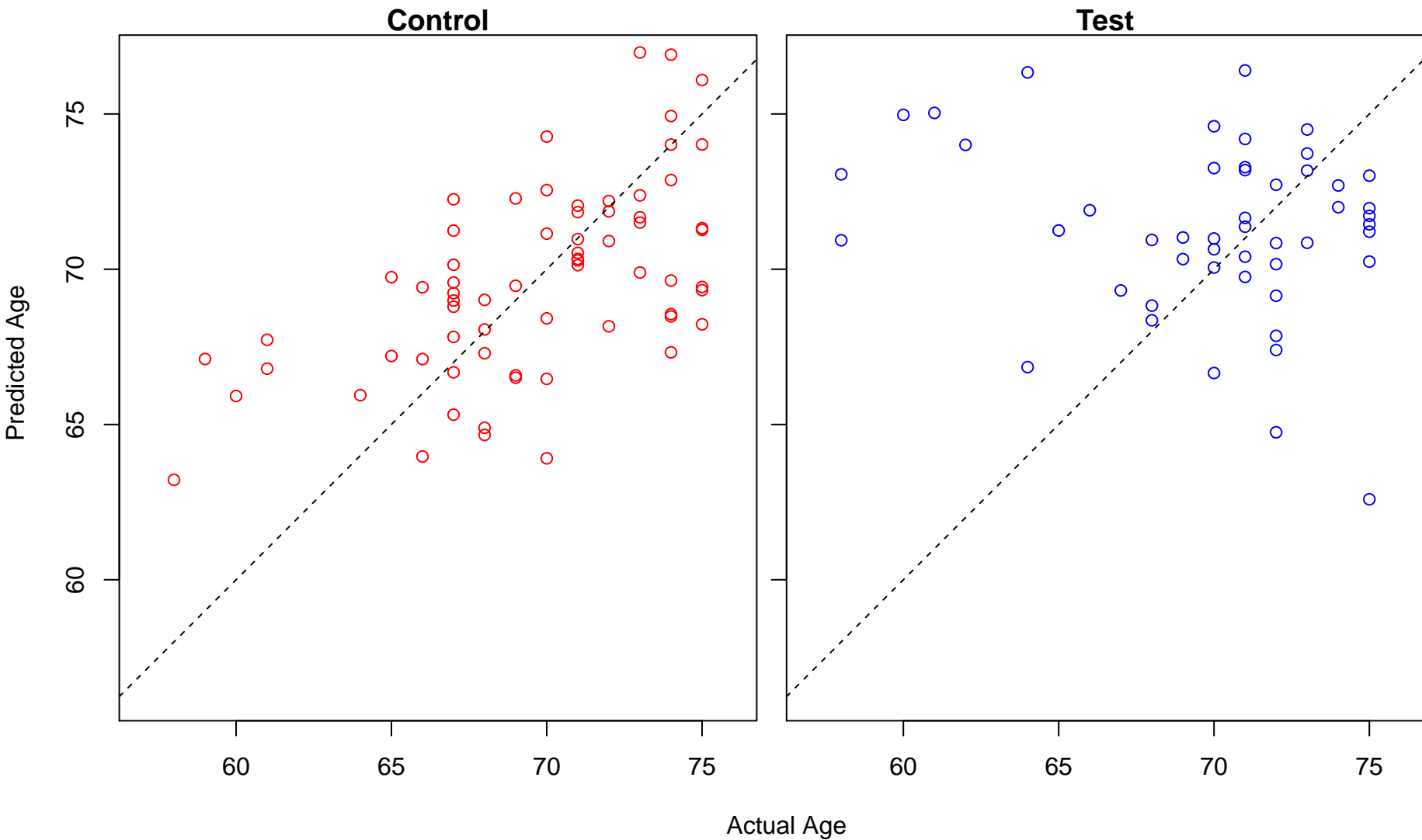
peptidyl-proline modification (Score: 1.190144)



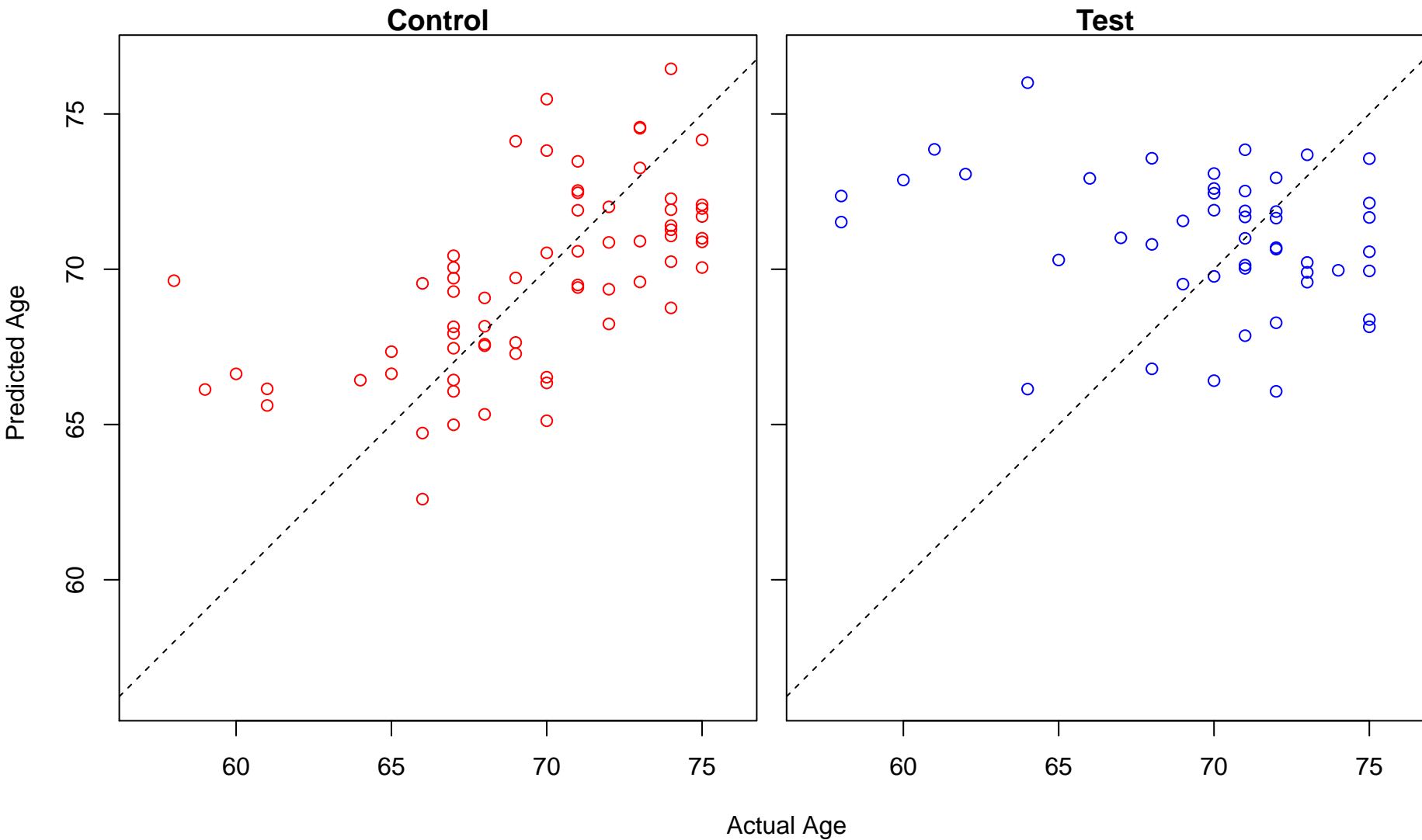
positive regulation of endothelial cell proliferation (Score: 1.189496)



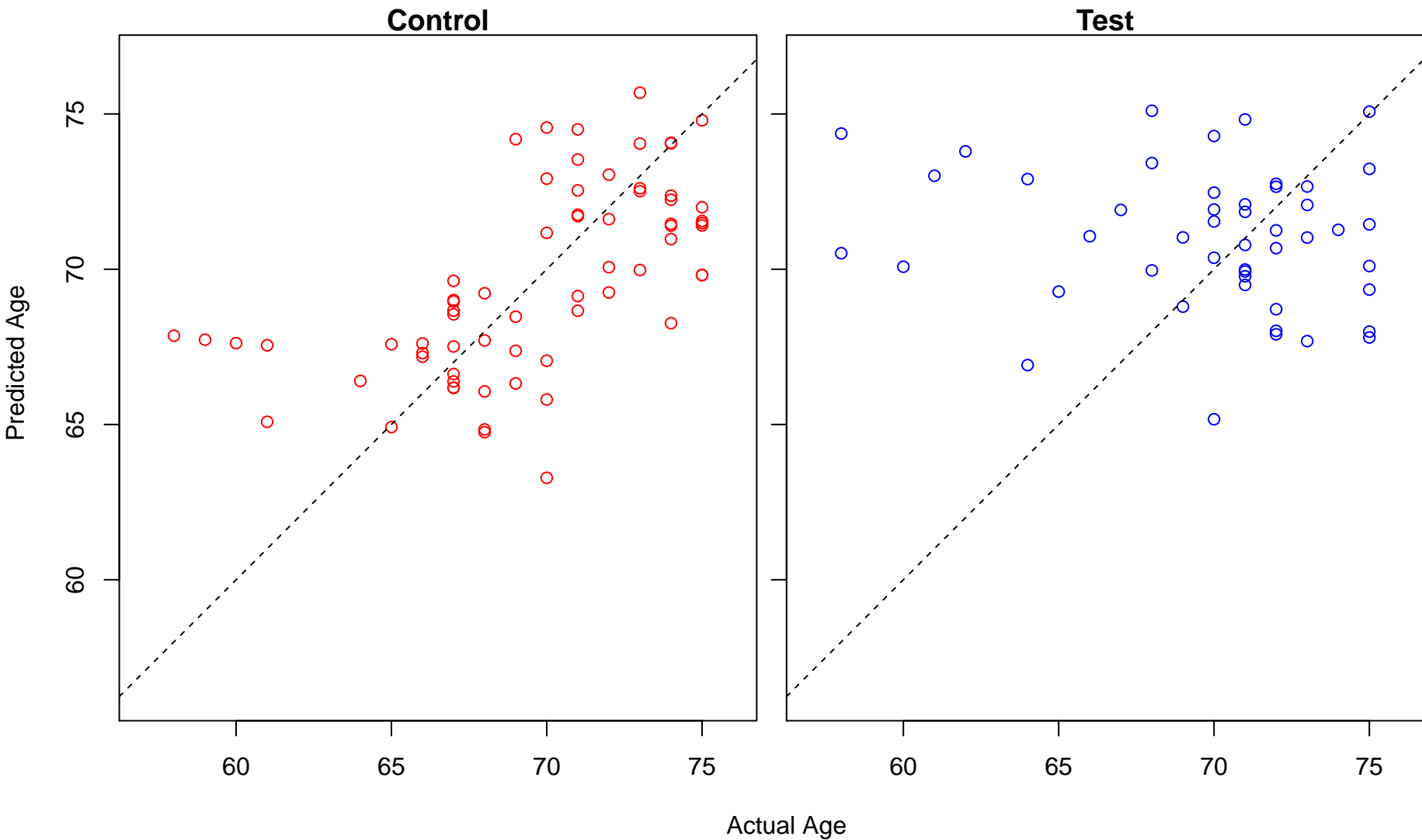
intestinal absorption (Score: 1.187950)



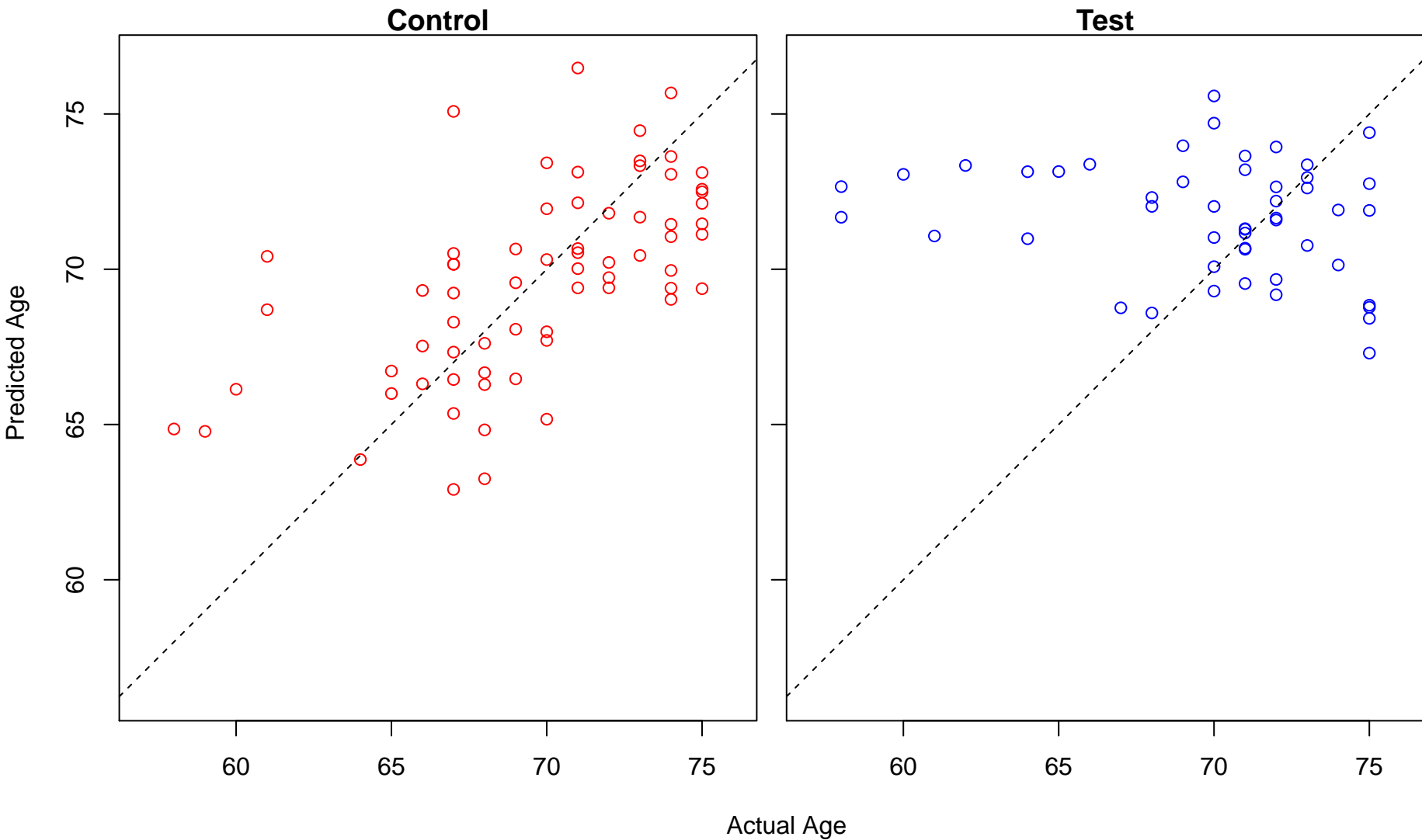
intracellular steroid hormone receptor signaling pathway (Score: 1.187657)



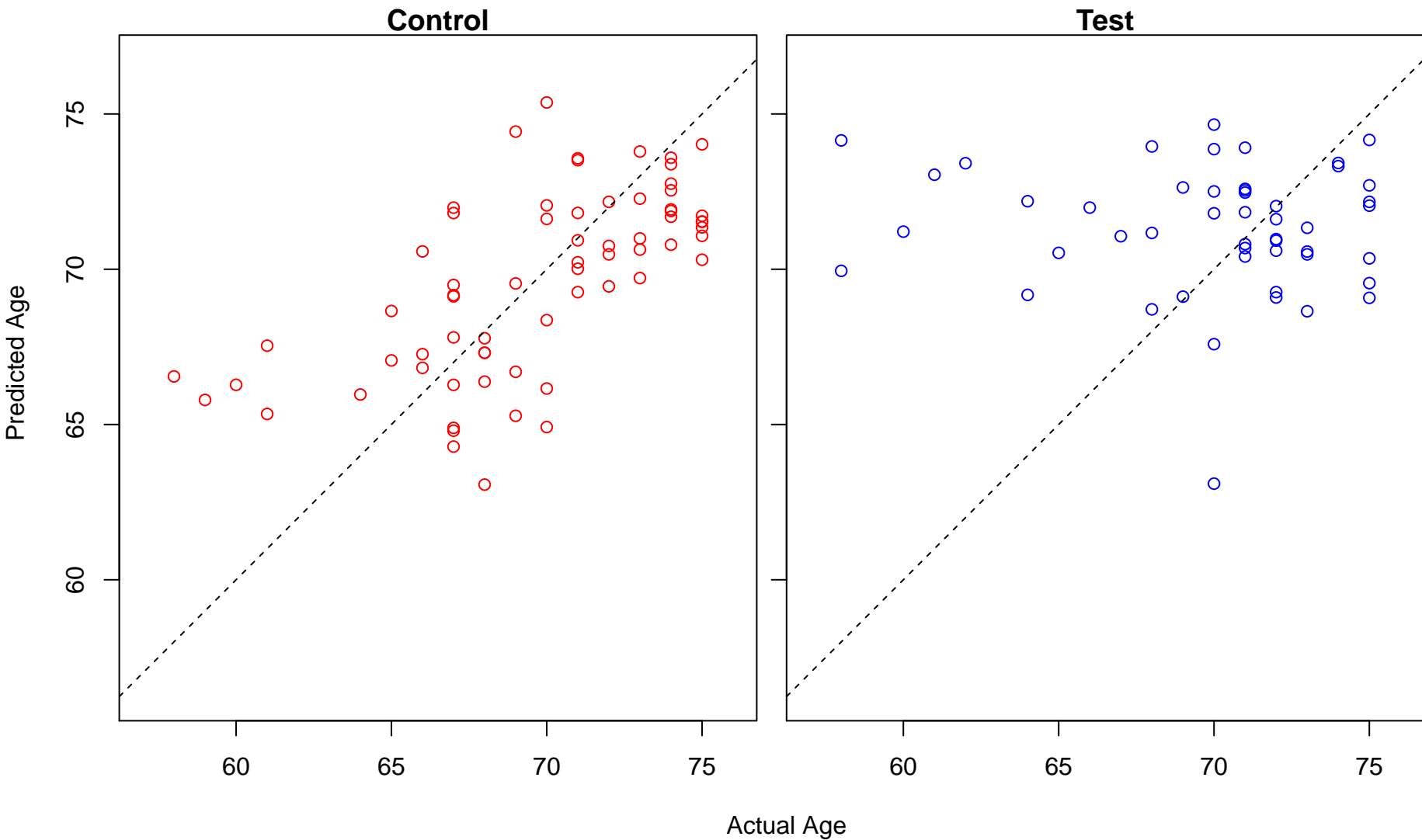
negative regulation of homeostatic process (Score: 1.187565)



sister chromatid cohesion (Score: 1.187474)

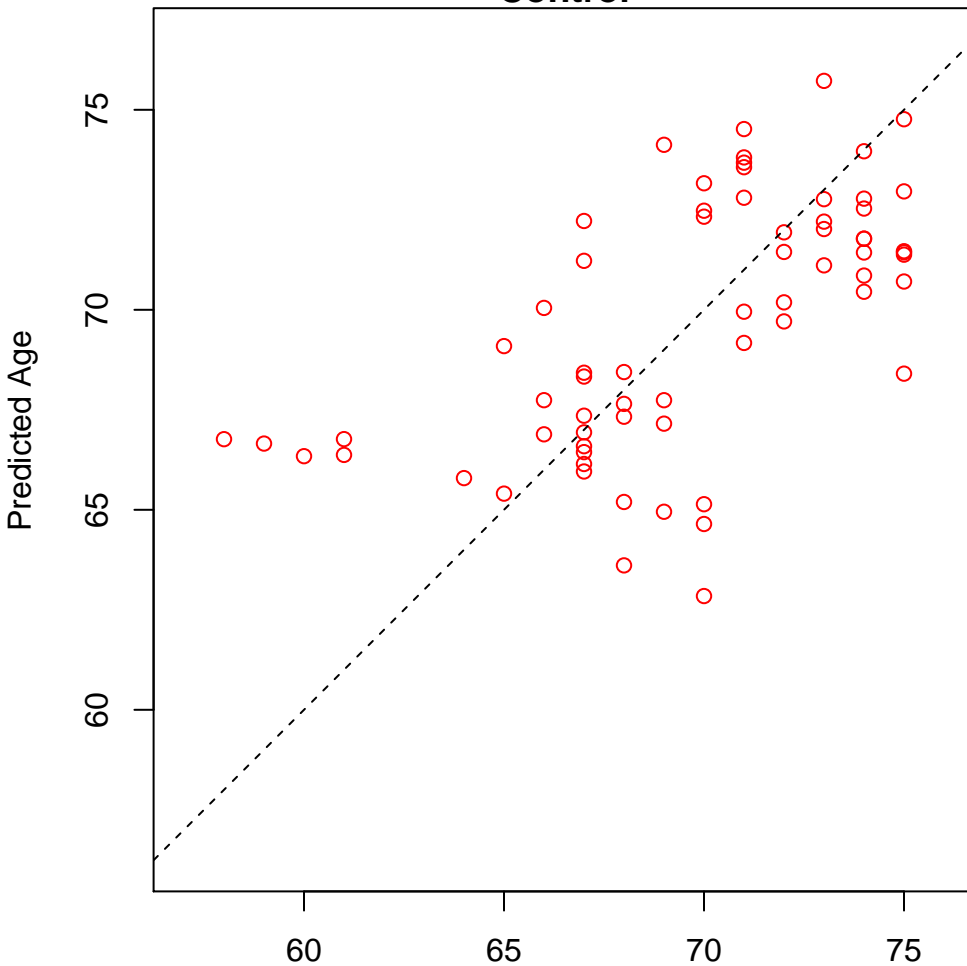


lymphocyte apoptotic process (Score: 1.187159)

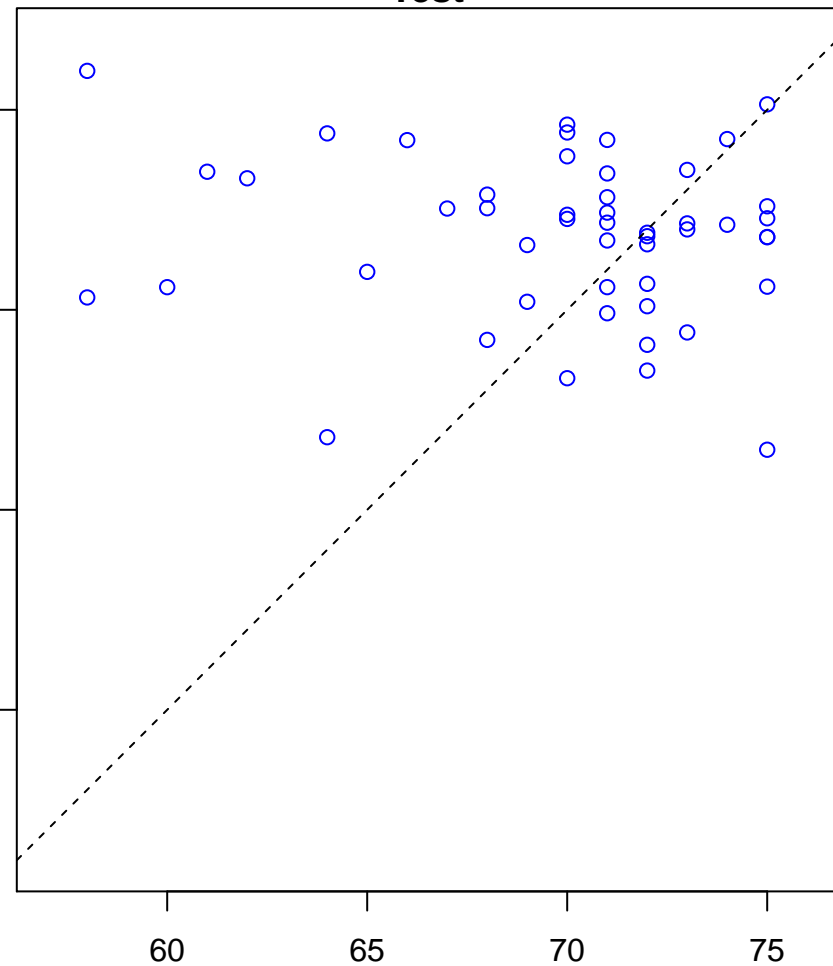


peptidyl-tyrosine dephosphorylation (Score: 1.186895)

Control

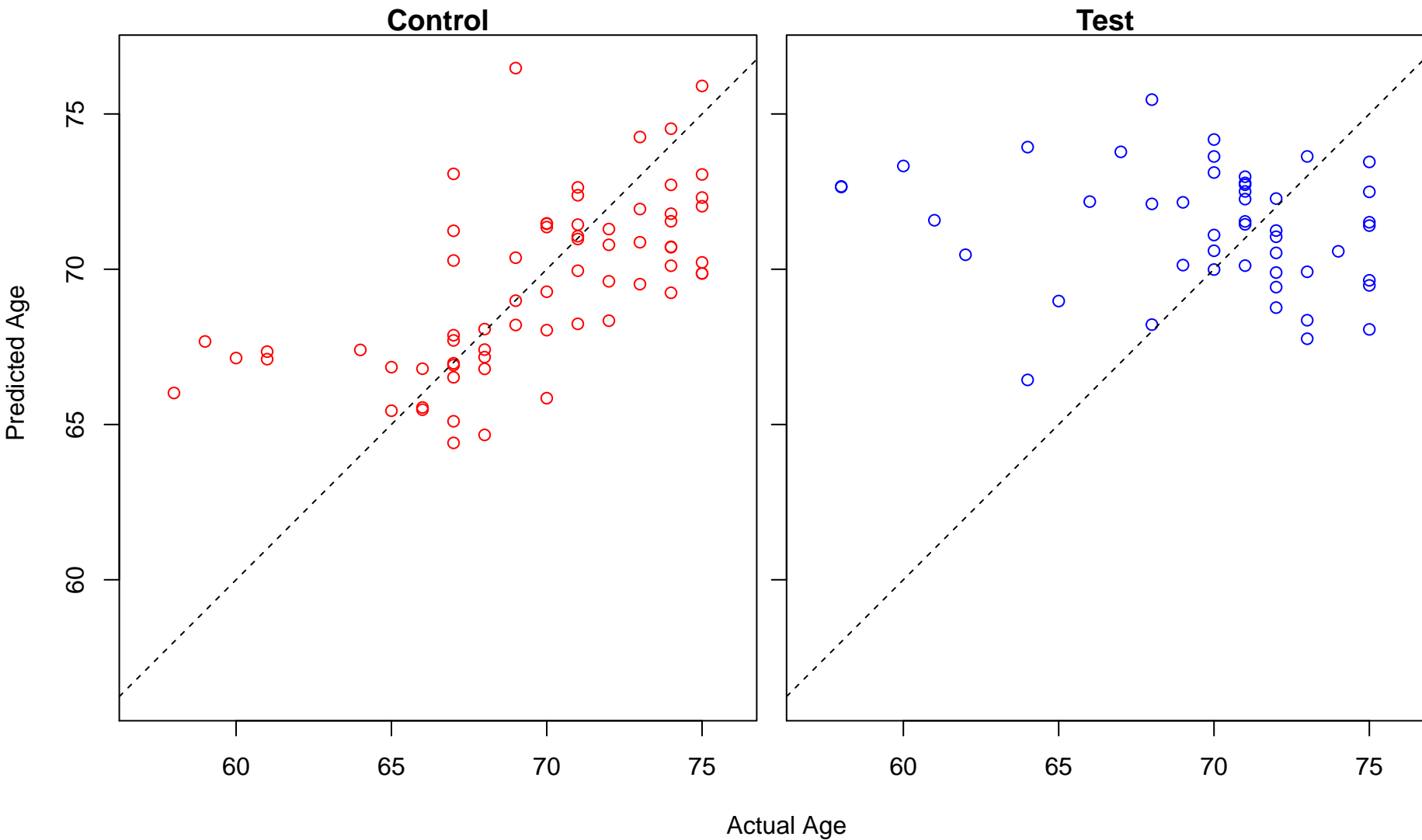


Test

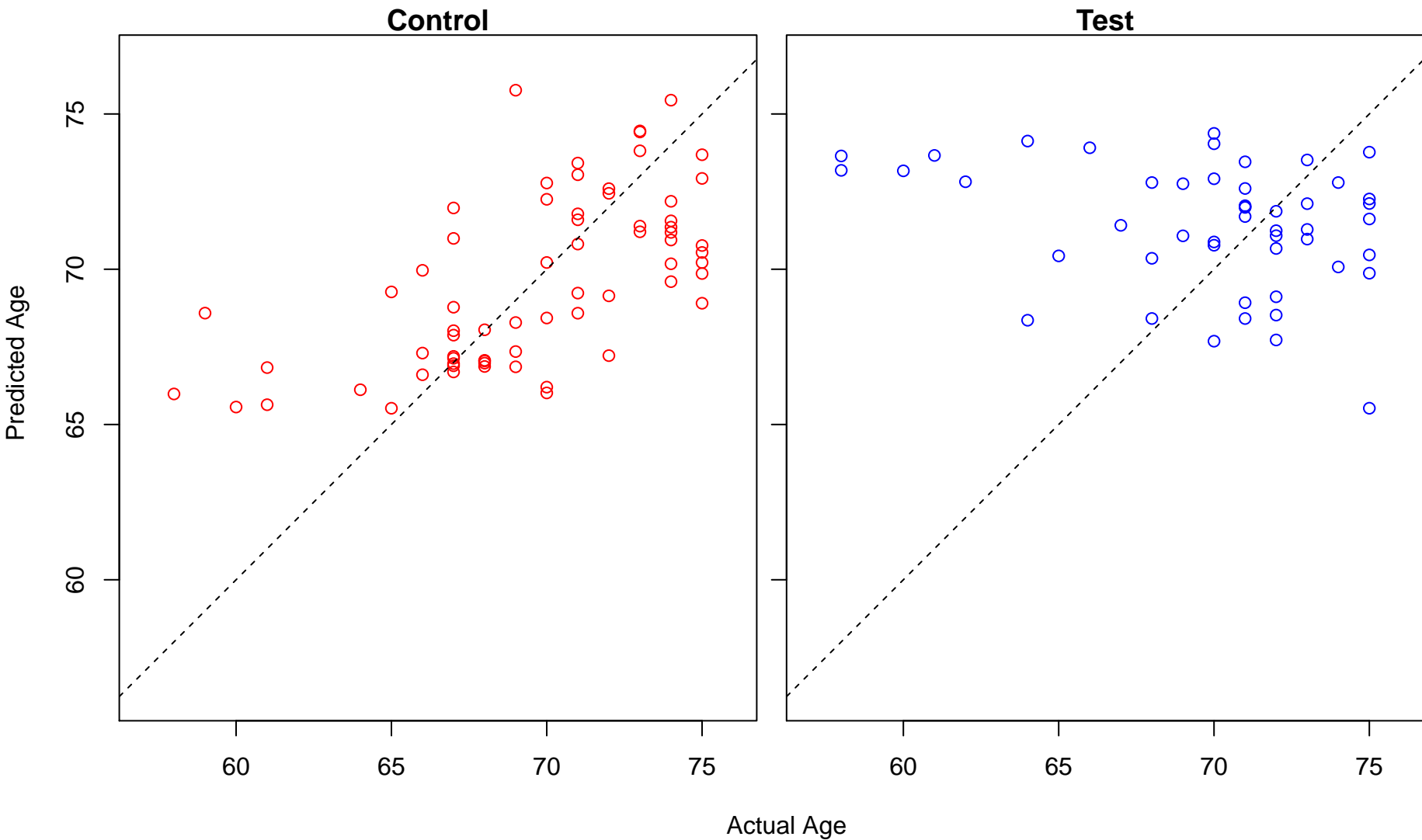


Actual Age

regulation of vesicle fusion (Score: 1.186813)

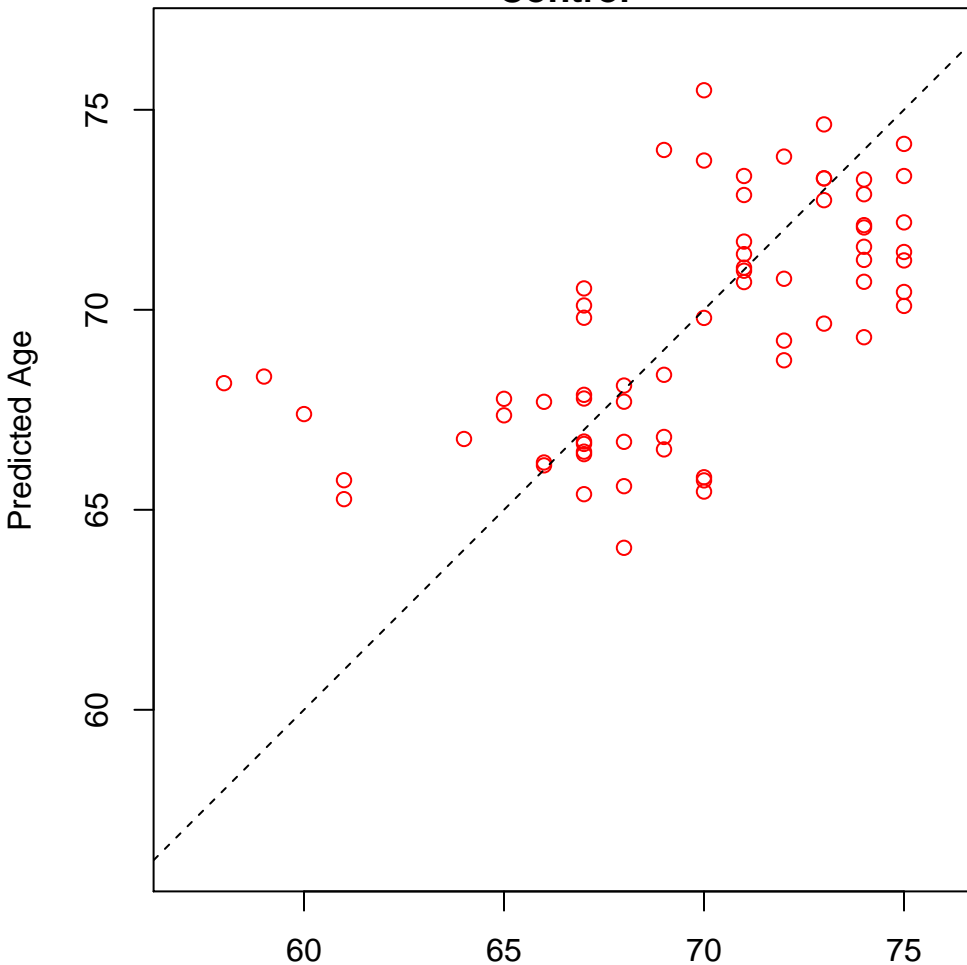


regulation of organ growth (Score: 1.186682)

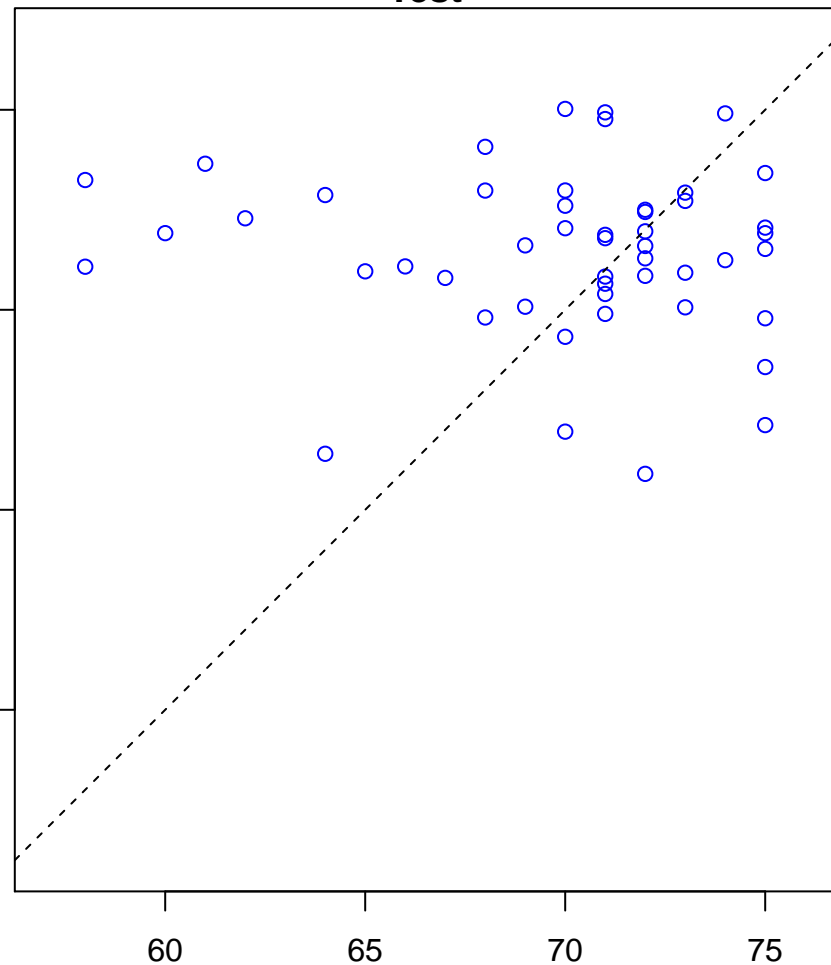


regulation of erythrocyte differentiation (Score: 1.186086)

Control

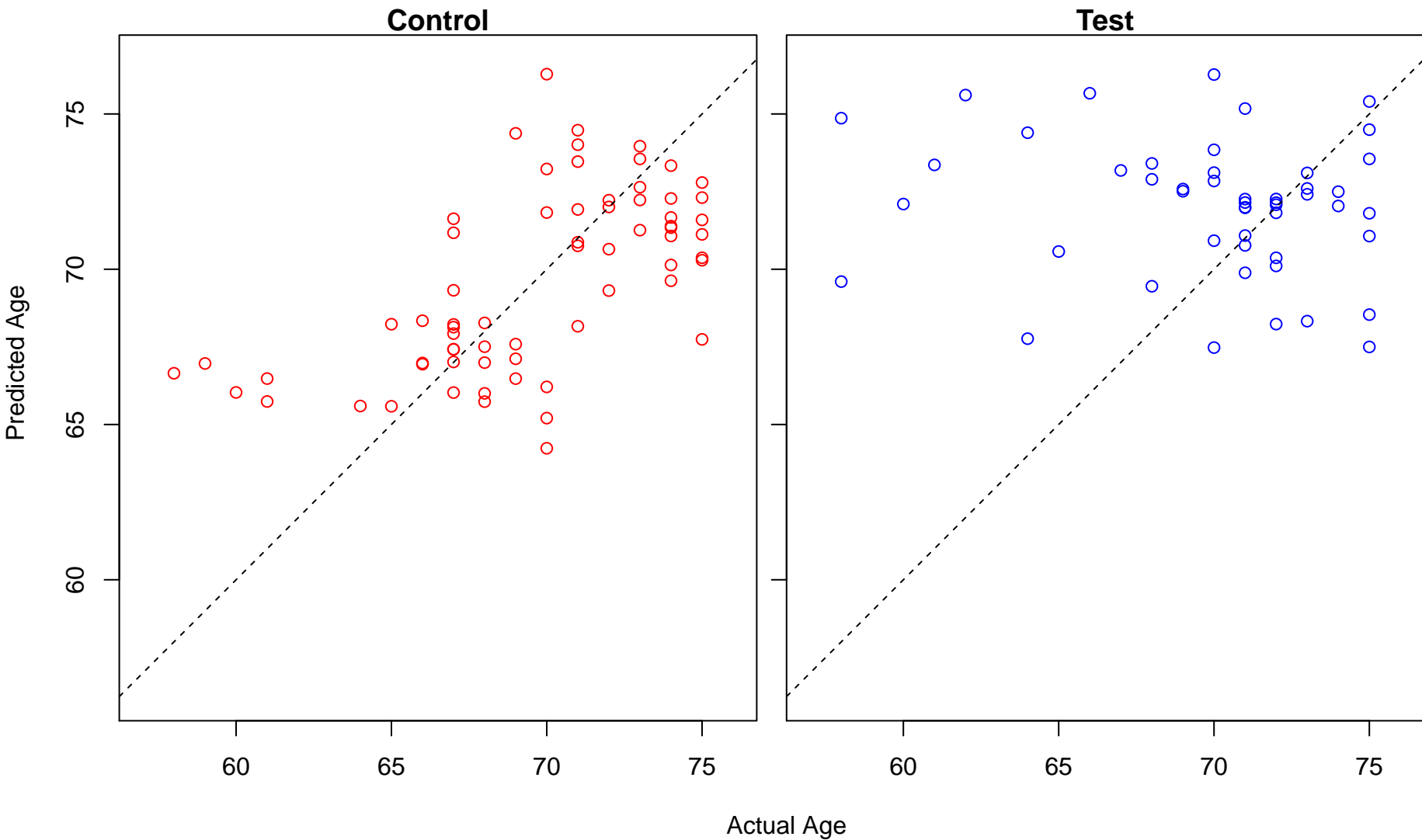


Test

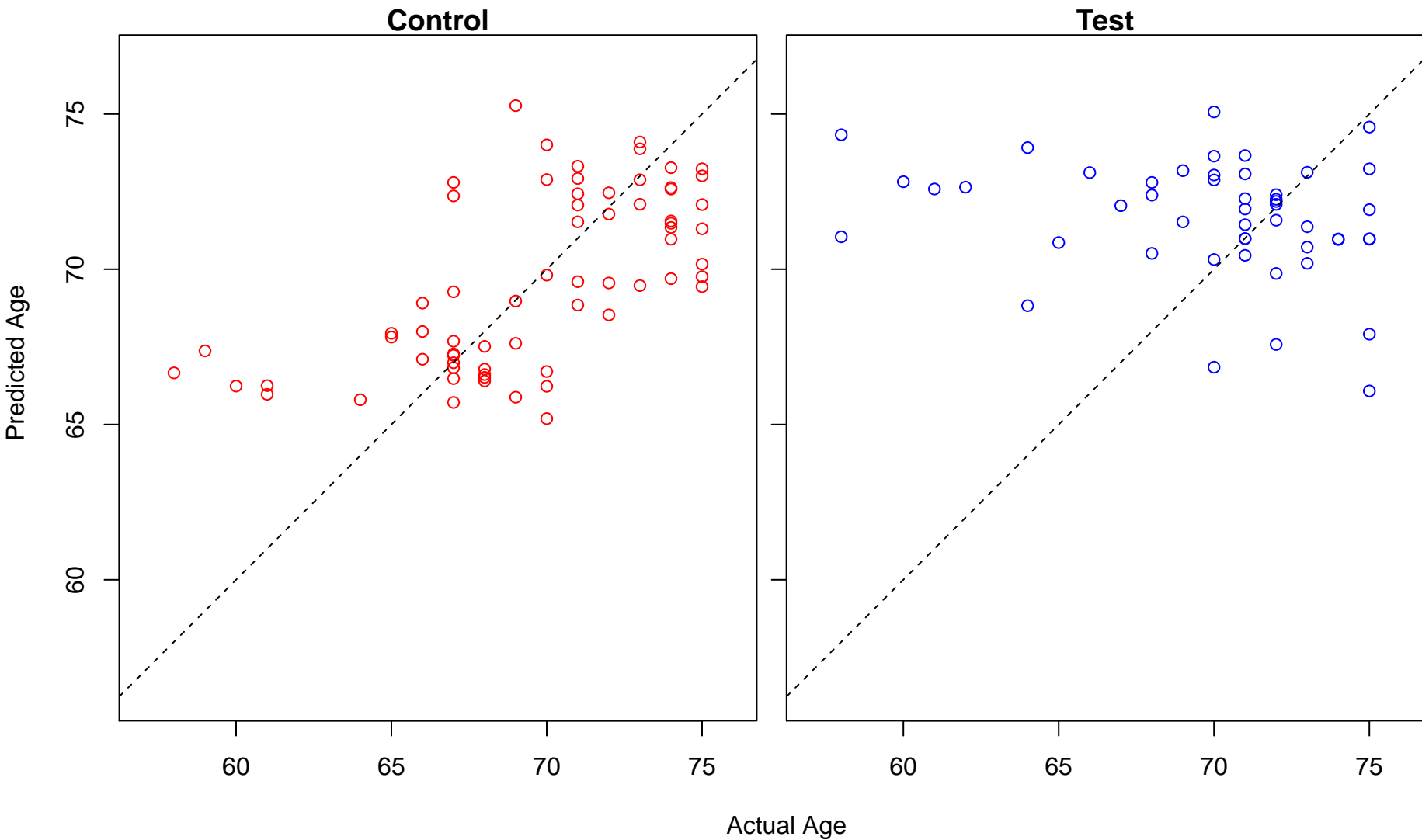


Actual Age

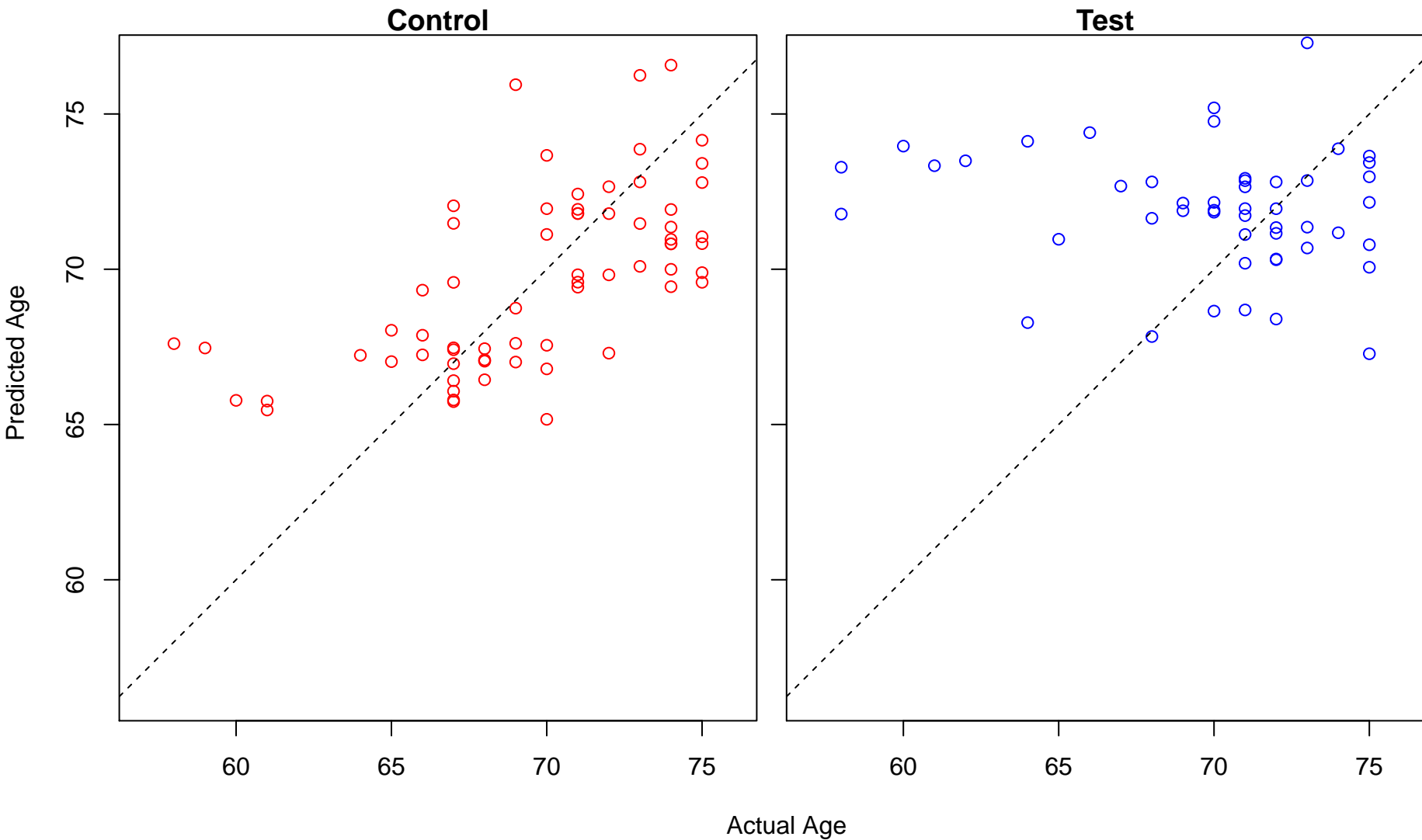
DNA damage response, detection of DNA damage (Score: 1.185773)



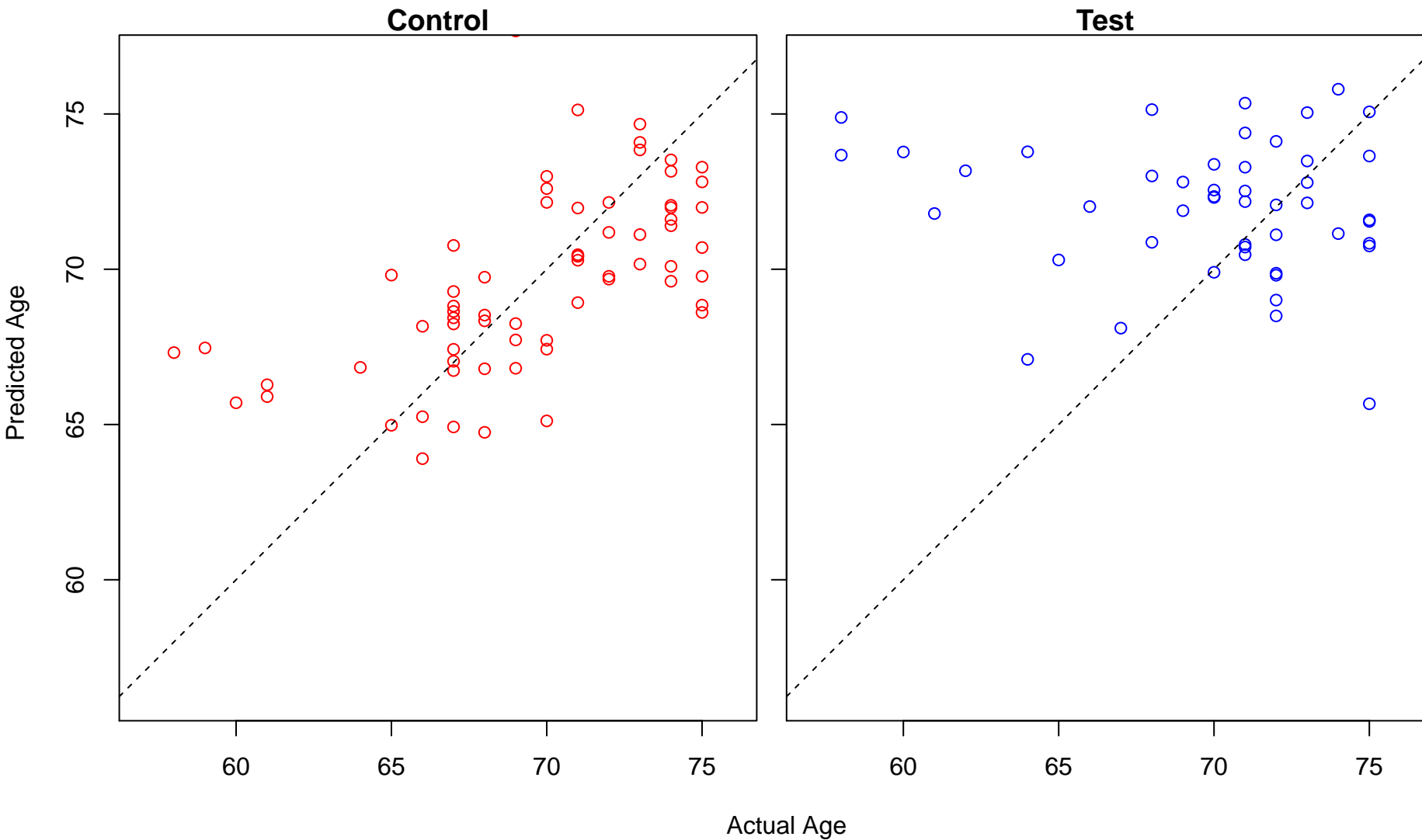
negative regulation of endothelial cell migration (Score: 1.185754)



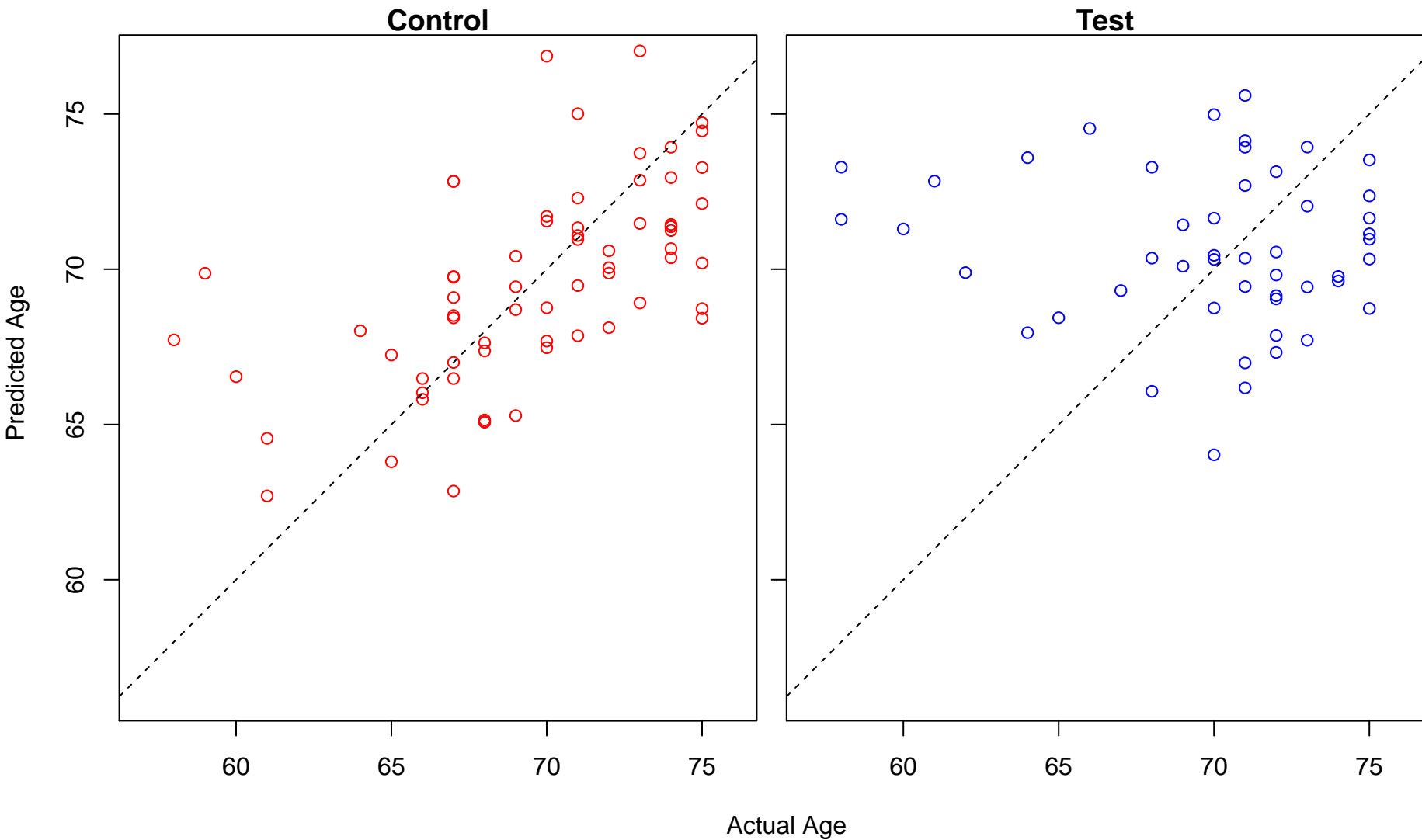
myelin maintenance (Score: 1.185576)



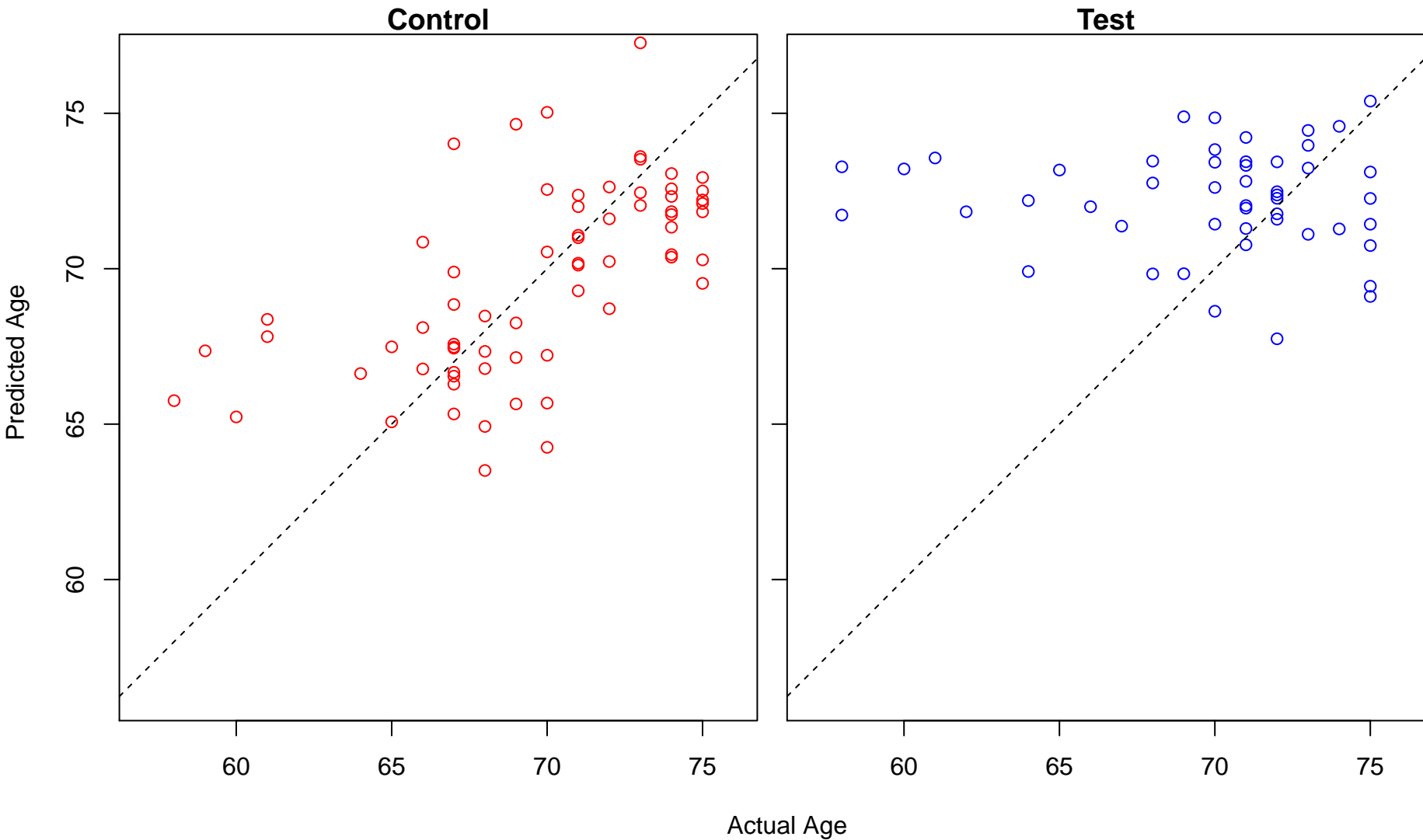
mesenchymal cell development (Score: 1.185212)



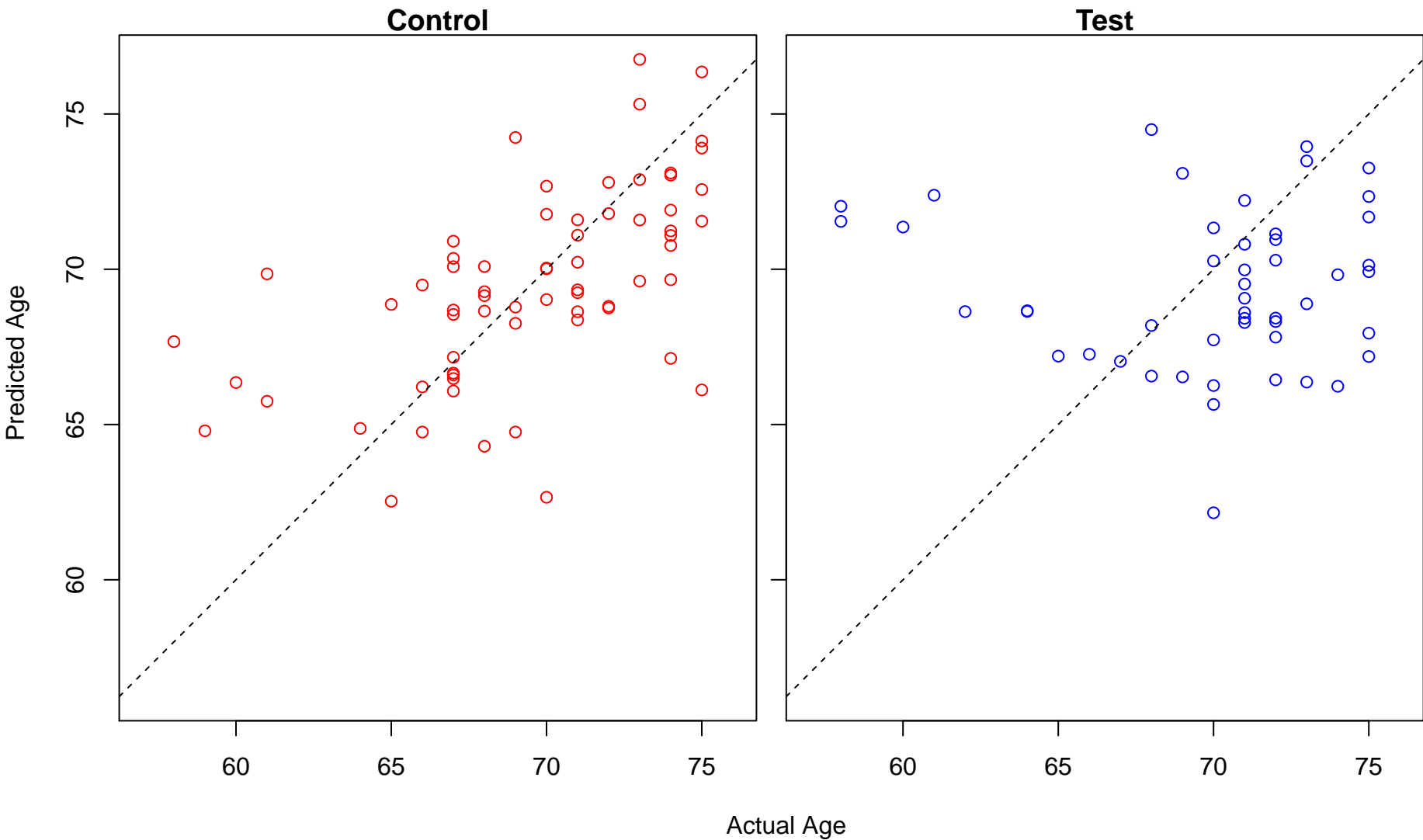
guanosine-containing compound metabolic process (Score: 1.184438)



double-strand break repair via synthesis-dependent strand annealing (Score: 1.183966)

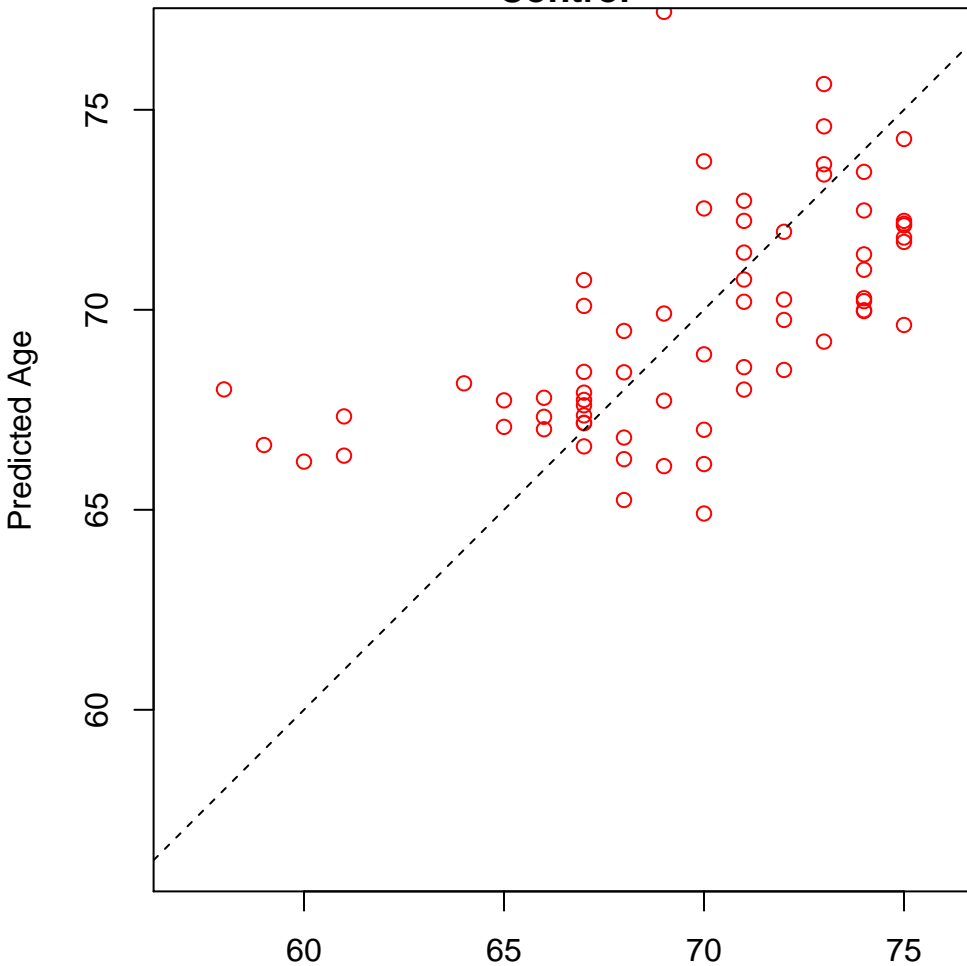


tion of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell

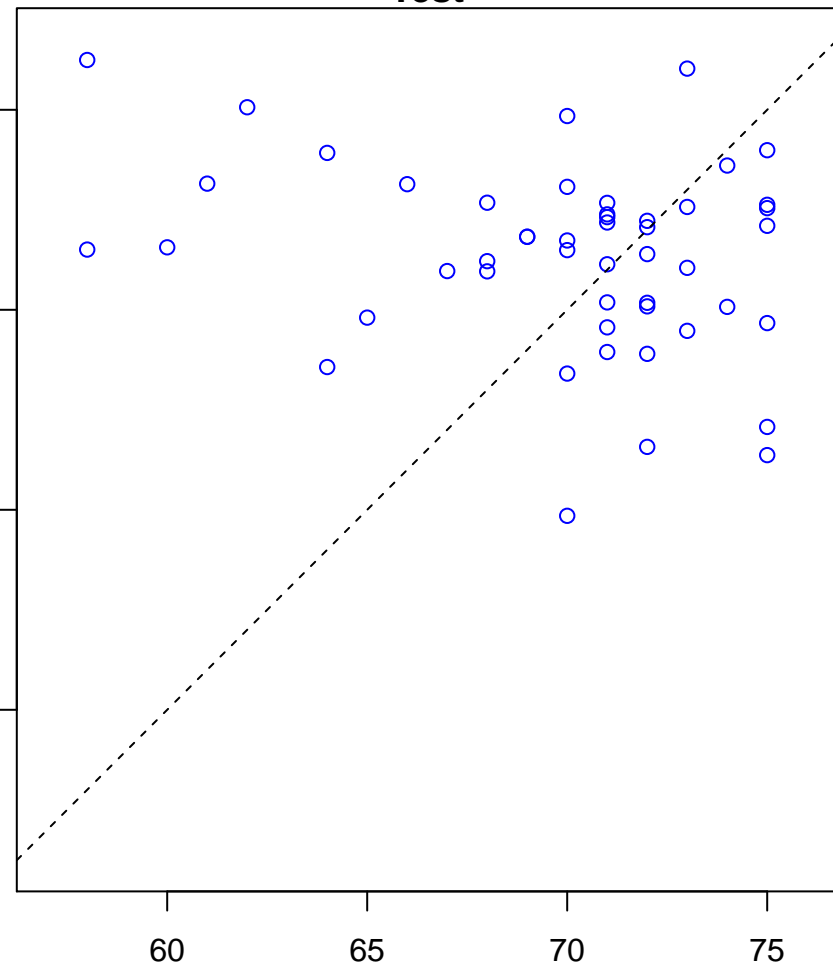


cellular response to estrogen stimulus (Score: 1.183554)

Control

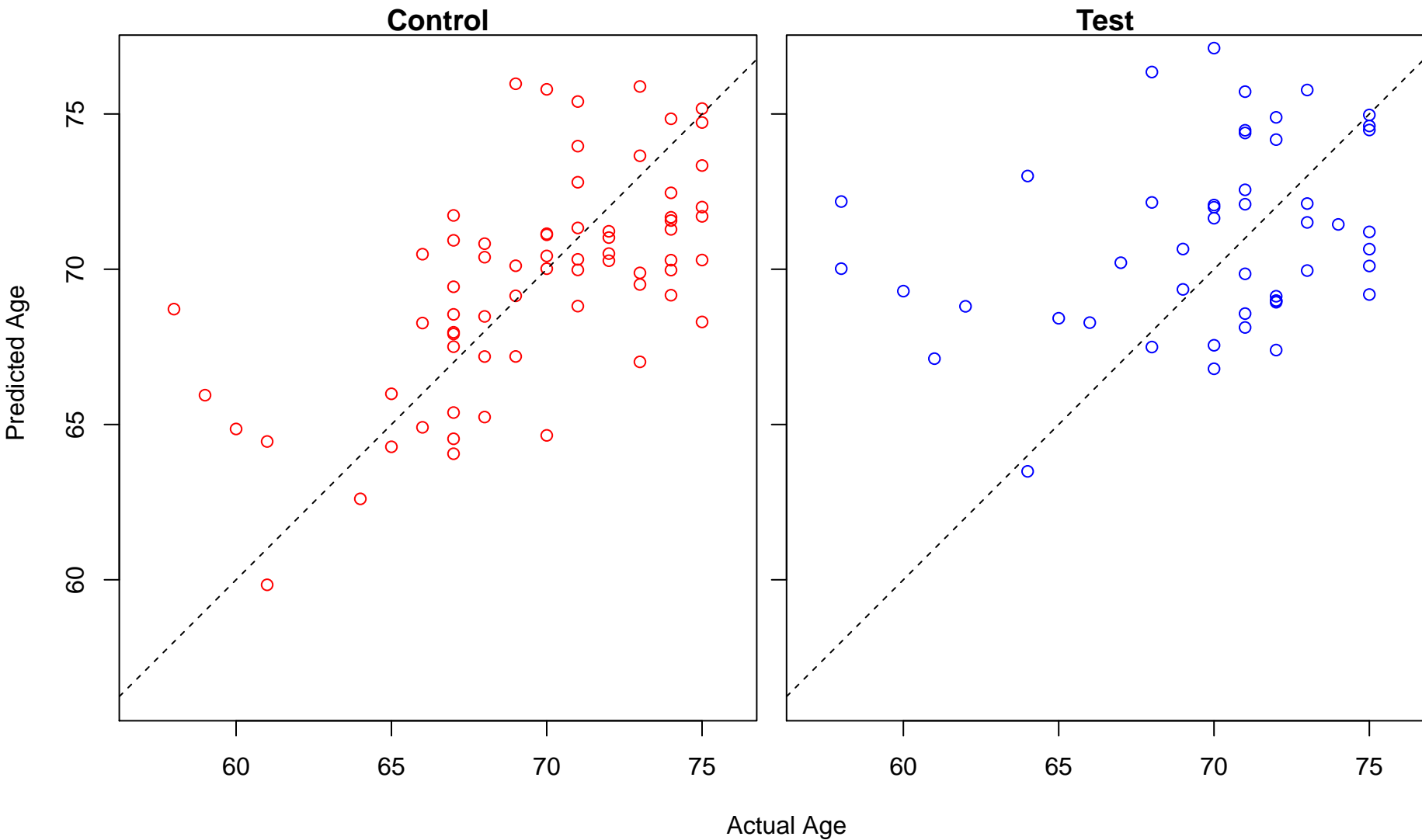


Test

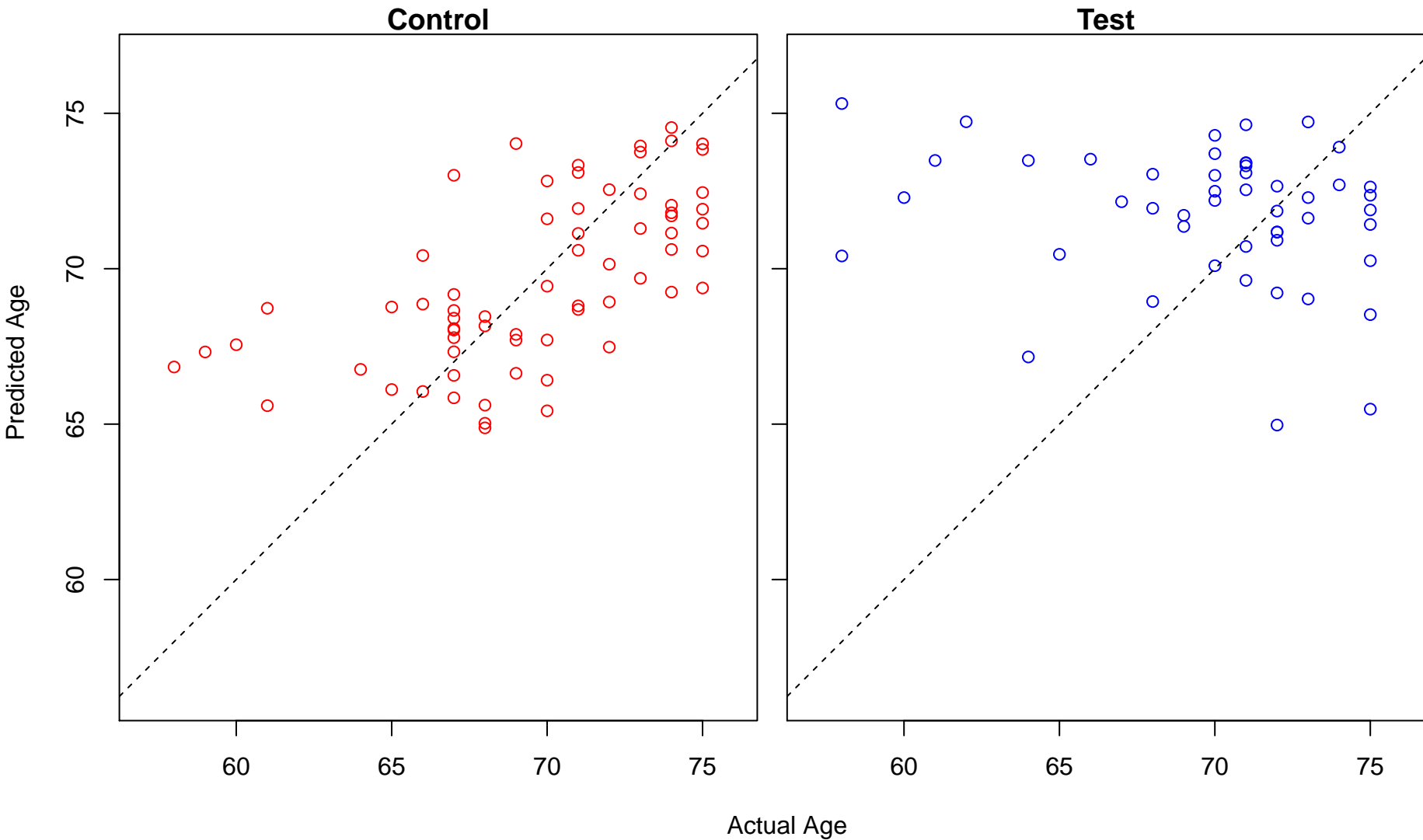


Actual Age

regionalization (Score: 1.182121)

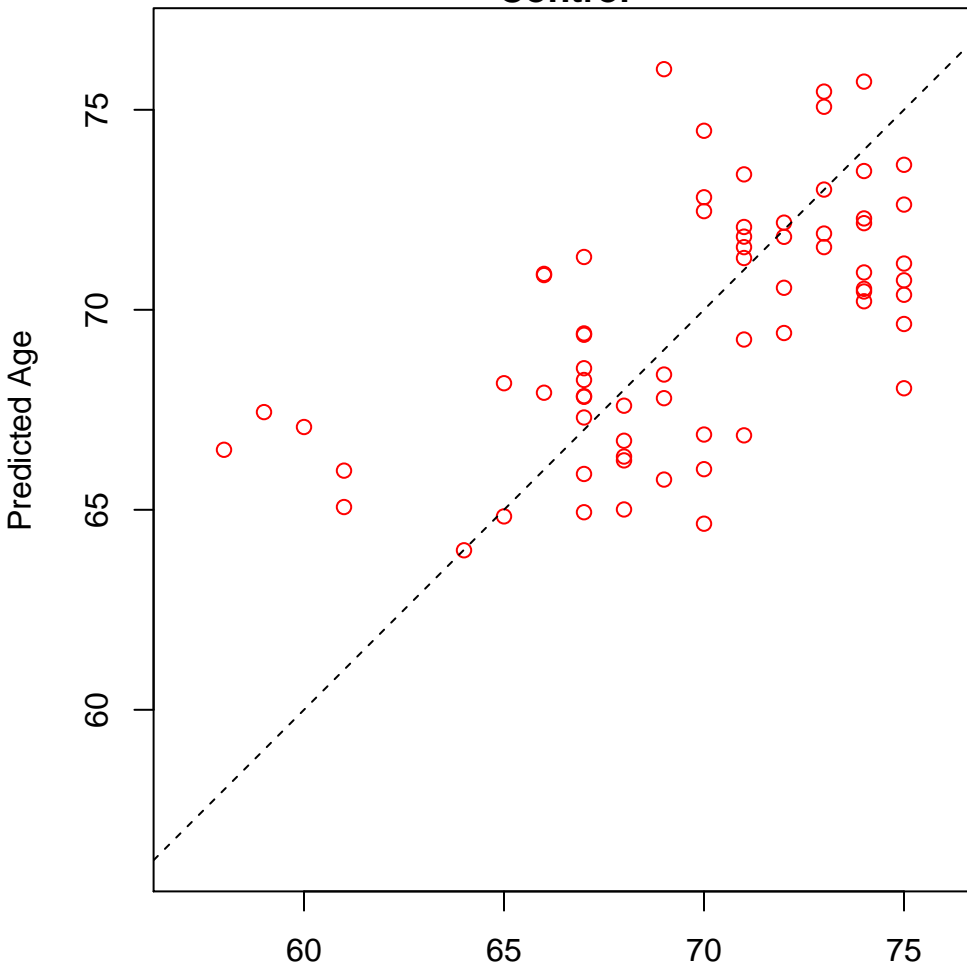


positive regulation of protein sumoylation (Score: 1.180988)

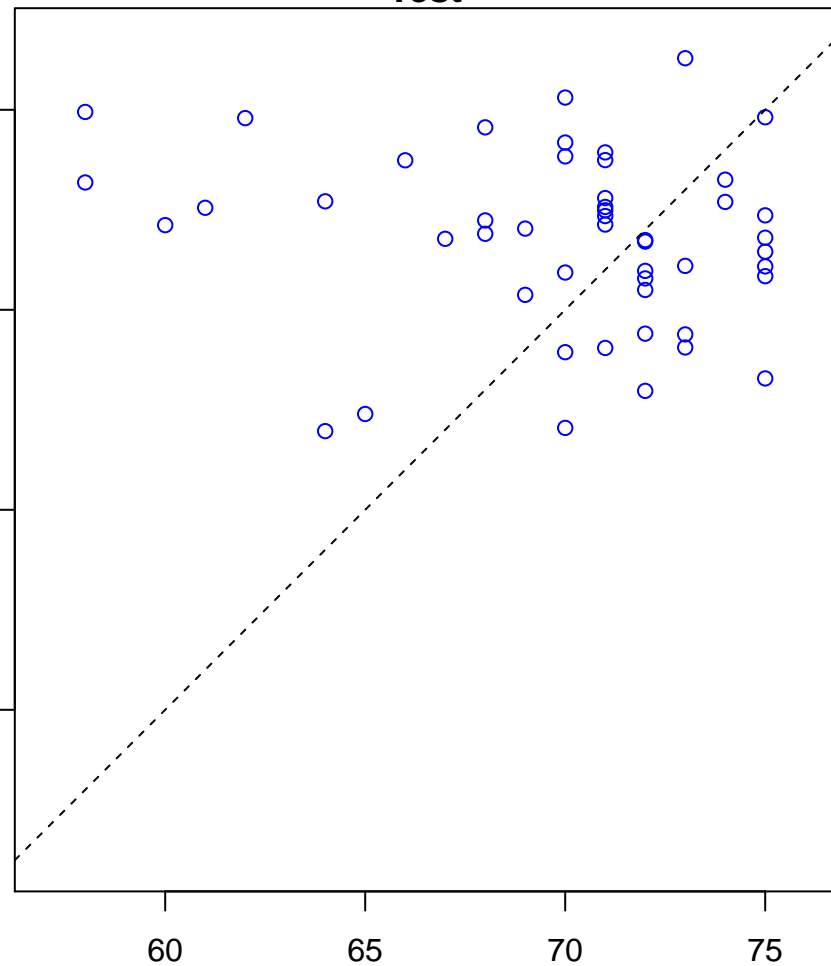


organelle transport along microtubule (Score: 1.180616)

Control

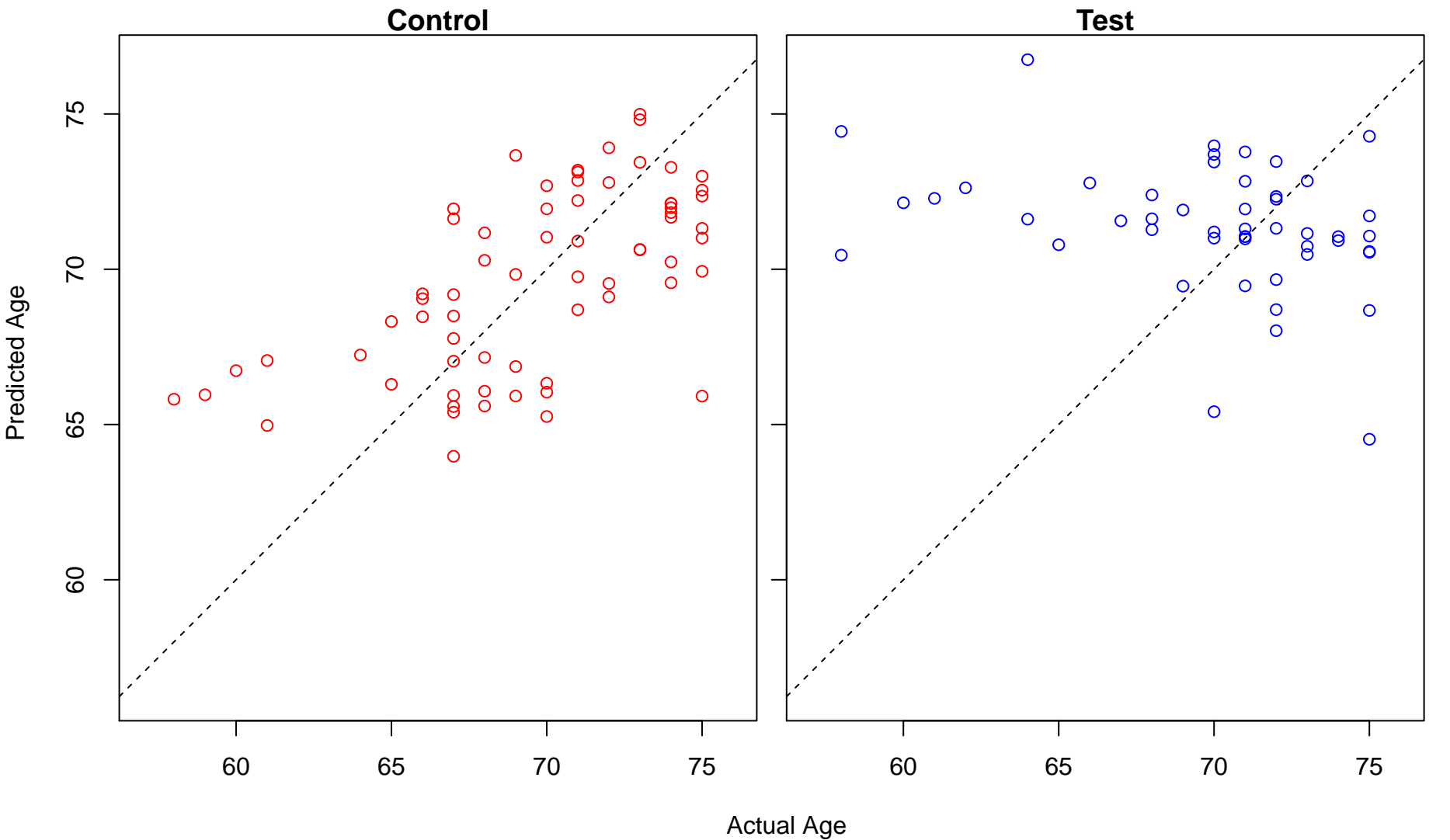


Test

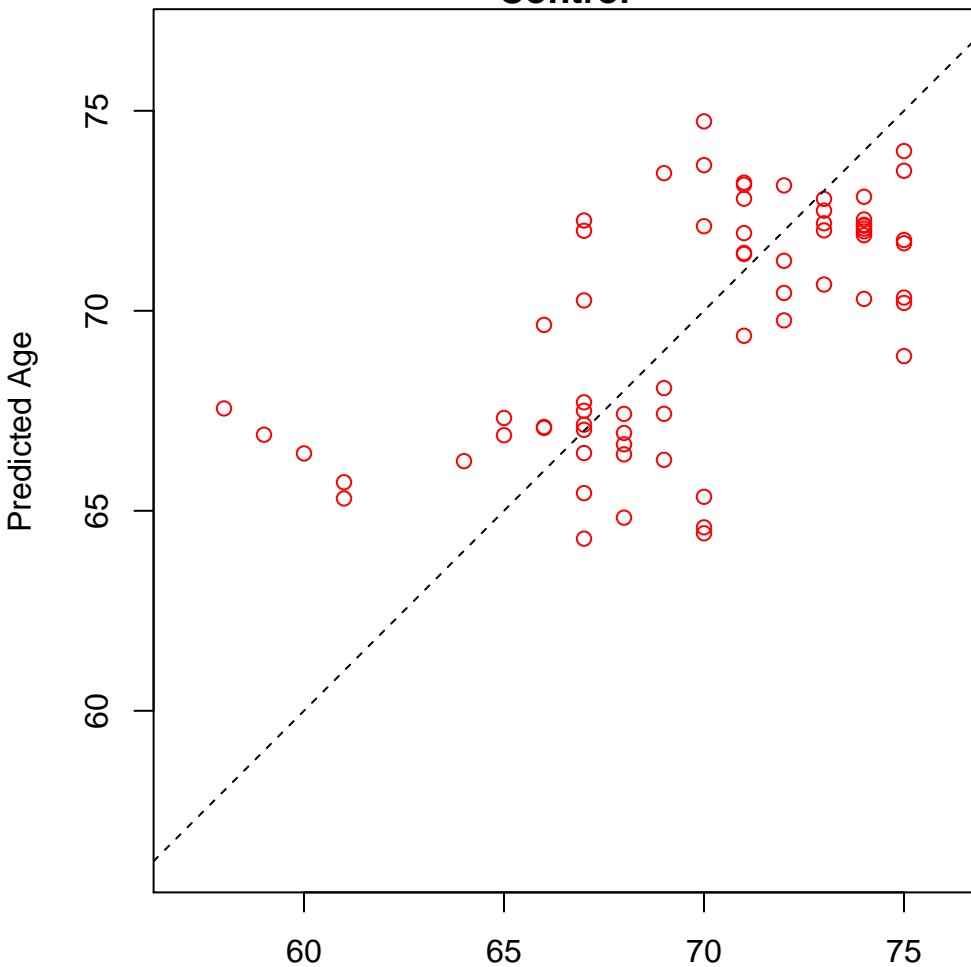


Actual Age

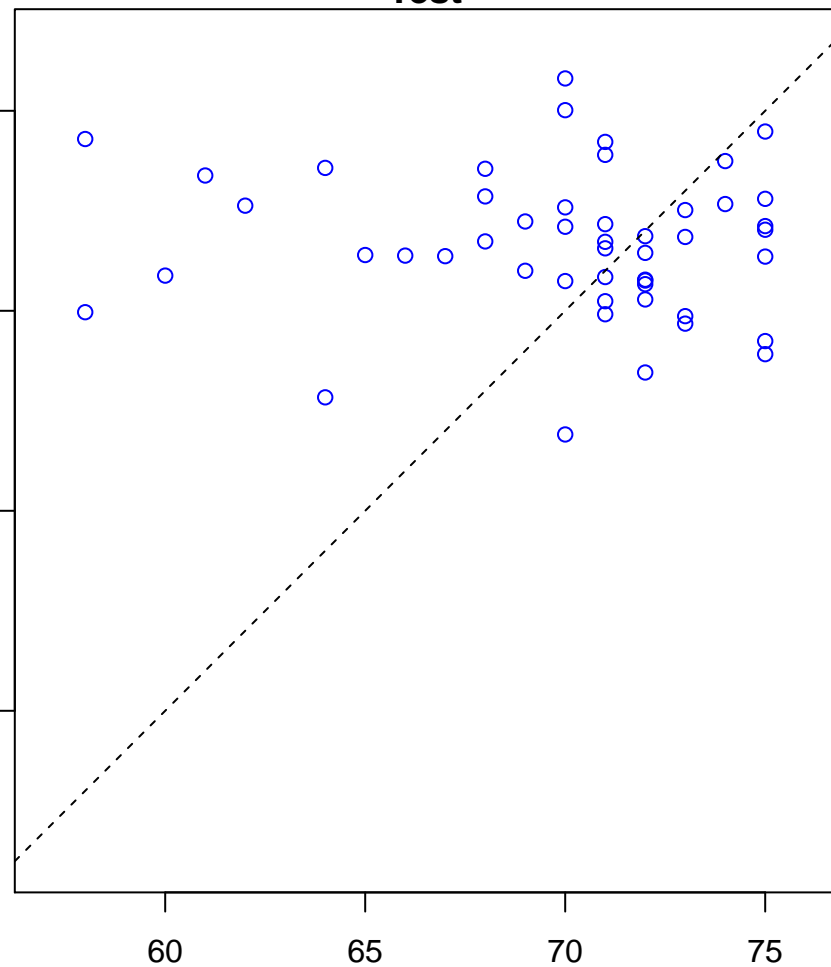
Negative regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis (Score: 1)



Control

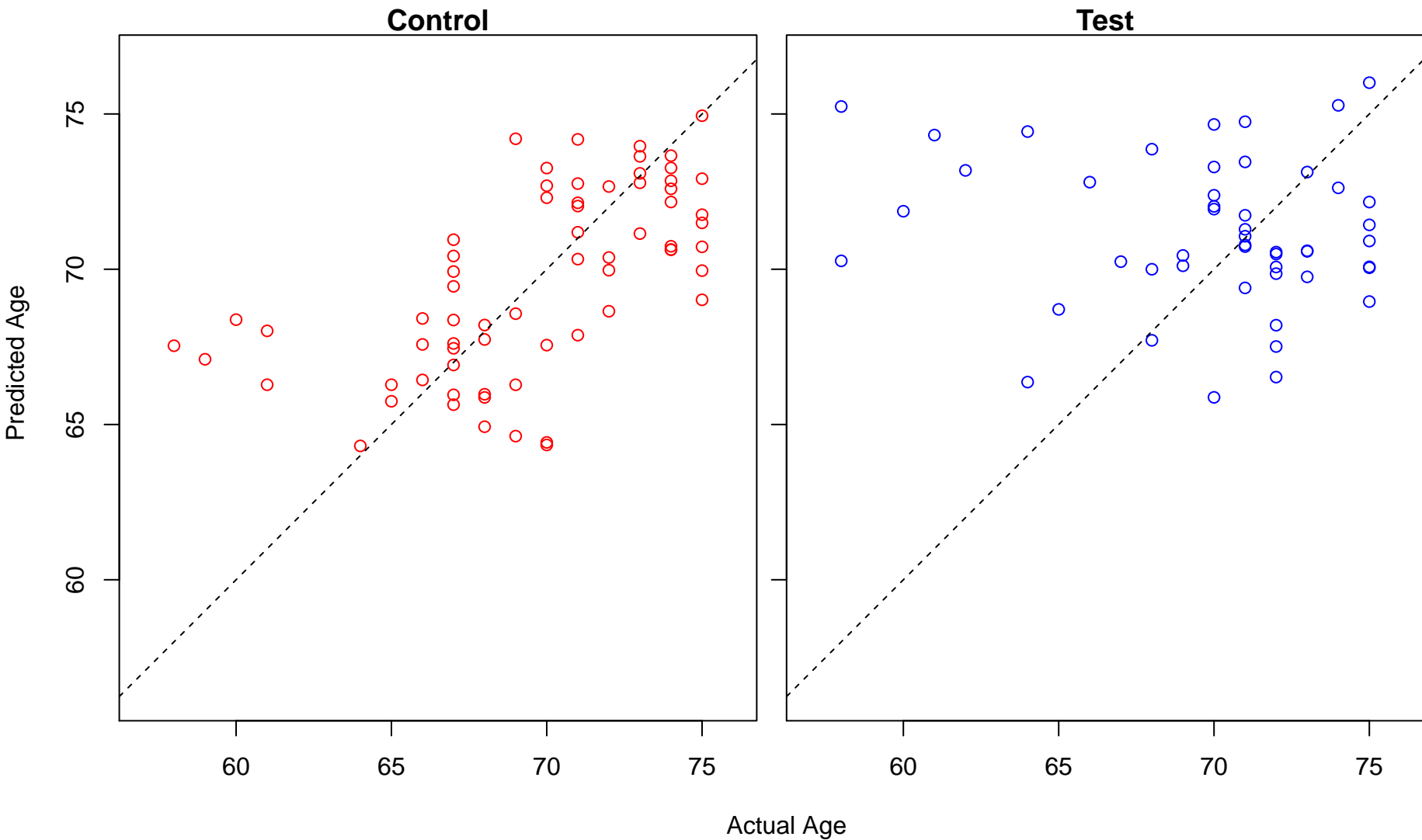


Test

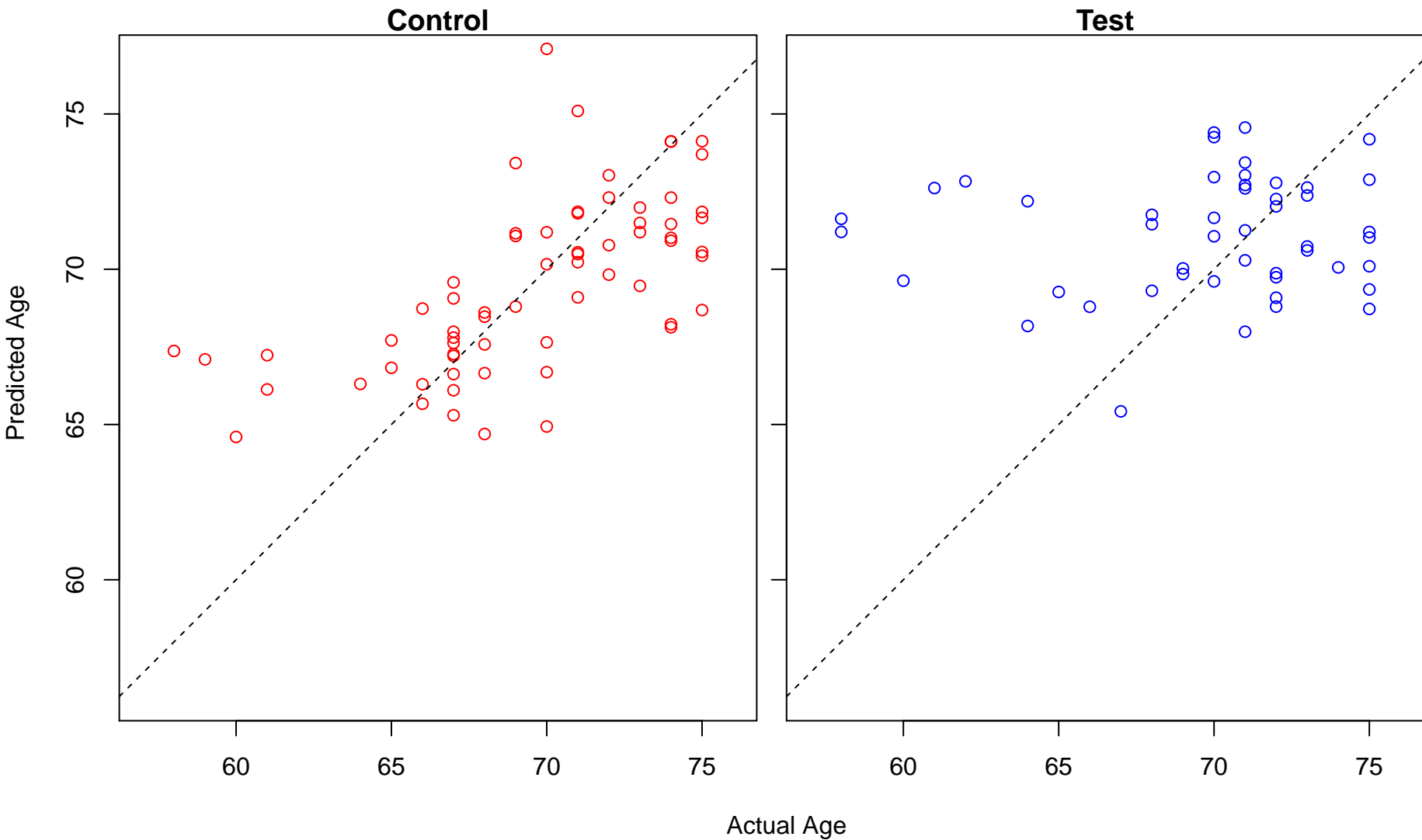


Actual Age

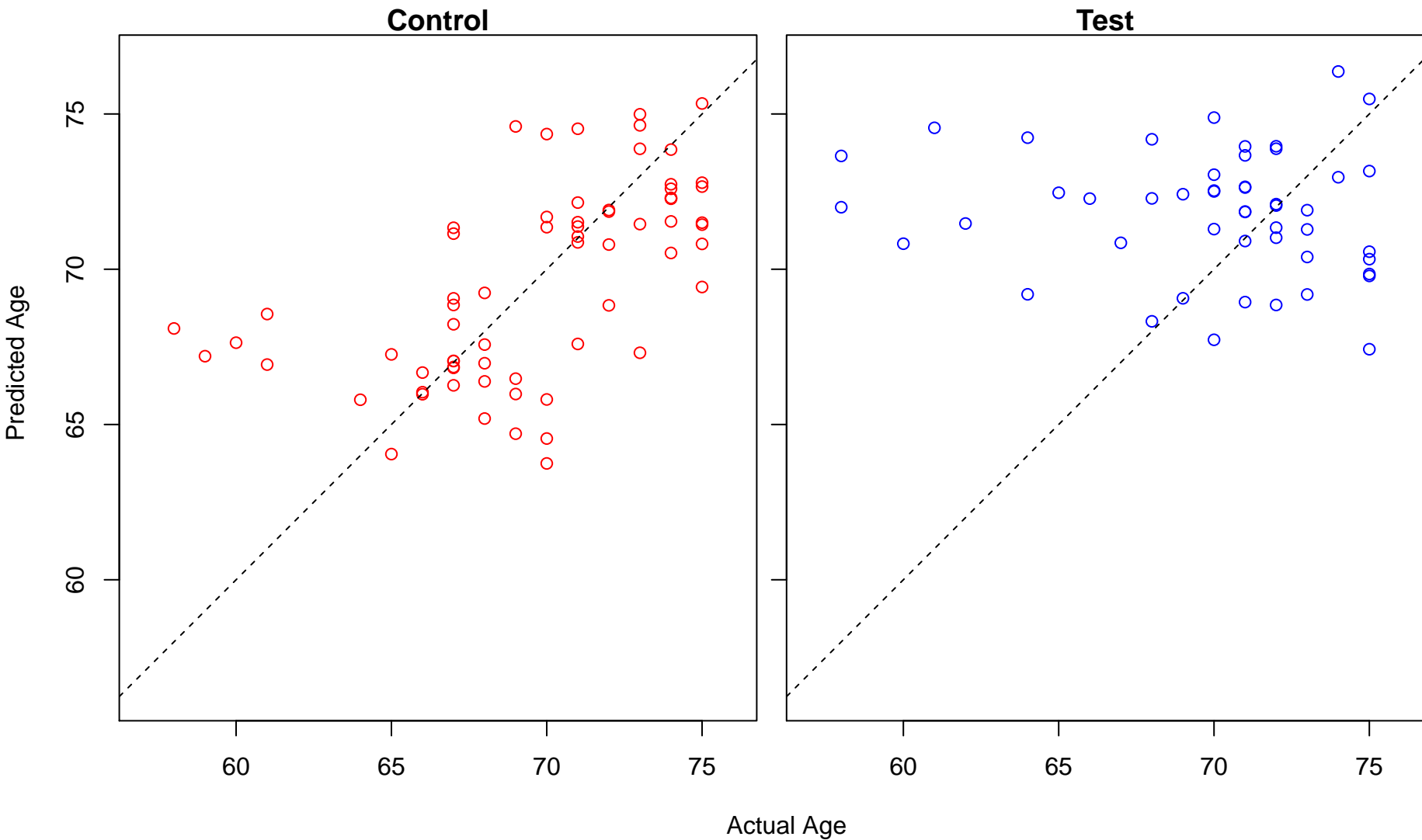
peptidyl-threonine modification (Score: 1.179711)



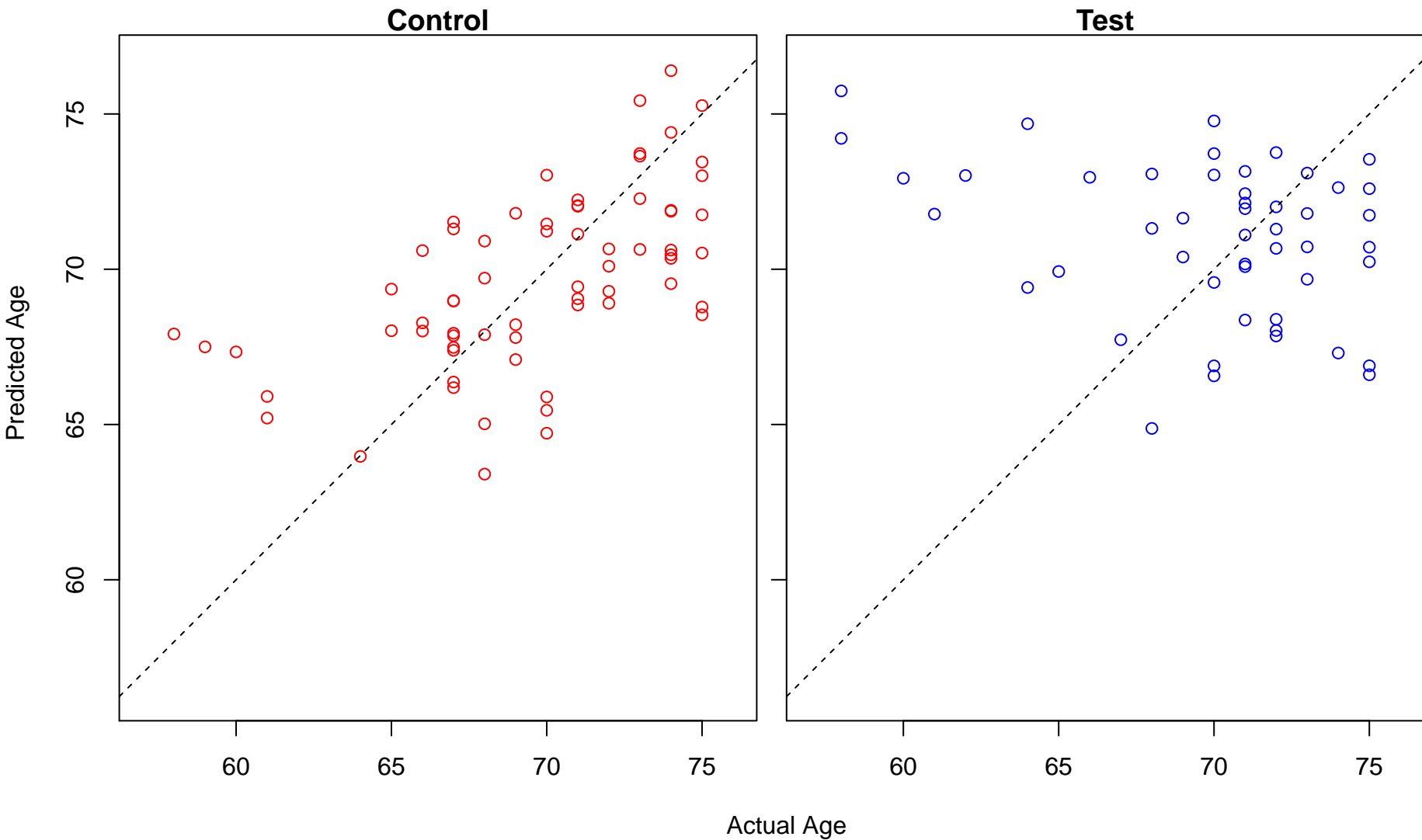
respiratory burst (Score: 1.179613)



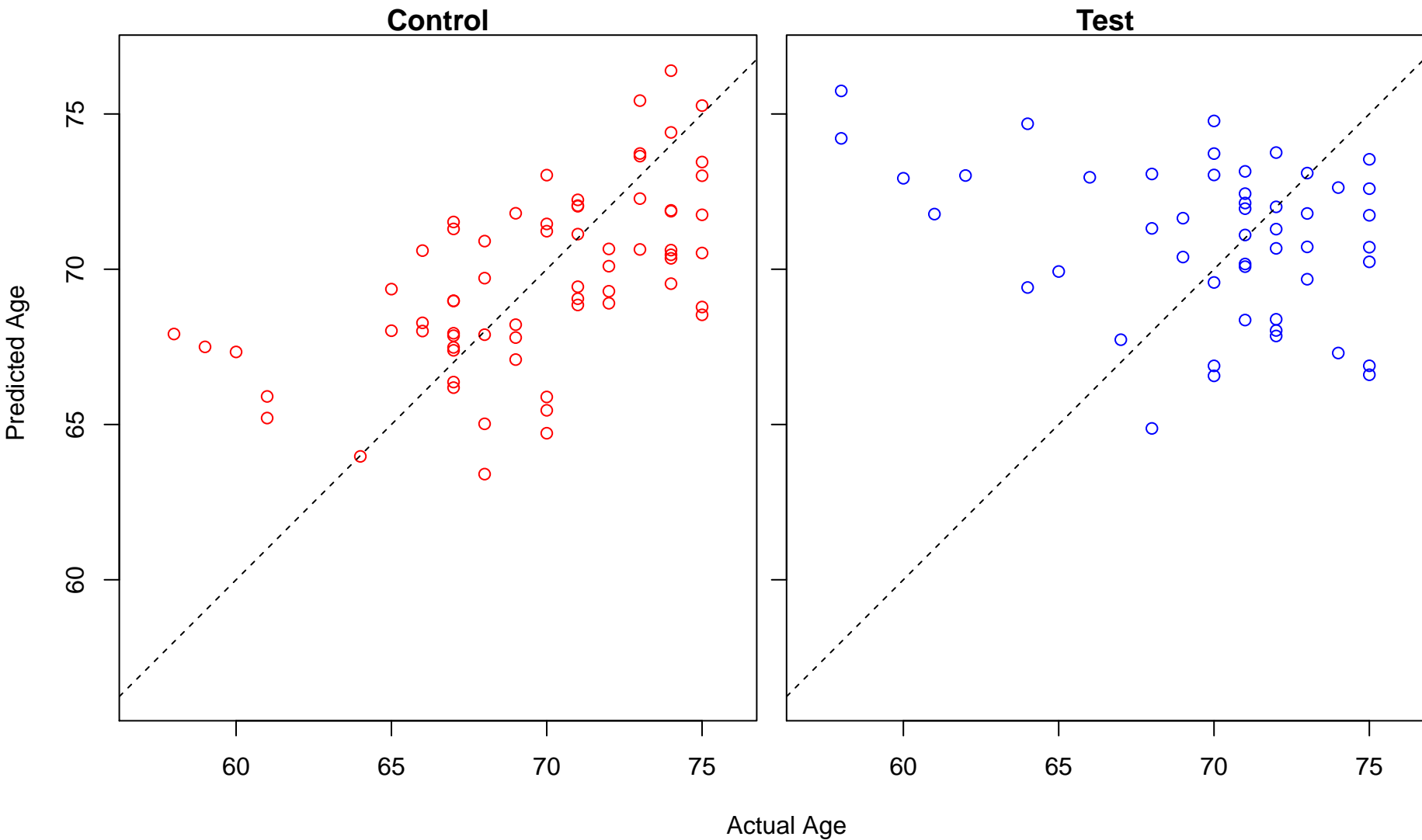
negative regulation of cellular protein localization (Score: 1.178597)



protein targeting to vacuole (Score: 1.178172)

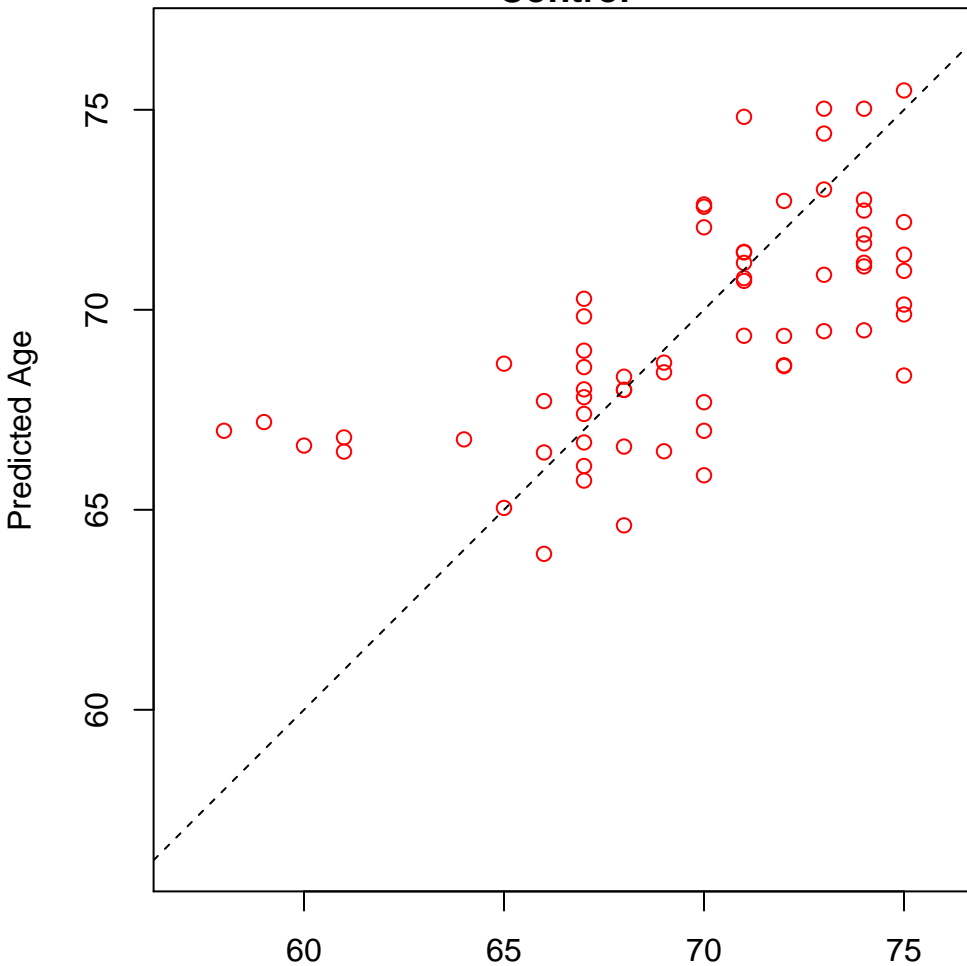


establishment of protein localization to vacuole (Score: 1.178172)

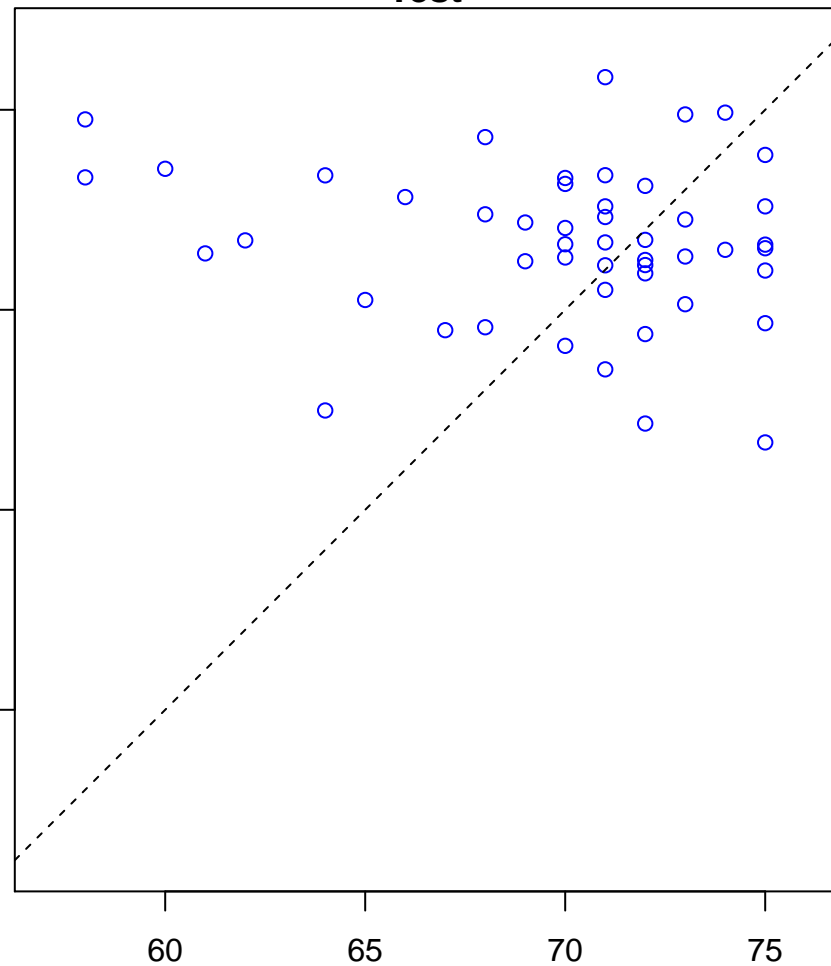


mesenchymal cell differentiation (Score: 1.177988)

Control

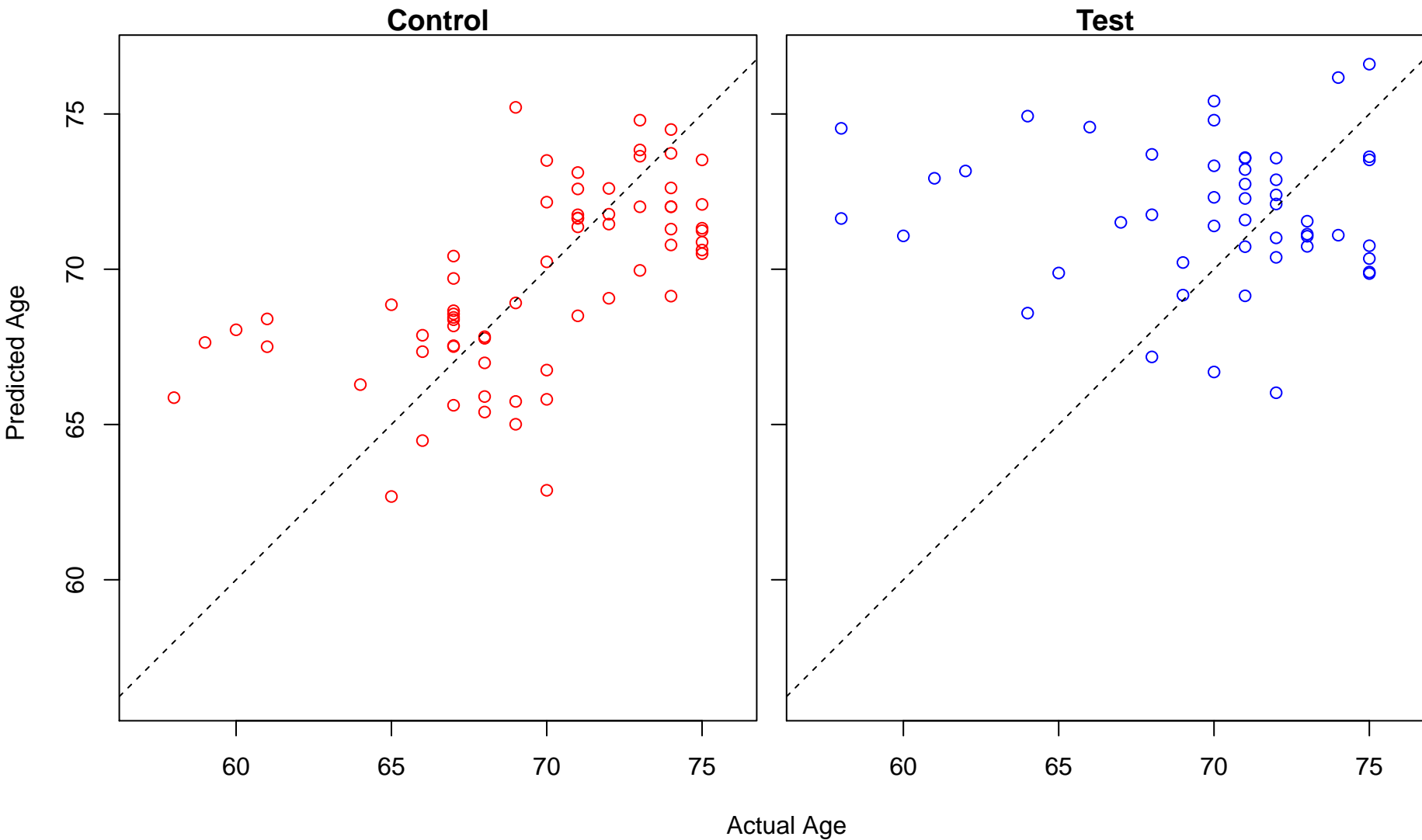


Test

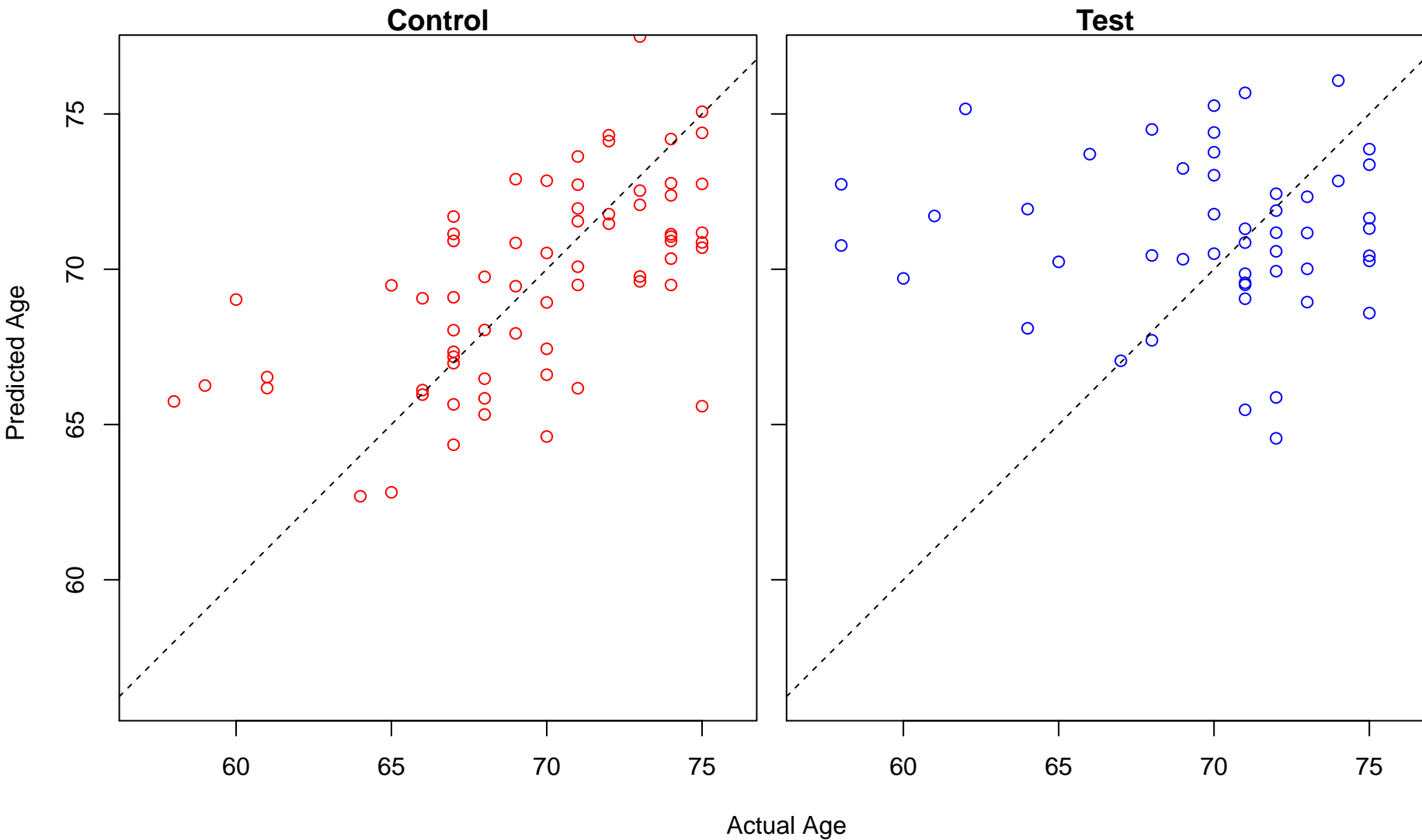


Actual Age

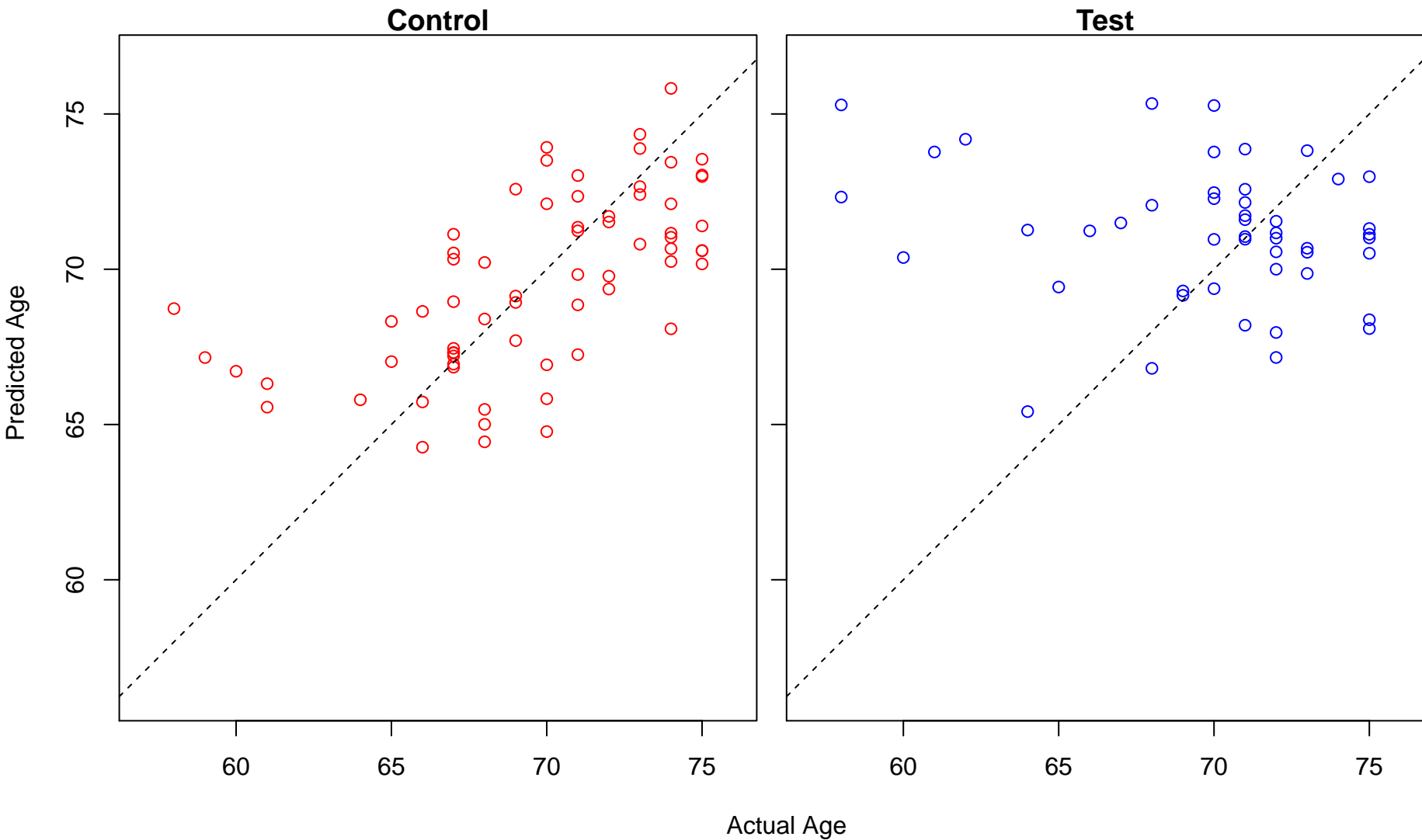
establishment or maintenance of cell polarity (Score: 1.177441)



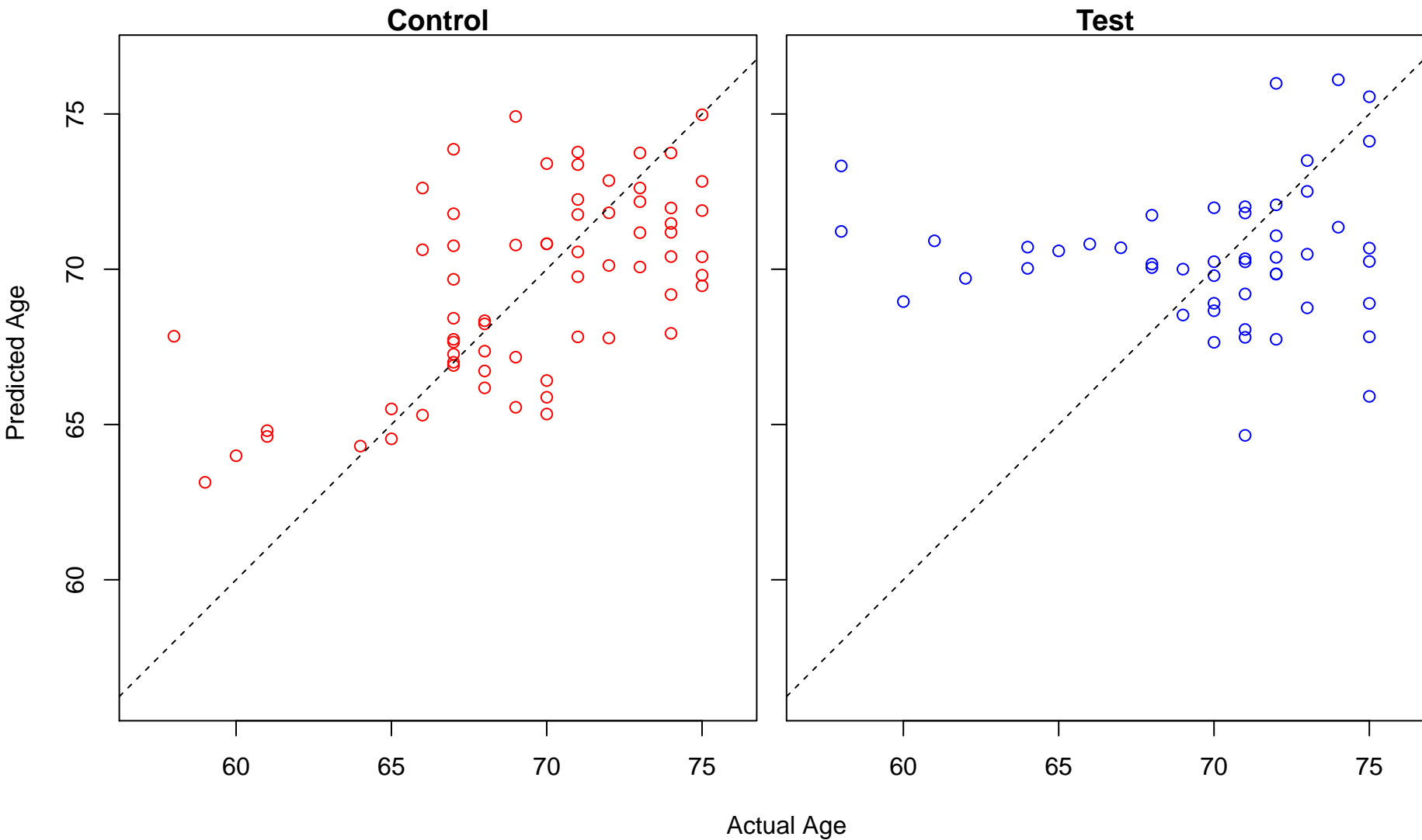
regulation of heterotypic cell-cell adhesion (Score: 1.177073)



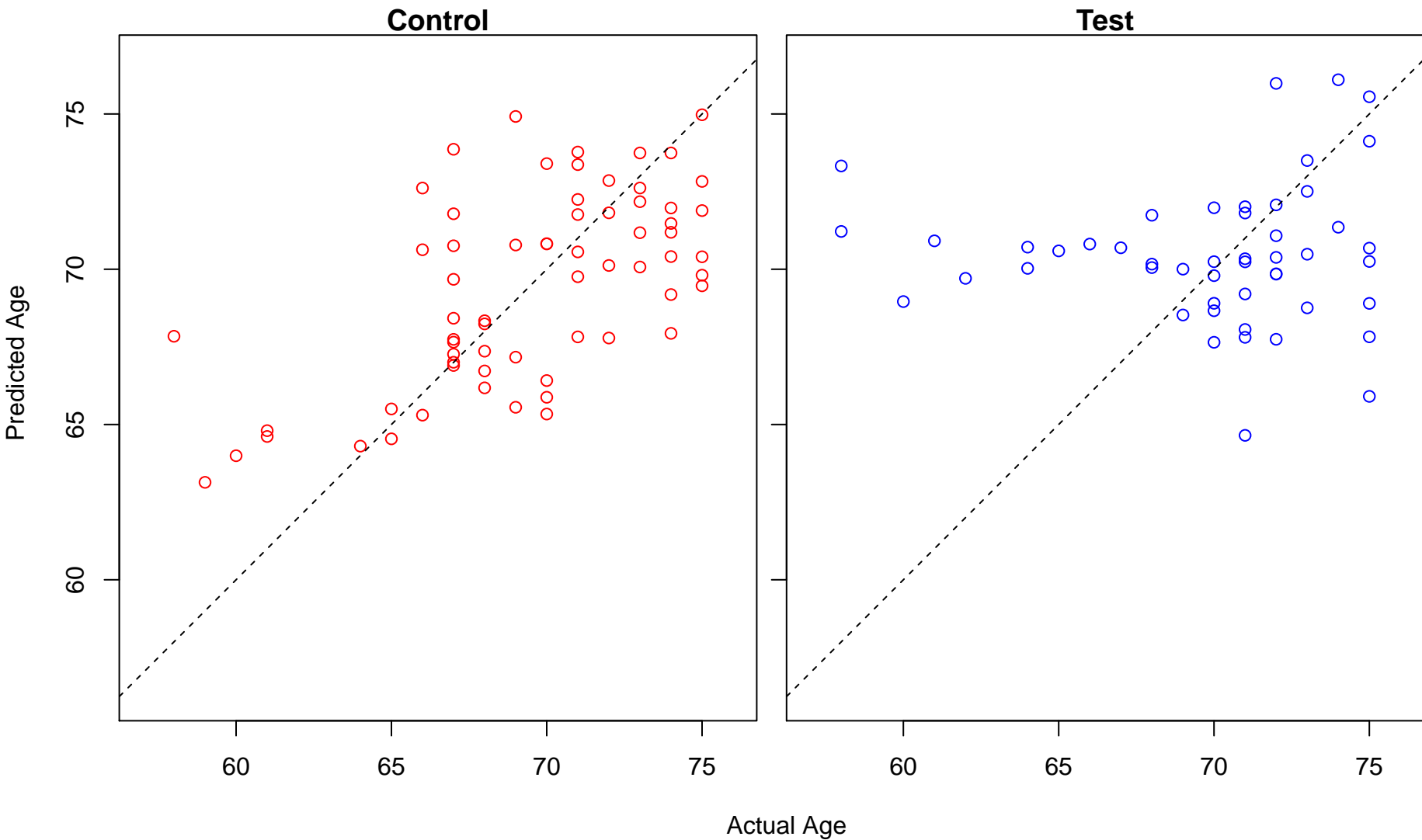
positive regulation of DNA-templated transcription, elongation (Score: 1.176744)



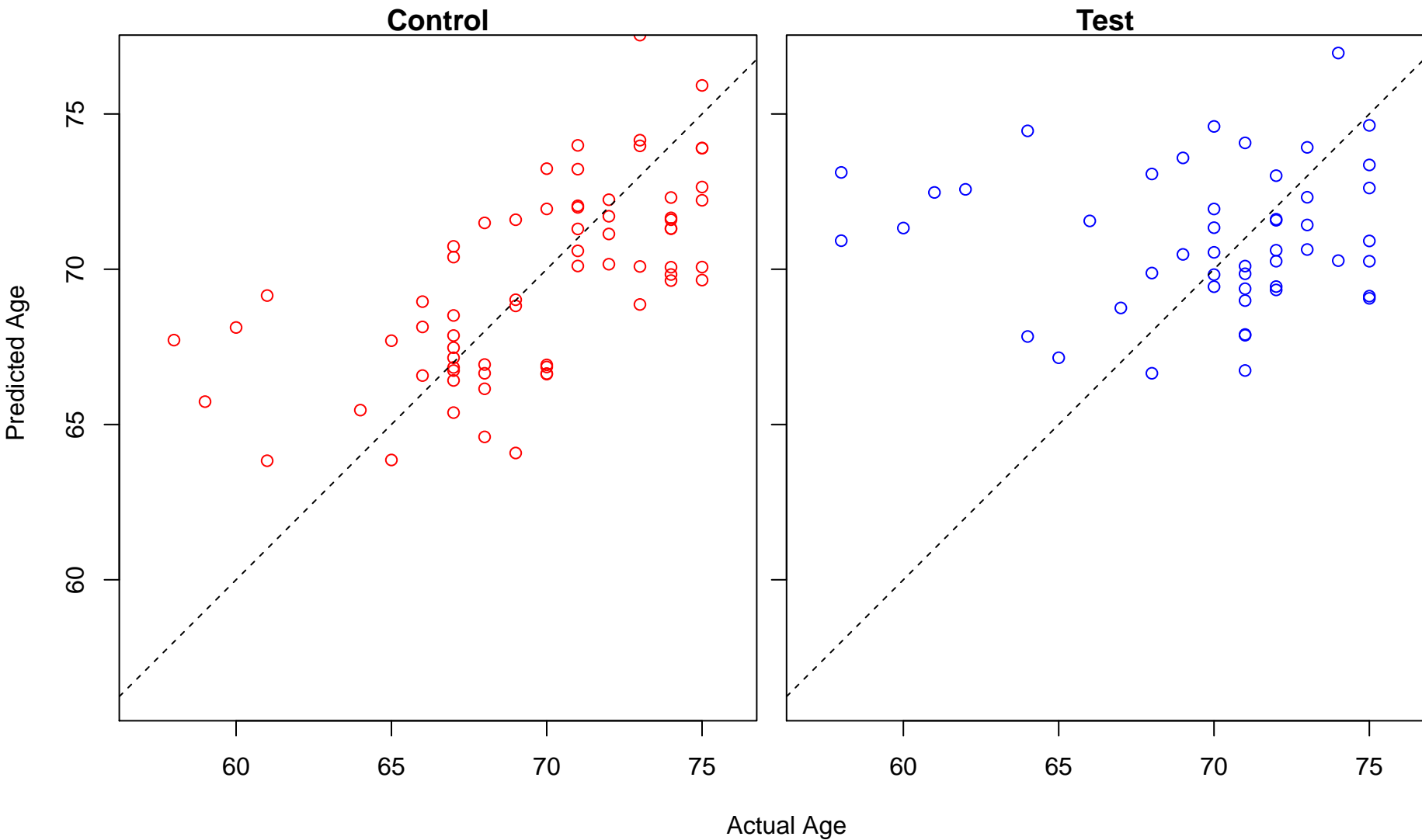
positive regulation of transforming growth factor beta receptor signaling pathway (Score: 1.176473)



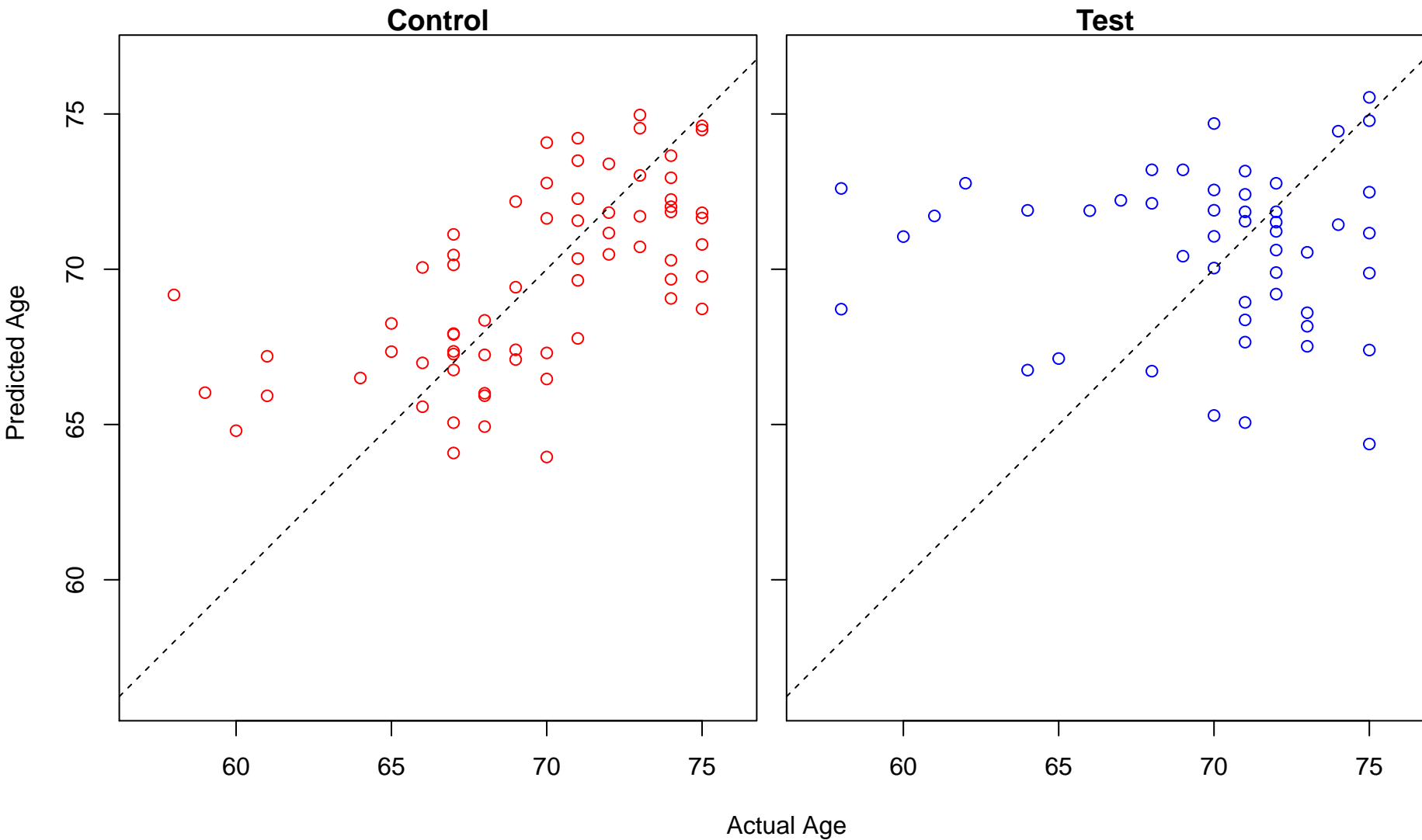
positive regulation of cellular response to transforming growth factor beta stimulus (Score: 1.17647)



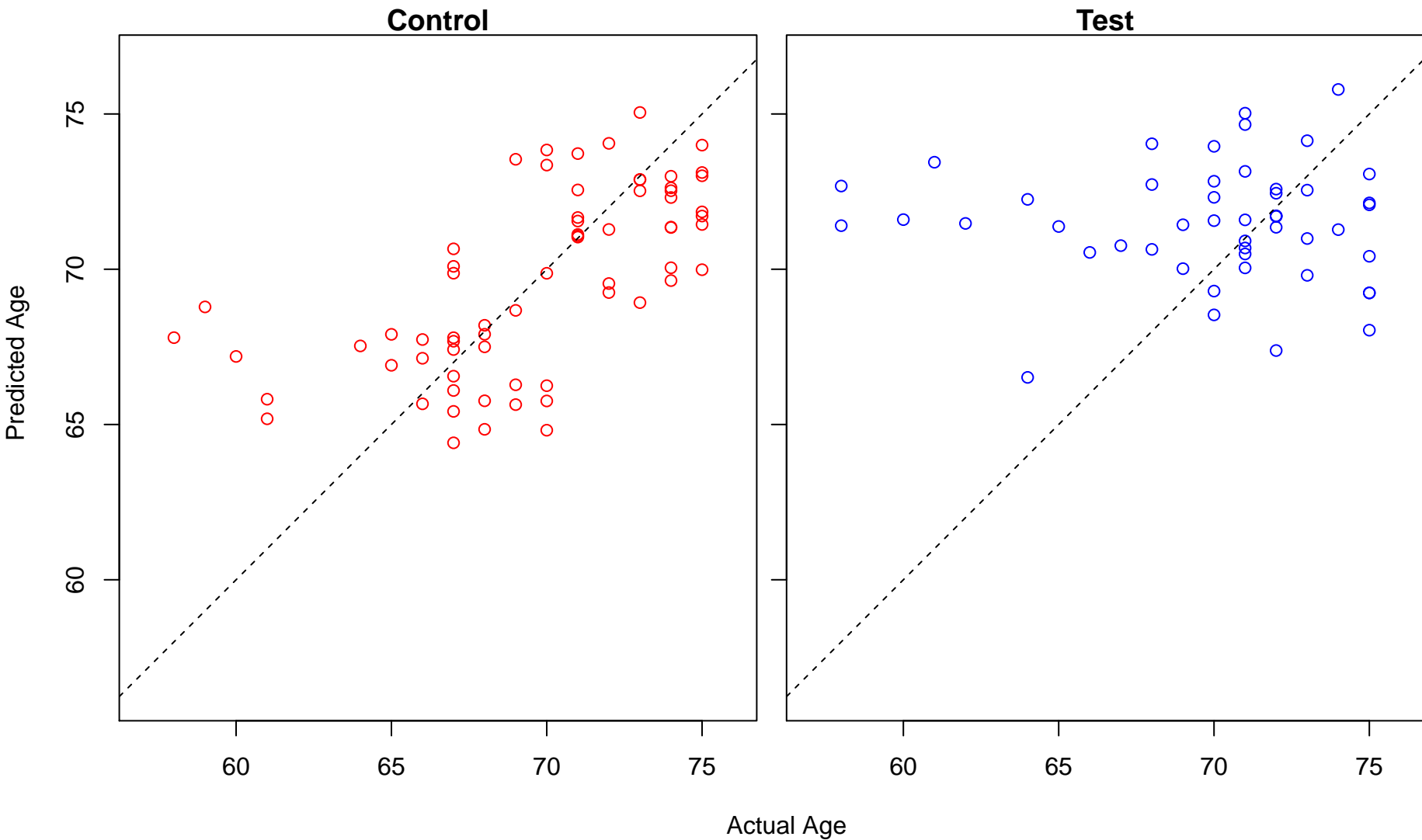
spinal cord development (Score: 1.176023)



innate immune response in mucosa (Score: 1.175510)

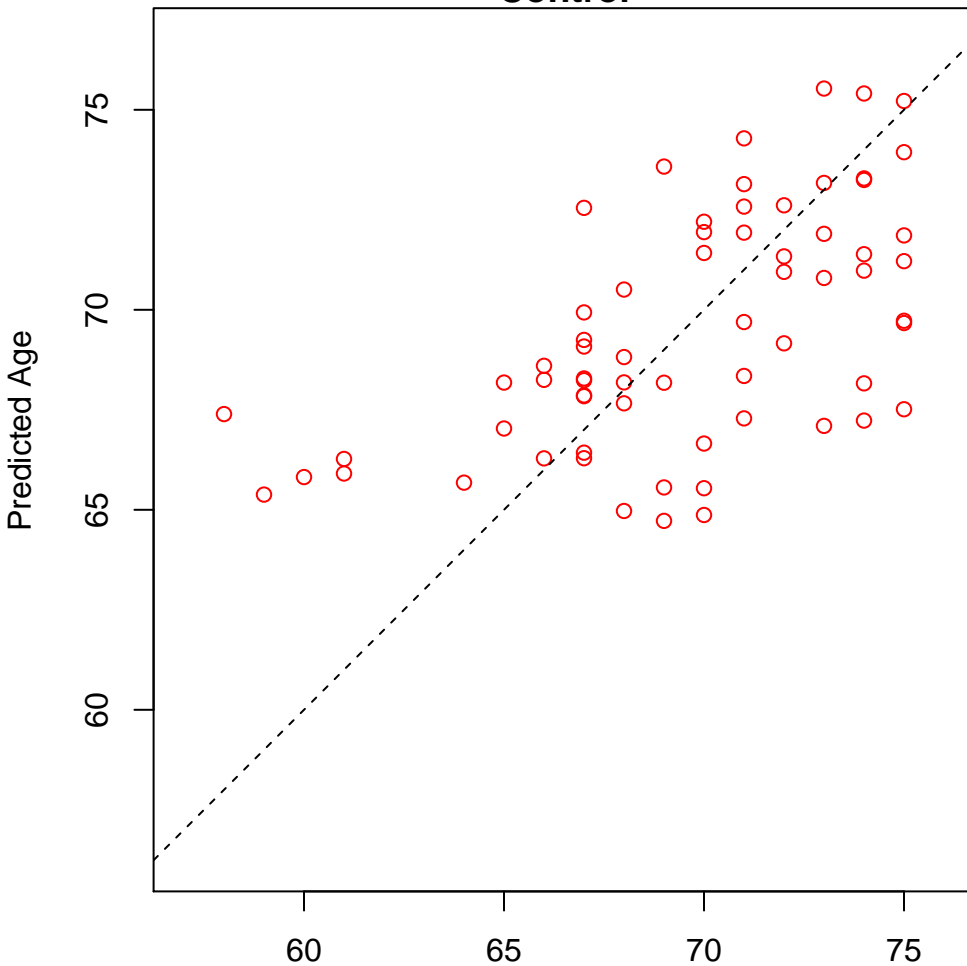


positive regulation of erythrocyte differentiation (Score: 1.175445)

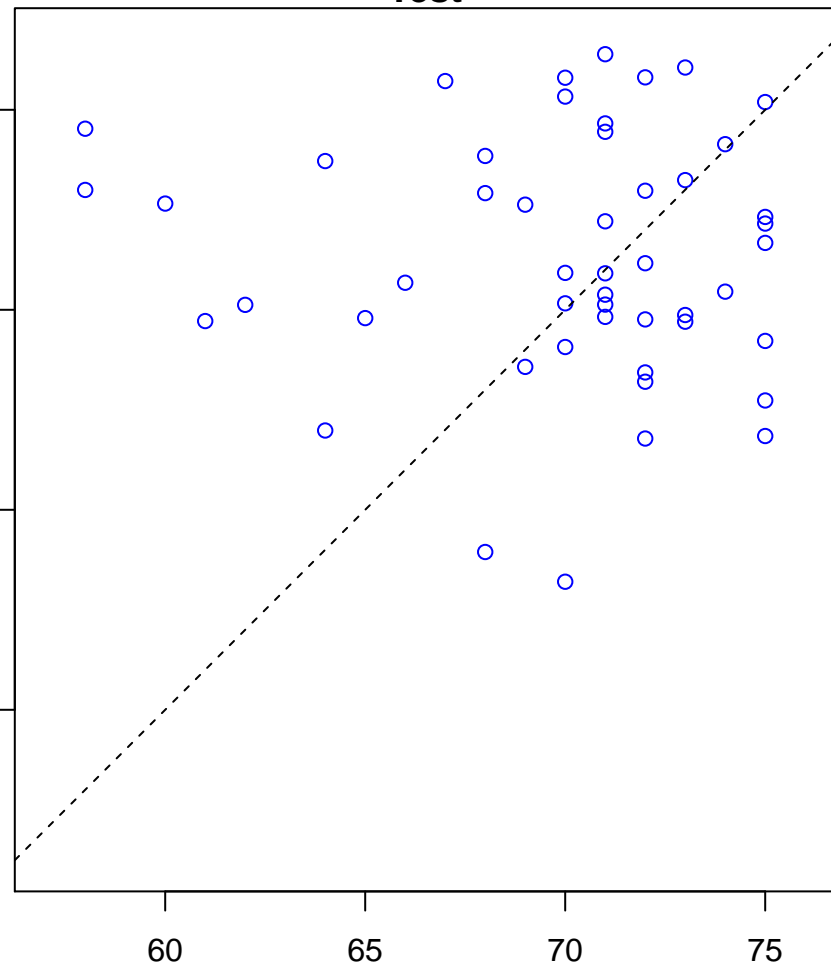


regulation of immunoglobulin production (Score: 1.175349)

Control

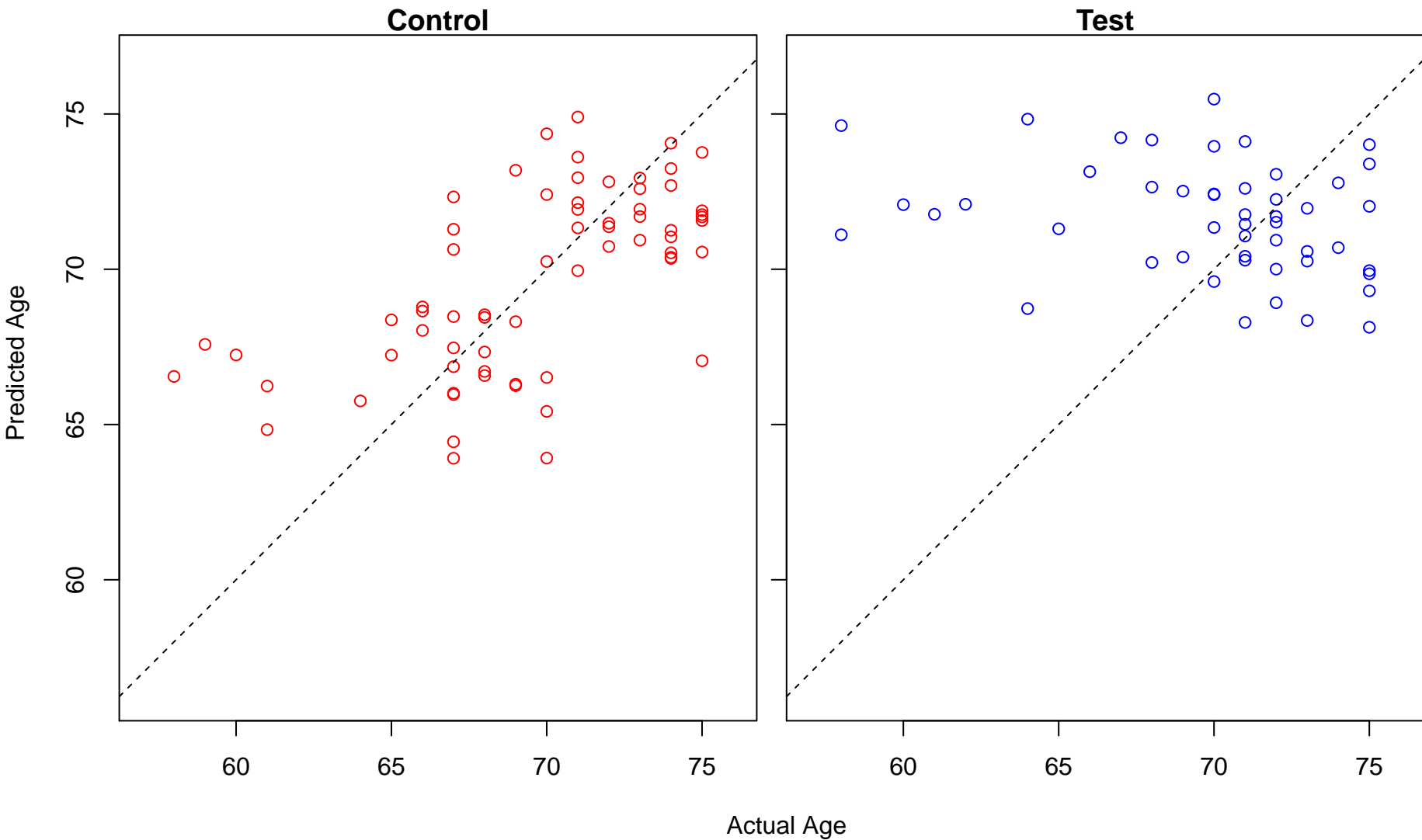


Test

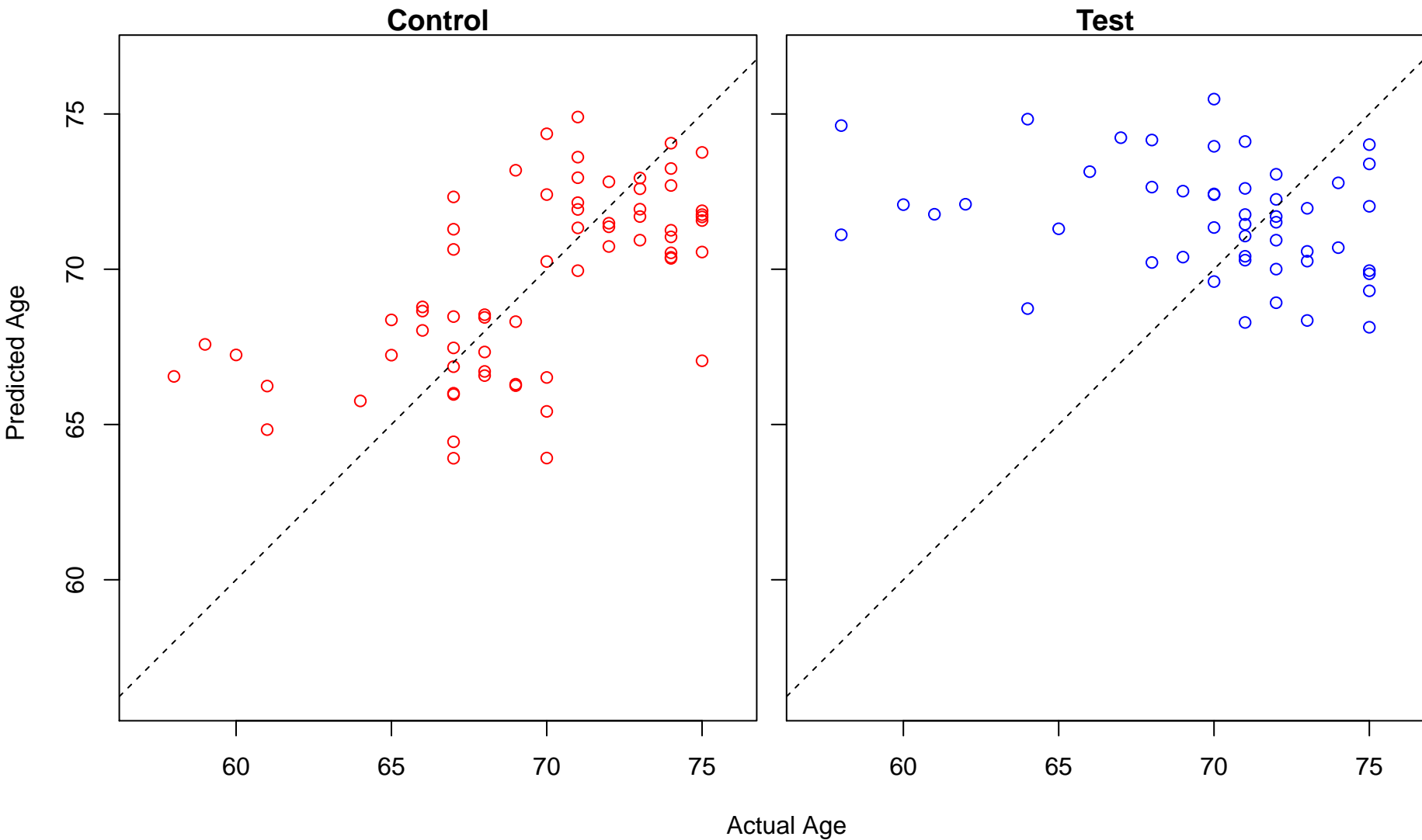


Actual Age

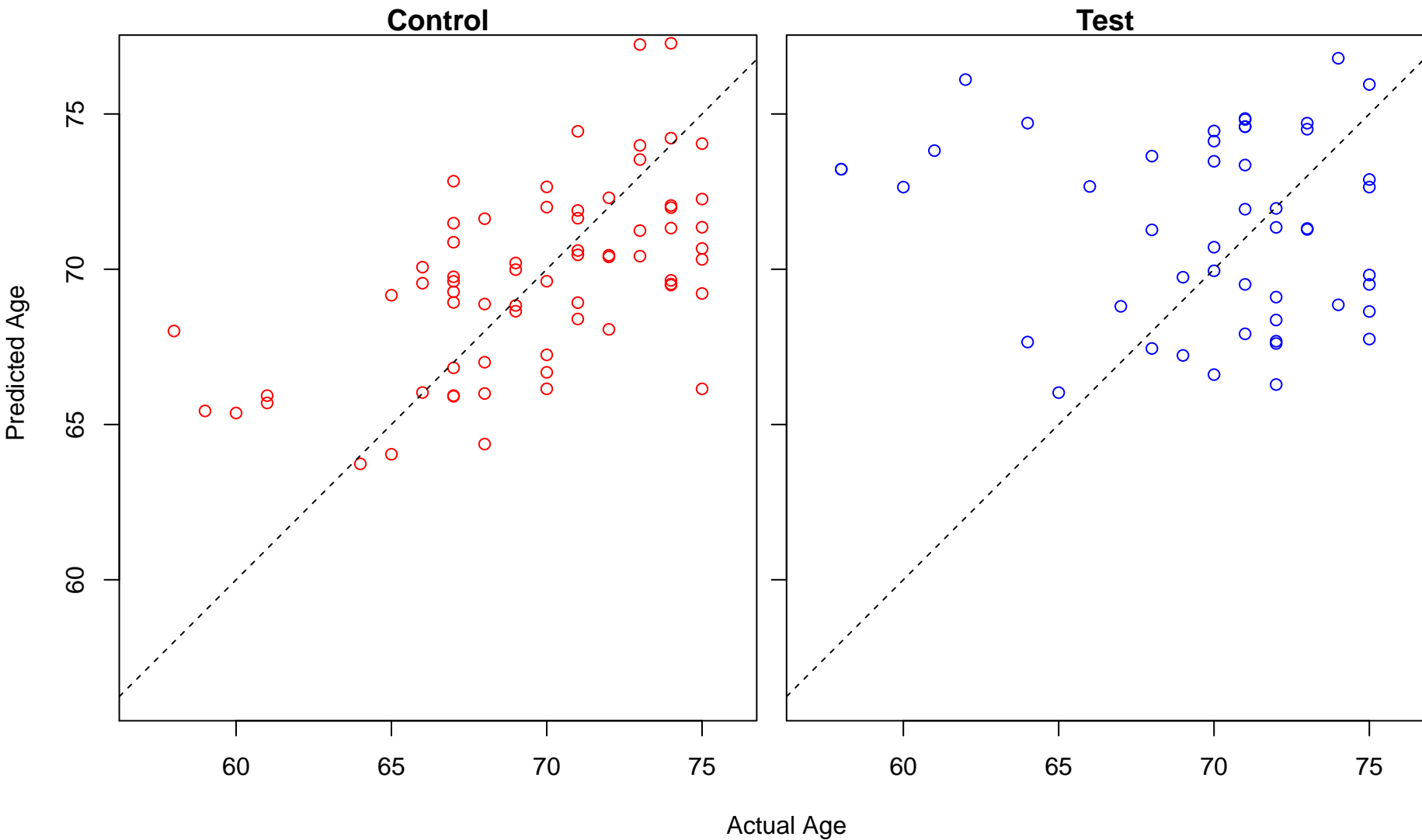
organelle inheritance (Score: 1.174630)



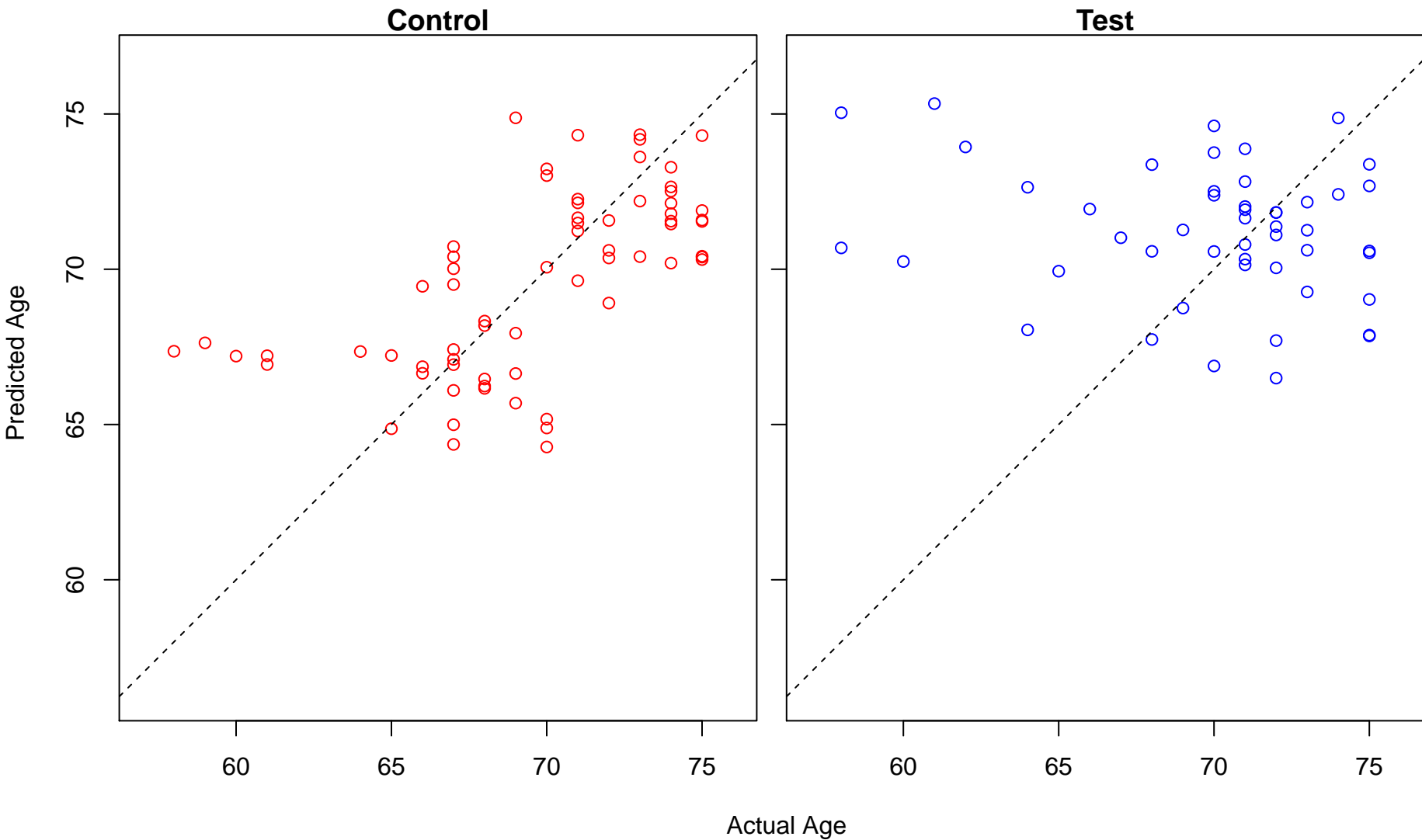
Golgi inheritance (Score: 1.174630)



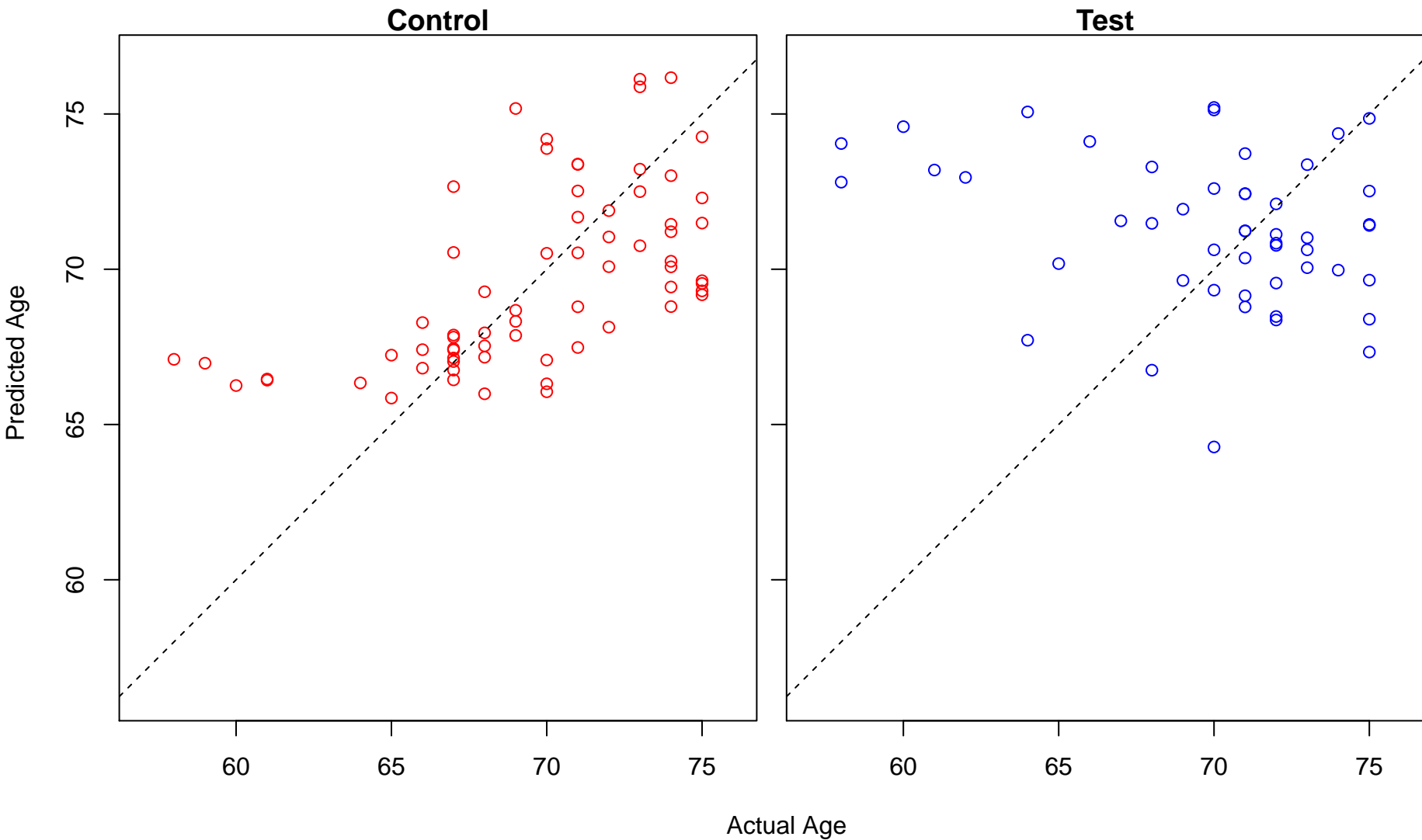
mast cell mediated immunity (Score: 1.174538)



vitamin metabolic process (Score: 1.174490)

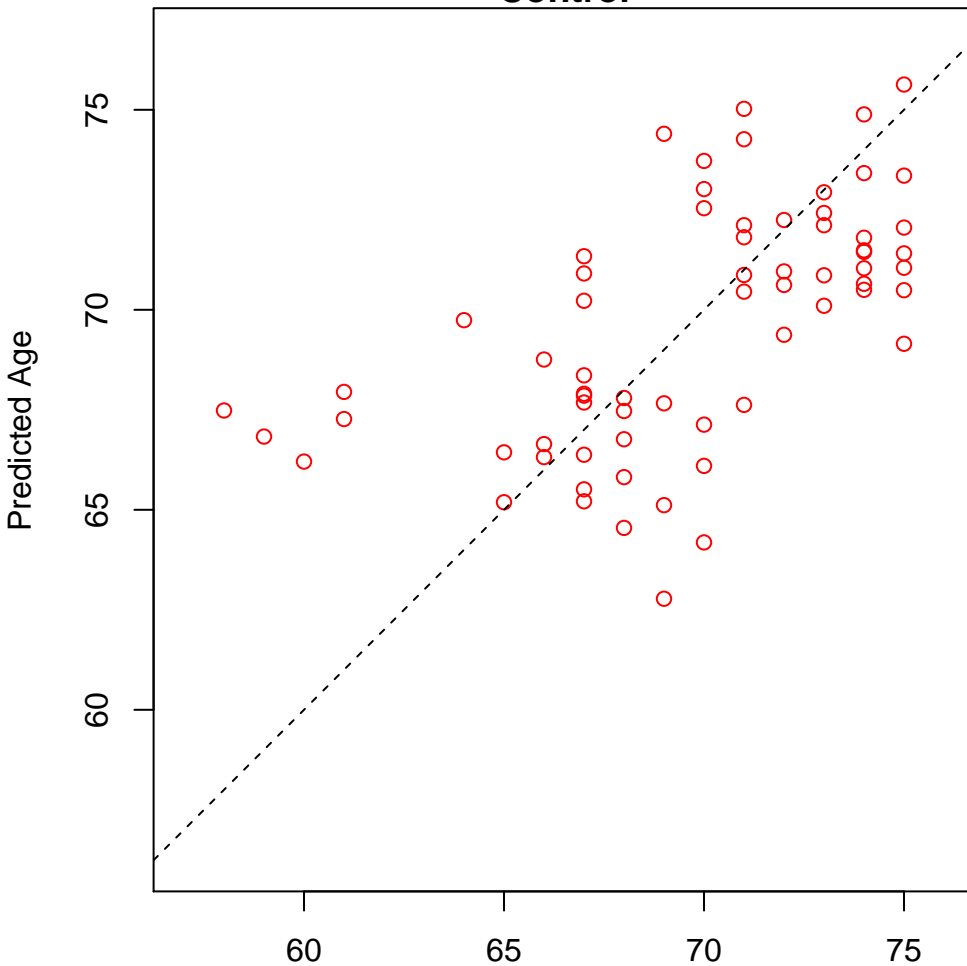


regulation of phosphatidylinositol 3-kinase signaling (Score: 1.174144)

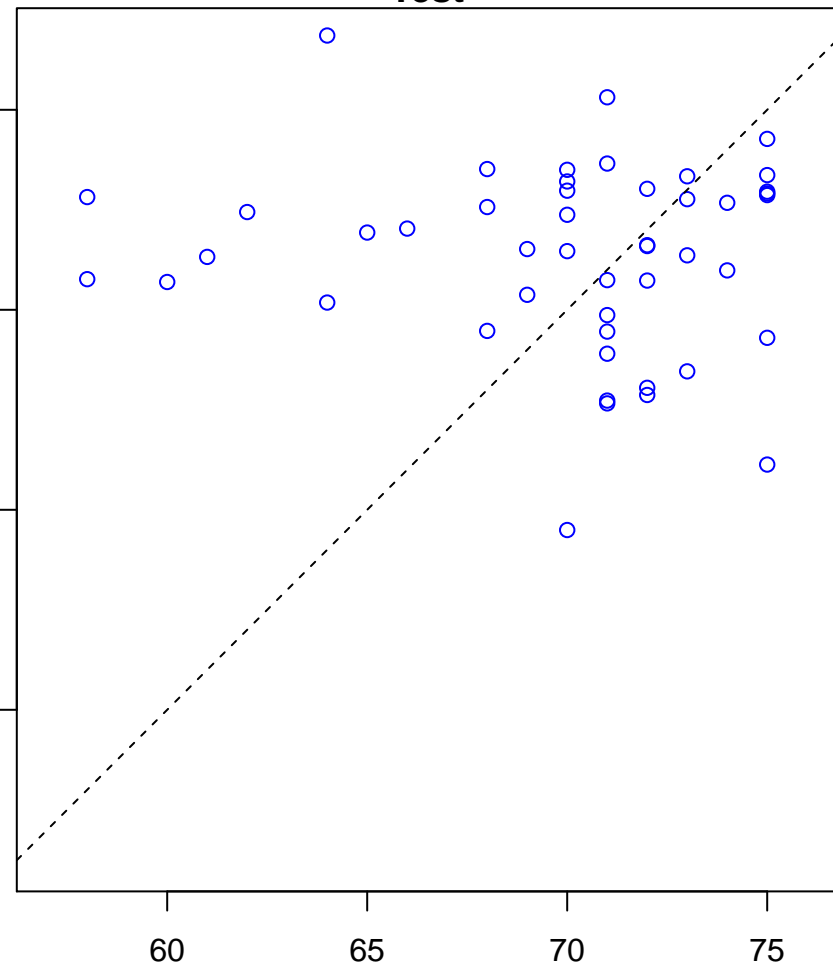


positive regulation of protein acetylation (Score: 1.174128)

Control

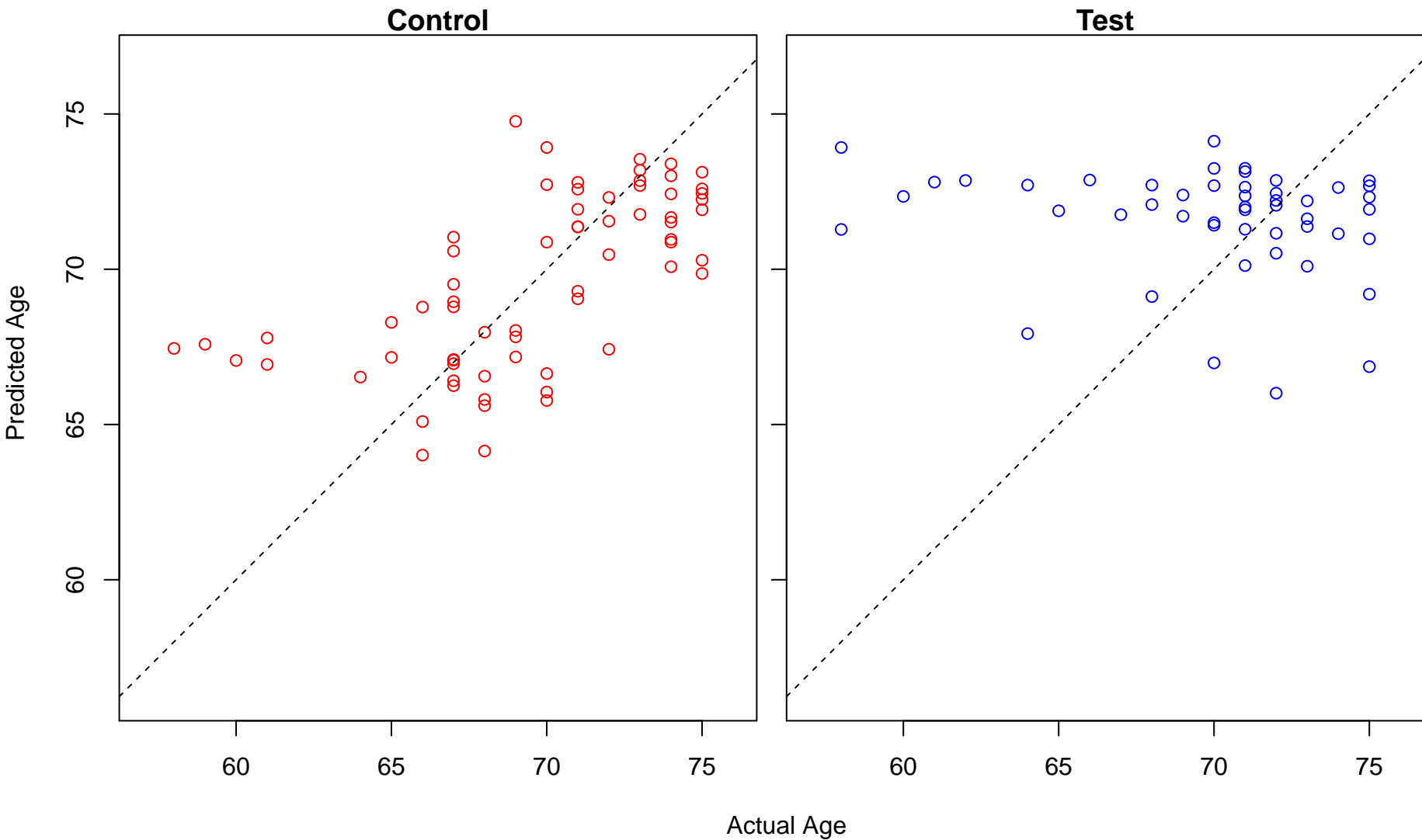


Test

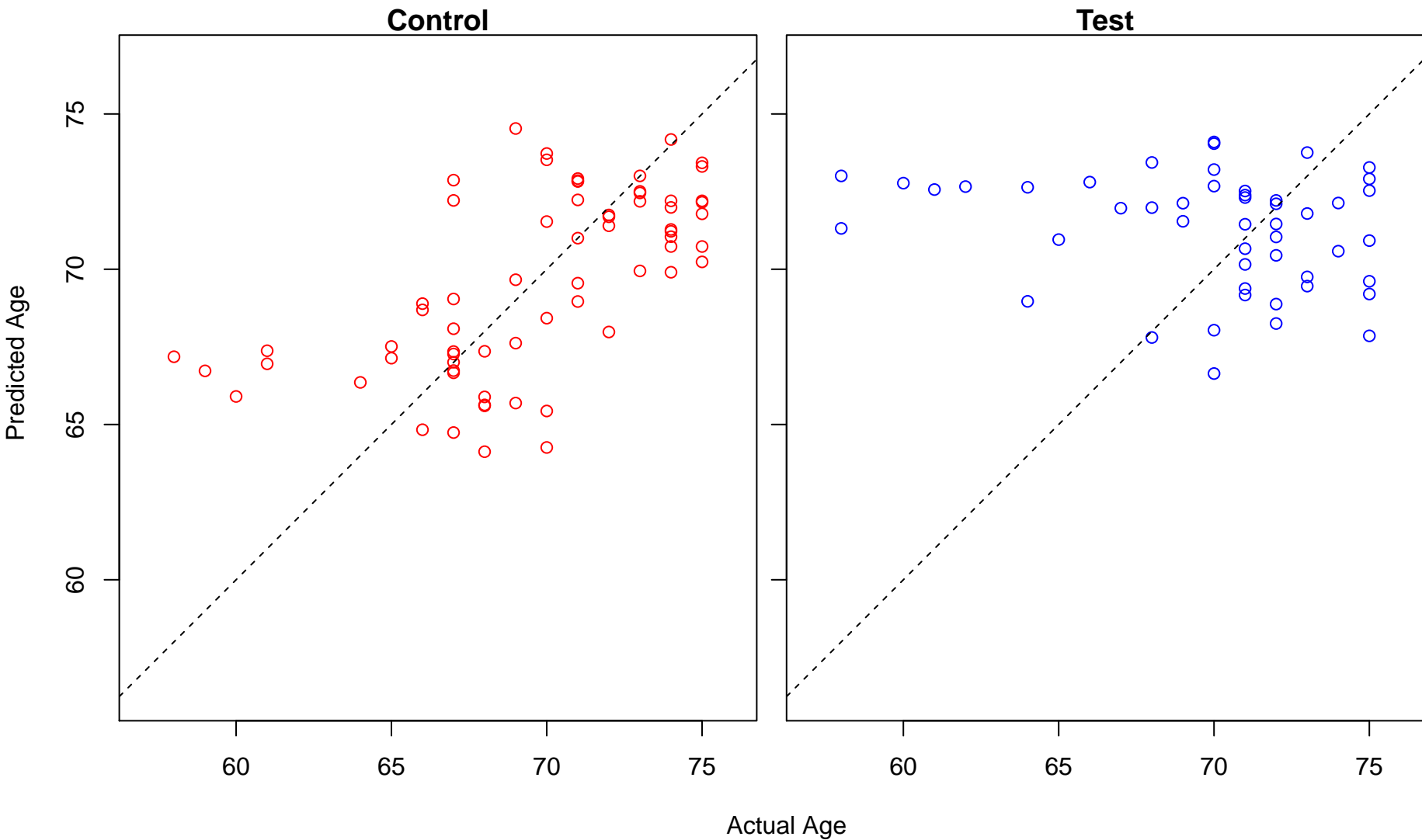


Actual Age

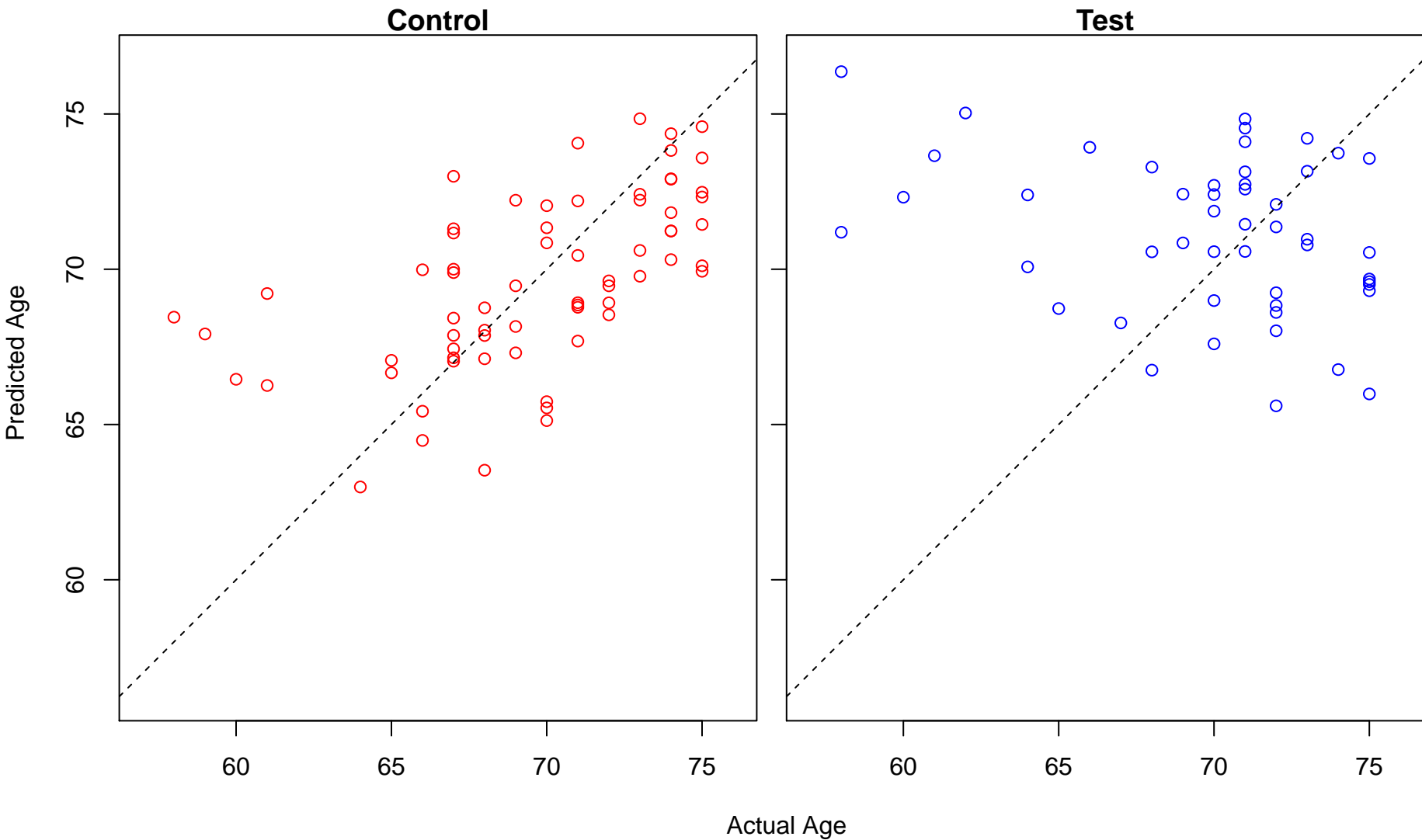
cranial nerve development (Score: 1.173766)



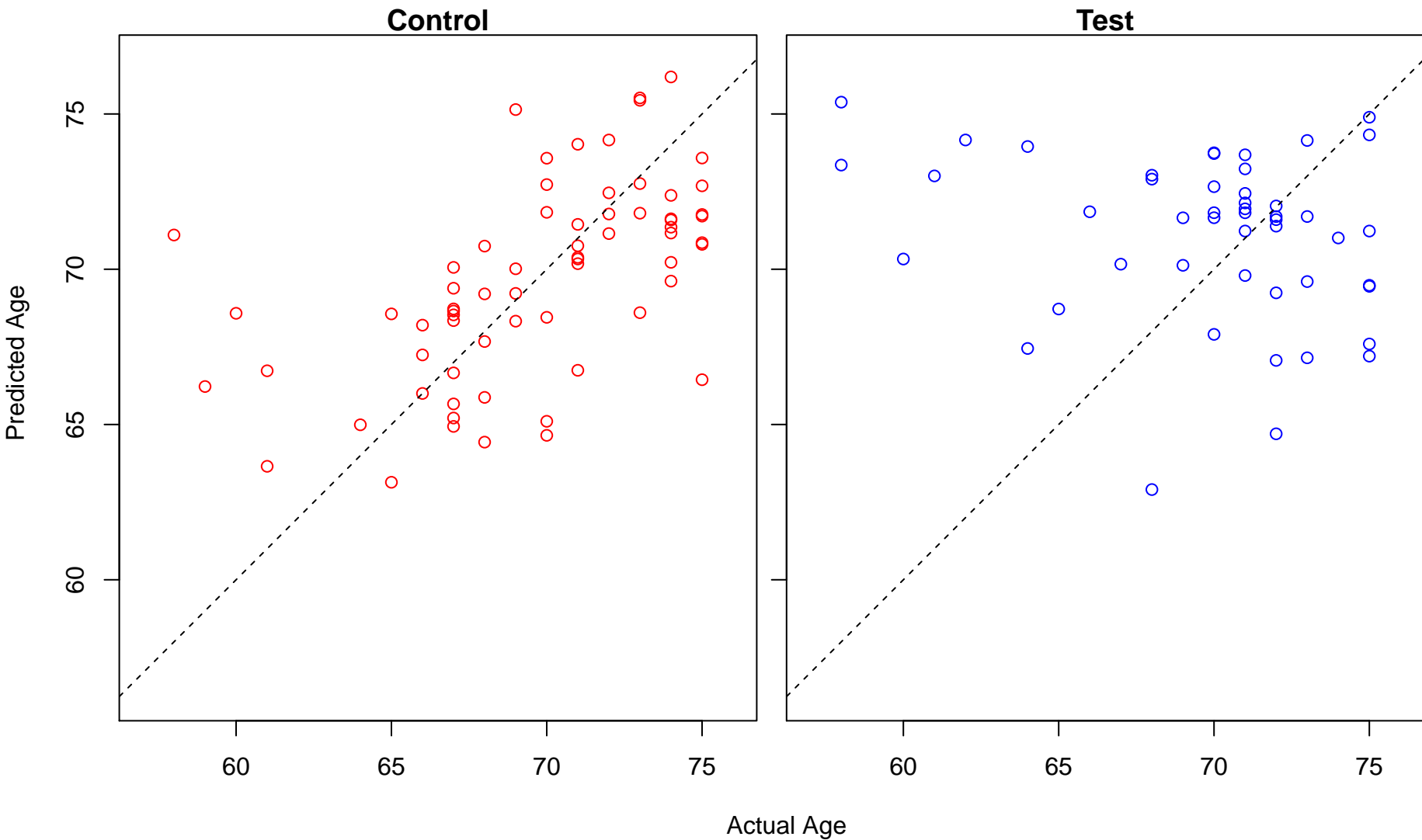
positive regulation of G2/M transition of mitotic cell cycle (Score: 1.172597)



negative regulation of actin filament bundle assembly (Score: 1.172411)

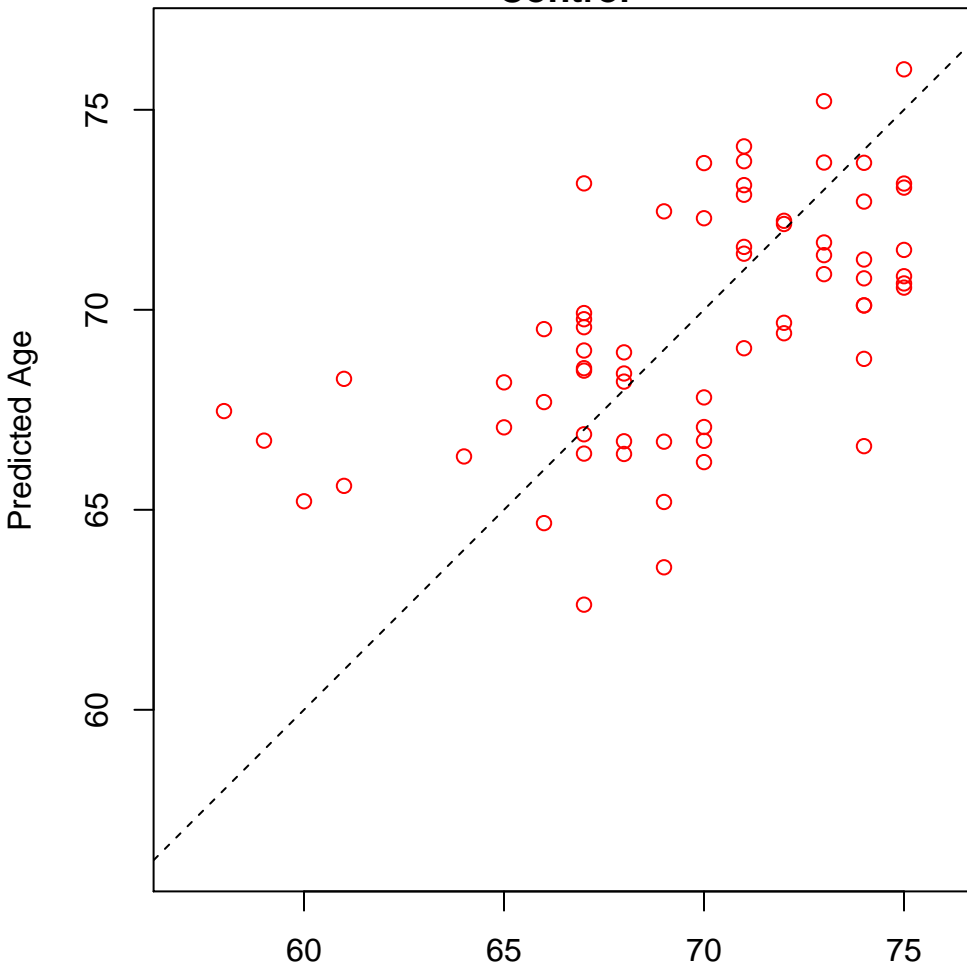


regulation of leukocyte mediated cytotoxicity (Score: 1.172184)

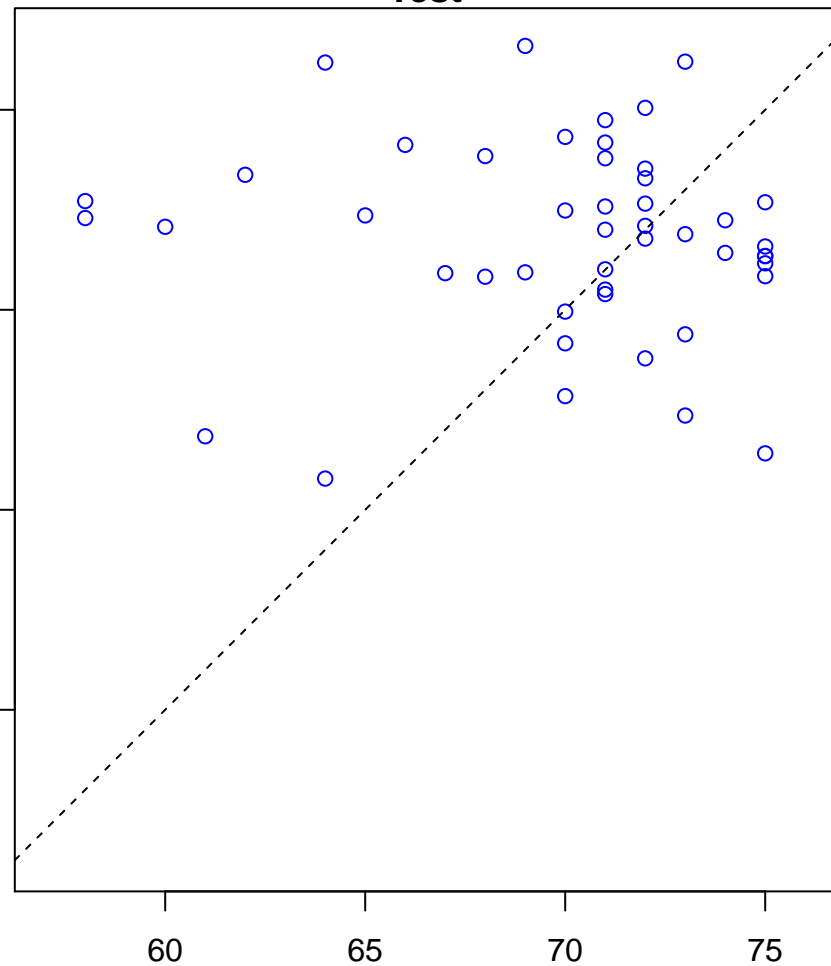


regulation of sister chromatid cohesion (Score: 1.171820)

Control

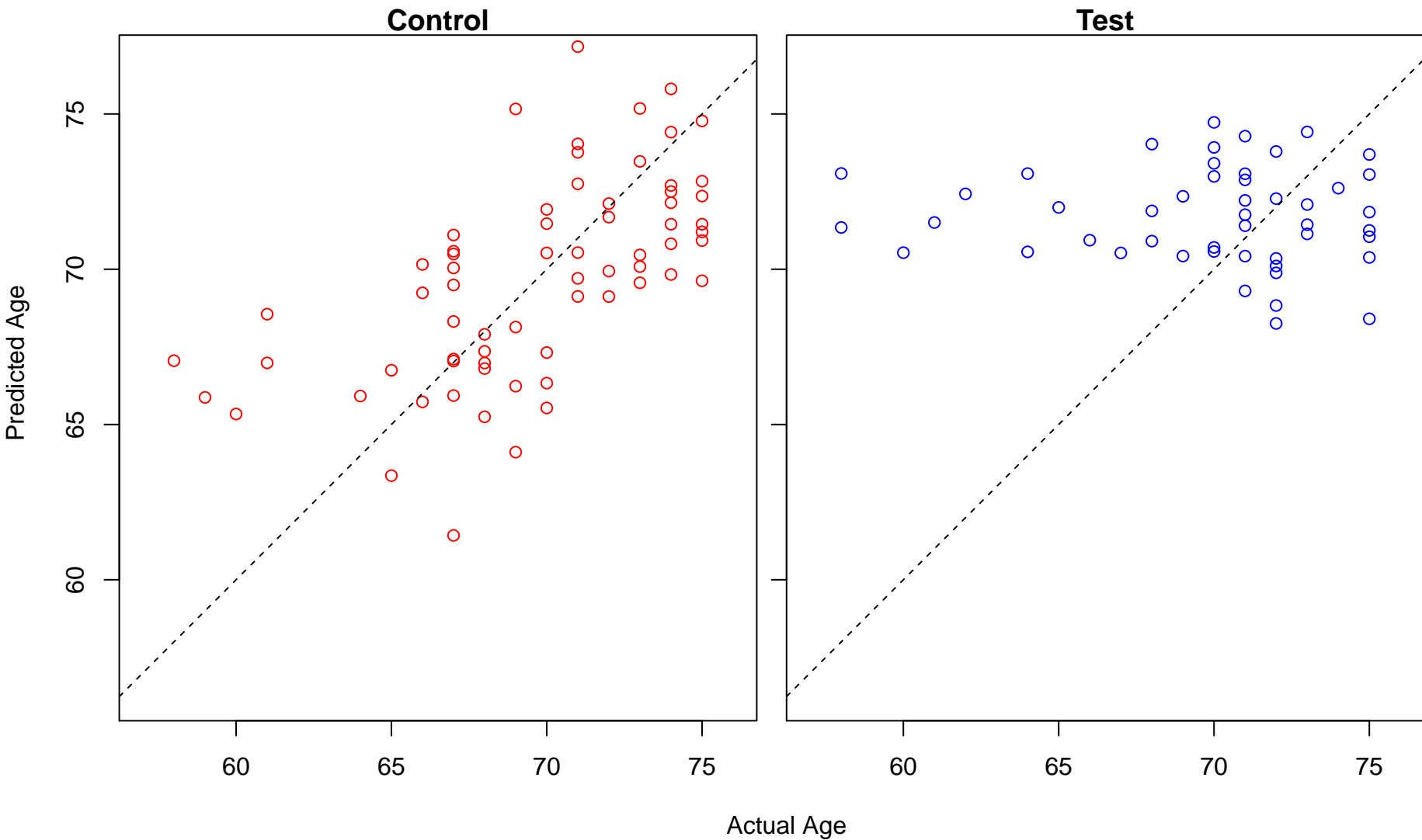


Test



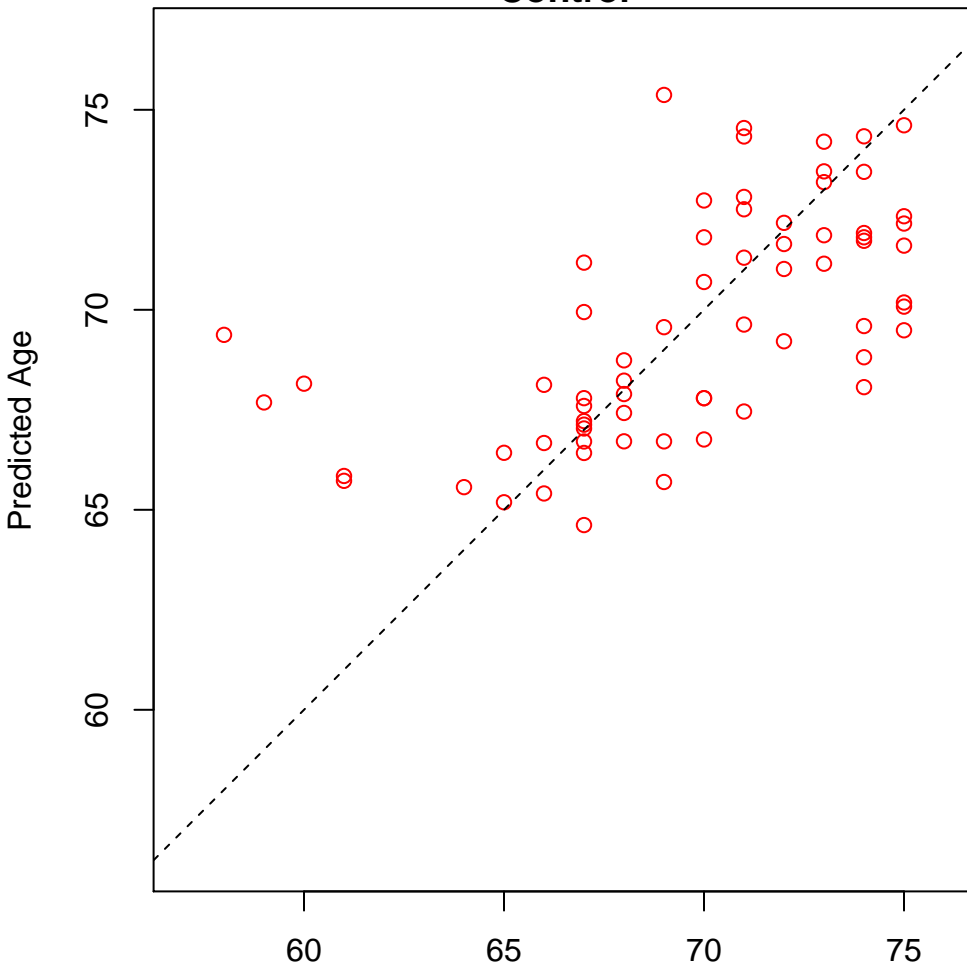
Actual Age

chromatin remodeling (Score: 1.171712)

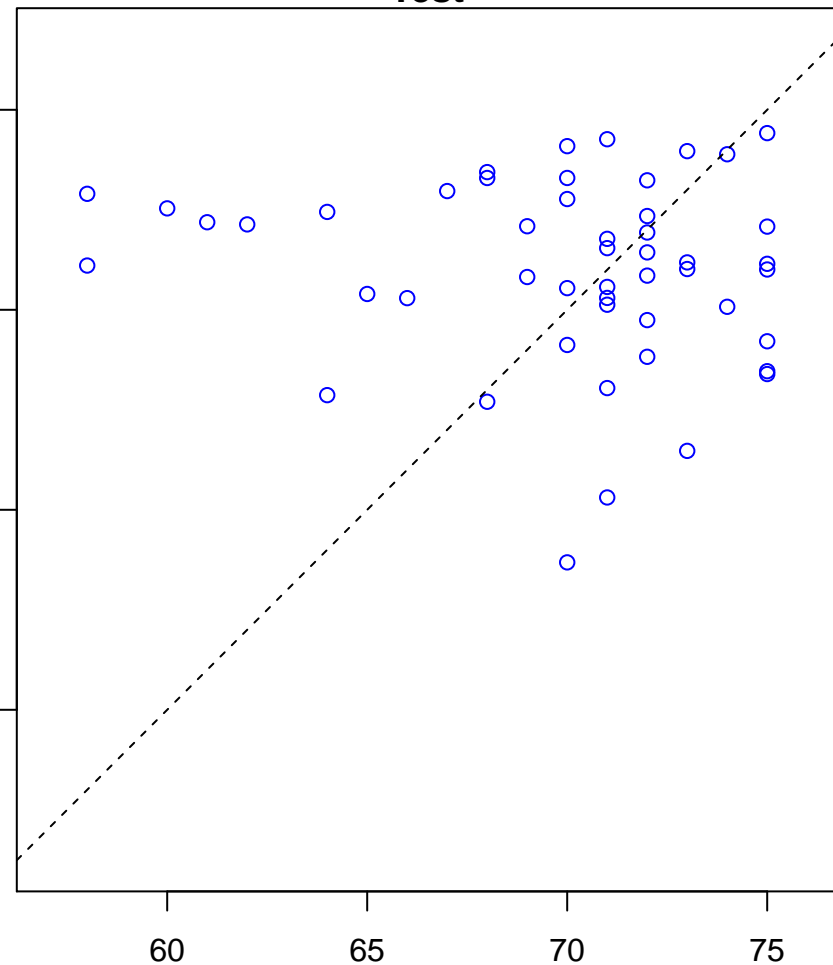


inositol phosphate-mediated signaling (Score: 1.171691)

Control

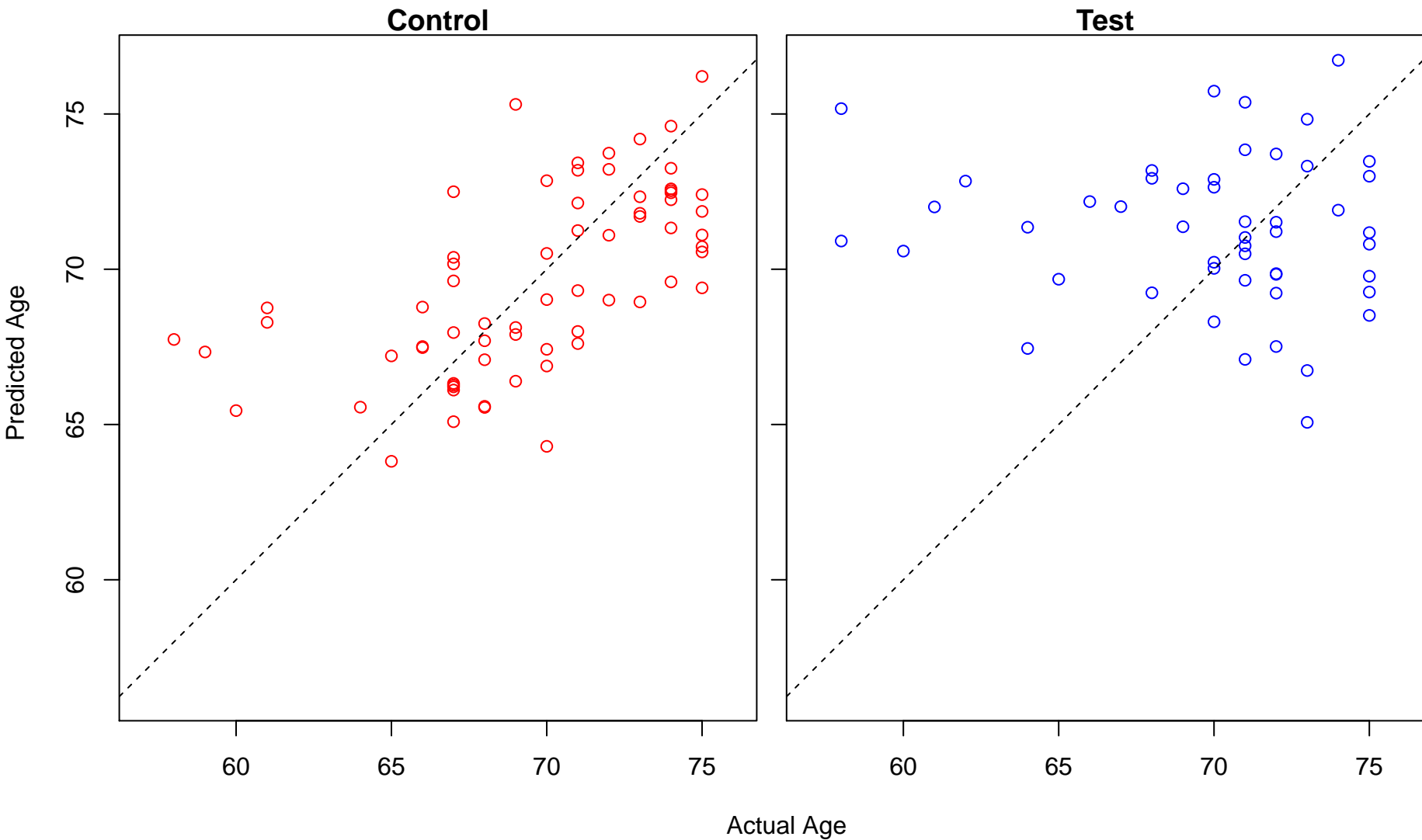


Test

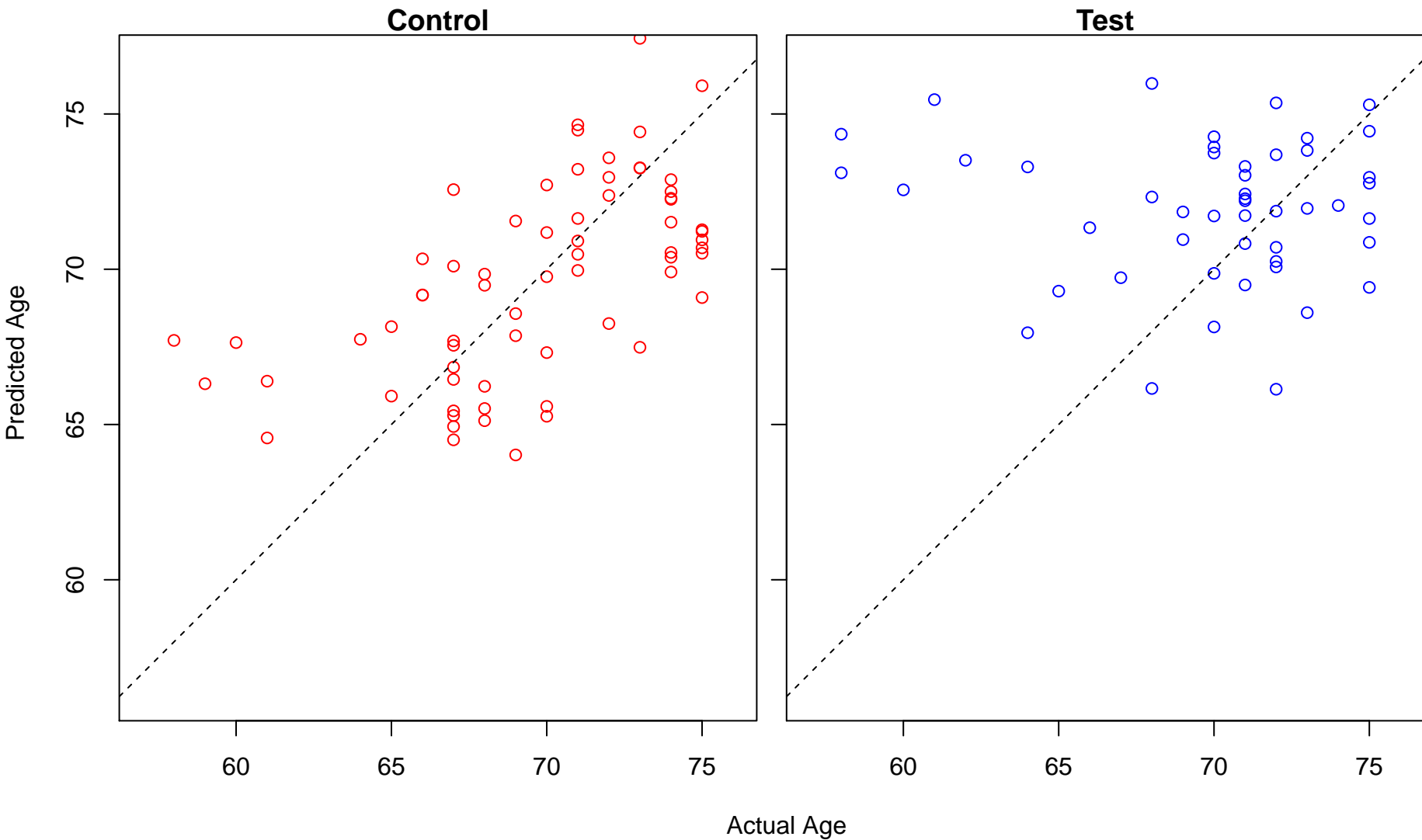


Actual Age

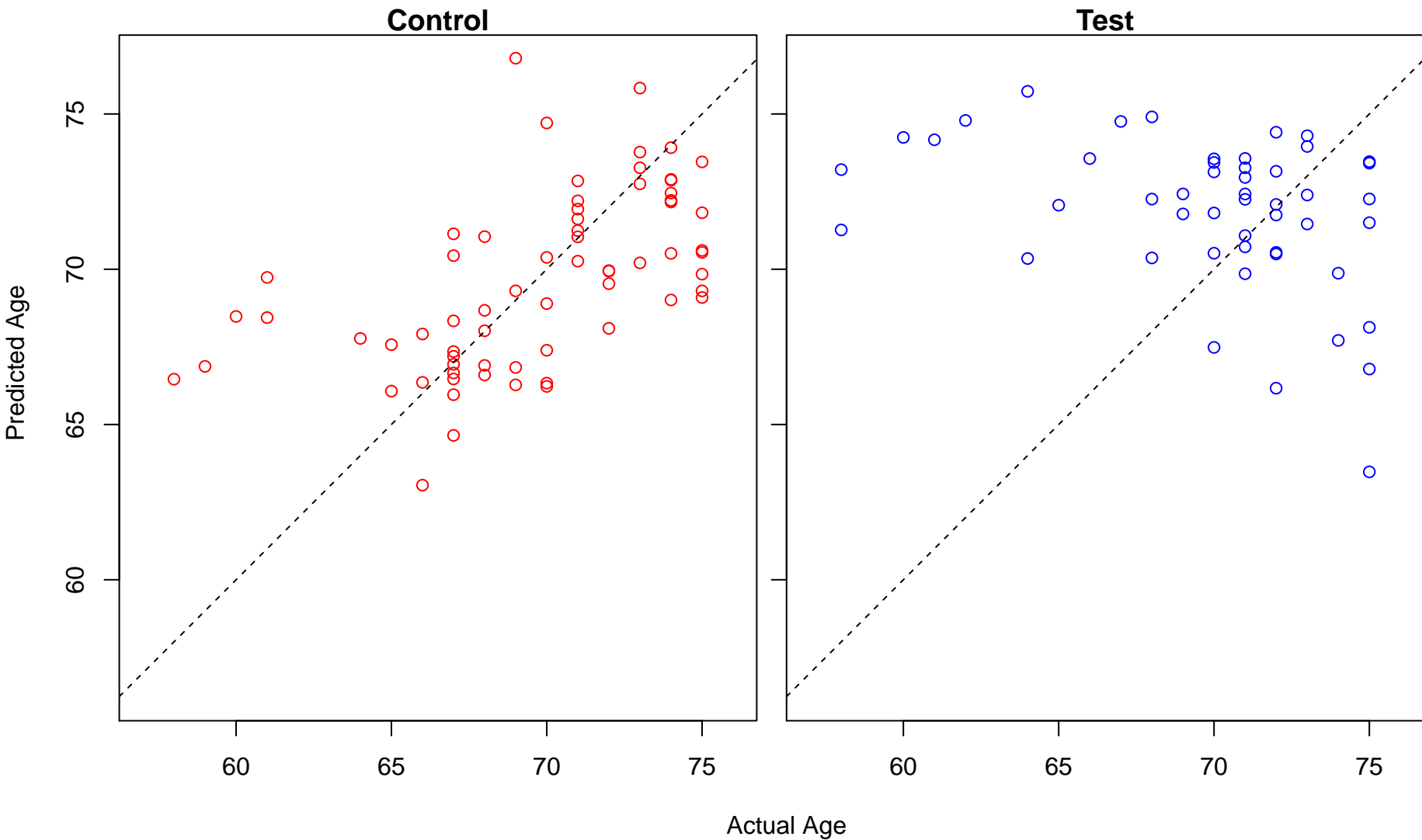
positive regulation of RIG-I signaling pathway (Score: 1.171690)



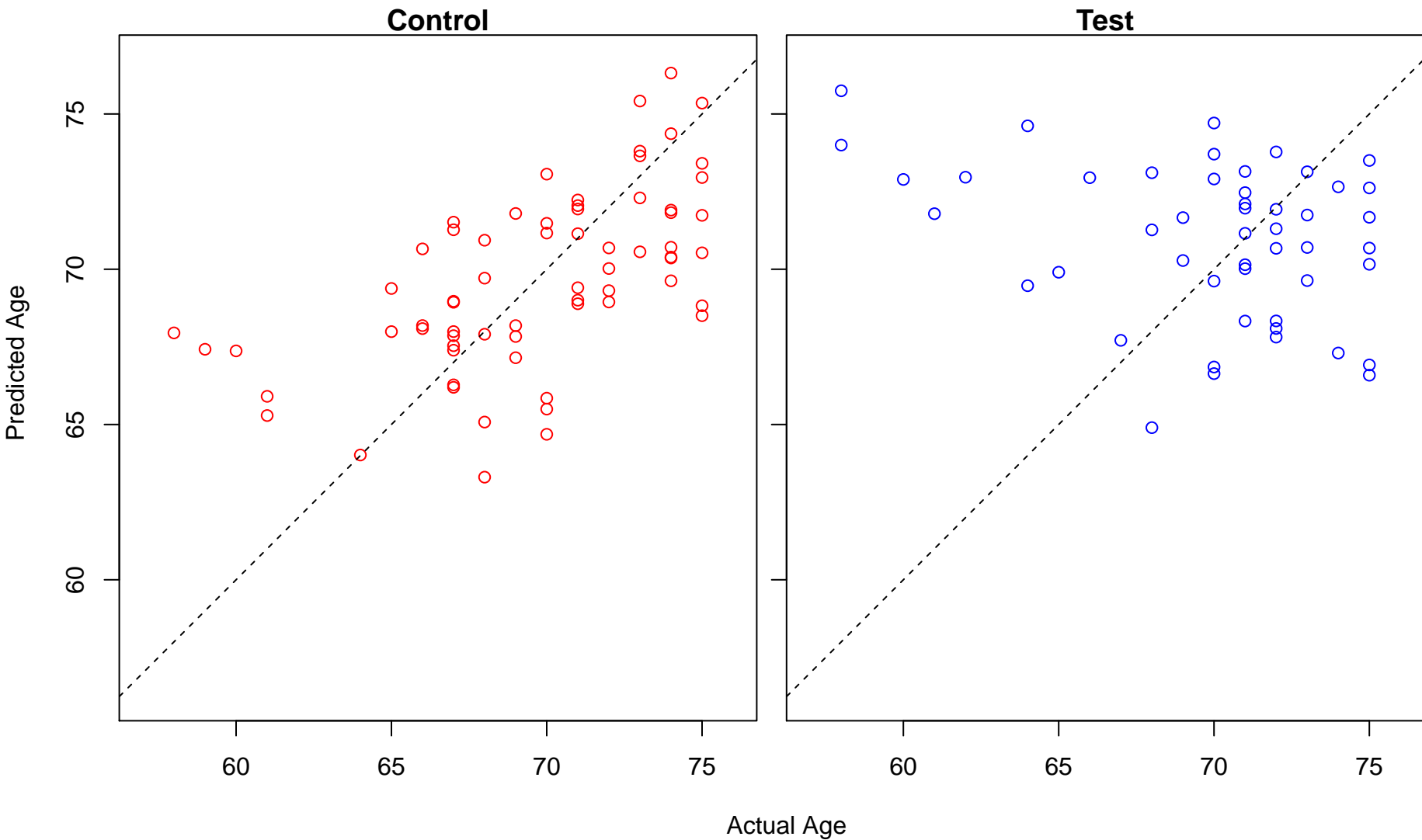
cofactor biosynthetic process (Score: 1.171543)



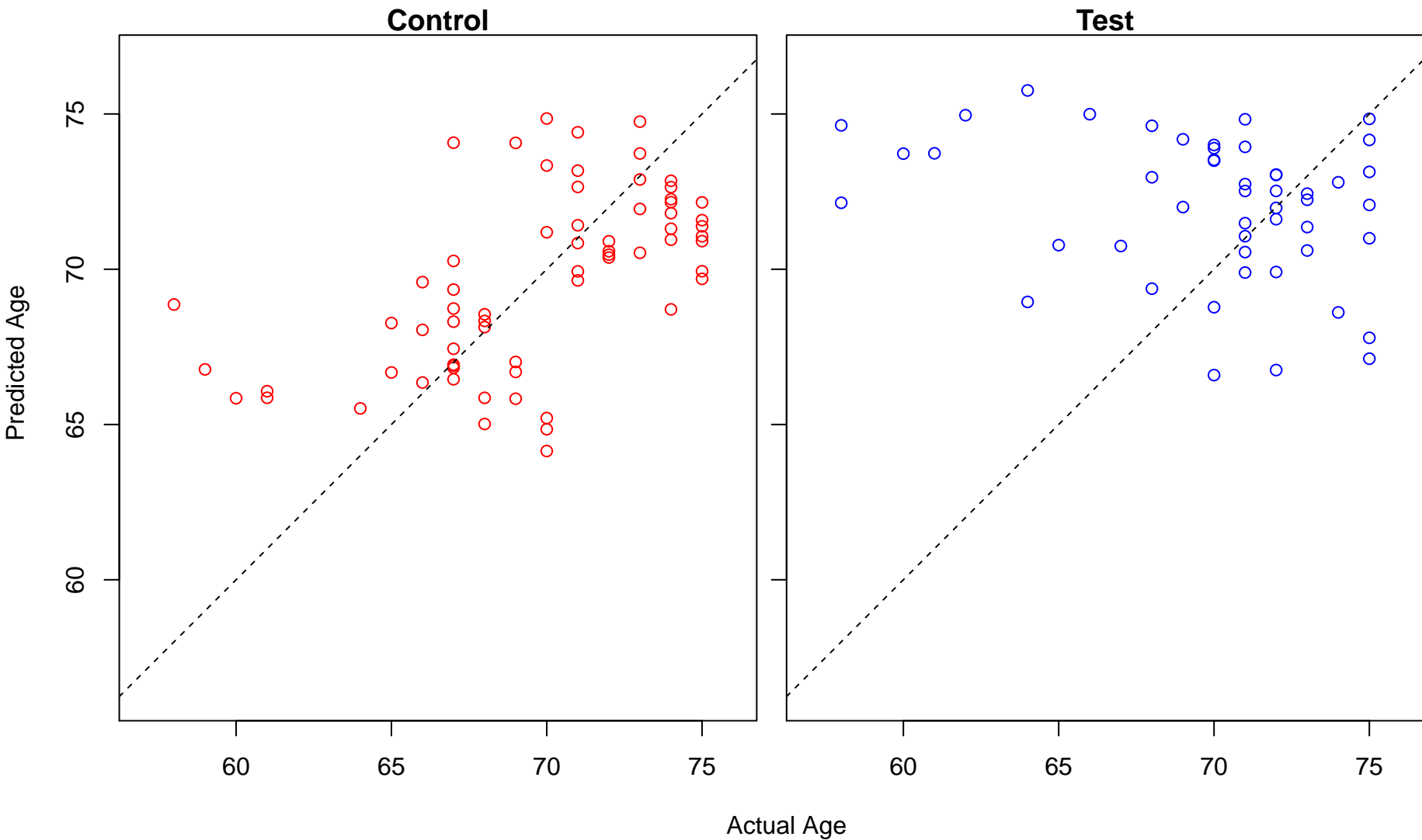
chaperone-mediated protein complex assembly (Score: 1.171318)



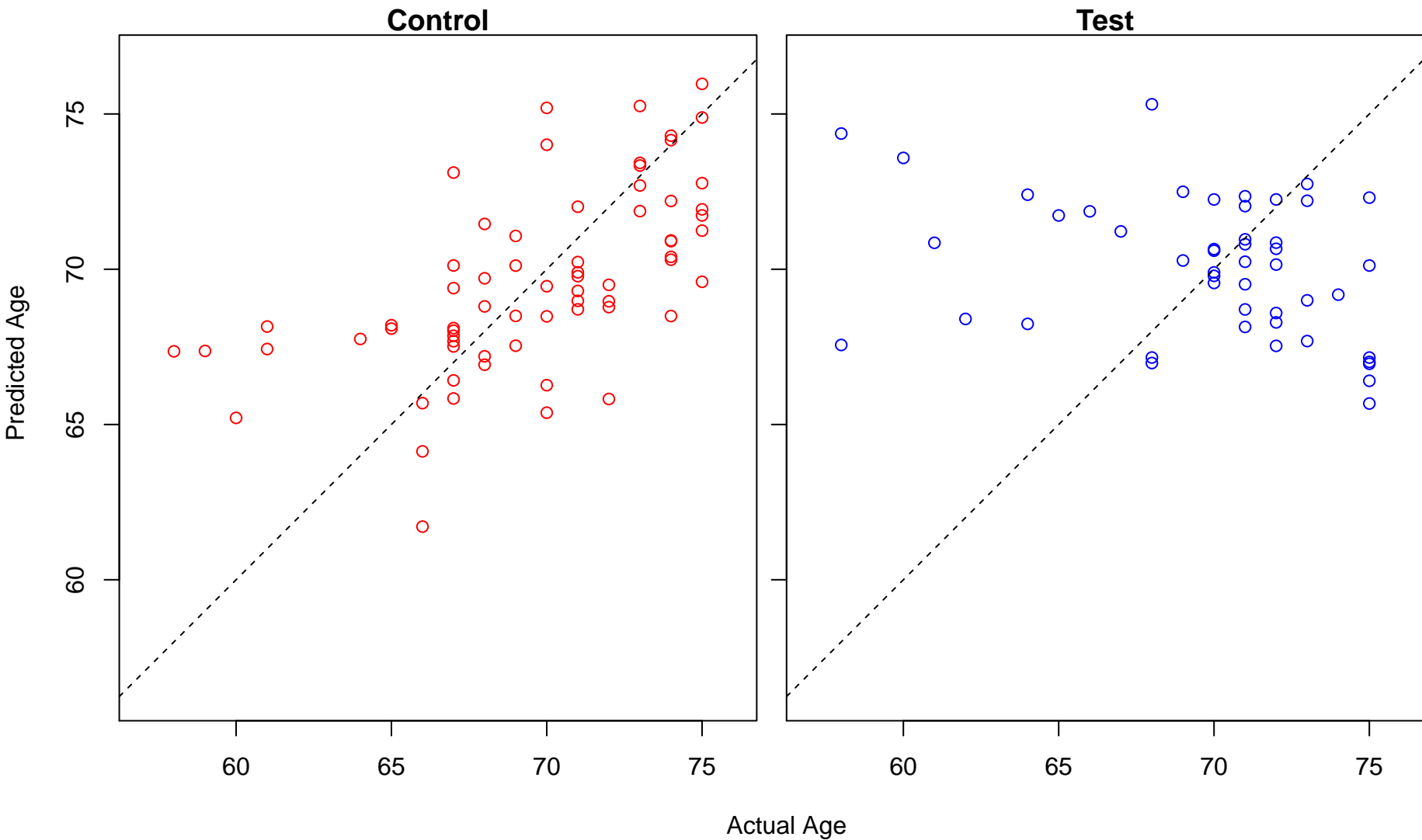
protein targeting to lysosome (Score: 1.171208)



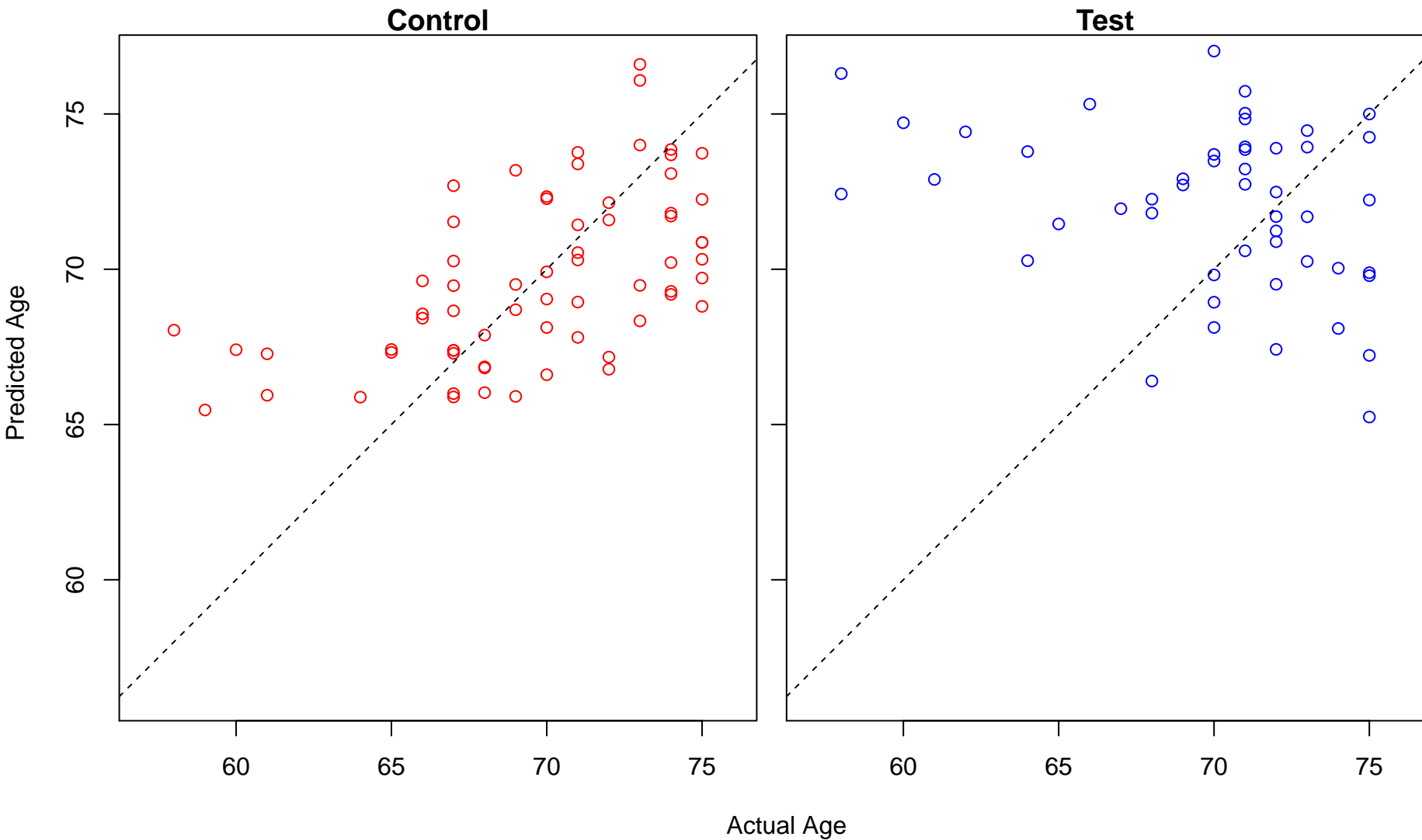
histone mRNA catabolic process (Score: 1.170549)



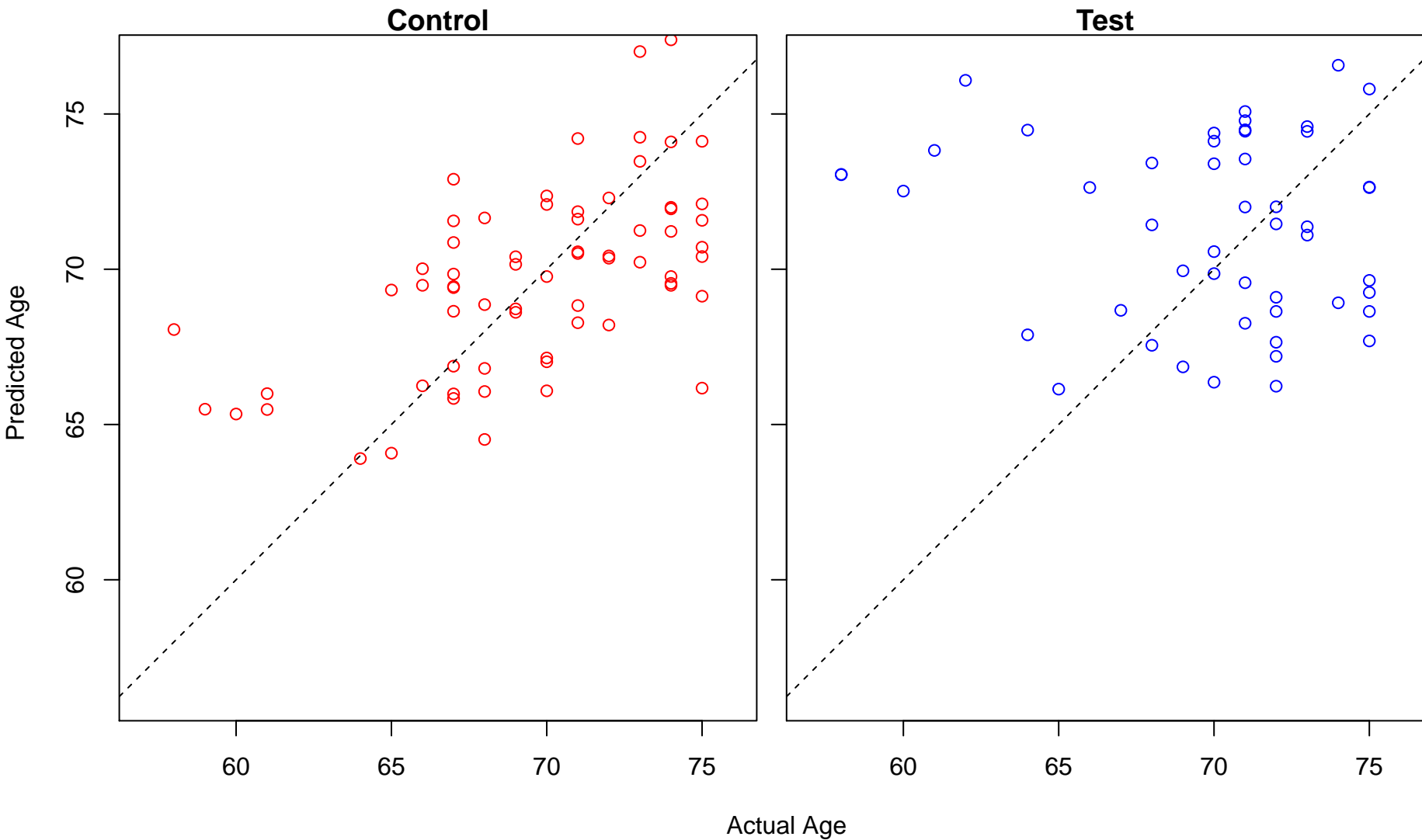
positive regulation of triglyceride metabolic process (Score: 1.170493)



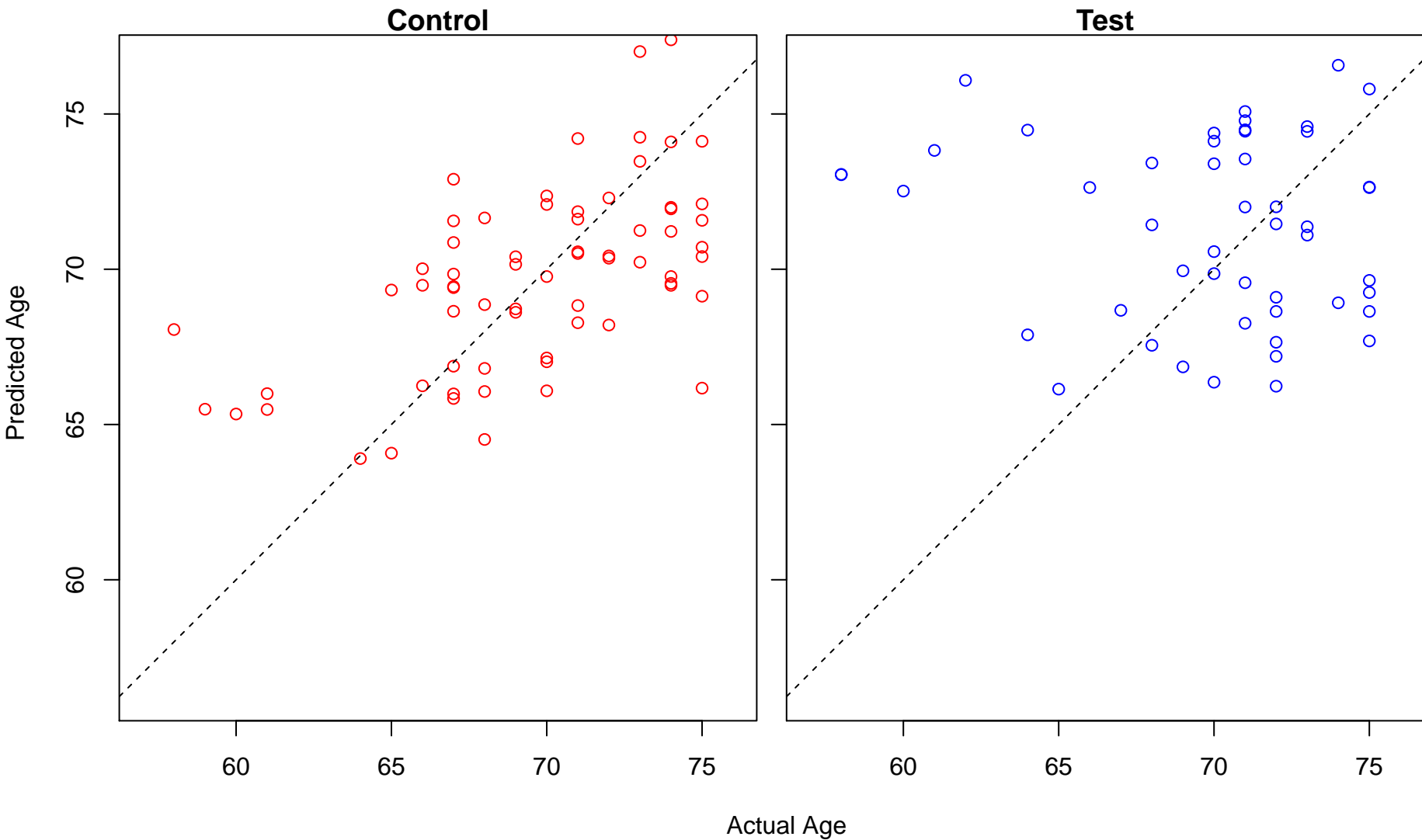
endosomal vesicle fusion (Score: 1.170254)



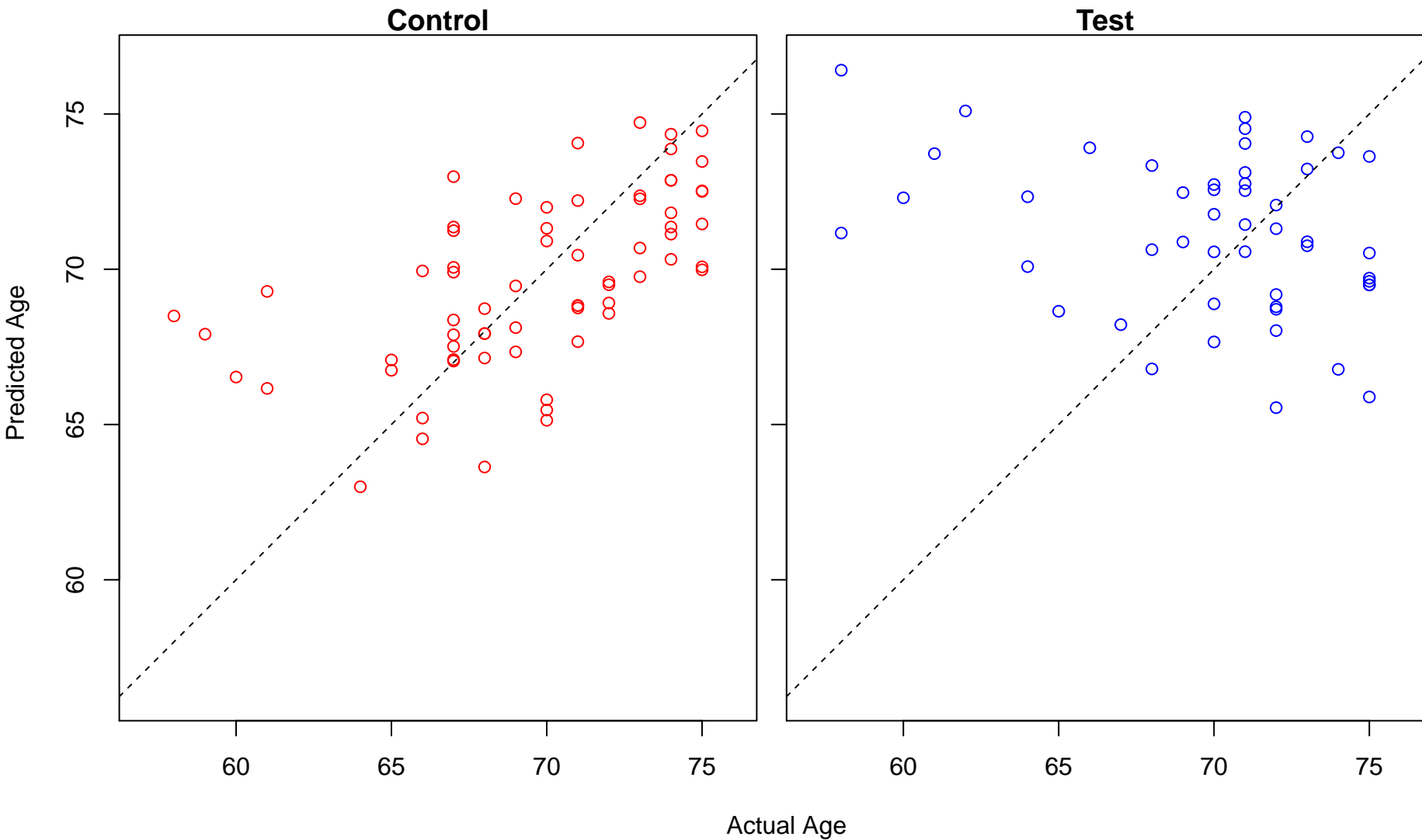
mast cell activation involved in immune response (Score: 1.169977)



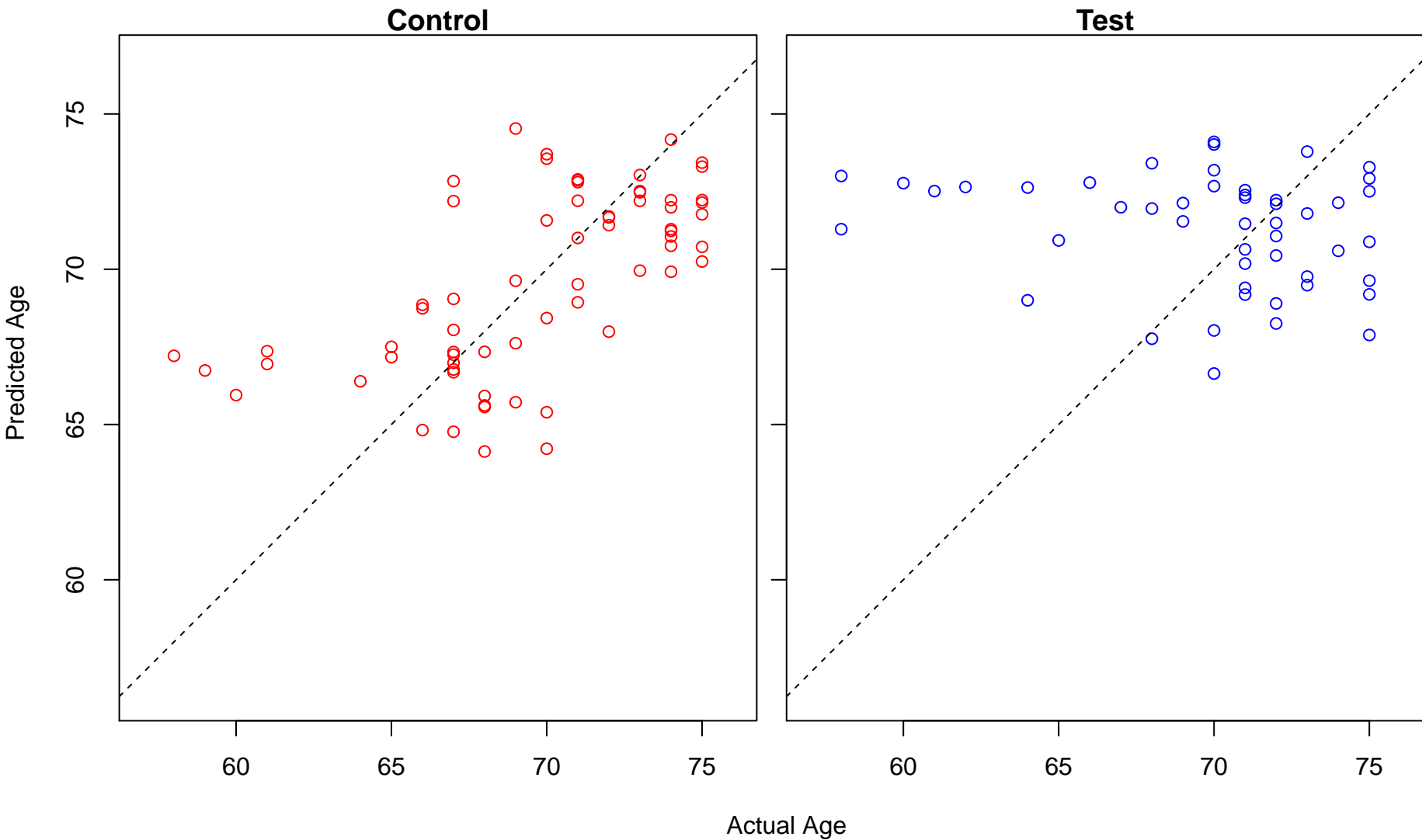
mast cell degranulation (Score: 1.169977)



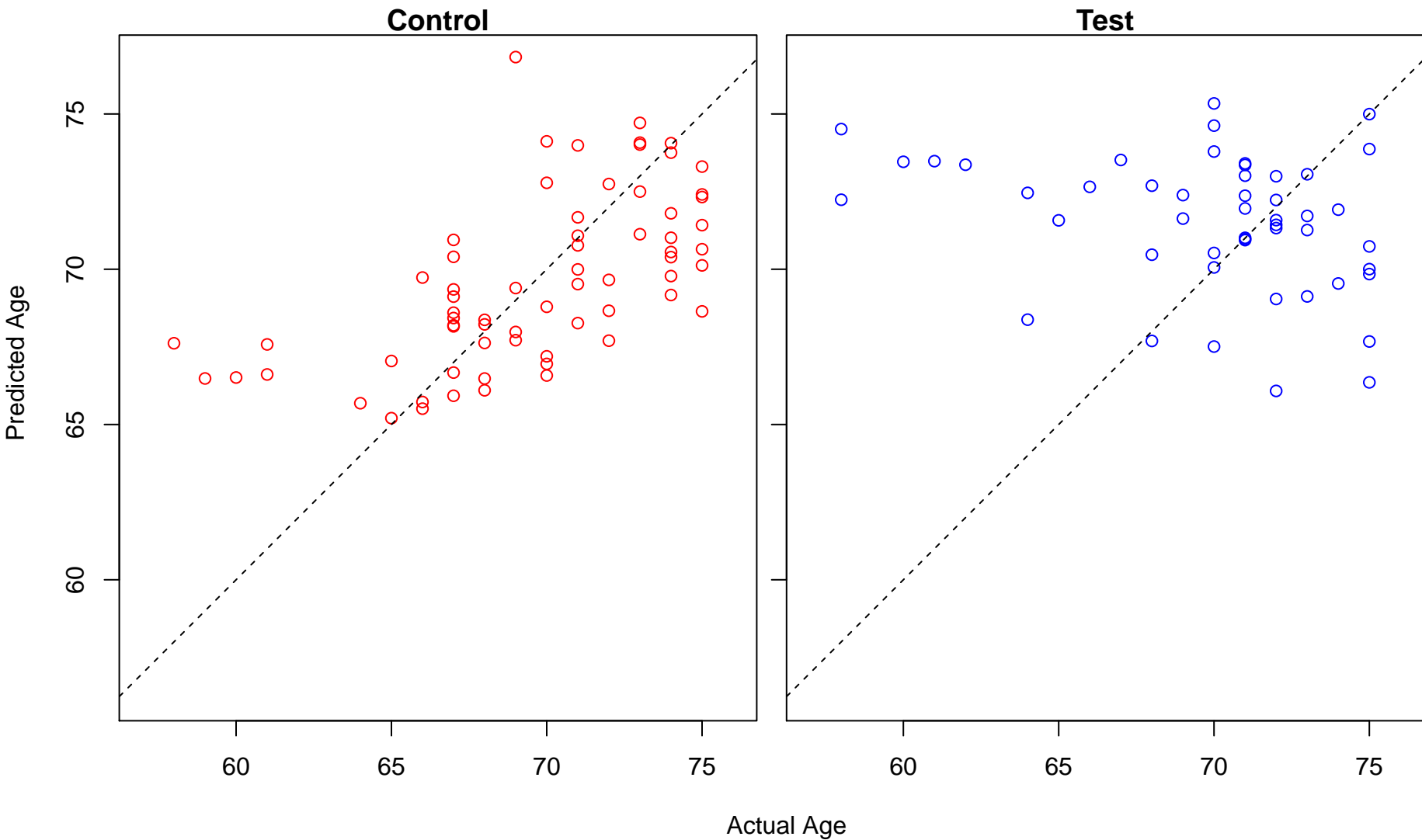
negative regulation of stress fiber assembly (Score: 1.169958)



positive regulation of cell cycle G2/M phase transition (Score: 1.169792)

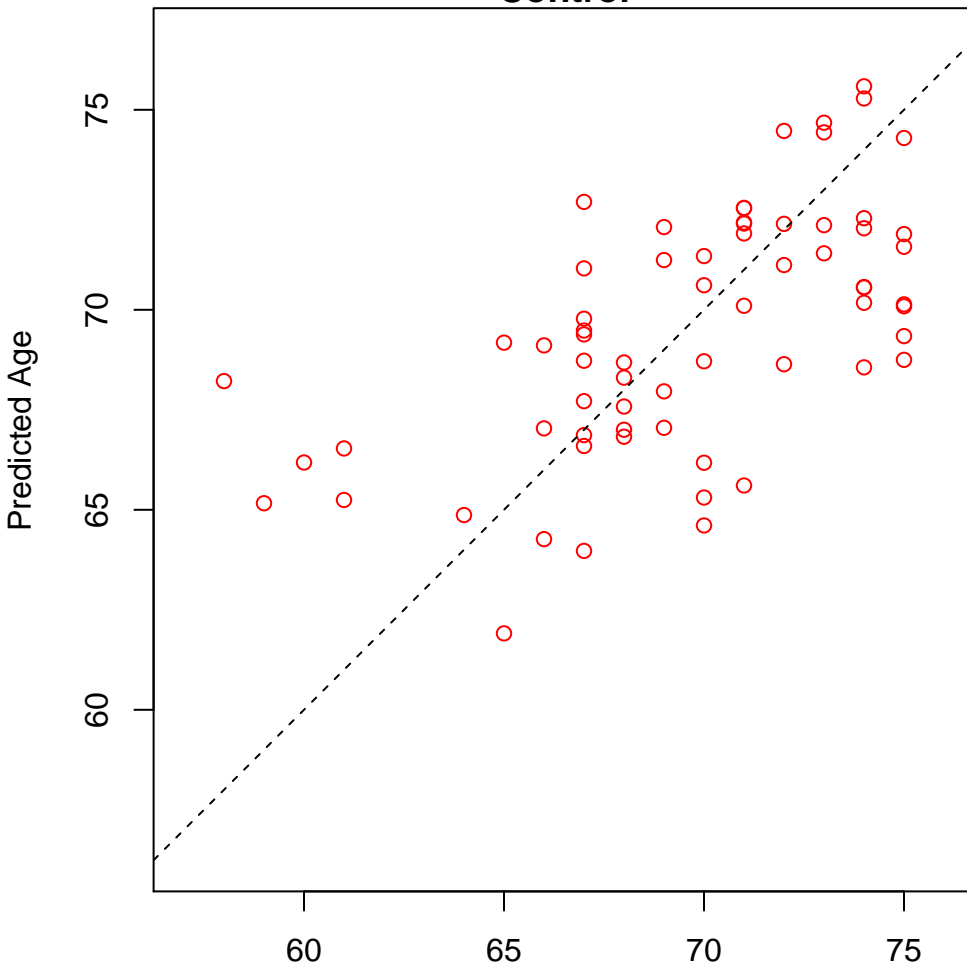


positive regulation of regulated secretory pathway (Score: 1.168911)

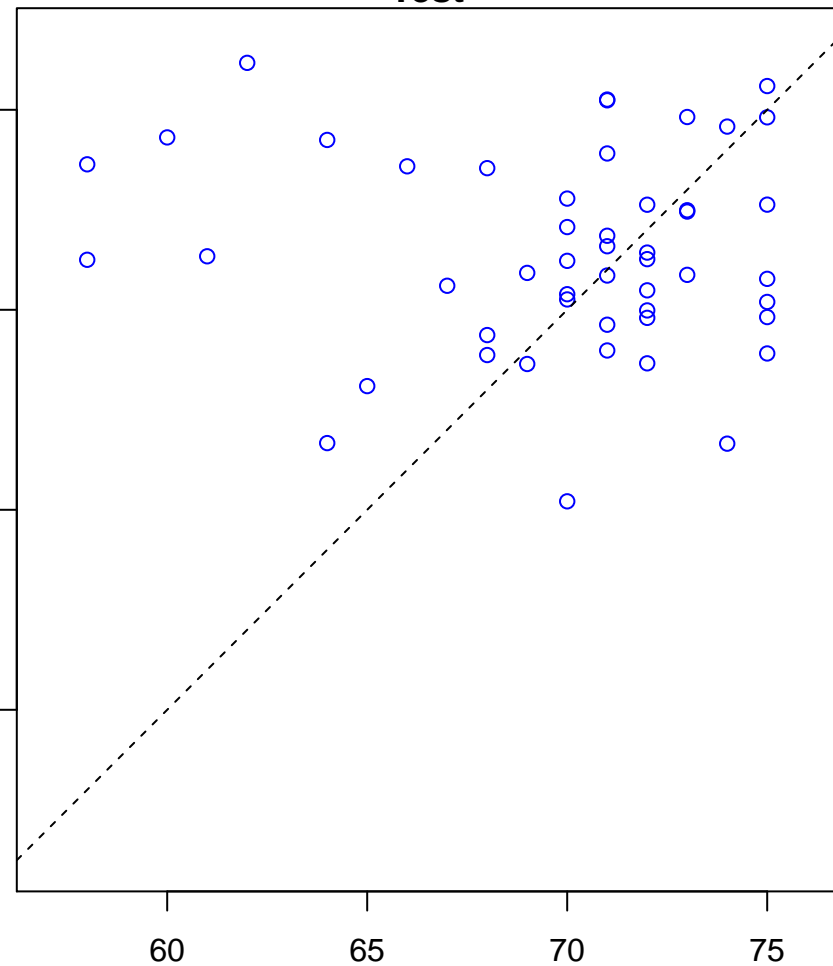


myeloid leukocyte mediated immunity (Score: 1.168632)

Control

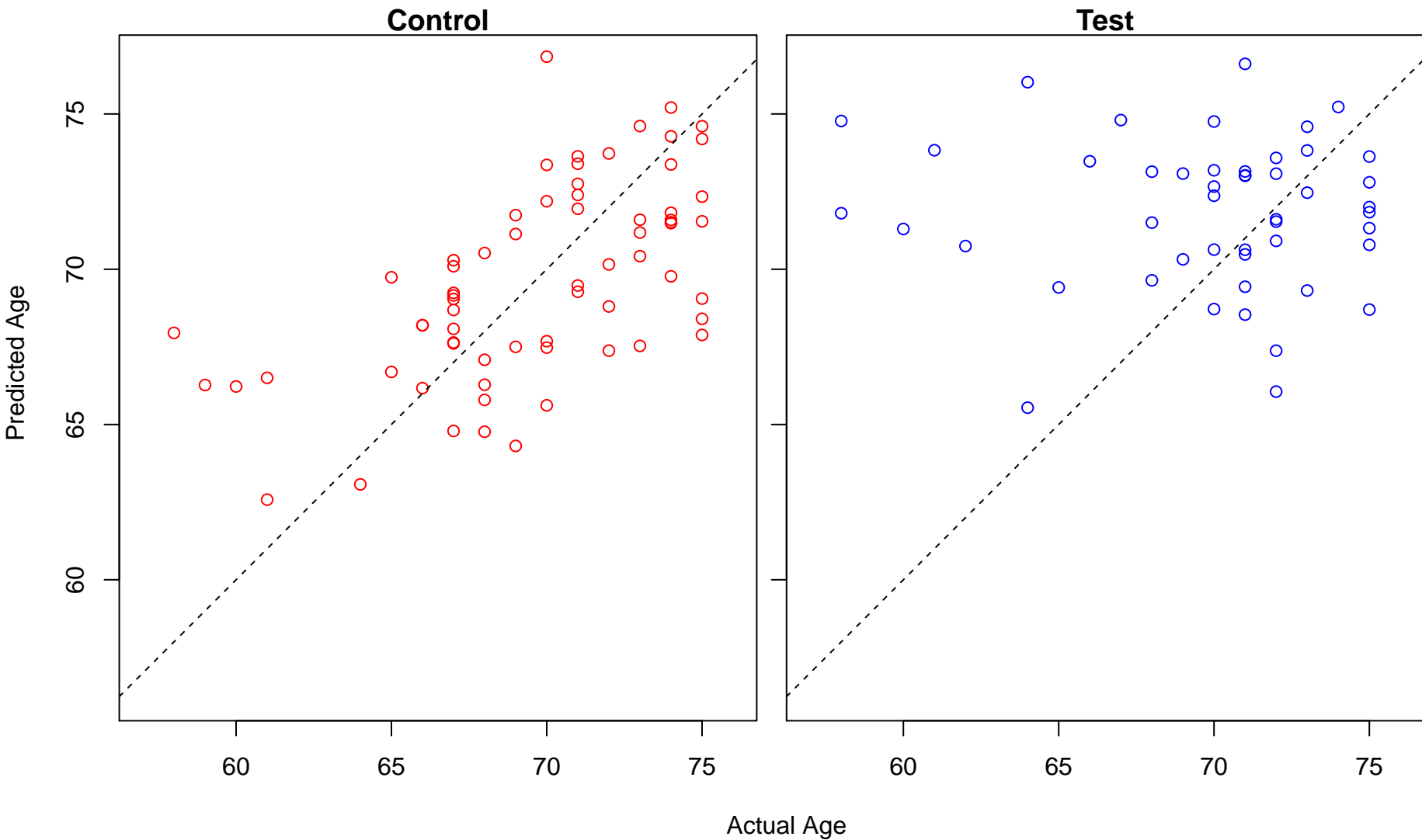


Test

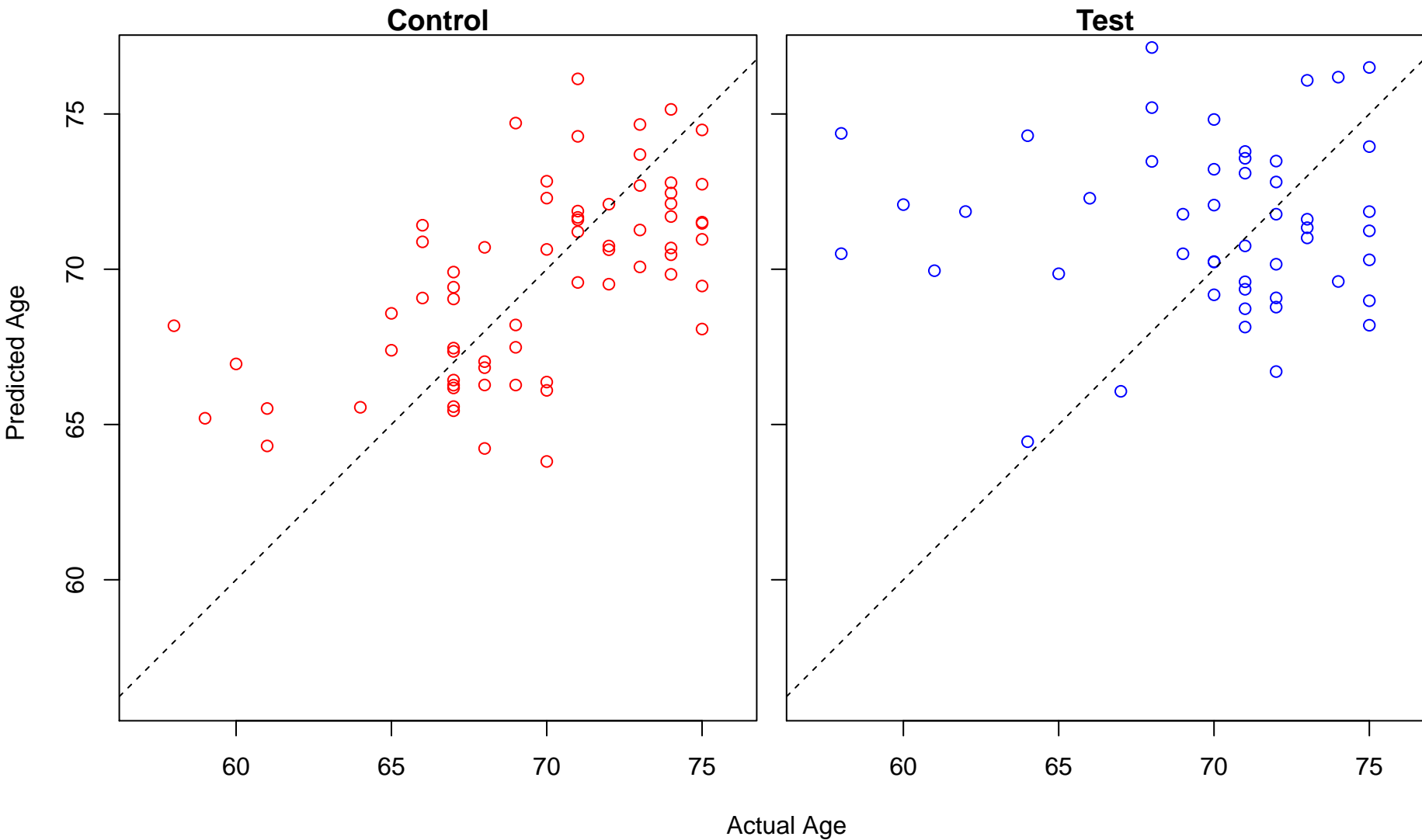


Actual Age

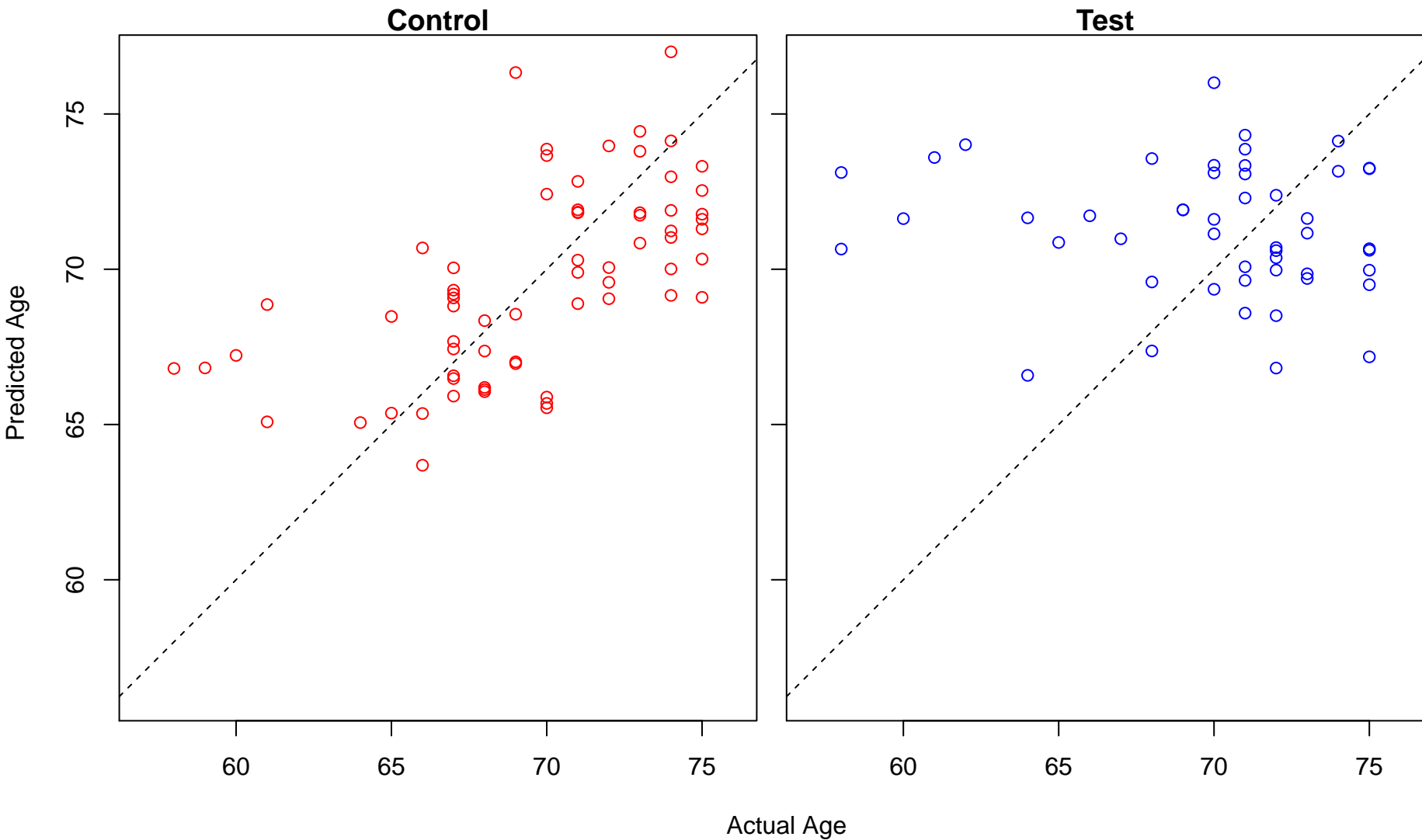
histone H2A monoubiquitination (Score: 1.167948)



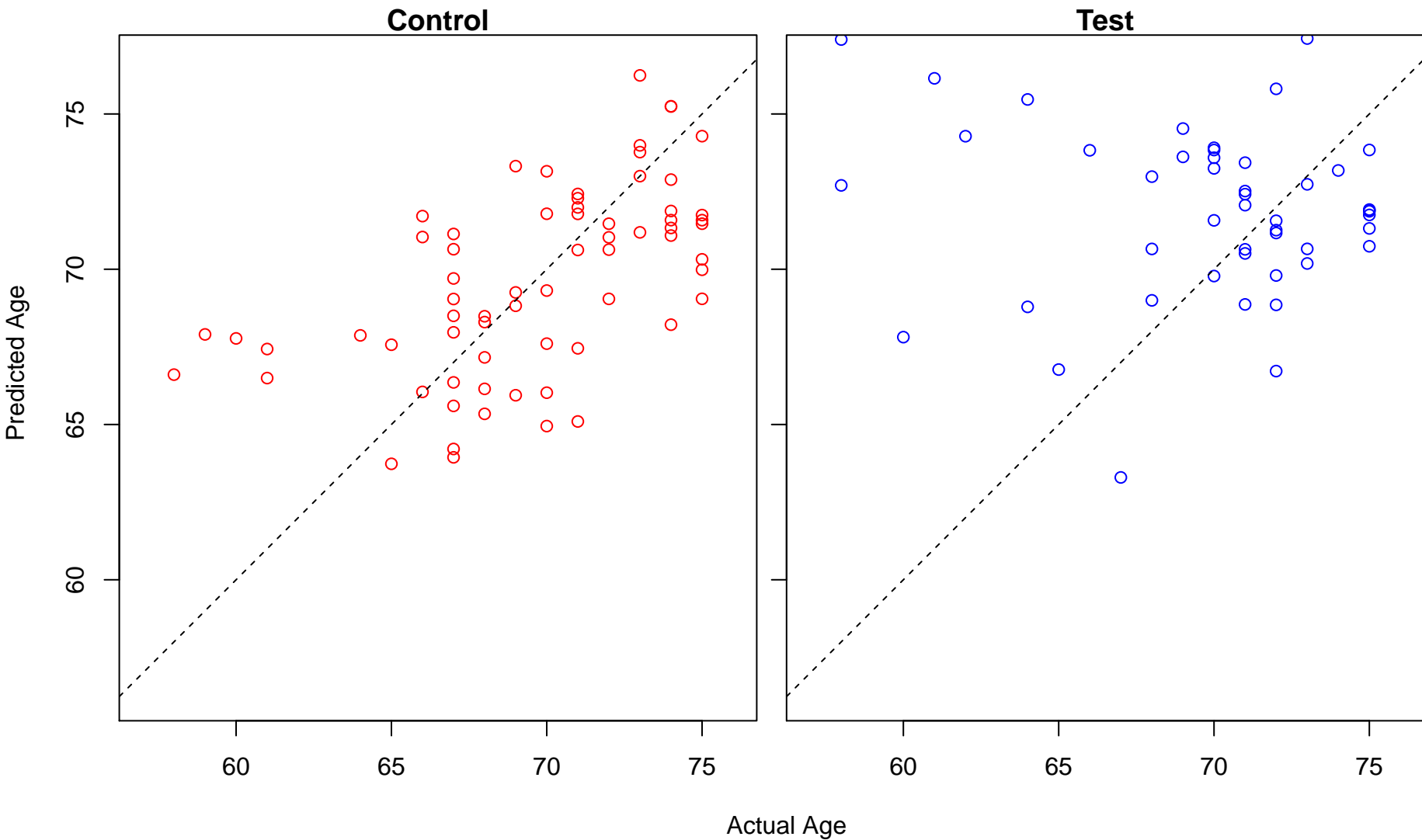
ncRNA catabolic process (Score: 1.167925)



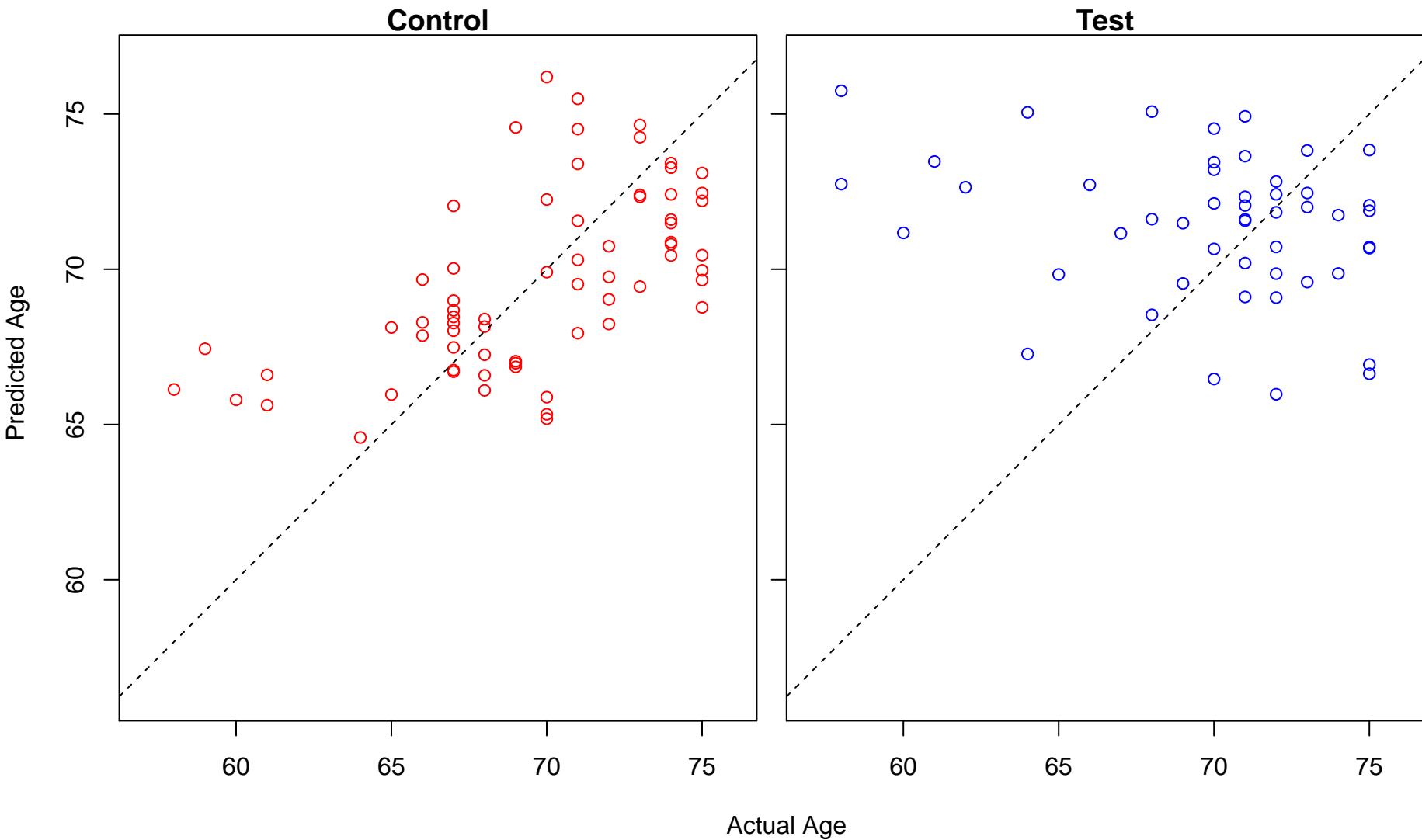
positive regulation of protein kinase B signaling (Score: 1.167859)



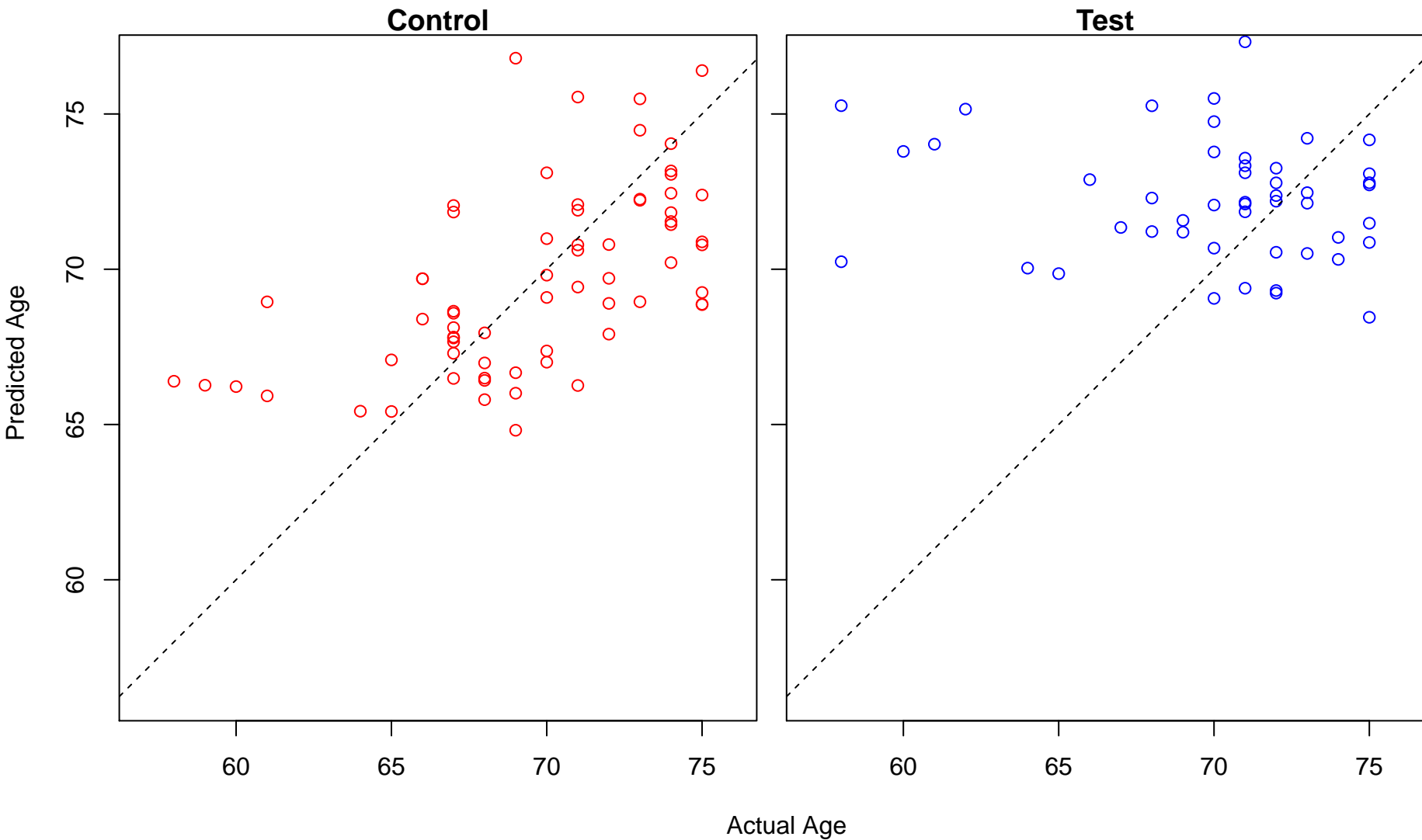
female pregnancy (Score: 1.167797)



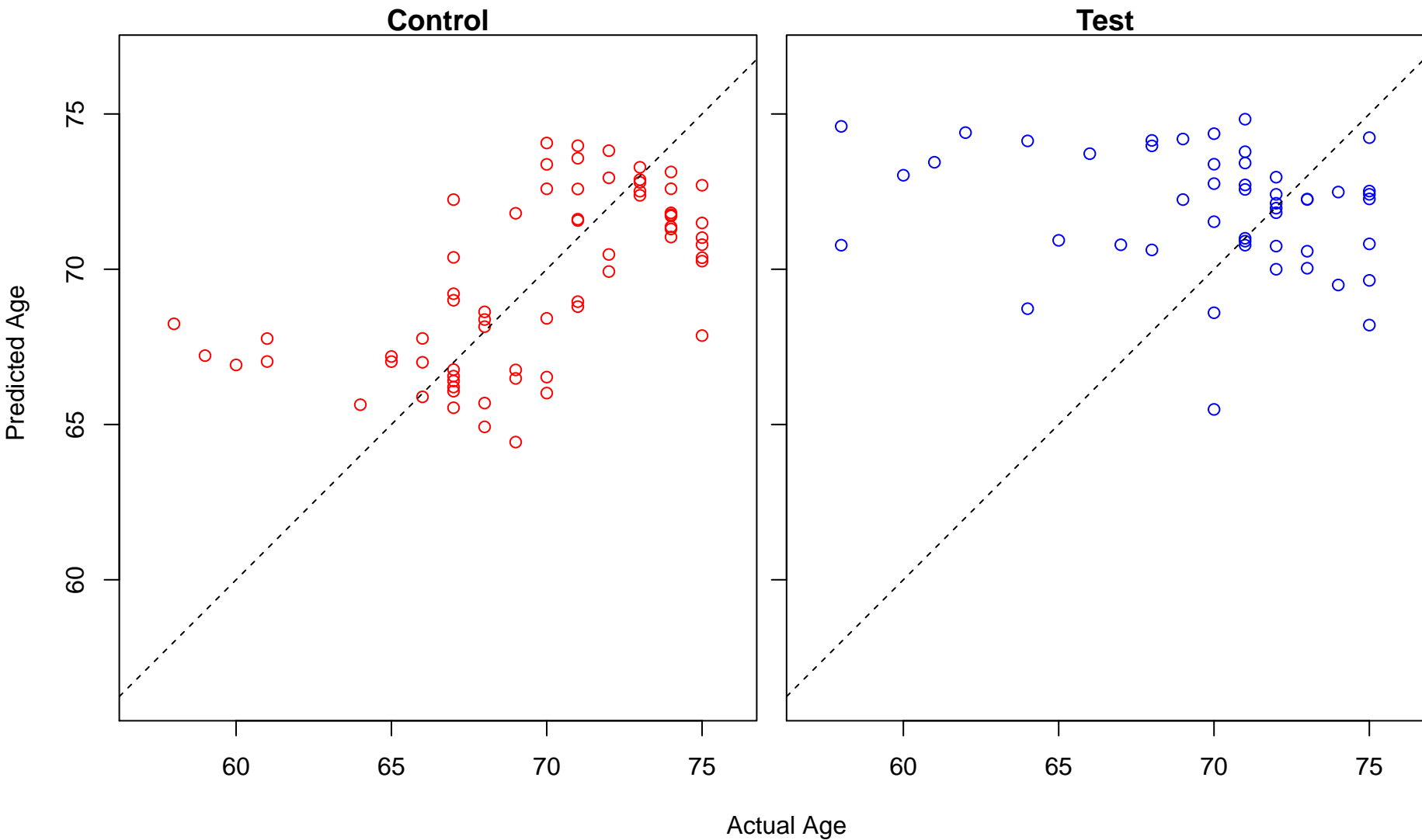
cellular response to UV (Score: 1.167775)



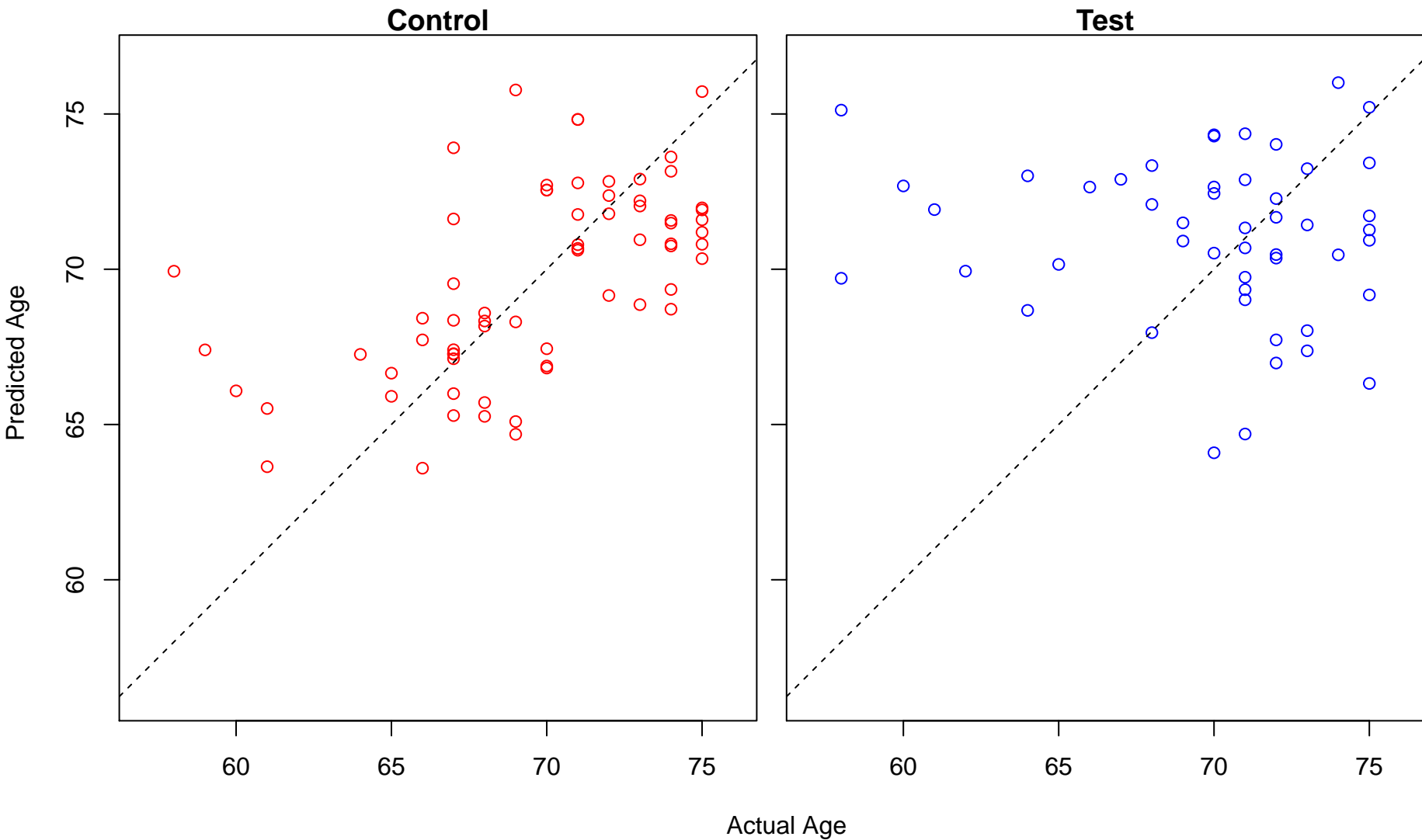
establishment of protein localization to mitochondrial membrane (Score: 1.167331)



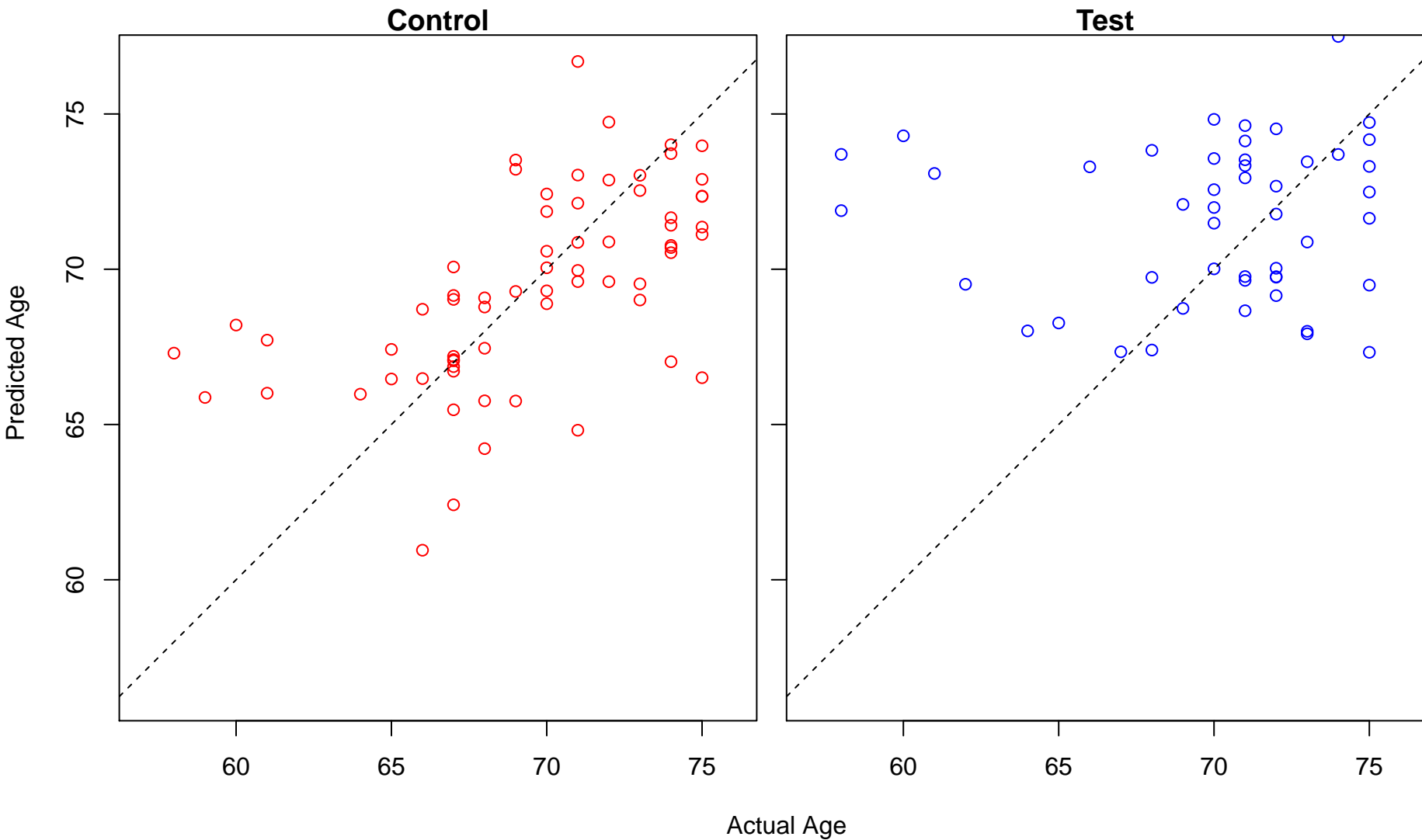
negative regulation of cell cycle G2/M phase transition (Score: 1.166949)



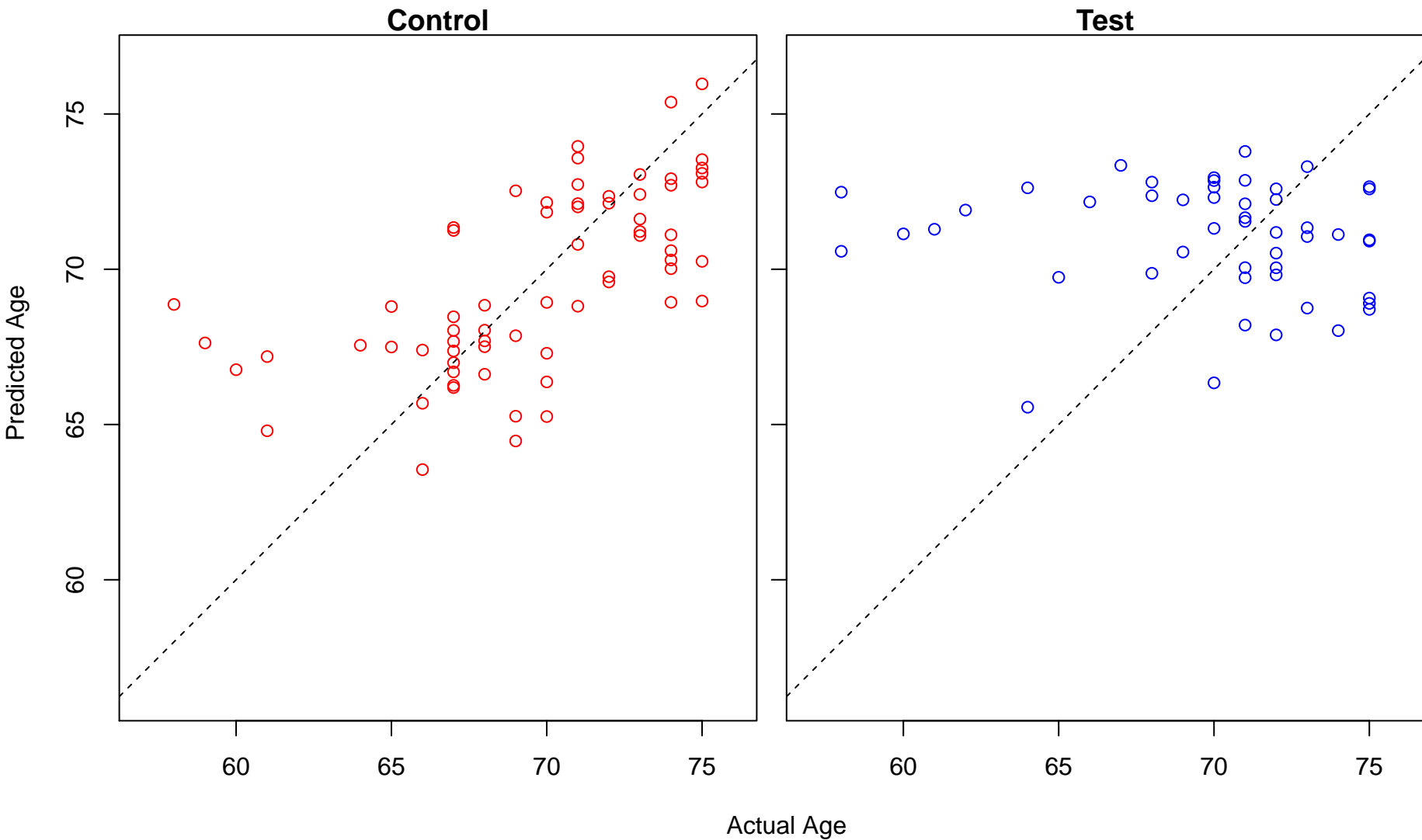
mitotic spindle assembly (Score: 1.166799)



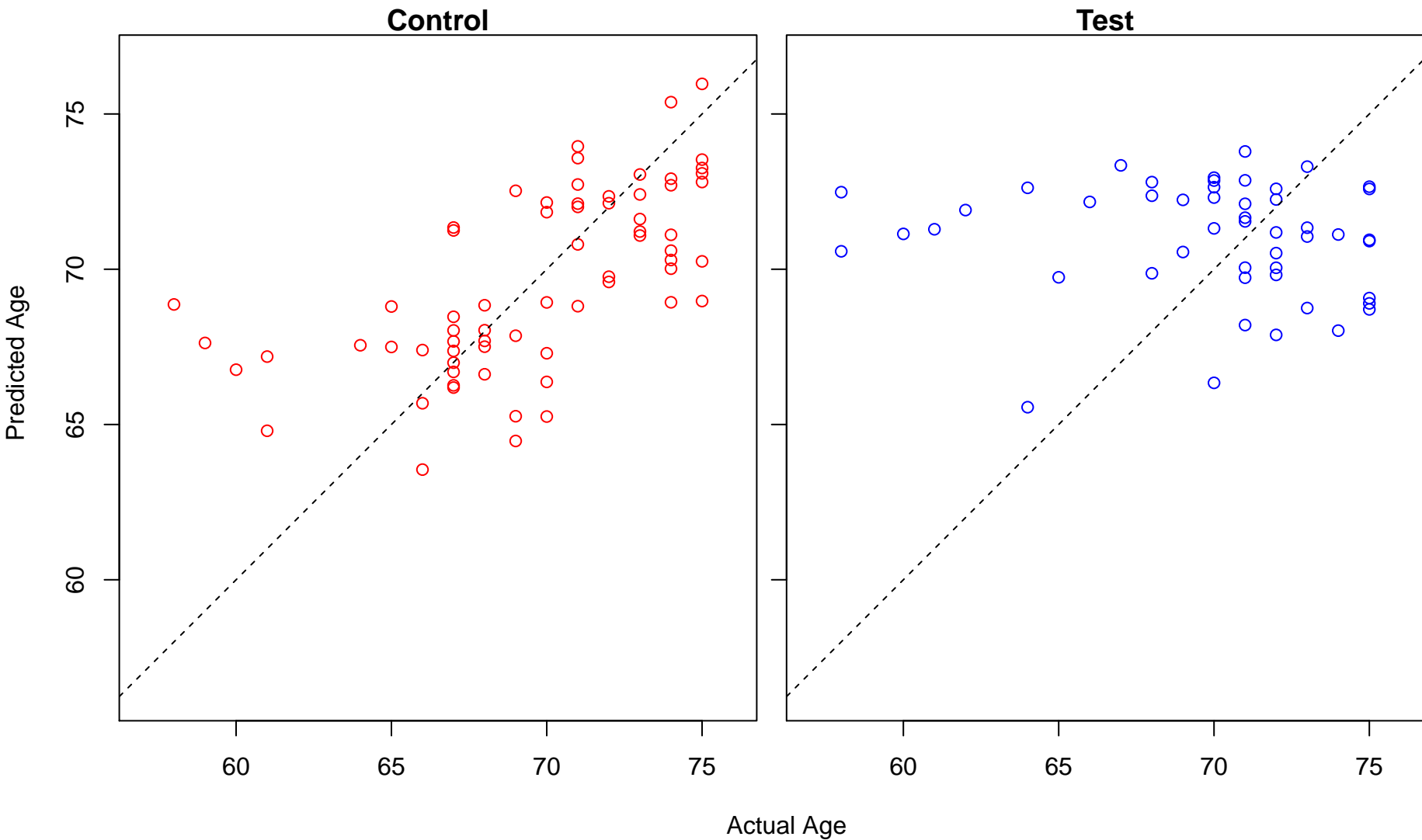
negative regulation of receptor binding (Score: 1.166580)



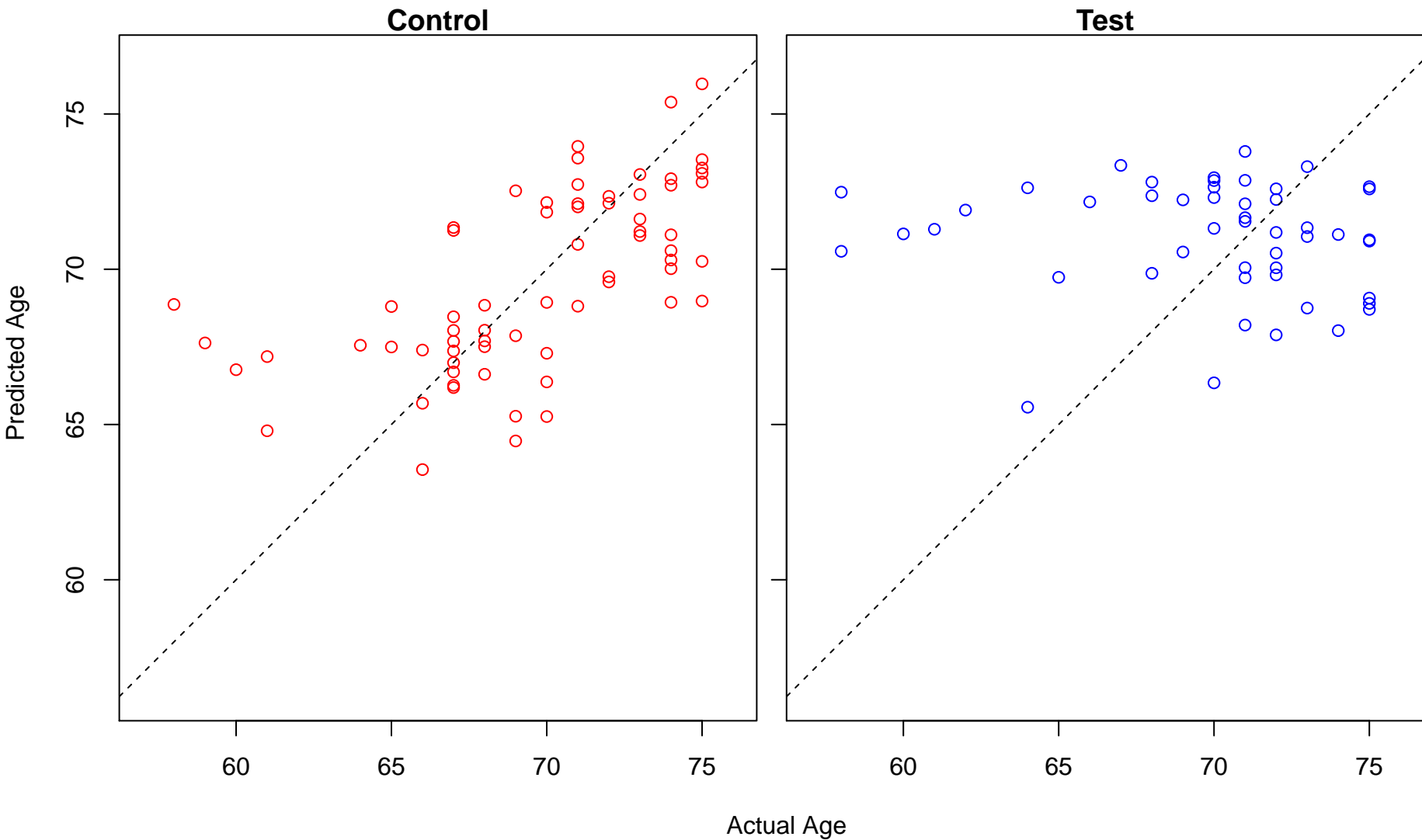
positive regulation of mitotic metaphase/anaphase transition (Score: 1.166153)



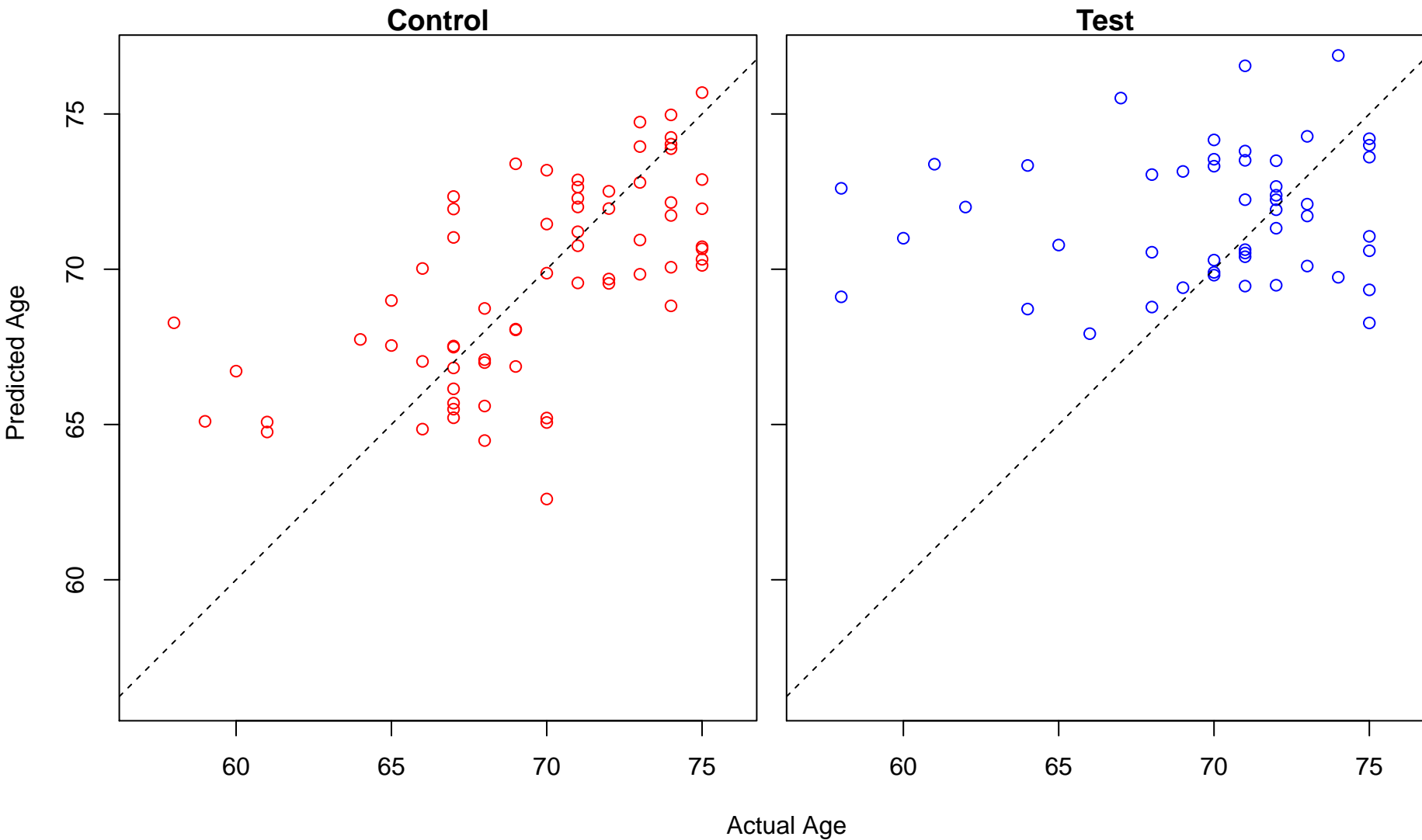
positive regulation of mitotic sister chromatid separation (Score: 1.166153)



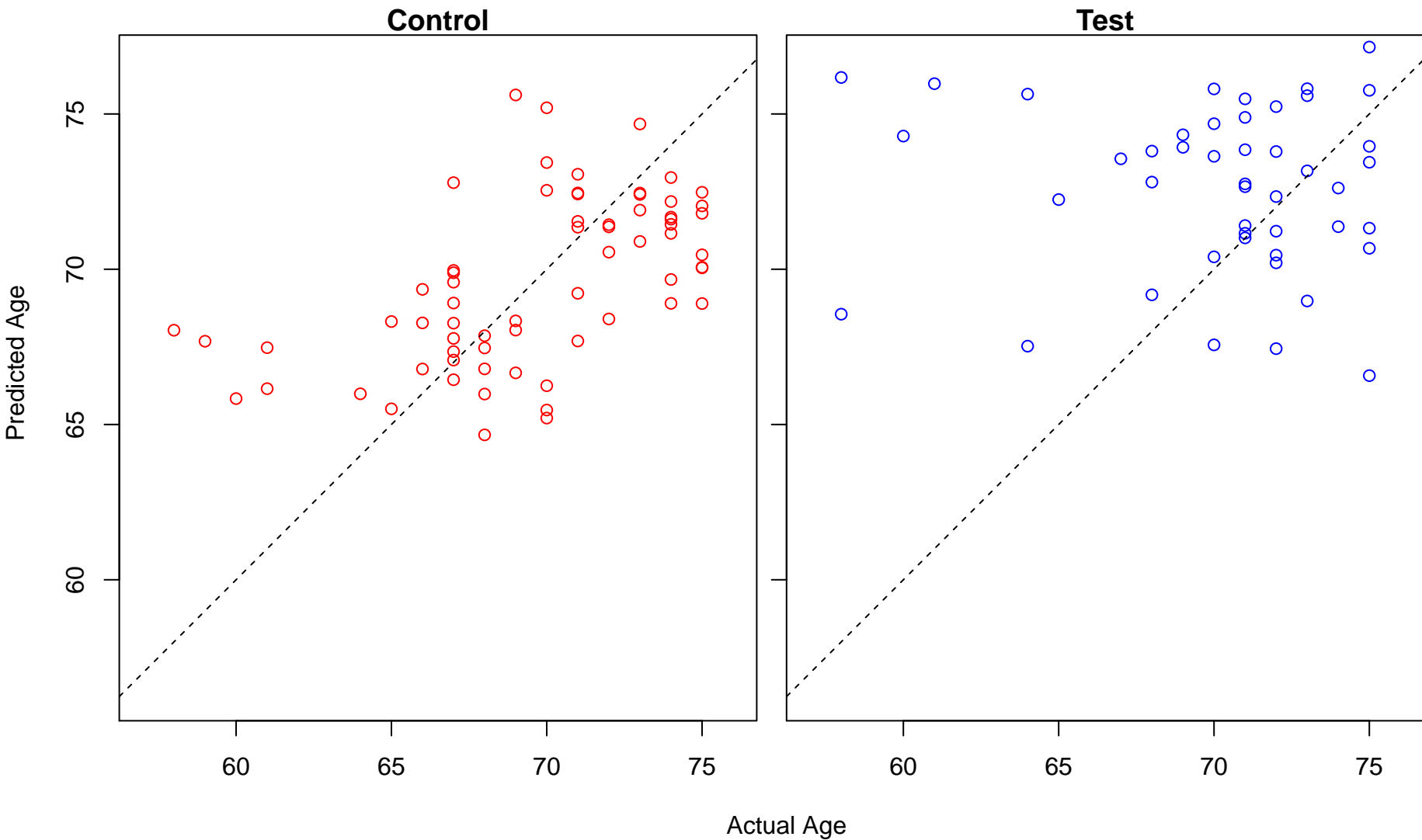
positive regulation of metaphase/anaphase transition of cell cycle (Score: 1.166153)



nucleobase metabolic process (Score: 1.165660)

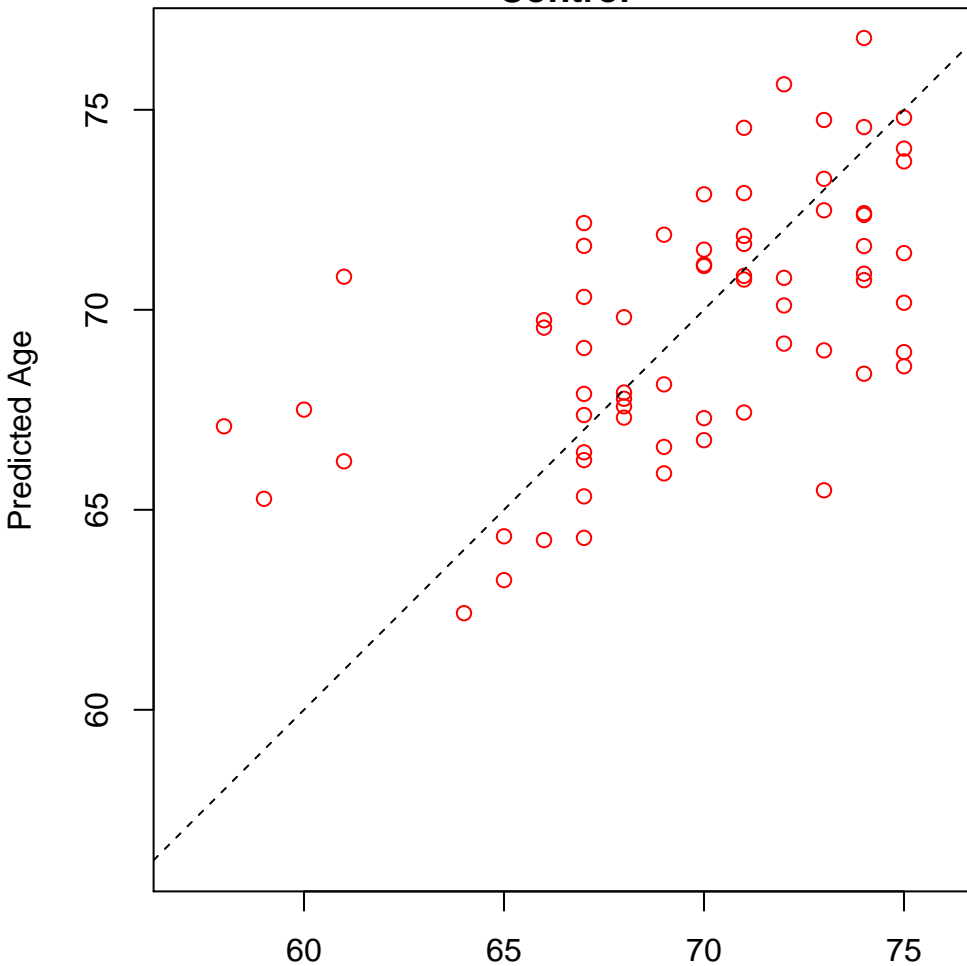


error-prone translesion synthesis (Score: 1.165466)

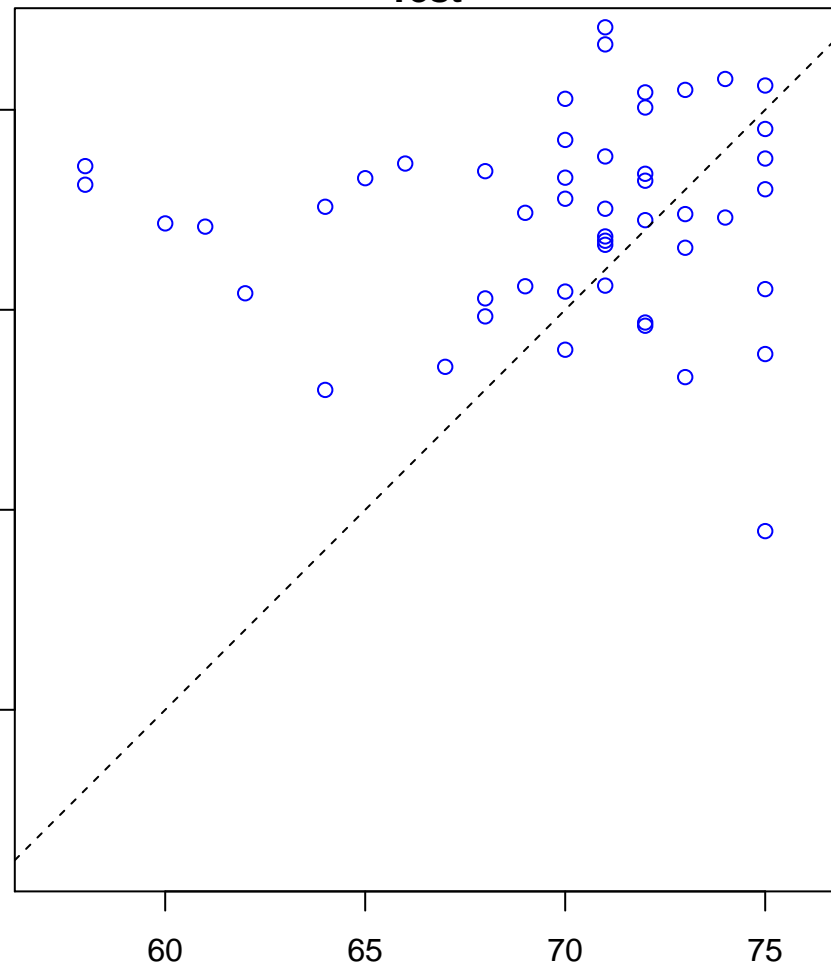


unsaturated fatty acid metabolic process (Score: 1.164803)

Control

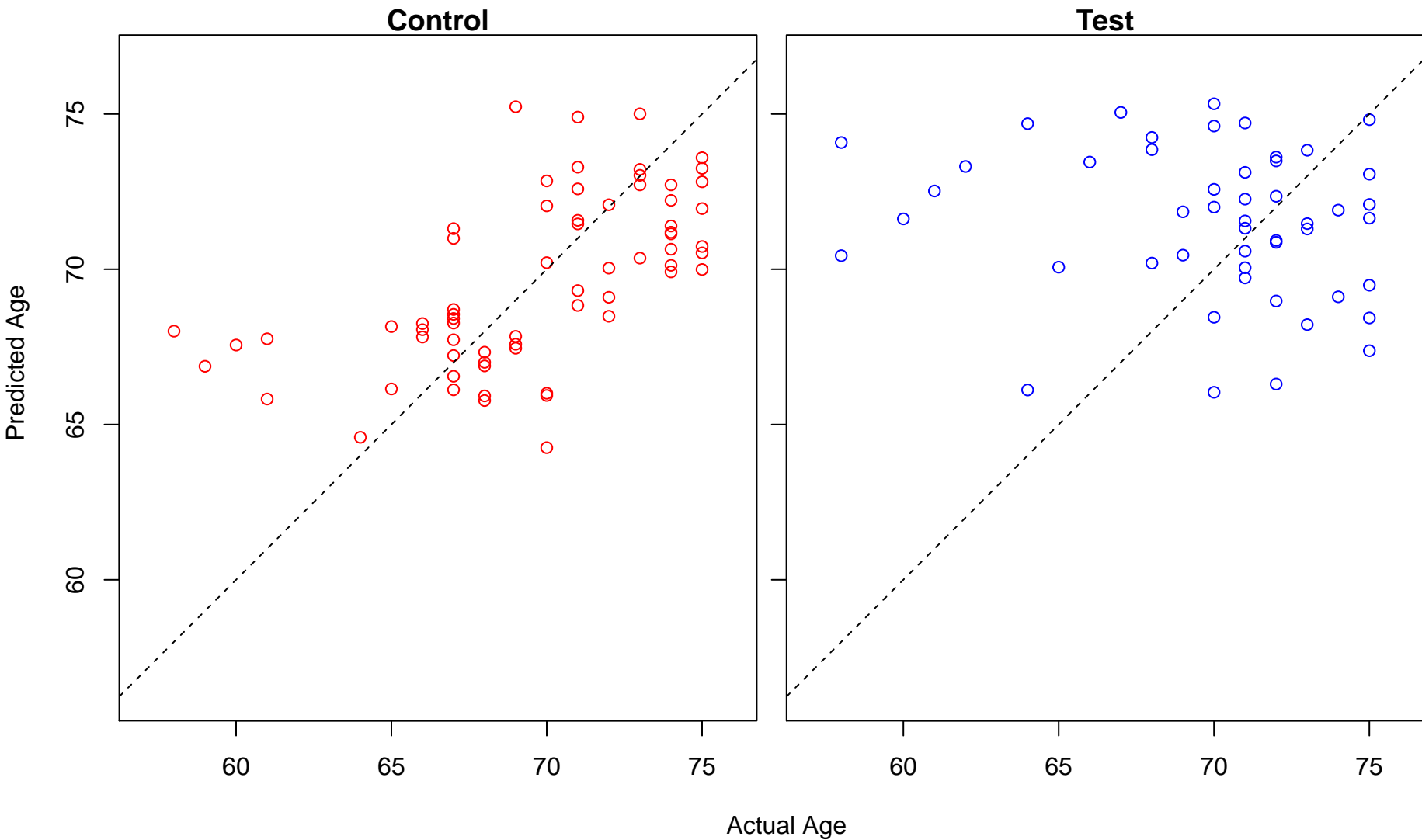


Test



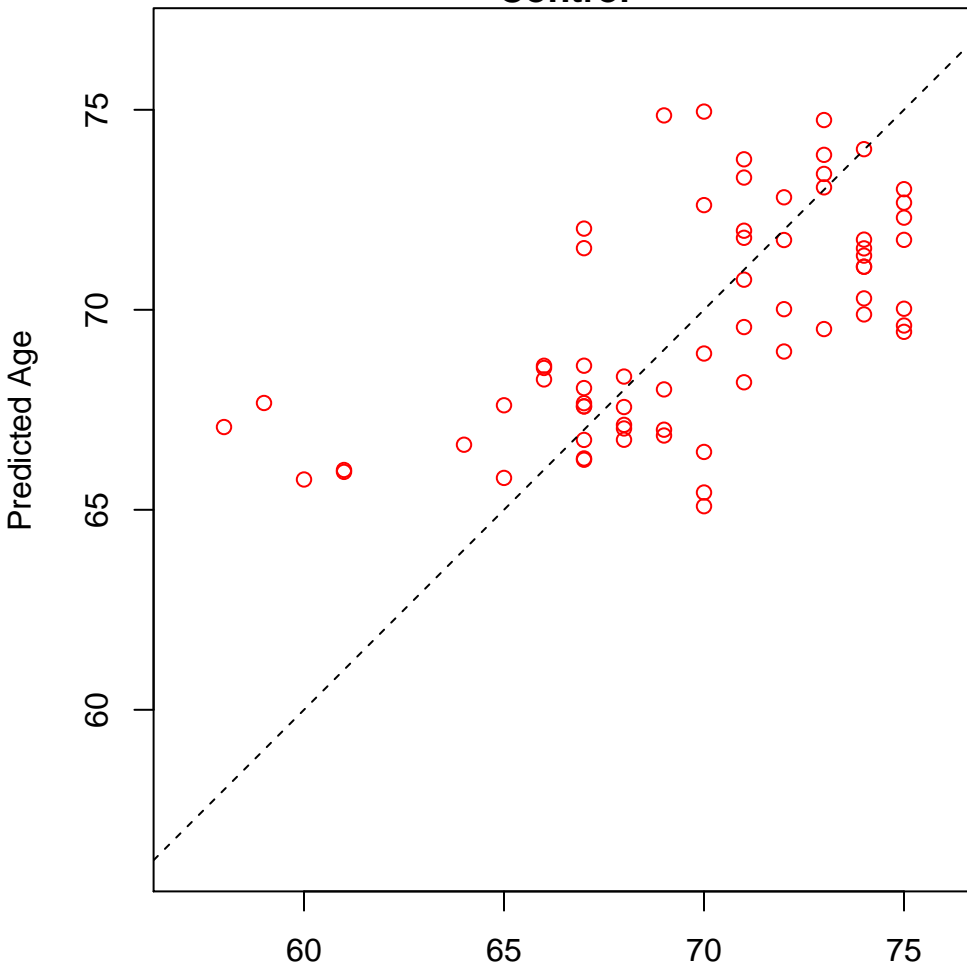
Actual Age

RNA methylation (Score: 1.164608)

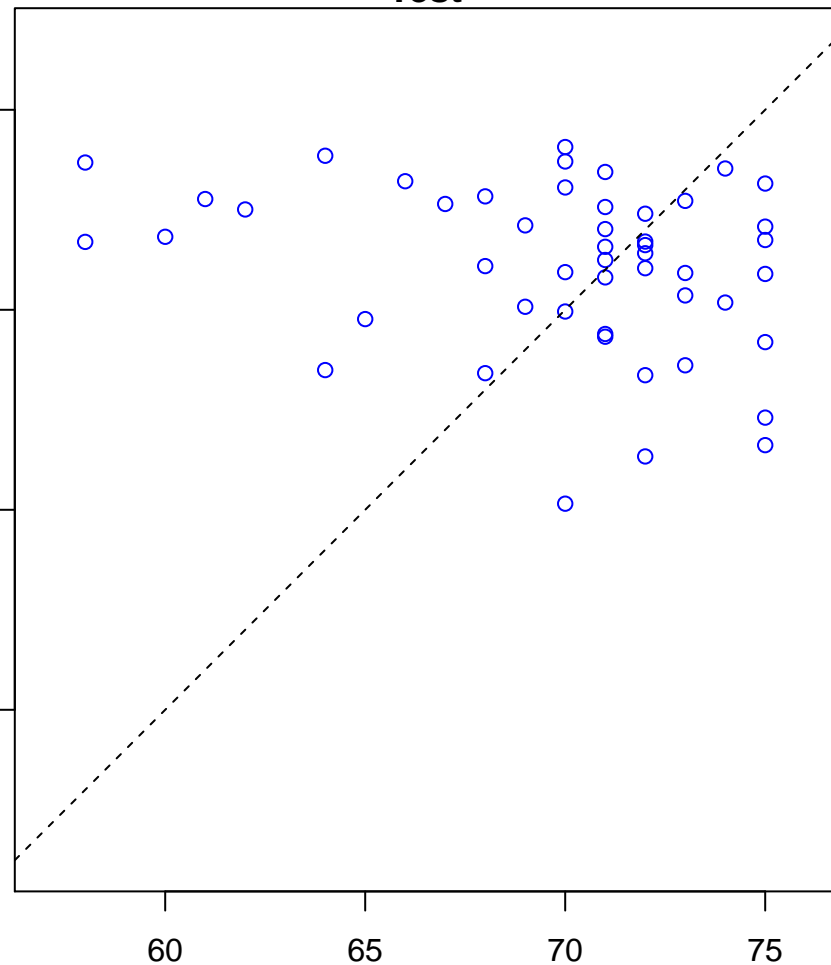


cellular response to biotic stimulus (Score: 1.164347)

Control

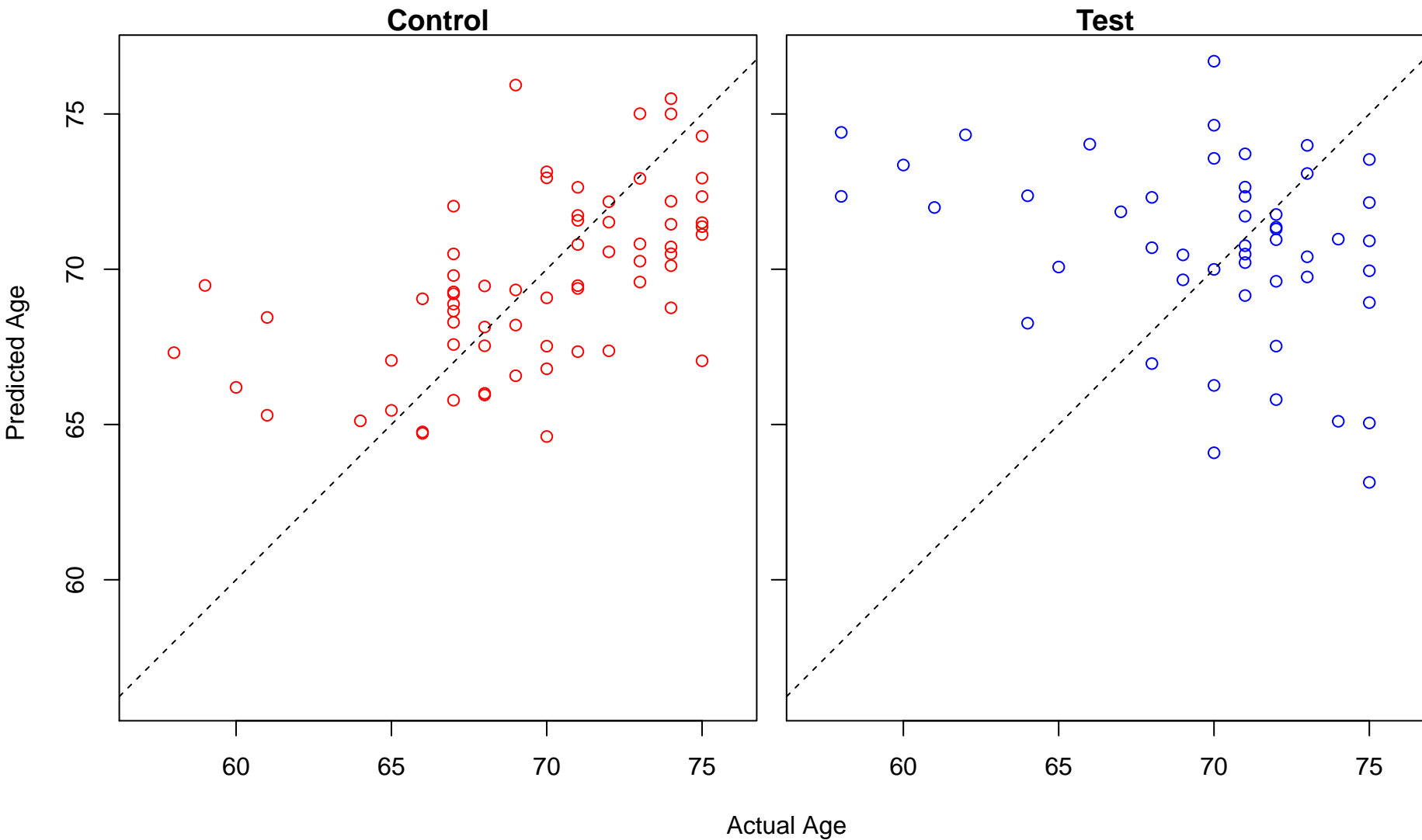


Test



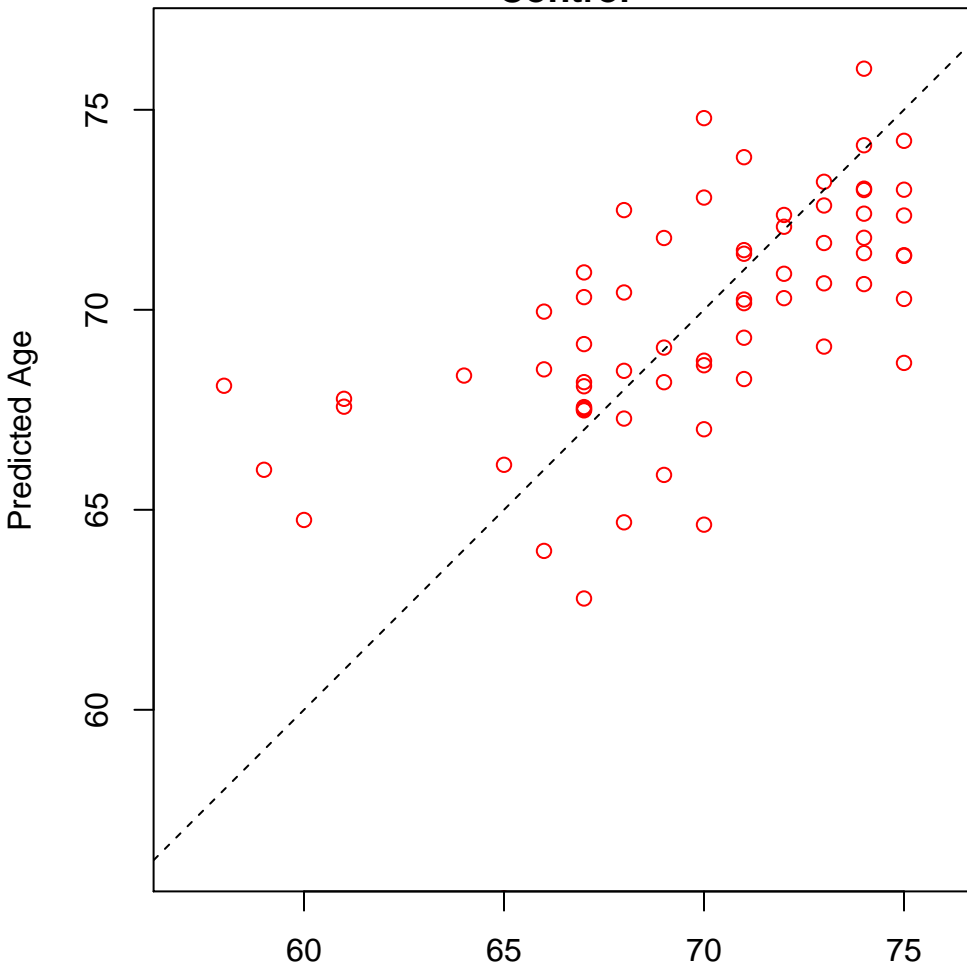
Actual Age

positive regulation of protein exit from endoplasmic reticulum (Score: 1.164249)

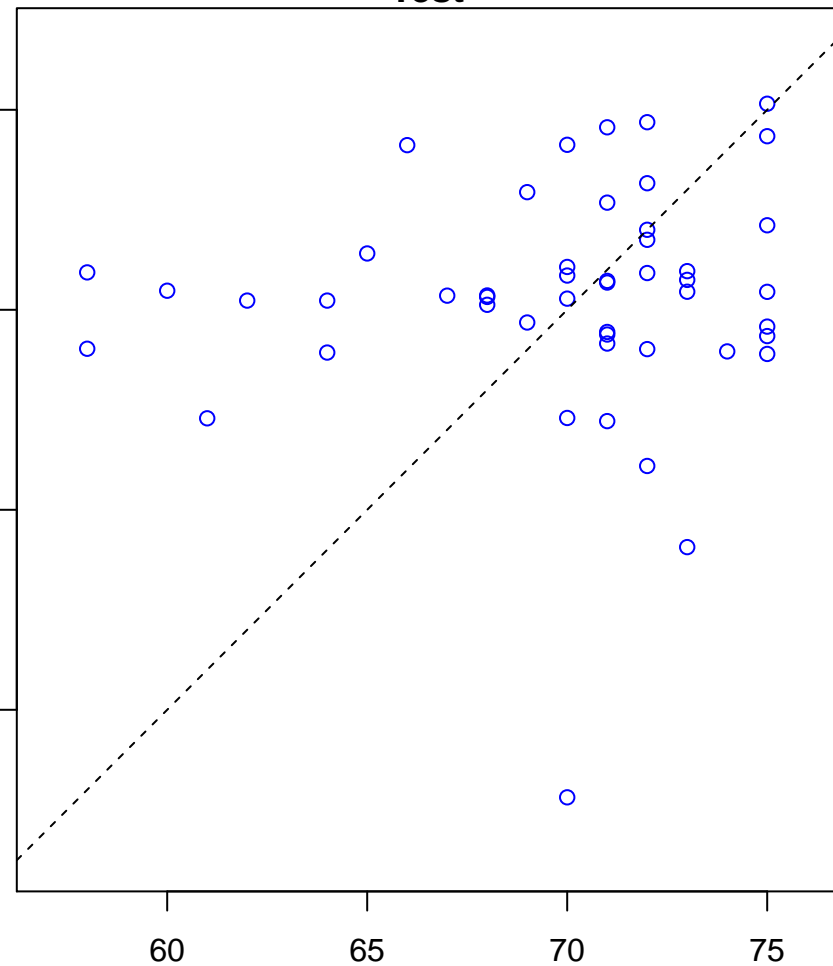


chemokine-mediated signaling pathway (Score: 1.163786)

Control

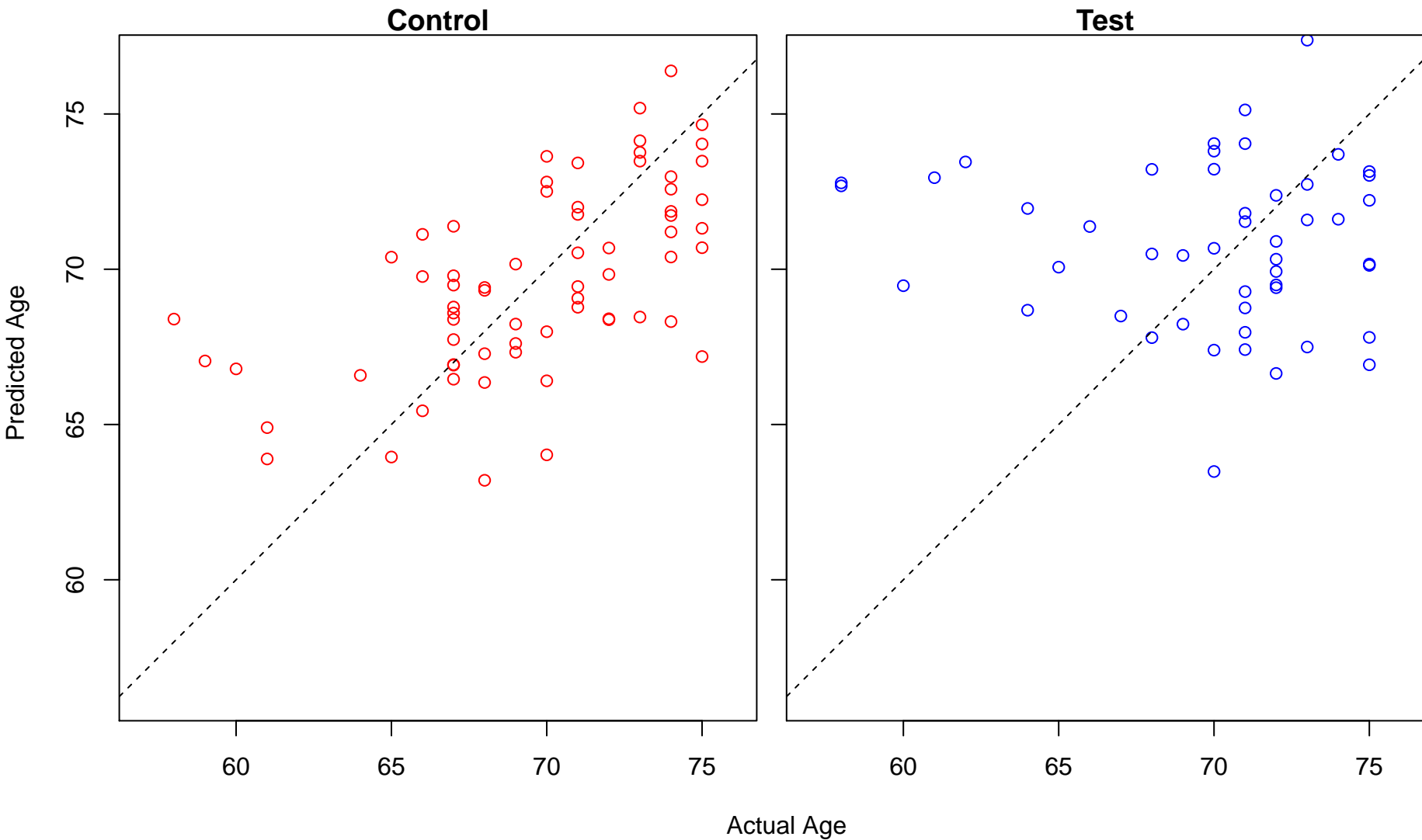


Test

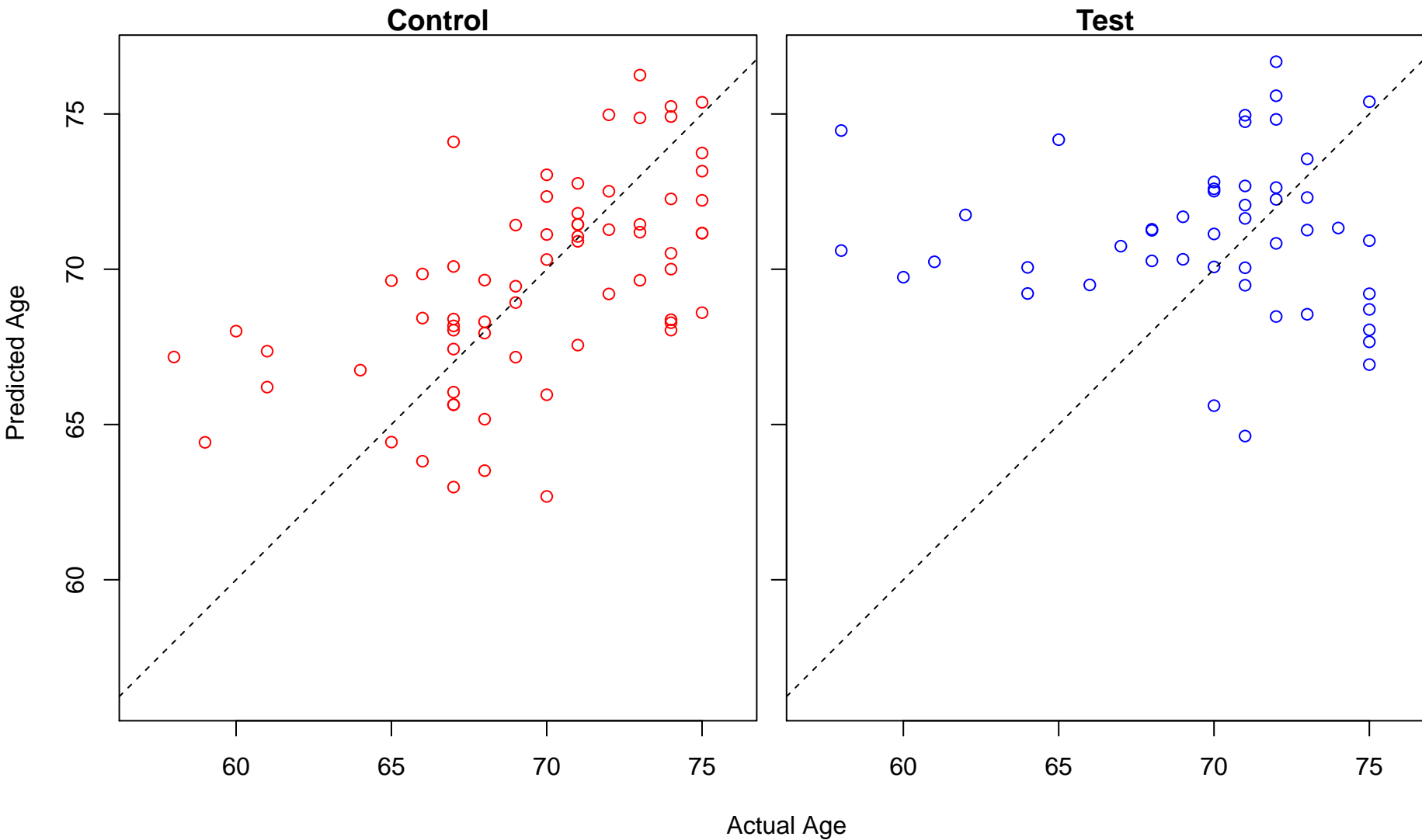


Actual Age

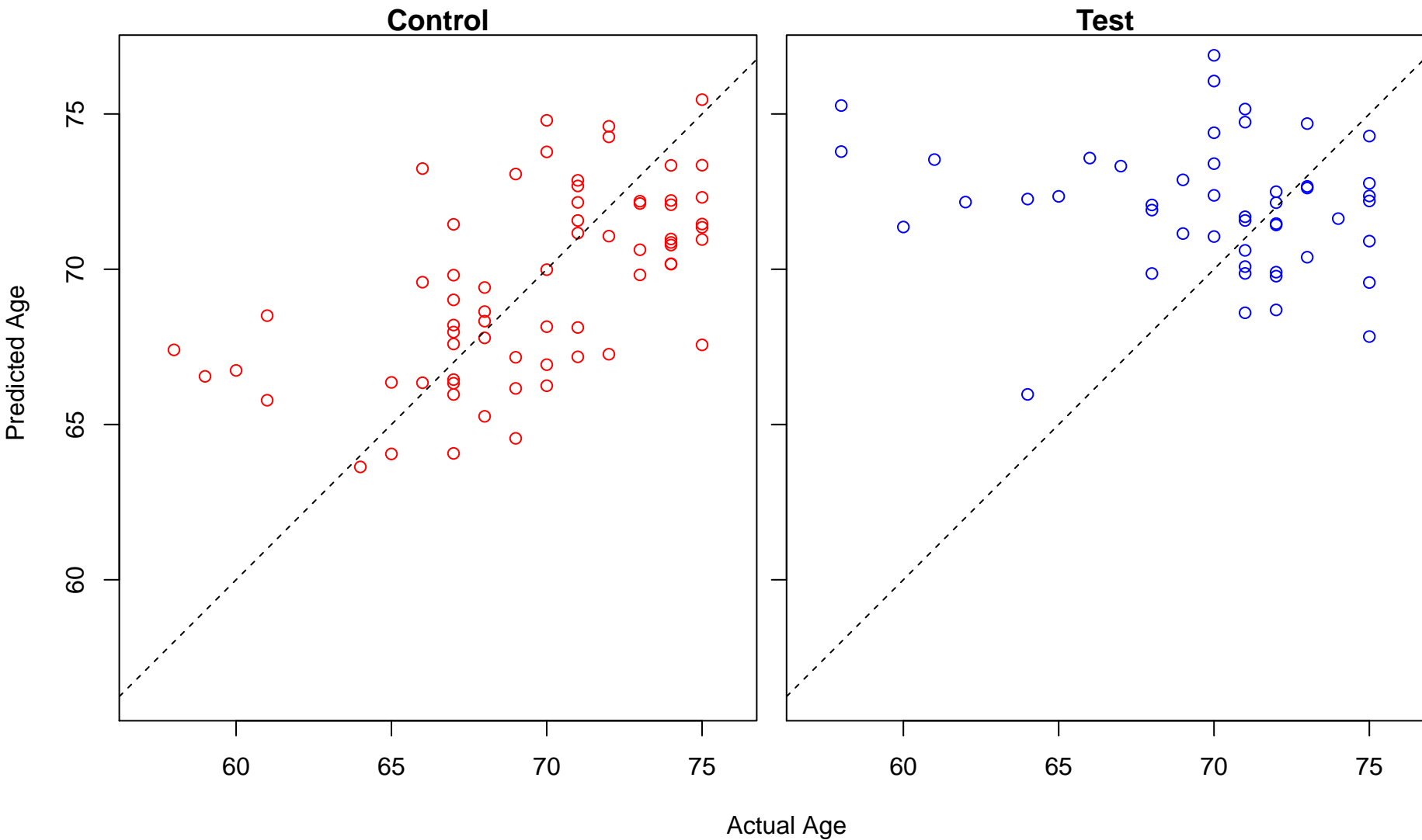
negative regulation of protein polymerization (Score: 1.163576)



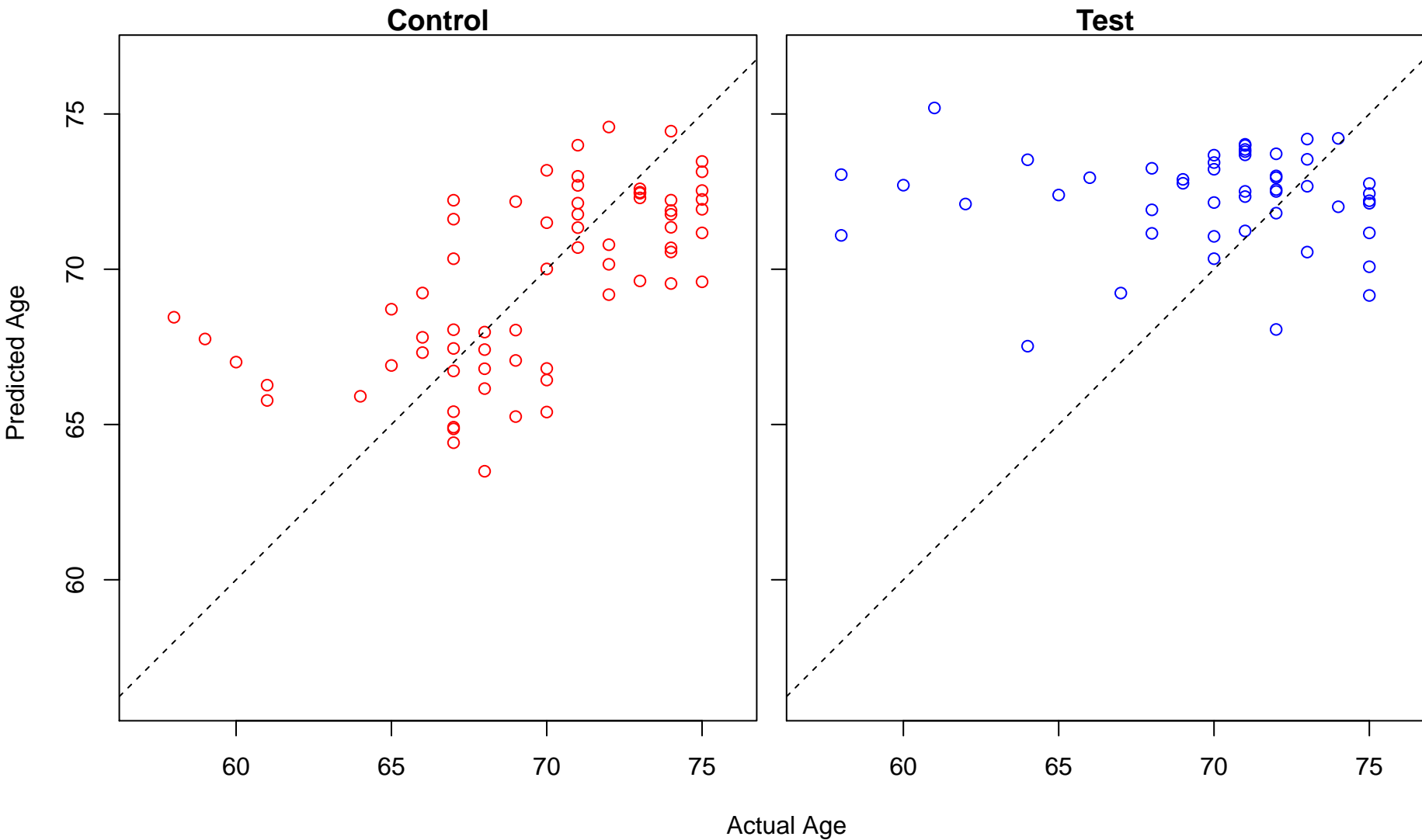
regulation of protein tyrosine kinase activity (Score: 1.163418)



learning (Score: 1.162896)

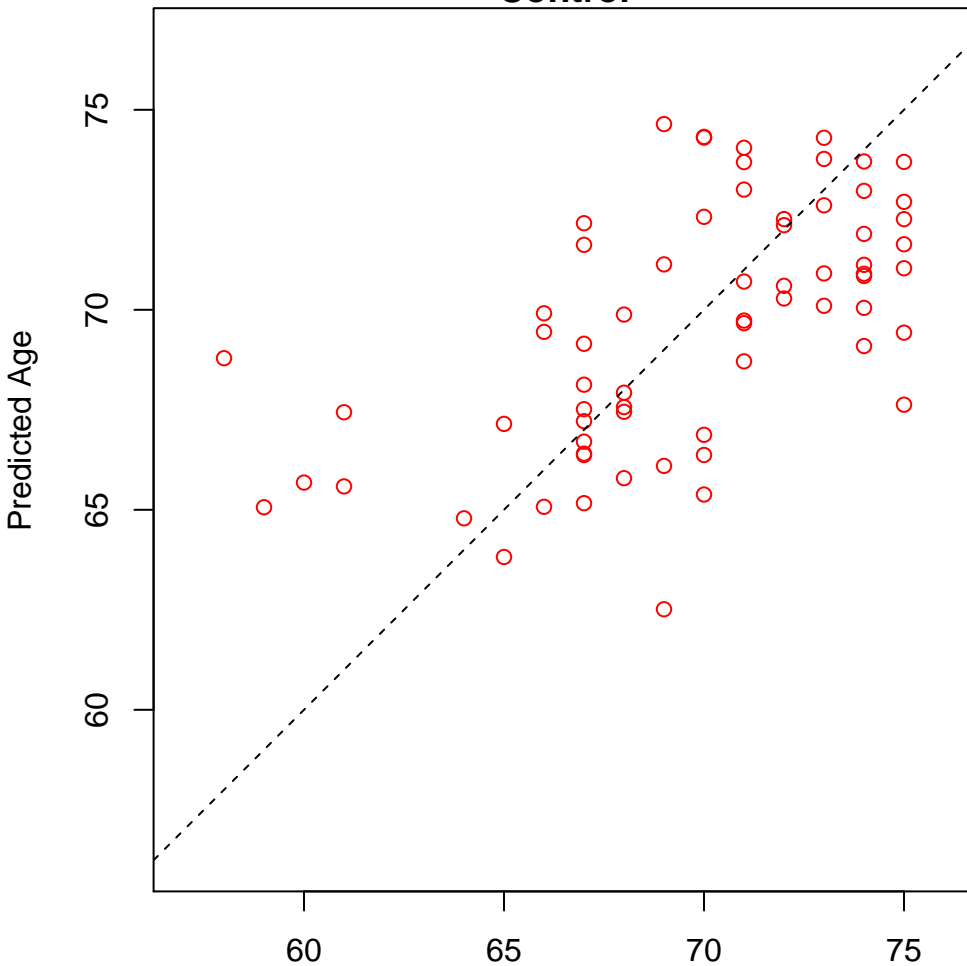


regulation of megakaryocyte differentiation (Score: 1.162631)

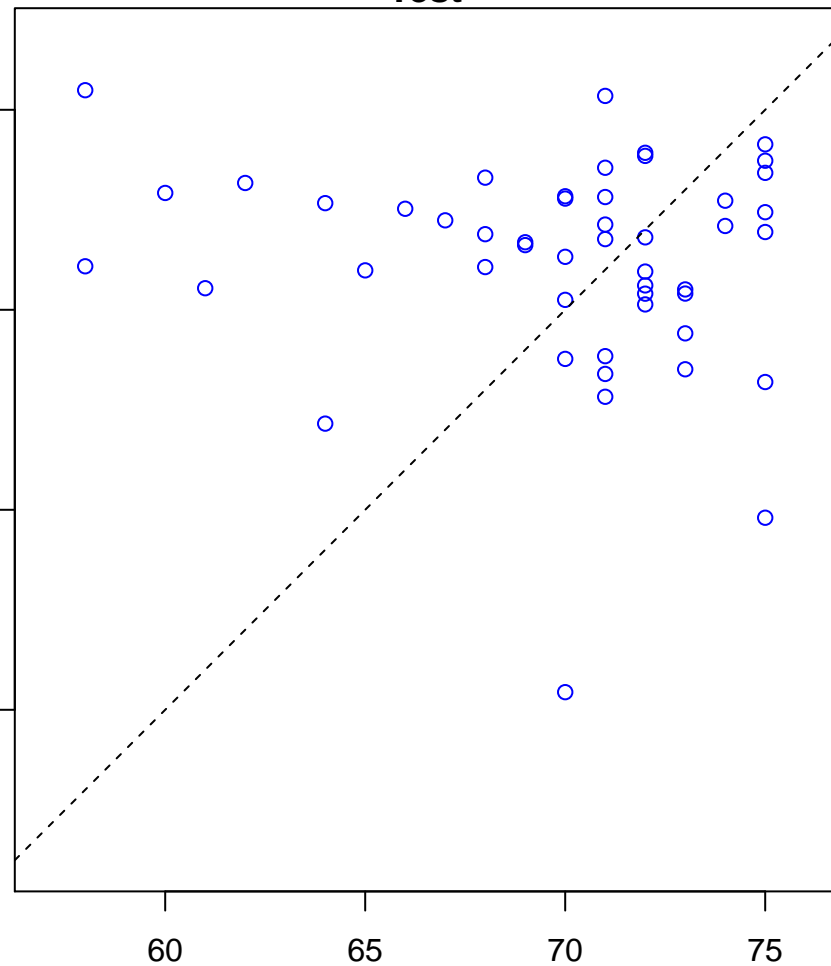


regulation of epithelial cell differentiation (Score: 1.162516)

Control



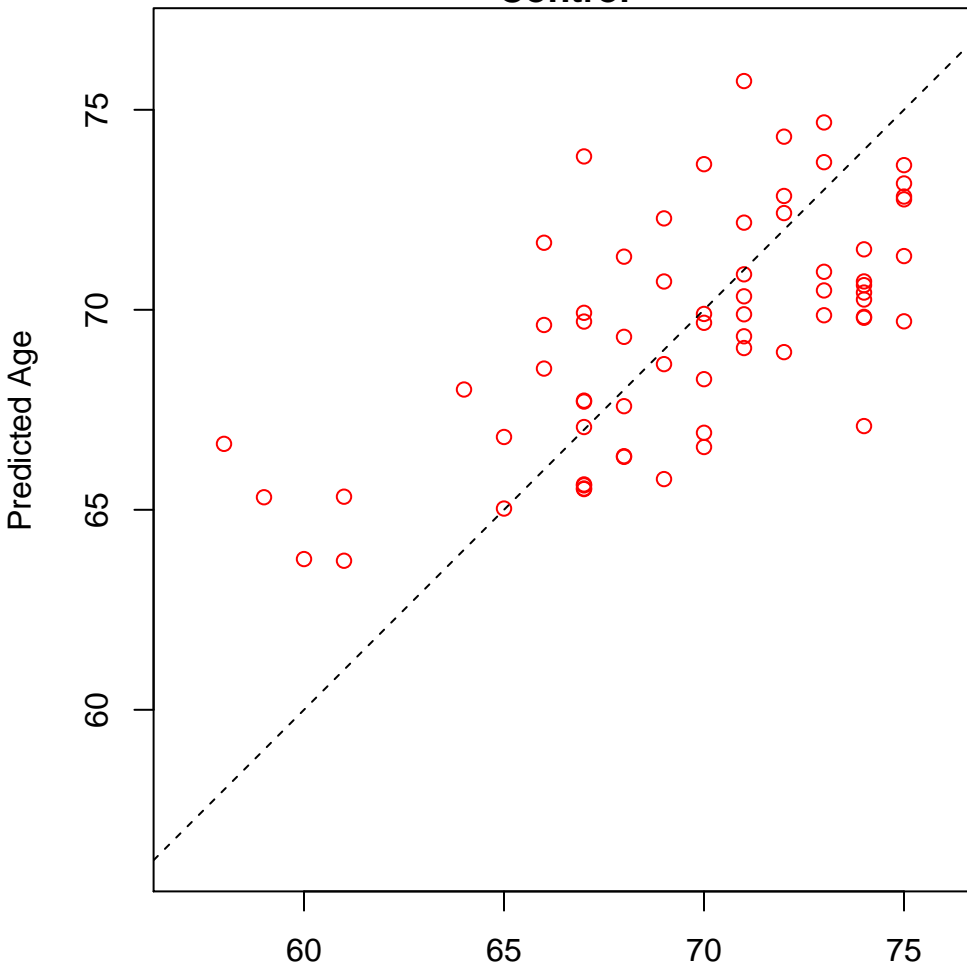
Test



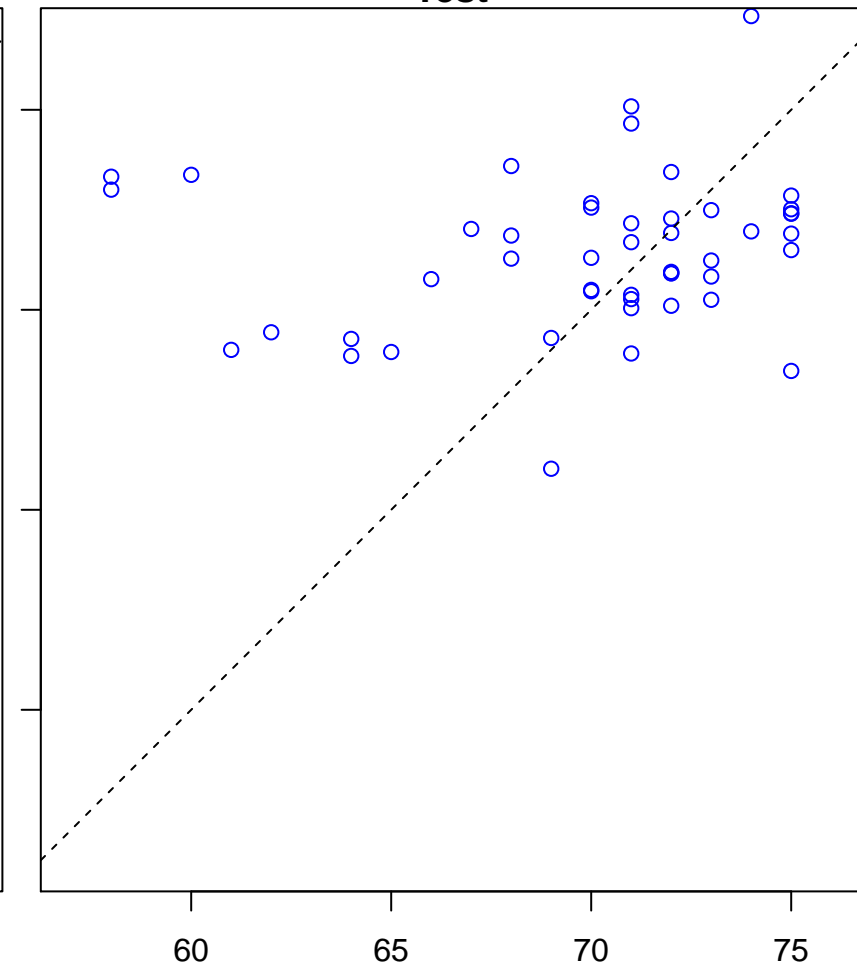
Actual Age

glycosylceramide metabolic process (Score: 1.161354)

Control

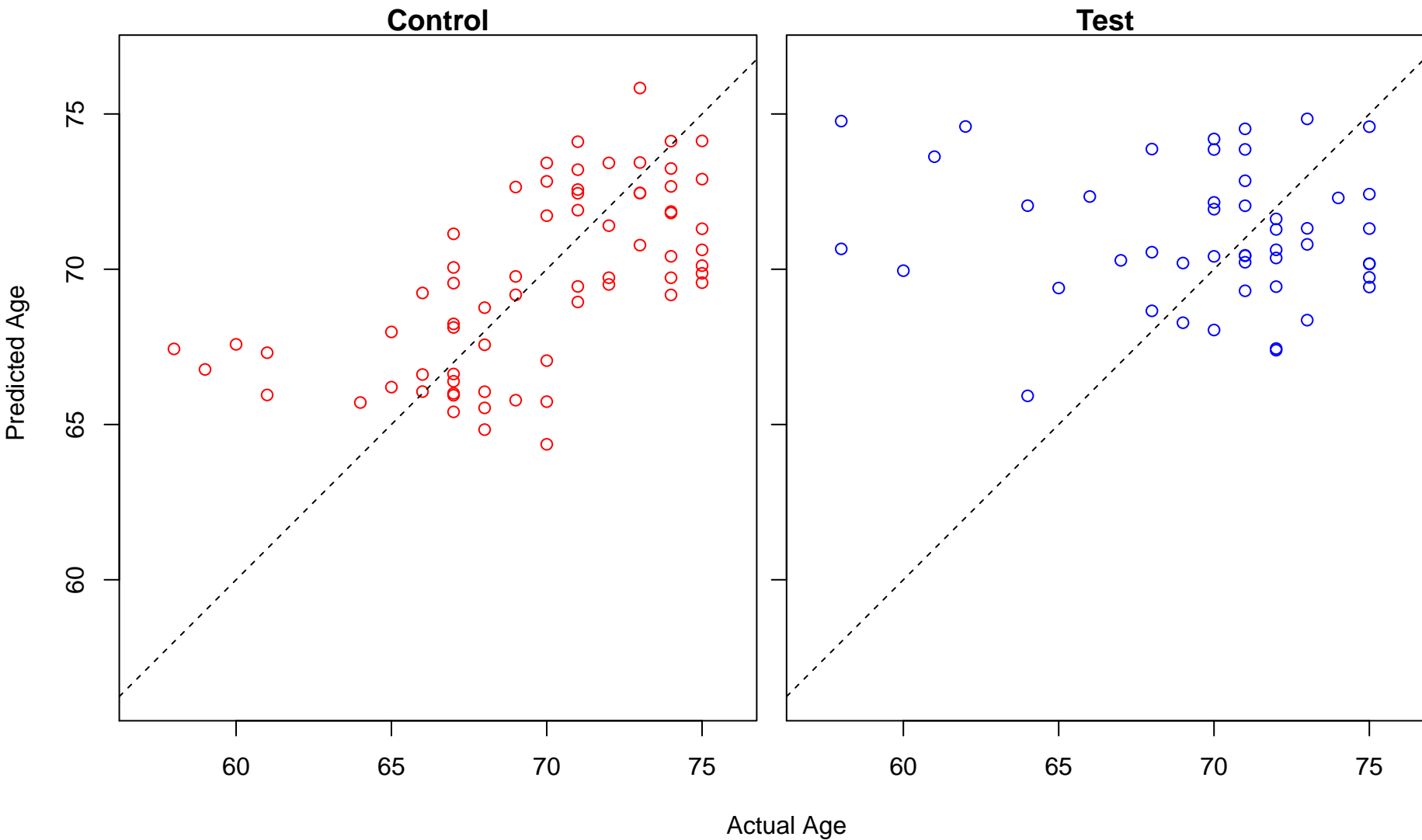


Test

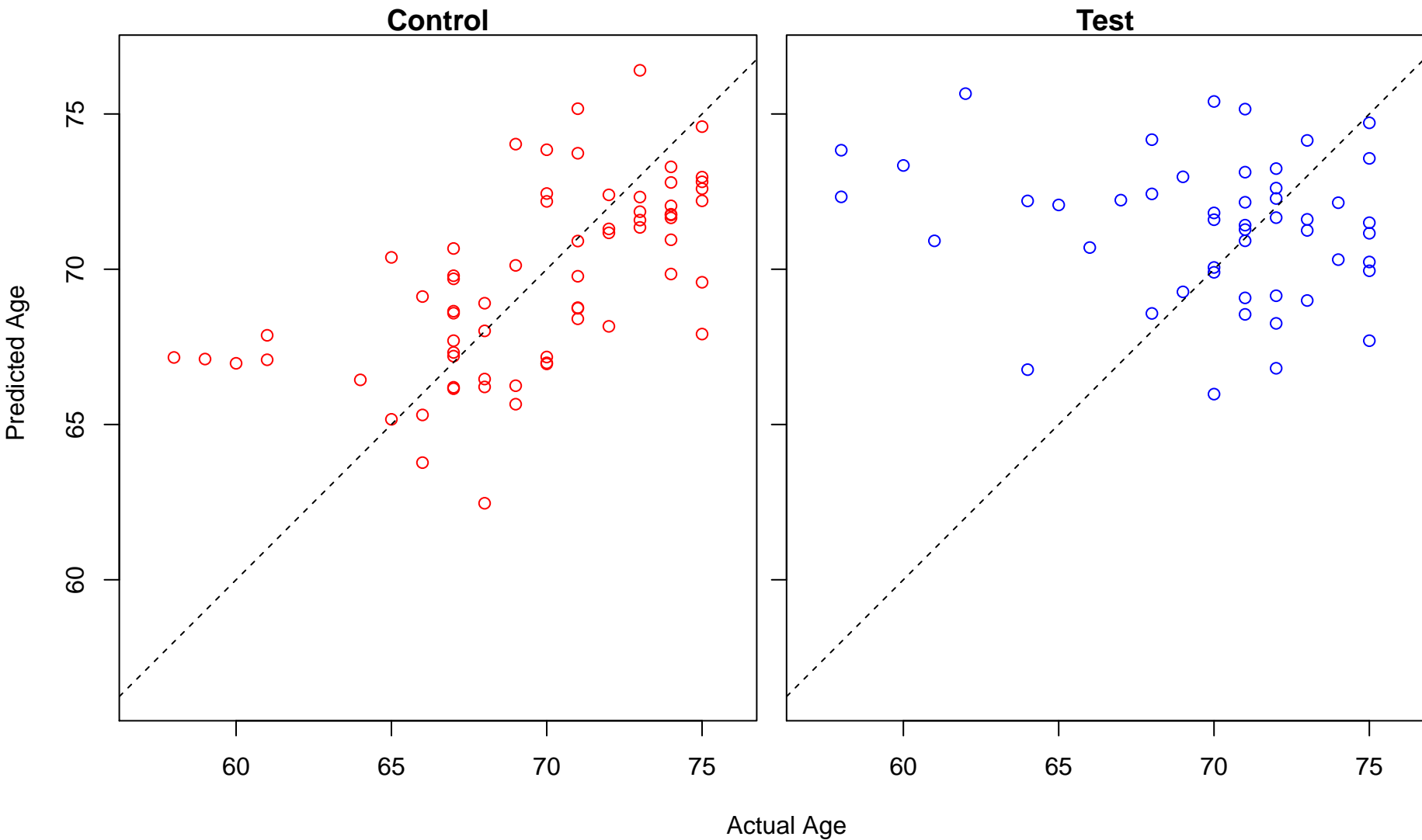


Actual Age

coenzyme metabolic process (Score: 1.160492)

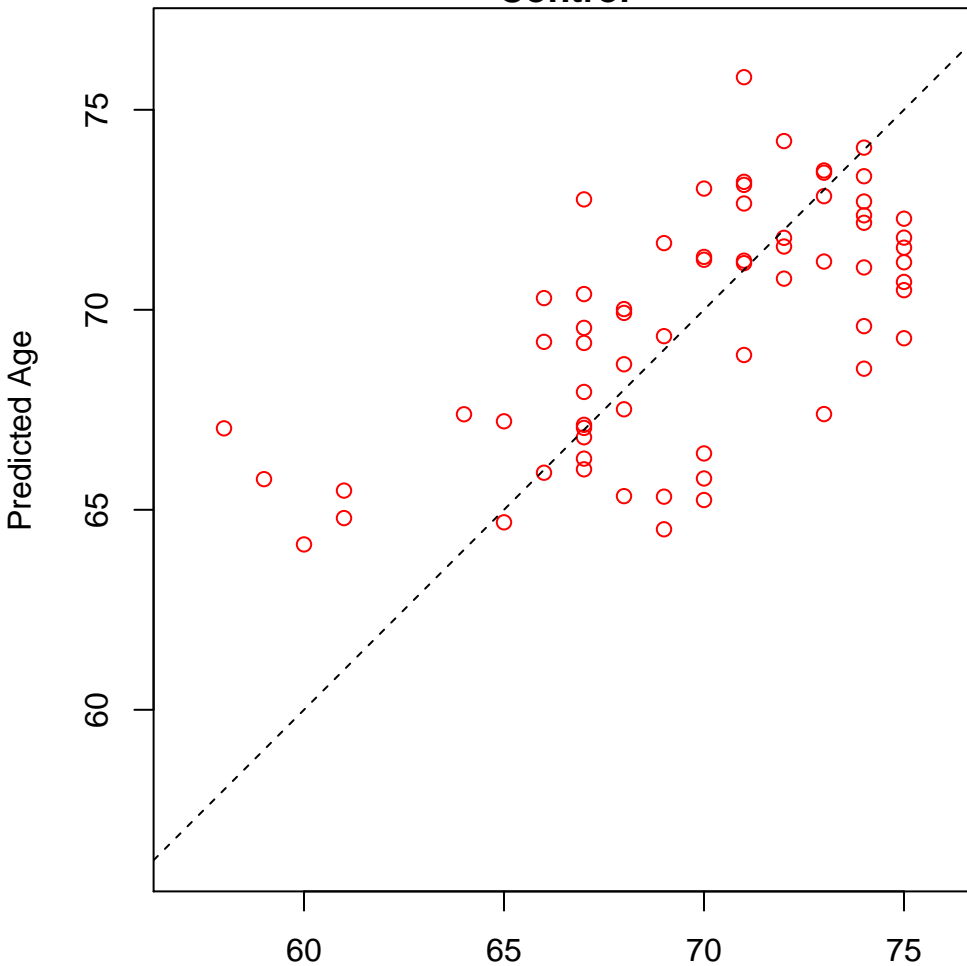


cellular response to vascular endothelial growth factor stimulus (Score: 1.159153)

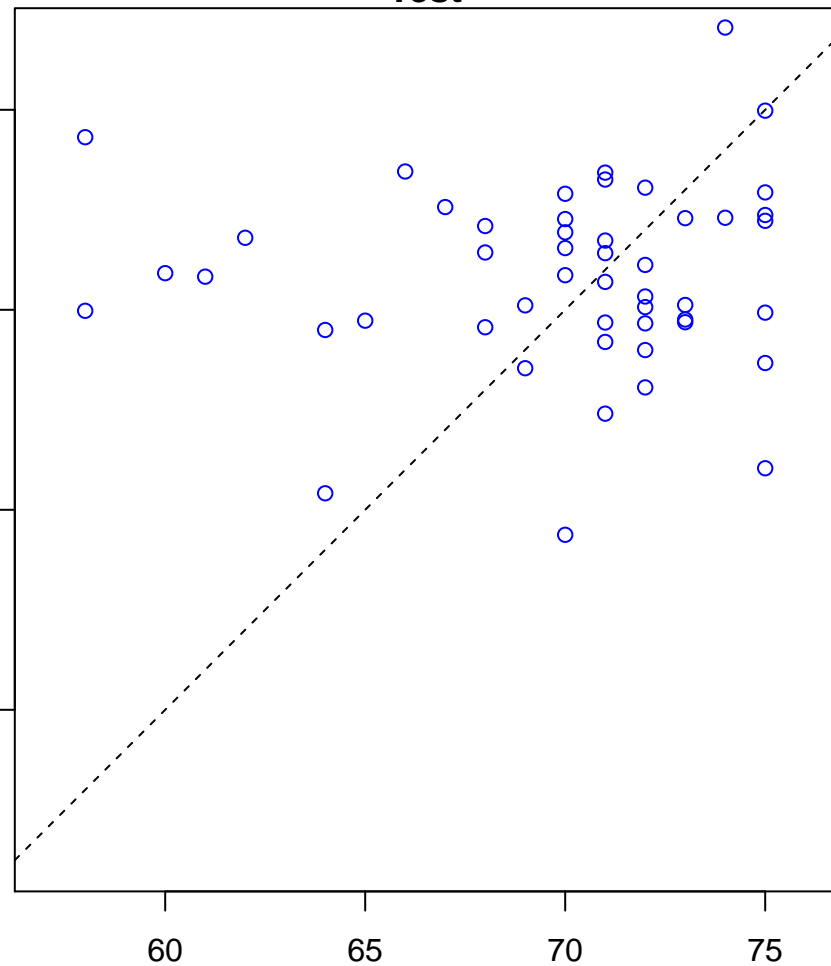


cellular response to glucagon stimulus (Score: 1.159100)

Control

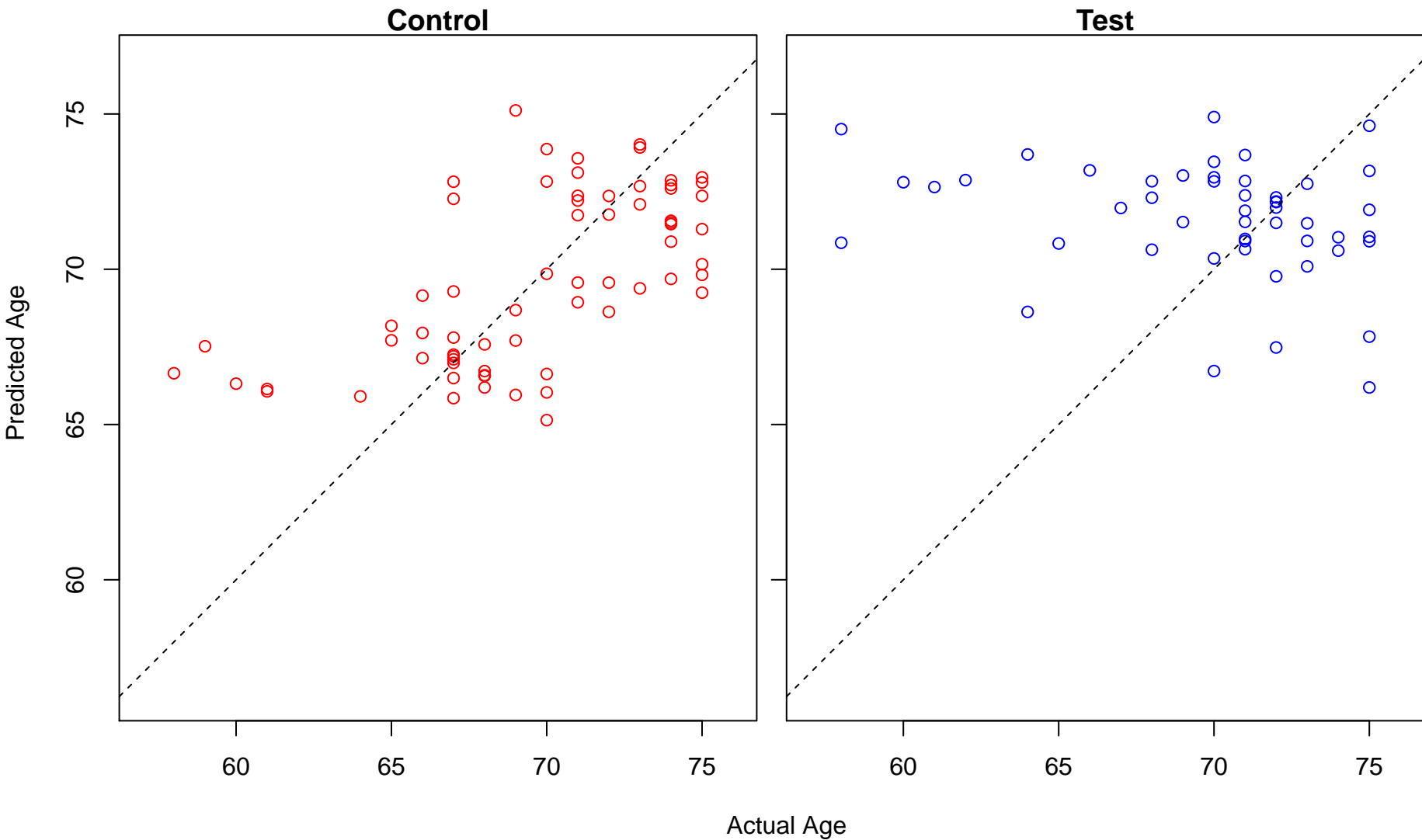


Test

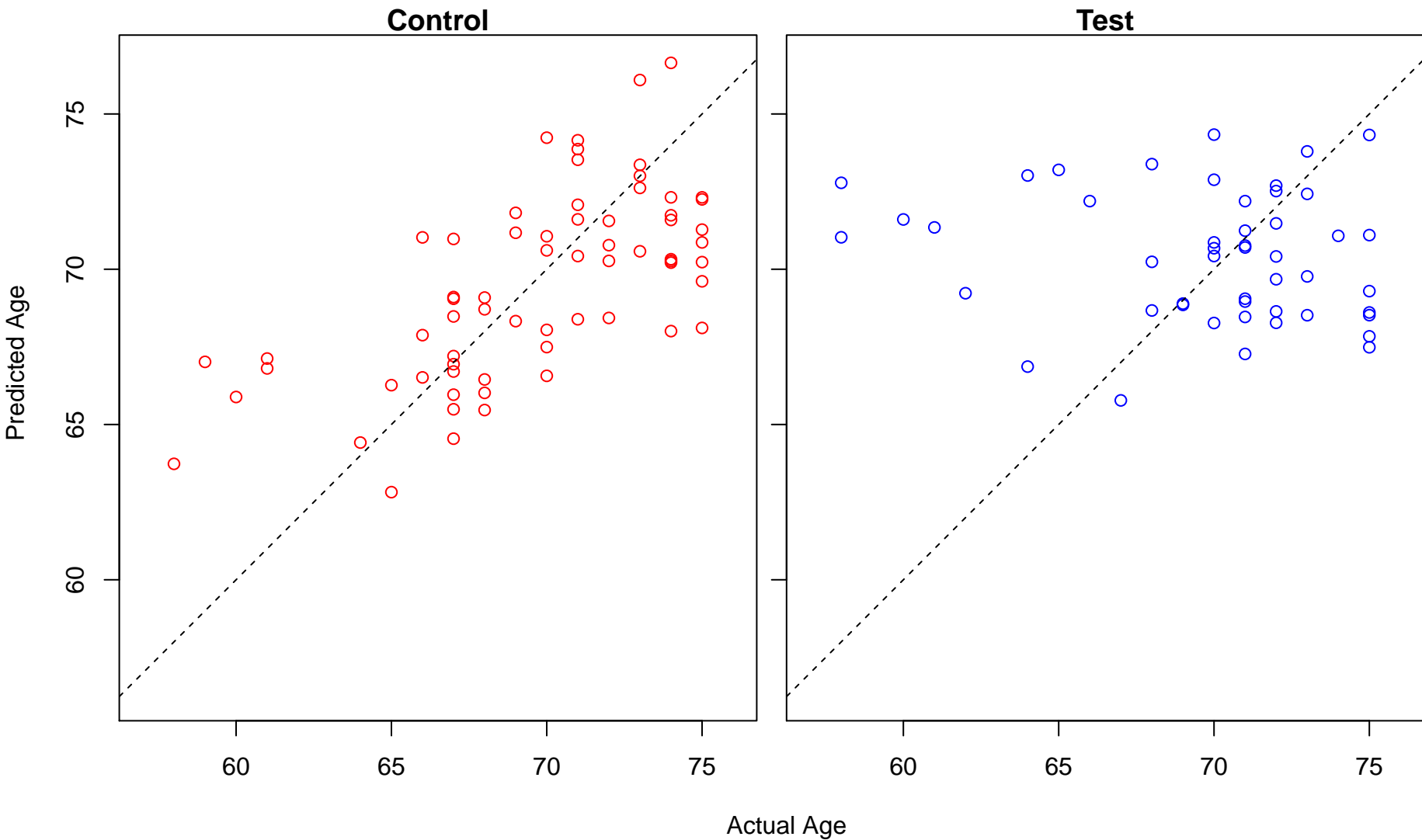


Actual Age

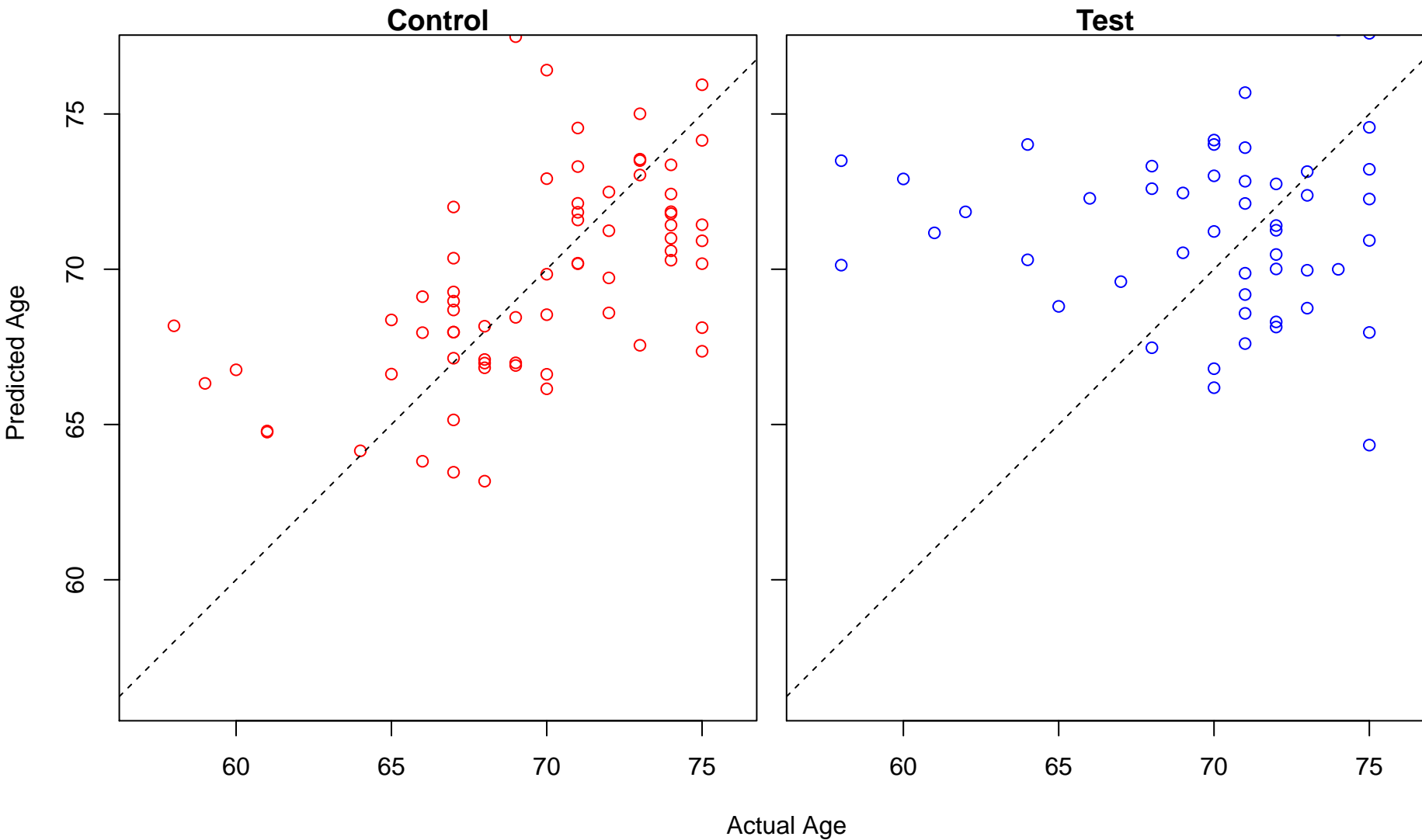
negative regulation of blood vessel endothelial cell migration (Score: 1.159061)



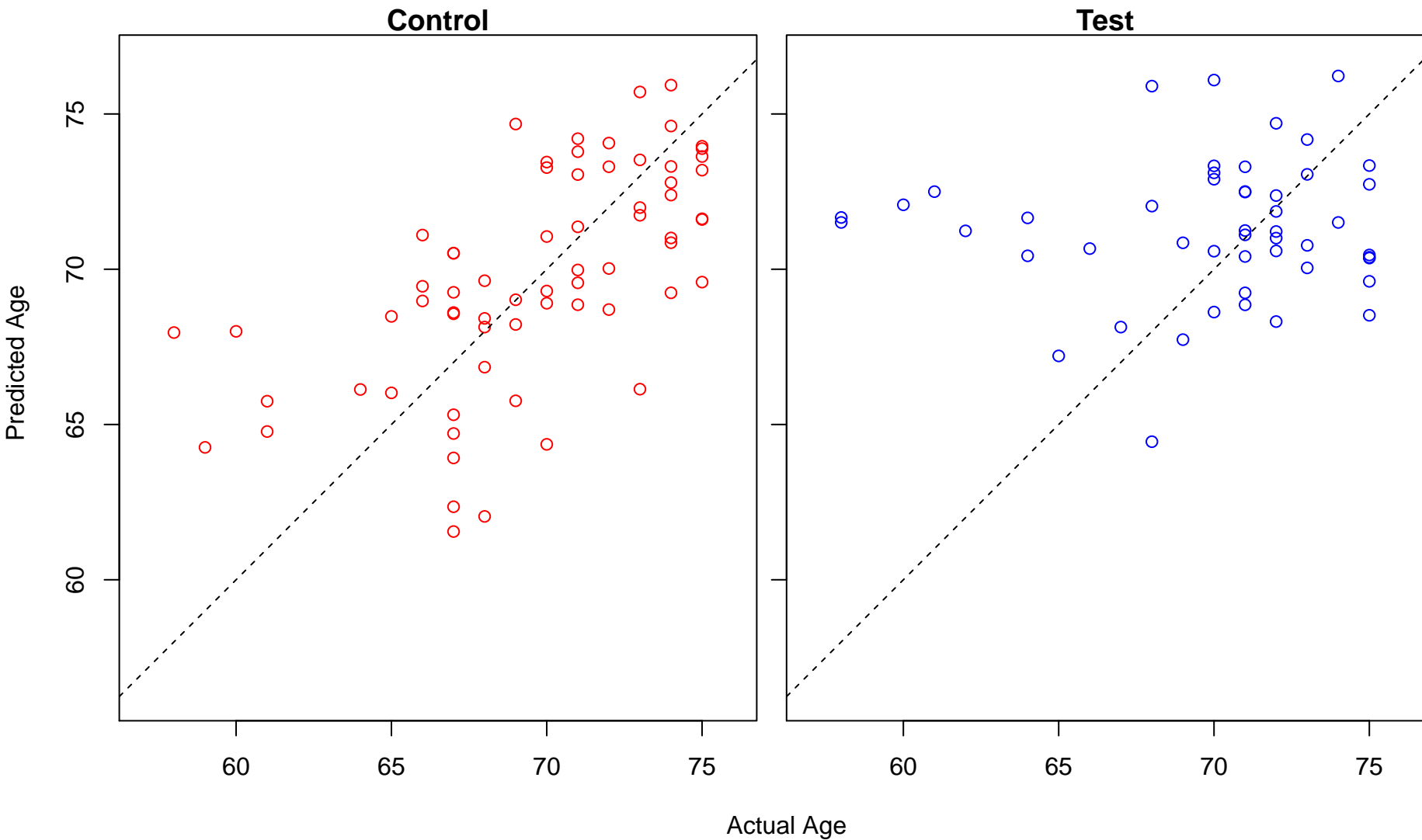
immunoglobulin mediated immune response (Score: 1.159010)



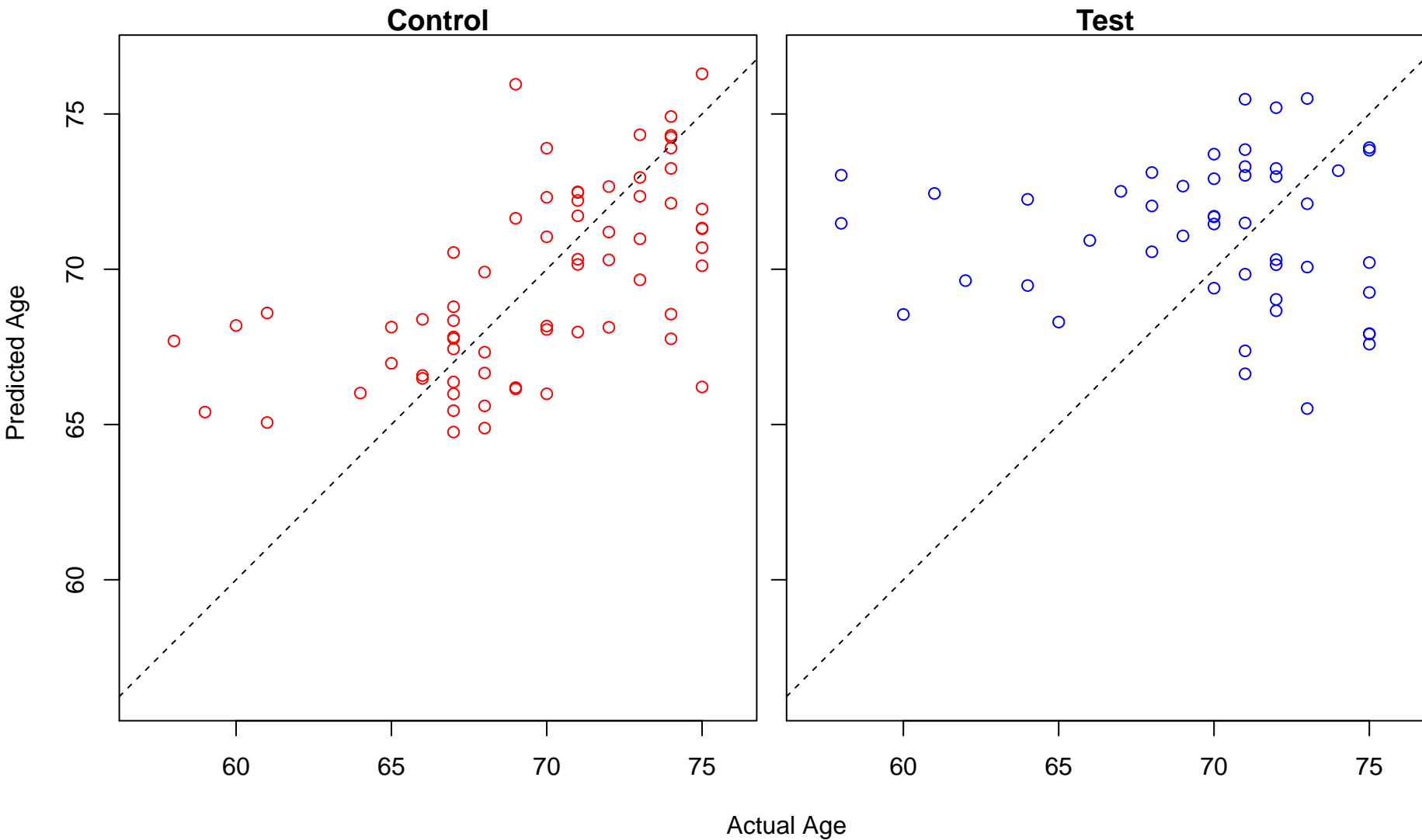
camera-type eye development (Score: 1.158946)



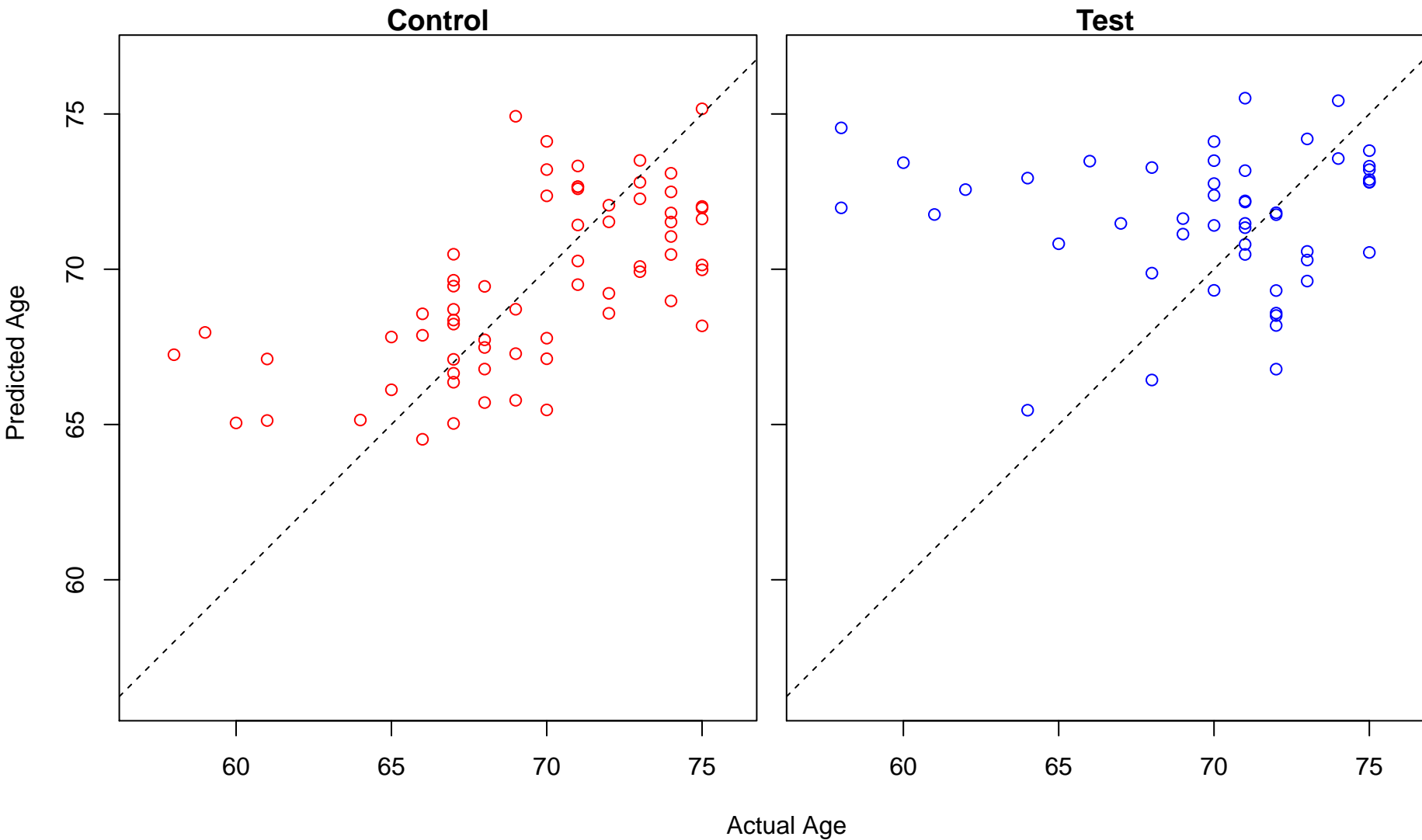
tetrapyrrole metabolic process (Score: 1.158797)



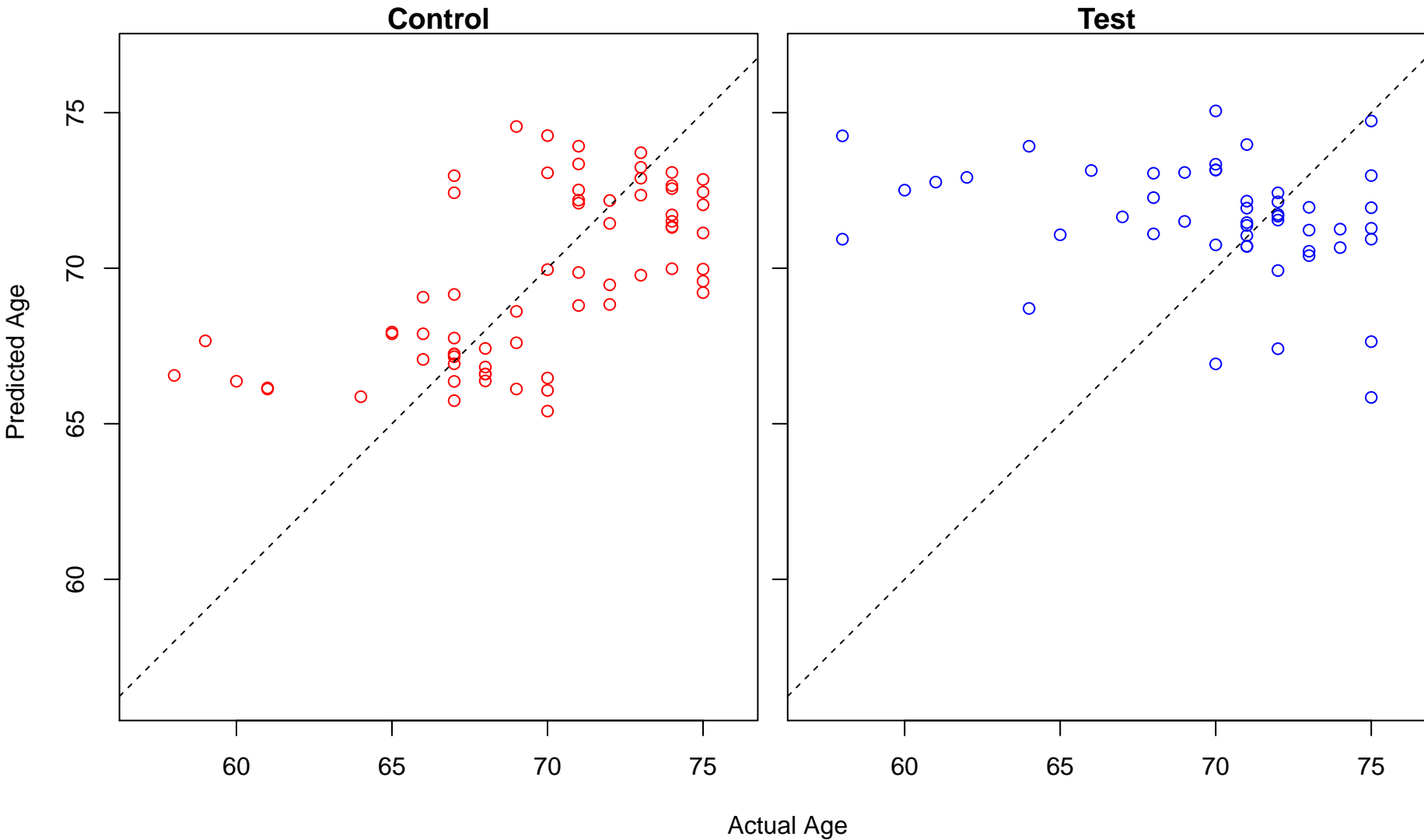
mitochondrial RNA processing (Score: 1.158538)



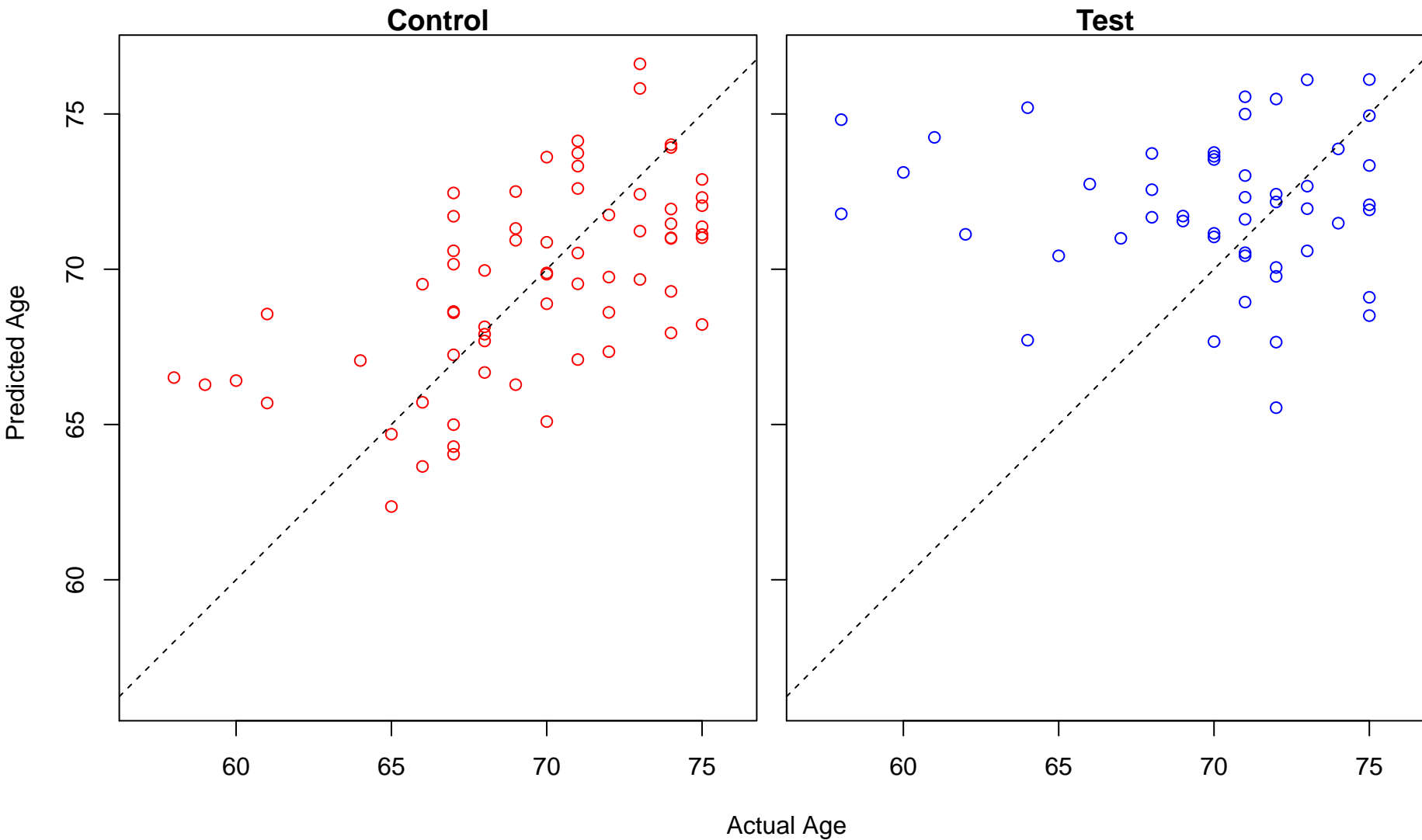
regulation of dendritic spine development (Score: 1.158247)



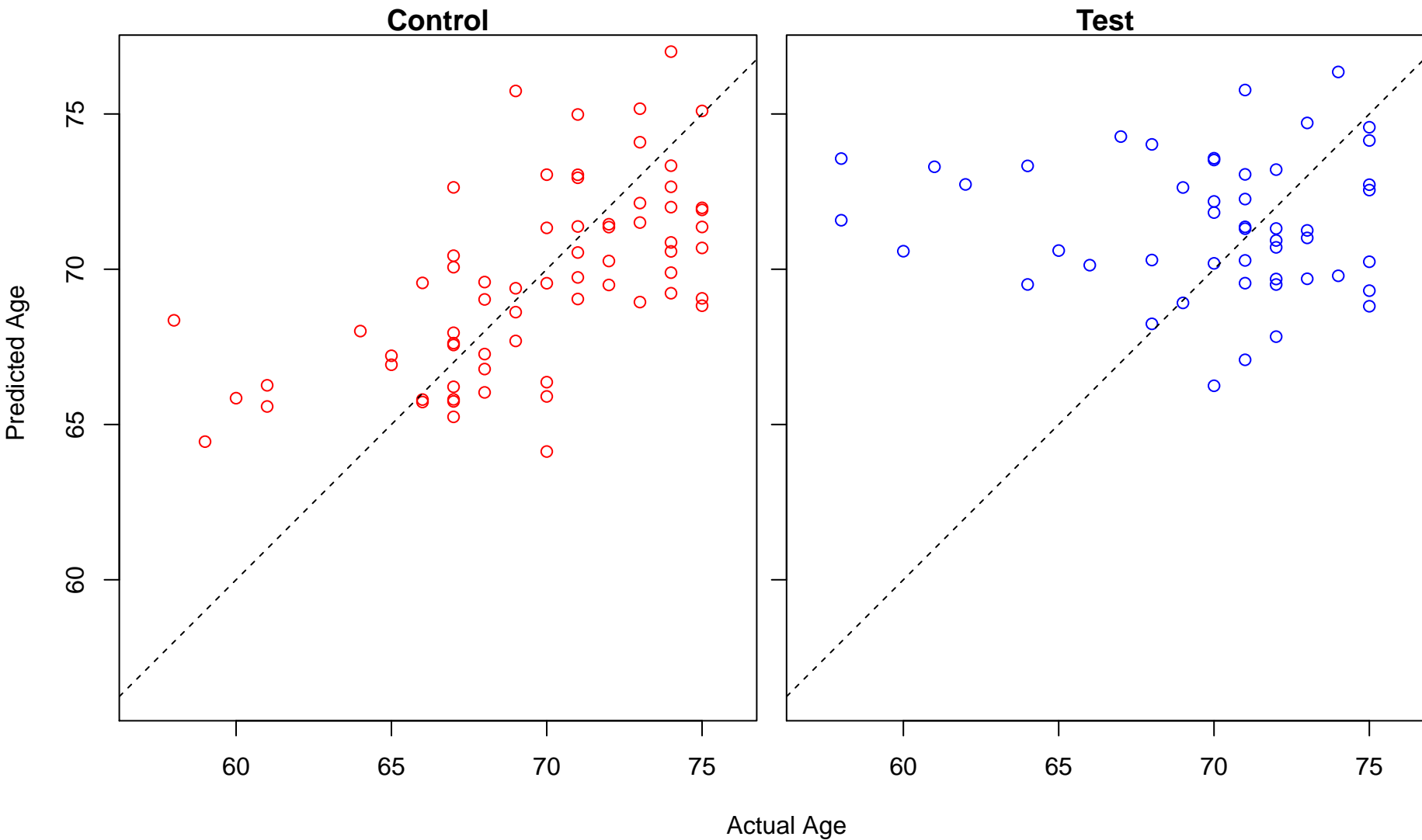
negative regulation of sprouting angiogenesis (Score: 1.158105)



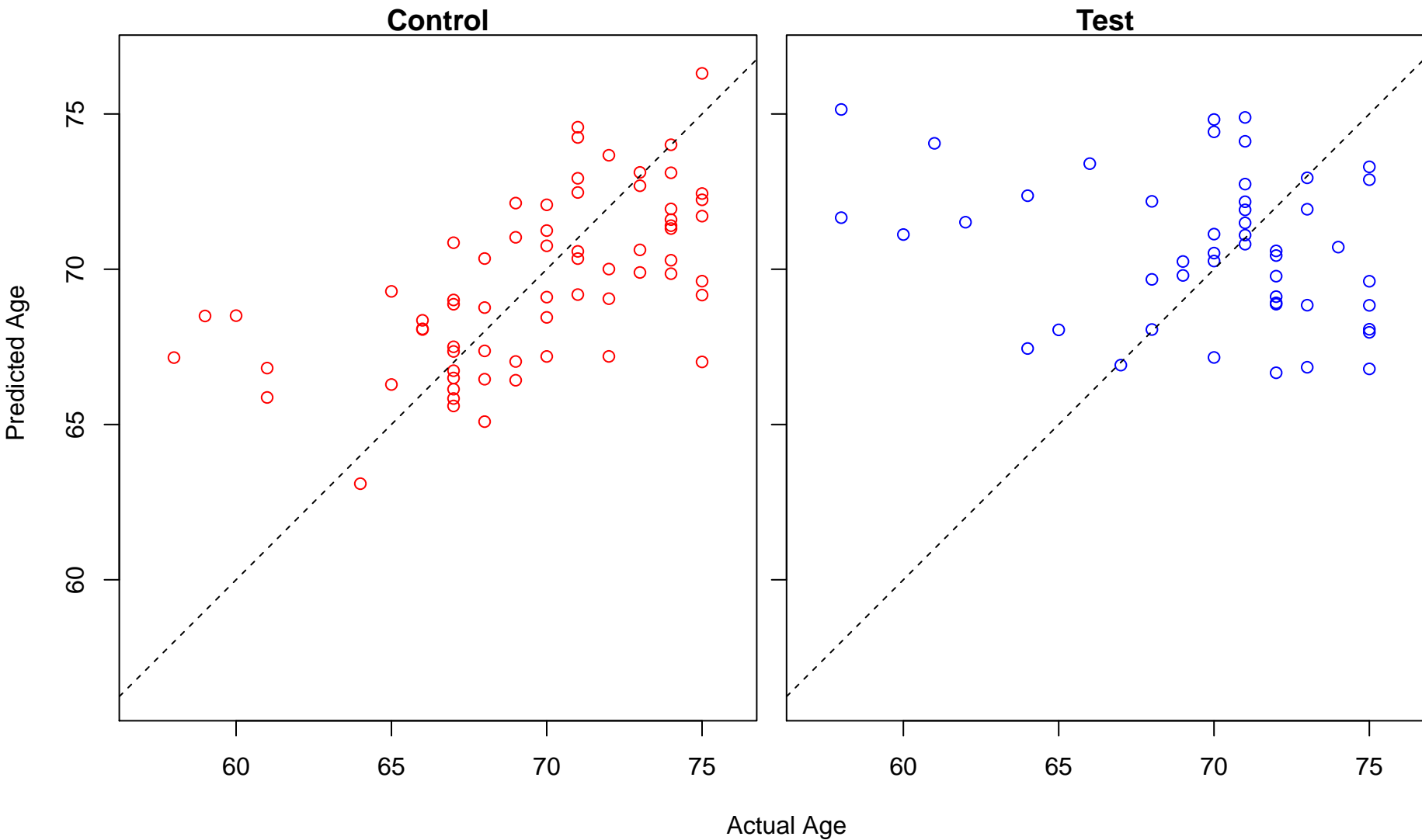
hippo signaling (Score: 1.157676)



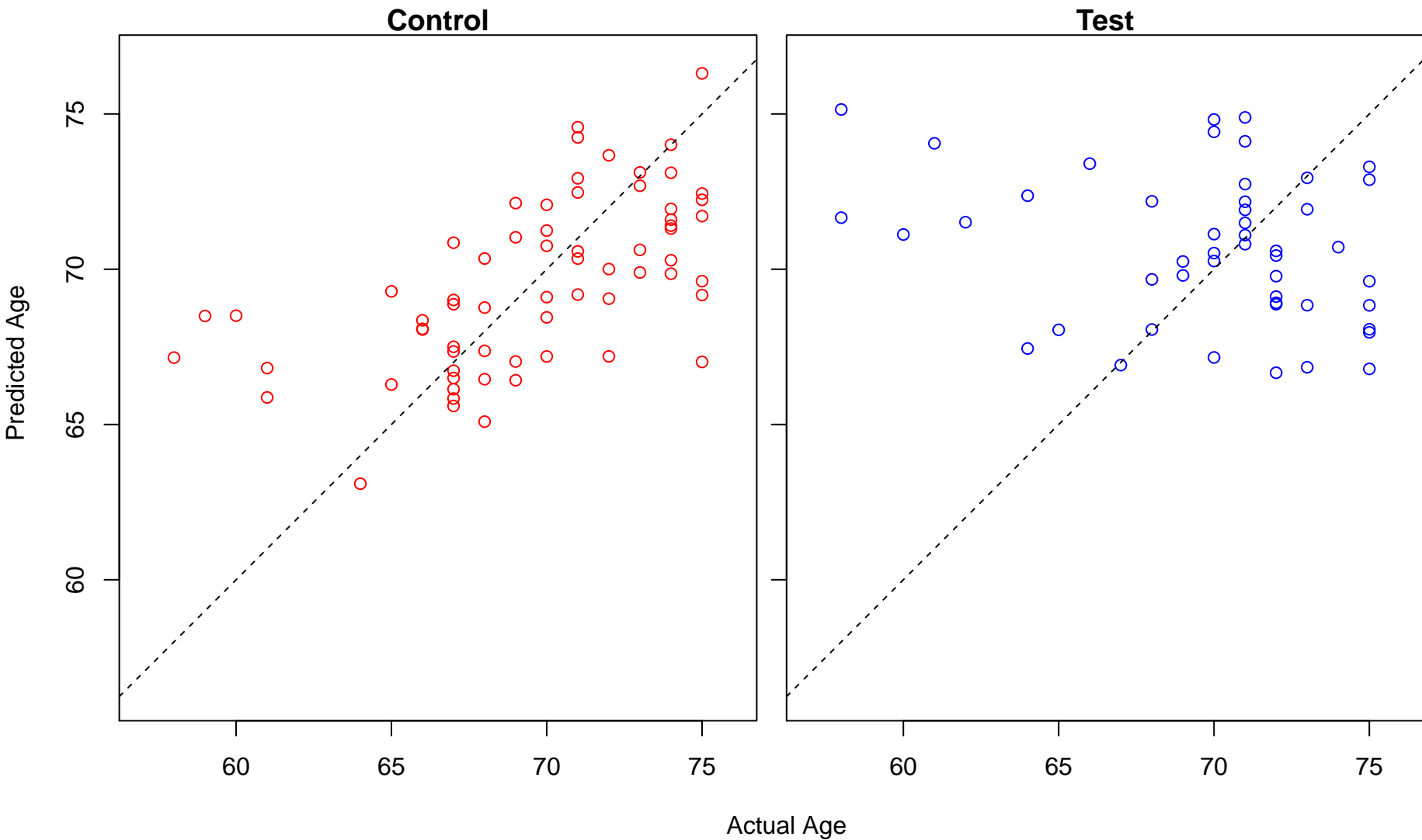
purine nucleobase metabolic process (Score: 1.156927)



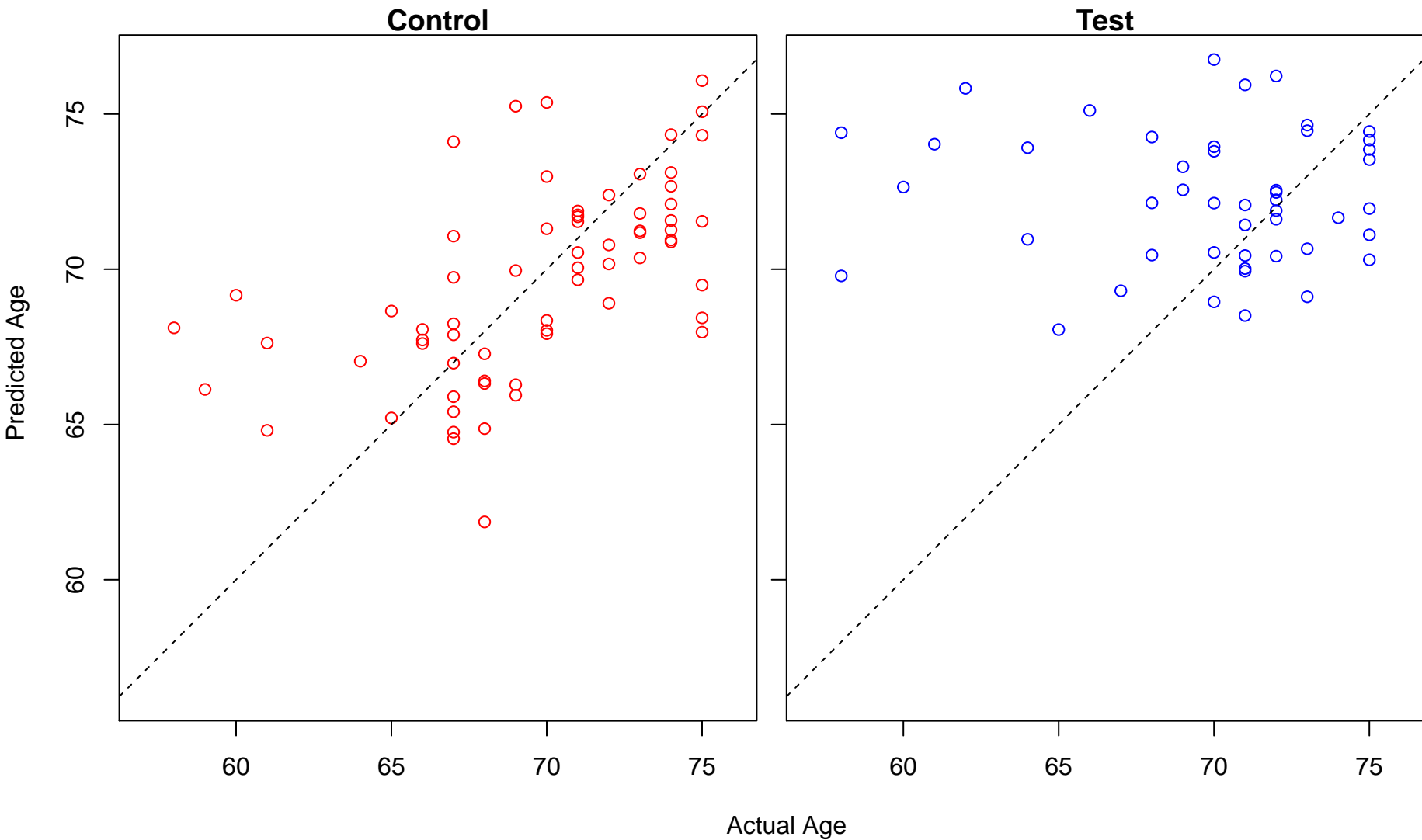
ethanol metabolic process (Score: 1.156737)



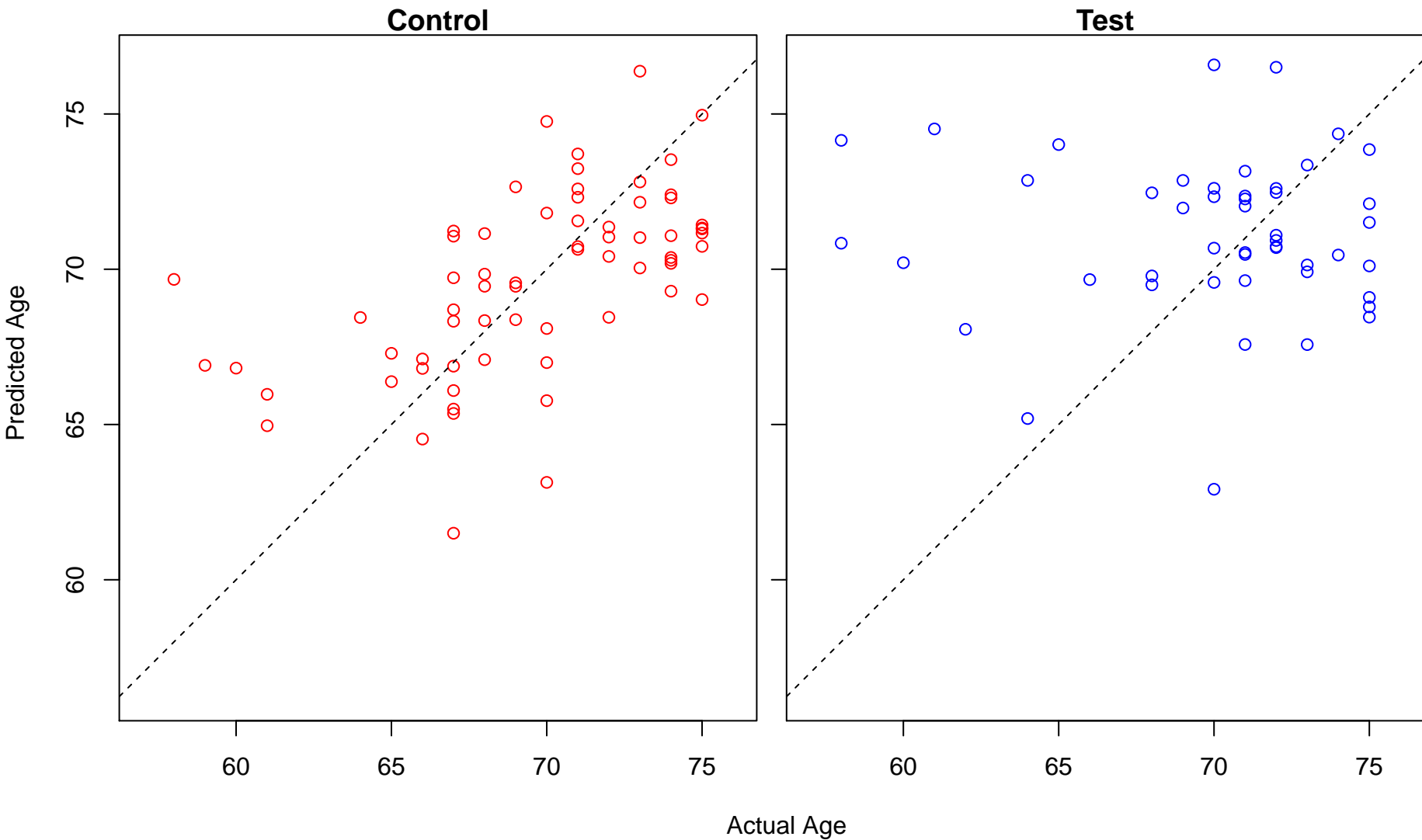
ethanol oxidation (Score: 1.156737)



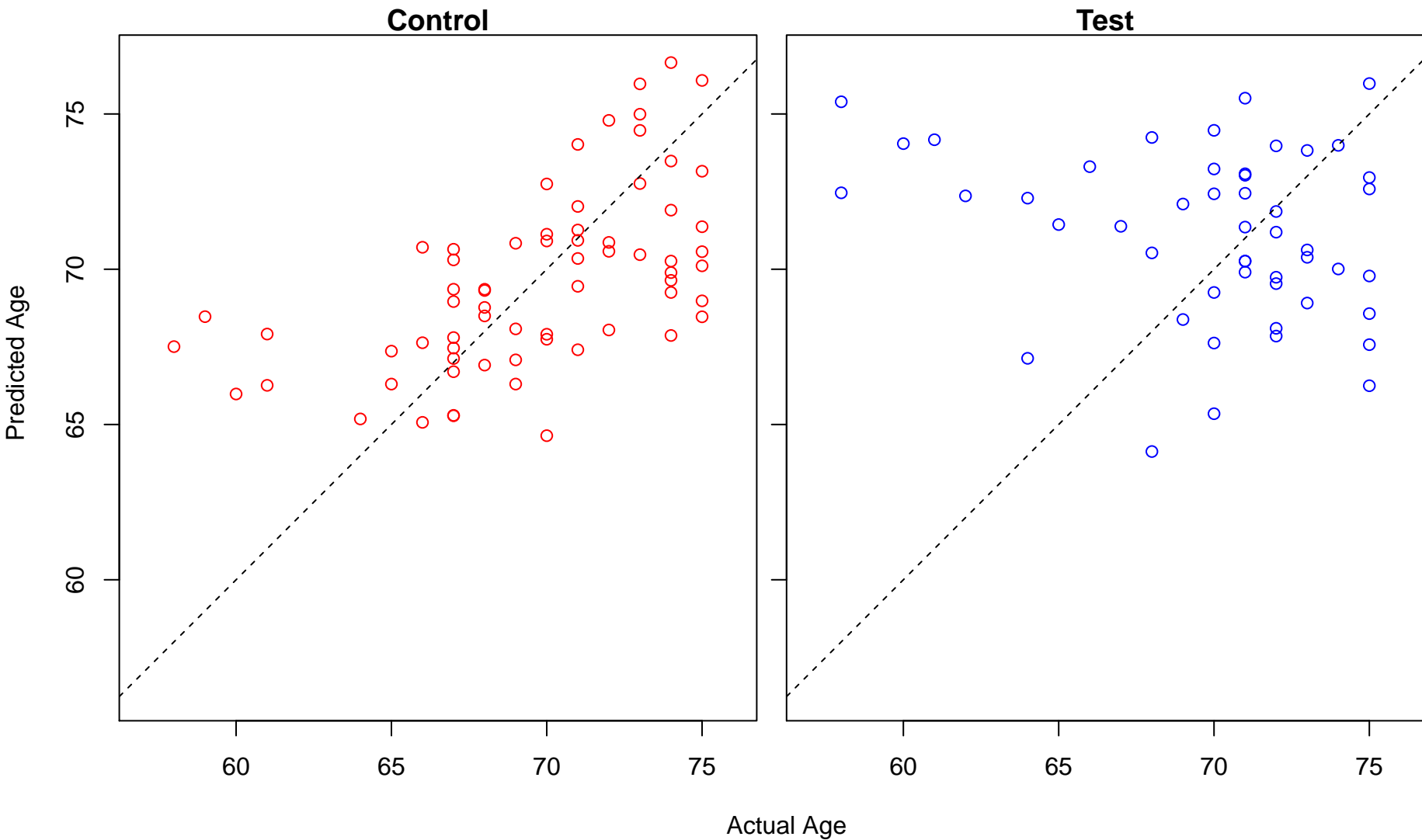
sensory organ morphogenesis (Score: 1.156589)



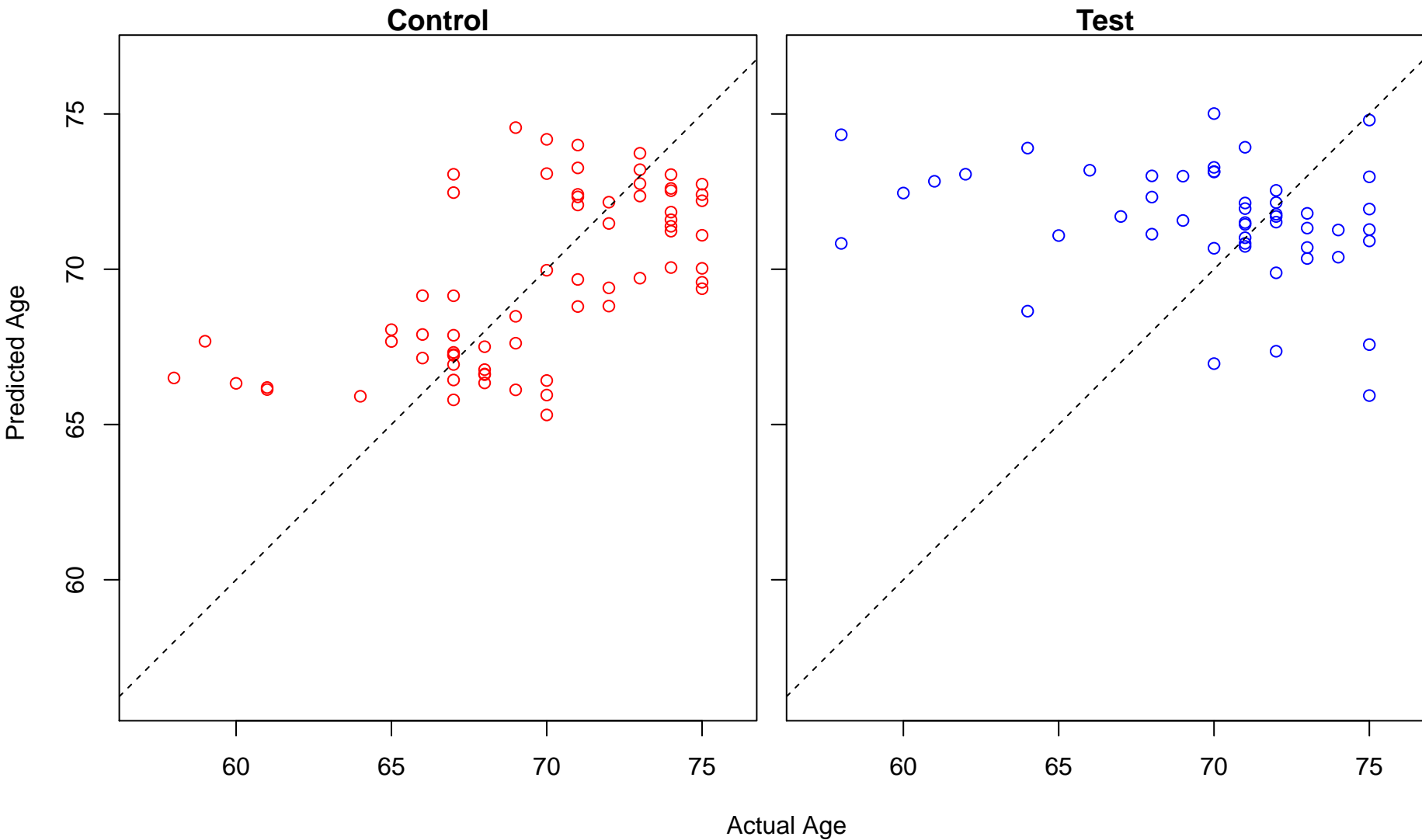
tetrahydrofolate interconversion (Score: 1.156194)



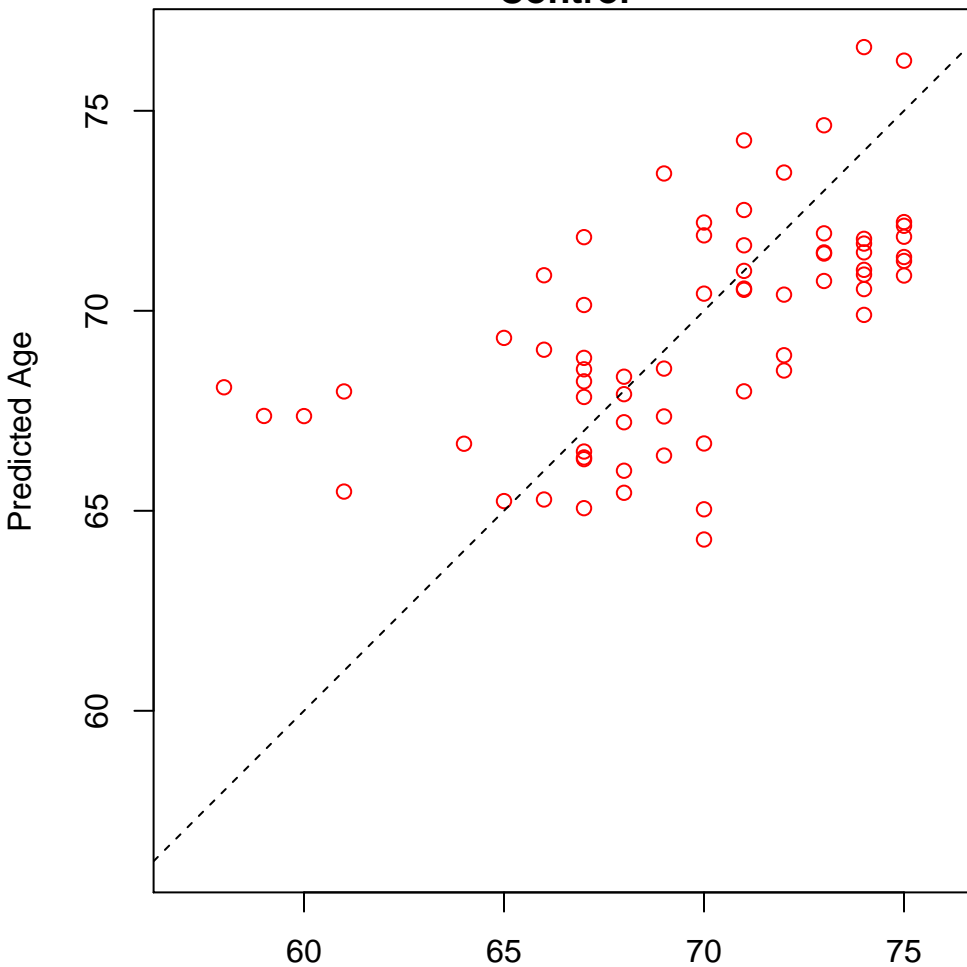
central nervous system neuron development (Score: 1.155883)



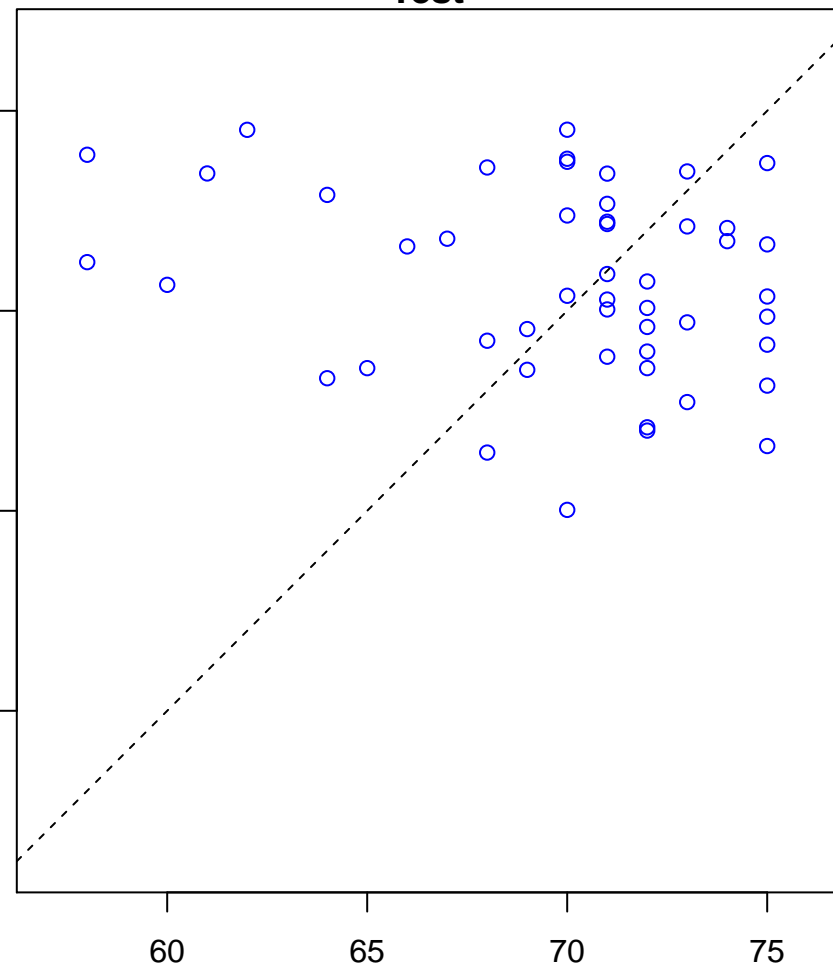
negative regulation of cell migration involved in sprouting angiogenesis (Score: 1.155690)



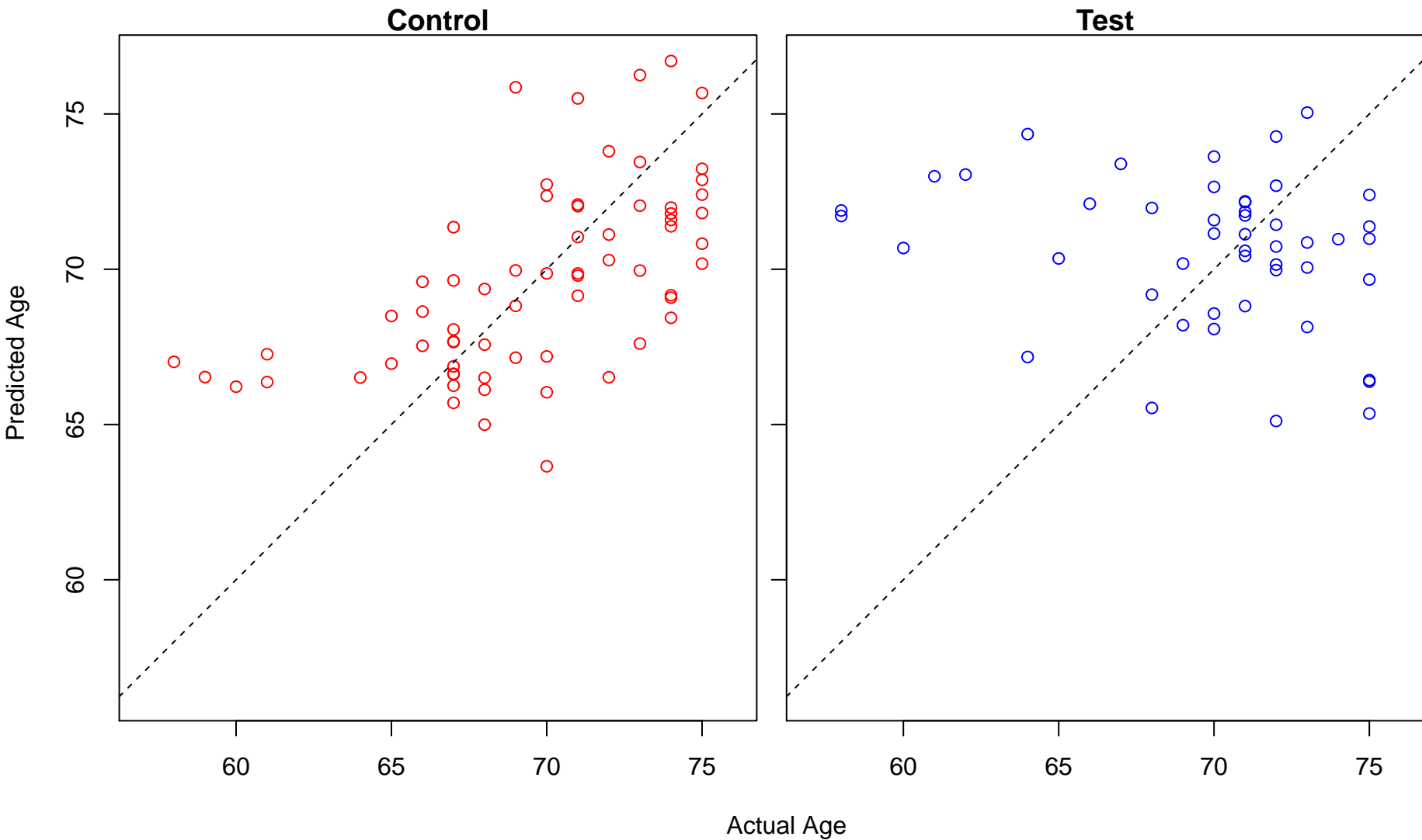
Control



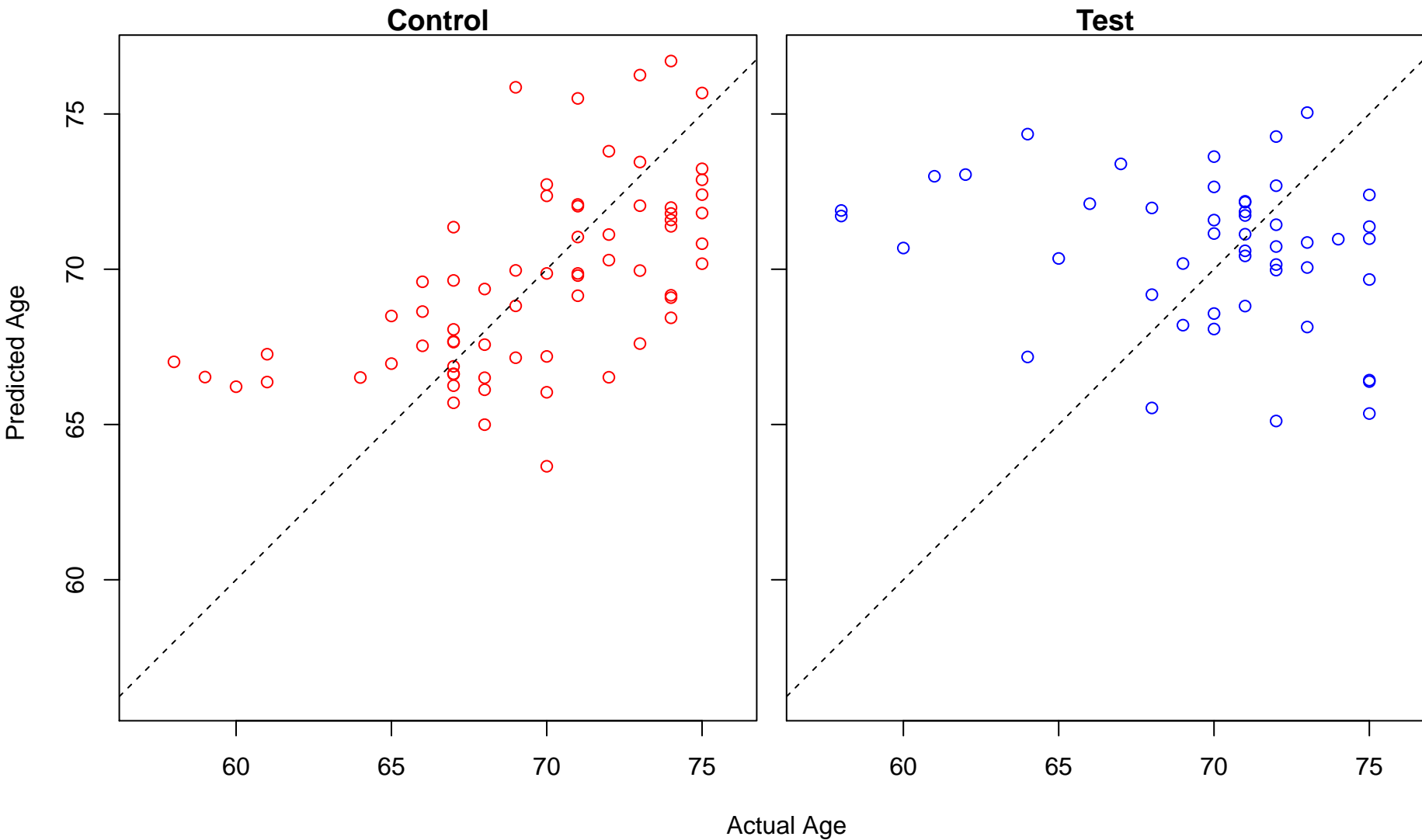
Test



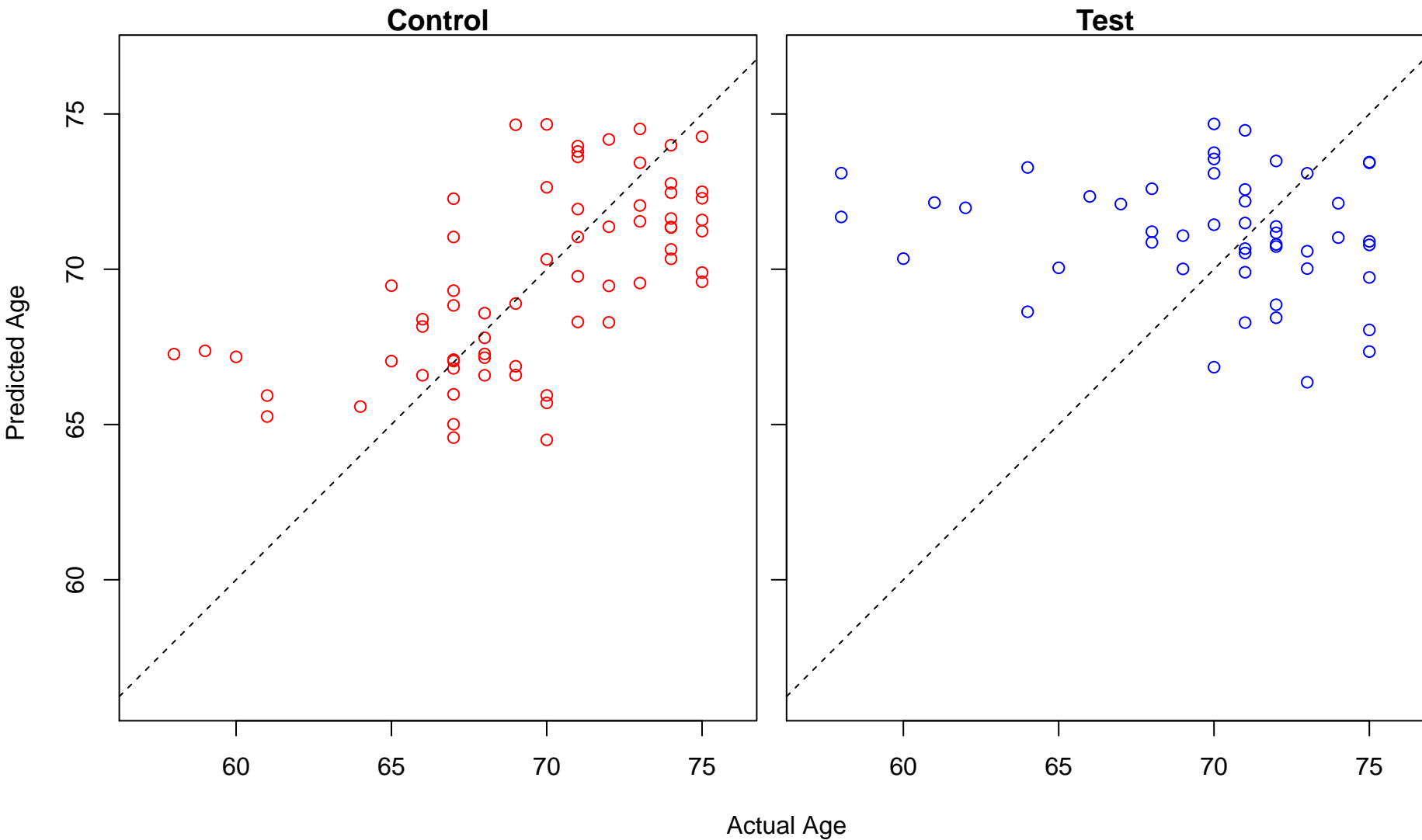
regulation of protein localization to Cajal body (Score: 1.154171)



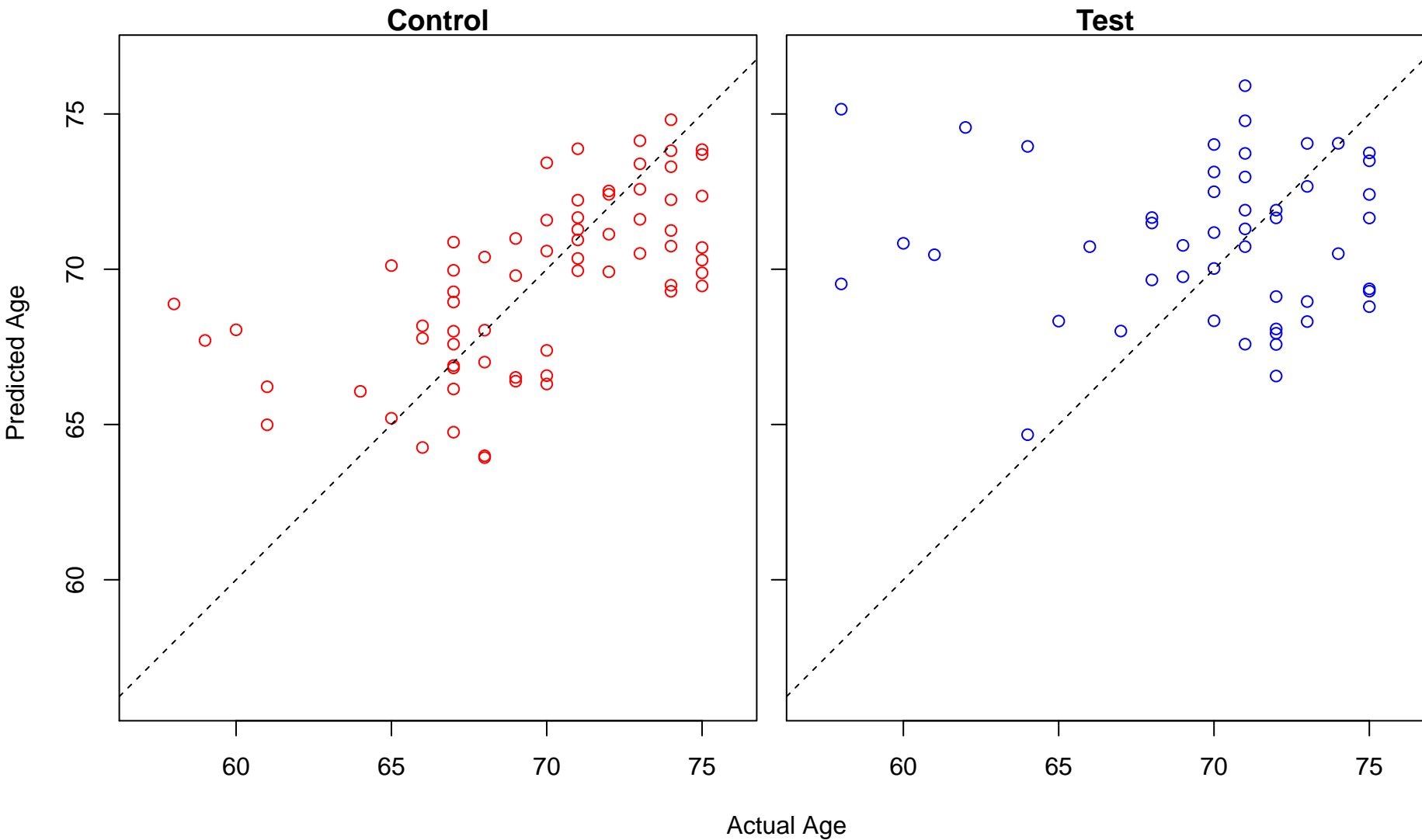
positive regulation of protein localization to Cajal body (Score: 1.154171)



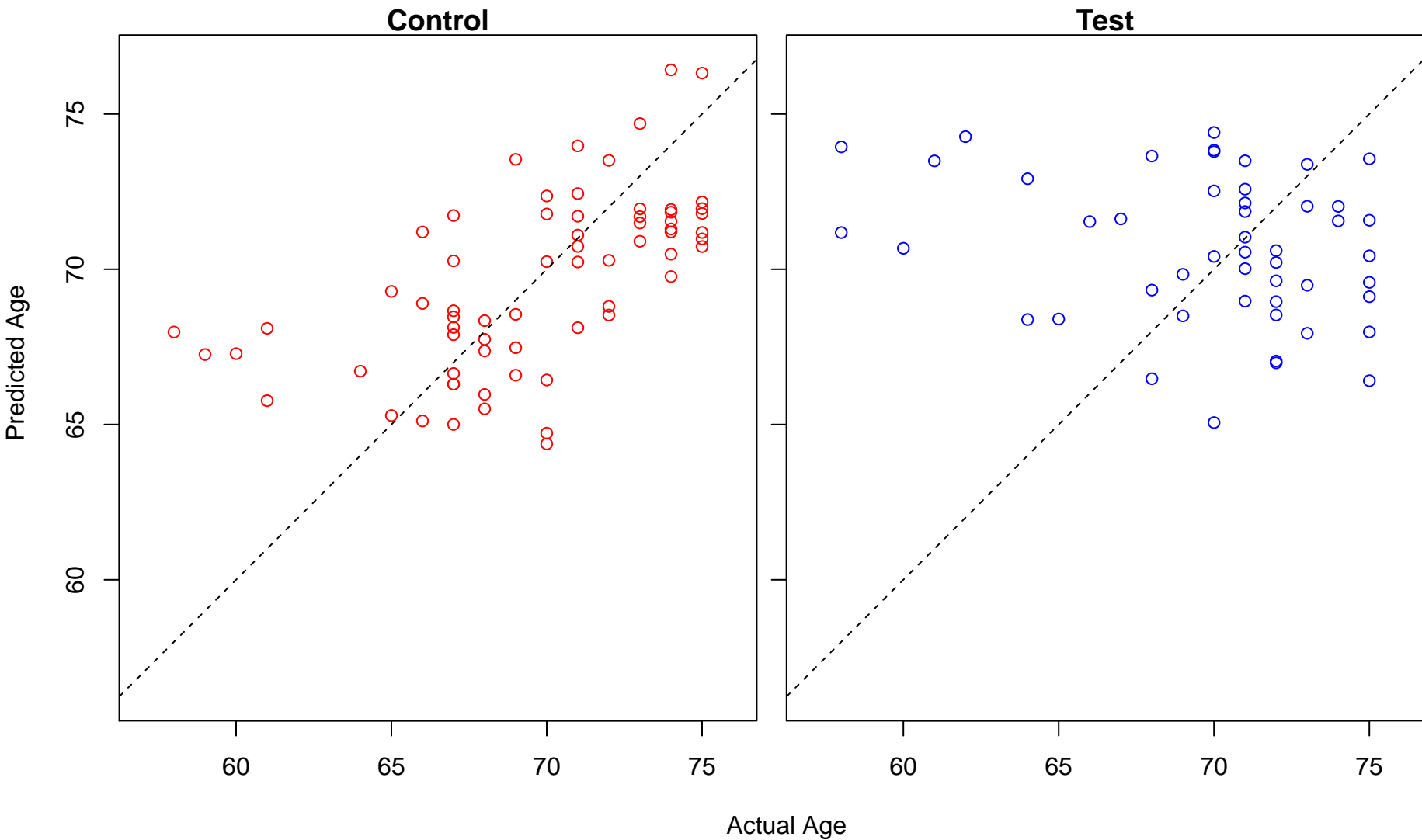
Golgi localization (Score: 1.154163)



stress granule assembly (Score: 1.154142)

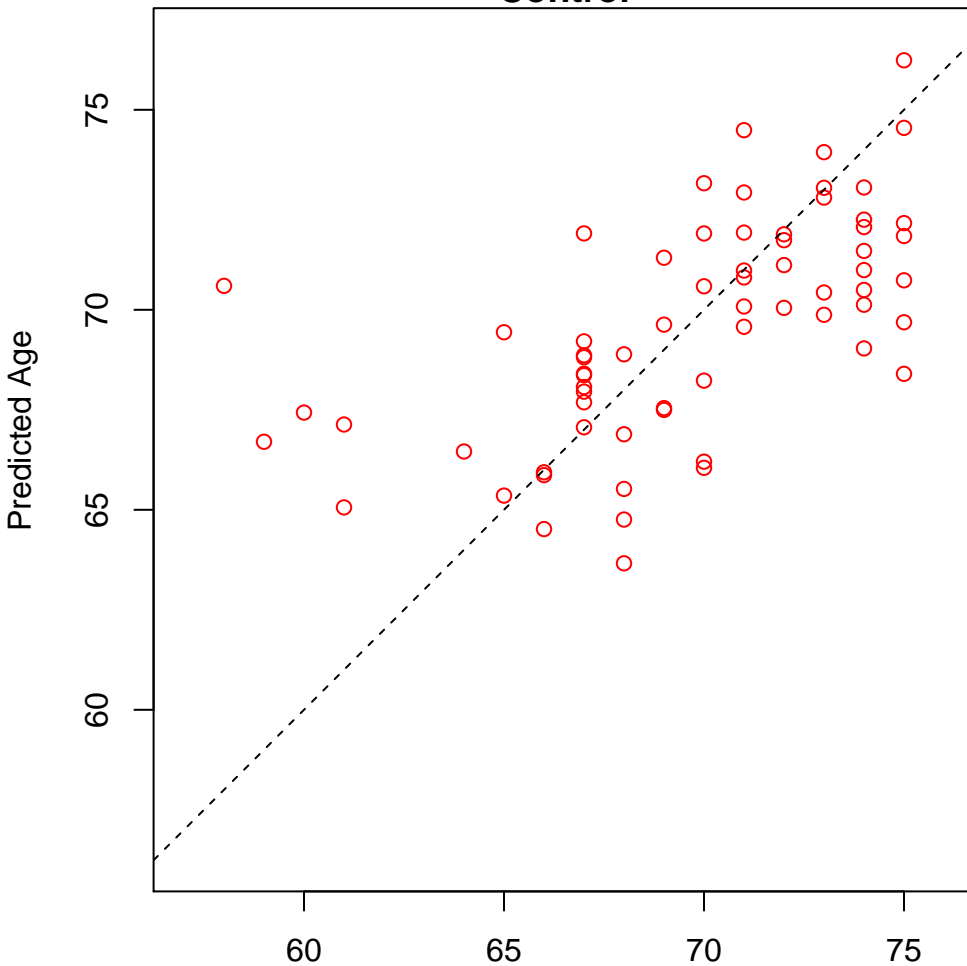


phospholipid dephosphorylation (Score: 1.152591)

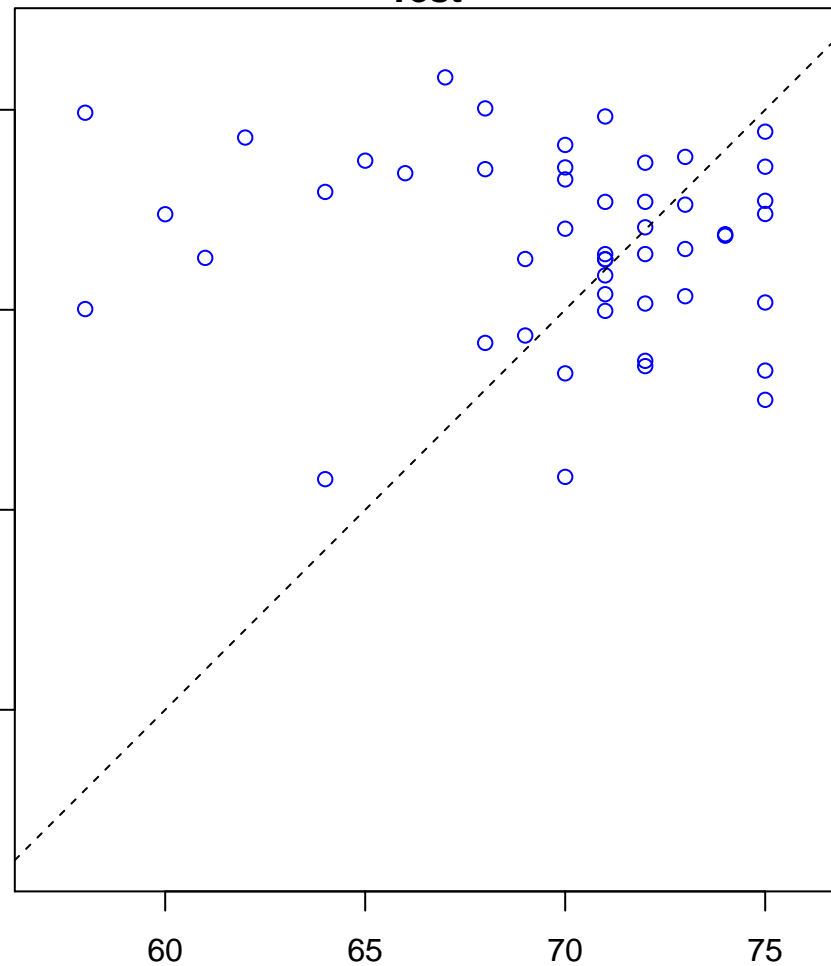


negative regulation of cell cycle arrest (Score: 1.152479)

Control

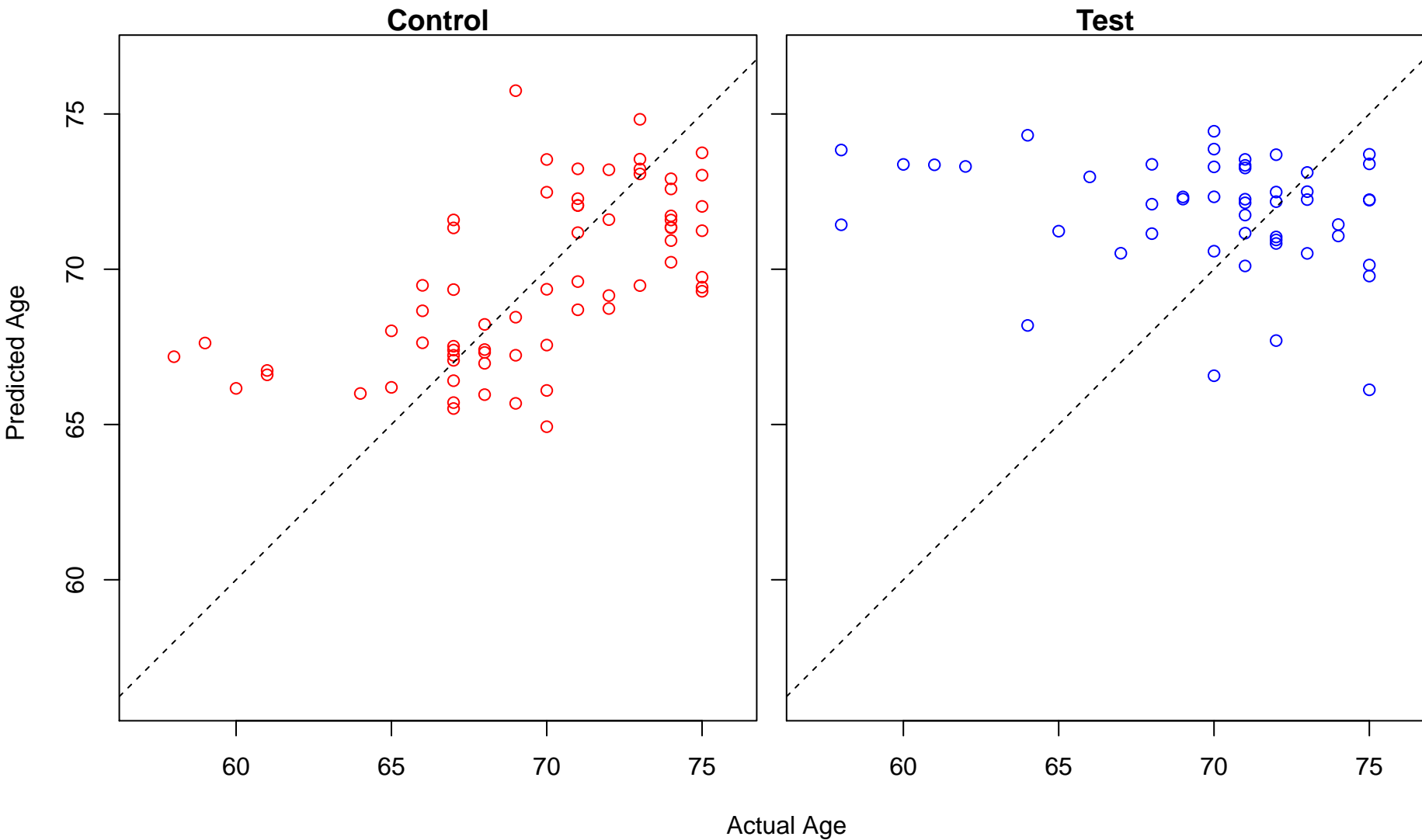


Test



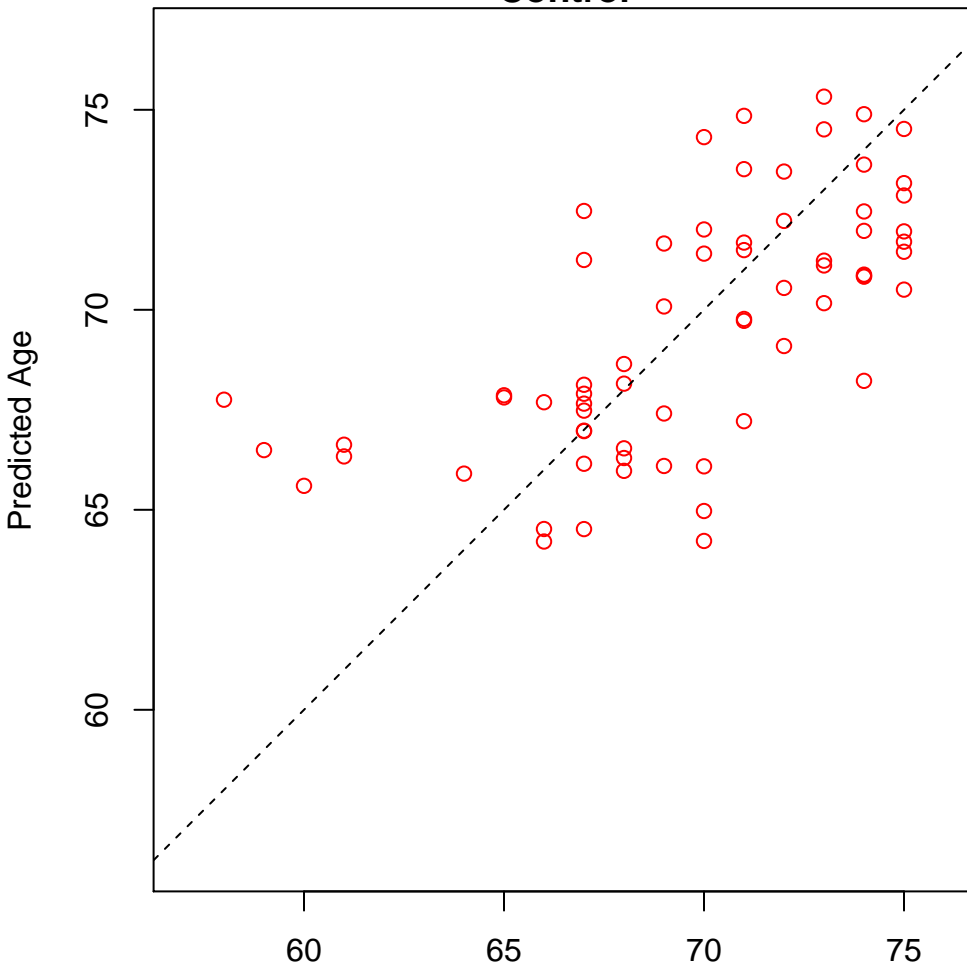
Actual Age

positive regulation of epithelial cell proliferation (Score: 1.152011)

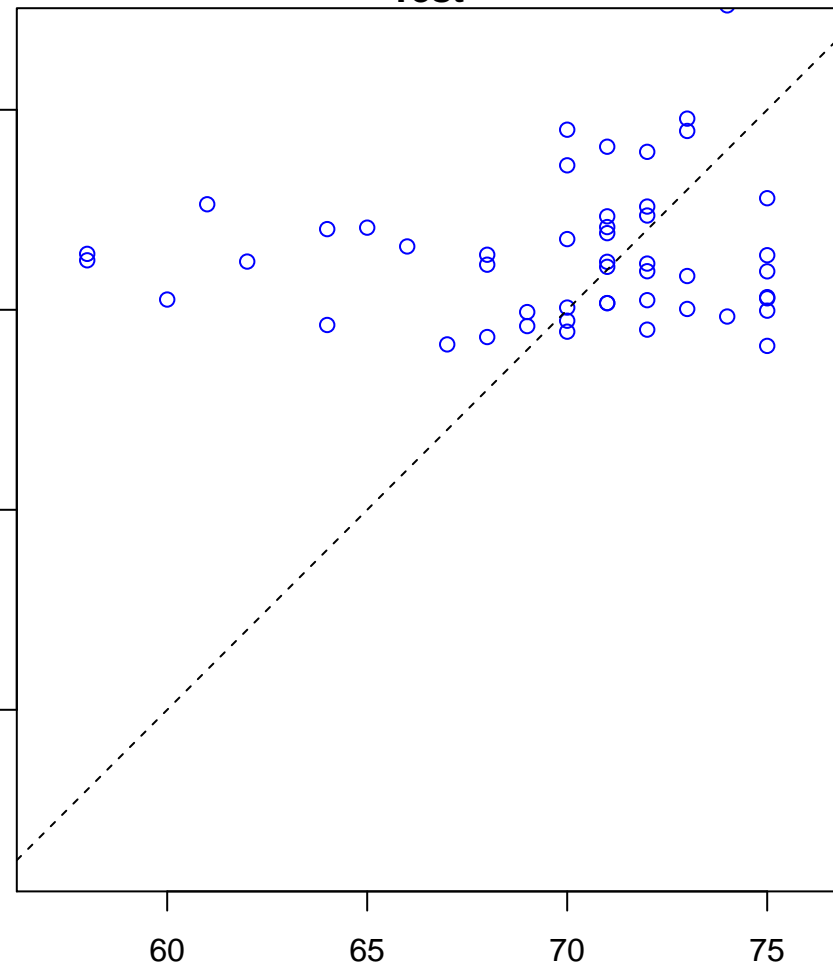


cellular potassium ion transport (Score: 1.151304)

Control



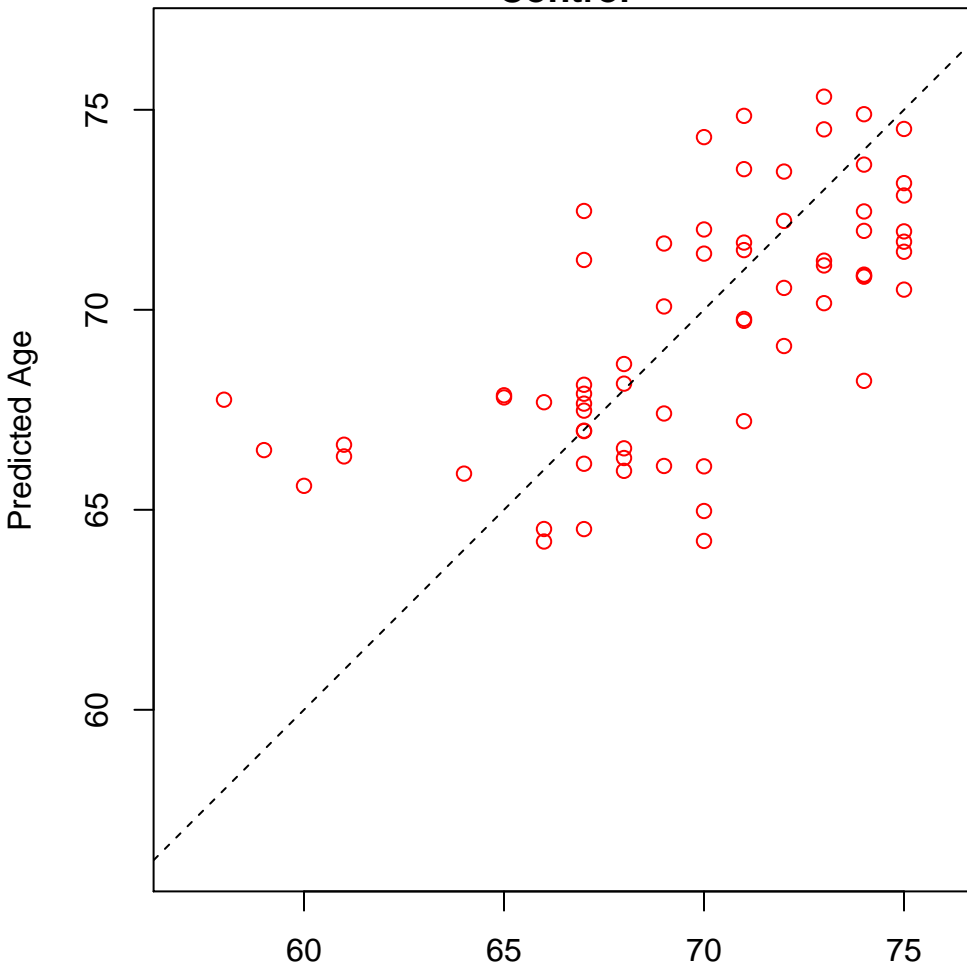
Test



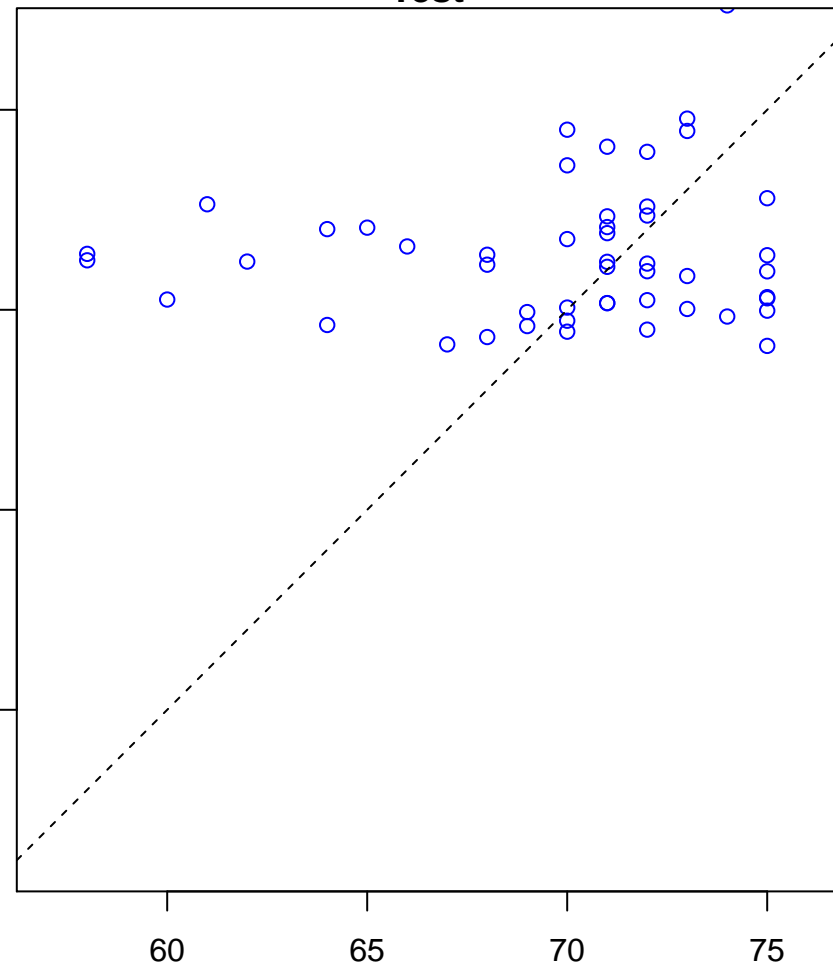
Actual Age

potassium ion transmembrane transport (Score: 1.151304)

Control



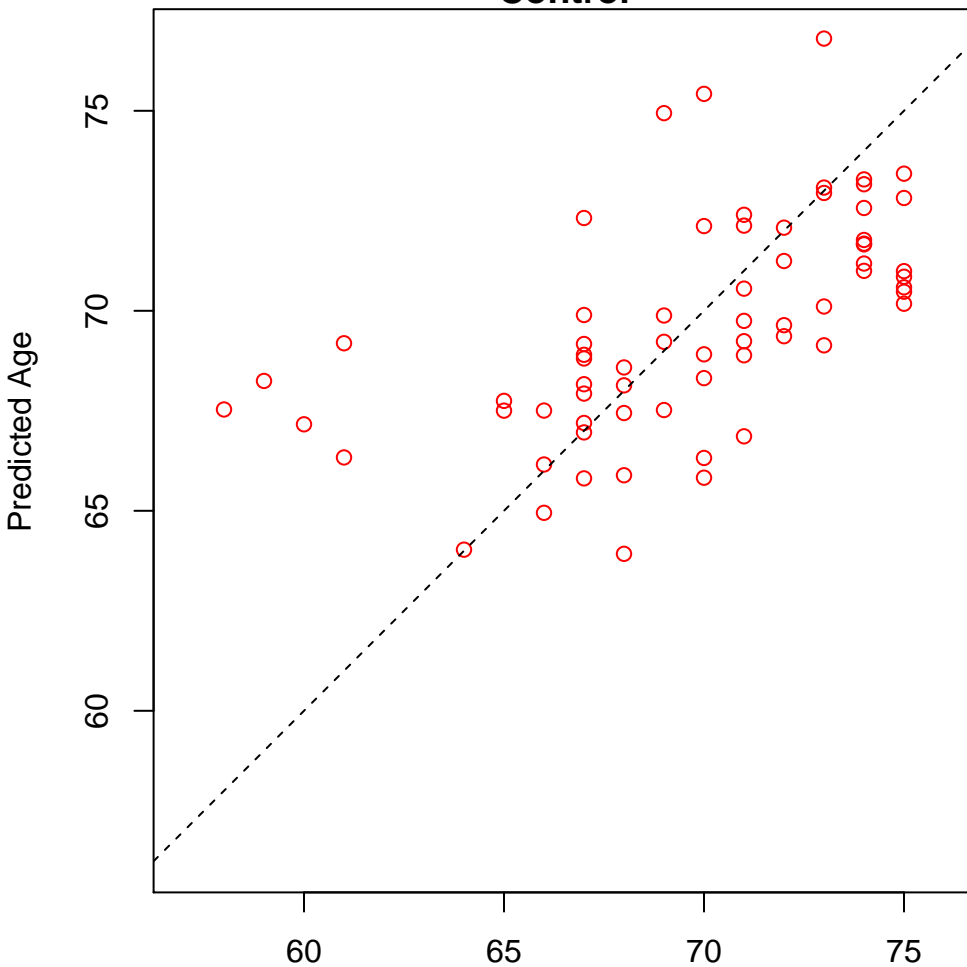
Test



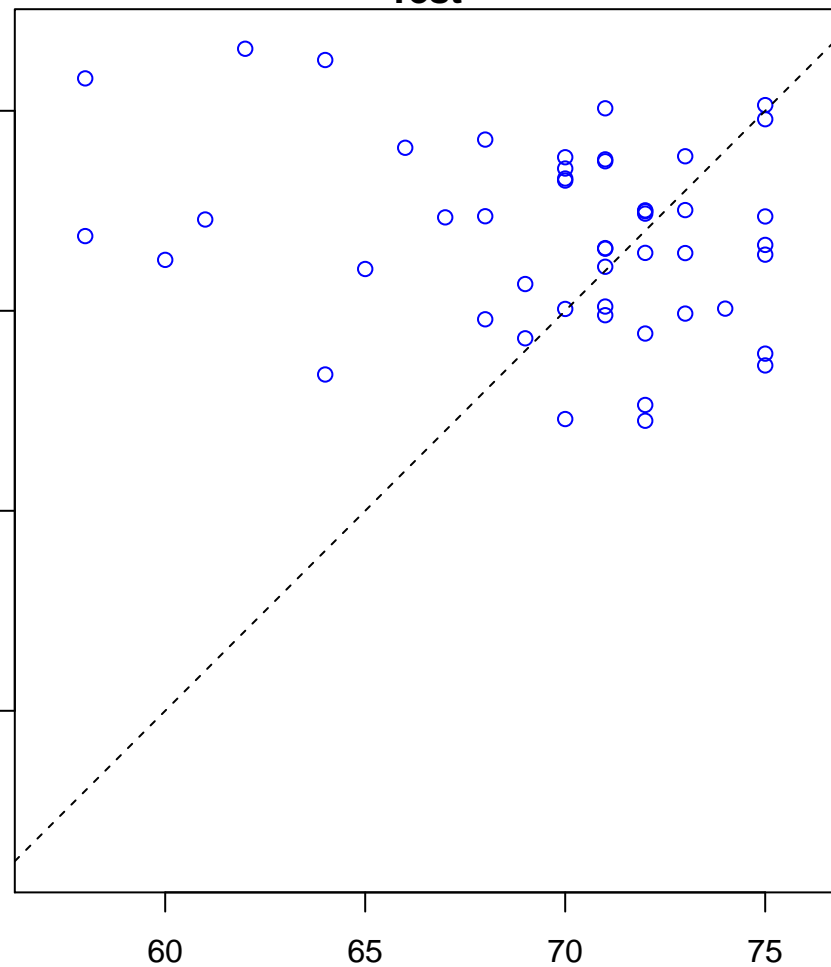
Actual Age

glutathione derivative metabolic process (Score: 1.150680)

Control

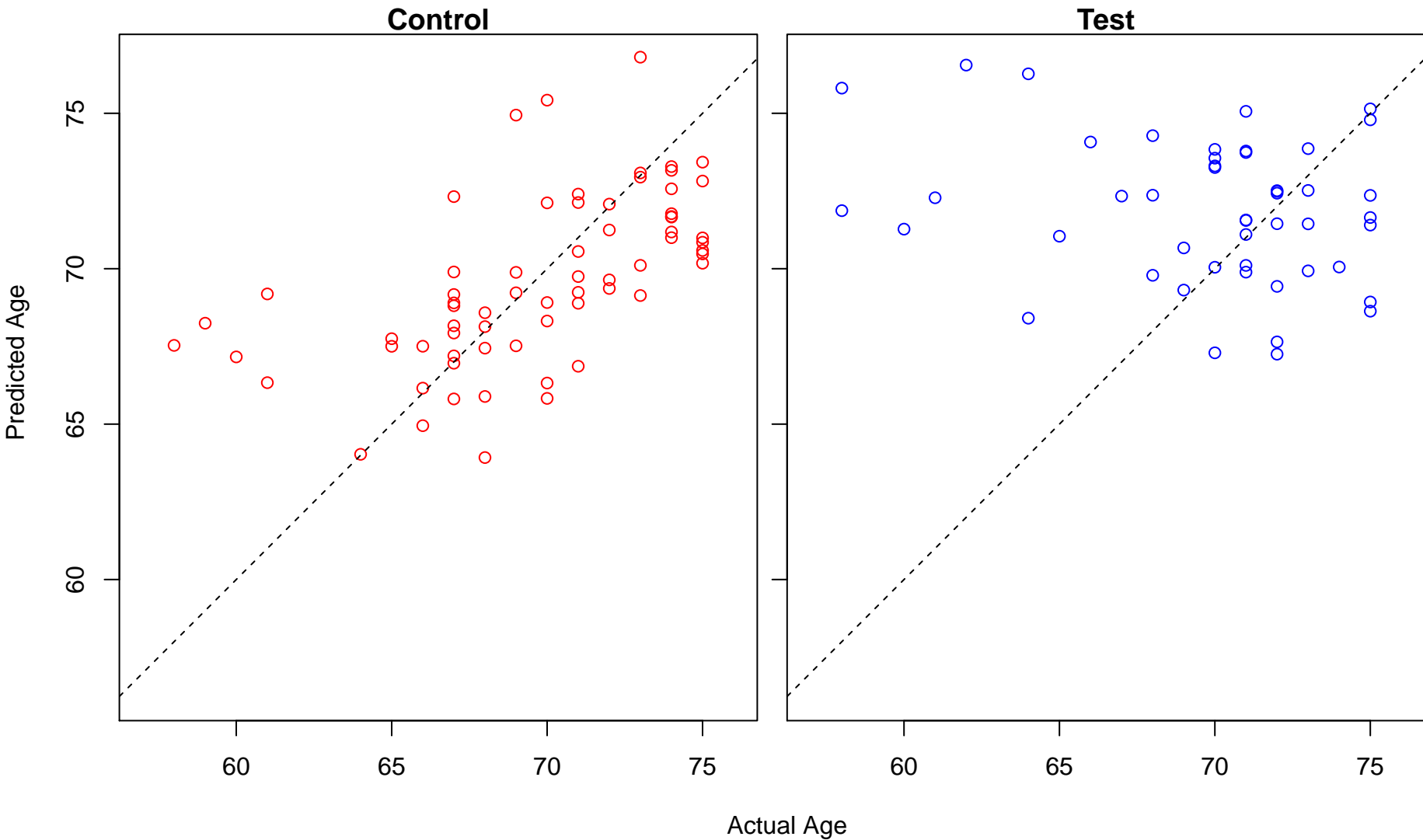


Test

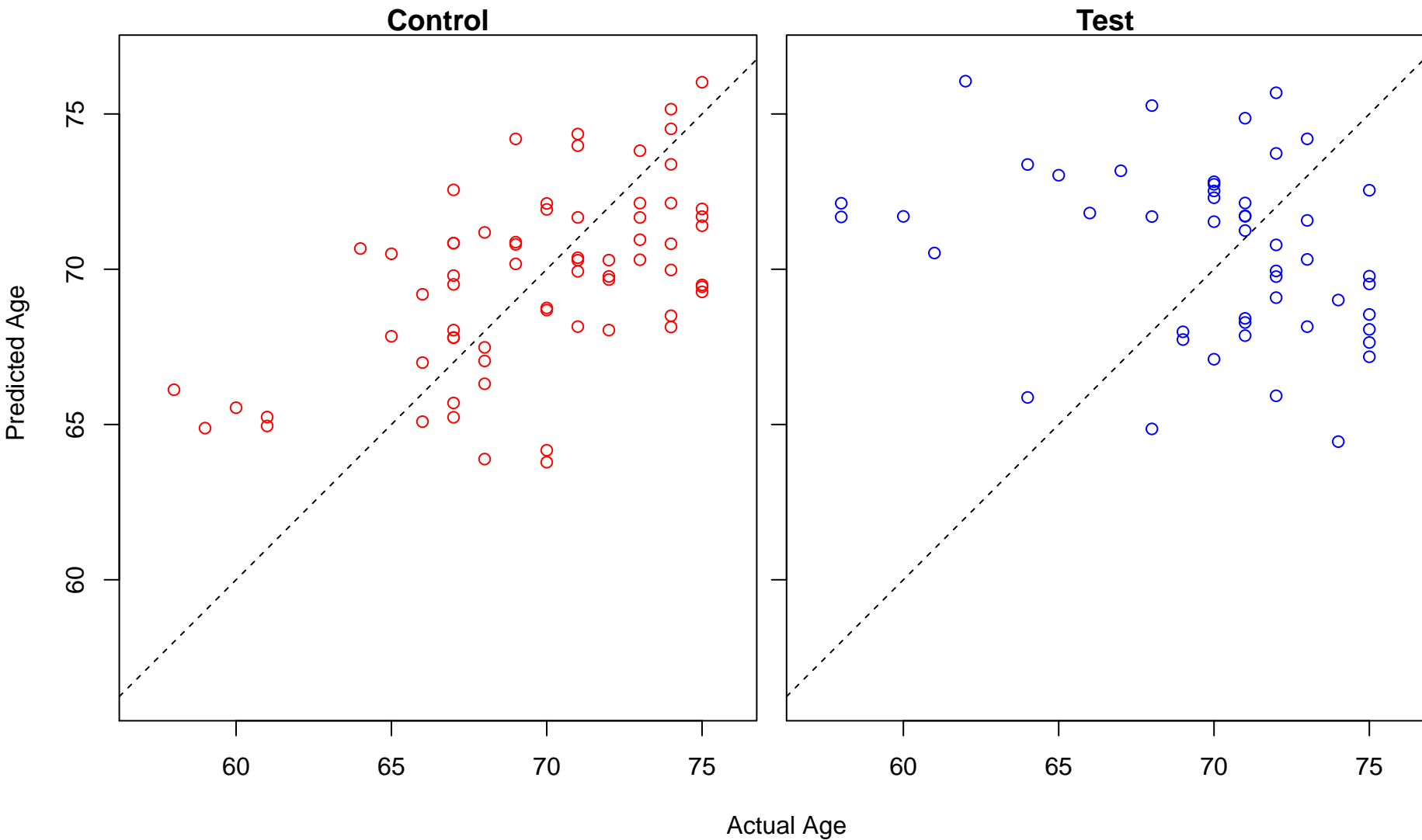


Actual Age

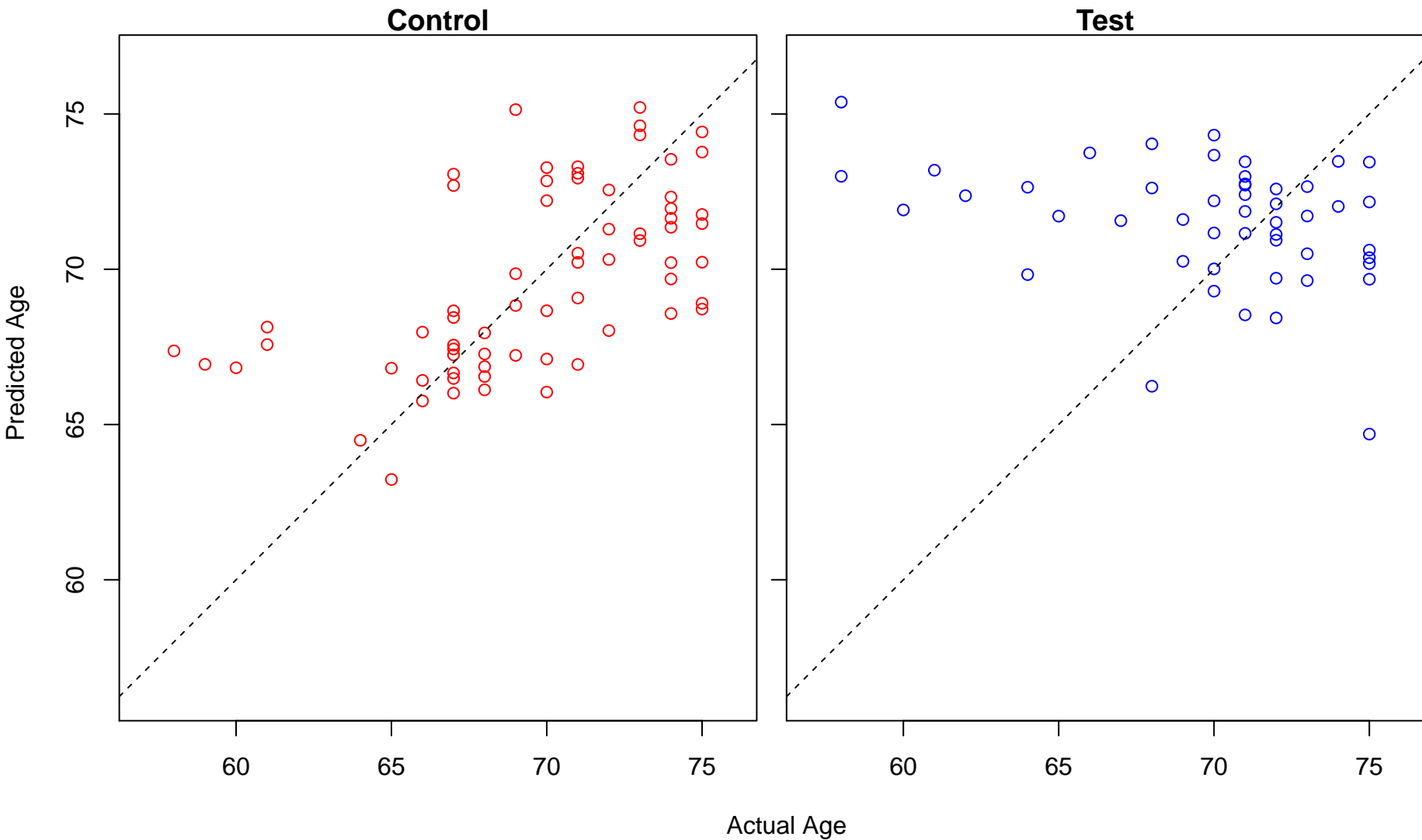
glutathione derivative biosynthetic process (Score: 1.150680)



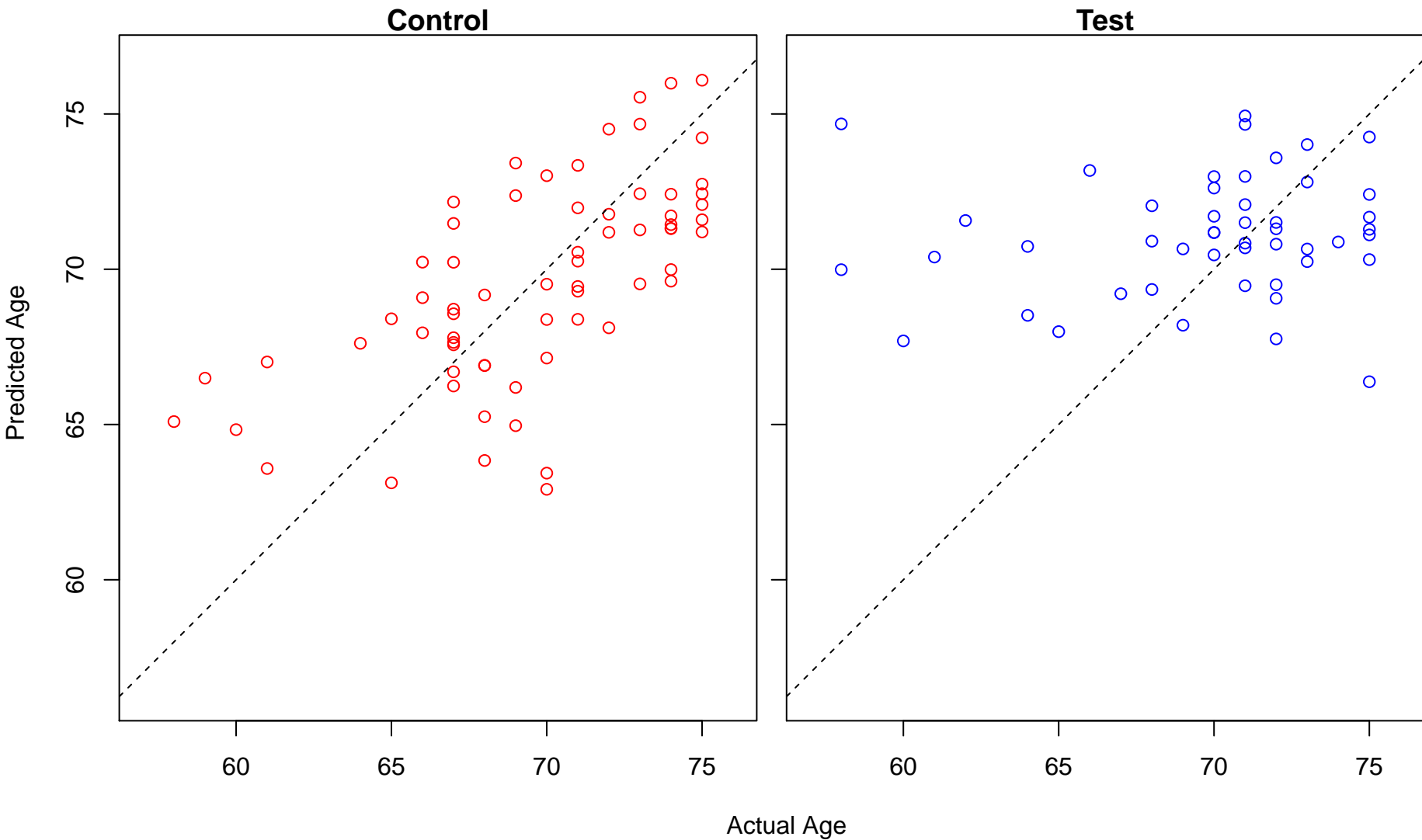
regulation of protein glycosylation (Score: 1.150347)



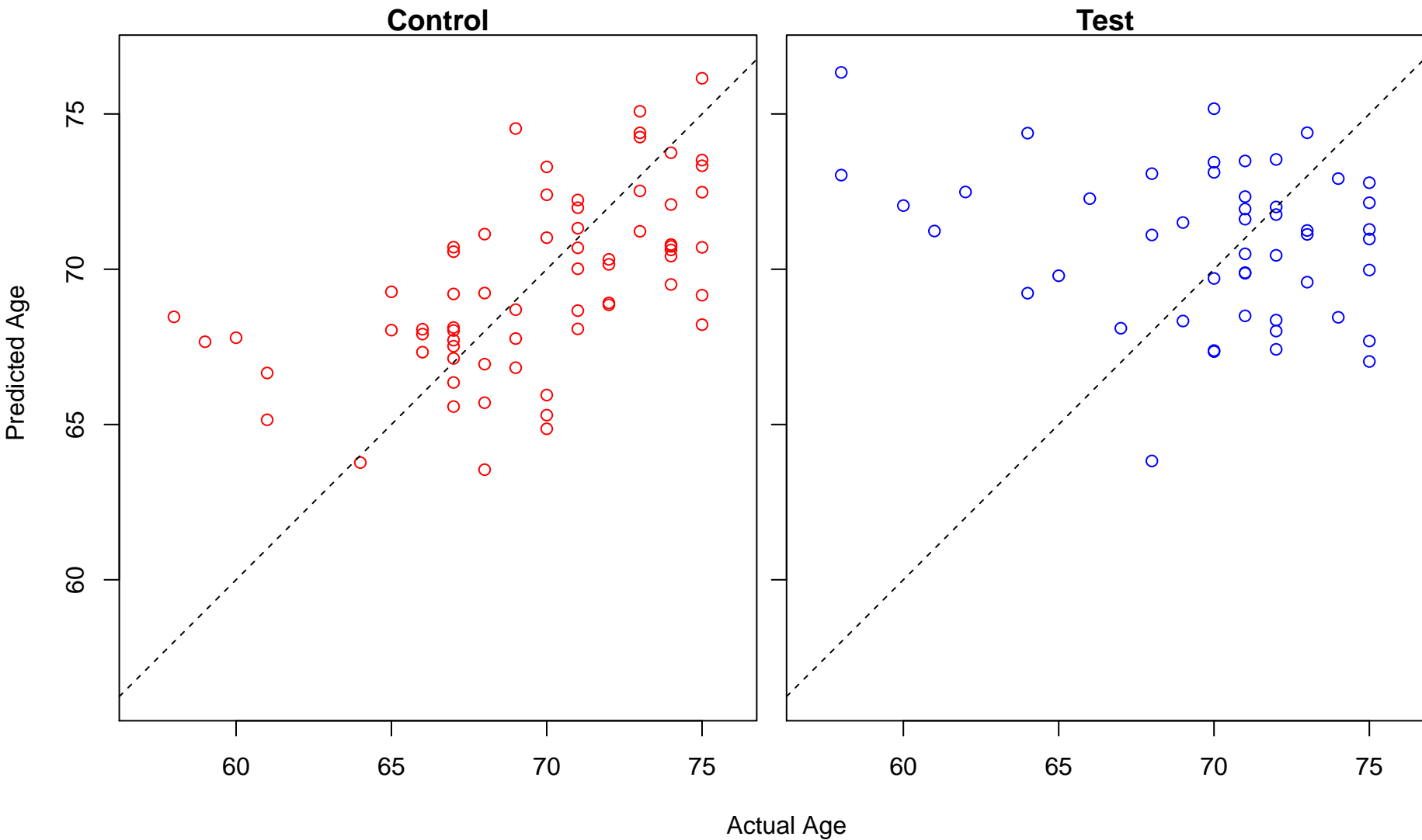
positive regulation of stress fiber assembly (Score: 1.149858)



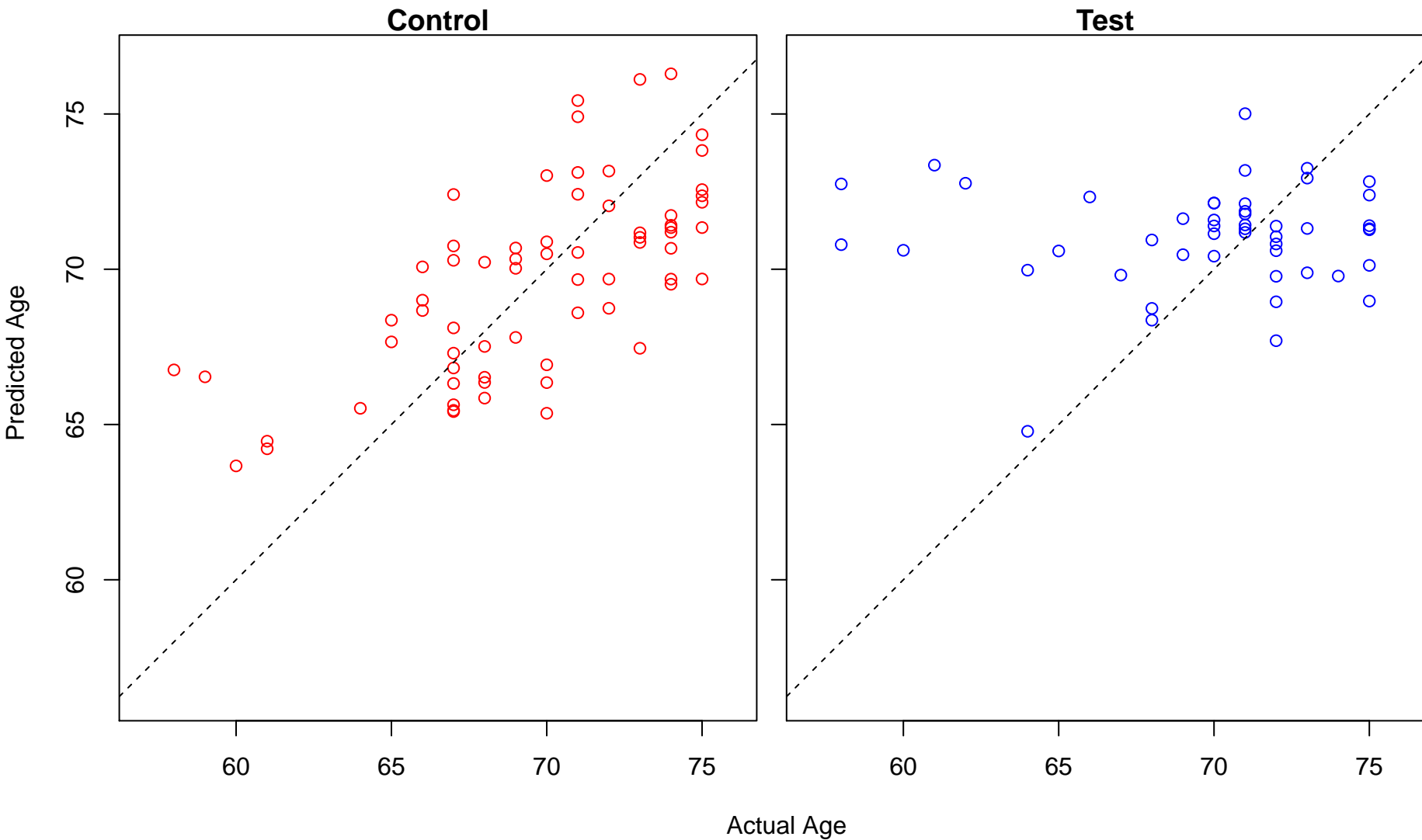
negative regulation of response to wounding (Score: 1.149411)



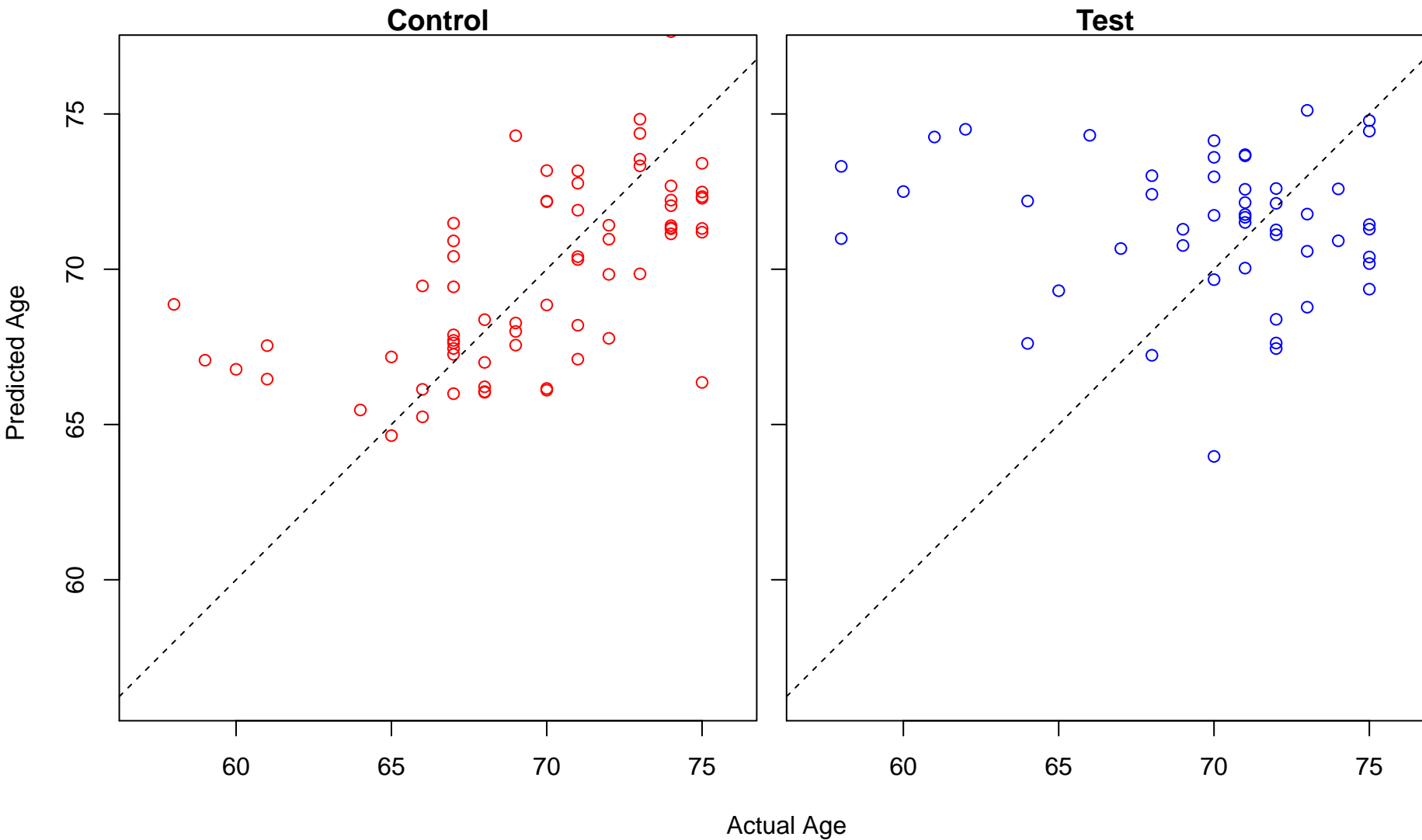
protein localization to lysosome (Score: 1.148867)



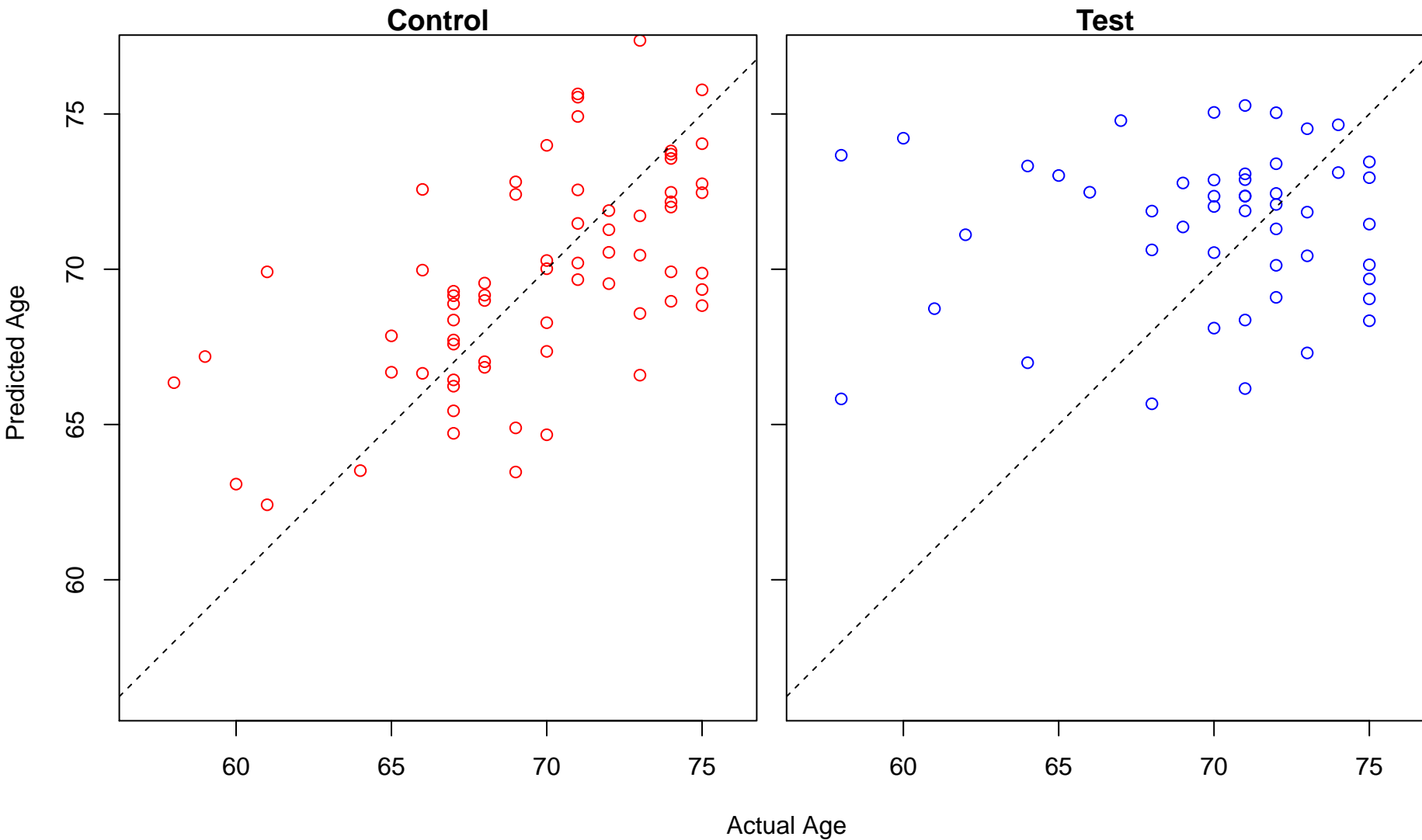
endothelial tube morphogenesis (Score: 1.148612)



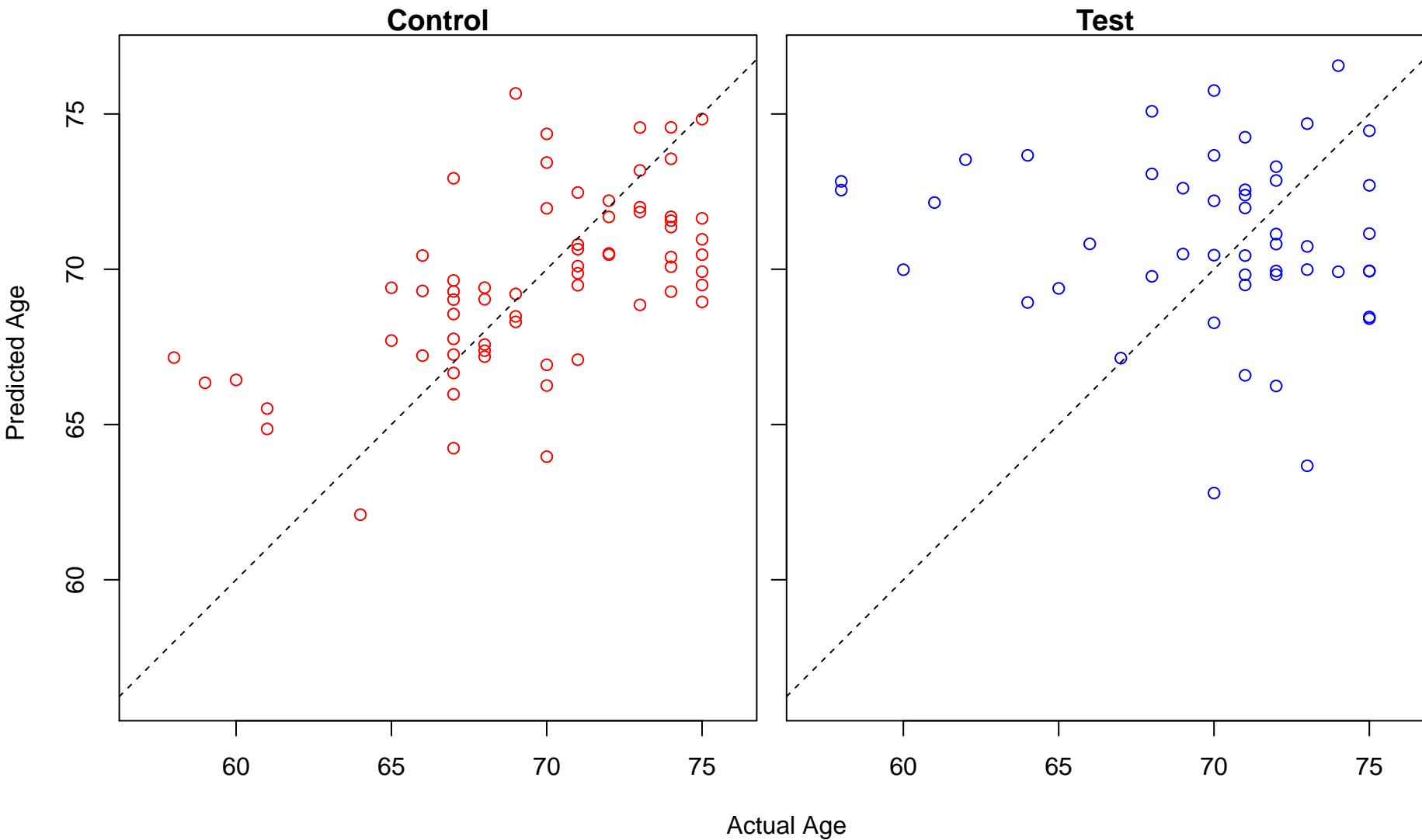
regulation of anion transport (Score: 1.148258)



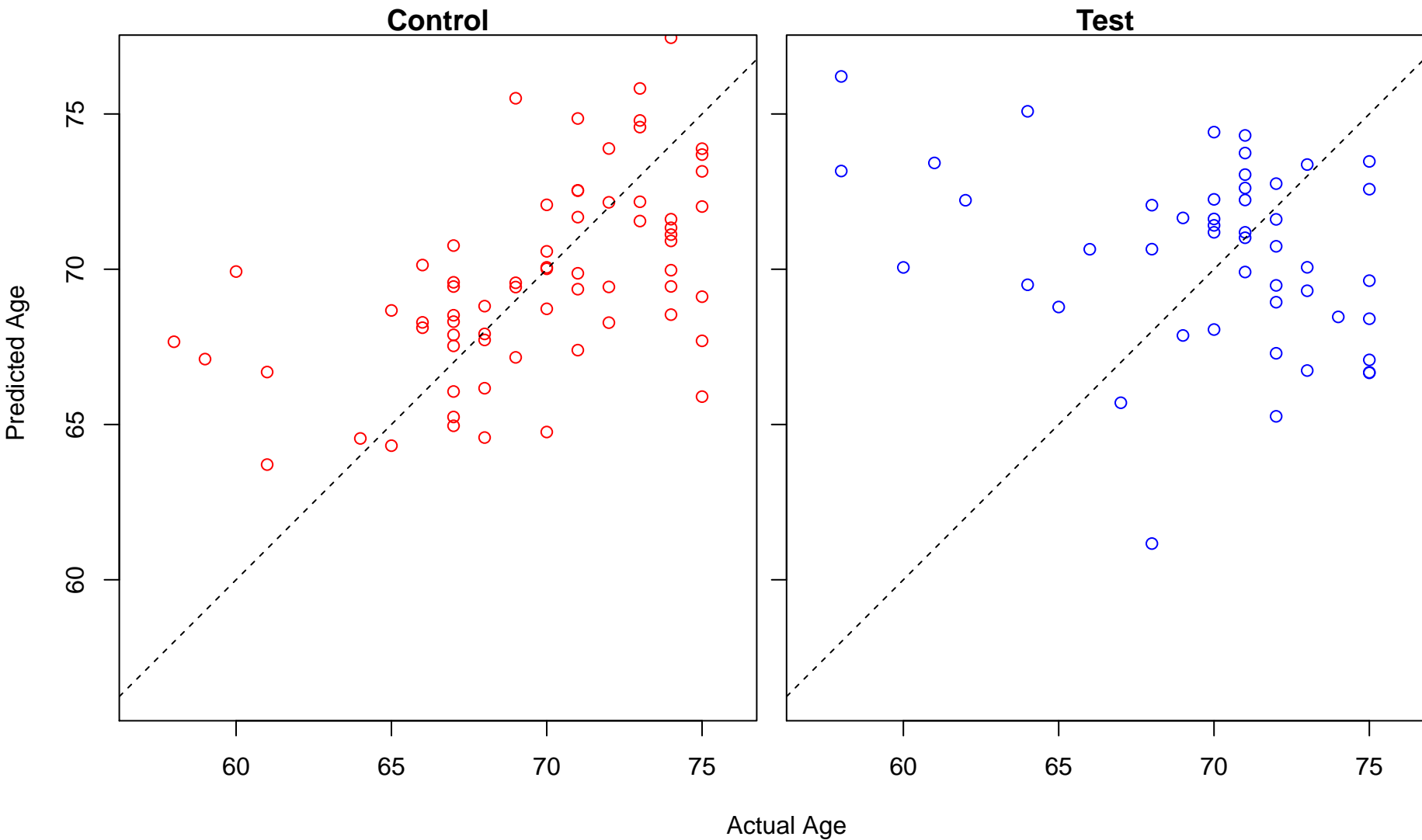
cellular process involved in reproduction in multicellular organism (Score: 1.148074)



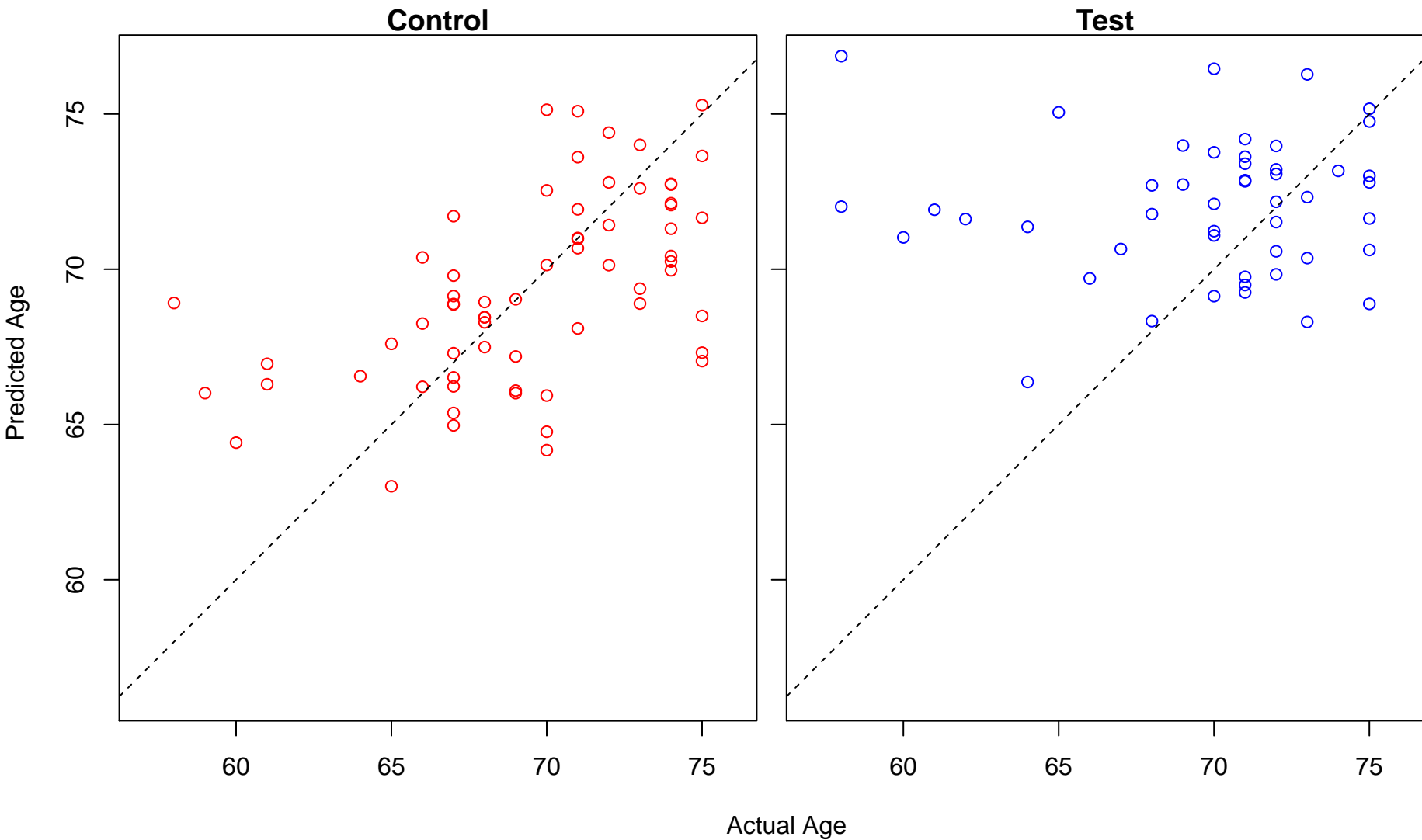
regulation of protein export from nucleus (Score: 1.148012)



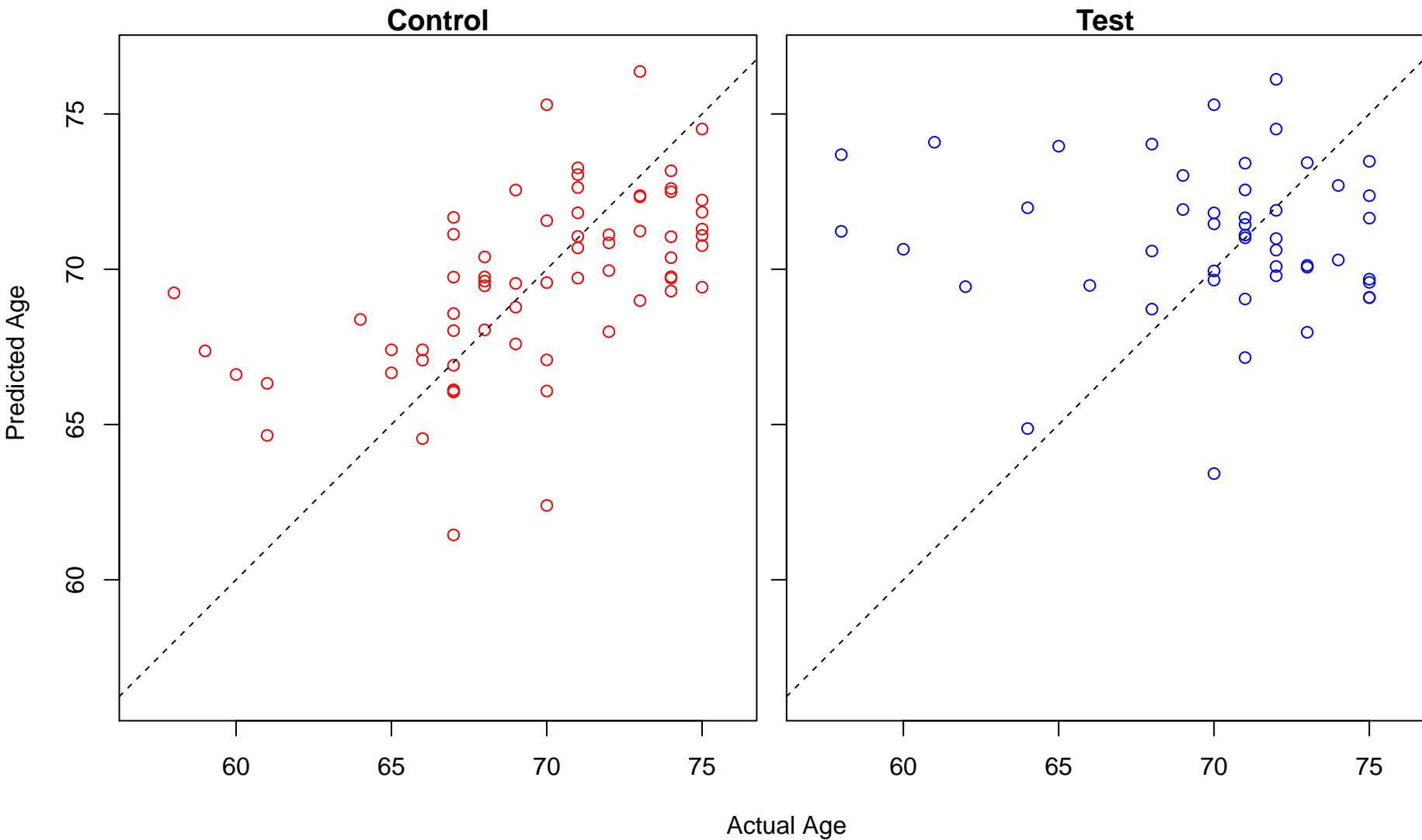
negative regulation of T cell proliferation (Score: 1.147947)



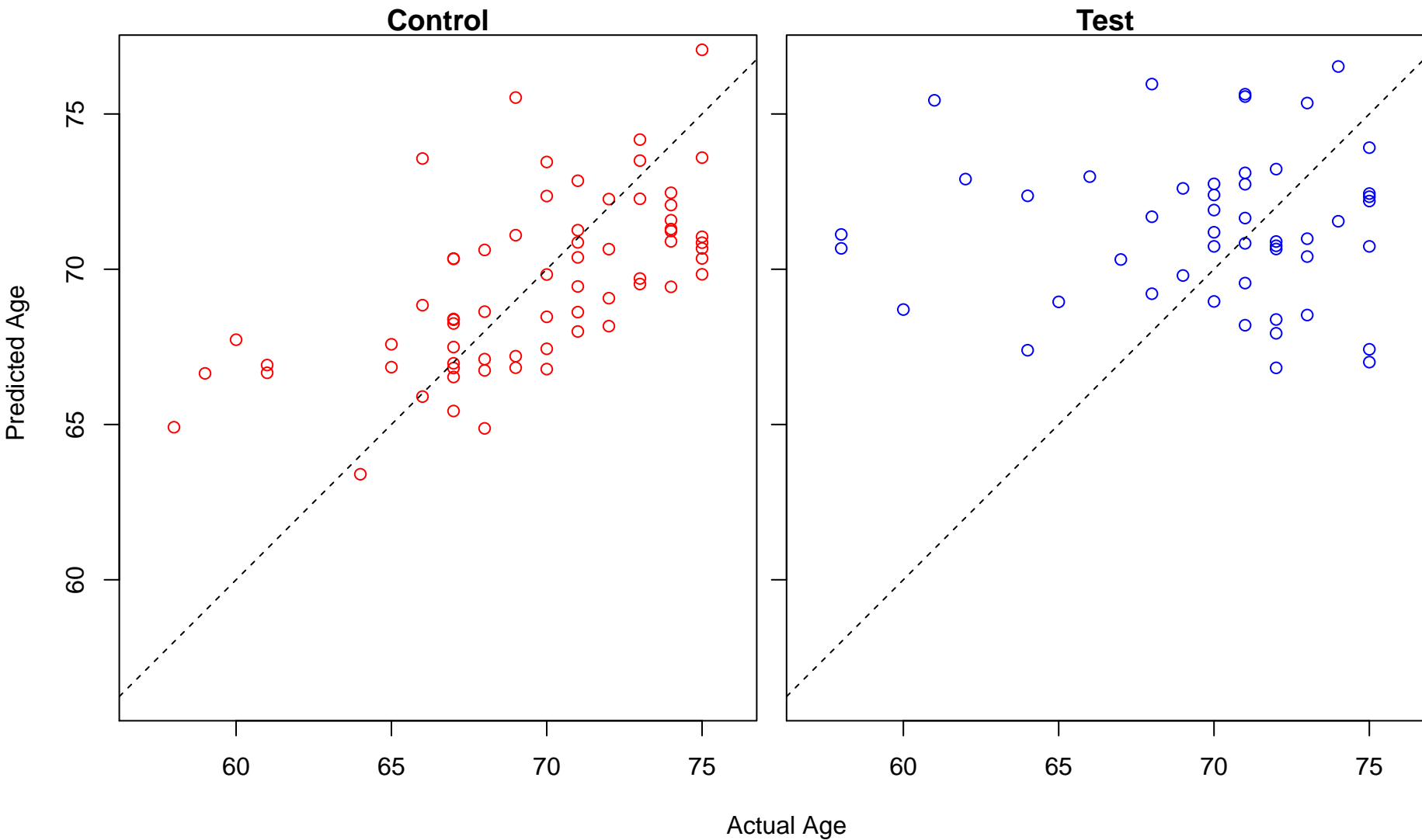
triglyceride biosynthetic process (Score: 1.147745)



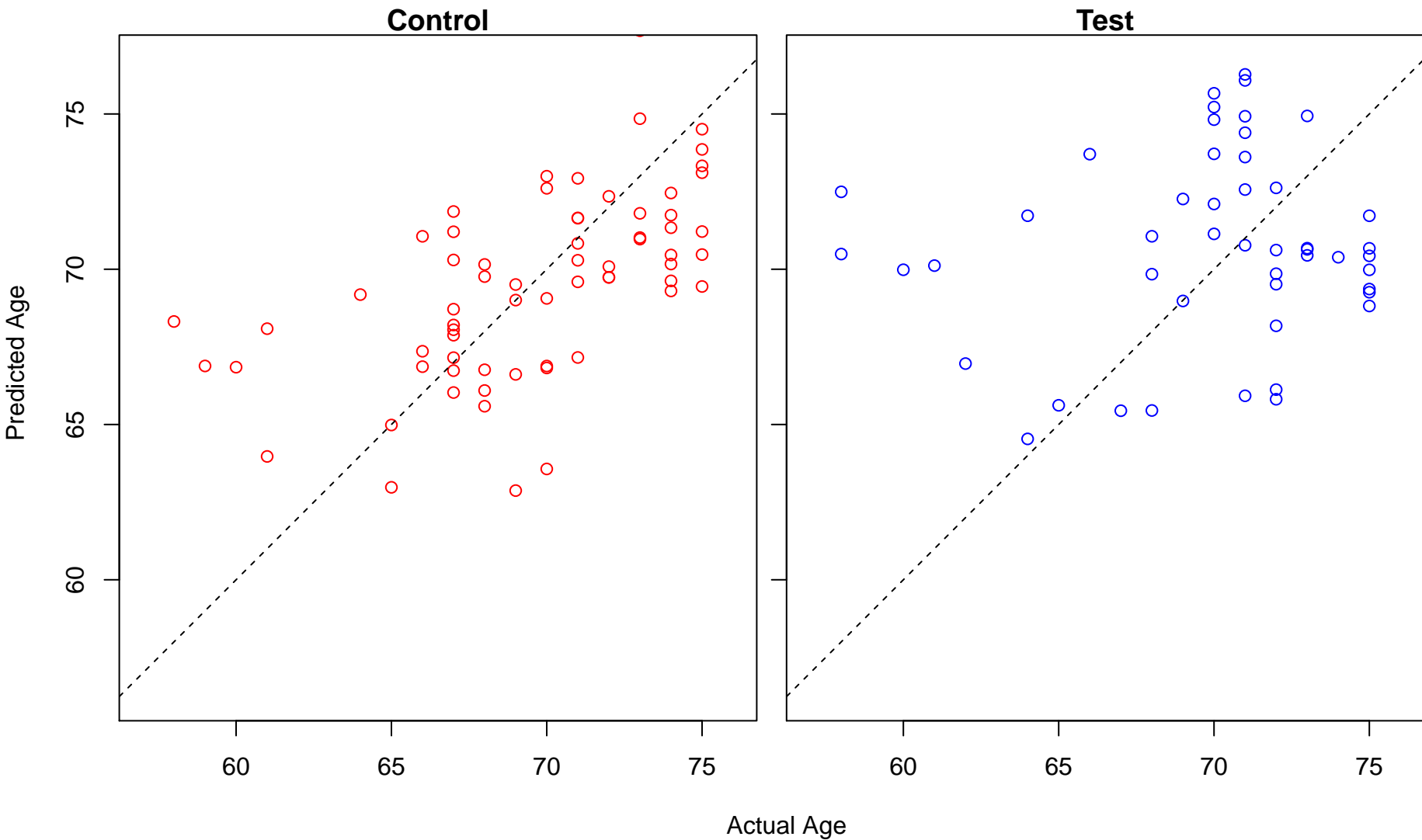
one-carbon metabolic process (Score: 1.147365)



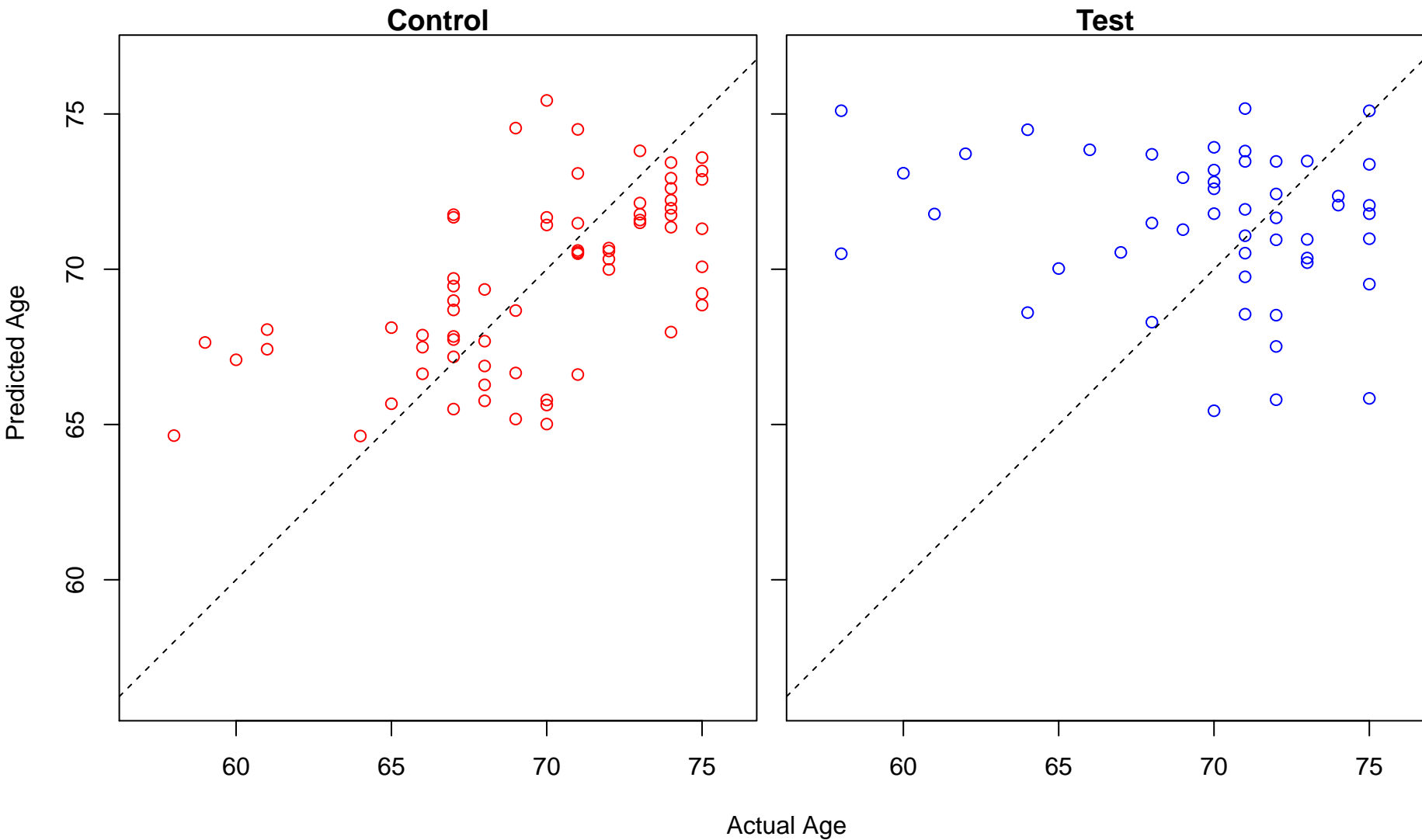
ribosome disassembly (Score: 1.147152)



negative regulation of wound healing (Score: 1.146724)

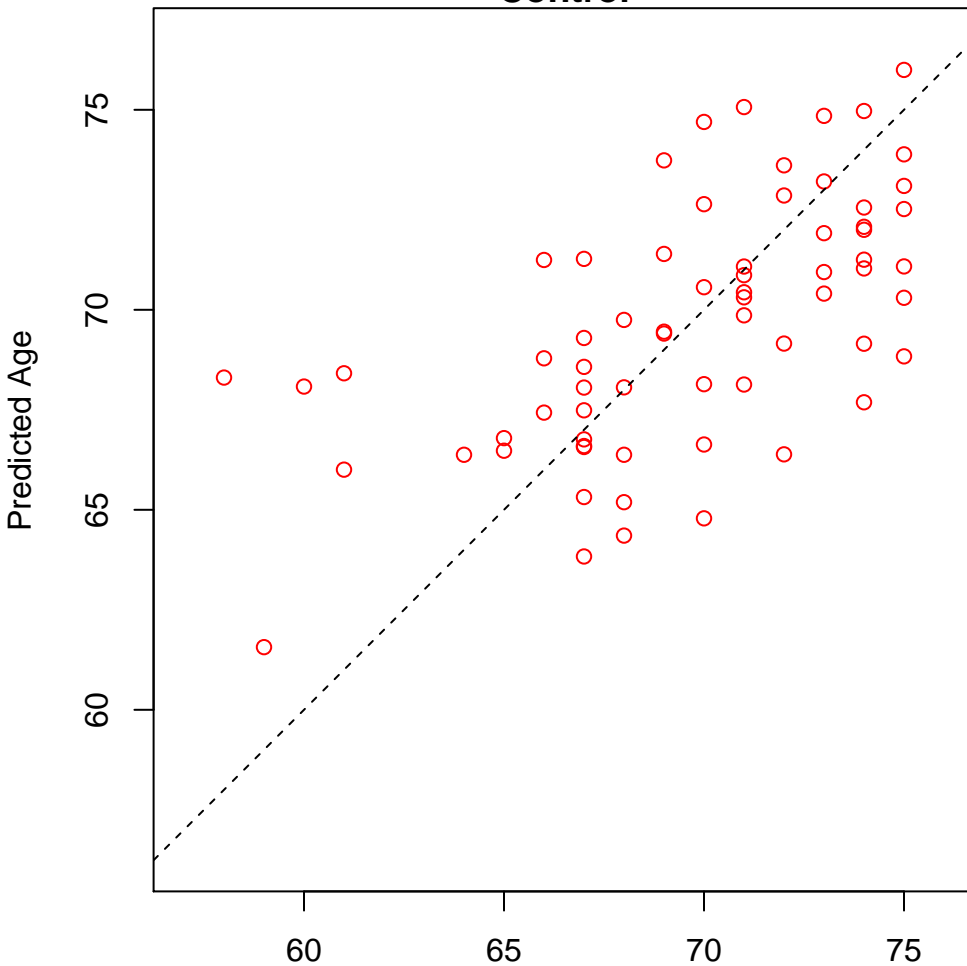


histone phosphorylation (Score: 1.146360)

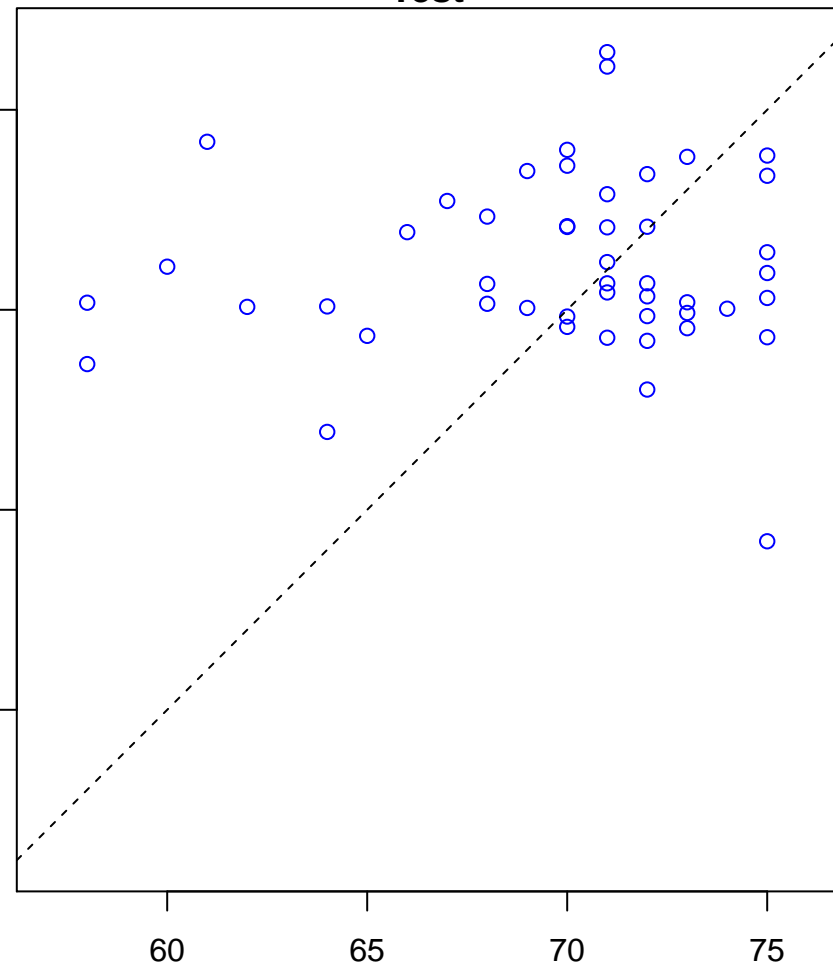


pyrimidine nucleoside catabolic process (Score: 1.146356)

Control

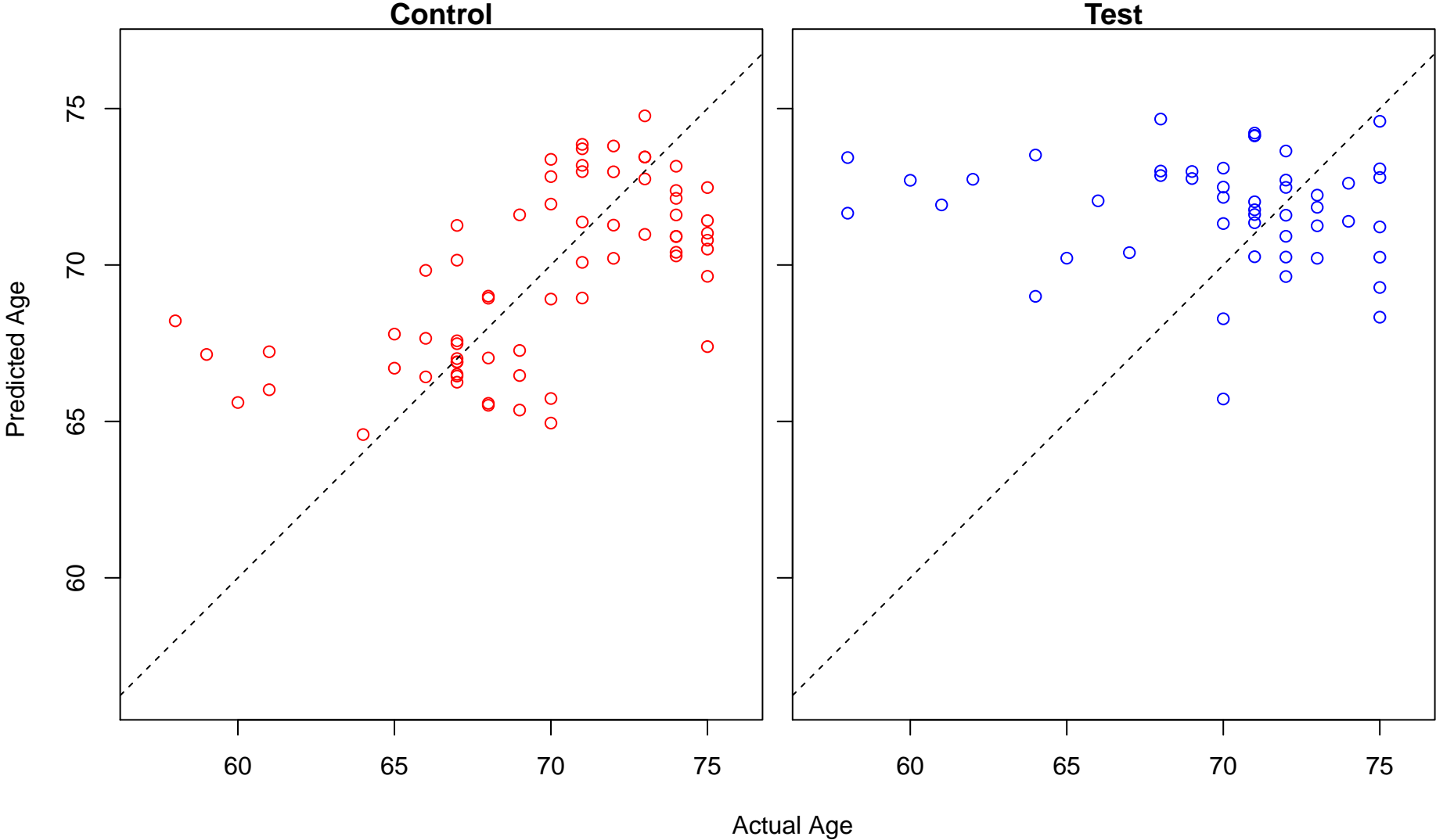


Test

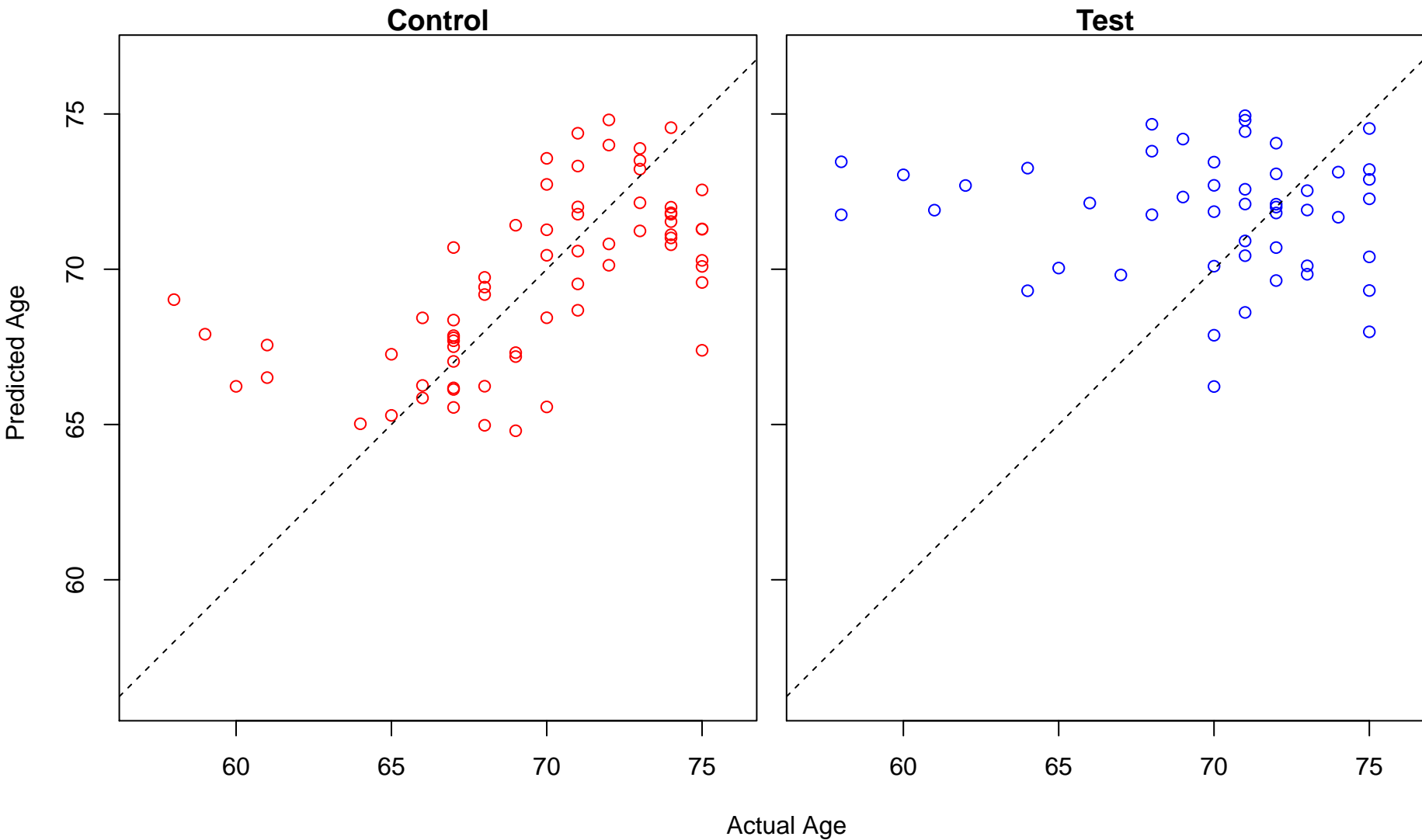


Actual Age

positive regulation of signal transduction by p53 class mediator (Score: 1.145948)

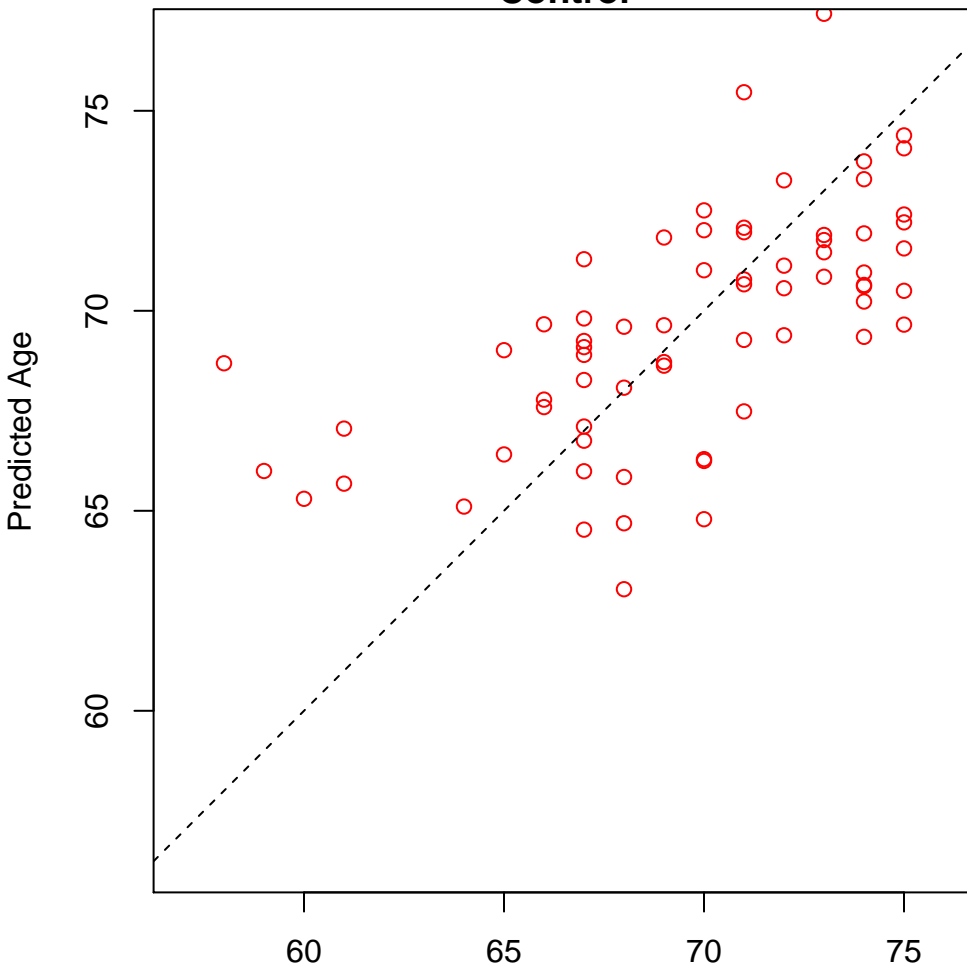


mitotic G2 DNA damage checkpoint (Score: 1.145484)

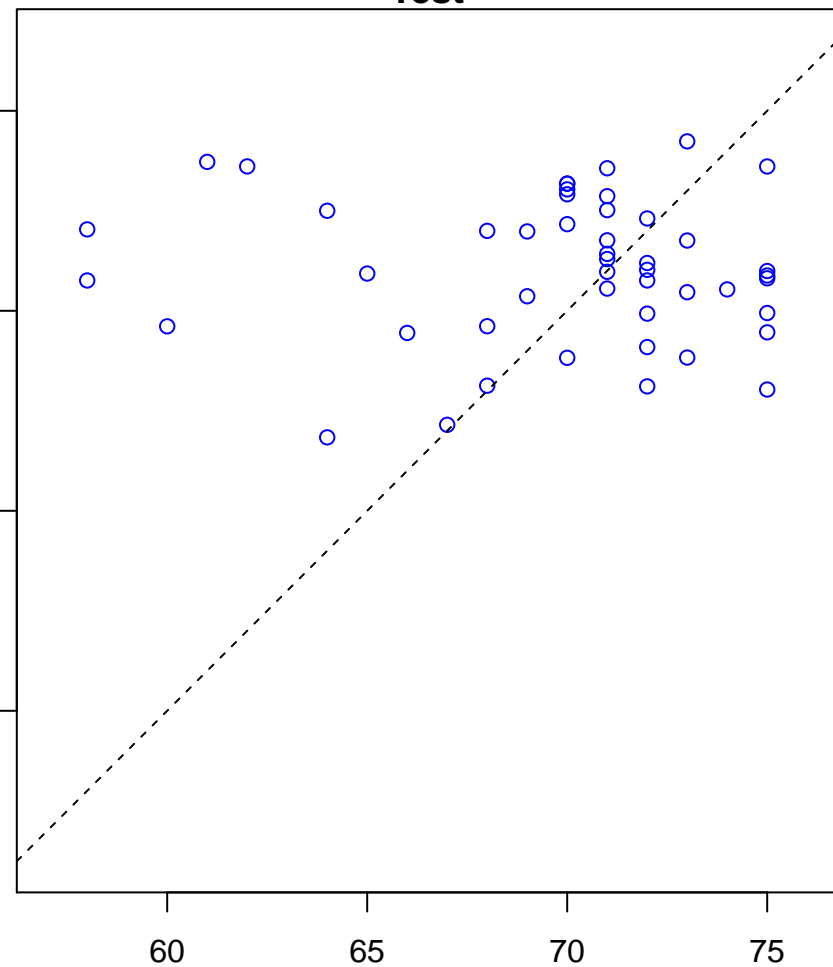


nucleoside diphosphate phosphorylation (Score: 1.145111)

Control

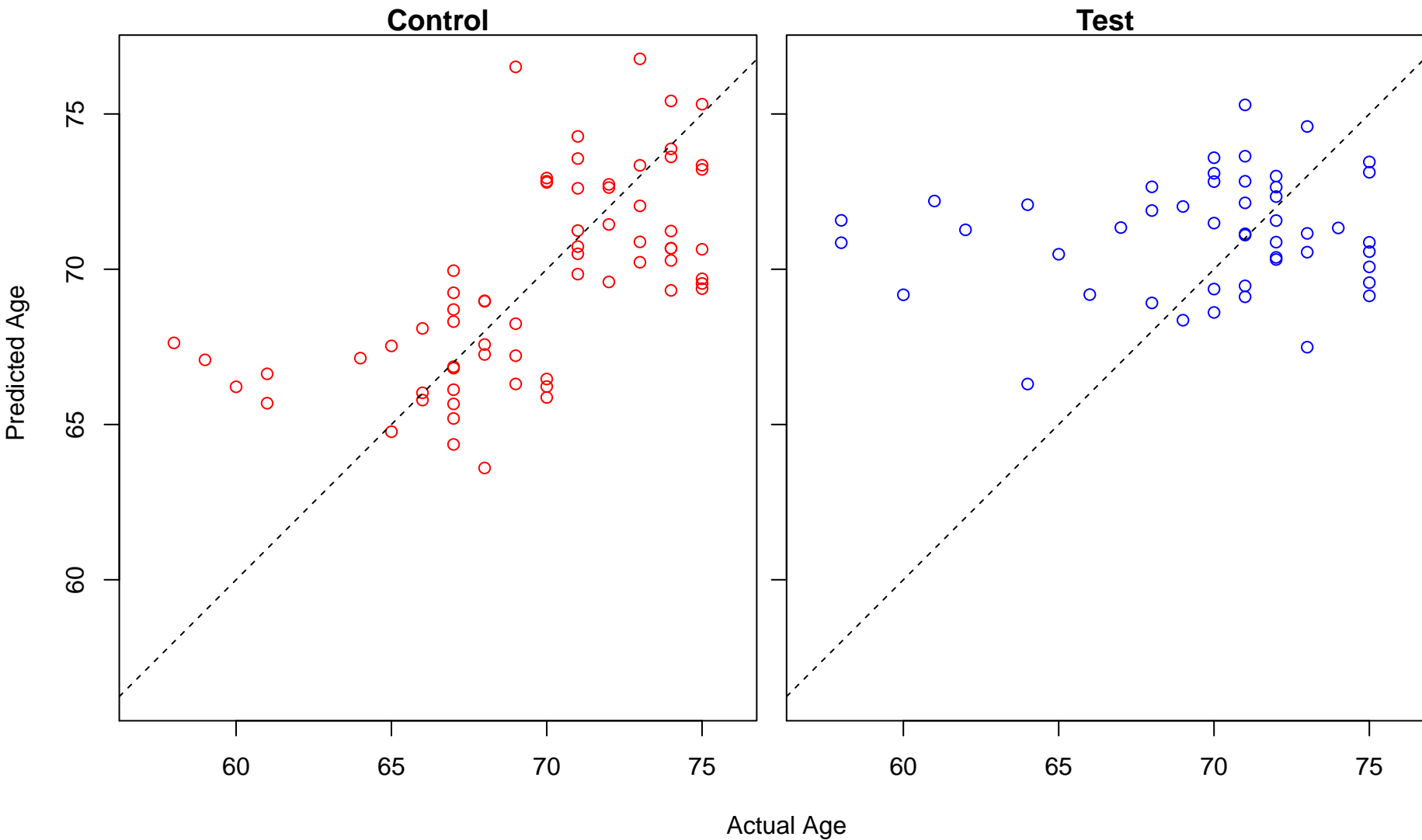


Test

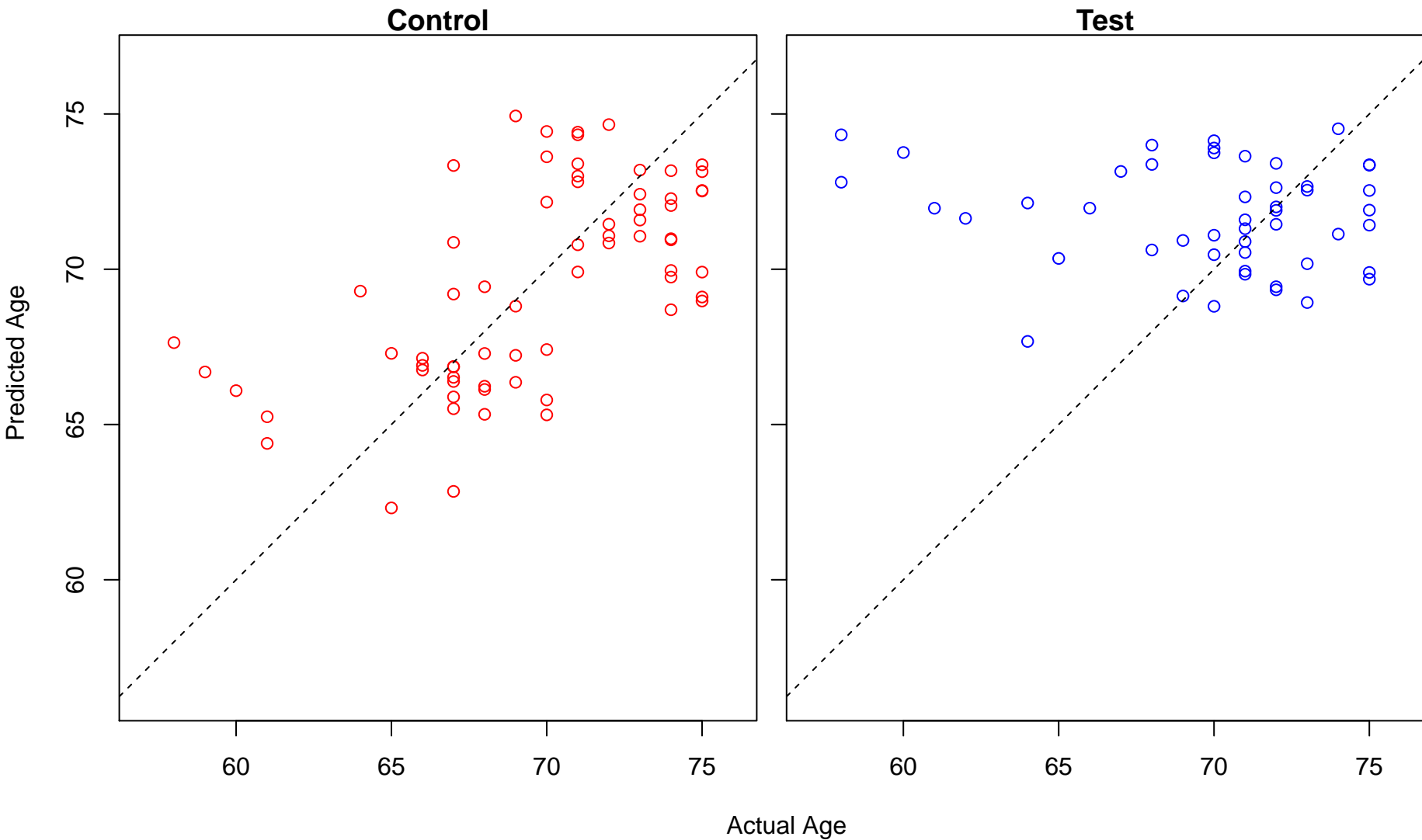


Actual Age

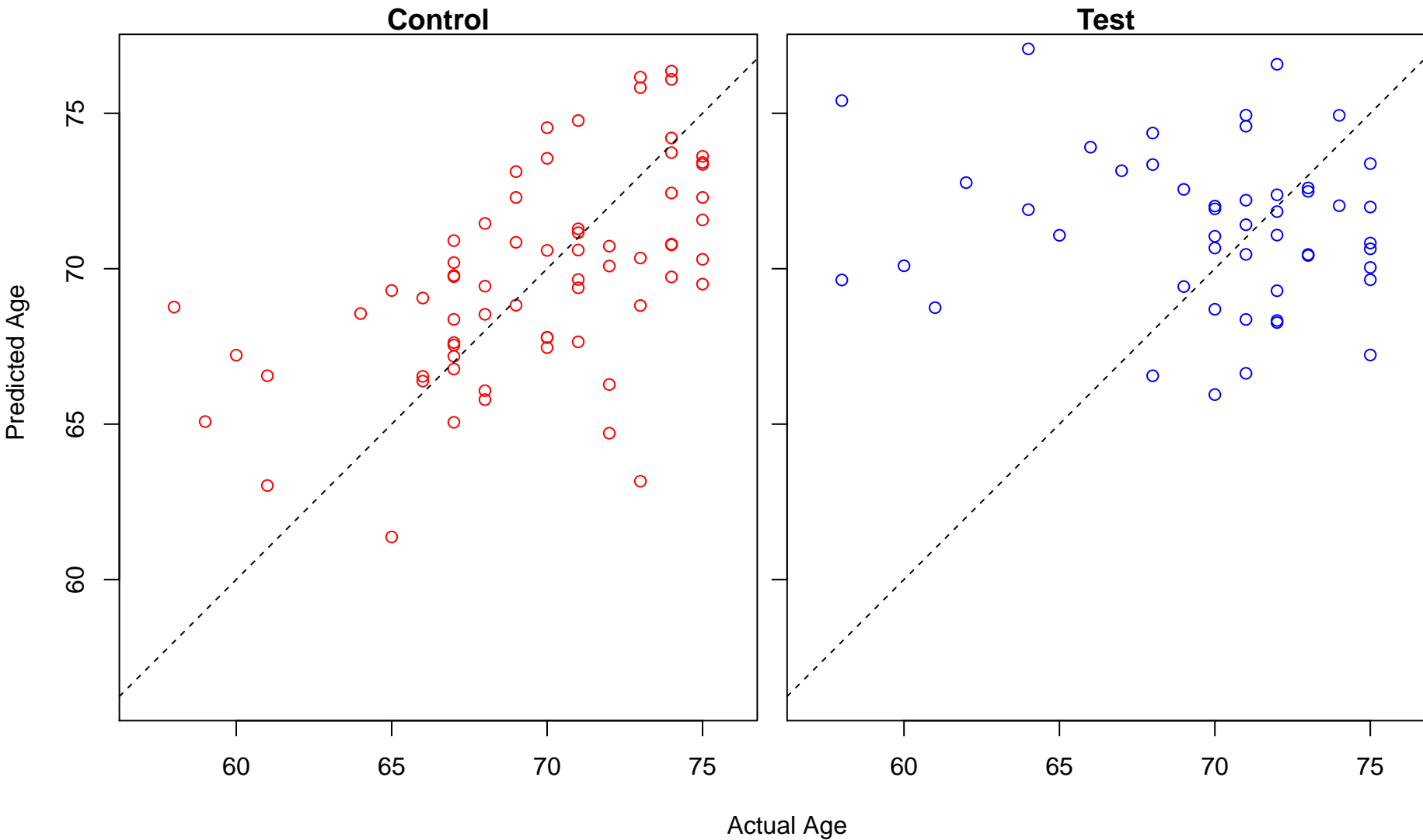
regulation of endocytosis (Score: 1.144518)



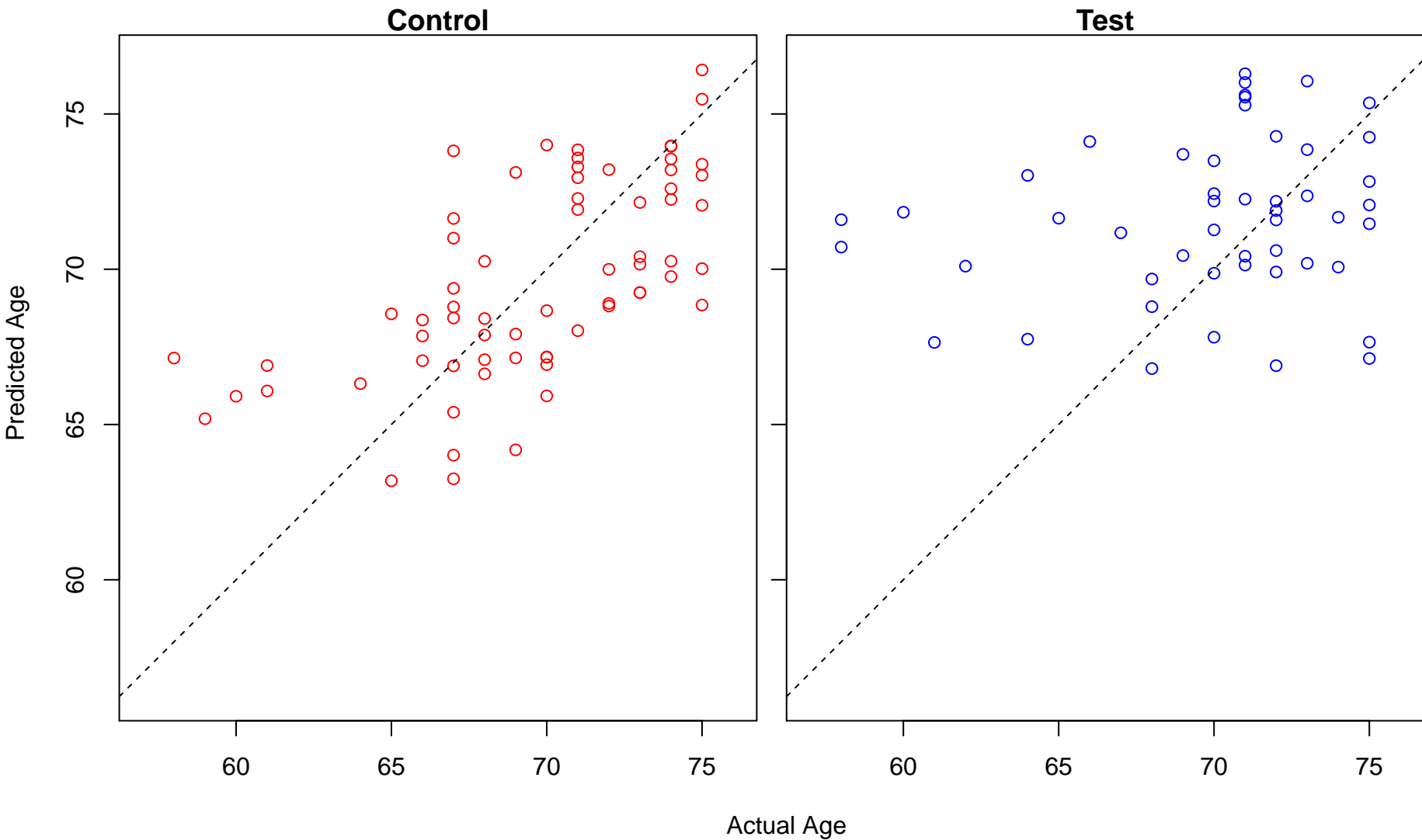
sphingolipid metabolic process (Score: 1.144233)



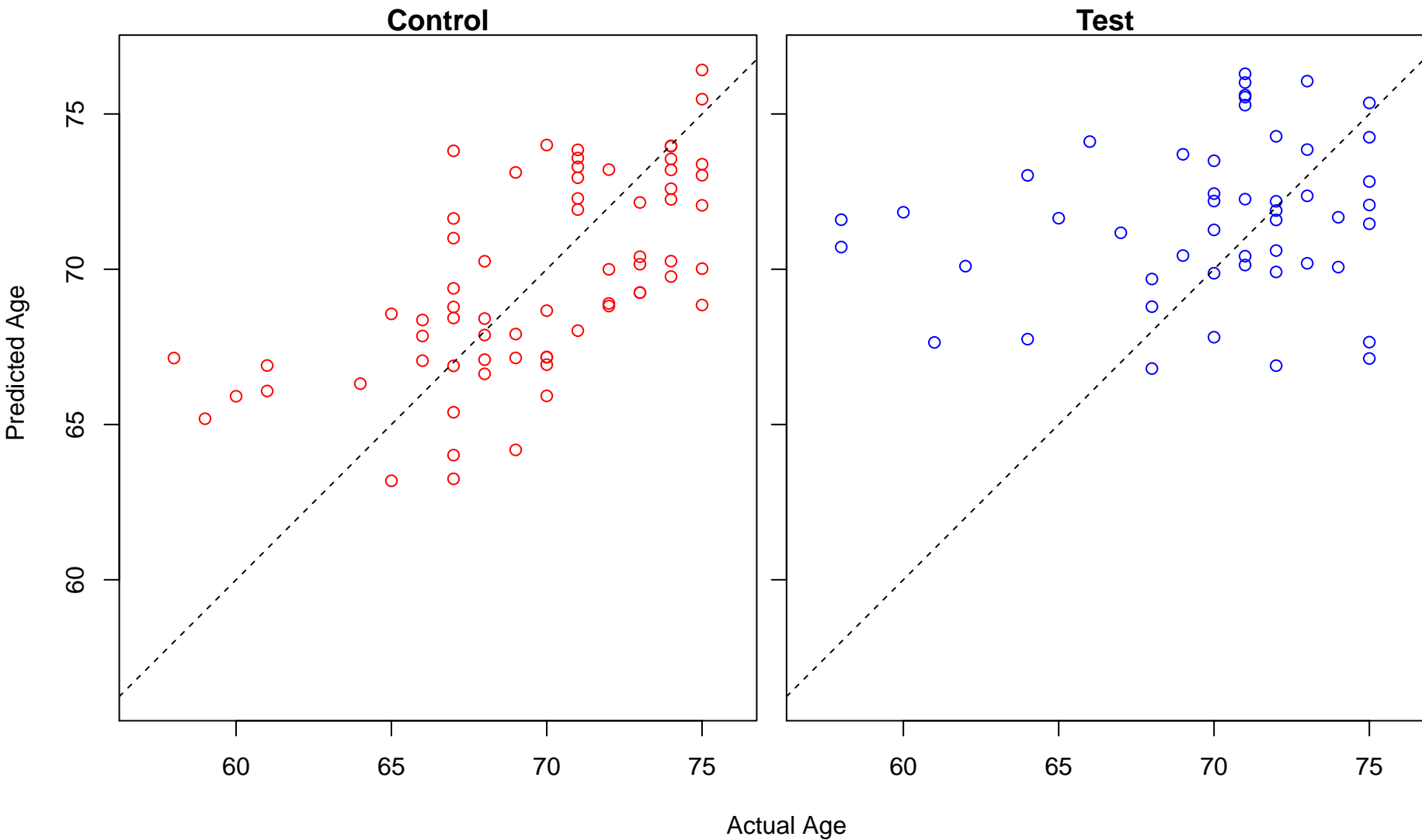
purine deoxyribonucleotide metabolic process (Score: 1.143991)



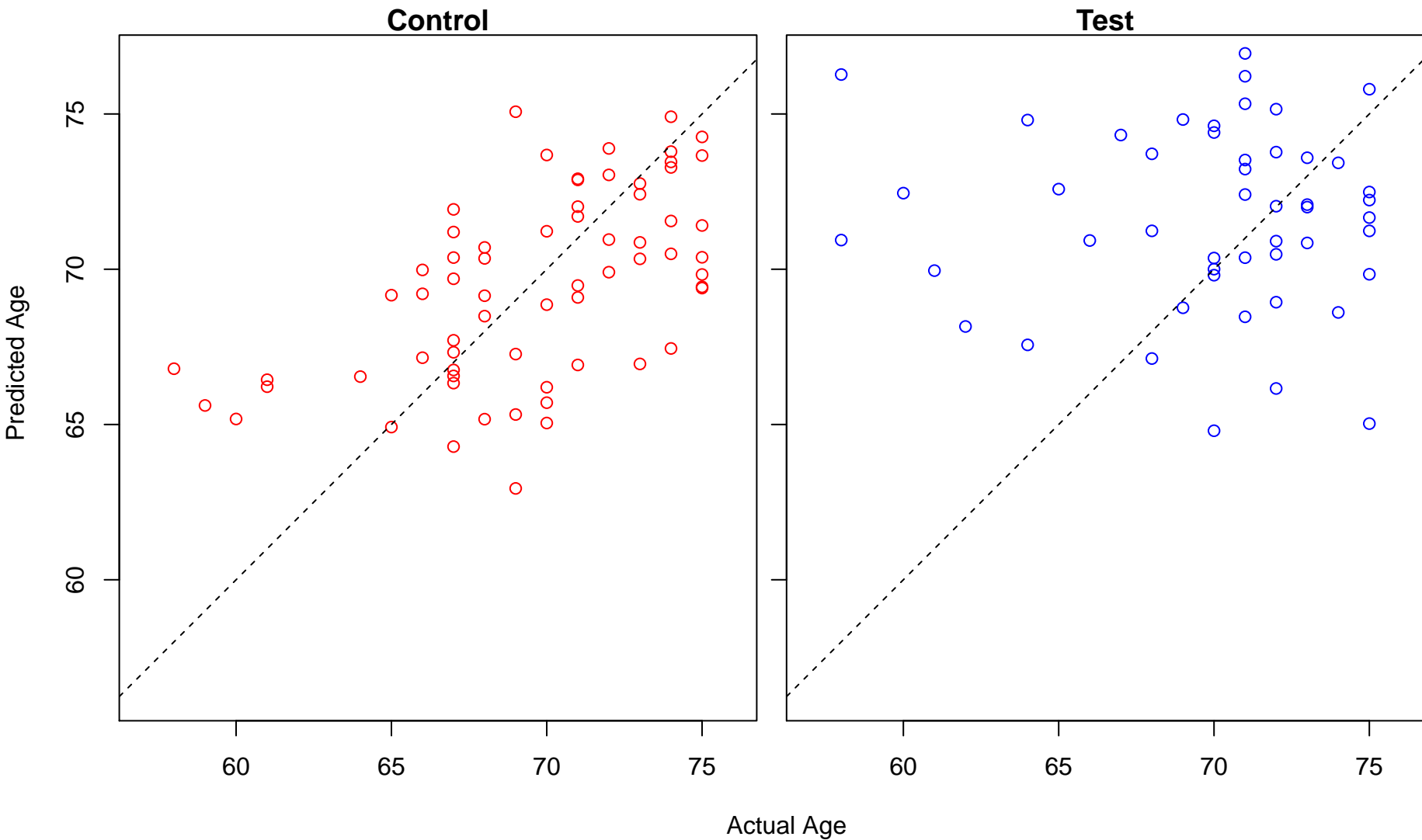
positive regulation of B cell mediated immunity (Score: 1.142685)



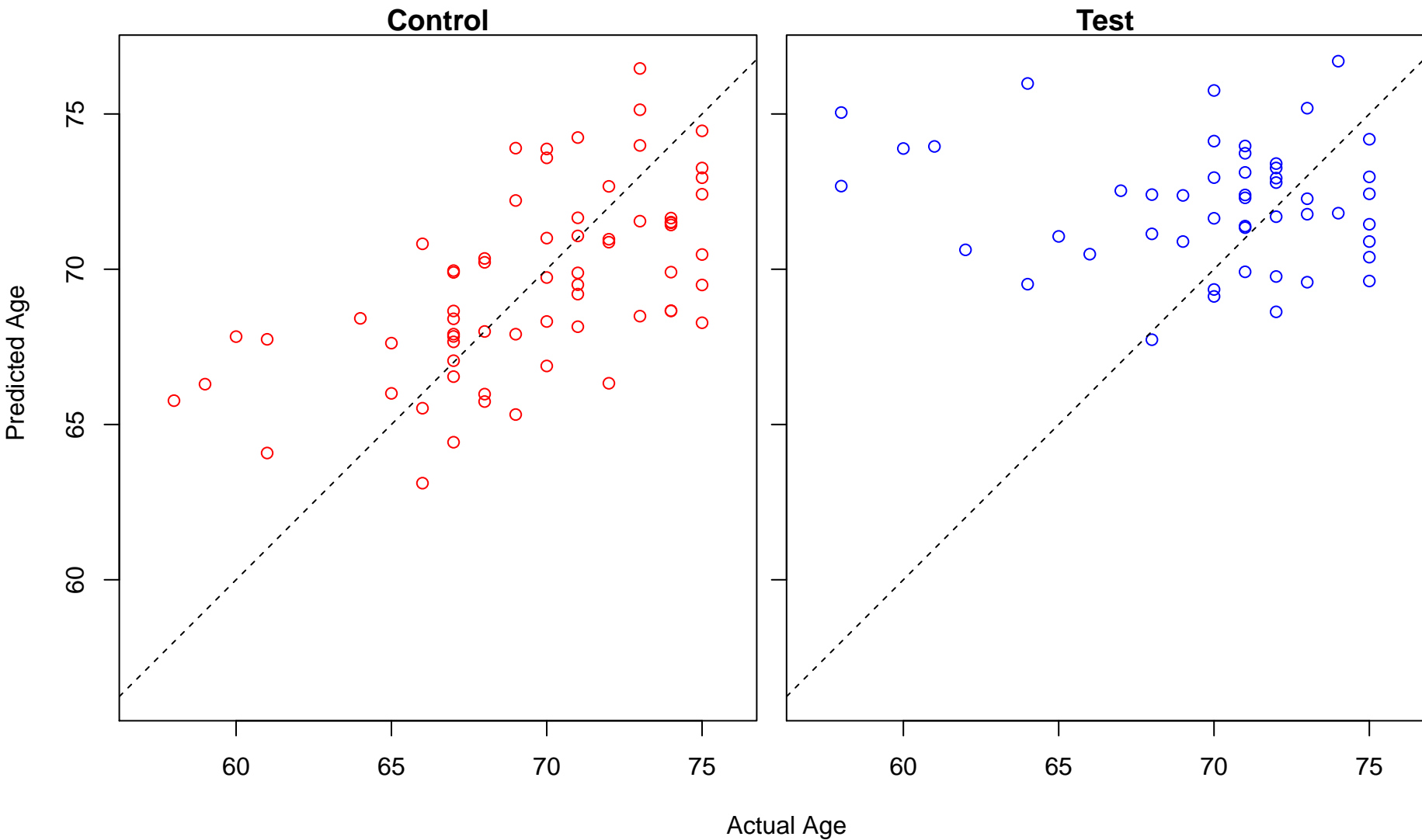
positive regulation of immunoglobulin mediated immune response (Score: 1.142685)



positive regulation of immunoglobulin production (Score: 1.142614)

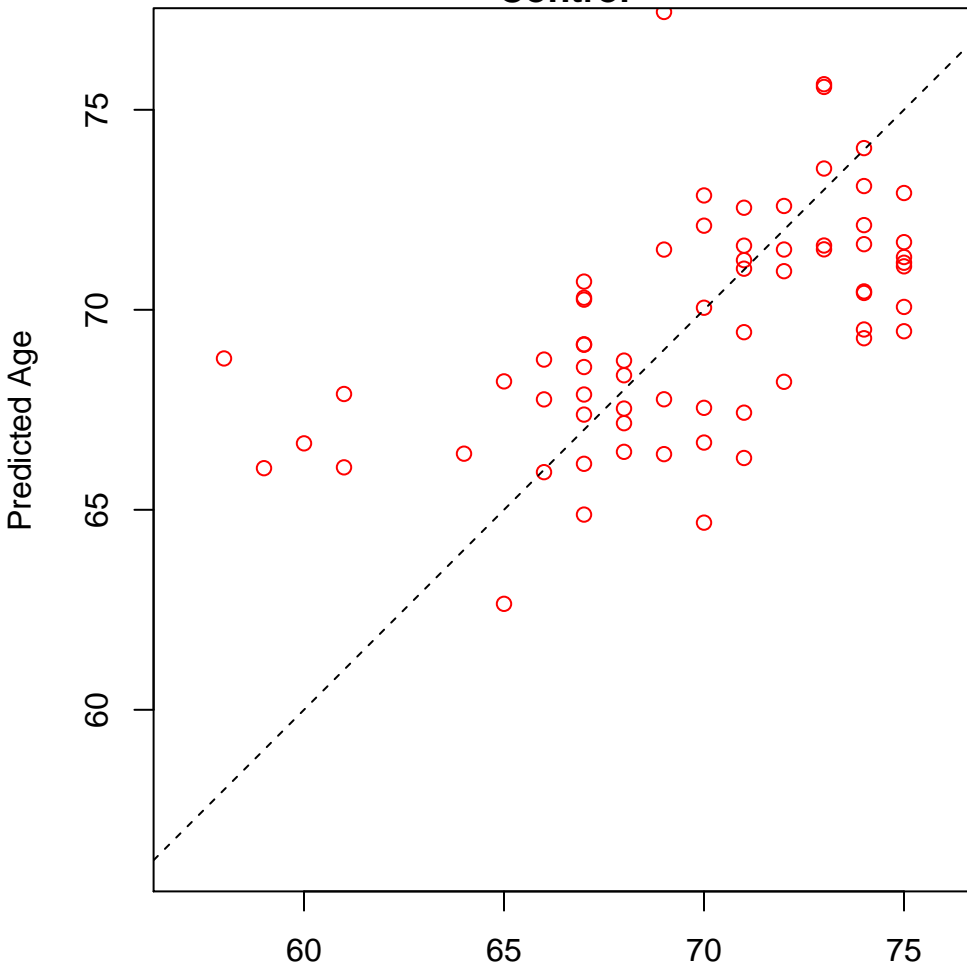


glyoxylate metabolic process (Score: 1.142584)

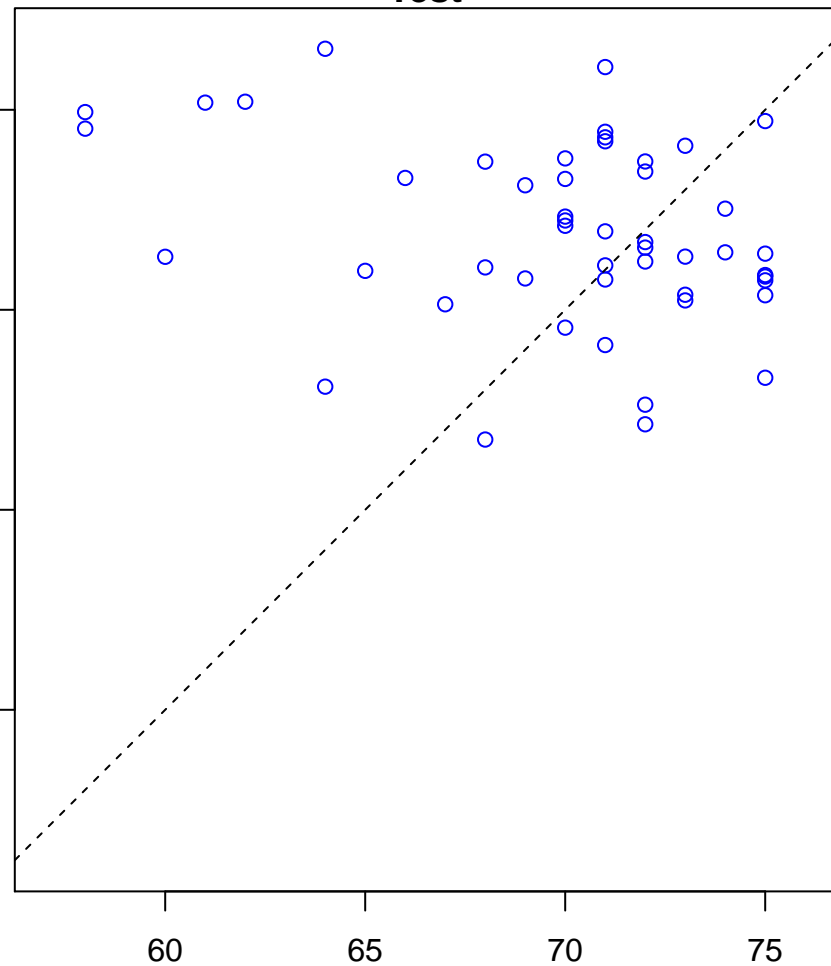


regulation of mast cell degranulation (Score: 1.142337)

Control

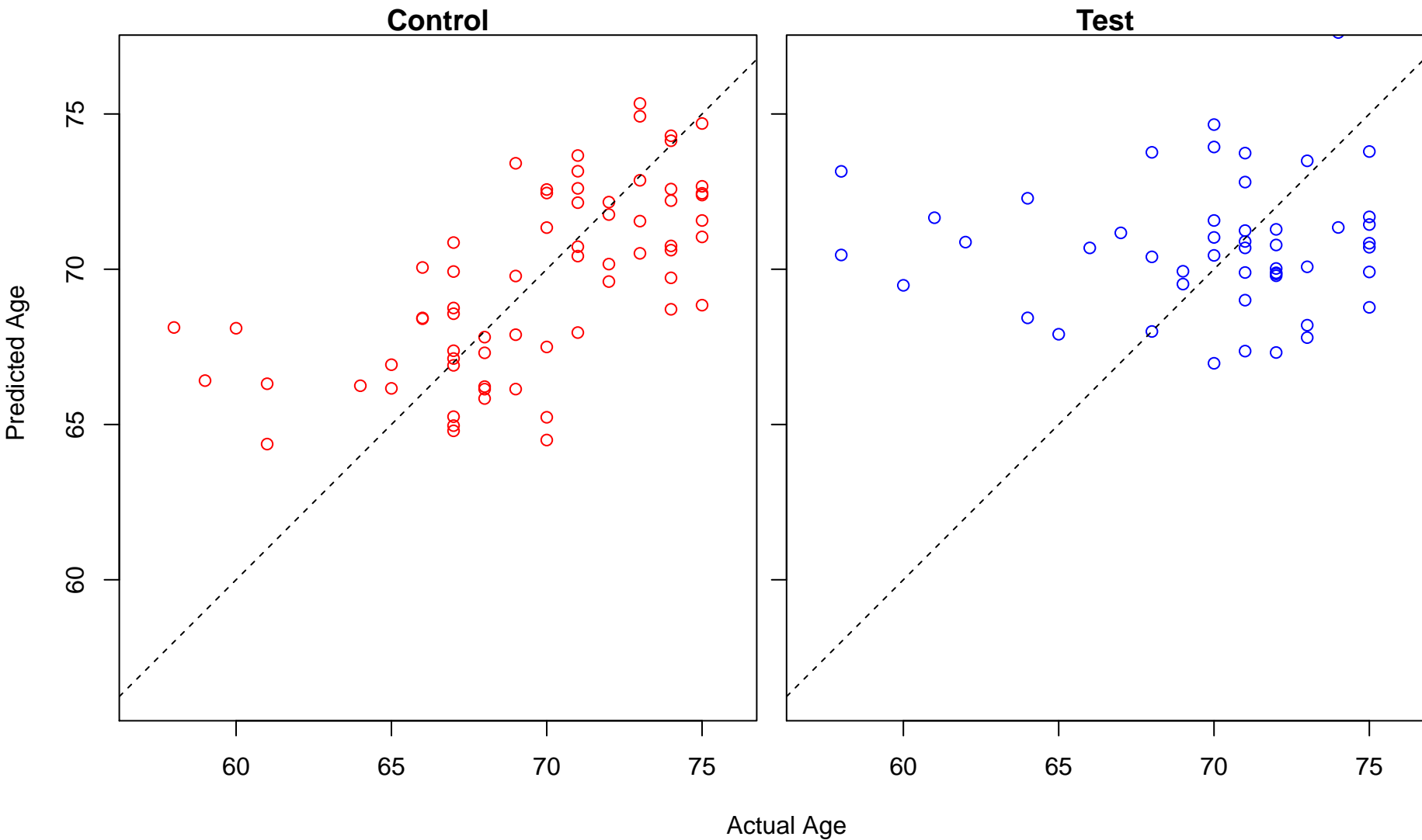


Test

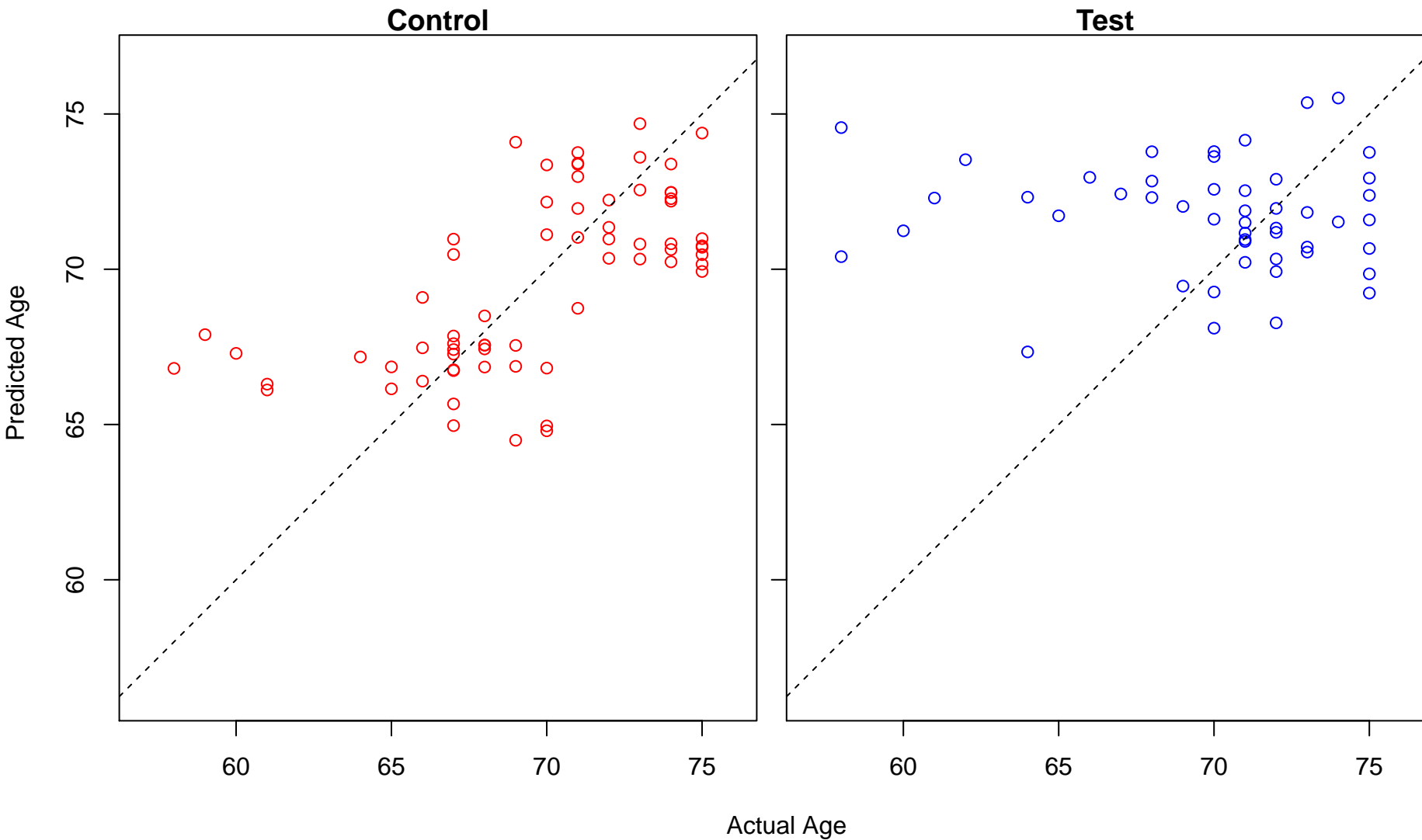


Actual Age

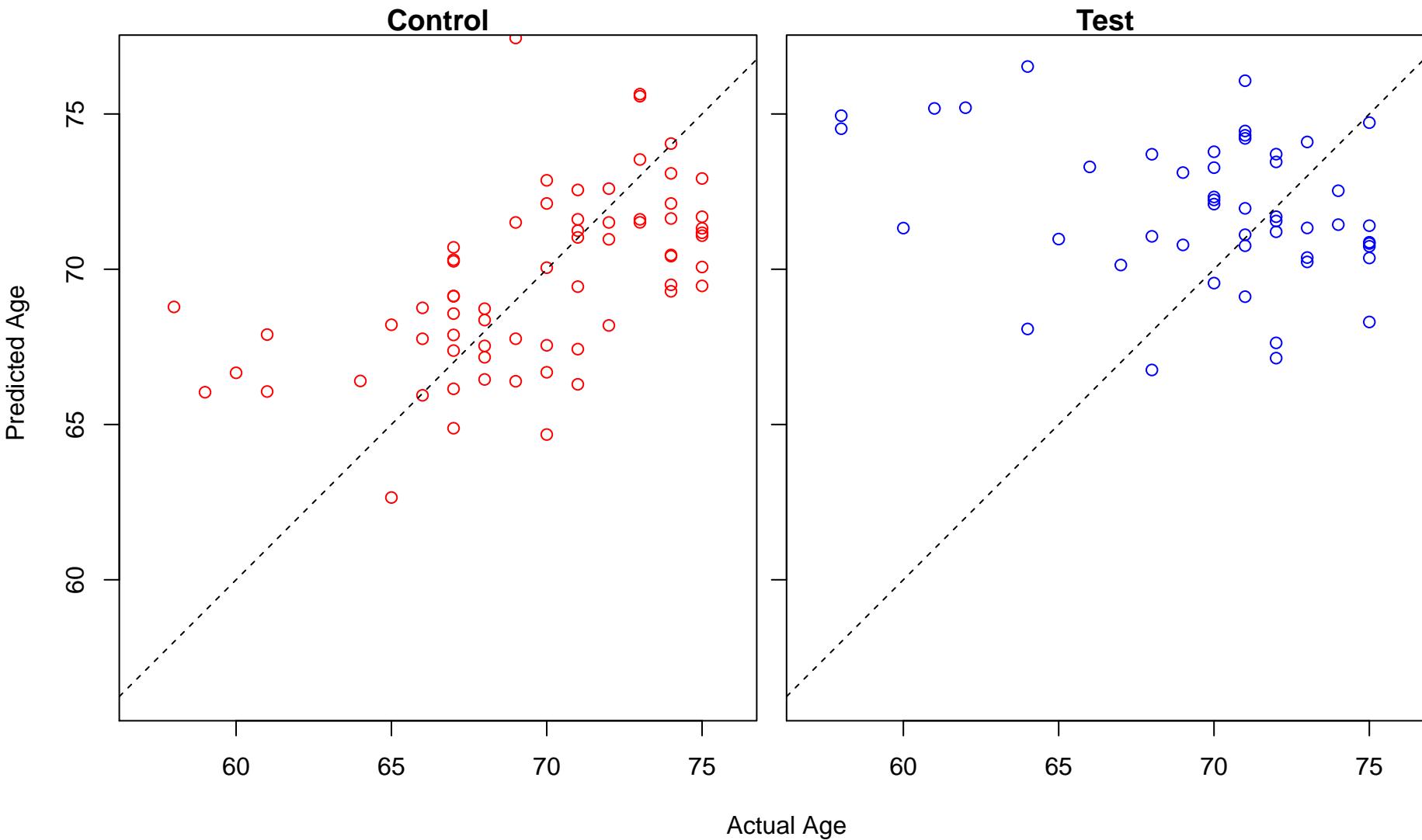
endosome organization (Score: 1.142041)



cellular response to reactive oxygen species (Score: 1.141426)

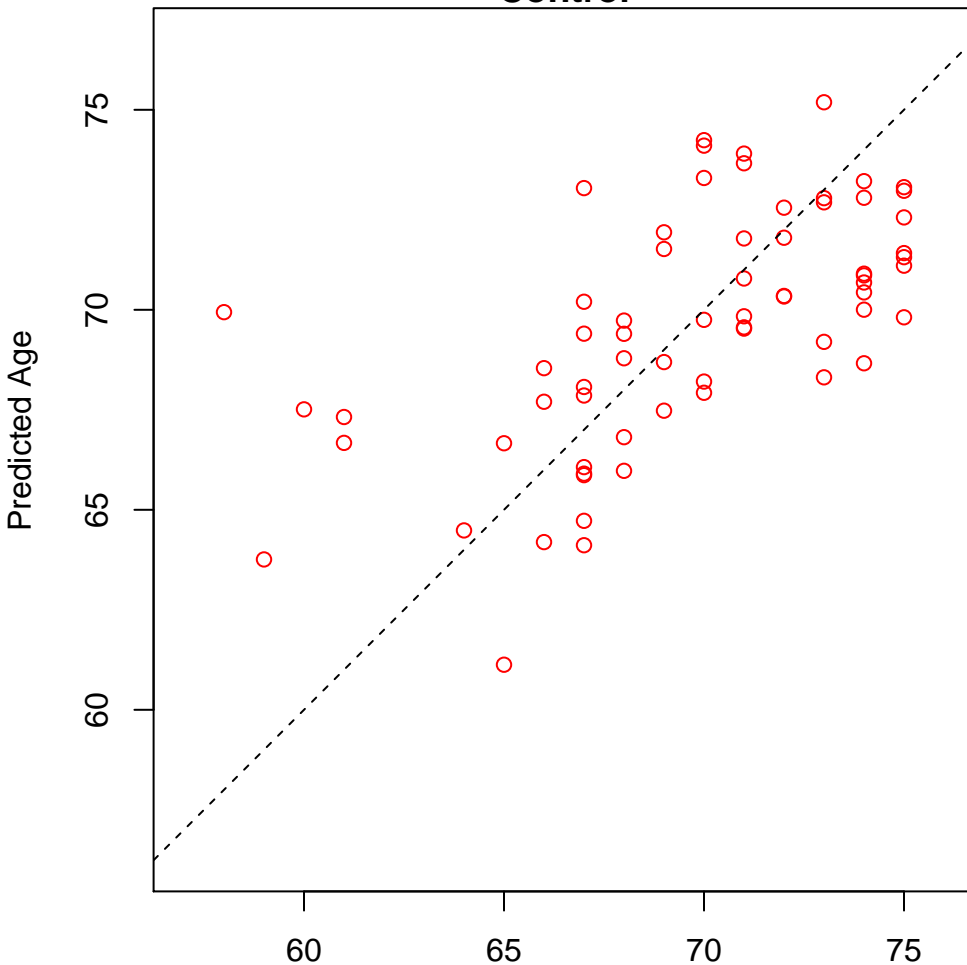


regulation of mast cell activation involved in immune response (Score: 1.141232)

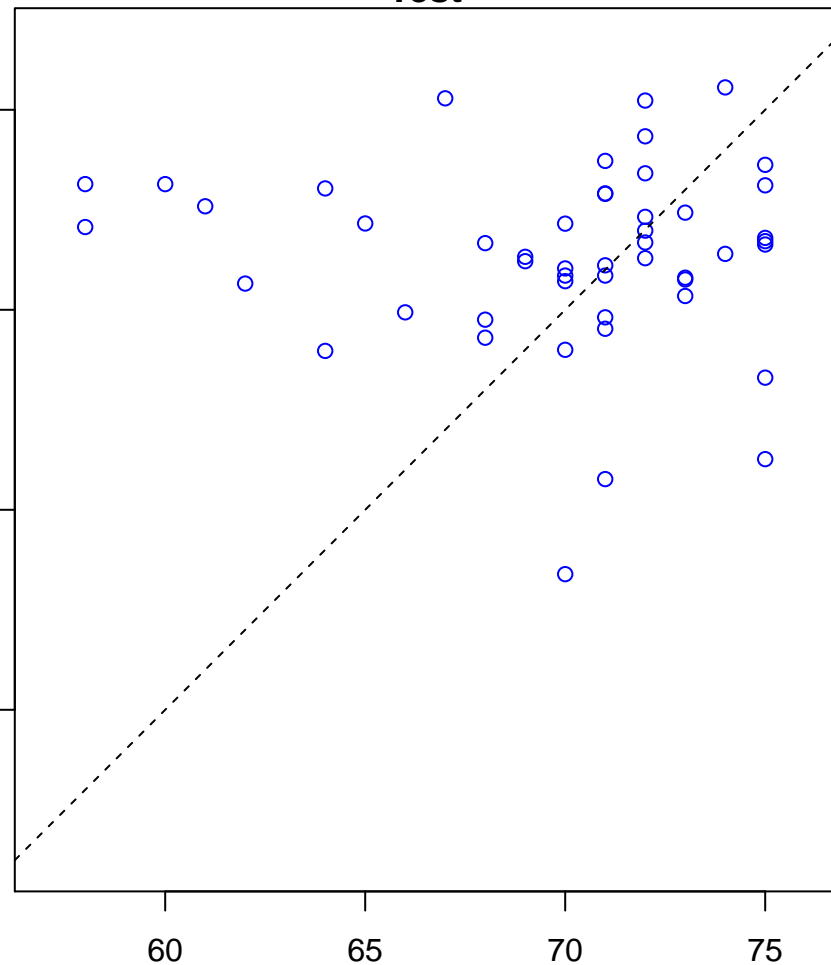


regulation of keratinocyte differentiation (Score: 1.140352)

Control

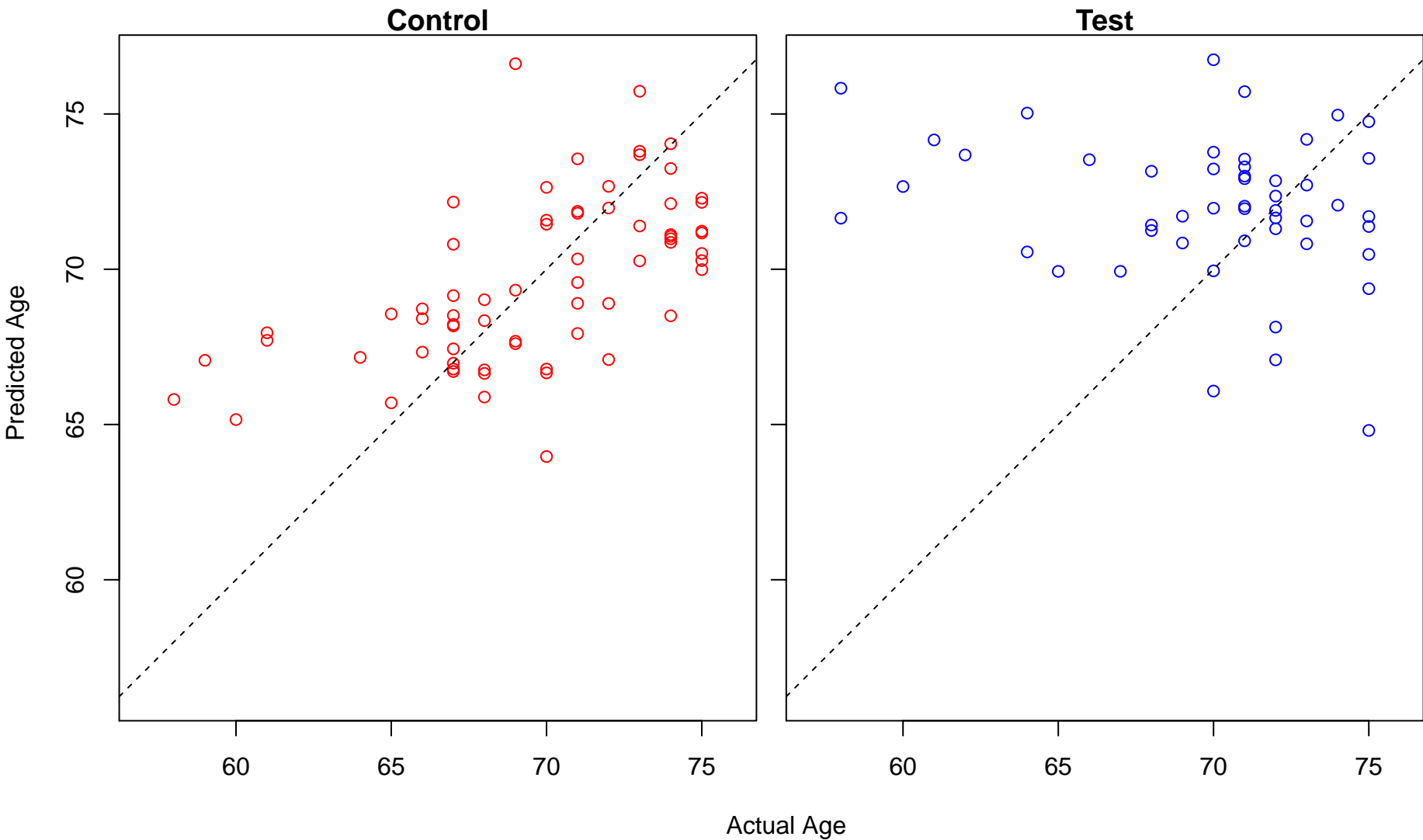


Test

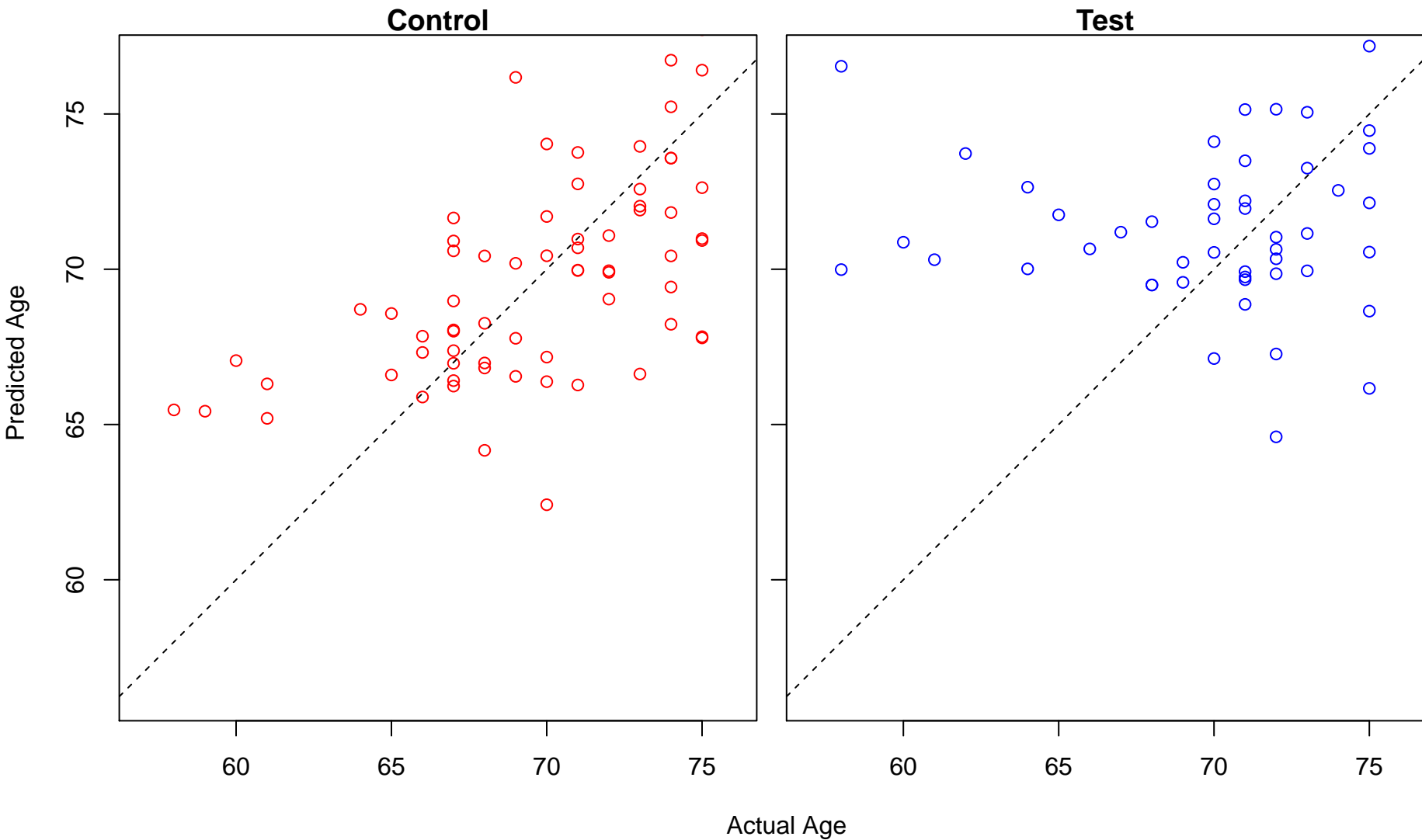


Actual Age

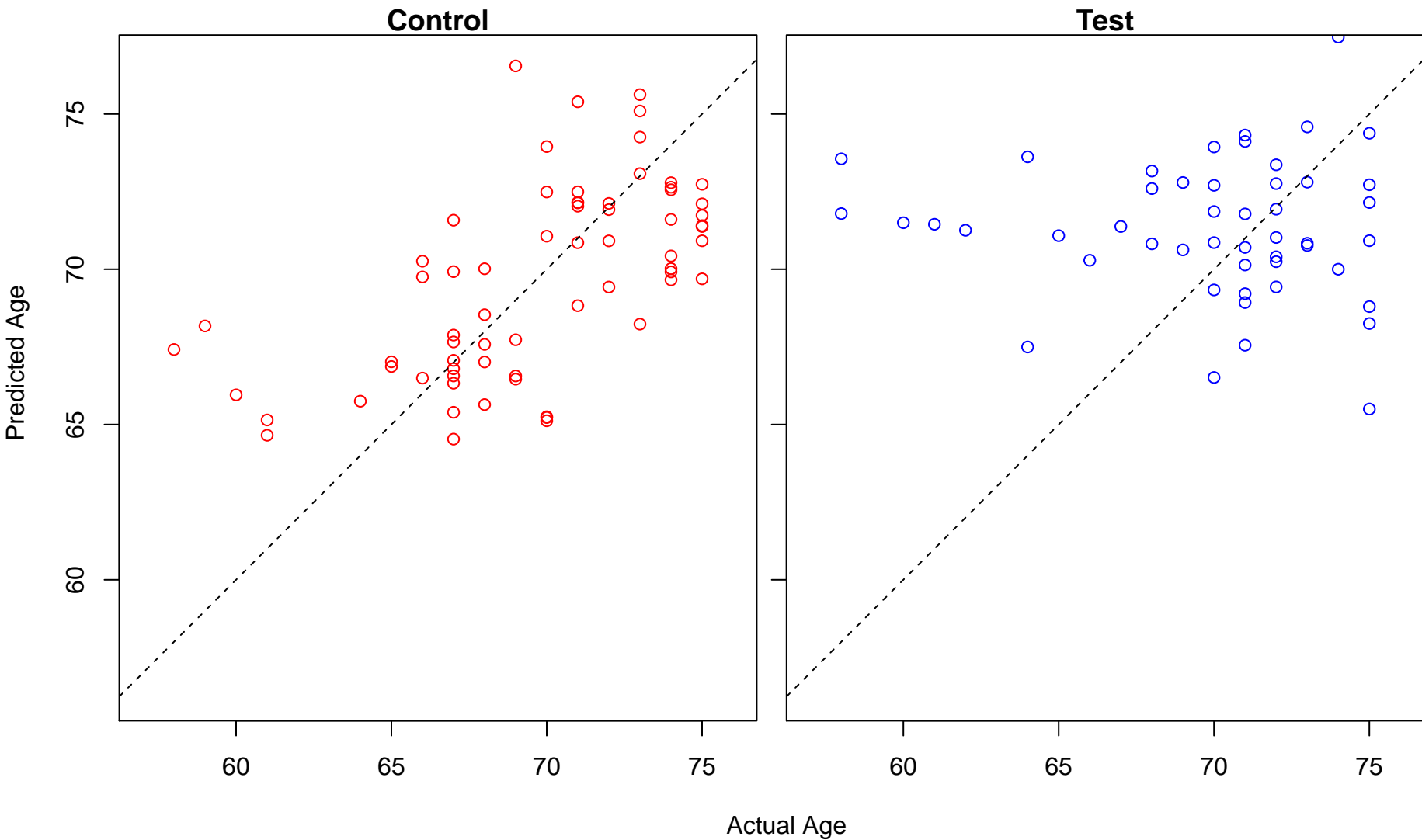
pH reduction (Score: 1.140342)



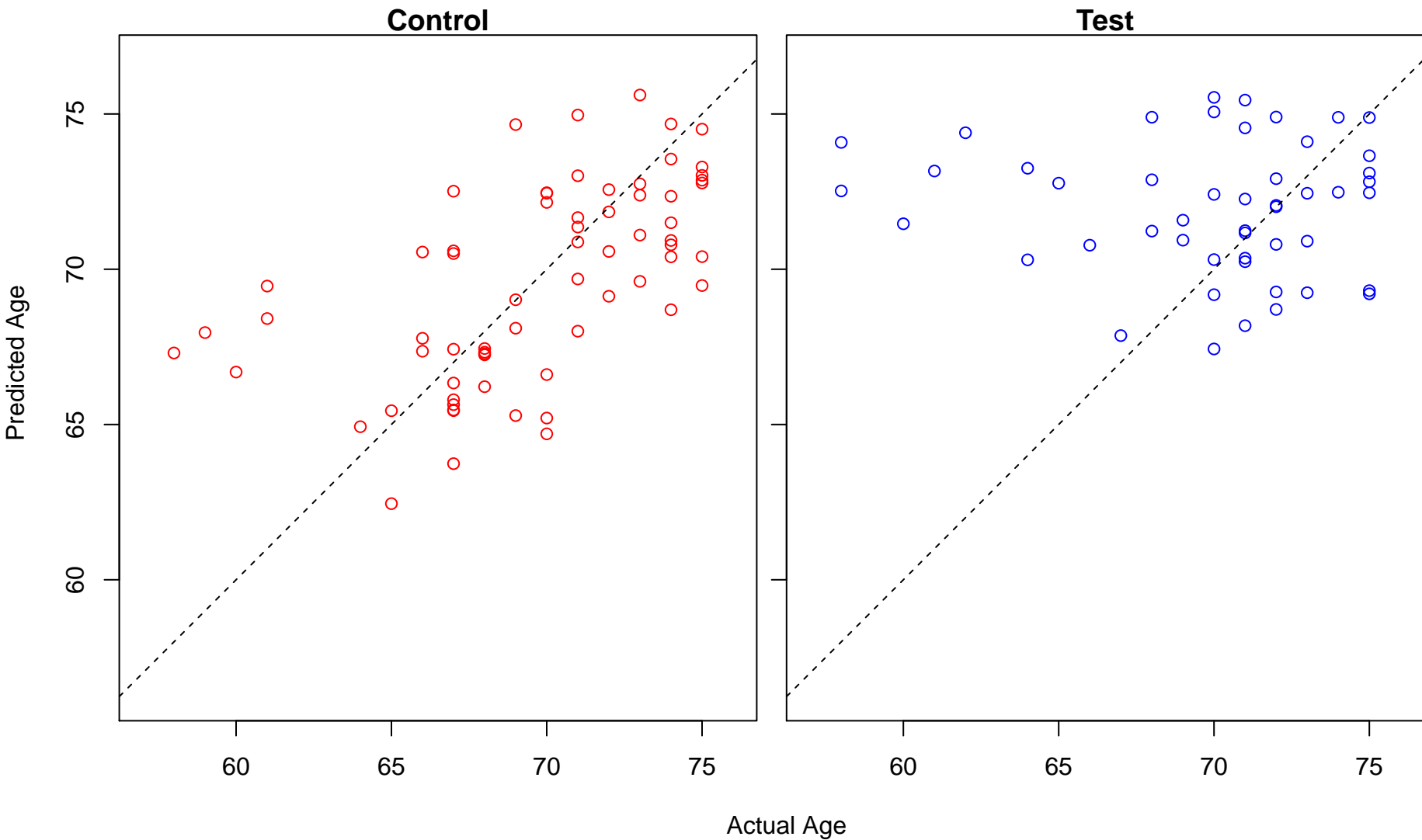
negative regulation of cation transmembrane transport (Score: 1.140293)



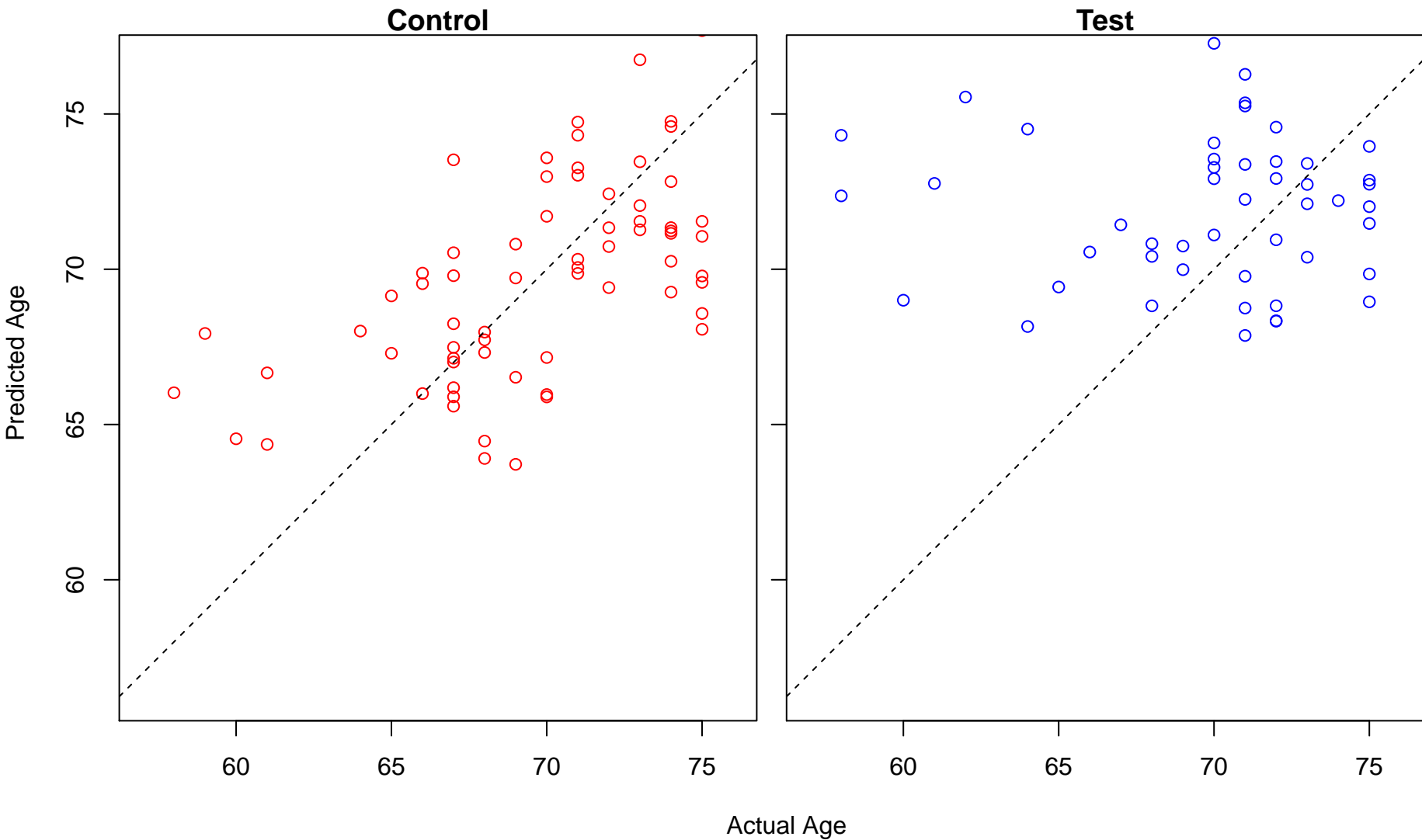
gene silencing by RNA (Score: 1.140243)



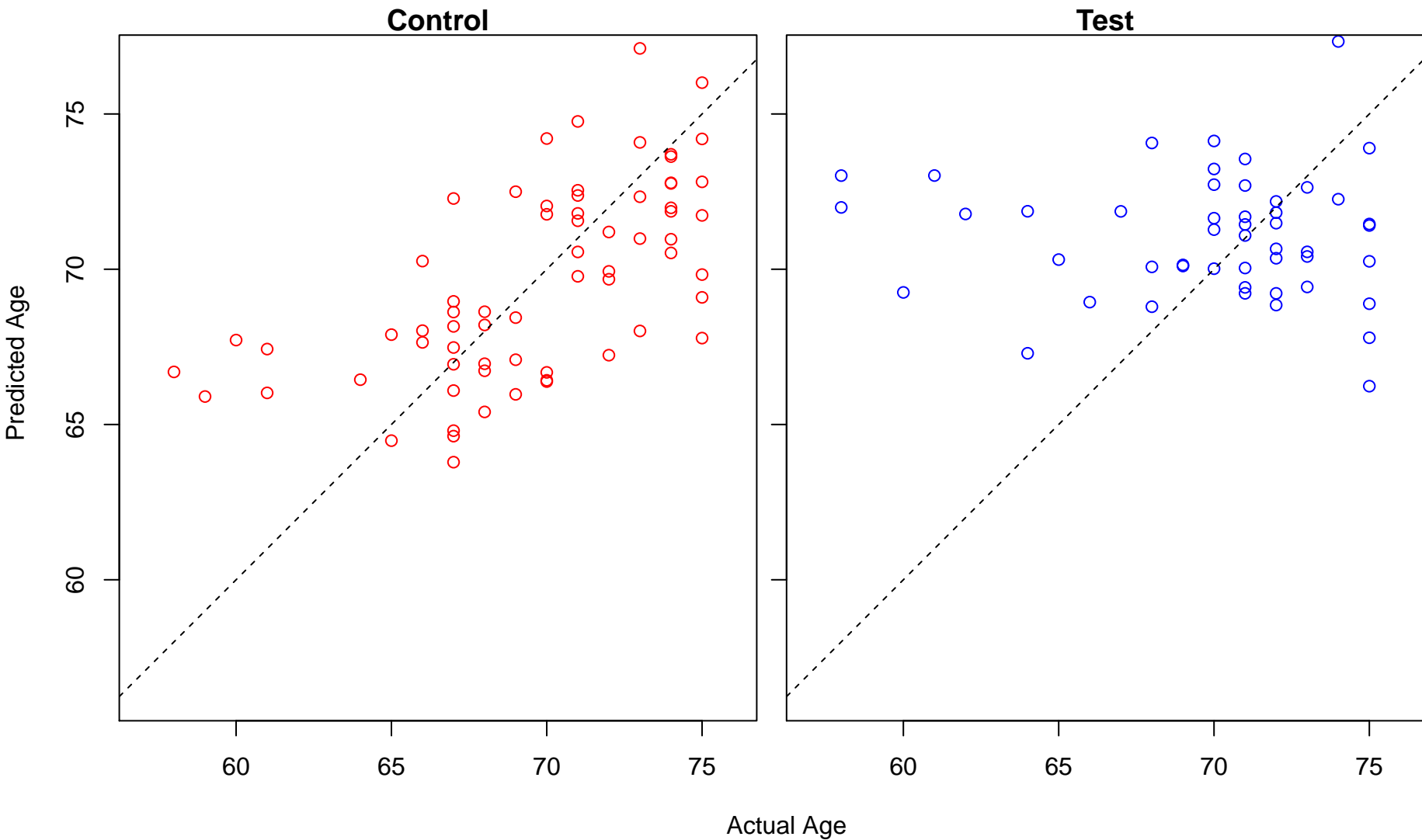
positive regulation of JNK cascade (Score: 1.140131)



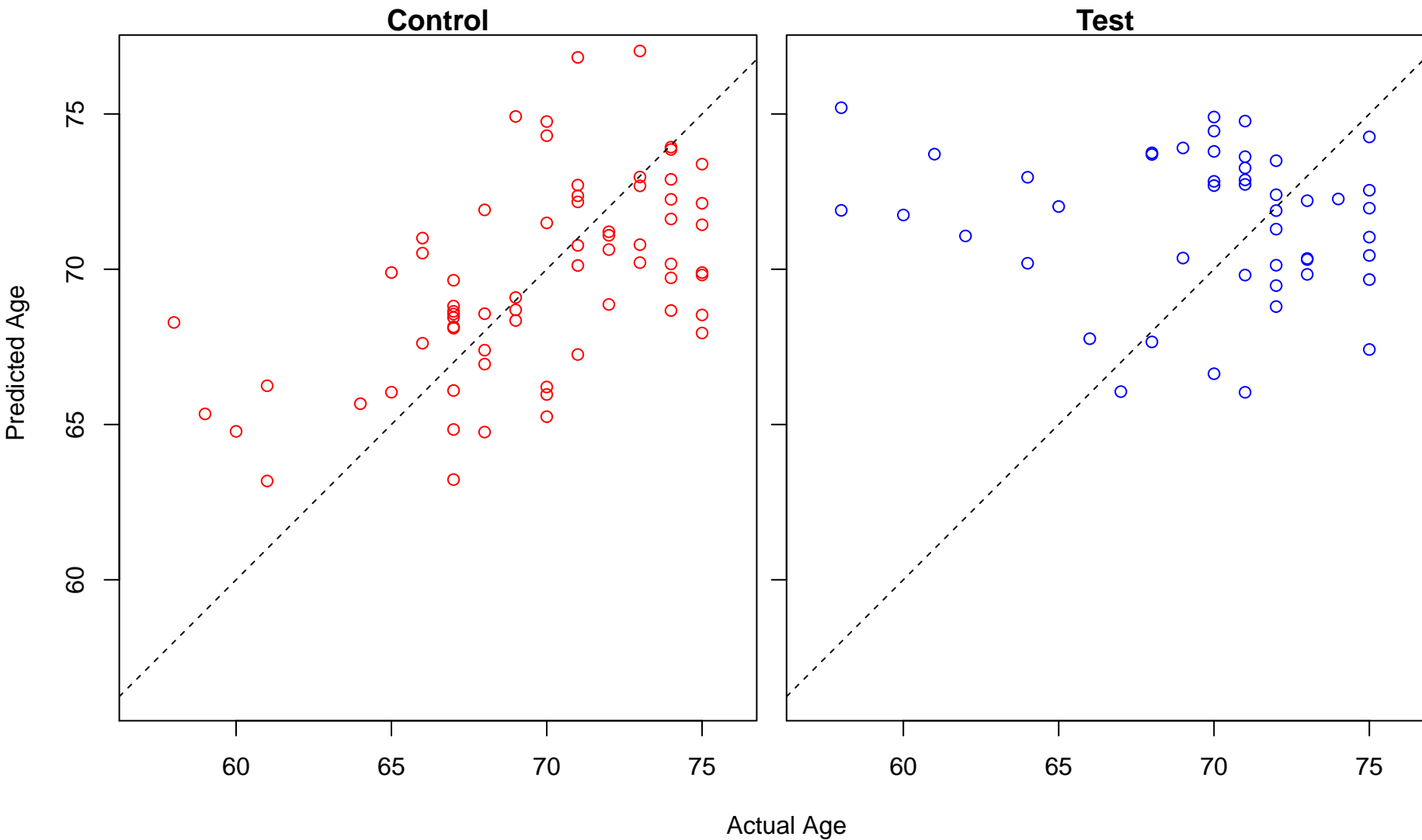
ammonium transport (Score: 1.139980)



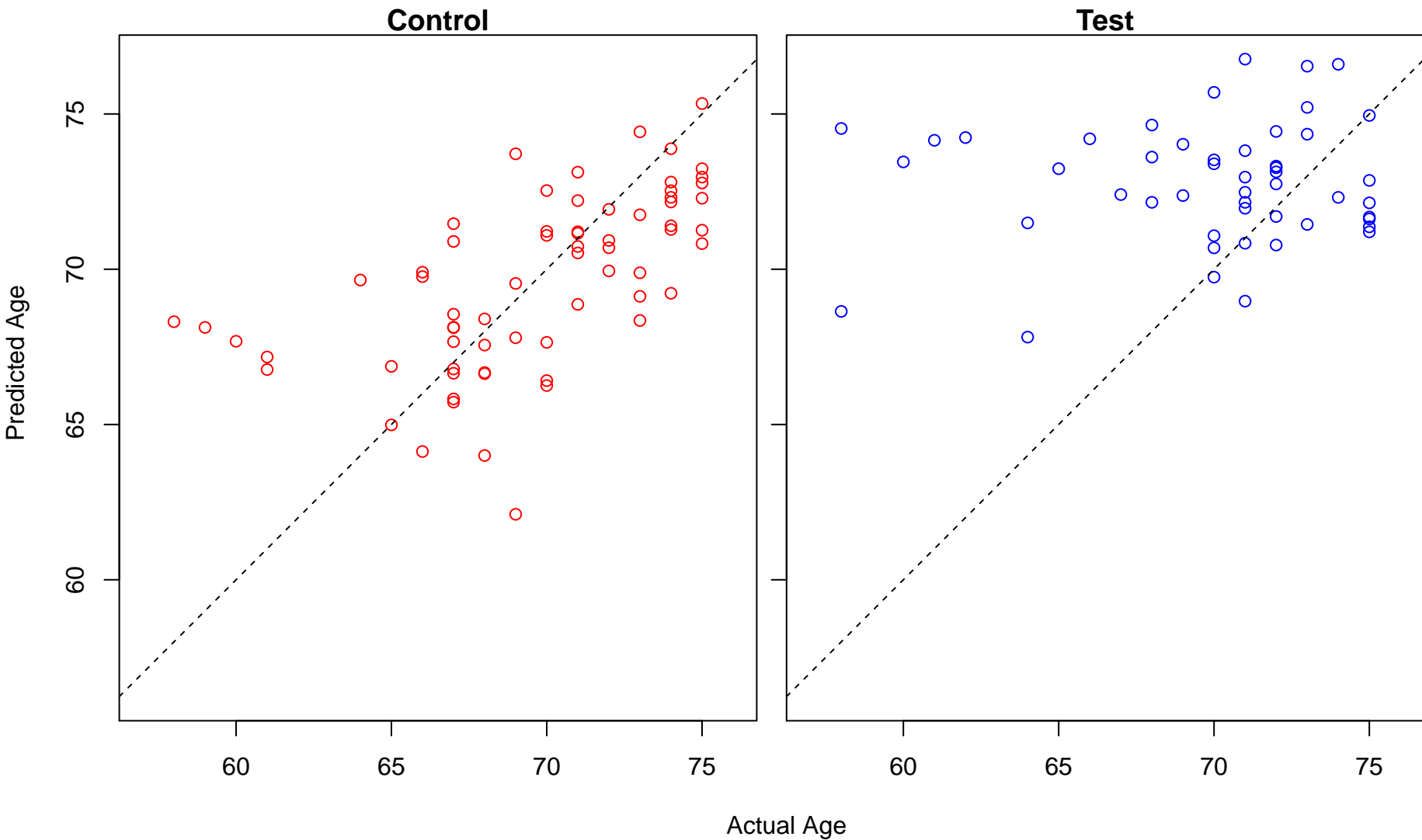
regulation of intrinsic apoptotic signaling pathway in response to DNA damage (Score: 1.139916)



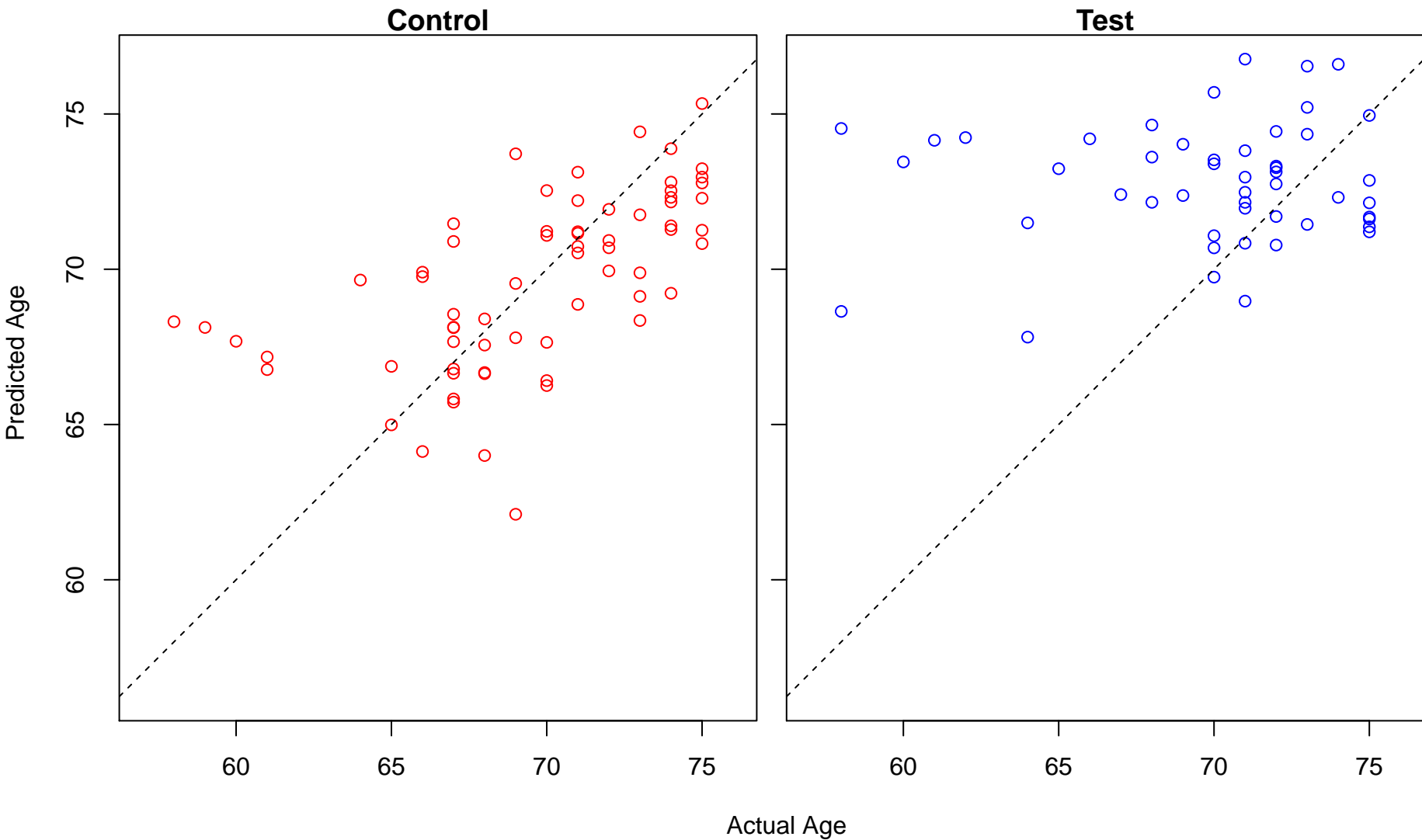
leukocyte proliferation (Score: 1.139661)



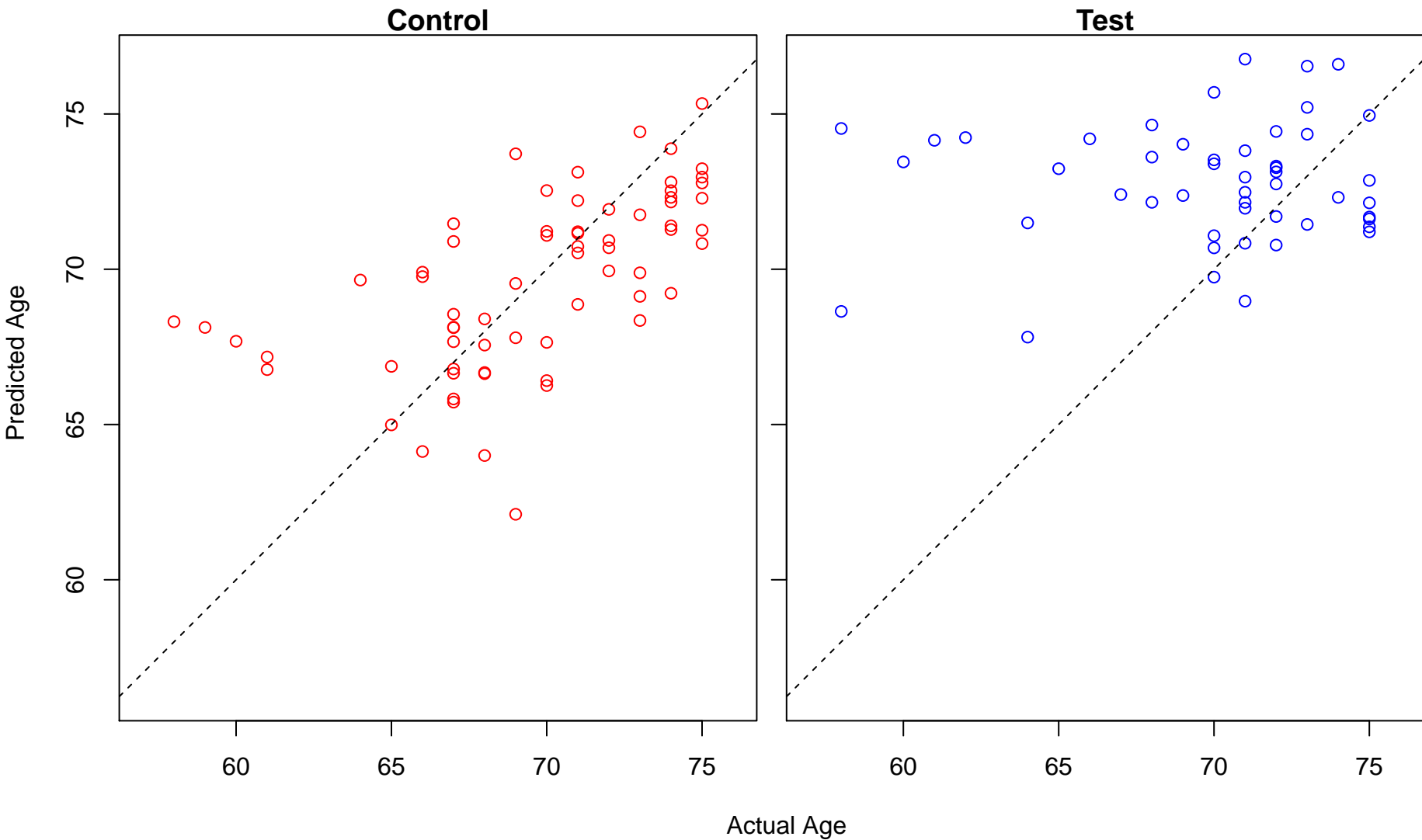
response to superoxide (Score: 1.139492)



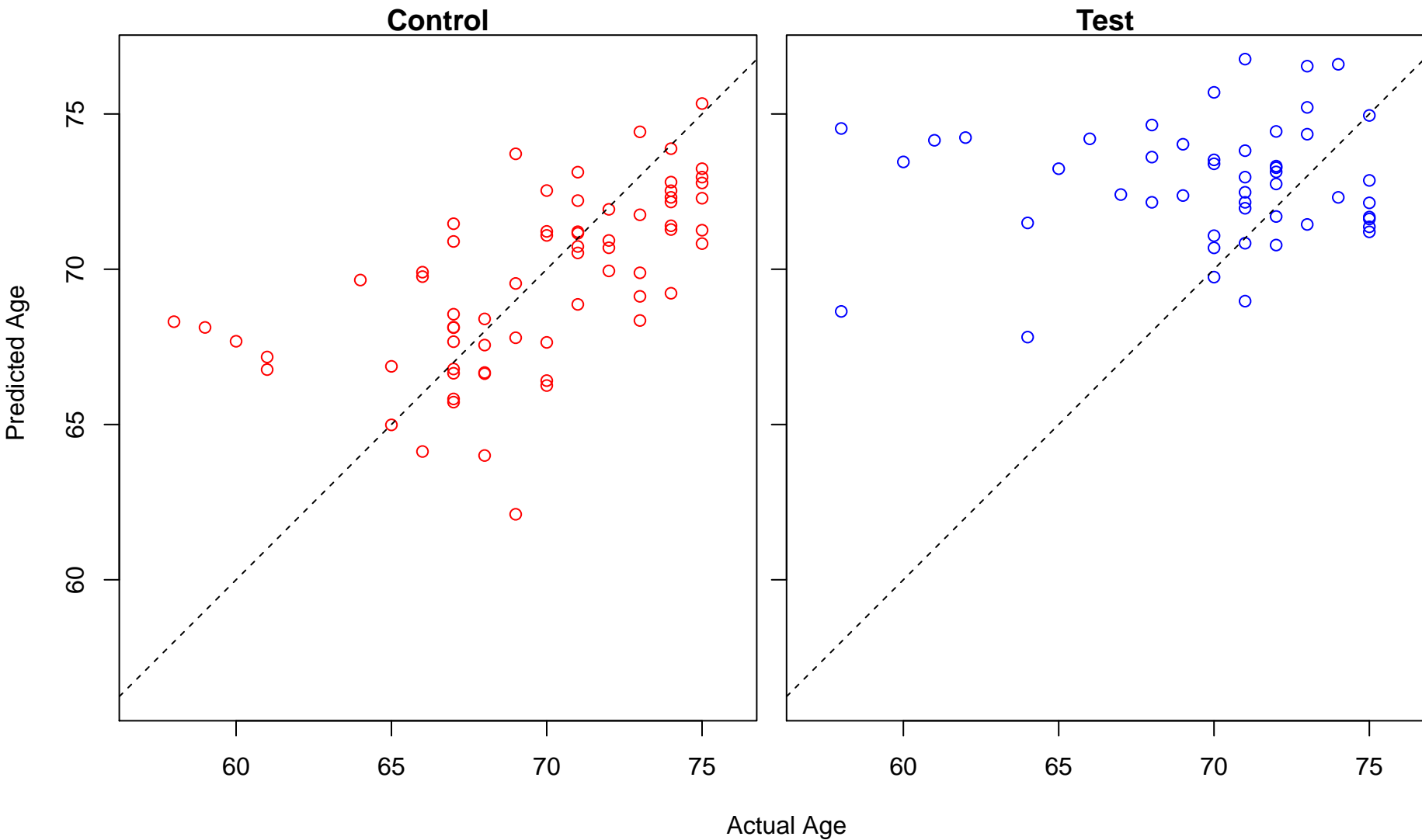
removal of superoxide radicals (Score: 1.139492)



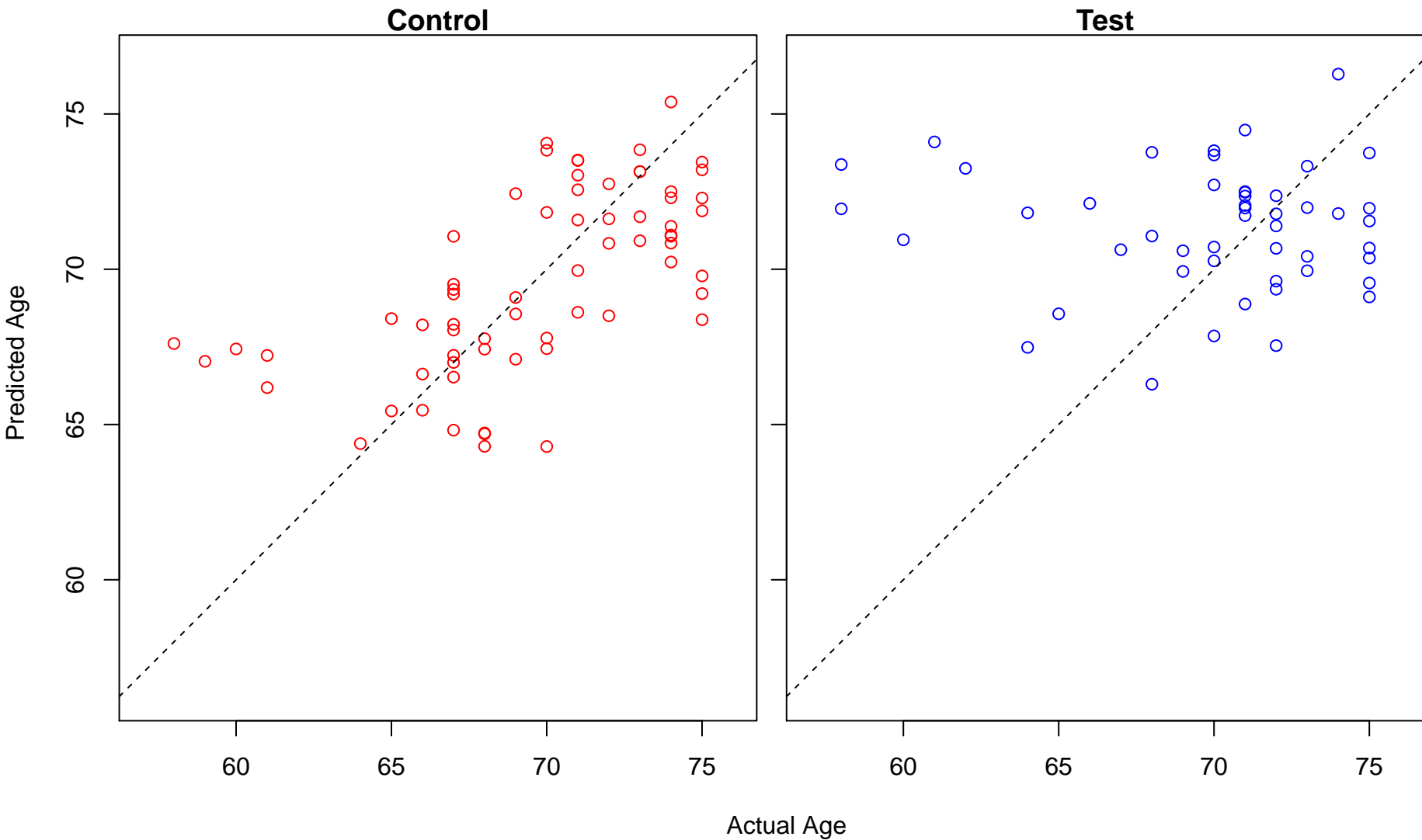
cellular response to oxygen radical (Score: 1.139492)



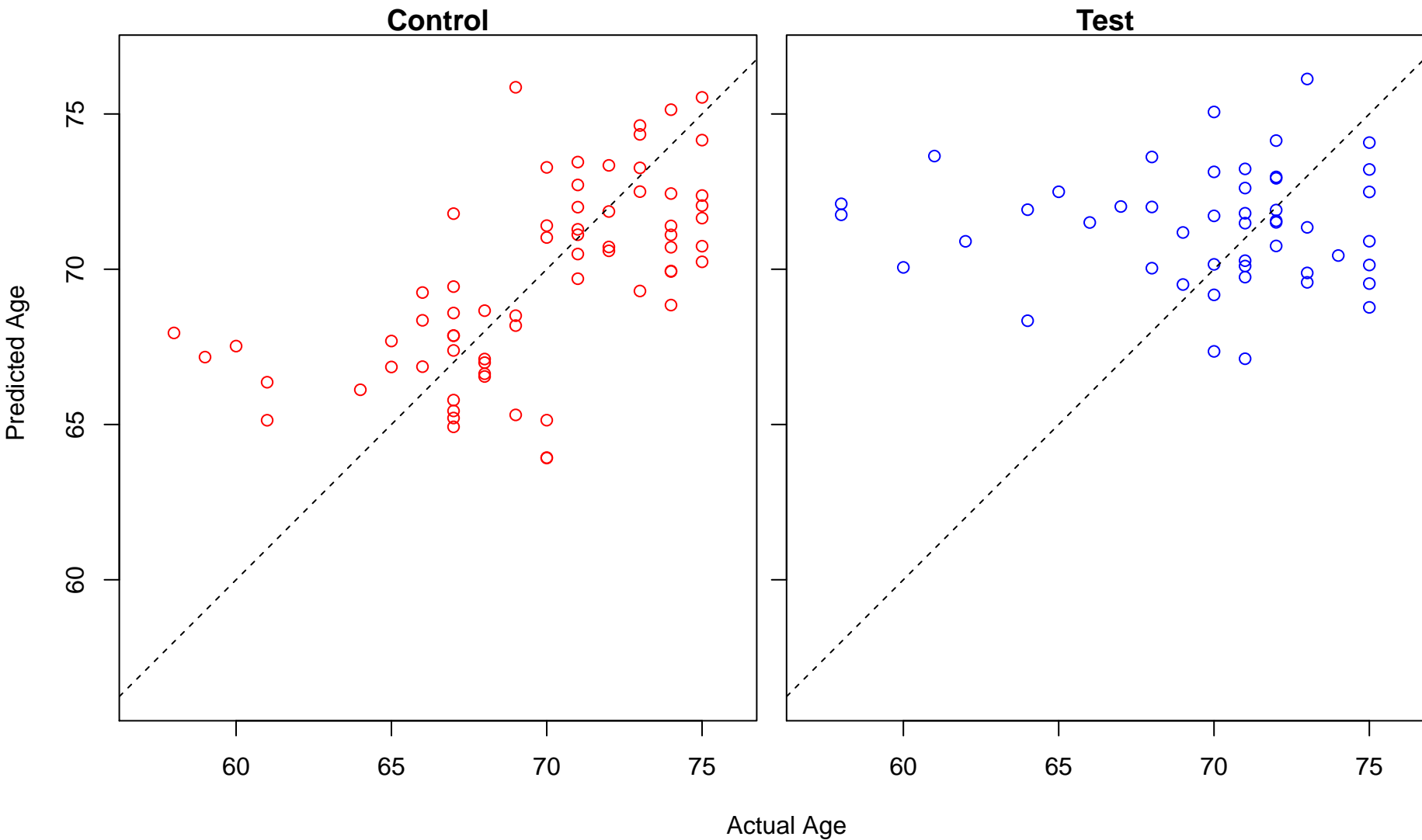
cellular response to superoxide (Score: 1.139492)



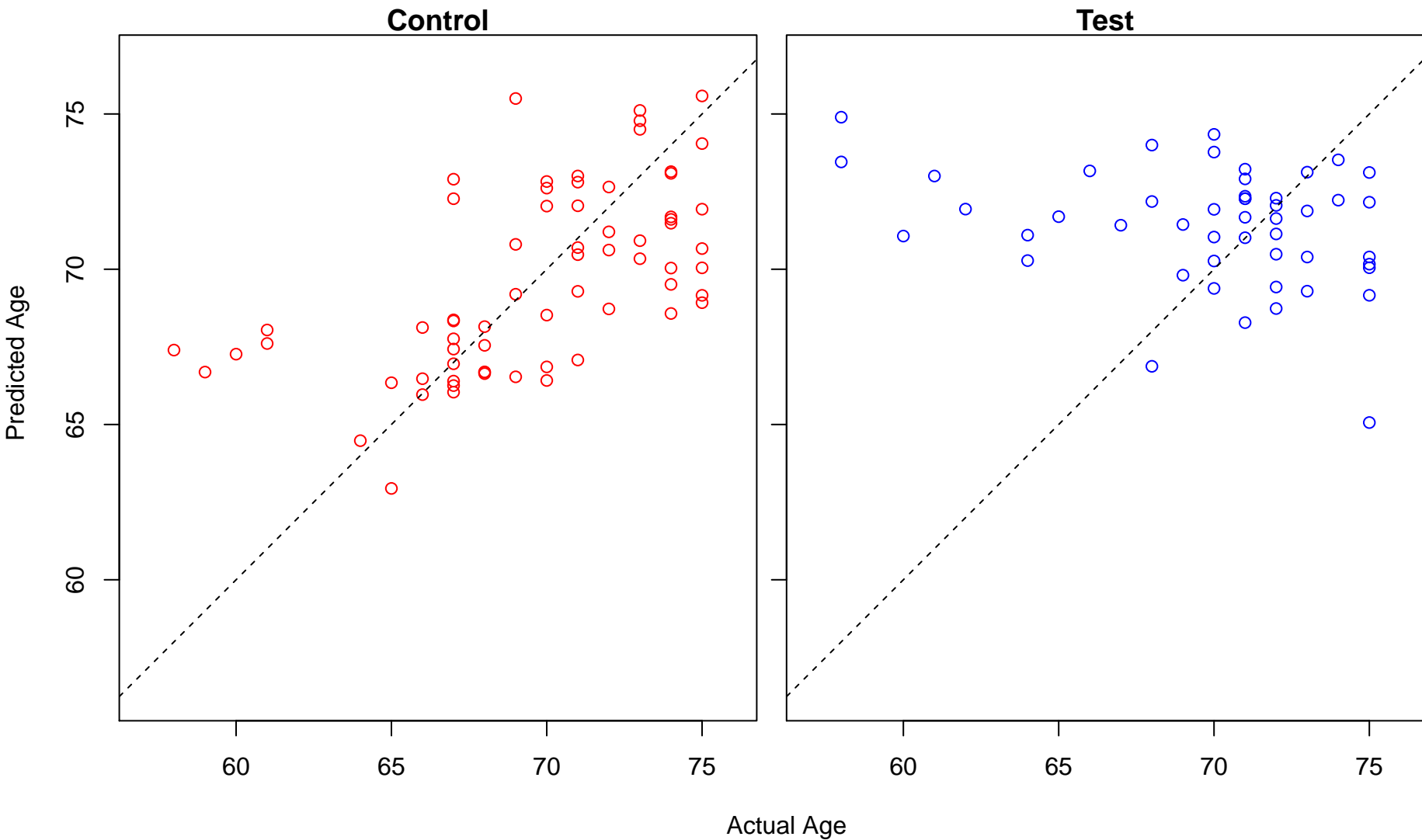
muscle cell differentiation (Score: 1.138102)



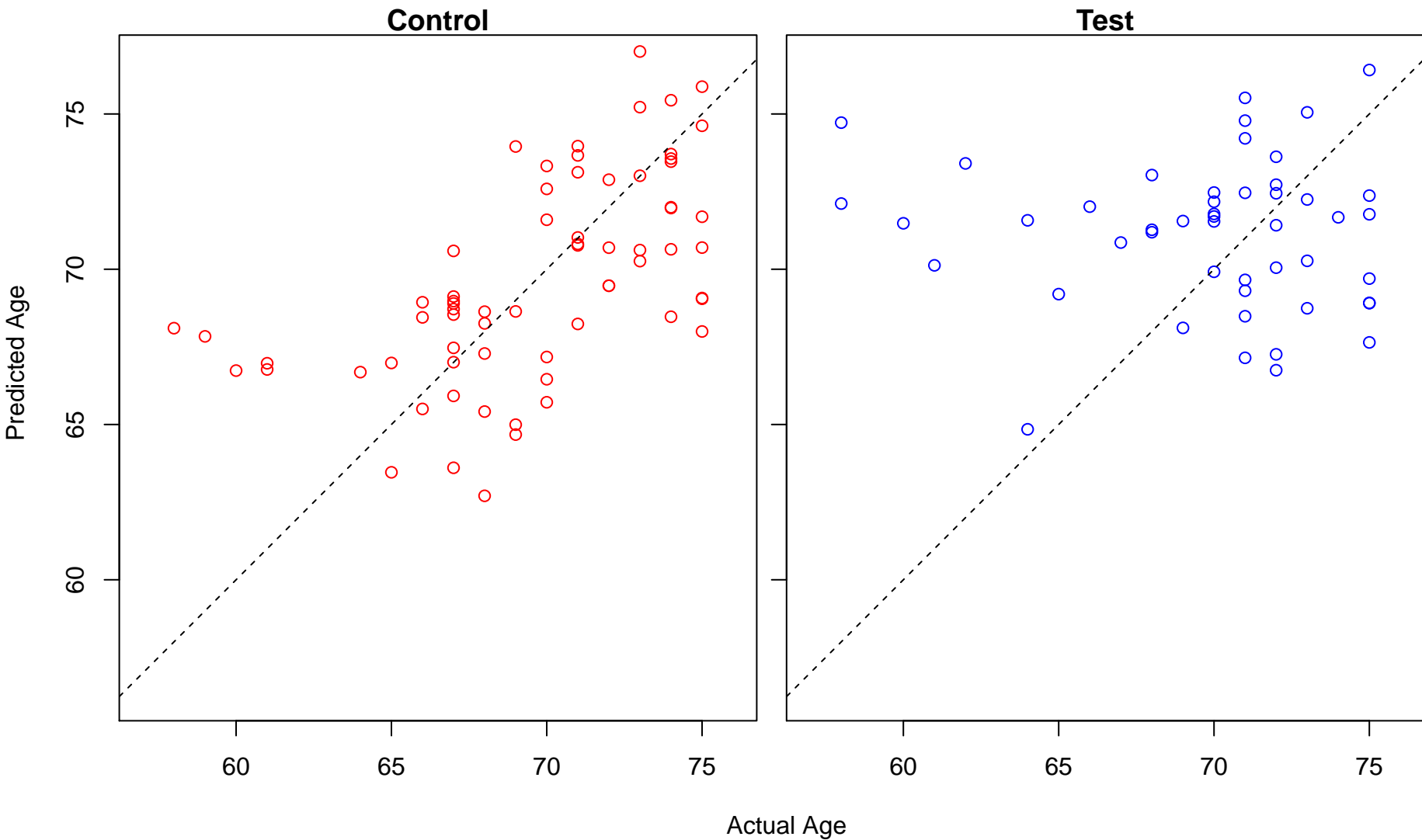
regulation of phosphoprotein phosphatase activity (Score: 1.137997)



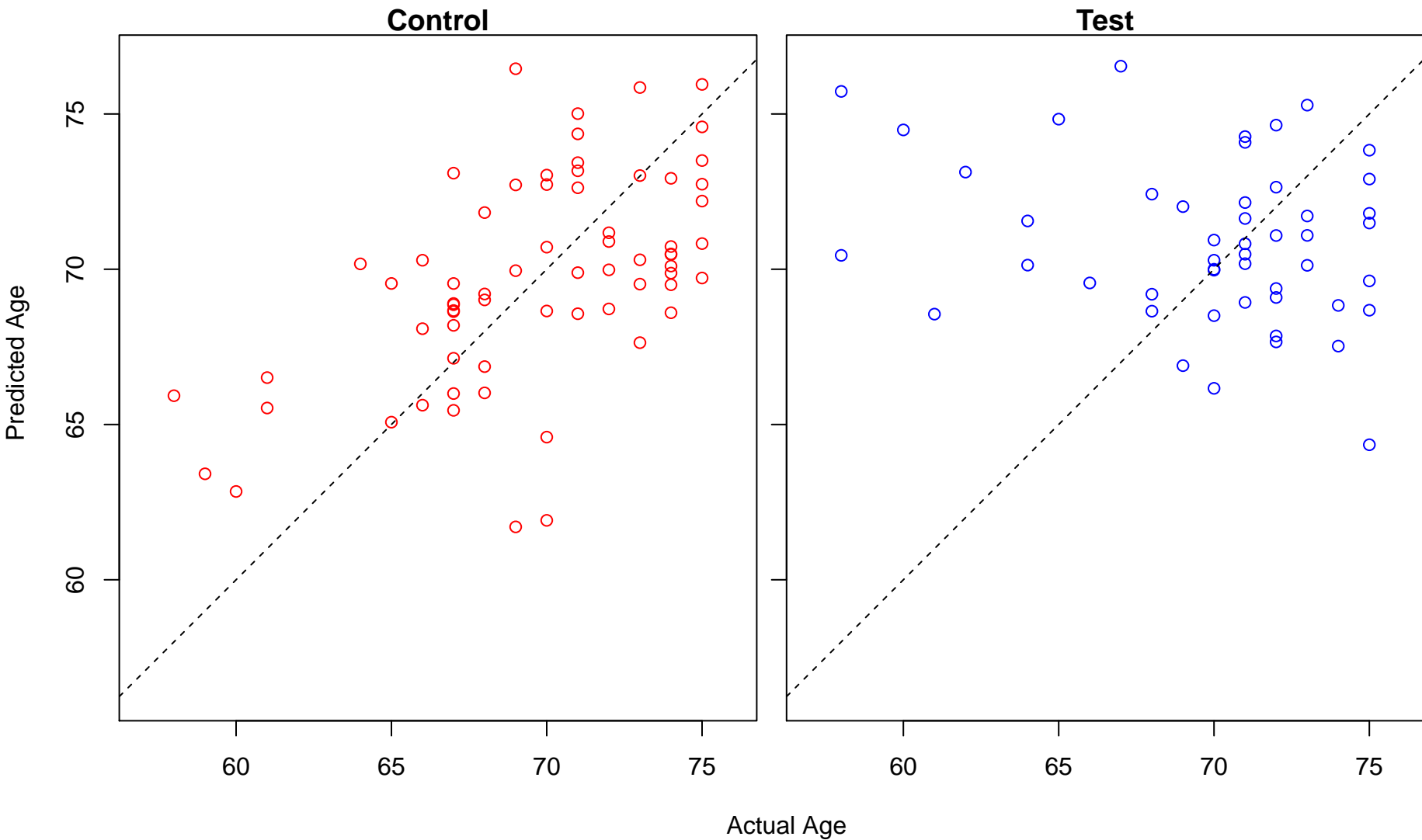
positive regulation of actin filament bundle assembly (Score: 1.137890)



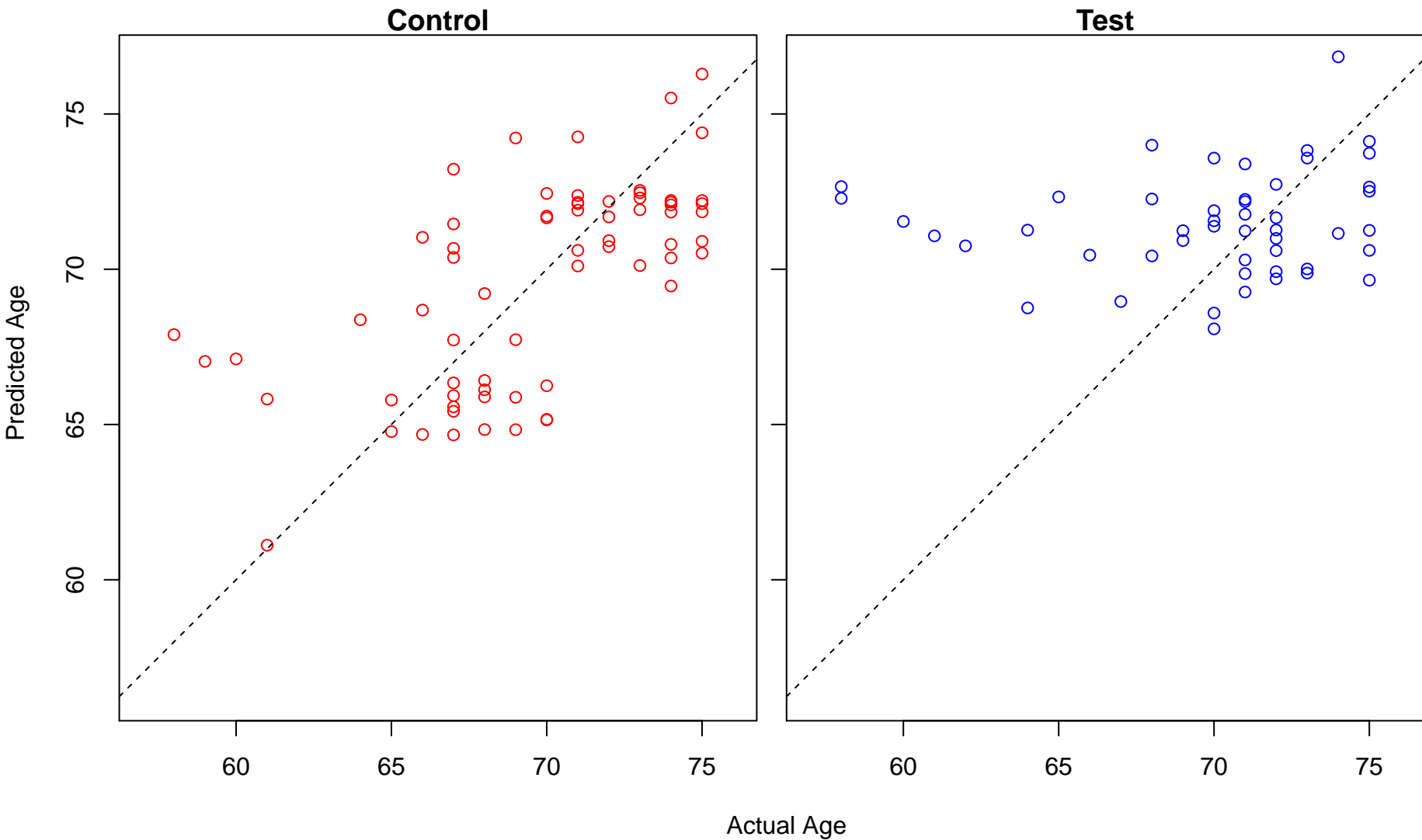
positive regulation of cell morphogenesis involved in differentiation (Score: 1.137514)



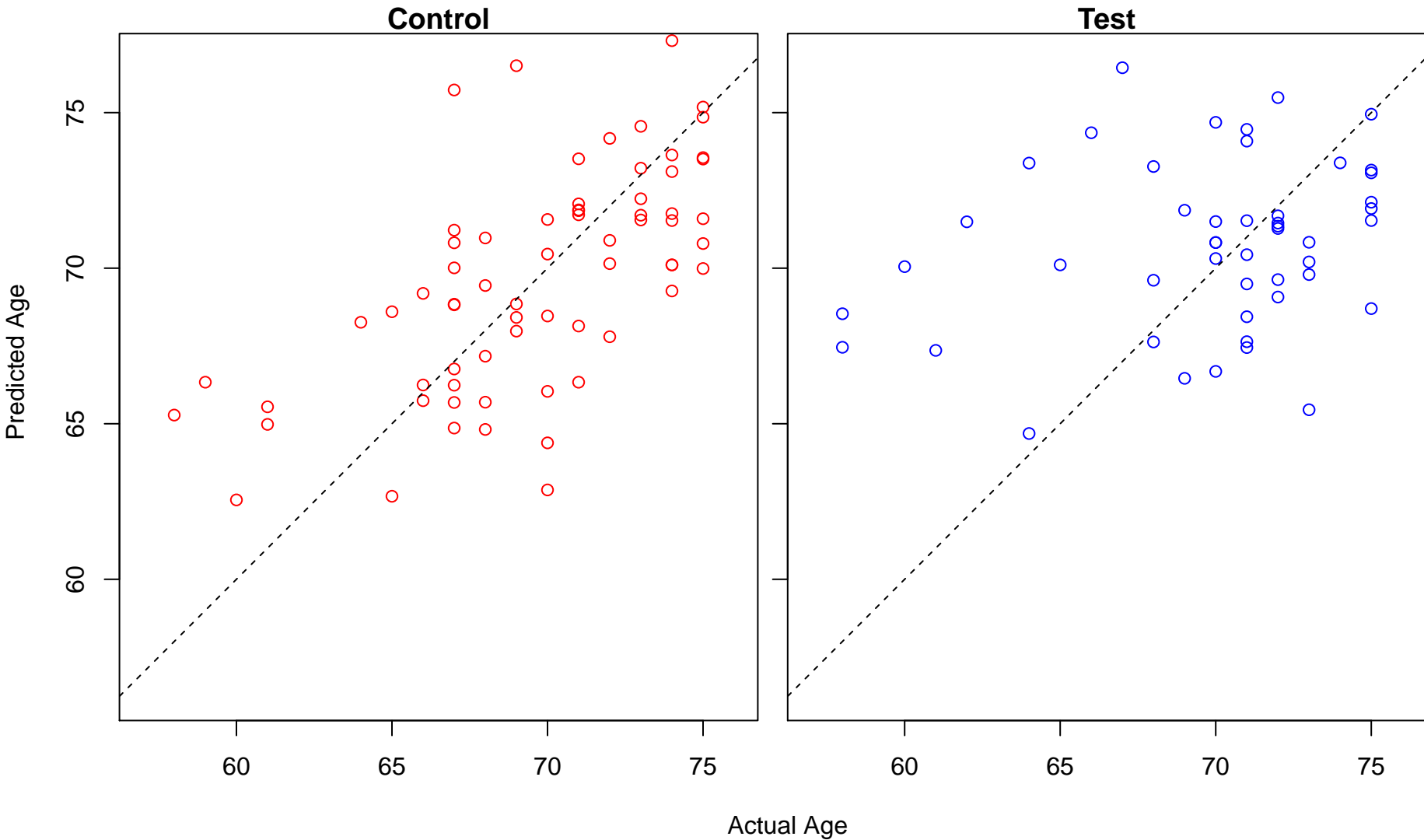
regulation of energy homeostasis (Score: 1.137082)



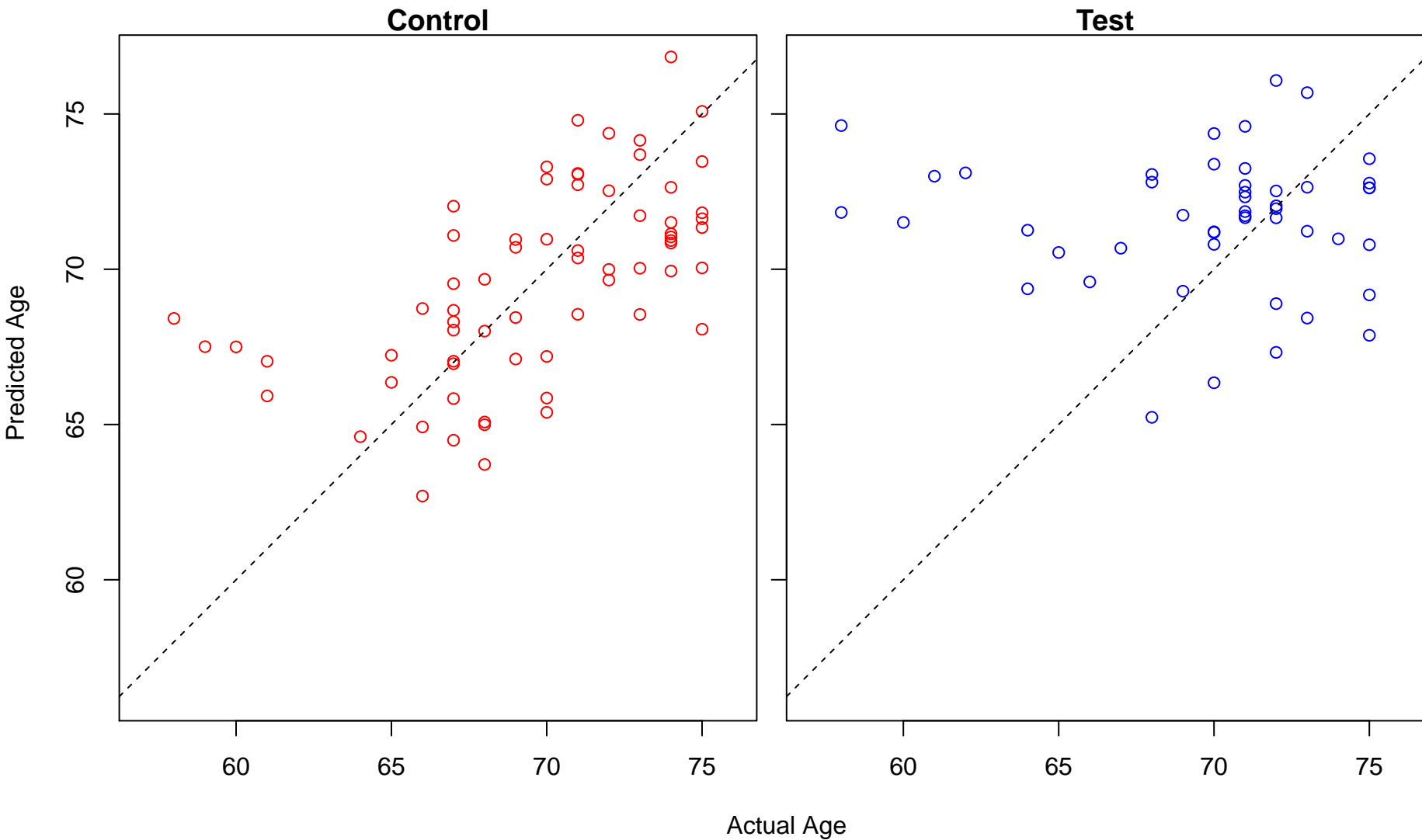
cytokinesis (Score: 1.137041)



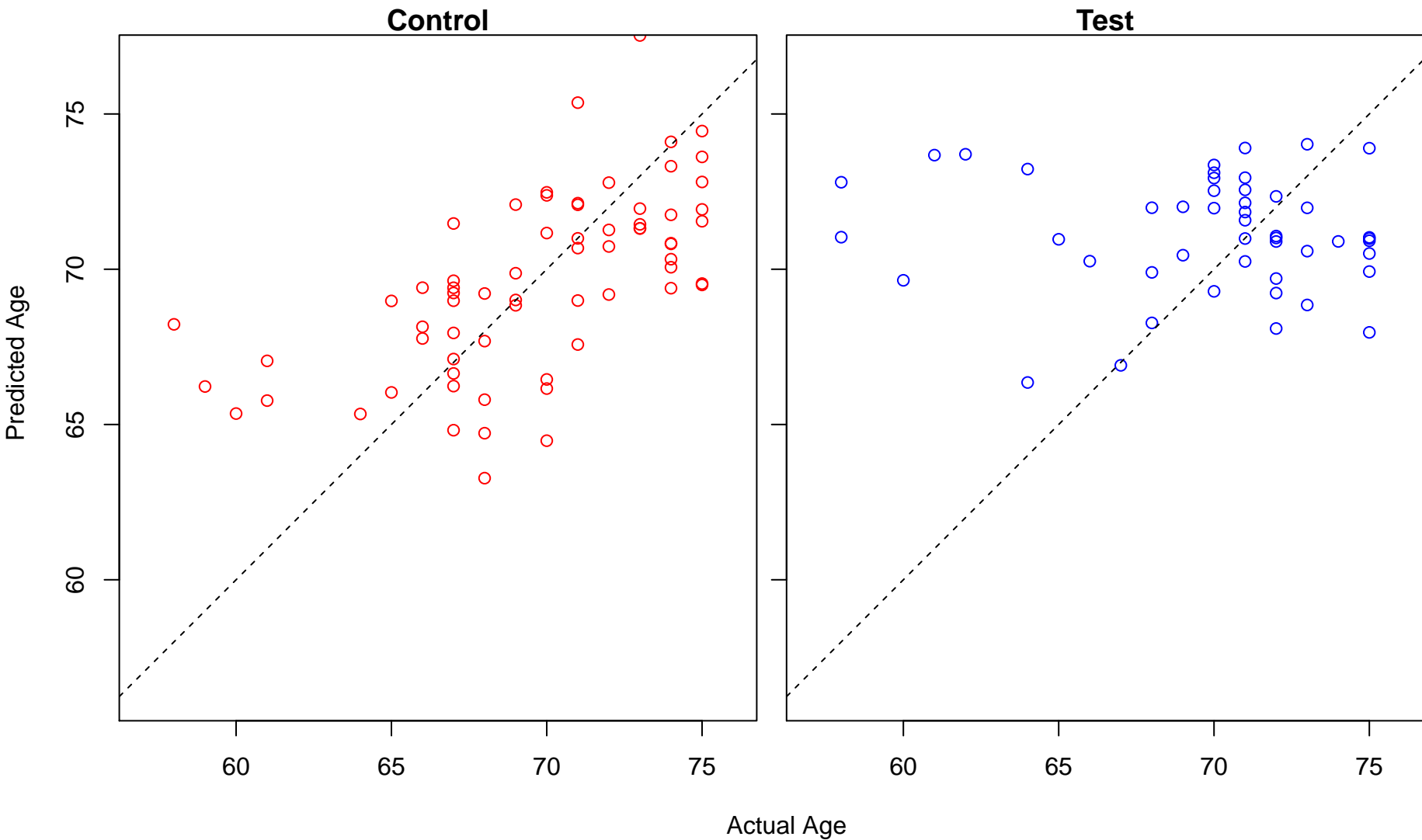
regulation of biomineral tissue development (Score: 1.136437)



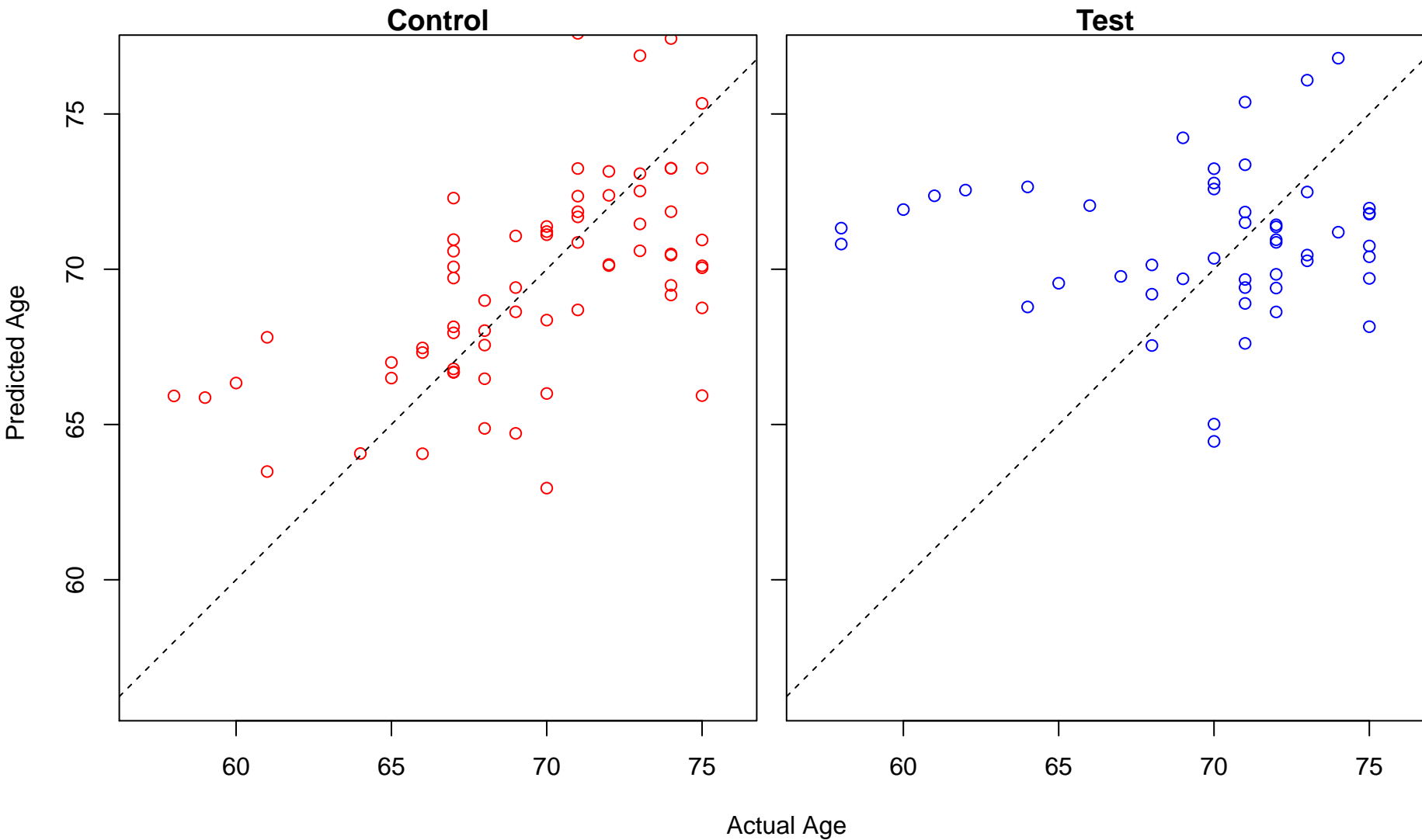
negative regulation of extrinsic apoptotic signaling pathway via death domain receptors (Score: 1.136)



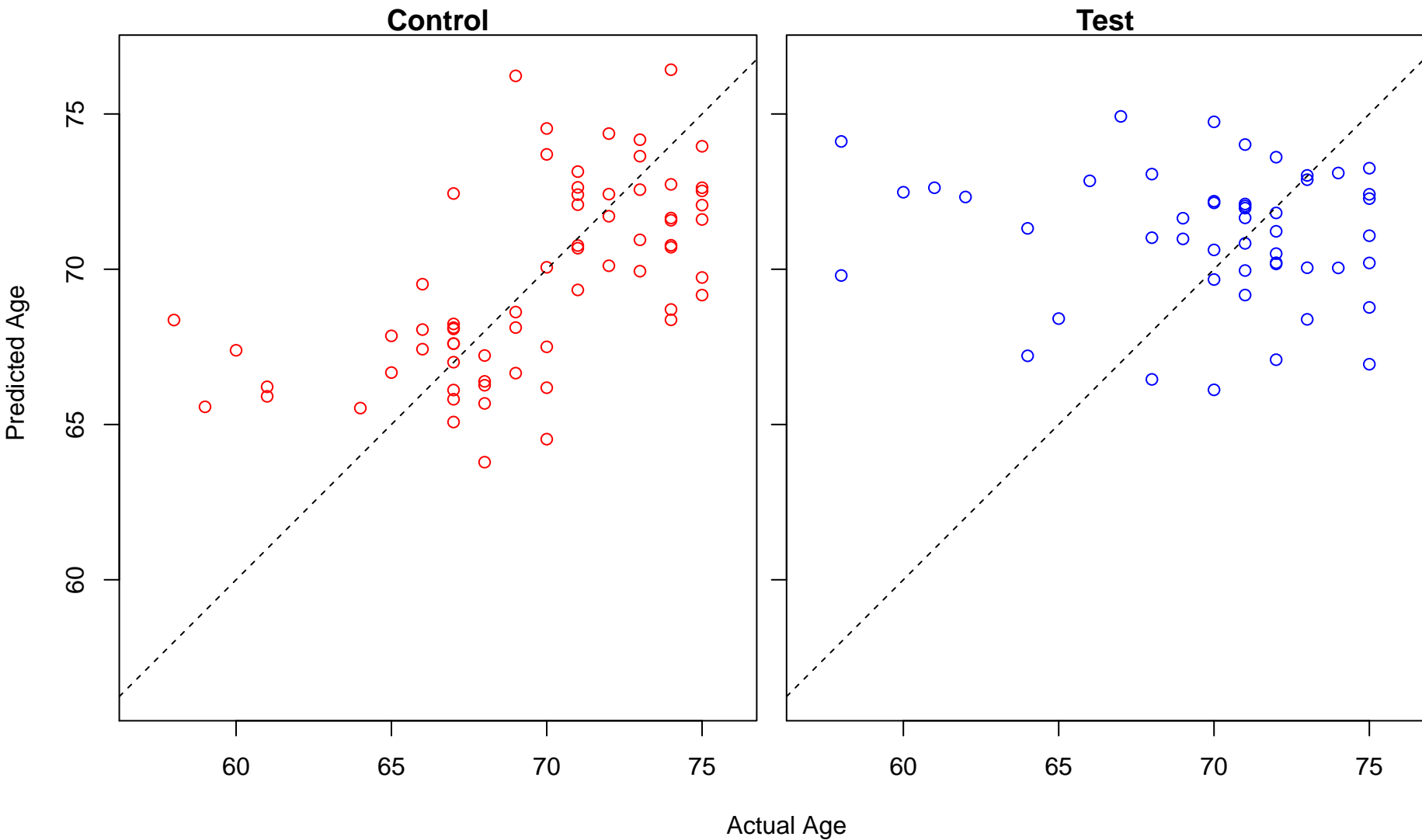
nucleotide phosphorylation (Score: 1.135104)



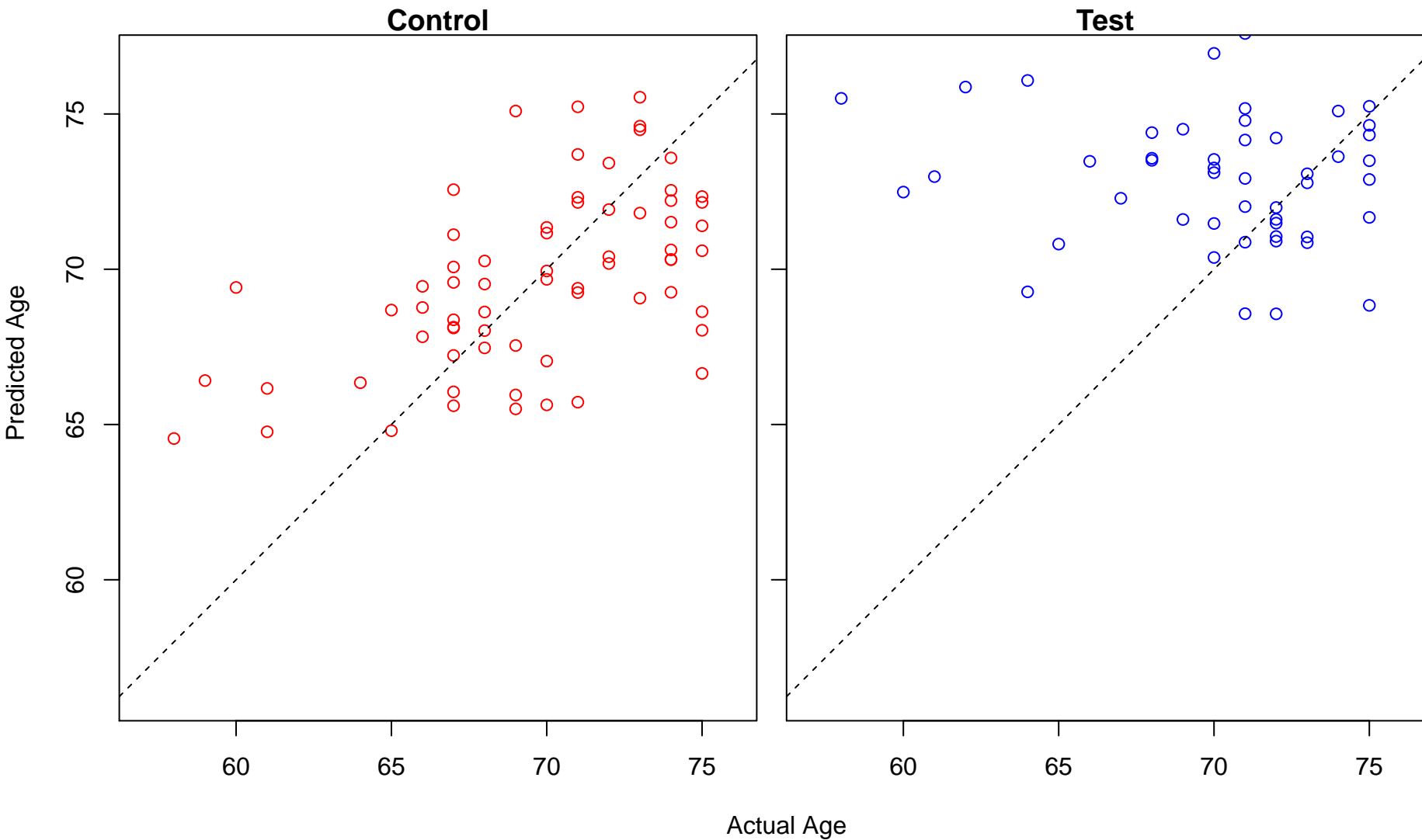
positive regulation of organelle assembly (Score: 1.132979)



regulation of cell aging (Score: 1.132821)

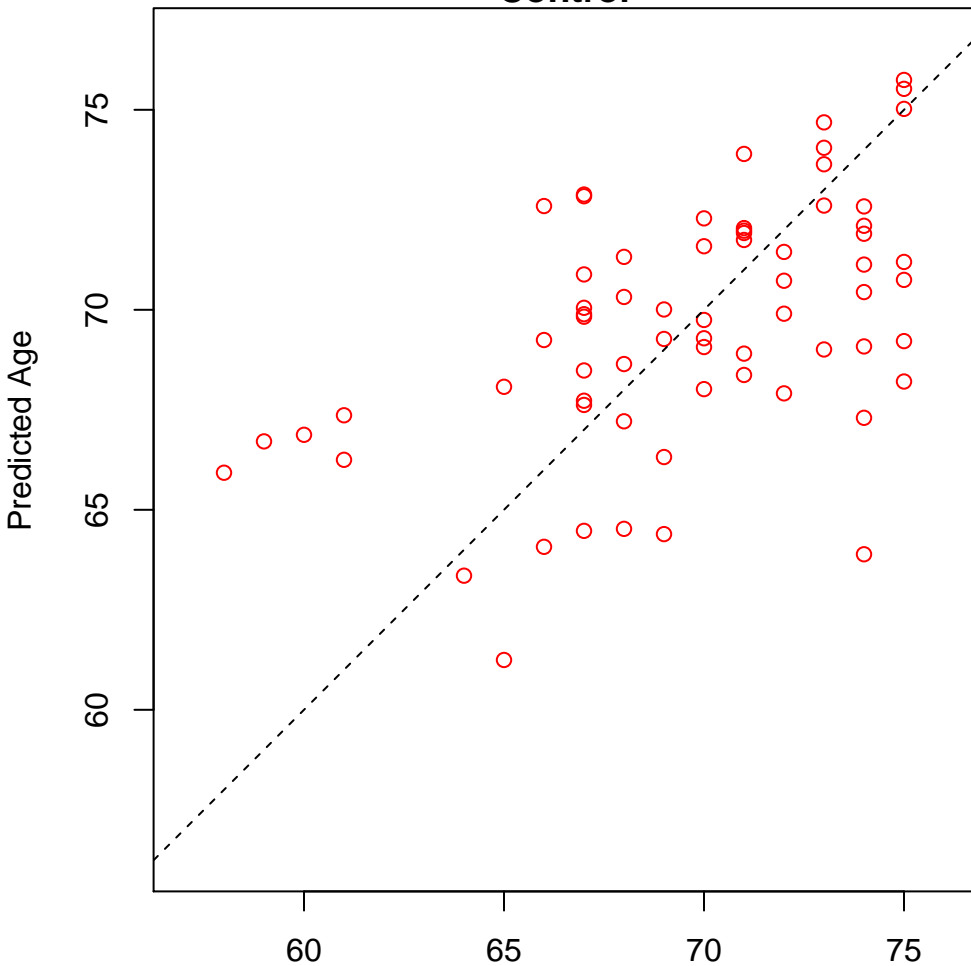


snRNA transcription (Score: 1.132124)

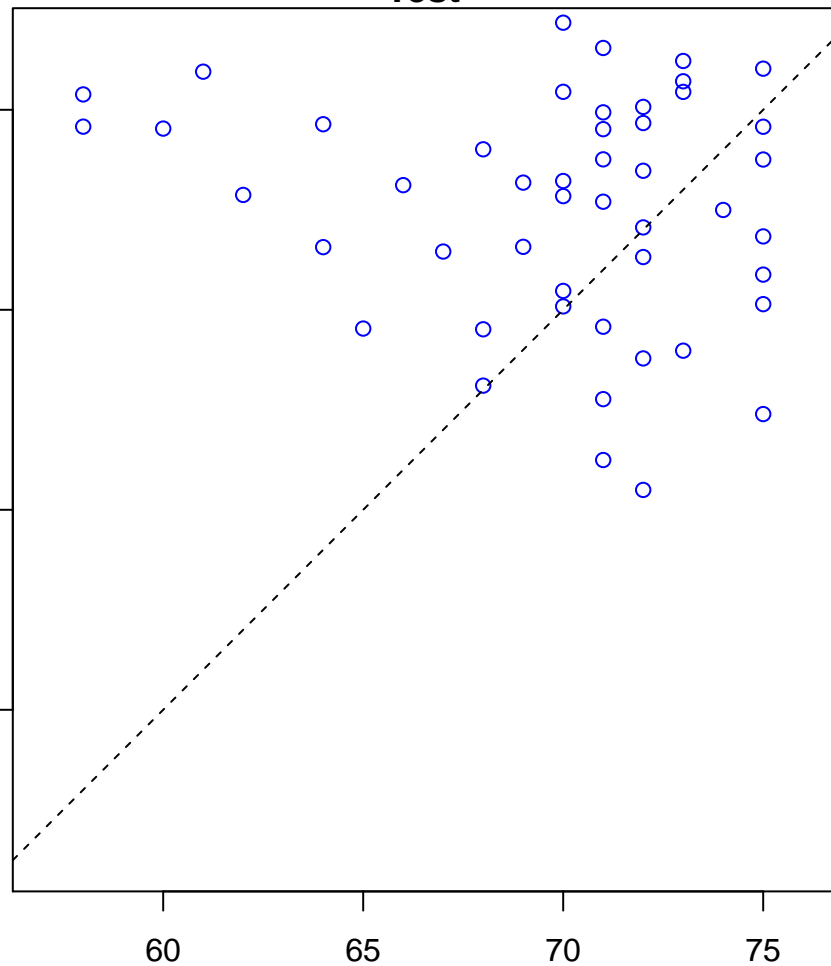


regulation of sulfur metabolic process (Score: 1.131852)

Control

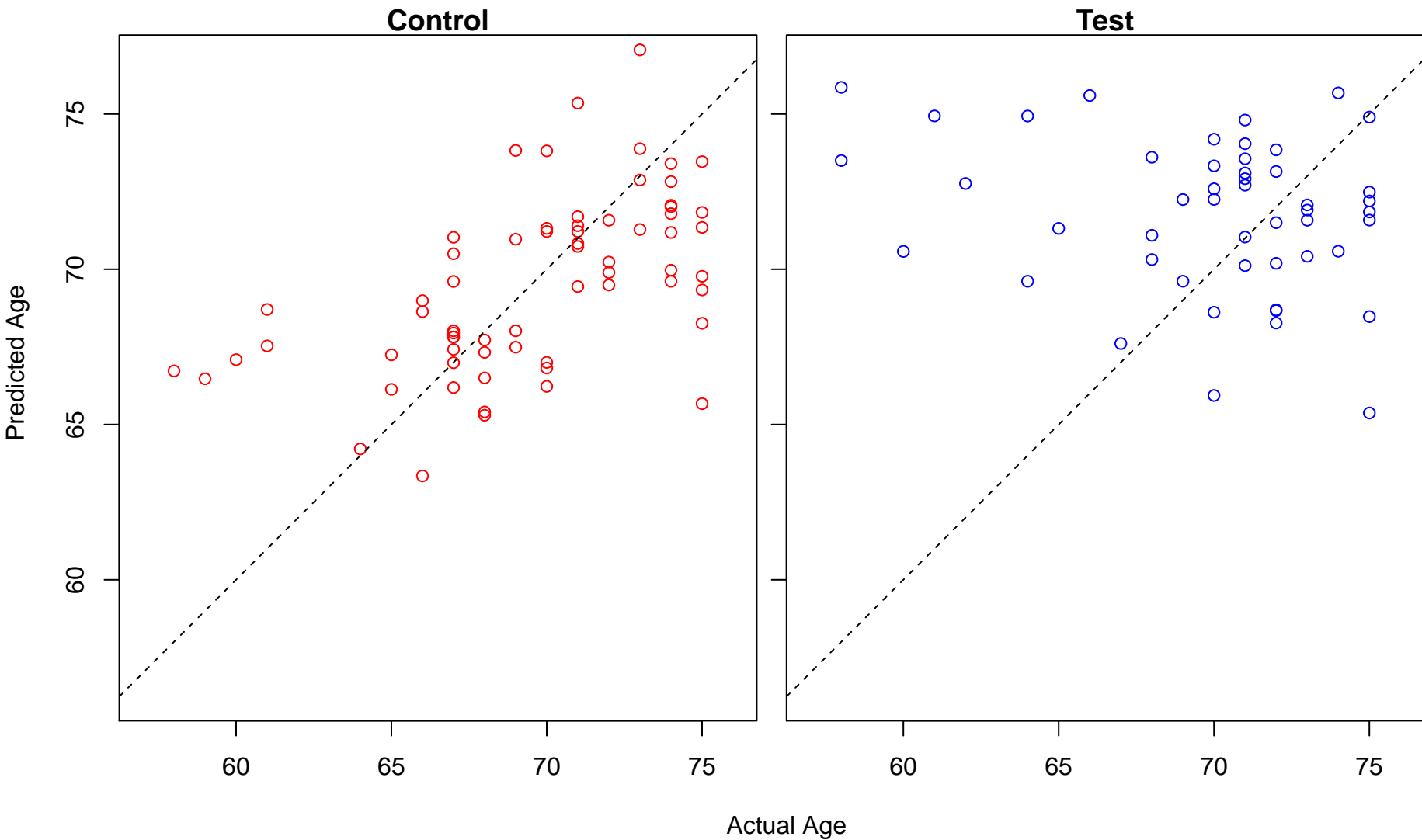


Test

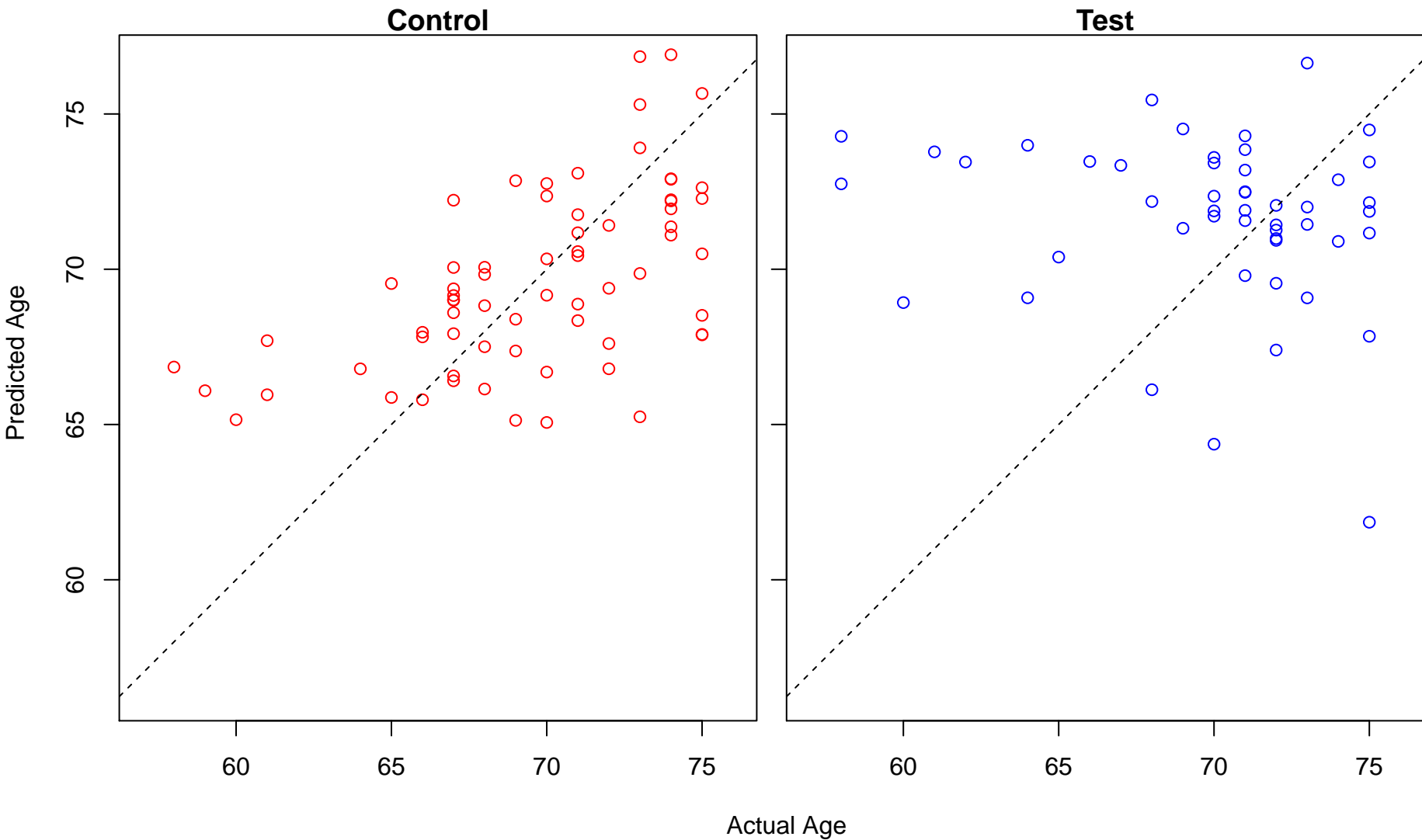


Actual Age

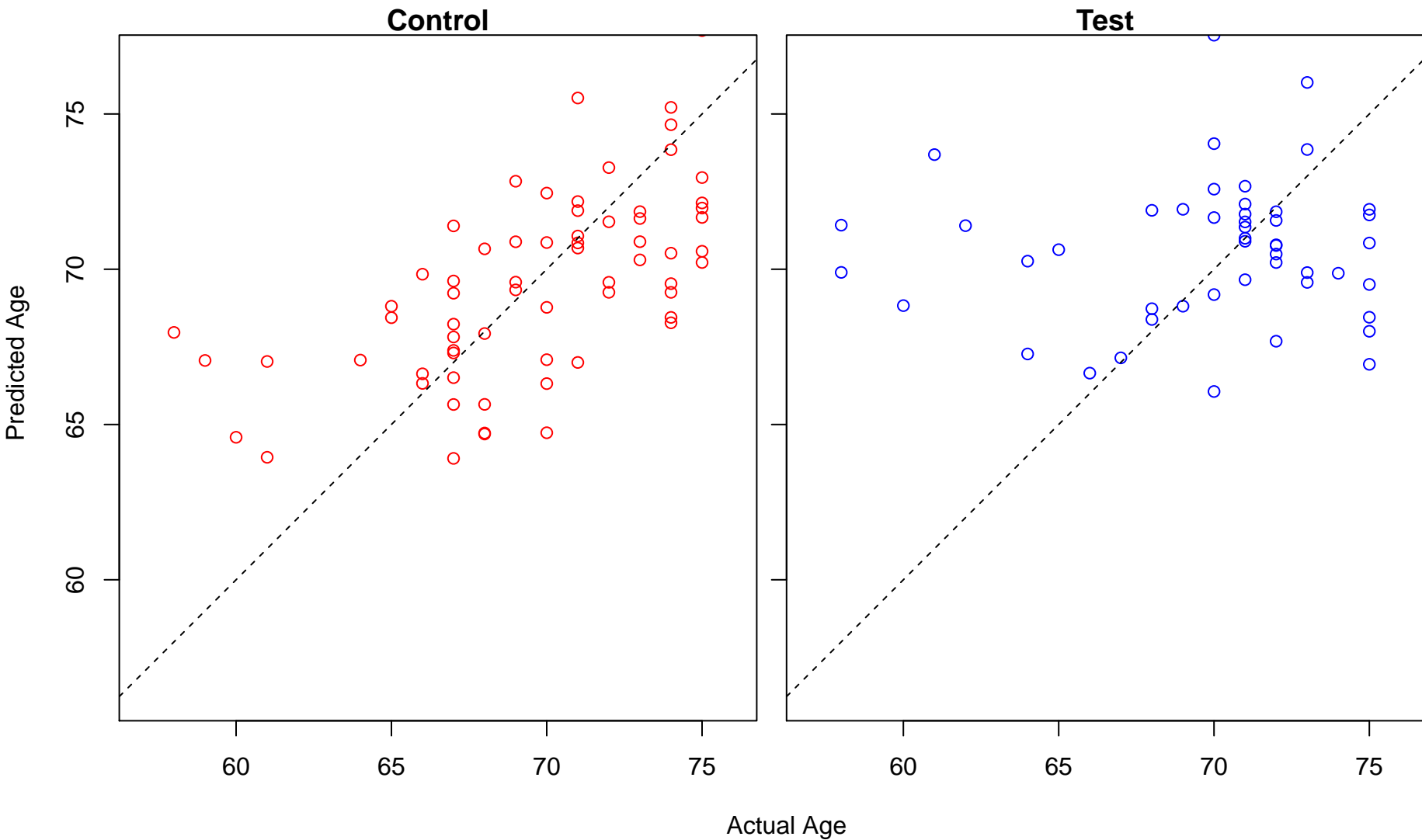
visual perception (Score: 1.130155)



regulation of sodium ion transmembrane transporter activity (Score: 1.129944)

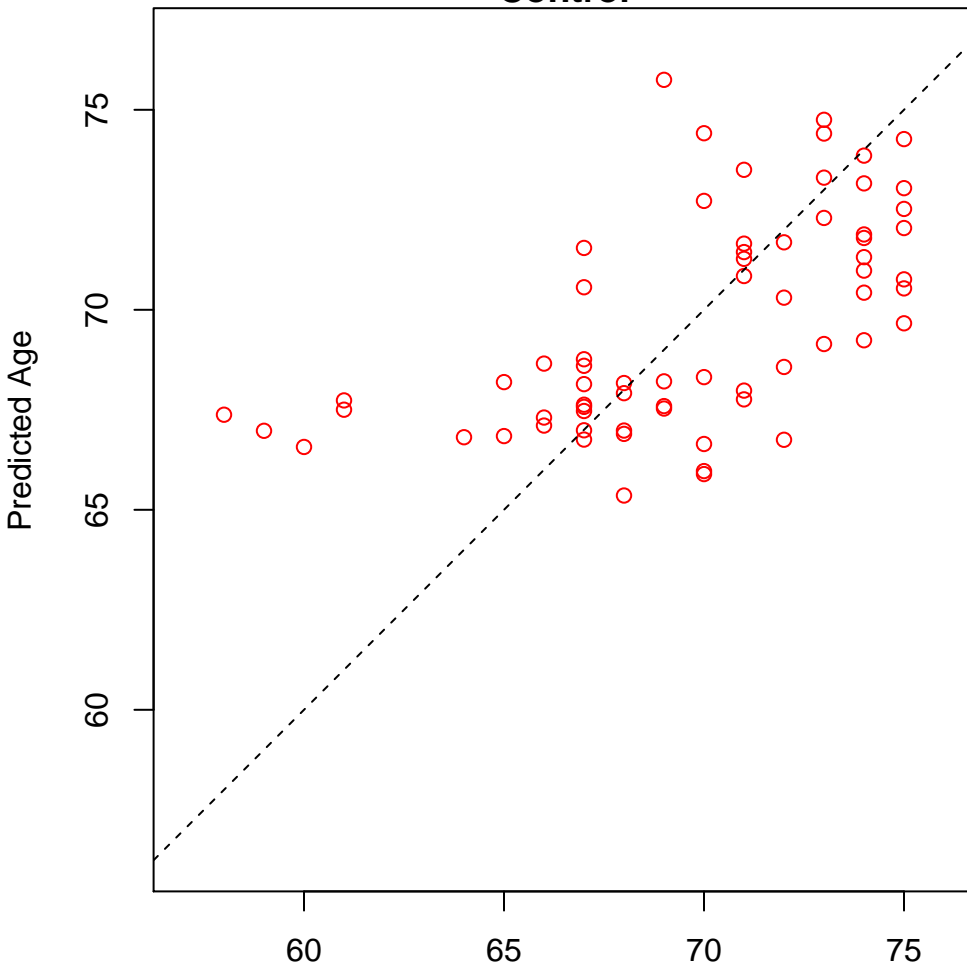


pyruvate metabolic process (Score: 1.129795)

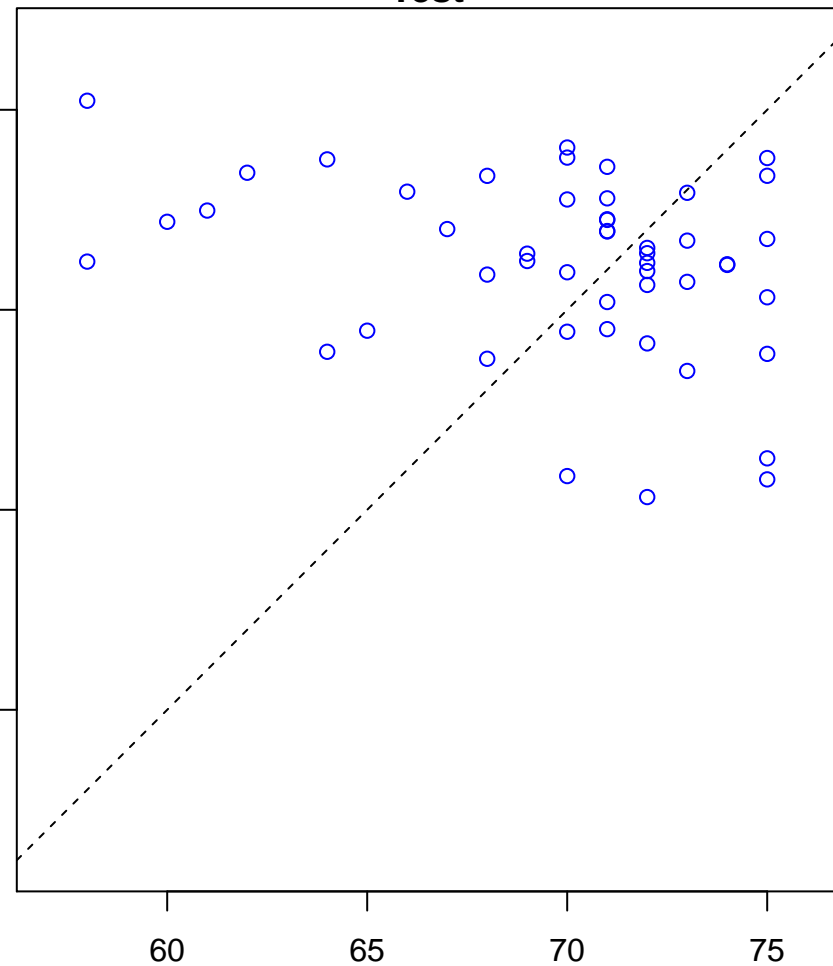


purine ribonucleotide catabolic process (Score: 1.128555)

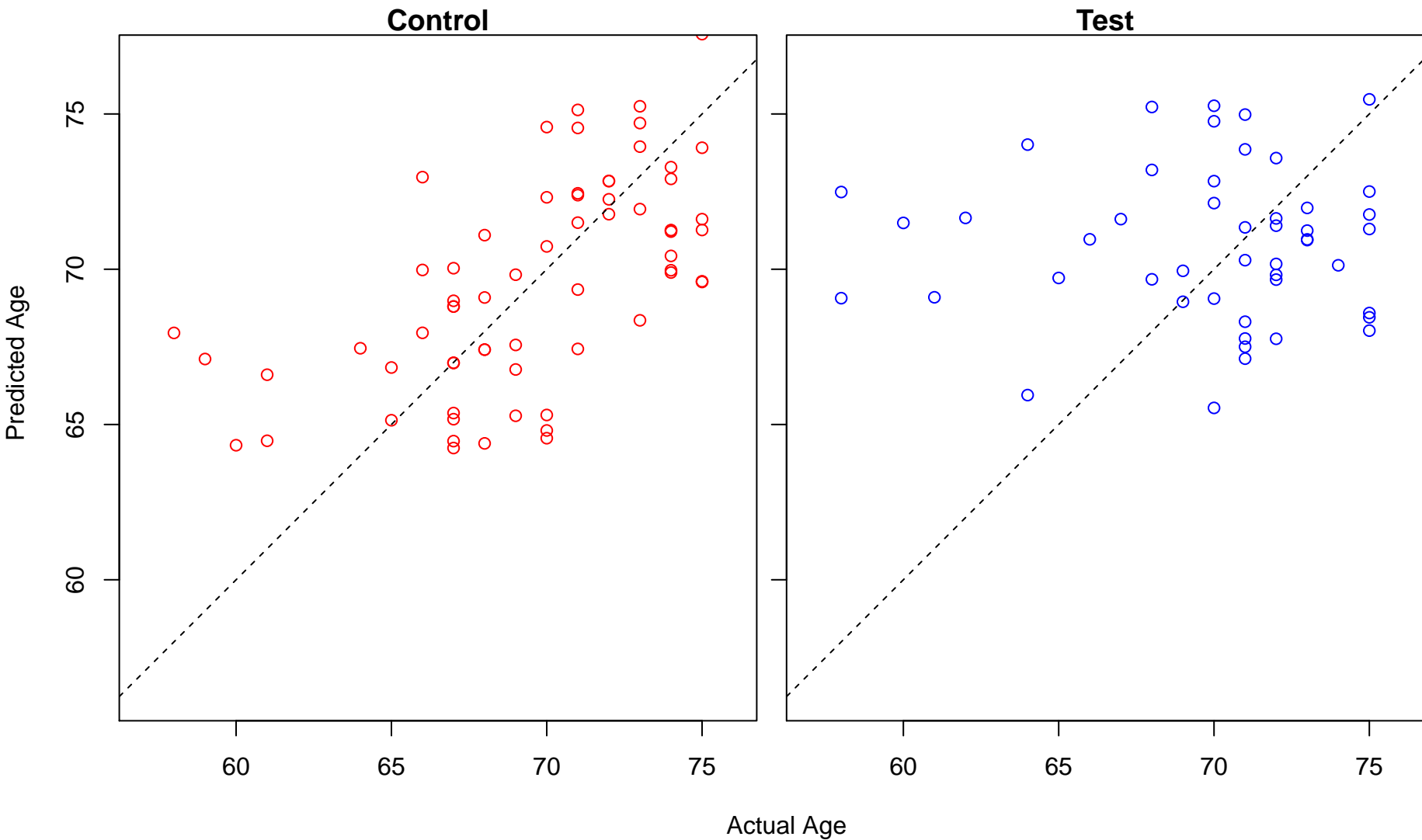
Control



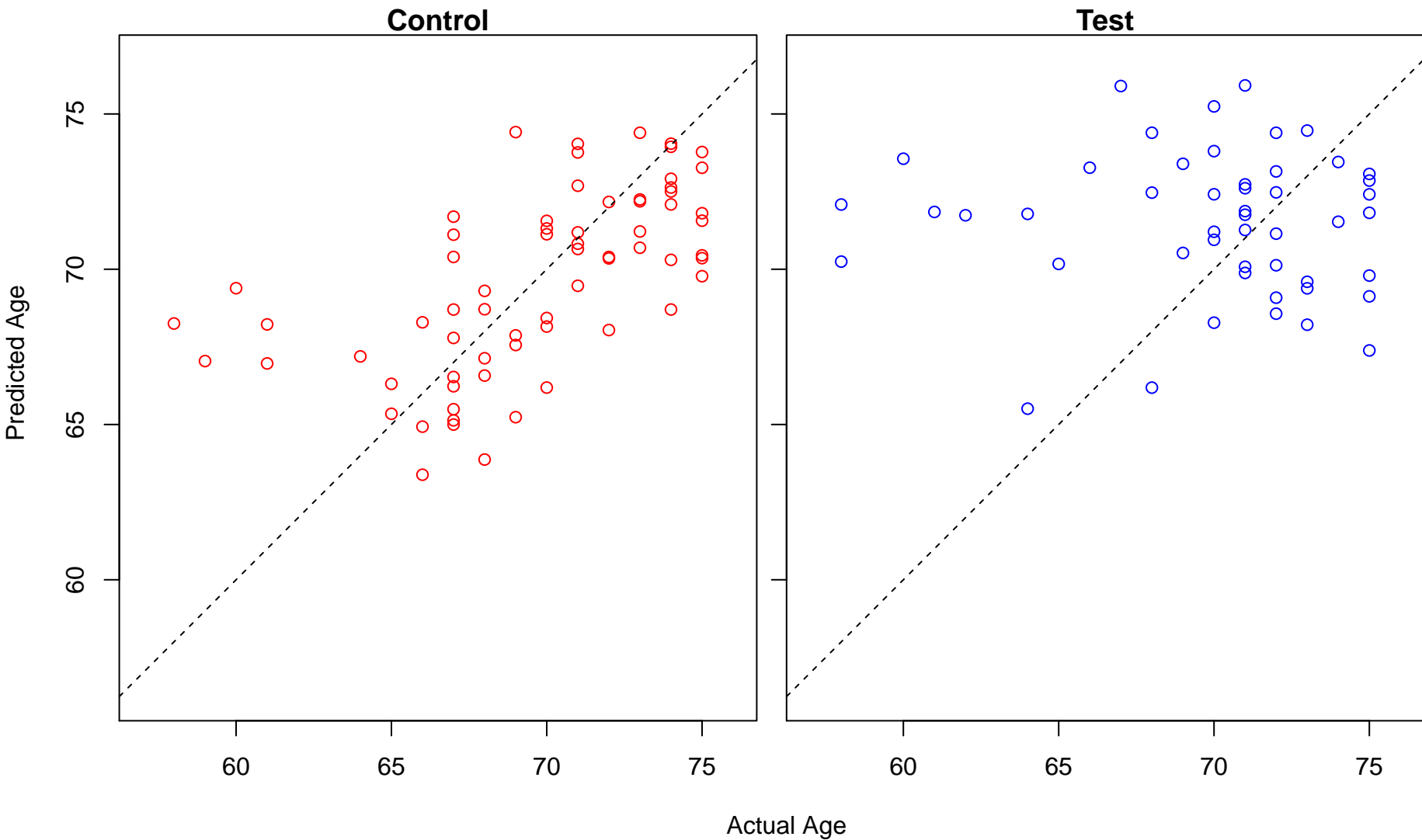
Test



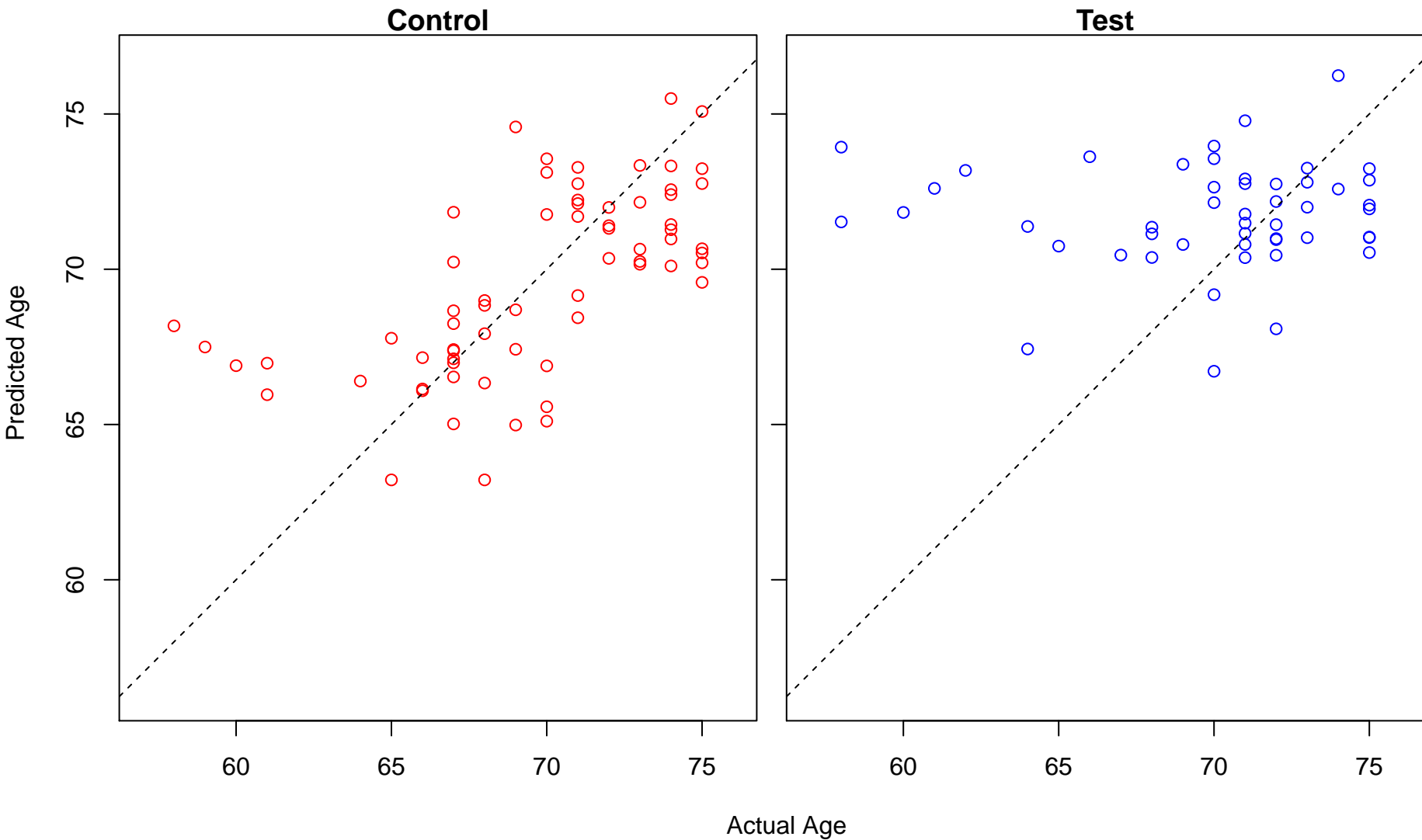
regulation of androgen receptor signaling pathway (Score: 1.127850)



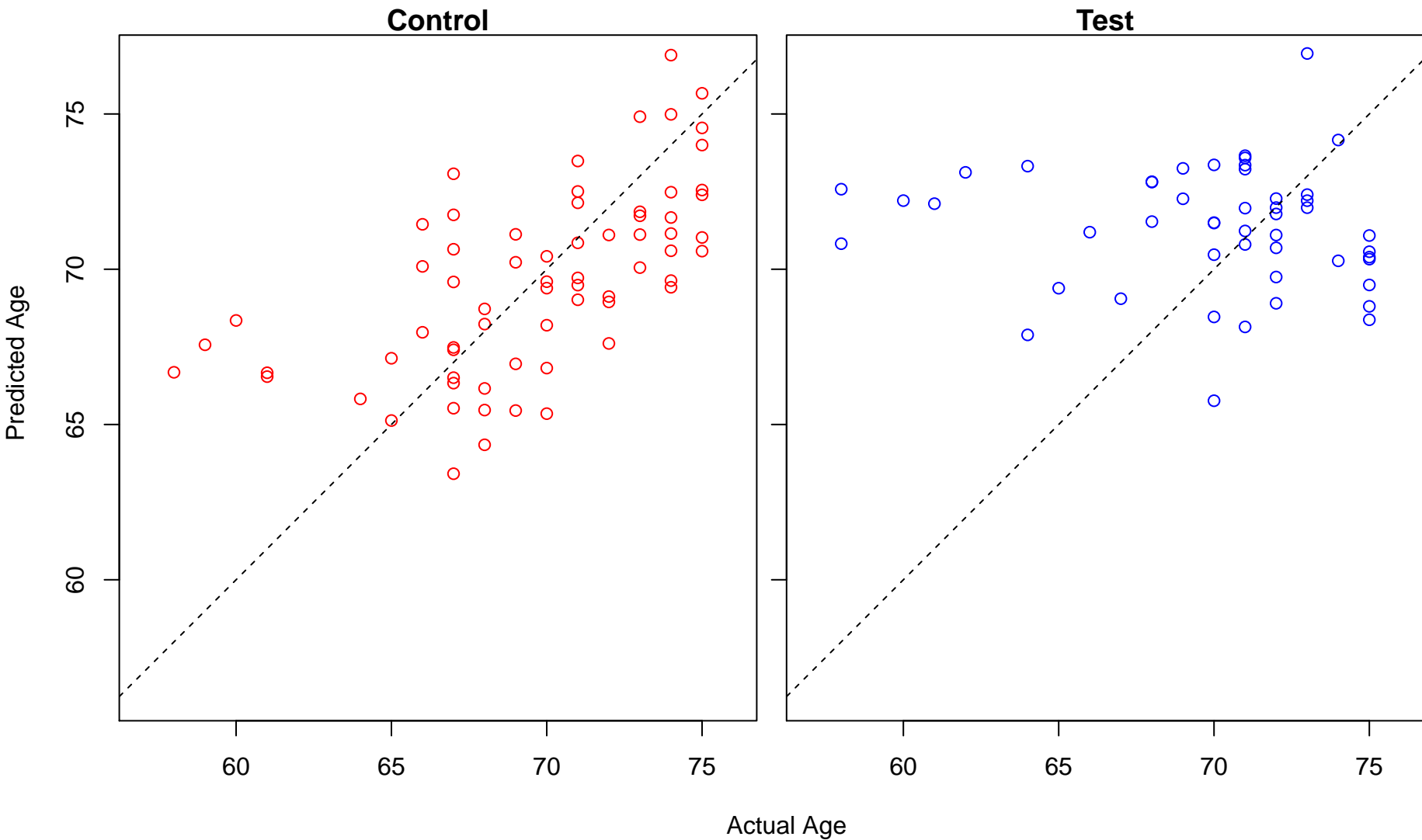
negative regulation of interleukin-8 production (Score: 1.127388)



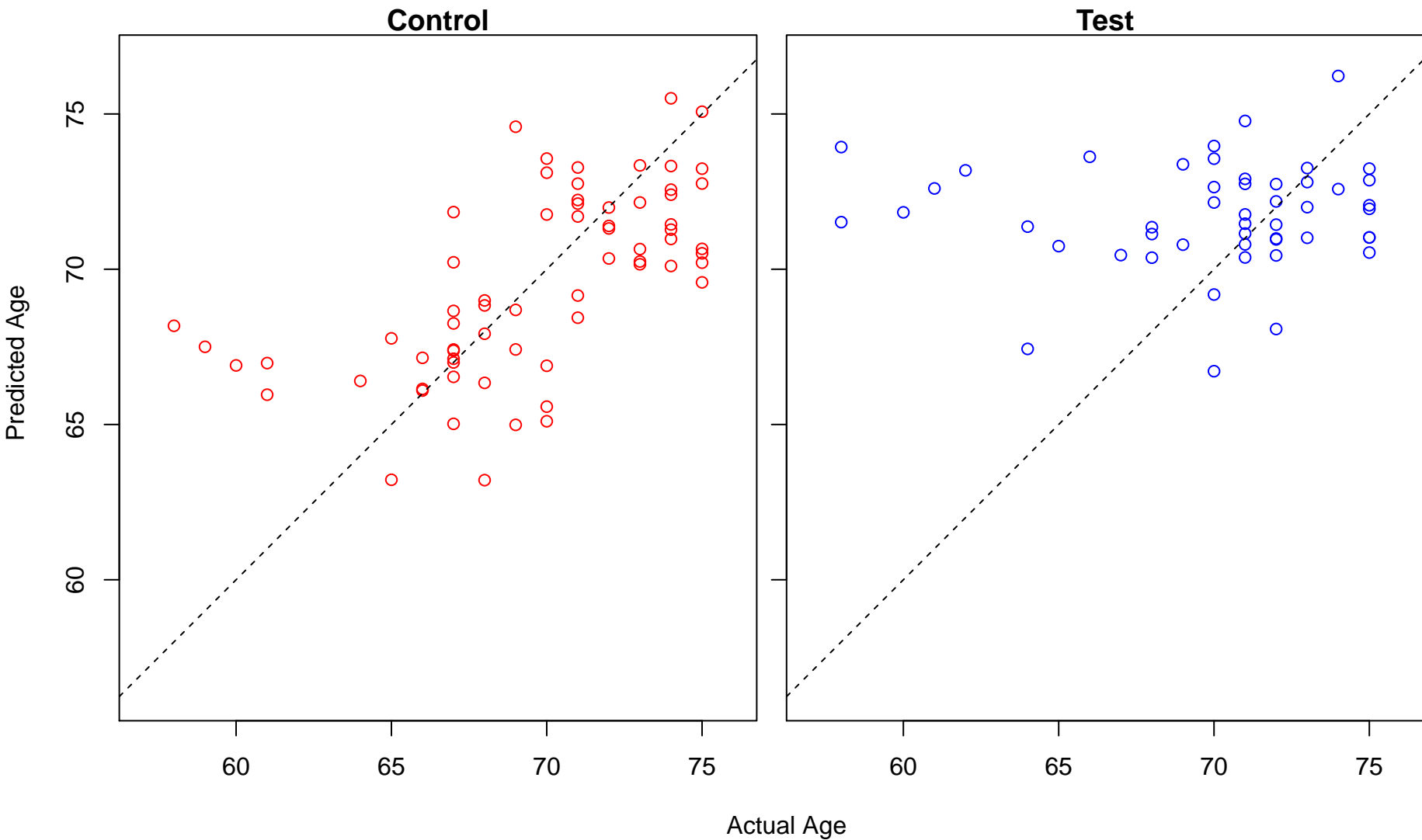
blood circulation (Score: 1.127384)



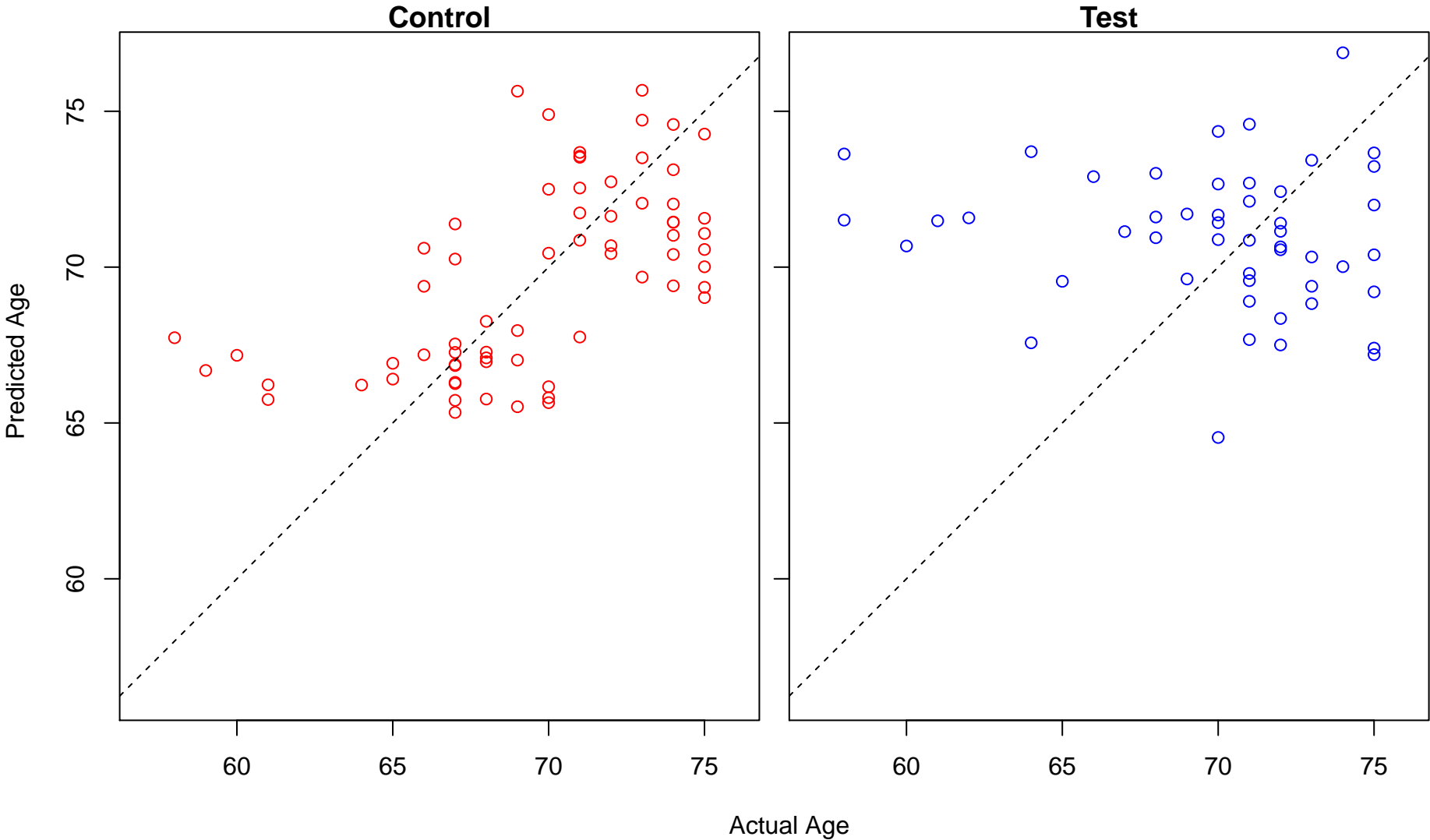
ovarian follicle development (Score: 1.126181)



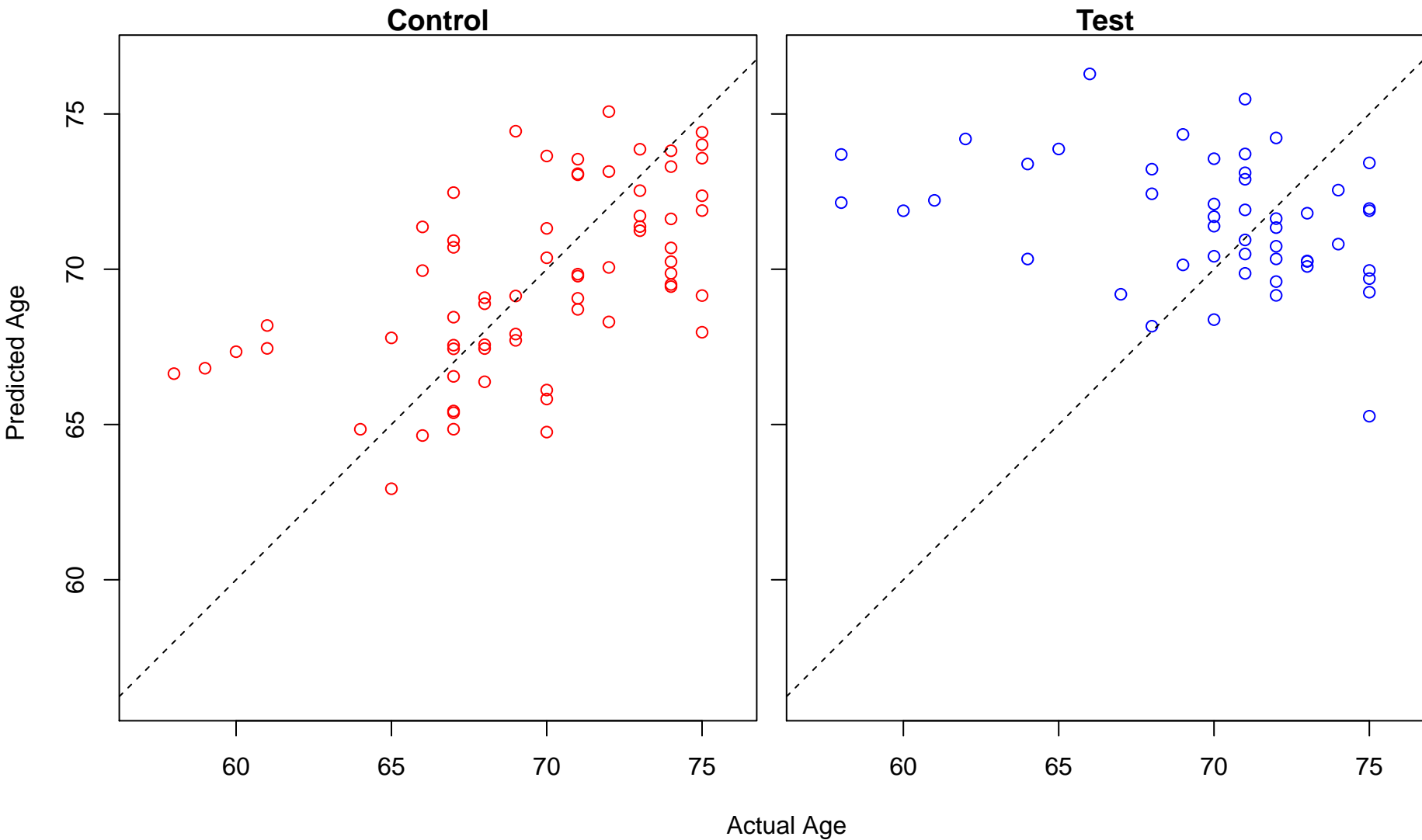
circulatory system process (Score: 1.126110)



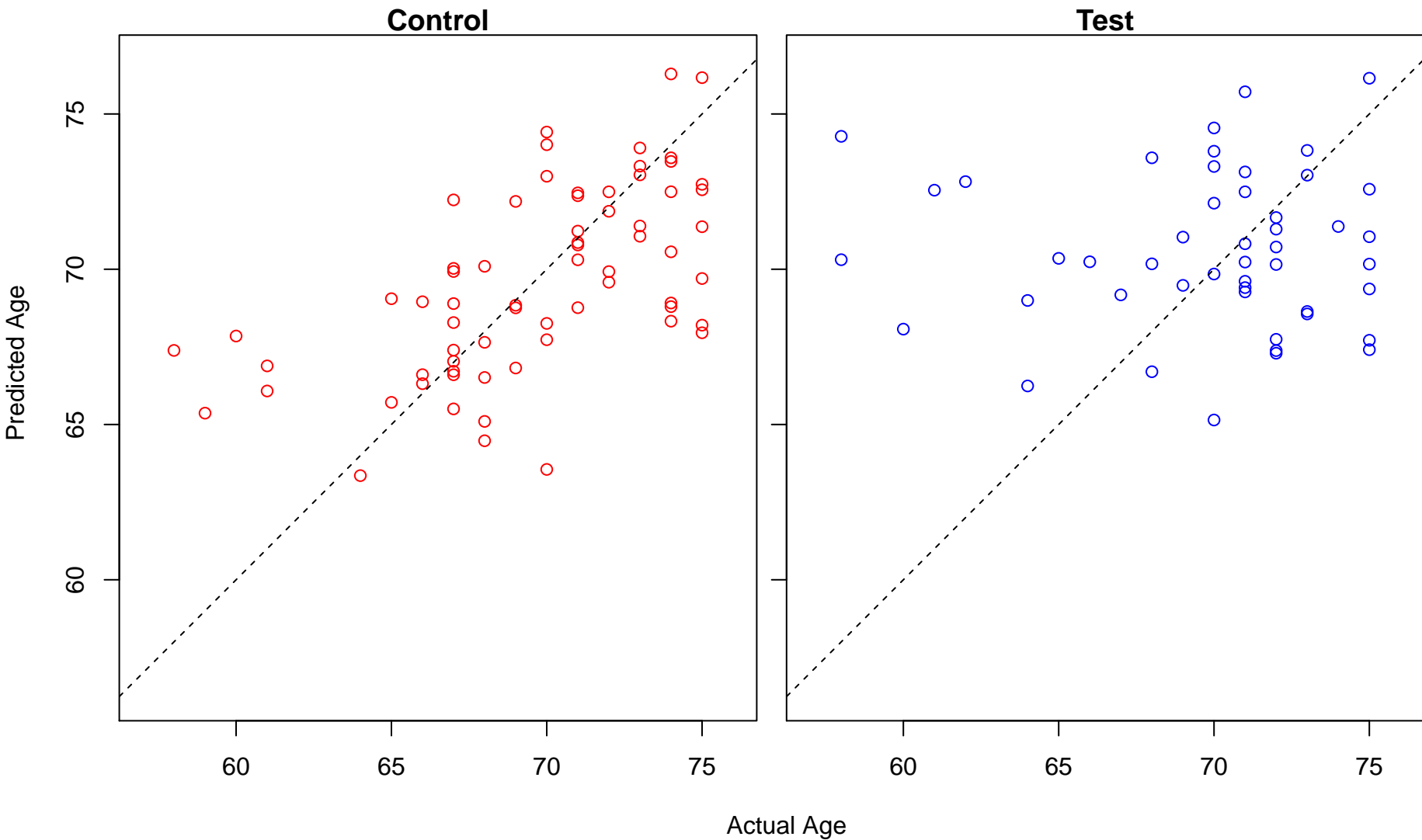
modification of morphology or physiology of other organism involved in symbiotic interaction (Score: 1.



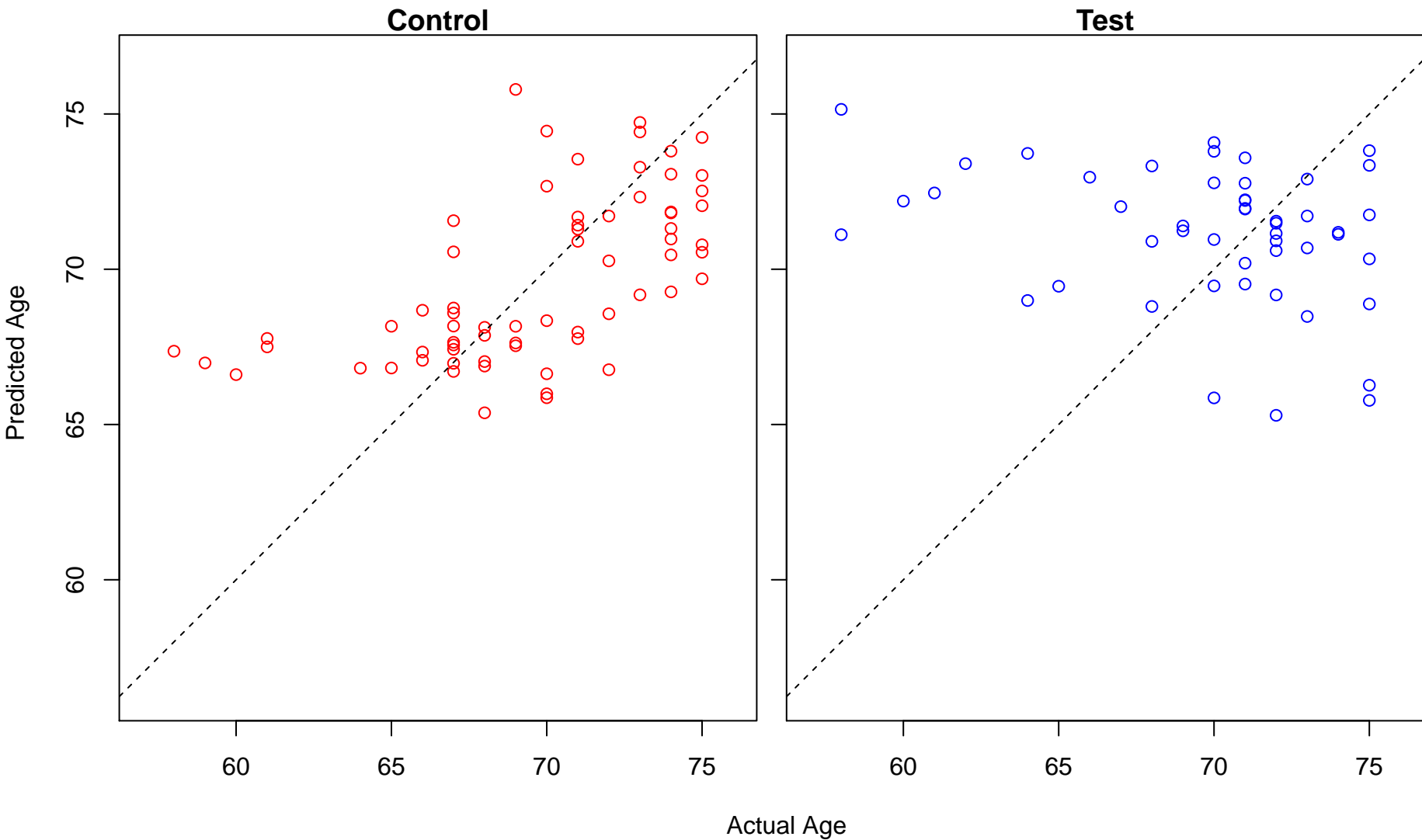
liver development (Score: 1.125868)



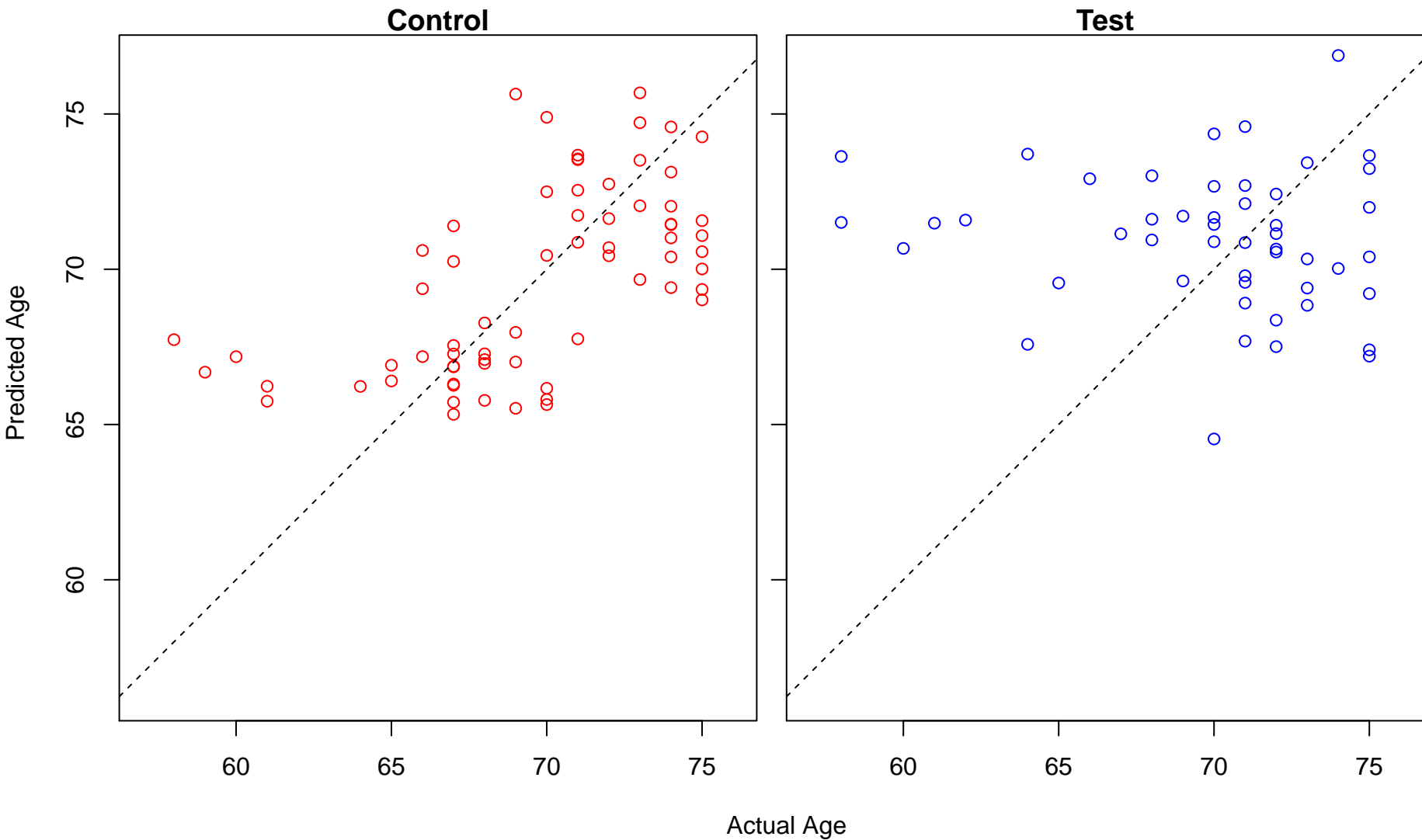
cell-cell junction organization (Score: 1.125667)



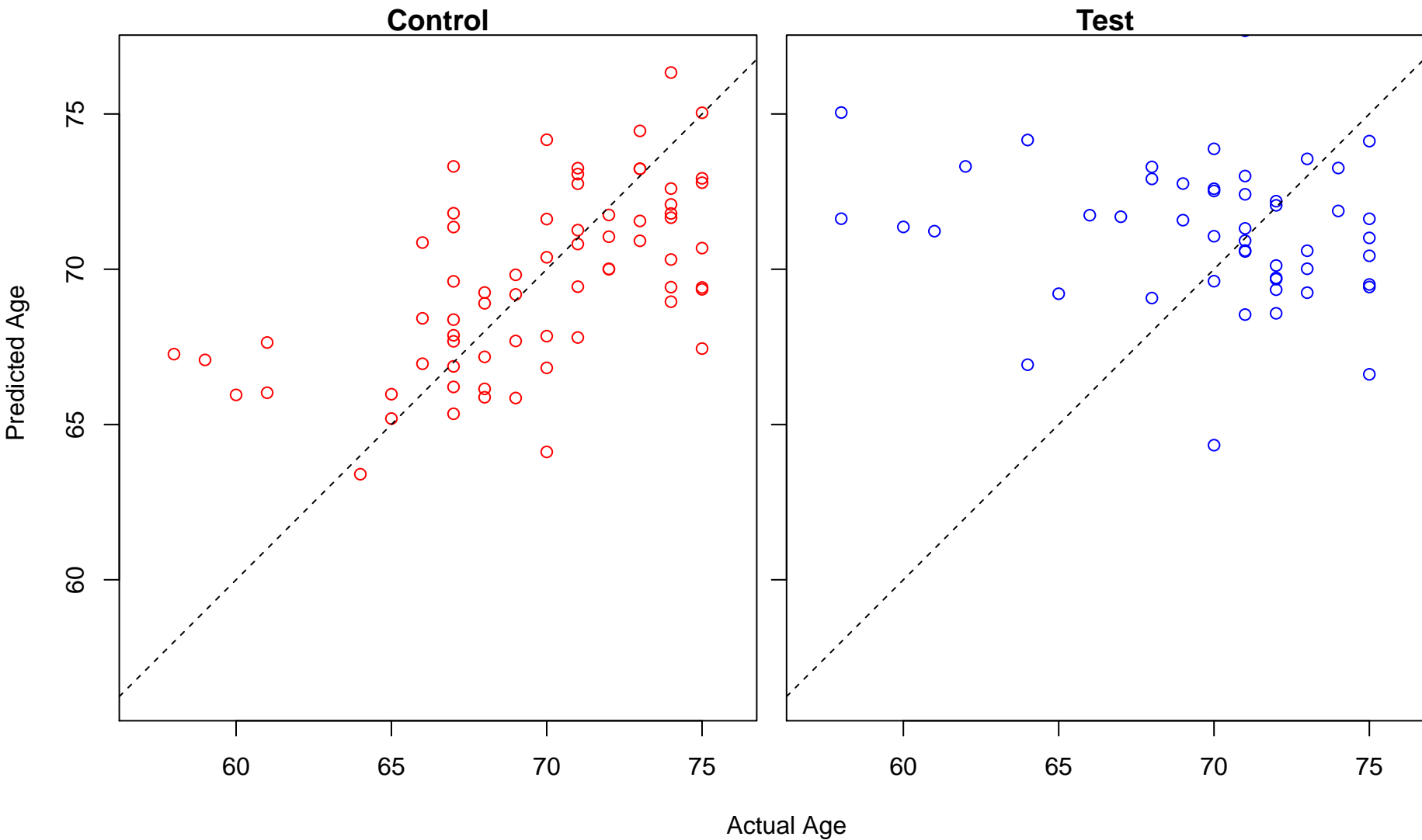
ribonucleotide catabolic process (Score: 1.125215)



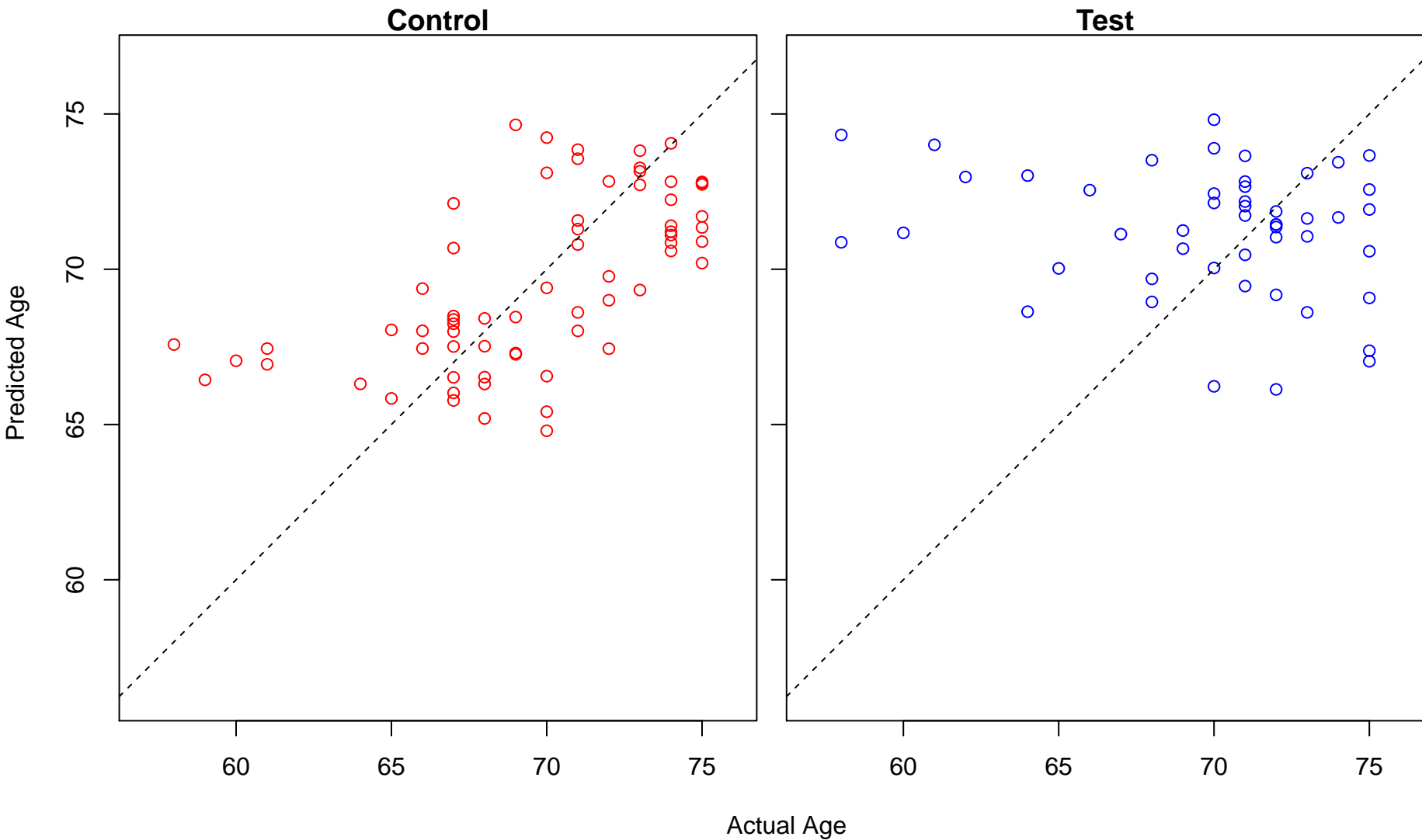
modification of morphology or physiology of other organism (Score: 1.125006)



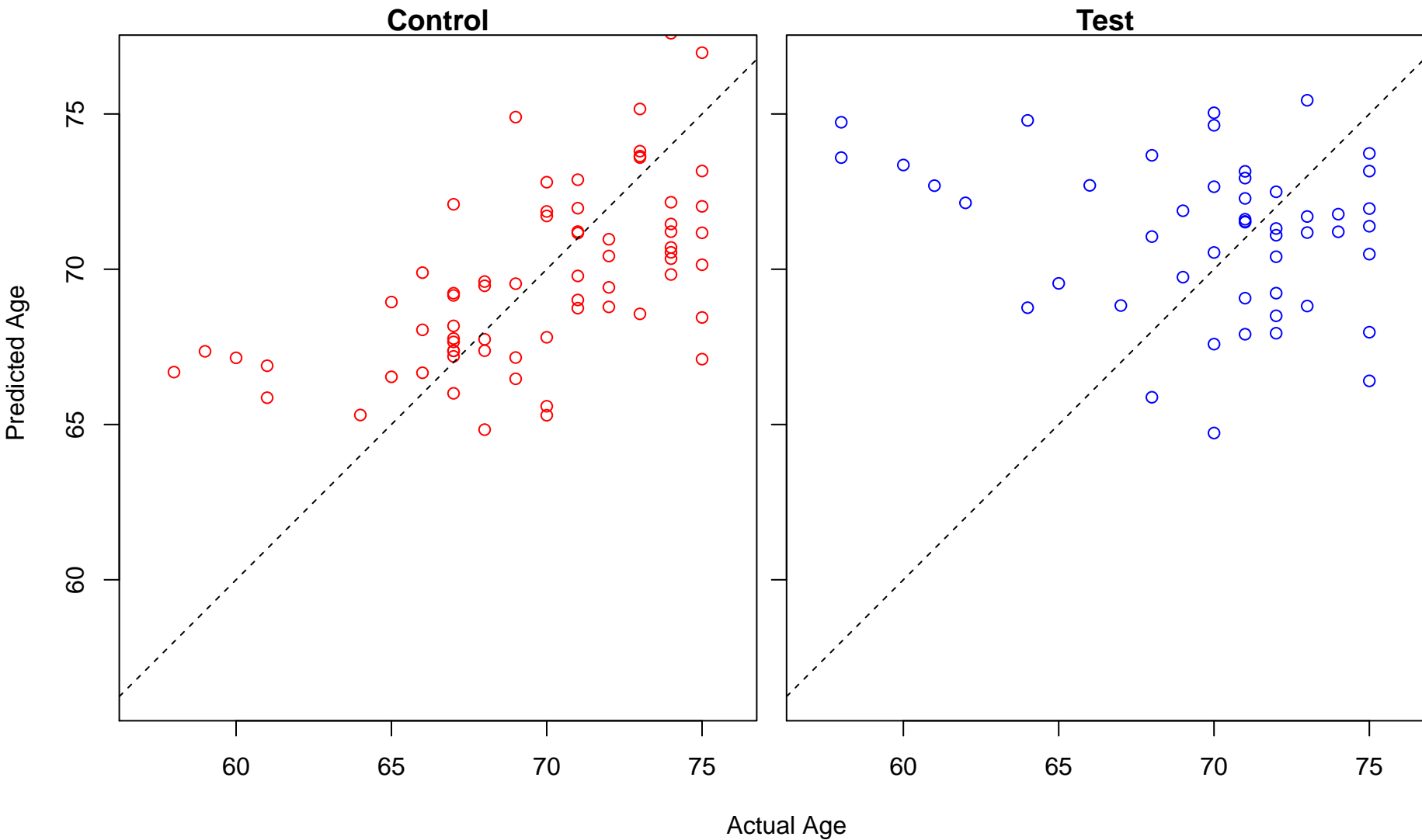
response to glucose (Score: 1.124814)



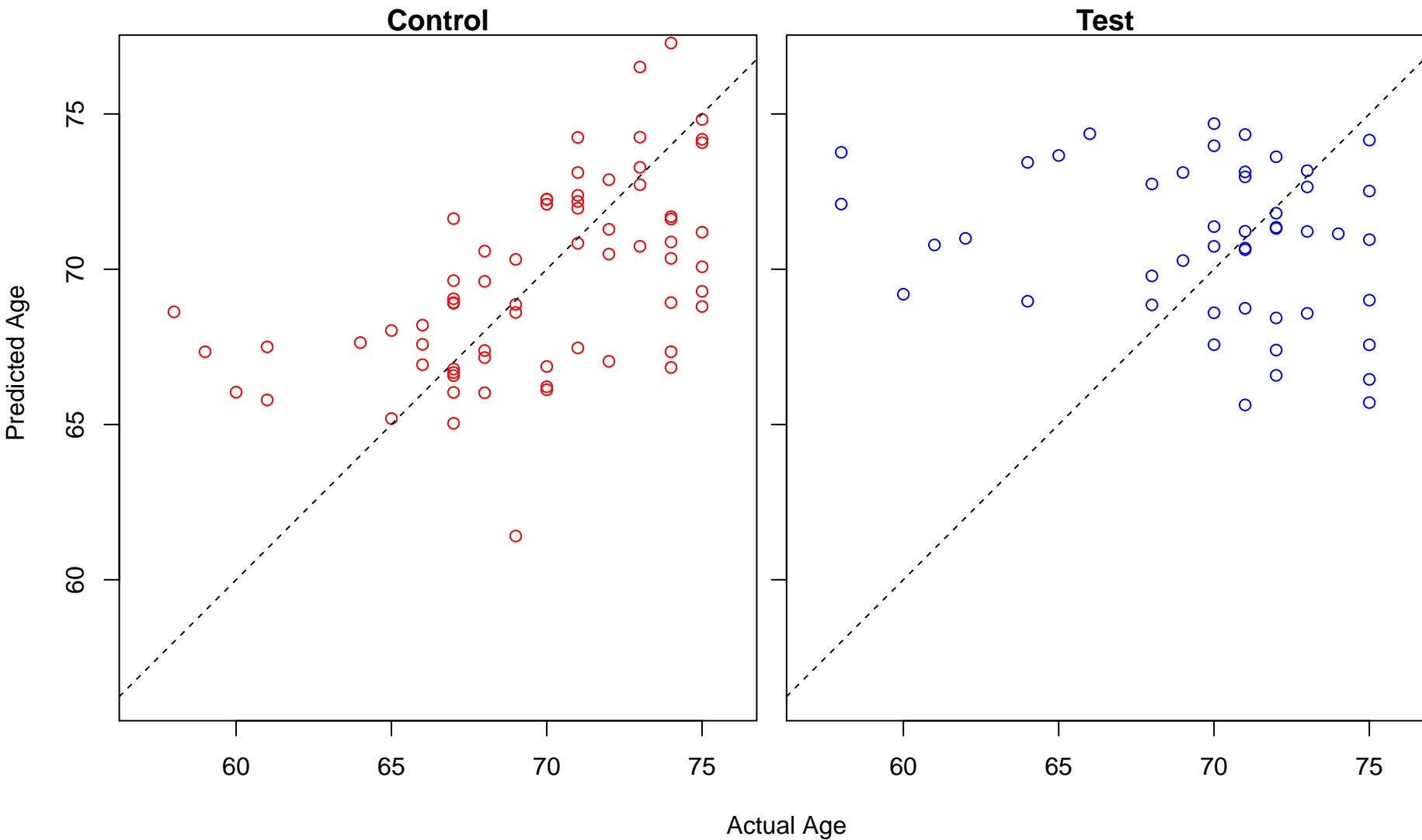
organonitrogen compound catabolic process (Score: 1.124606)



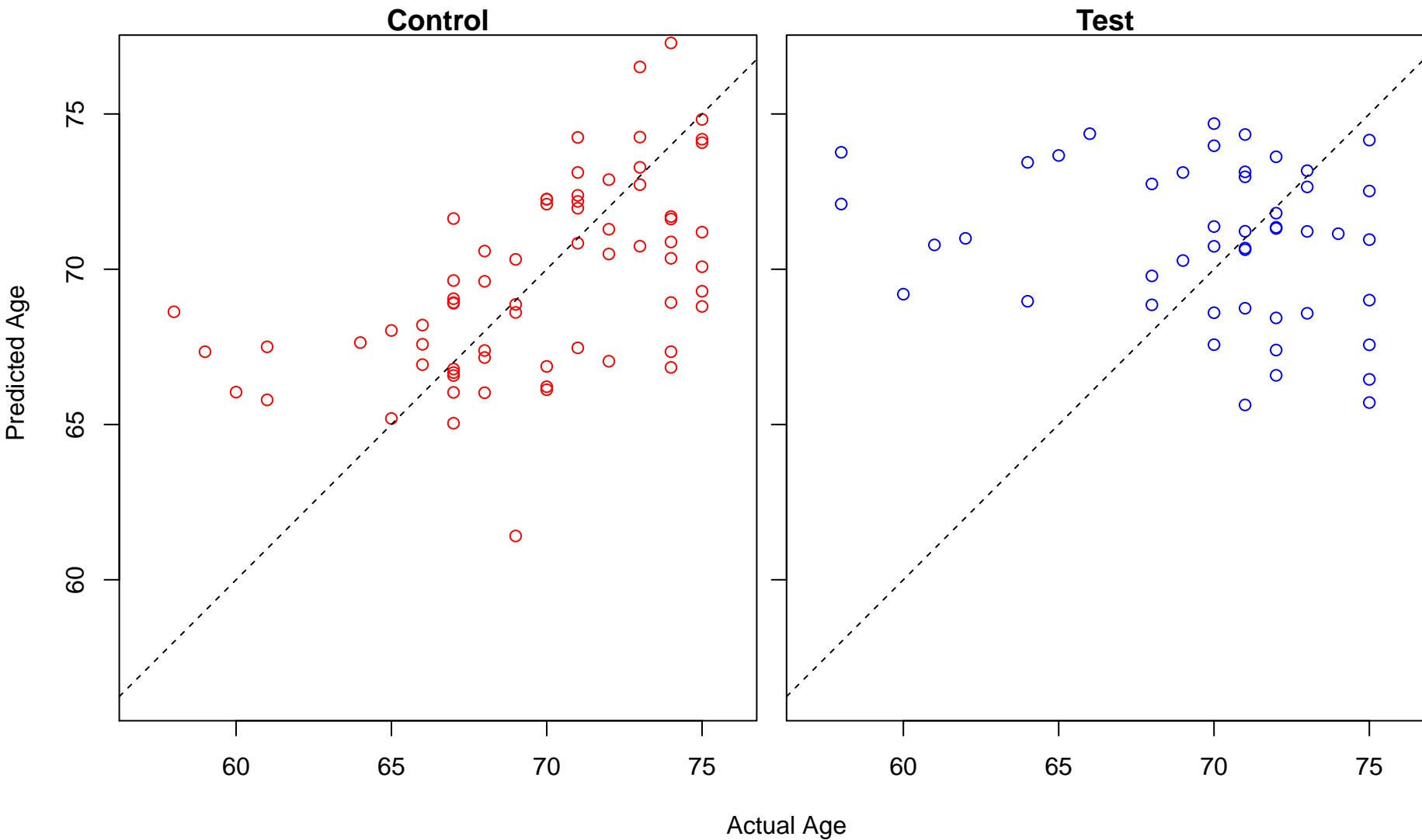
protein localization to vacuole (Score: 1.124551)



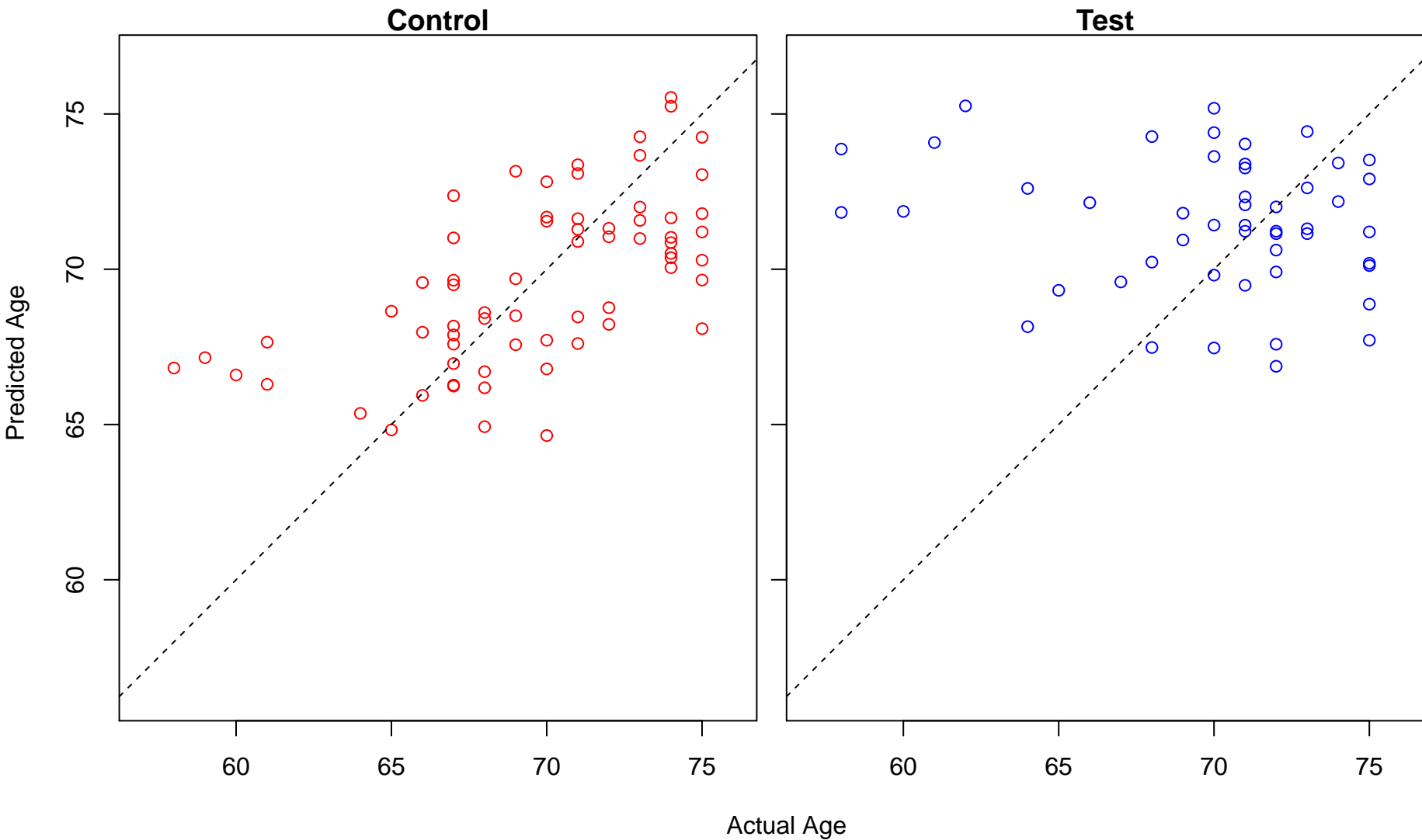
replication fork processing (Score: 1.124242)



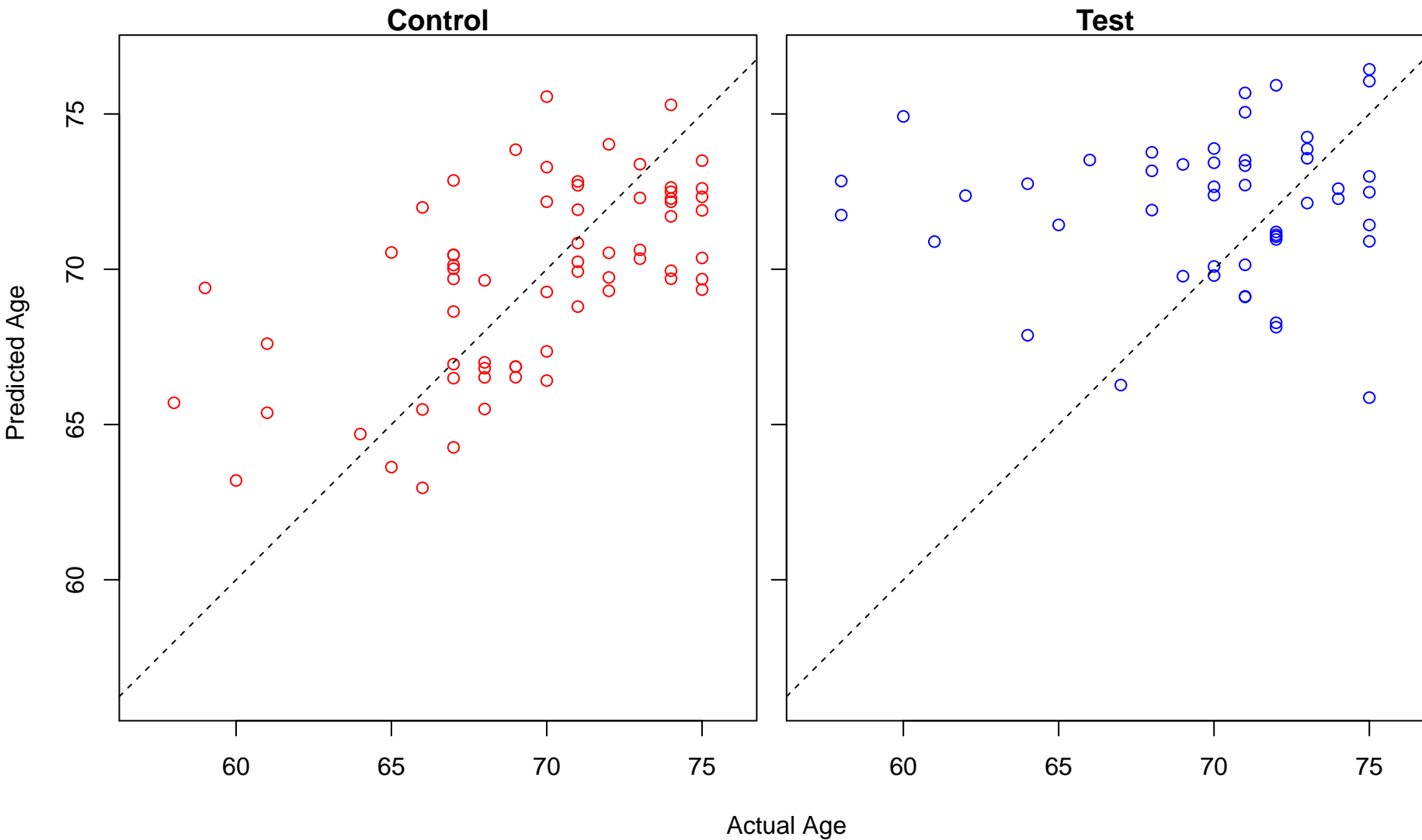
DNA-dependent DNA replication maintenance of fidelity (Score: 1.124242)



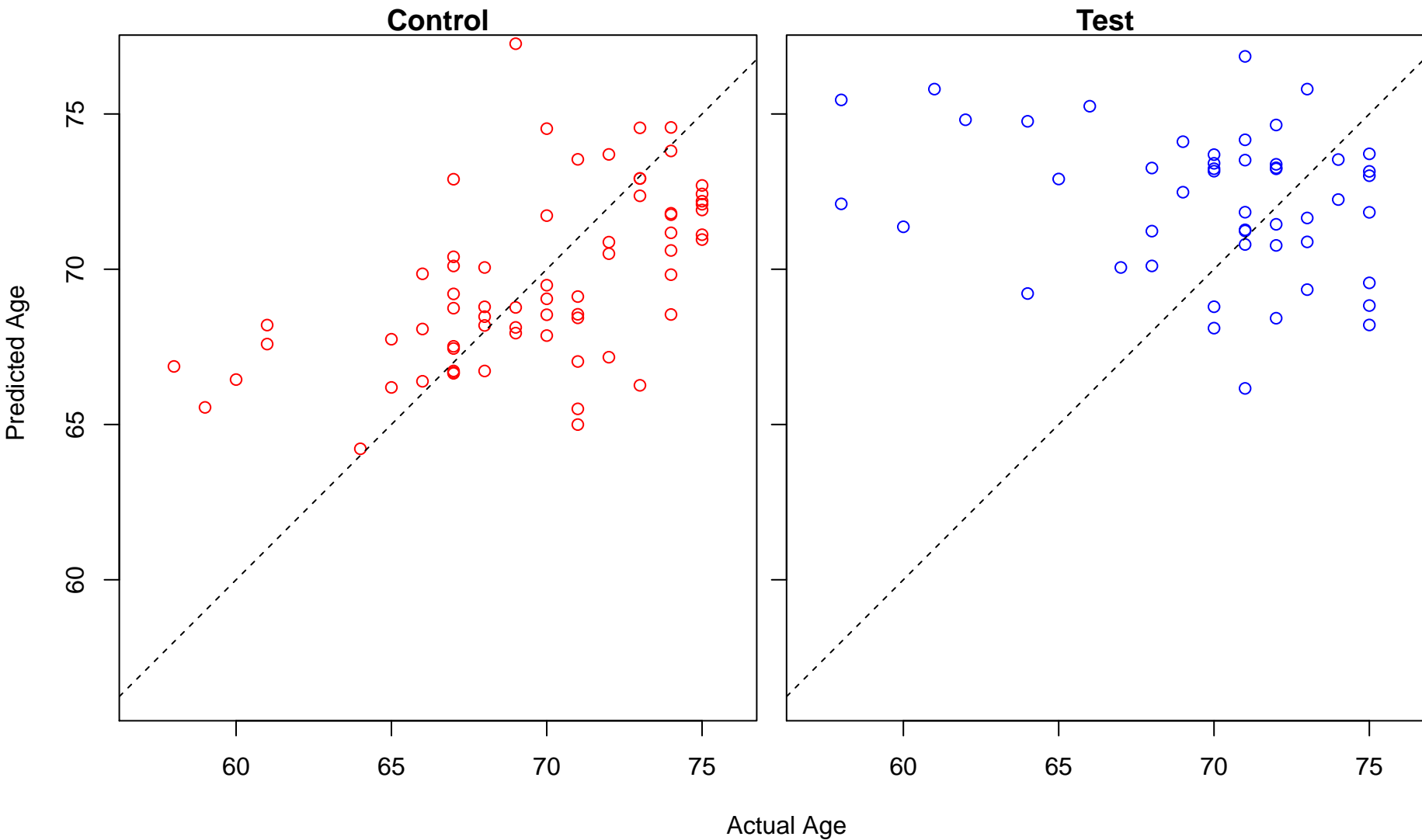
lipid transport (Score: 1.123218)



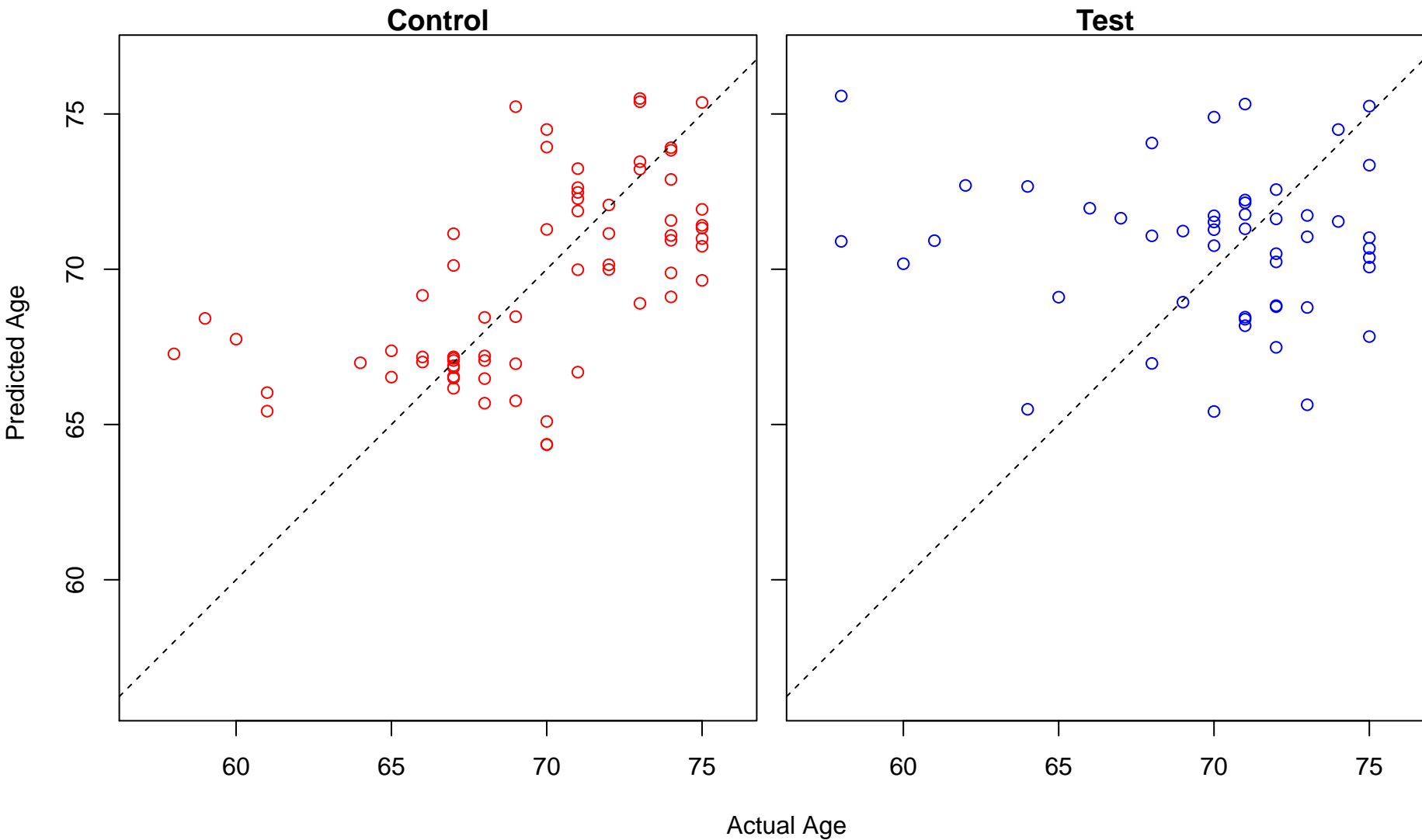
organ growth (Score: 1.122758)



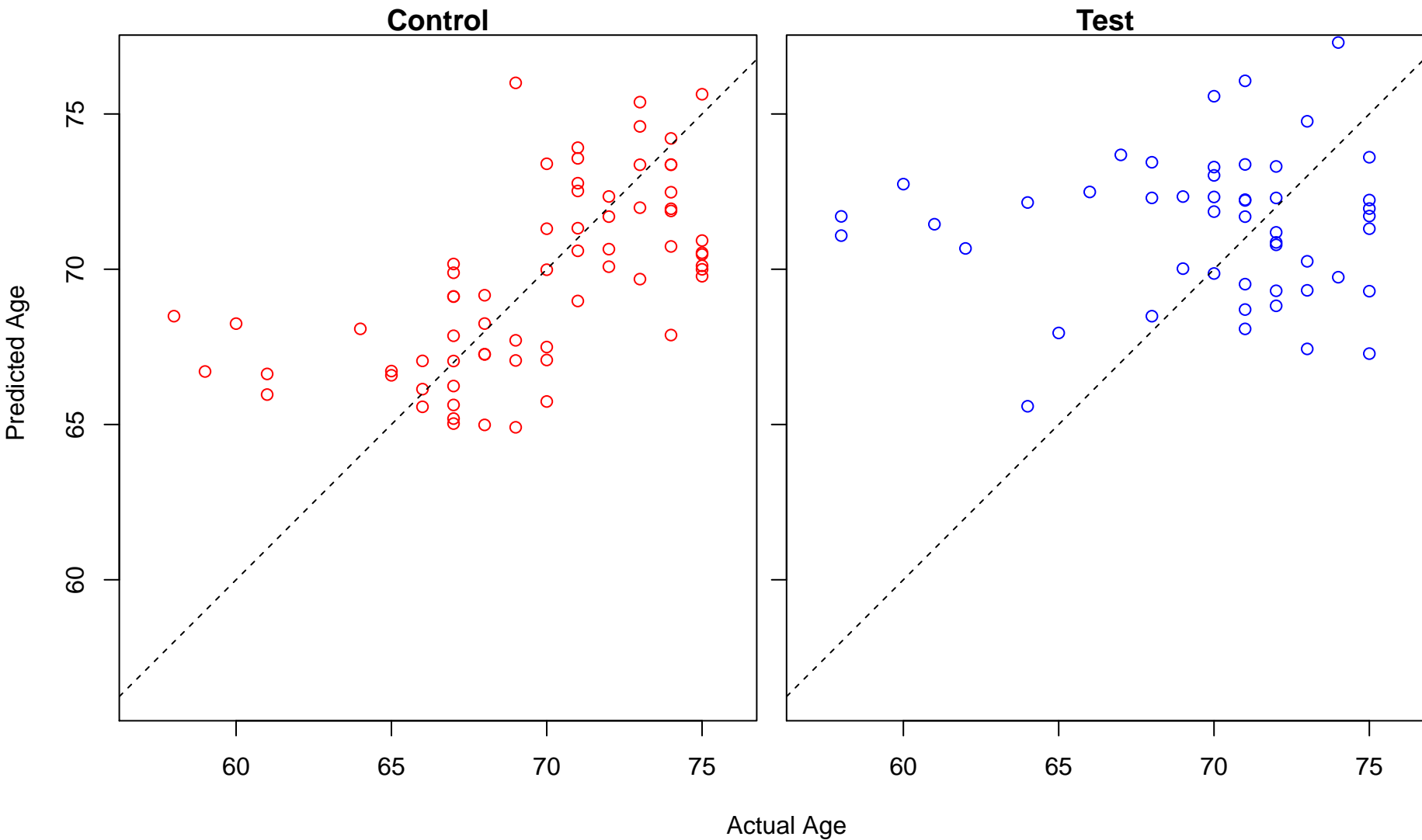
regulation of helicase activity (Score: 1.122162)



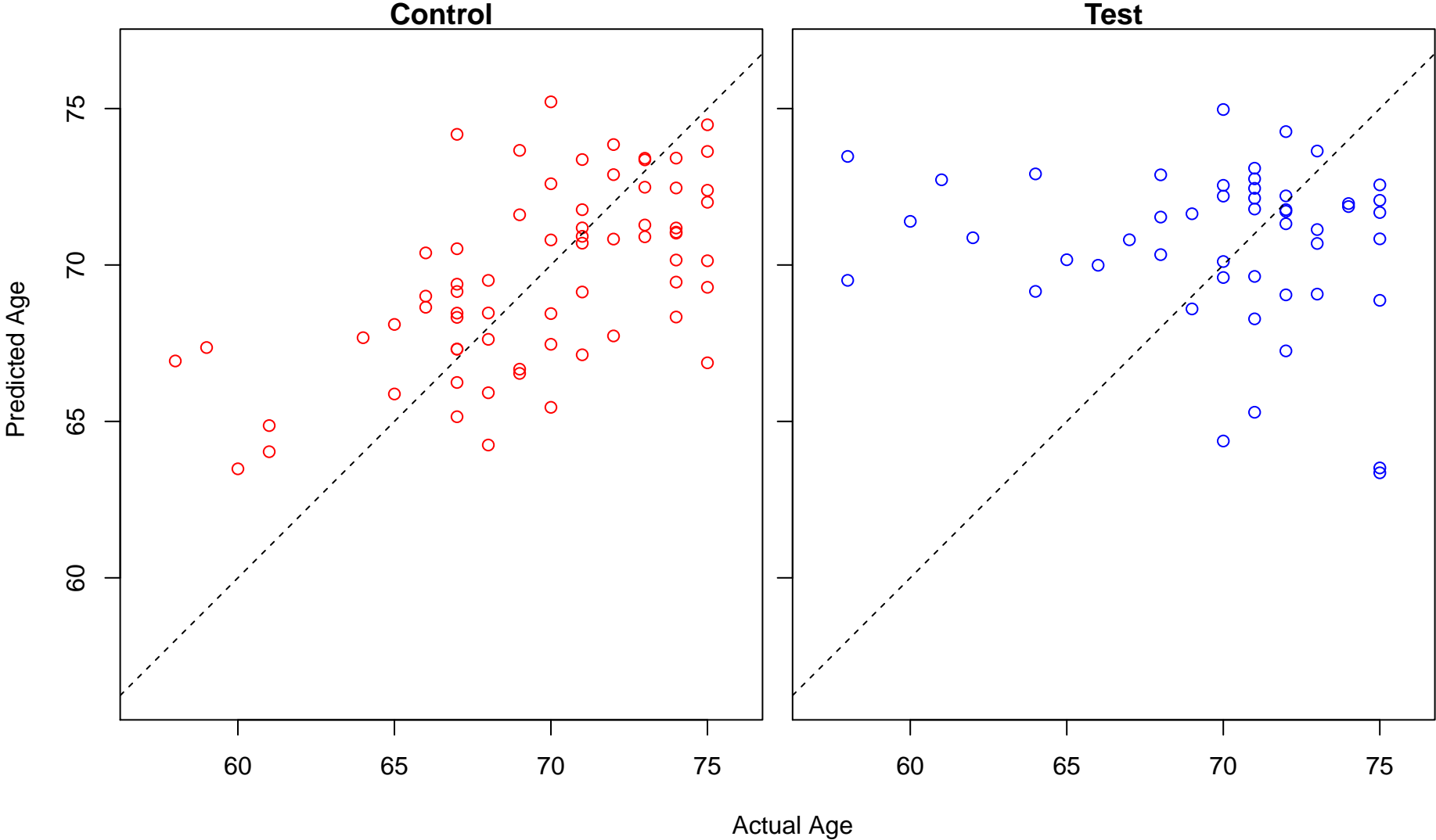
synaptic vesicle localization (Score: 1.121772)



regulation of wound healing (Score: 1.121755)

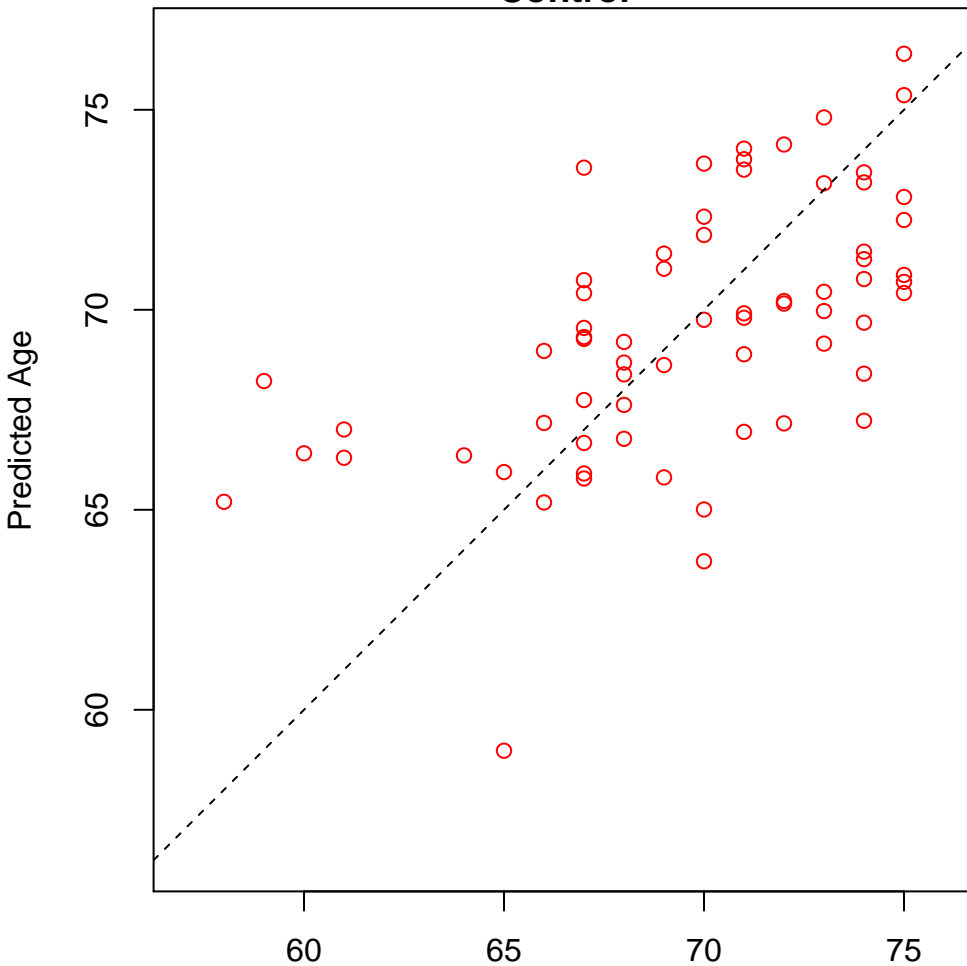


positive regulation of potassium ion transmembrane transporter activity (Score: 1.121640)

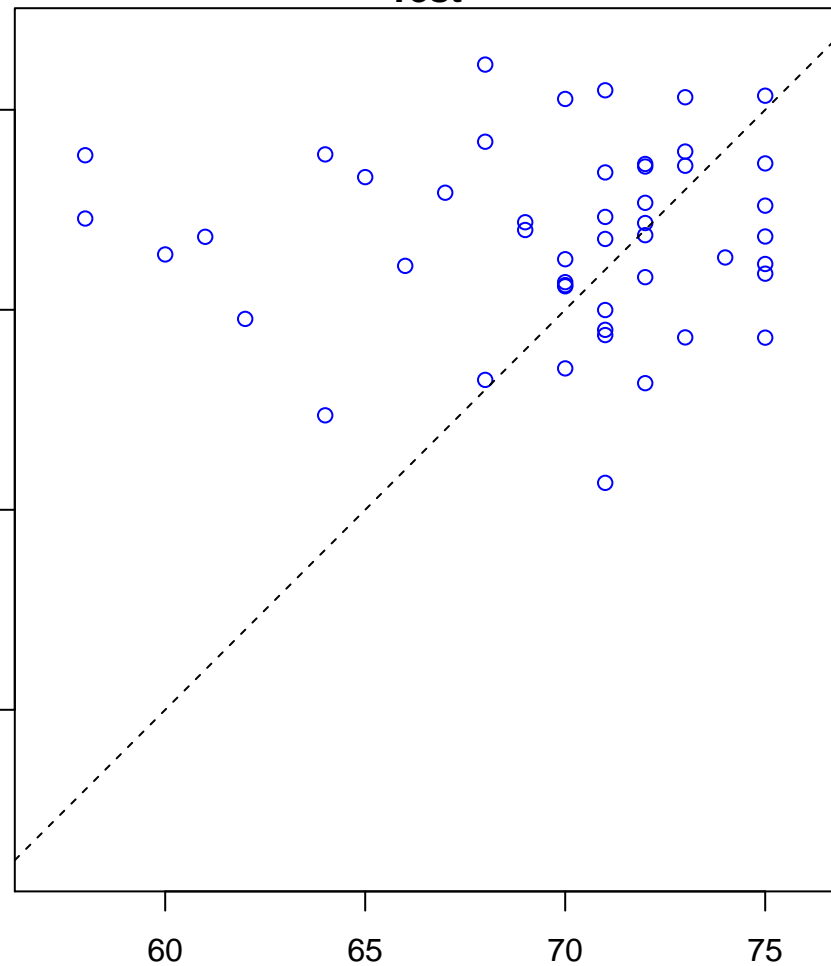


positive regulation of B cell proliferation (Score: 1.121610)

Control

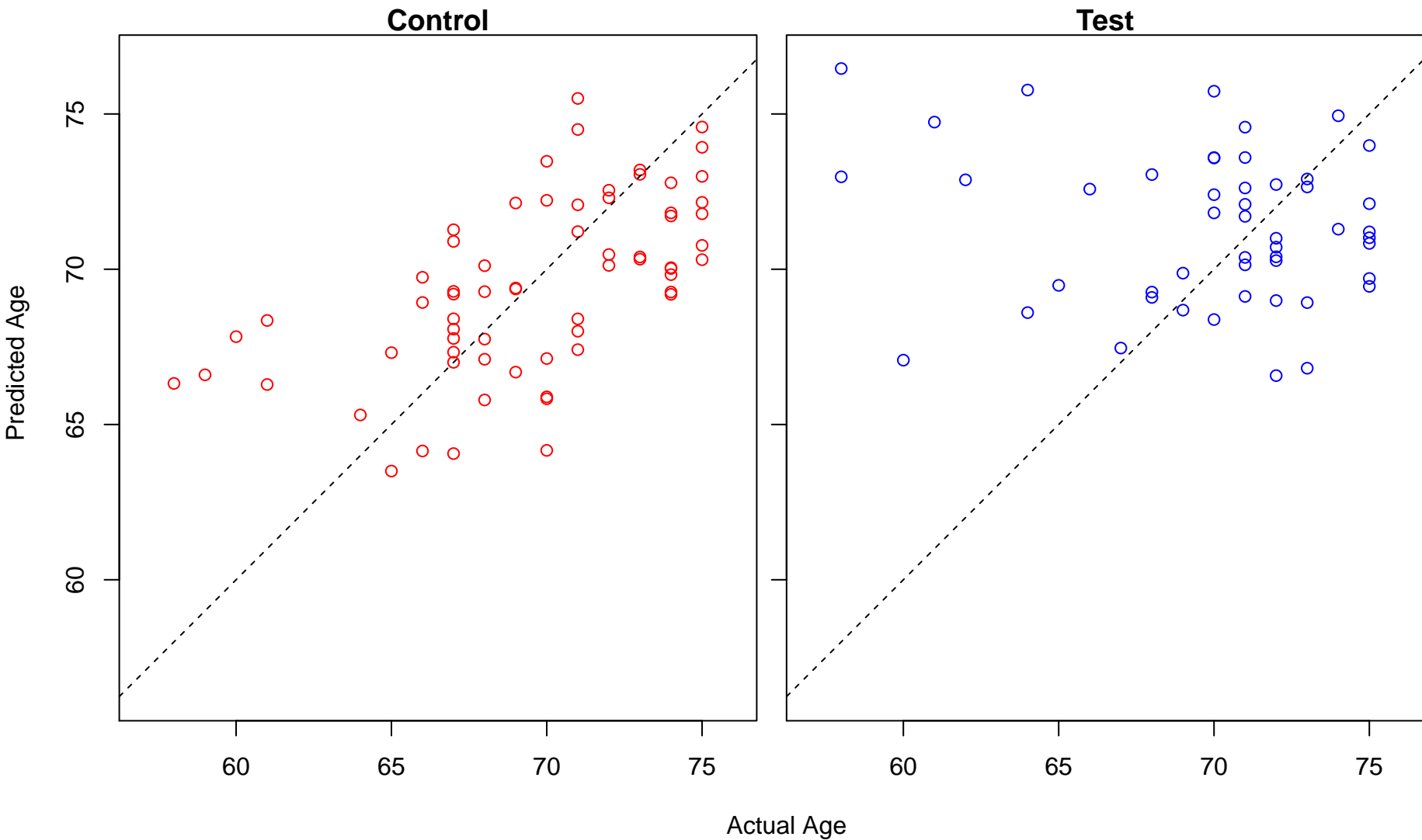


Test

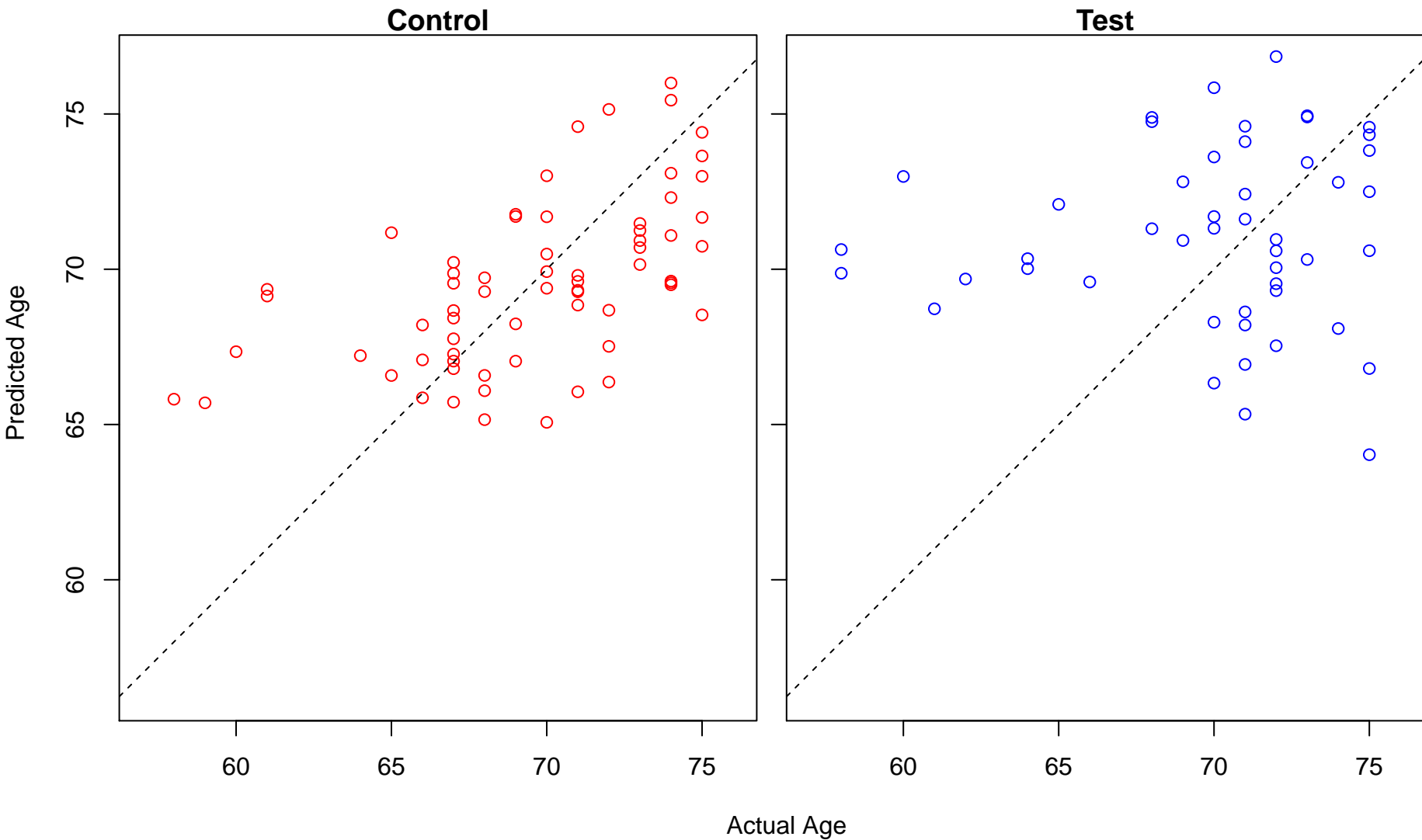


Actual Age

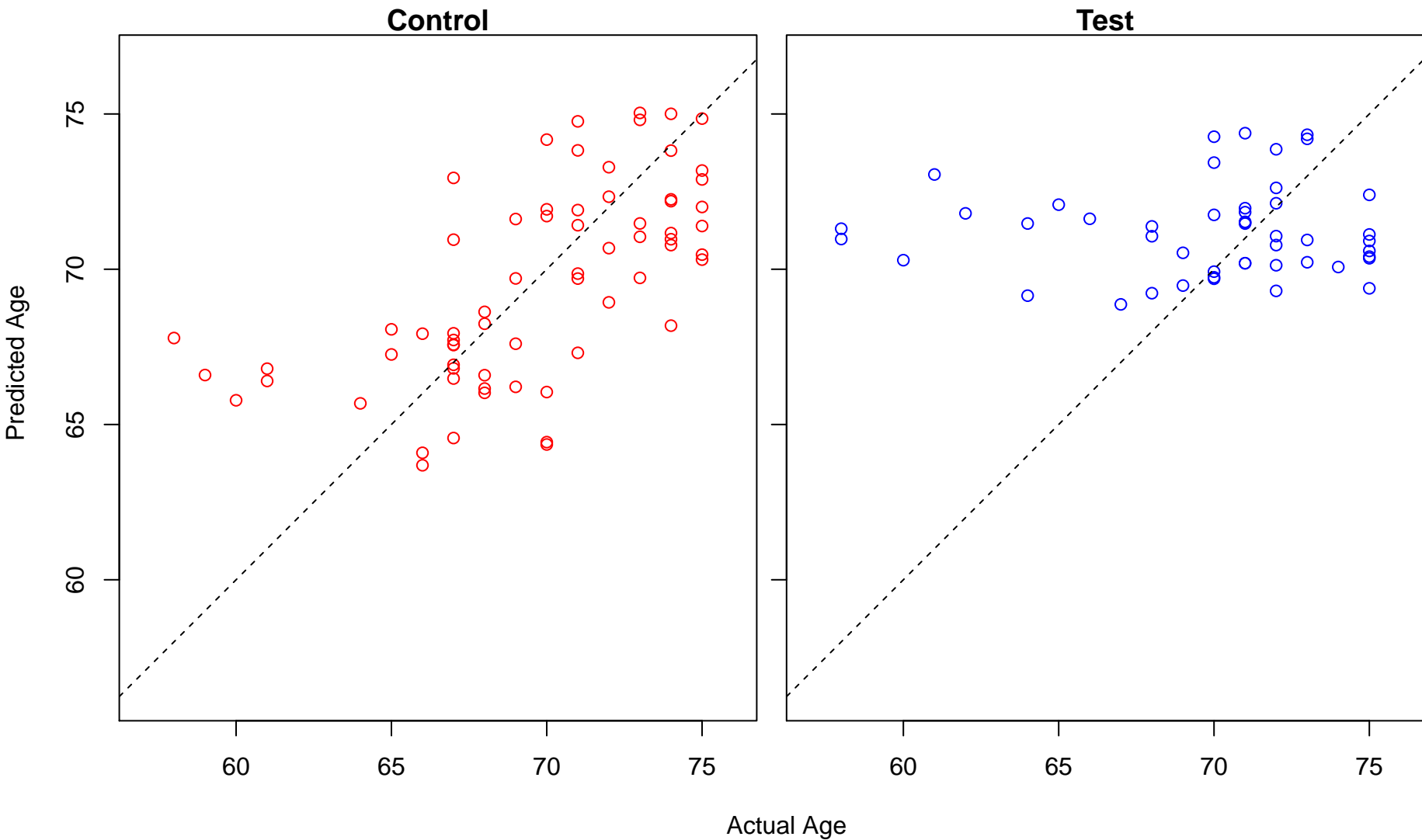
regulation of viral entry into host cell (Score: 1.120873)



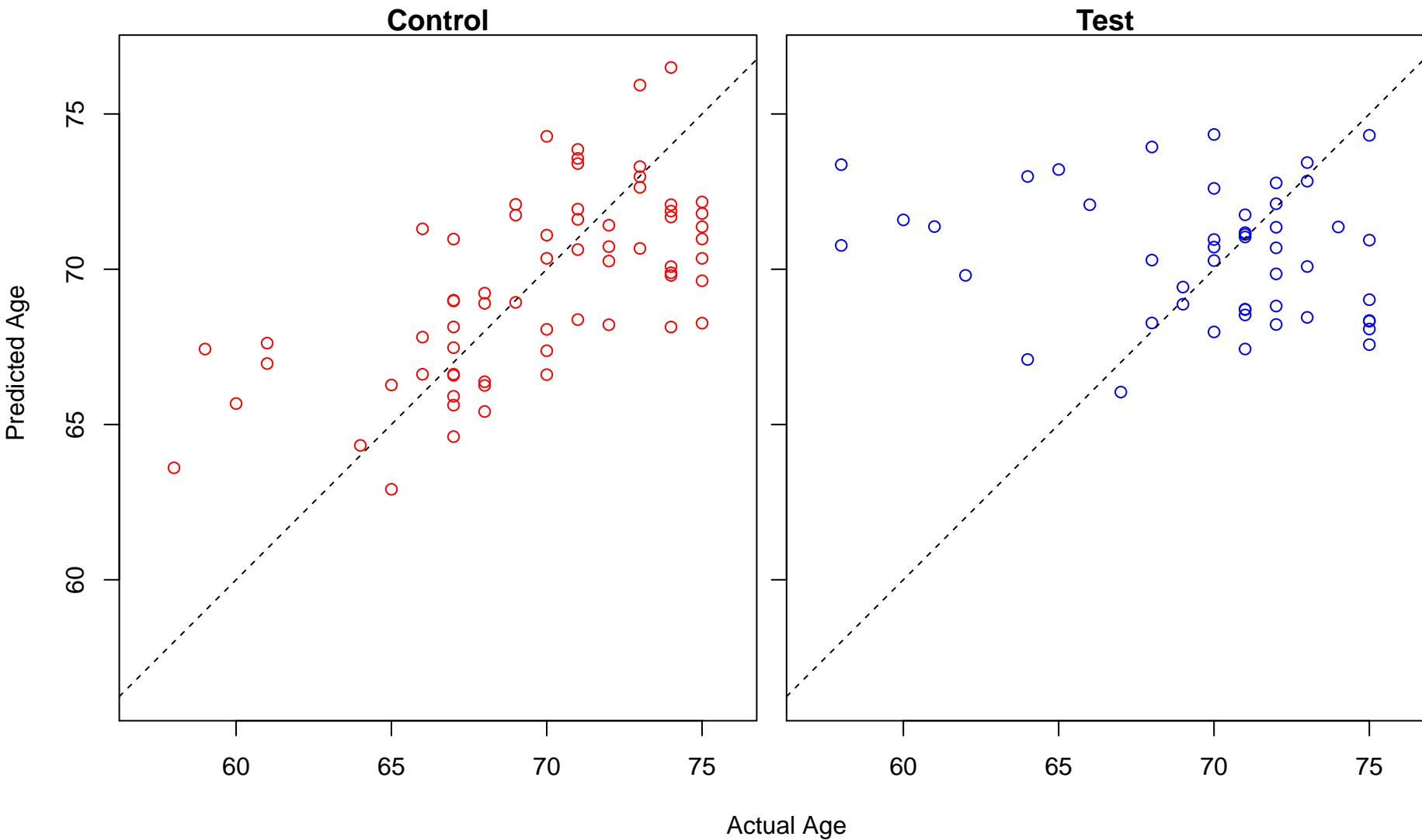
anion homeostasis (Score: 1.120870)



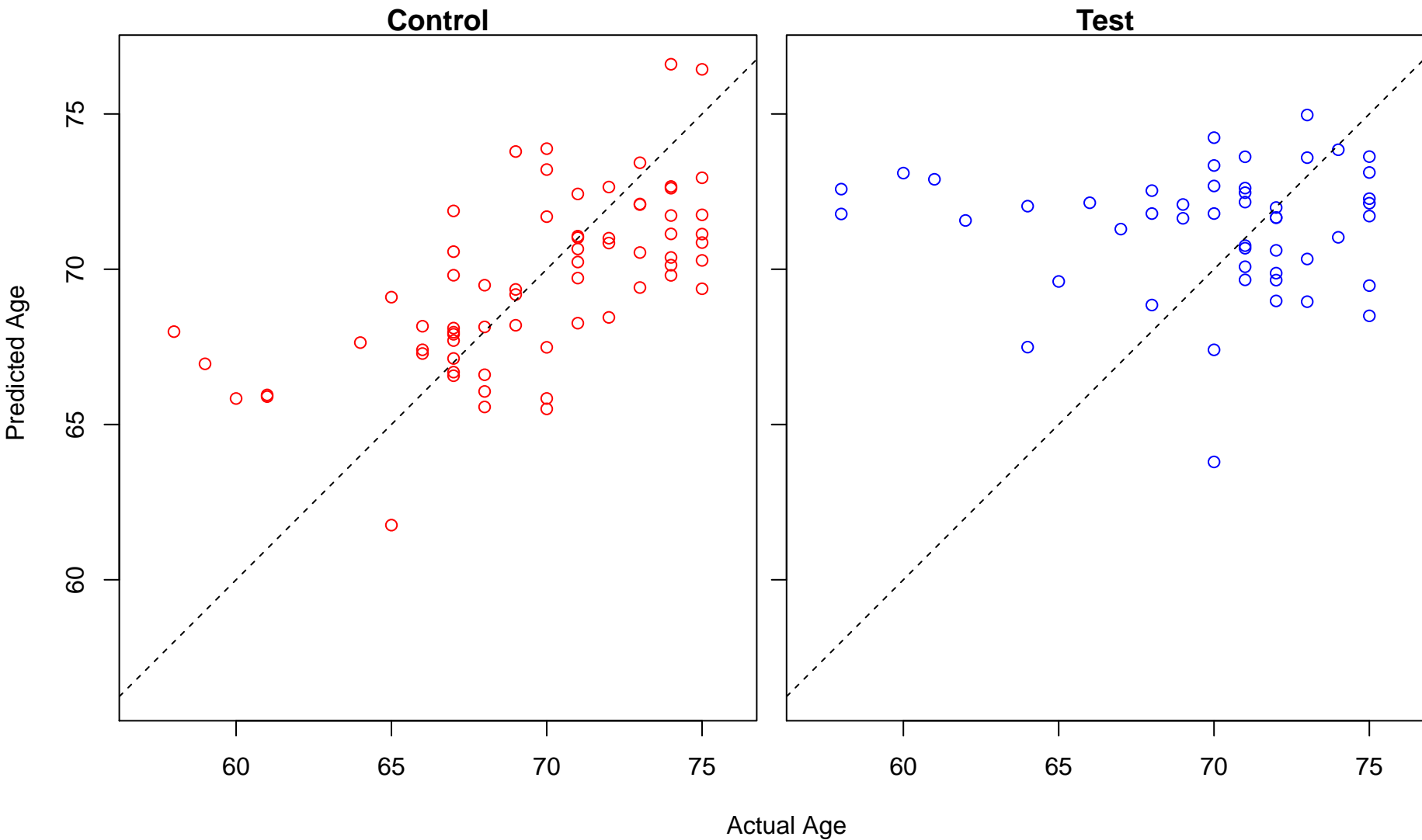
potassium ion transport (Score: 1.120841)



B cell mediated immunity (Score: 1.120623)

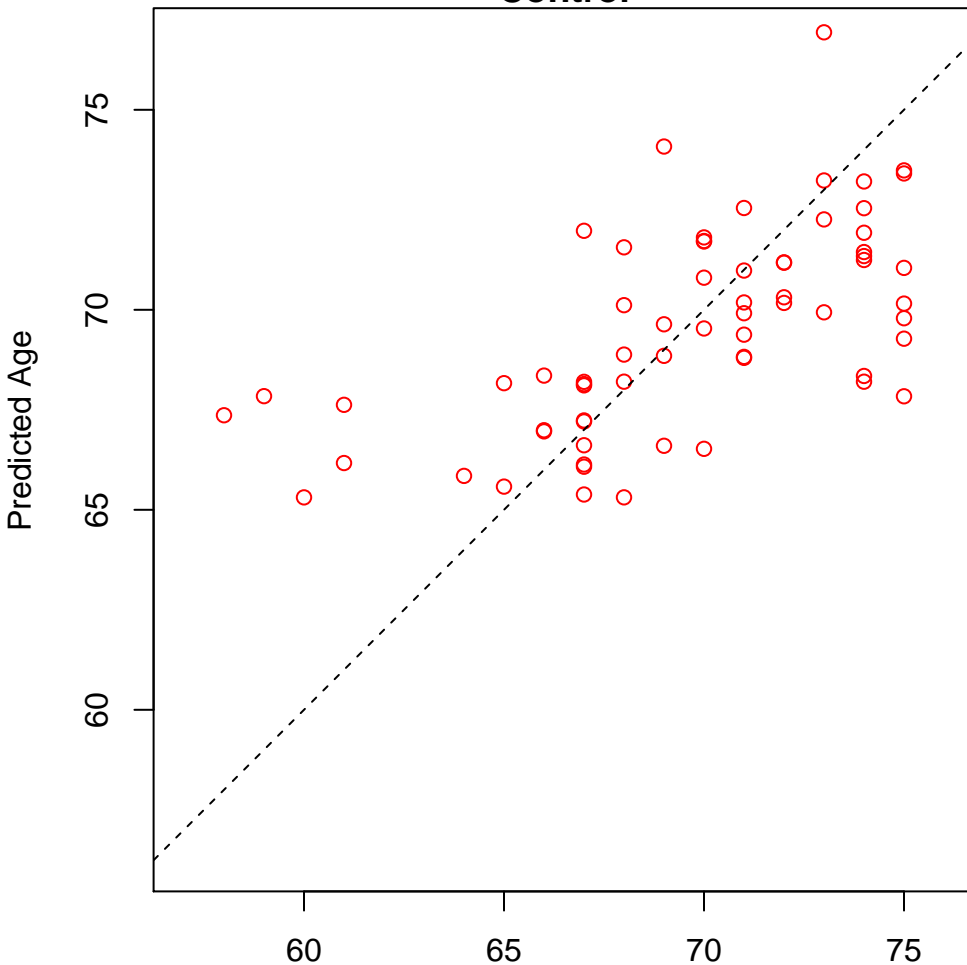


T cell migration (Score: 1.120511)

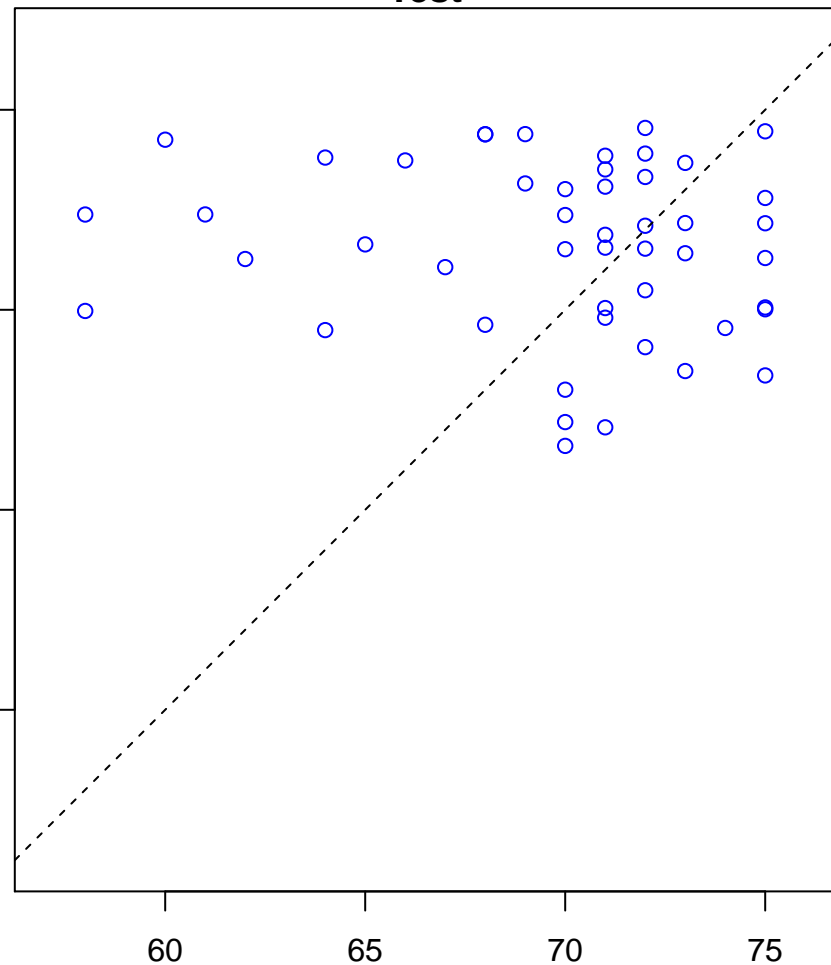


glycerophospholipid catabolic process (Score: 1.120273)

Control

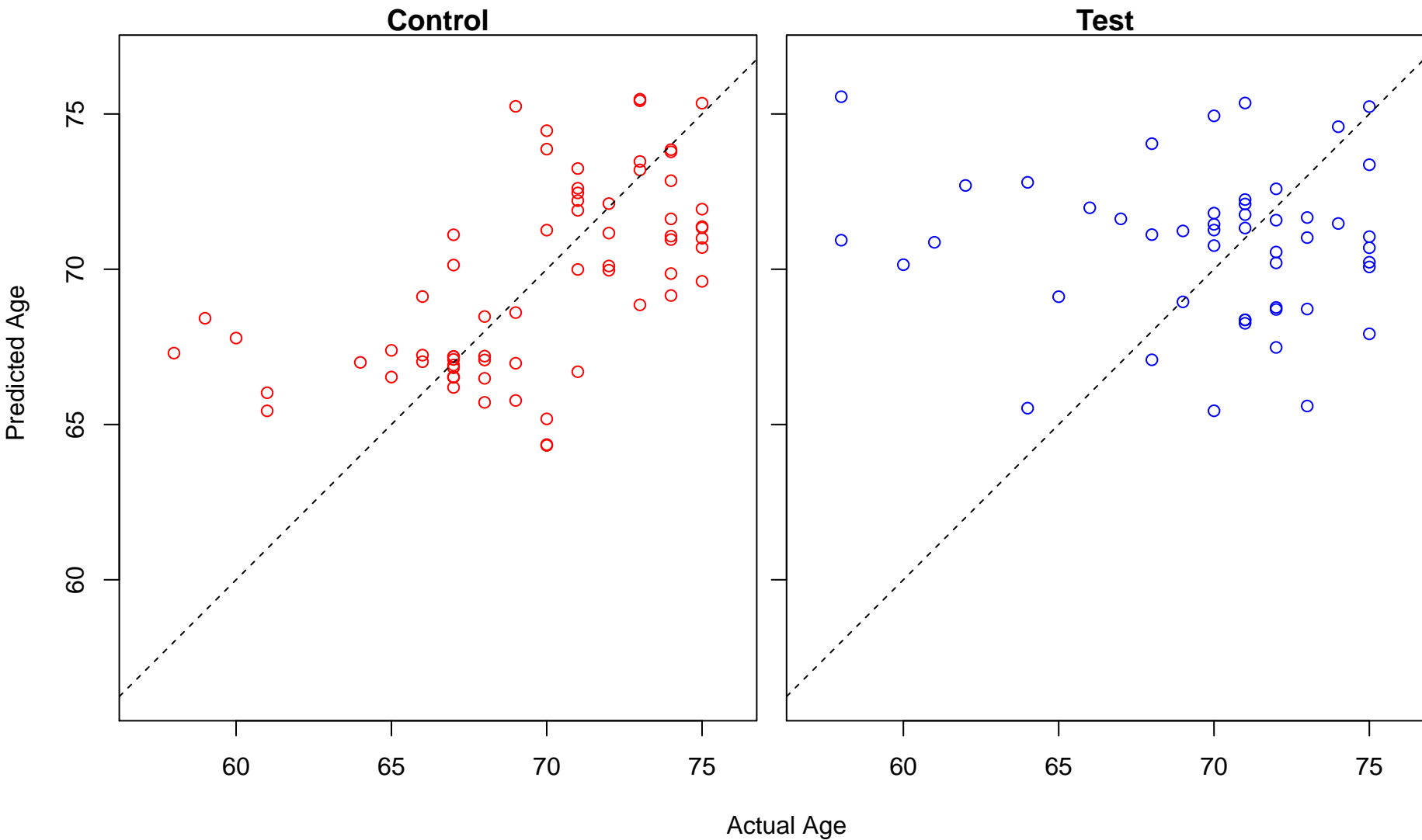


Test

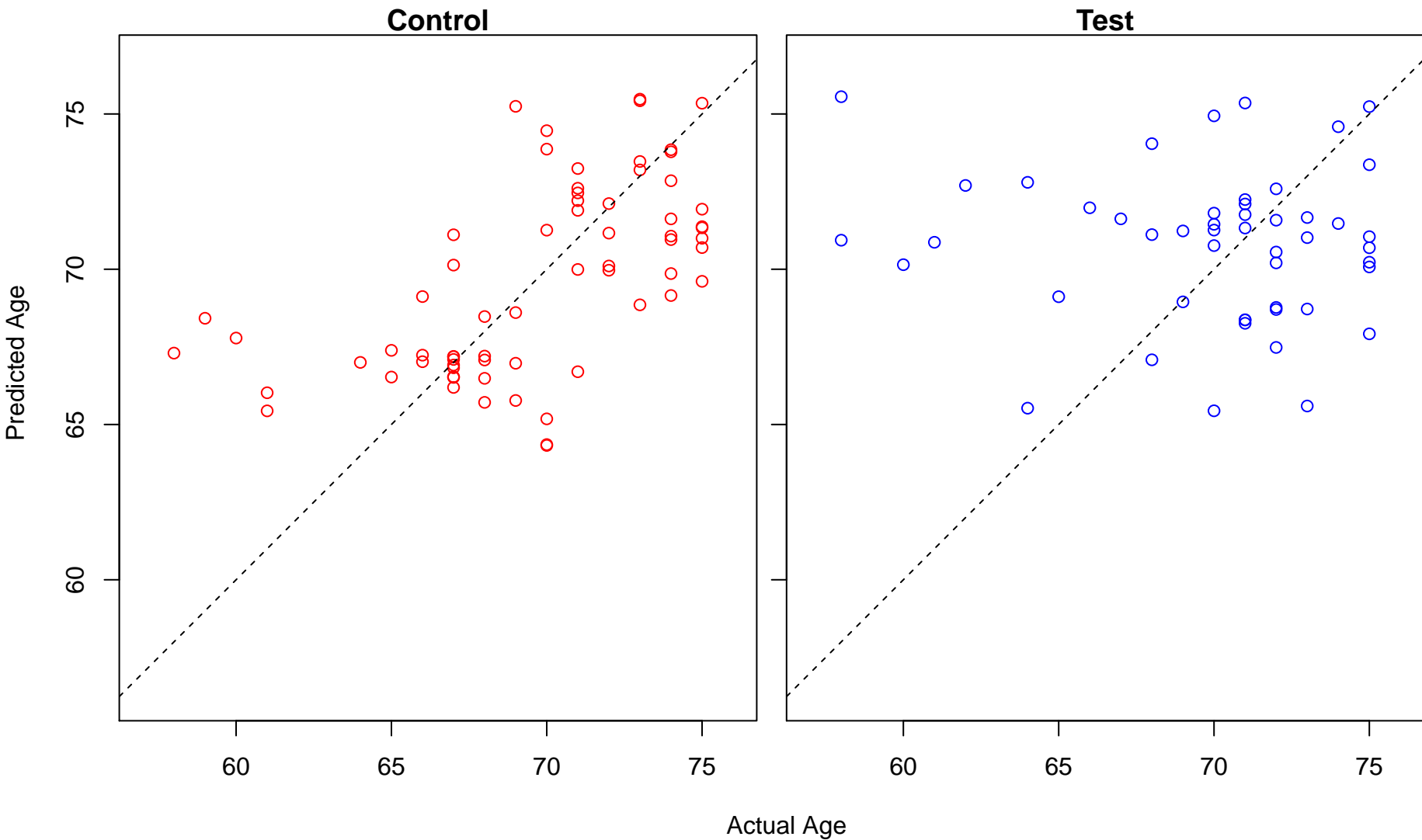


Actual Age

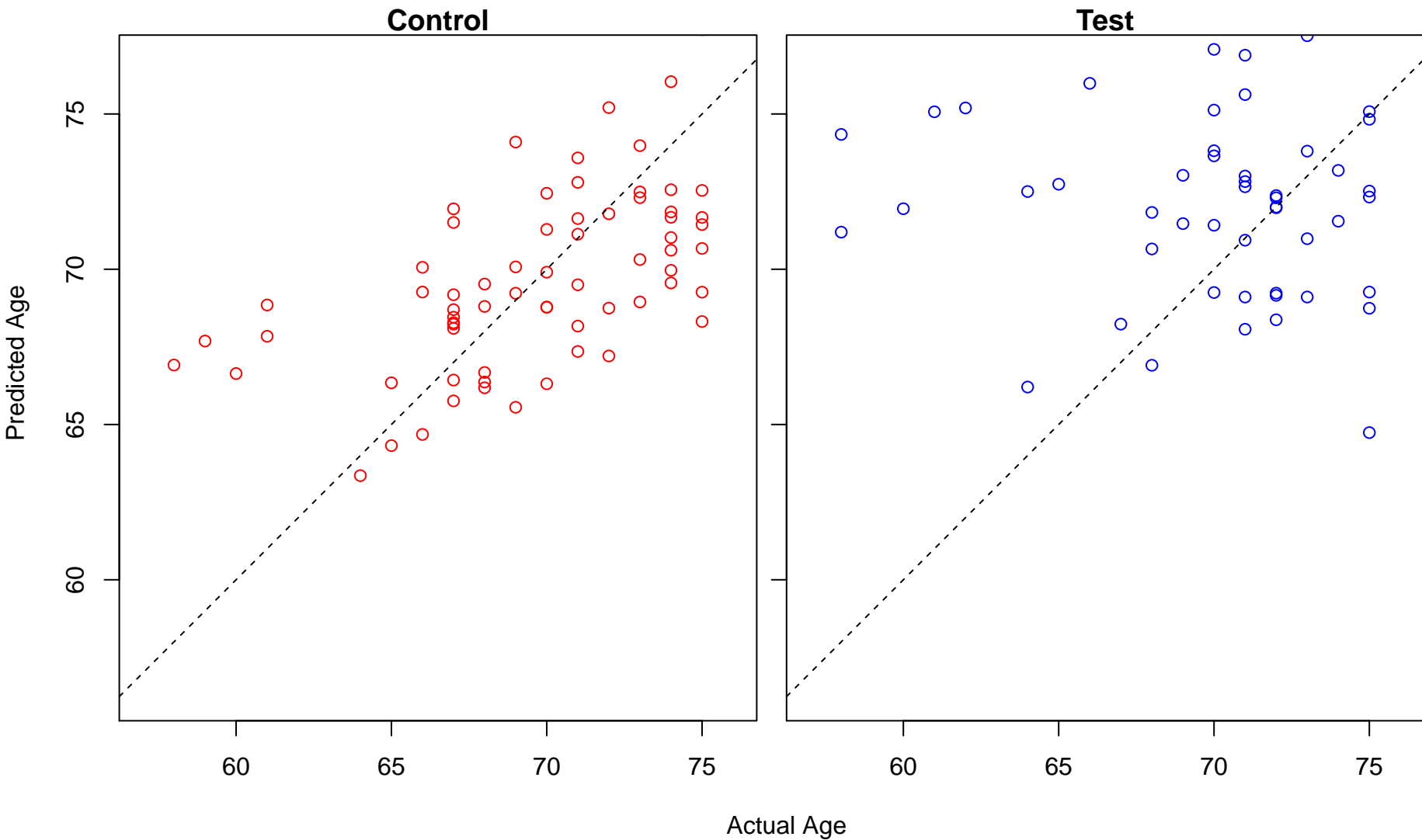
synaptic vesicle transport (Score: 1.119689)



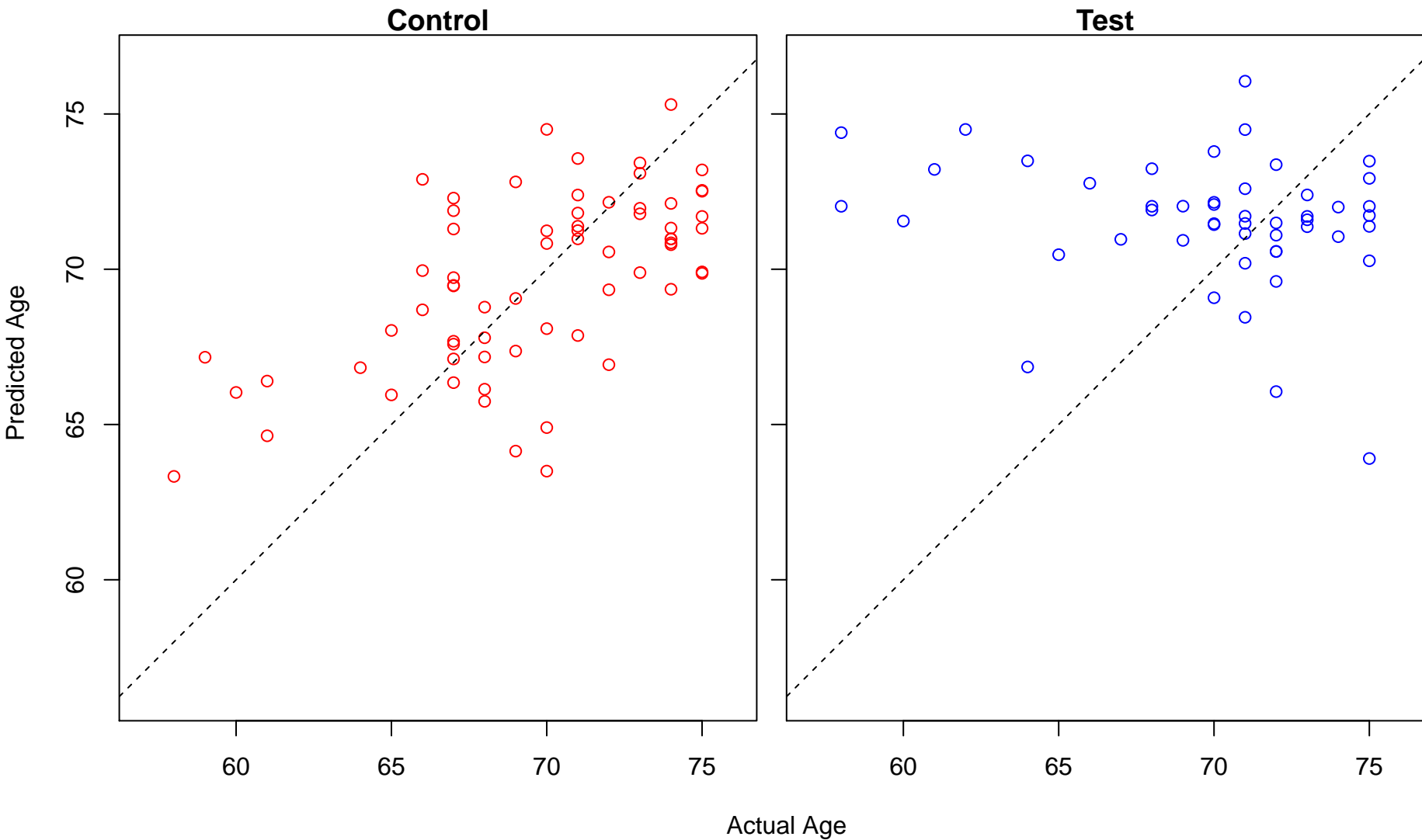
establishment of synaptic vesicle localization (Score: 1.119689)



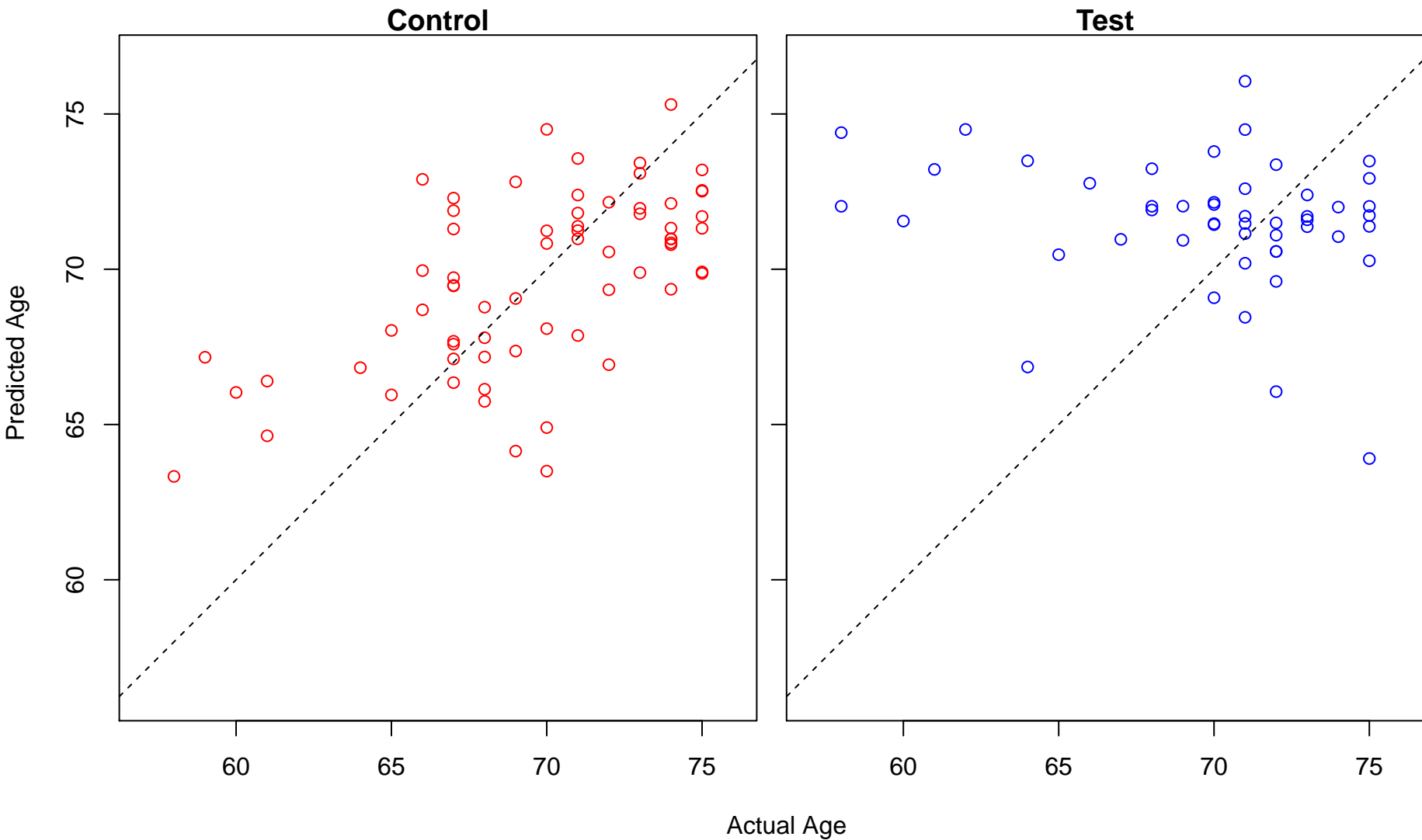
visual learning (Score: 1.119212)



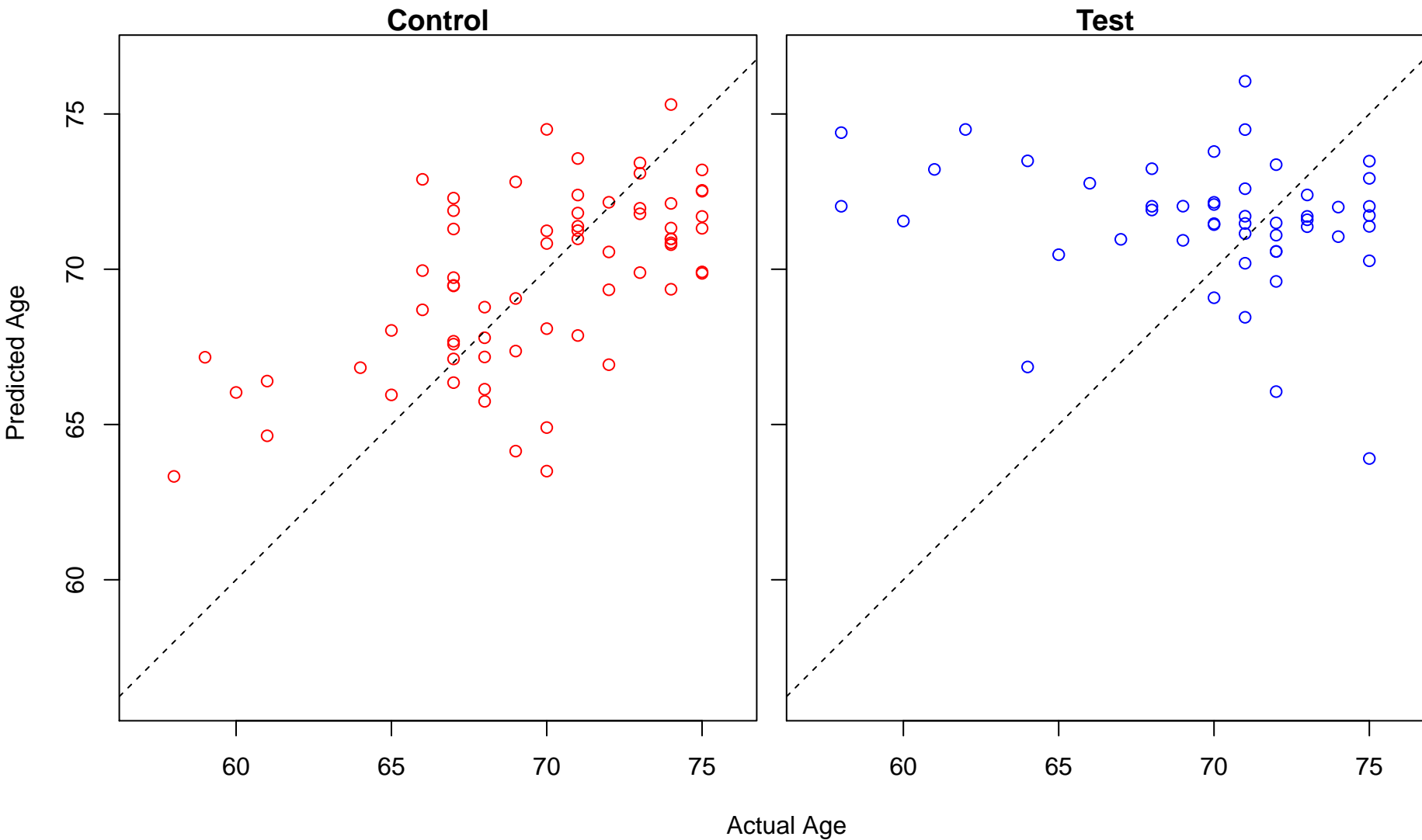
histidine metabolic process (Score: 1.118968)



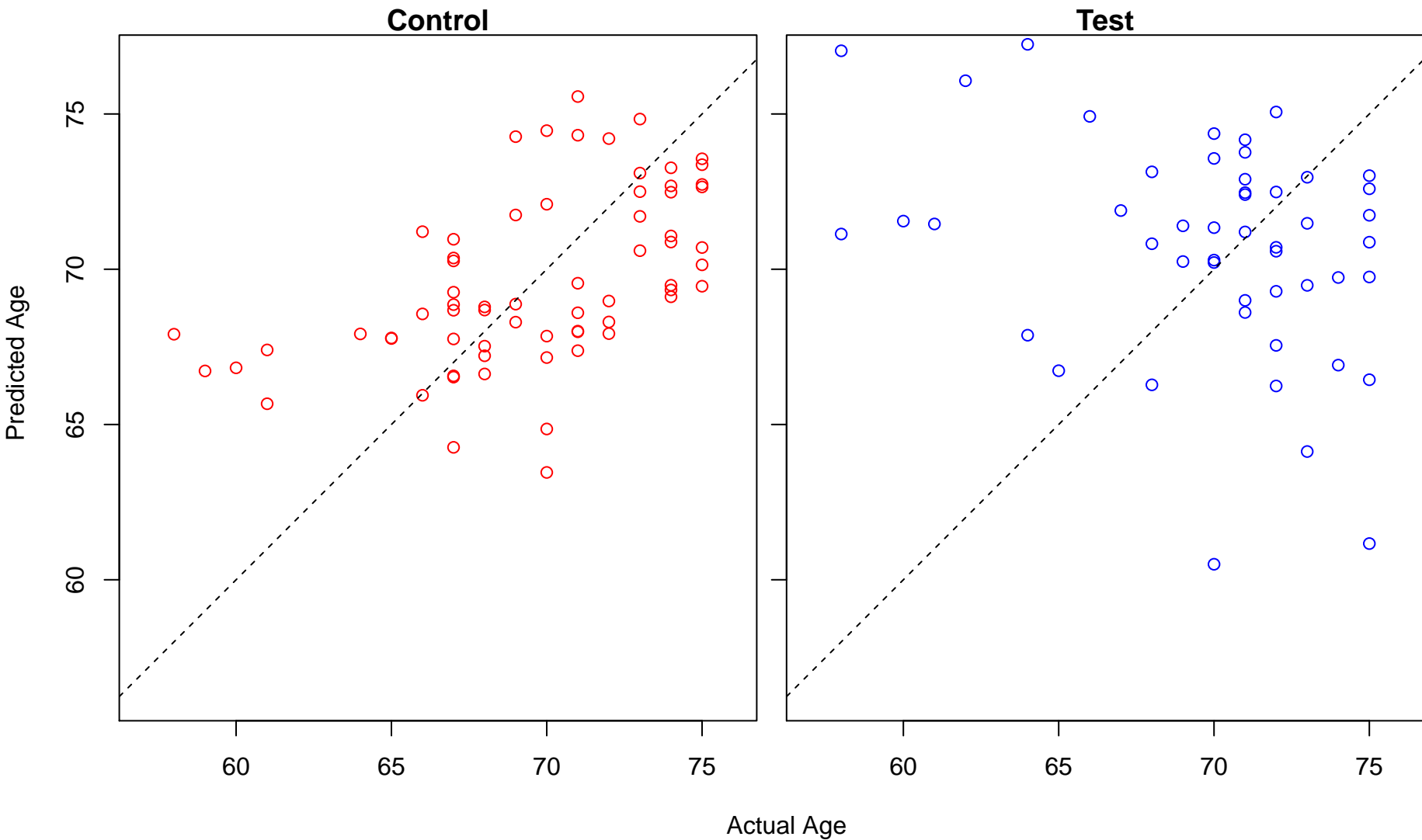
histidine catabolic process (Score: 1.118968)



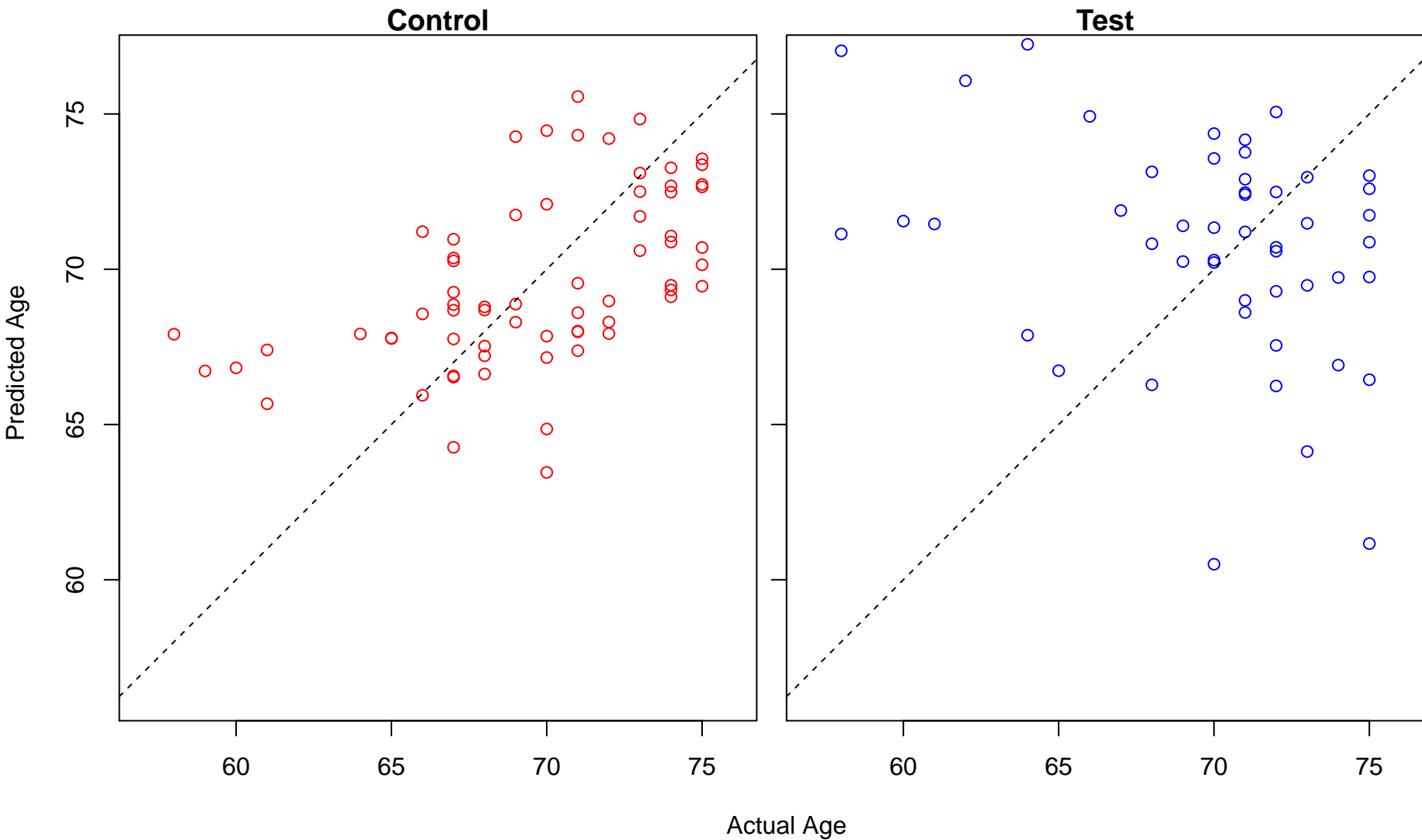
imidazole-containing compound catabolic process (Score: 1.118968)



positive regulation of sphingolipid biosynthetic process (Score: 1.118884)

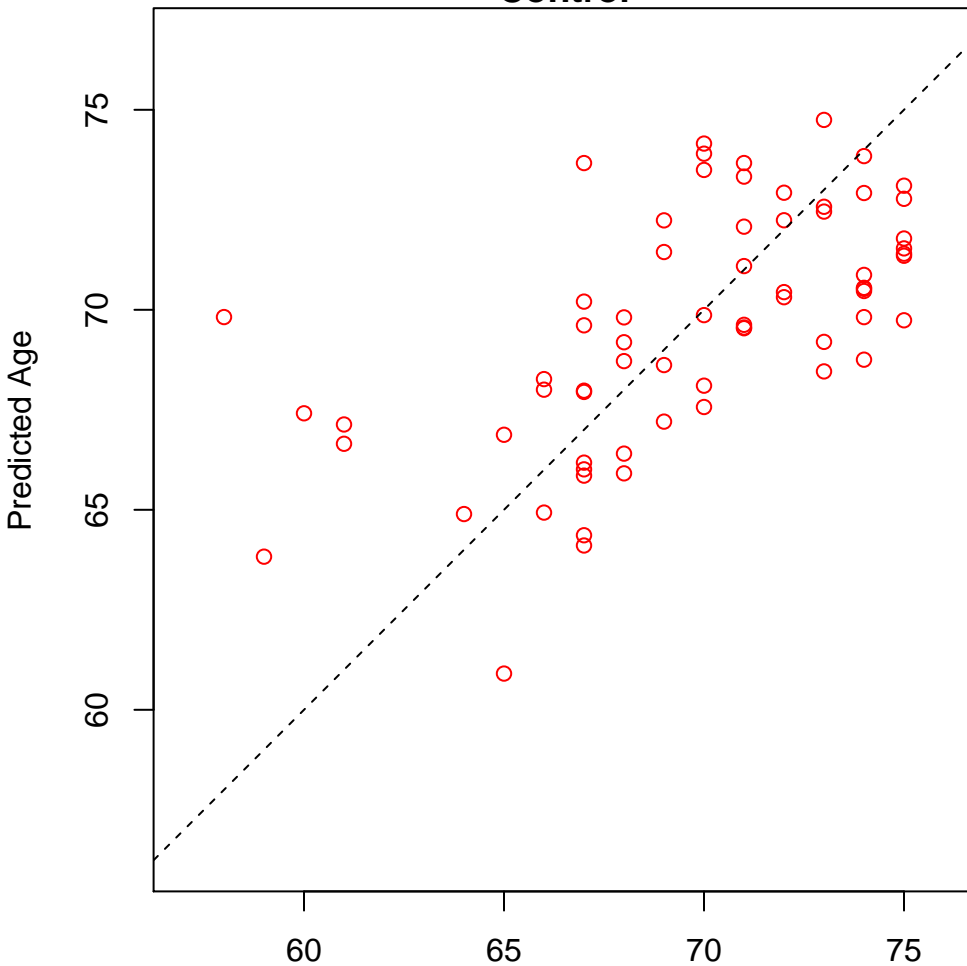


positive regulation of ceramide biosynthetic process (Score: 1.118884)

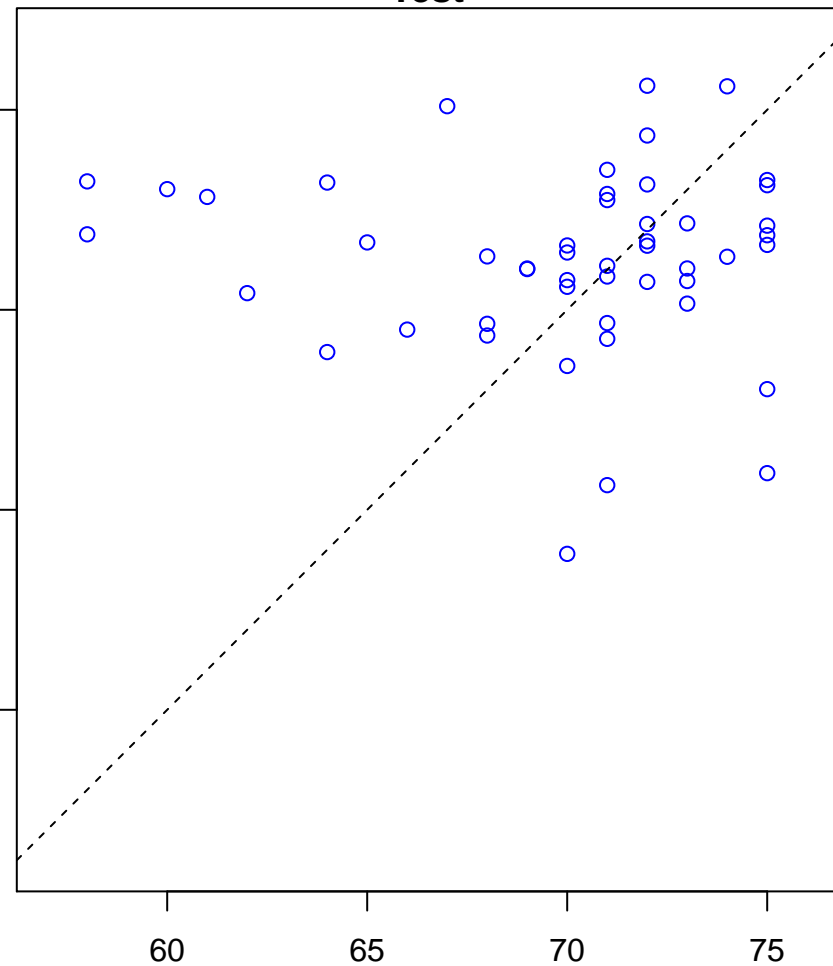


regulation of epidermal cell differentiation (Score: 1.118532)

Control

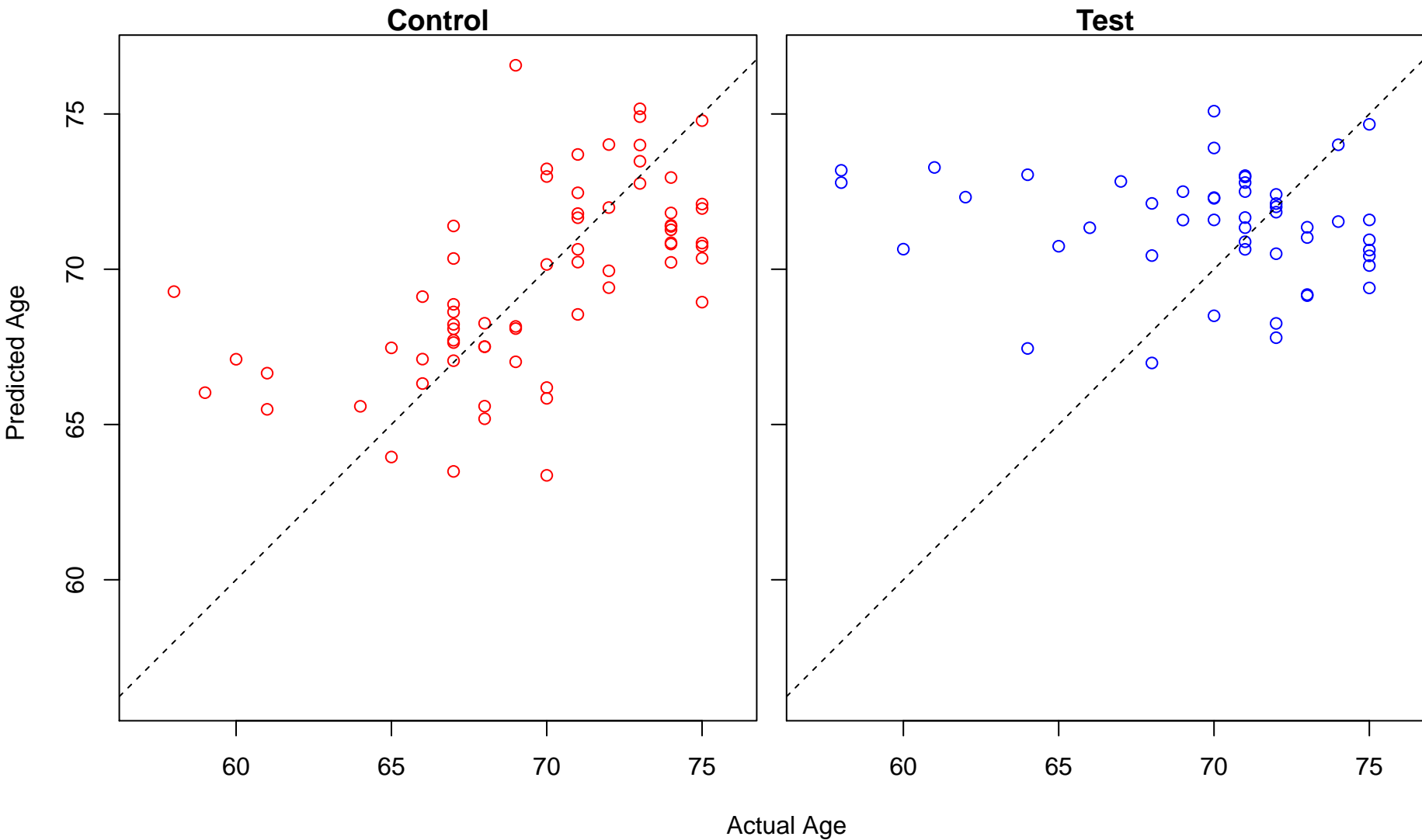


Test

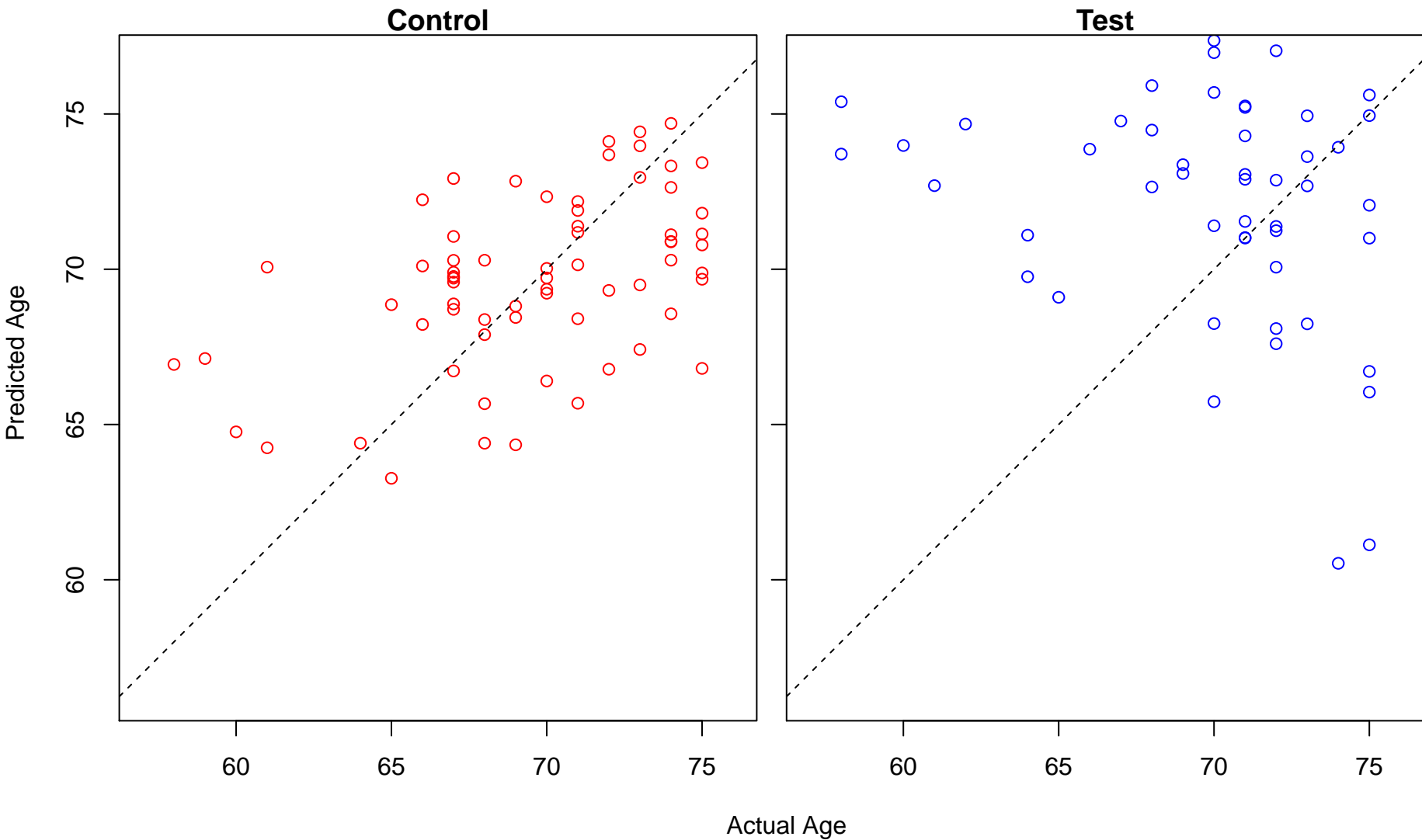


Actual Age

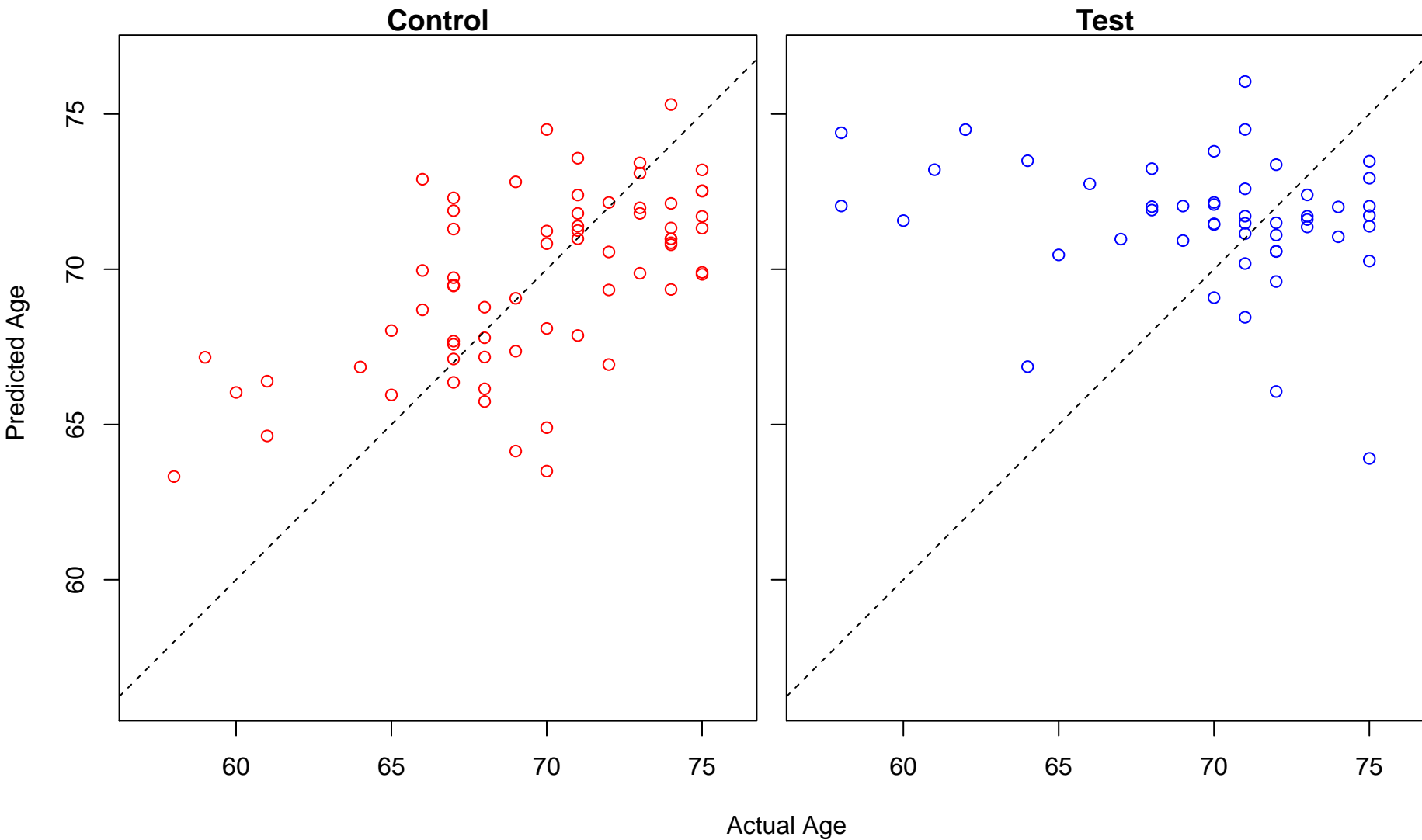
regulation of regulated secretory pathway (Score: 1.118367)



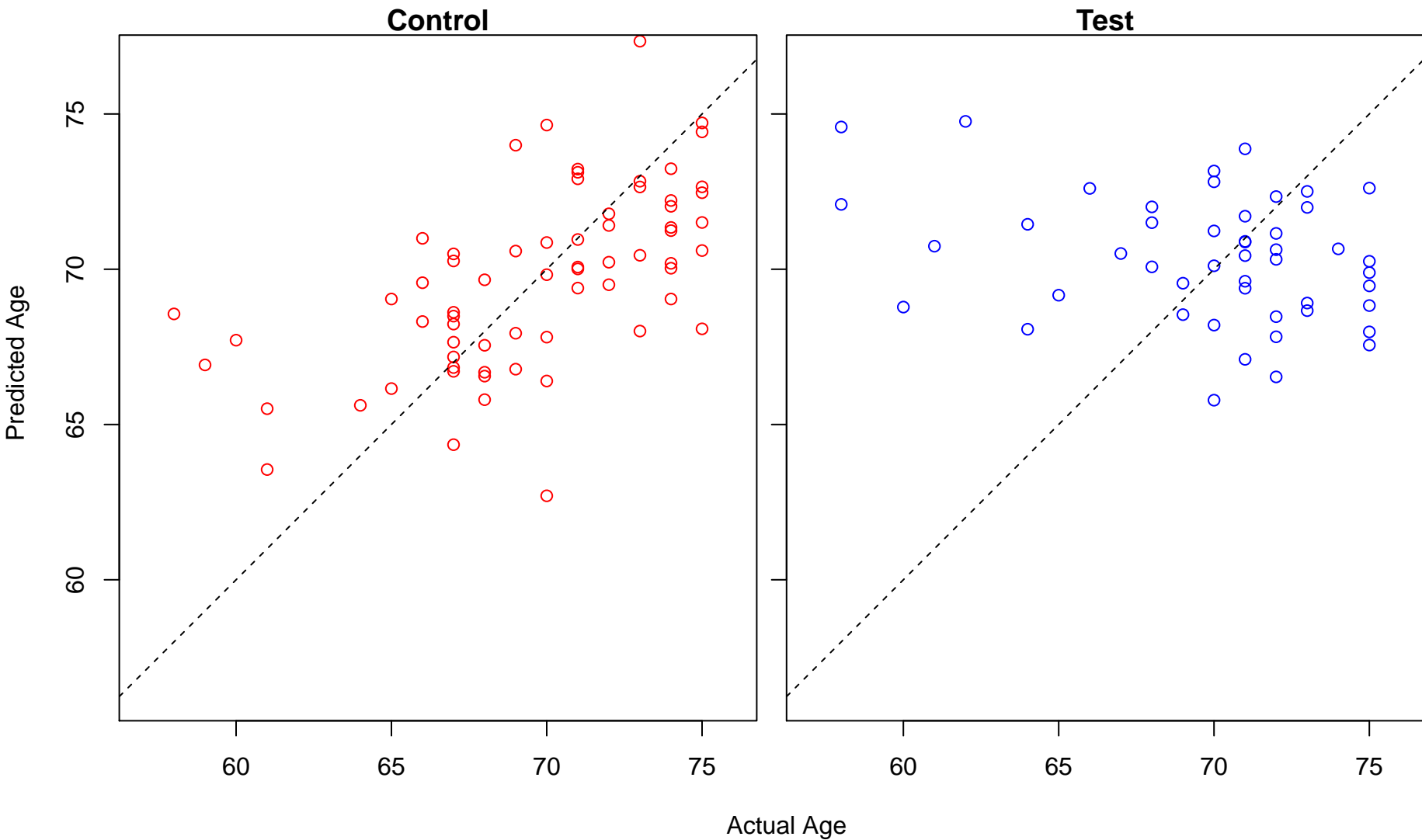
sodium-independent organic anion transport (Score: 1.118280)



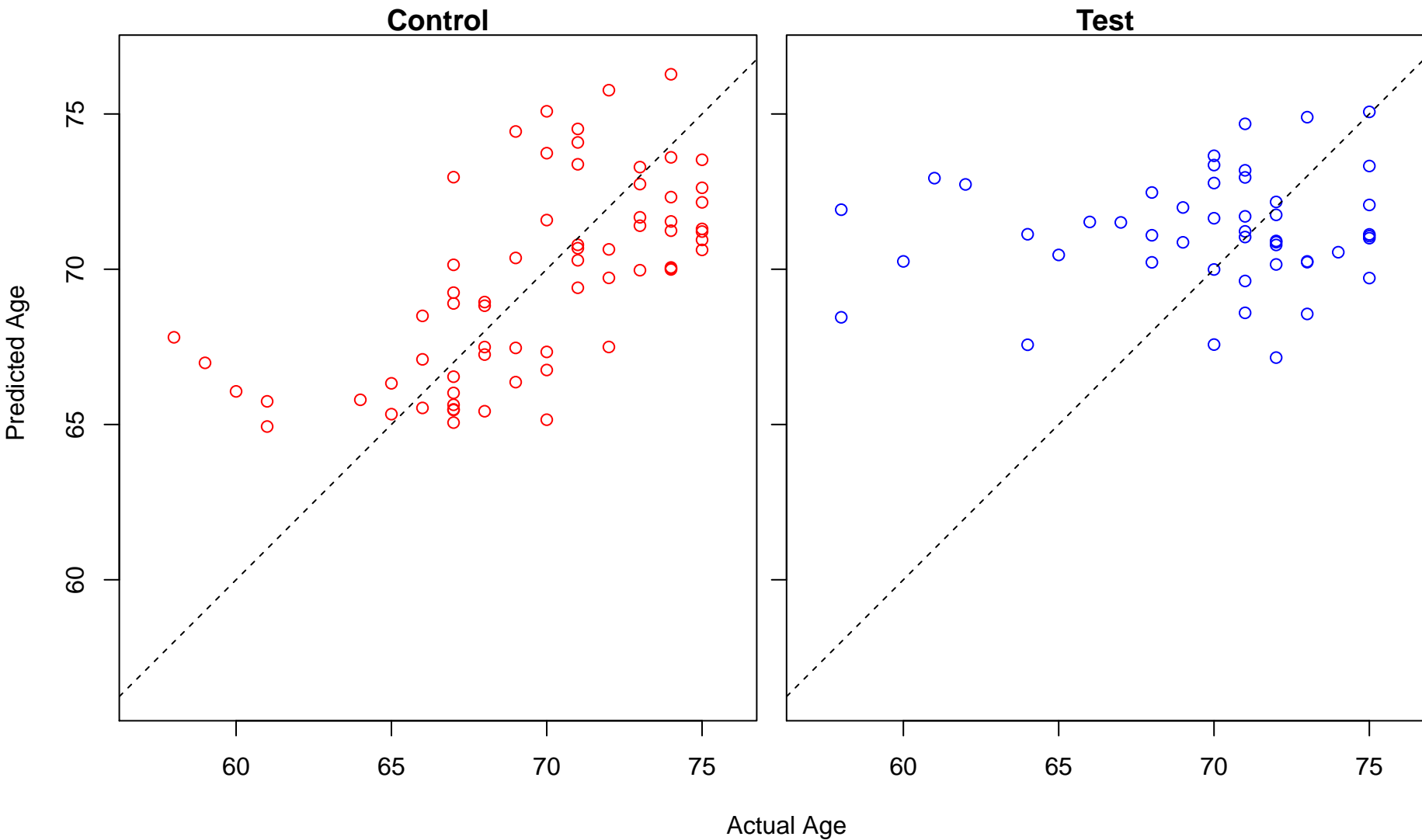
imidazole-containing compound metabolic process (Score: 1.117944)



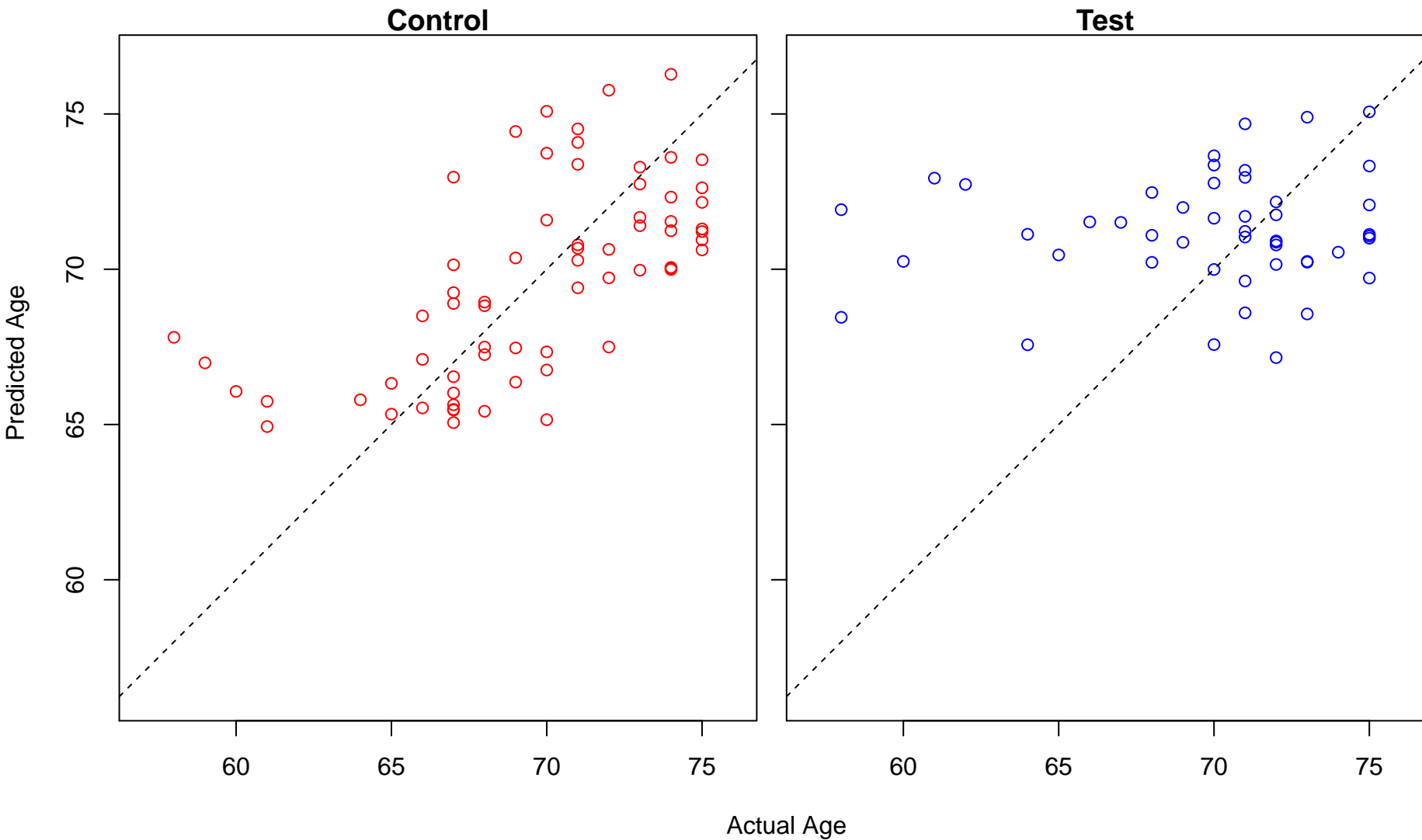
extrinsic apoptotic signaling pathway via death domain receptors (Score: 1.117504)



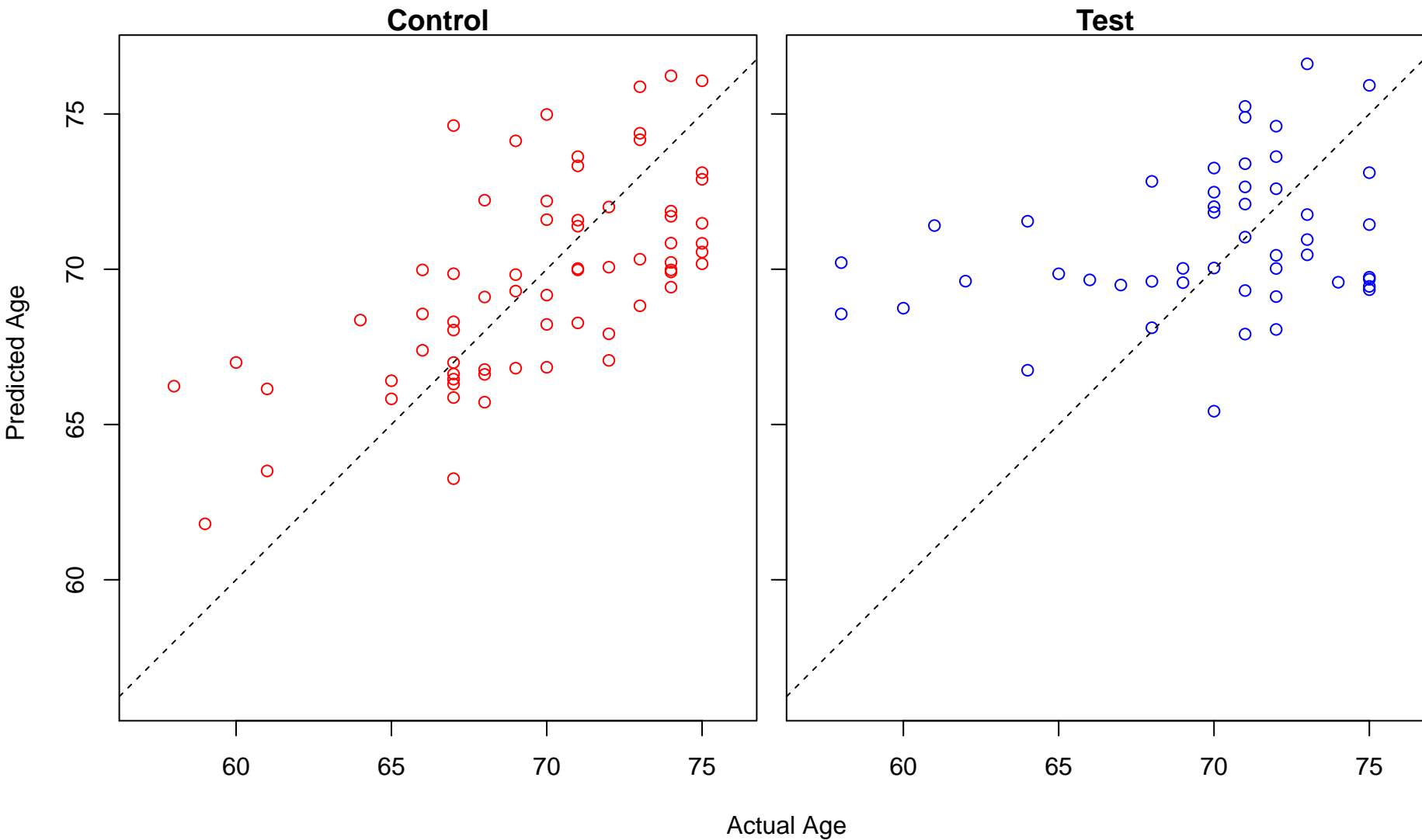
platelet formation (Score: 1.117309)



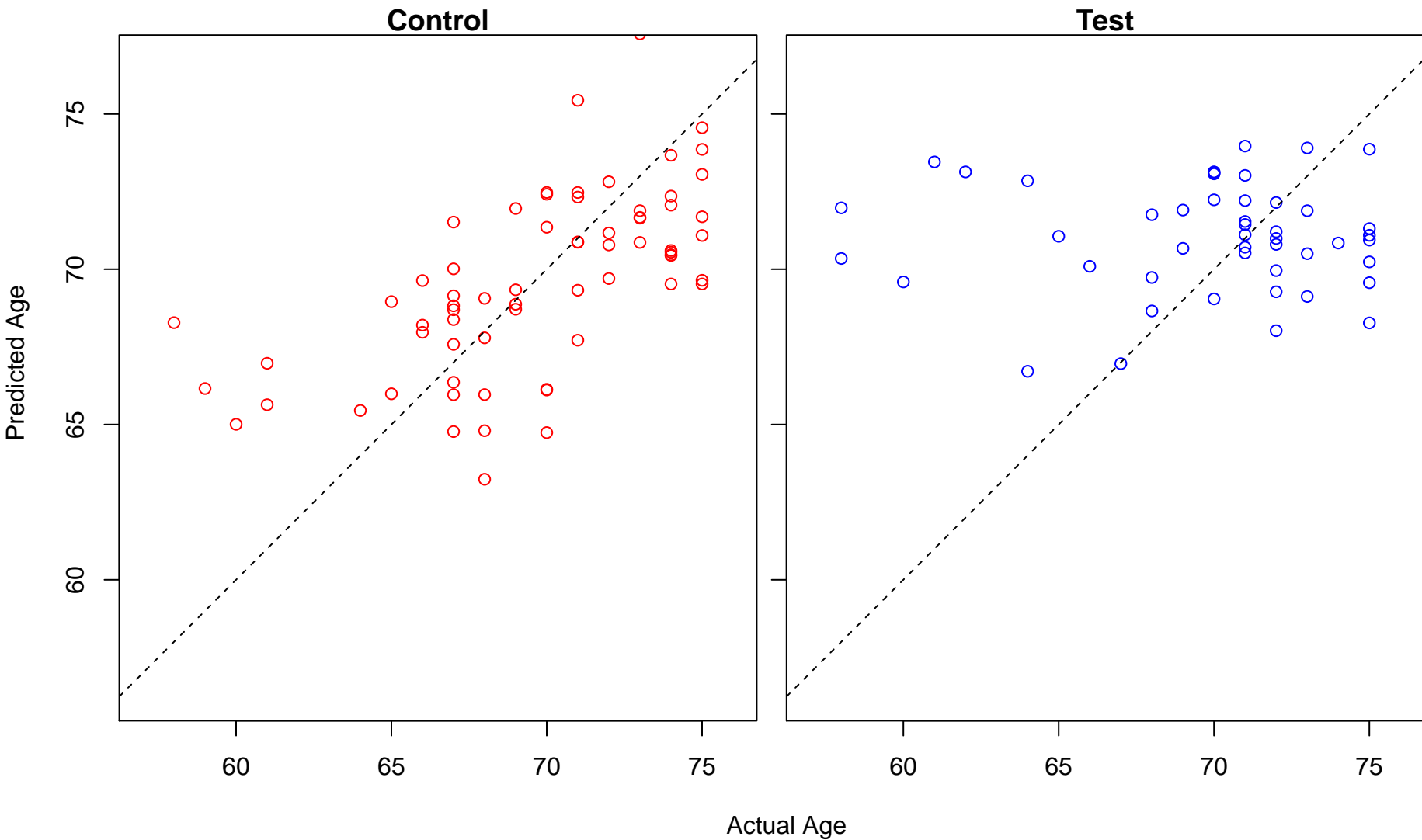
platelet morphogenesis (Score: 1.117309)



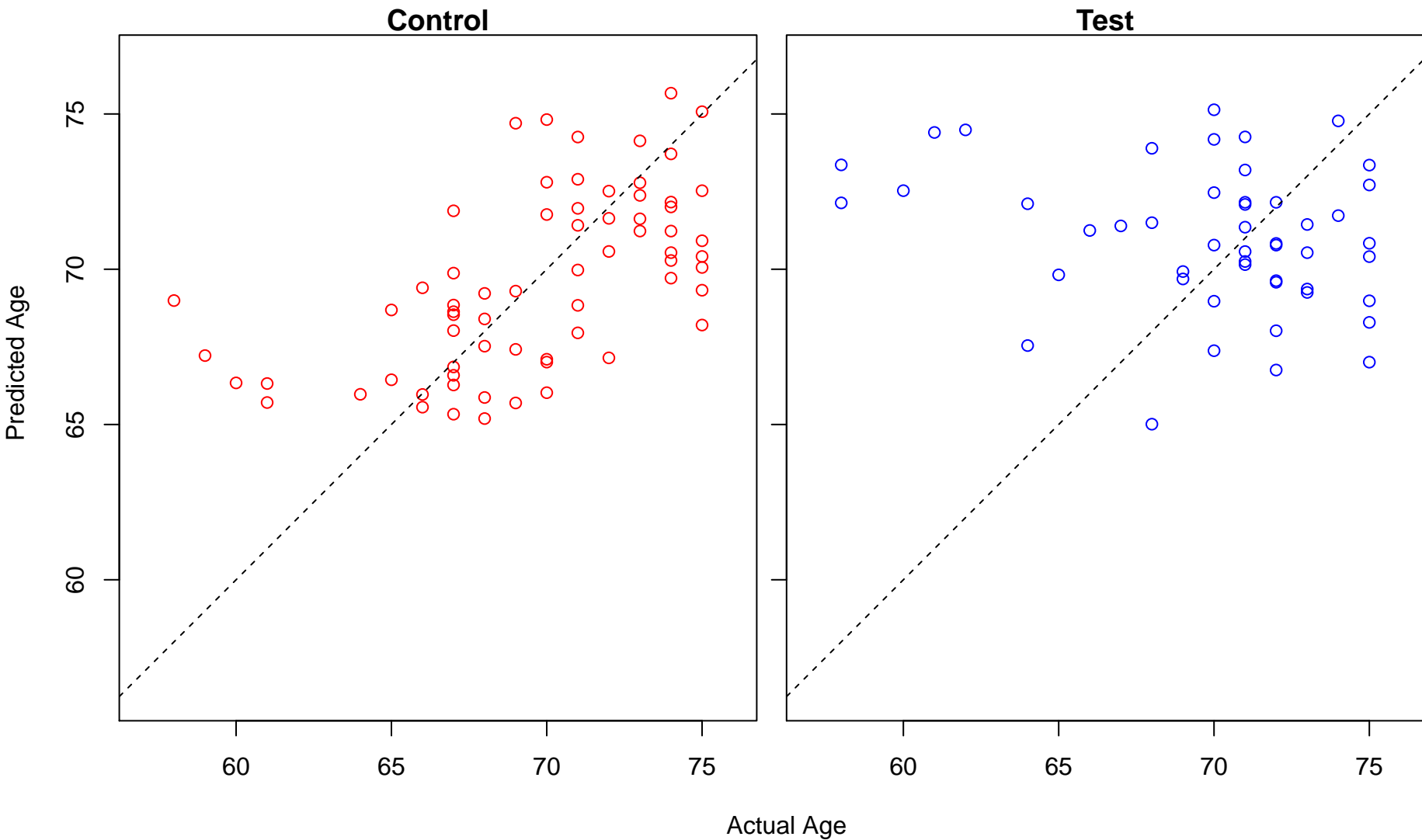
misfolded or incompletely synthesized protein catabolic process (Score: 1.117175)



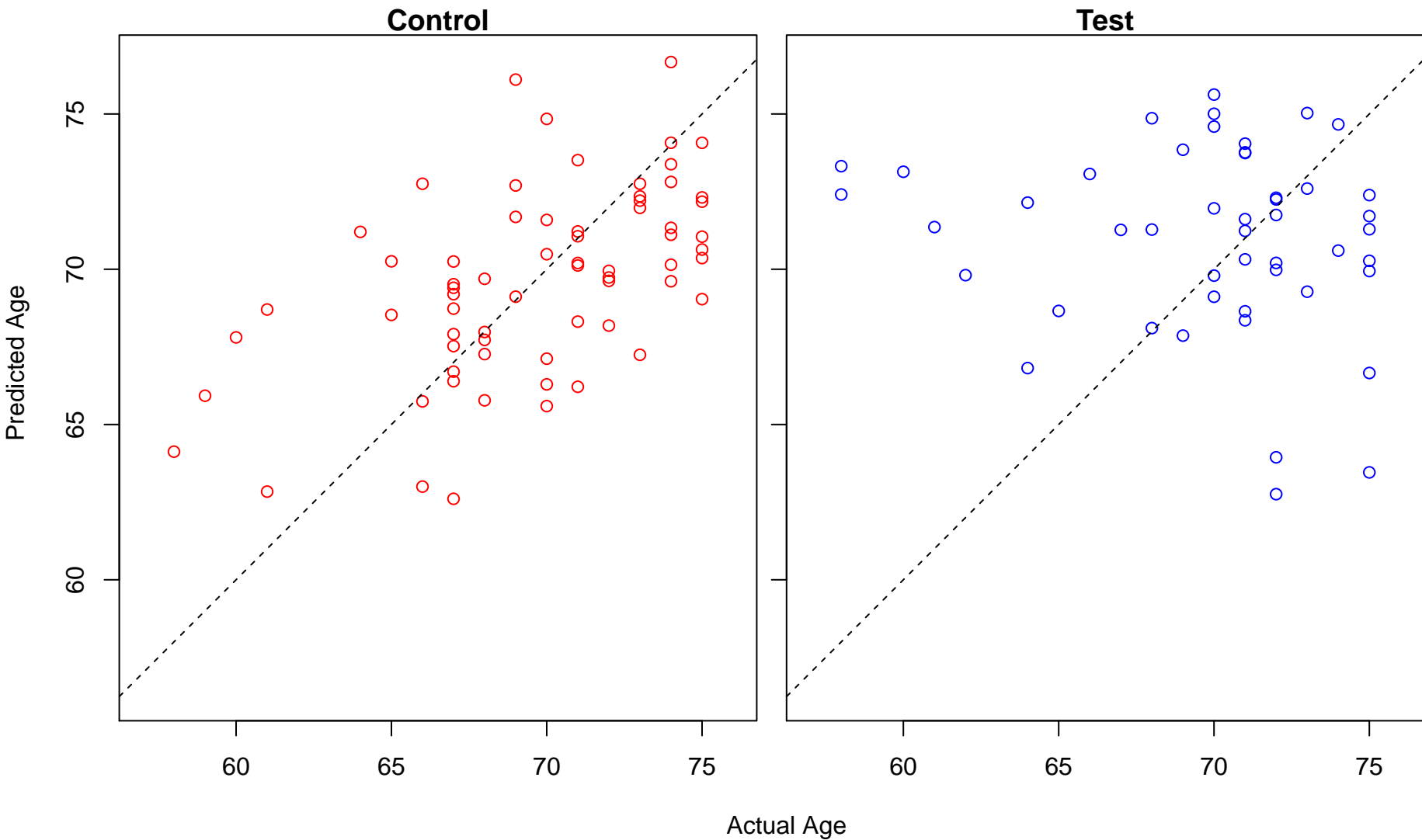
nucleoside diphosphate metabolic process (Score: 1.116232)



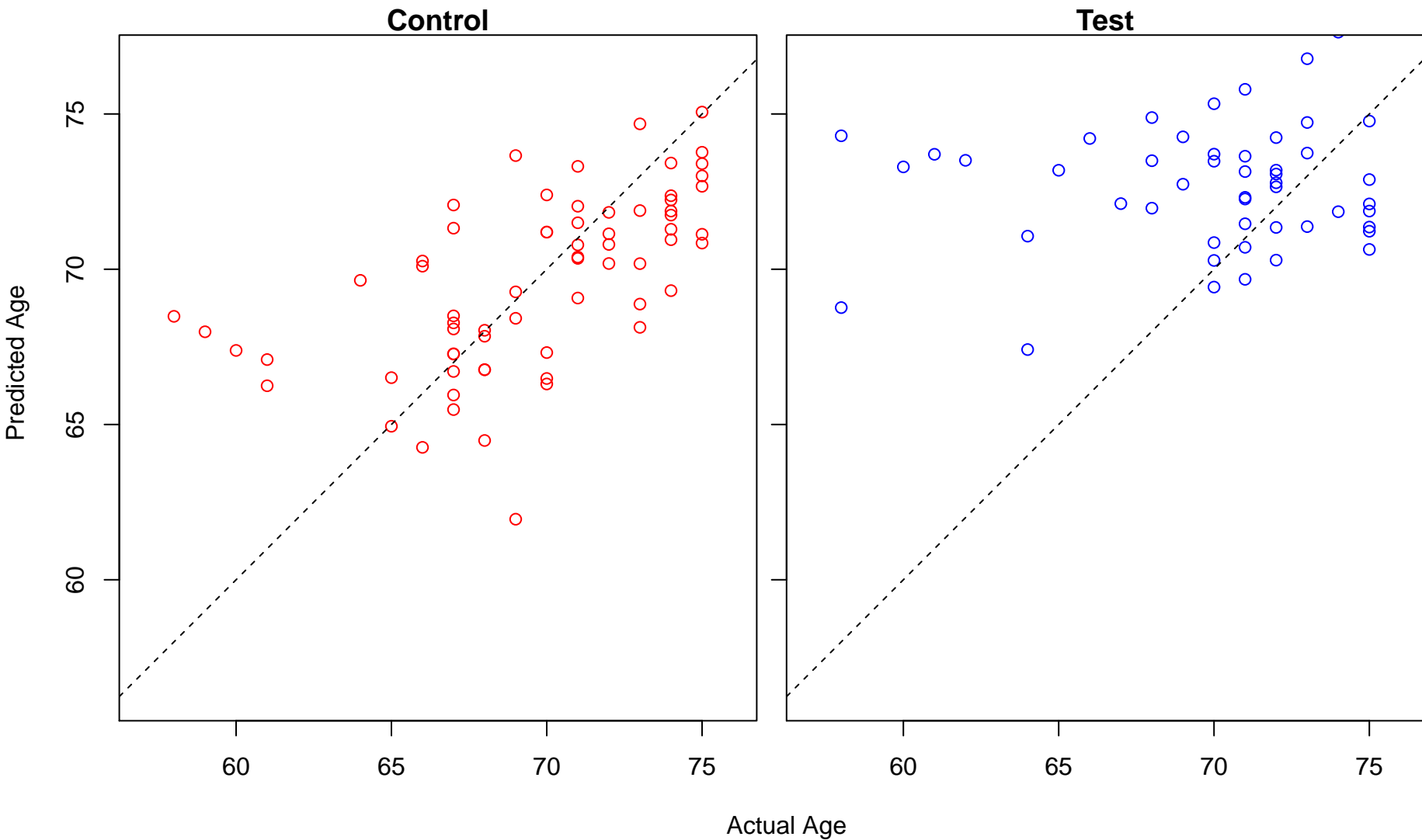
negative regulation of macroautophagy (Score: 1.116150)



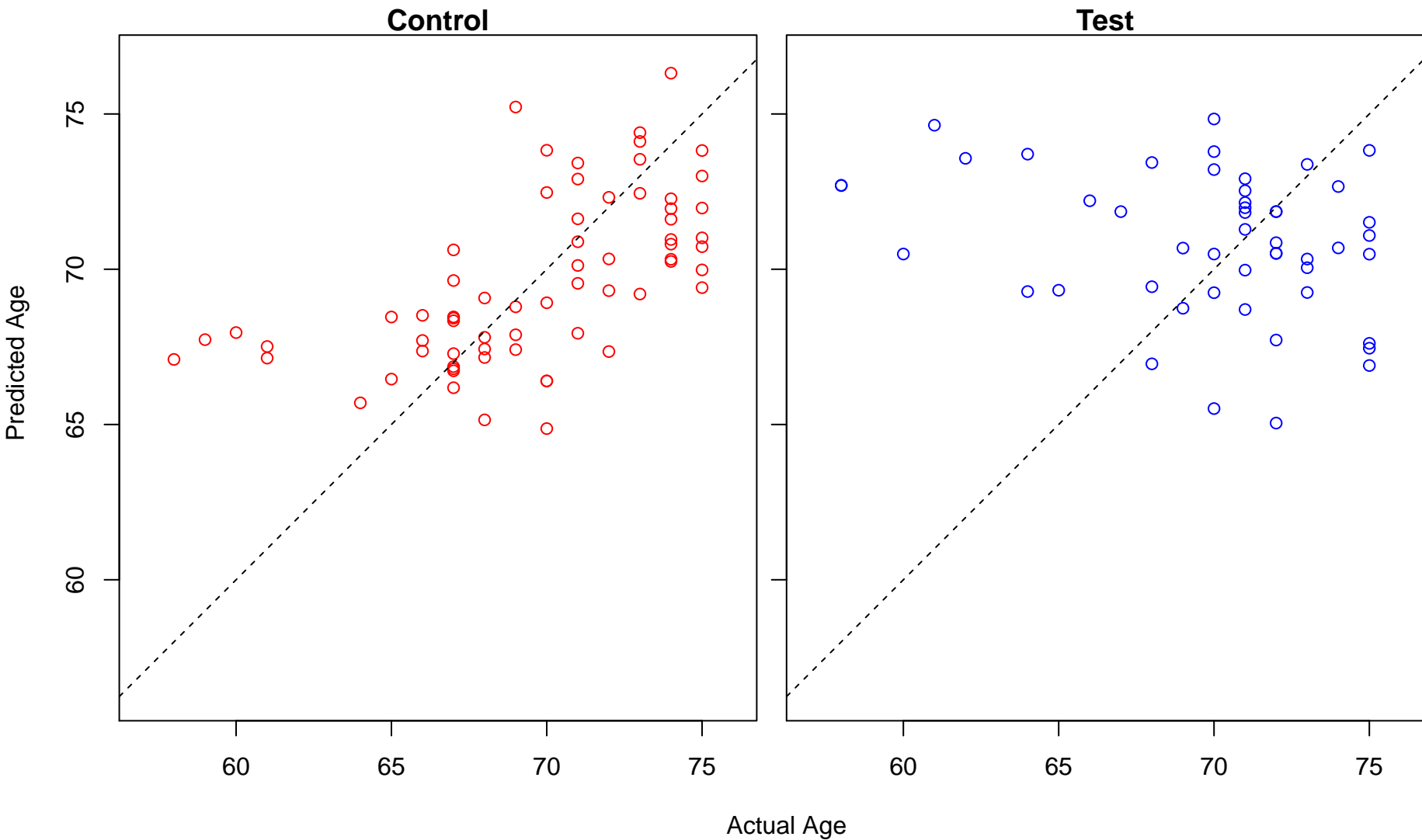
negative regulation of endoplasmic reticulum calcium ion concentration (Score: 1.115660)



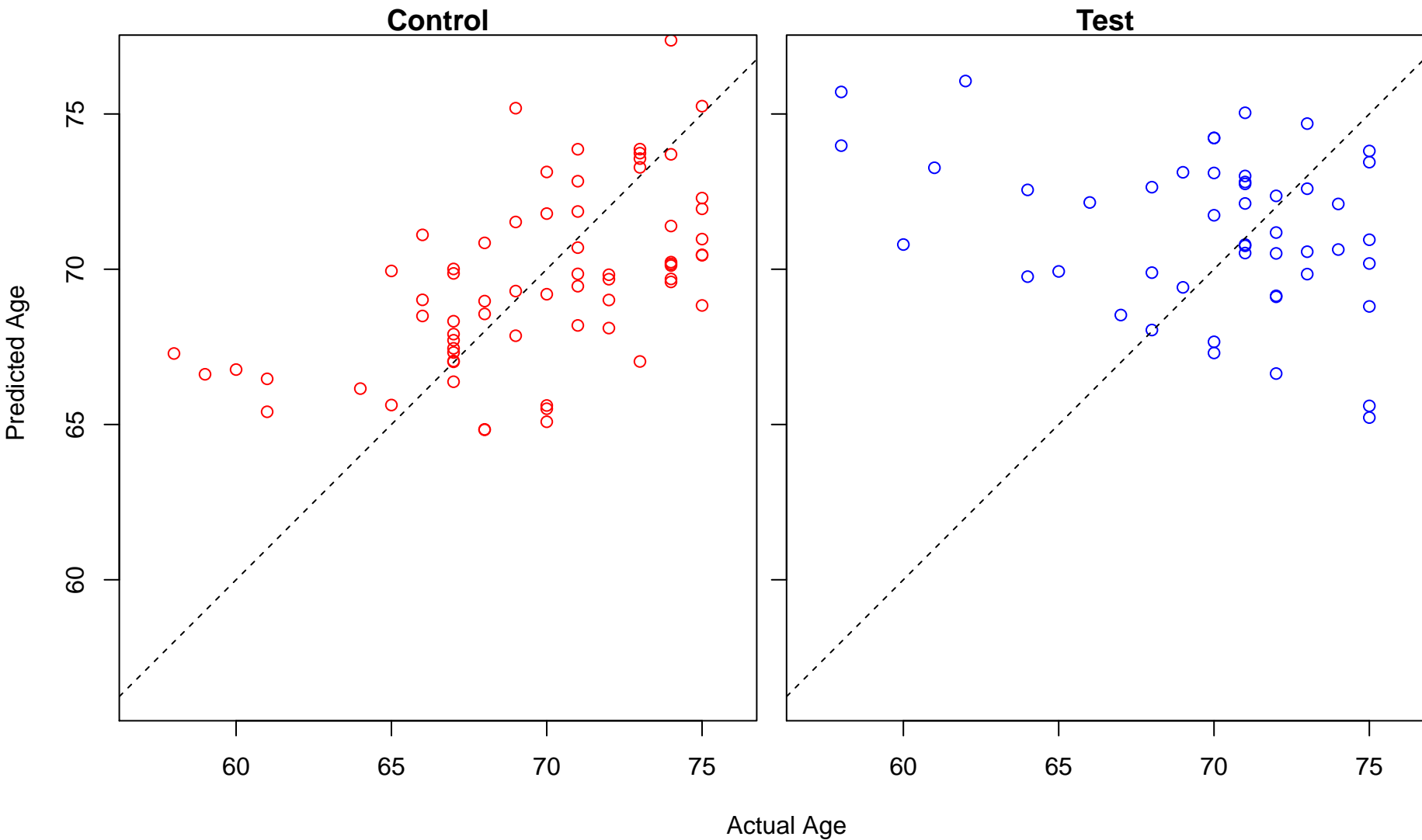
response to oxygen radical (Score: 1.115400)



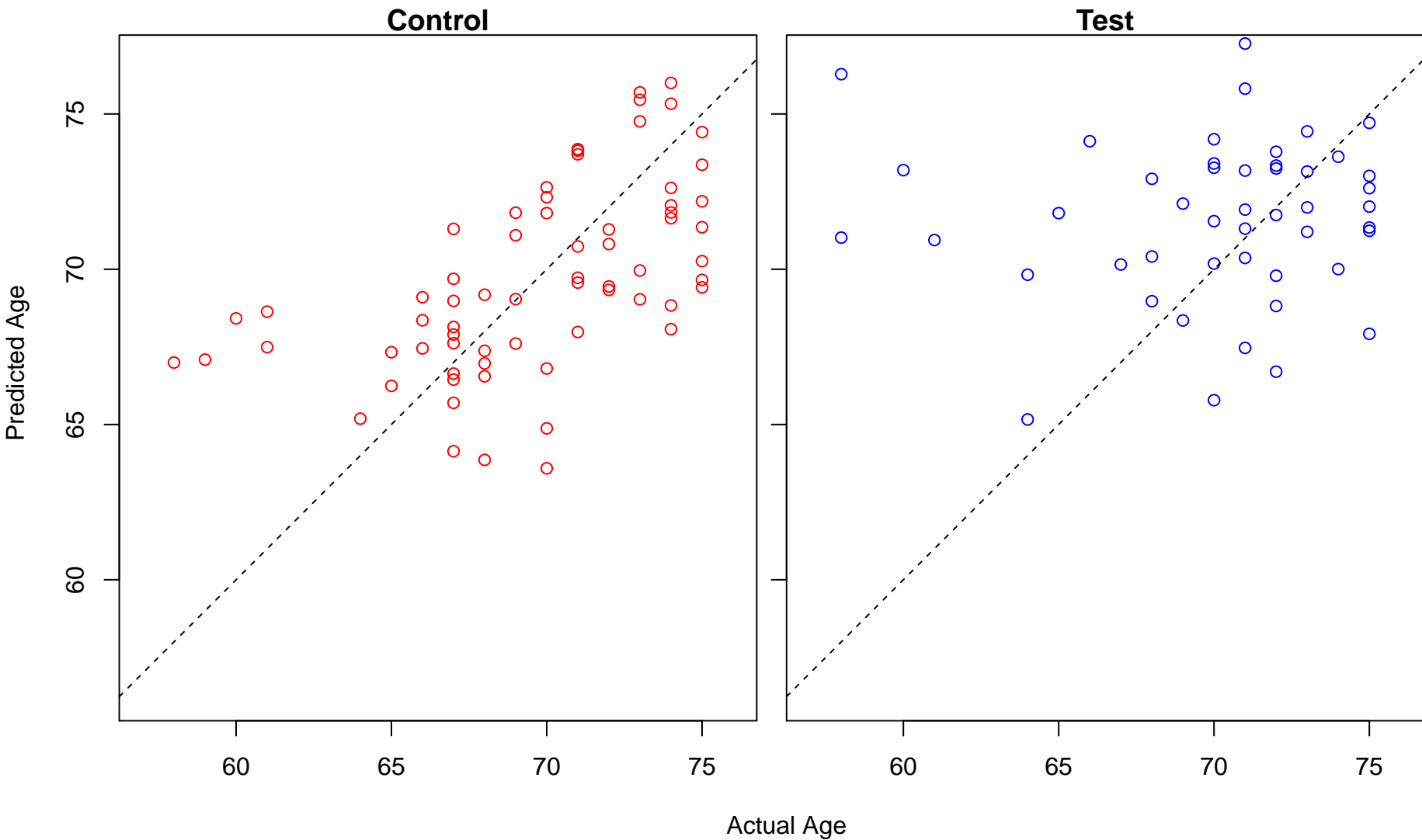
negative regulation of neurogenesis (Score: 1.115216)



regulation of inclusion body assembly (Score: 1.114628)

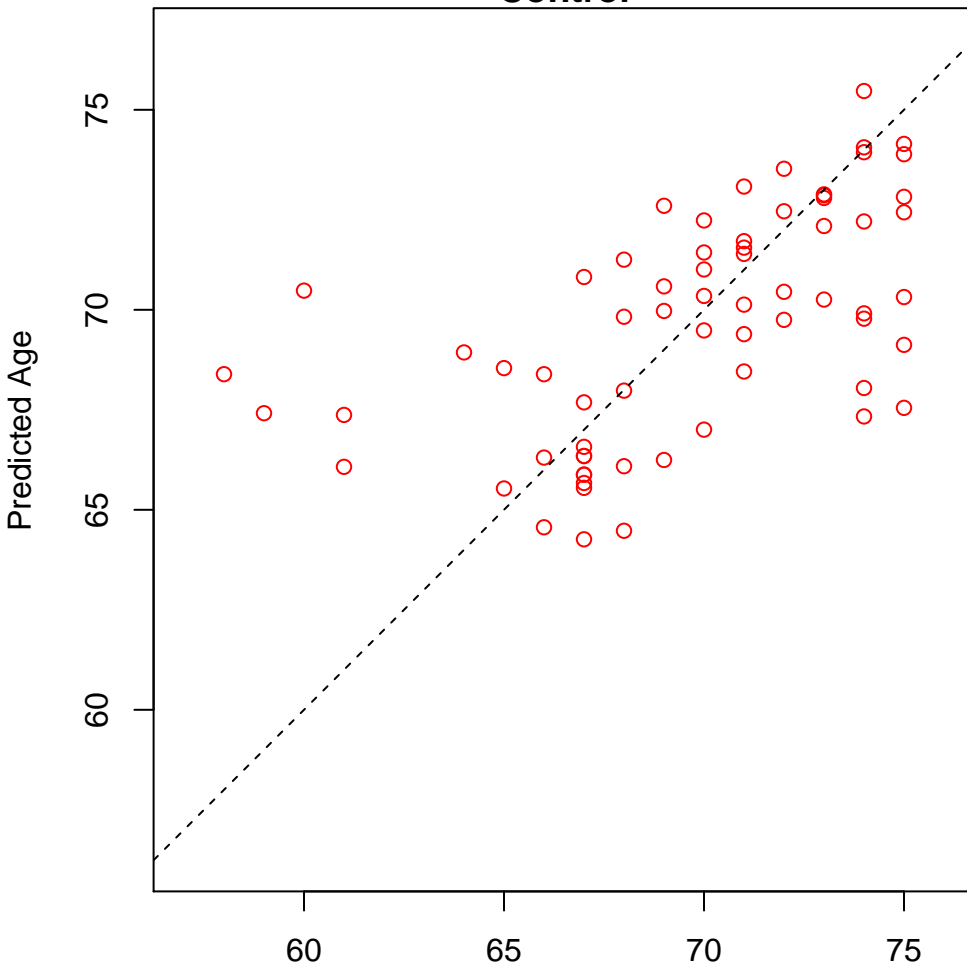


positive regulation of endothelial cell migration (Score: 1.114574)

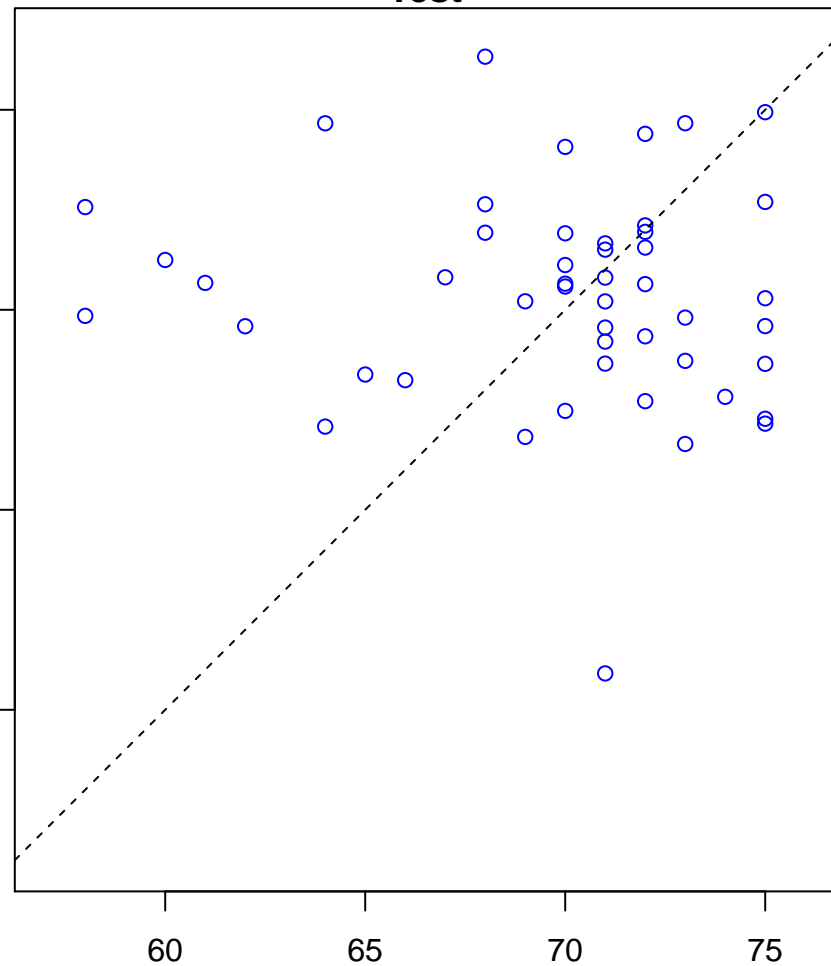


negative regulation of B cell activation (Score: 1.114342)

Control

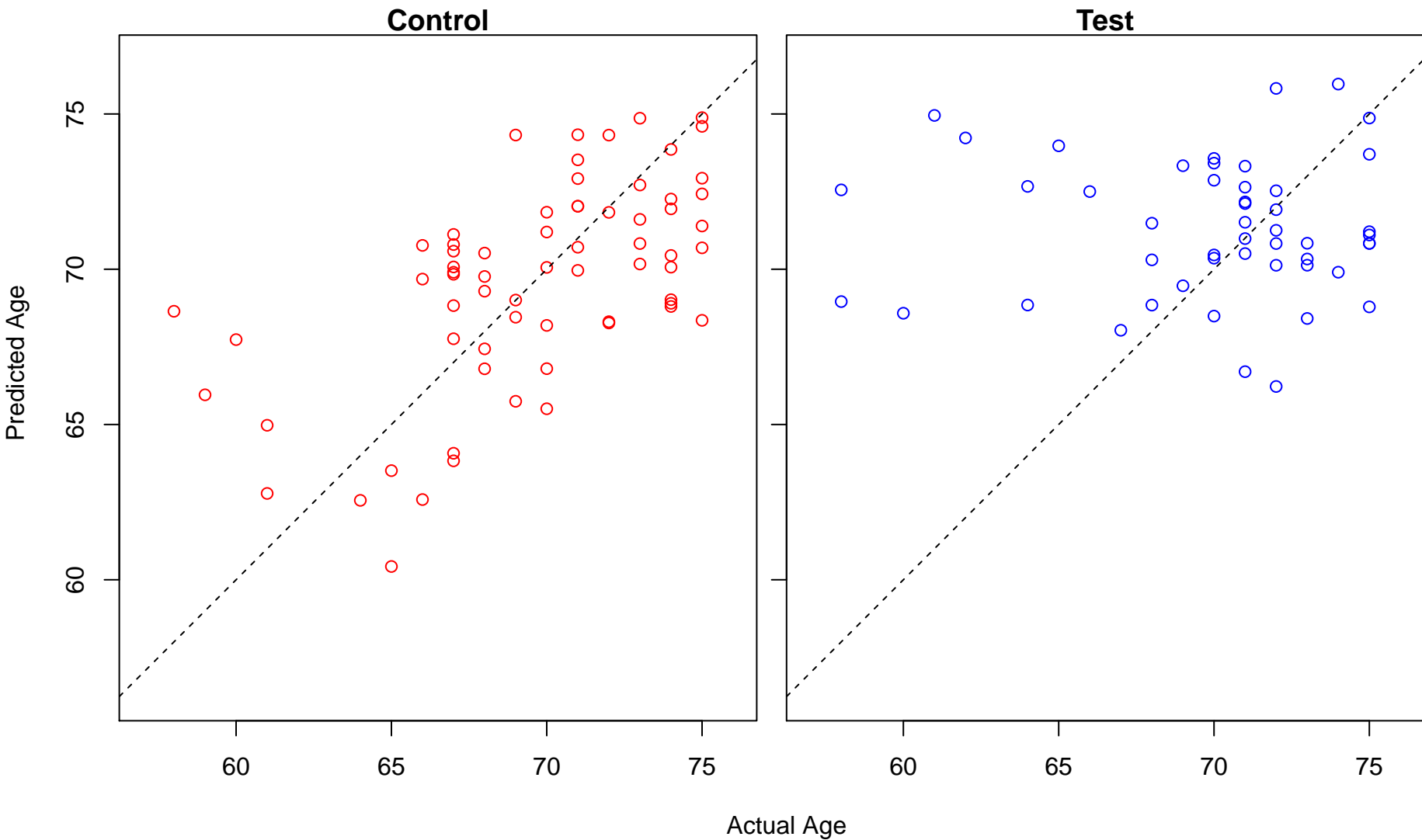


Test

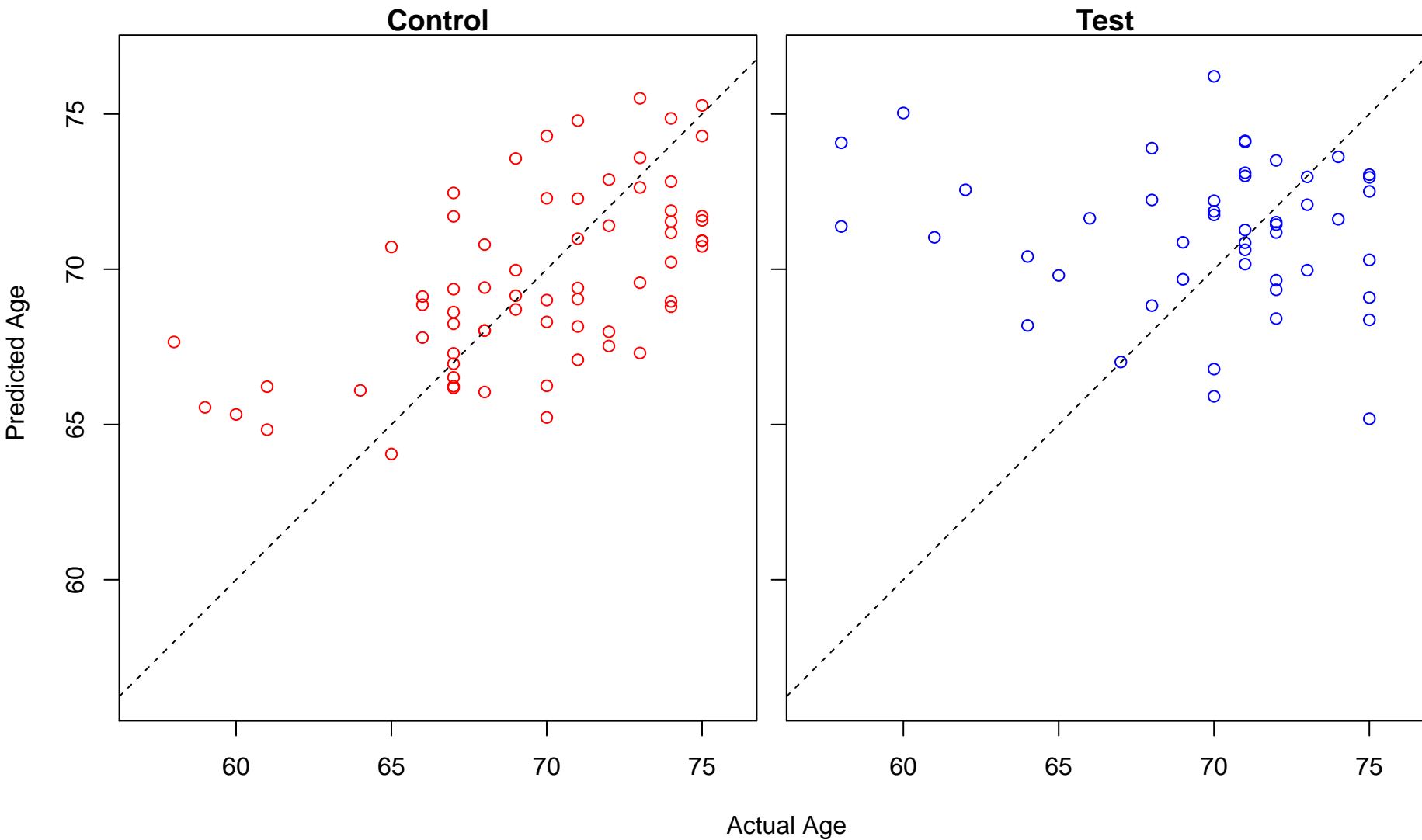


Actual Age

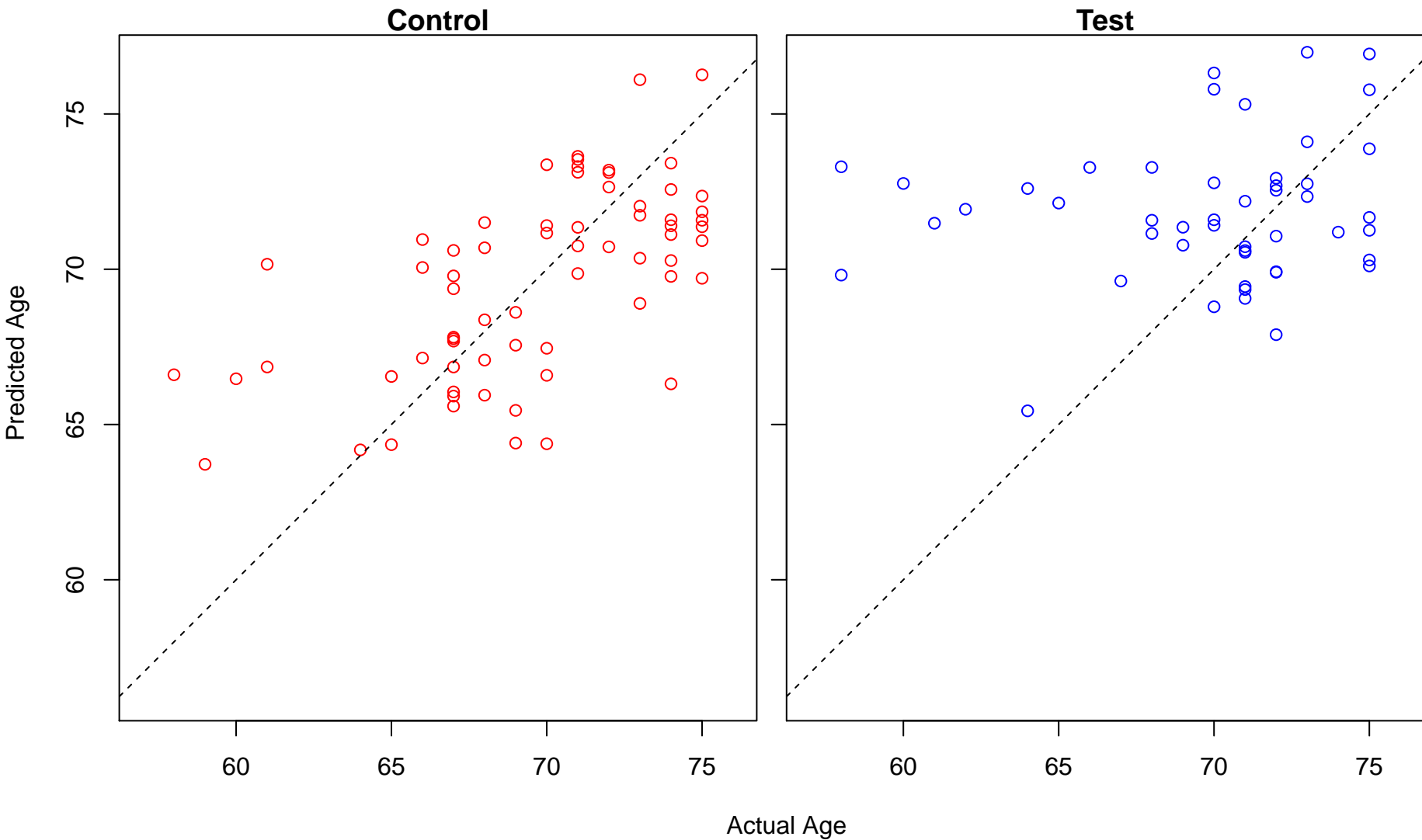
membrane docking (Score: 1.114238)



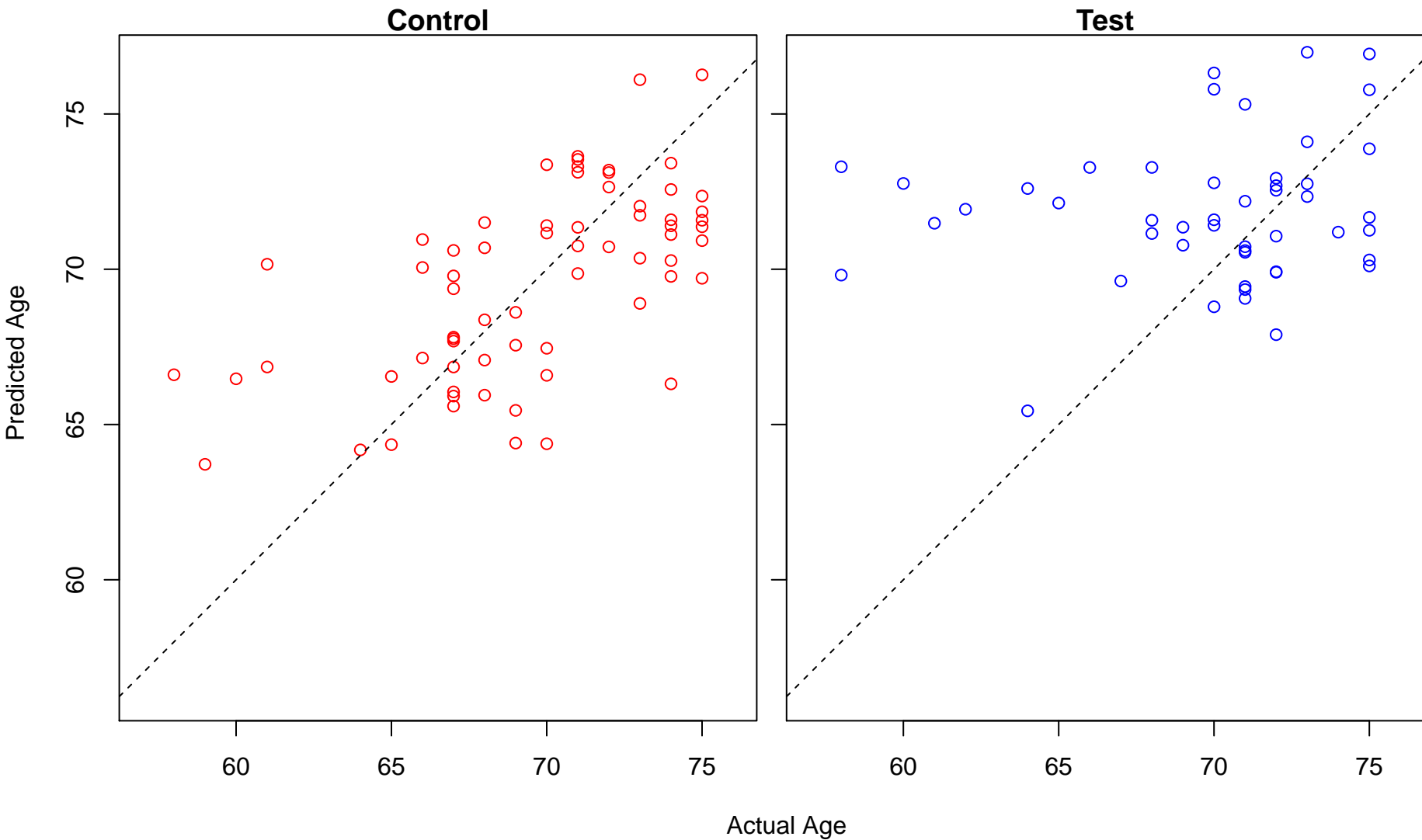
heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules (Score: 1.113998)



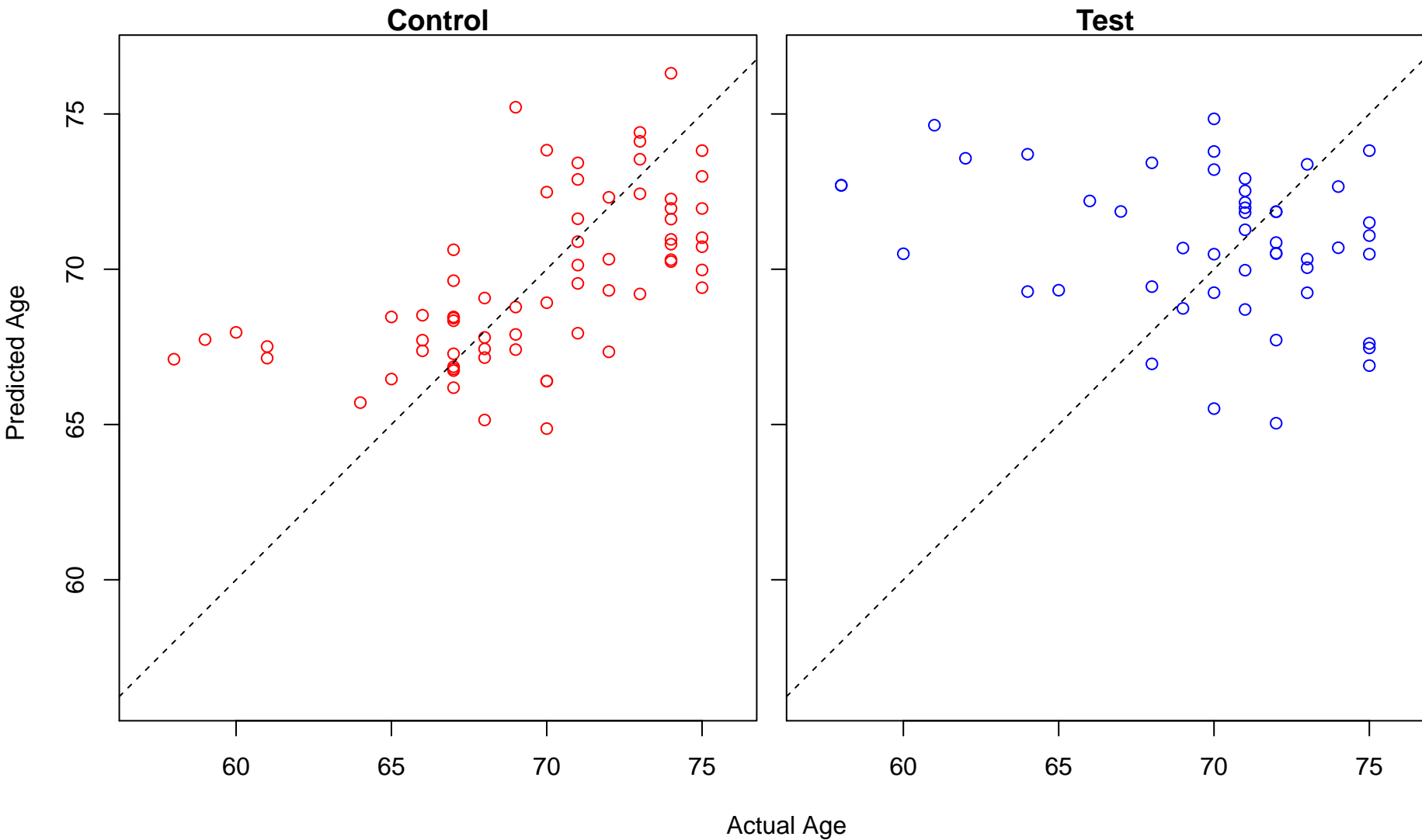
cerebellum development (Score: 1.113851)



metencephalon development (Score: 1.113851)

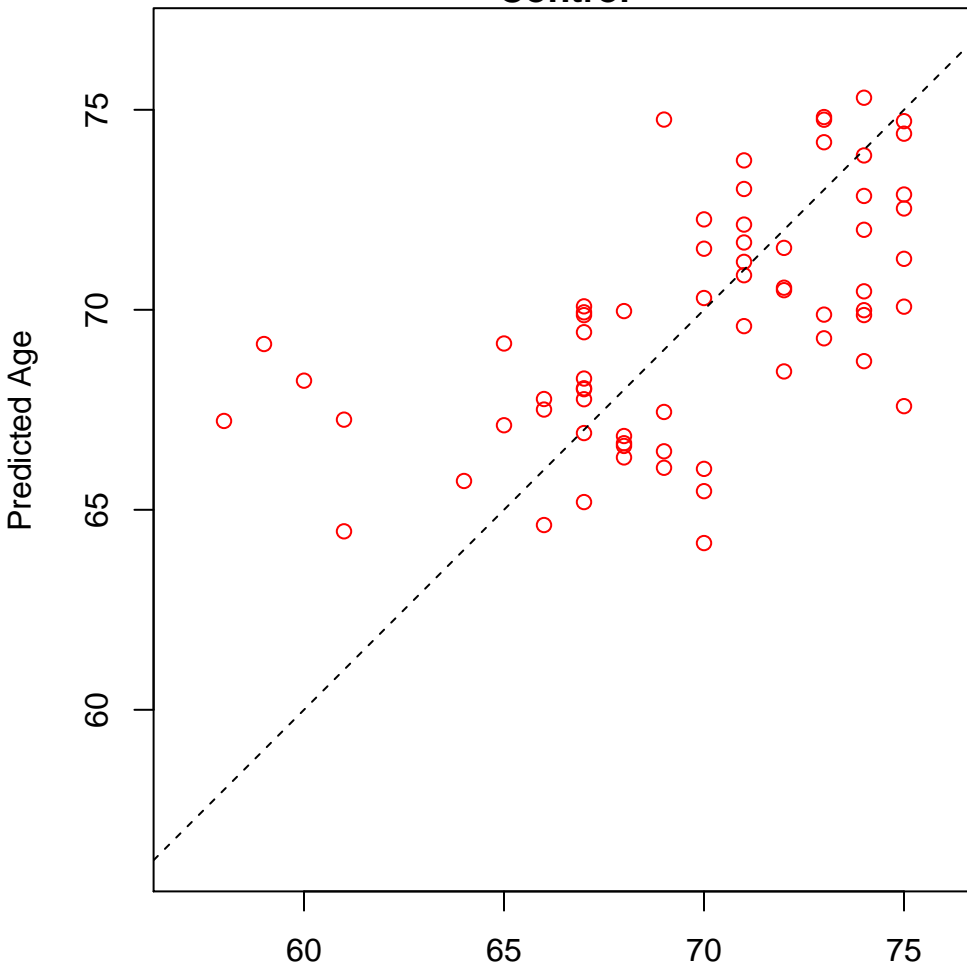


negative regulation of nervous system development (Score: 1.113740)

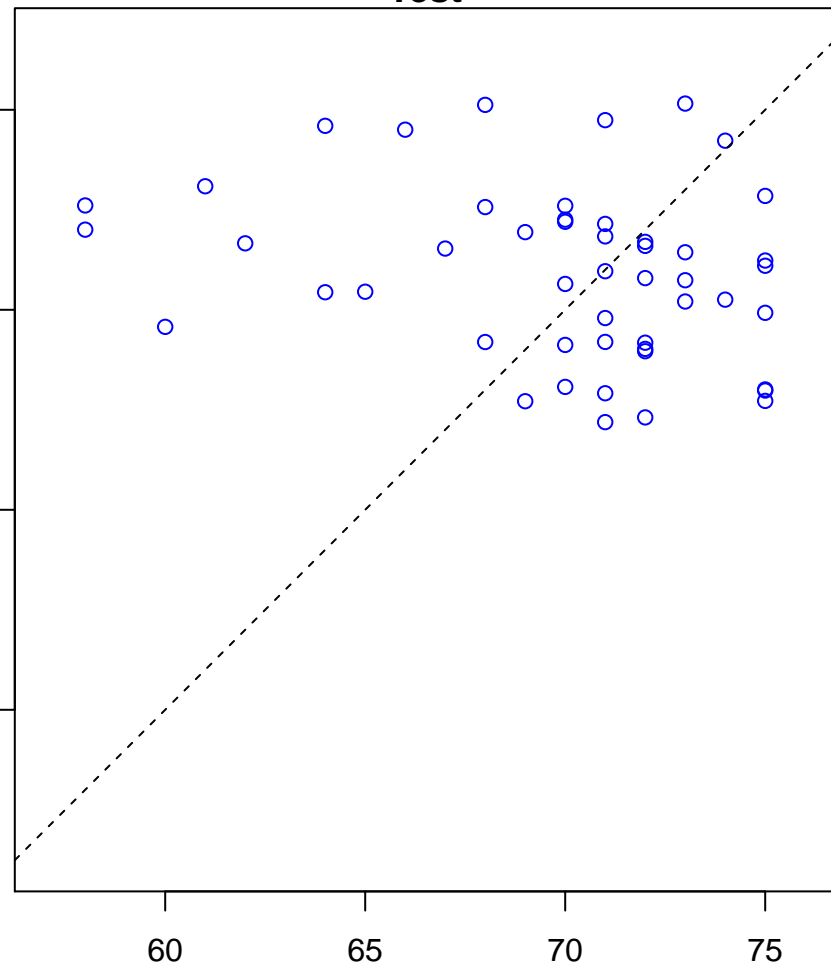


regulation of lamellipodium organization (Score: 1.112908)

Control

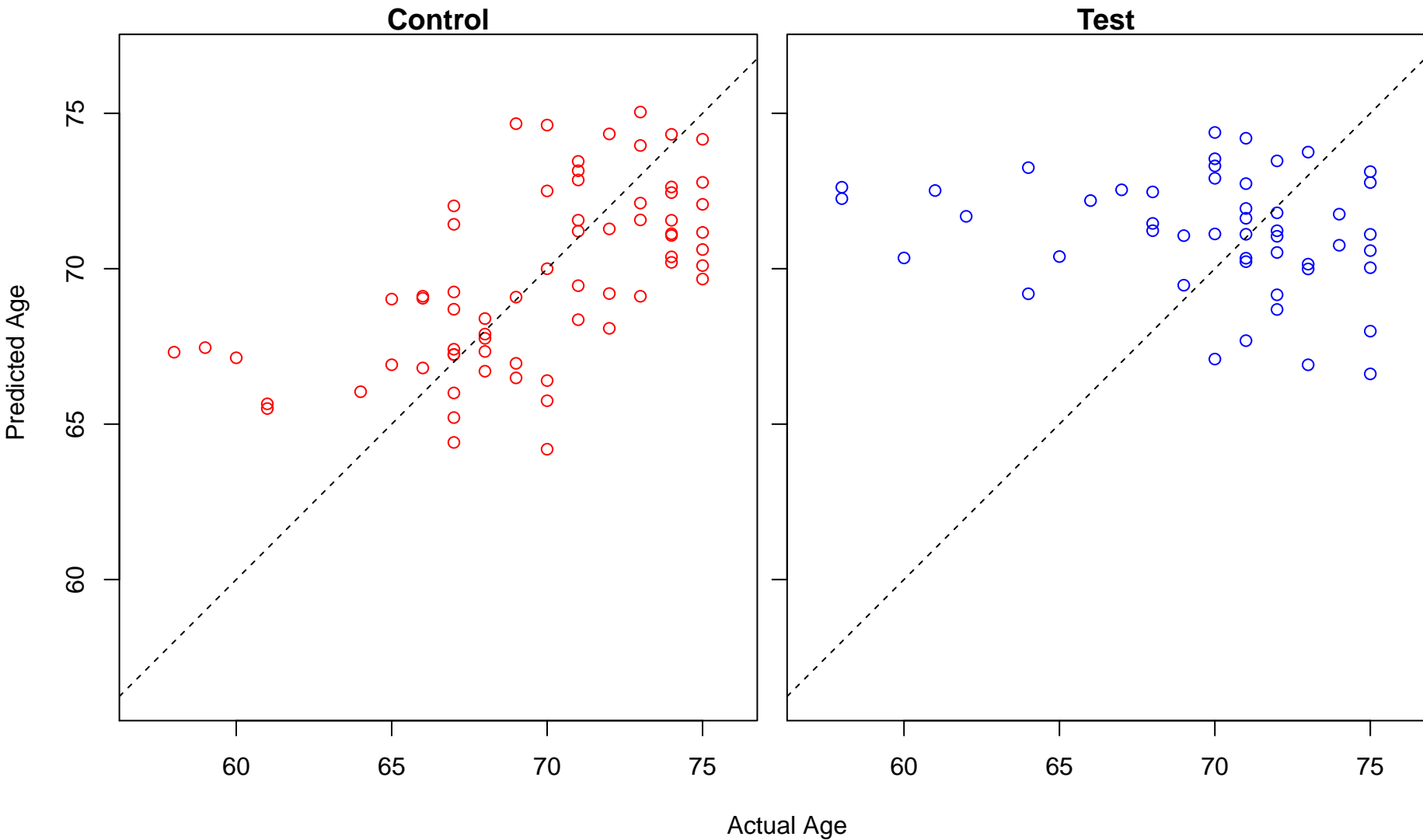


Test

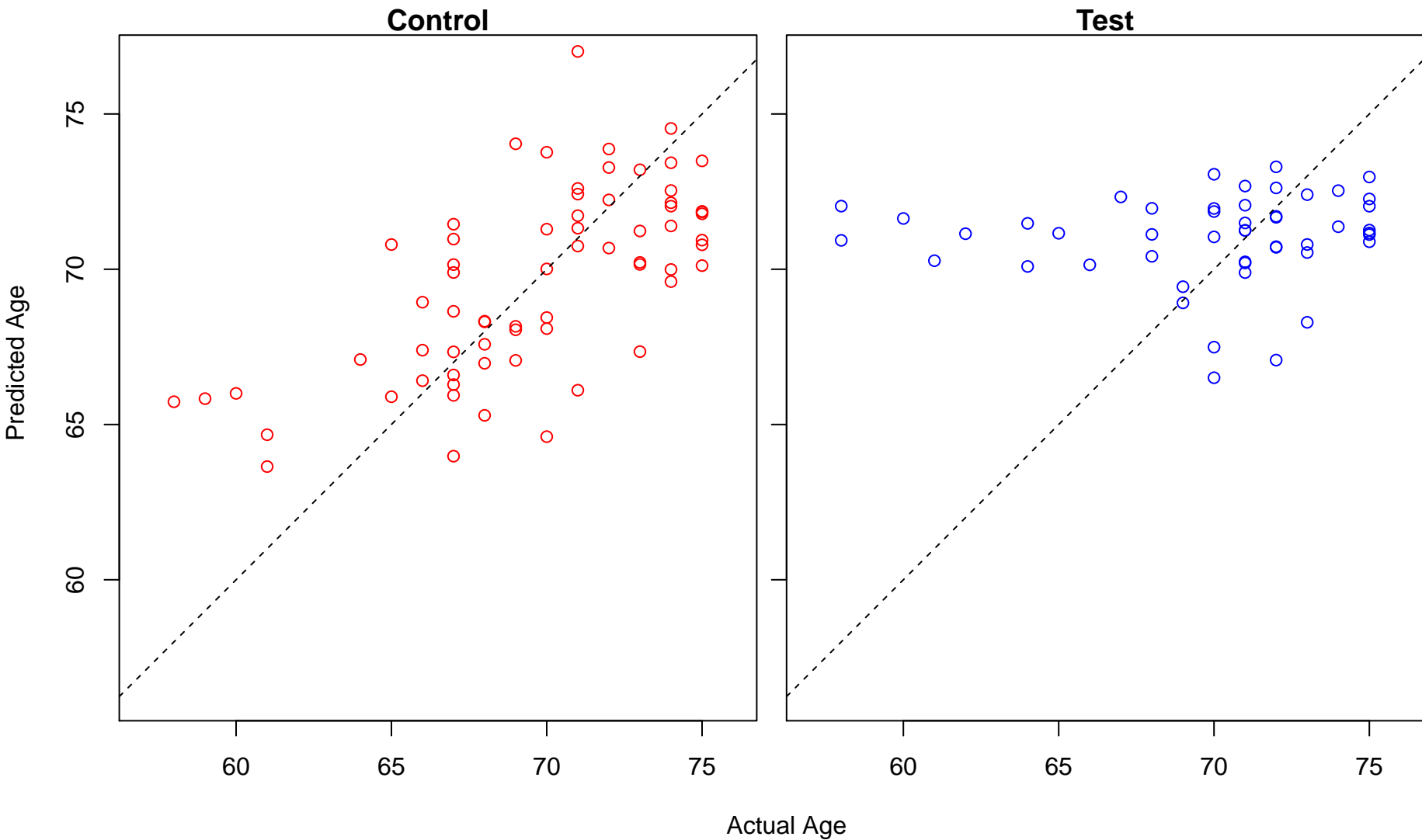


Actual Age

establishment of Golgi localization (Score: 1.112306)

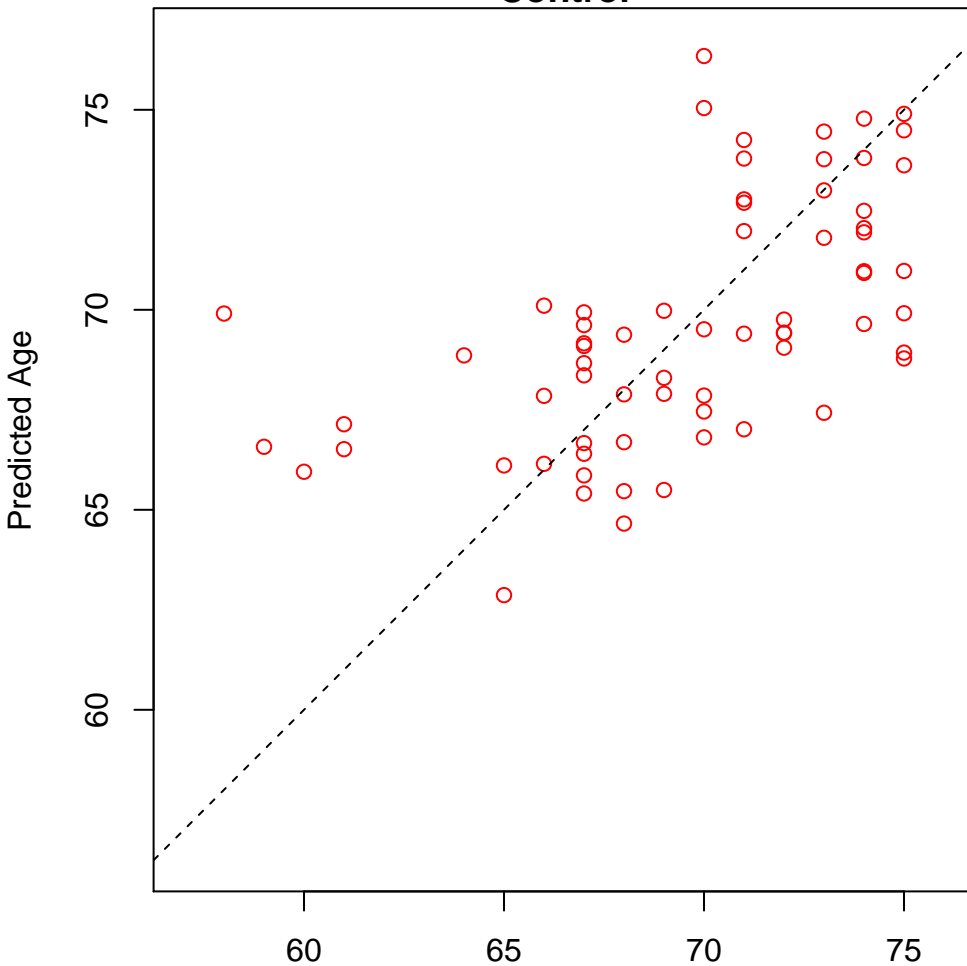


positive regulation of IRE1-mediated unfolded protein response (Score: 1.111950)

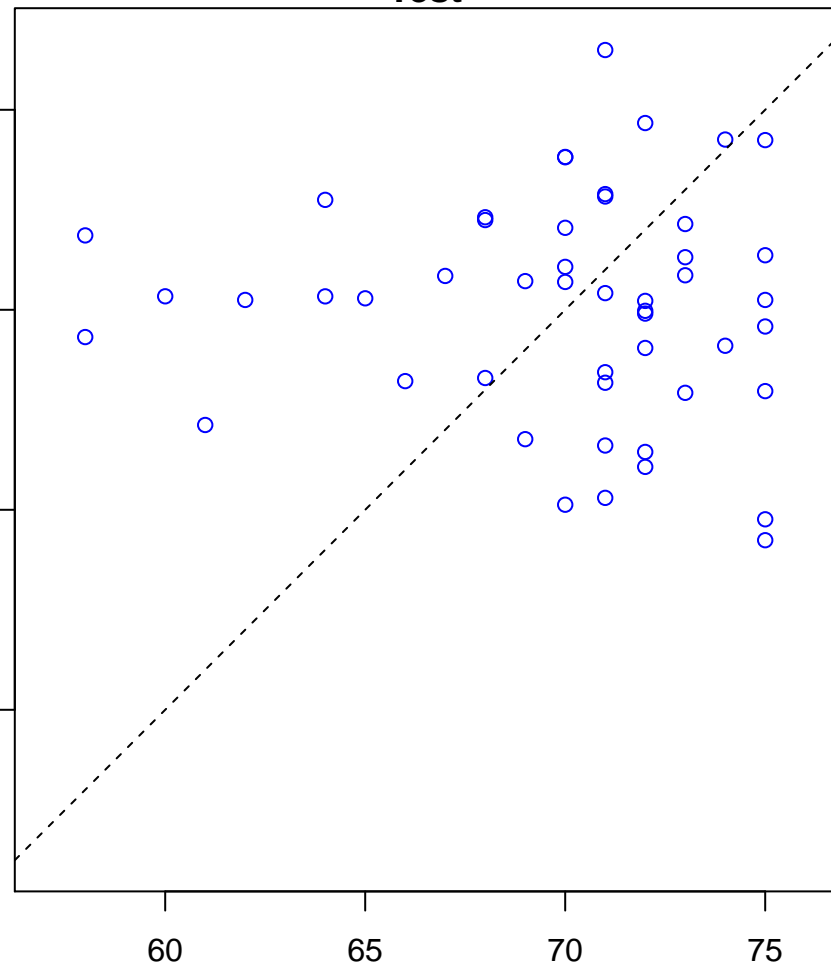


modulation by host of viral transcription (Score: 1.111524)

Control

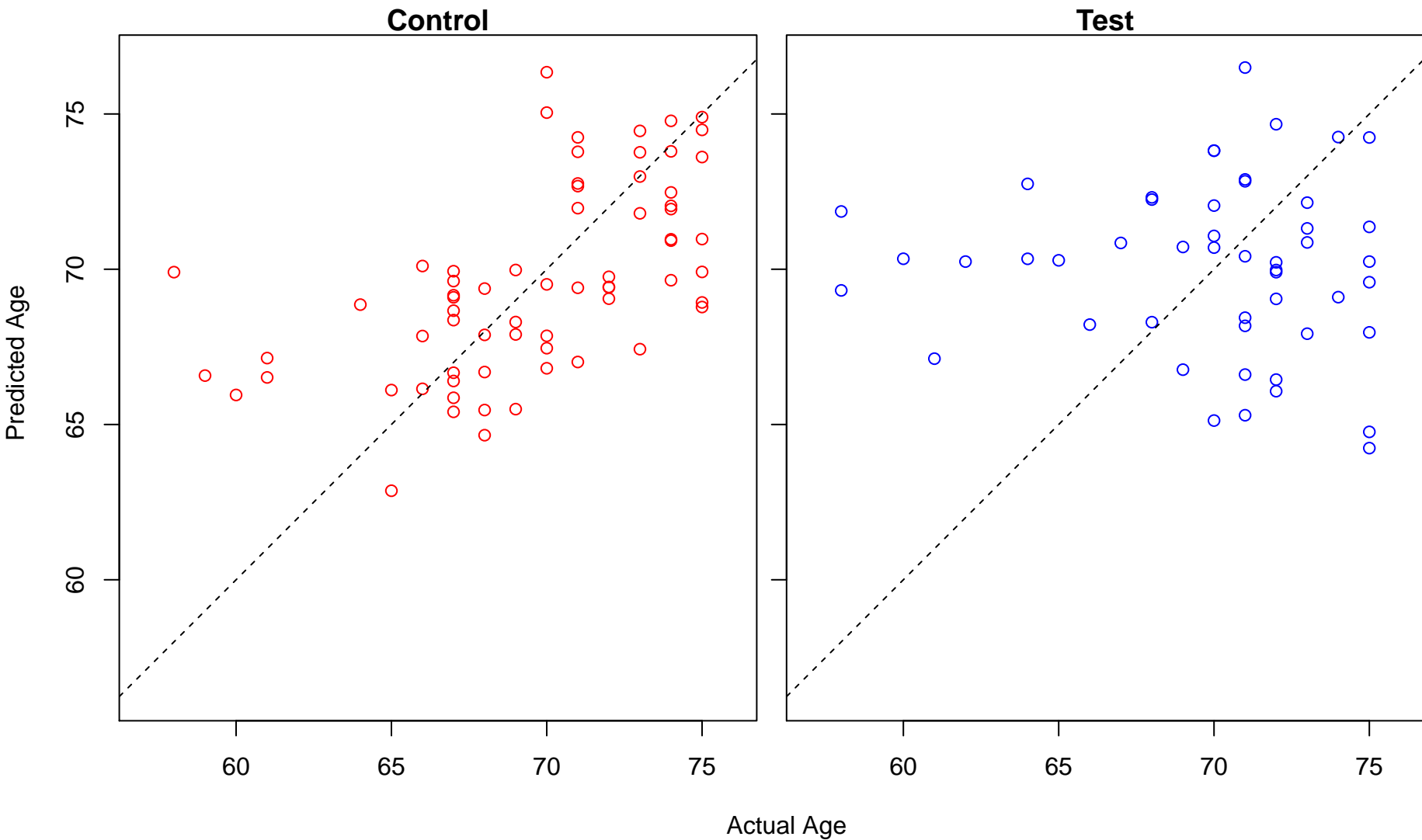


Test

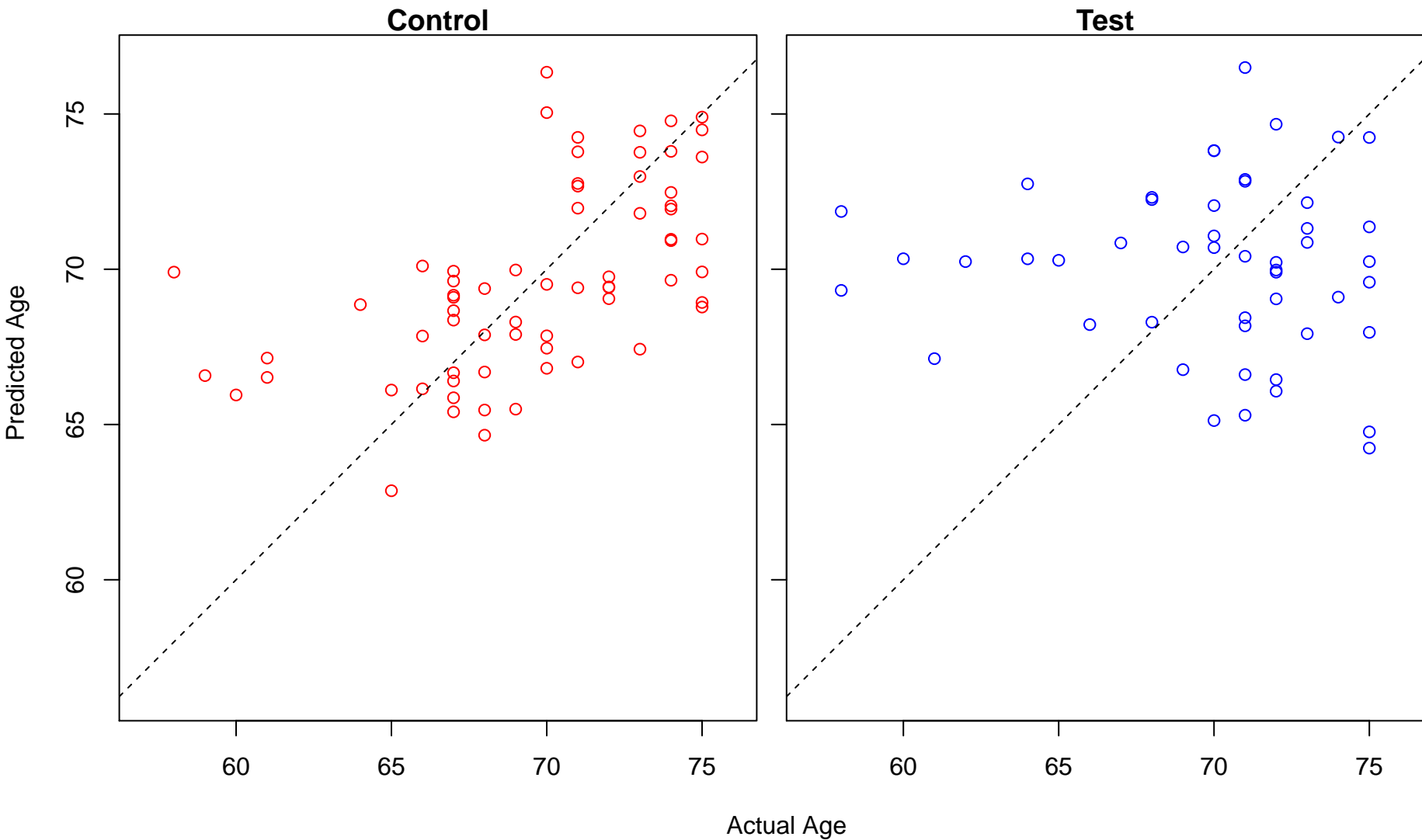


Actual Age

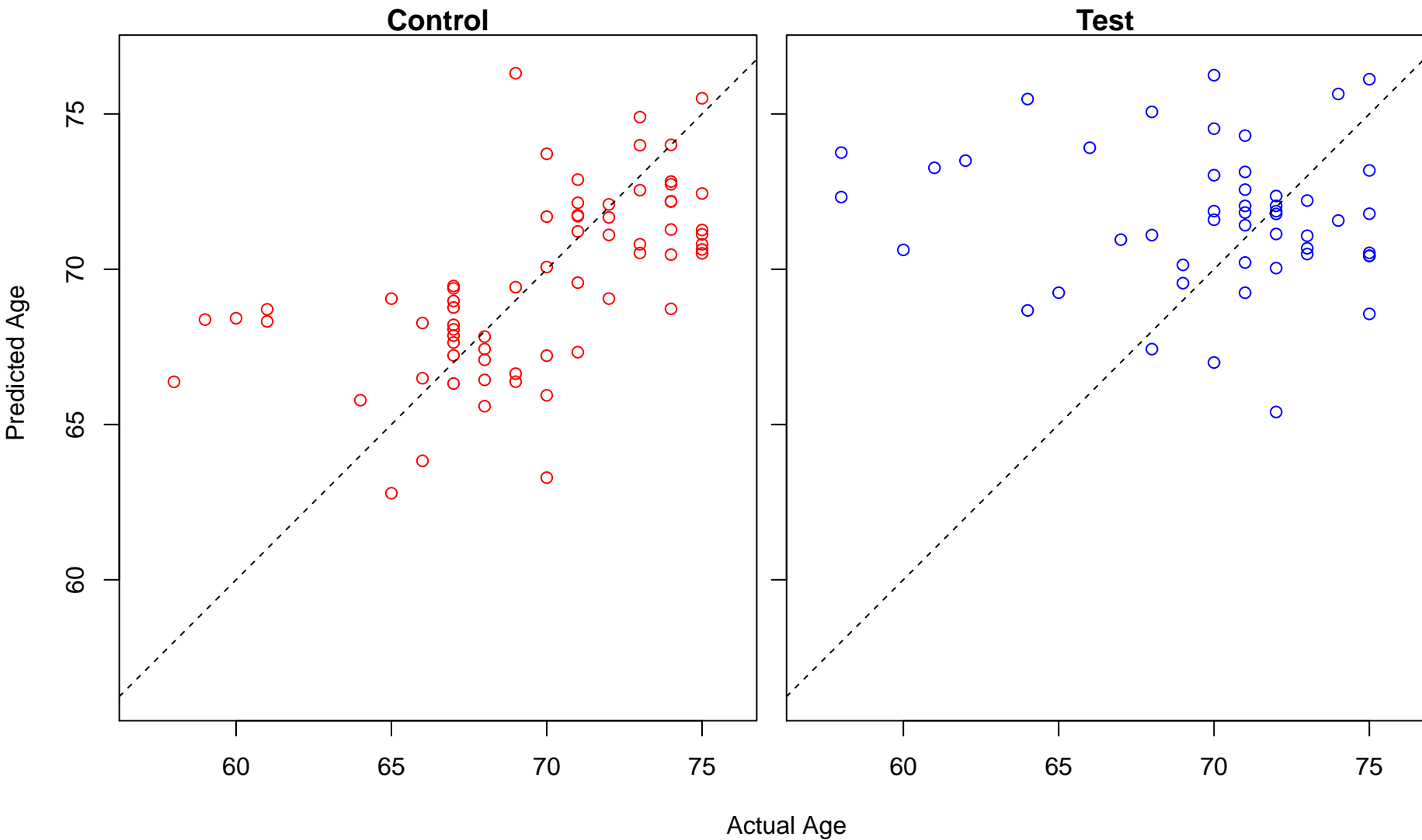
modulation of transcription in other organism involved in symbiotic interaction (Score: 1.111524)



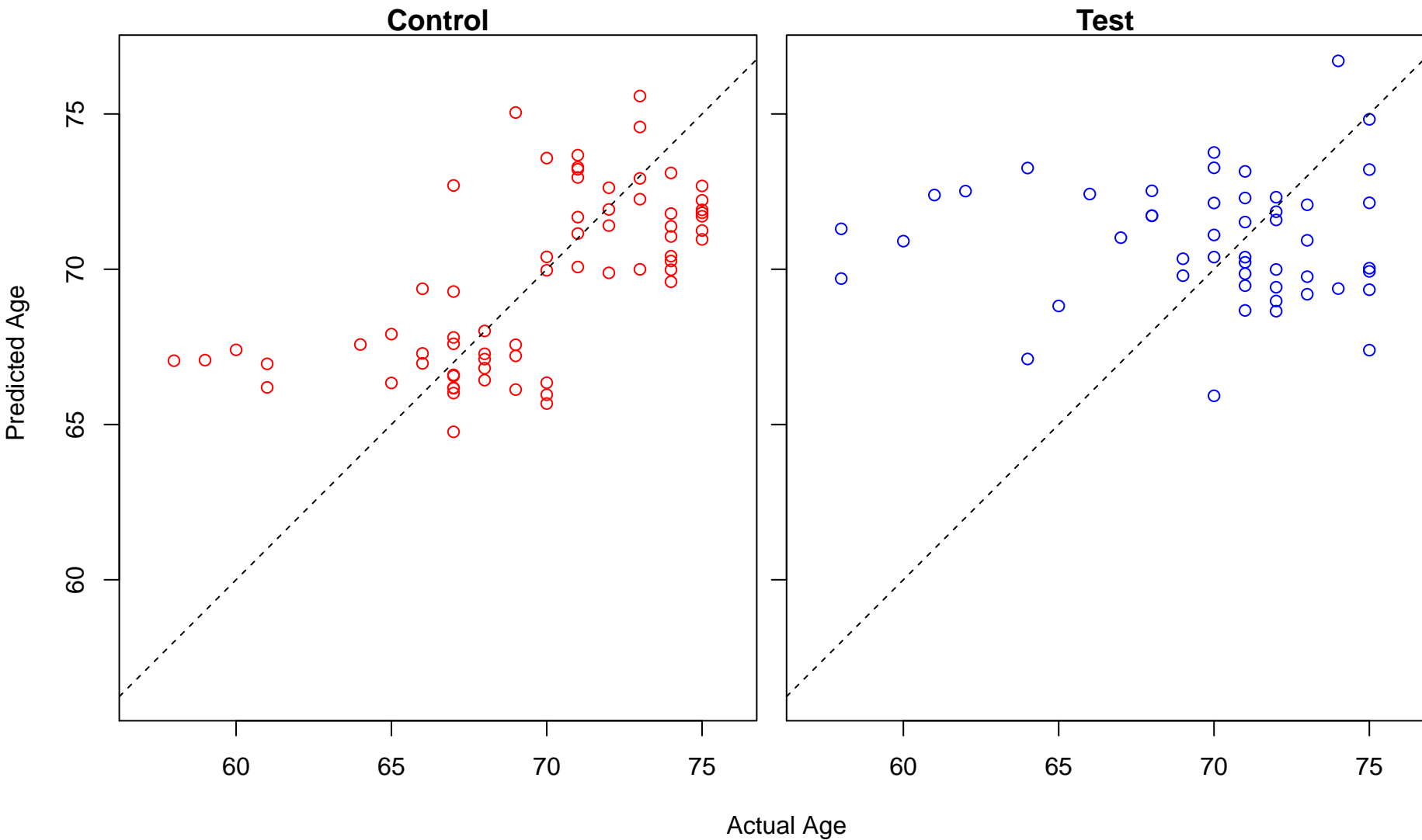
modulation by host of symbiont transcription (Score: 1.111524)



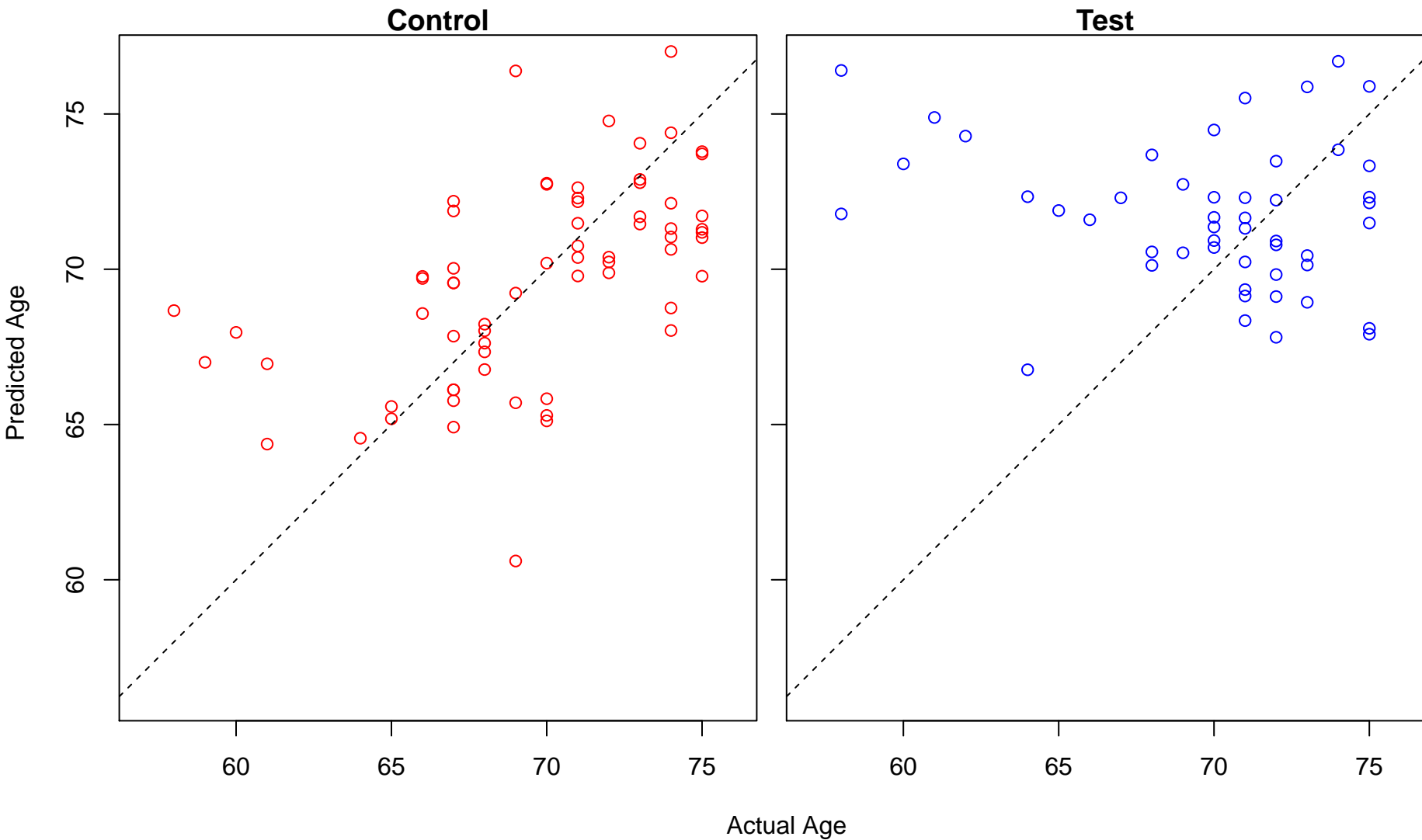
establishment of cell polarity (Score: 1.111474)



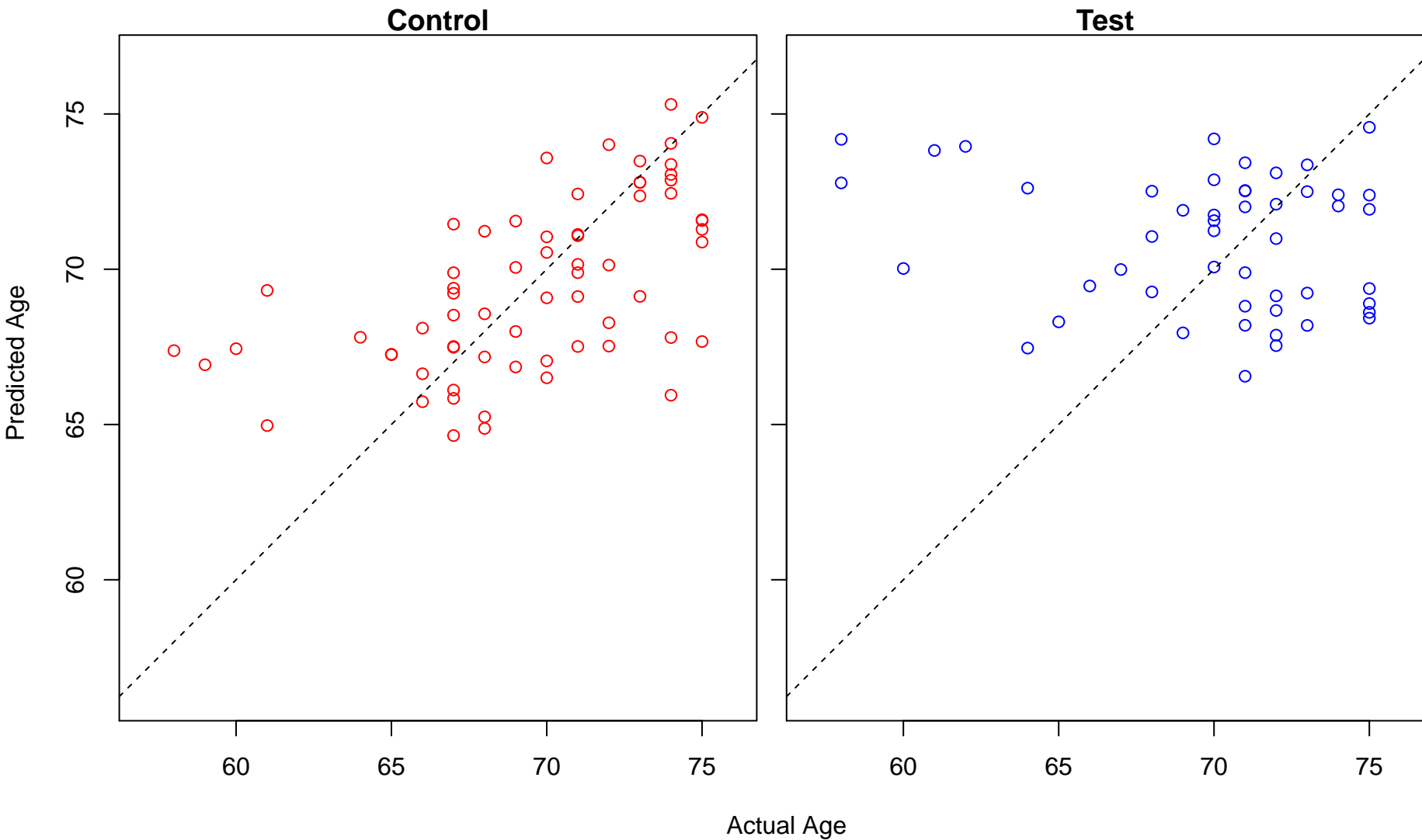
macrophage chemotaxis (Score: 1.111316)



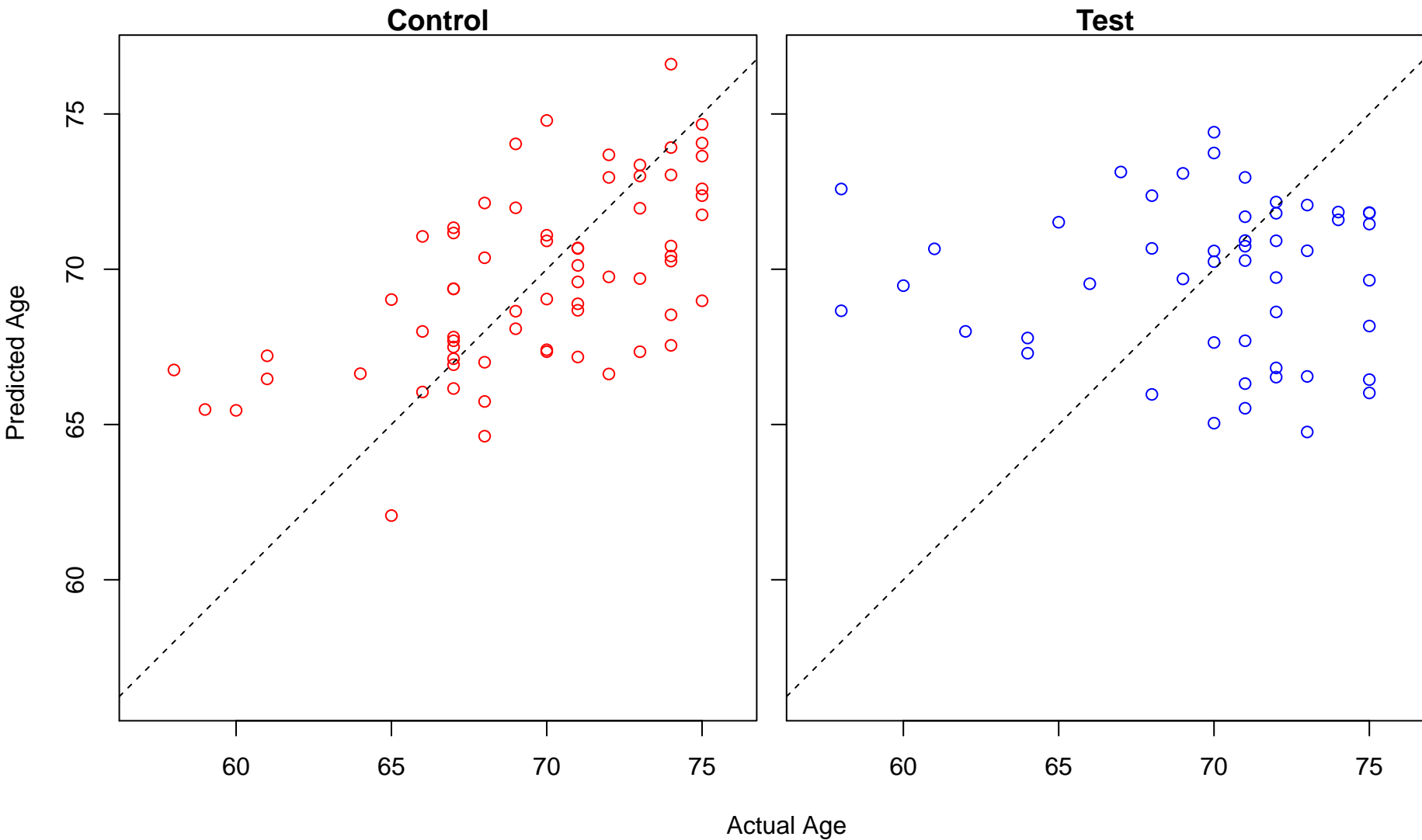
ameboidal-type cell migration (Score: 1.110753)



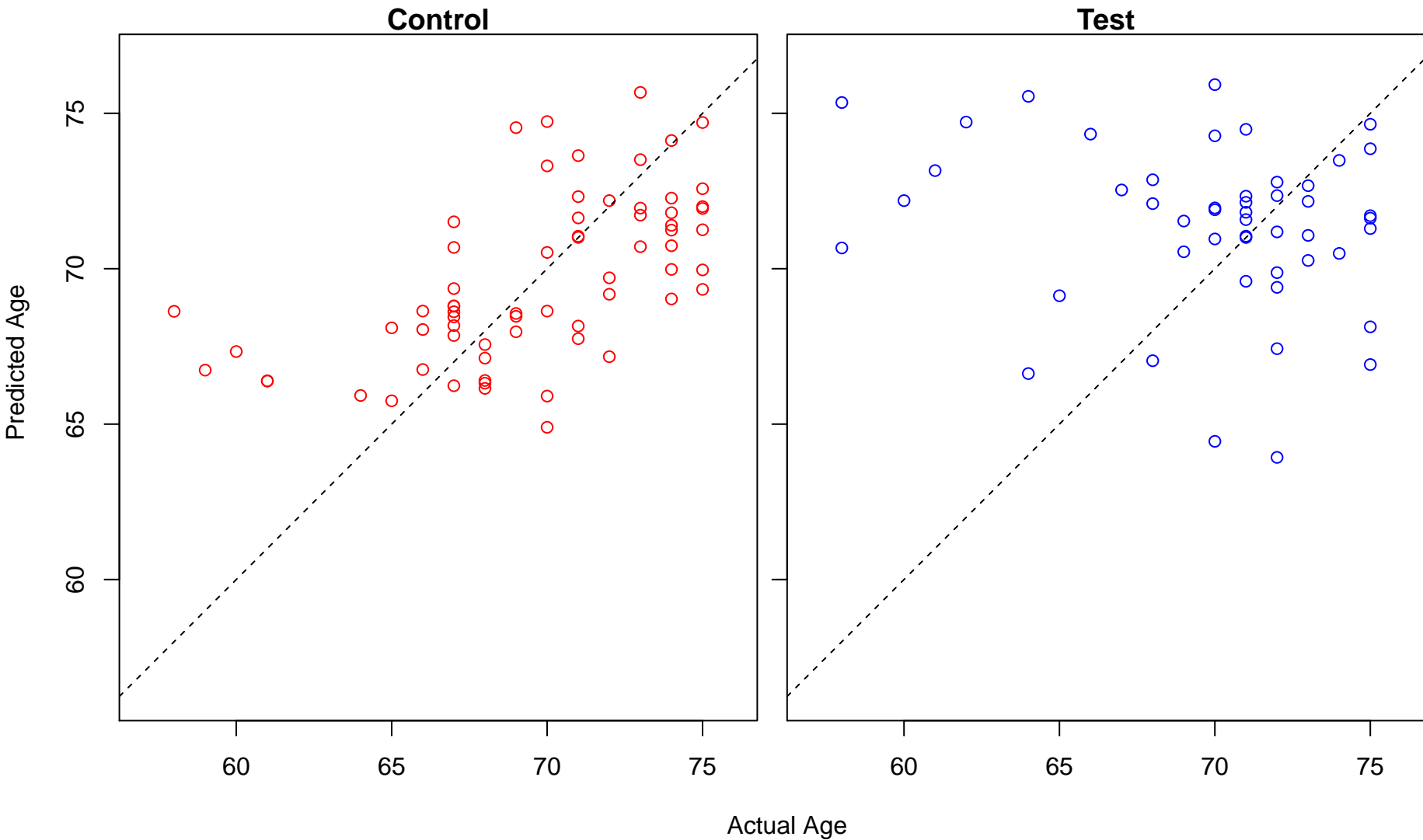
keratan sulfate biosynthetic process (Score: 1.110735)



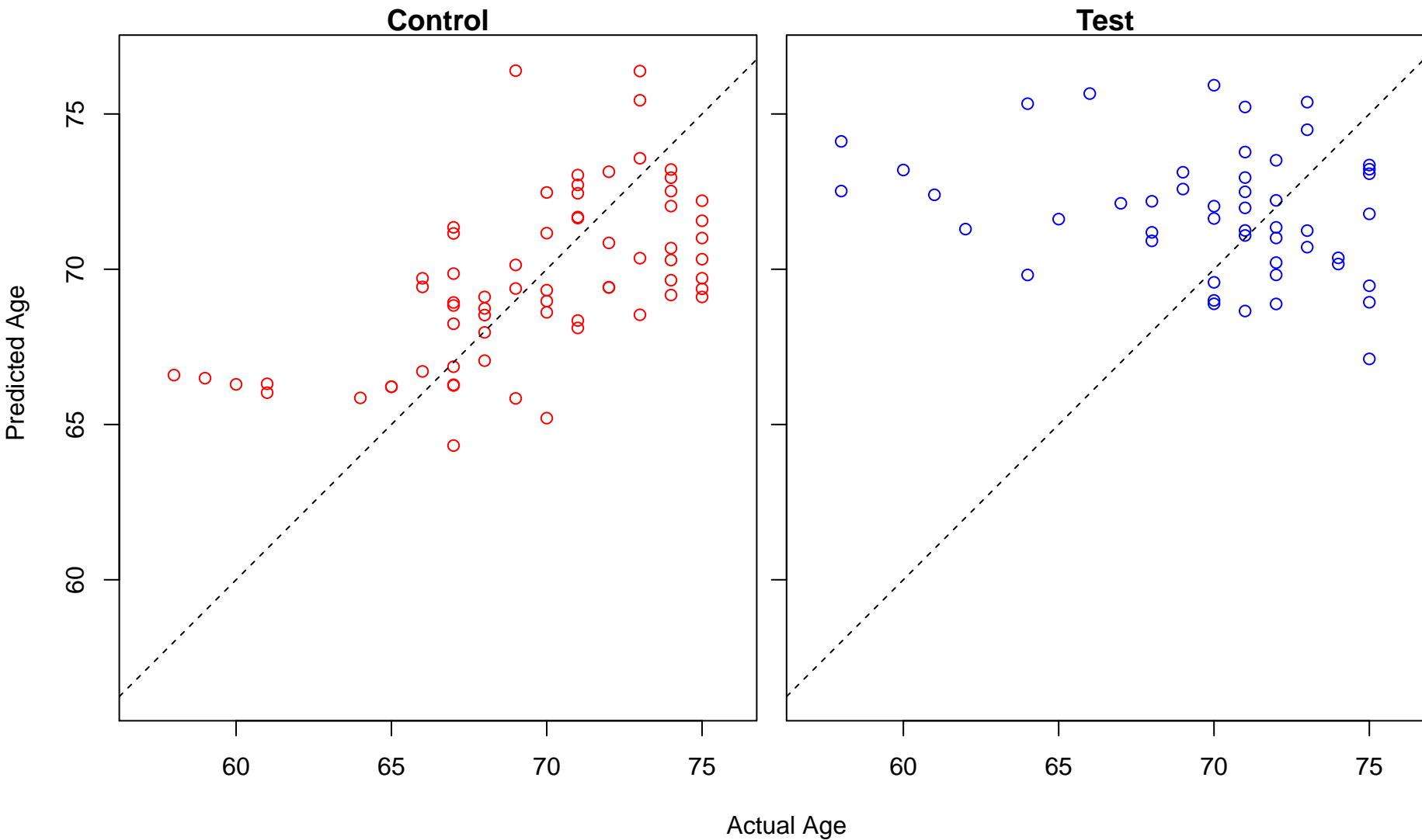
regulation of phospholipid biosynthetic process (Score: 1.110509)



negative regulation of histone modification (Score: 1.110074)

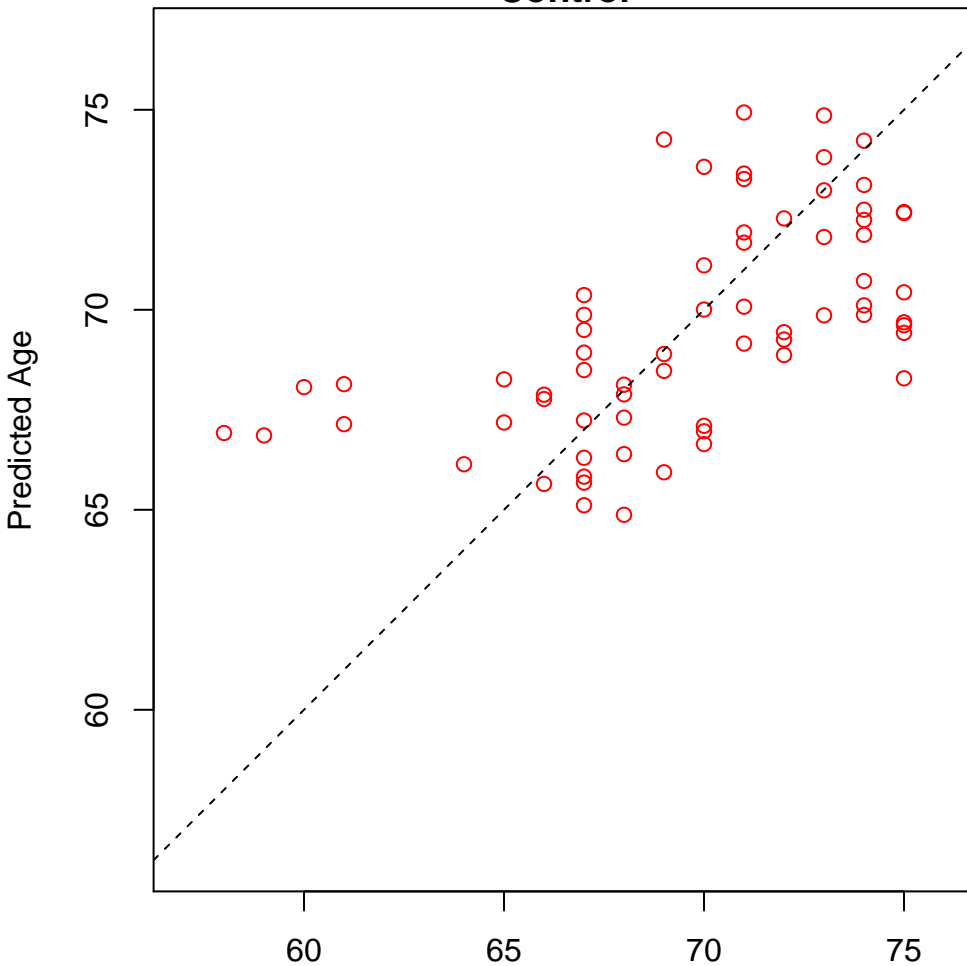


adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway (Score: 1.109966)

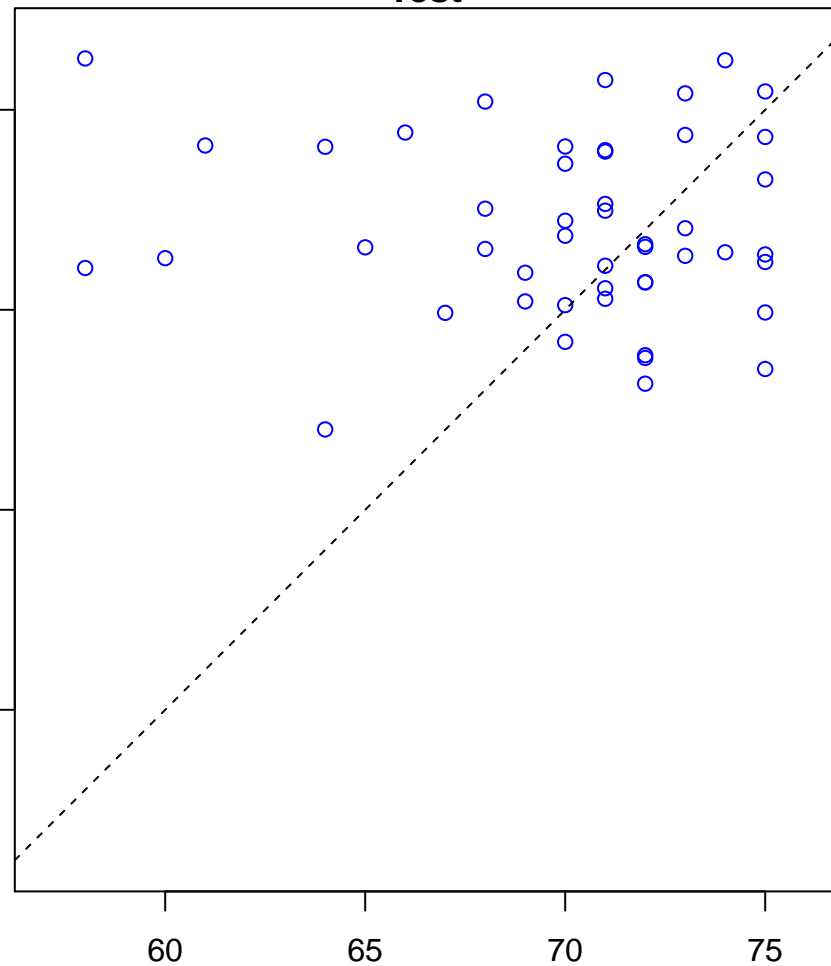


hydrogen peroxide metabolic process (Score: 1.109710)

Control



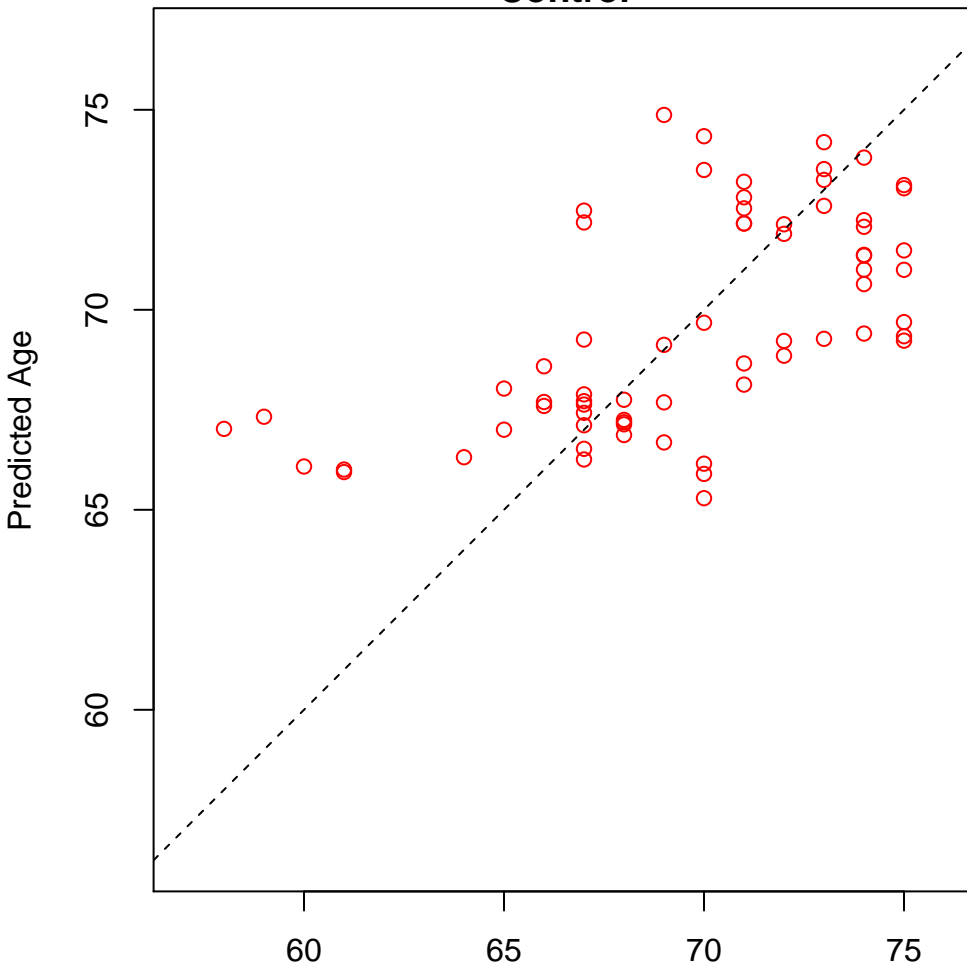
Test



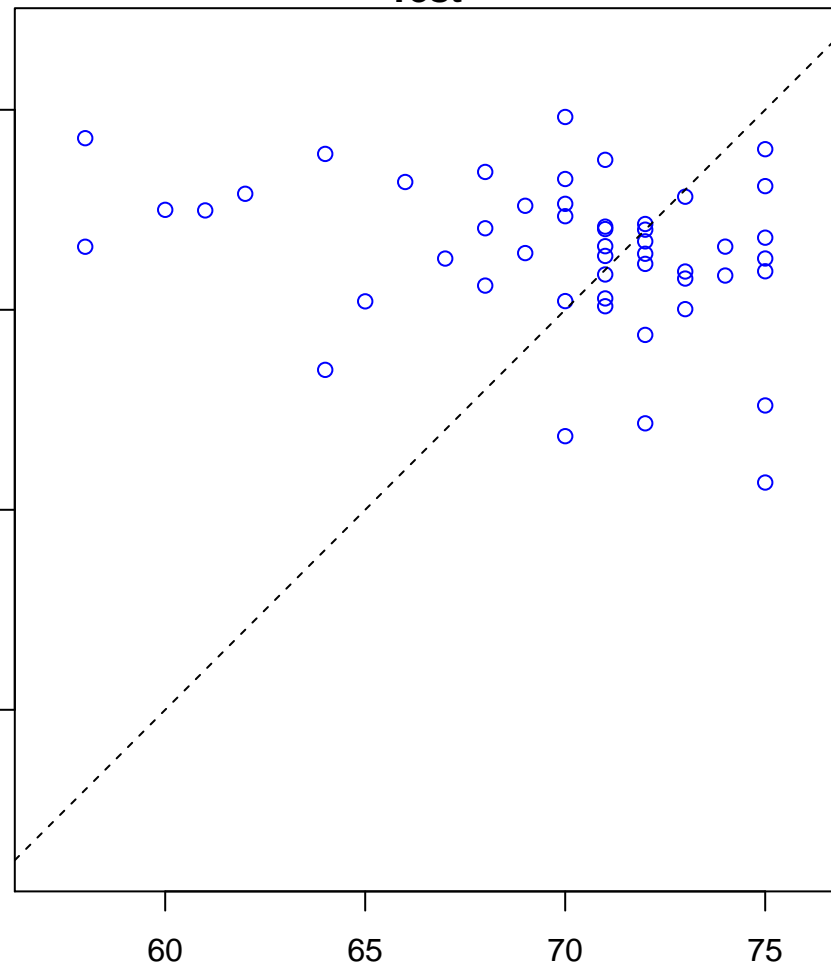
Actual Age

regulation of sprouting angiogenesis (Score: 1.109621)

Control

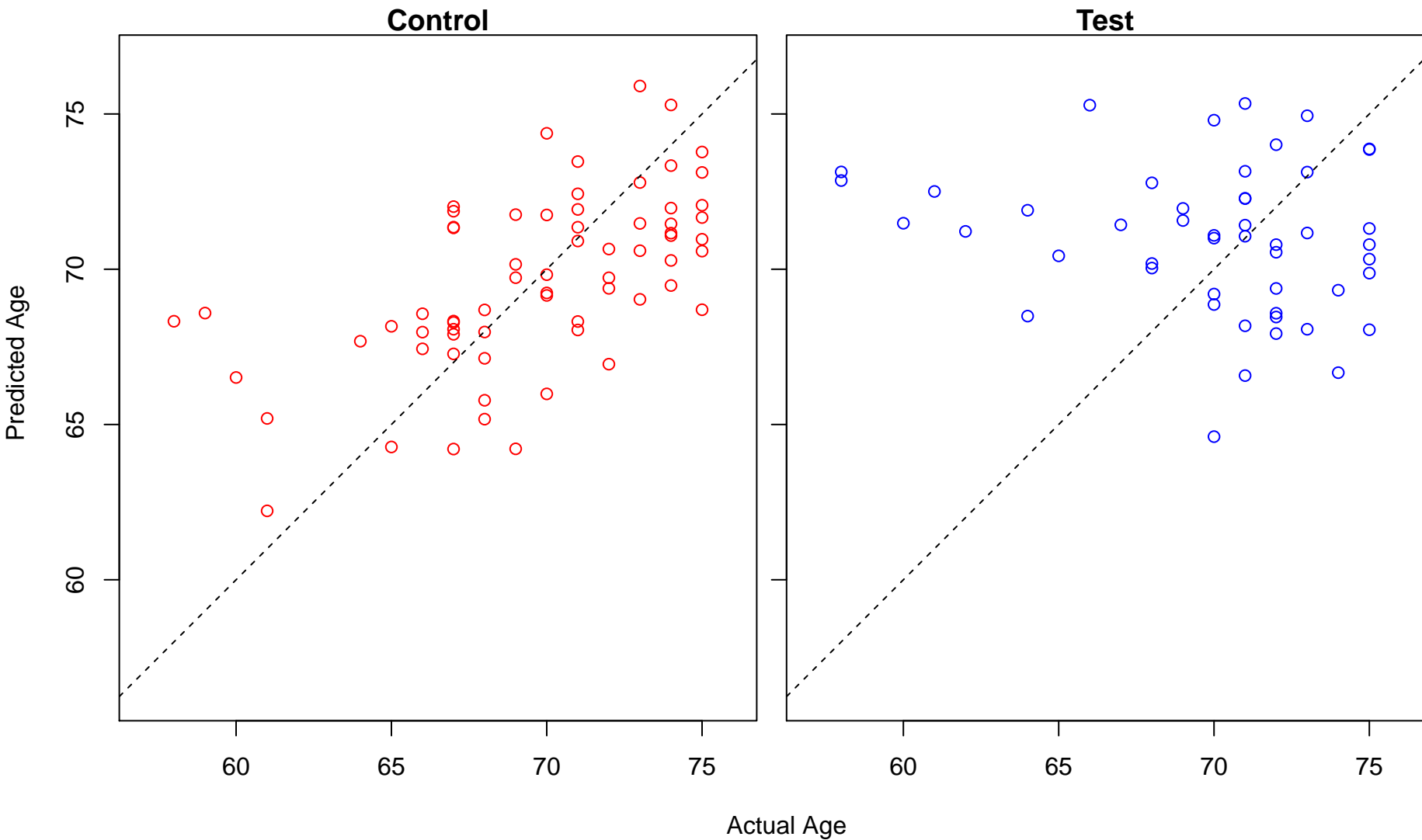


Test

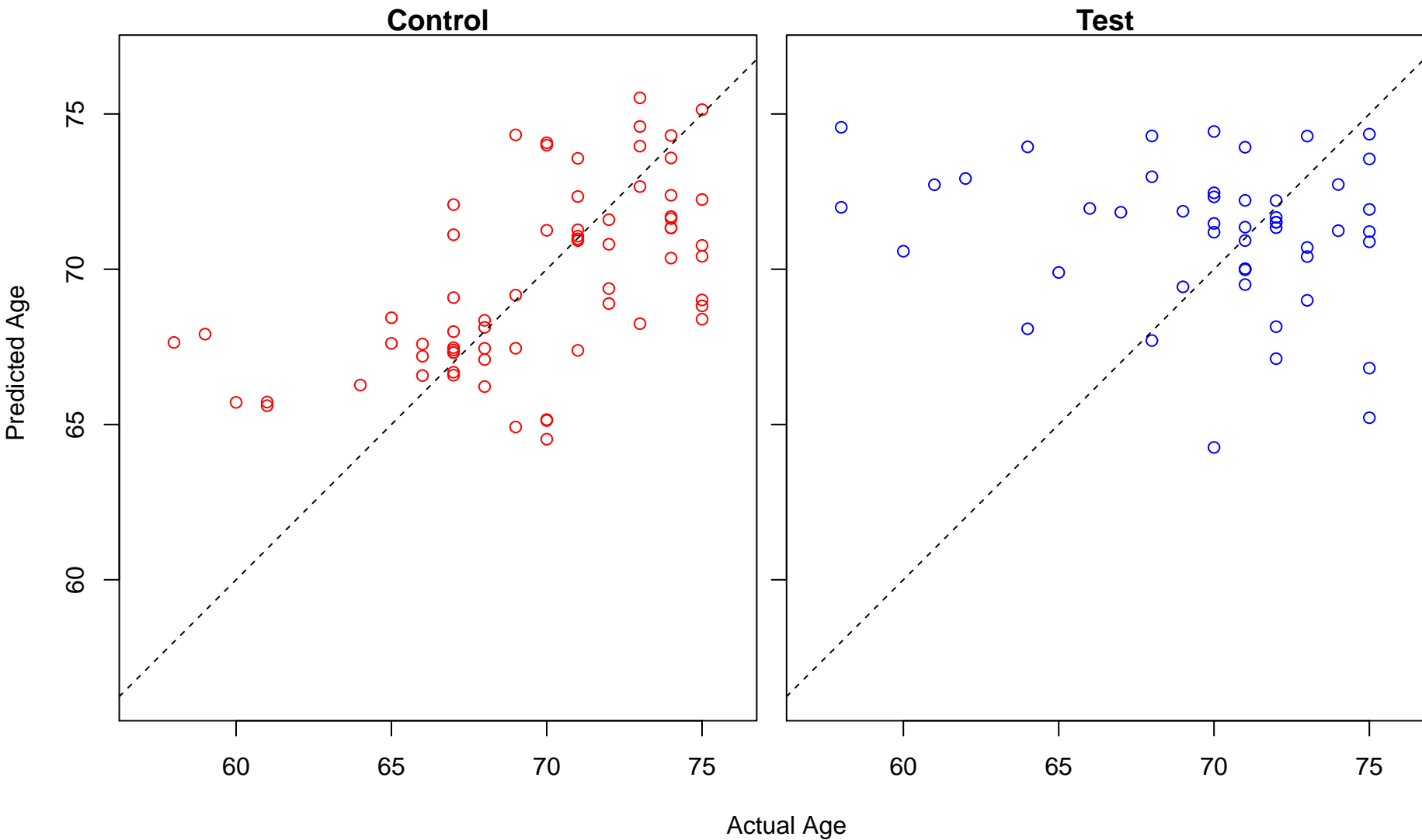


Actual Age

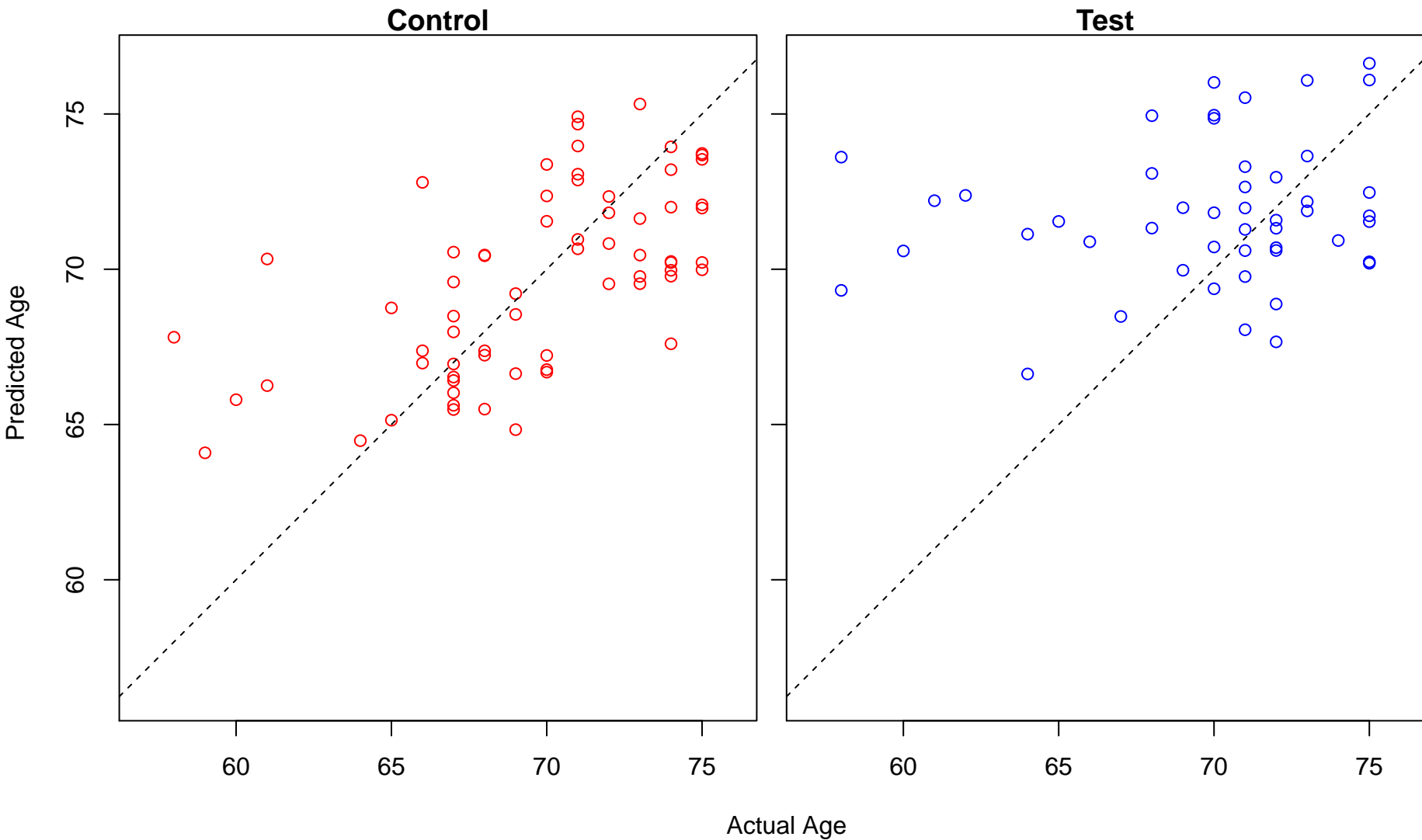
GTP metabolic process (Score: 1.109230)



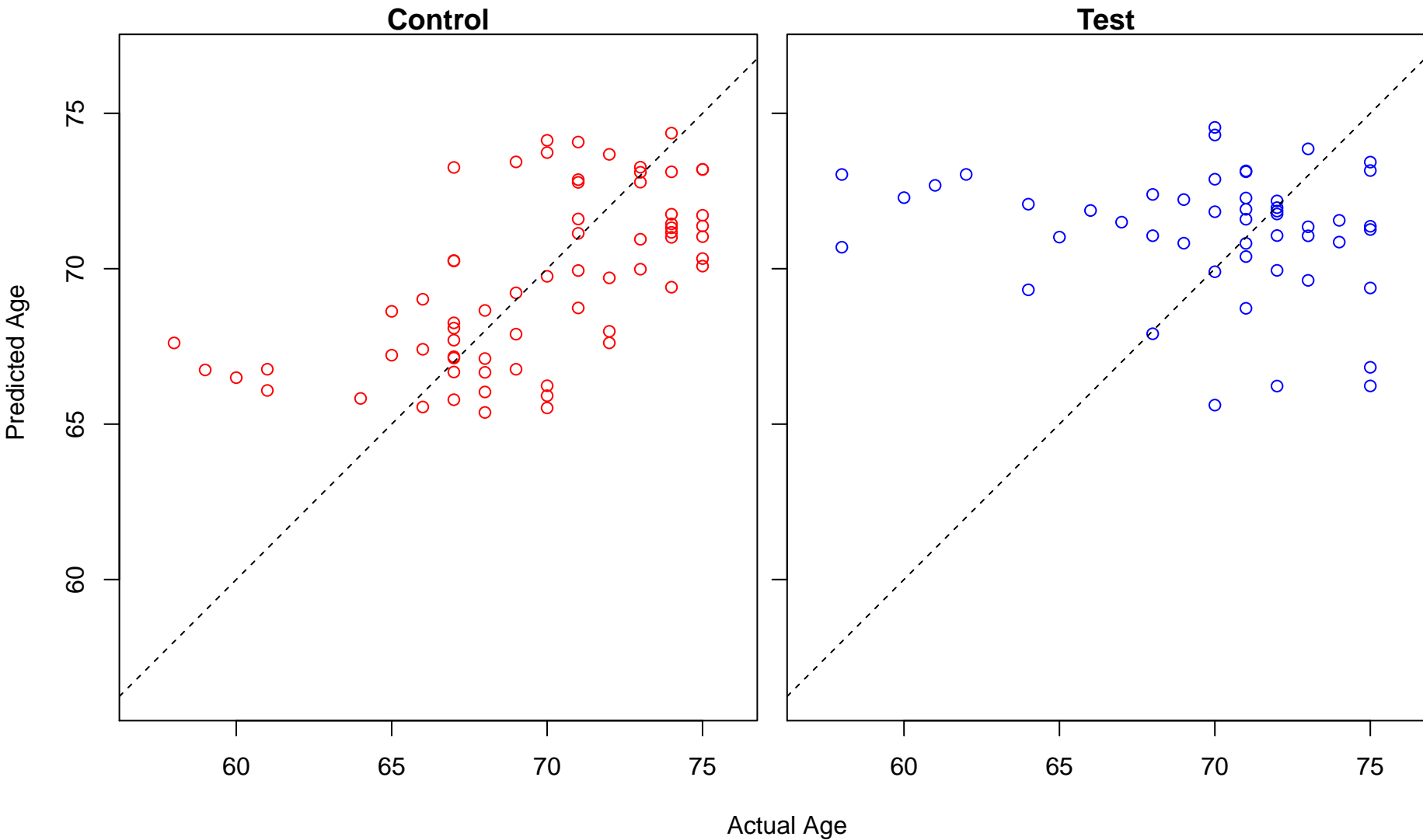
regulation of sodium ion transport (Score: 1.108987)



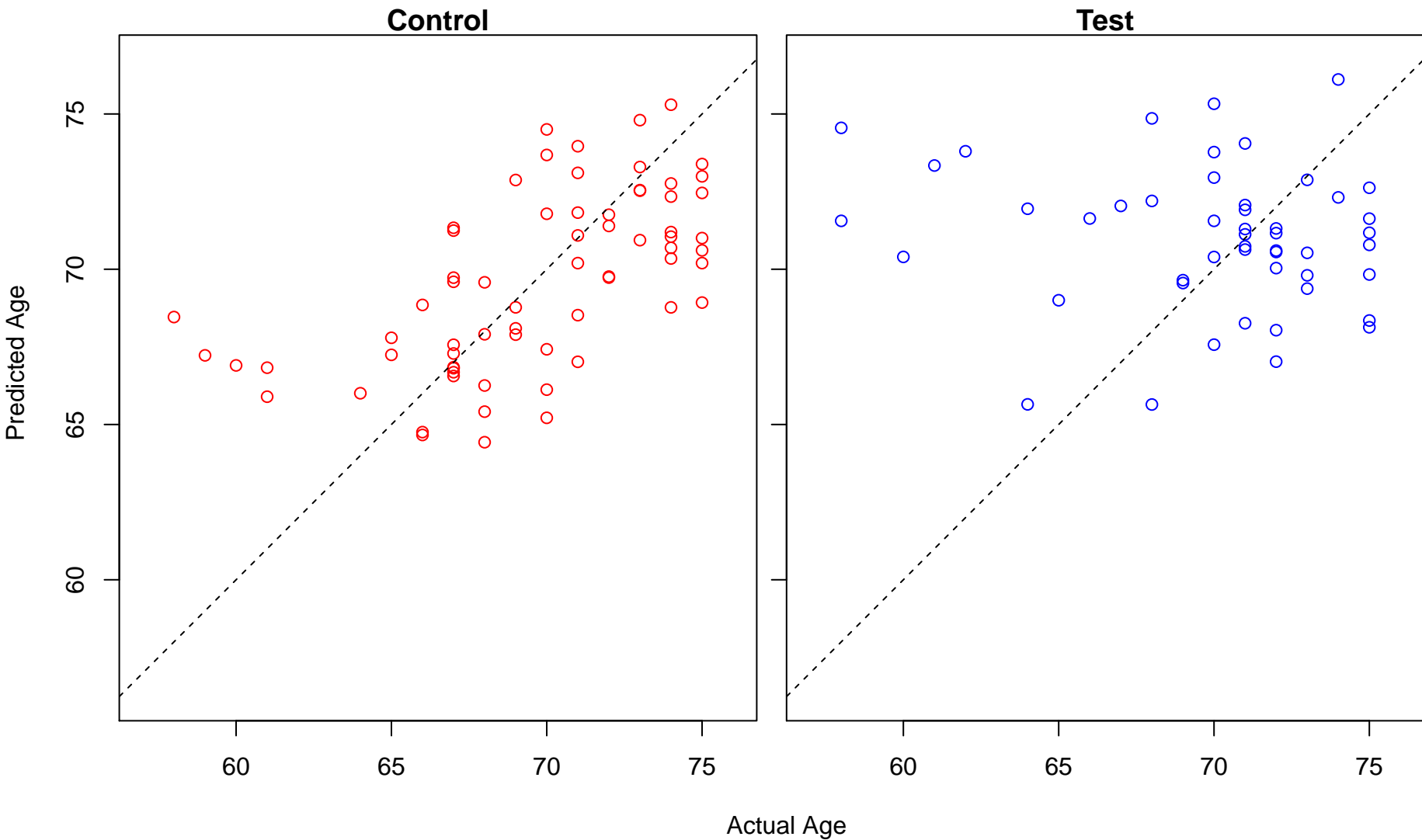
UV protection (Score: 1.108936)



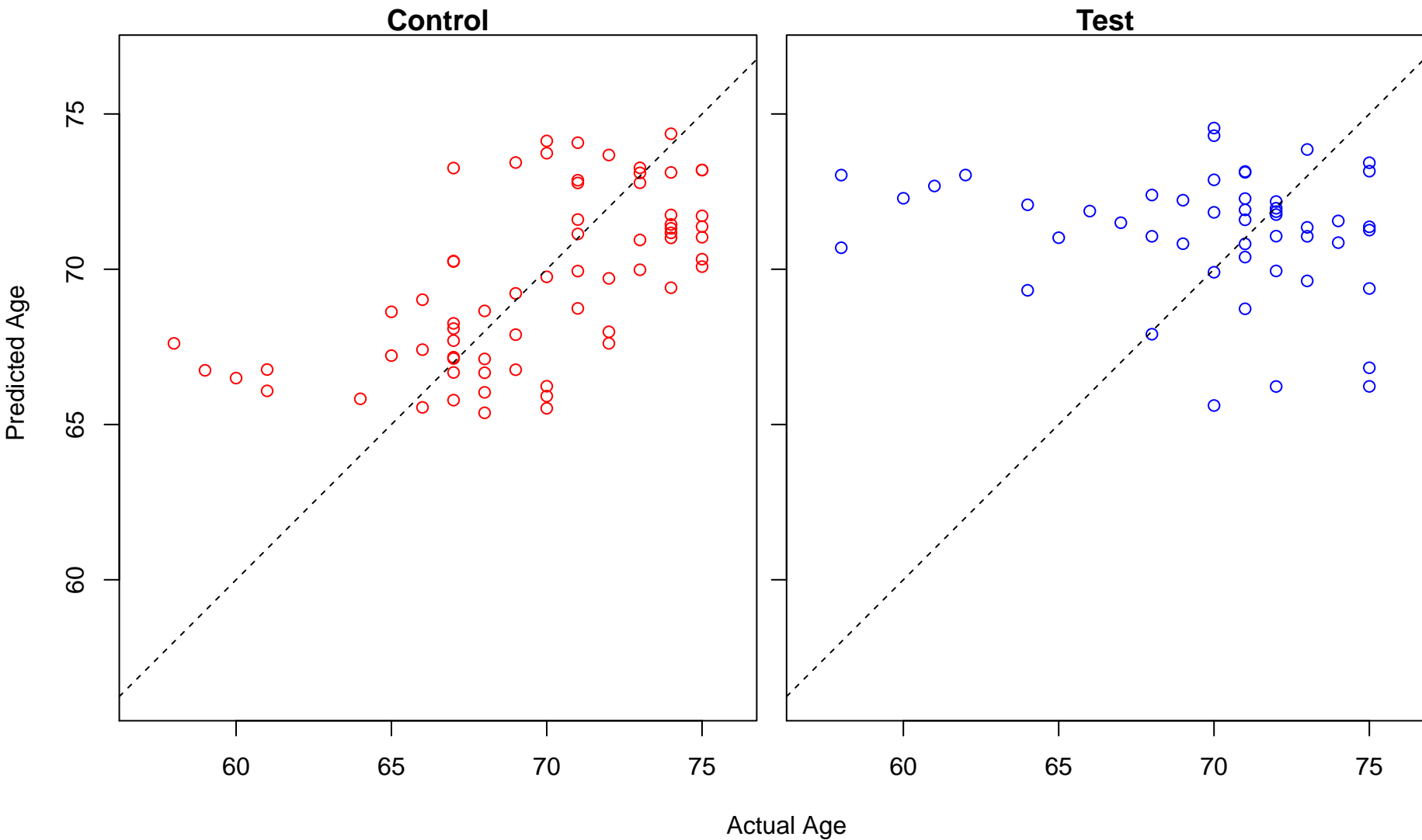
negative regulation of angiogenesis (Score: 1.108608)



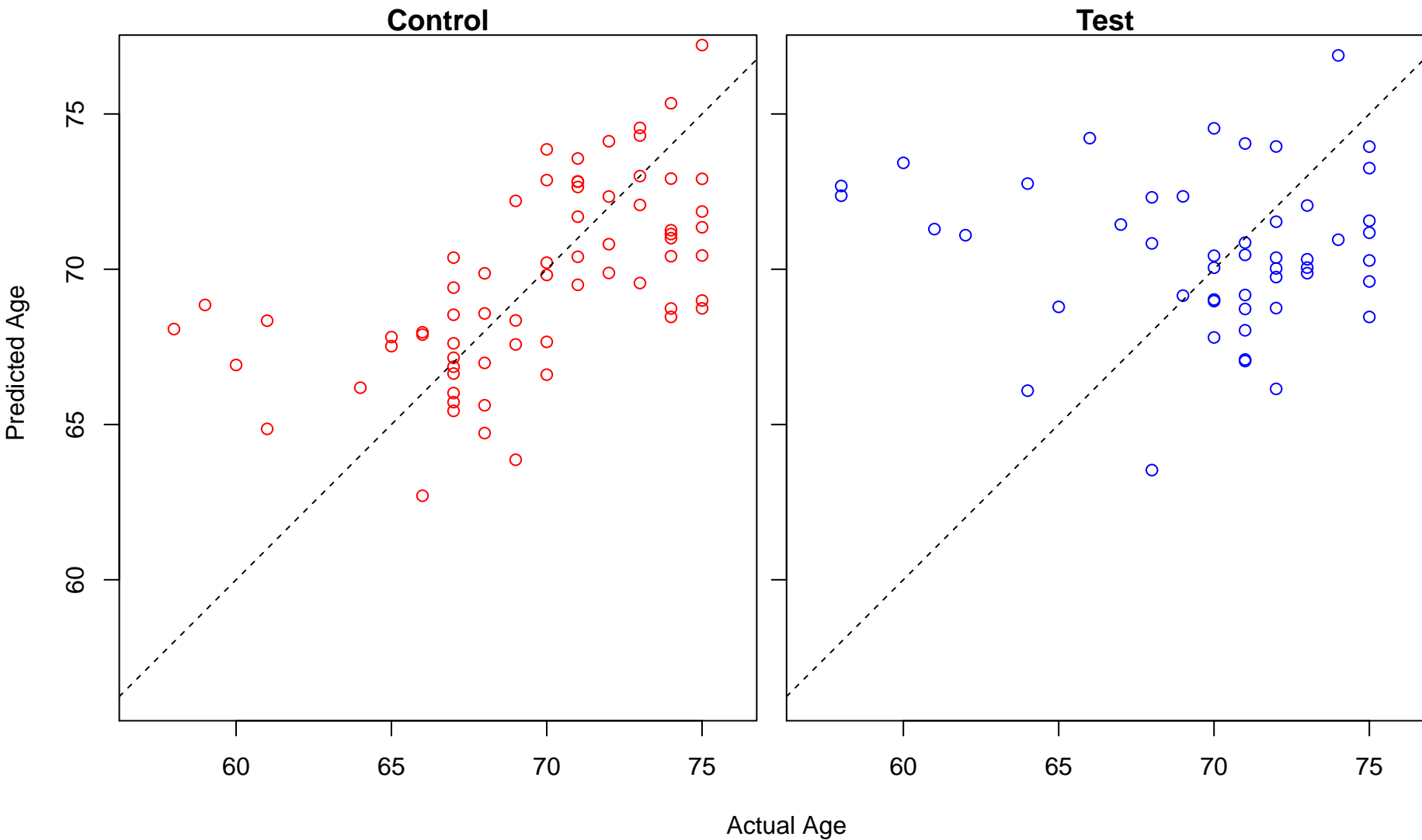
regulation of DNA-templated transcription, elongation (Score: 1.108532)



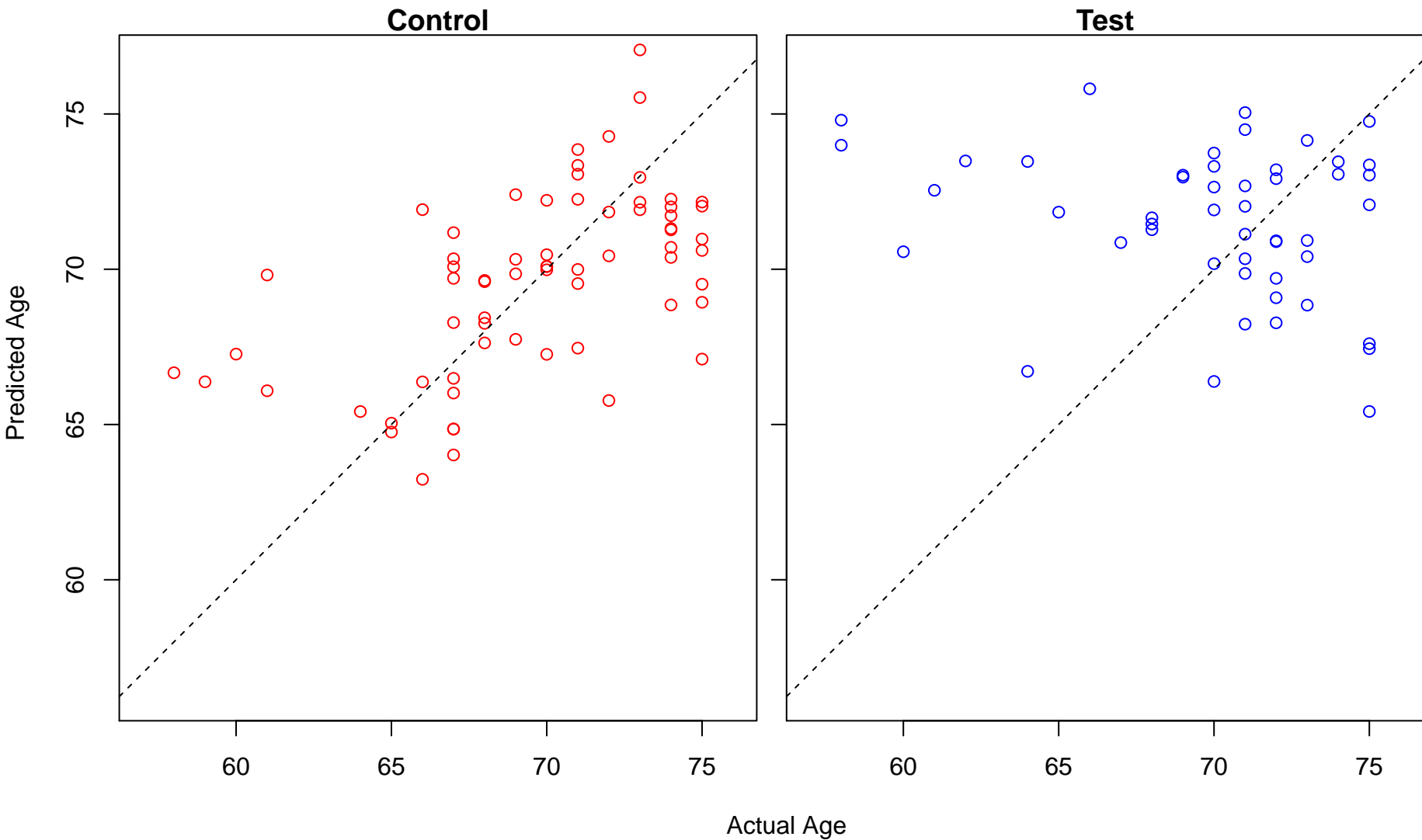
negative regulation of blood vessel morphogenesis (Score: 1.108227)



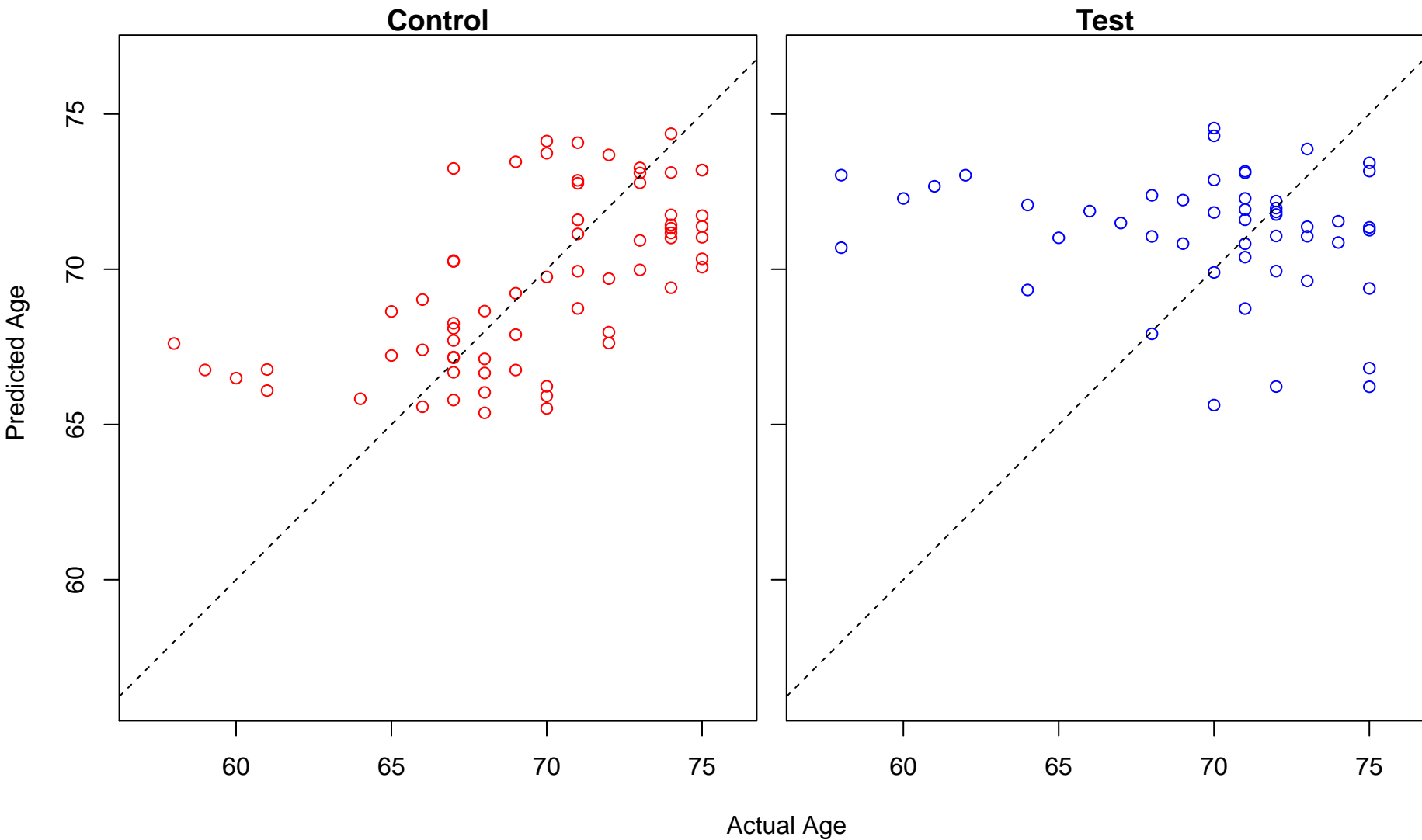
brain morphogenesis (Score: 1.107640)



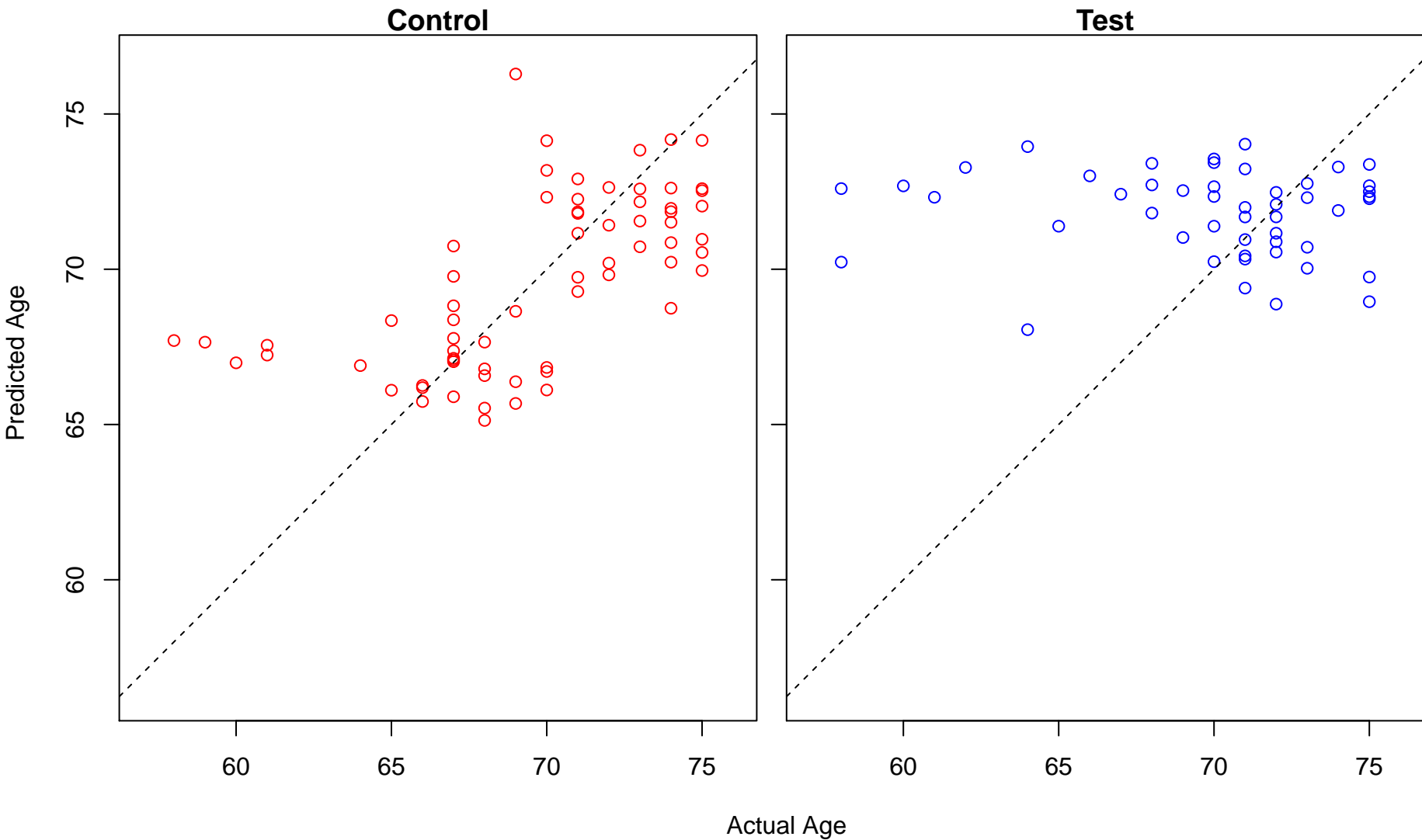
fucosylation (Score: 1.106742)



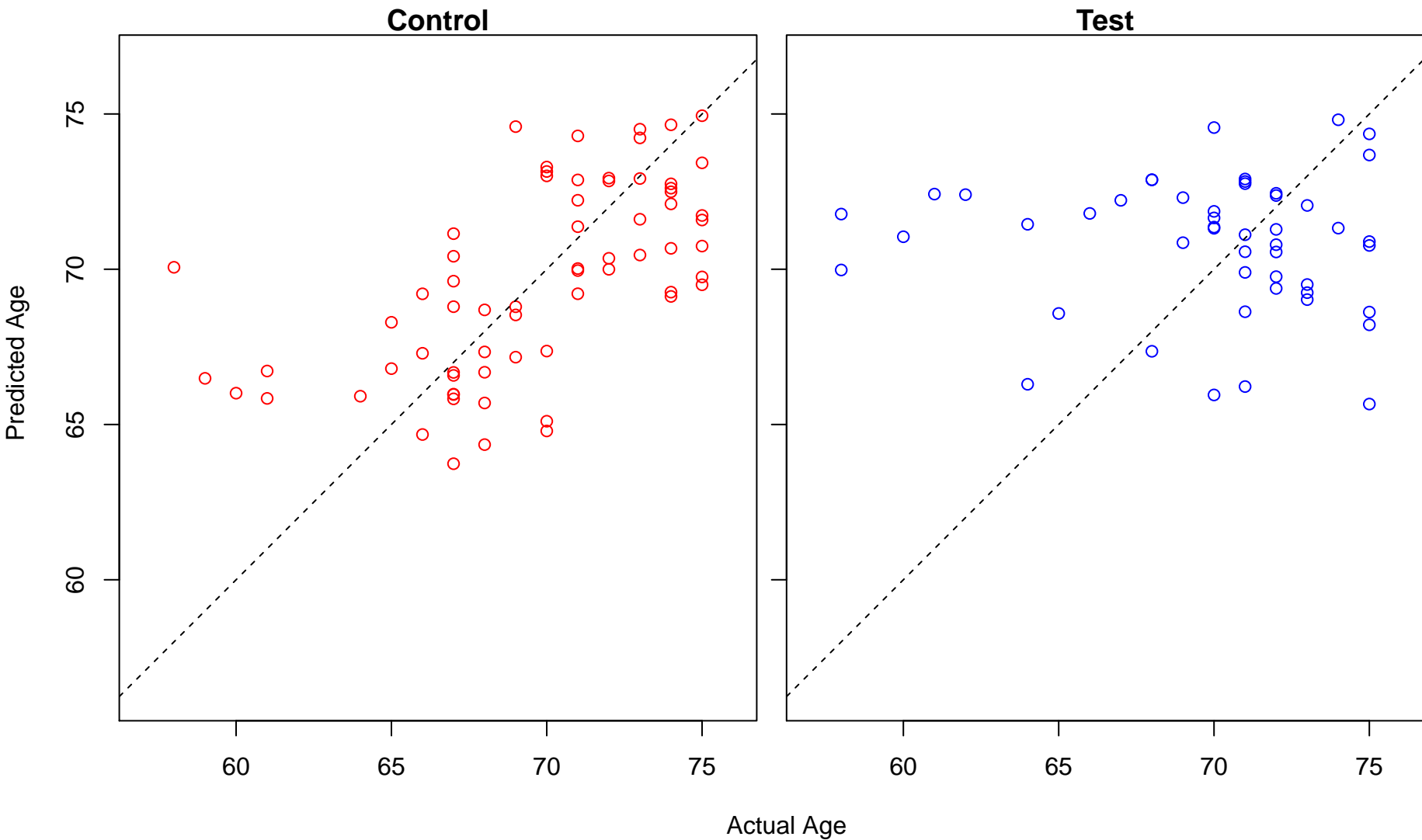
negative regulation of vasculature development (Score: 1.106251)



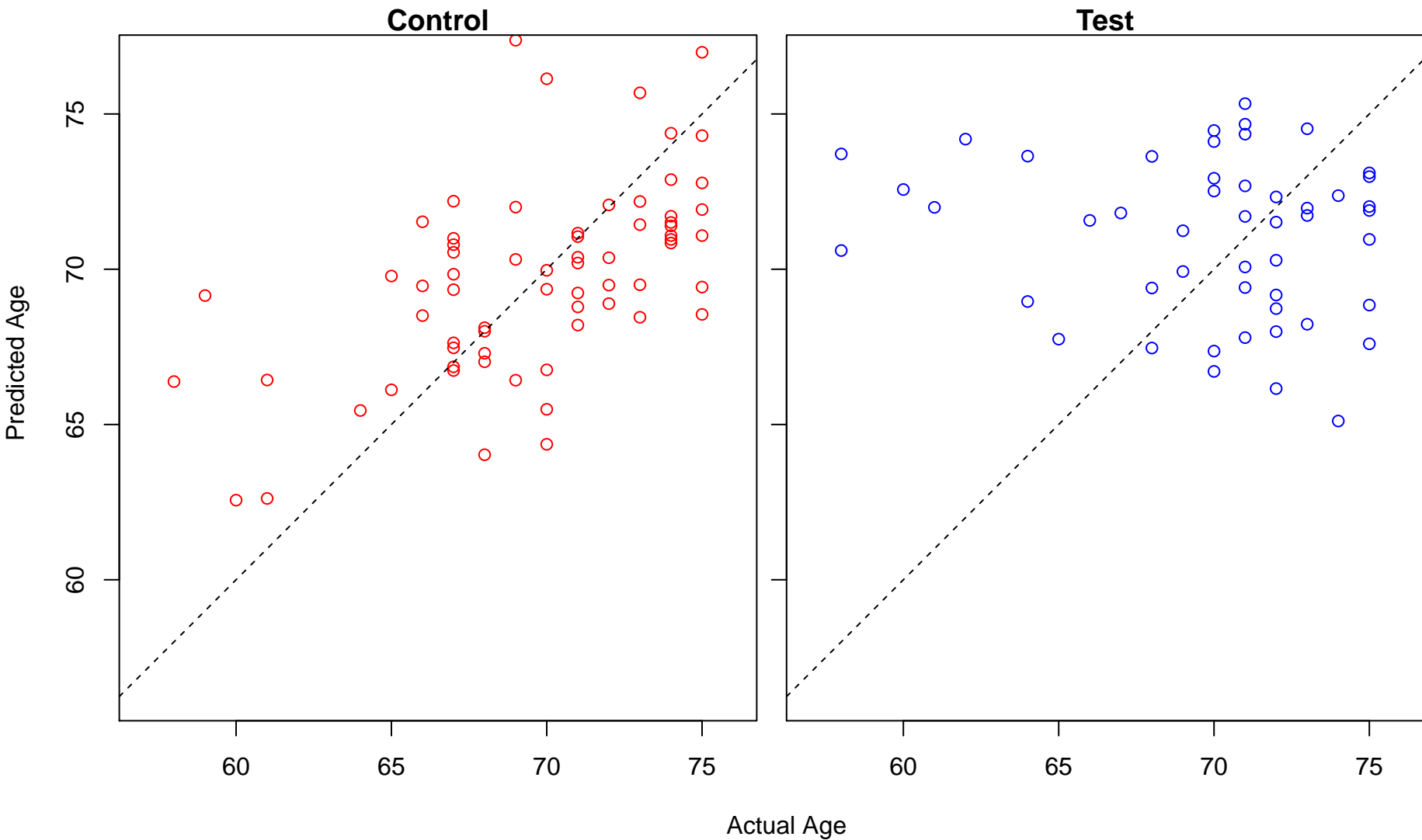
positive regulation of anoikis (Score: 1.105609)



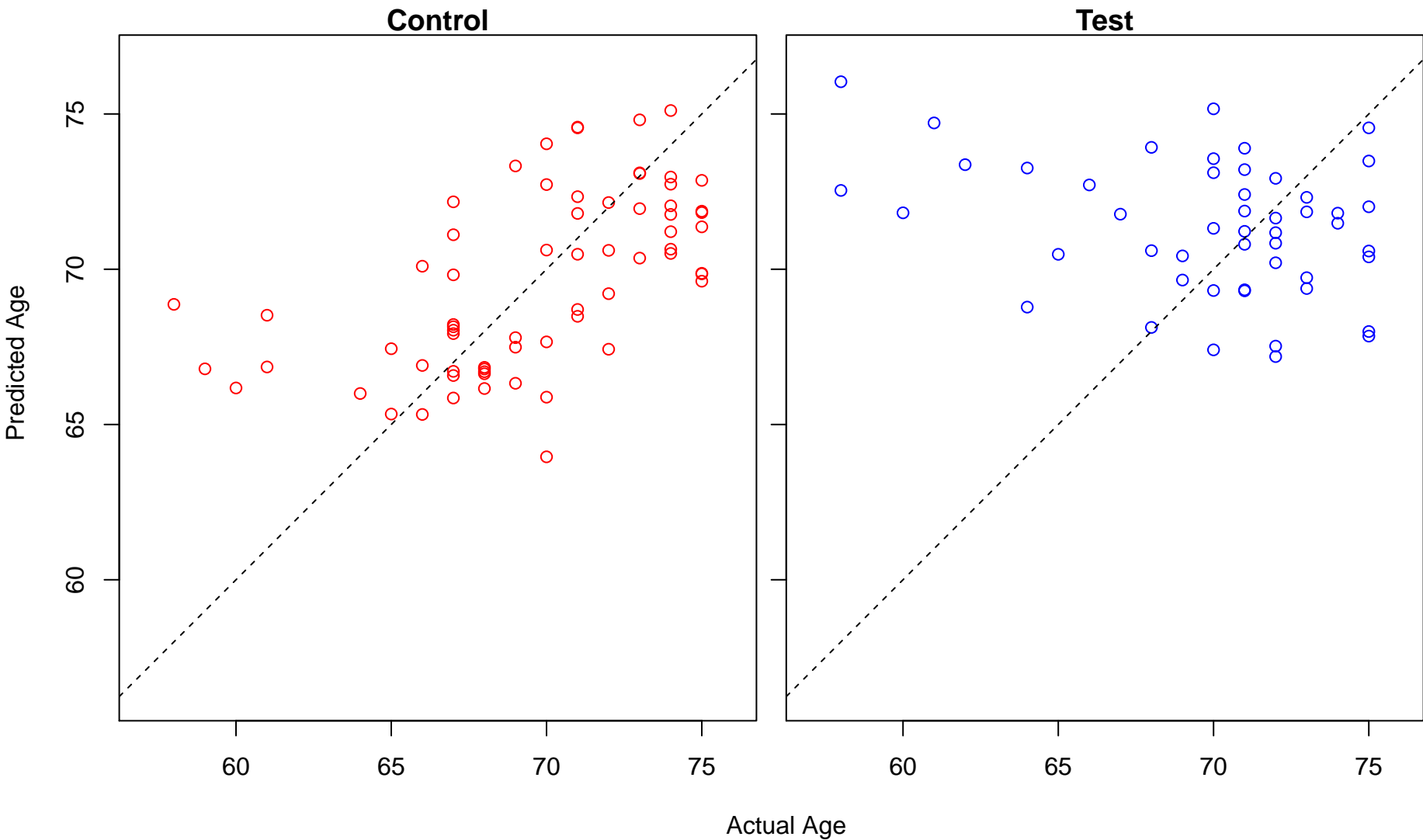
defense response to Gram-positive bacterium (Score: 1.105602)



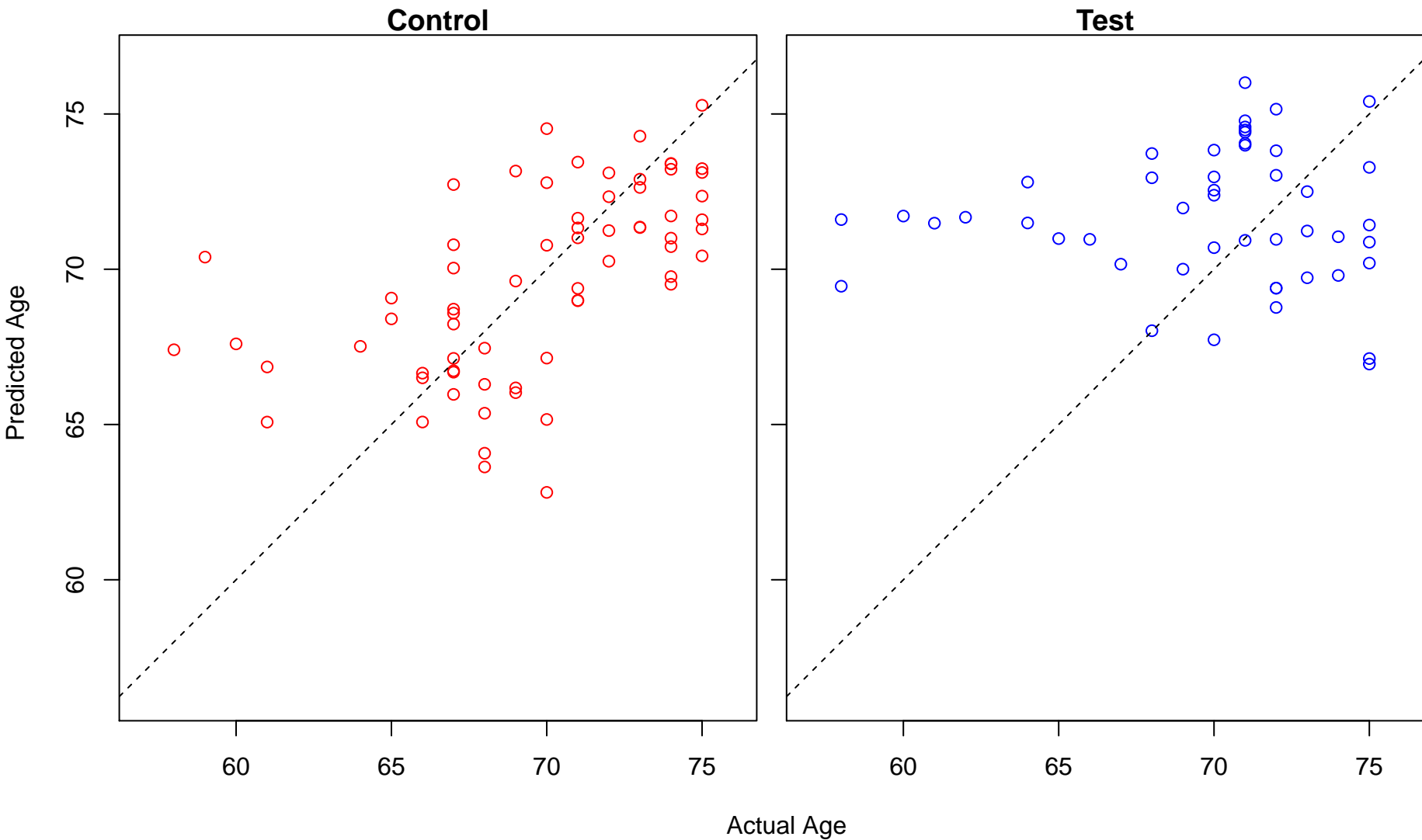
histone H2B ubiquitination (Score: 1.105542)



renal system process (Score: 1.105472)

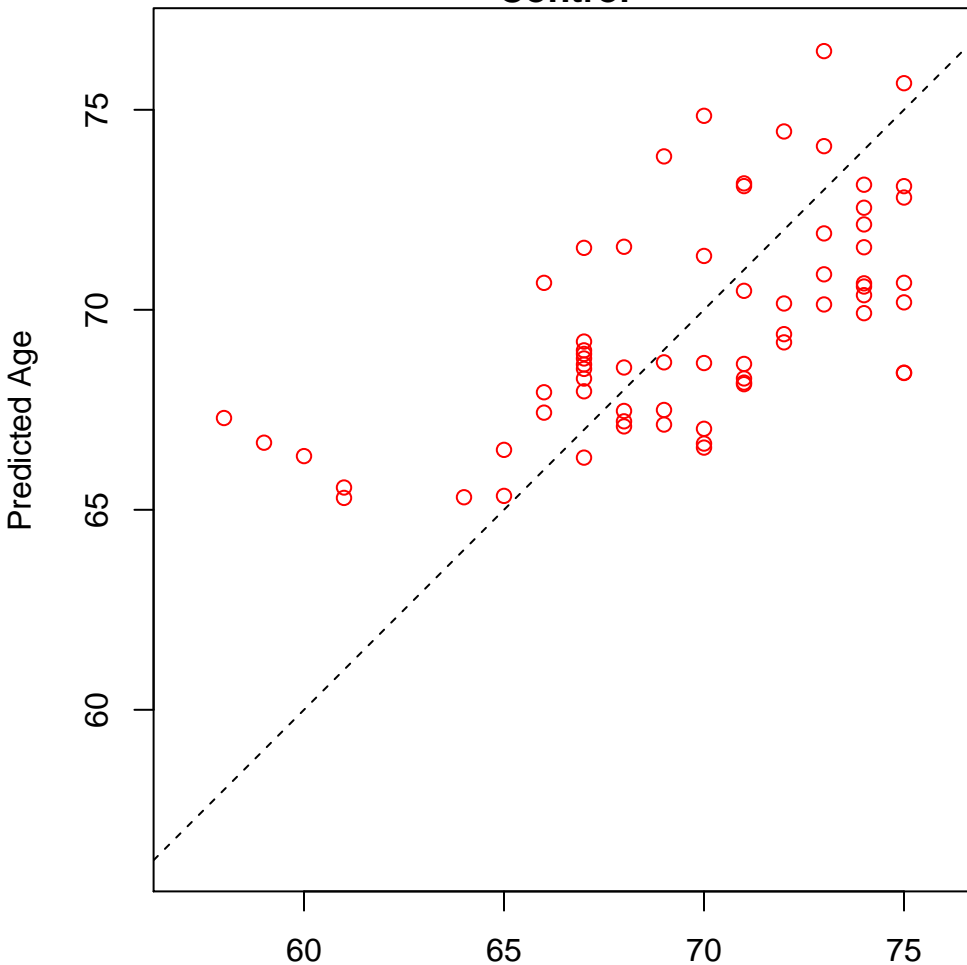


cellular metabolic compound salvage (Score: 1.104815)

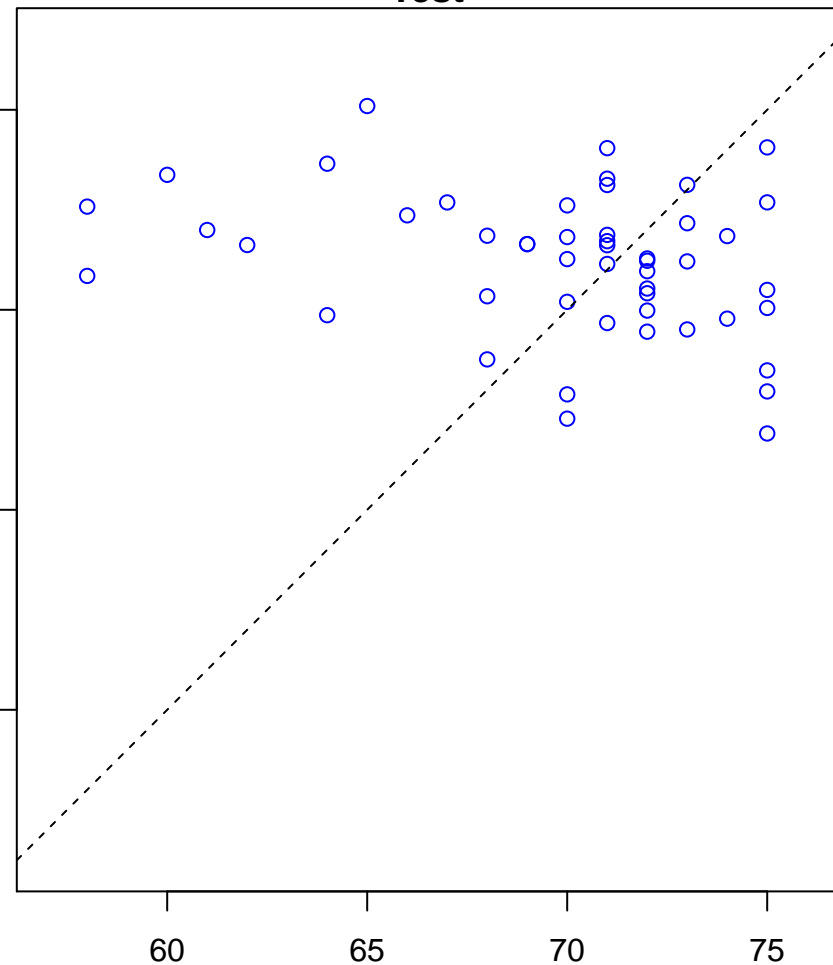


negative regulation of gluconeogenesis (Score: 1.104582)

Control

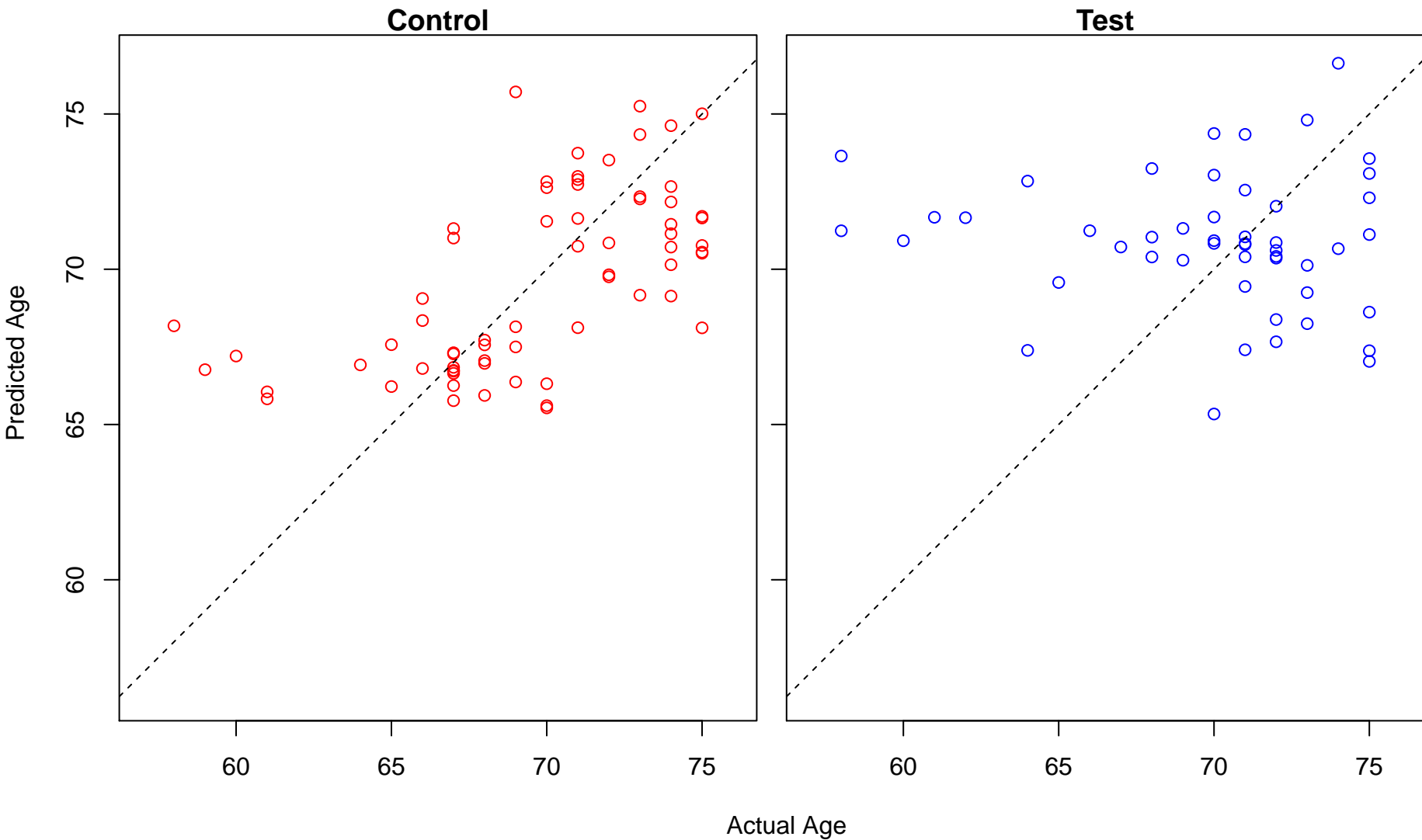


Test

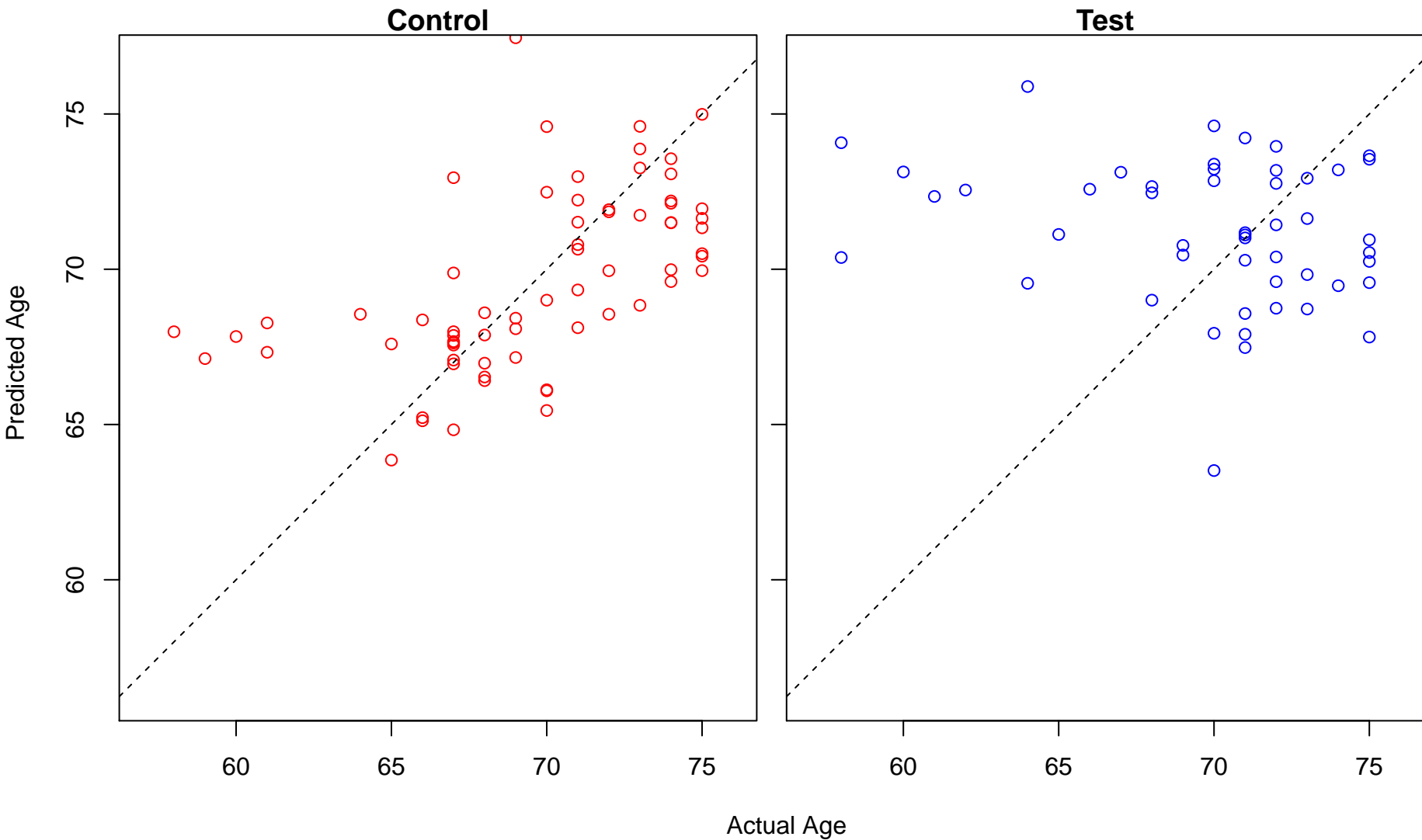


Actual Age

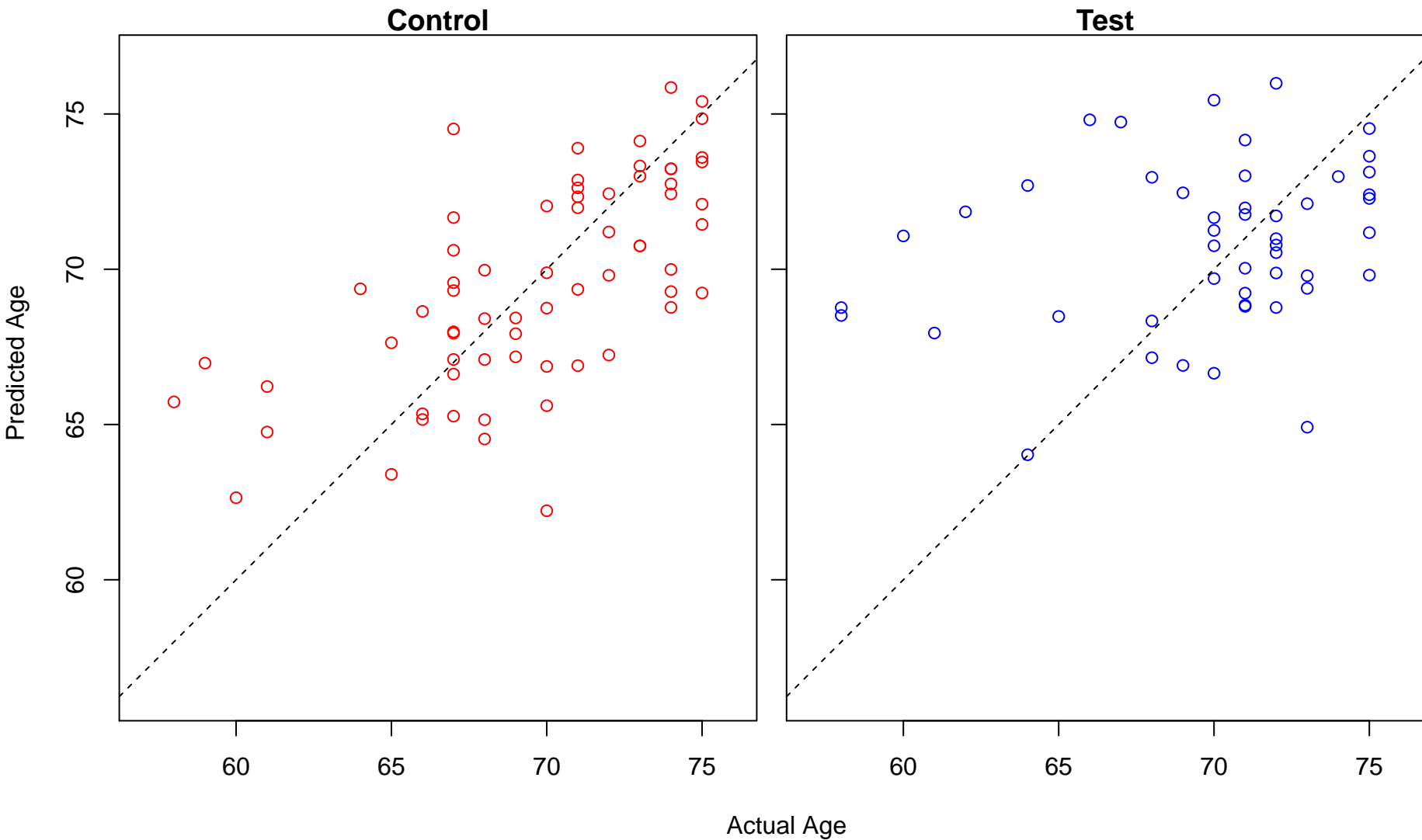
modulation by virus of host morphology or physiology (Score: 1.104360)



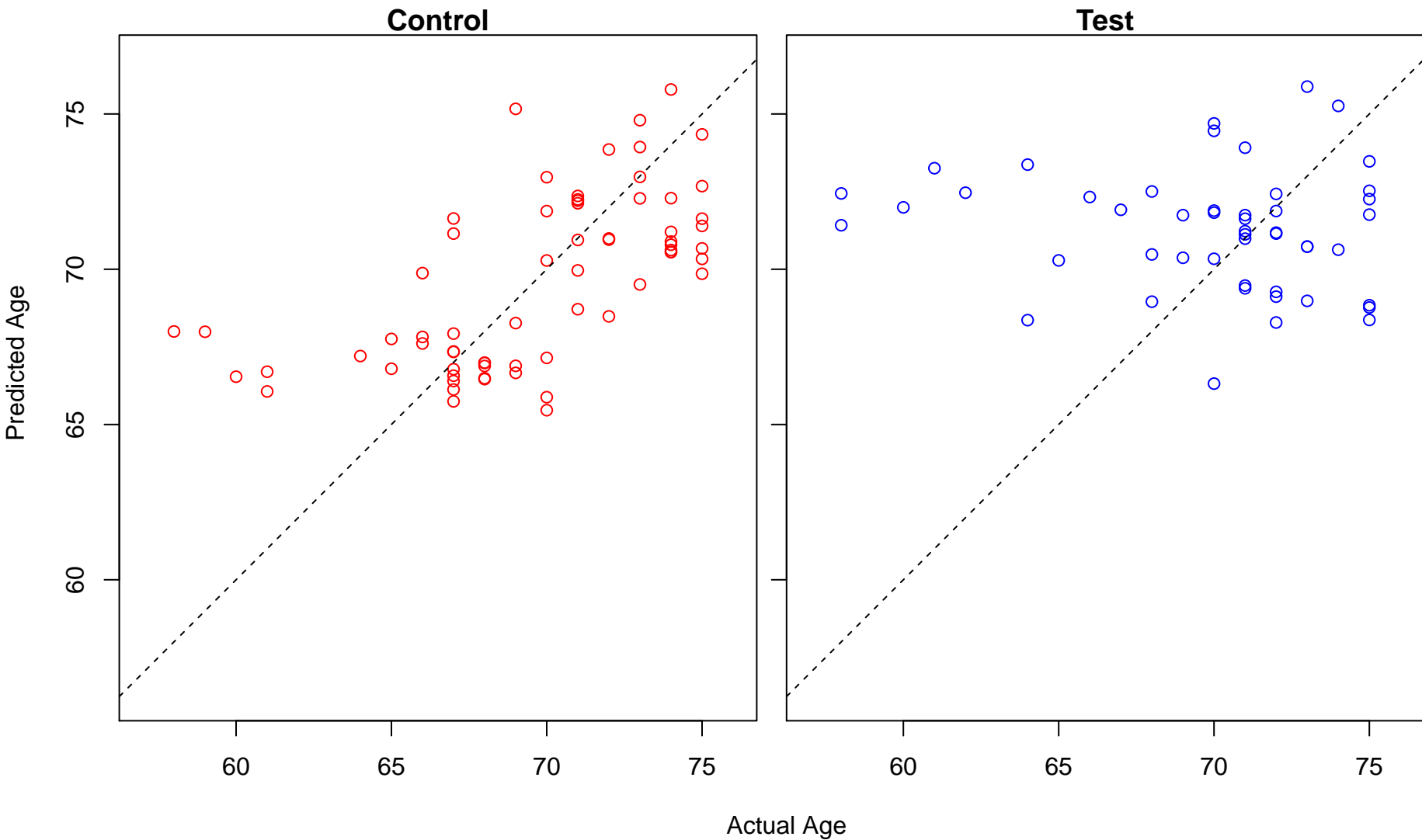
regulation of calcium-mediated signaling (Score: 1.104322)



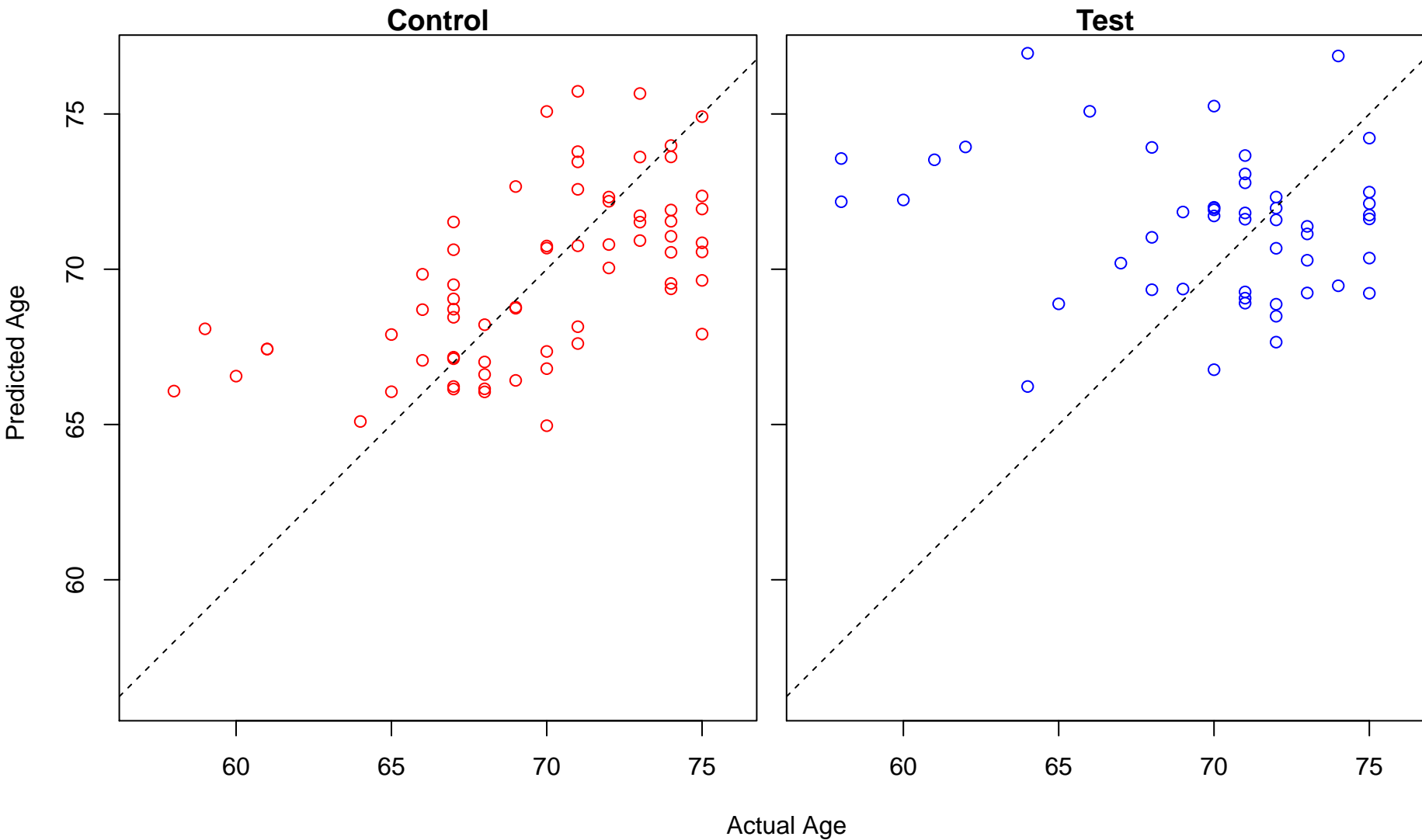
regulation of bone mineralization (Score: 1.104308)



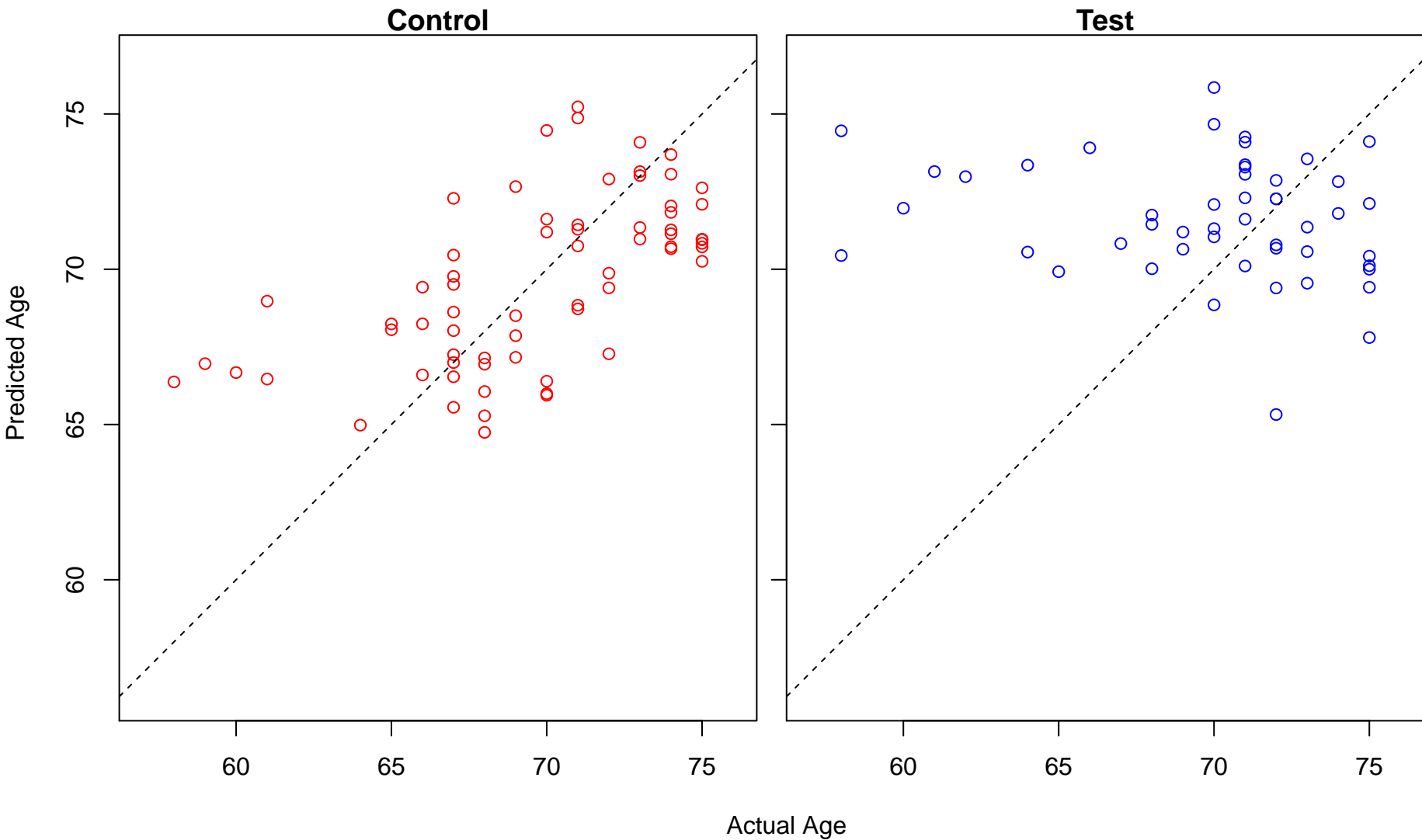
locomotory behavior (Score: 1.103435)



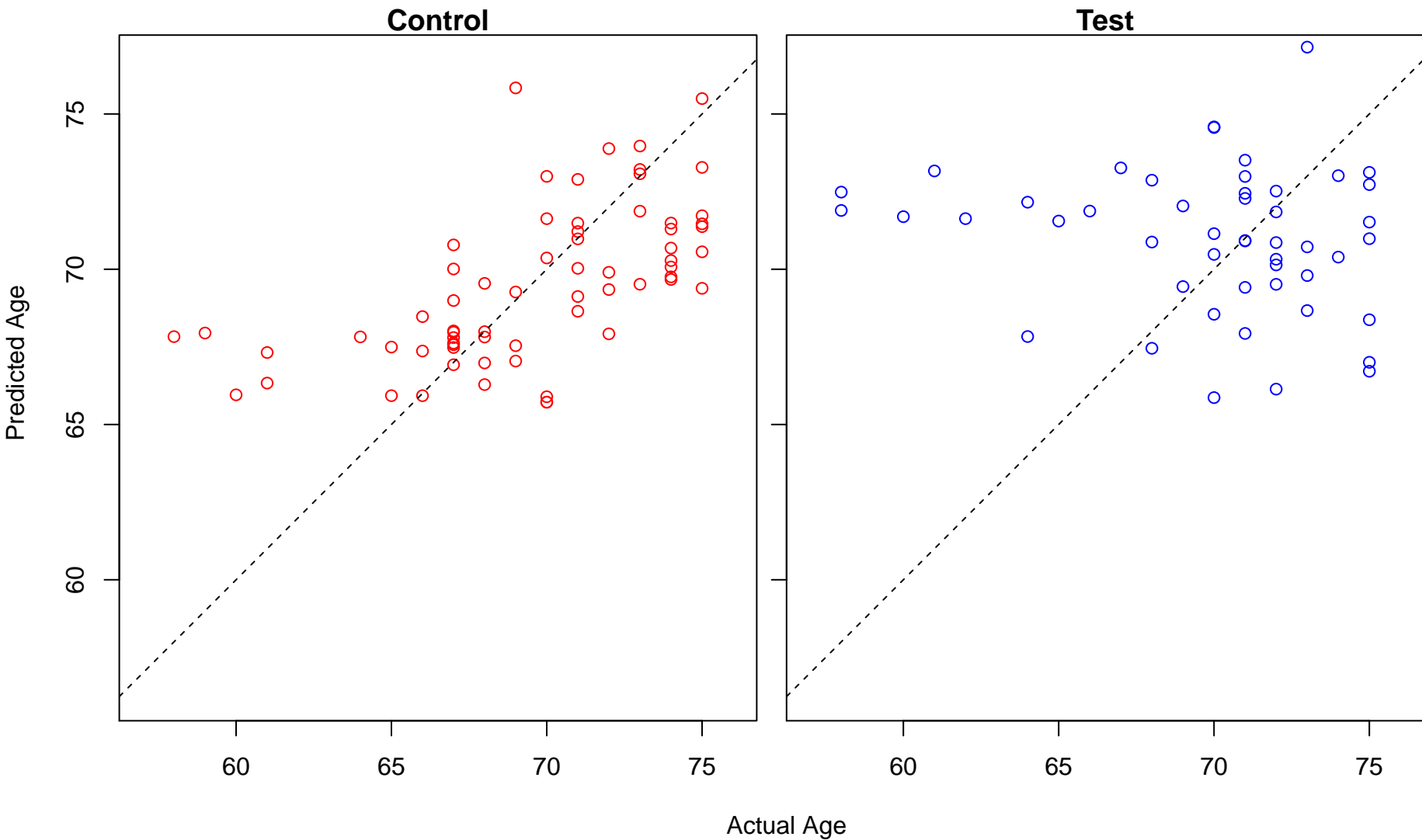
response to interleukin-1 (Score: 1.103080)



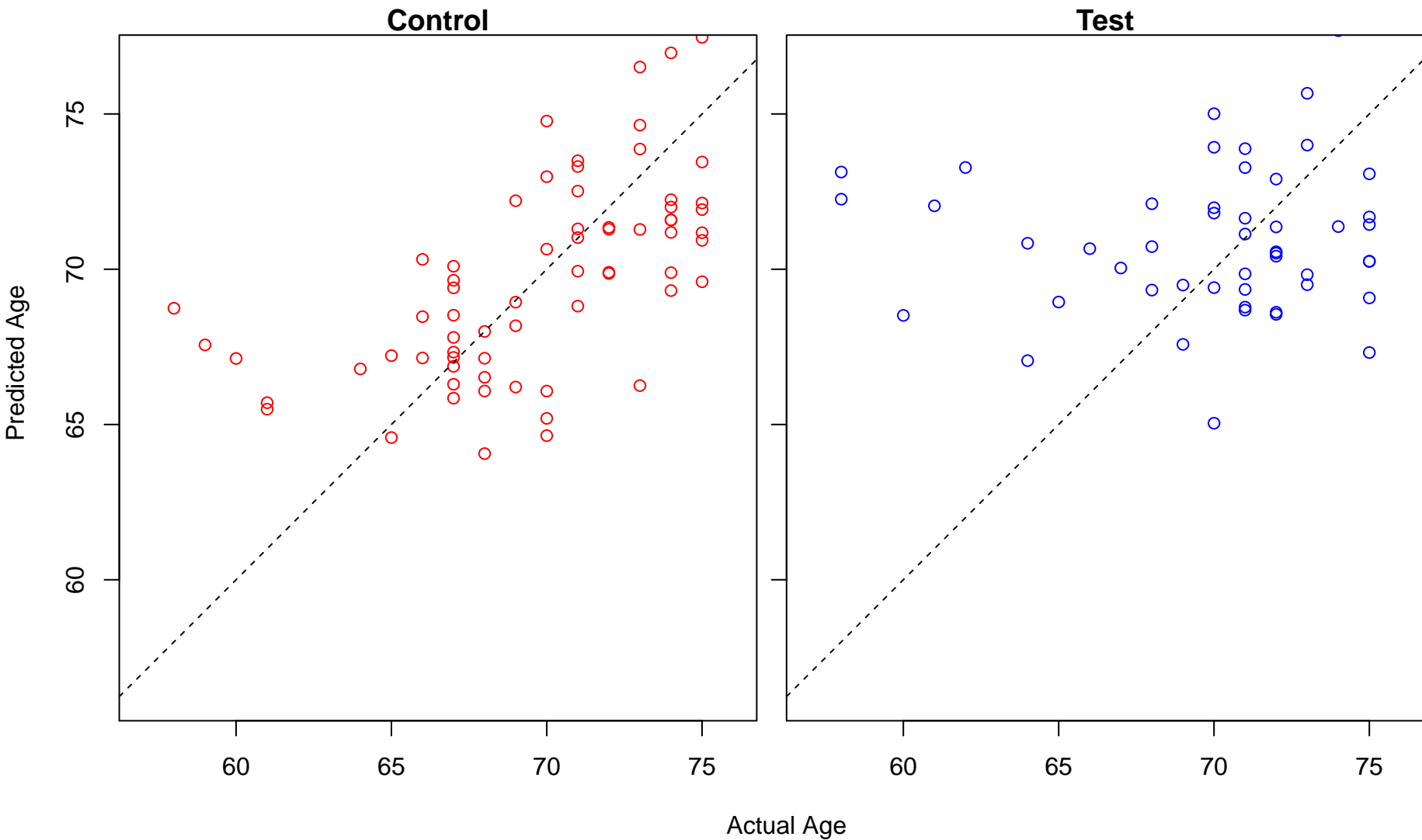
sulfur amino acid metabolic process (Score: 1.102481)



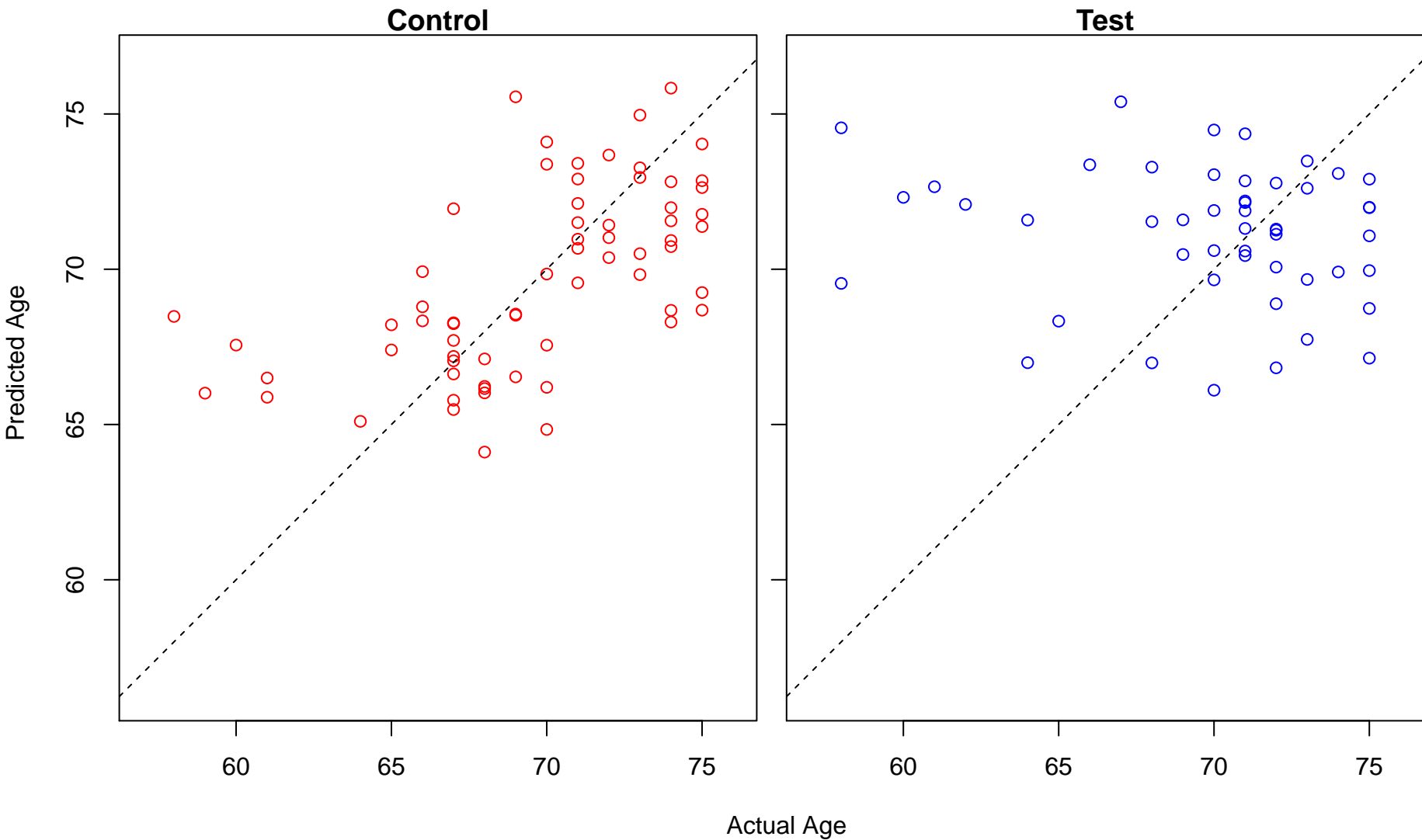
protein K11-linked ubiquitination (Score: 1.100222)



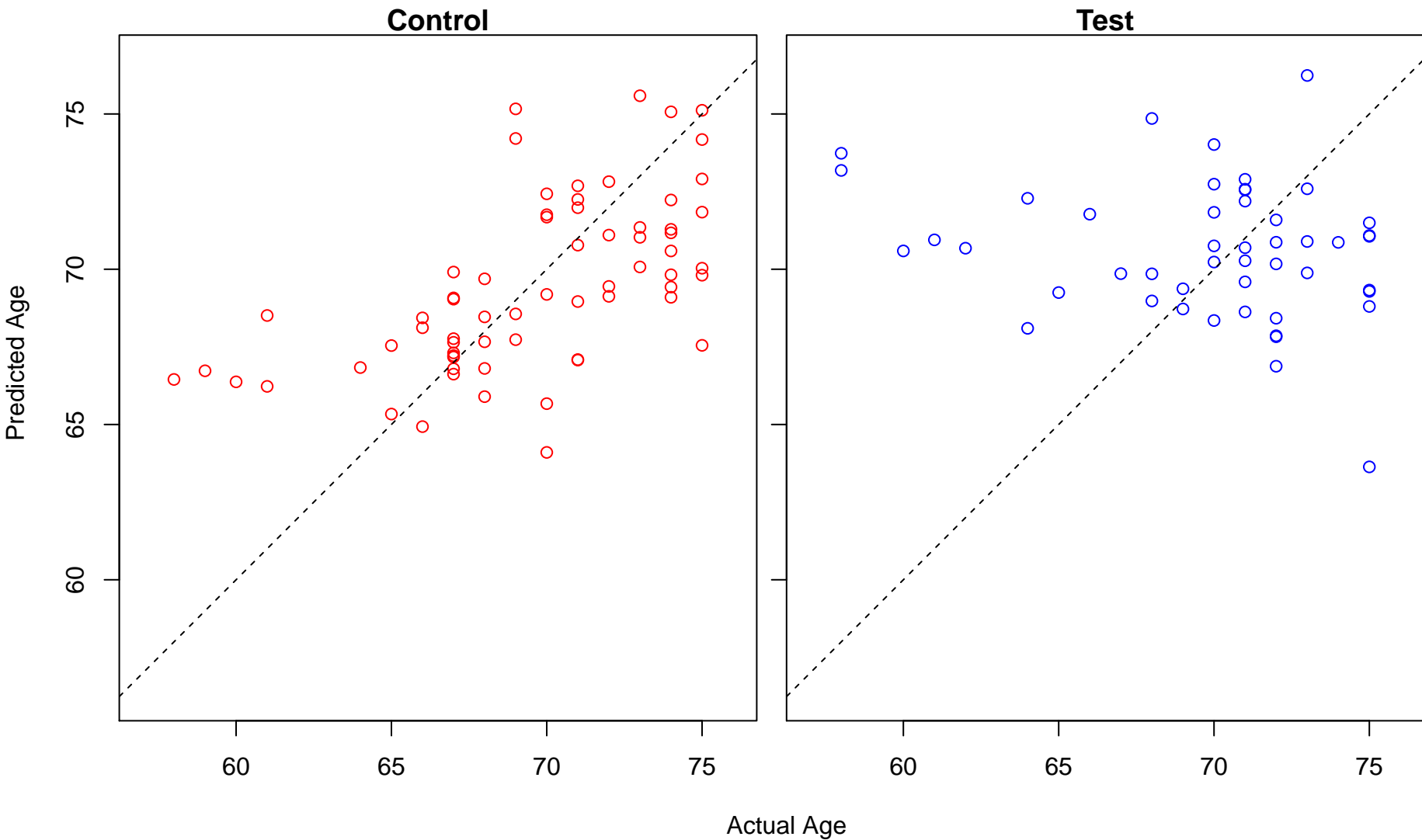
regulation of protein depolymerization (Score: 1.100213)



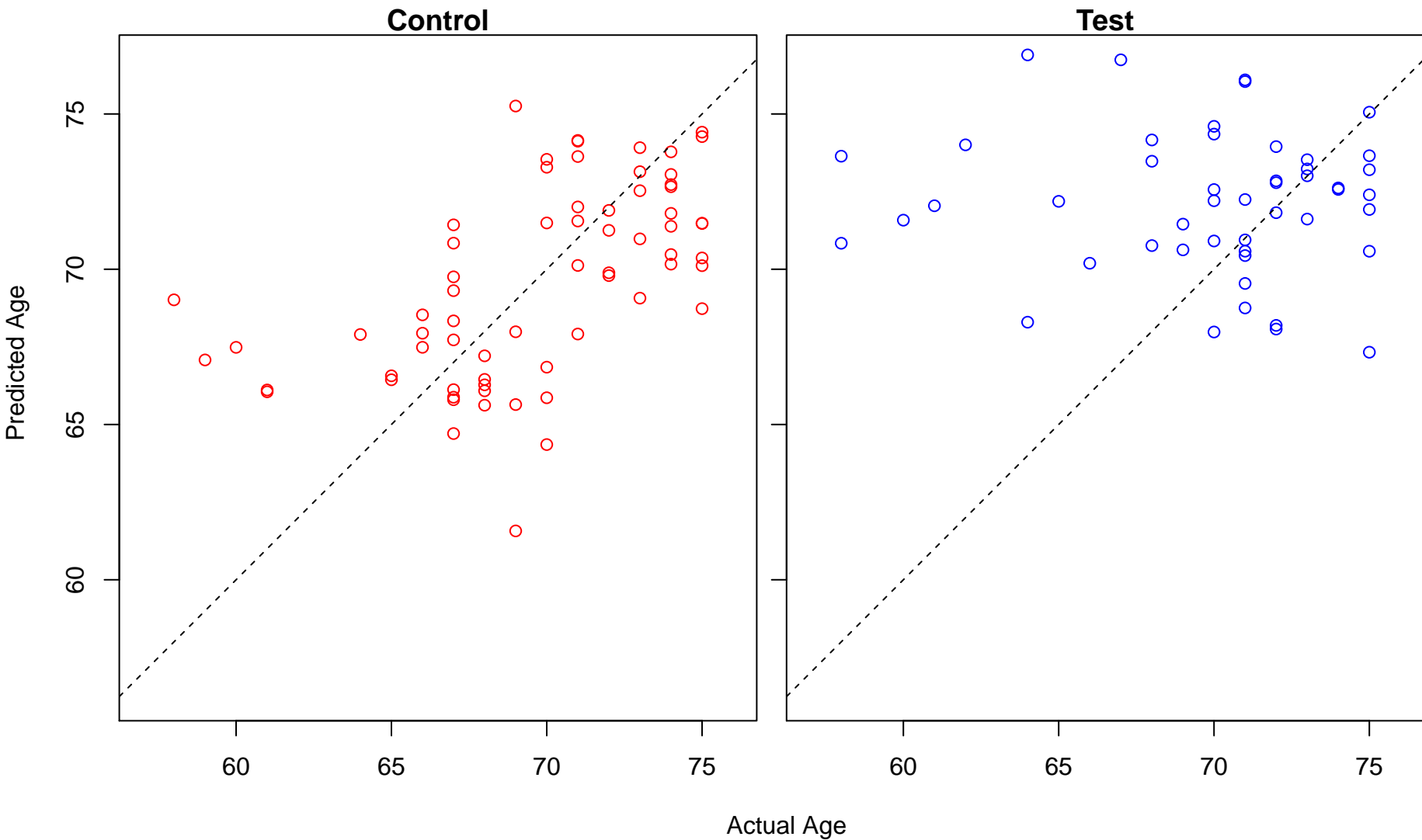
regulation of cellular senescence (Score: 1.099967)



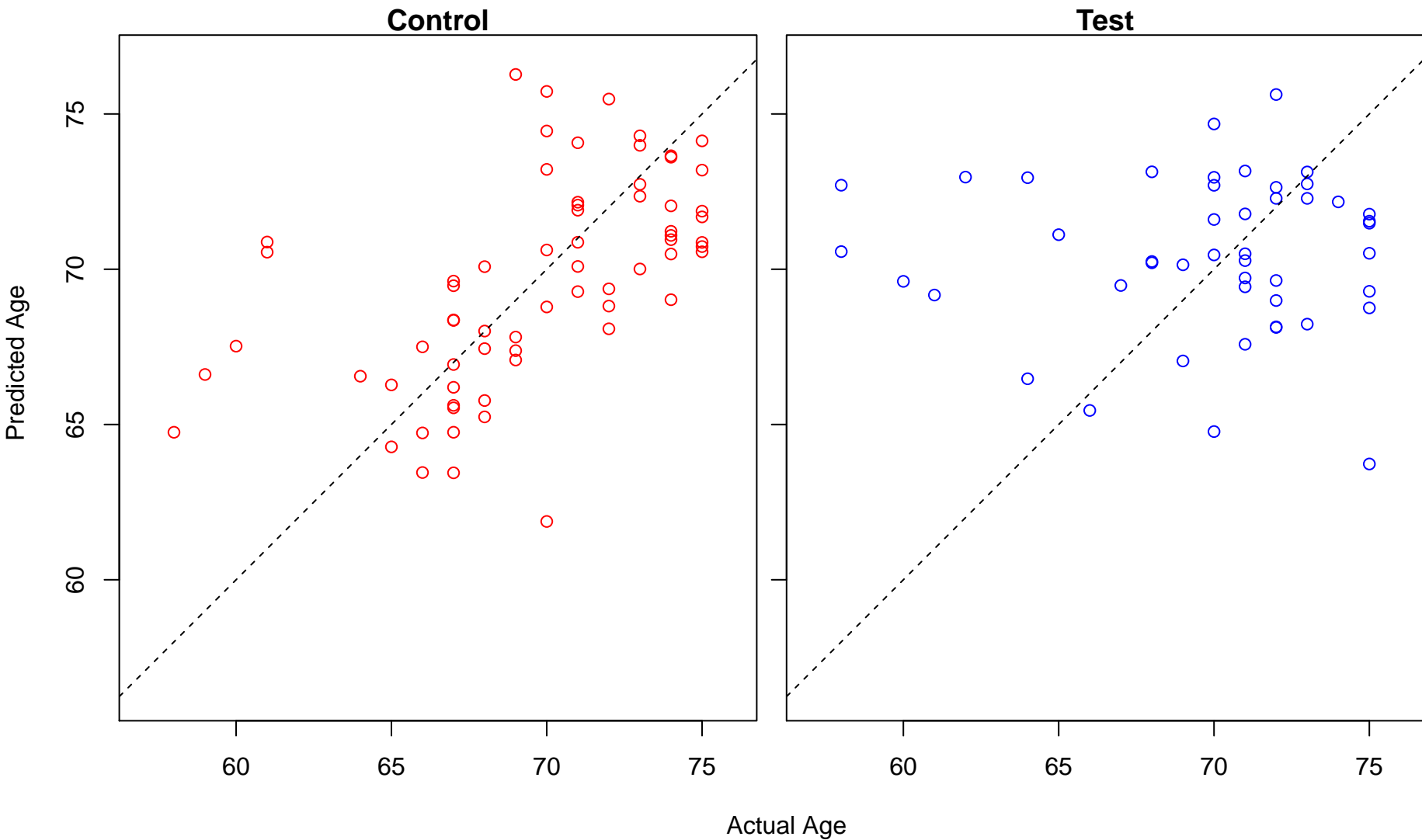
osteoclast differentiation (Score: 1.099963)



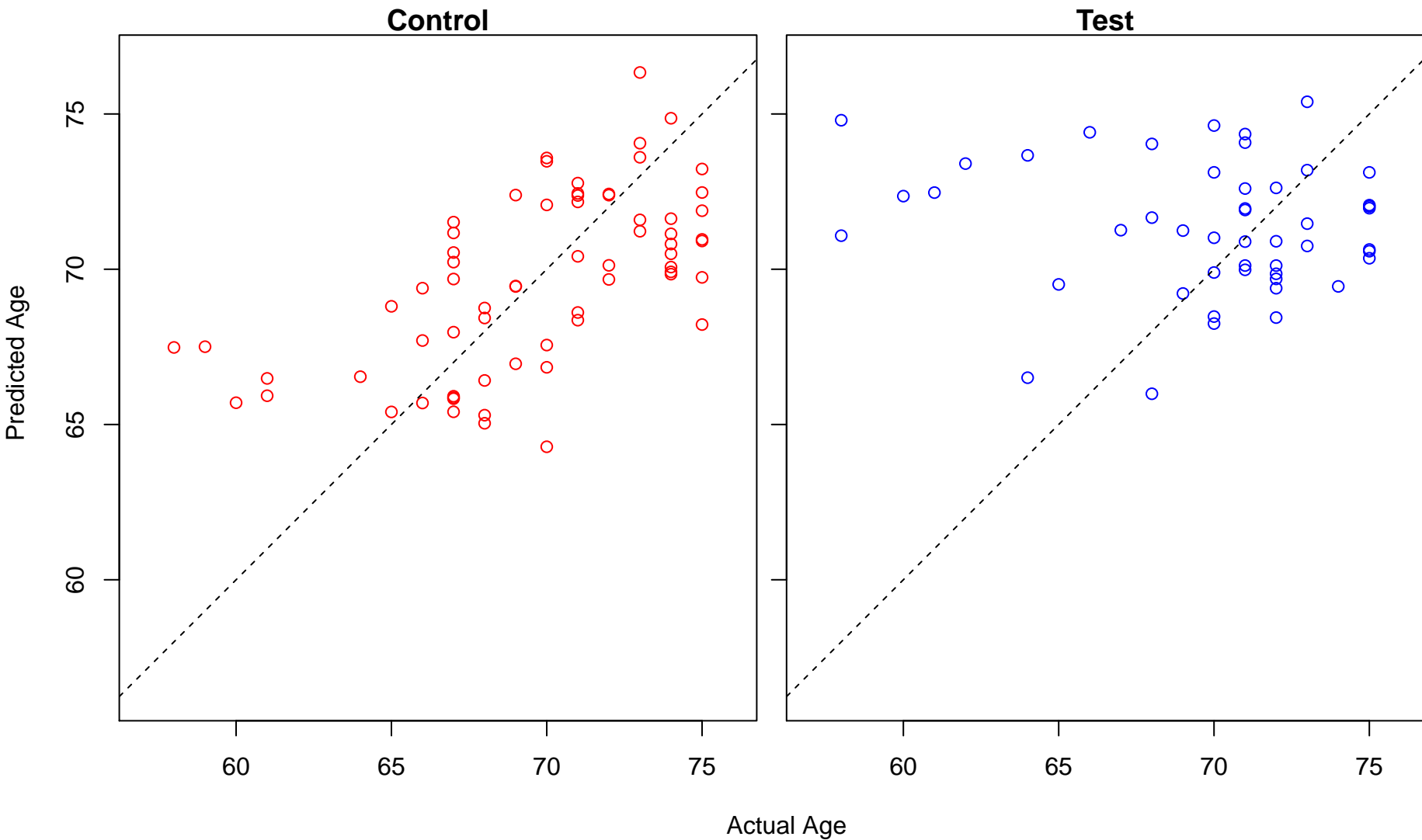
regulation of protein acetylation (Score: 1.098703)



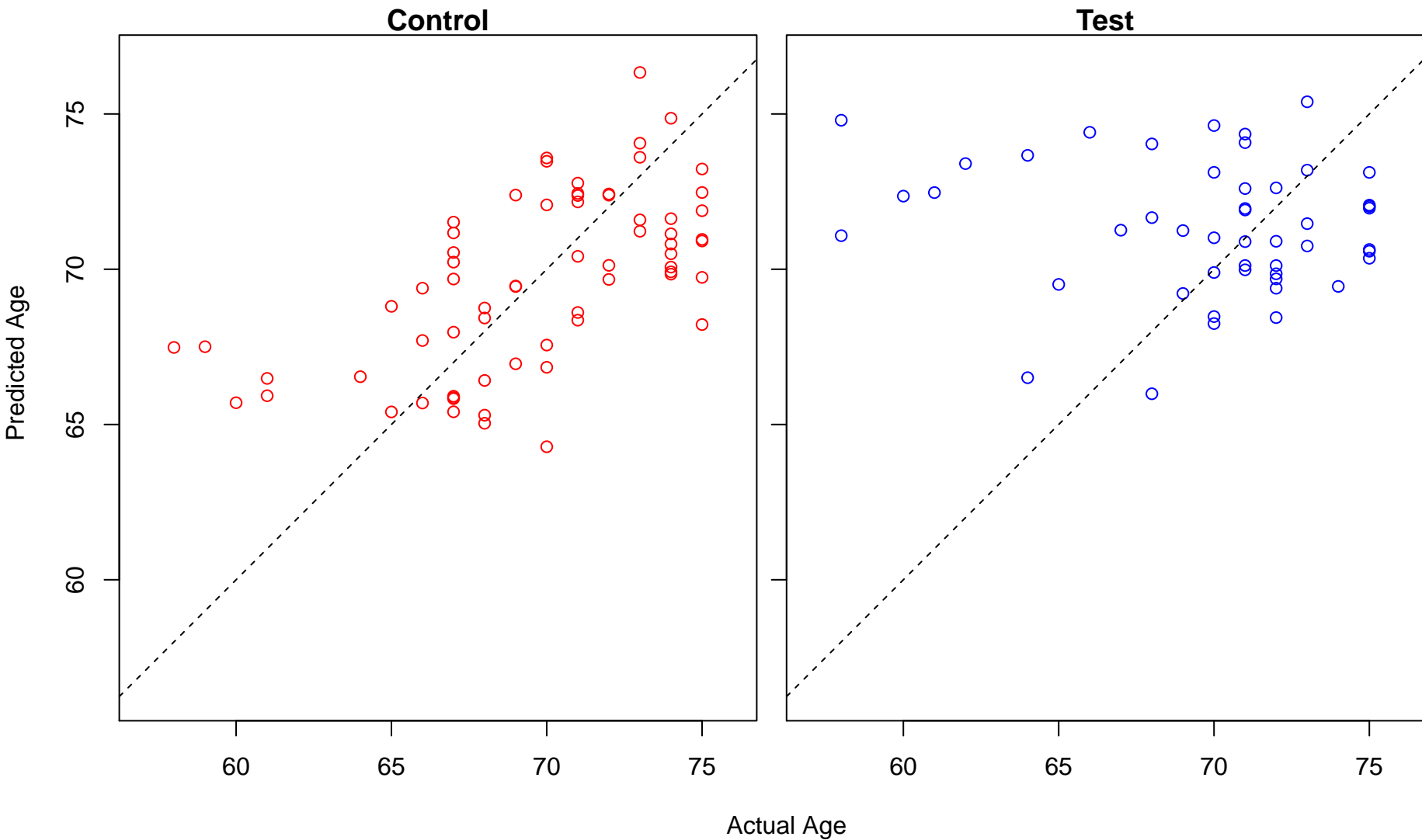
mRNA stabilization (Score: 1.098388)



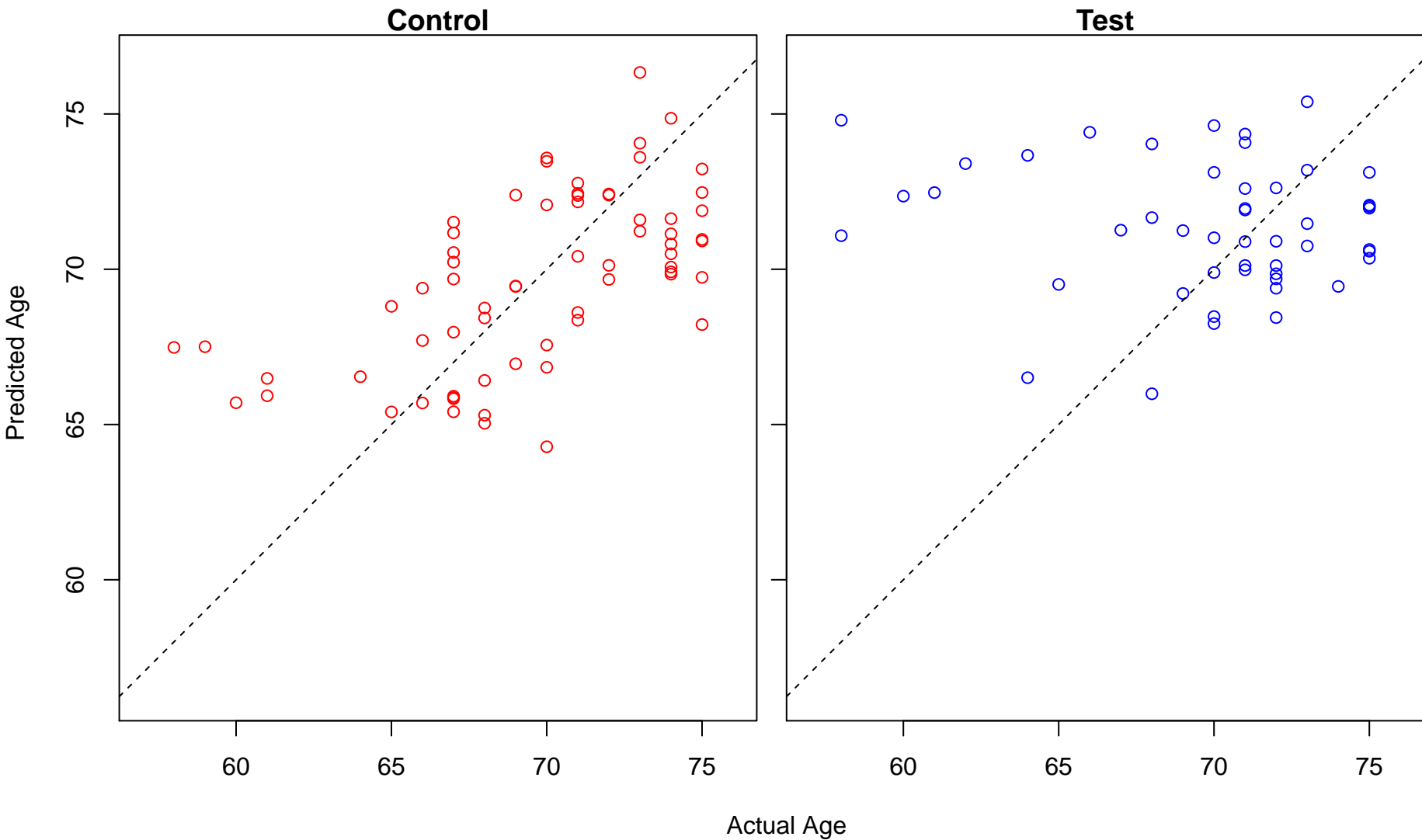
COPI-coated vesicle budding (Score: 1.098283)



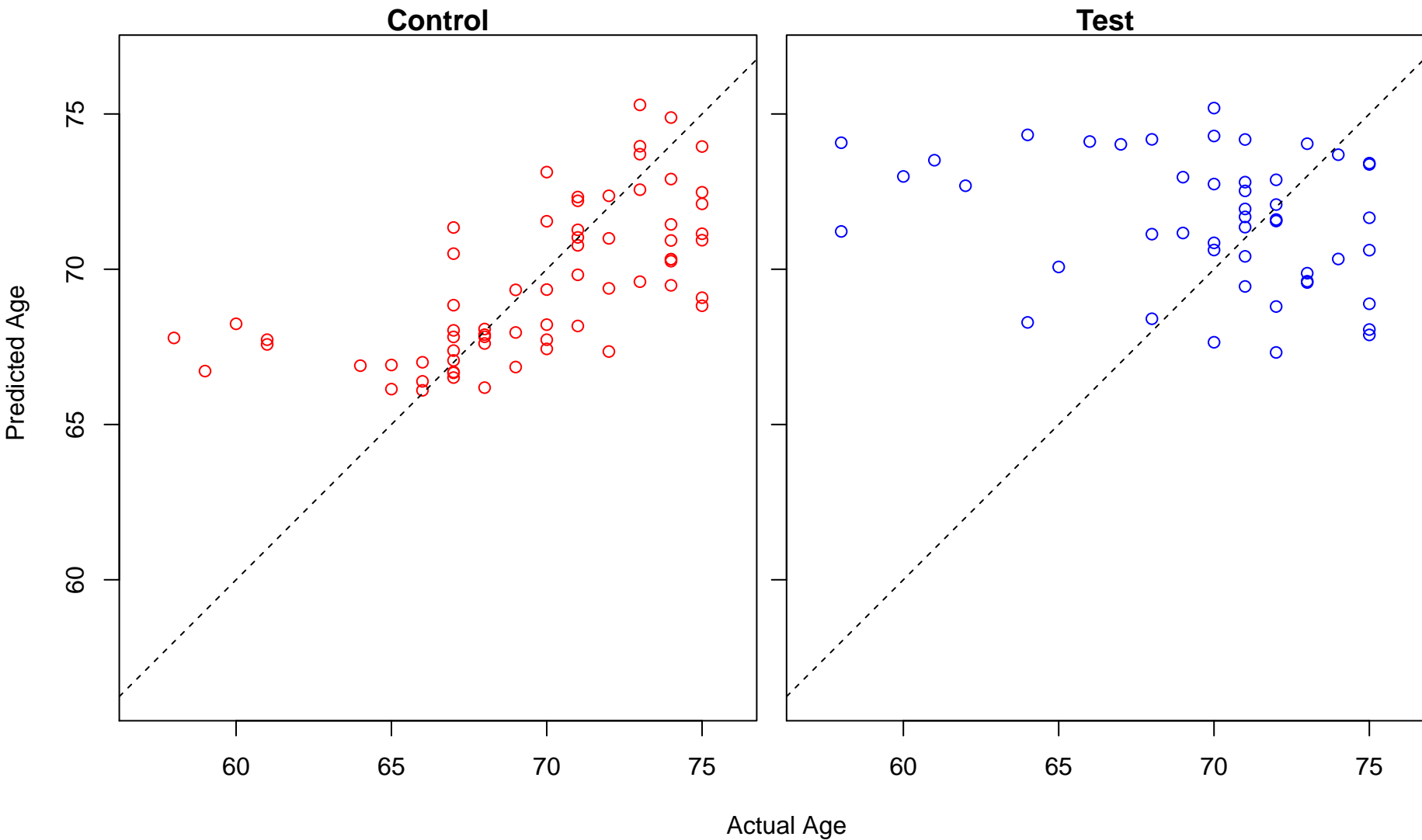
Golgi transport vesicle coating (Score: 1.098283)



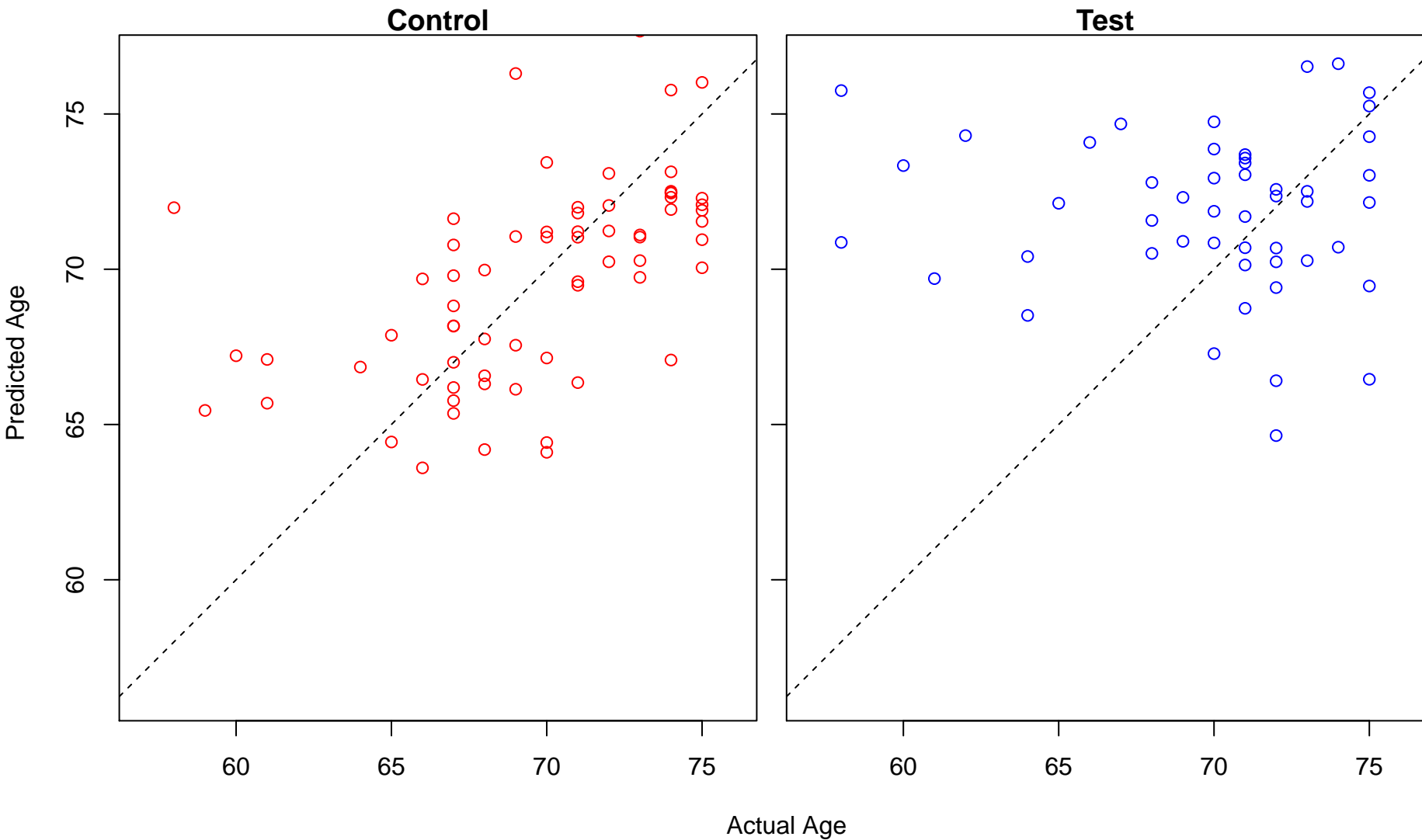
COPI coating of Golgi vesicle (Score: 1.098283)



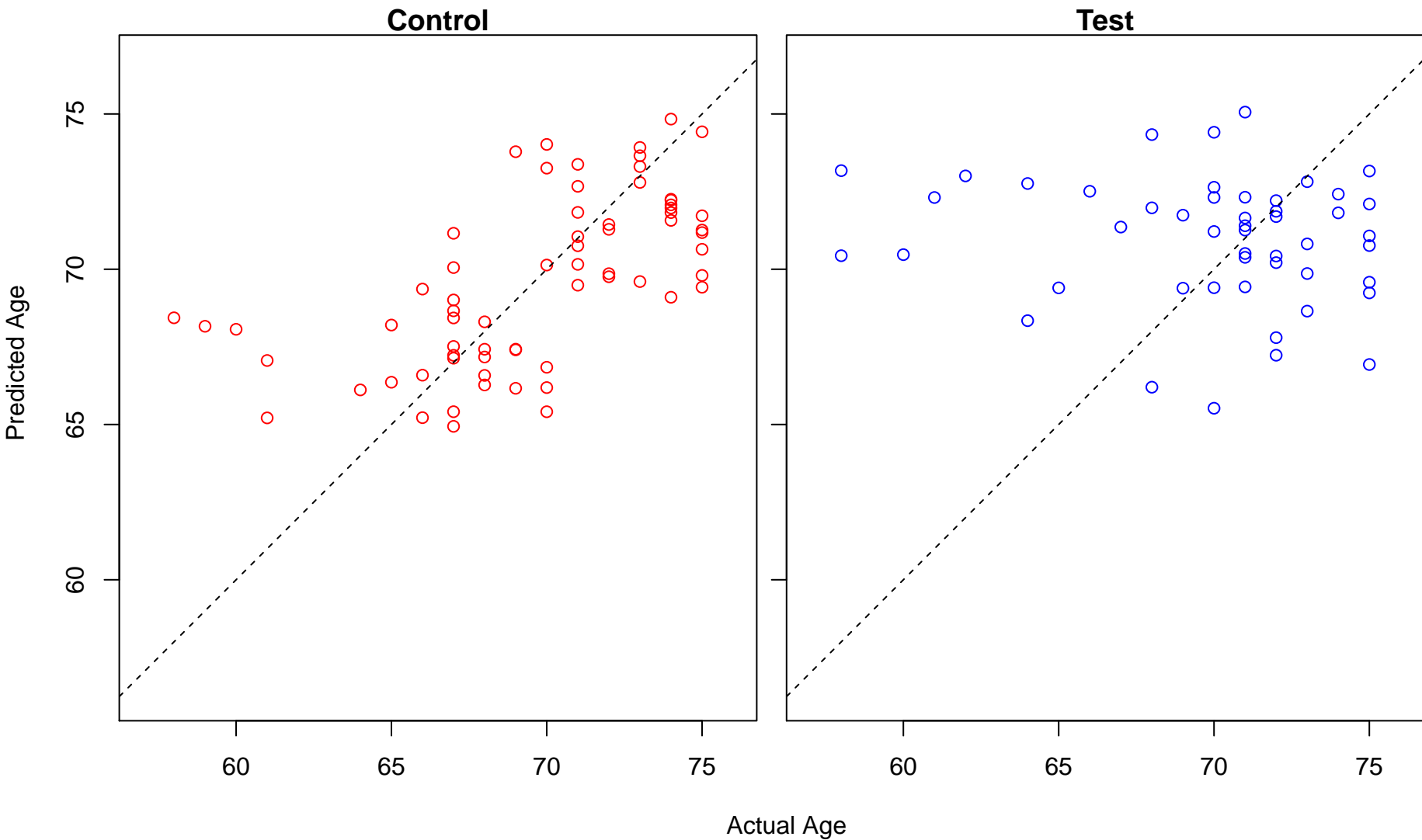
negative regulation of cytokine secretion (Score: 1.097880)



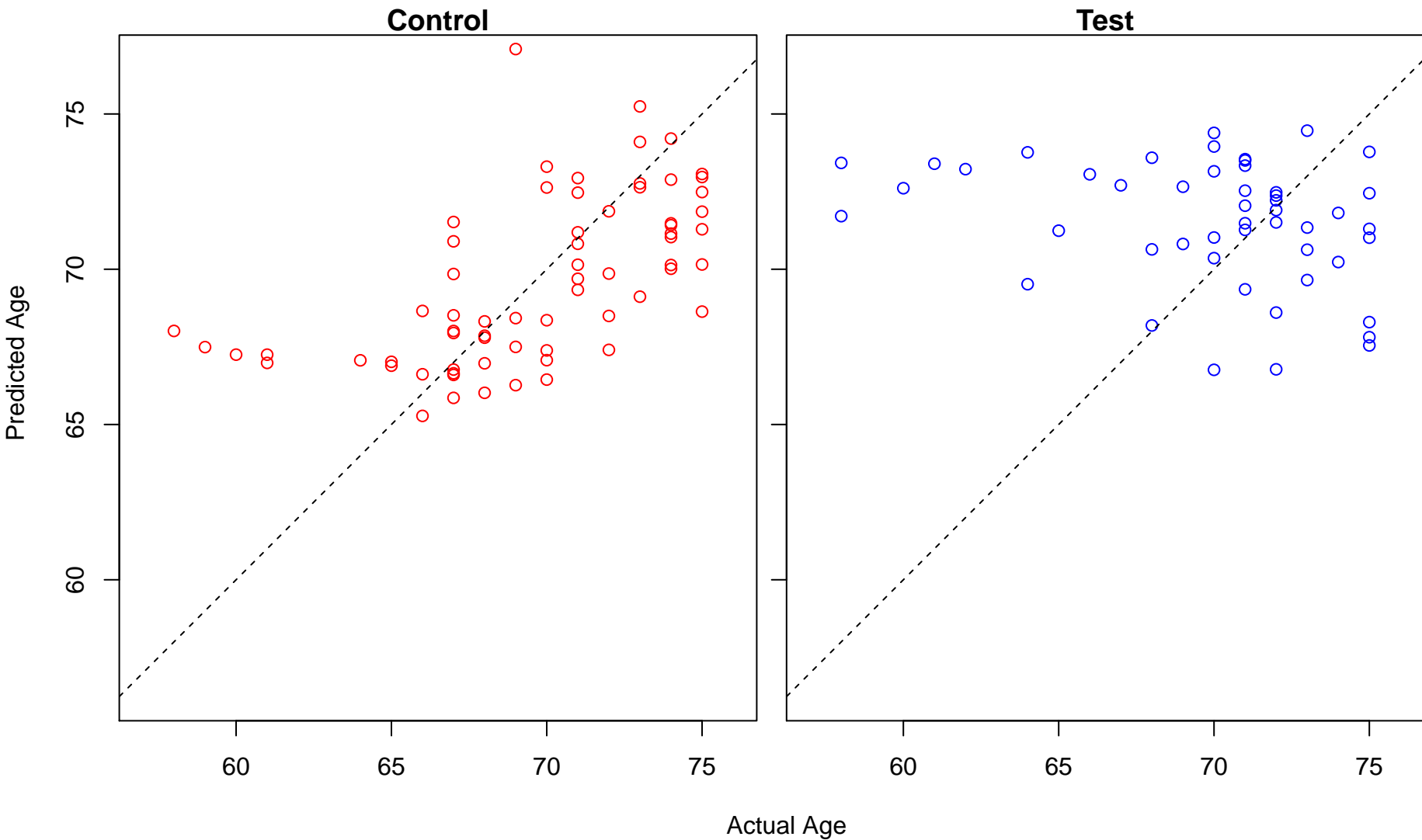
positive regulation of cell killing (Score: 1.097394)



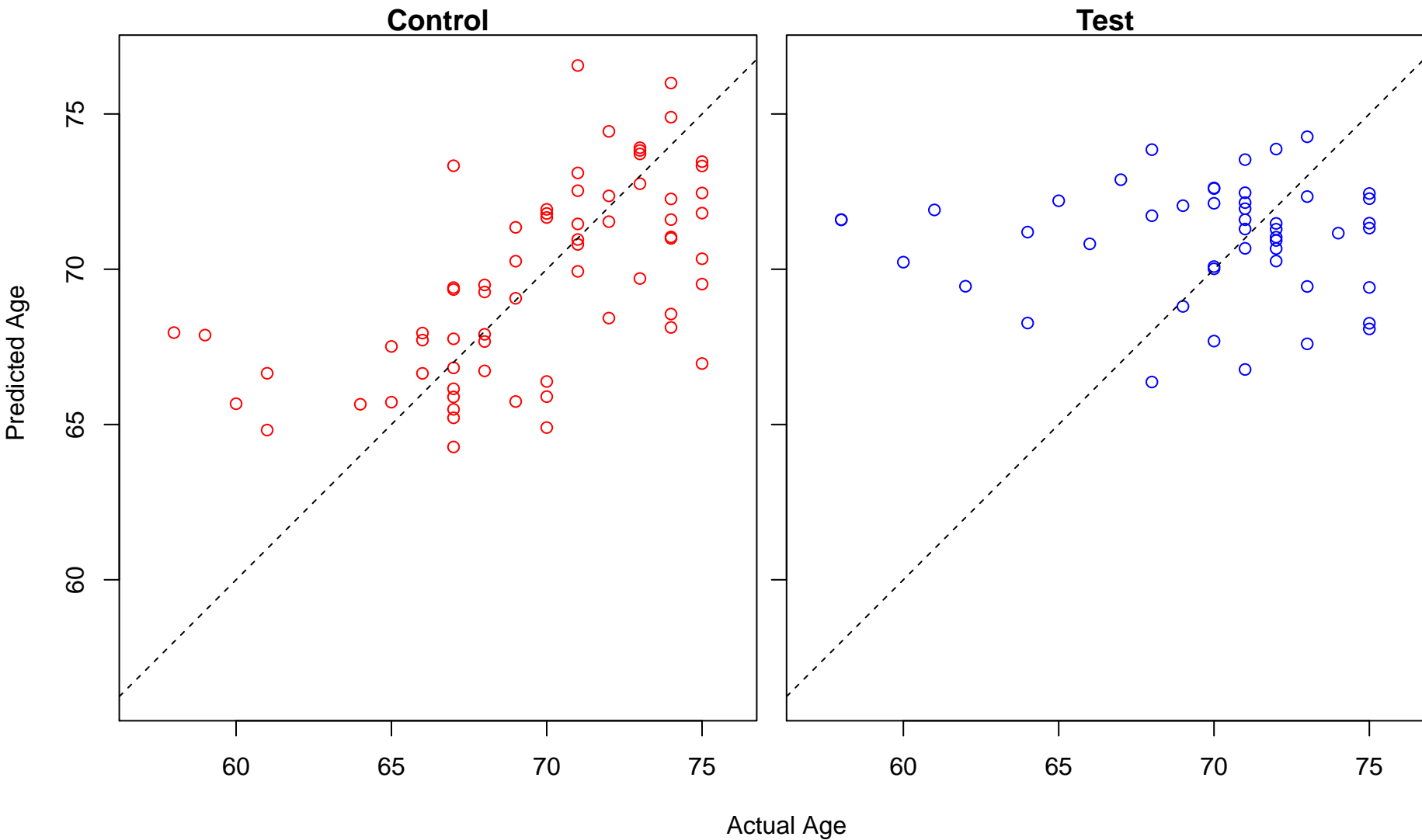
response to calcium ion (Score: 1.096958)



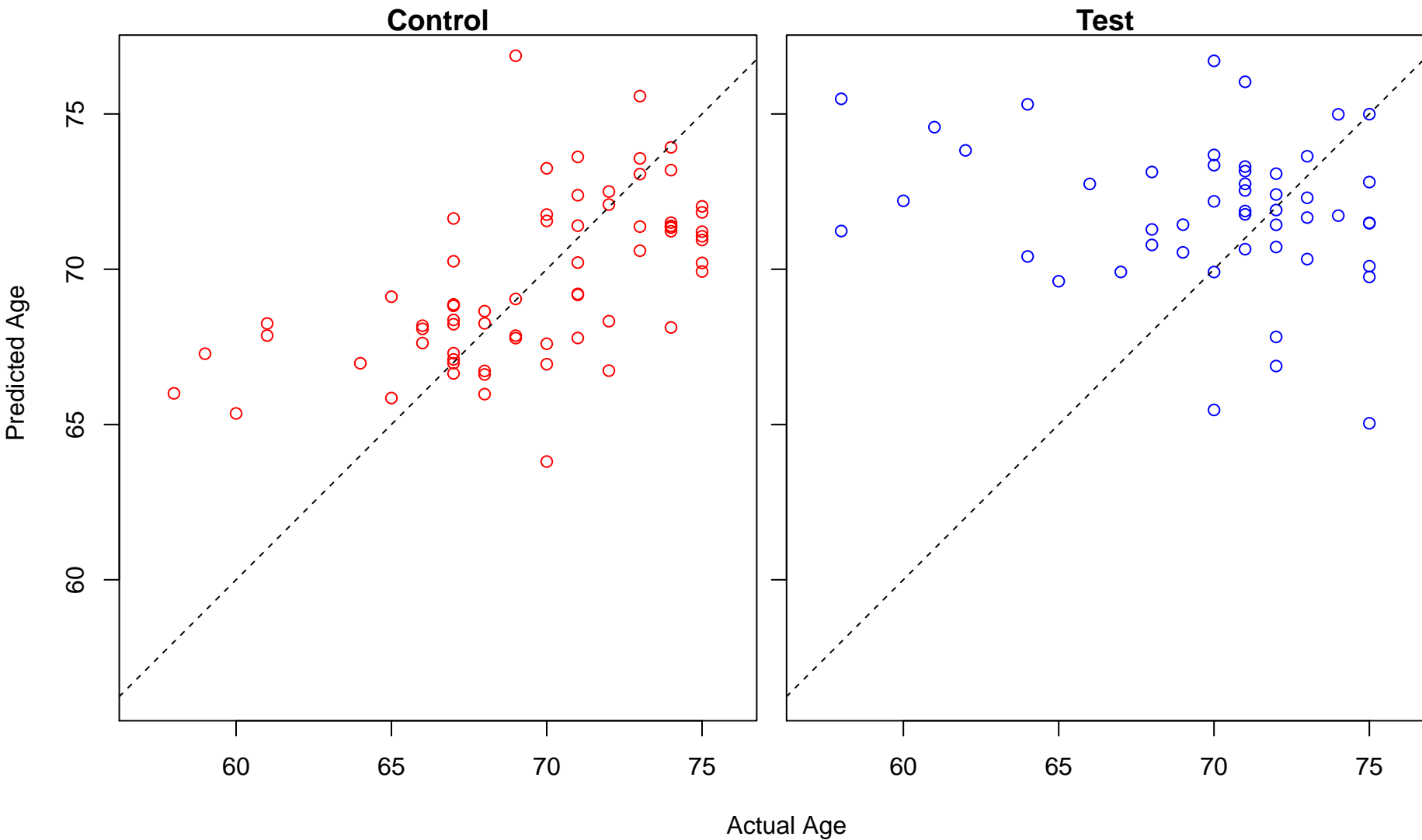
regulation of hormone levels (Score: 1.096952)



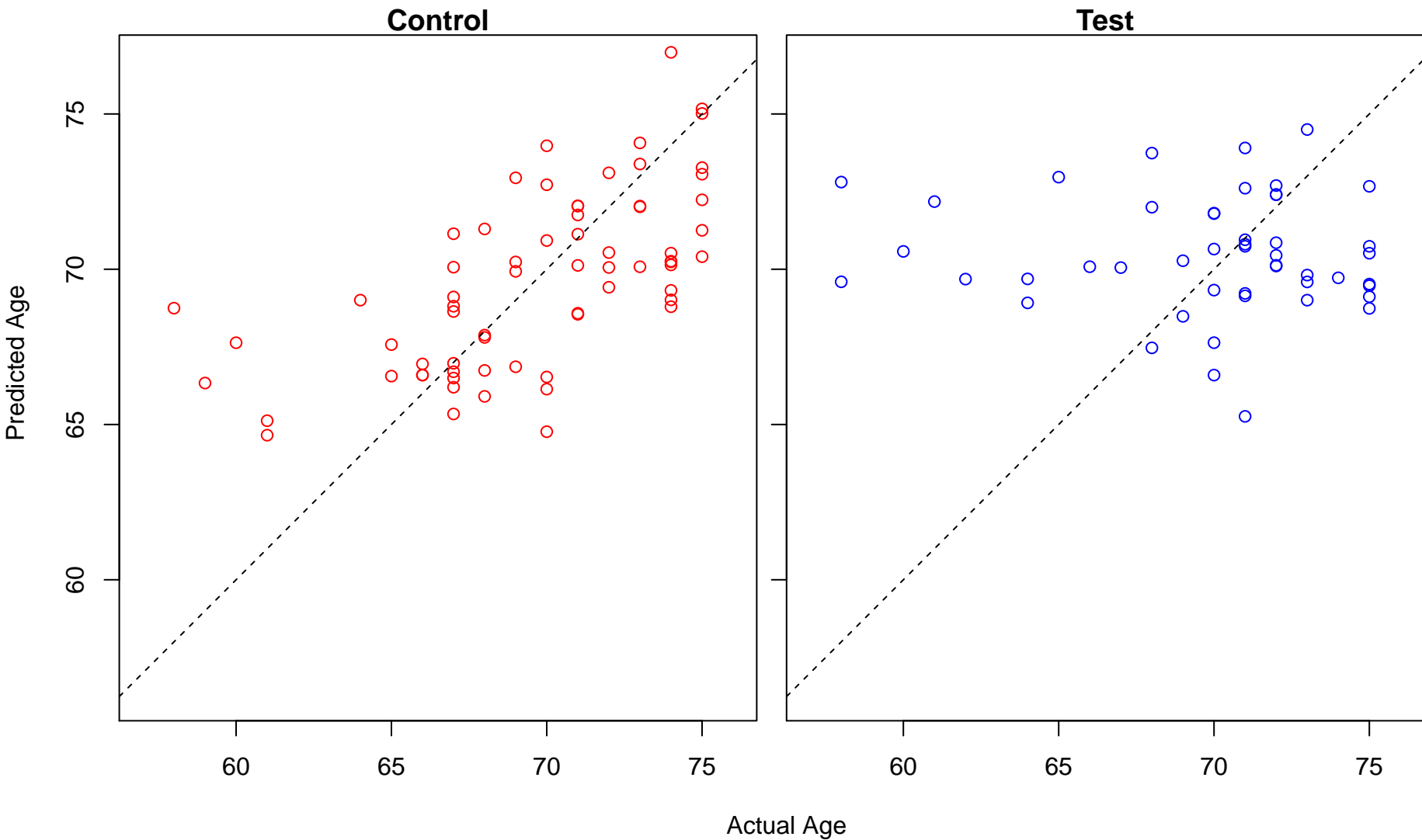
regulation of translation in response to stress (Score: 1.096952)



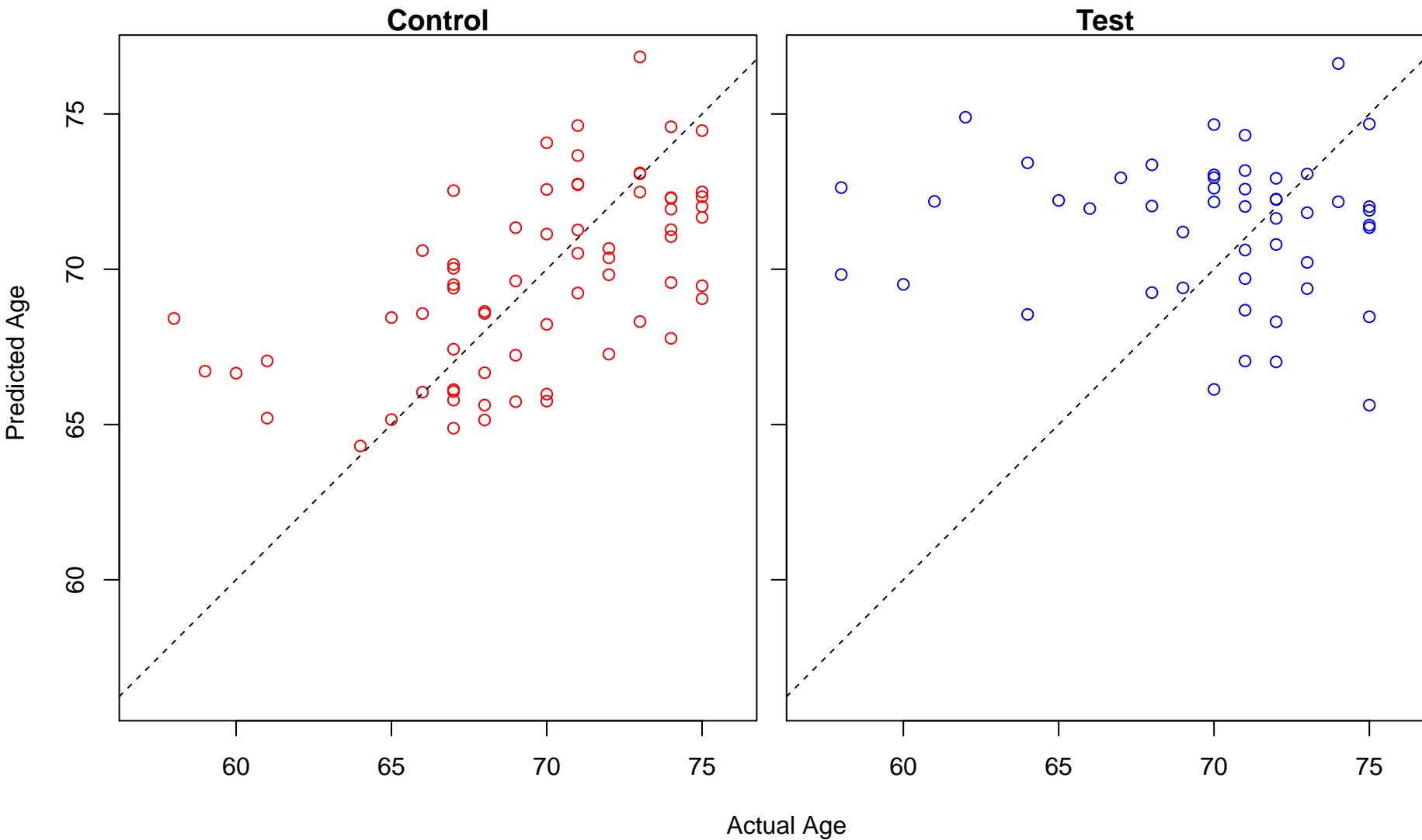
intracellular pH reduction (Score: 1.096320)



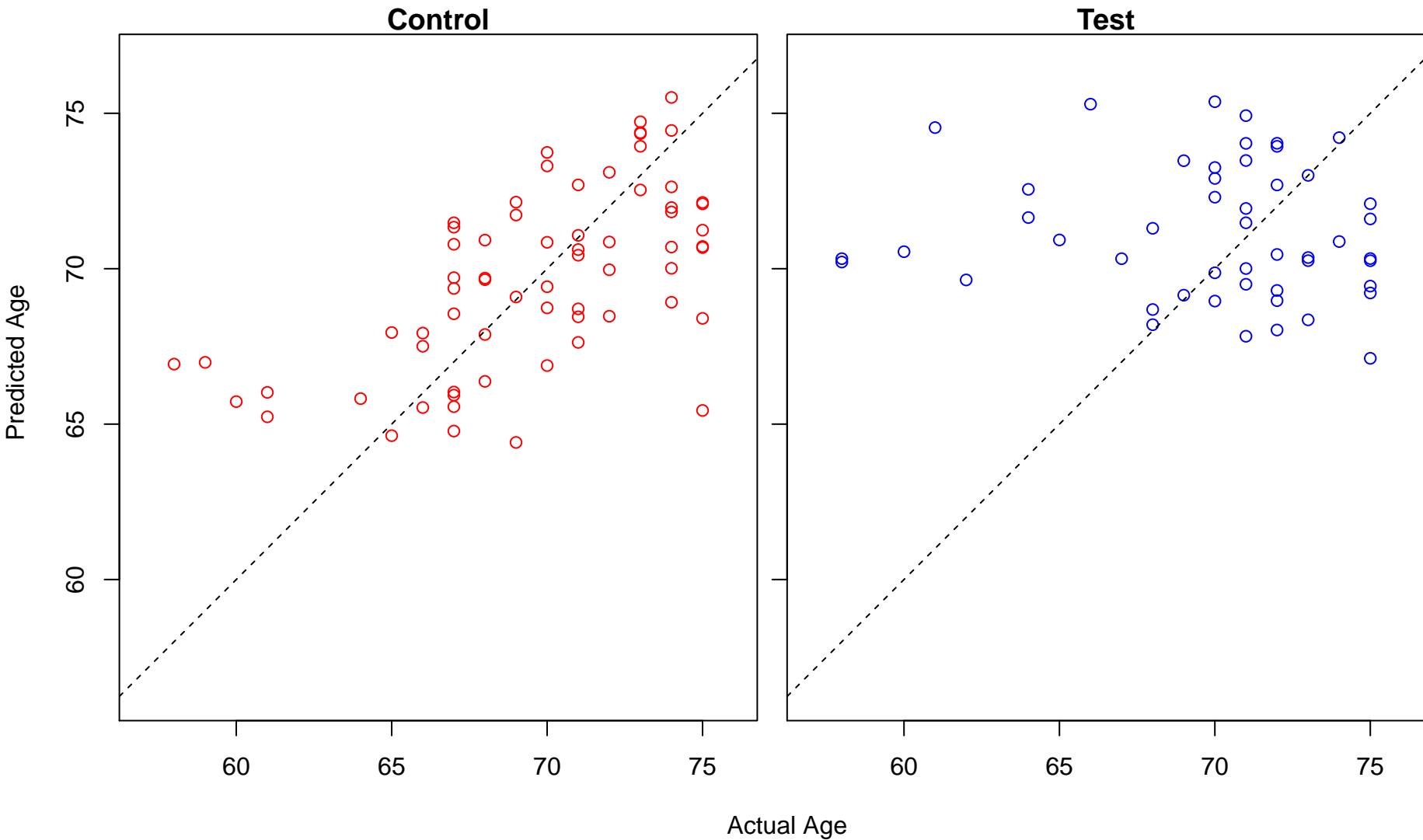
negative regulation of phosphoprotein phosphatase activity (Score: 1.094914)



receptor internalization (Score: 1.094222)

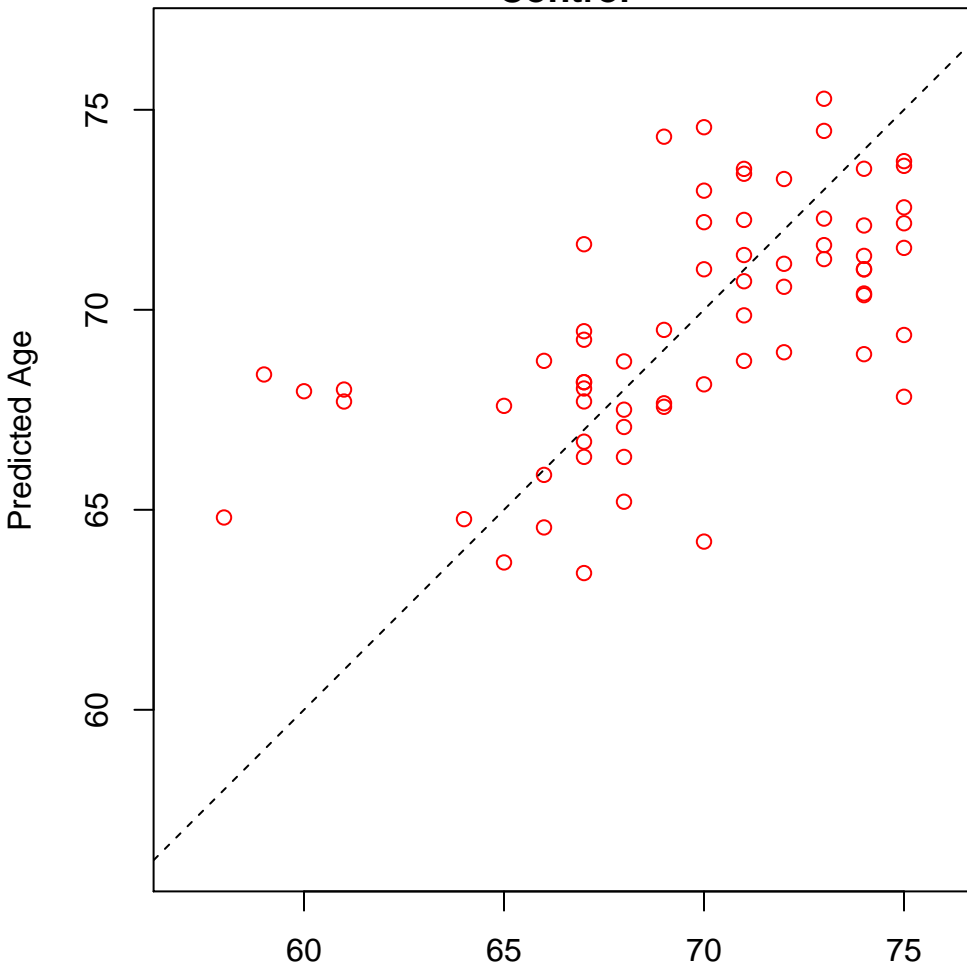


phosphatidylglycerol biosynthetic process (Score: 1.094128)

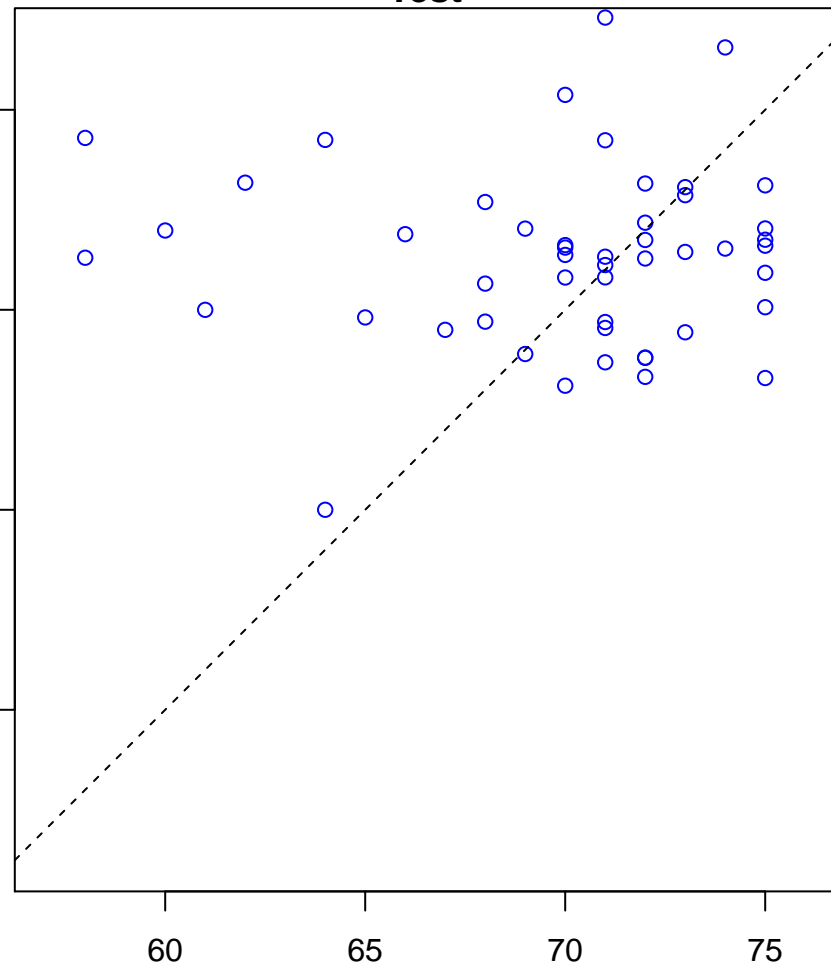


regulation of myoblast differentiation (Score: 1.093848)

Control

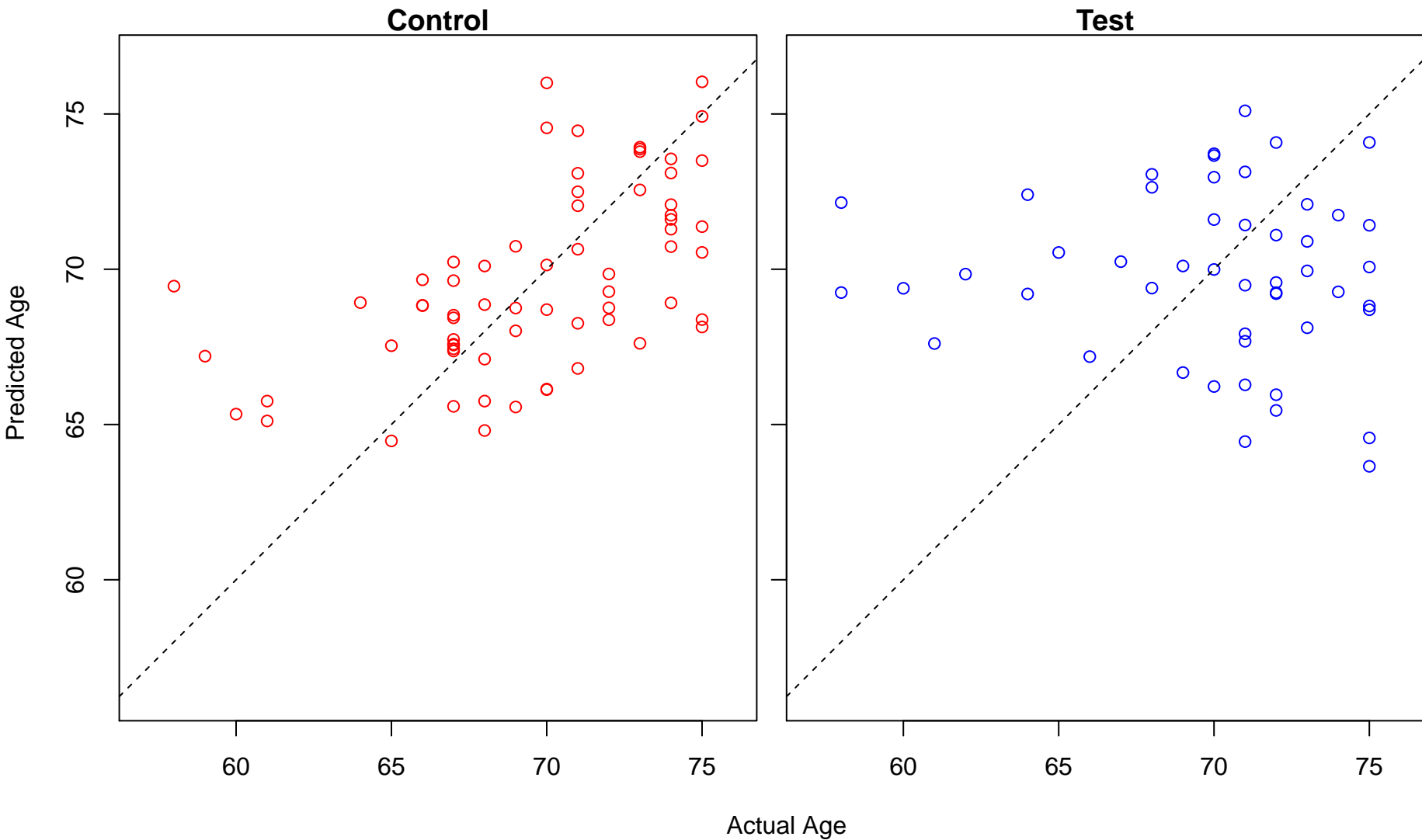


Test

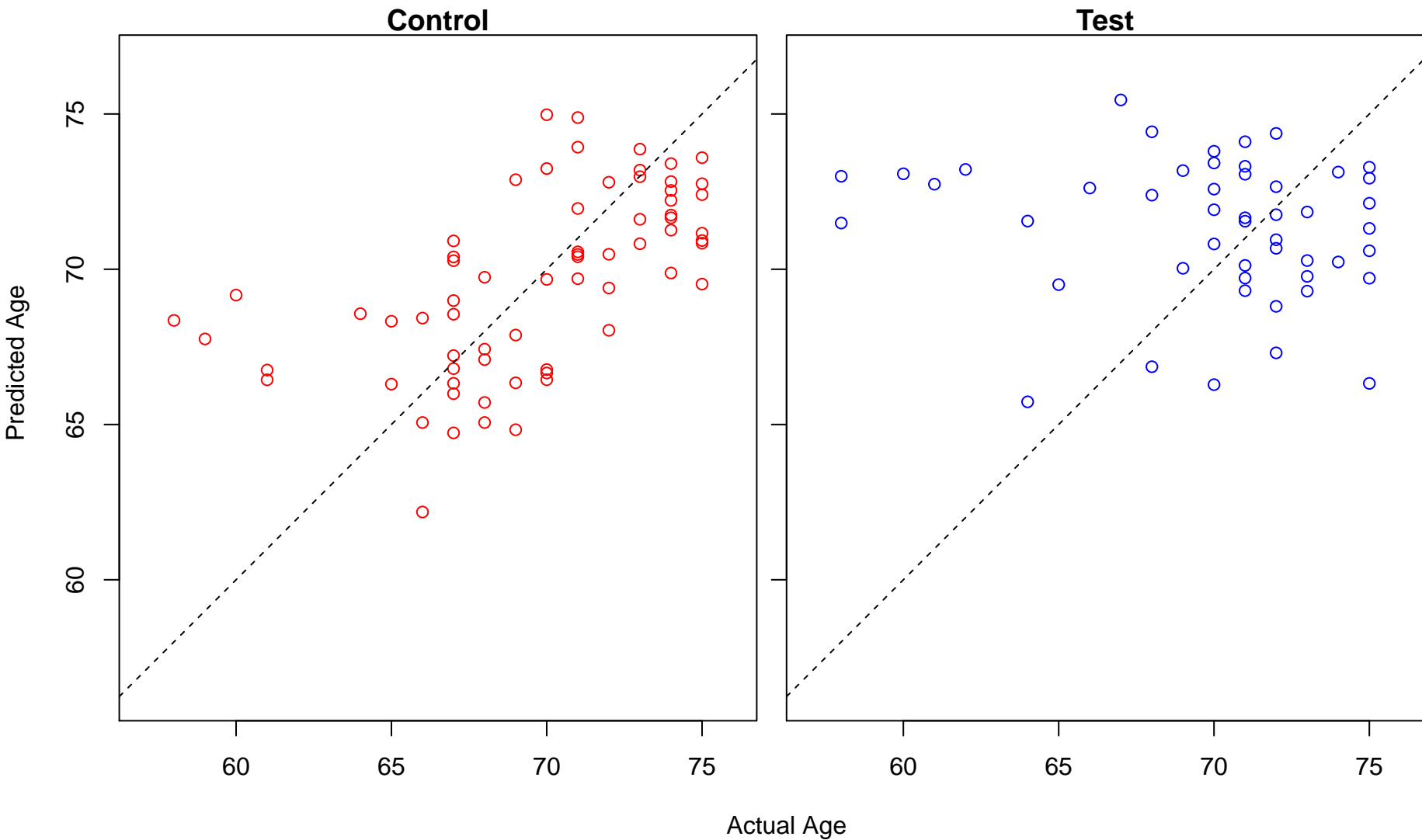


Actual Age

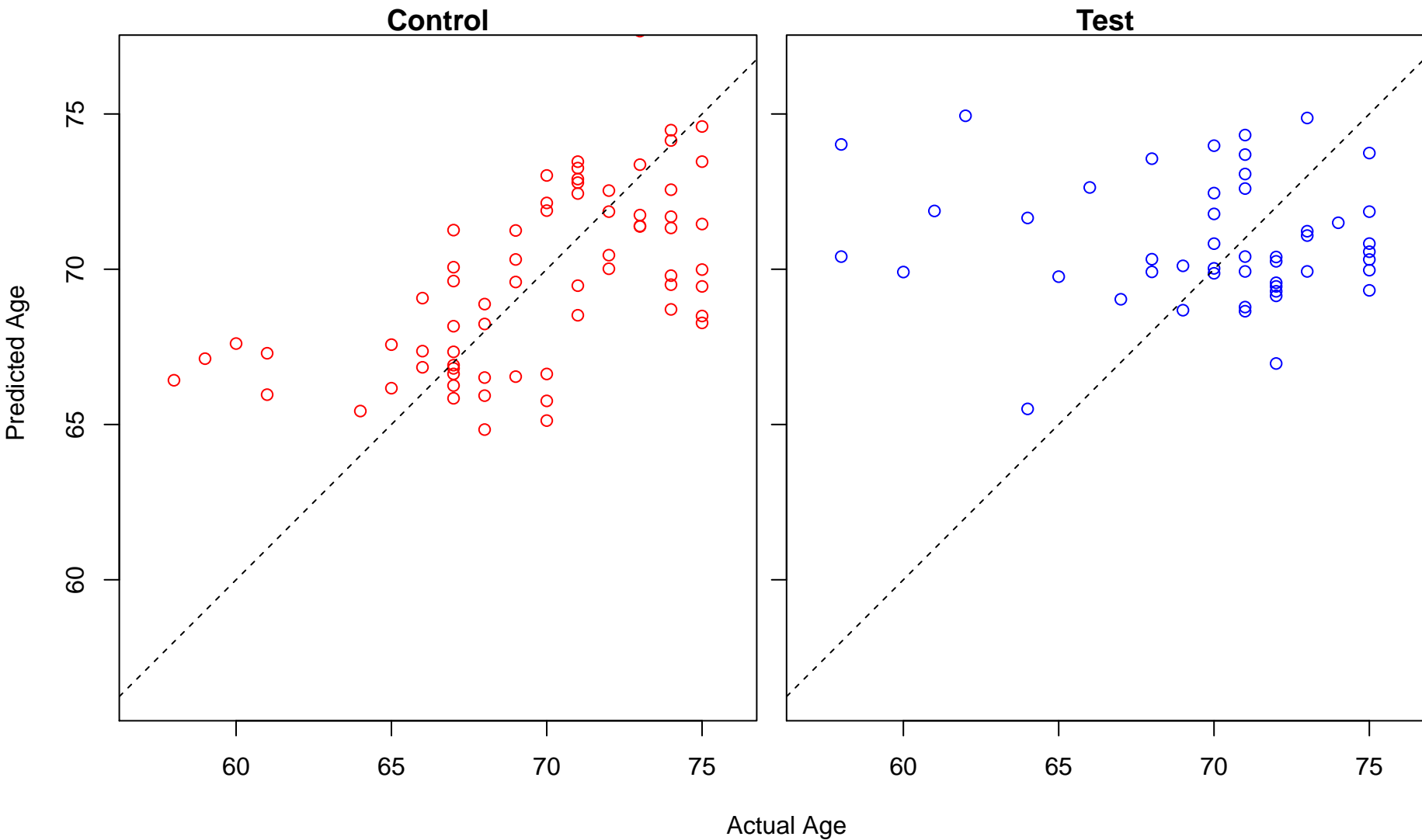
positive regulation by host of viral transcription (Score: 1.093782)



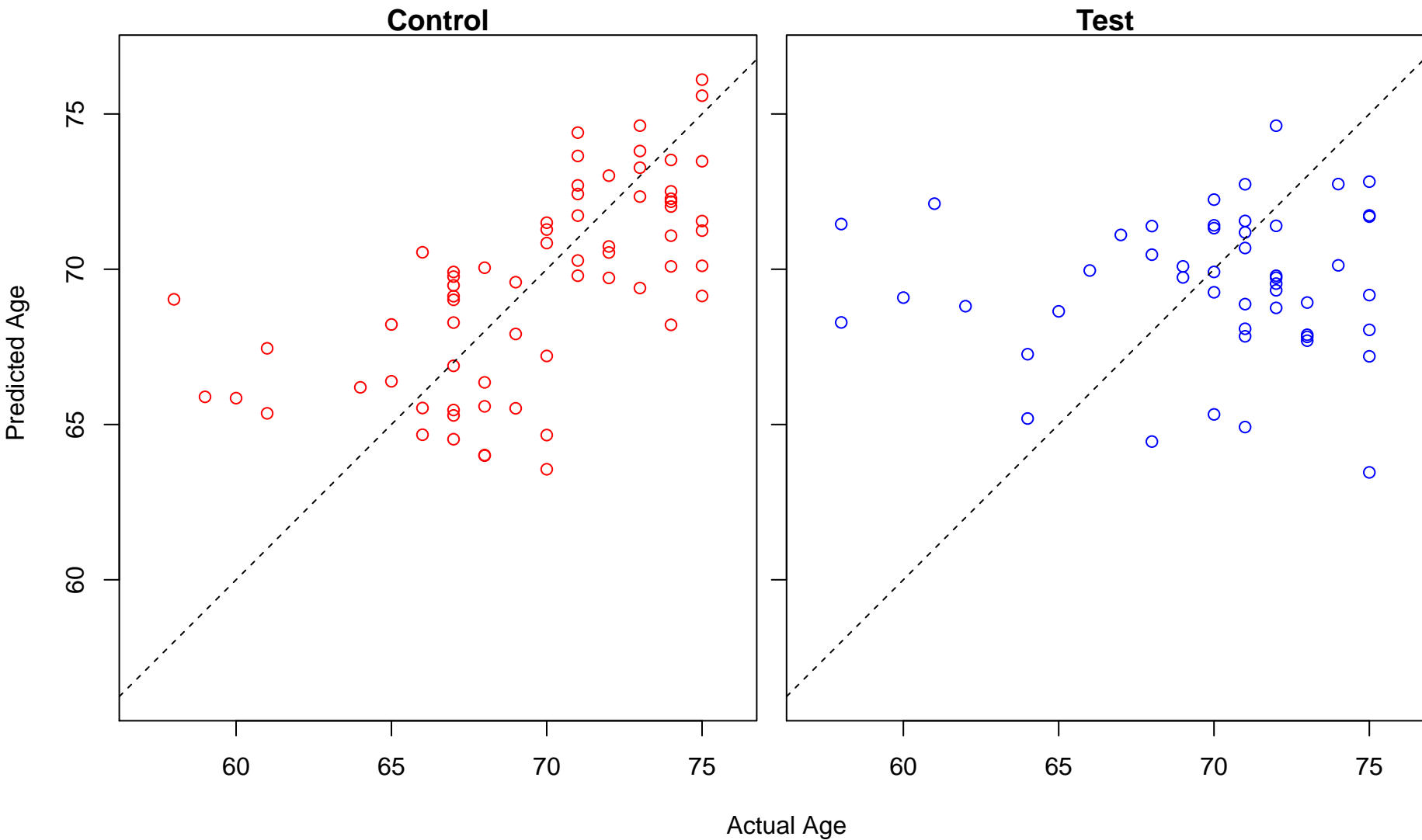
skin development (Score: 1.093649)



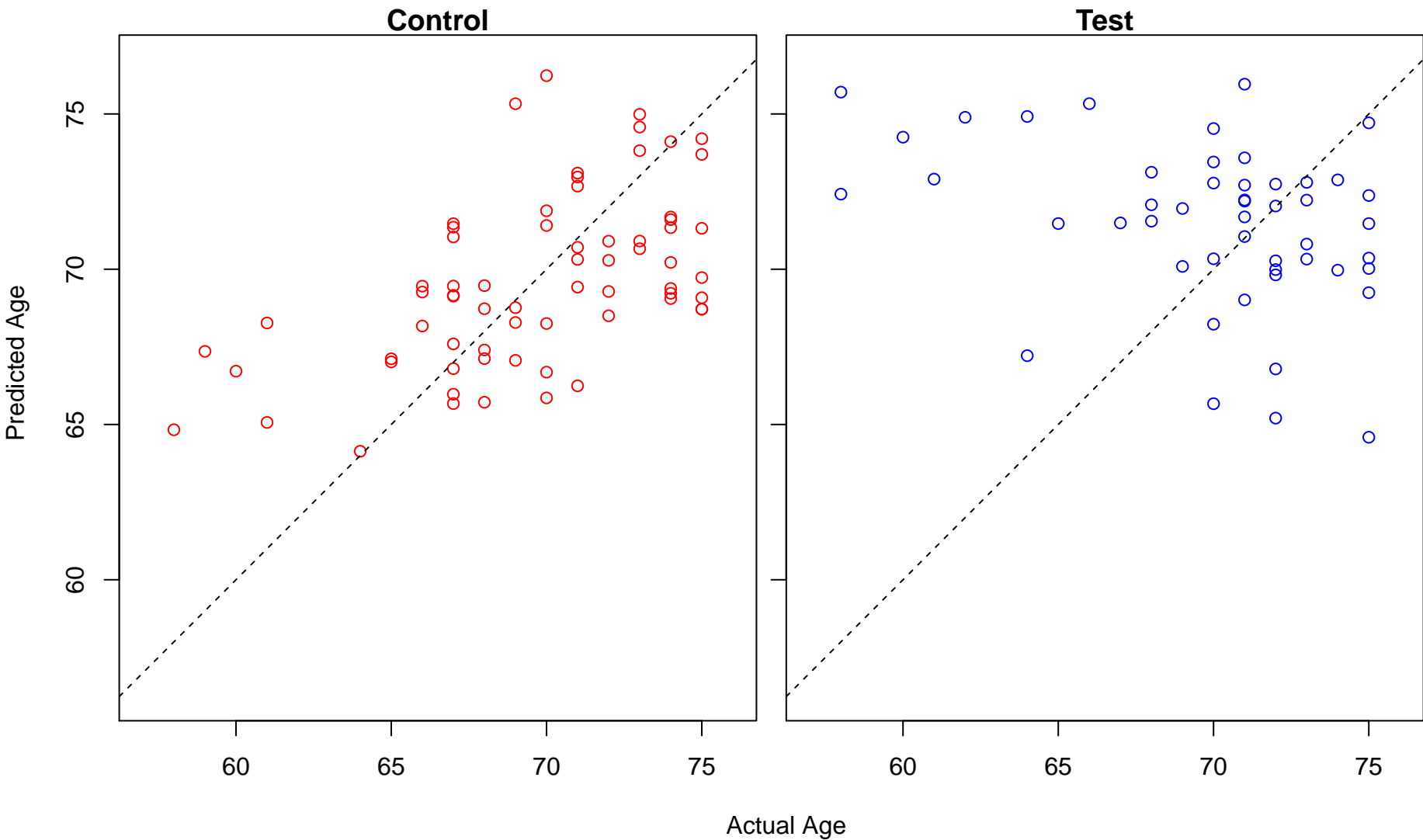
pyridine-containing compound metabolic process (Score: 1.093167)



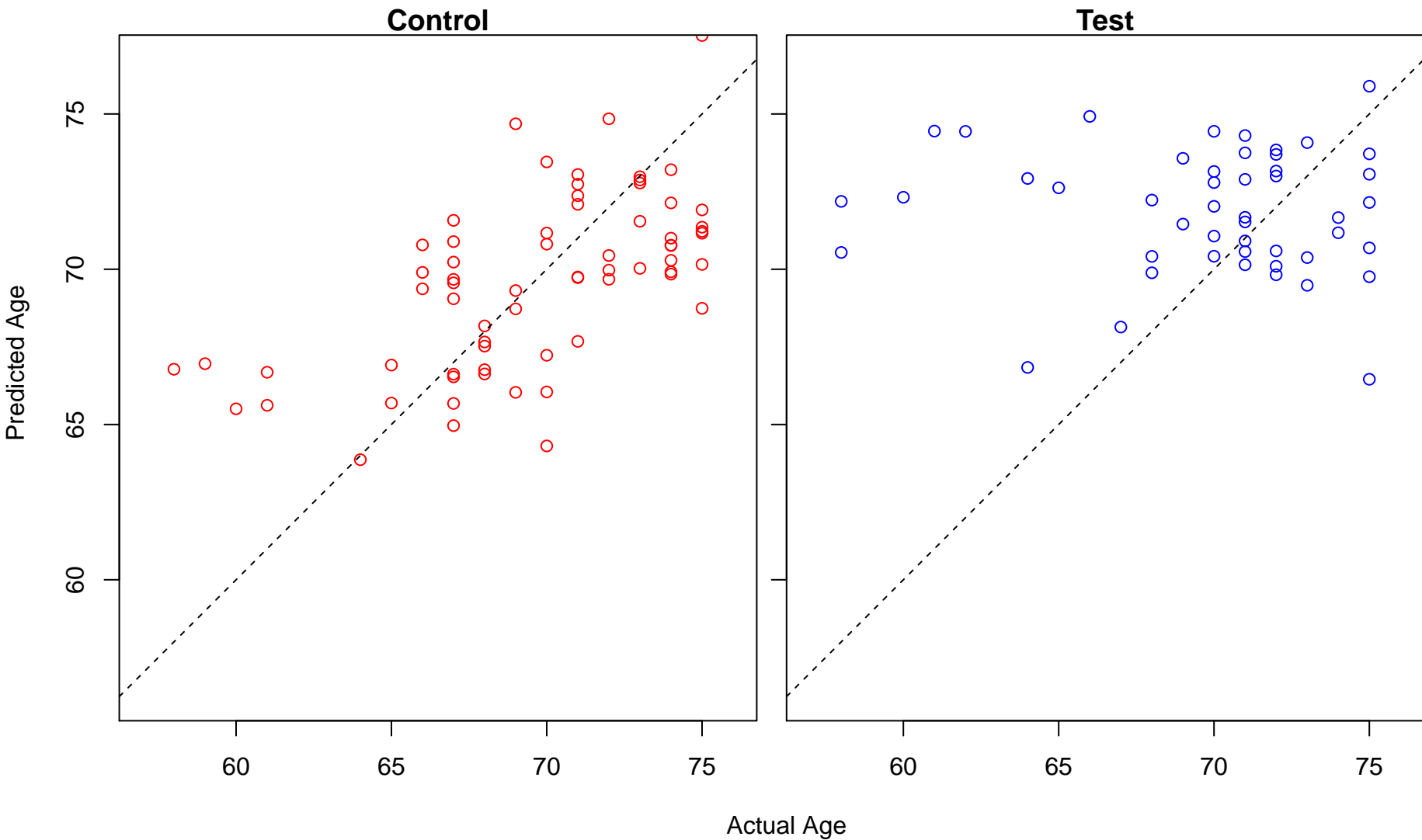
humoral immune response (Score: 1.092954)



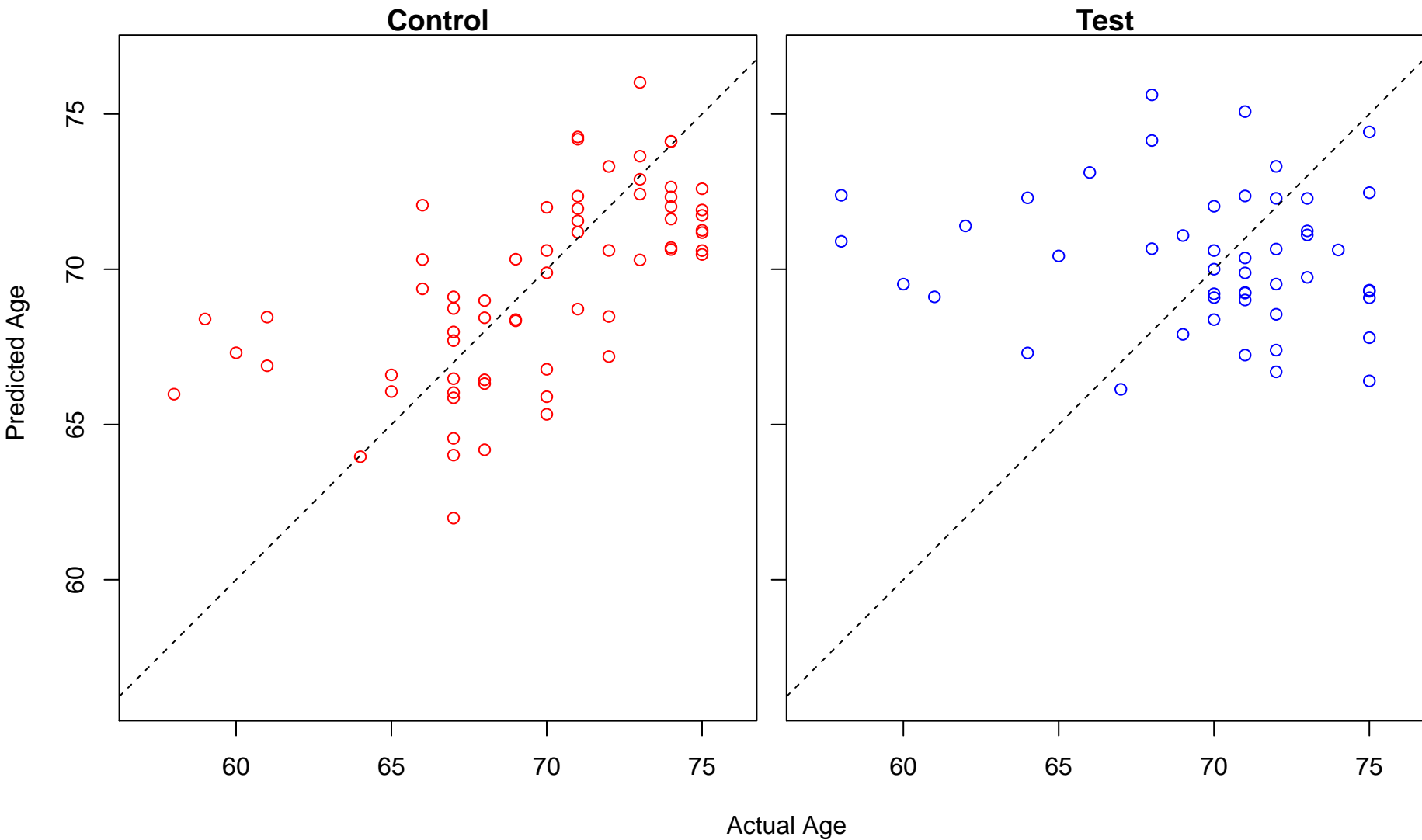
digestion (Score: 1.092653)



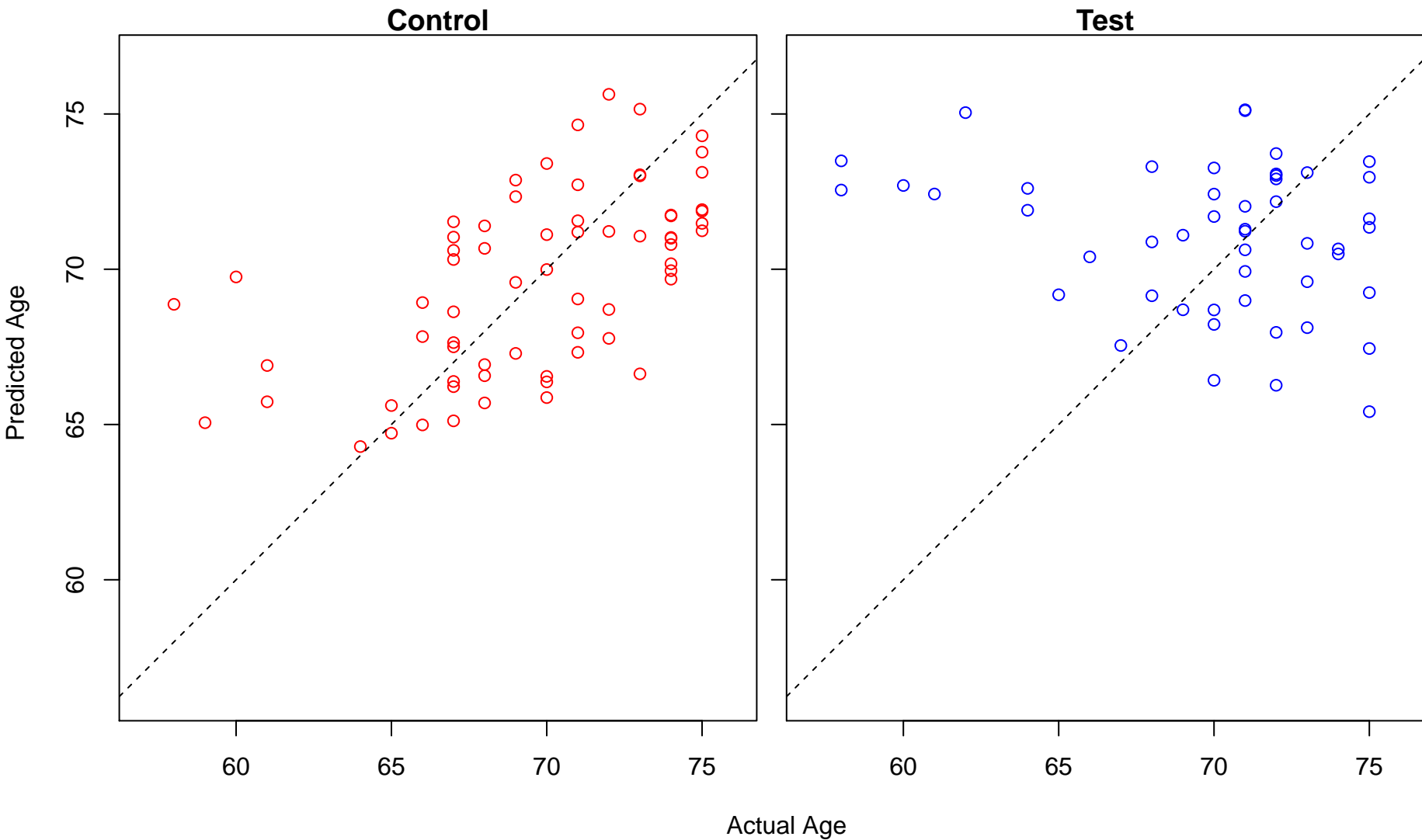
asymmetric cell division (Score: 1.092499)



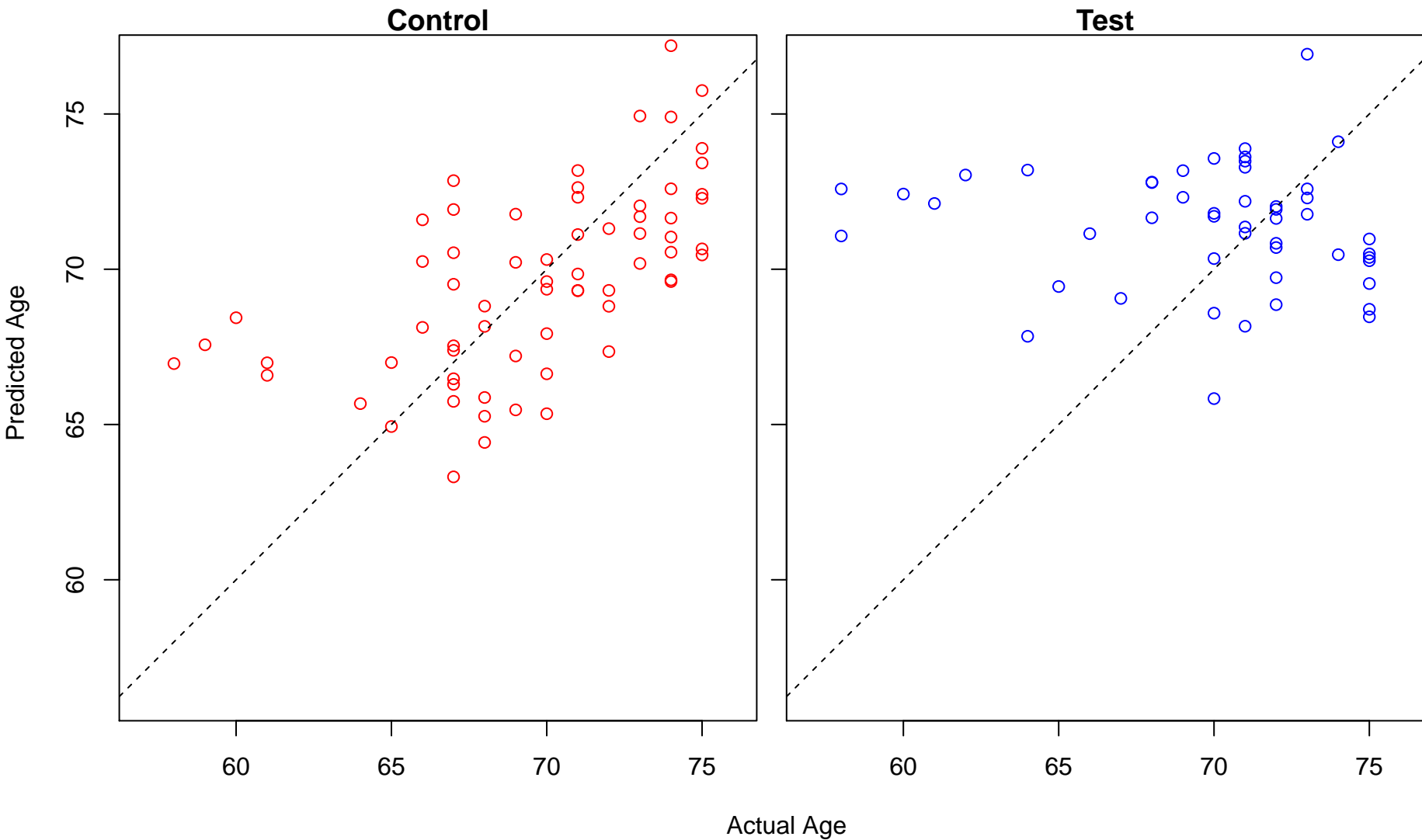
immunoglobulin production (Score: 1.092039)



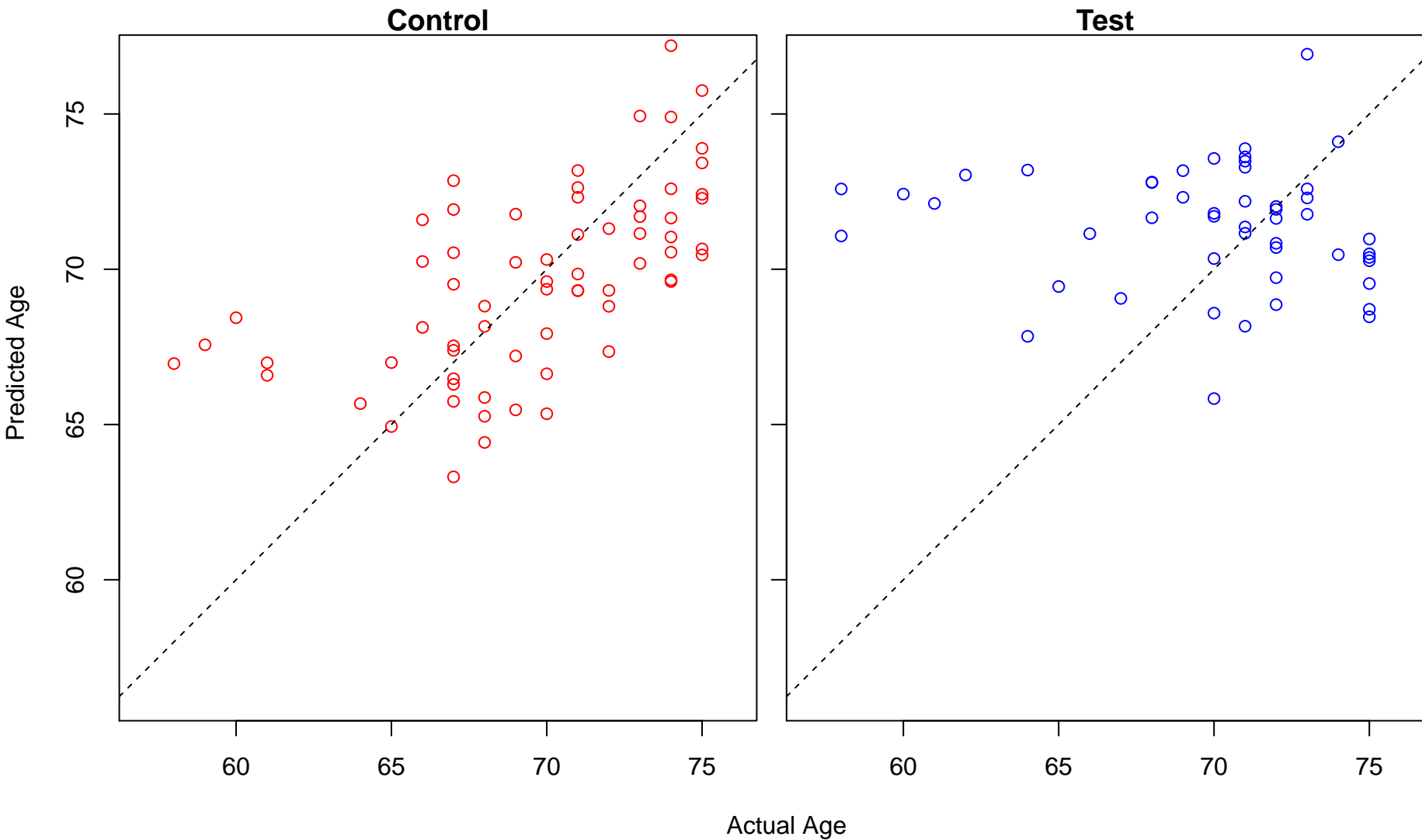
short-chain fatty acid metabolic process (Score: 1.091714)



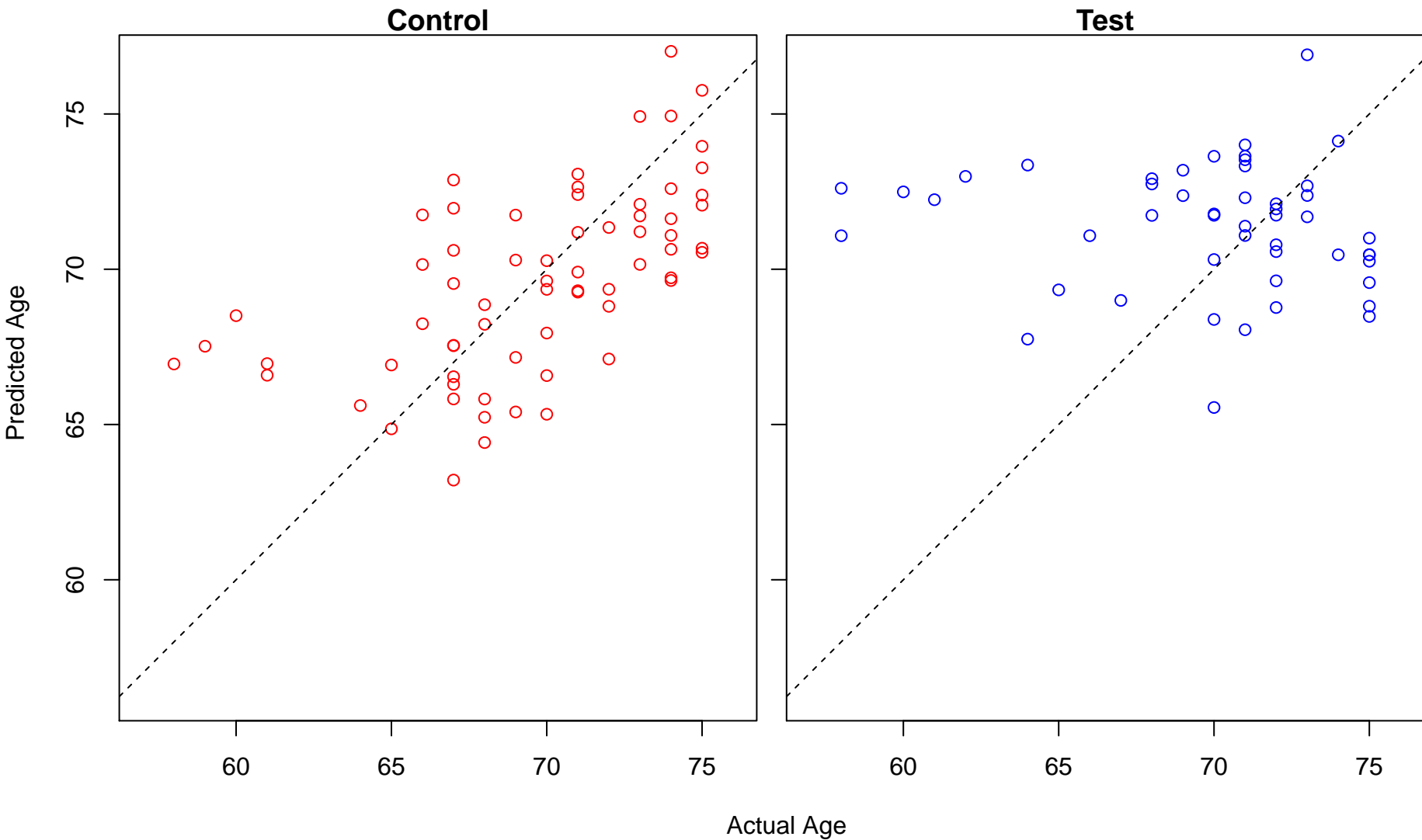
female gonad development (Score: 1.091611)



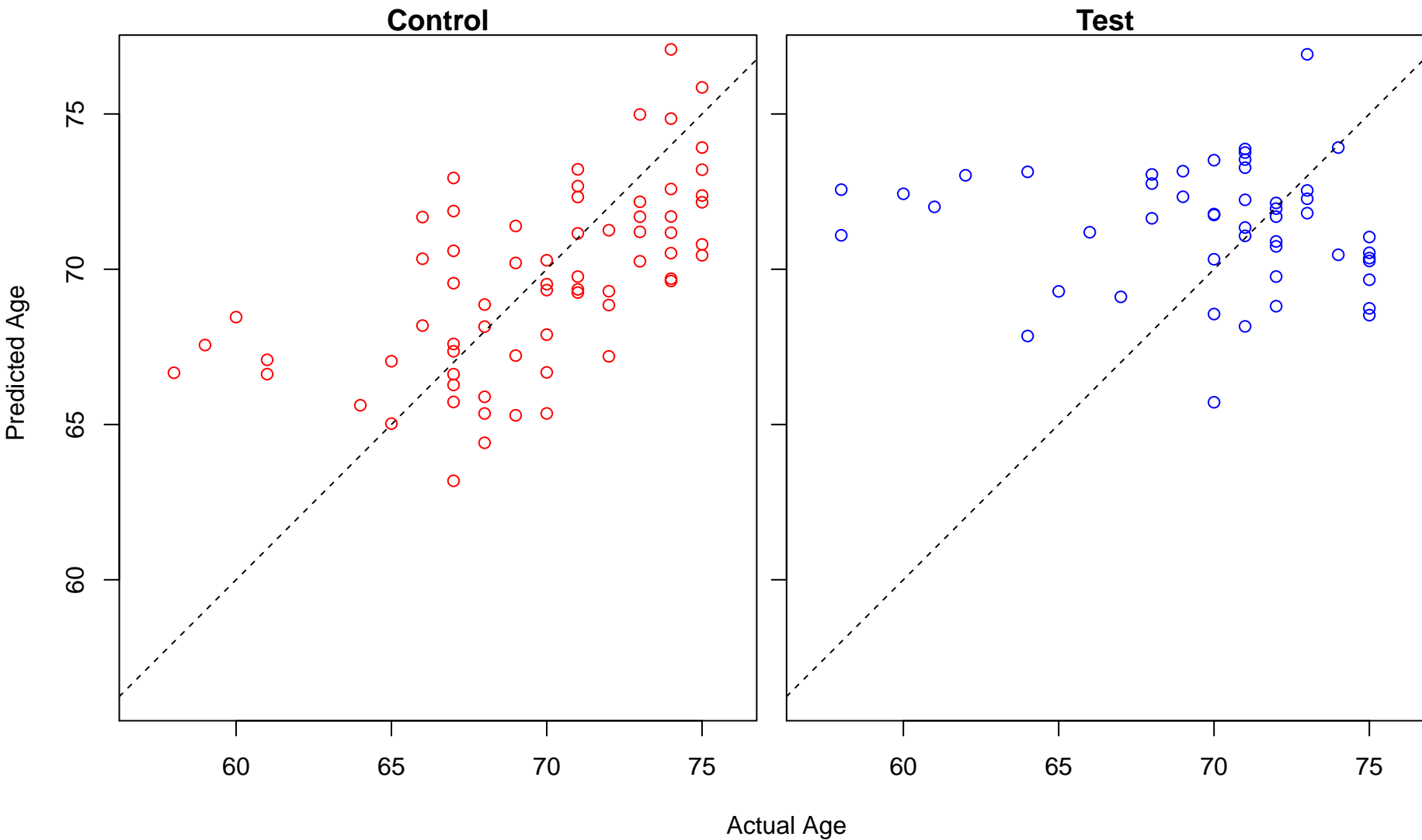
development of primary female sexual characteristics (Score: 1.091611)



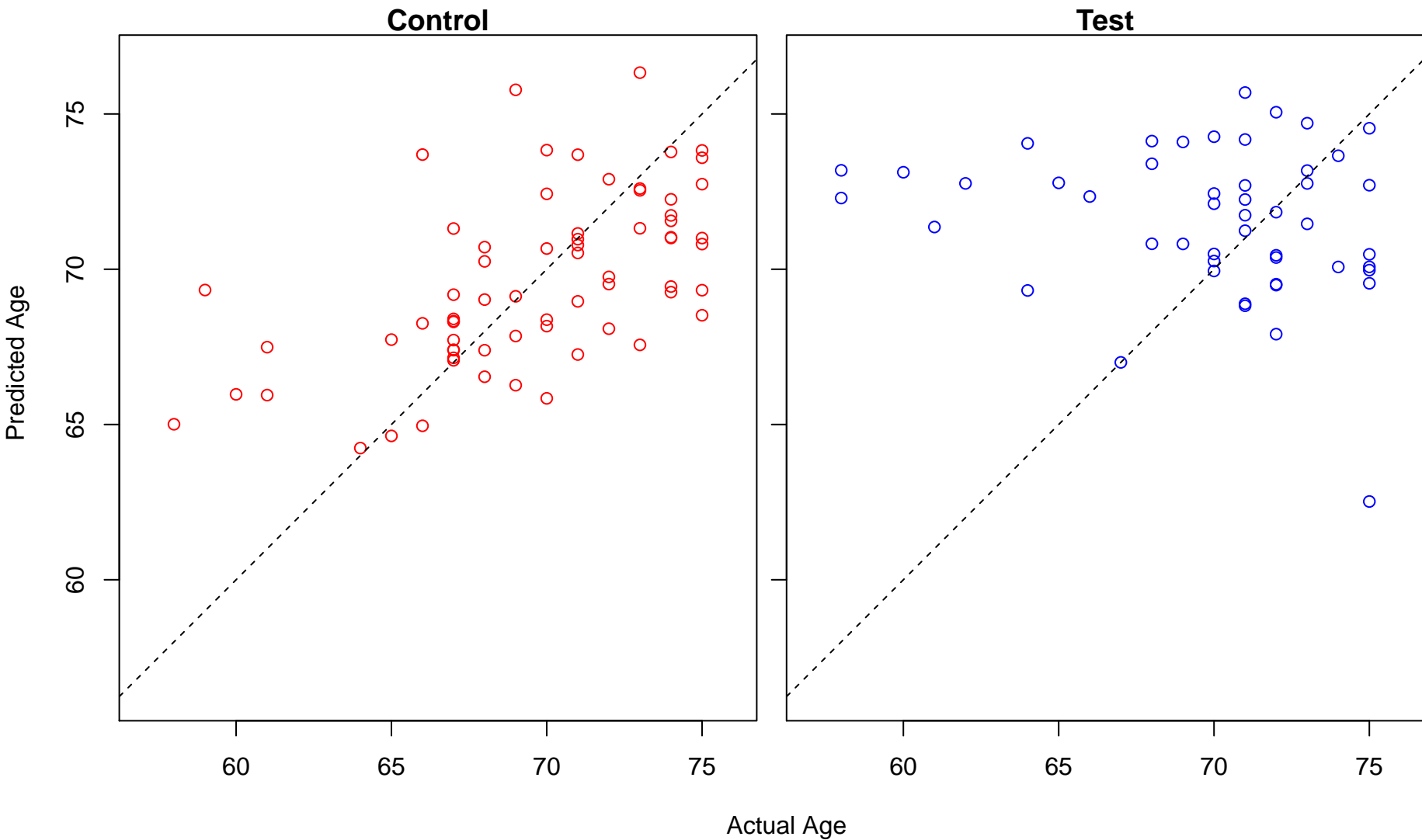
female sex differentiation (Score: 1.091511)



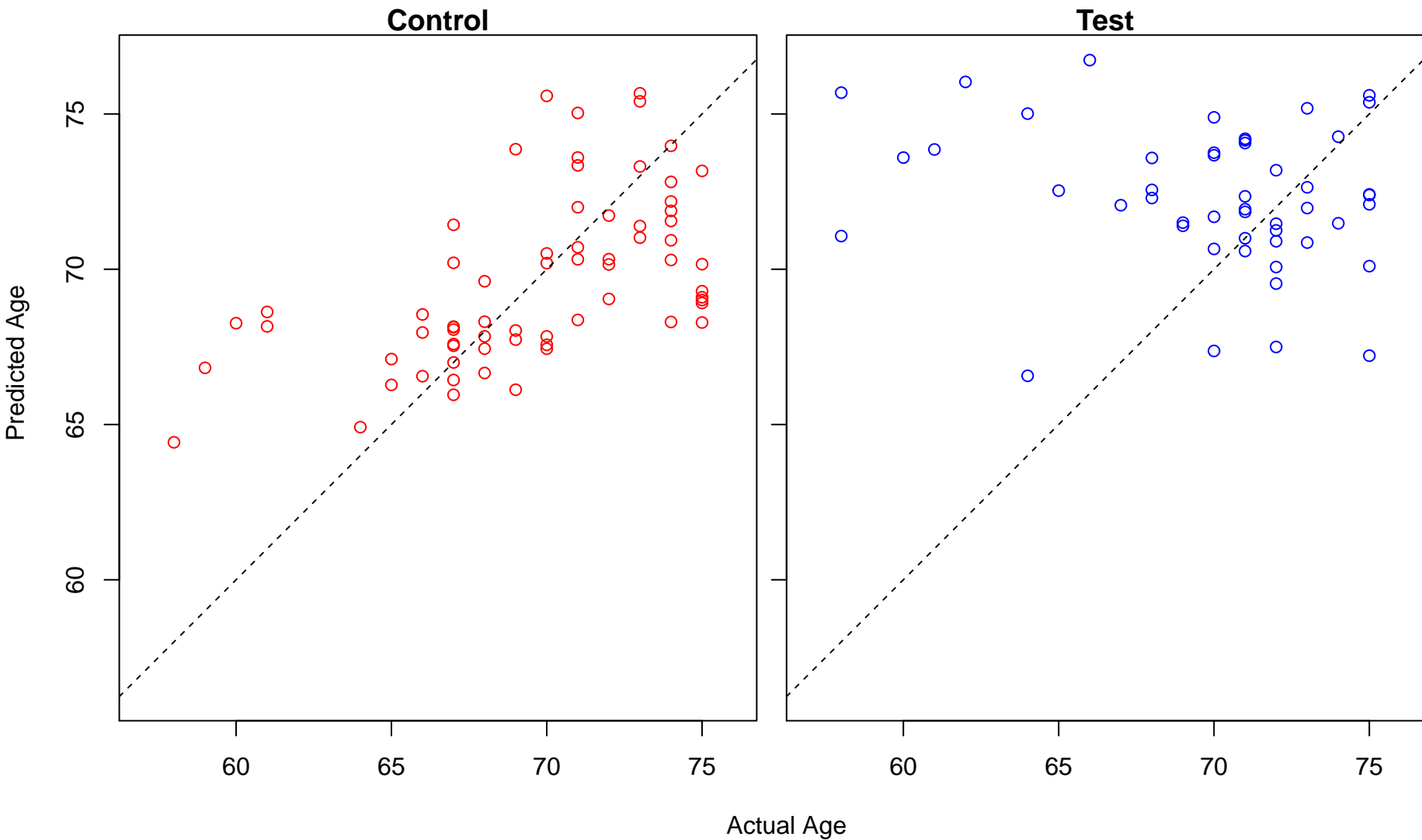
ovulation cycle process (Score: 1.091475)



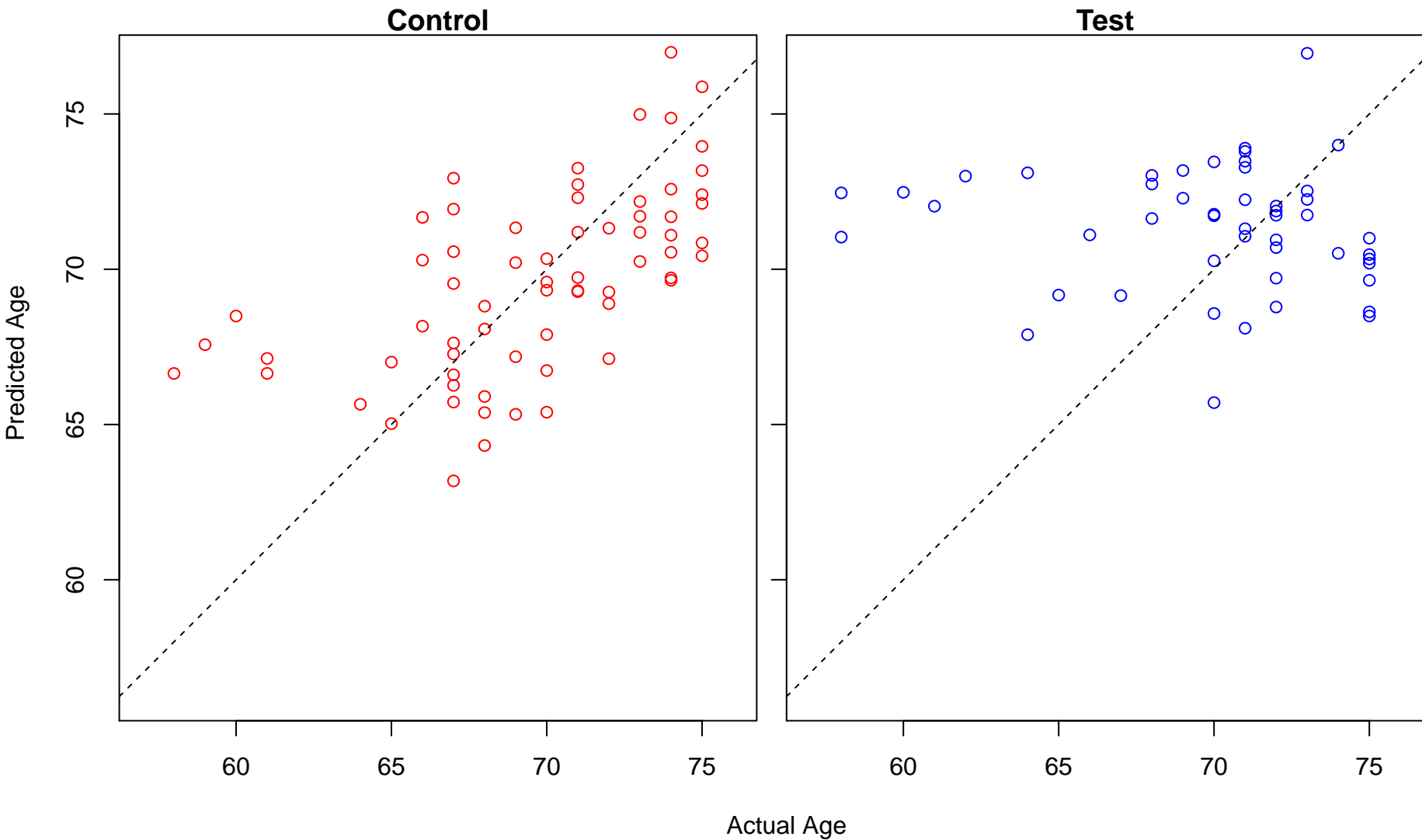
regulation of extracellular matrix assembly (Score: 1.091043)



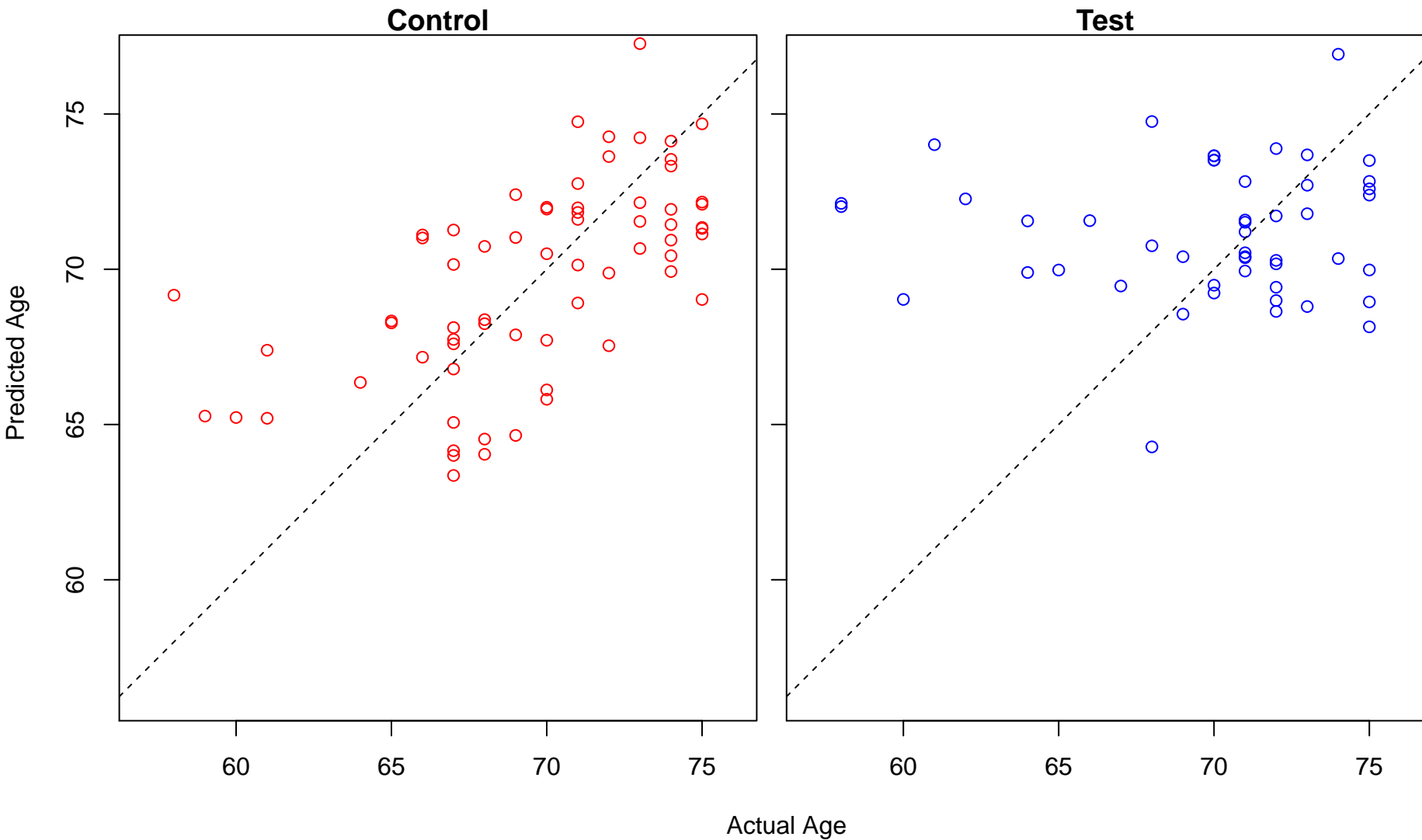
reactive nitrogen species metabolic process (Score: 1.090978)



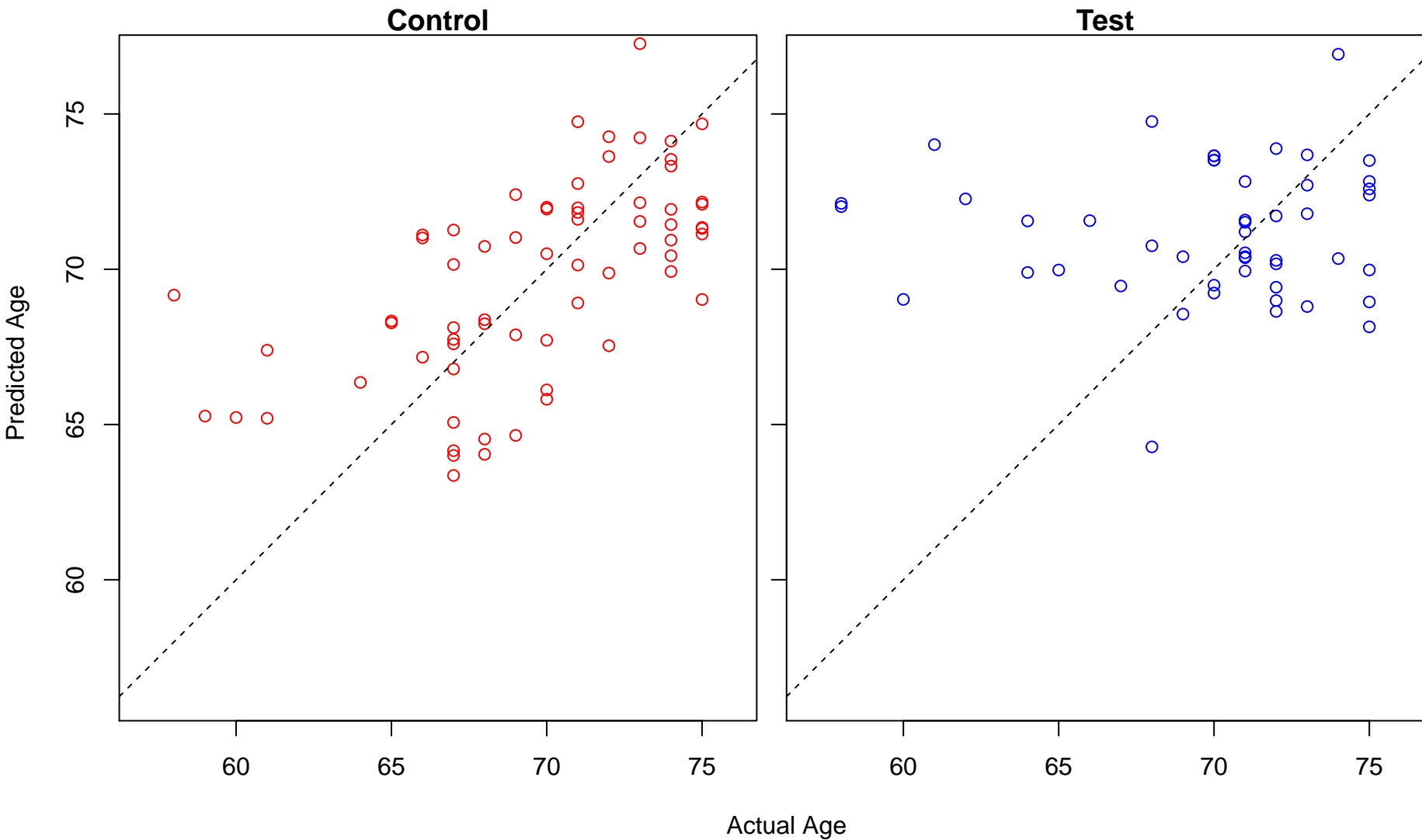
ovulation cycle (Score: 1.090884)



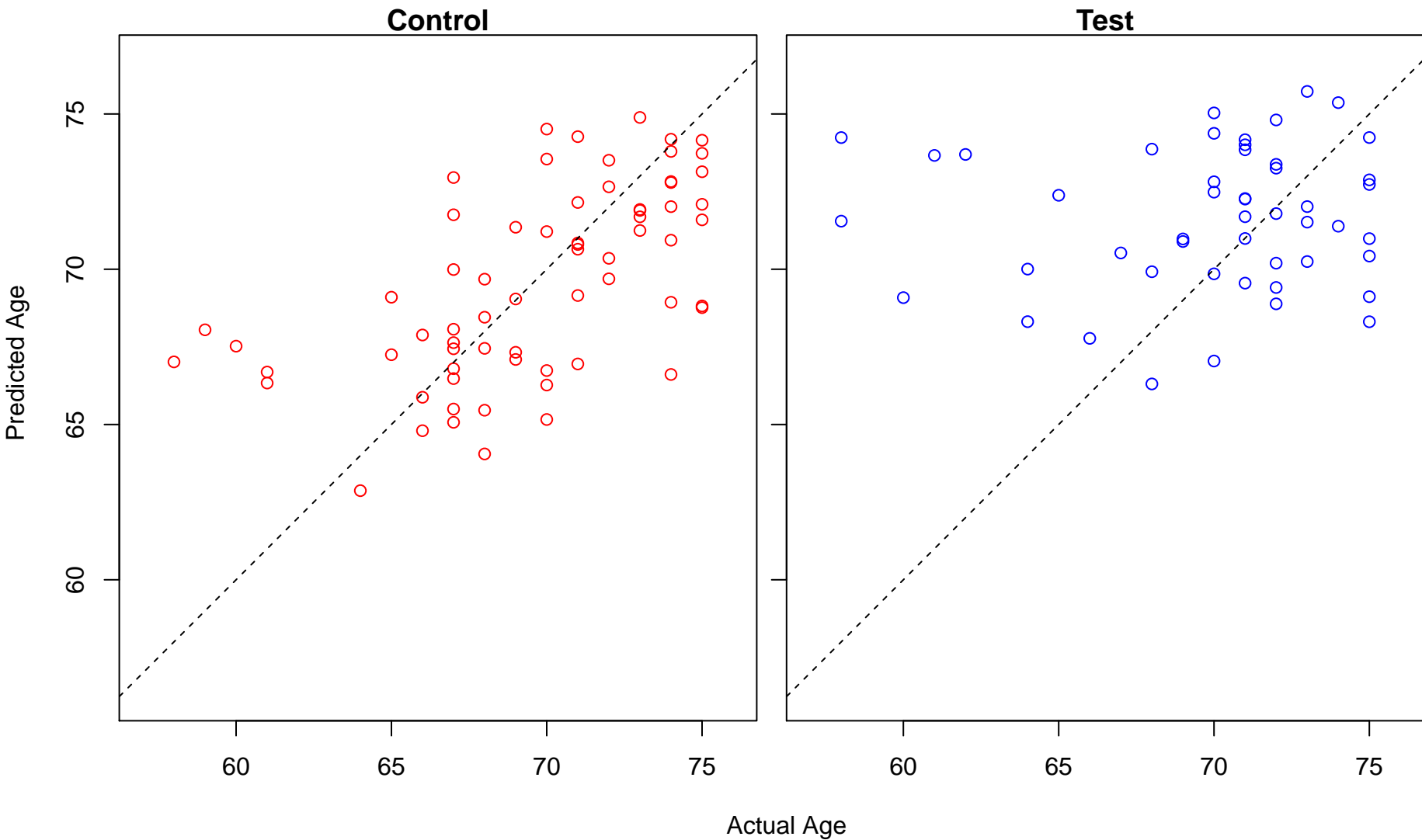
porphyrin-containing compound biosynthetic process (Score: 1.090824)



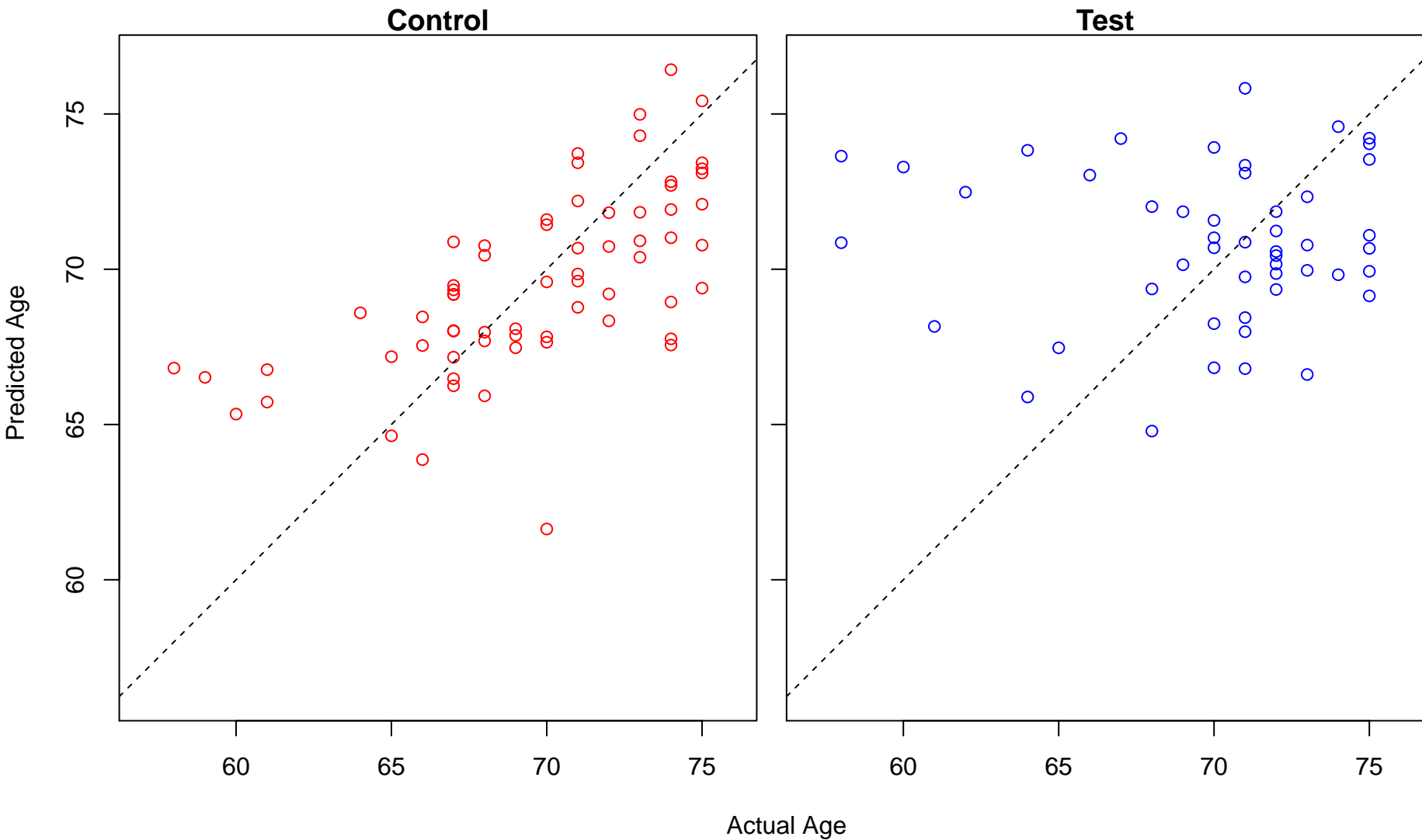
tetrapyrrole biosynthetic process (Score: 1.090824)



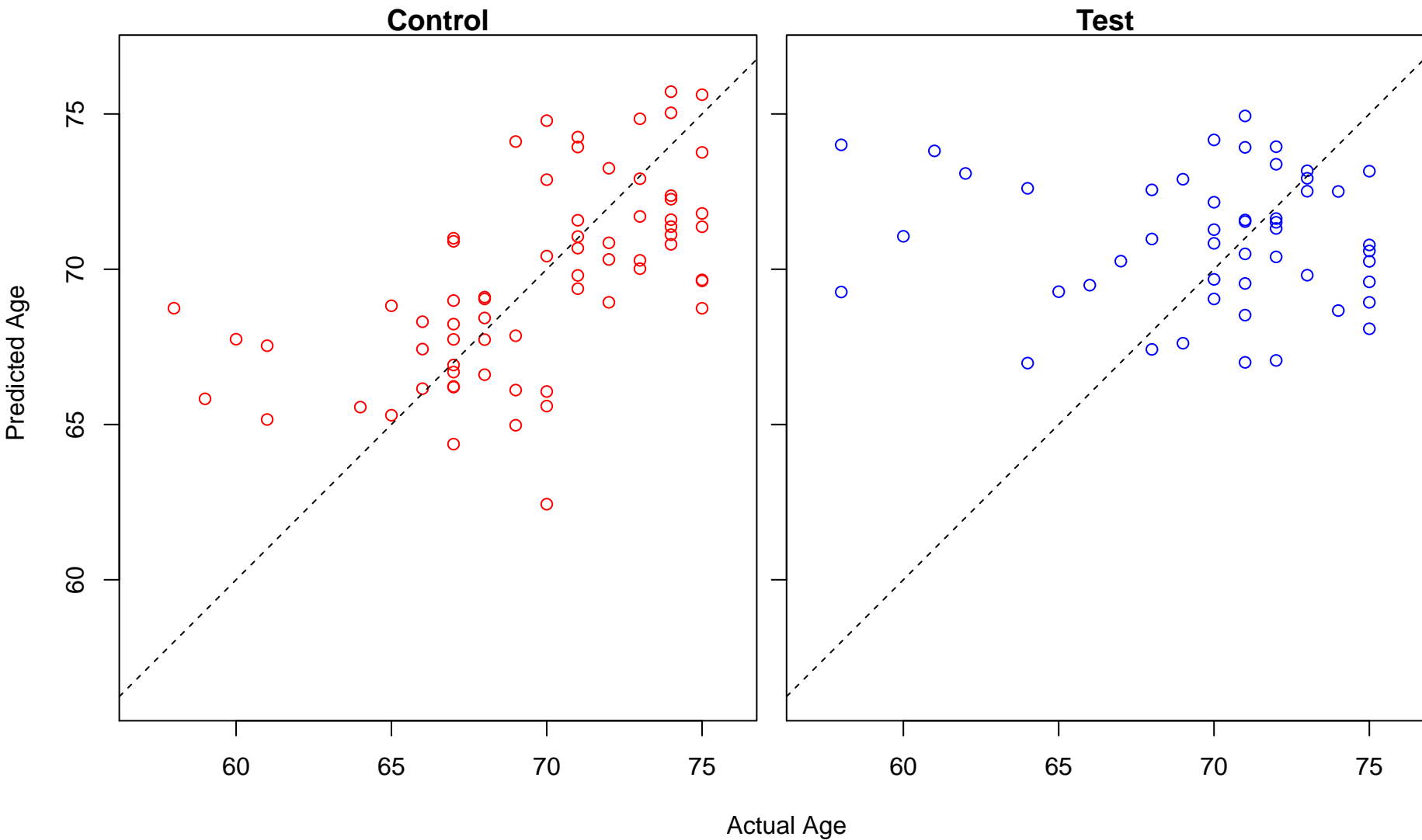
regulation of heart contraction (Score: 1.090819)



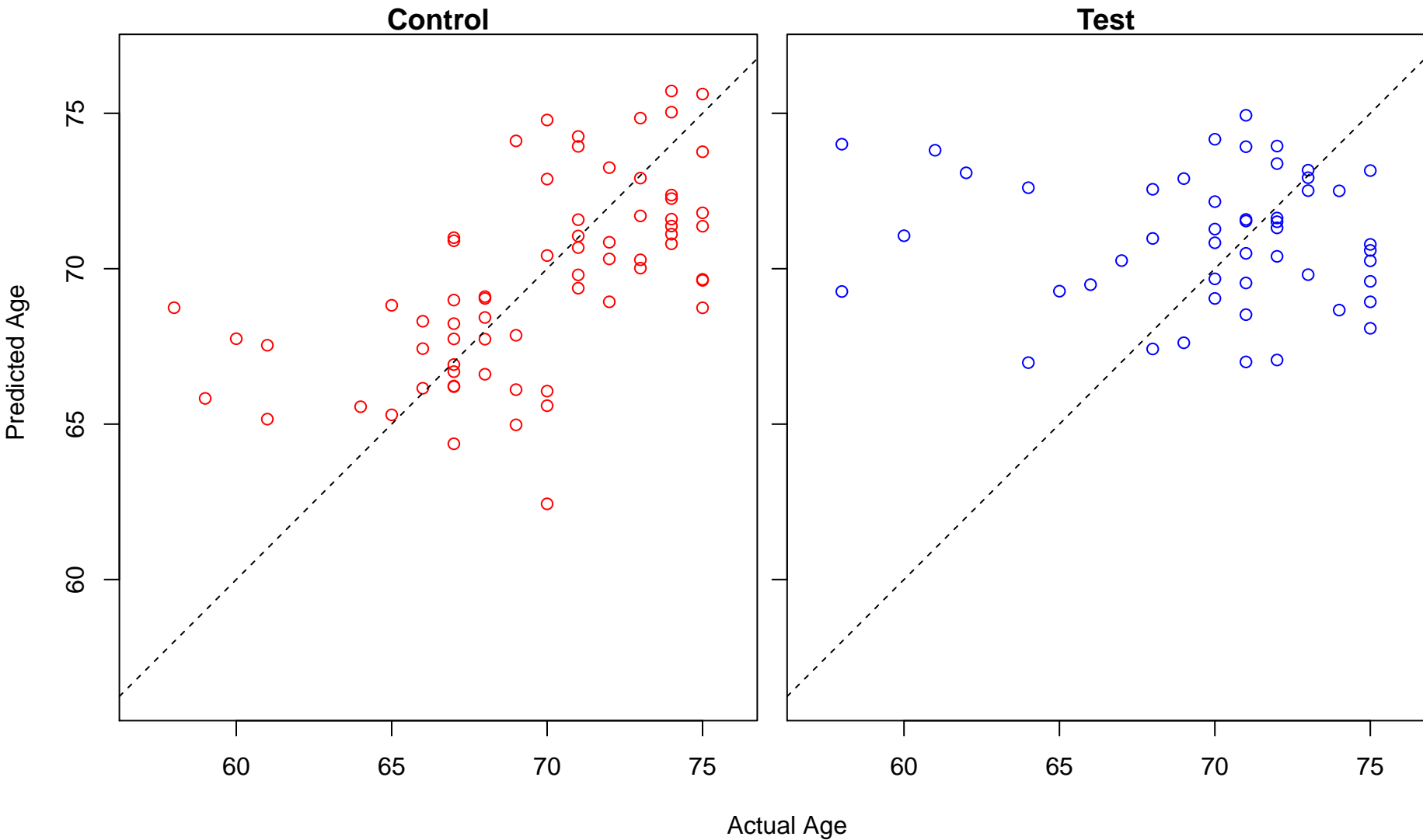
negative regulation of bone mineralization (Score: 1.090450)



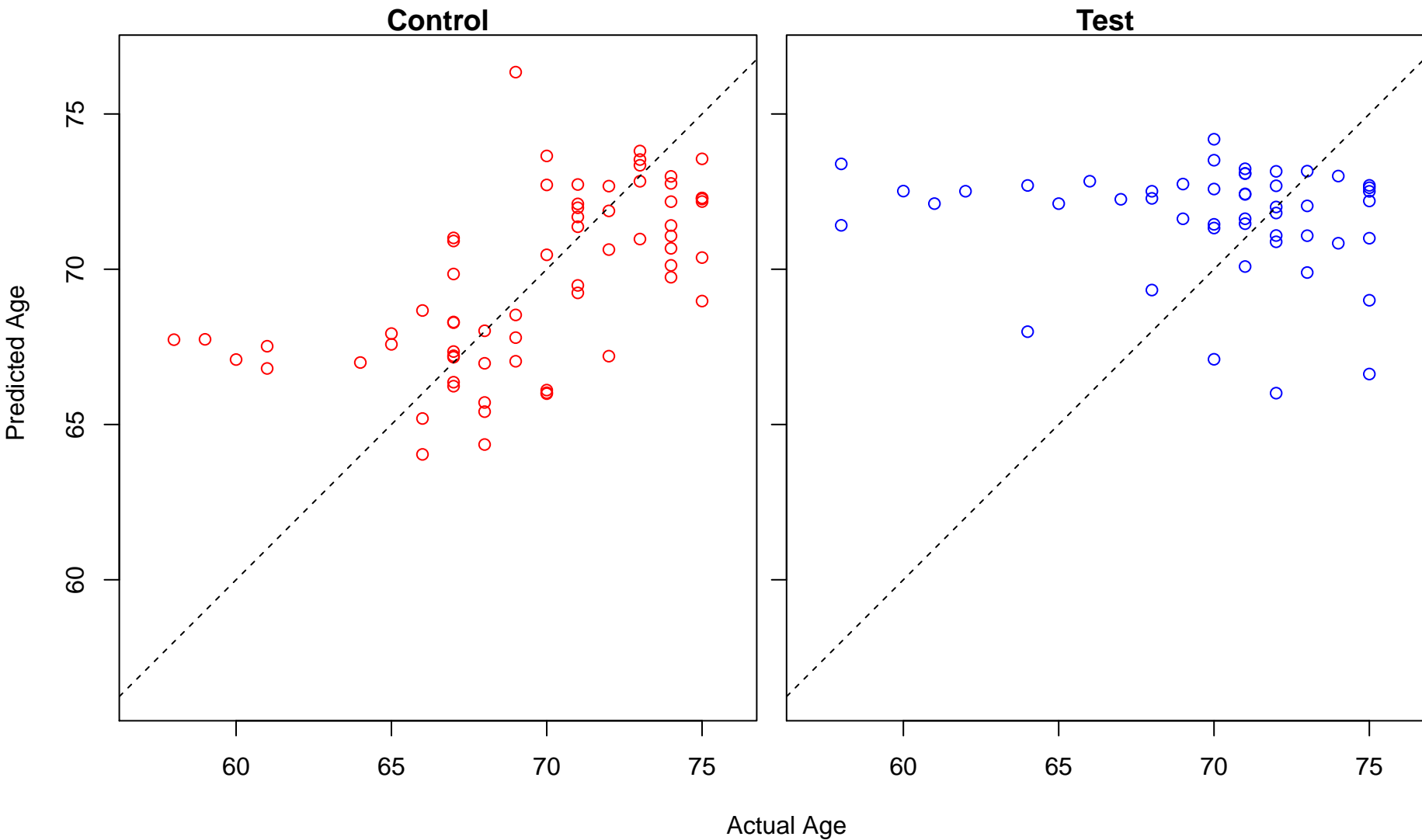
male gonad development (Score: 1.090065)



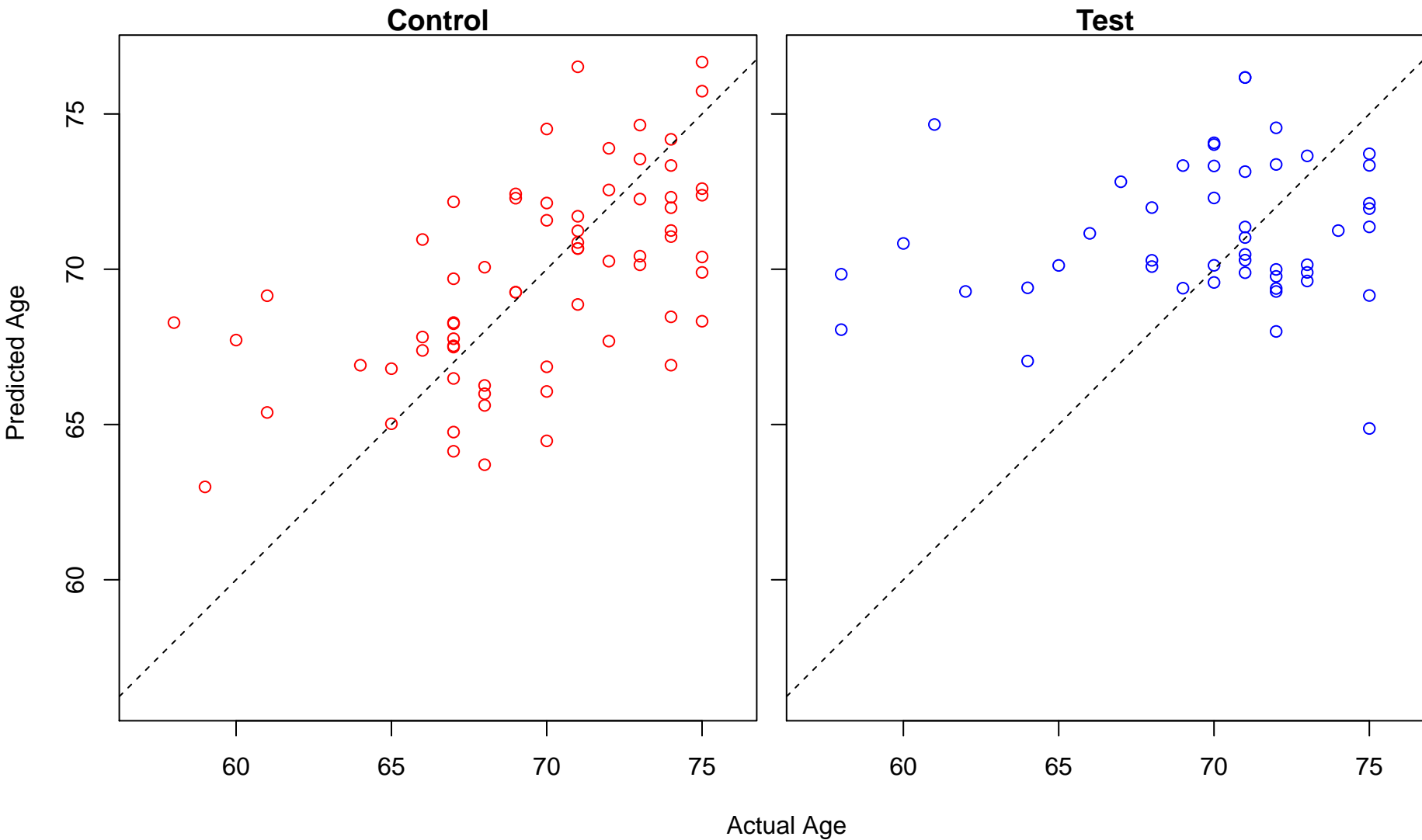
development of primary male sexual characteristics (Score: 1.090065)



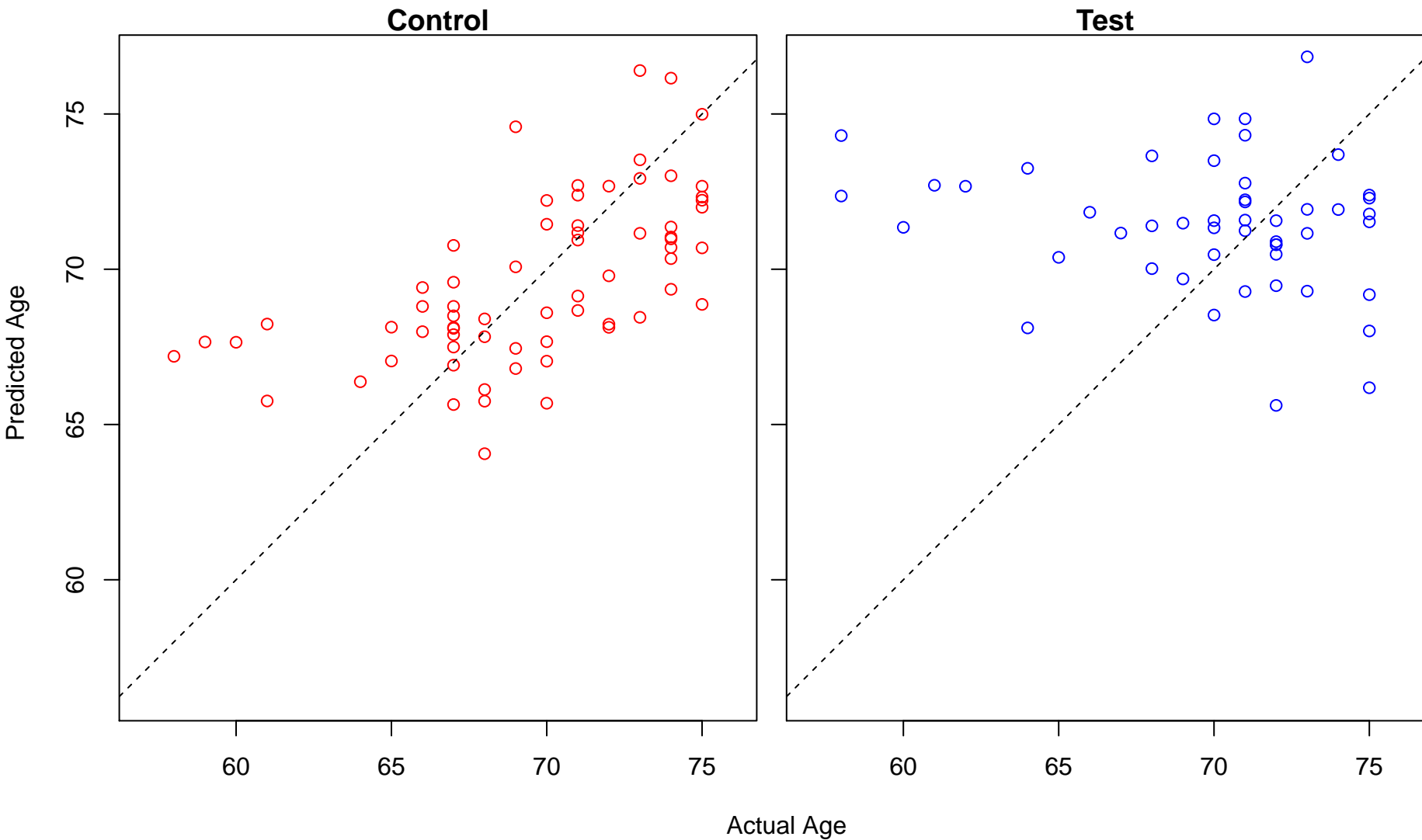
nerve development (Score: 1.089888)



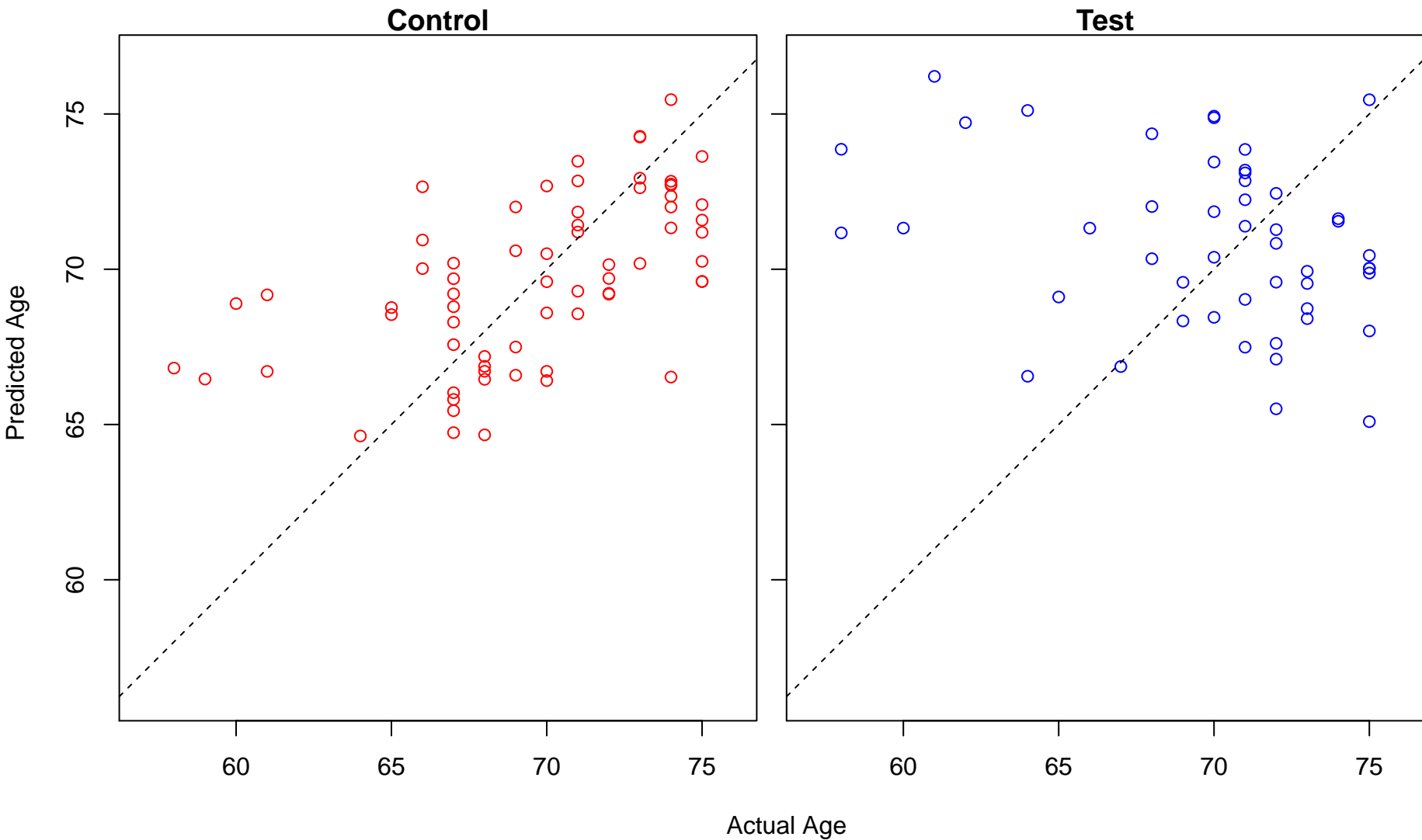
pyrimidine-containing compound catabolic process (Score: 1.089774)



regulation of protein sumoylation (Score: 1.089363)

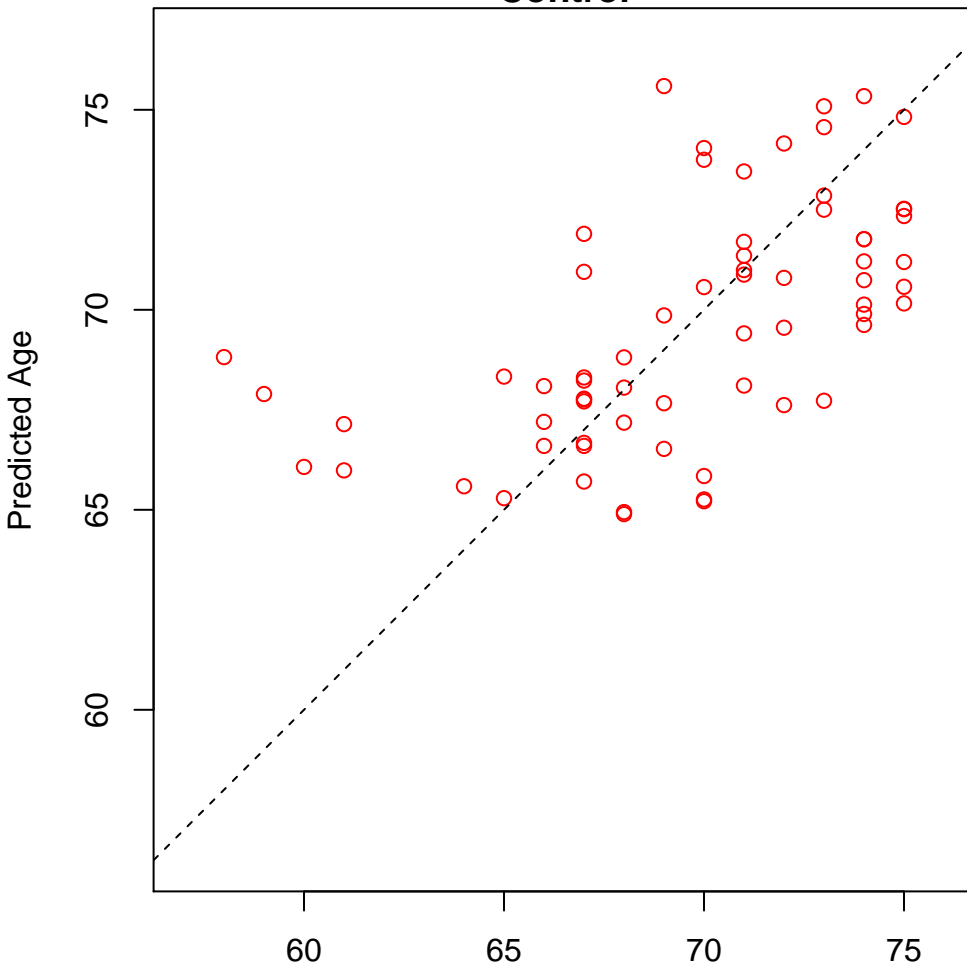


hormone-mediated signaling pathway (Score: 1.089242)

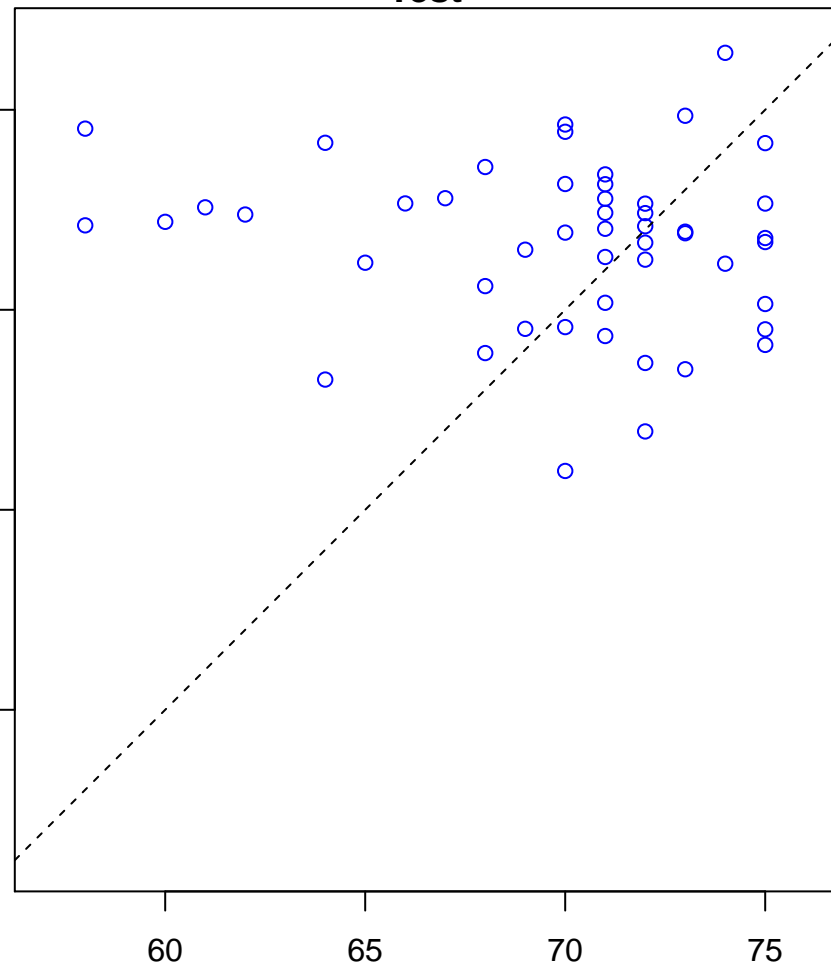


sulfur compound biosynthetic process (Score: 1.089143)

Control

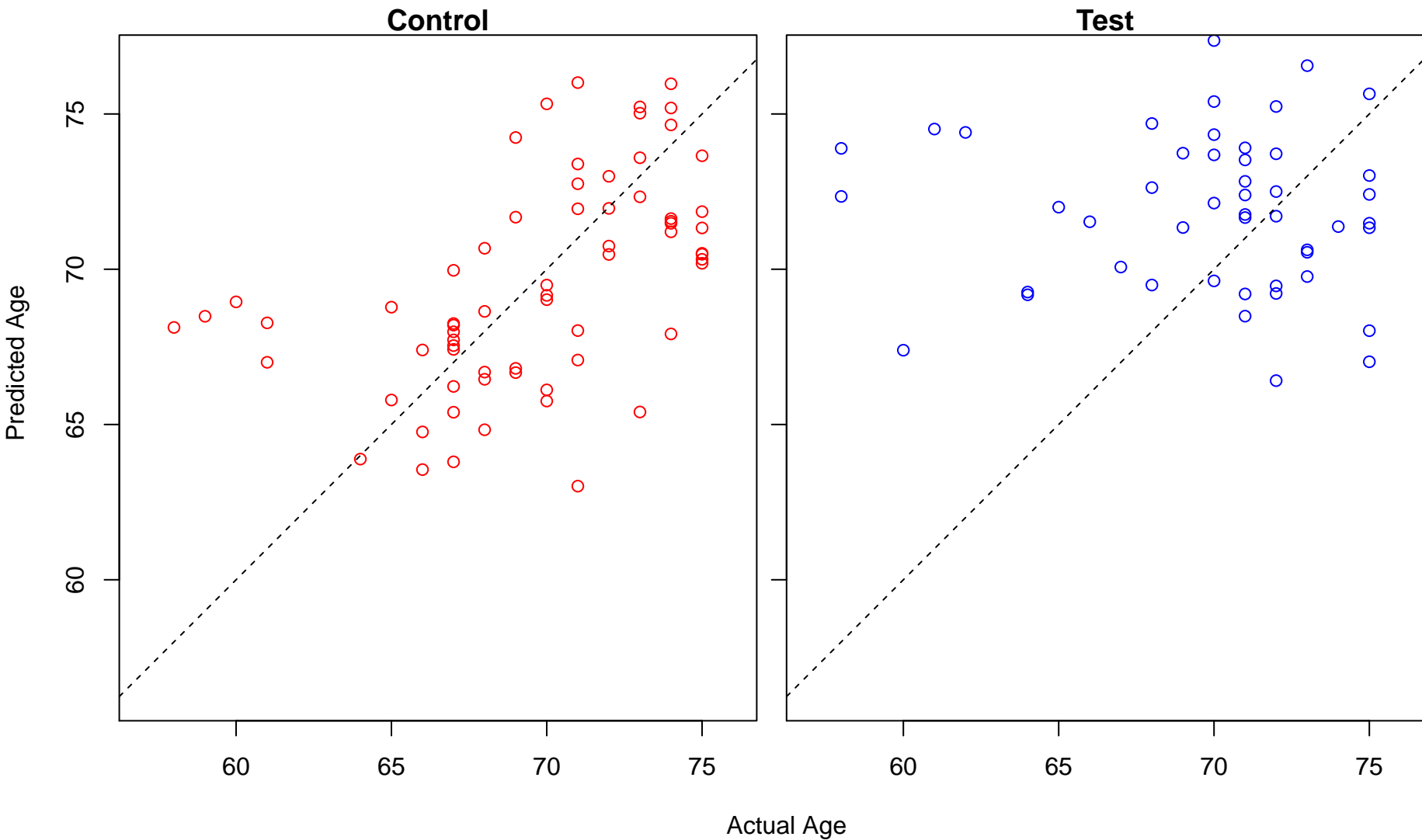


Test

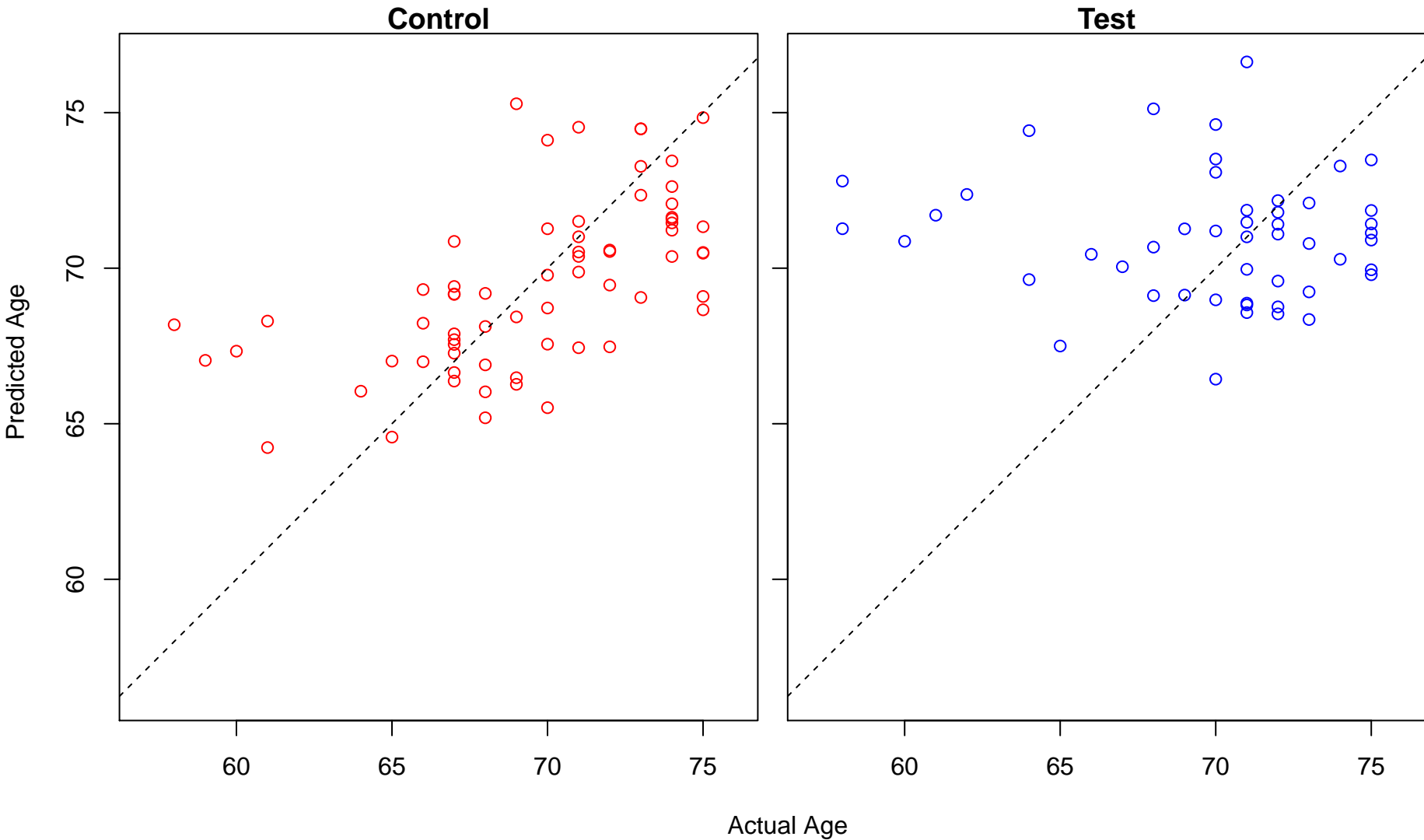


Actual Age

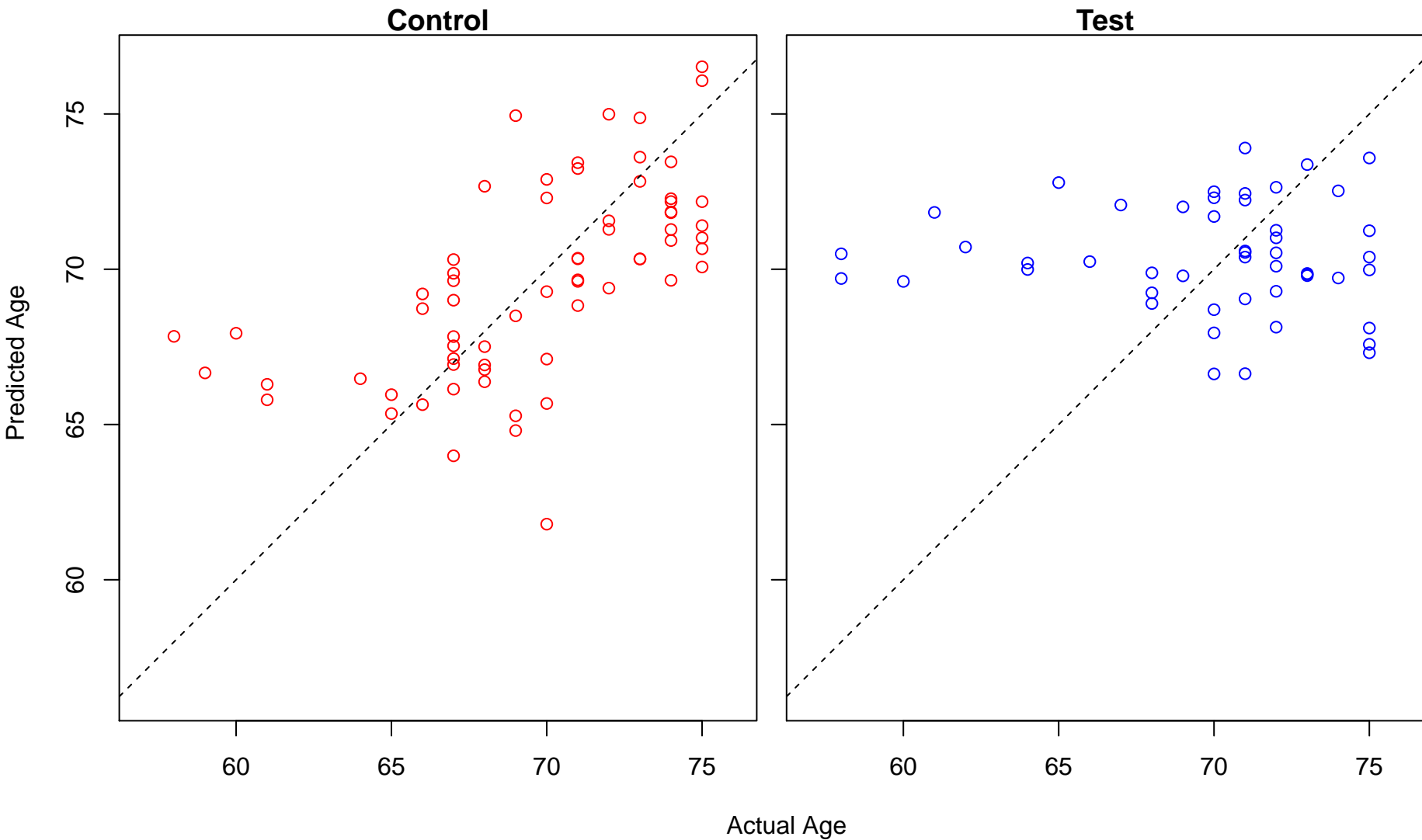
regulation of toll-like receptor signaling pathway (Score: 1.088861)



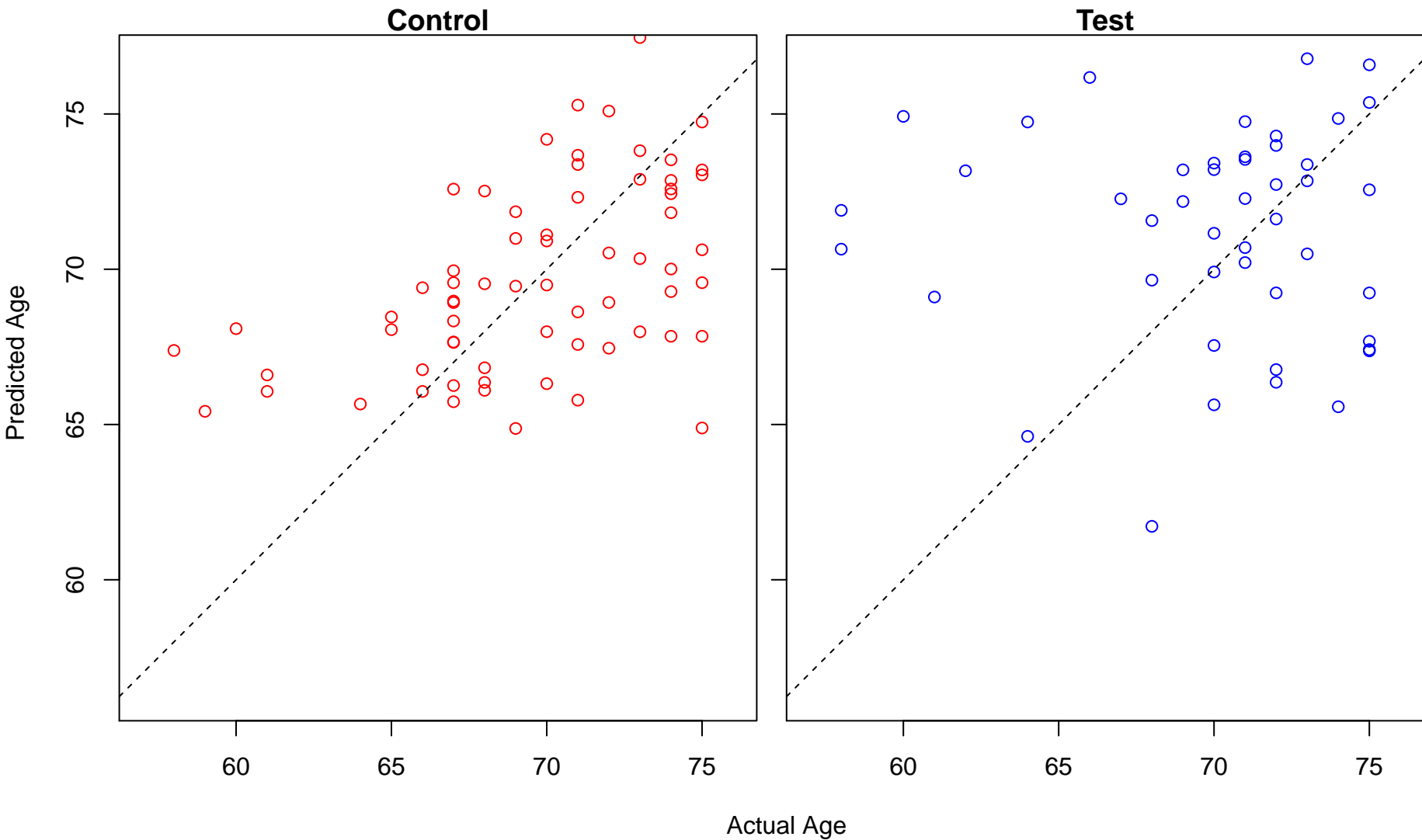
inner mitochondrial membrane organization (Score: 1.087523)



negative regulation of cellular carbohydrate metabolic process (Score: 1.087228)

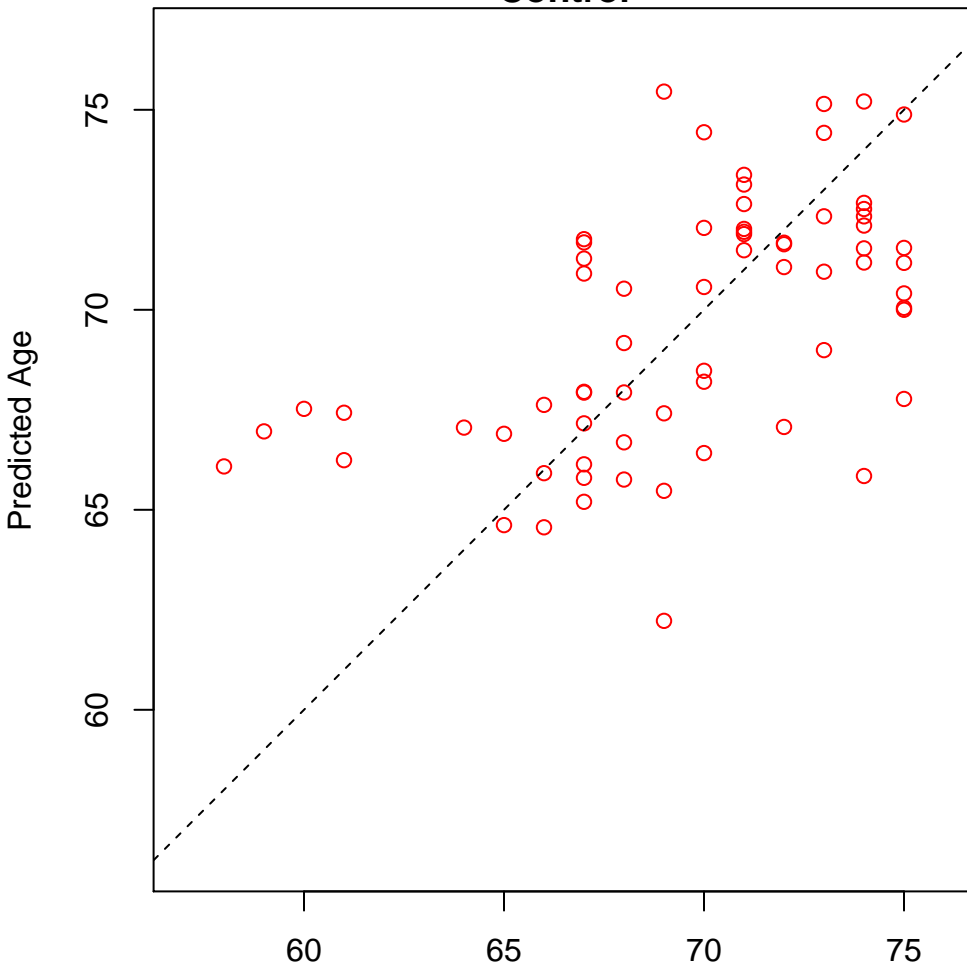


phenol-containing compound metabolic process (Score: 1.086591)

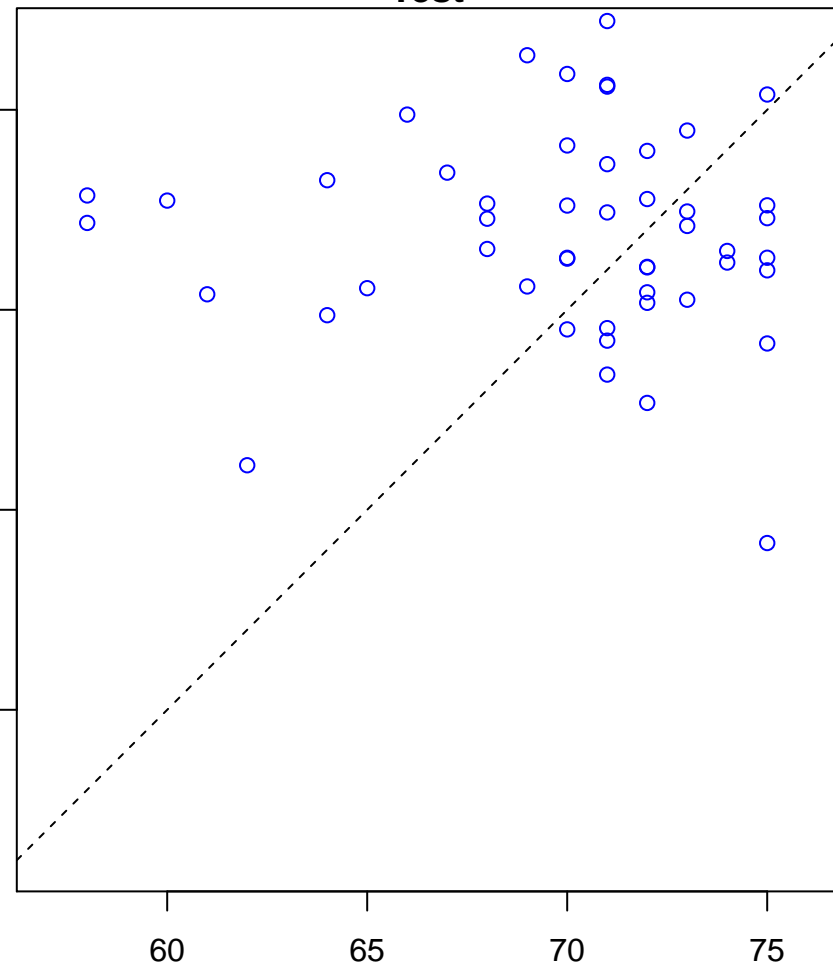


N-terminal protein amino acid modification (Score: 1.086395)

Control

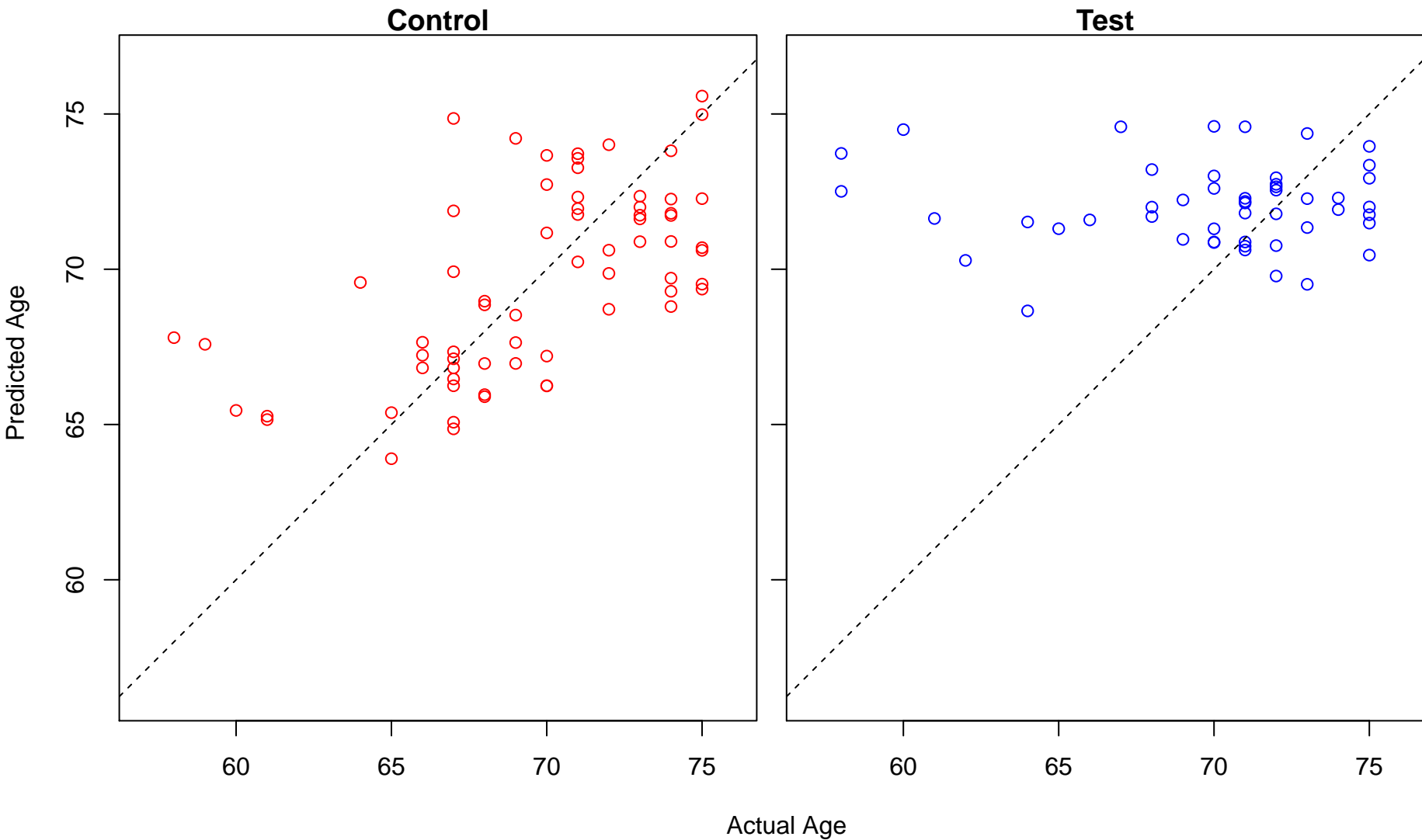


Test



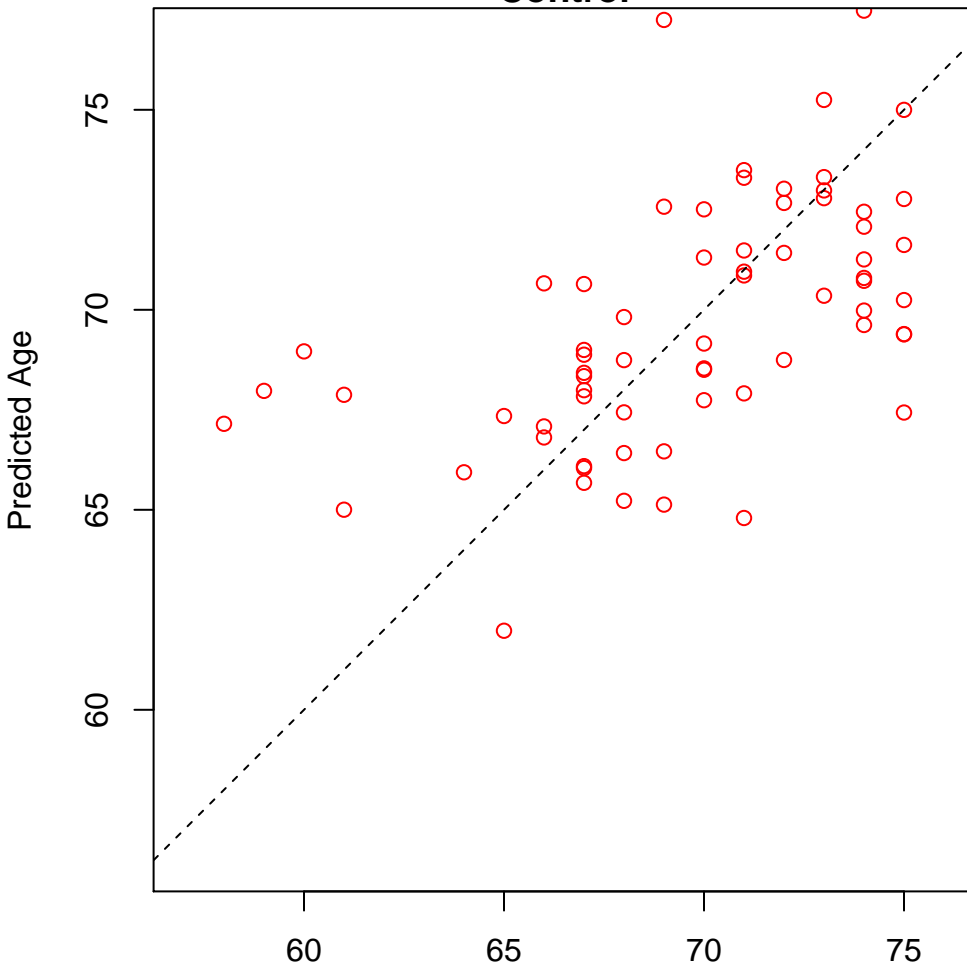
Actual Age

sphingolipid biosynthetic process (Score: 1.085448)

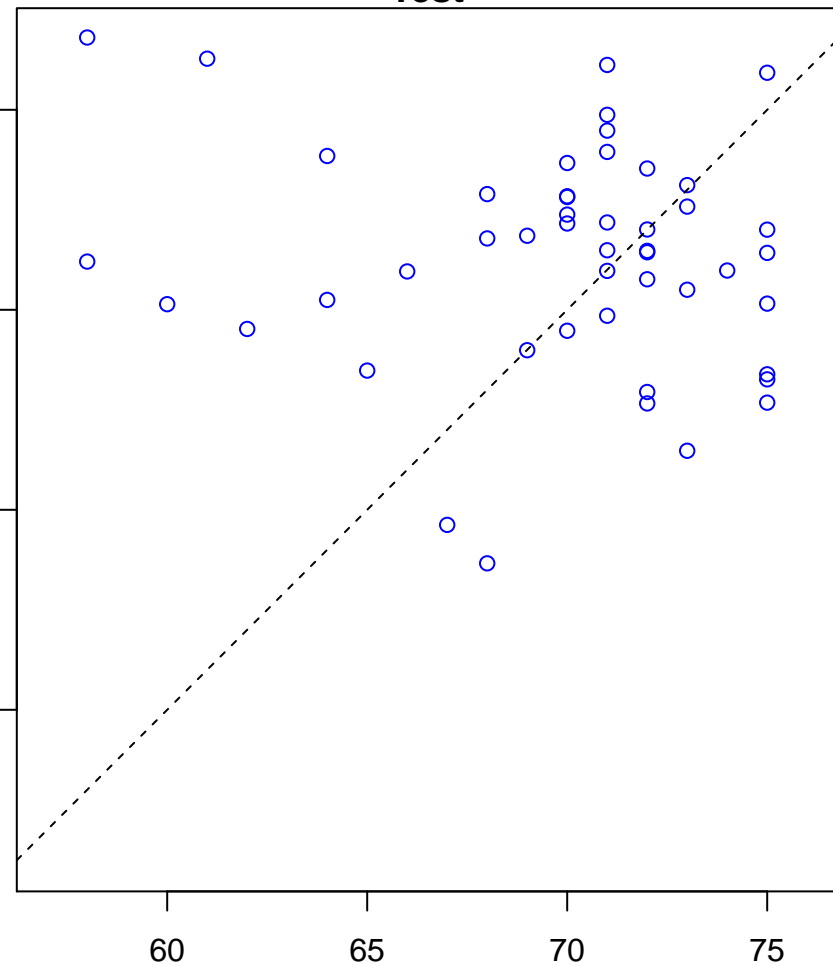


regulation of interleukin-10 production (Score: 1.085430)

Control

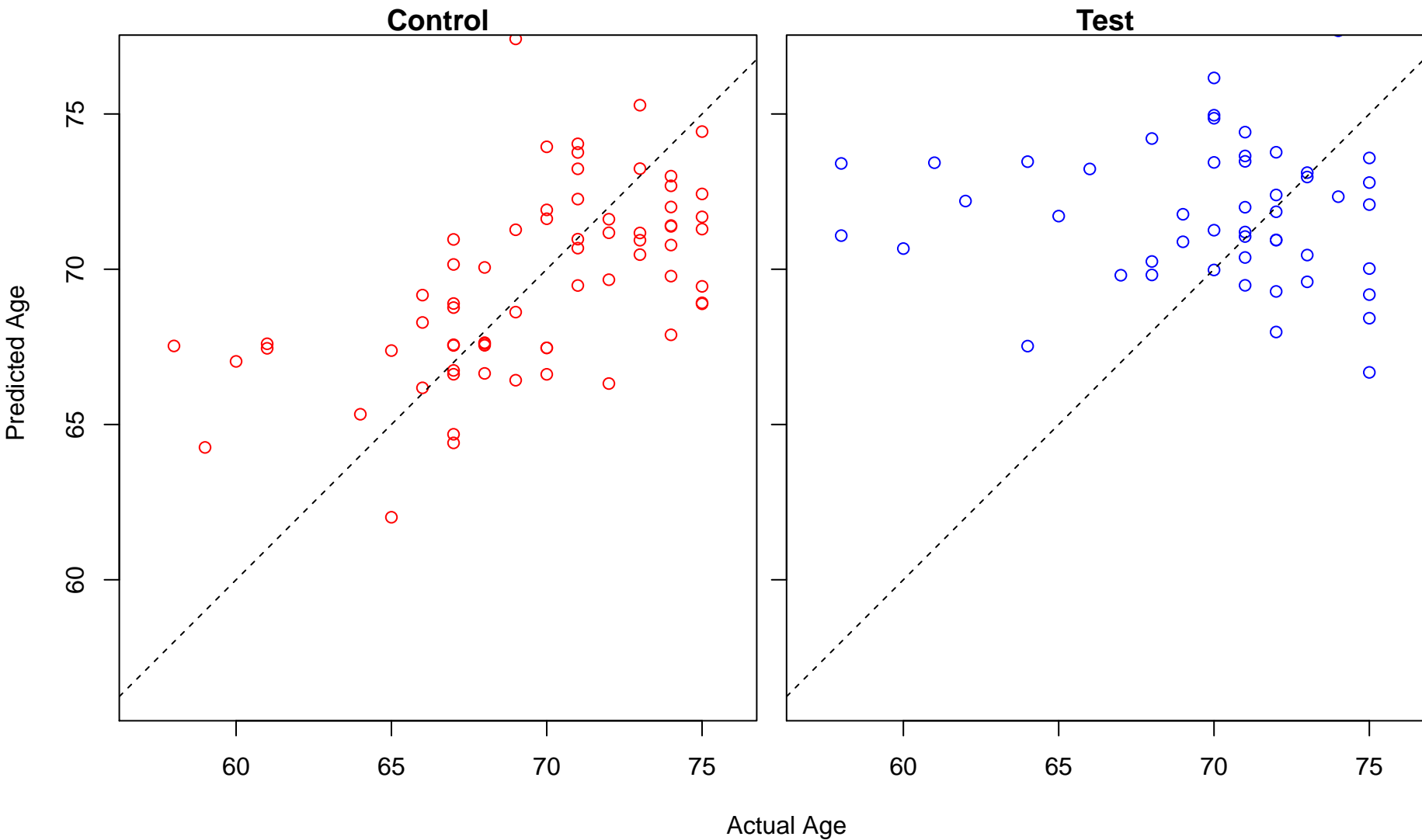


Test

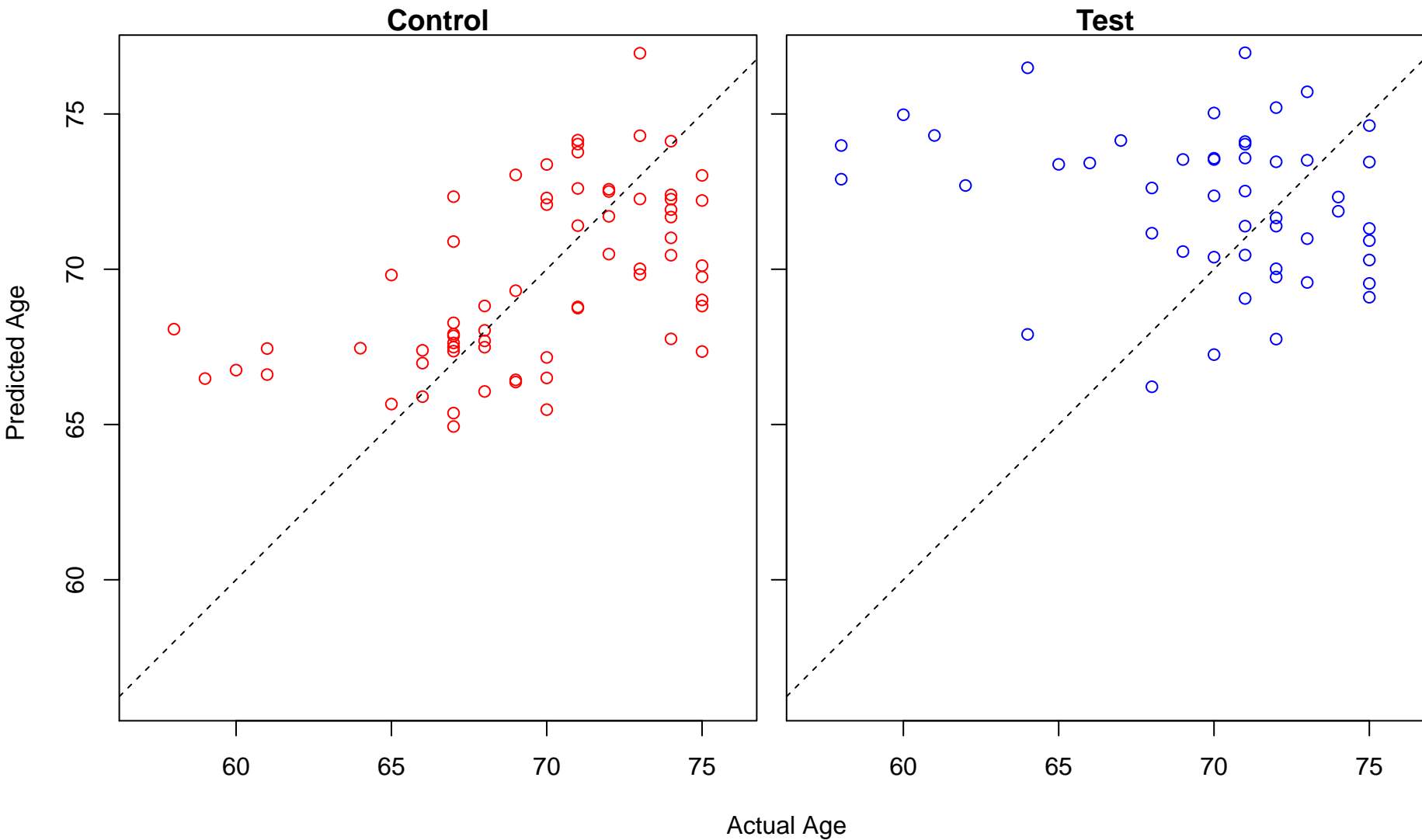


Actual Age

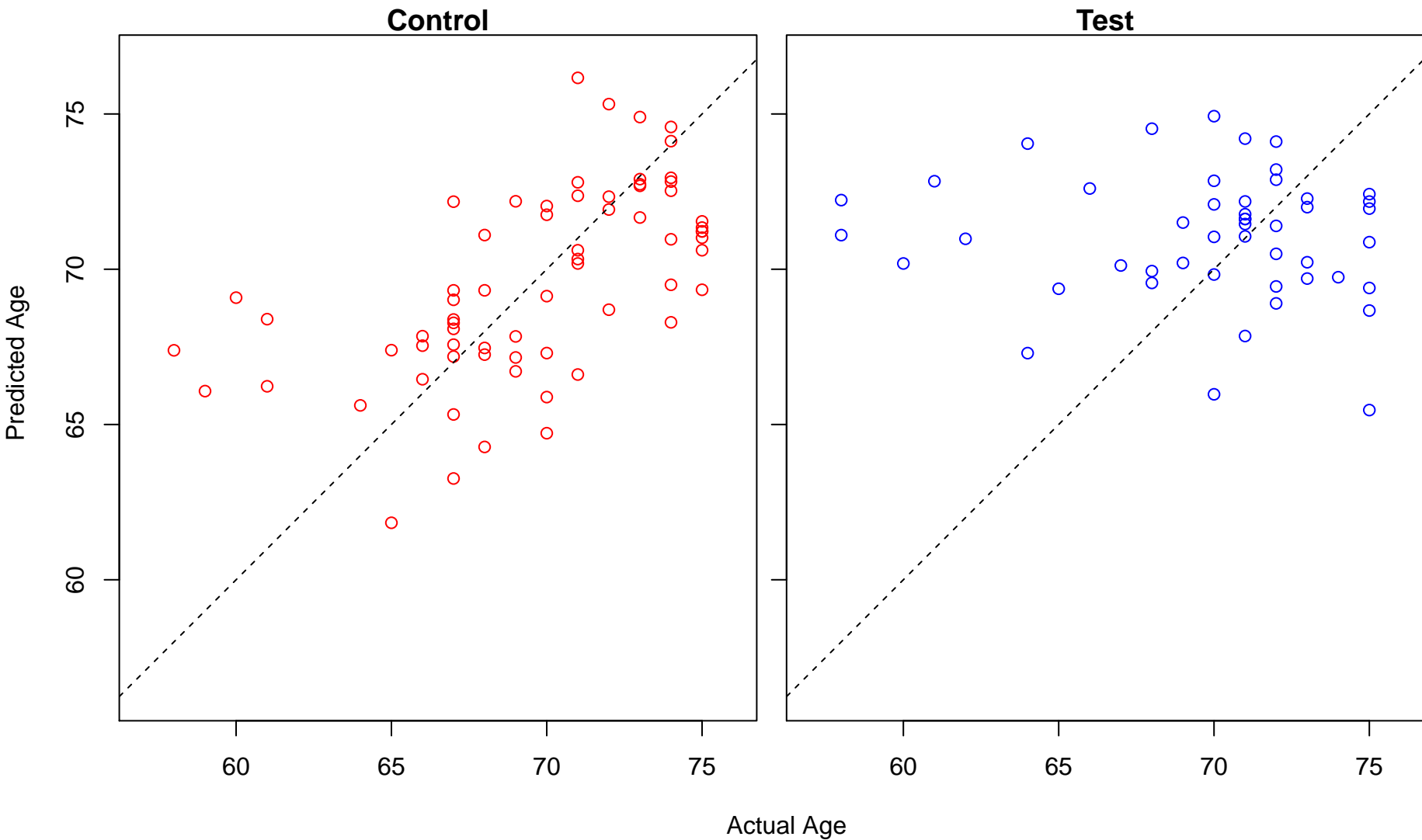
negative regulation of DNA damage response, signal transduction by p53 class mediator (Score: 1.085)



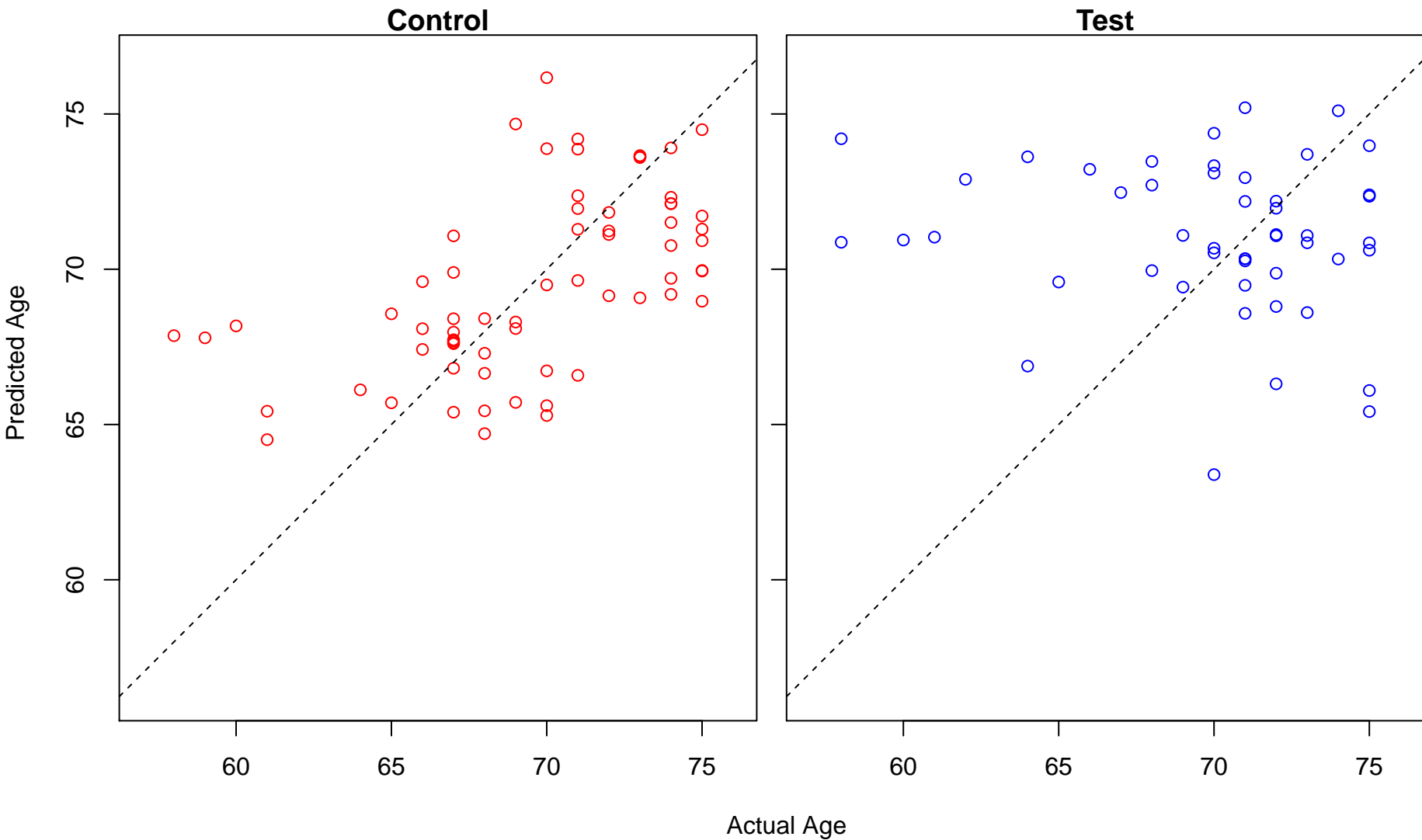
cyclic nucleotide metabolic process (Score: 1.084873)



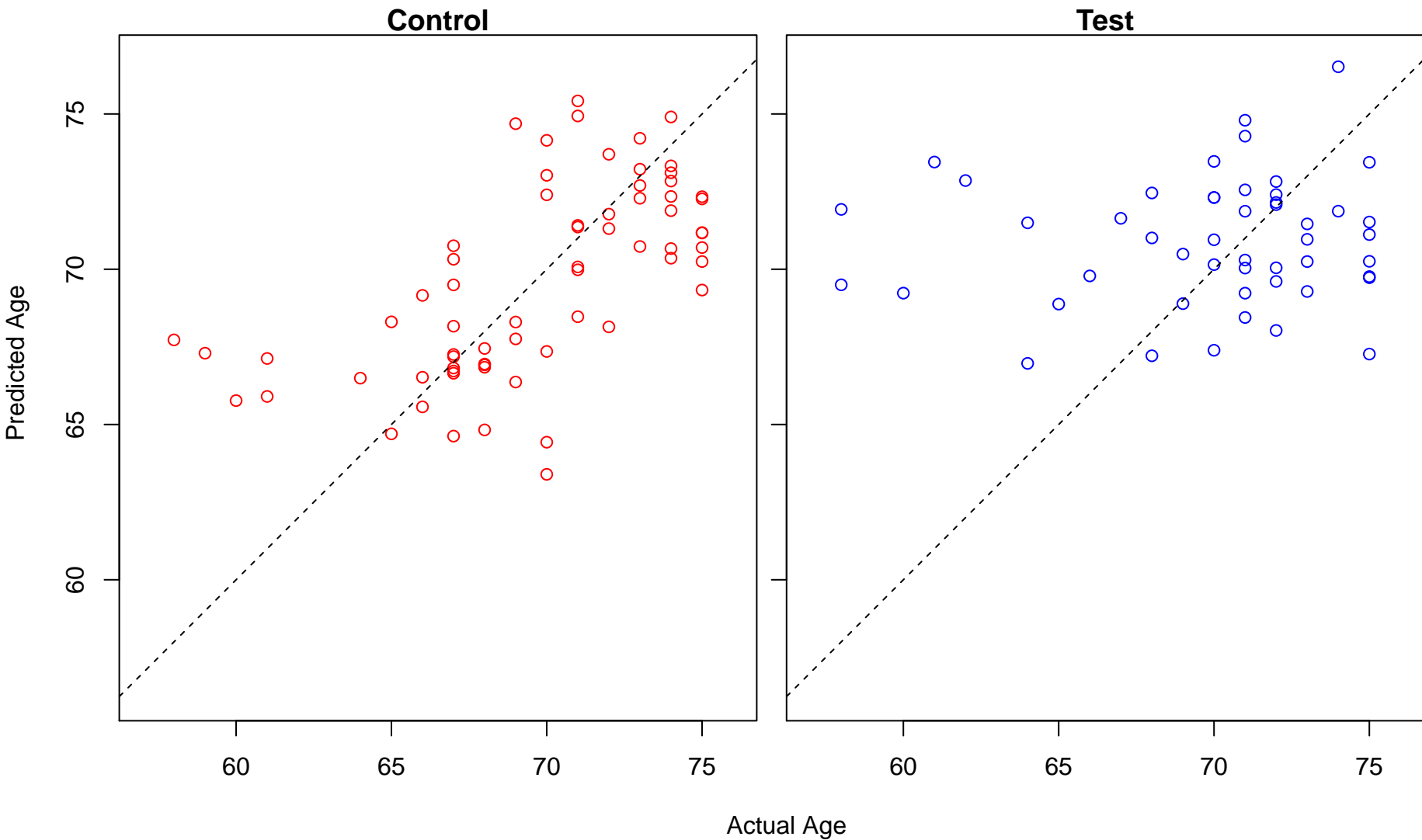
regulation of interleukin-1 beta production (Score: 1.084592)



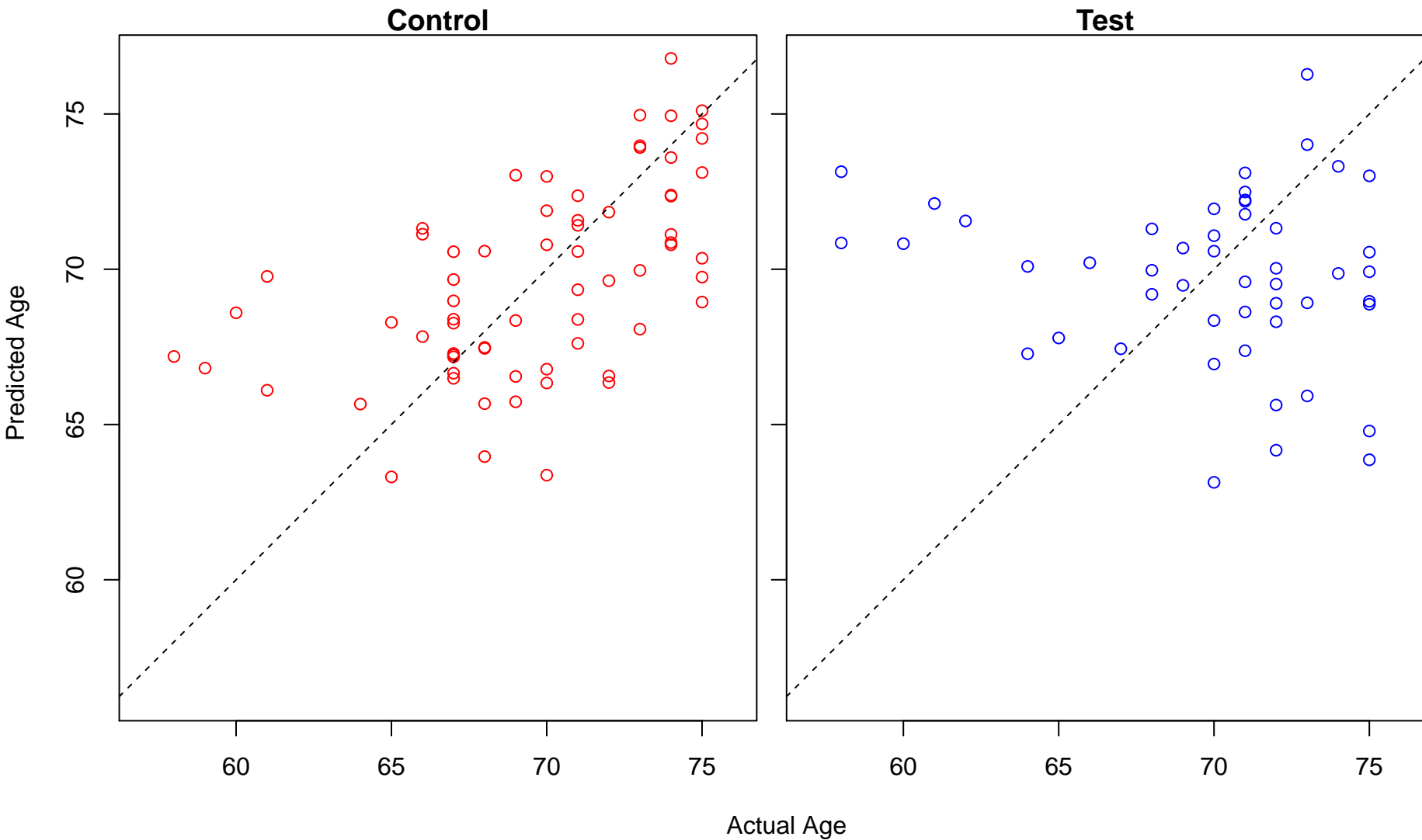
interaction with symbiont (Score: 1.084512)



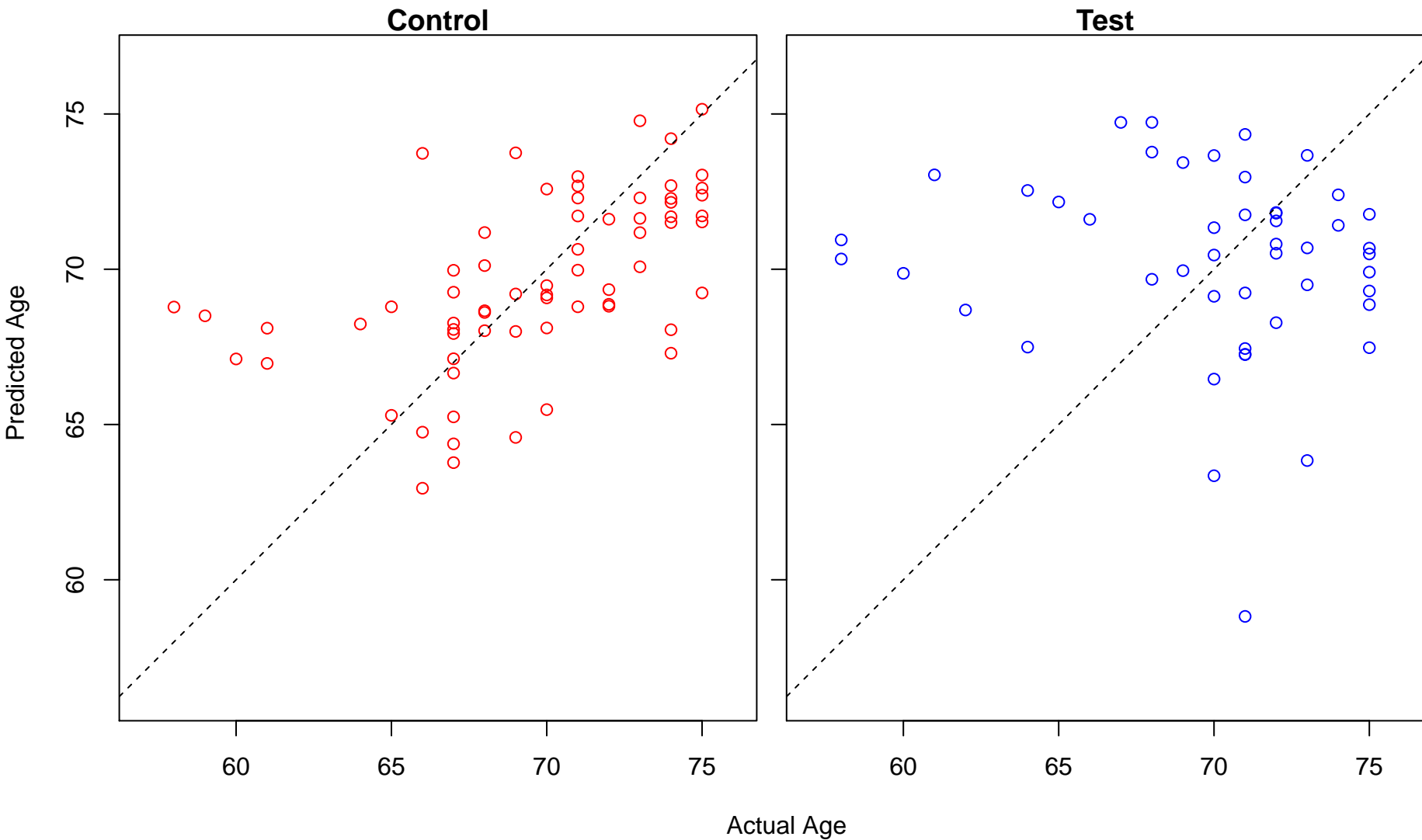
positive regulation of endocytosis (Score: 1.084188)



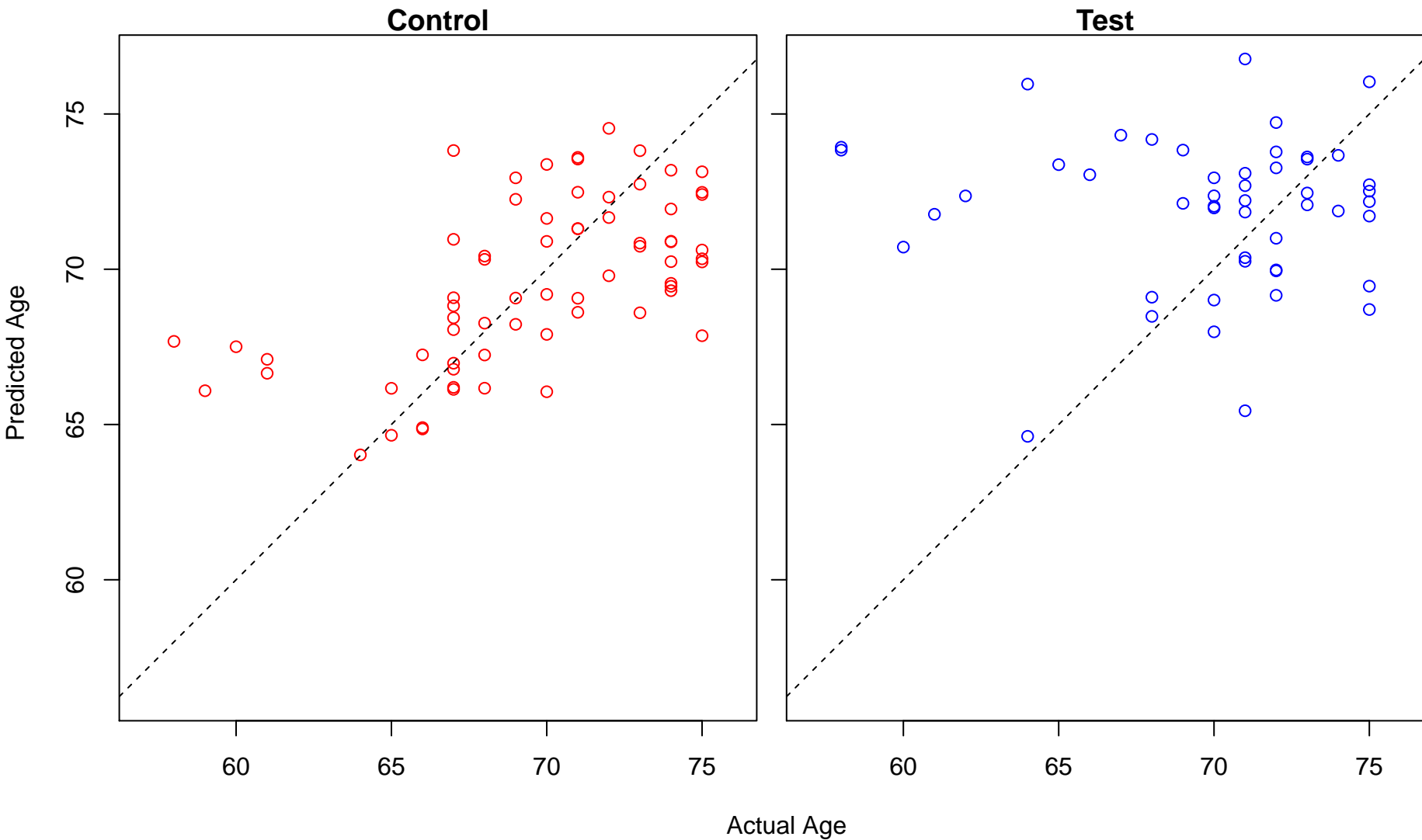
positive regulation of cyclin–dependent protein kinase activity (Score: 1.083938)



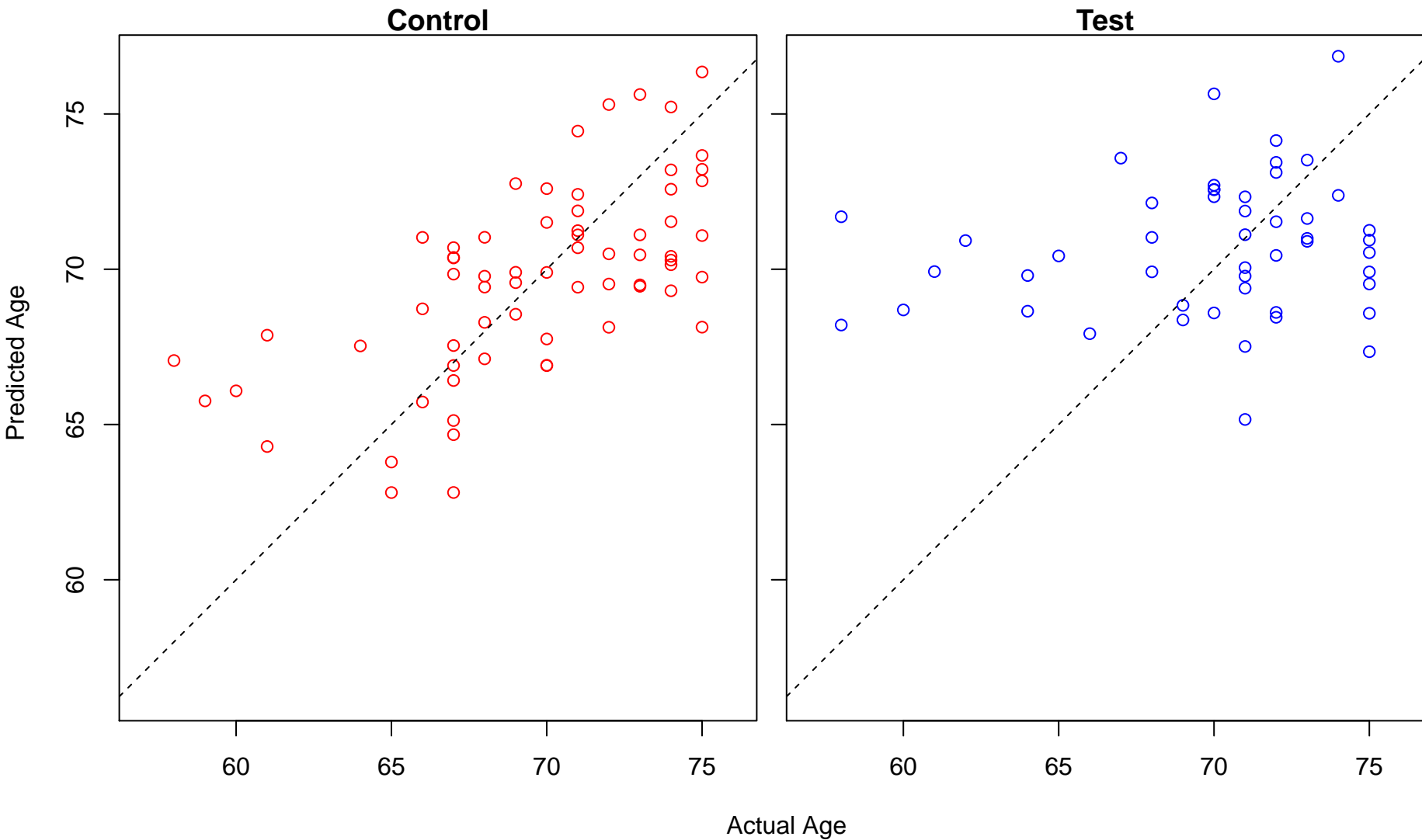
vitamin catabolic process (Score: 1.083938)



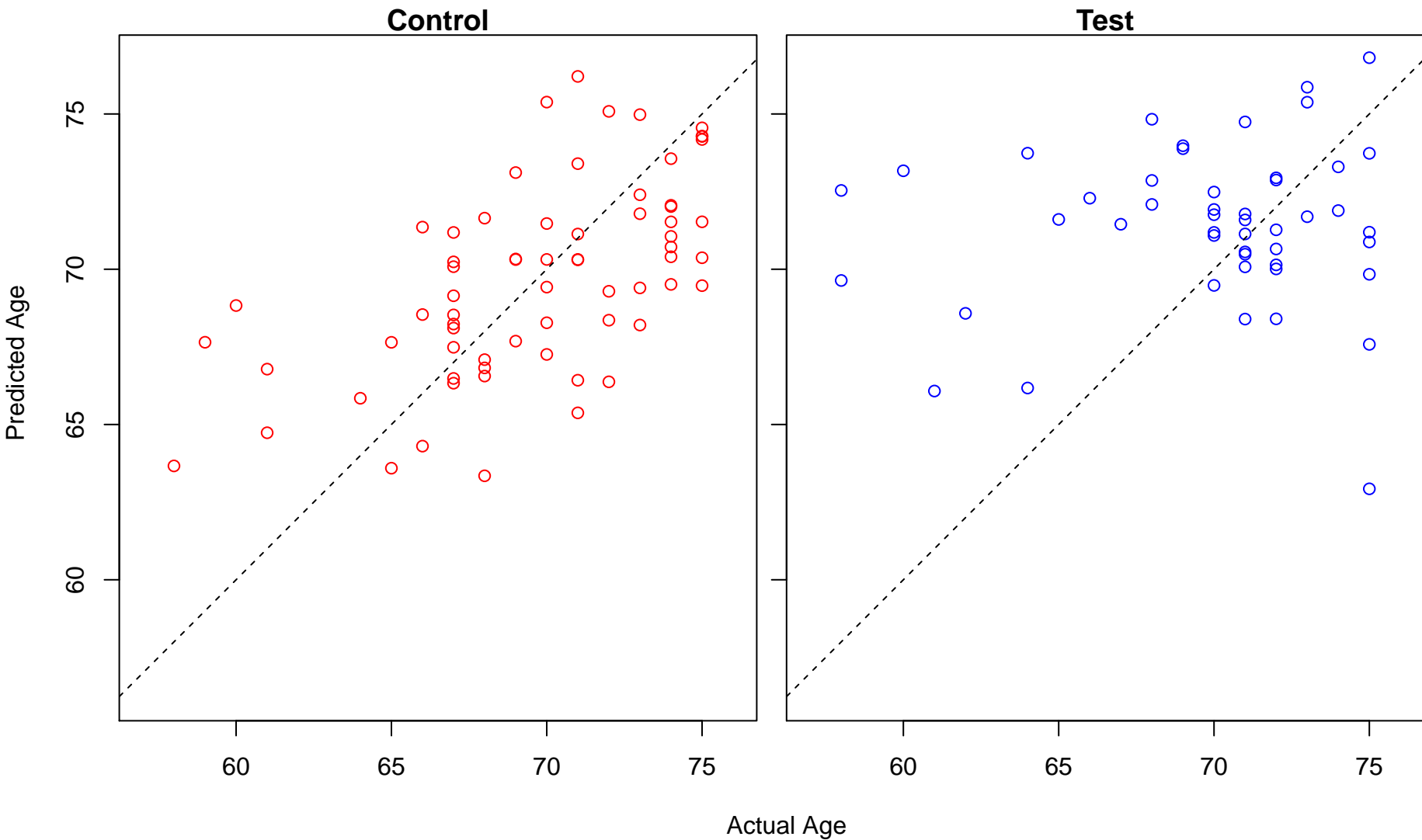
axonemal dynein complex assembly (Score: 1.082811)



viral genome replication (Score: 1.082761)

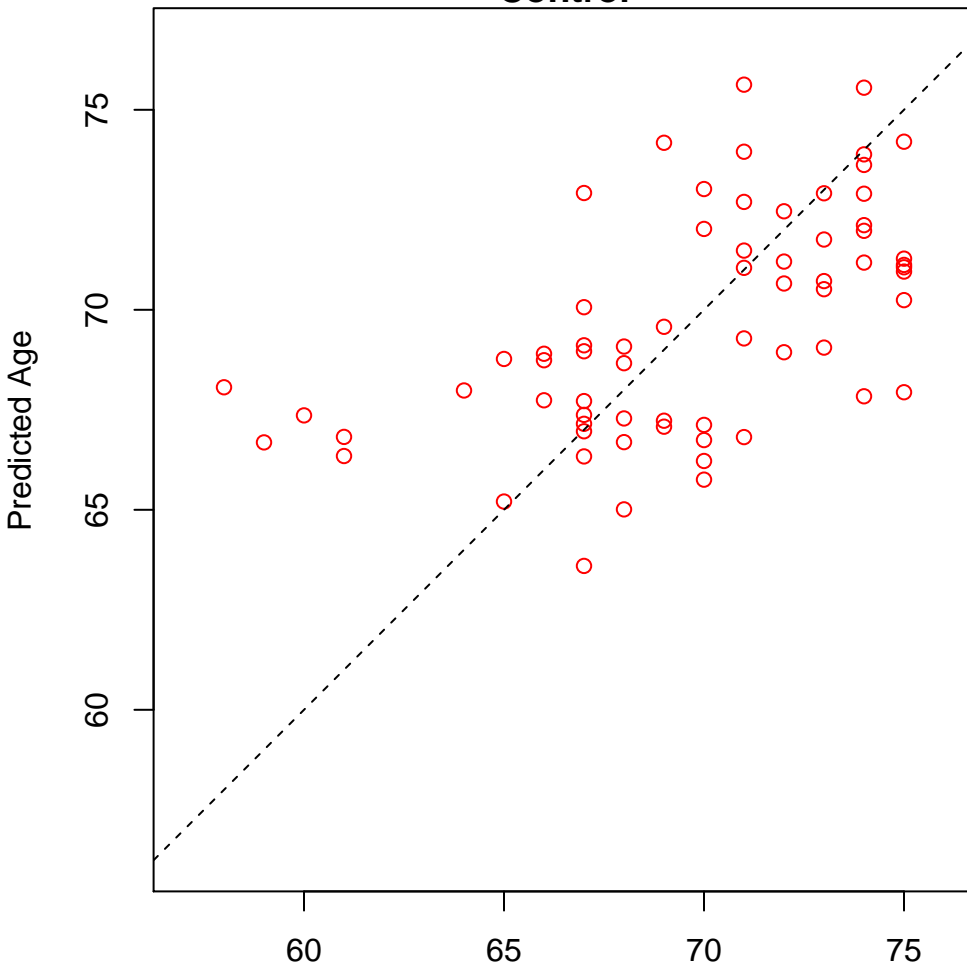


interleukin-1 production (Score: 1.082194)

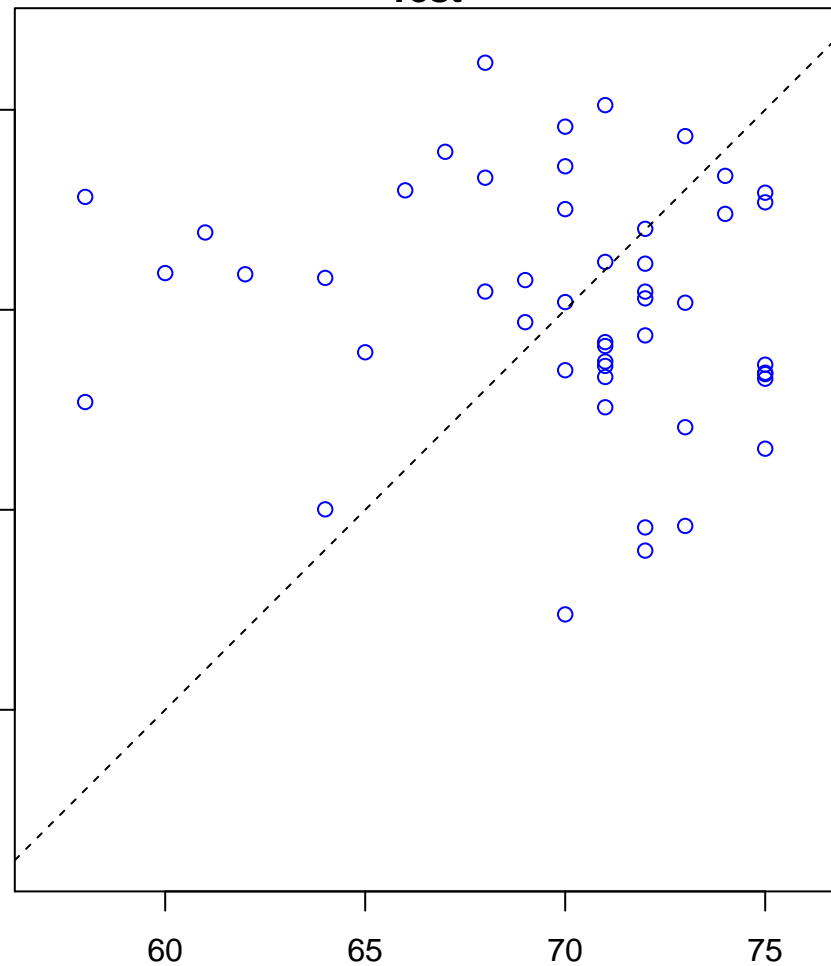


negative regulation of telomere capping (Score: 1.082192)

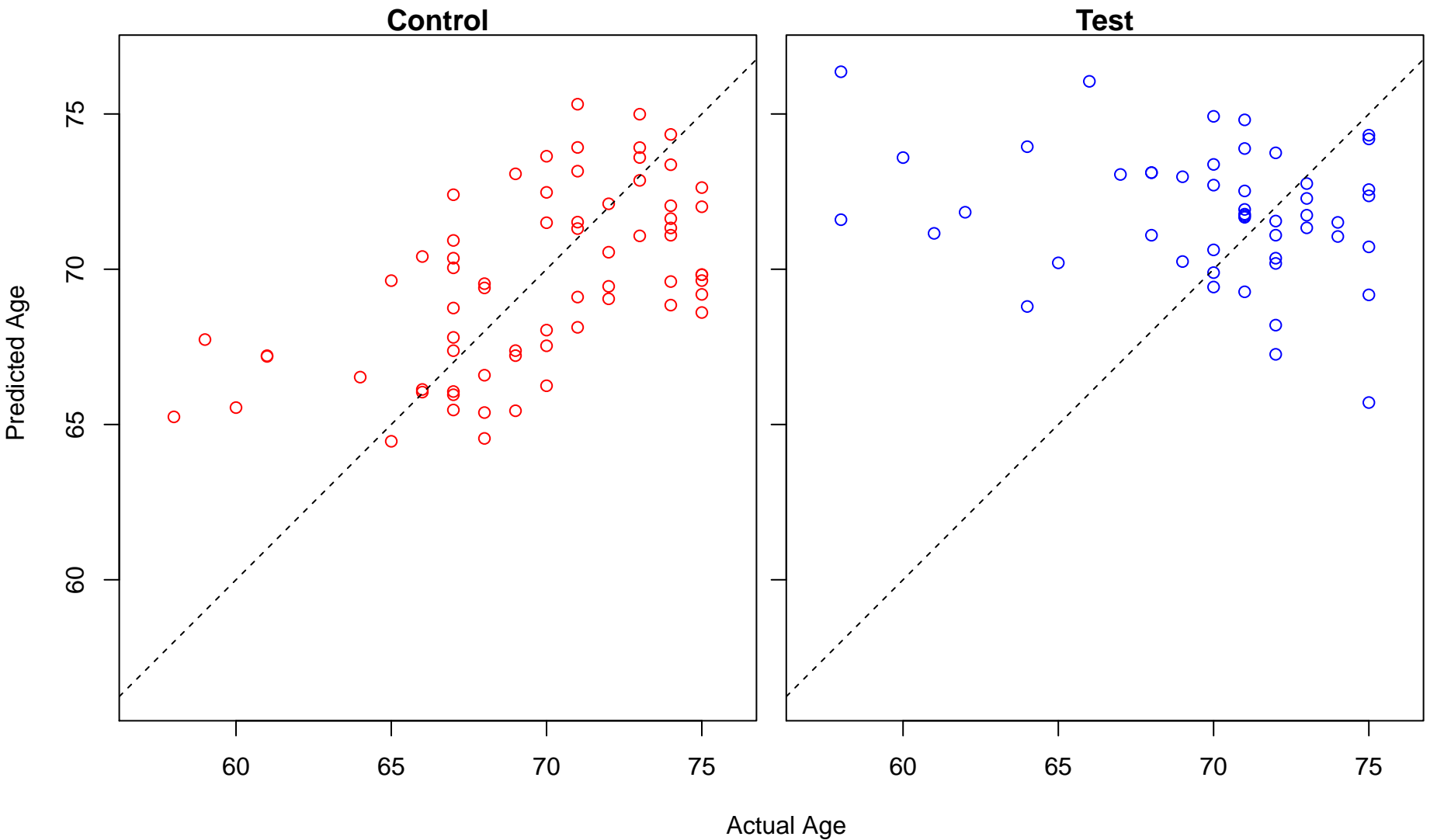
Control



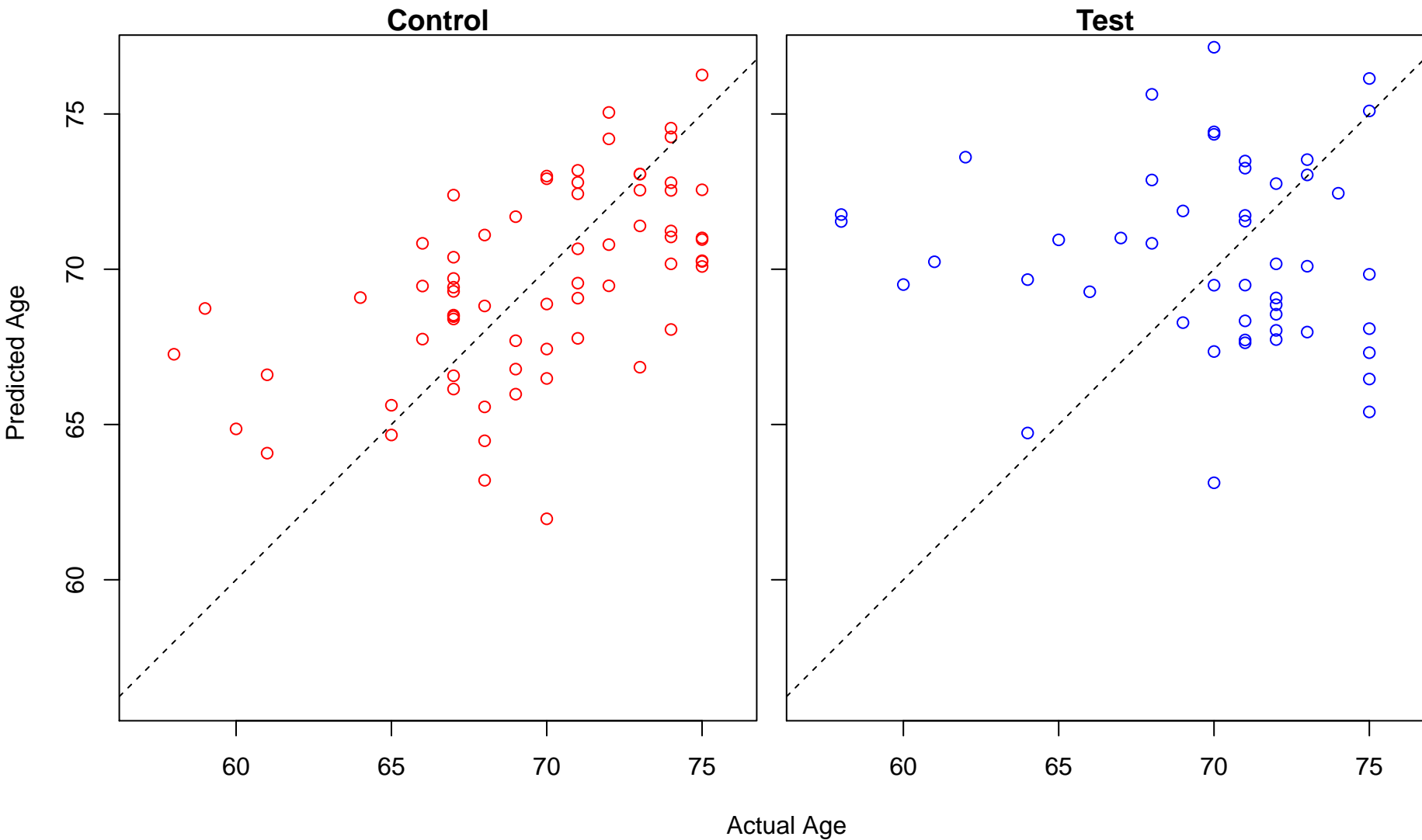
Test



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

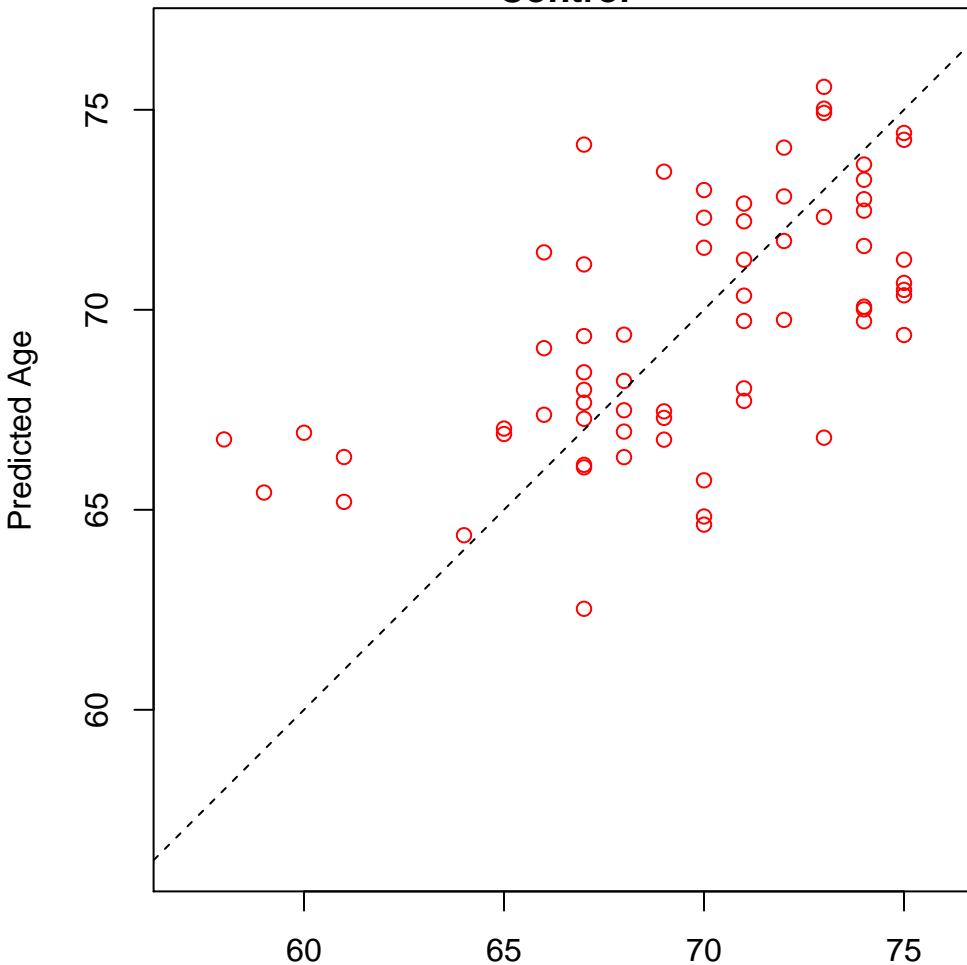


negative regulation of intracellular steroid hormone receptor signaling pathway (Score: 1.081931)

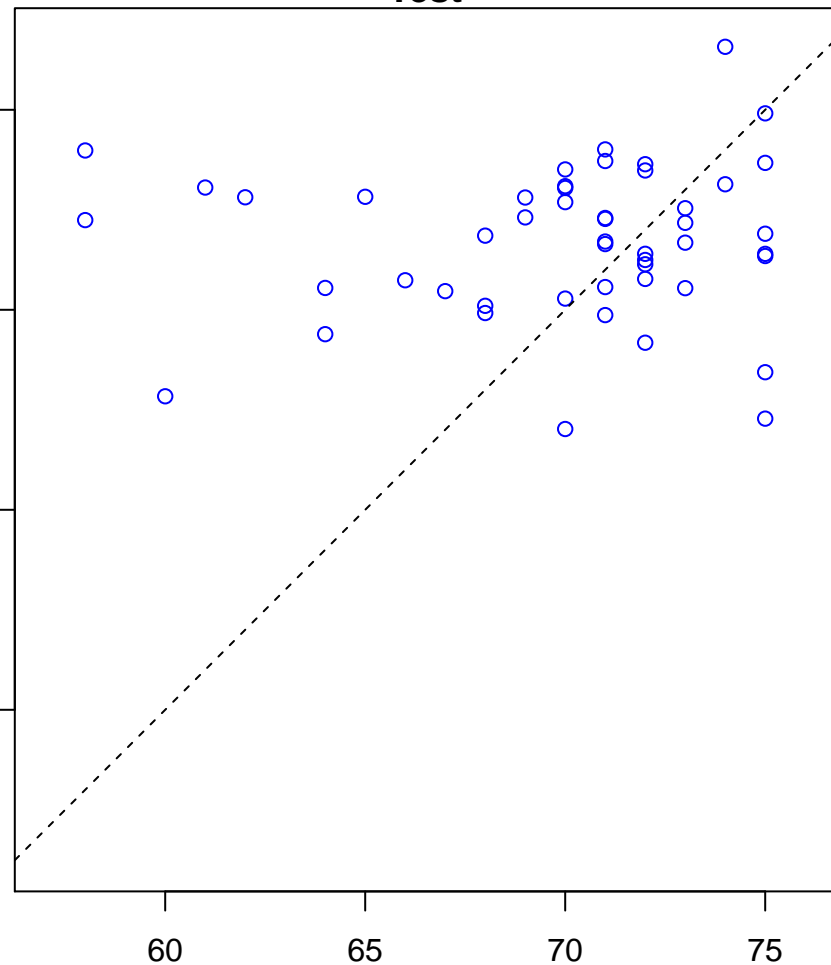


protein localization to plasma membrane (Score: 1.081763)

Control



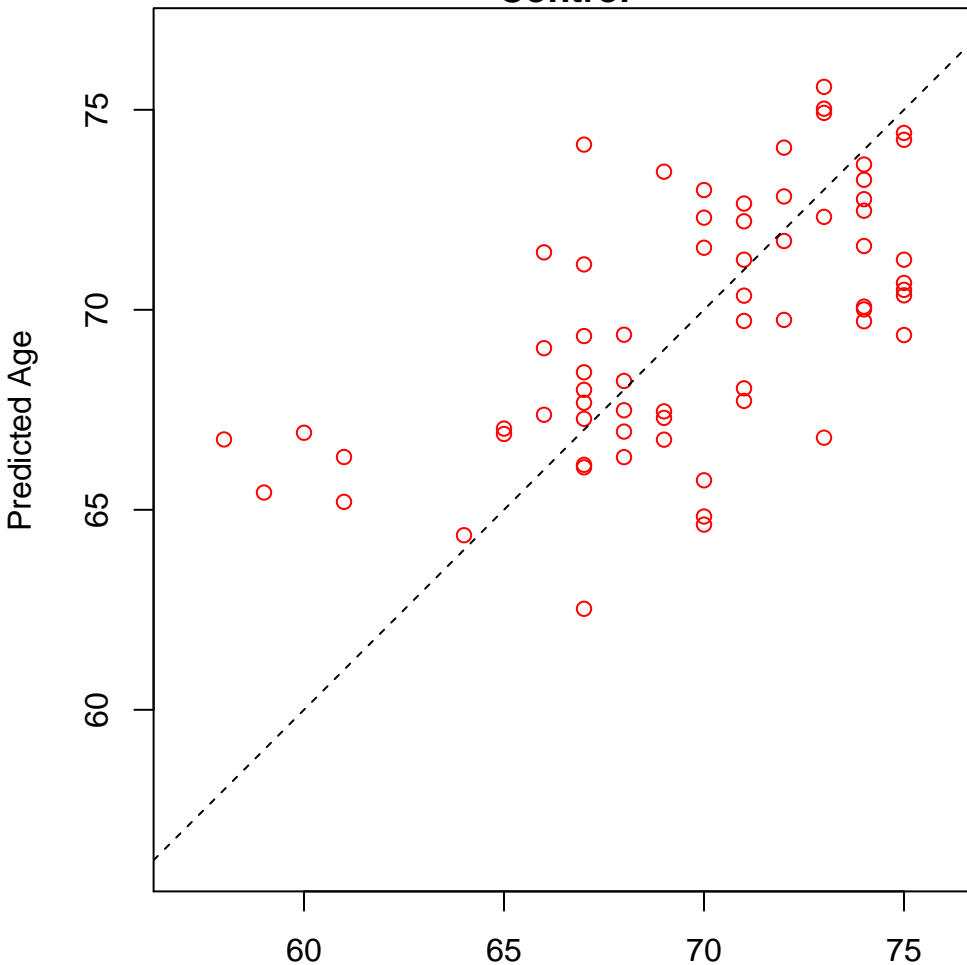
Test



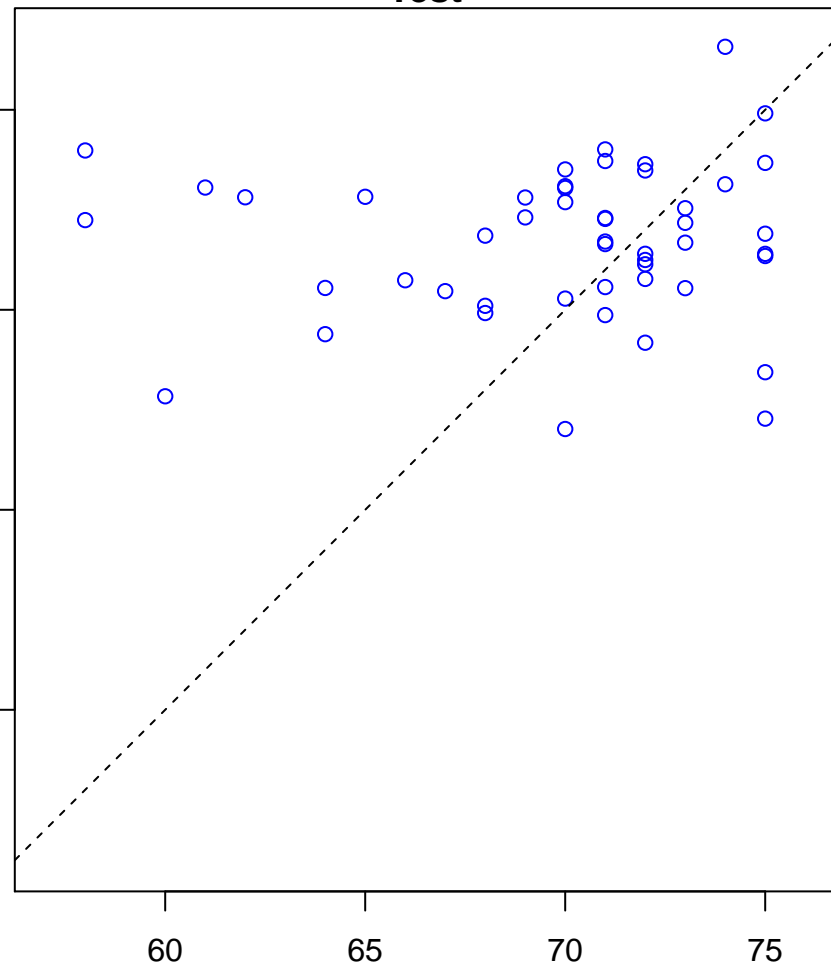
Actual Age

protein localization to cell periphery (Score: 1.081763)

Control

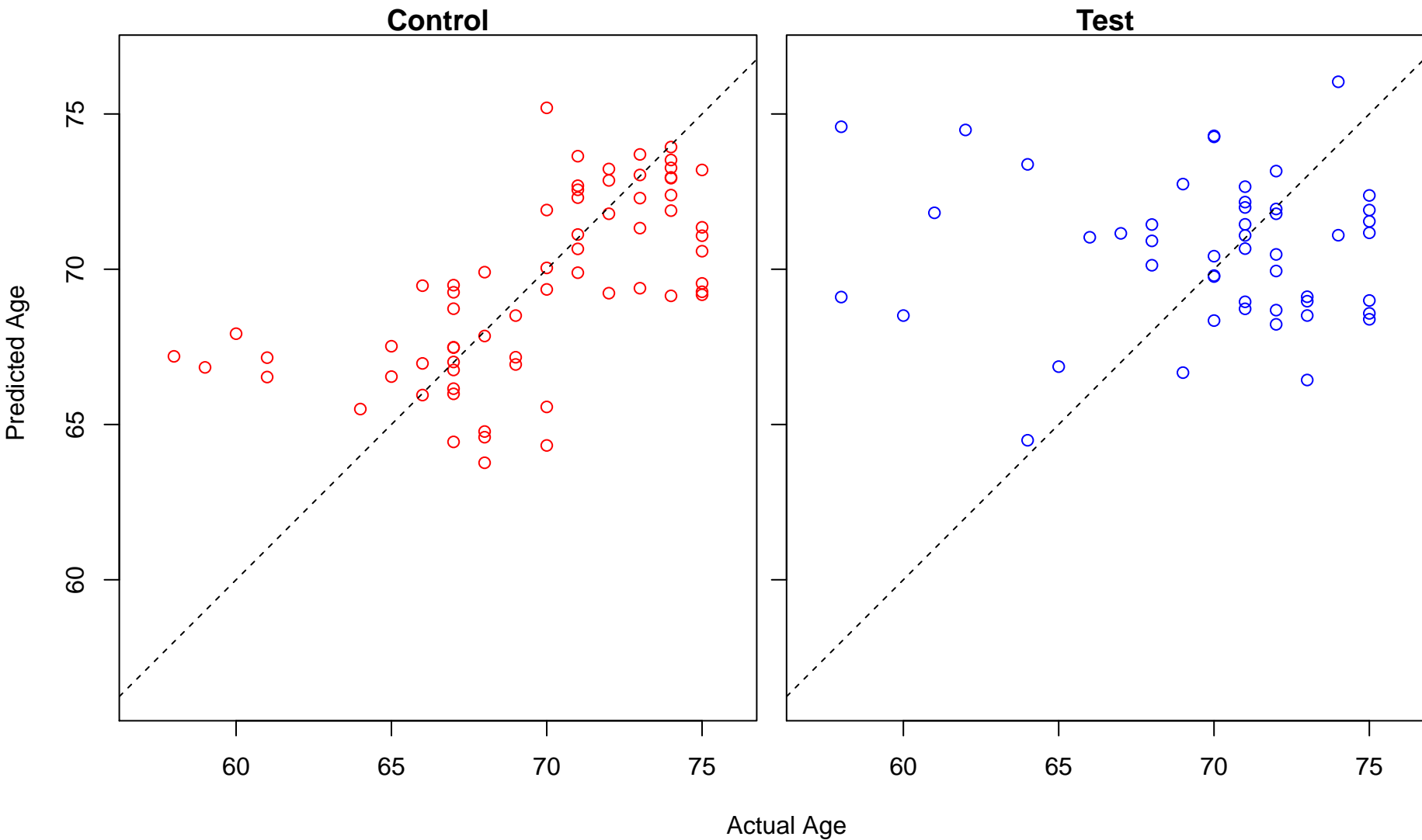


Test

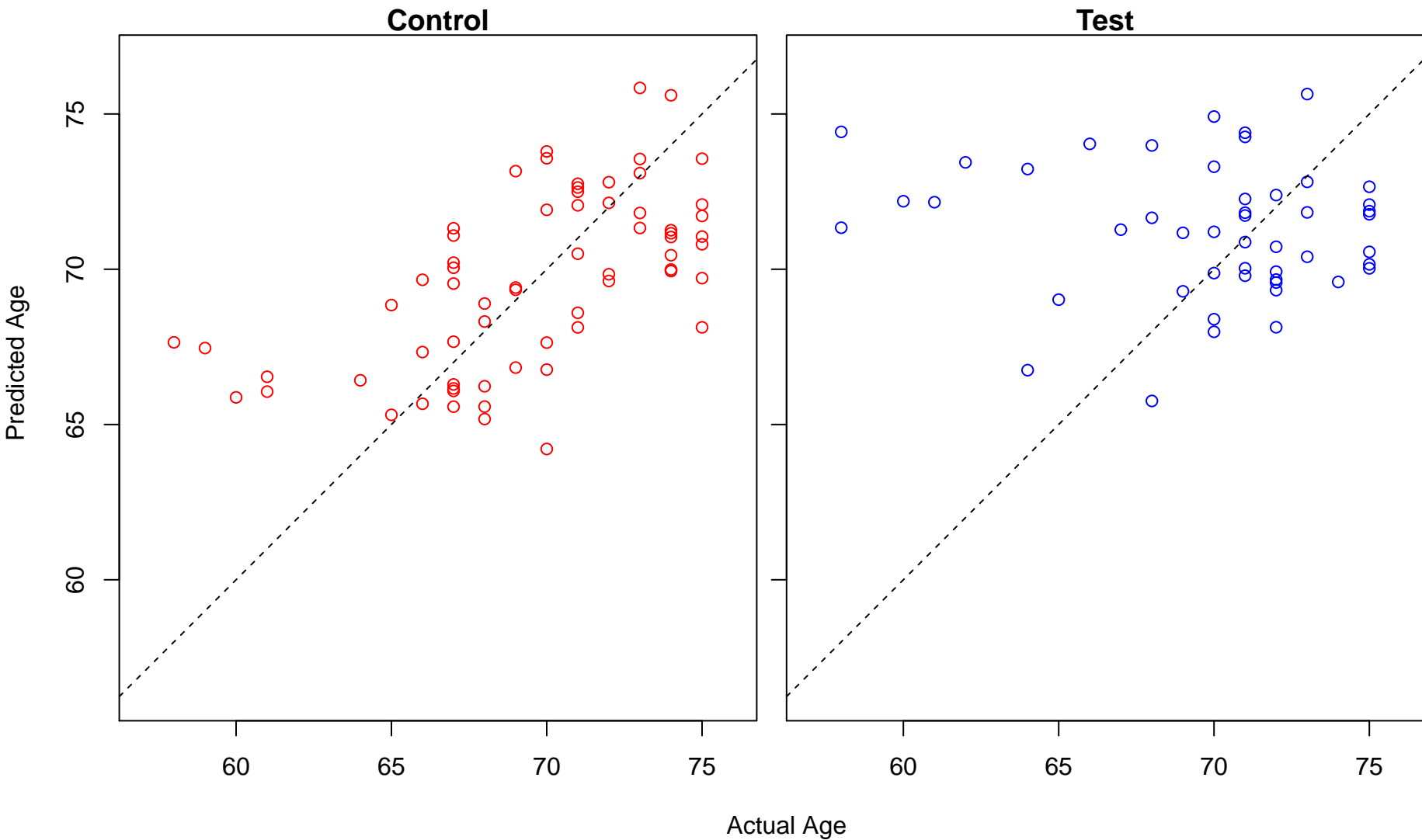


Actual Age

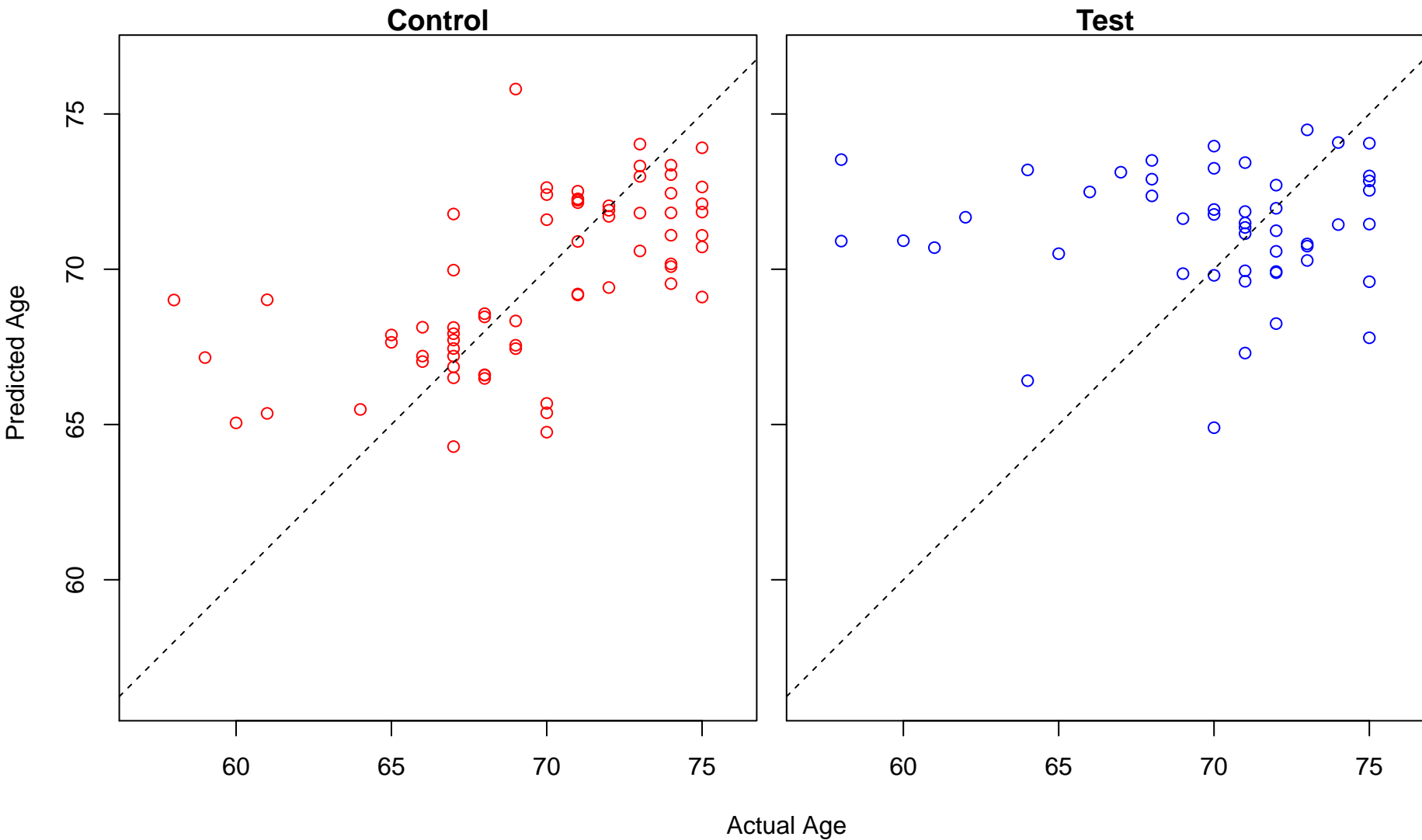
positive regulation of receptor-mediated endocytosis (Score: 1.081644)



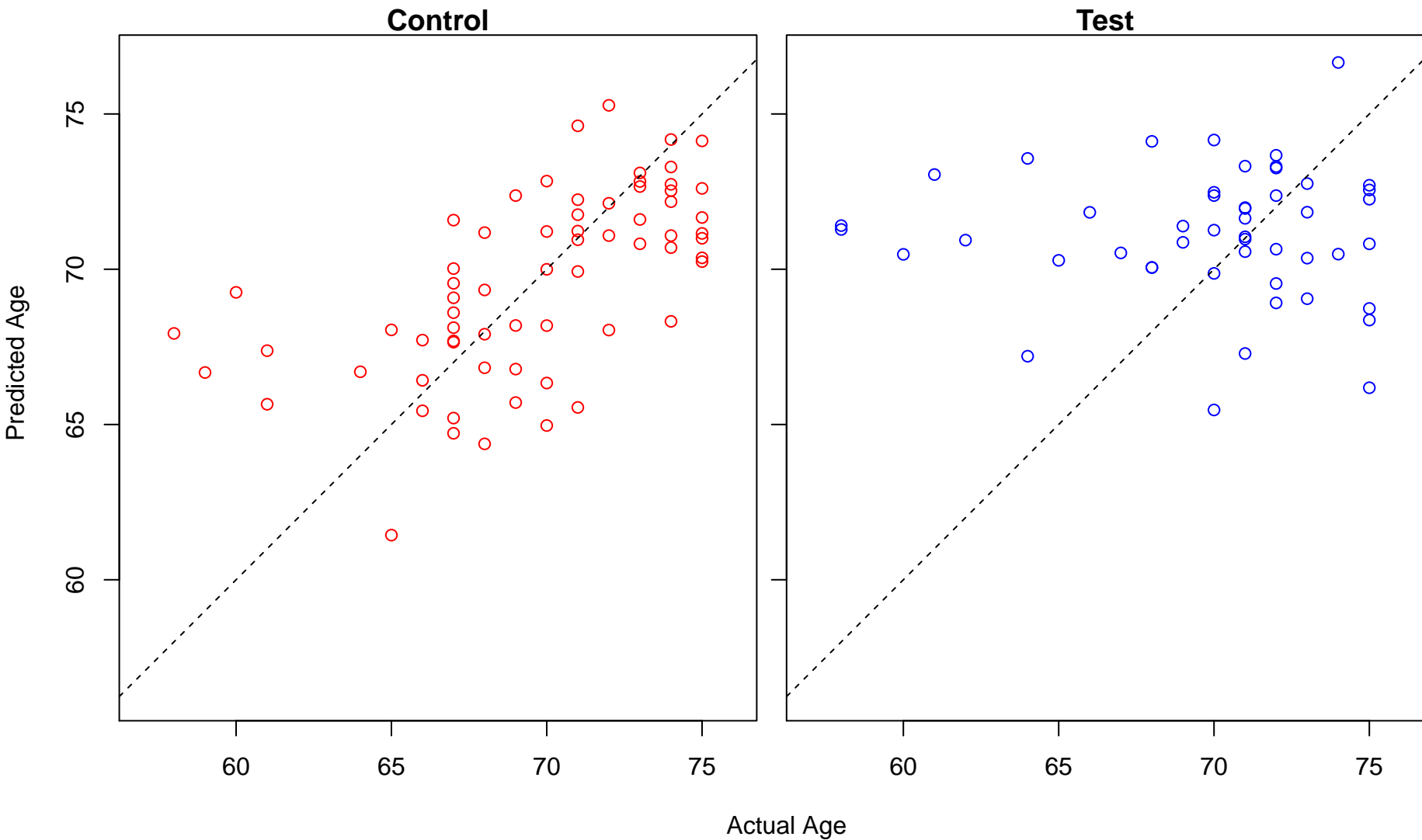
Golgi vesicle budding (Score: 1.081078)



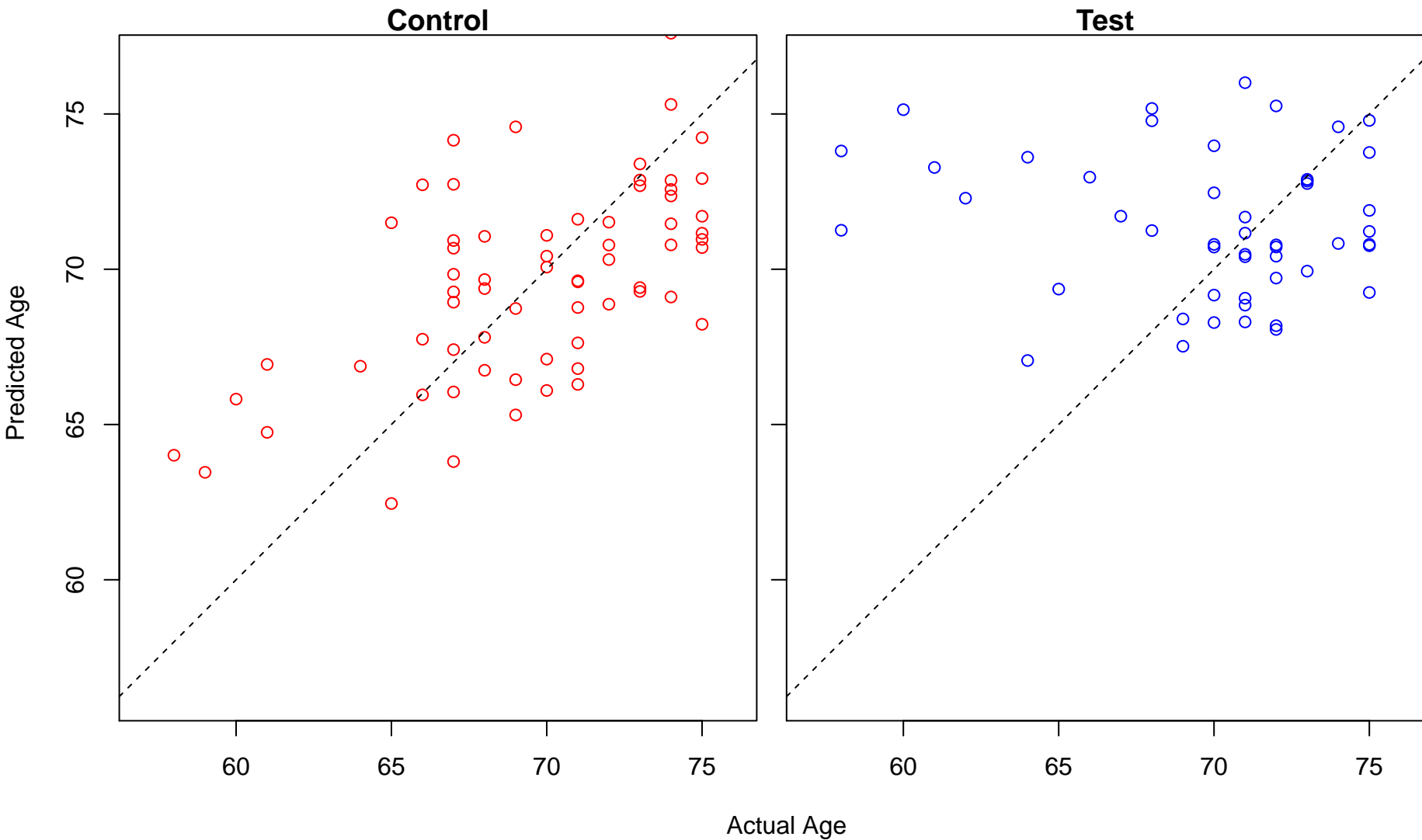
peptidyl-histidine modification (Score: 1.081024)



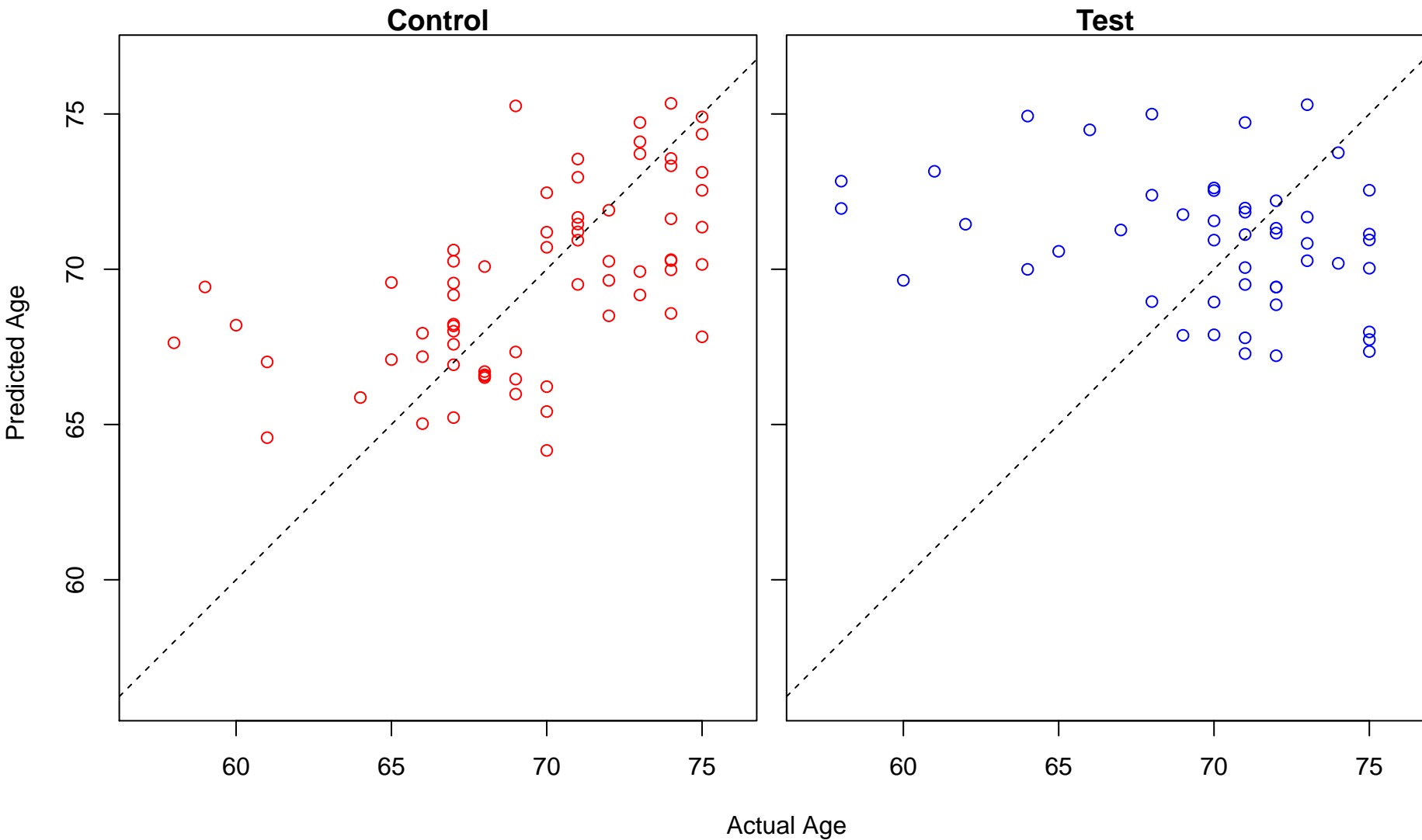
positive regulation of interleukin-1 beta production (Score: 1.080892)



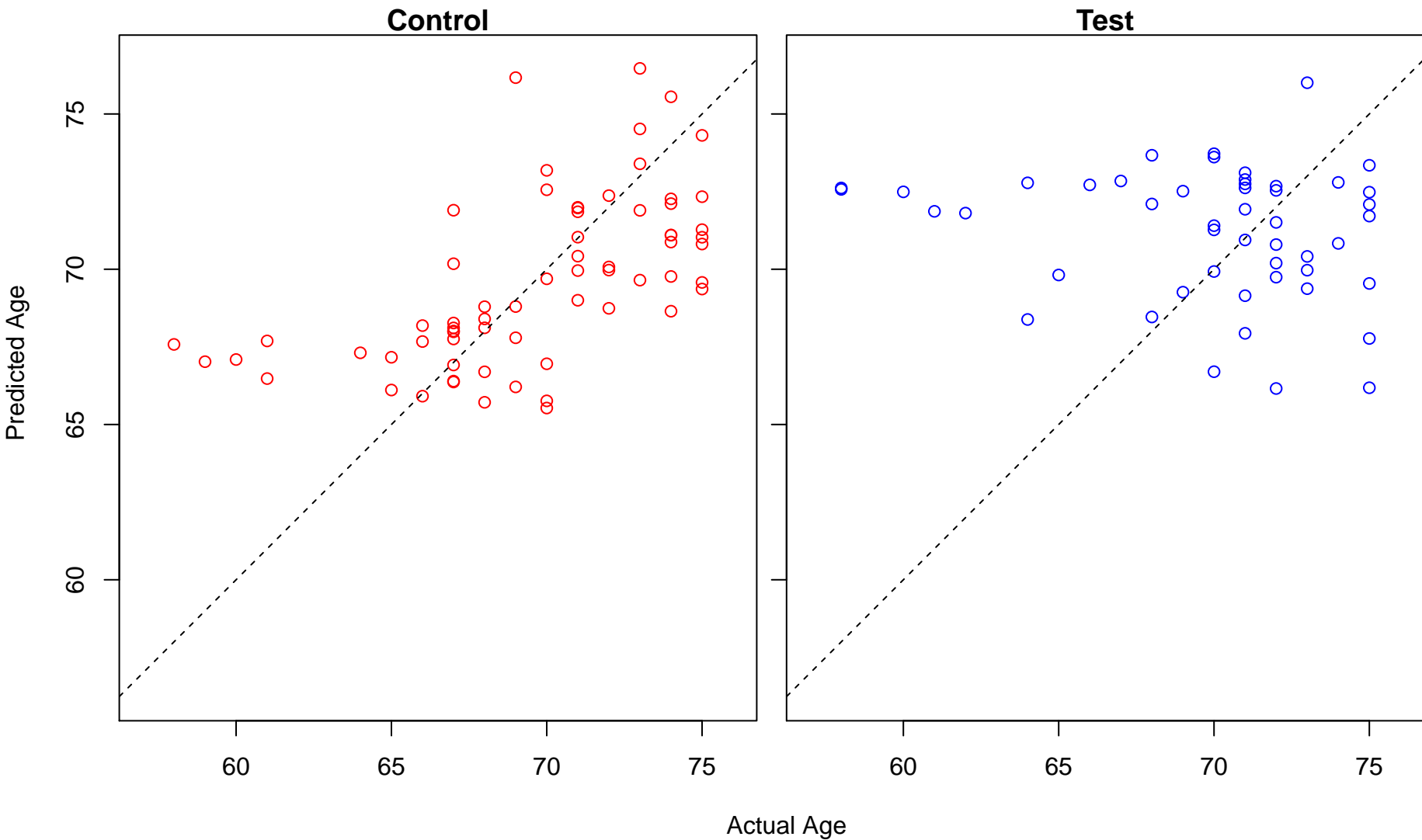
amyloid precursor protein catabolic process (Score: 1.080600)



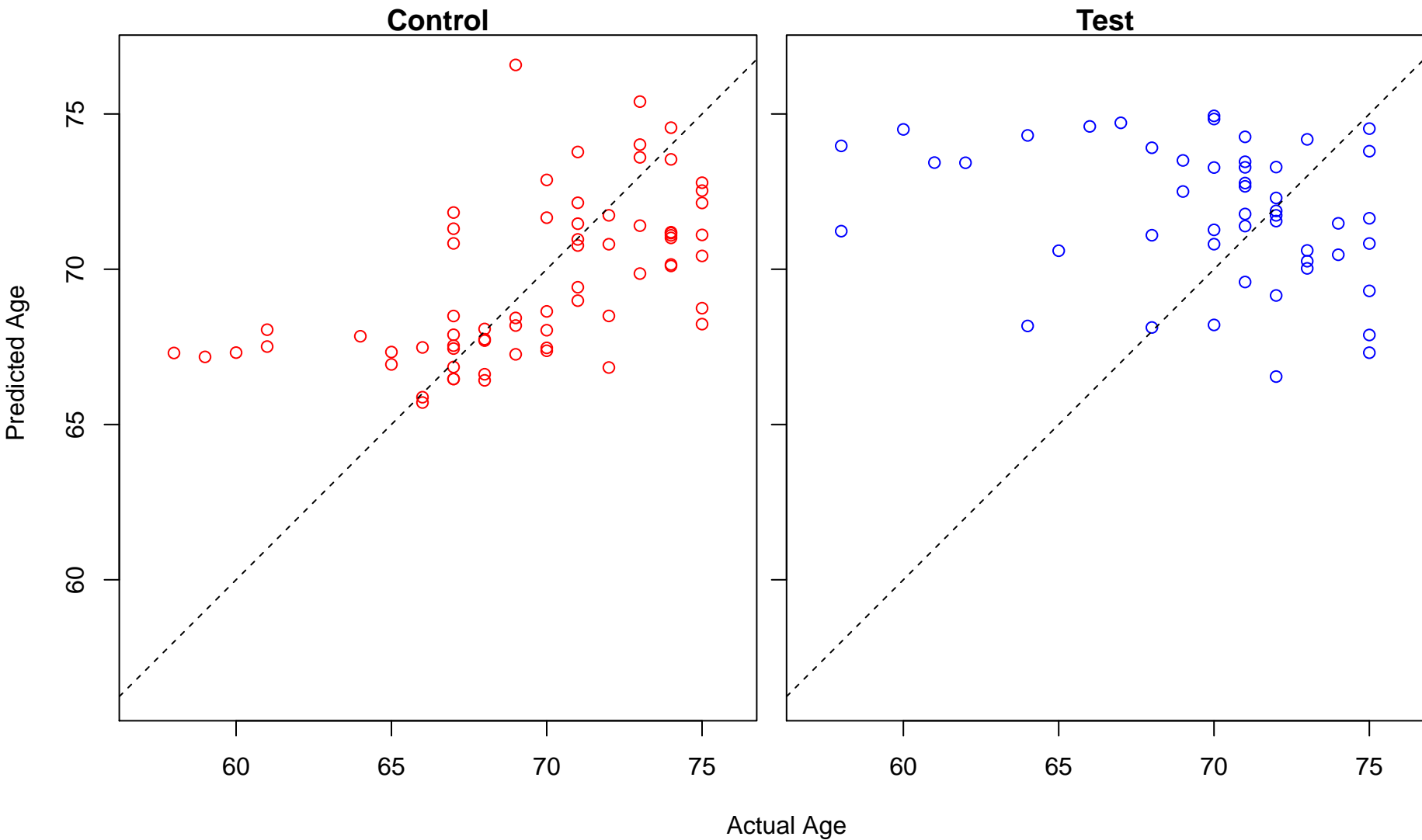
positive regulation of lamellipodium organization (Score: 1.079900)



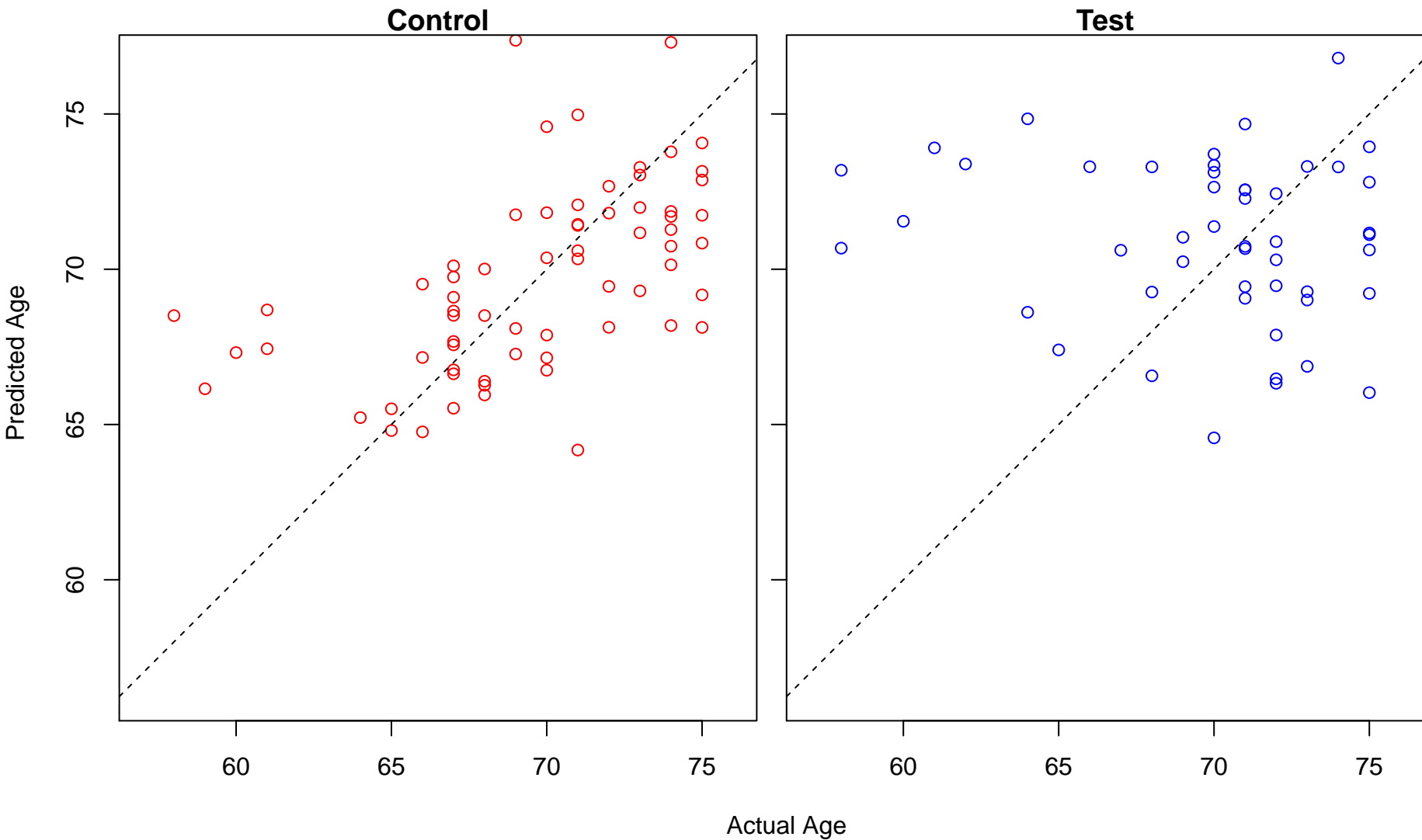
regulation of cell projection assembly (Score: 1.078518)



regulation of T-helper cell differentiation (Score: 1.078509)

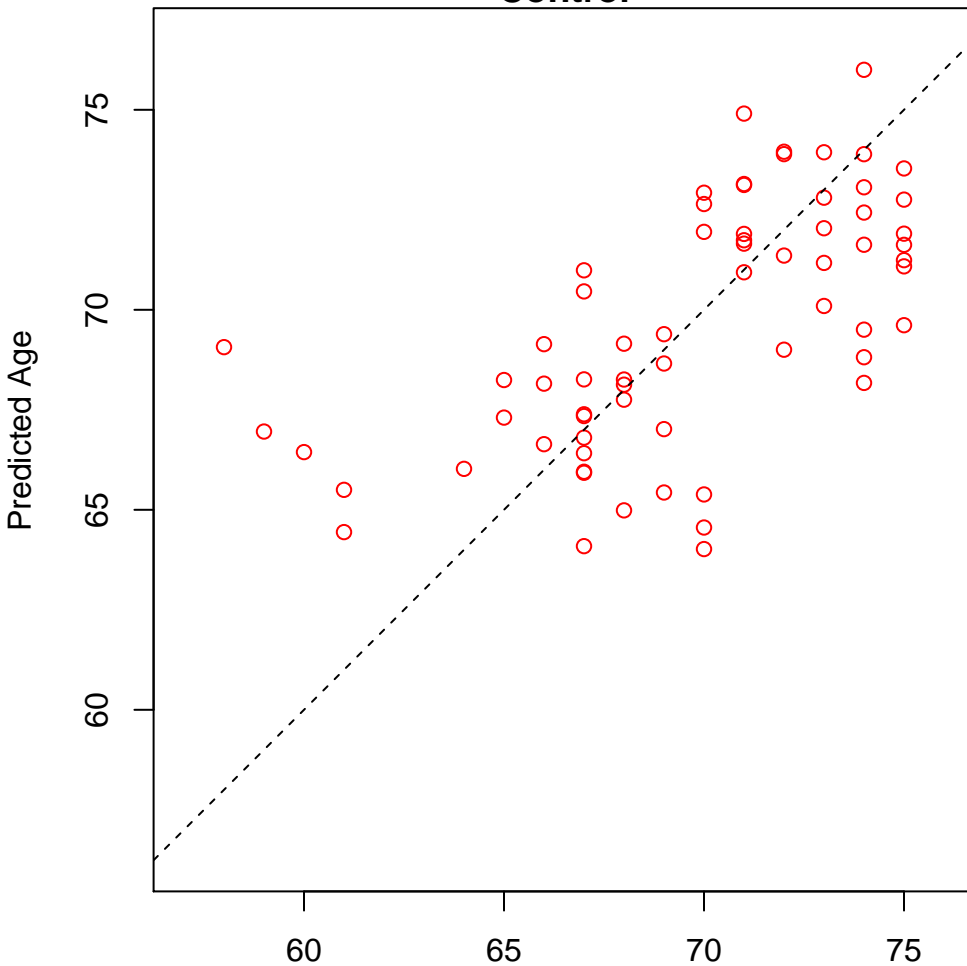


regulation of receptor binding (Score: 1.078504)

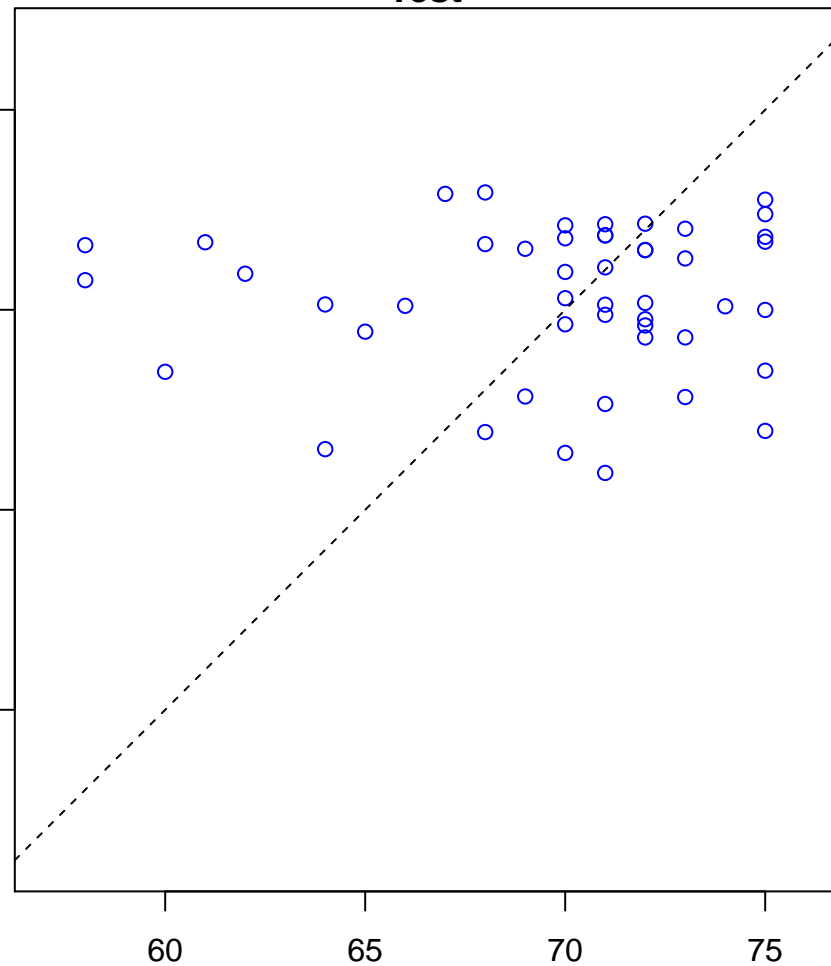


regulation of translational initiation (Score: 1.078234)

Control

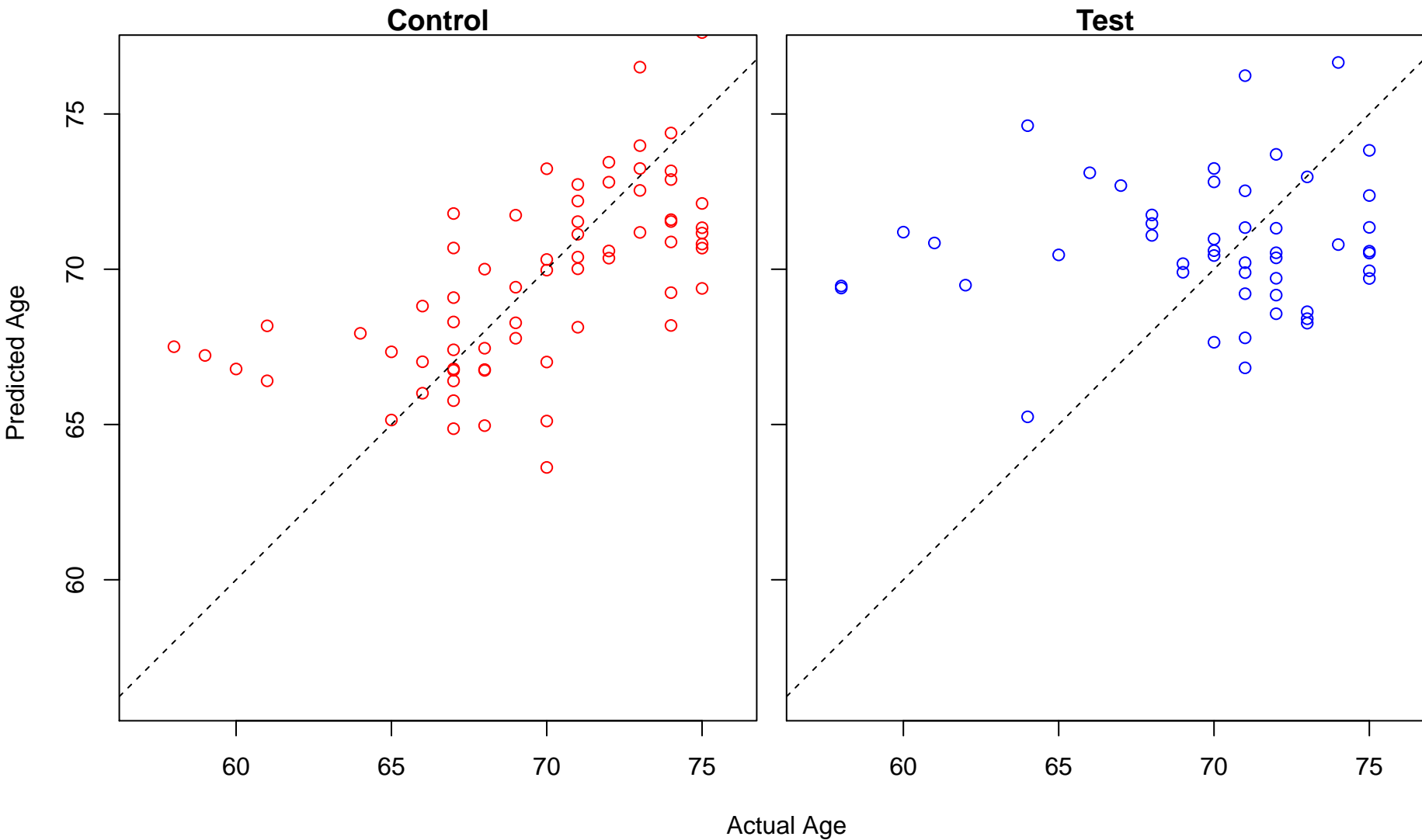


Test

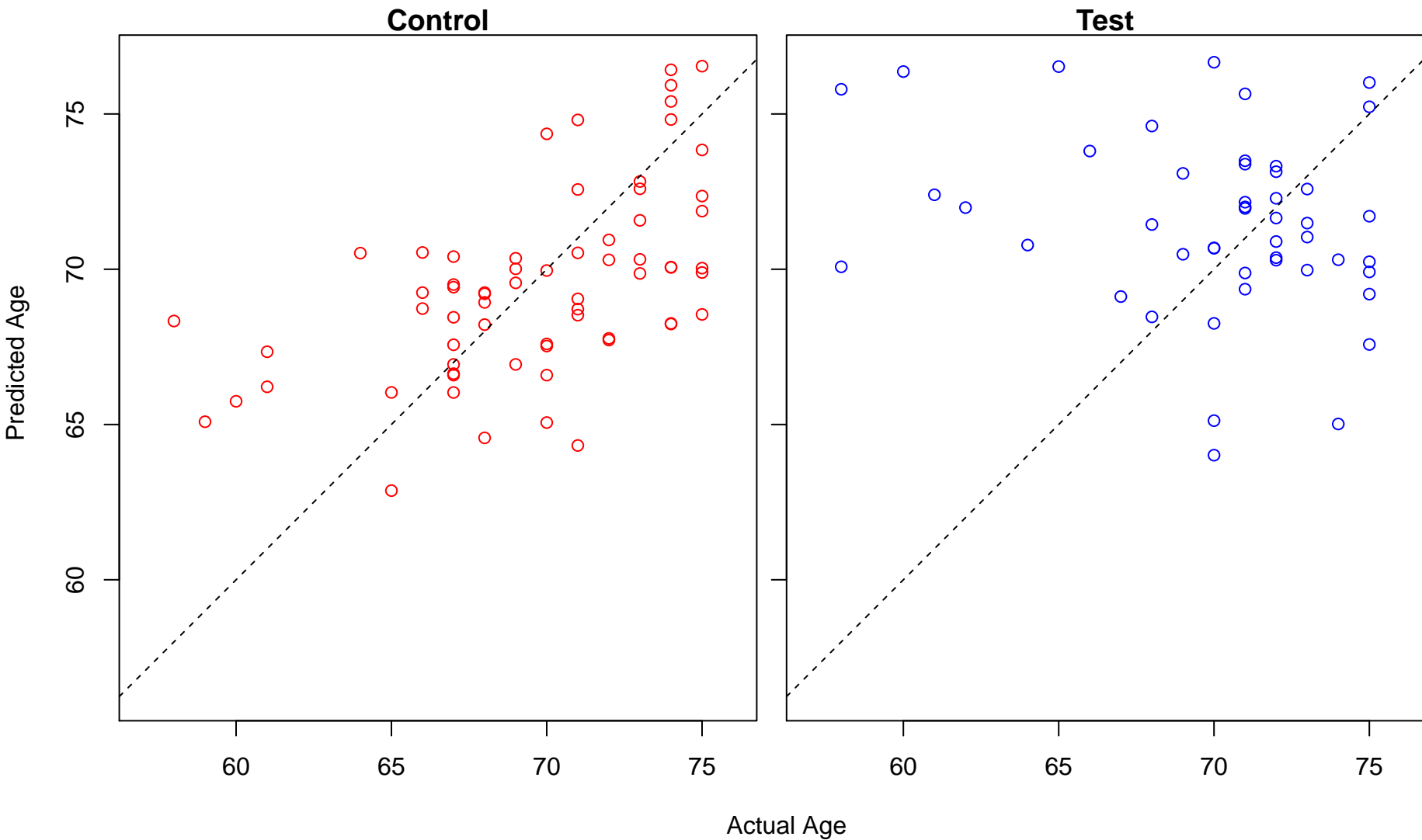


Actual Age

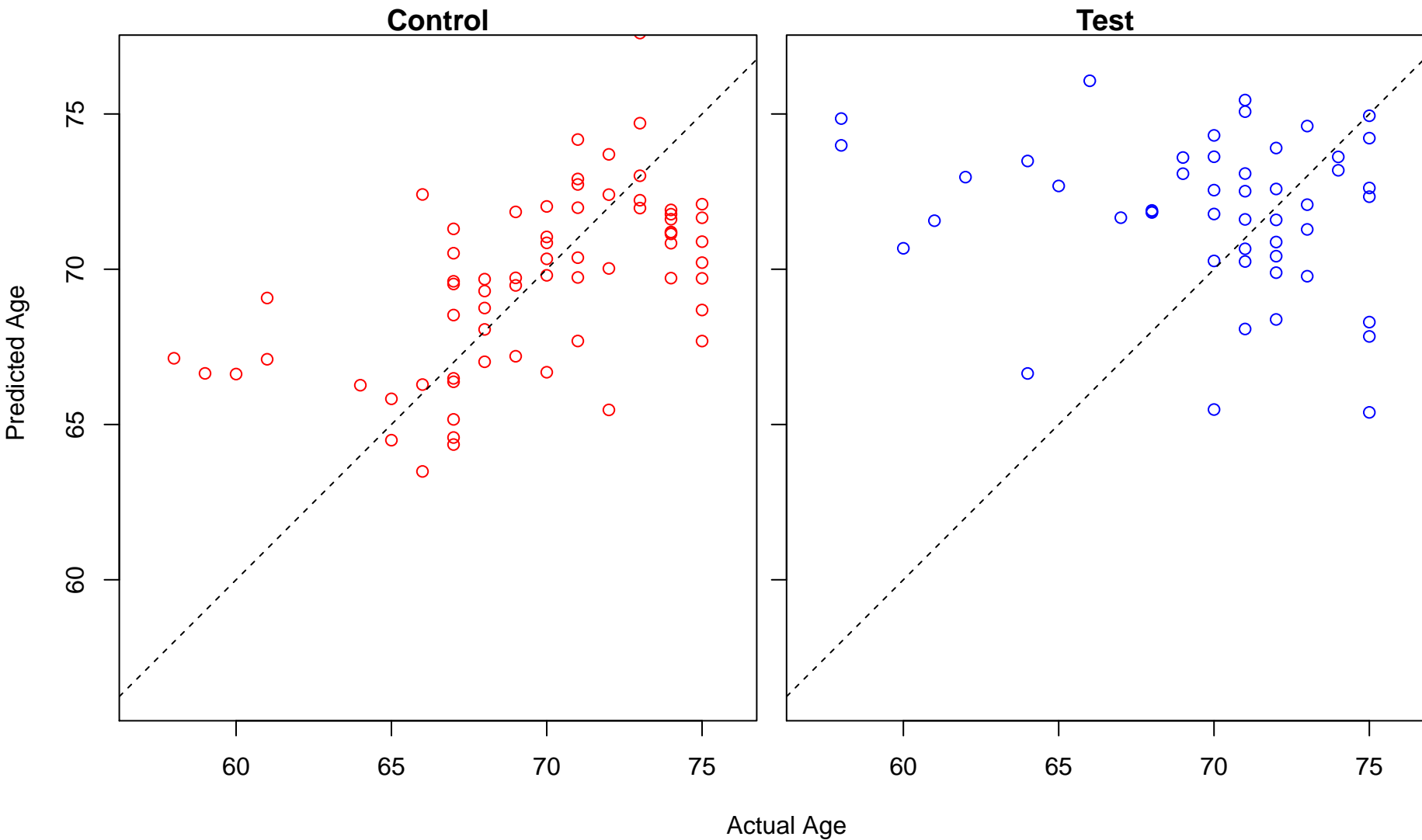
locomotor rhythm (Score: 1.077293)



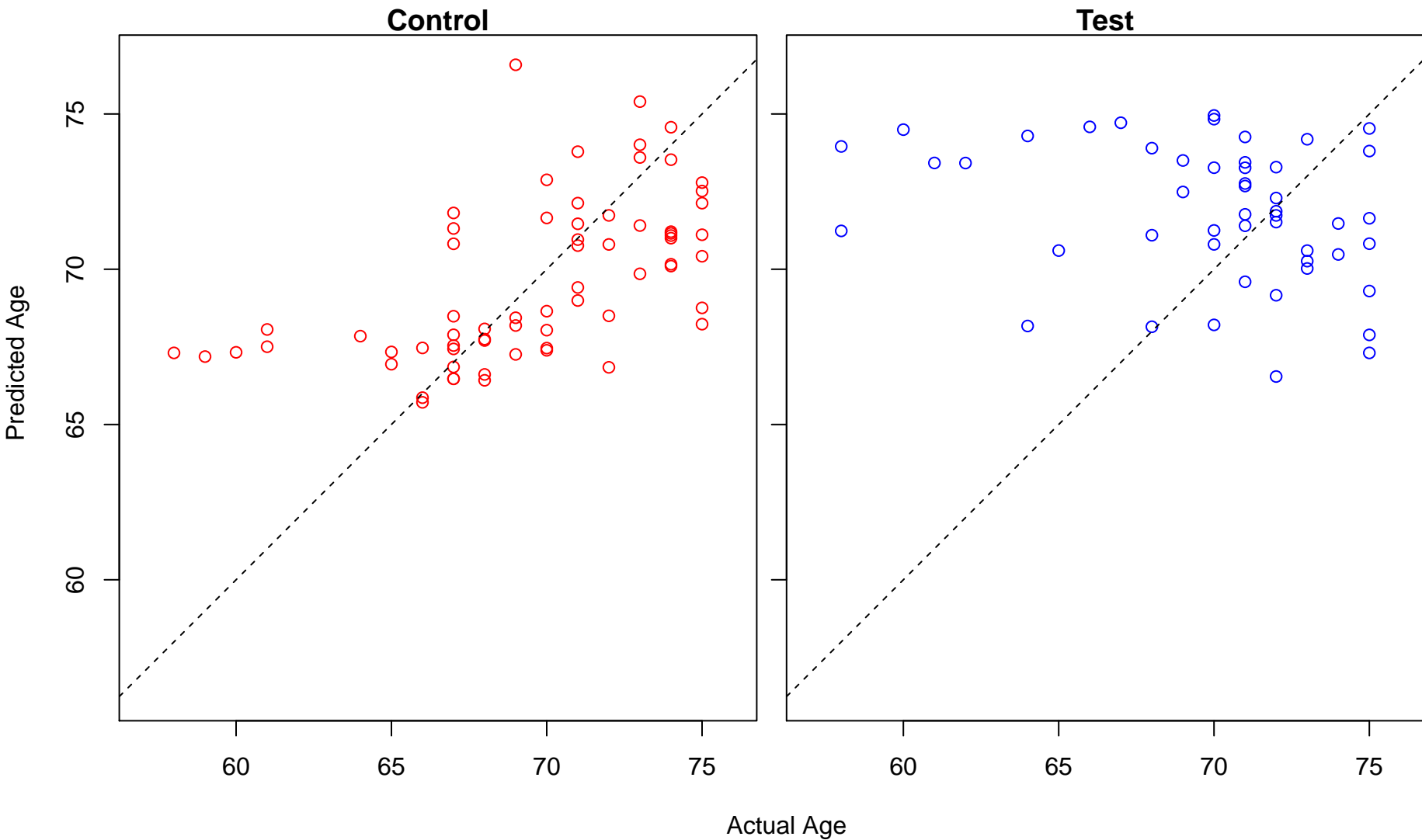
cellular response to retinoic acid (Score: 1.077214)



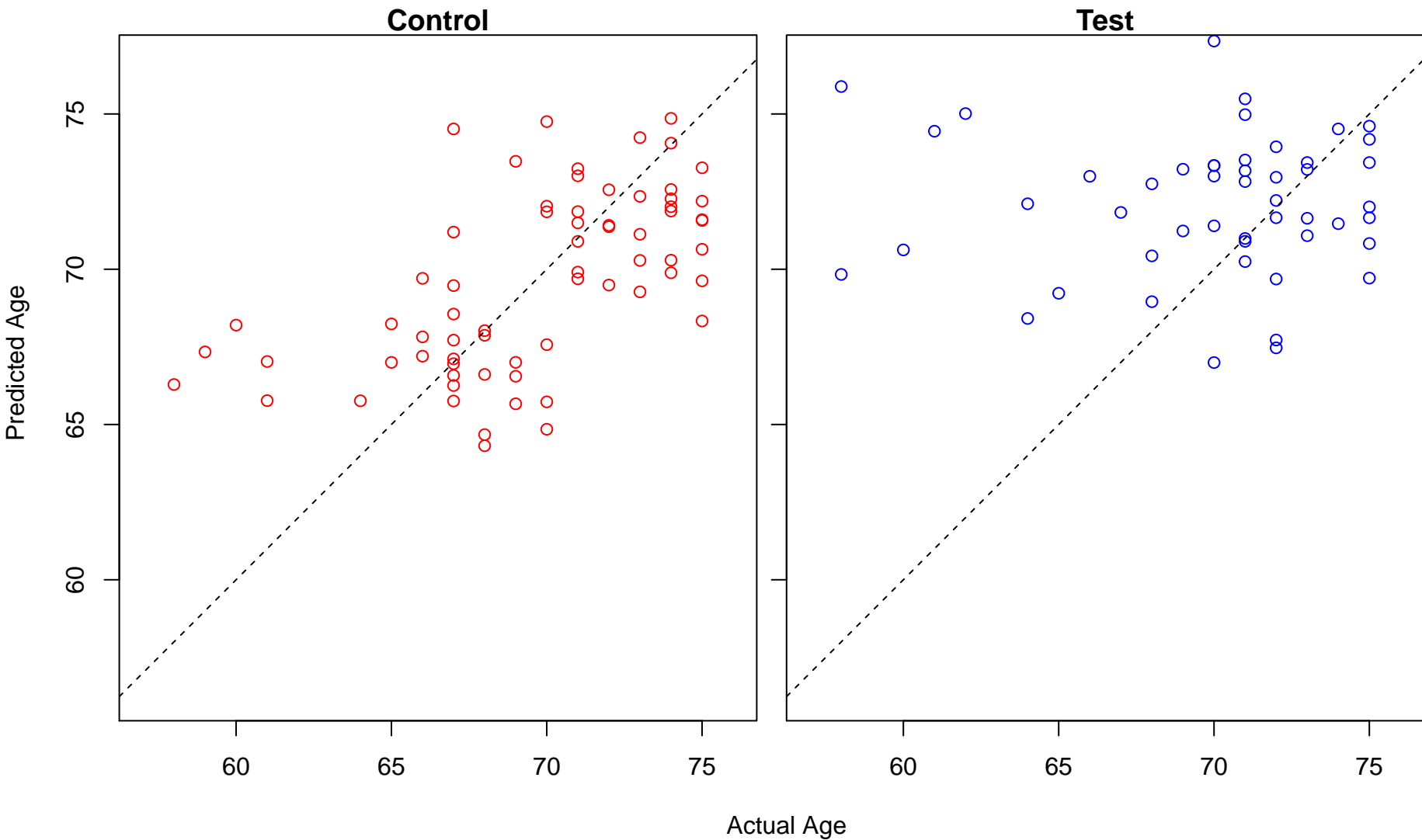
protein O-linked fucosylation (Score: 1.077091)



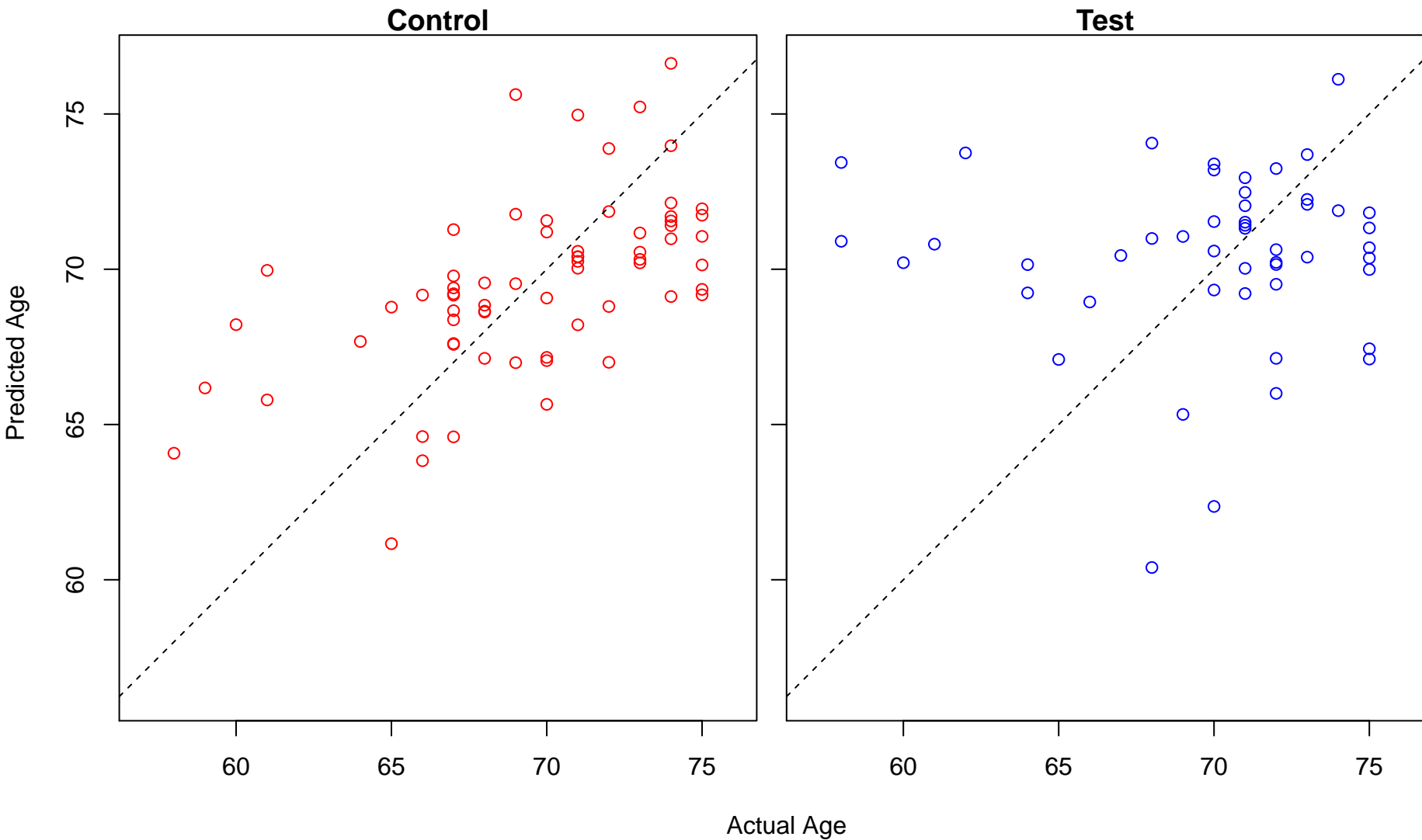
positive regulation of T-helper cell differentiation (Score: 1.076984)



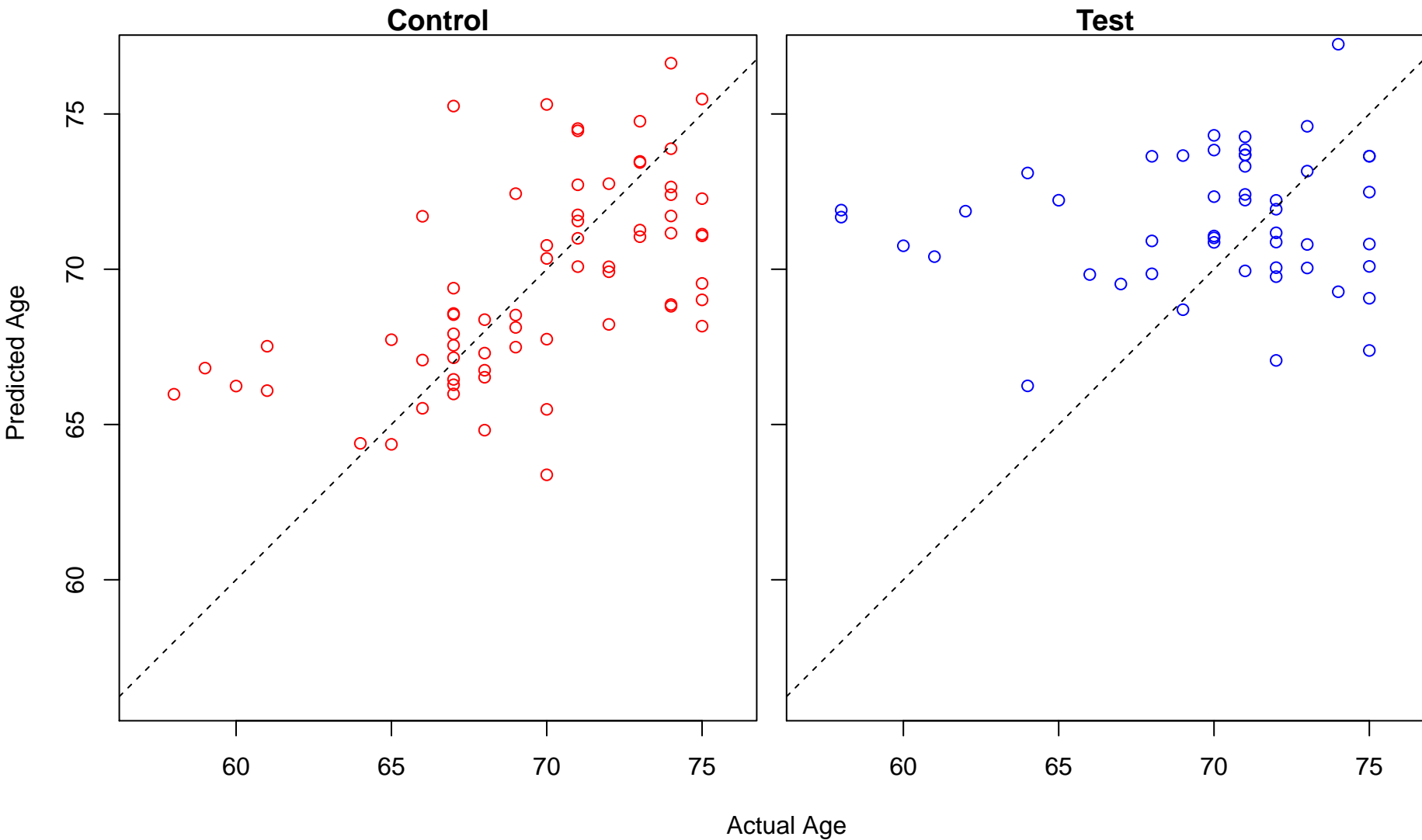
regulation of muscle system process (Score: 1.076727)



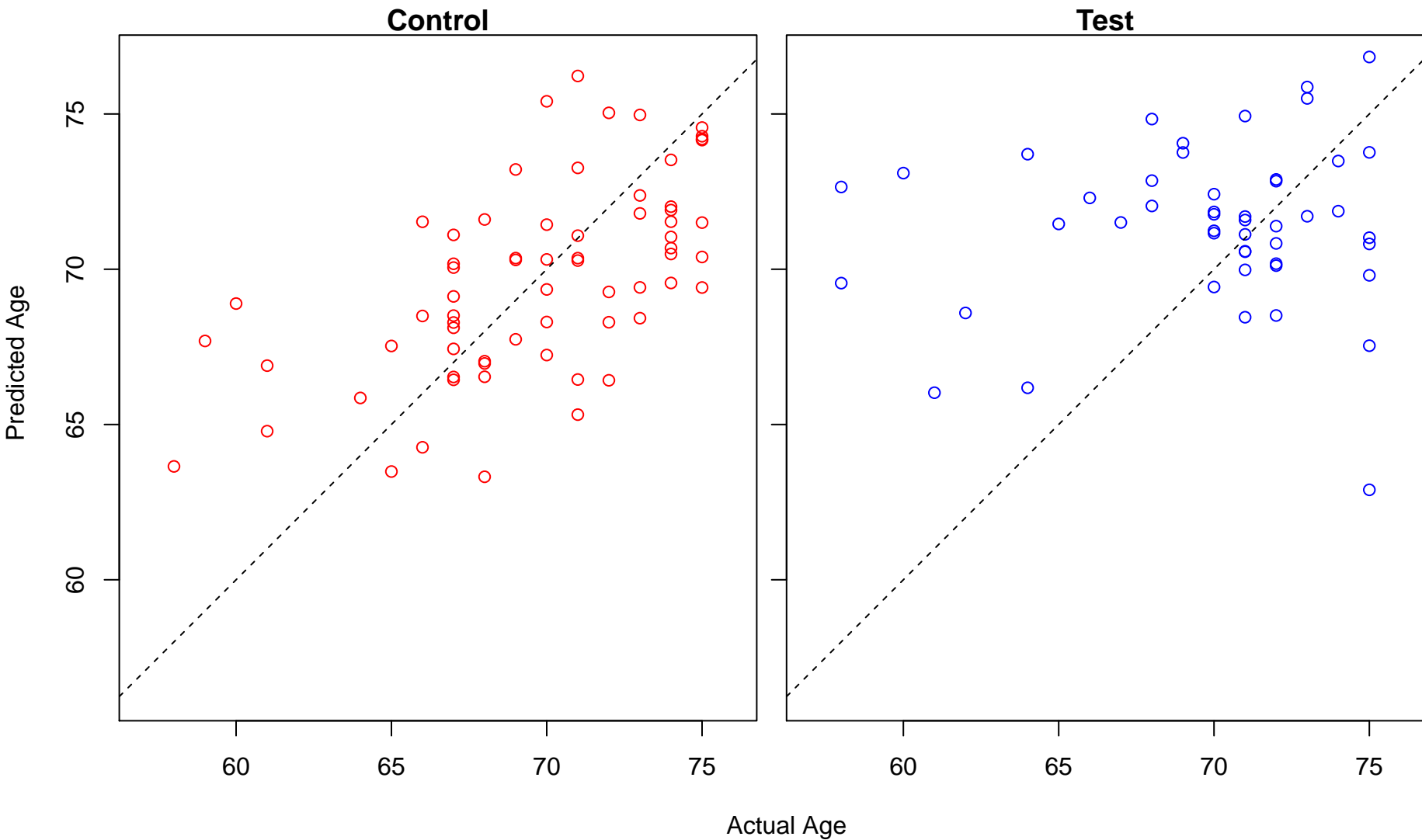
regulation of tyrosine phosphorylation of Stat5 protein (Score: 1.075594)



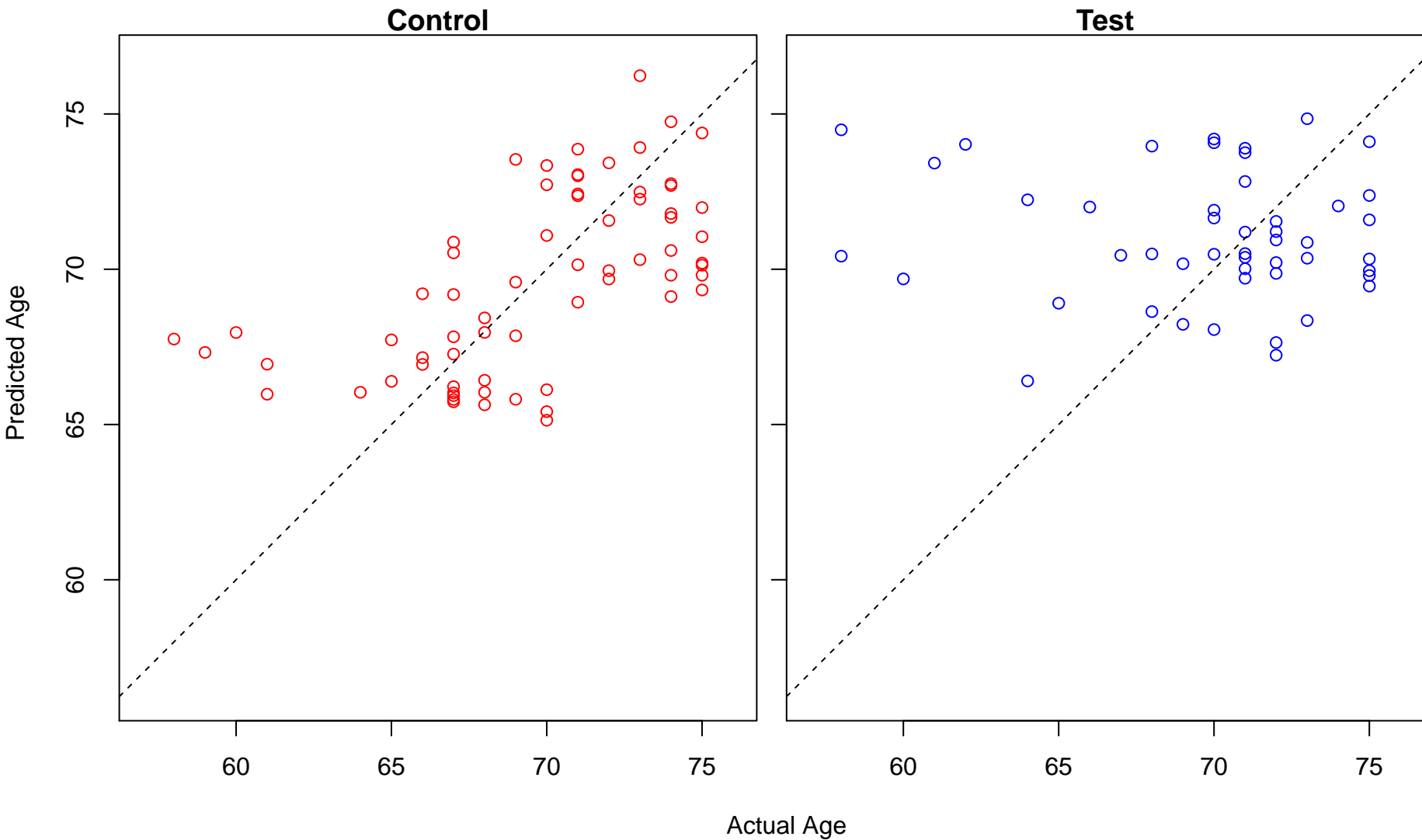
membrane protein proteolysis (Score: 1.075555)



interleukin-1 secretion (Score: 1.075409)

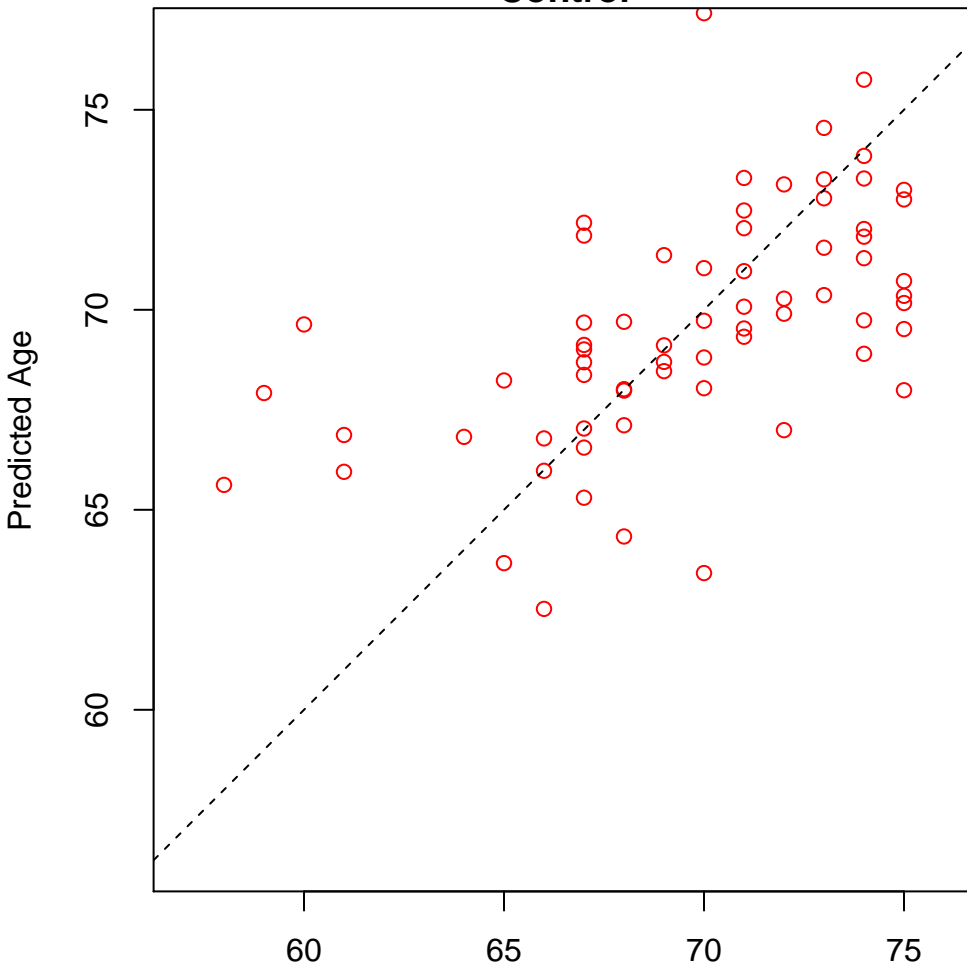


cofactor metabolic process (Score: 1.075078)

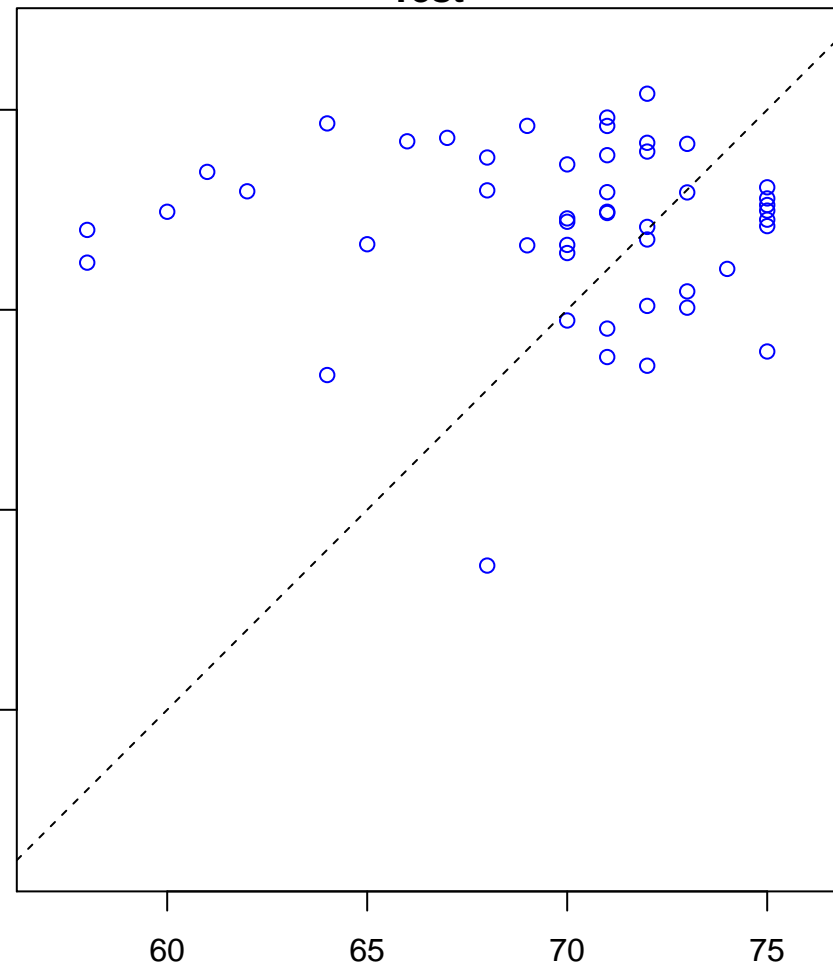


deoxyribonucleotide metabolic process (Score: 1.074980)

Control

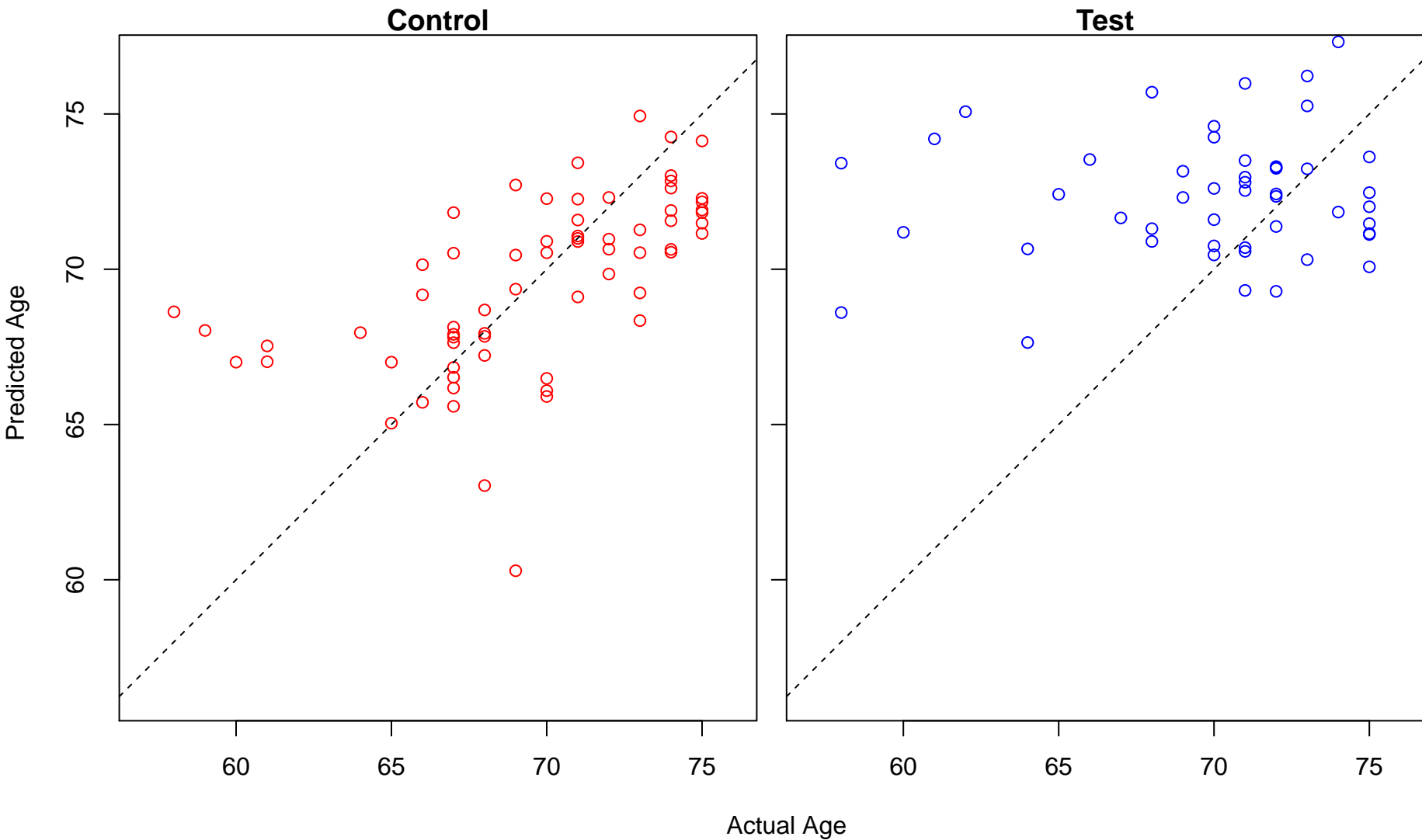


Test

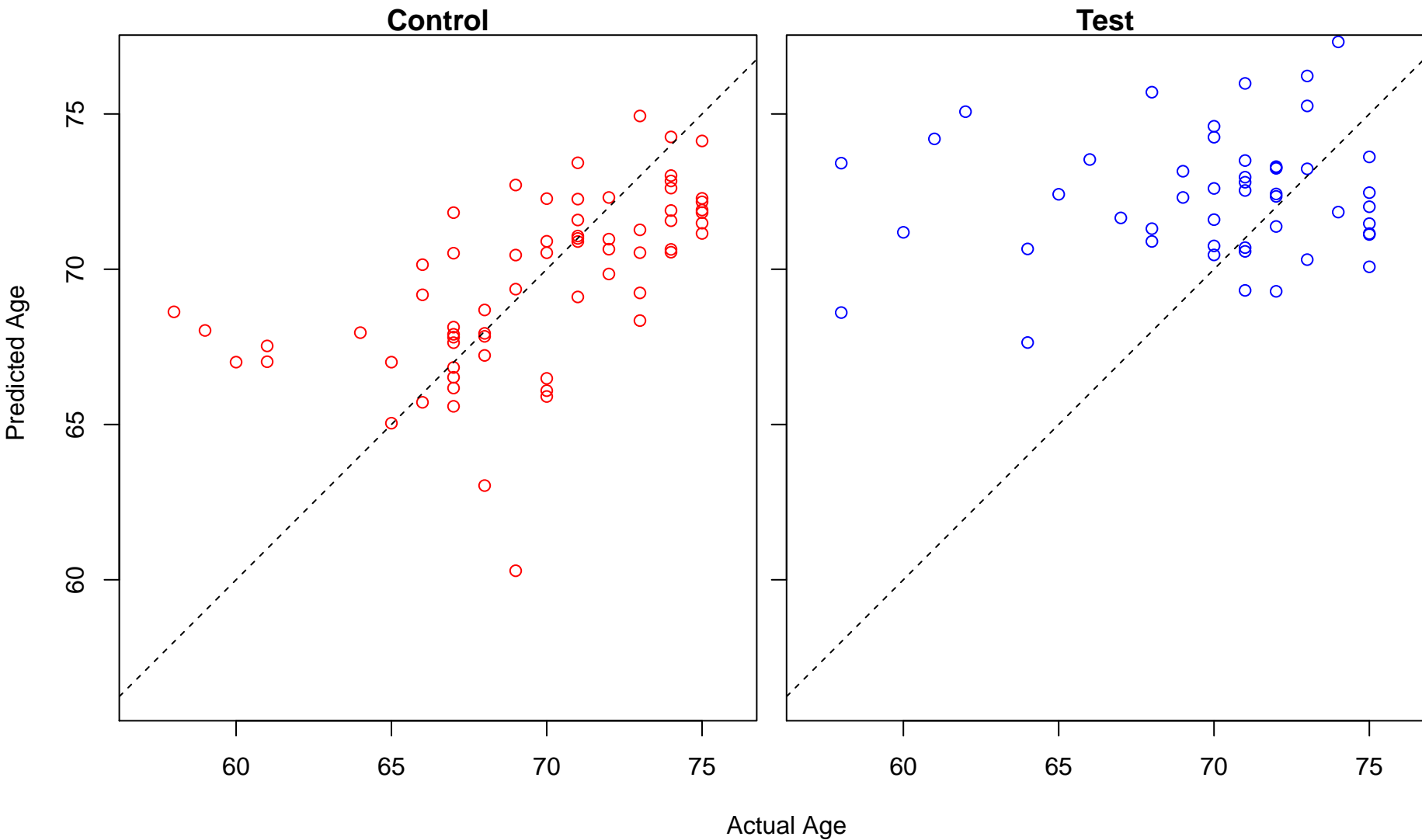


Actual Age

regulation of tube size (Score: 1.074105)

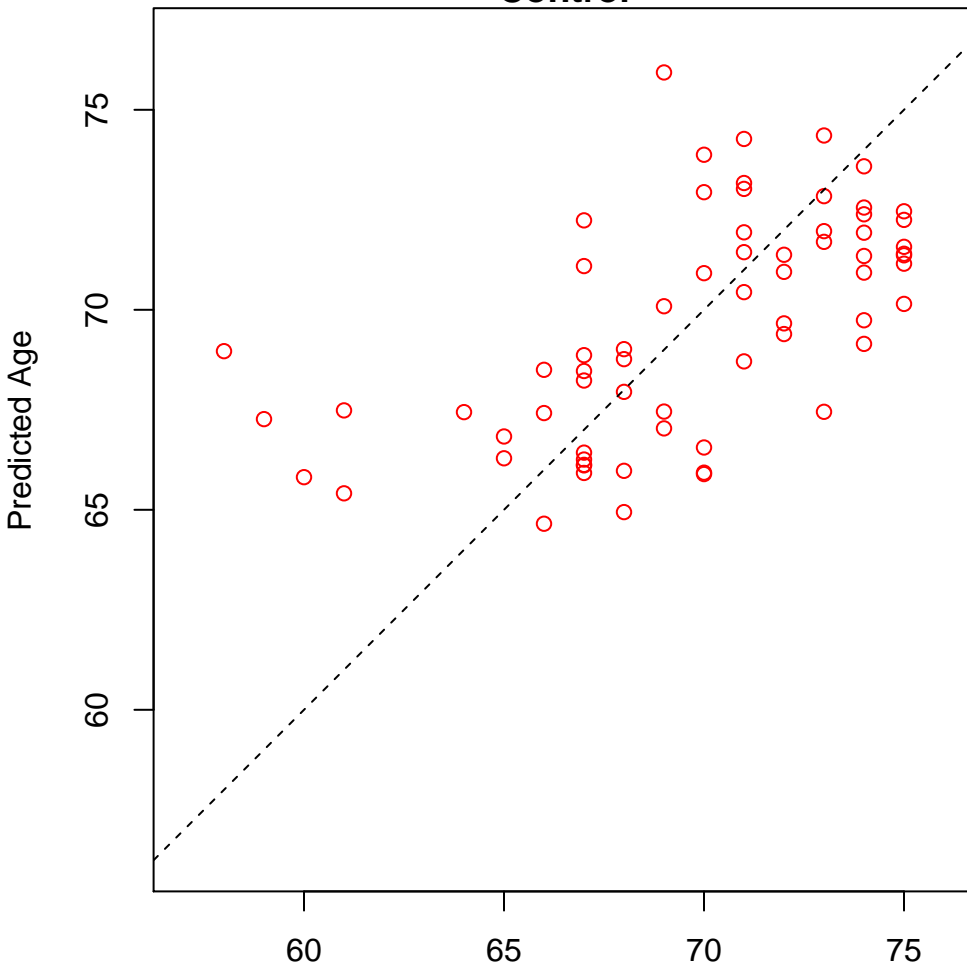


regulation of blood vessel size (Score: 1.074105)

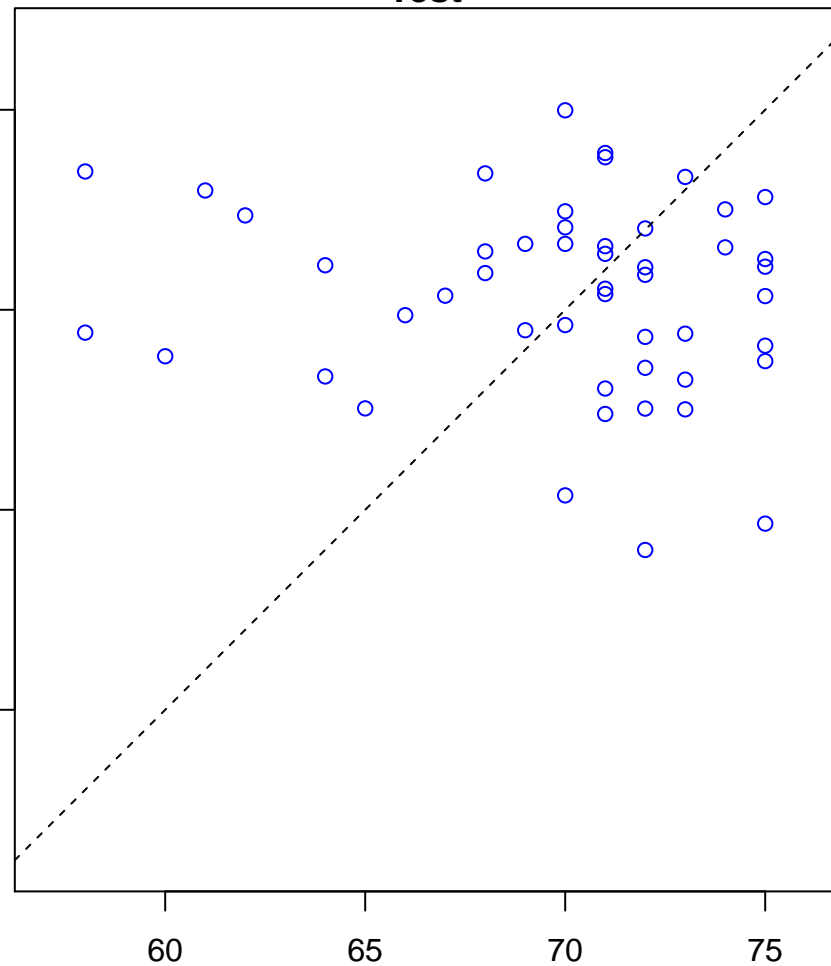


signal transduction in absence of ligand (Score: 1.074000)

Control

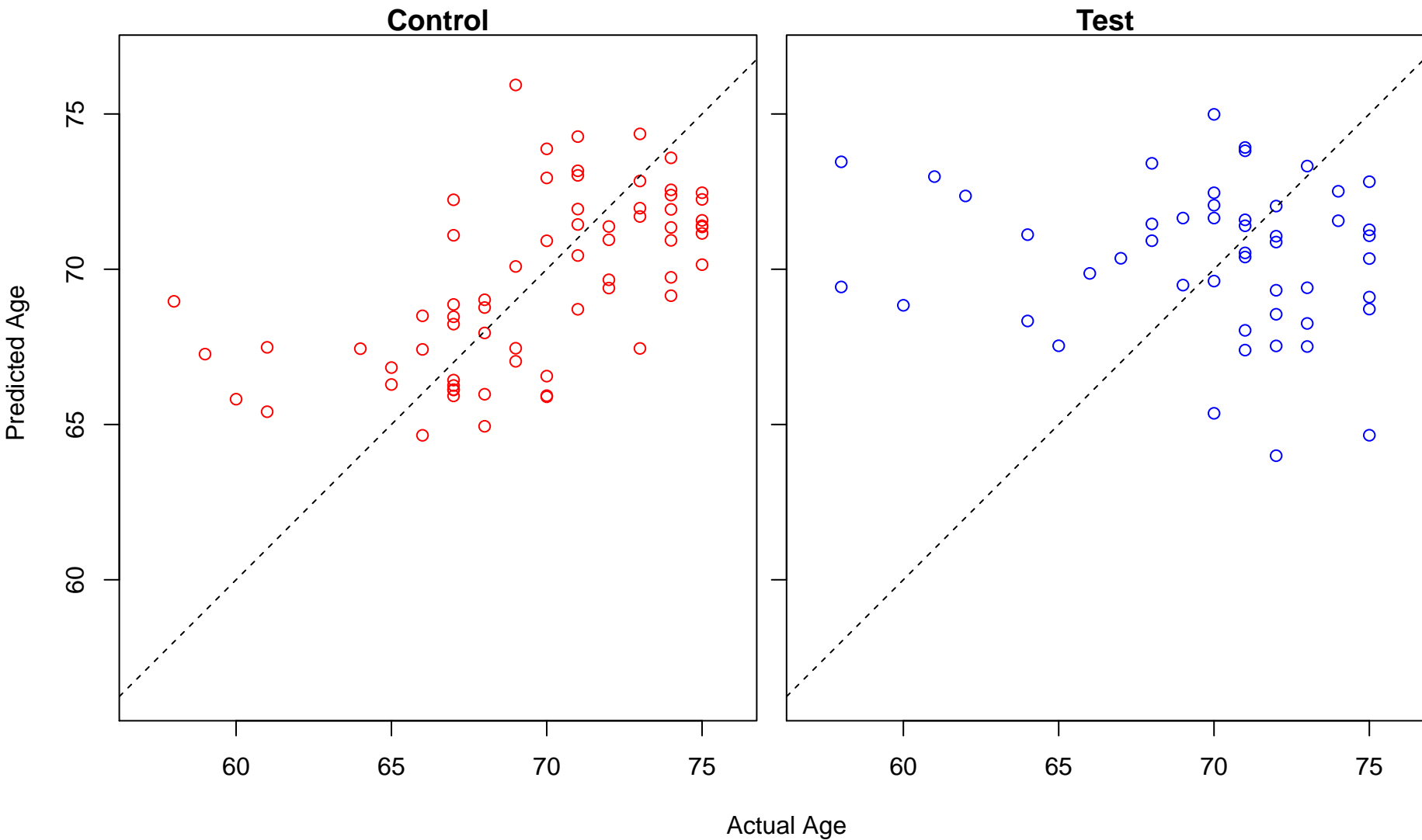


Test

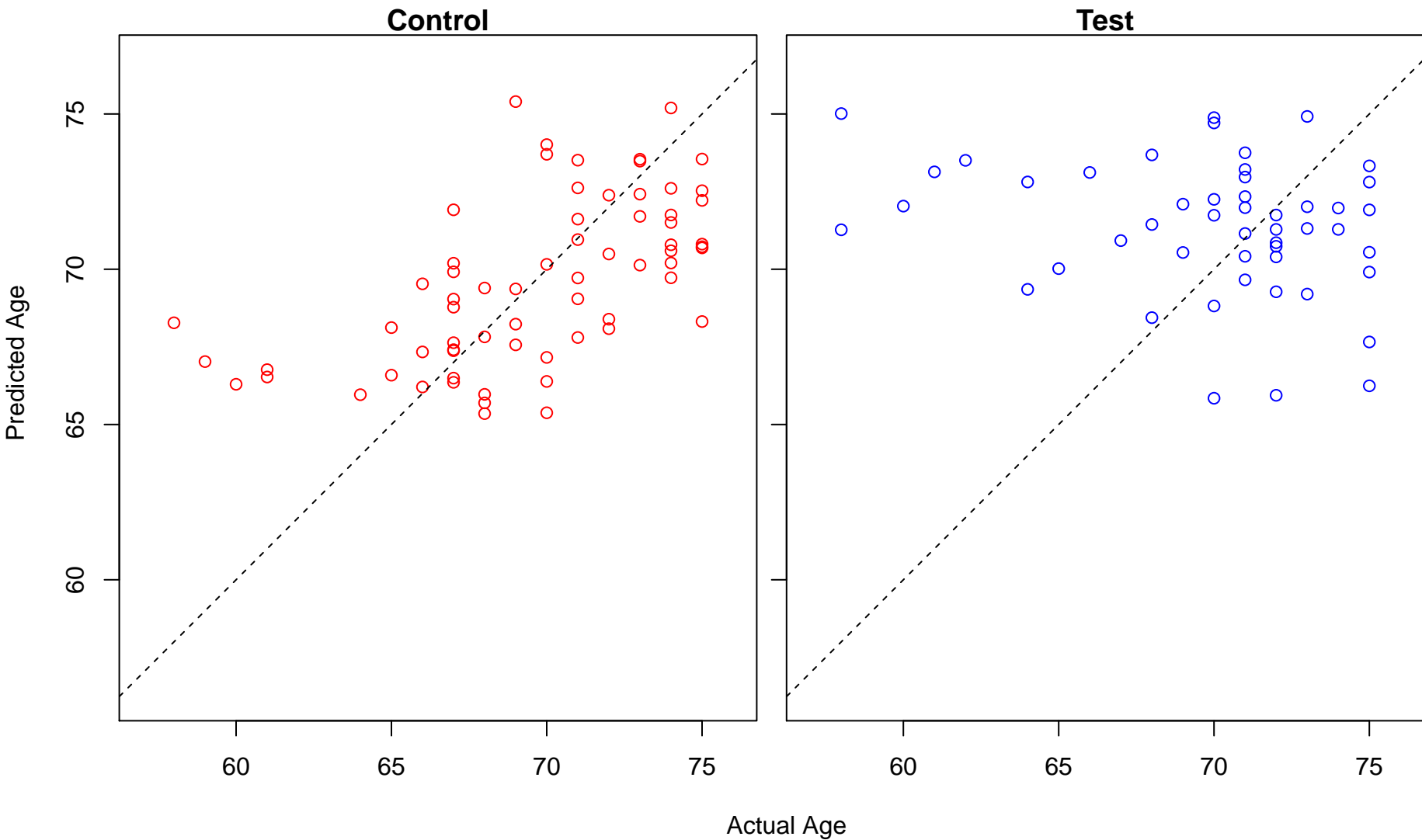


Actual Age

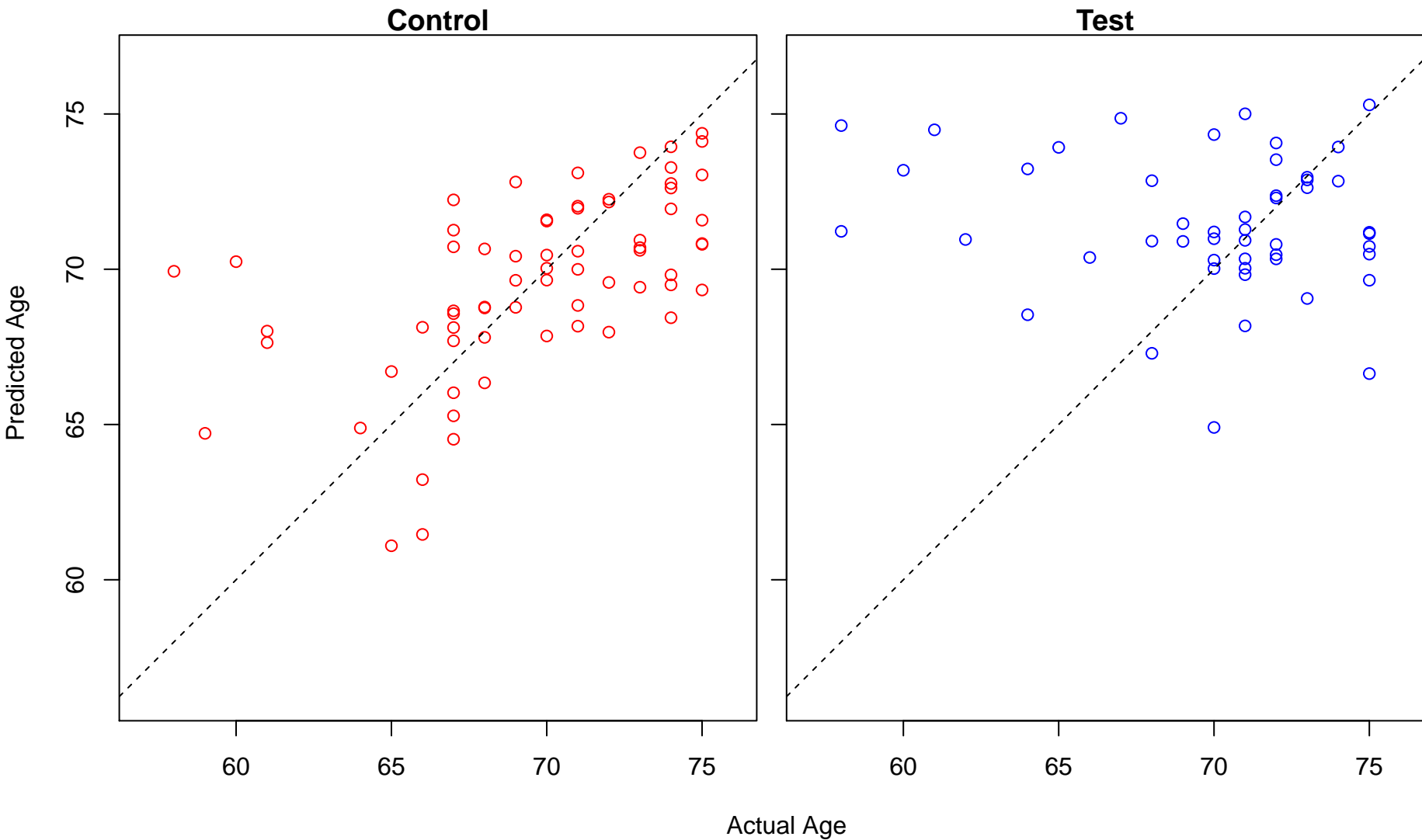
extrinsic apoptotic signaling pathway in absence of ligand (Score: 1.074000)



single-organism membrane budding (Score: 1.073868)

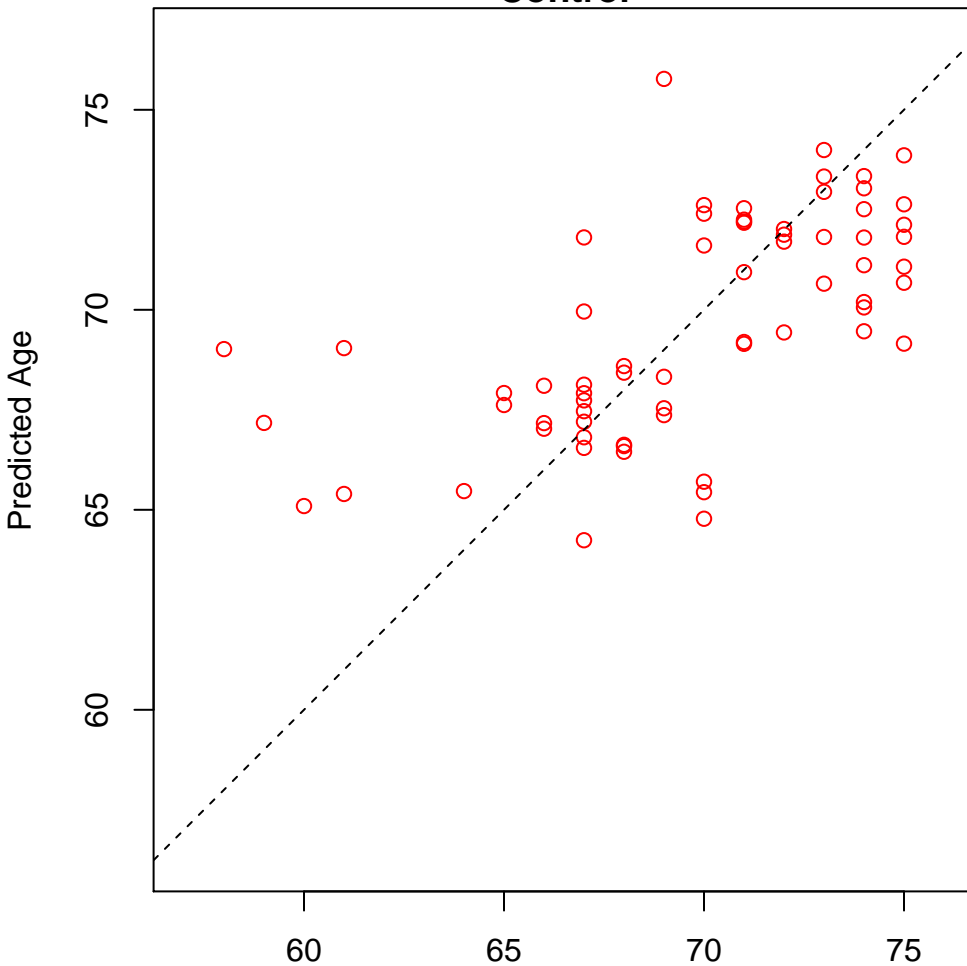


muscle cell migration (Score: 1.073791)

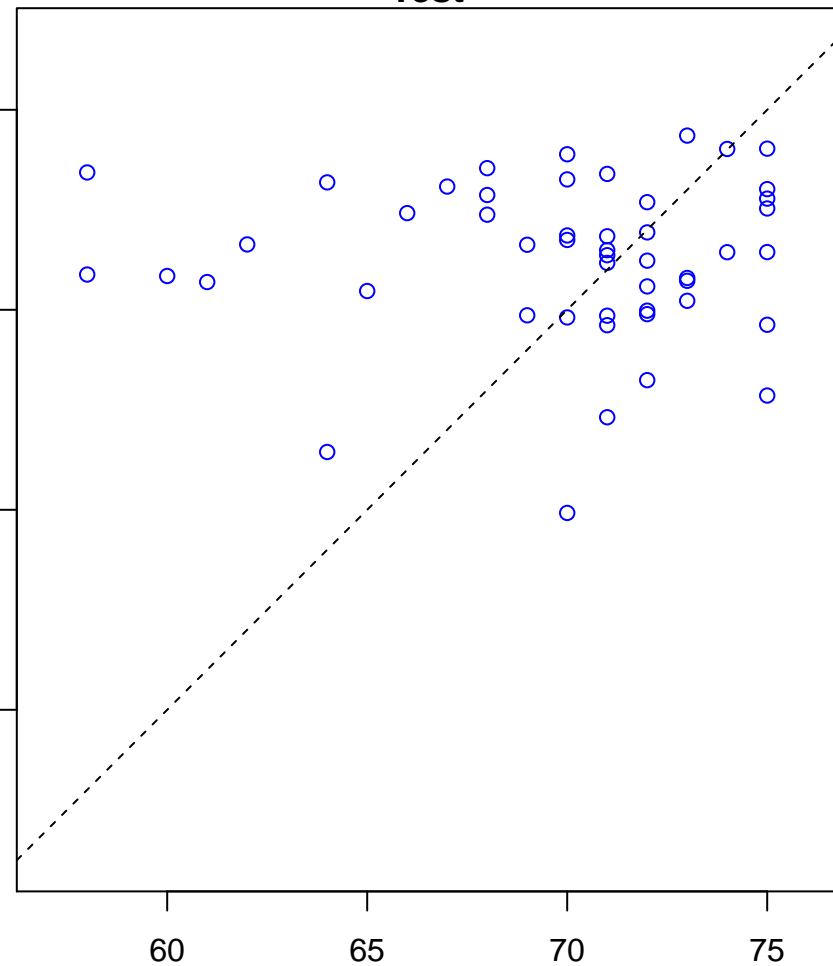


peptidyl-diphthamide metabolic process (Score: 1.073776)

Control

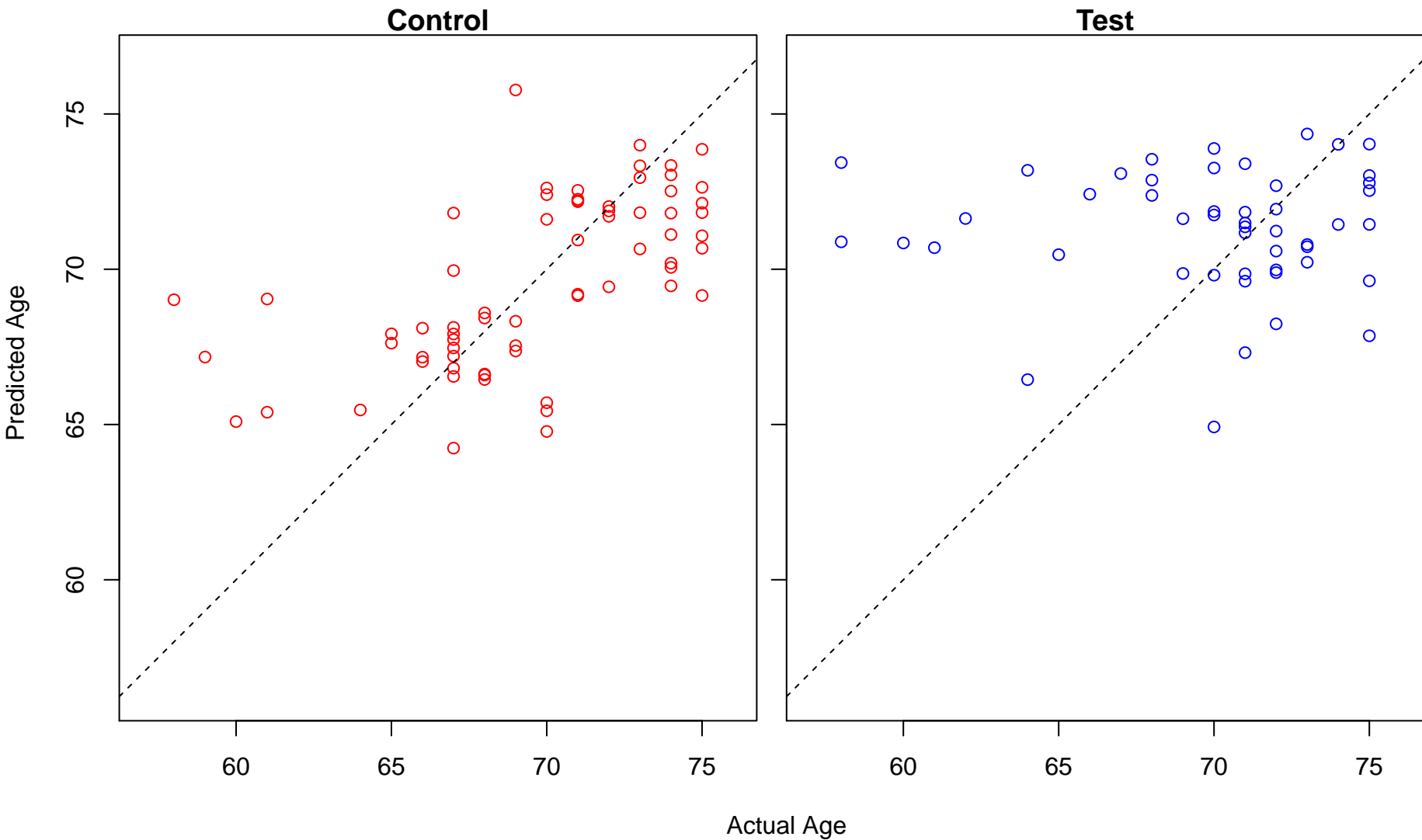


Test

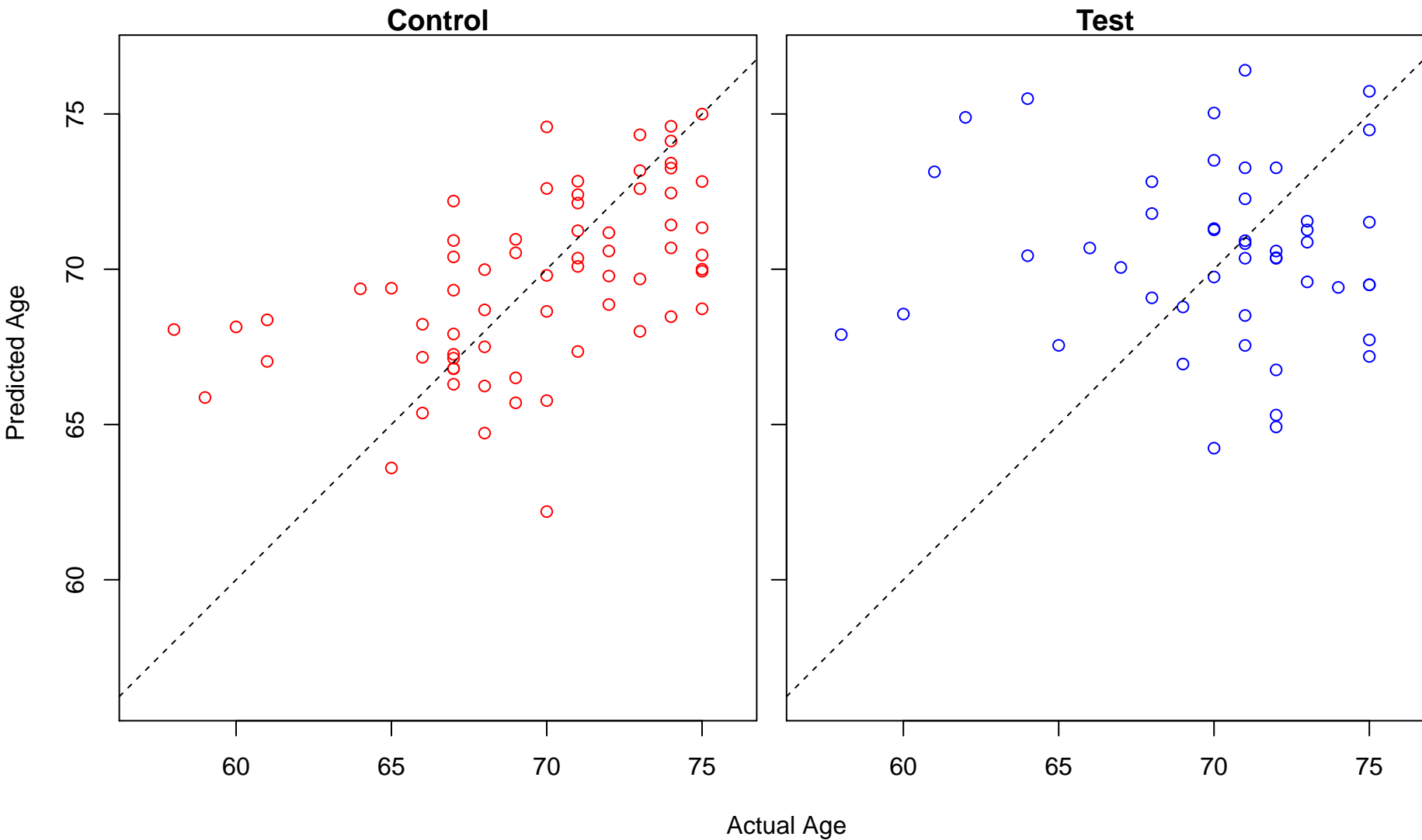


Actual Age

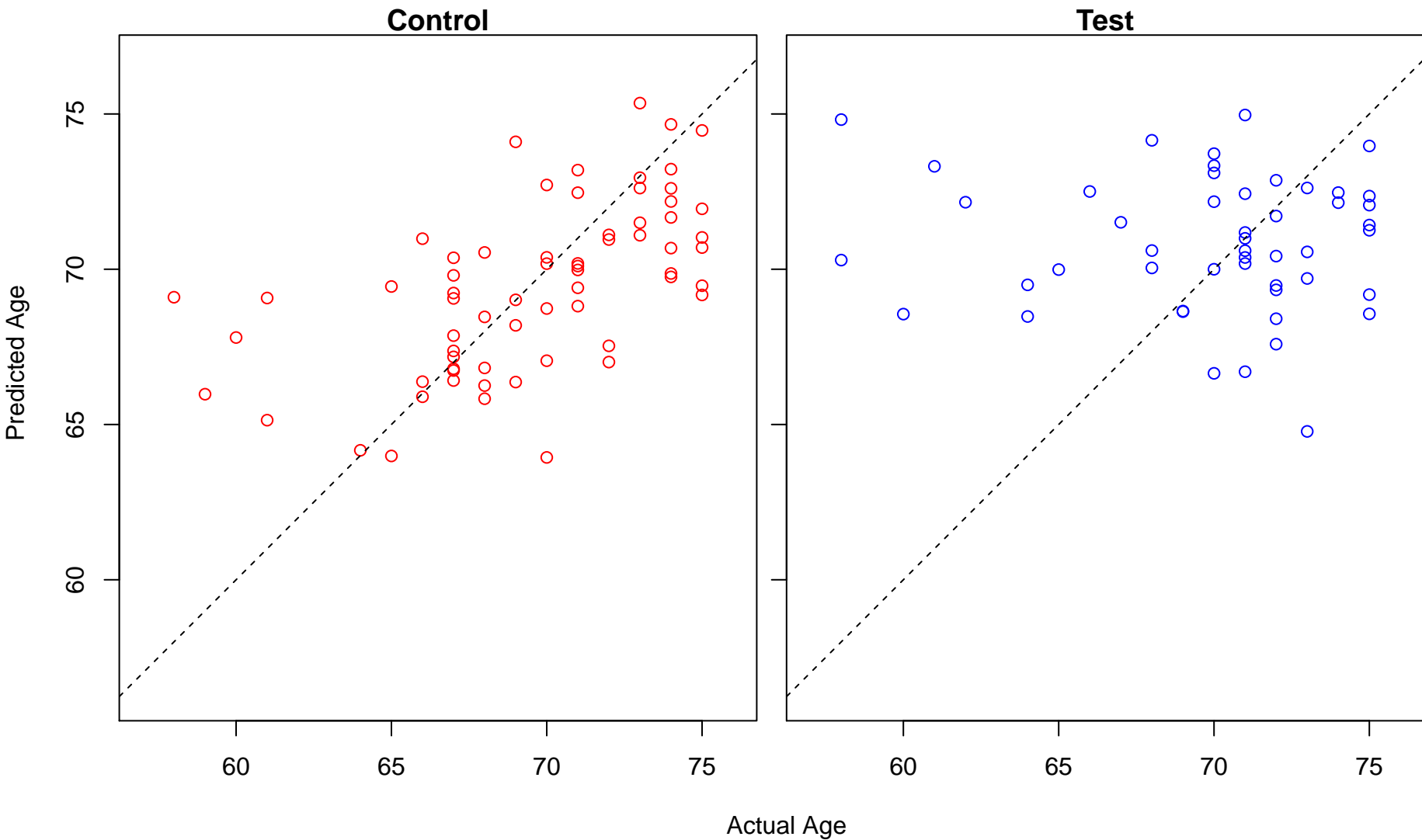
peptidyl-diphthamide biosynthetic process from peptidyl-histidine (Score: 1.073776)



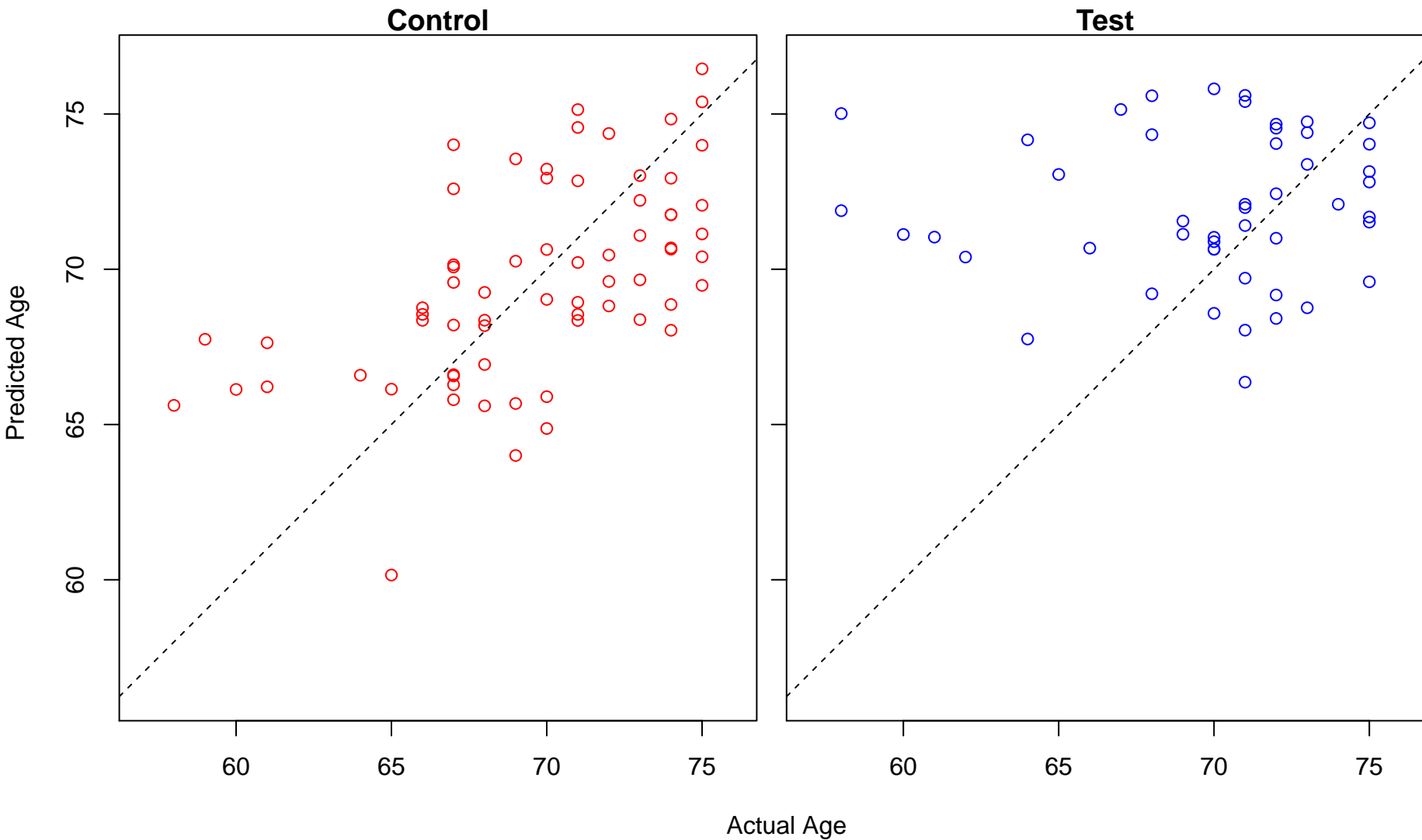
regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum (Score: 1.073)



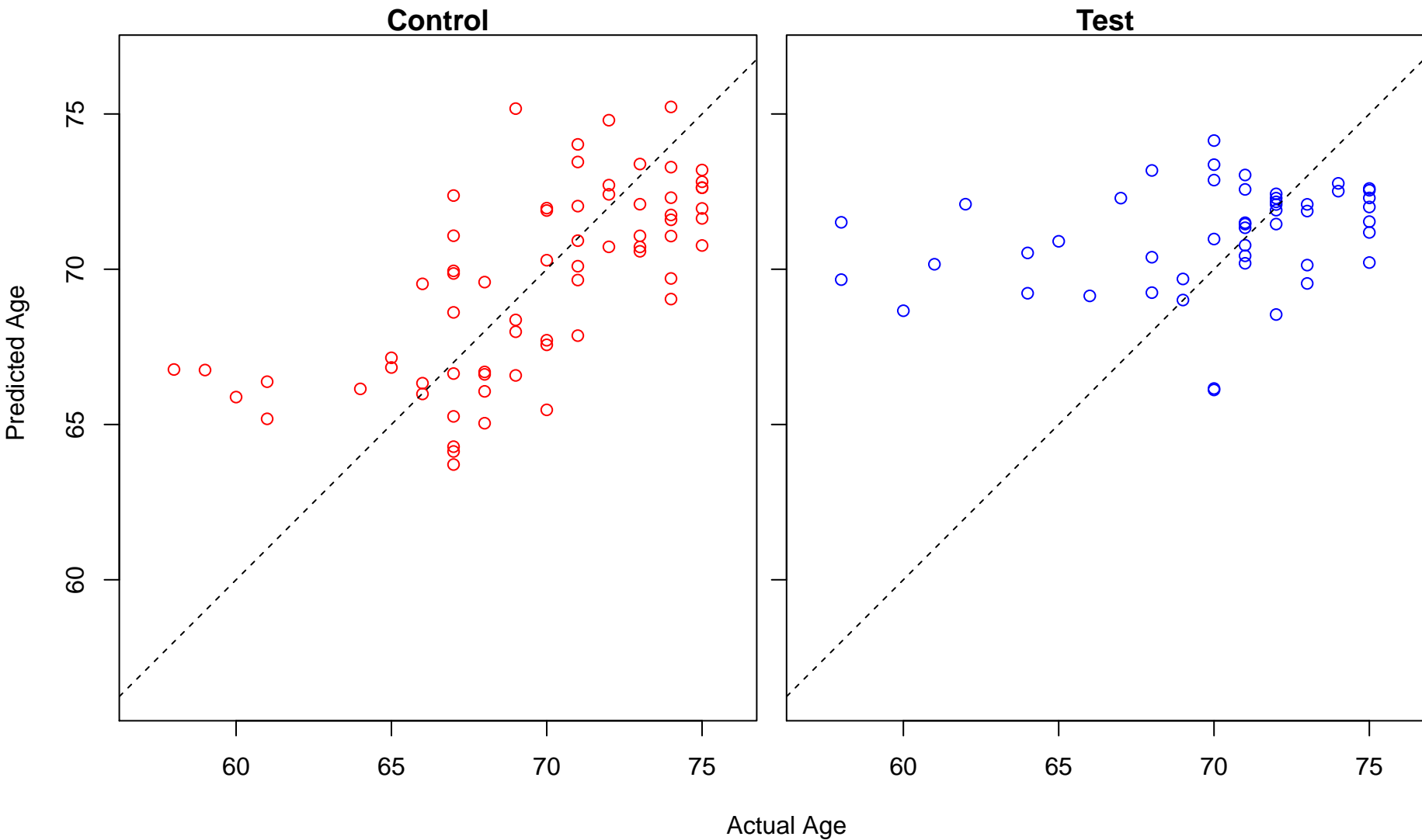
response to interferon-beta (Score: 1.073412)



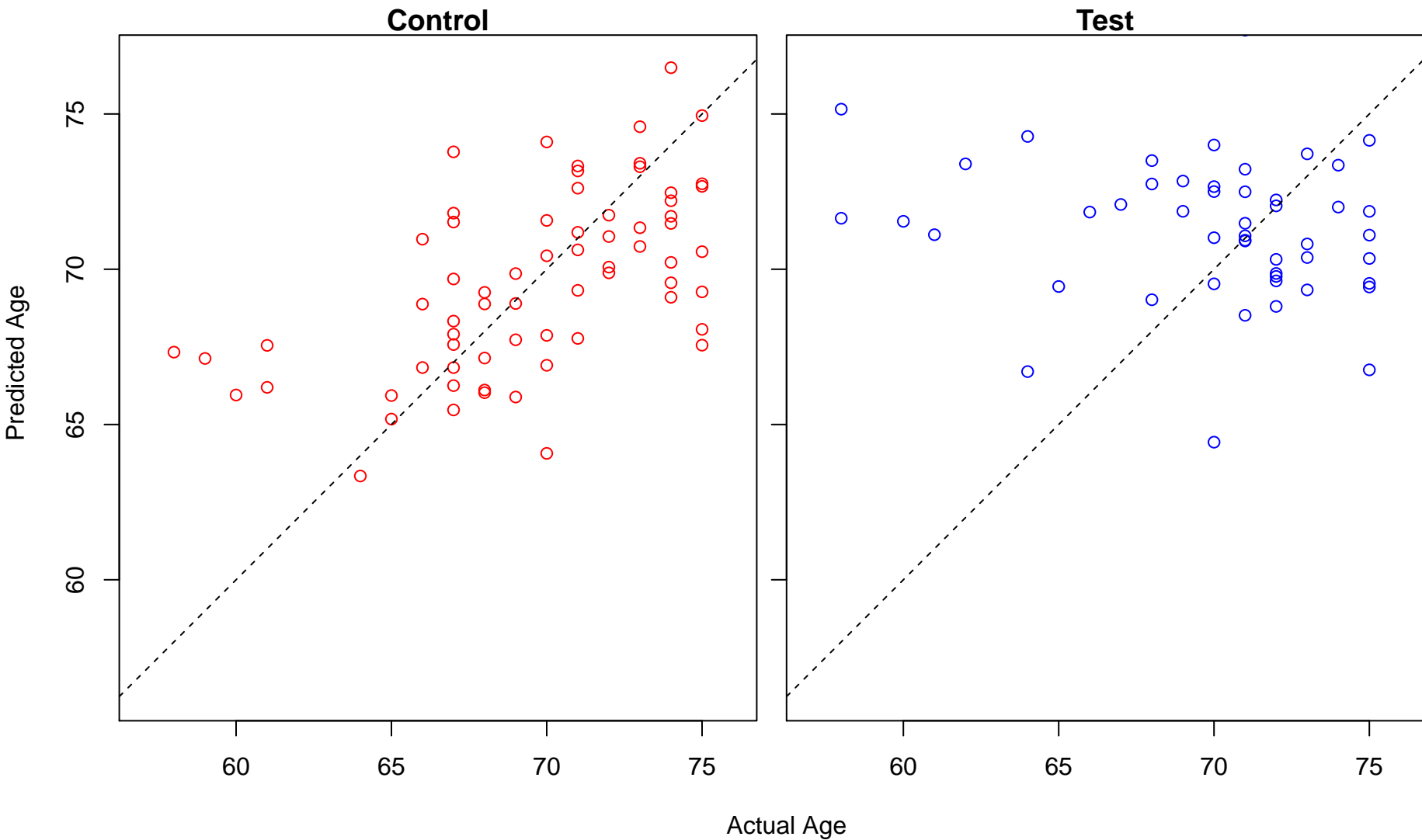
positive regulation of B cell activation (Score: 1.073391)



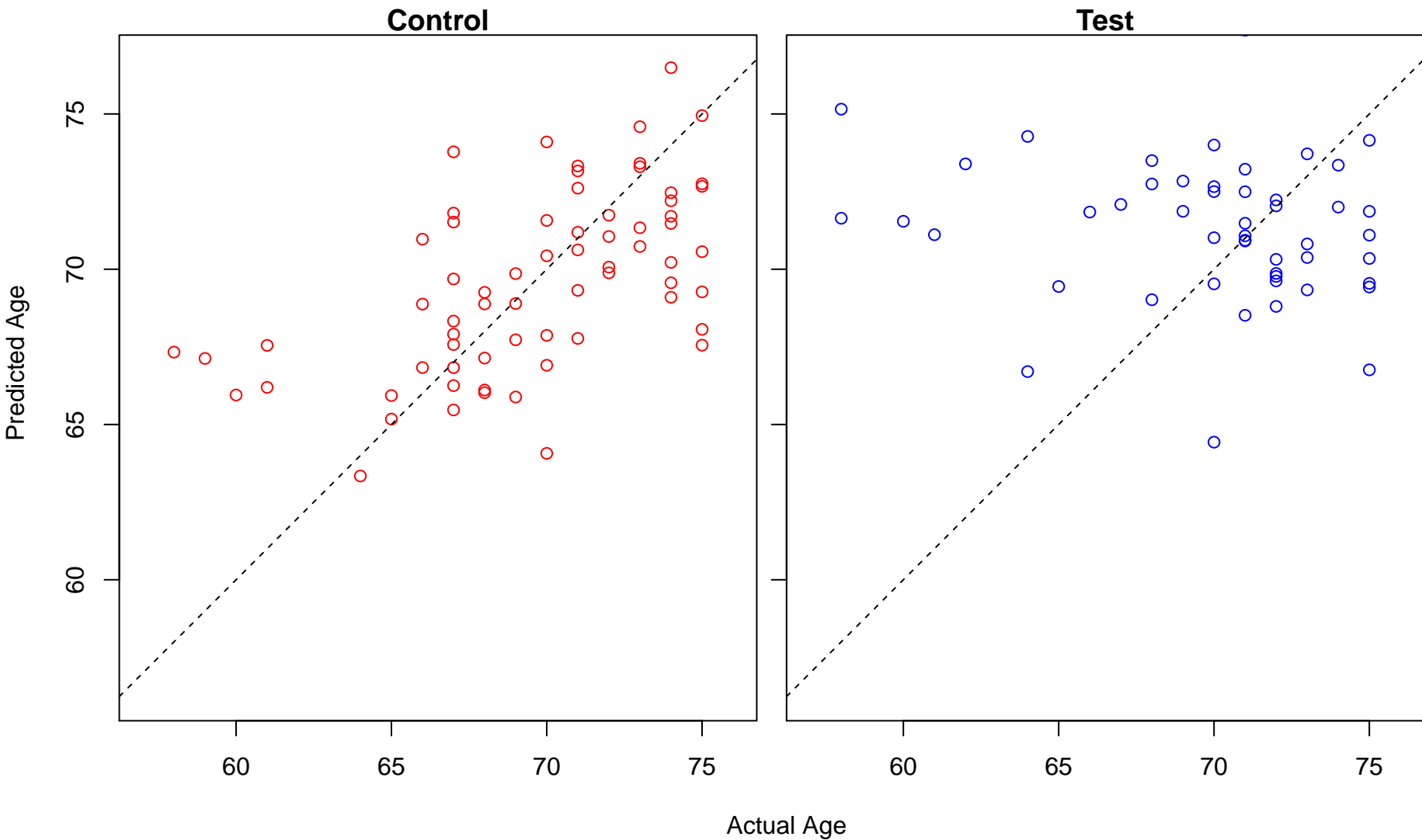
positive regulation of execution phase of apoptosis (Score: 1.073252)



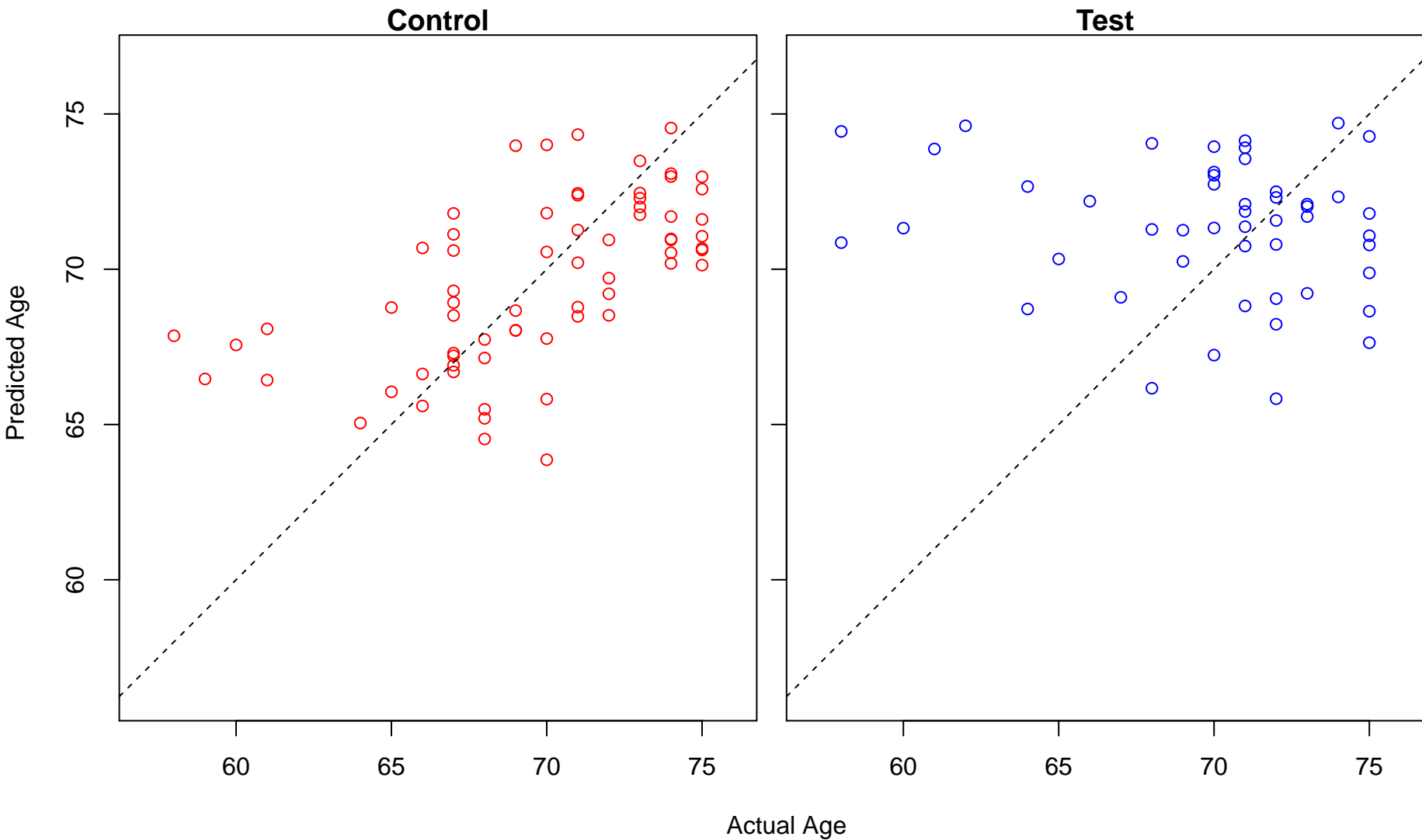
response to hexose (Score: 1.072417)



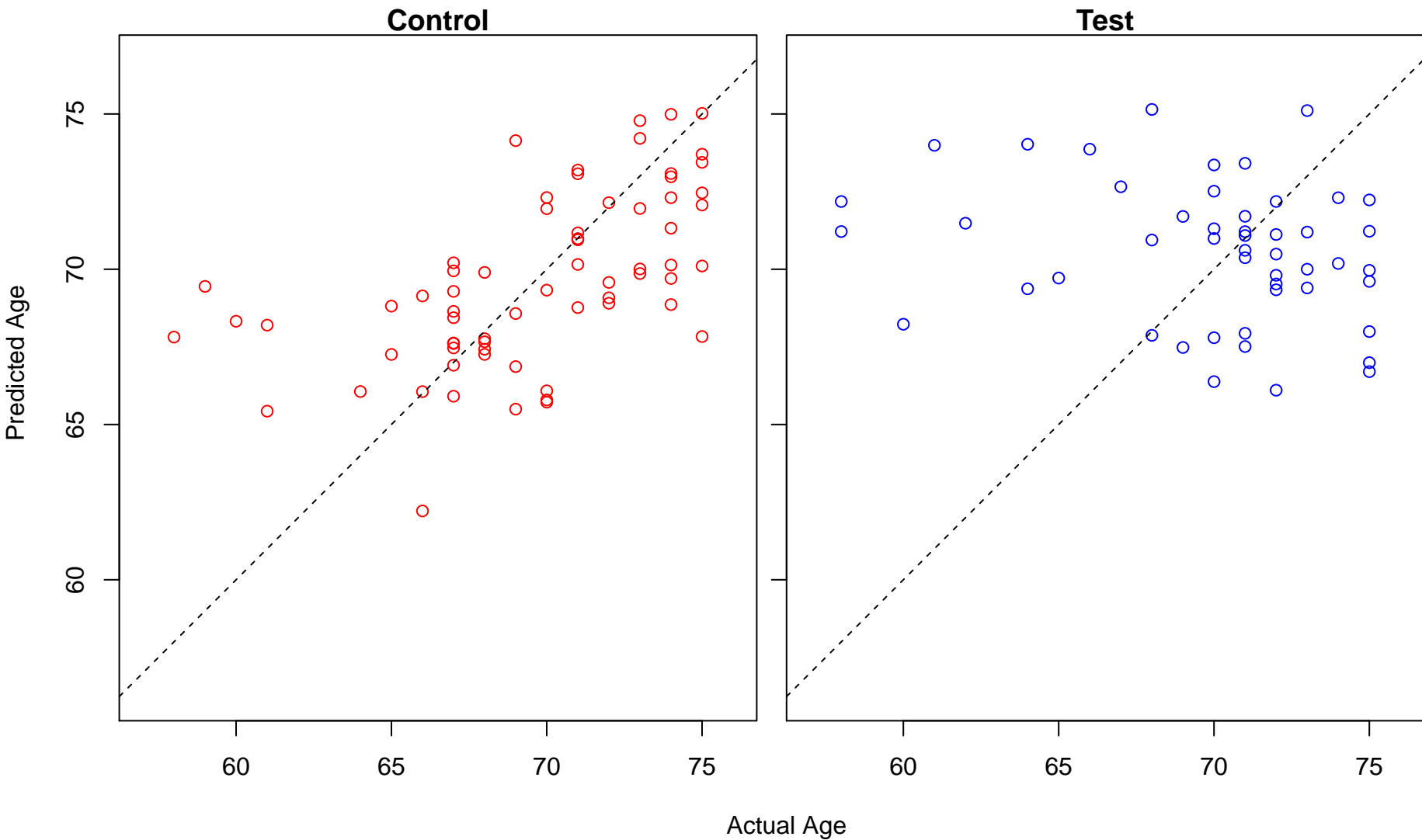
response to monosaccharide (Score: 1.072417)



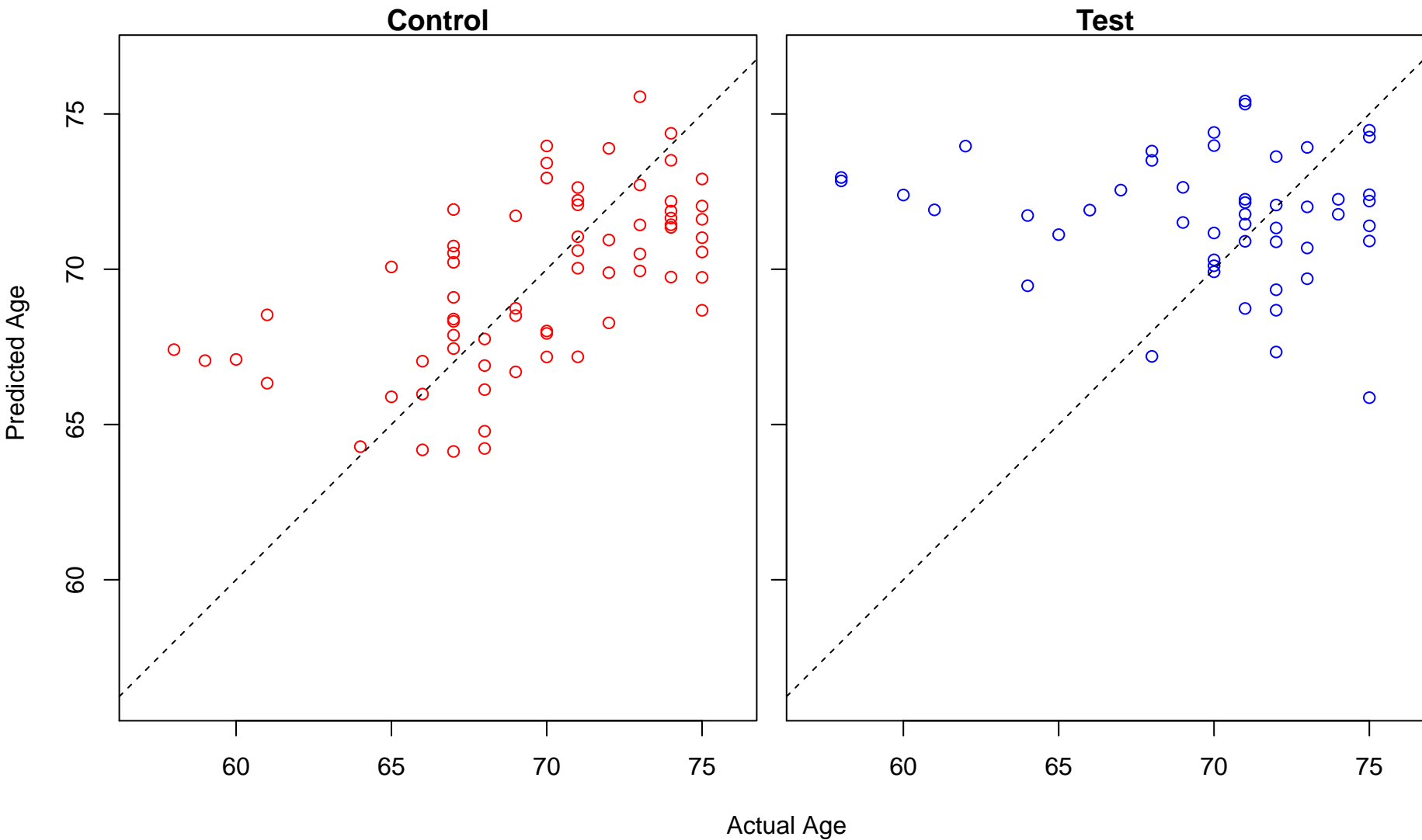
negative regulation of myeloid cell differentiation (Score: 1.072094)



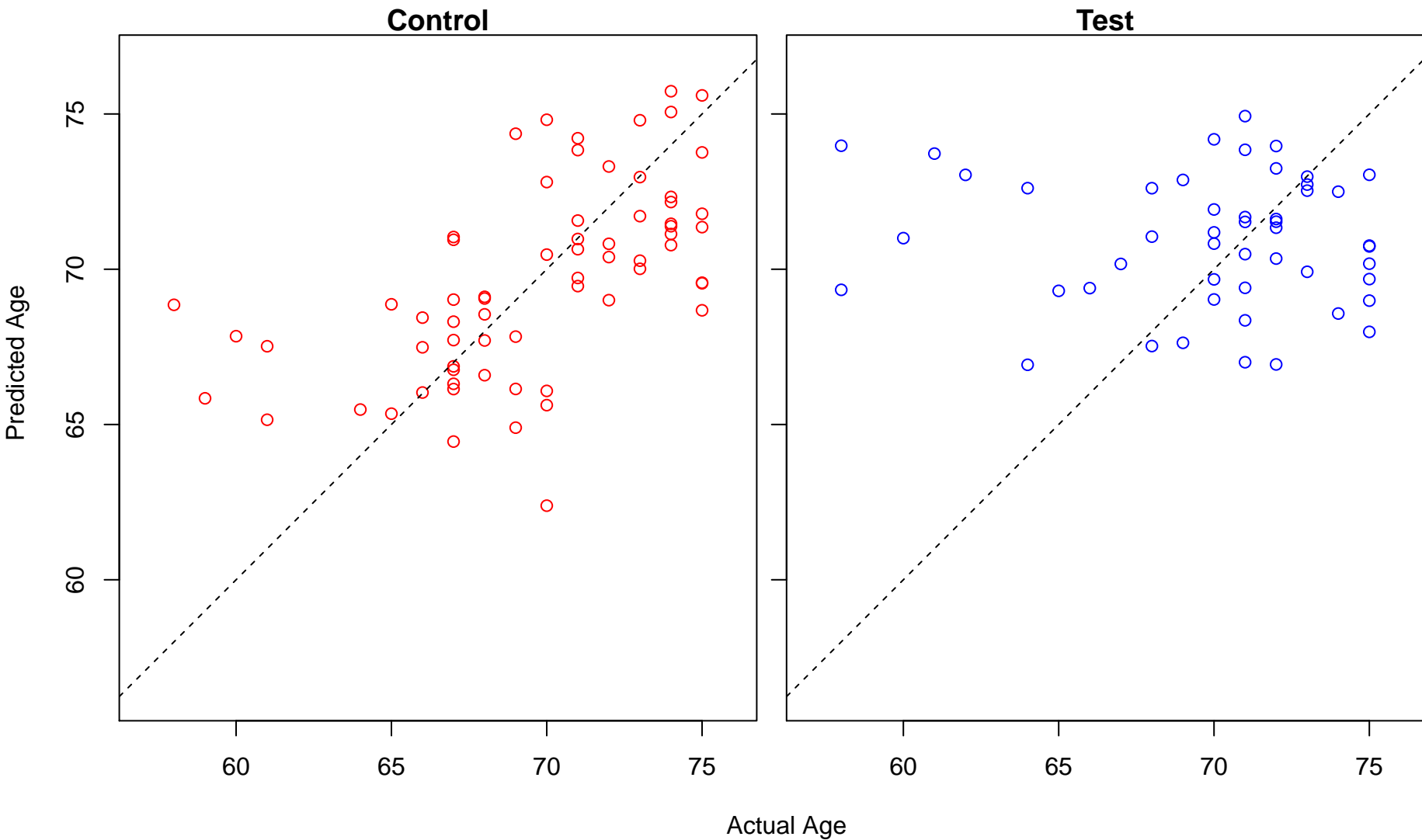
regulation of lamellipodium assembly (Score: 1.071895)



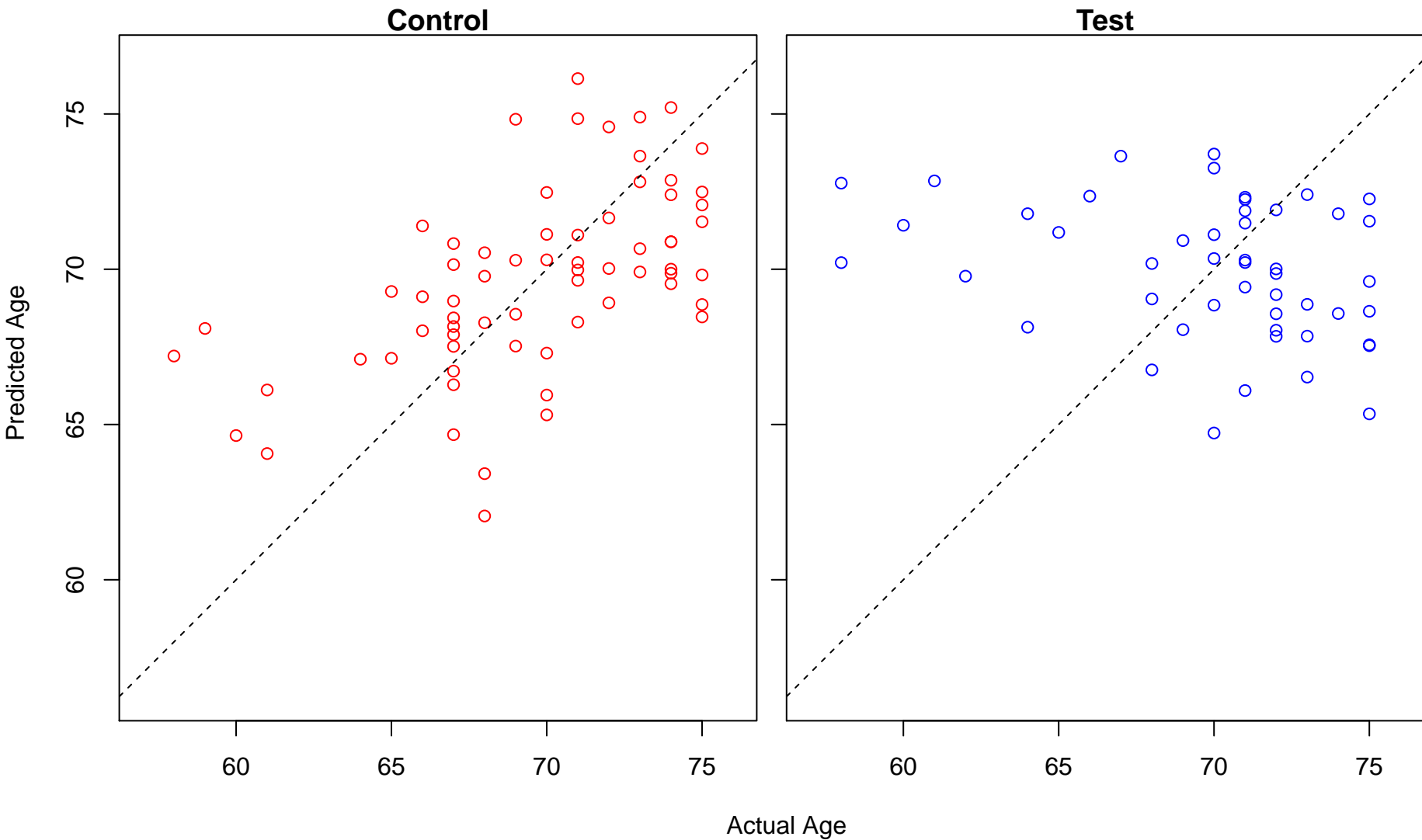
negative regulation of myotube differentiation (Score: 1.071354)



male sex differentiation (Score: 1.071239)

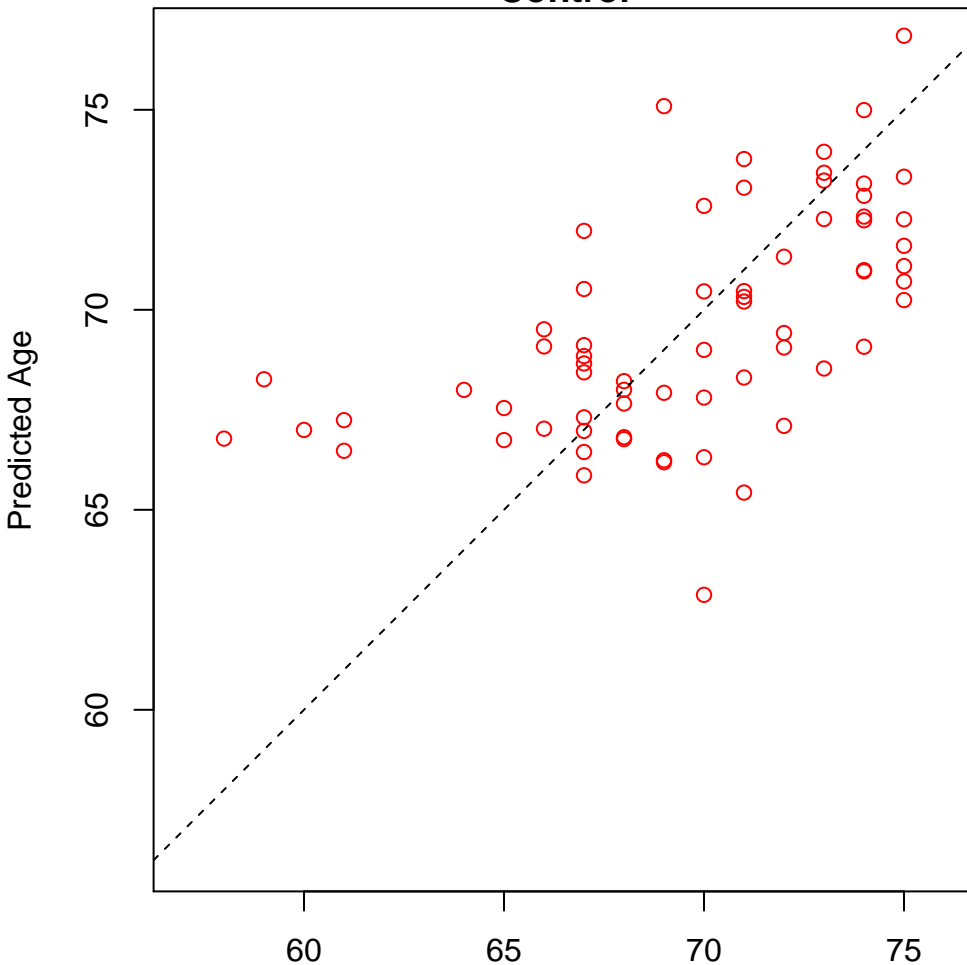


dendritic spine development (Score: 1.071011)

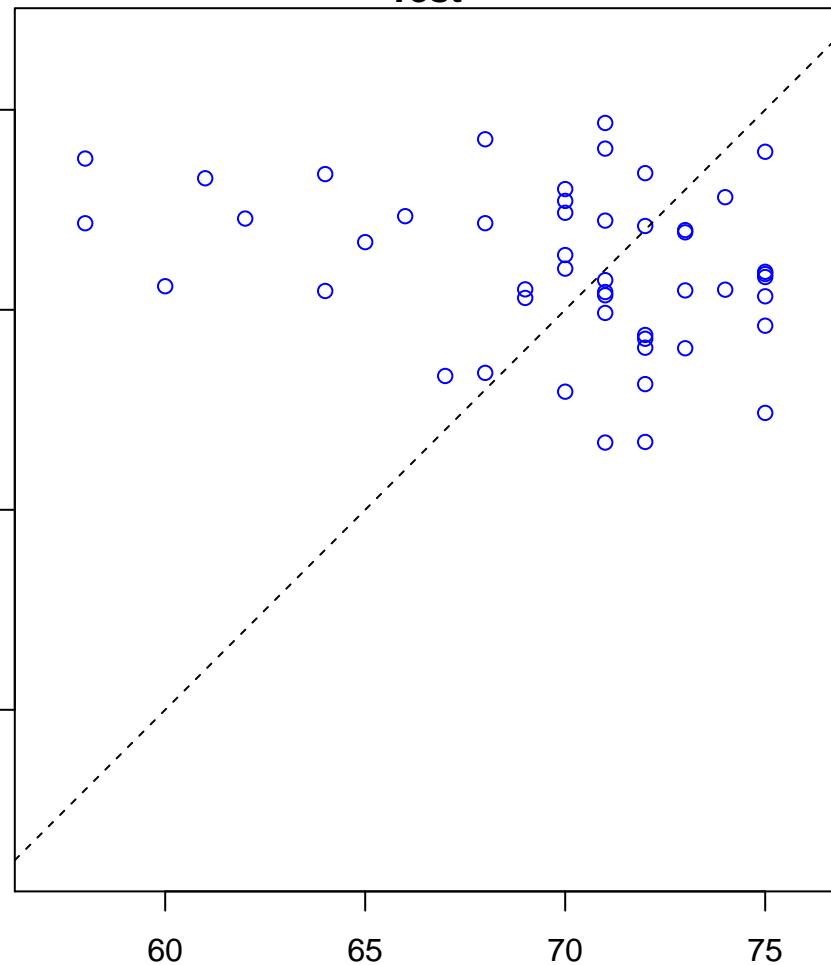


N-acetylneuraminate metabolic process (Score: 1.069805)

Control

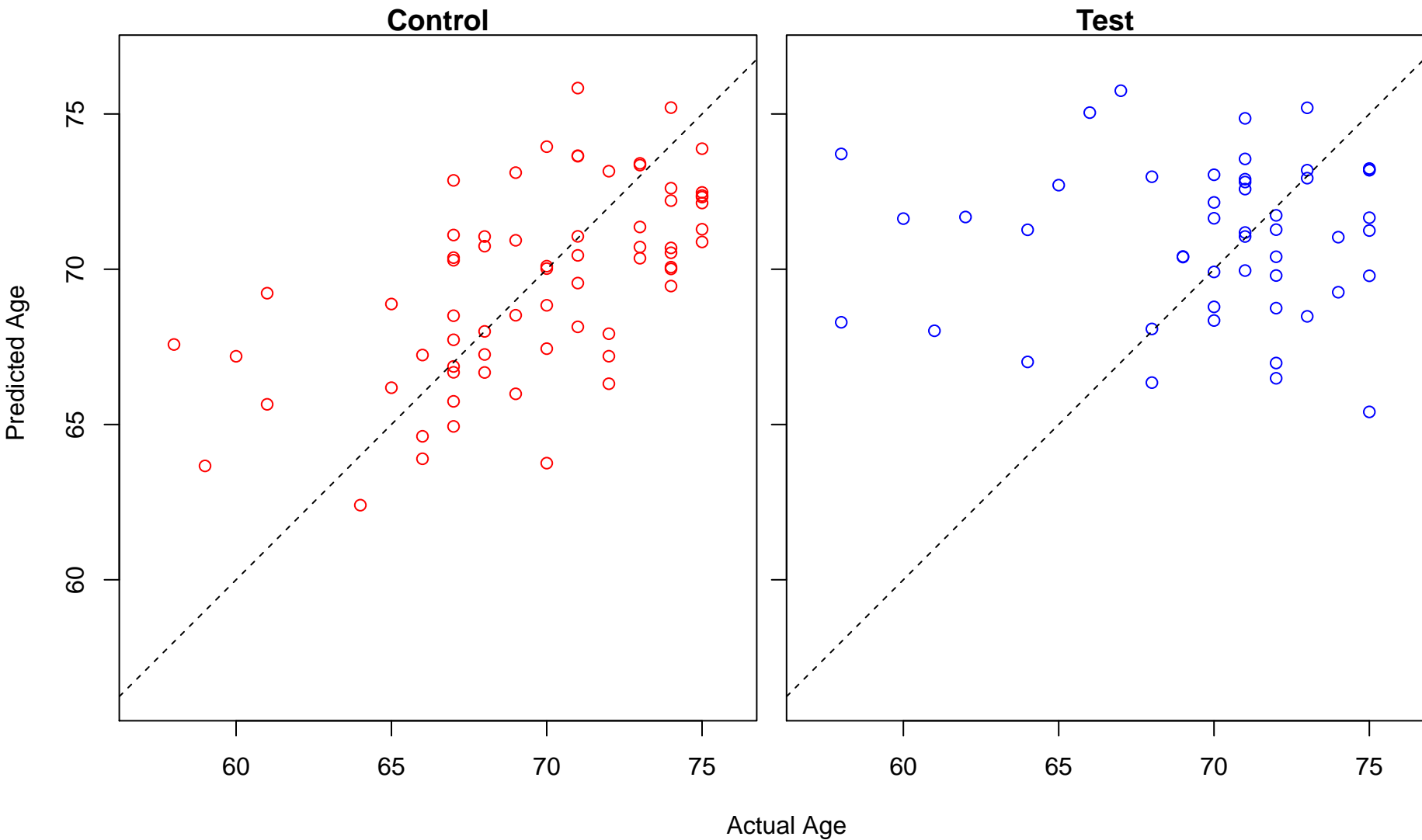


Test

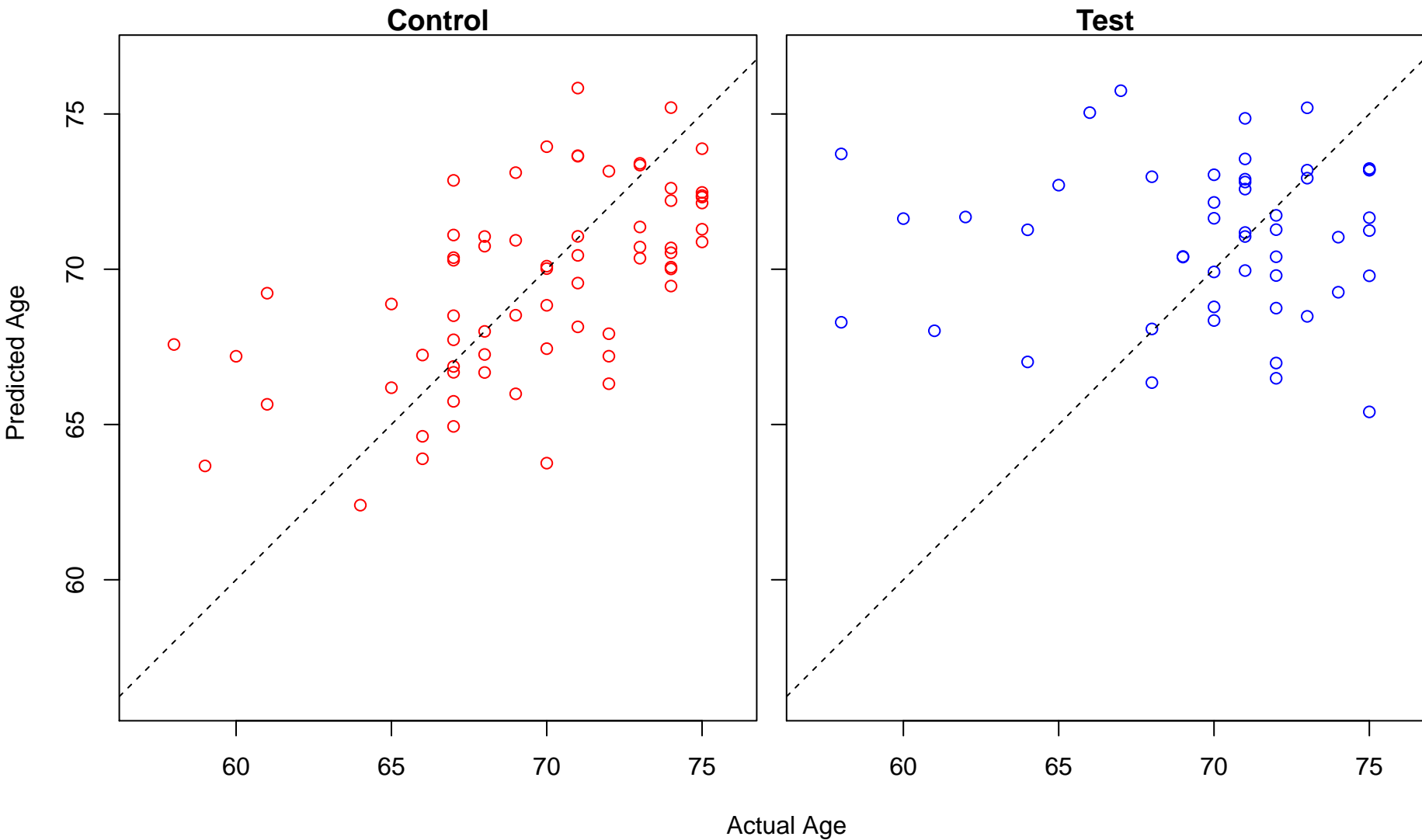


Actual Age

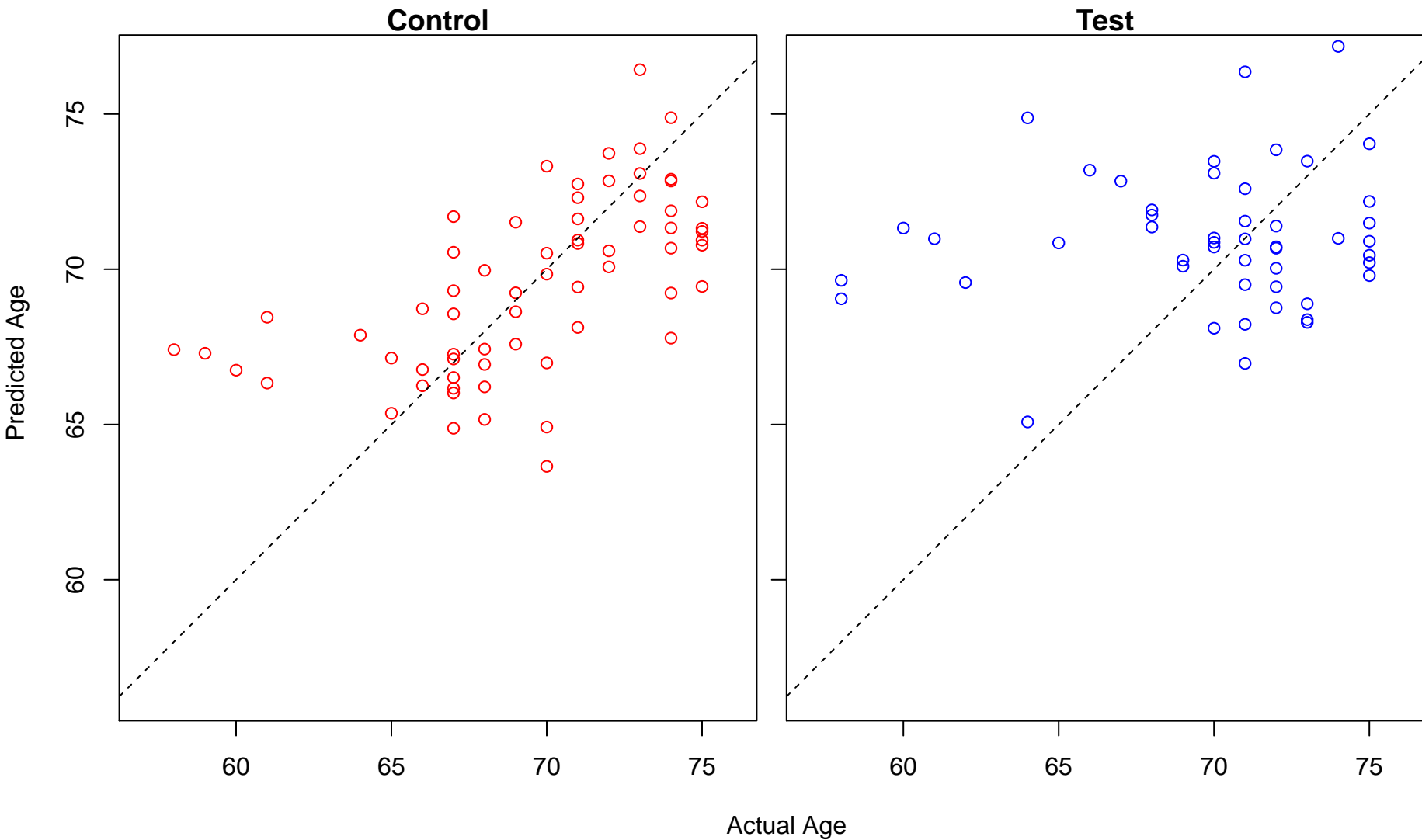
positive regulation of response to tumor cell (Score: 1.069597)



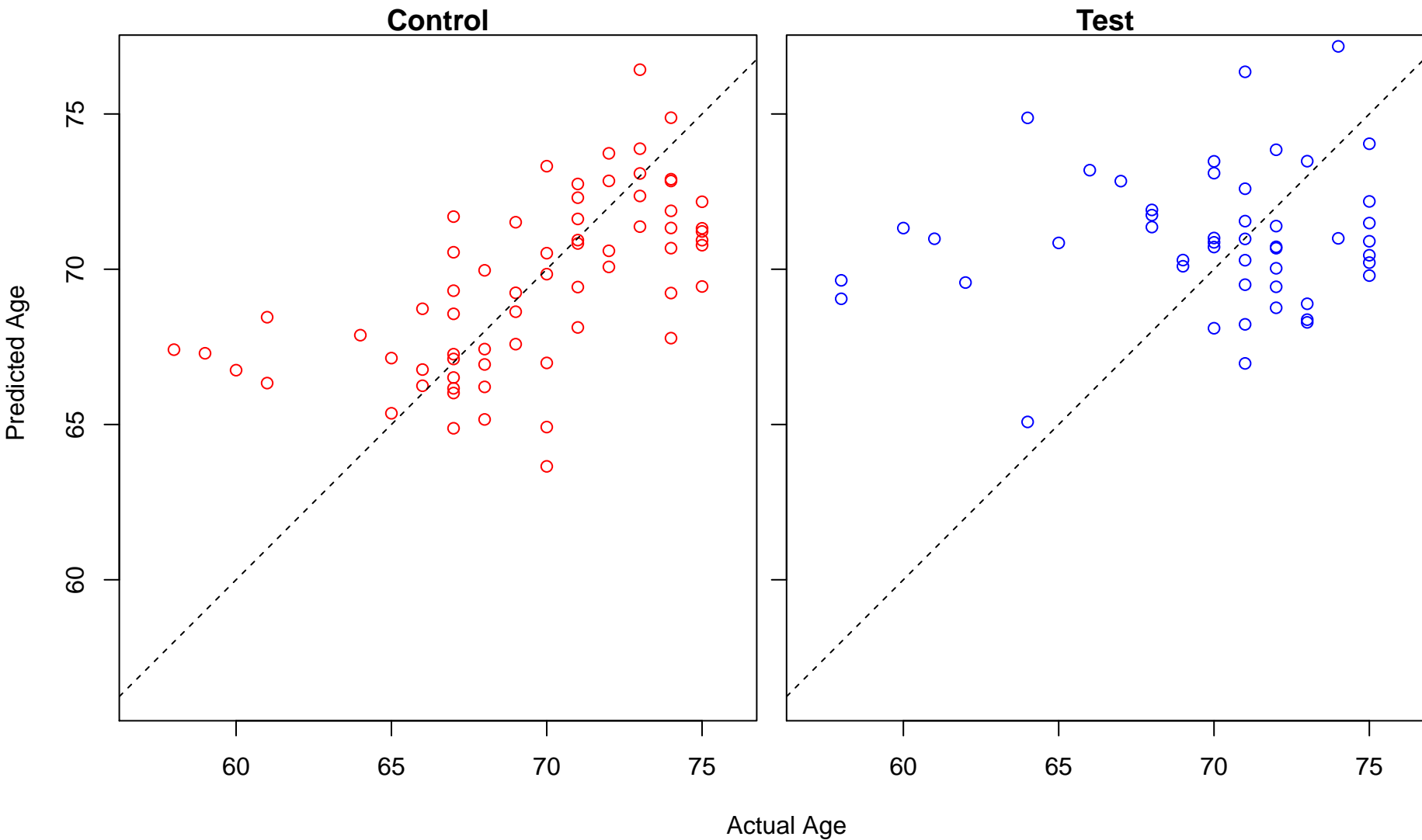
positive regulation of immune response to tumor cell (Score: 1.069597)



rhythmic behavior (Score: 1.069393)

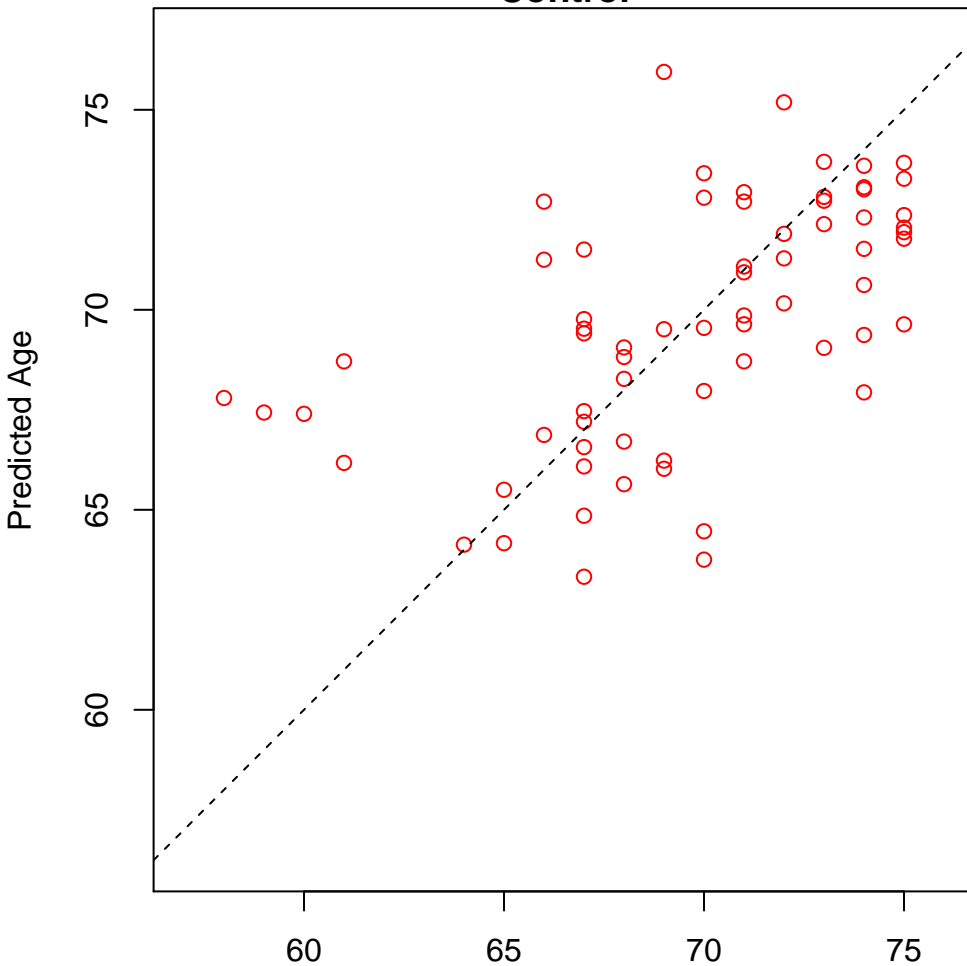


circadian behavior (Score: 1.069393)

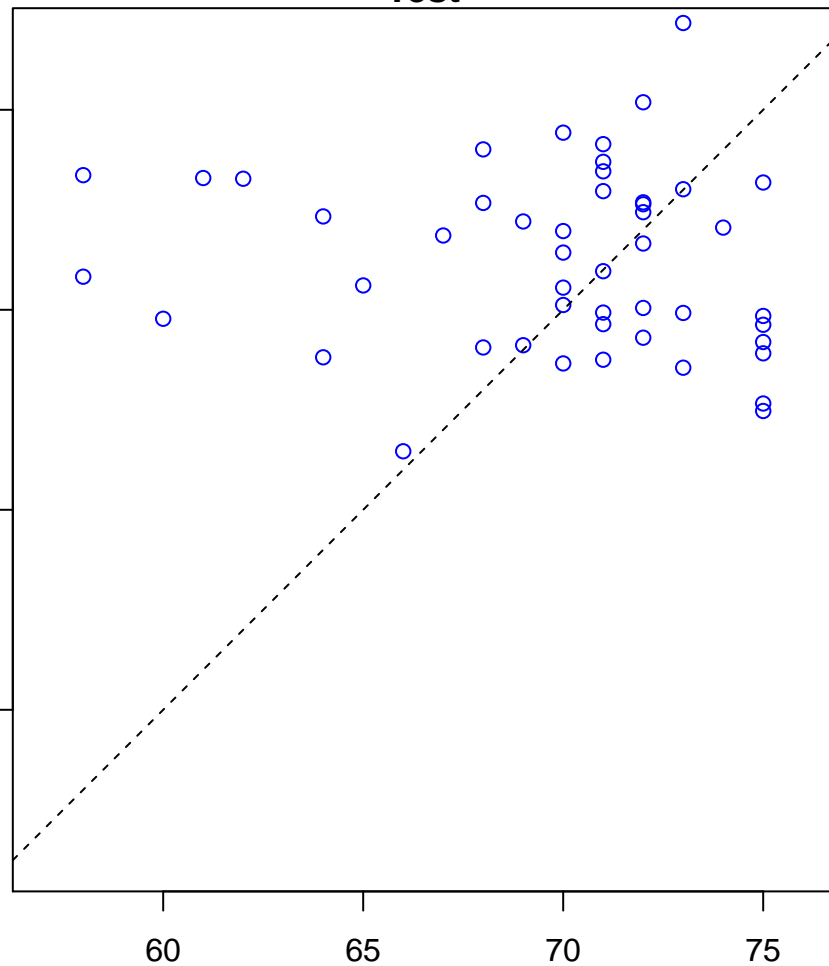


posttranscriptional gene silencing (Score: 1.068787)

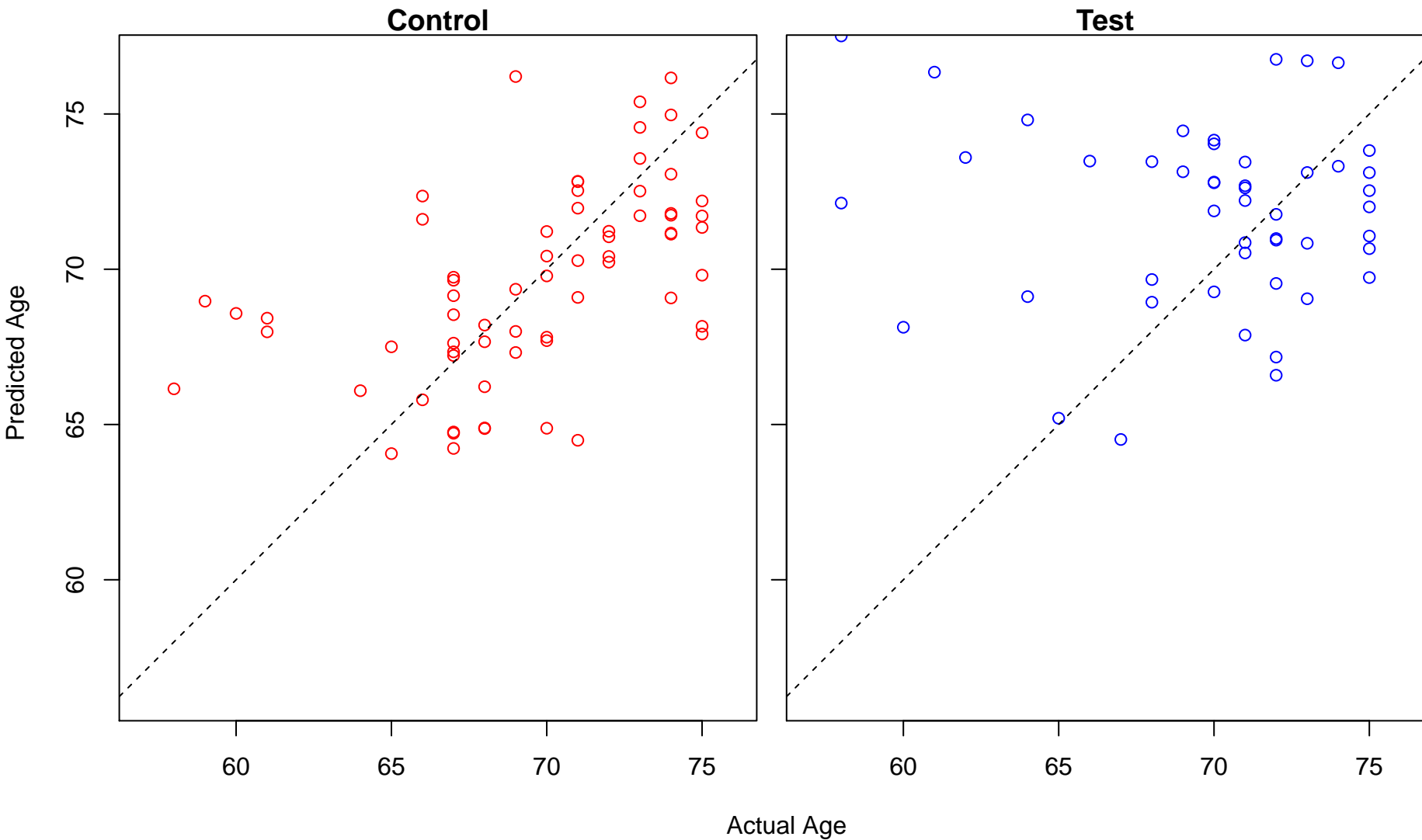
Control



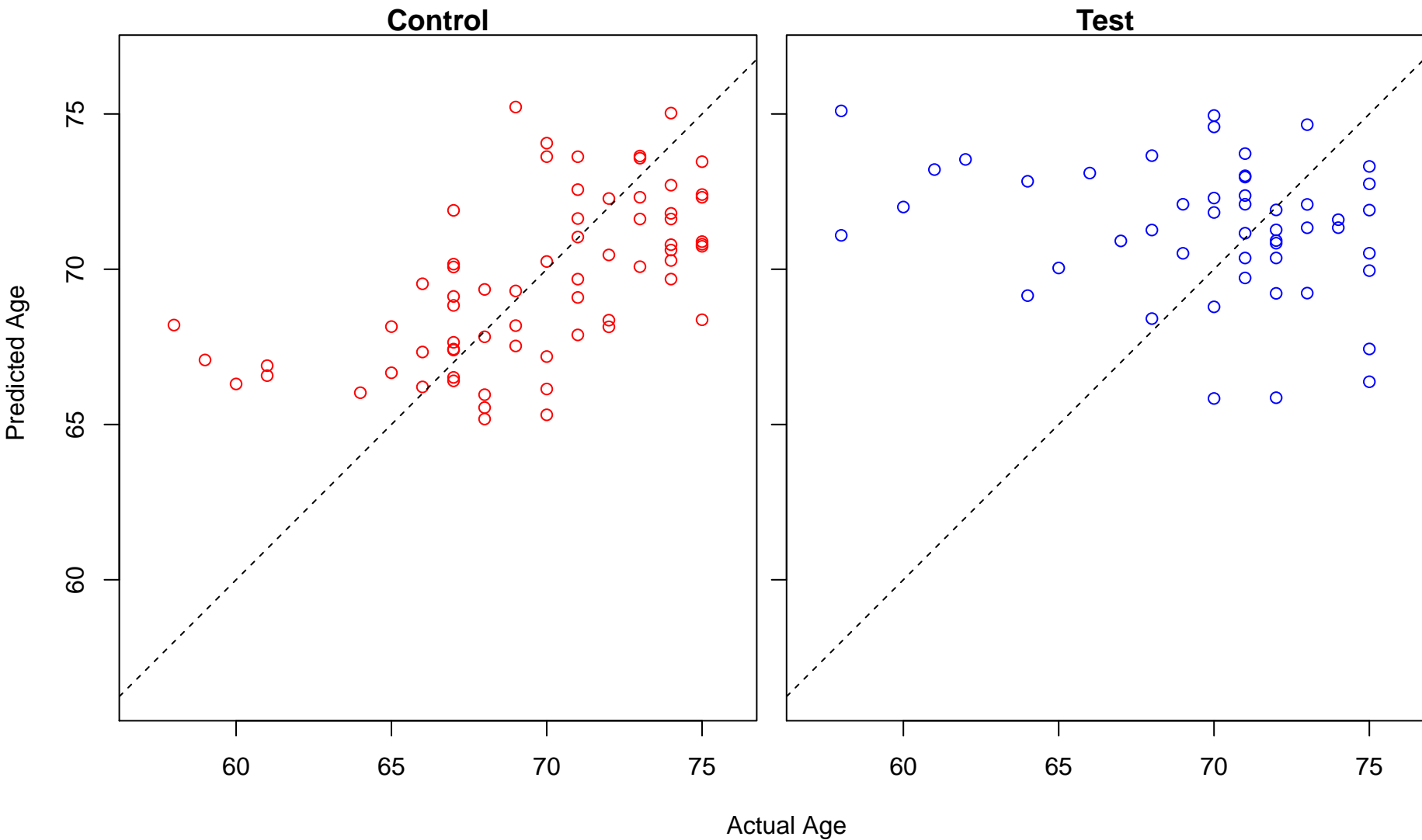
Test



multi-multicellular organism process (Score: 1.068512)

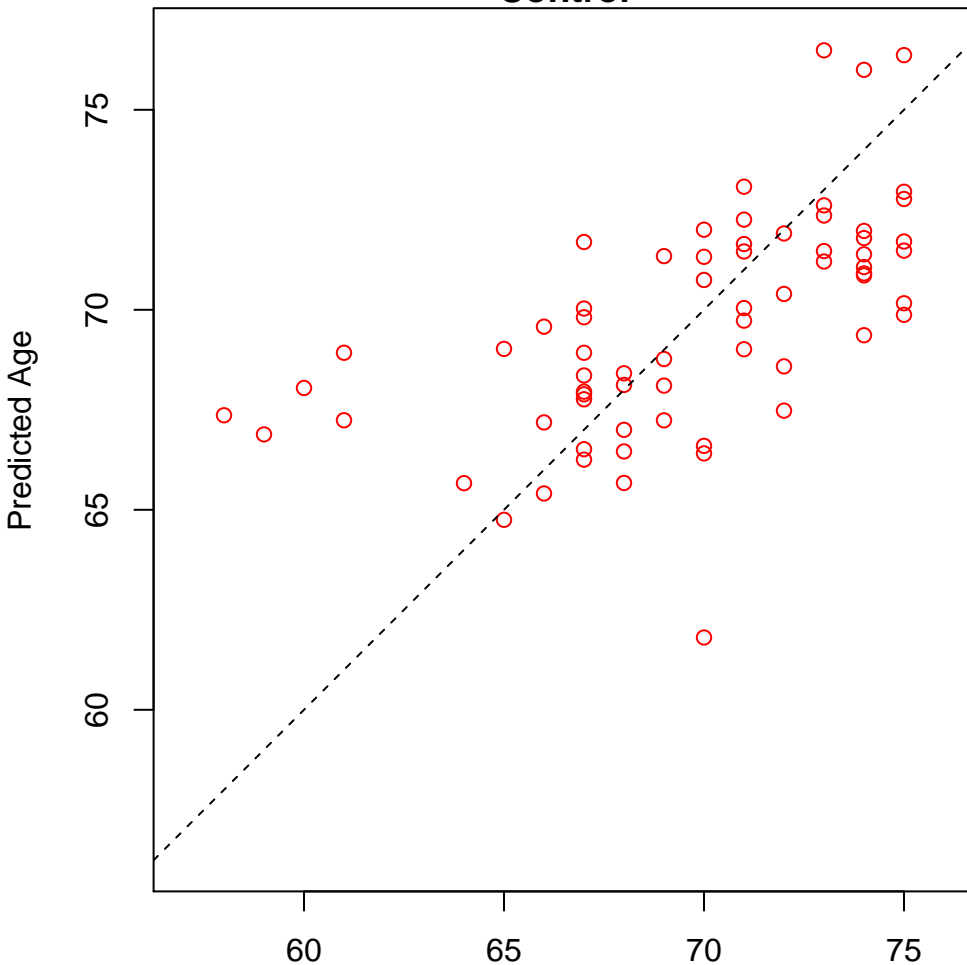


vesicle targeting, to, from or within Golgi (Score: 1.068149)

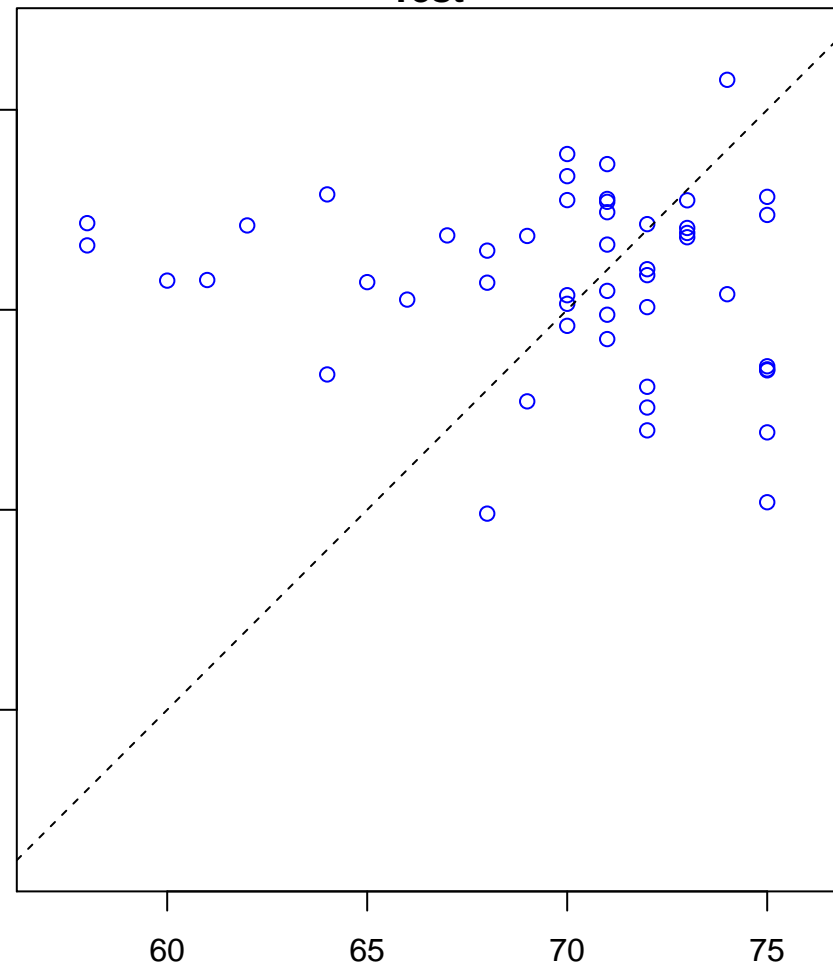


response to cell cycle checkpoint signaling (Score: 1.068090)

Control

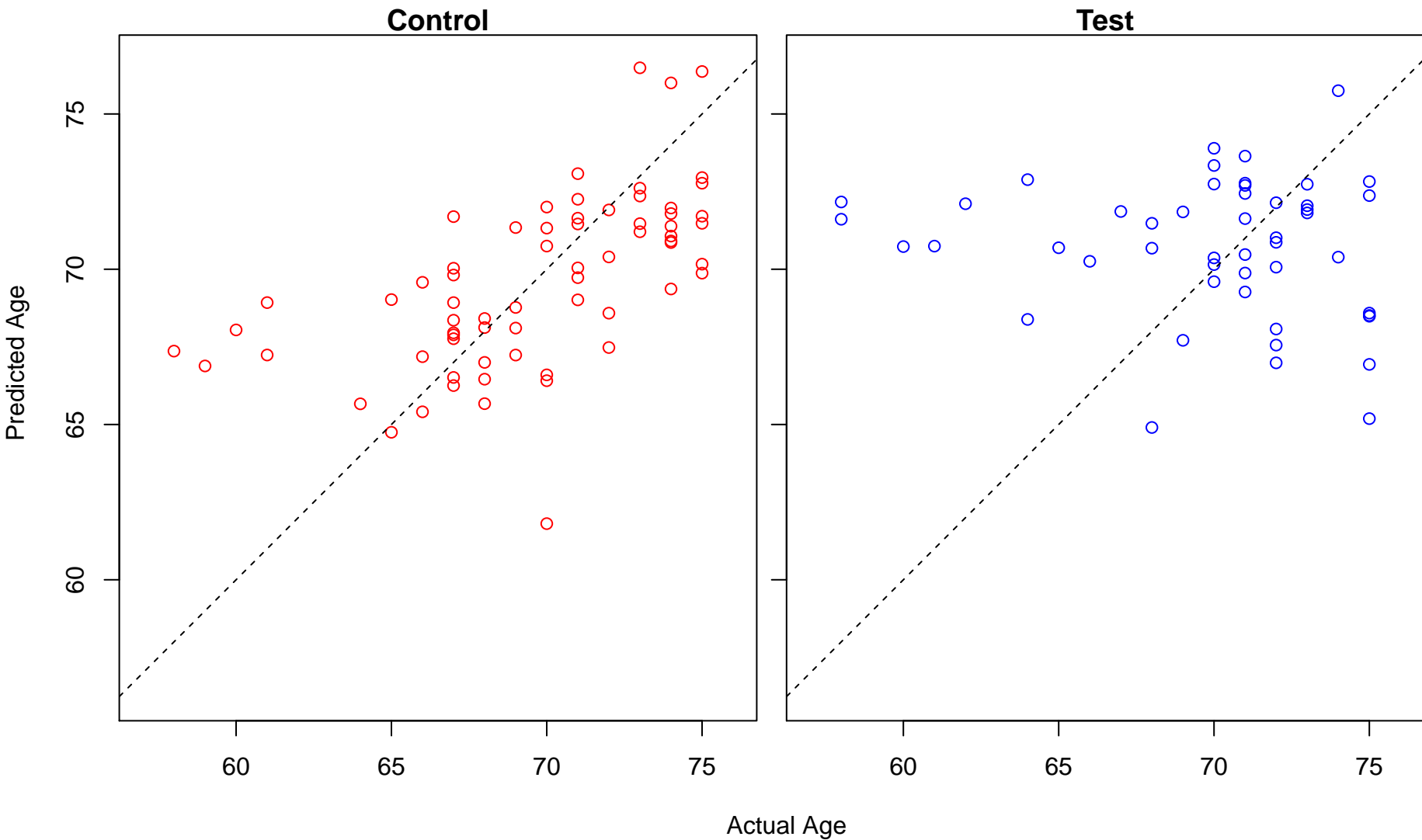


Test

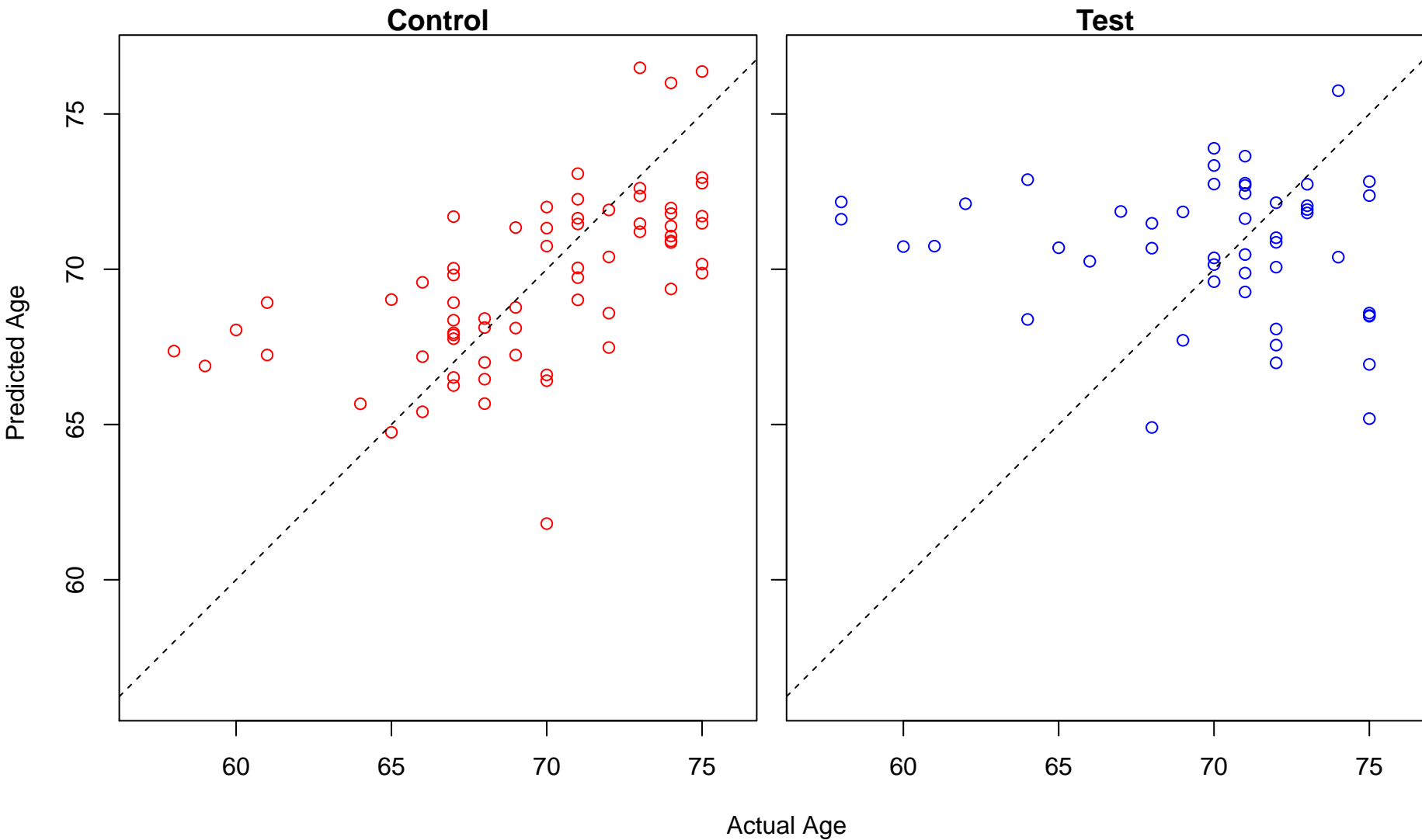


Actual Age

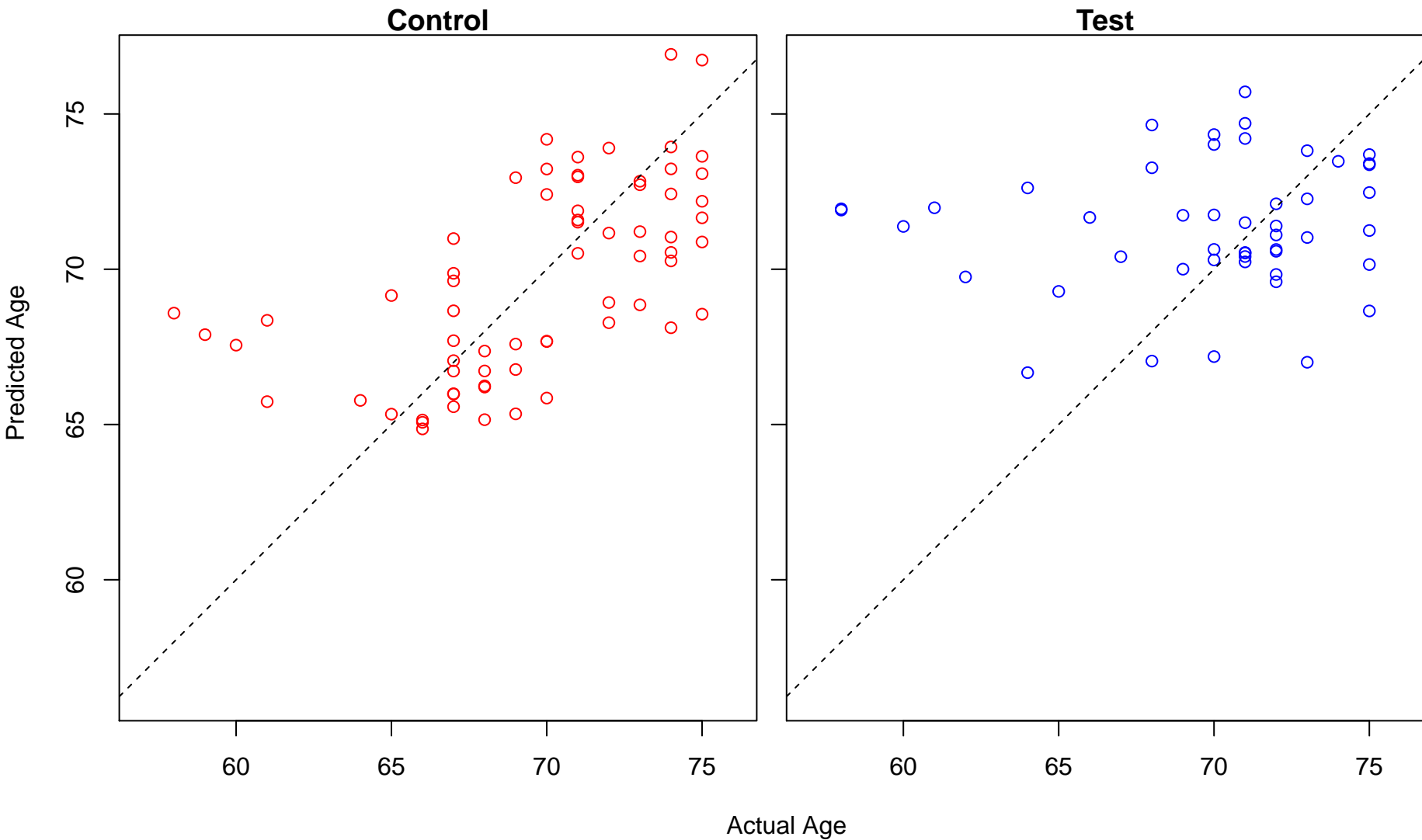
response to DNA integrity checkpoint signaling (Score: 1.068090)



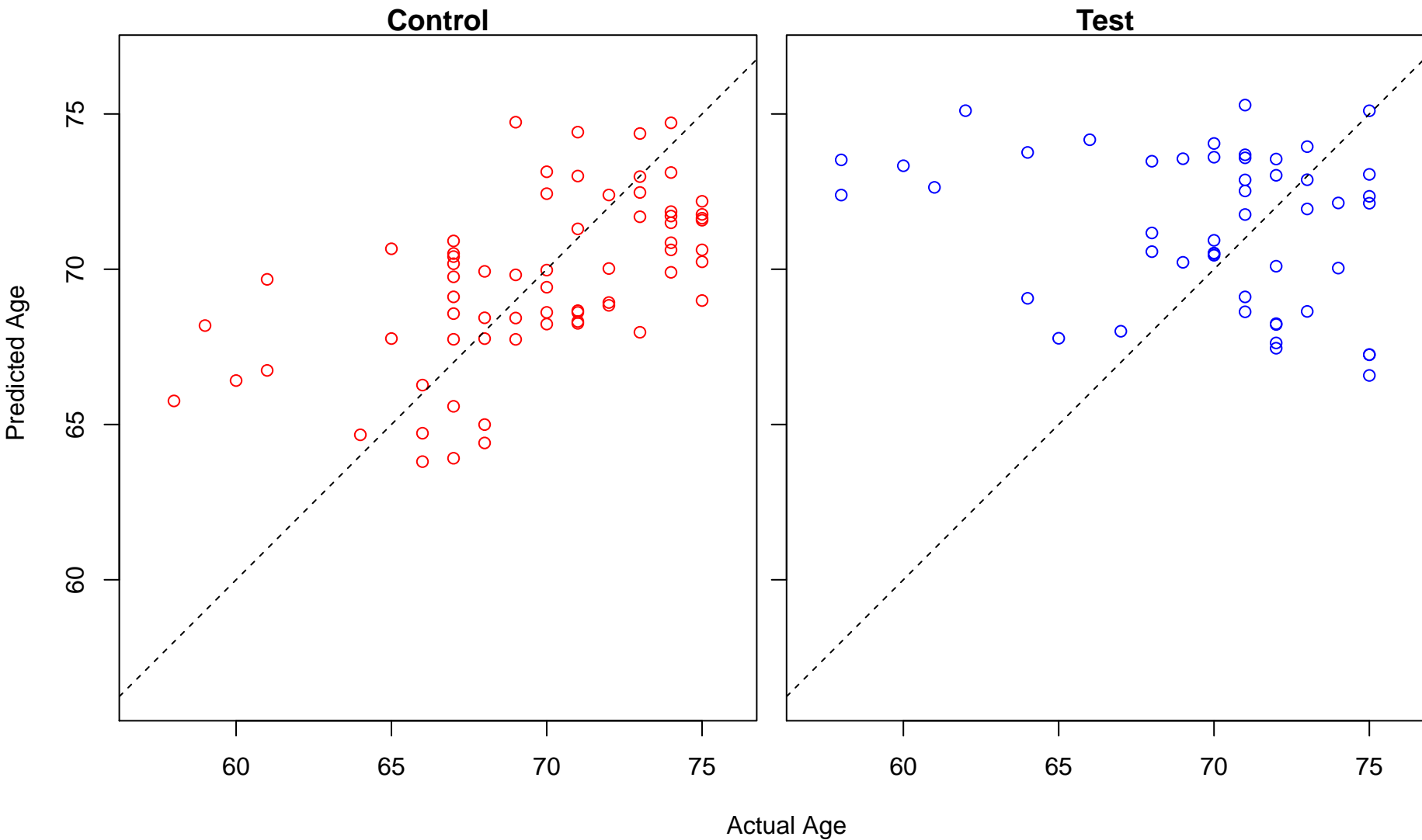
response to DNA damage checkpoint signaling (Score: 1.068090)



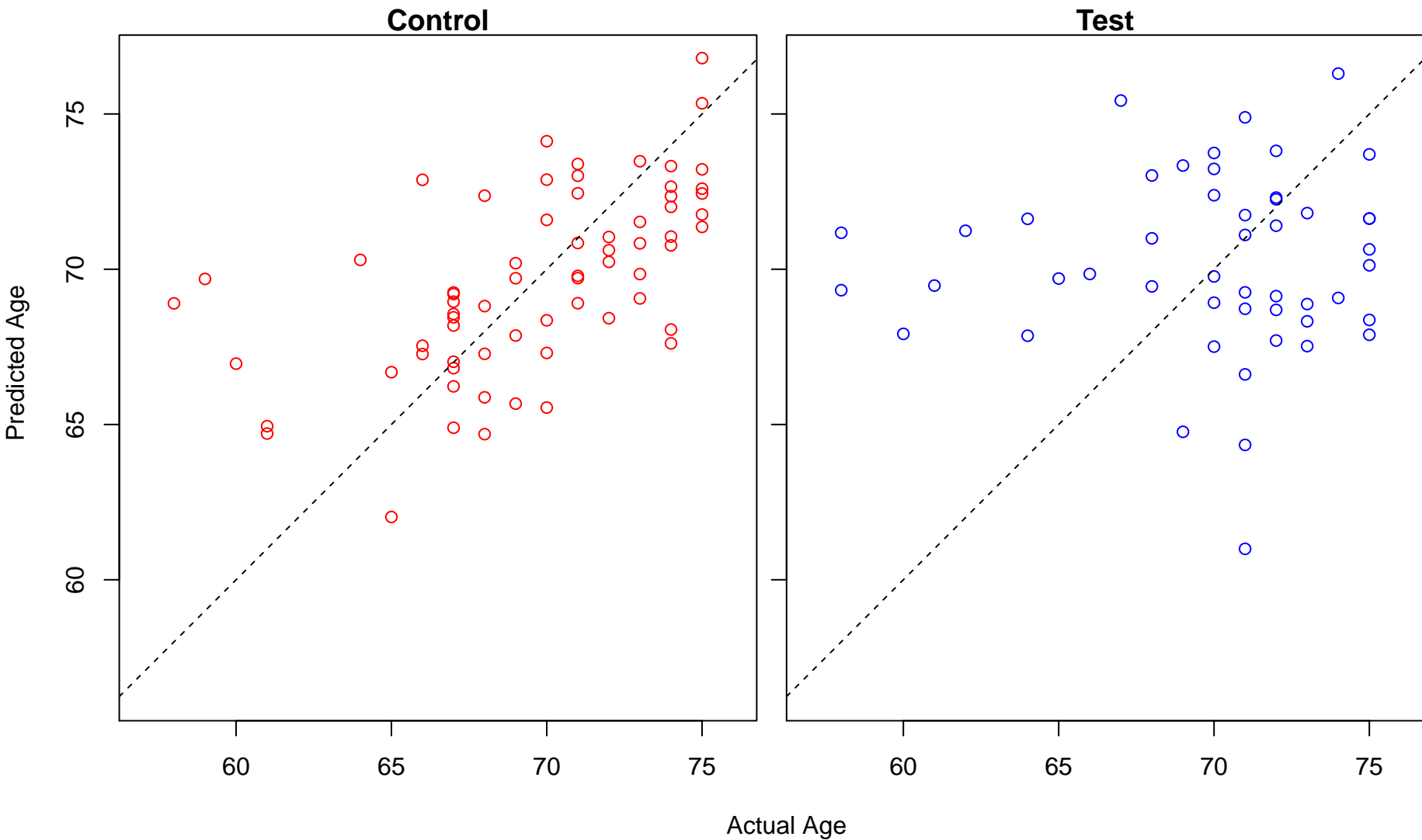
regulation of neurotransmitter levels (Score: 1.067907)



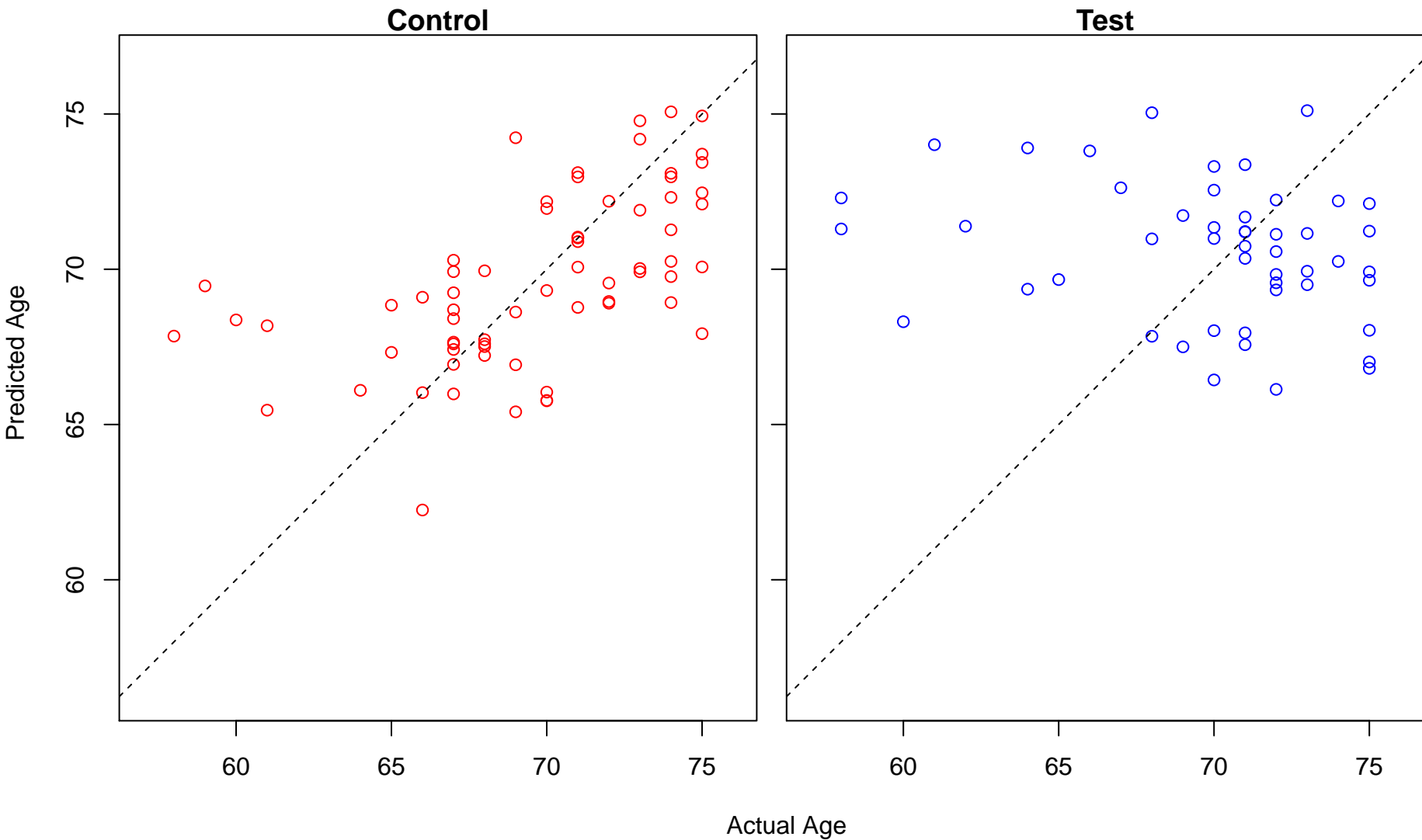
negative regulation of BMP signaling pathway (Score: 1.067621)



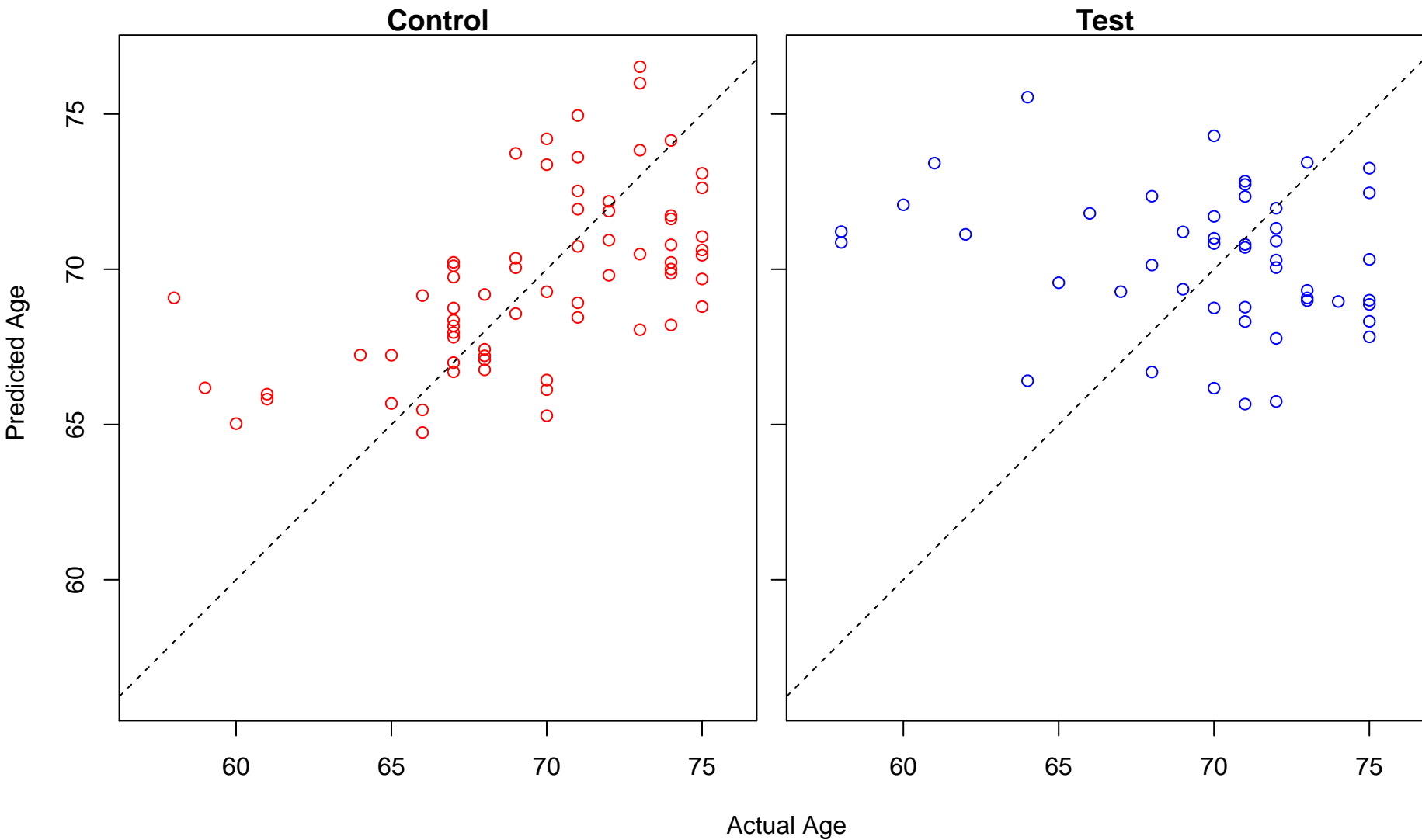
negative regulation of histone H3–K9 methylation (Score: 1.067234)



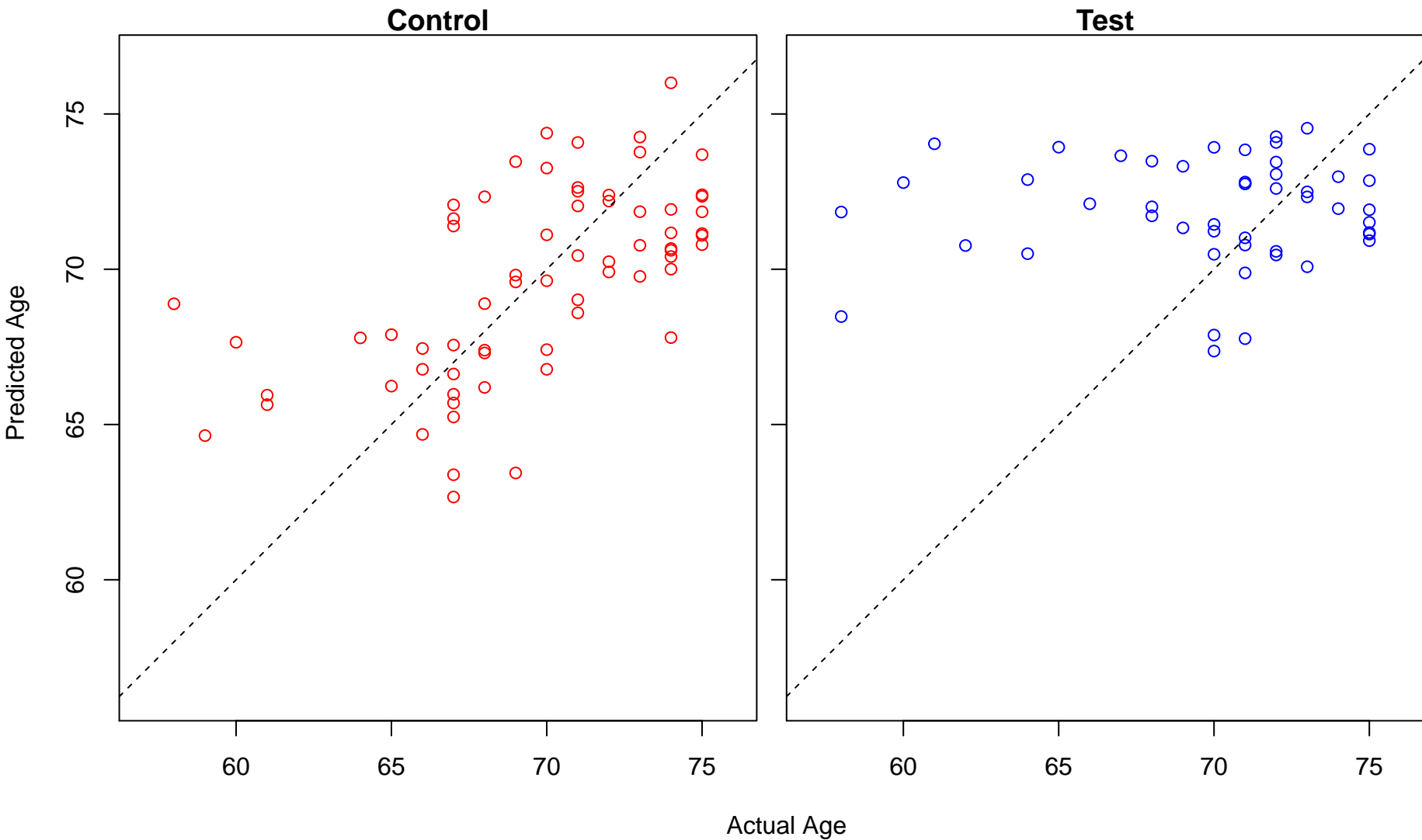
positive regulation of lamellipodium assembly (Score: 1.066903)



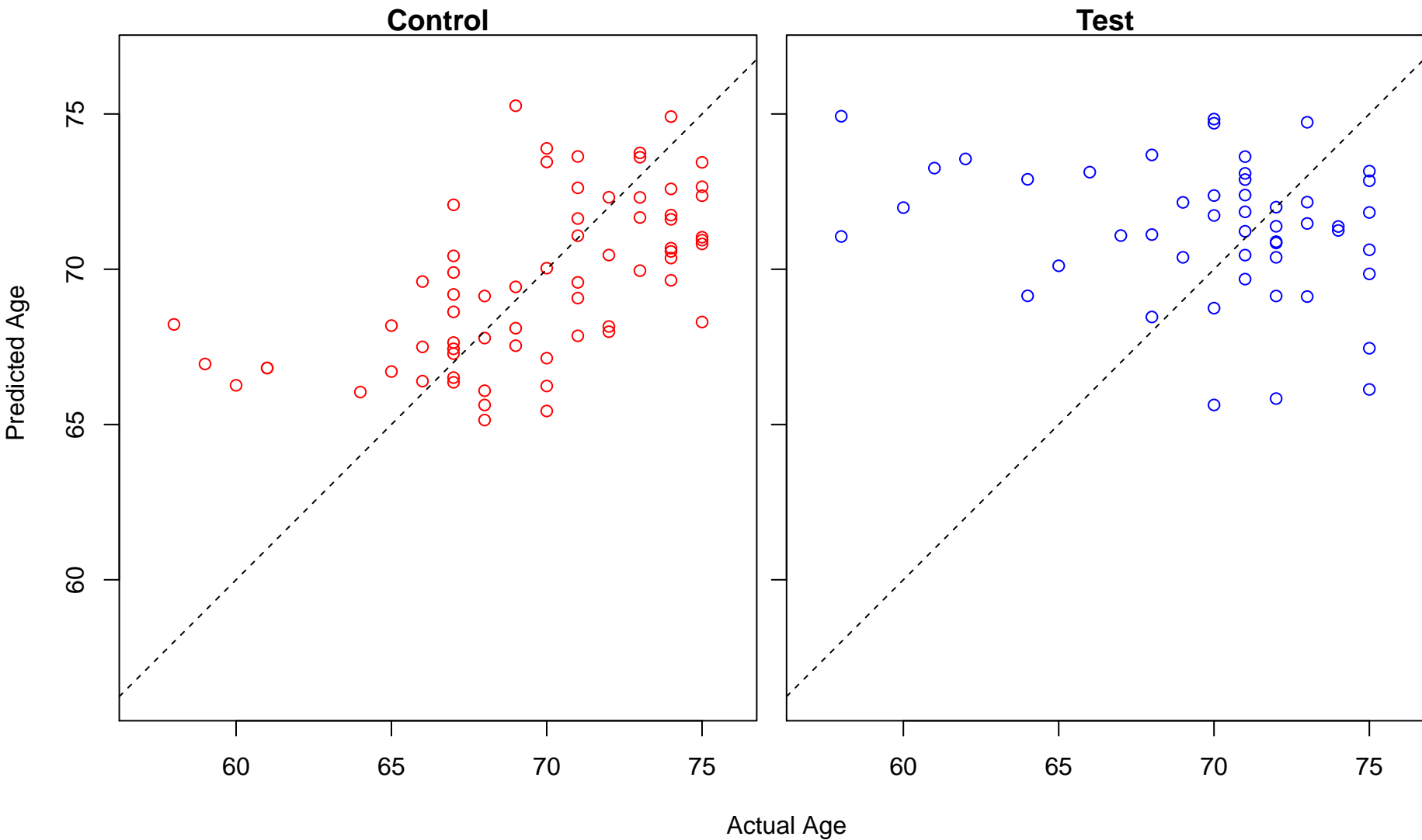
androgen receptor signaling pathway (Score: 1.066872)



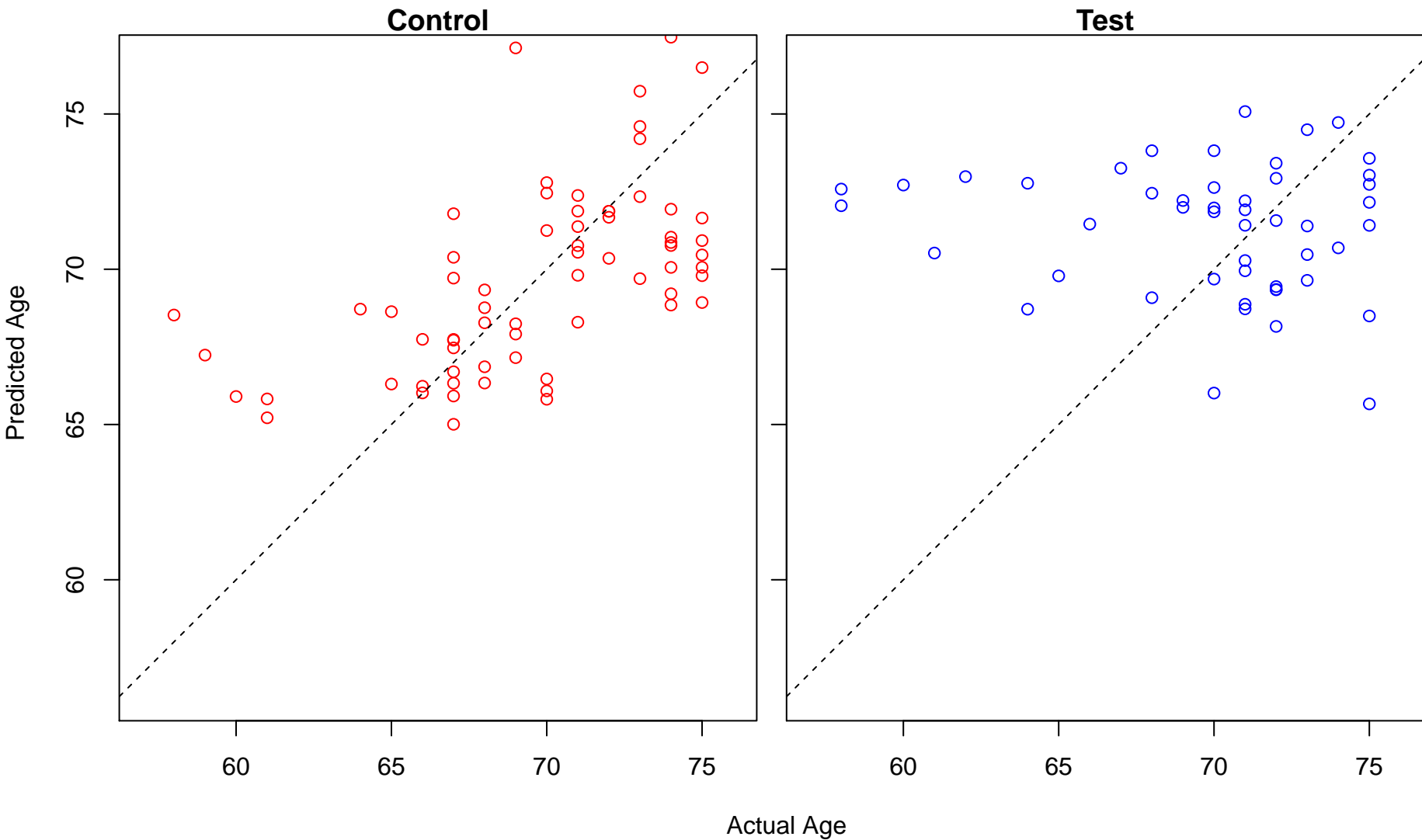
meiosis I (Score: 1.066865)



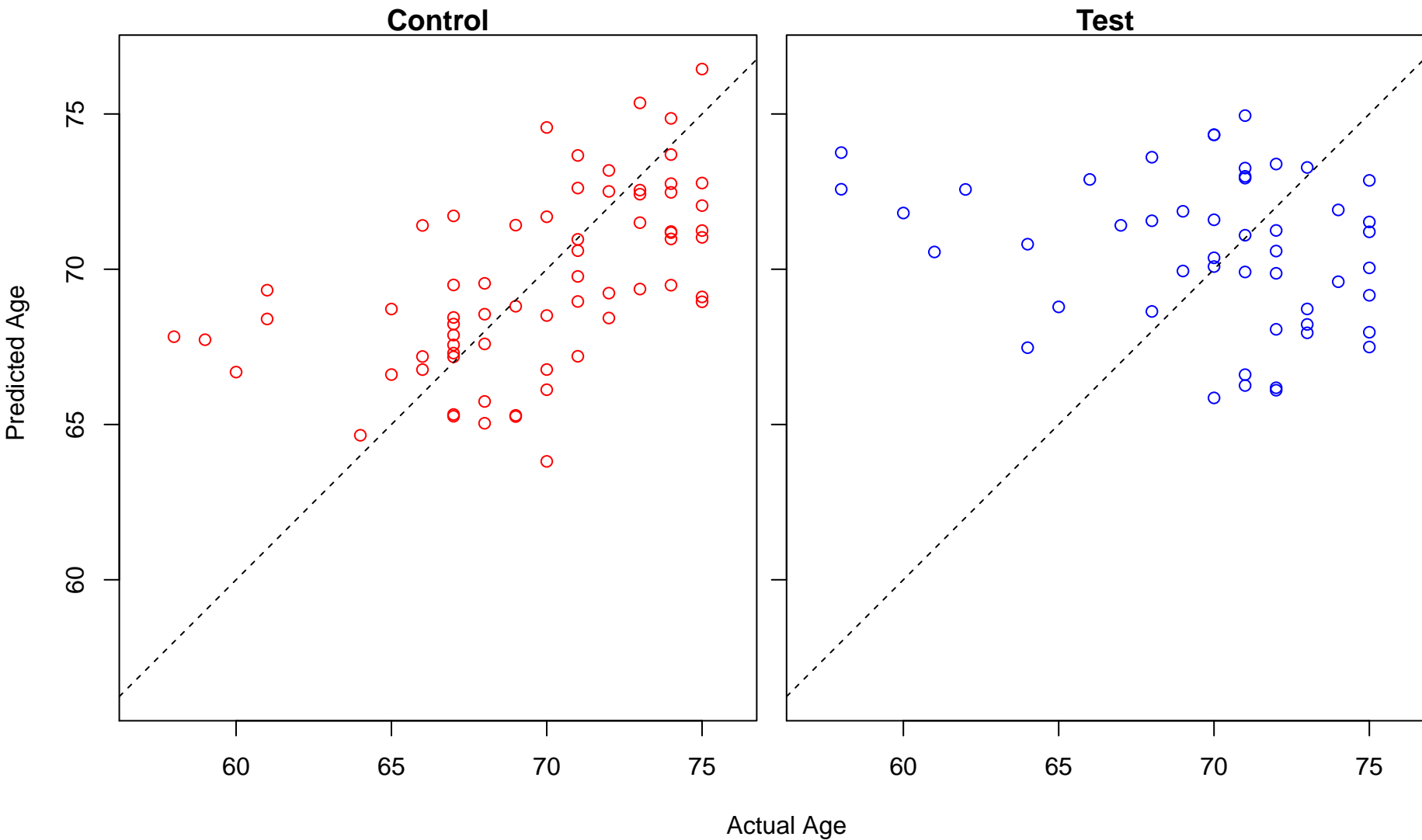
vesicle coating (Score: 1.066817)



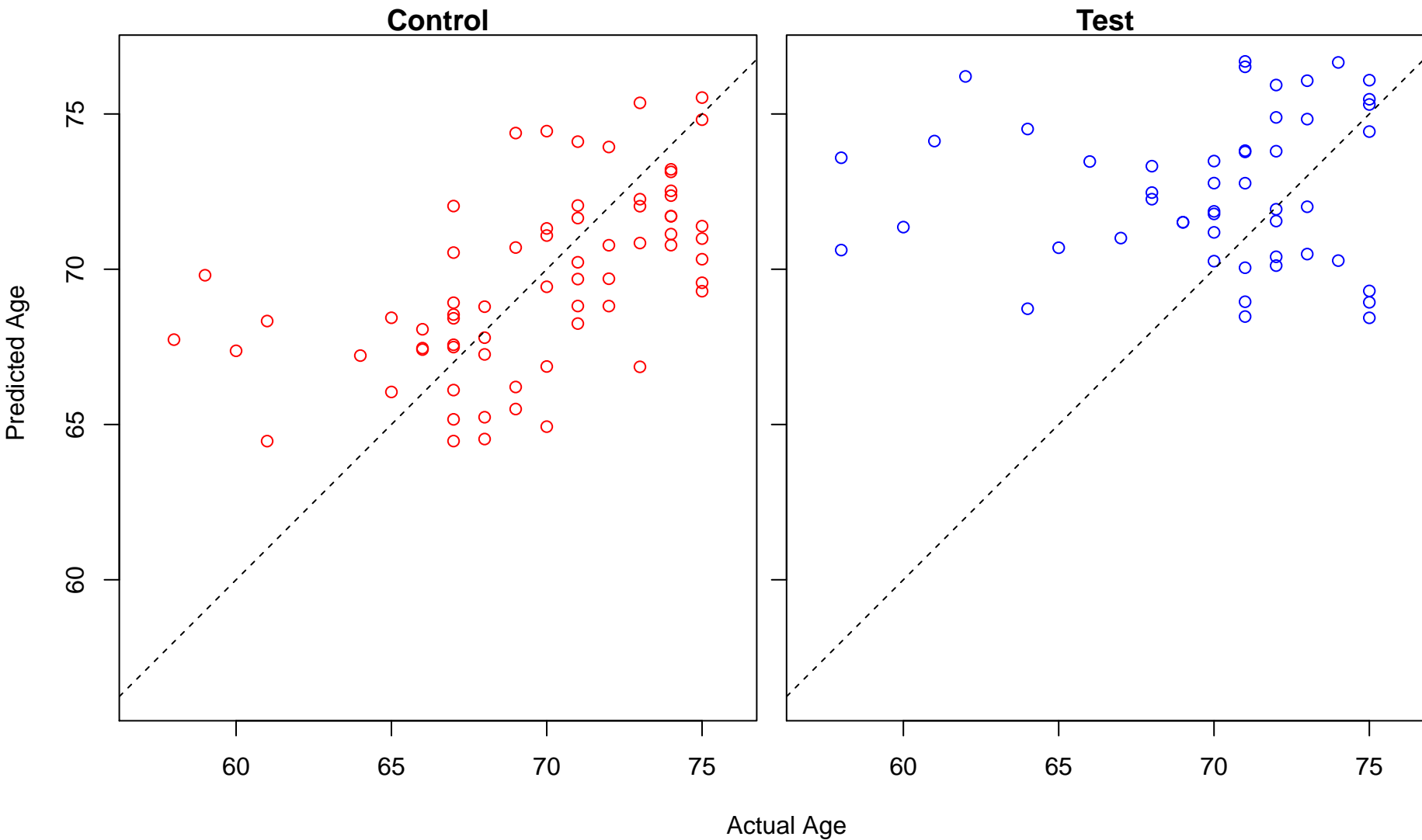
cell growth (Score: 1.066340)



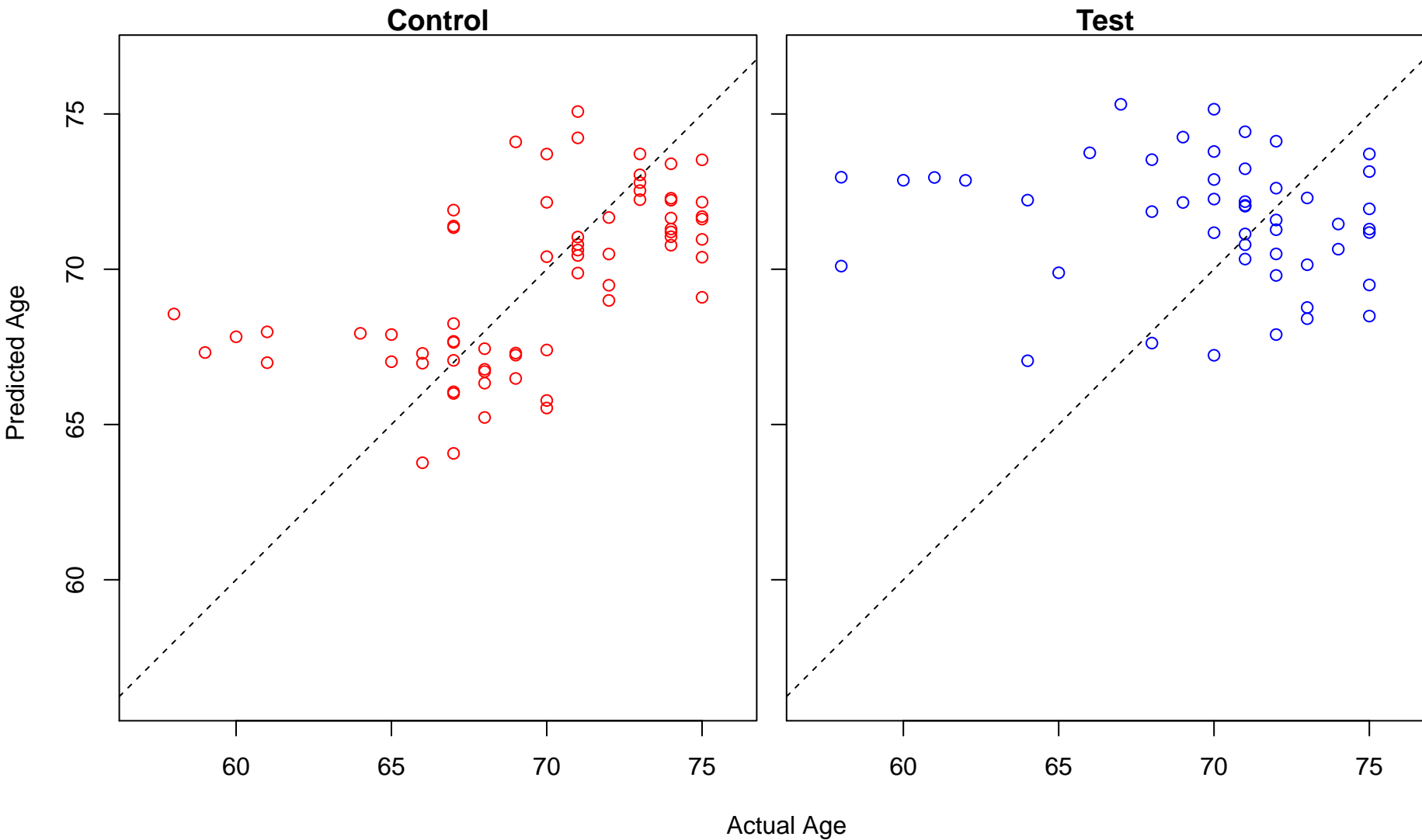
establishment of protein localization to Golgi (Score: 1.065948)



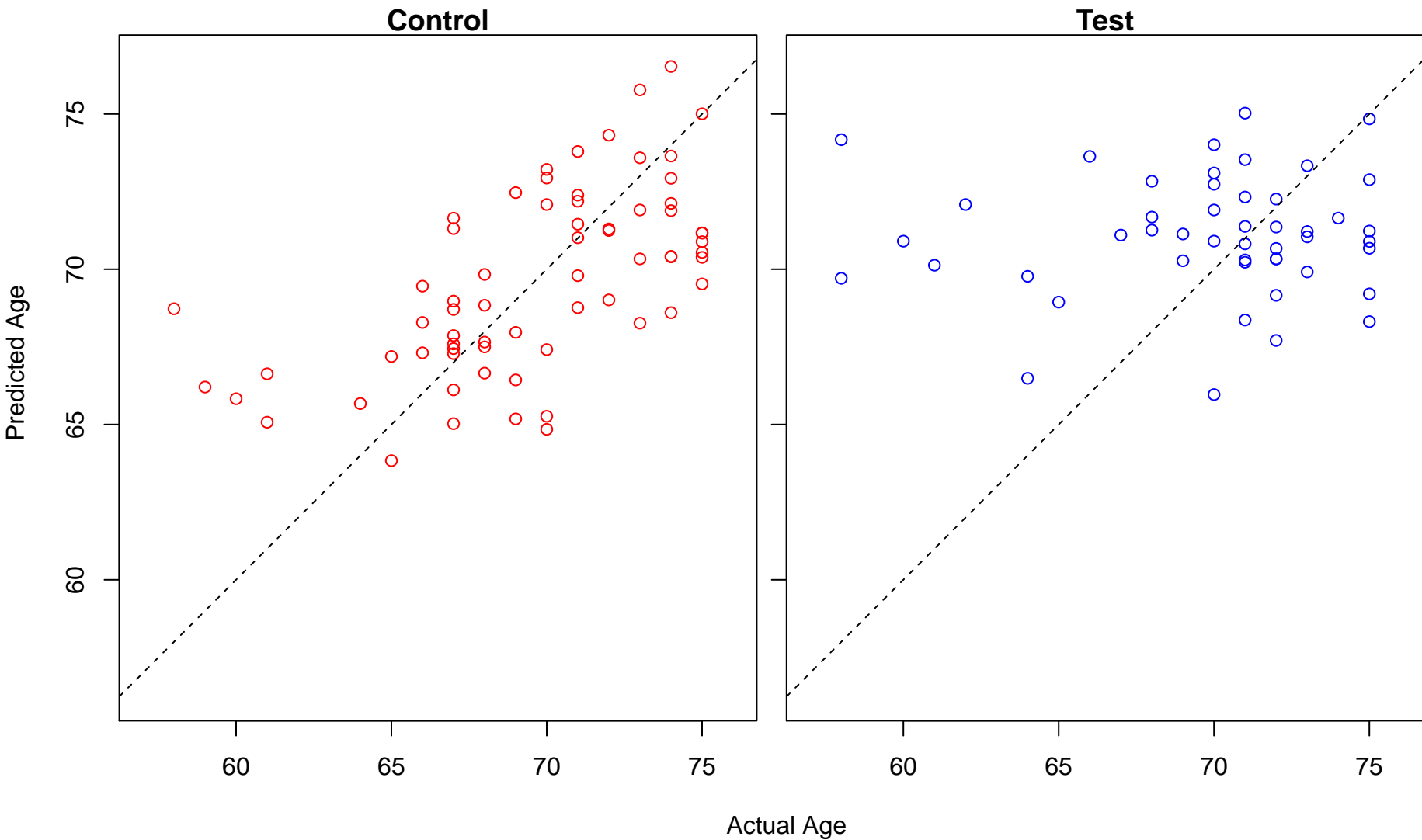
glutathione metabolic process (Score: 1.065323)



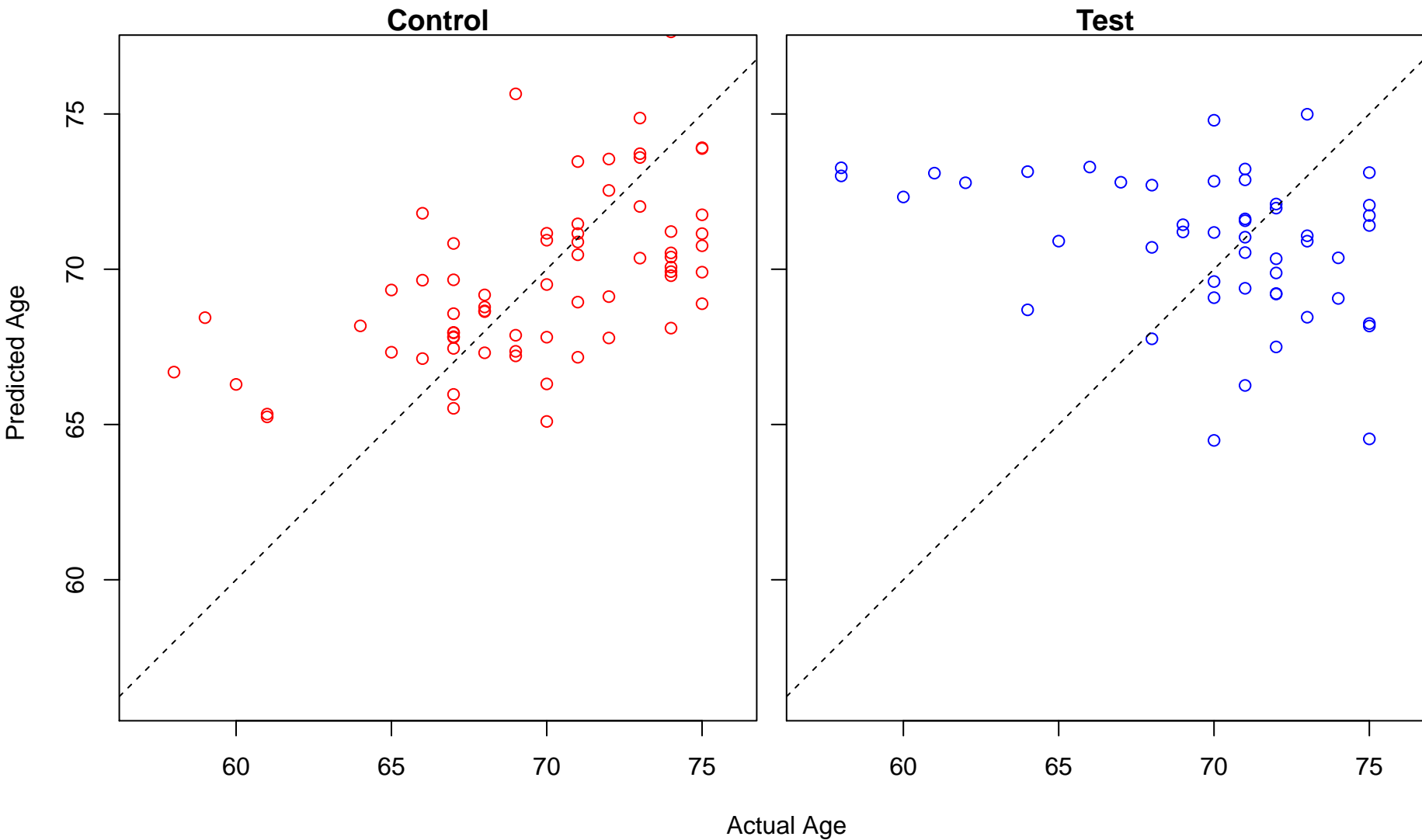
positive regulation of interleukin-2 production (Score: 1.064998)



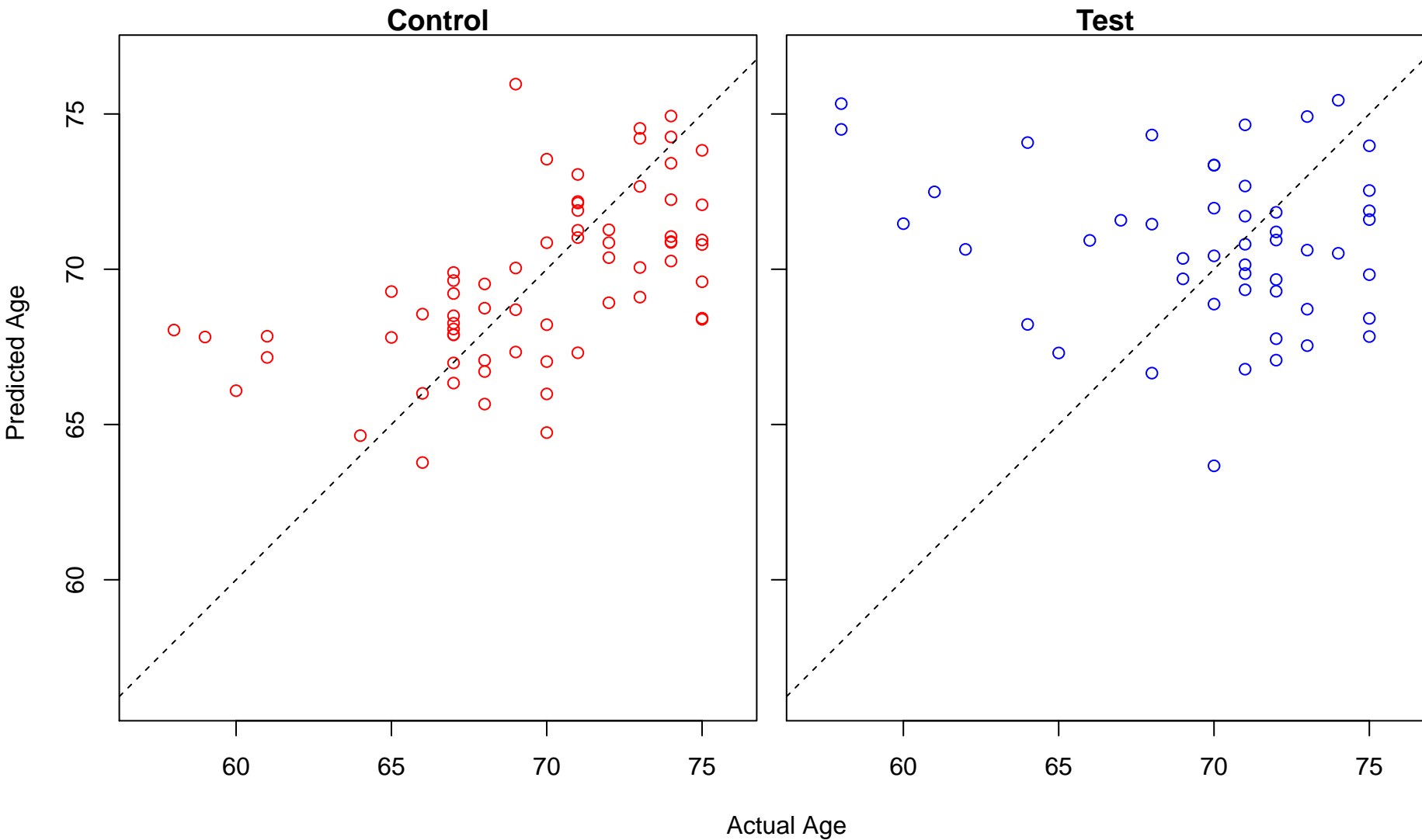
cell-substrate adhesion (Score: 1.064826)



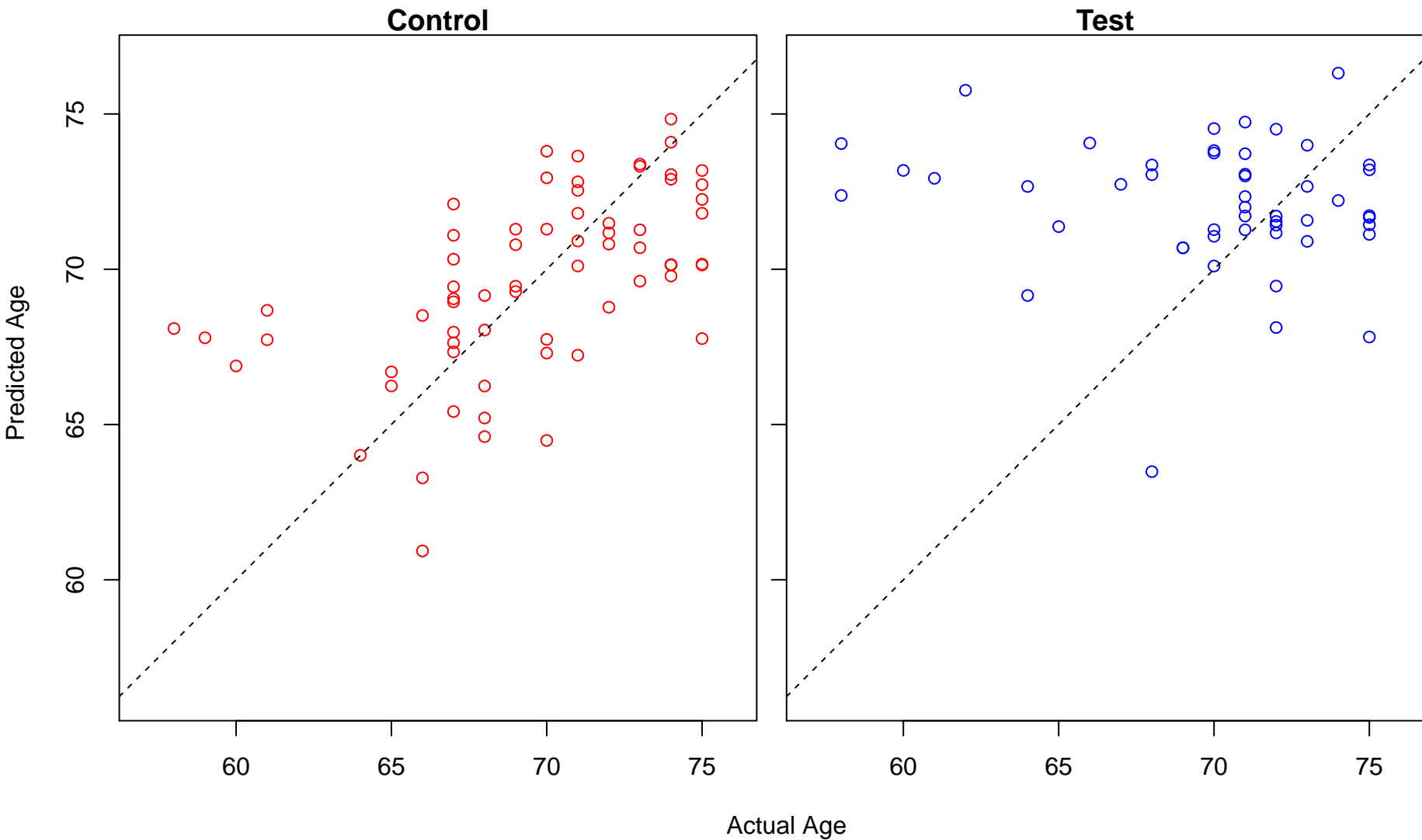
negative regulation of organ growth (Score: 1.063703)



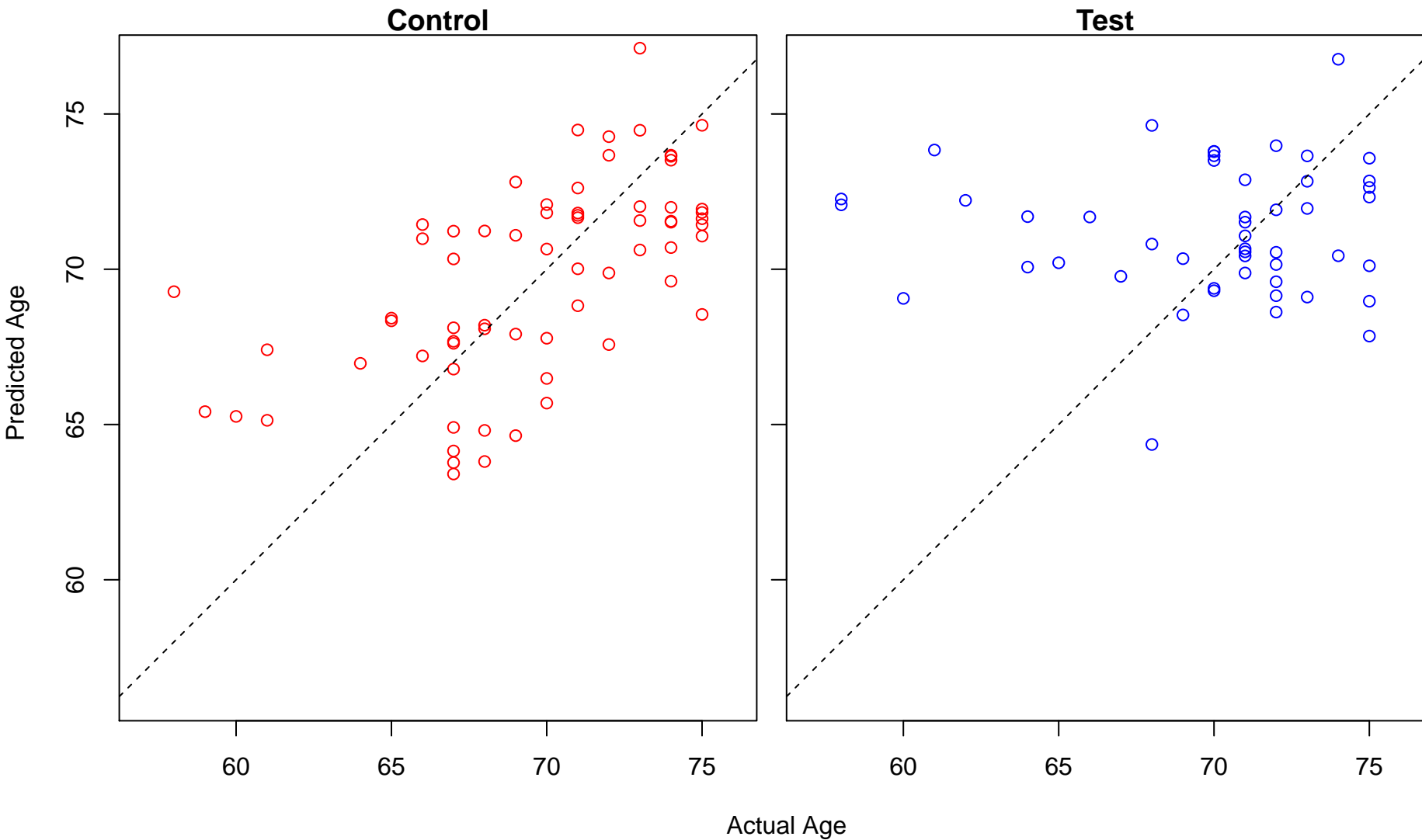
heparan sulfate proteoglycan metabolic process (Score: 1.063147)



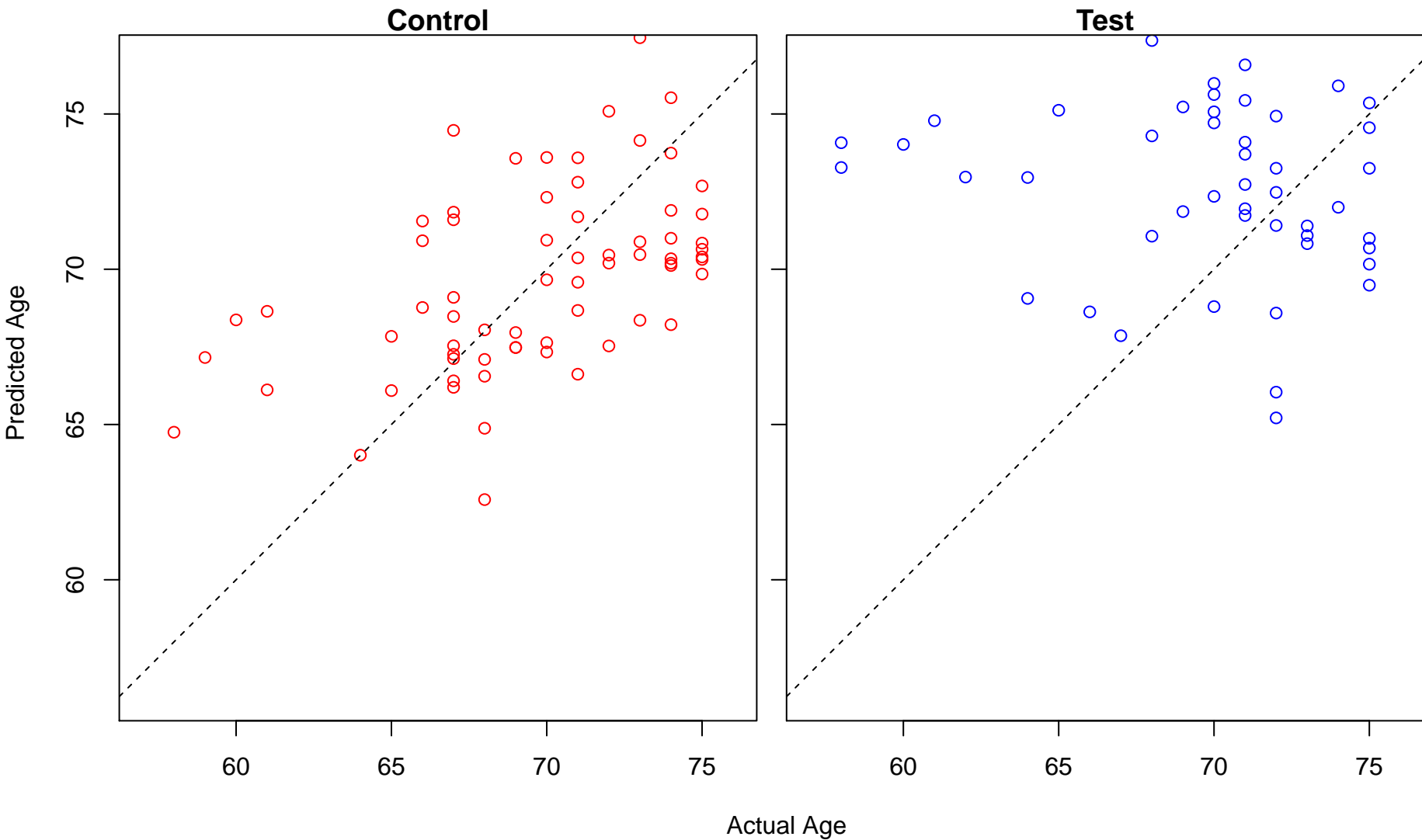
regulation of necroptotic process (Score: 1.062909)



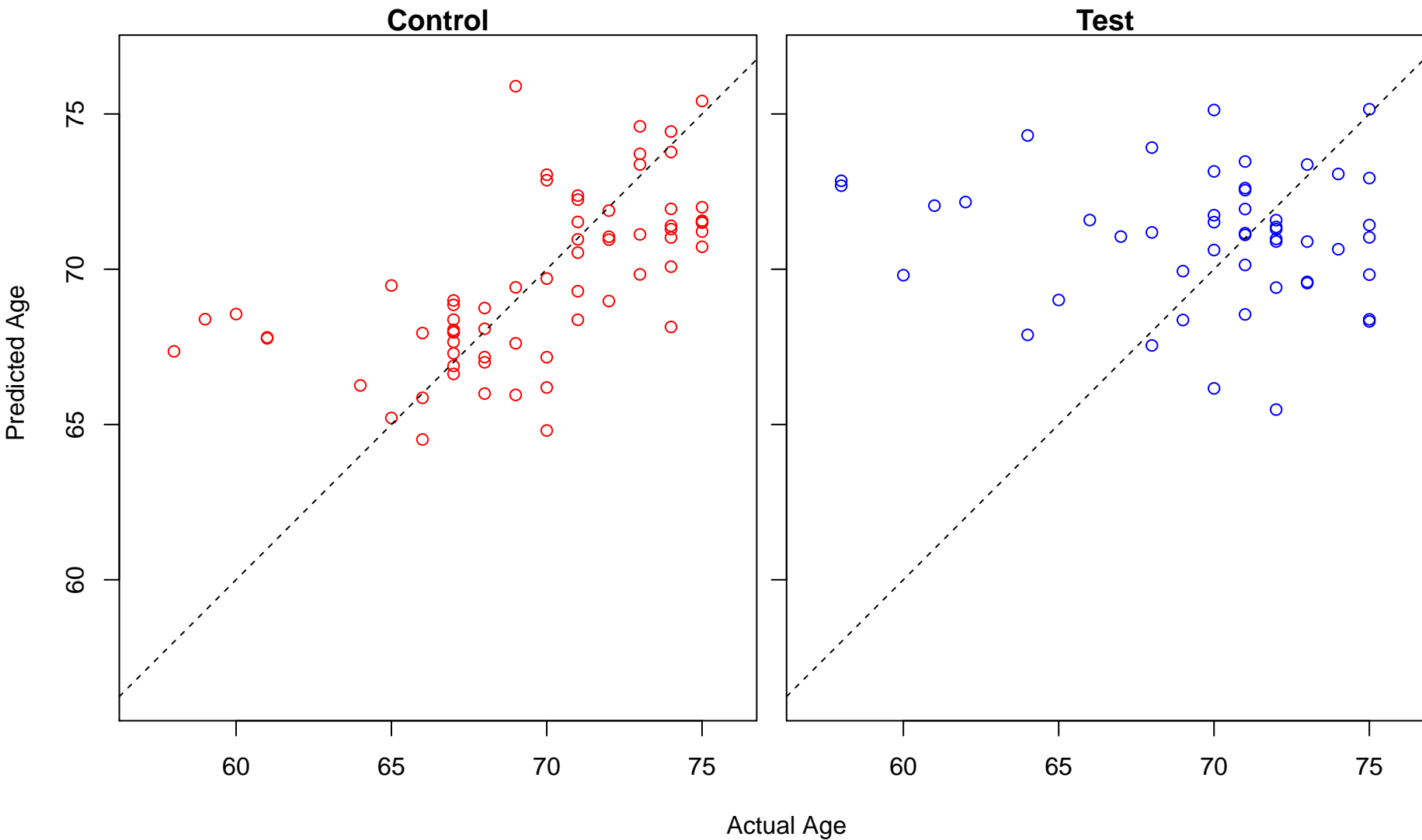
heme biosynthetic process (Score: 1.062729)



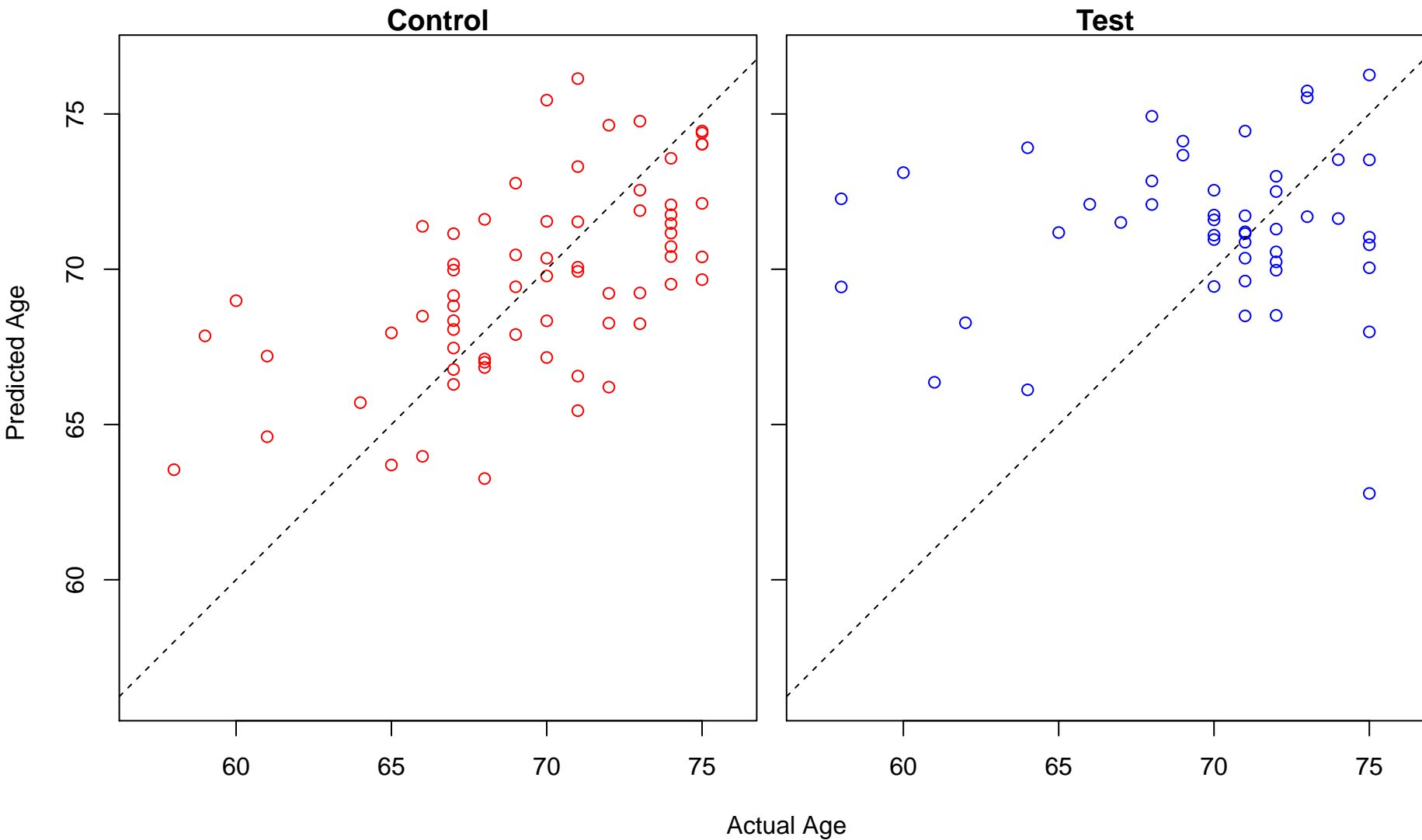
transmission of nerve impulse (Score: 1.062698)



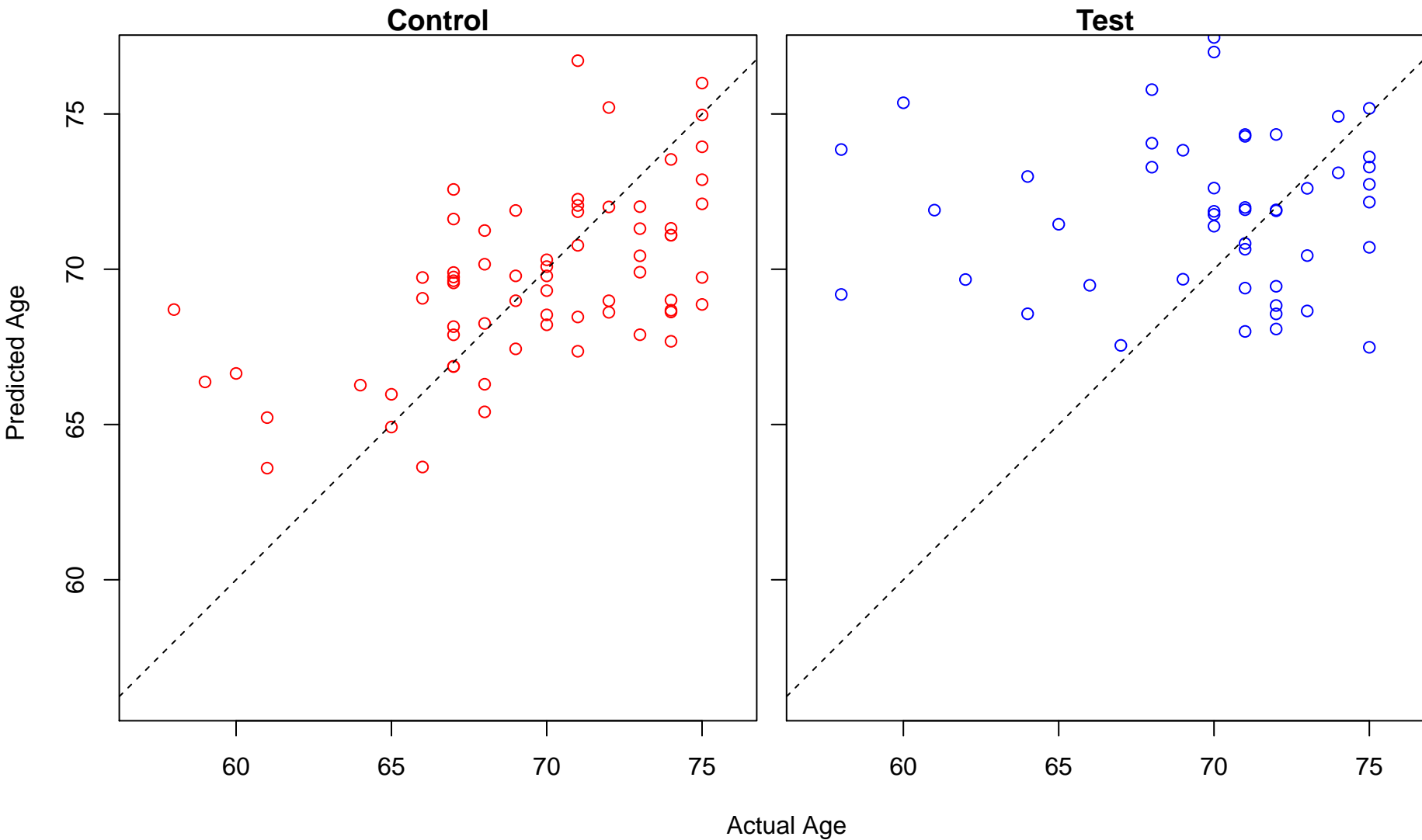
establishment of spindle localization (Score: 1.062054)



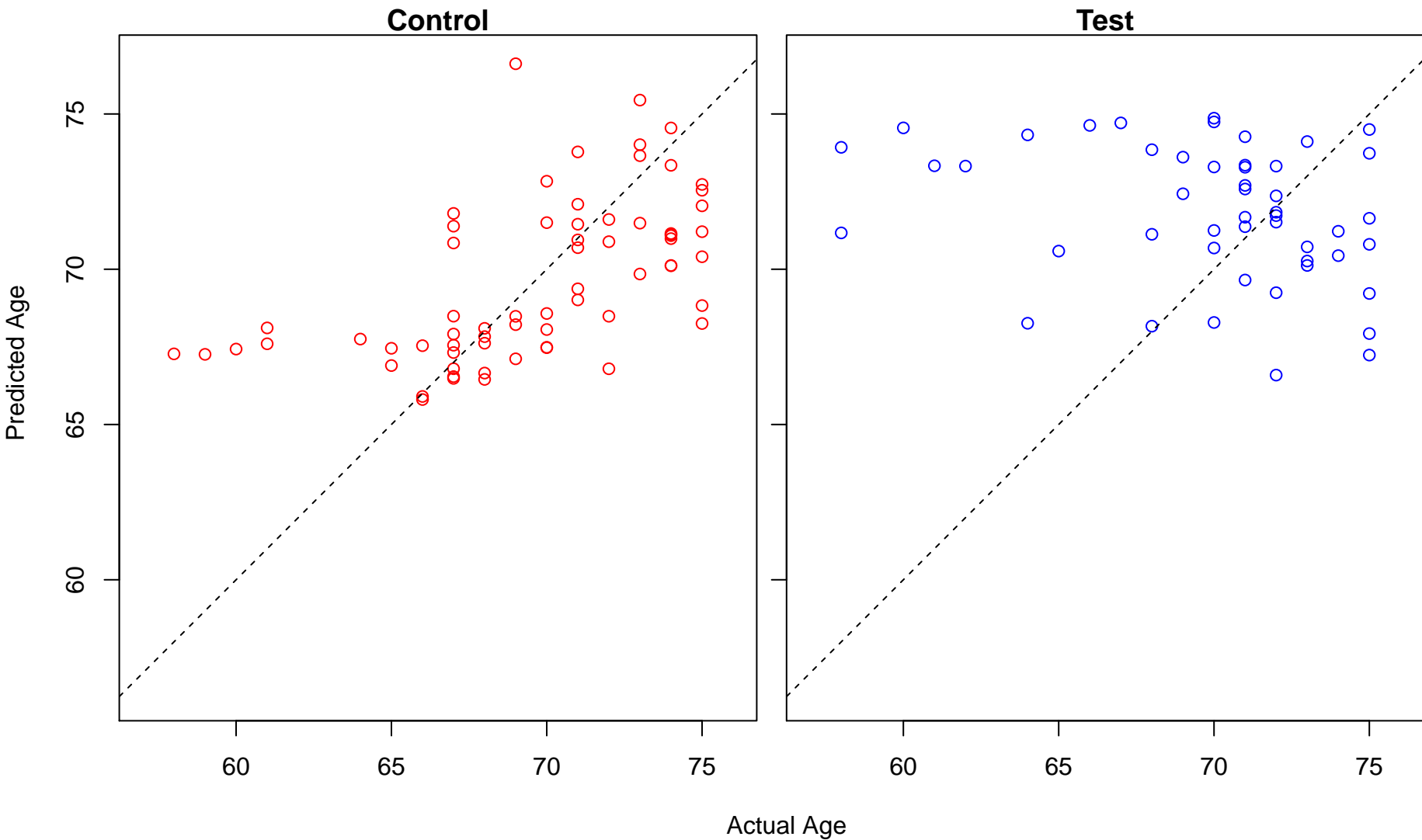
interleukin-1 beta production (Score: 1.062016)



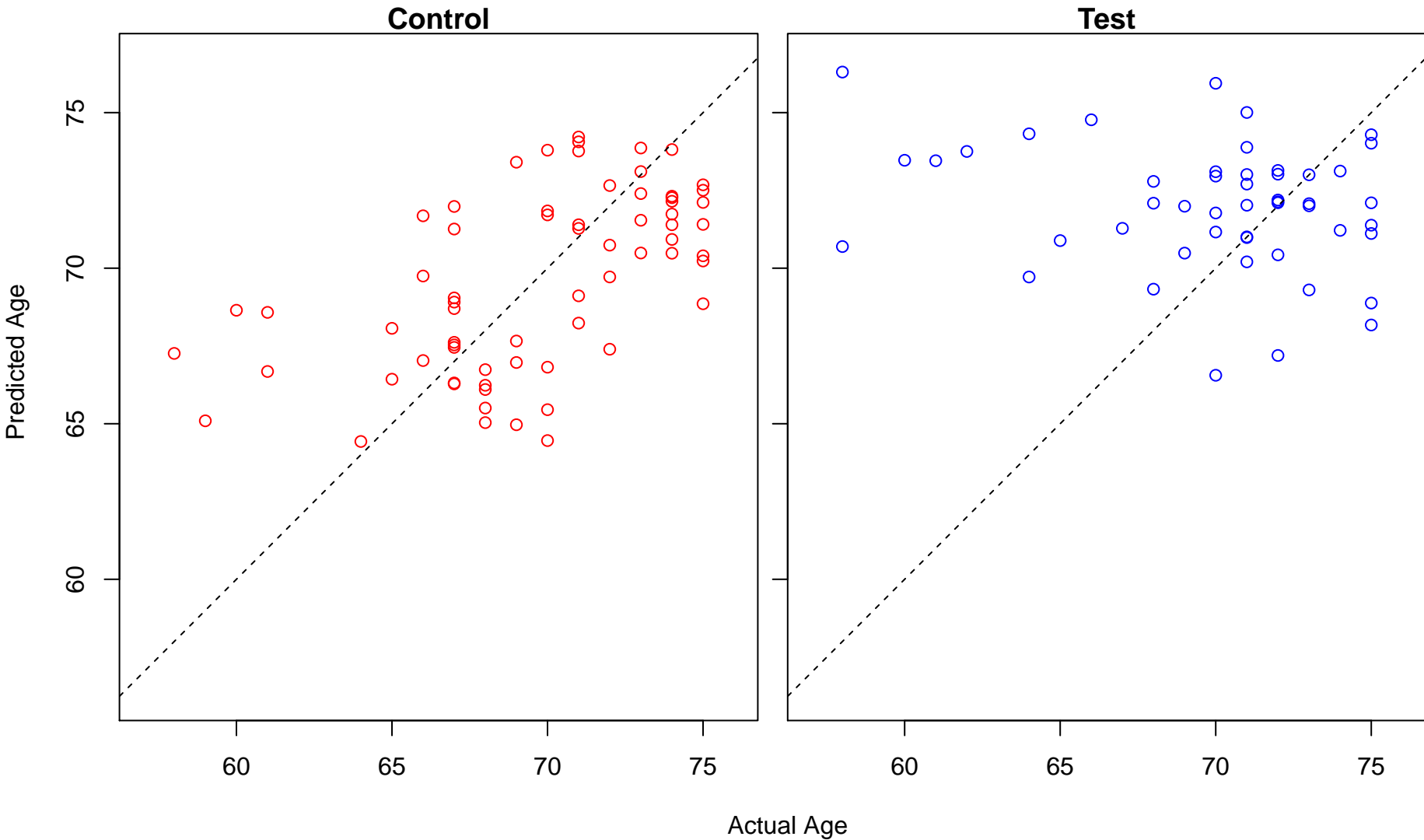
response to ATP (Score: 1.061687)



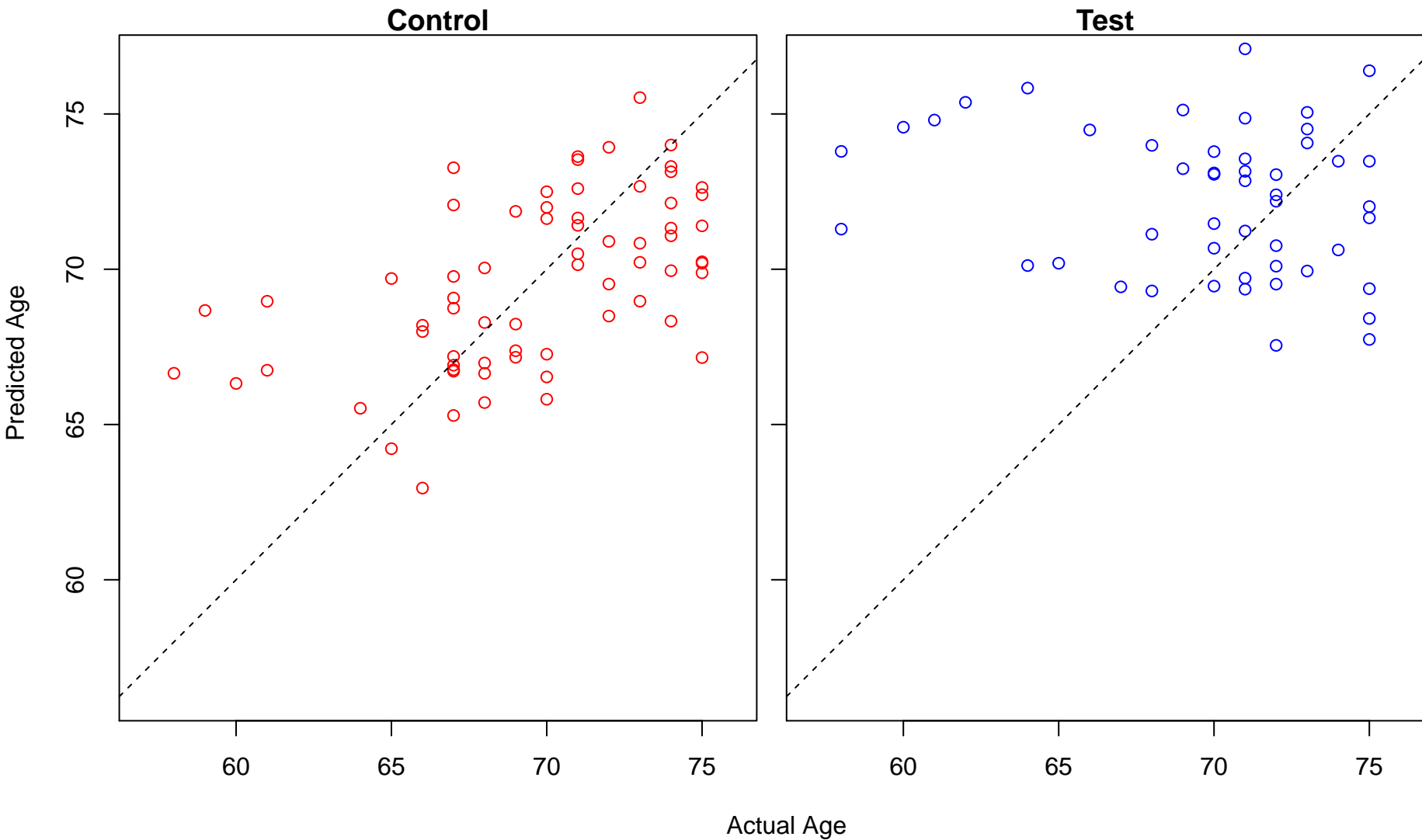
regulation of T-helper 2 cell differentiation (Score: 1.061673)



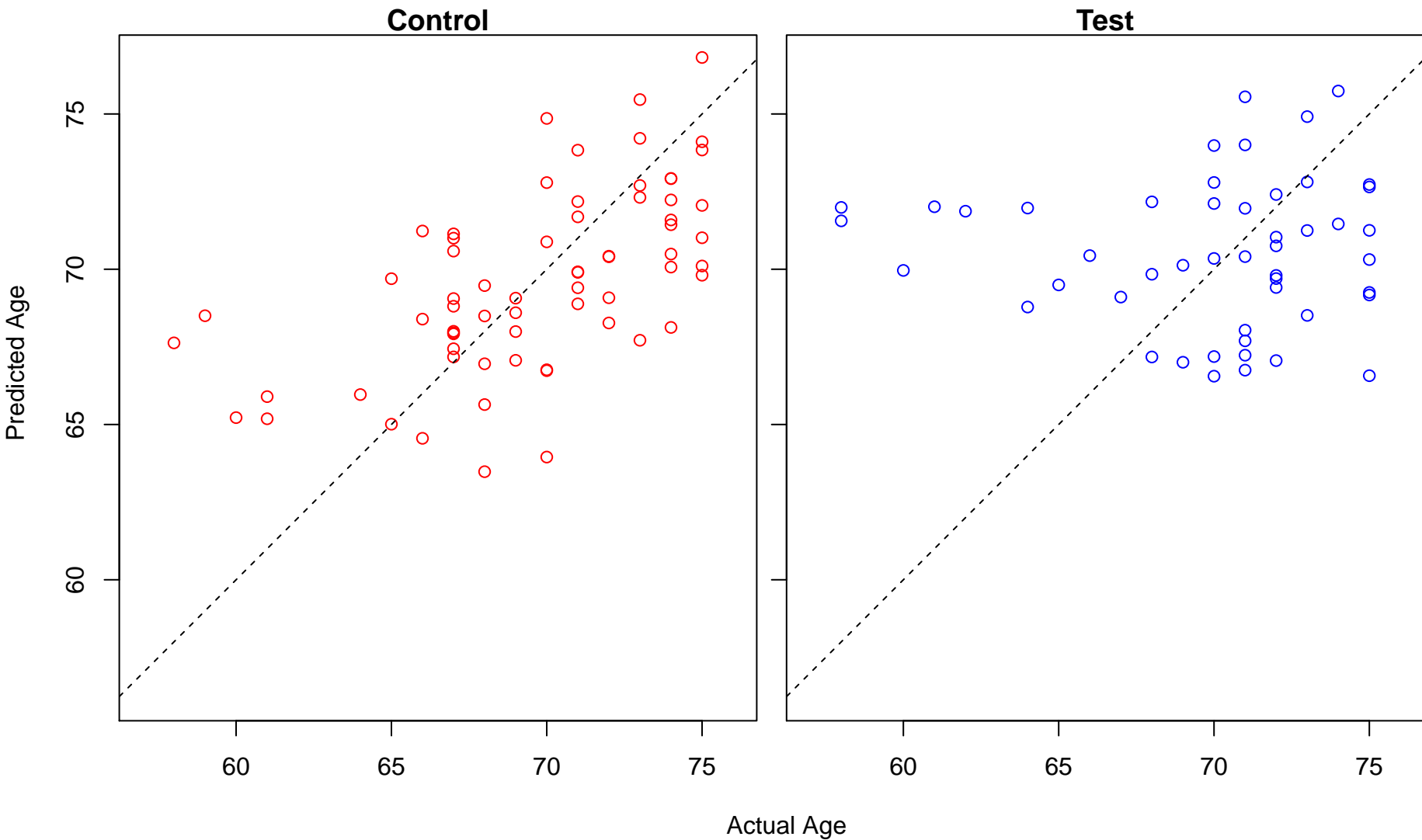
sulfur compound catabolic process (Score: 1.061400)



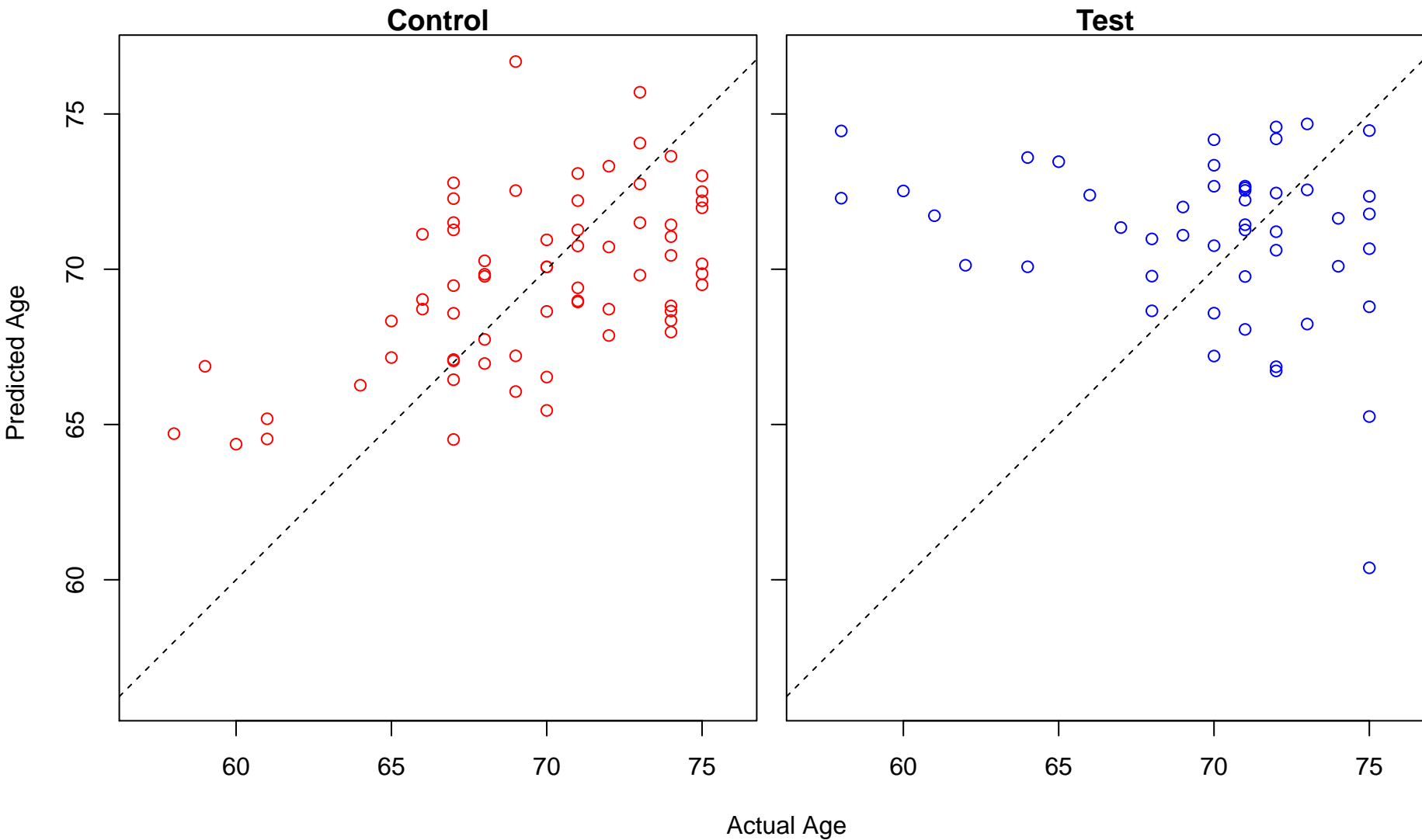
myoblast differentiation (Score: 1.061239)



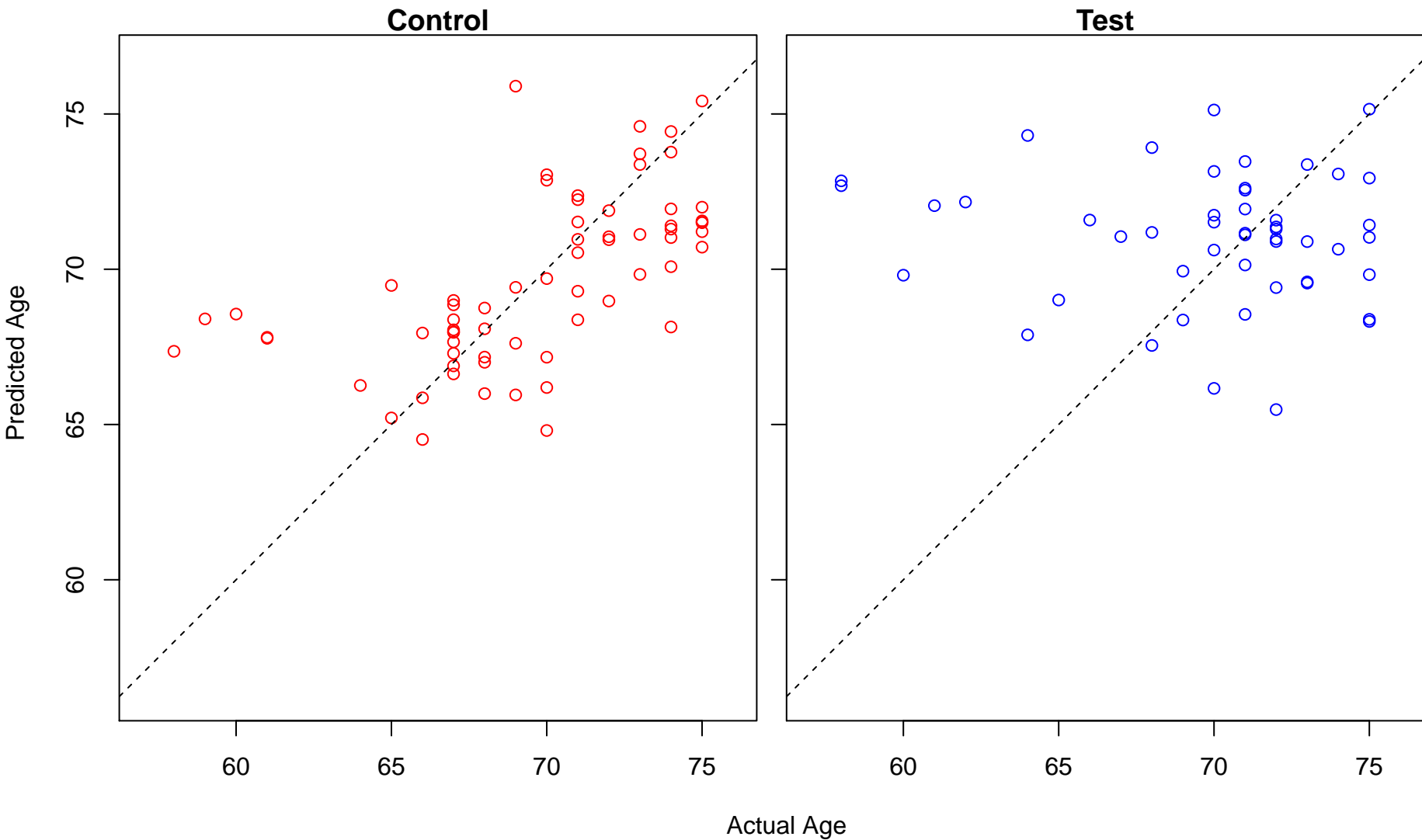
negative regulation of actin filament polymerization (Score: 1.061162)



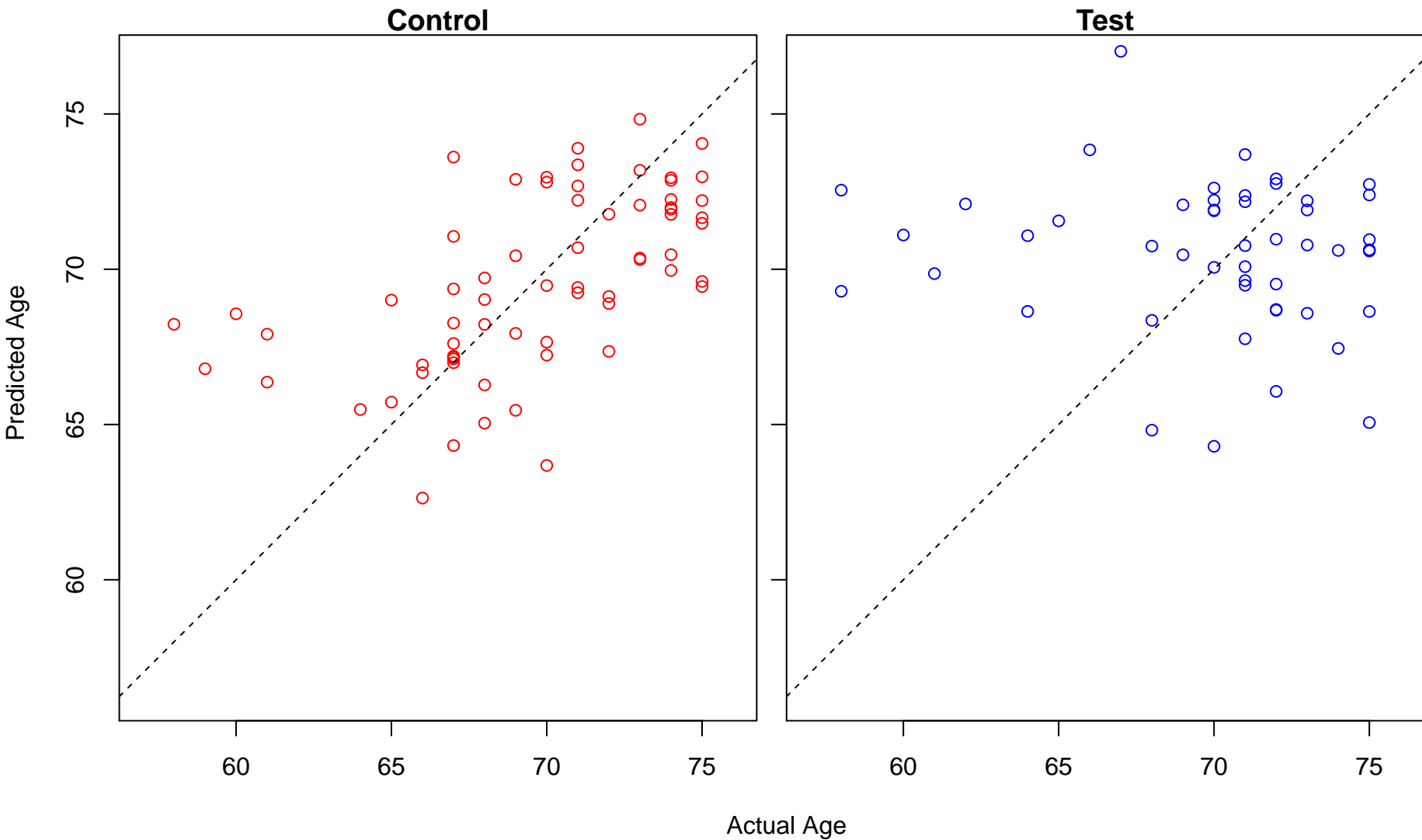
regulation of membrane repolarization (Score: 1.061149)



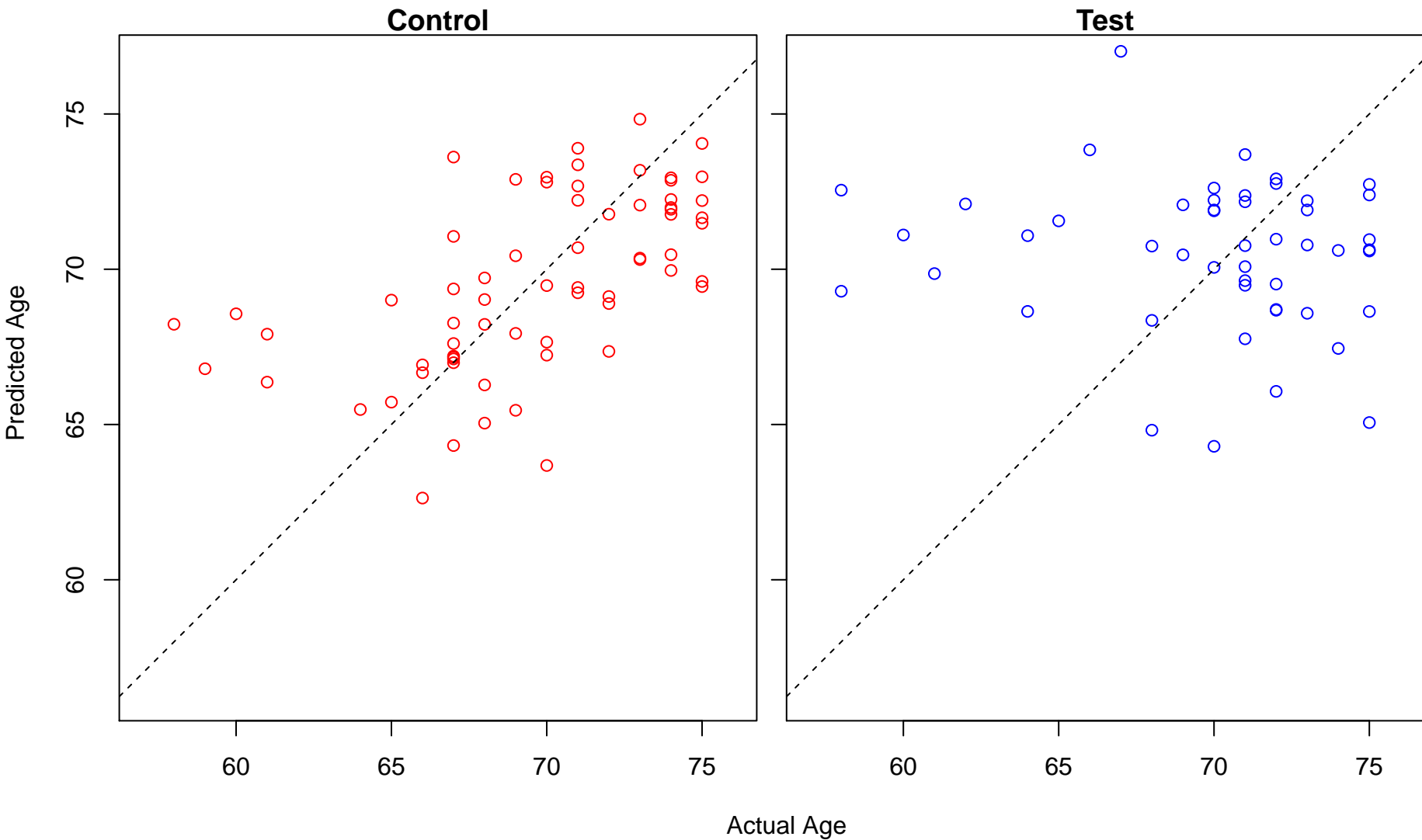
spindle localization (Score: 1.061092)



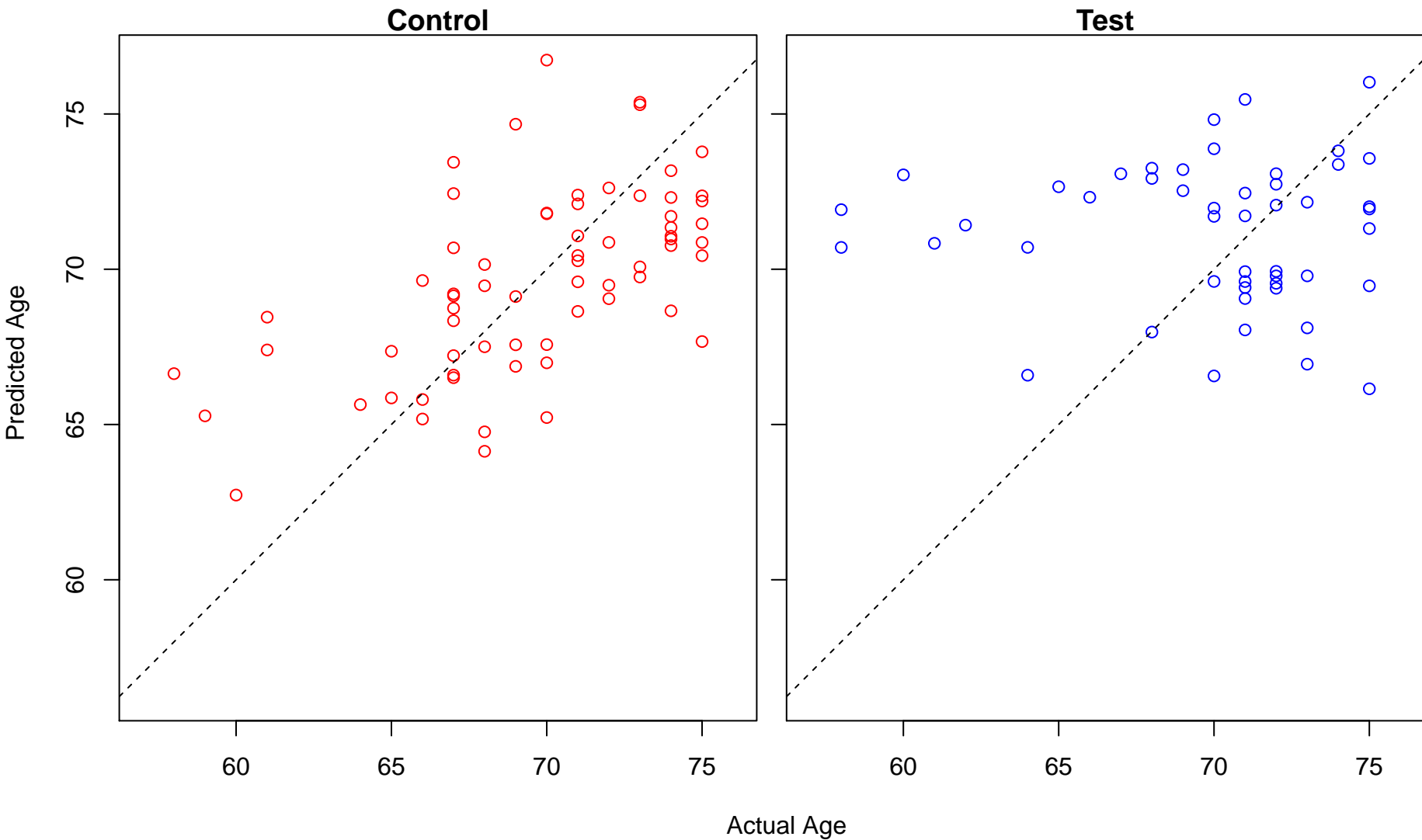
regulation of response to tumor cell (Score: 1.060744)



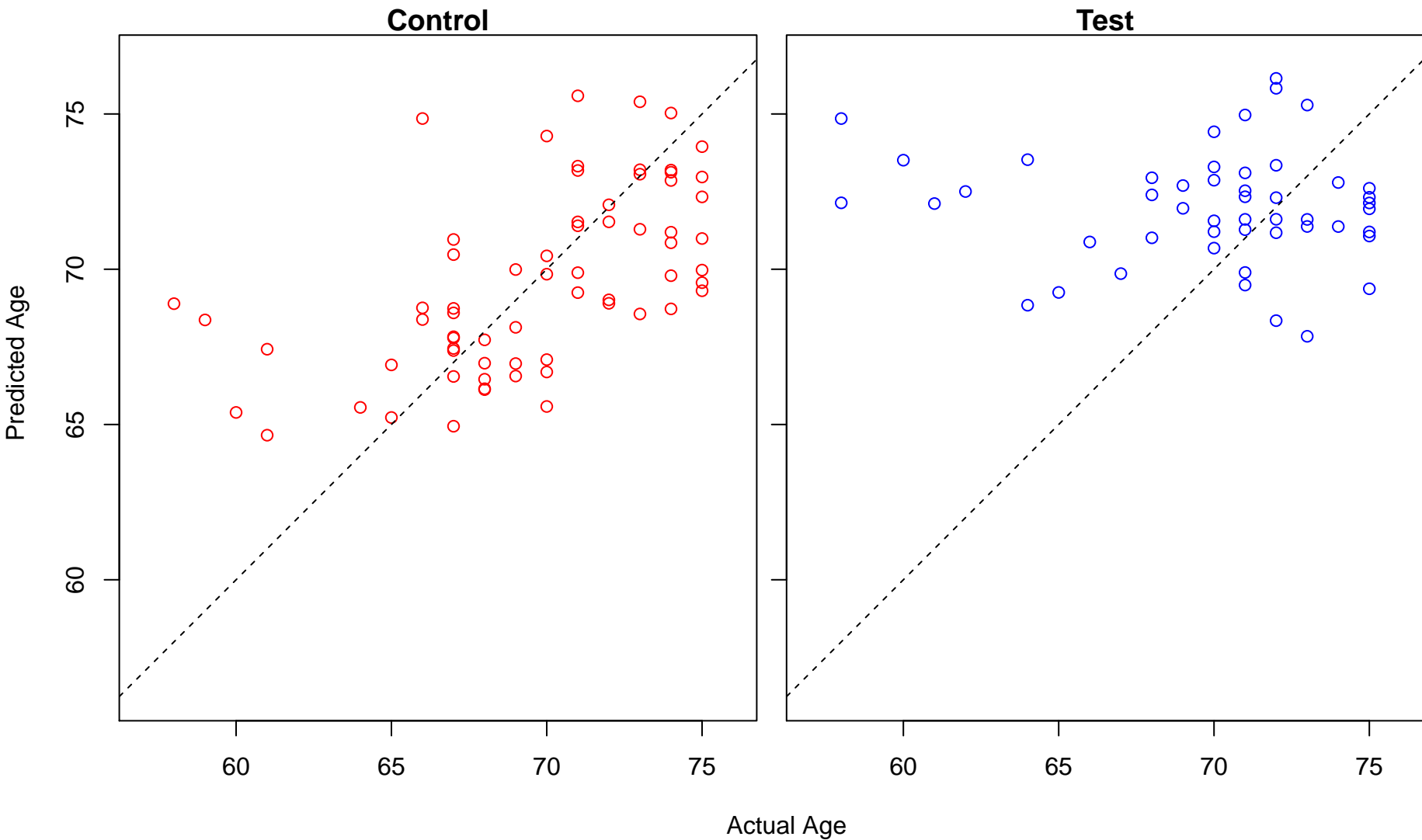
regulation of immune response to tumor cell (Score: 1.060744)



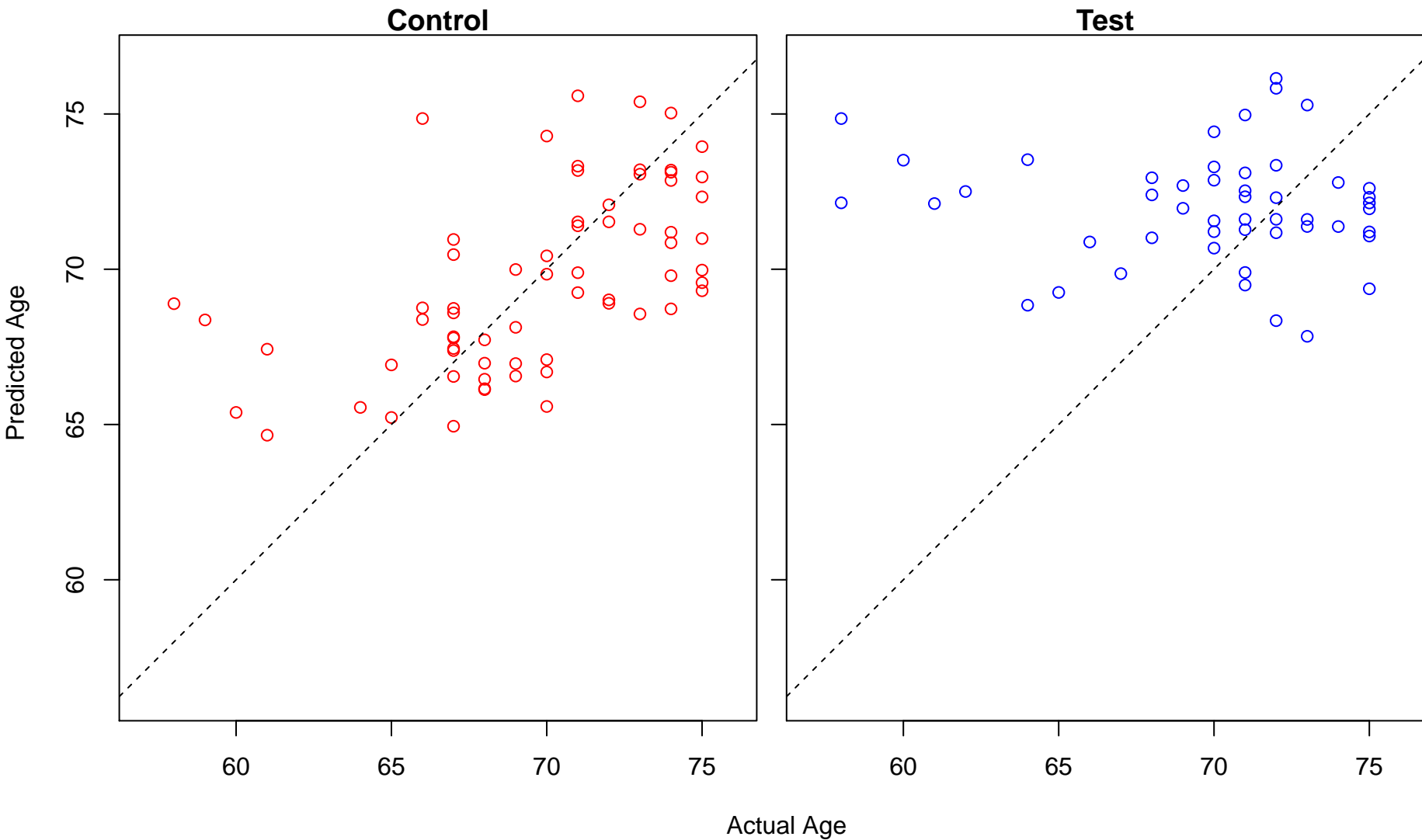
regulation of phospholipid metabolic process (Score: 1.060643)



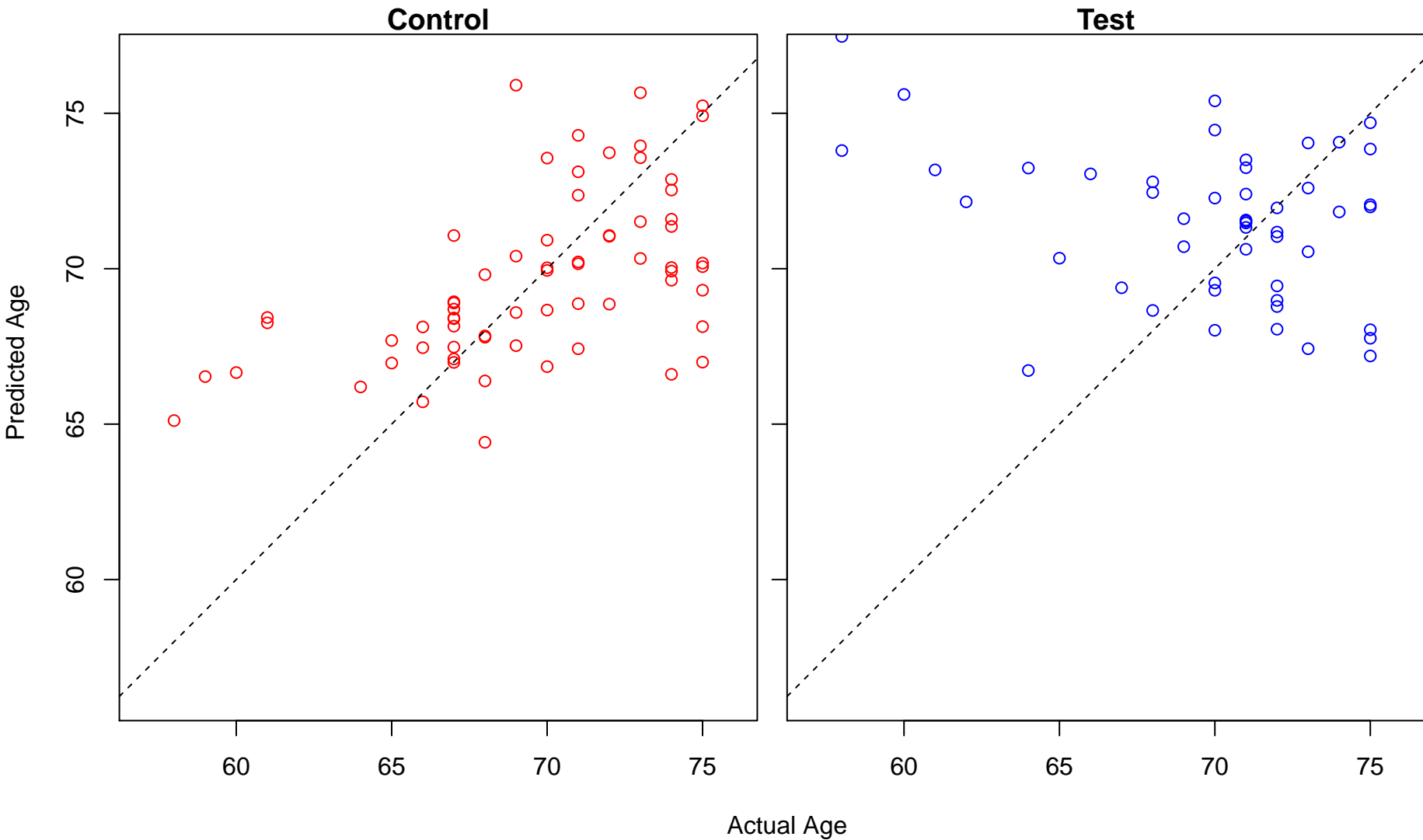
RNA destabilization (Score: 1.060395)



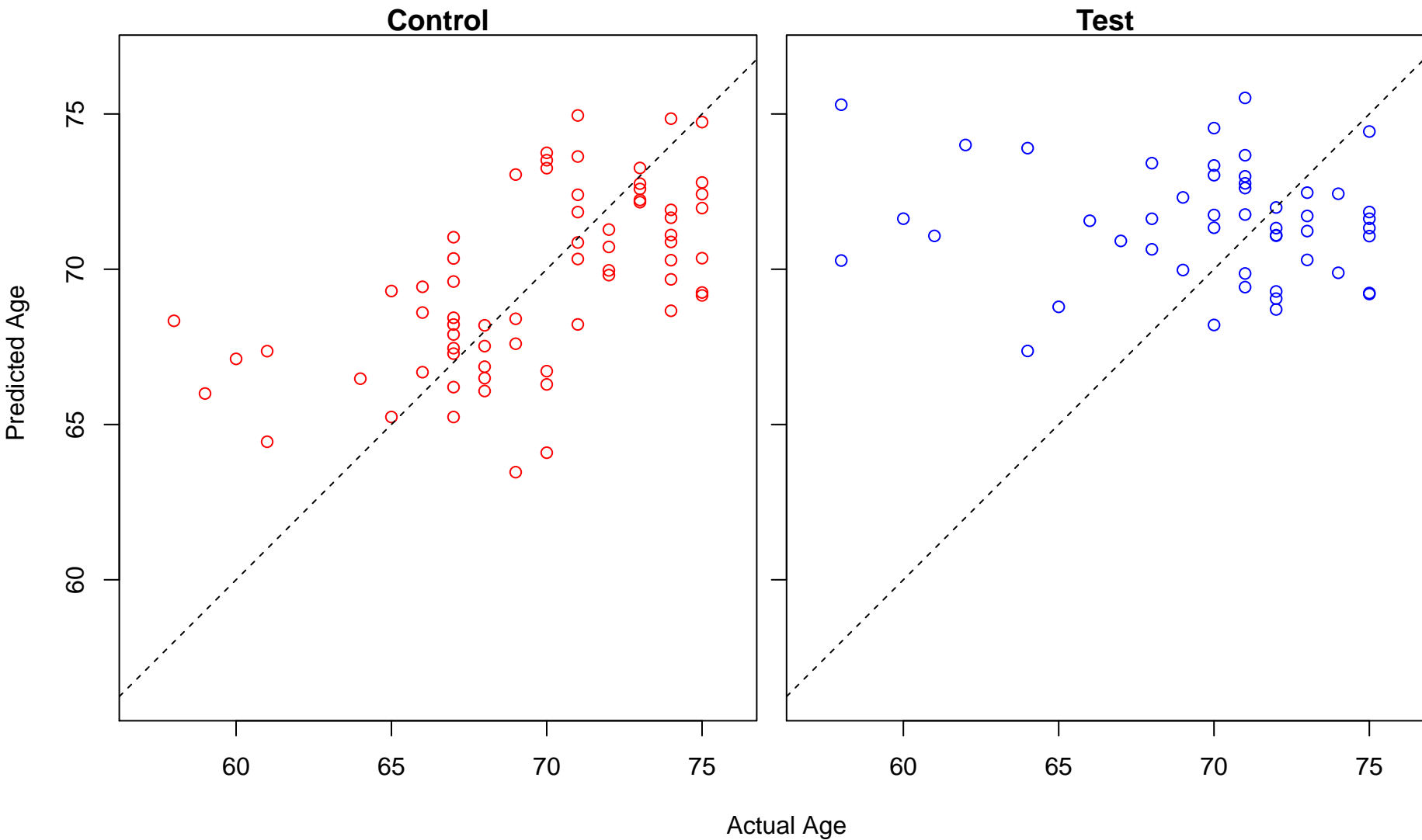
mRNA destabilization (Score: 1.060395)



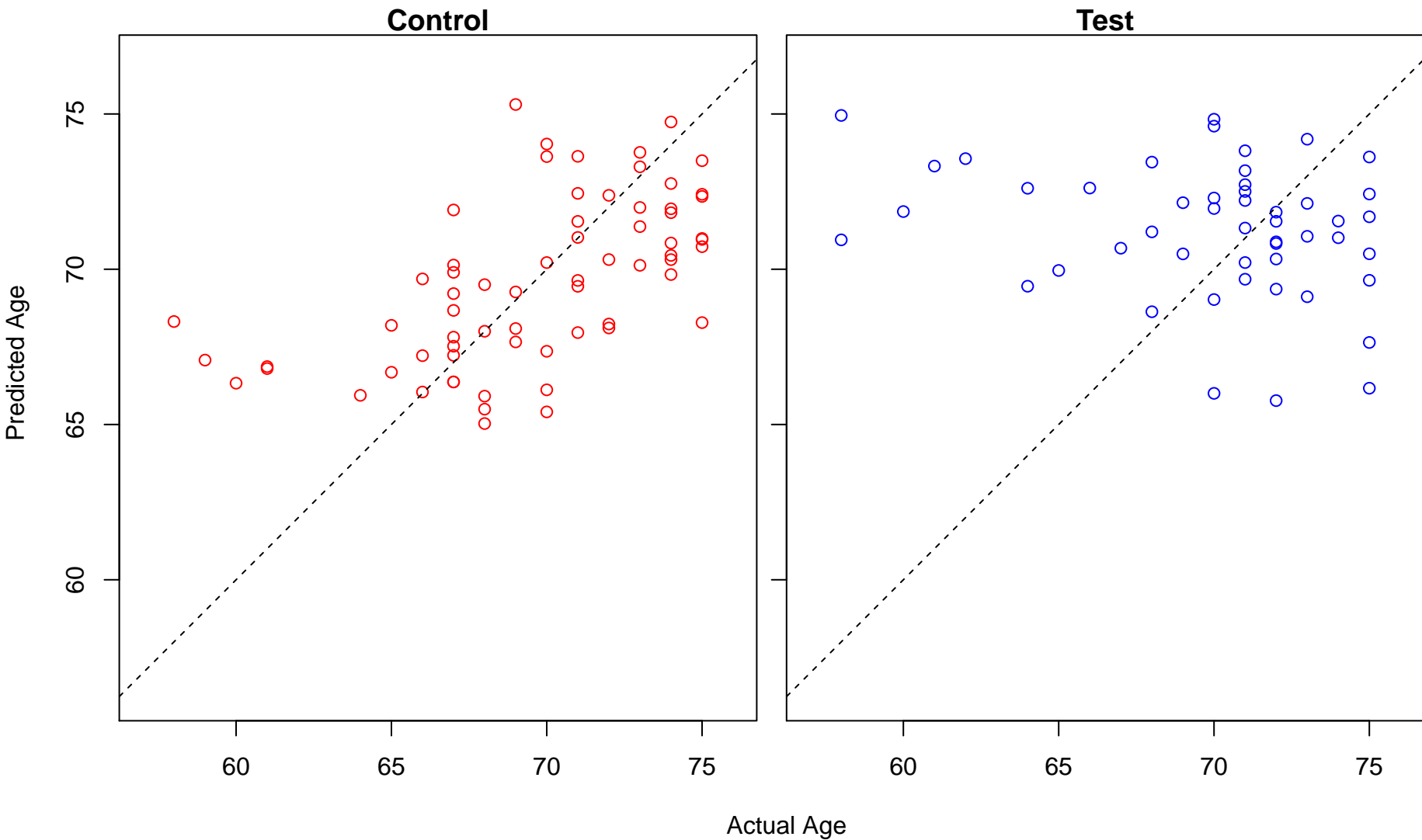
neuromuscular process controlling balance (Score: 1.060013)



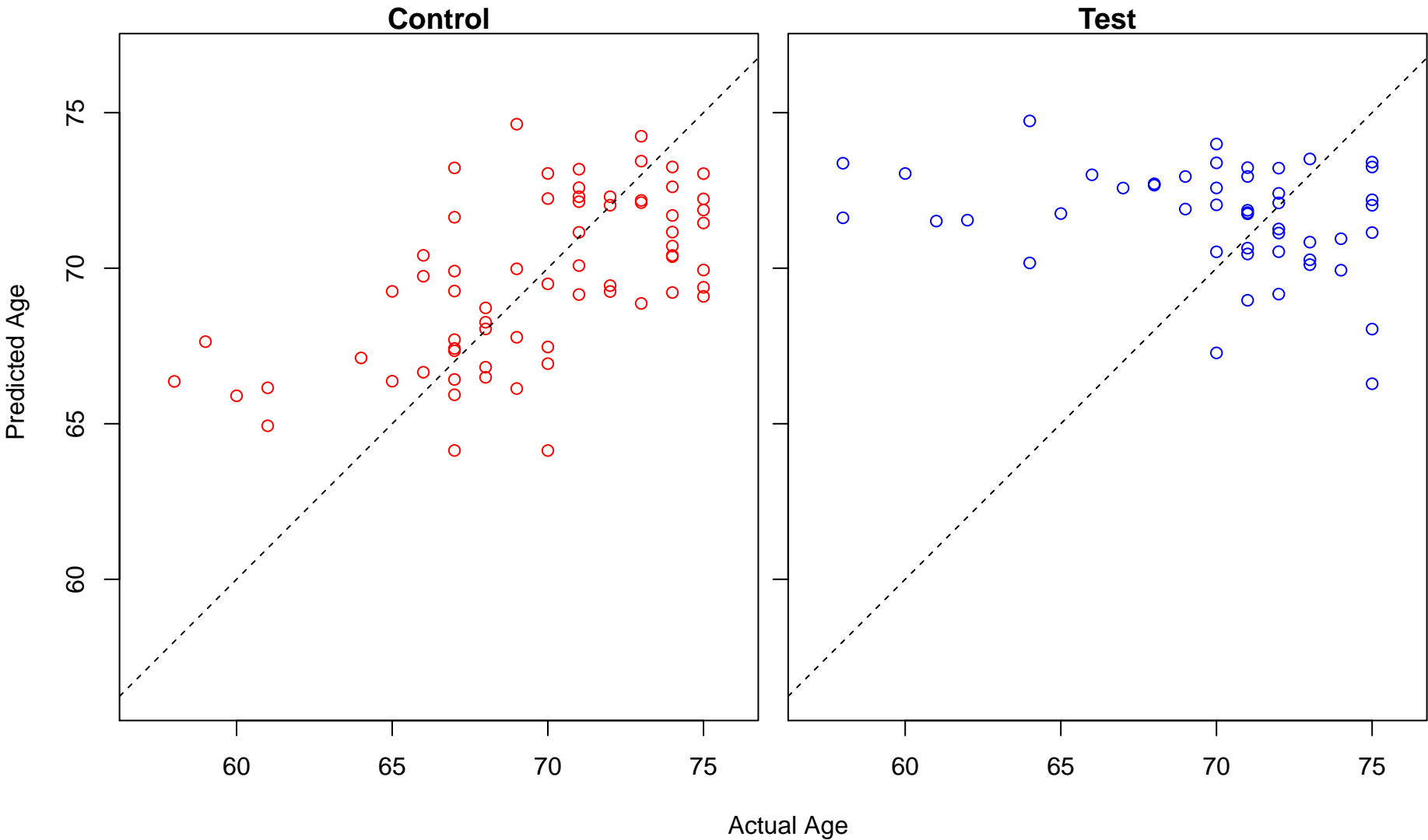
regulation of protein deacetylation (Score: 1.059931)



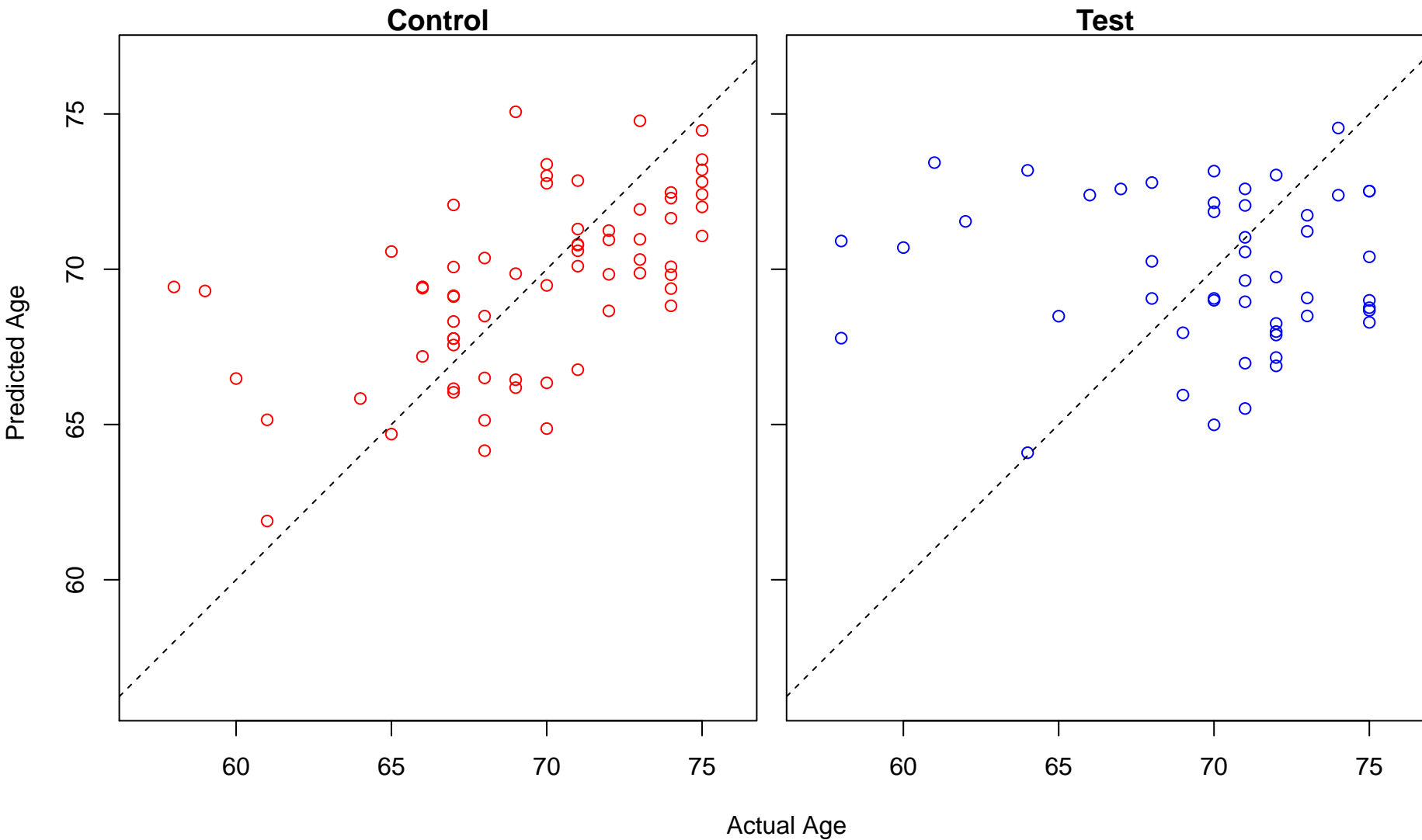
COPII-coated vesicle budding (Score: 1.059446)



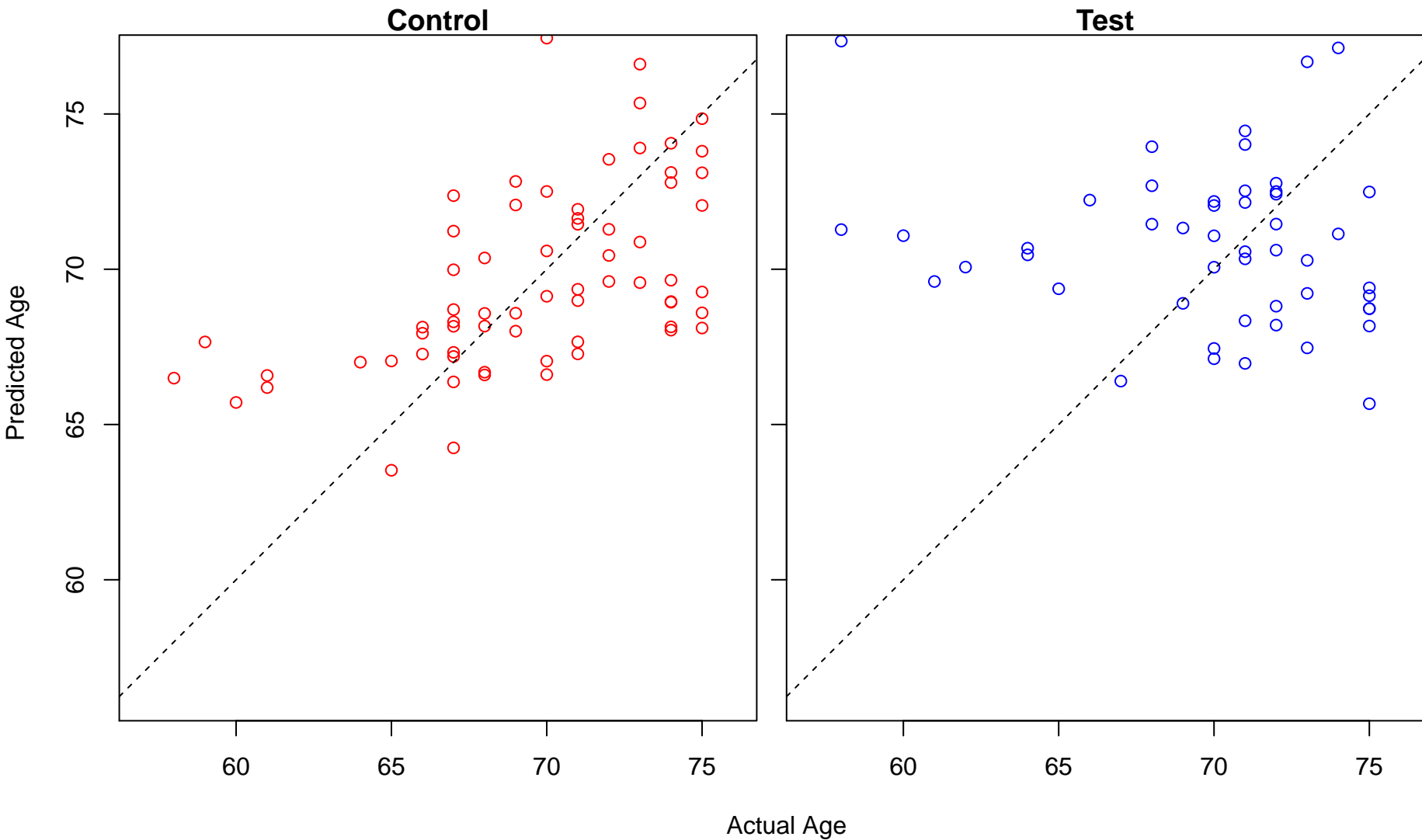
regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis (Score: 1.05)



negative regulation of protein kinase B signaling (Score: 1.058236)

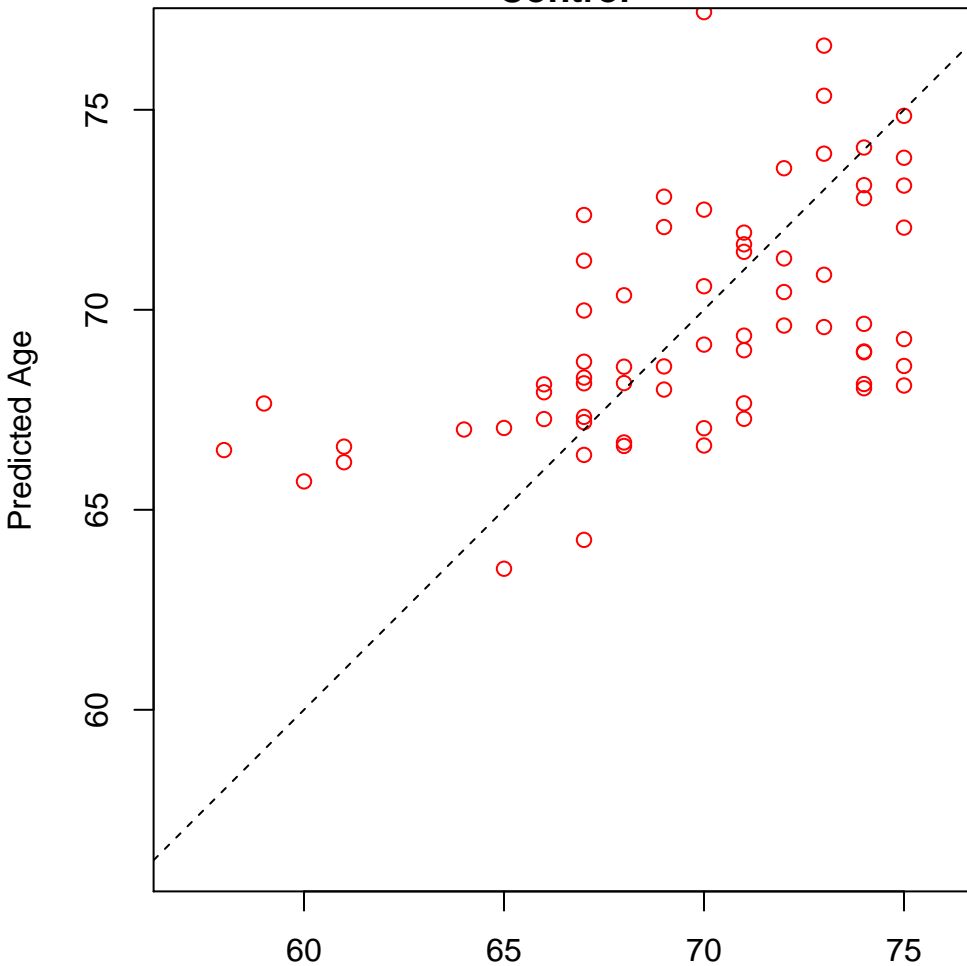


intraciliary transport (Score: 1.058010)

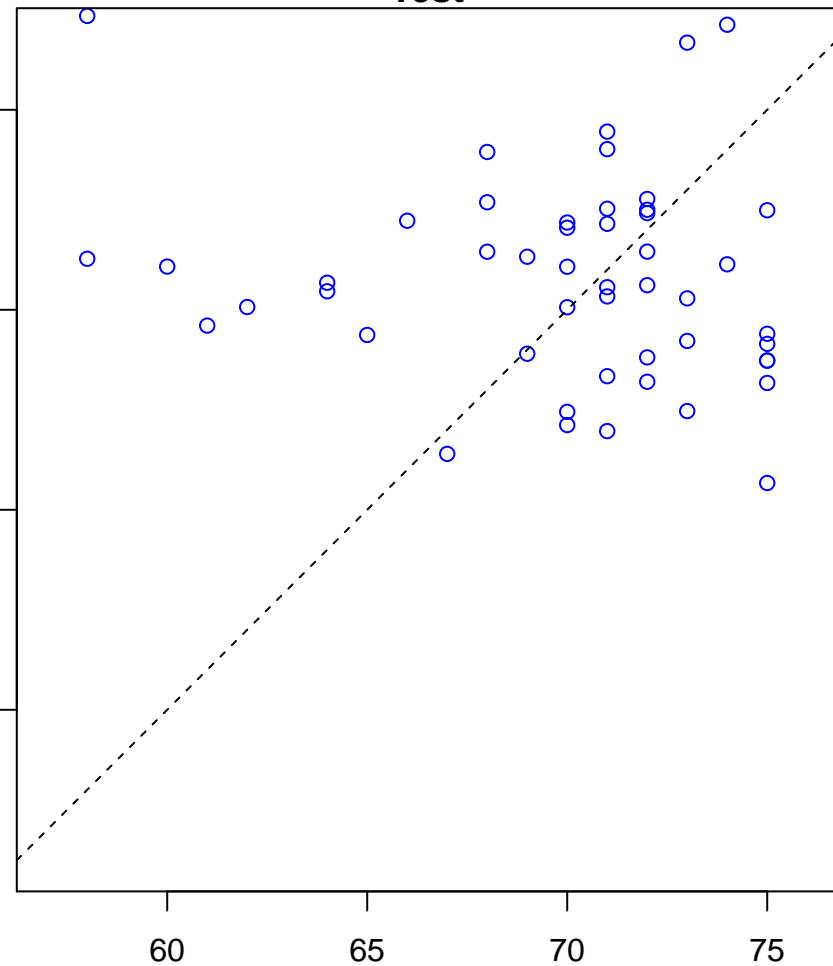


protein transport along microtubule (Score: 1.058010)

Control

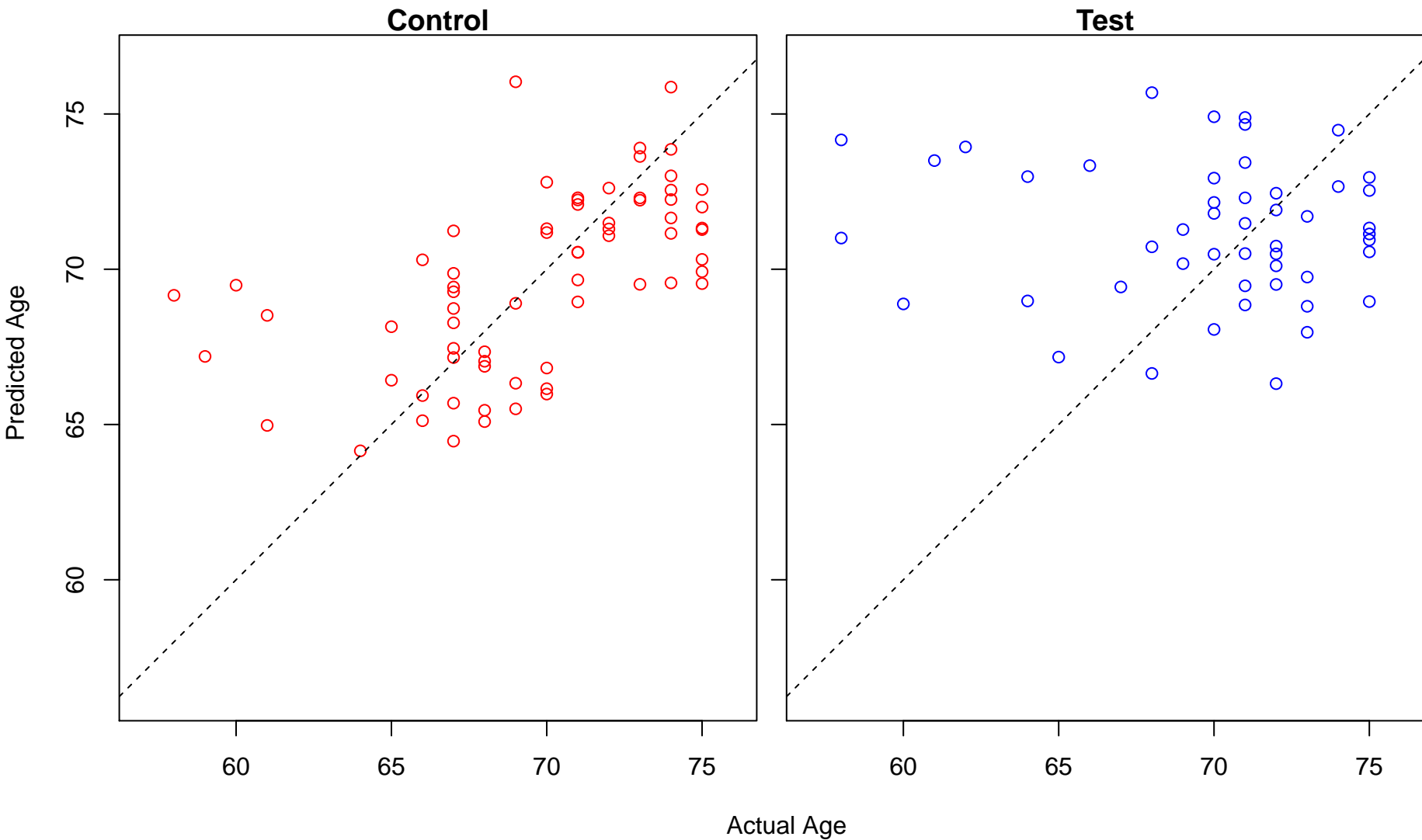


Test

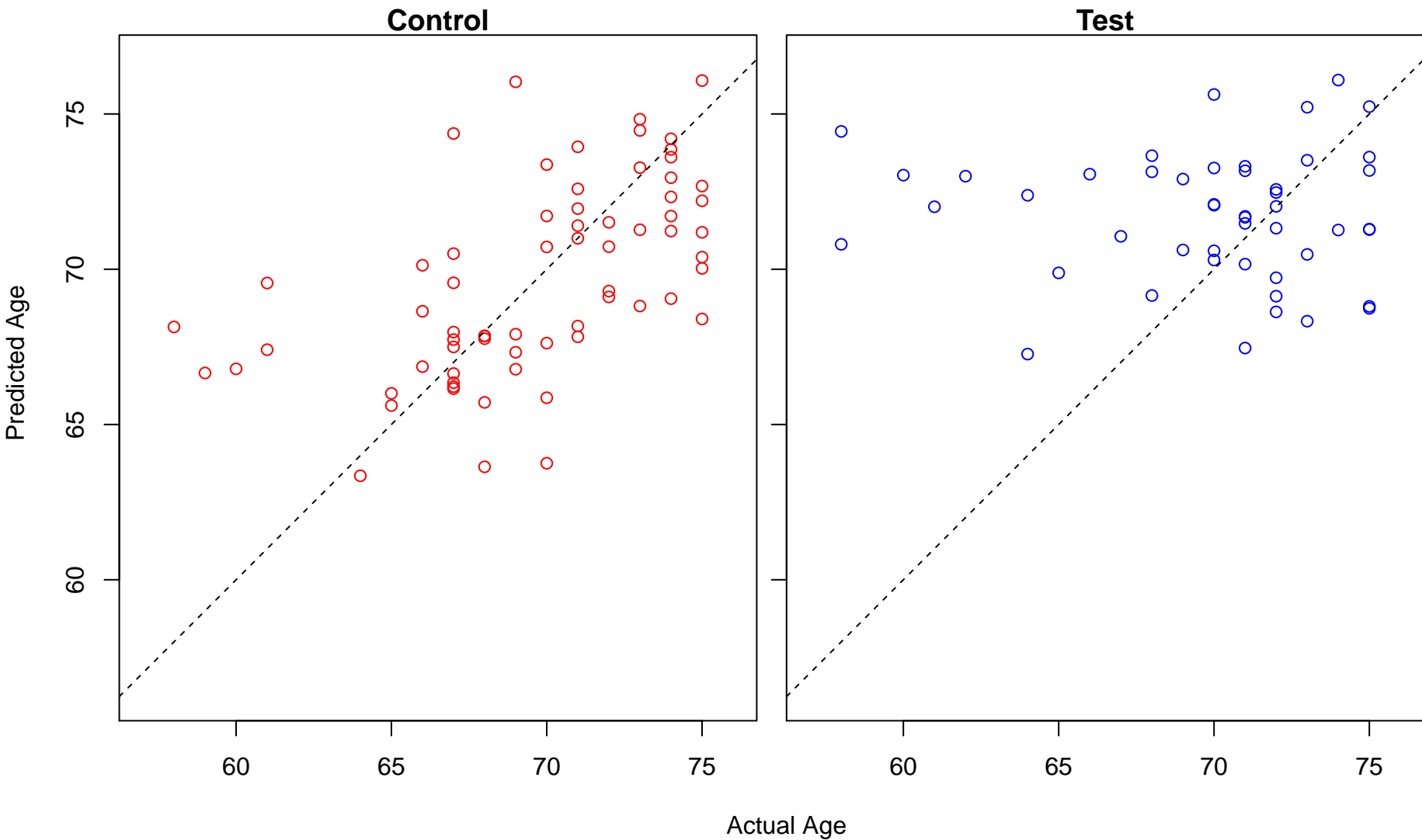


Actual Age

cellular response to metal ion (Score: 1.057900)

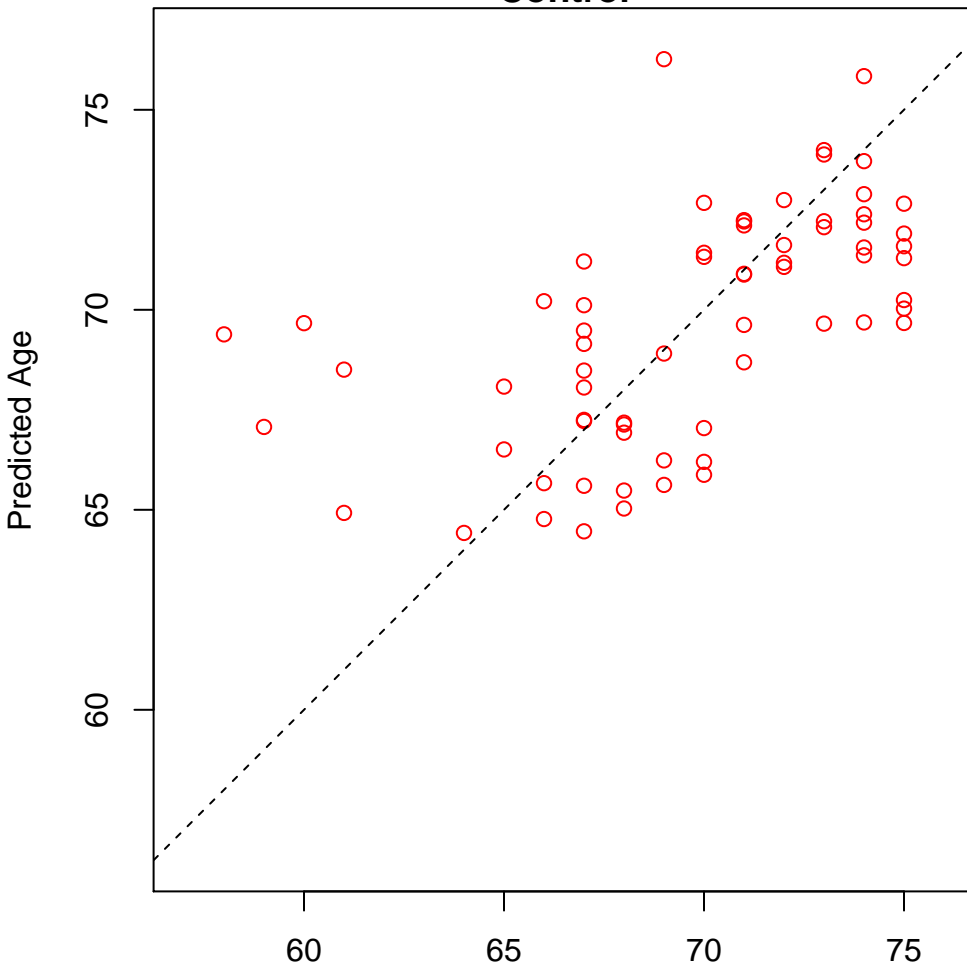


positive regulation of response to biotic stimulus (Score: 1.057465)

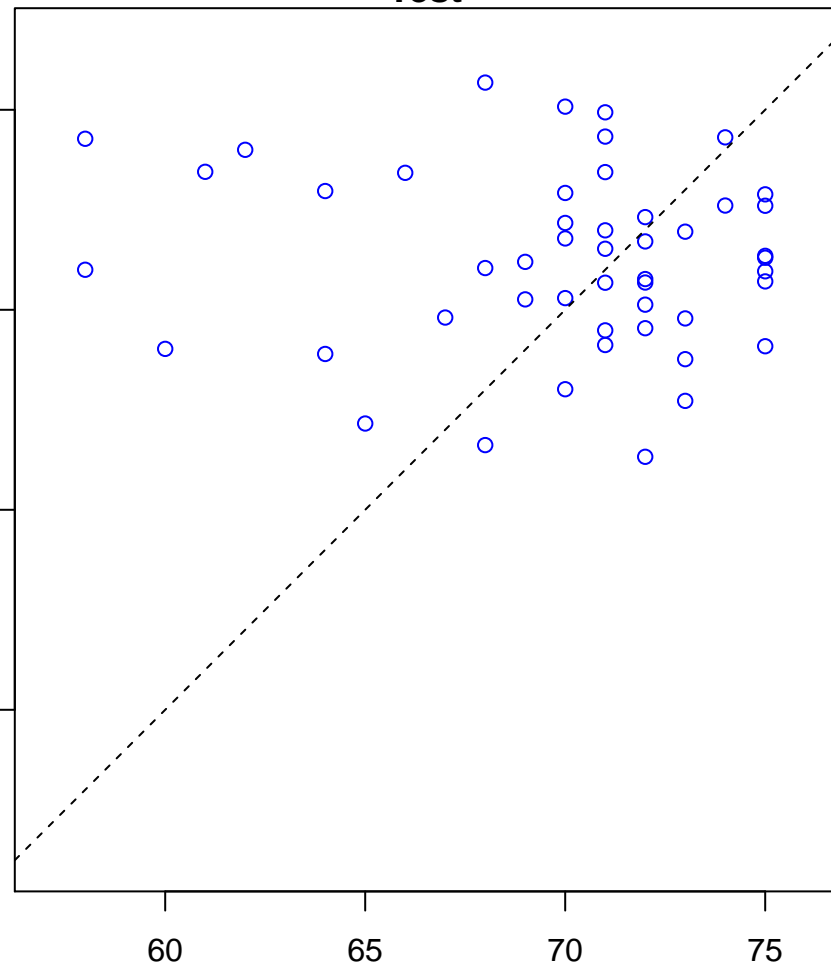


cellular response to inorganic substance (Score: 1.057185)

Control

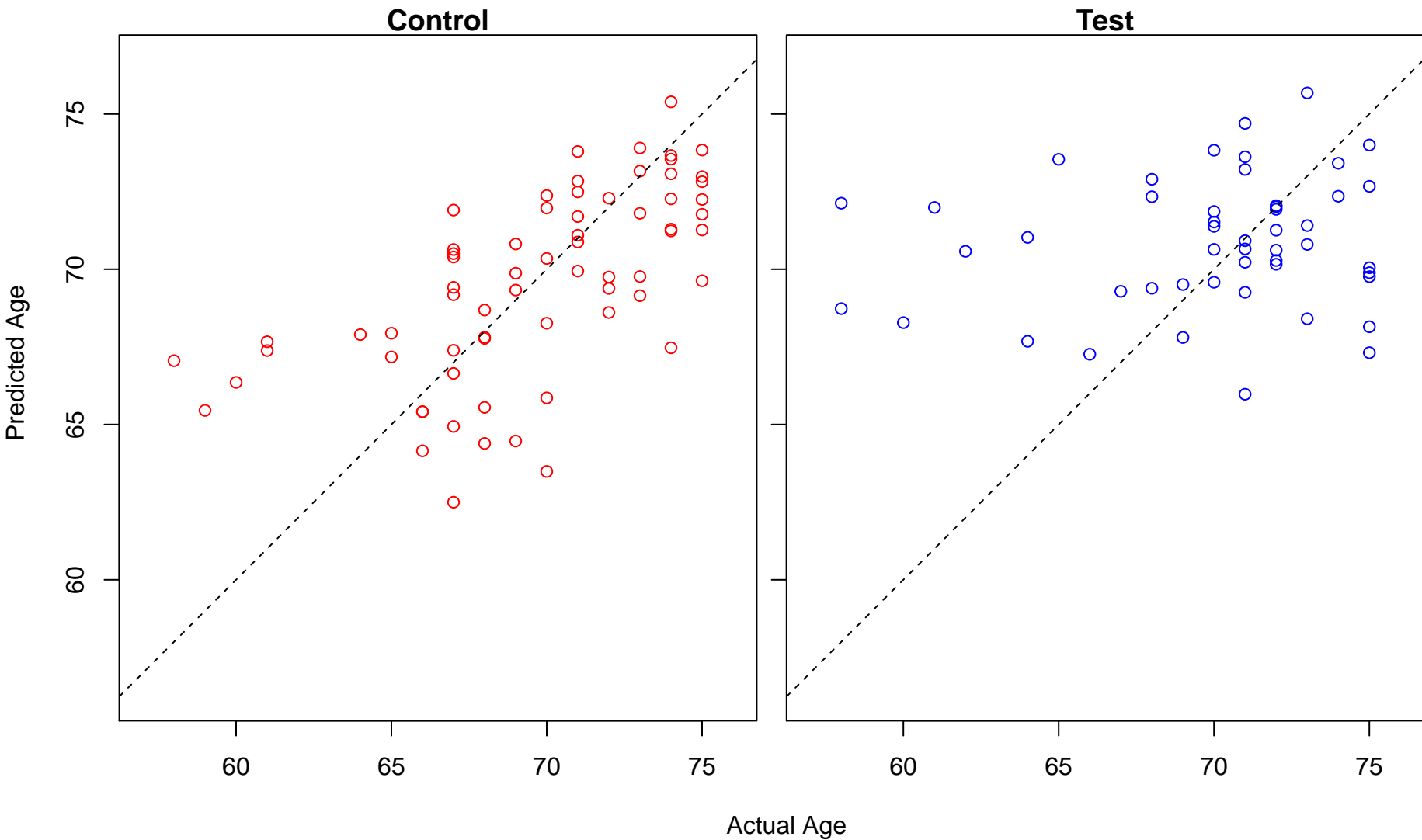


Test

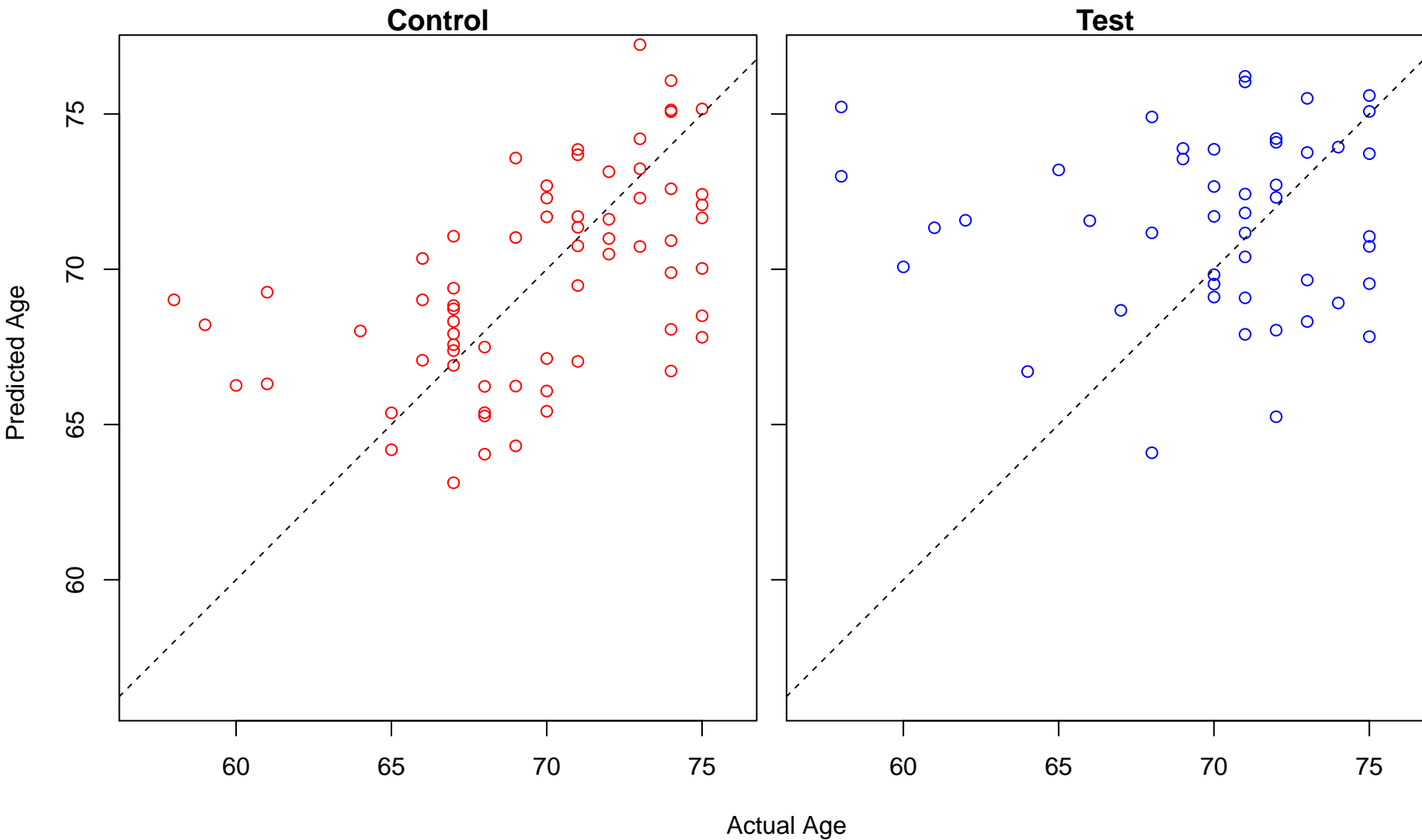


Actual Age

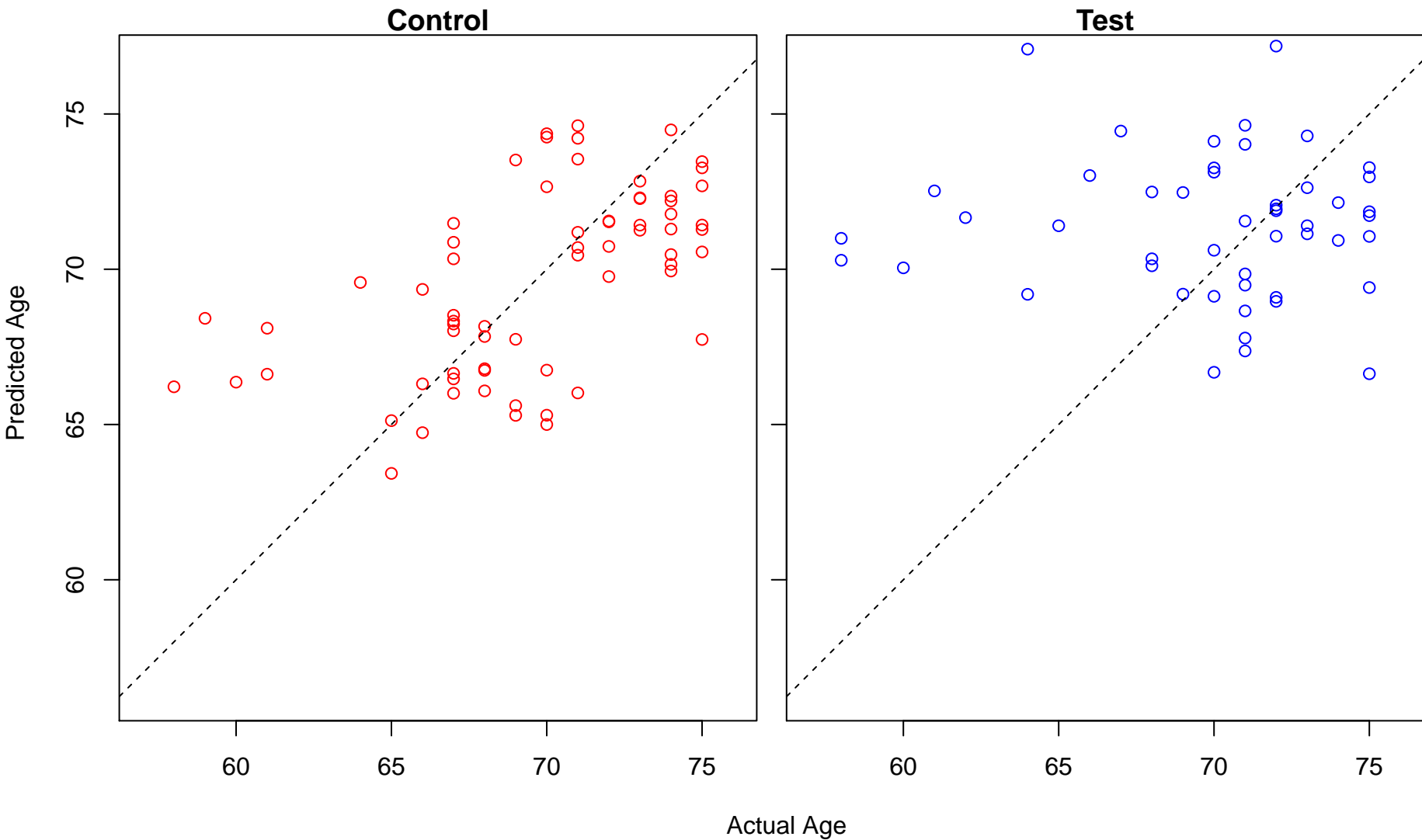
ribosome assembly (Score: 1.056465)



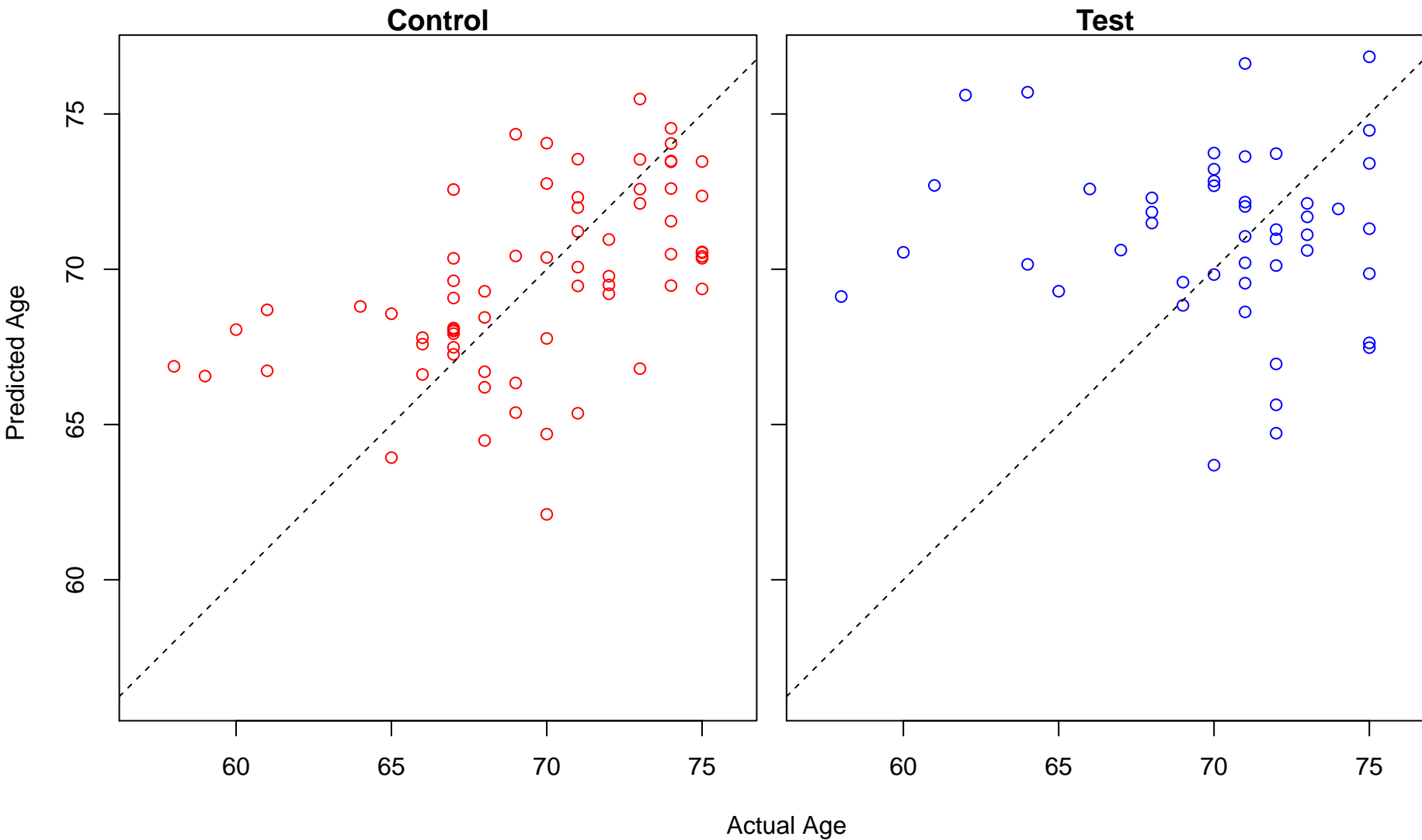
positive regulation of dendrite morphogenesis (Score: 1.056434)



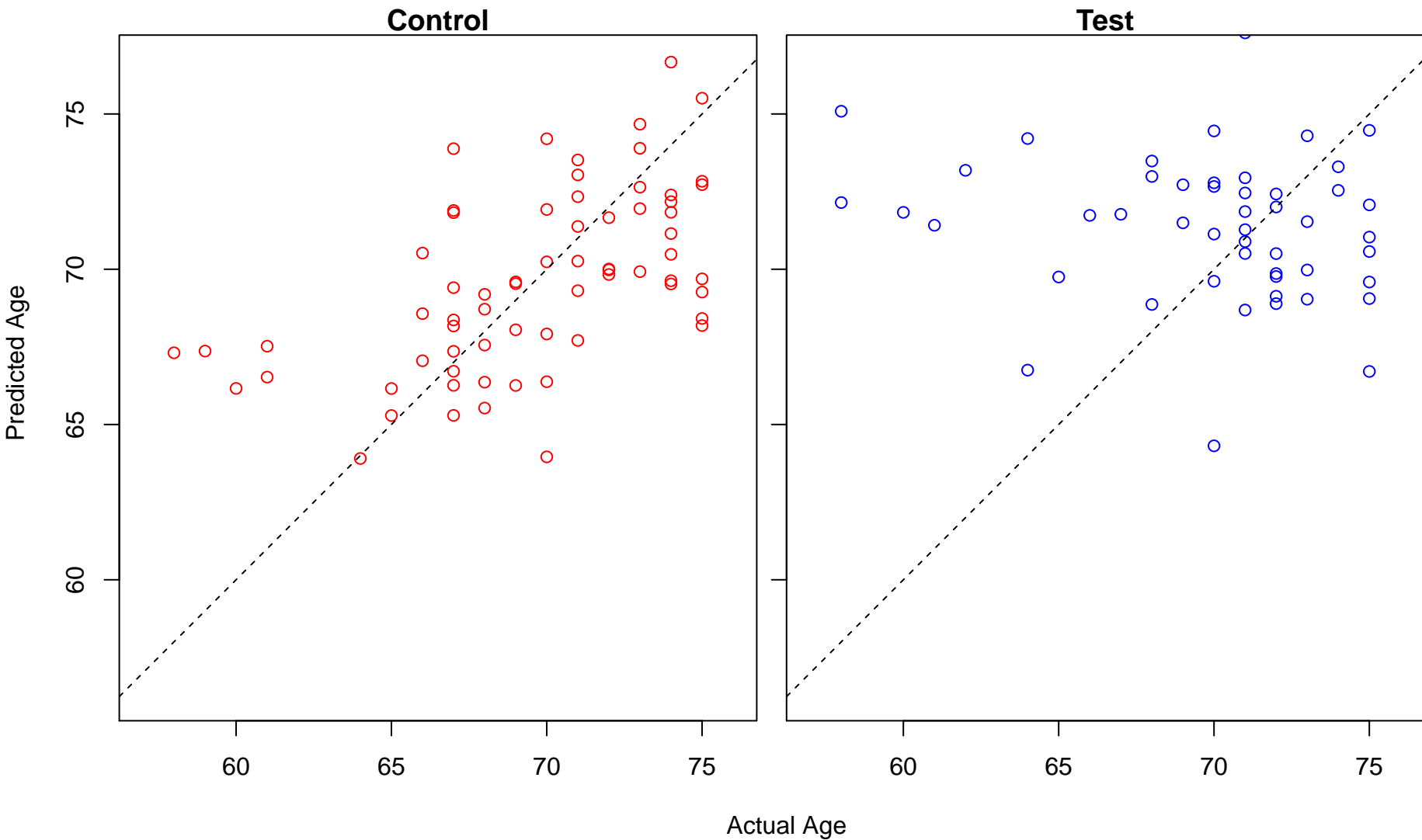
positive regulation of histone acetylation (Score: 1.056304)



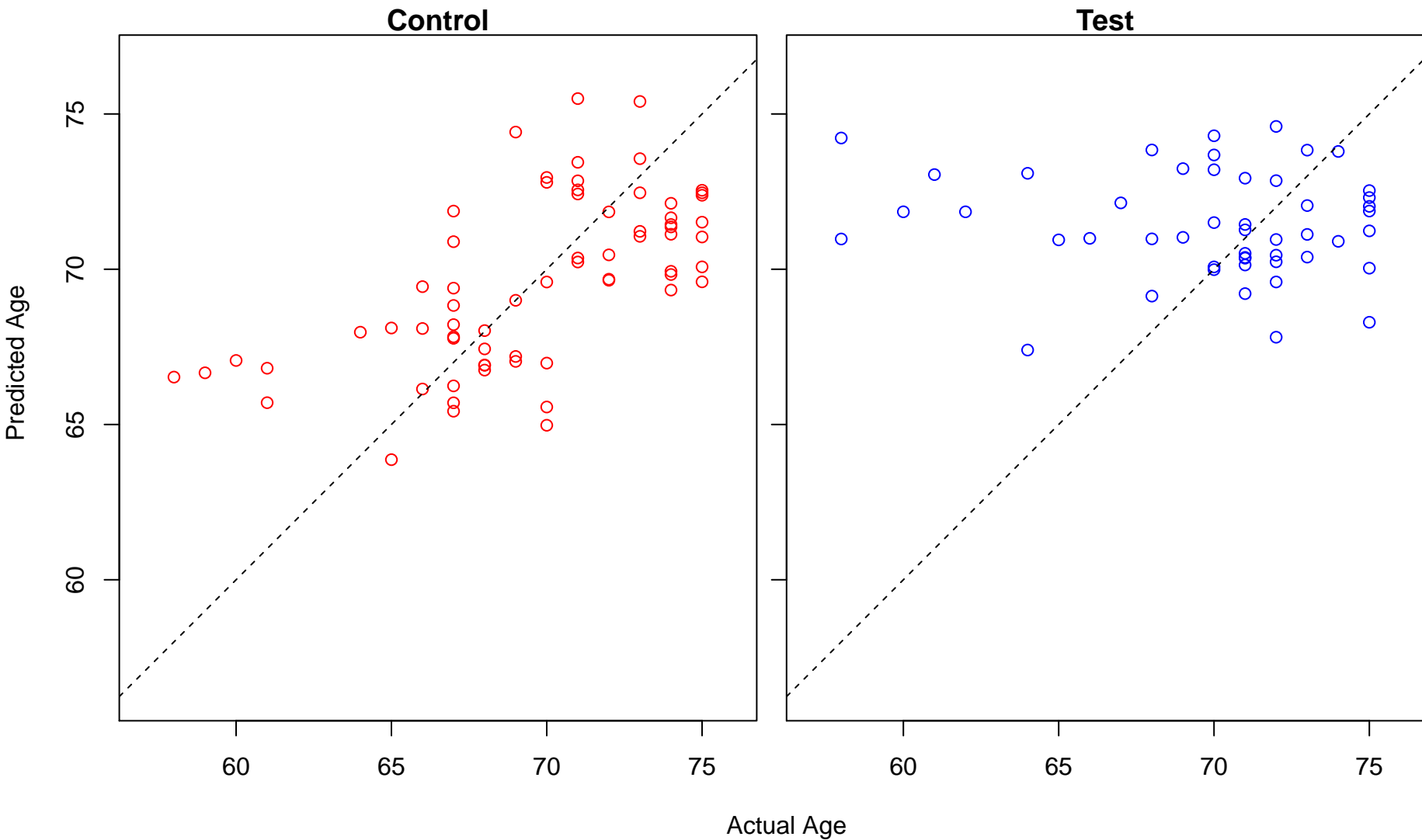
negative regulation of ion transmembrane transporter activity (Score: 1.056162)



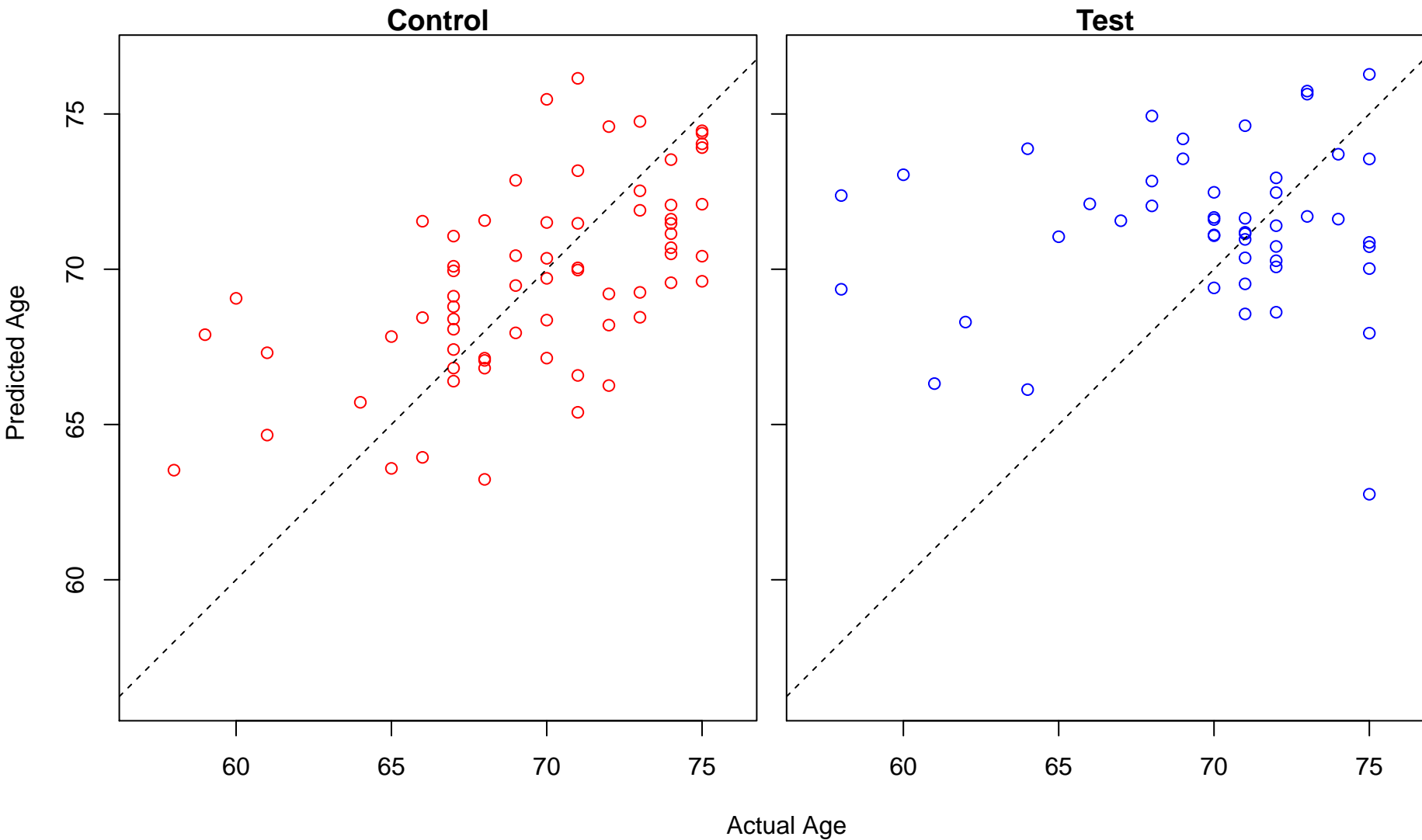
response to carbohydrate (Score: 1.055945)



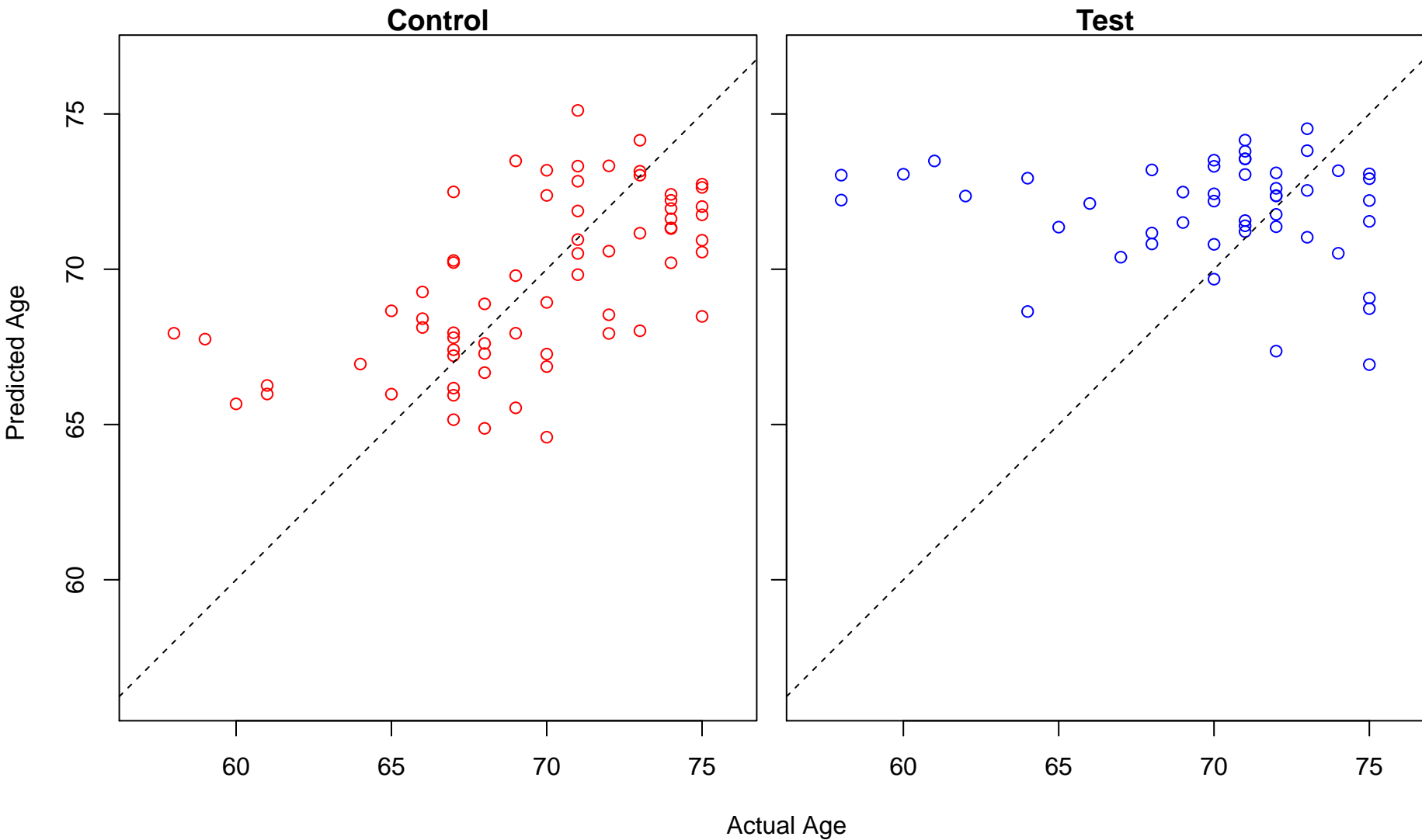
negative regulation of telomerase activity (Score: 1.055631)



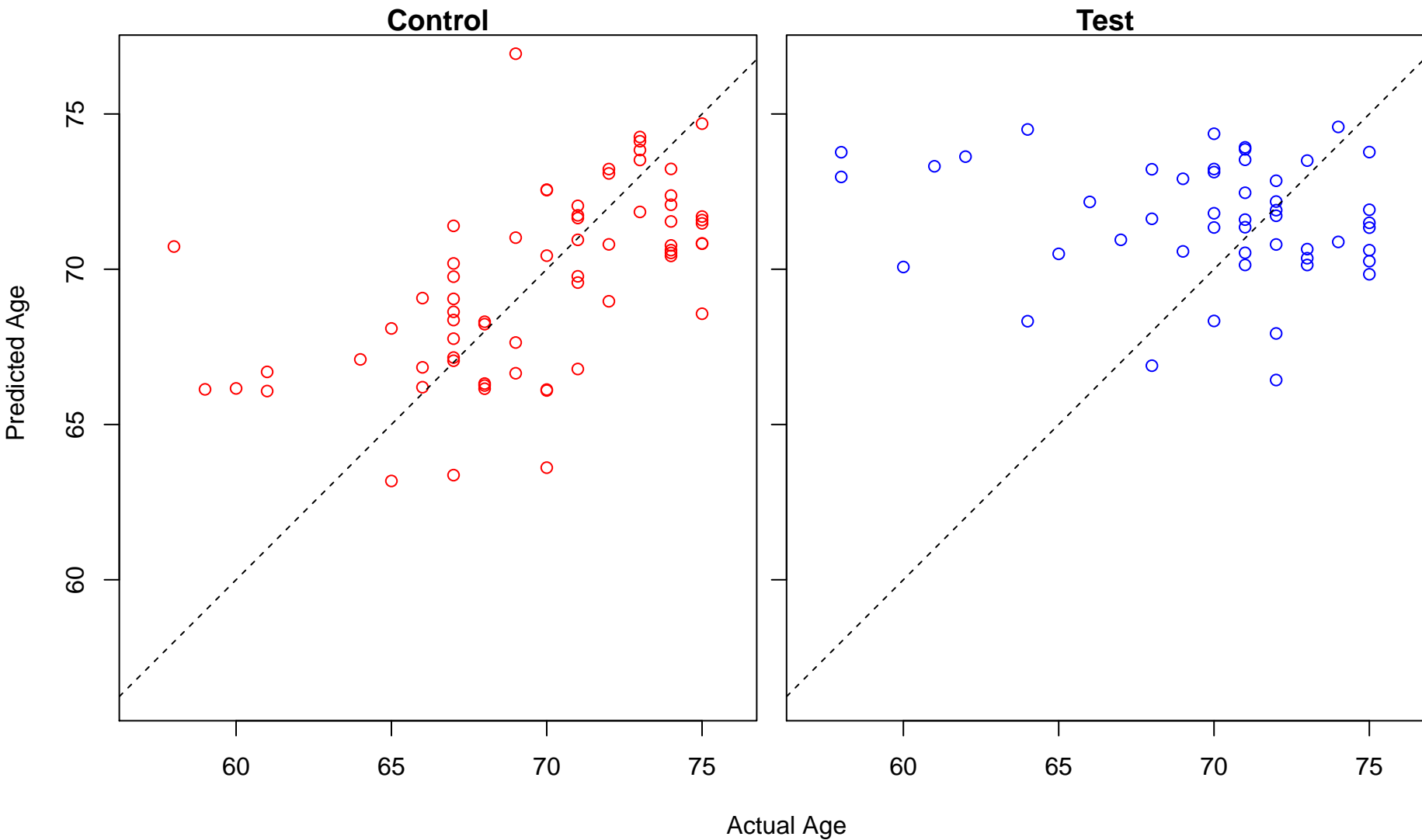
interleukin-1 beta secretion (Score: 1.055396)



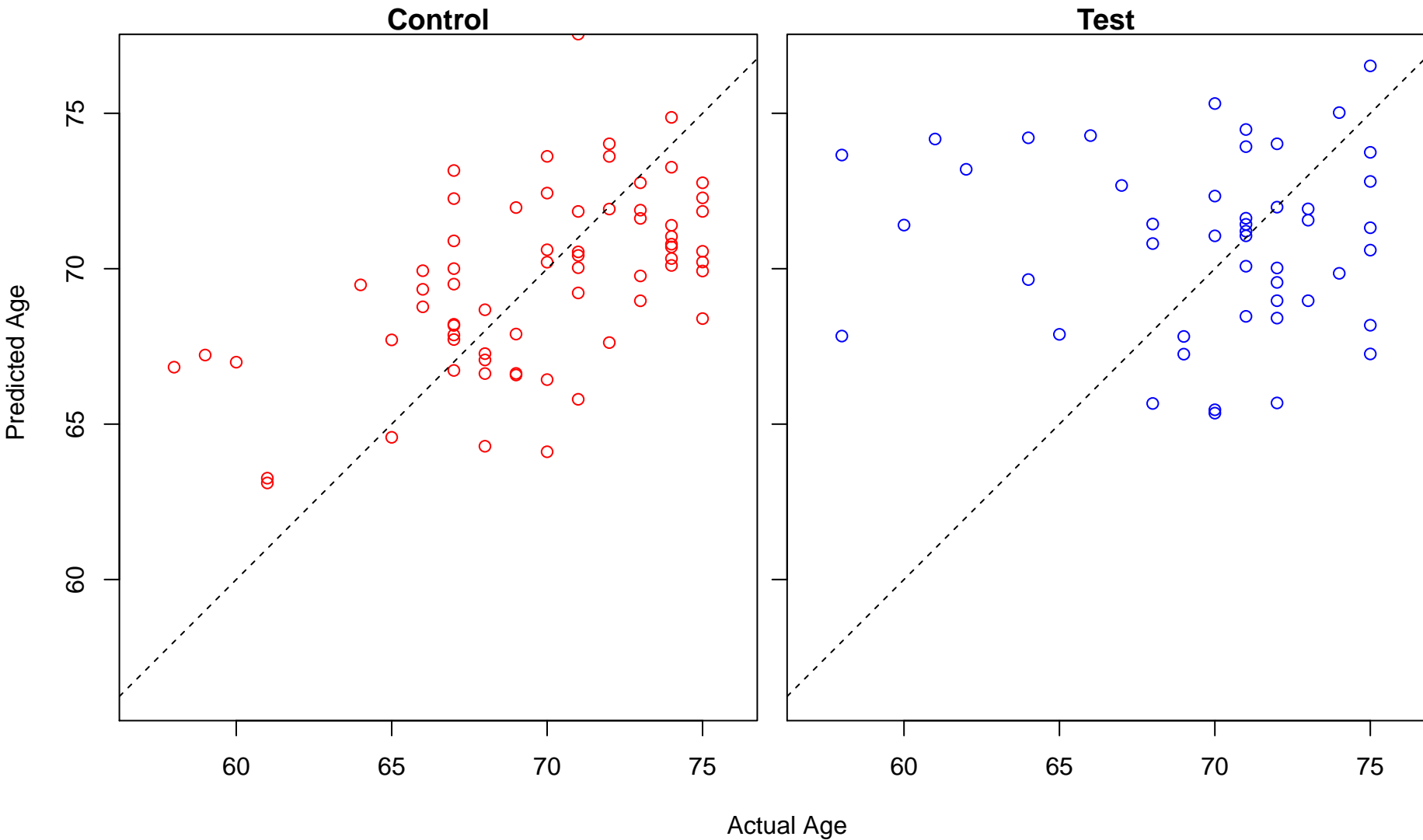
regulation of hematopoietic progenitor cell differentiation (Score: 1.055280)



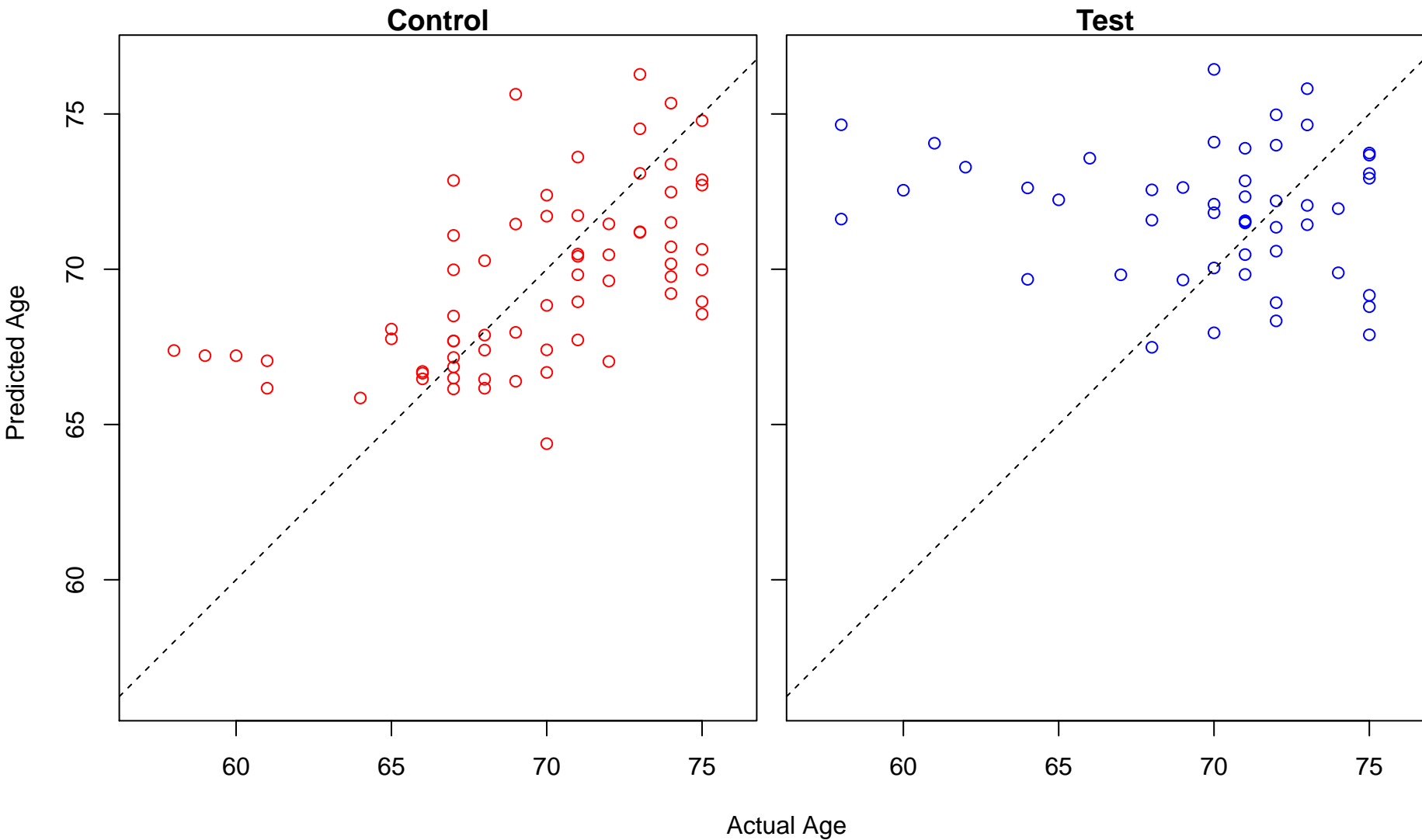
regulation of leukocyte degranulation (Score: 1.055251)



regulation of cardiac muscle contraction by calcium ion signaling (Score: 1.054929)

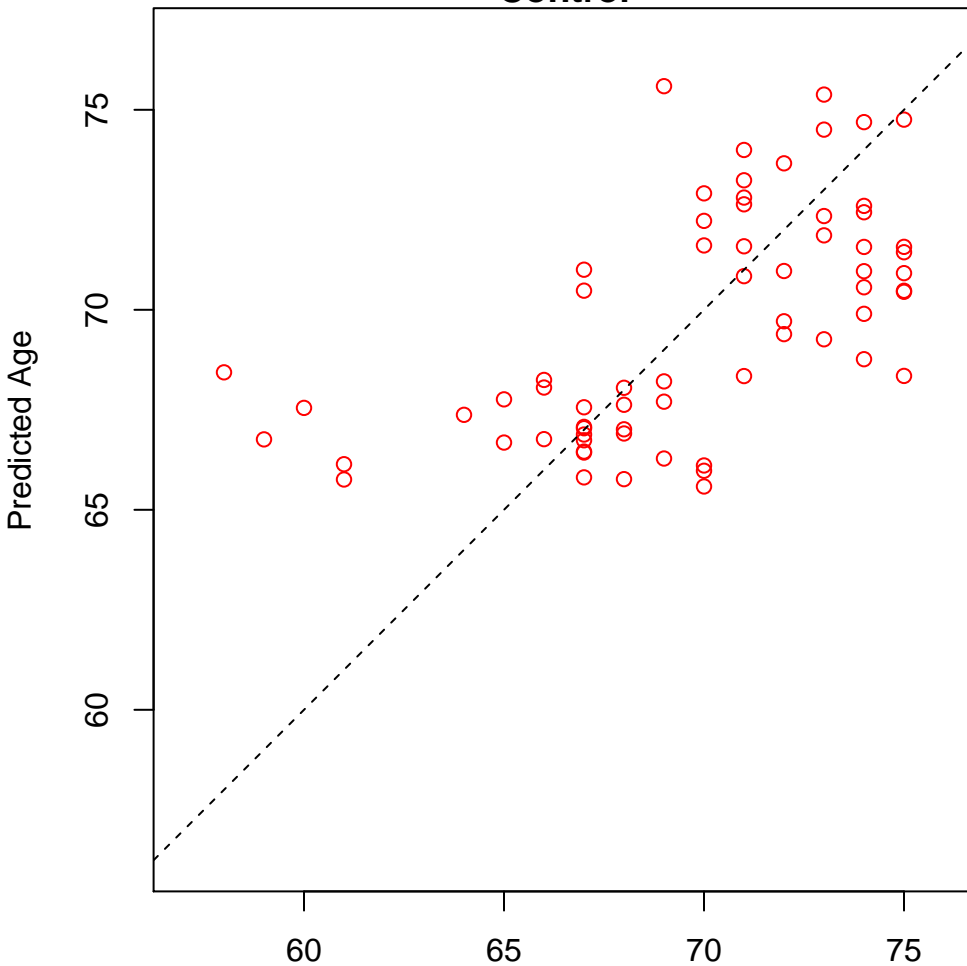


heart process (Score: 1.054466)

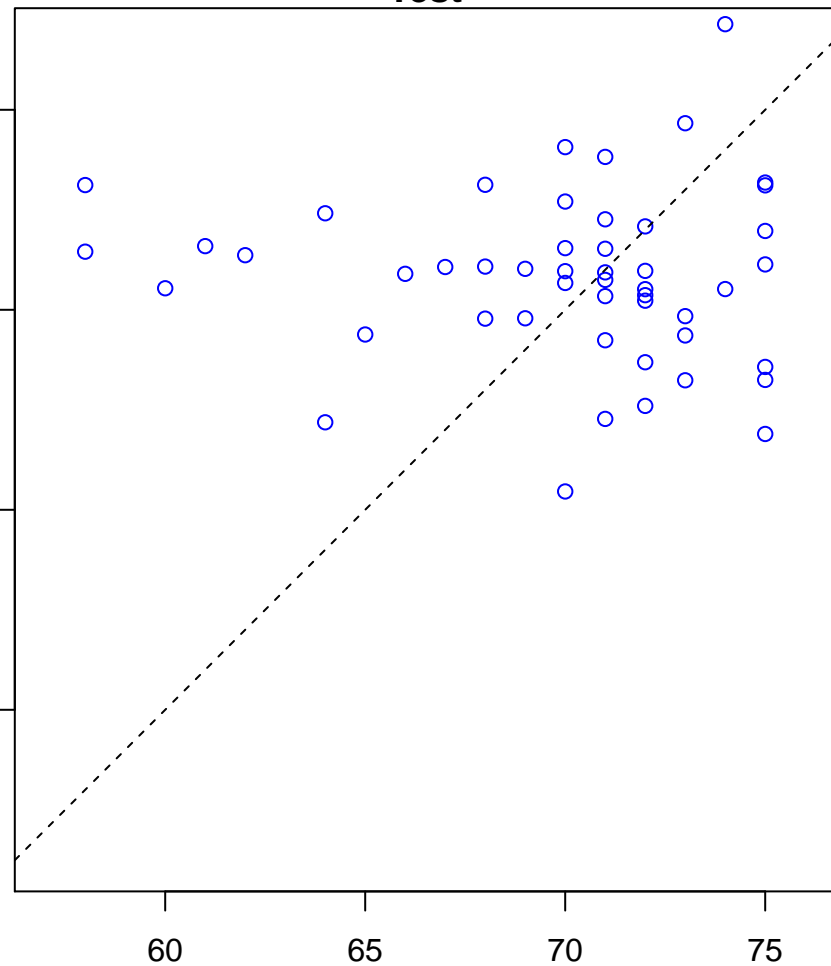


modulation by virus of host process (Score: 1.054370)

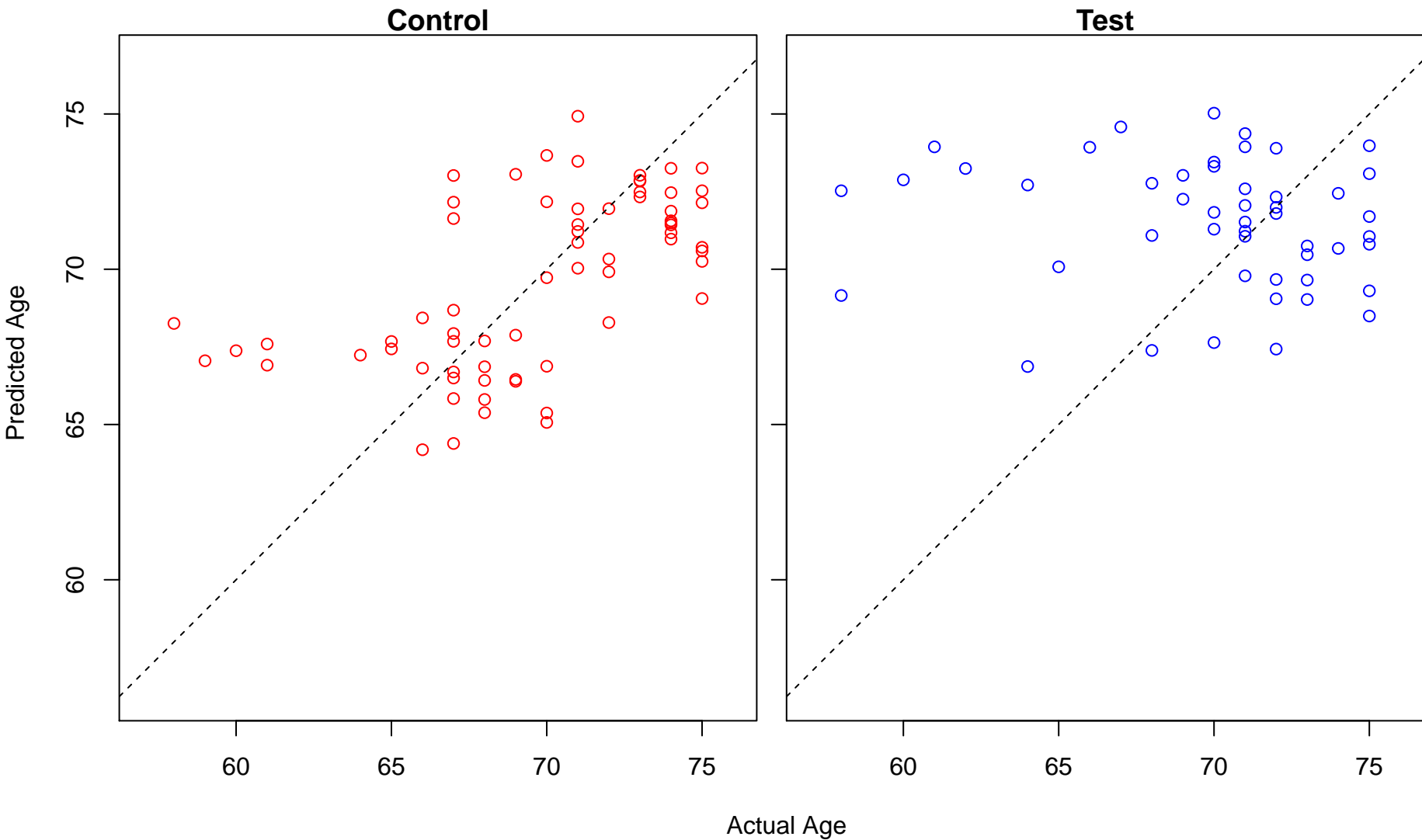
Control



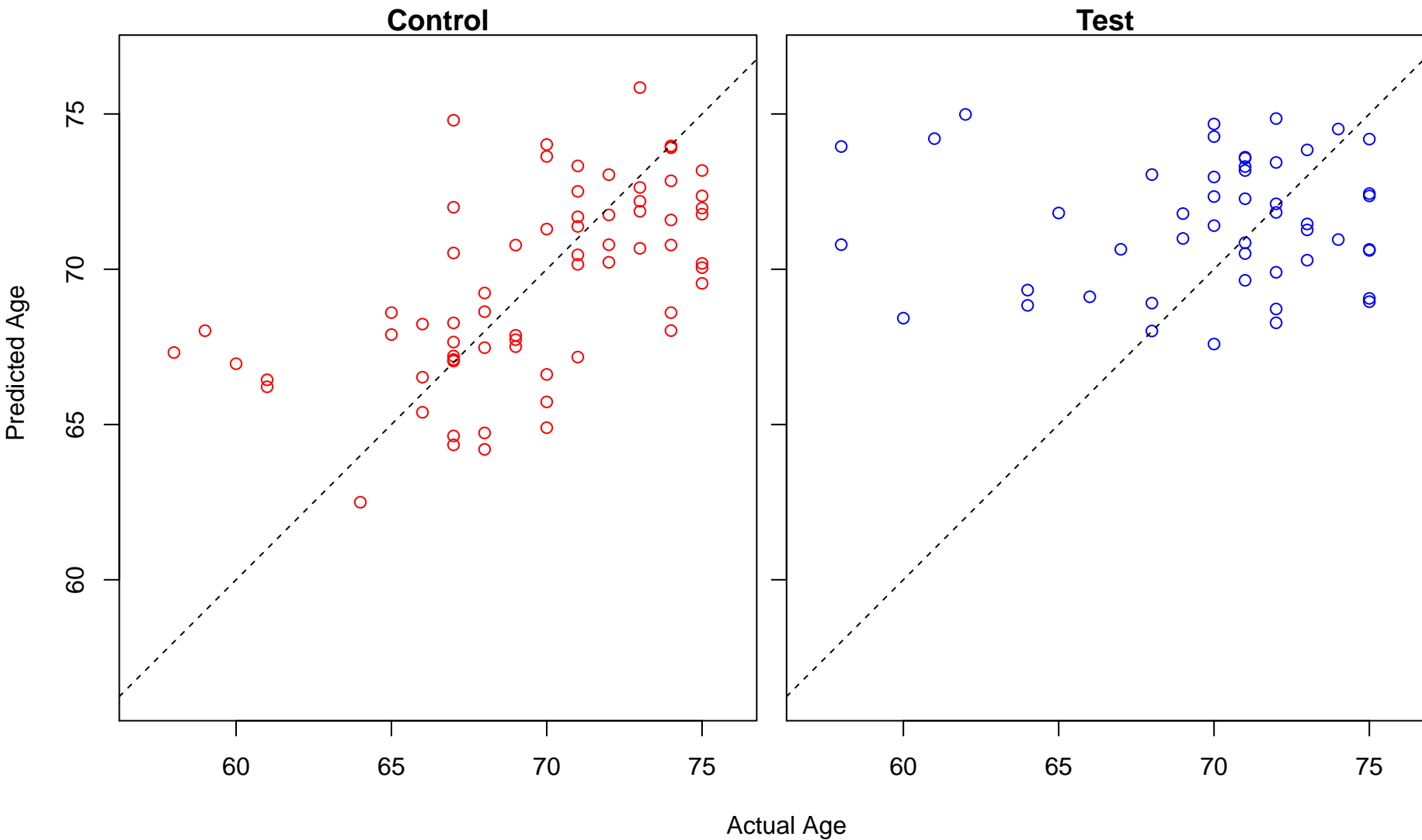
Test



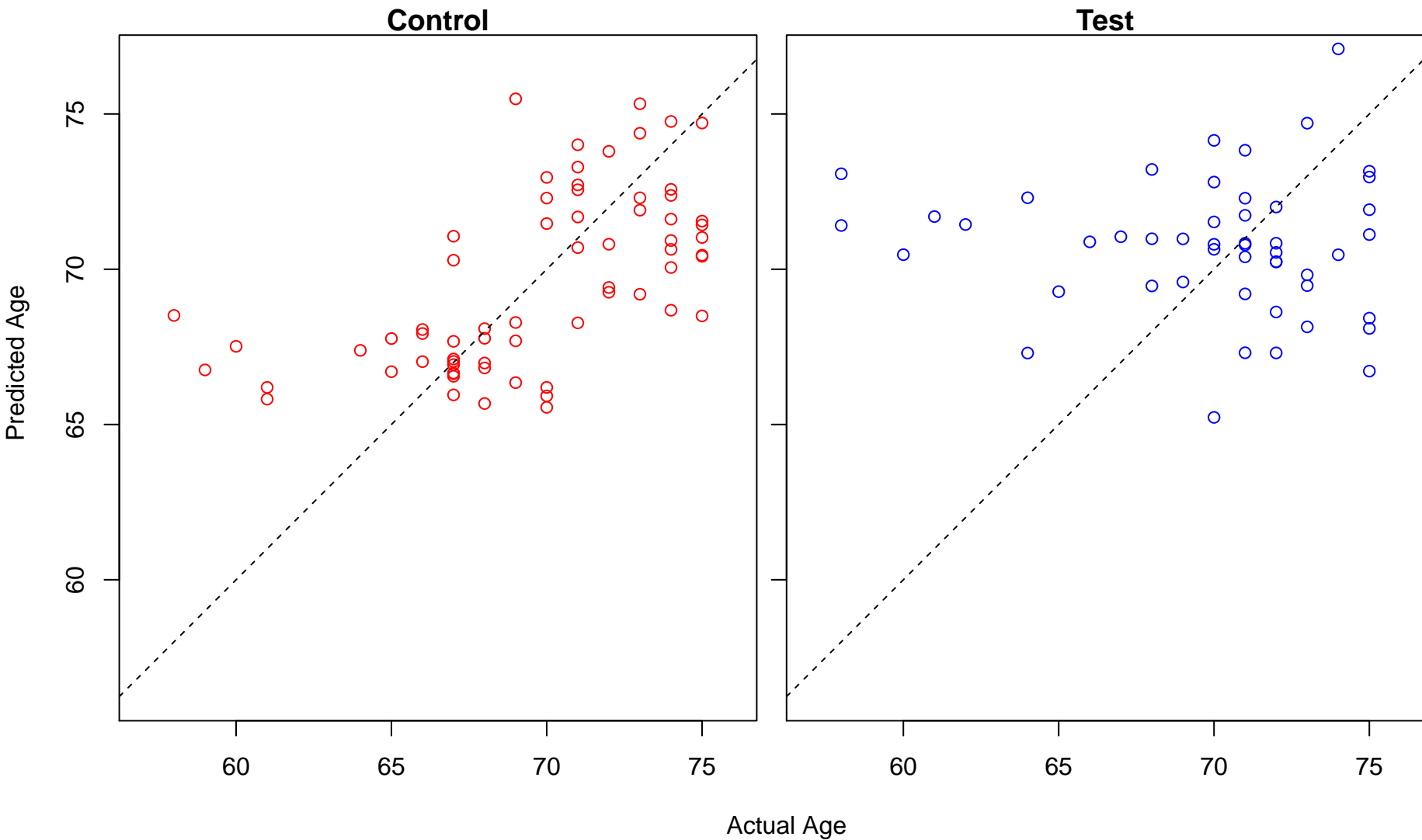
tissue remodeling (Score: 1.053892)



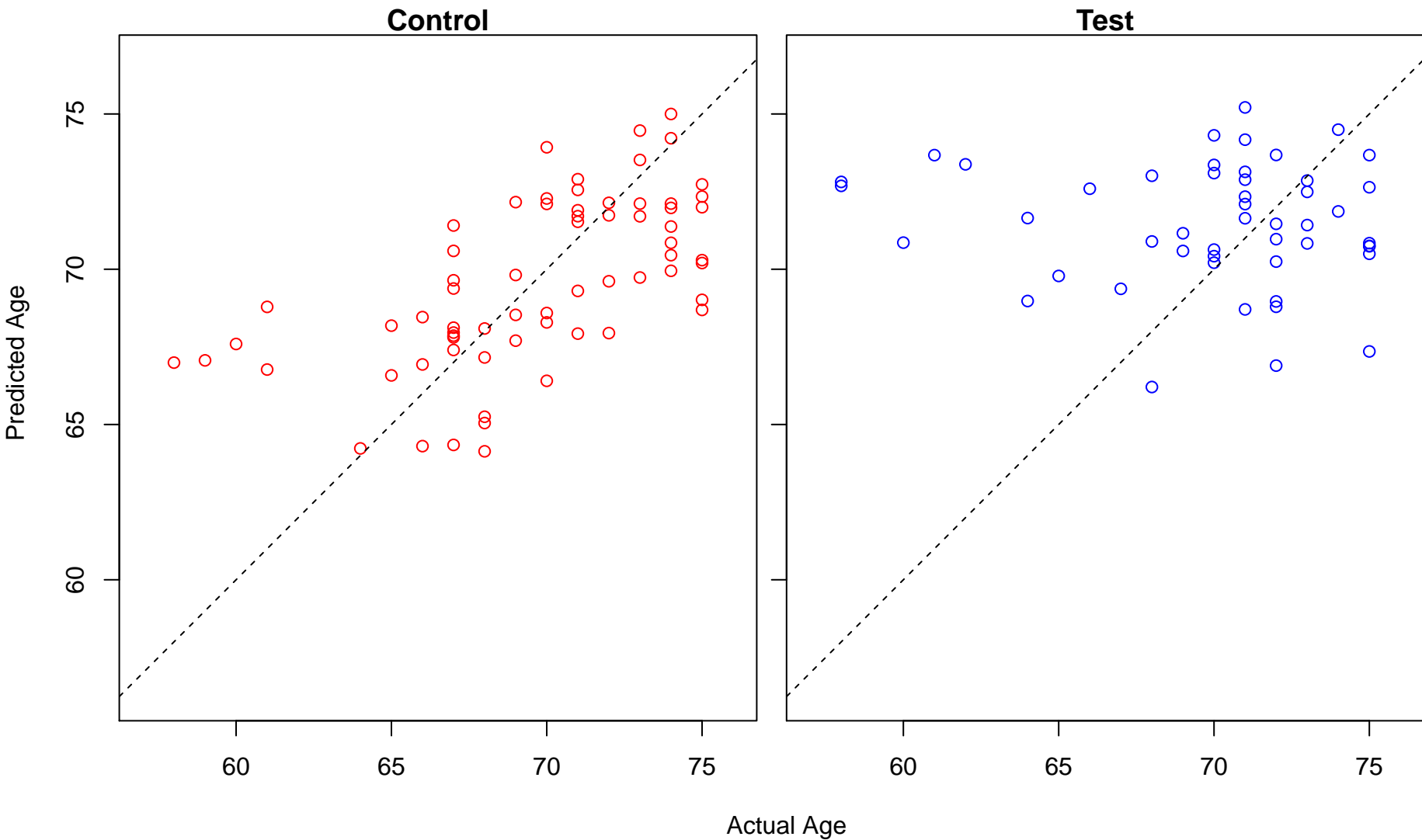
regulation of blood circulation (Score: 1.053288)



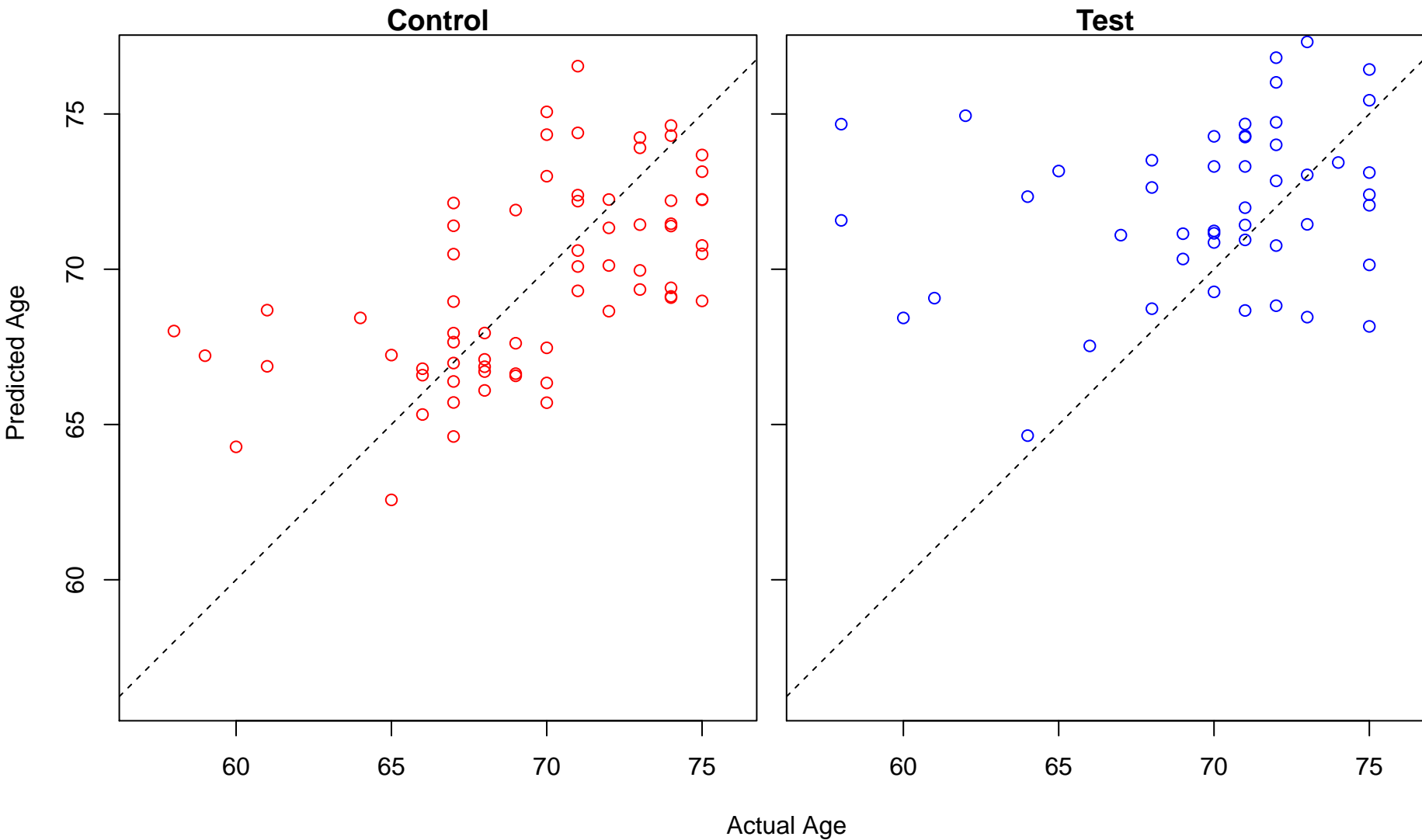
modulation by symbiont of host cellular process (Score: 1.053176)



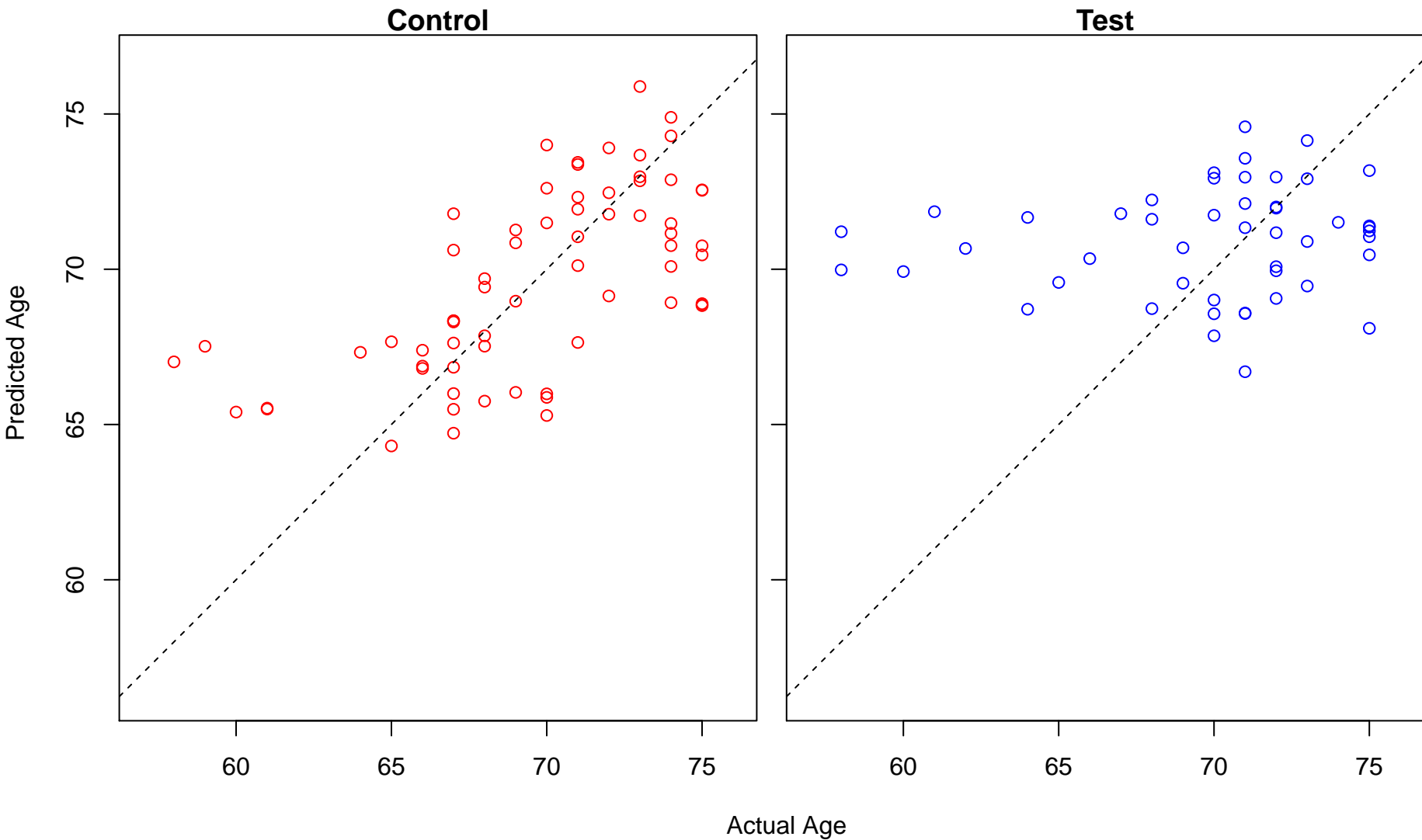
muscle cell development (Score: 1.052708)



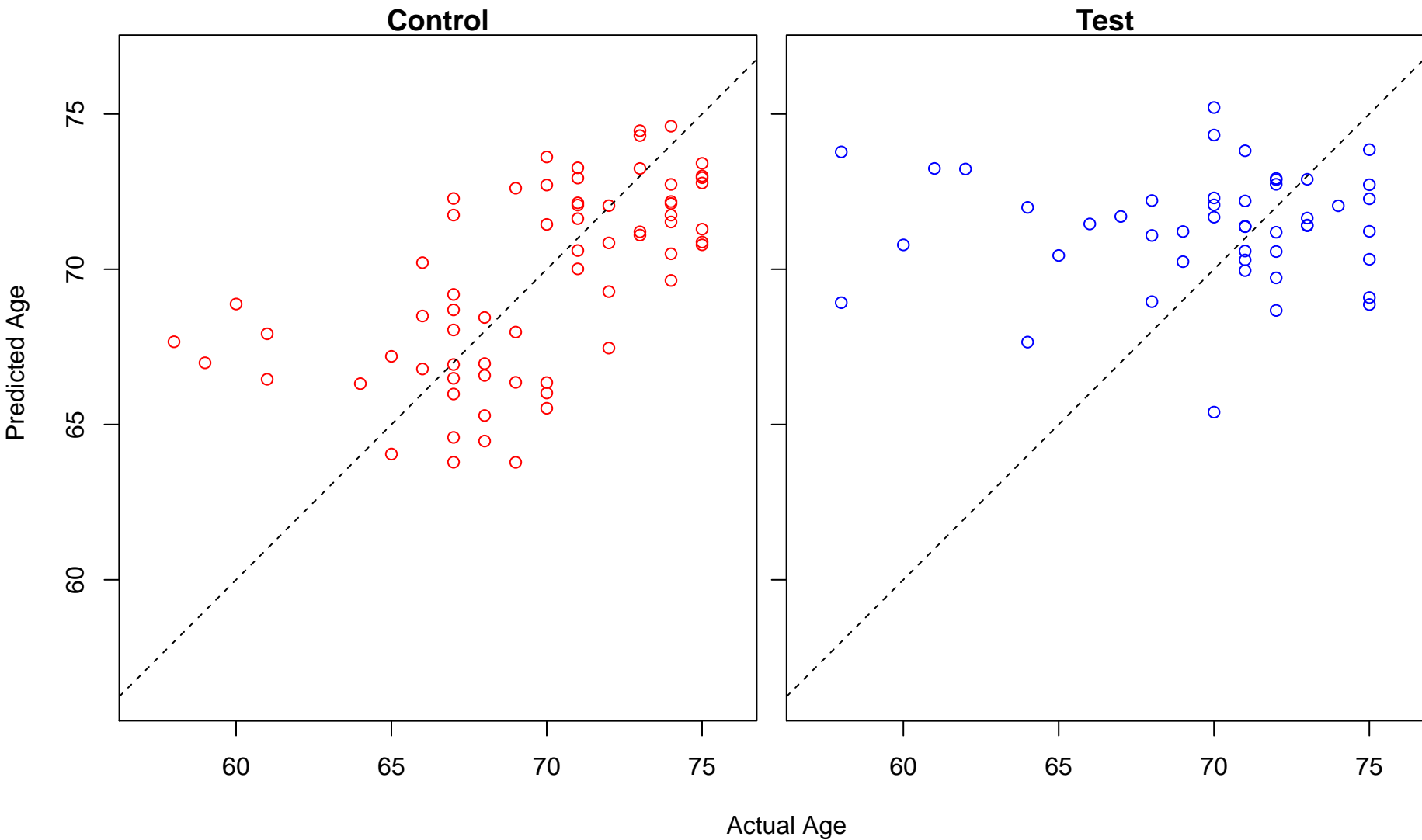
positive regulation of neuron projection development (Score: 1.052388)



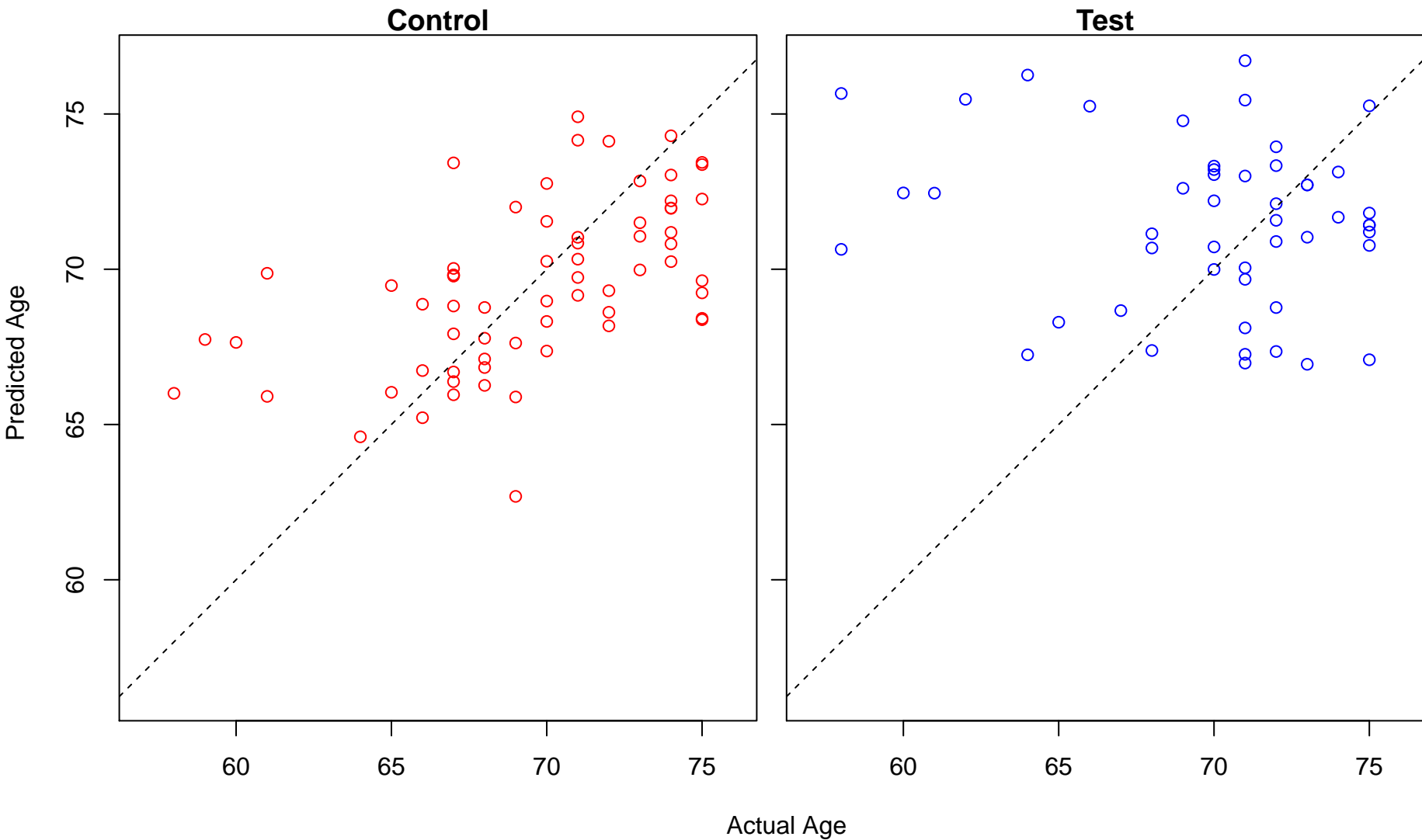
positive regulation of phagocytosis (Score: 1.052293)



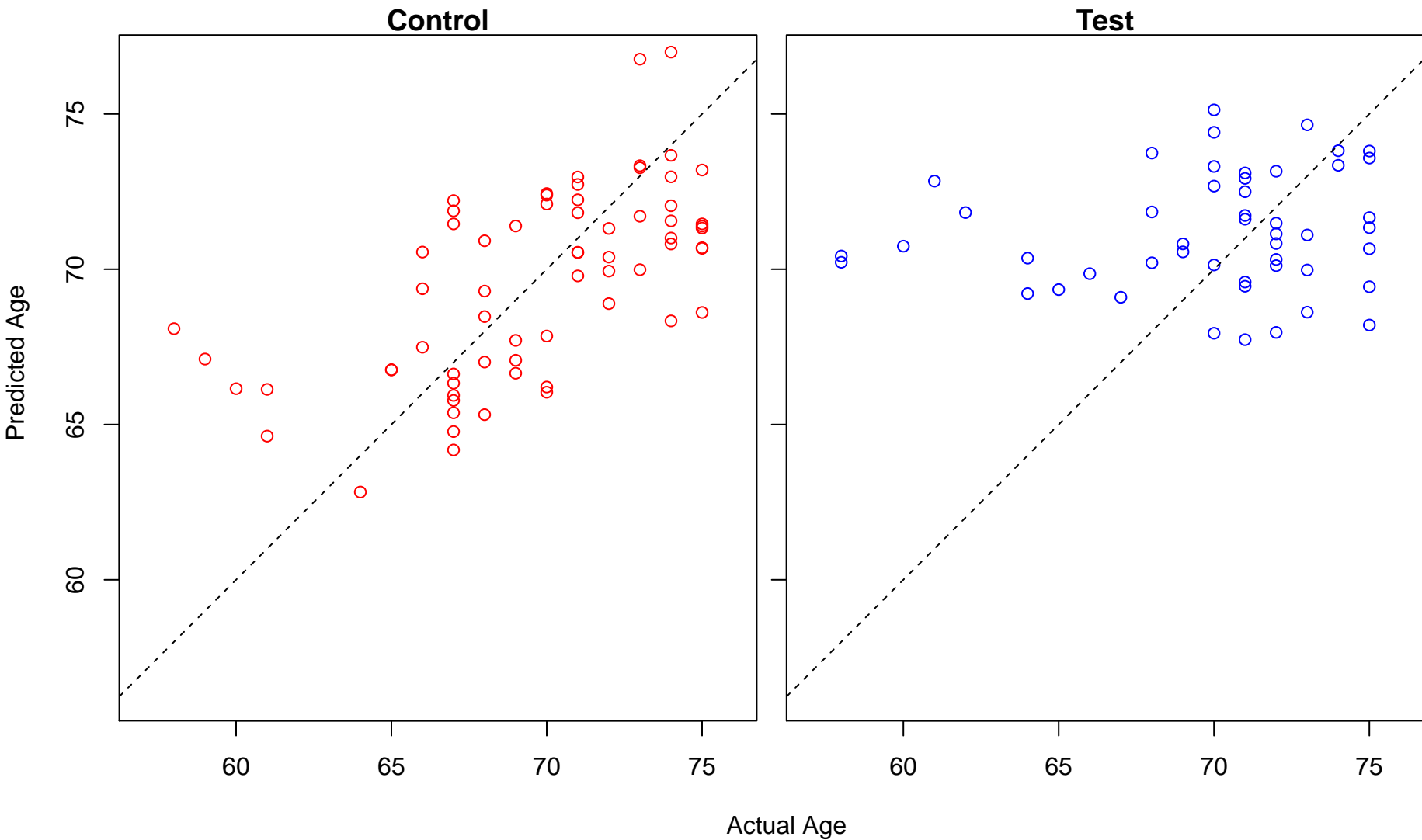
regulation of reactive oxygen species metabolic process (Score: 1.052066)



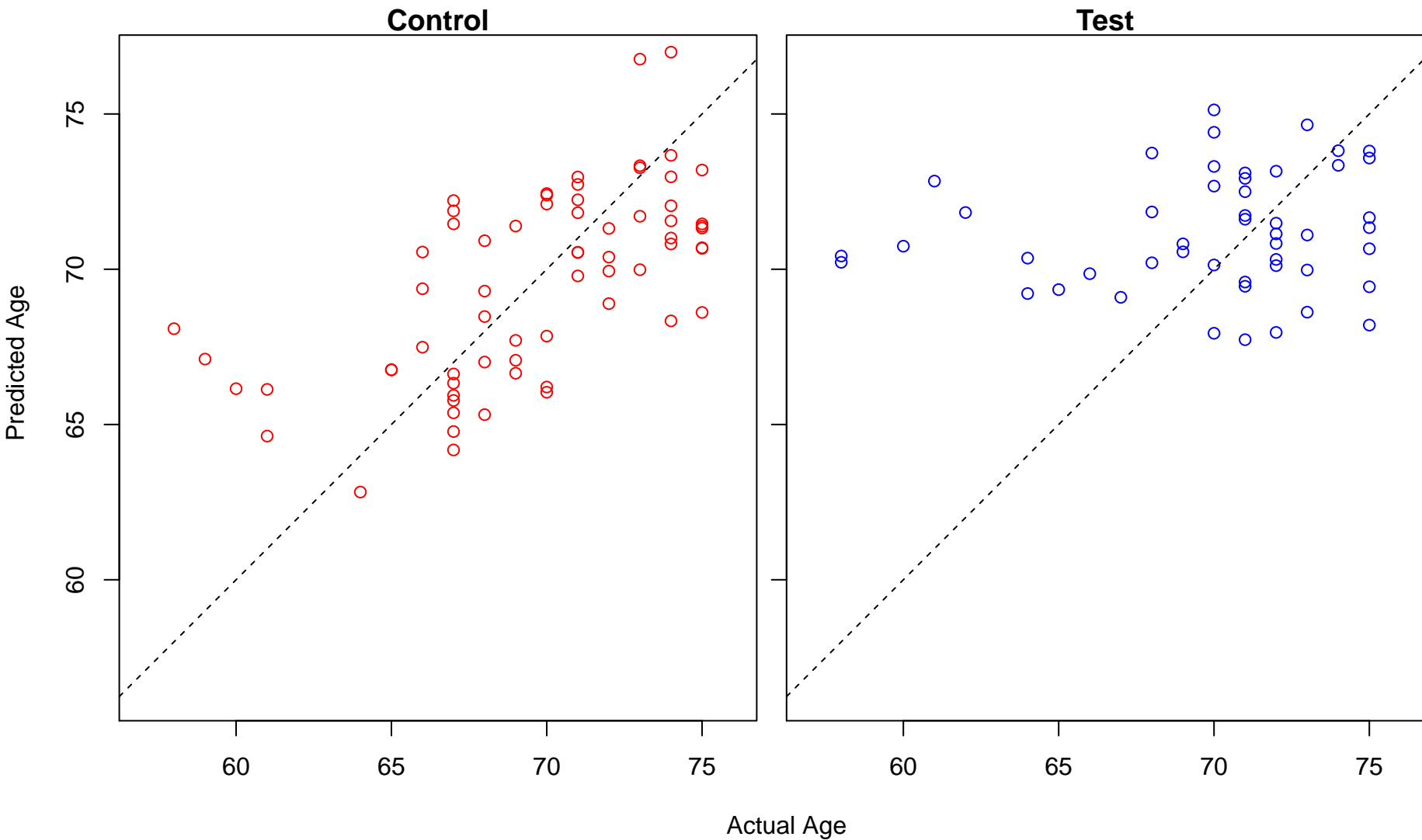
negative regulation of glial cell differentiation (Score: 1.051758)



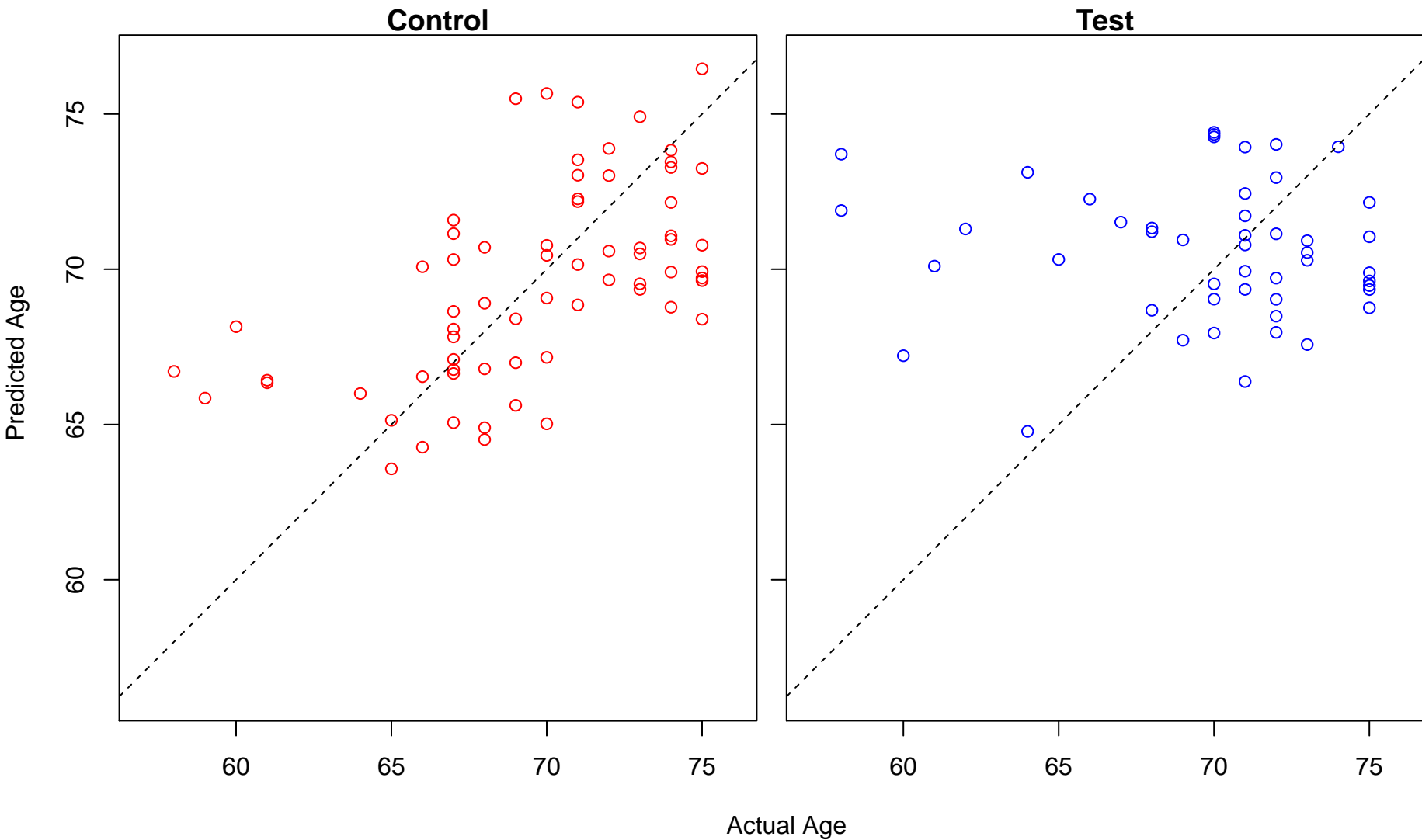
transcription elongation from RNA polymerase III promoter (Score: 1.051510)



termination of RNA polymerase III transcription (Score: 1.051510)

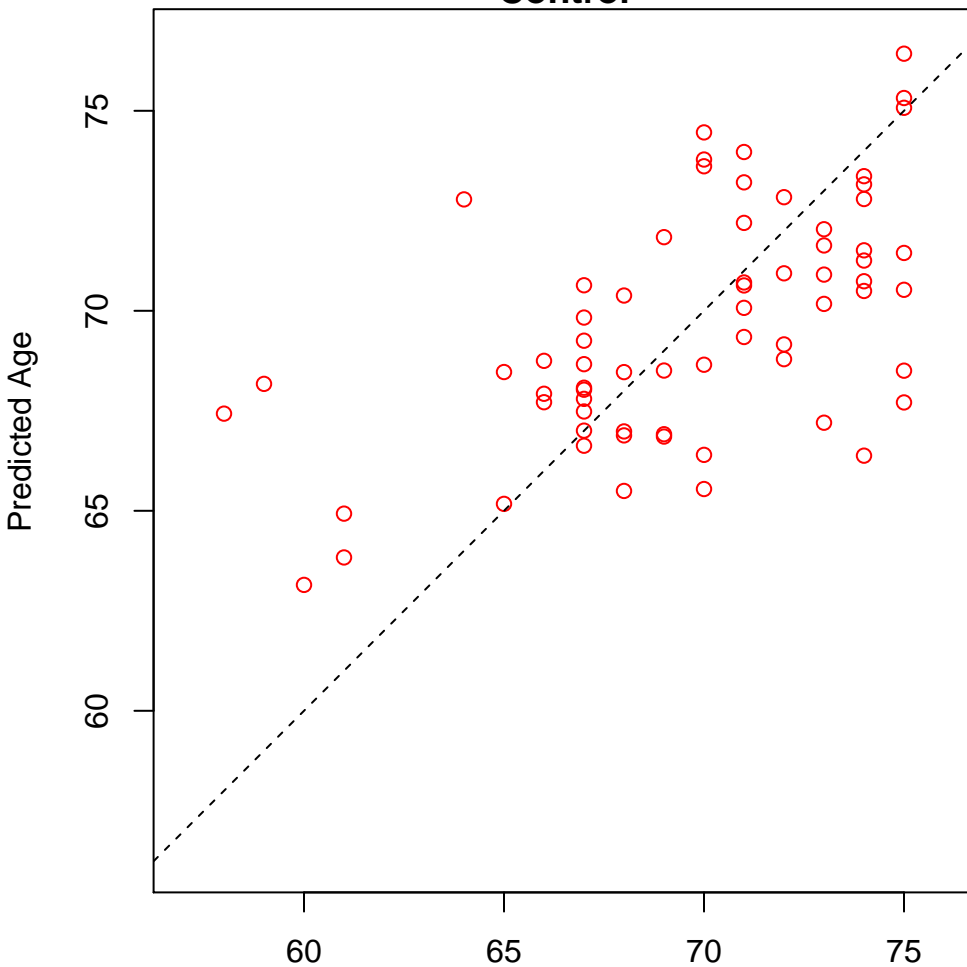


regulation of early endosome to late endosome transport (Score: 1.051129)

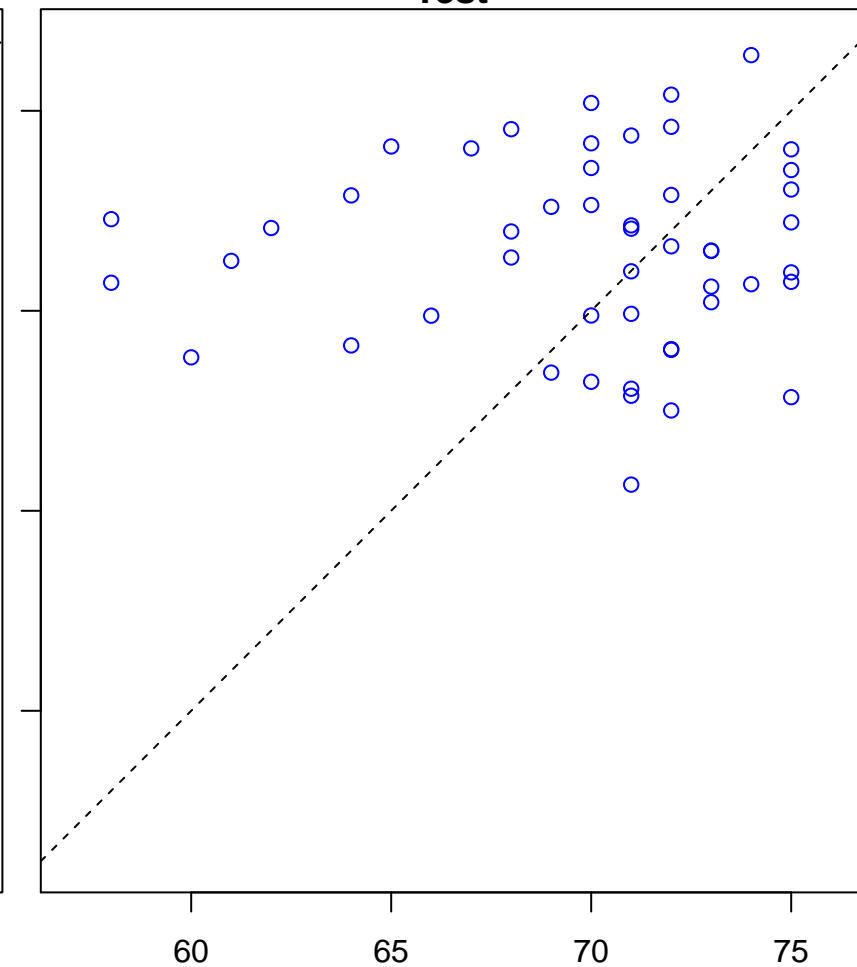


regulation of histone H3-K9 methylation (Score: 1.051064)

Control

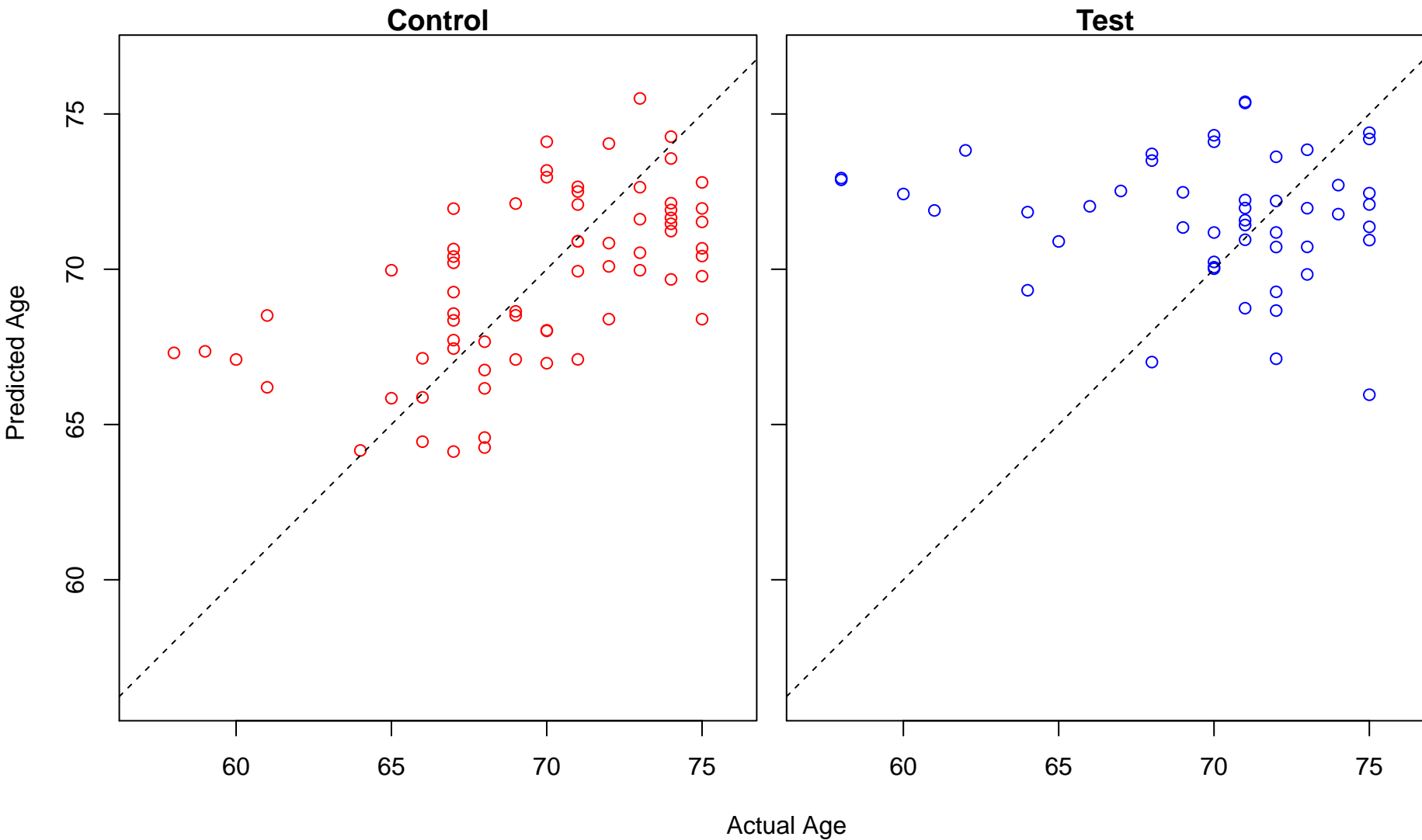


Test

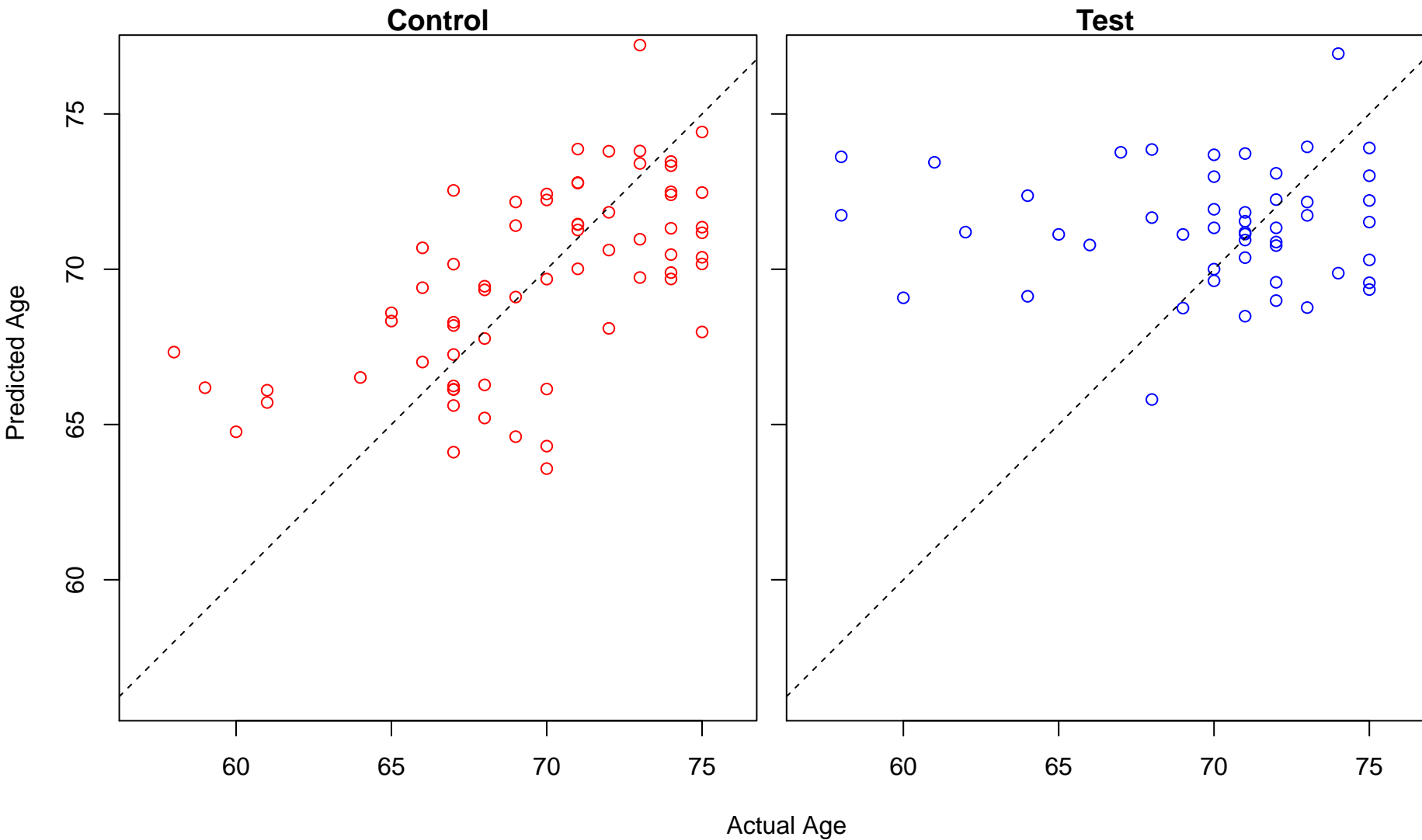


Actual Age

negative regulation of striated muscle cell differentiation (Score: 1.050780)

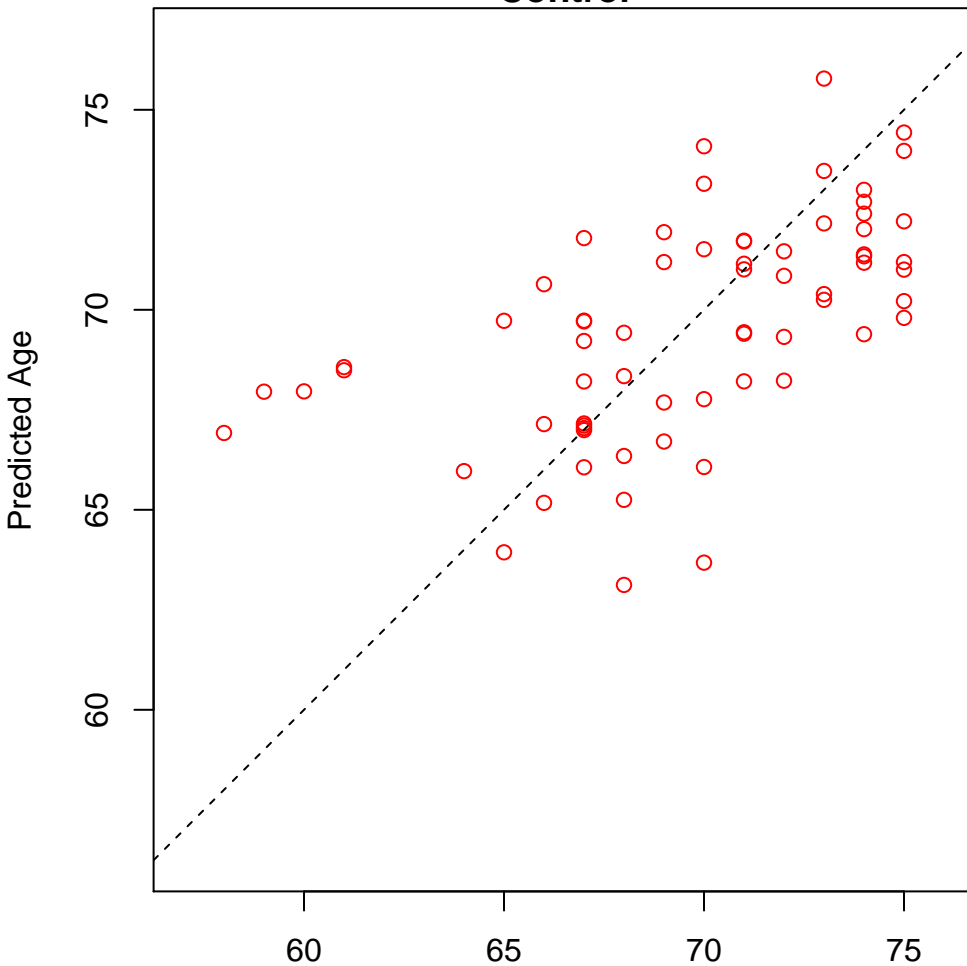


pigment biosynthetic process (Score: 1.050722)

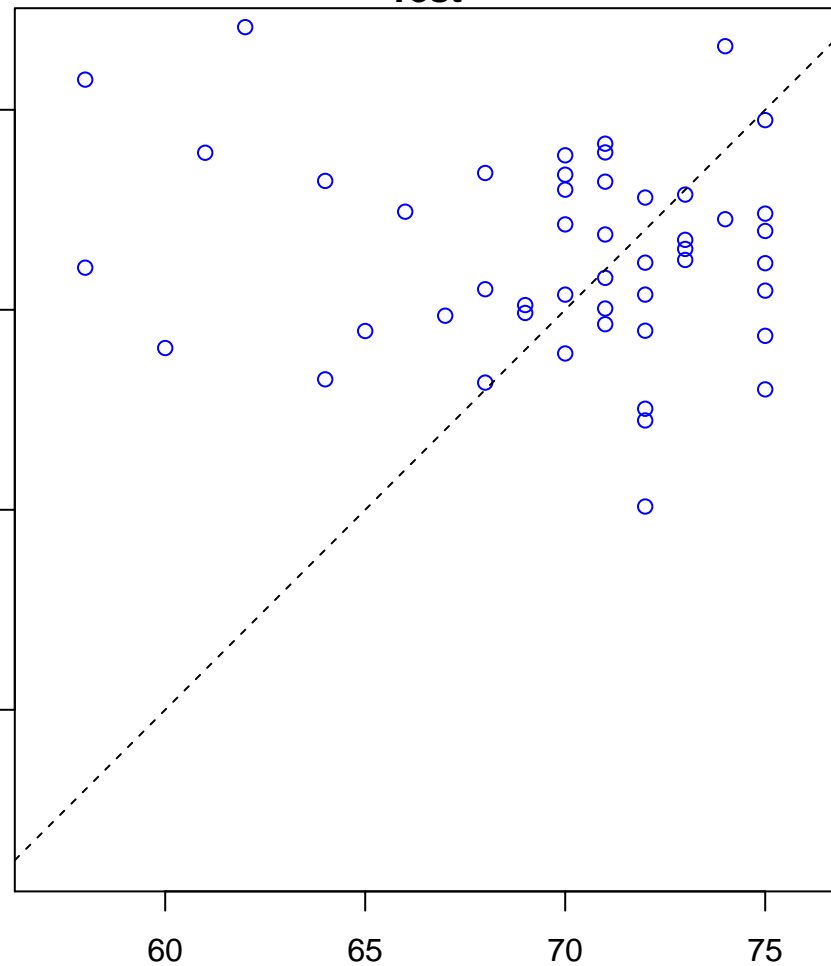


response to arsenic-containing substance (Score: 1.050714)

Control

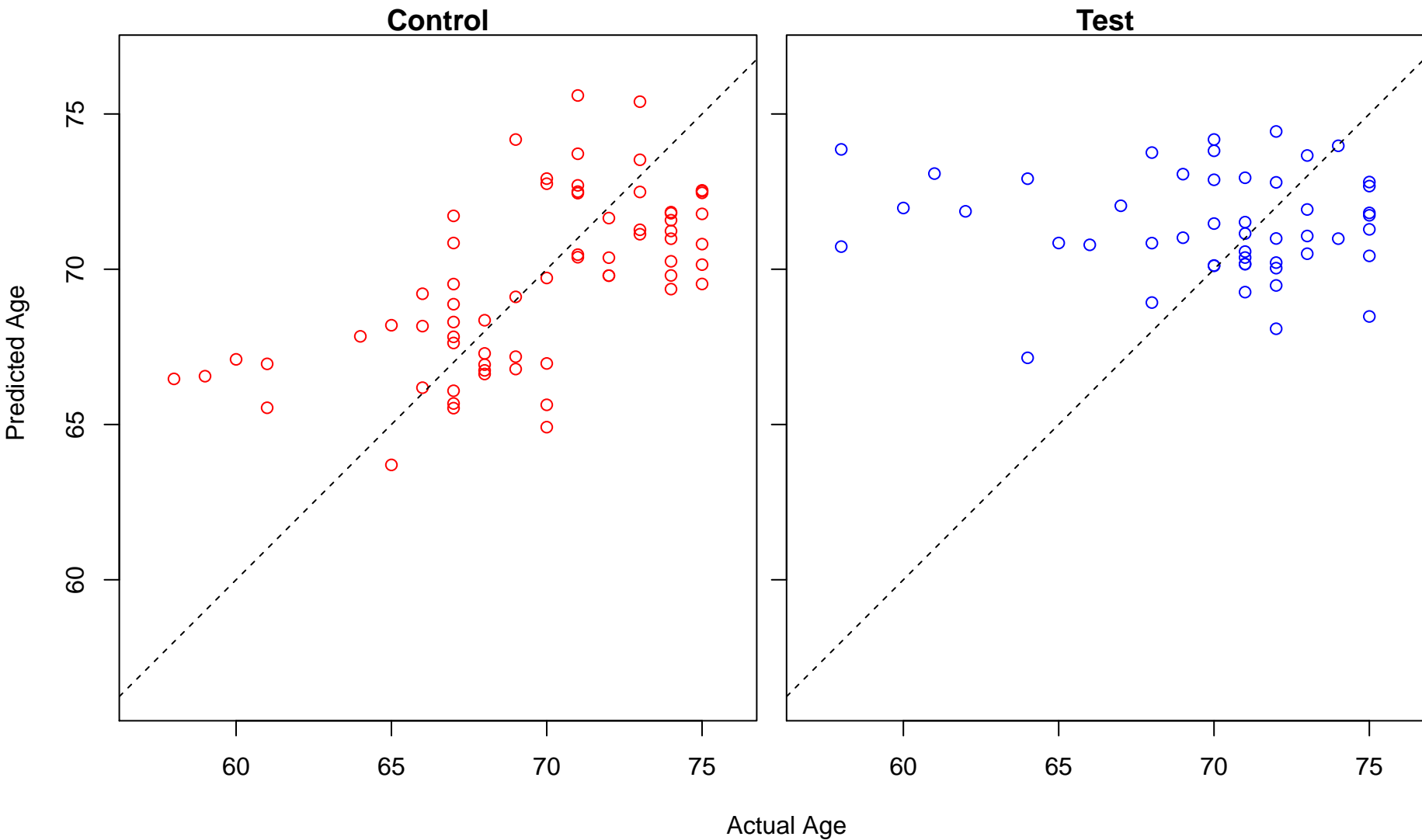


Test

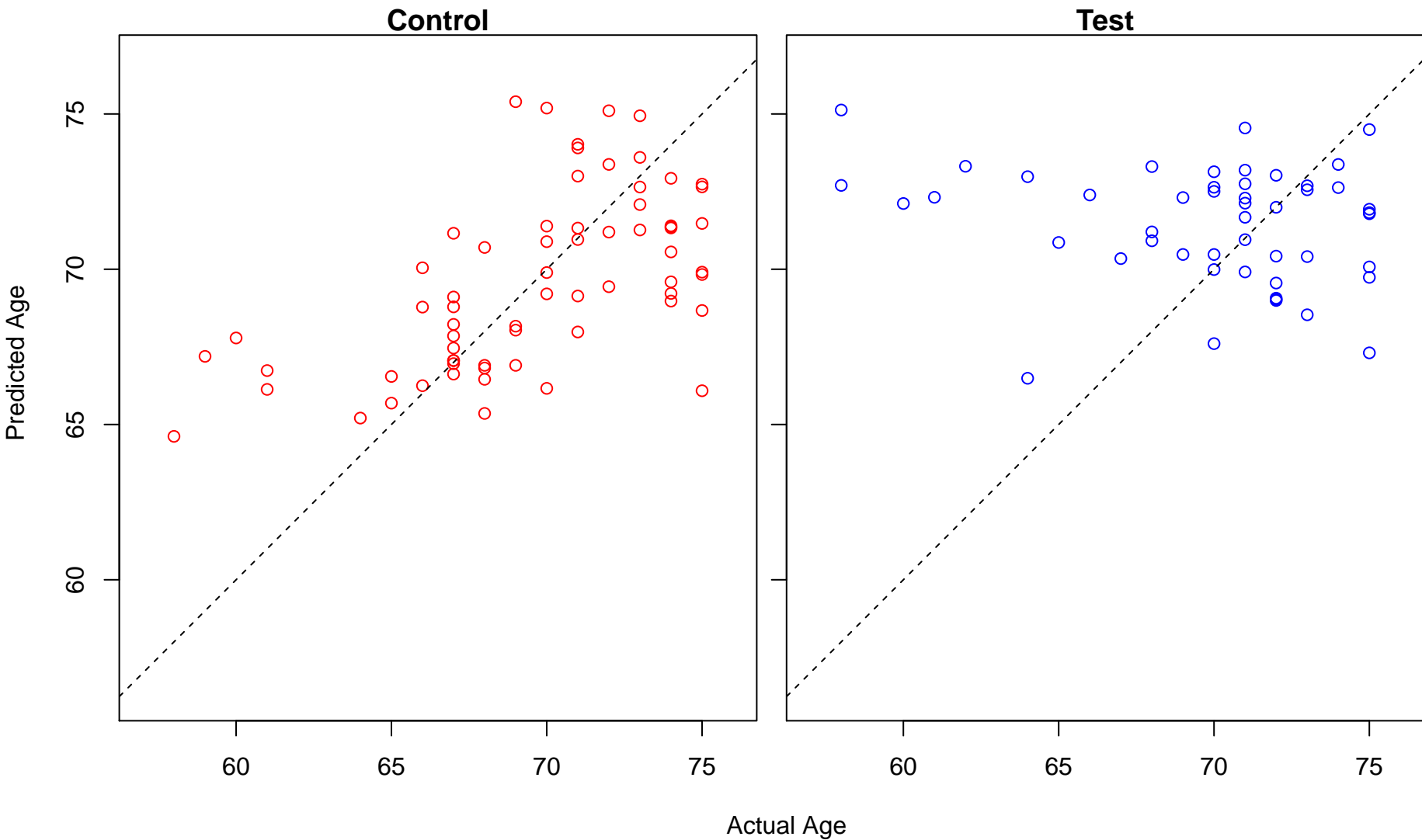


Actual Age

negative regulation of DNA biosynthetic process (Score: 1.050362)

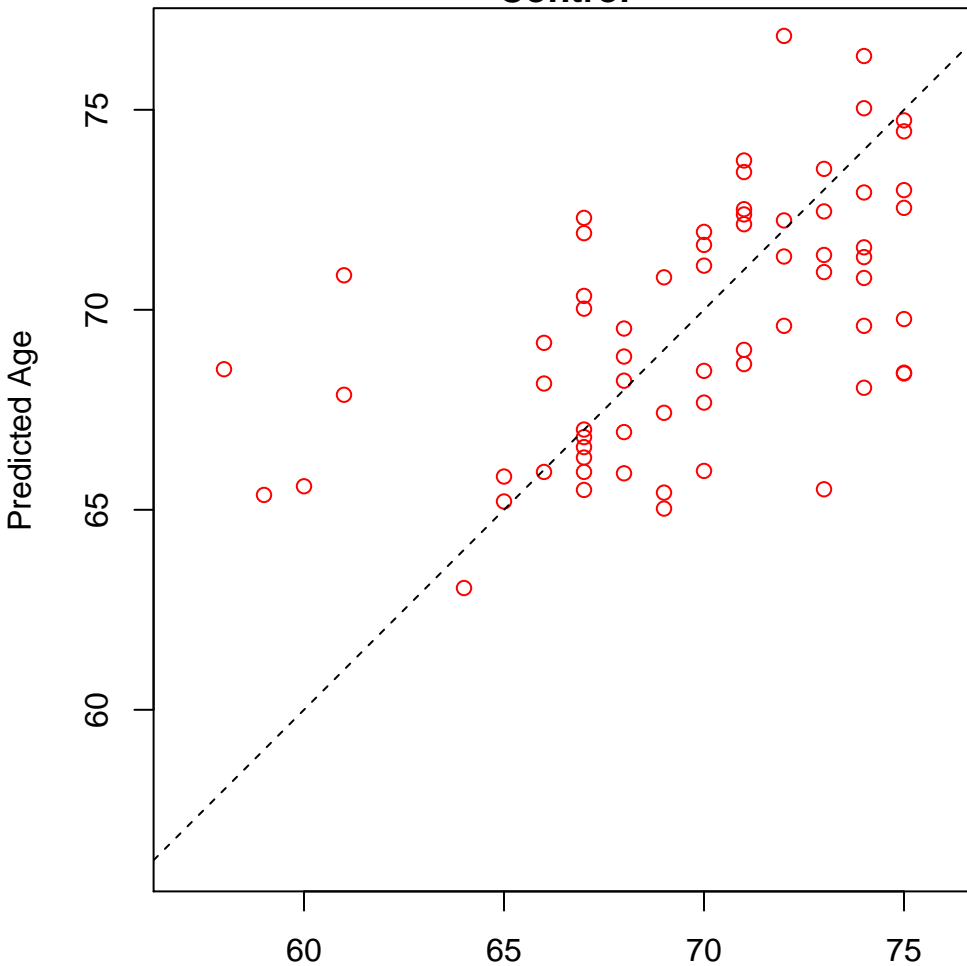


photoreceptor cell maintenance (Score: 1.049897)

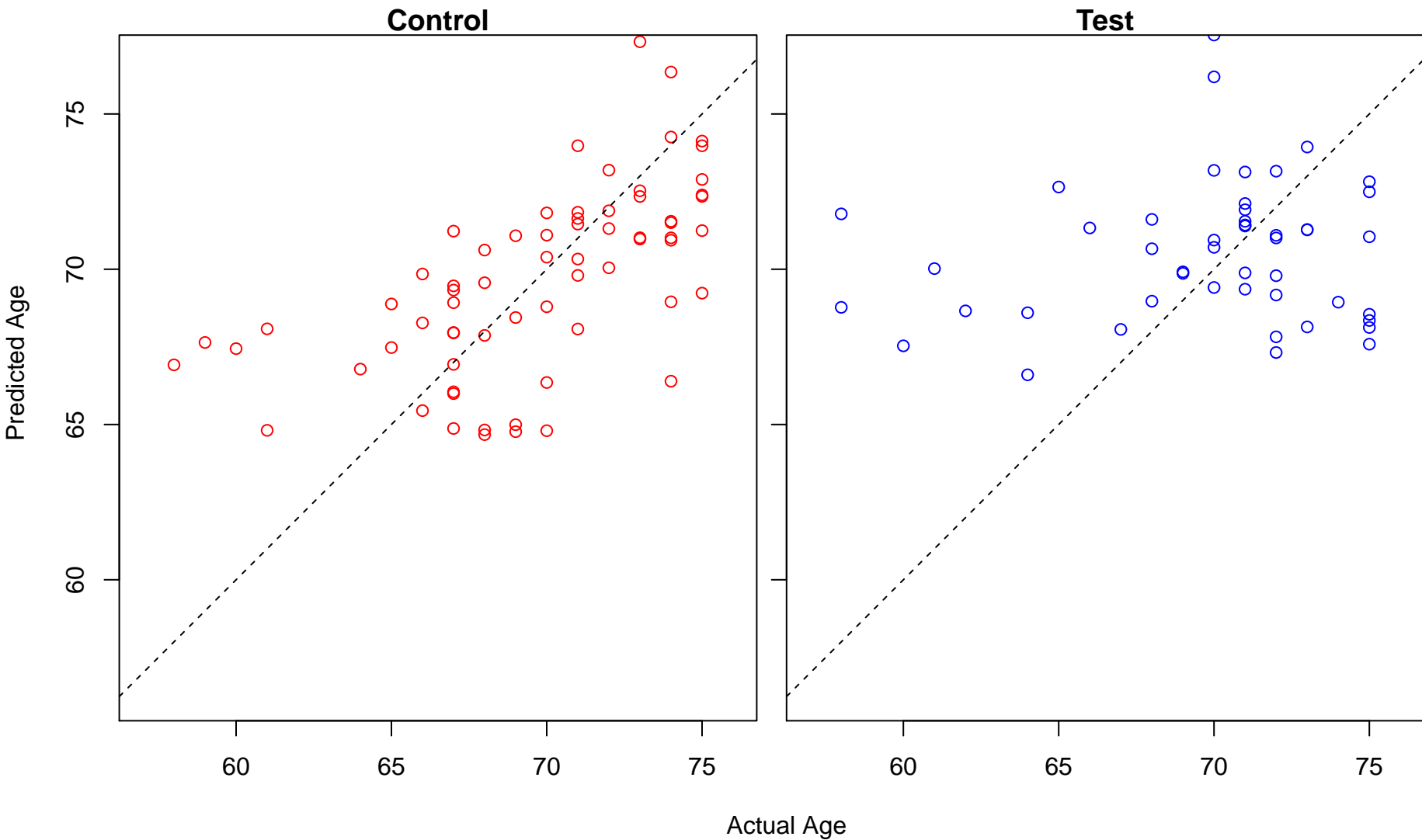


long-chain fatty acid metabolic process (Score: 1.049676)

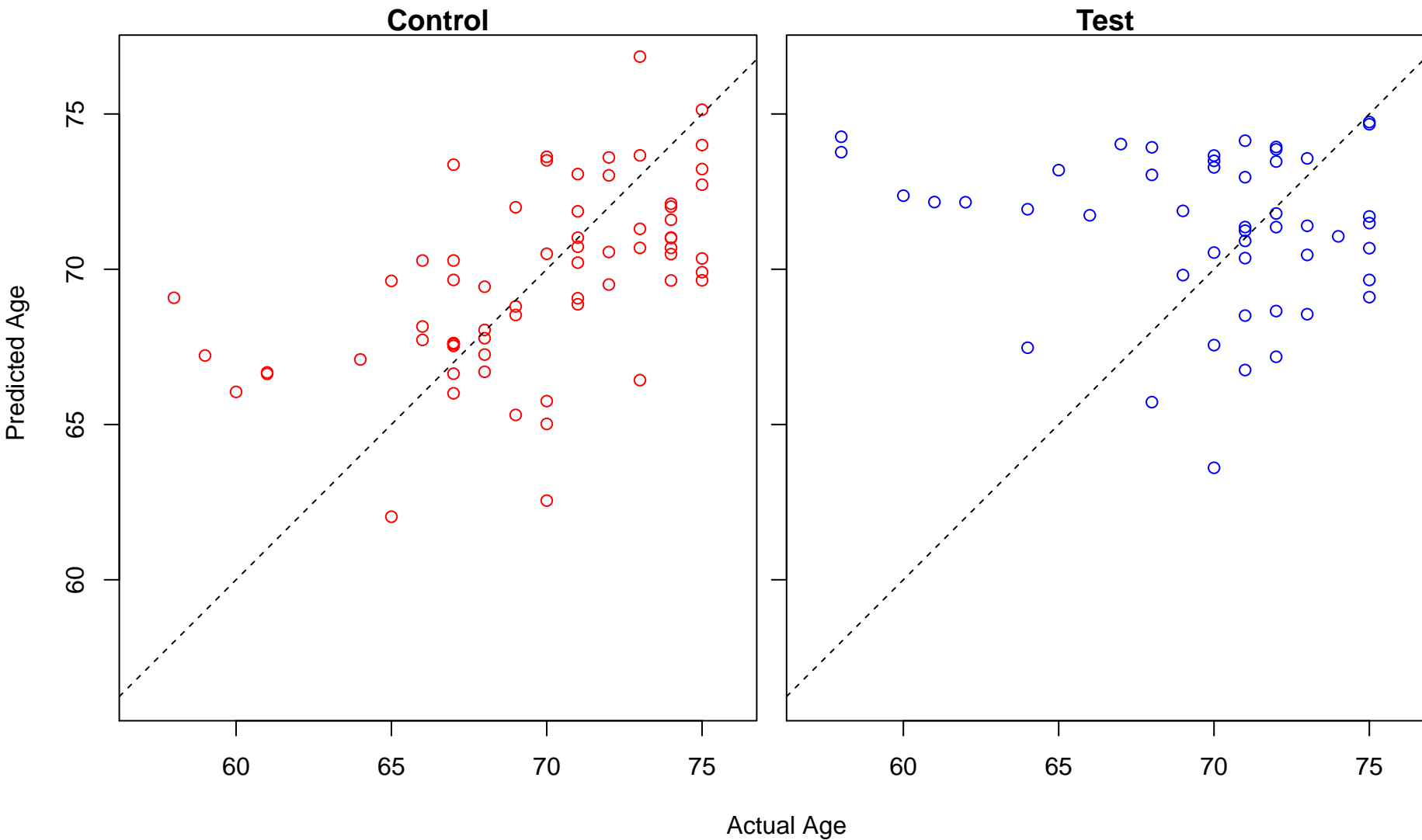
Control



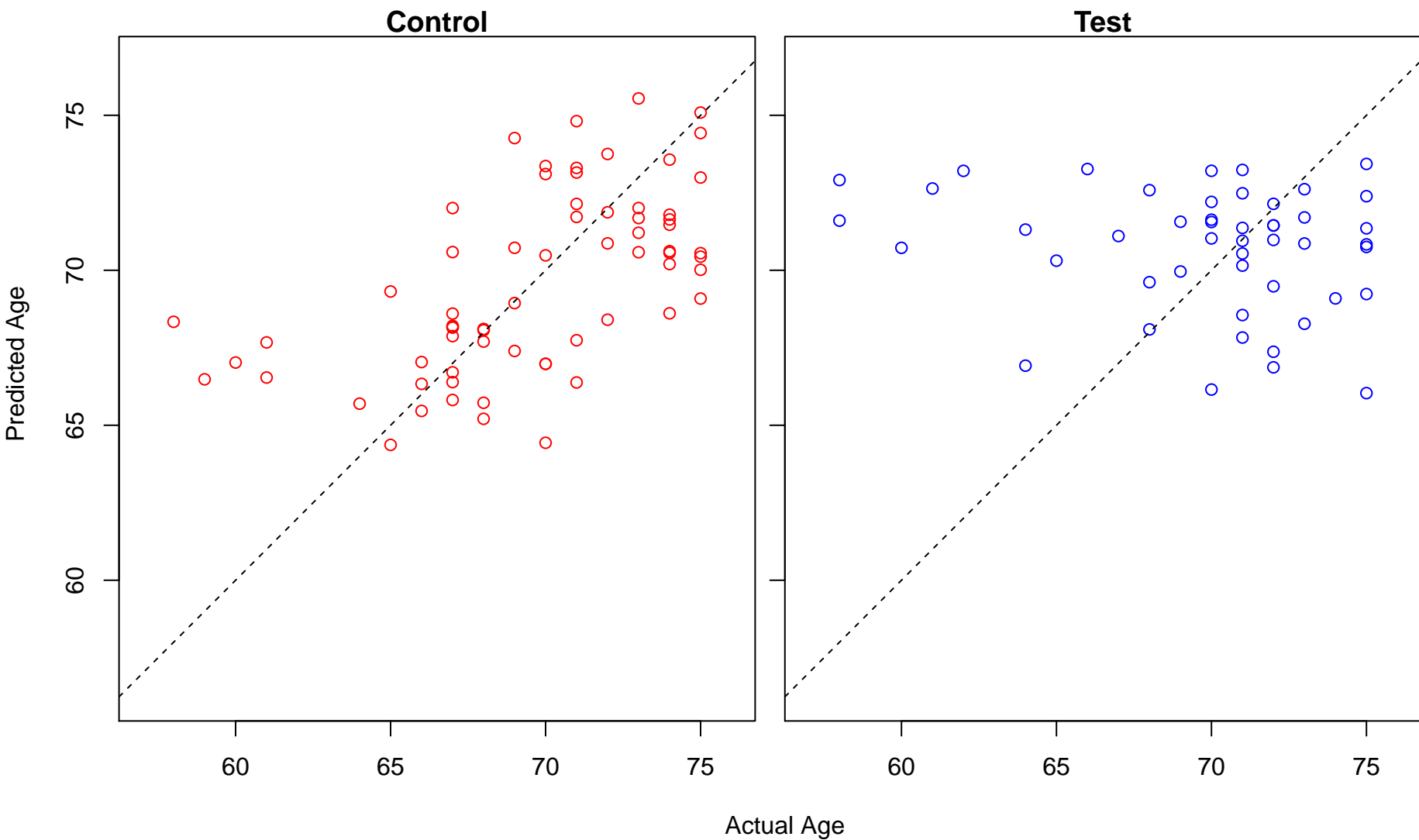
triglyceride catabolic process (Score: 1.049172)



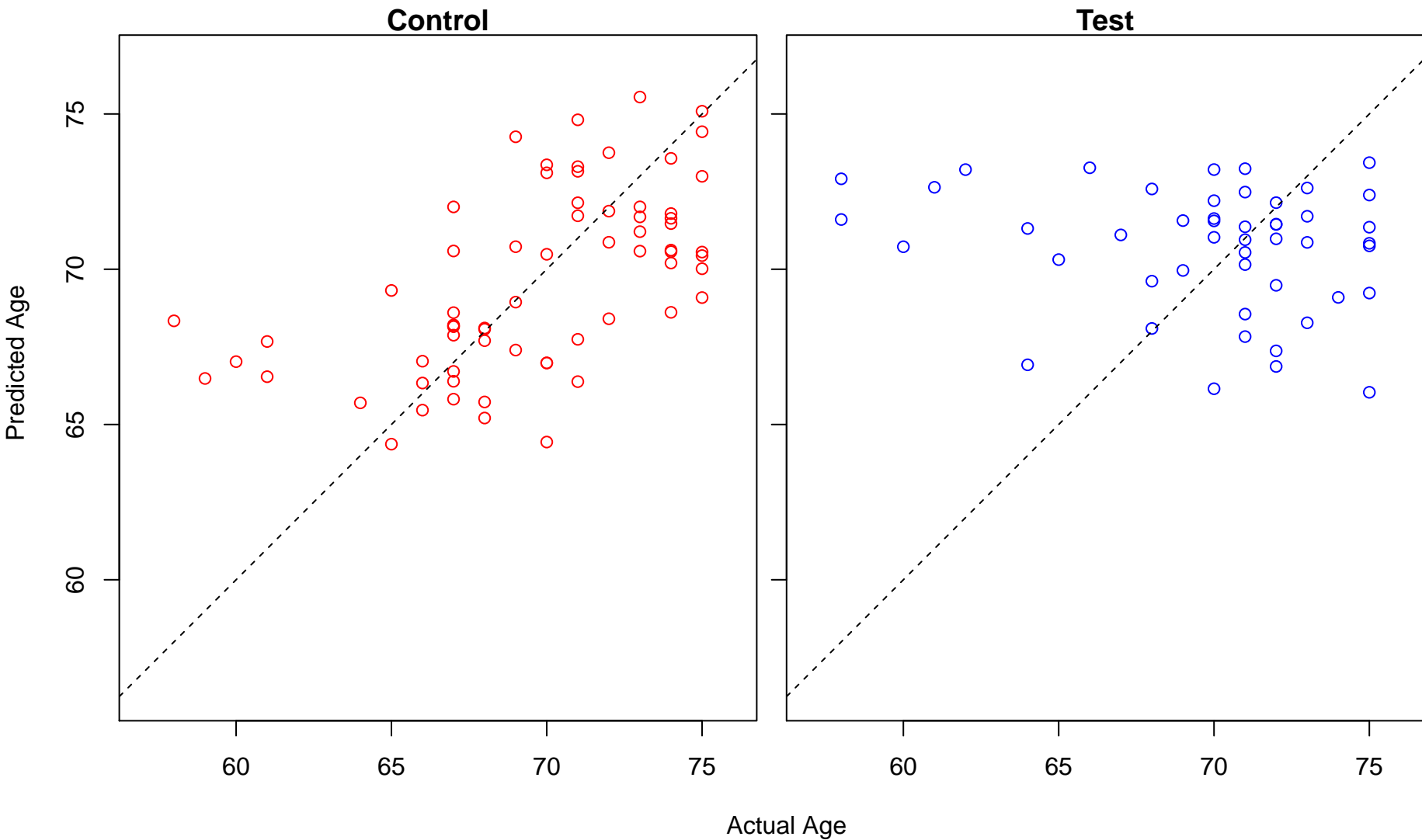
long-chain fatty-acyl-CoA metabolic process (Score: 1.049028)



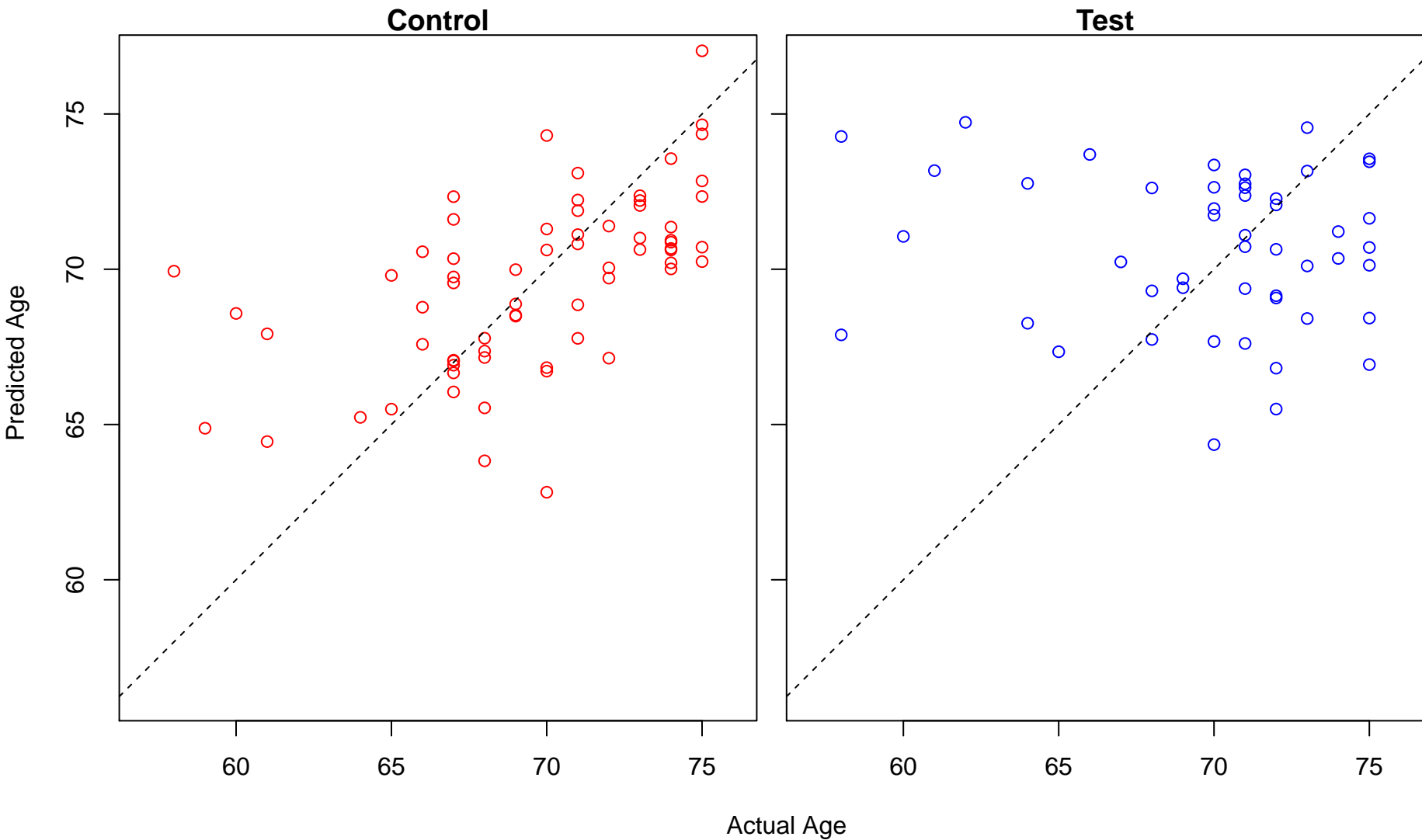
positive regulation of JAK-STAT cascade (Score: 1.048933)



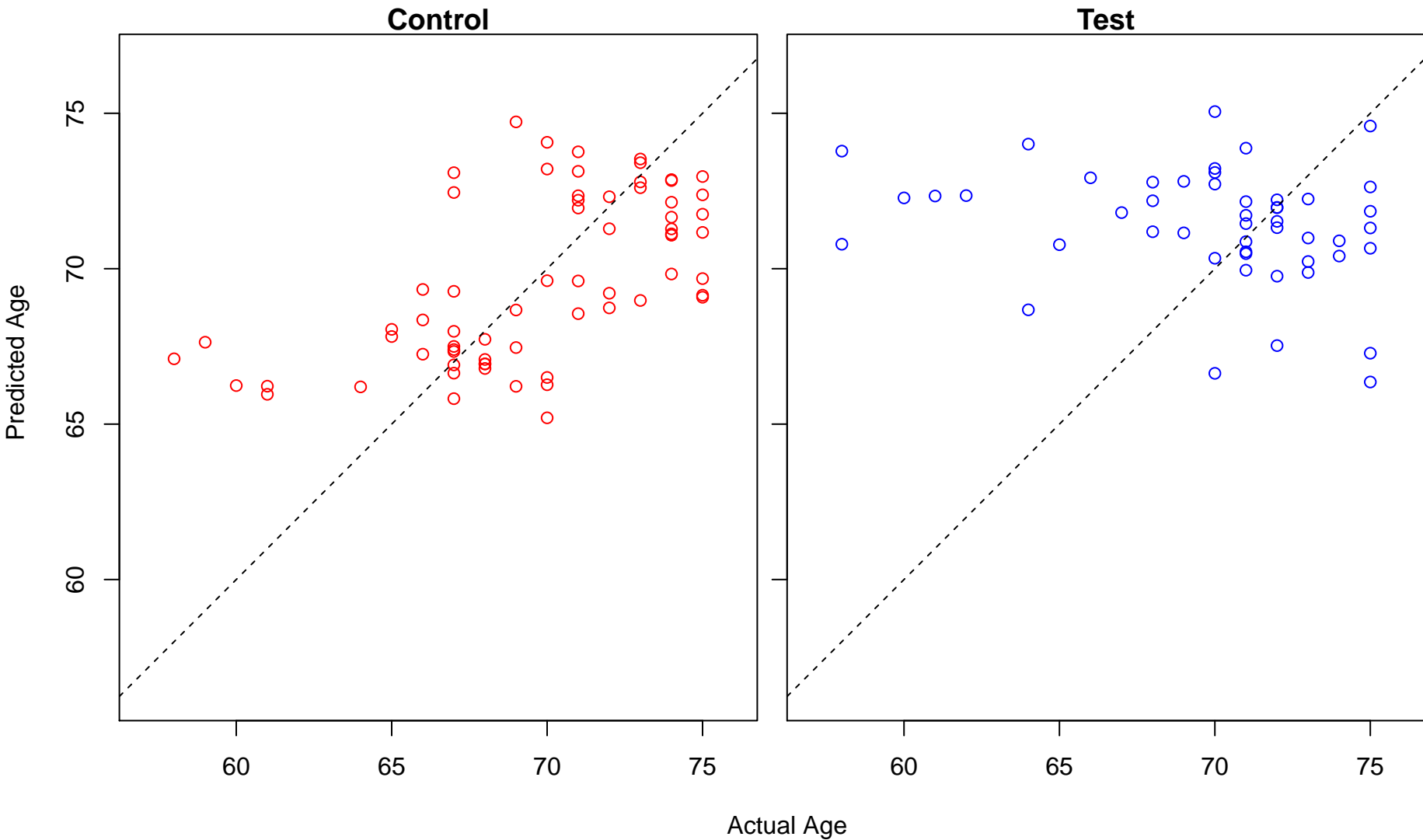
positive regulation of STAT cascade (Score: 1.048933)



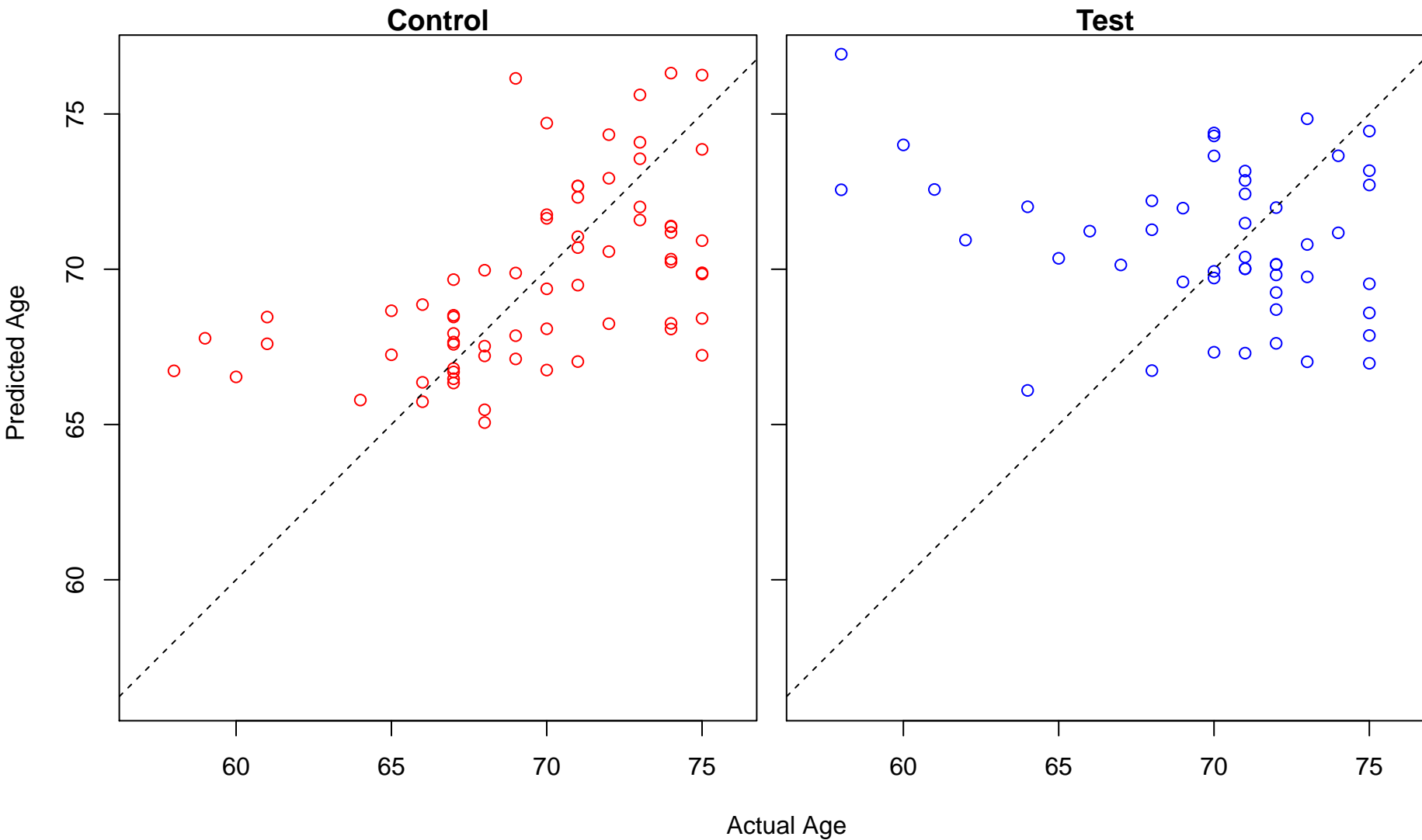
clathrin-mediated endocytosis (Score: 1.048822)



regulation of cell migration involved in sprouting angiogenesis (Score: 1.048785)

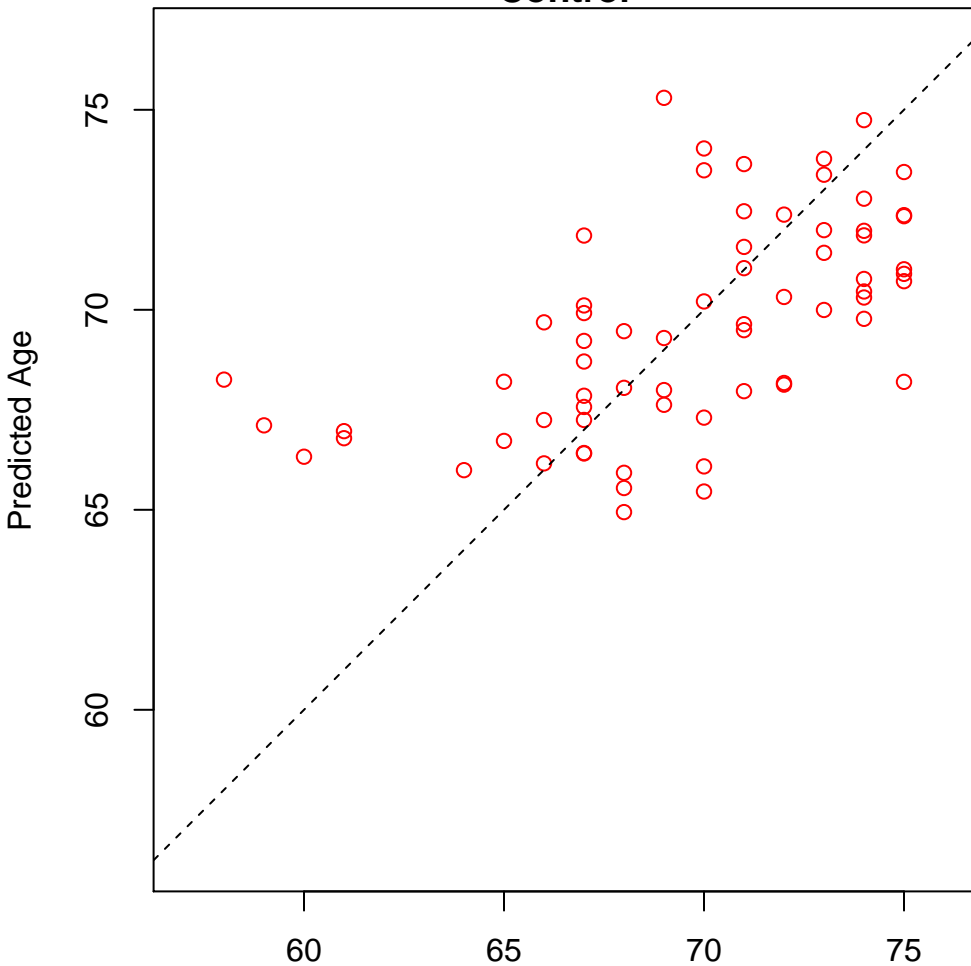


neuromuscular process (Score: 1.047871)

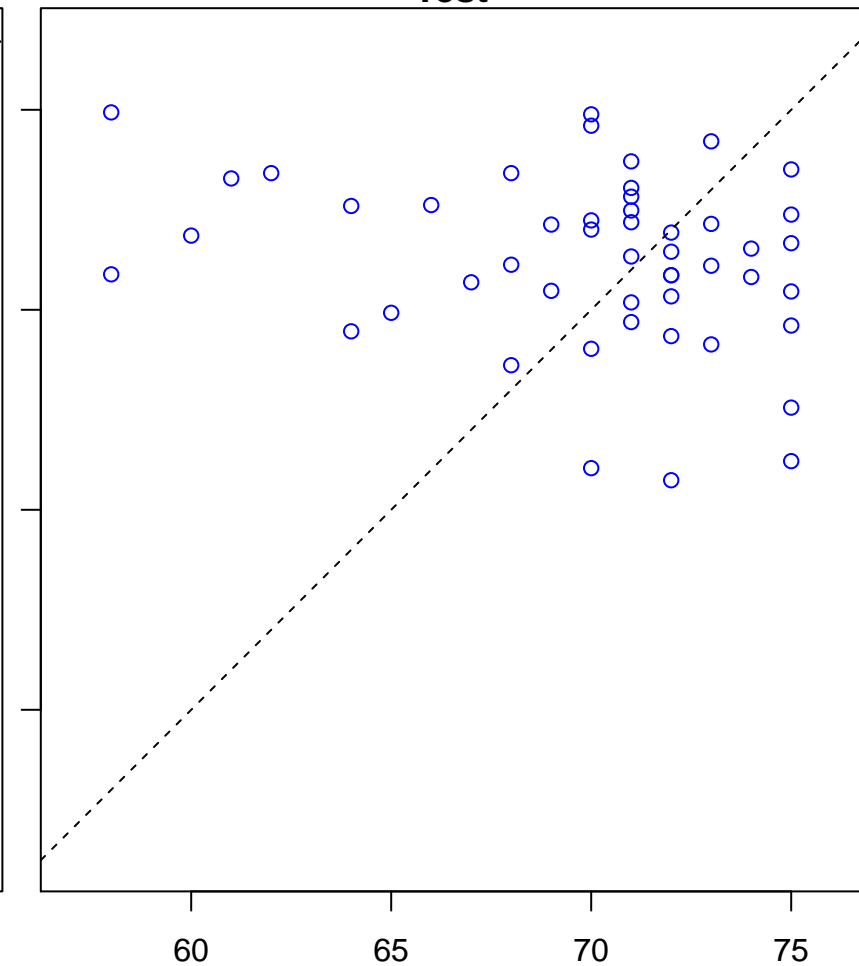


vesicle targeting, rough ER to cis-Golgi (Score: 1.047834)

Control

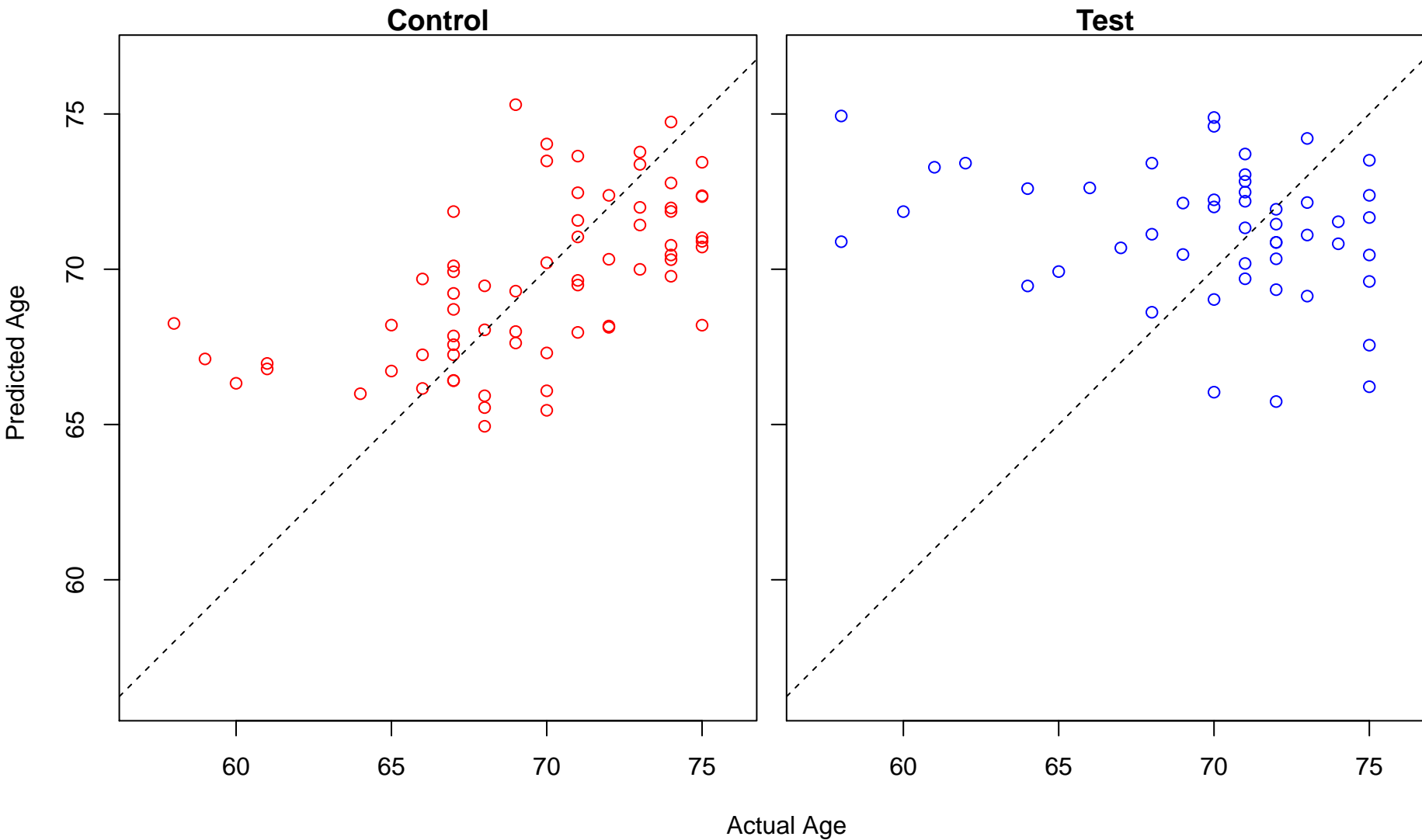


Test

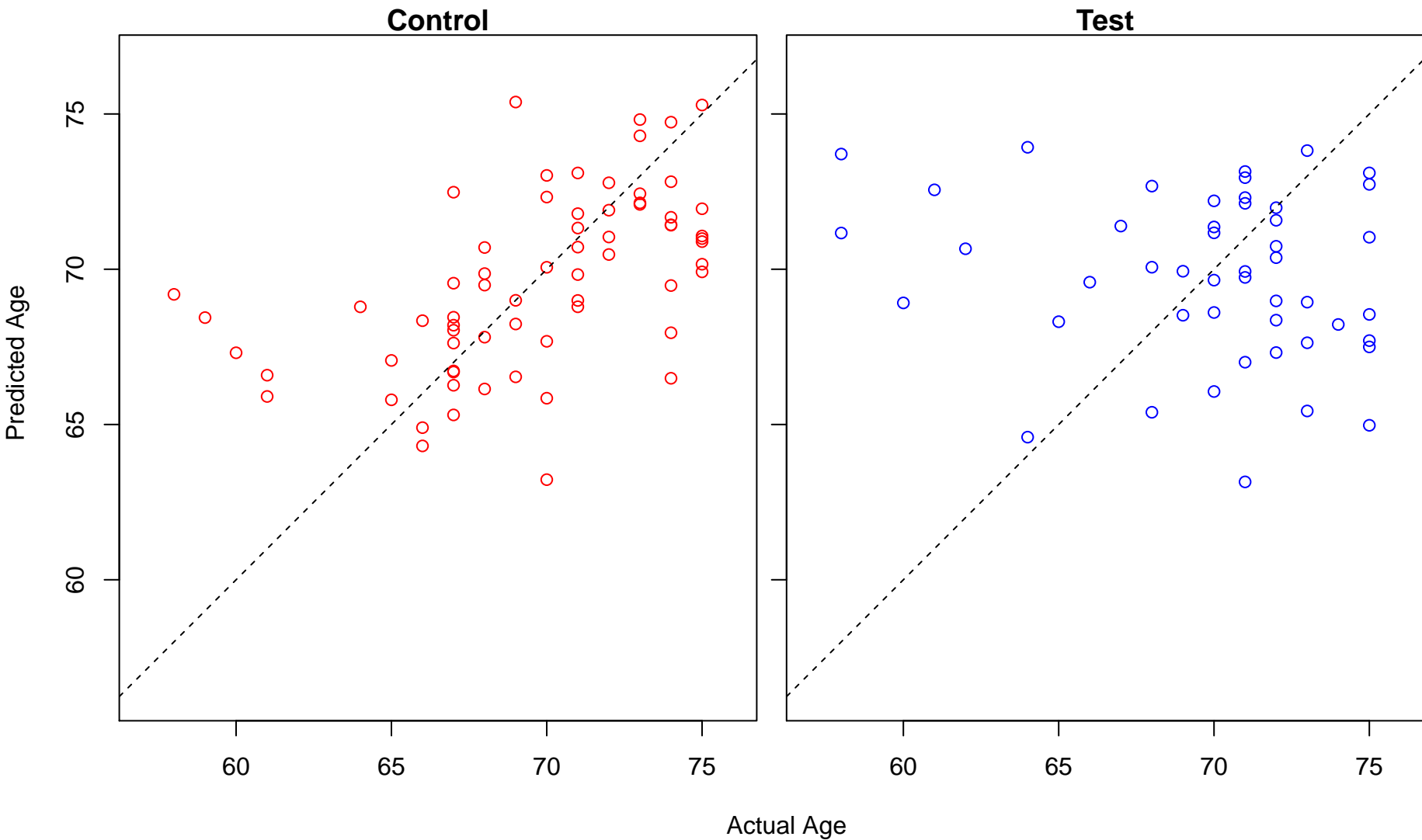


Actual Age

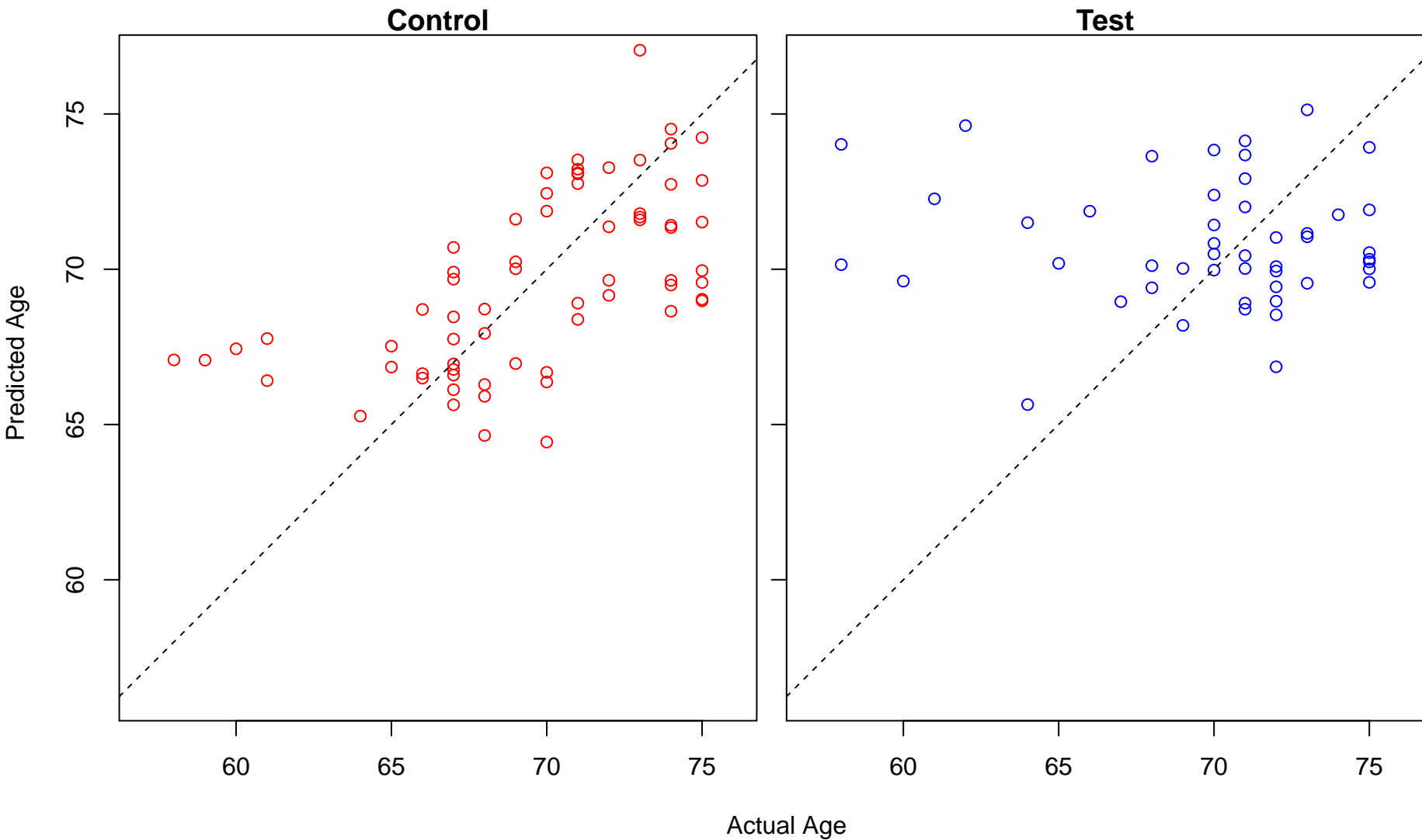
COPII vesicle coating (Score: 1.047834)



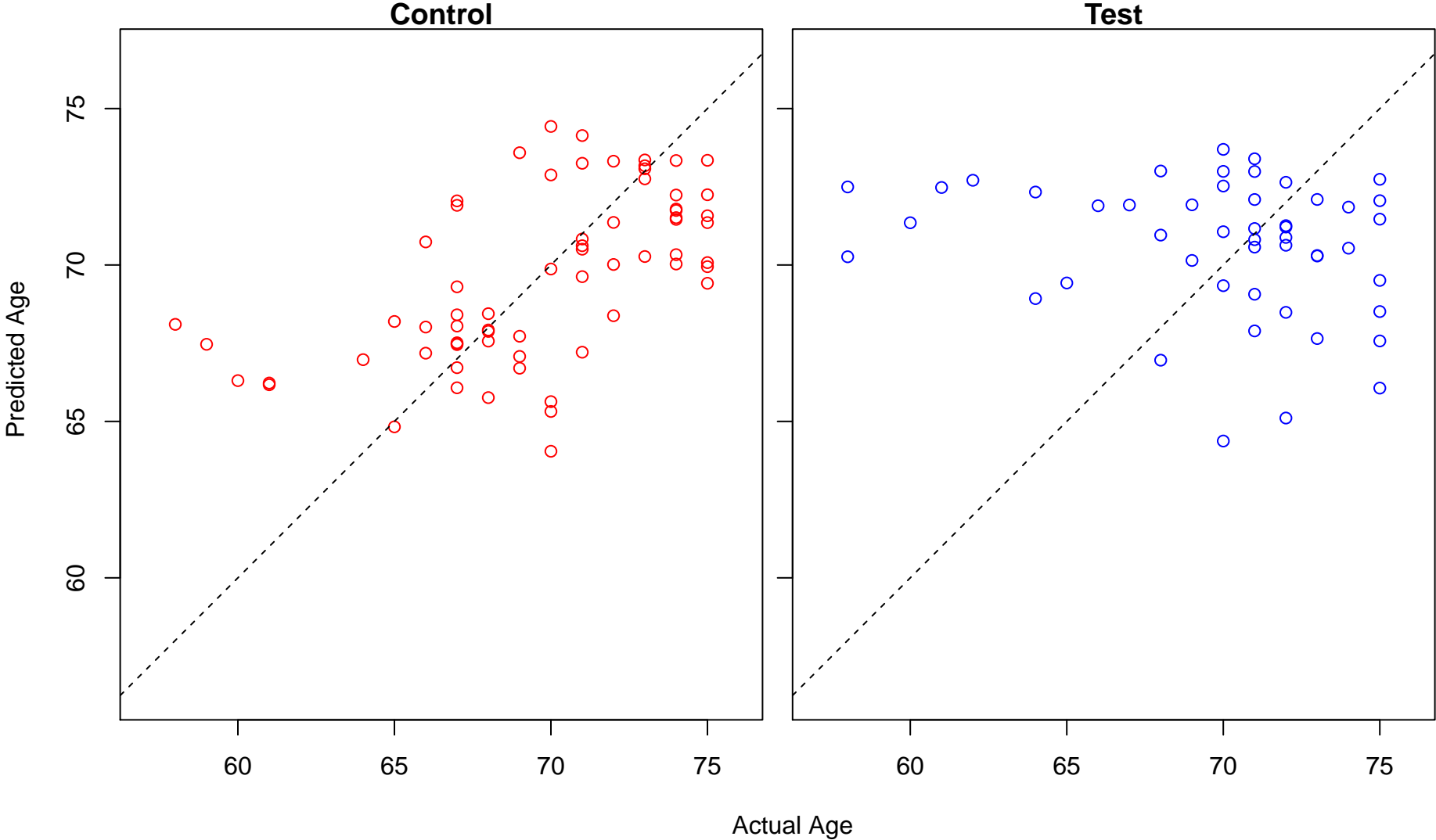
positive regulation of interleukin-8 secretion (Score: 1.047508)



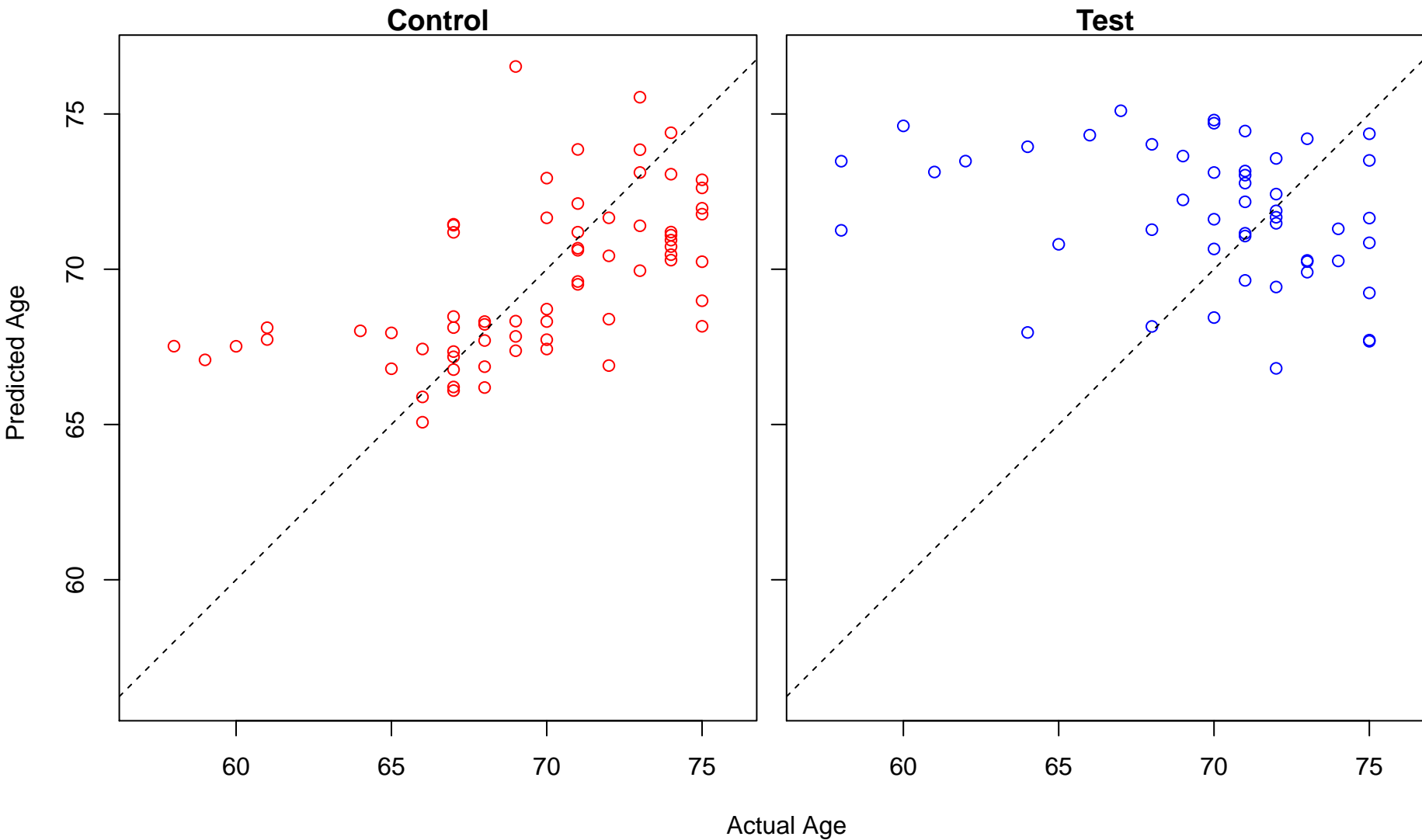
oxidoreduction coenzyme metabolic process (Score: 1.047446)



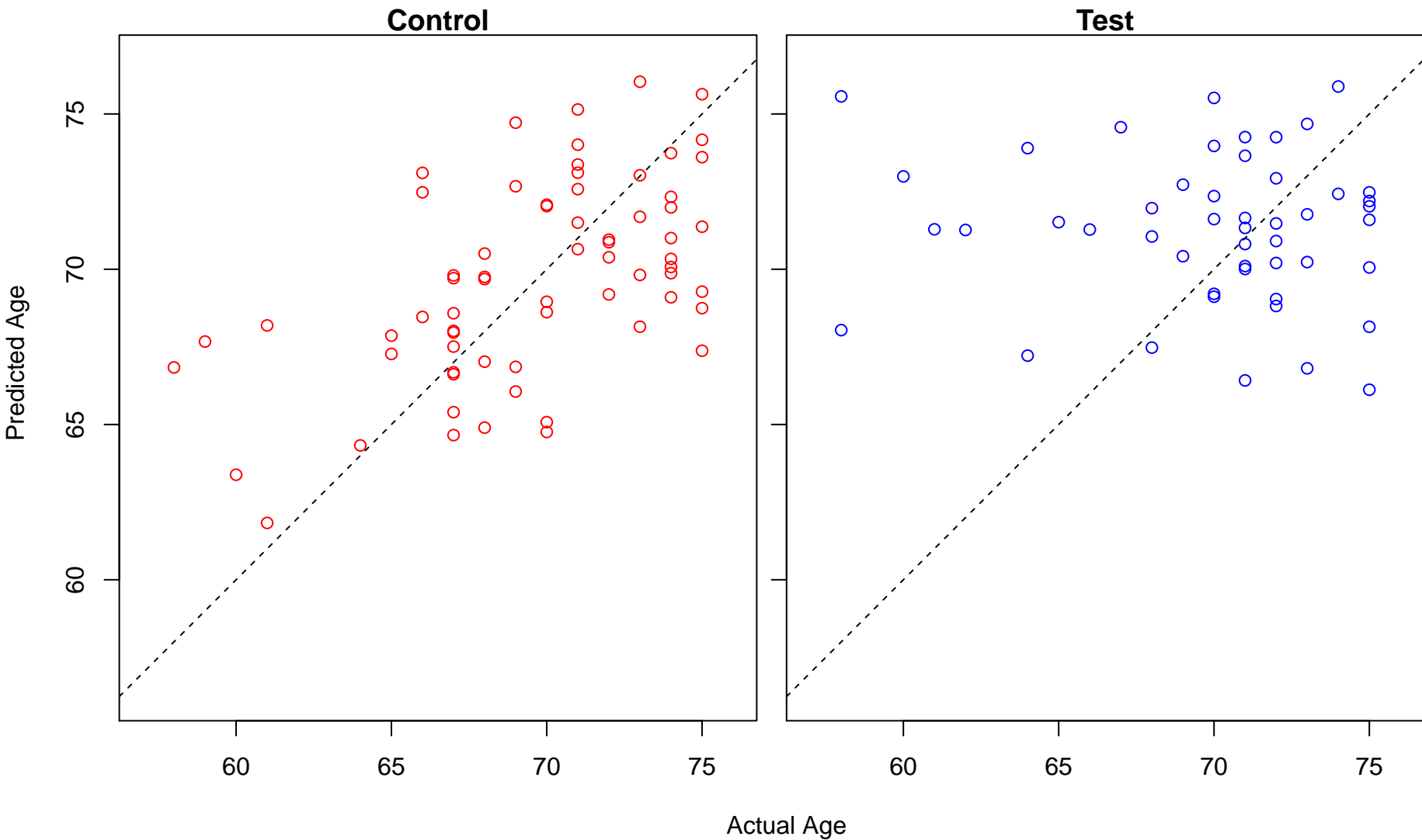
regulation of tumor necrosis factor superfamily cytokine production (Score: 1.047311)



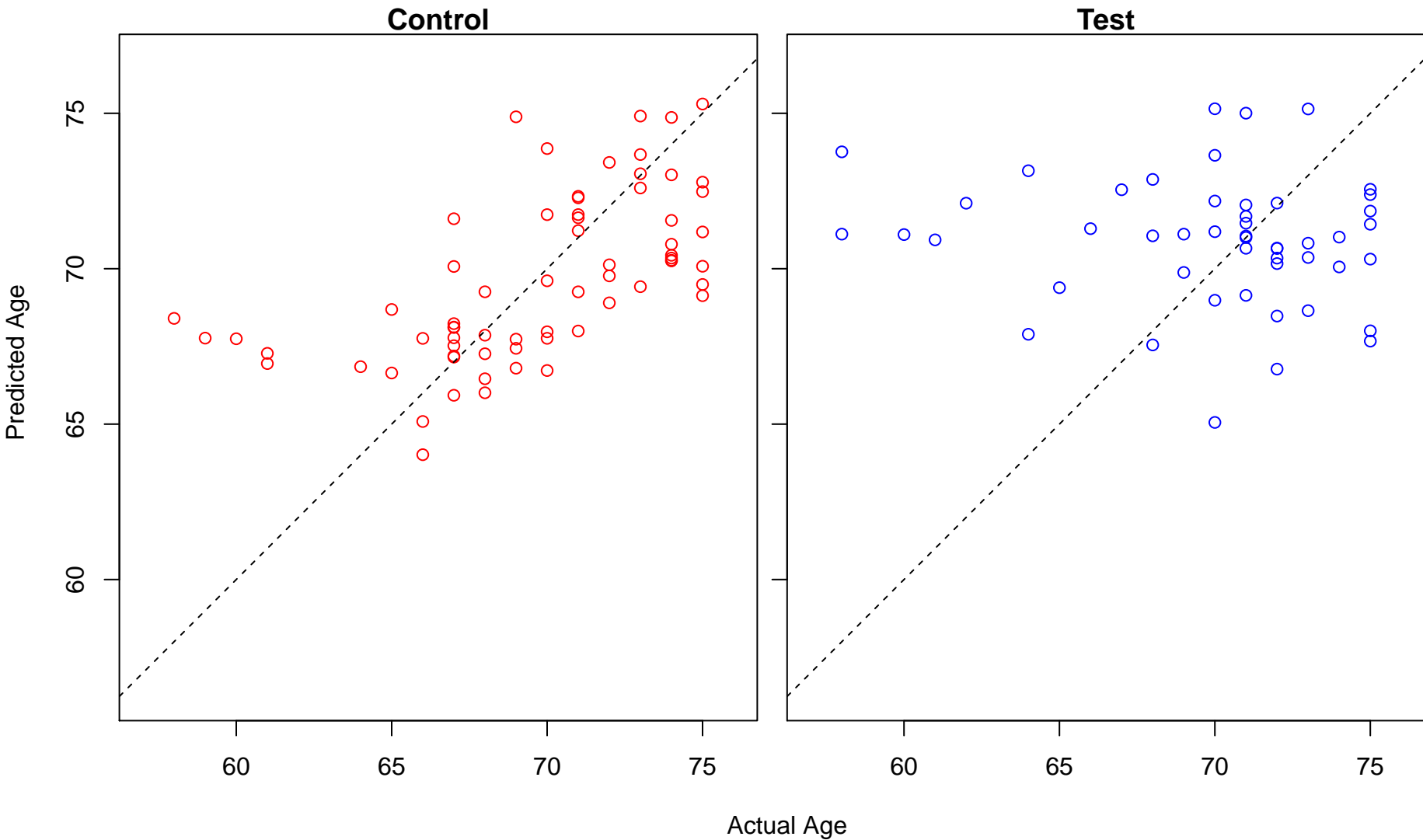
negative regulation of T-helper cell differentiation (Score: 1.046265)



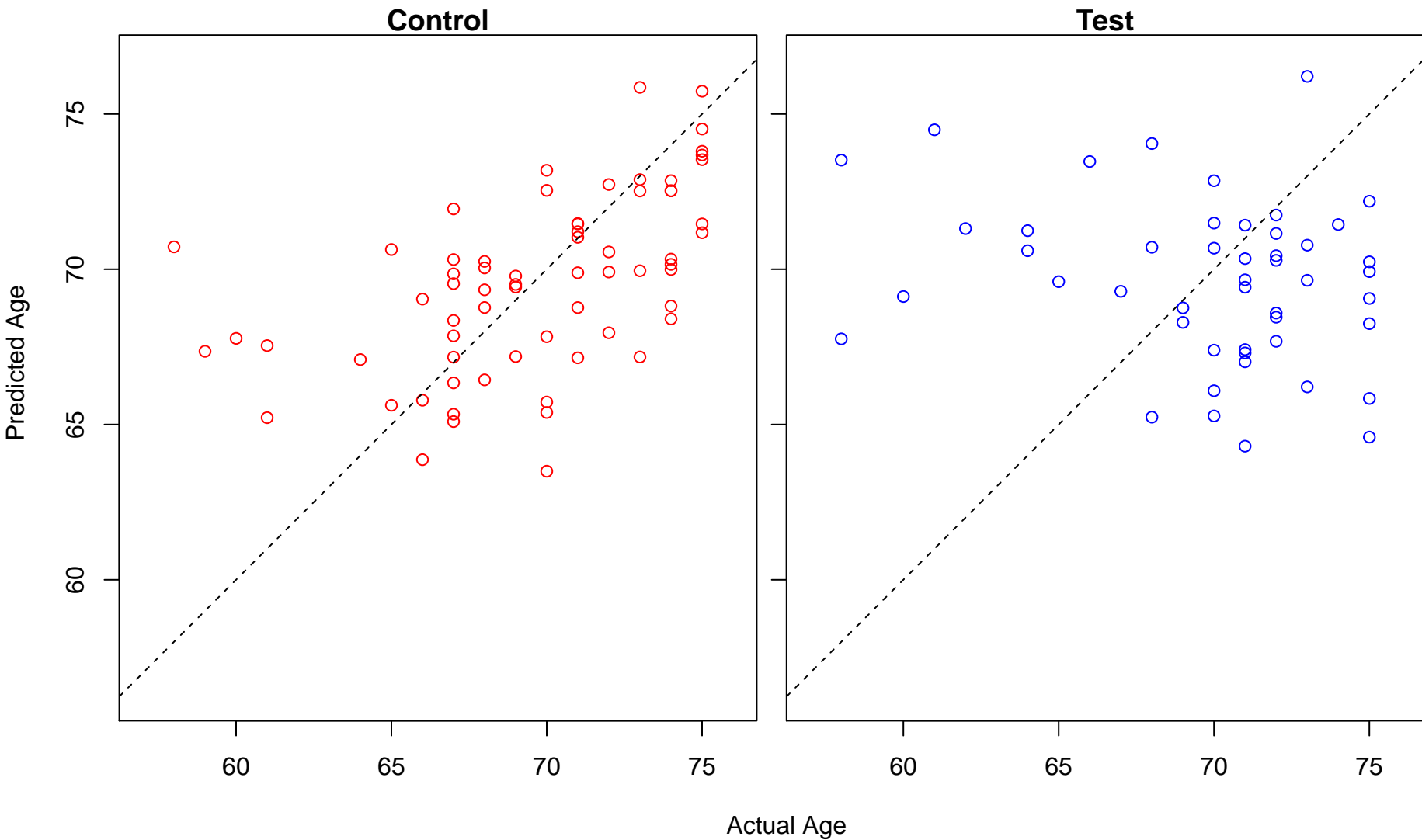
germ cell development (Score: 1.046065)



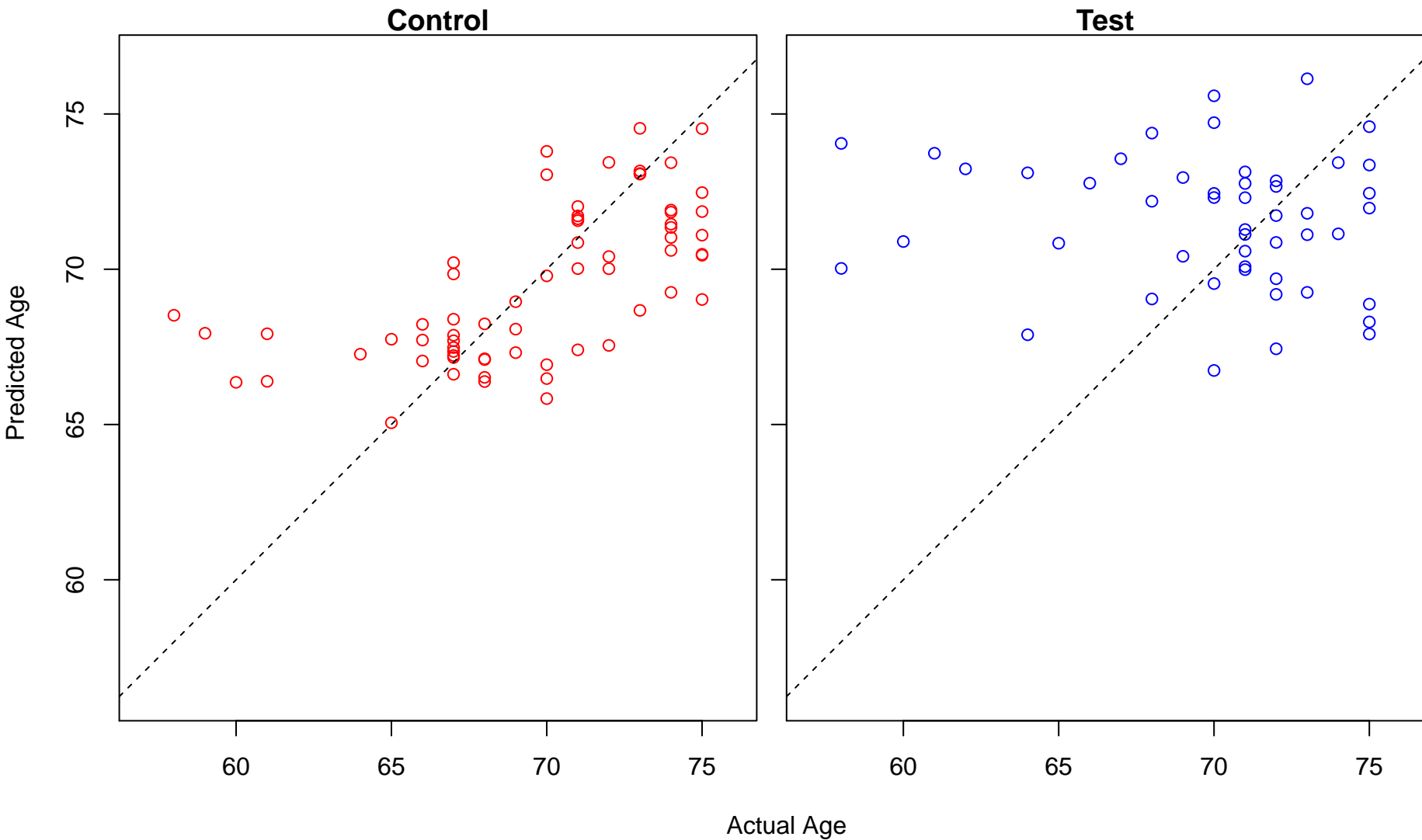
cytoplasmic mRNA processing body assembly (Score: 1.046009)



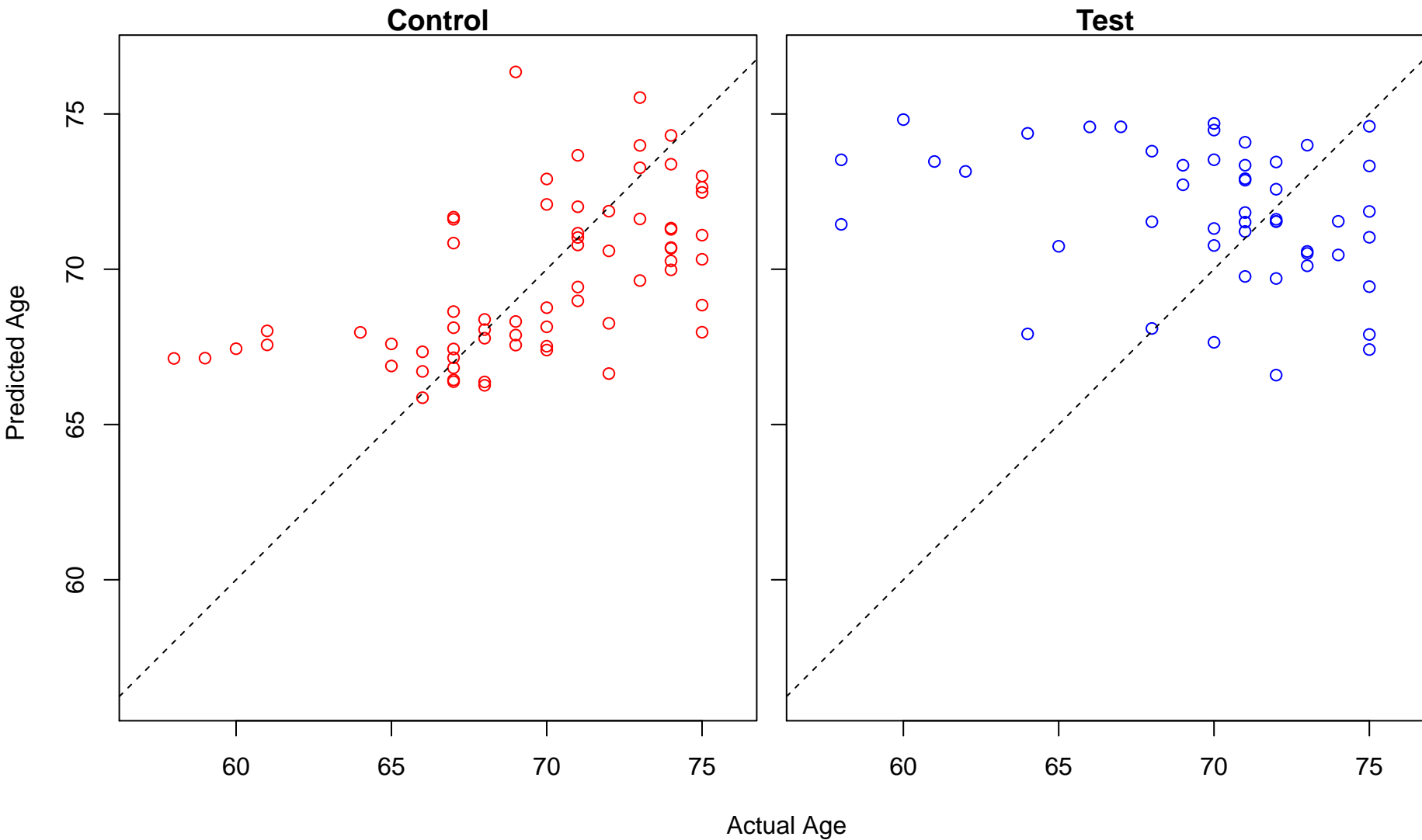
regulation of activin receptor signaling pathway (Score: 1.045982)



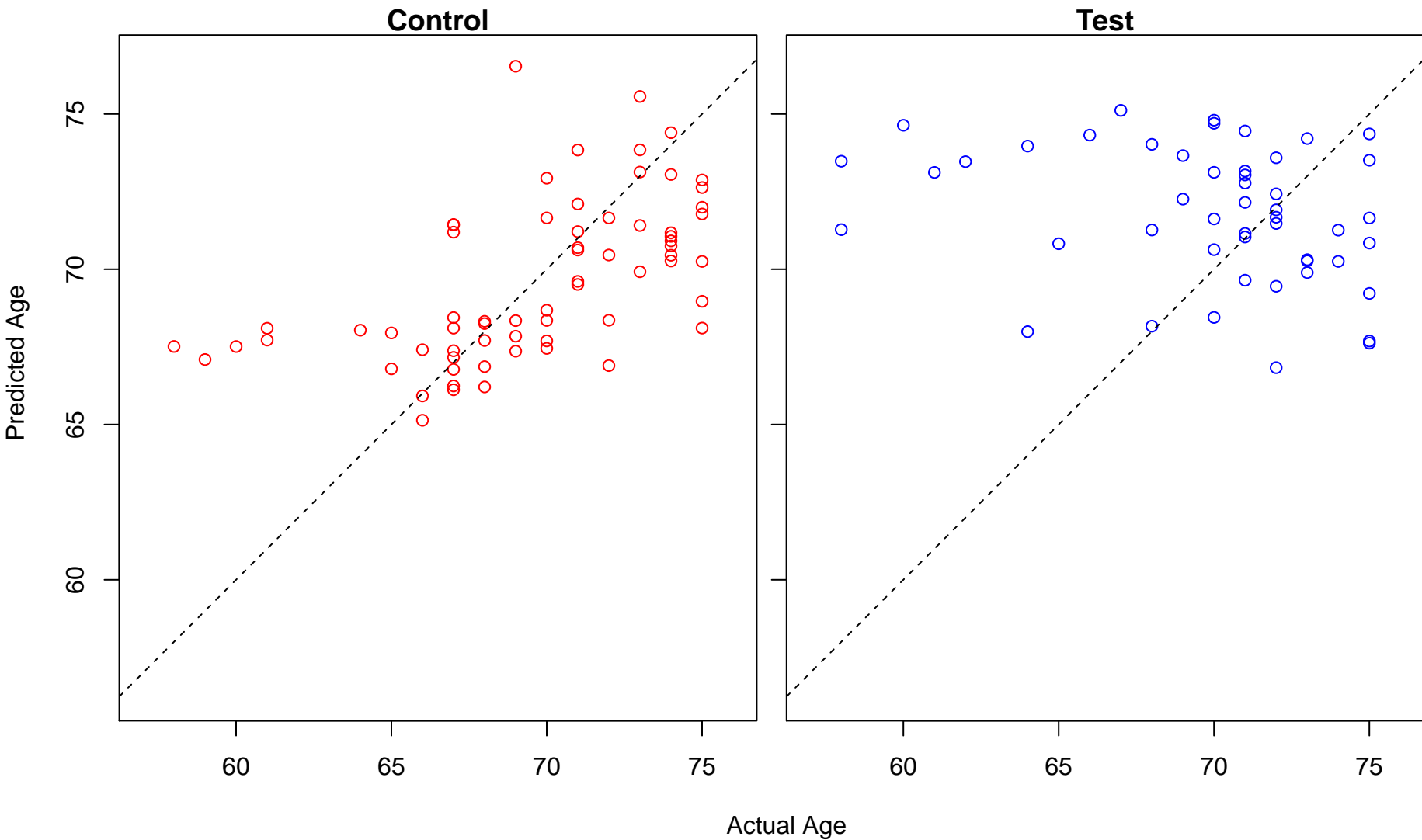
base-excision repair (Score: 1.045815)



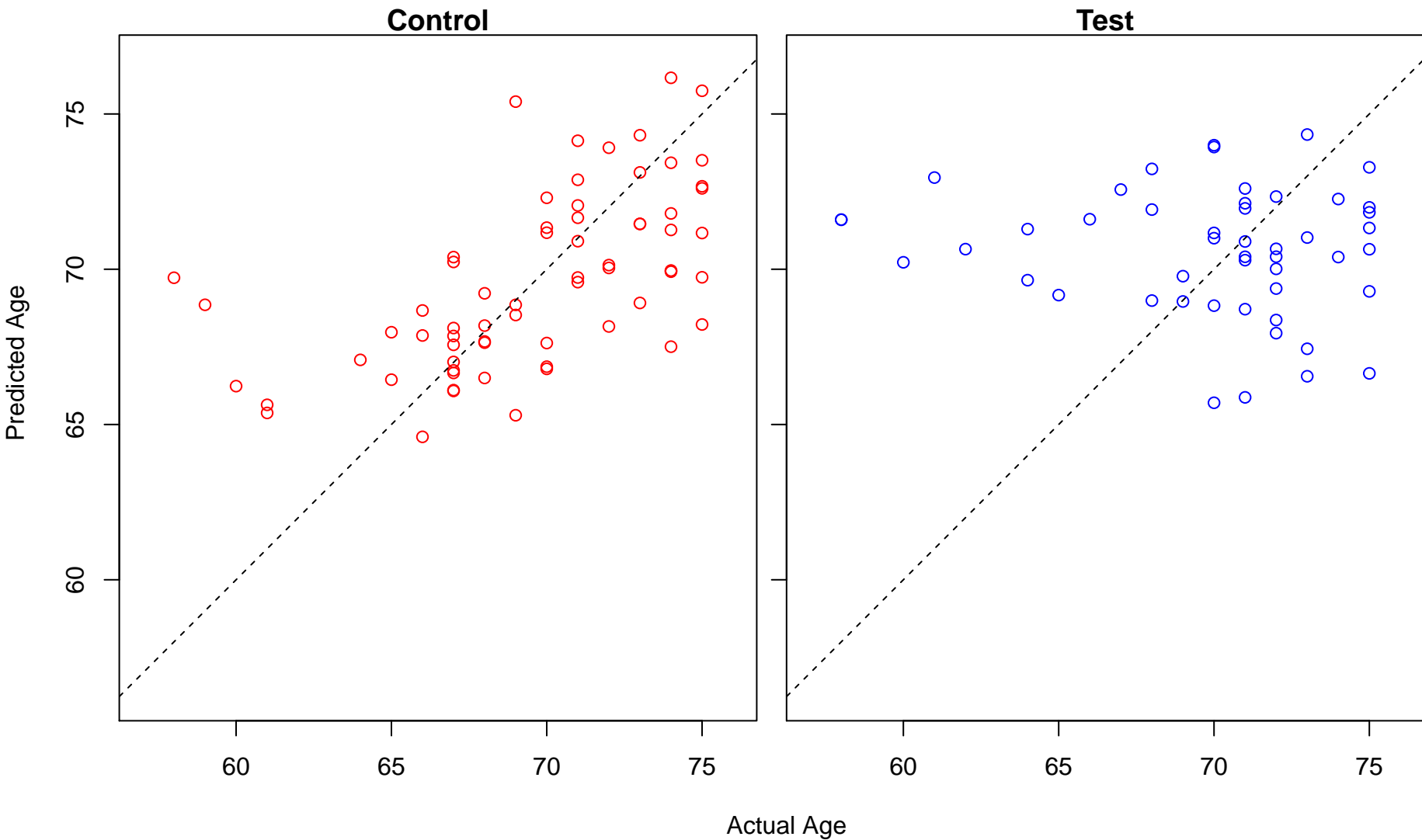
leukocyte homeostasis (Score: 1.045351)



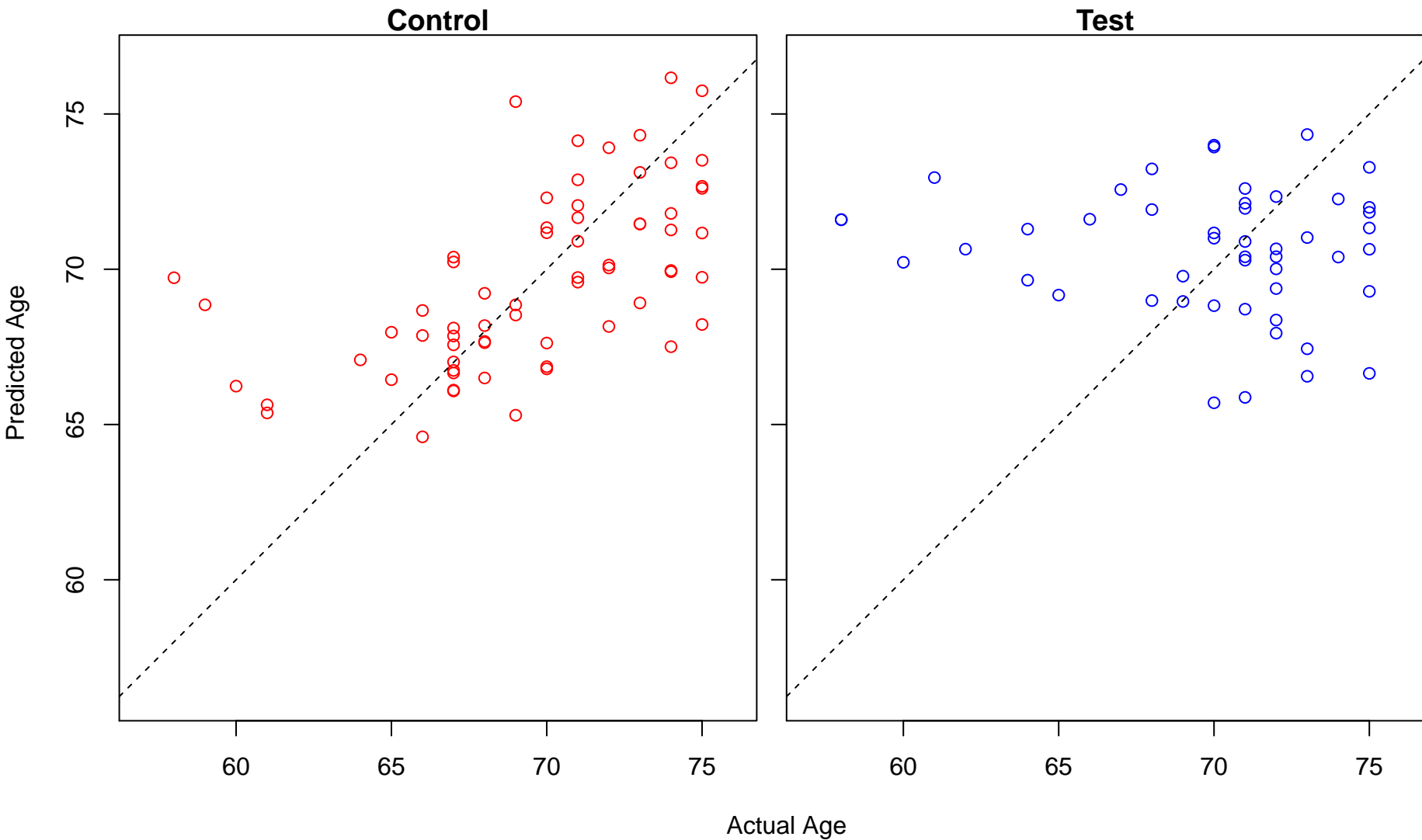
negative regulation of CD4-positive, alpha-beta T cell differentiation (Score: 1.045282)



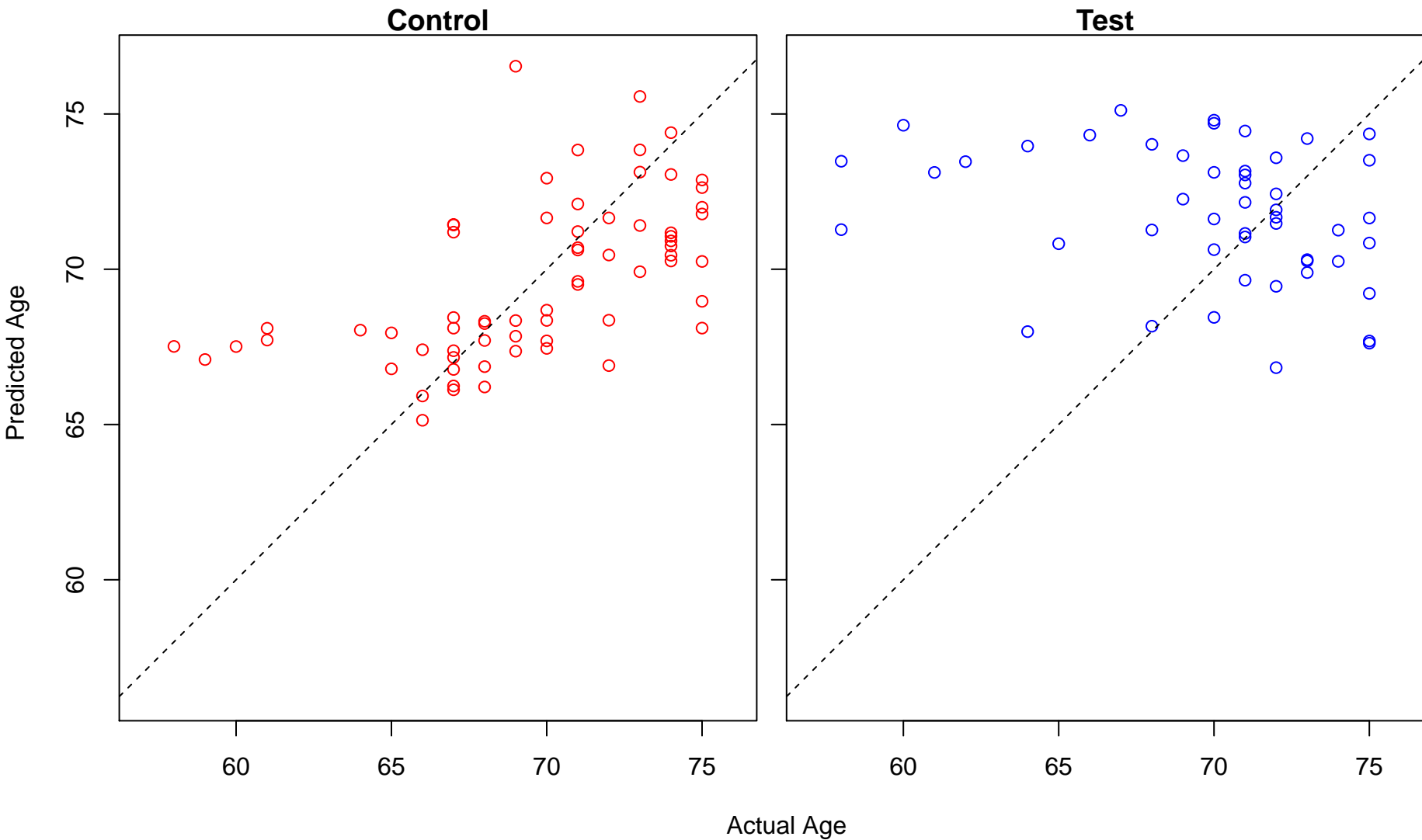
melanosome transport (Score: 1.045268)



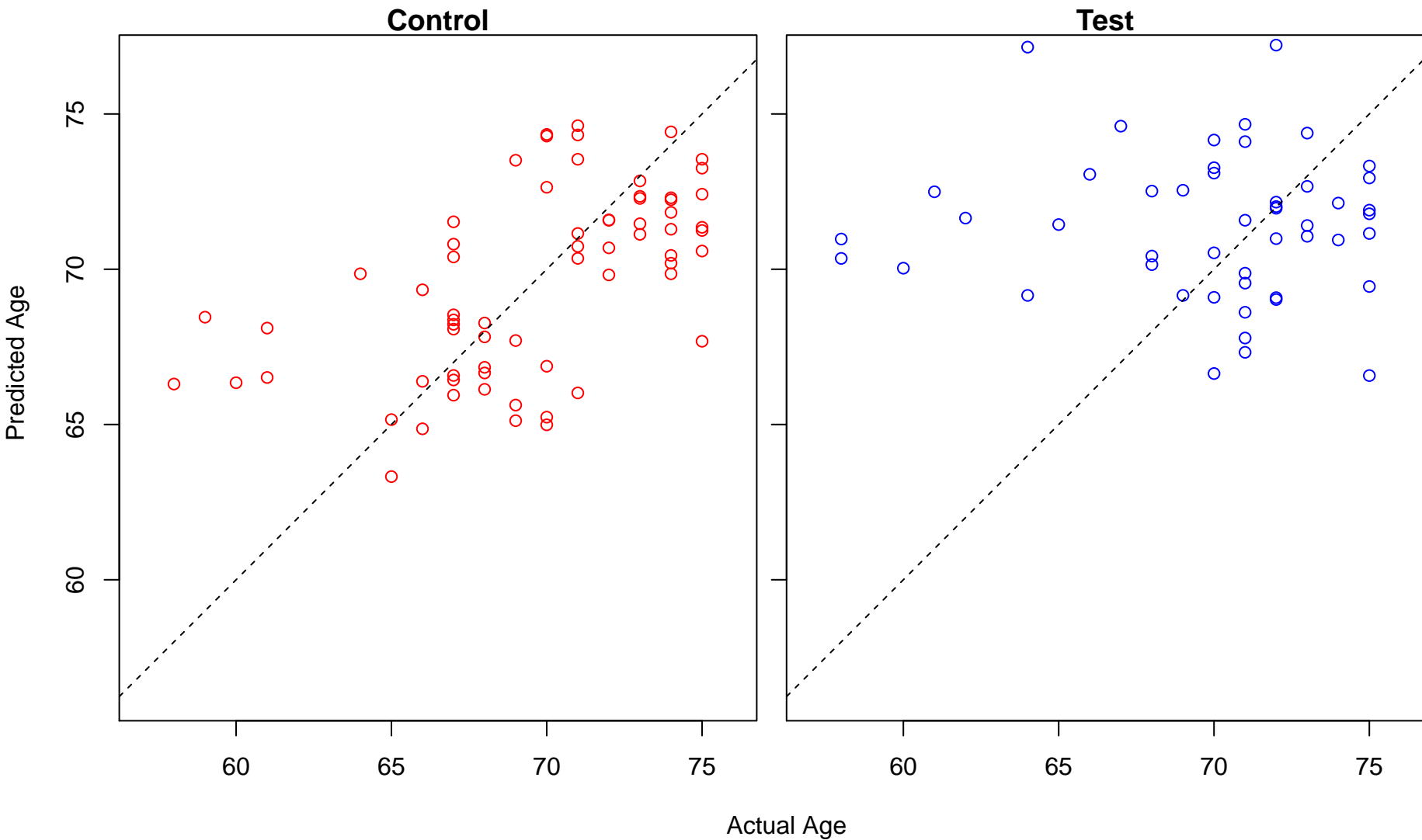
pigment granule transport (Score: 1.045268)



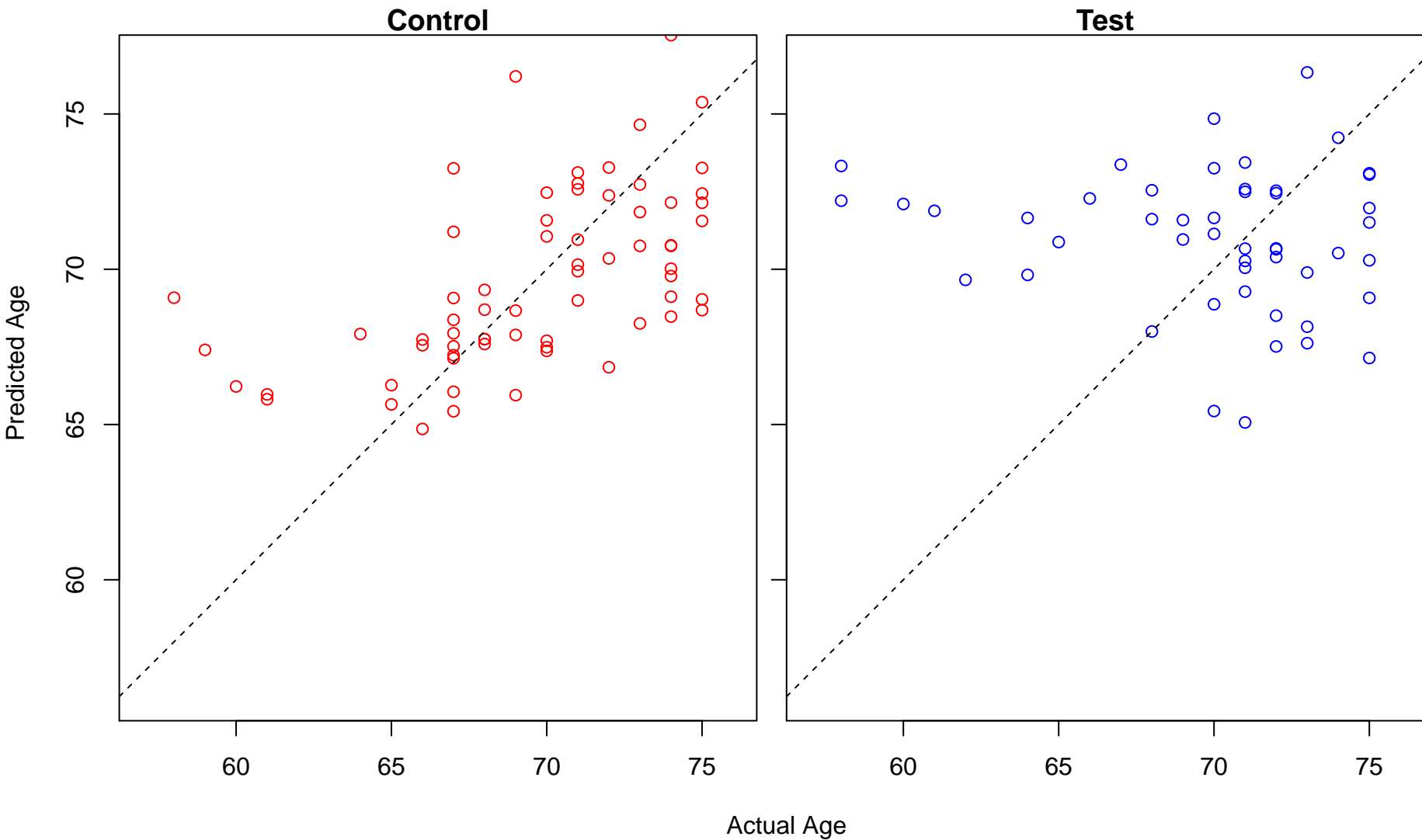
negative regulation of alpha-beta T cell differentiation (Score: 1.045062)



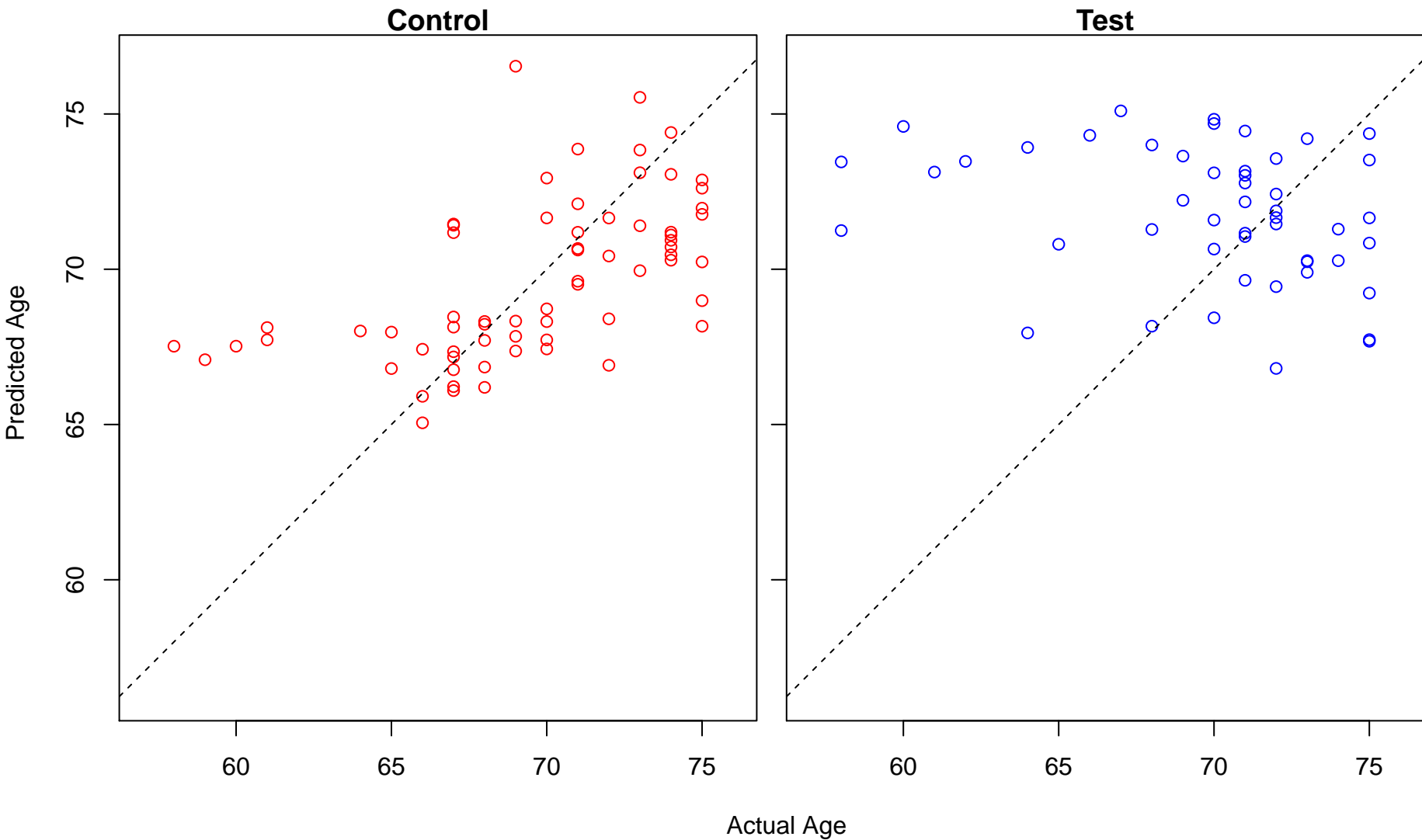
positive regulation of peptidyl-lysine acetylation (Score: 1.044821)



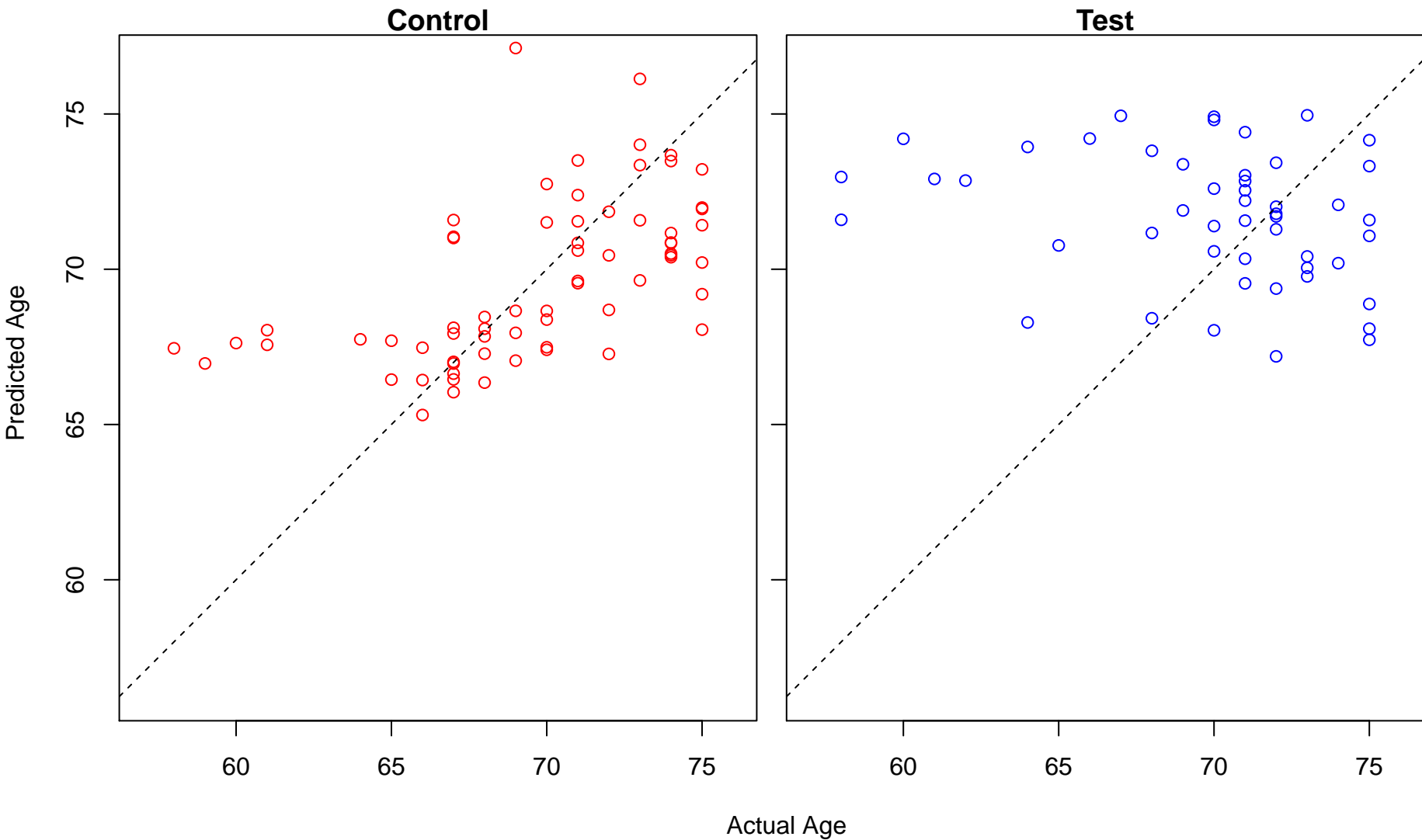
microtubule cytoskeleton organization involved in mitosis (Score: 1.044673)



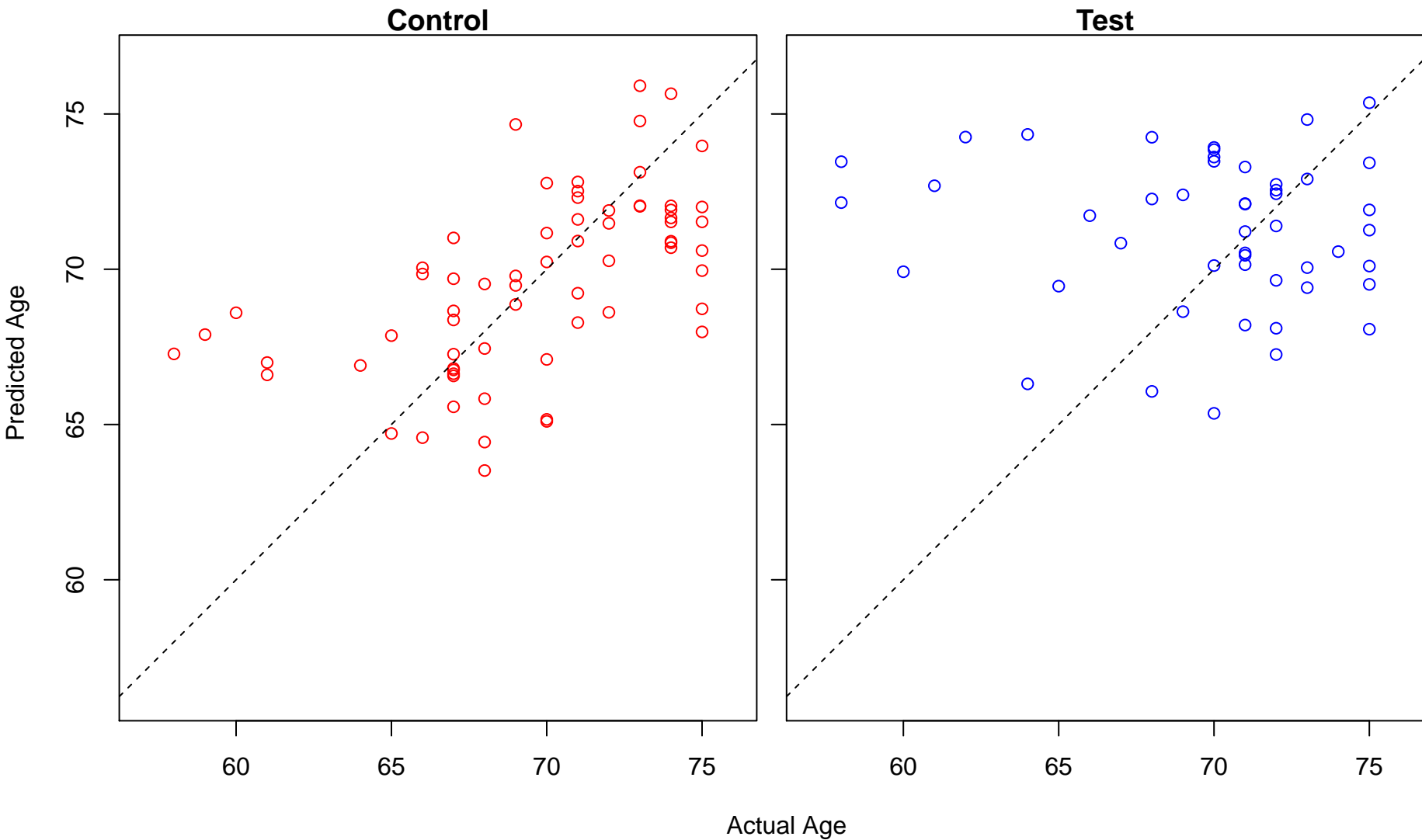
regulation of T-helper 1 cell differentiation (Score: 1.044320)



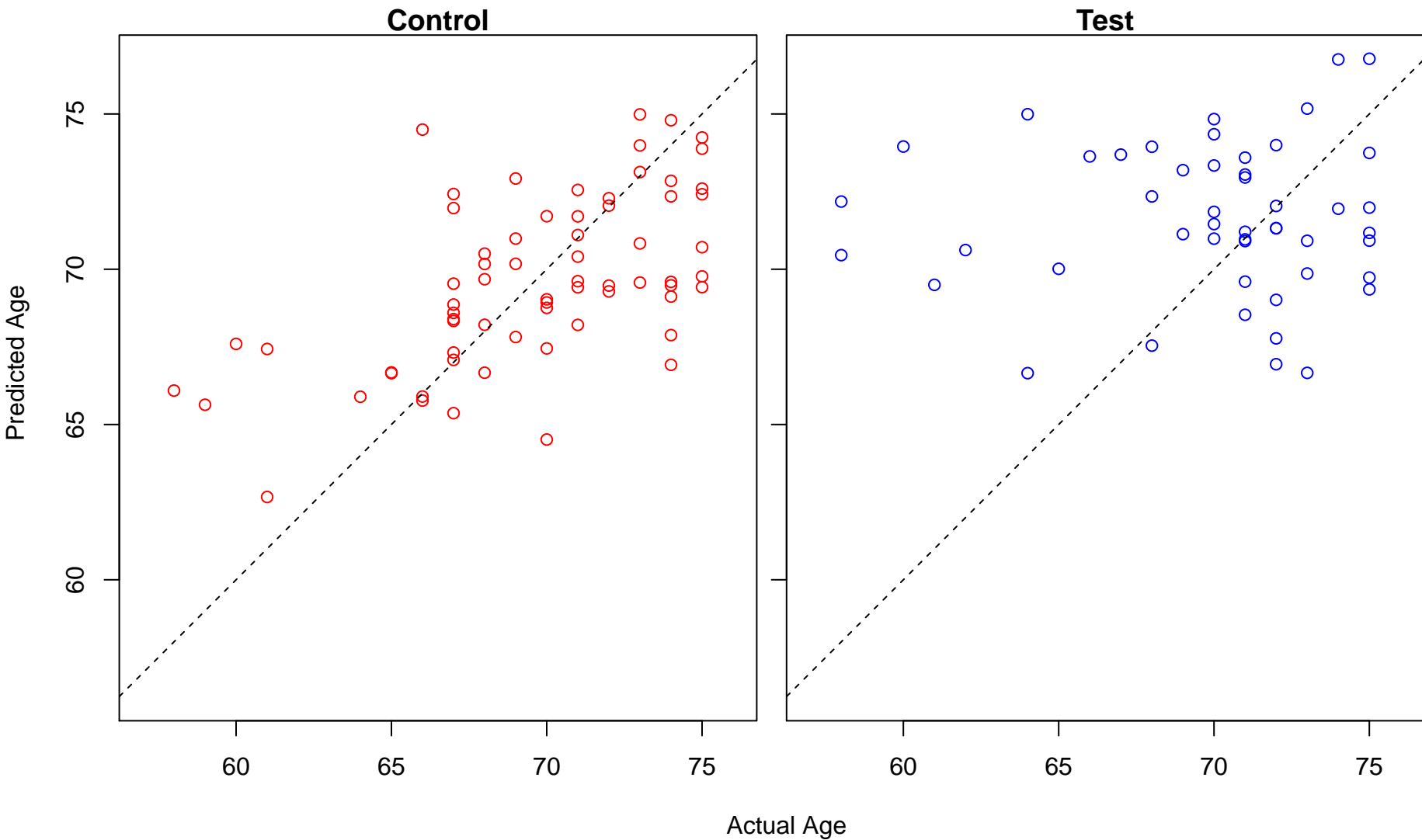
positive regulation of wound healing (Score: 1.044289)



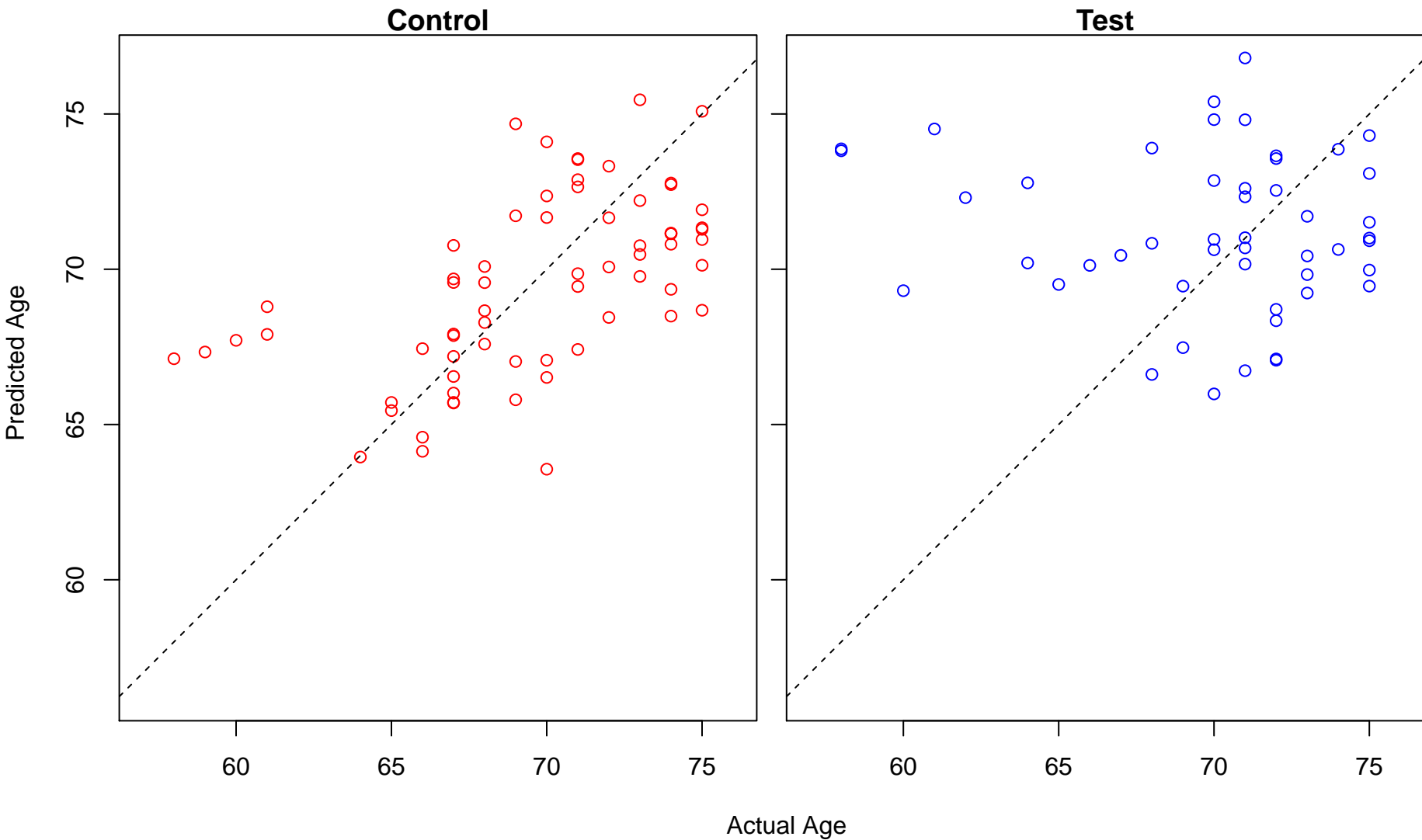
negative regulation of peptidyl-tyrosine phosphorylation (Score: 1.044012)



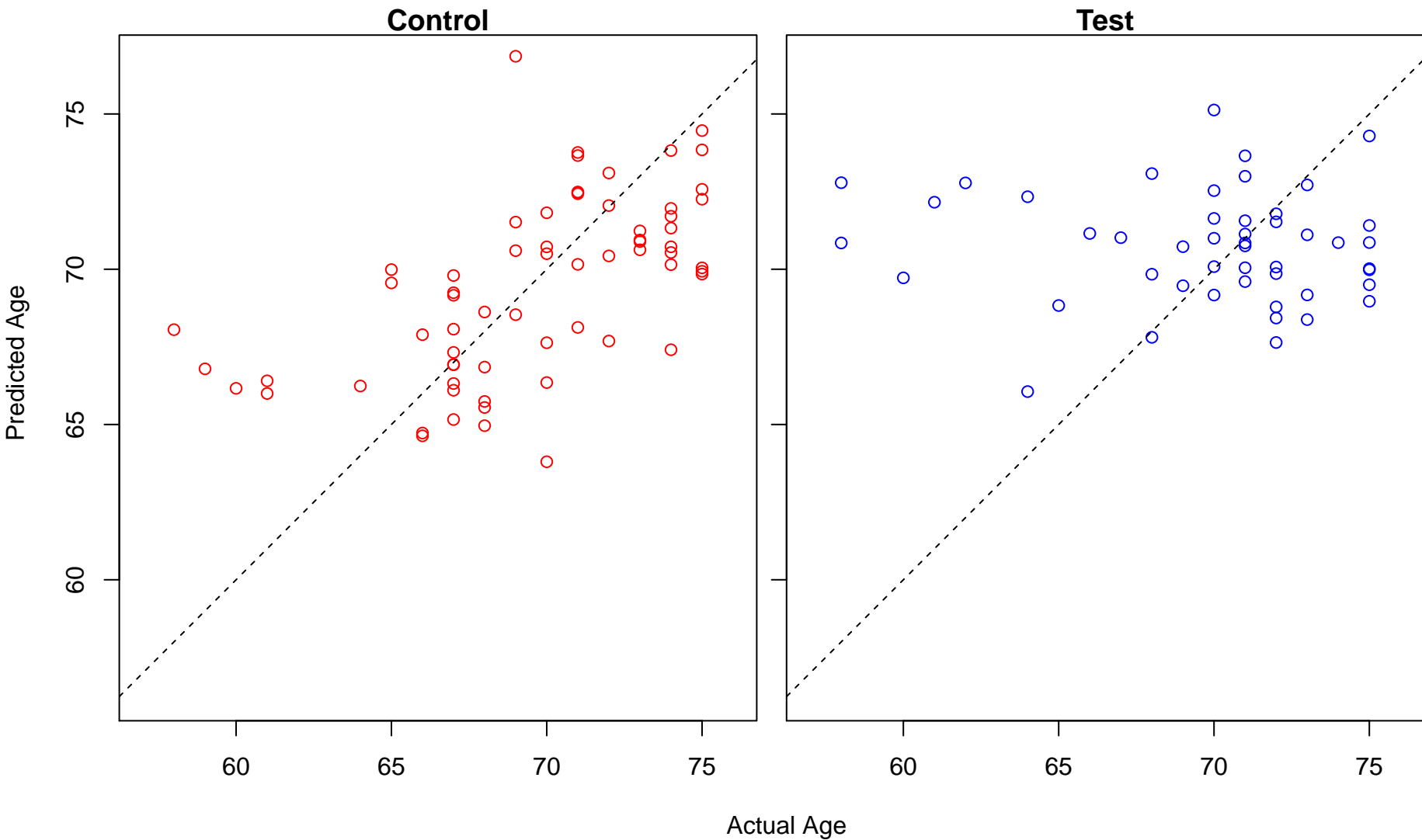
disaccharide metabolic process (Score: 1.043984)



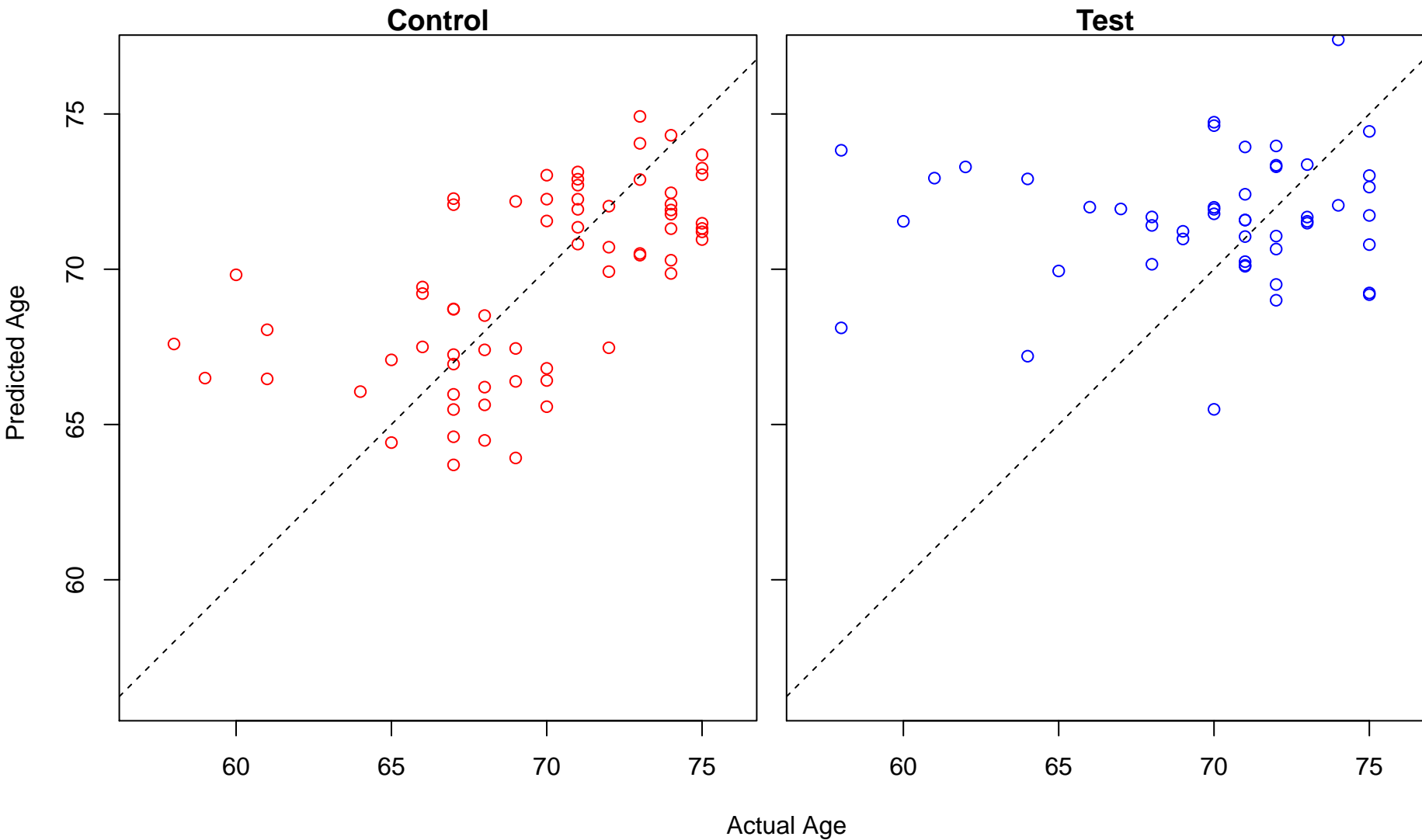
activation of JUN kinase activity (Score: 1.043880)



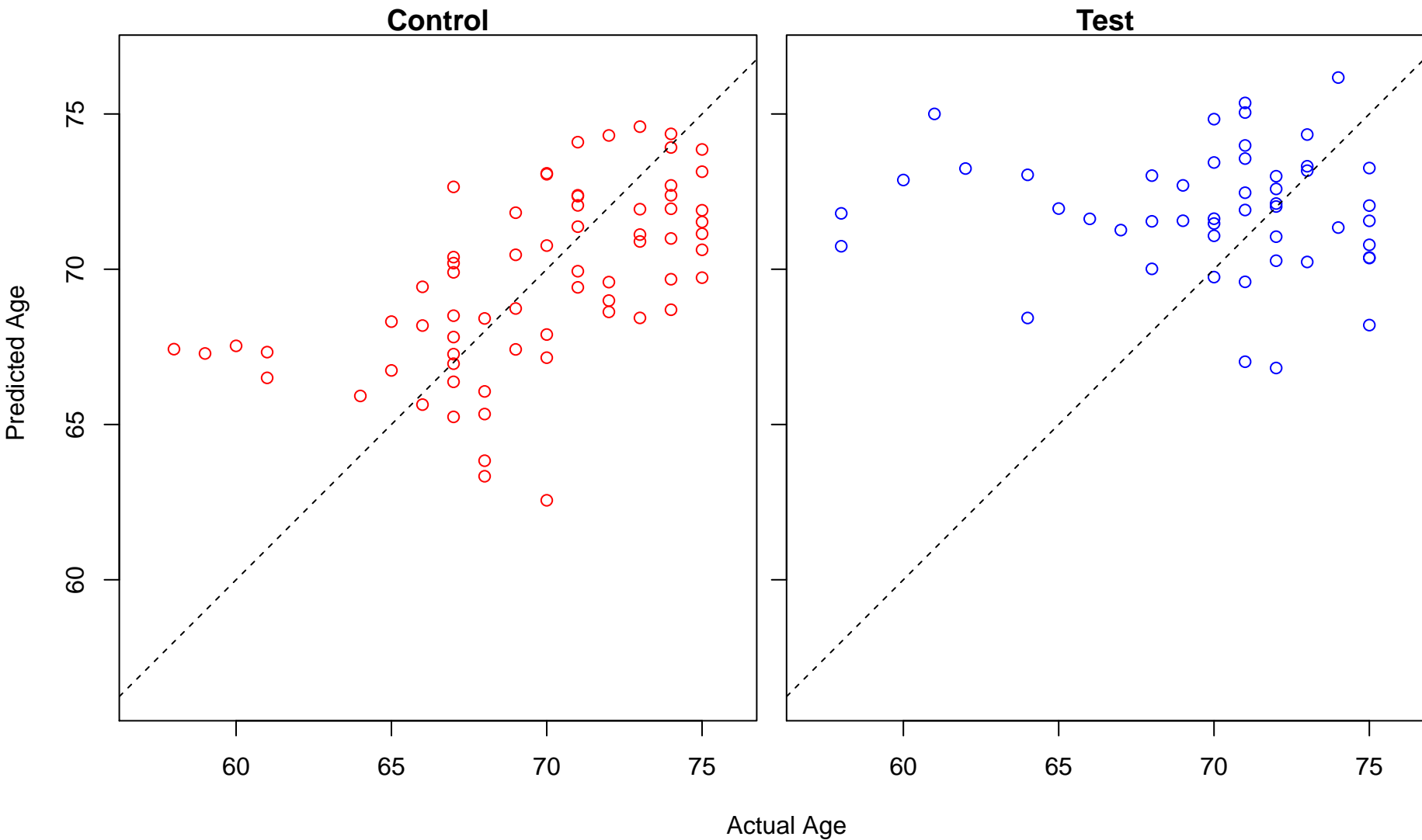
hexose biosynthetic process (Score: 1.043788)



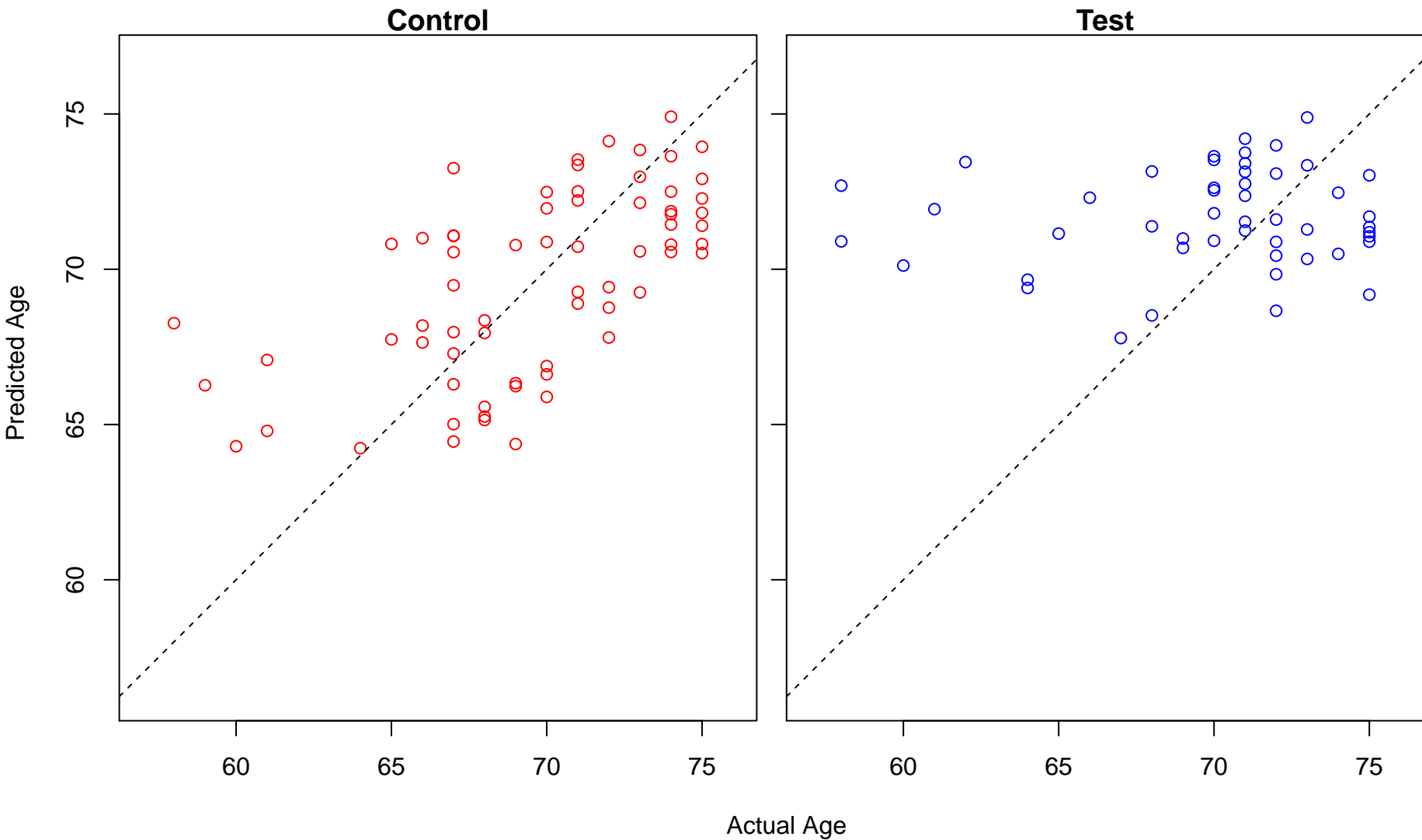
positive regulation of reactive oxygen species metabolic process (Score: 1.043684)



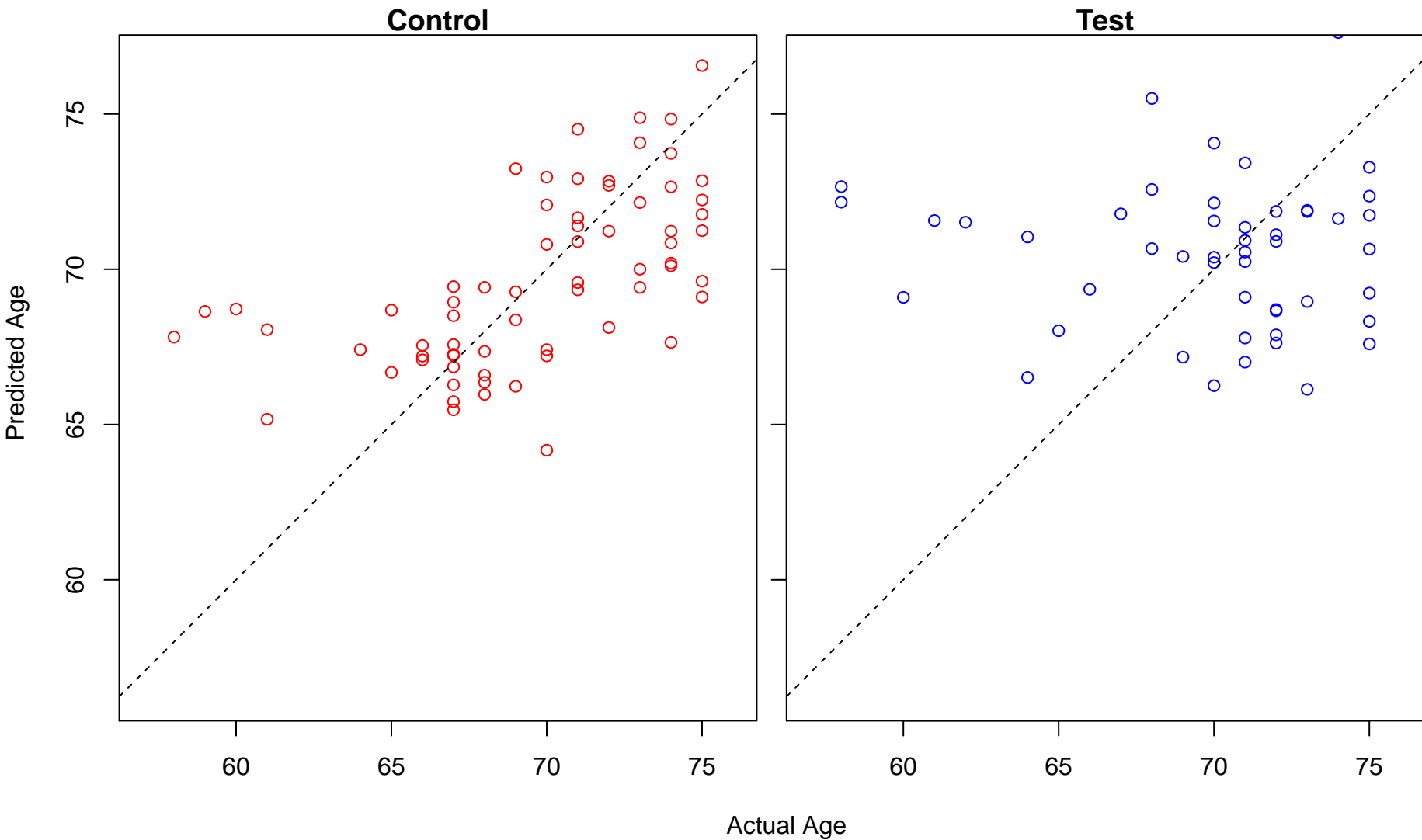
columnar/cuboidal epithelial cell differentiation (Score: 1.043368)



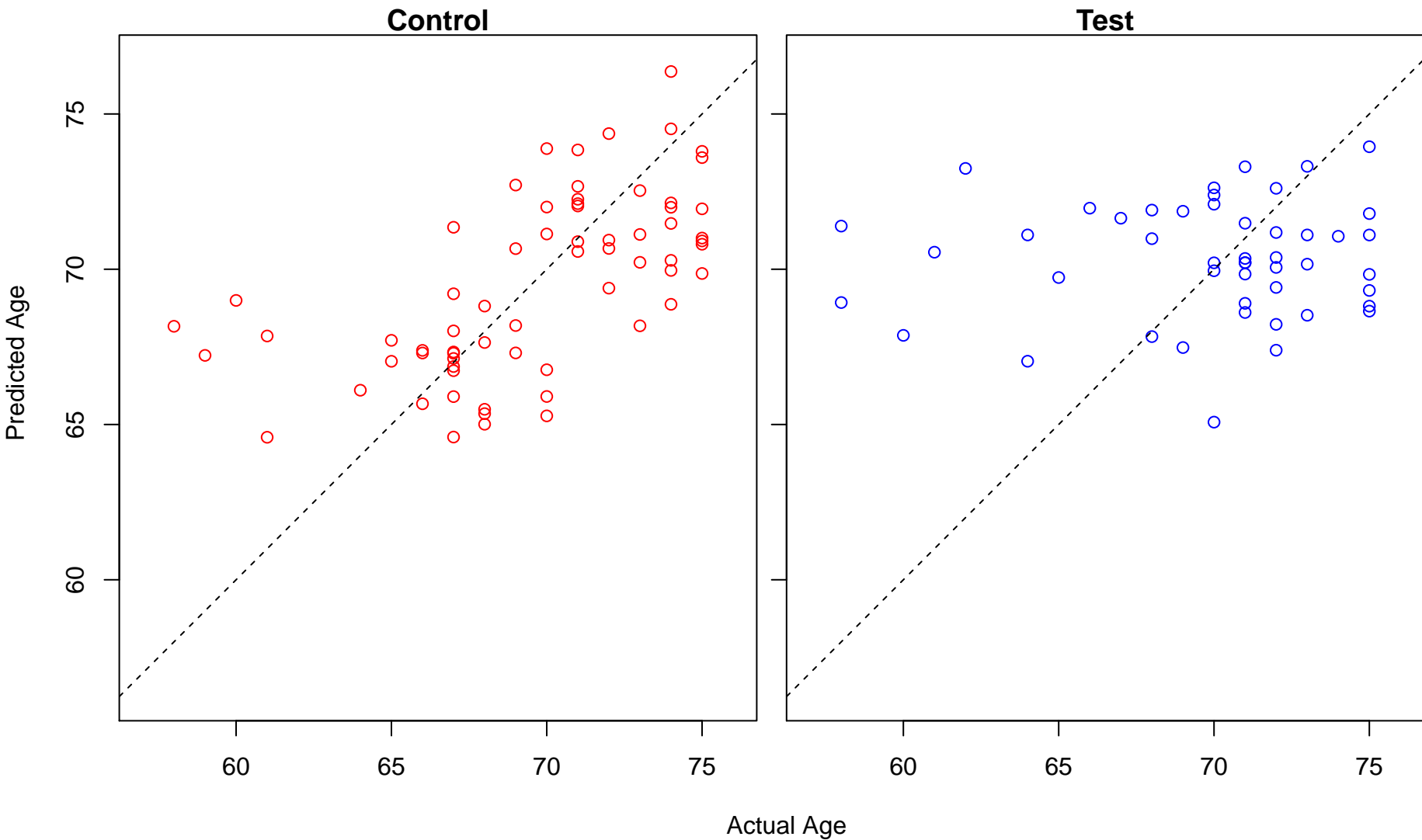
membrane depolarization (Score: 1.042747)



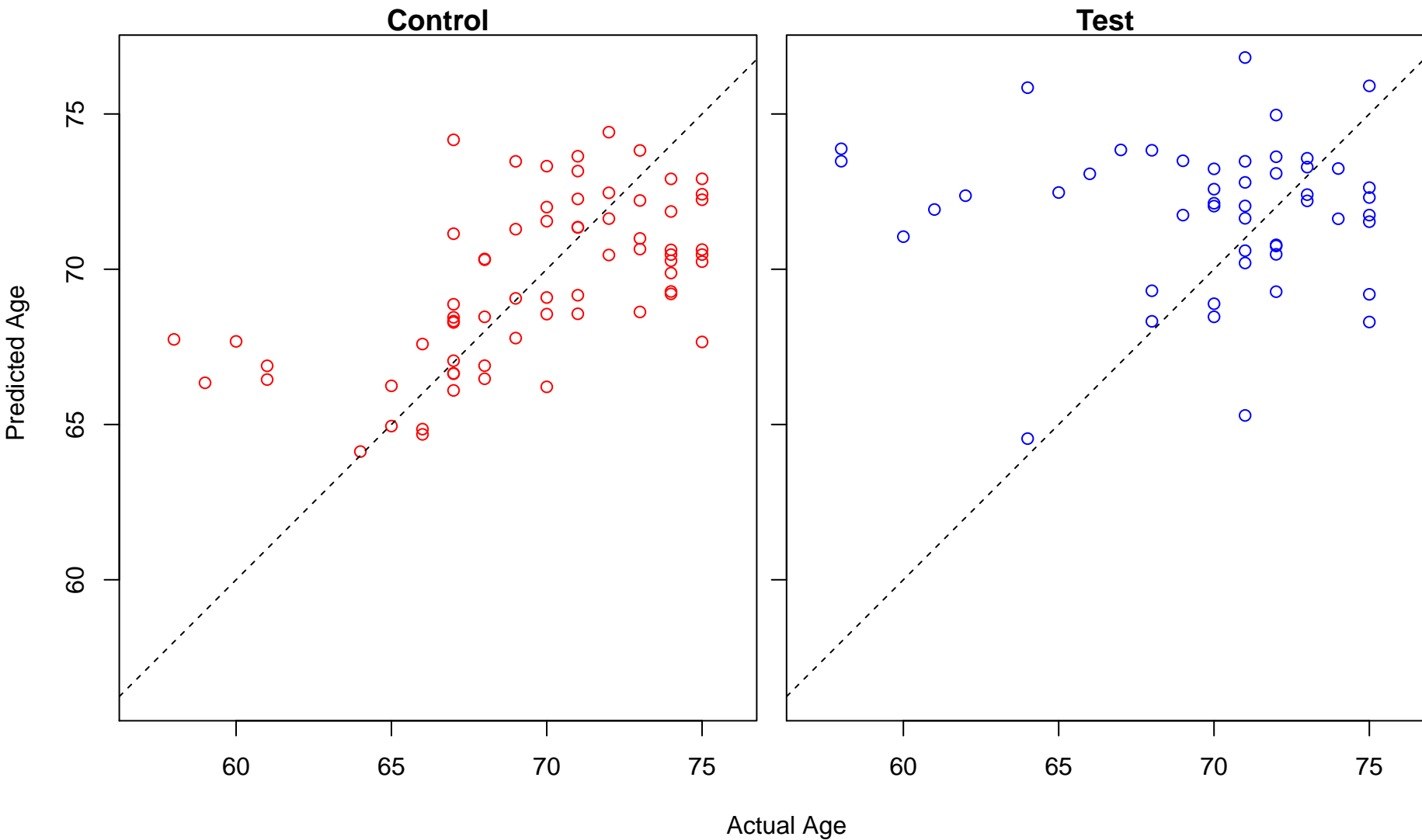
negative regulation of telomere maintenance (Score: 1.042579)



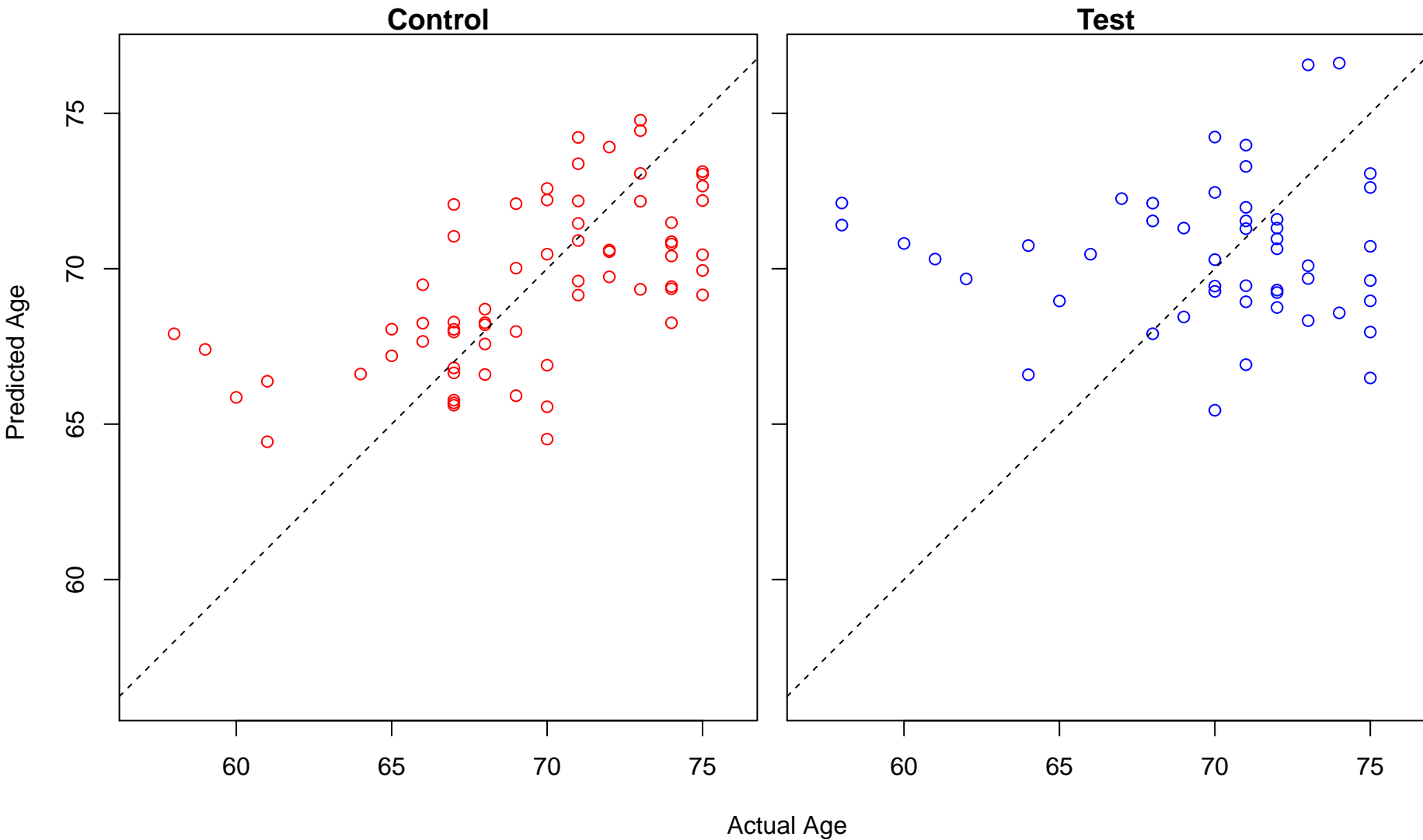
negative regulation of cytokine-mediated signaling pathway (Score: 1.042294)



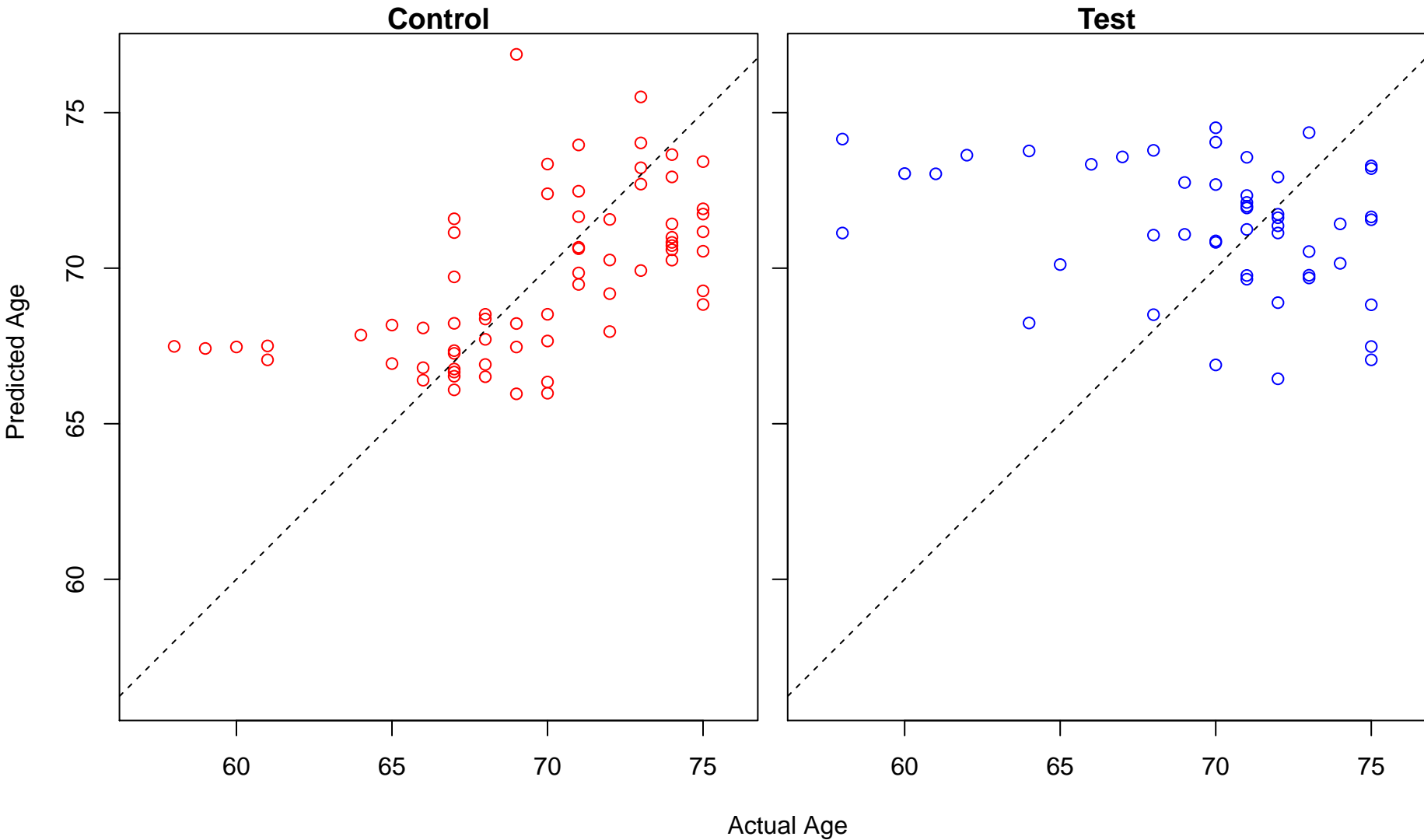
inner dynein arm assembly (Score: 1.042054)



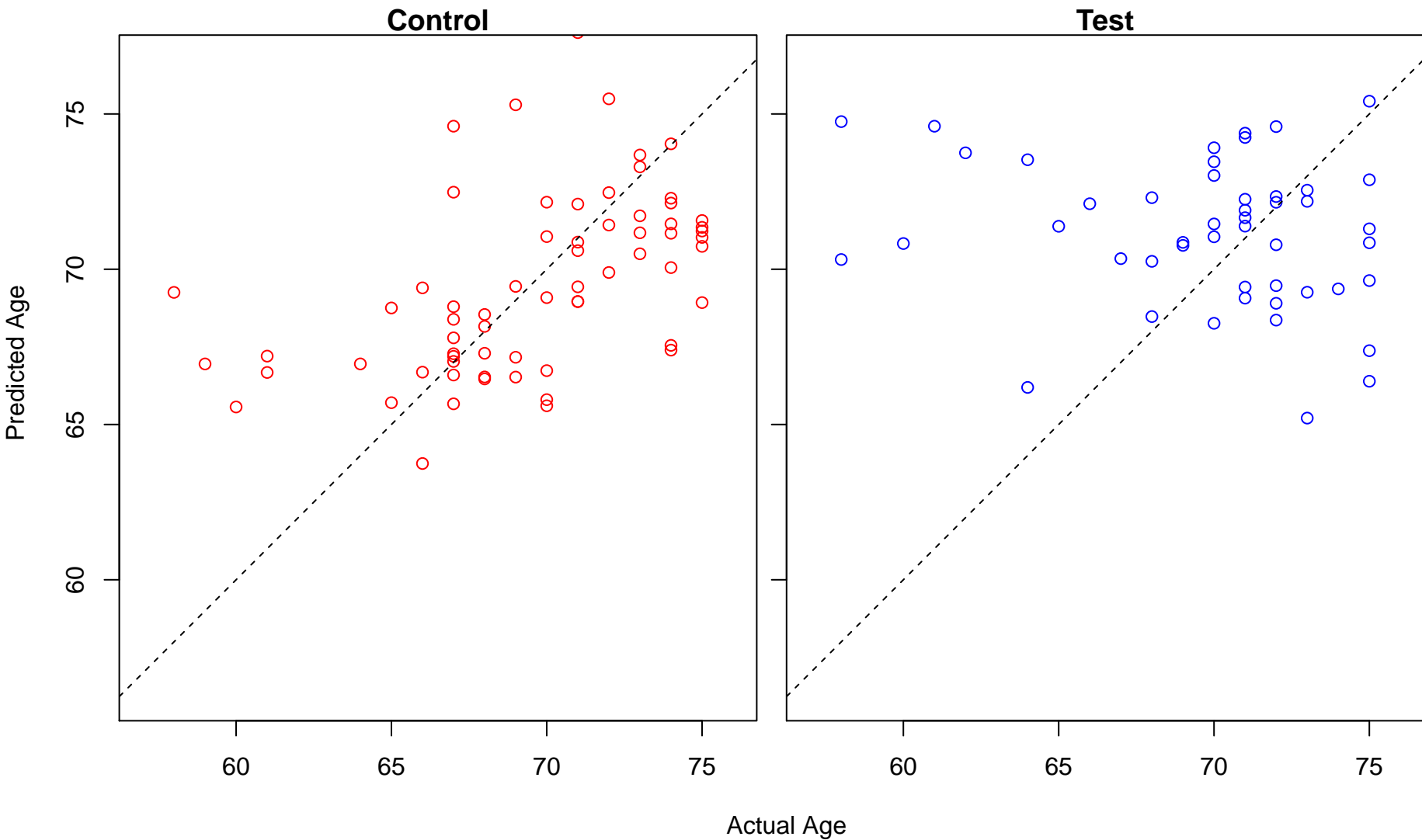
negative regulation of translational initiation (Score: 1.041939)



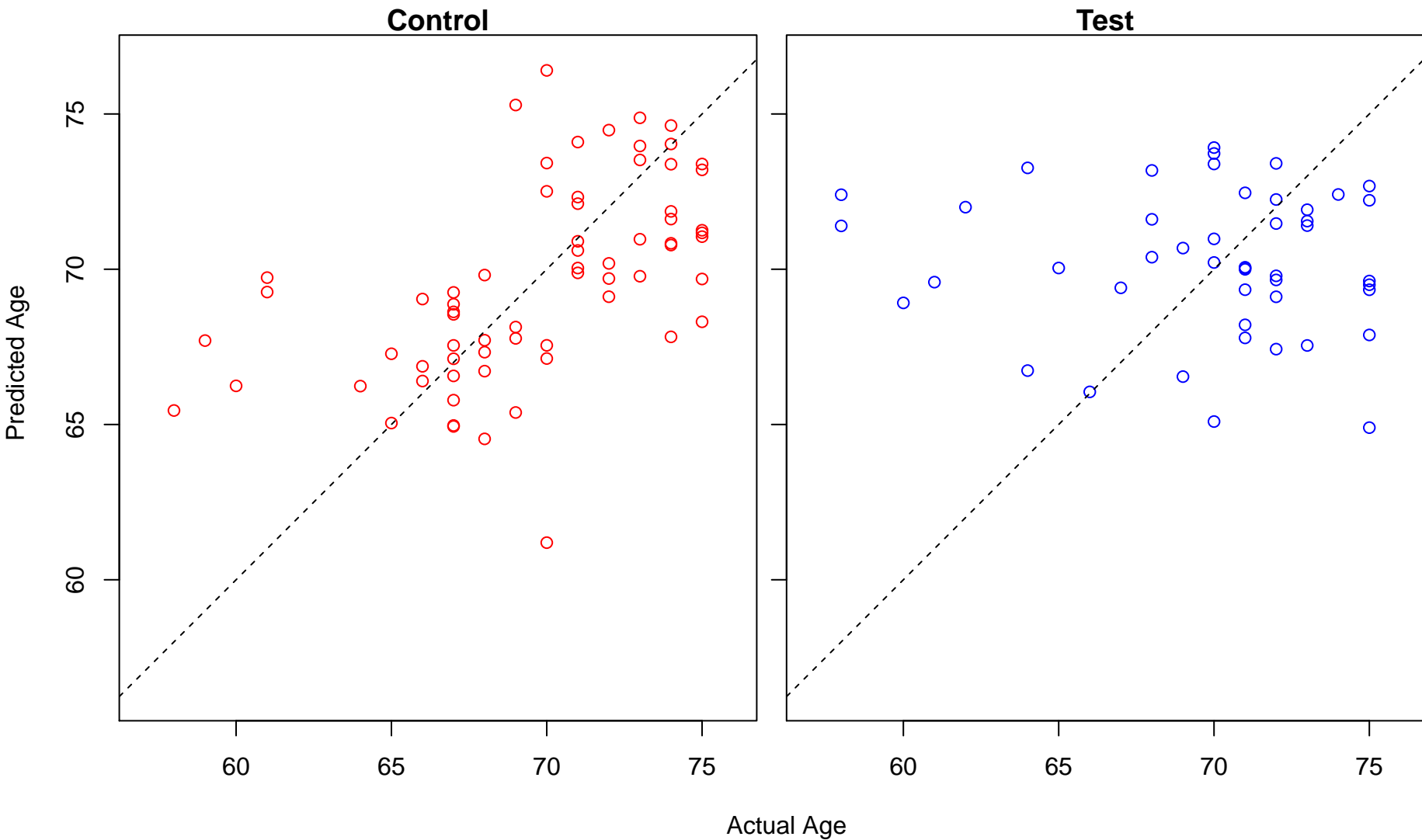
cellular response to steroid hormone stimulus (Score: 1.041160)



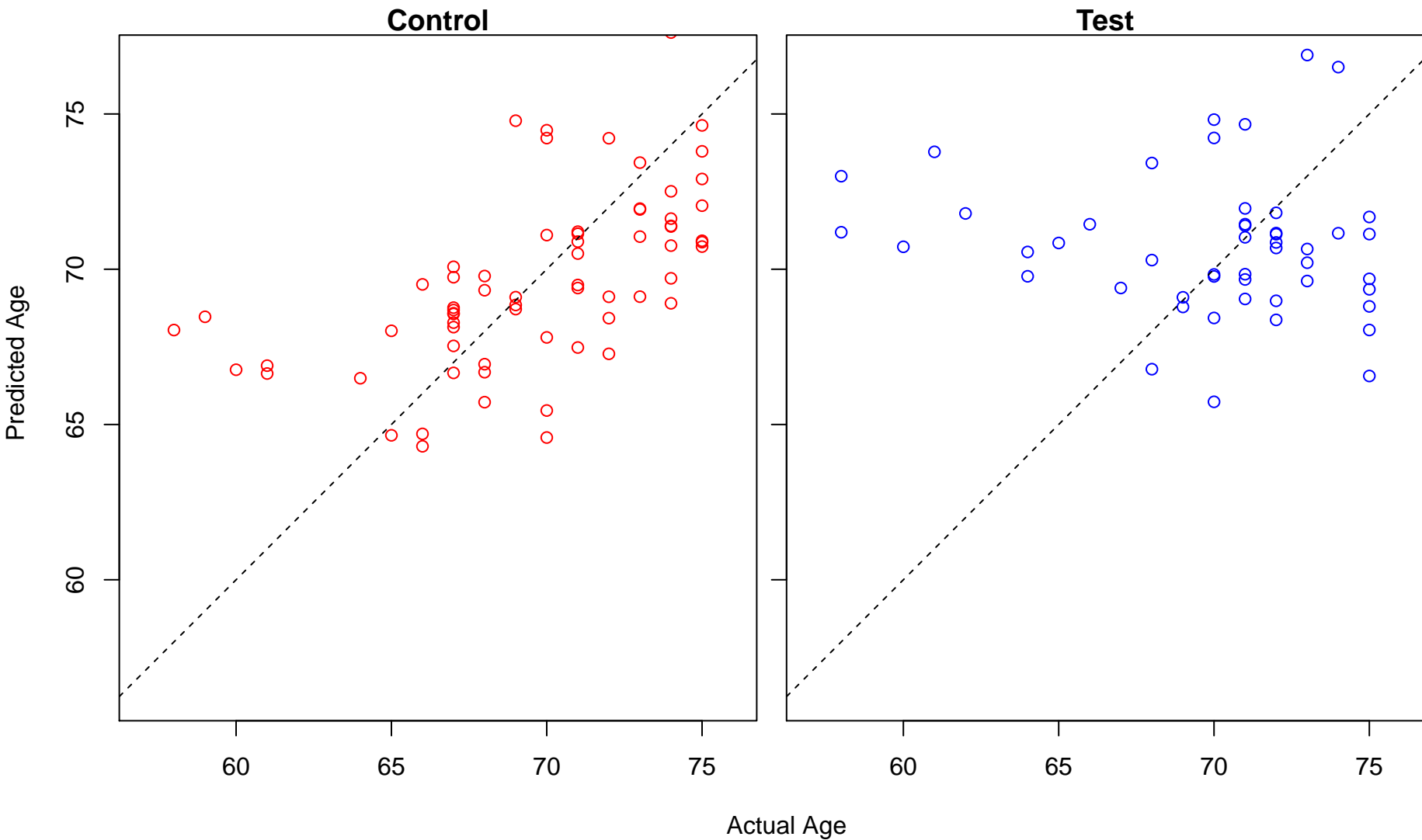
positive regulation of interleukin-6 production (Score: 1.041125)



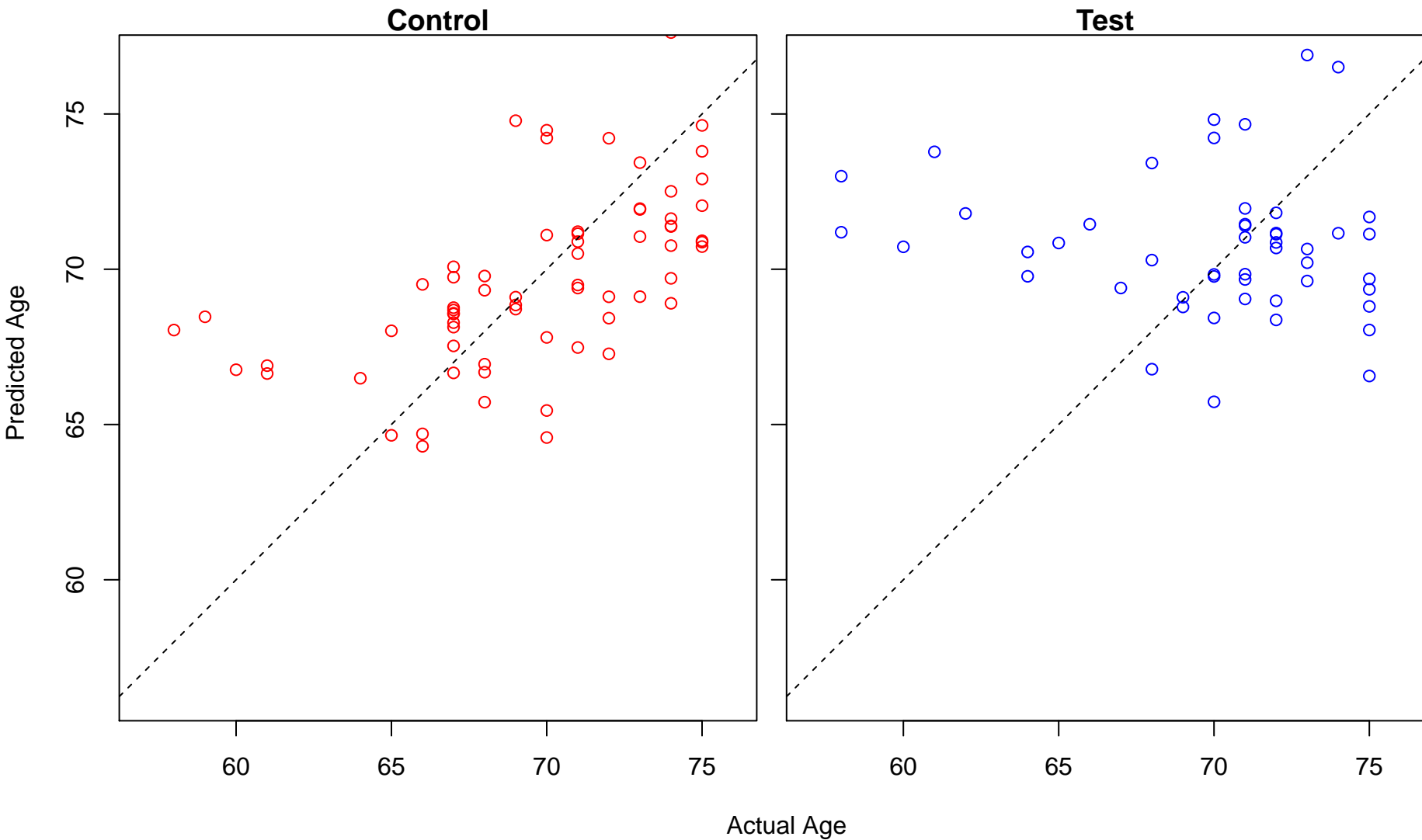
RNA stabilization (Score: 1.040982)



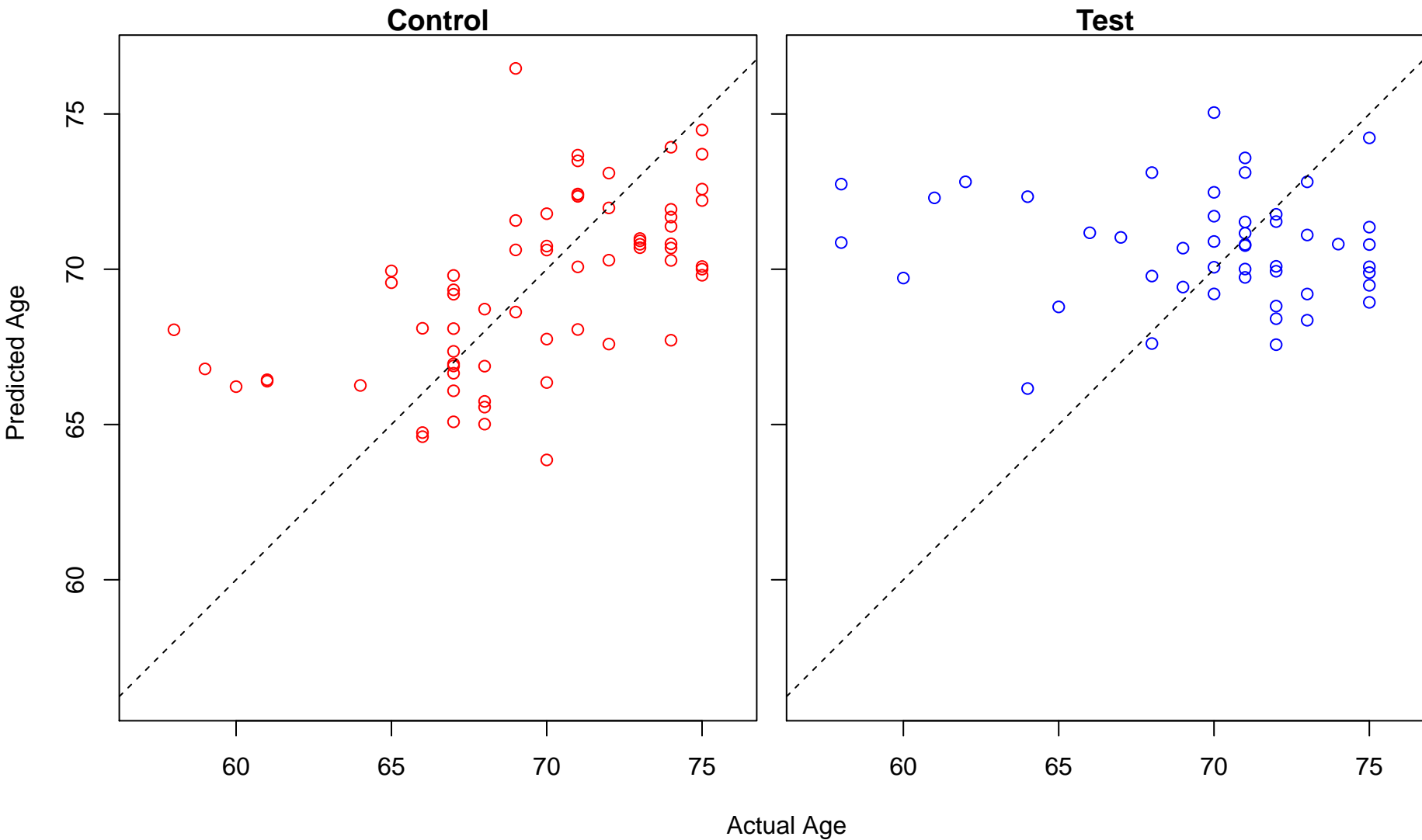
mitotic nuclear envelope reassembly (Score: 1.040959)



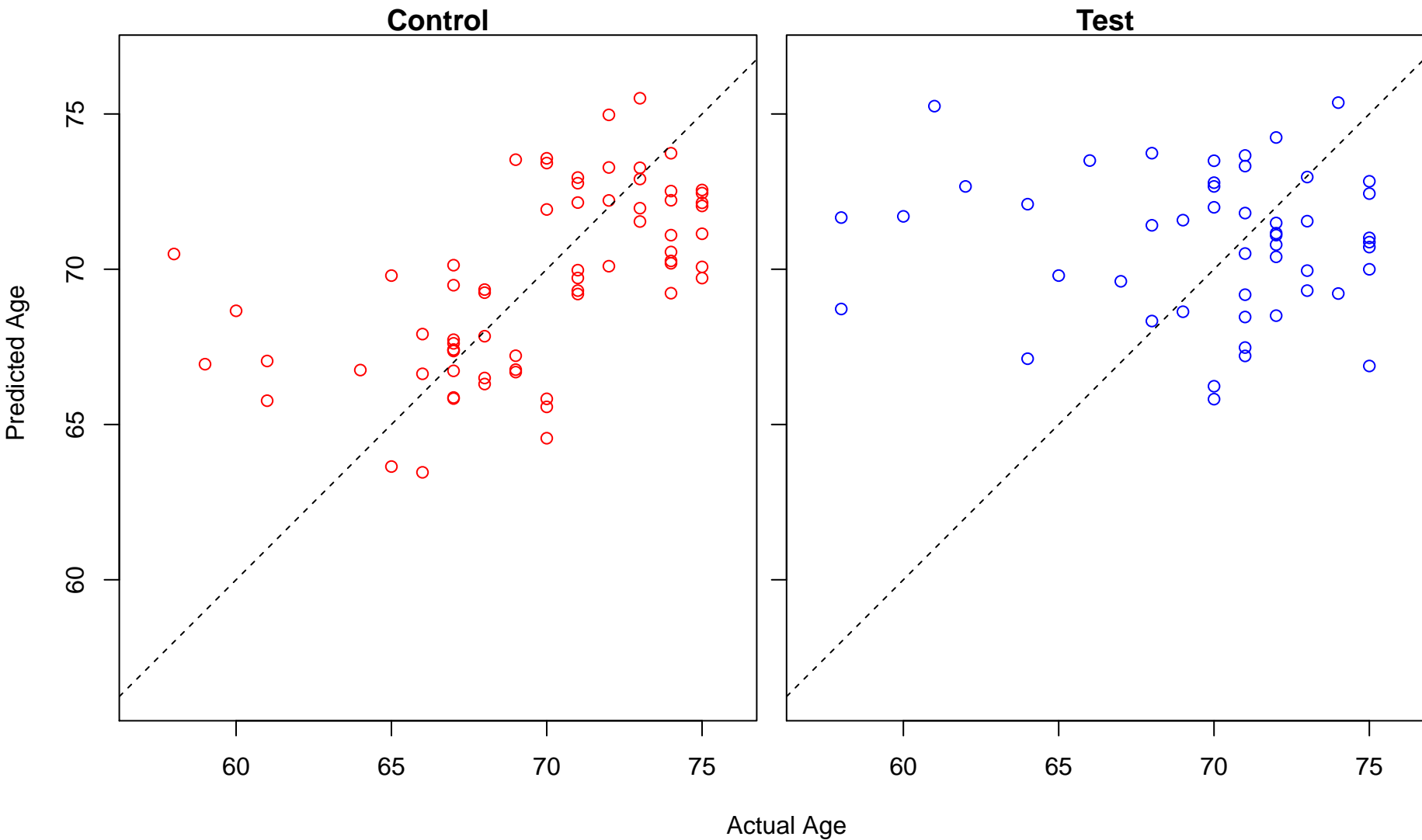
nuclear envelope reassembly (Score: 1.040959)



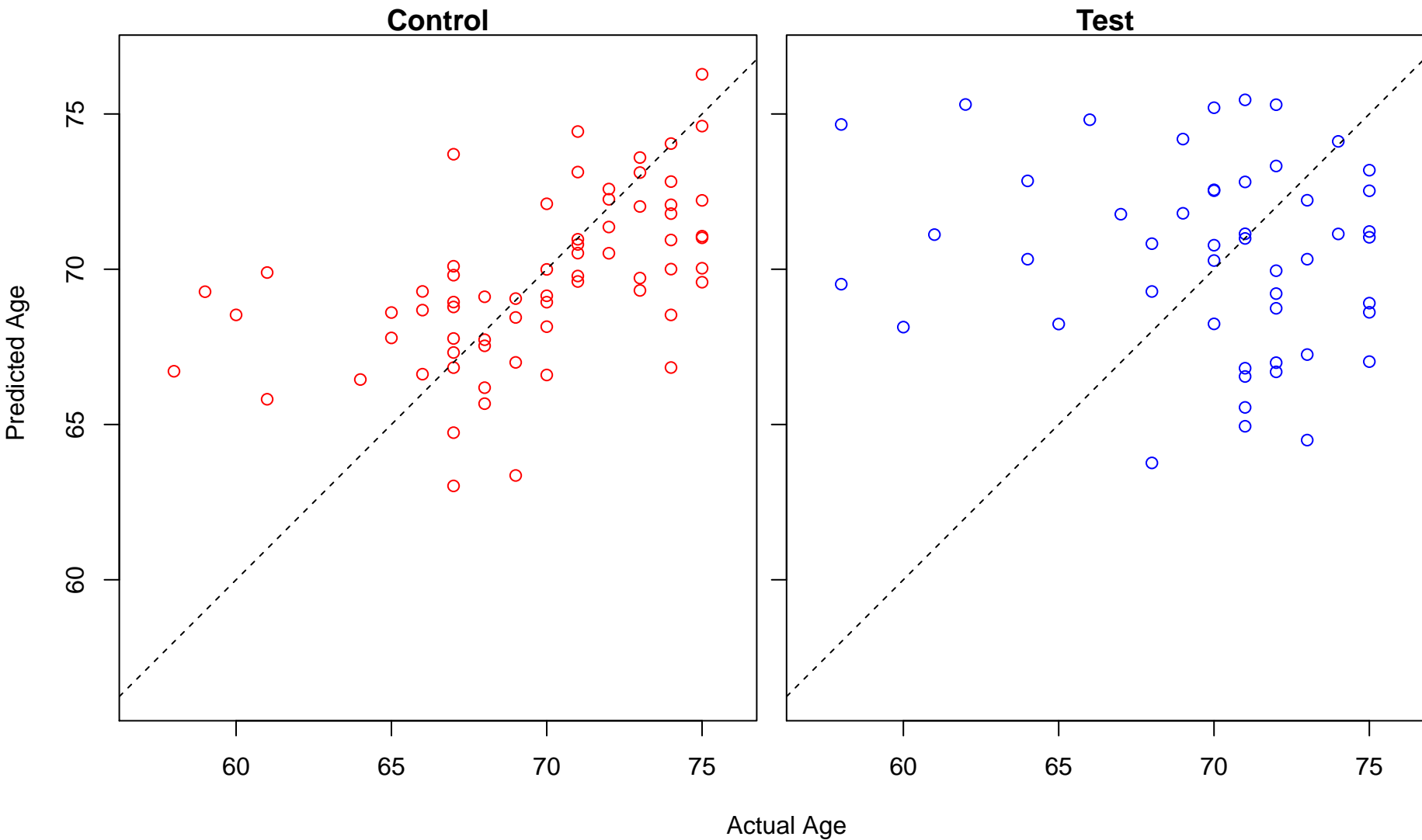
gluconeogenesis (Score: 1.040847)



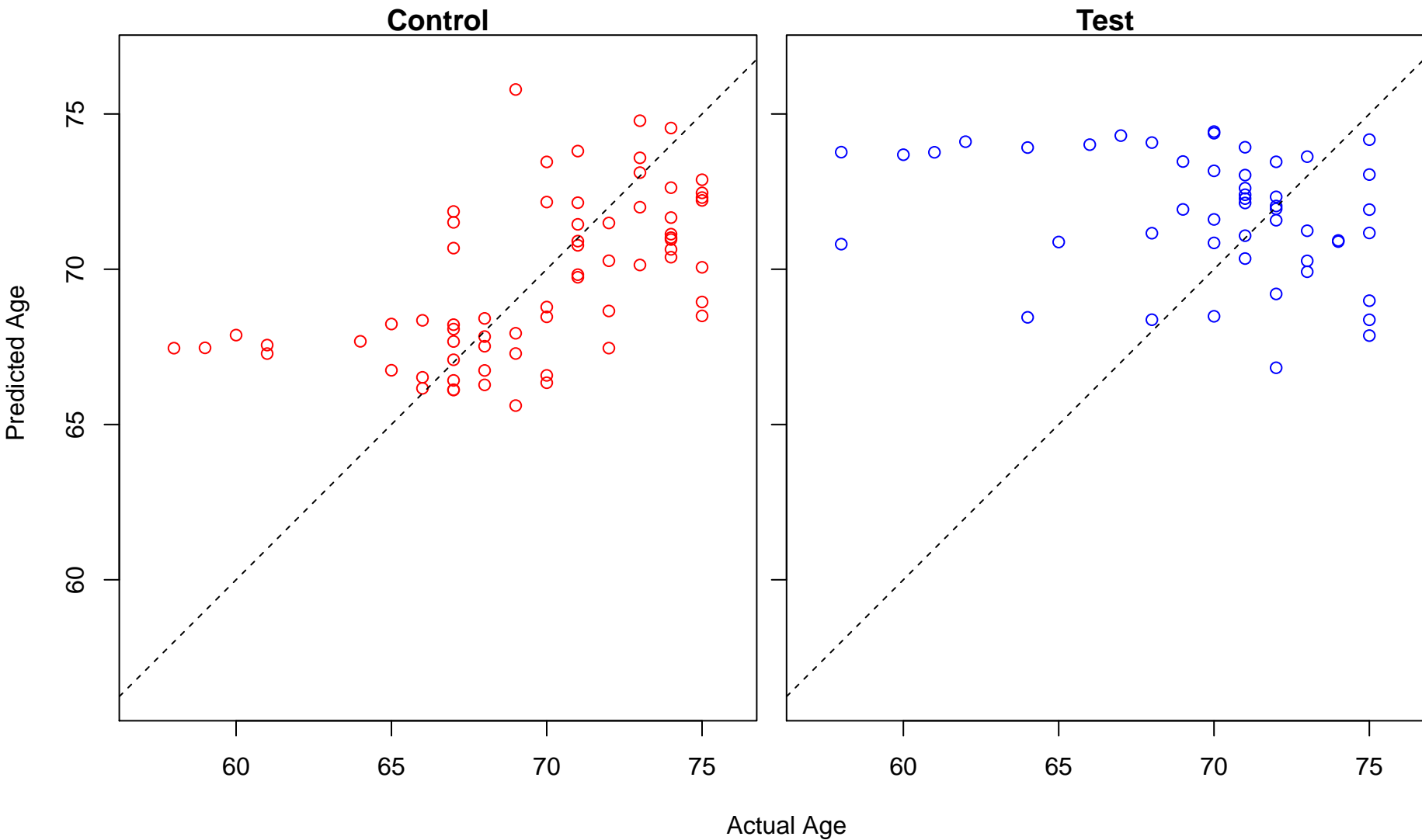
RNA phosphodiester bond hydrolysis, exonucleolytic (Score: 1.040571)



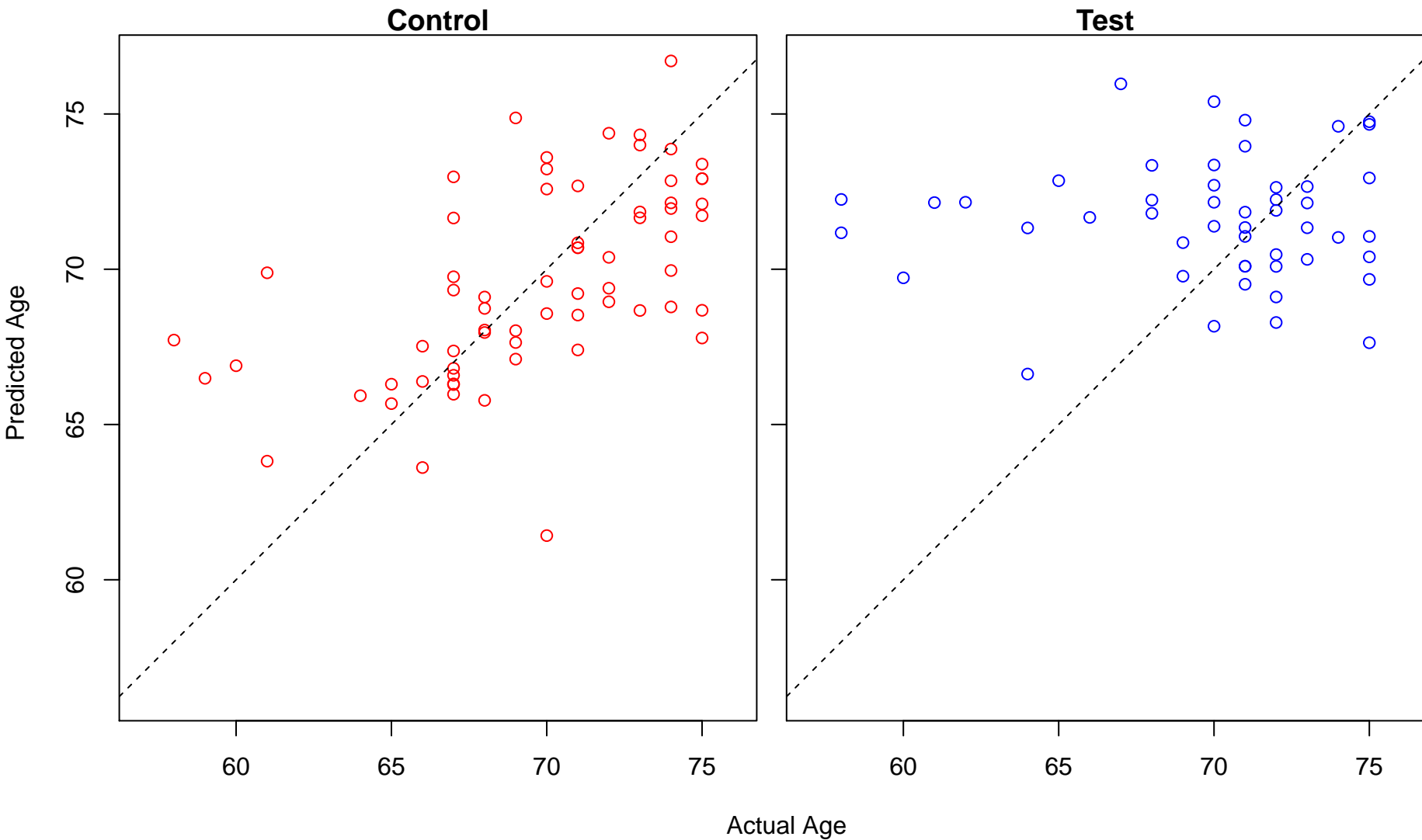
negative regulation of neural precursor cell proliferation (Score: 1.040088)



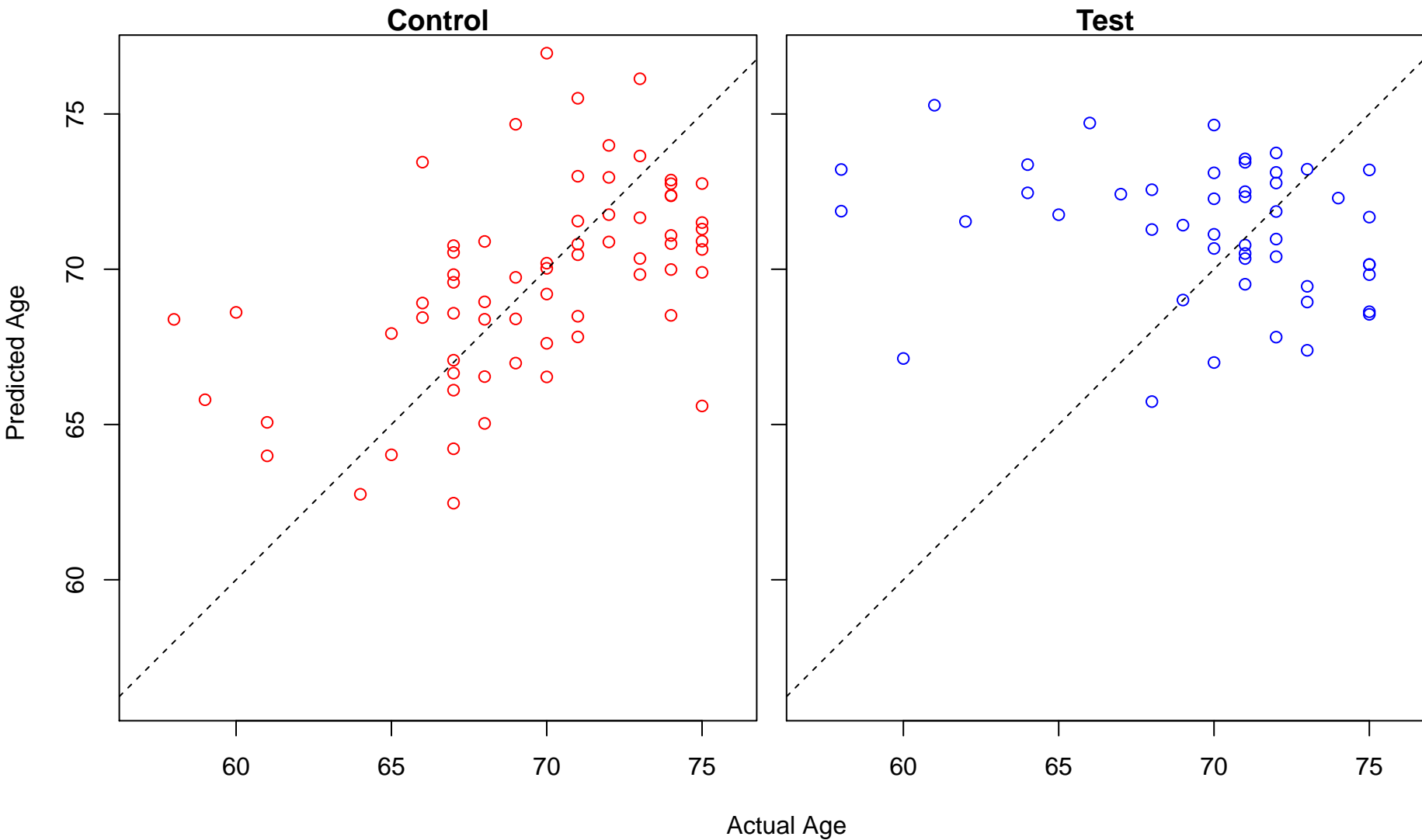
epidermal cell differentiation (Score: 1.039837)



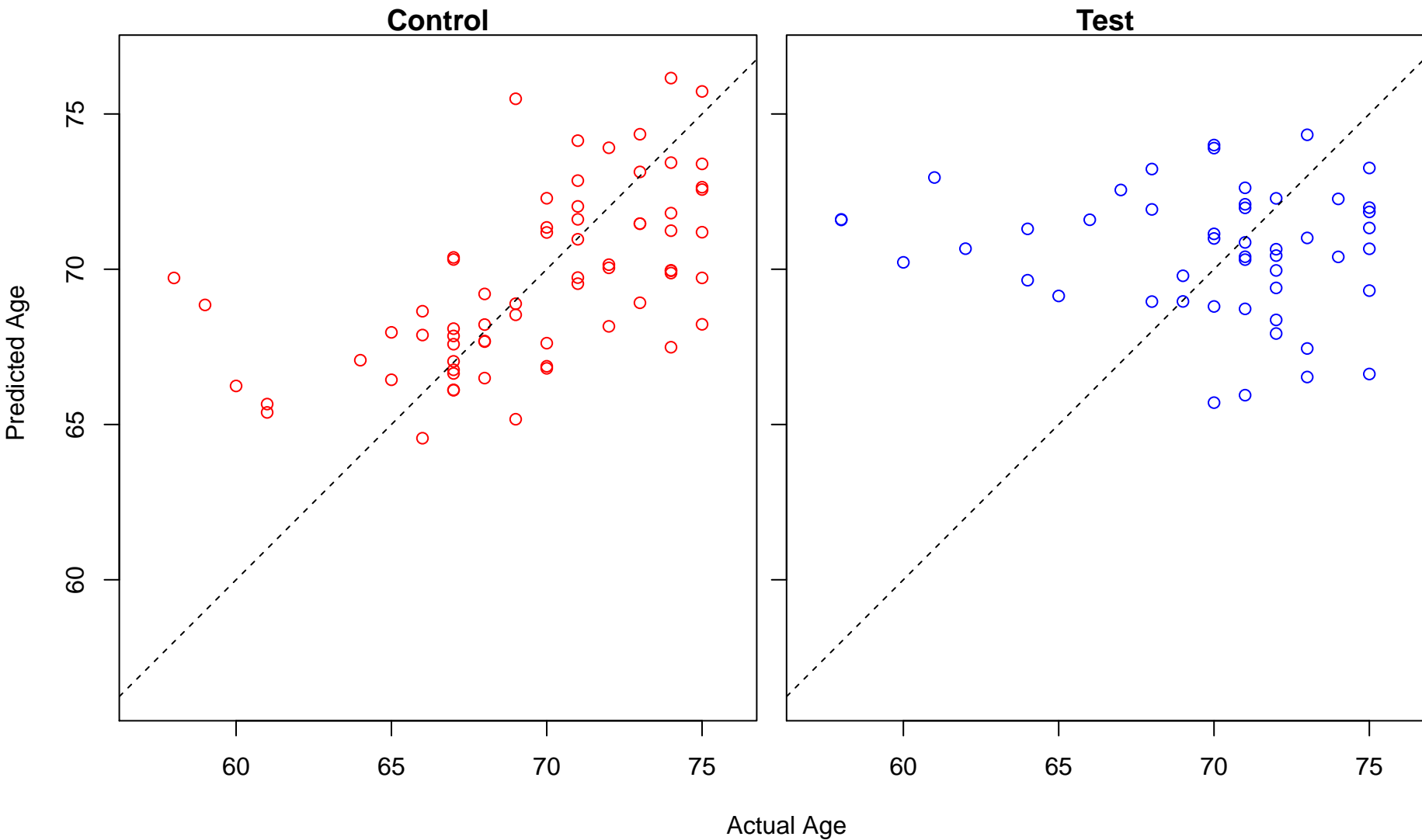
viral entry into host cell (Score: 1.039774)



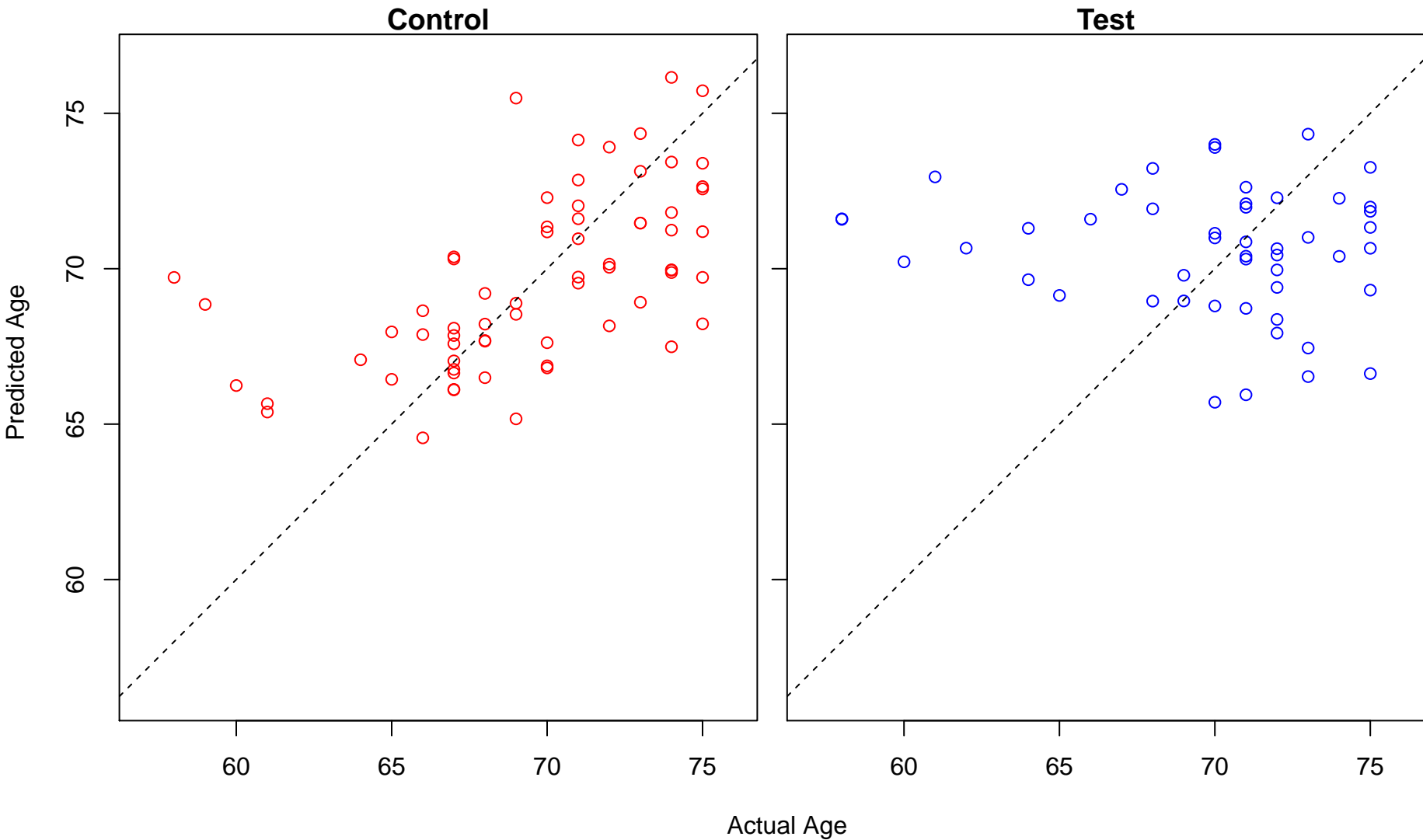
negative regulation of leukocyte apoptotic process (Score: 1.039493)



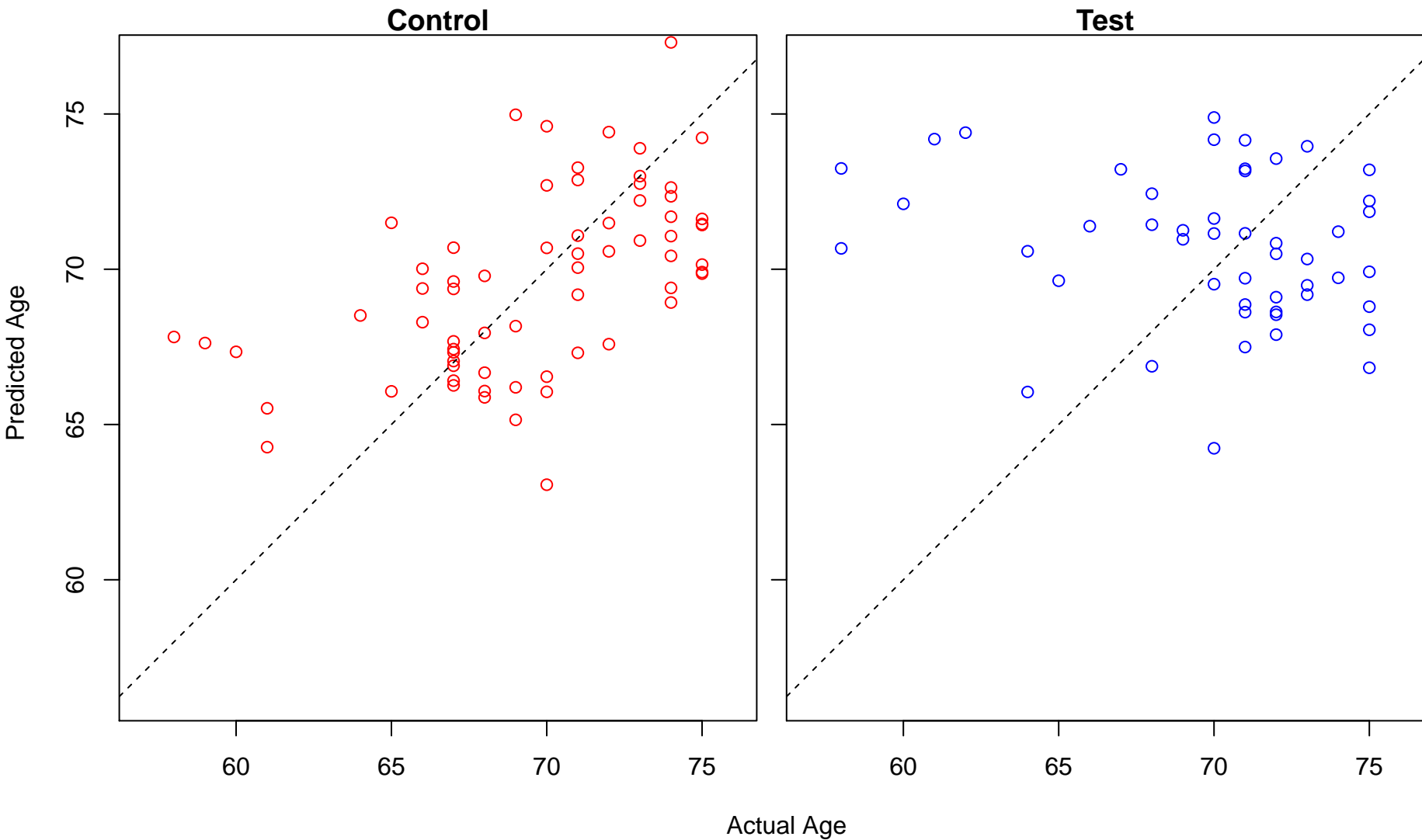
establishment of melanosome localization (Score: 1.039389)



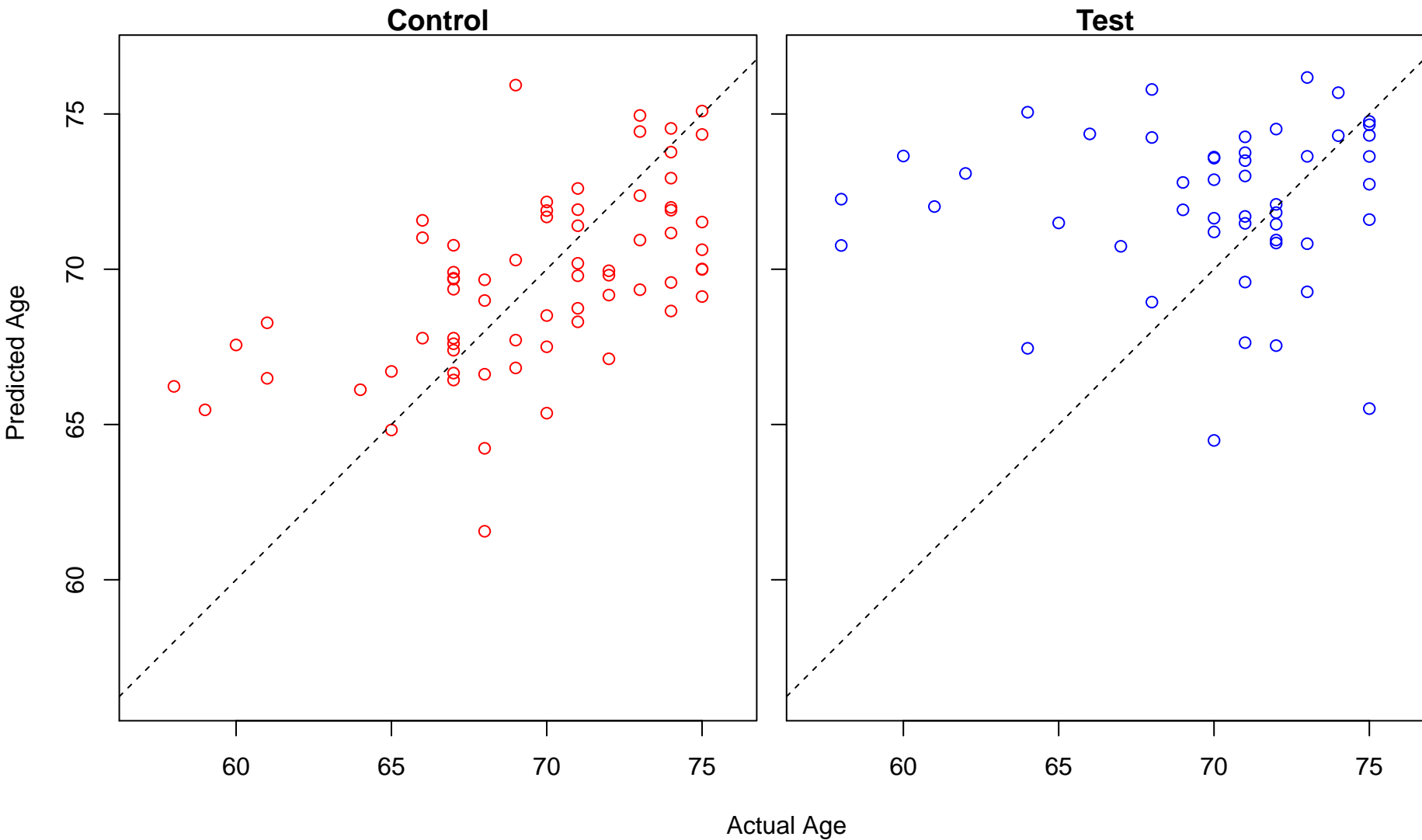
establishment of pigment granule localization (Score: 1.039389)



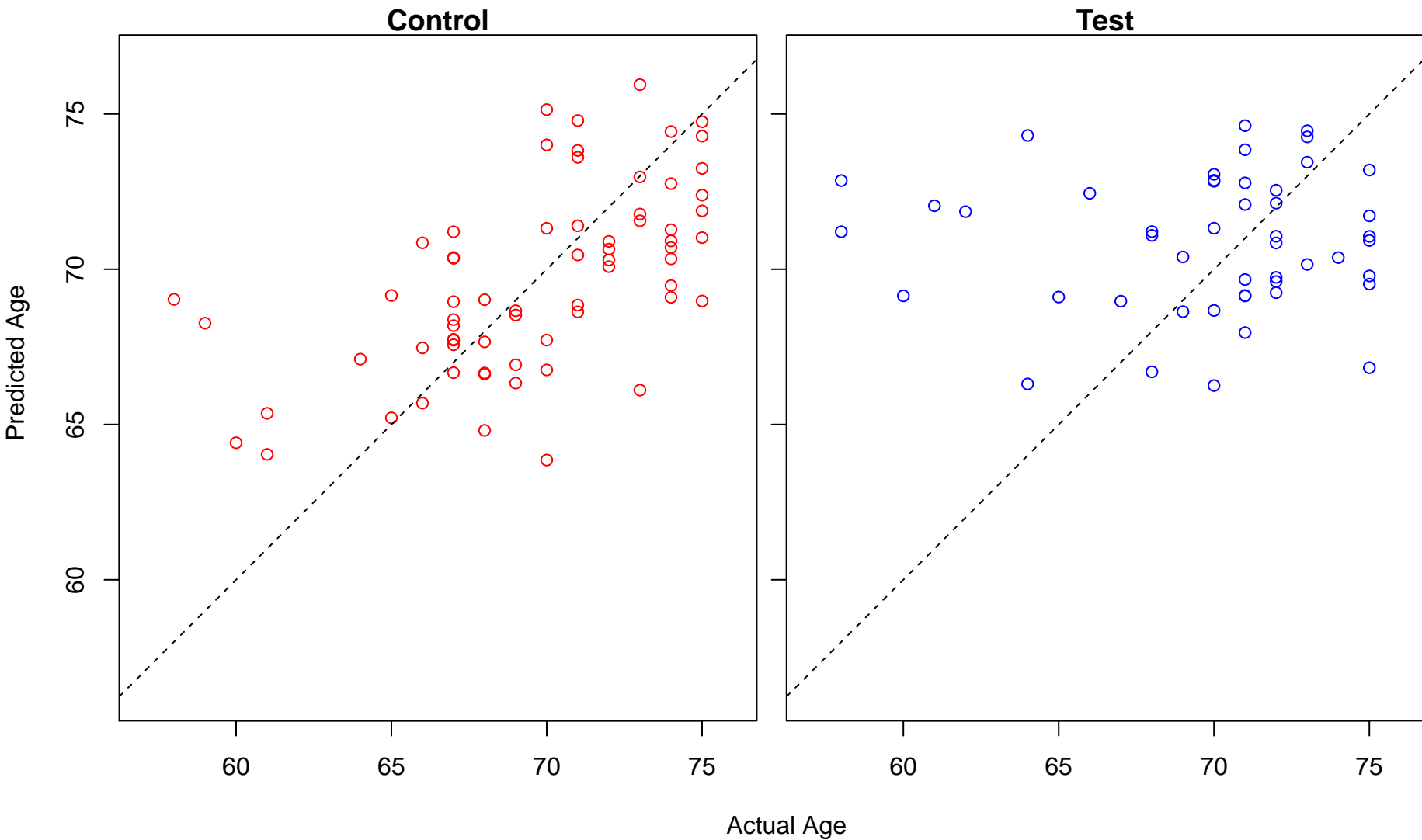
negative regulation of developmental growth (Score: 1.038392)



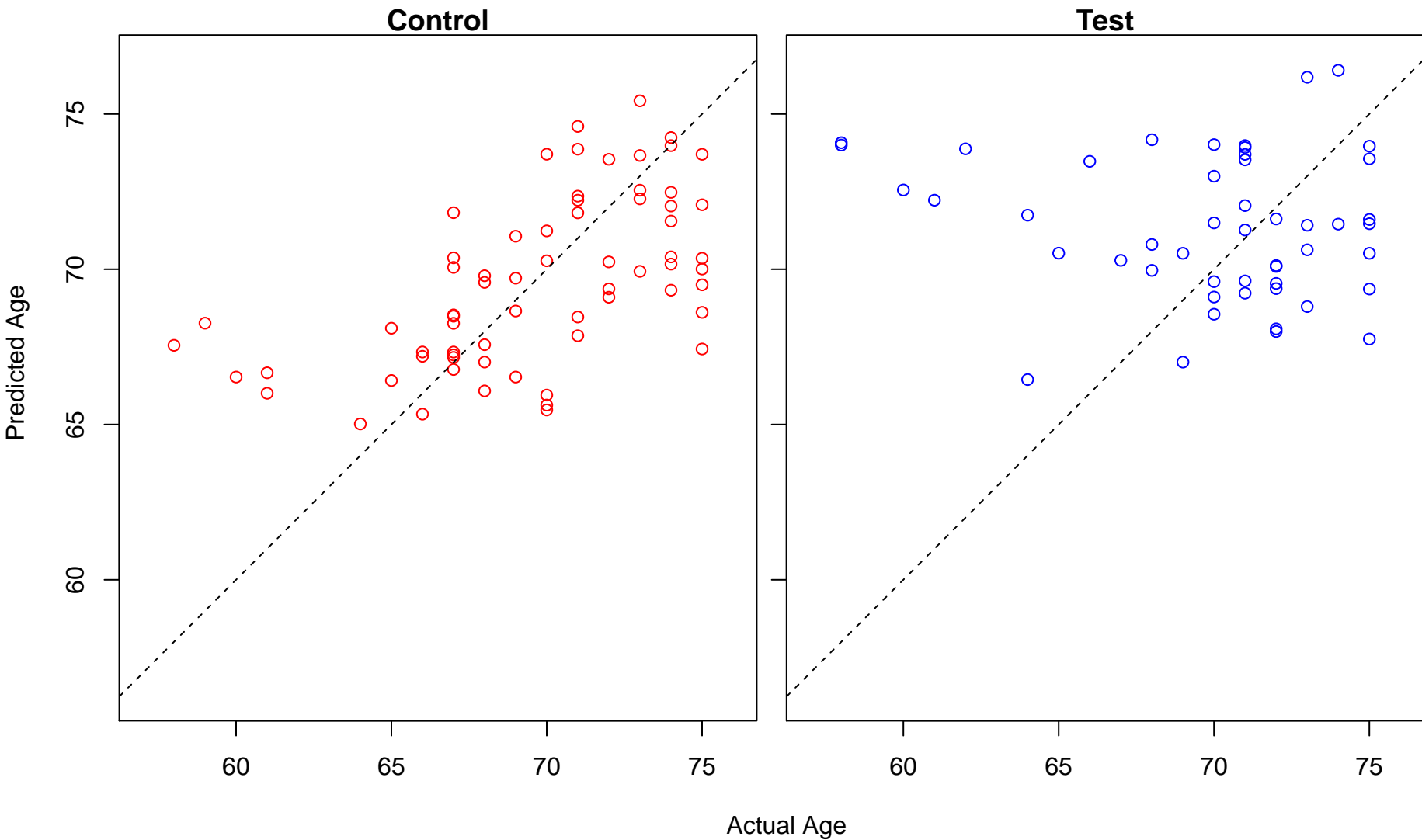
positive regulation of glucose metabolic process (Score: 1.038294)



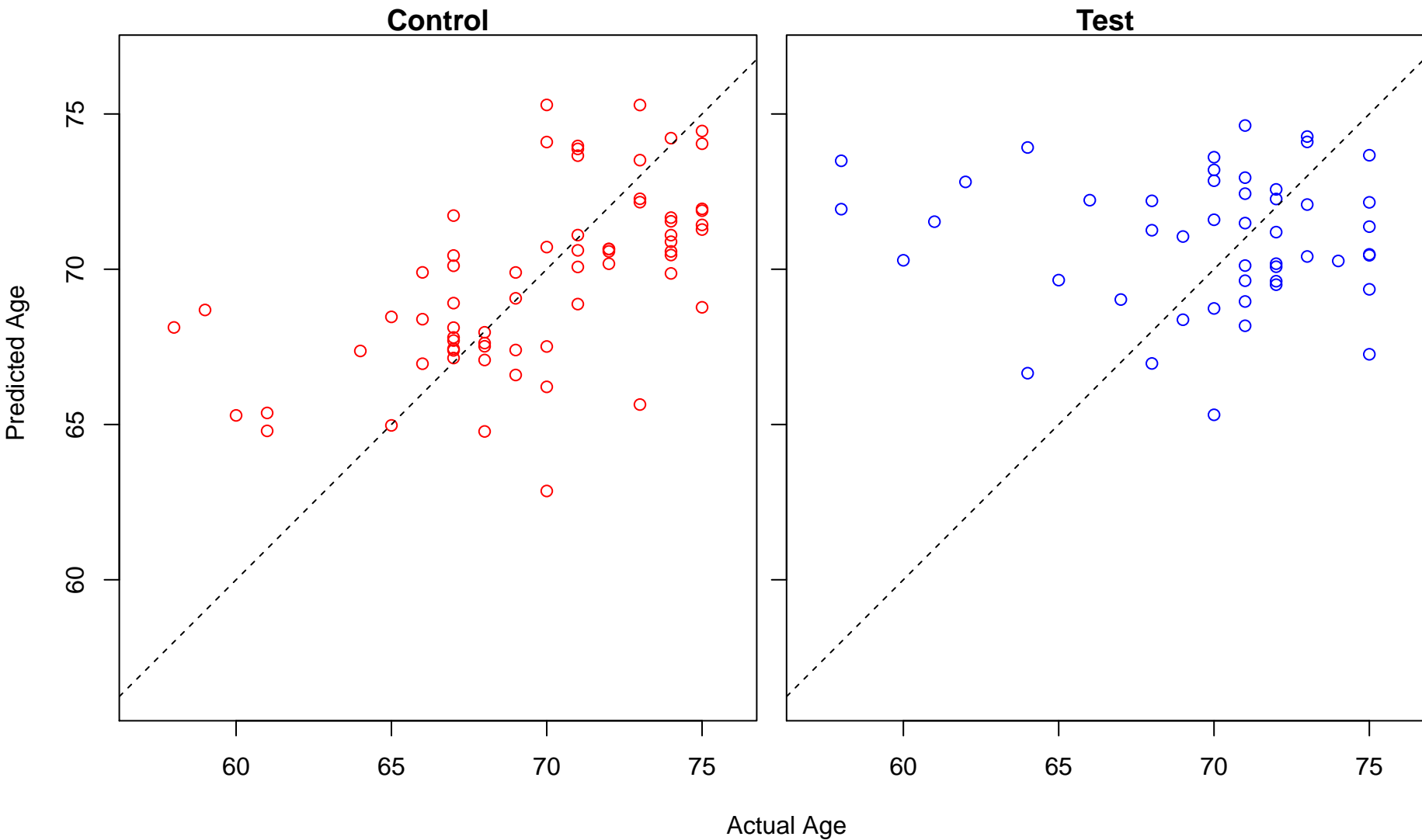
negative regulation of protein complex disassembly (Score: 1.038234)



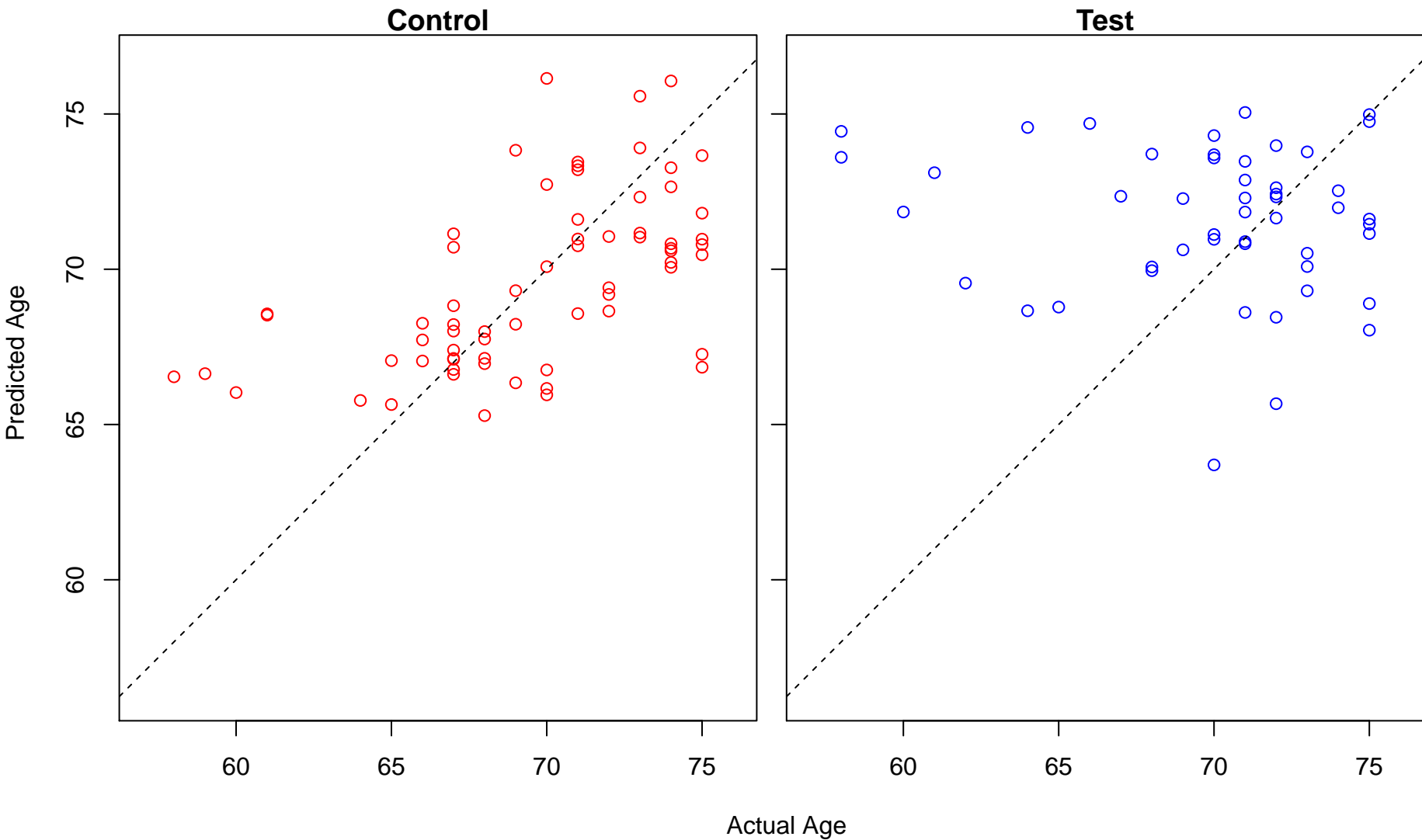
regulation of transcription from RNA polymerase III promoter (Score: 1.038122)



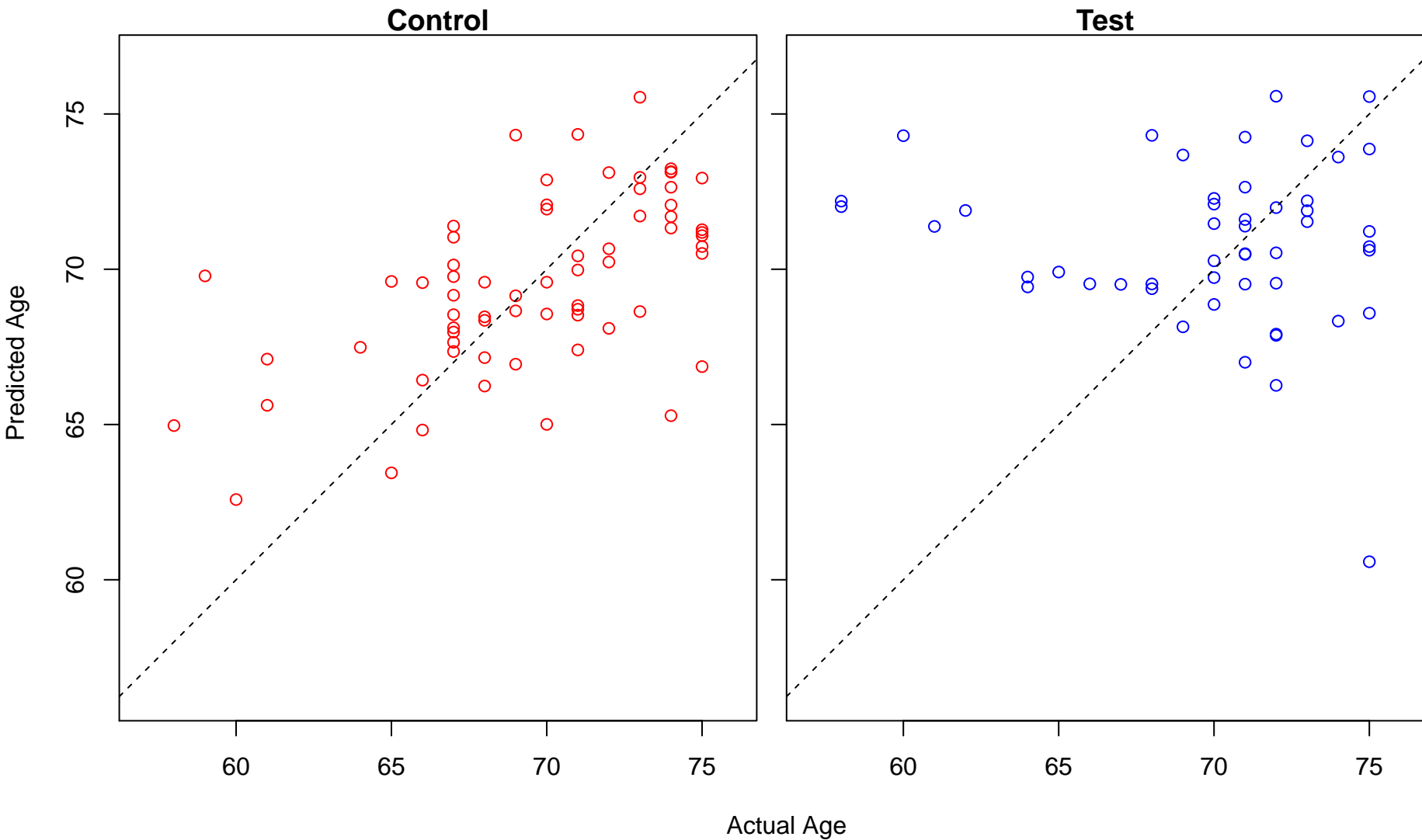
negative regulation of protein depolymerization (Score: 1.038079)



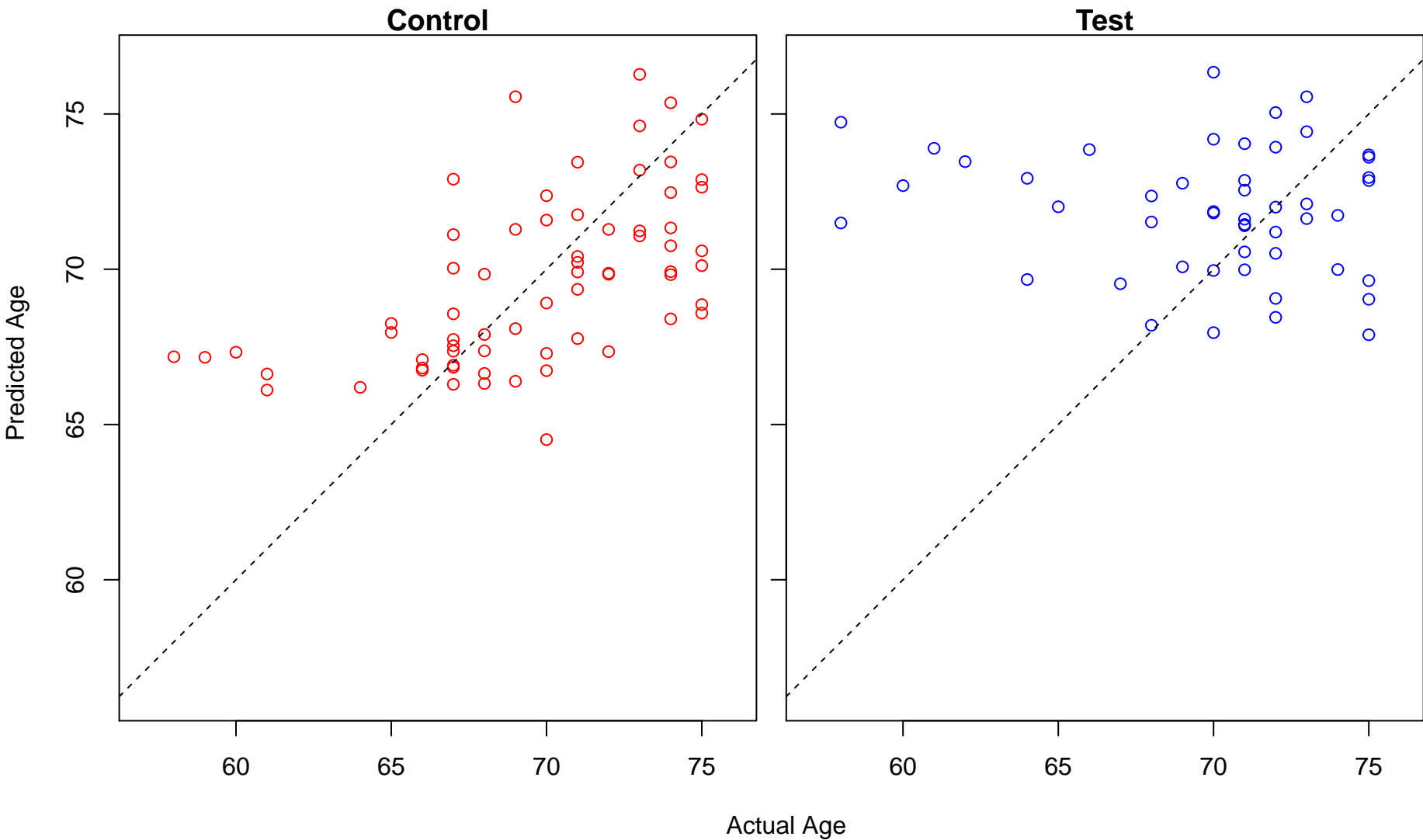
urogenital system development (Score: 1.037994)



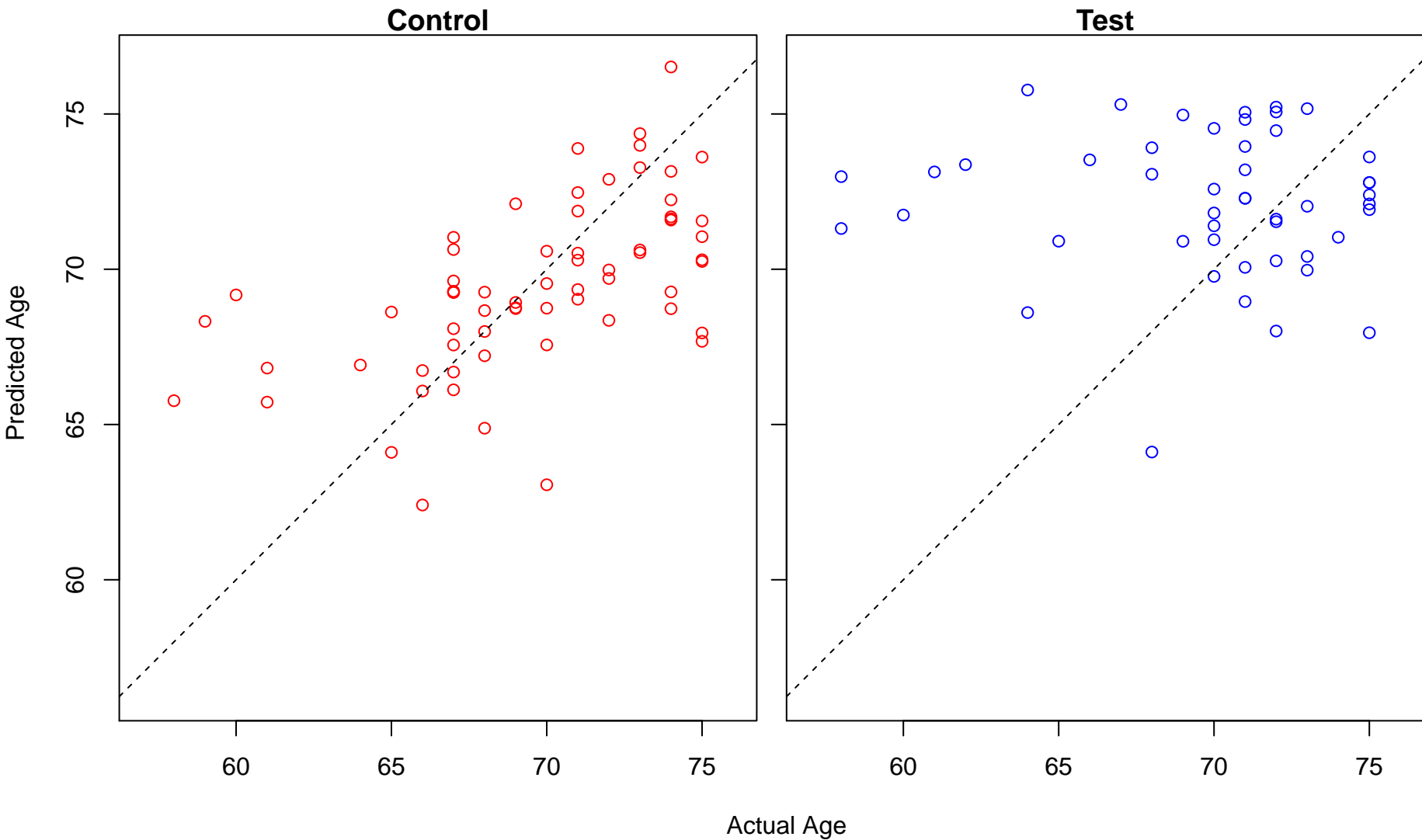
regulation of glial cell proliferation (Score: 1.037691)



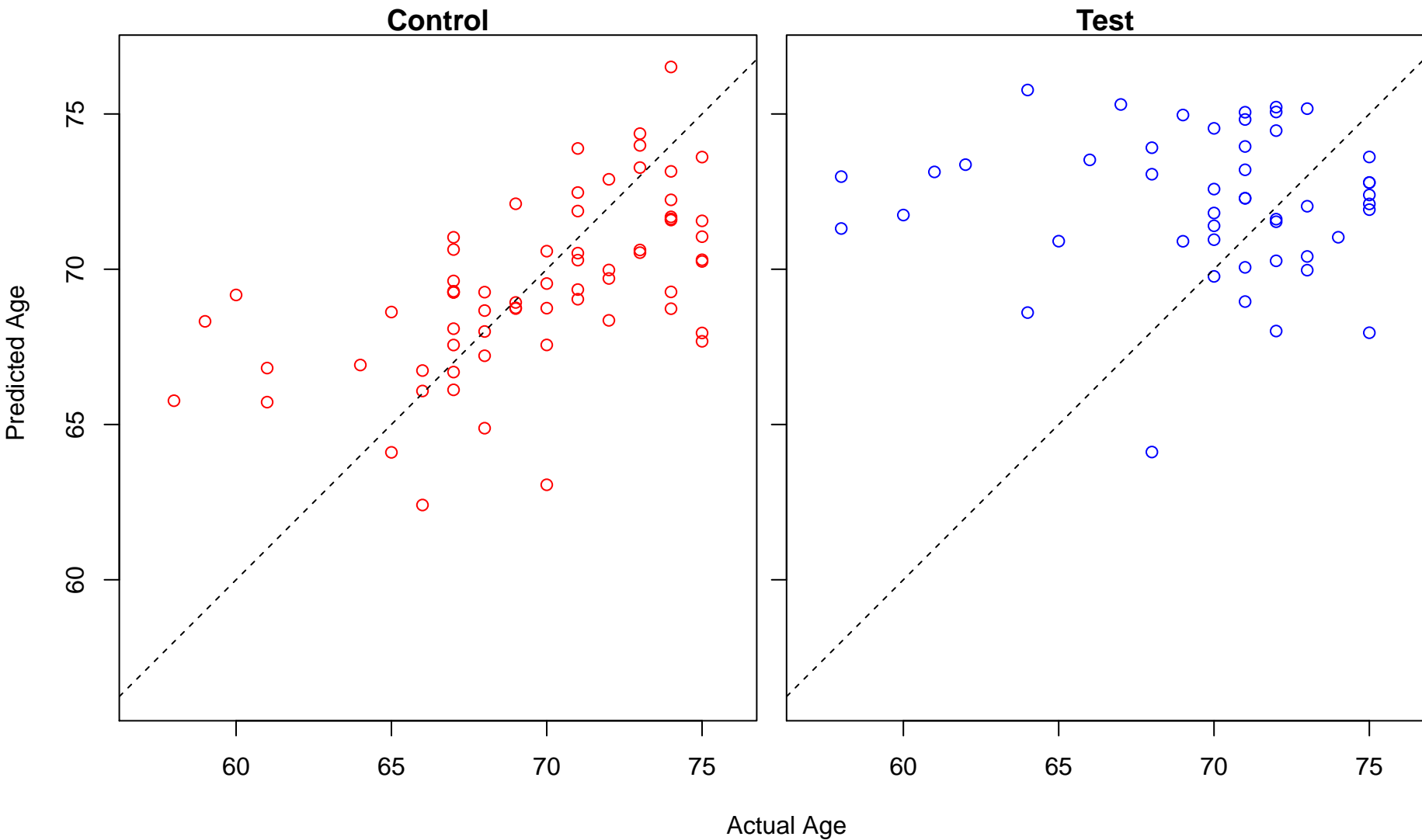
heart contraction (Score: 1.037627)



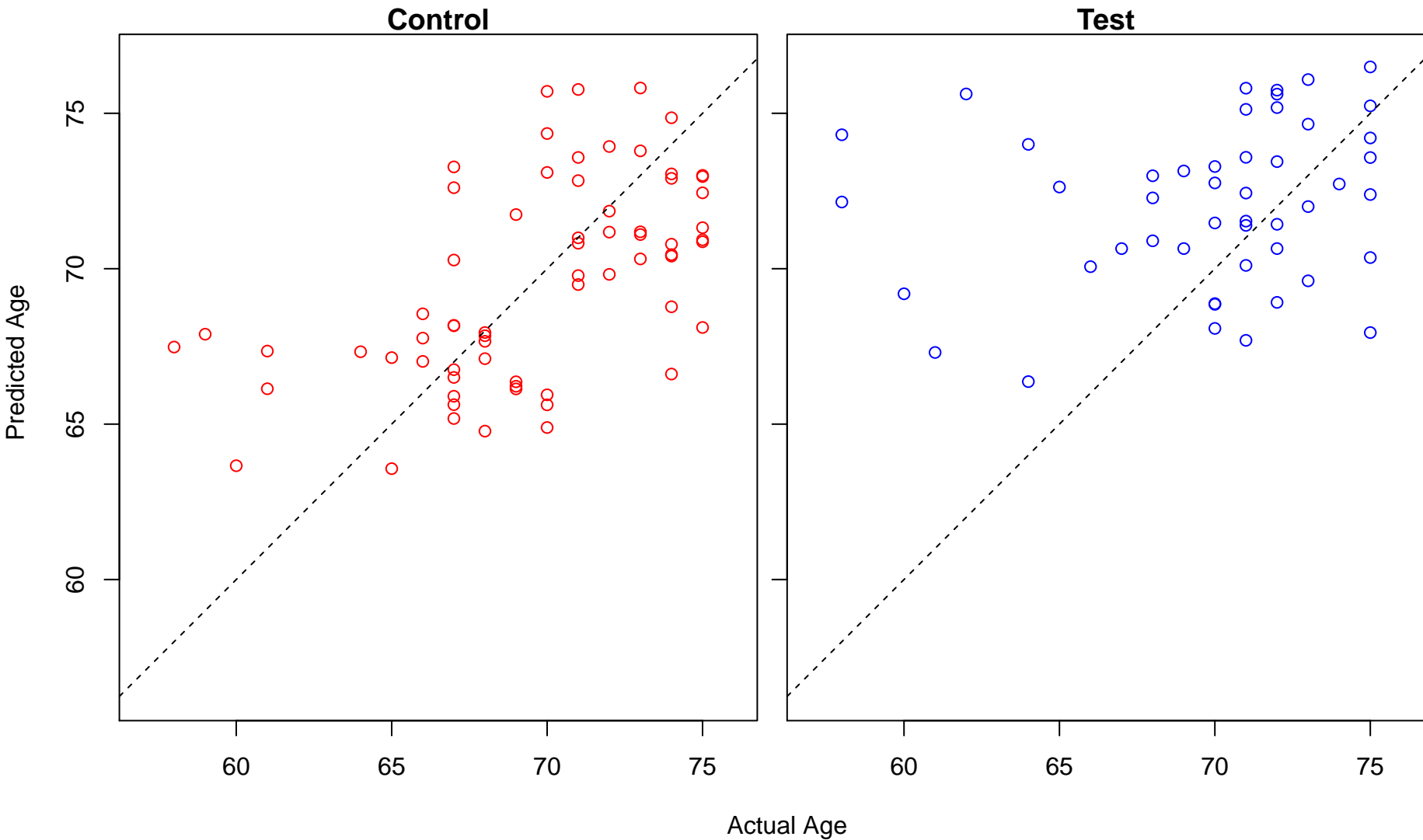
2'-deoxyribonucleotide metabolic process (Score: 1.036863)



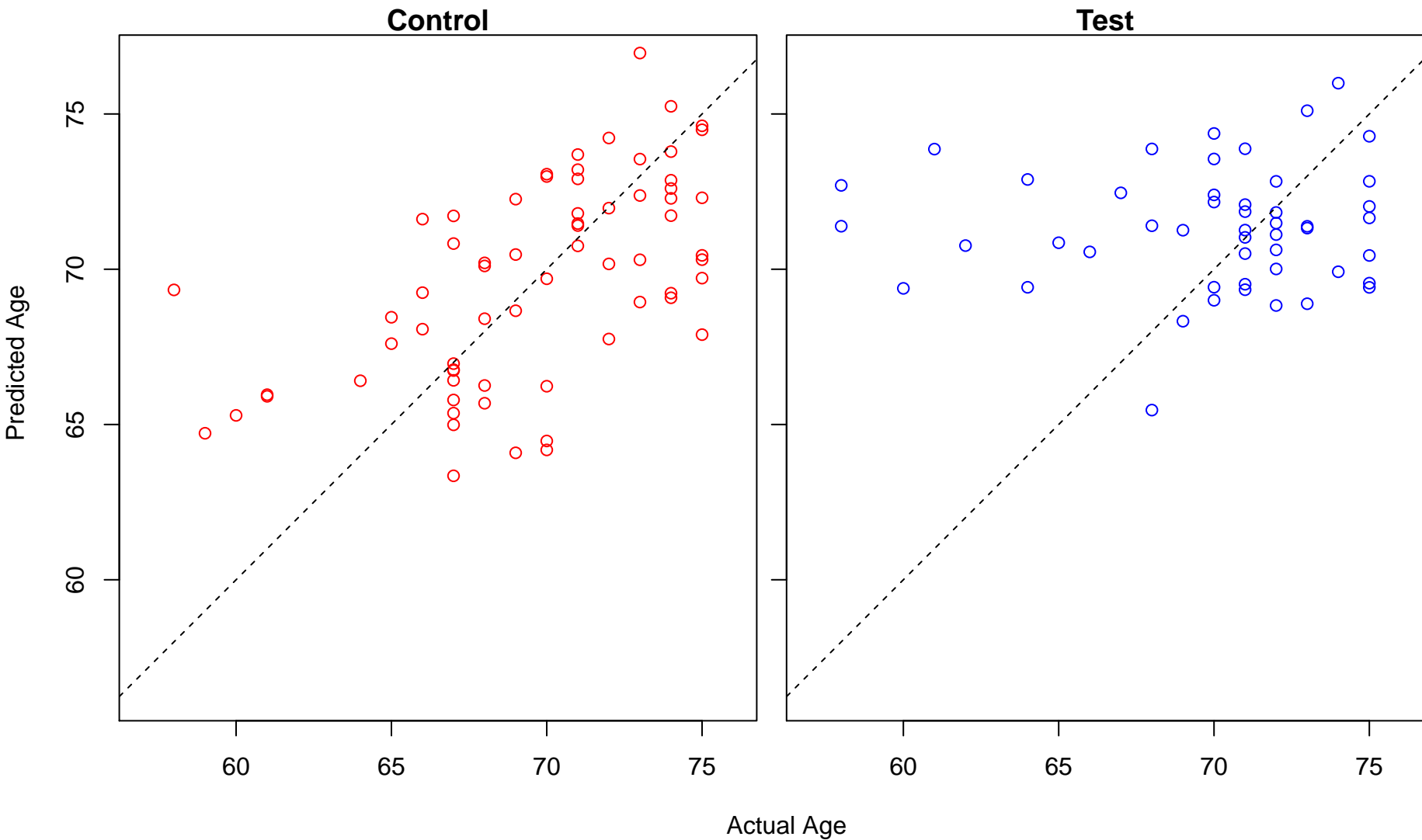
deoxyribose phosphate metabolic process (Score: 1.036863)



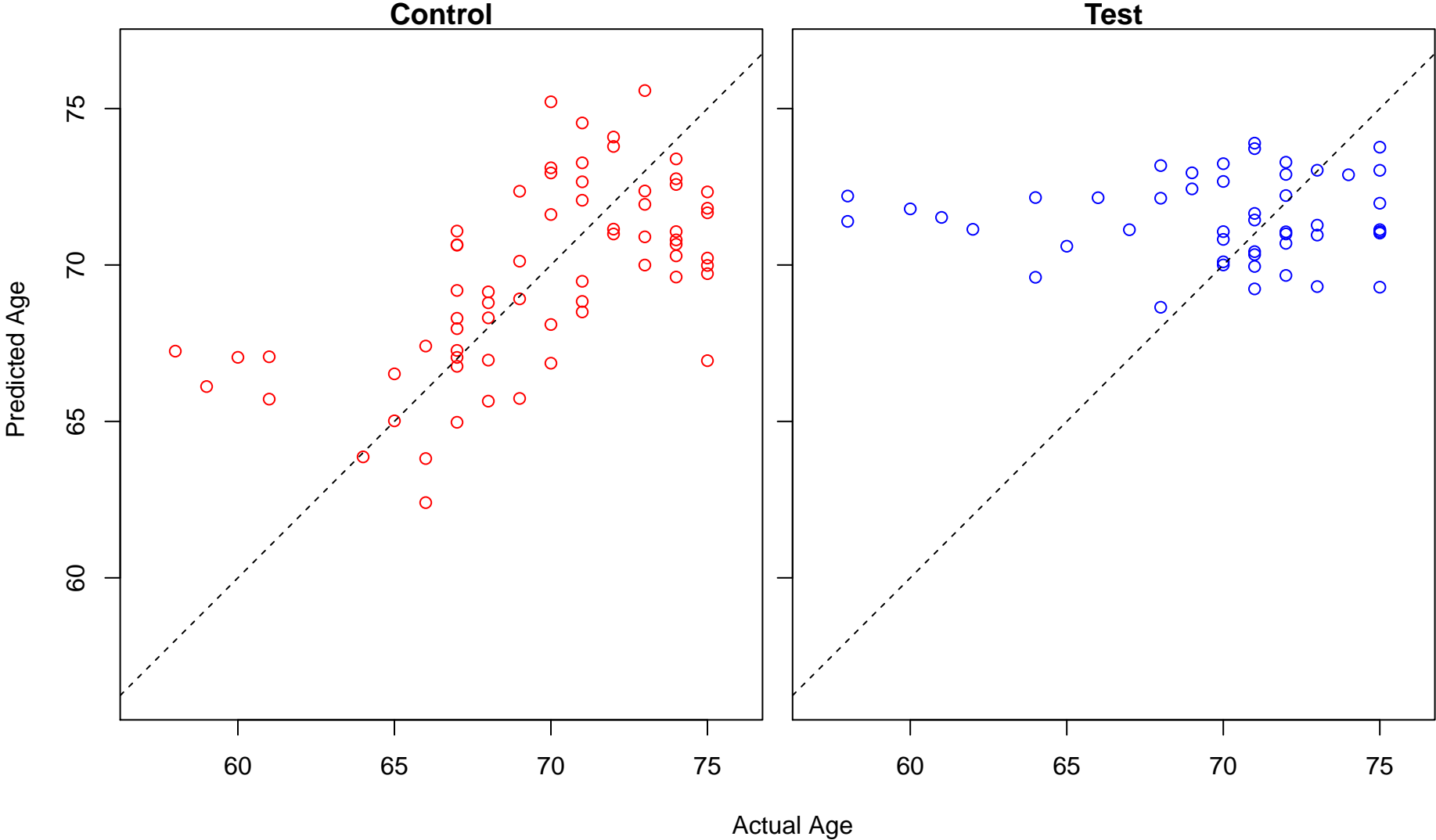
positive regulation of neuron differentiation (Score: 1.036100)



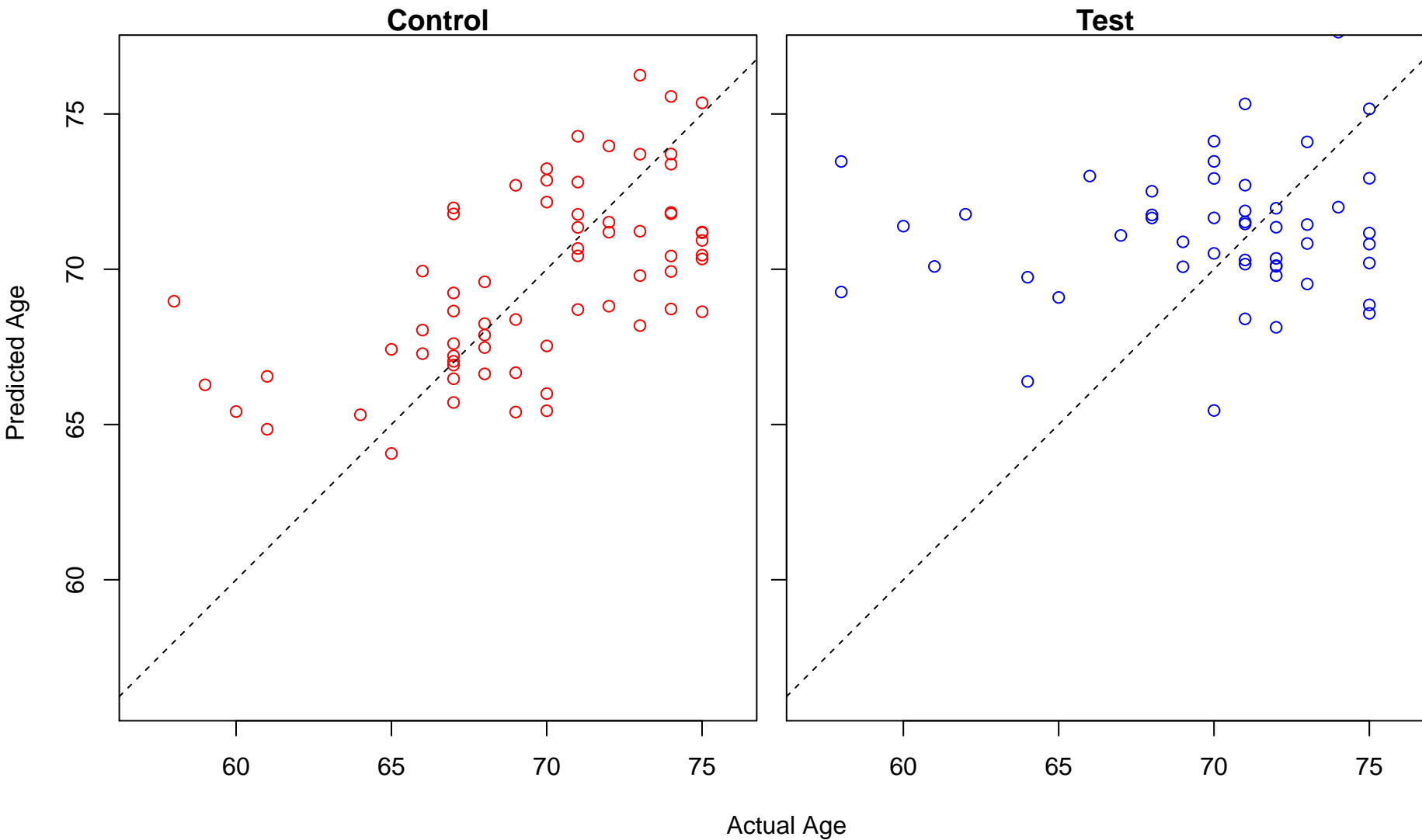
pigment metabolic process (Score: 1.035016)



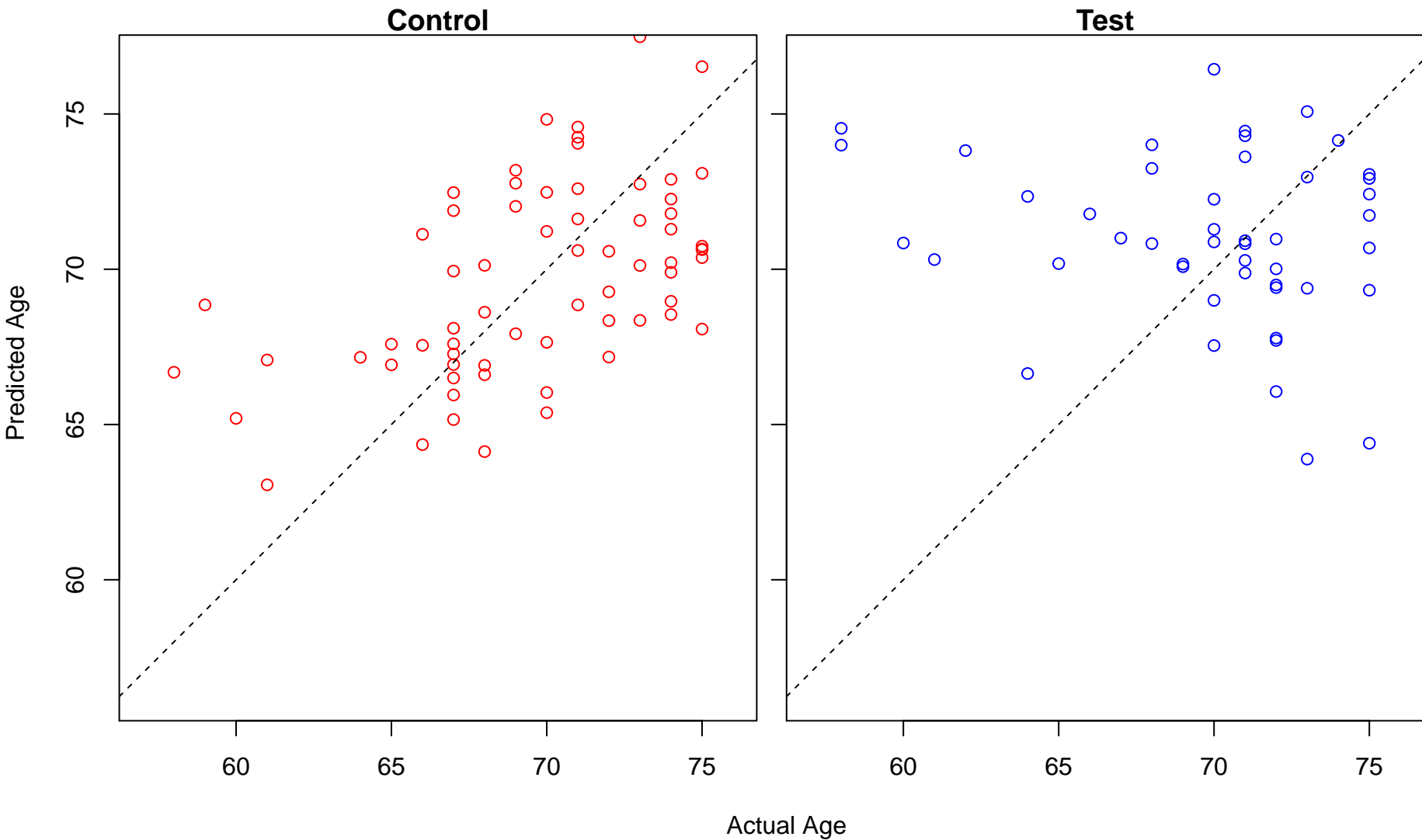
negative regulation of protein kinase activity by regulation of protein phosphorylation (Score: 1.0346)



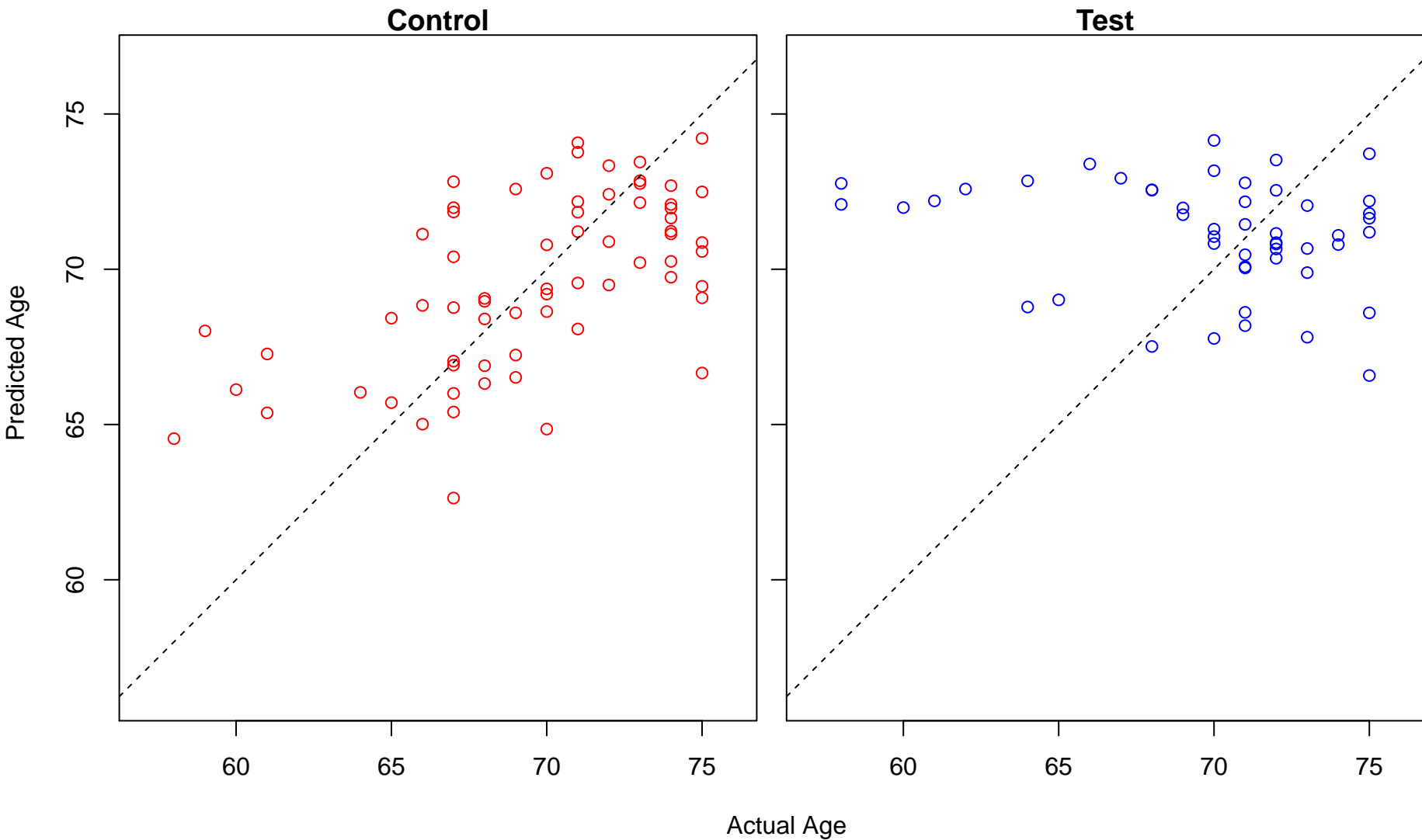
cell-matrix adhesion (Score: 1.034547)



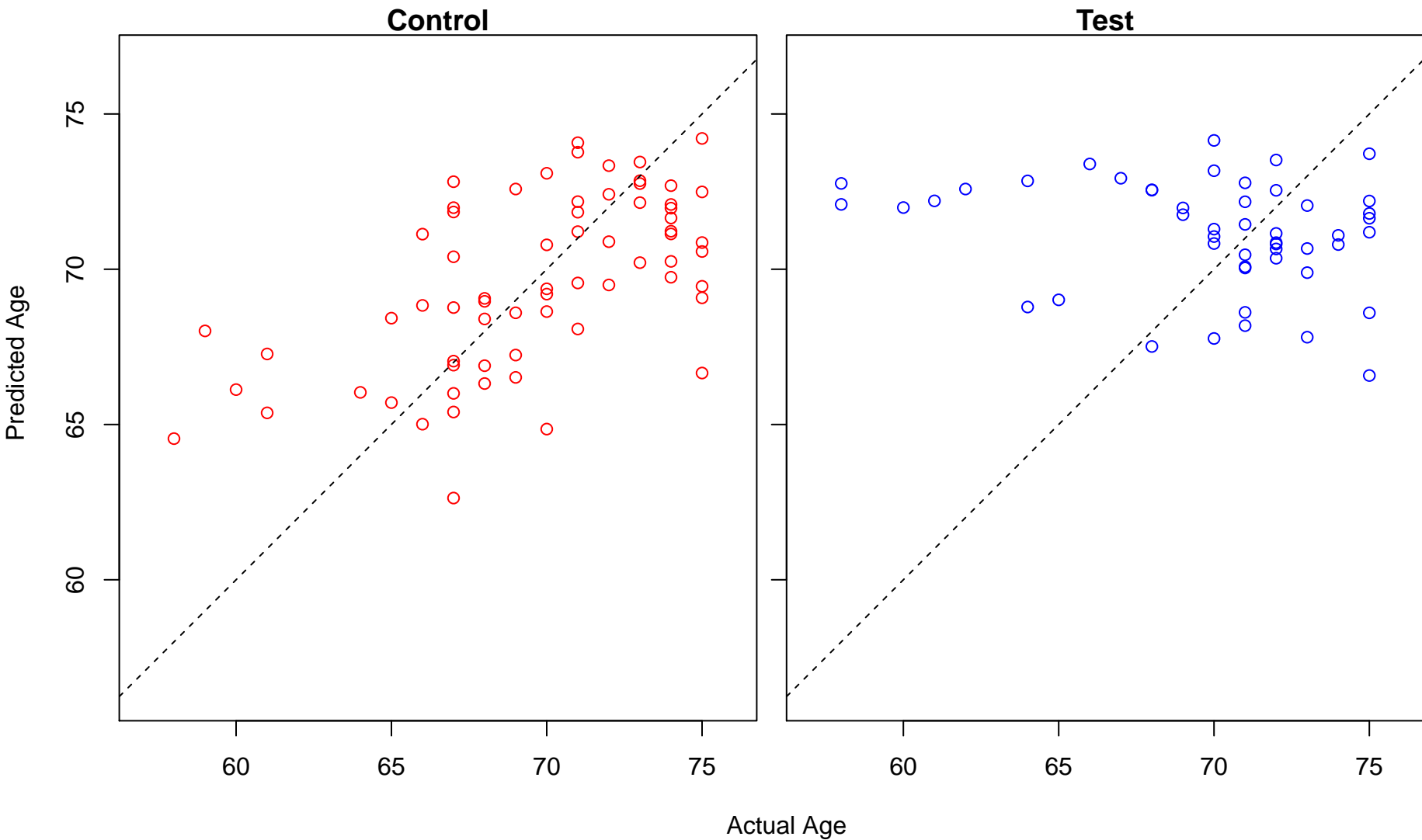
inactivation of MAPK activity (Score: 1.034122)



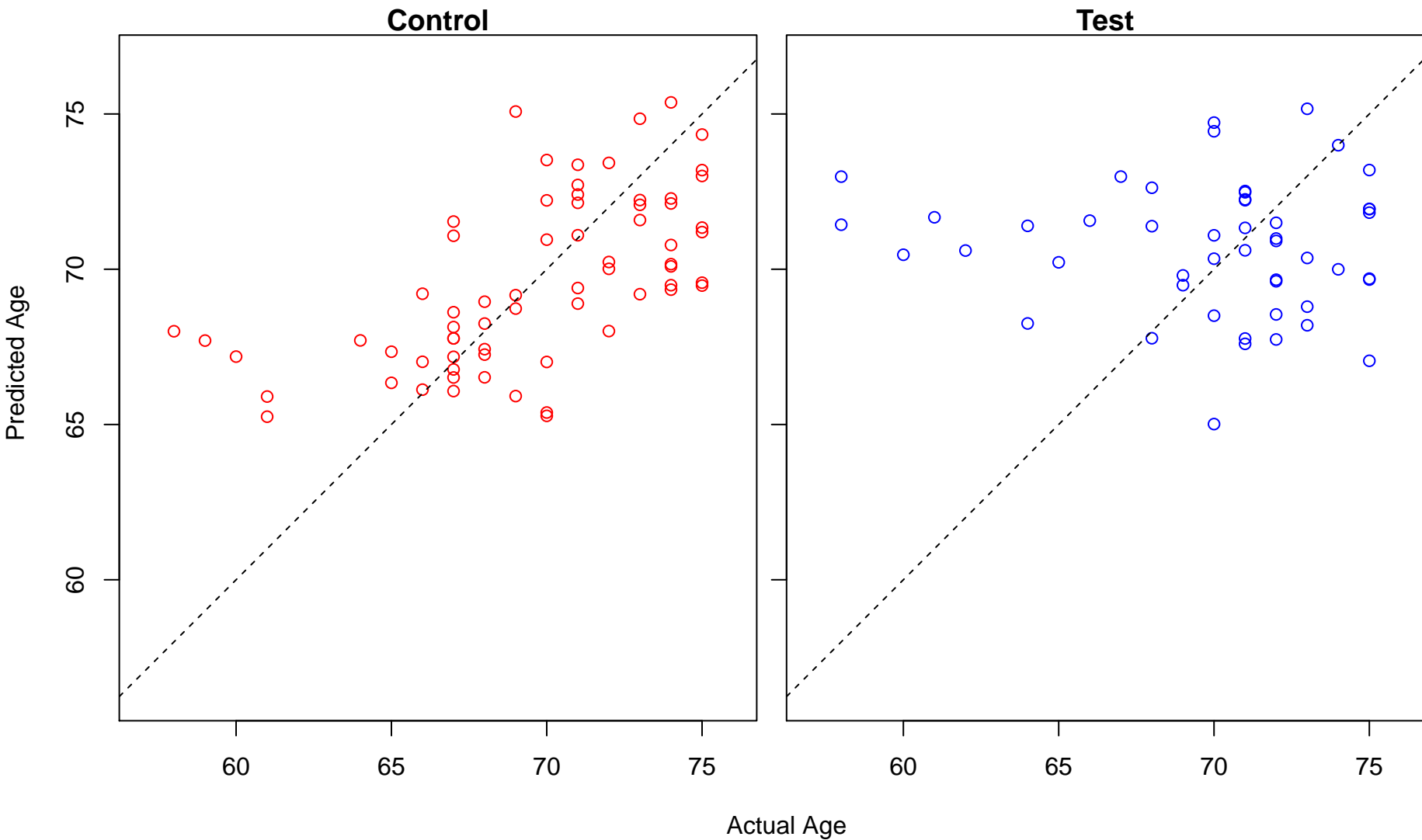
DNA replication-dependent nucleosome assembly (Score: 1.033922)



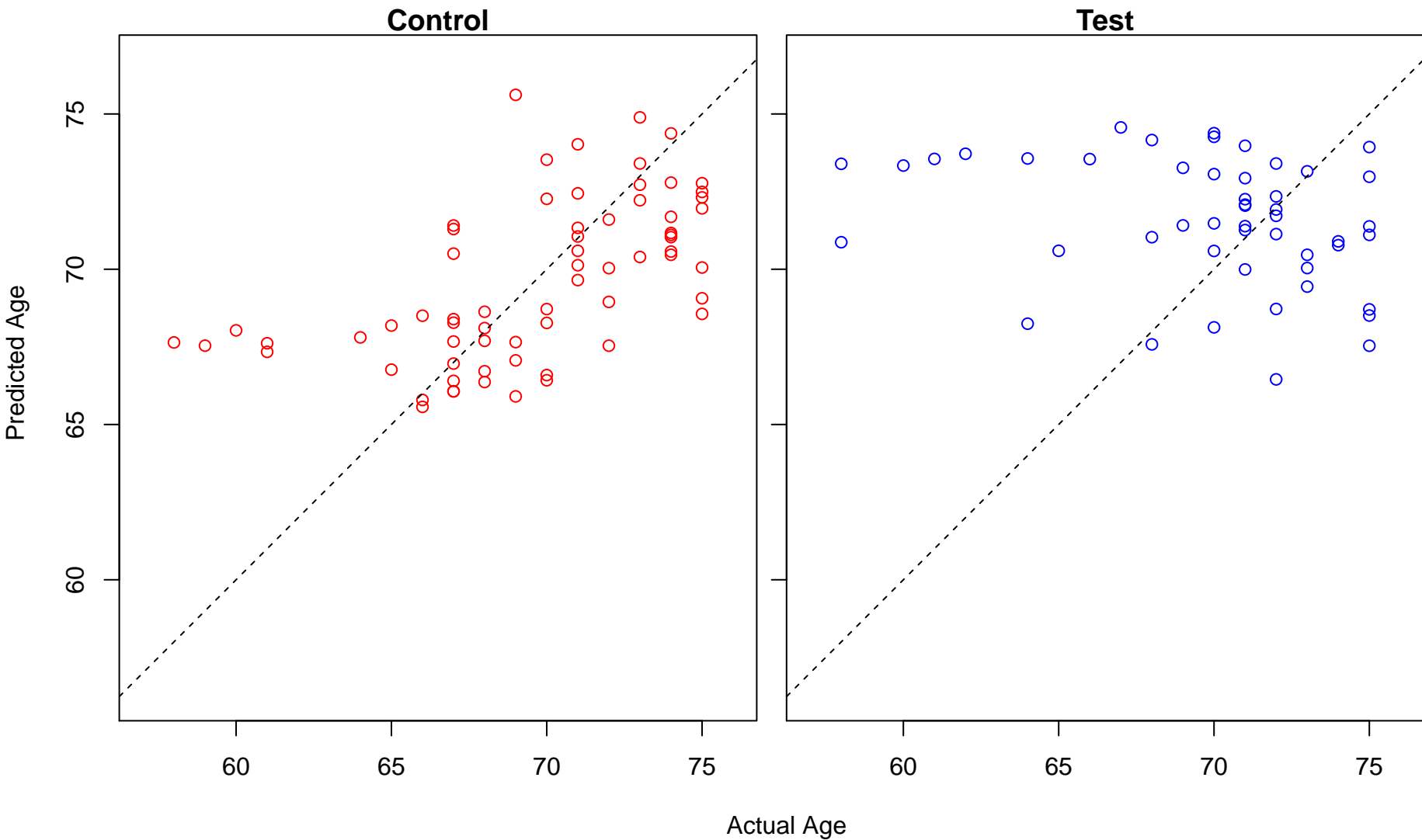
DNA replication-dependent nucleosome organization (Score: 1.033922)



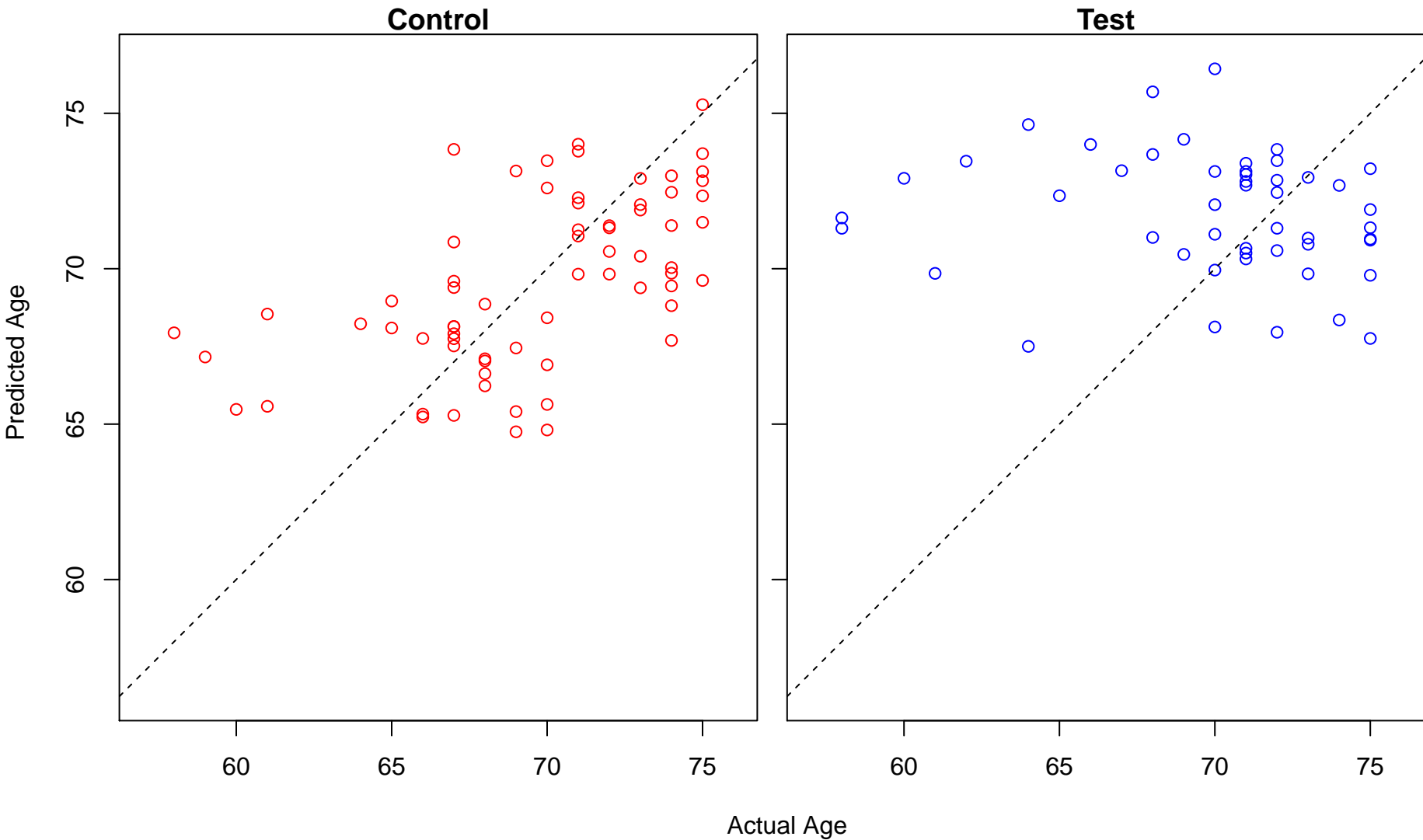
cellular pigmentation (Score: 1.032973)



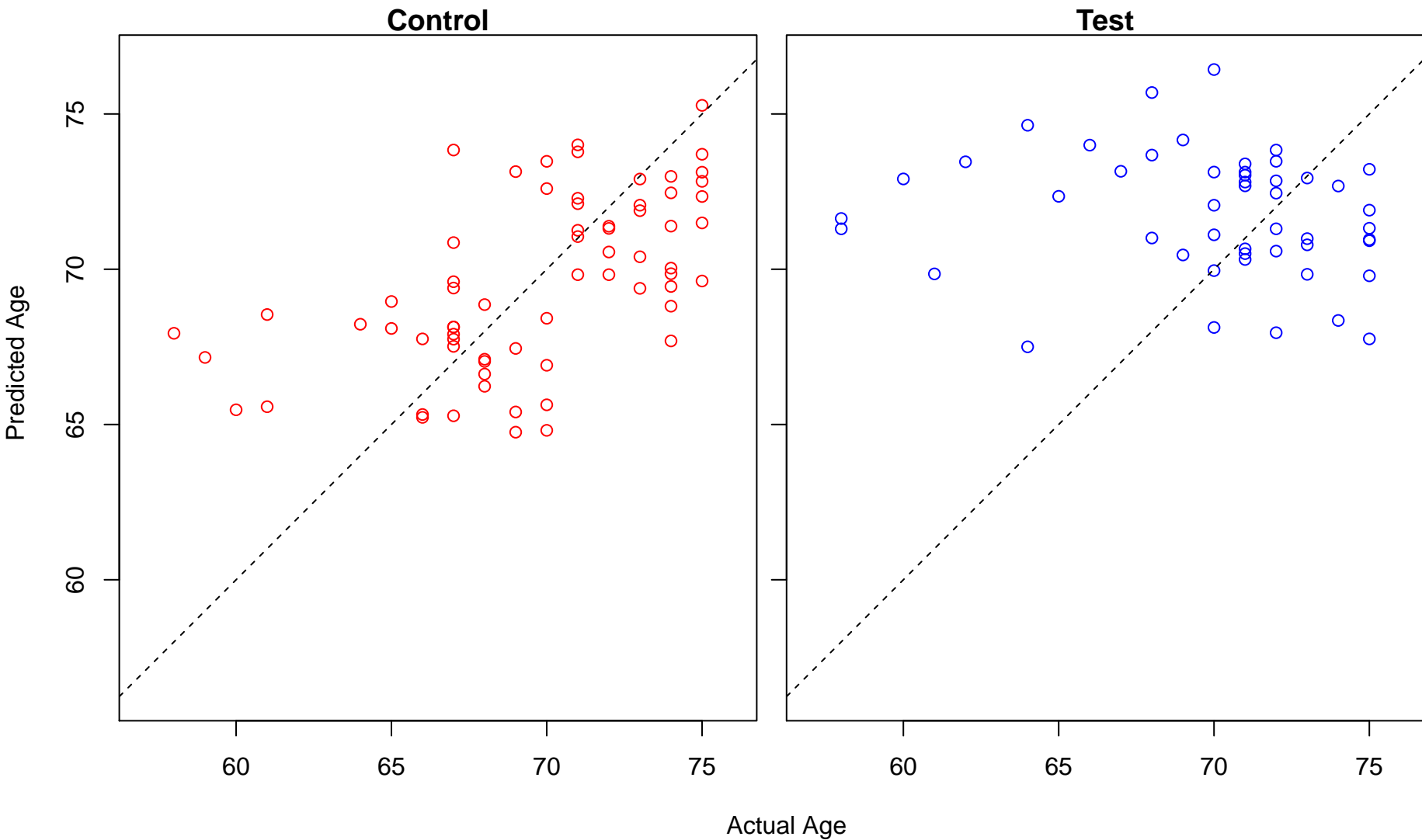
keratinocyte differentiation (Score: 1.032638)



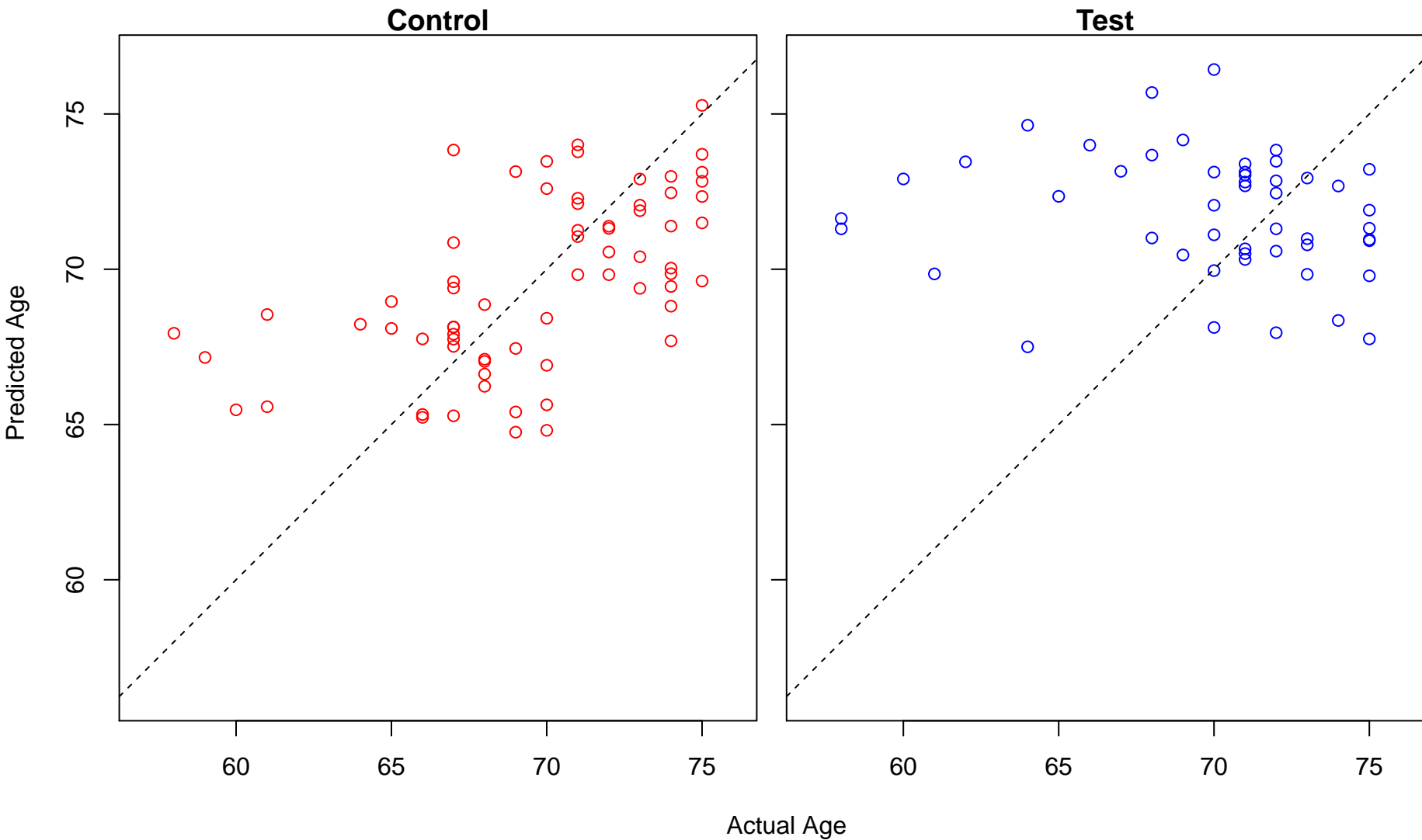
positive regulation of maintenance of sister chromatid cohesion (Score: 1.032308)



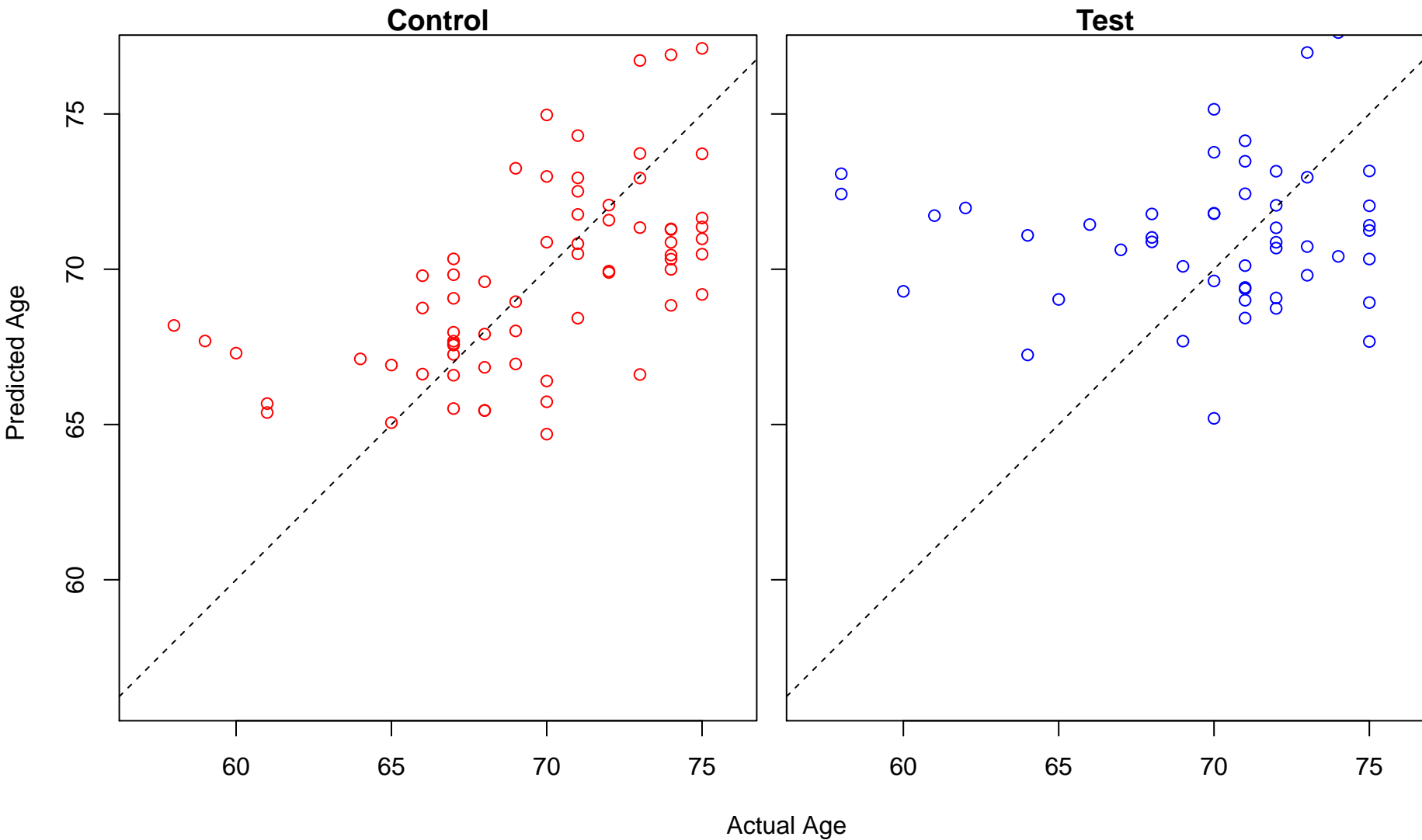
positive regulation of maintenance of mitotic sister chromatid cohesion (Score: 1.032308)



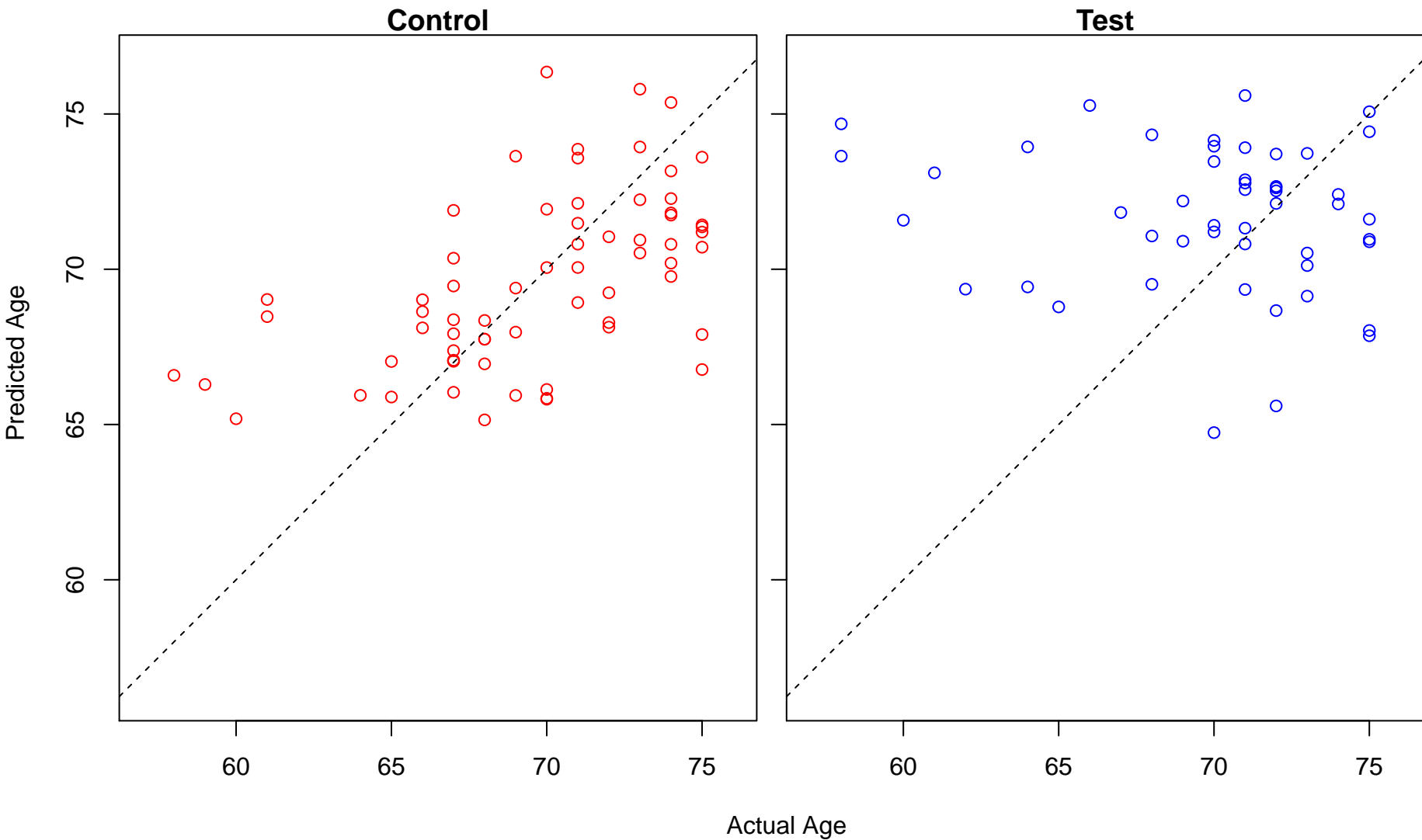
positive regulation of sister chromatid cohesion (Score: 1.032308)



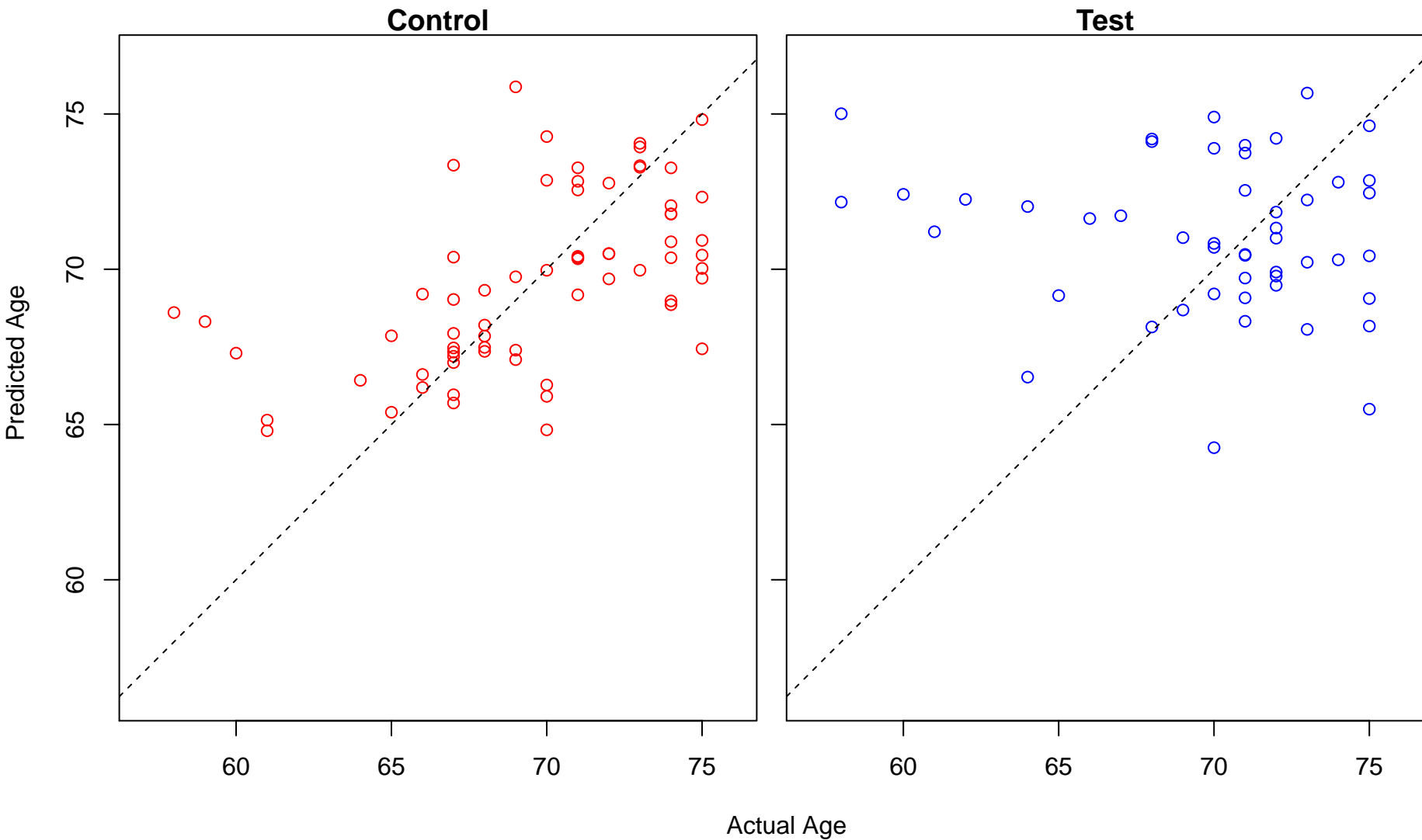
regulation of protein complex disassembly (Score: 1.032008)



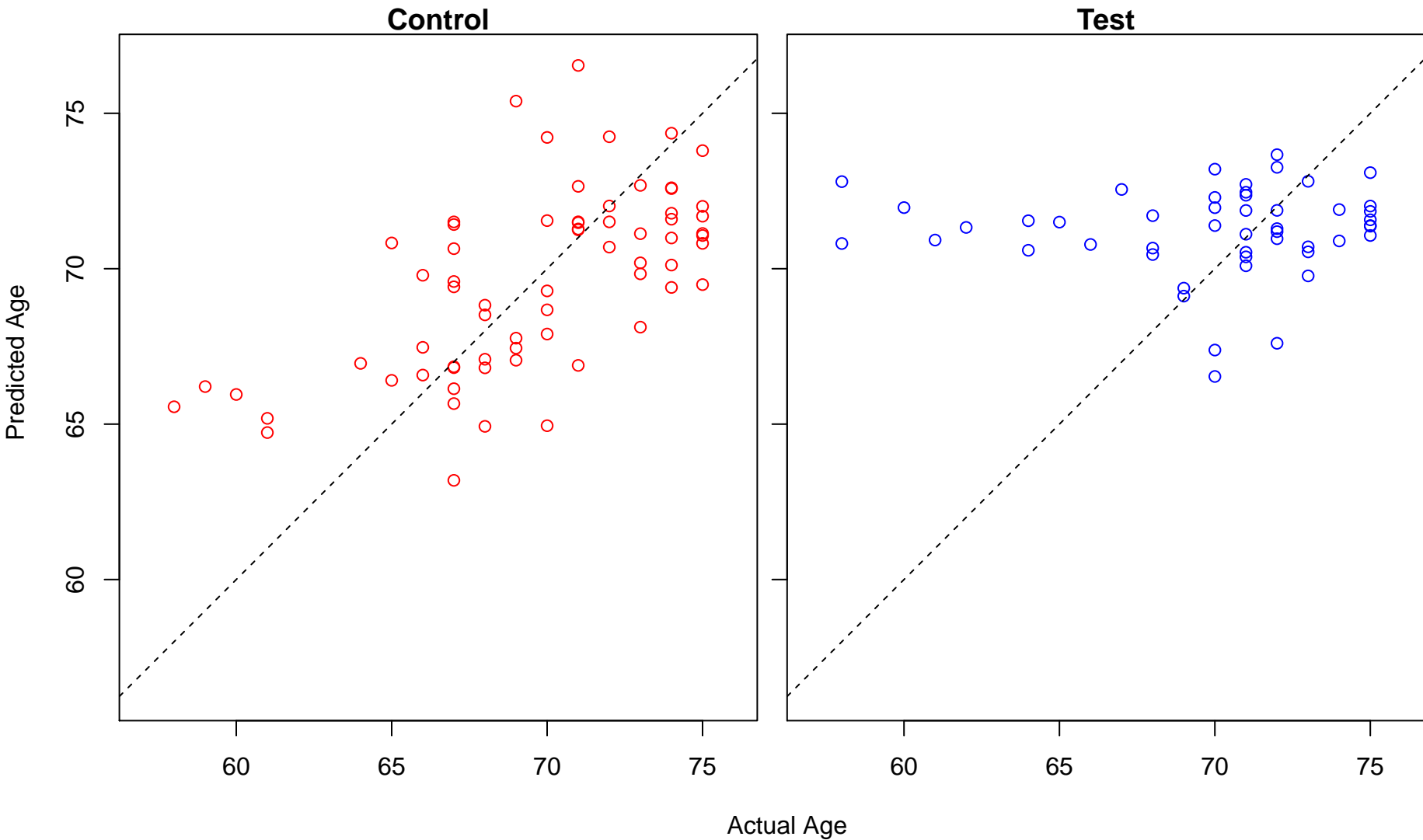
renal system development (Score: 1.031647)



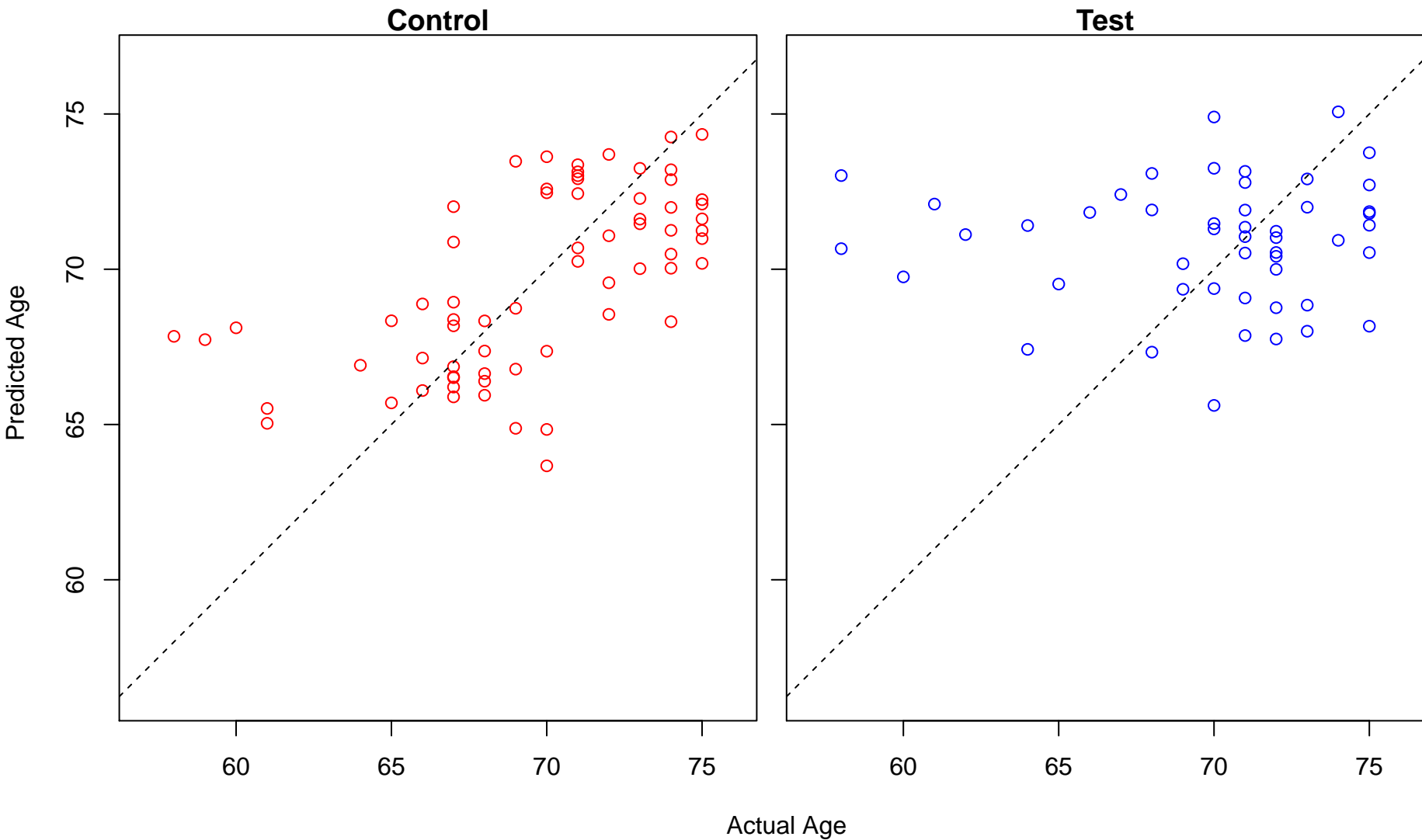
regulation of cardiac conduction (Score: 1.031231)



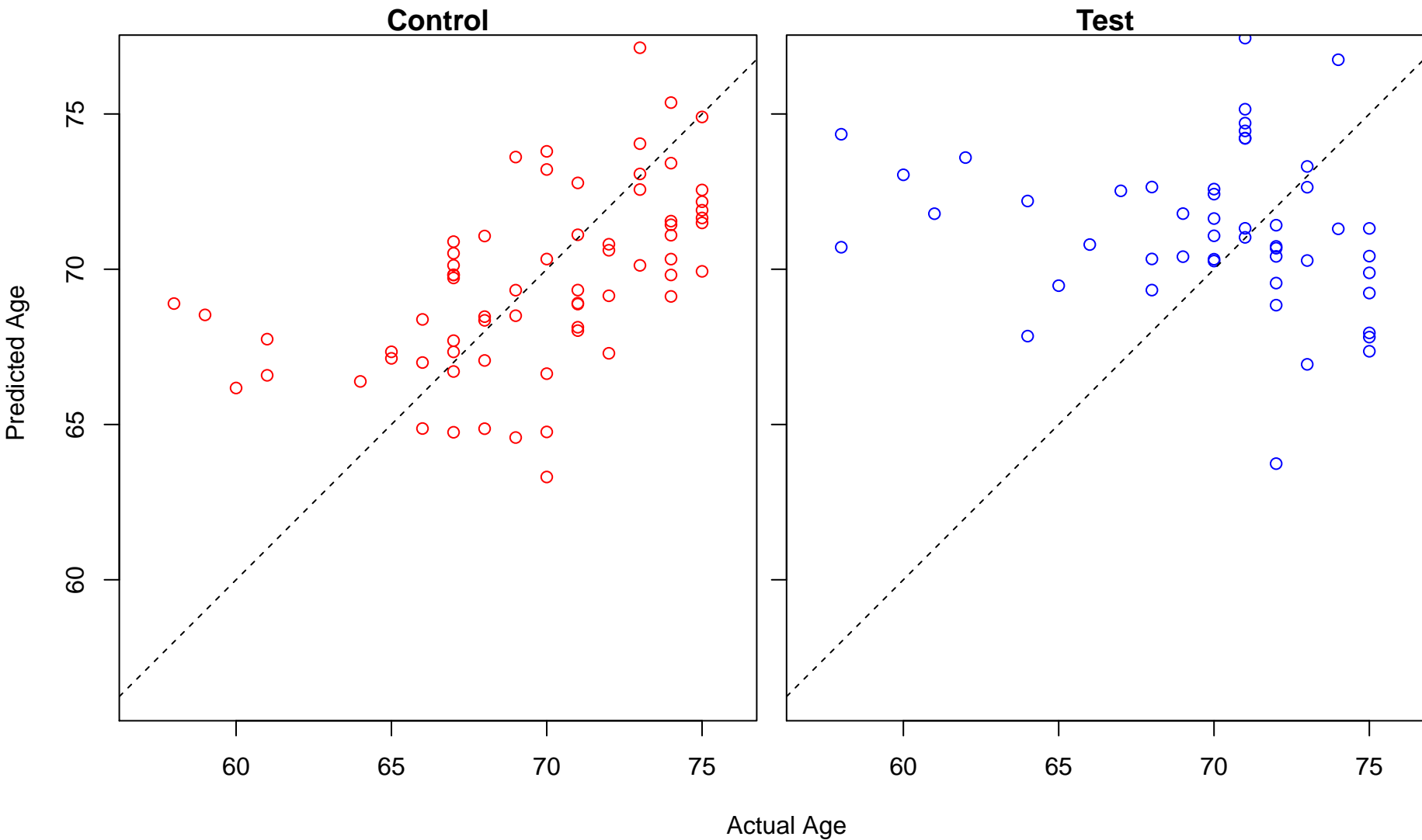
positive regulation of endoplasmic reticulum unfolded protein response (Score: 1.030676)



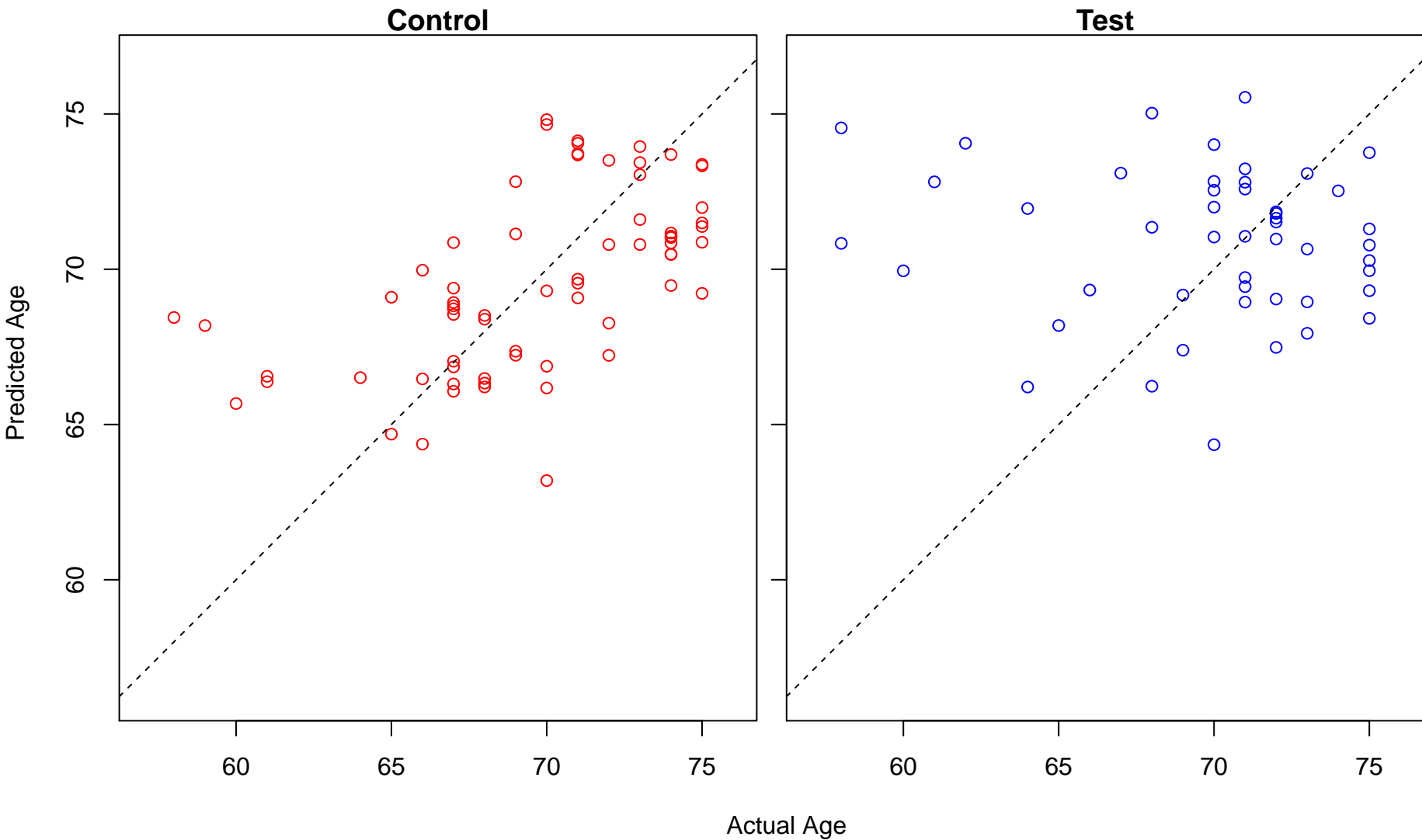
pigmentation (Score: 1.030433)



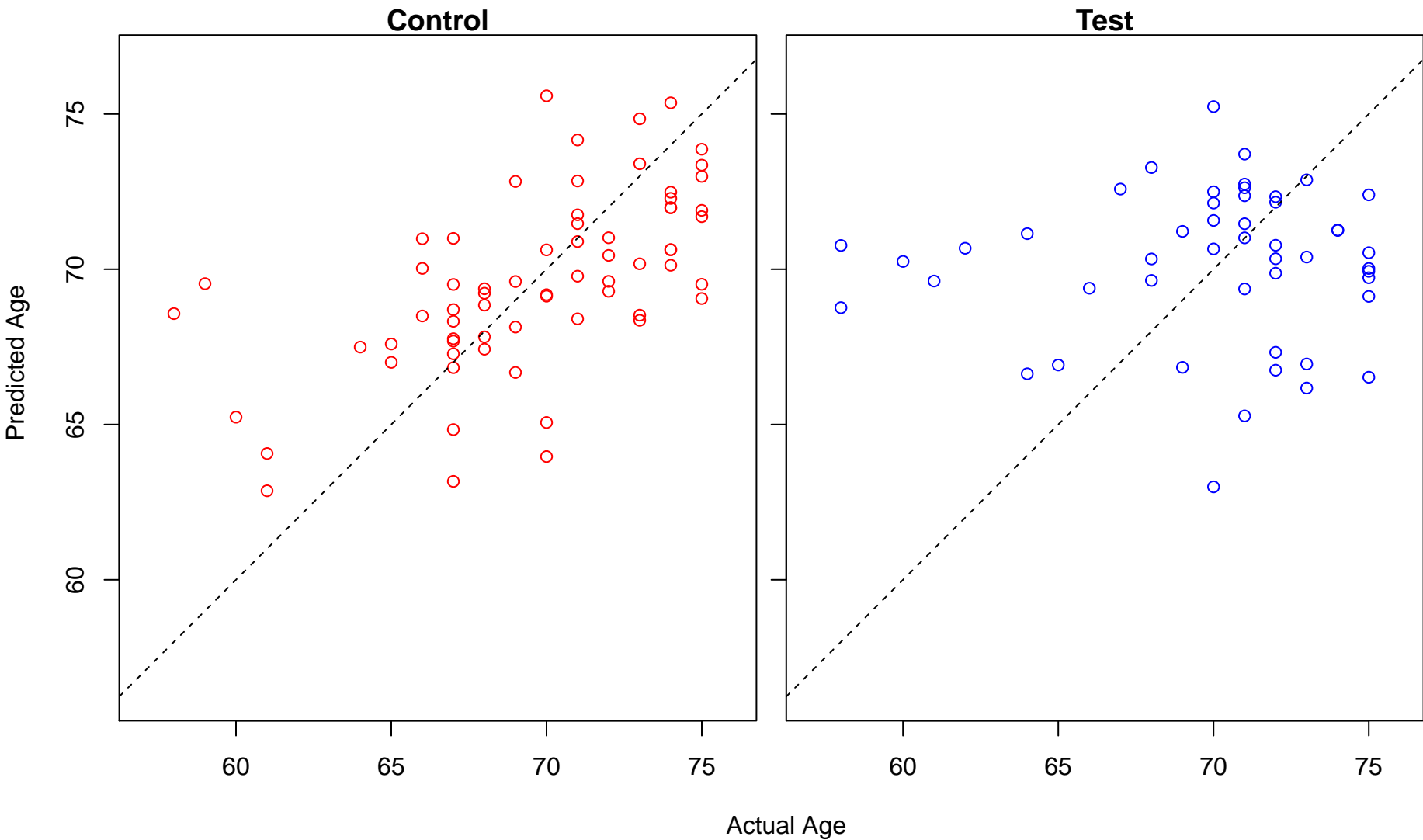
positive regulation of lipid catabolic process (Score: 1.029947)



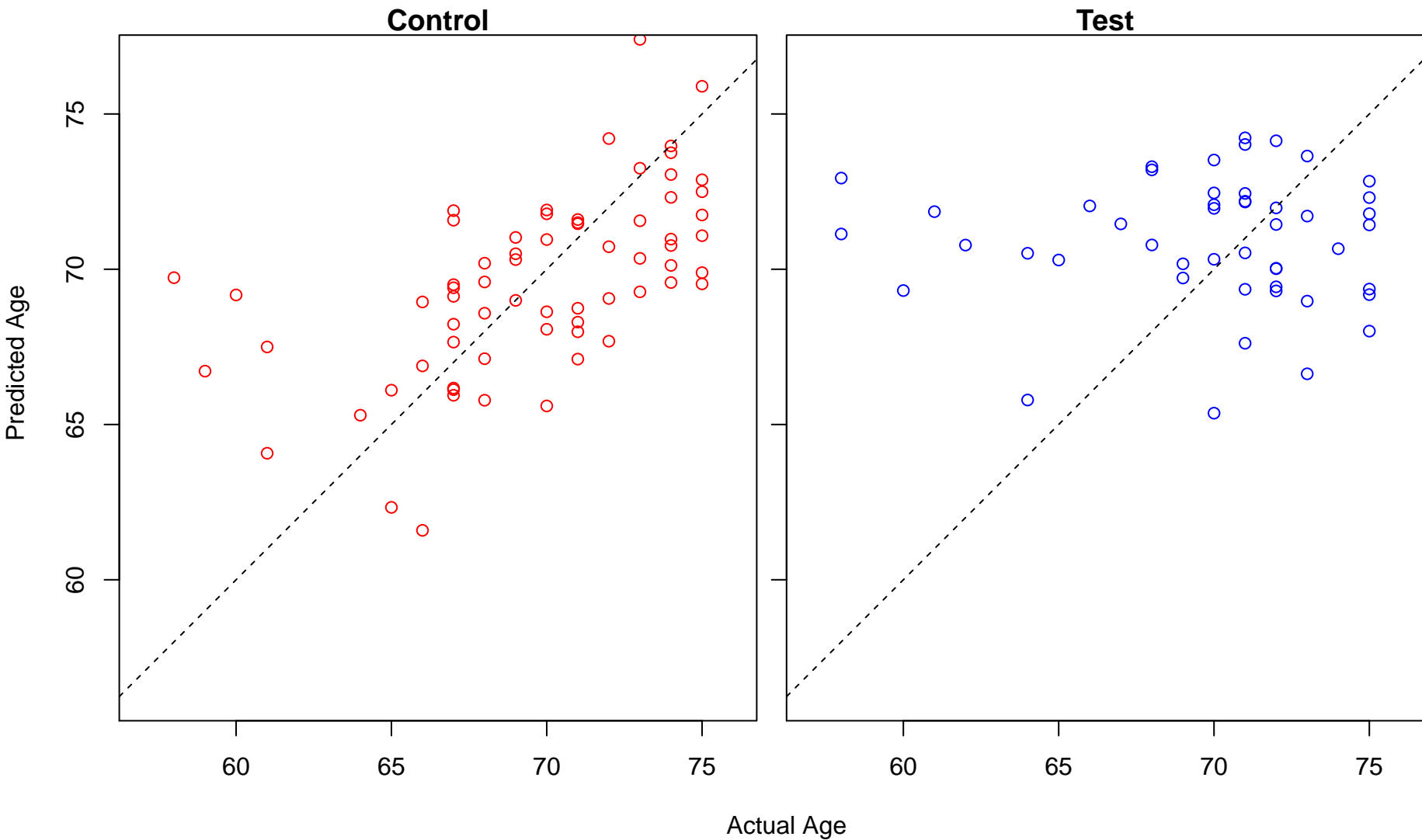
positive regulation of muscle cell differentiation (Score: 1.029924)



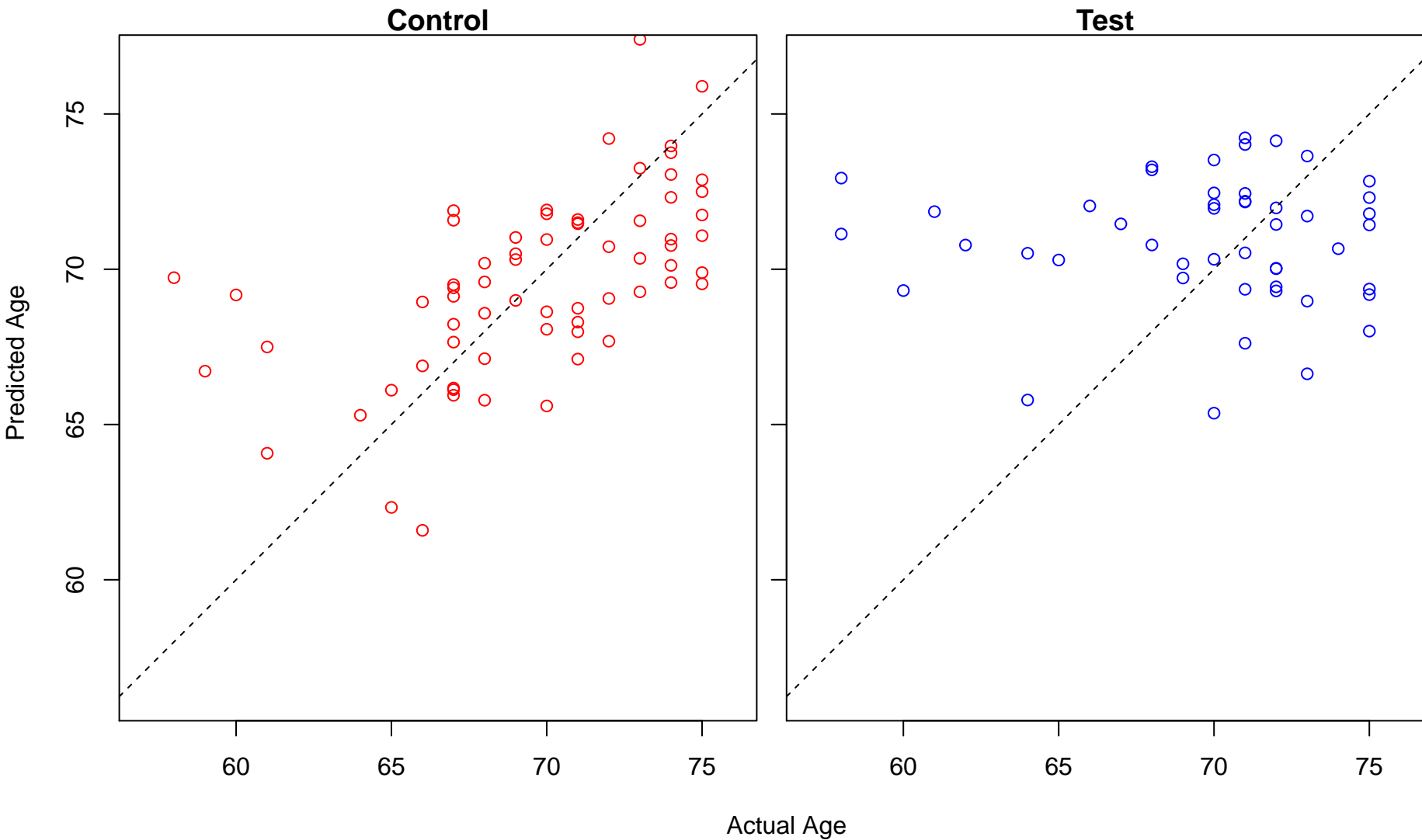
regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress



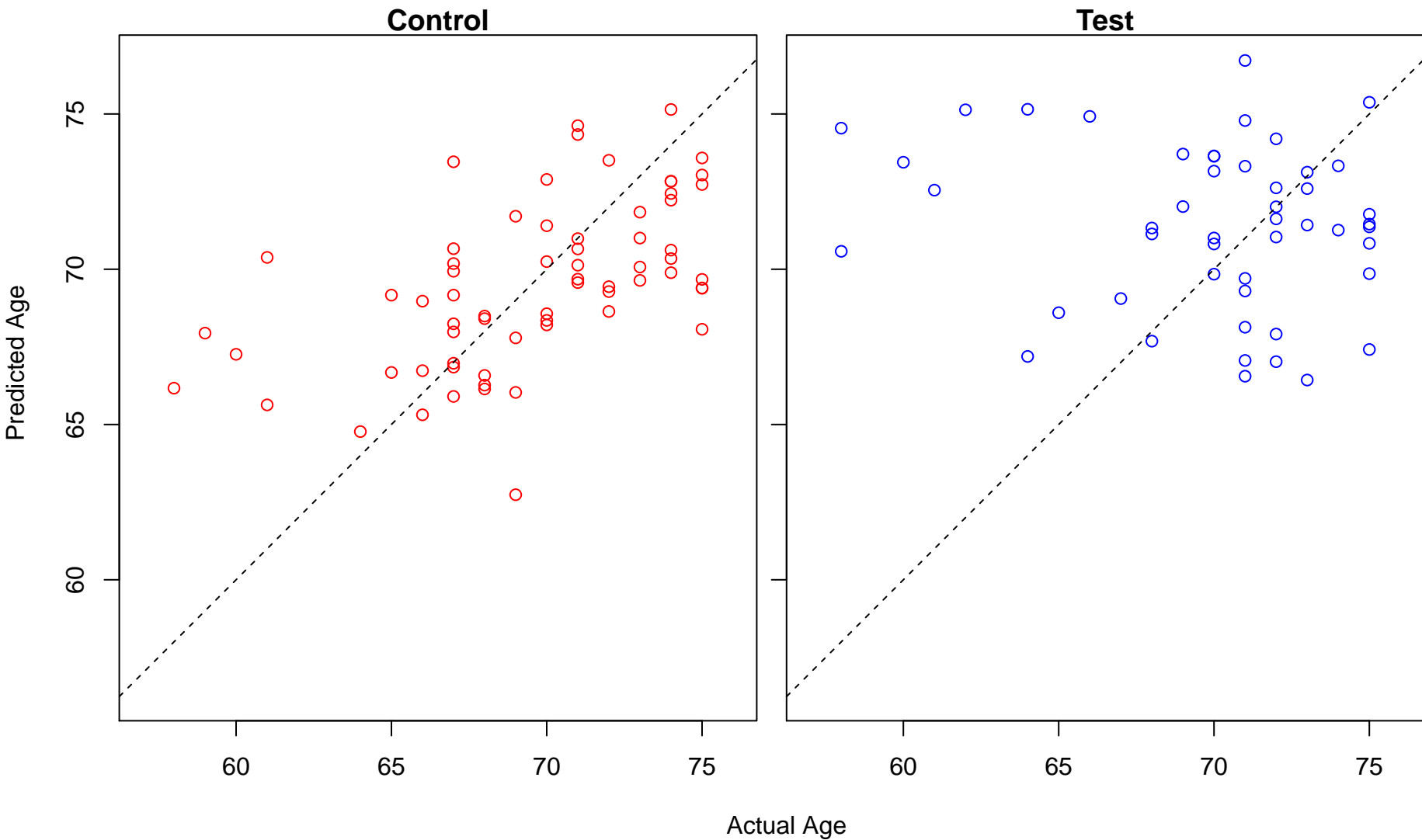
contractile actin filament bundle assembly (Score: 1.029353)



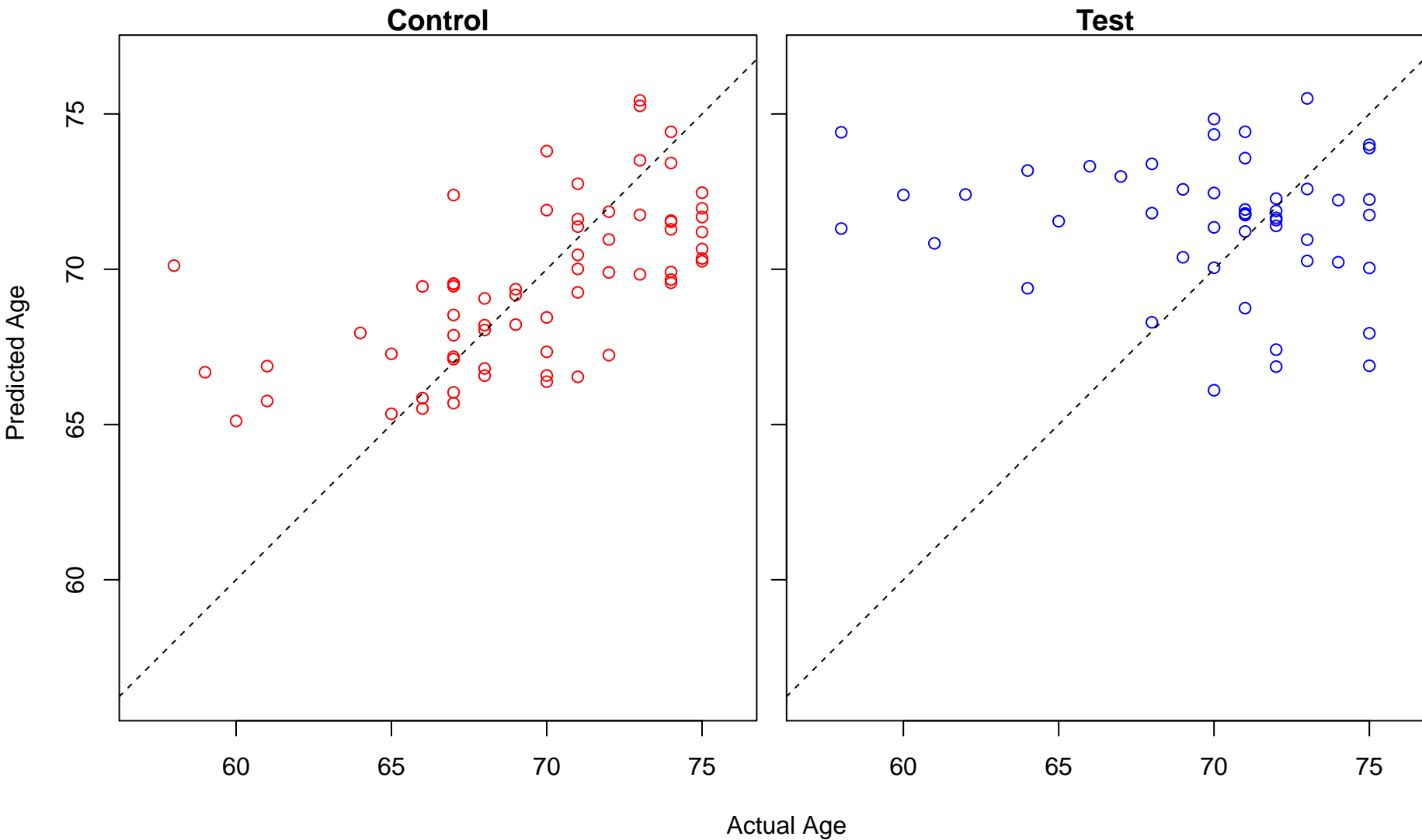
stress fiber assembly (Score: 1.029353)



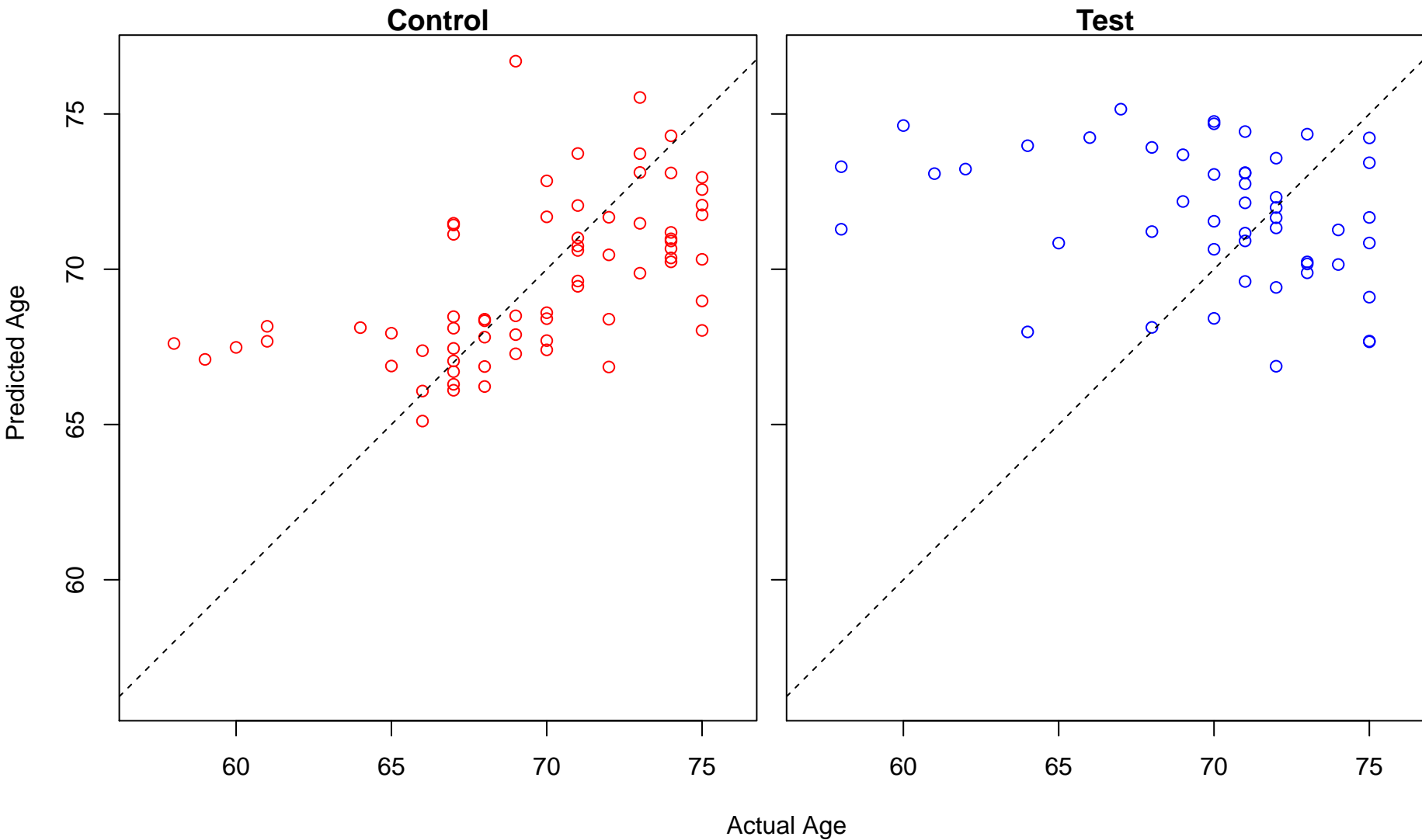
negative regulation of oligodendrocyte differentiation (Score: 1.029237)



positive regulation of leukocyte degranulation (Score: 1.029032)

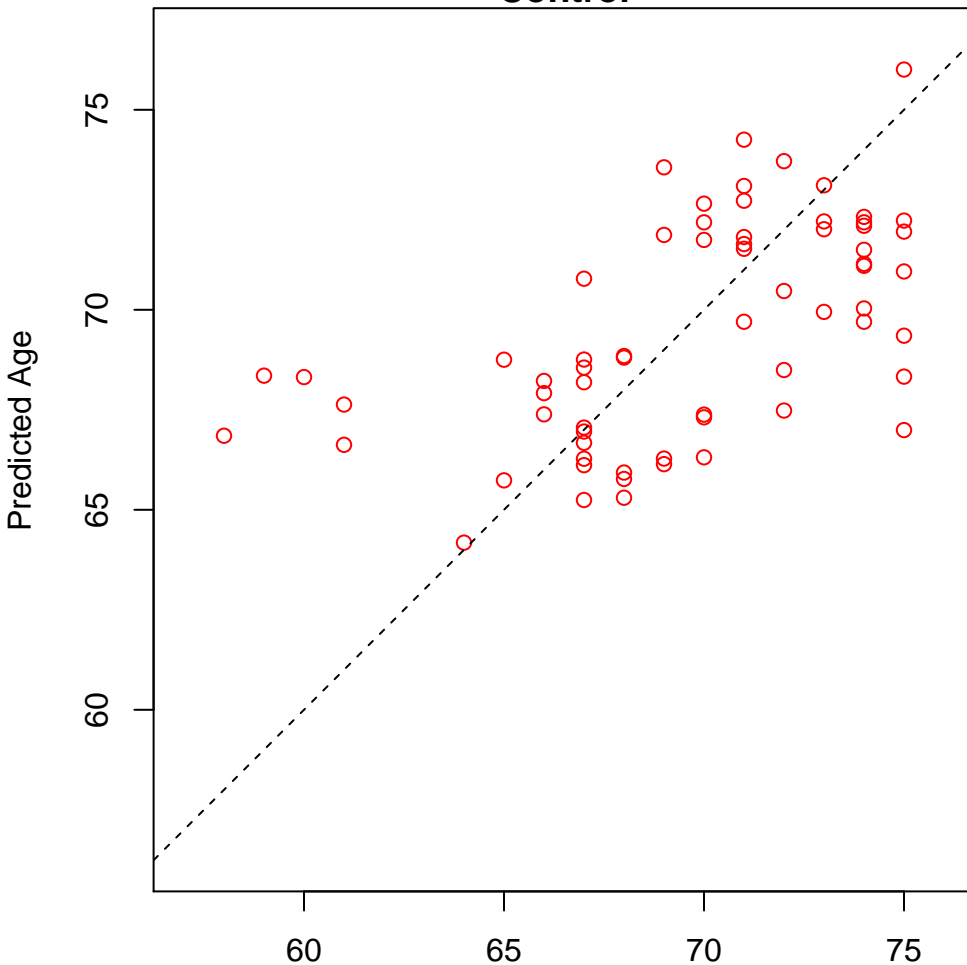


neutrophil homeostasis (Score: 1.028852)

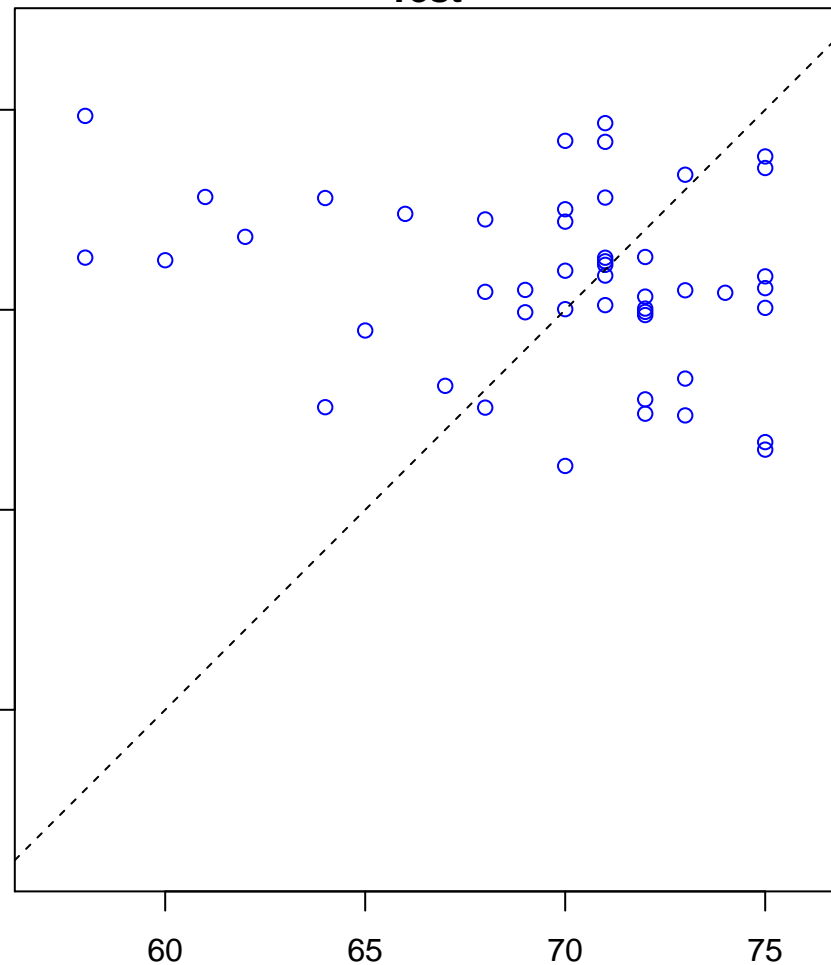


primary alcohol metabolic process (Score: 1.028307)

Control

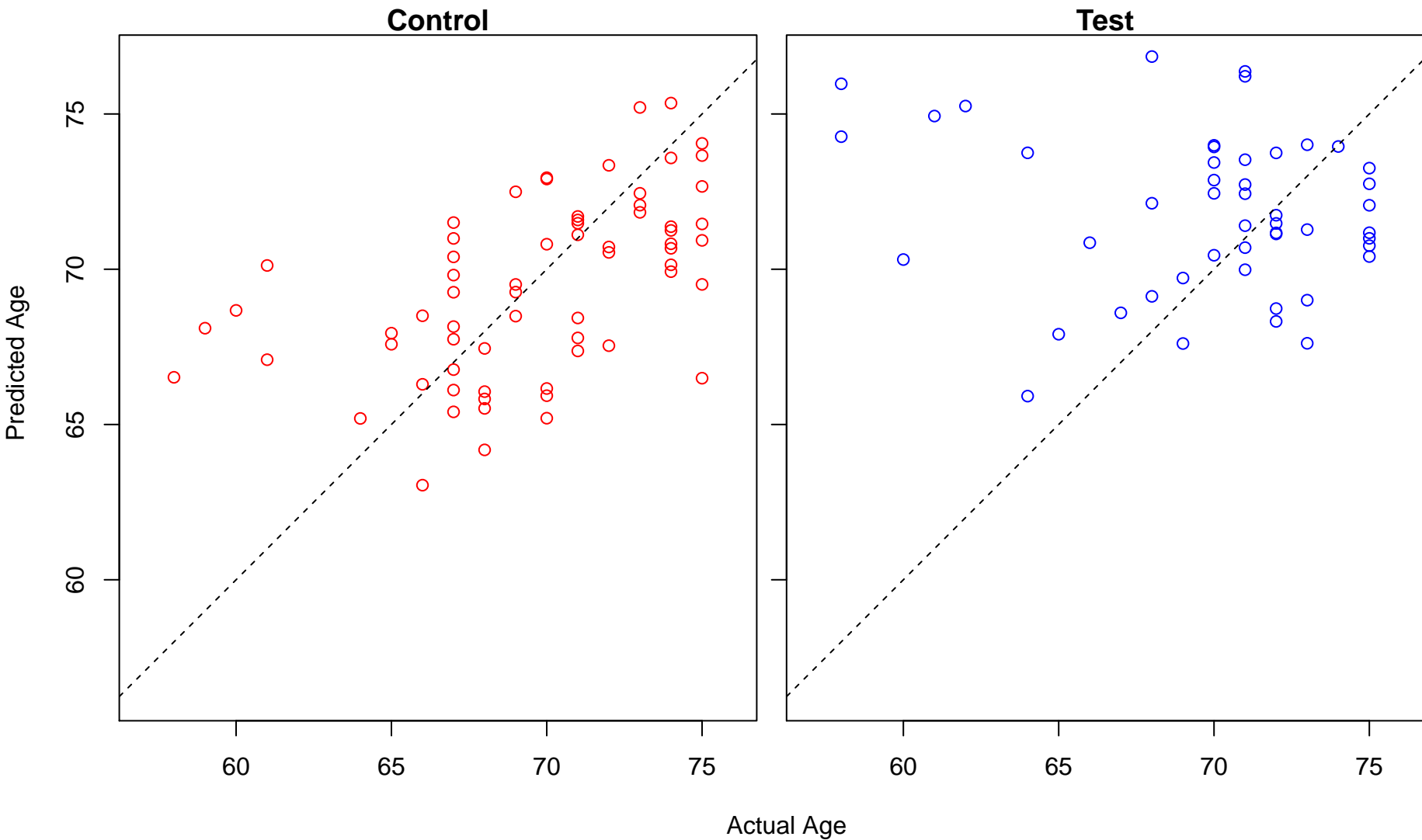


Test

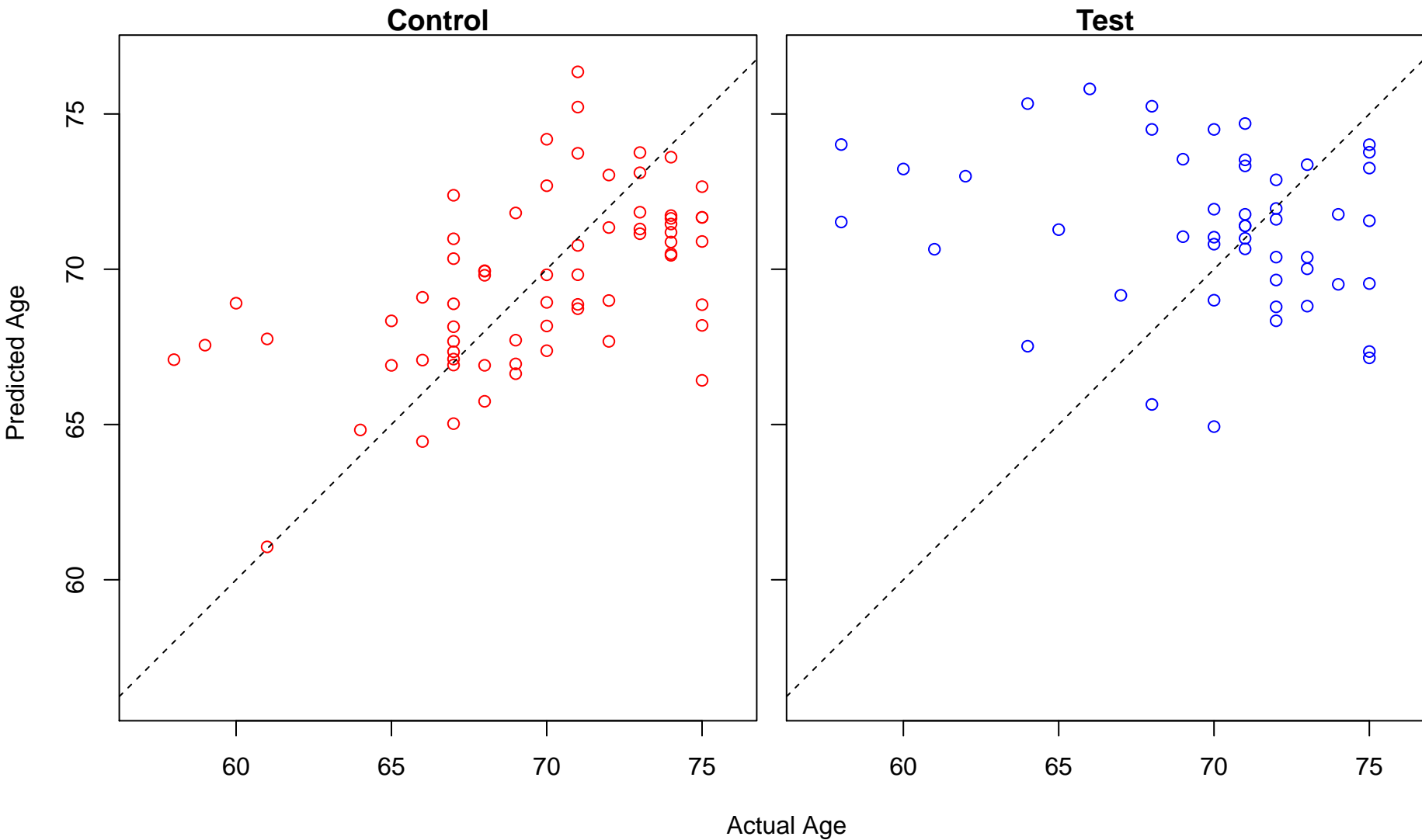


Actual Age

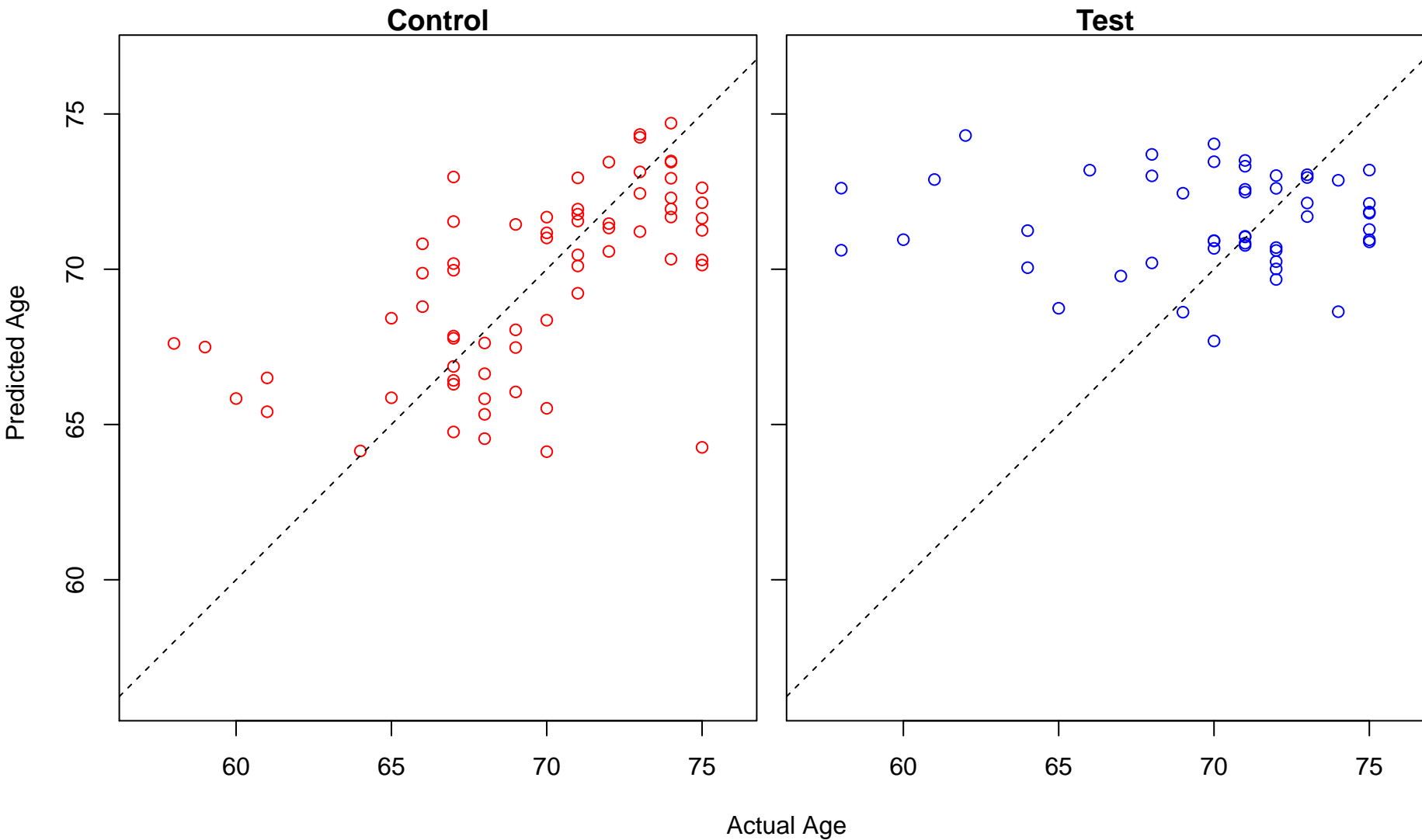
bone development (Score: 1.028095)



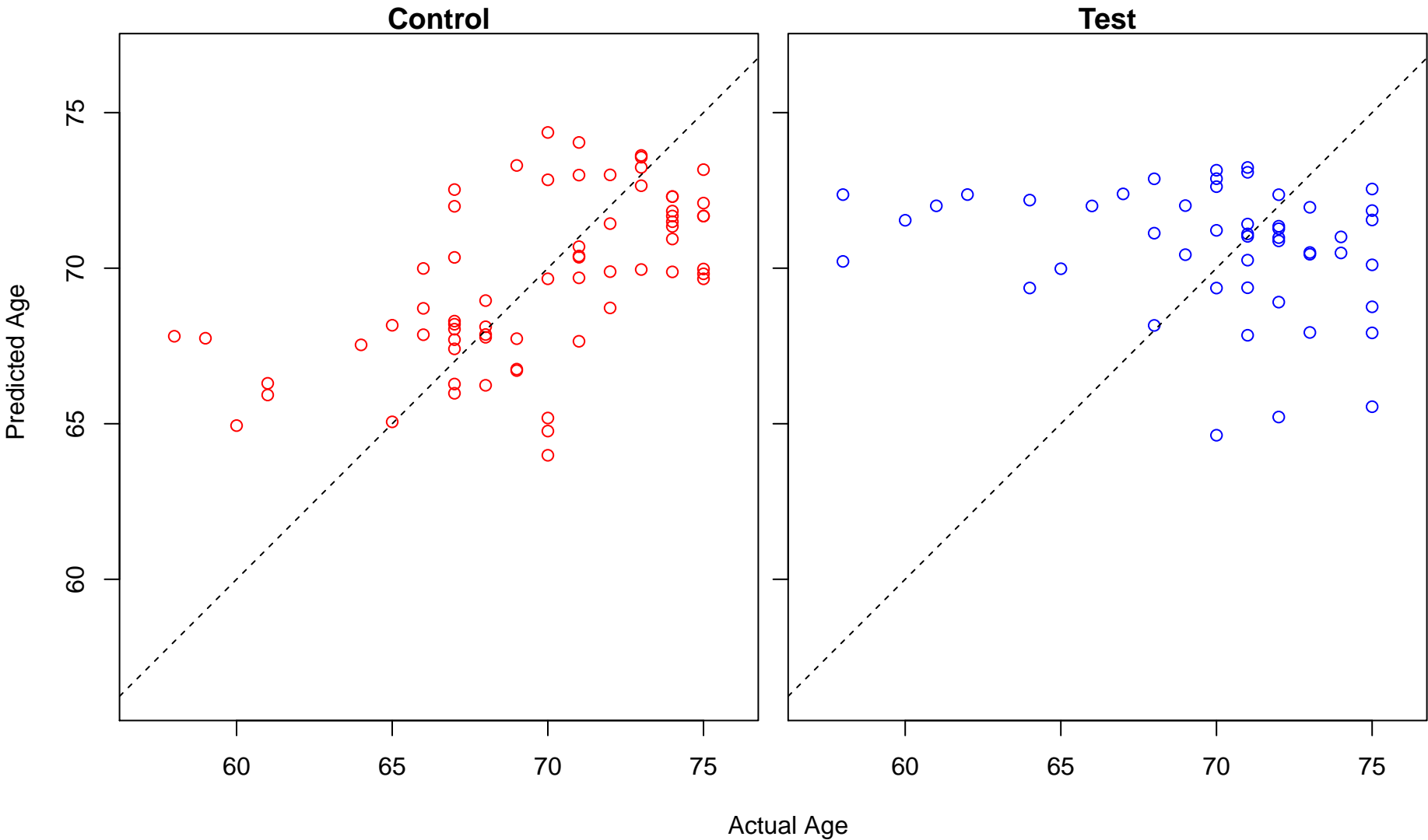
regulation of clathrin-mediated endocytosis (Score: 1.027707)



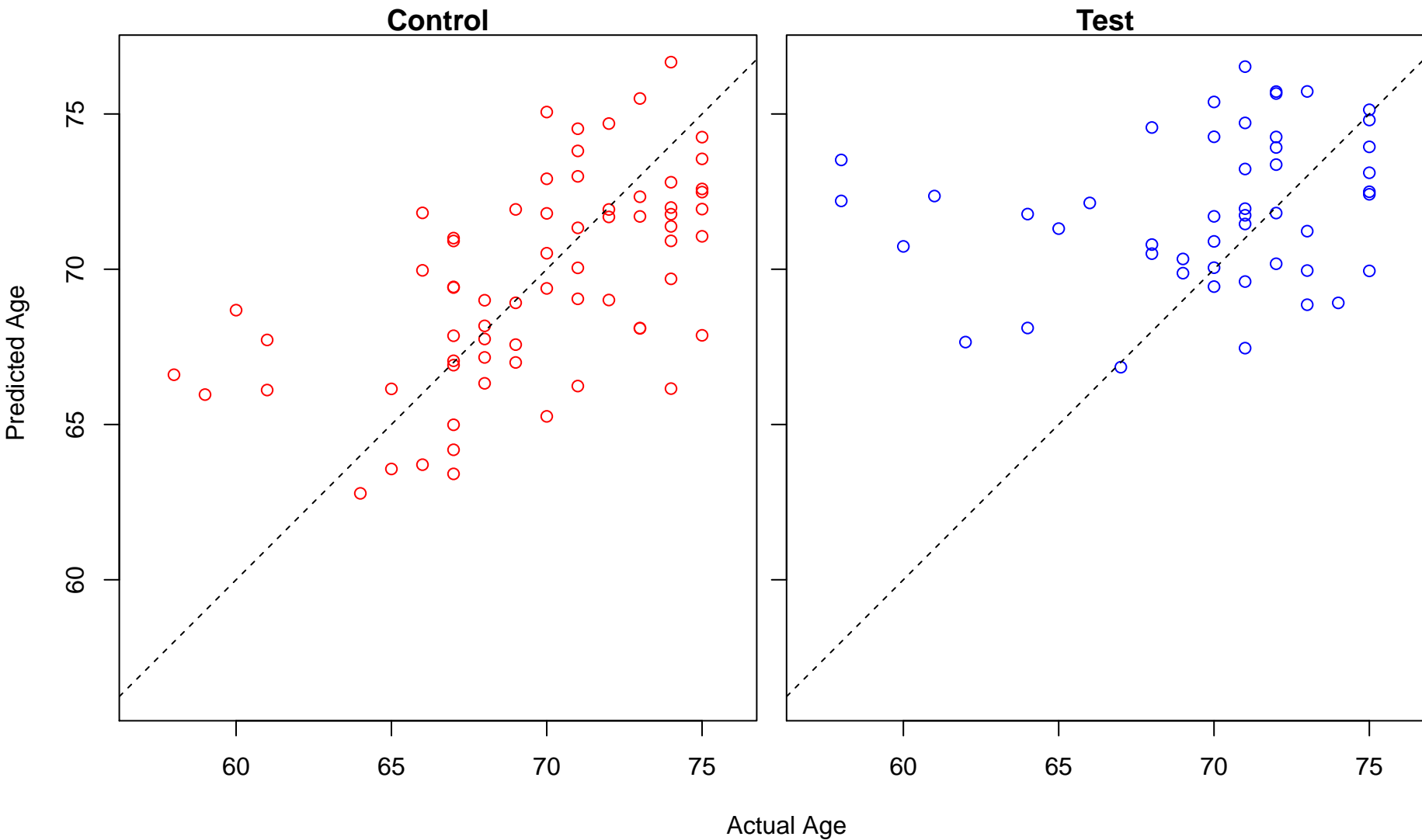
negative regulation of ATPase activity (Score: 1.027577)



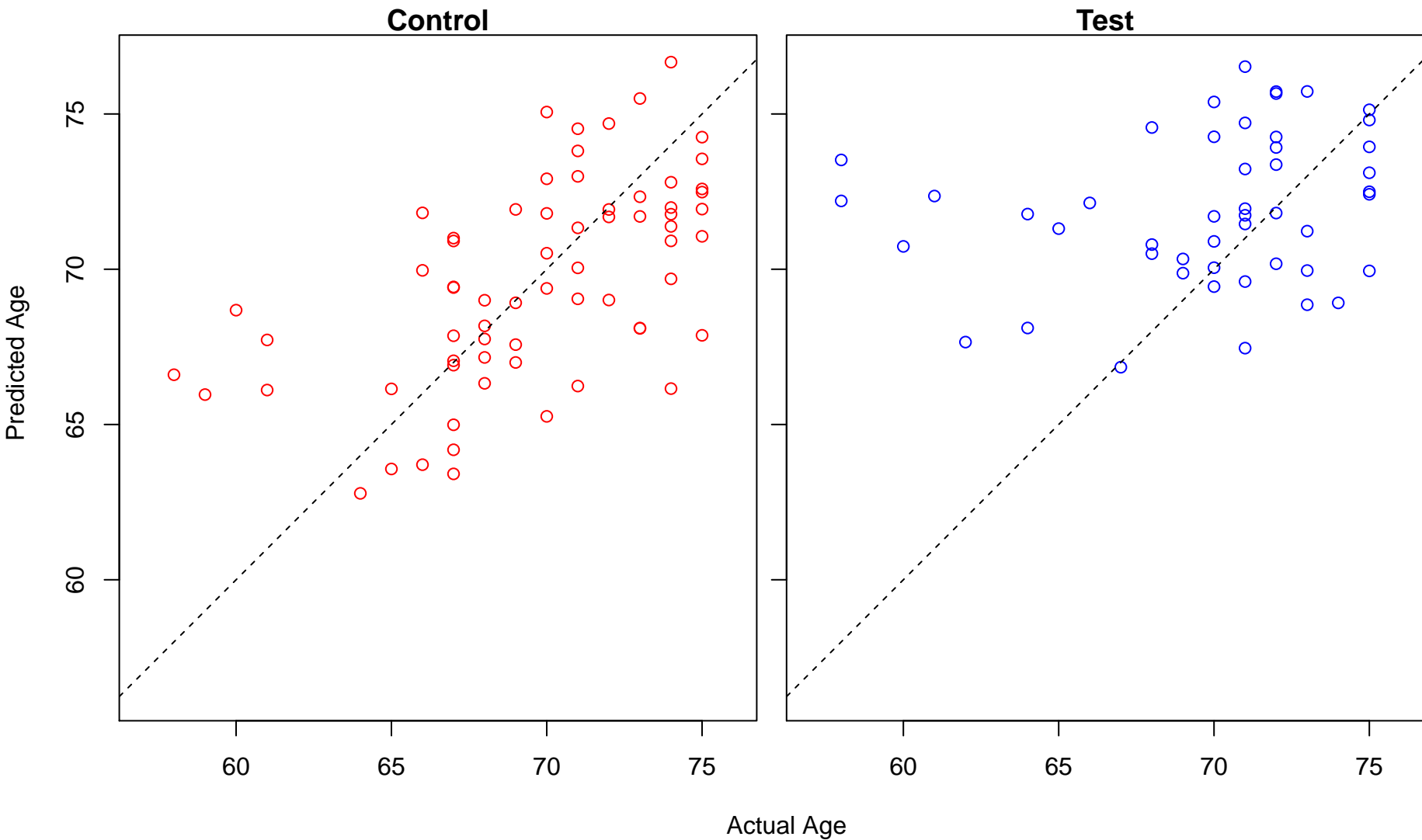
positive regulation of tumor necrosis factor superfamily cytokine production (Score: 1.026942)



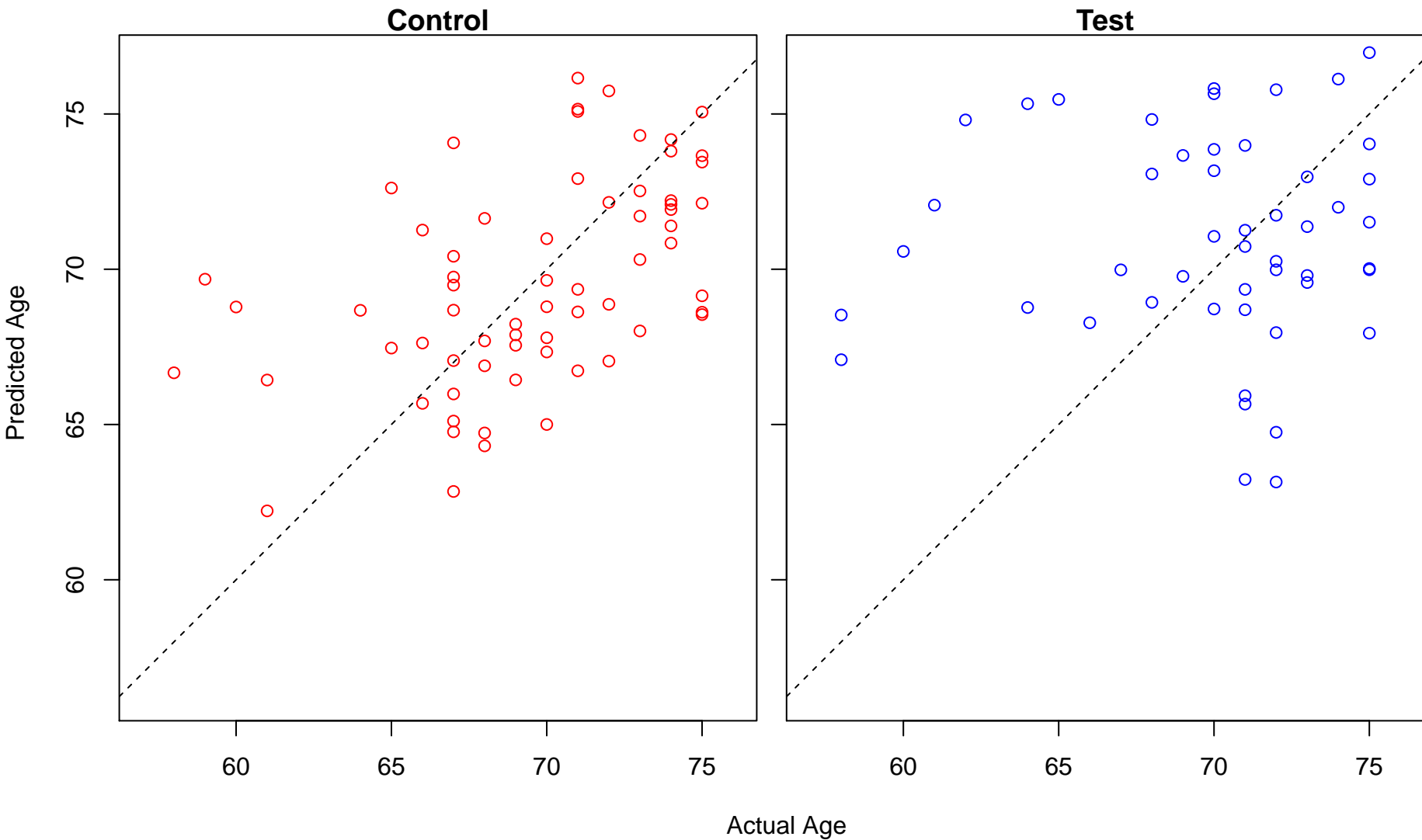
icosanoid biosynthetic process (Score: 1.026872)



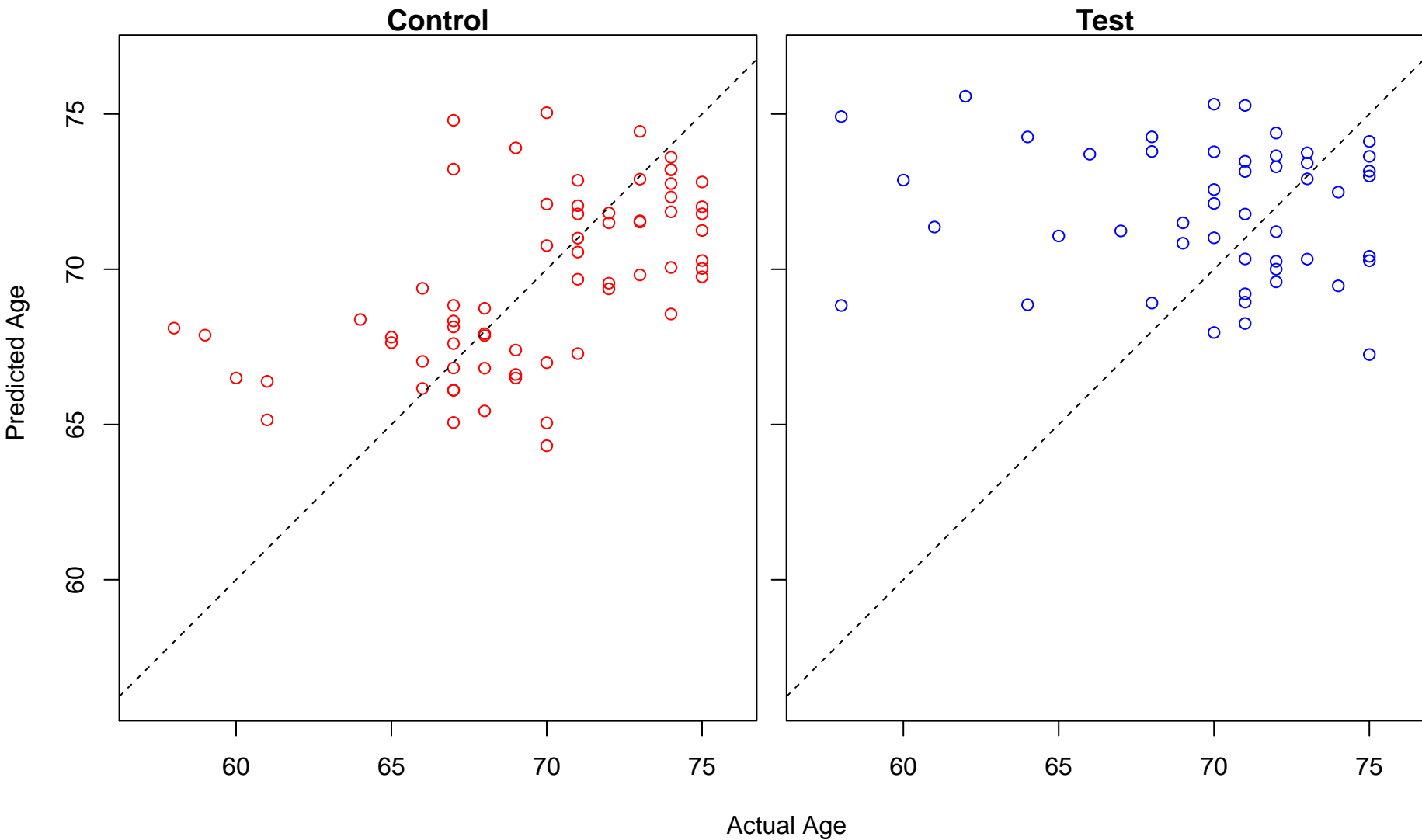
fatty acid derivative biosynthetic process (Score: 1.026872)



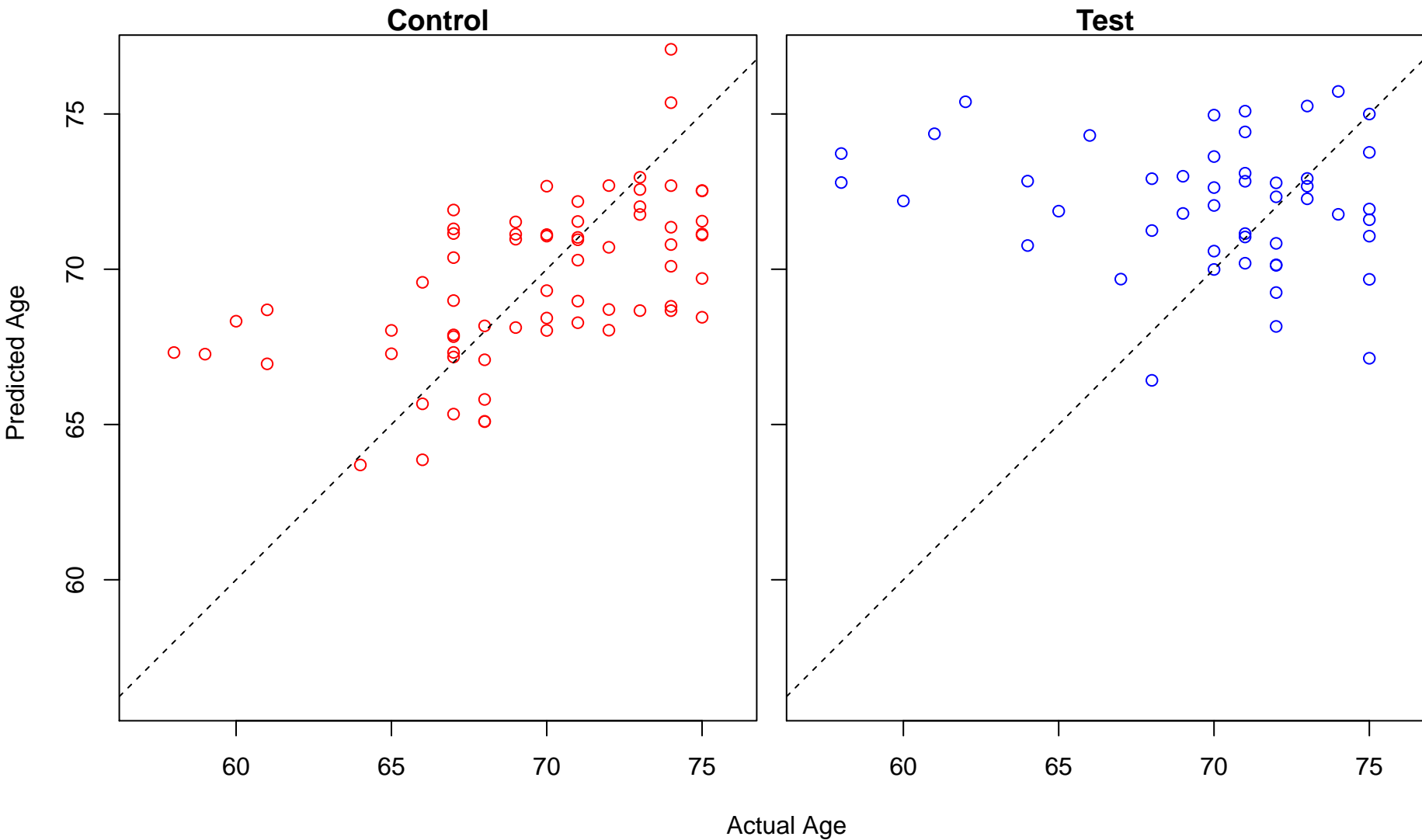
regulation of lamellipodium morphogenesis (Score: 1.026508)



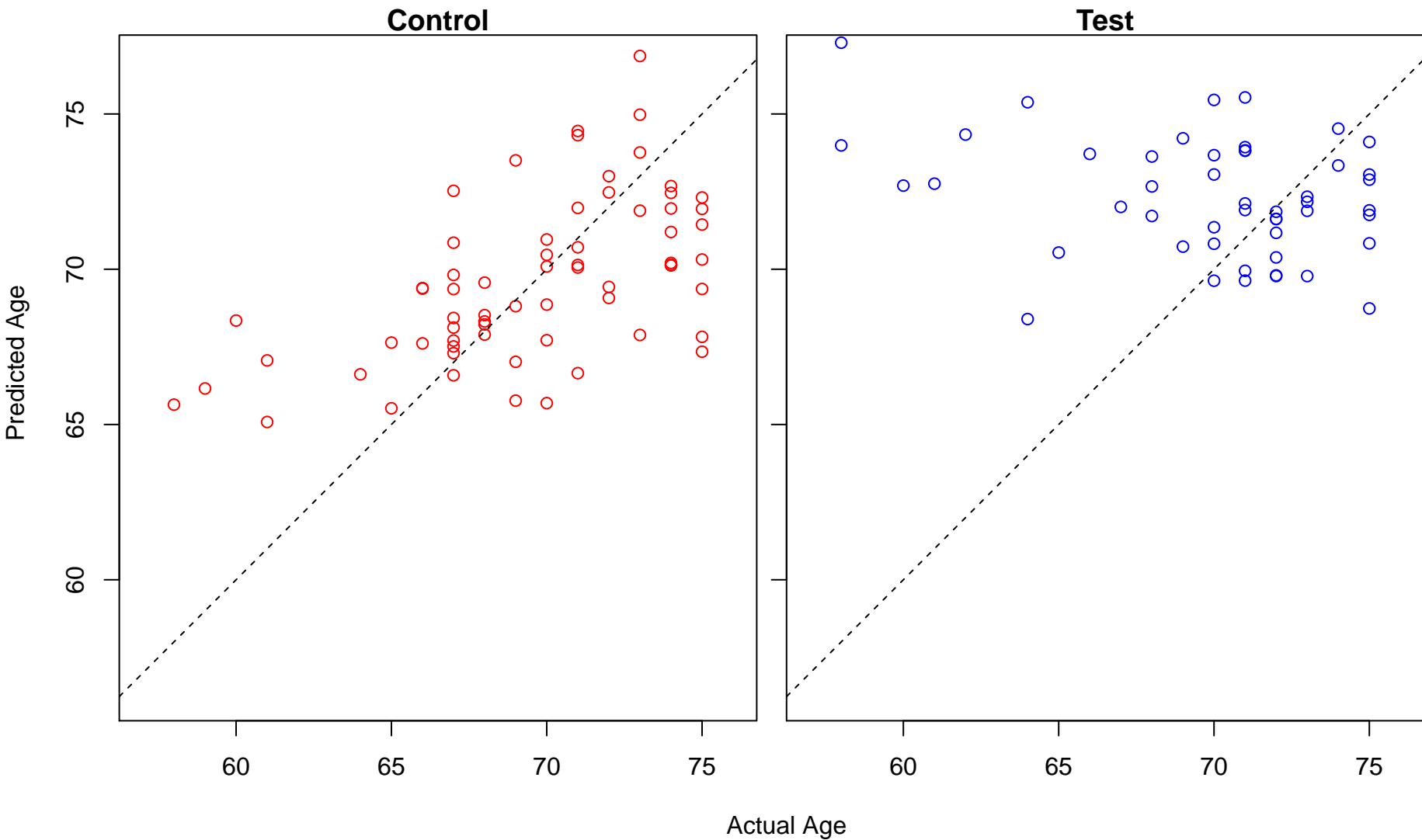
relaxation of muscle (Score: 1.025935)



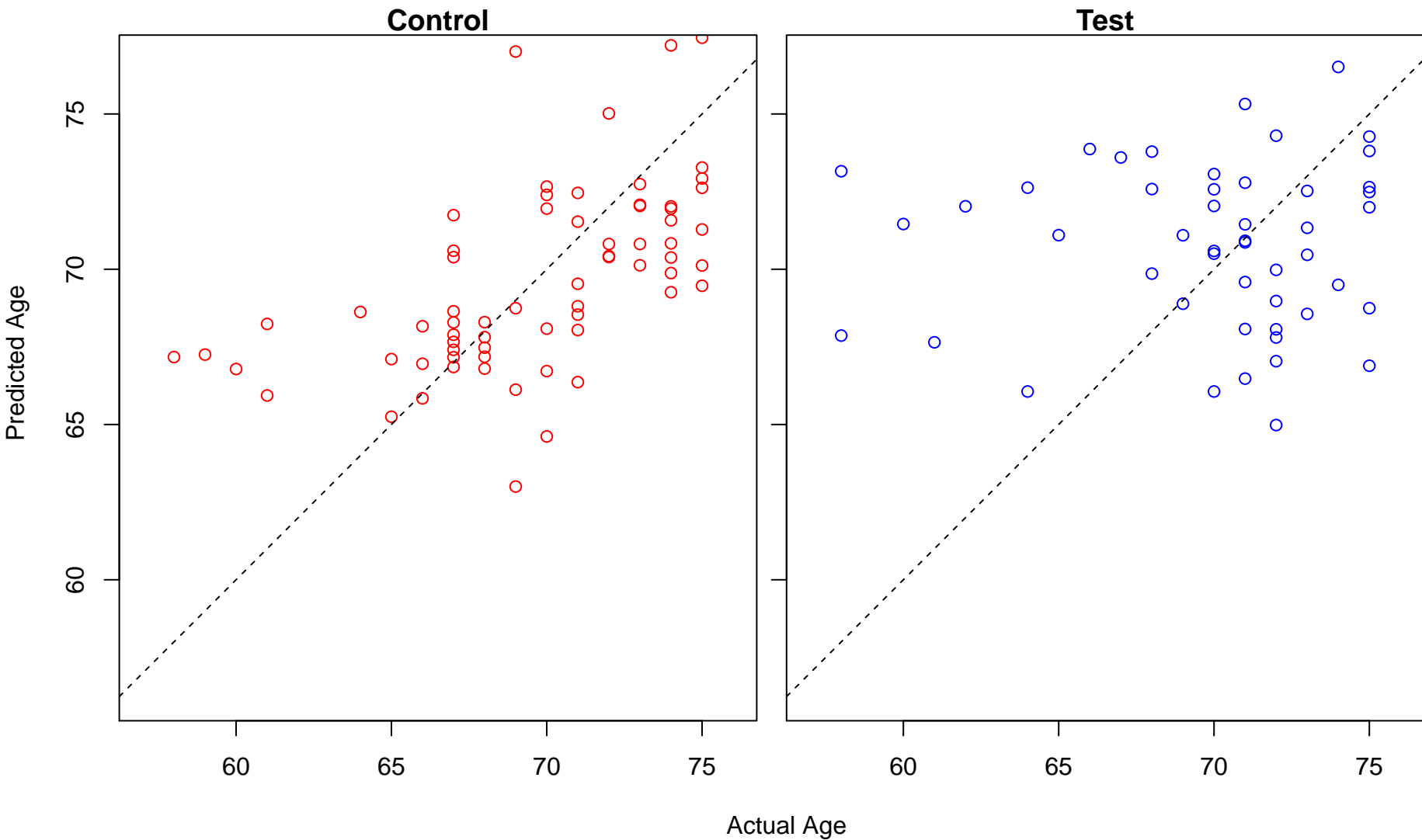
tissue regeneration (Score: 1.025637)



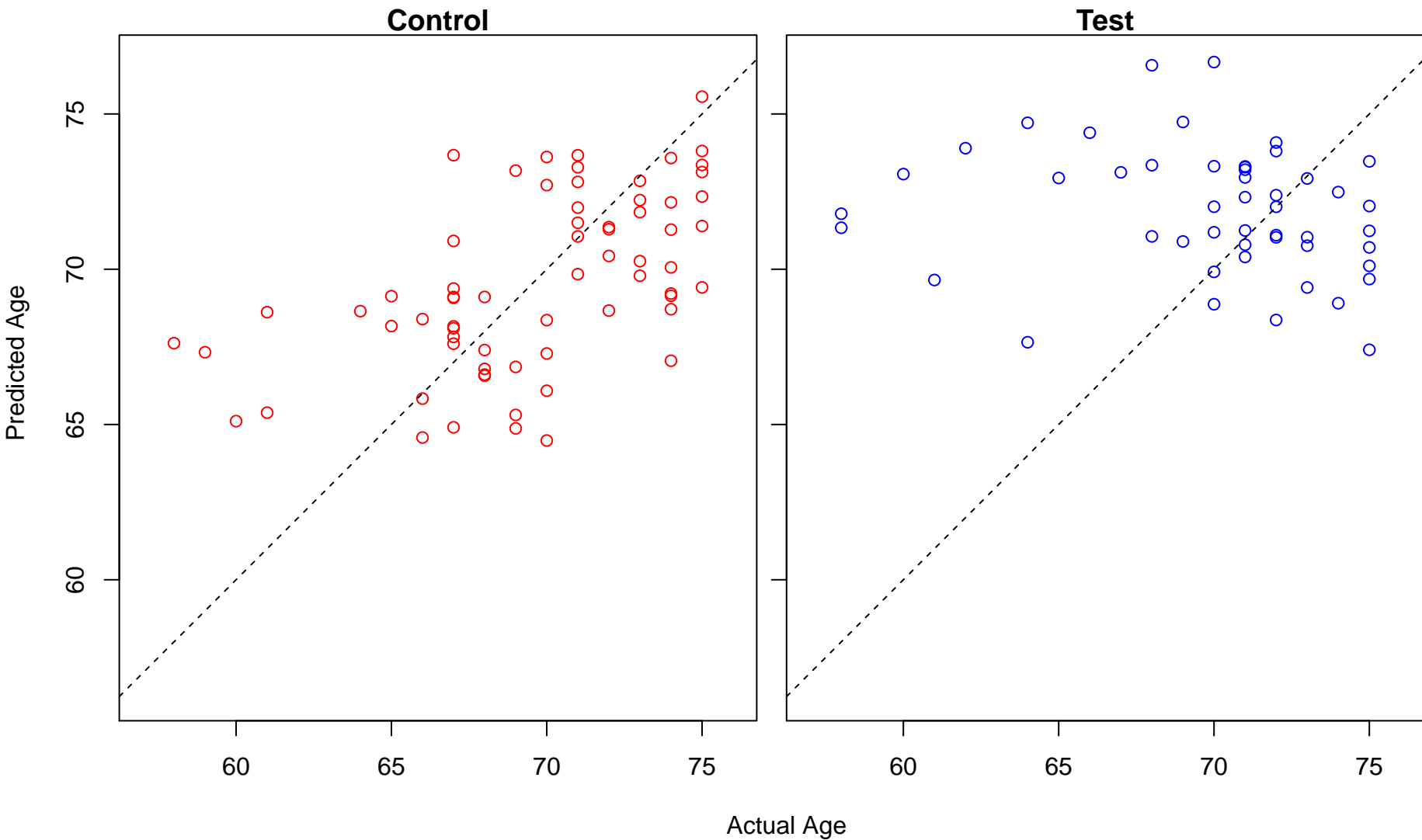
snRNA transcription from RNA polymerase III promoter (Score: 1.025558)



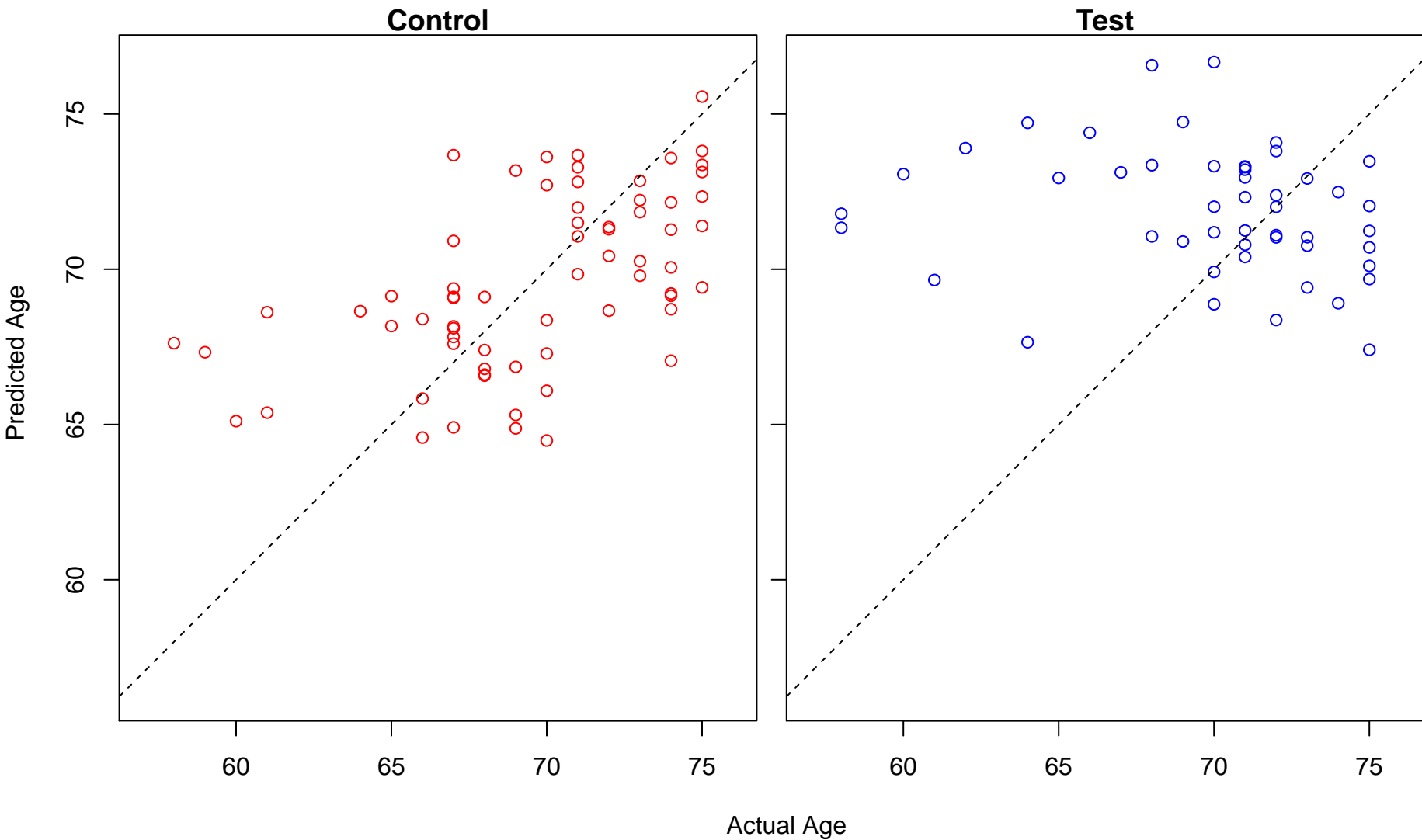
regulation of ER-associated ubiquitin-dependent protein catabolic process (Score: 1.024935)



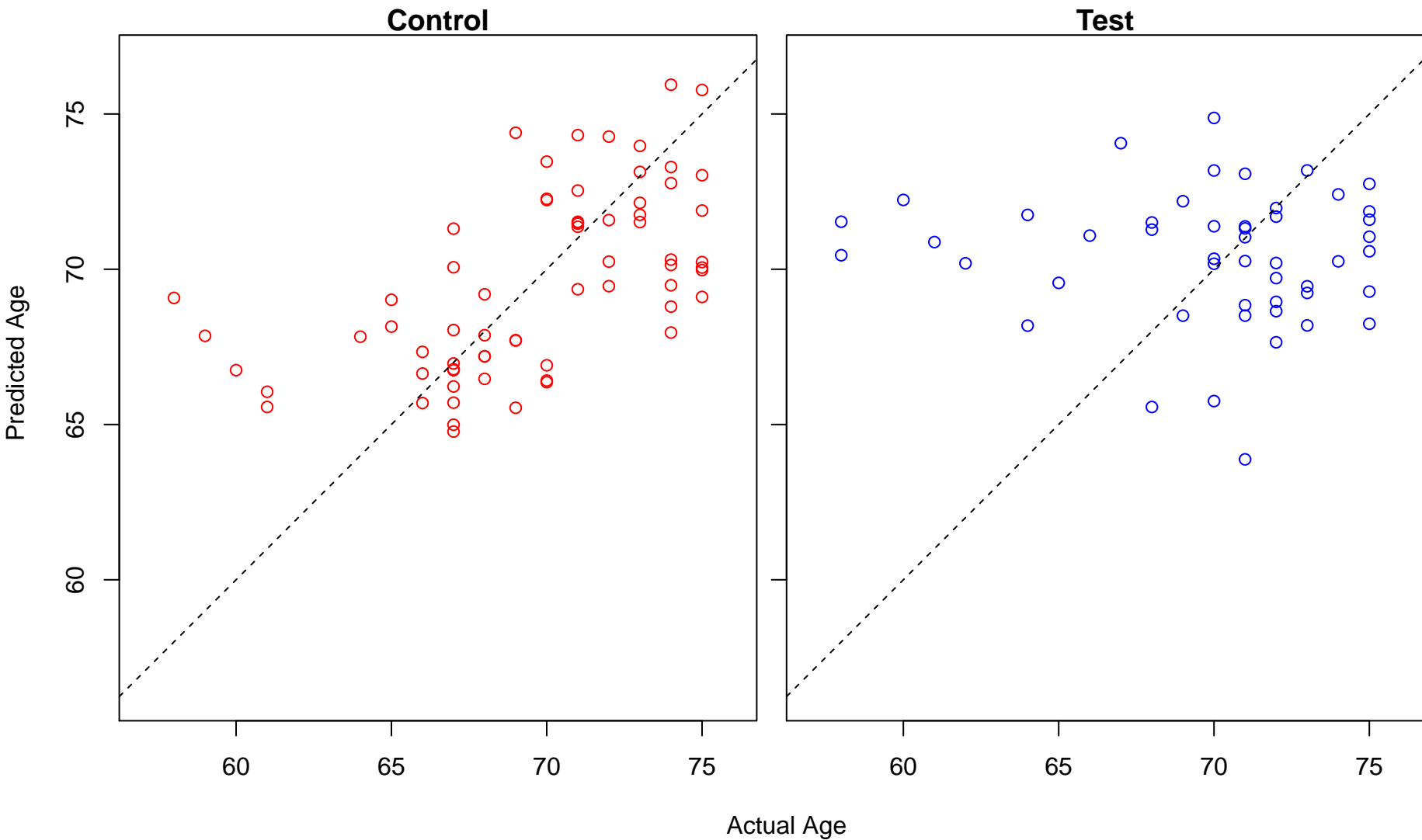
regulation of maintenance of sister chromatid cohesion (Score: 1.024536)



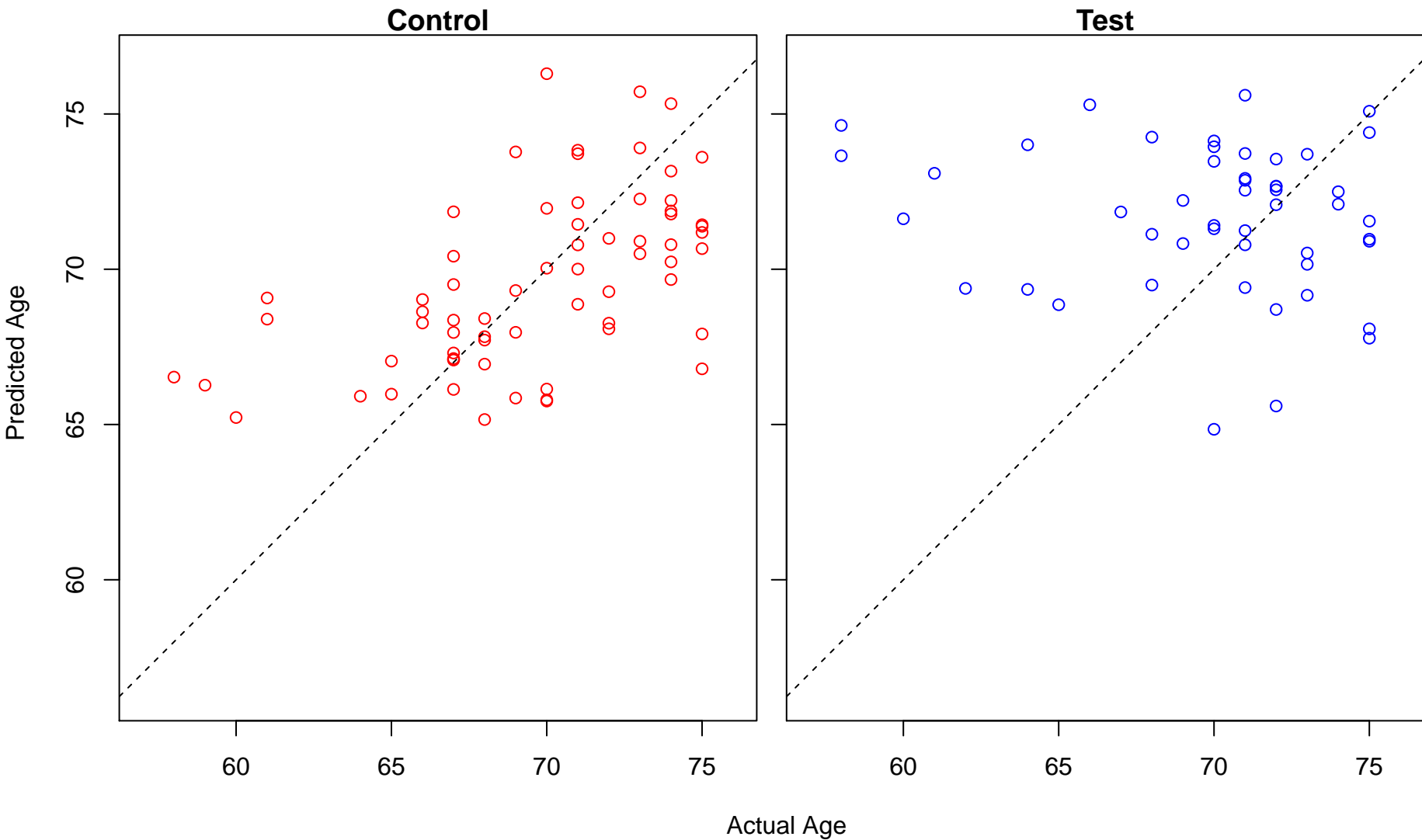
regulation of maintenance of mitotic sister chromatid cohesion (Score: 1.024536)



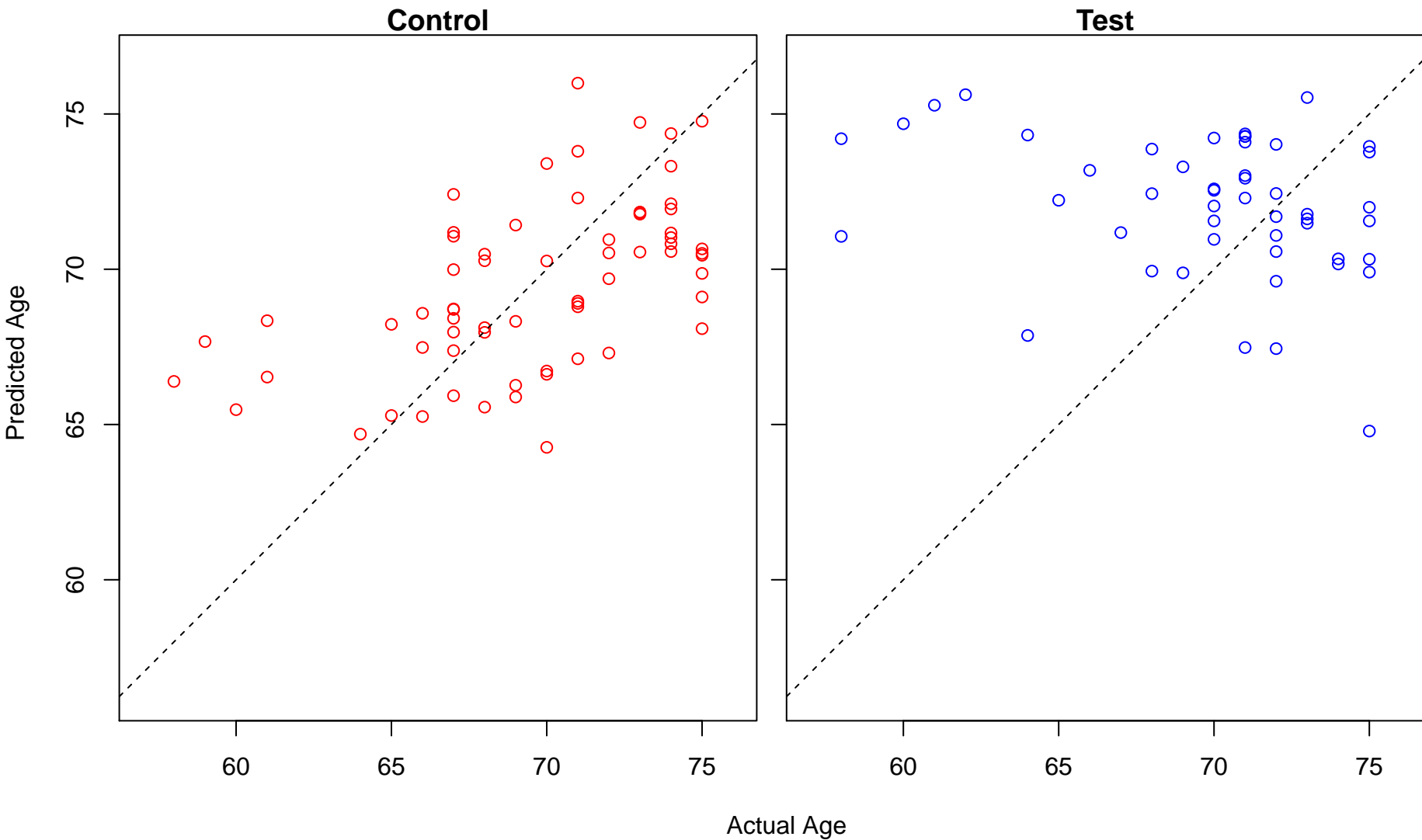
positive regulation of mitotic nuclear division (Score: 1.024023)



kidney development (Score: 1.024022)

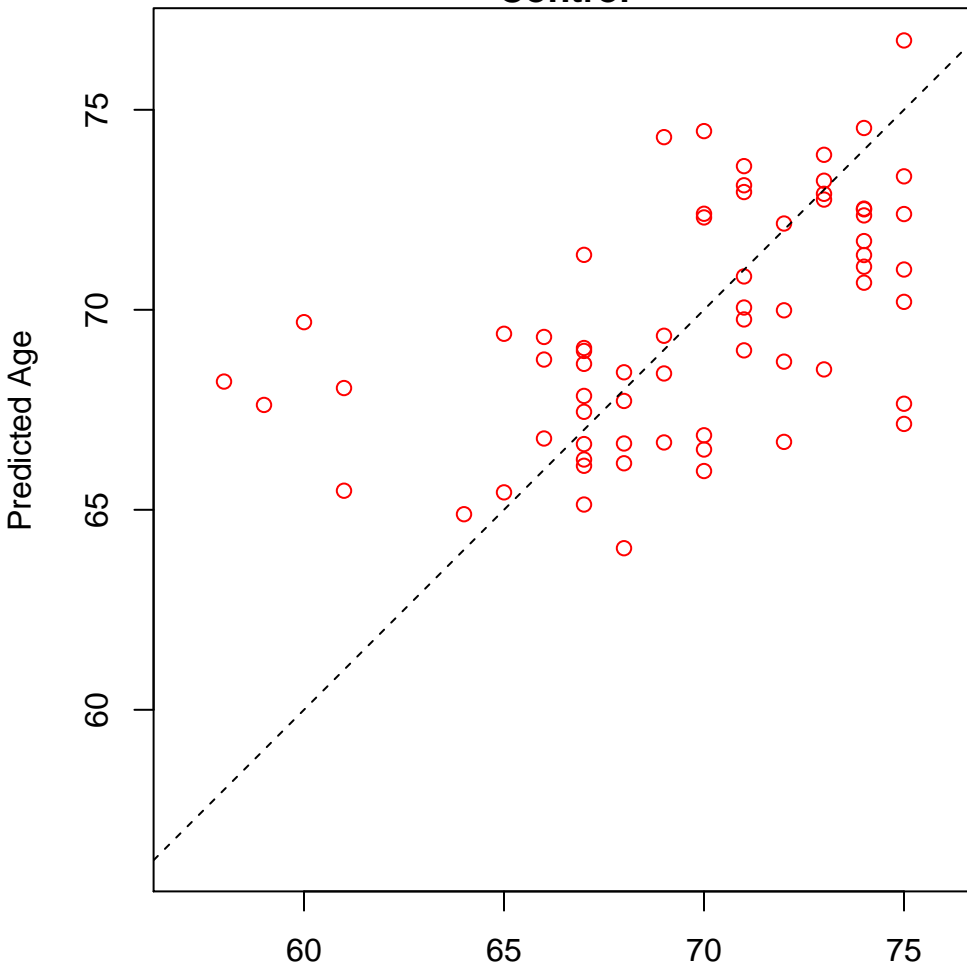


Notch receptor processing (Score: 1.023527)

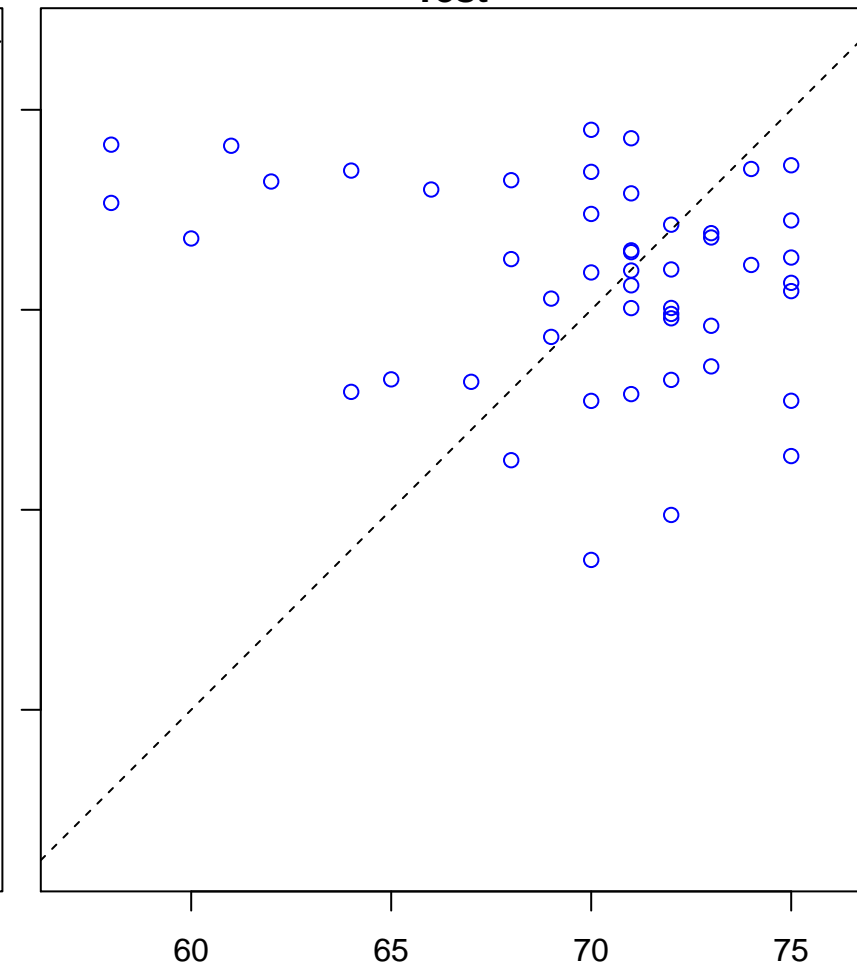


maintenance of protein location in cell (Score: 1.023513)

Control

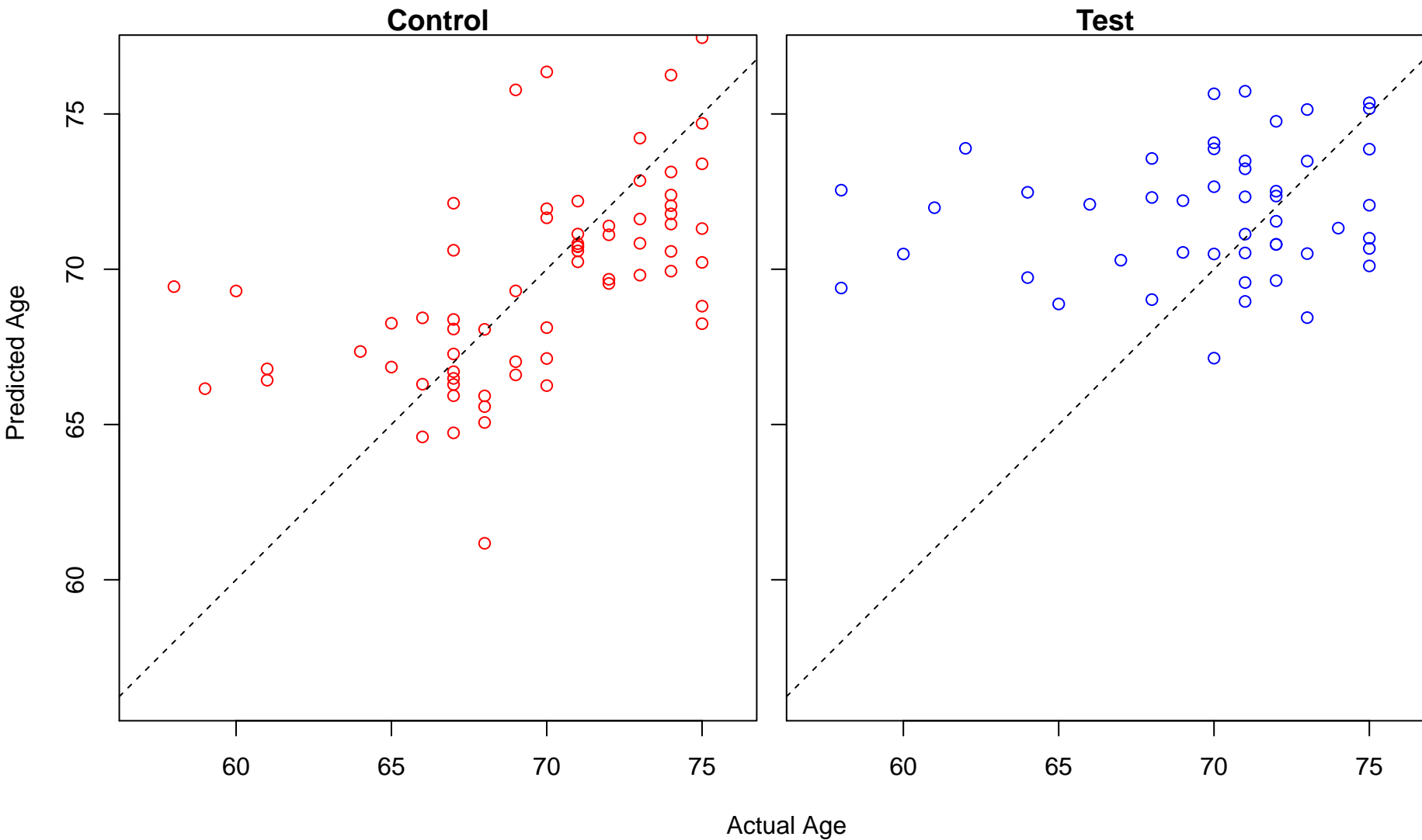


Test

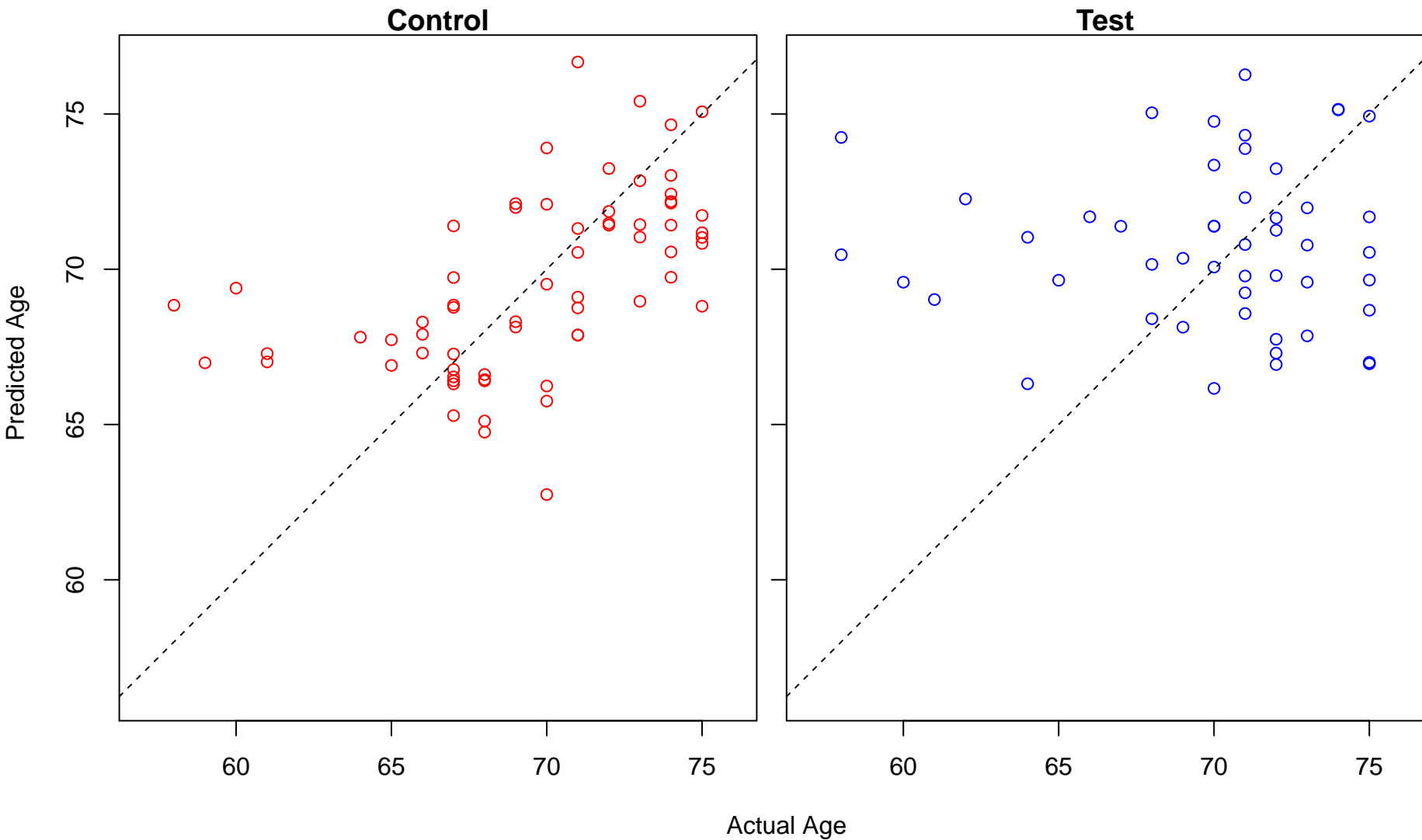


Actual Age

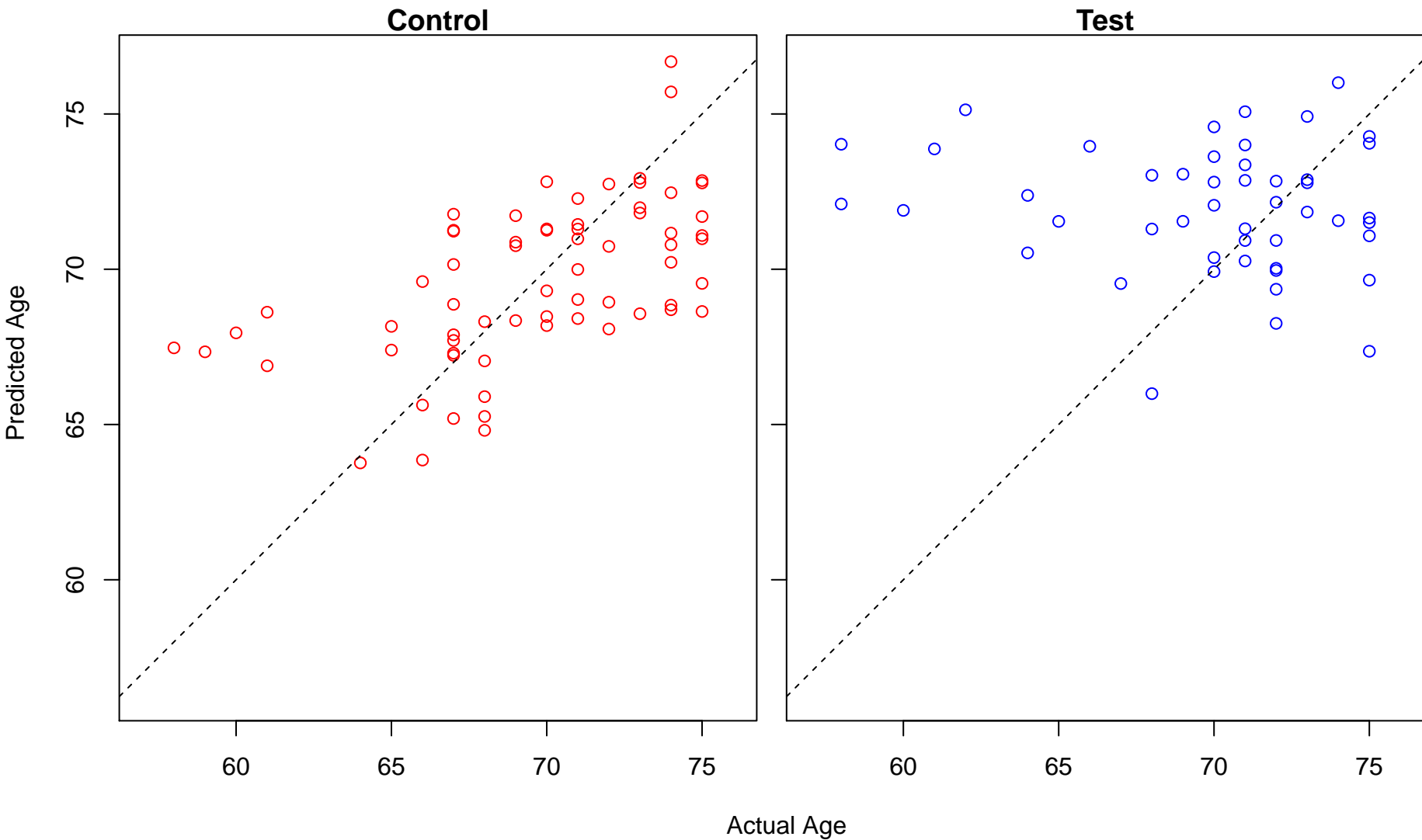
sensory organ development (Score: 1.022285)



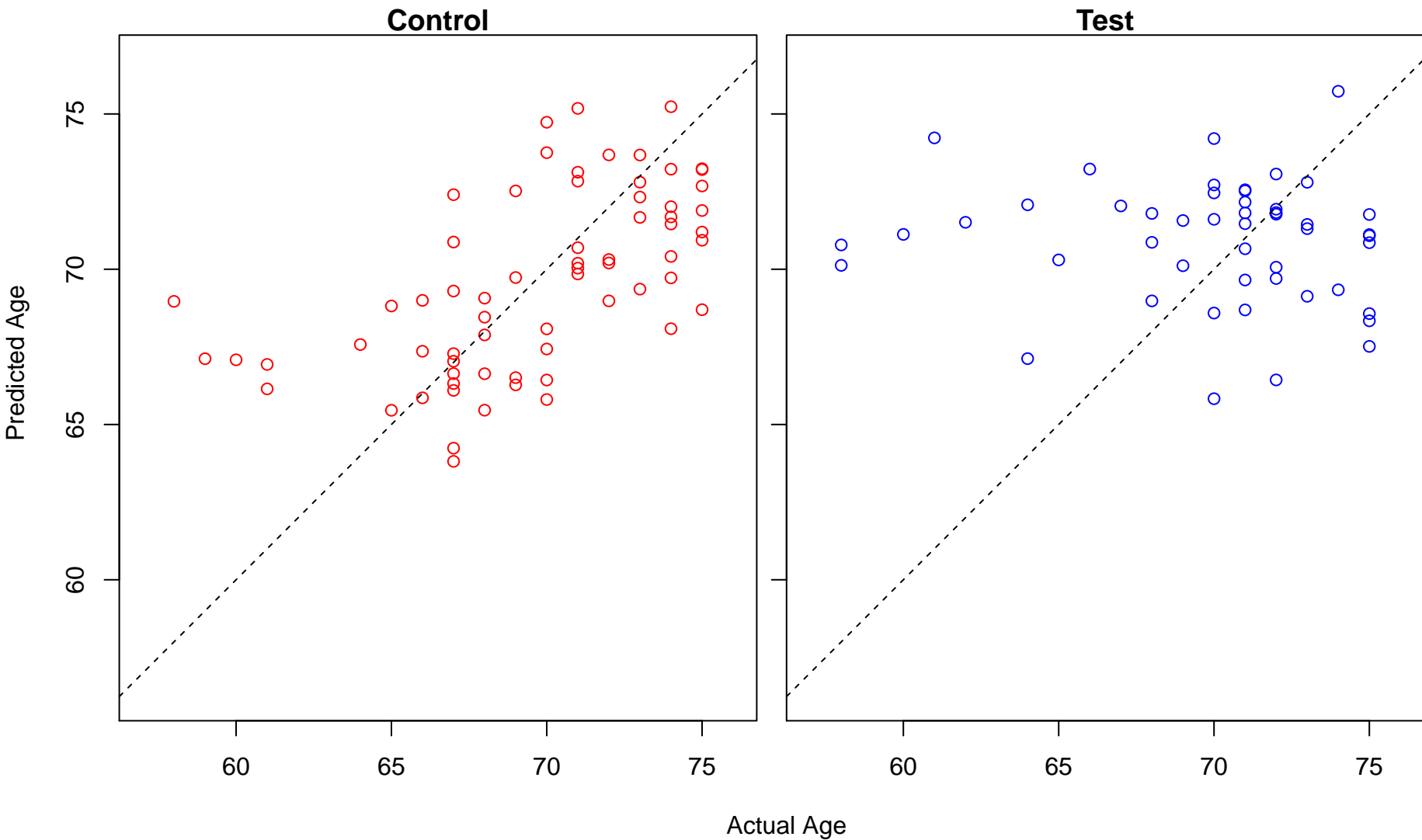
synaptic vesicle recycling (Score: 1.021608)



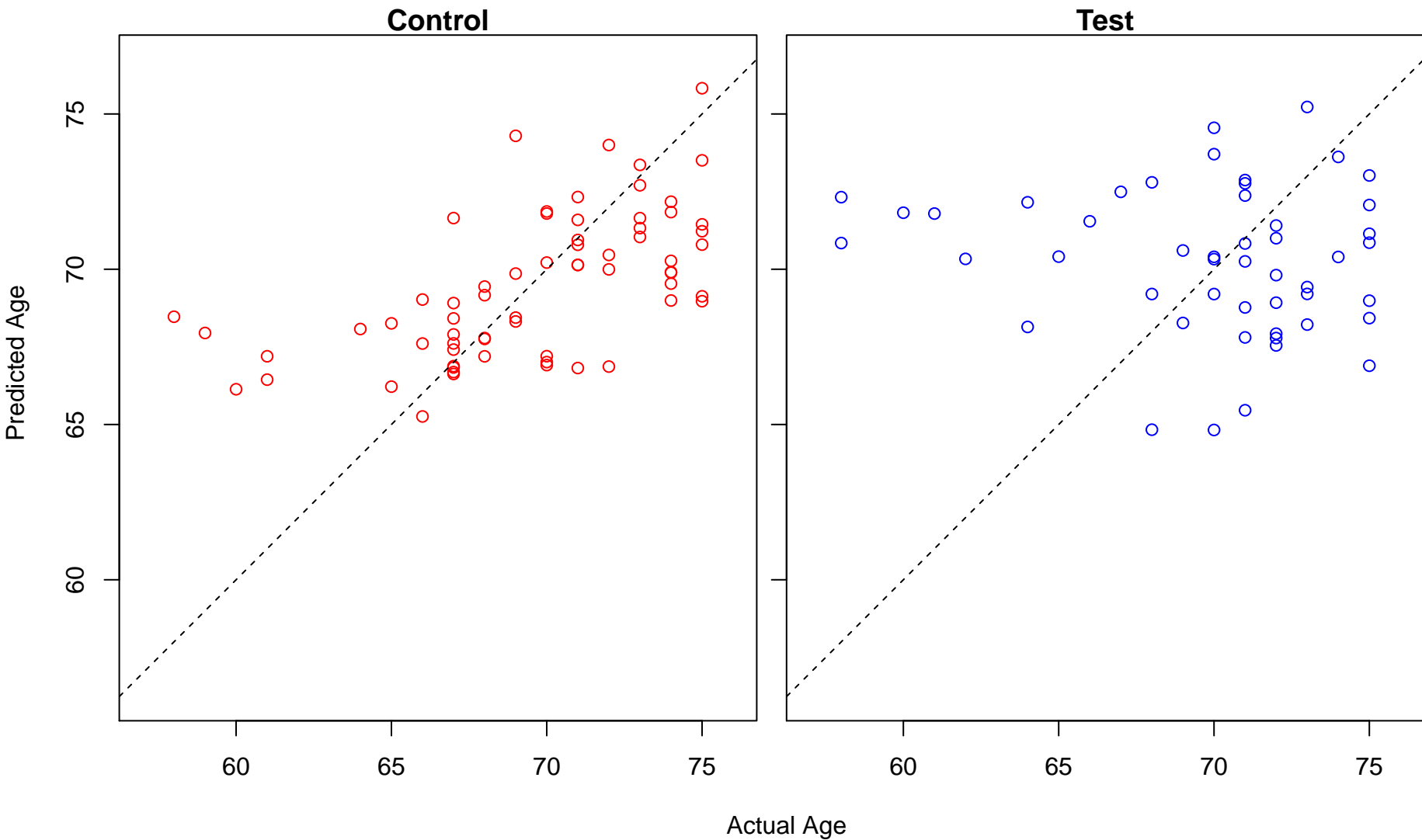
skeletal muscle tissue regeneration (Score: 1.021584)



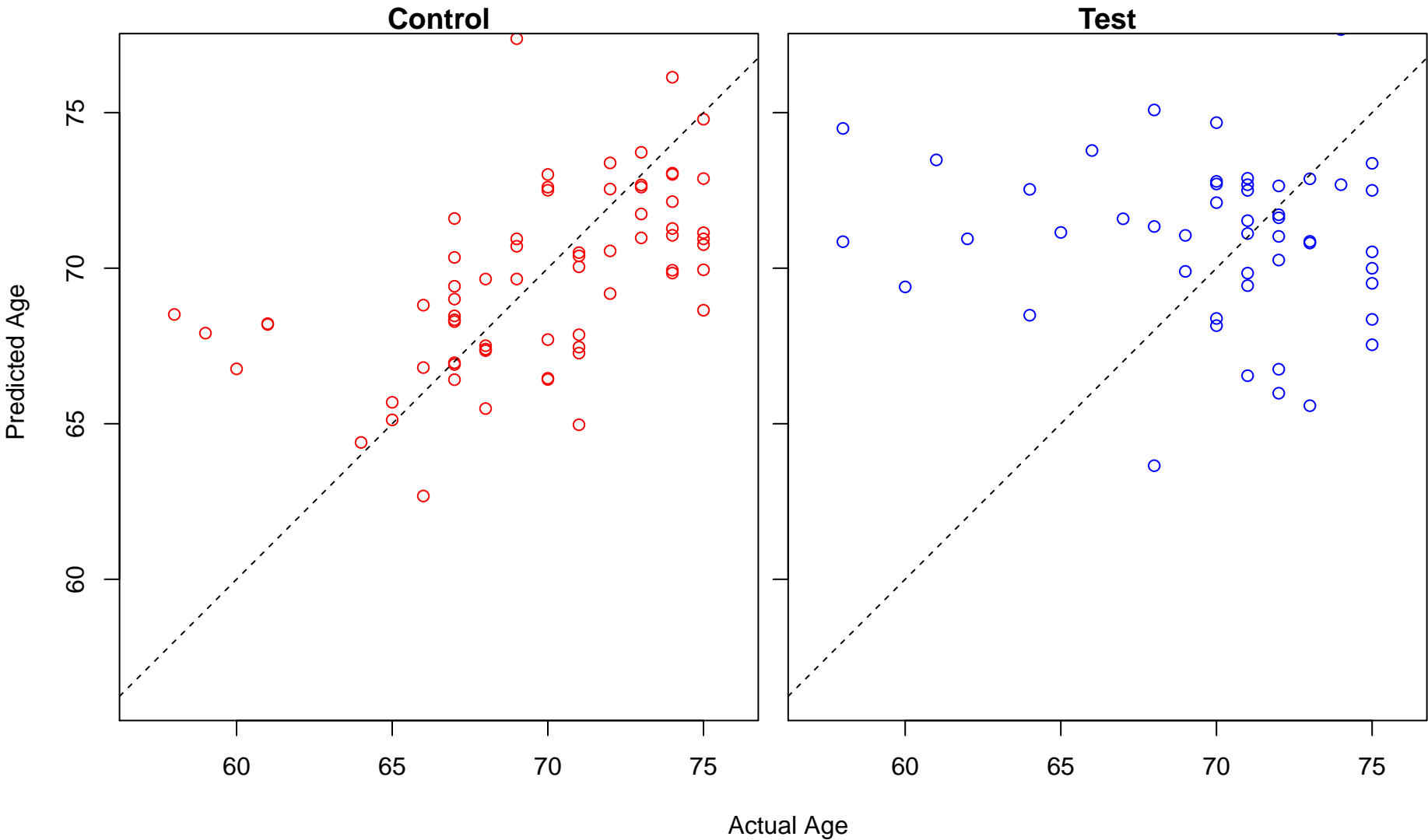
positive chemotaxis (Score: 1.021410)



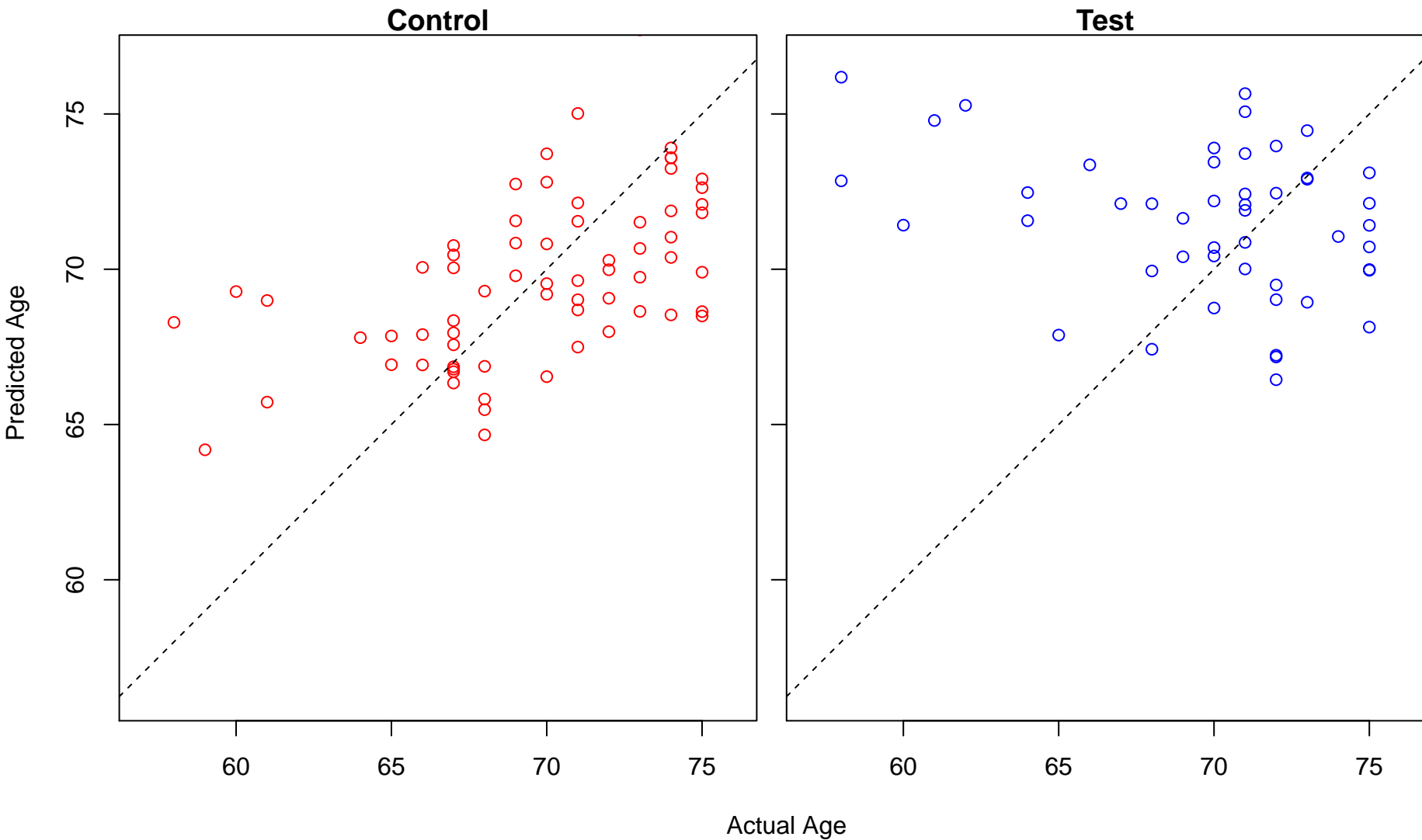
modulation of excitatory postsynaptic potential (Score: 1.020944)



positive regulation of production of molecular mediator of immune response (Score: 1.020937)

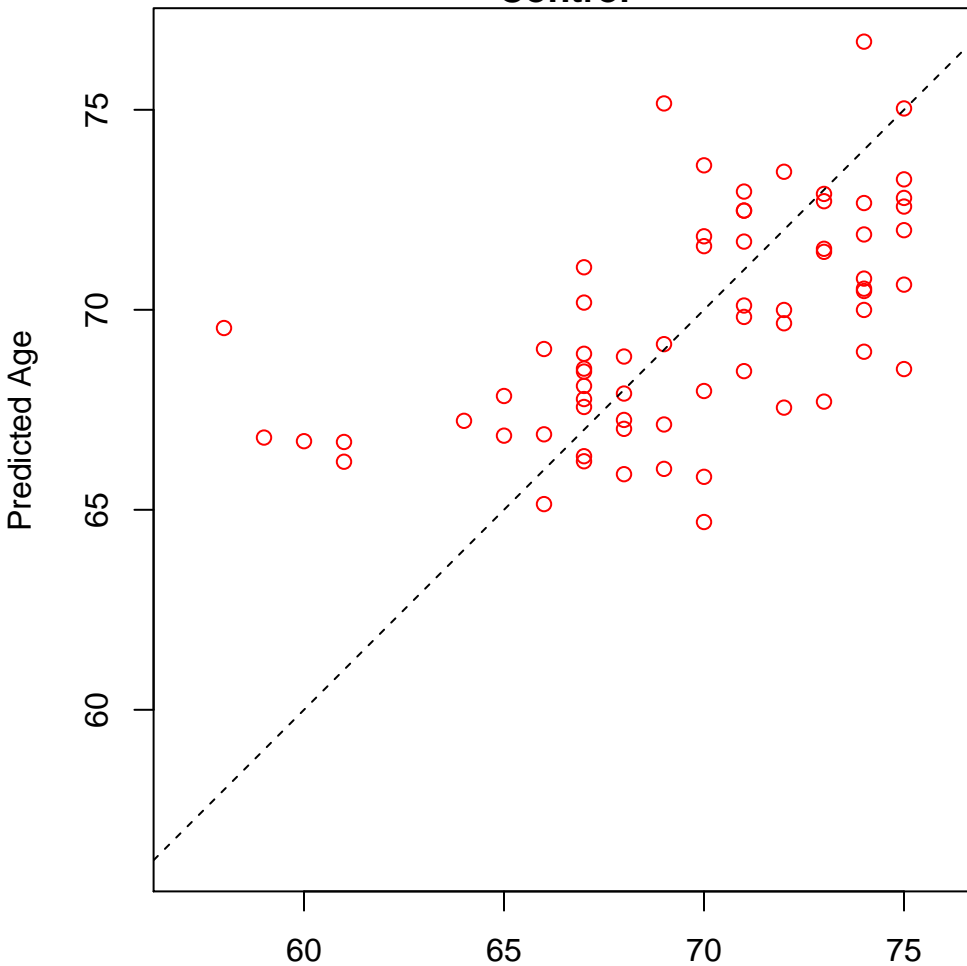


cellular response to pH (Score: 1.020821)

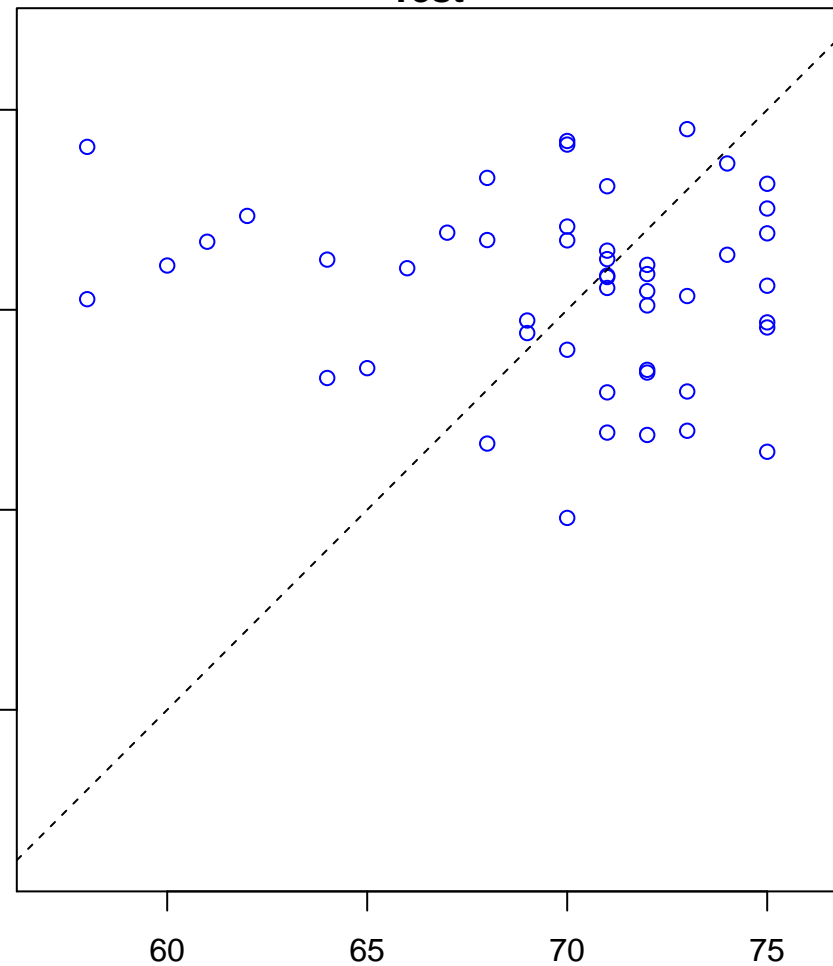


cytoplasmic microtubule organization (Score: 1.020571)

Control

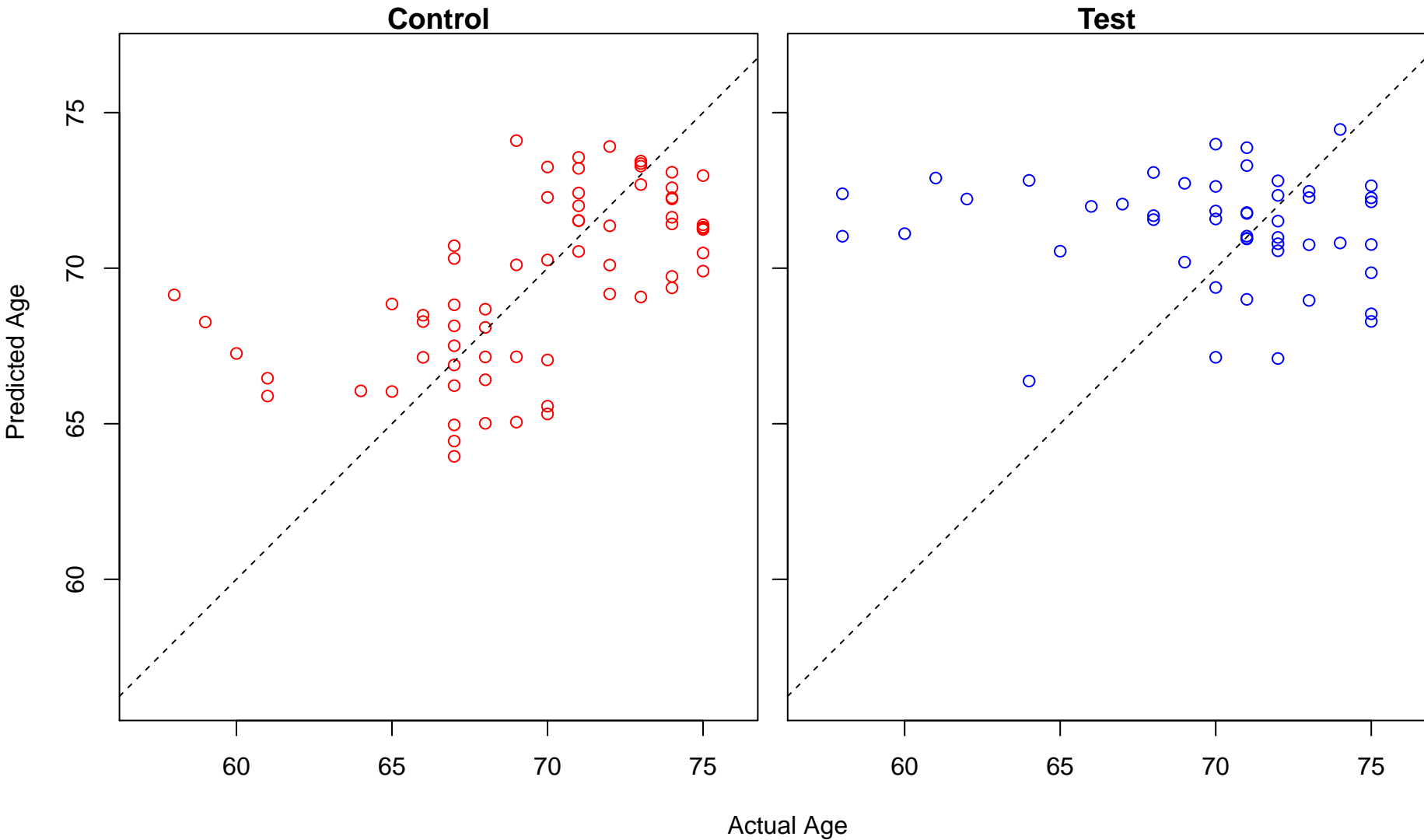


Test

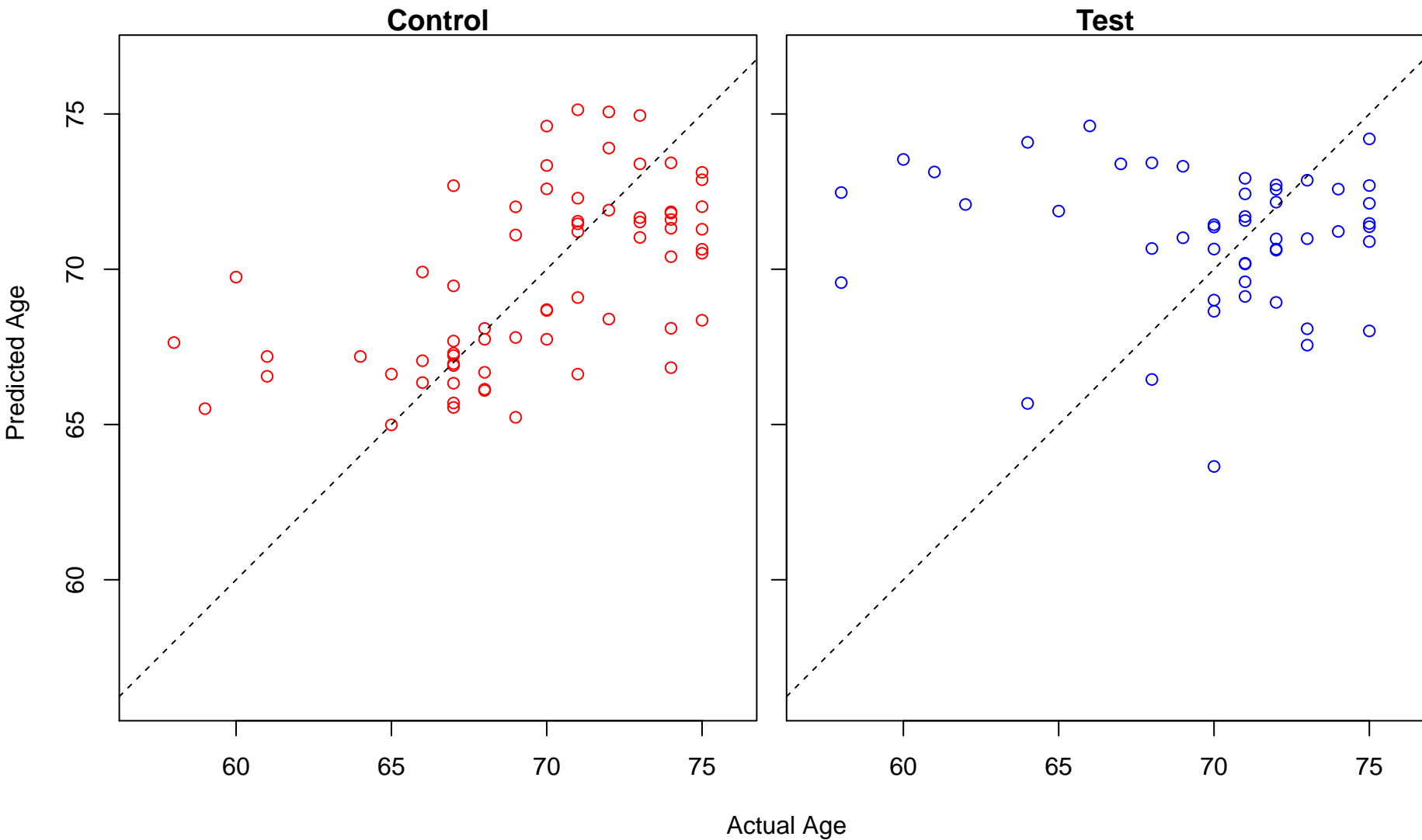


Actual Age

somatic diversification of immune receptors (Score: 1.020256)

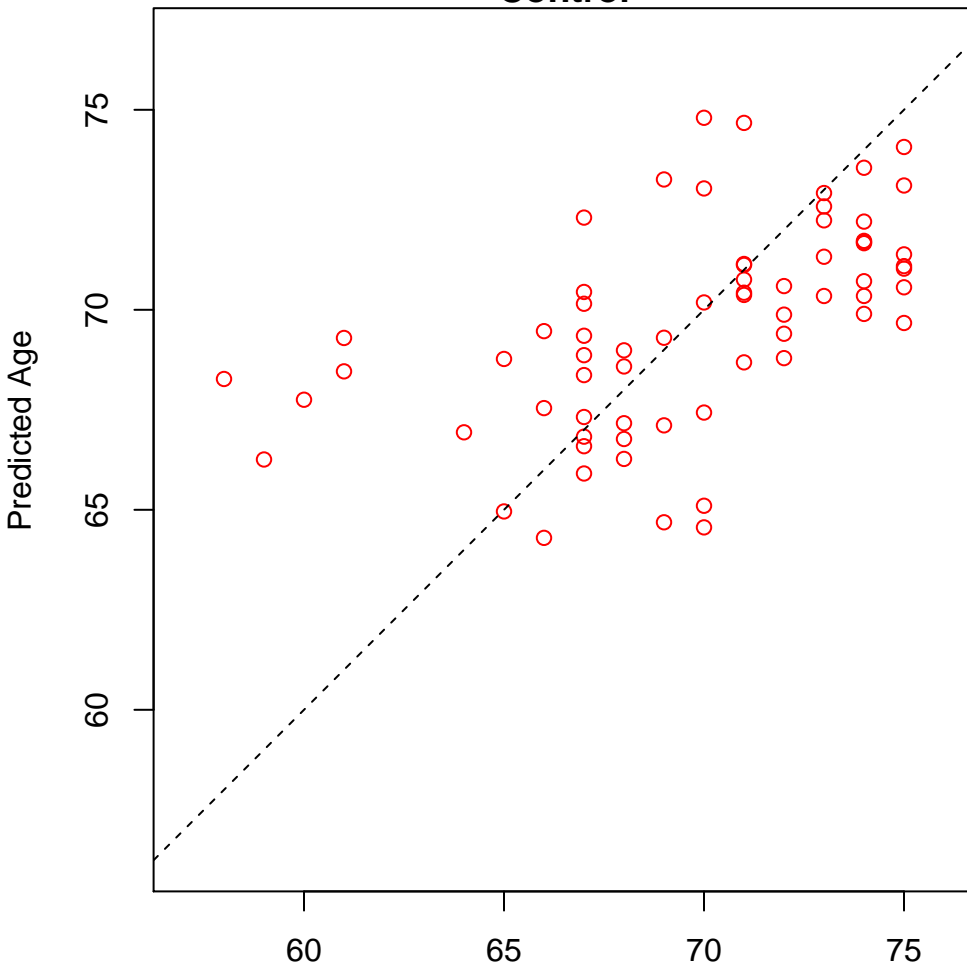


pancreas development (Score: 1.019136)

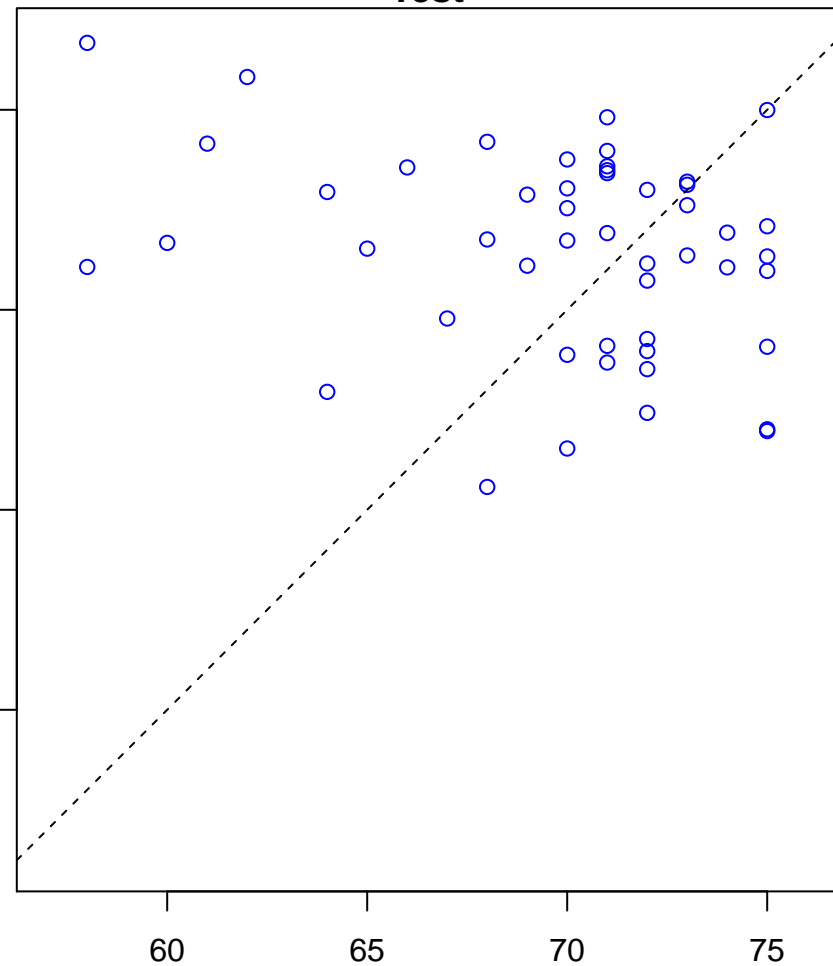


odontogenesis of dentin-containing tooth (Score: 1.018928)

Control

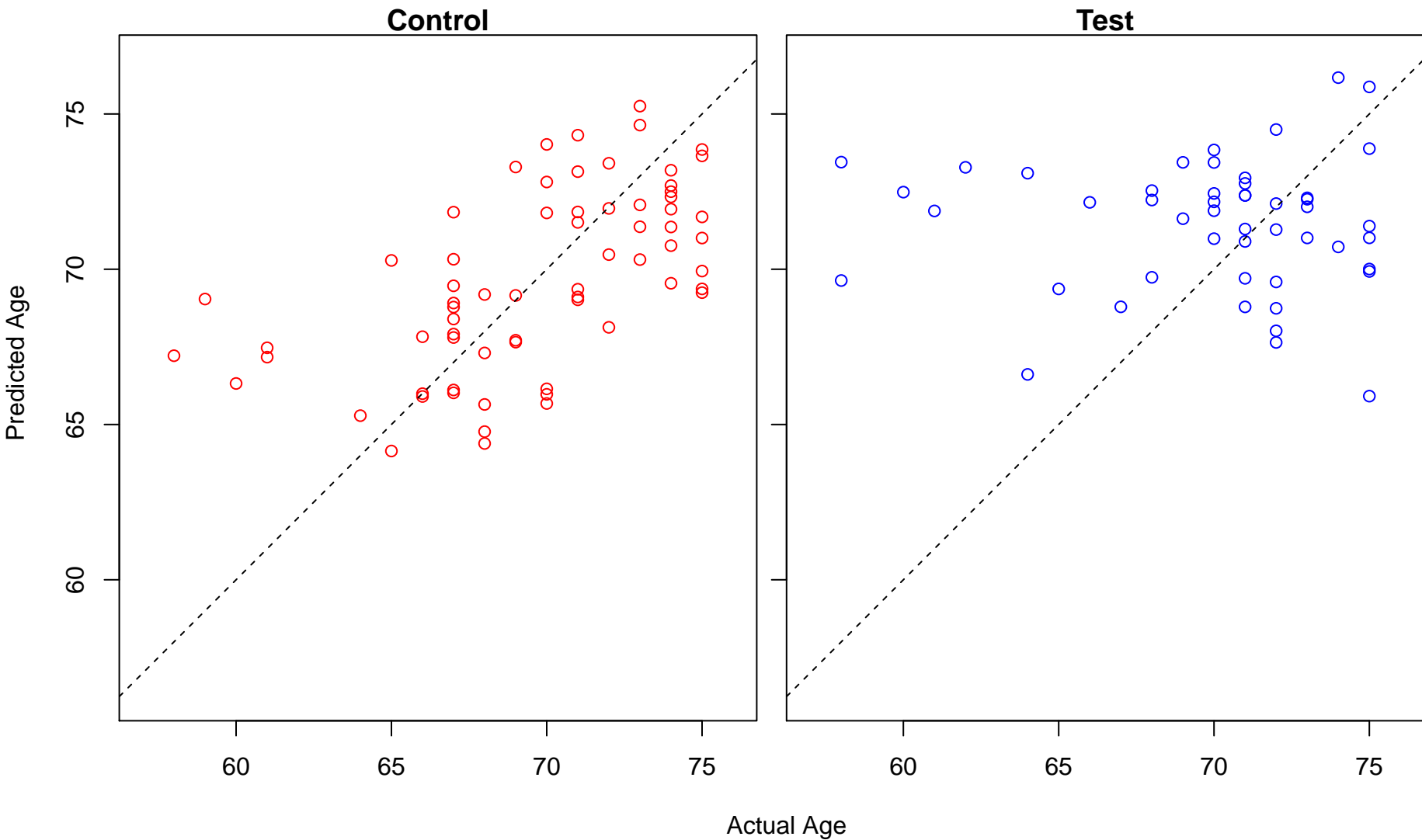


Test

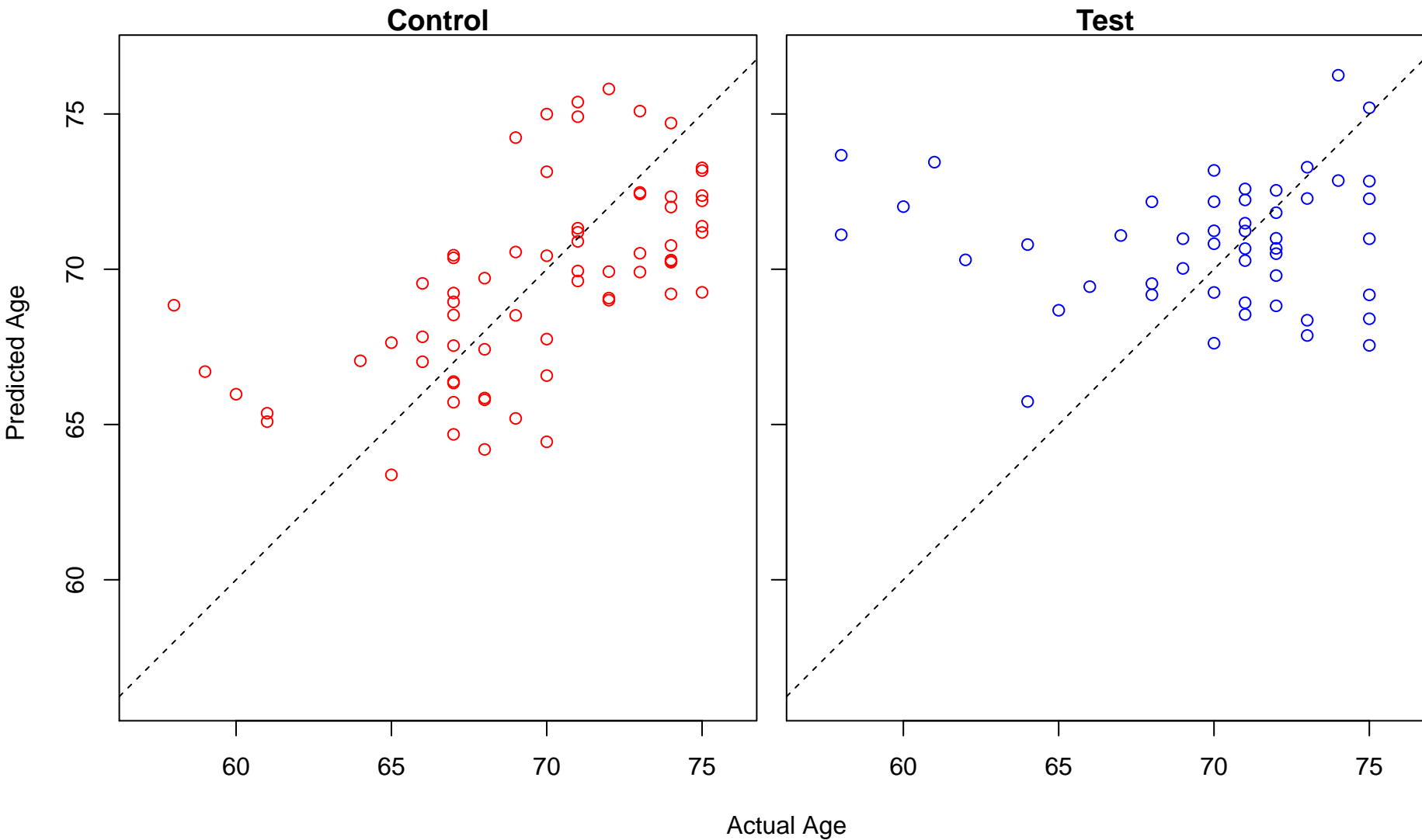


Actual Age

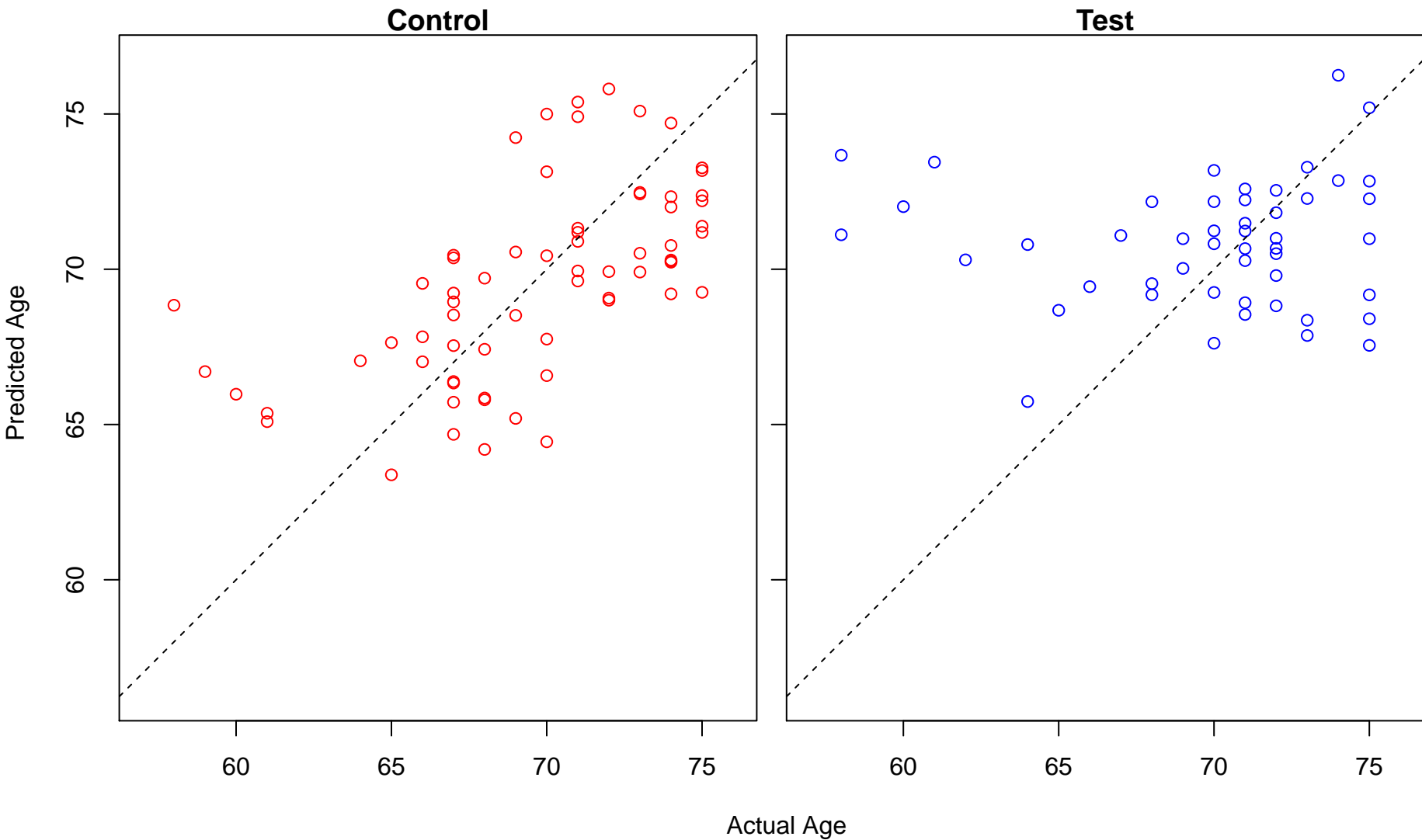
positive regulation of gliogenesis (Score: 1.018701)



embryo development ending in birth or egg hatching (Score: 1.017832)

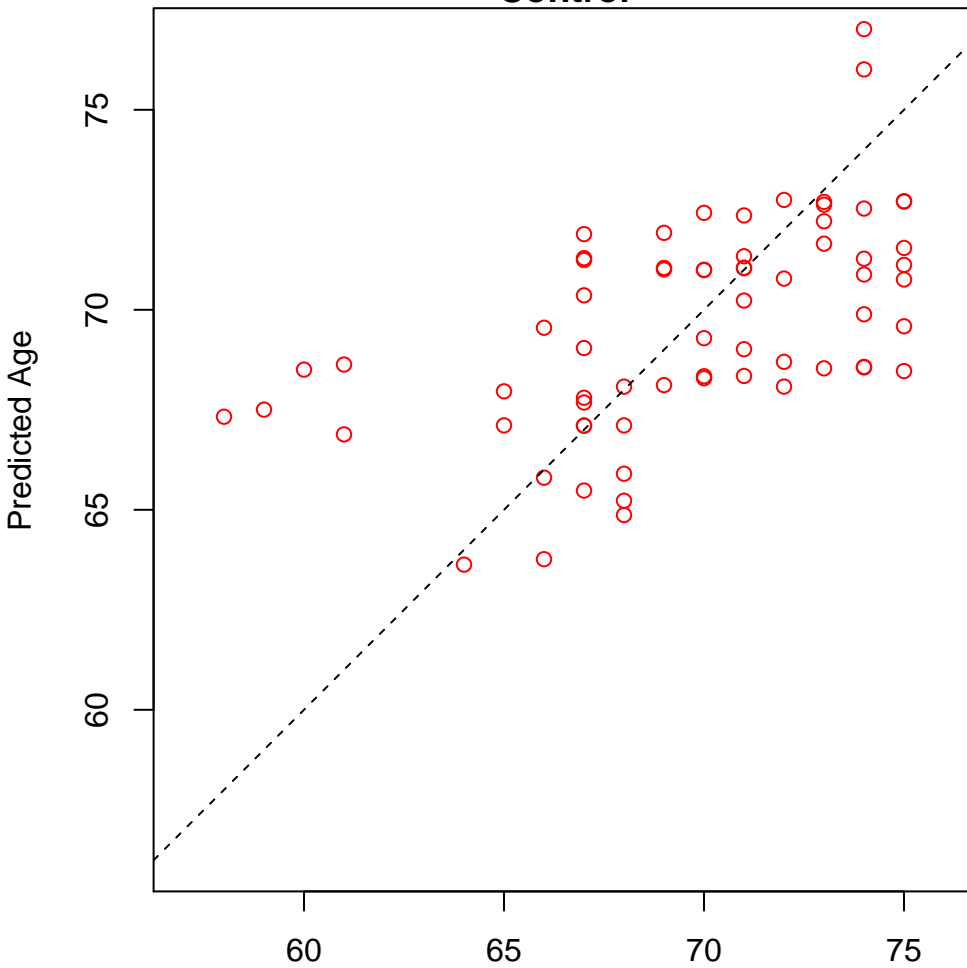


chordate embryonic development (Score: 1.017832)

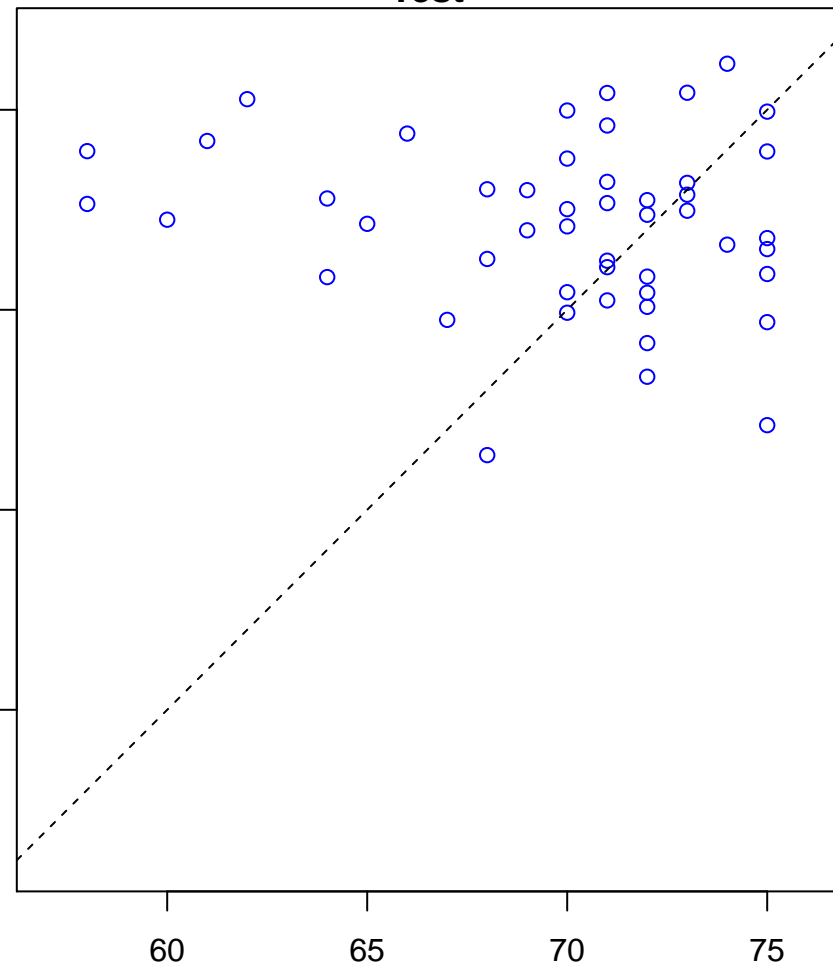


regeneration (Score: 1.017725)

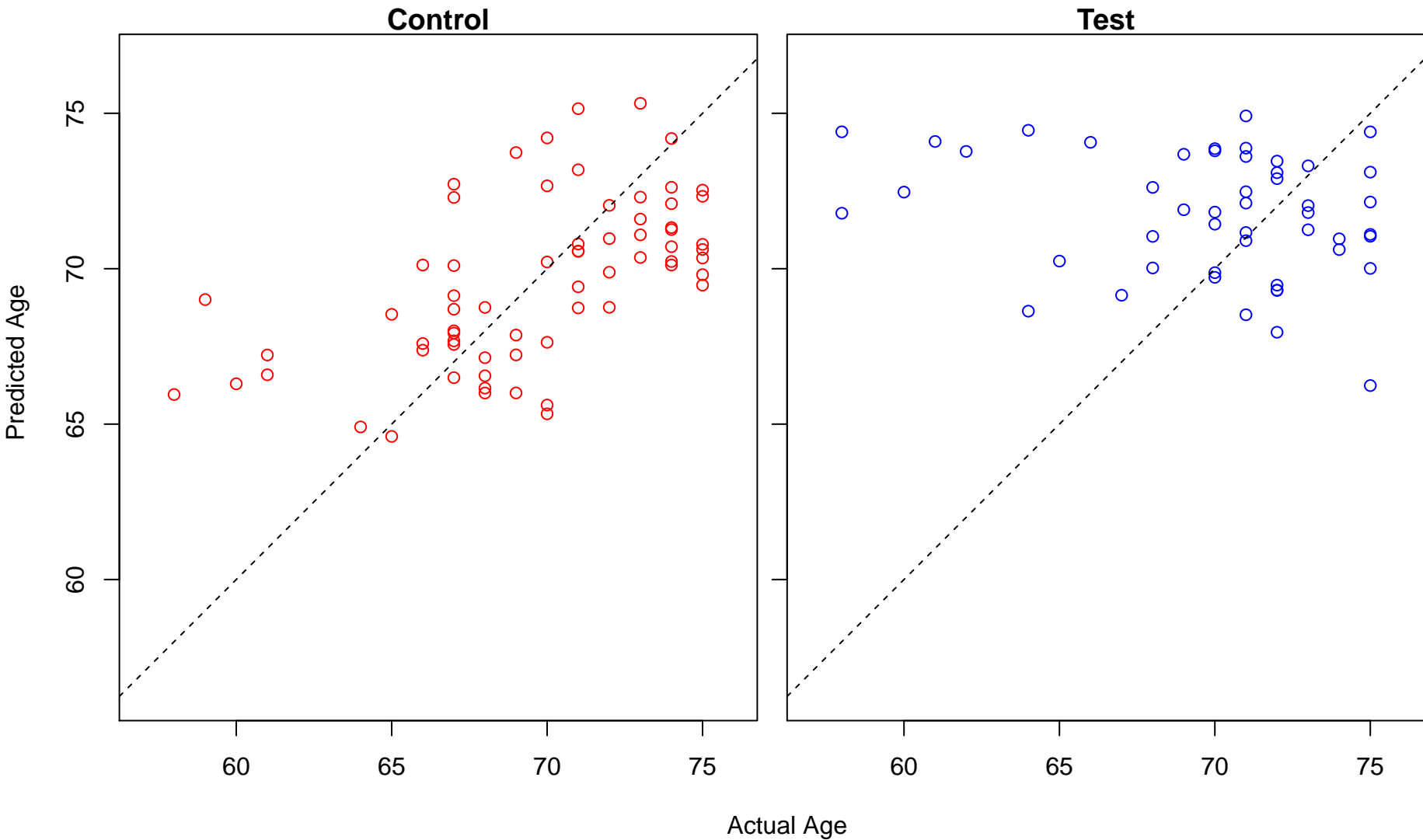
Control



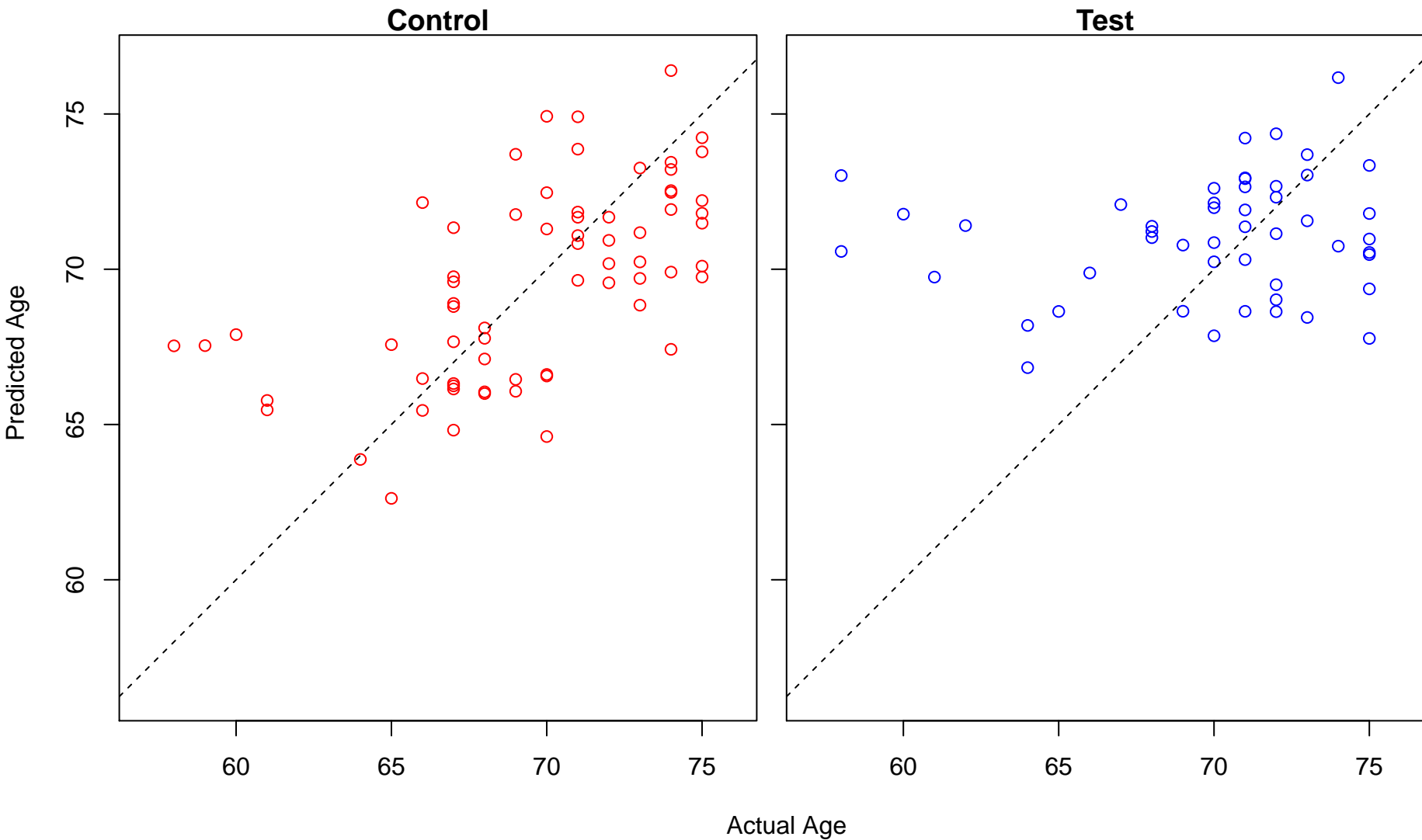
Test



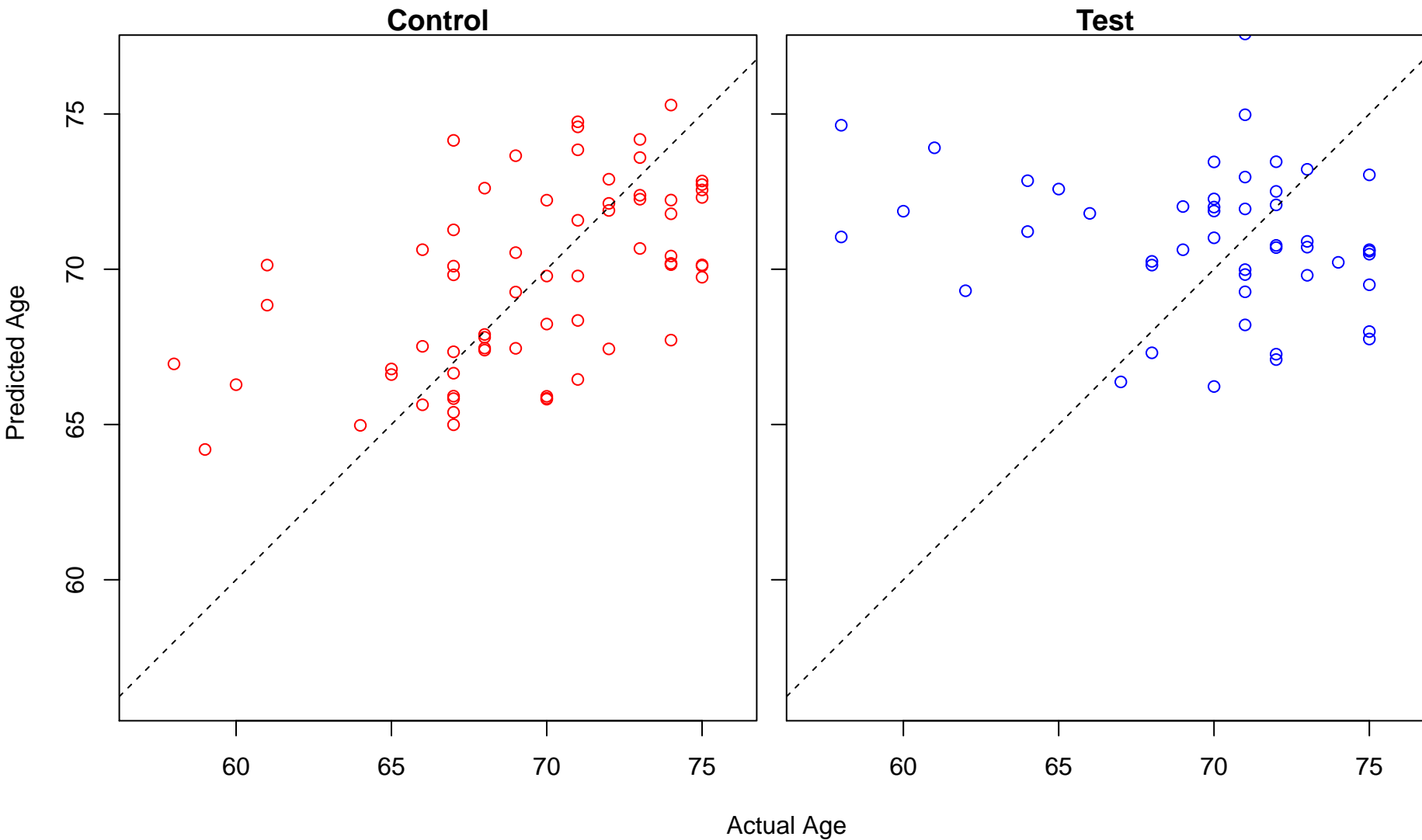
determination of left/right symmetry (Score: 1.017691)



mesoderm development (Score: 1.017659)

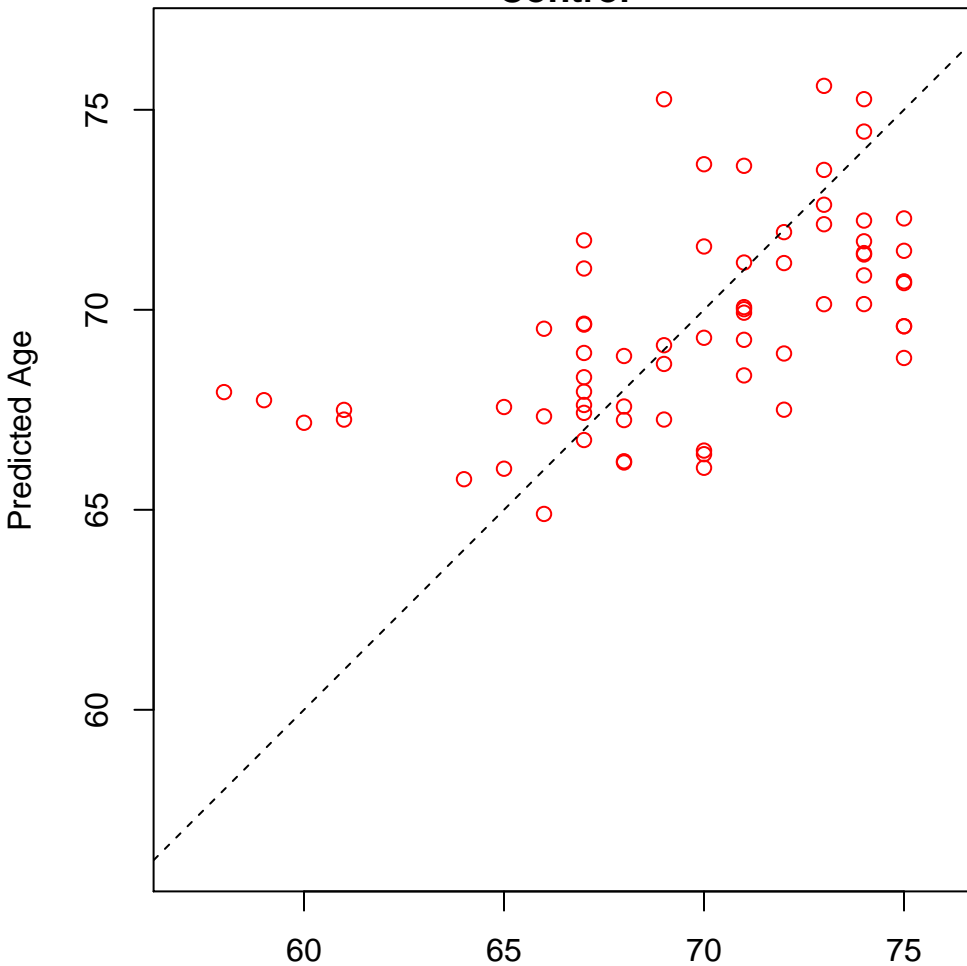


response to thyroid hormone (Score: 1.017505)

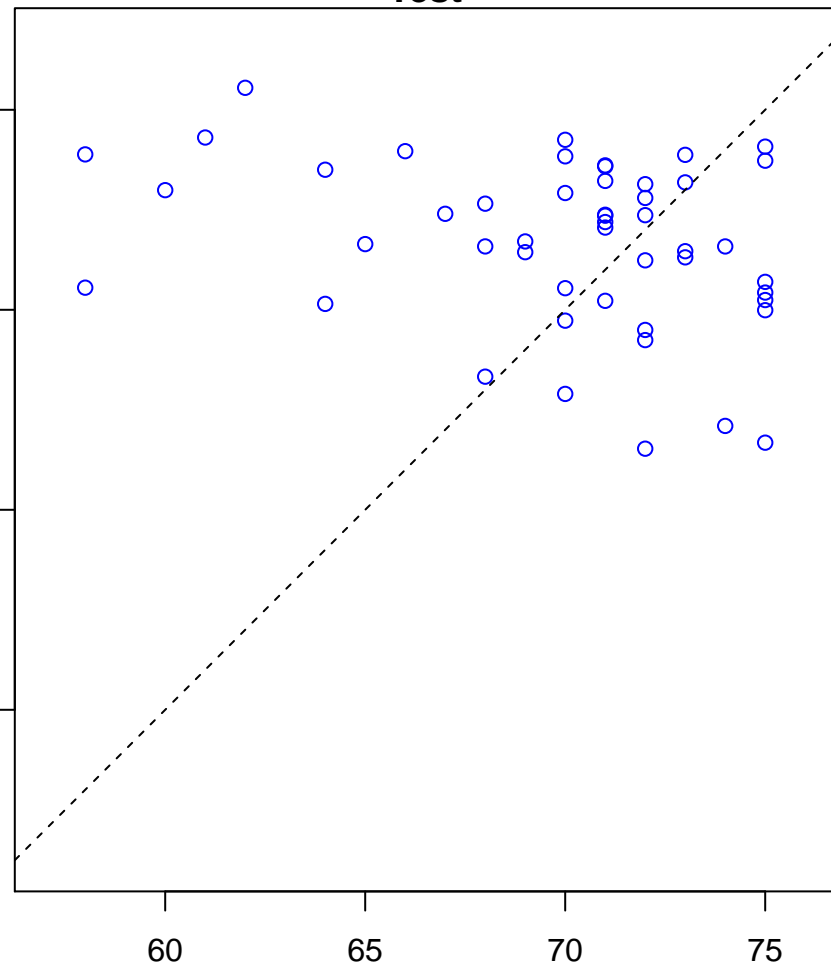


positive regulation of anion transport (Score: 1.017424)

Control

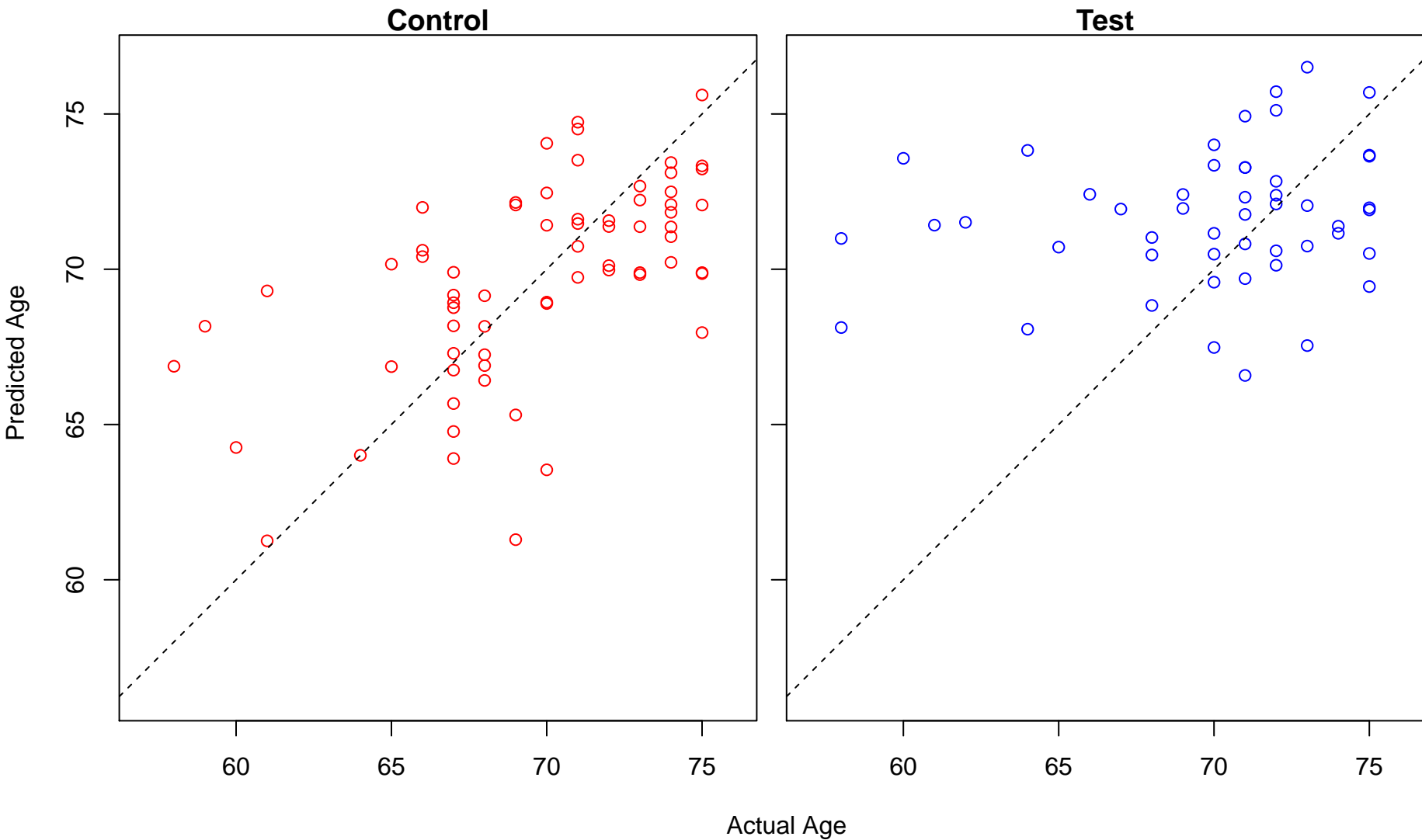


Test

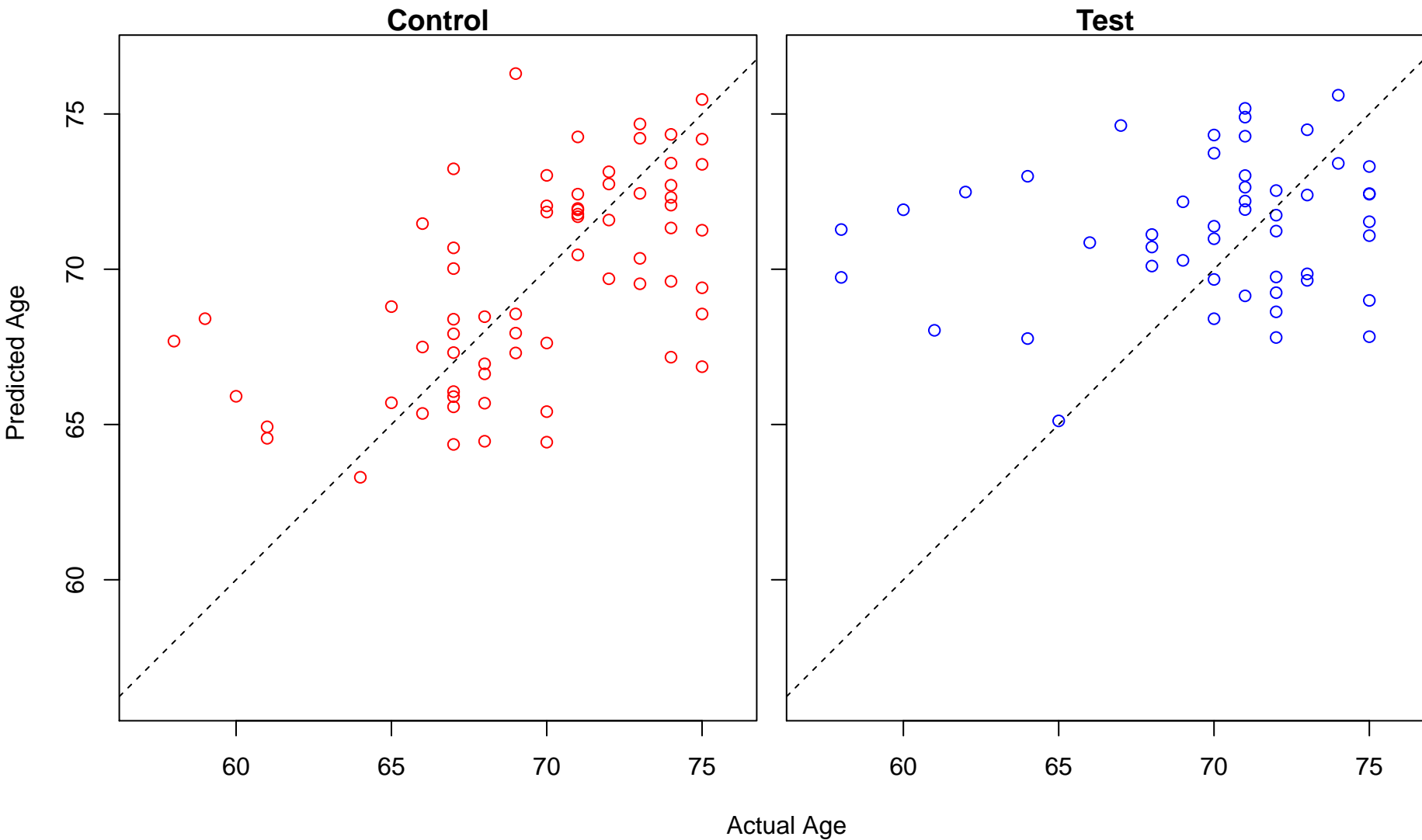


Actual Age

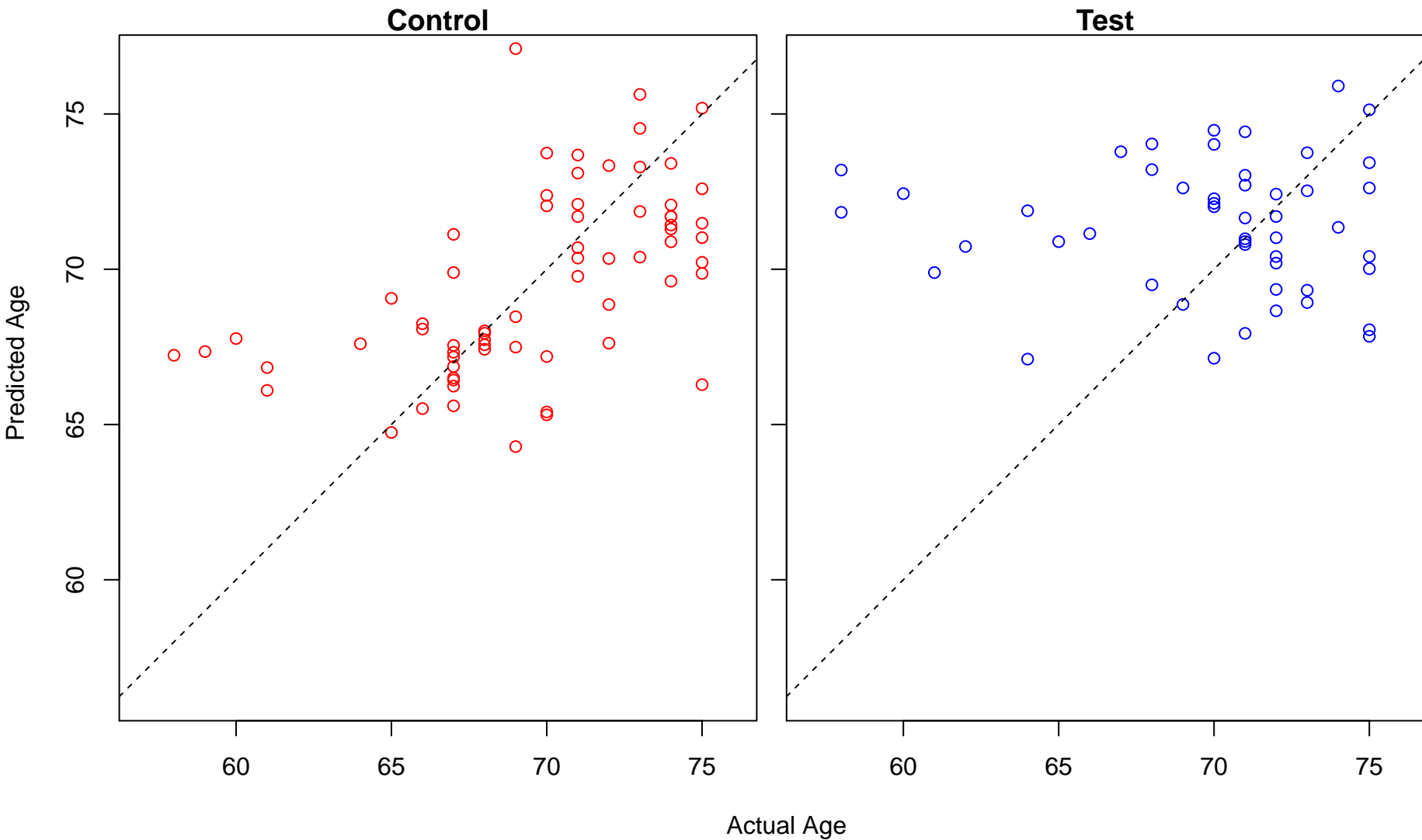
spermatid differentiation (Score: 1.017041)



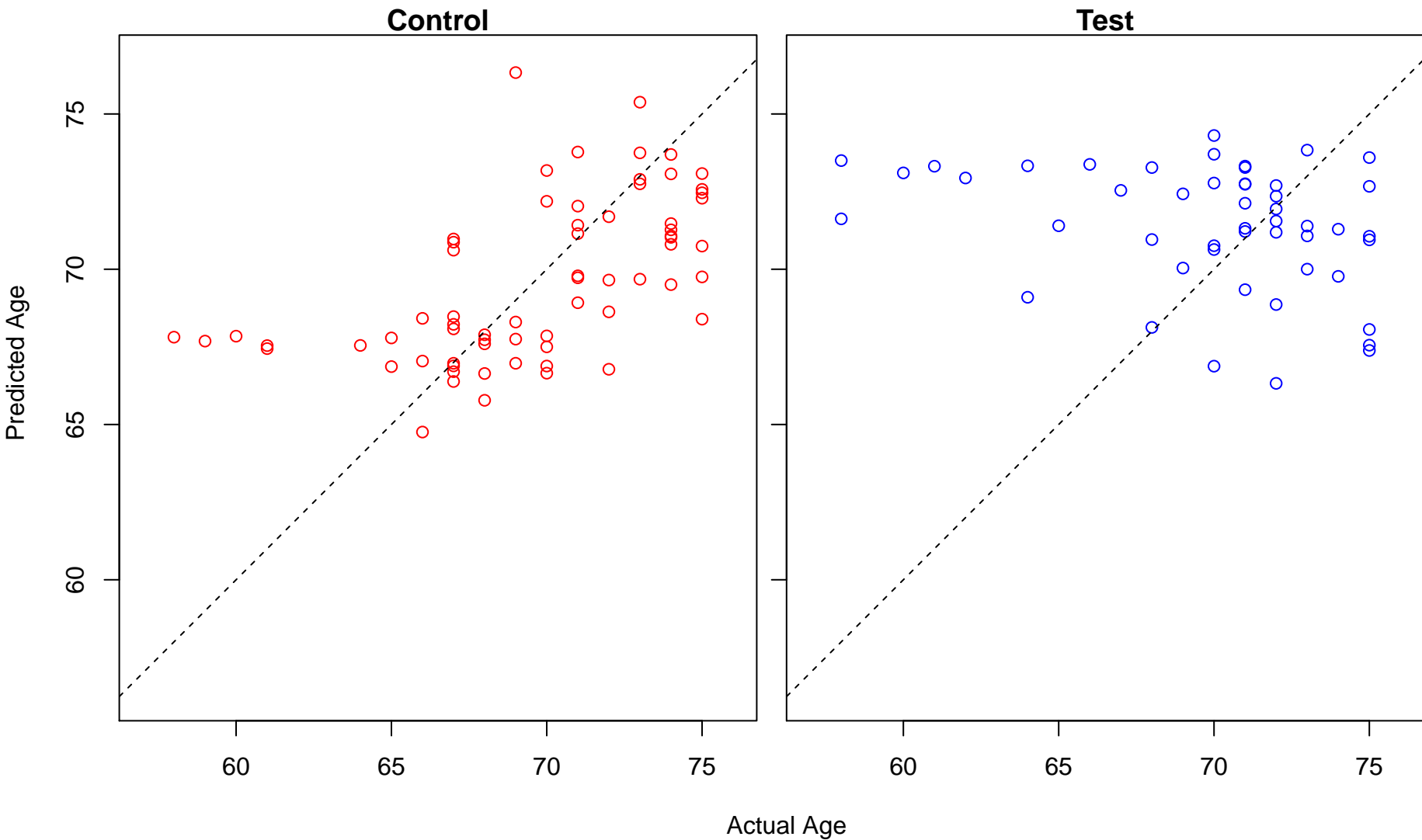
proteoglycan biosynthetic process (Score: 1.017002)



detection of light stimulus (Score: 1.016797)

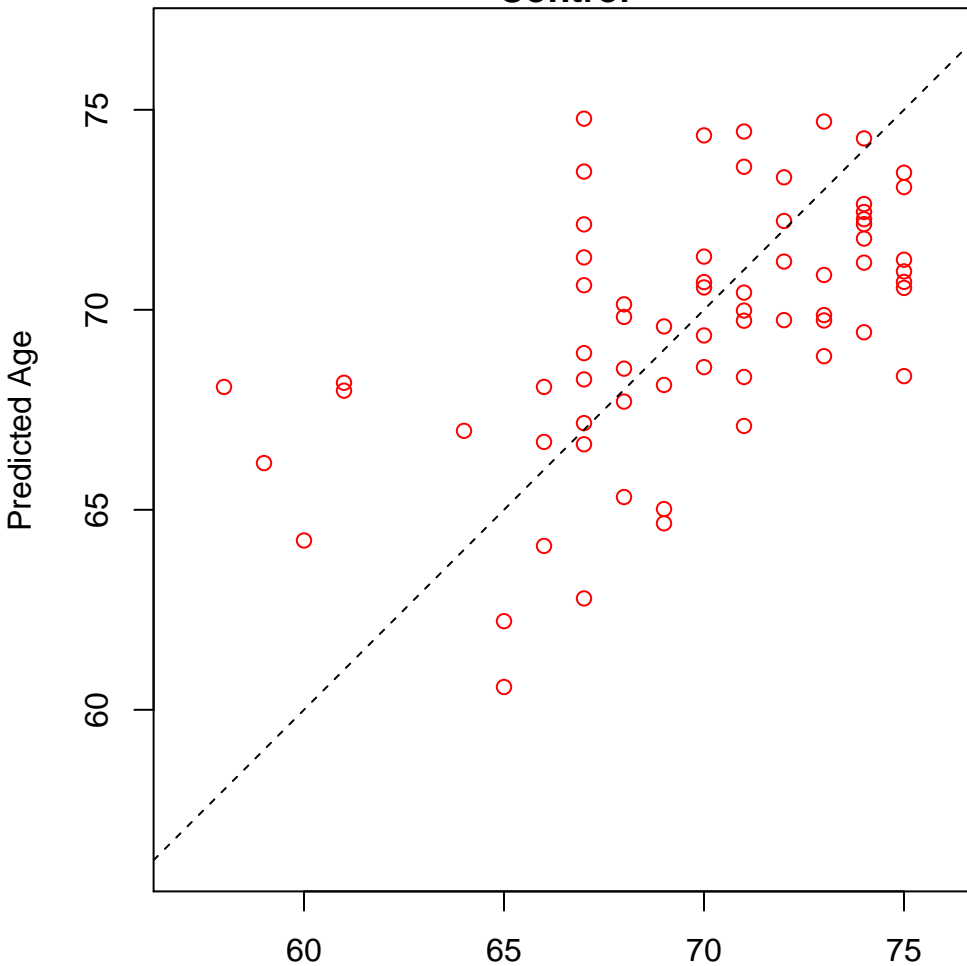


regulation of hormone secretion (Score: 1.016420)

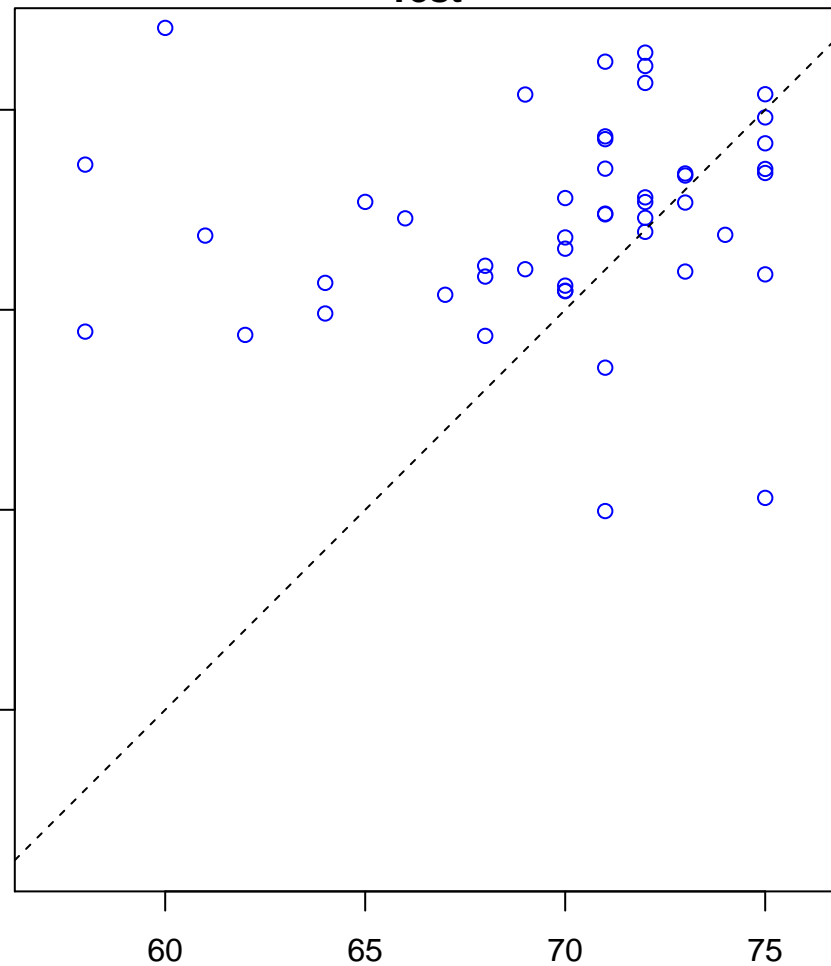


negative regulation of viral transcription (Score: 1.015234)

Control

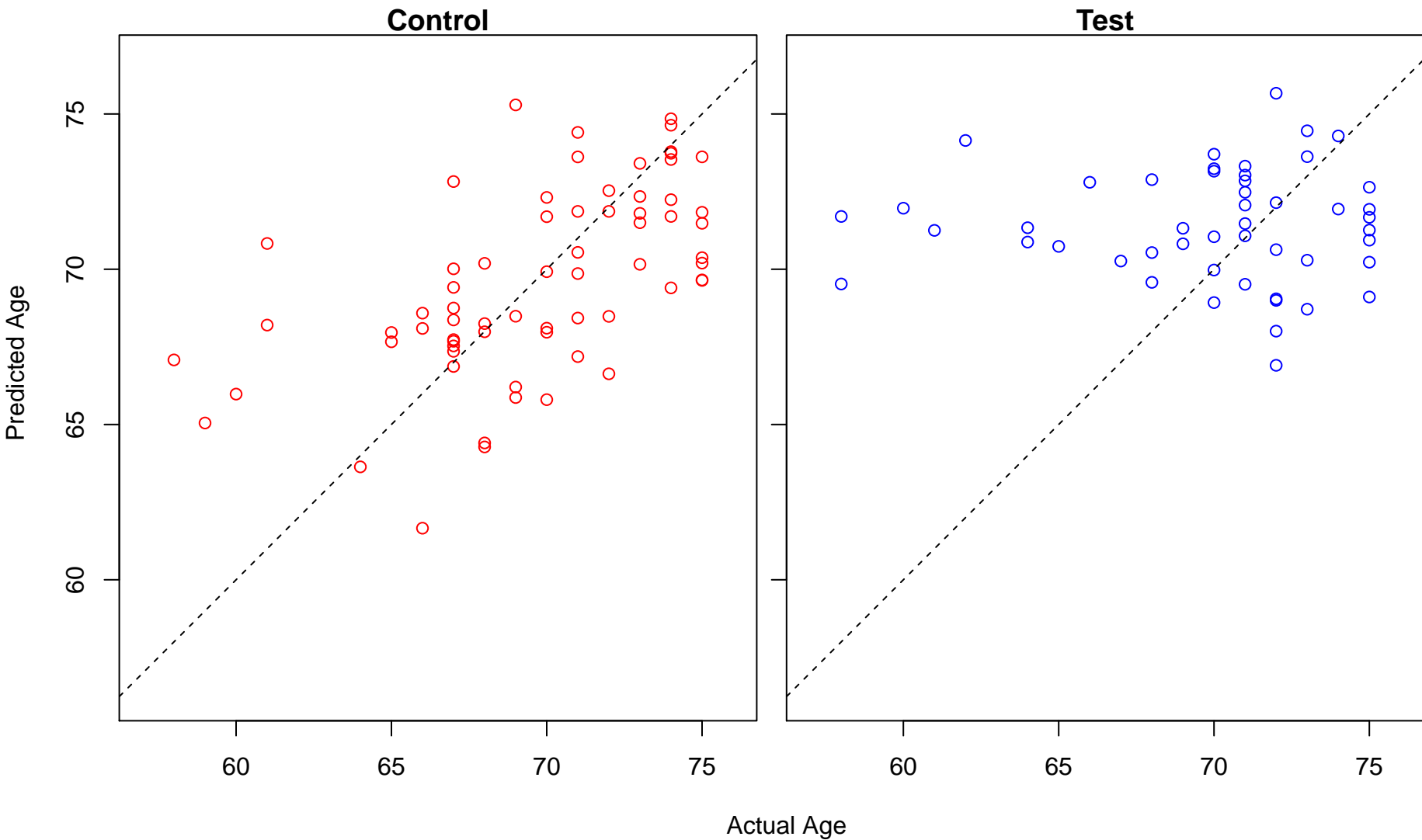


Test

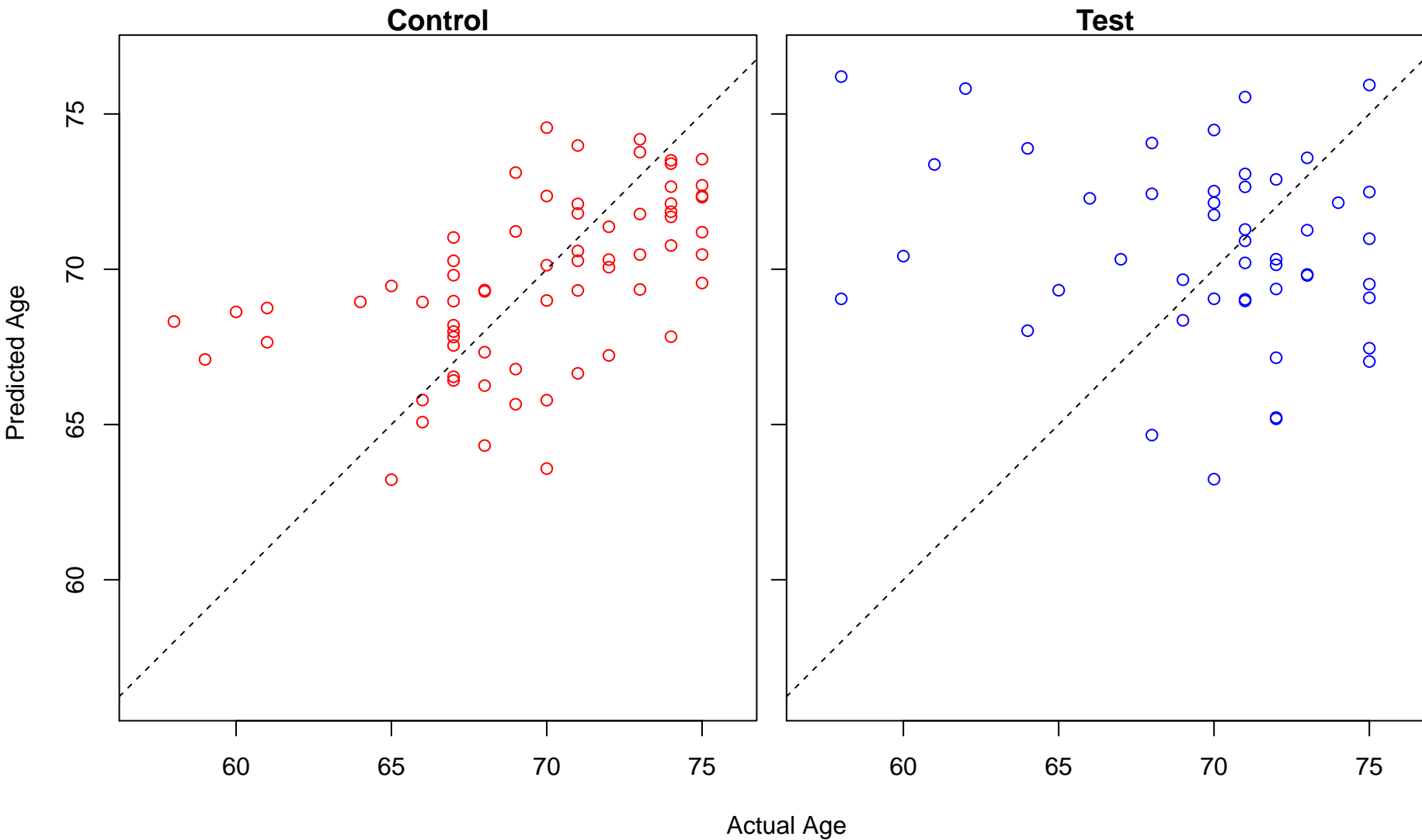


Actual Age

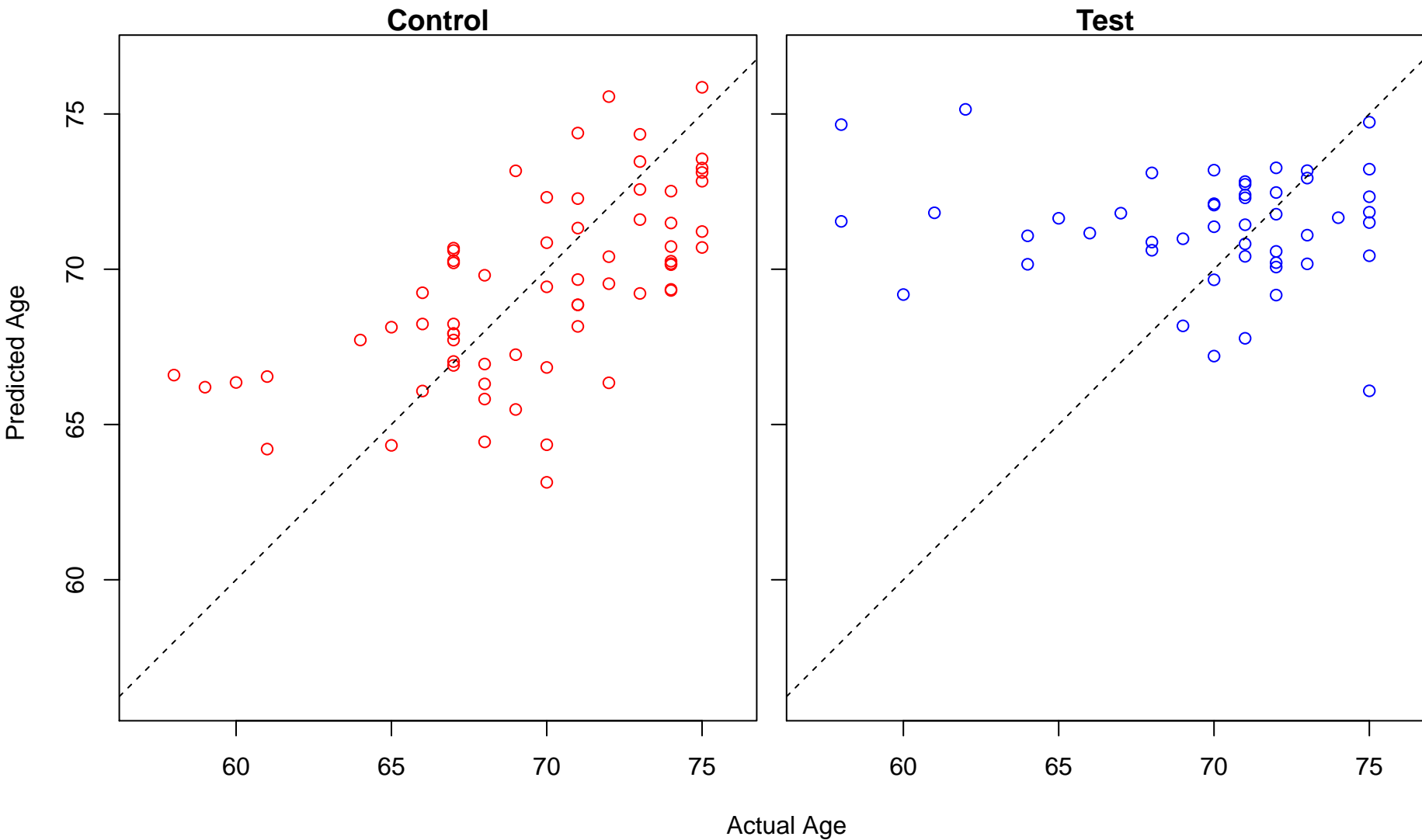
sensory perception of pain (Score: 1.015135)



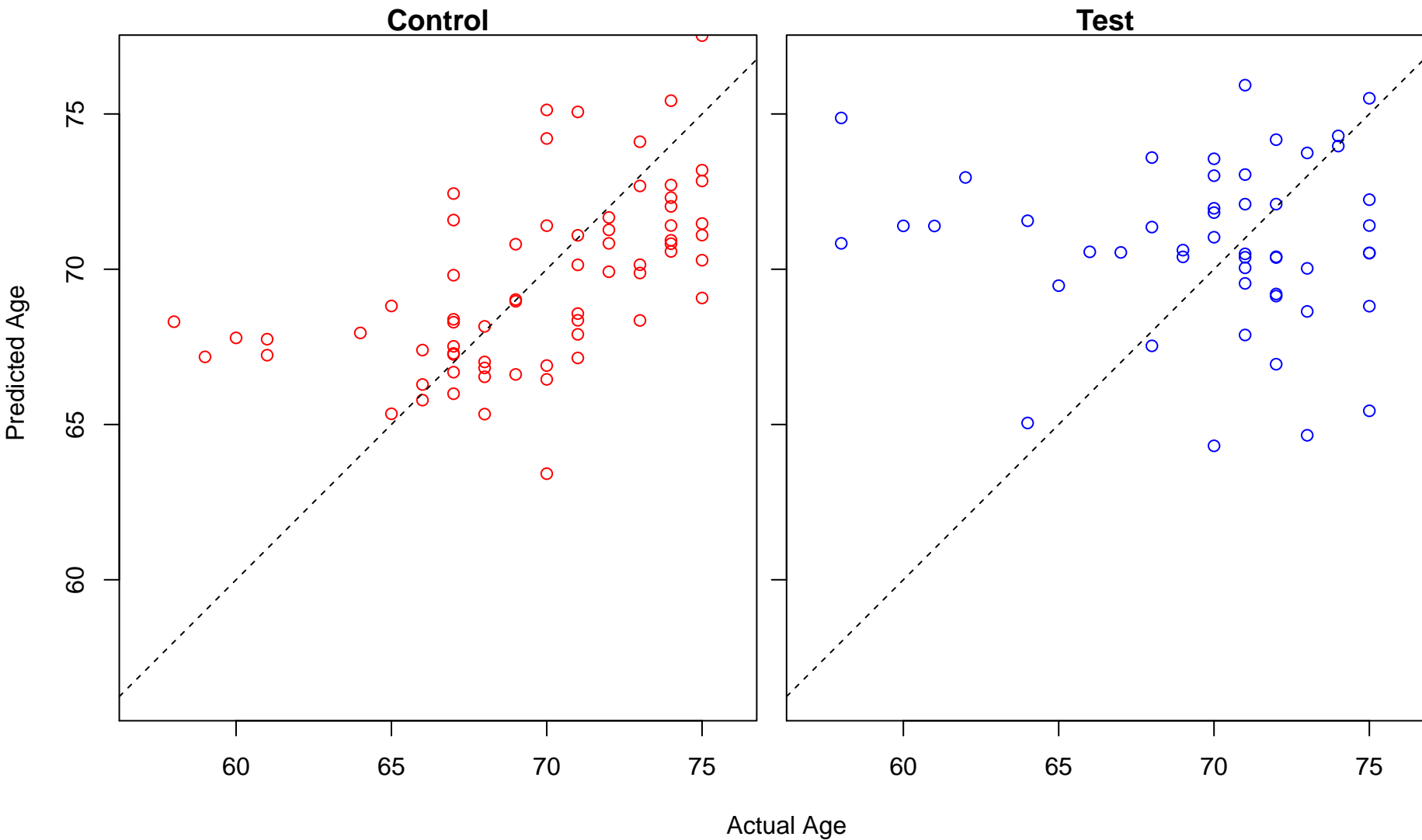
positive regulation of calcium ion transmembrane transporter activity (Score: 1.014895)



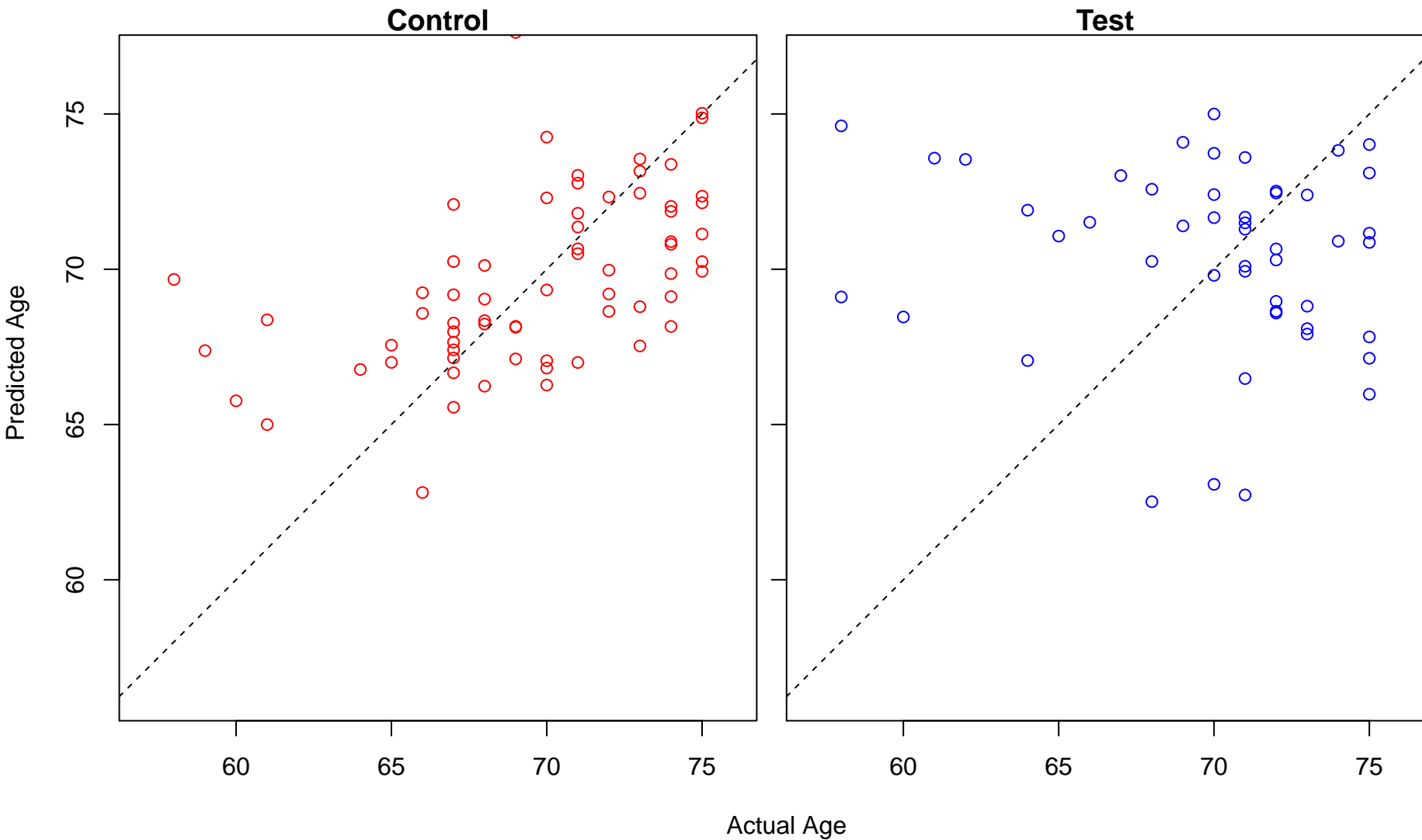
negative regulation of inflammatory response (Score: 1.014406)



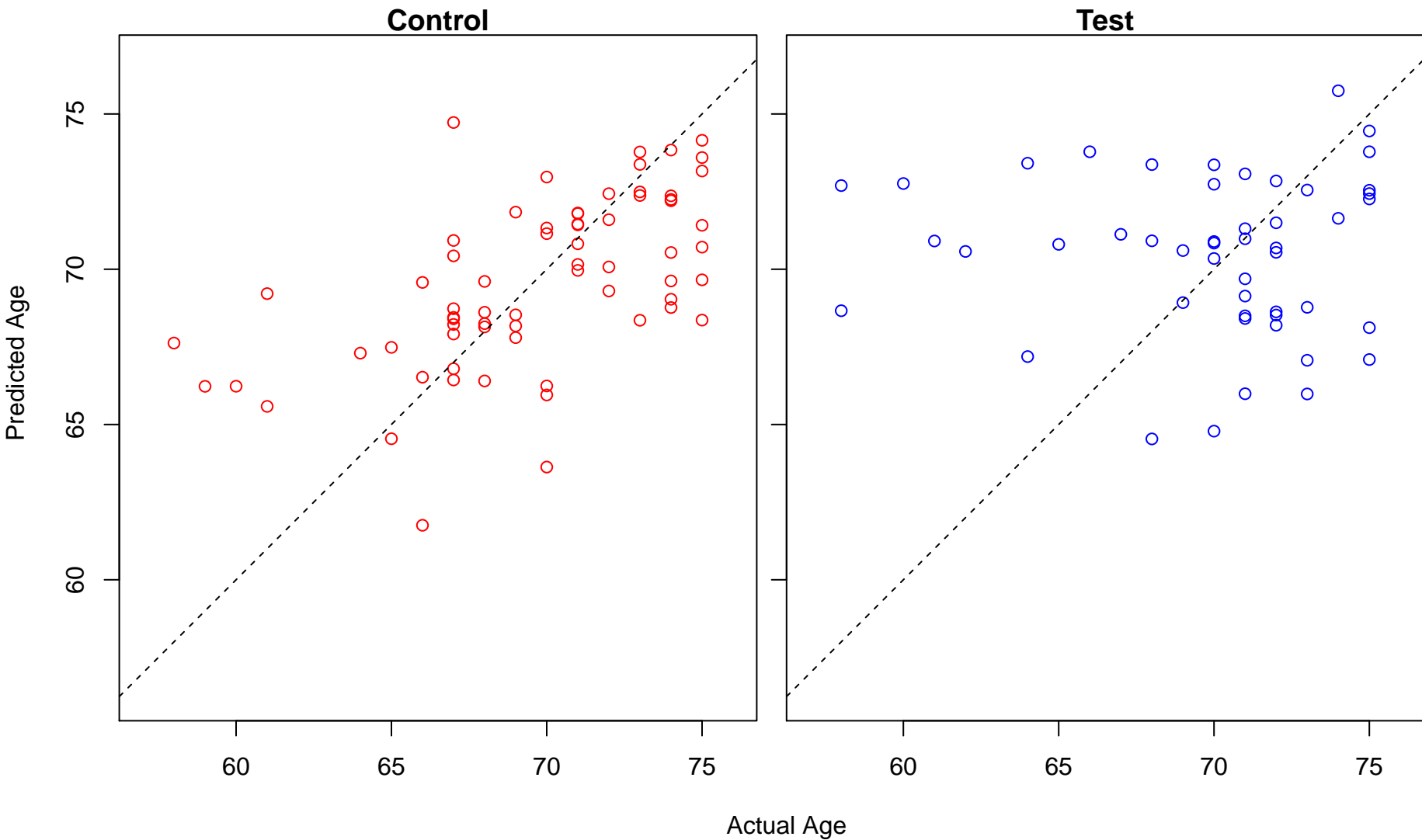
synaptic vesicle cycle (Score: 1.014068)



isoprenoid biosynthetic process (Score: 1.013969)

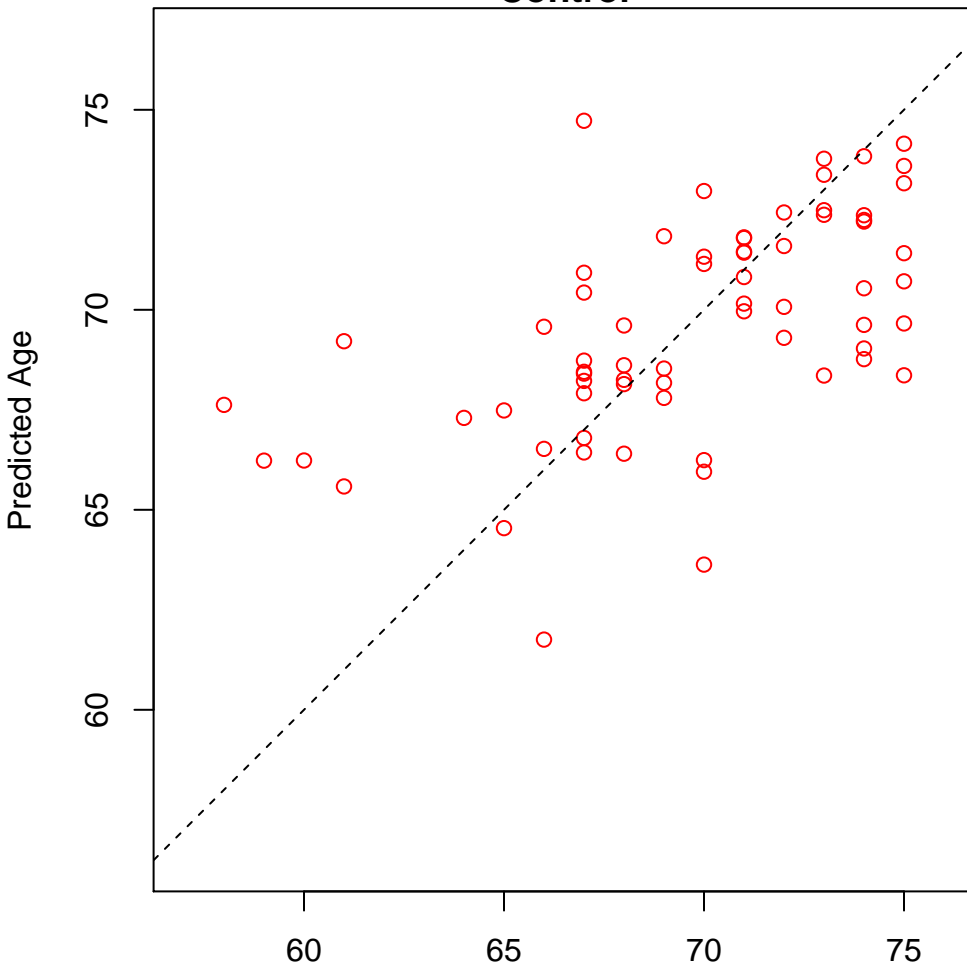


mature B cell differentiation involved in immune response (Score: 1.013928)

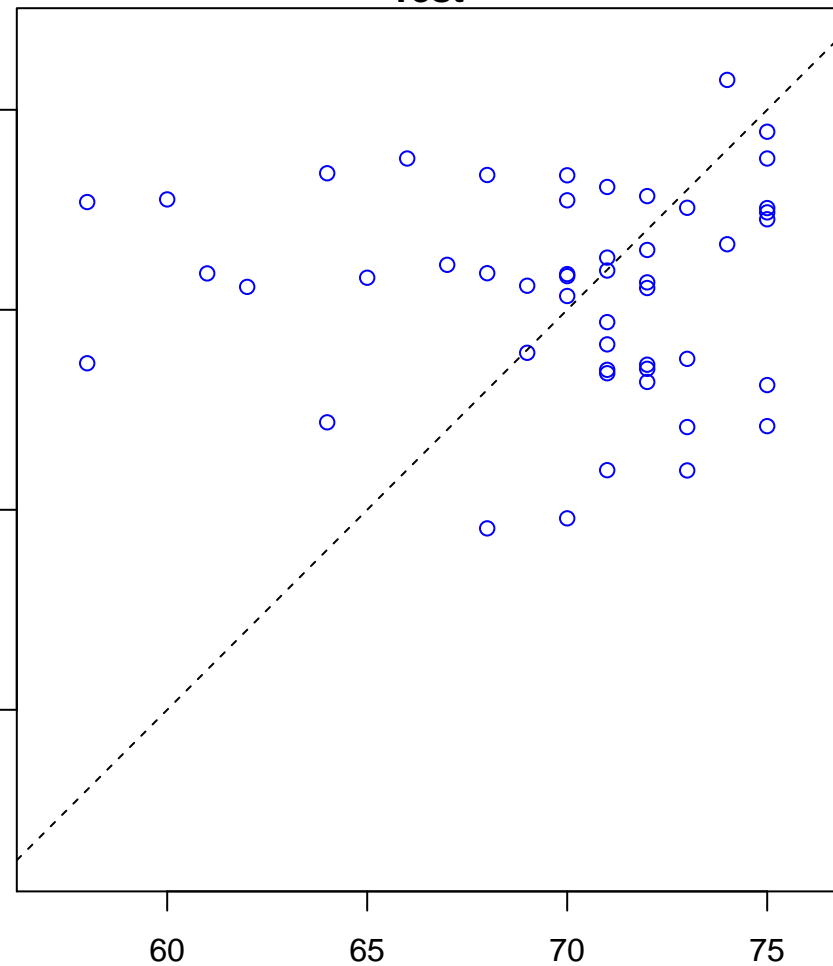


marginal zone B cell differentiation (Score: 1.013928)

Control

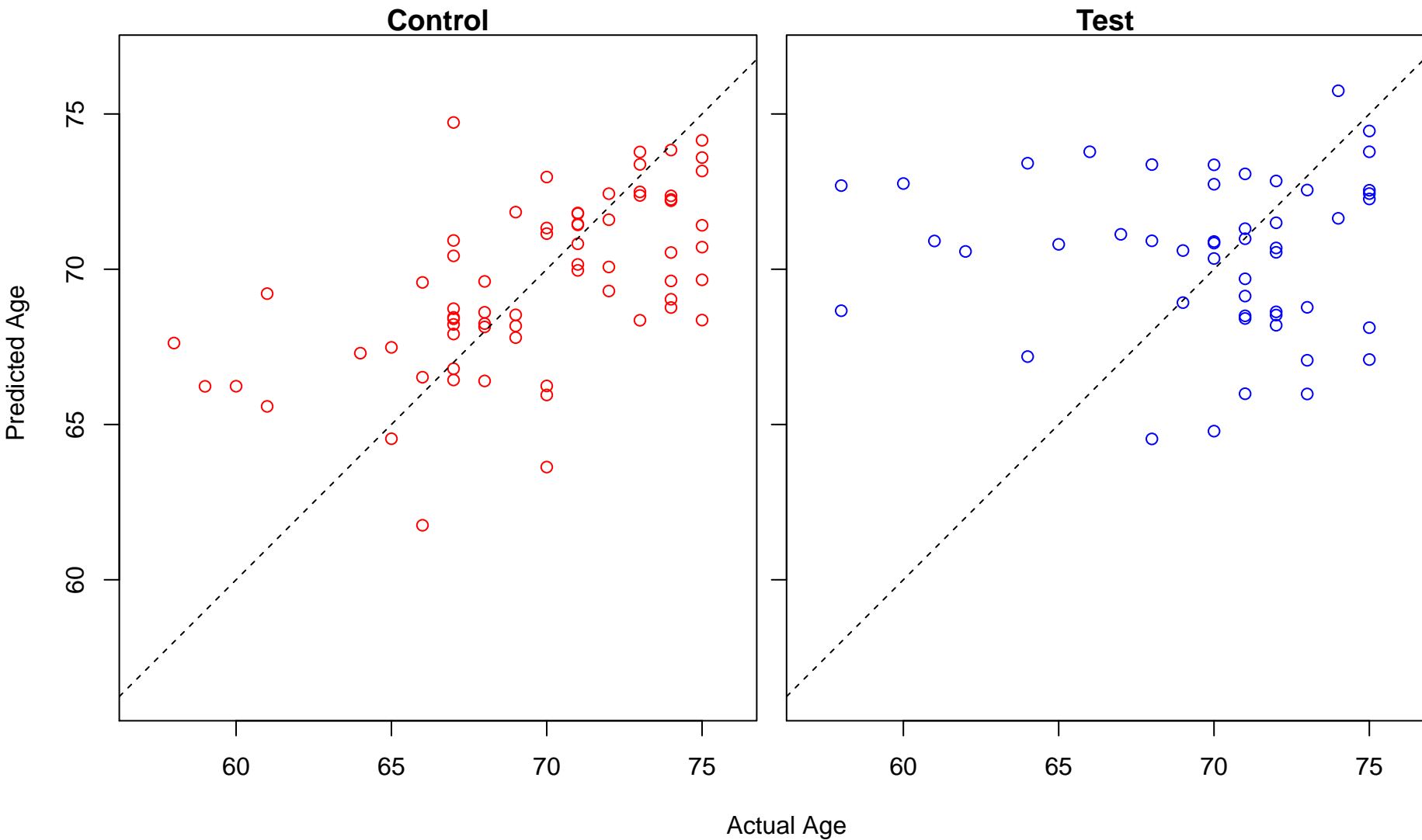


Test

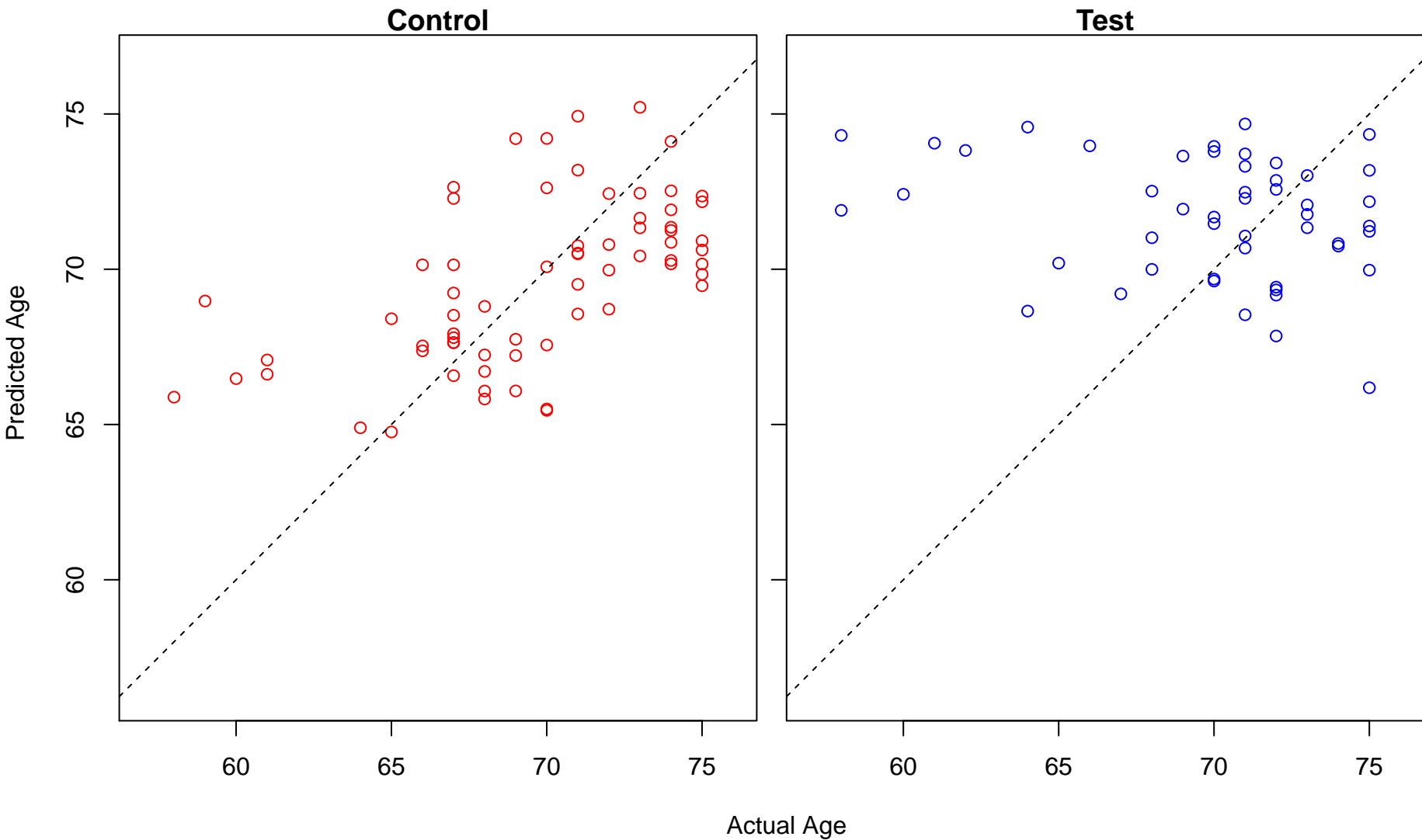


Actual Age

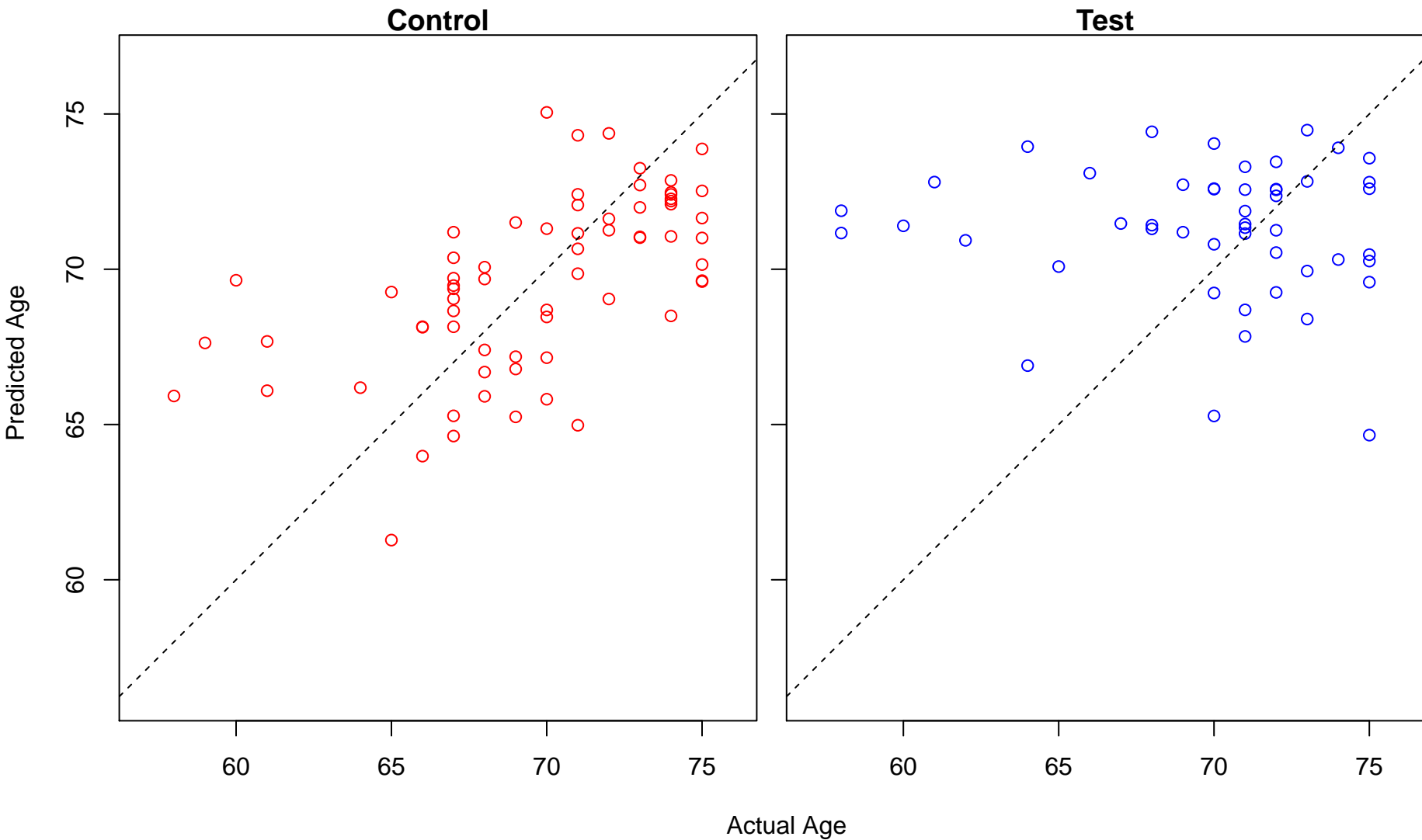
mature B cell differentiation (Score: 1.013928)



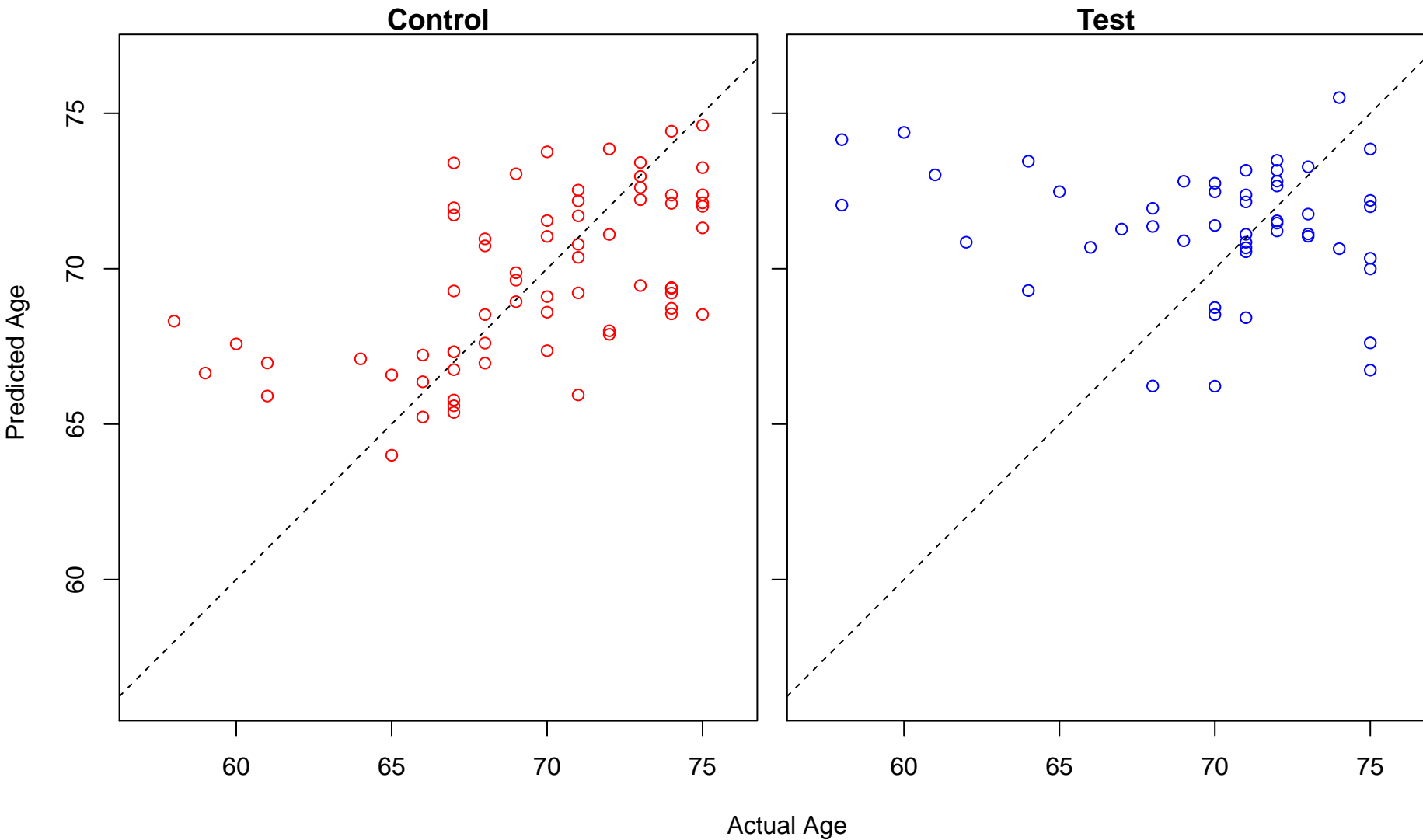
determination of bilateral symmetry (Score: 1.013697)



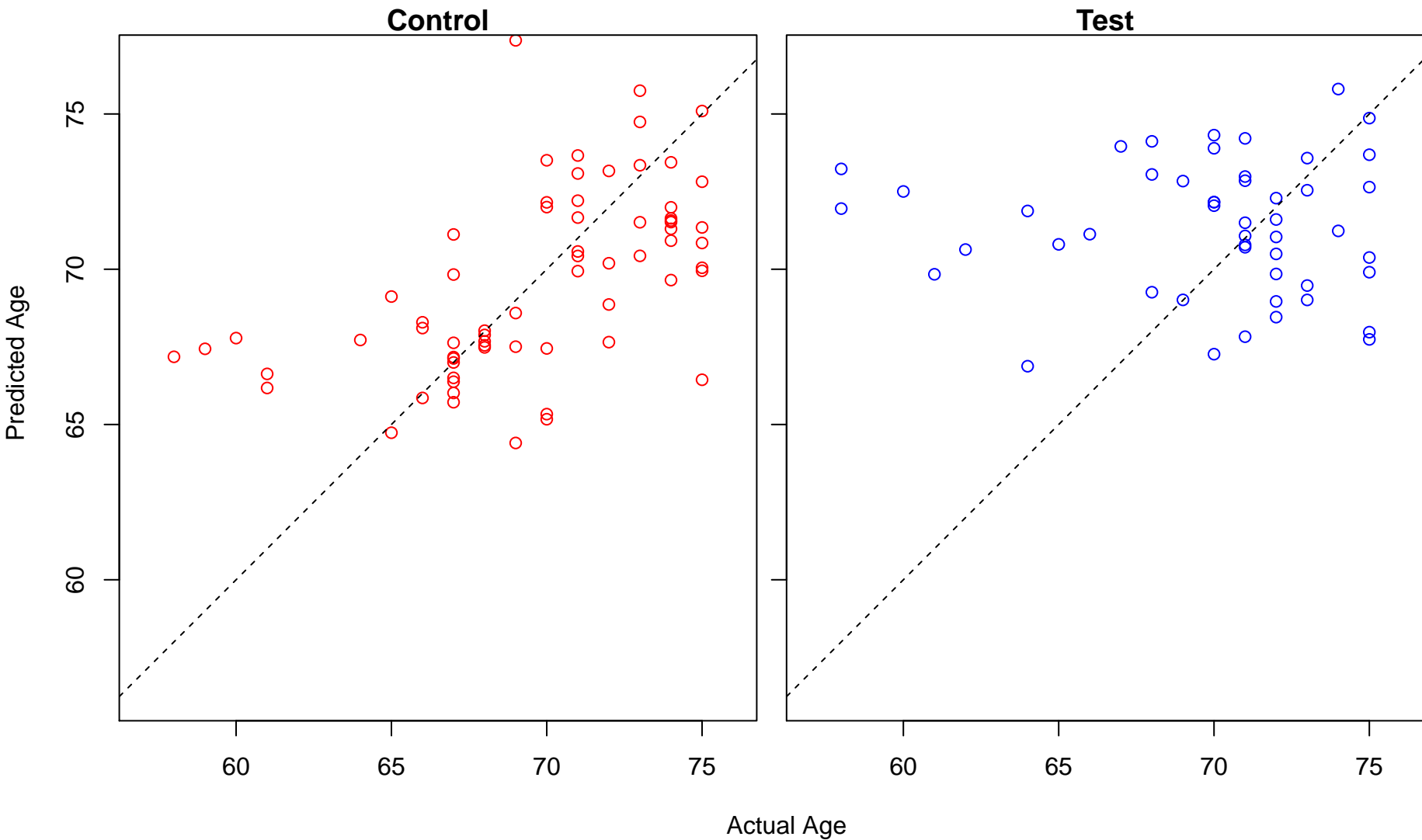
positive regulation of interleukin-1 beta secretion (Score: 1.013561)



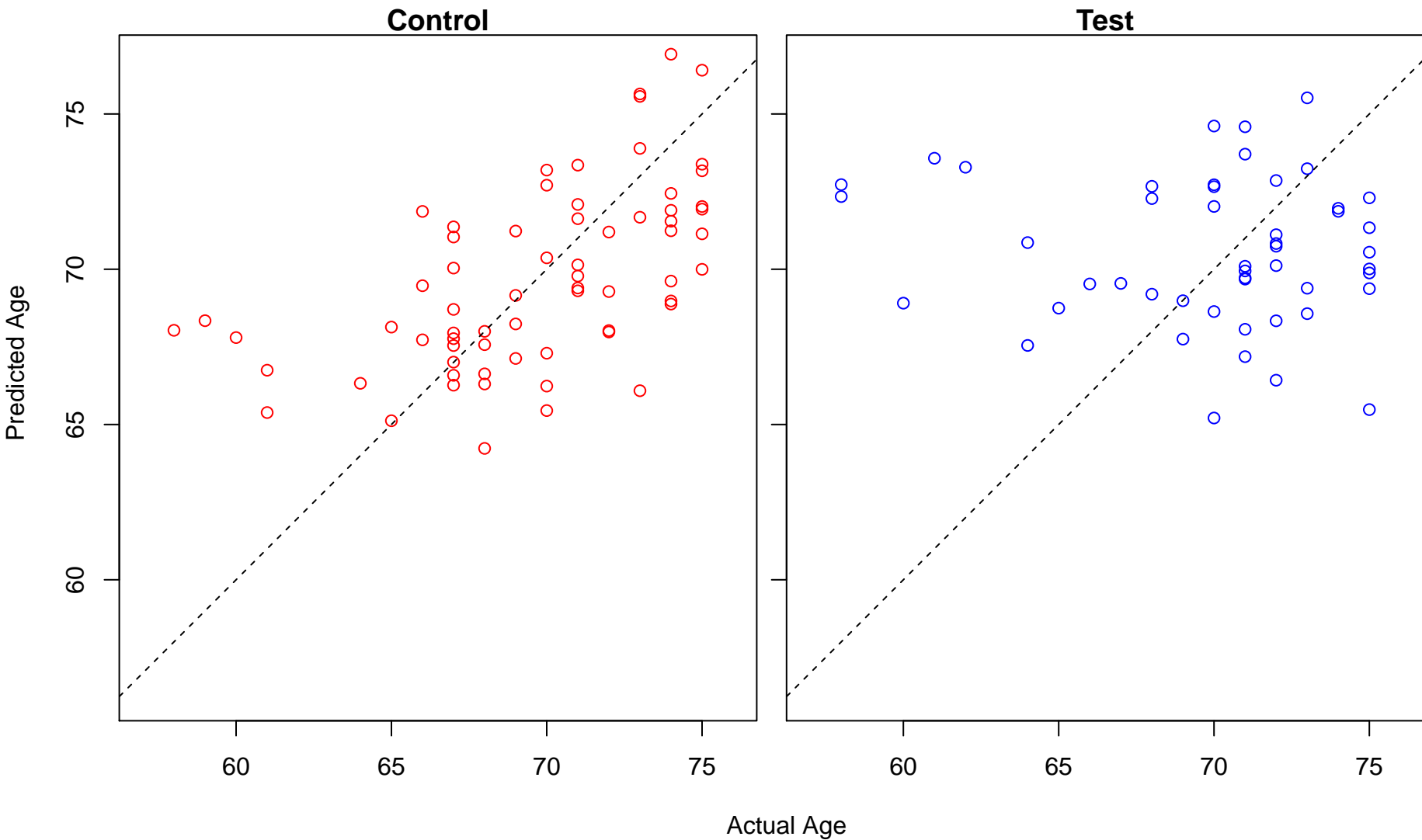
negative regulation of myosin–light–chain–phosphatase activity (Score: 1.013560)



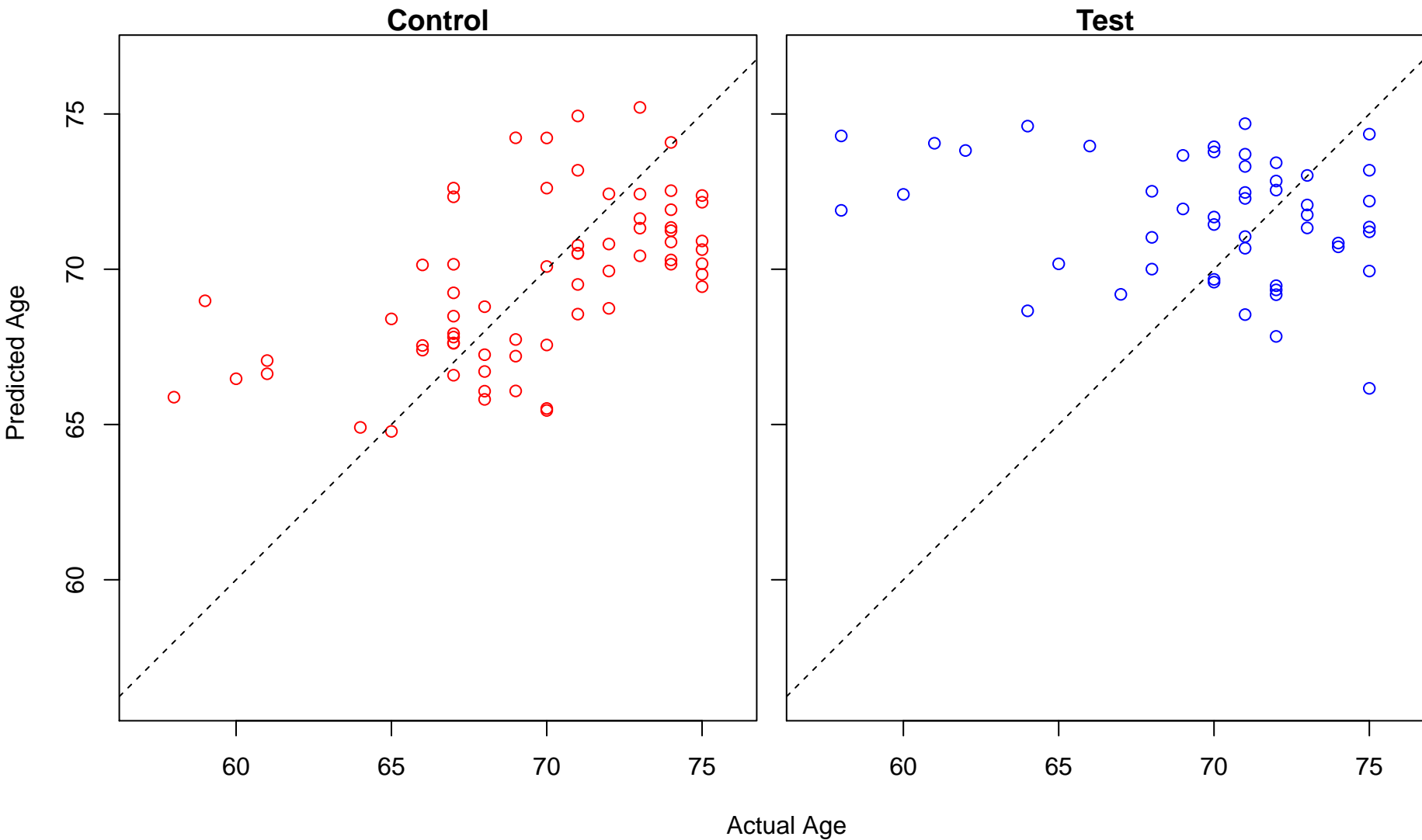
phototransduction (Score: 1.012767)



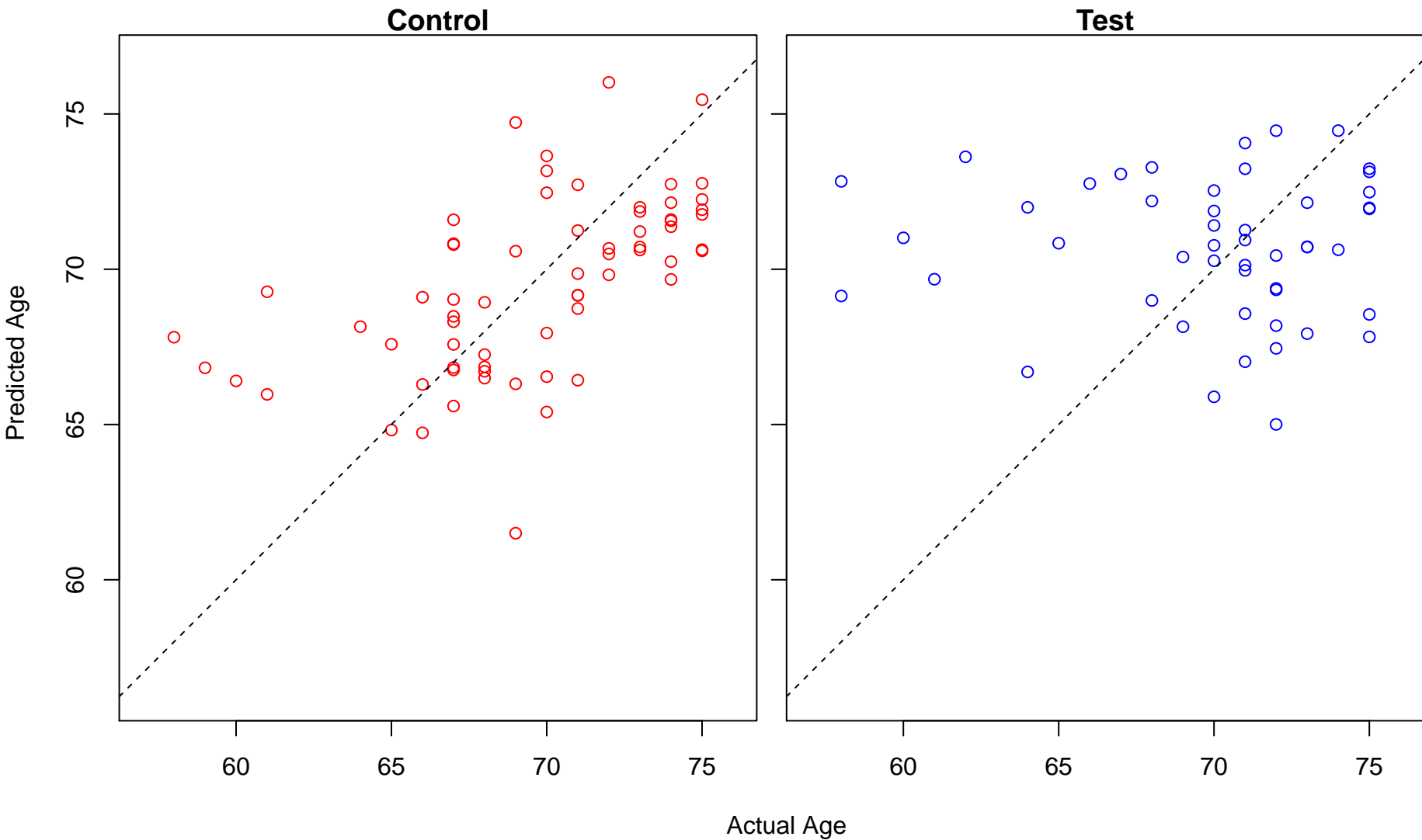
regulation of actin filament depolymerization (Score: 1.012313)



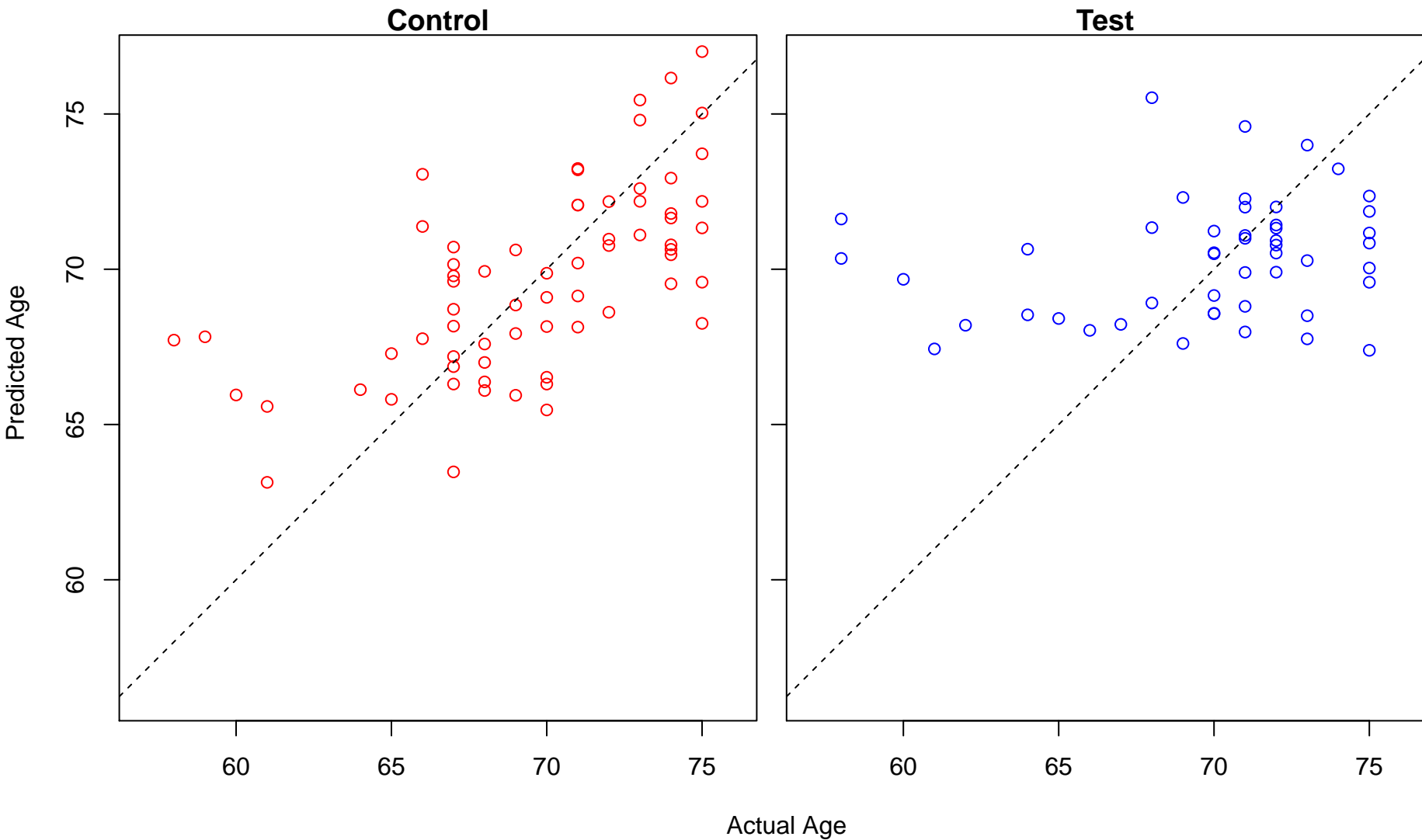
specification of symmetry (Score: 1.012249)



positive regulation of ERAD pathway (Score: 1.012151)

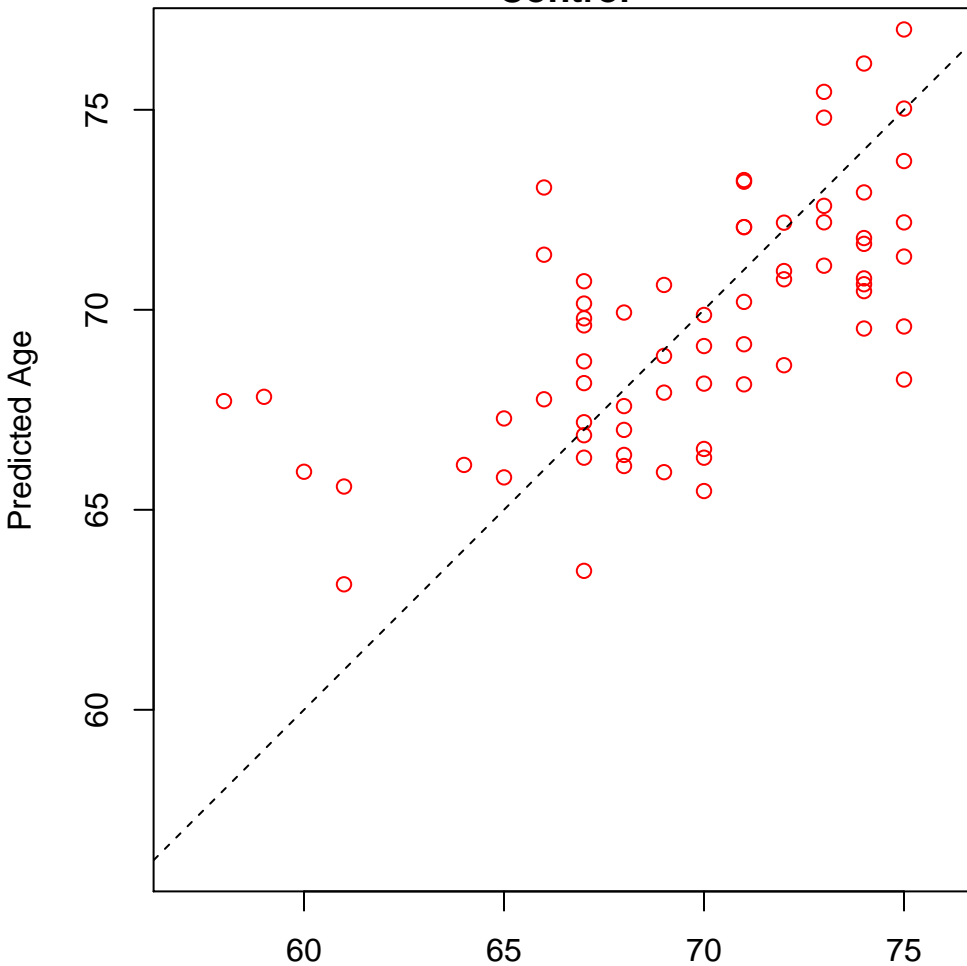


regulation of exosomal secretion (Score: 1.011792)

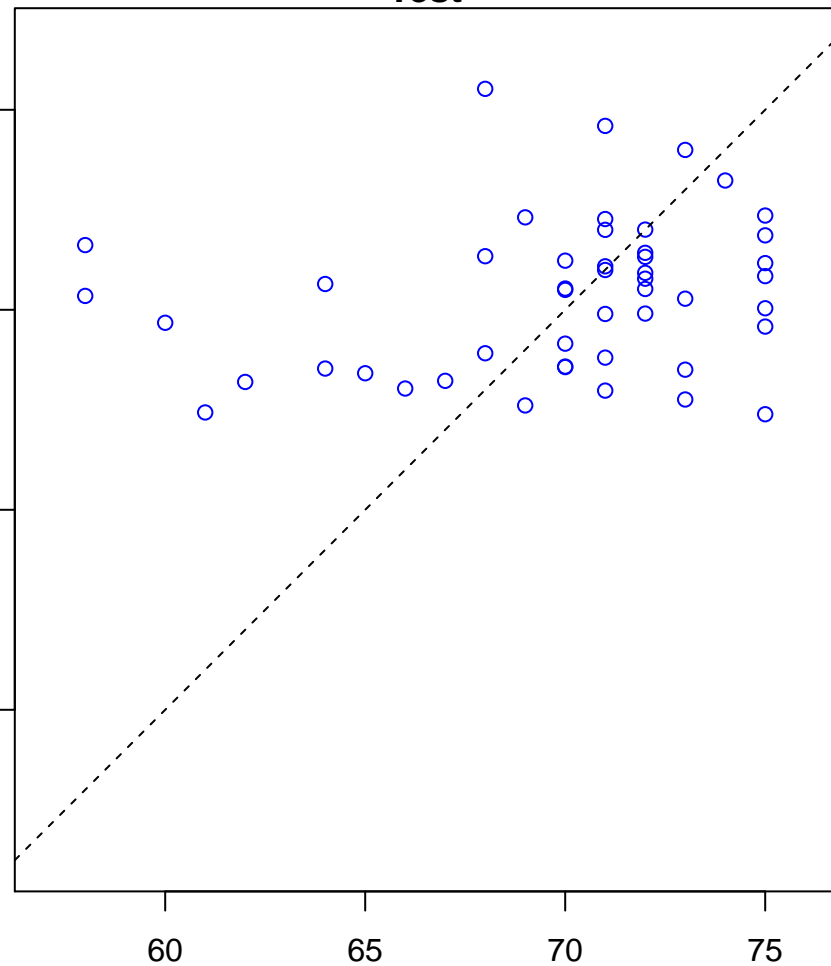


positive regulation of exosomal secretion (Score: 1.011792)

Control

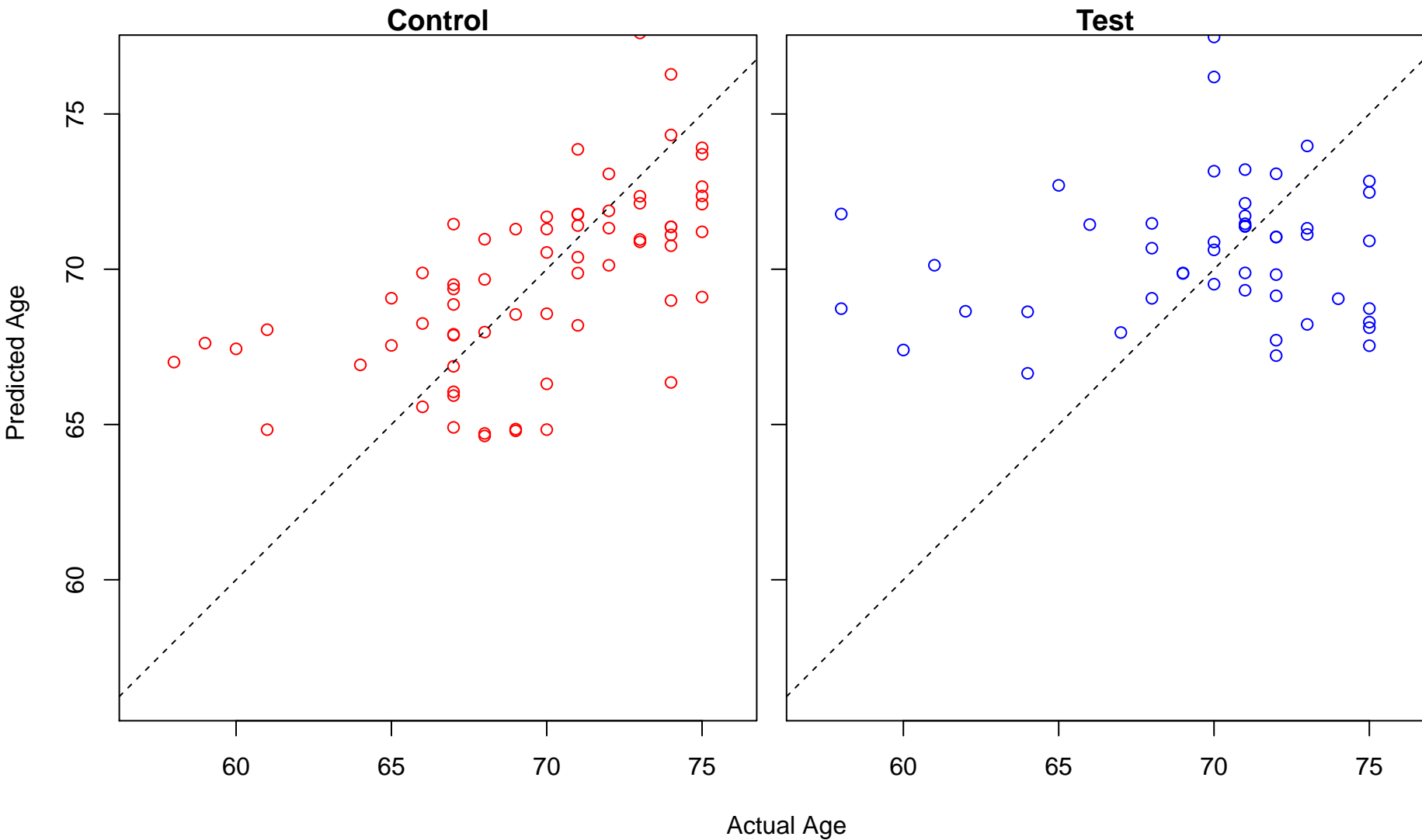


Test

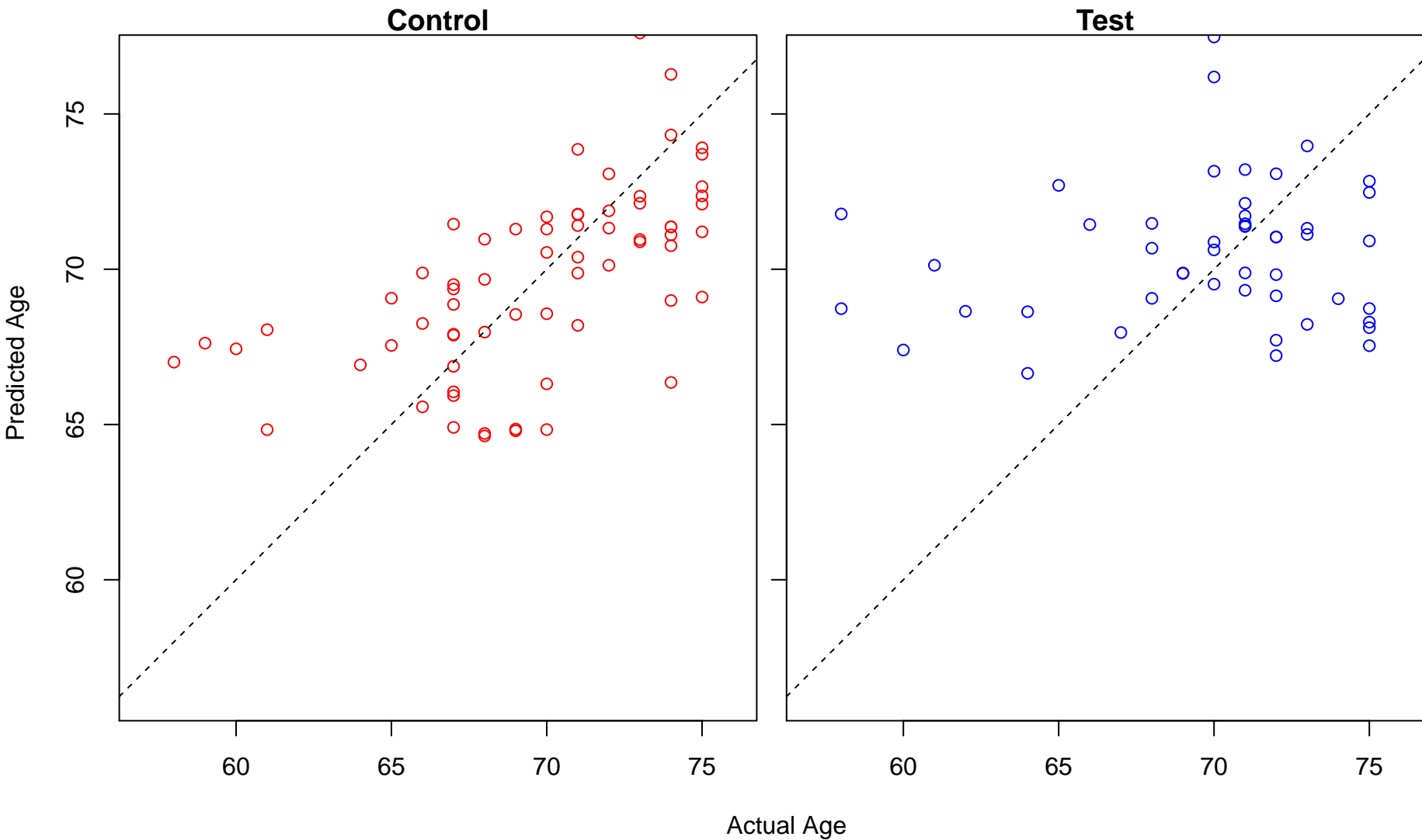


Actual Age

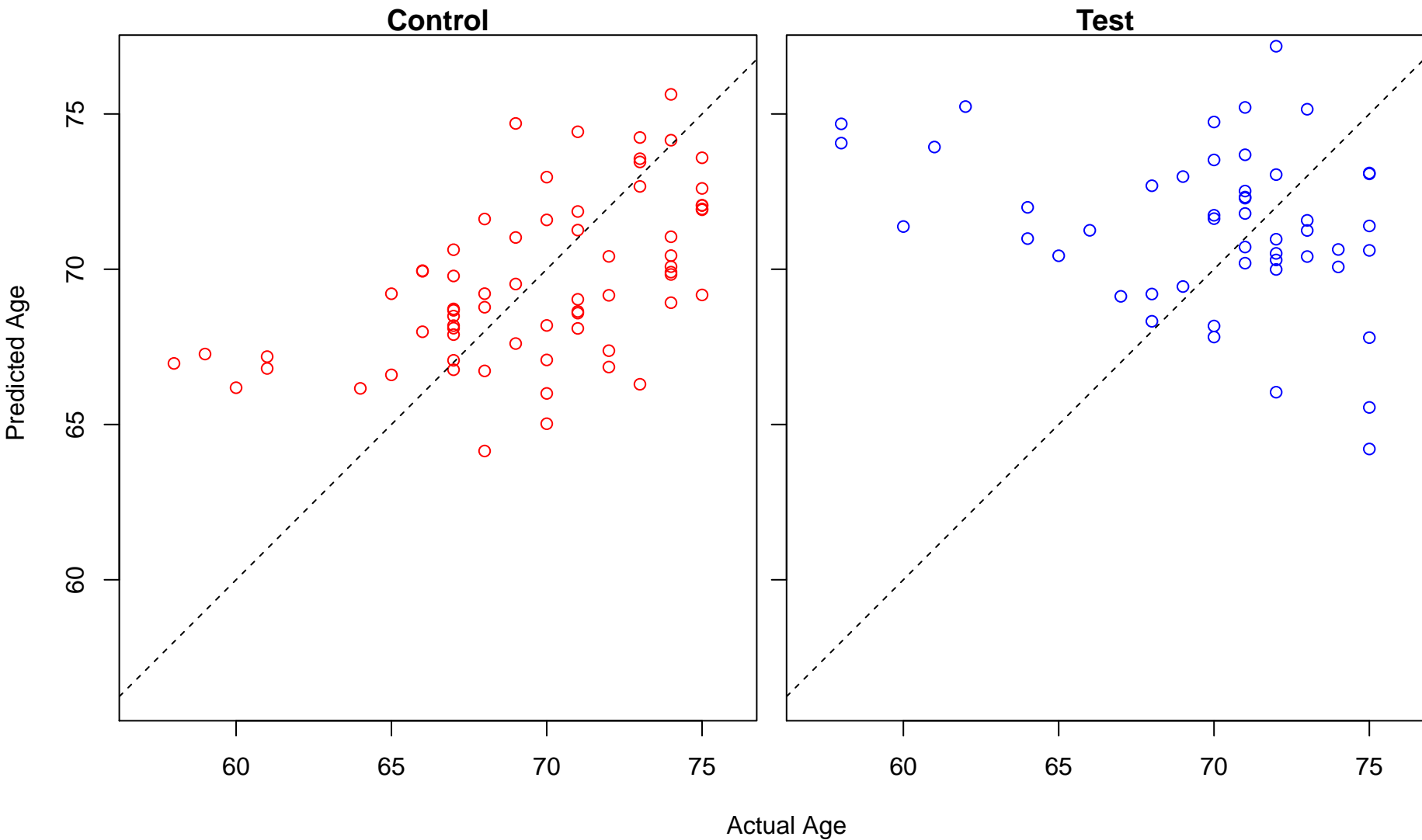
neutral lipid catabolic process (Score: 1.011679)



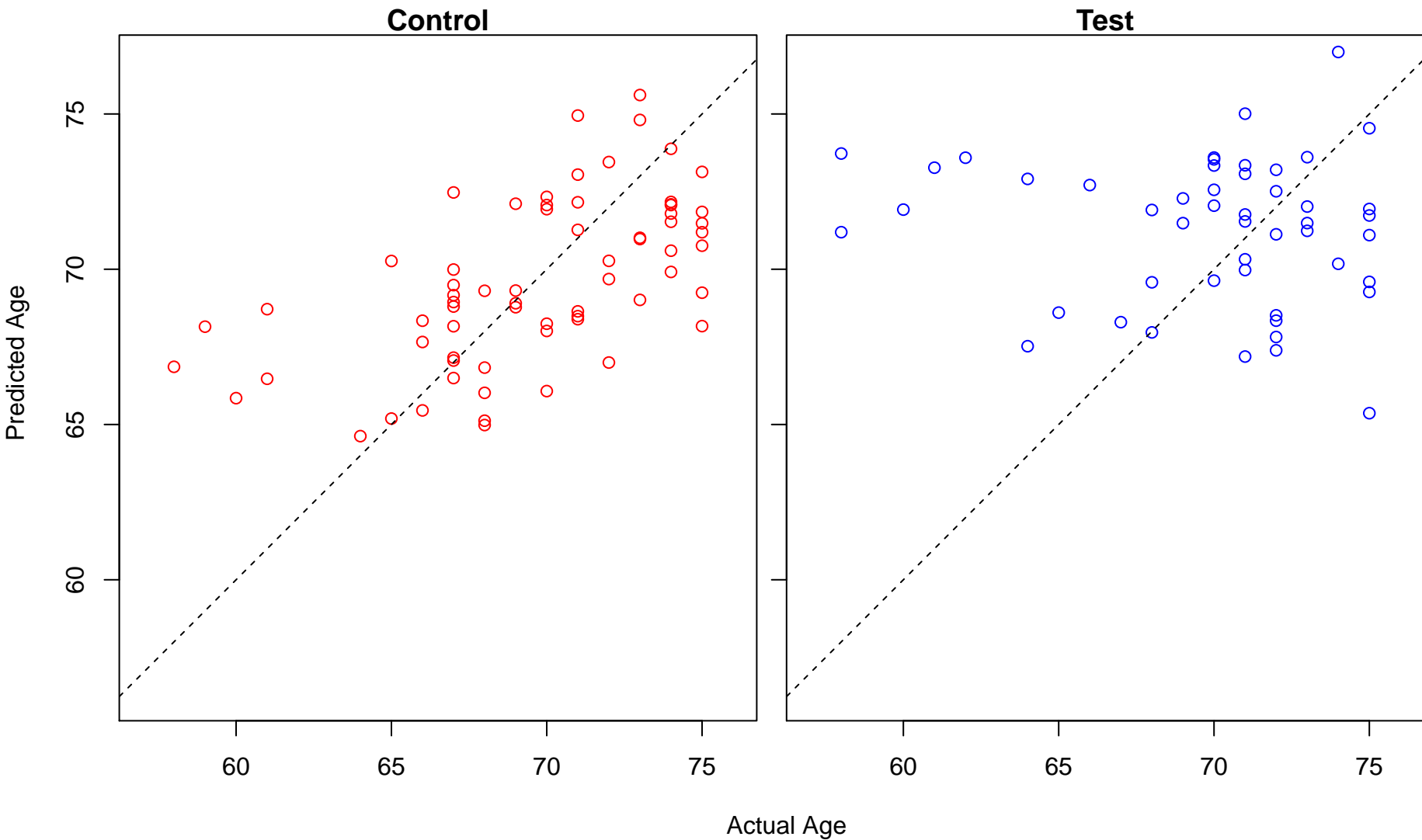
acylglycerol catabolic process (Score: 1.011679)



negative regulation of inclusion body assembly (Score: 1.011463)

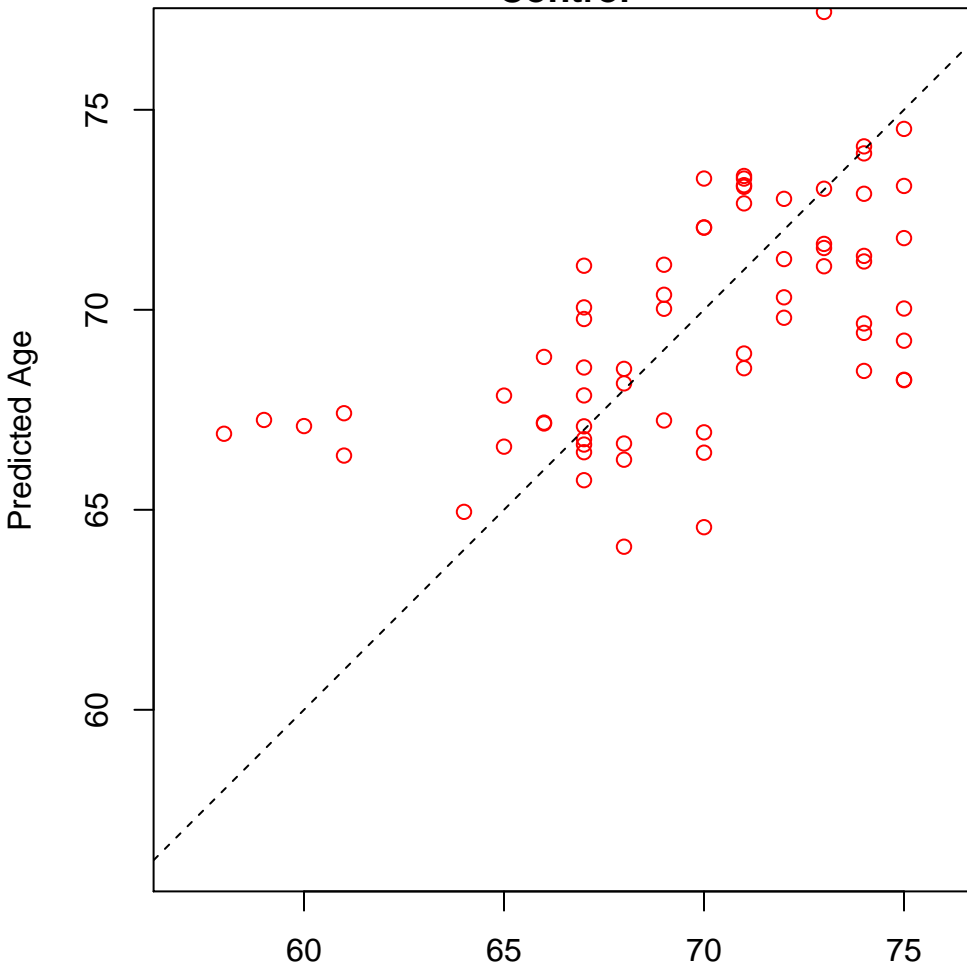


regulation of oligodendrocyte differentiation (Score: 1.011442)

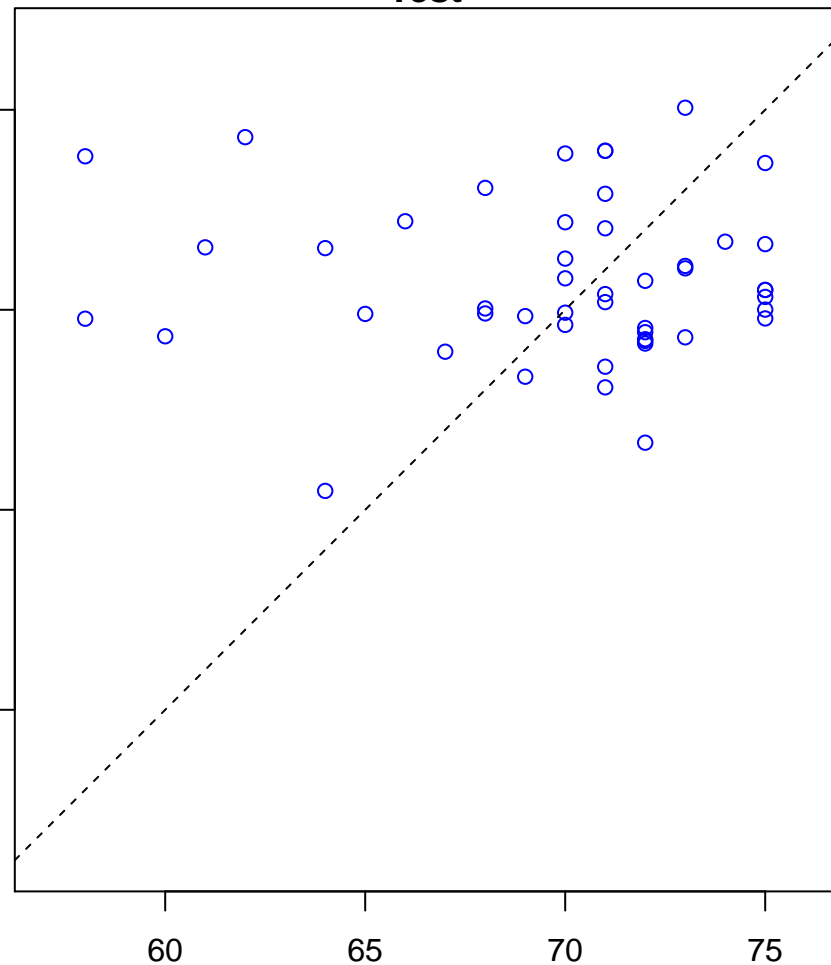


pyridine nucleotide metabolic process (Score: 1.011296)

Control

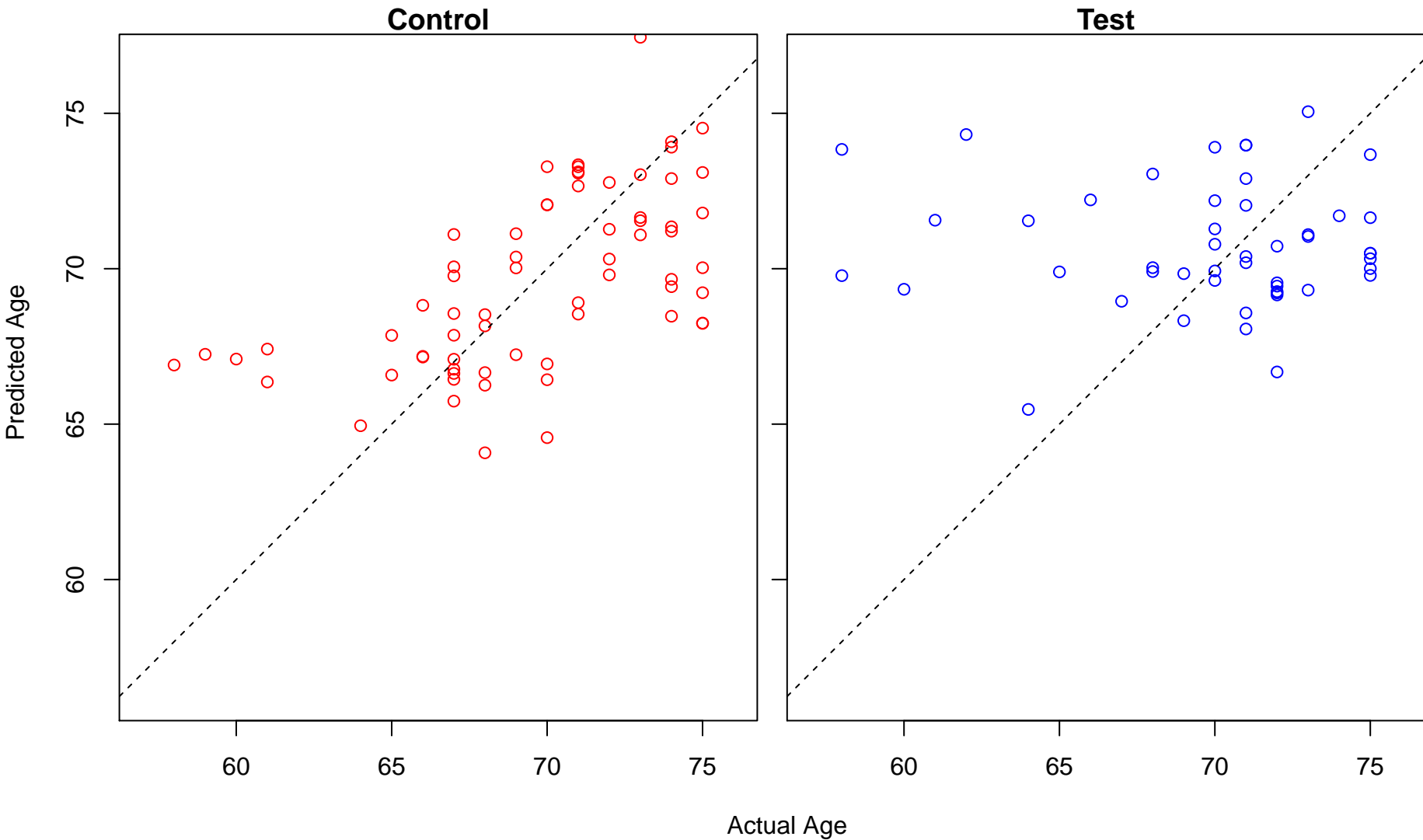


Test

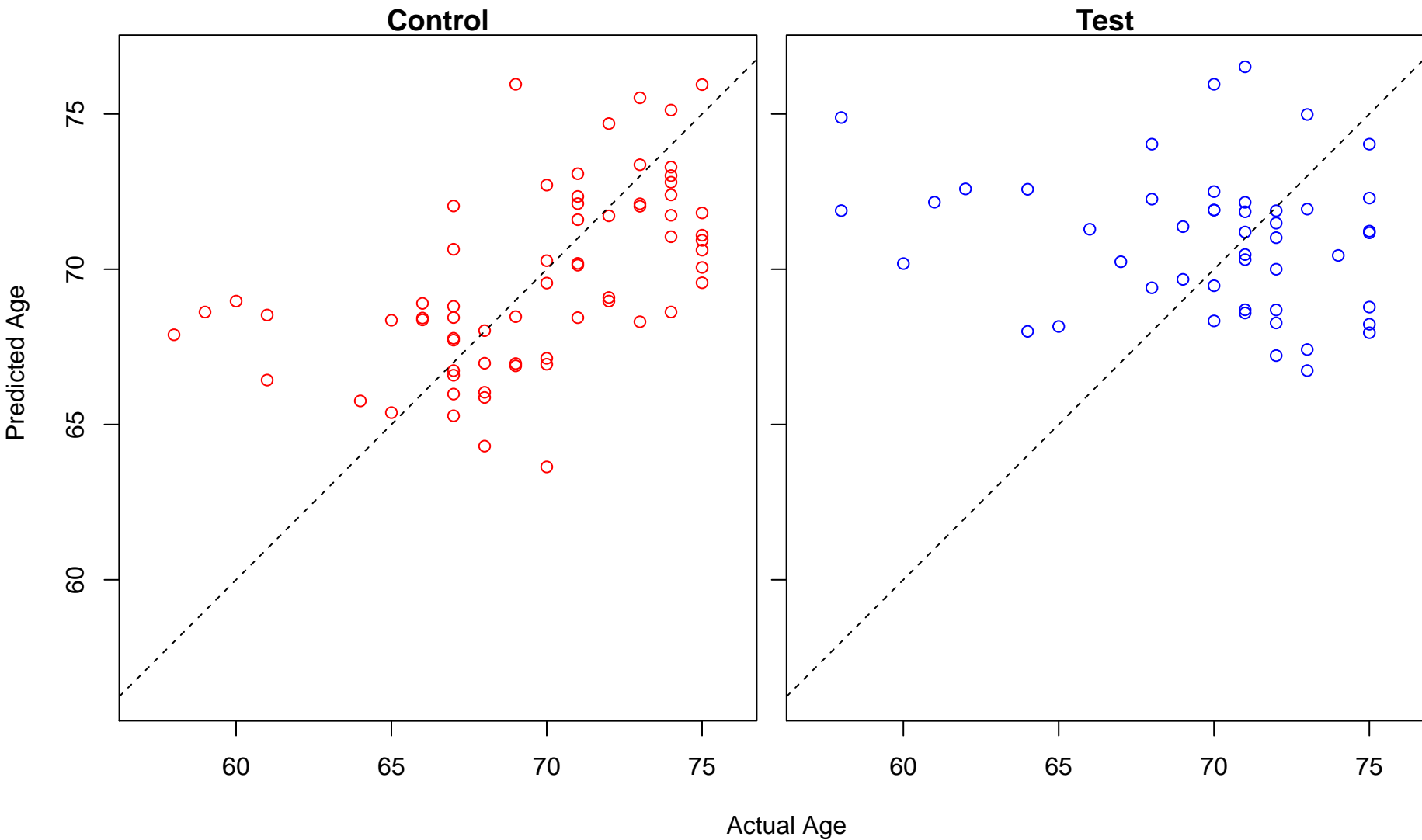


Actual Age

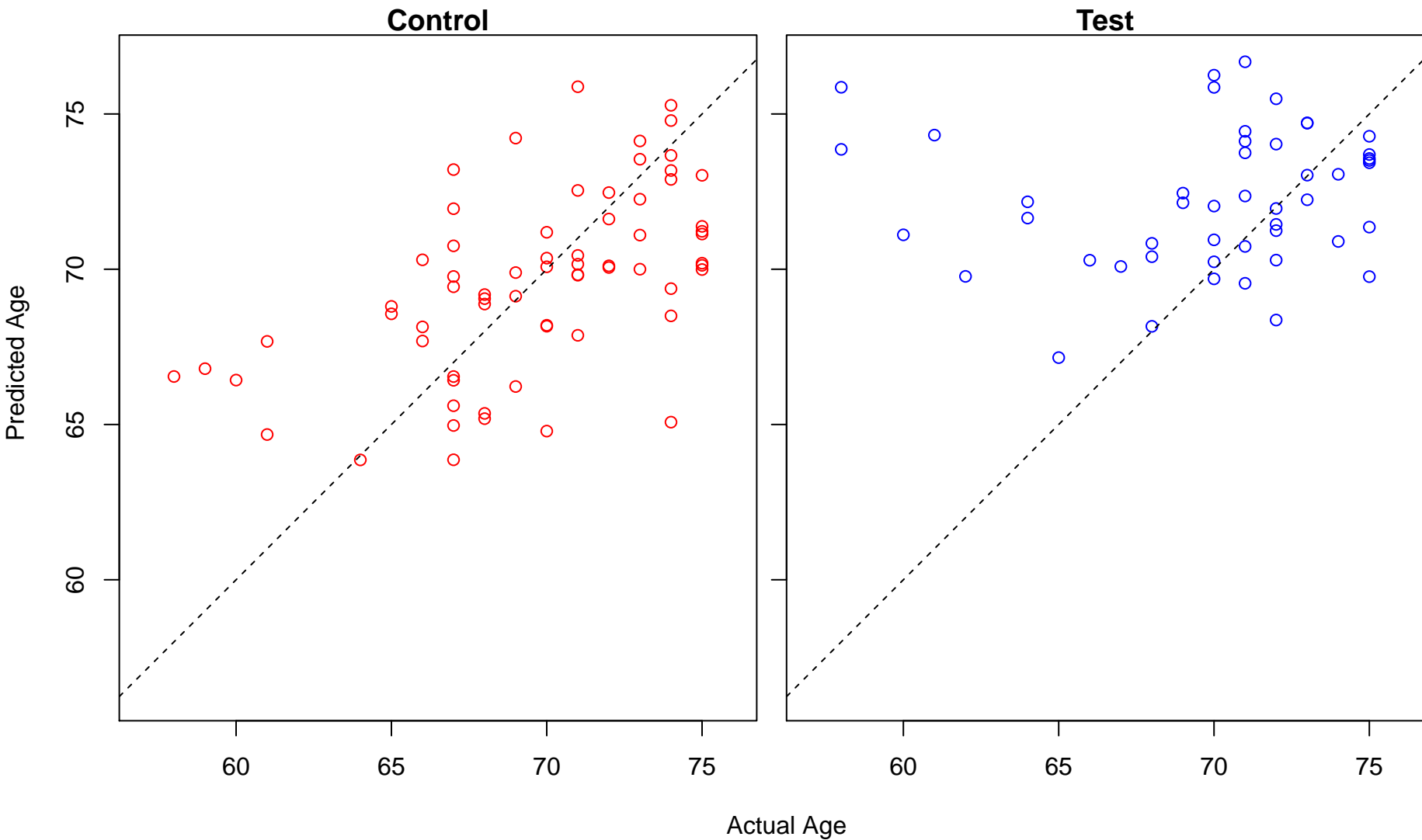
nicotinamide nucleotide metabolic process (Score: 1.011296)



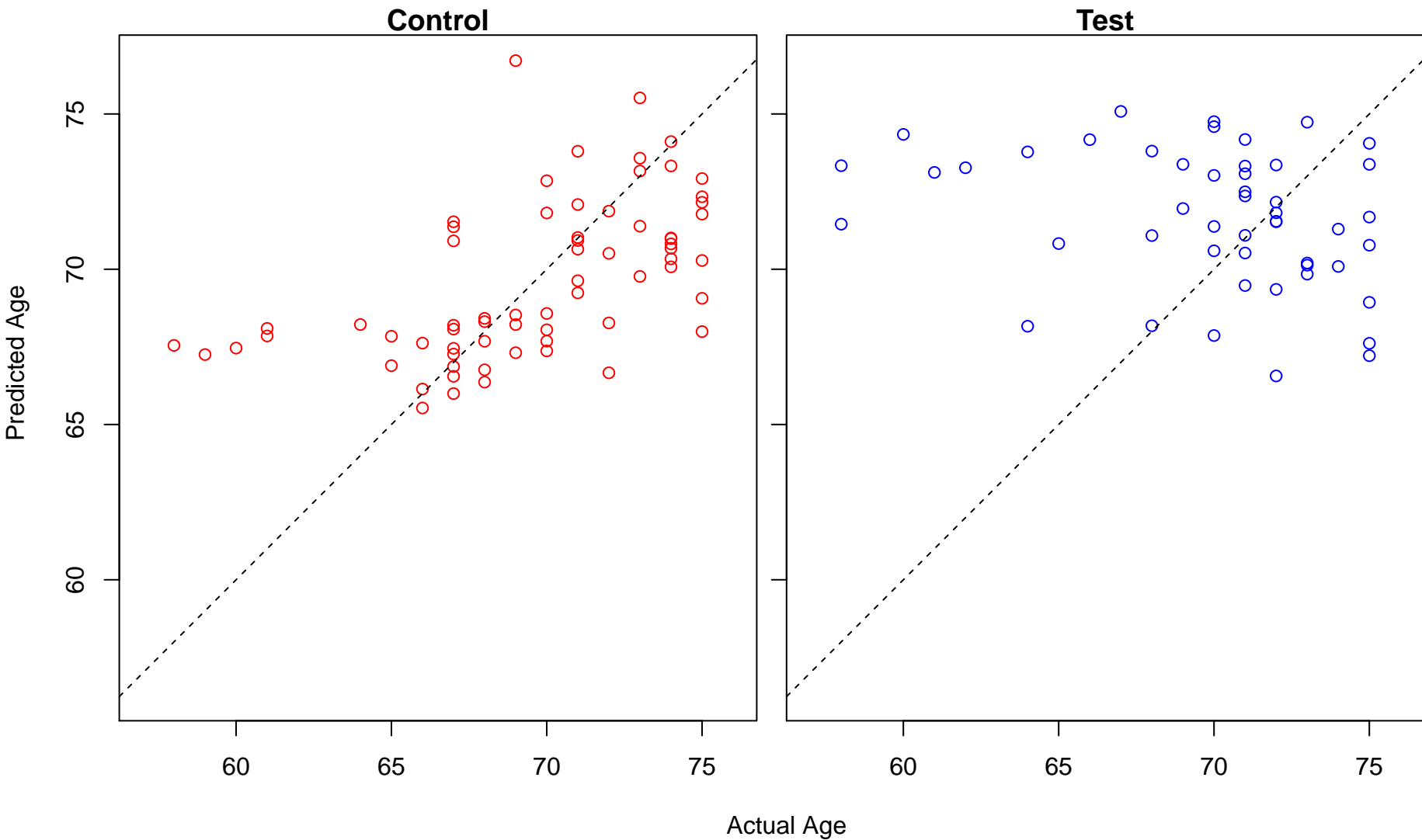
regulation of RIG-I signaling pathway (Score: 1.011055)



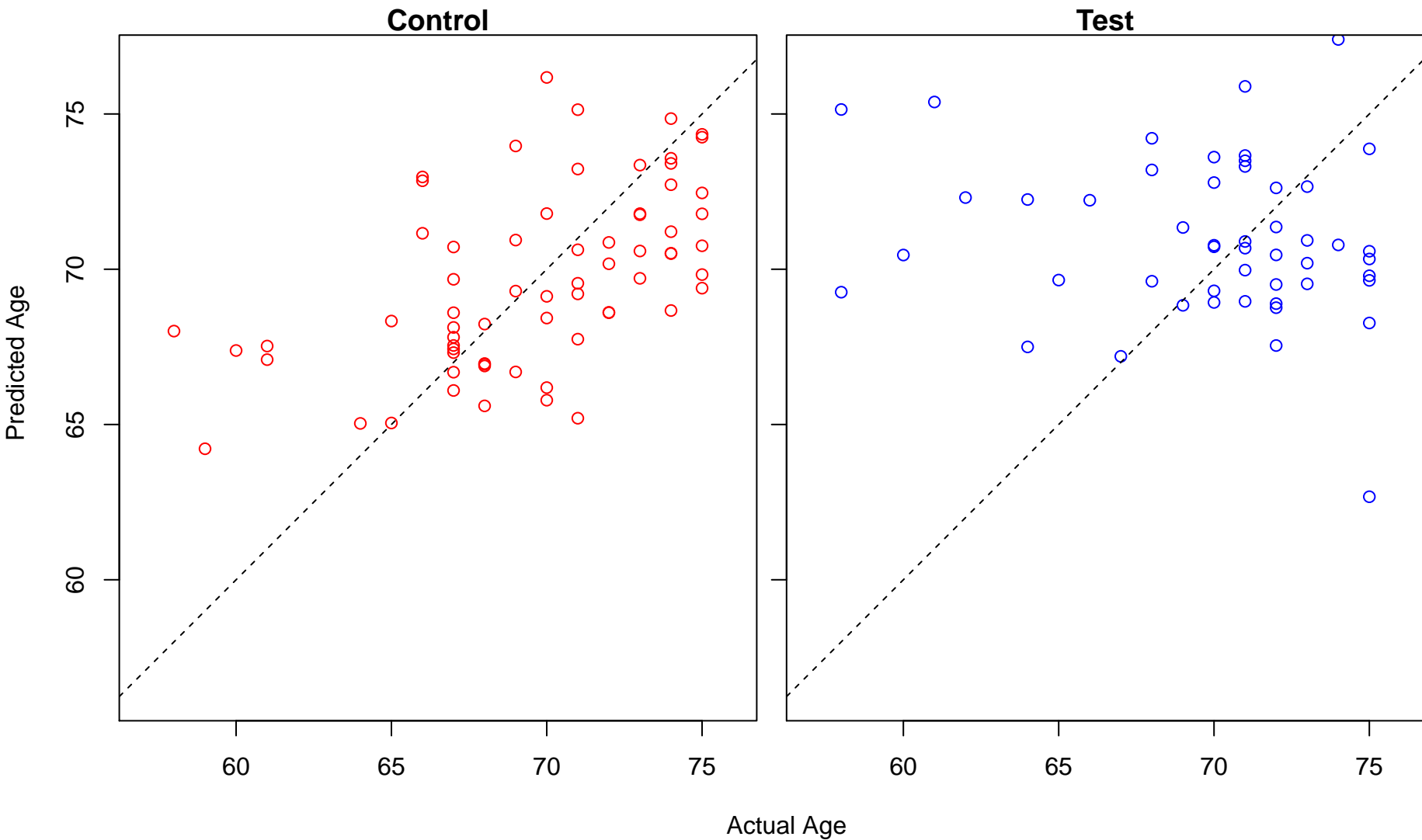
regulation of actin filament-based movement (Score: 1.010212)



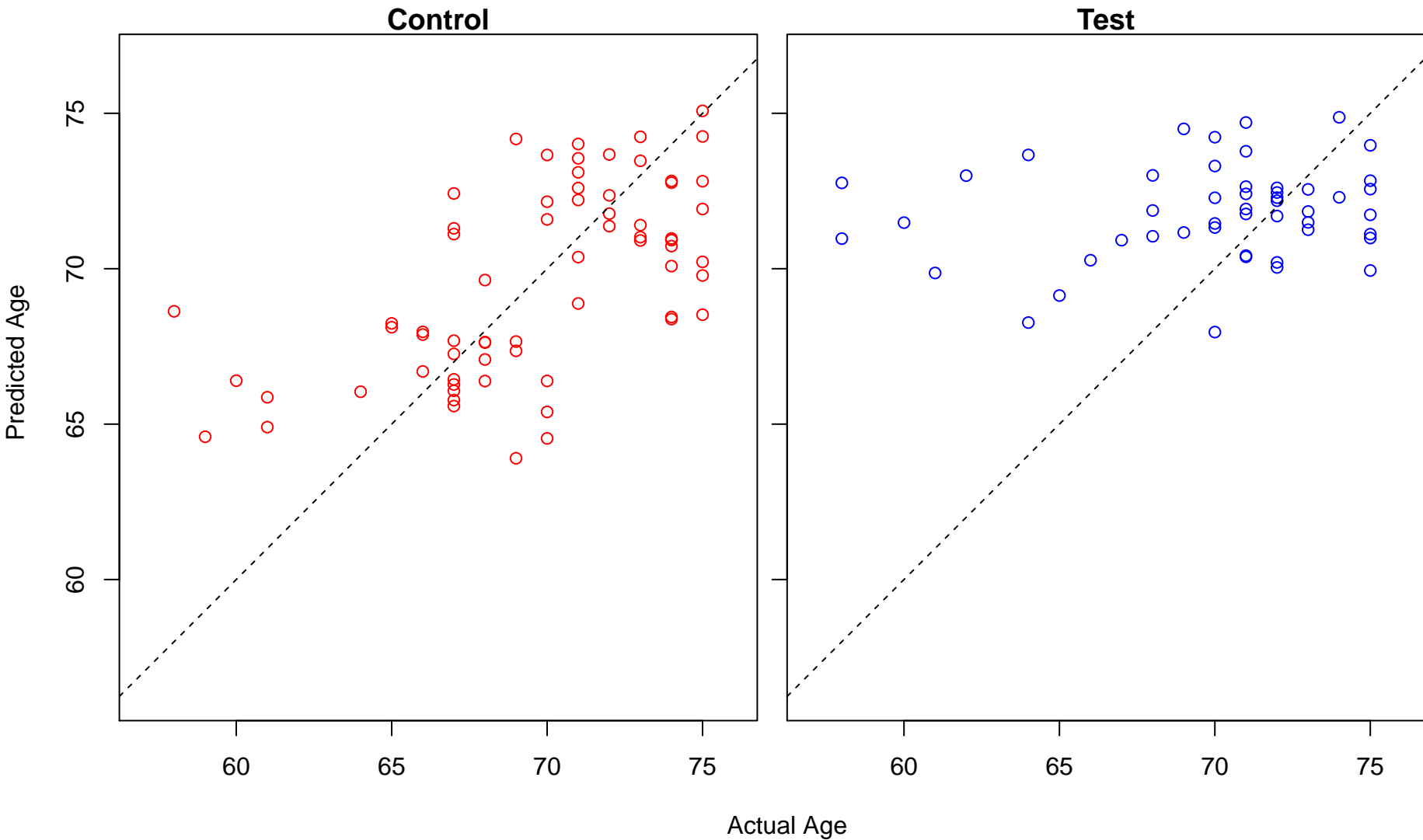
cellular response to glucocorticoid stimulus (Score: 1.009242)



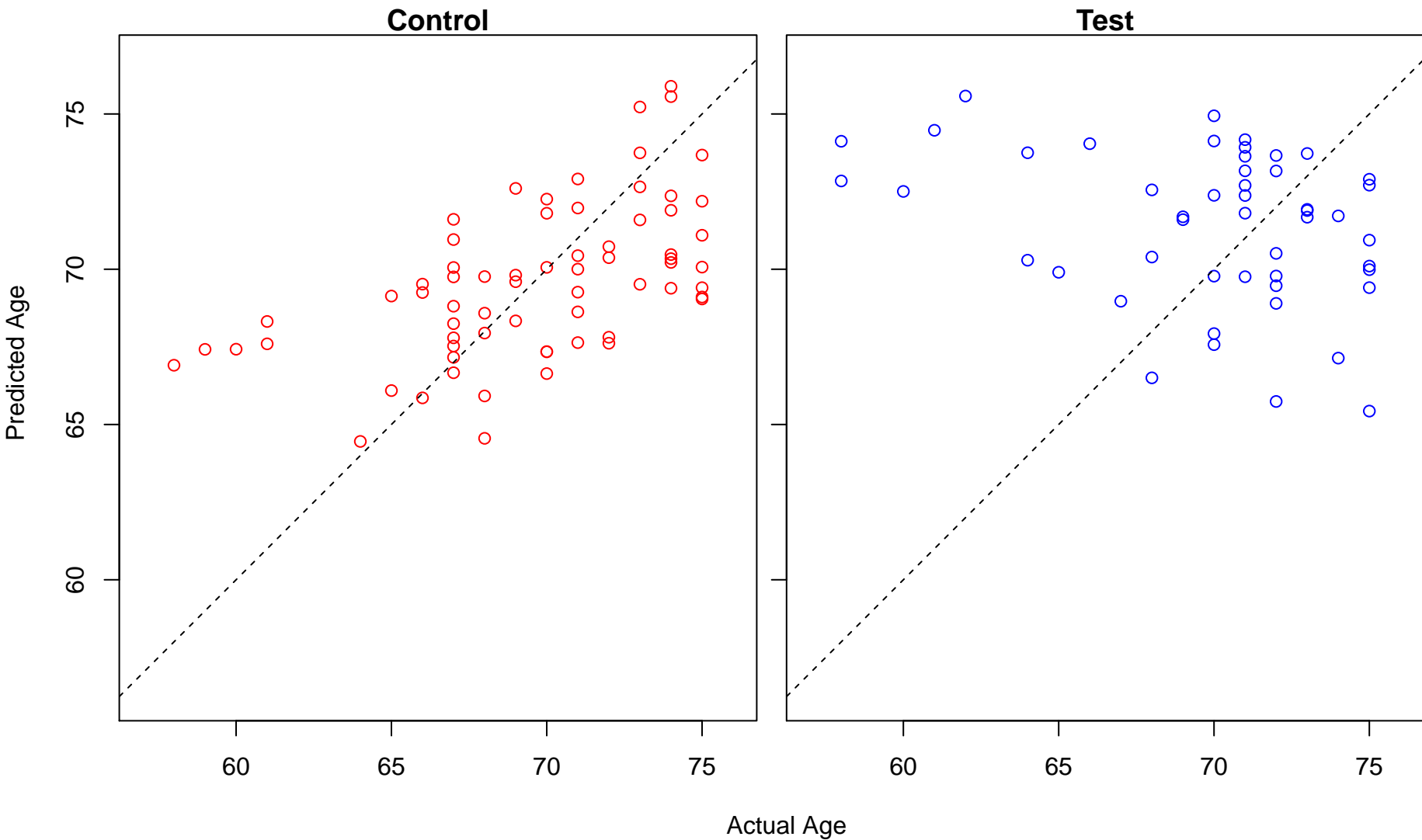
DNA deamination (Score: 1.008911)



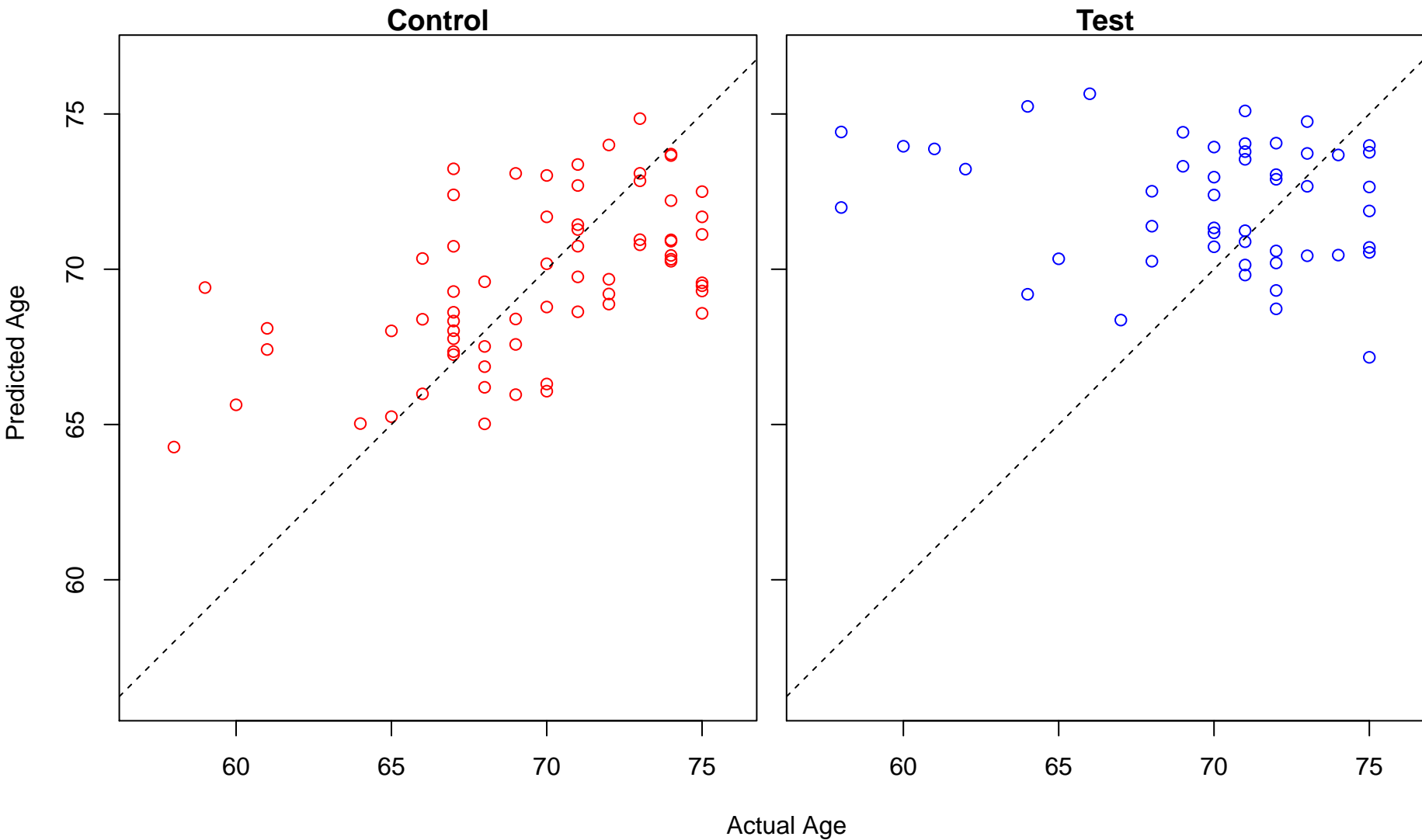
positive regulation of protein deacetylation (Score: 1.008805)



regulation of beta-amyloid formation (Score: 1.007708)



cardiocyte differentiation (Score: 1.007139)

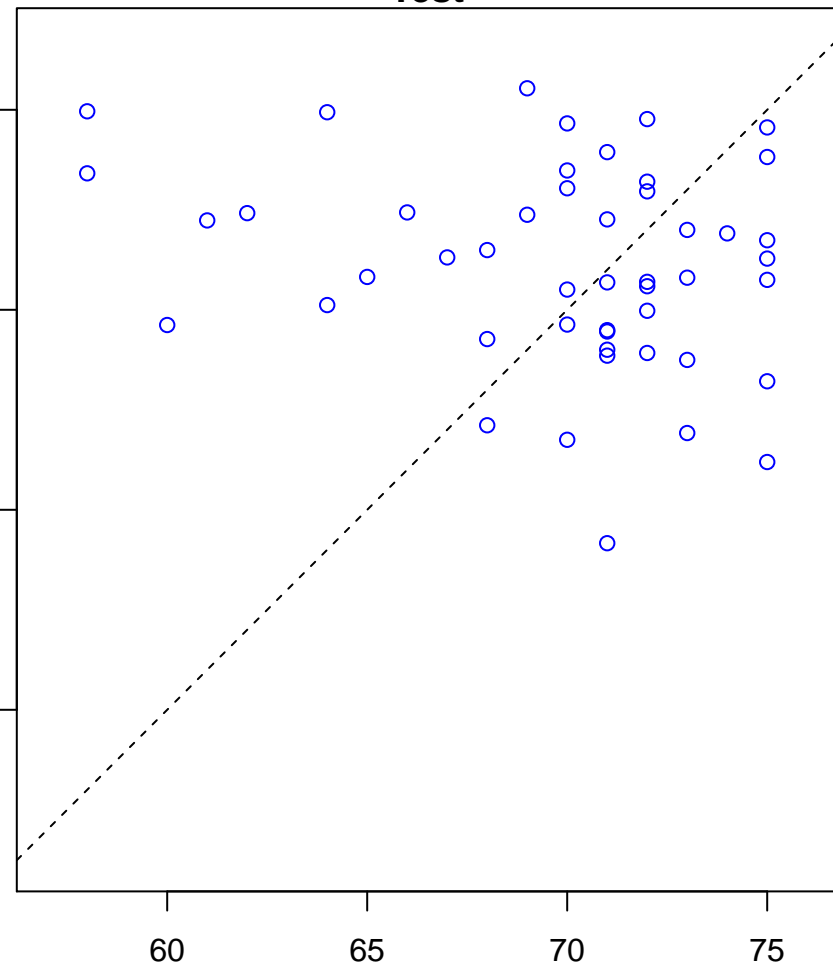
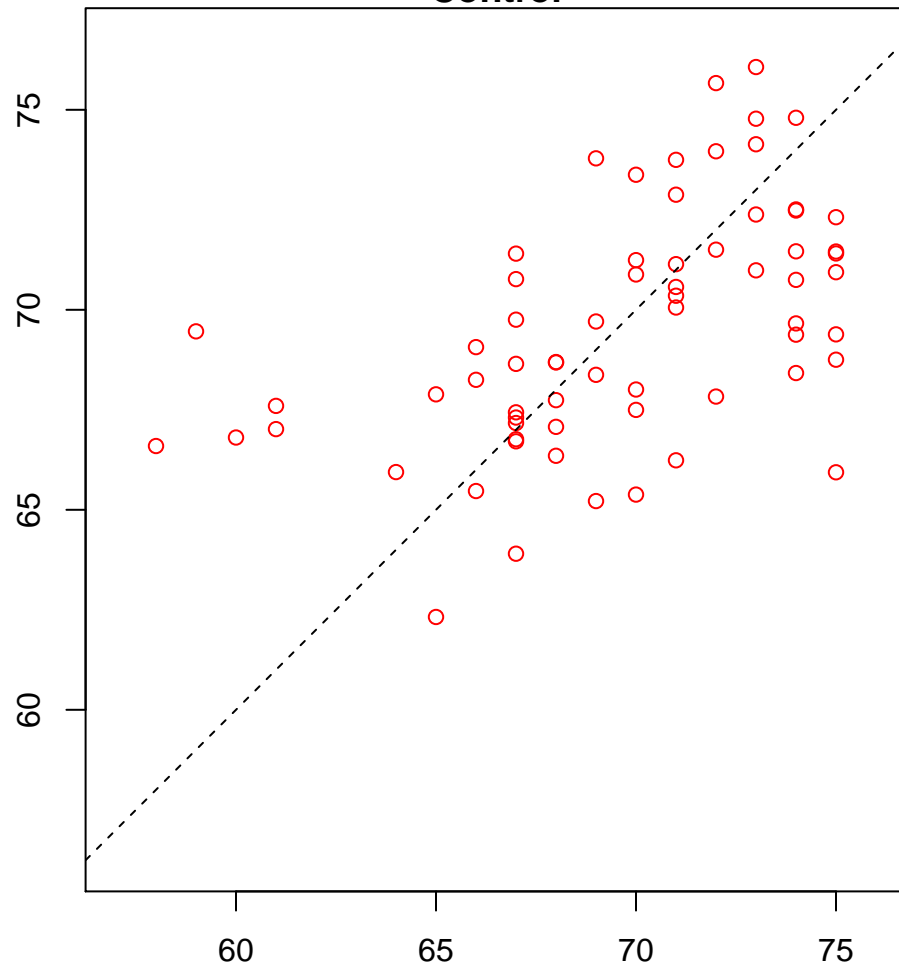


CD4-positive, alpha-beta T cell activation (Score: 1.006562)

Control

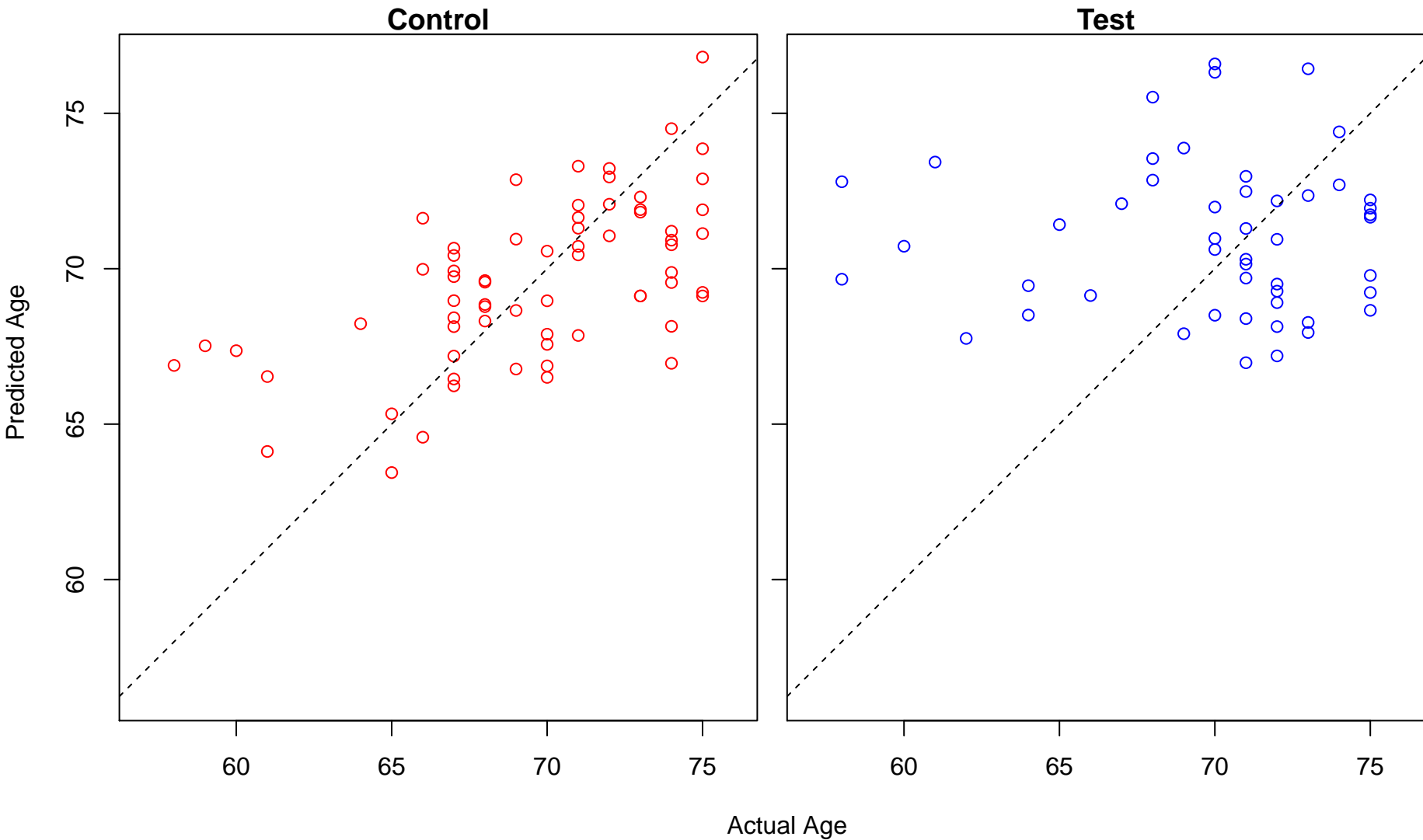
Test

Predicted Age

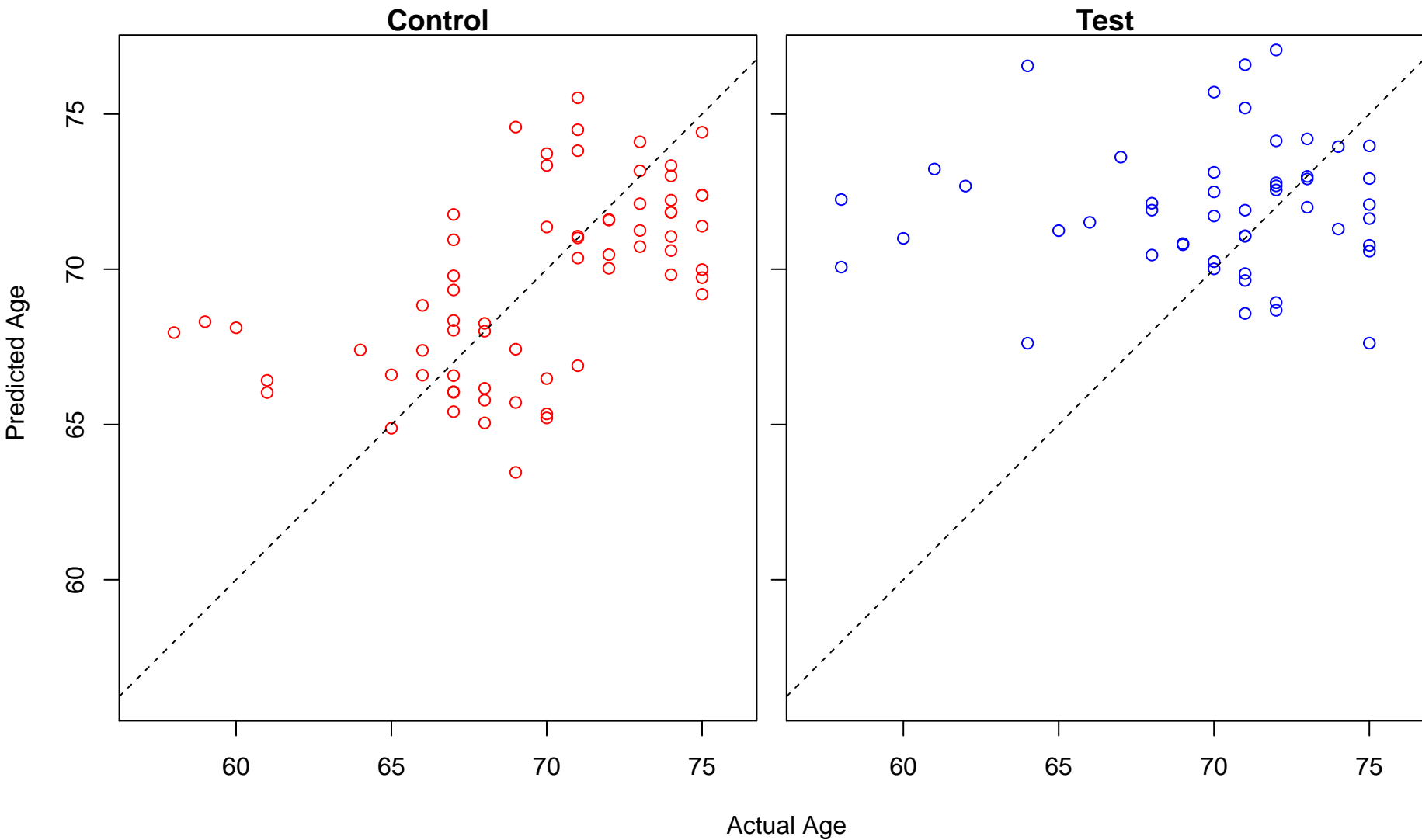


Actual Age

thrombin receptor signaling pathway (Score: 1.006439)

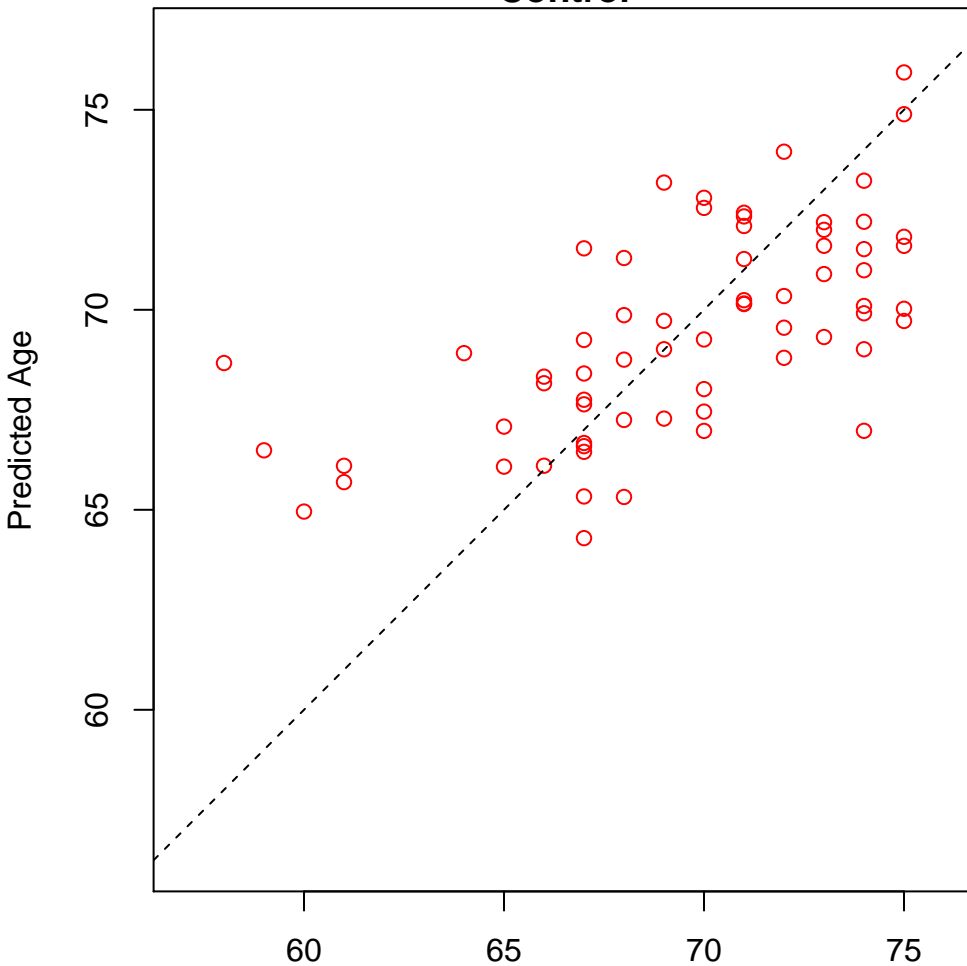


regulation of histone acetylation (Score: 1.006171)

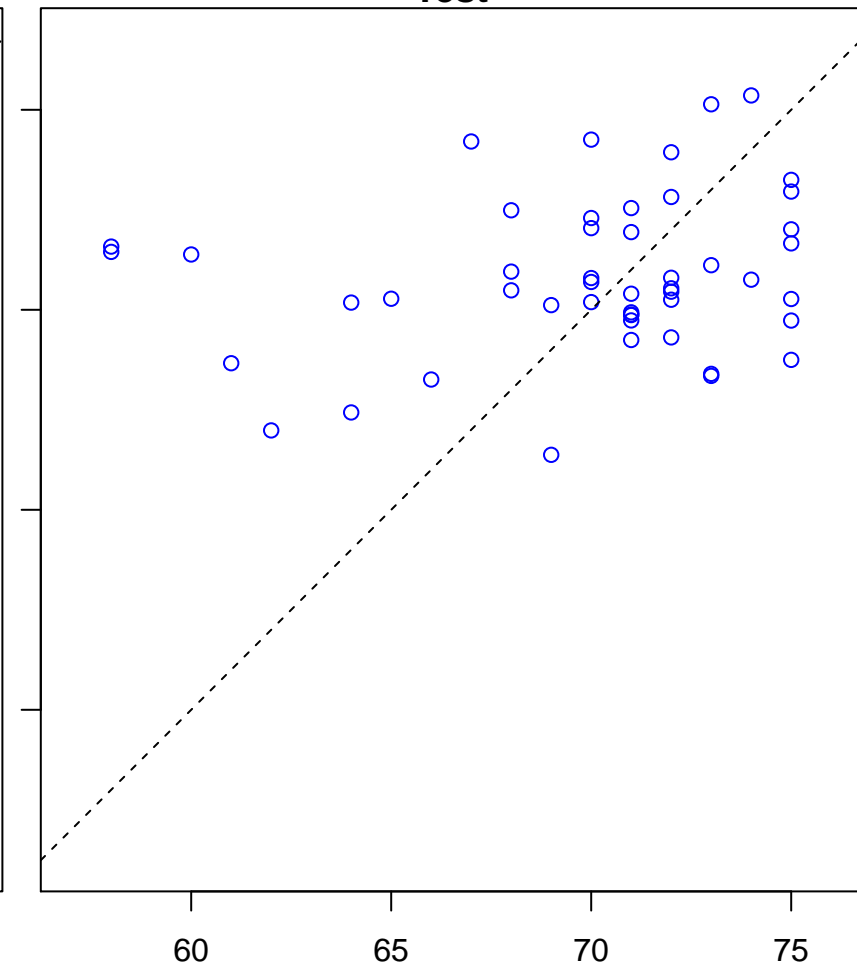


glycosphingolipid biosynthetic process (Score: 1.006073)

Control

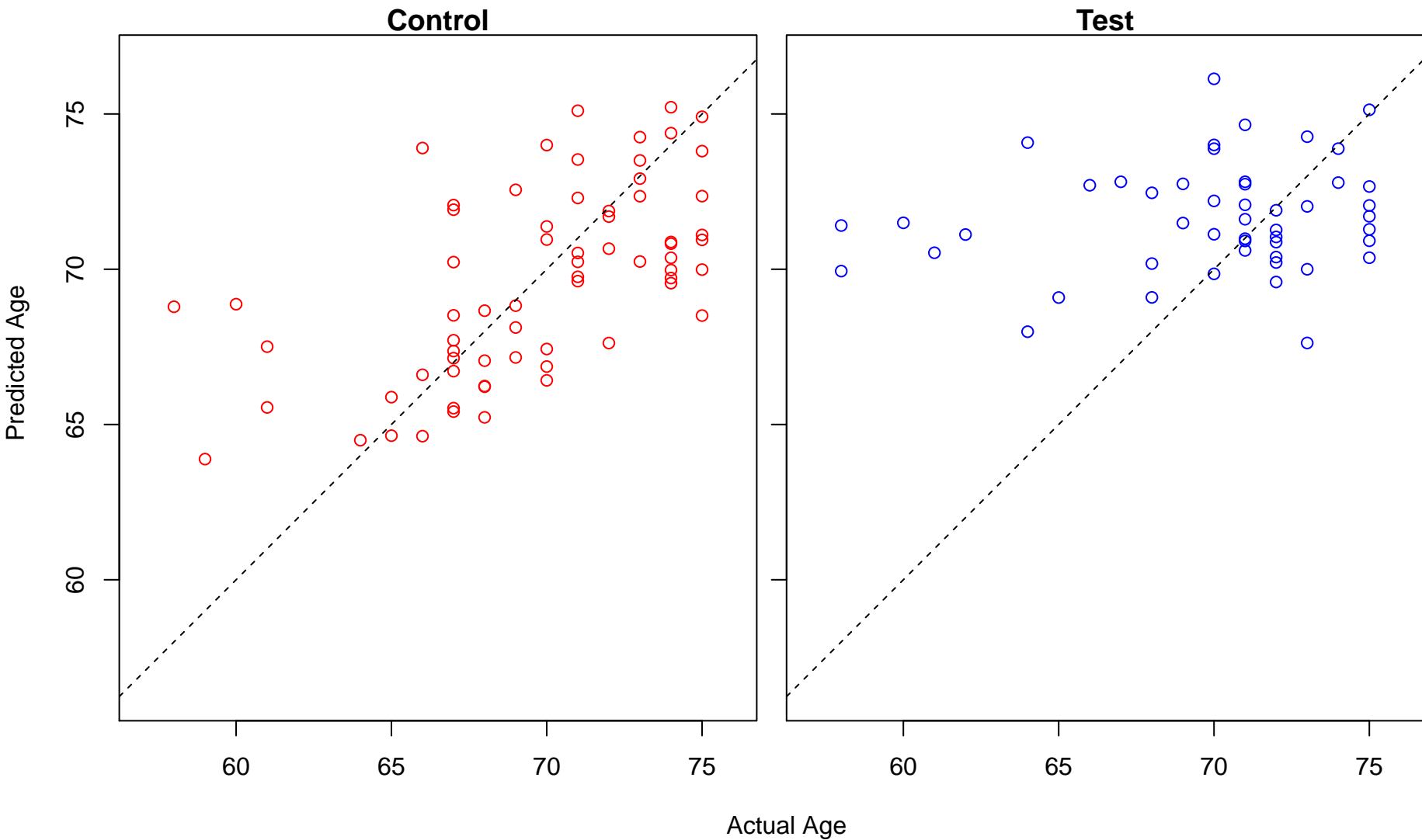


Test

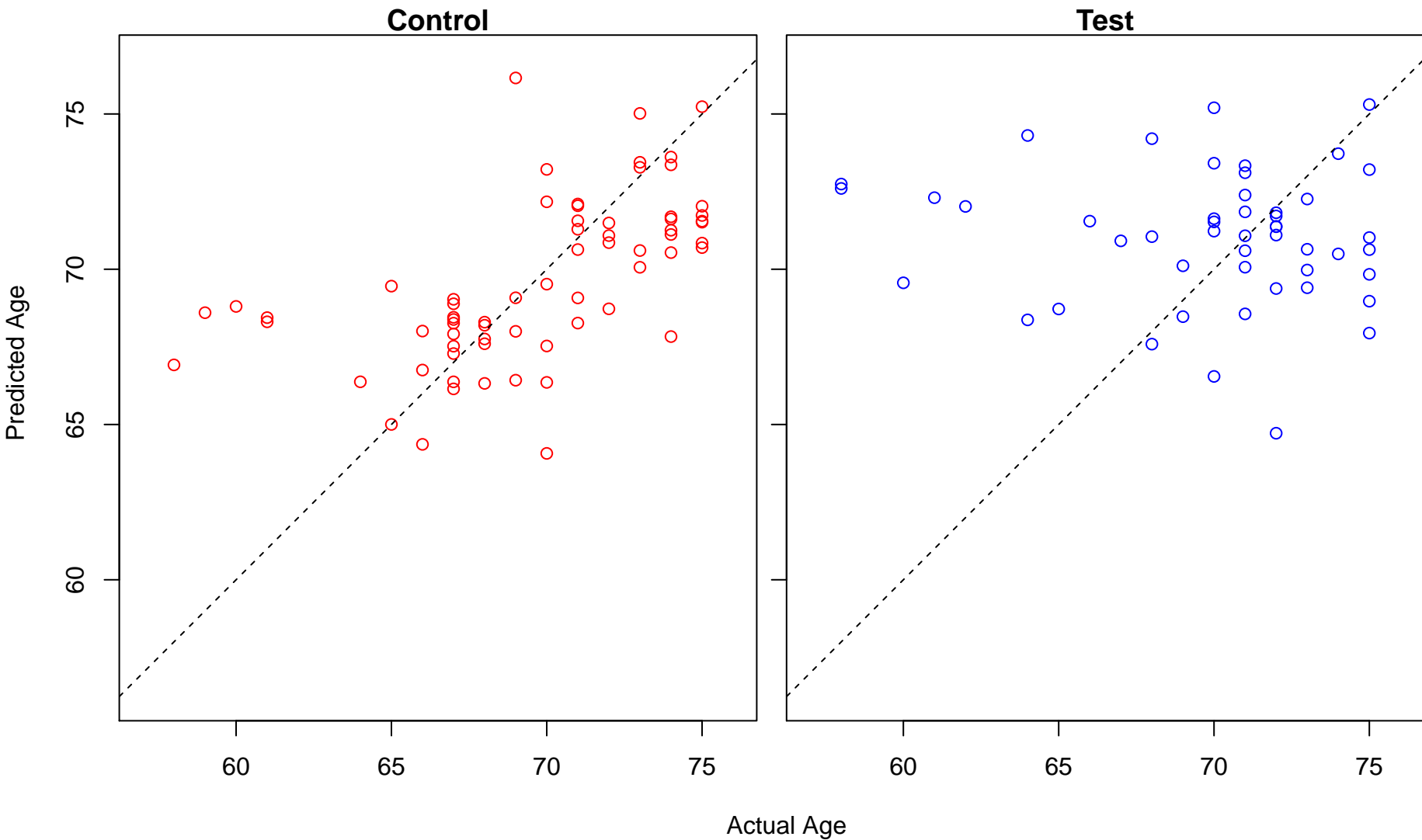


Actual Age

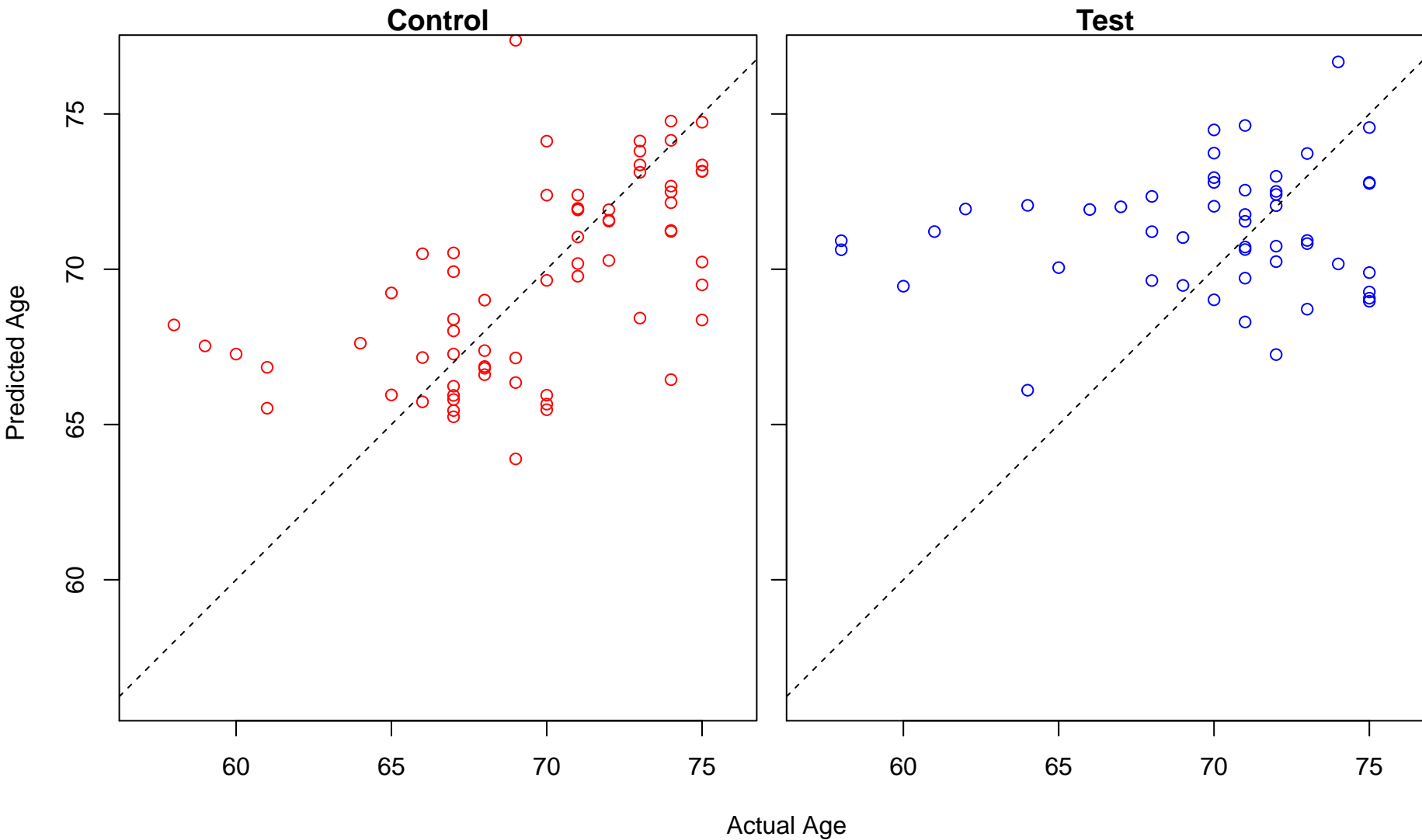
chondroitin sulfate catabolic process (Score: 1.005894)



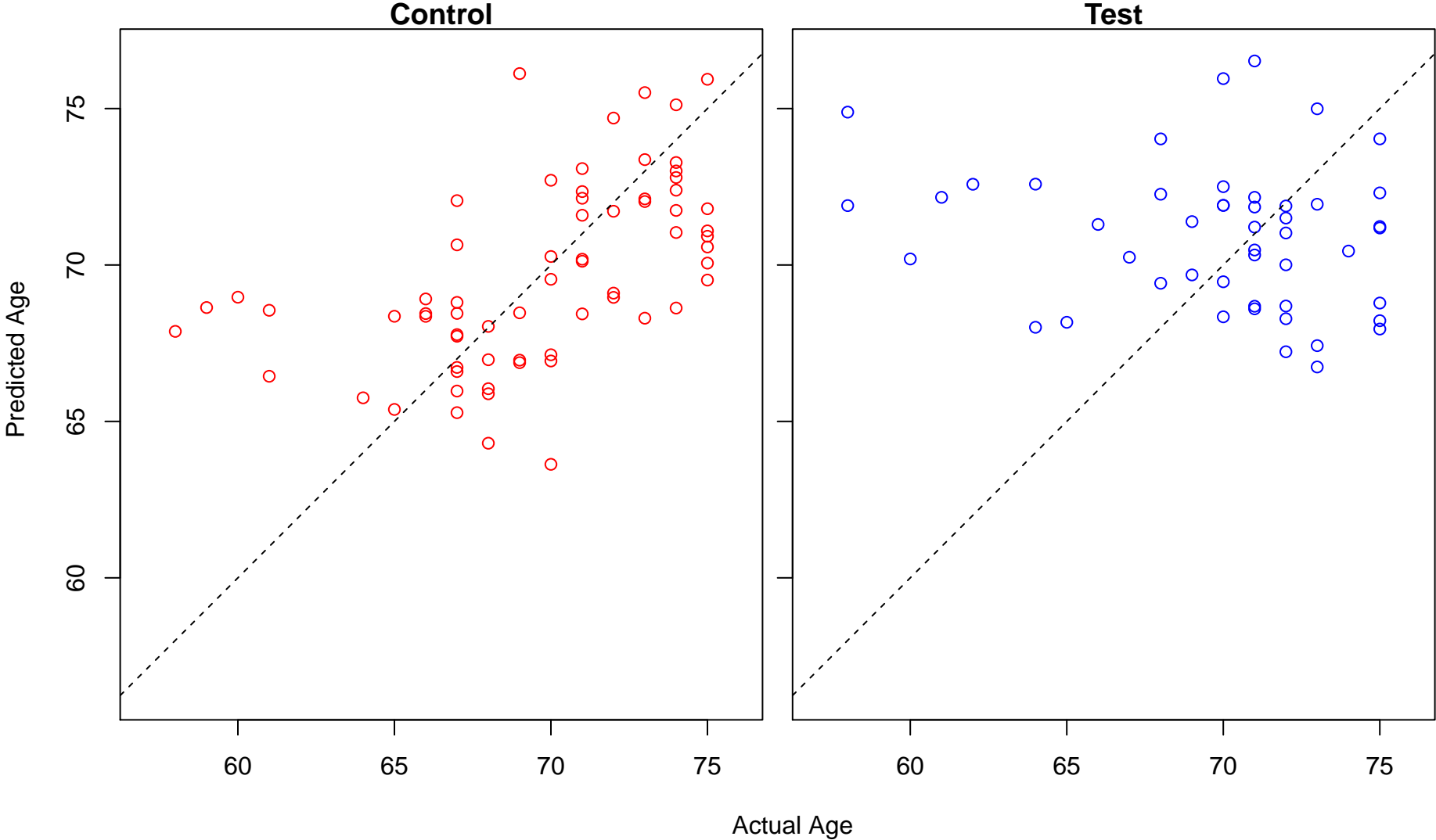
establishment of mitotic spindle localization (Score: 1.005793)



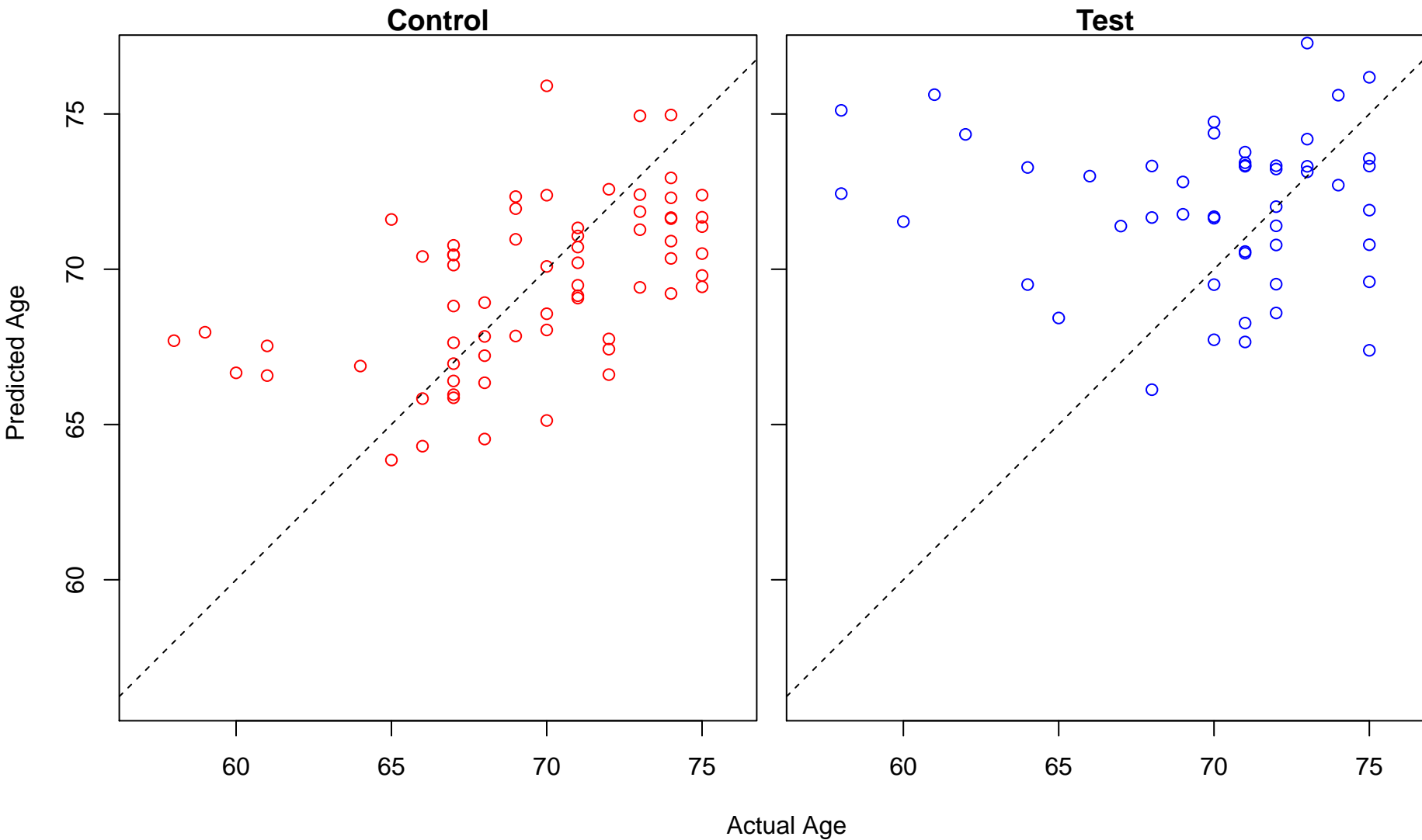
regulation of G-protein coupled receptor protein signaling pathway (Score: 1.005785)



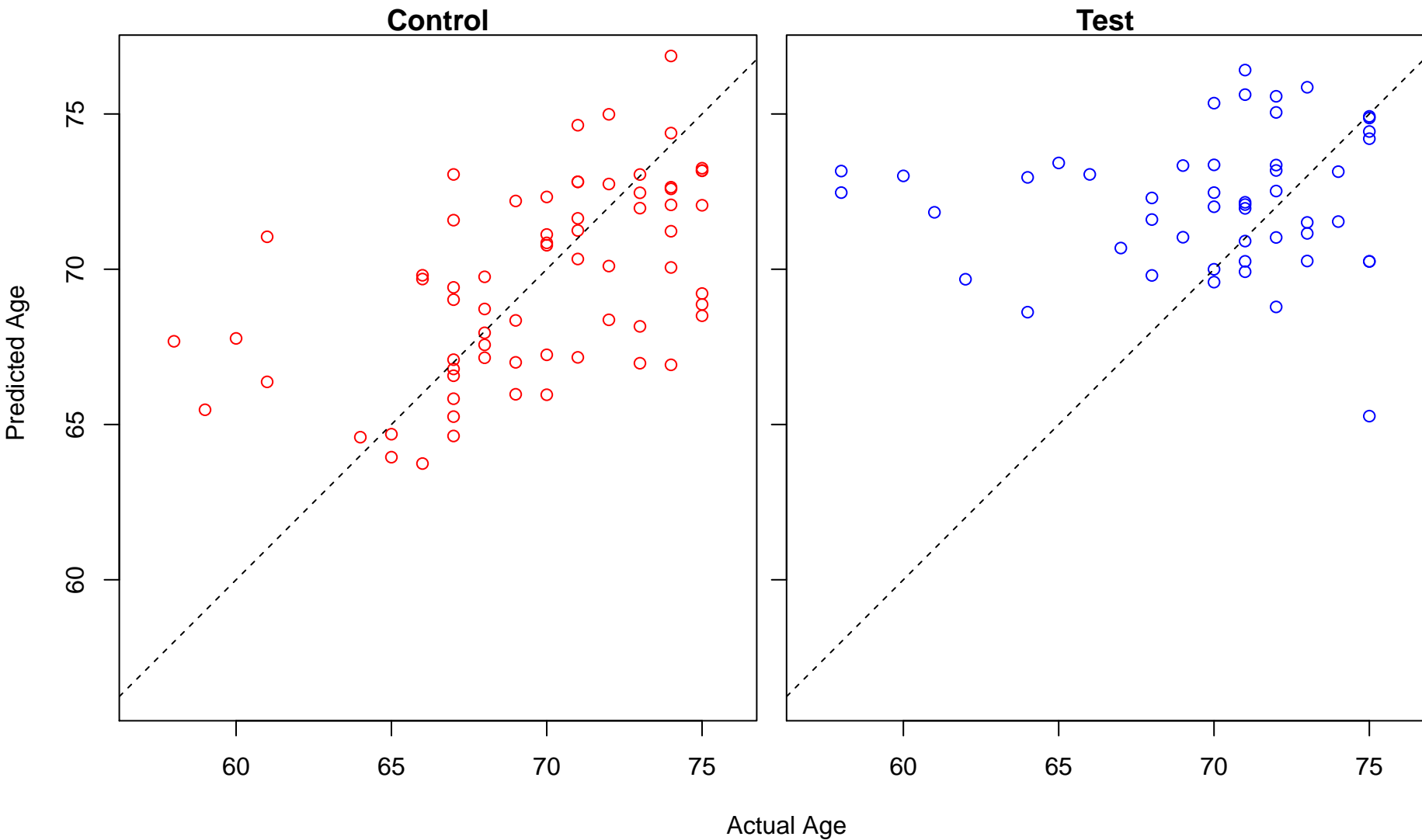
regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway (Score: 1.005)



cellular modified amino acid biosynthetic process (Score: 1.005473)

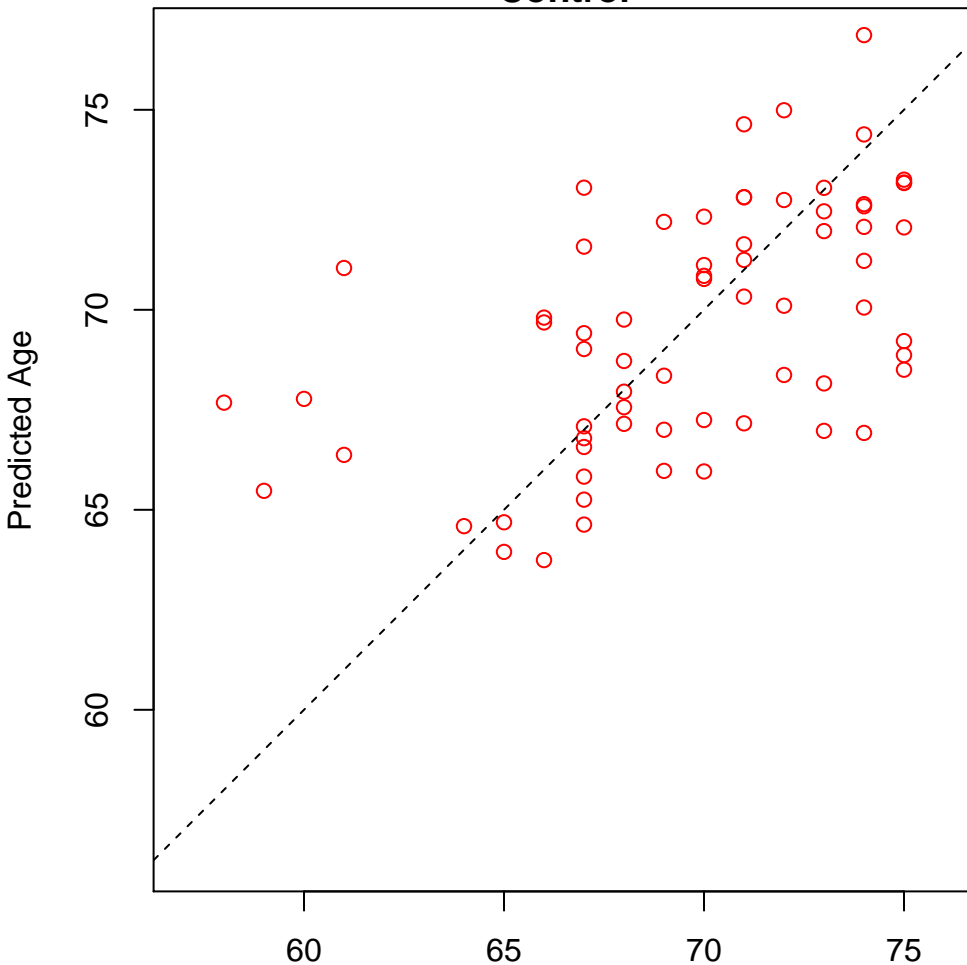


icosanoid metabolic process (Score: 1.003724)

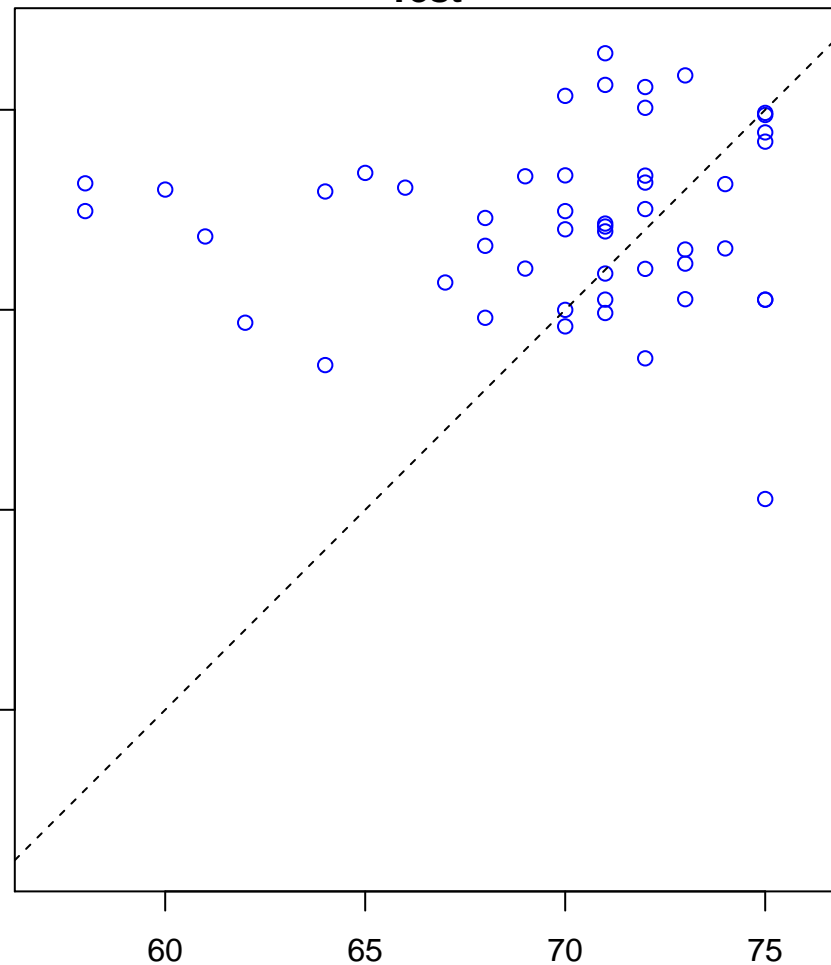


fatty acid derivative metabolic process (Score: 1.003724)

Control



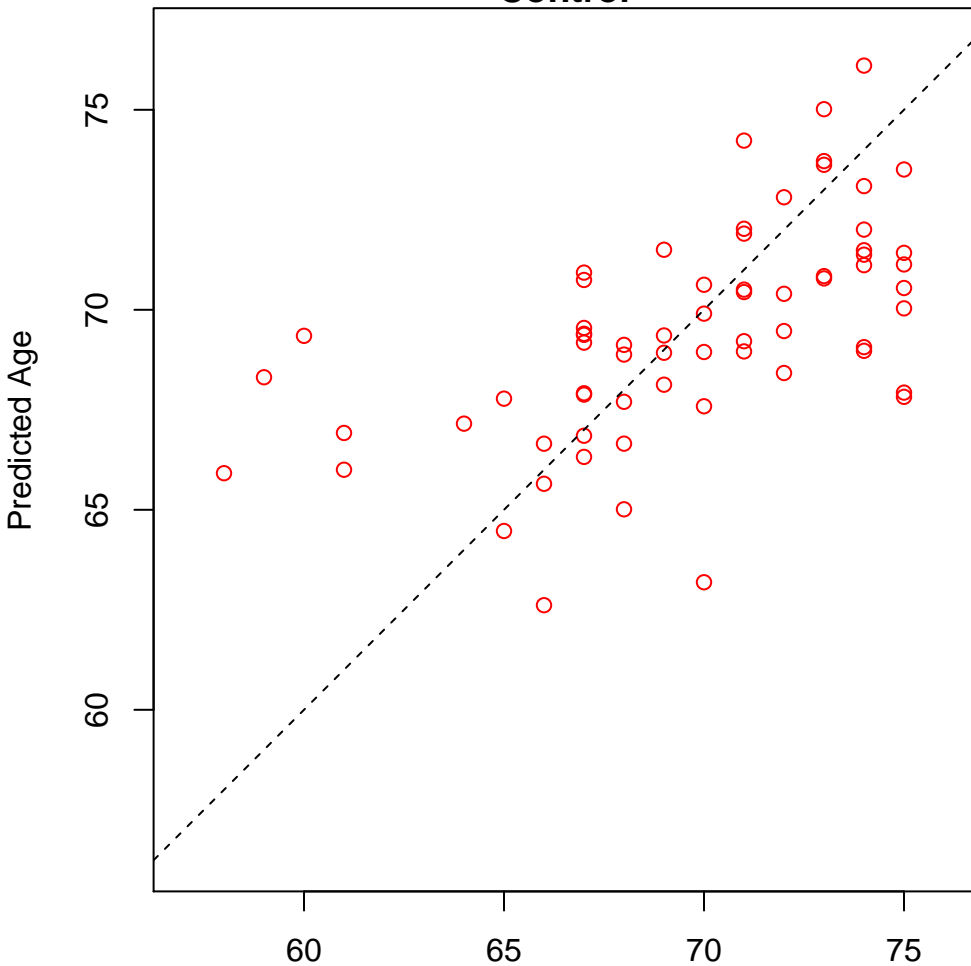
Test



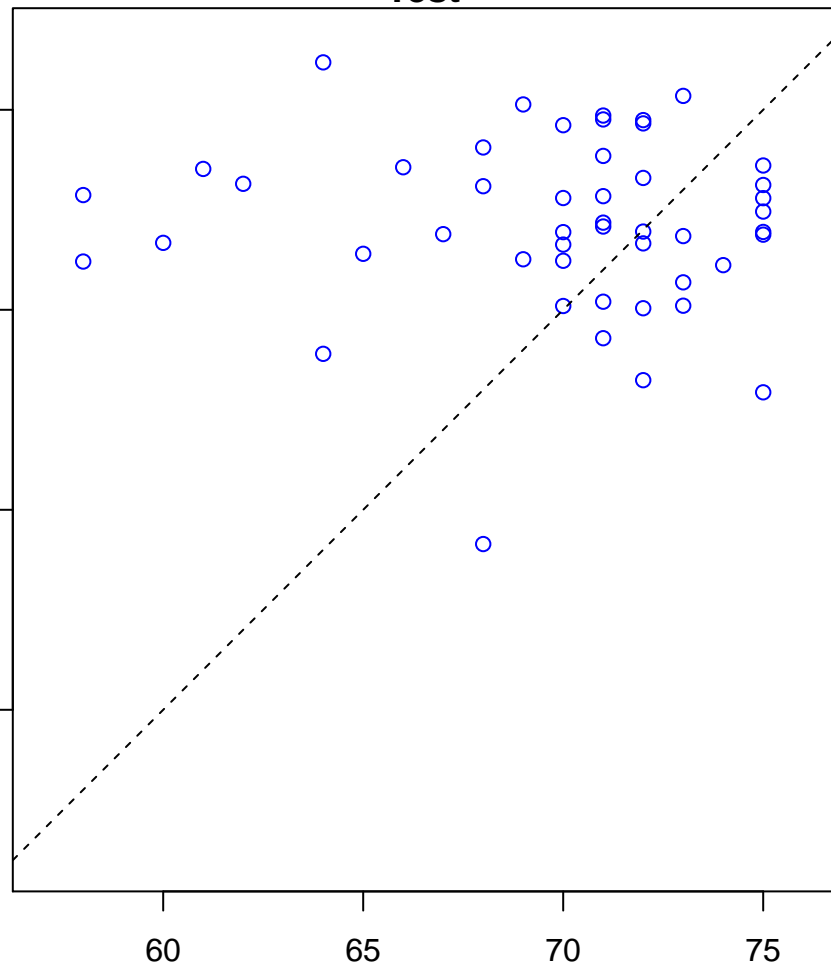
Actual Age

deoxyribonucleotide catabolic process (Score: 1.003688)

Control

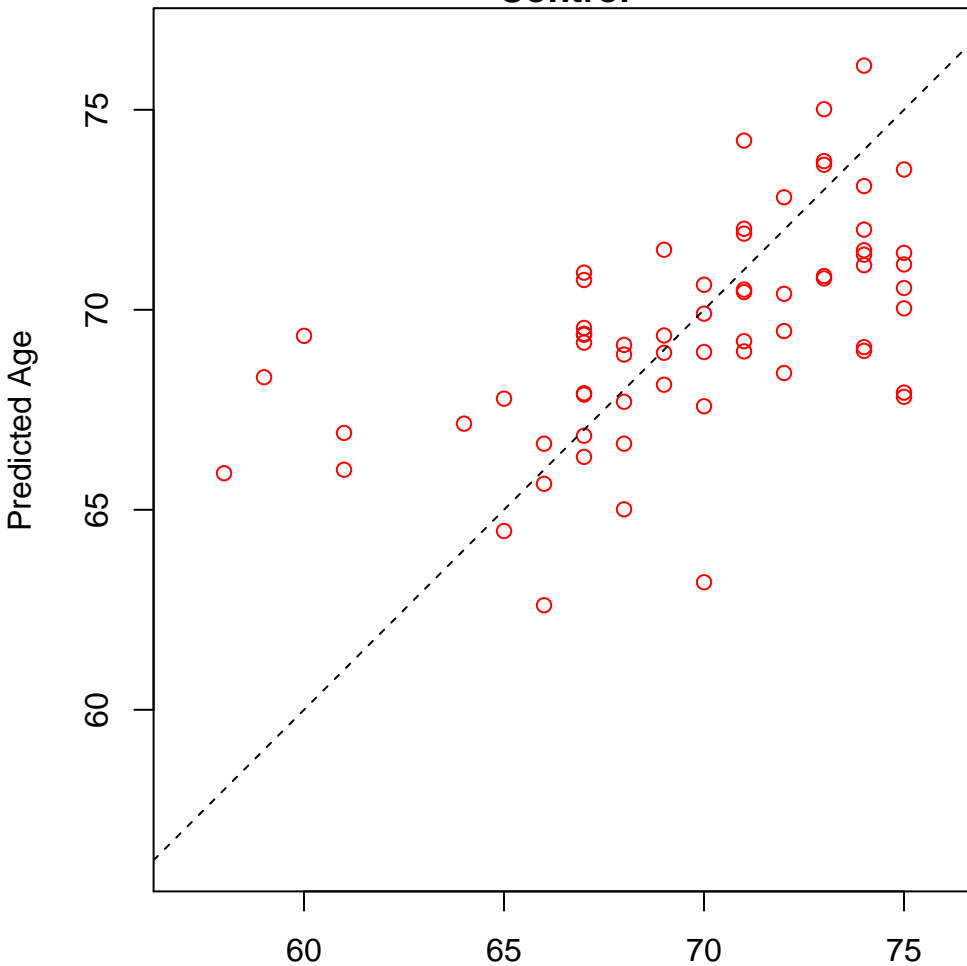


Test

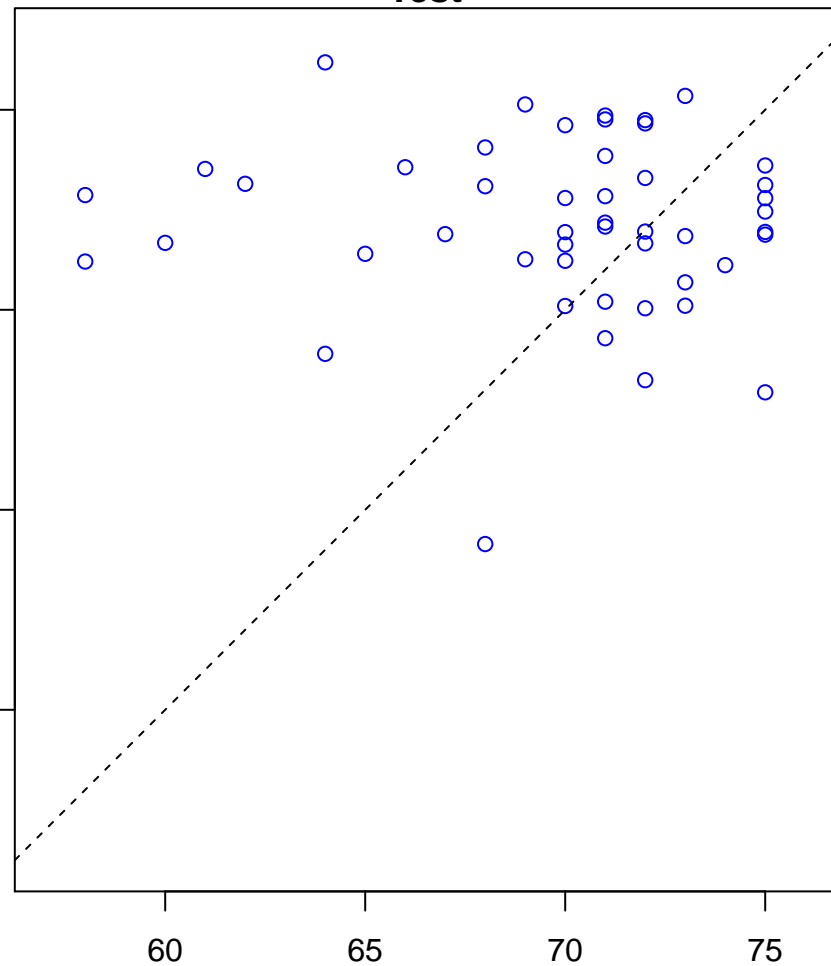


deoxyribose phosphate catabolic process (Score: 1.003688)

Control

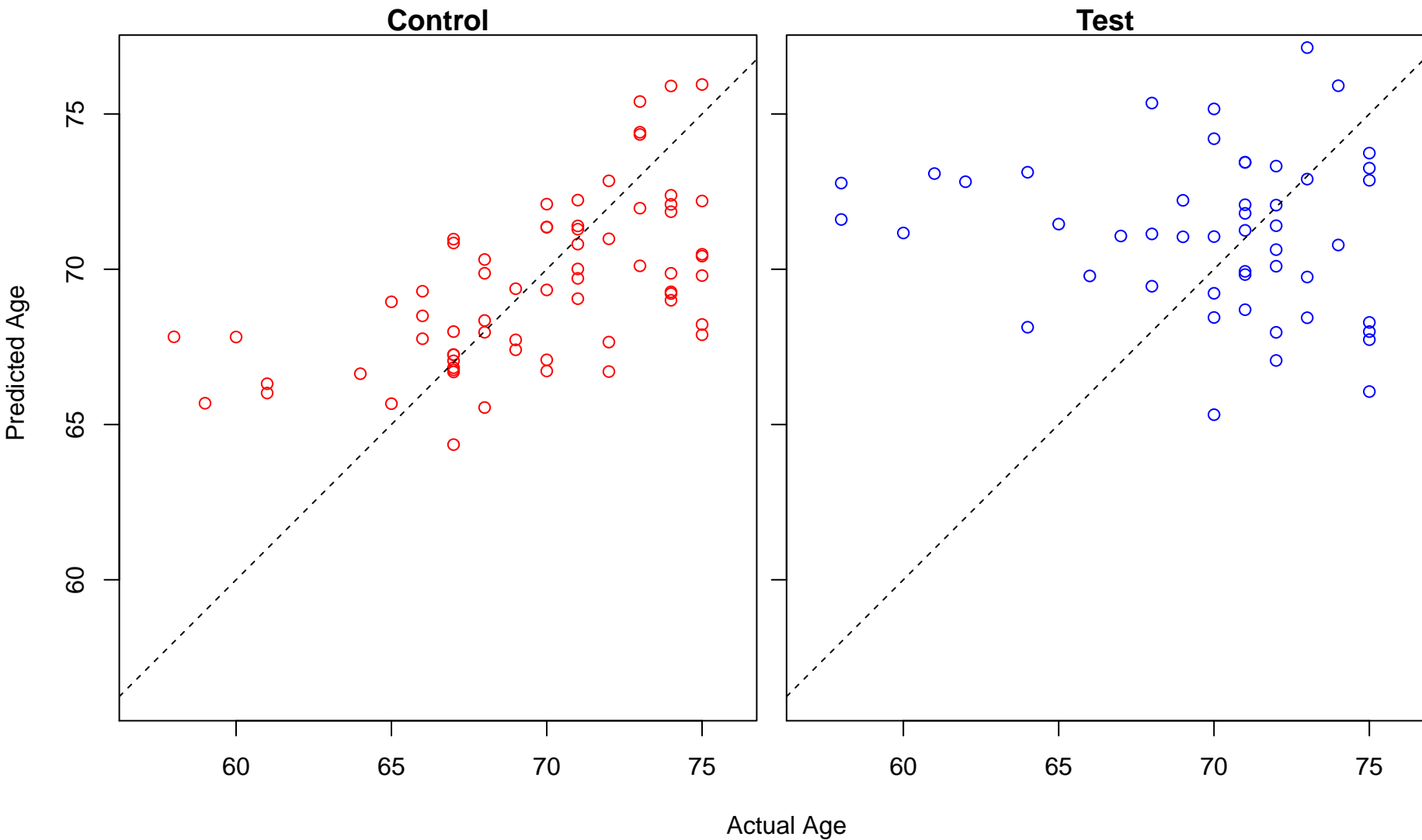


Test

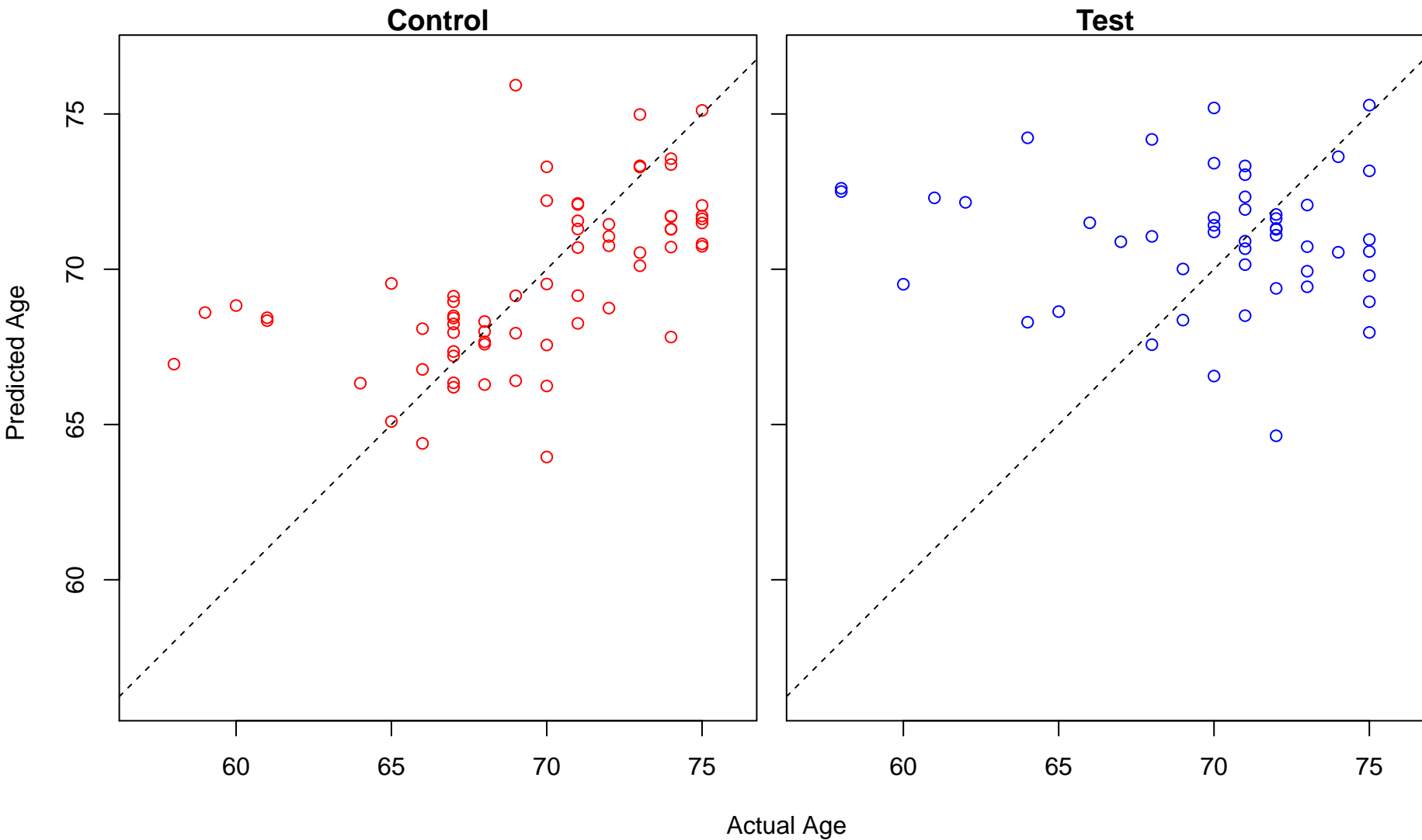


Actual Age

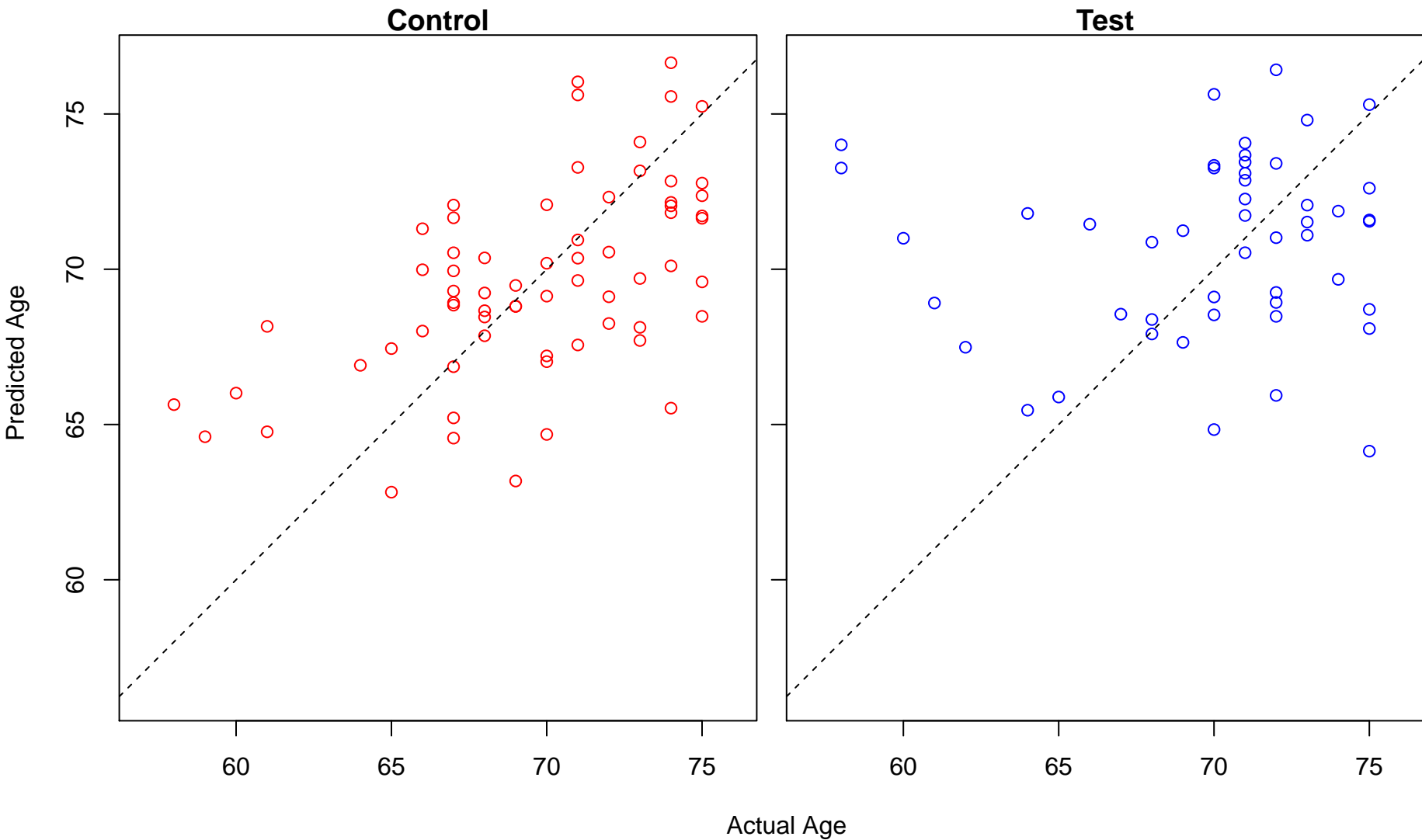
apical junction assembly (Score: 1.003390)



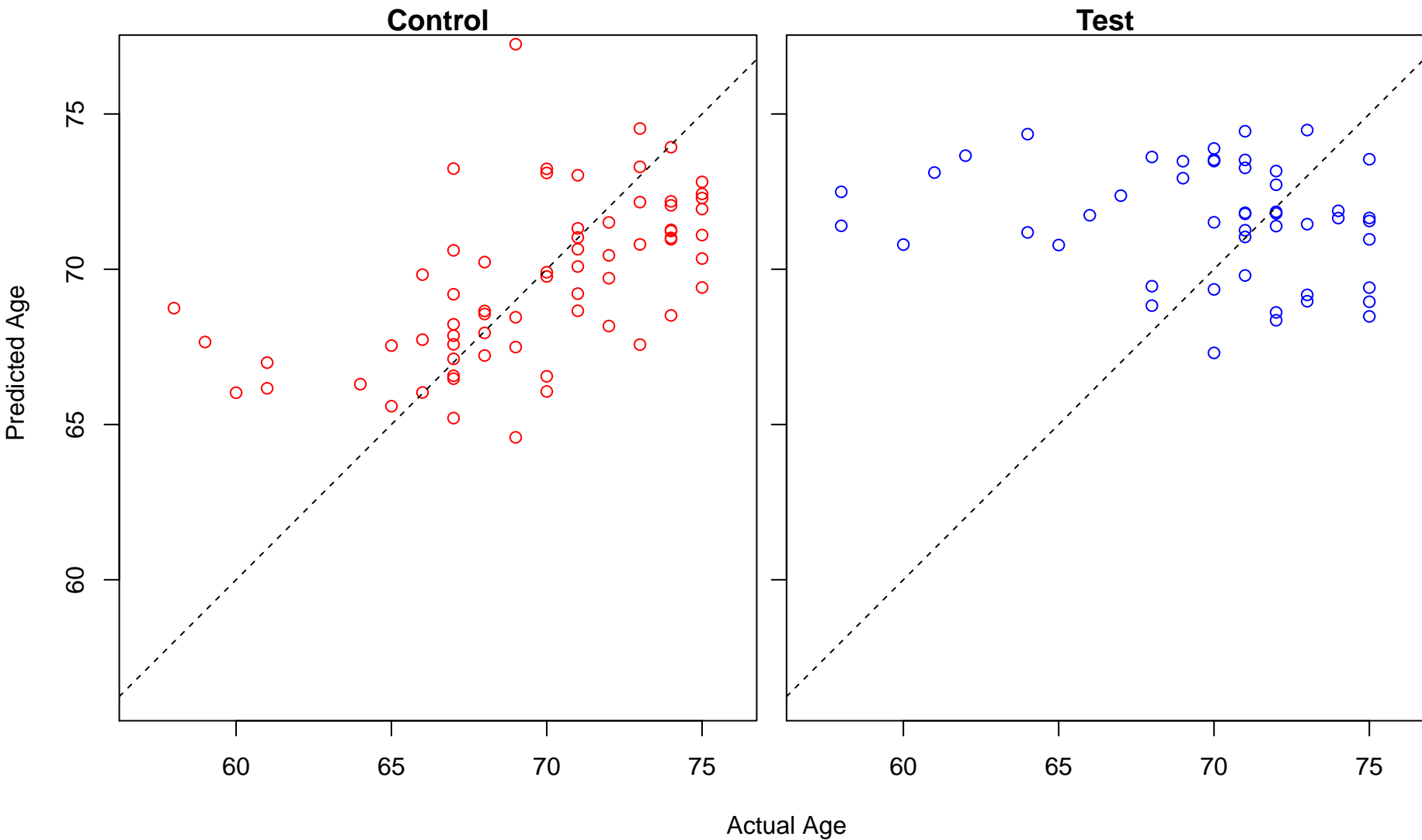
establishment of spindle orientation (Score: 1.003310)



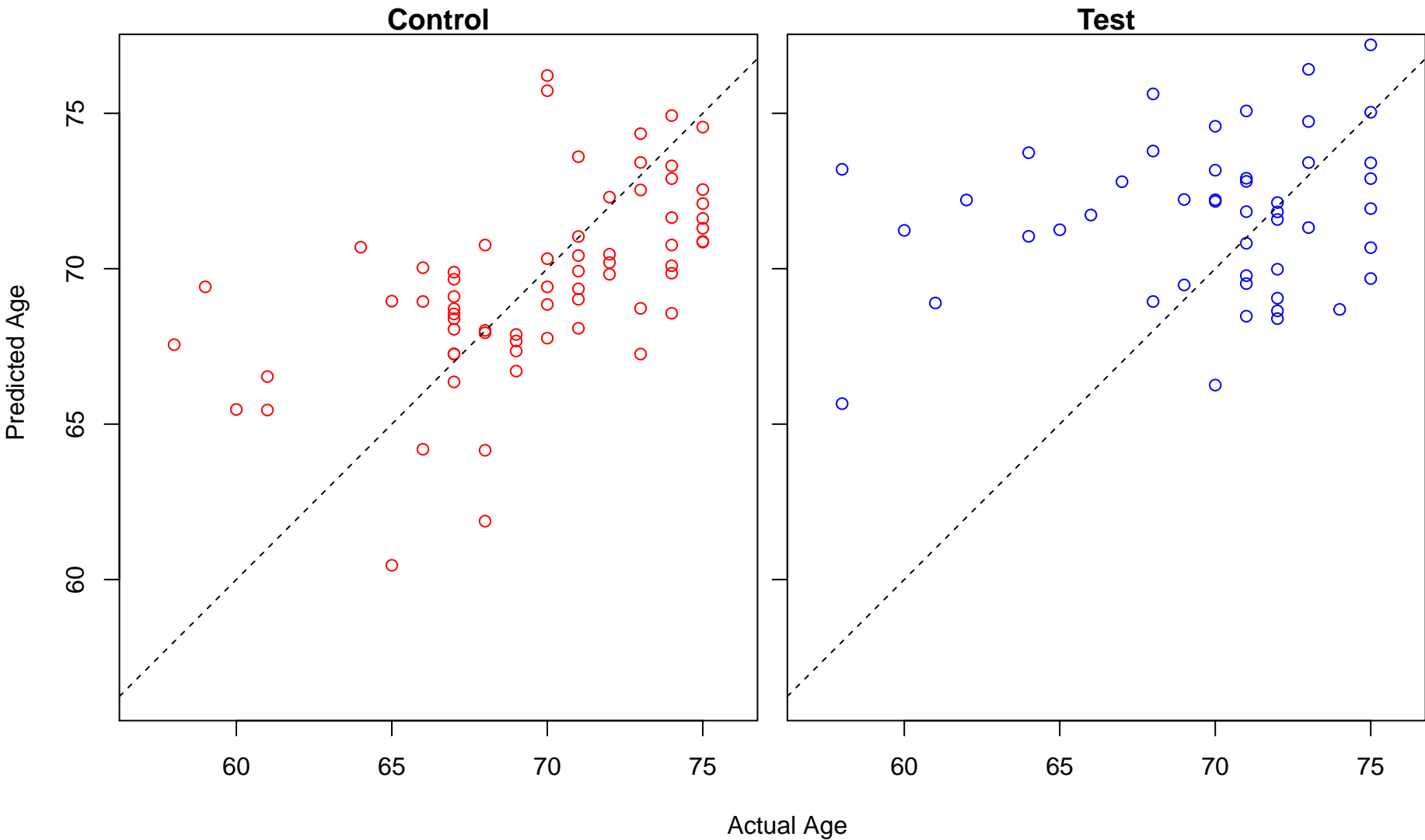
regulation of isotype switching (Score: 1.002985)



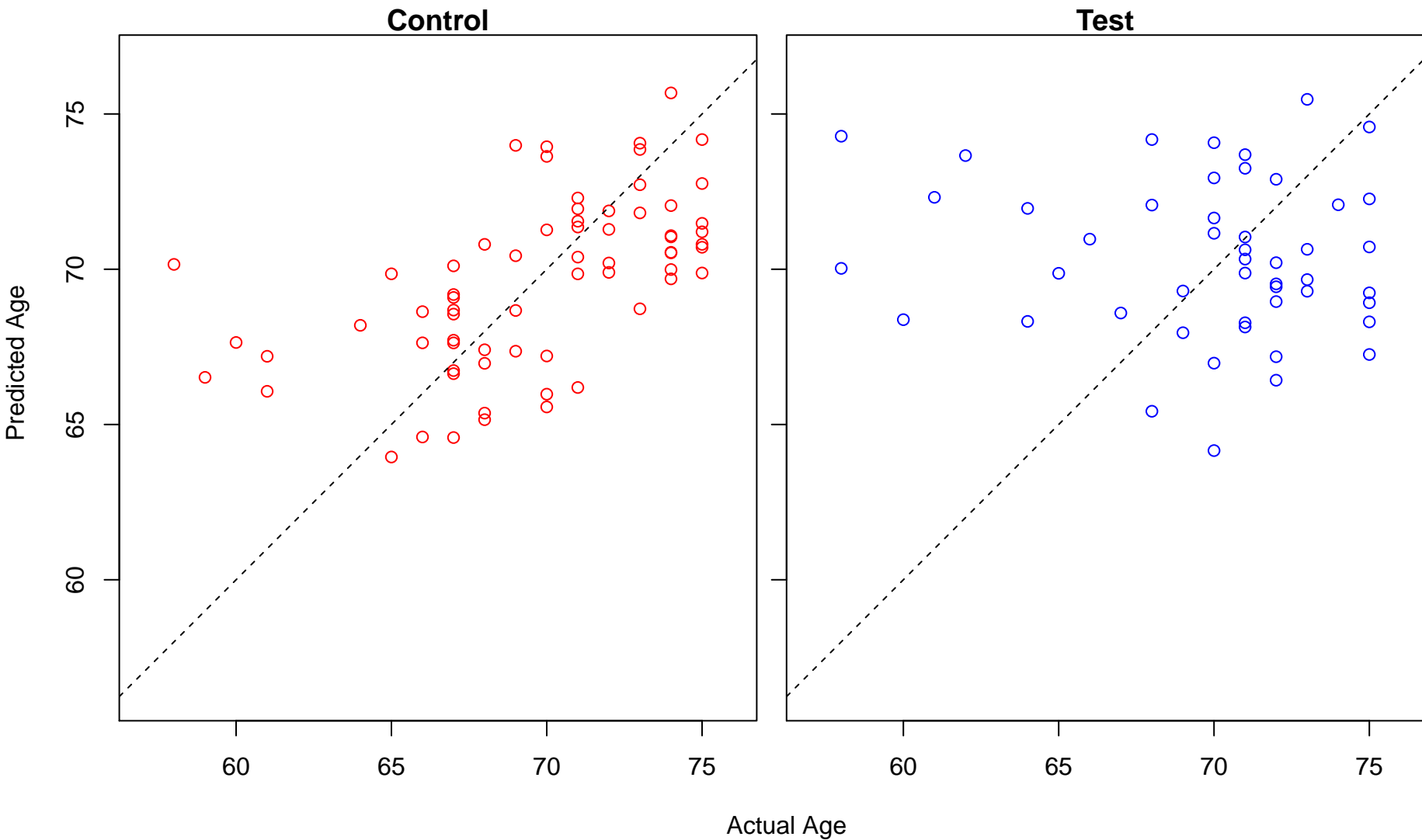
hormone metabolic process (Score: 1.002633)



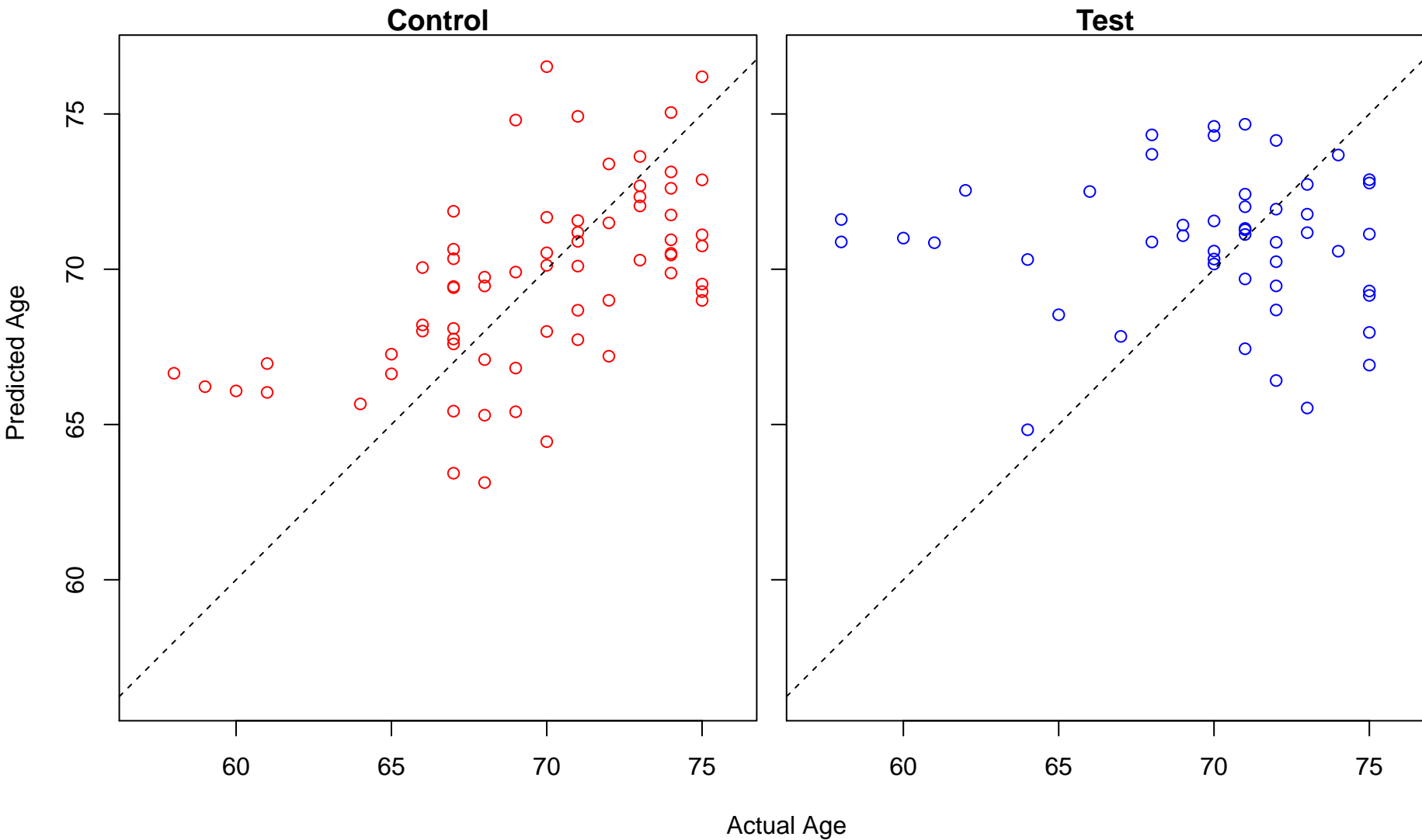
positive regulation of transcription from RNA polymerase I promoter (Score: 1.001895)



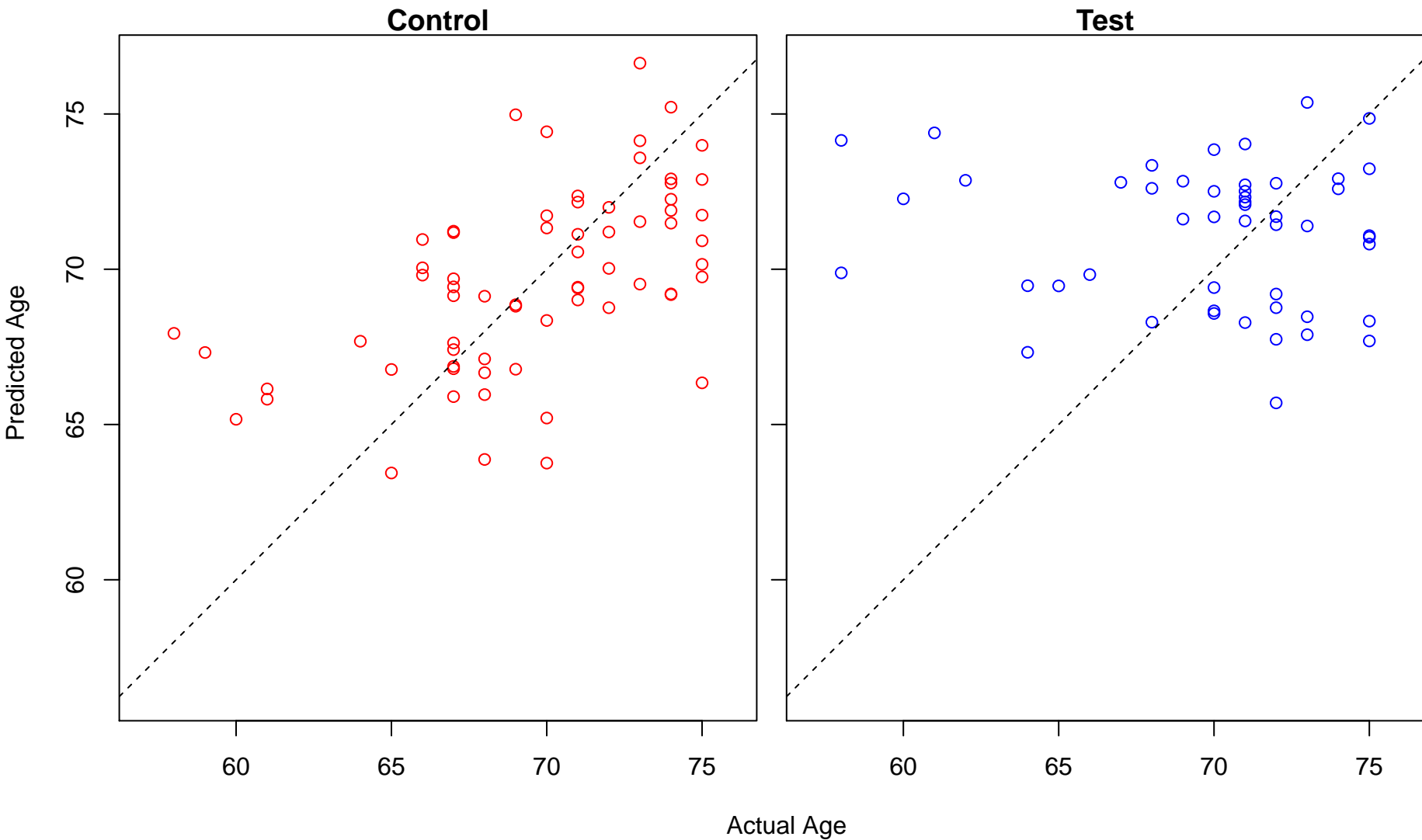
regulation of calcium ion transmembrane transporter activity (Score: 1.001816)



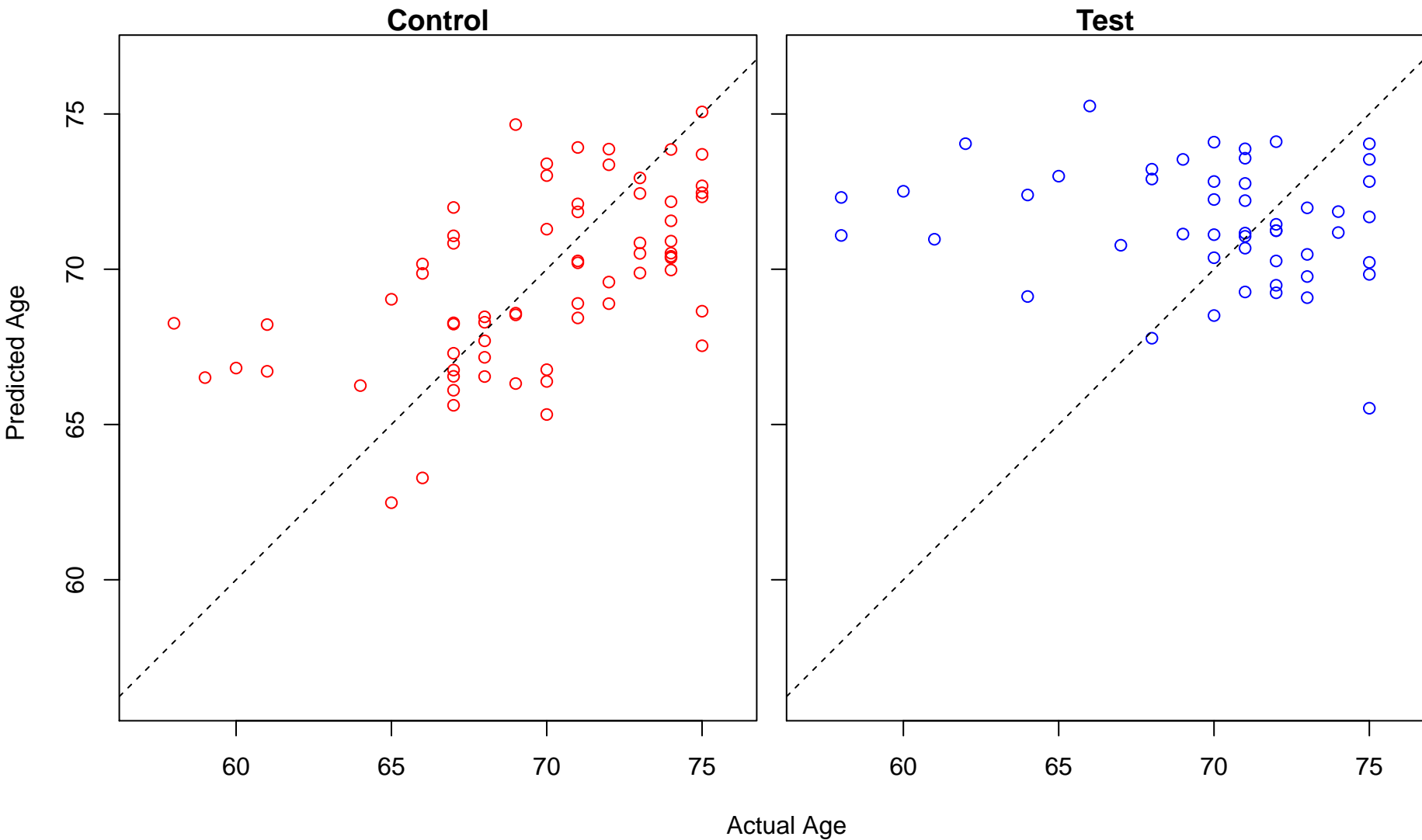
bile acid metabolic process (Score: 1.001466)



positive regulation of cytokinesis (Score: 1.001443)

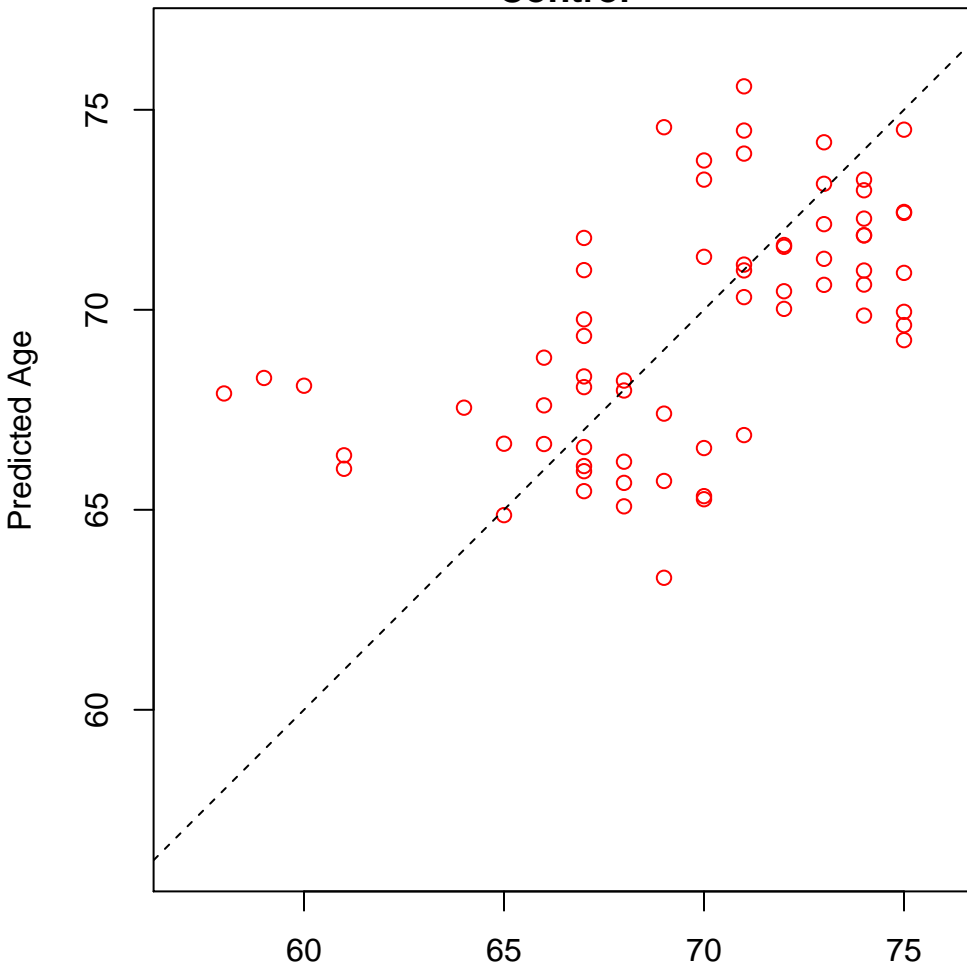


hepaticobiliary system development (Score: 1.001170)

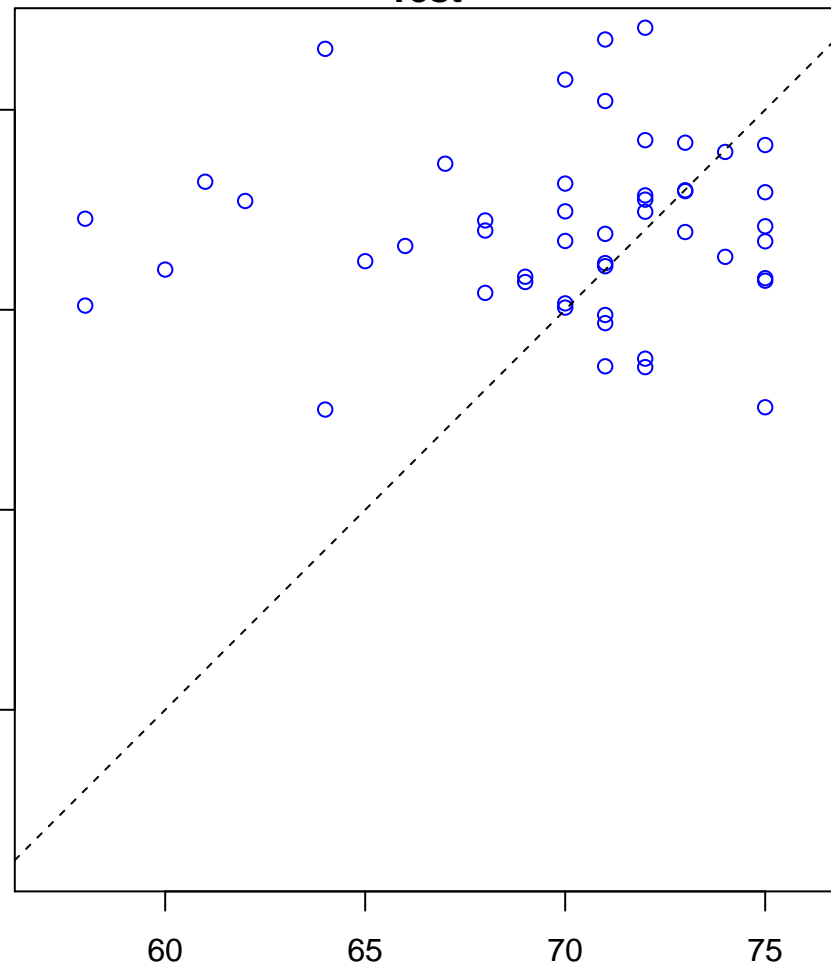


regulation of peptidyl-lysine acetylation (Score: 1.000657)

Control

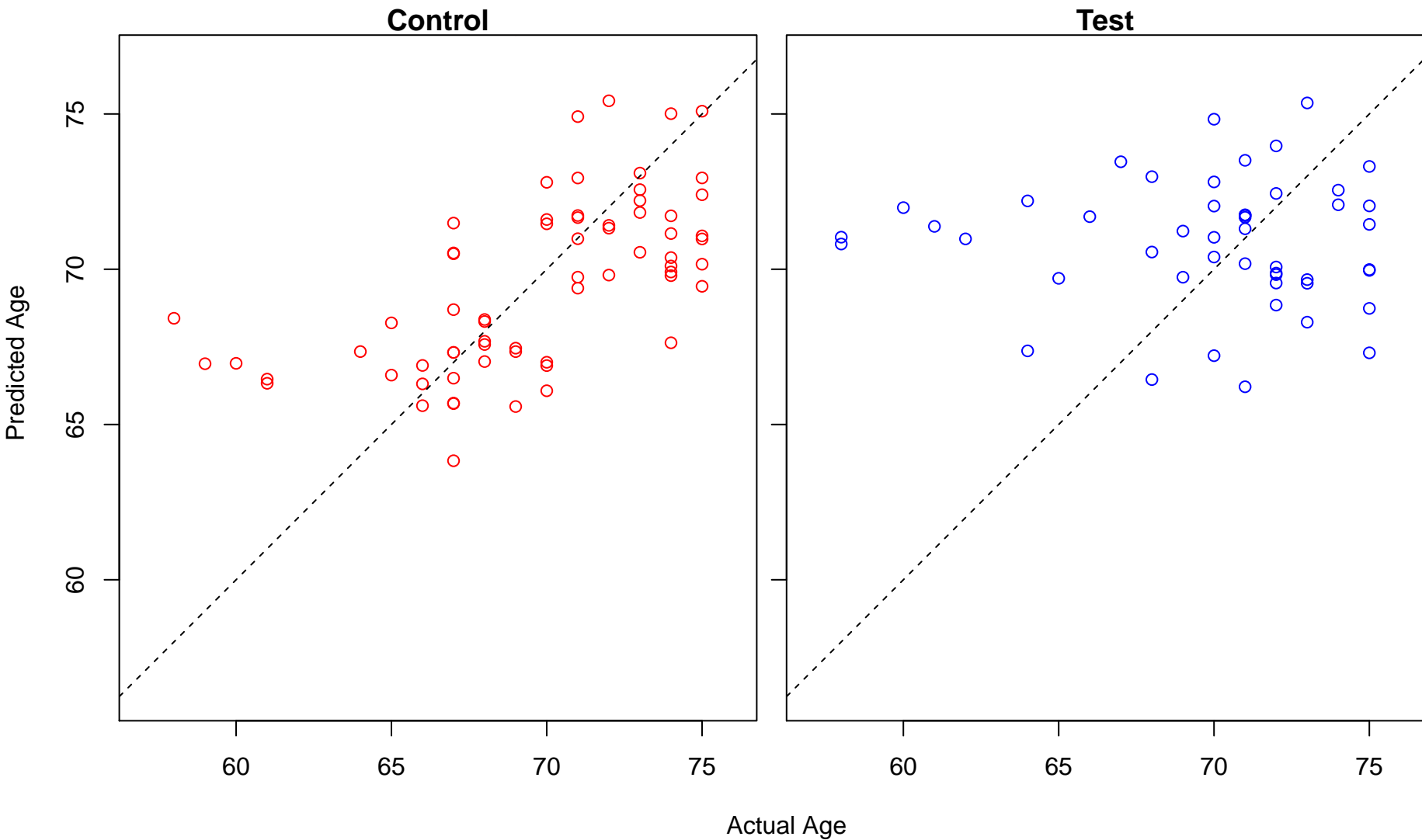


Test

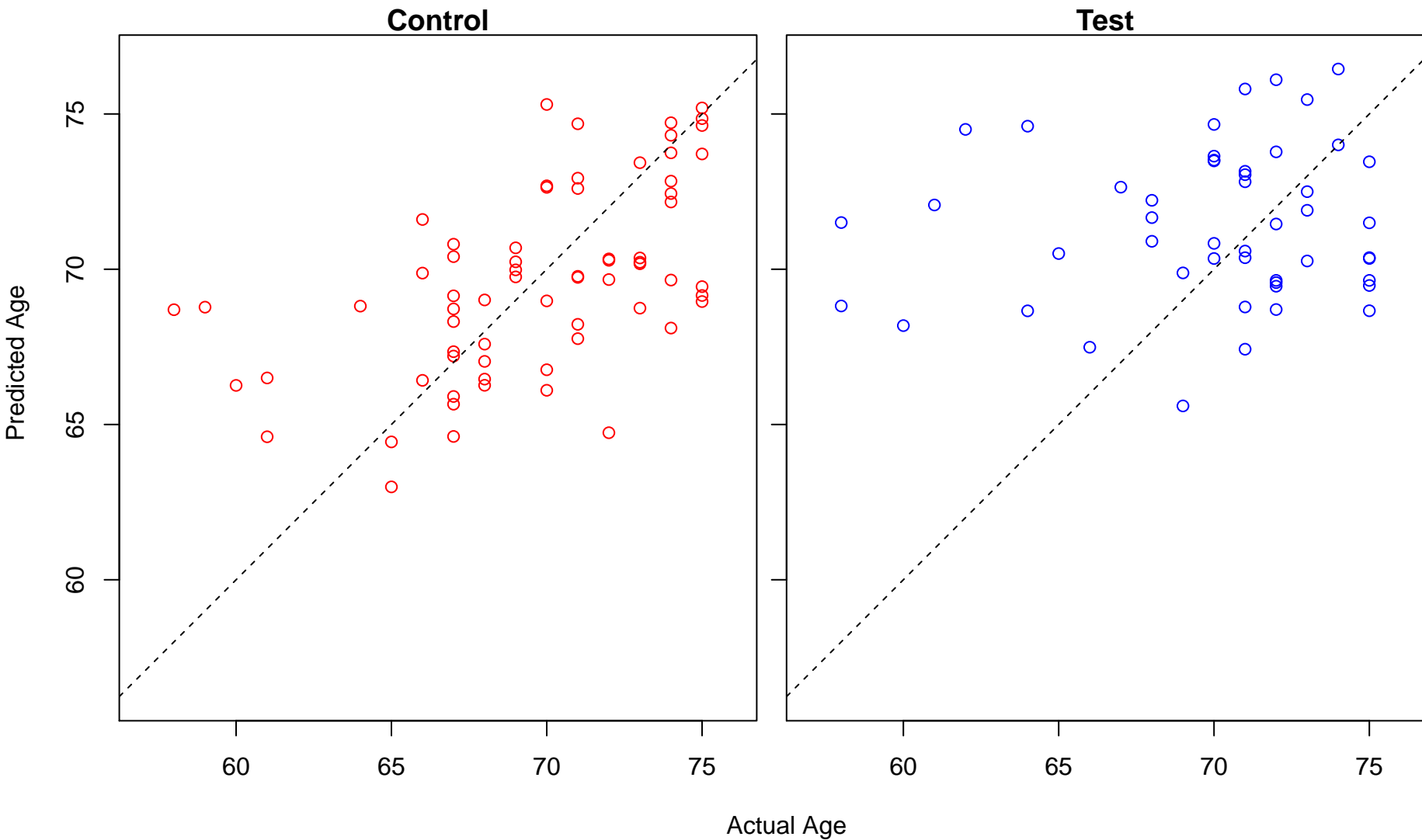


Actual Age

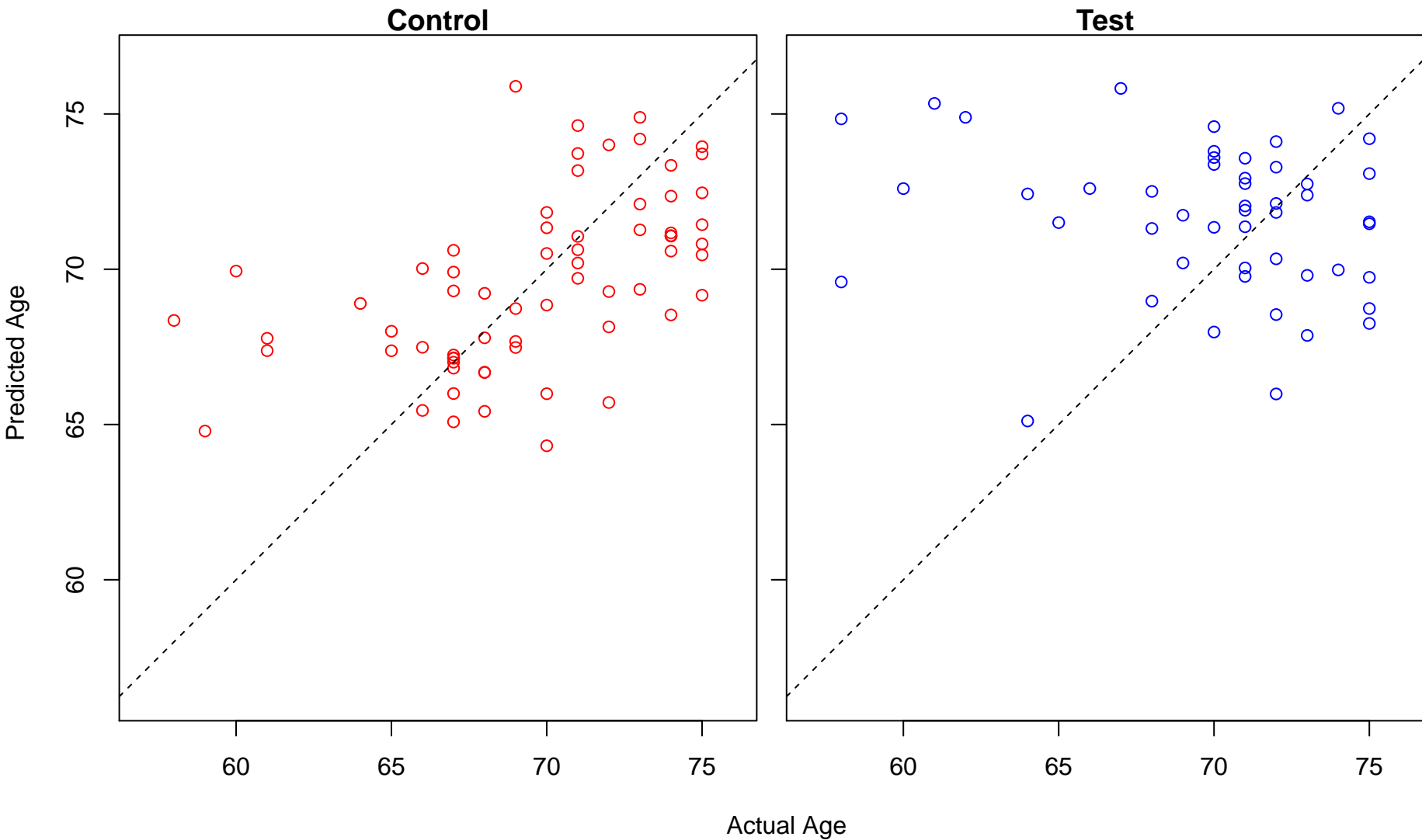
negative regulation of cyclin–dependent protein kinase activity (Score: 1.000220)



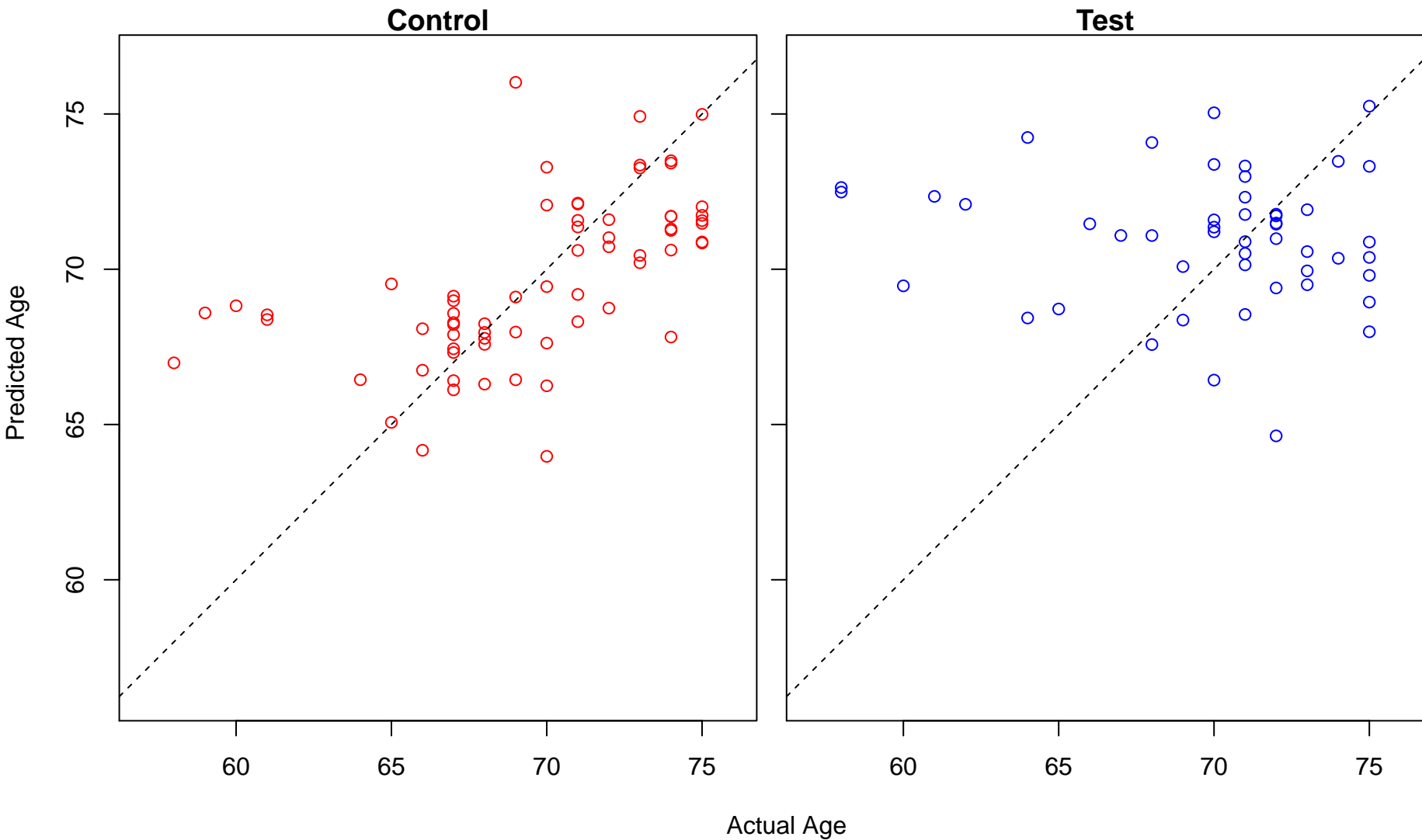
regulation of histone H4 acetylation (Score: 1.000192)



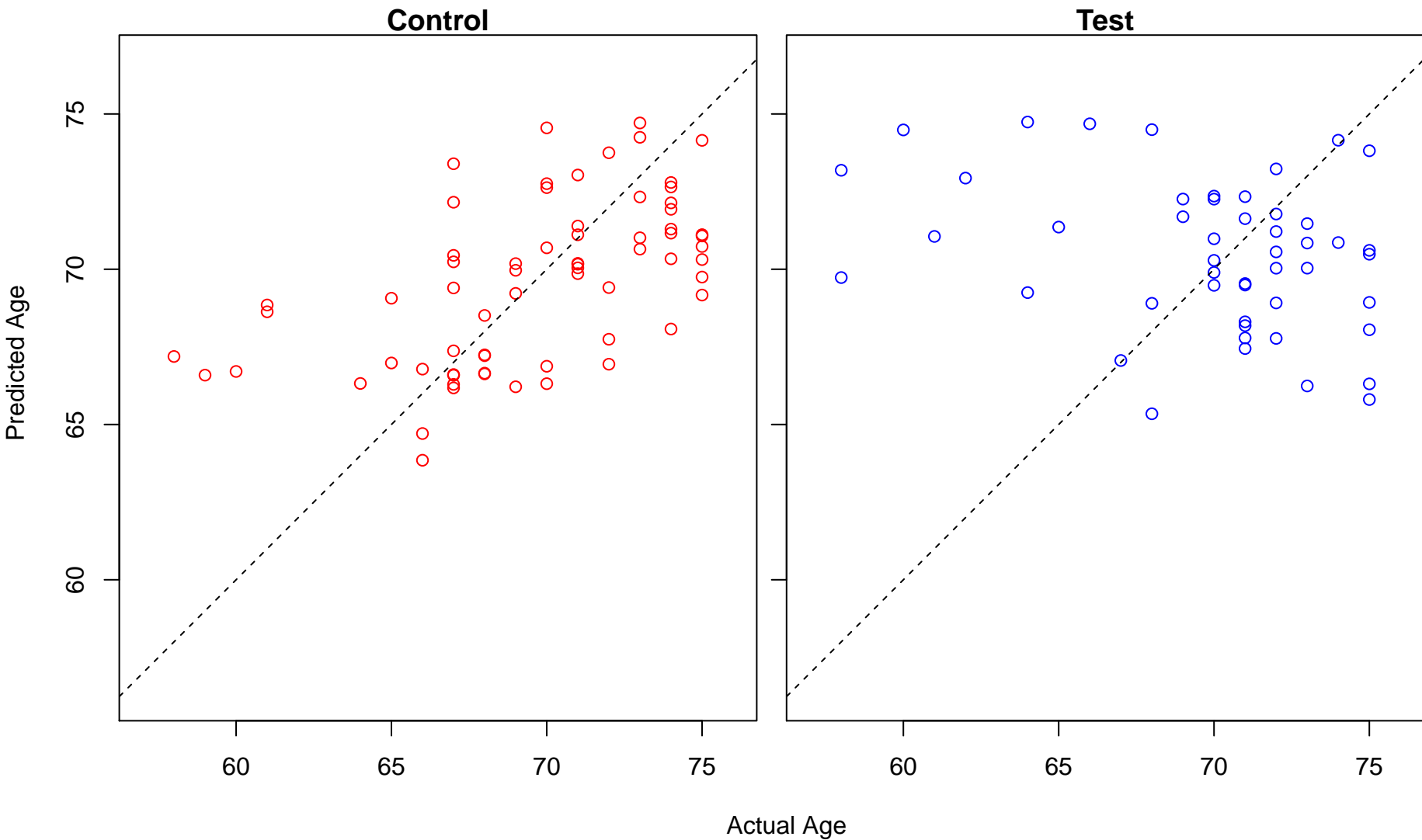
response to cold (Score: 1.000051)



establishment of mitotic spindle orientation (Score: 0.999532)

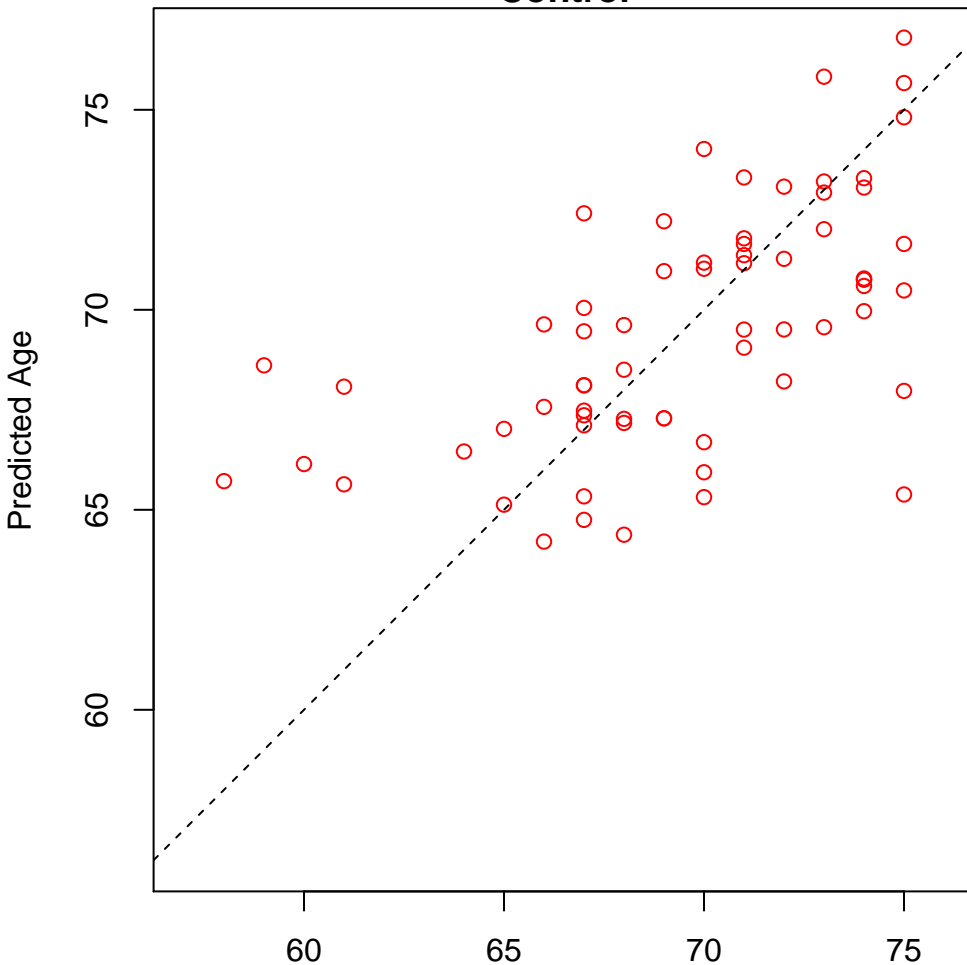


regulation of triglyceride biosynthetic process (Score: 0.998463)

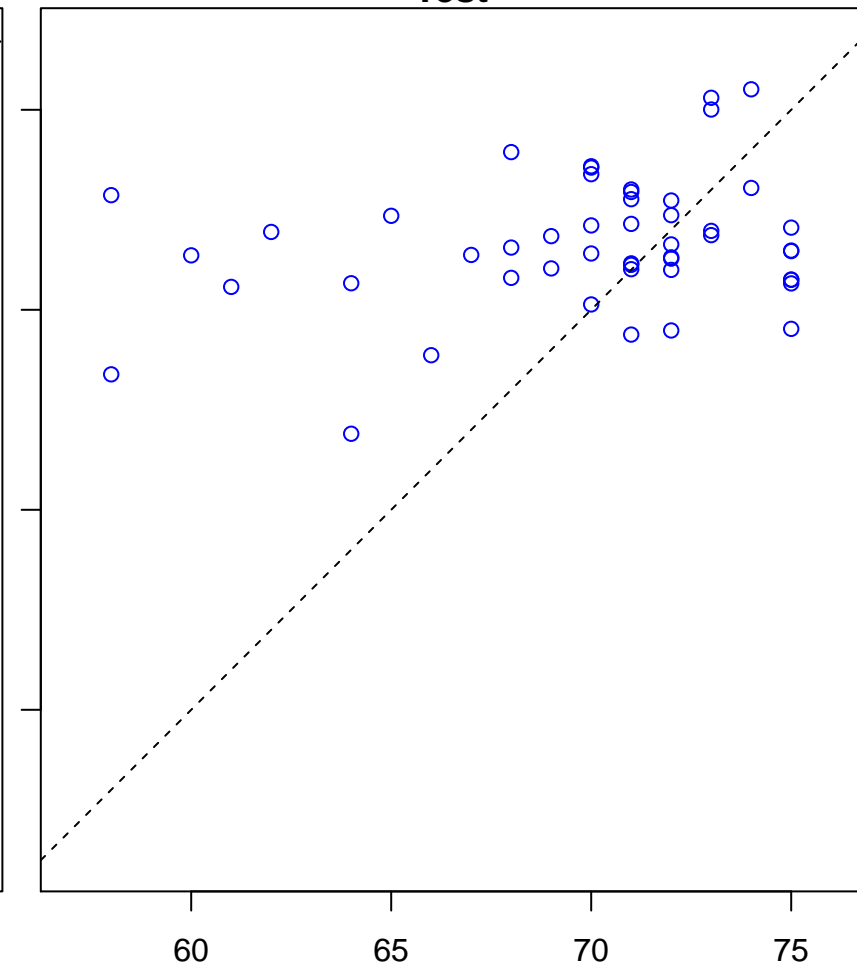


organic hydroxy compound transport (Score: 0.998379)

Control

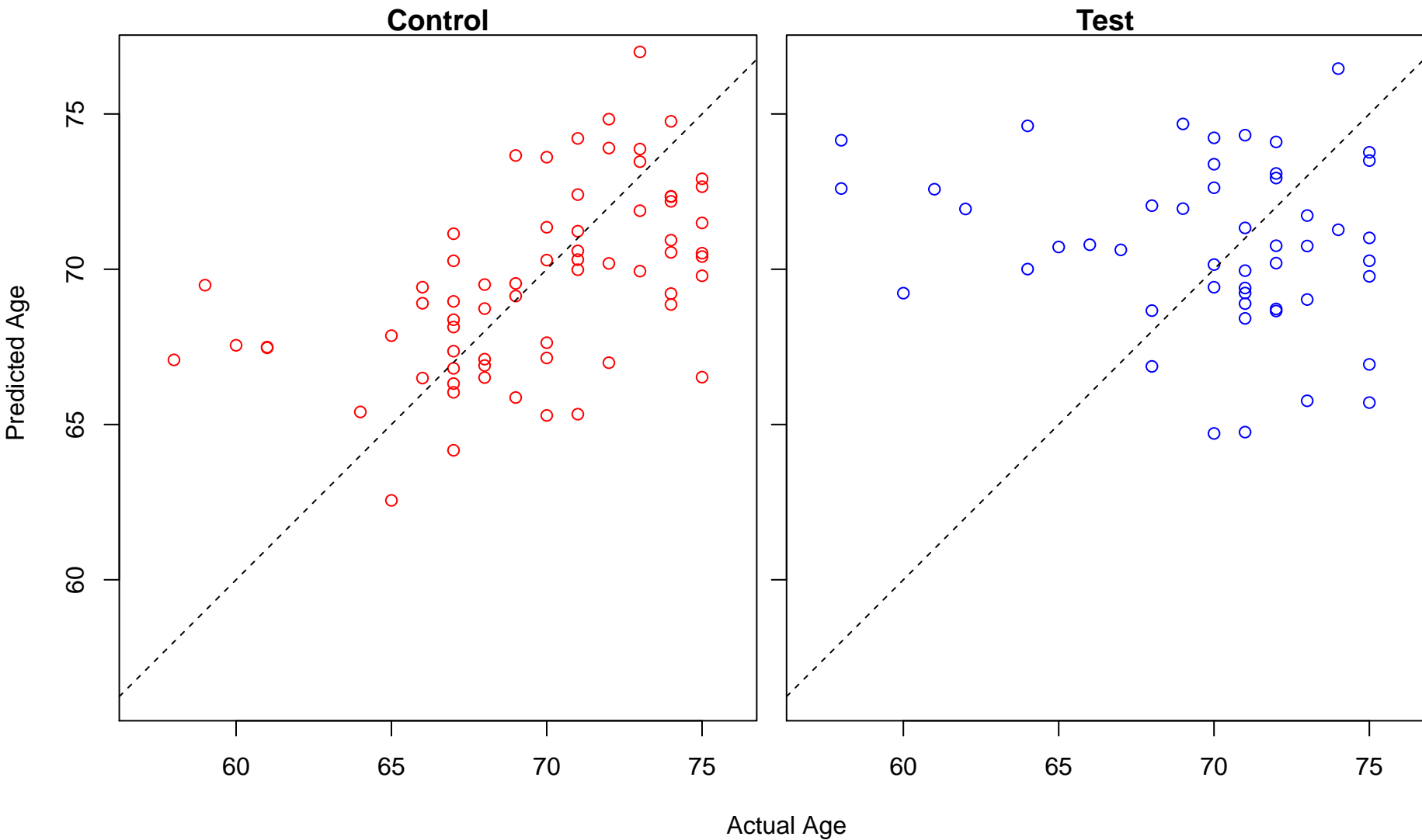


Test

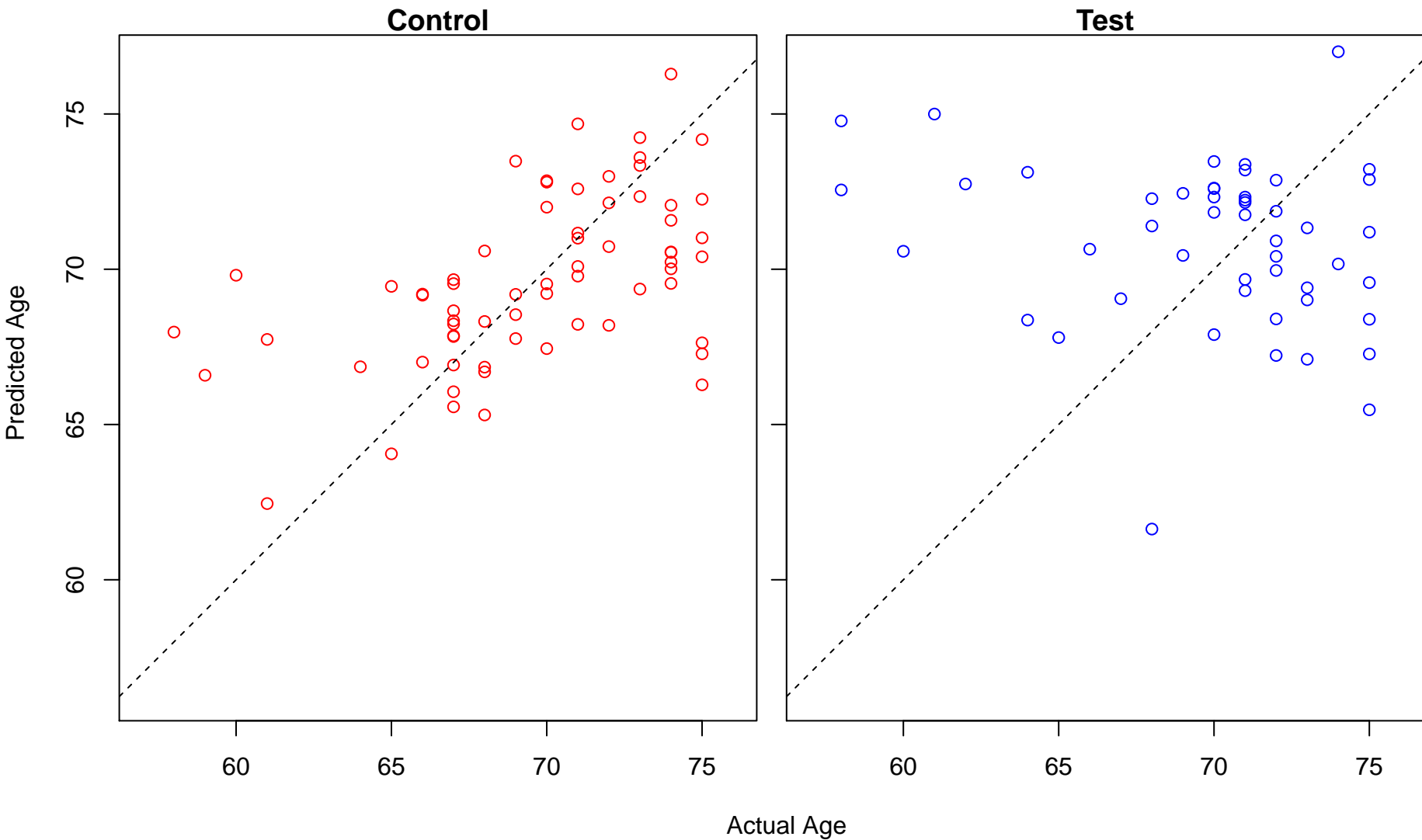


Actual Age

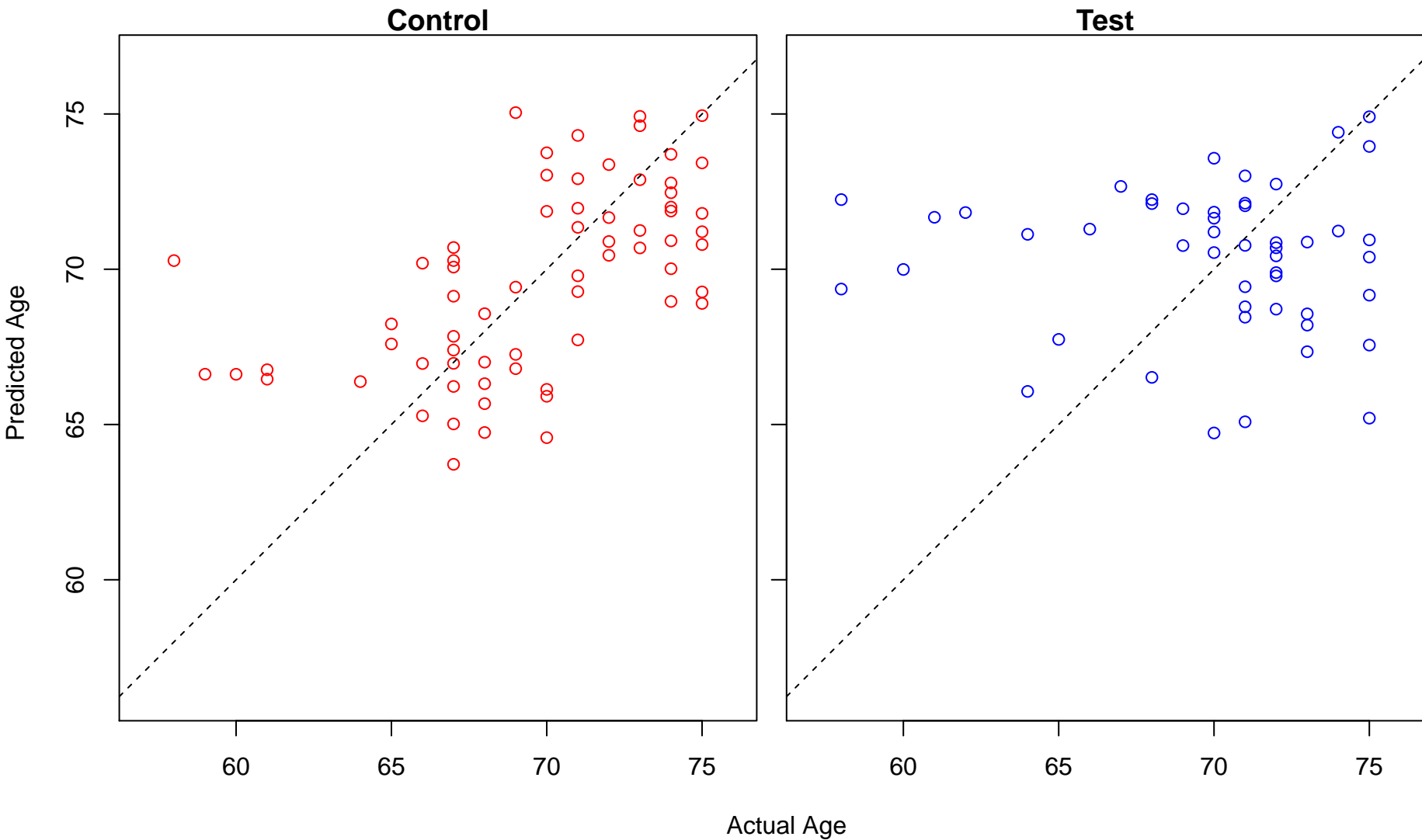
CD4-positive, alpha-beta T cell differentiation (Score: 0.998036)



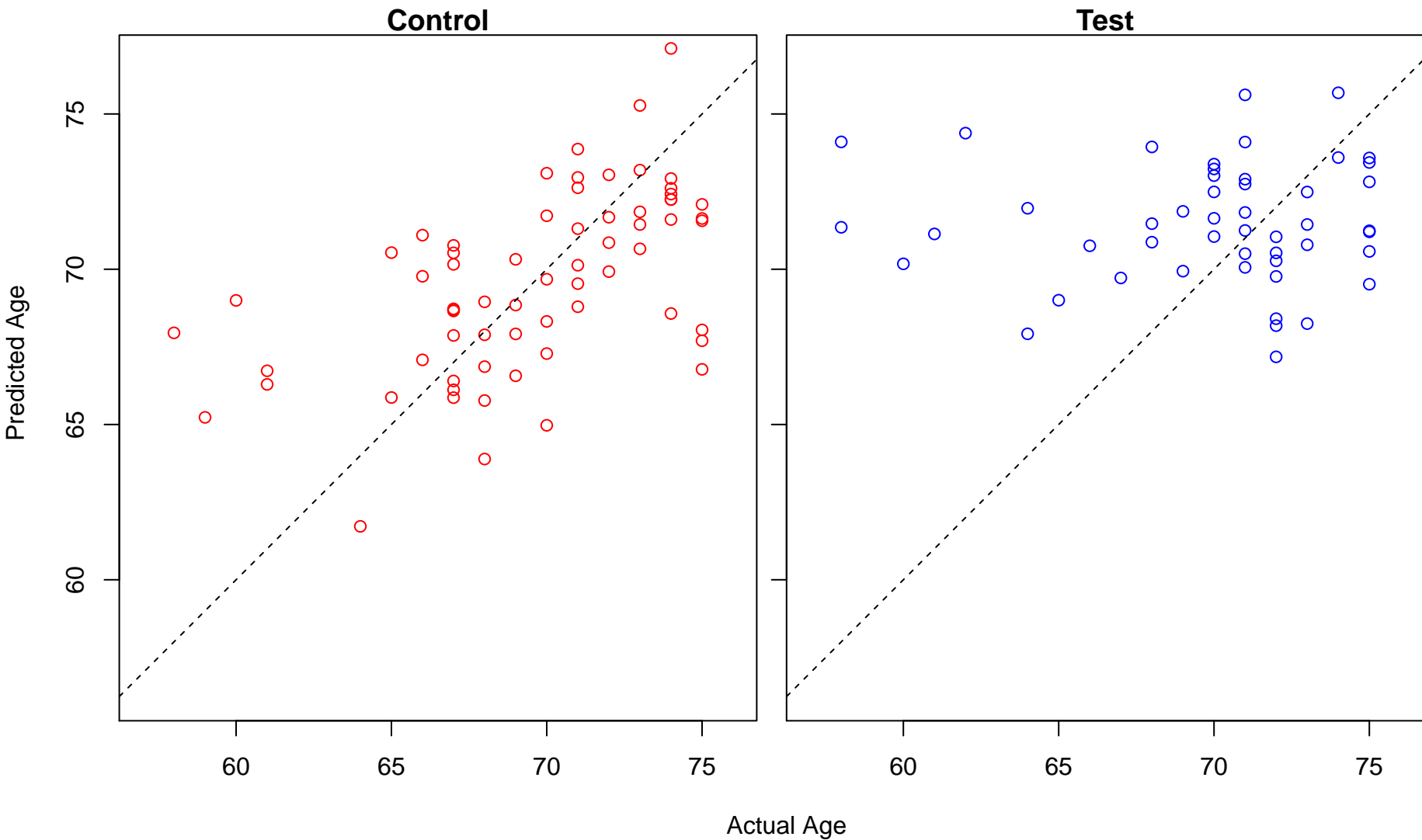
regulation of dendritic cell differentiation (Score: 0.997626)



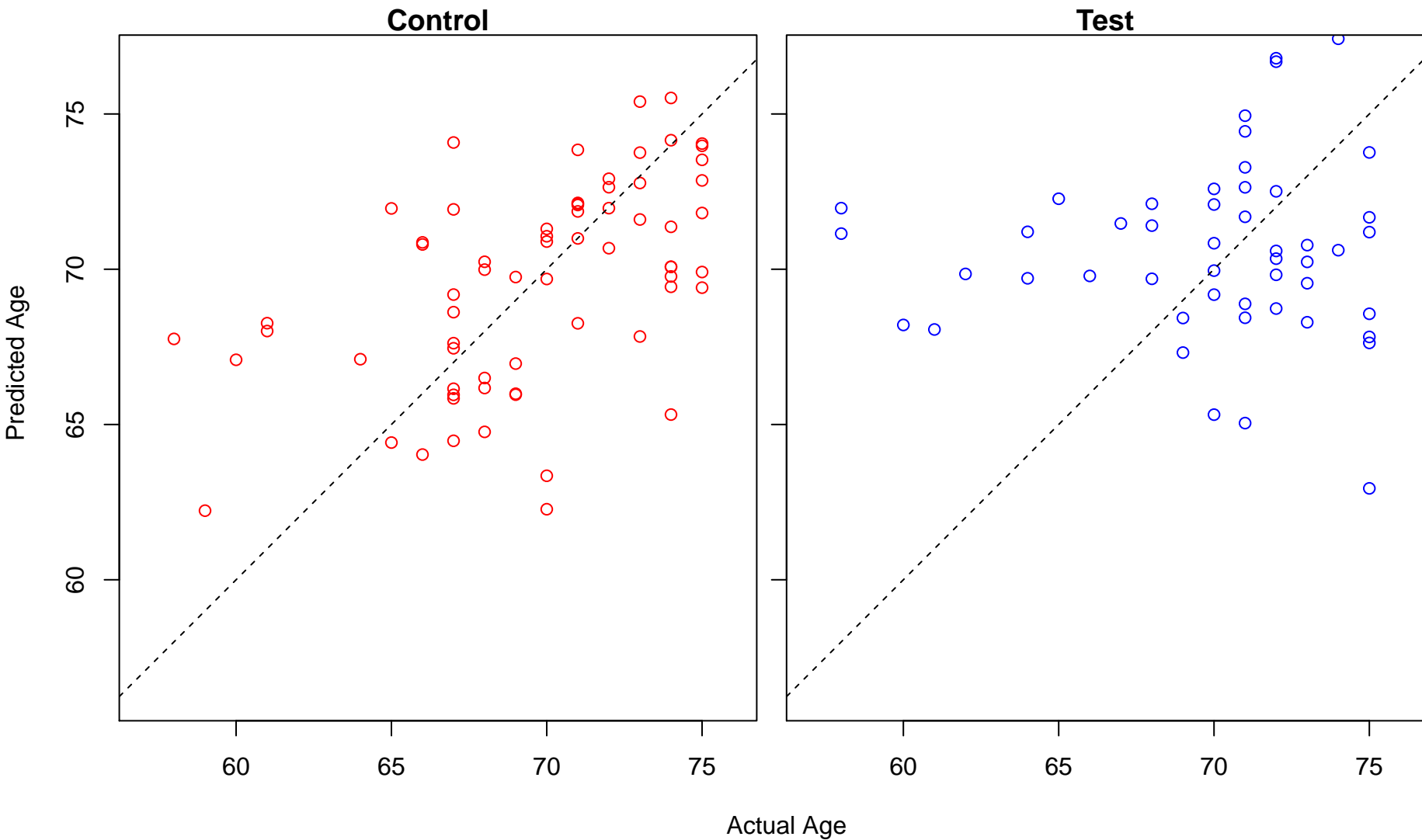
antimicrobial humoral response (Score: 0.997426)



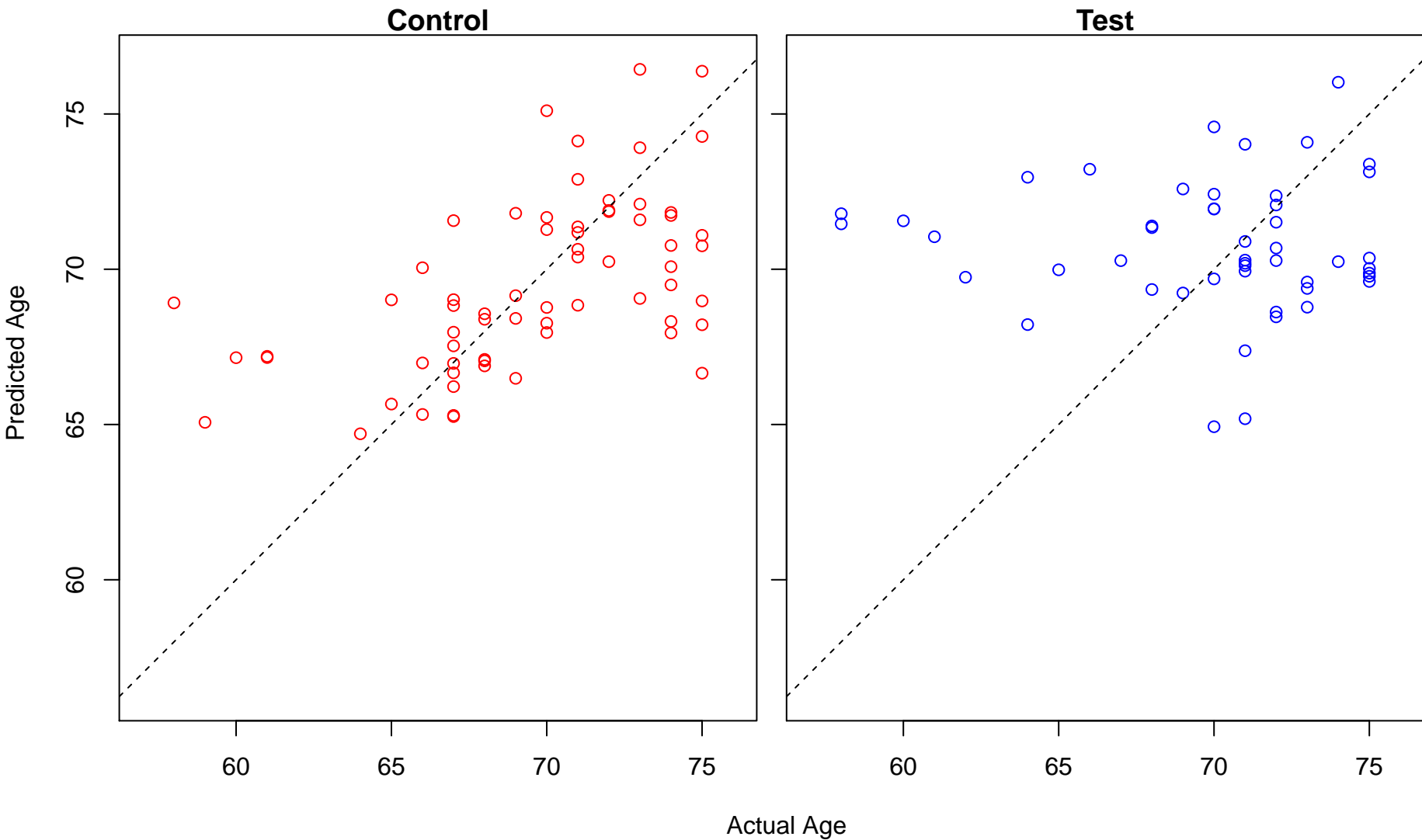
cellular carbohydrate catabolic process (Score: 0.997320)



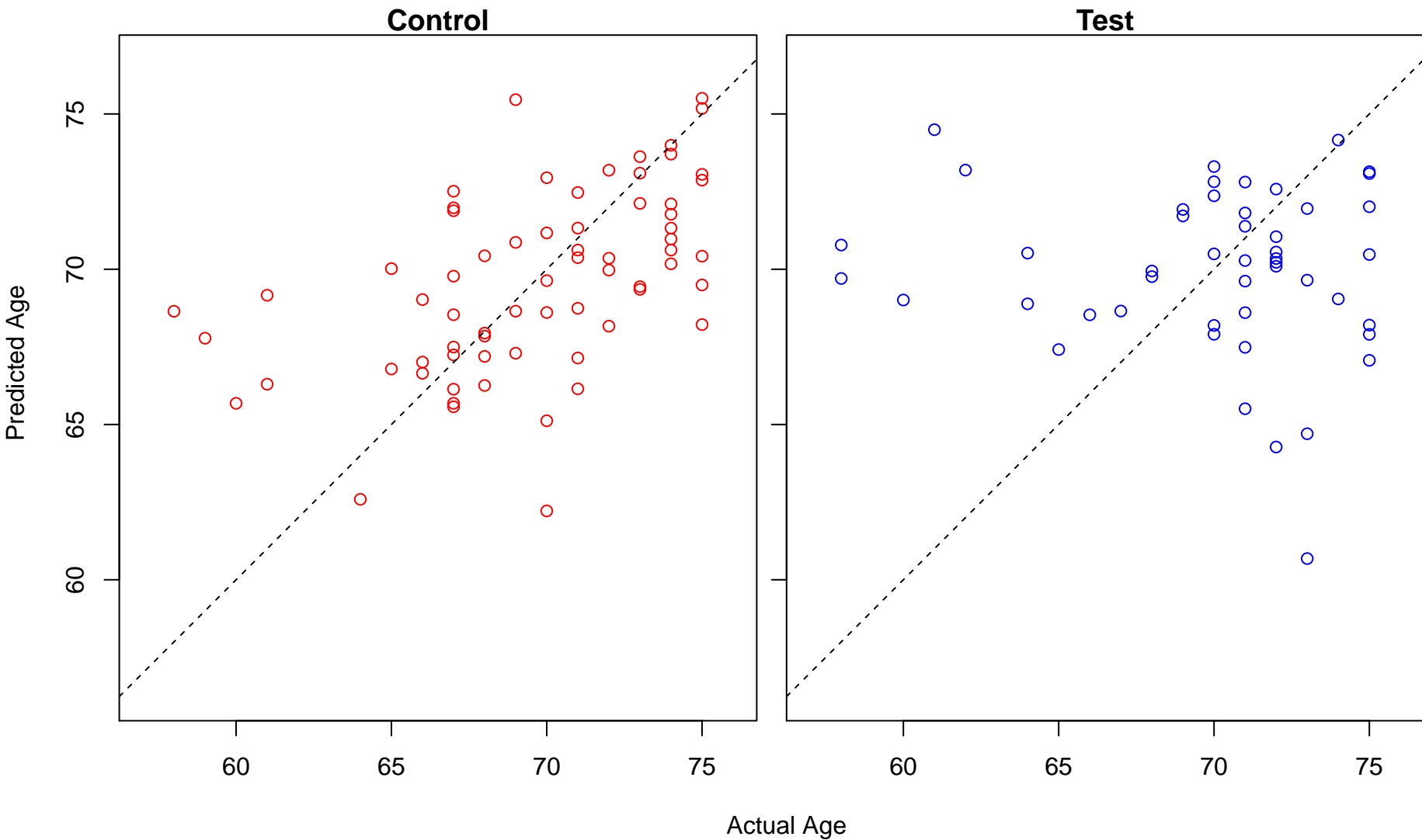
positive regulation of protein tyrosine kinase activity (Score: 0.996997)



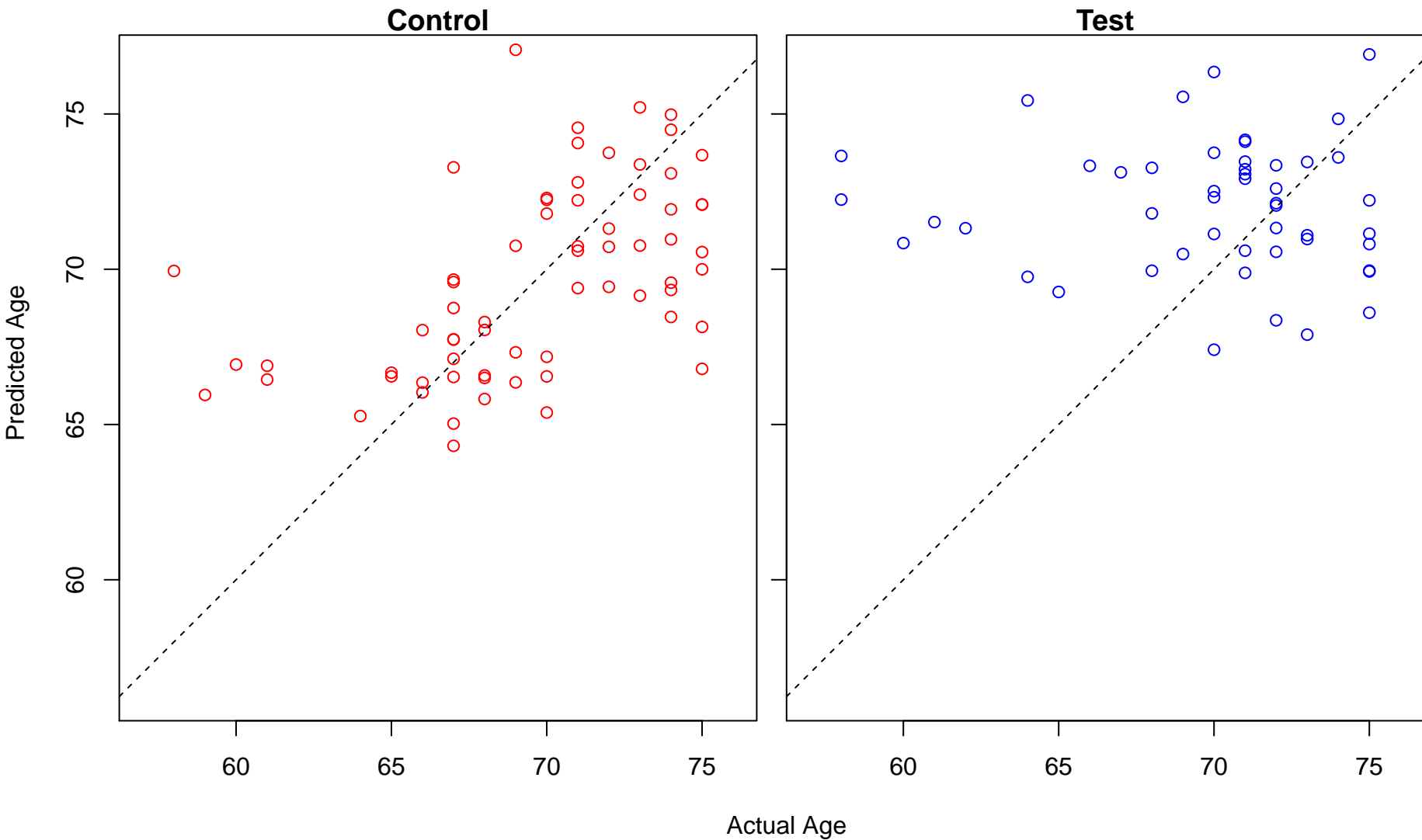
negative regulation of cell morphogenesis involved in differentiation (Score: 0.996783)



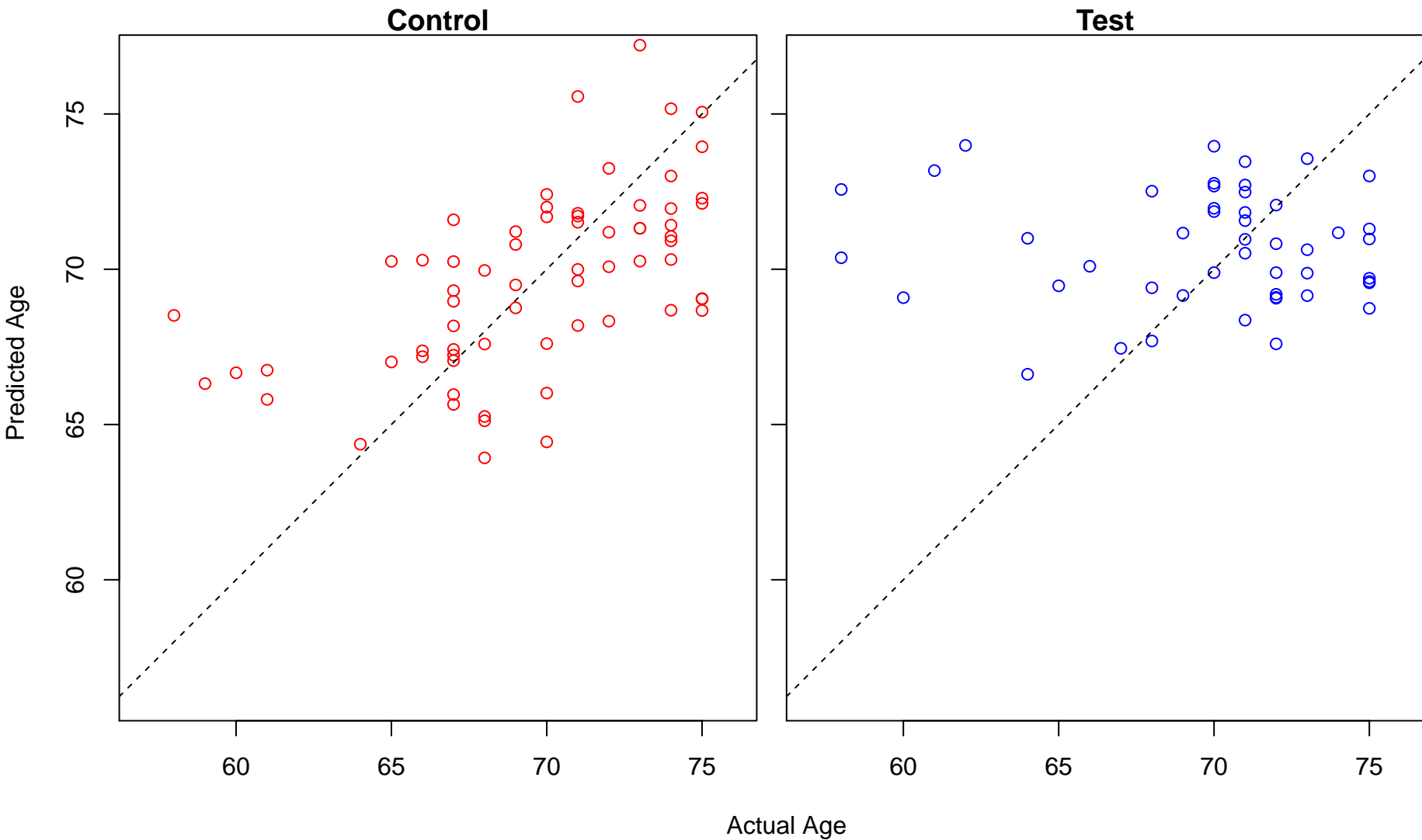
regulation of mitochondrial depolarization (Score: 0.996709)



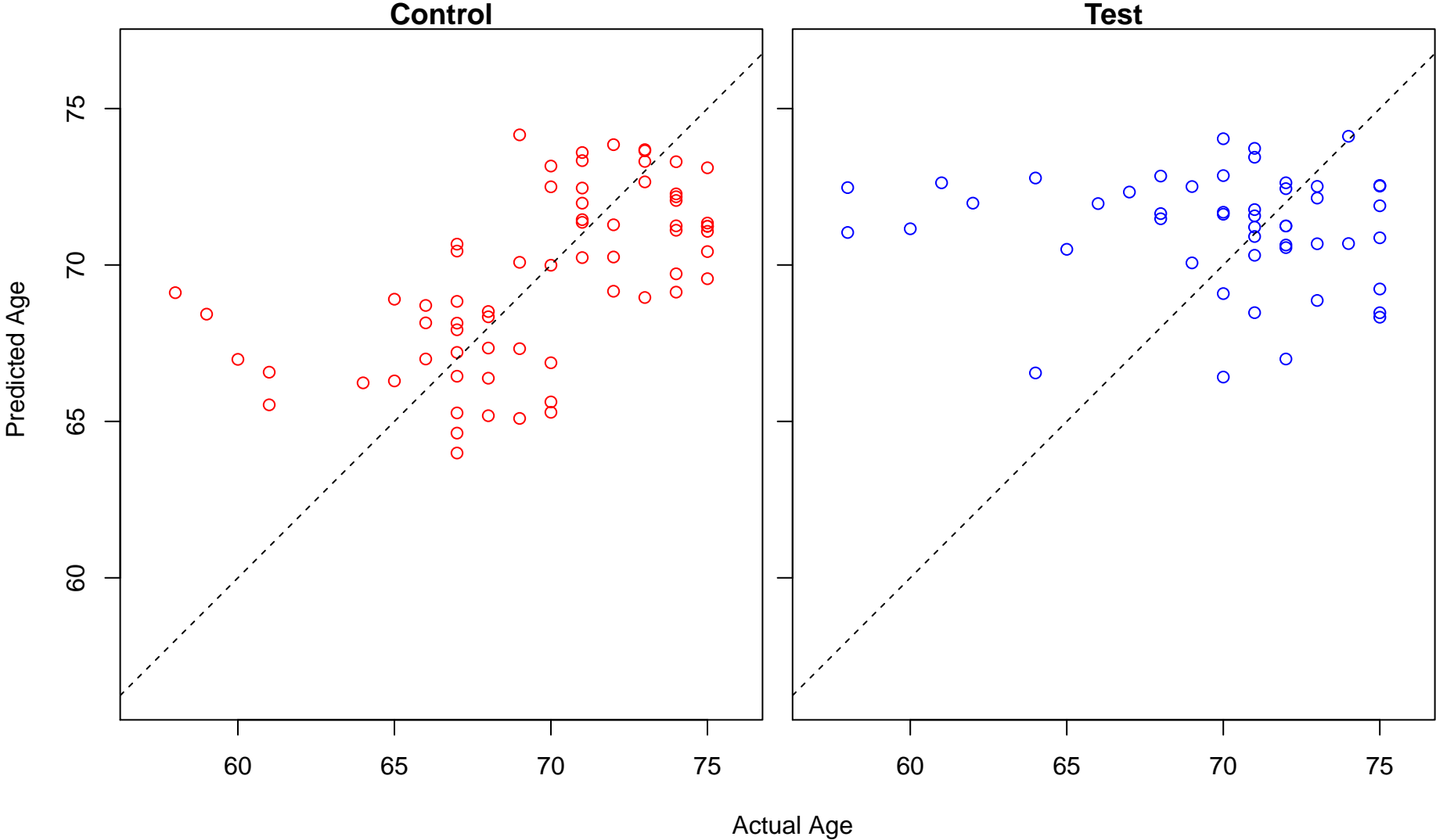
chondroitin sulfate proteoglycan metabolic process (Score: 0.996503)



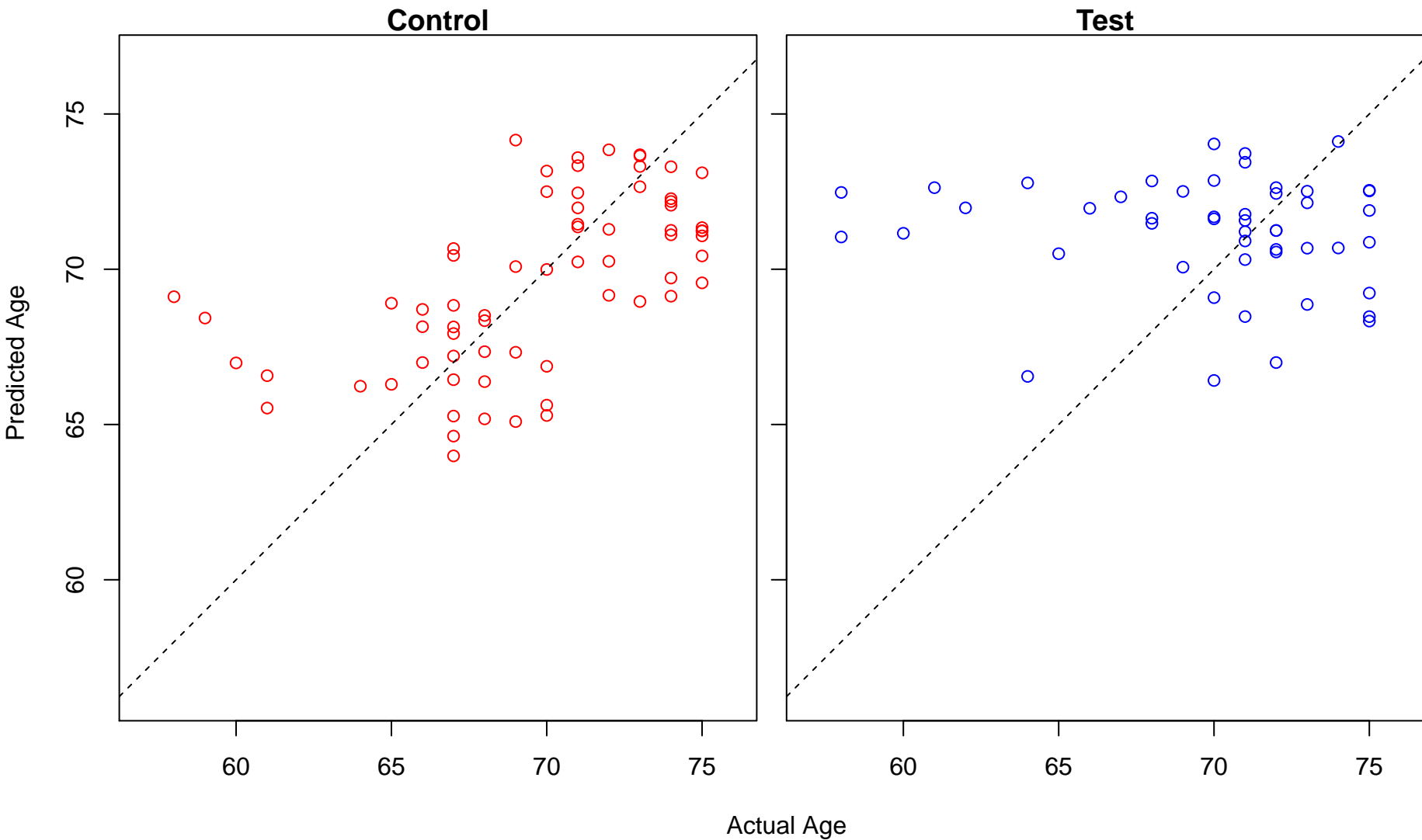
carbohydrate catabolic process (Score: 0.996481)



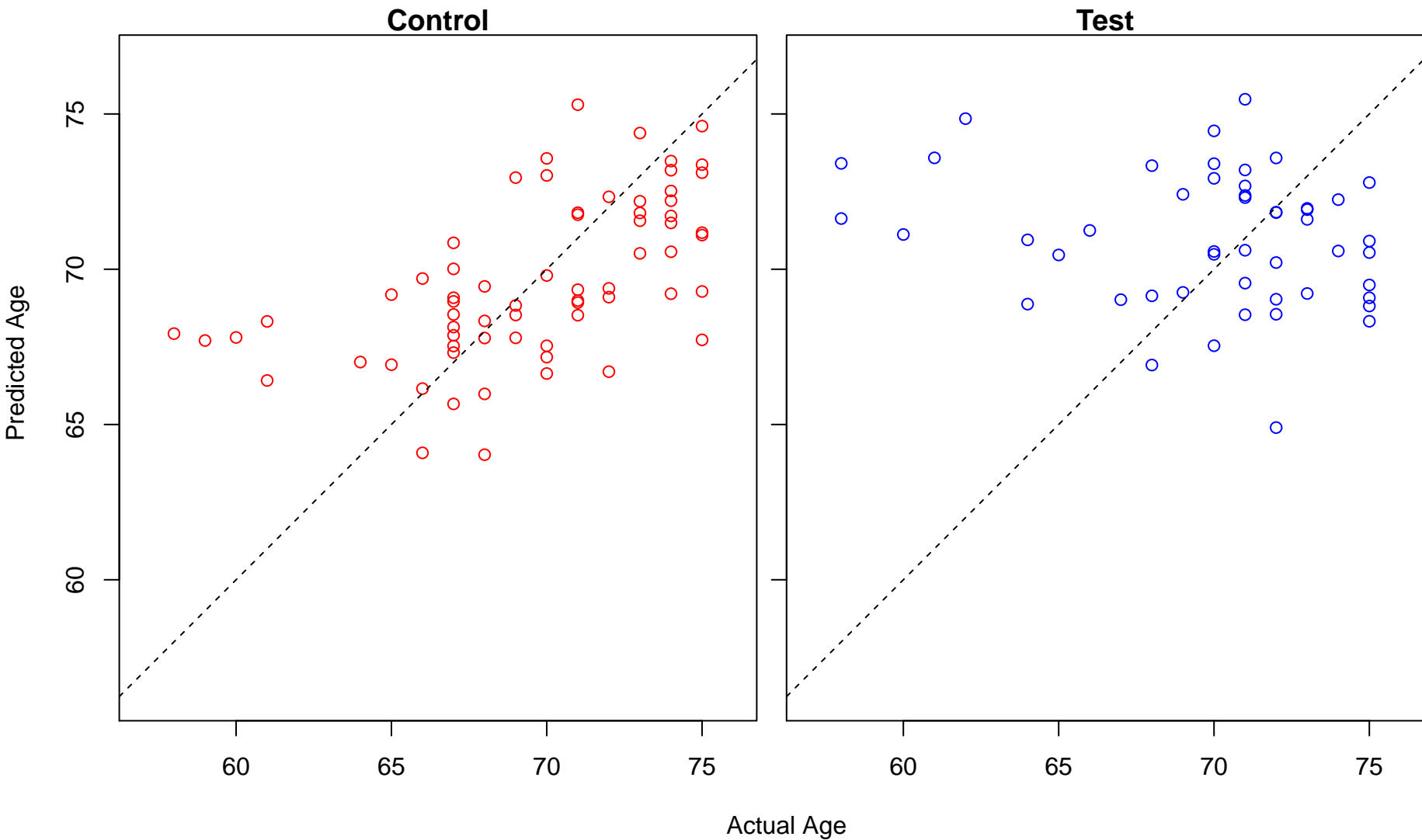
somatic diversification of immune receptors via germline recombination within a single locus (Score: 0.9



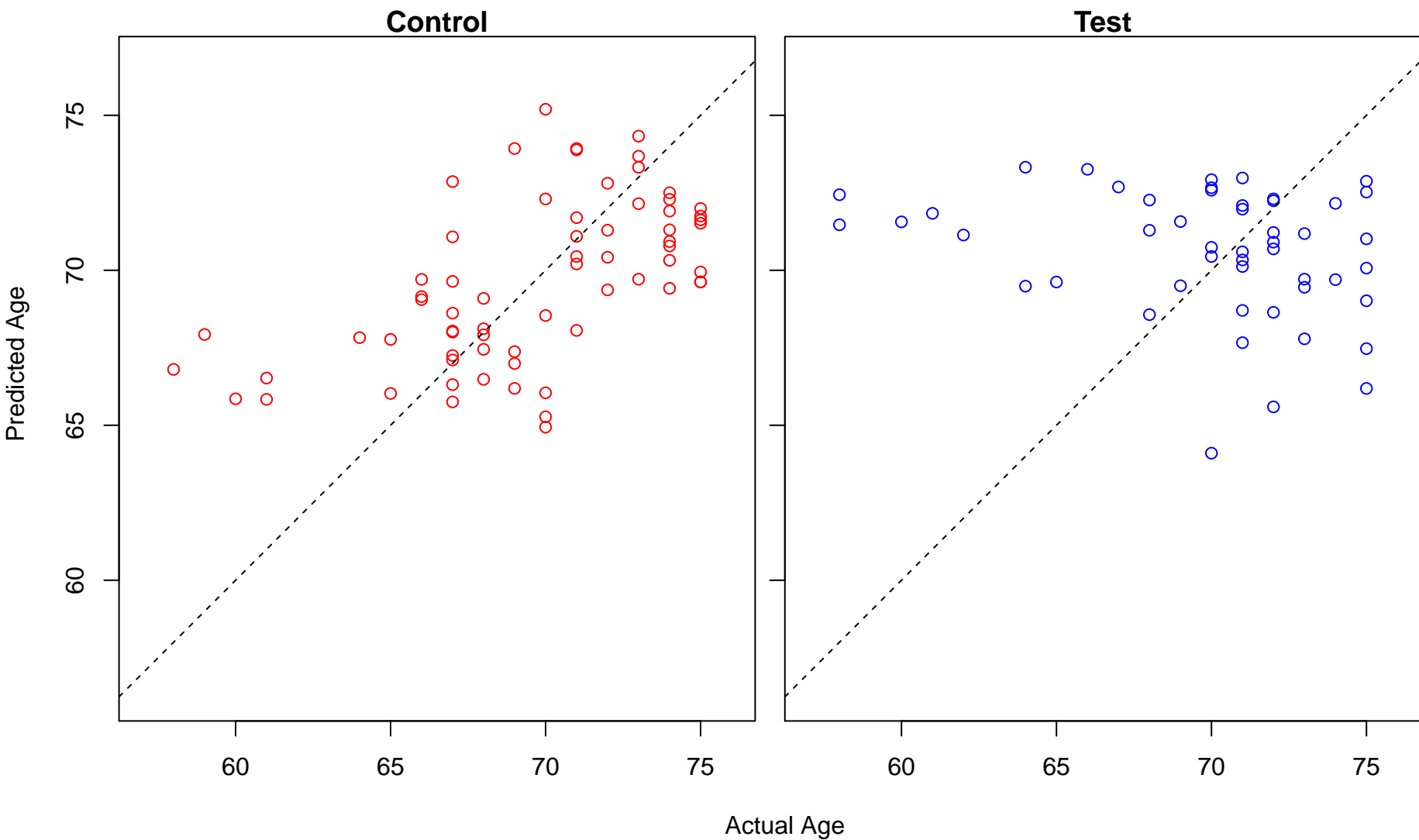
somatic cell DNA recombination (Score: 0.996457)



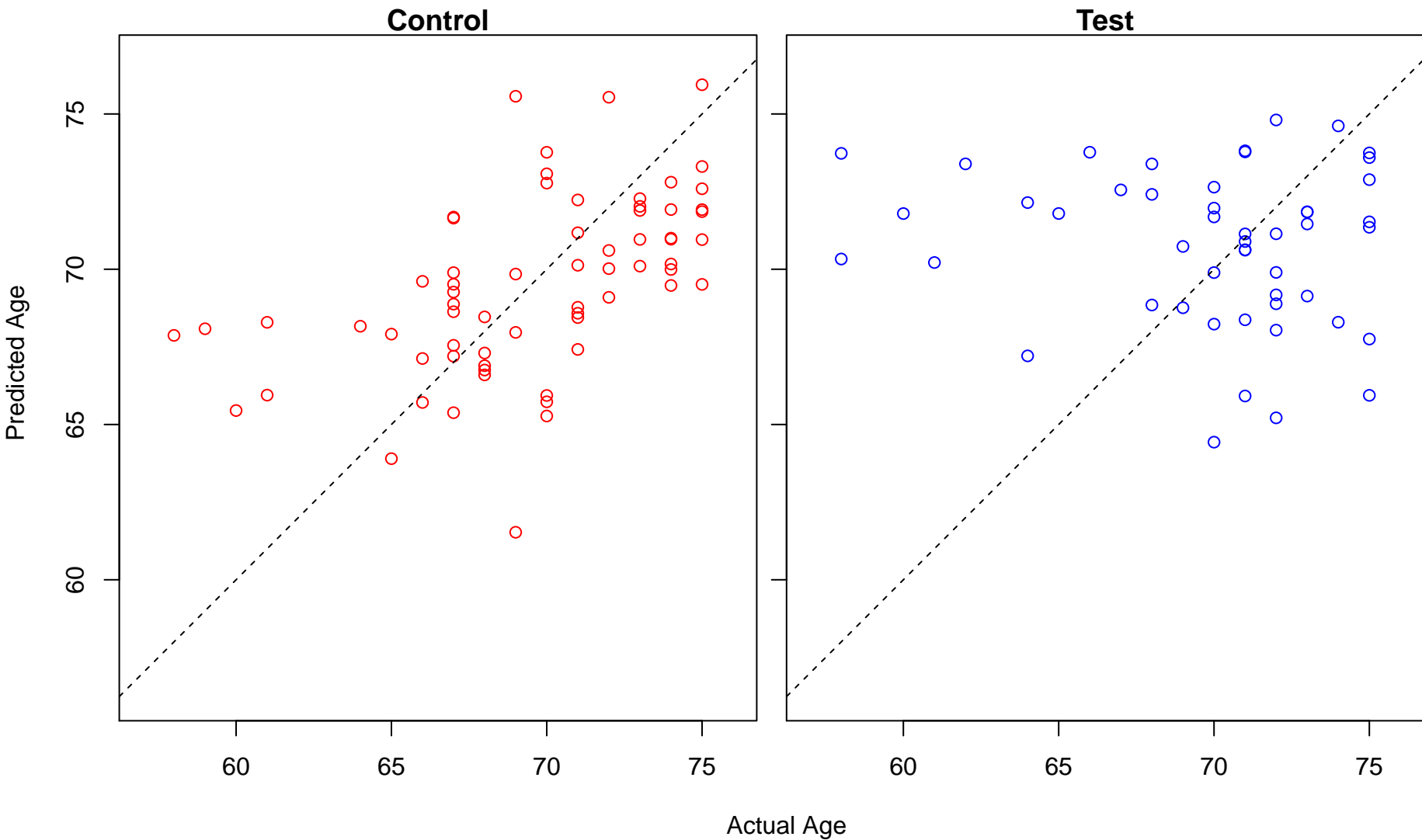
regulation of endothelial cell chemotaxis (Score: 0.996449)



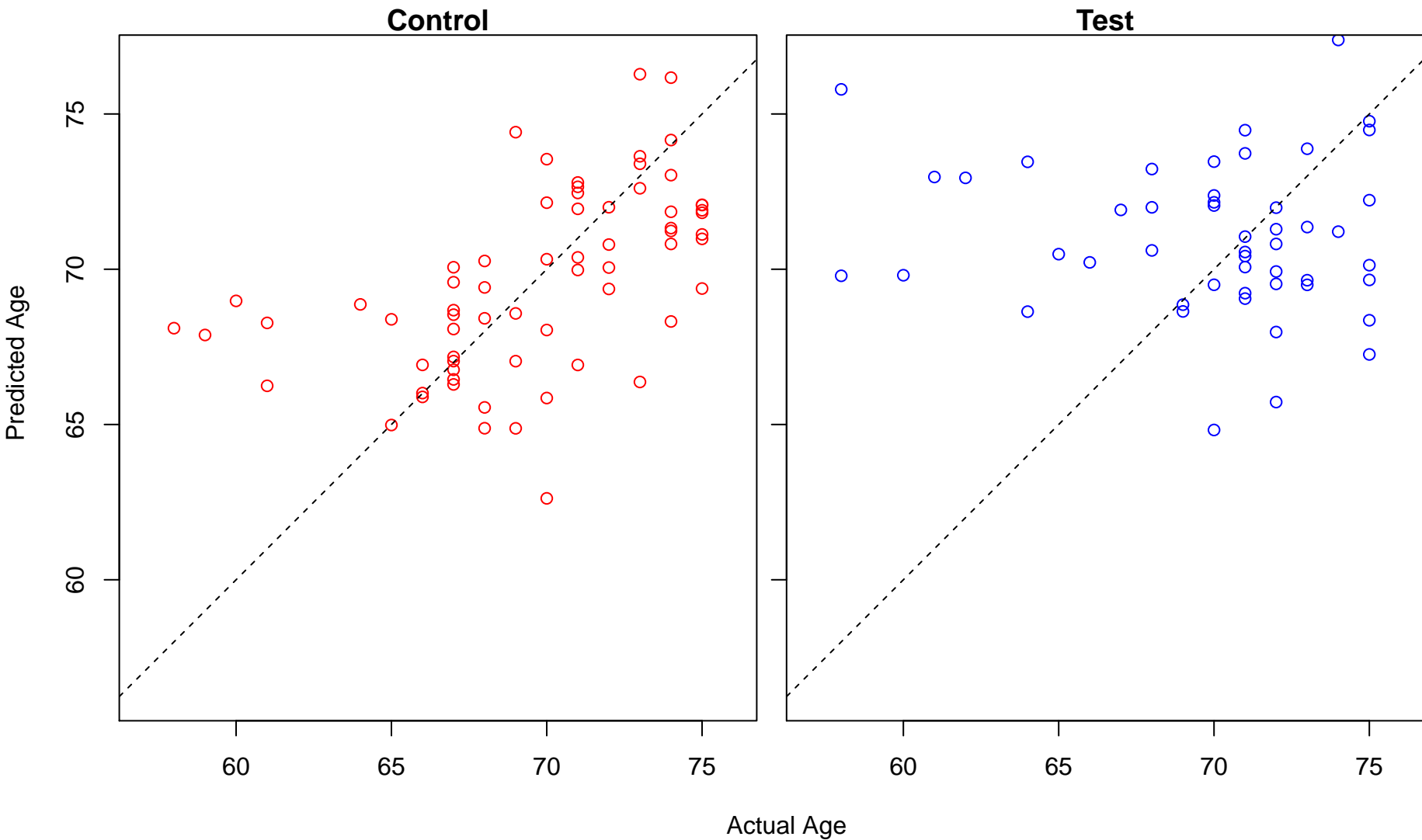
lipopolysaccharide-mediated signaling pathway (Score: 0.995277)



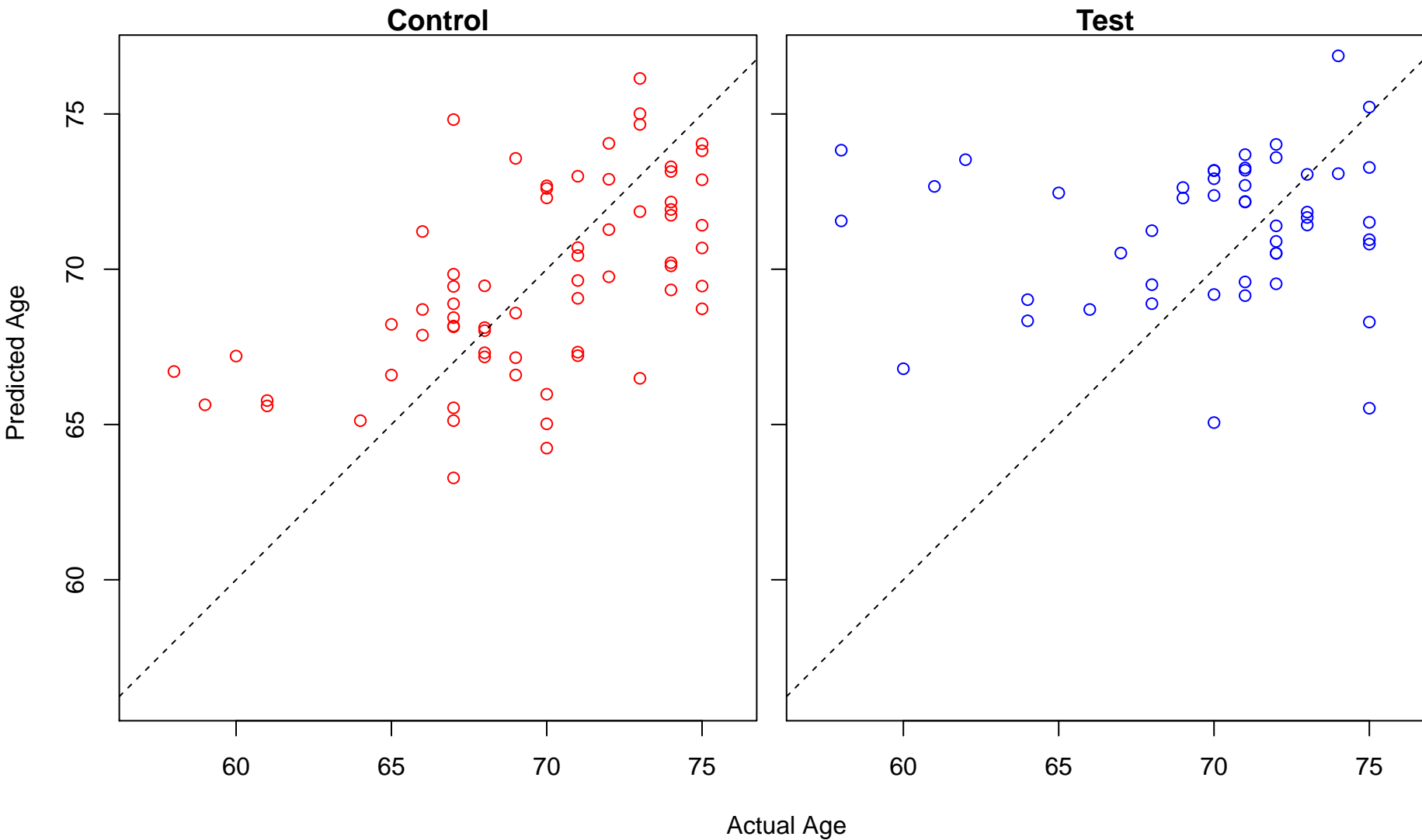
regulation of ERAD pathway (Score: 0.994841)



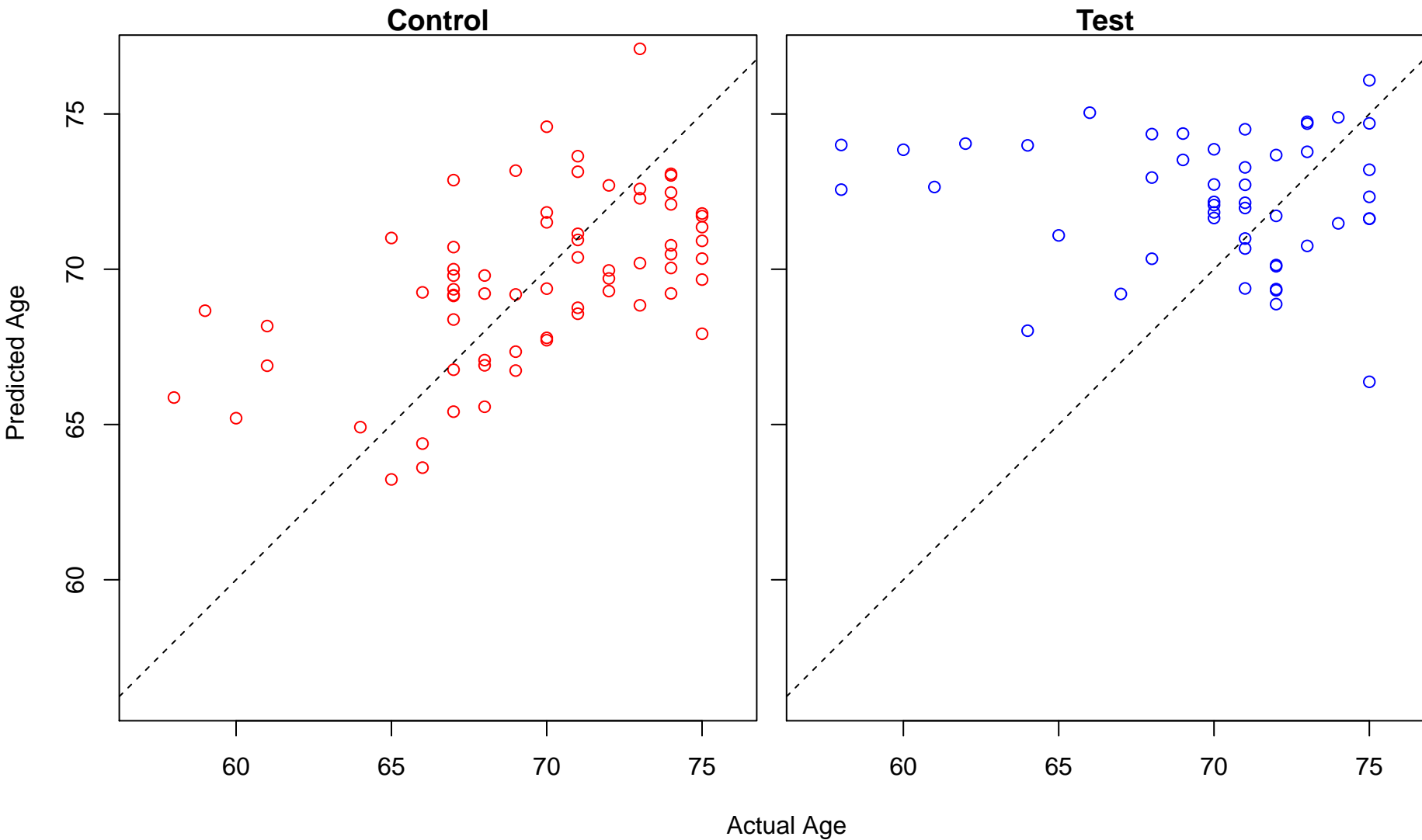
negative regulation of transporter activity (Score: 0.994711)



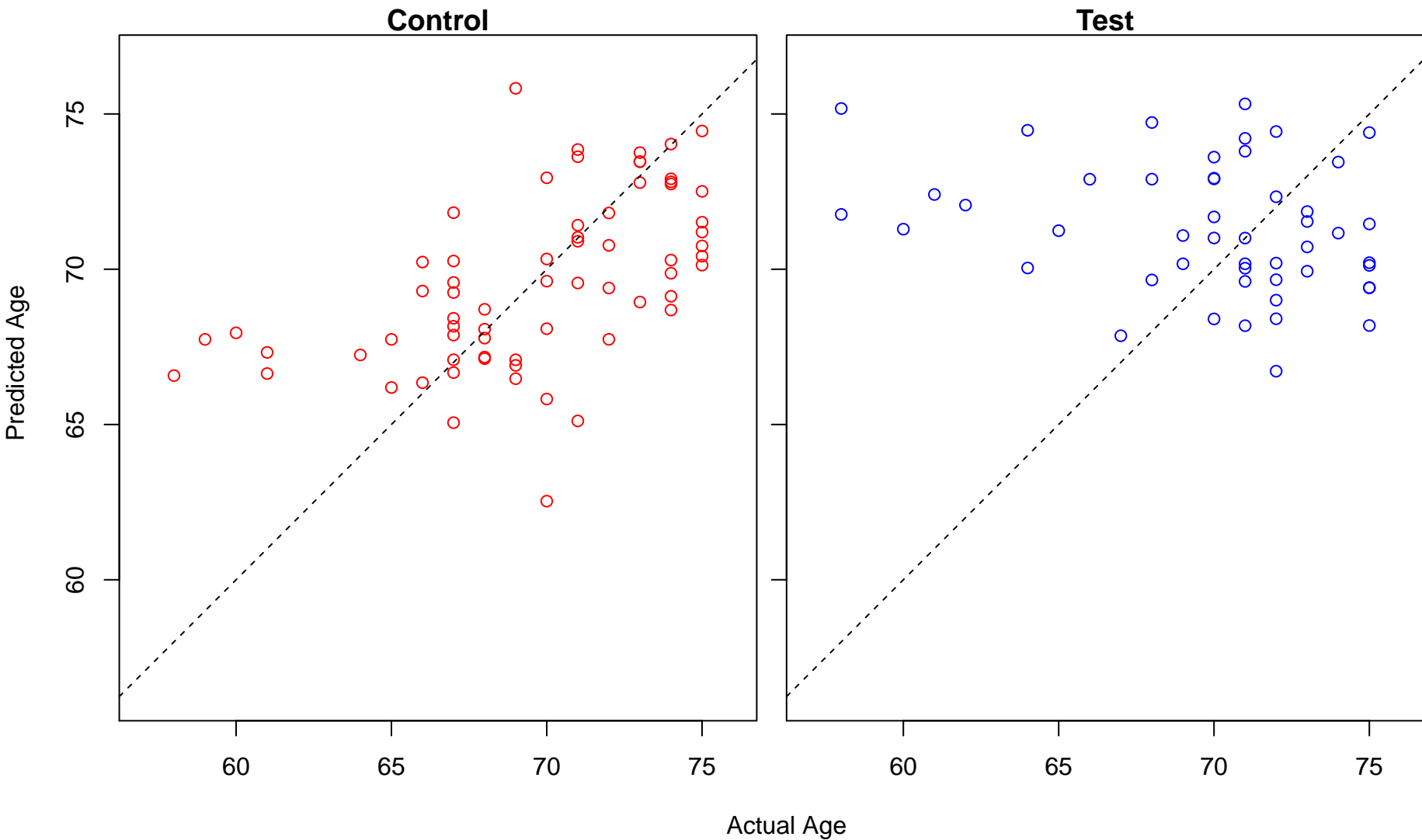
establishment of protein localization to plasma membrane (Score: 0.994550)



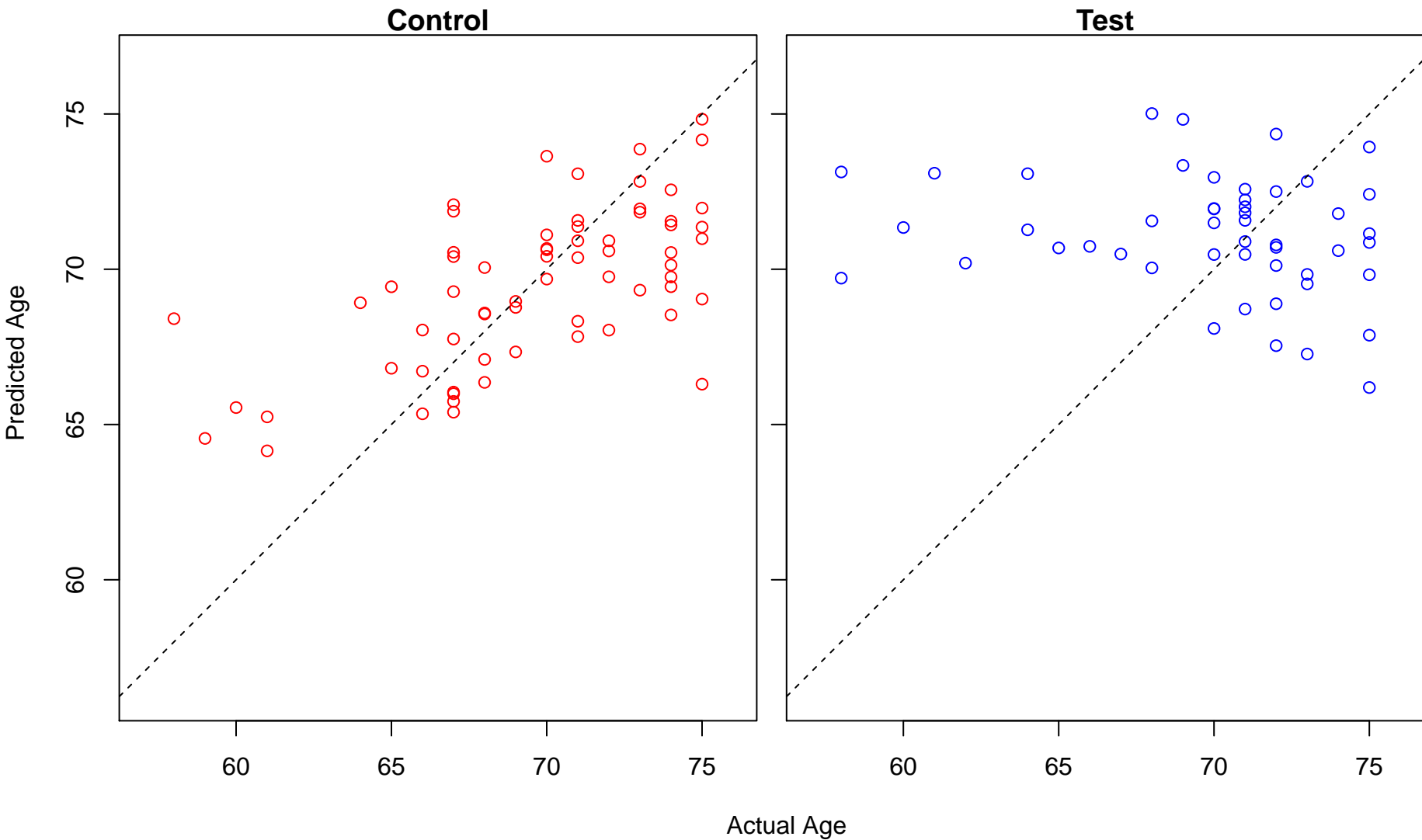
cardiac epithelial to mesenchymal transition (Score: 0.994286)



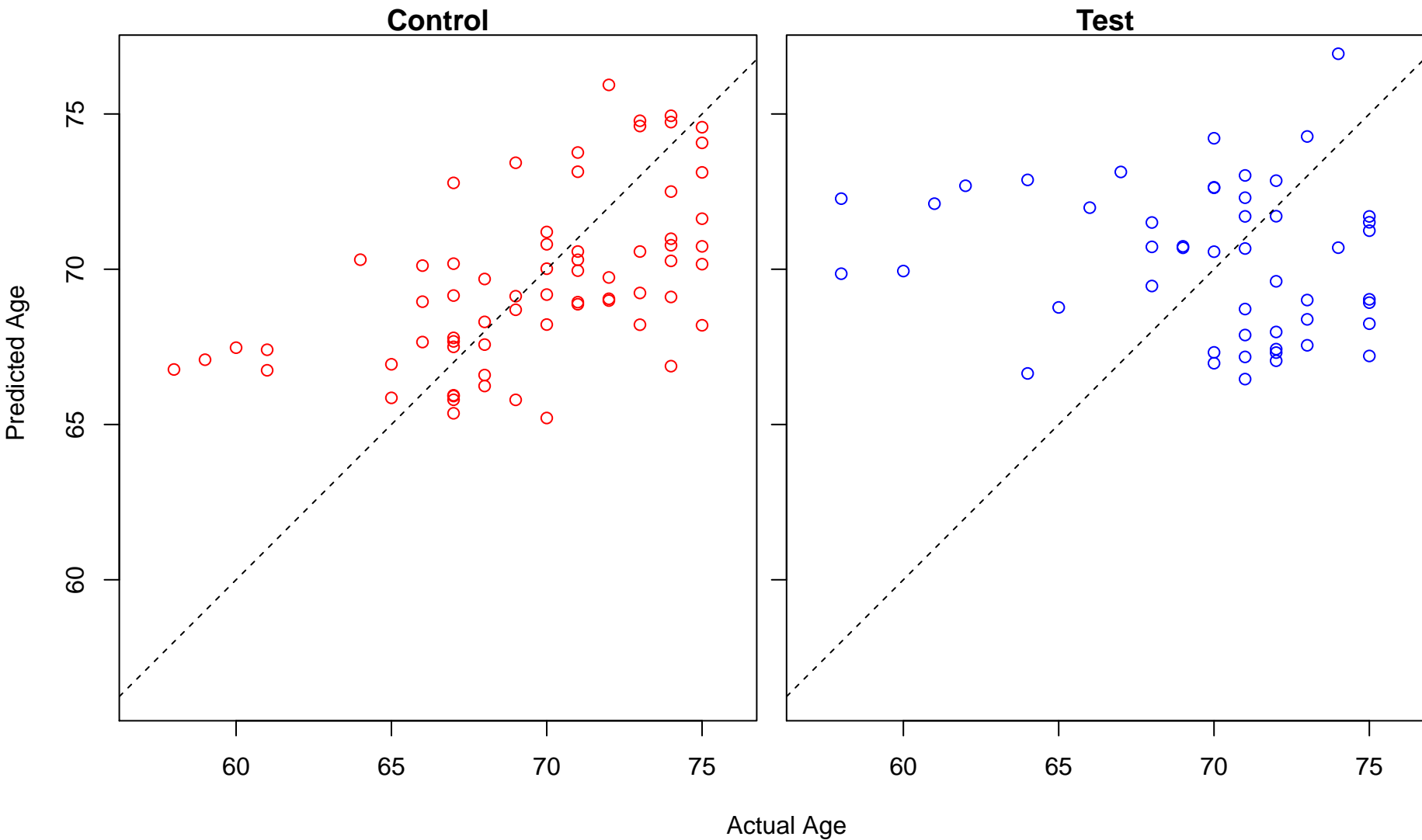
amino sugar metabolic process (Score: 0.994168)



ncRNA 3'-end processing (Score: 0.993998)

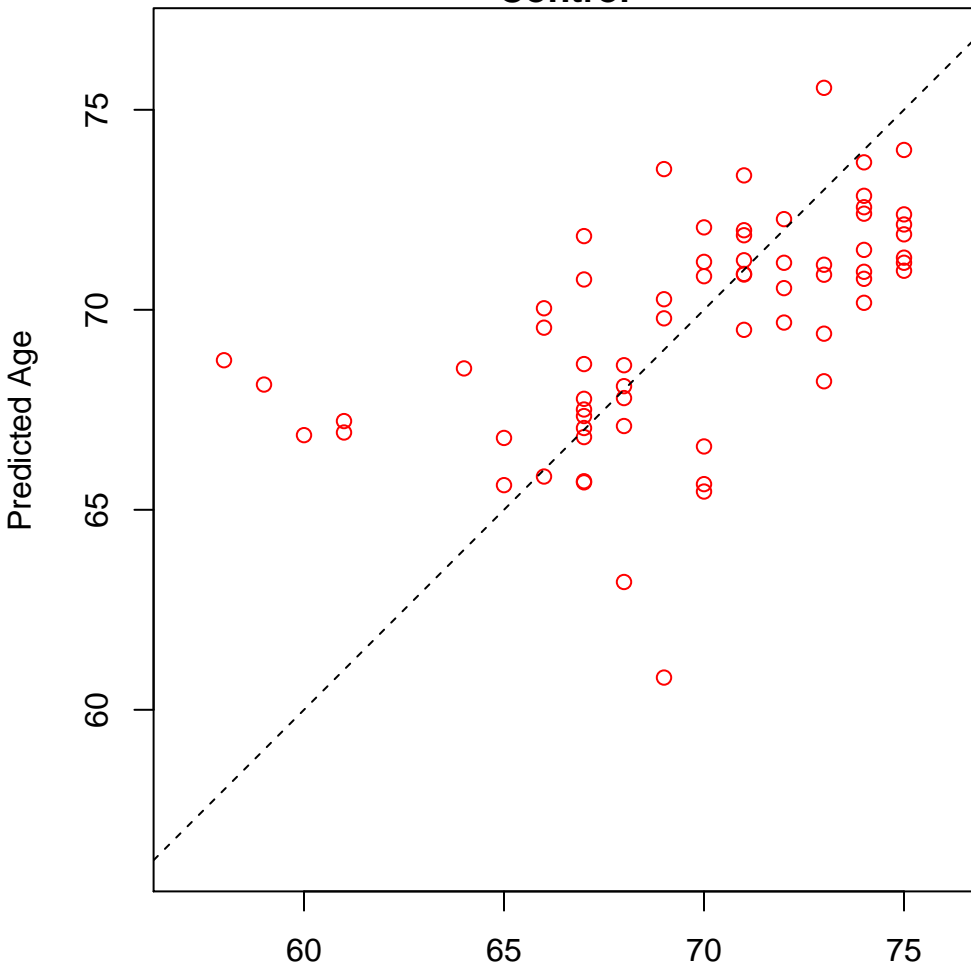


histone deacetylation (Score: 0.993207)

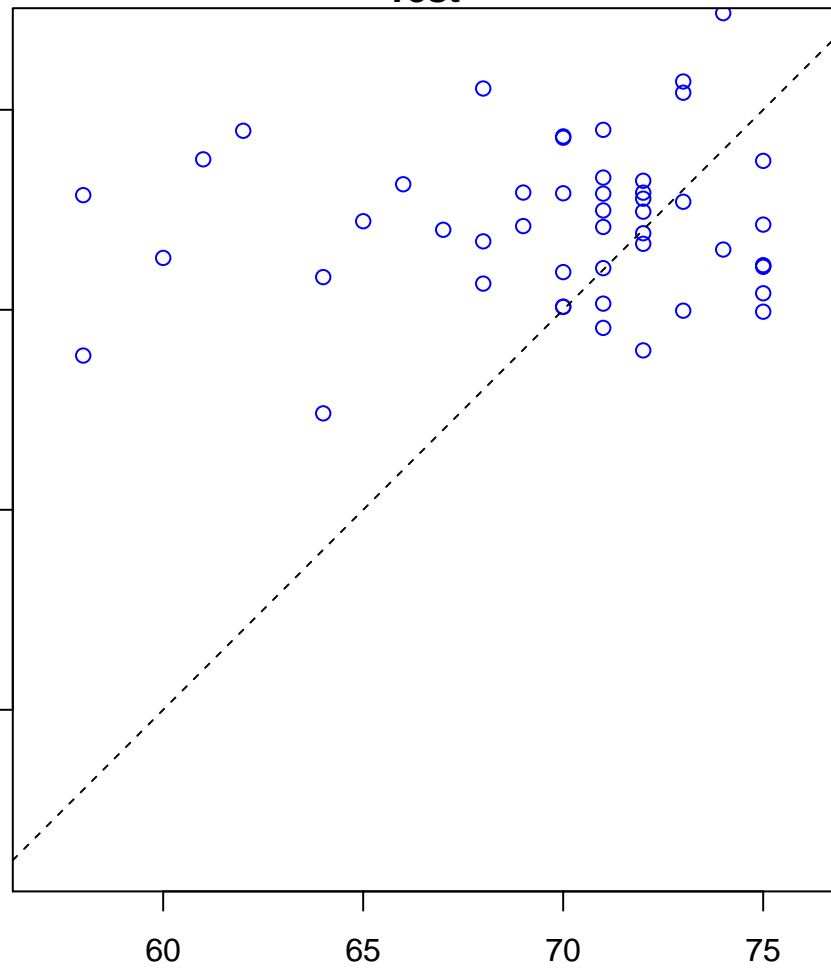


vascular process in circulatory system (Score: 0.993140)

Control

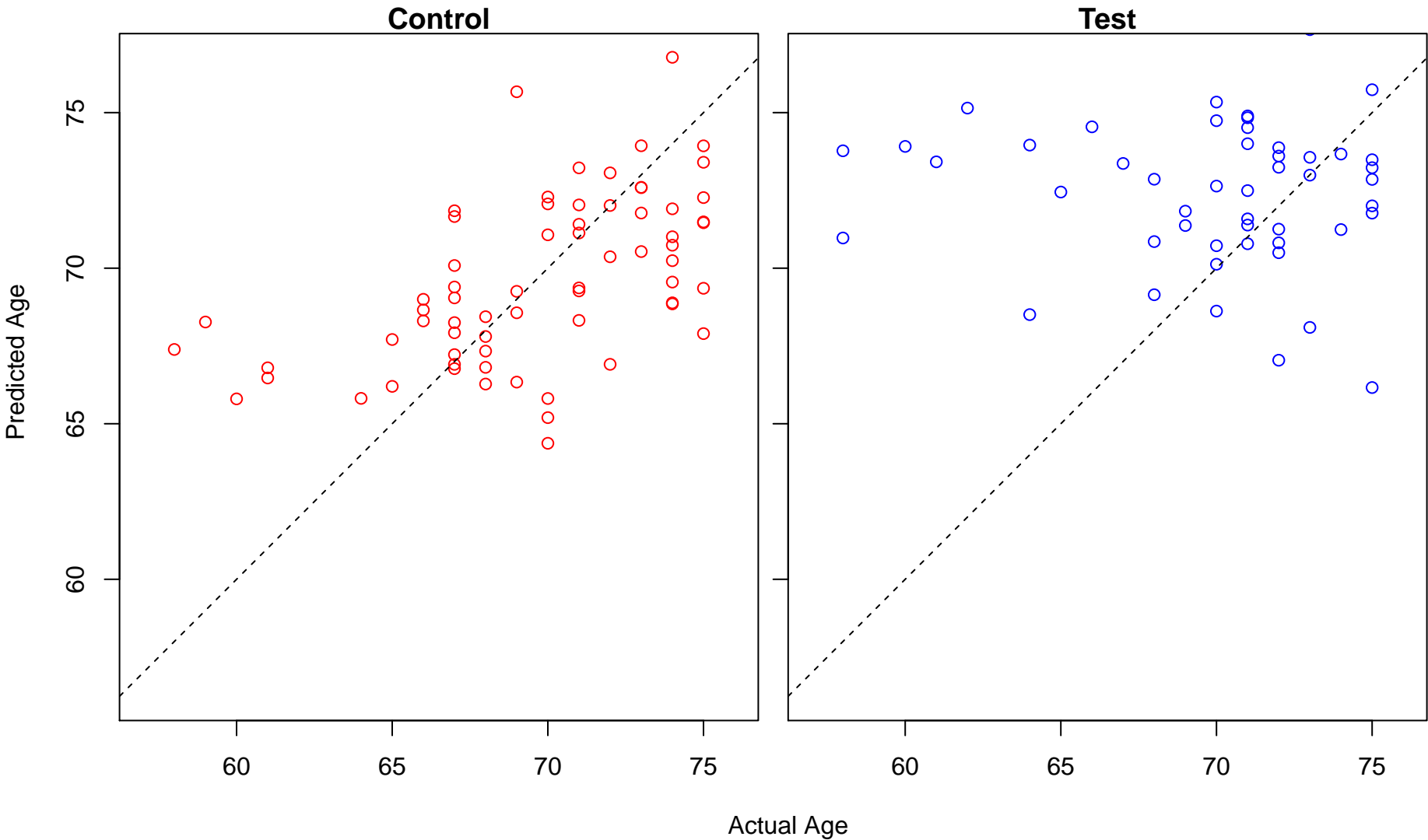


Test

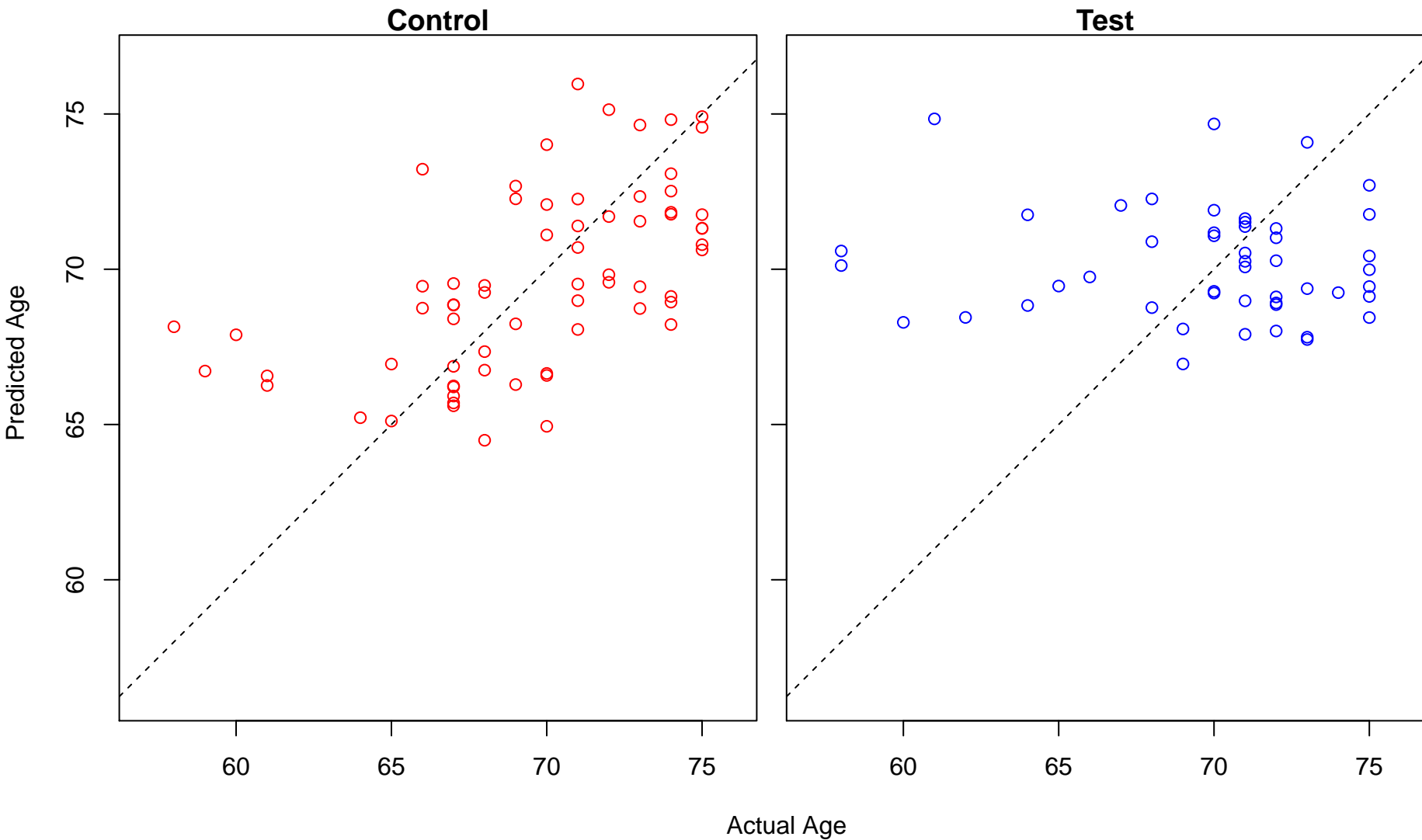


Actual Age

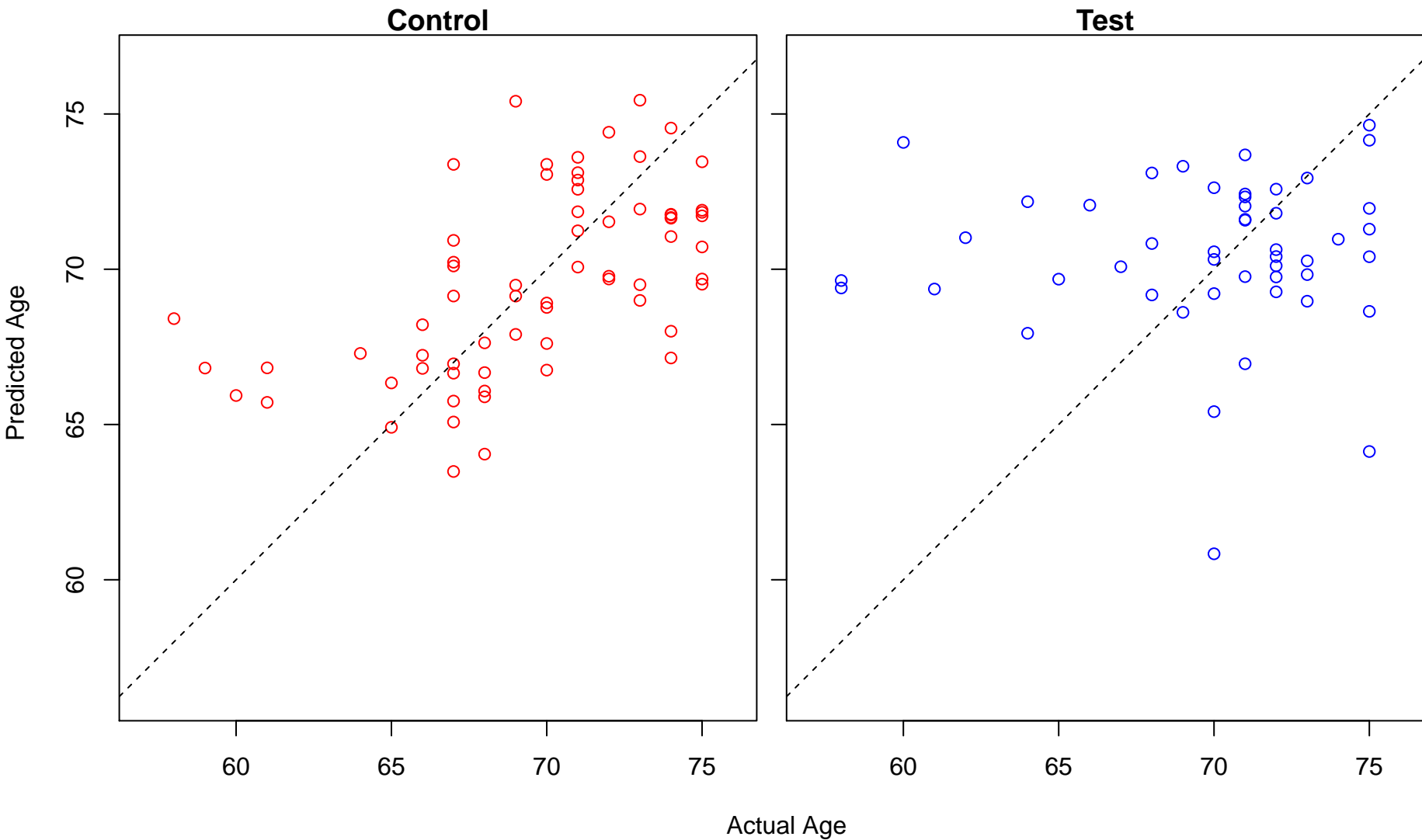
cellular carbohydrate biosynthetic process (Score: 0.992989)



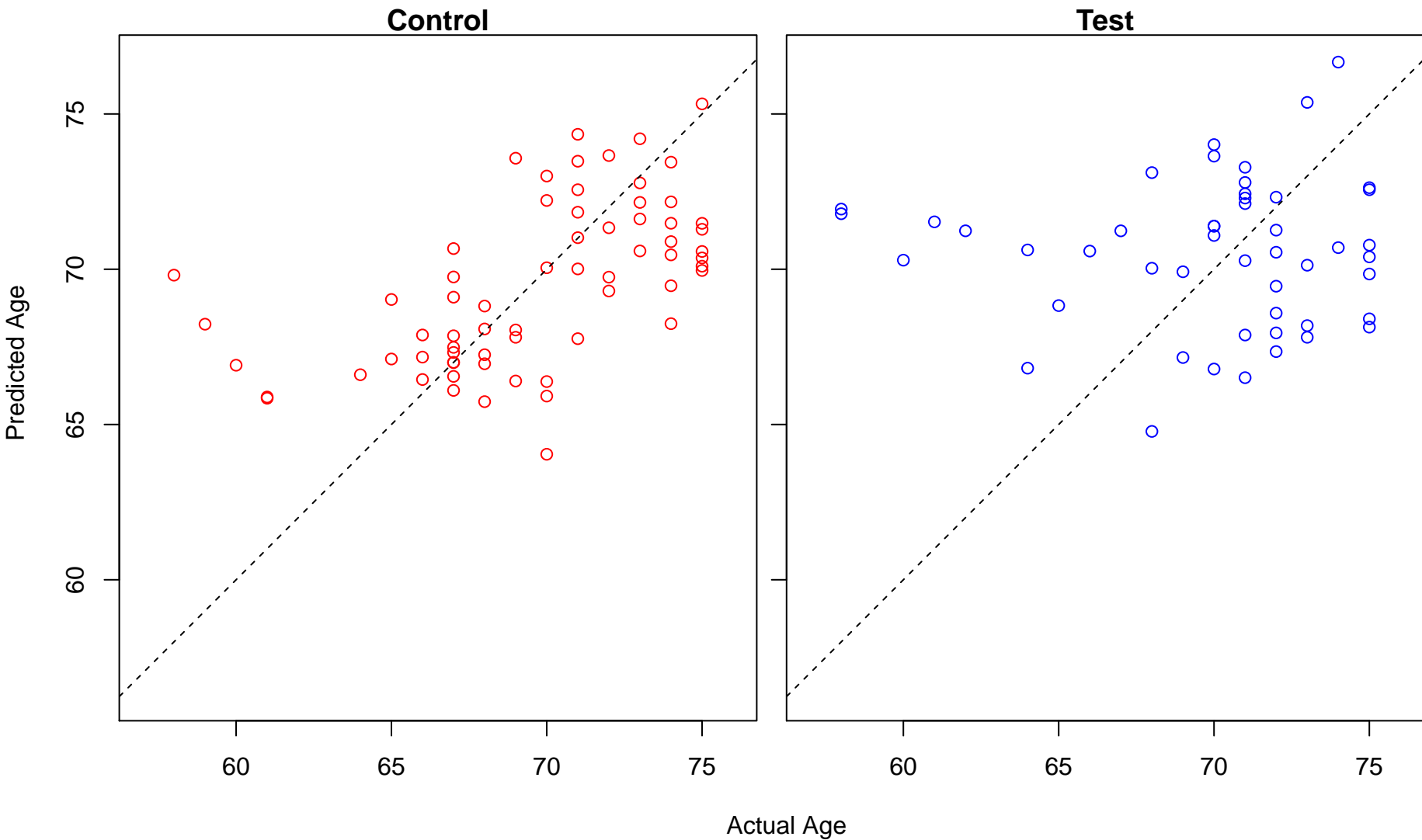
DNA dealkylation (Score: 0.992503)



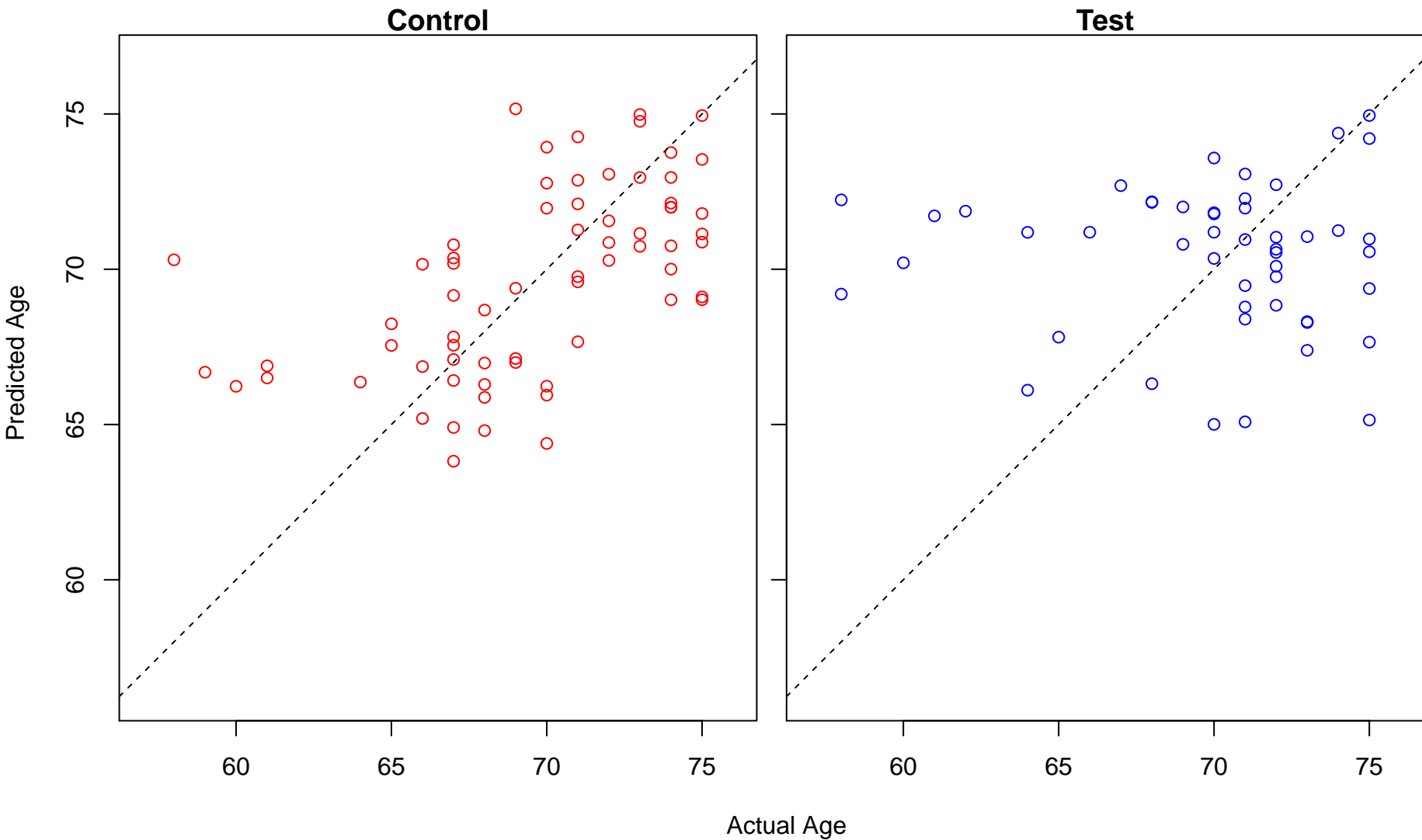
nucleotide transport (Score: 0.991691)



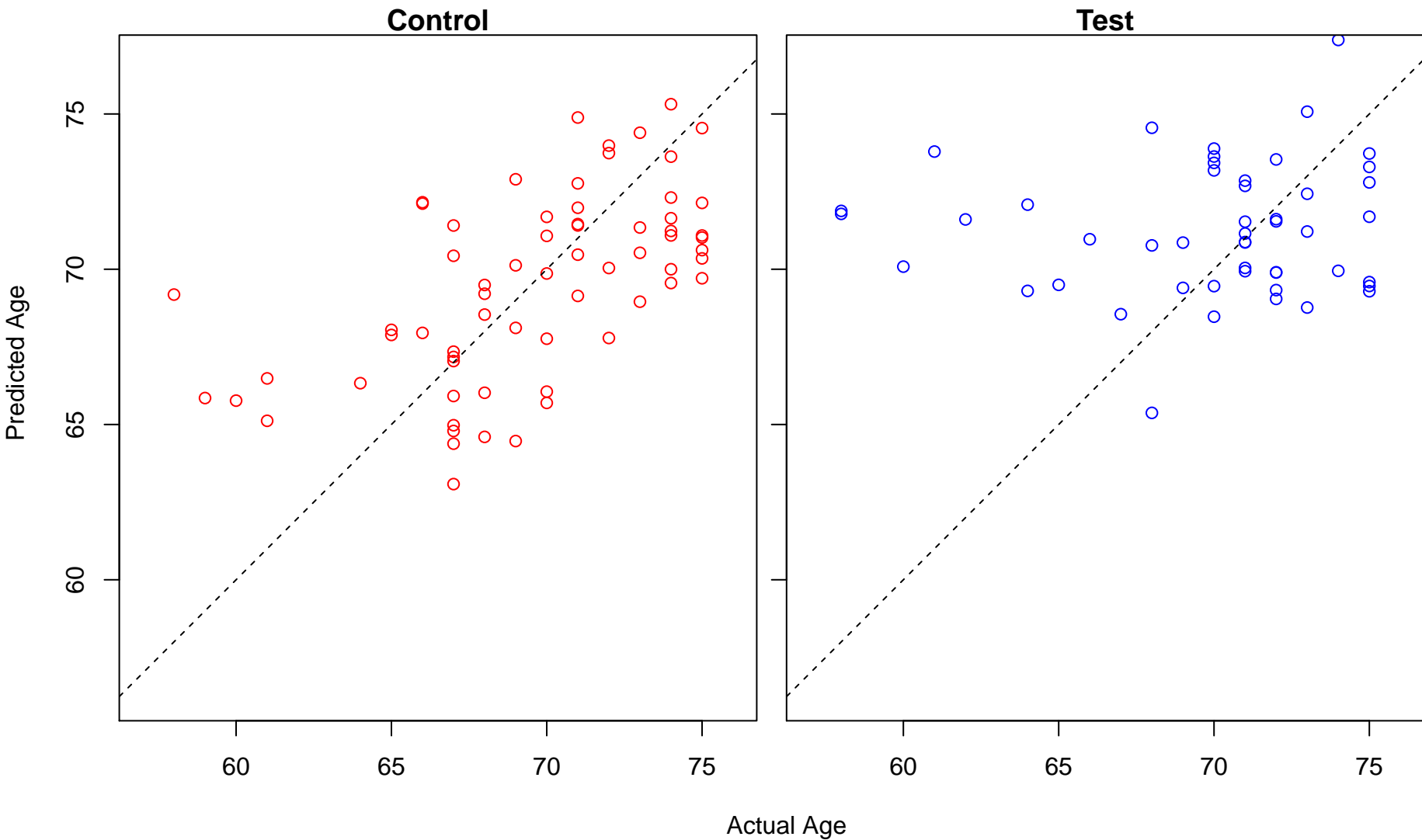
canonical Wnt signaling pathway (Score: 0.991657)



antibacterial humoral response (Score: 0.991648)

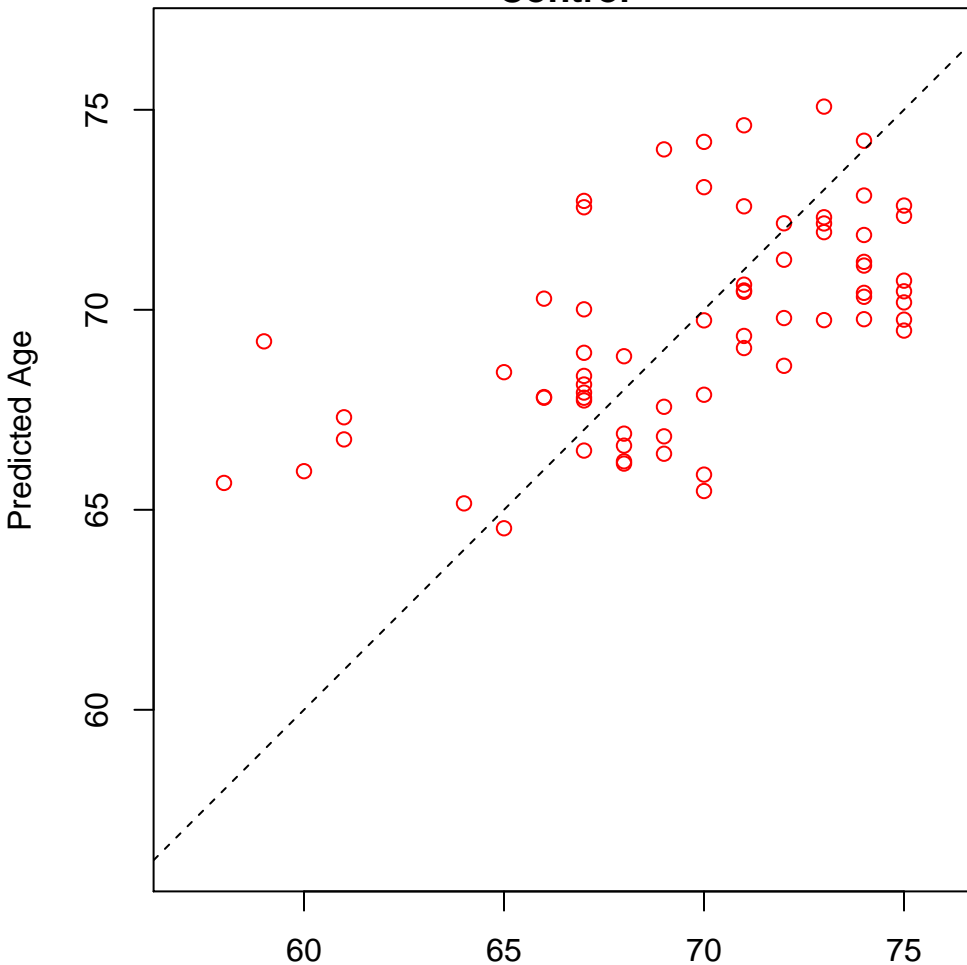


porphyrin-containing compound metabolic process (Score: 0.991366)

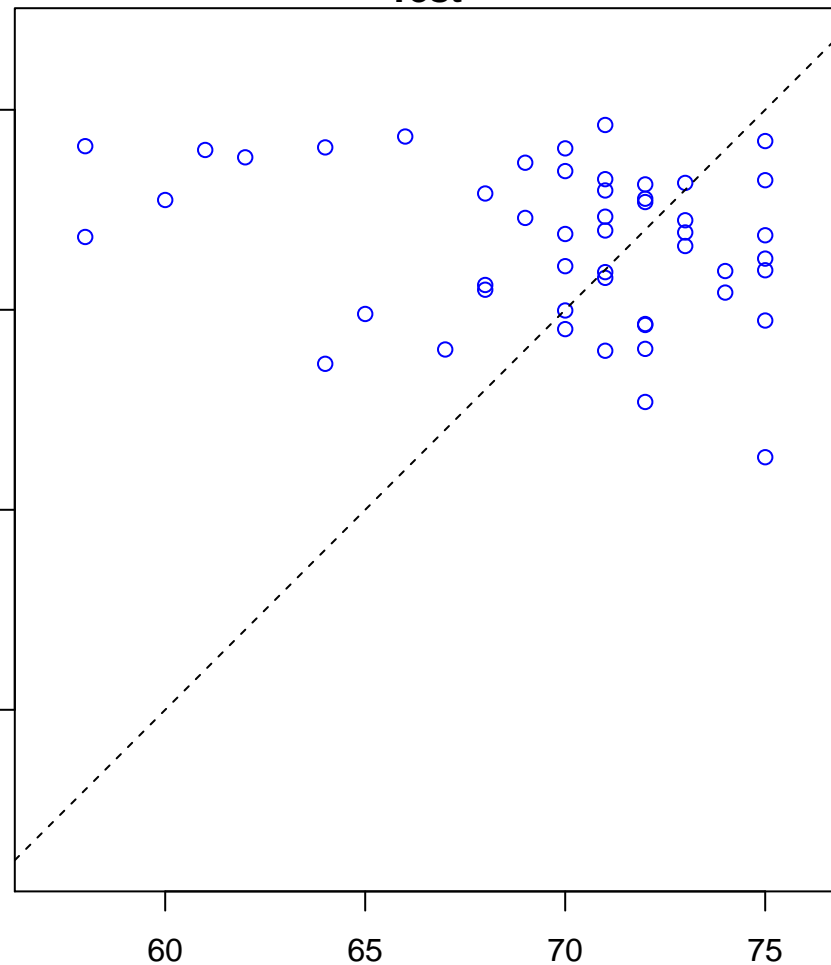


embryonic heart tube development (Score: 0.991313)

Control

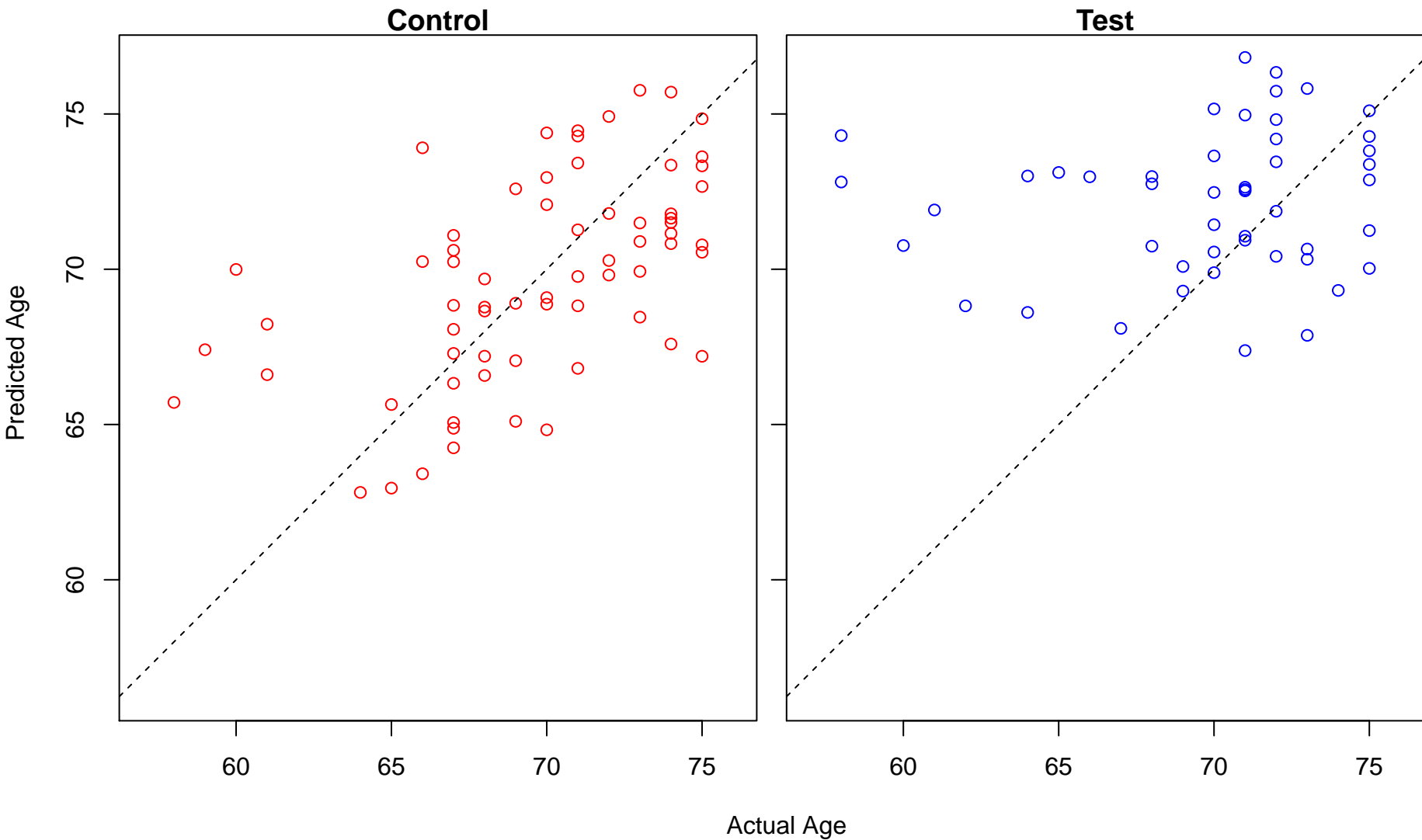


Test

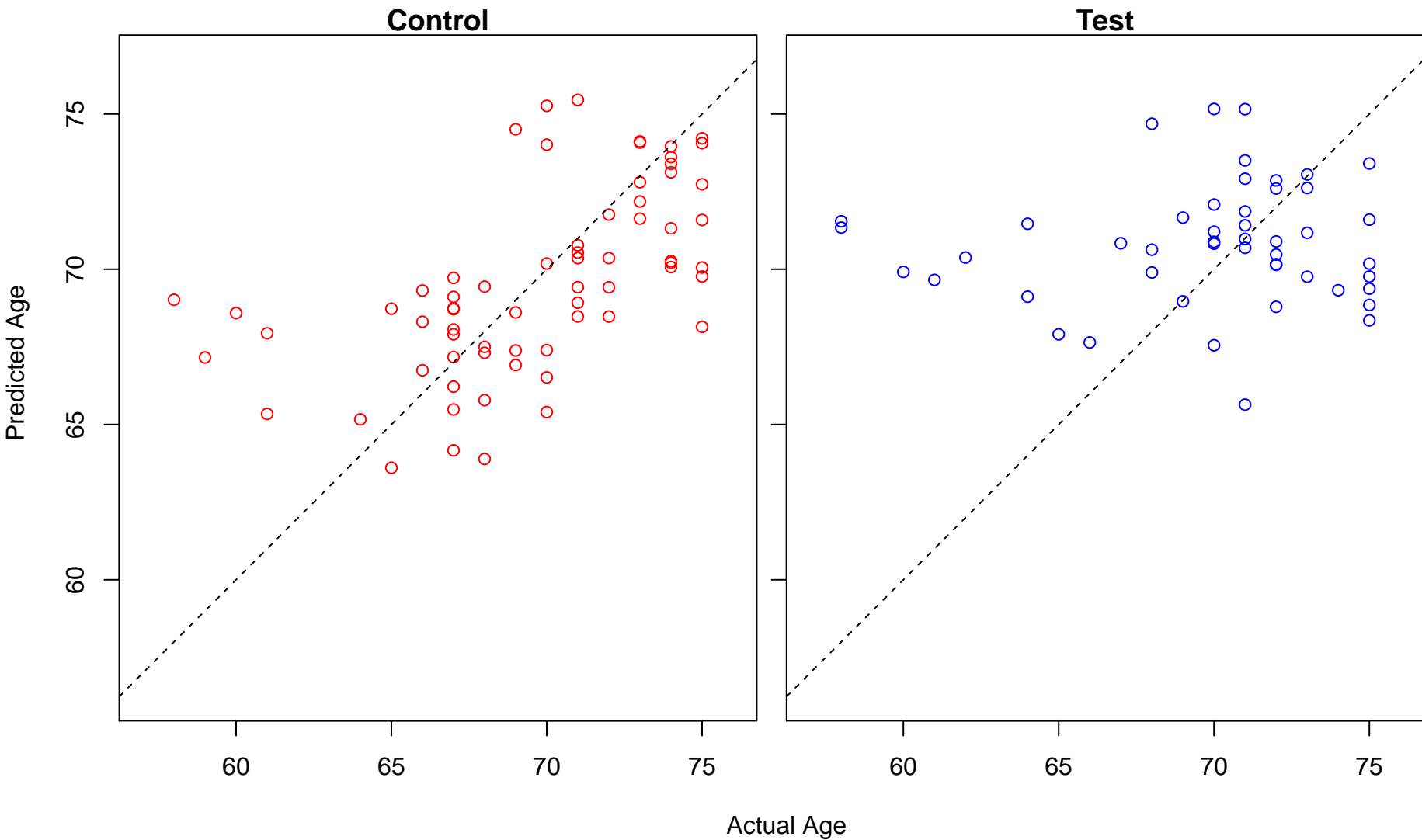


Actual Age

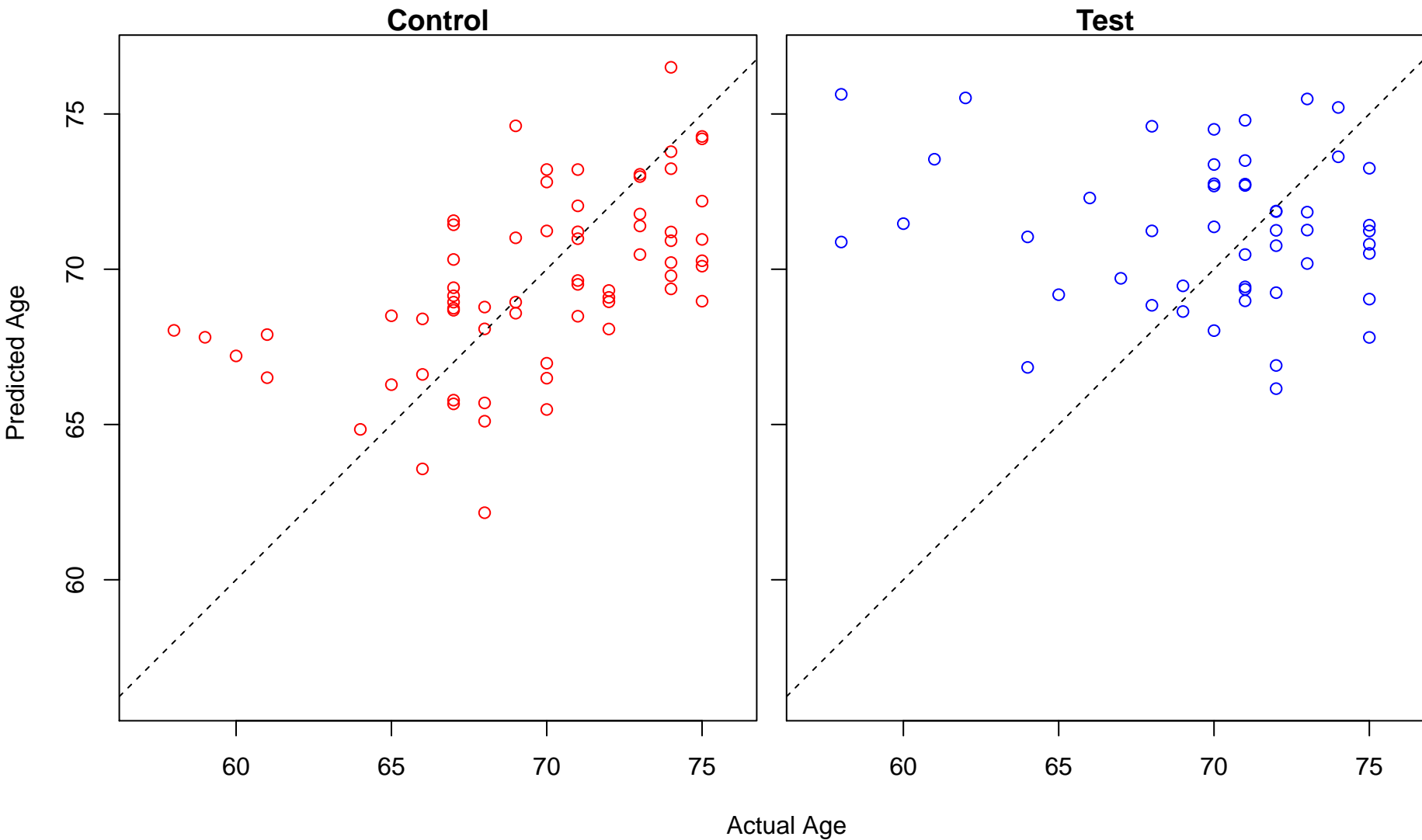
fatty acid biosynthetic process (Score: 0.991211)



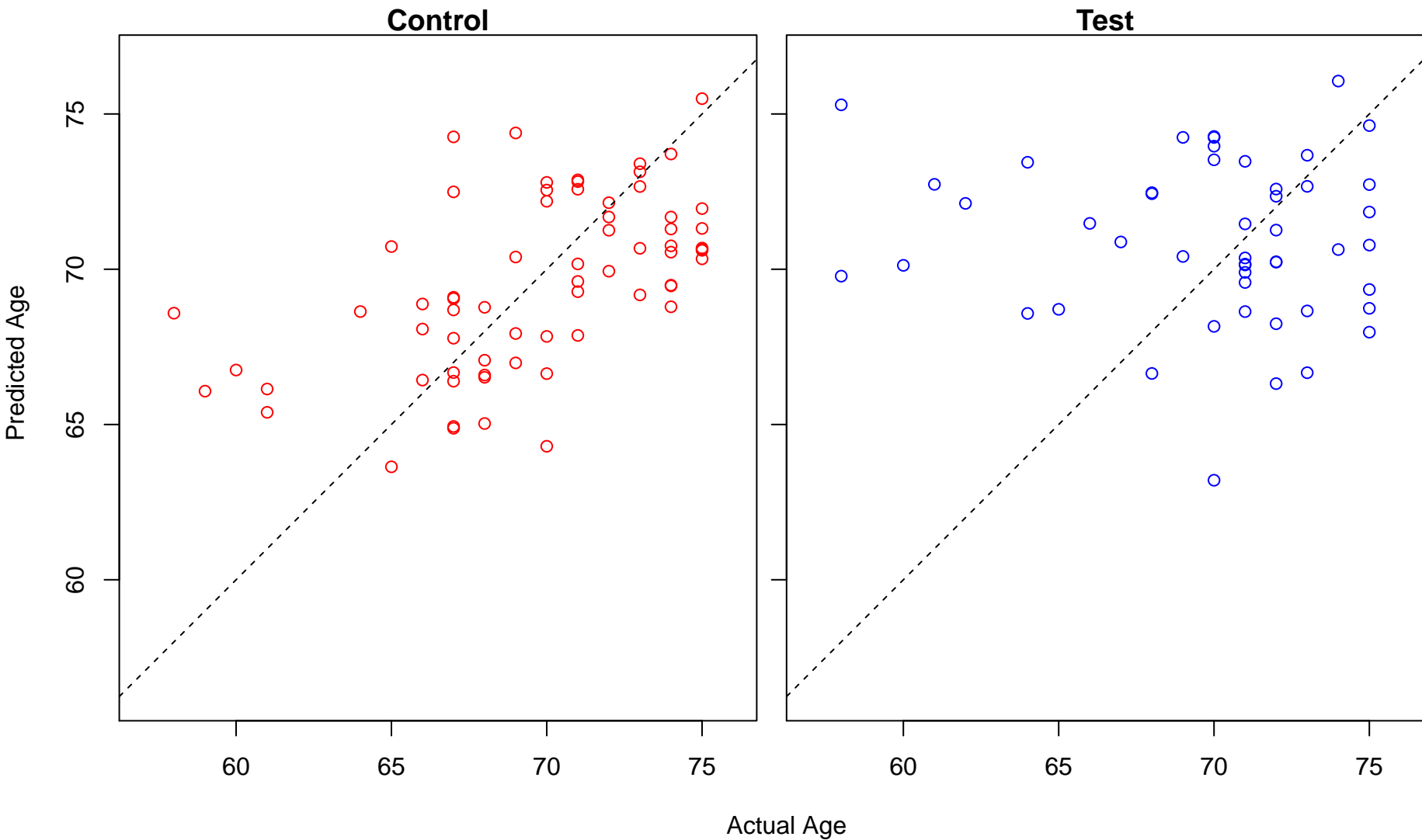
stem cell population maintenance (Score: 0.991080)



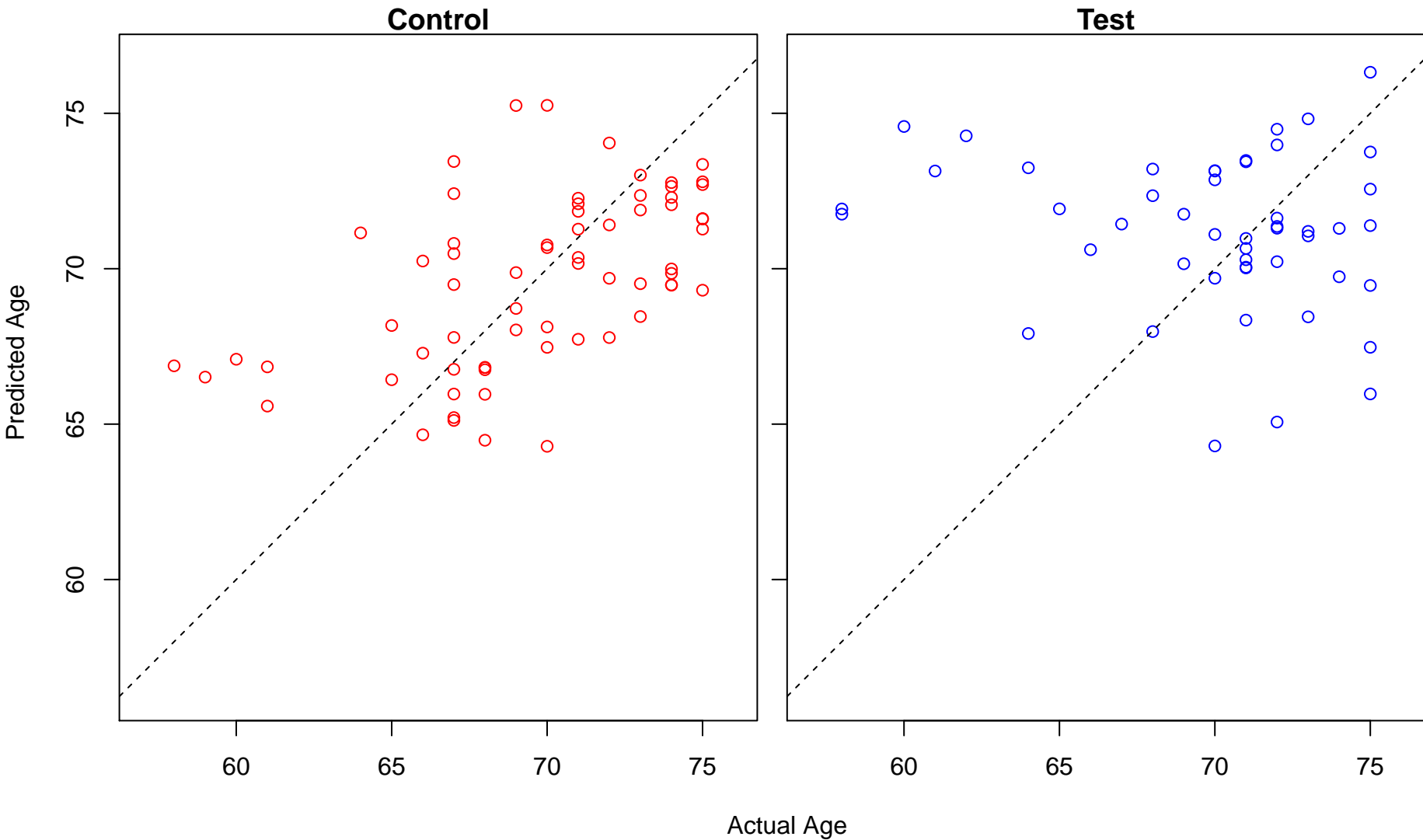
regulation of transcription elongation from RNA polymerase II promoter (Score: 0.990637)



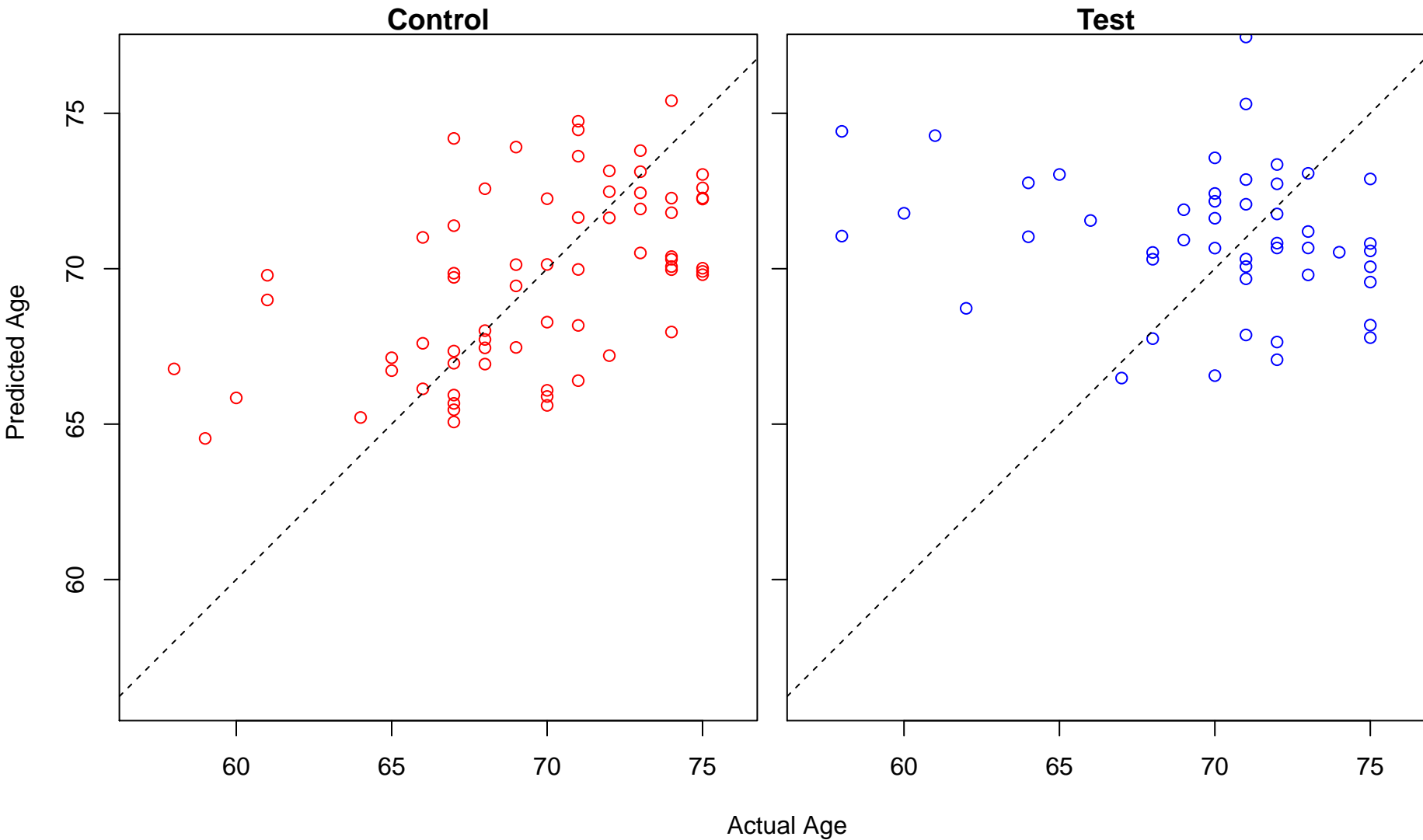
regulation of antigen receptor-mediated signaling pathway (Score: 0.990606)



monoubiquitinated protein deubiquitination (Score: 0.990386)

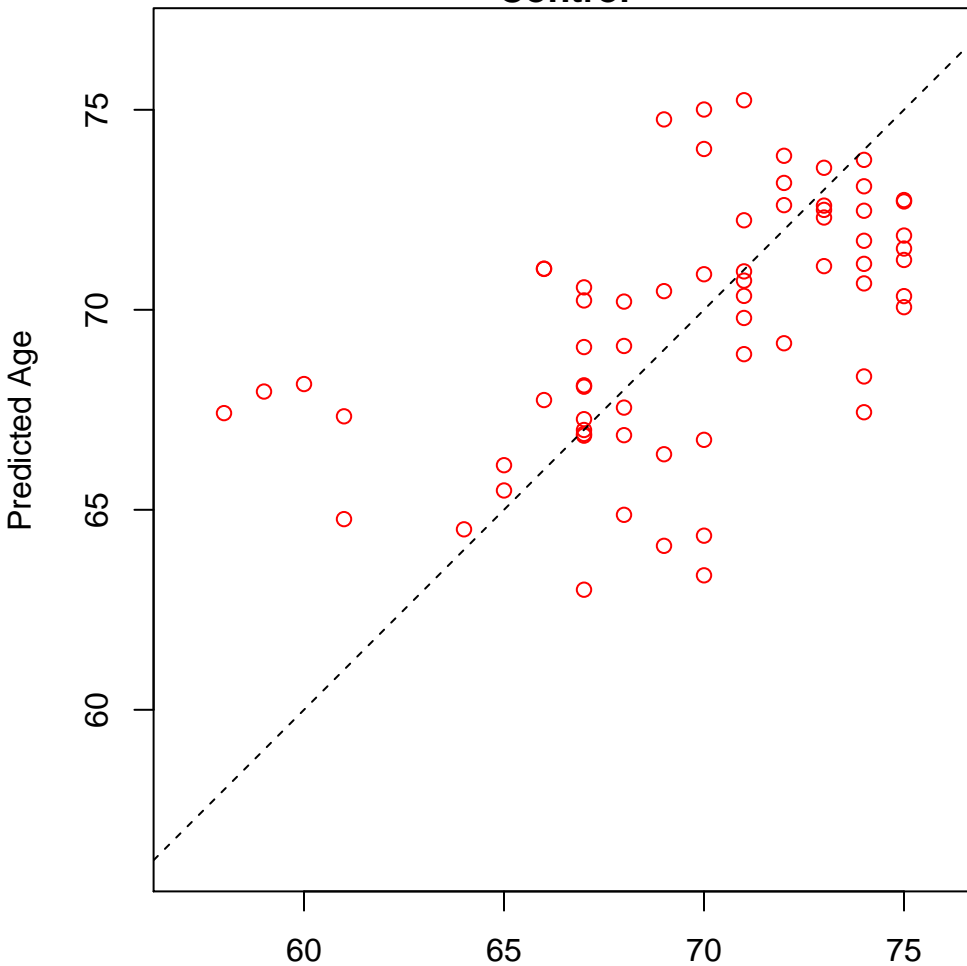


cellular response to thyroid hormone stimulus (Score: 0.990317)

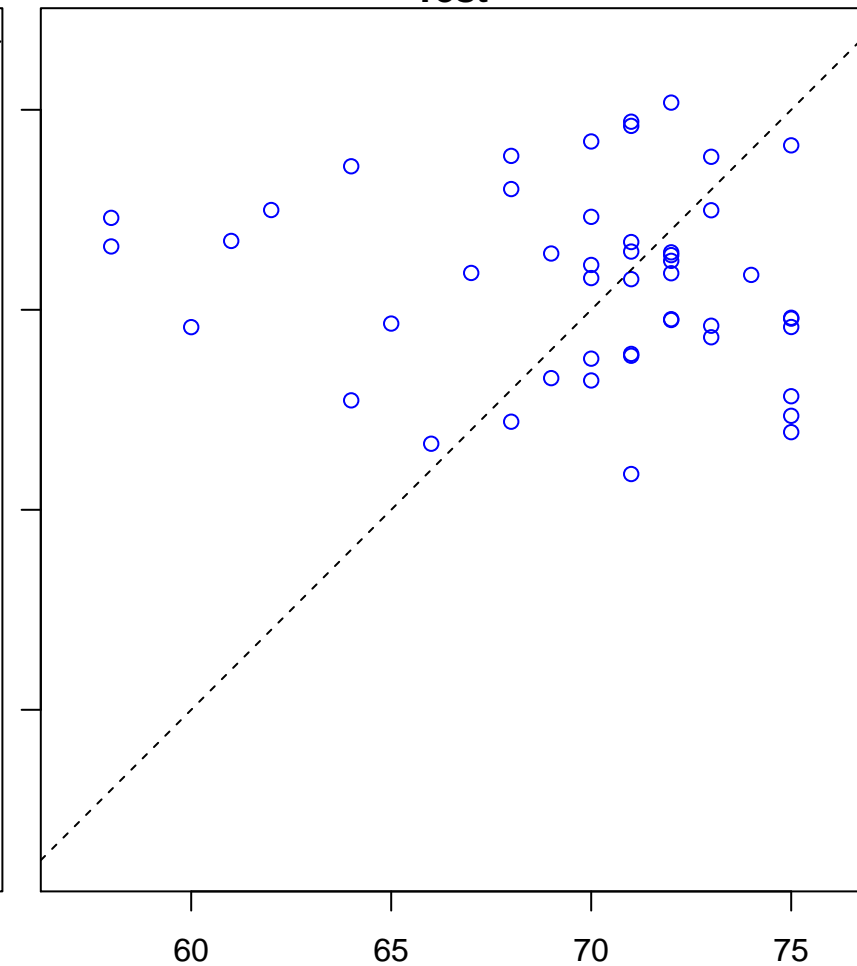


posttranscriptional gene silencing by RNA (Score: 0.990310)

Control

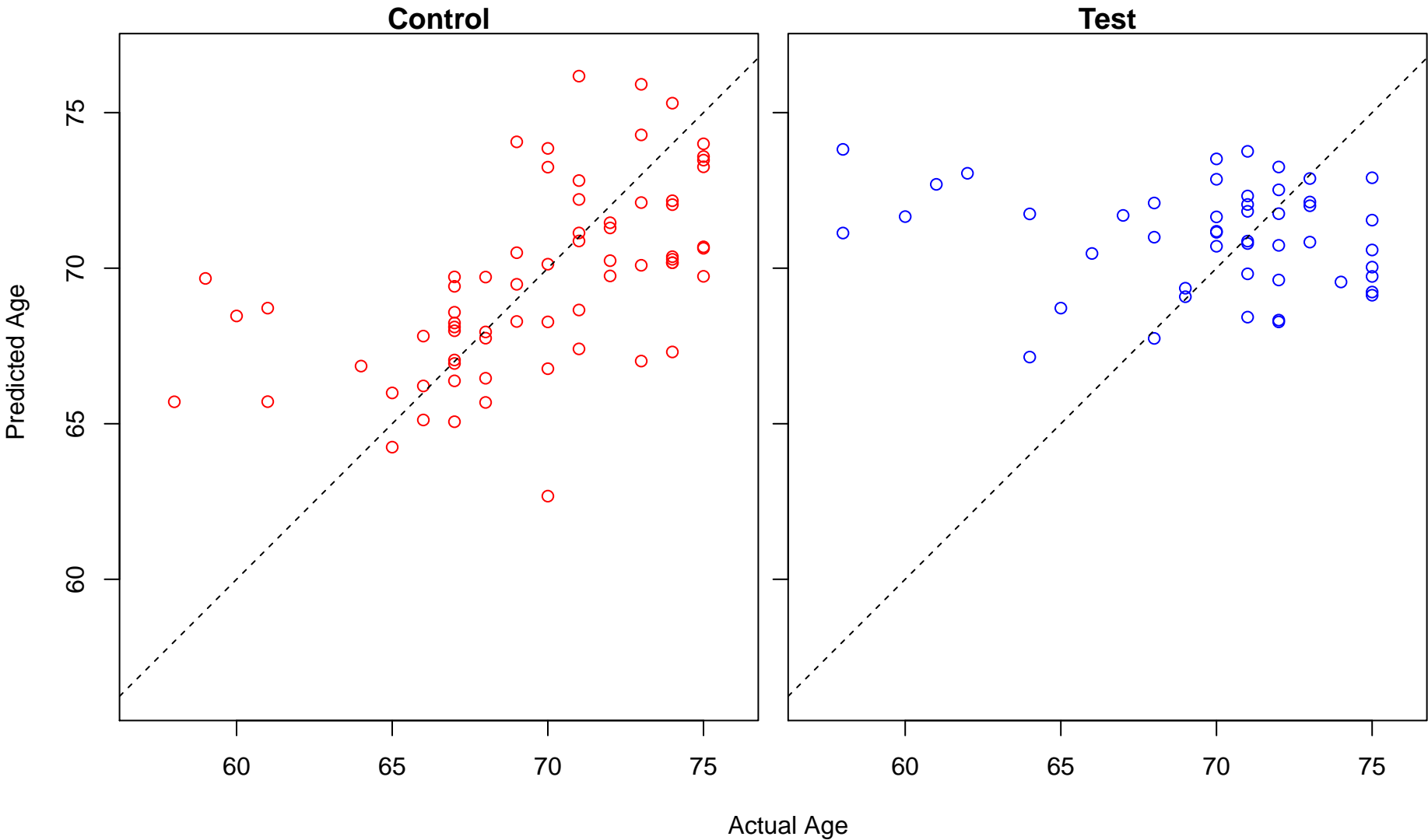


Test

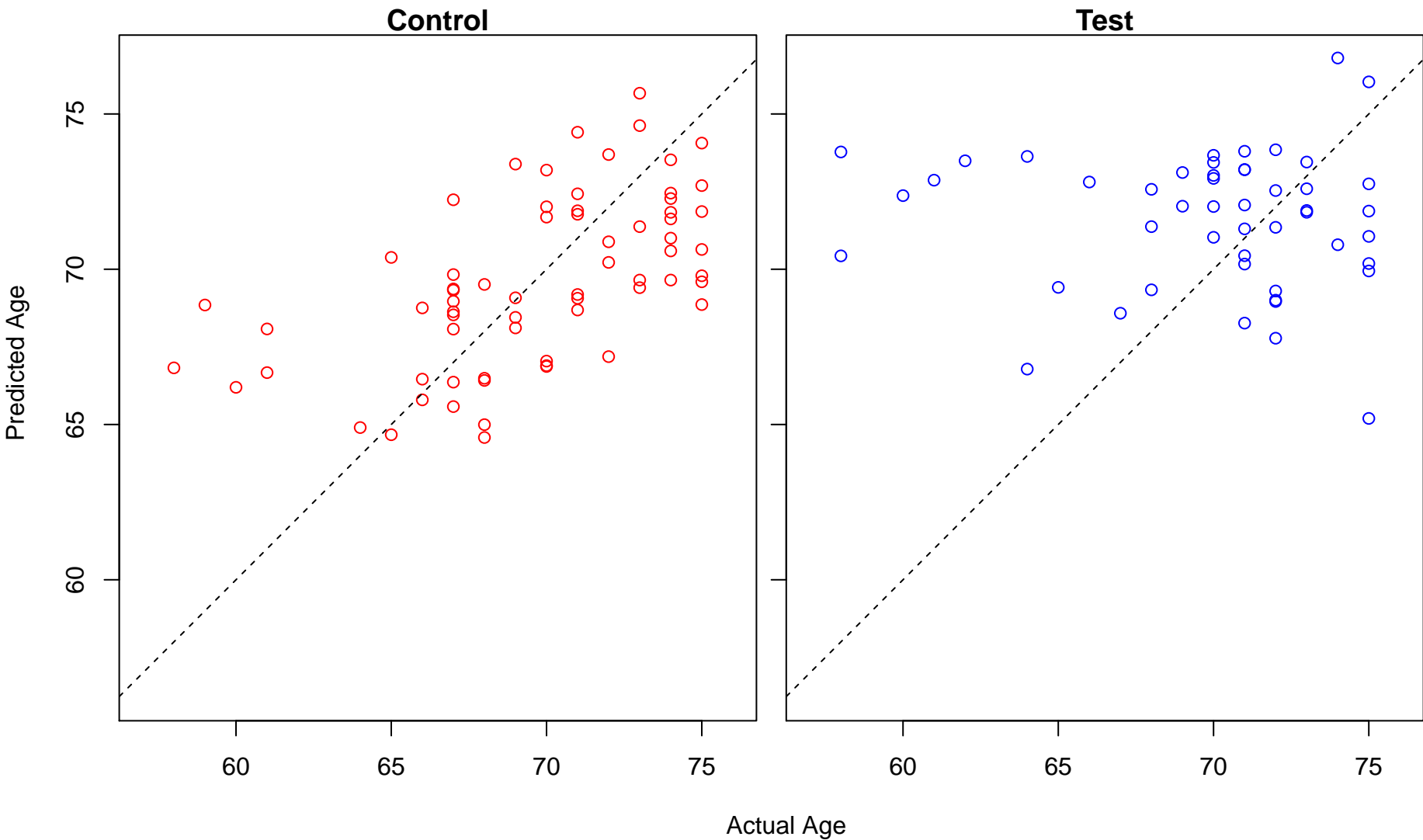


Actual Age

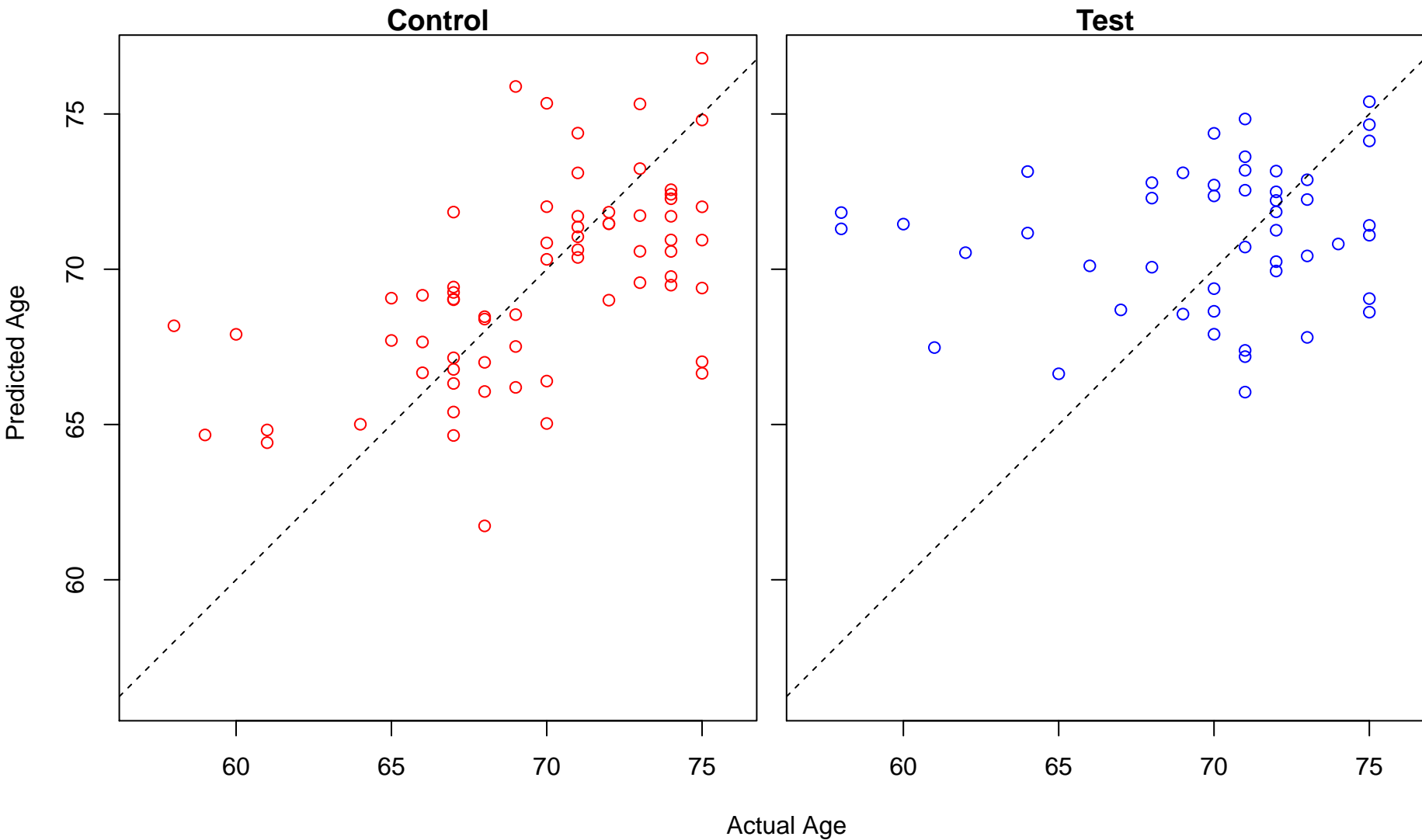
negative regulation of telomere maintenance via telomere lengthening (Score: 0.989263)



regulation of glial cell differentiation (Score: 0.989078)

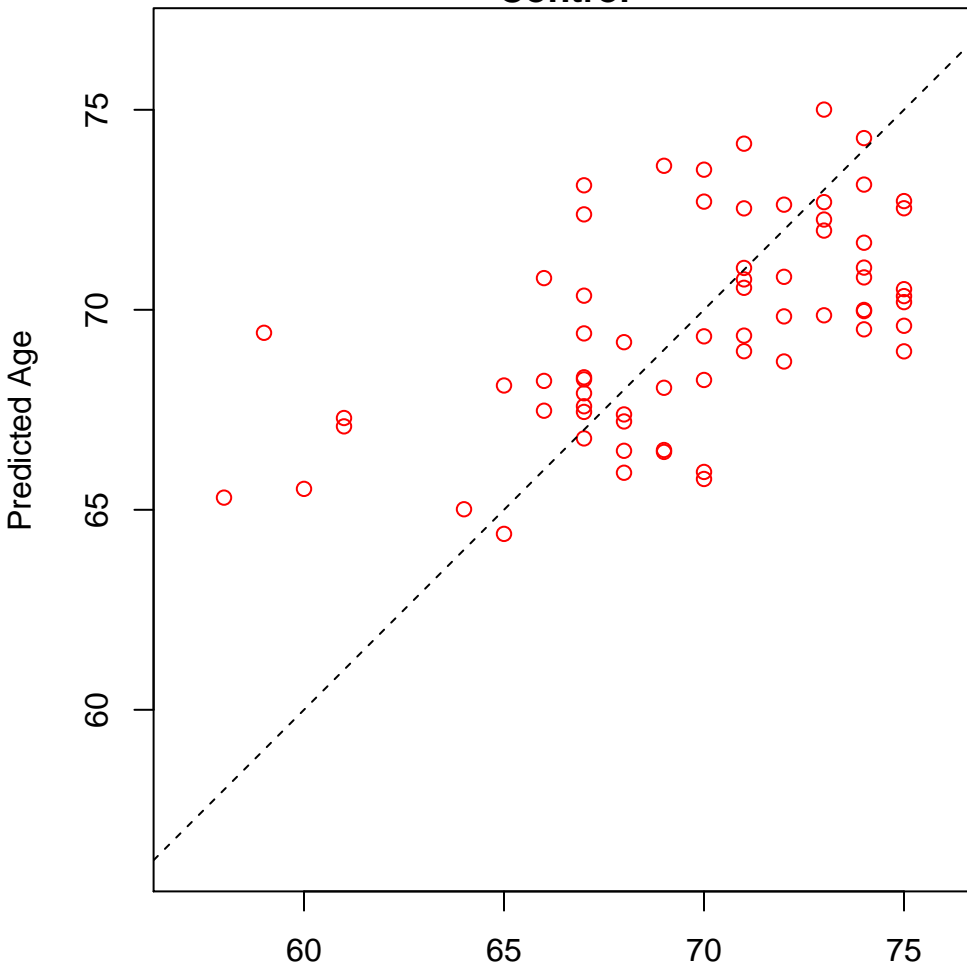


eye development (Score: 0.989066)

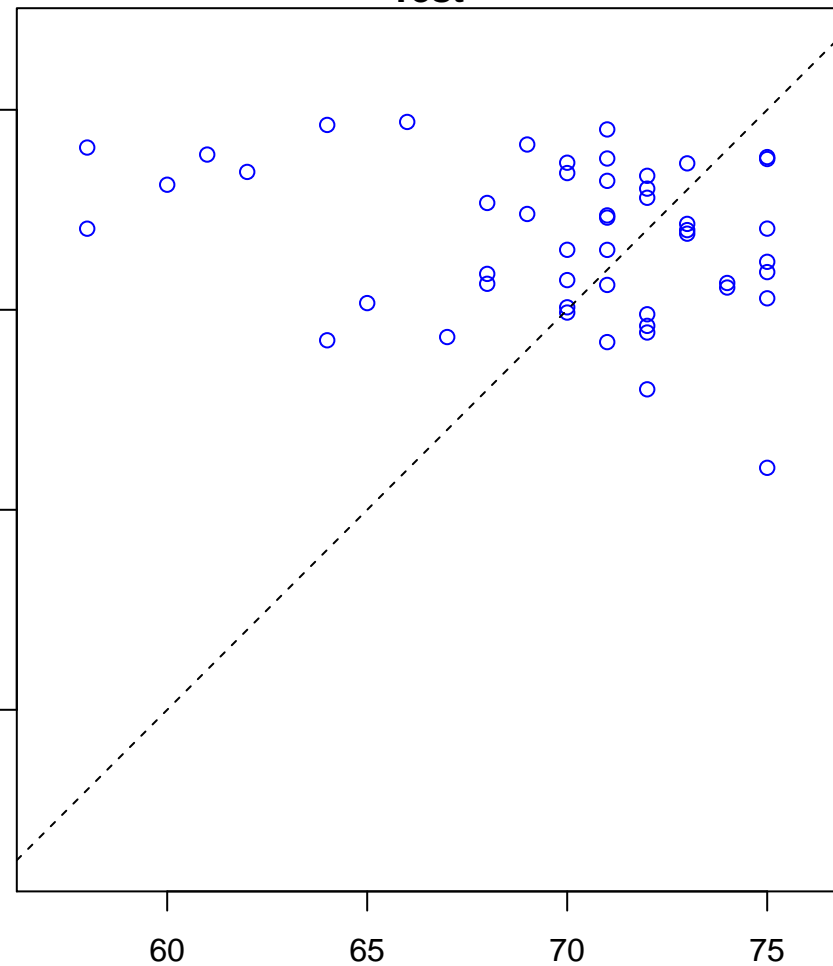


embryonic heart tube morphogenesis (Score: 0.988999)

Control

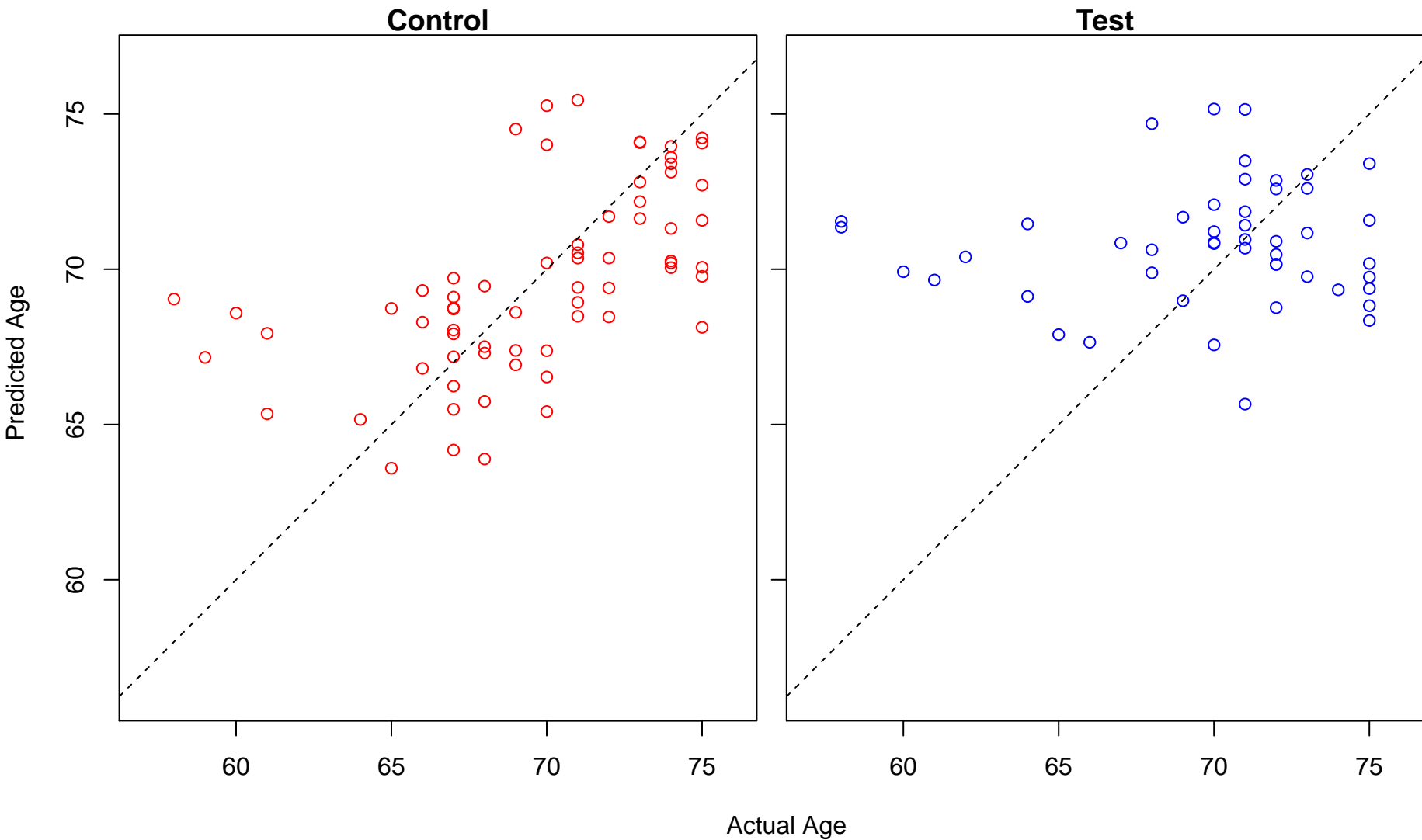


Test

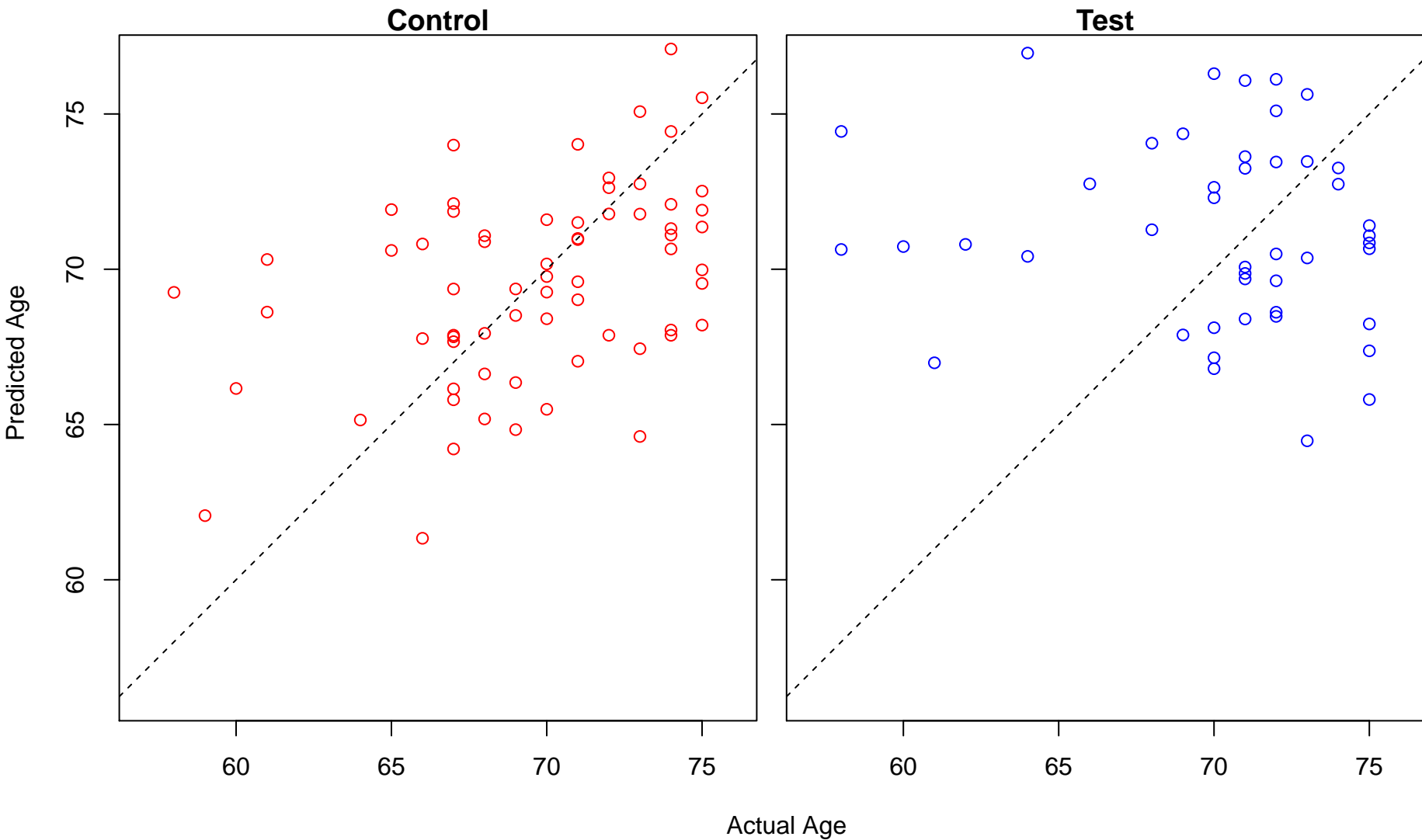


Actual Age

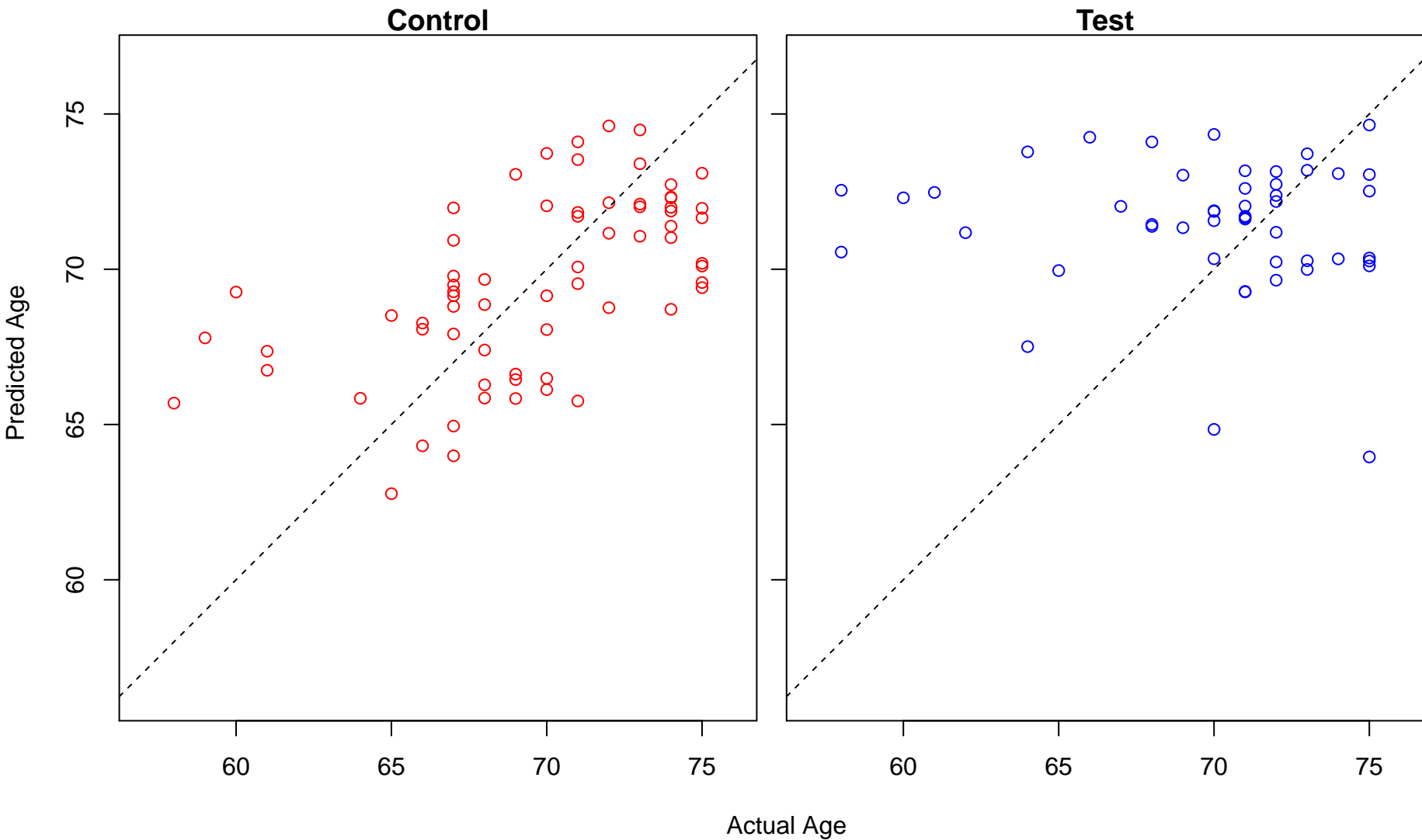
maintenance of cell number (Score: 0.988944)



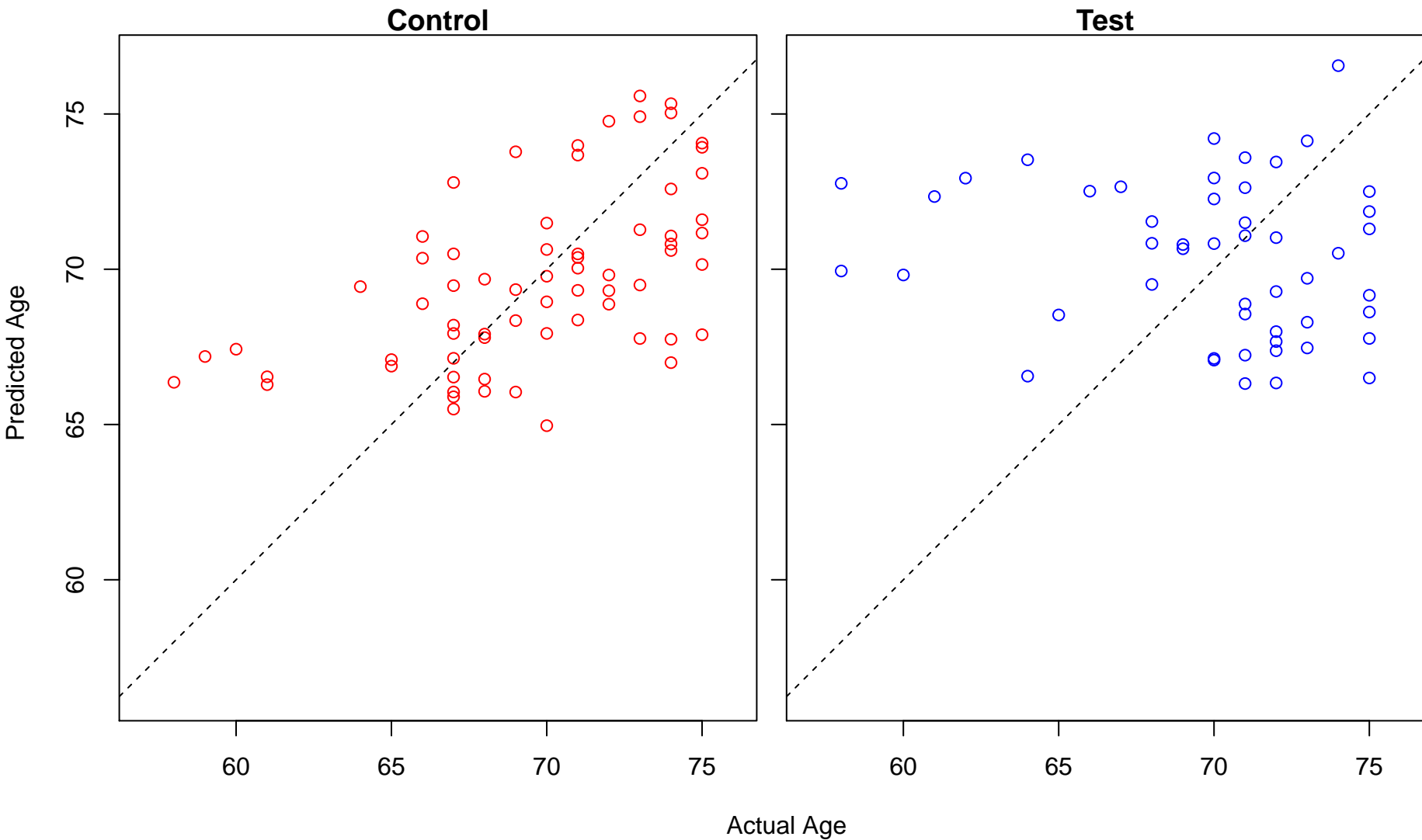
cellular response to carbohydrate stimulus (Score: 0.988419)



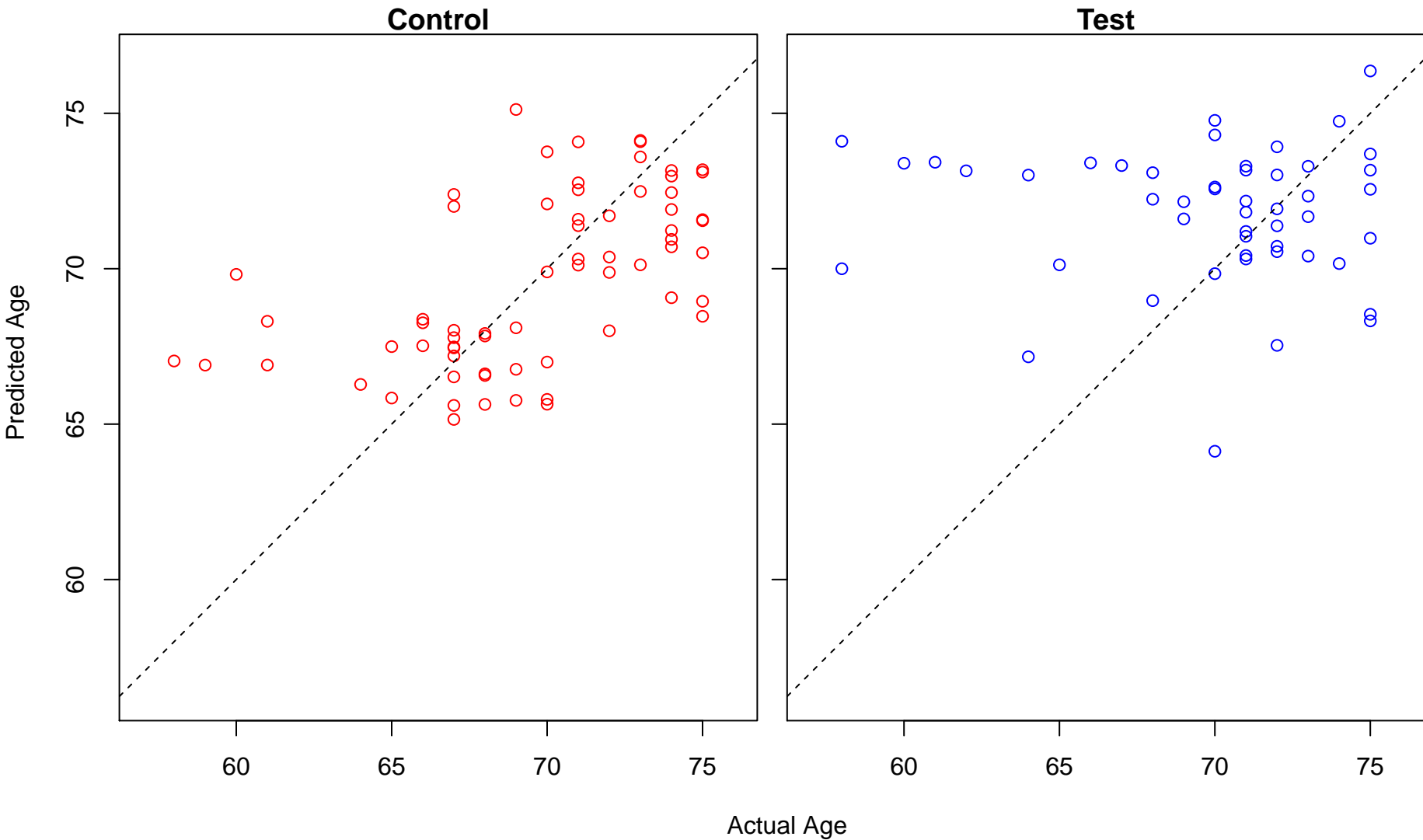
regulation of interleukin-1 beta secretion (Score: 0.988234)



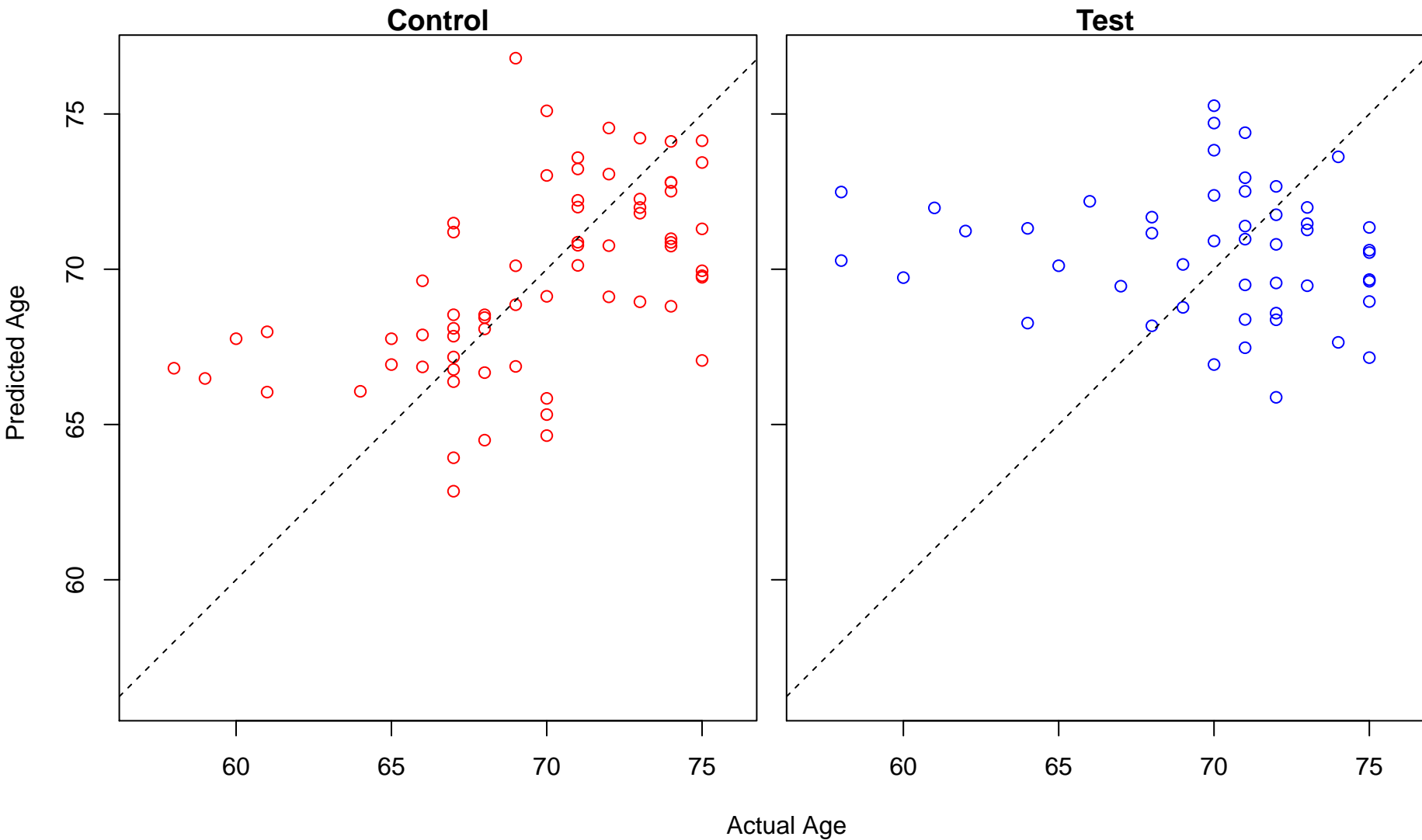
protein deacetylation (Score: 0.987383)



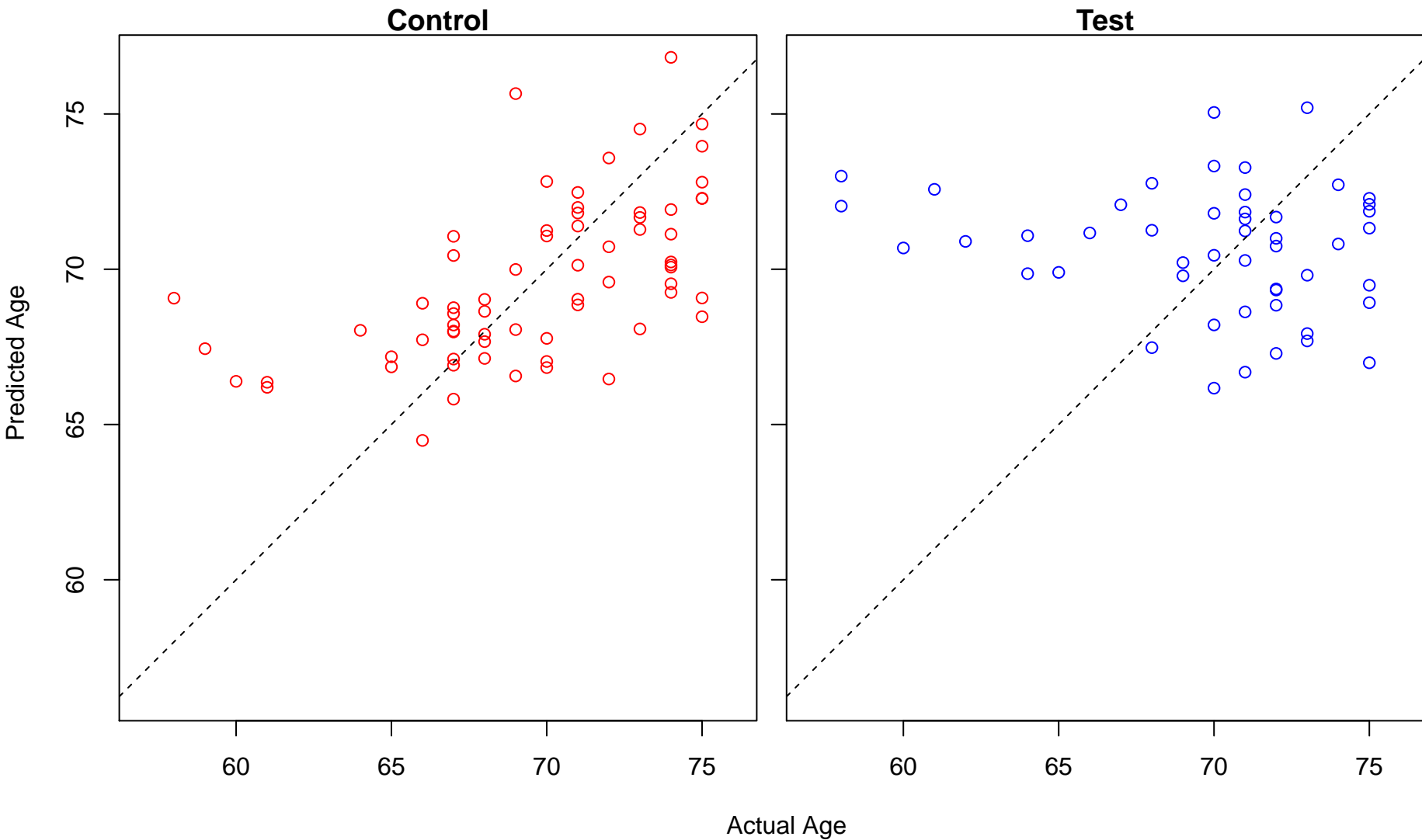
positive regulation of reactive oxygen species biosynthetic process (Score: 0.987021)



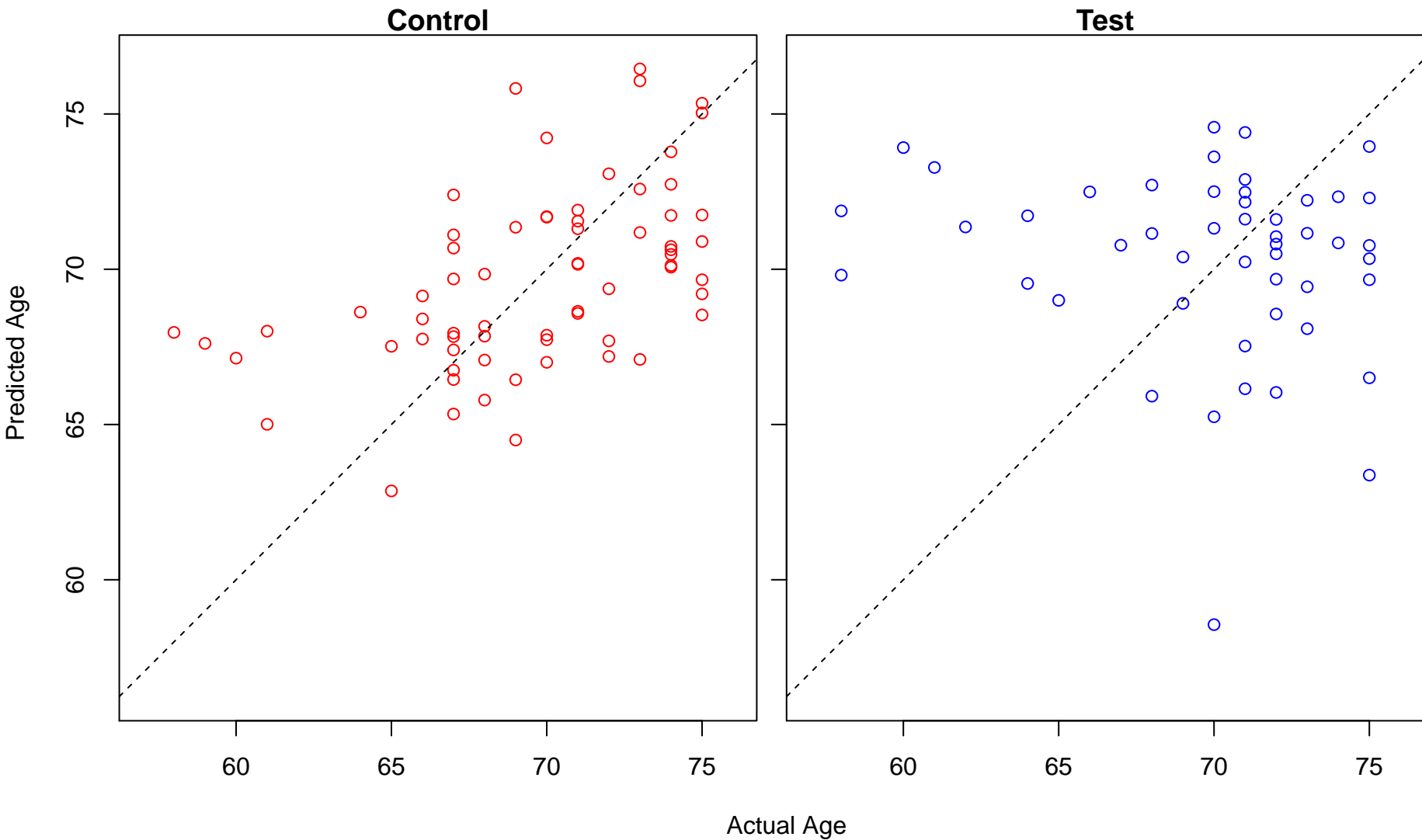
positive regulation of cytokine biosynthetic process (Score: 0.986820)



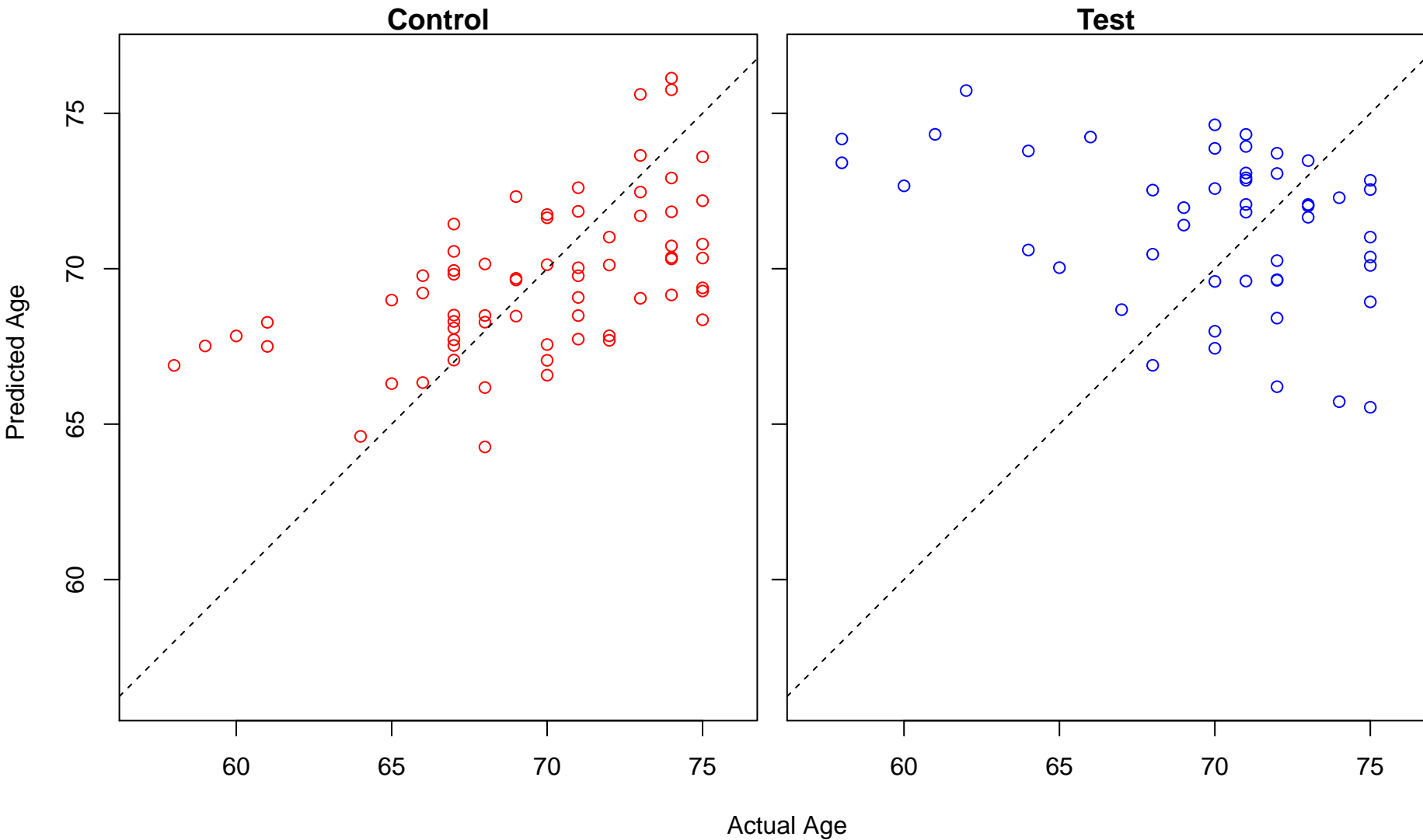
astral microtubule organization (Score: 0.986652)



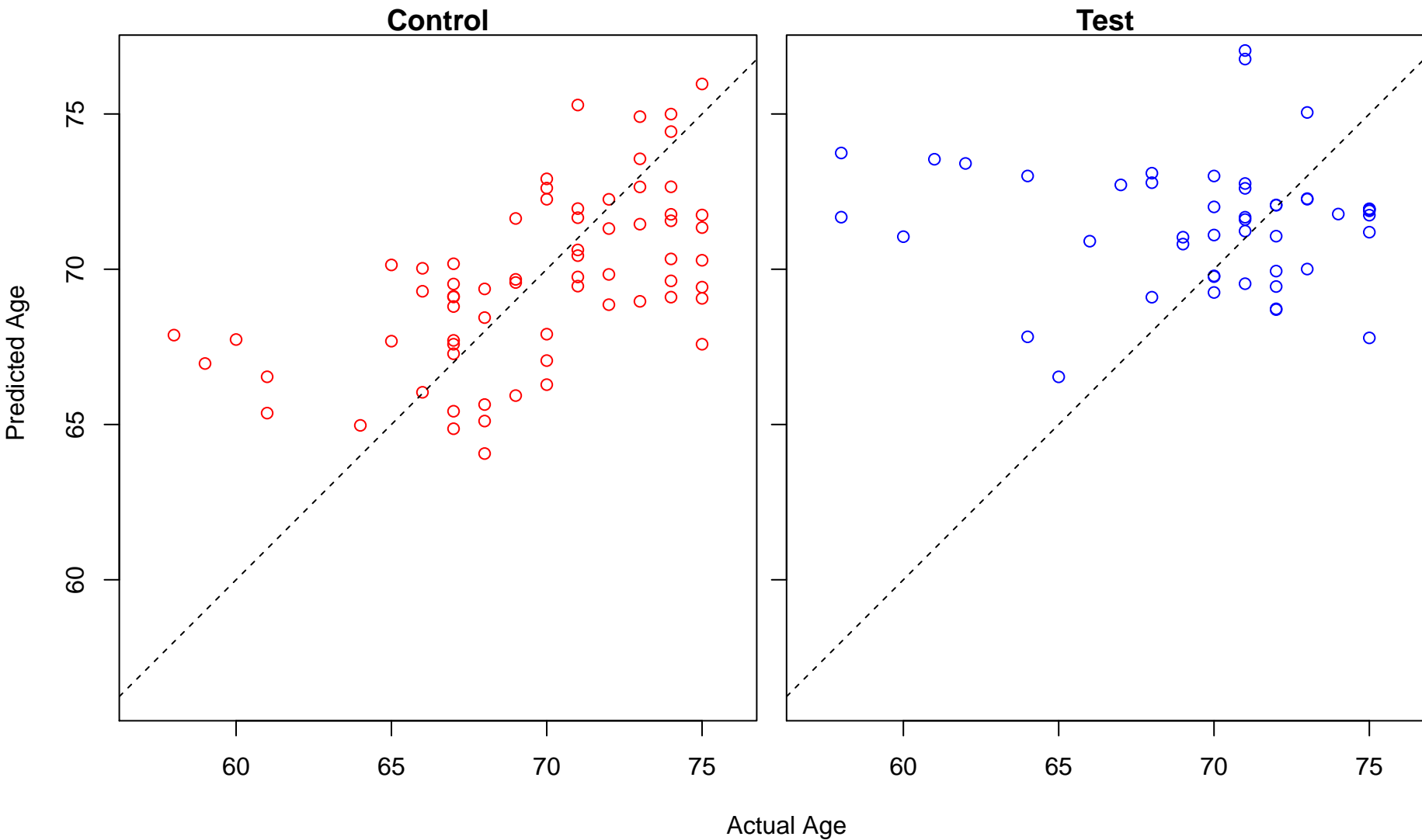
maintenance of protein localization in organelle (Score: 0.986575)



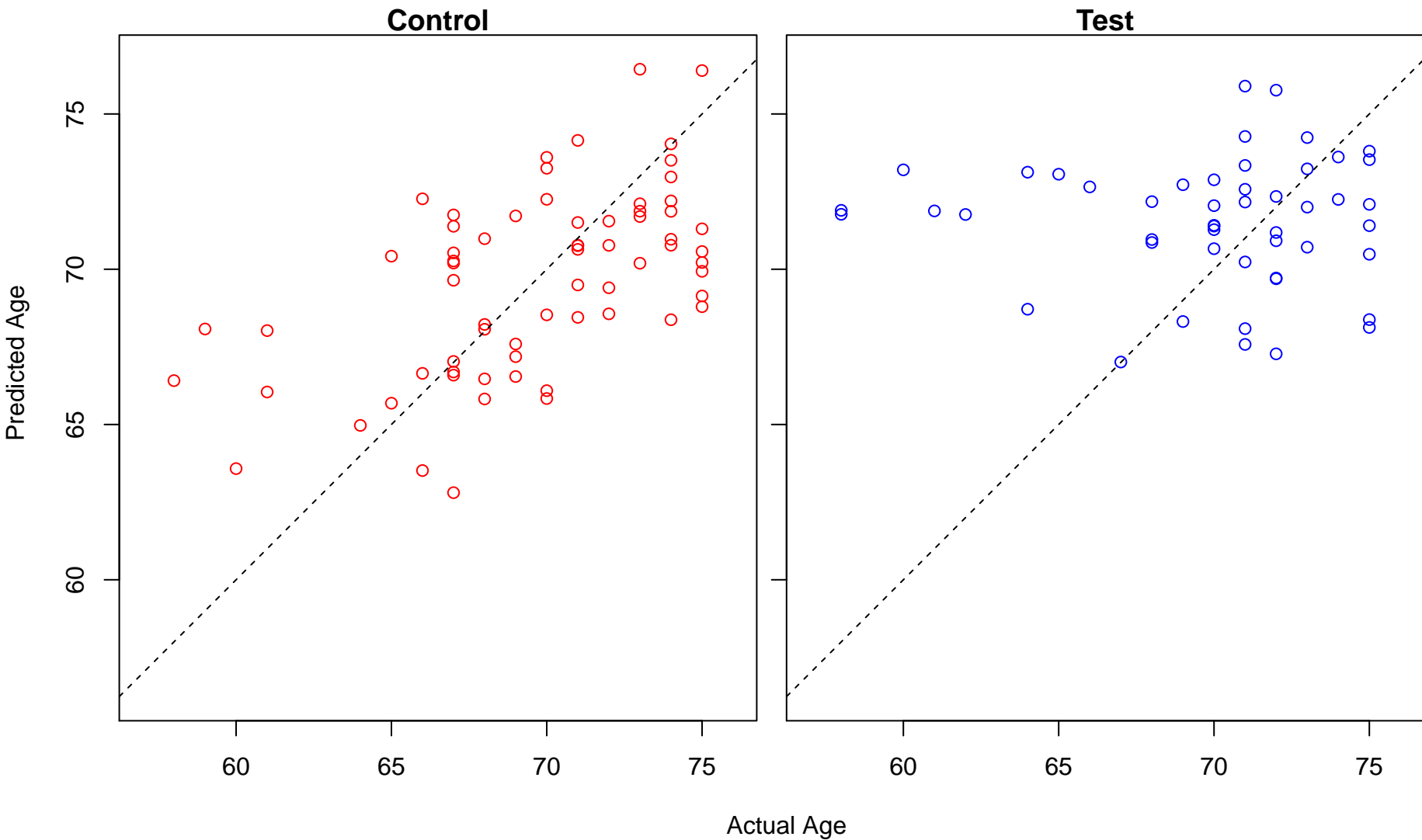
negative regulation of beta-amyloid formation (Score: 0.986347)



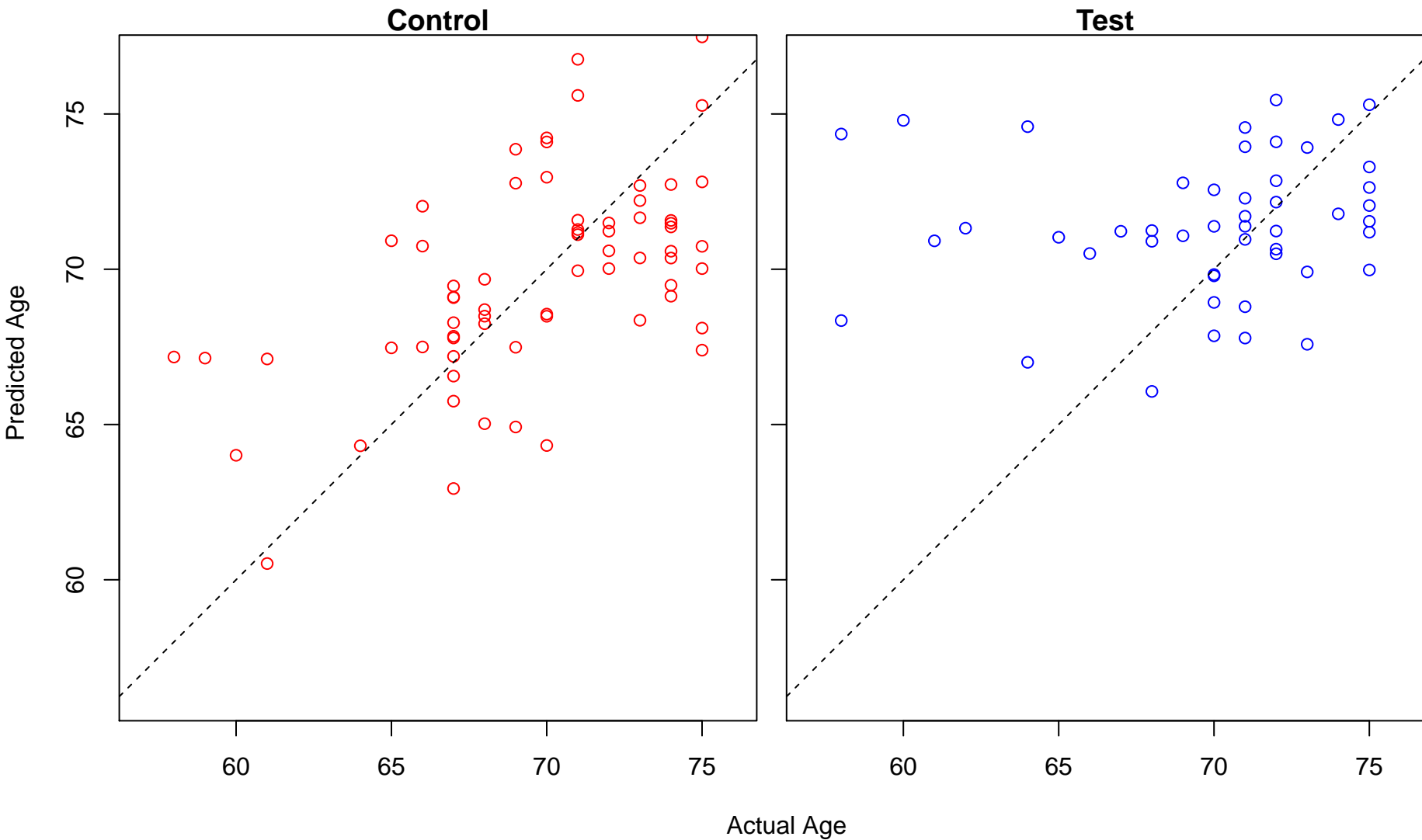
plasma membrane to endosome transport (Score: 0.986203)



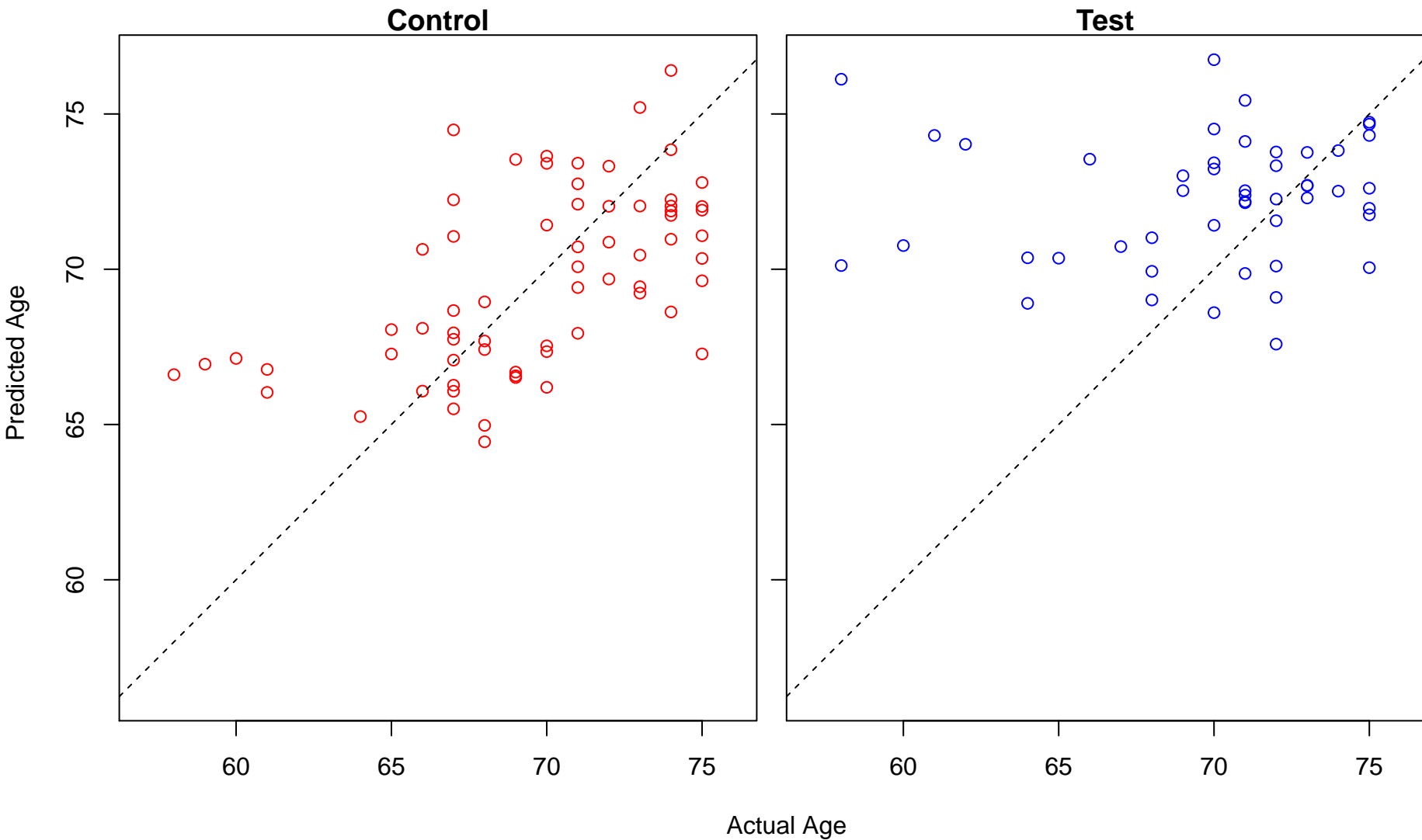
heart growth (Score: 0.985090)



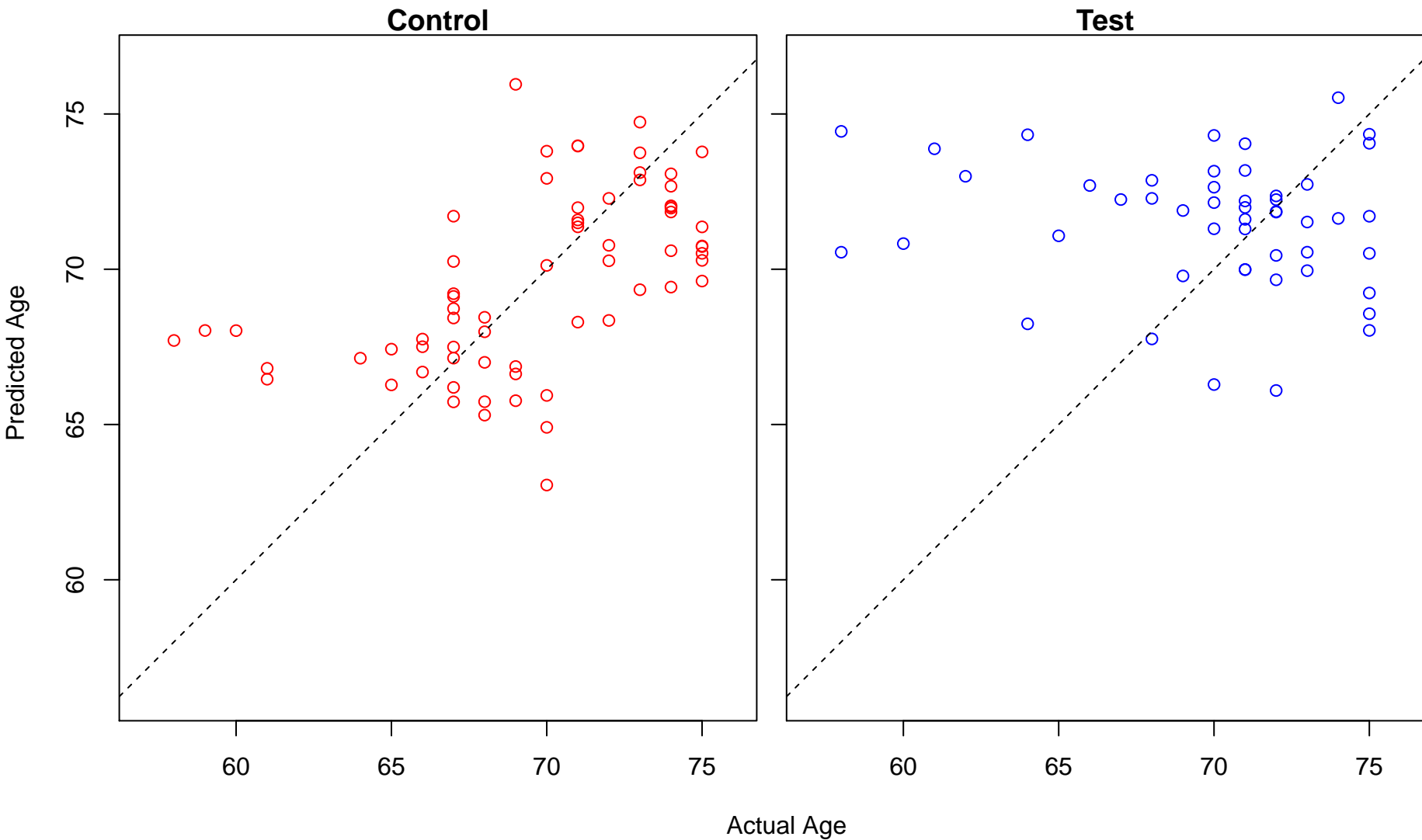
spermatid development (Score: 0.984863)



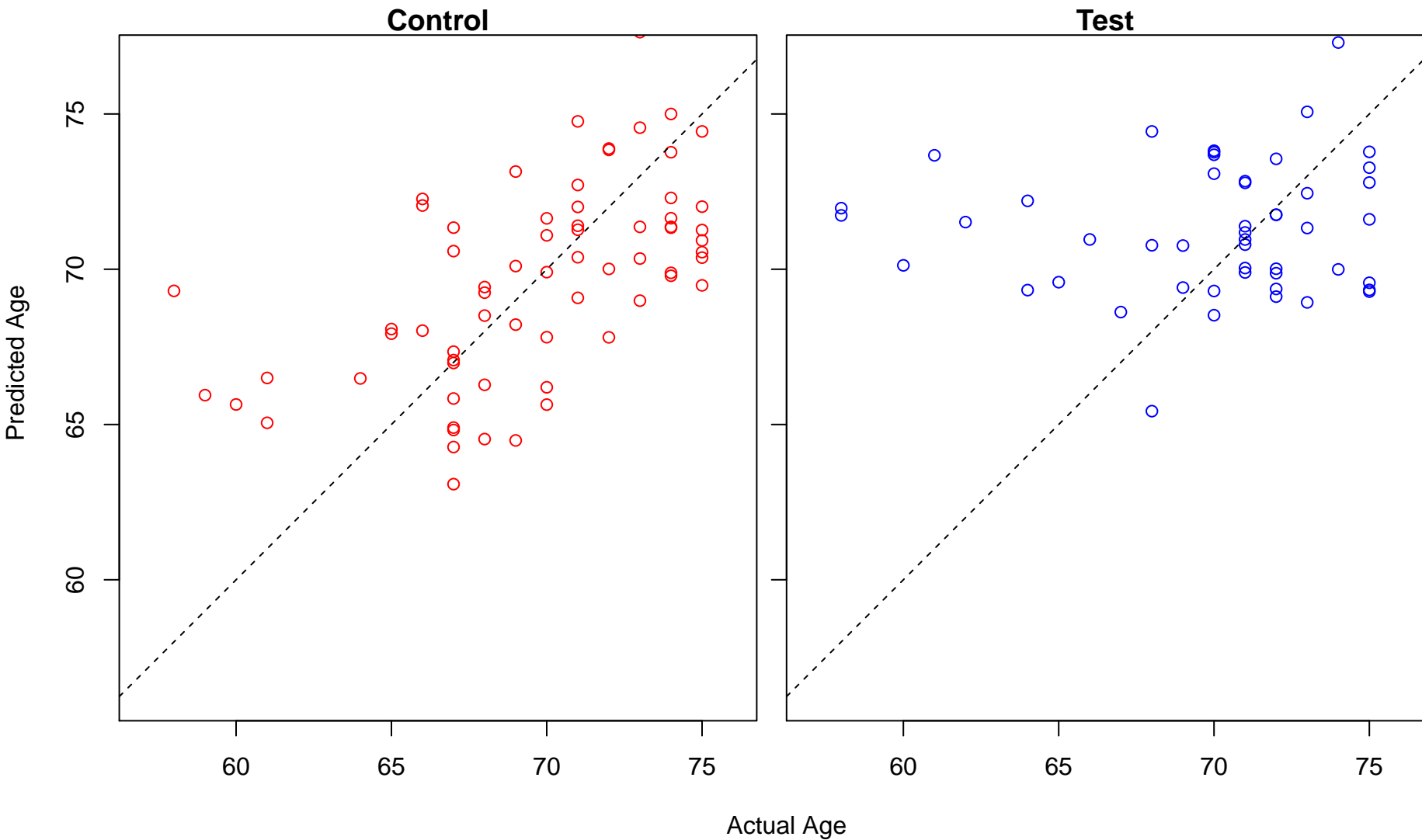
regulation of muscle contraction (Score: 0.984704)



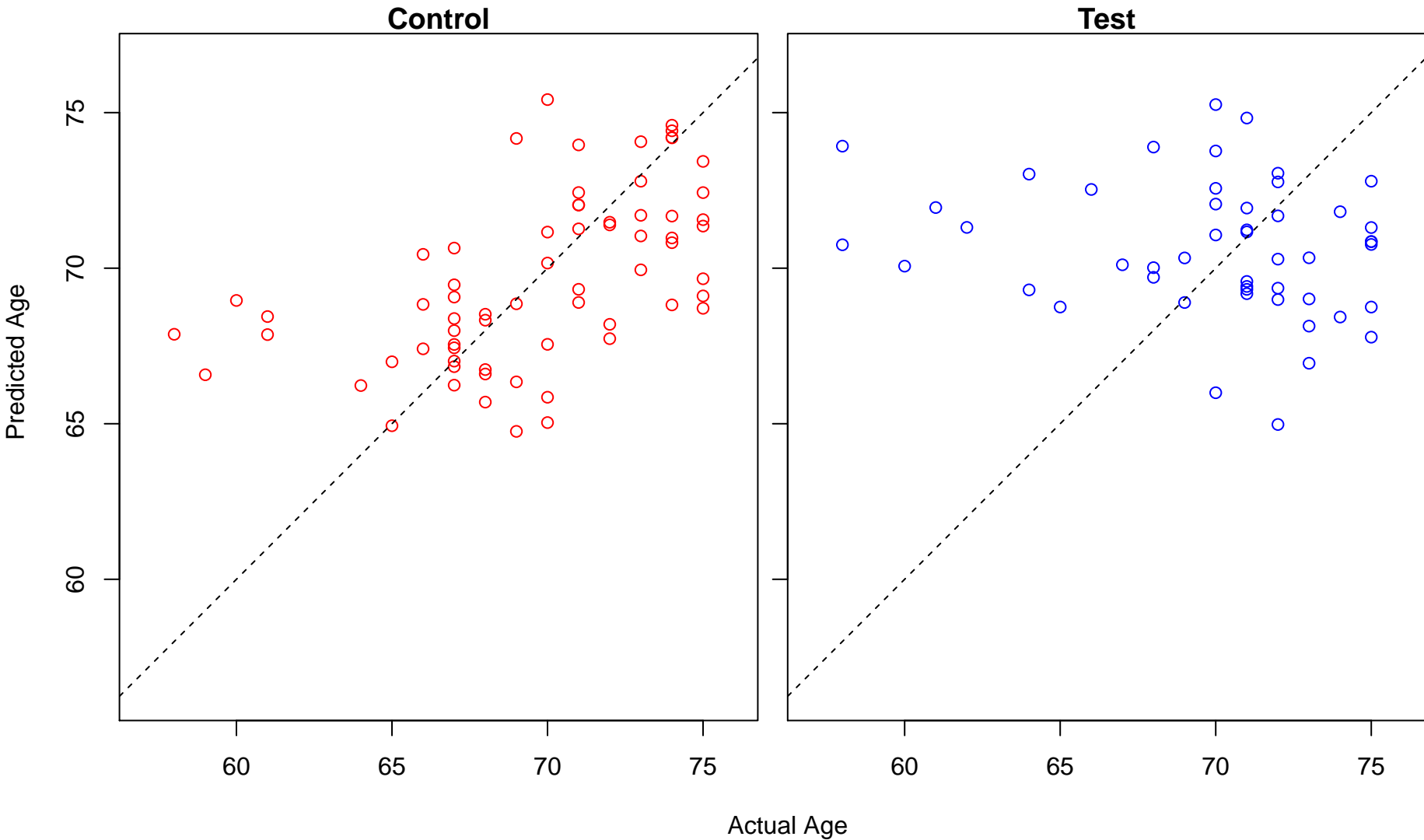
negative regulation of cytoplasmic transport (Score: 0.984618)



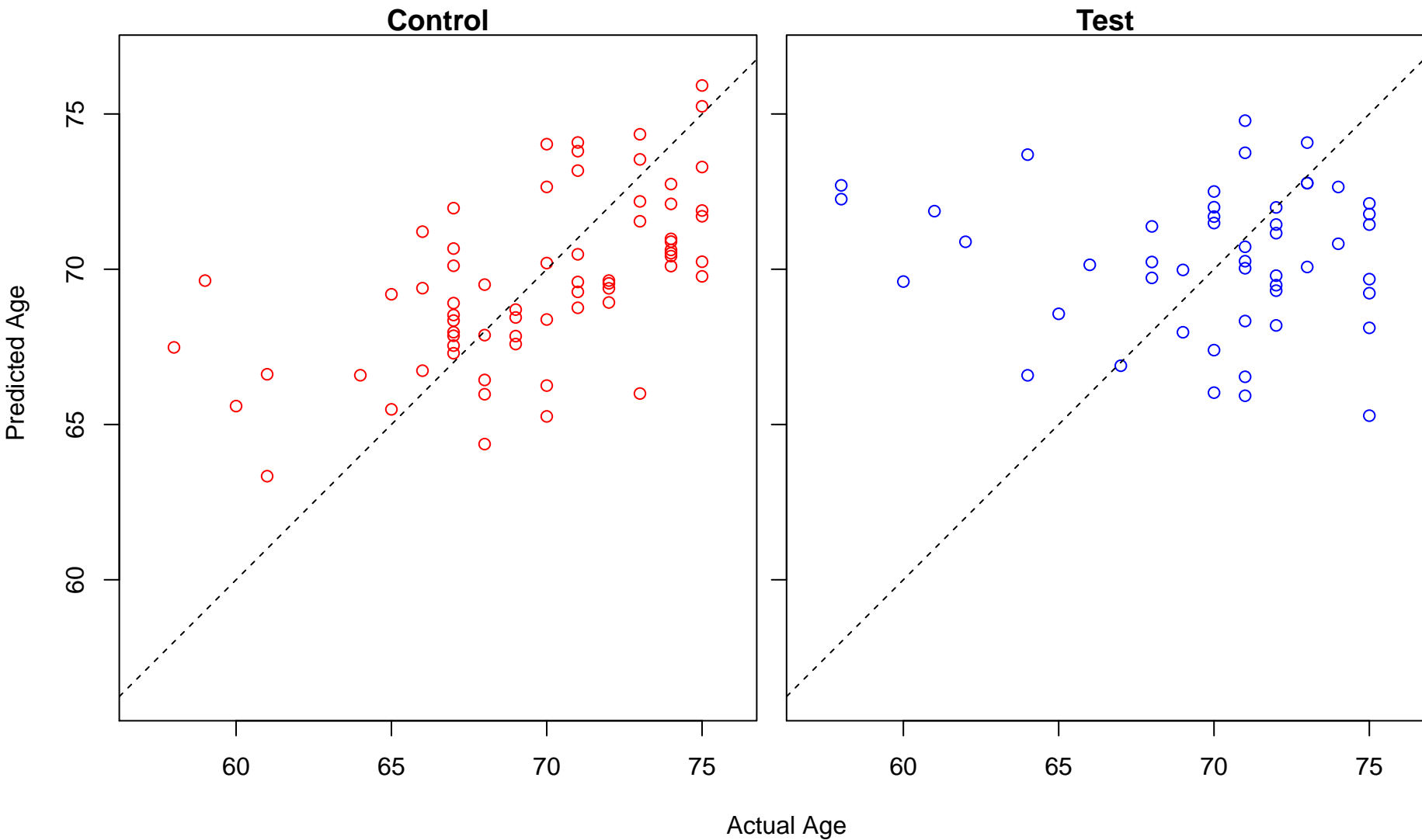
heme metabolic process (Score: 0.983863)



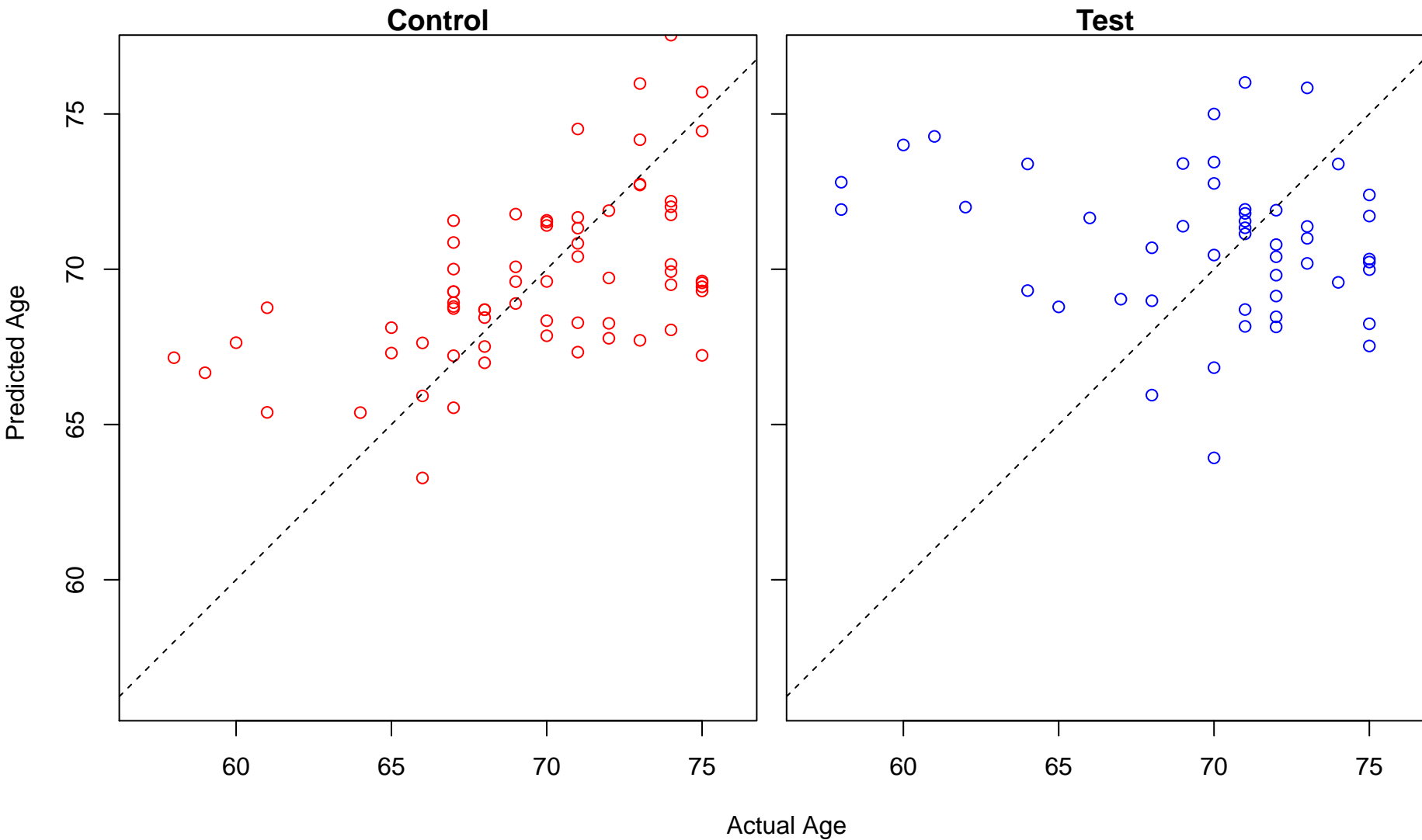
regulation of mesenchymal cell proliferation (Score: 0.983431)



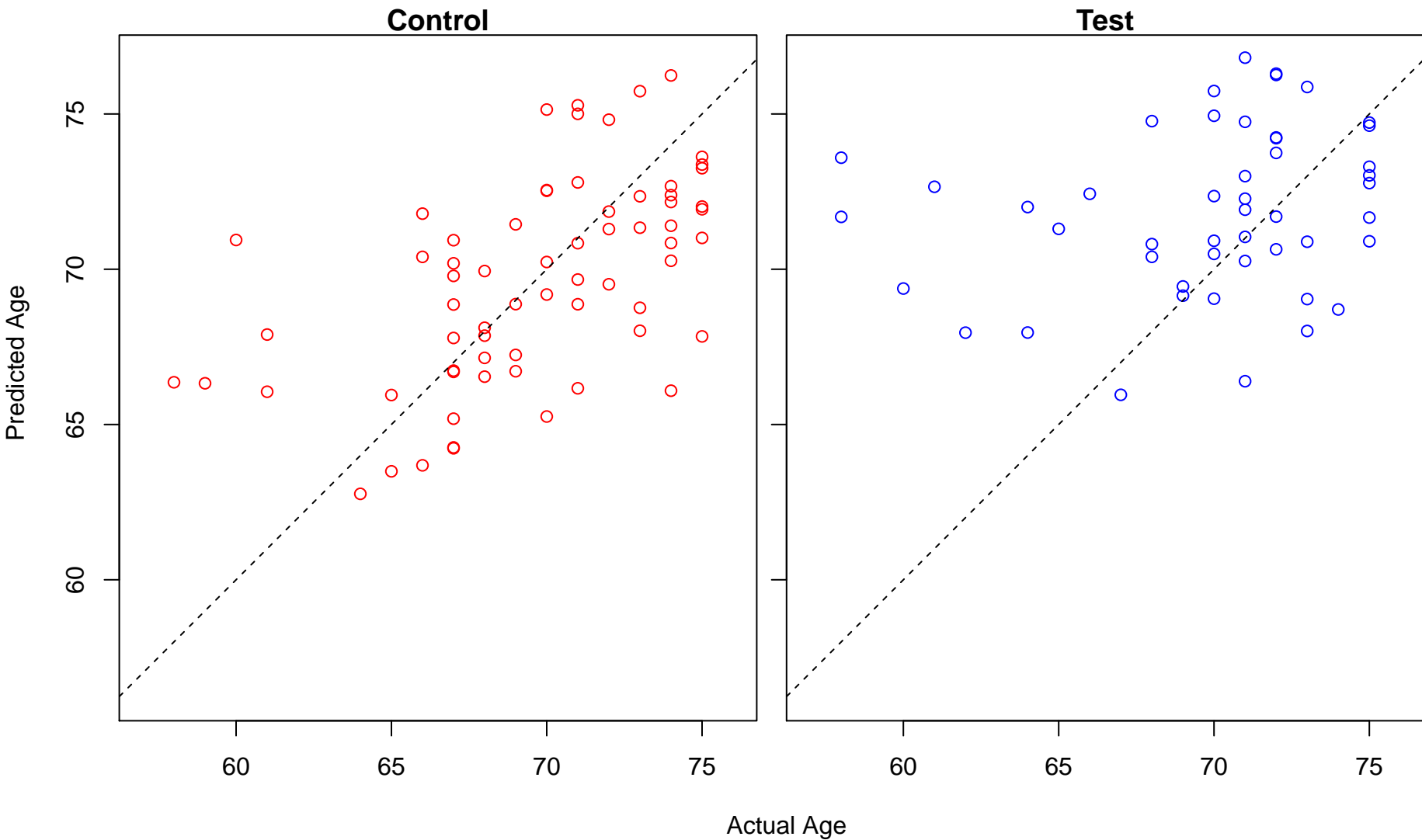
negative regulation of actin filament depolymerization (Score: 0.982968)



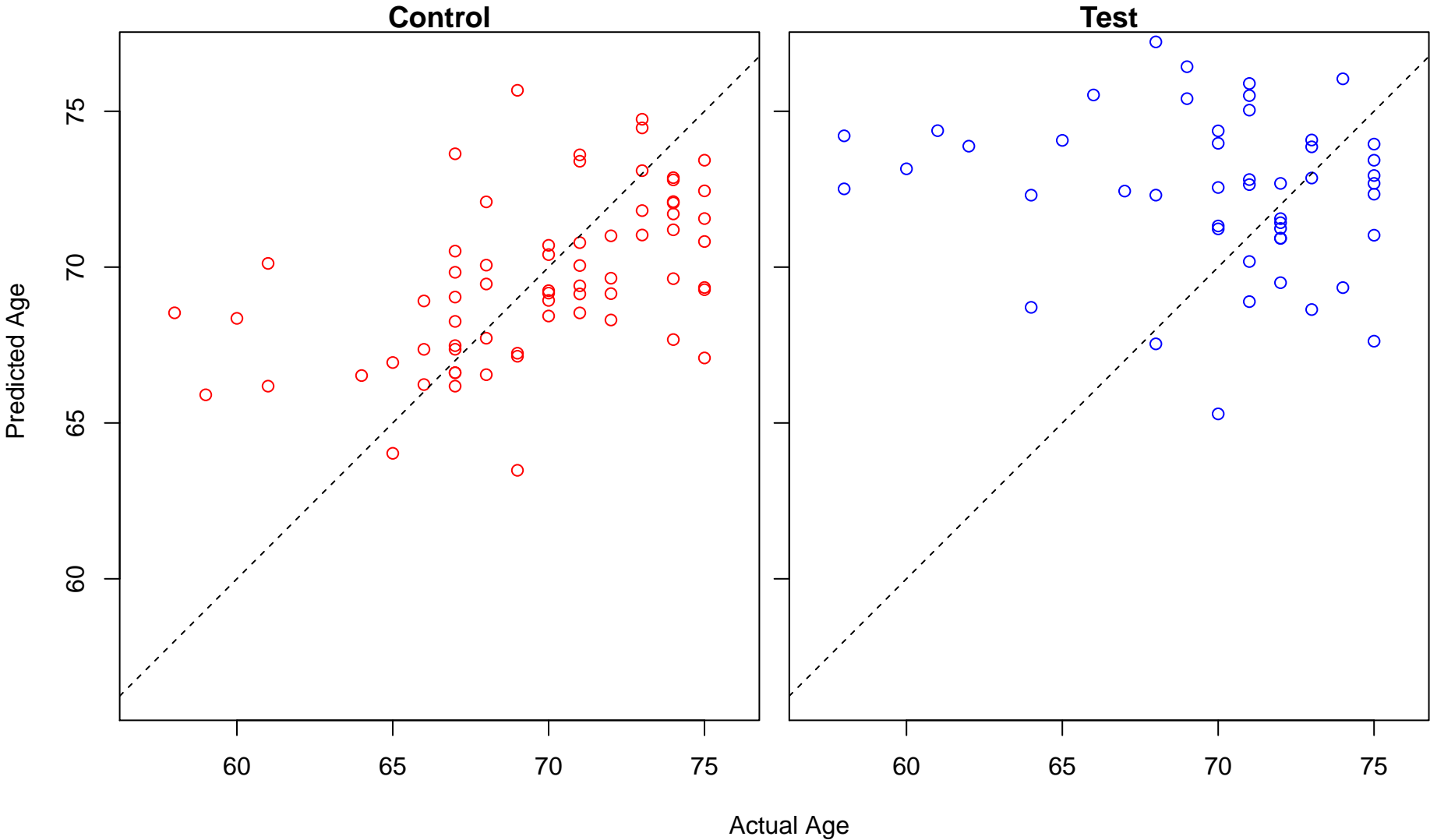
positive regulation of autophagosome assembly (Score: 0.982851)



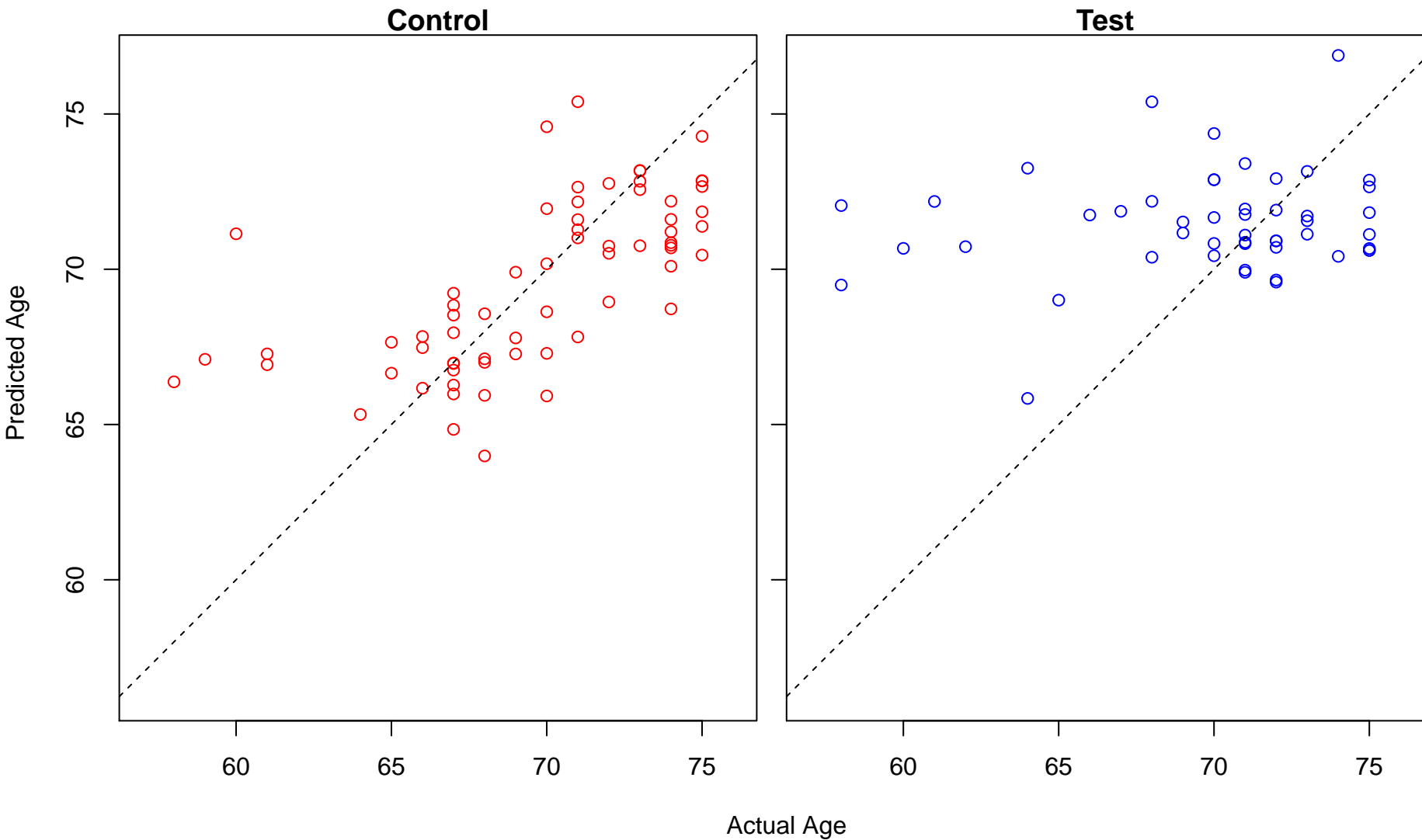
unsaturated fatty acid biosynthetic process (Score: 0.982137)



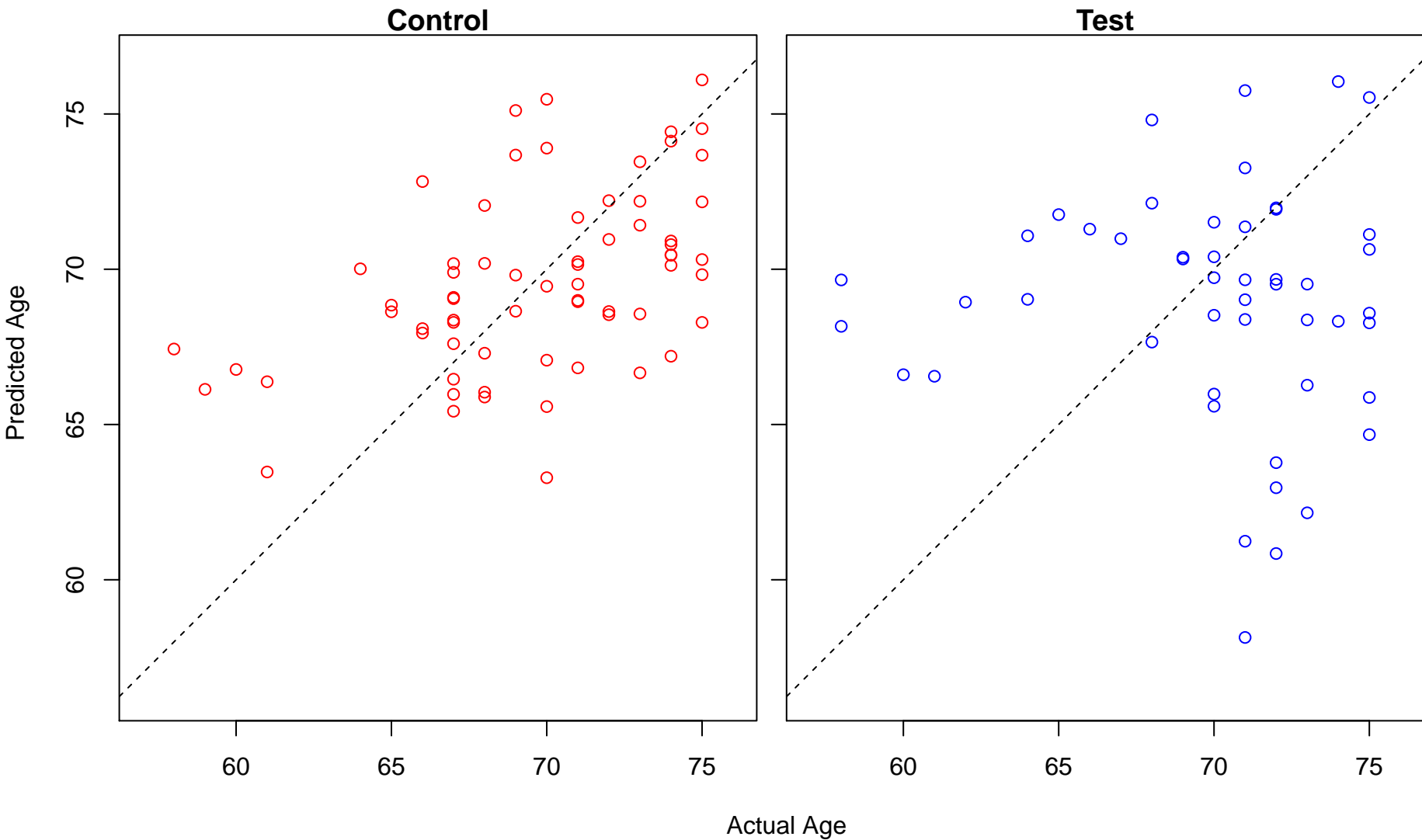
calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules (Score: 0.981)



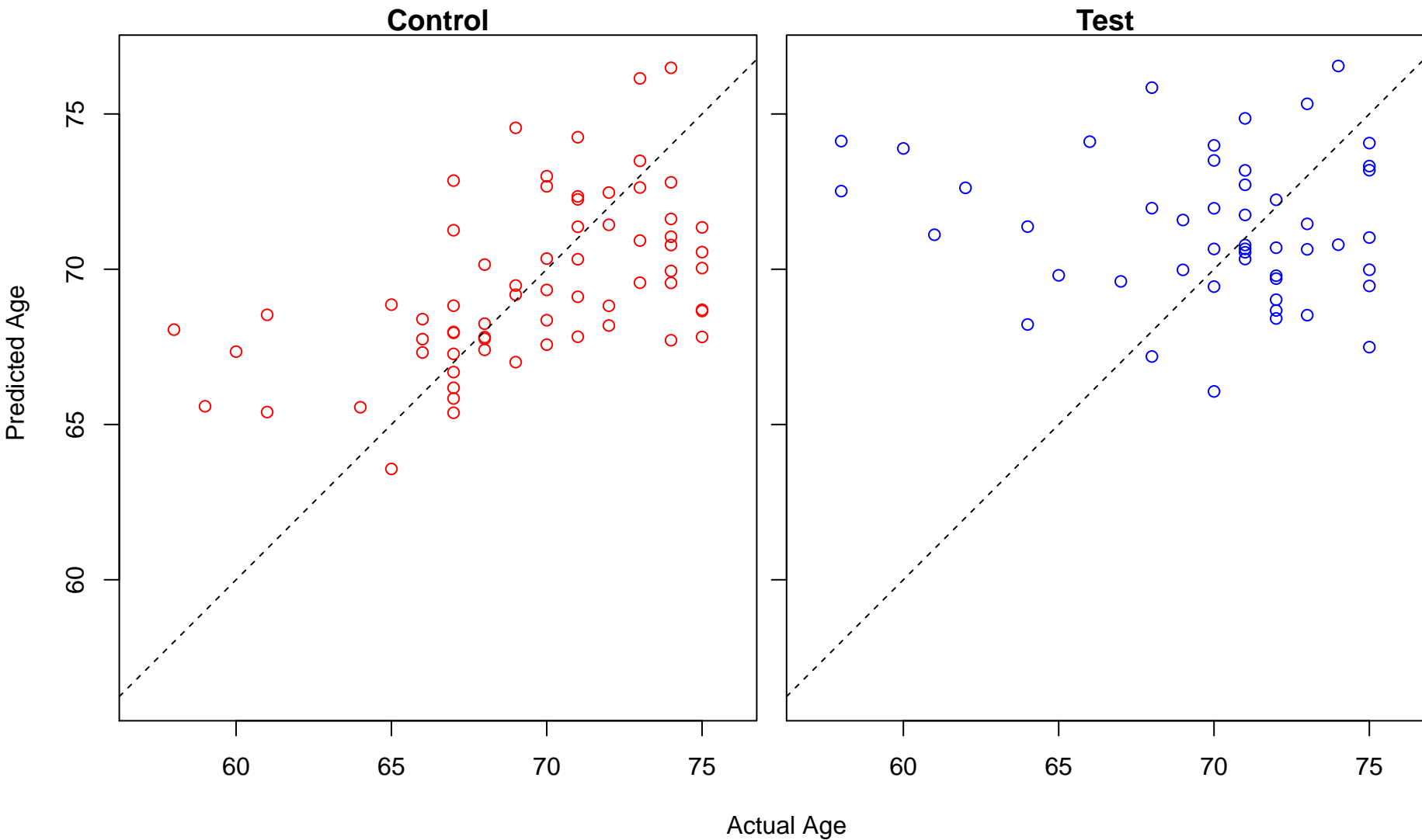
secretory granule organization (Score: 0.980959)



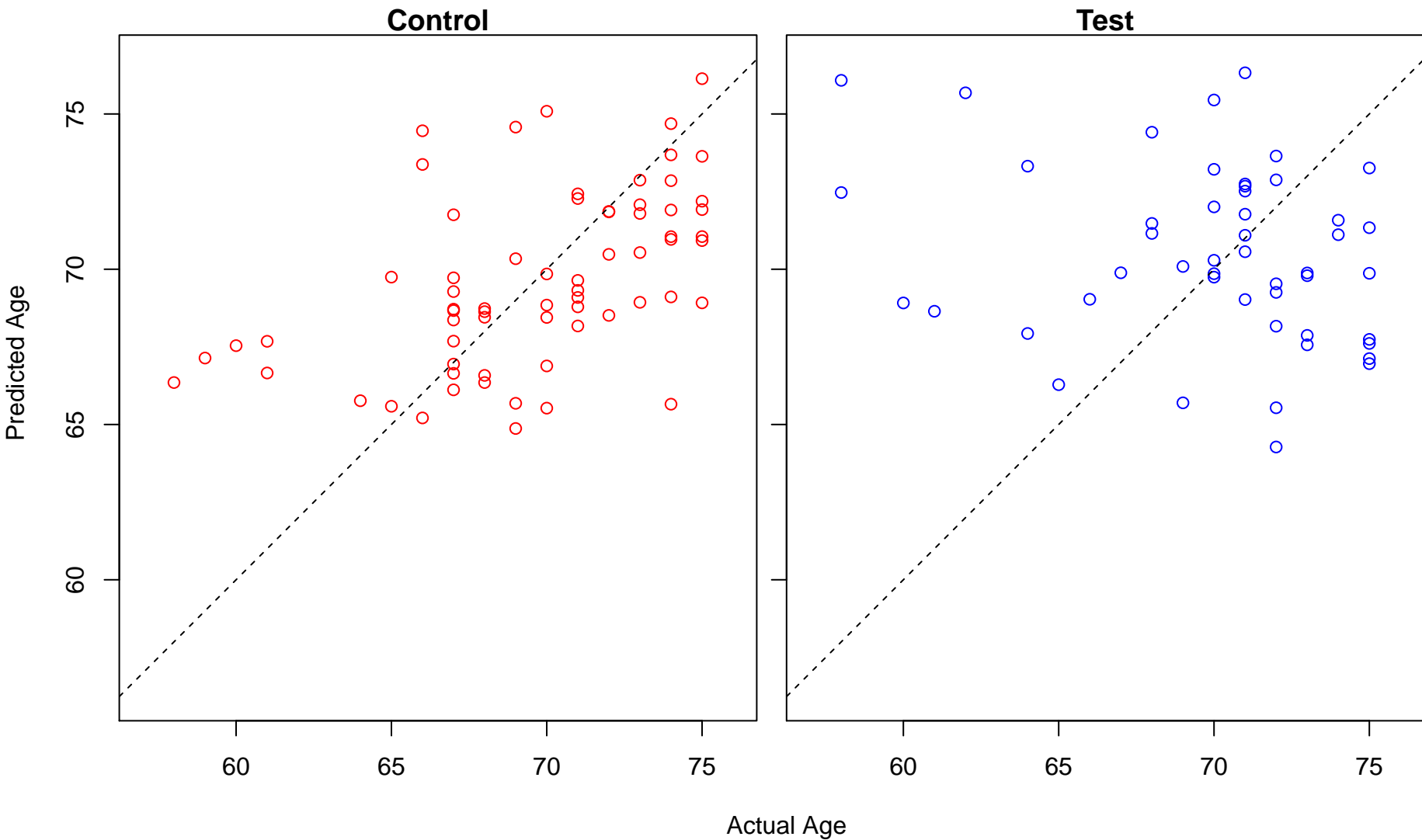
response to yeast (Score: 0.980896)



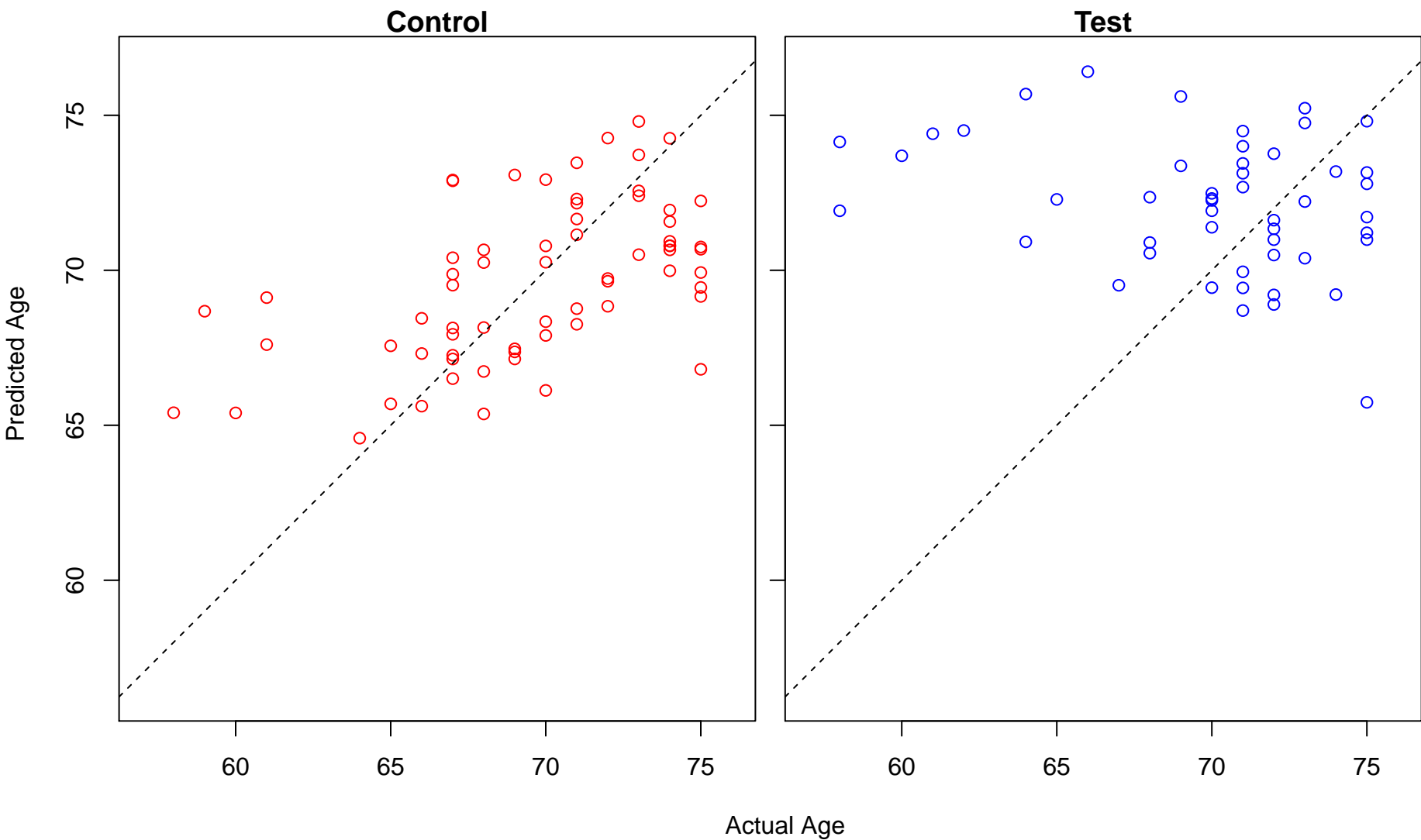
cell-cell adhesion via plasma-membrane adhesion molecules (Score: 0.980853)



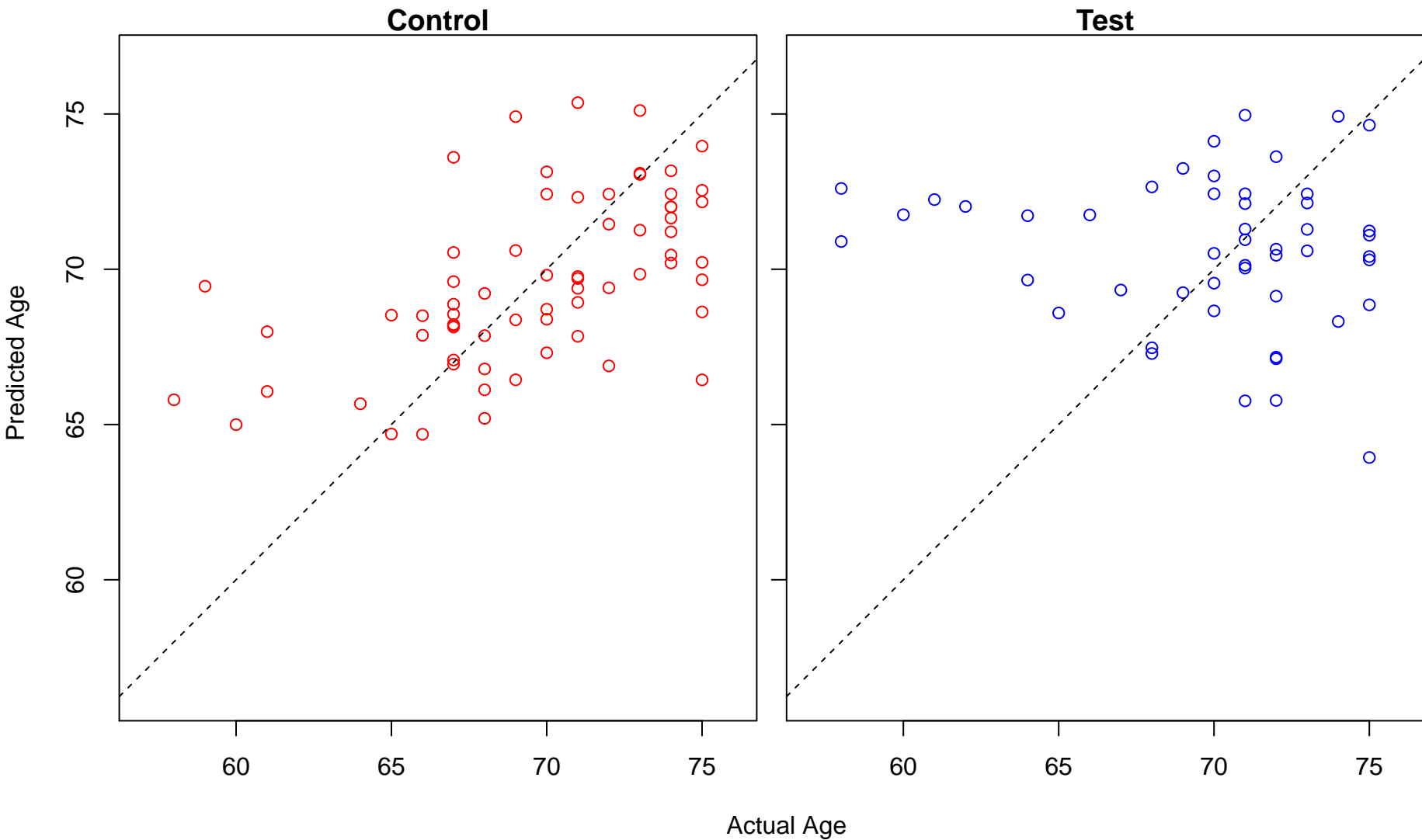
adipose tissue development (Score: 0.980747)



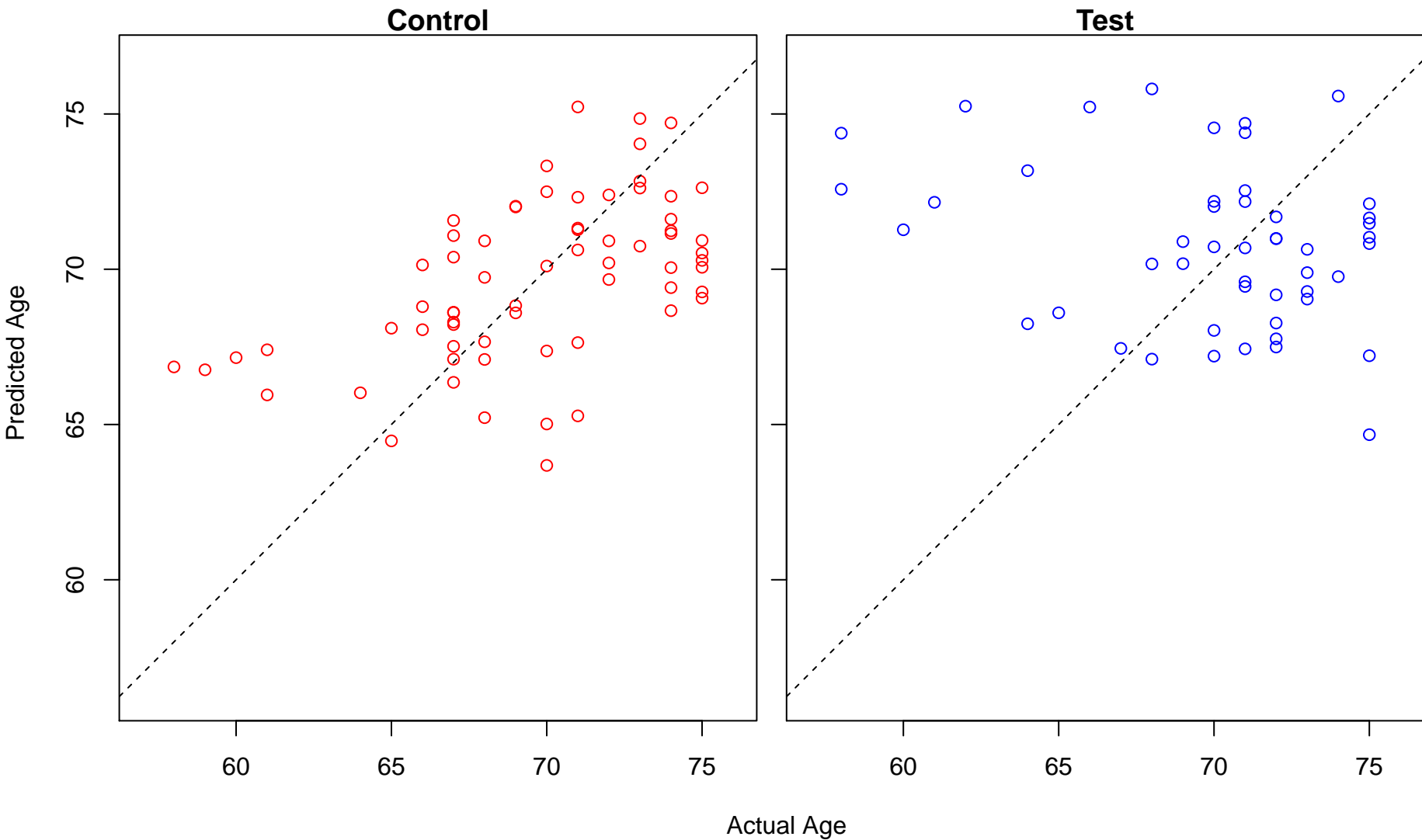
on of transcription from RNA polymerase II promoter involved in myocardial precursor cell differentiation (



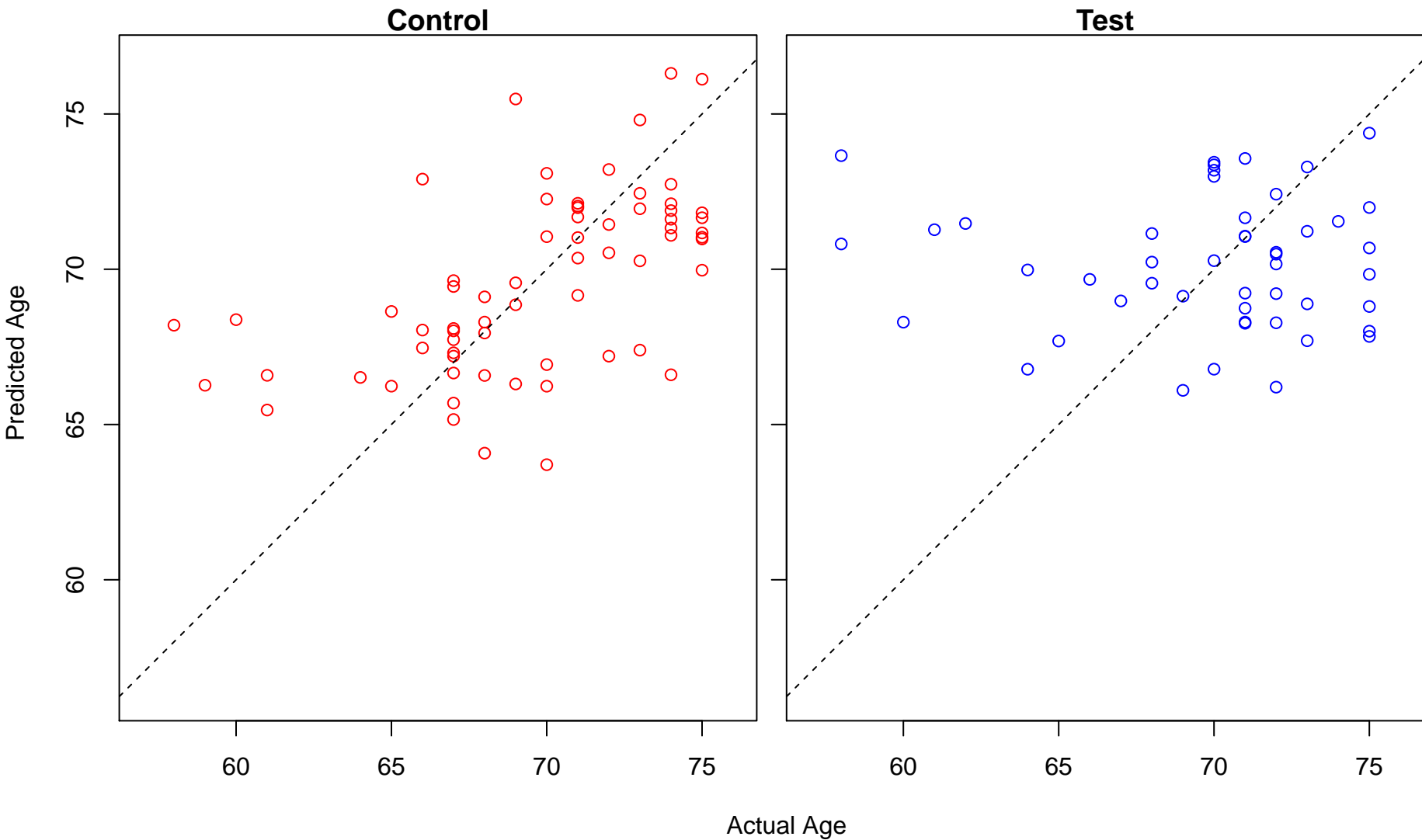
negative regulation of gliogenesis (Score: 0.980072)



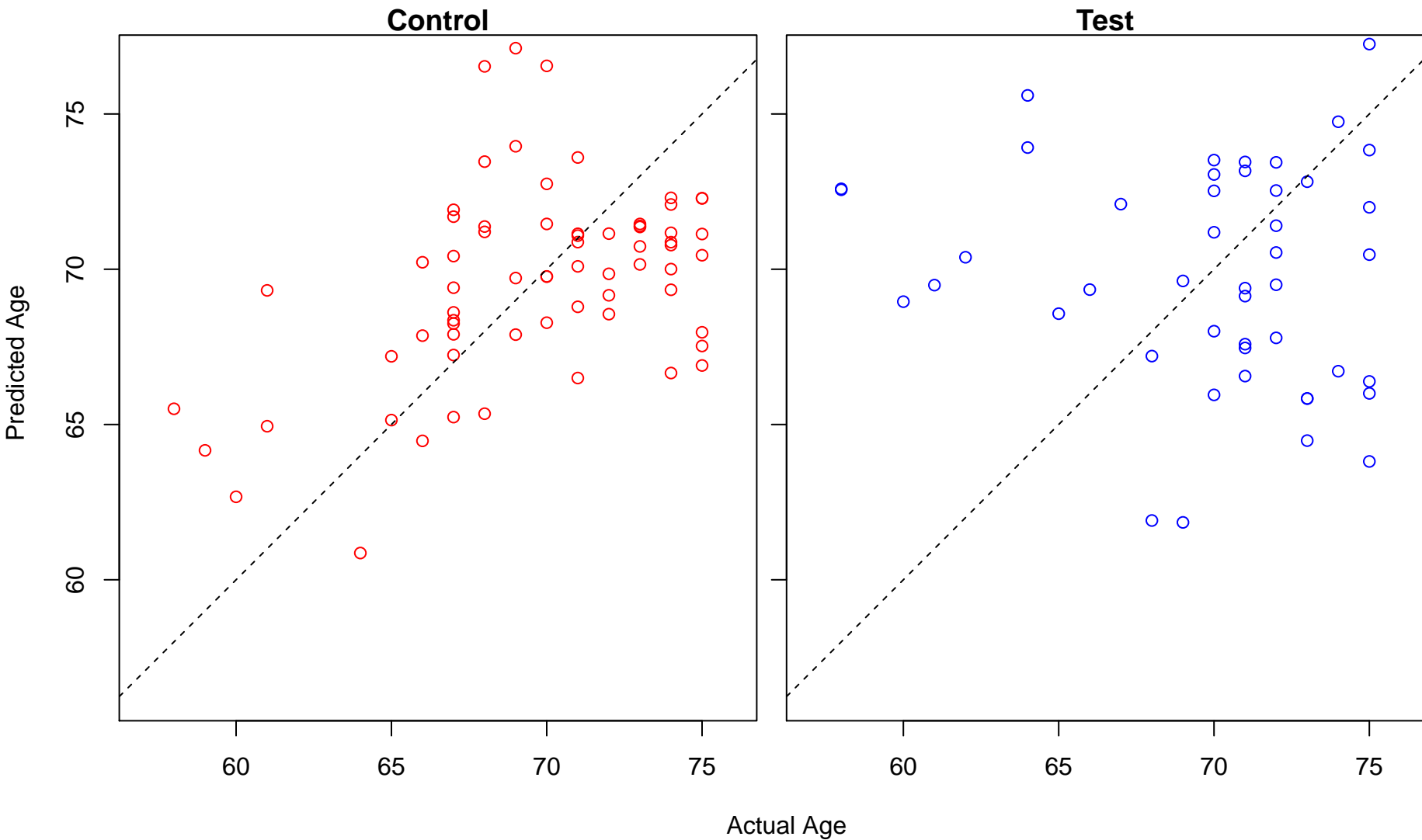
wound healing, spreading of epidermal cells (Score: 0.979783)



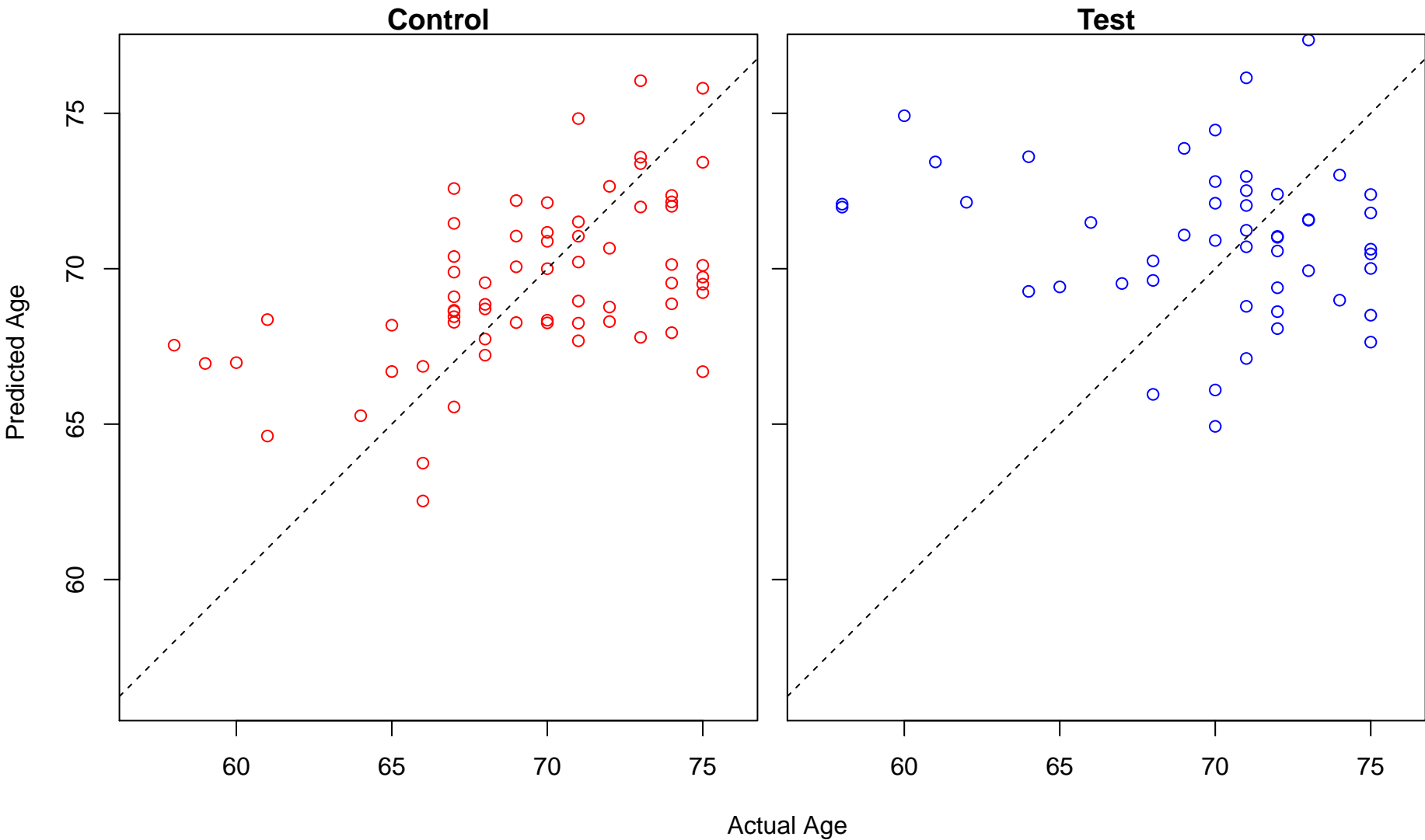
platelet aggregation (Score: 0.979652)



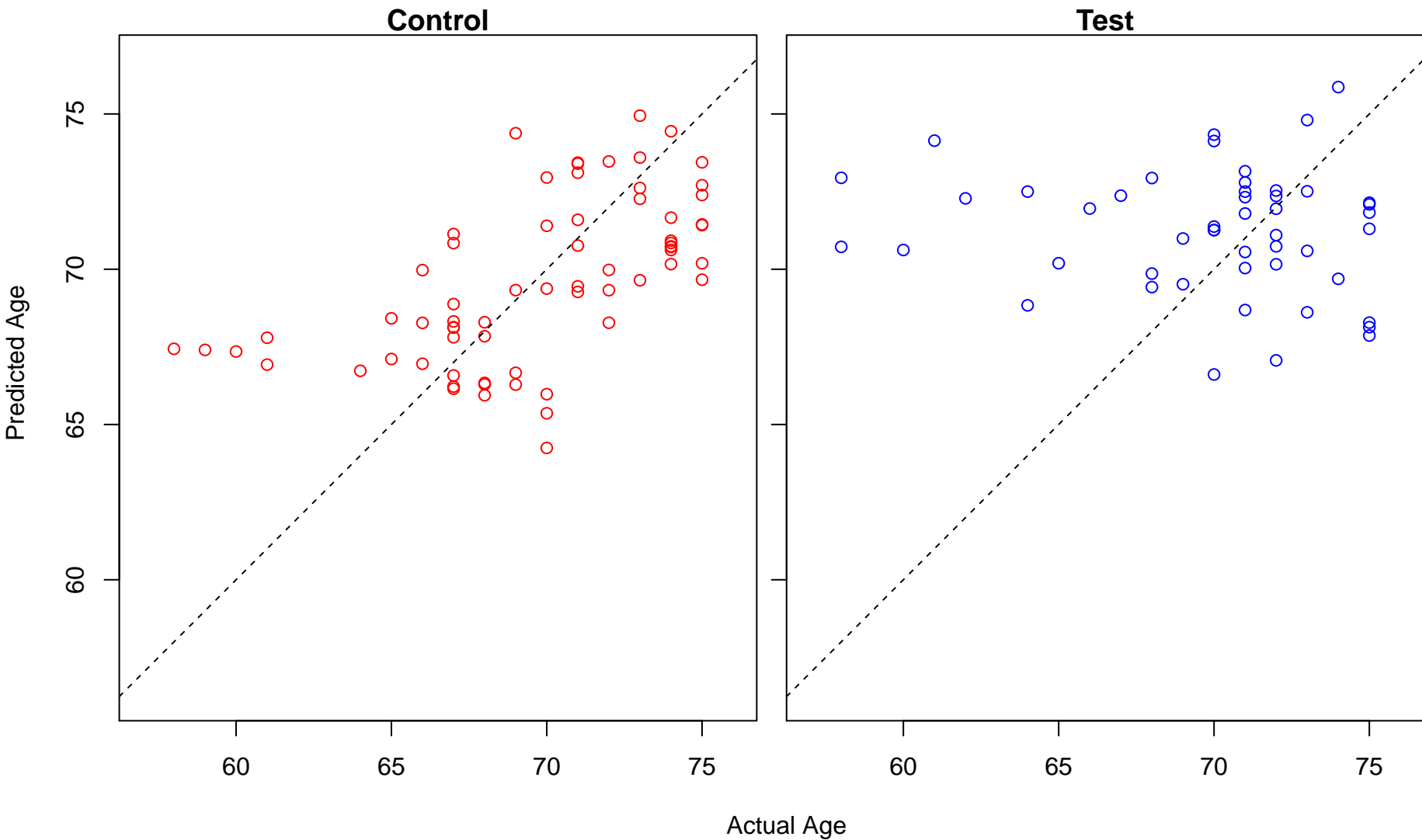
lens development in camera-type eye (Score: 0.979557)



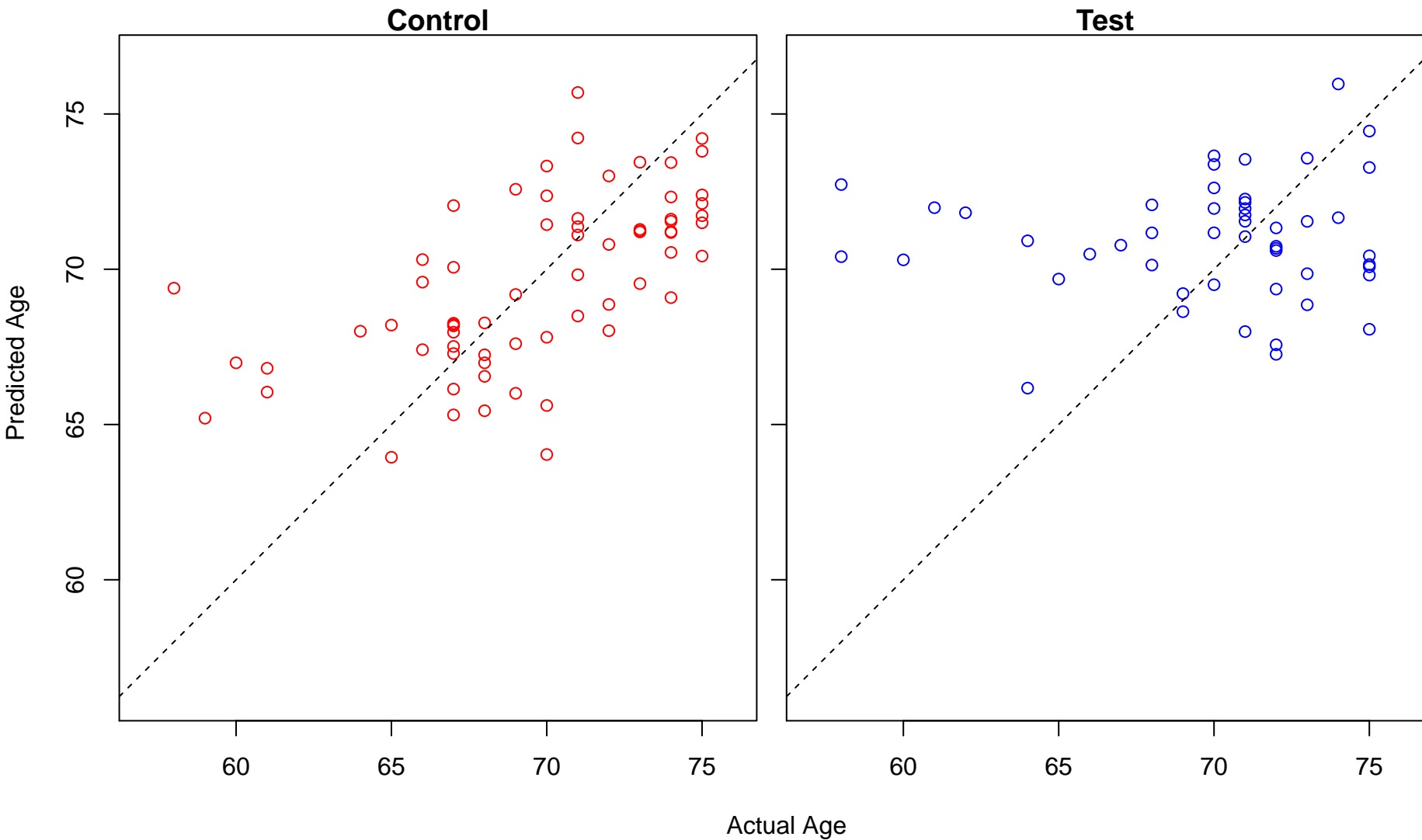
positive regulation of vacuole organization (Score: 0.977926)



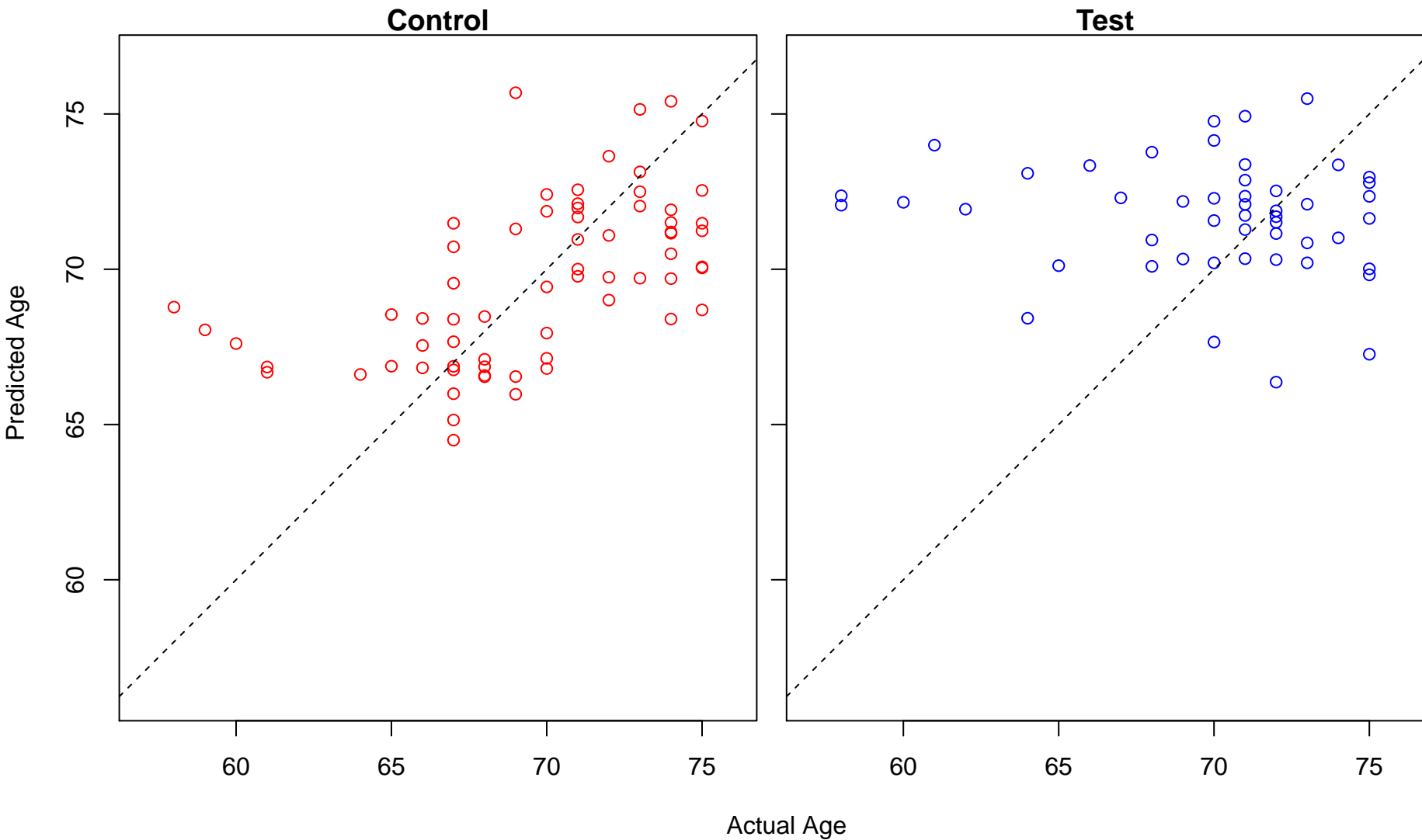
regulation of protein phosphatase type 2A activity (Score: 0.977148)



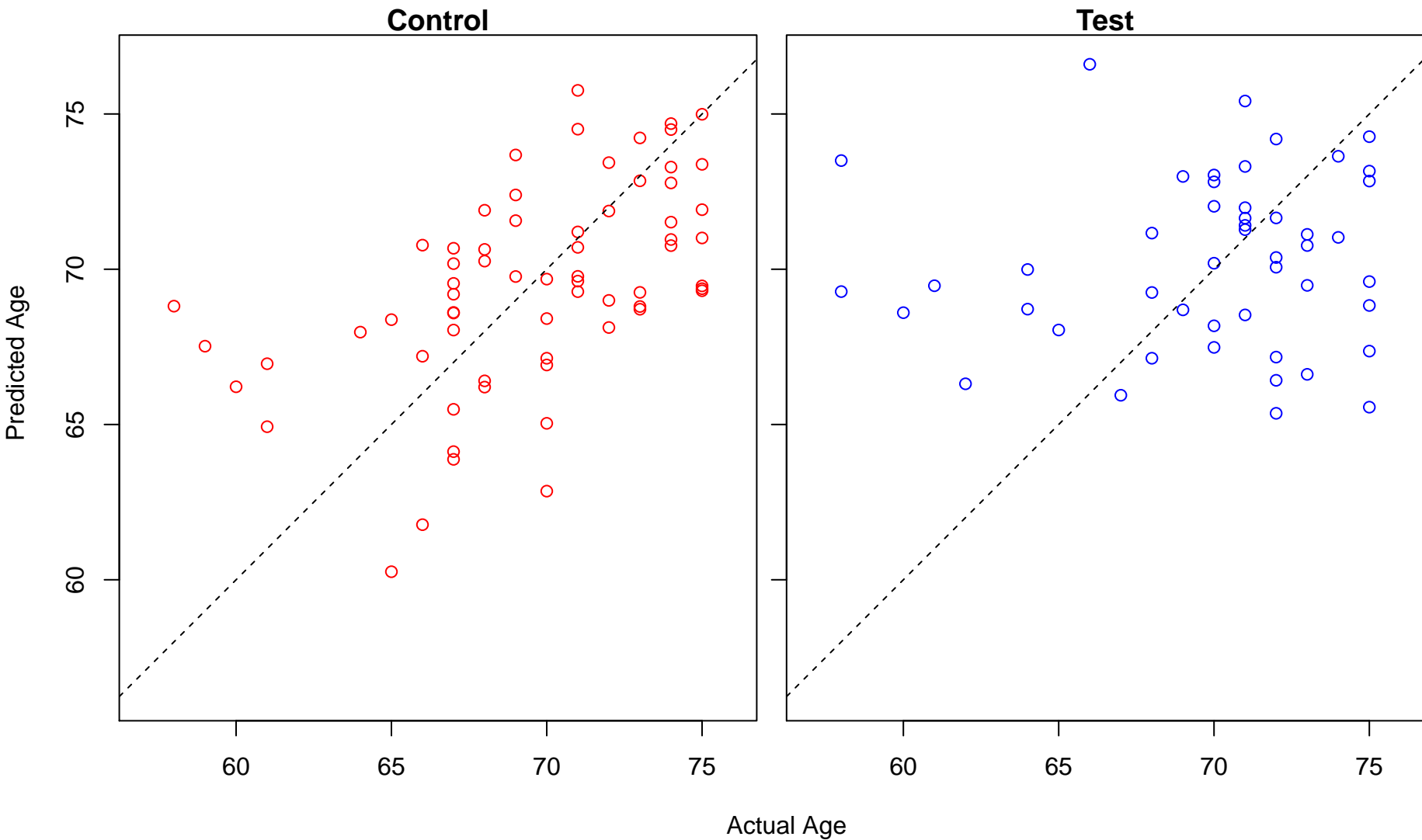
fat cell differentiation (Score: 0.976845)



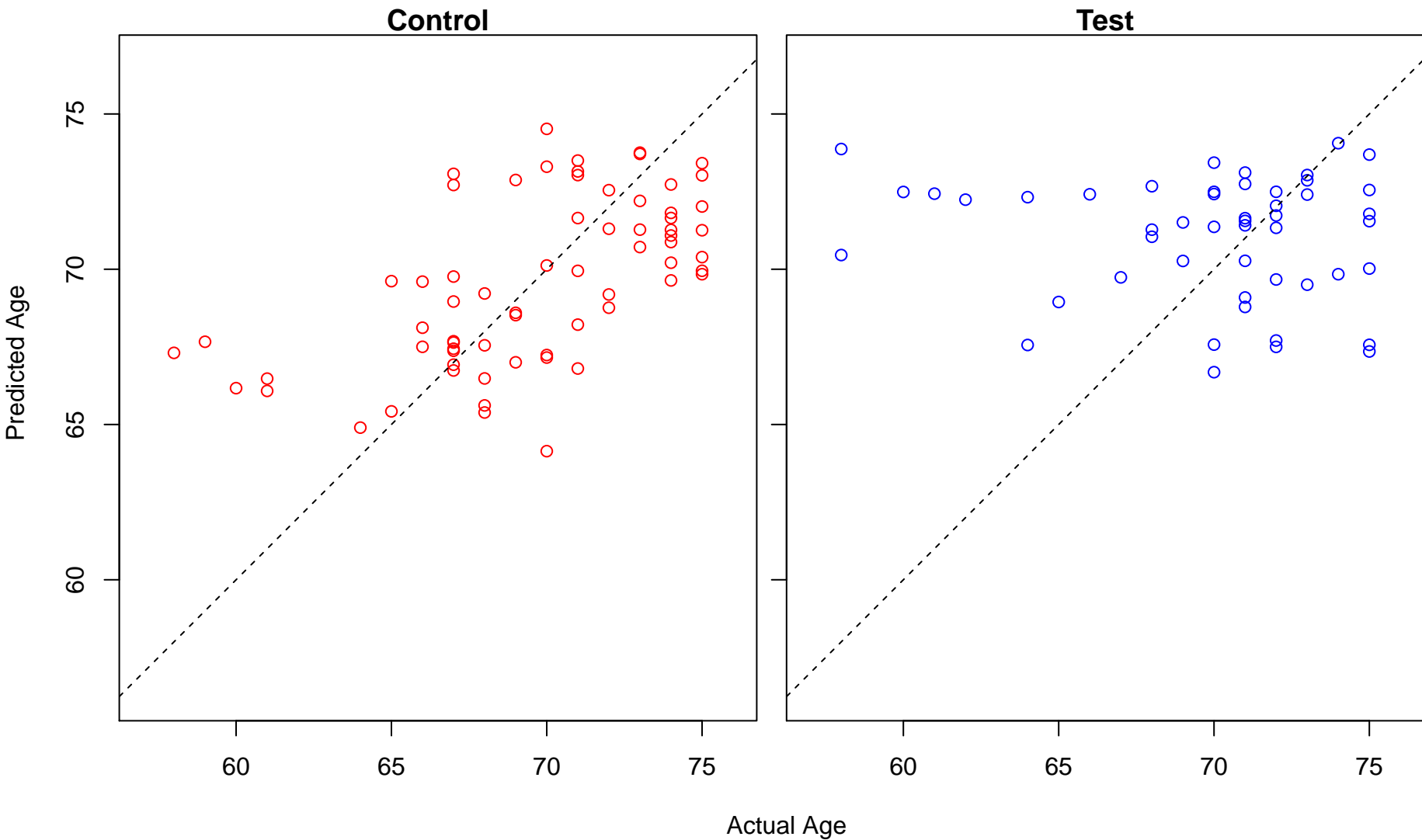
DNA topological change (Score: 0.975961)



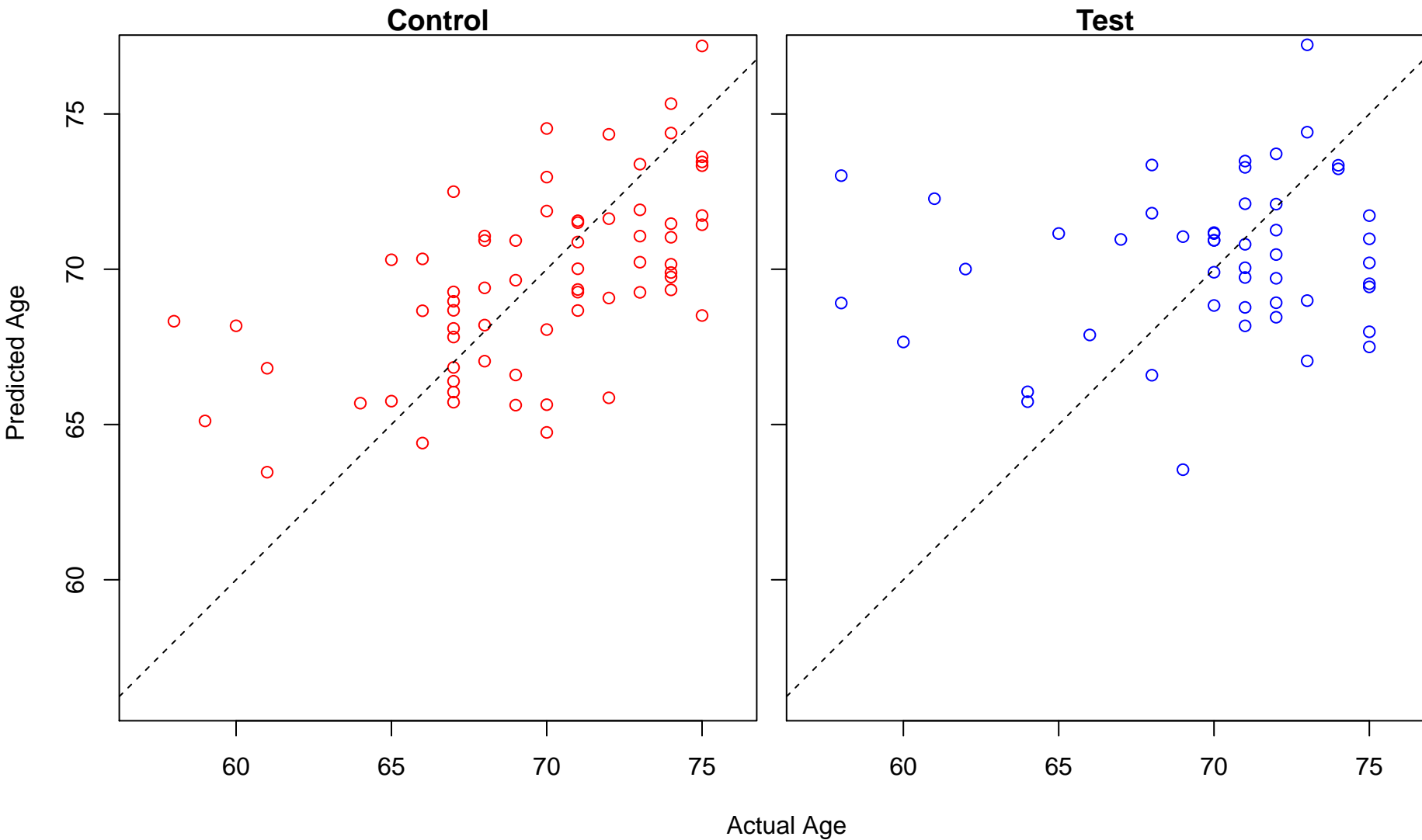
positive regulation of interleukin-13 production (Score: 0.974086)



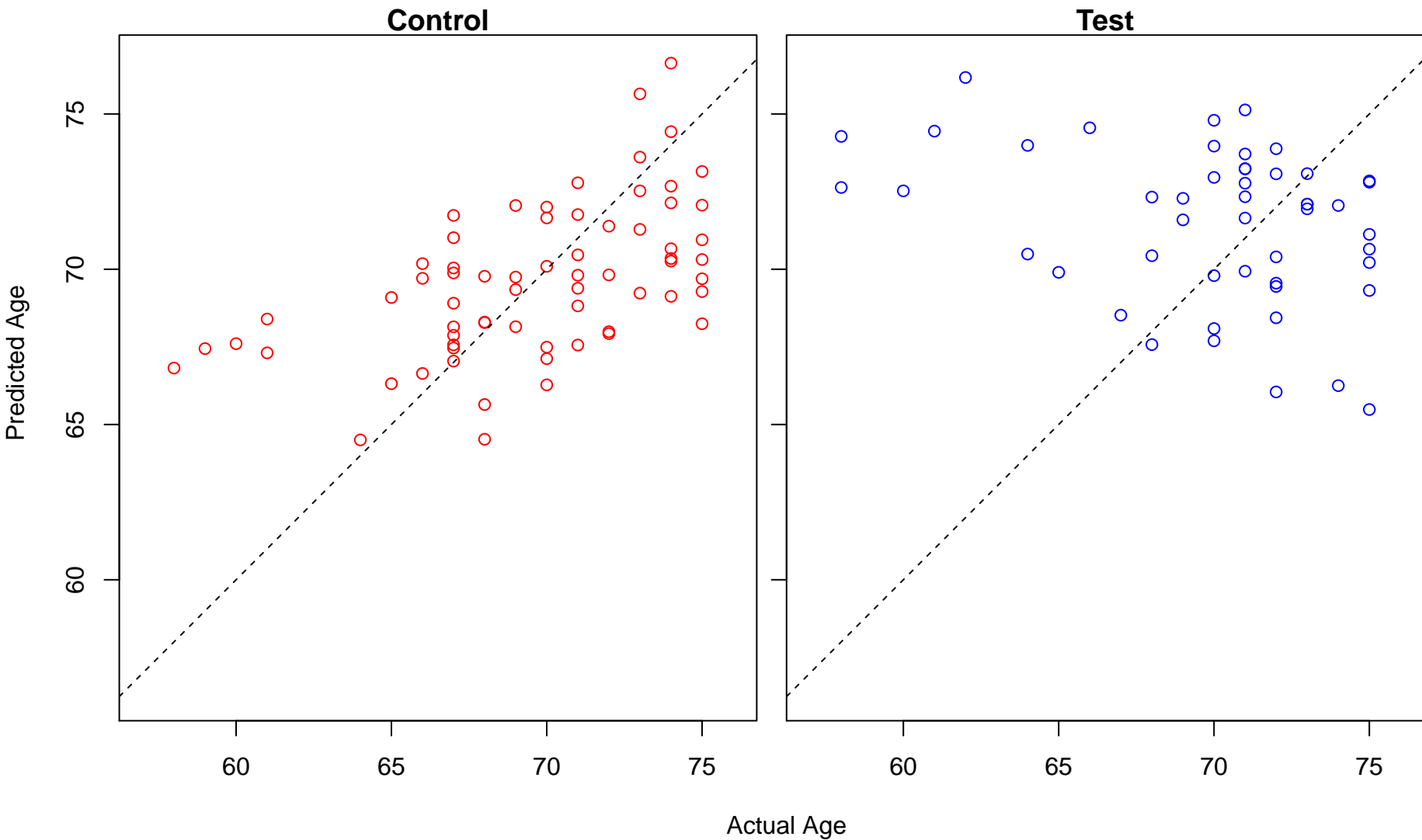
tube formation (Score: 0.973278)



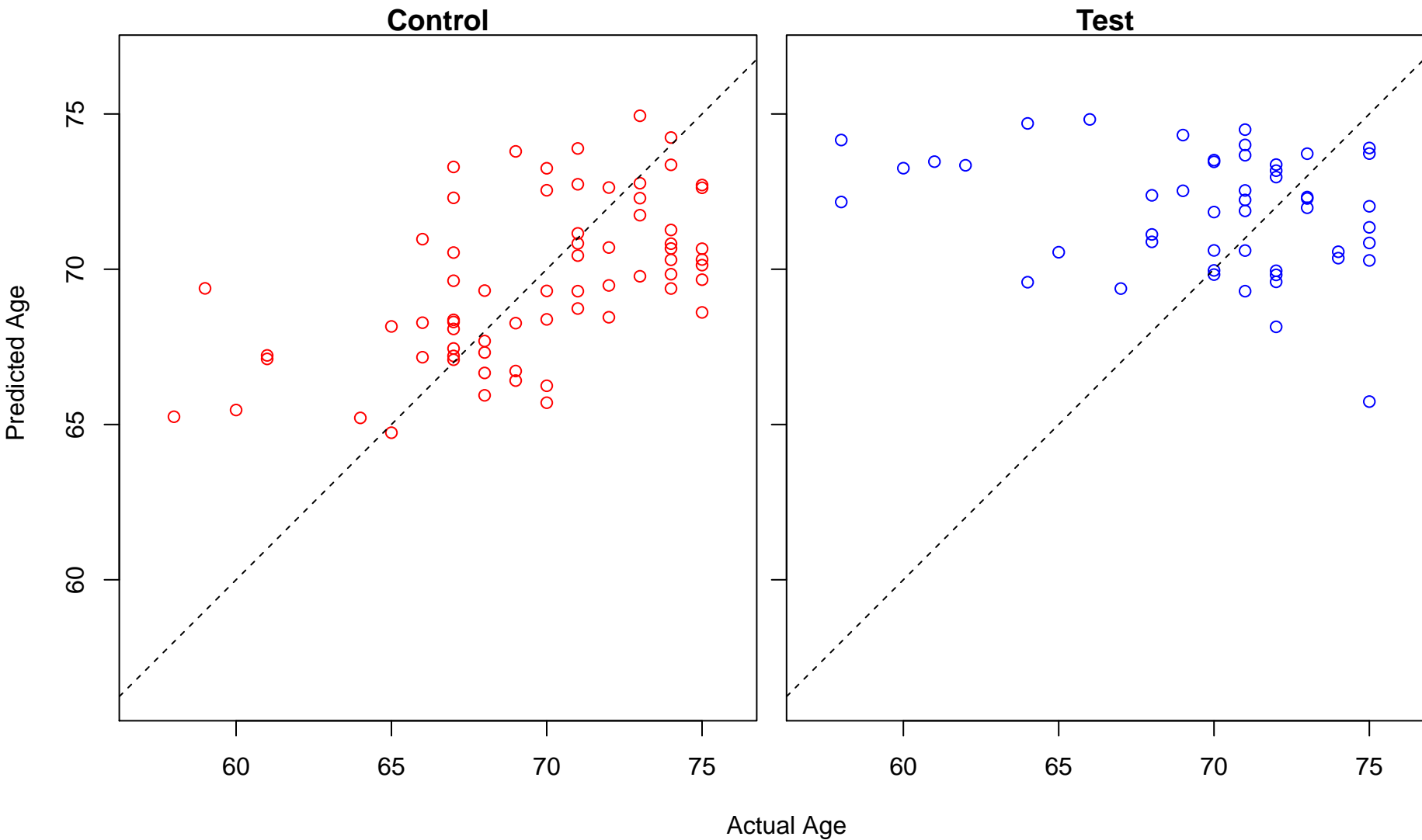
protein maturation by protein folding (Score: 0.973228)



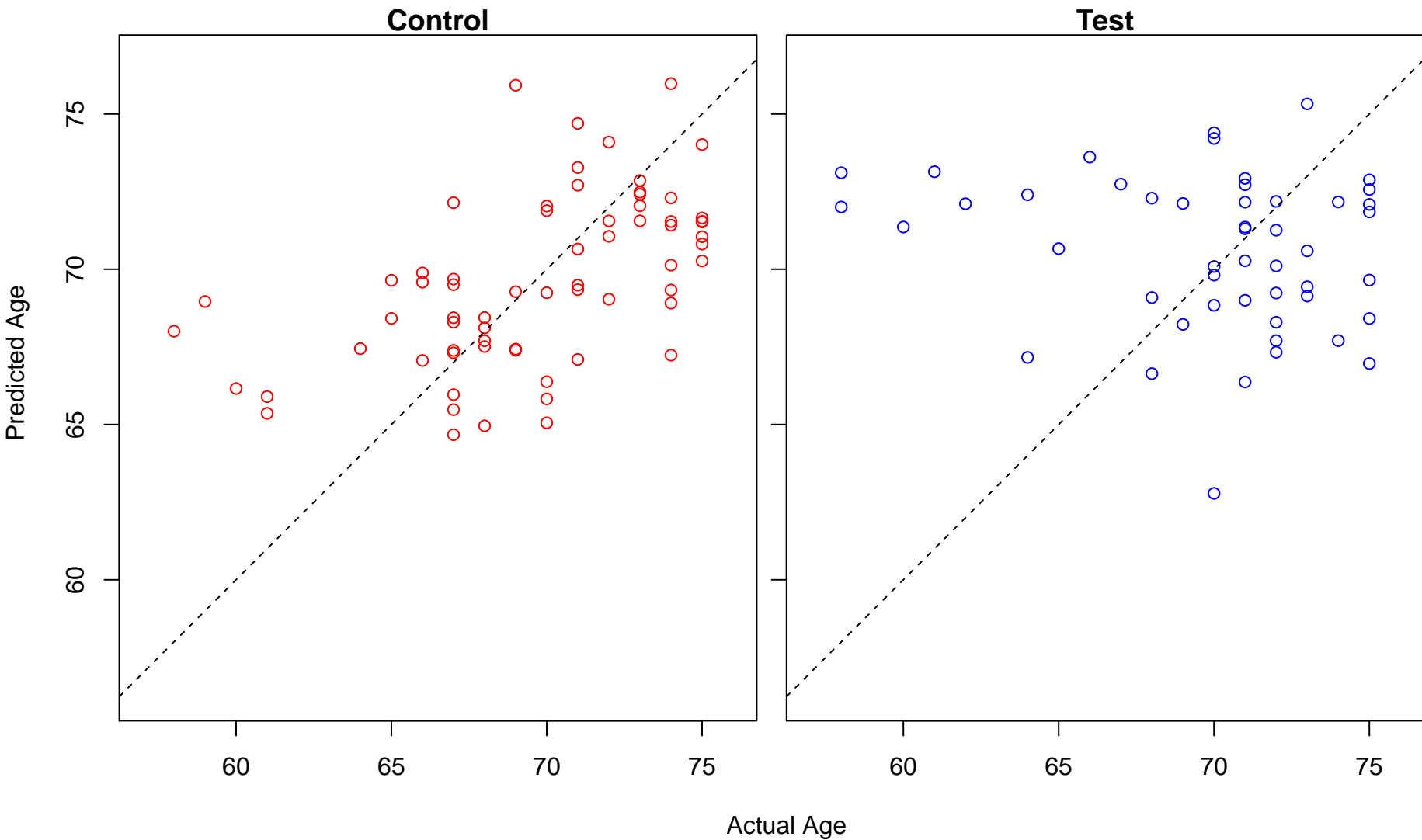
negative regulation of amyloid precursor protein catabolic process (Score: 0.973191)



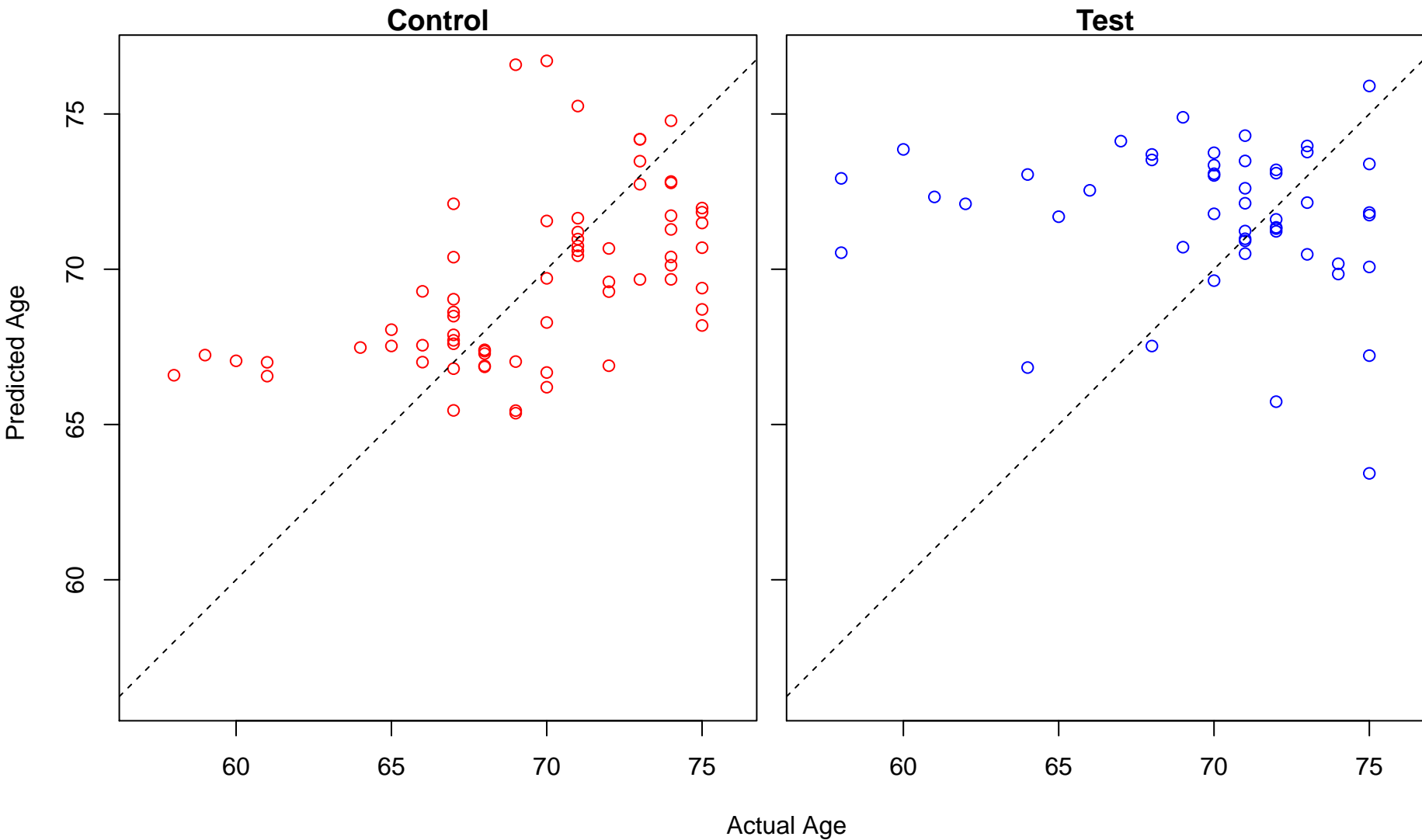
heart looping (Score: 0.972264)



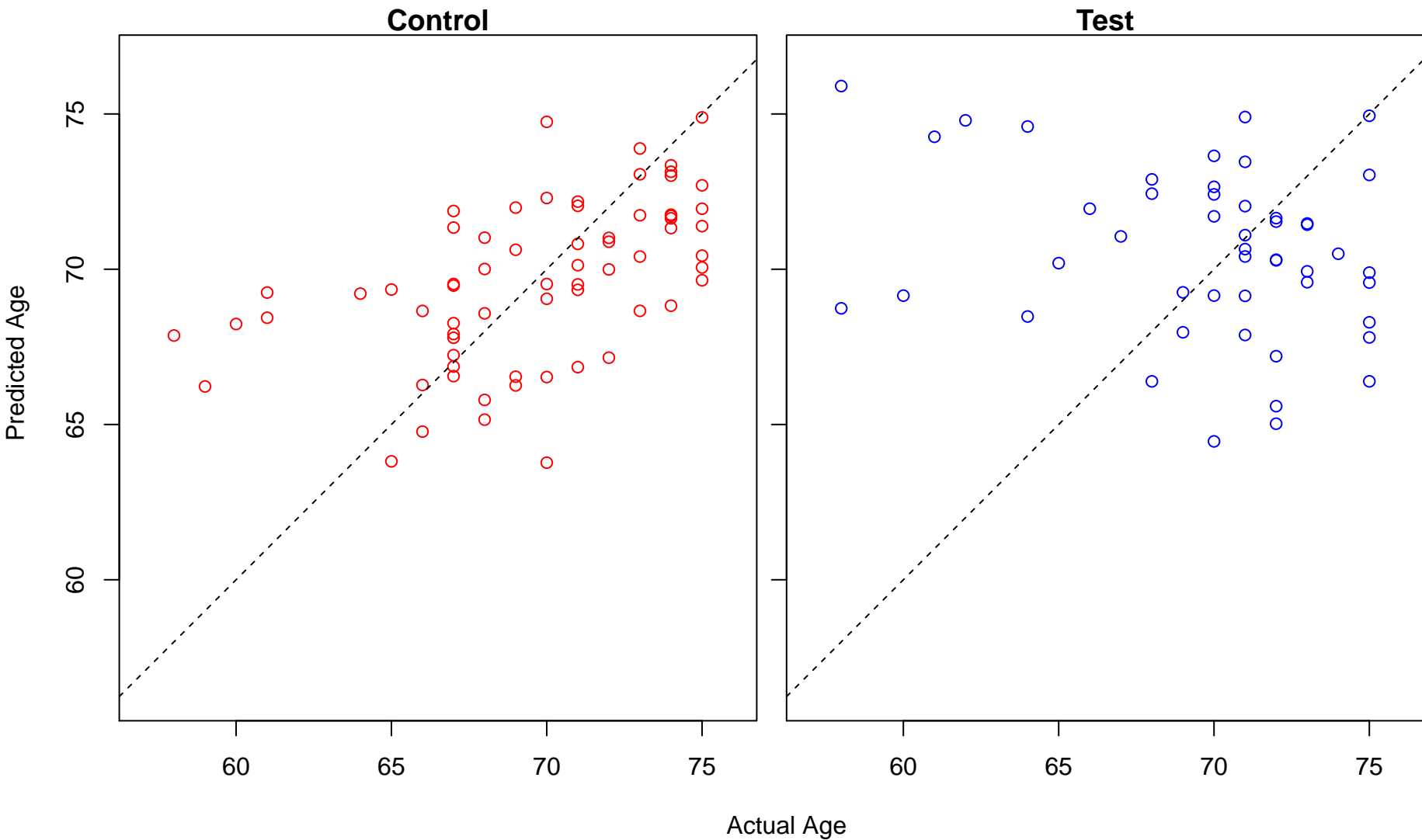
dendritic spine organization (Score: 0.972259)



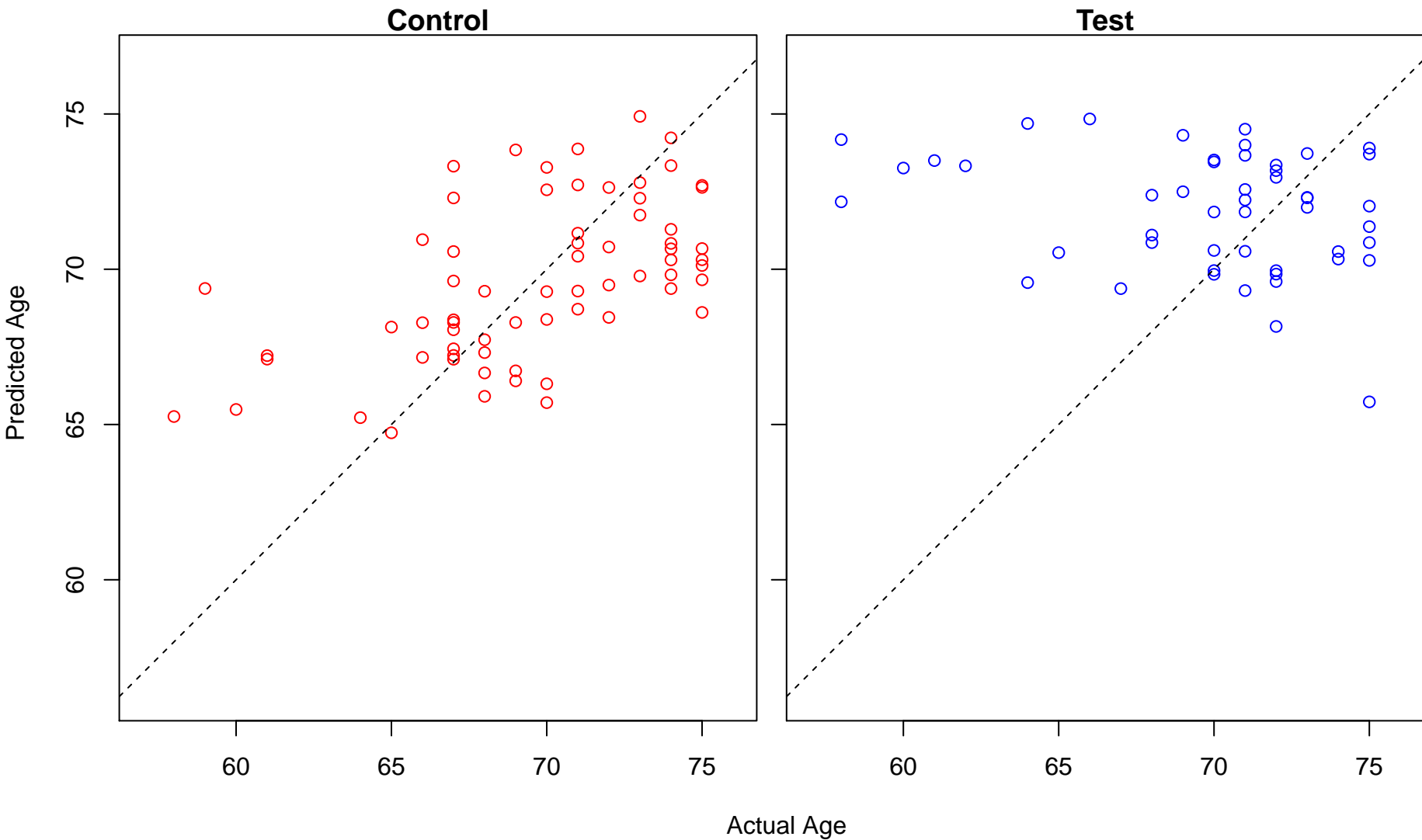
rhodopsin mediated signaling pathway (Score: 0.972058)



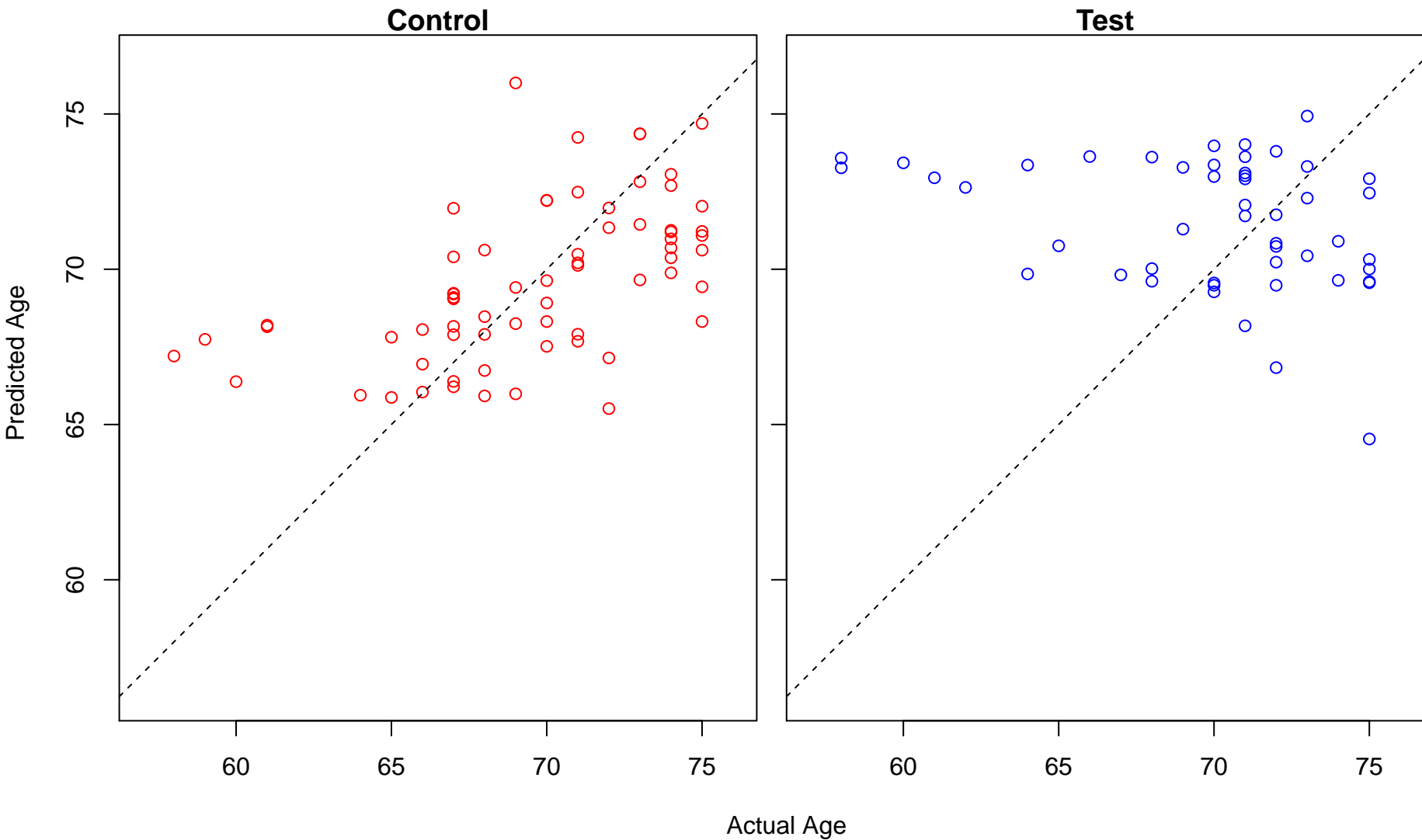
positive regulation of ryanodine-sensitive calcium-release channel activity (Score: 0.971567)



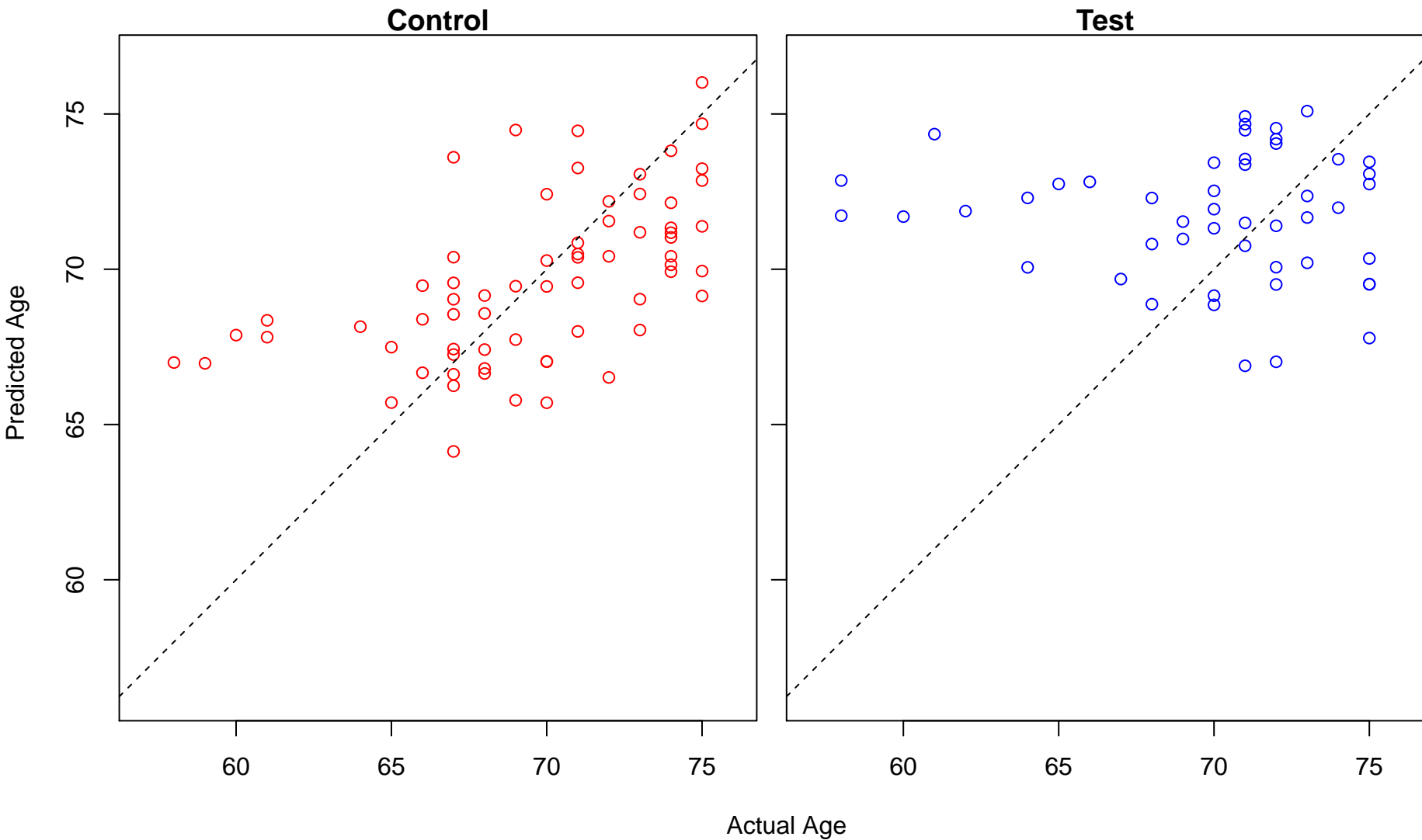
determination of heart left/right asymmetry (Score: 0.971466)



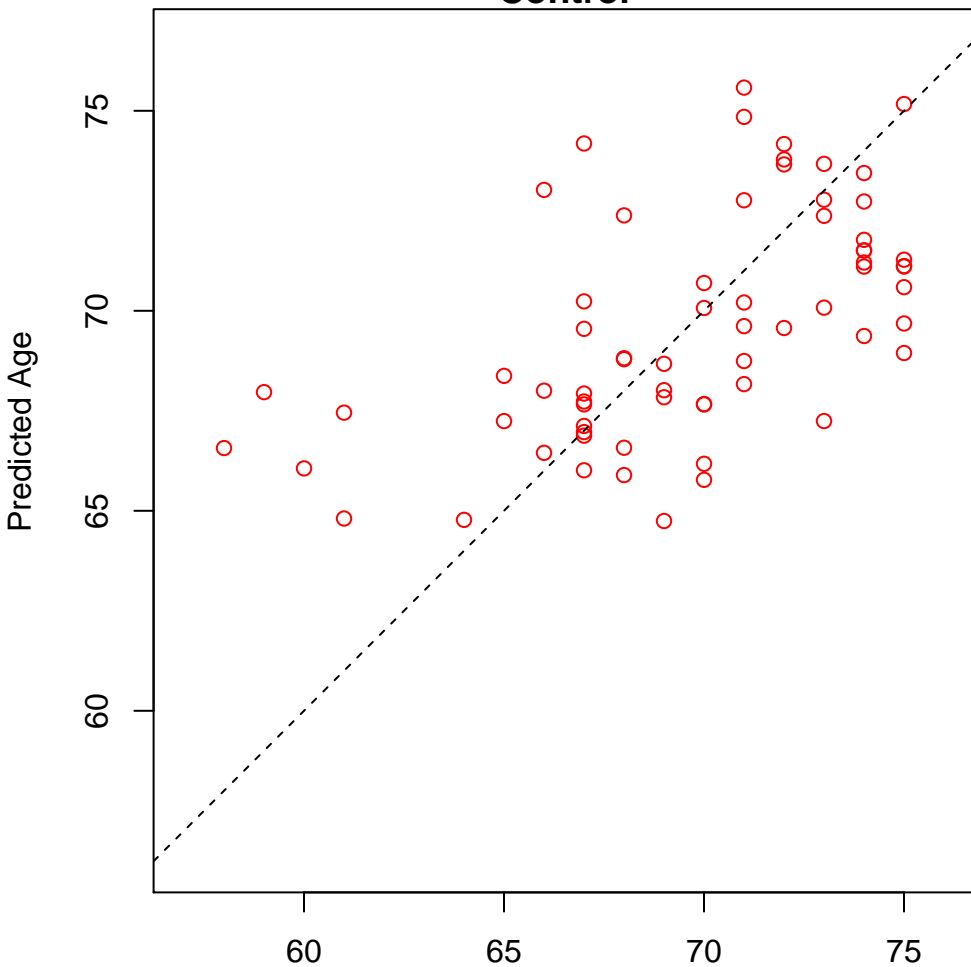
negative regulation of stem cell differentiation (Score: 0.971226)



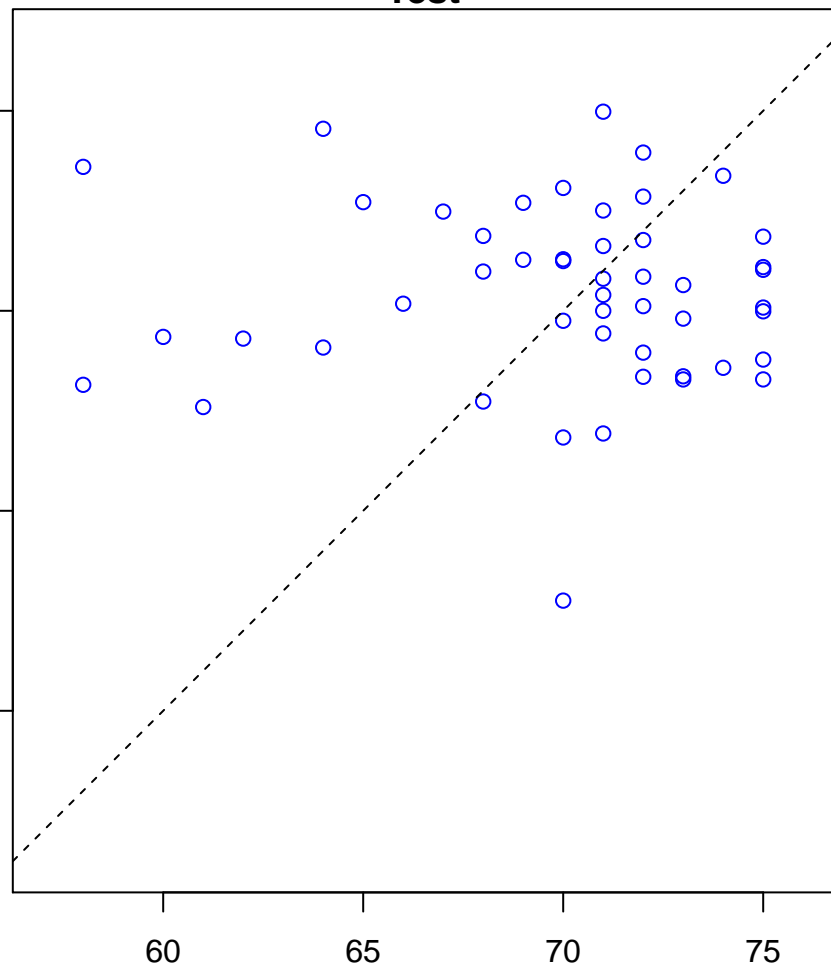
positive regulation of cellular response to insulin stimulus (Score: 0.971168)



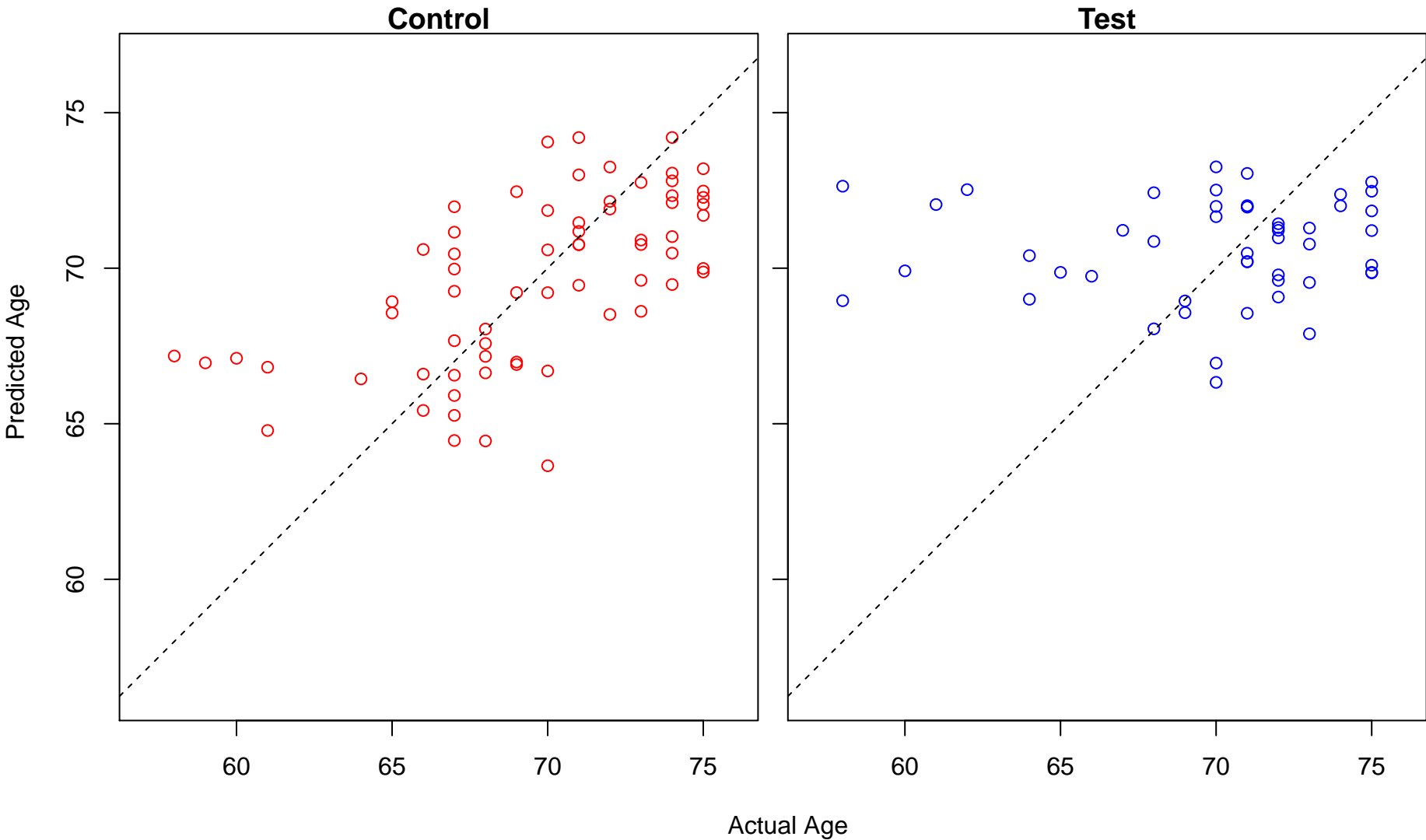
Control



Test

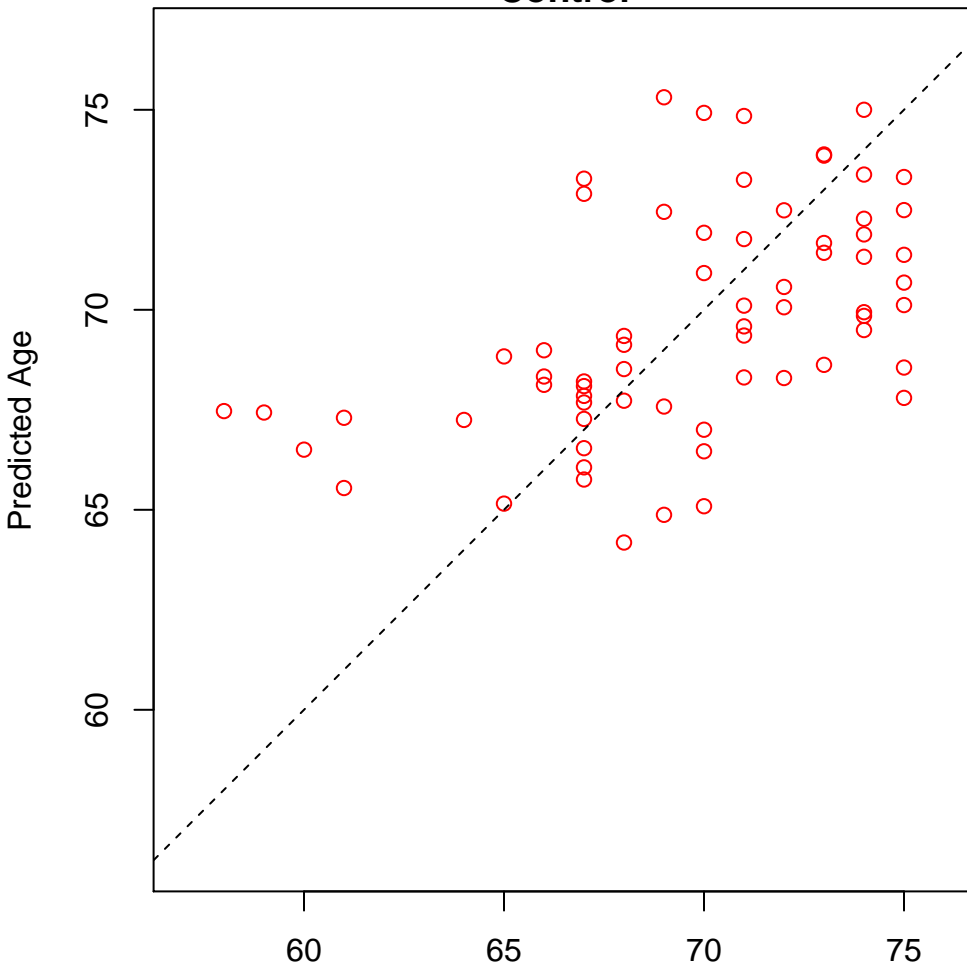


activation of signaling protein activity involved in unfolded protein response (Score: 0.970943)

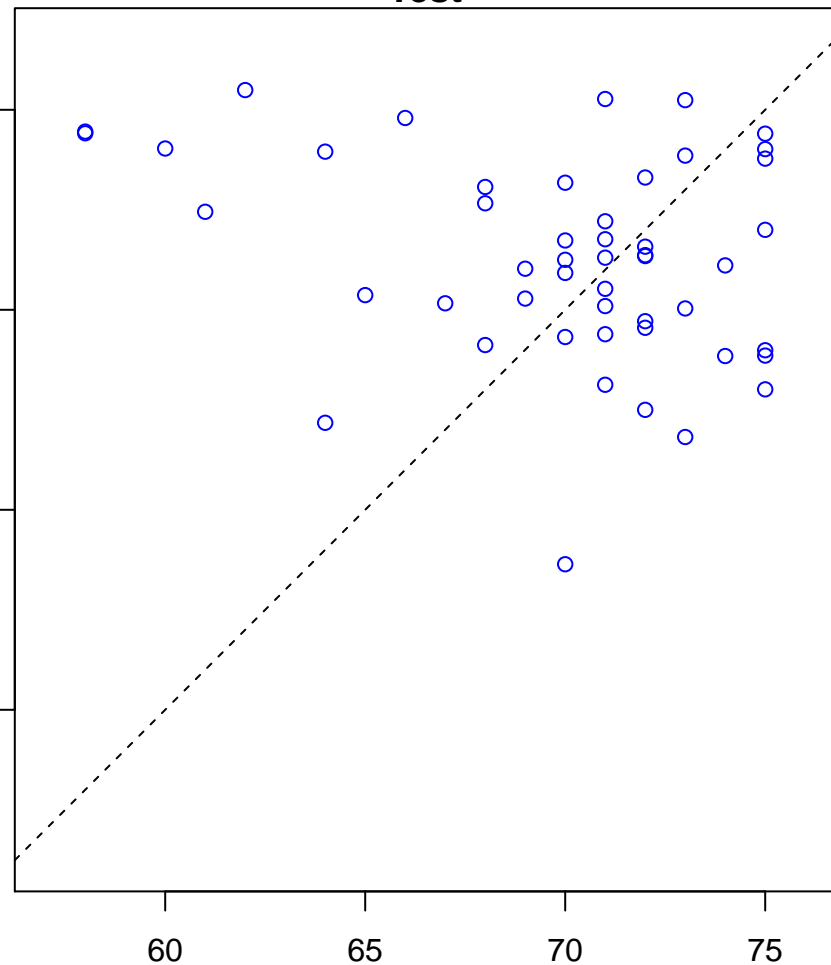


protein K48-linked deubiquitination (Score: 0.970730)

Control



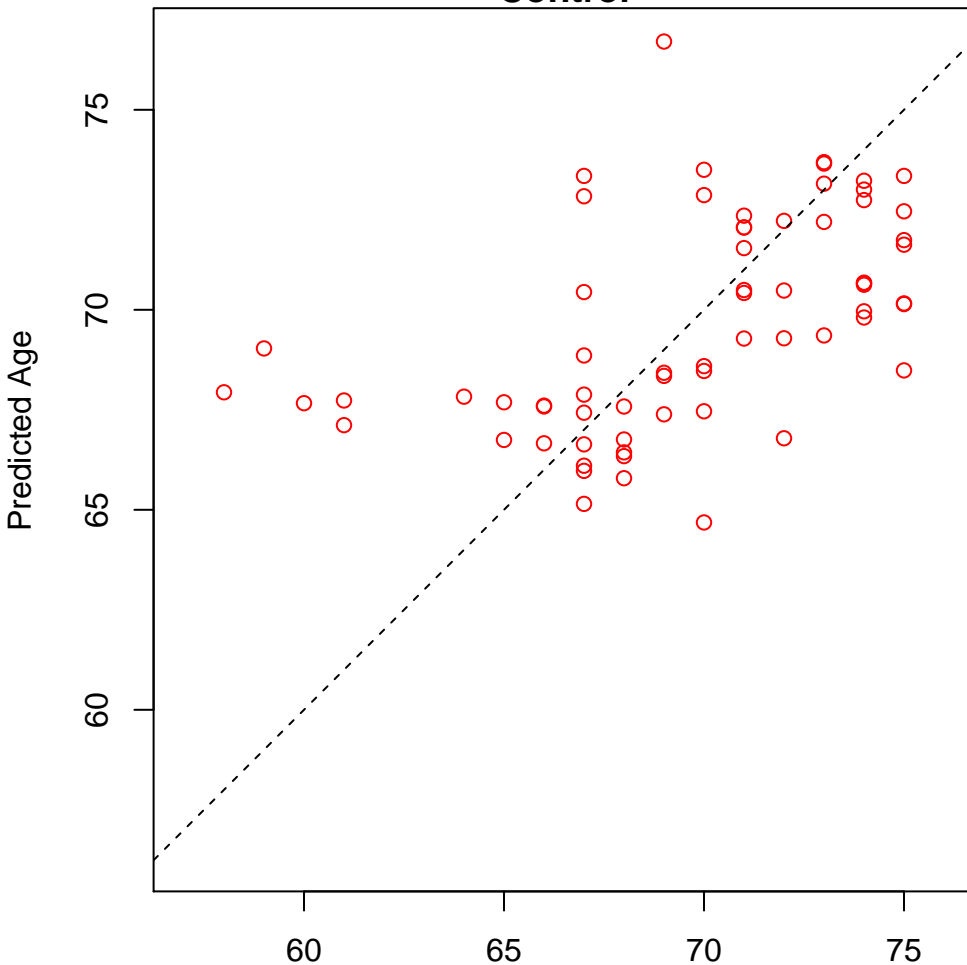
Test



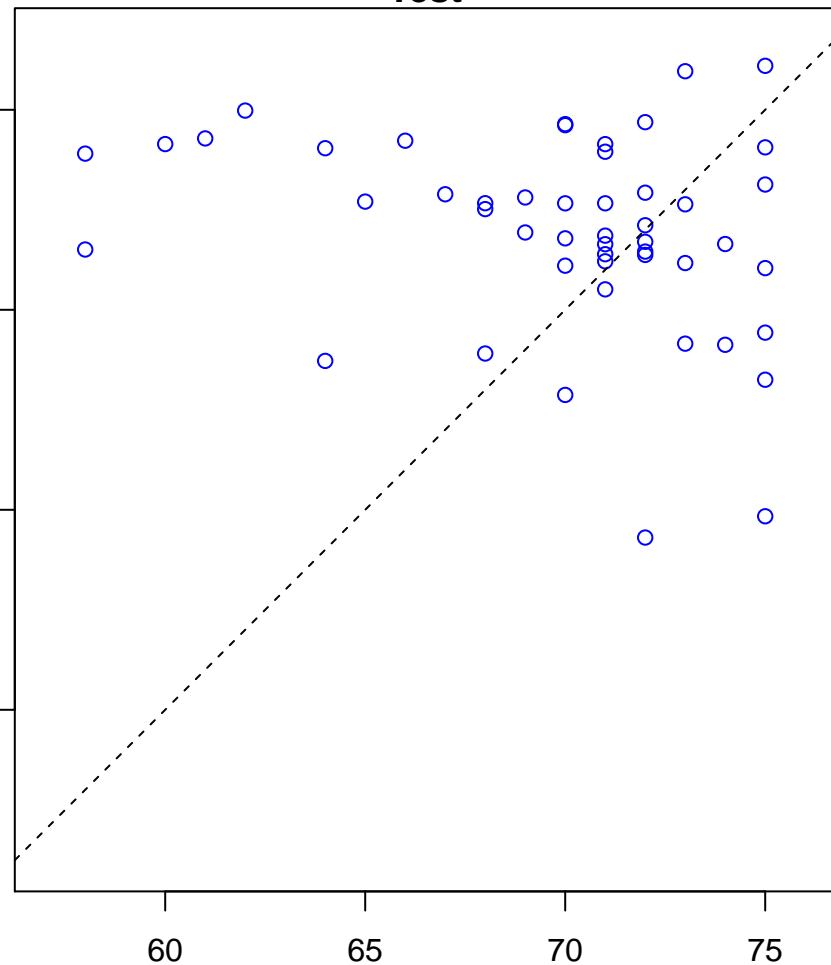
Actual Age

protein K63-linked deubiquitination (Score: 0.970485)

Control

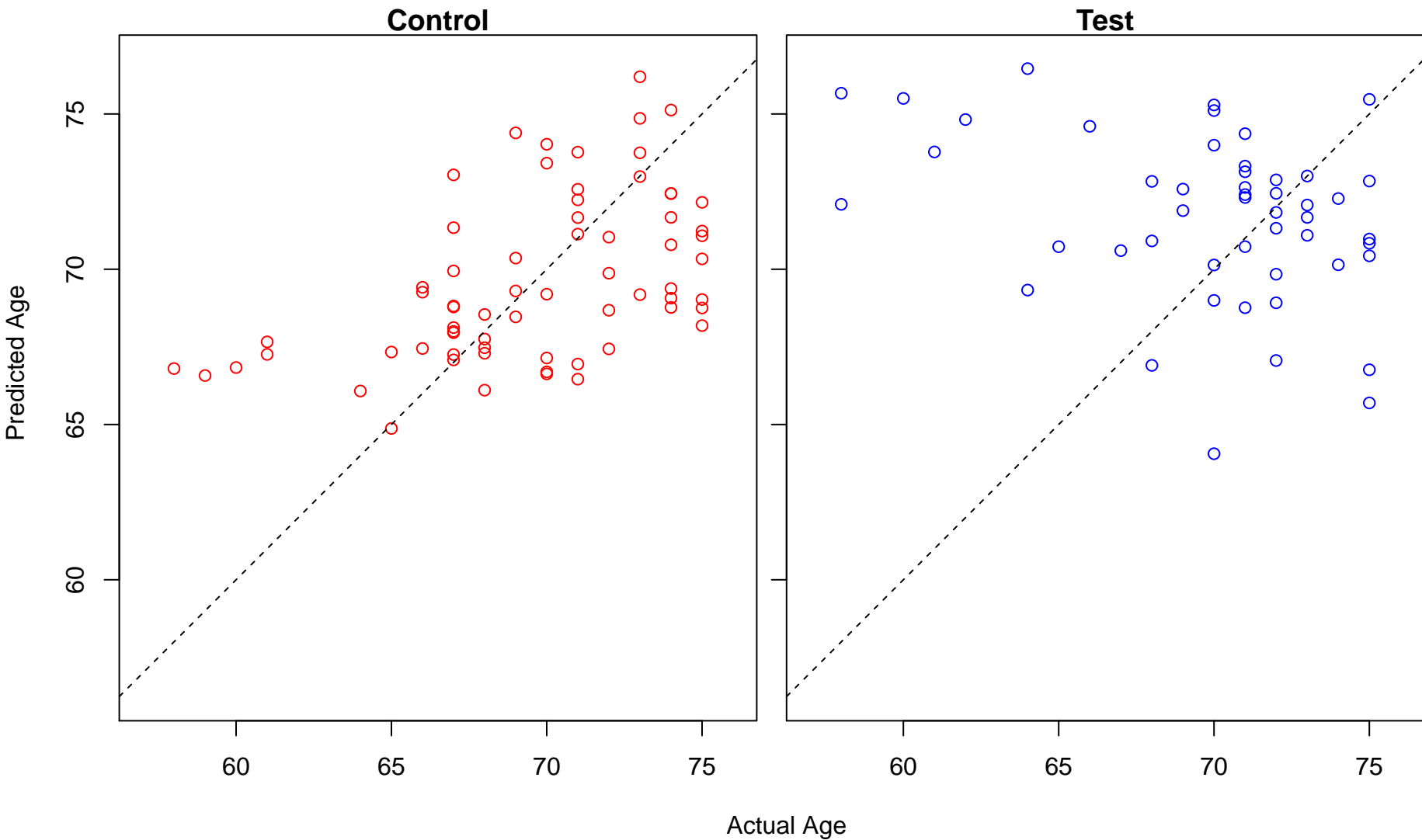


Test

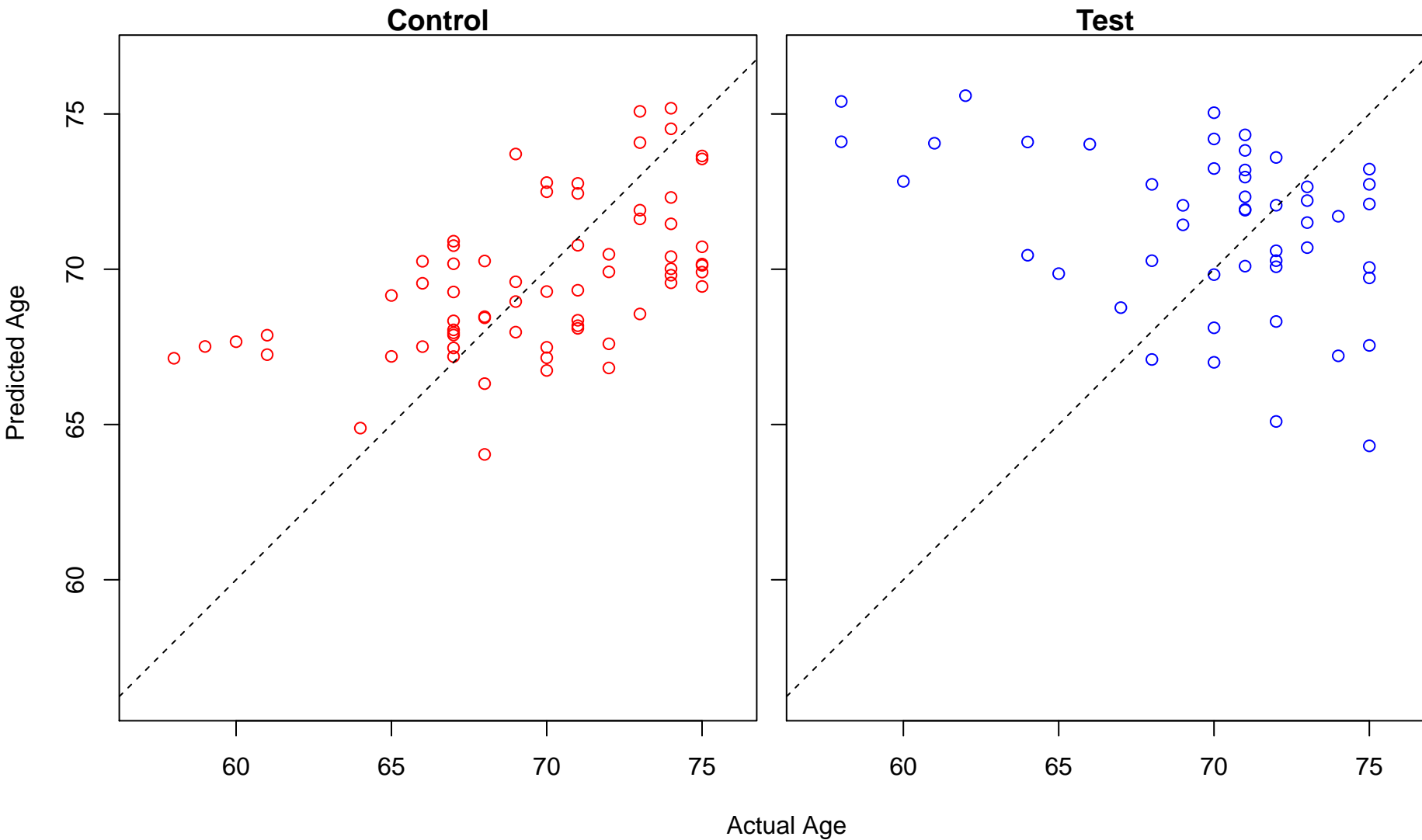


Actual Age

positive regulation of phosphatidylinositol 3-kinase signaling (Score: 0.970256)

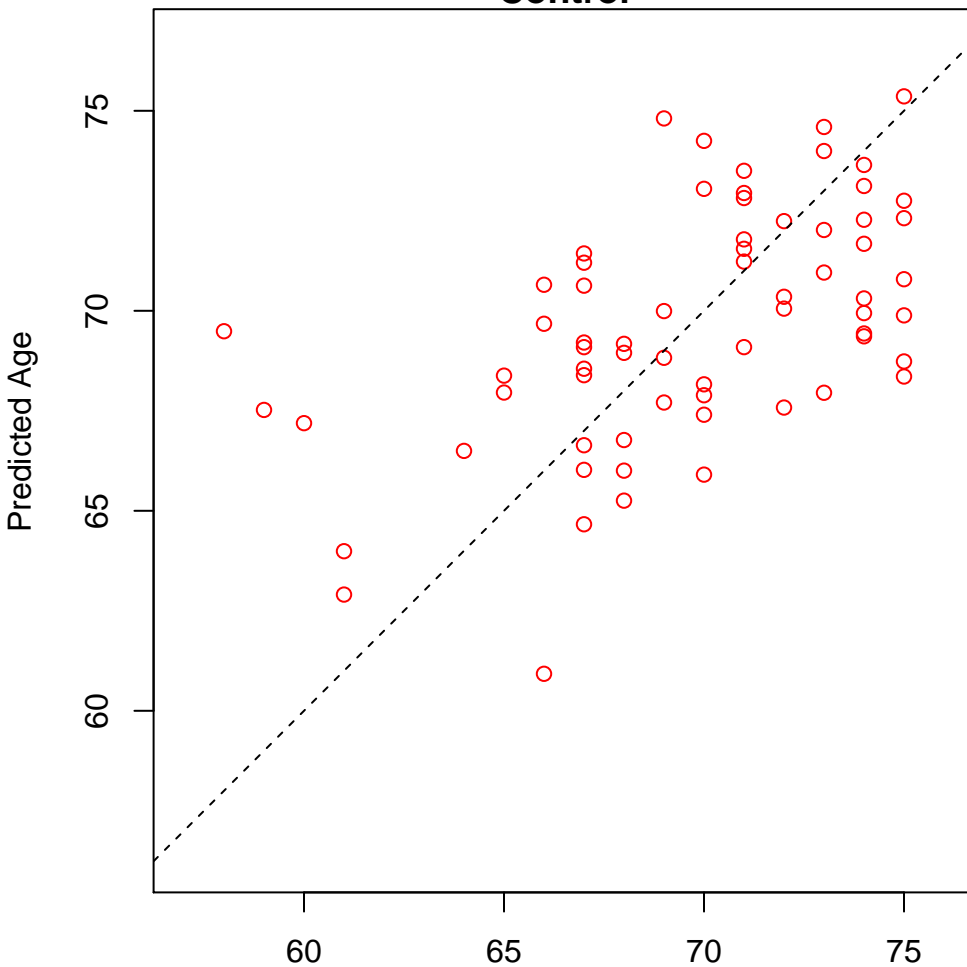


regulation of ER to Golgi vesicle-mediated transport (Score: 0.970087)

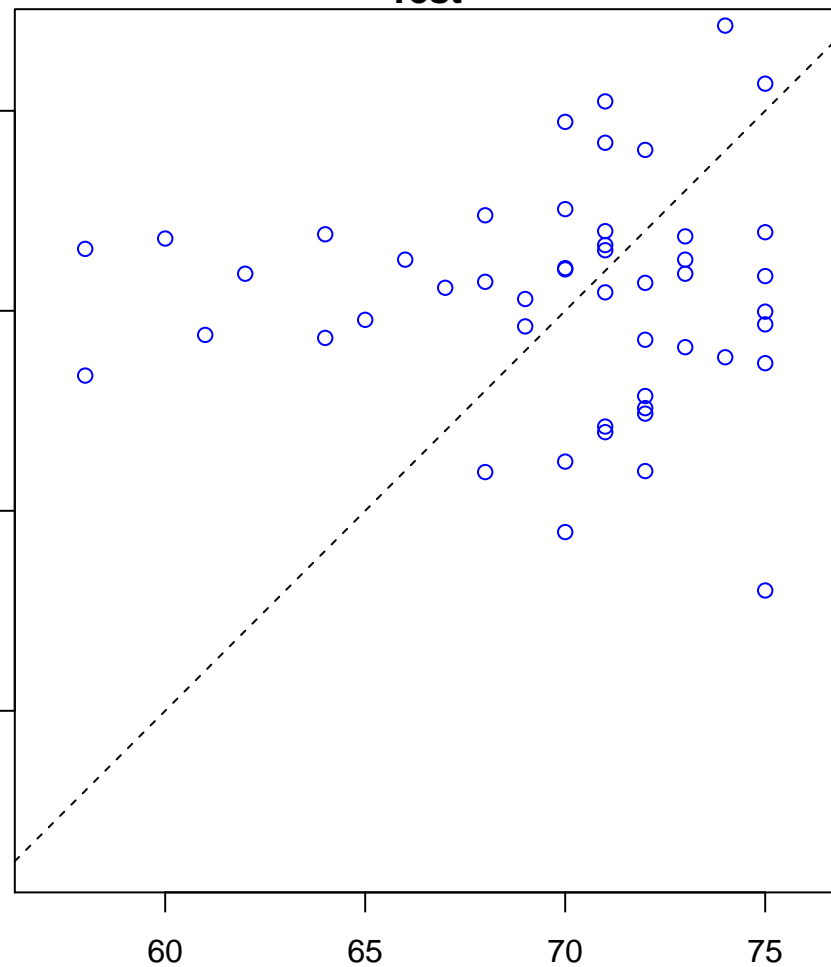


retina development in camera-type eye (Score: 0.969546)

Control



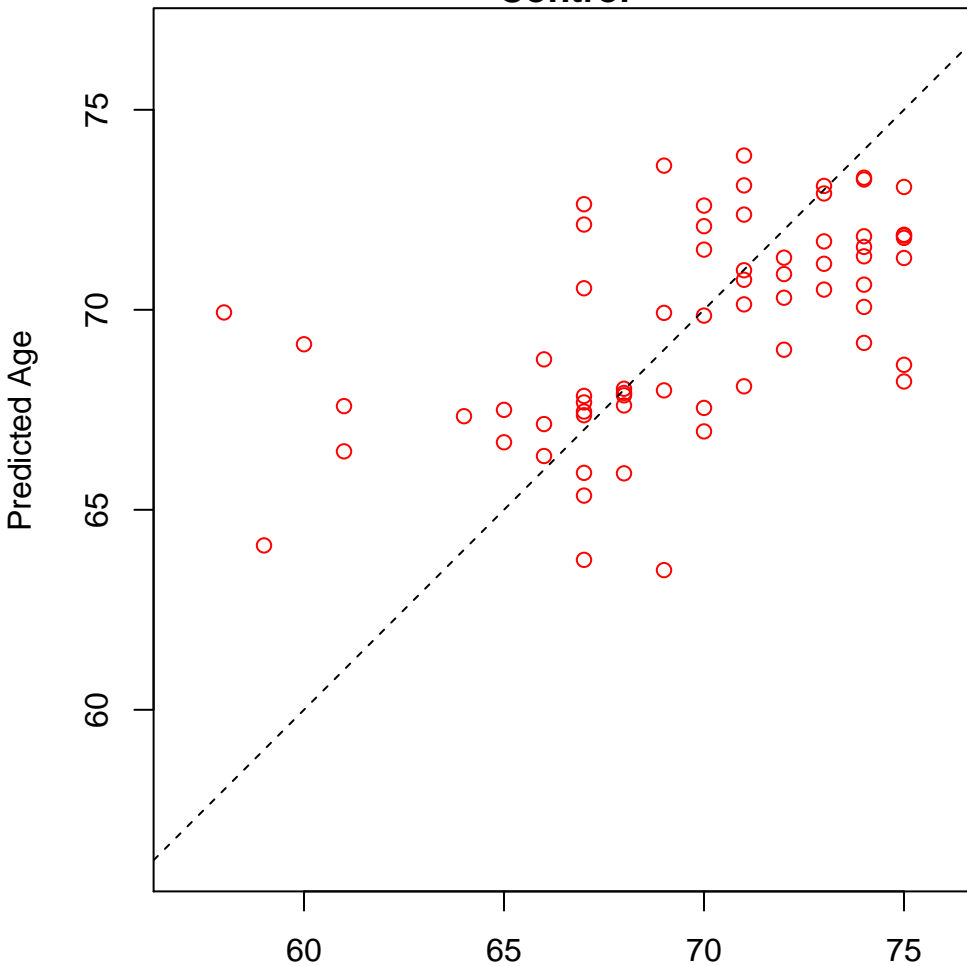
Test



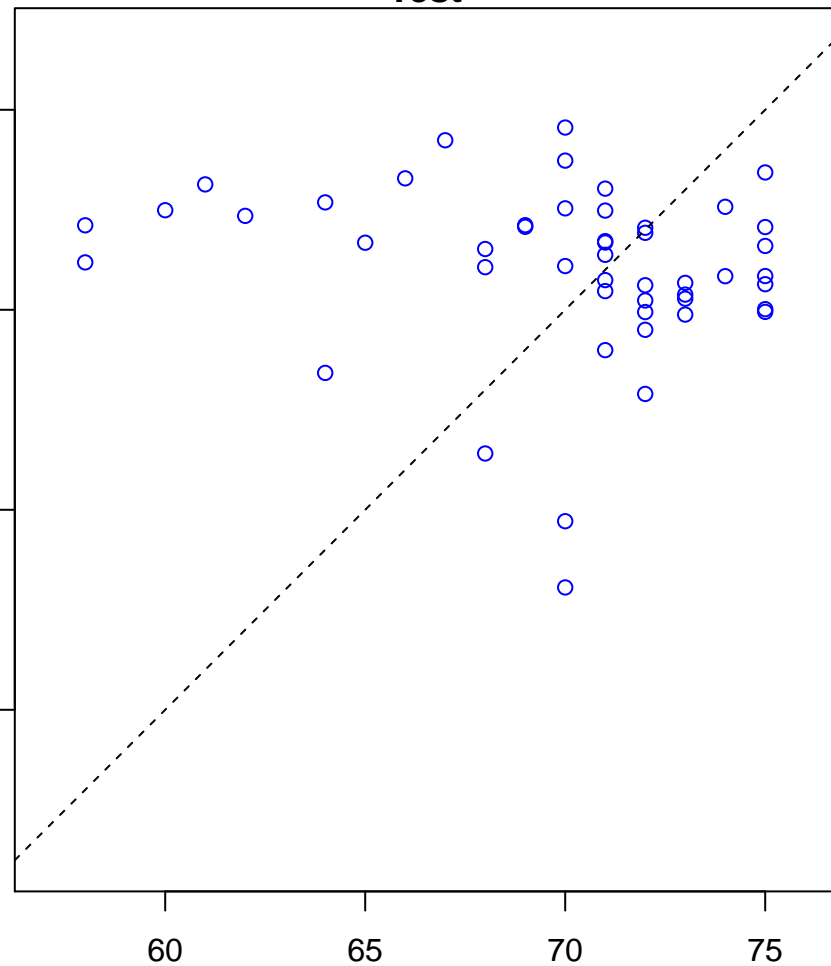
Actual Age

protein localization to chromosome (Score: 0.969518)

Control

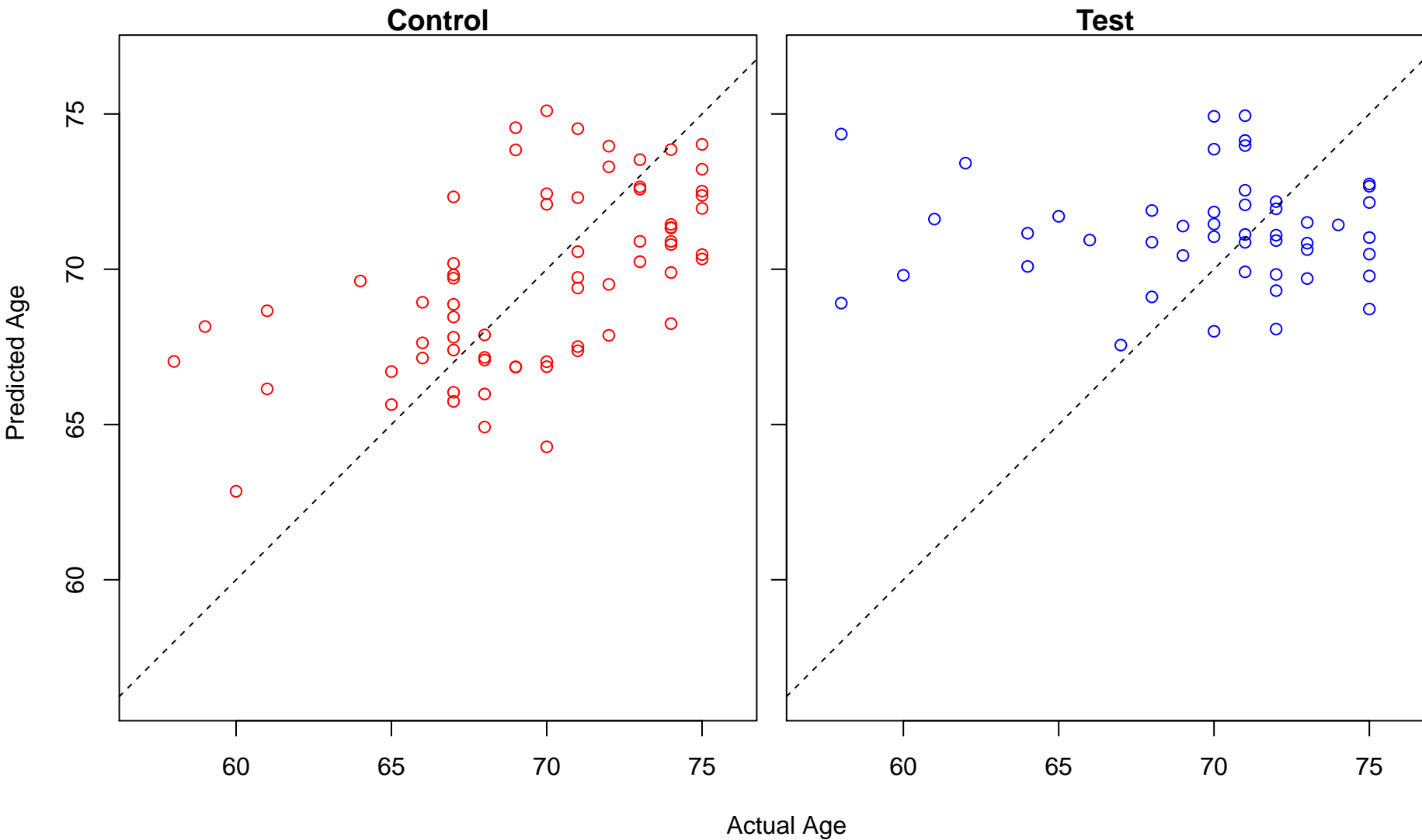


Test

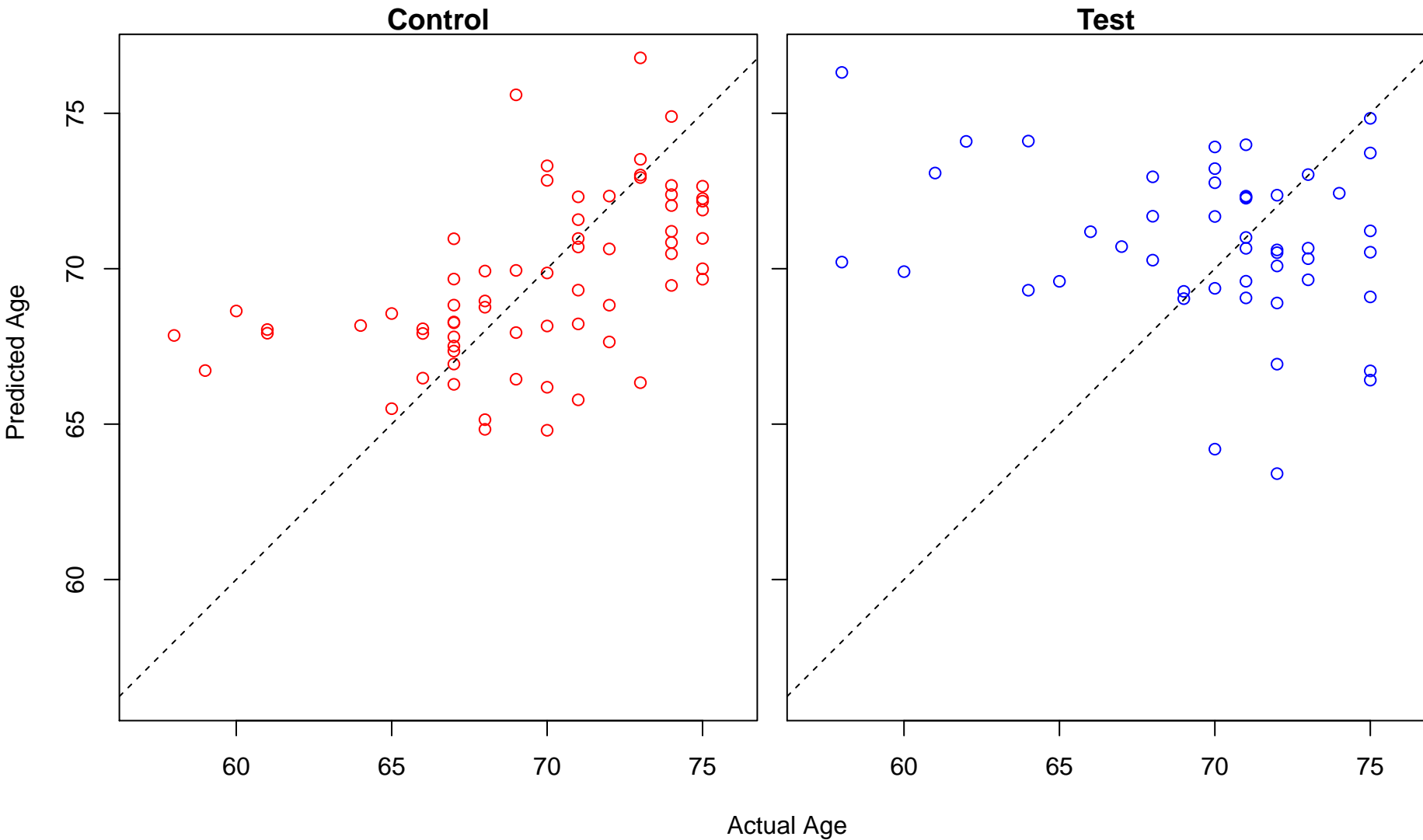


Actual Age

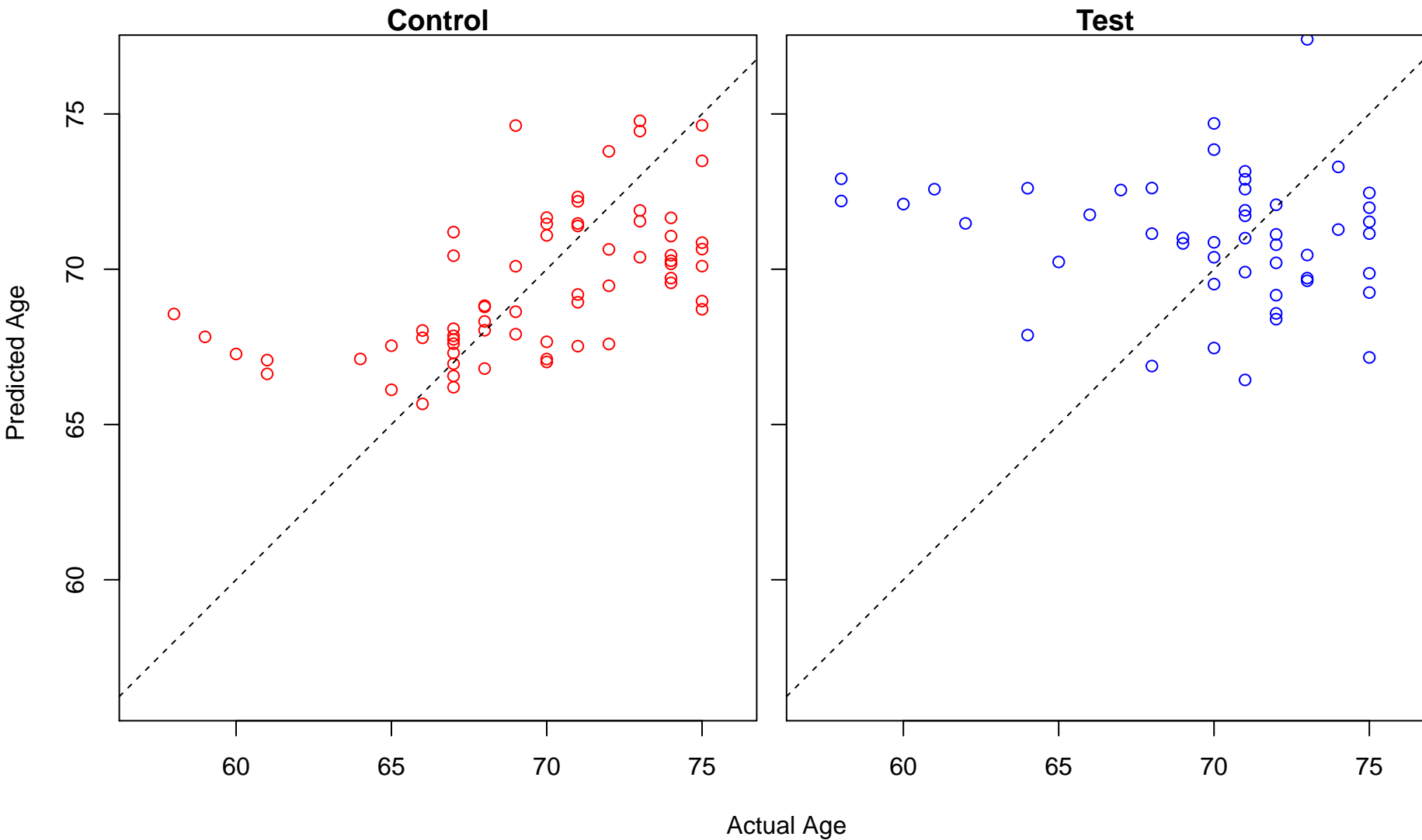
L-amino acid transport (Score: 0.969516)



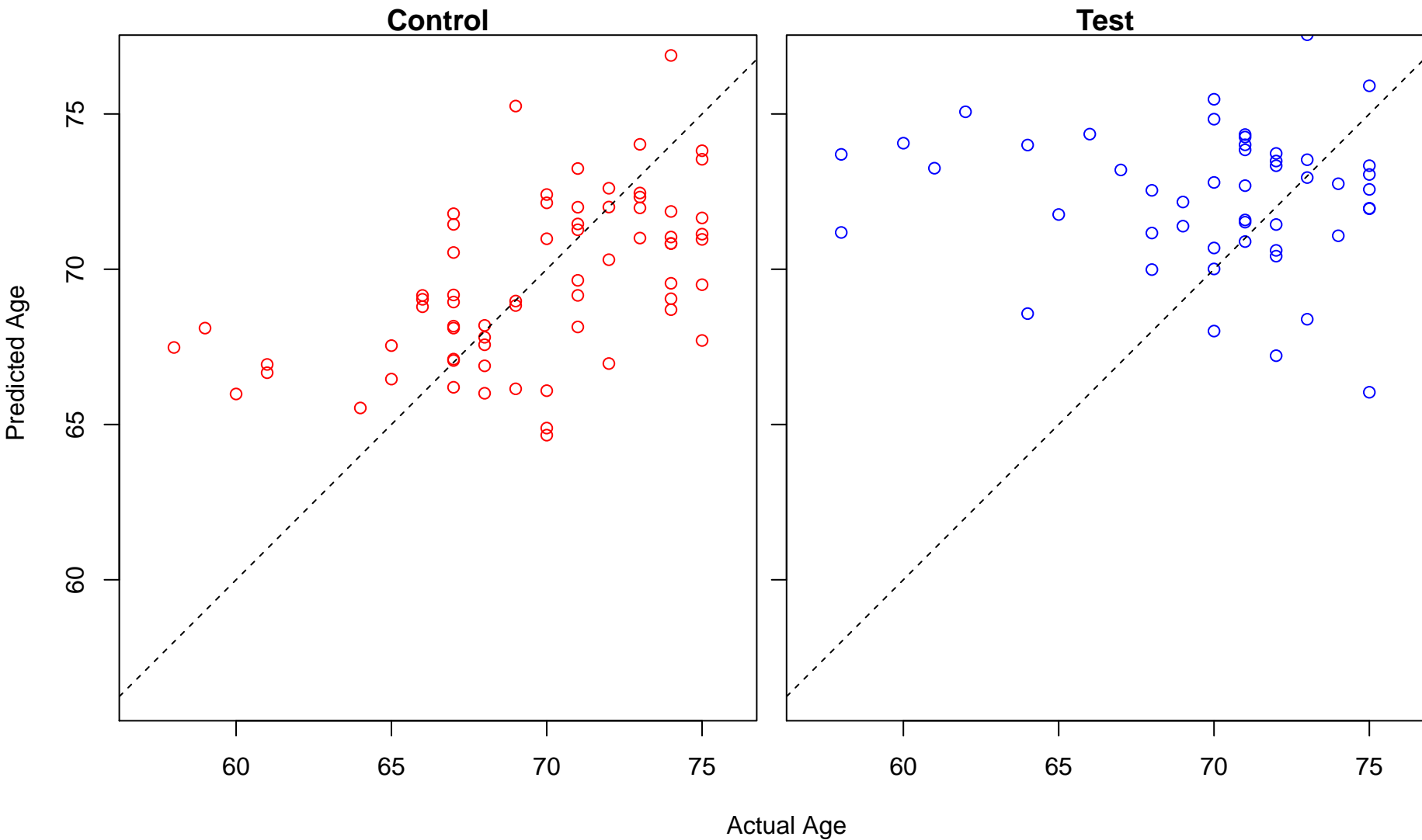
negative regulation of cation channel activity (Score: 0.968926)



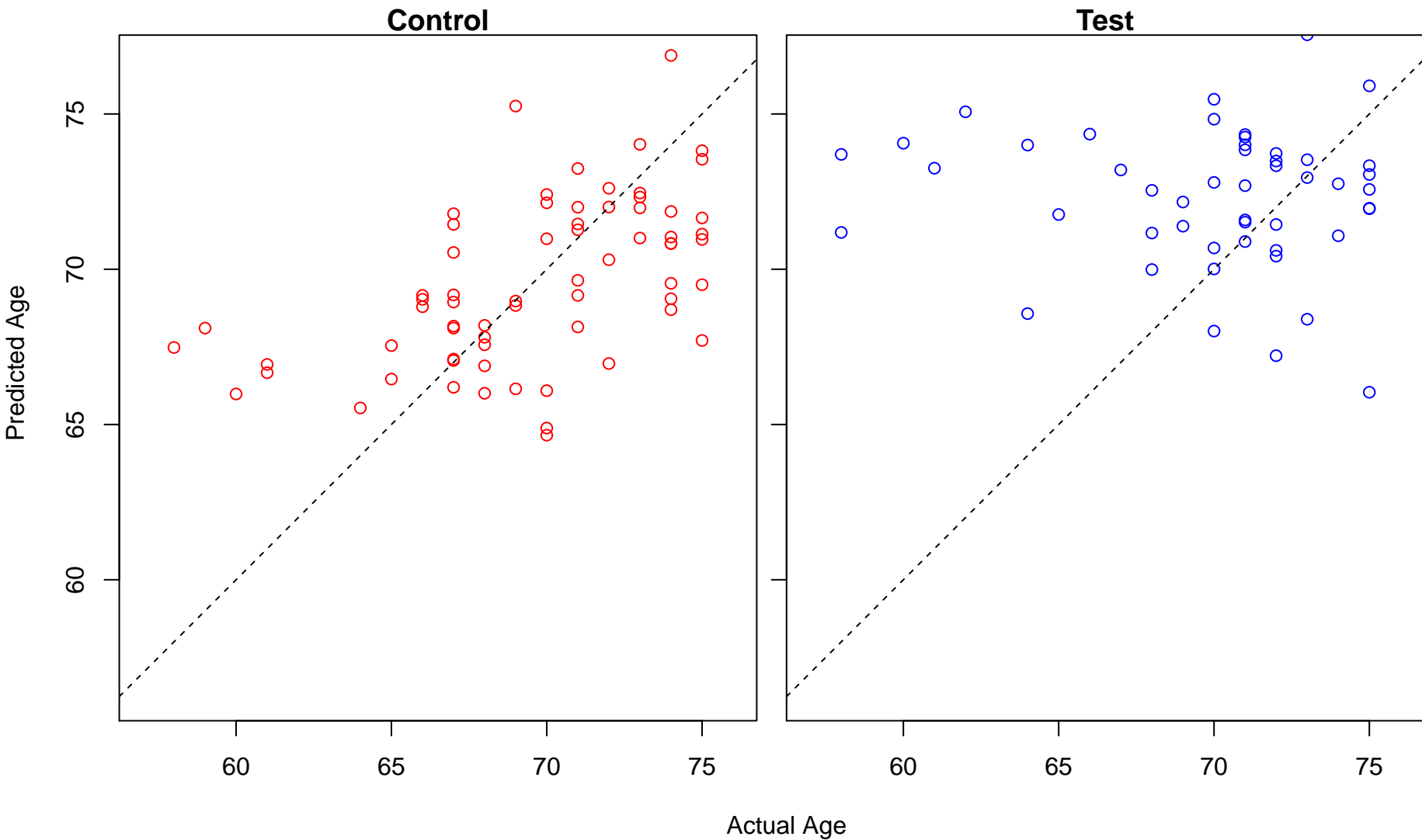
learning or memory (Score: 0.968924)



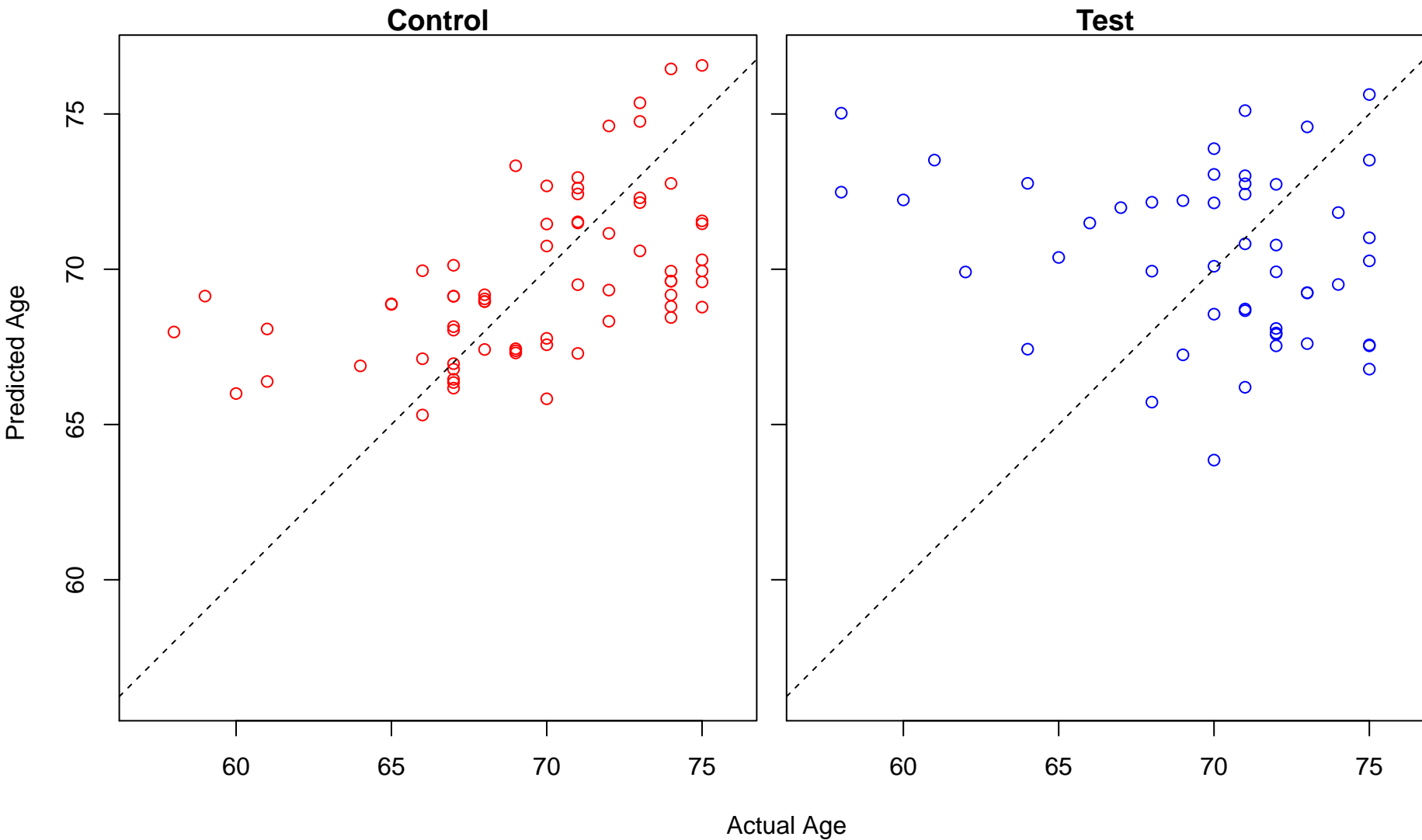
glycogen biosynthetic process (Score: 0.968923)



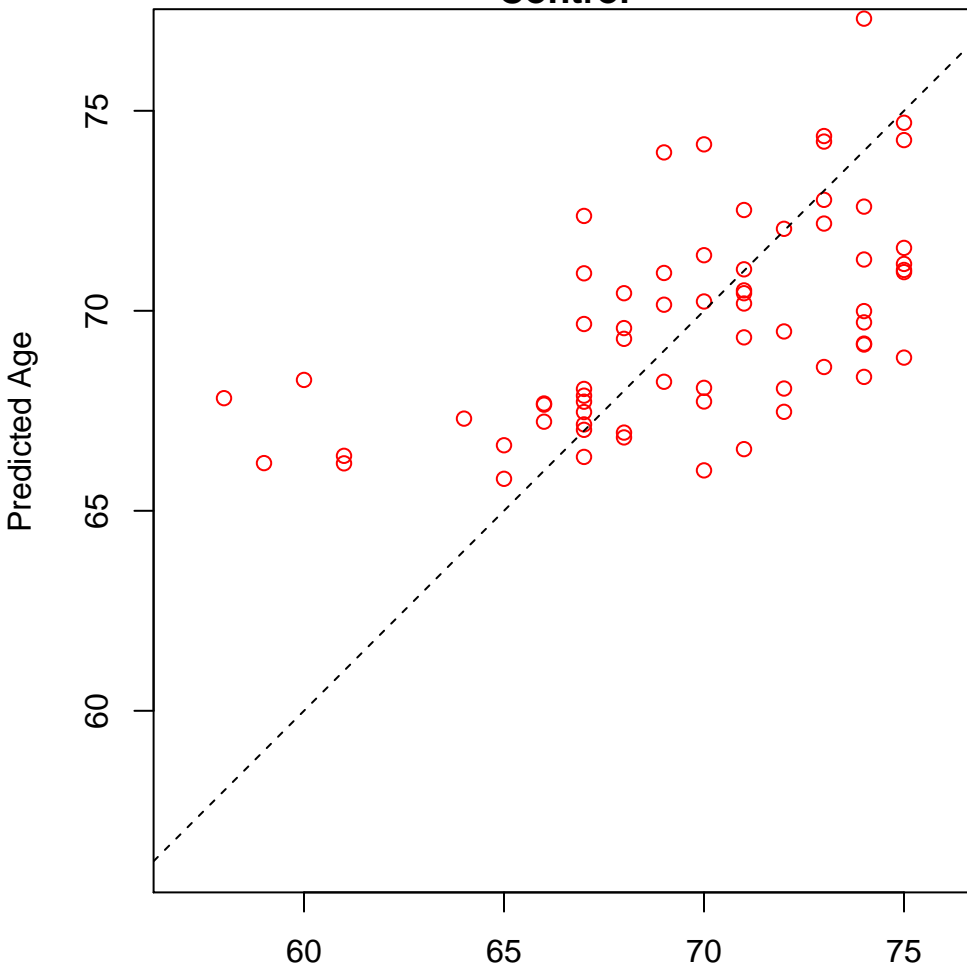
glucan biosynthetic process (Score: 0.968923)



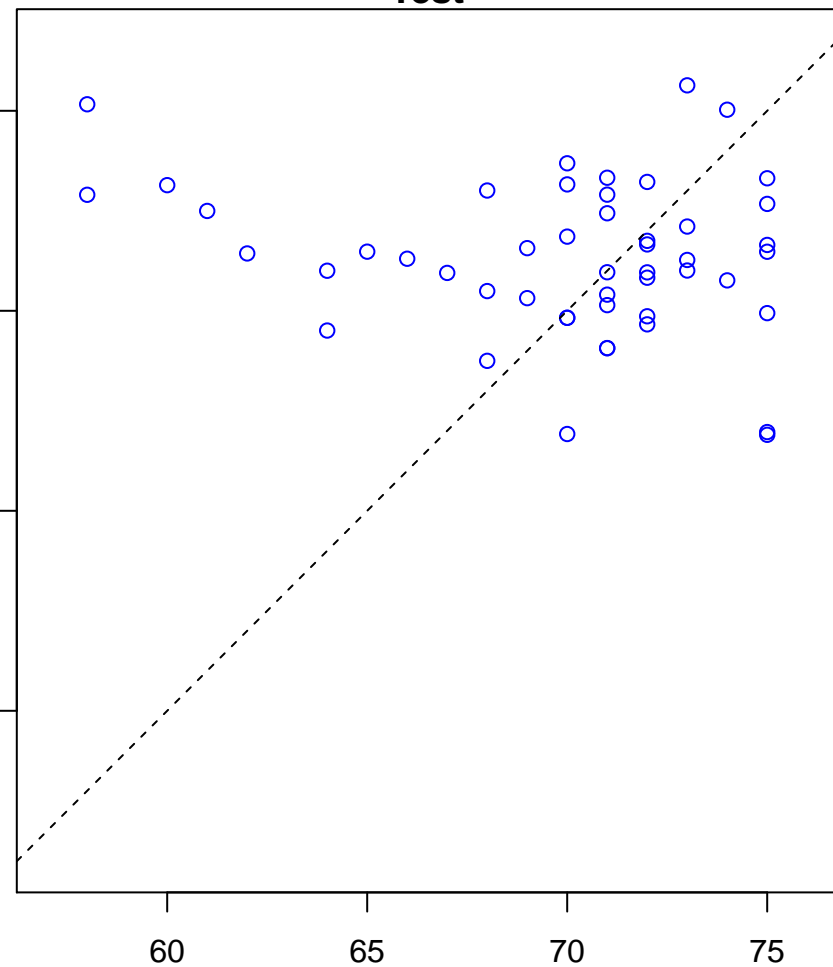
central nervous system neuron axonogenesis (Score: 0.968884)



Control

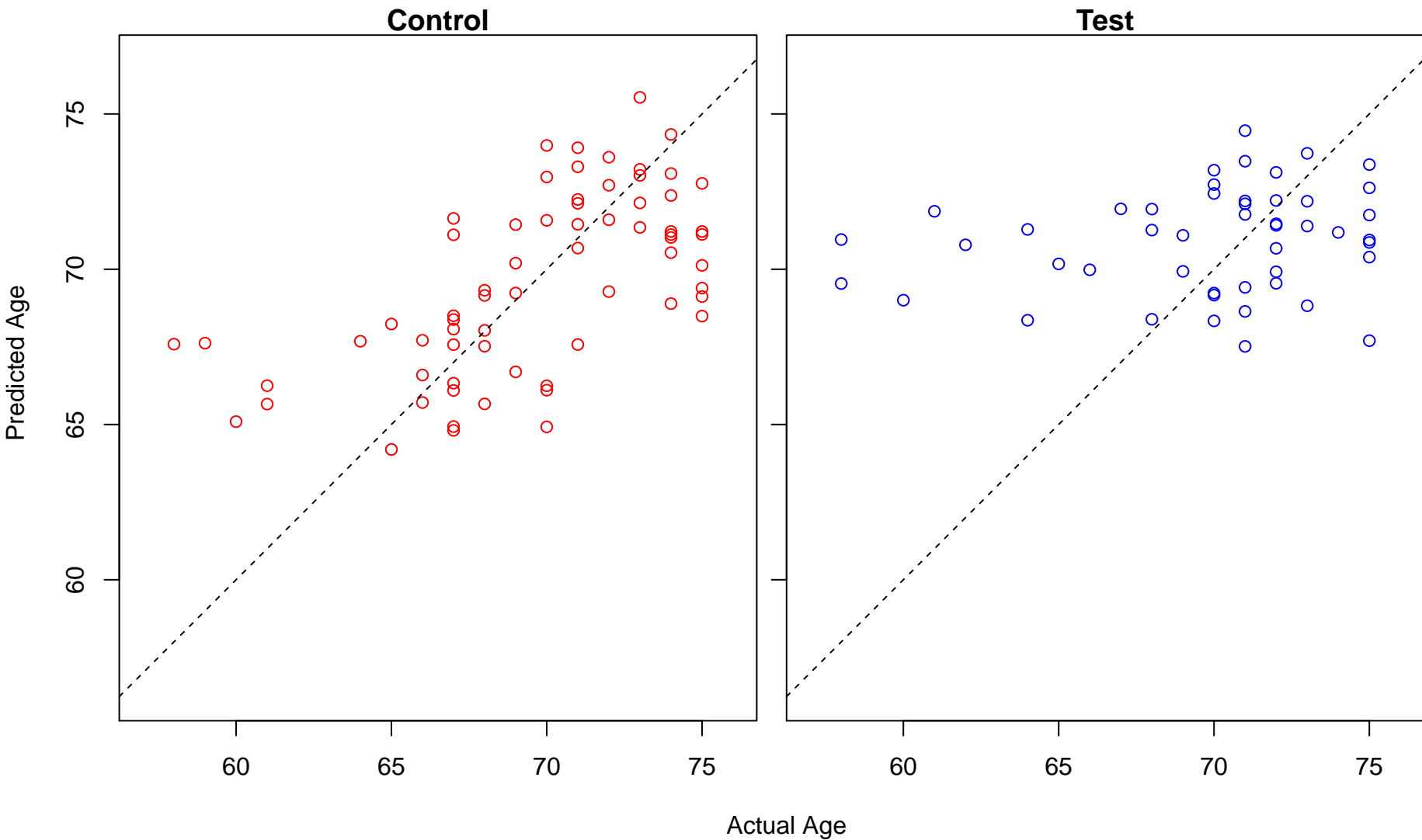


Test

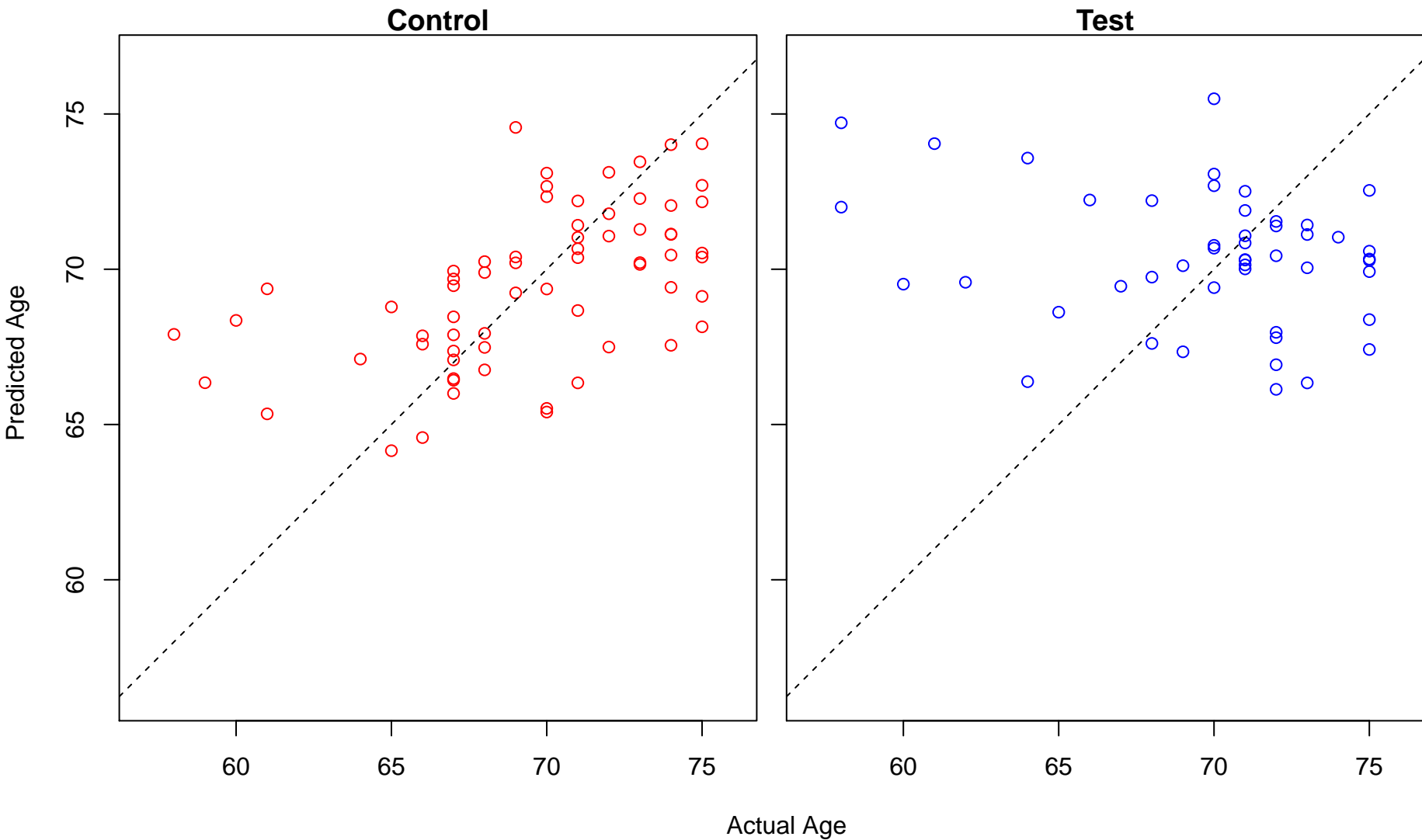


Actual Age

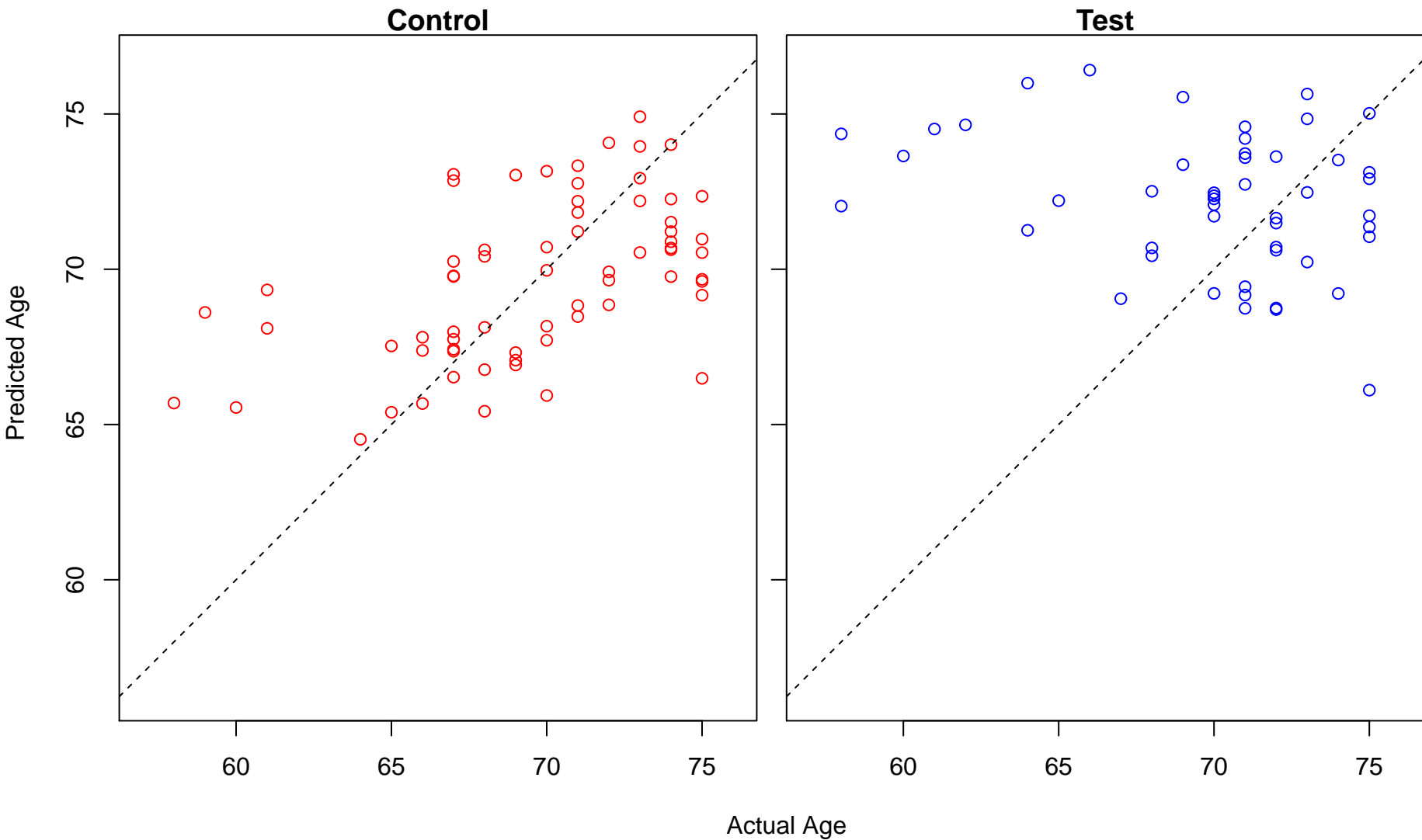
regulation of phagocytosis (Score: 0.968772)



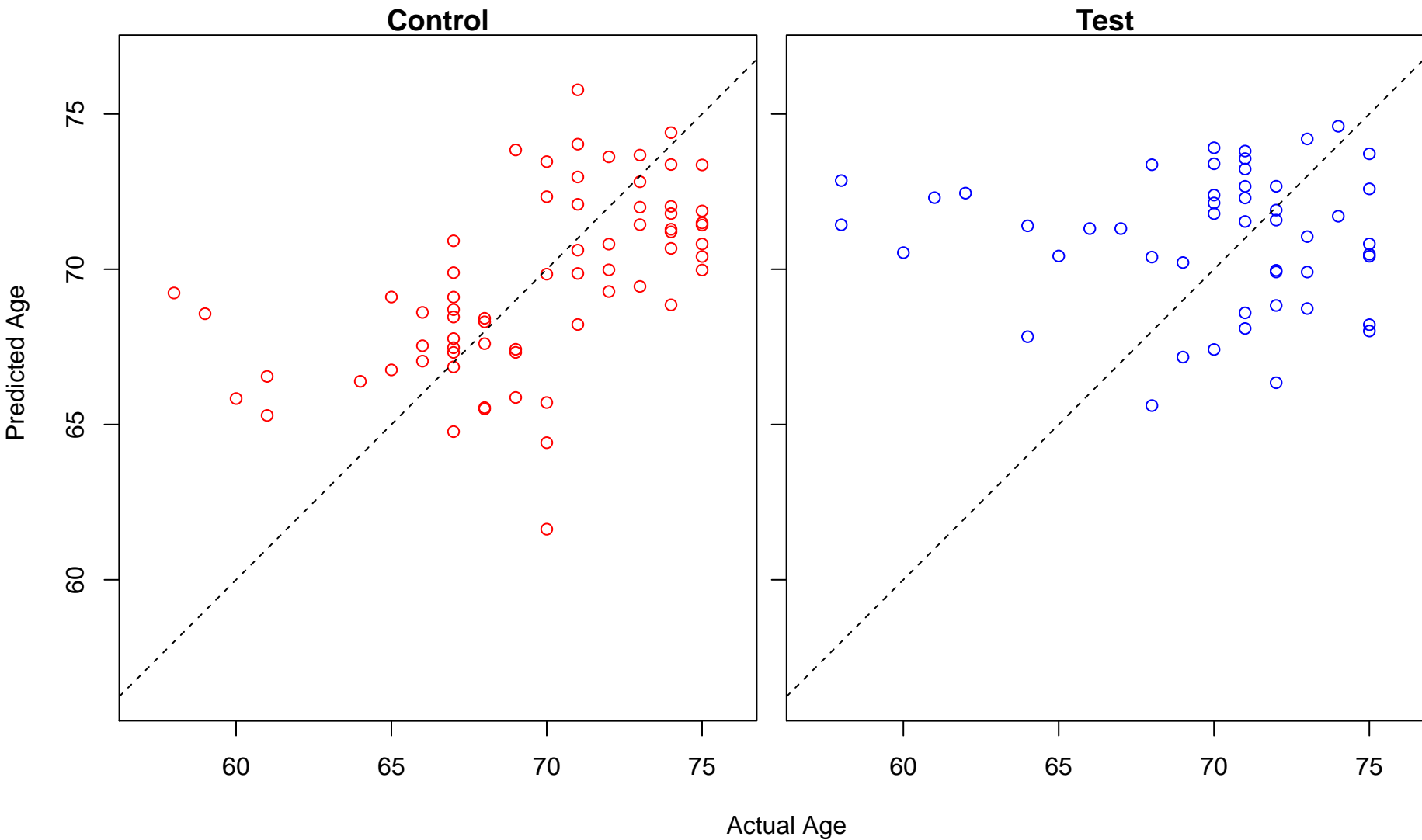
positive regulation of NF-kappaB import into nucleus (Score: 0.968752)



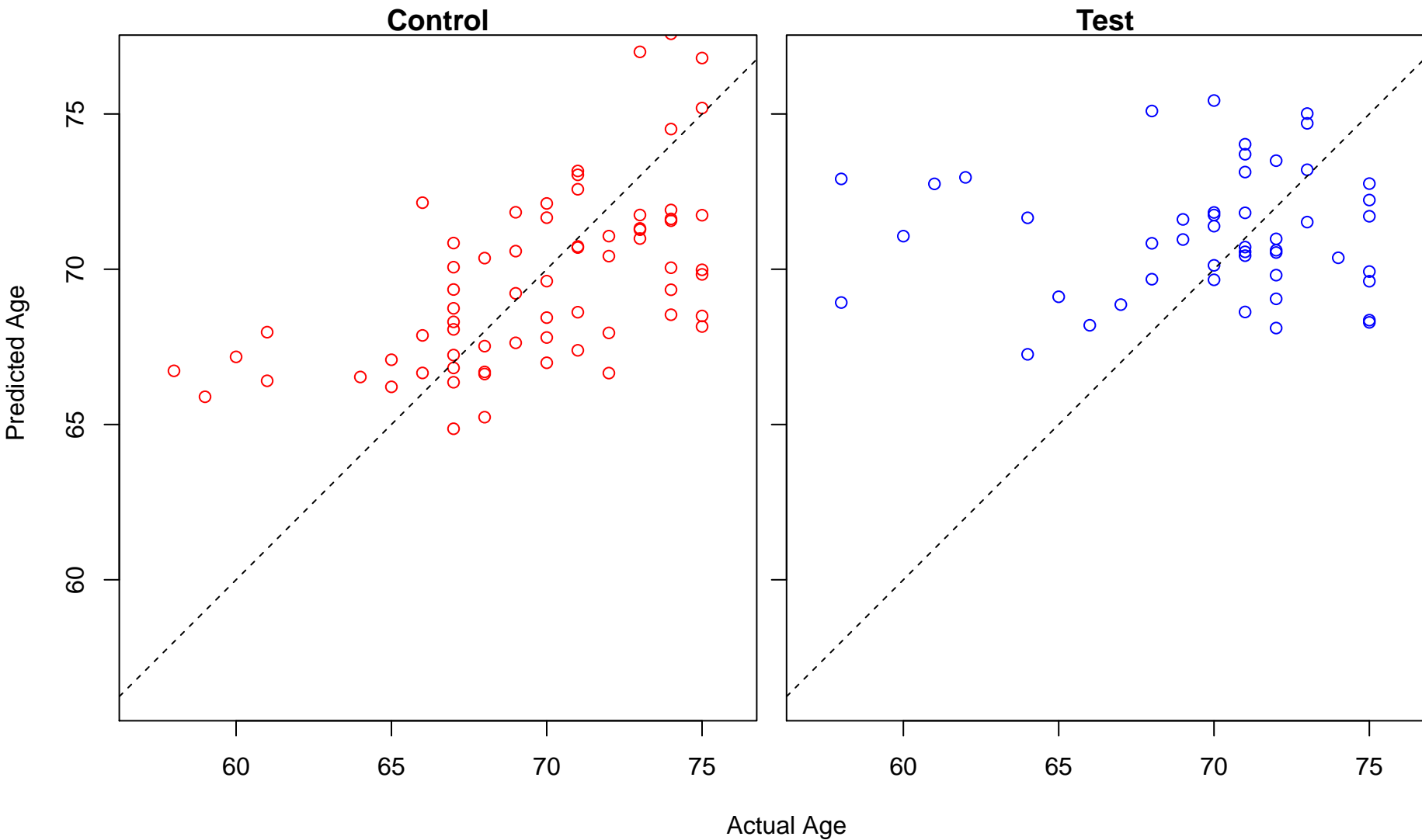
cardioblast differentiation (Score: 0.967541)



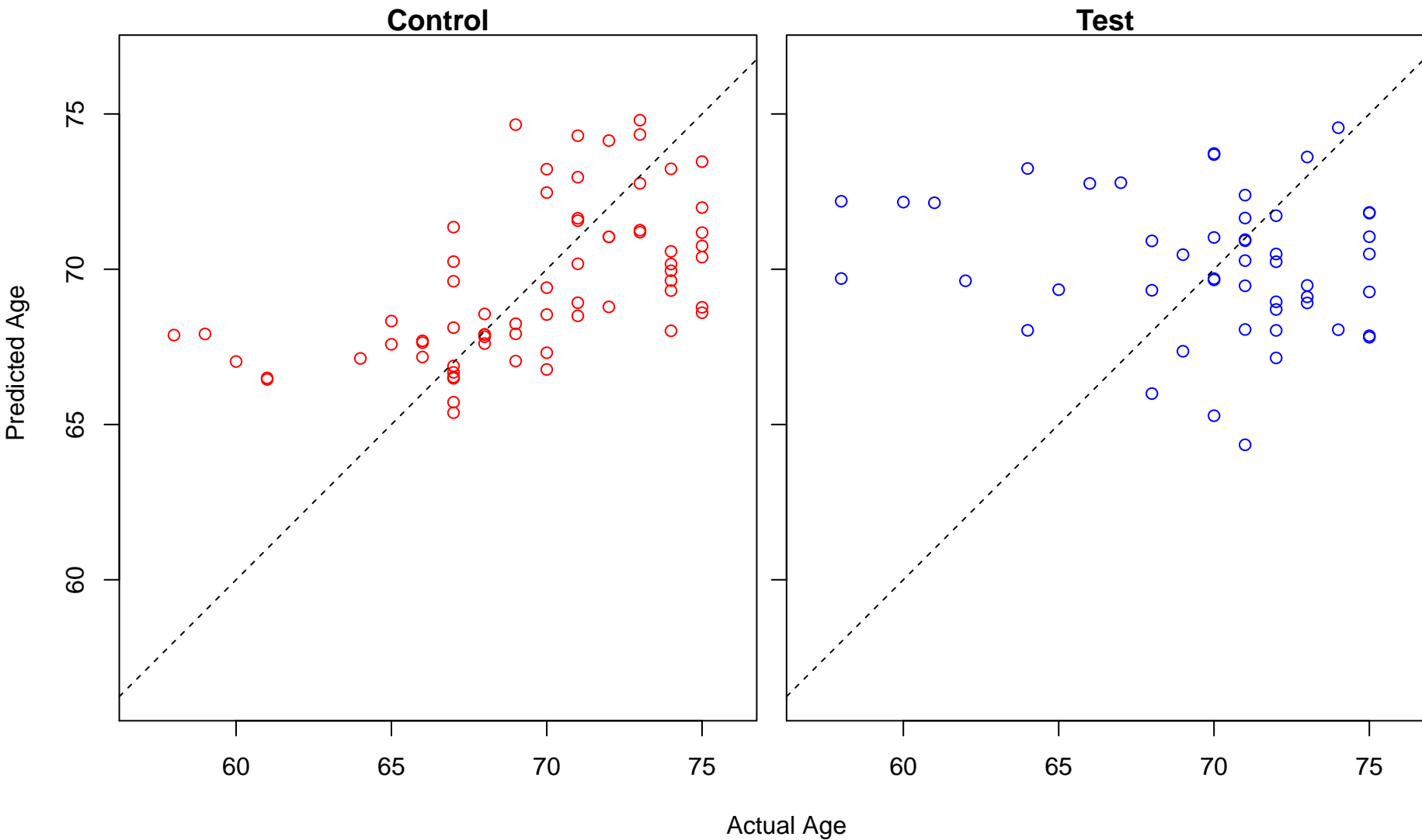
Wnt signaling pathway (Score: 0.967456)



intracellular lipid transport (Score: 0.967370)

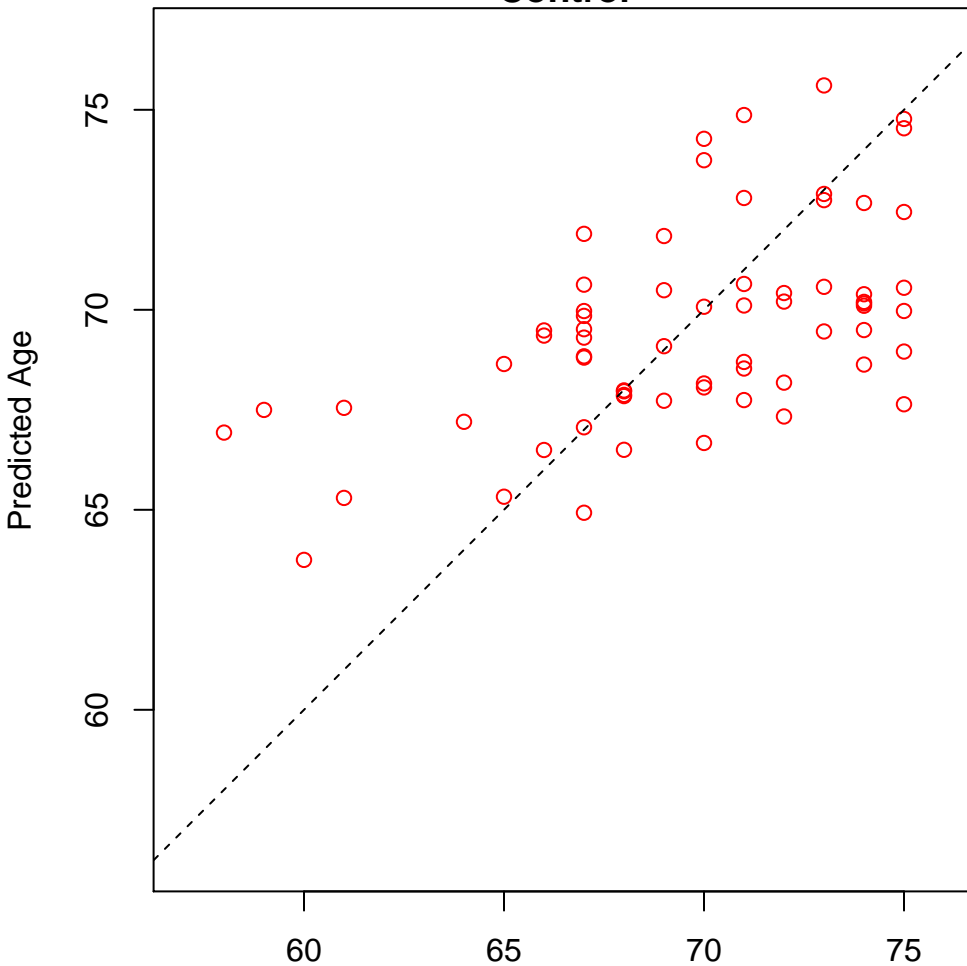


protein kinase B signaling (Score: 0.967287)

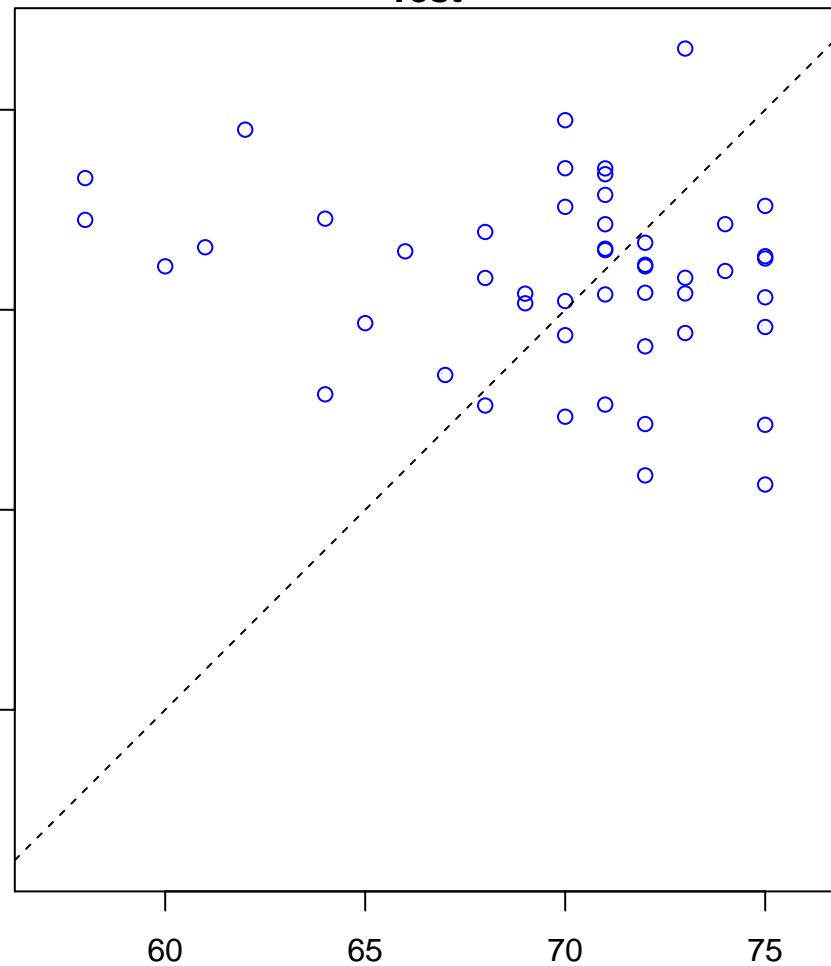


long-chain fatty acid transport (Score: 0.967173)

Control

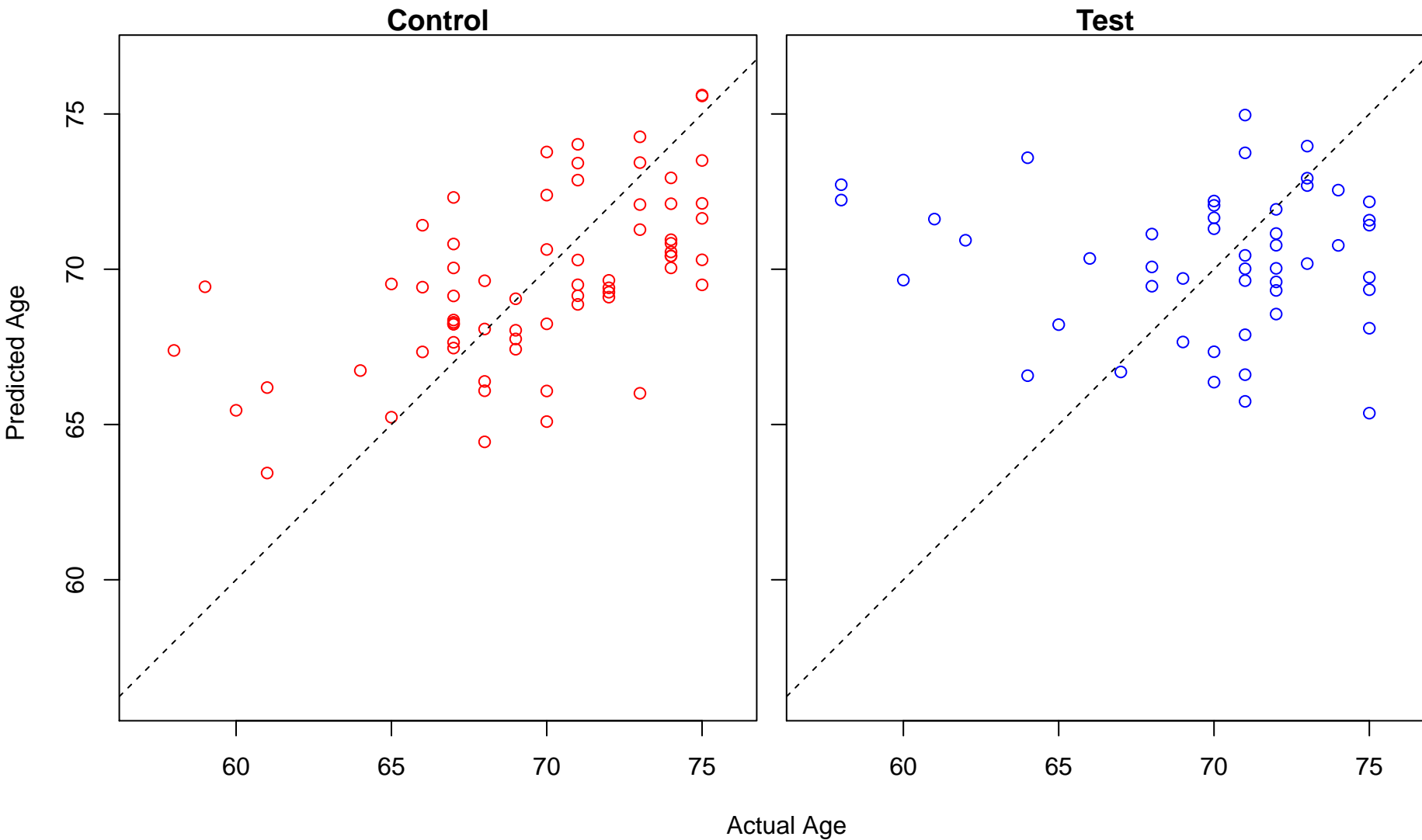


Test

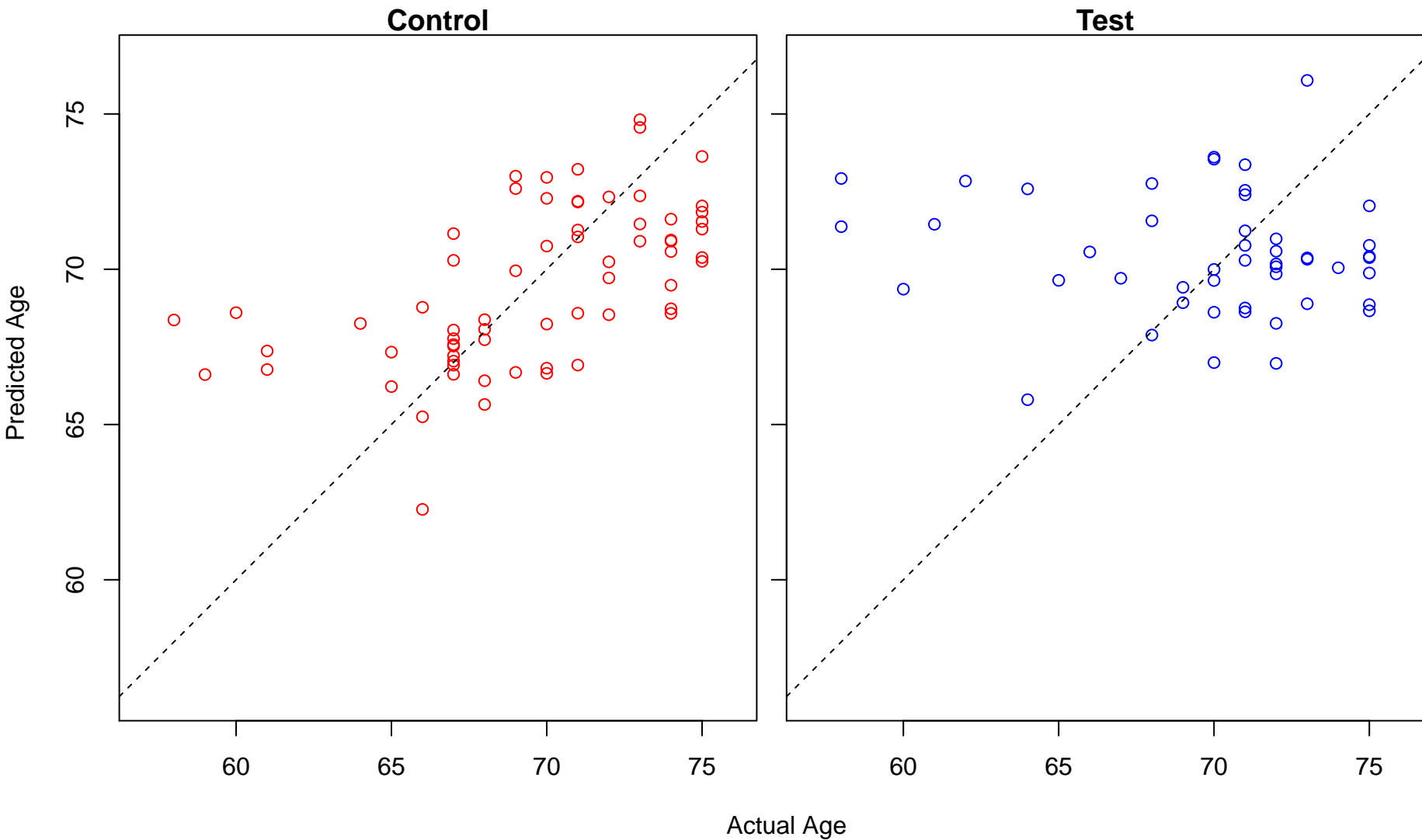


Actual Age

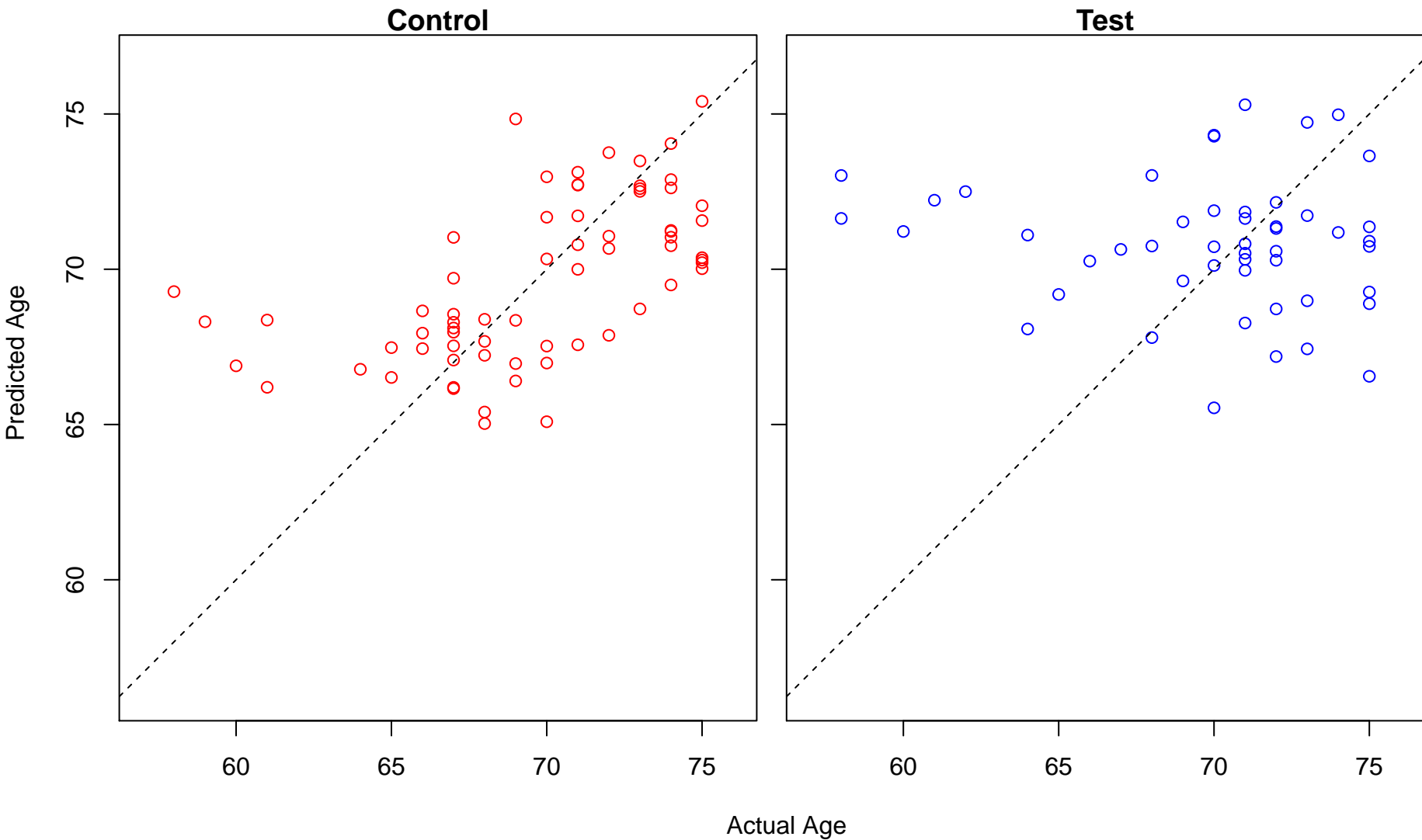
actin filament capping (Score: 0.967009)



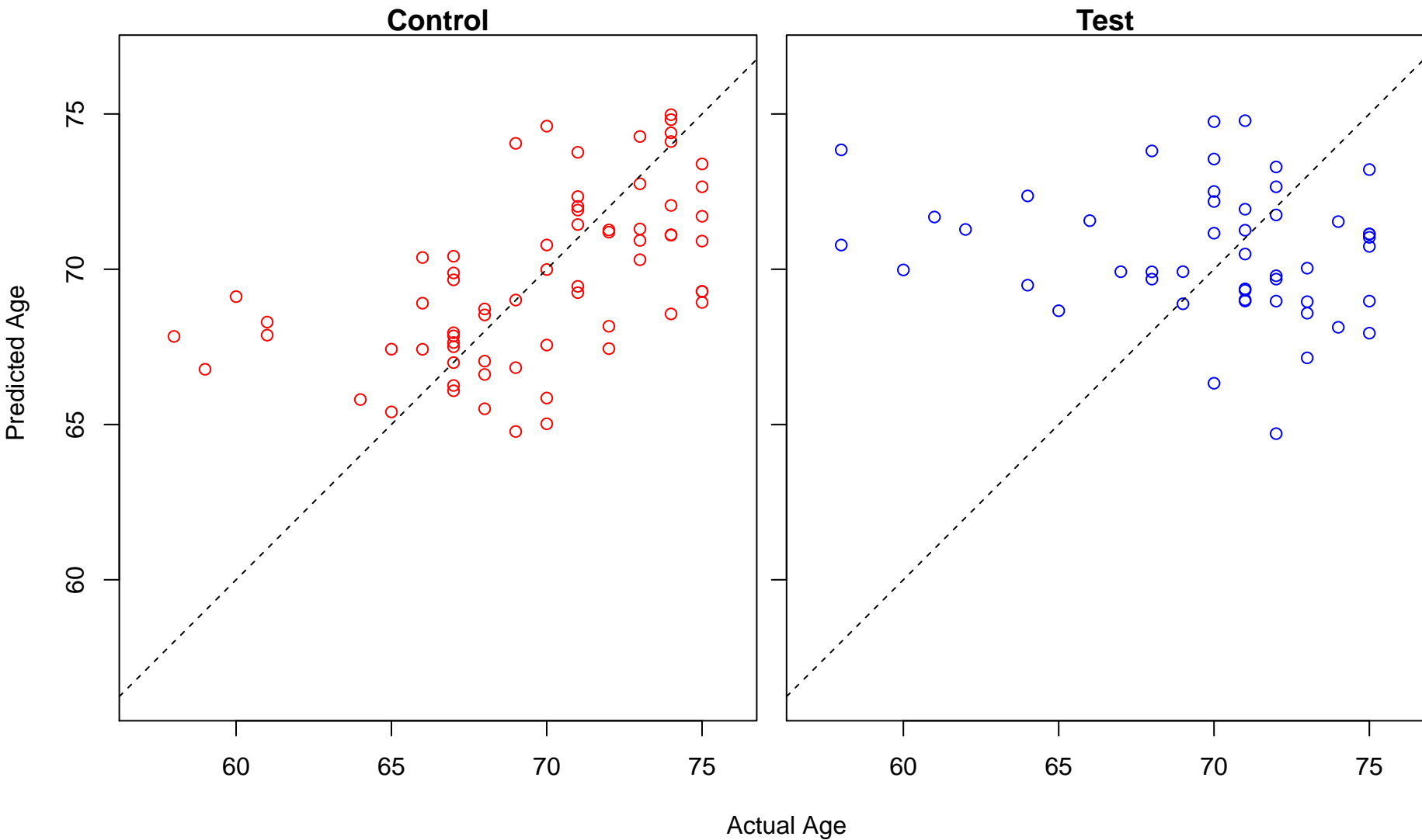
peroxisome organization (Score: 0.966995)



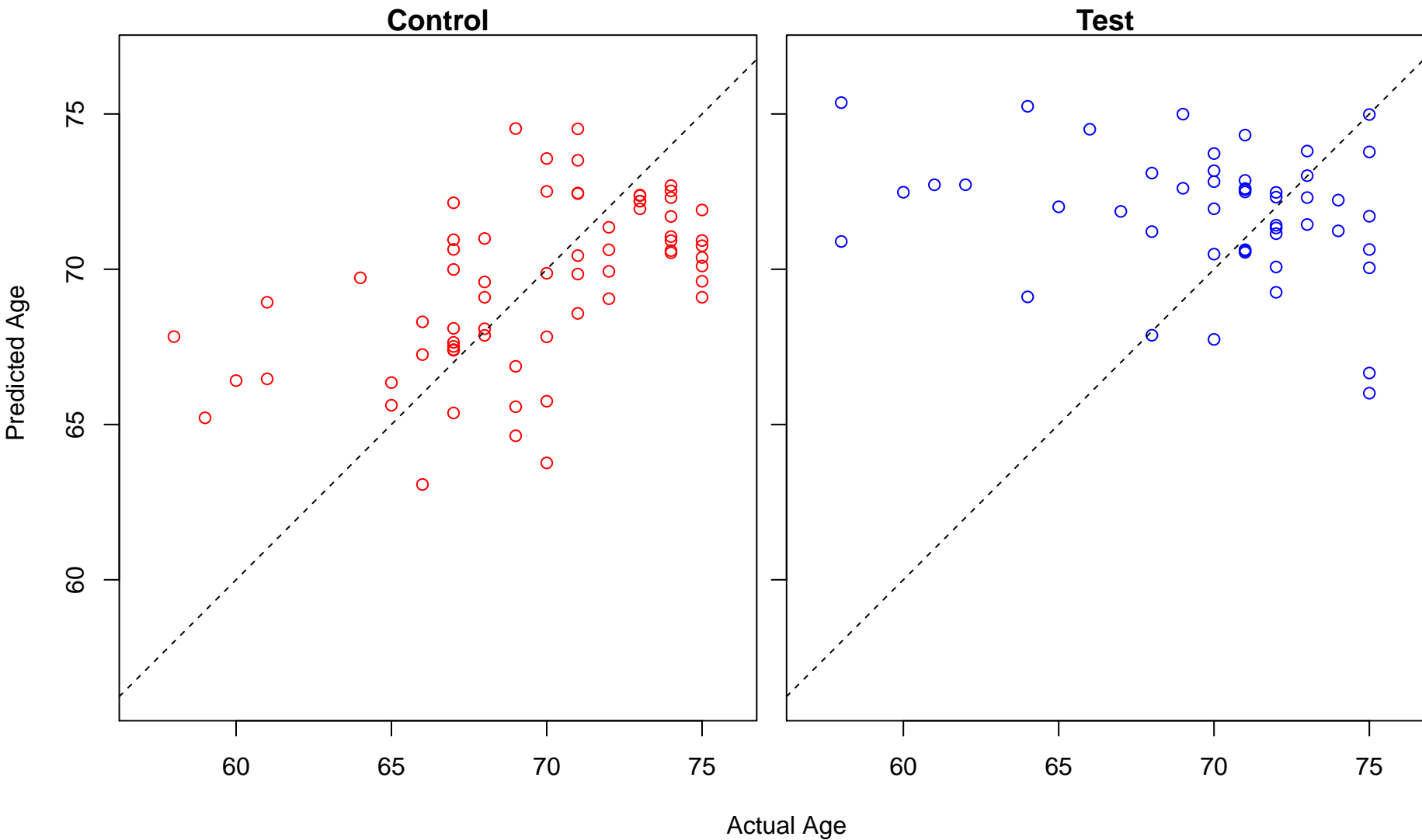
adult locomotory behavior (Score: 0.966943)



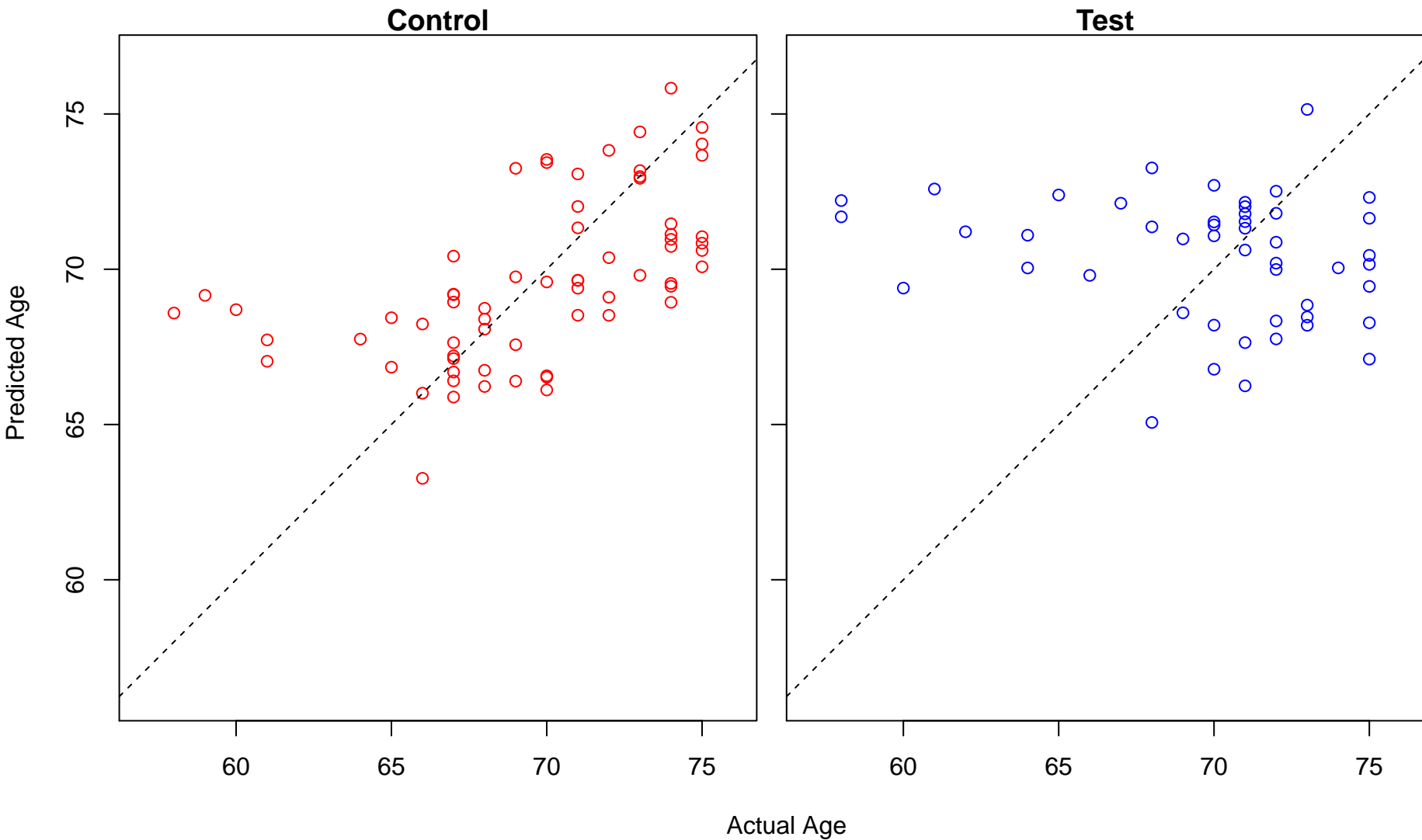
positive regulation of mesenchymal cell proliferation (Score: 0.966761)



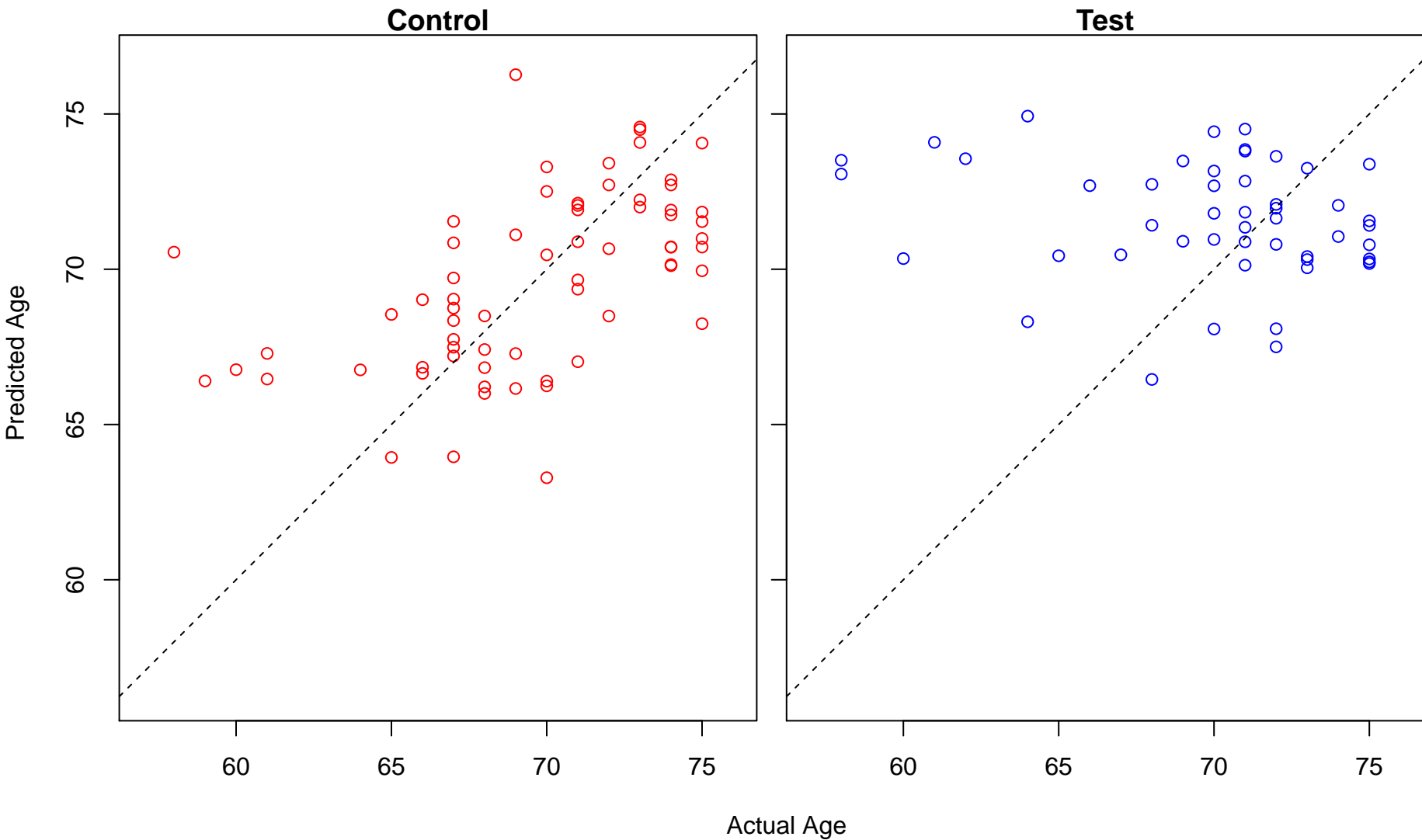
face morphogenesis (Score: 0.966264)



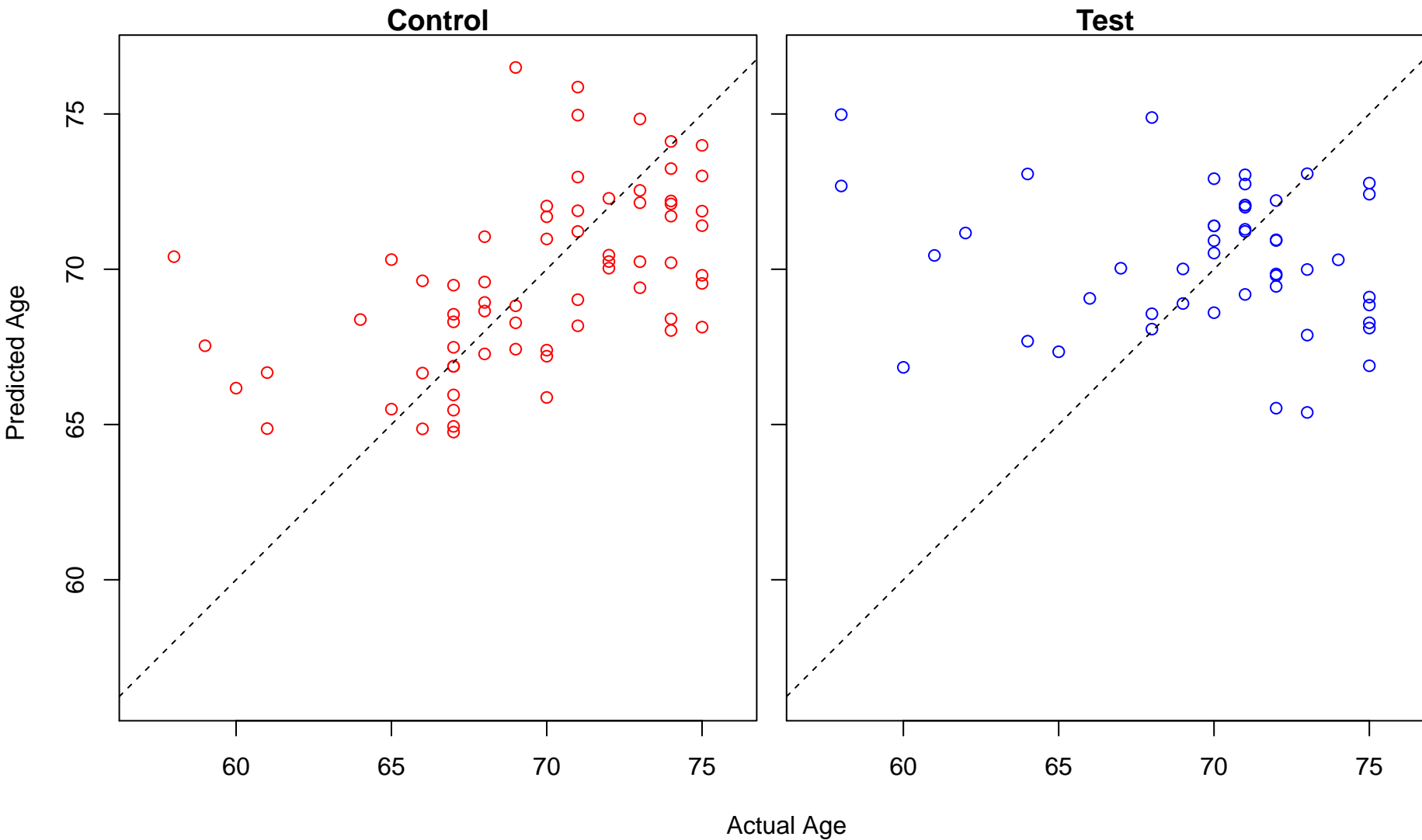
amino acid transmembrane transport (Score: 0.966025)



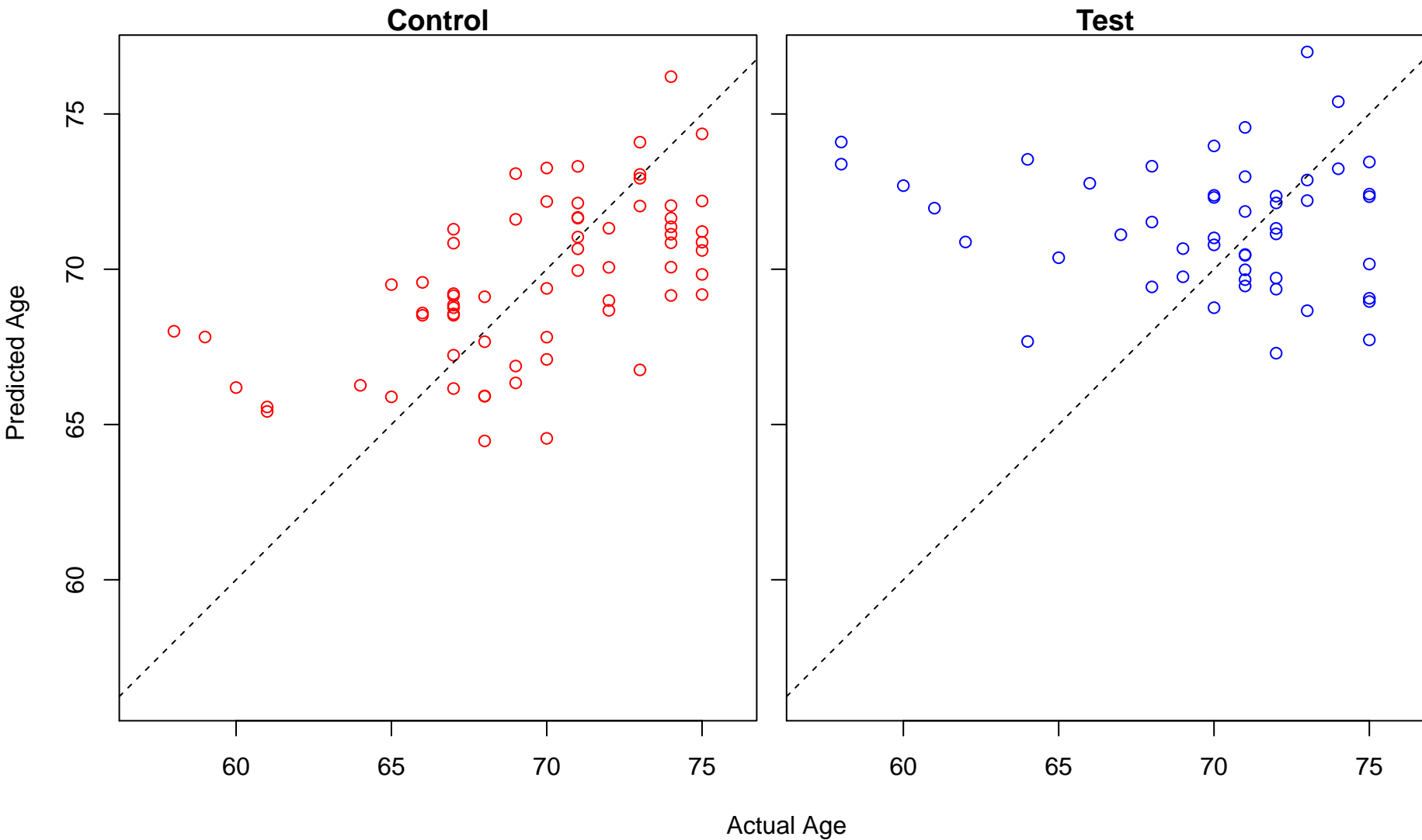
regulation of myeloid leukocyte mediated immunity (Score: 0.965978)



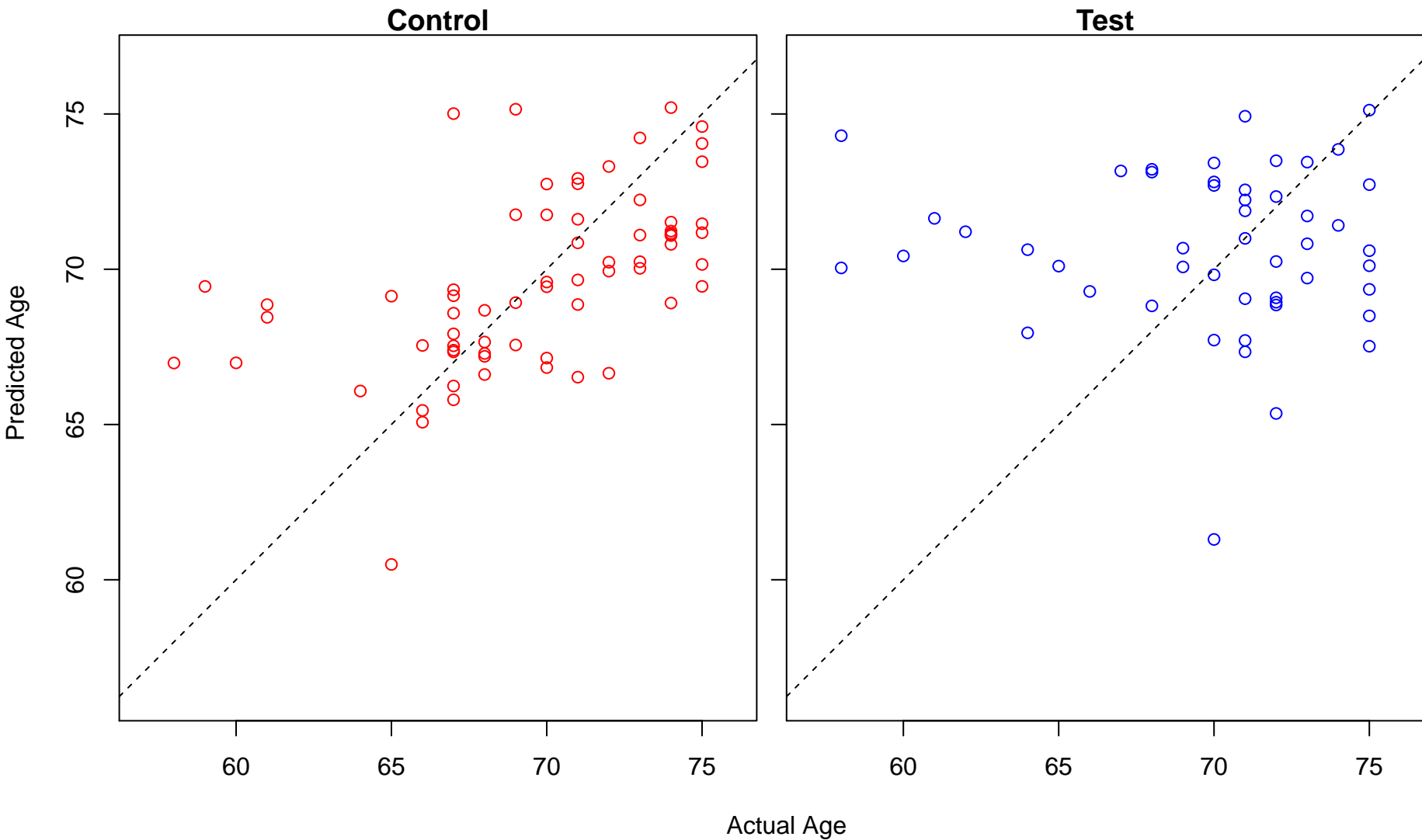
regulation of activated T cell proliferation (Score: 0.965790)



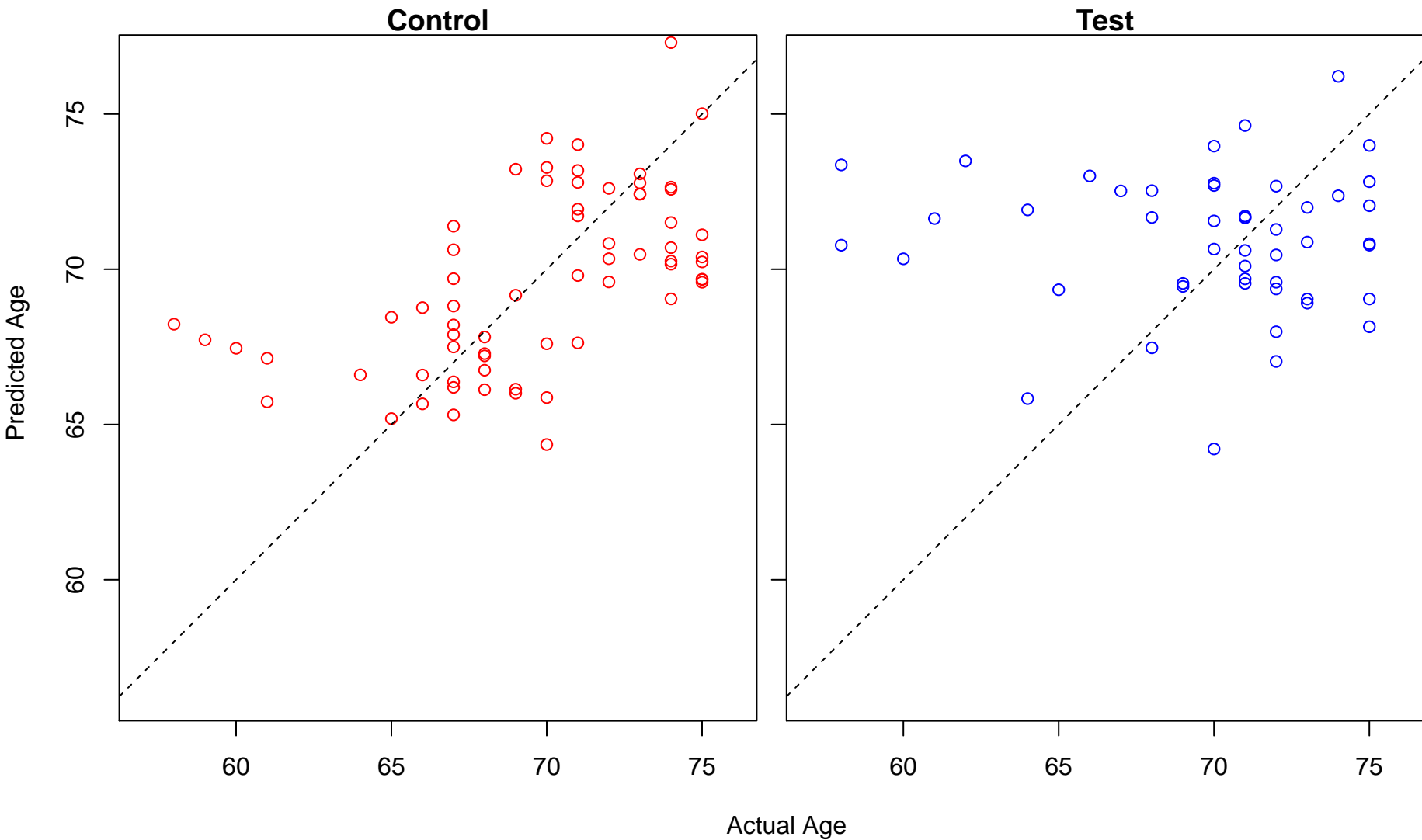
histone H2A ubiquitination (Score: 0.965592)



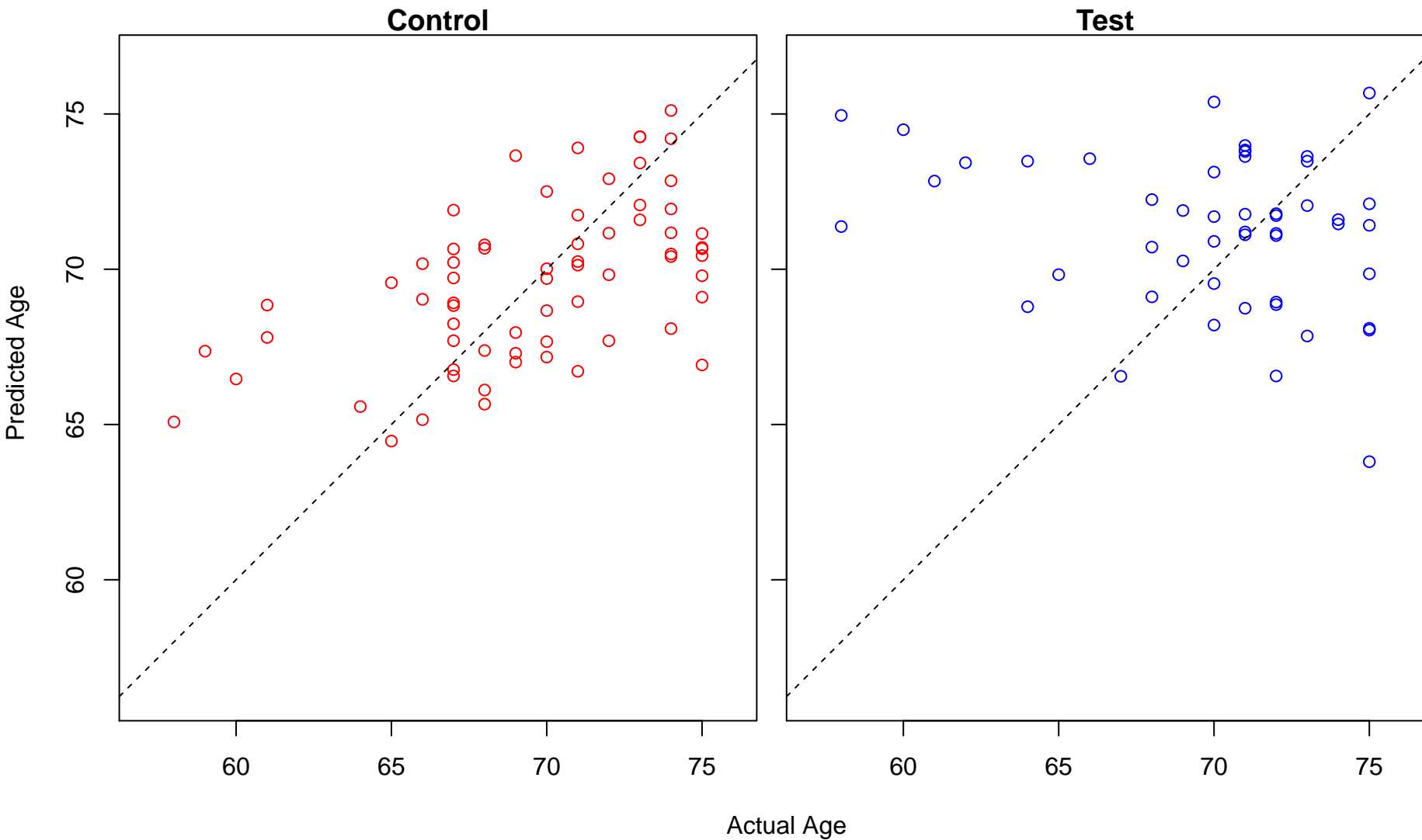
positive regulation of nitric-oxide synthase biosynthetic process (Score: 0.965338)



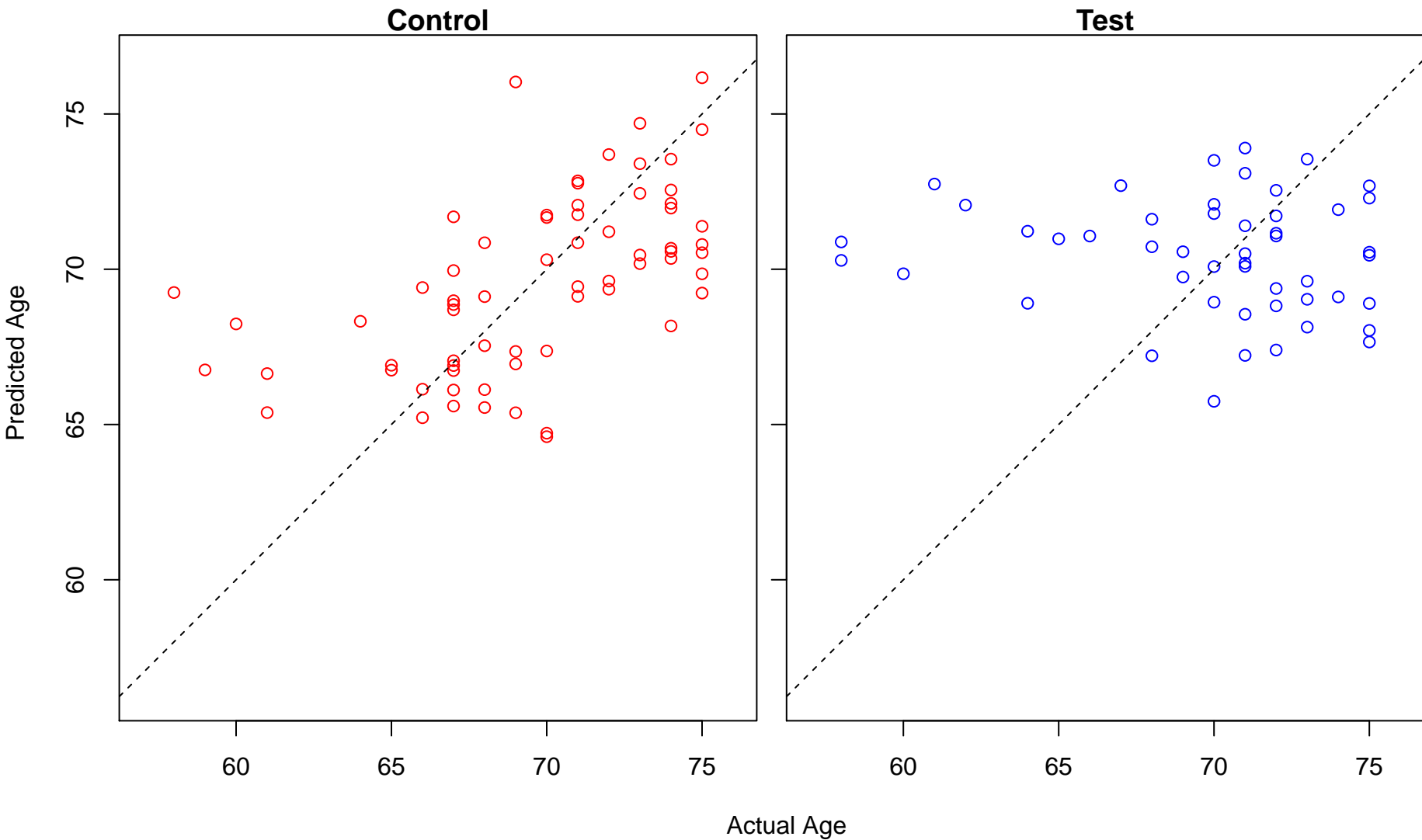
regulation of neuron differentiation (Score: 0.965271)



Notch signaling involved in heart development (Score: 0.965123)

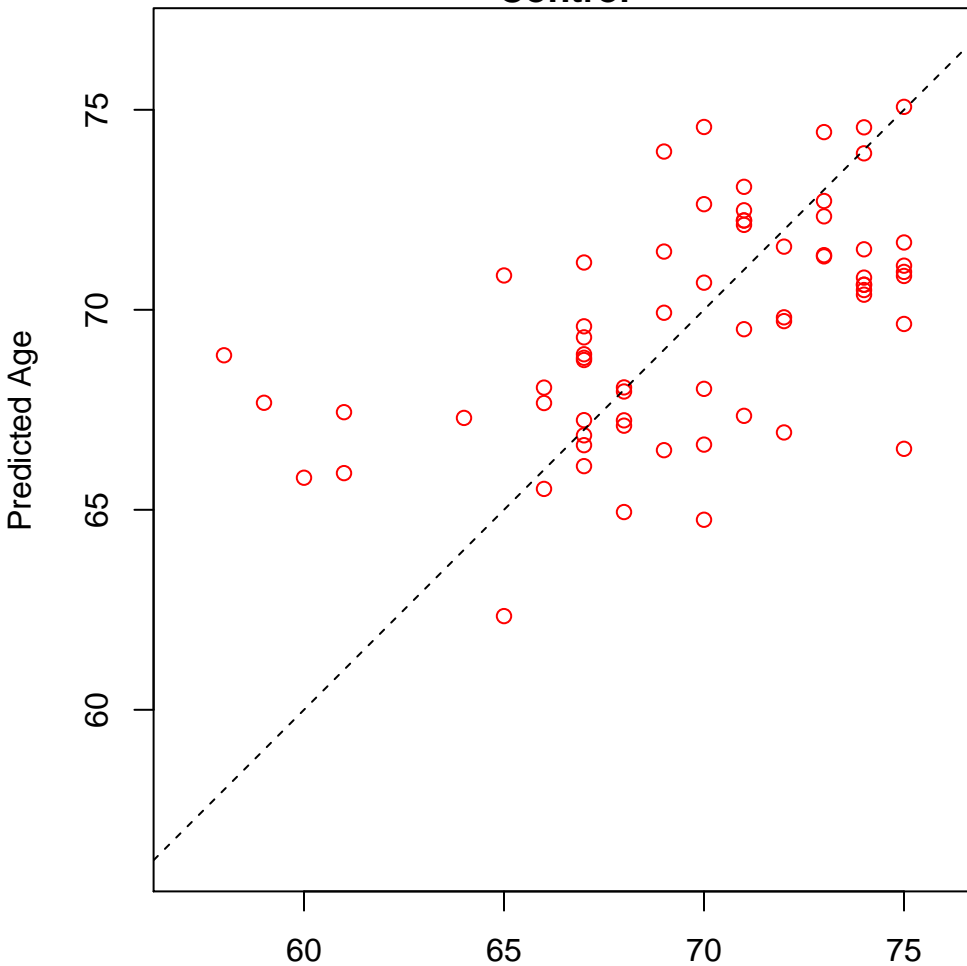


negative regulation of carbohydrate metabolic process (Score: 0.964283)

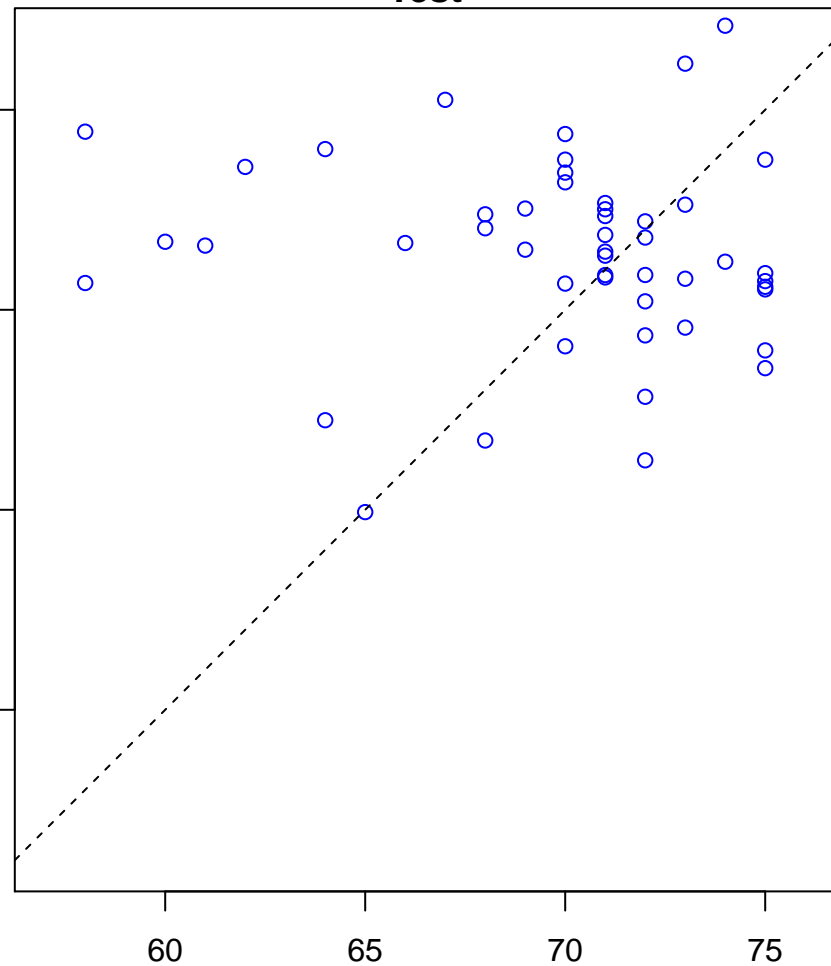


alpha-amino acid biosynthetic process (Score: 0.963775)

Control

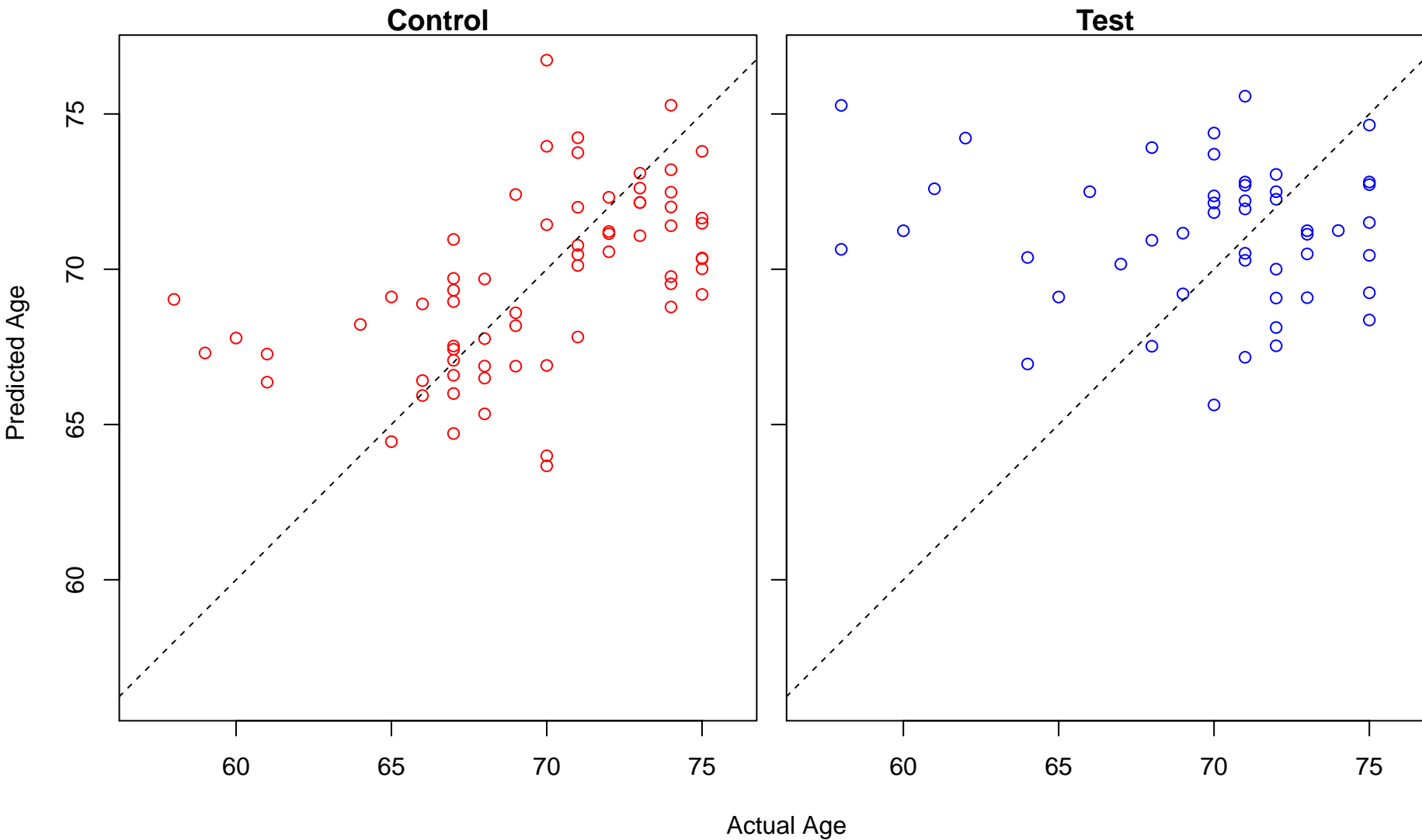


Test

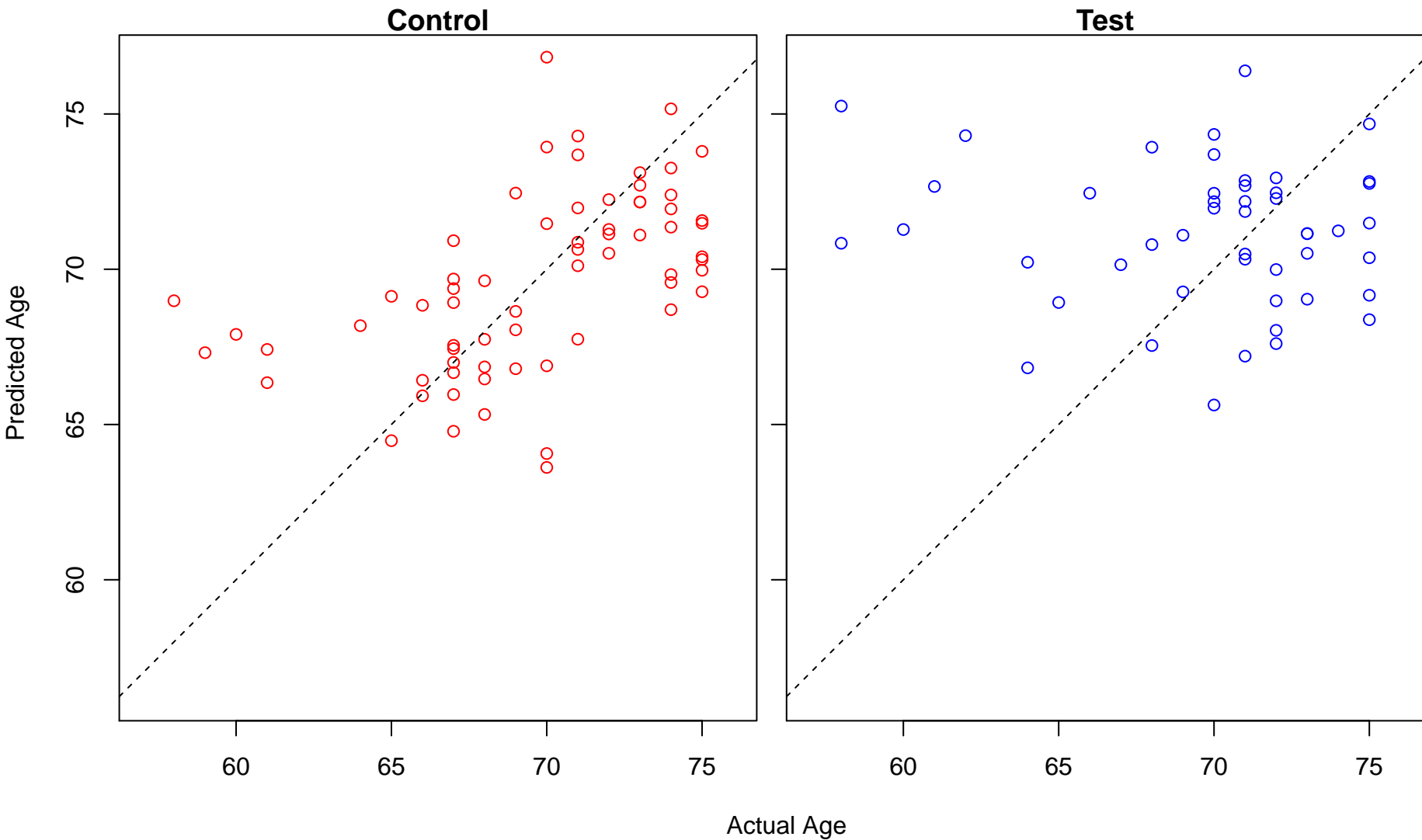


Actual Age

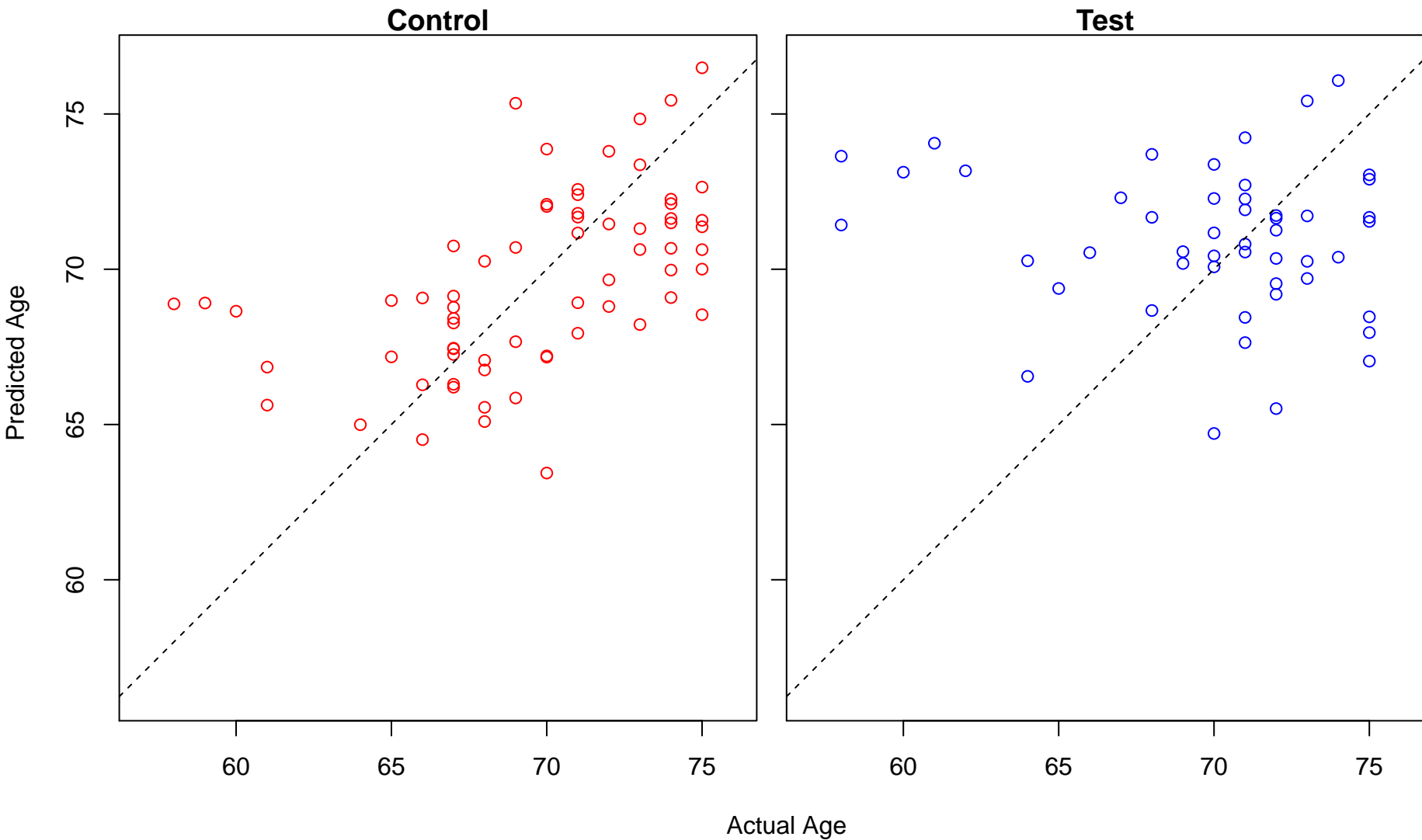
positive regulation of angiogenesis (Score: 0.963052)



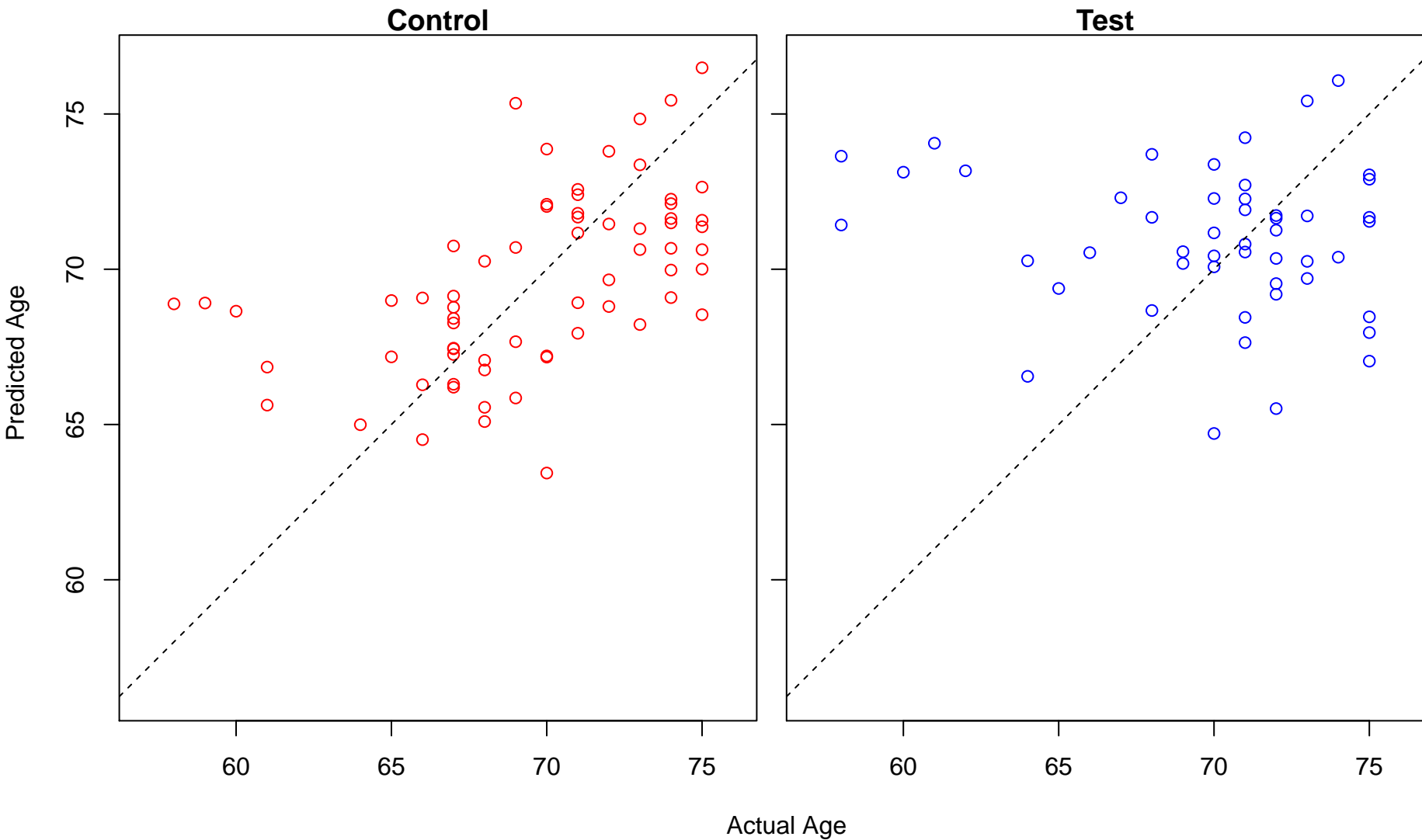
positive regulation of vasculature development (Score: 0.962976)



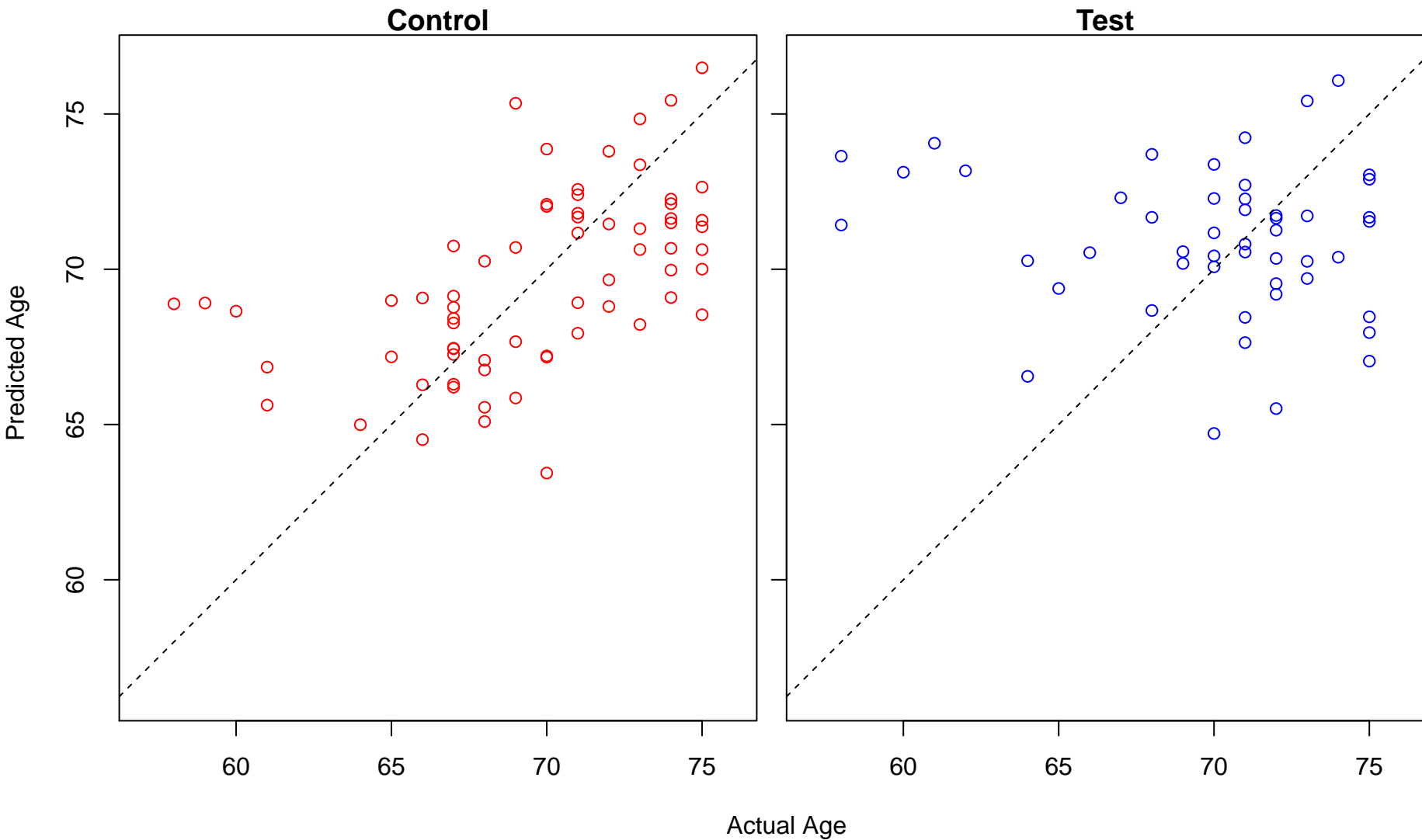
nucleoside bisphosphate metabolic process (Score: 0.962519)



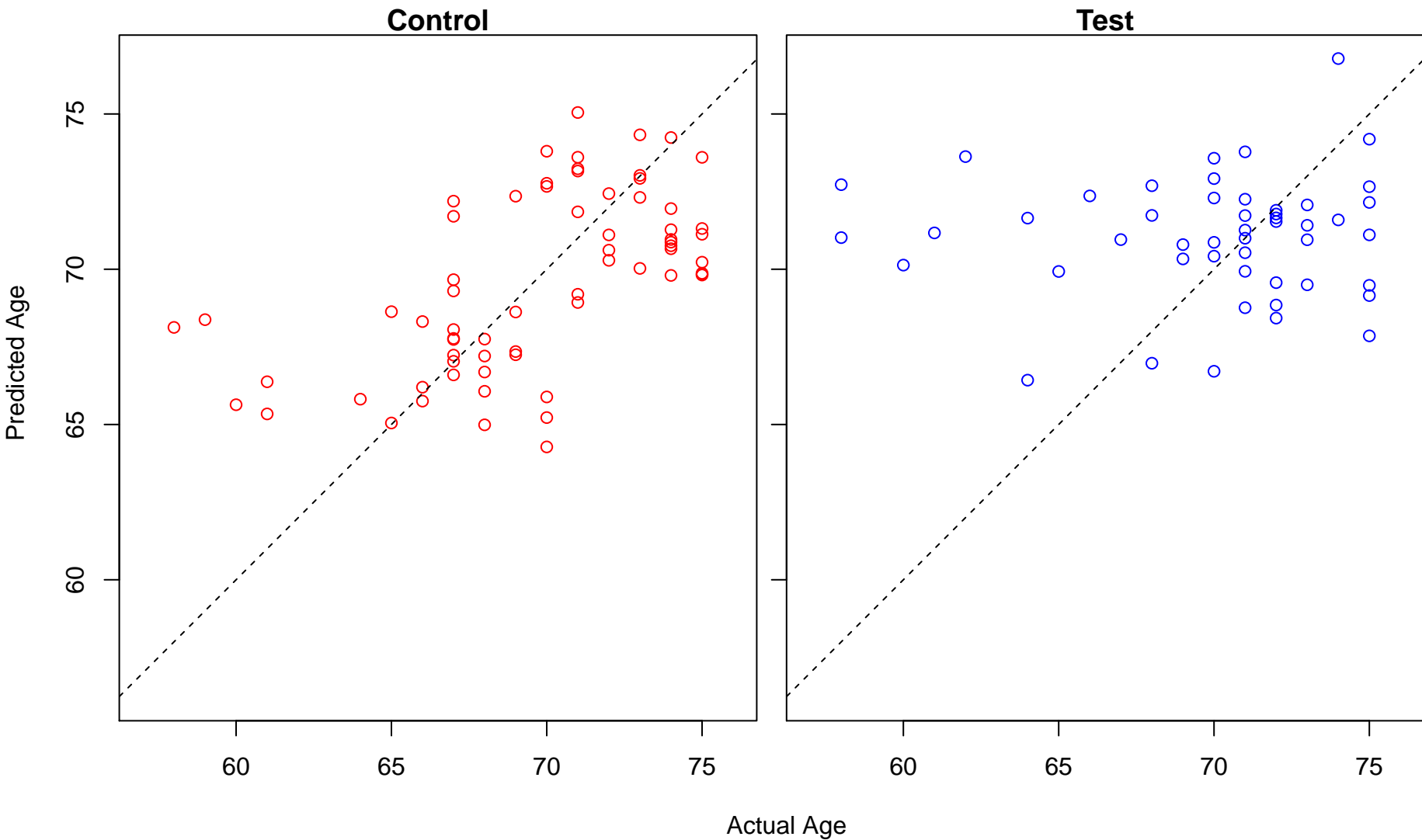
ribonucleoside biphosphate metabolic process (Score: 0.962519)



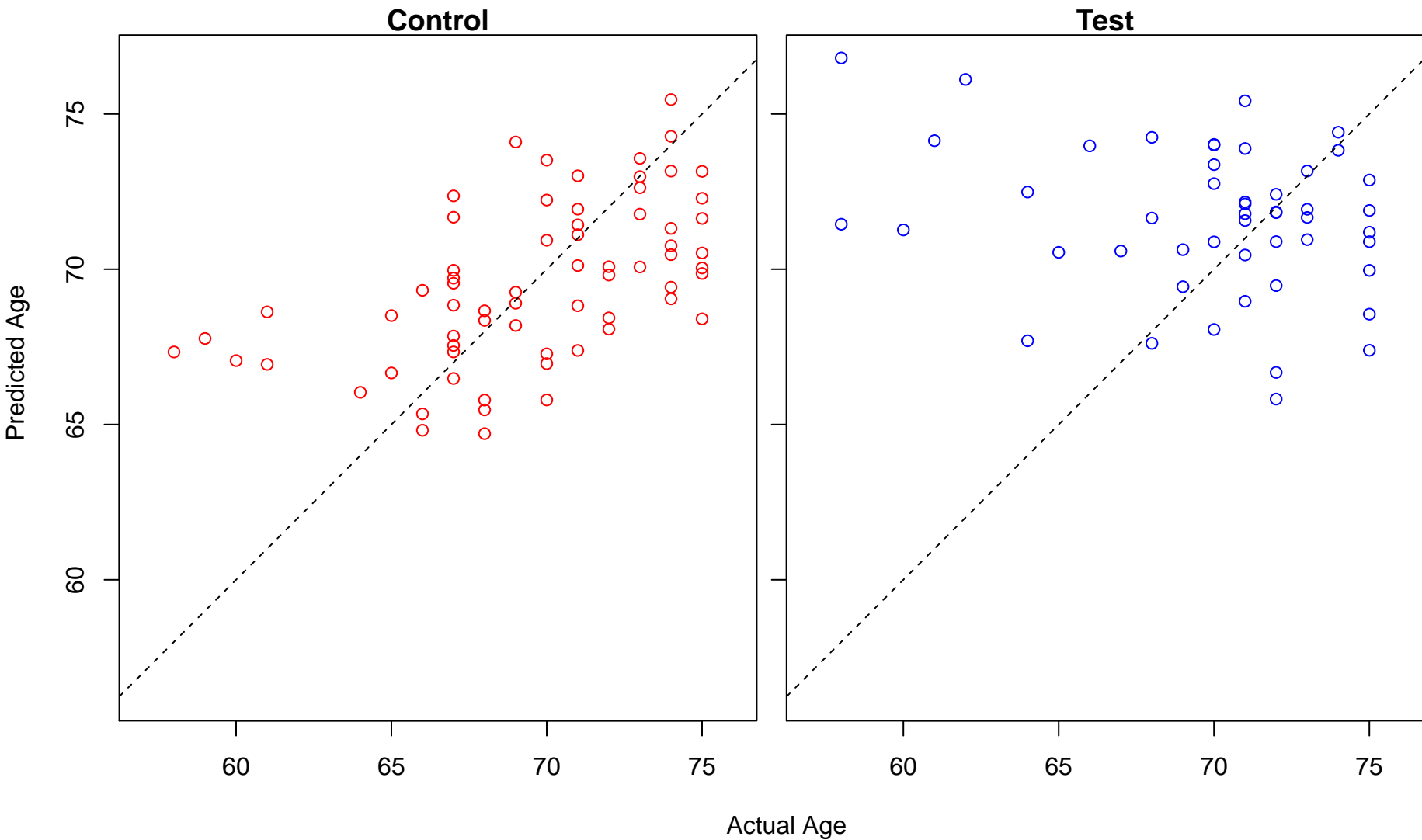
purine nucleoside bisphosphate metabolic process (Score: 0.962519)



positive regulation of nervous system development (Score: 0.961719)

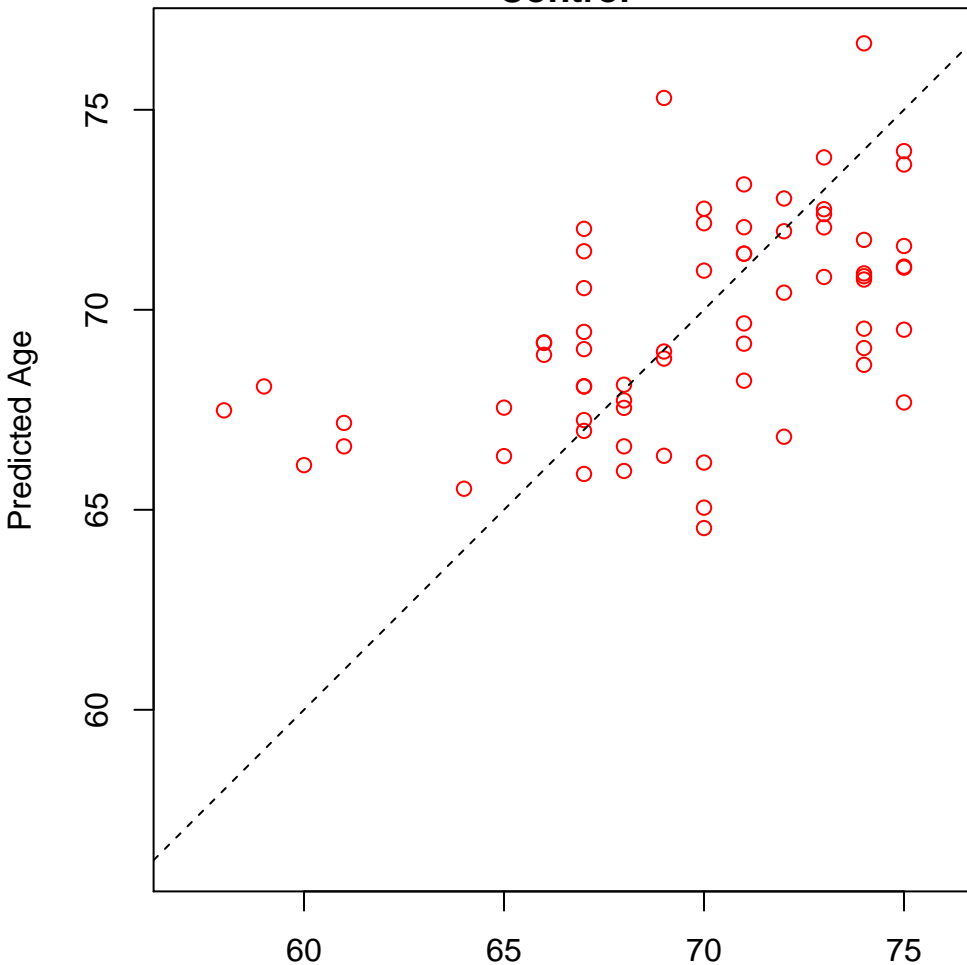


positive regulation of transcription elongation from RNA polymerase II promoter (Score: 0.961094)

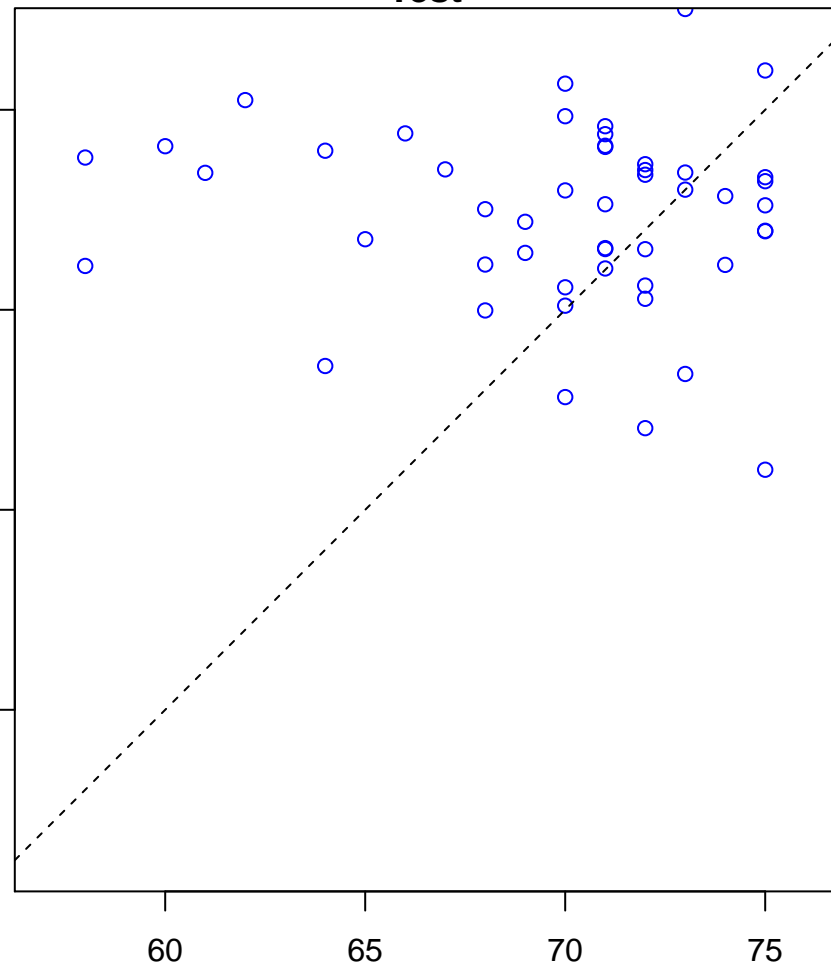


polysaccharide biosynthetic process (Score: 0.960795)

Control

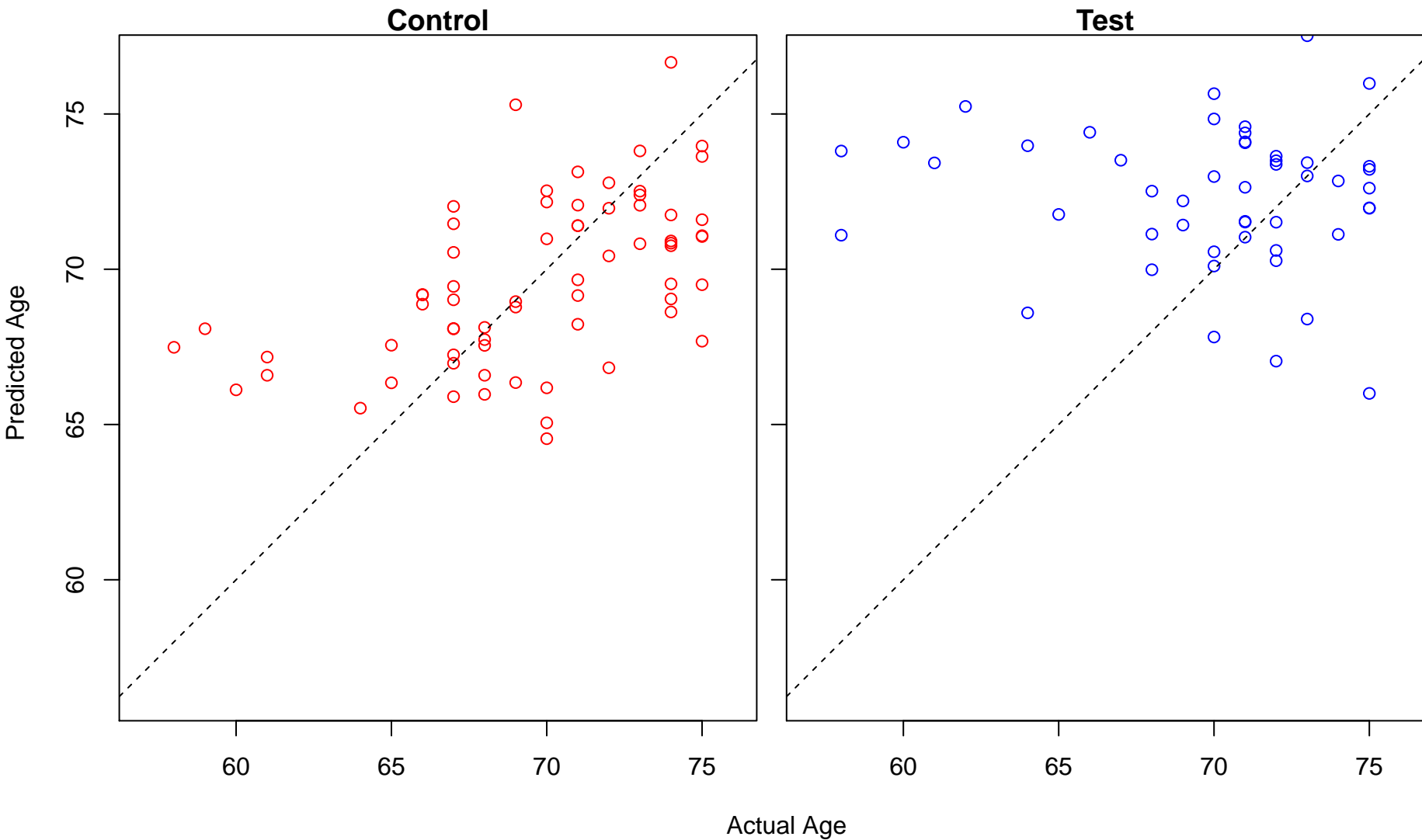


Test

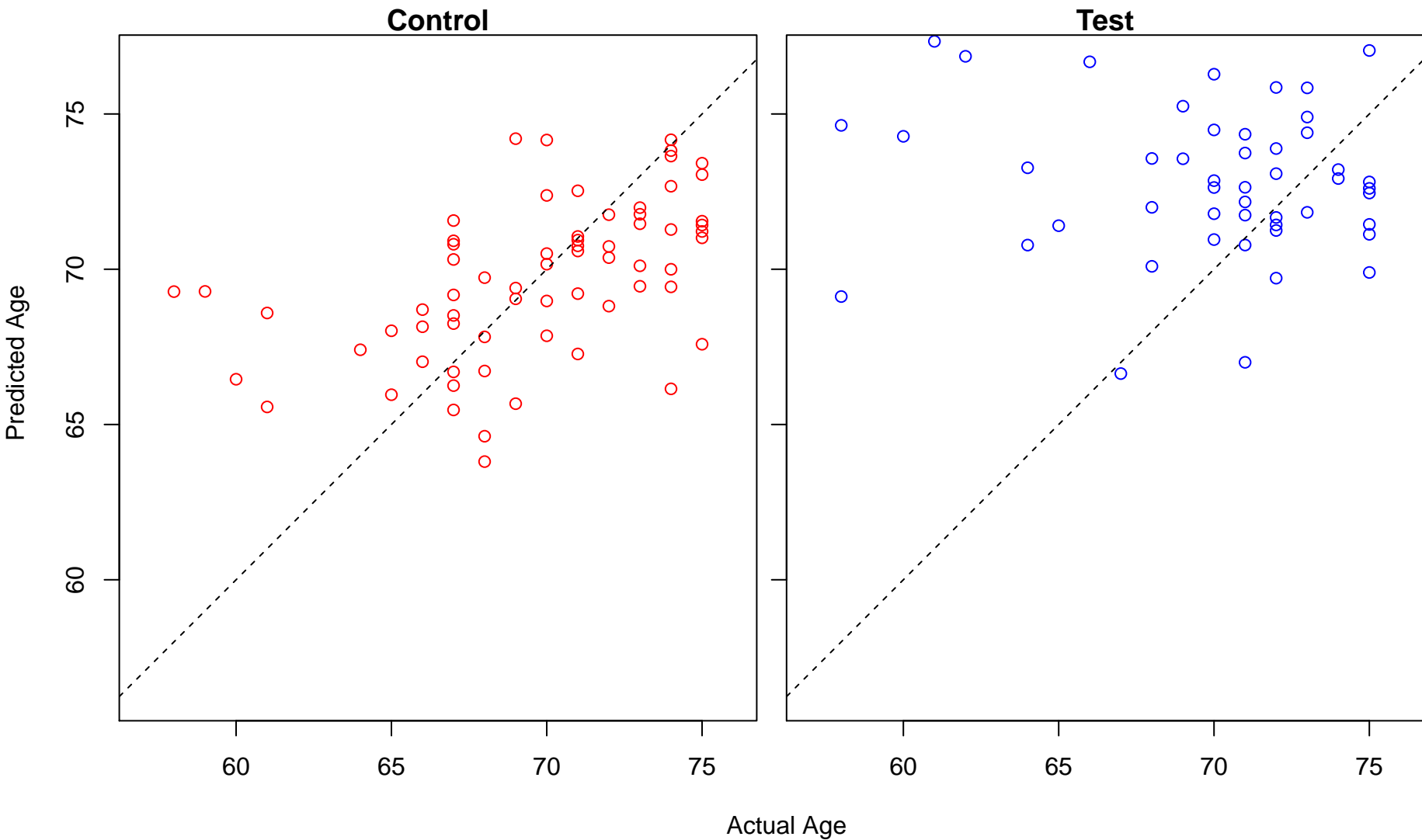


Actual Age

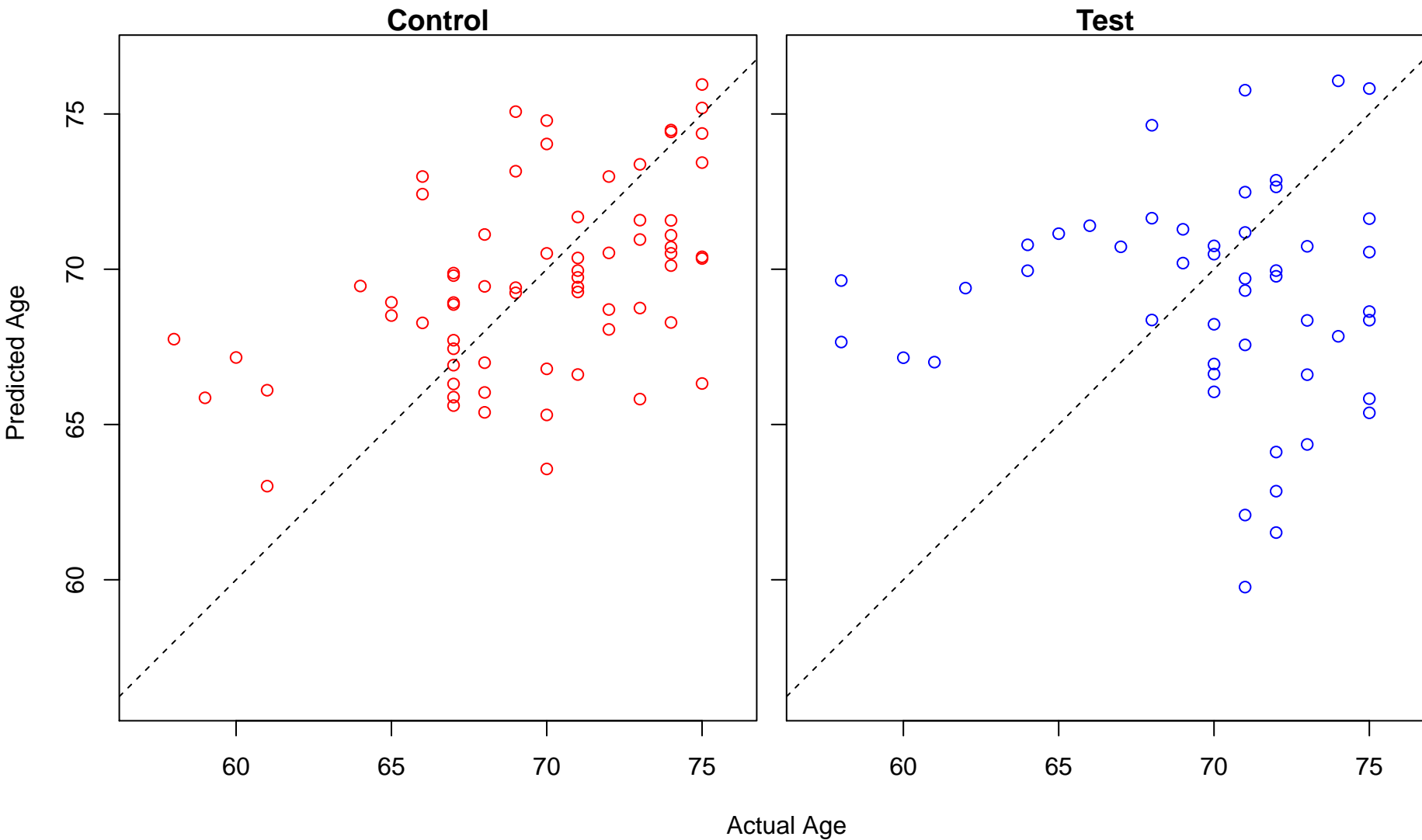
cellular polysaccharide biosynthetic process (Score: 0.960795)



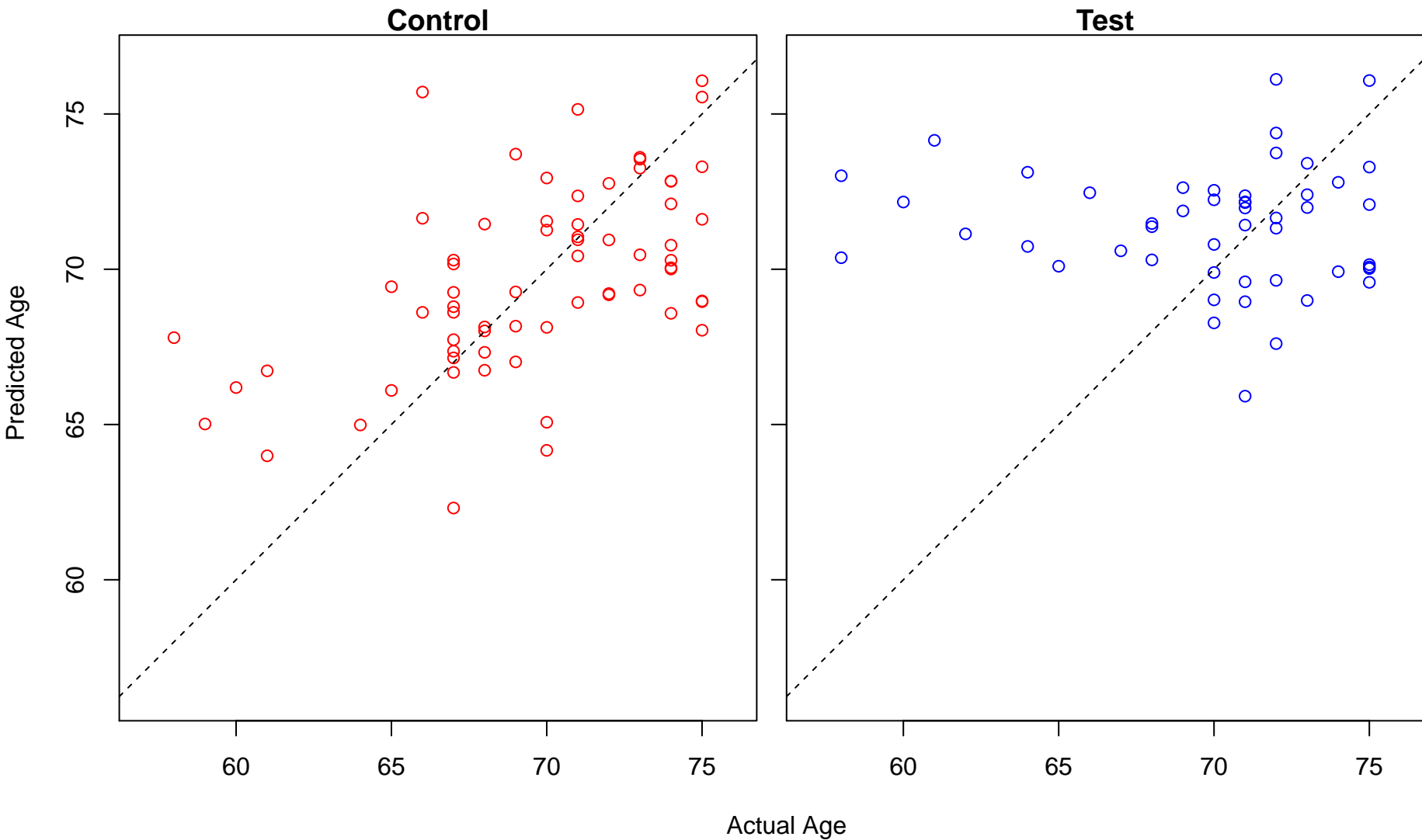
response to axon injury (Score: 0.960669)



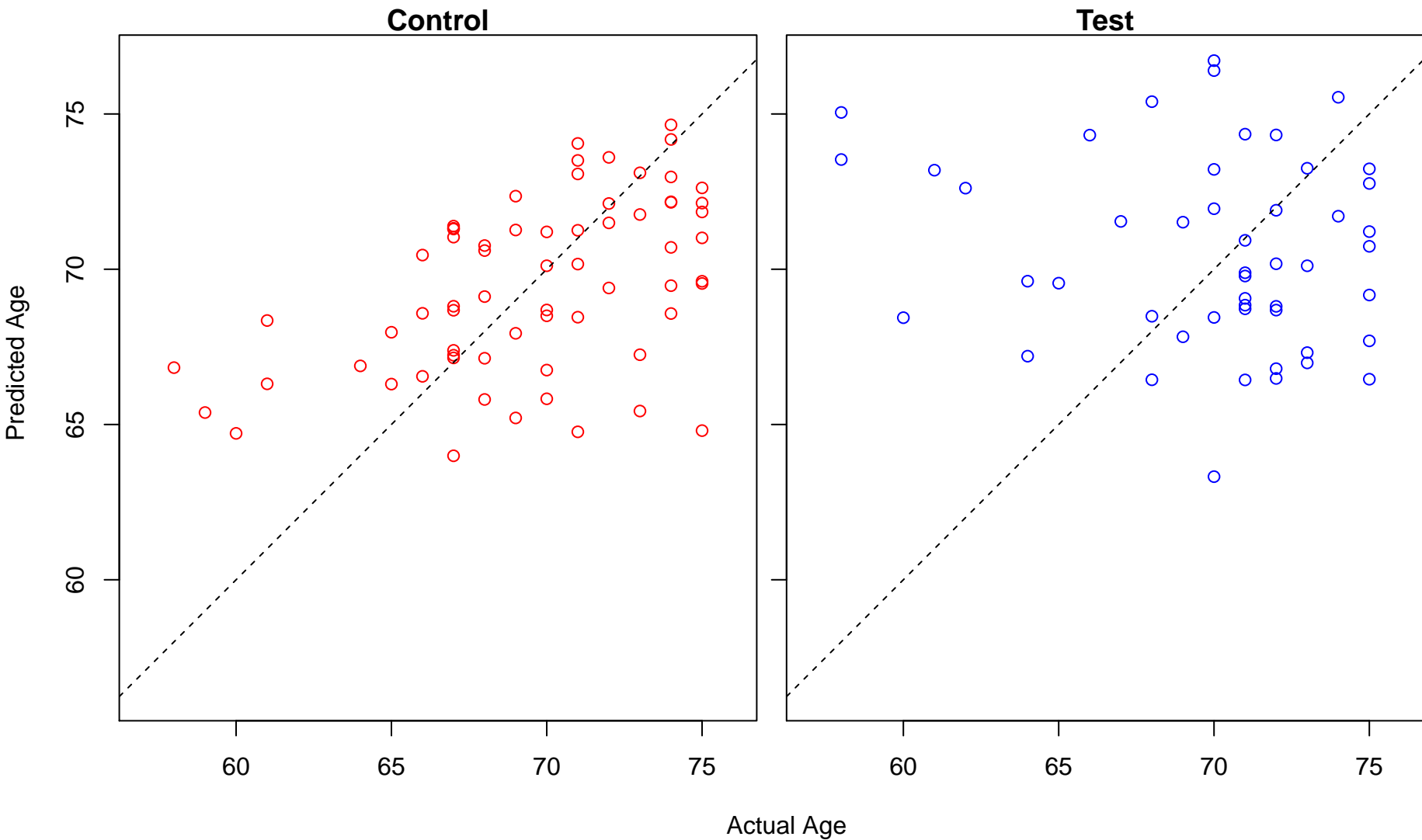
antifungal humoral response (Score: 0.960209)



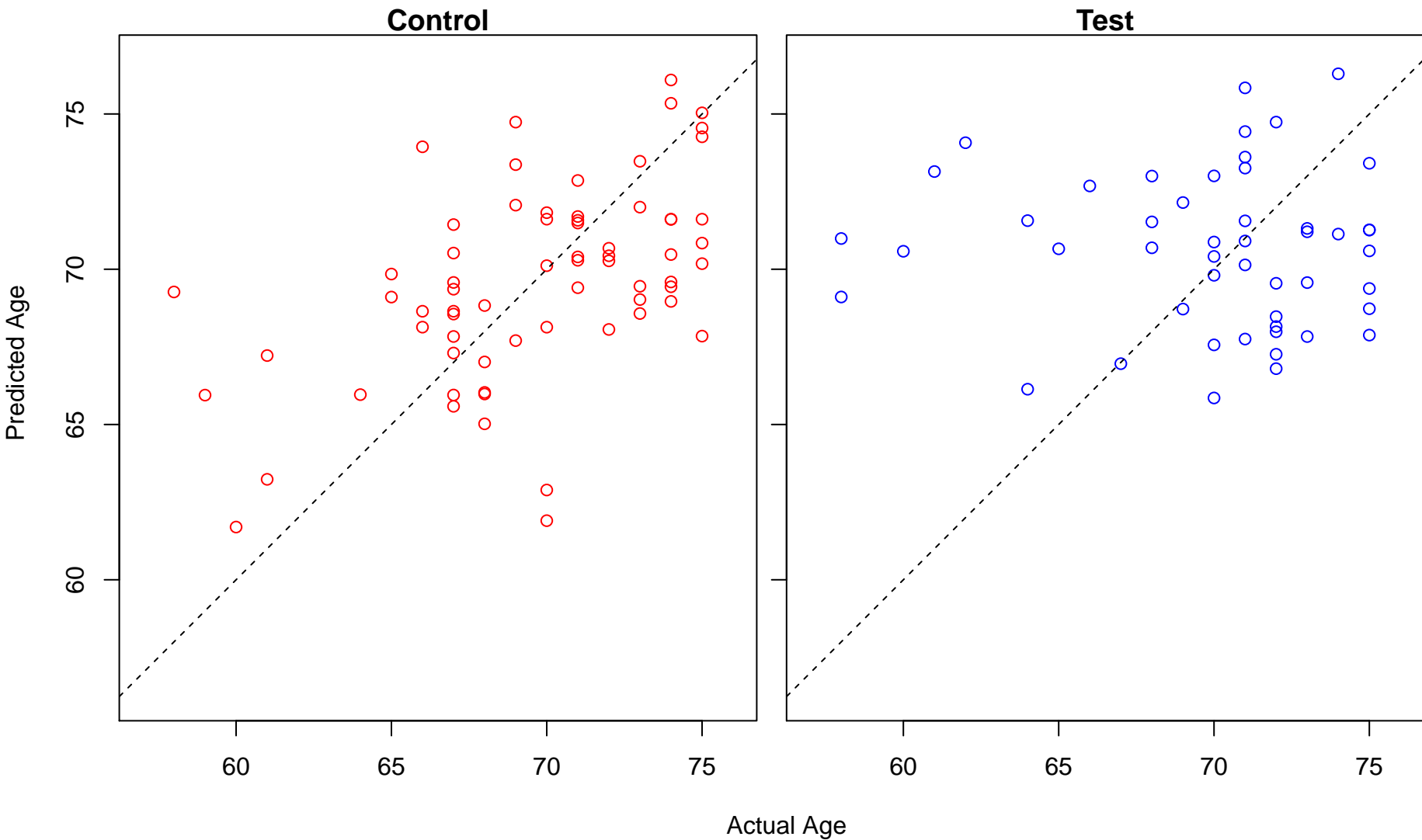
male meiosis (Score: 0.959972)



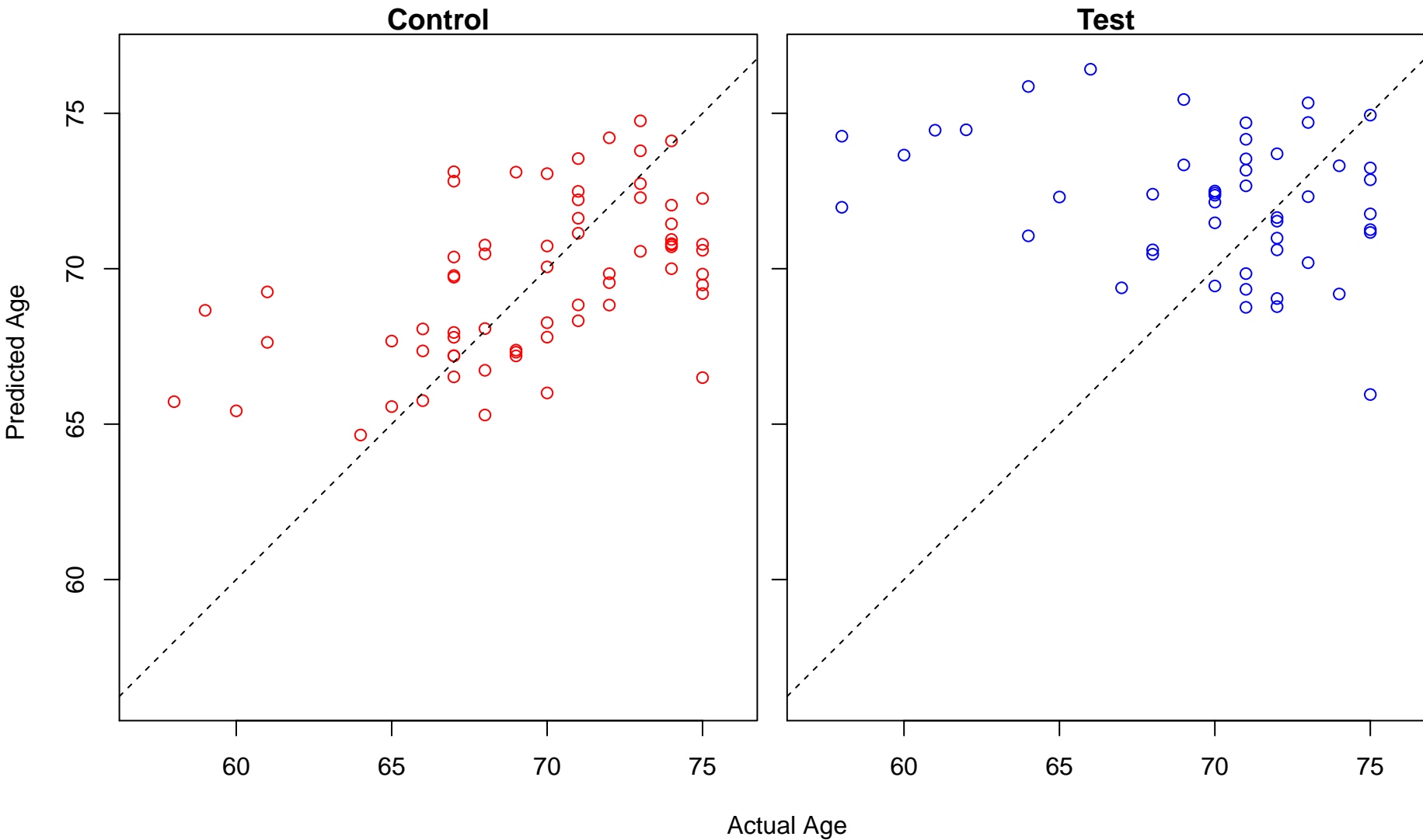
negative regulation of monooxygenase activity (Score: 0.959911)



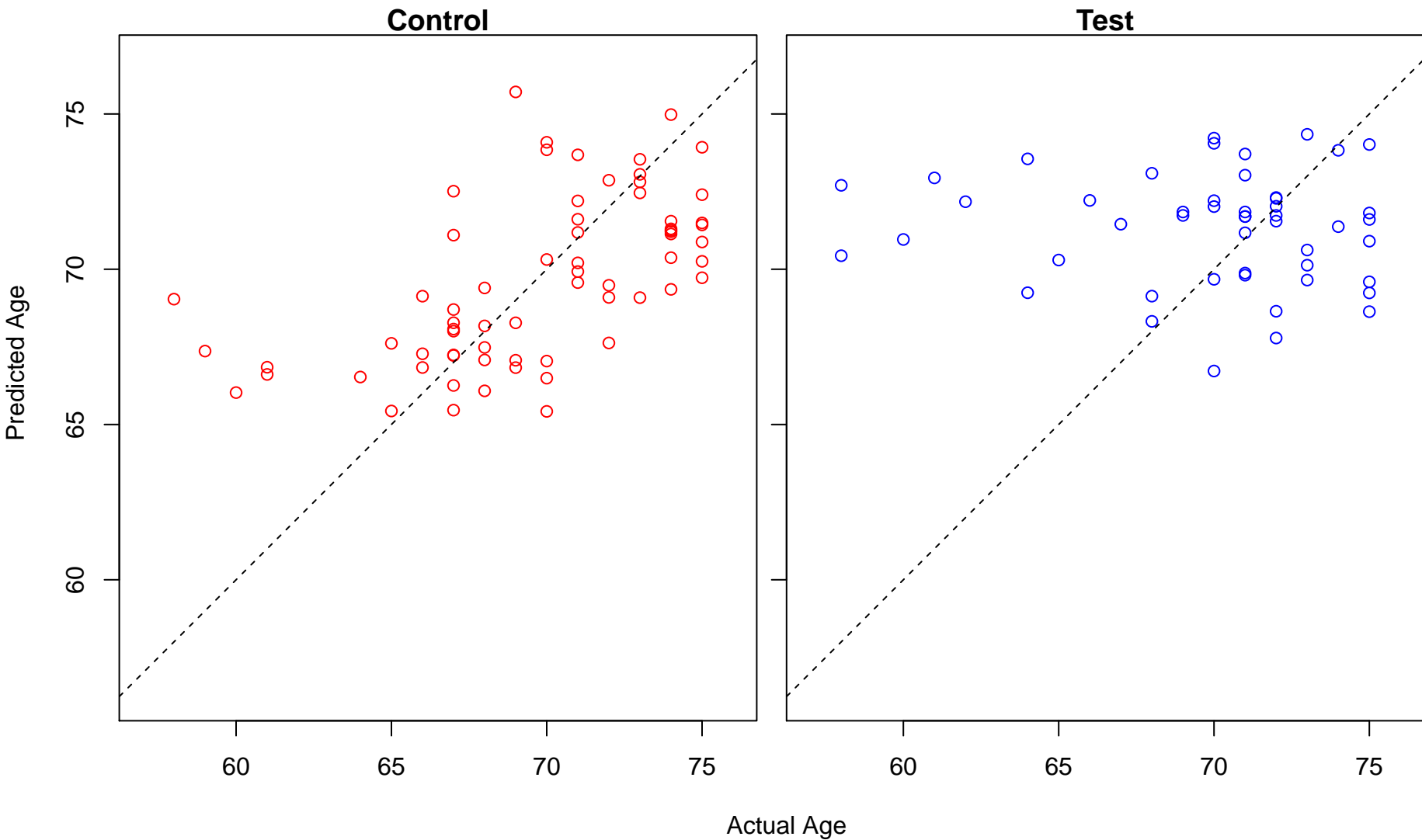
endothelial cell proliferation (Score: 0.959488)



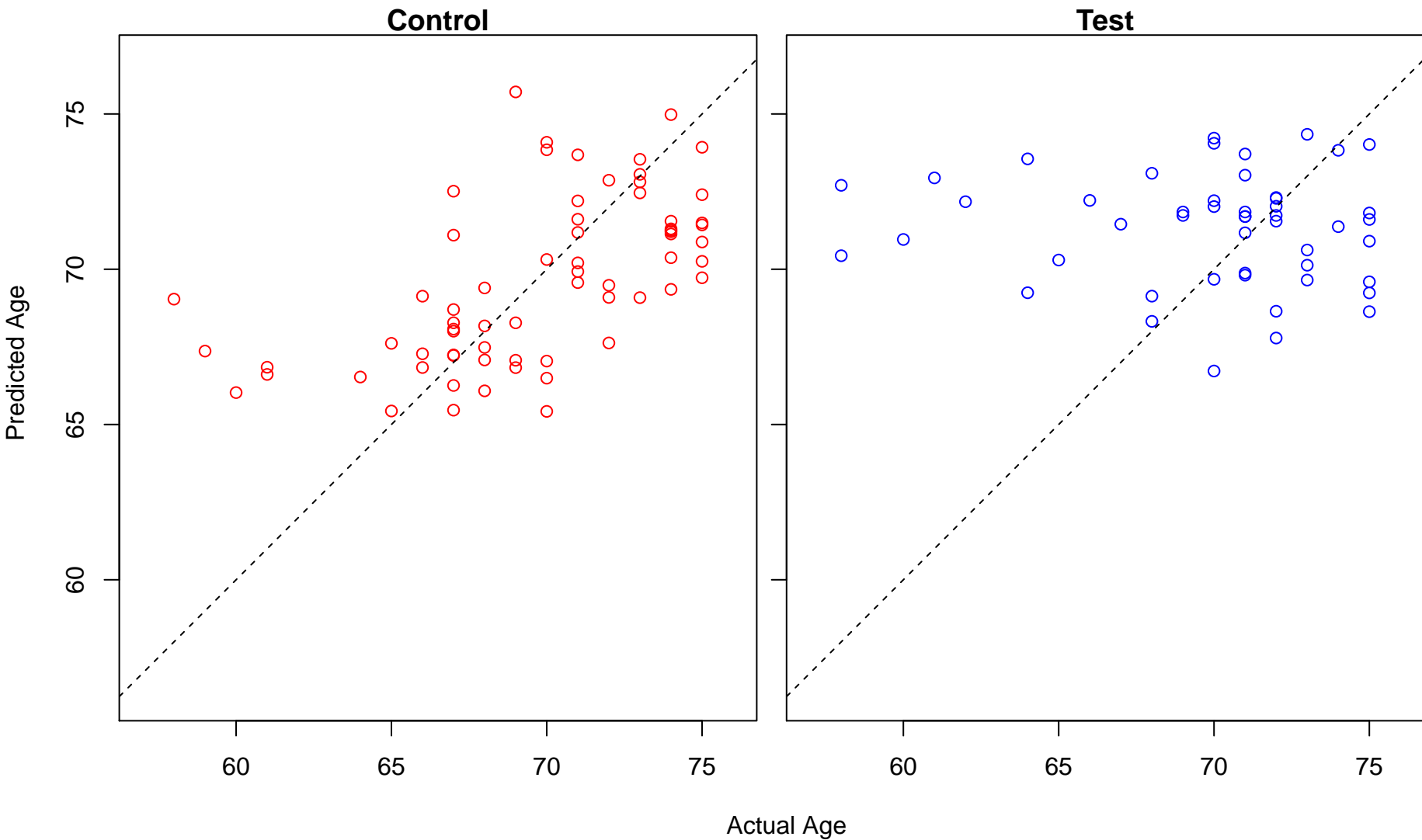
cardiac muscle cell myoblast differentiation (Score: 0.958925)



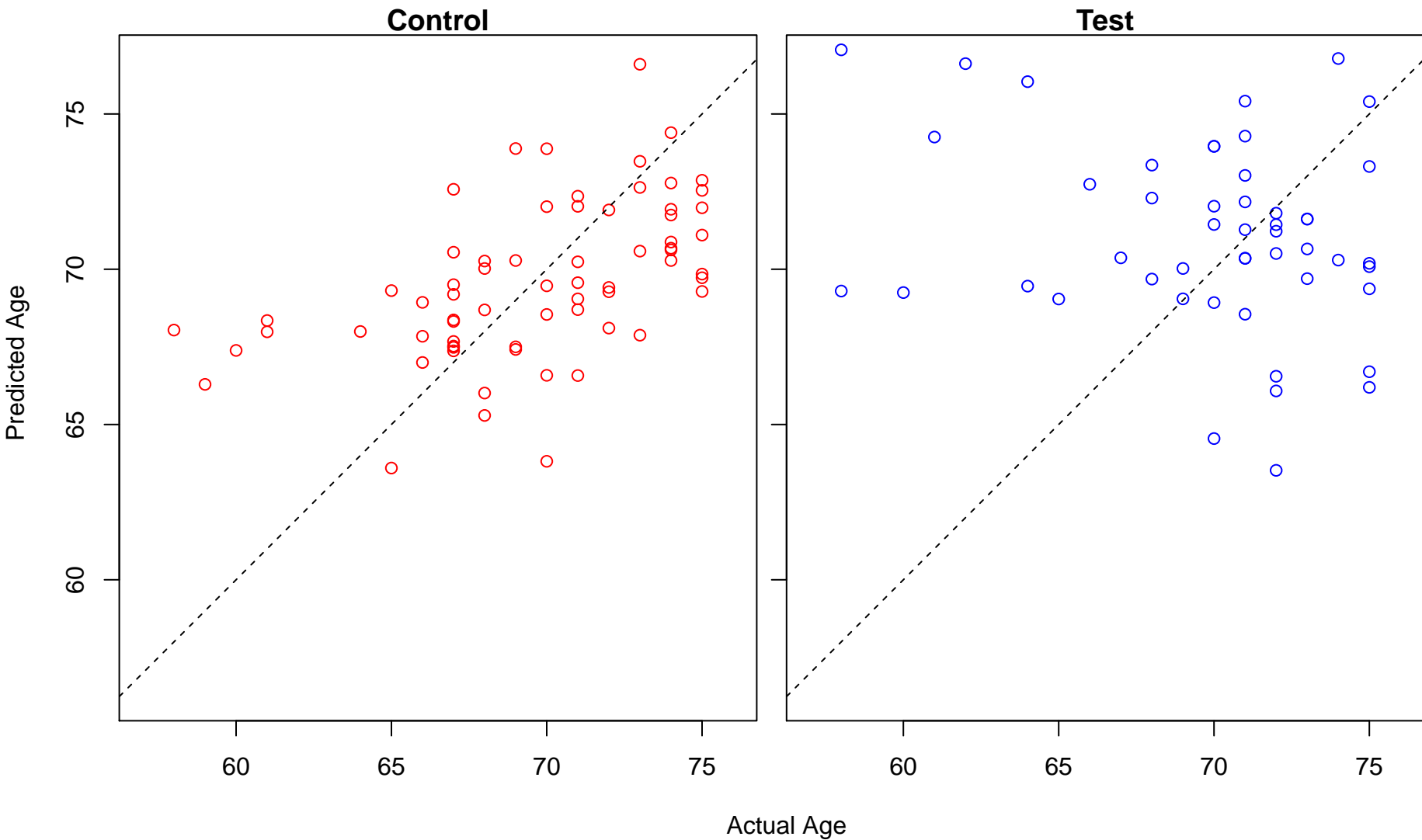
organic acid biosynthetic process (Score: 0.958756)



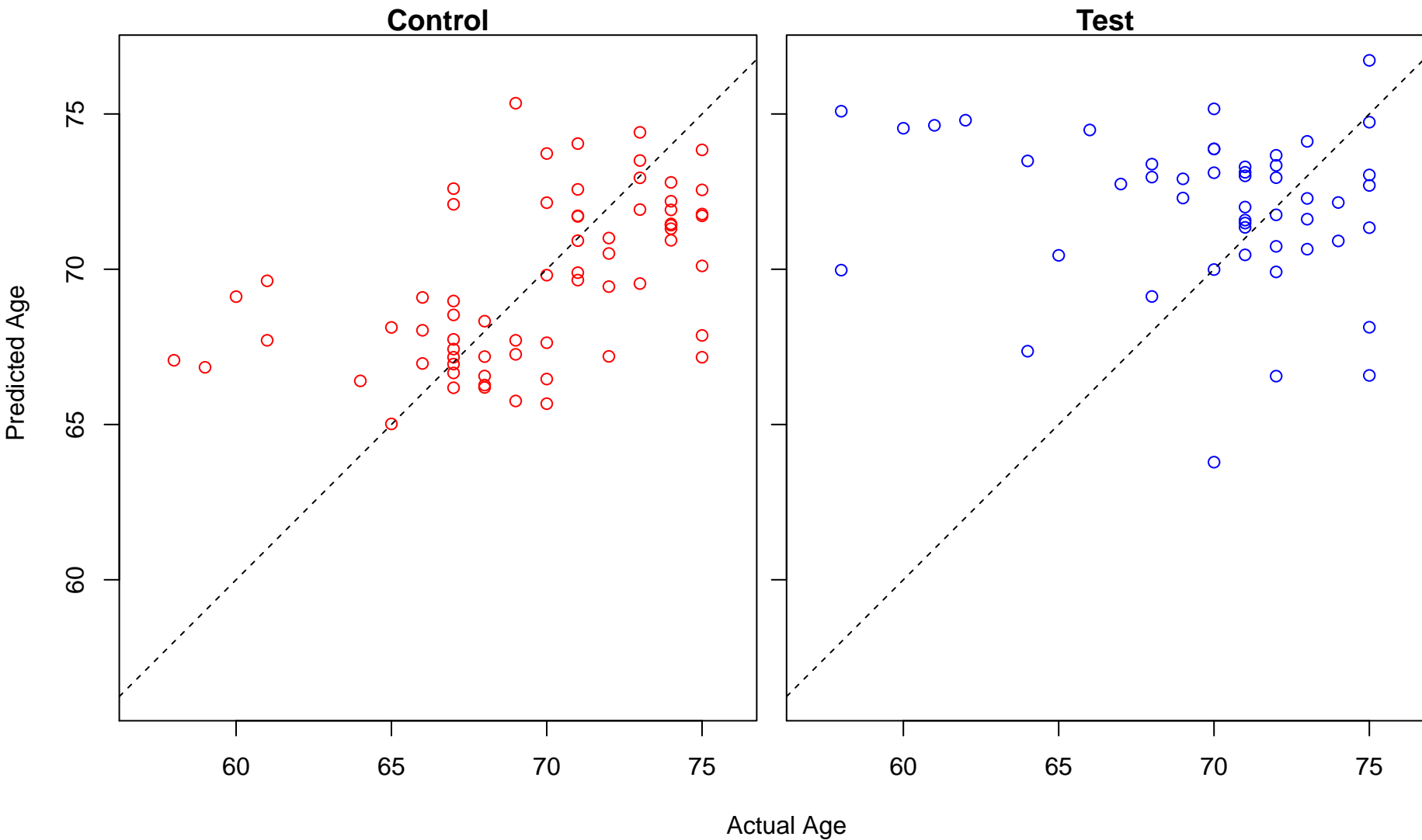
carboxylic acid biosynthetic process (Score: 0.958756)



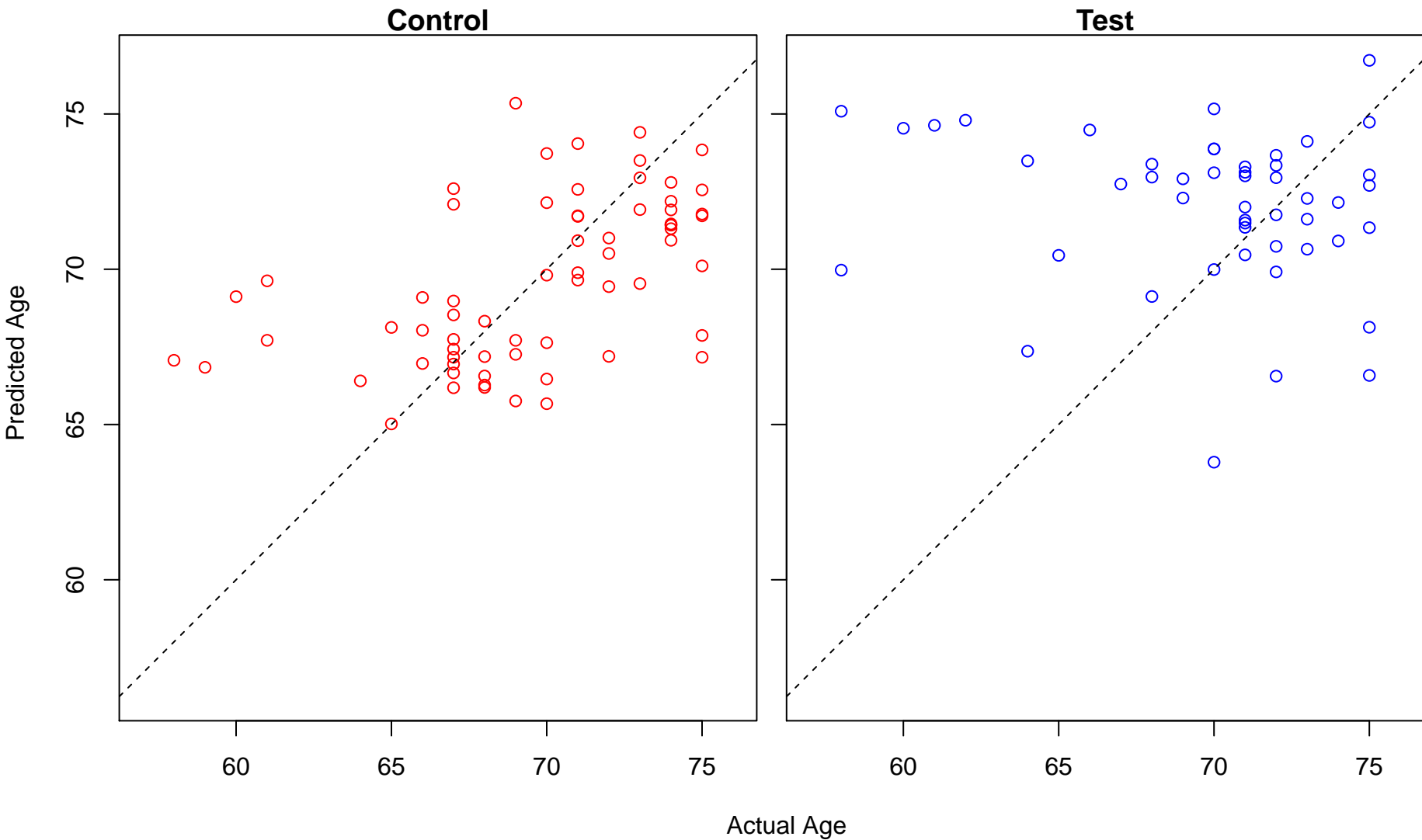
negative regulation of calcium ion import (Score: 0.958412)



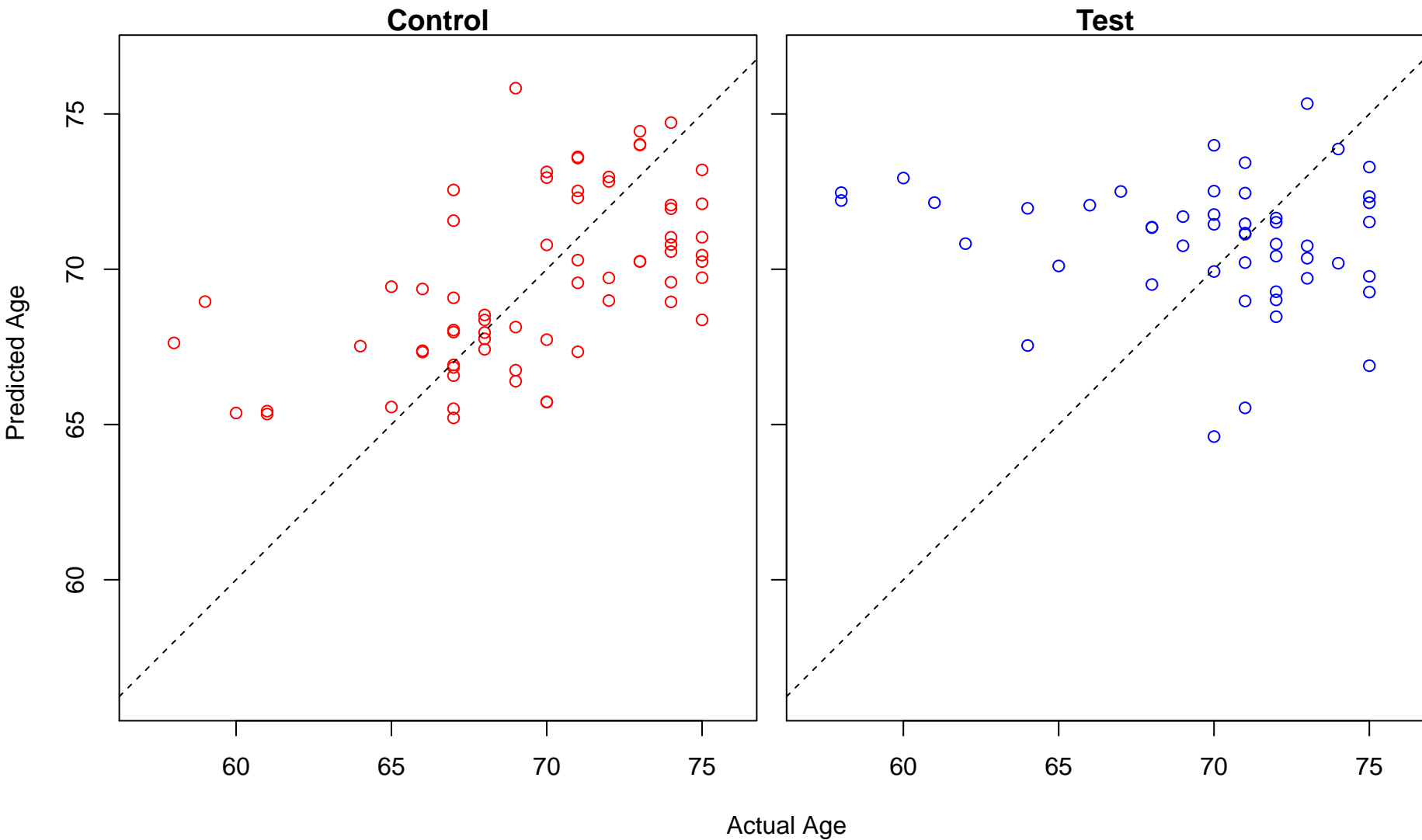
positive regulation of nitric oxide biosynthetic process (Score: 0.958277)



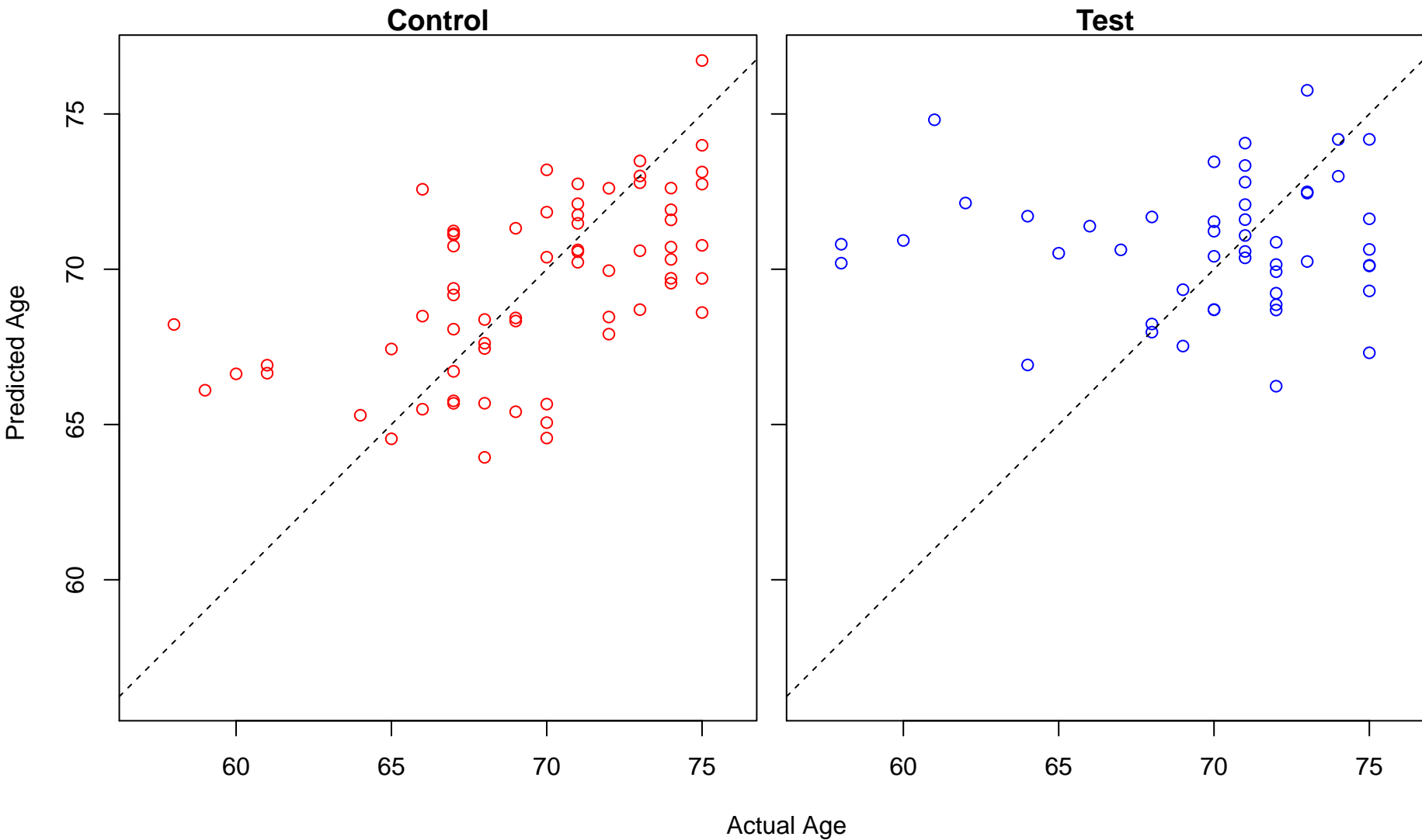
positive regulation of nitric oxide metabolic process (Score: 0.958277)



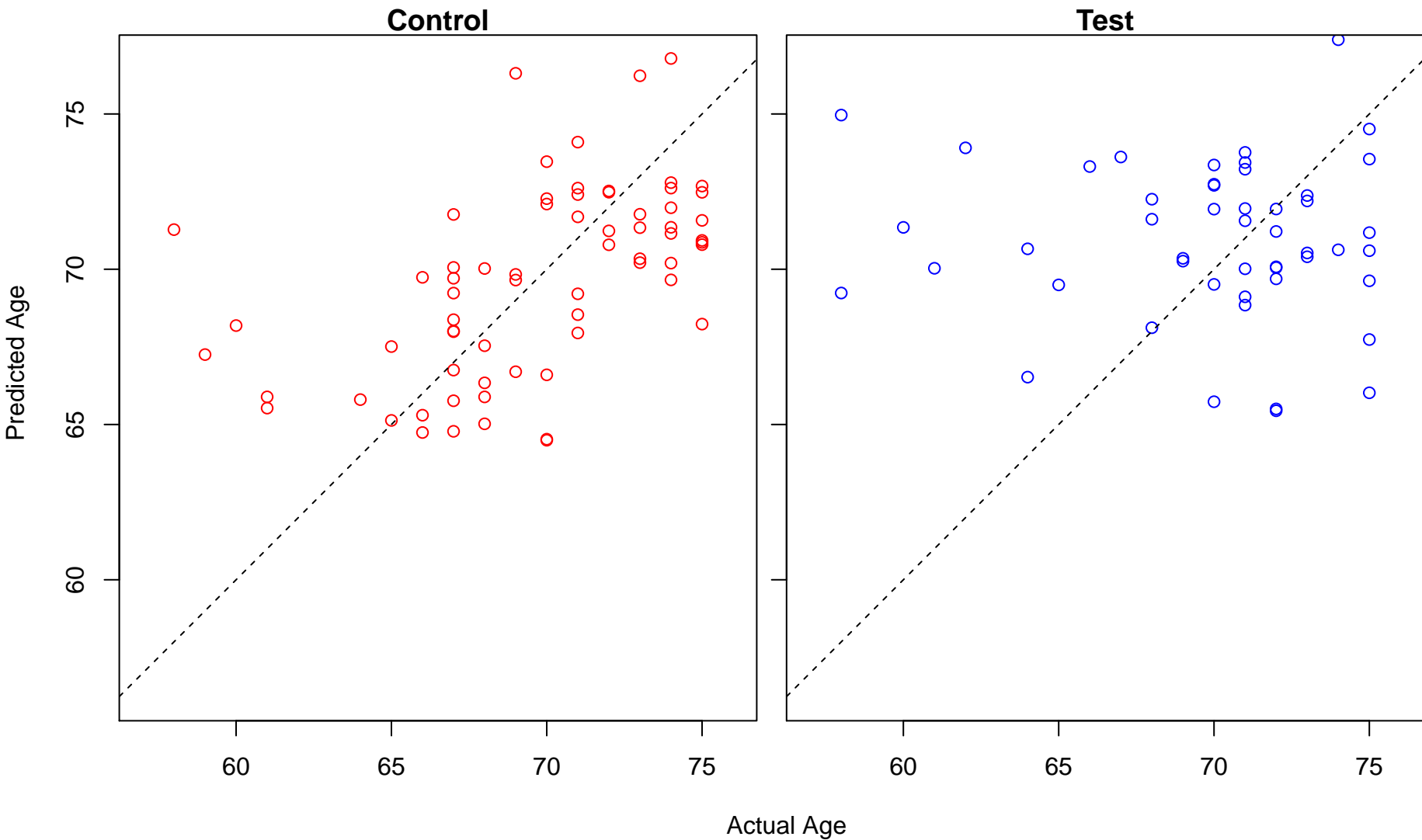
negative regulation of cell-substrate adhesion (Score: 0.958151)



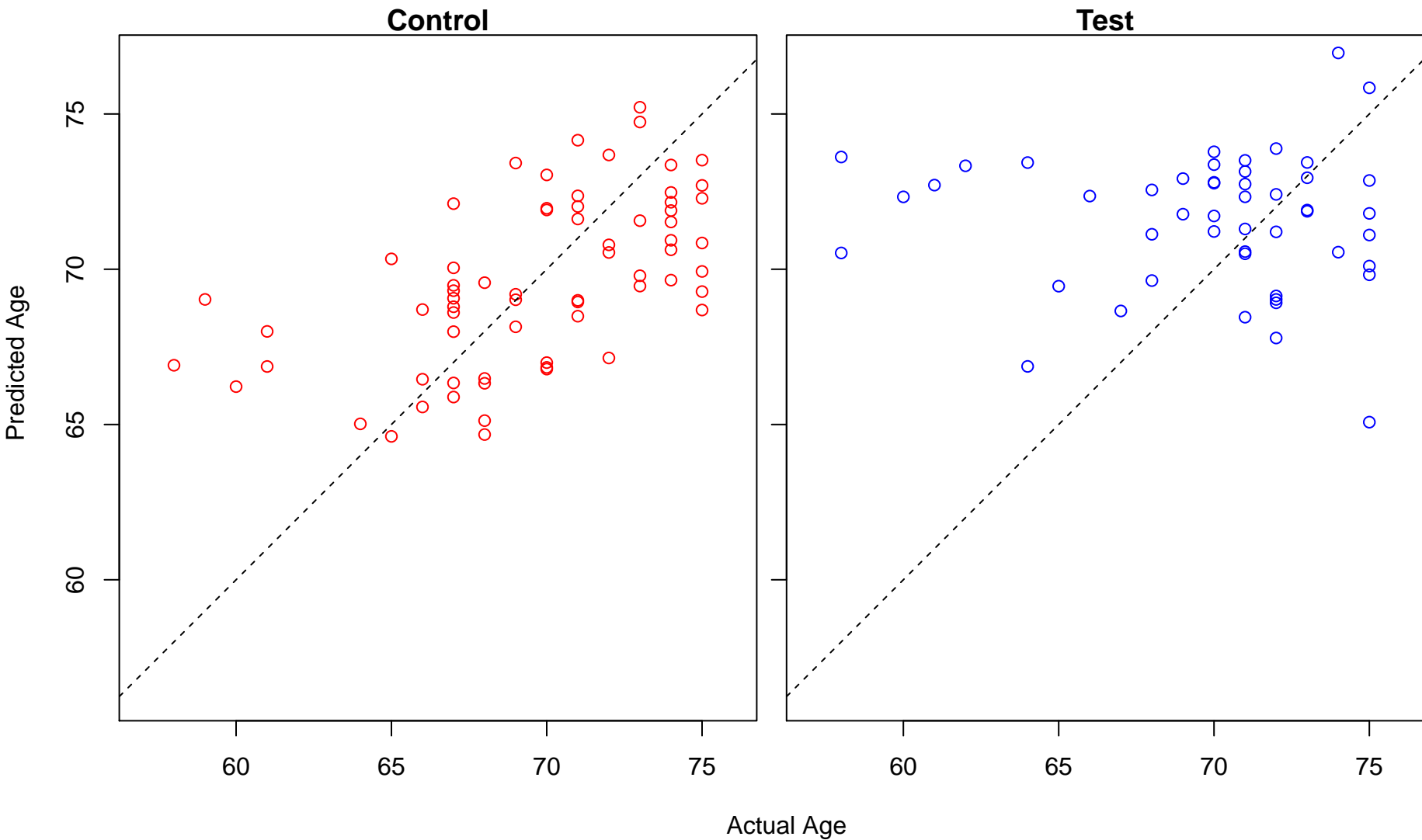
BMP signaling pathway (Score: 0.958124)



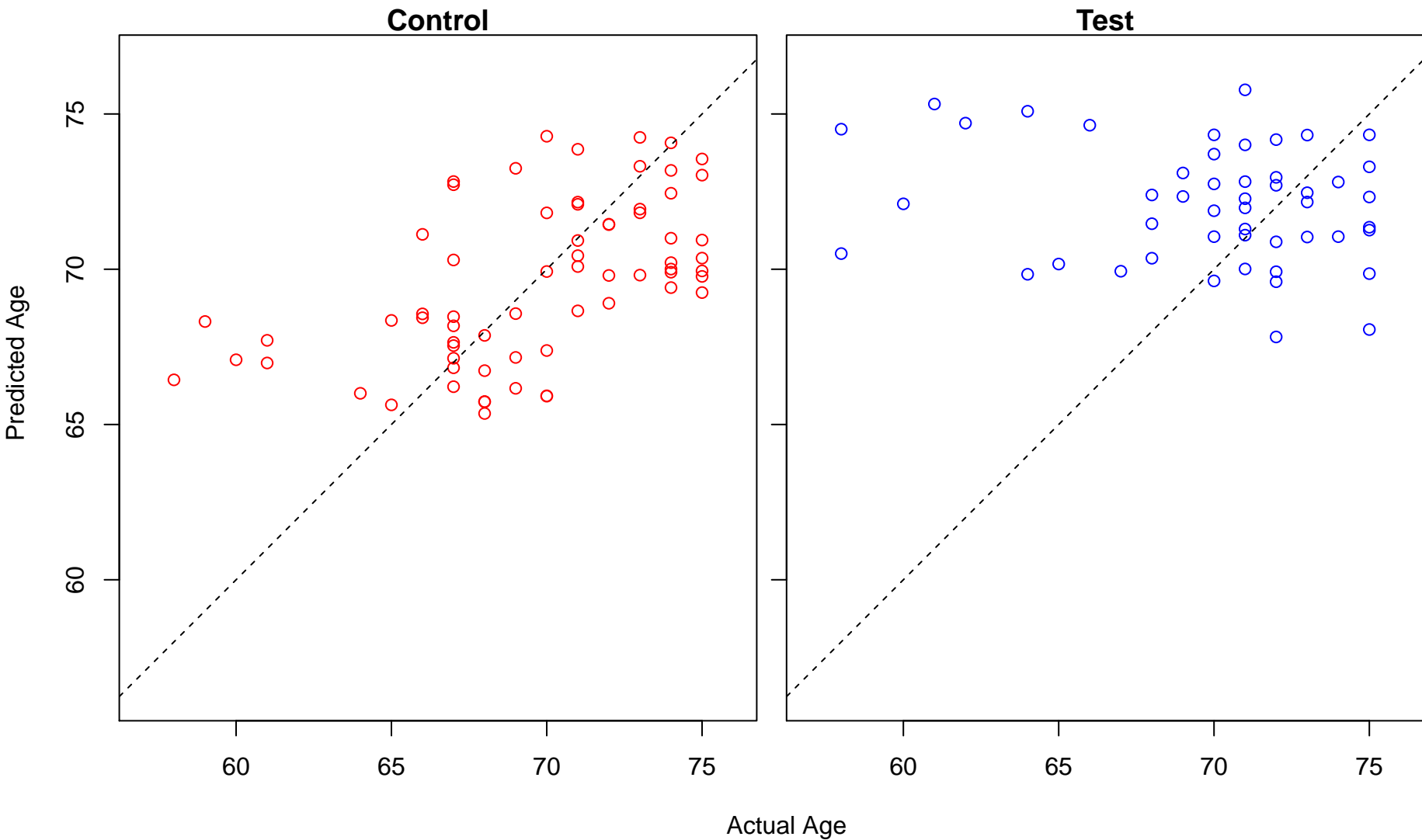
positive regulation of leukocyte mediated cytotoxicity (Score: 0.958014)



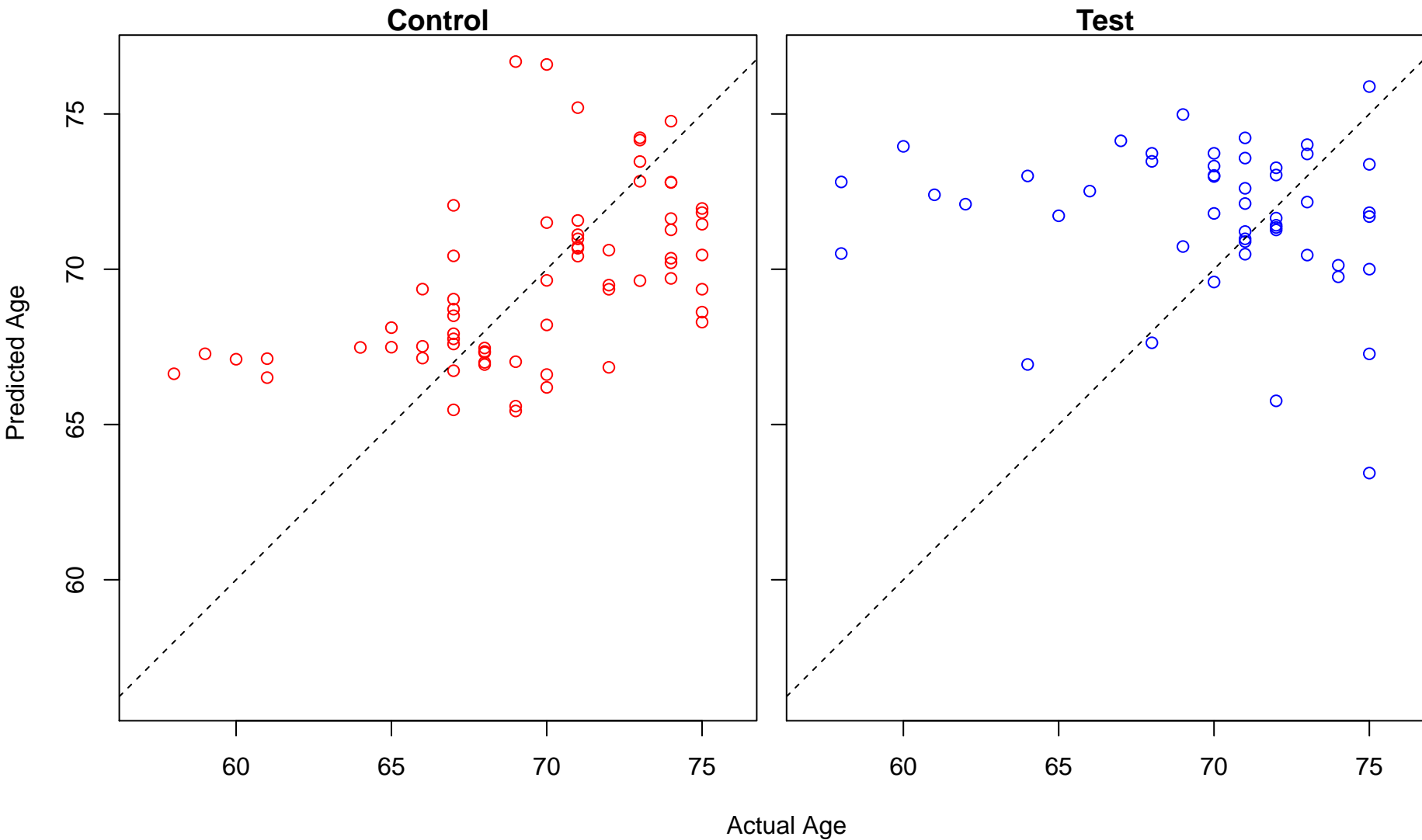
positive regulation of glial cell differentiation (Score: 0.957084)



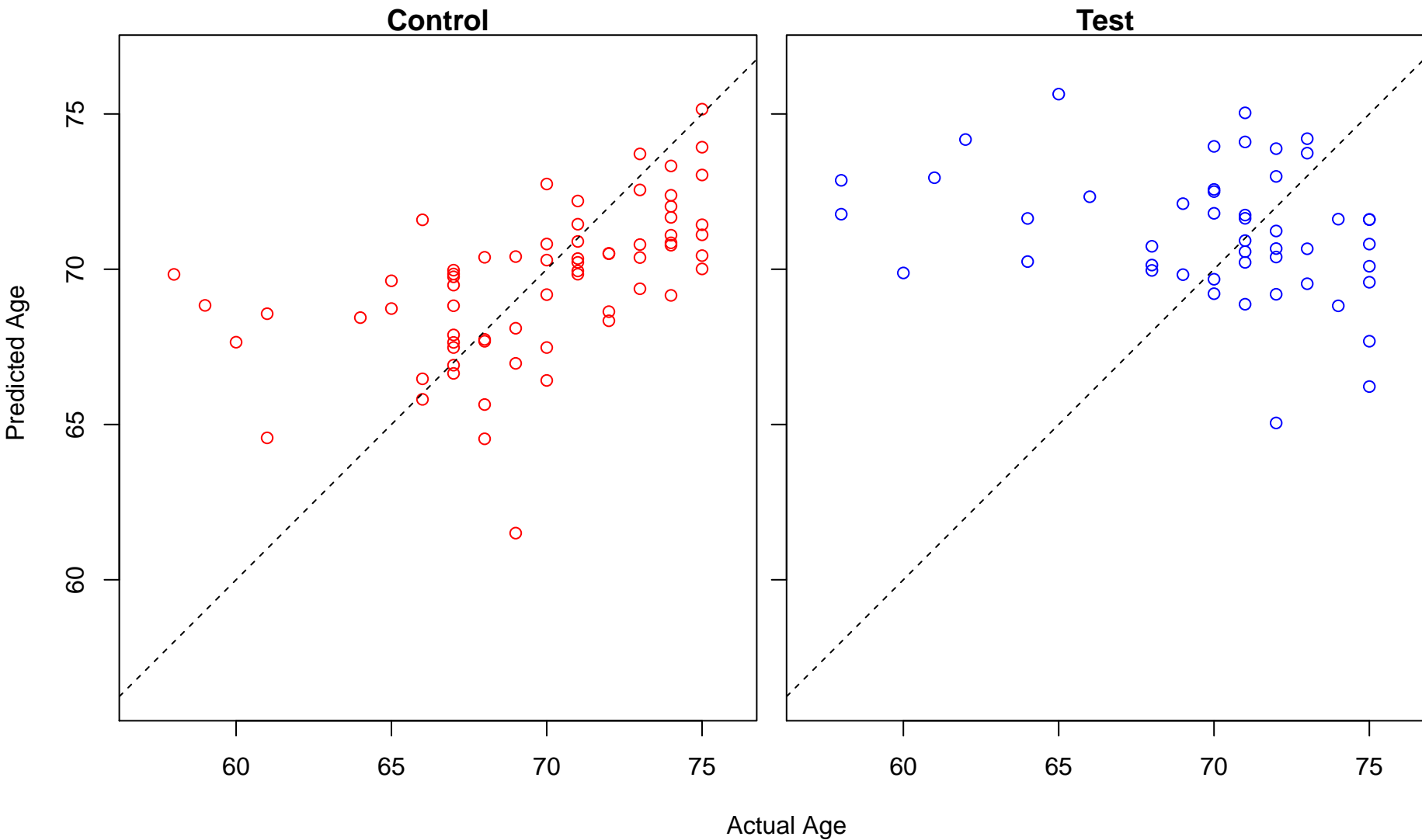
embryonic organ morphogenesis (Score: 0.956861)



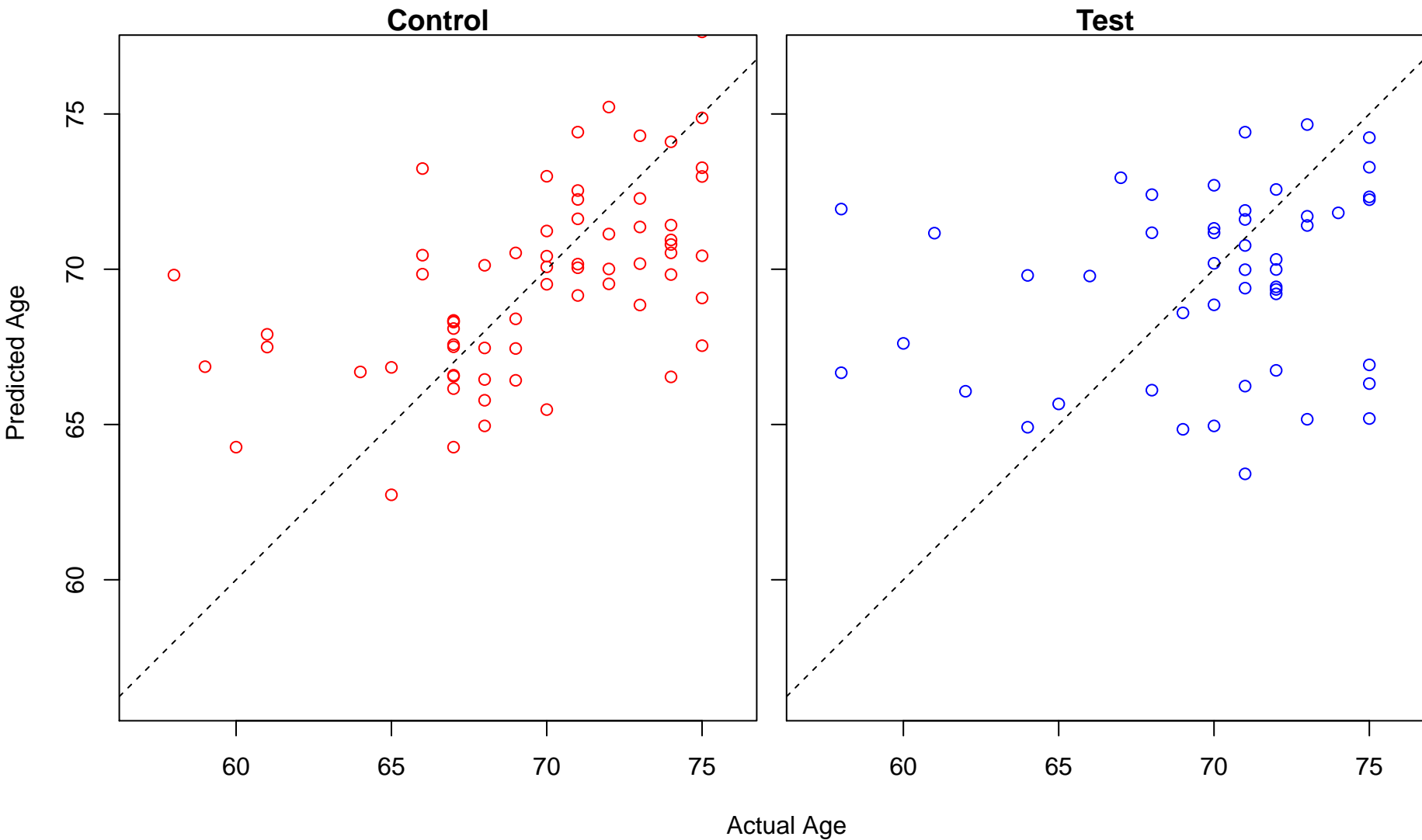
regulation of rhodopsin mediated signaling pathway (Score: 0.956736)



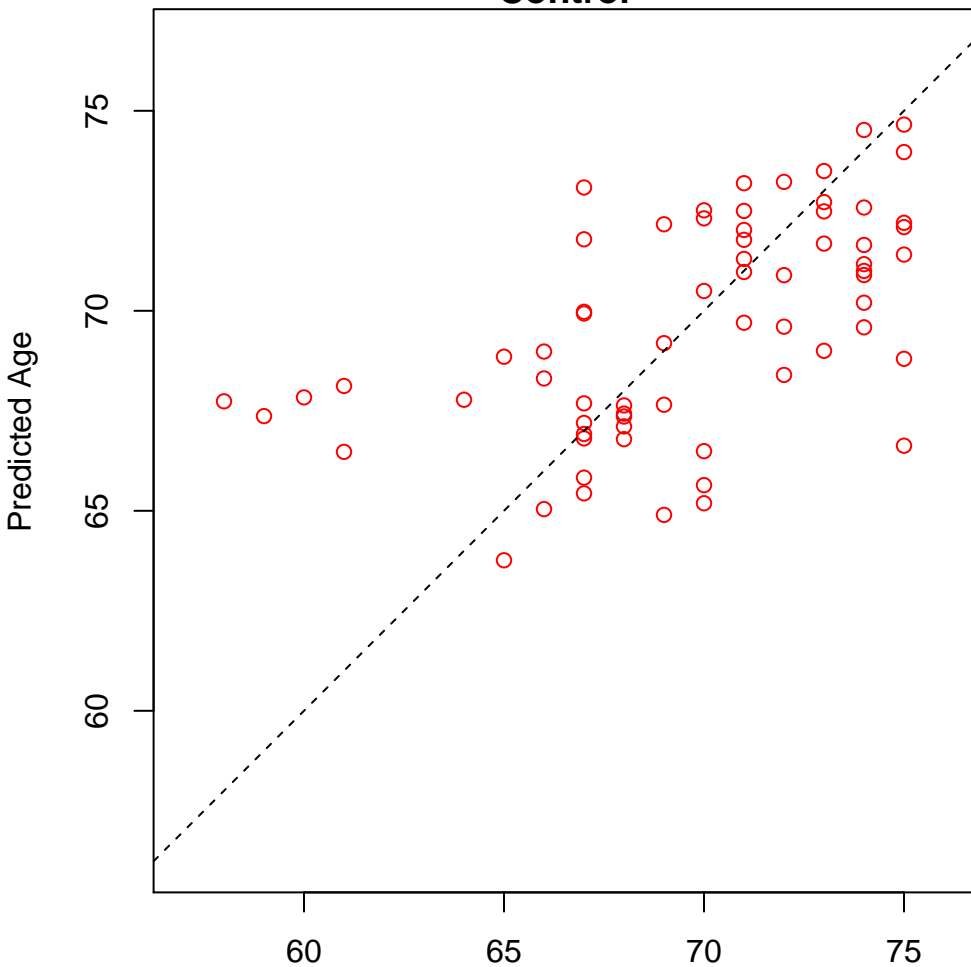
positive regulation of double-strand break repair (Score: 0.956477)



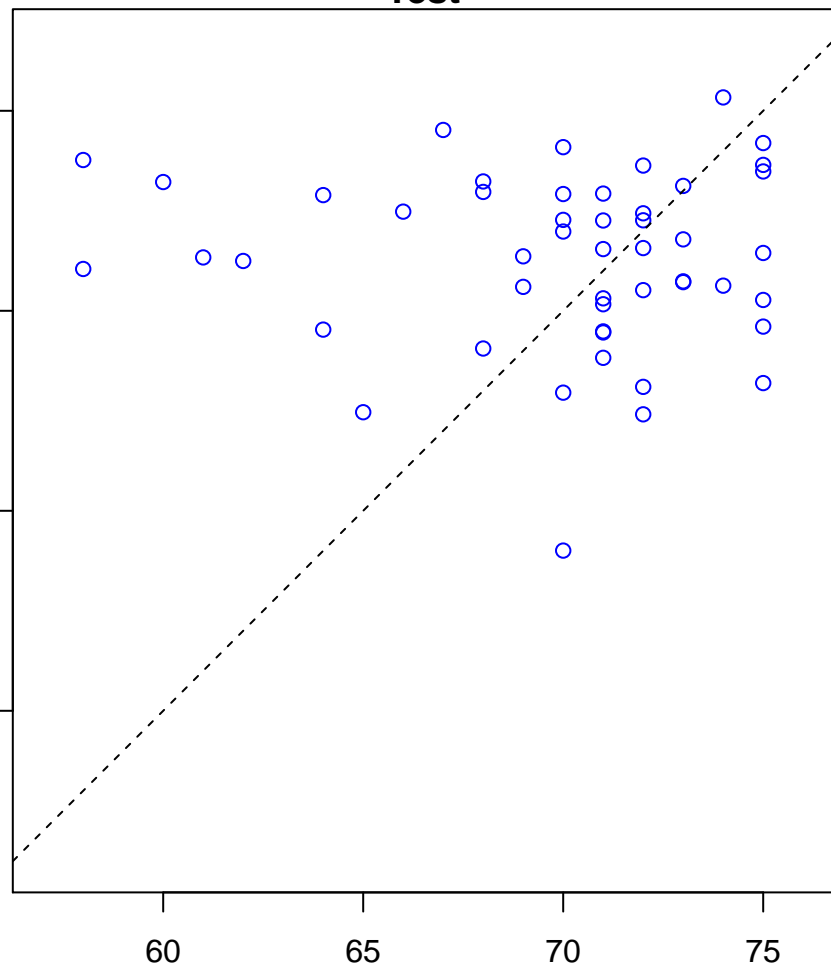
positive regulation of peptidyl–threonine phosphorylation (Score: 0.955733)



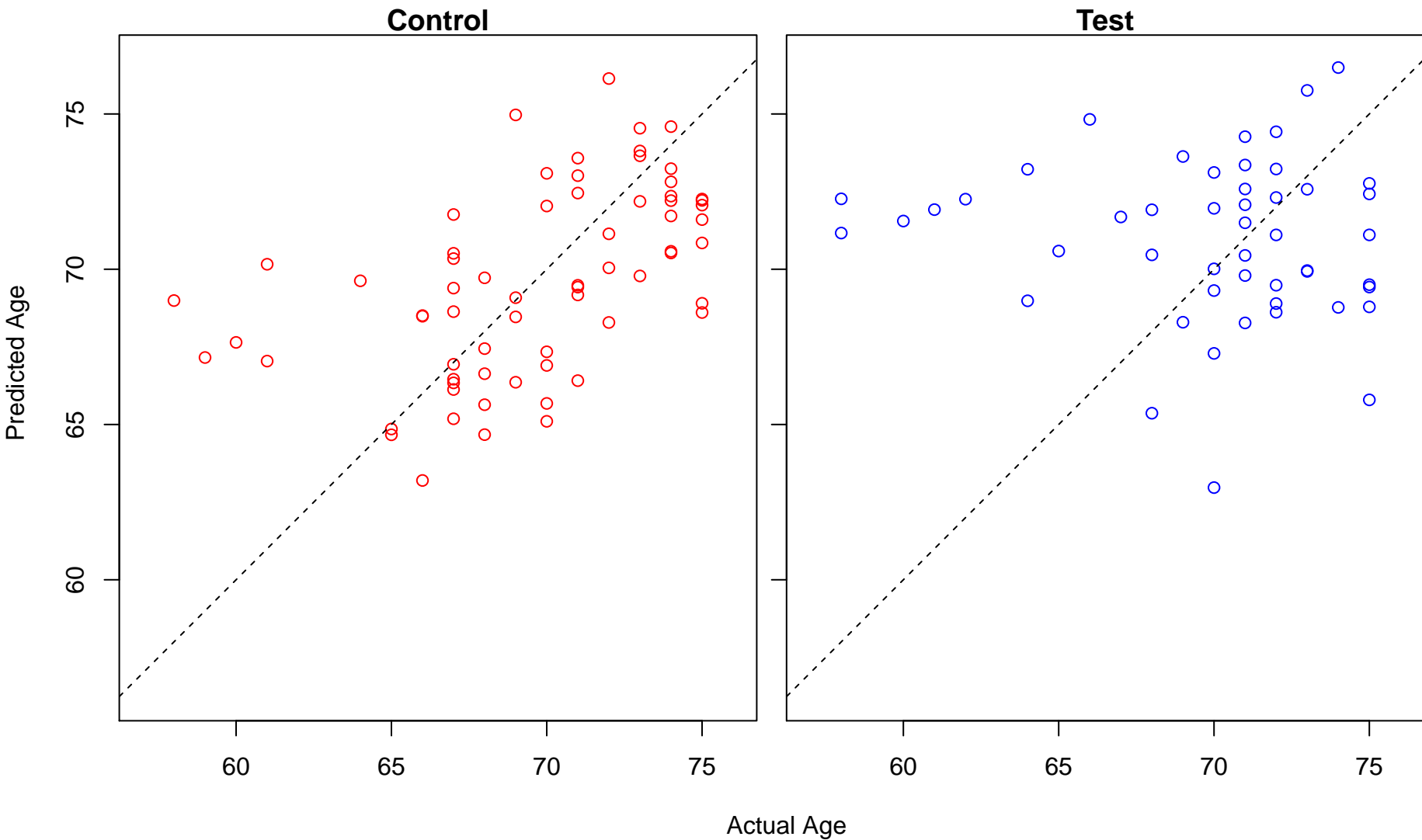
Control



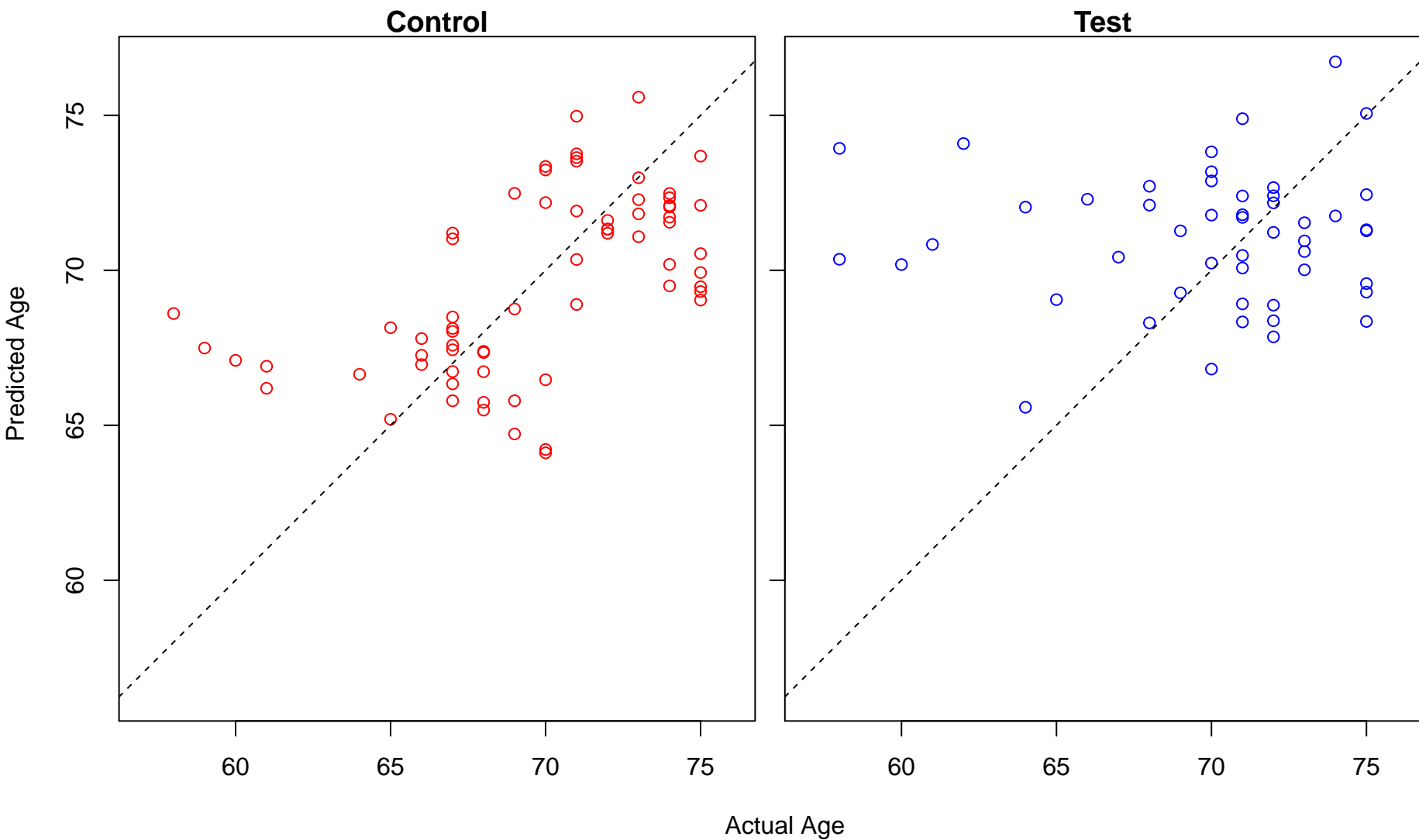
Test



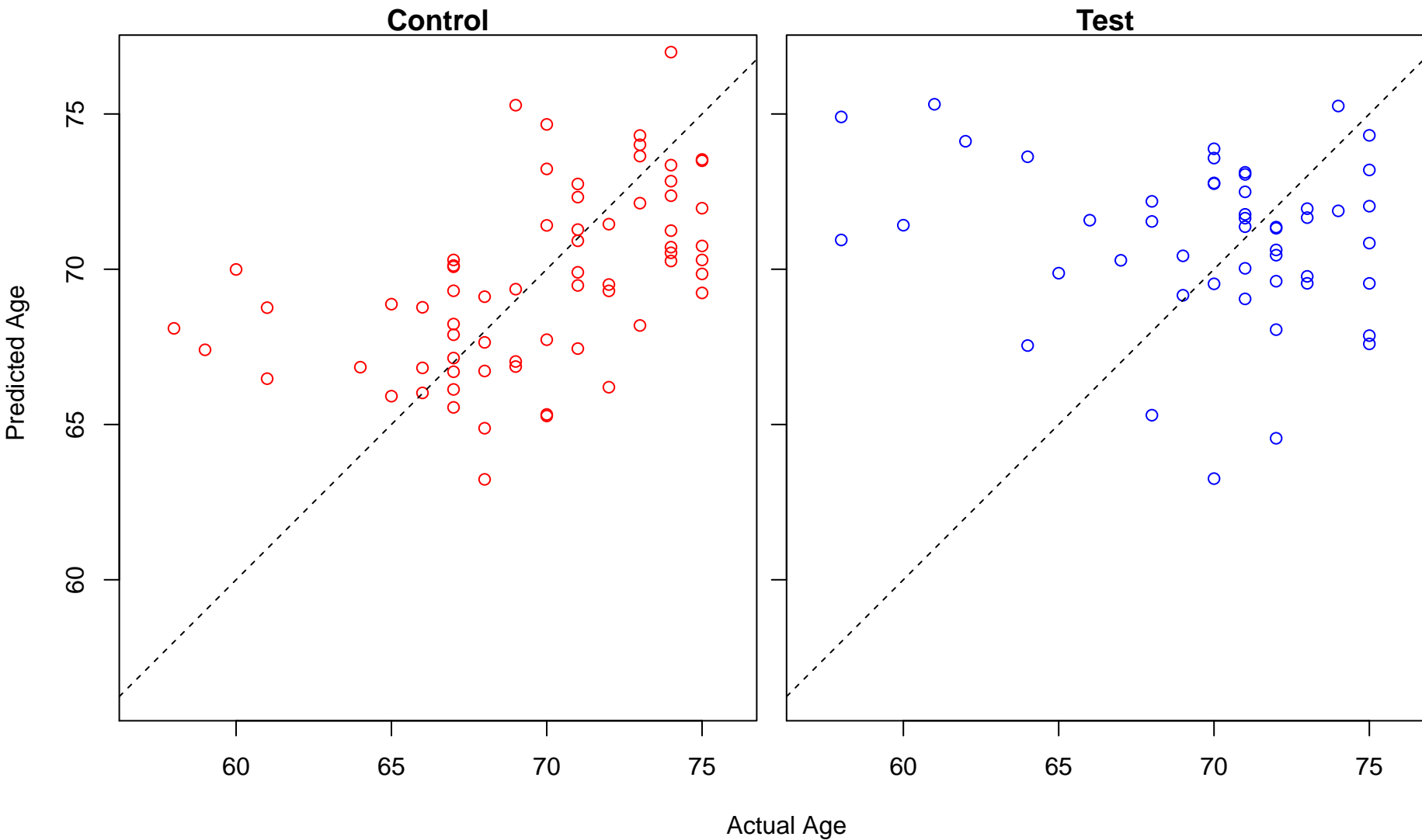
neutrophil activation (Score: 0.955320)



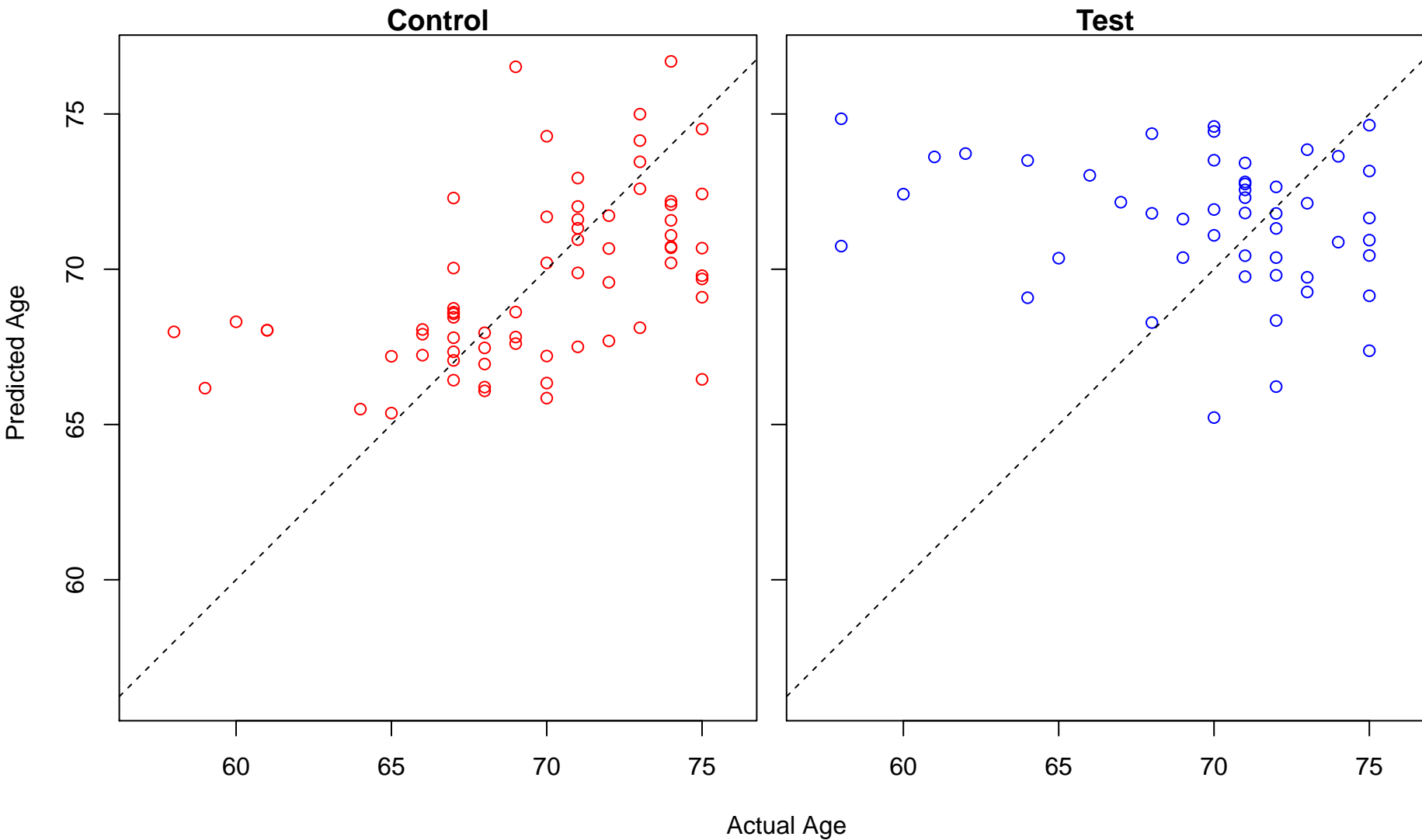
positive regulation of cell development (Score: 0.955109)



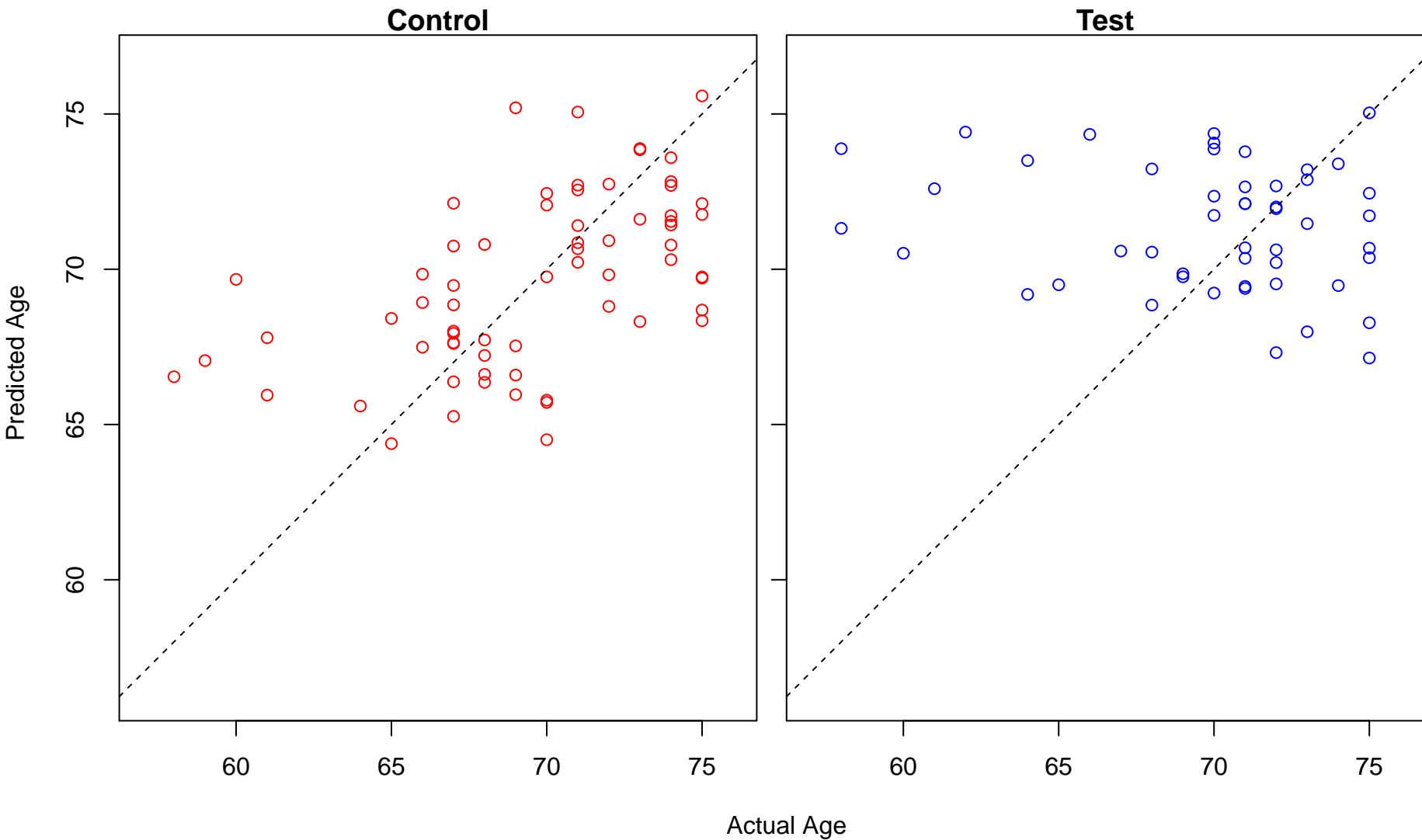
negative regulation of ion transport (Score: 0.955011)



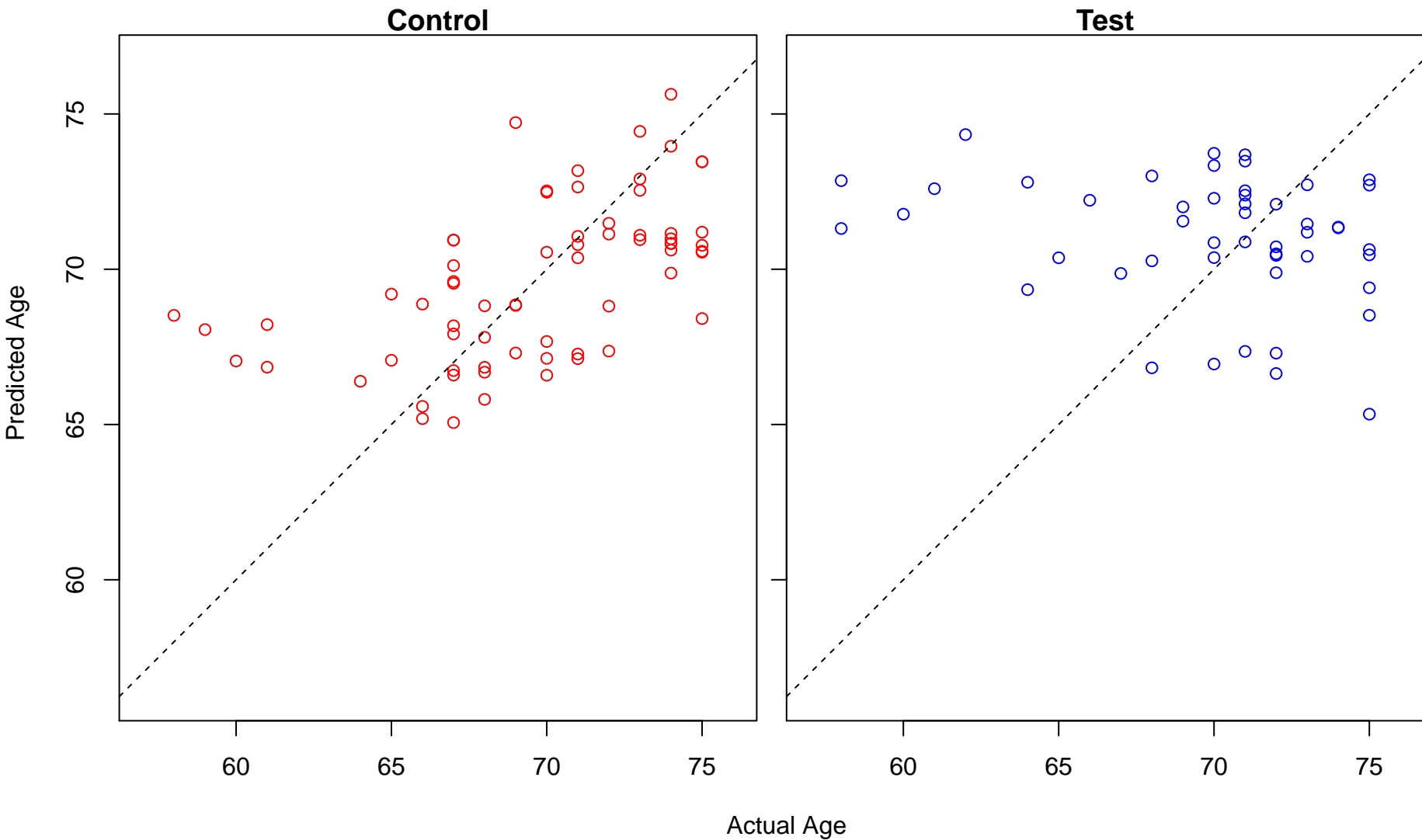
regulation of plasma membrane organization (Score: 0.954895)



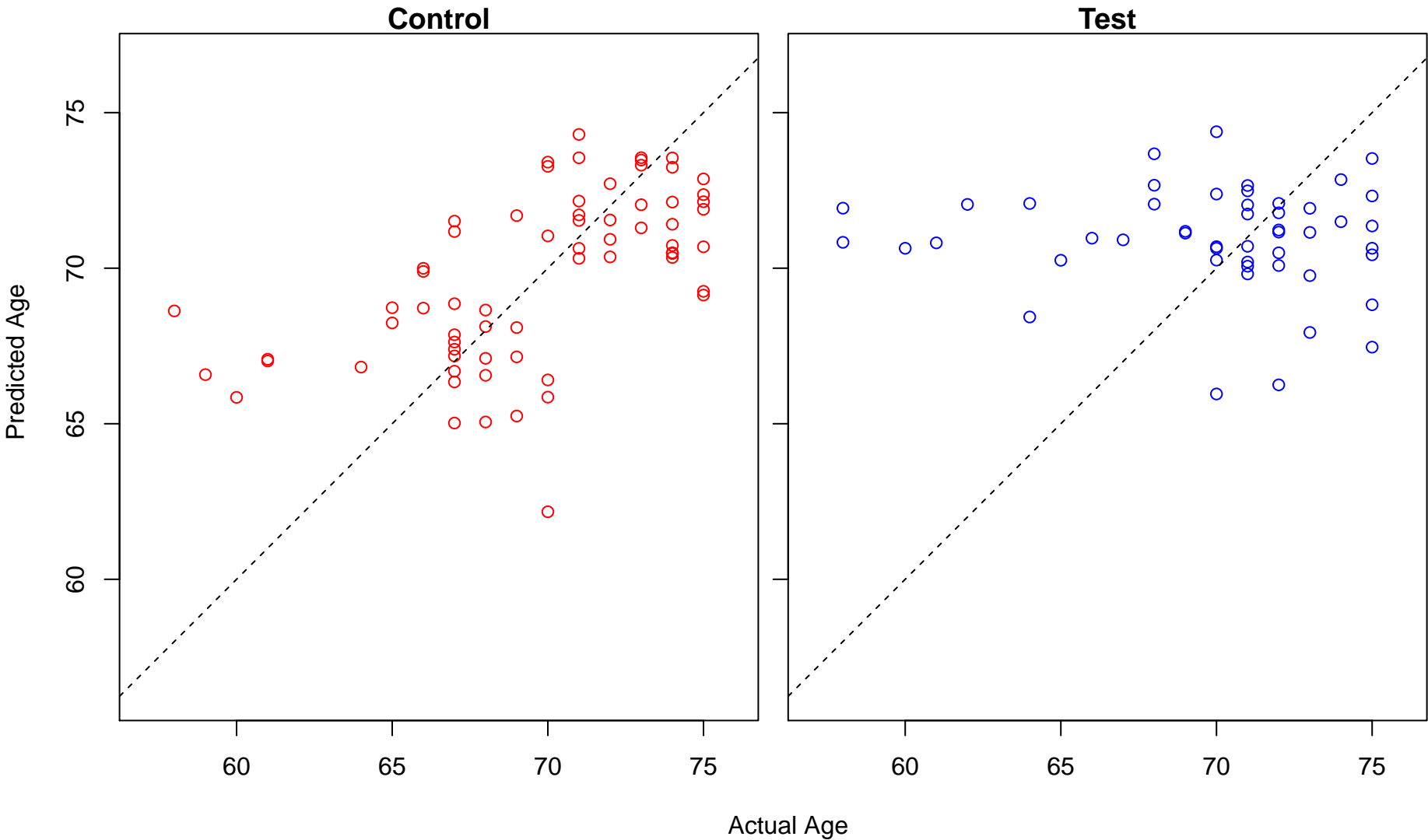
hyaluronan catabolic process (Score: 0.953999)



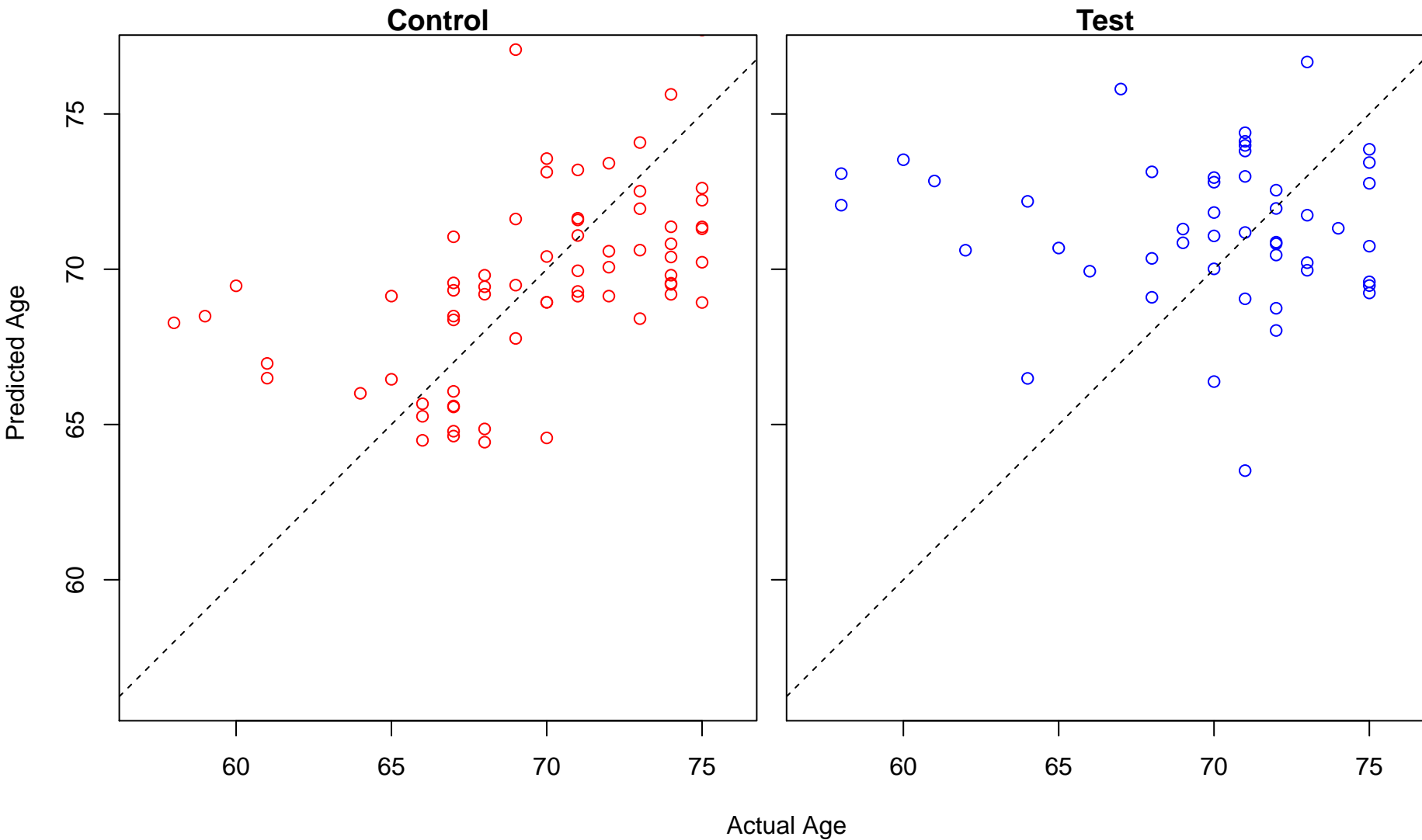
developmental growth involved in morphogenesis (Score: 0.953910)



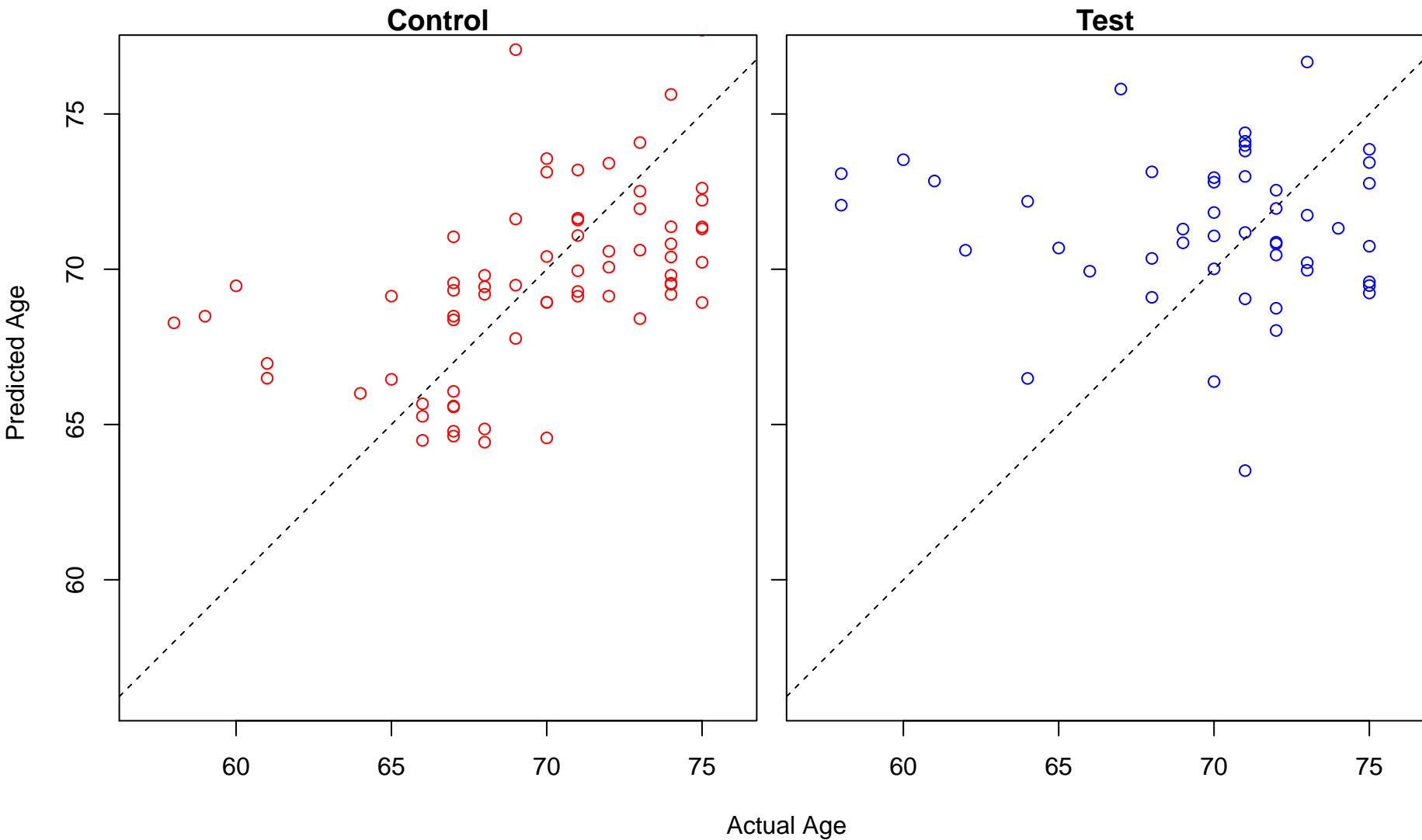
positive regulation of DNA damage response, signal transduction by p53 class mediator (Score: 0.953)



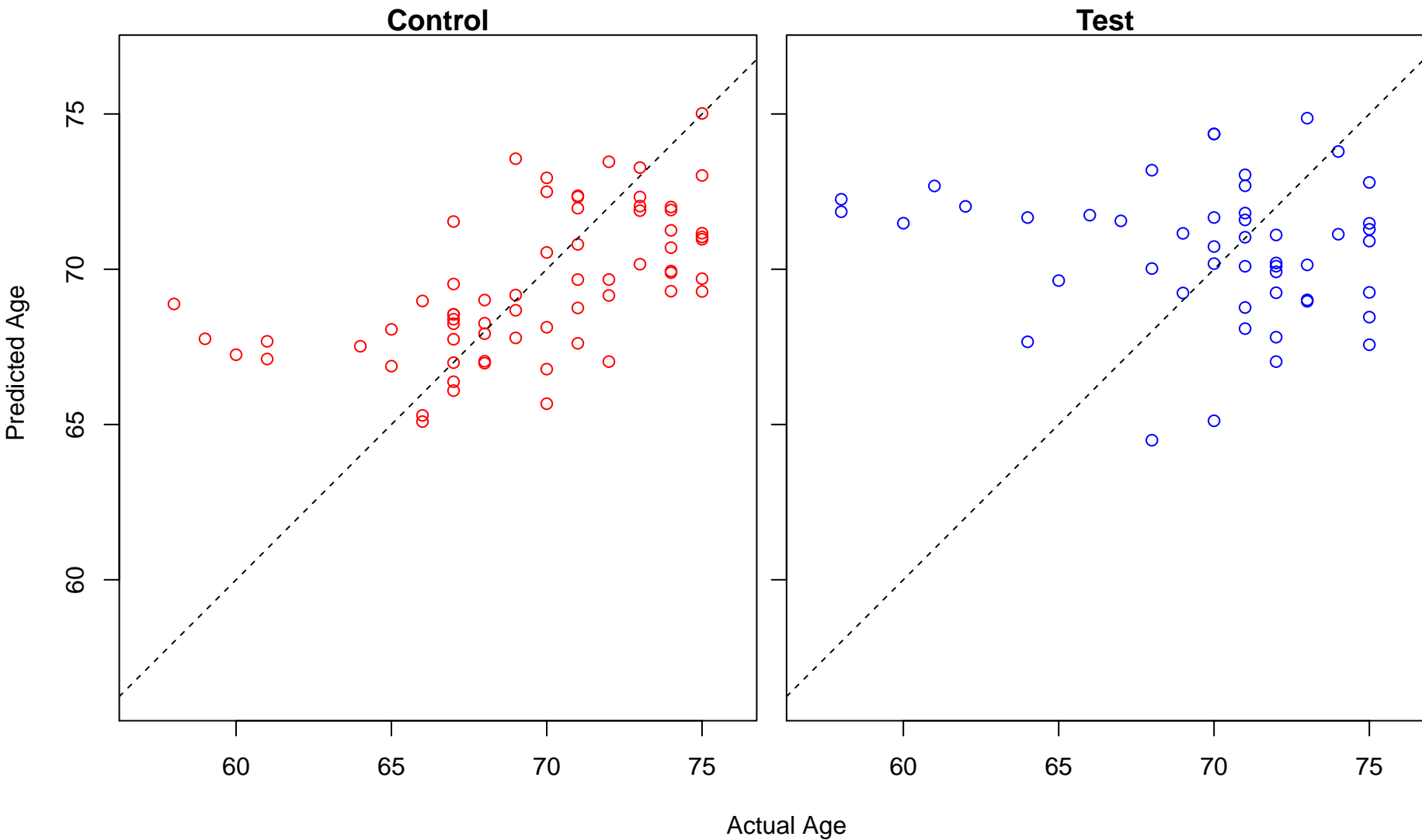
purine ribonucleoside bisphosphate metabolic process (Score: 0.953589)



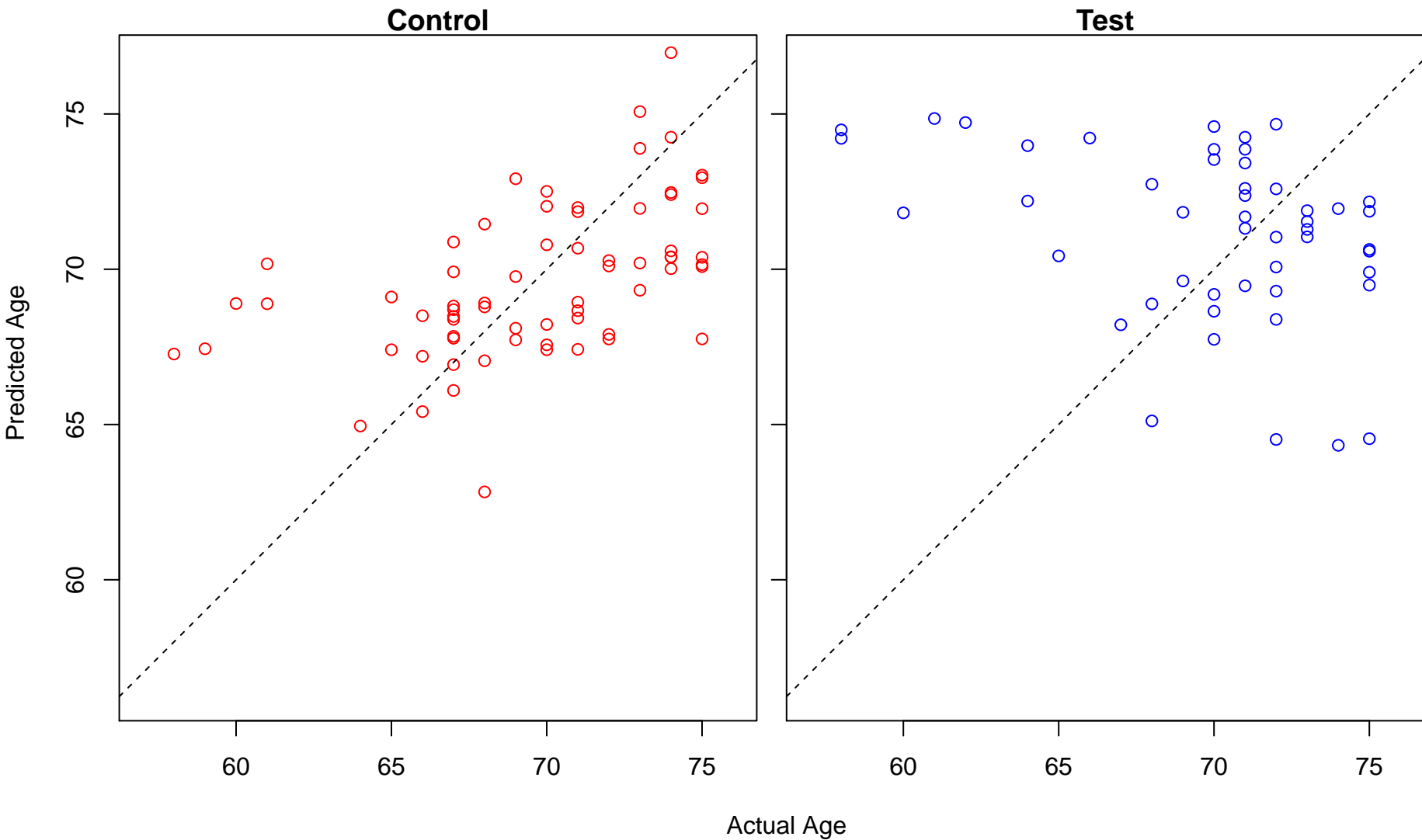
3'-phosphoadenosine 5'-phosphosulfate metabolic process (Score: 0.953589)



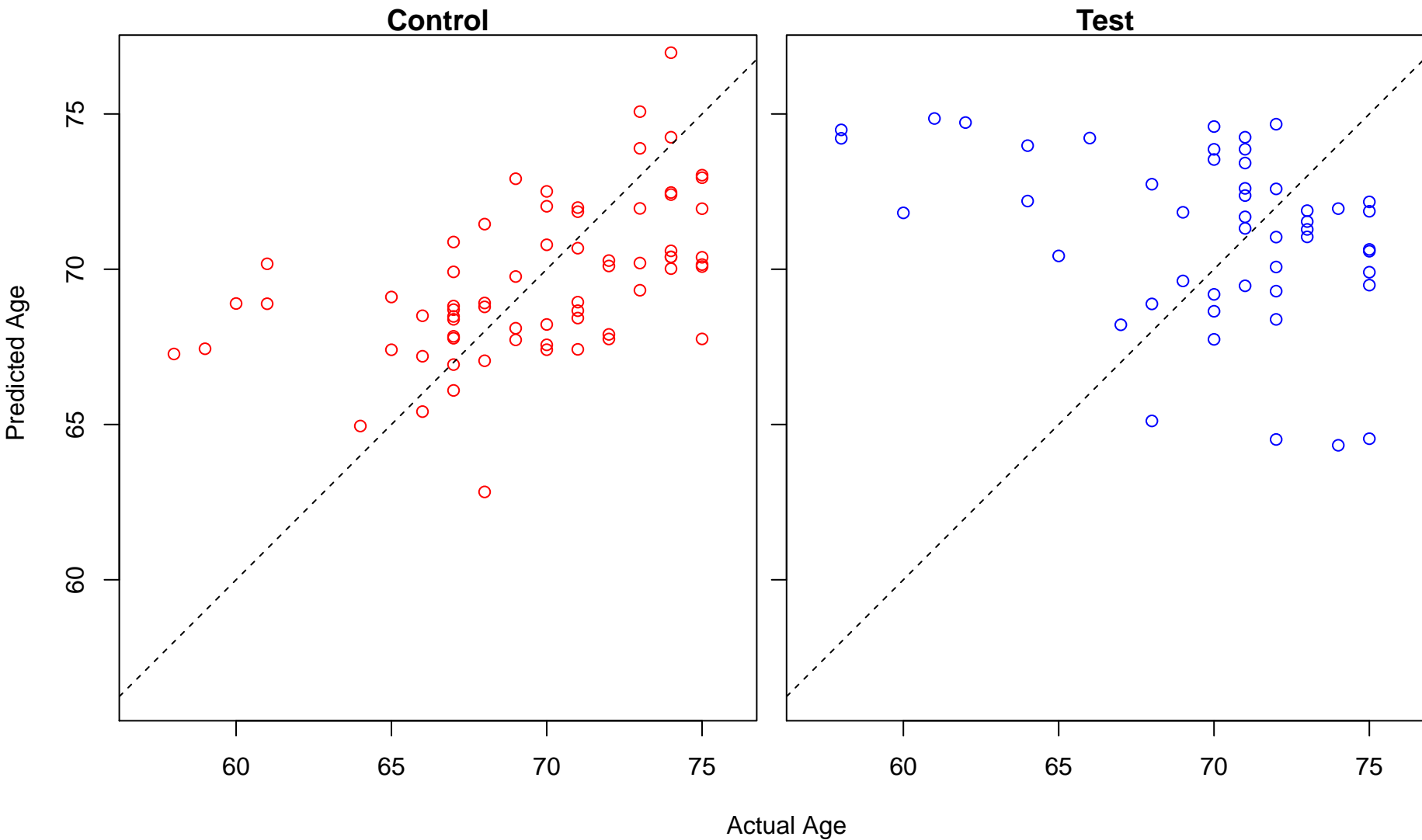
regulation of synapse structure or activity (Score: 0.953383)



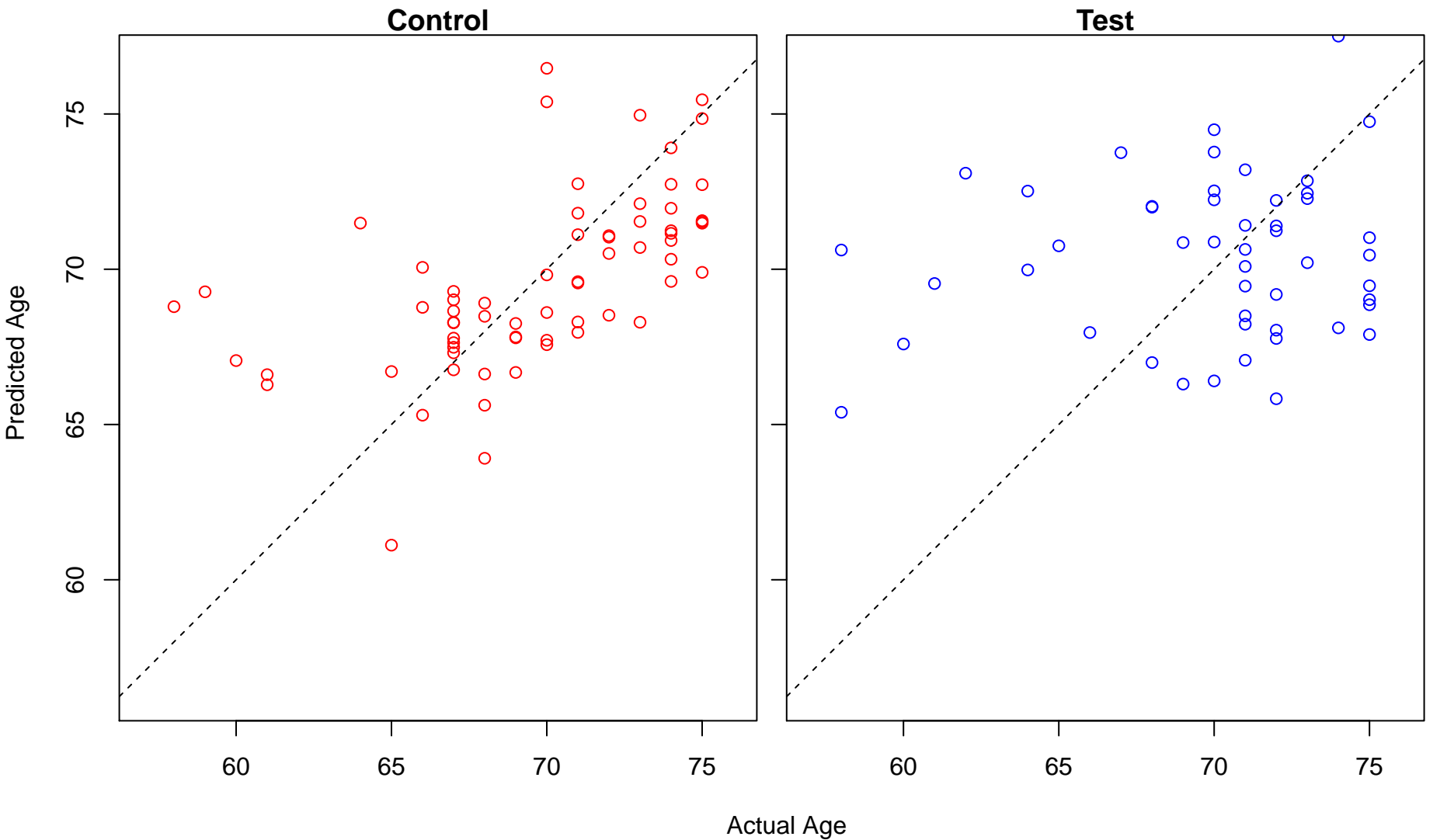
regulation of protein localization to early endosome (Score: 0.953120)



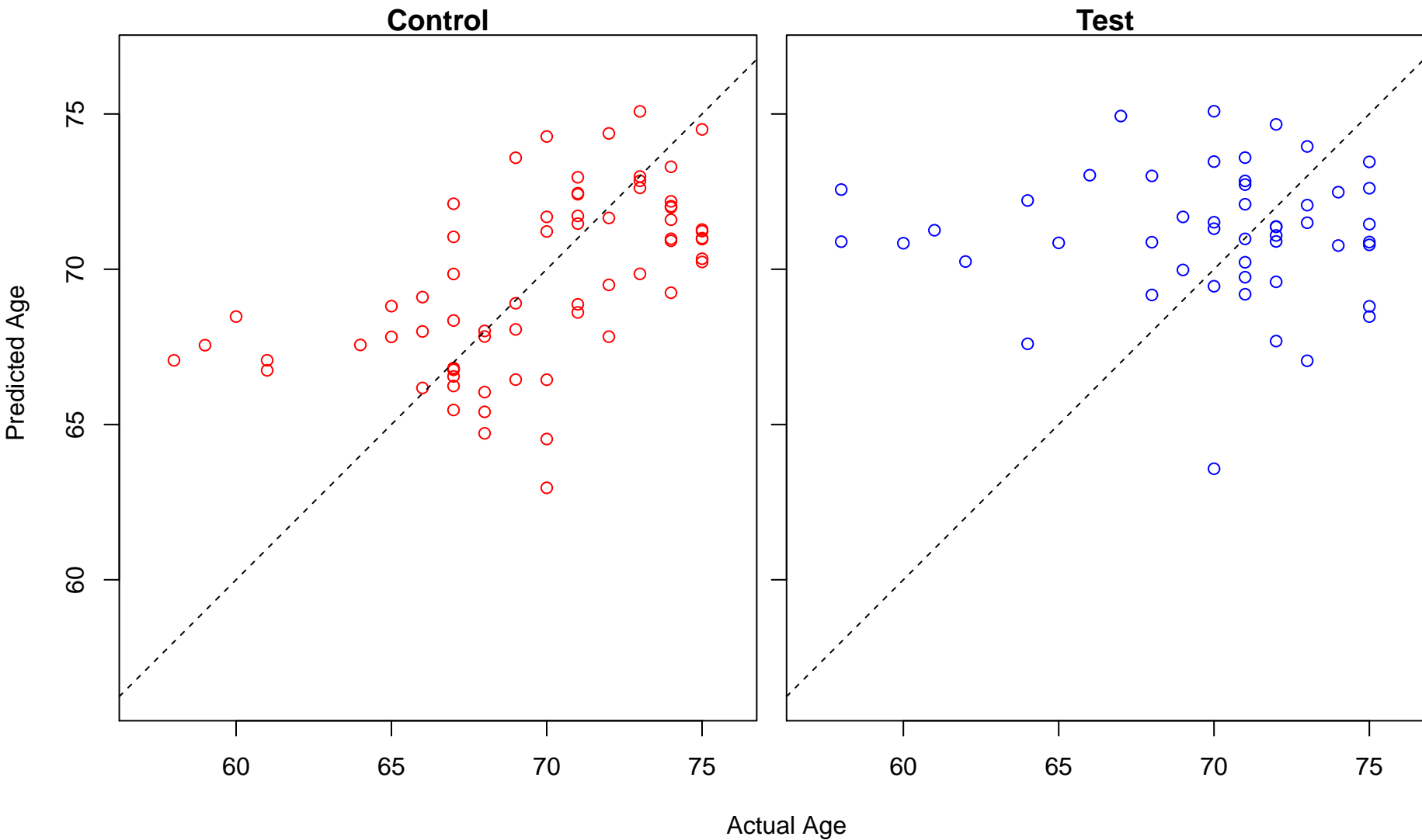
positive regulation of protein localization to early endosome (Score: 0.953120)



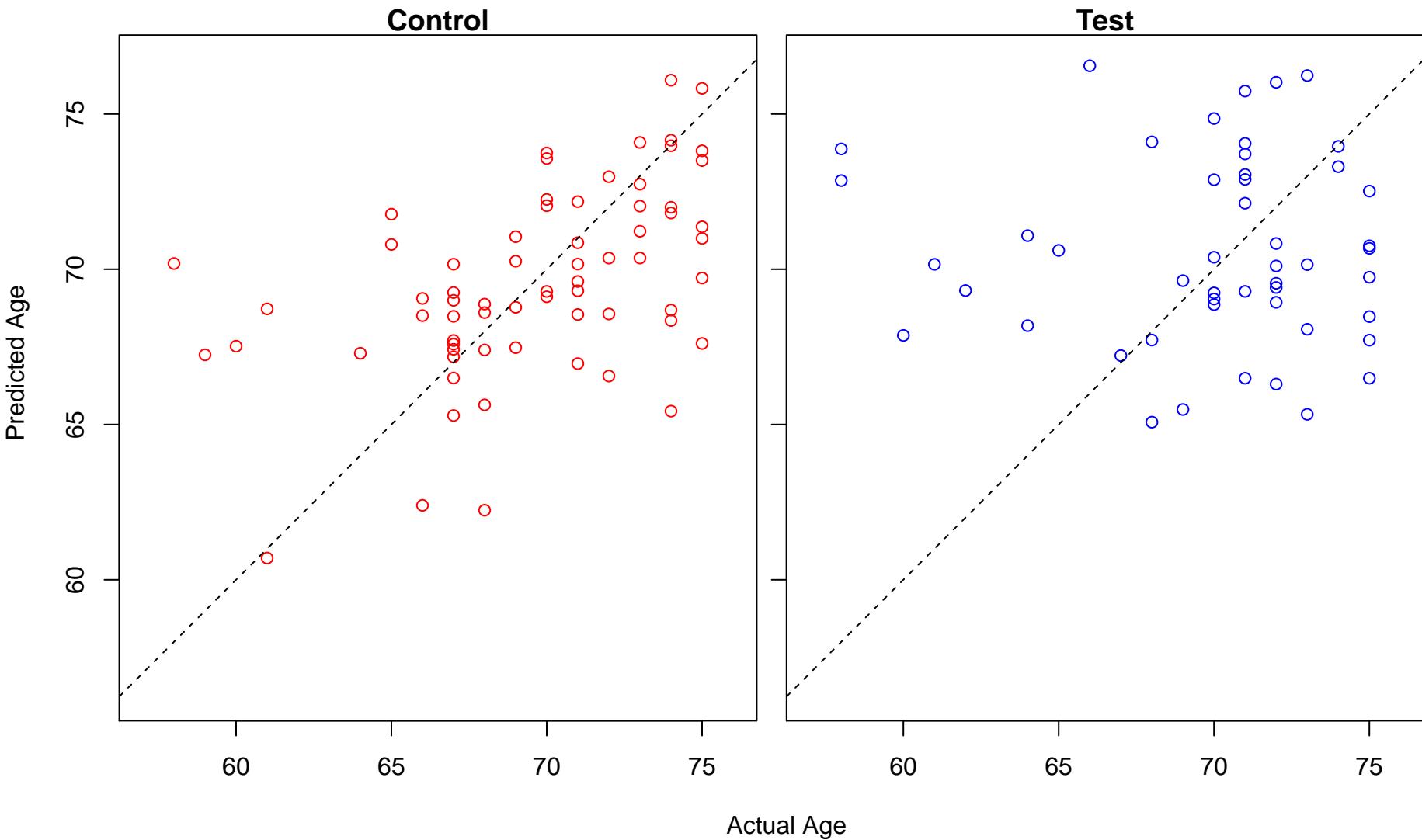
Positive regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter (Score



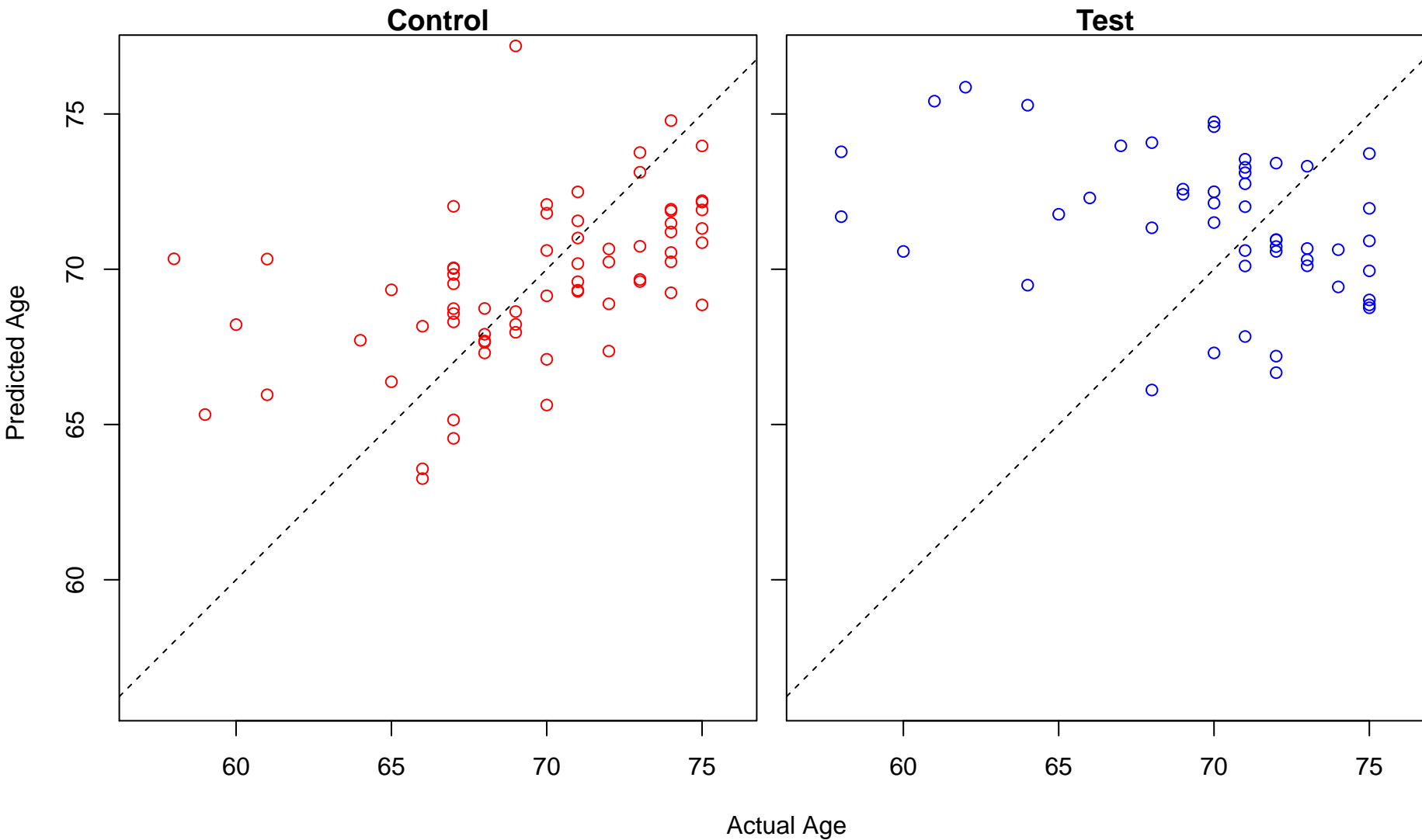
cell killing (Score: 0.952781)



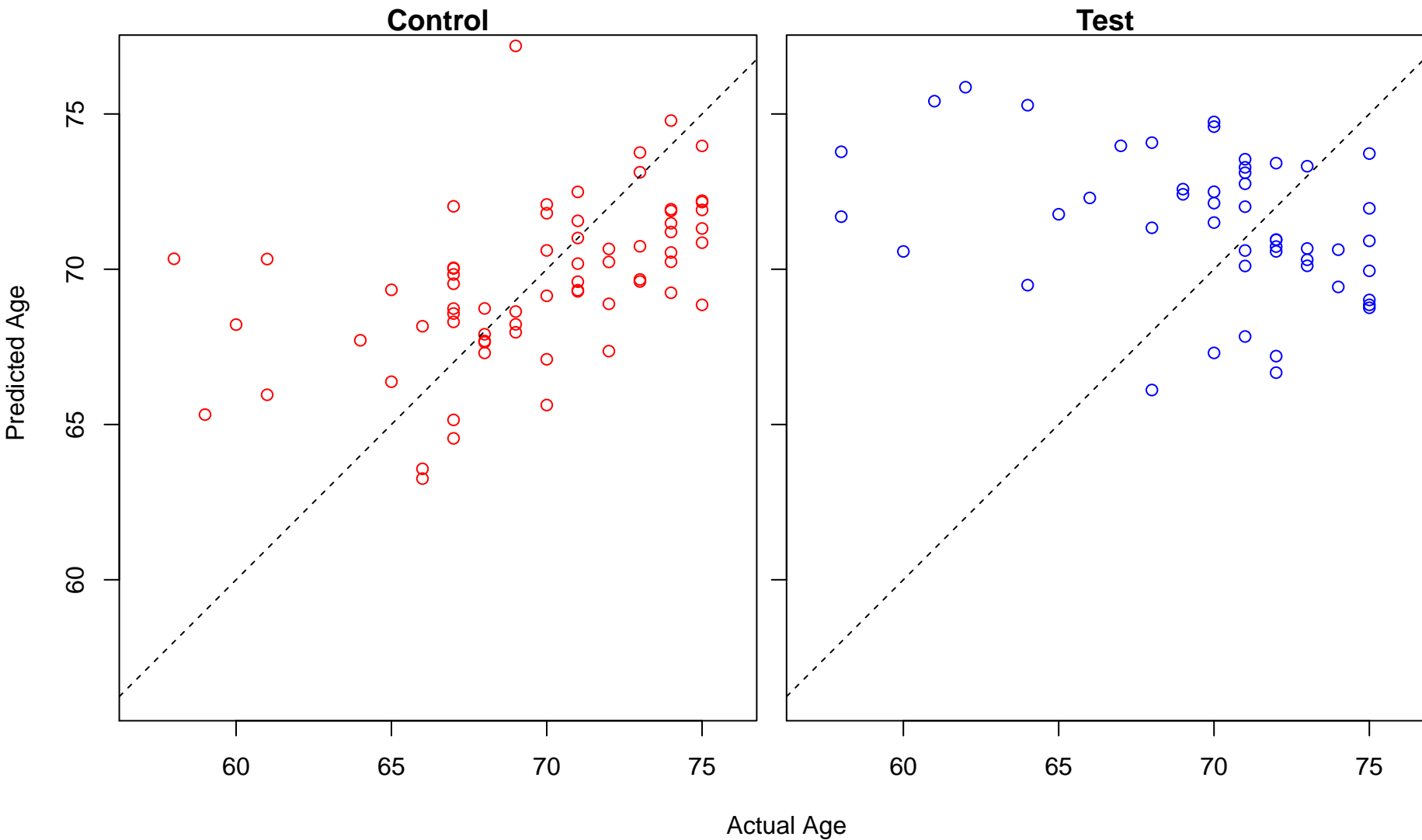
protein homotrimerization (Score: 0.952753)



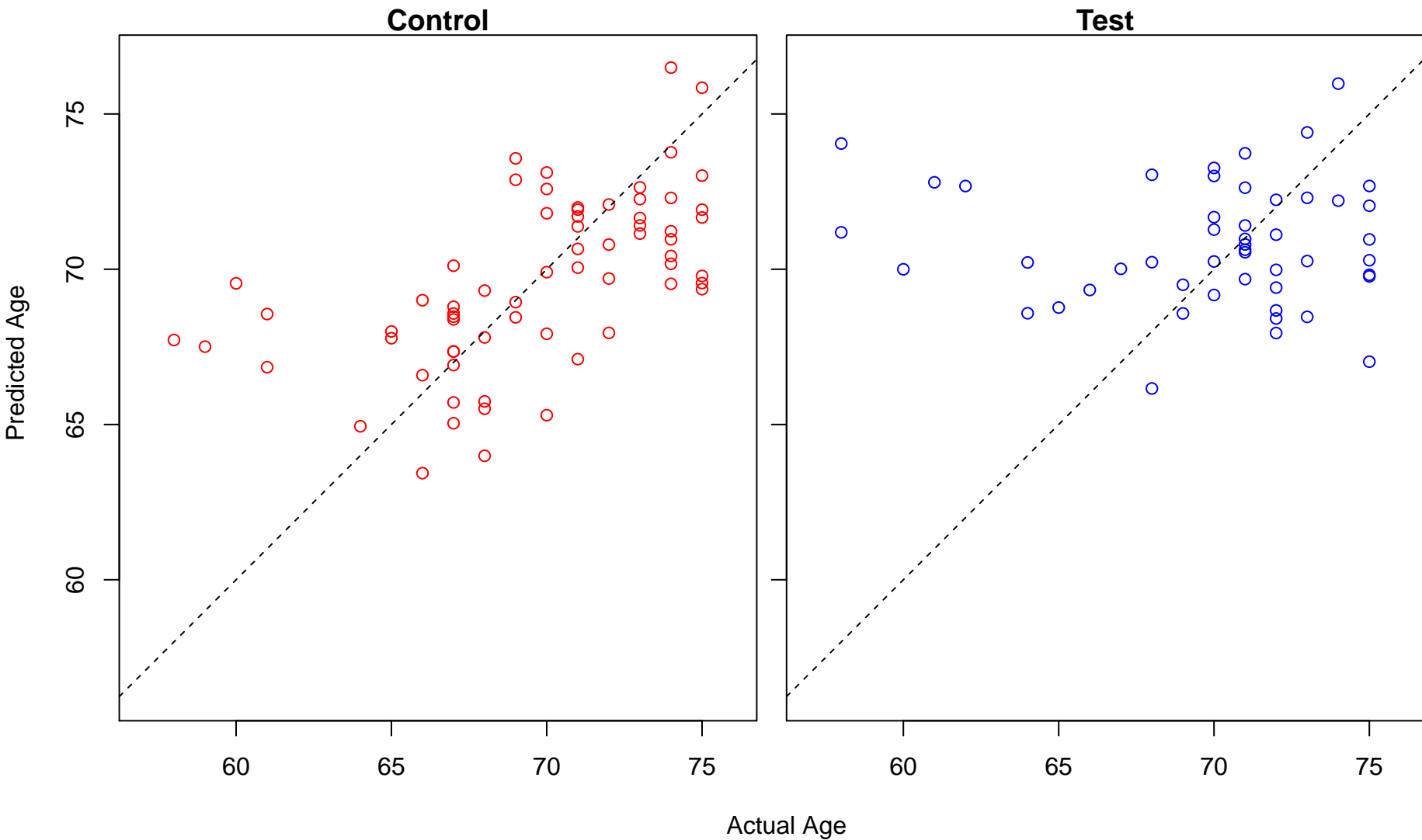
negative regulation of protein processing (Score: 0.952340)



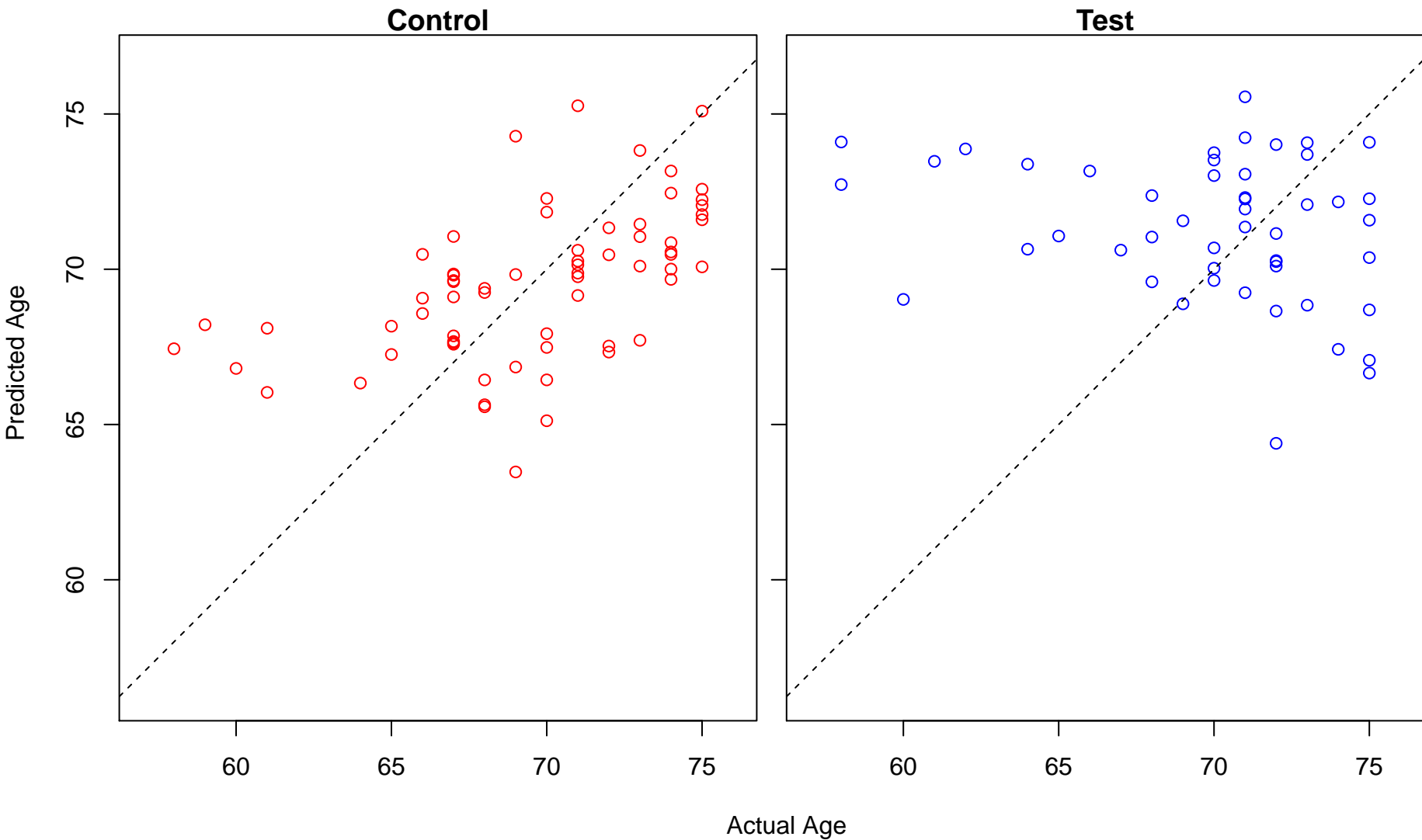
negative regulation of protein maturation (Score: 0.952340)



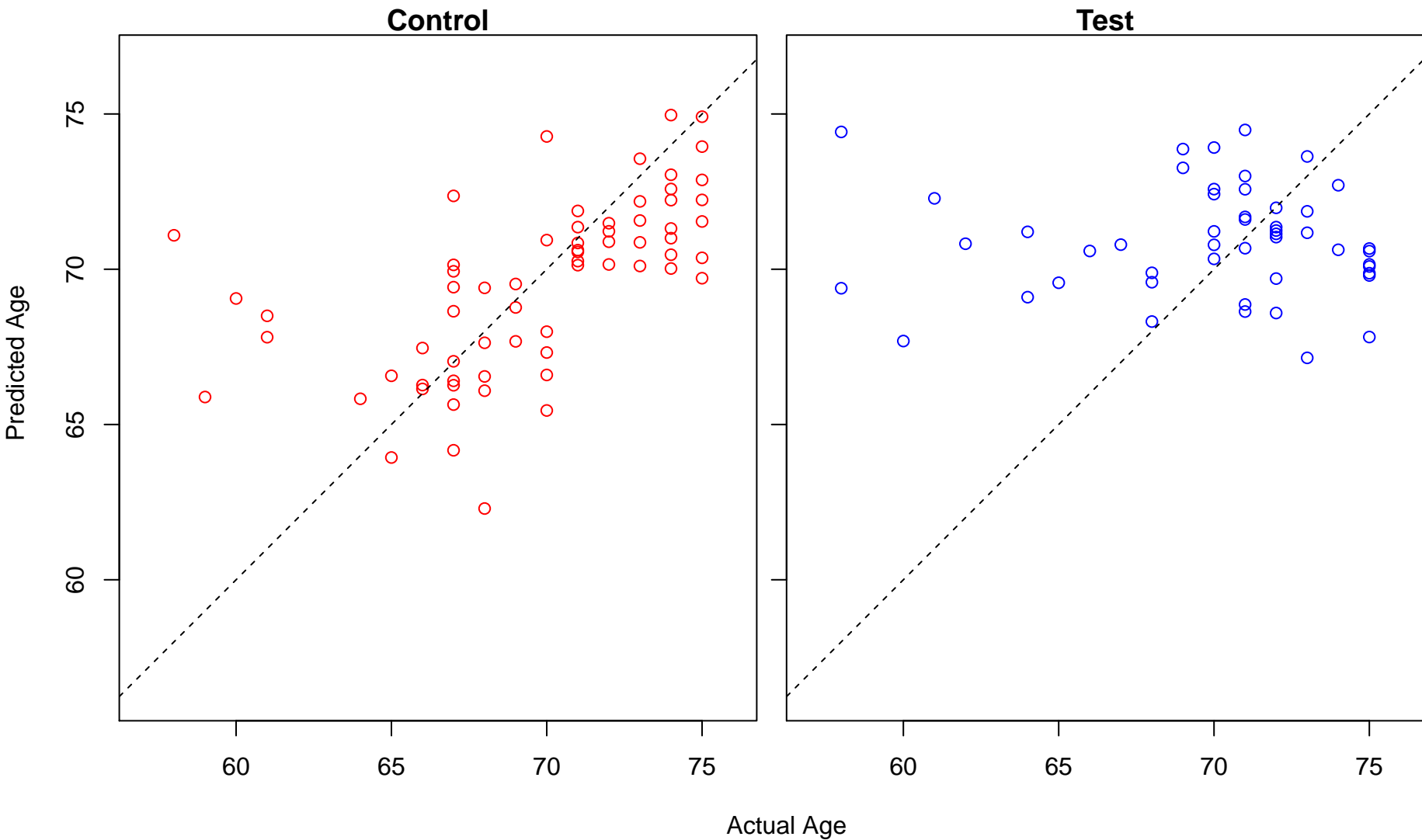
regulation of myoblast fusion (Score: 0.952088)



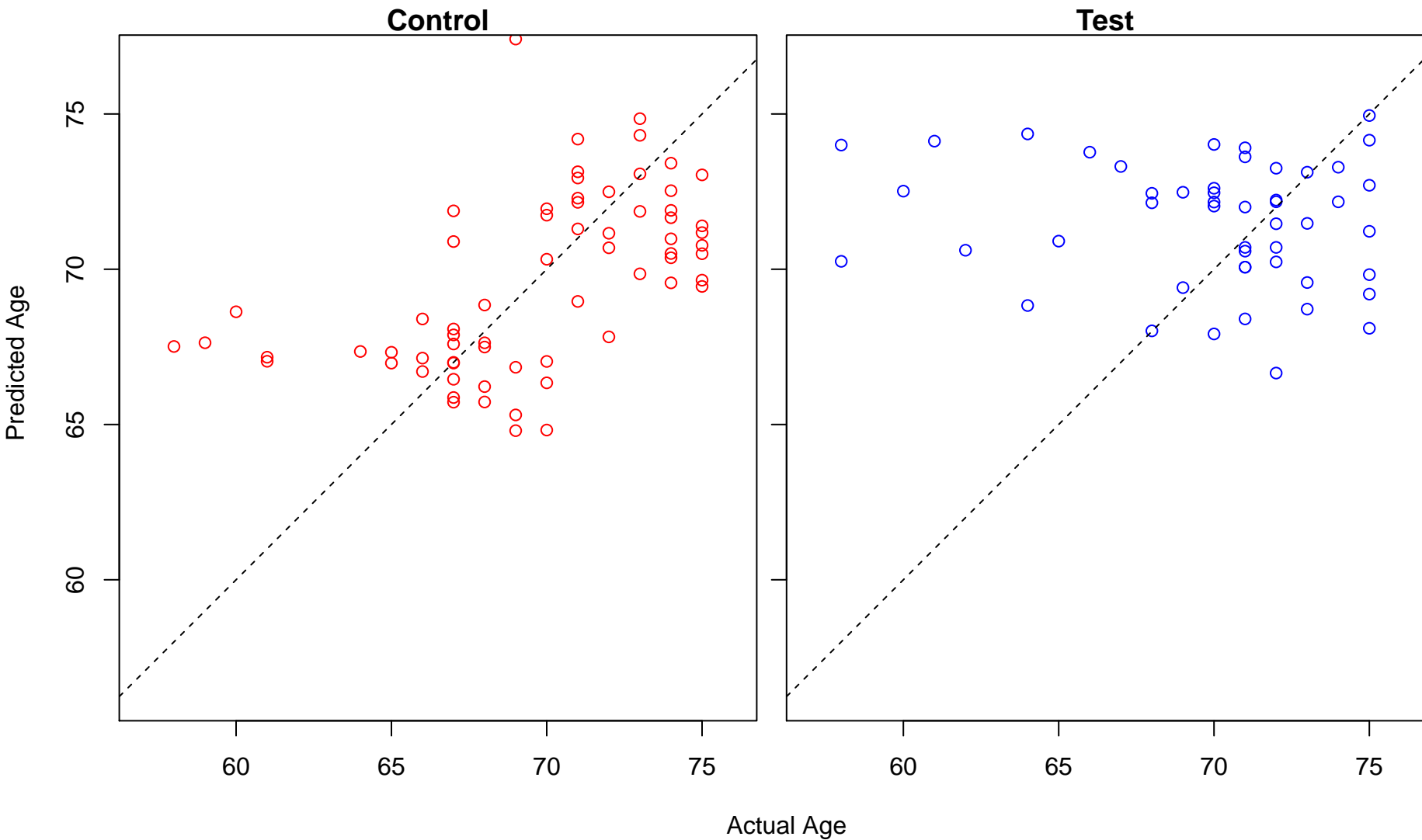
histone H3-K36 methylation (Score: 0.951378)



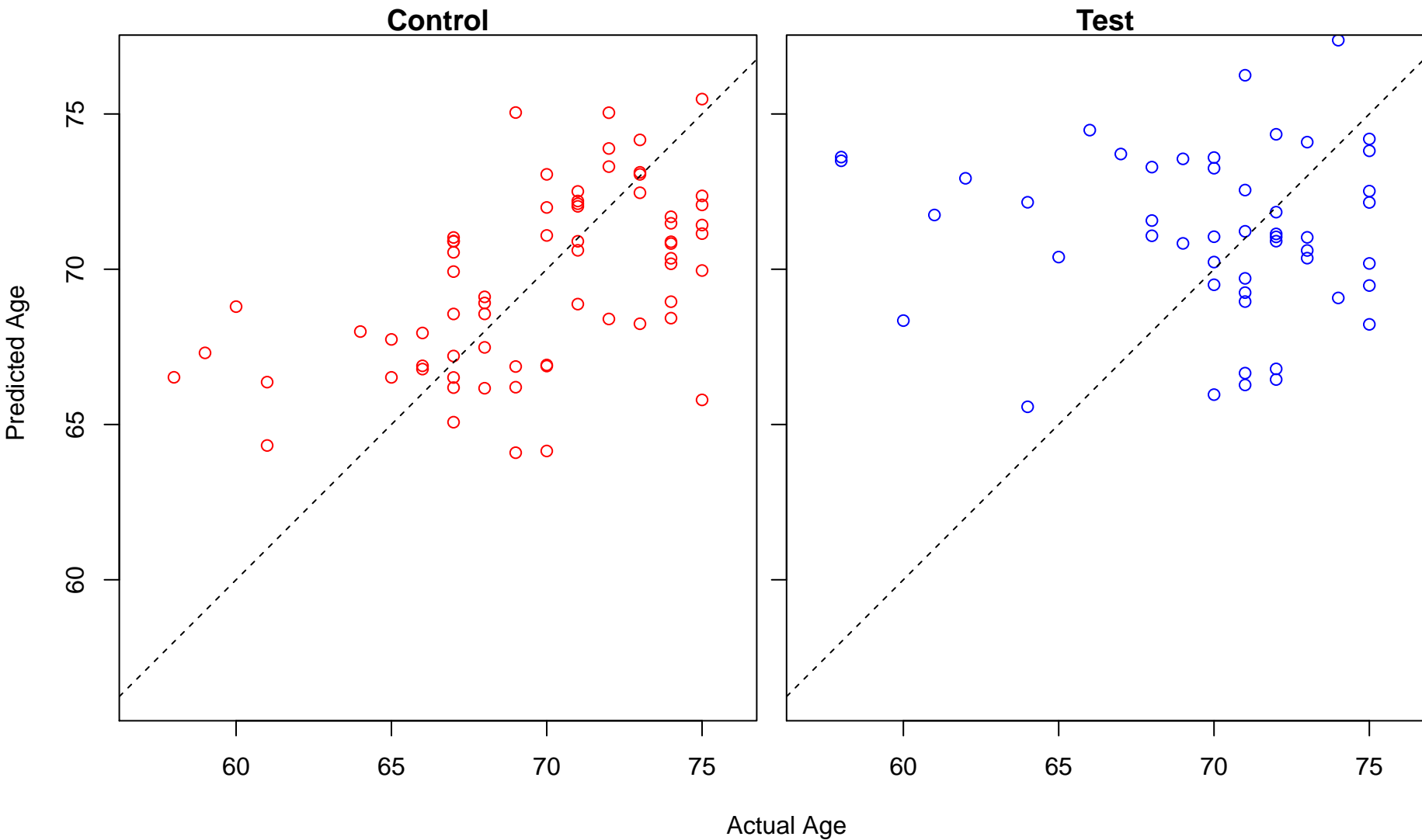
antigen processing and presentation of endogenous peptide antigen (Score: 0.951347)



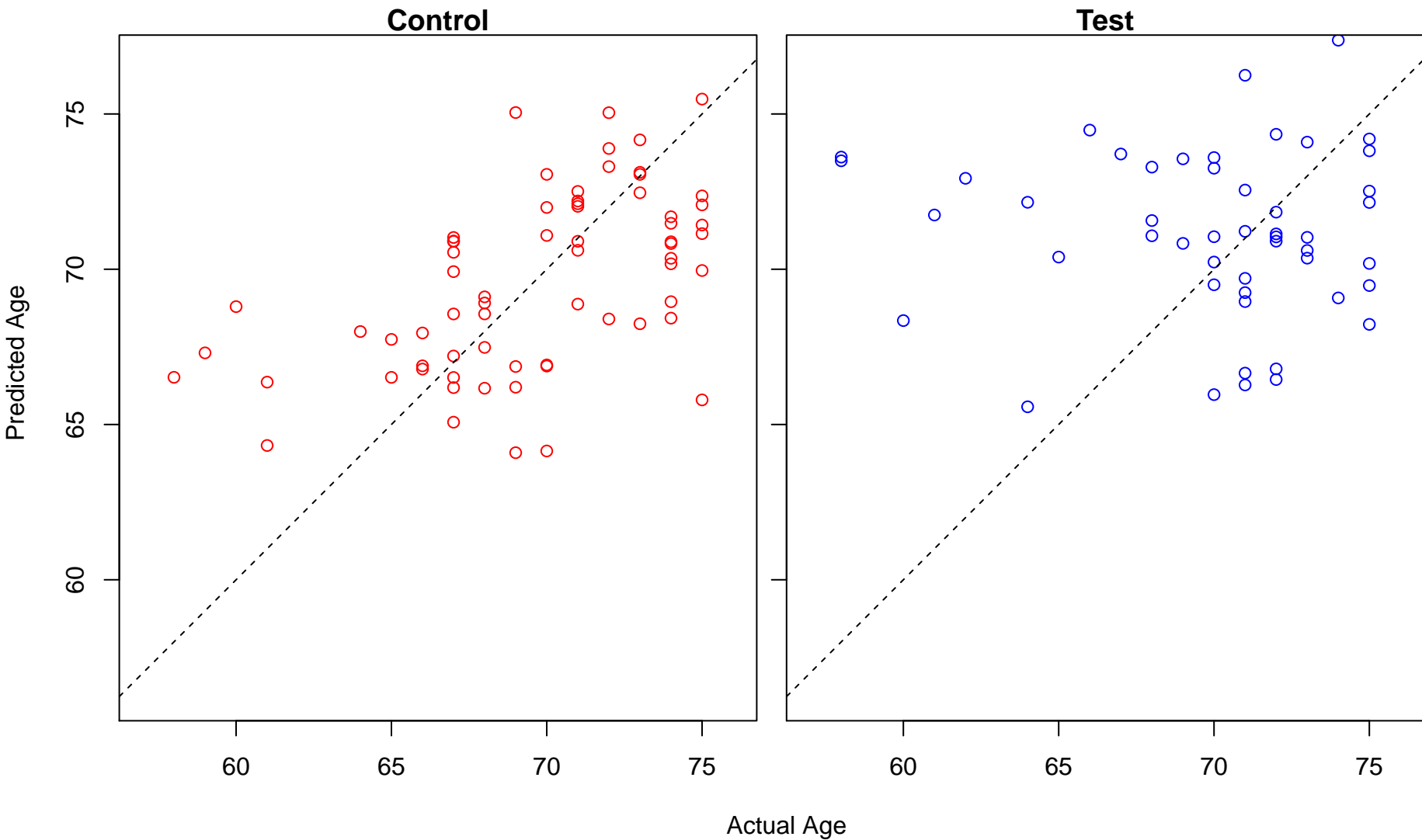
negative regulation of transcription factor import into nucleus (Score: 0.951307)



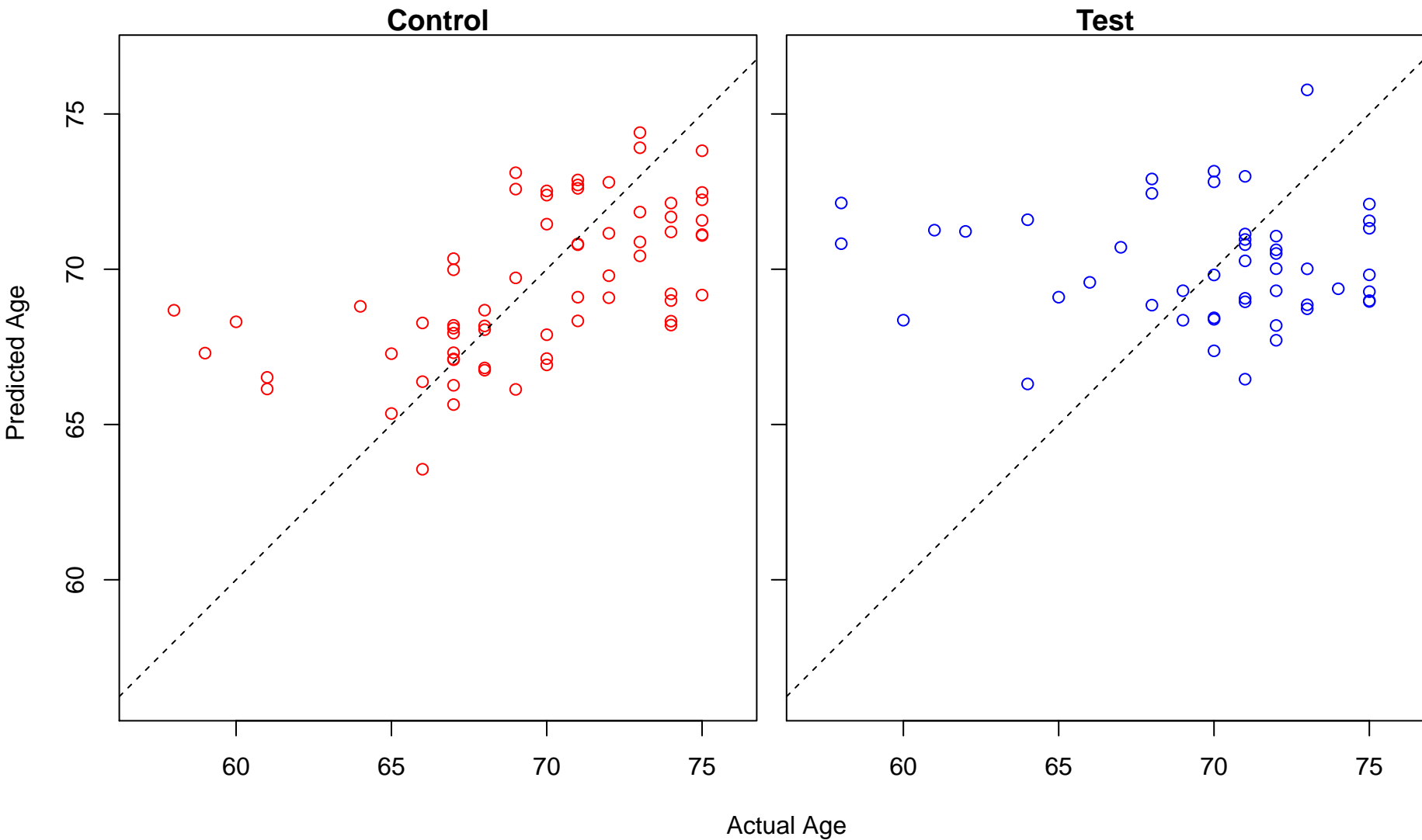
DNA alkylation (Score: 0.951001)



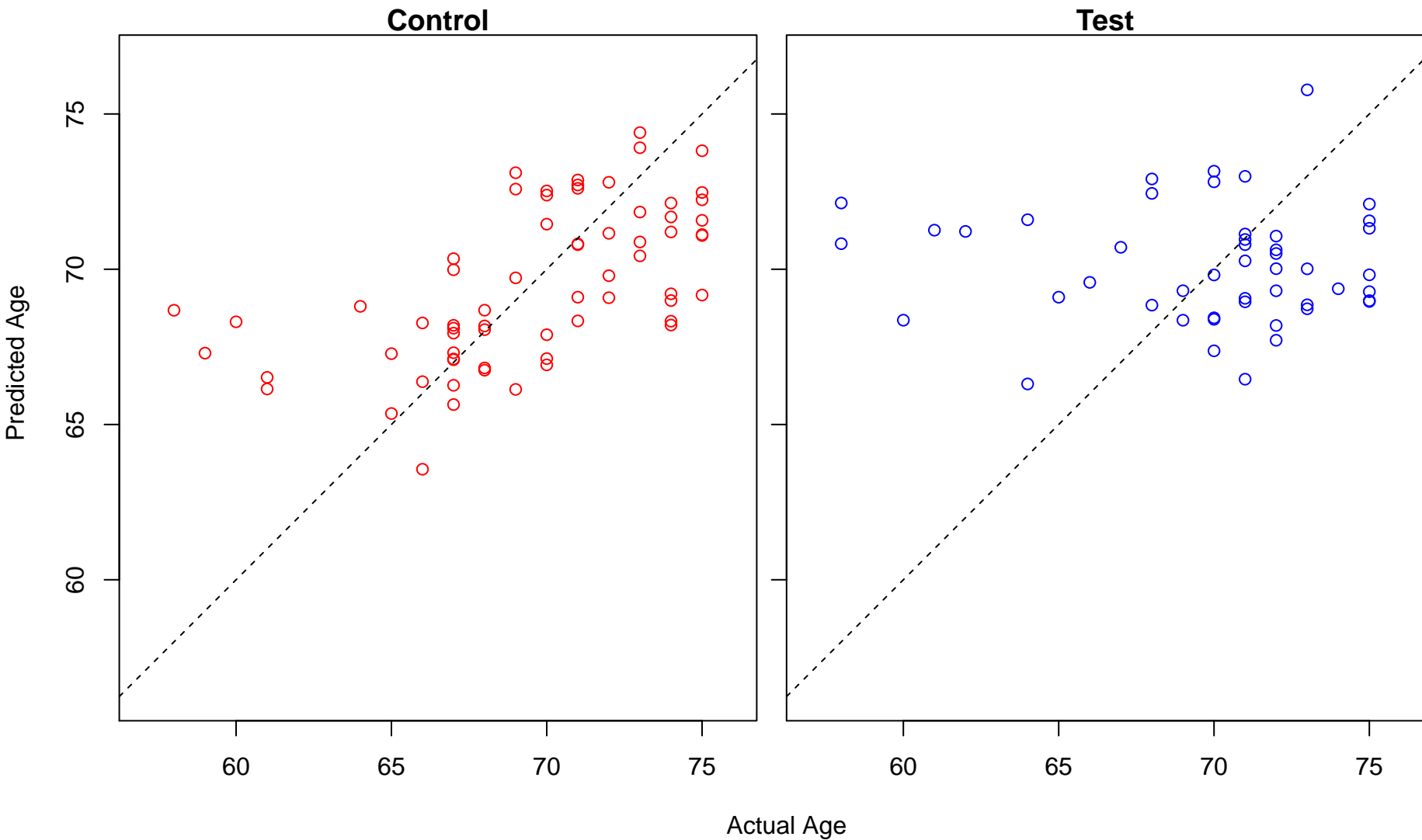
DNA methylation (Score: 0.951001)



protein targeting to peroxisome (Score: 0.950879)

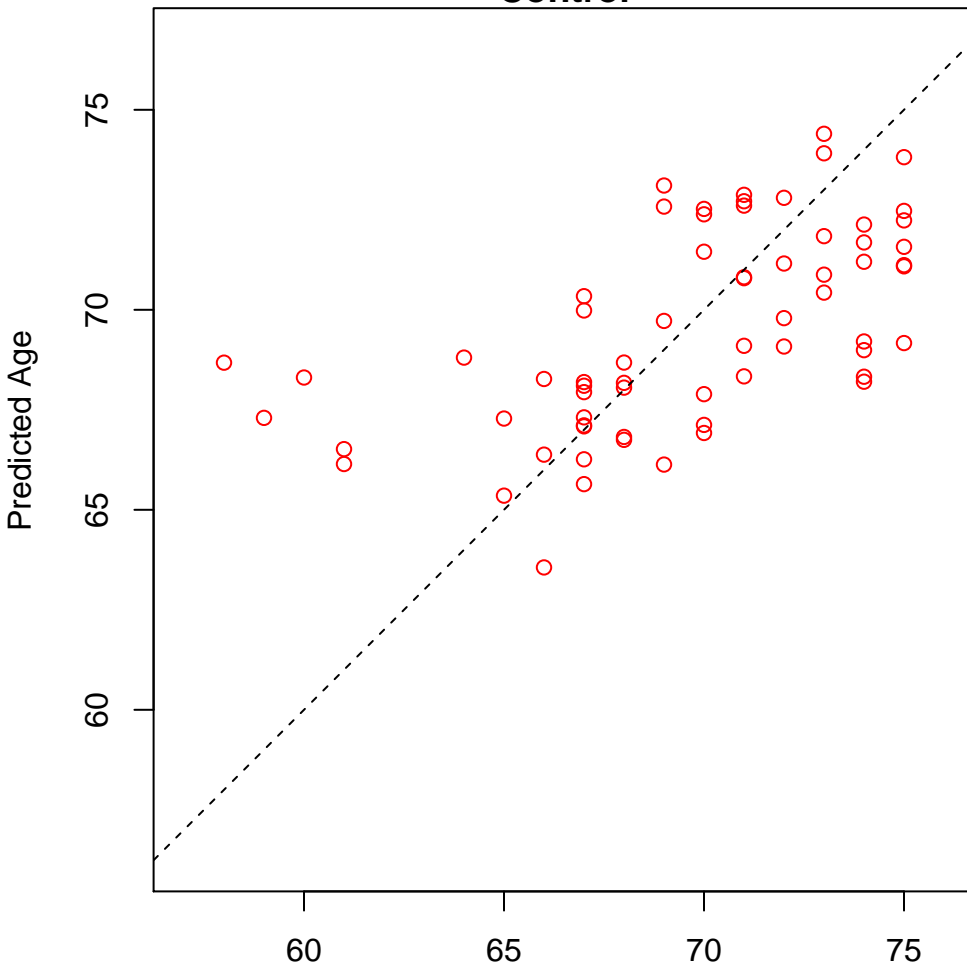


peroxisomal transport (Score: 0.950879)

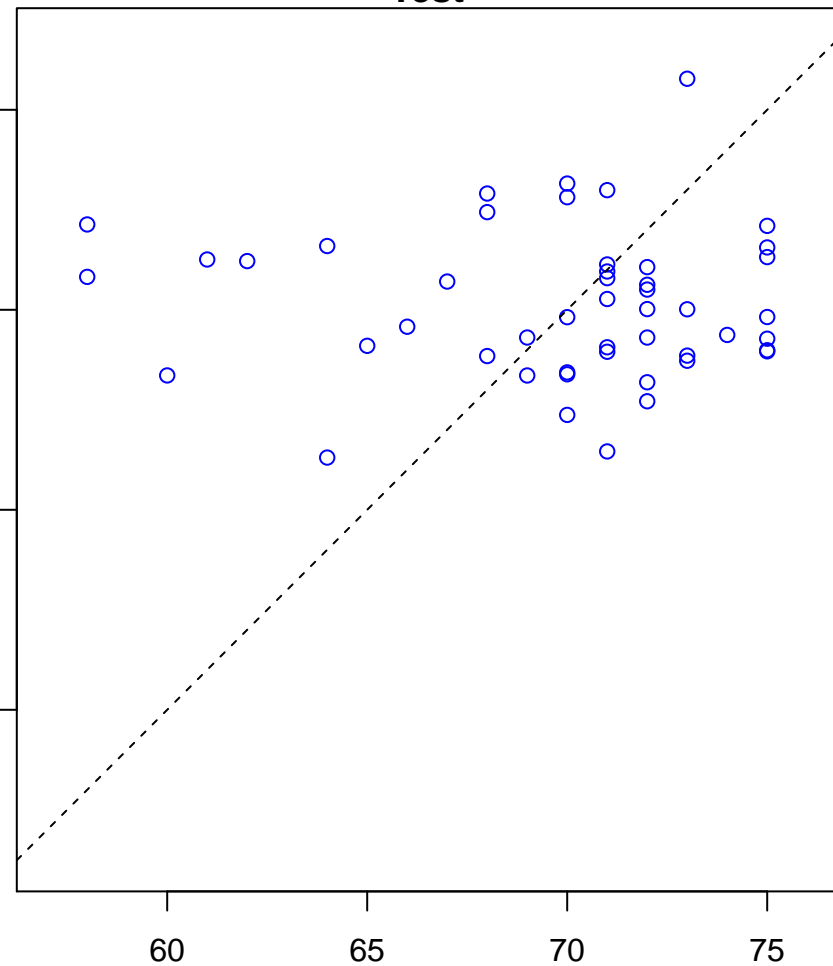


protein localization to peroxisome (Score: 0.950879)

Control

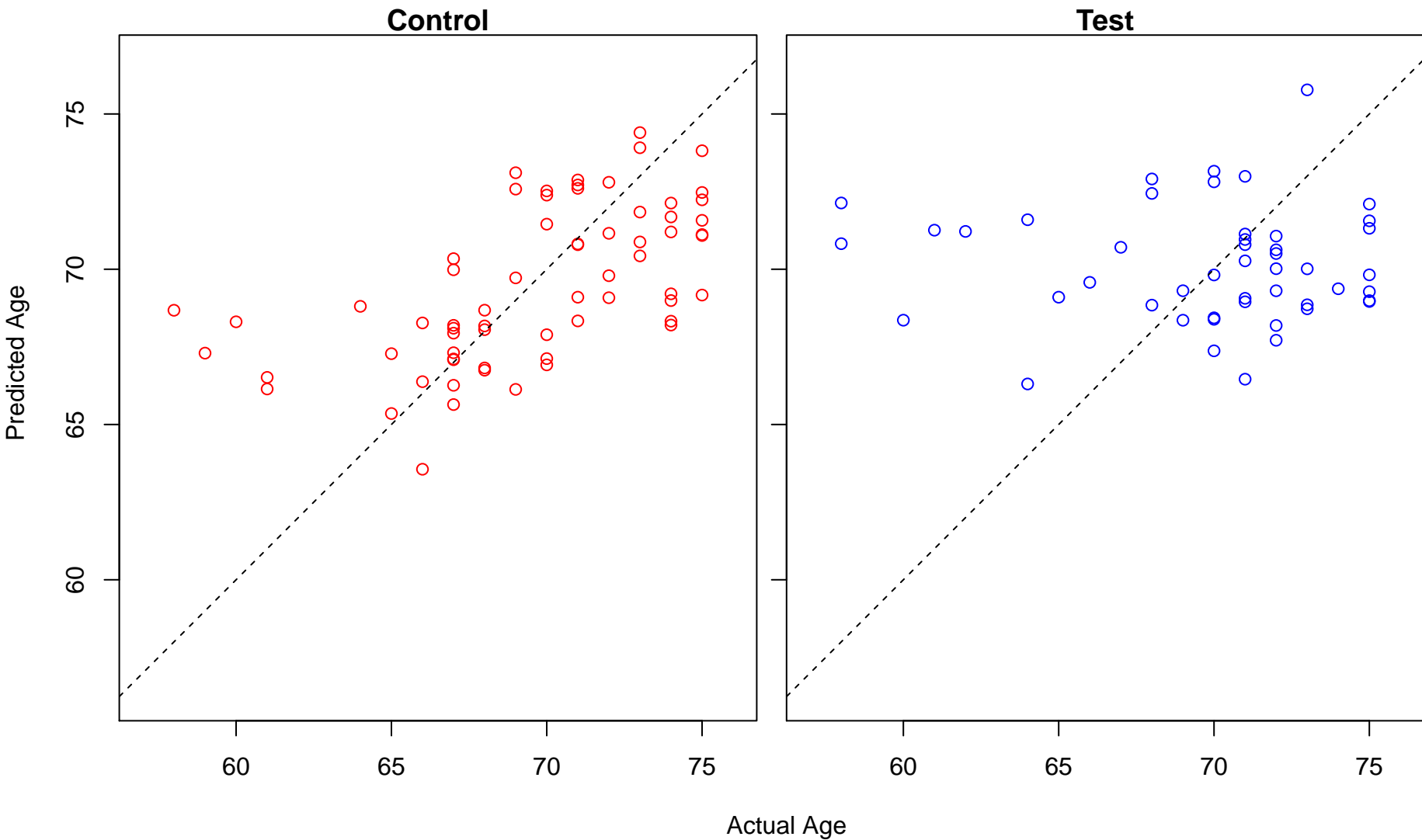


Test

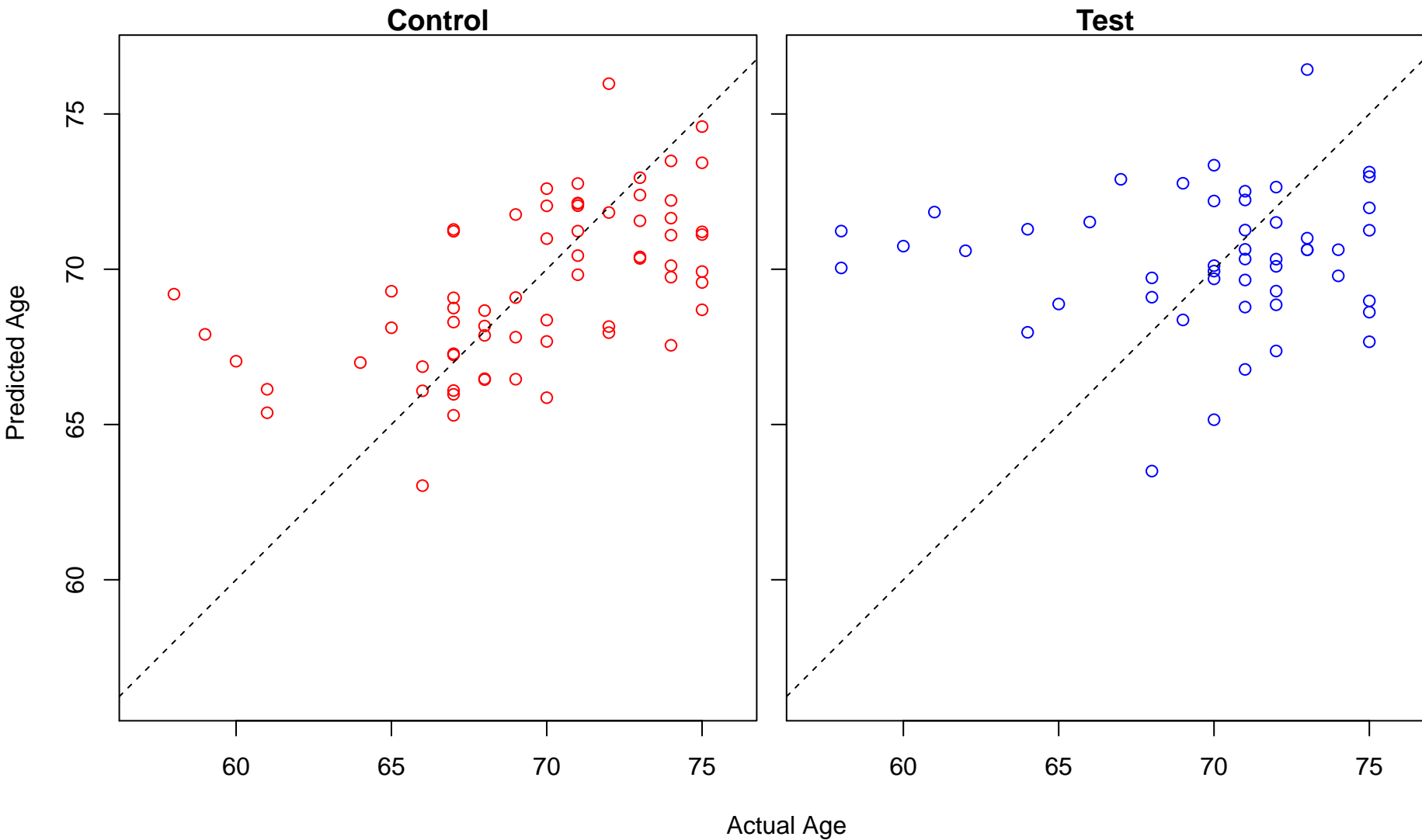


Actual Age

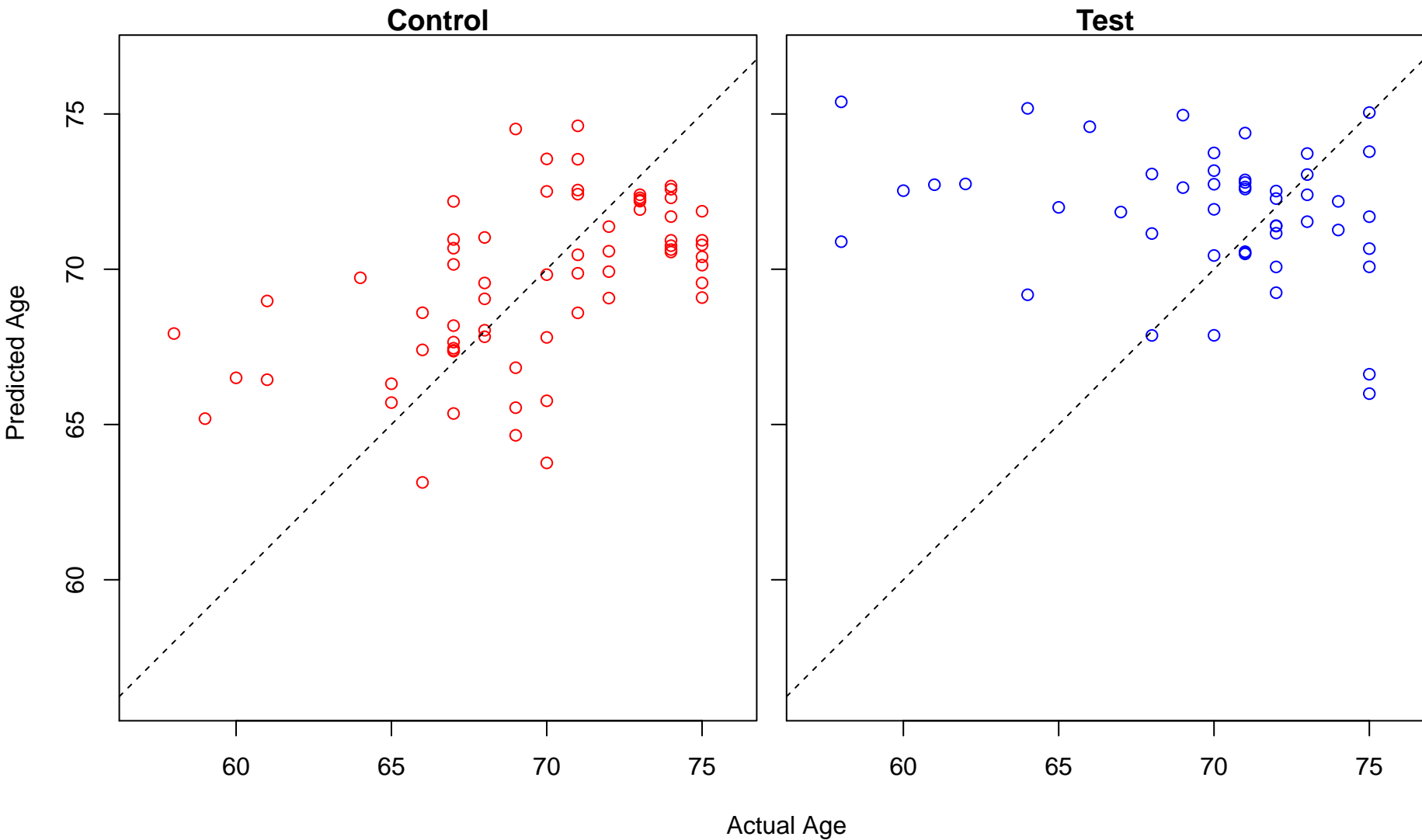
establishment of protein localization to peroxisome (Score: 0.950879)



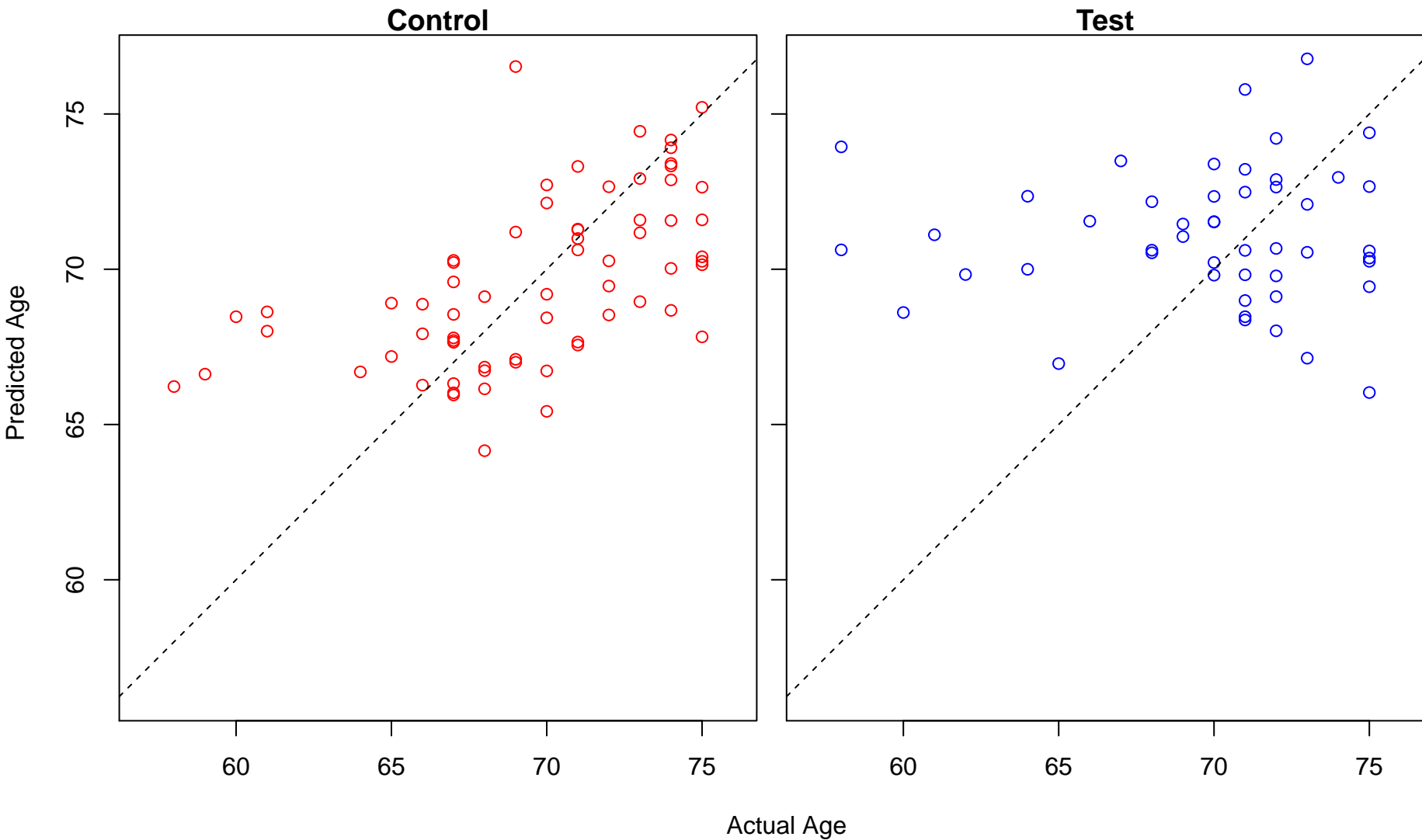
N-glycan processing (Score: 0.950261)



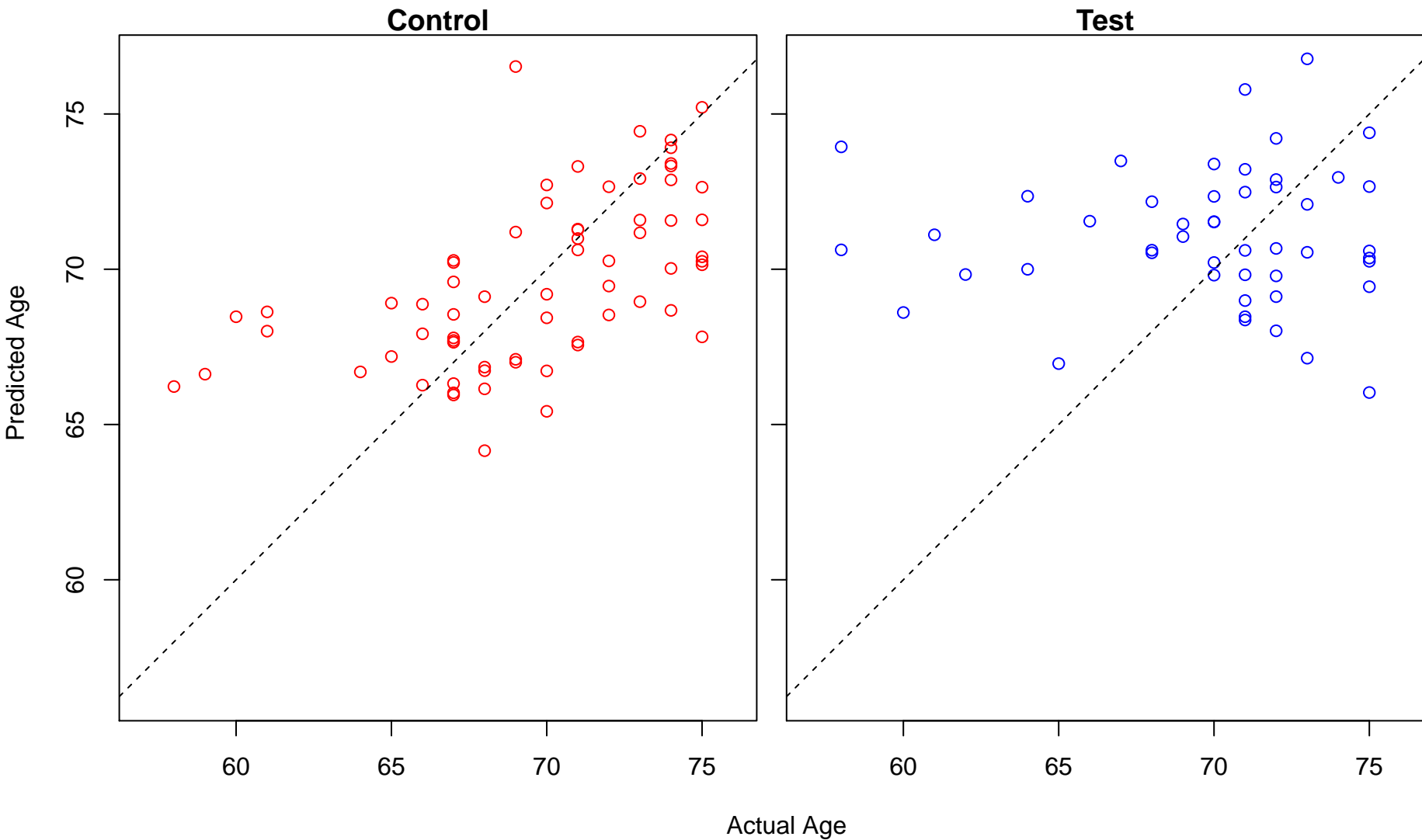
face development (Score: 0.950170)



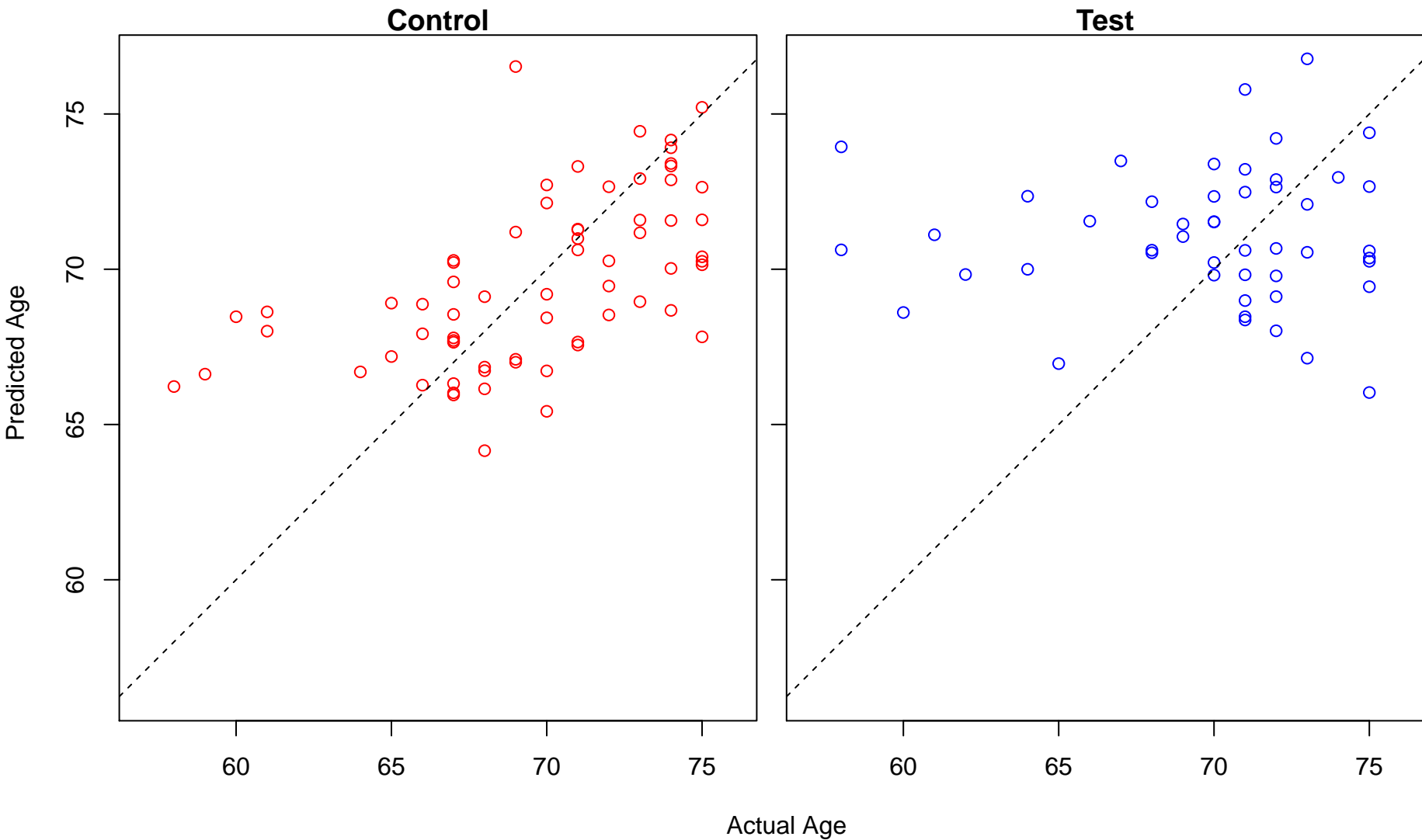
tRNA threonylcarbamoyladenosine metabolic process (Score: 0.949958)



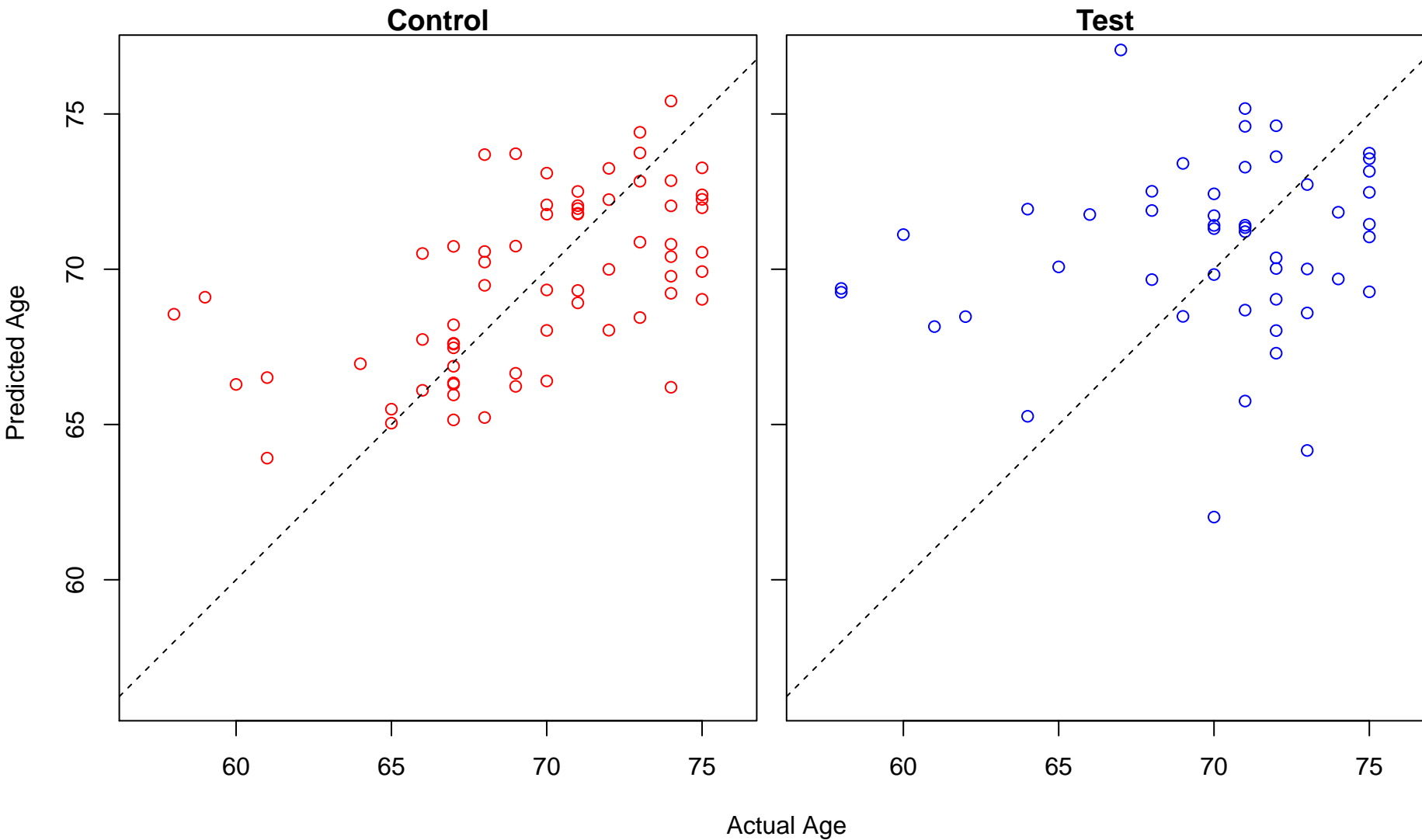
mitochondrial tRNA modification (Score: 0.949958)



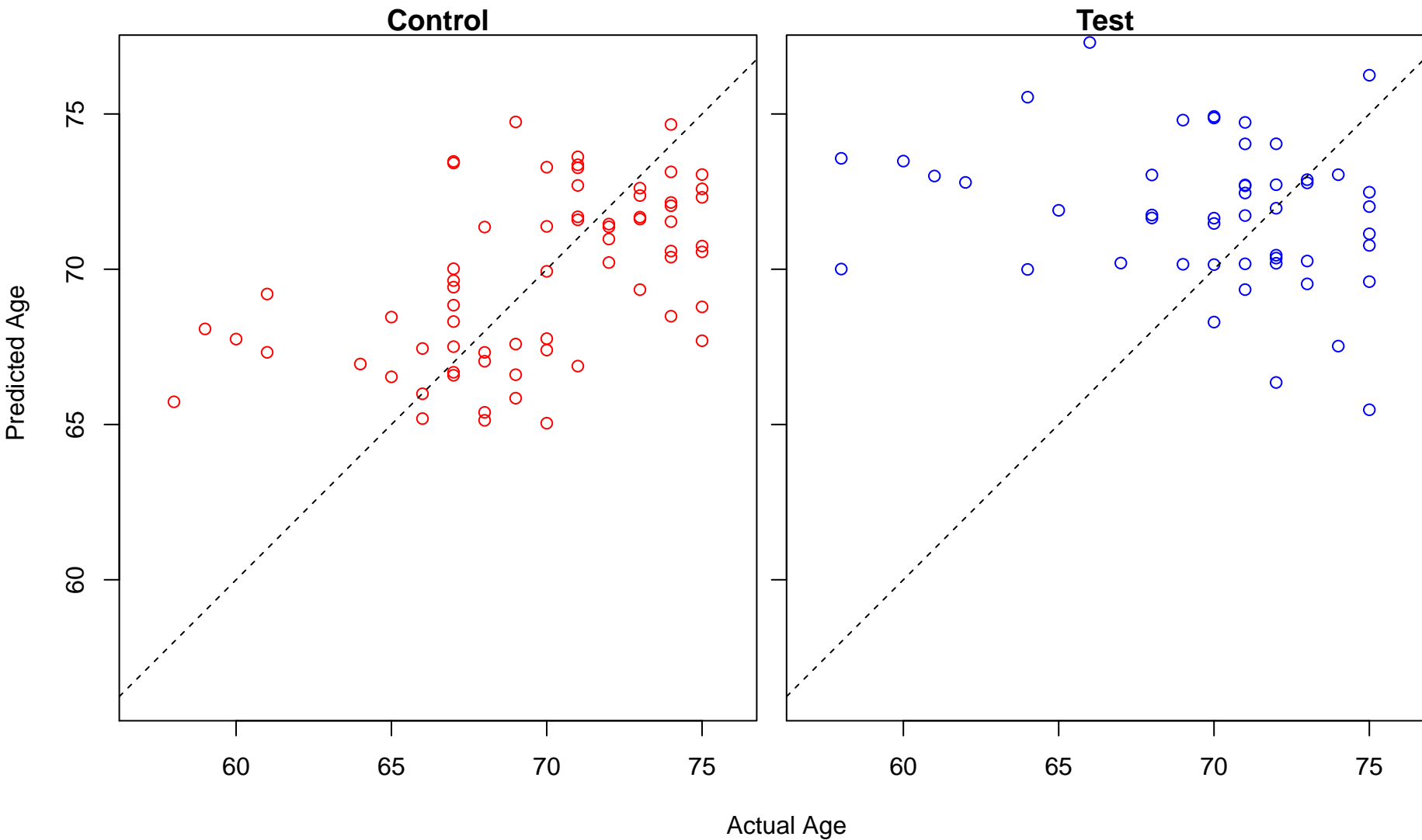
mitochondrial RNA modification (Score: 0.949958)



PERK-mediated unfolded protein response (Score: 0.949855)

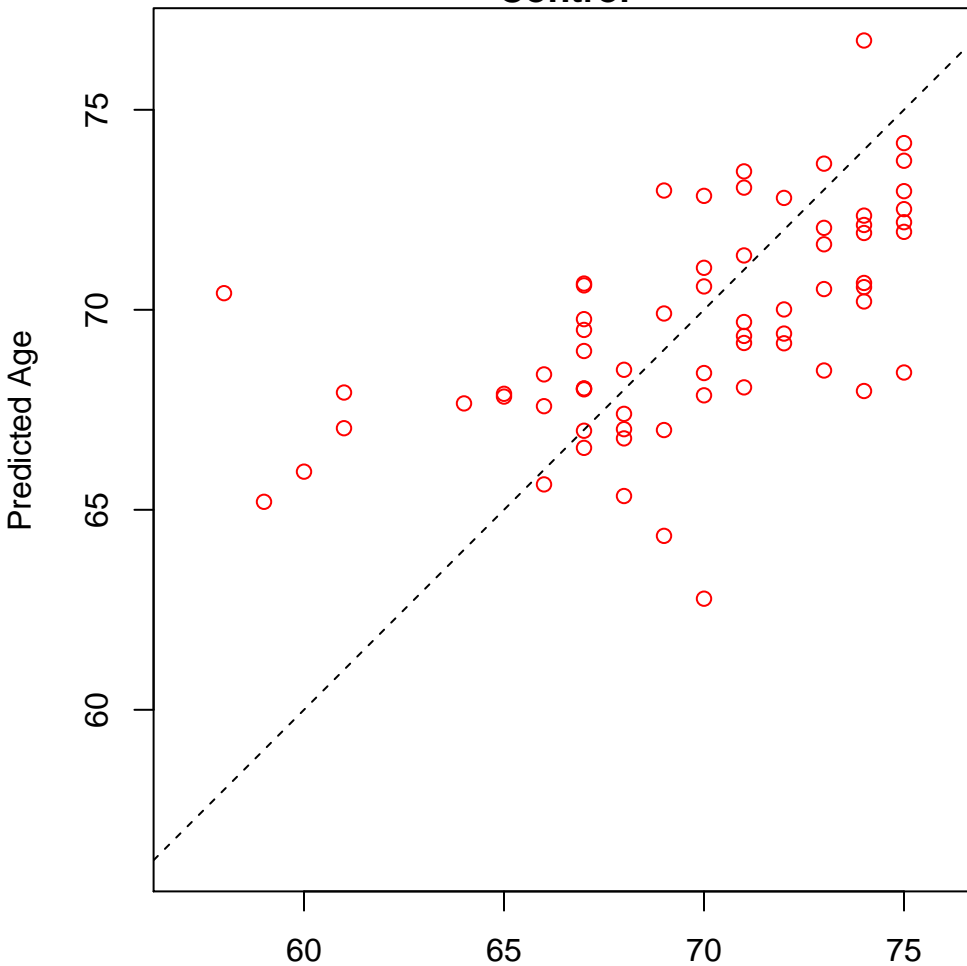


histone-serine phosphorylation (Score: 0.949013)

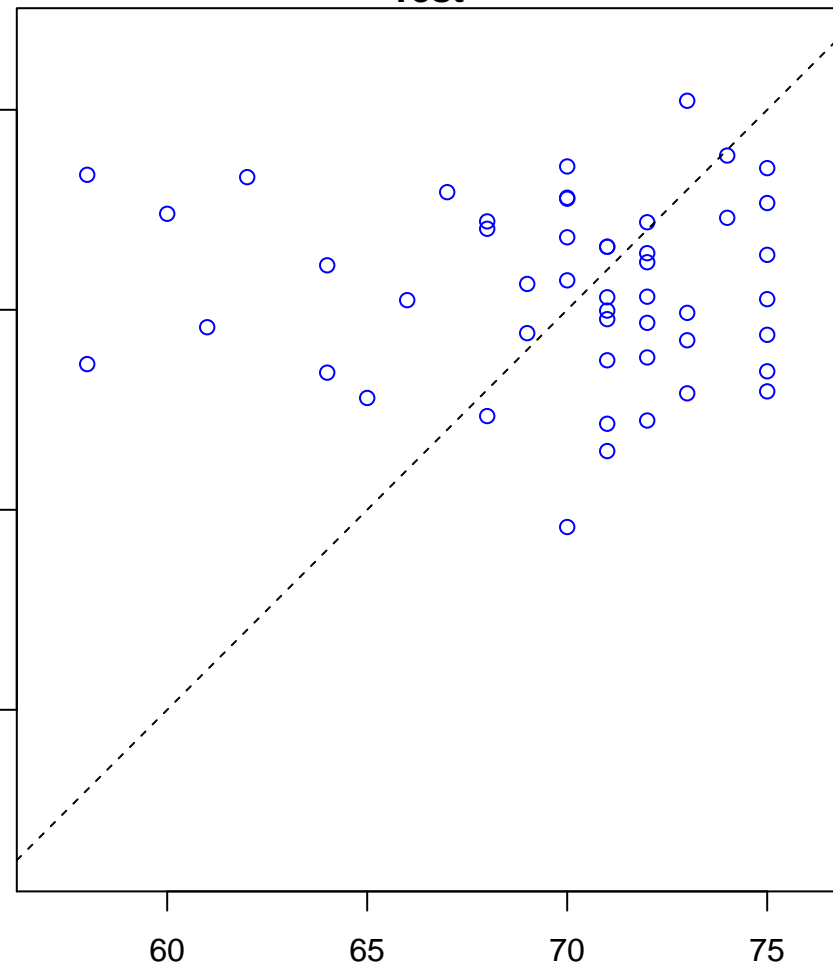


protein localization to microtubule (Score: 0.948703)

Control

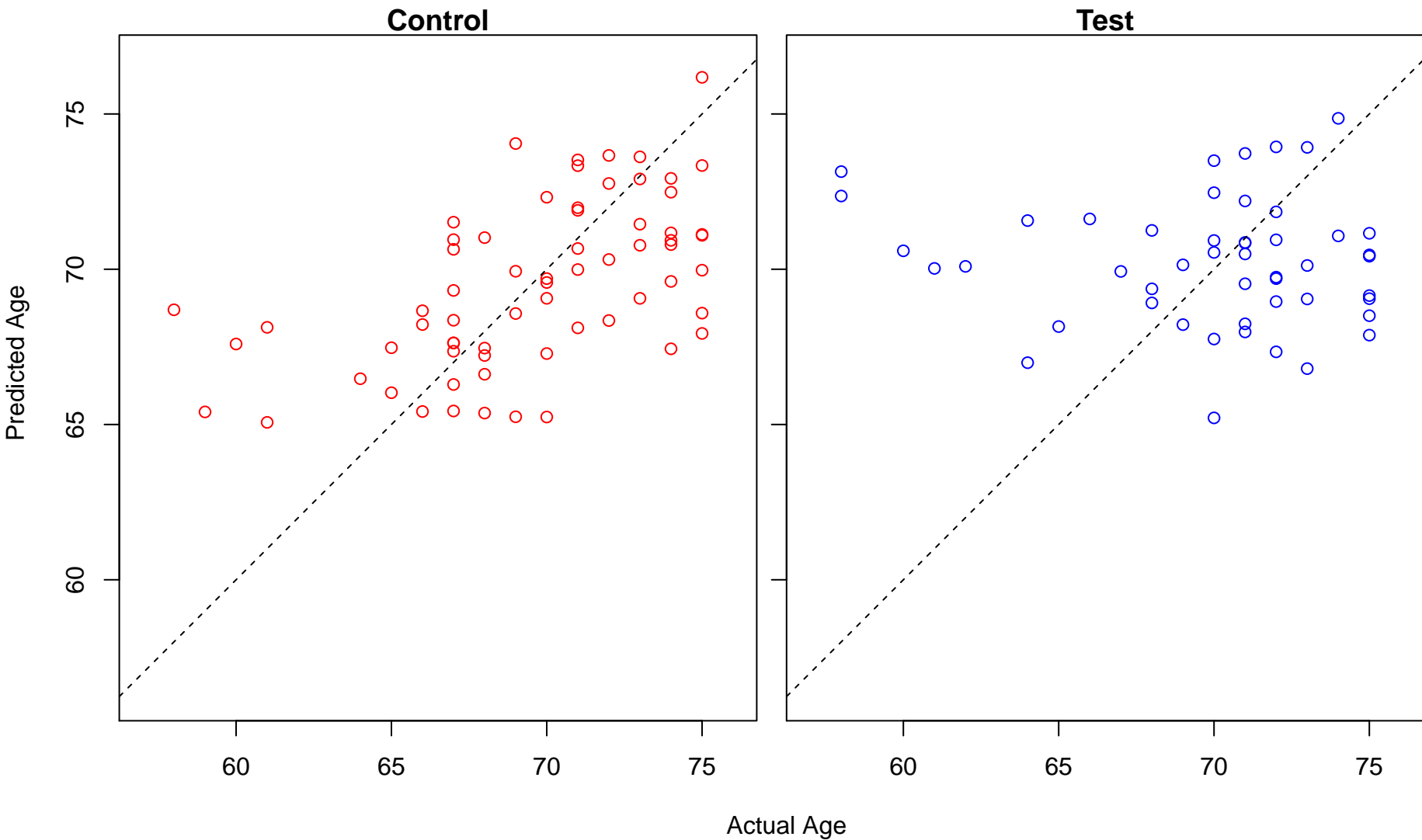


Test

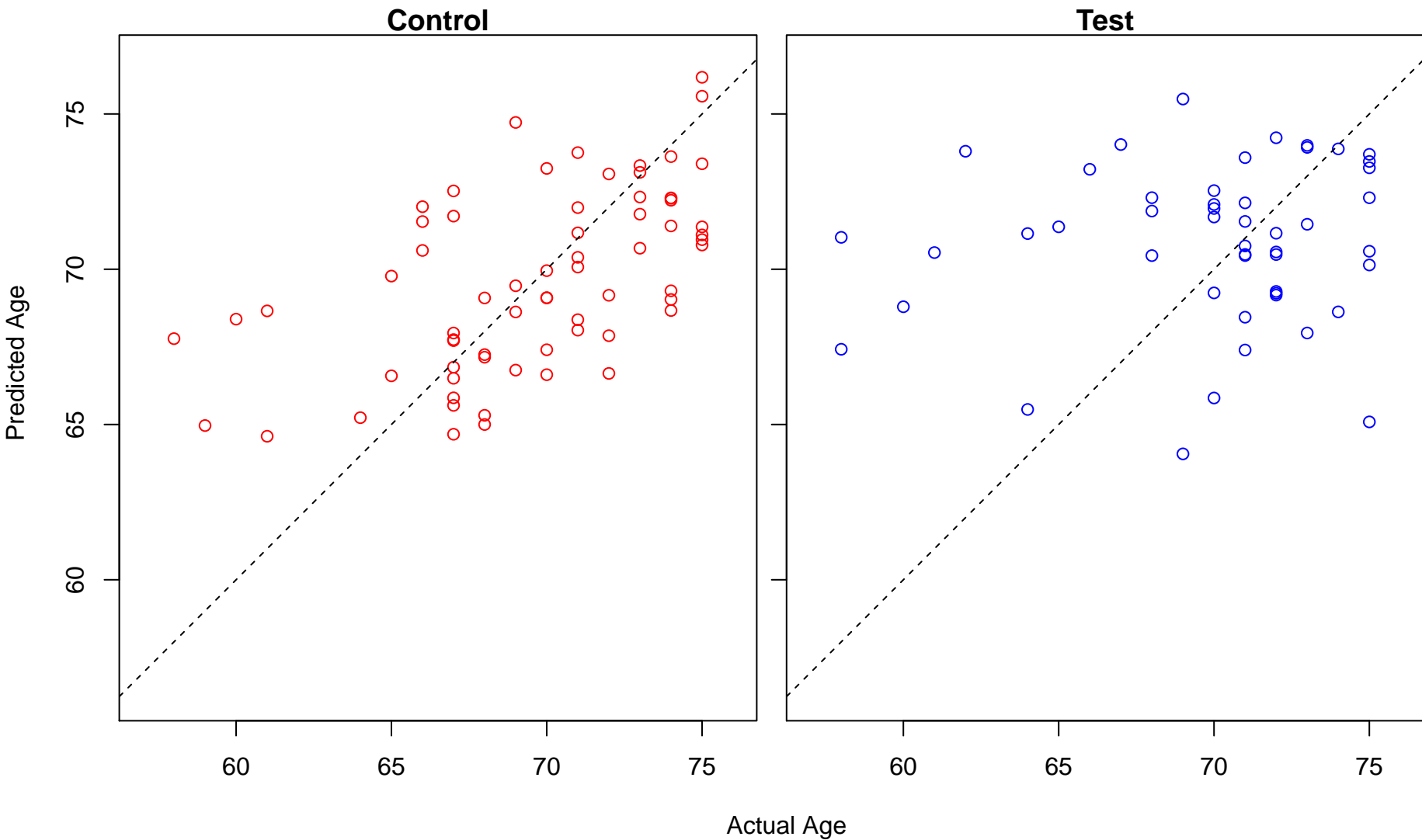


Actual Age

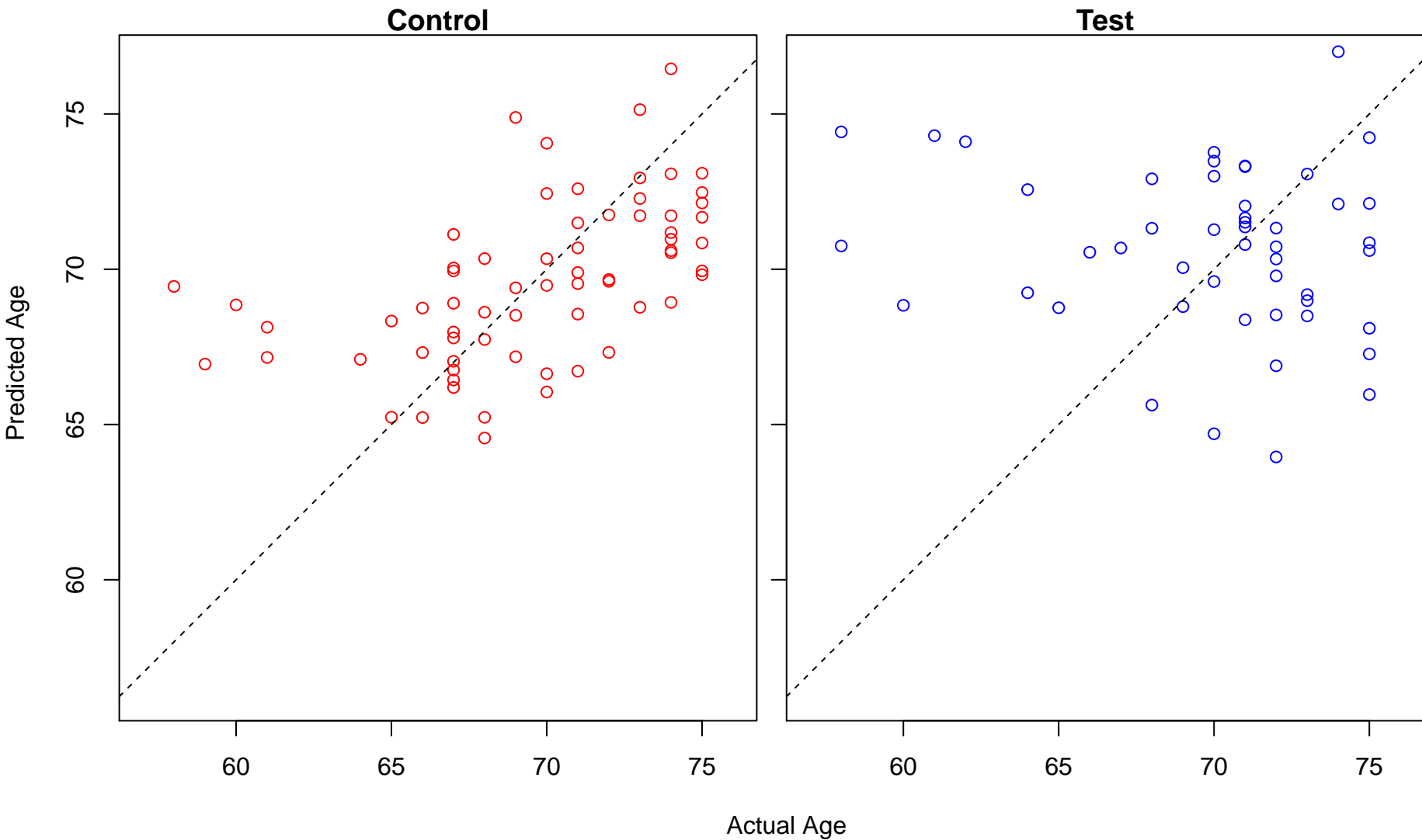
positive regulation of early endosome to late endosome transport (Score: 0.948330)



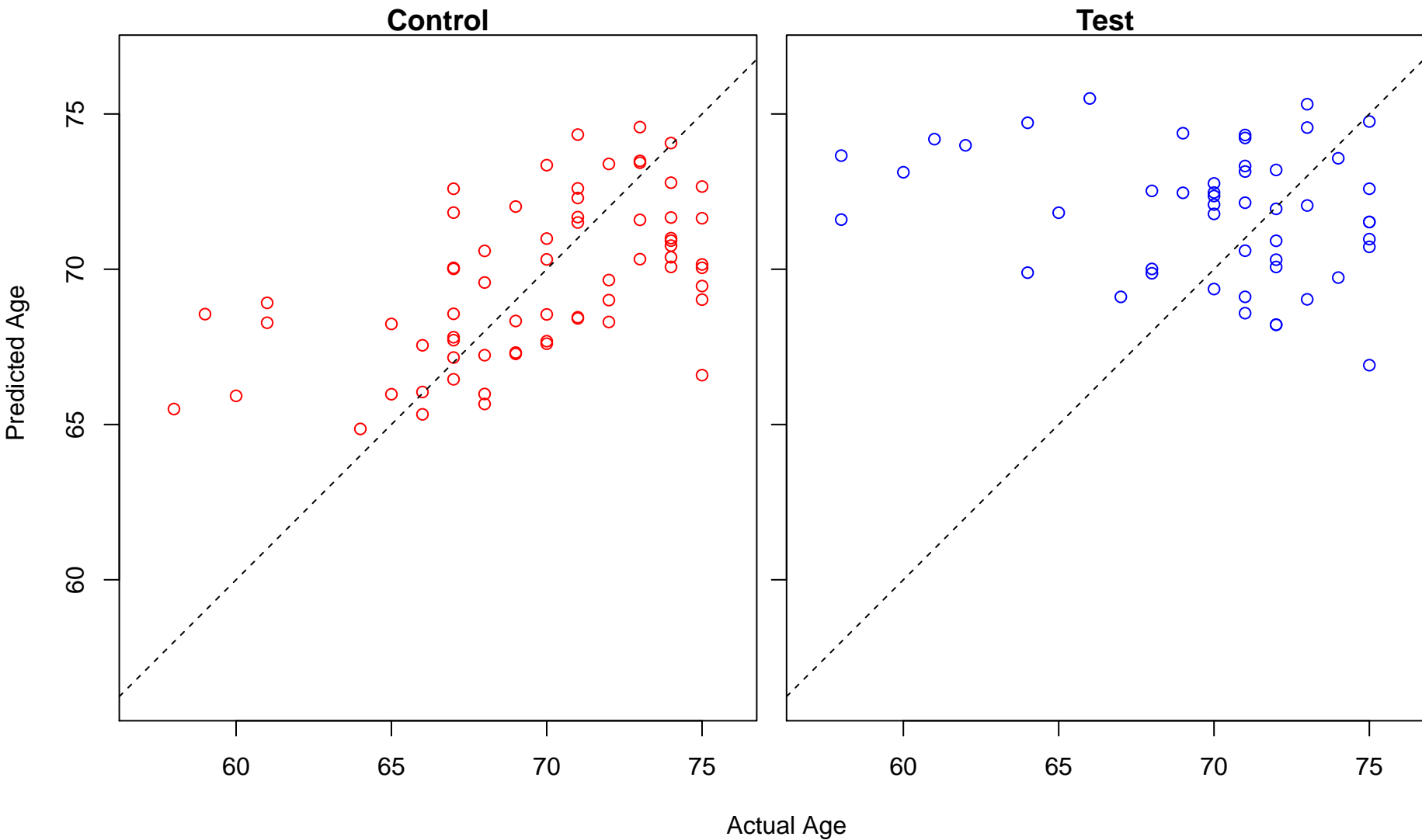
clathrin coat assembly (Score: 0.948044)



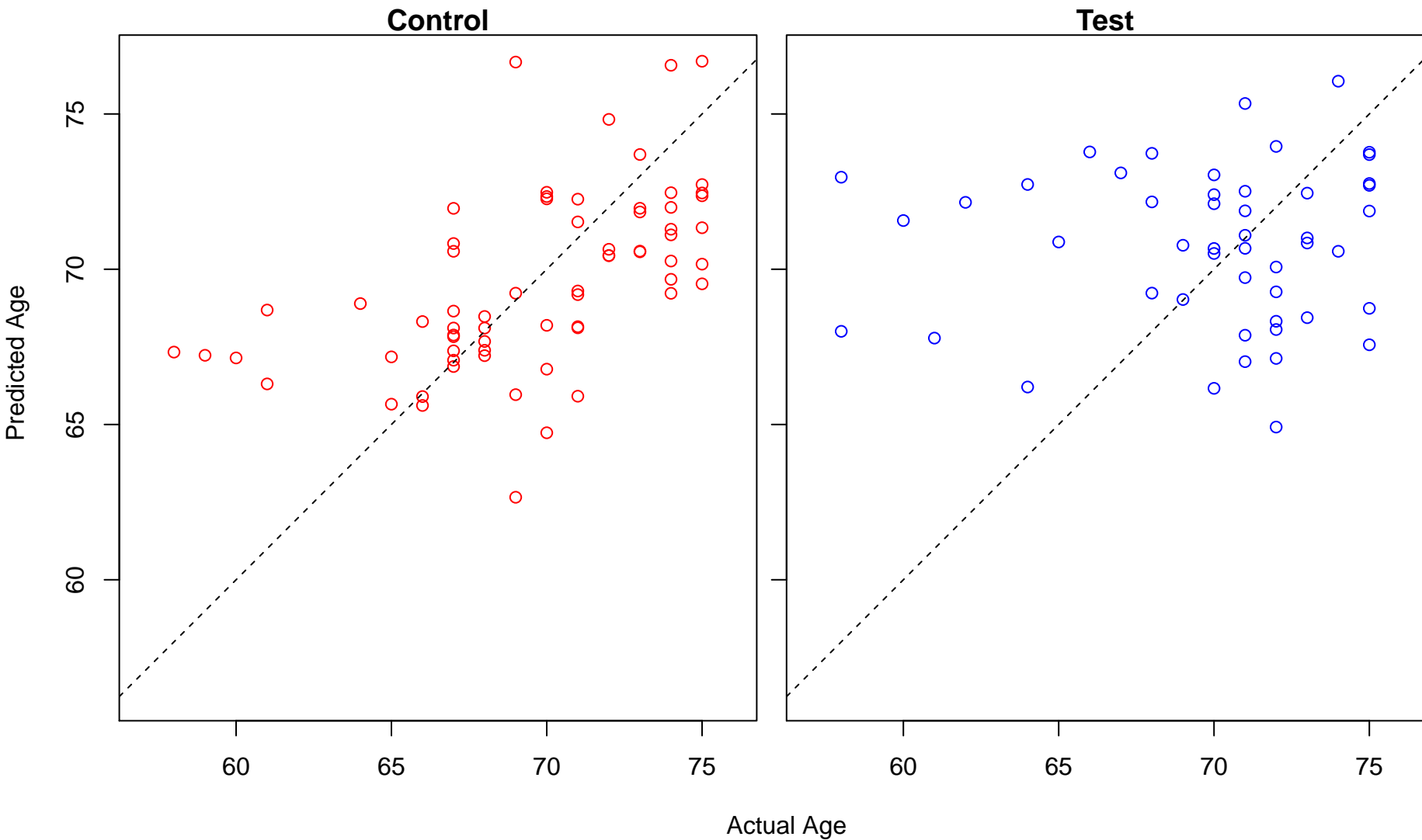
negative regulation of calcium ion transport (Score: 0.948019)



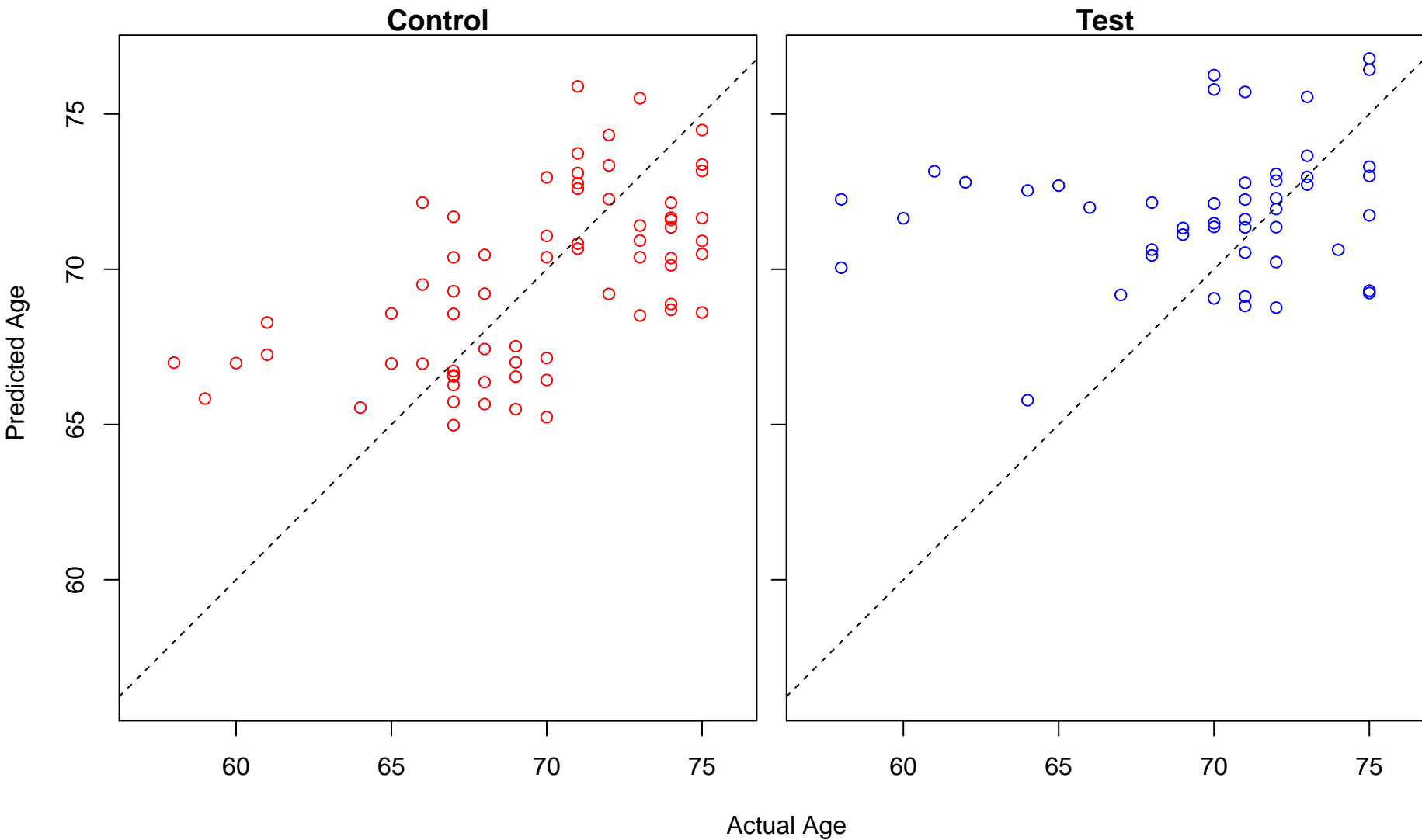
endocardium morphogenesis (Score: 0.947702)



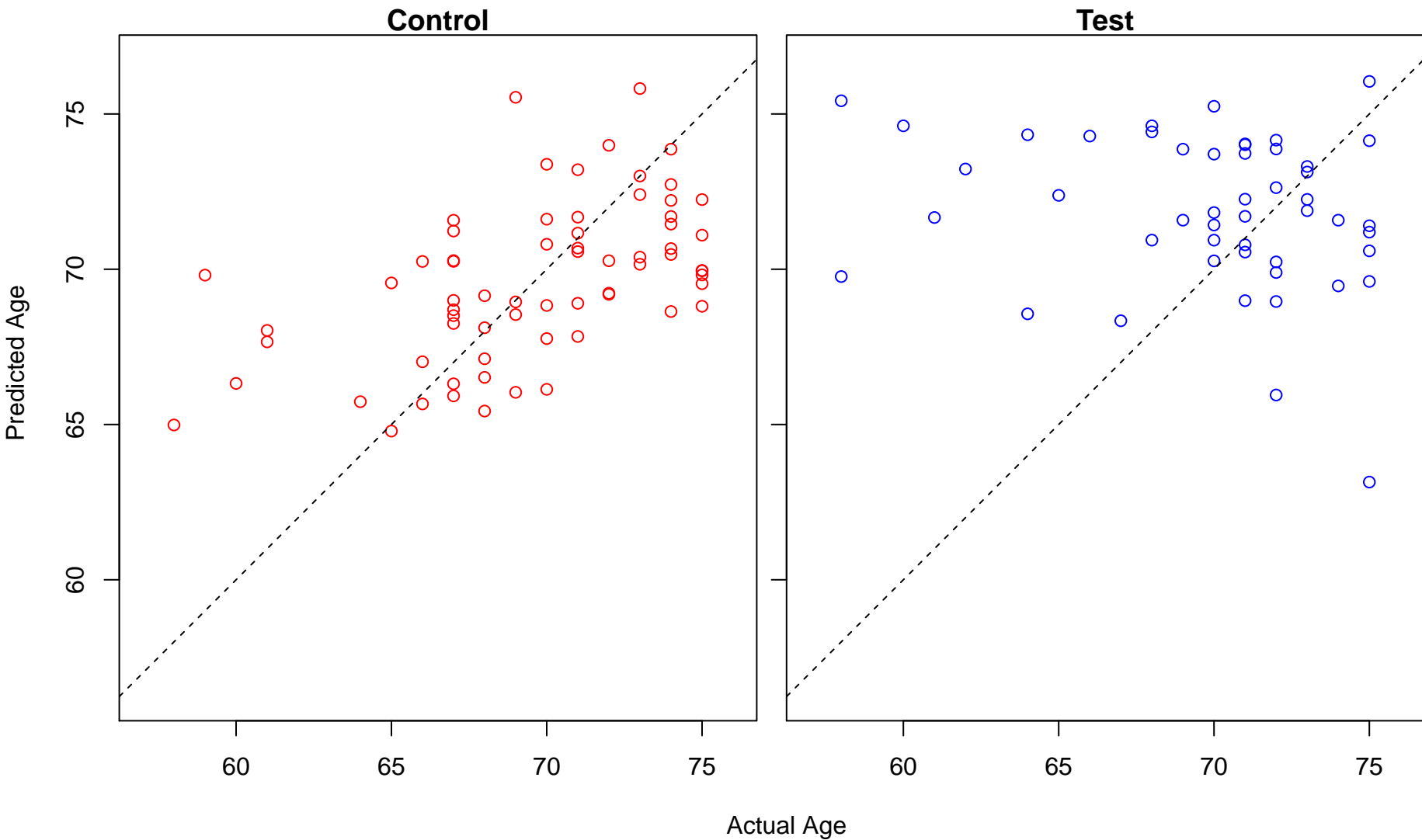
positive regulation of ER-associated ubiquitin-dependent protein catabolic process (Score: 0.94702)



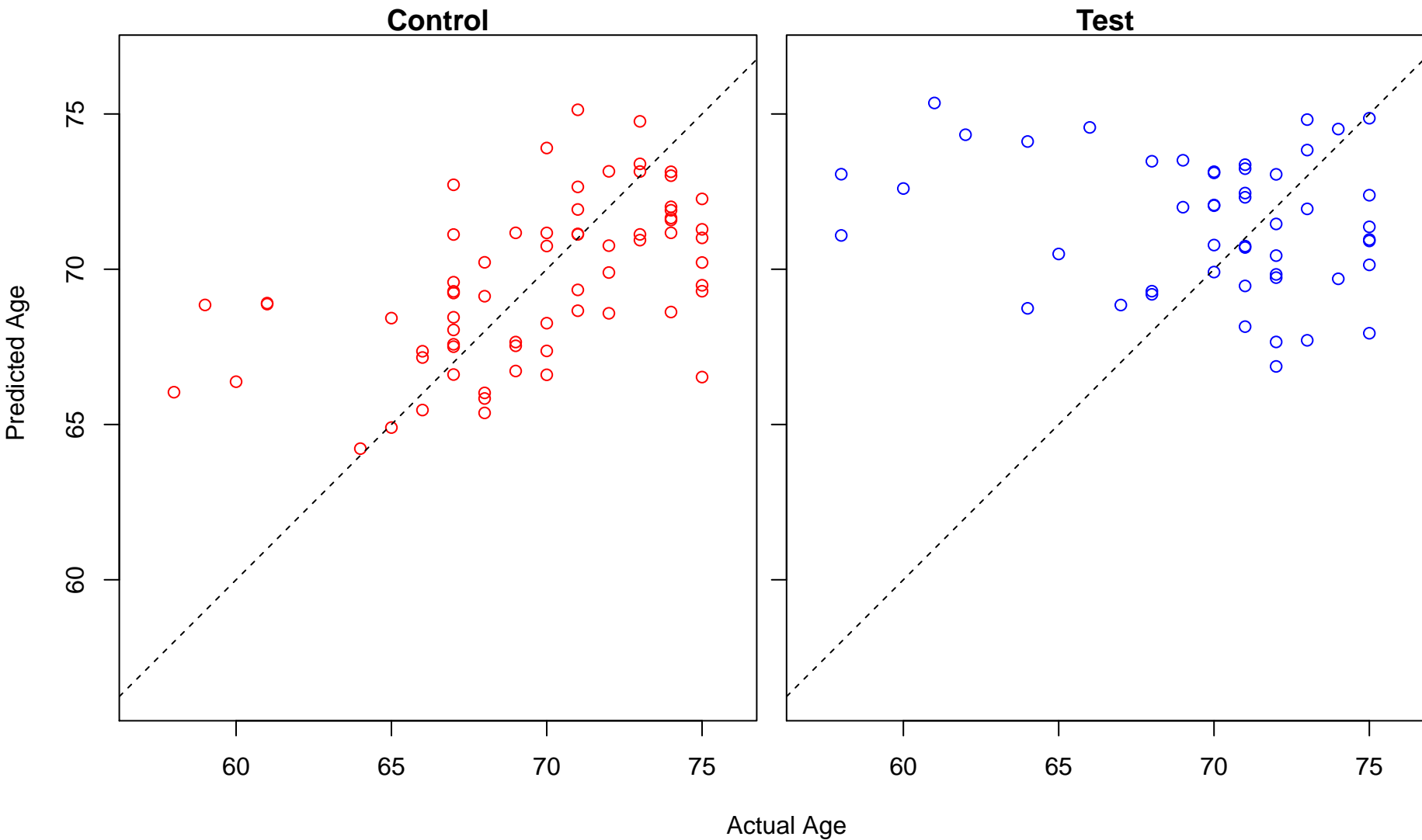
hindbrain development (Score: 0.946897)



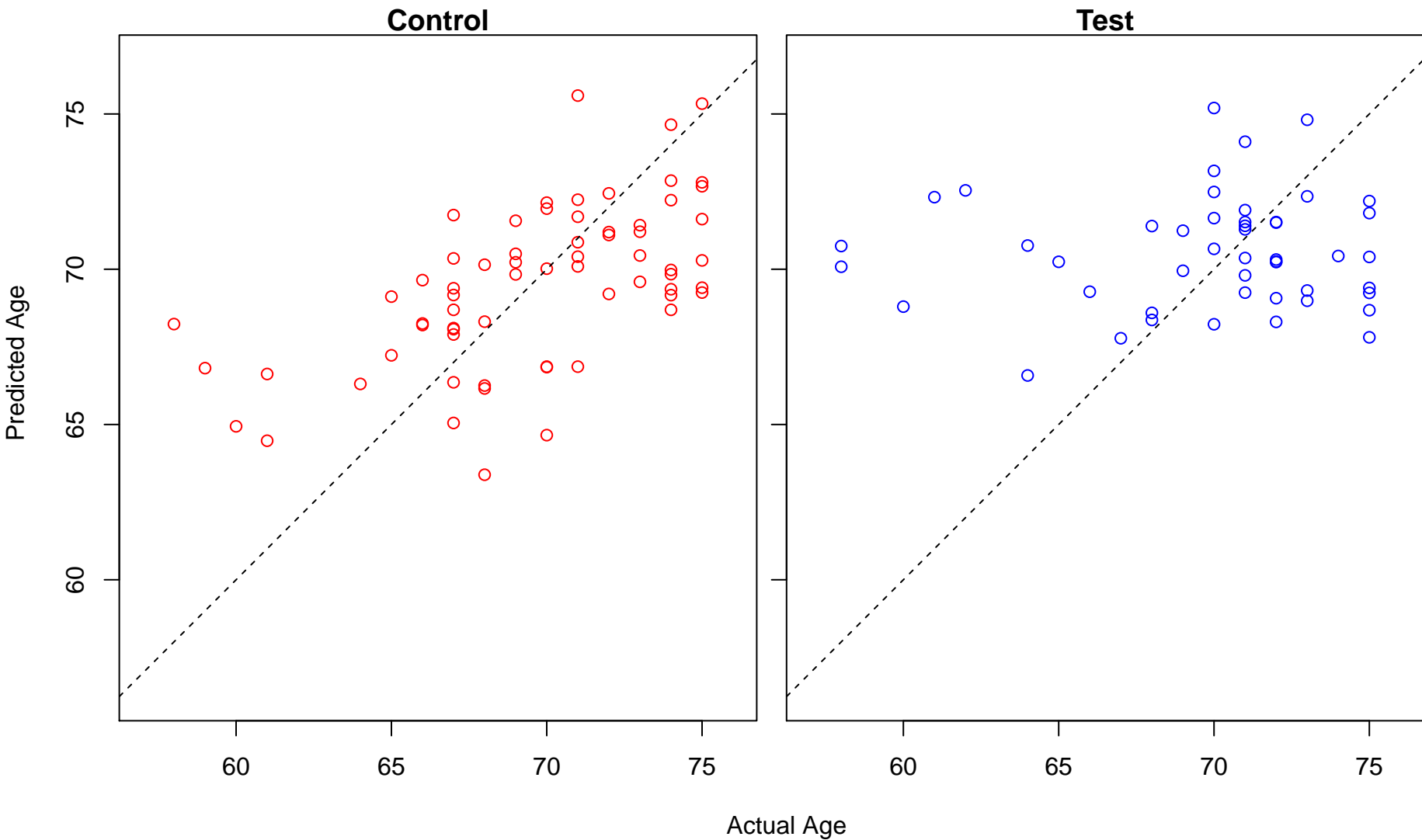
positive regulation of astrocyte differentiation (Score: 0.946645)



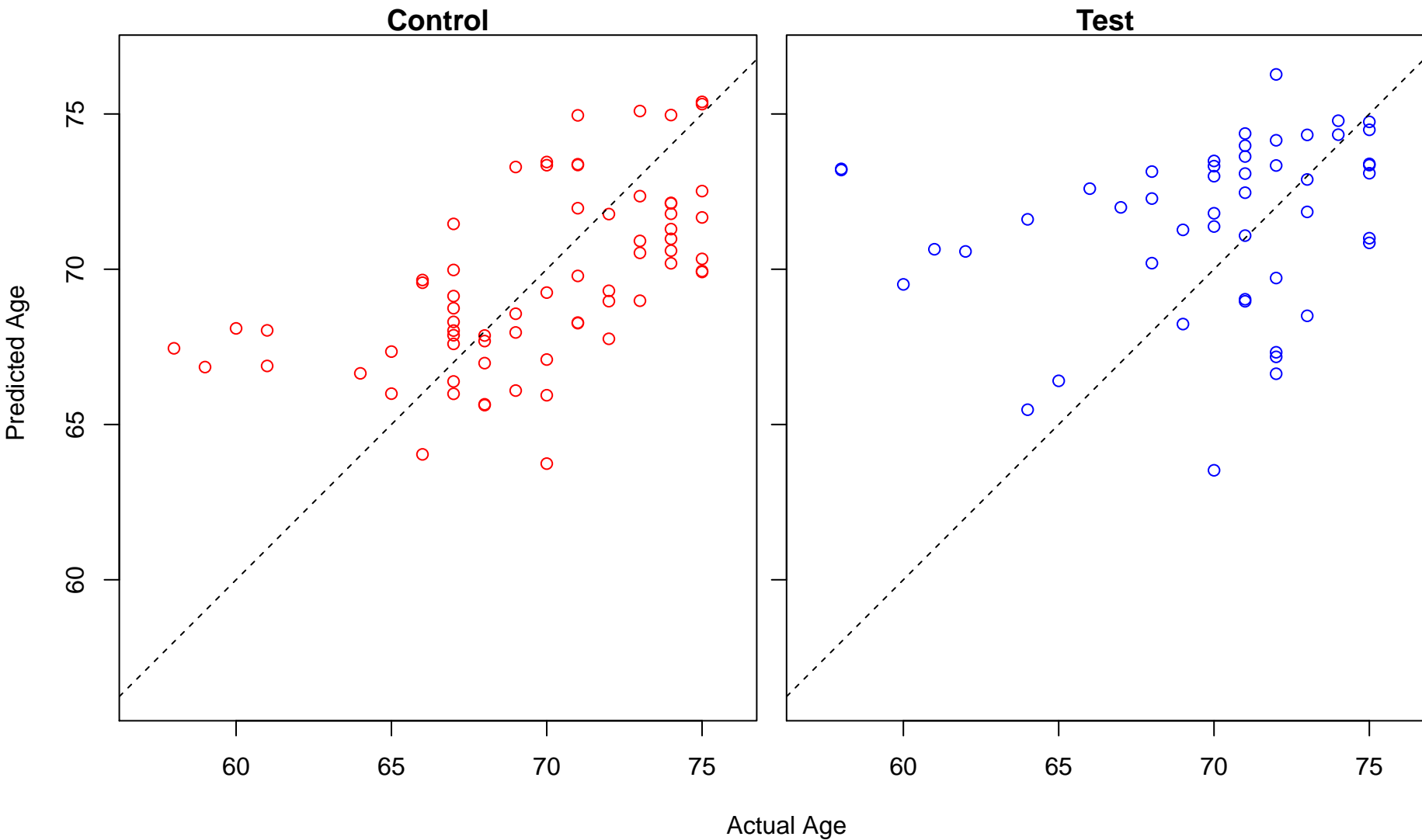
endocardium development (Score: 0.946611)



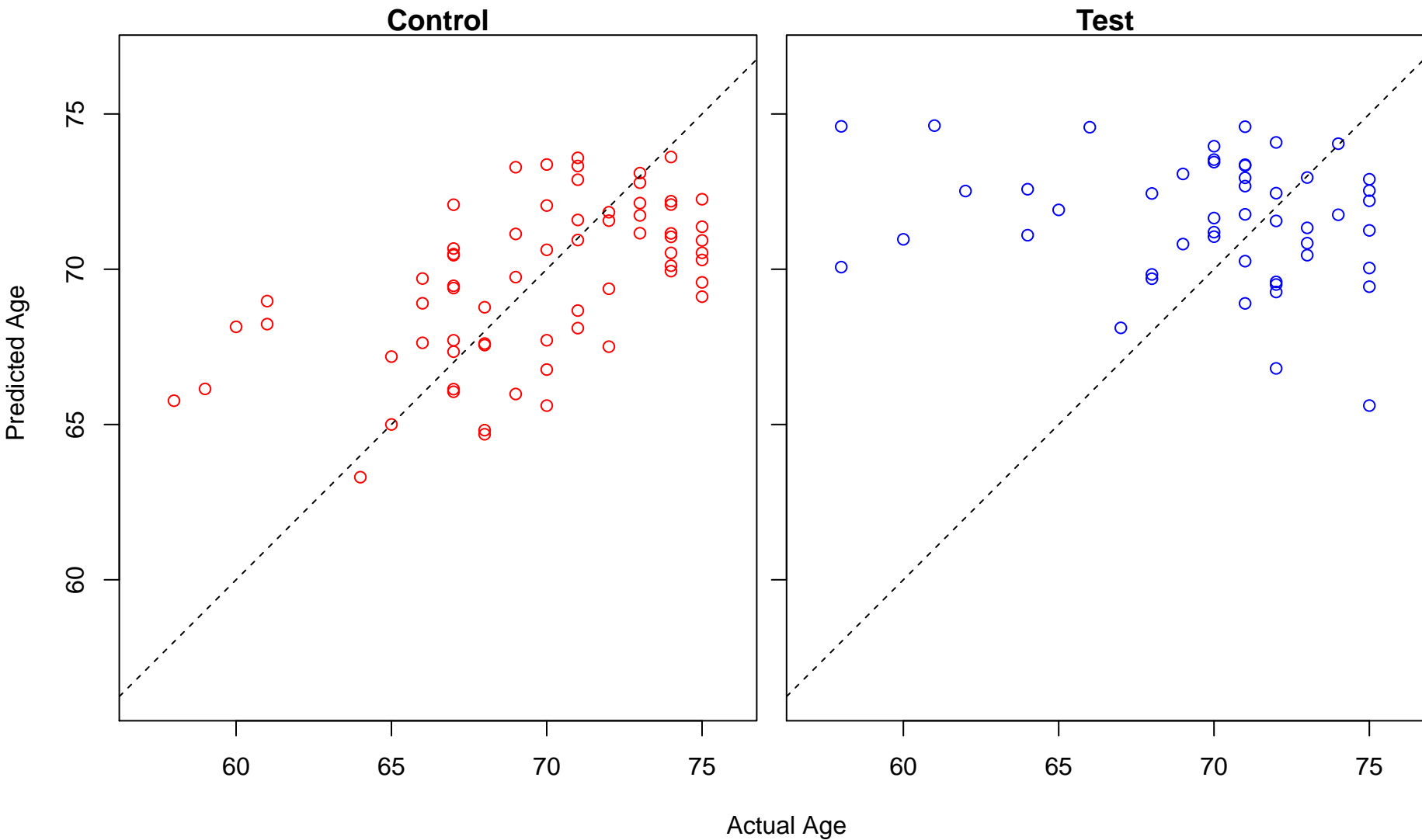
NADH metabolic process (Score: 0.946568)



connective tissue development (Score: 0.946080)

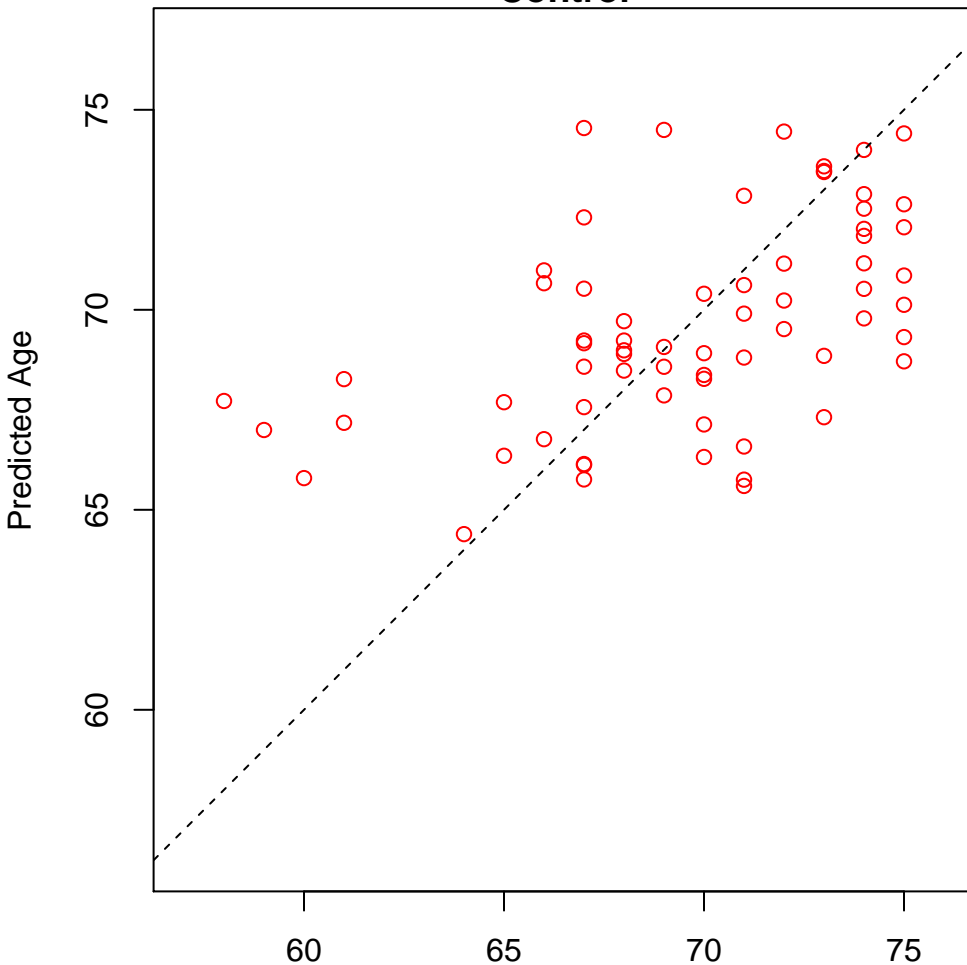


negative regulation of peptidyl-serine phosphorylation (Score: 0.945640)

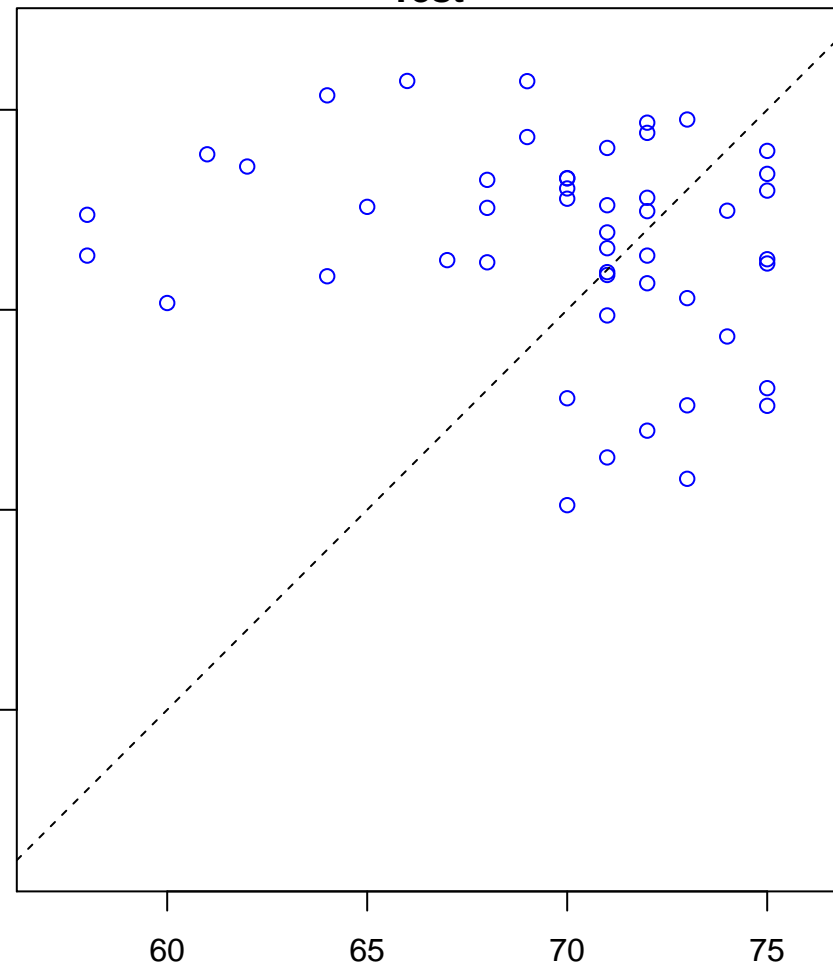


cellular response to exogenous dsRNA (Score: 0.945588)

Control

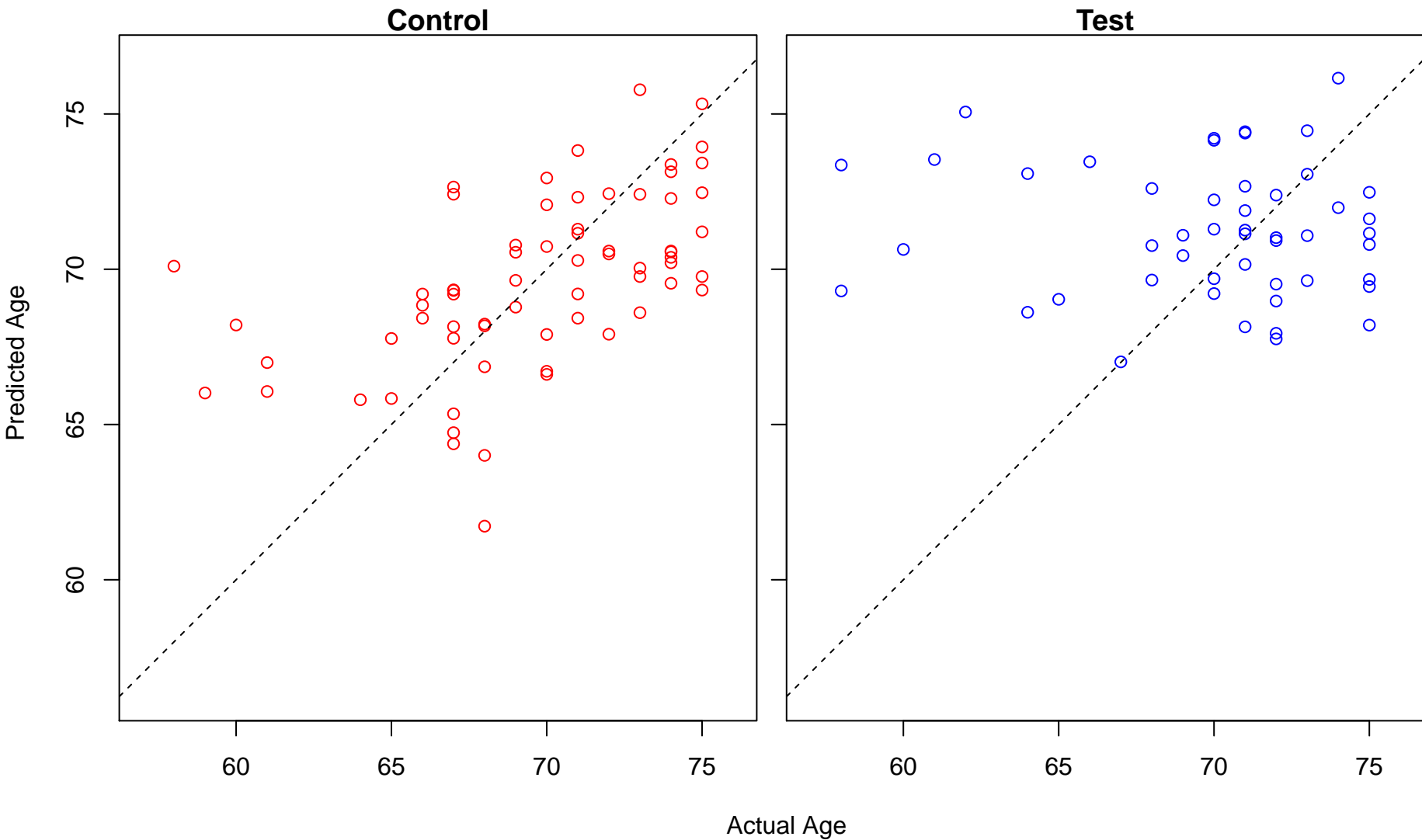


Test

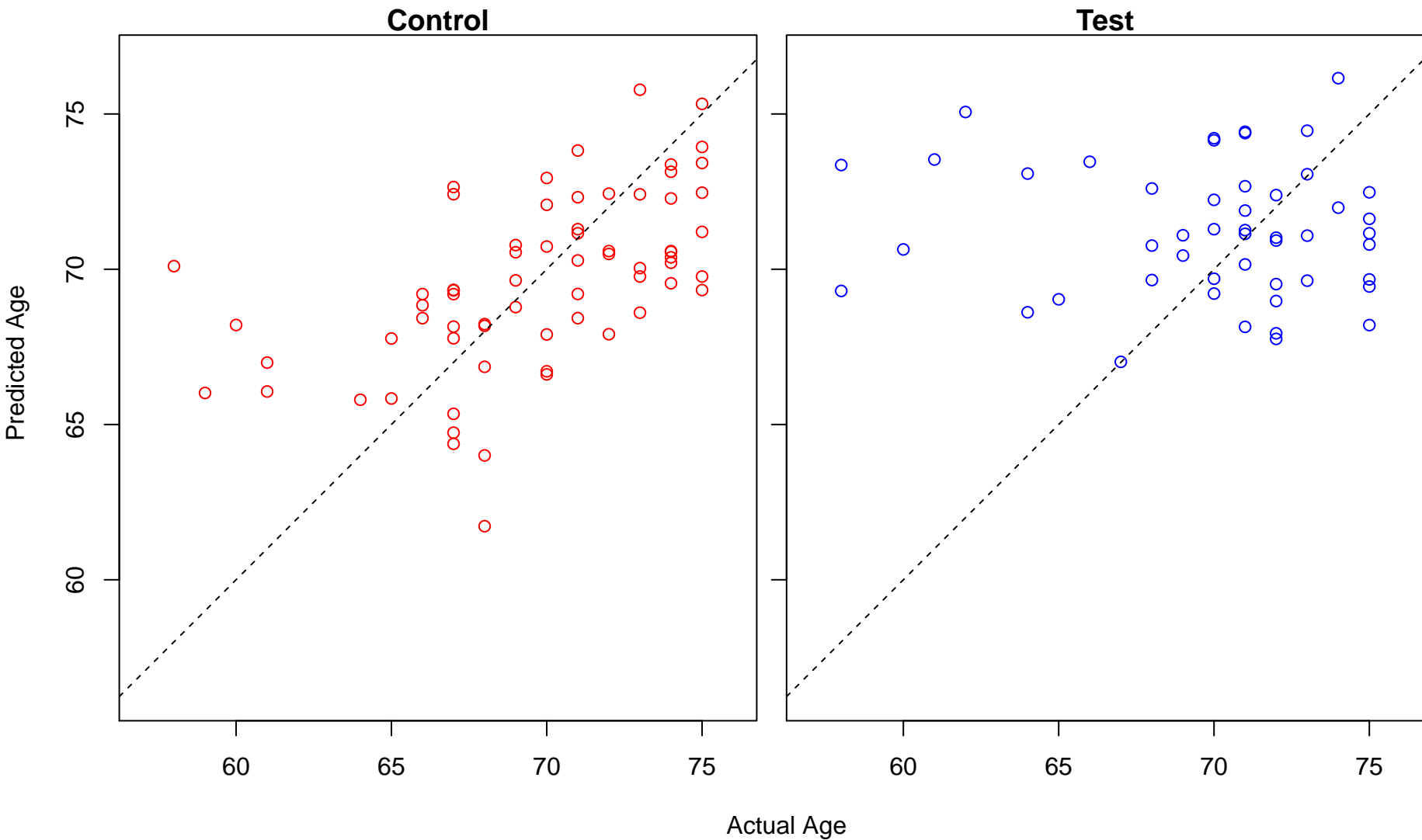


Actual Age

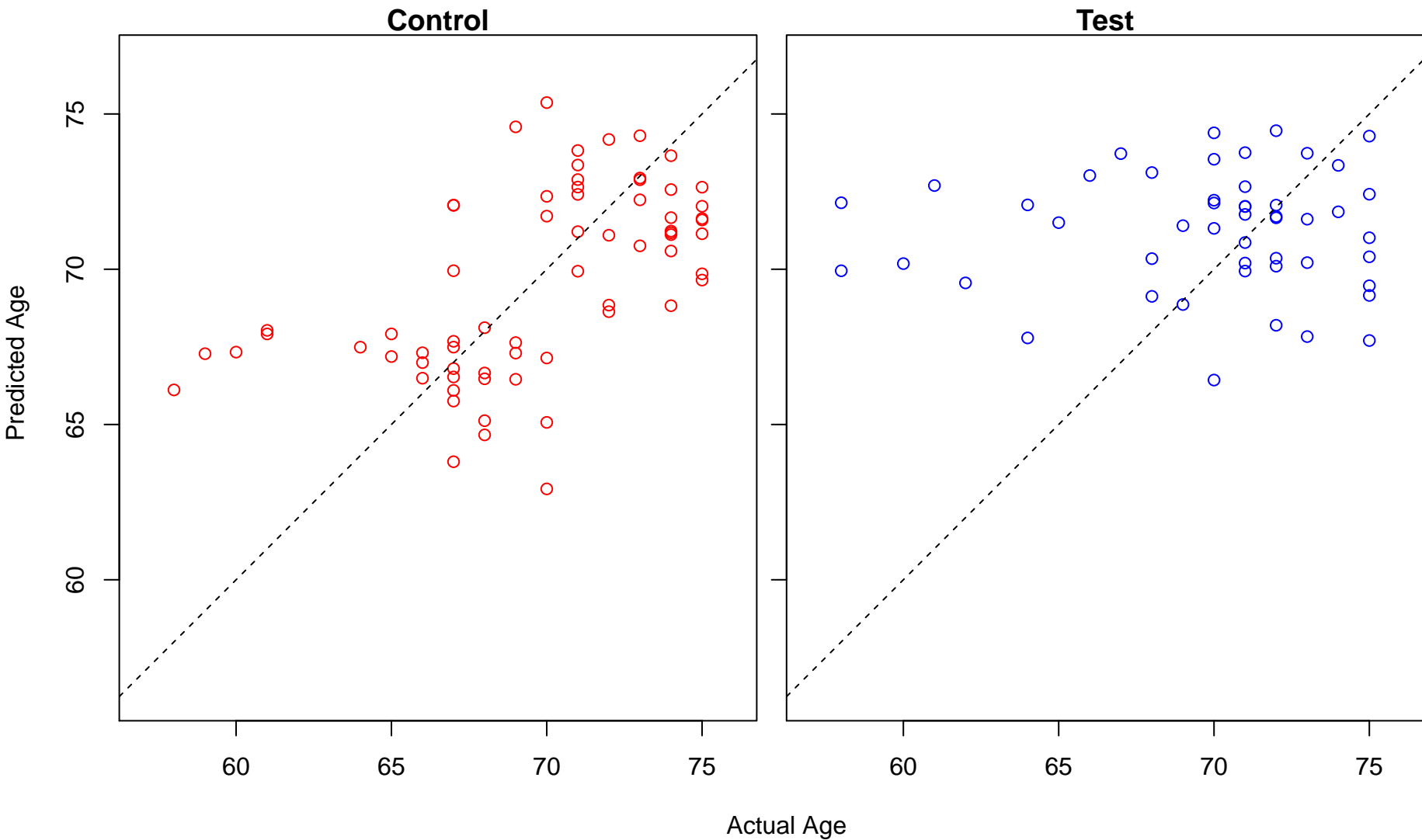
positive regulation of cellular response to oxidative stress (Score: 0.945477)



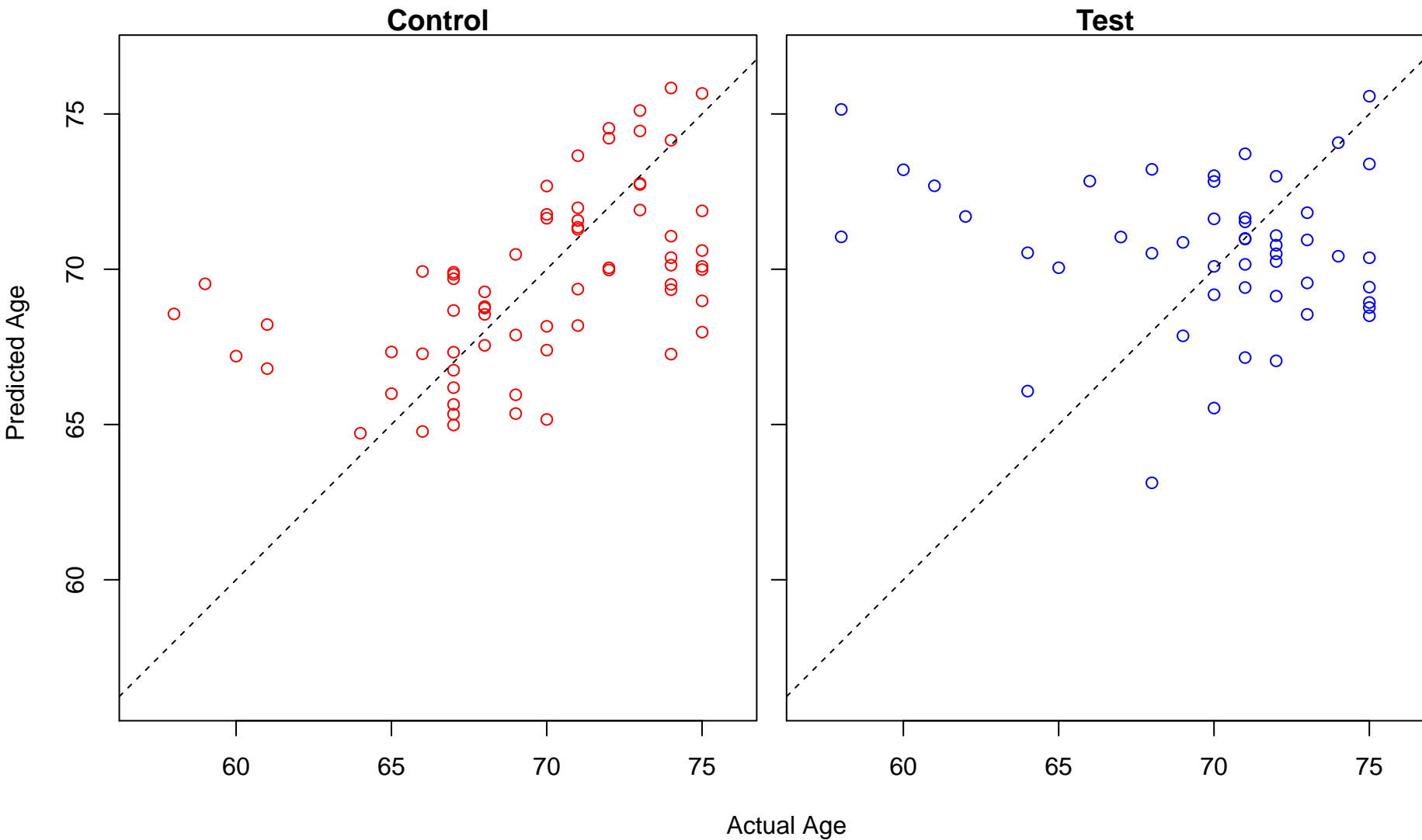
positive regulation of response to oxidative stress (Score: 0.945477)



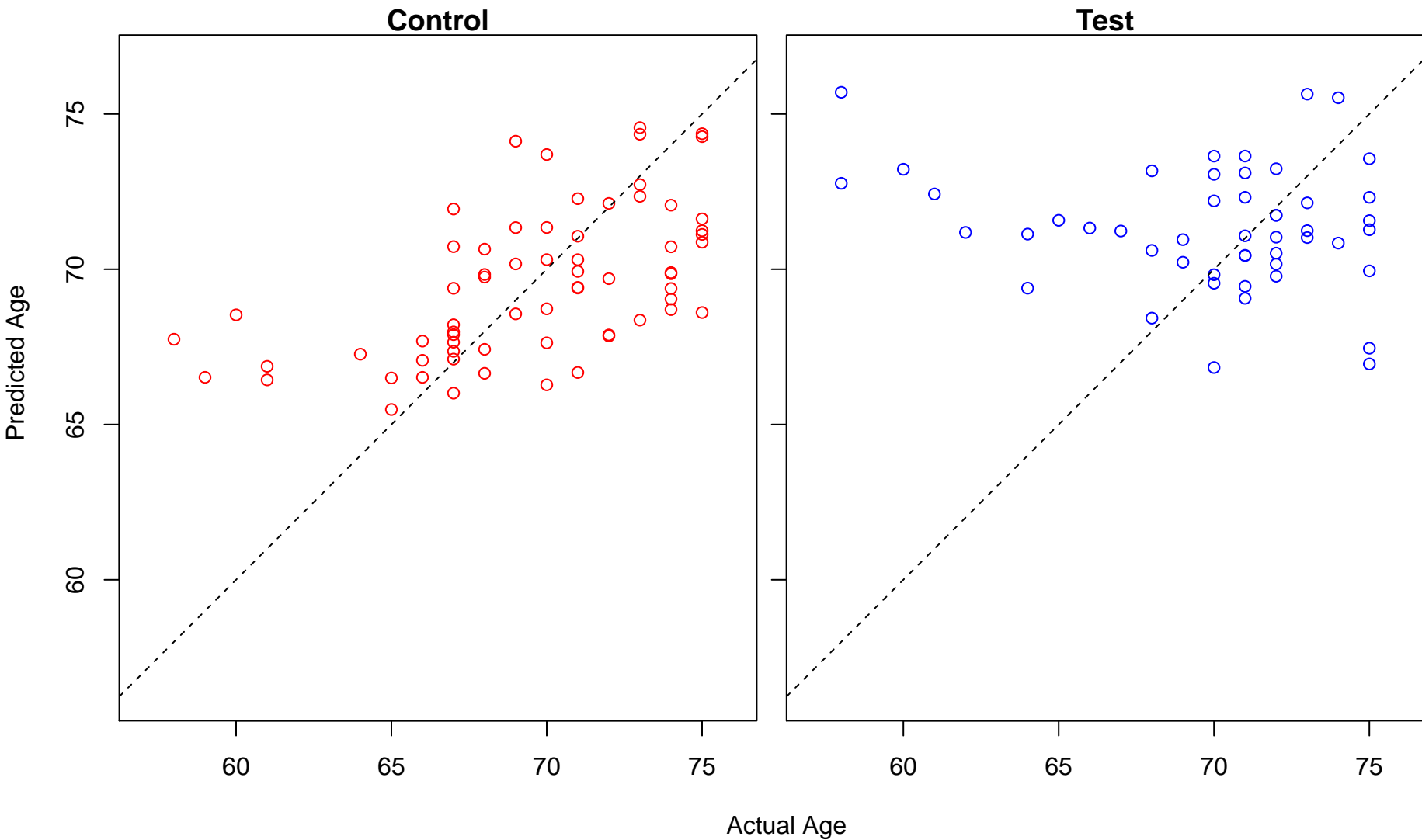
leukocyte mediated cytotoxicity (Score: 0.944852)



central nervous system neuron differentiation (Score: 0.944850)

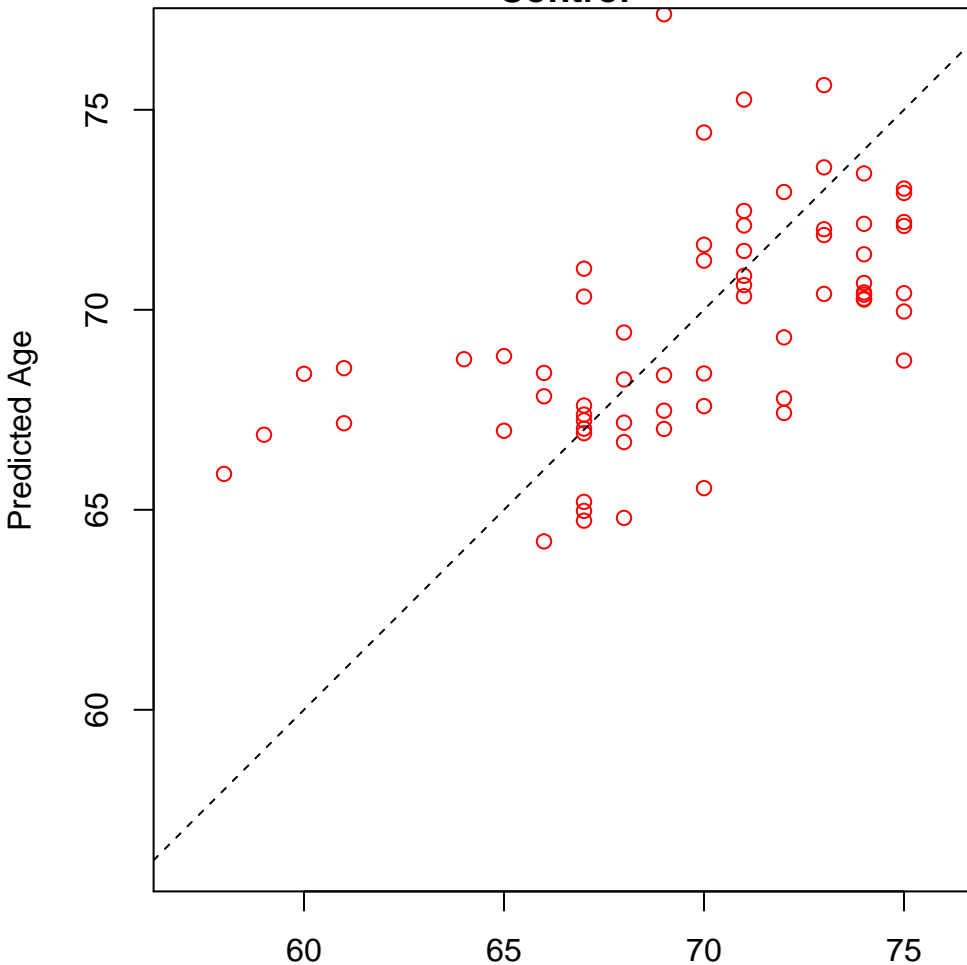


cortical cytoskeleton organization (Score: 0.944776)

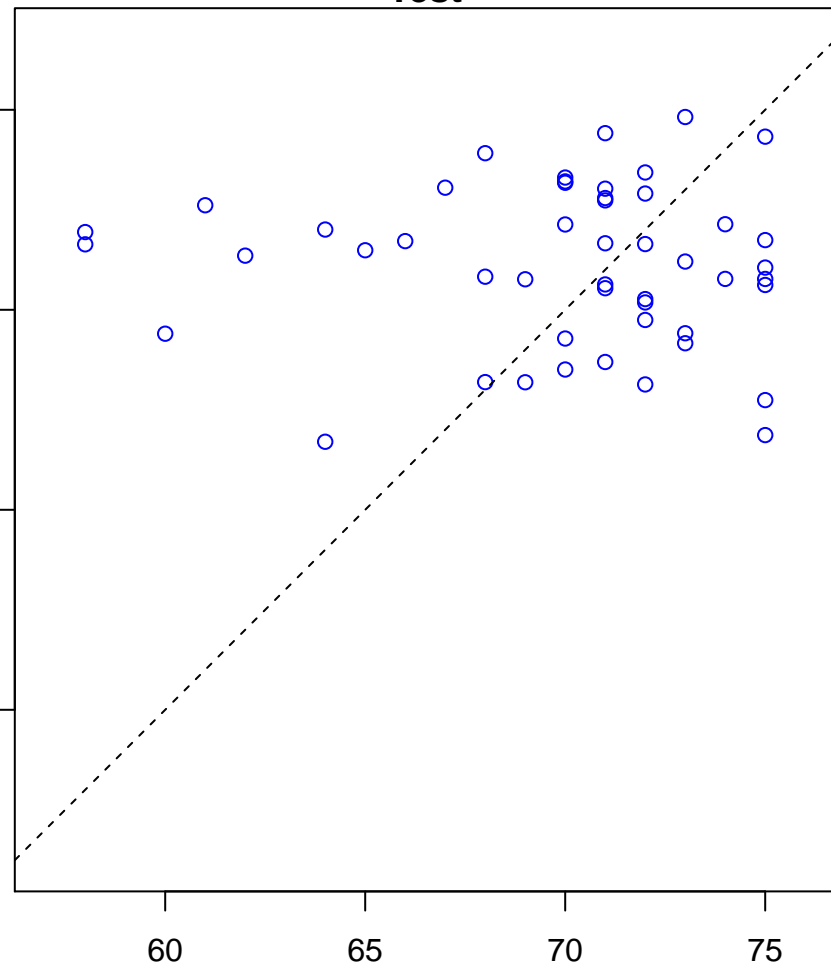


natural killer cell mediated cytotoxicity (Score: 0.944451)

Control

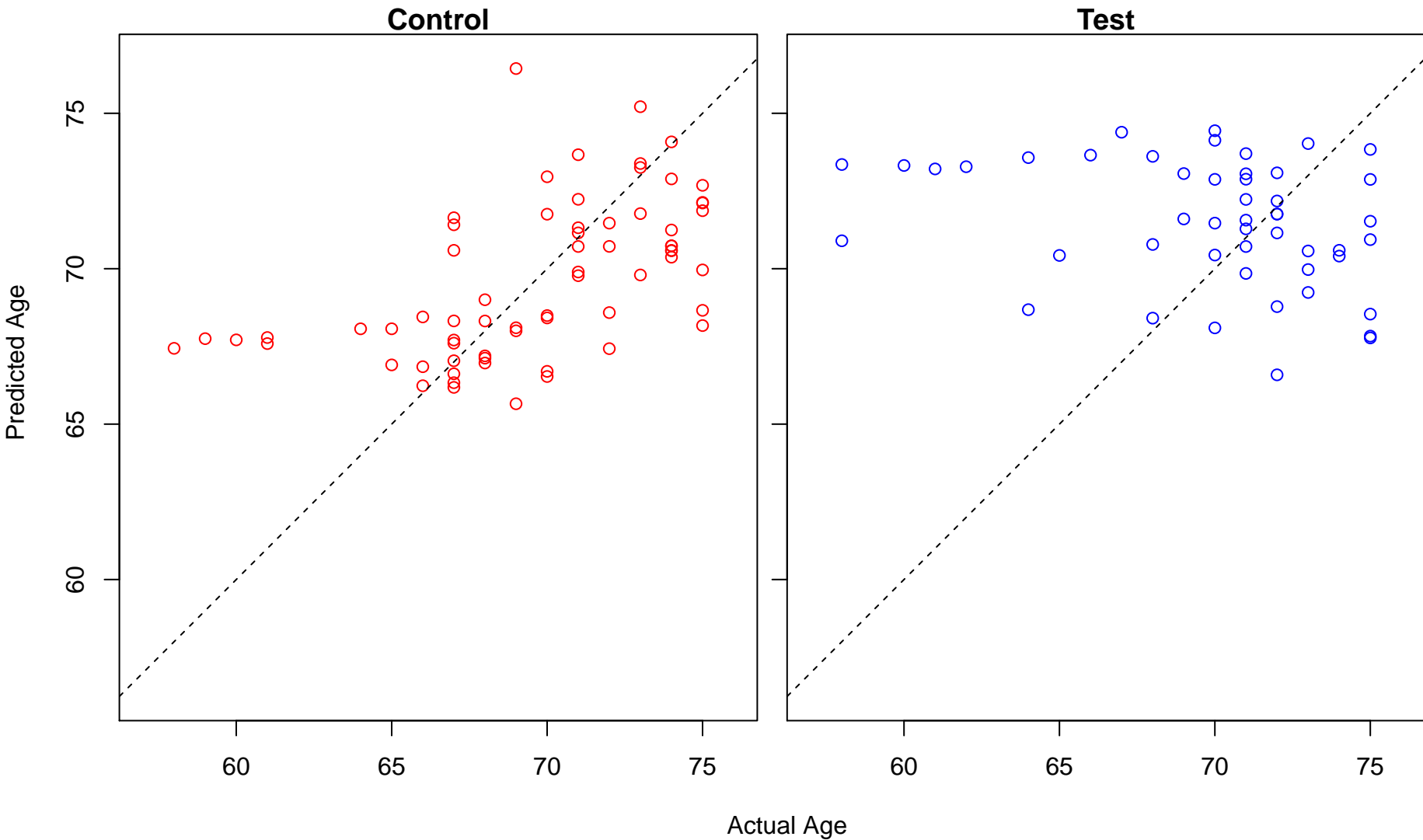


Test

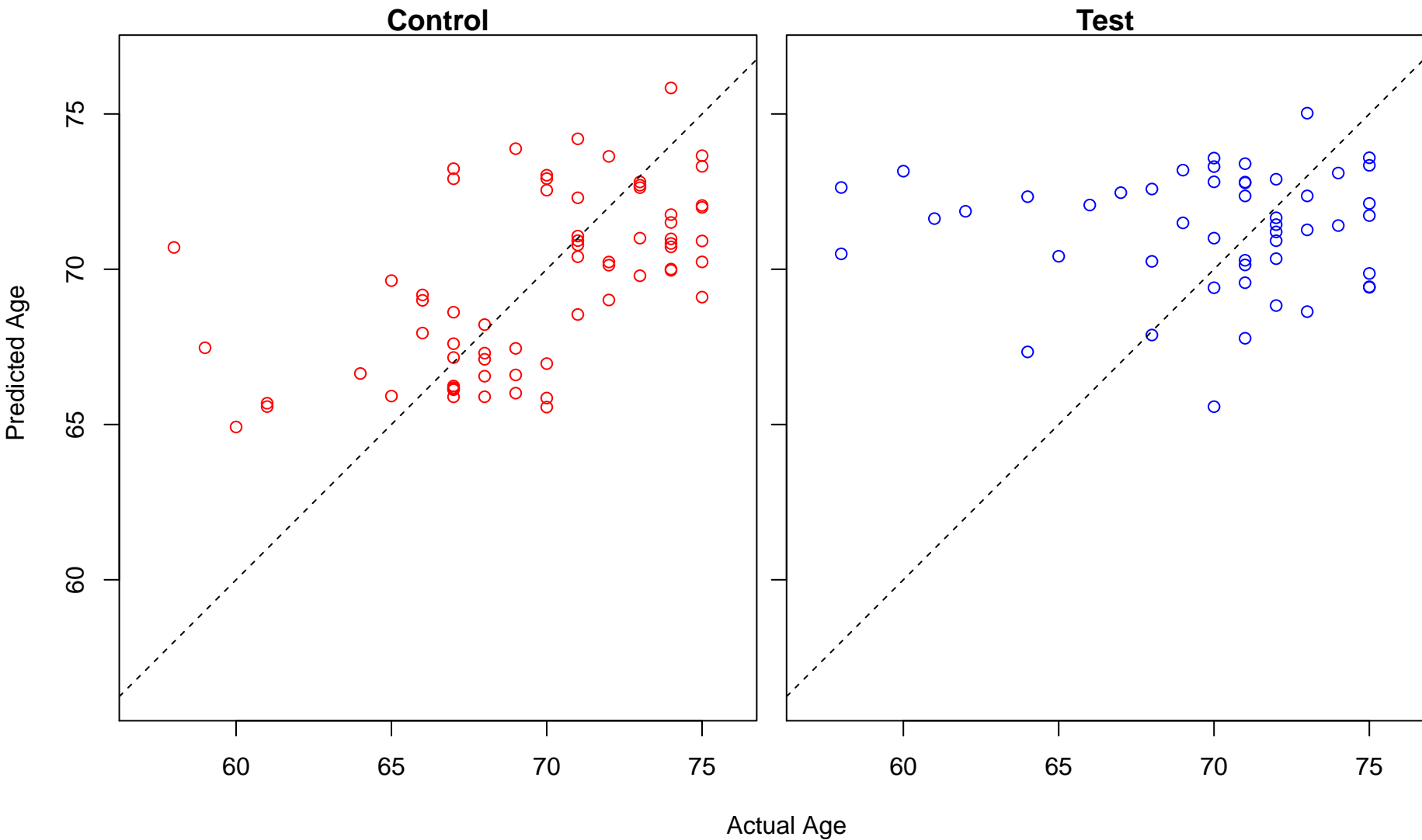


Actual Age

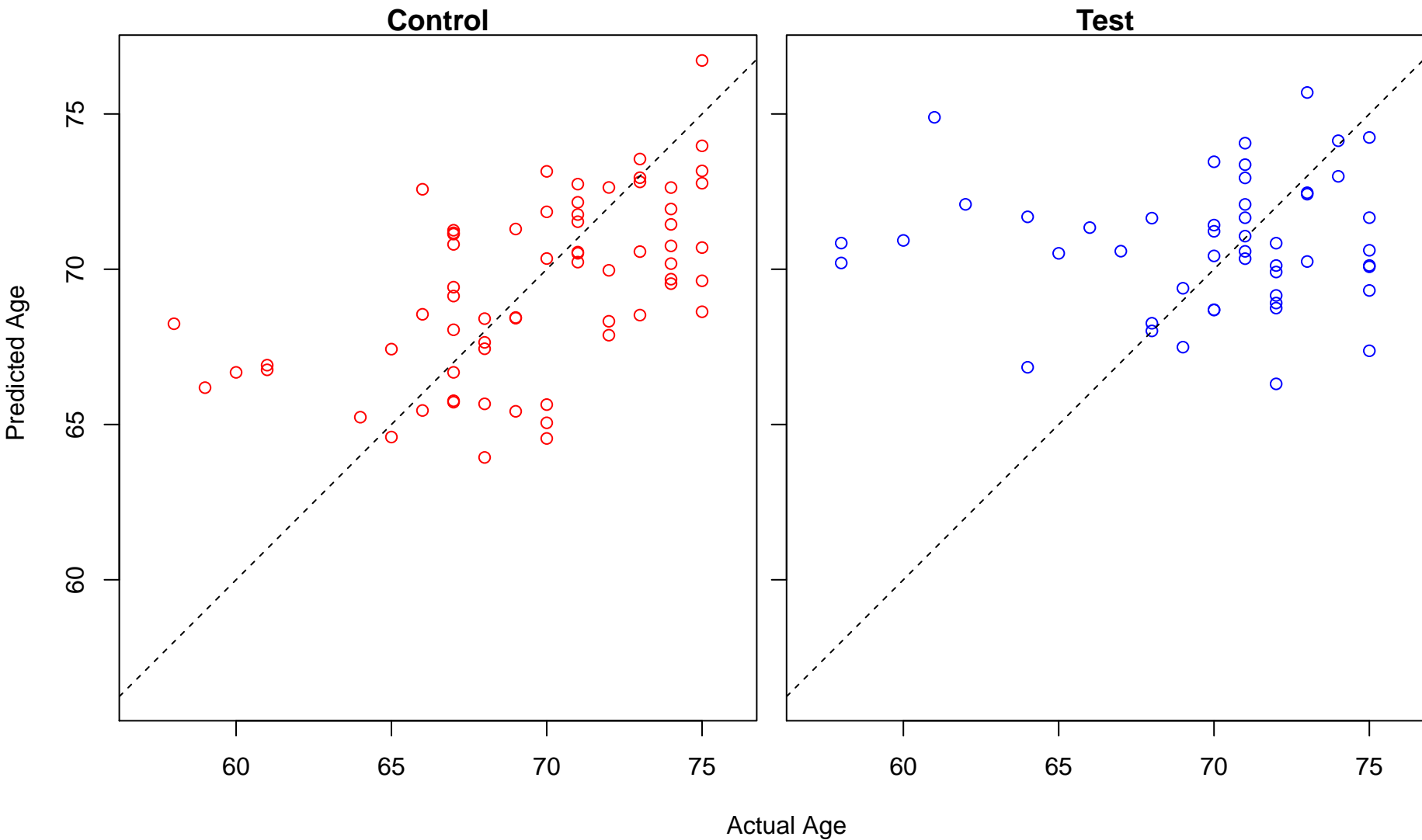
cellular response to corticosteroid stimulus (Score: 0.944408)



gliogenesis (Score: 0.944009)

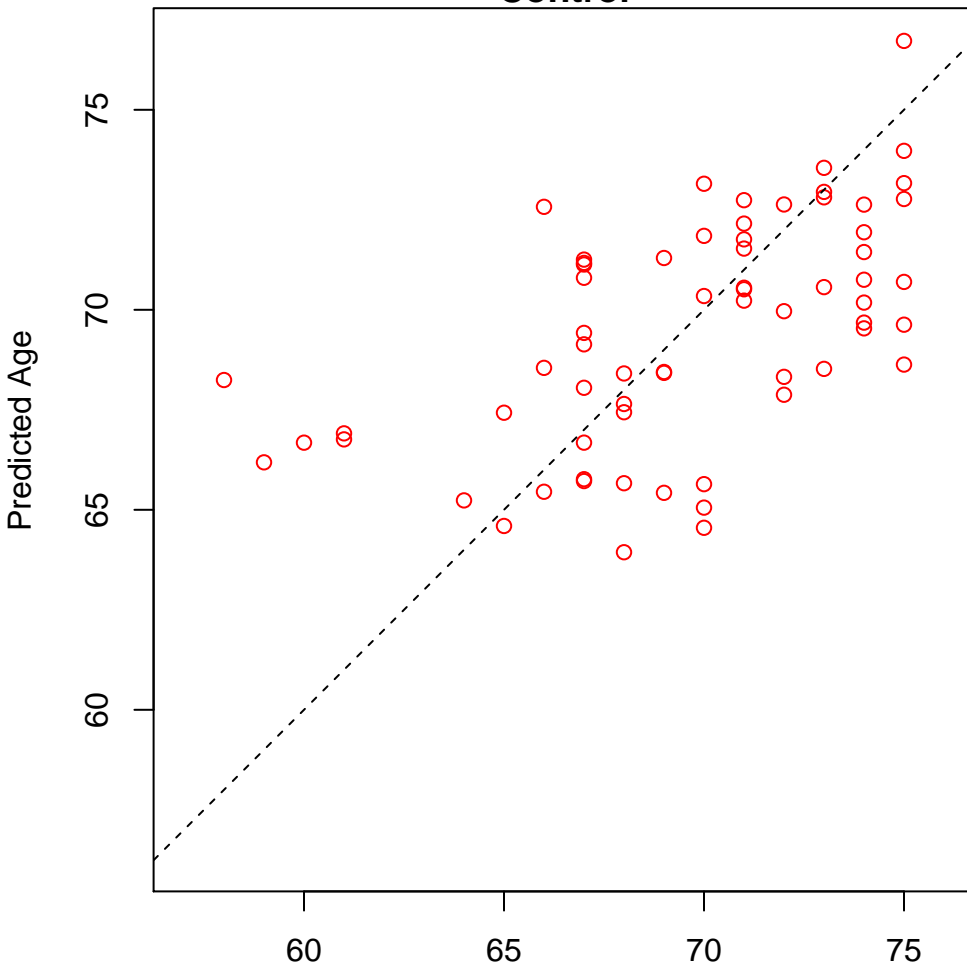


response to BMP (Score: 0.943859)

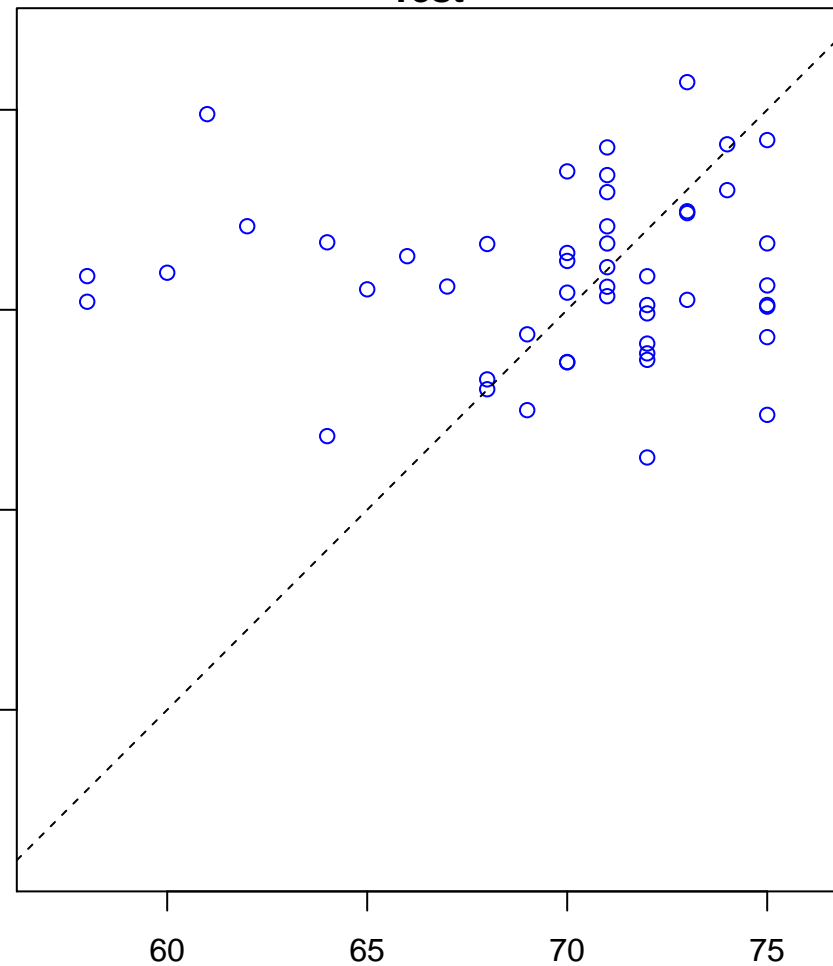


cellular response to BMP stimulus (Score: 0.943859)

Control



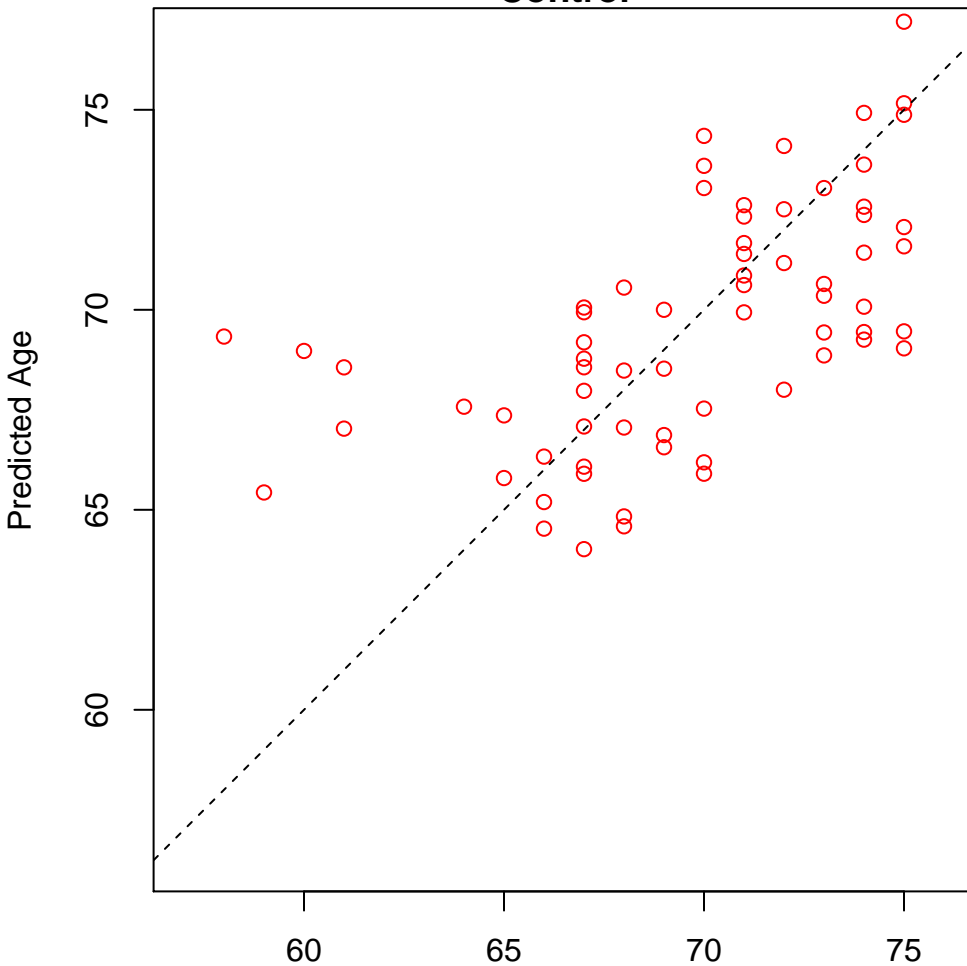
Test



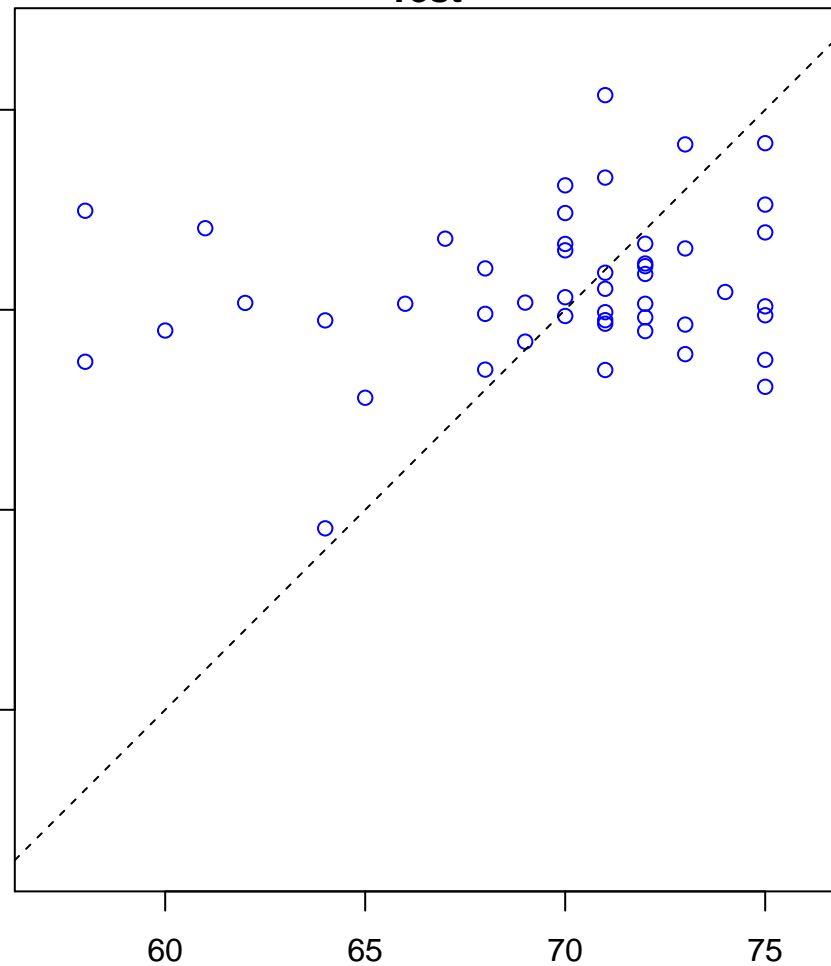
Actual Age

protein peptidyl–prolyl isomerization (Score: 0.943599)

Control

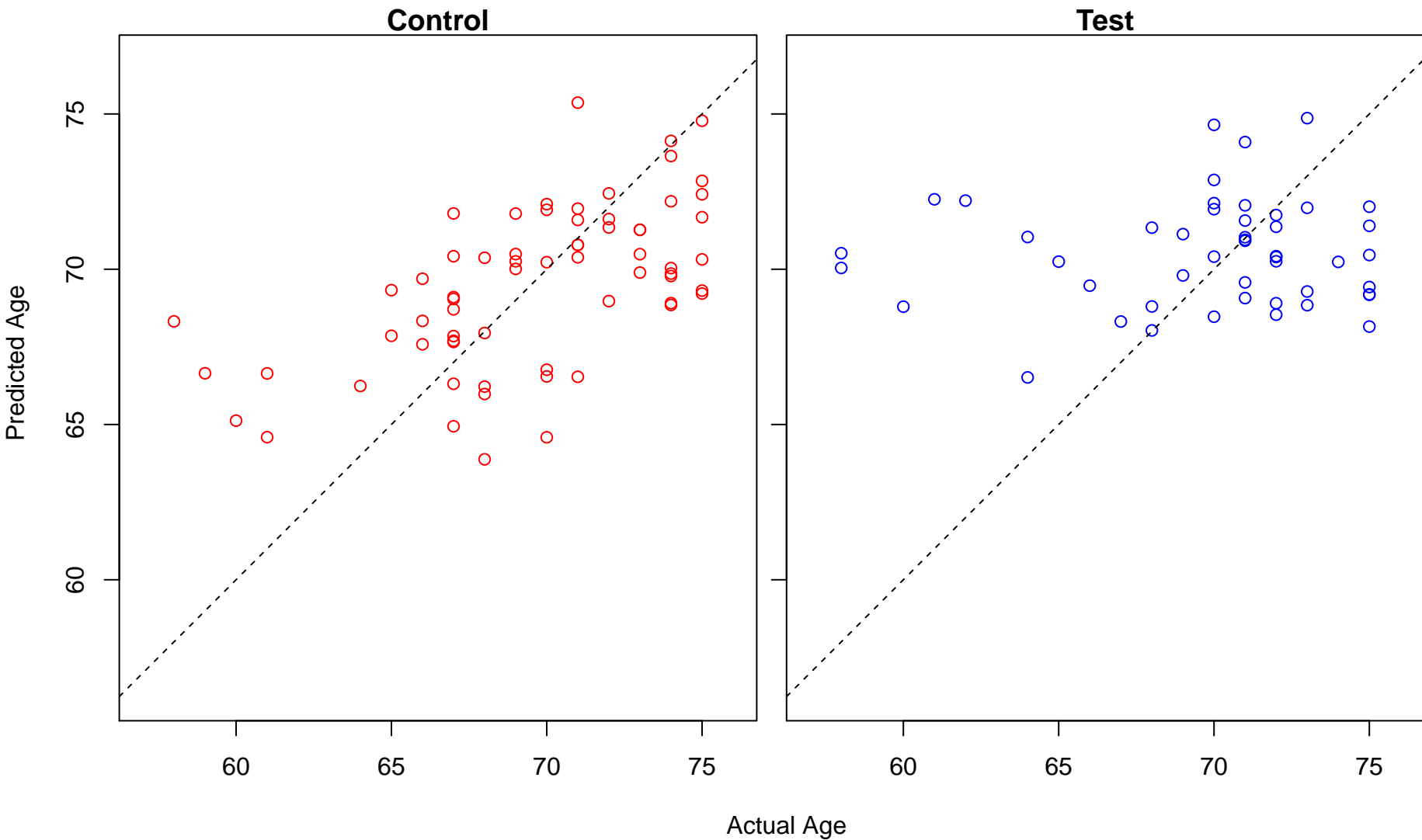


Test

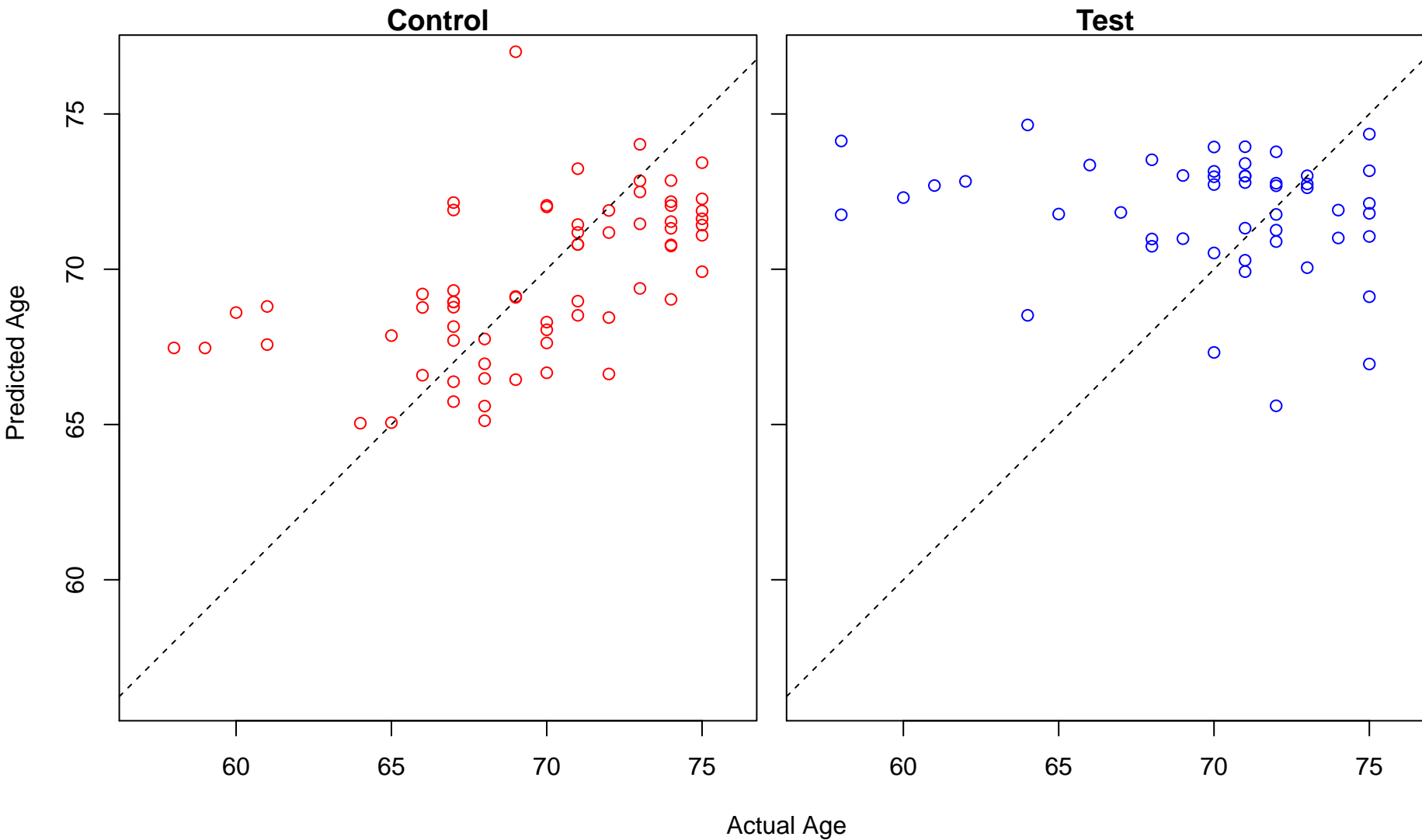


Actual Age

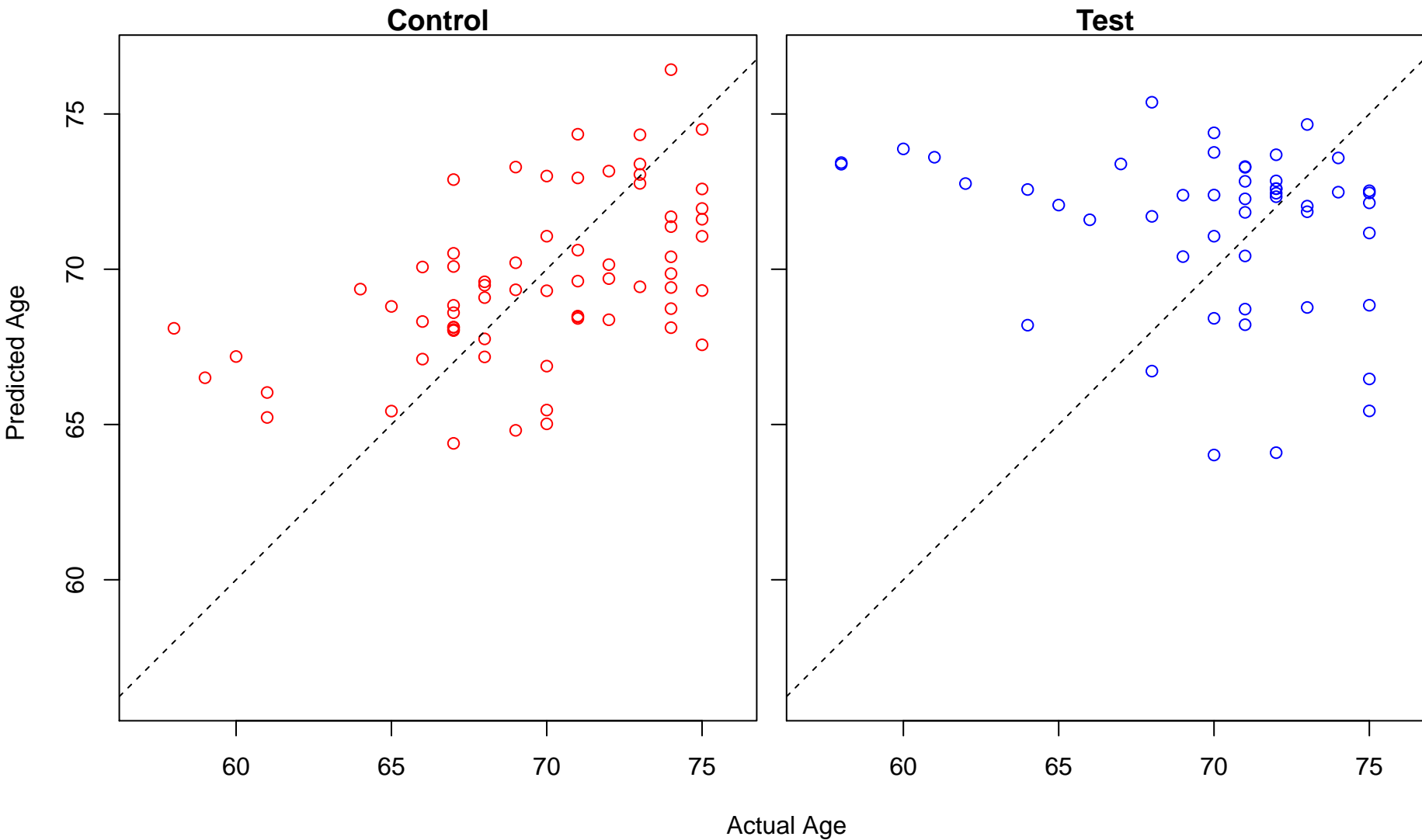
hexose catabolic process (Score: 0.943502)



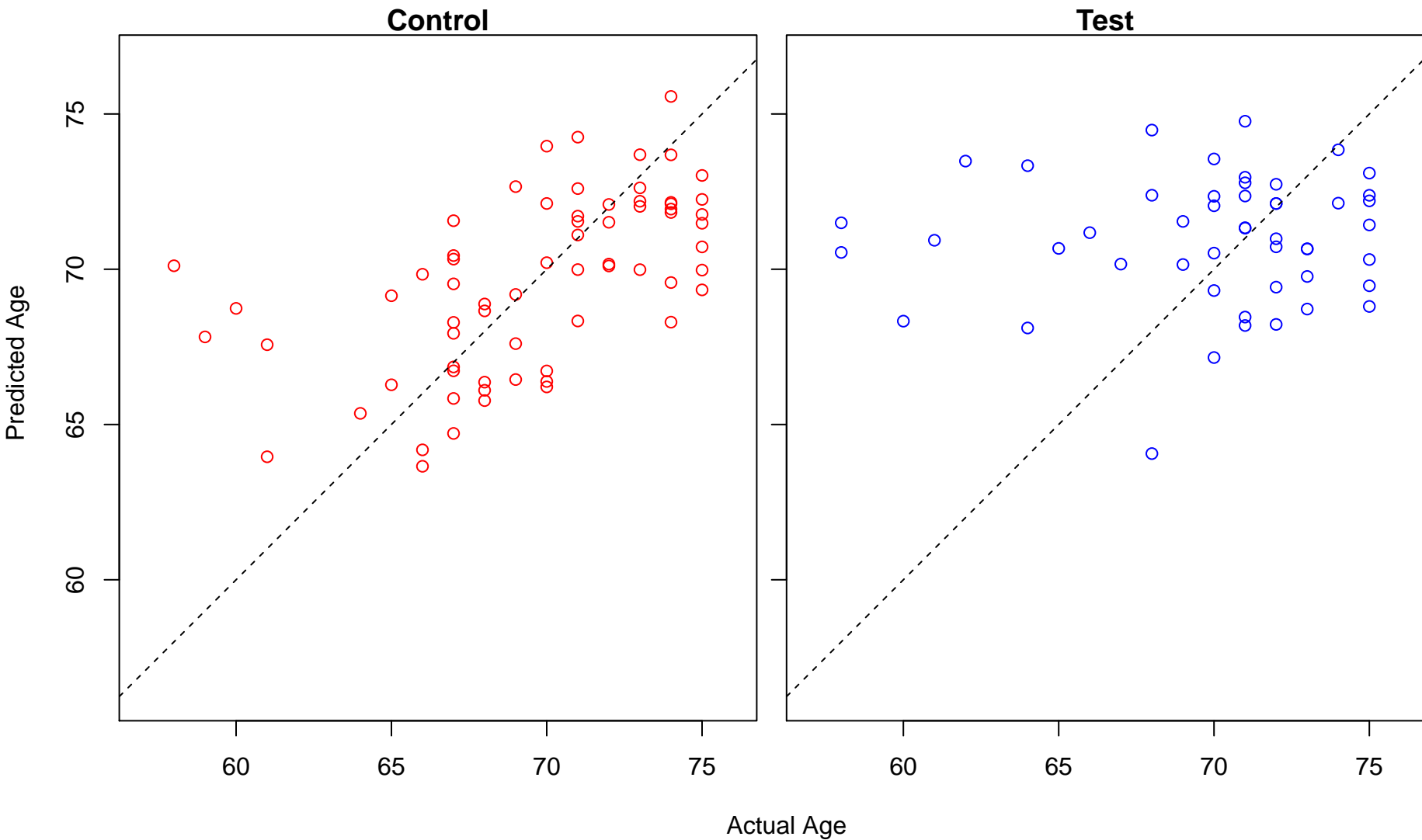
ketone body biosynthetic process (Score: 0.943137)



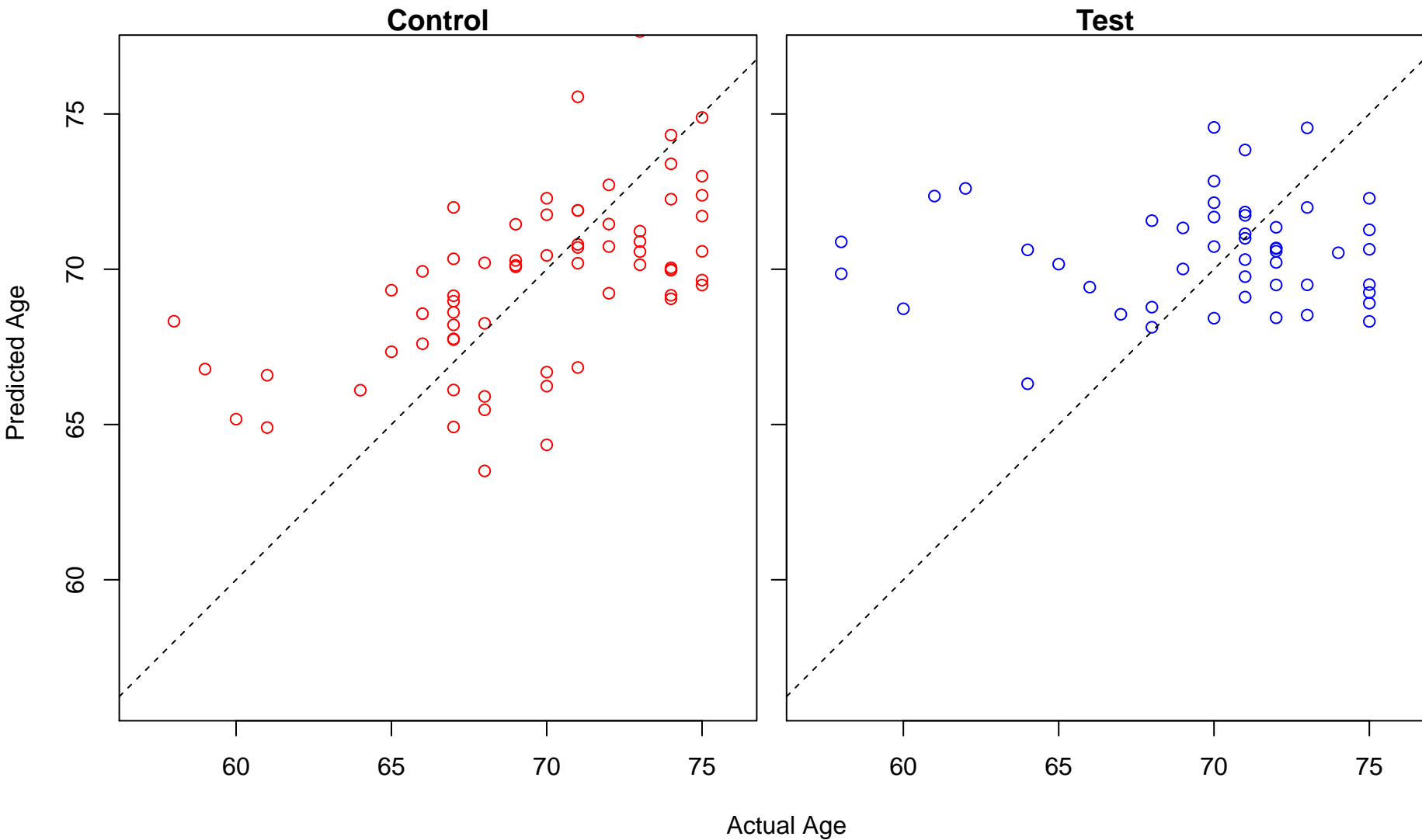
pantothenate metabolic process (Score: 0.942143)



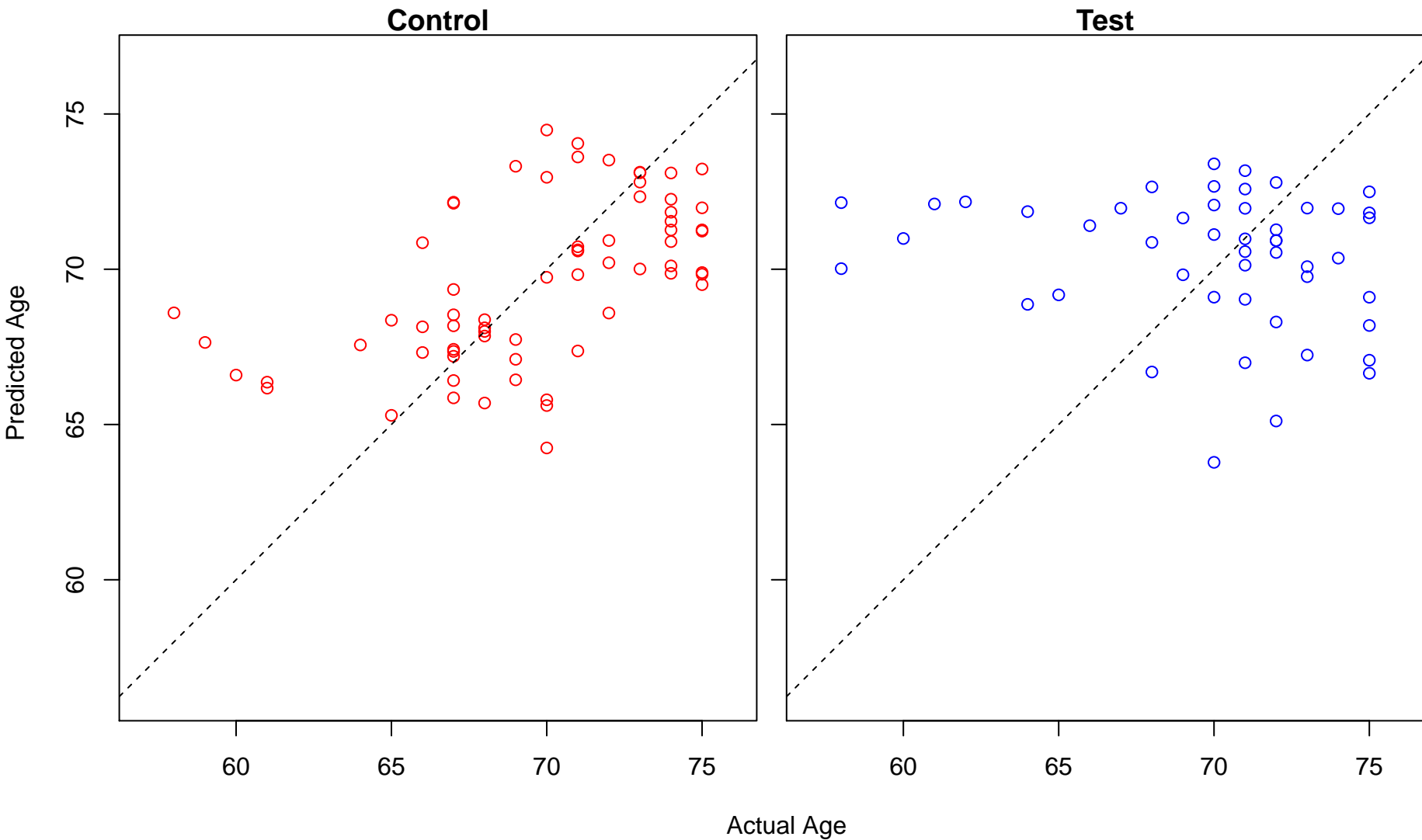
cellular response to calcium ion (Score: 0.941992)



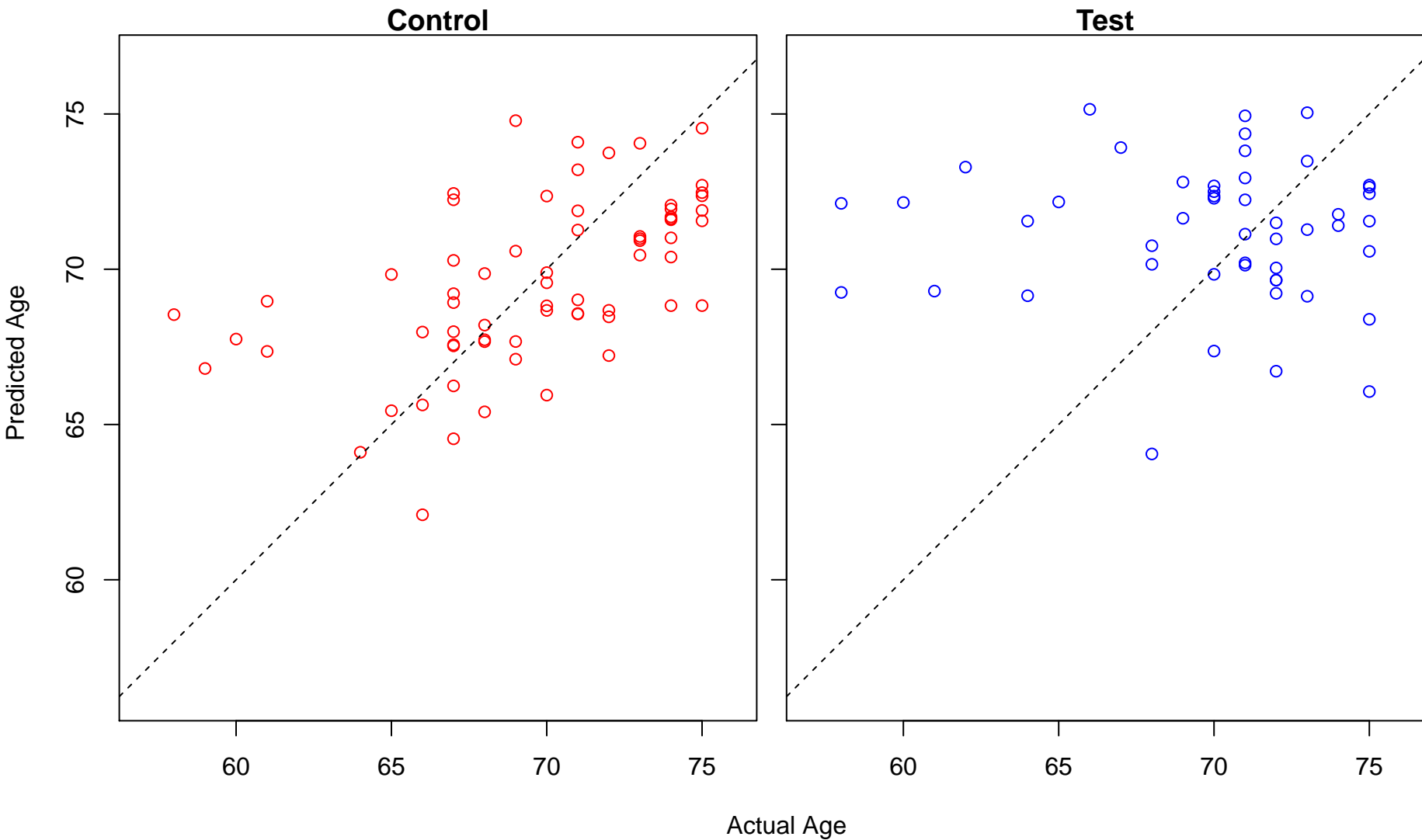
ADP metabolic process (Score: 0.941868)



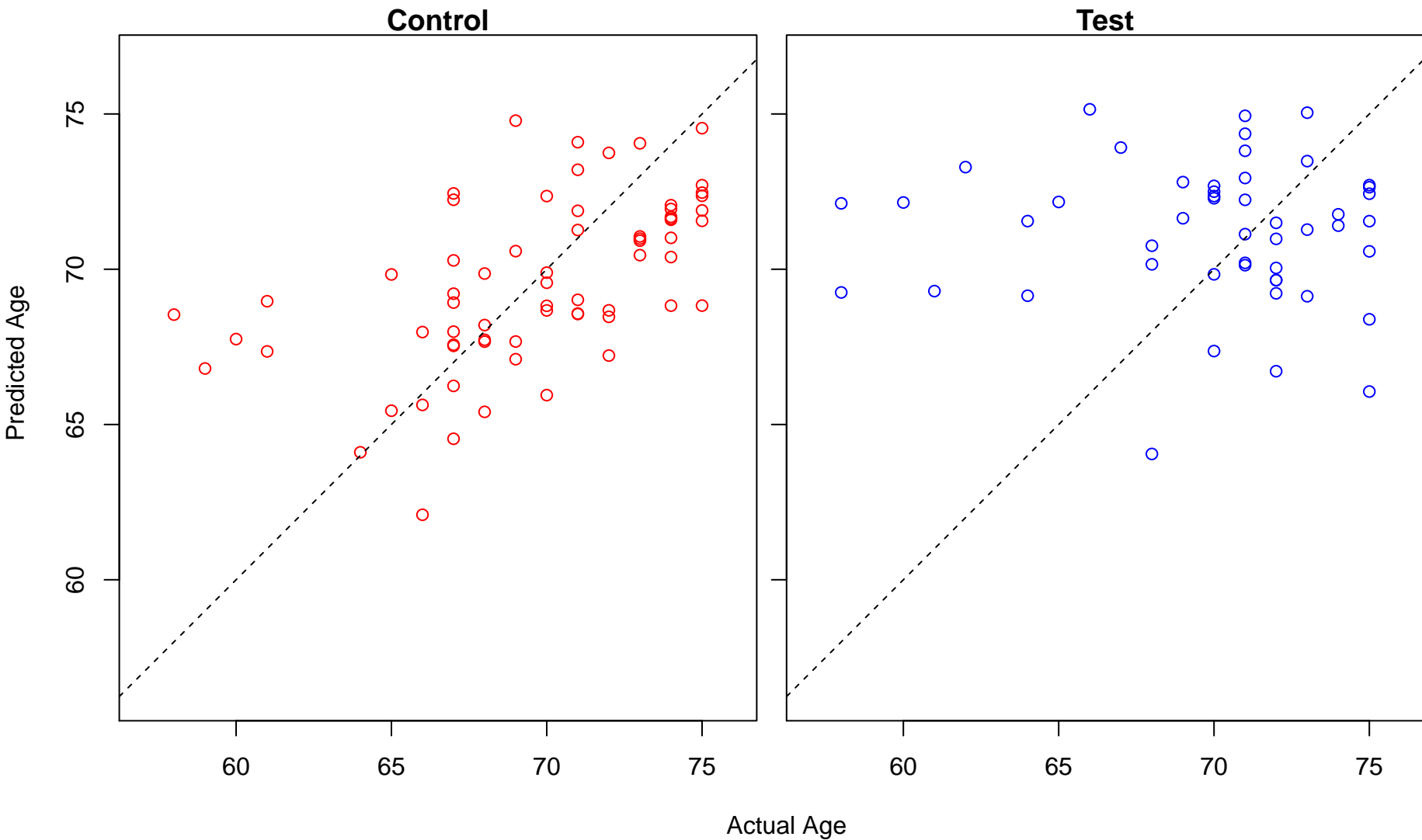
regulation of tumor necrosis factor production (Score: 0.941505)



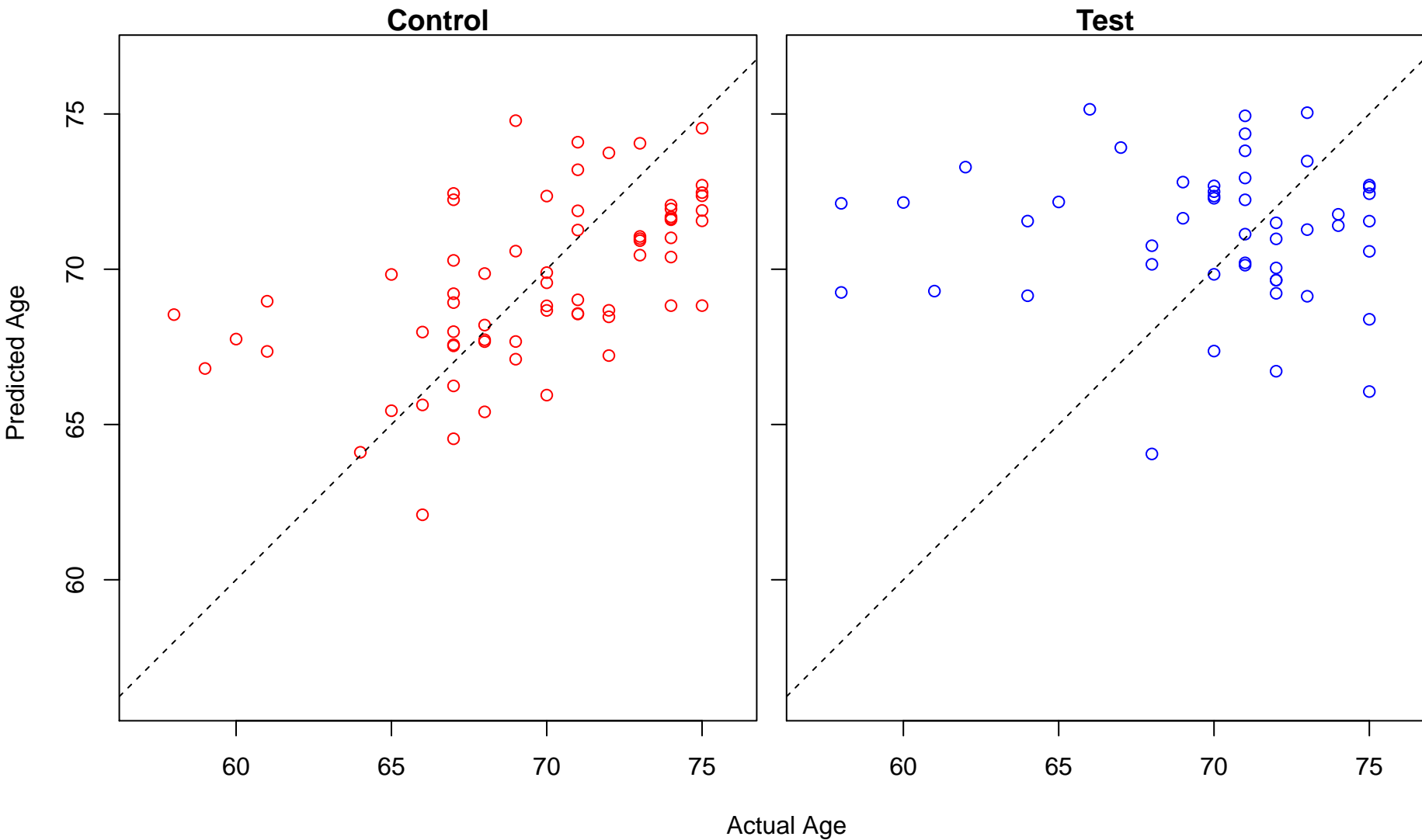
regulation of natural killer cell mediated immune response to tumor cell (Score: 0.941263)



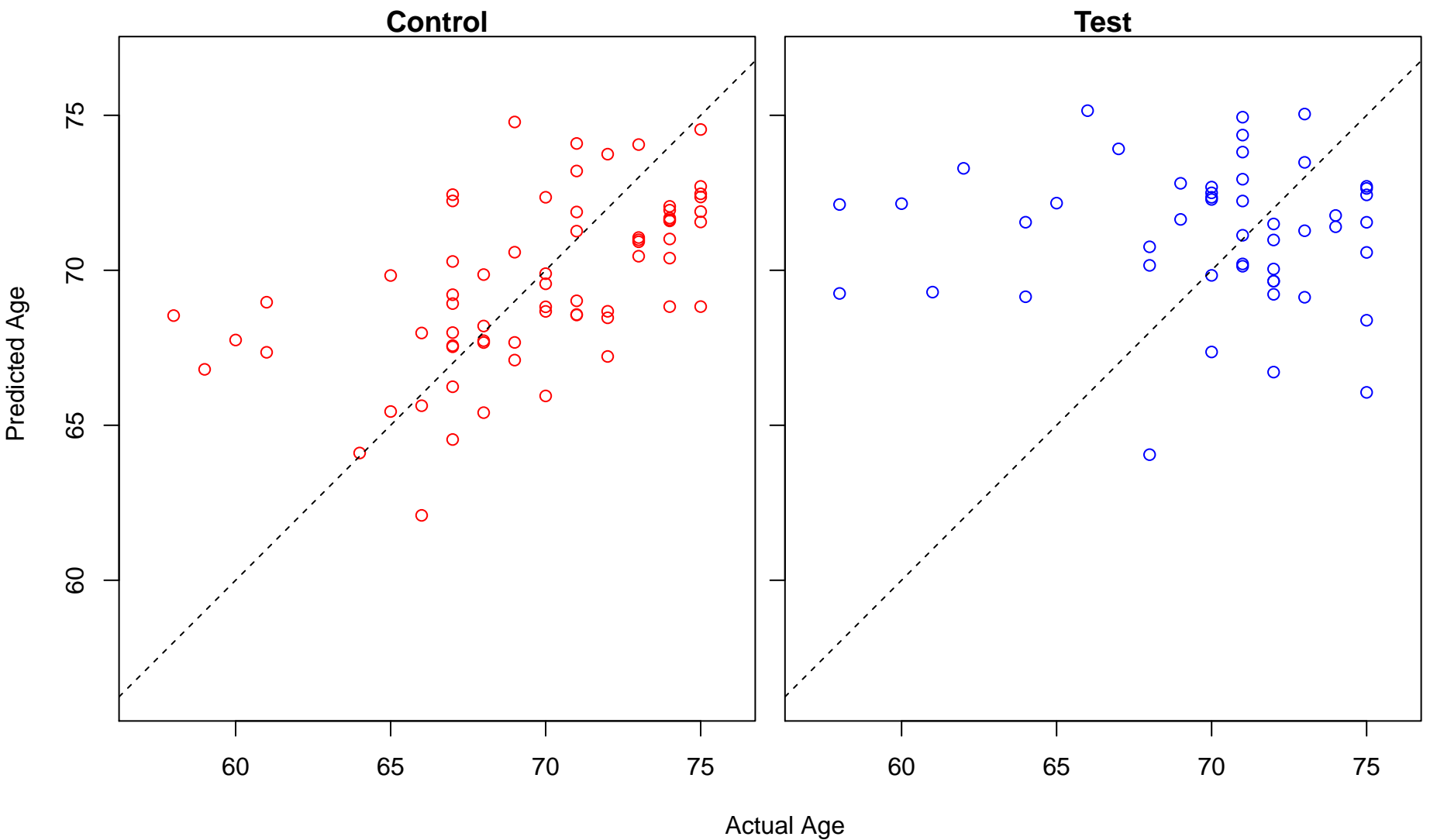
positive regulation of natural killer cell mediated immune response to tumor cell (Score: 0.941263)



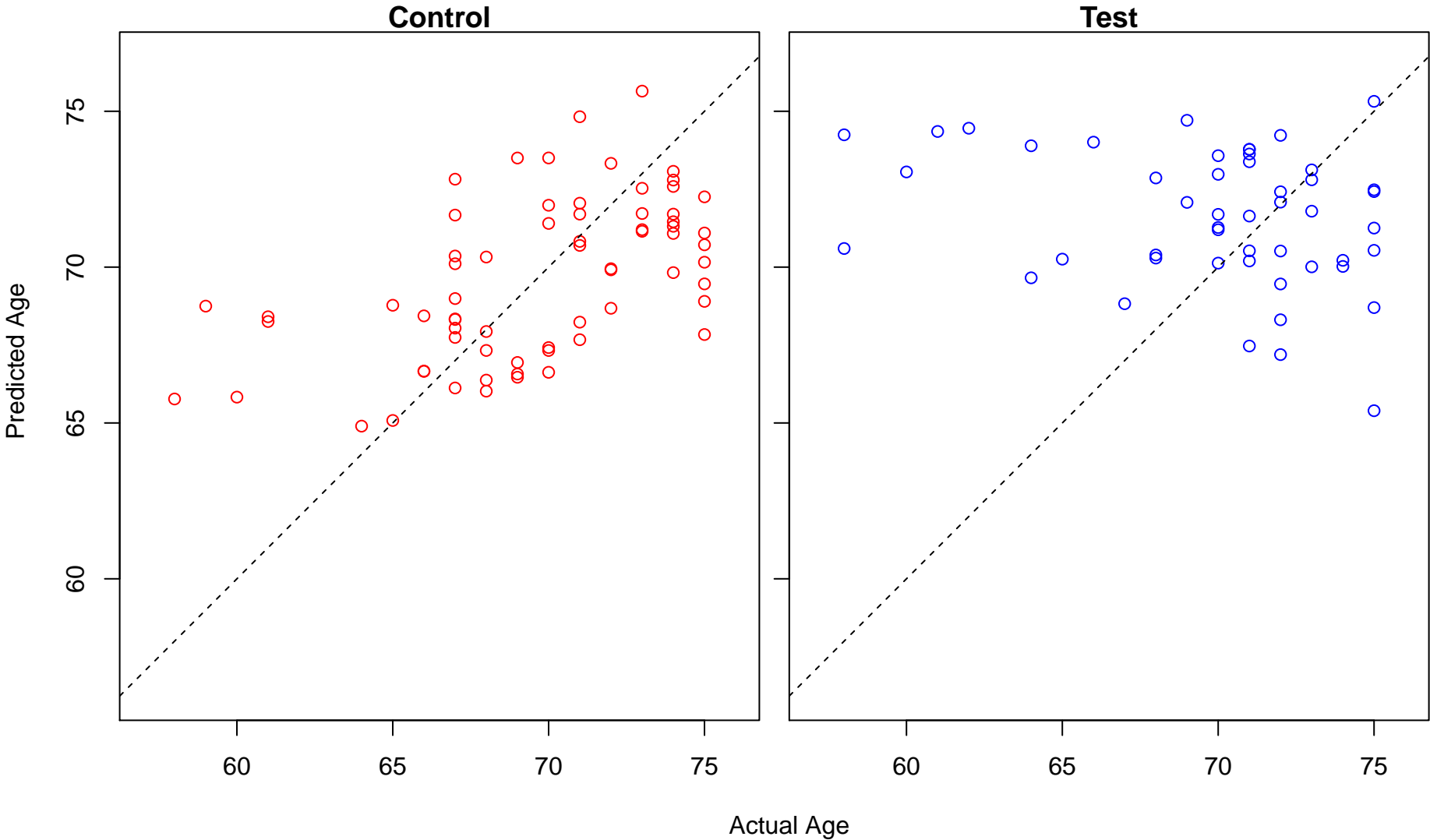
regulation of natural killer cell mediated cytotoxicity directed against tumor cell target (Score: 0.9412)



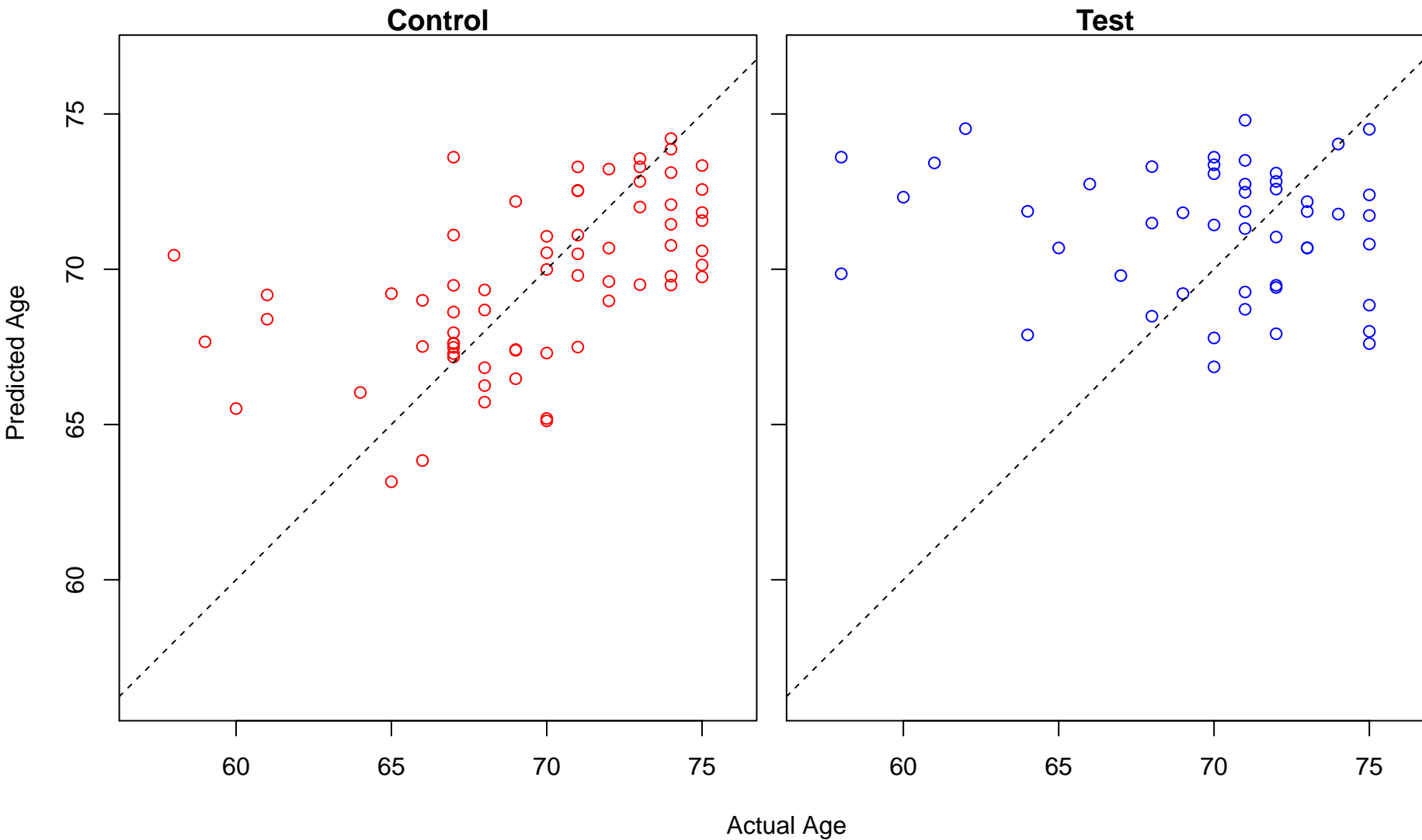
positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target (Score: 0.0)



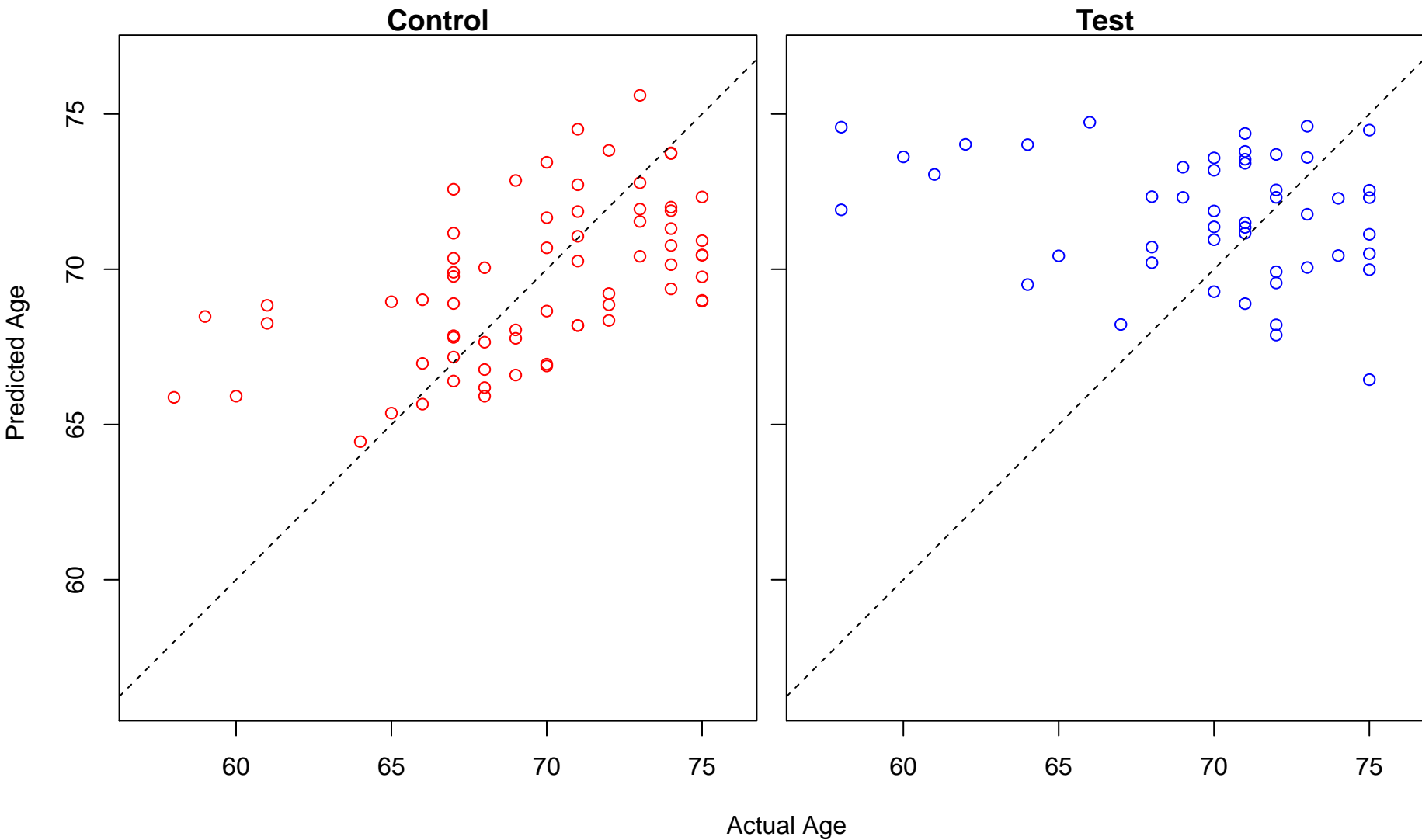
regulation of transcription from RNA polymerase II promoter involved in heart development (Score: 0.94)



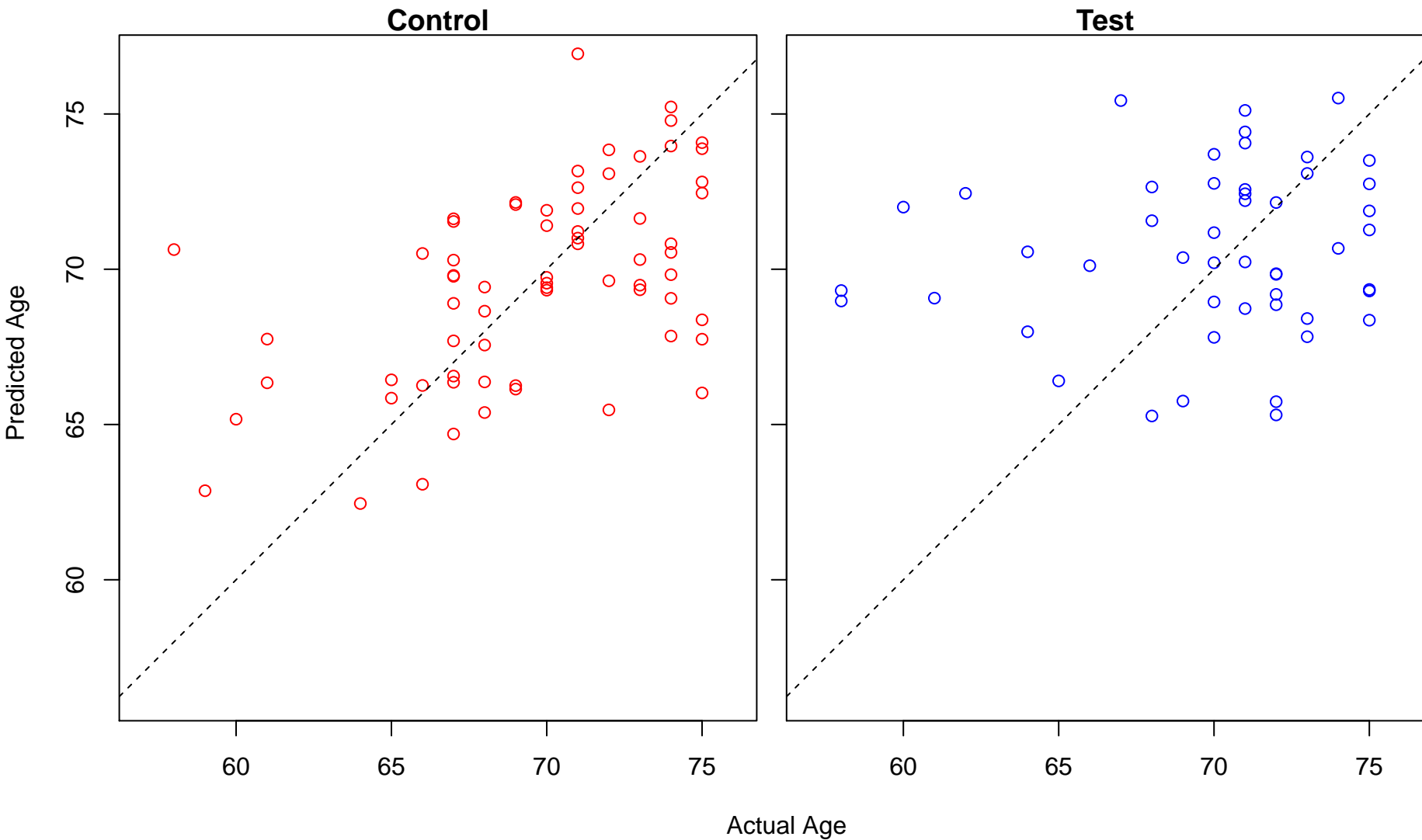
response to muramyl dipeptide (Score: 0.940025)



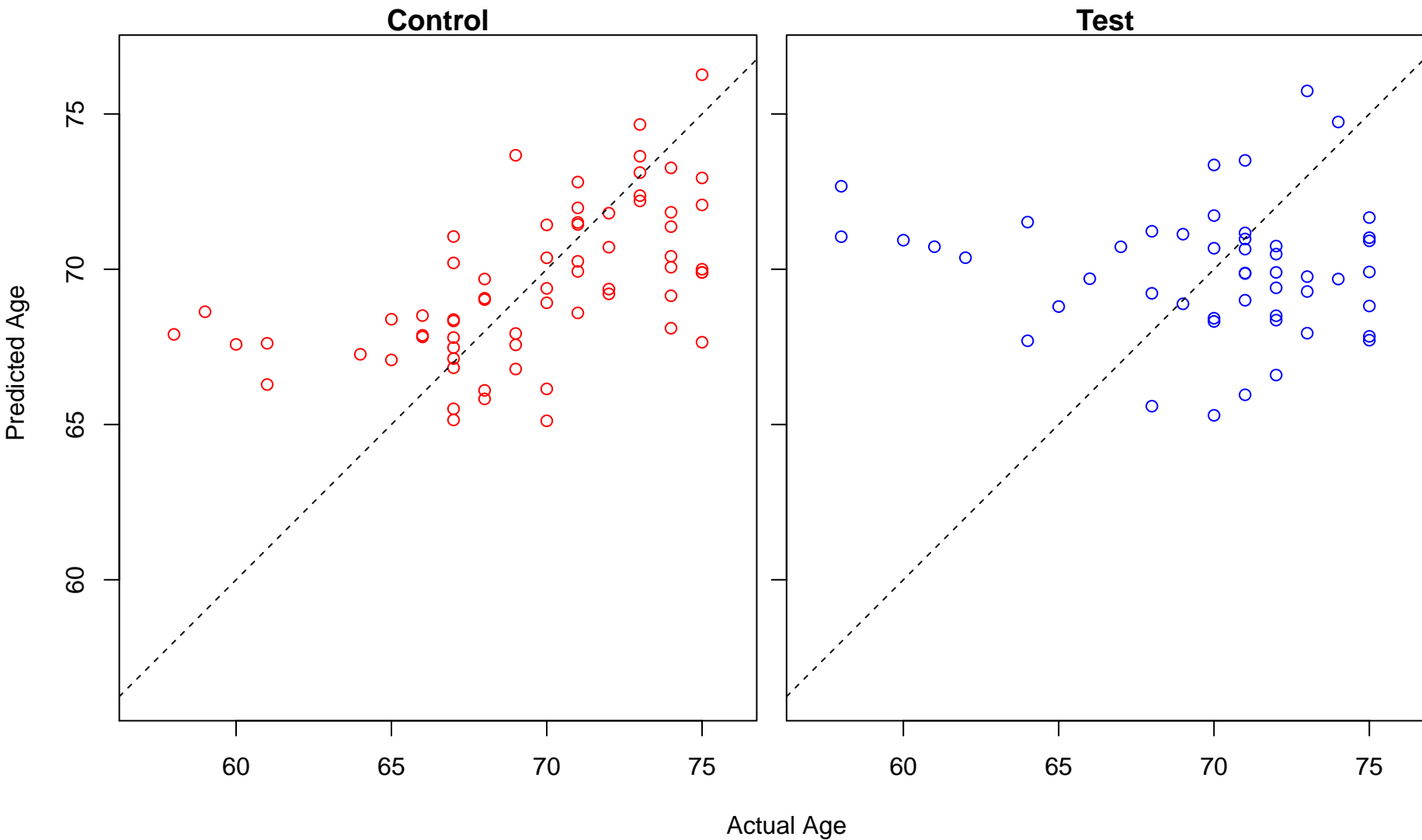
artery development (Score: 0.939673)



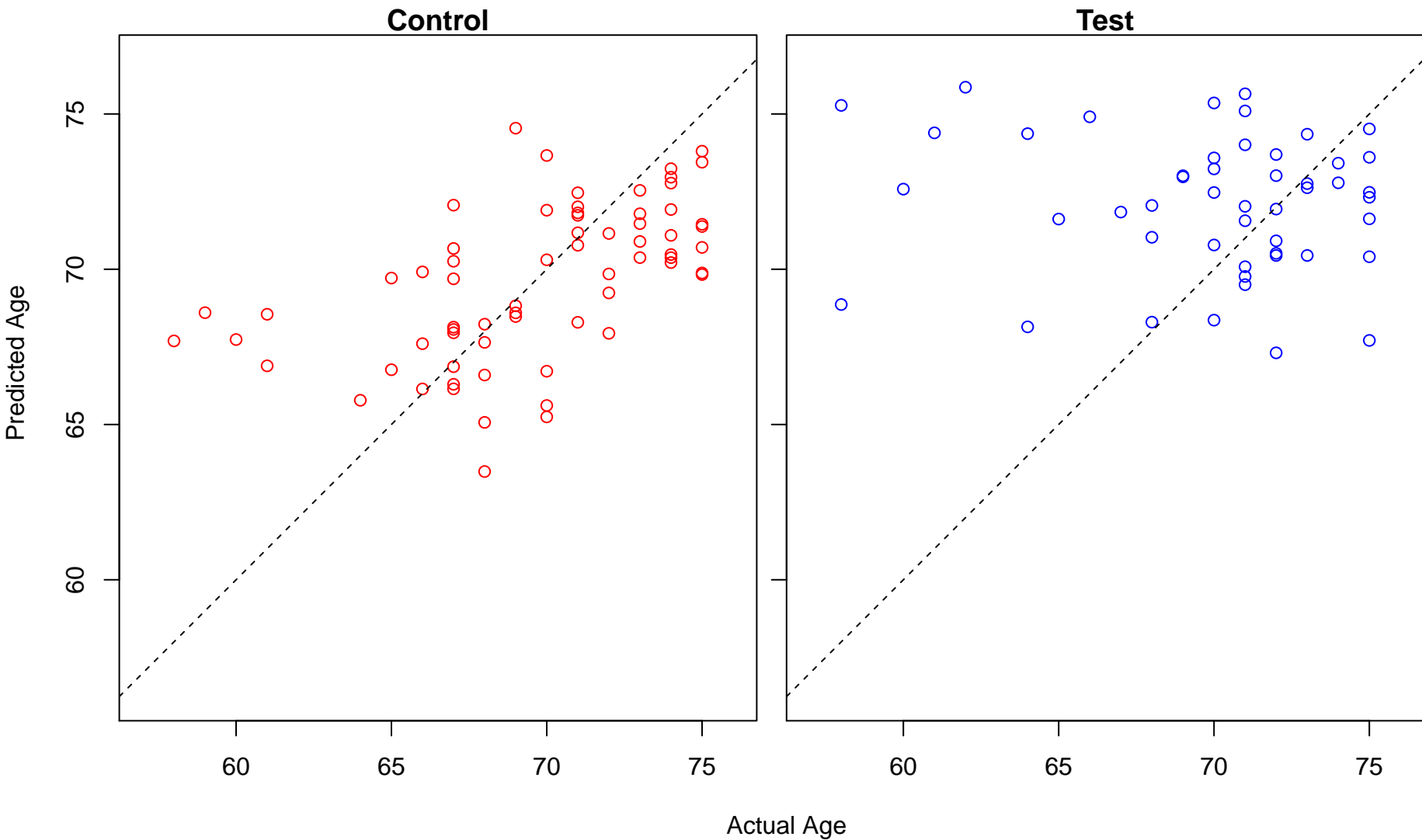
mesoderm formation (Score: 0.939620)



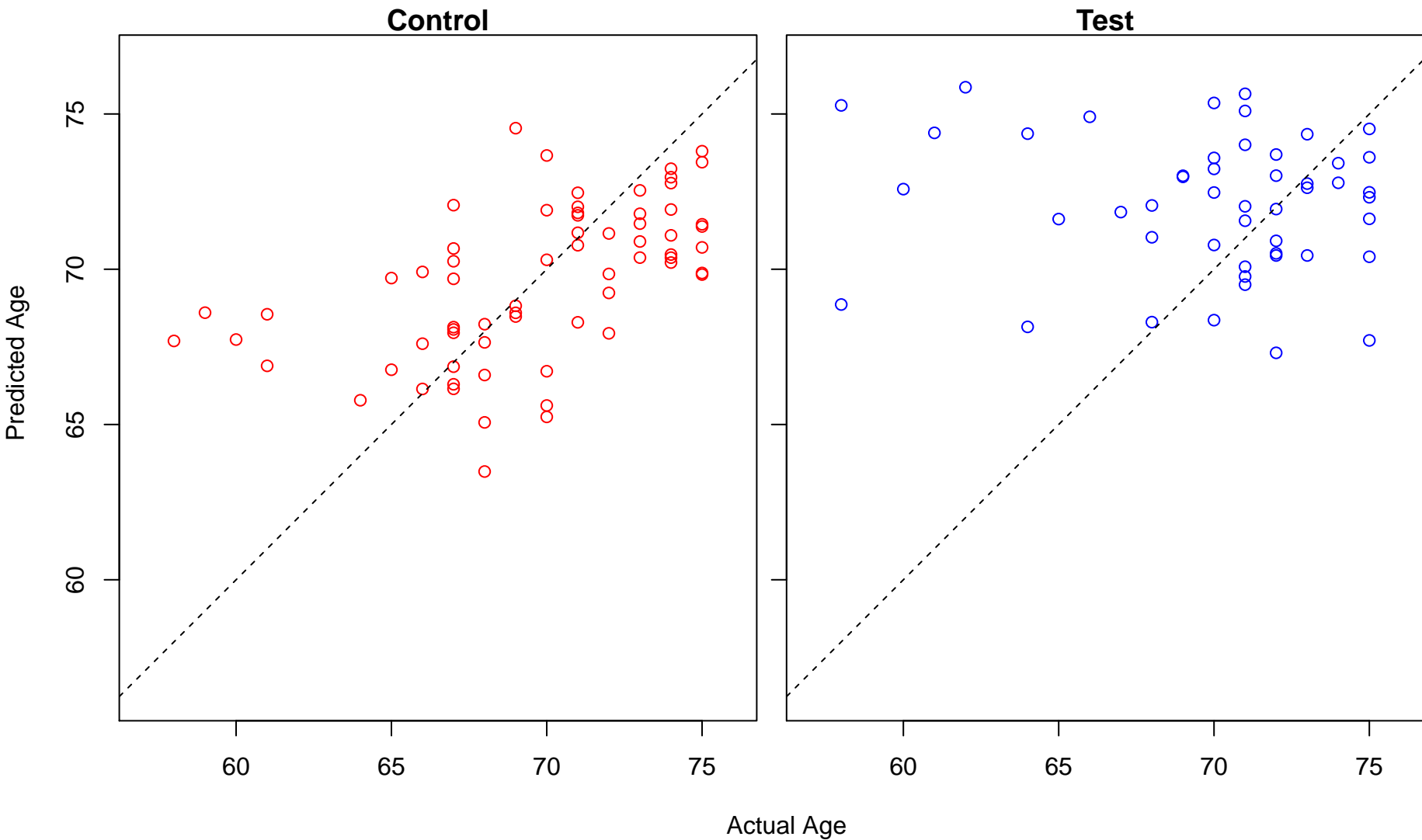
oligodendrocyte development (Score: 0.939590)



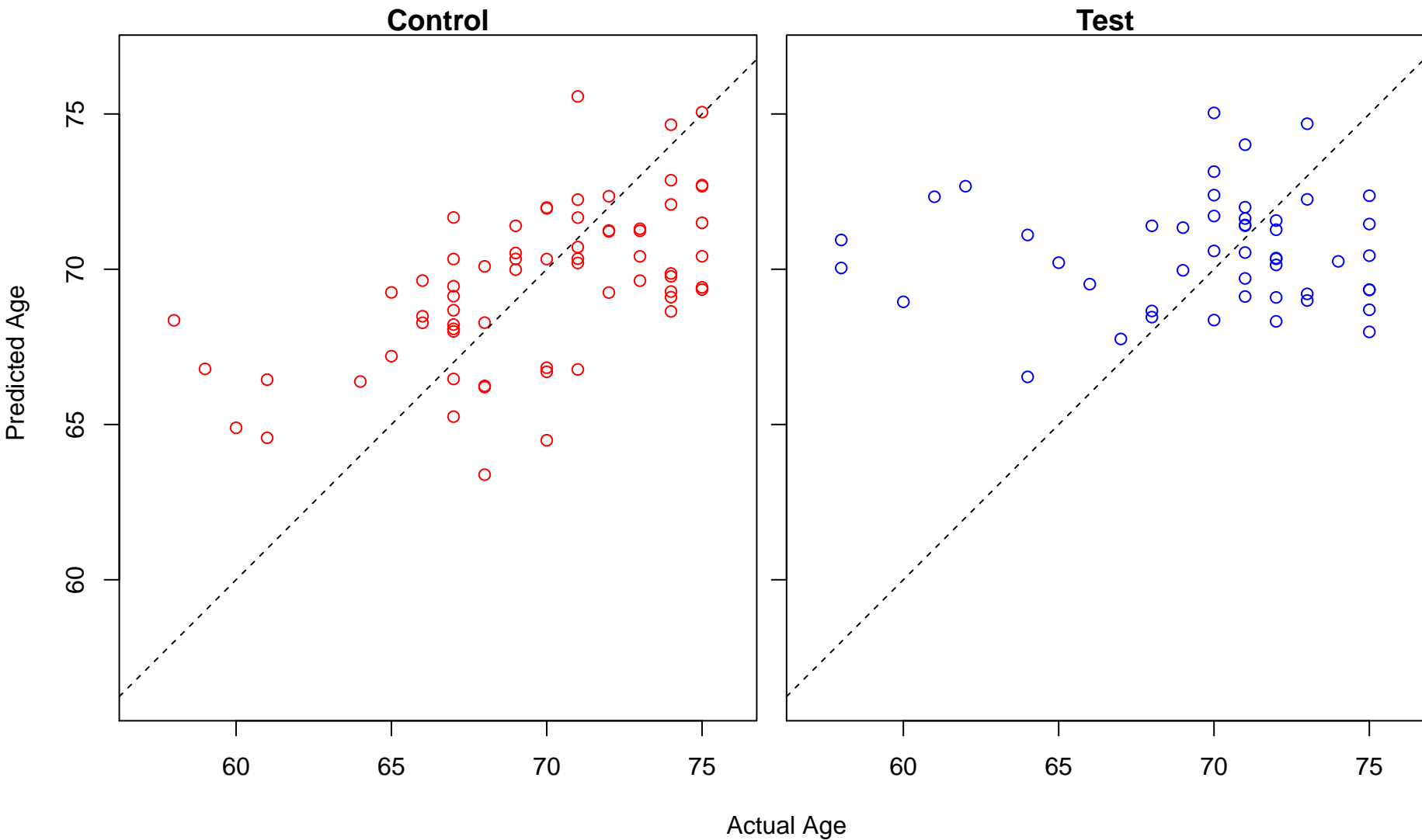
protein polyufmylation (Score: 0.938170)



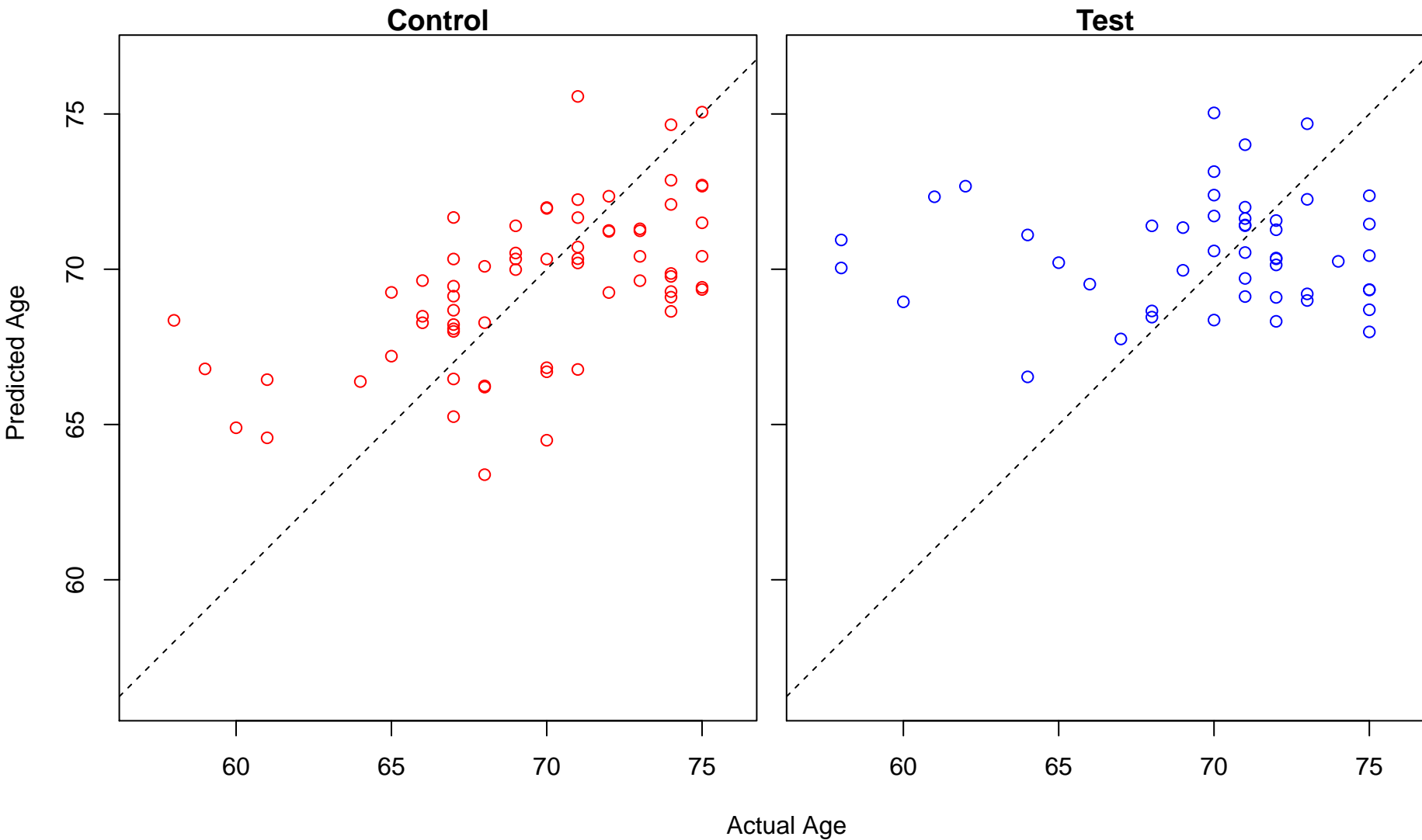
protein K69-linked ufmylation (Score: 0.938170)



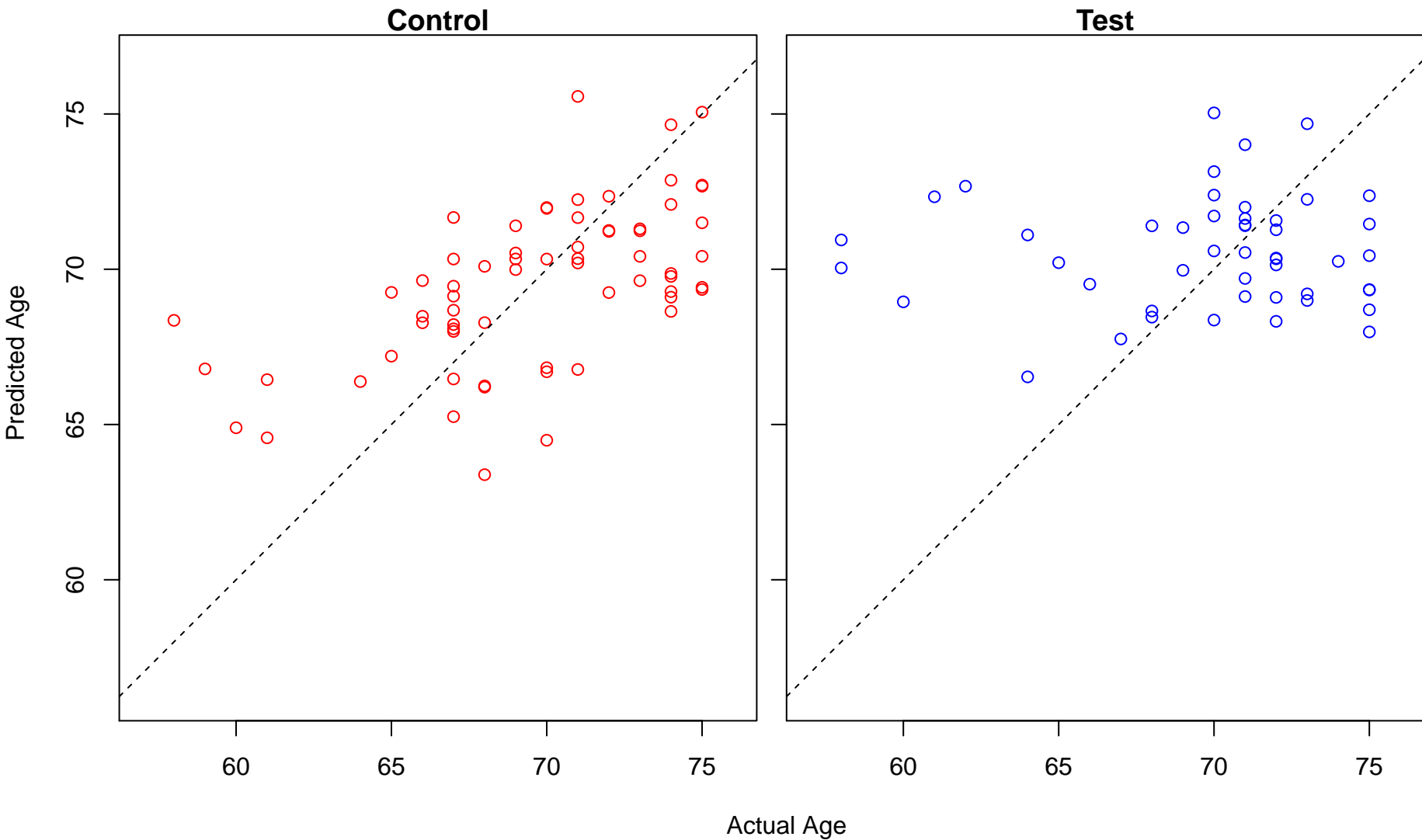
NADH regeneration (Score: 0.937843)



glycolytic process through glucose-6-phosphate (Score: 0.937843)

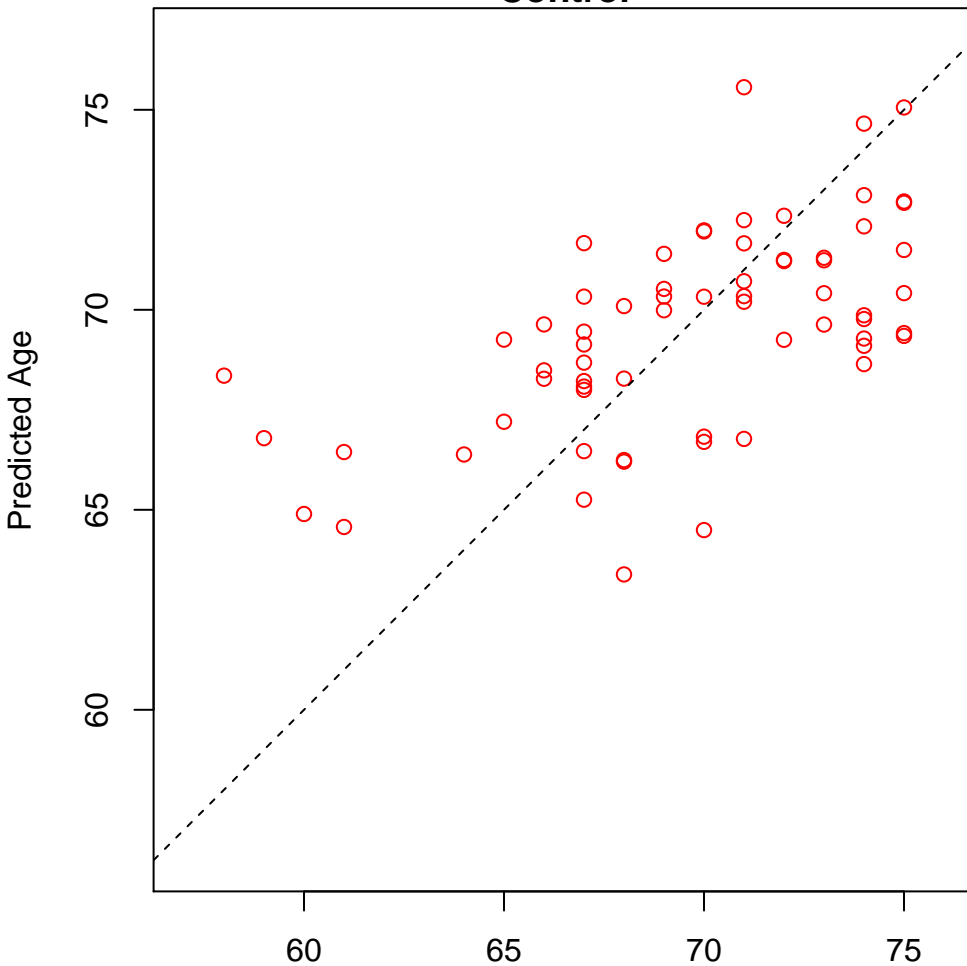


canonical glycolysis (Score: 0.937843)

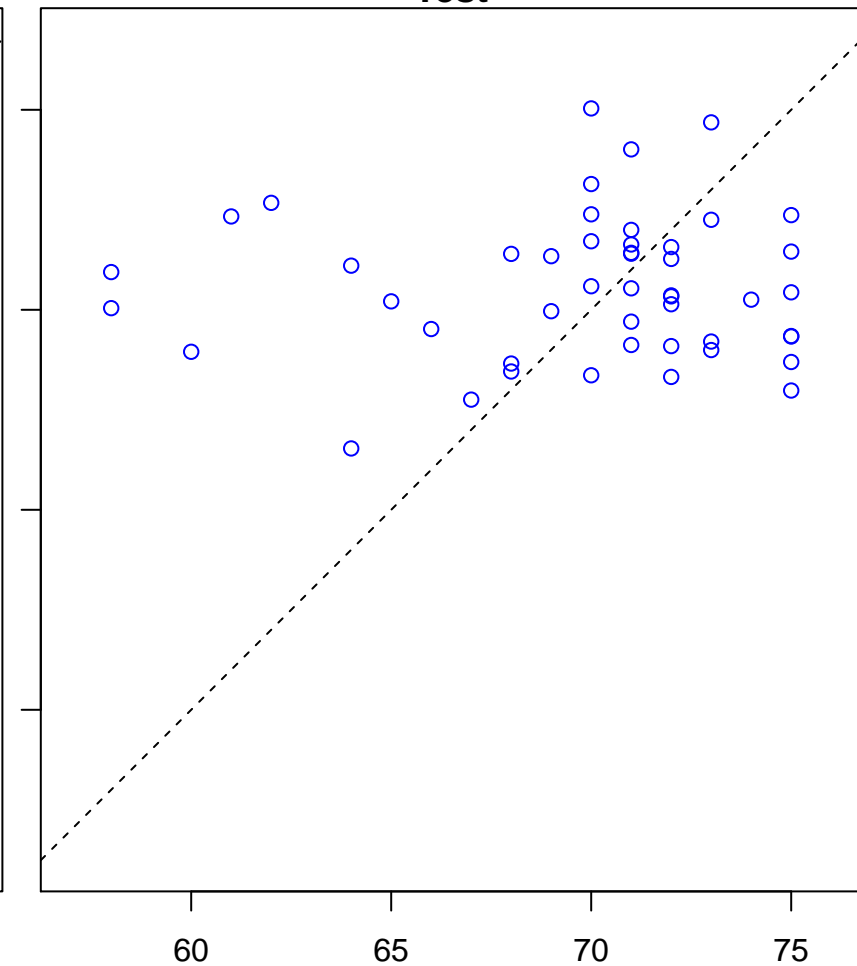


glucose catabolic process to pyruvate (Score: 0.937843)

Control

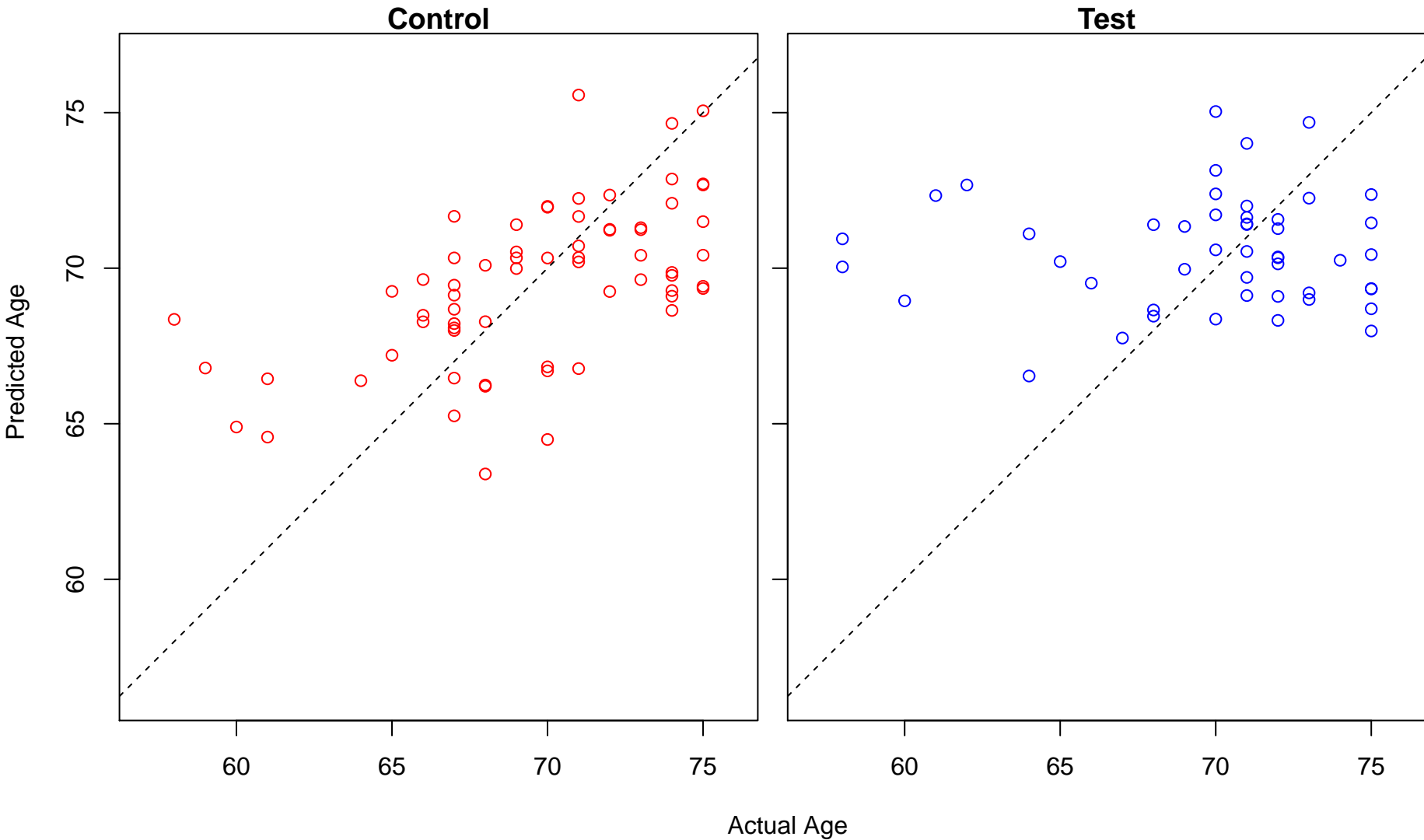


Test



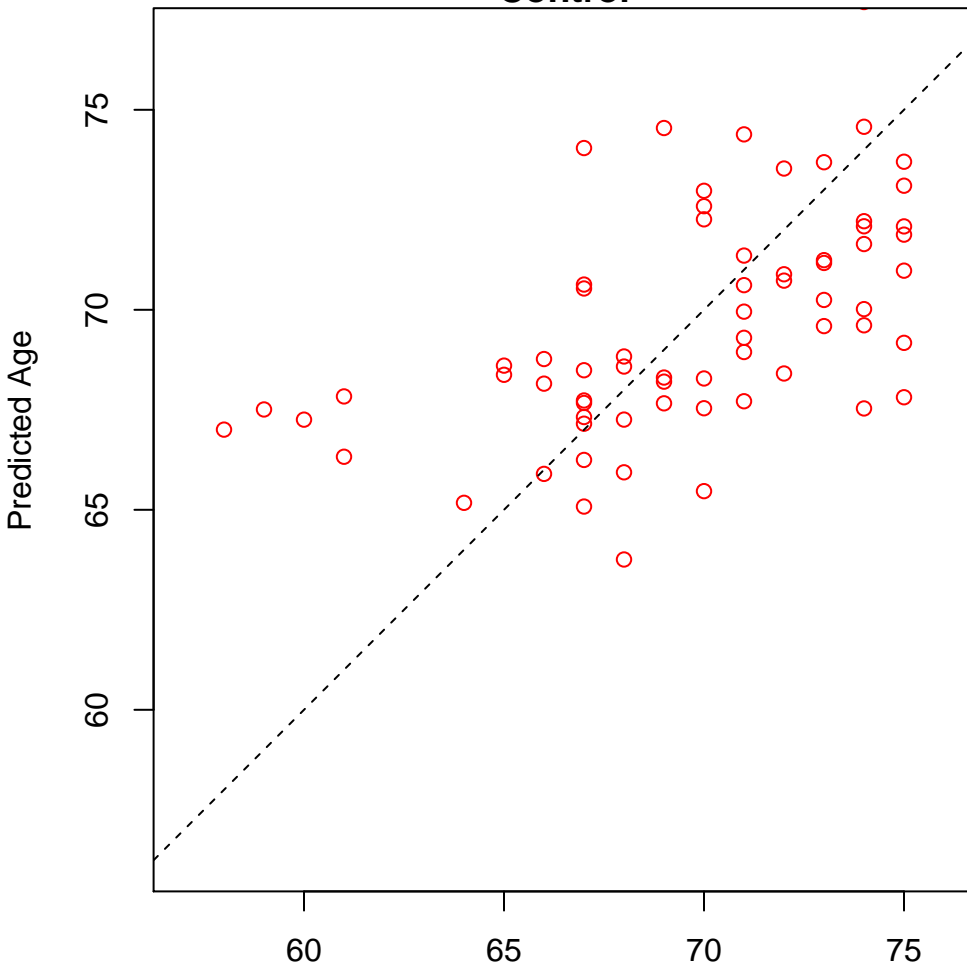
Actual Age

glycolytic process through fructose-6-phosphate (Score: 0.937843)

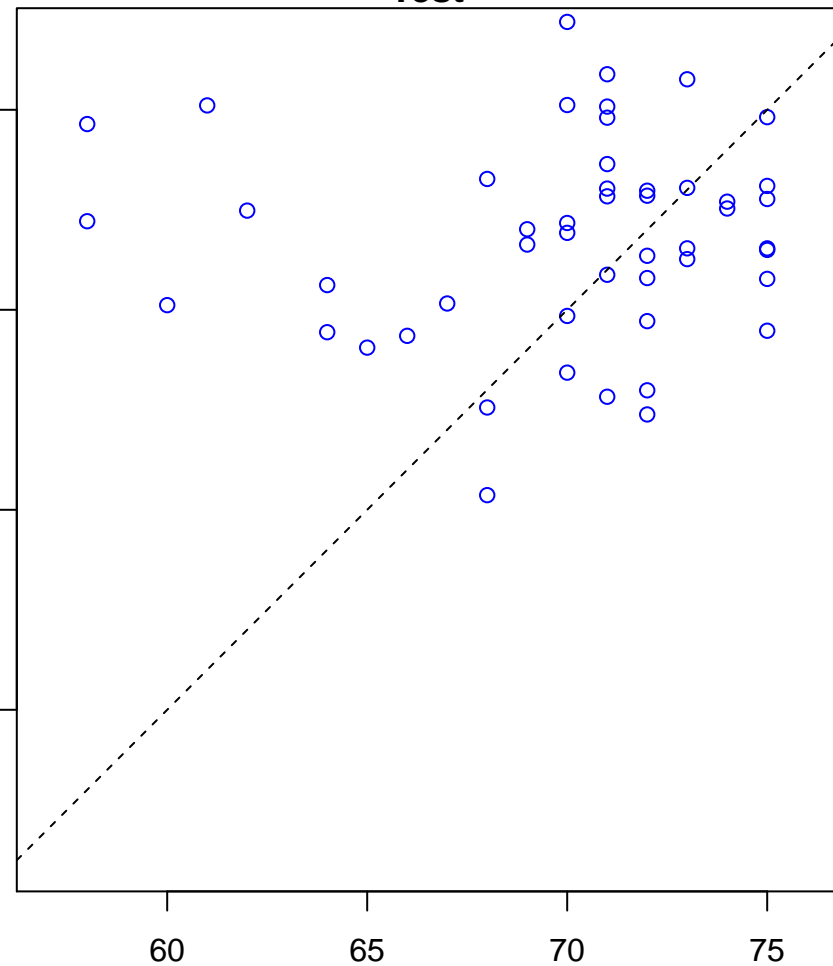


regulation of striated muscle contraction (Score: 0.937796)

Control

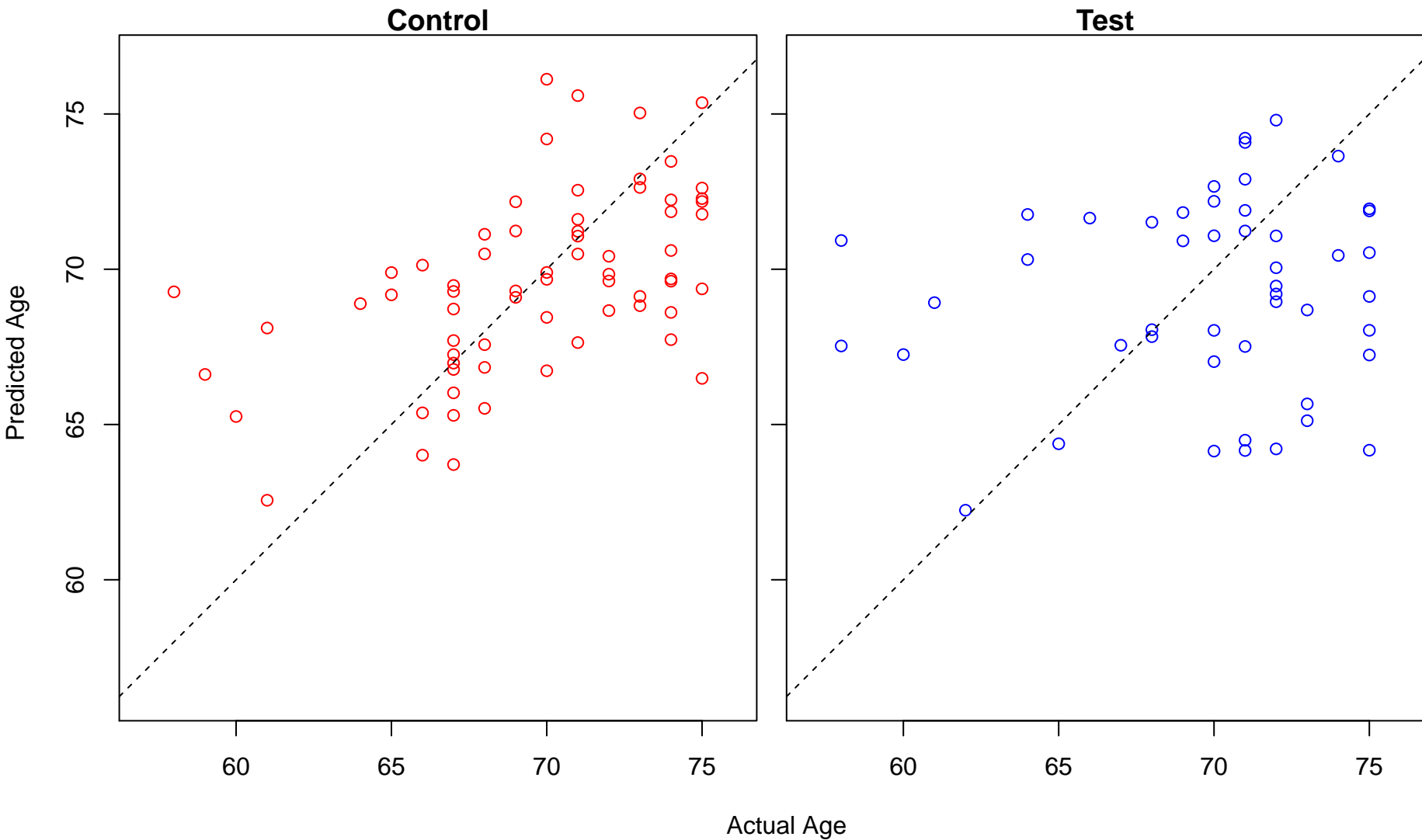


Test

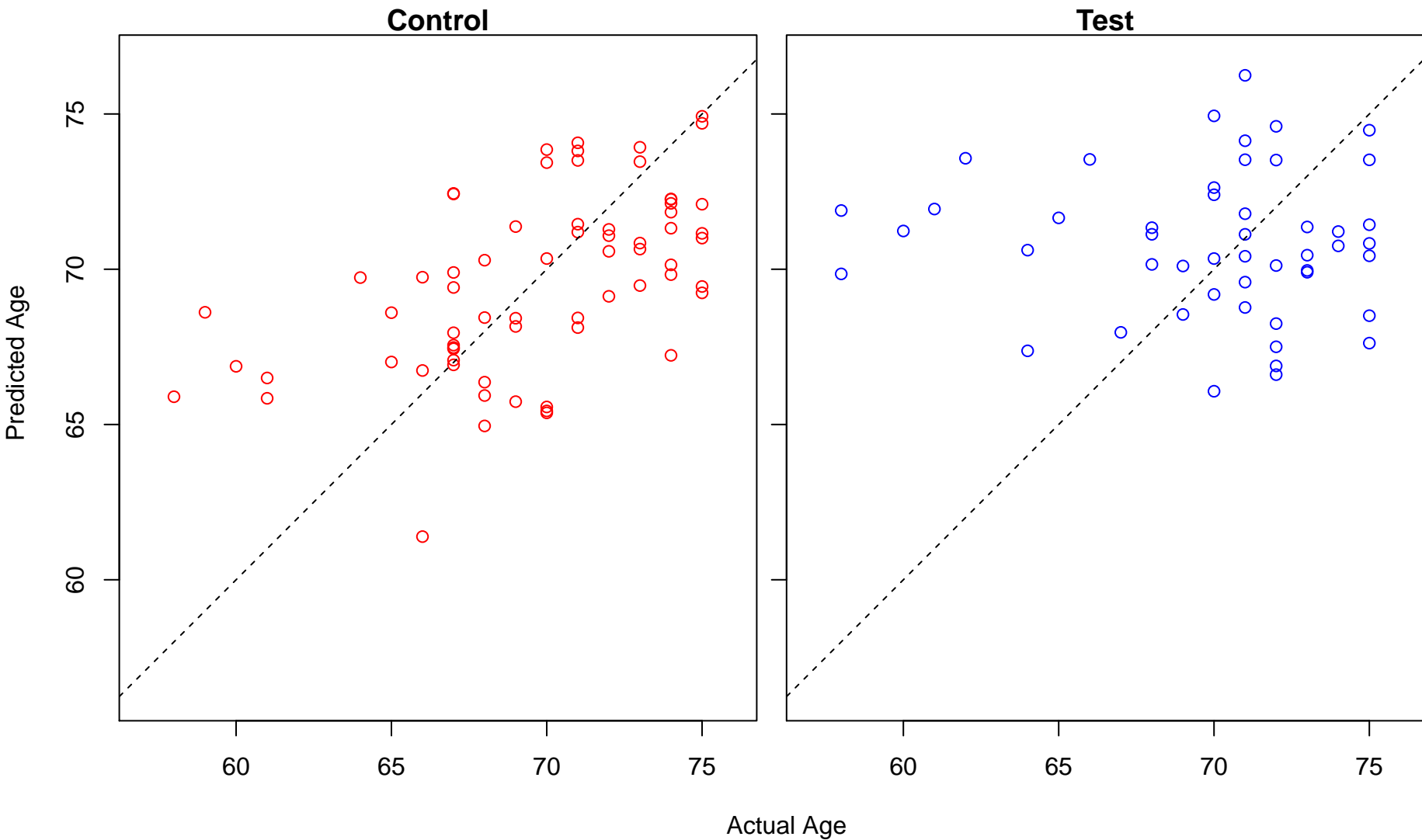


Actual Age

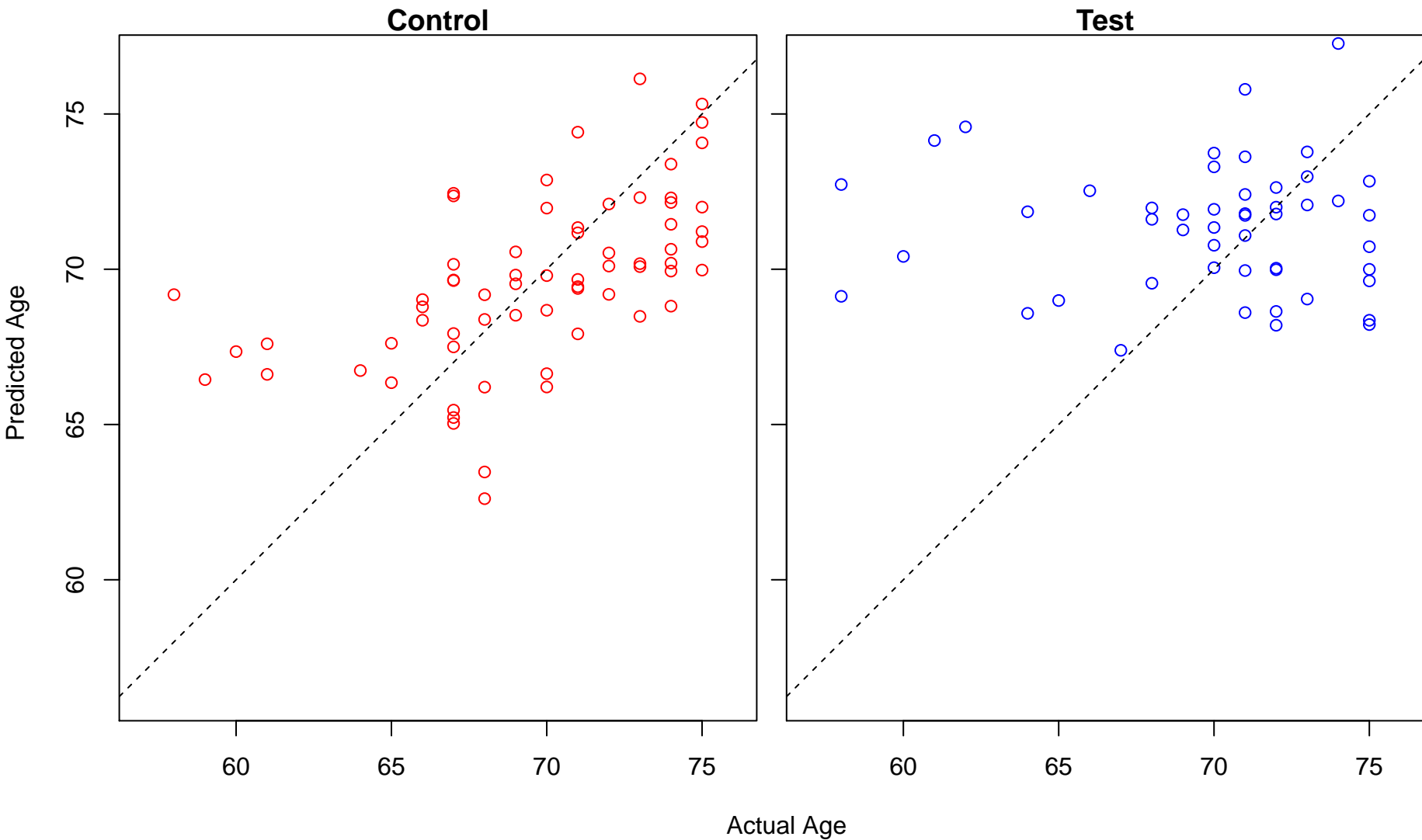
positive regulation of protein homooligomerization (Score: 0.937652)



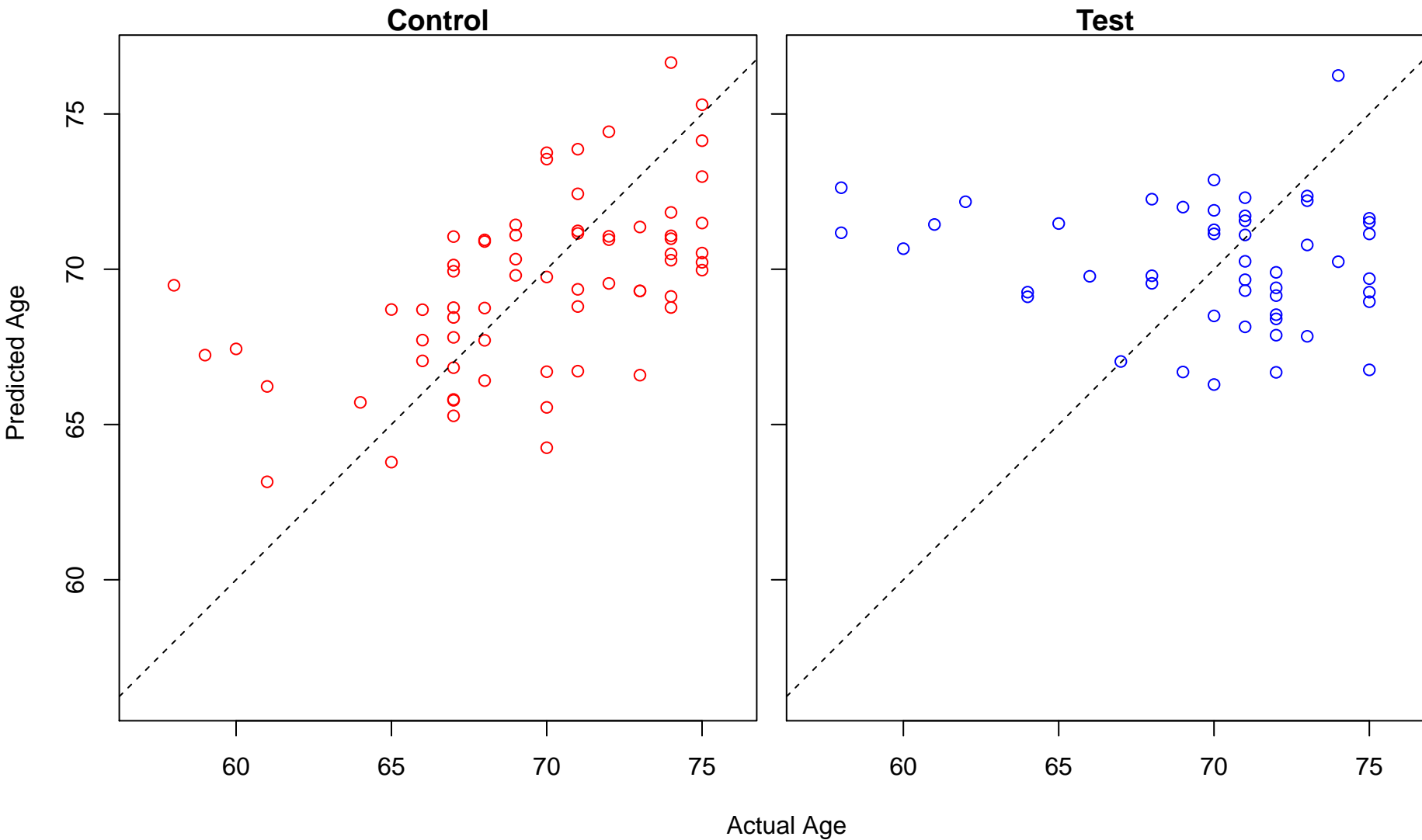
positive regulation of CREB transcription factor activity (Score: 0.936894)



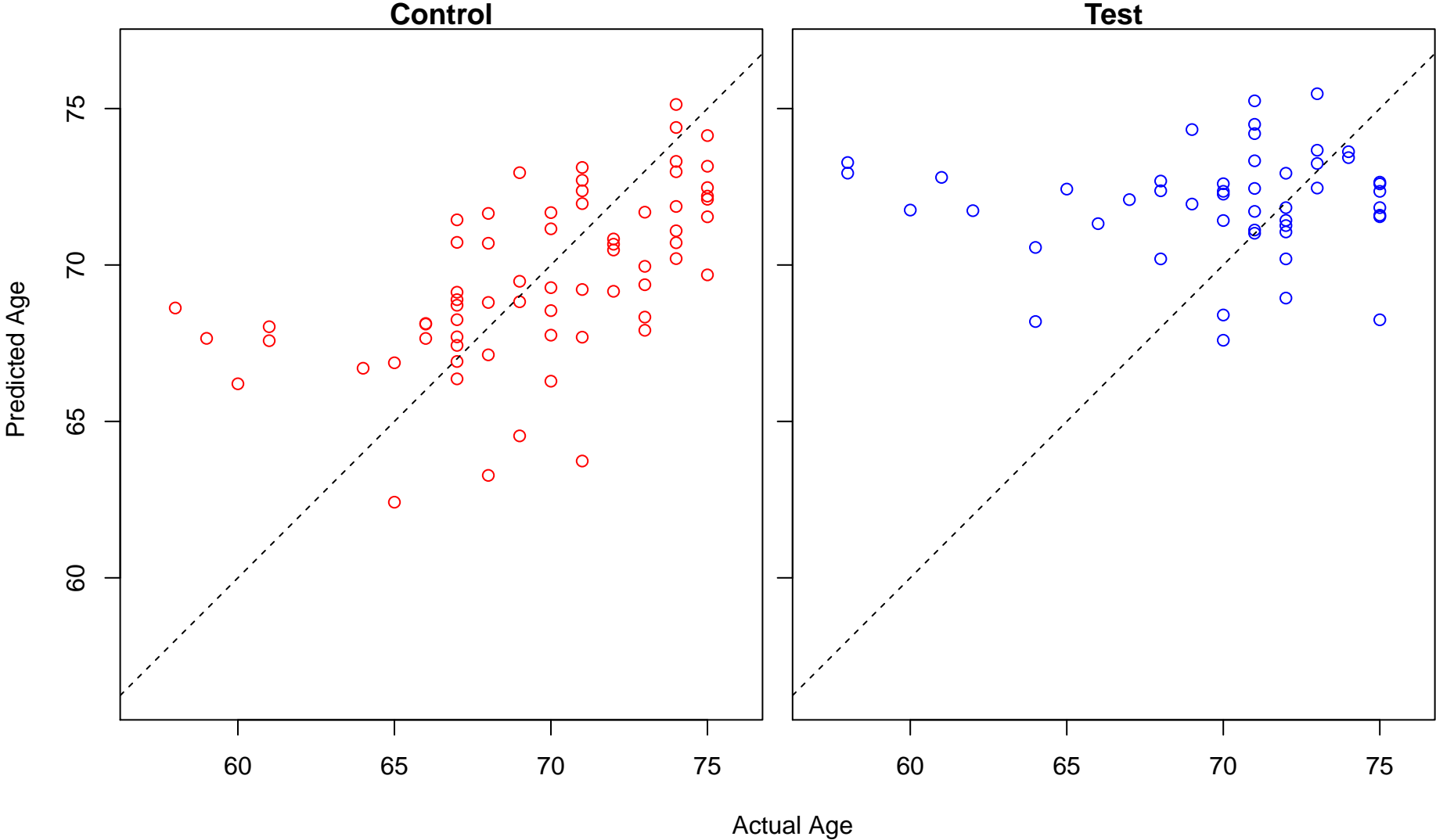
positive regulation of oxidative stress-induced cell death (Score: 0.936453)



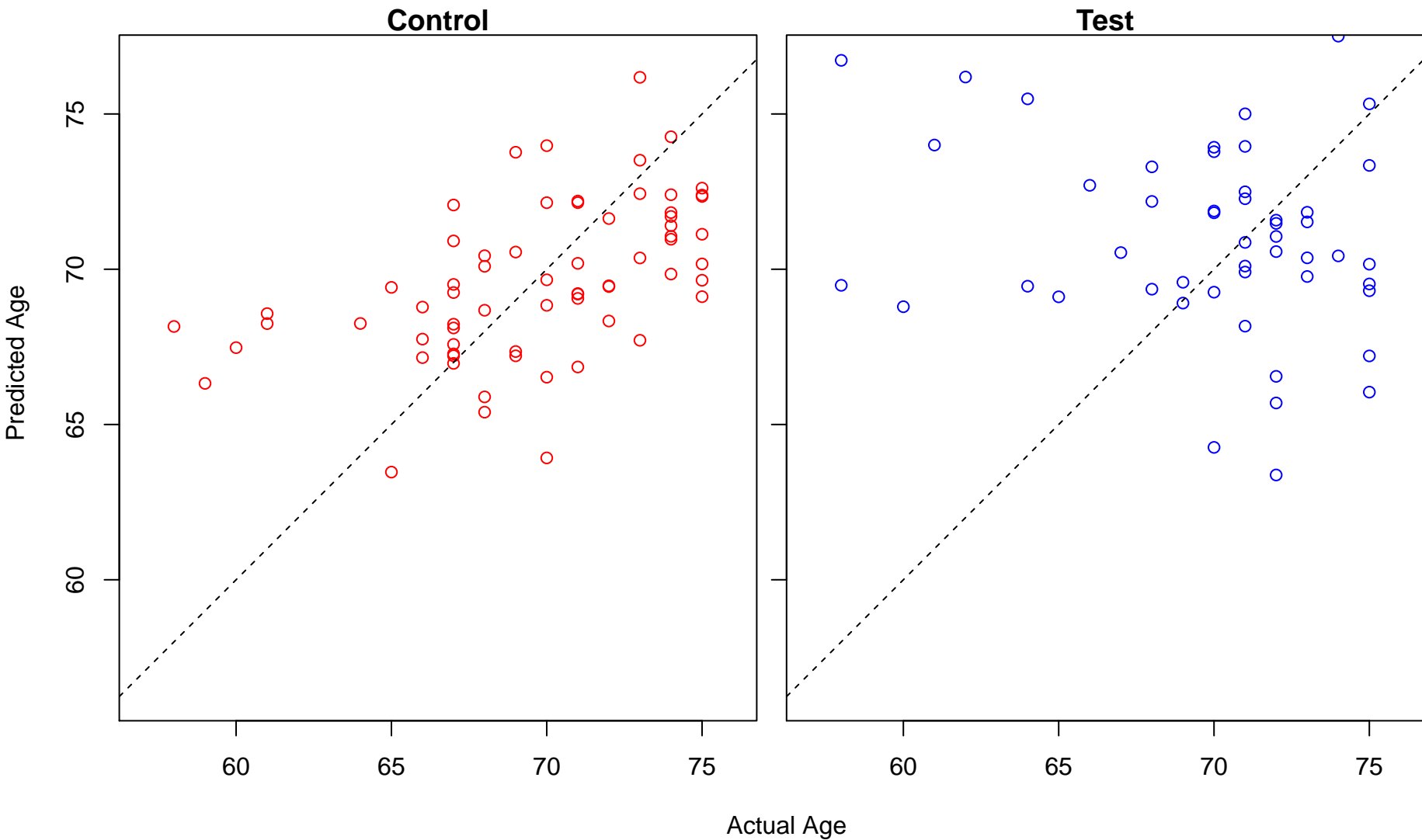
regulation of gastrulation (Score: 0.936370)



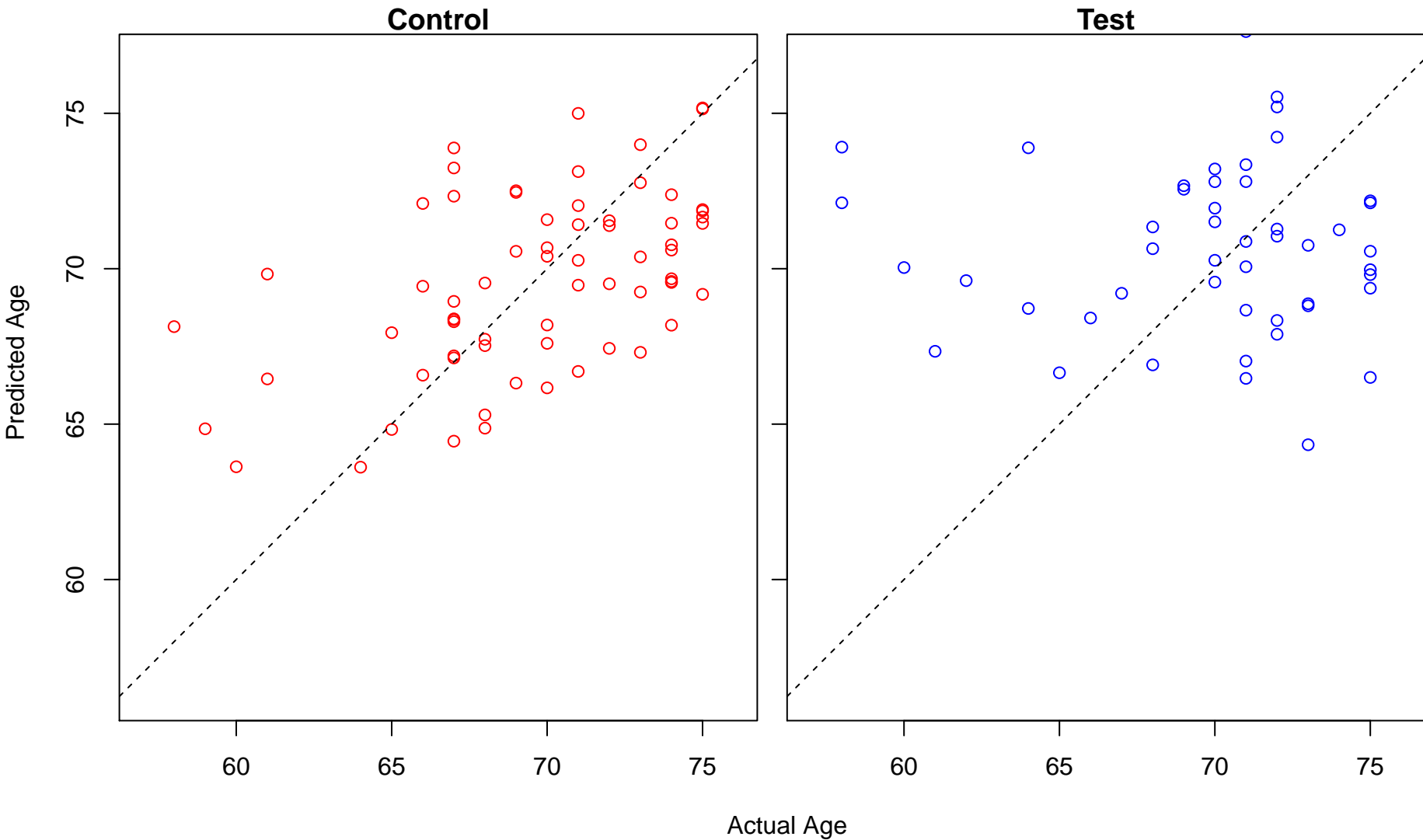
regulation of systemic arterial blood pressure mediated by a chemical signal (Score: 0.936292)



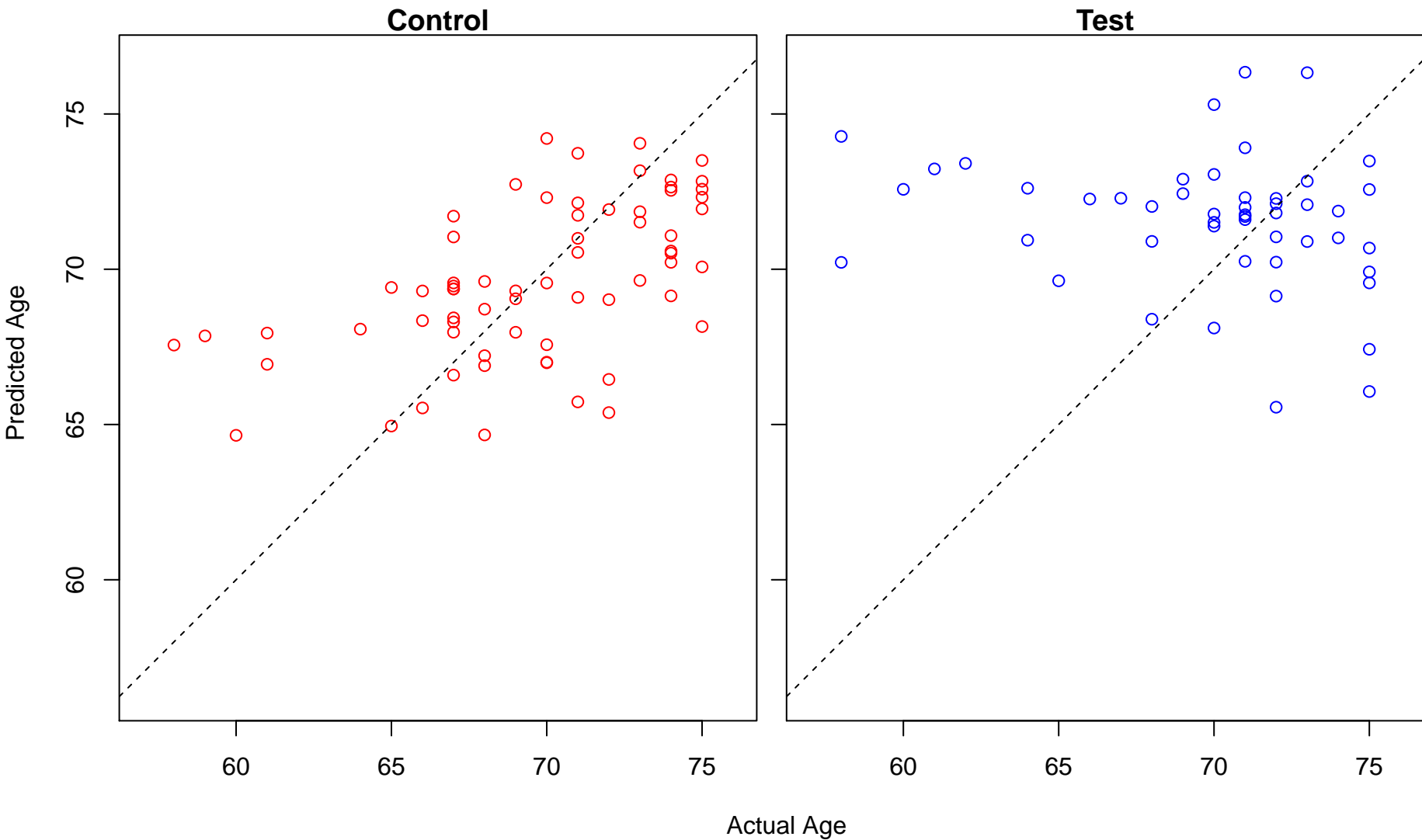
negative regulation of calcium ion transport into cytosol (Score: 0.935909)



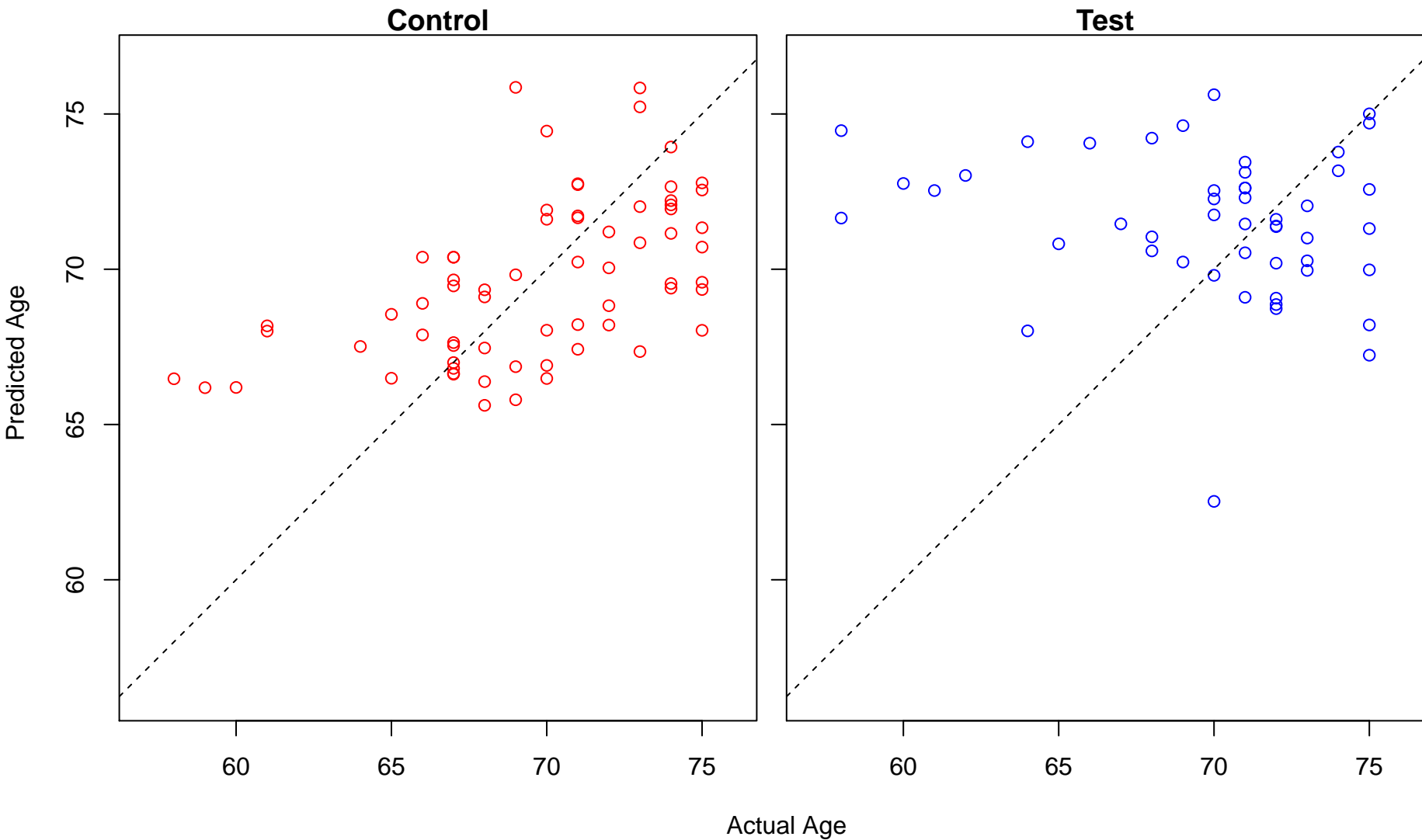
positive regulation of epidermal growth factor receptor signaling pathway (Score: 0.935169)



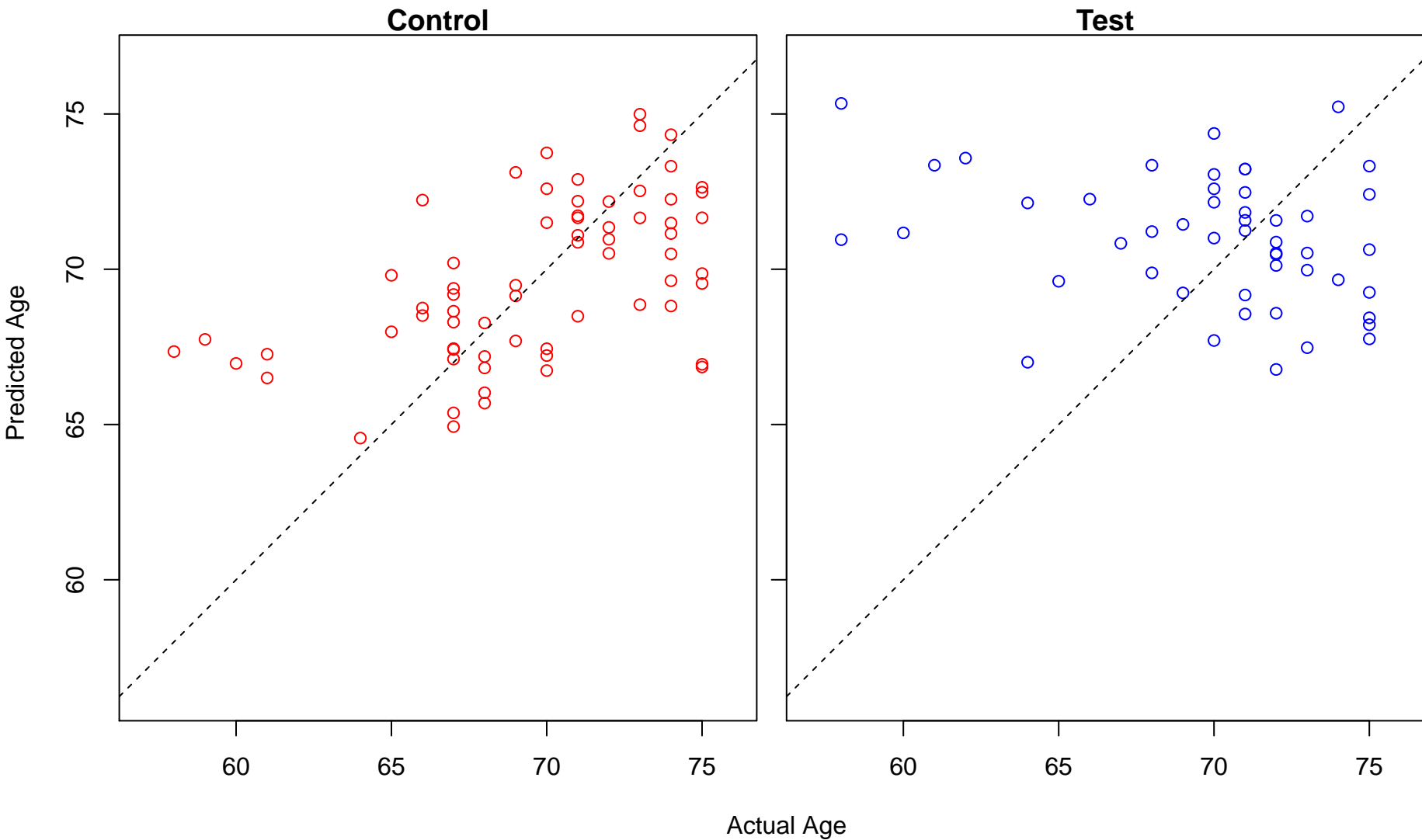
aspartate family amino acid biosynthetic process (Score: 0.934726)



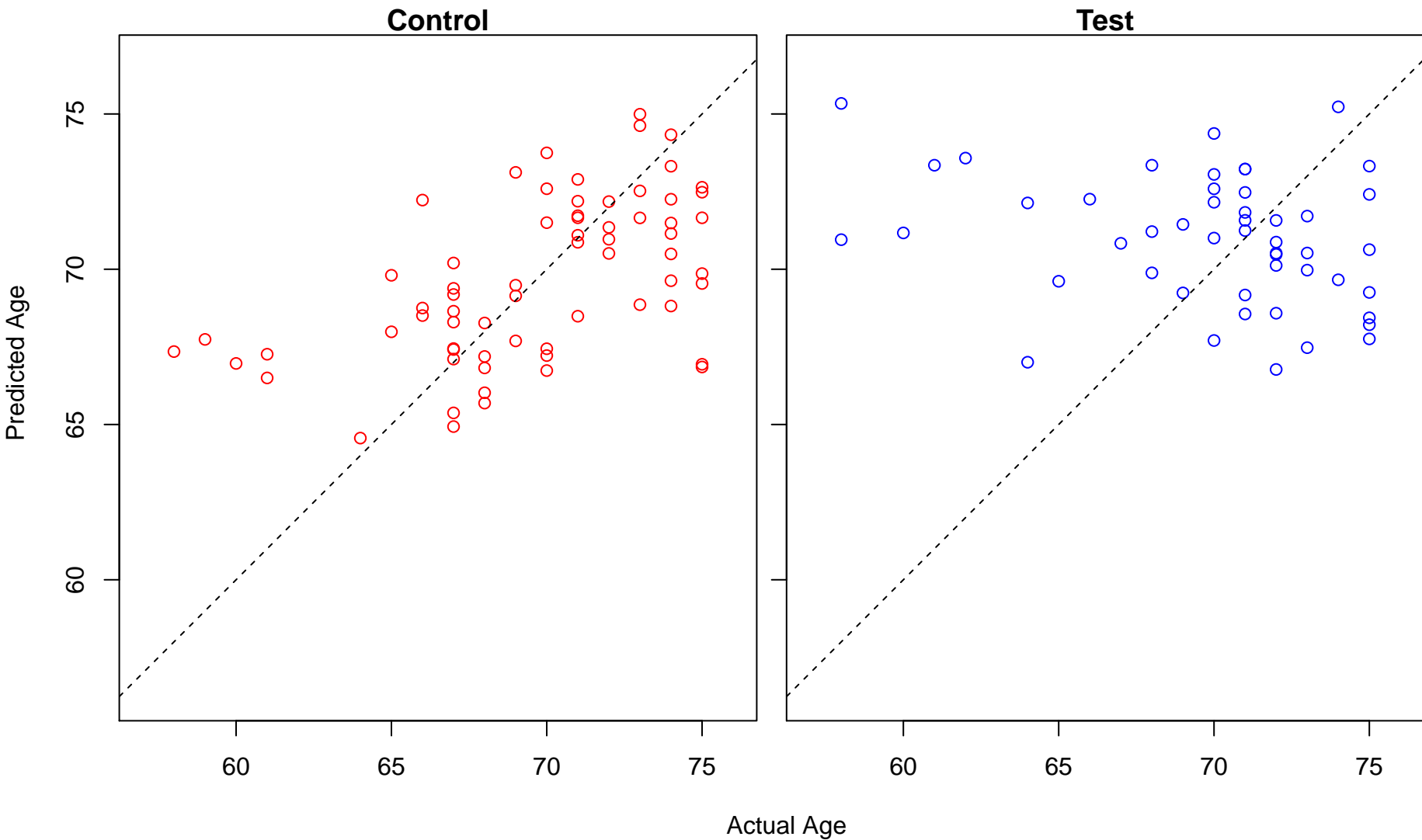
T cell apoptotic process (Score: 0.934260)



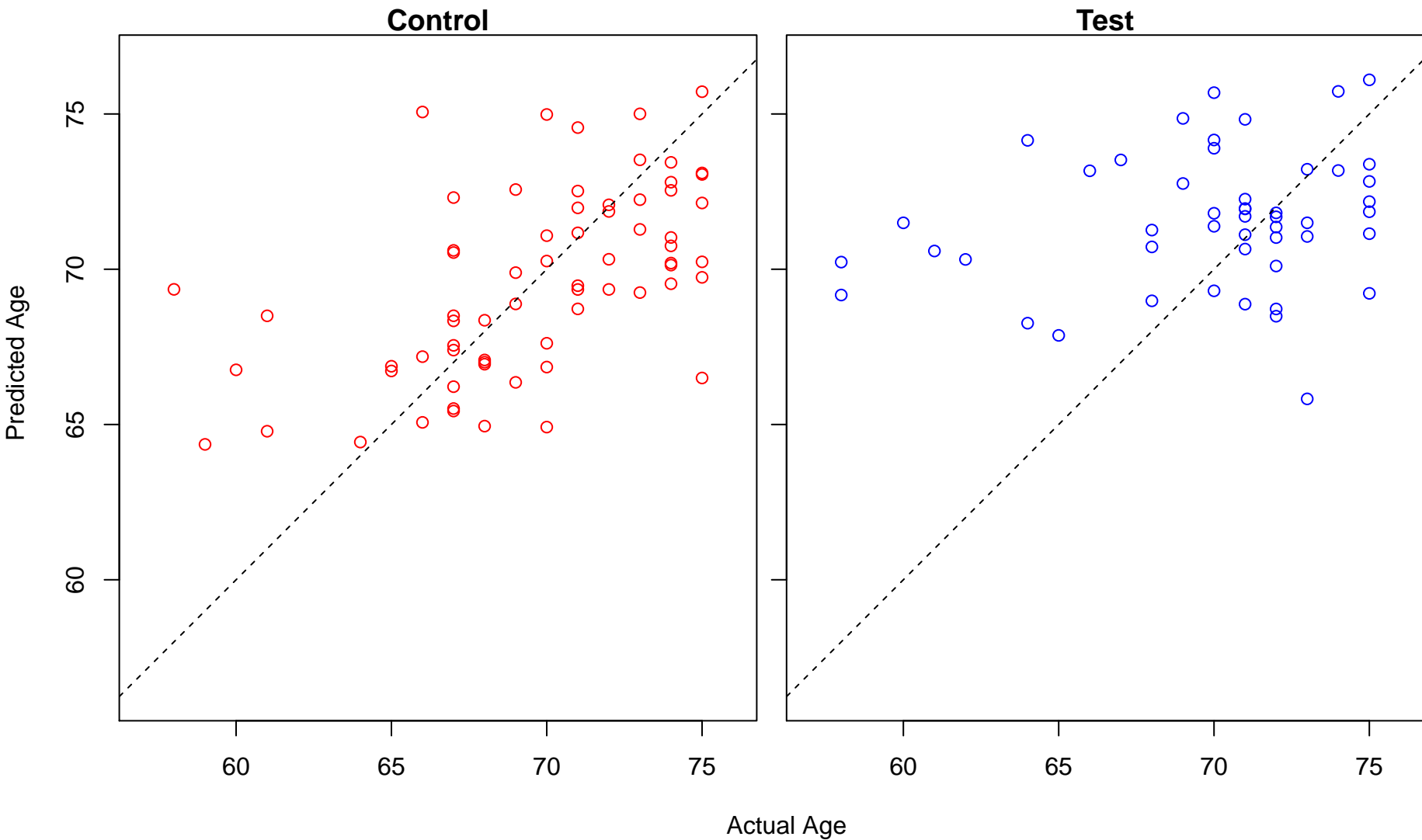
regulation of miRNA metabolic process (Score: 0.934081)



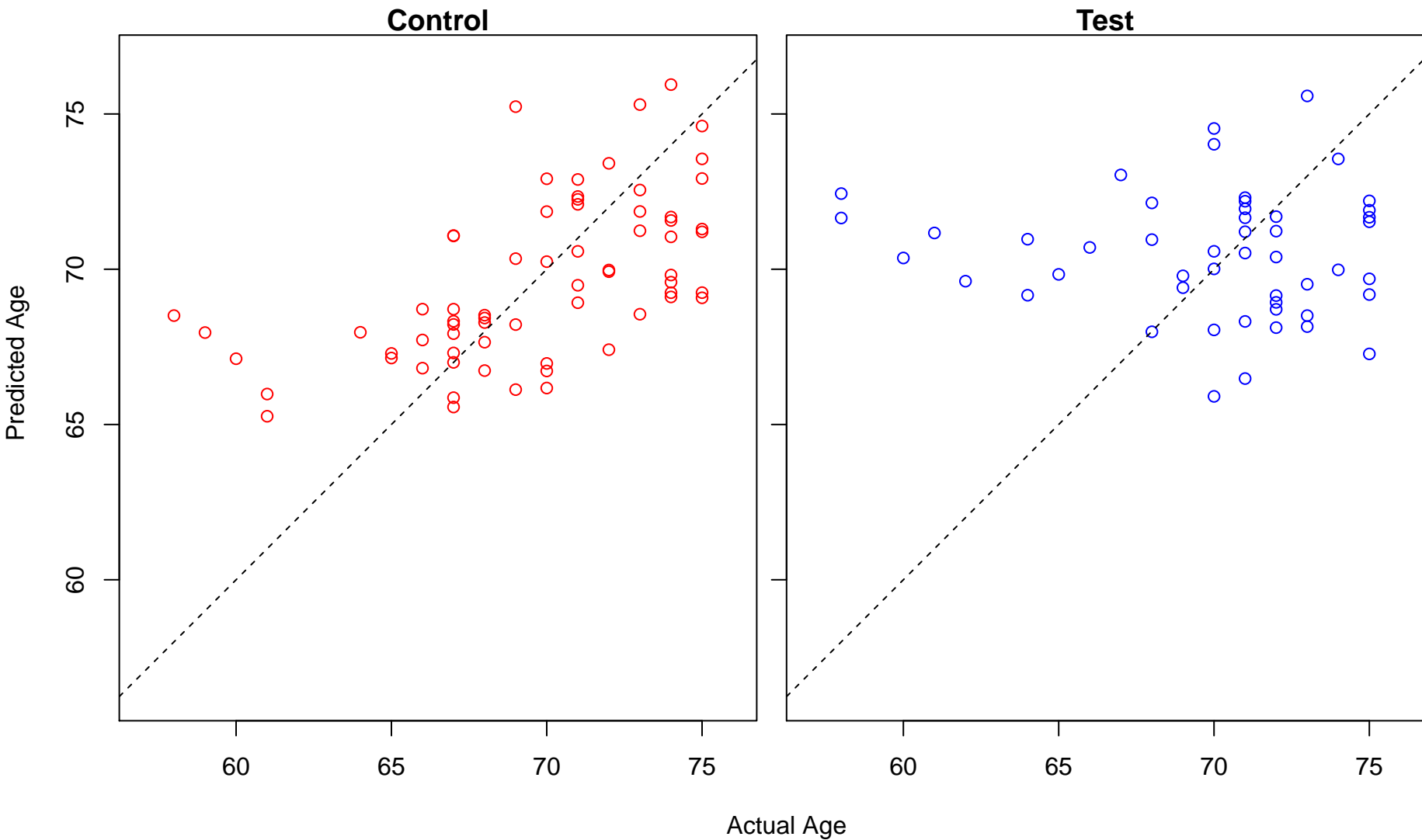
positive regulation of miRNA metabolic process (Score: 0.934081)



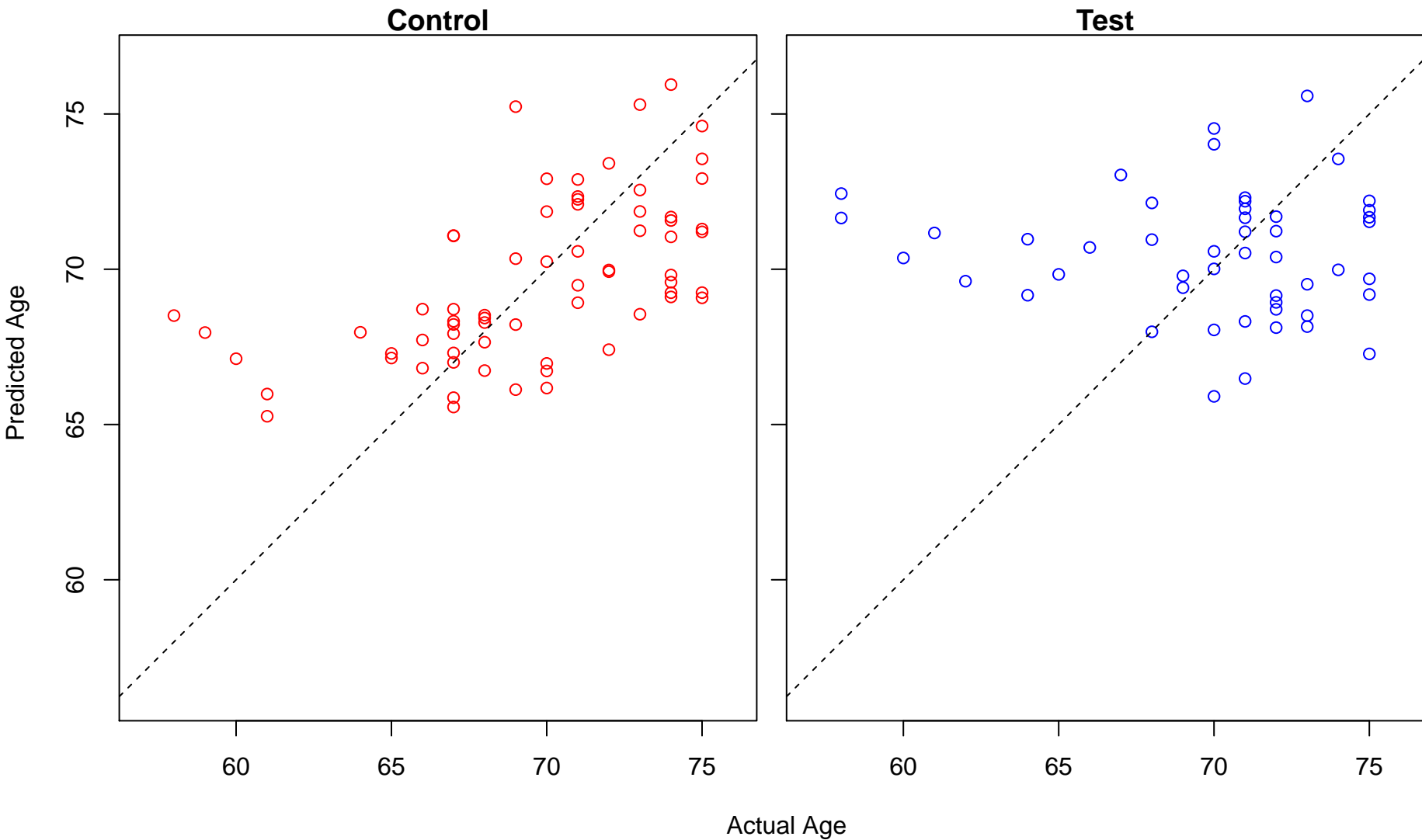
dermatan sulfate proteoglycan metabolic process (Score: 0.934002)



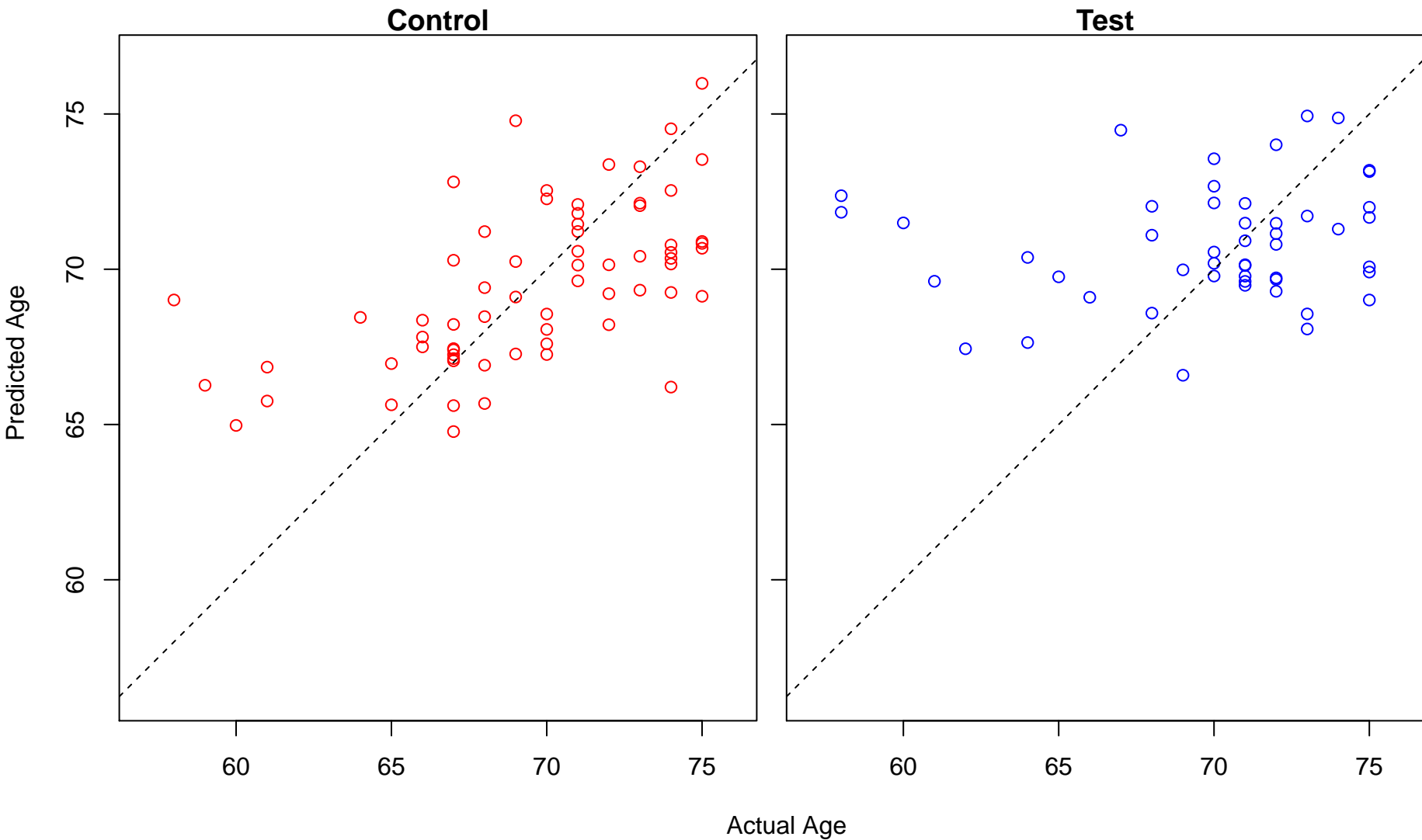
melanosome localization (Score: 0.933883)



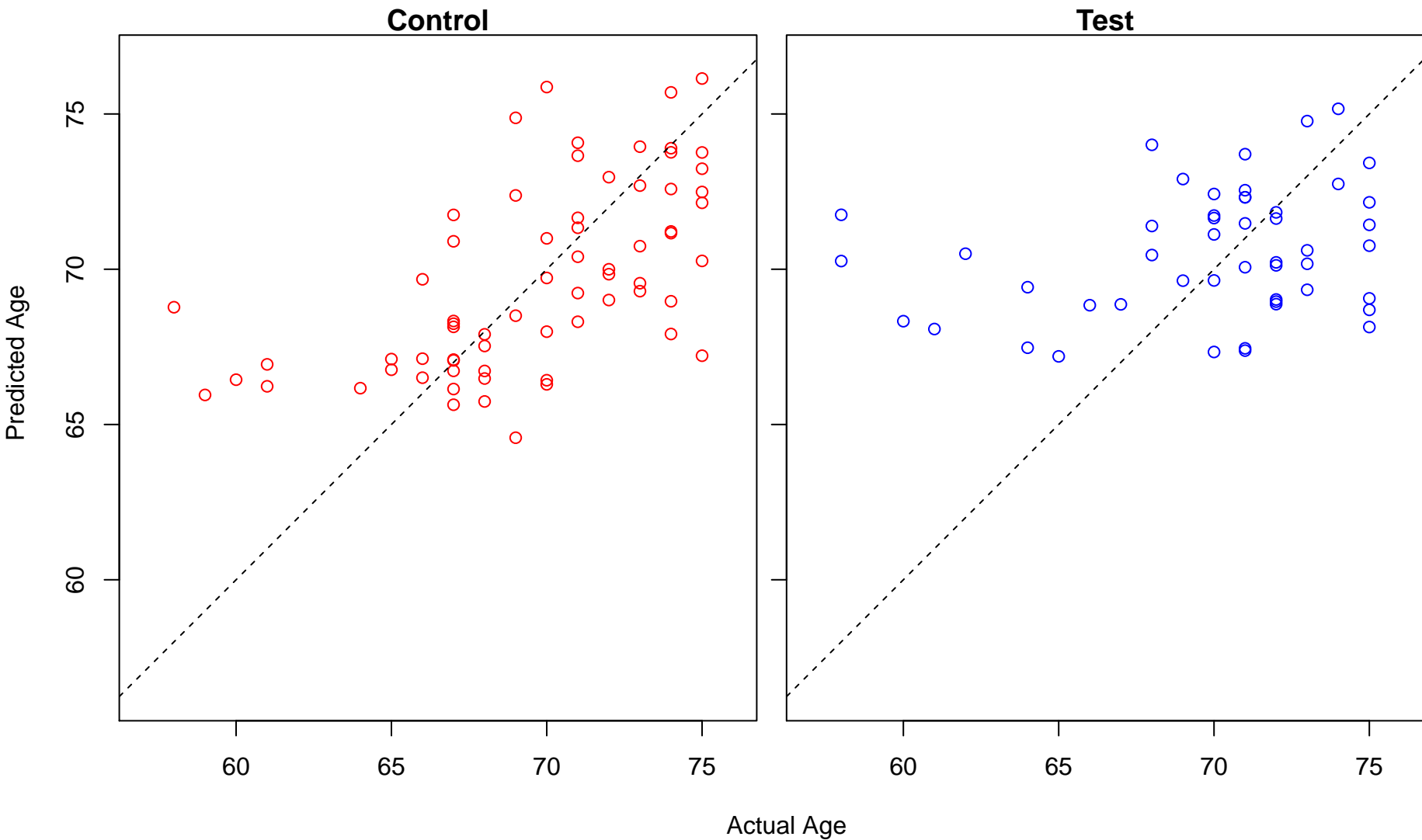
pigment granule localization (Score: 0.933883)



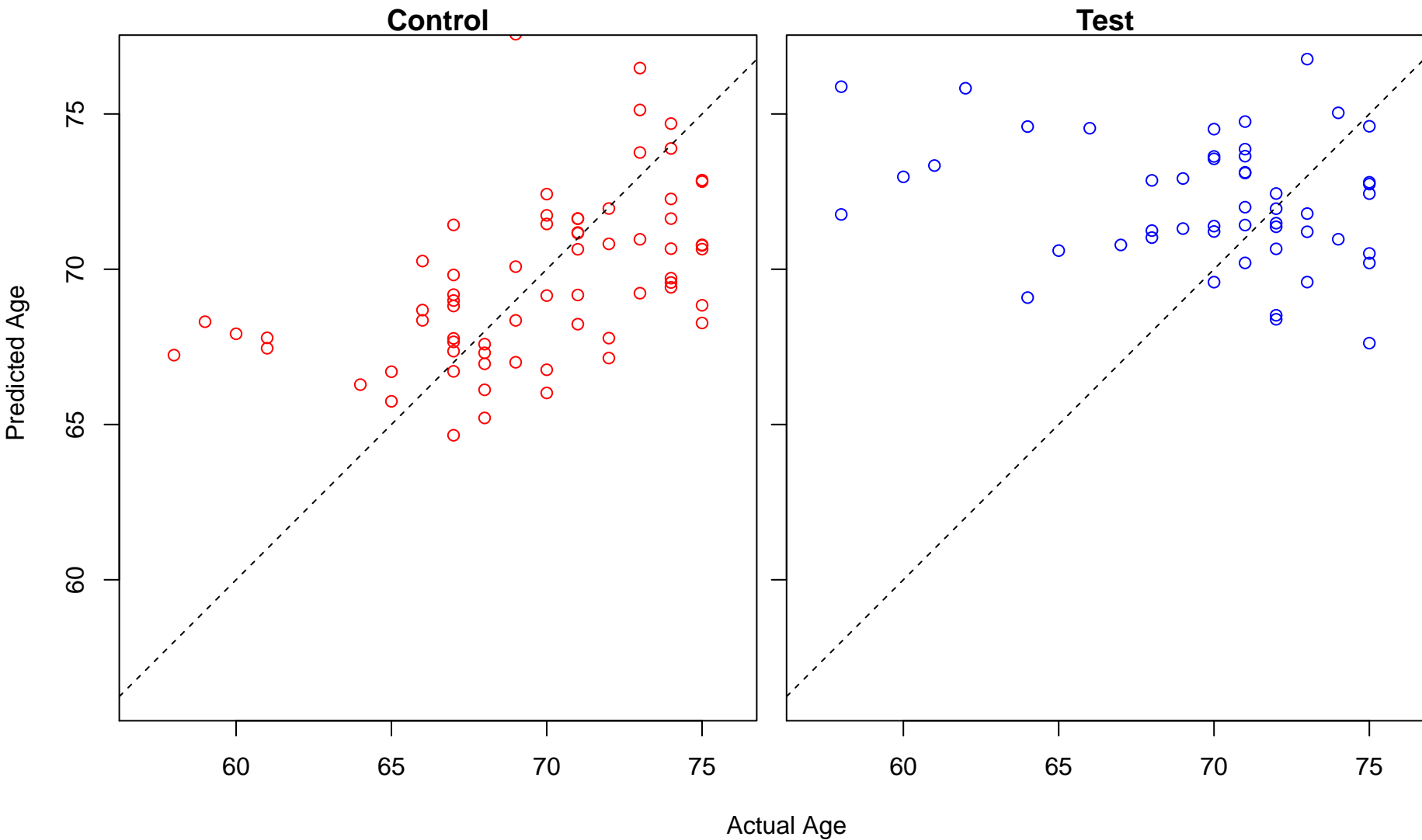
ceramide biosynthetic process (Score: 0.933585)



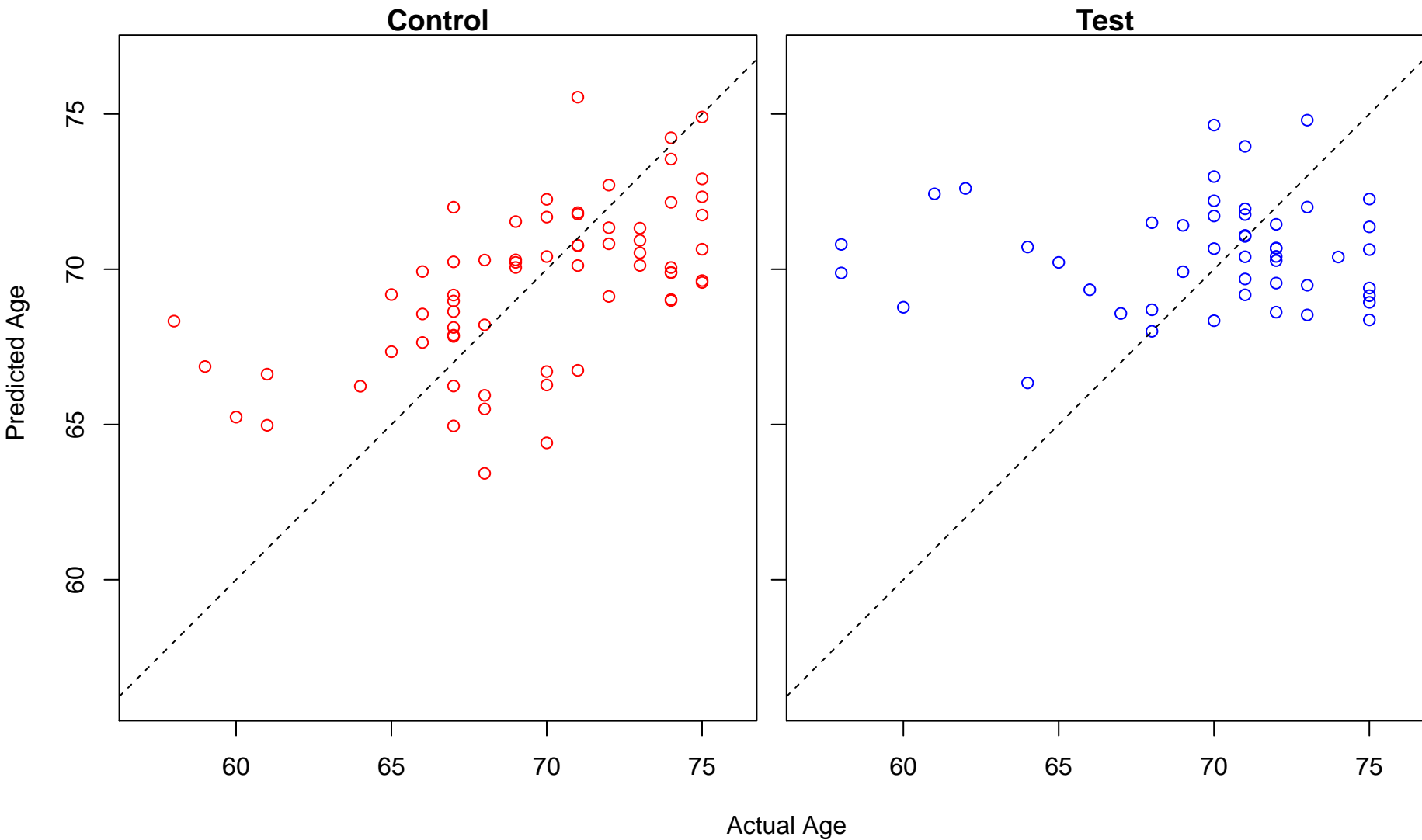
mesonephros development (Score: 0.933359)



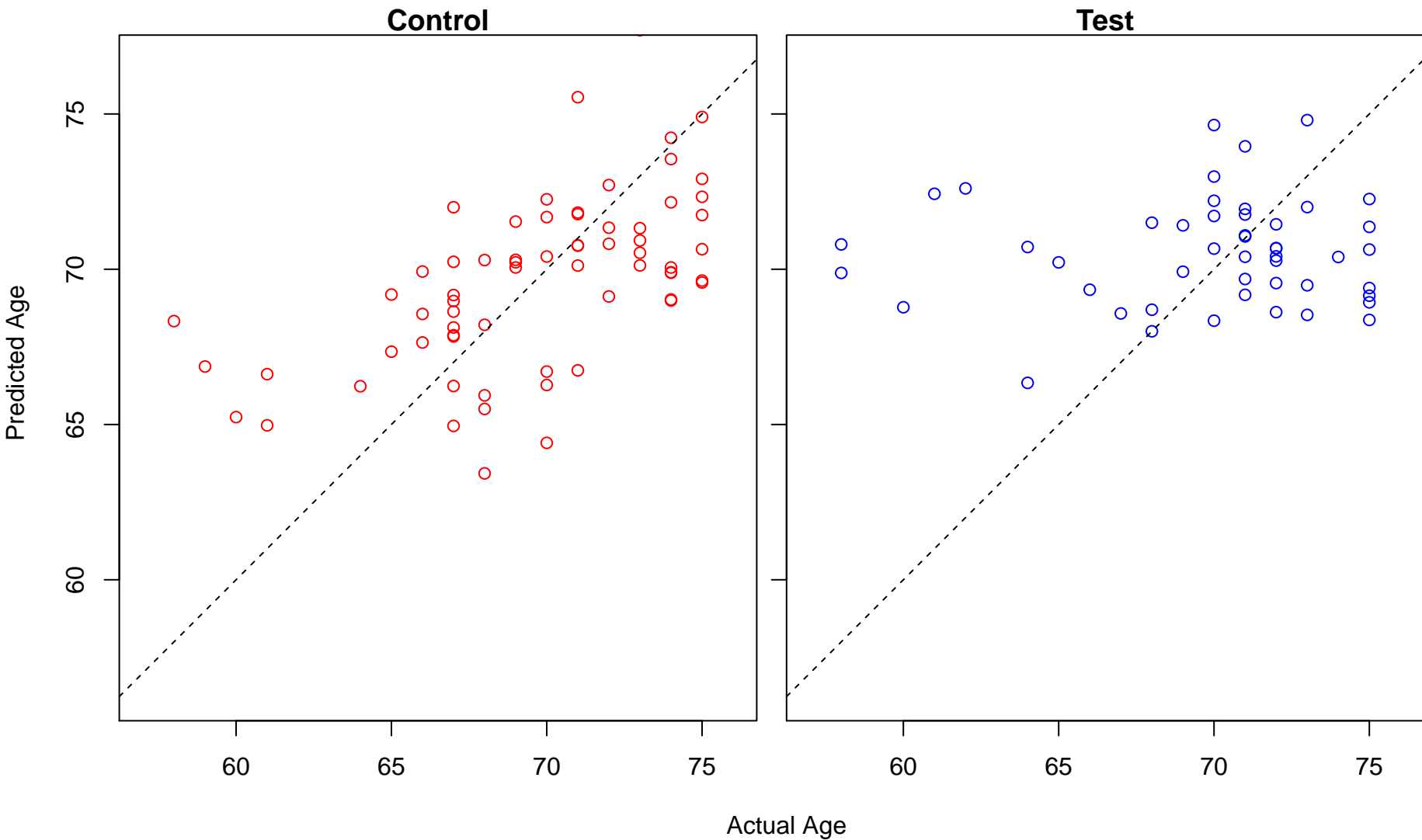
axo-dendritic transport (Score: 0.932510)



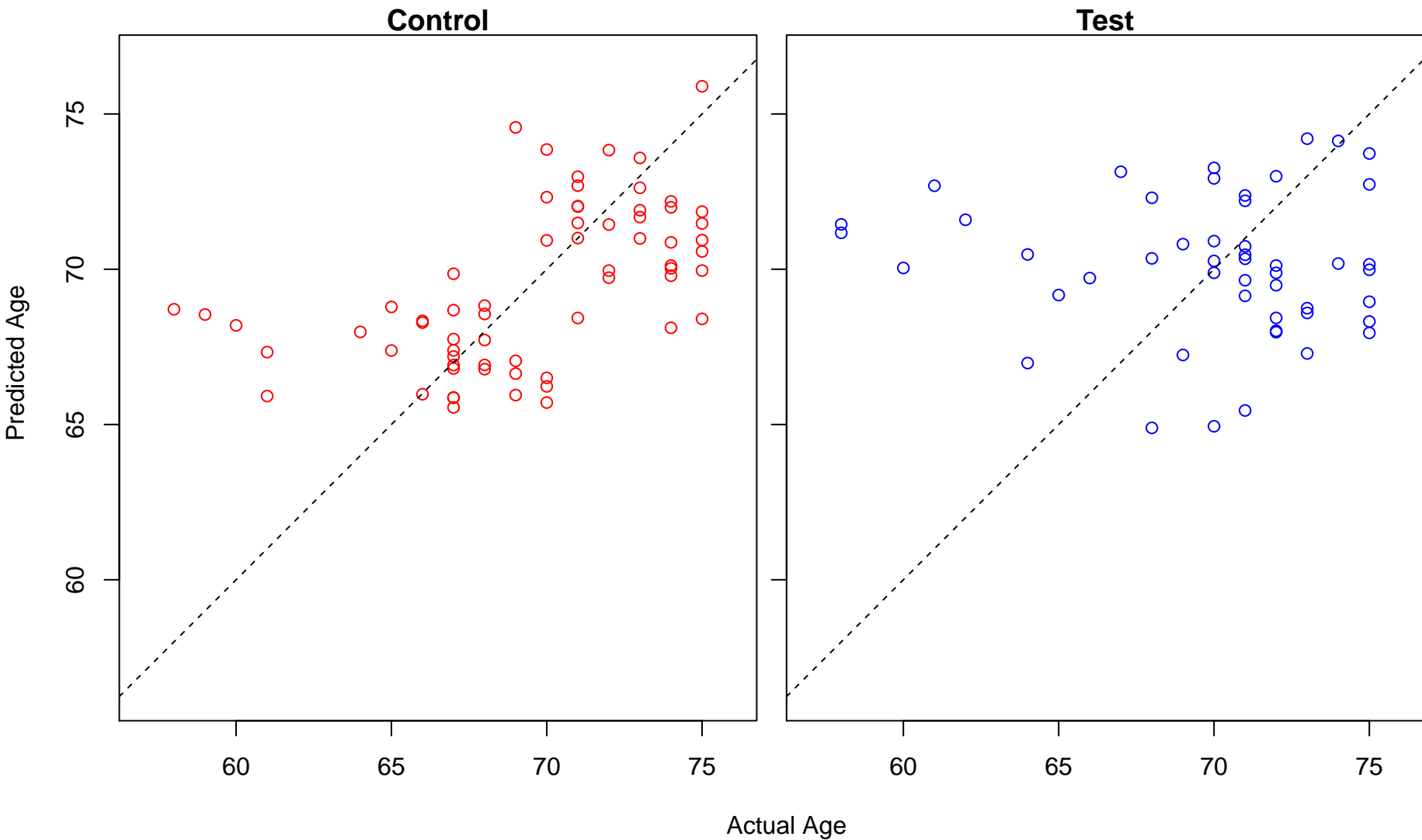
glycolytic process (Score: 0.932404)



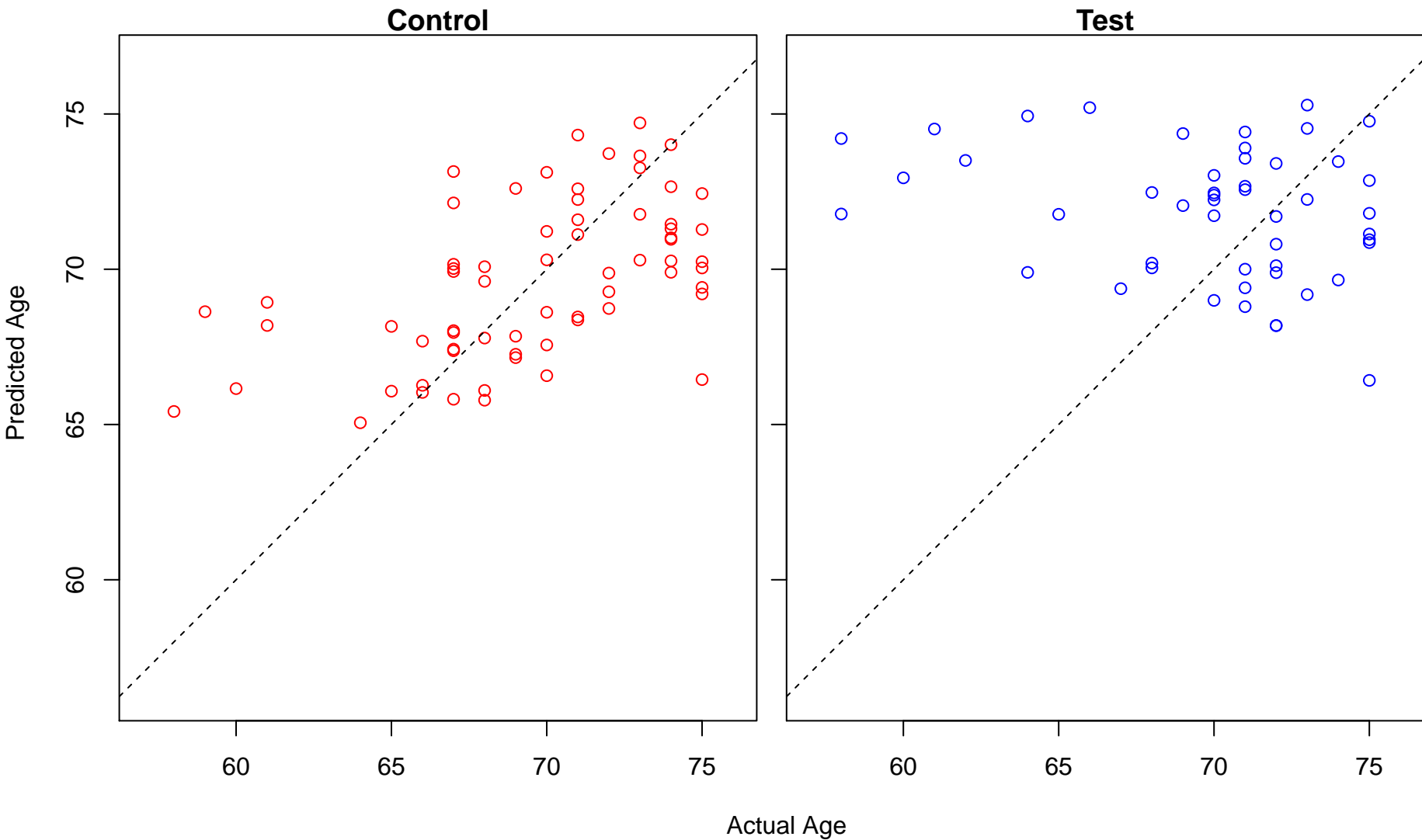
ATP generation from ADP (Score: 0.932404)



organic hydroxy compound catabolic process (Score: 0.932165)

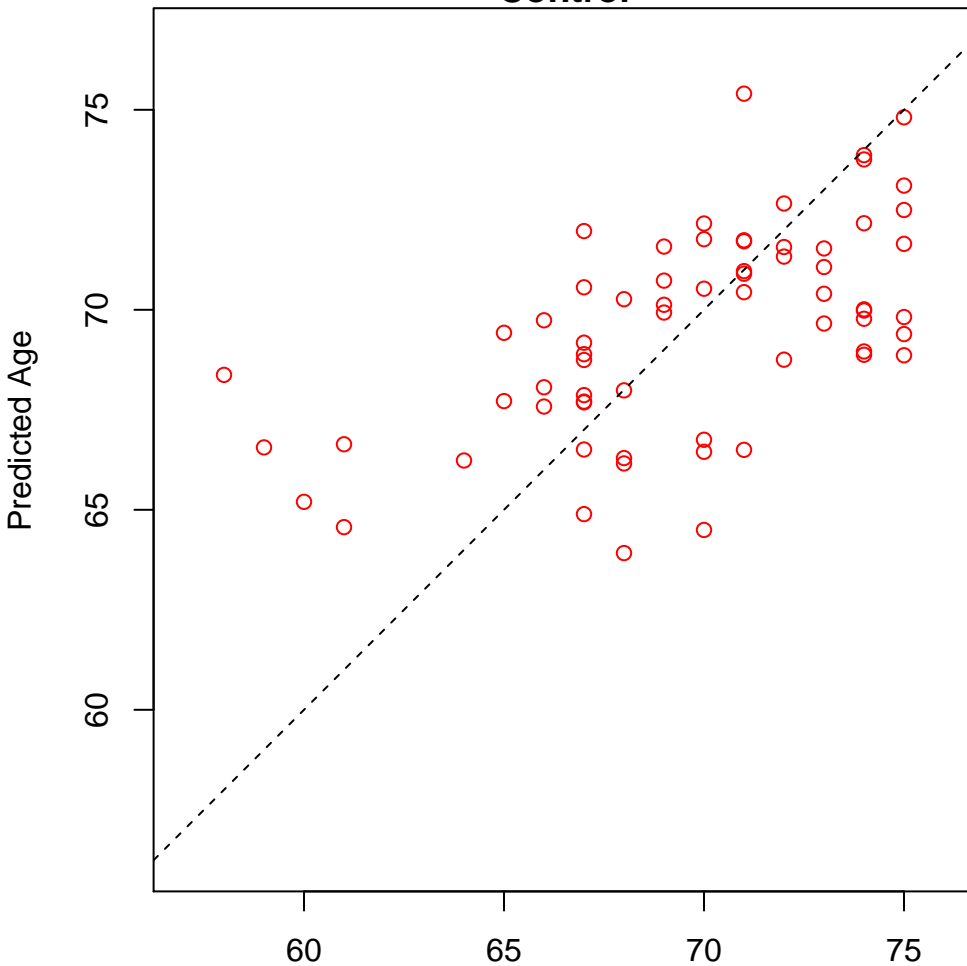


blood vessel endothelial cell differentiation (Score: 0.931282)

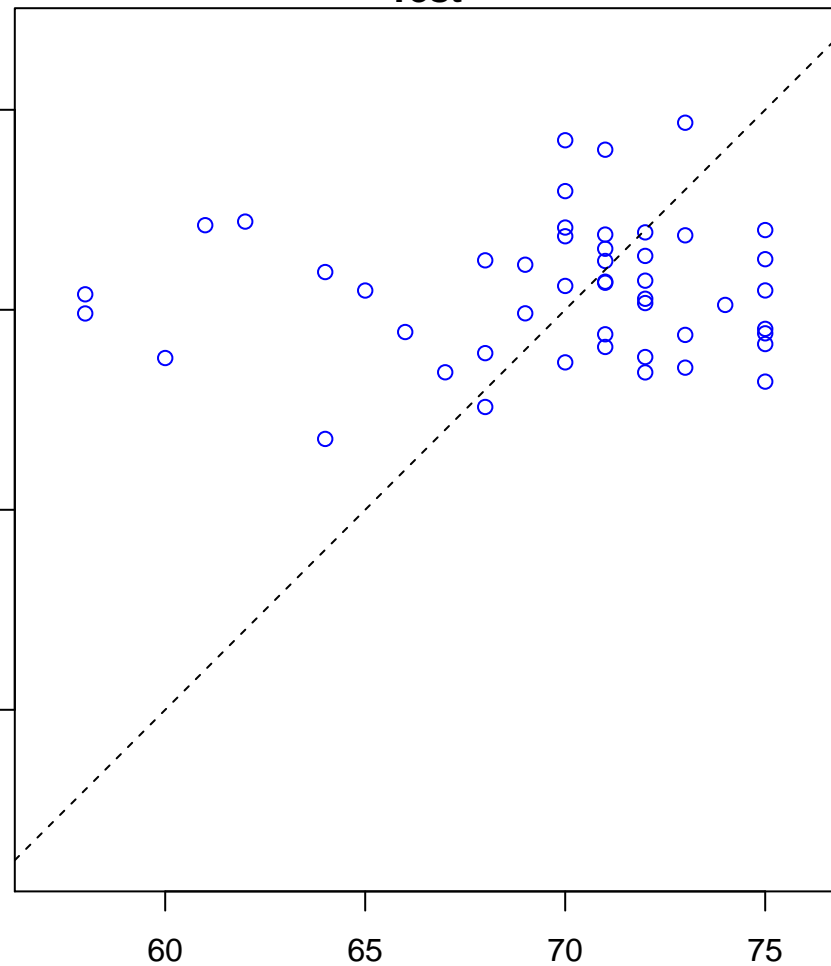


monosaccharide catabolic process (Score: 0.930995)

Control

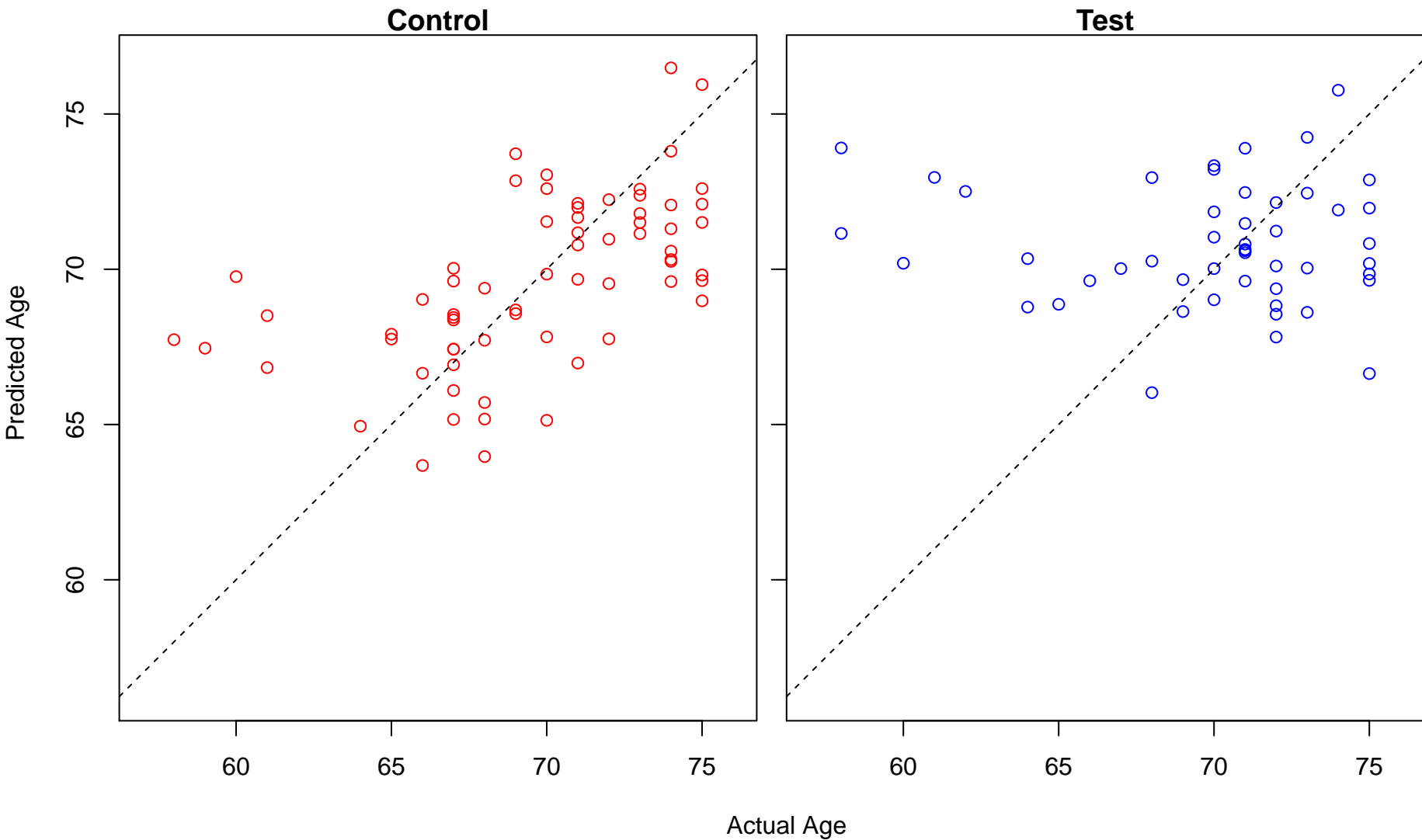


Test

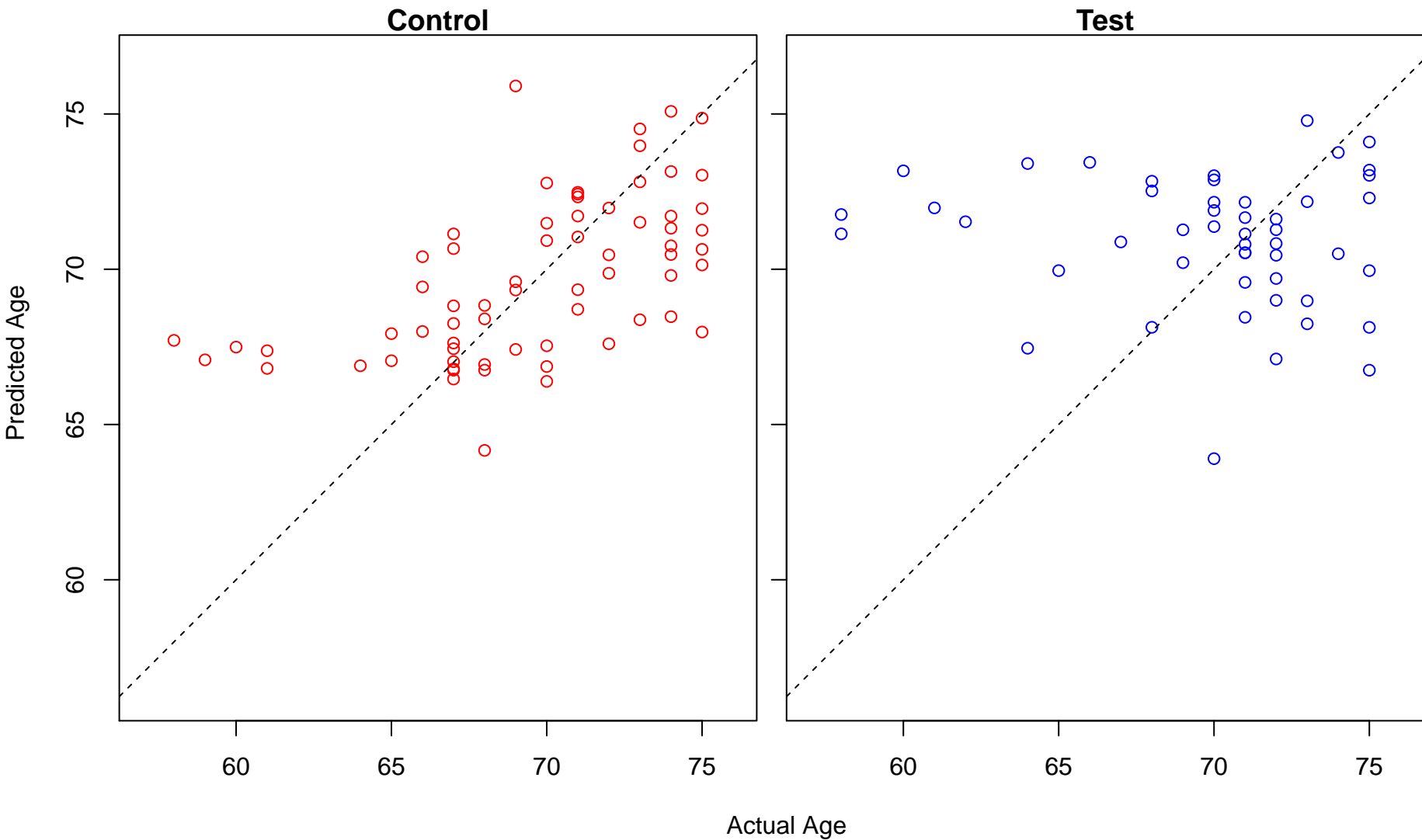


Actual Age

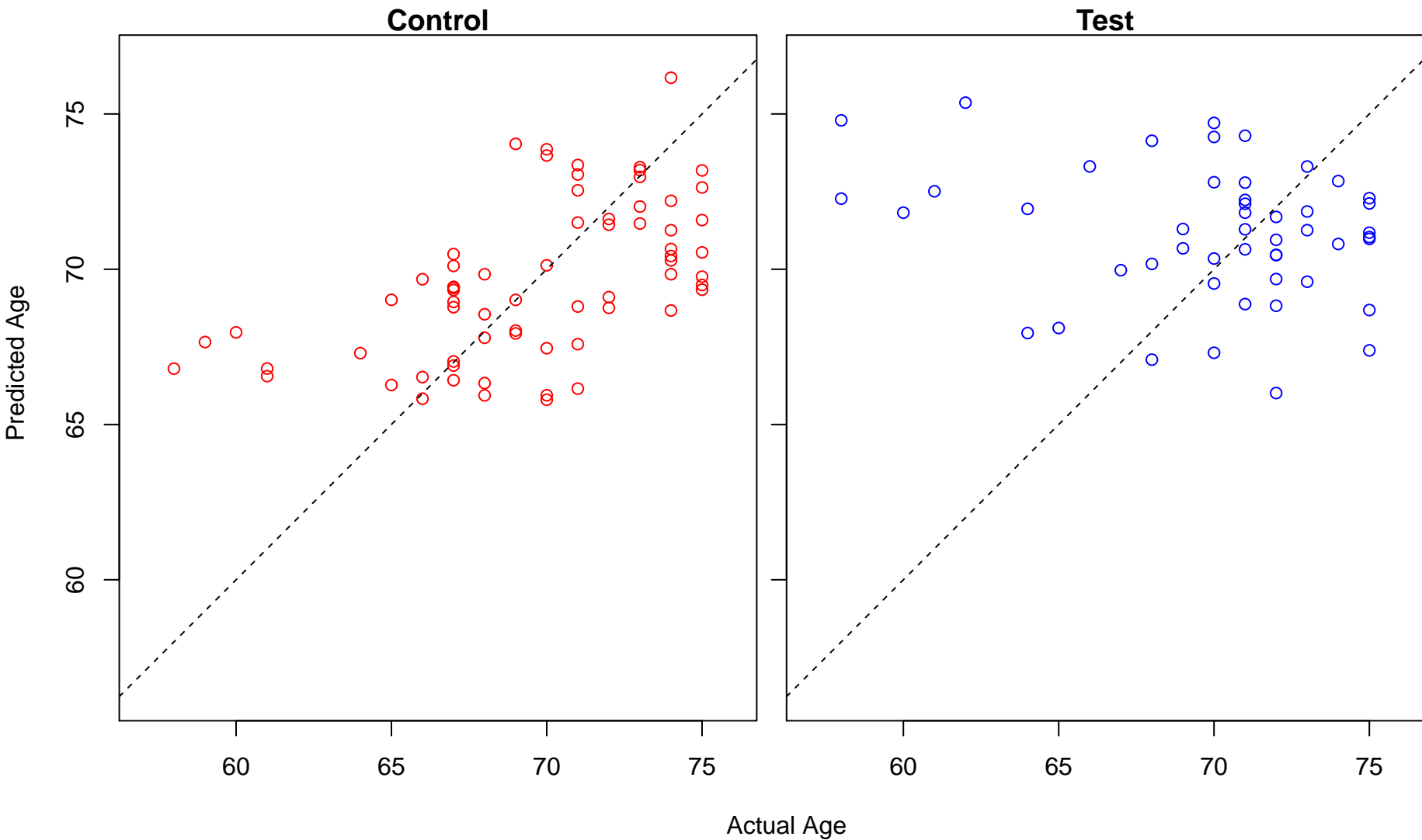
regulation of syncytium formation by plasma membrane fusion (Score: 0.930890)



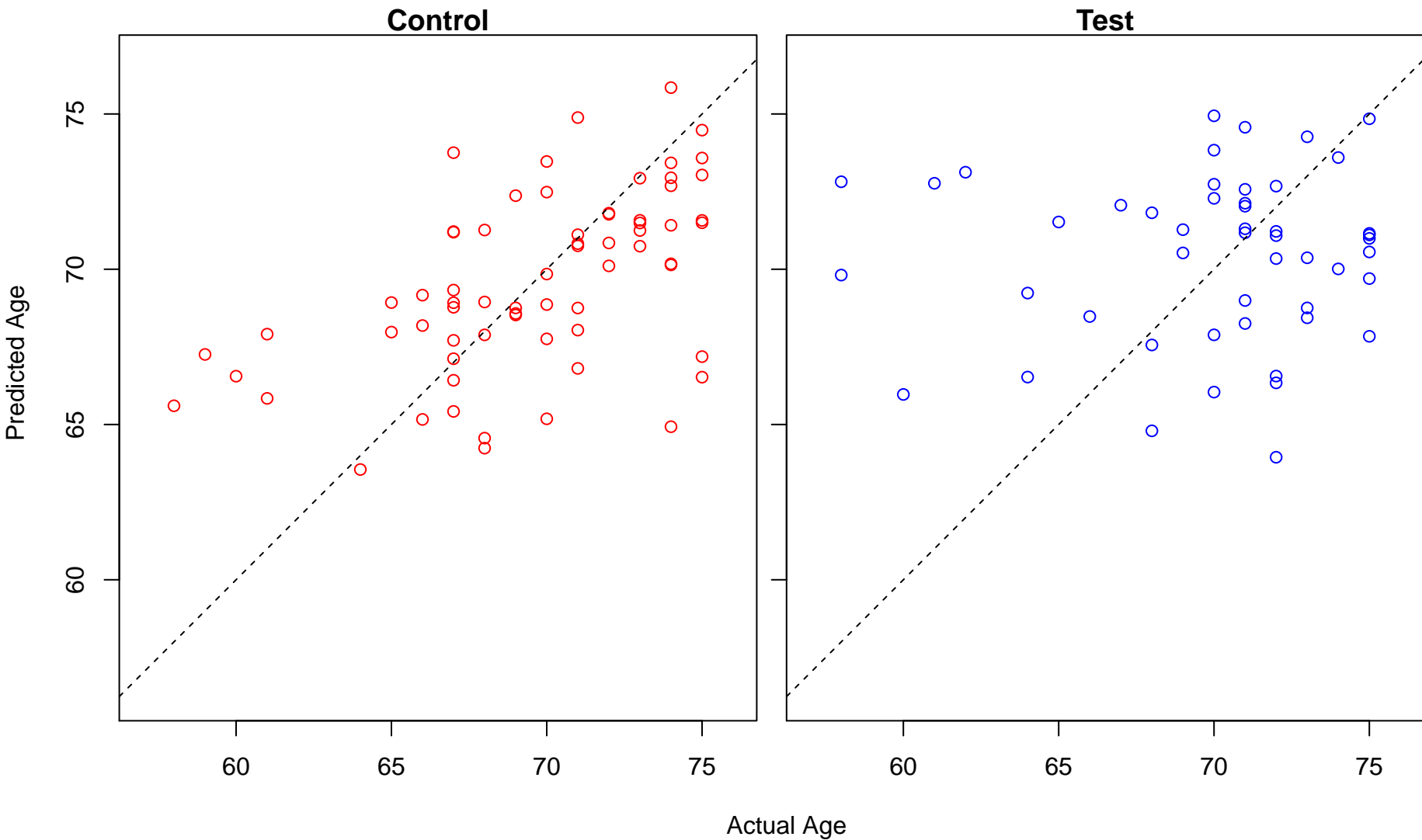
positive regulation of carbohydrate metabolic process (Score: 0.930785)



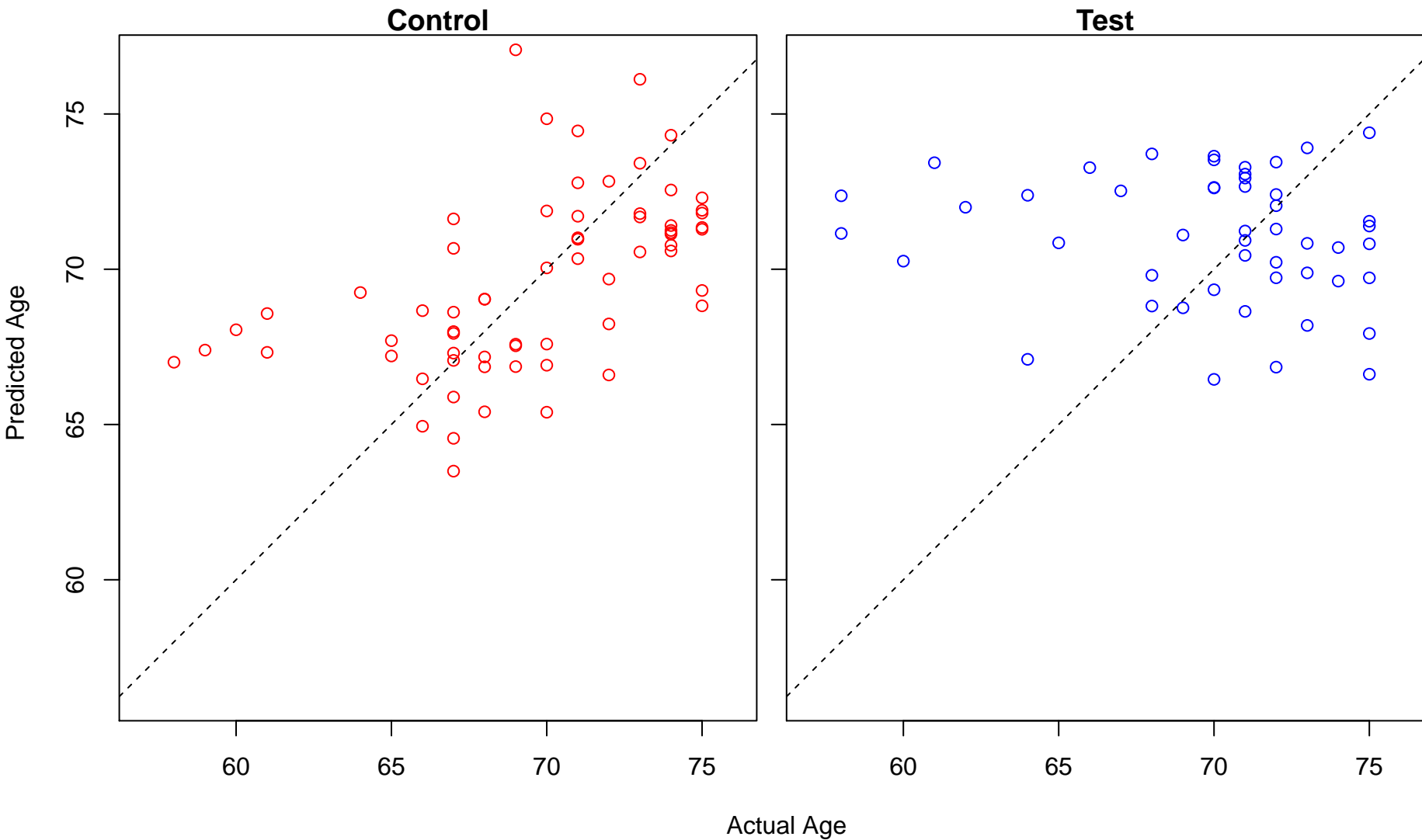
regulation of vascular endothelial growth factor receptor signaling pathway (Score: 0.930759)



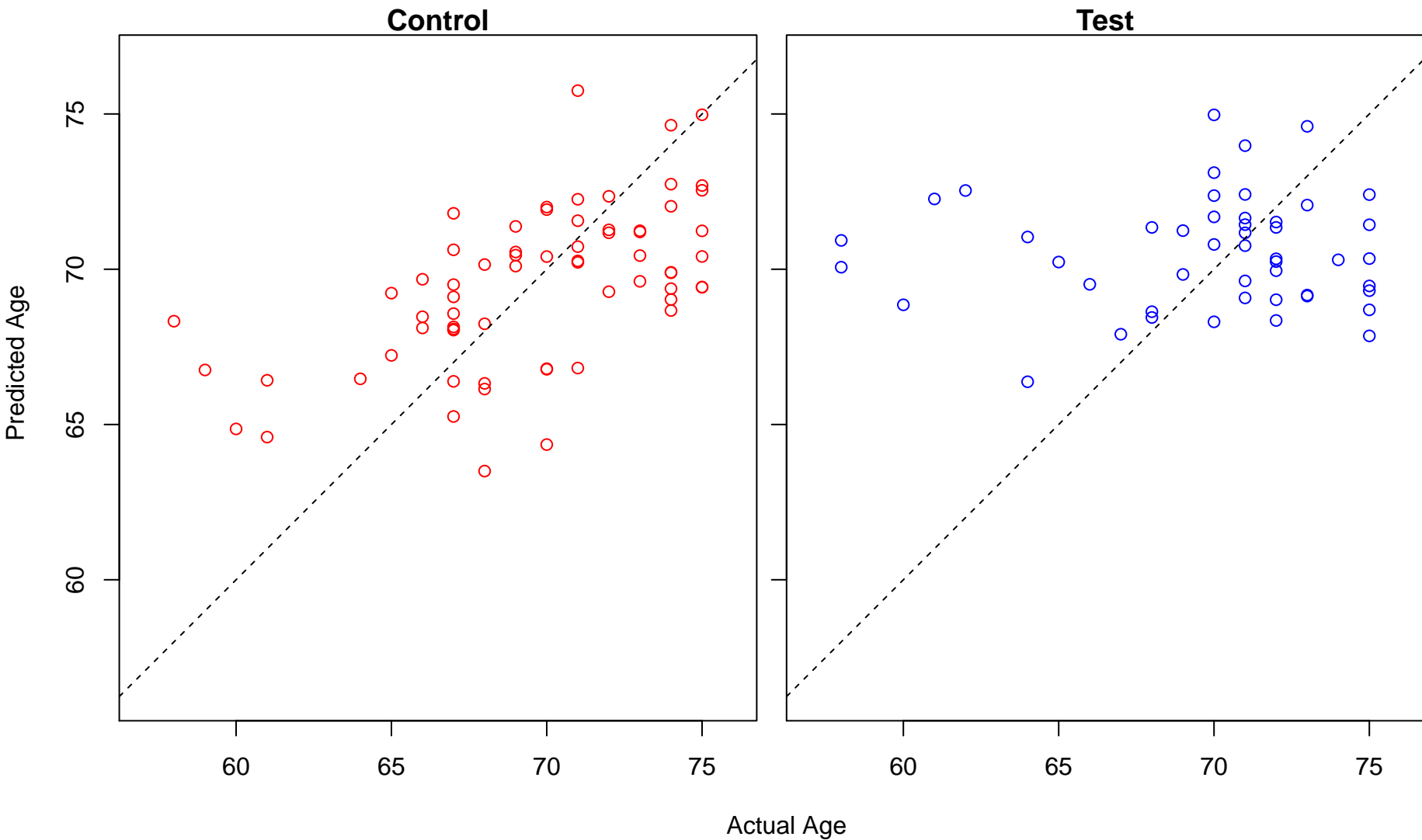
regulation of heart rate (Score: 0.929847)



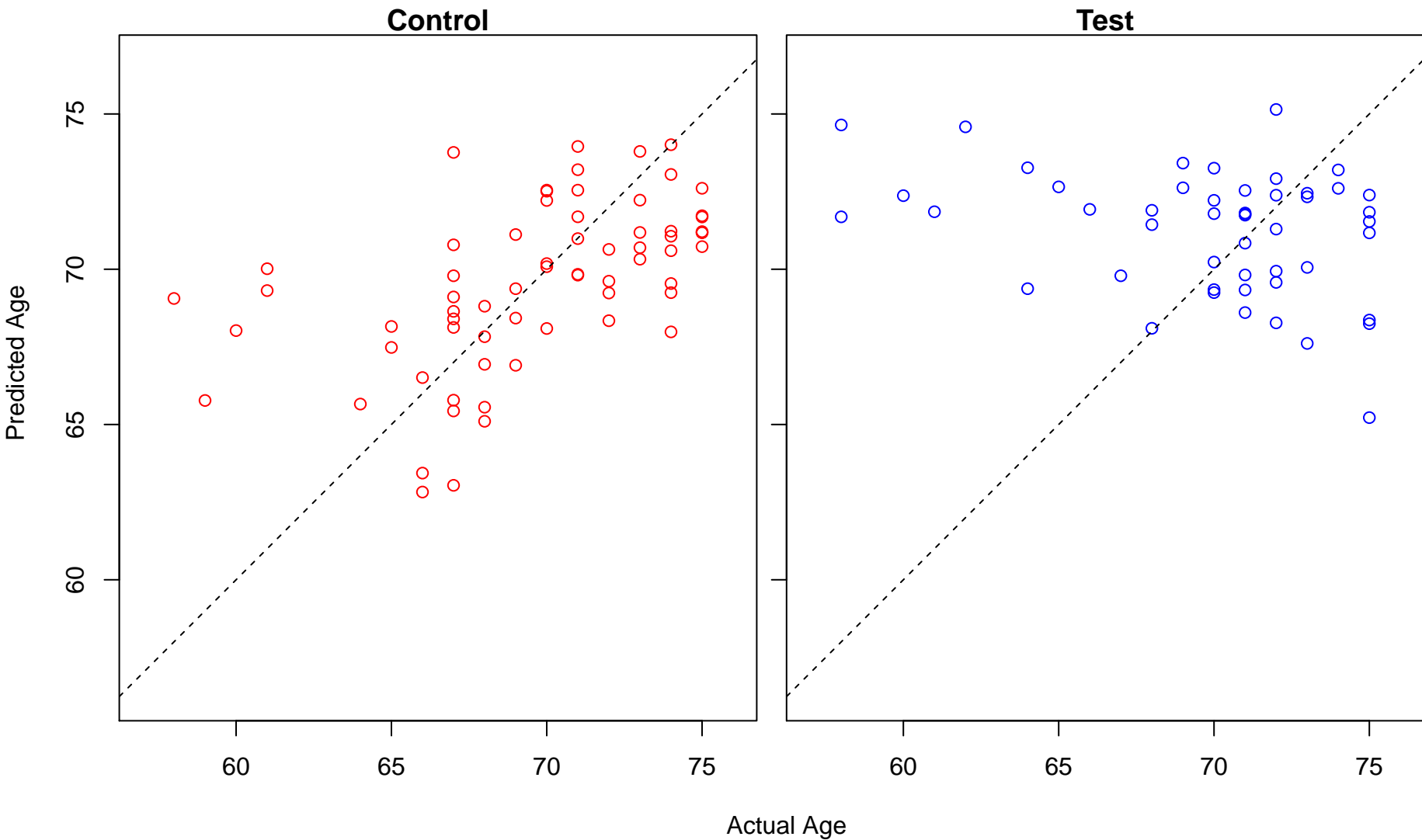
natural killer cell mediated immunity (Score: 0.929182)



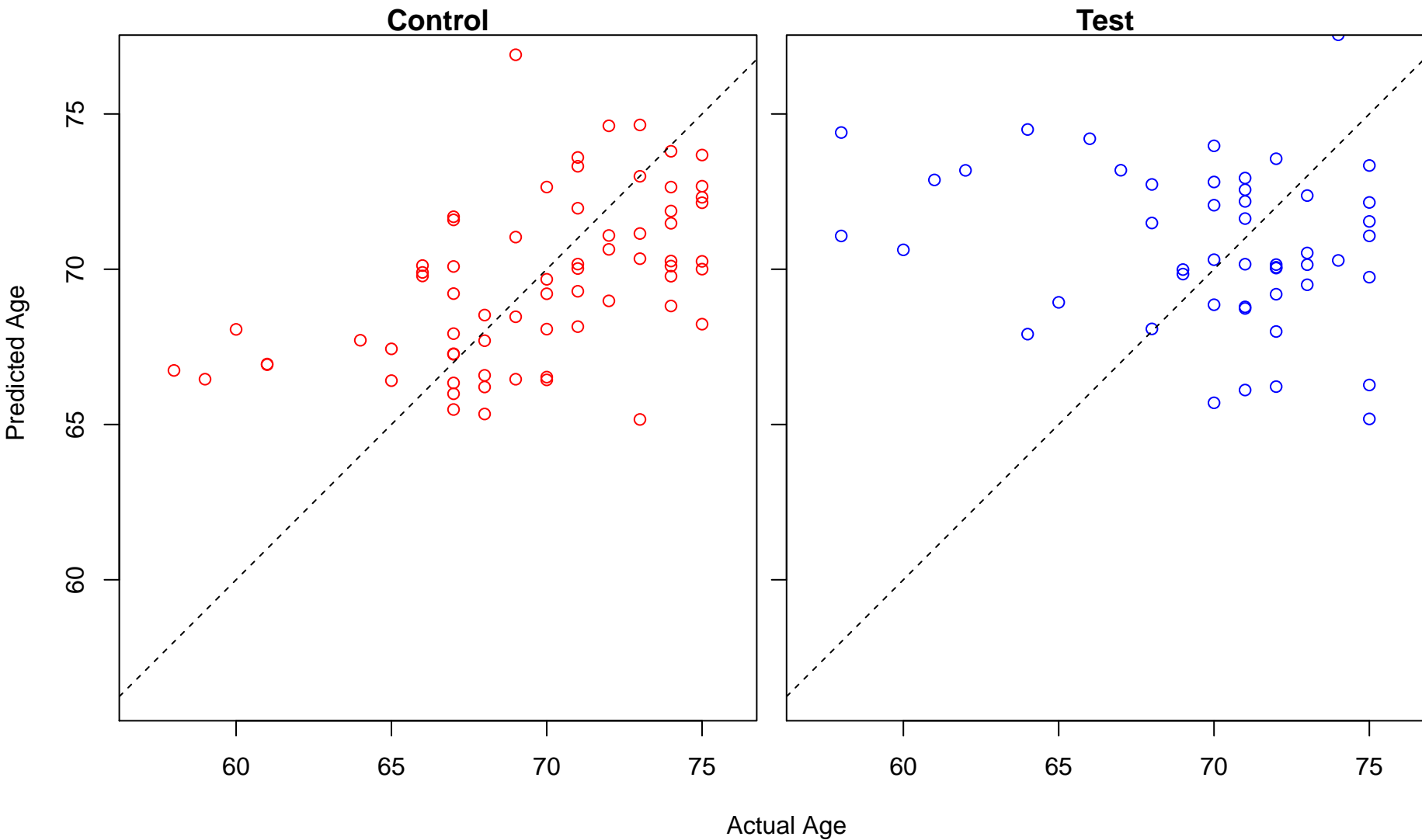
glucose catabolic process (Score: 0.929125)



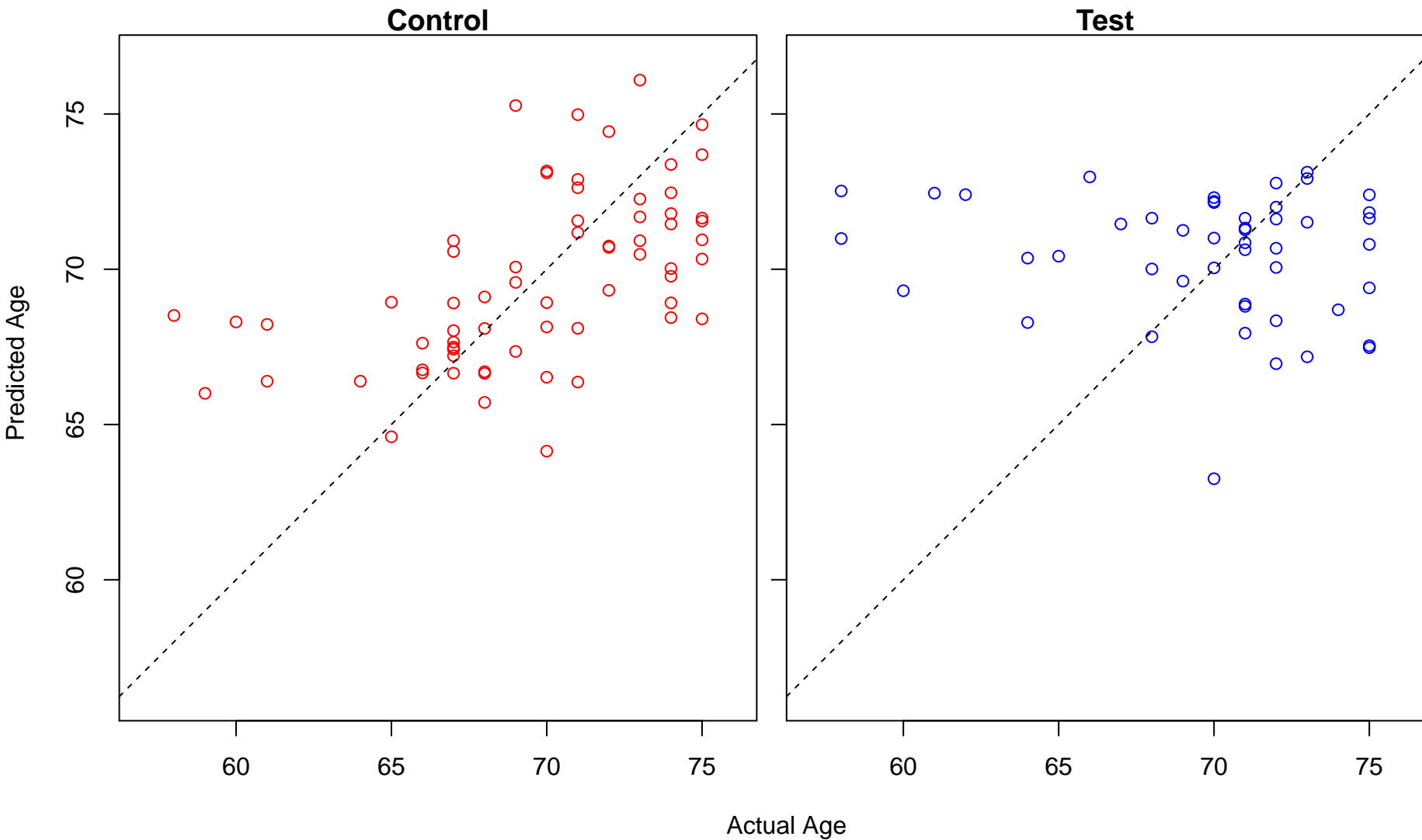
negative regulation of DNA endoreduplication (Score: 0.927908)



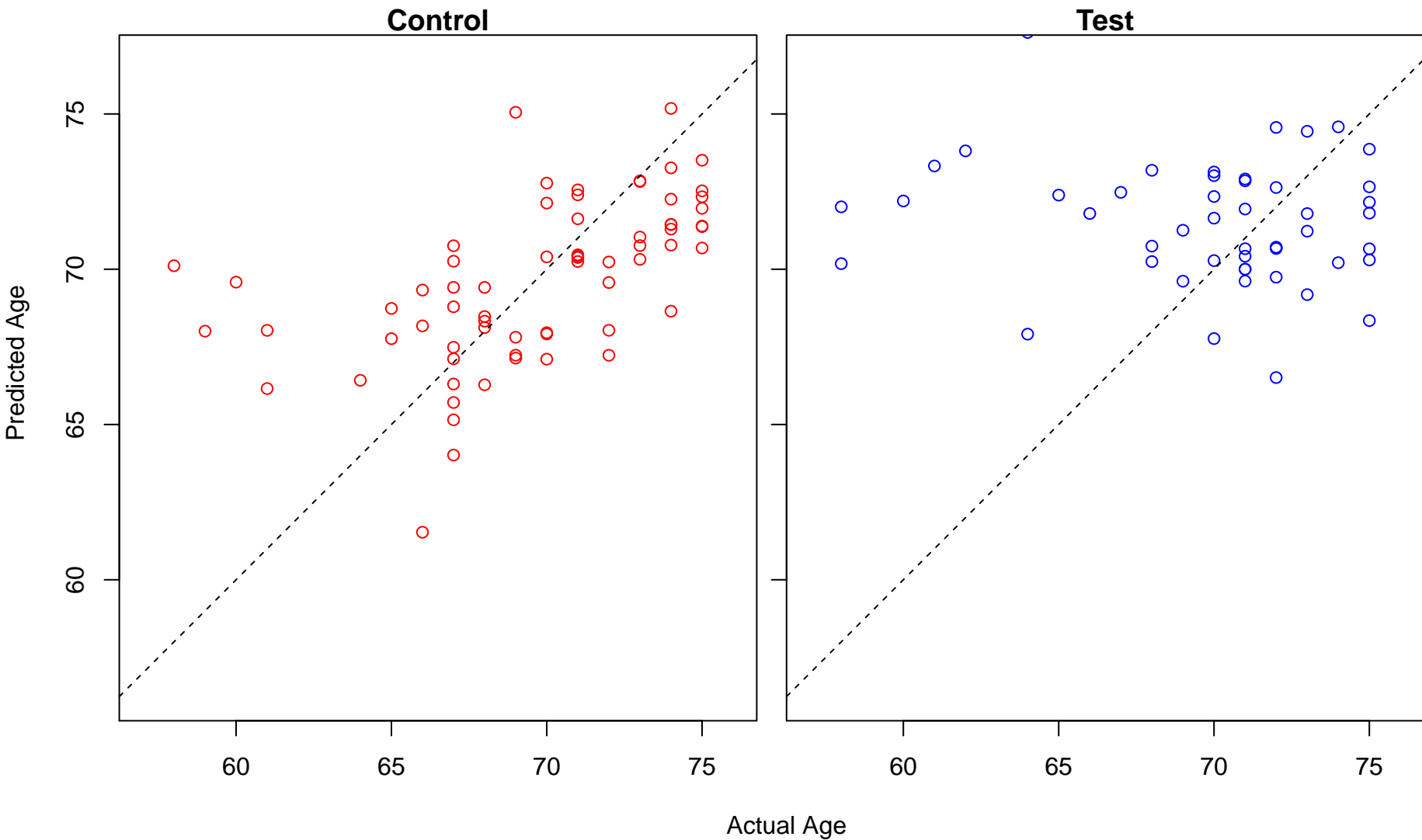
protein deacylation (Score: 0.927706)



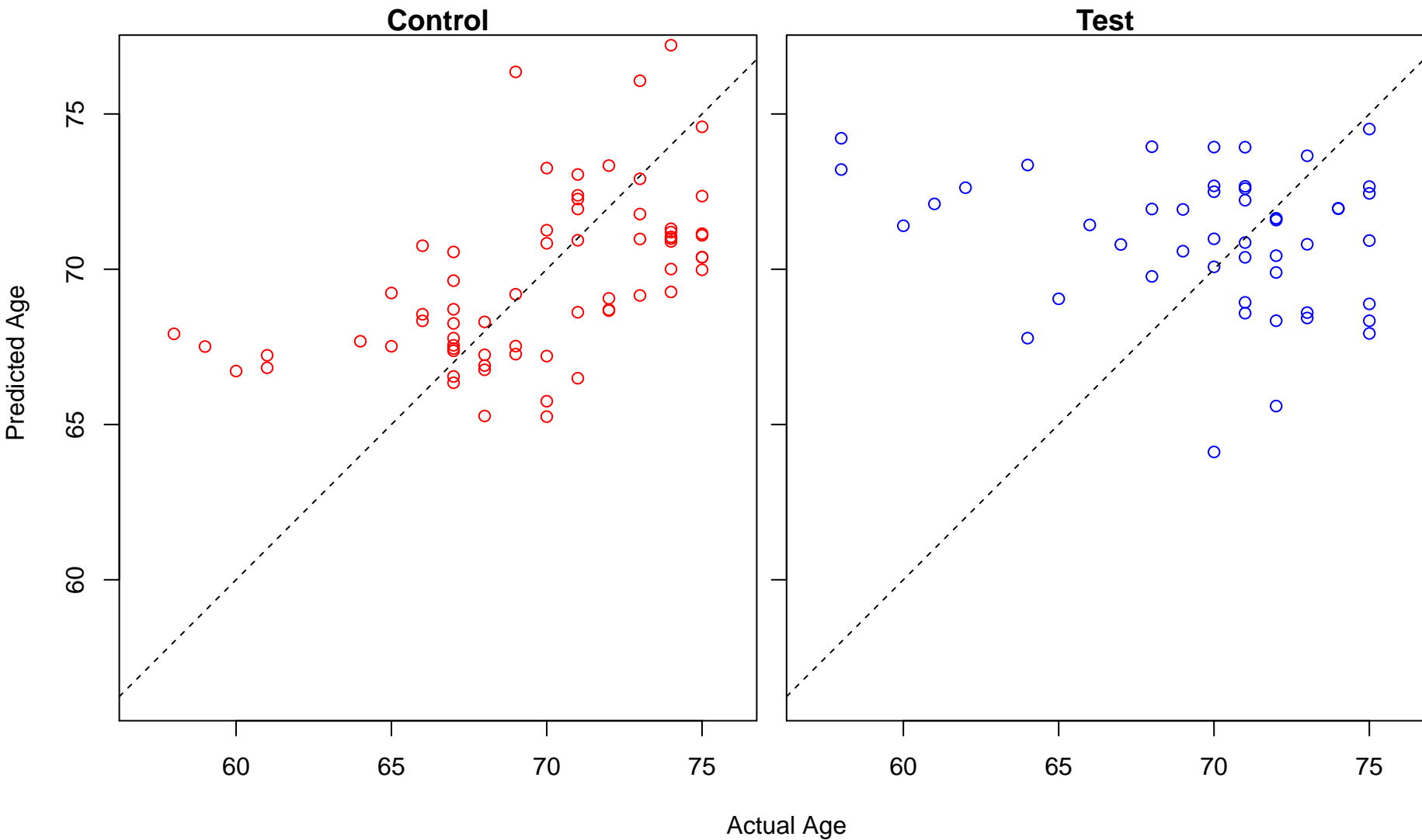
regulation of tyrosine phosphorylation of STAT protein (Score: 0.927661)



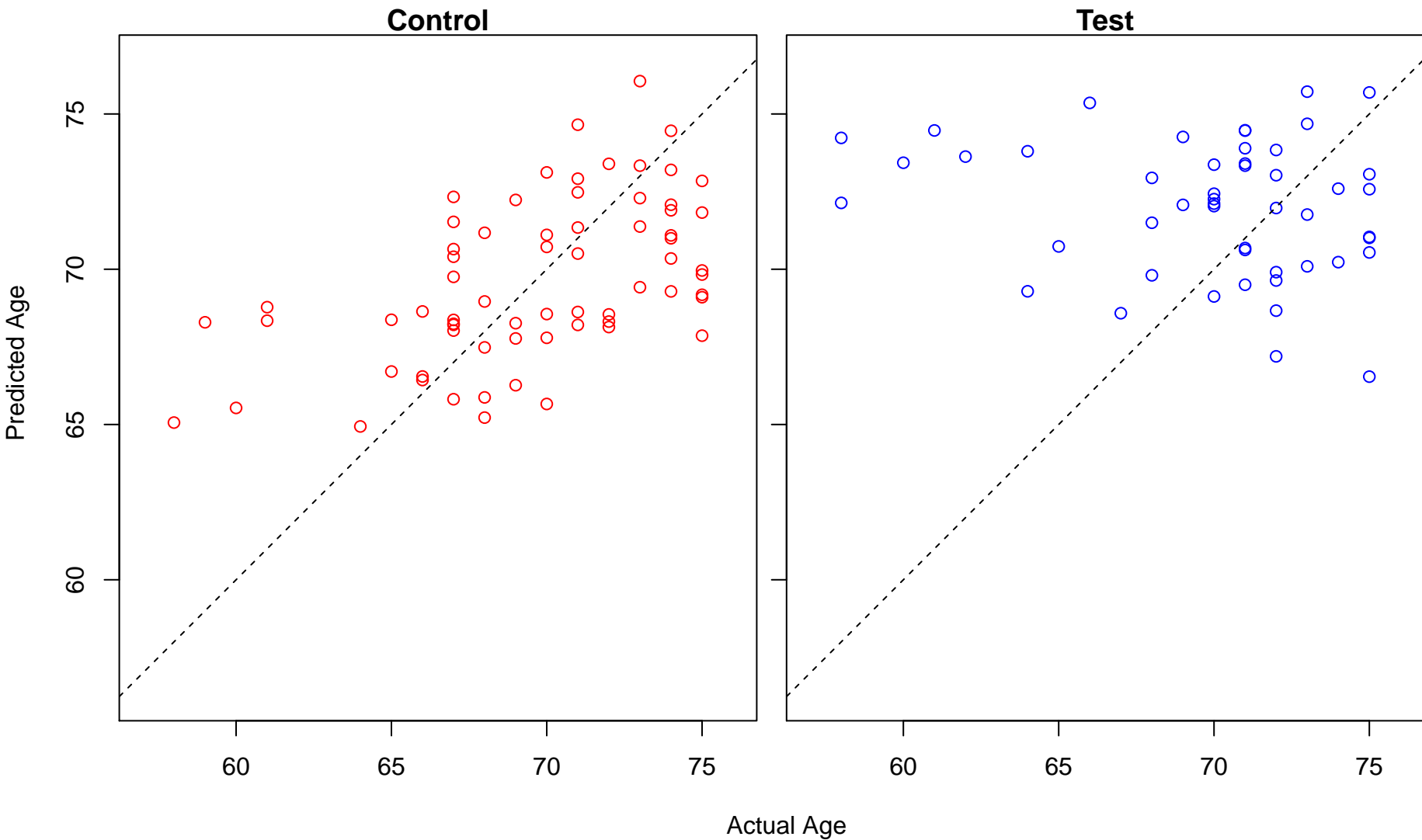
intracellular estrogen receptor signaling pathway (Score: 0.927547)



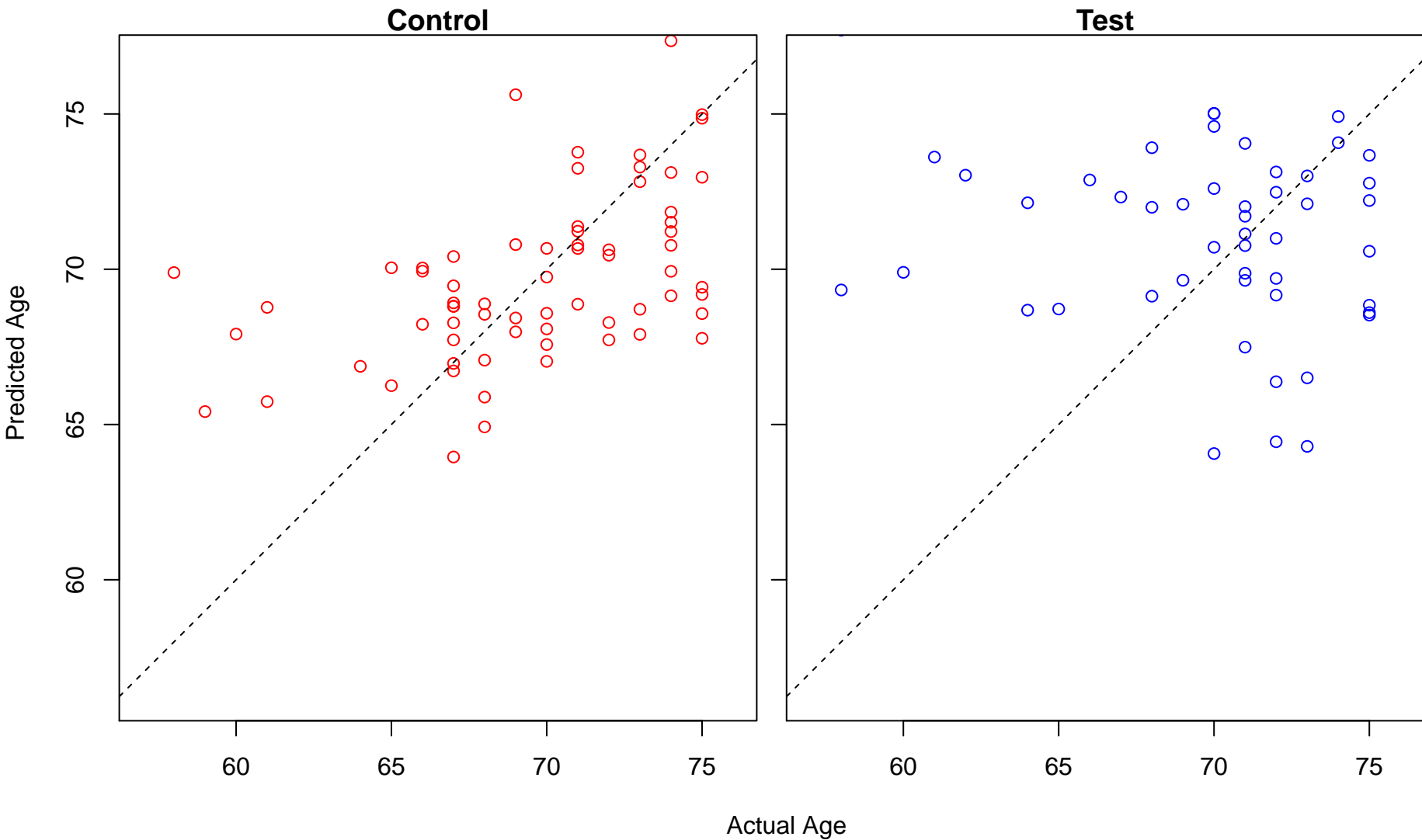
NLS-bearing protein import into nucleus (Score: 0.927232)



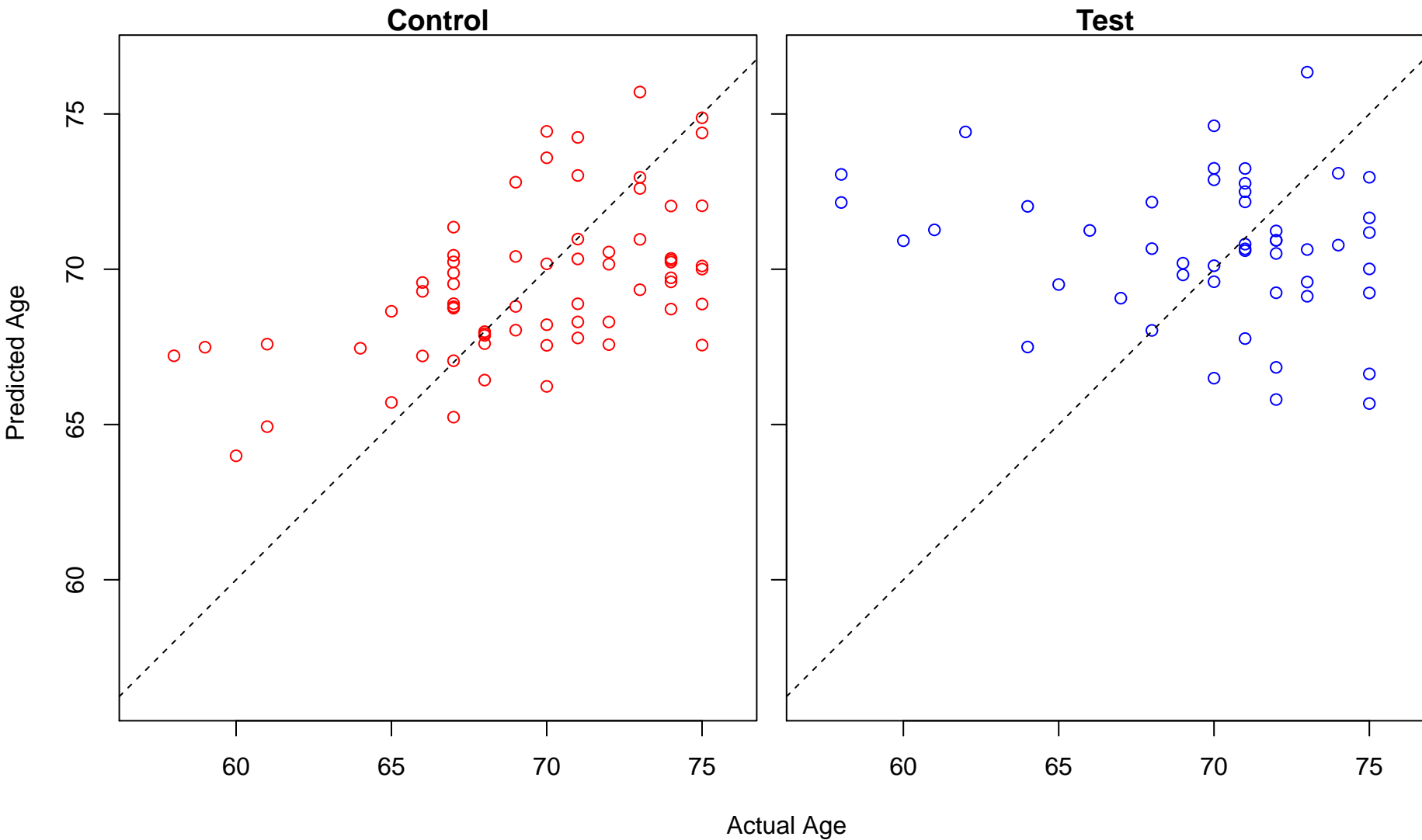
mesenchyme morphogenesis (Score: 0.926317)



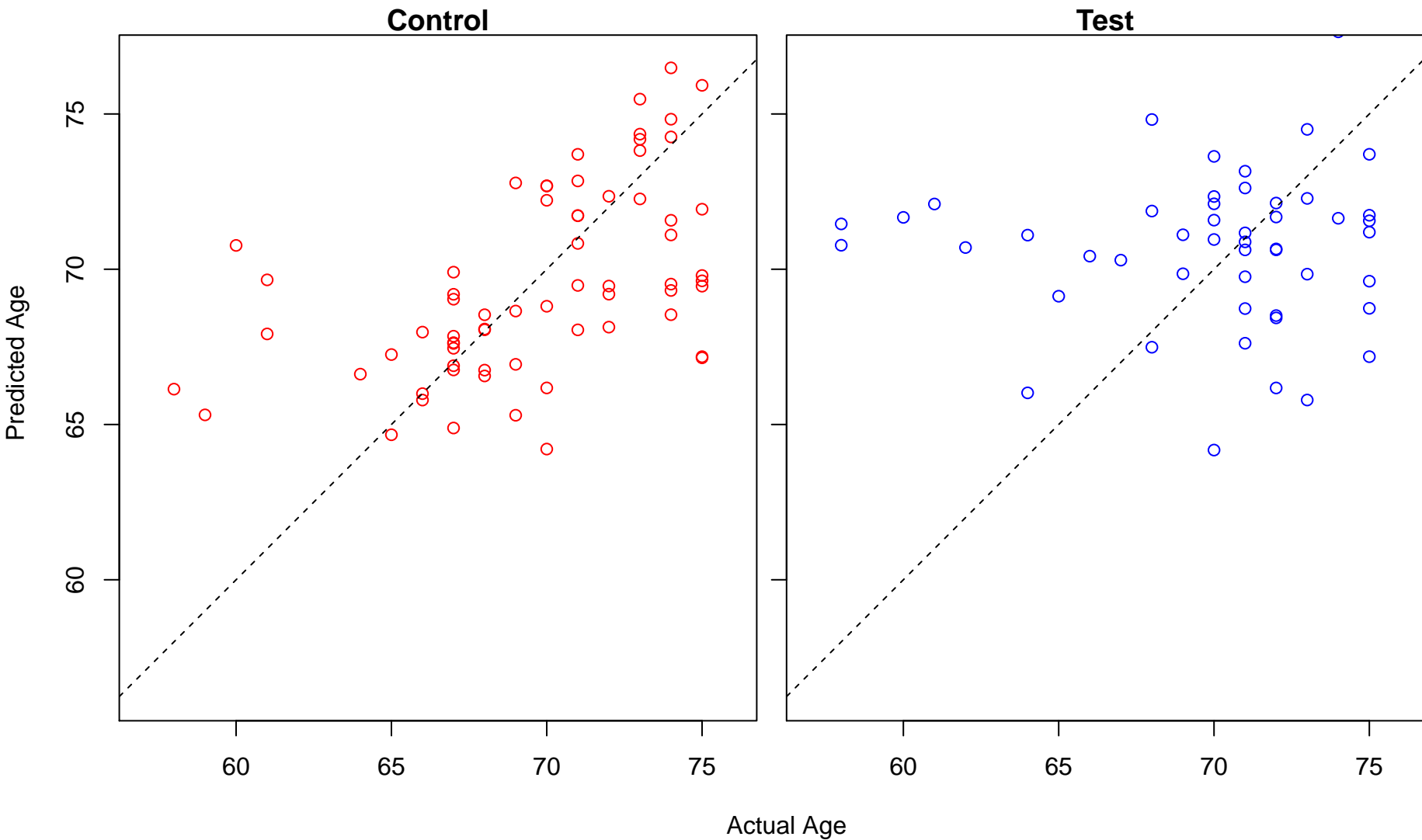
telomere capping (Score: 0.926115)



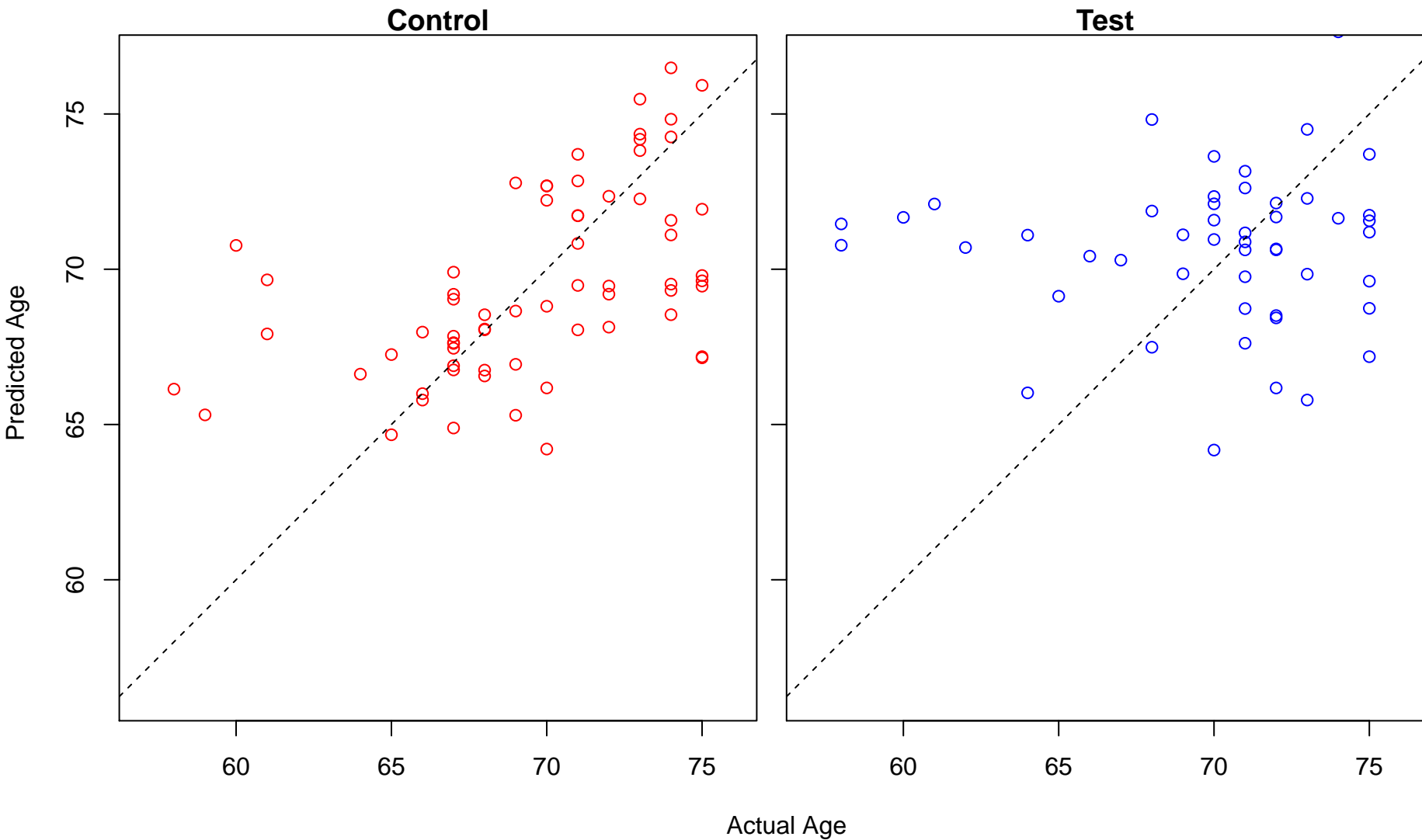
fatty acid transport (Score: 0.925923)



positive regulation of protein localization to plasma membrane (Score: 0.925716)

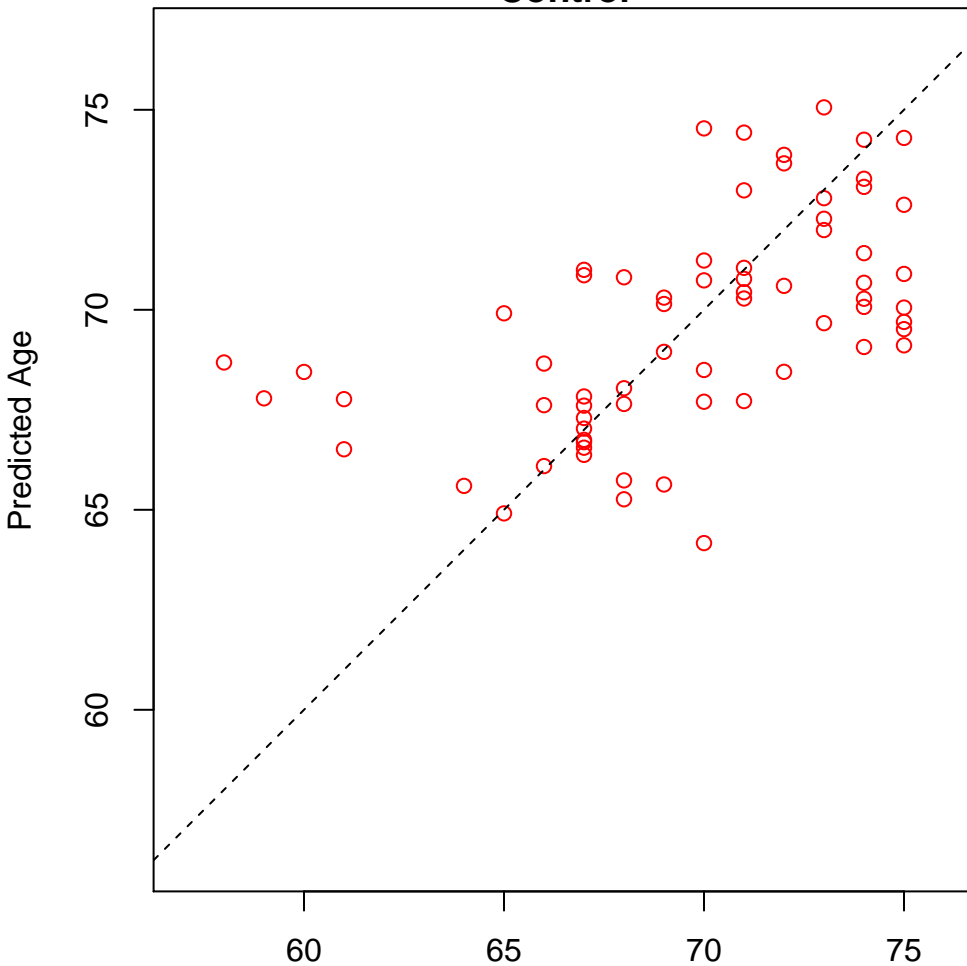


positive regulation of protein localization to cell periphery (Score: 0.925716)

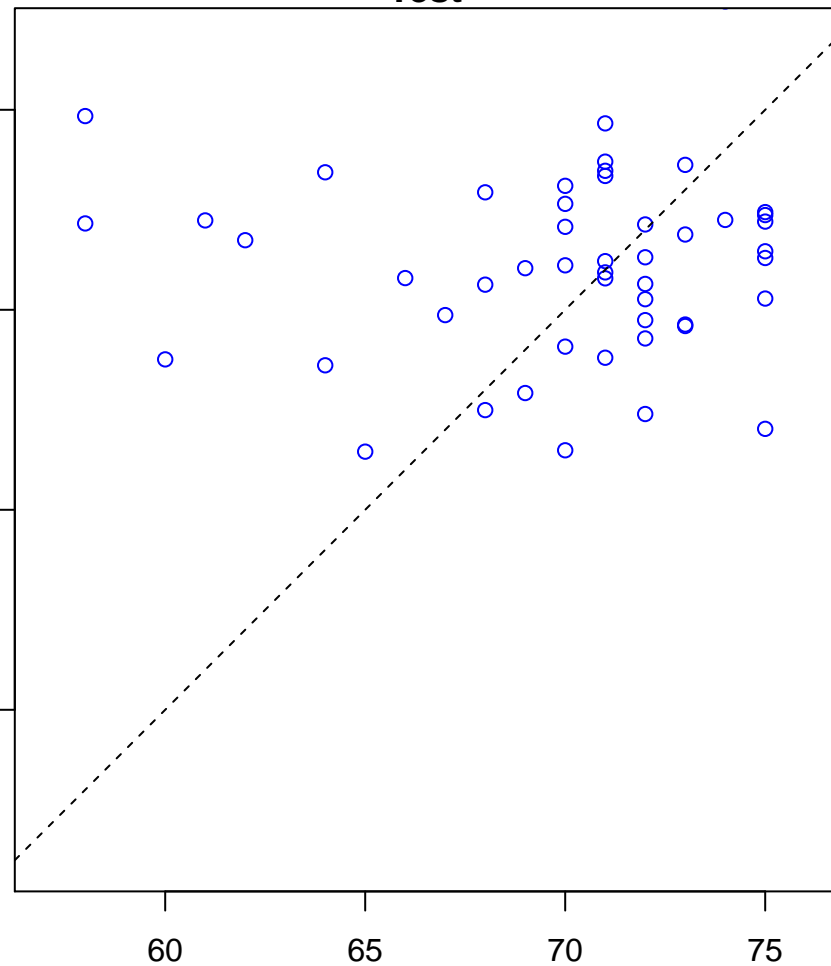


digestive tract development (Score: 0.925560)

Control

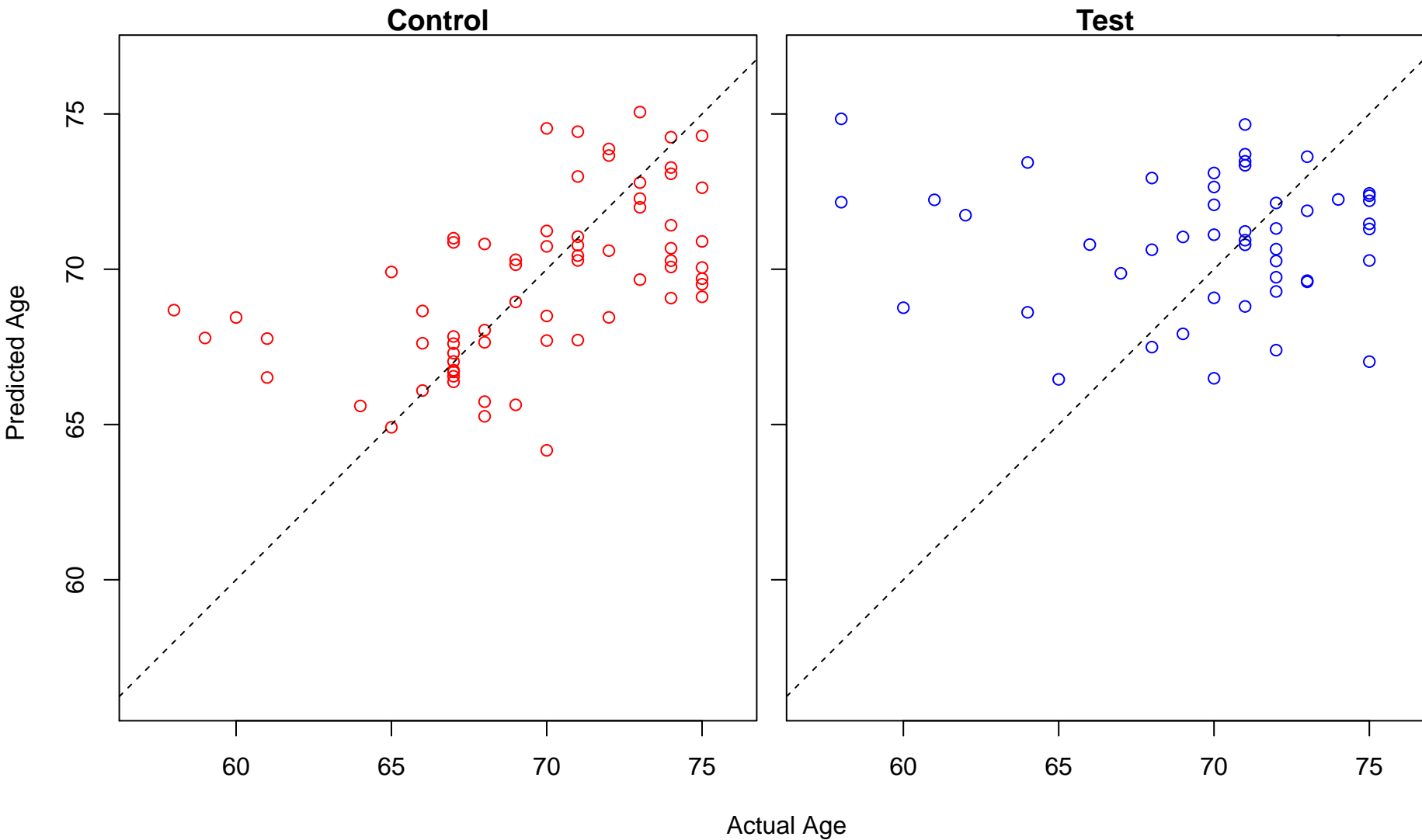


Test



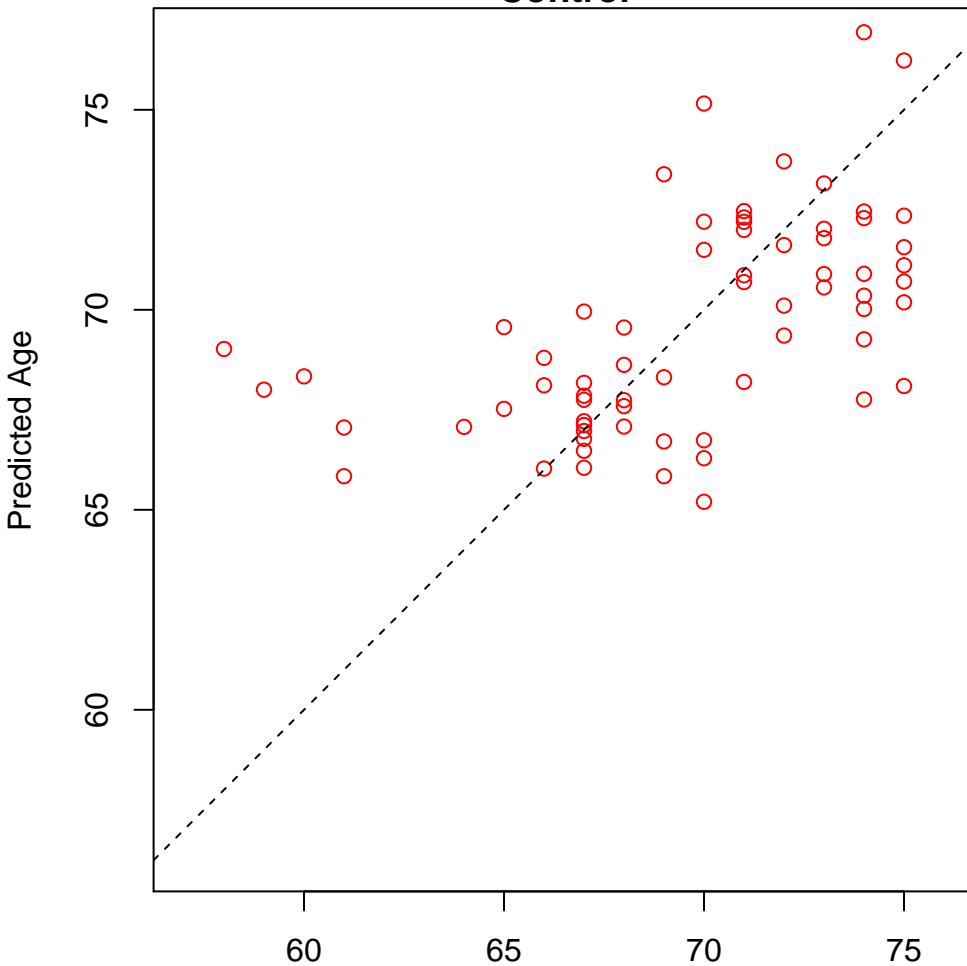
Actual Age

digestive system development (Score: 0.925560)

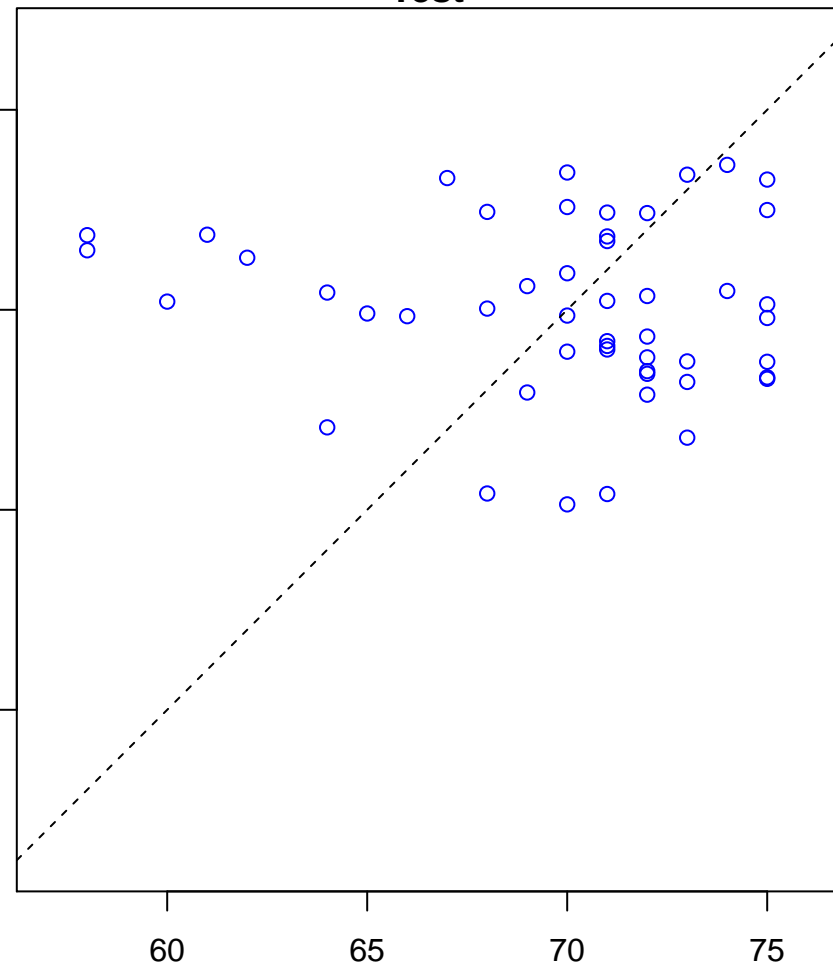


inositol phosphate catabolic process (Score: 0.925540)

Control

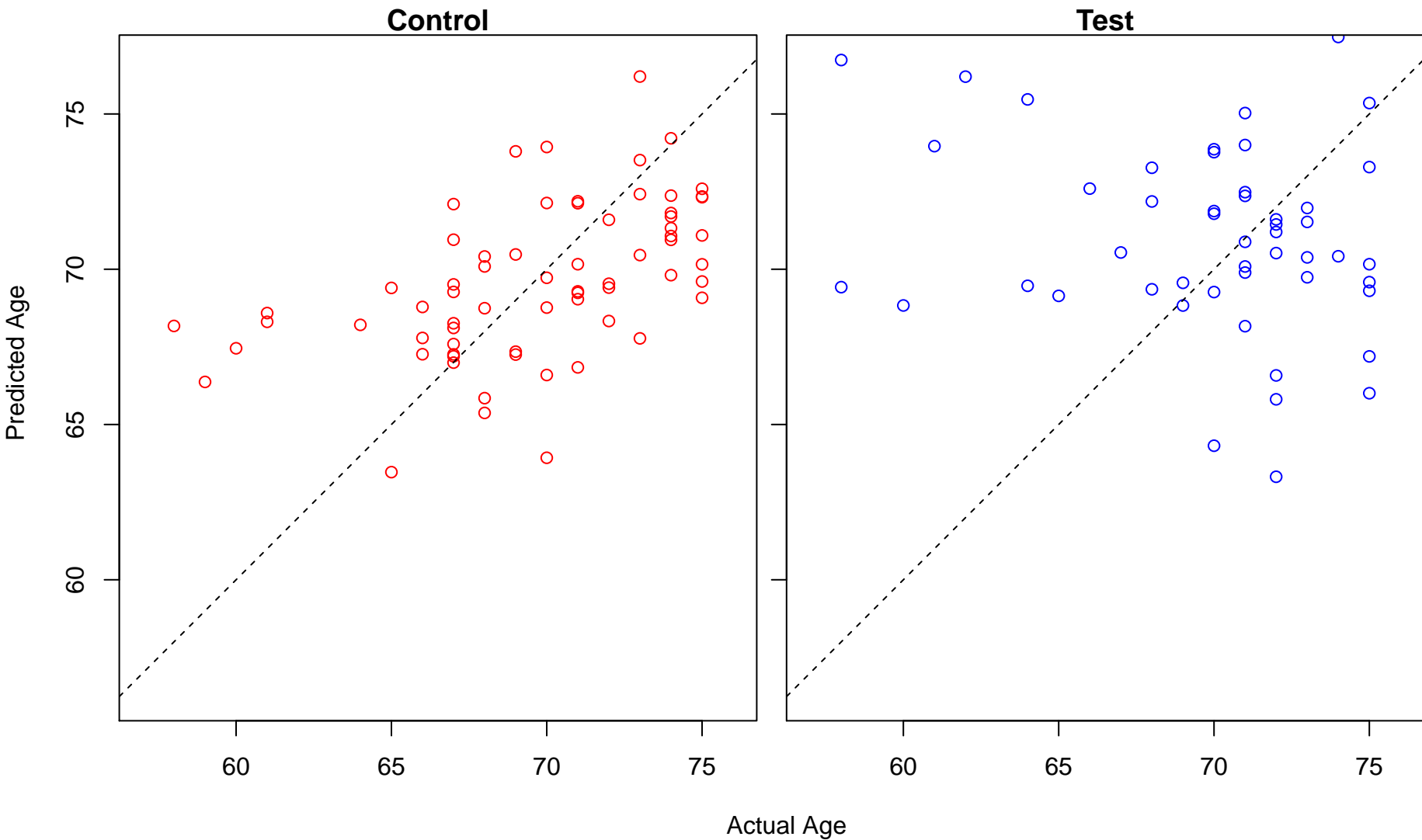


Test

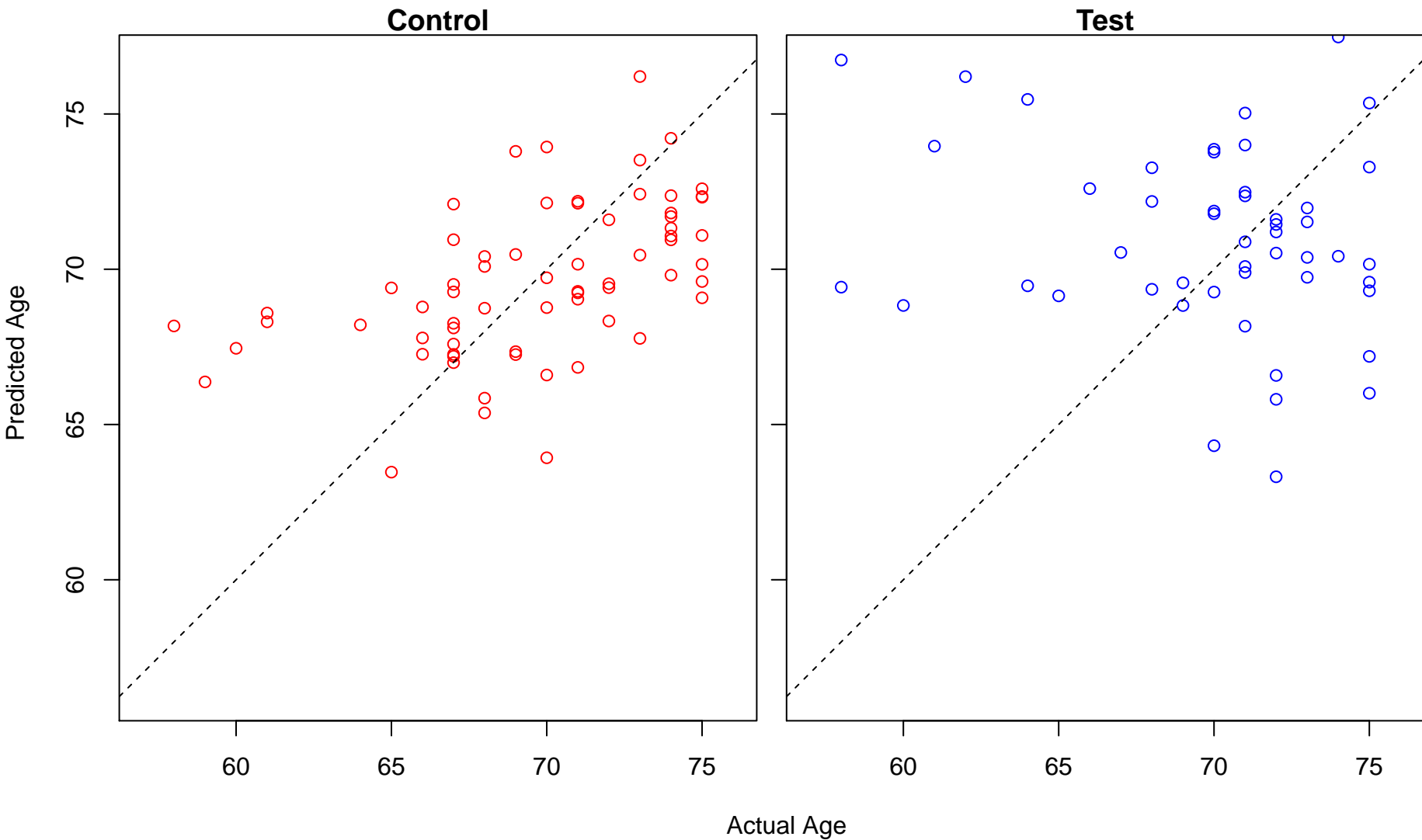


Actual Age

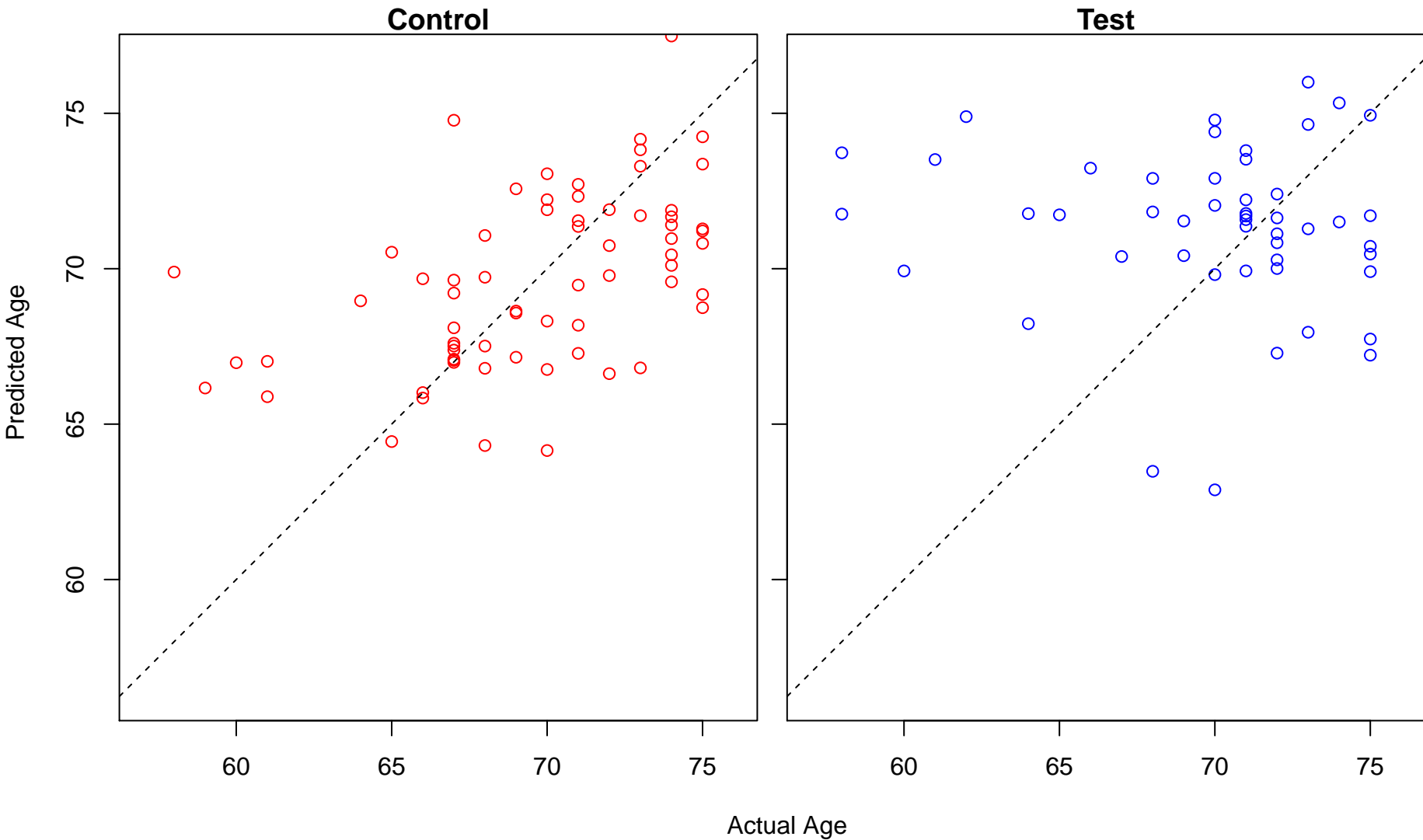
negative regulation of release of sequestered calcium ion into cytosol (Score: 0.925470)



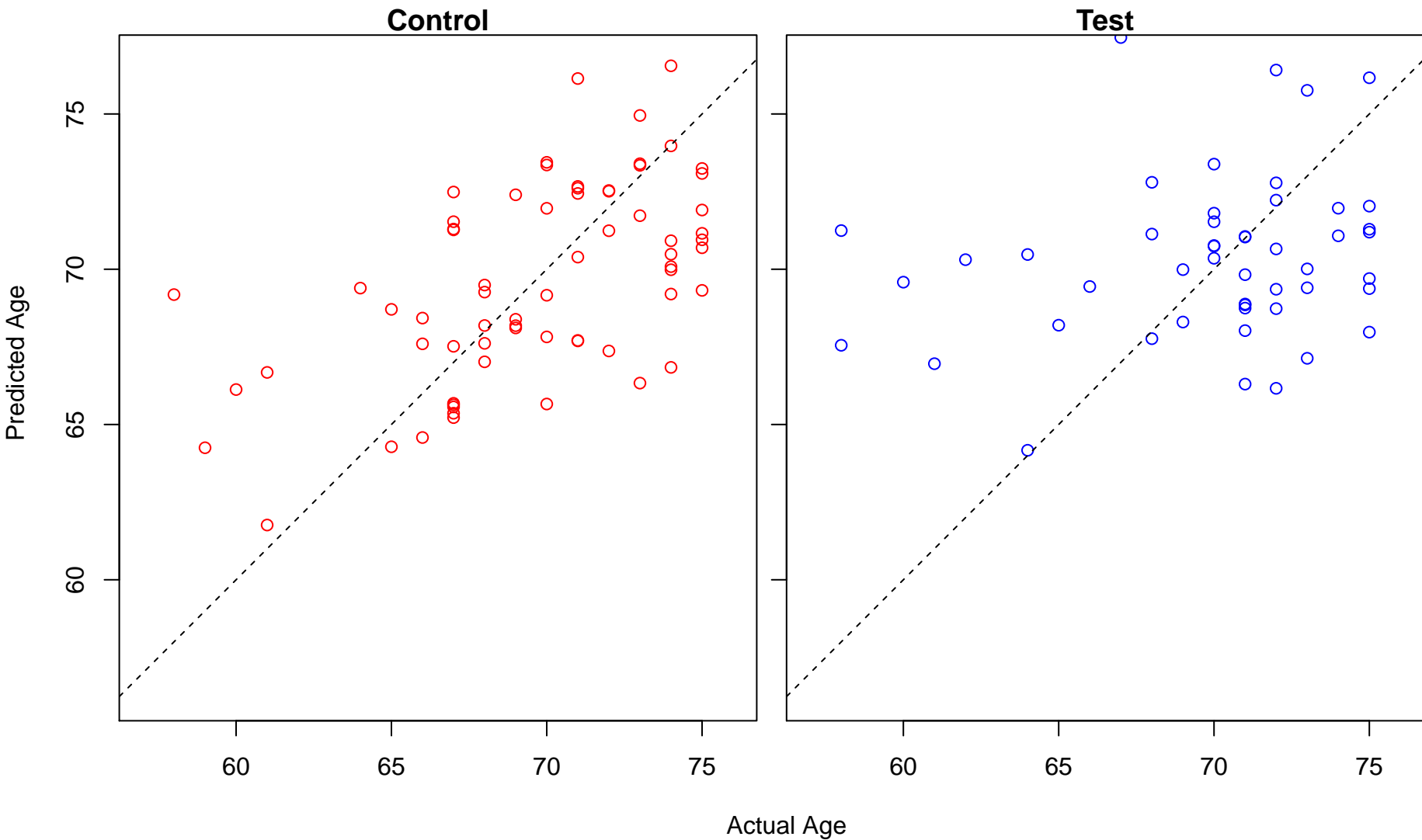
negative regulation of ryanodine-sensitive calcium-release channel activity (Score: 0.925470)



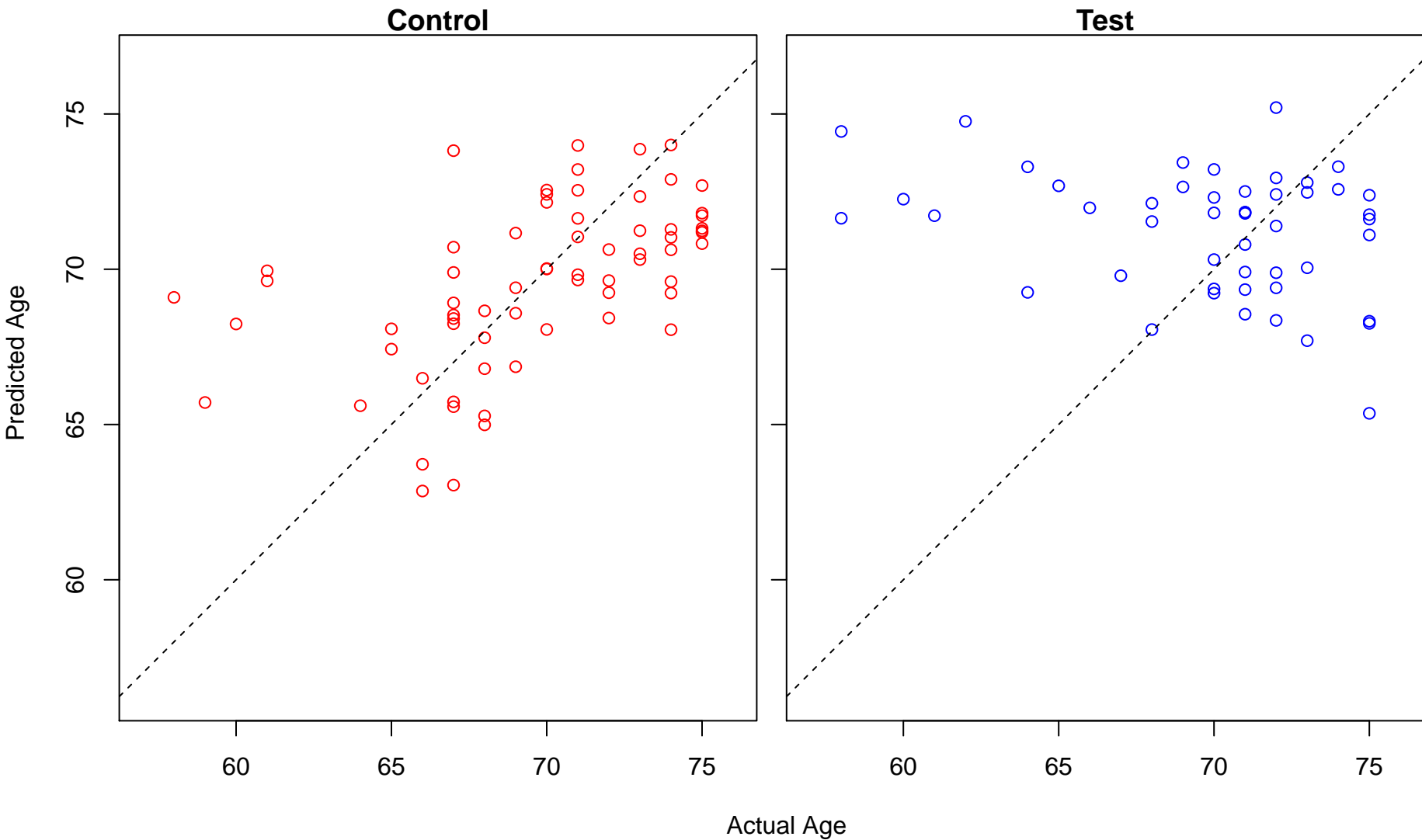
negative regulation of microtubule polymerization or depolymerization (Score: 0.925001)



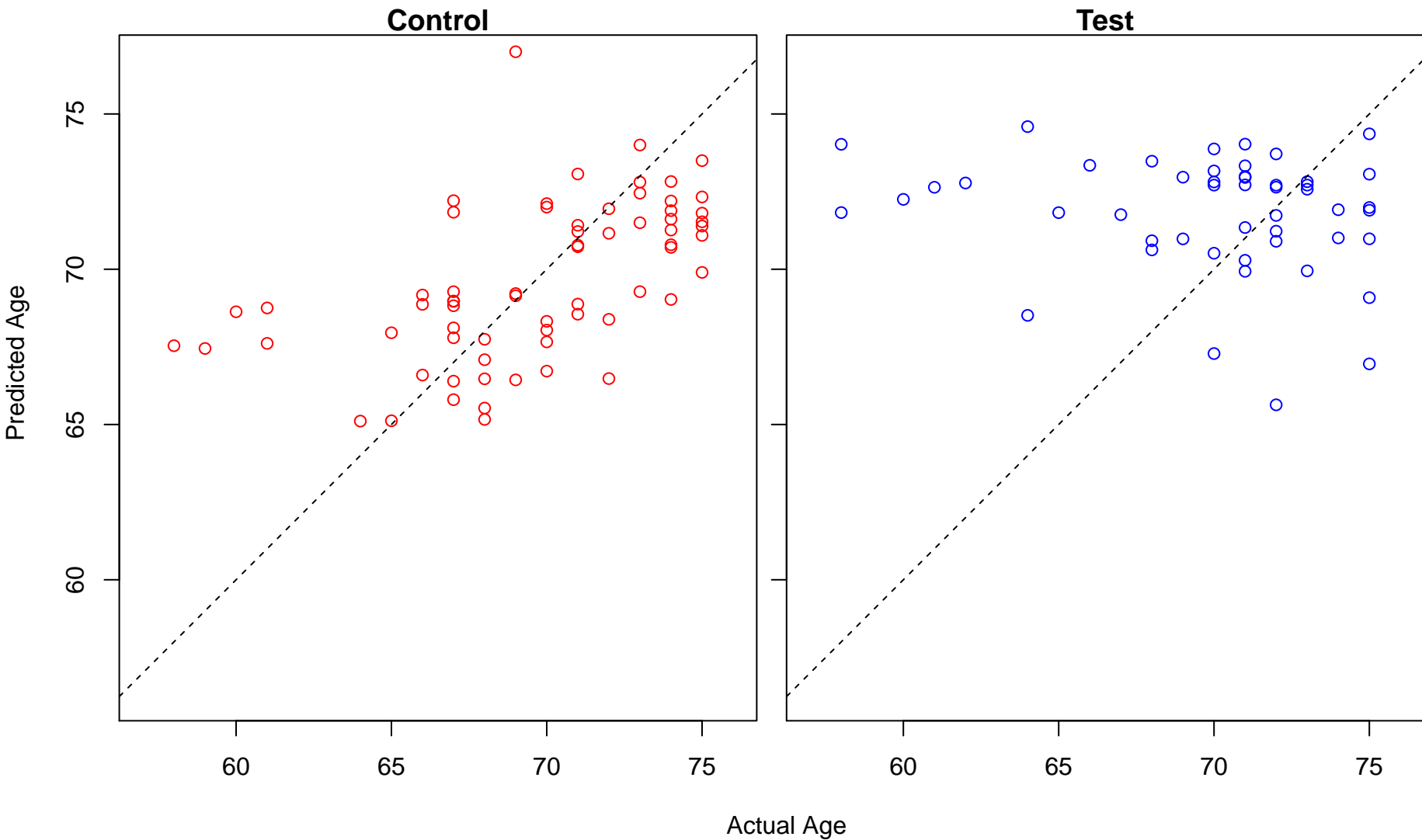
mRNA modification (Score: 0.924802)



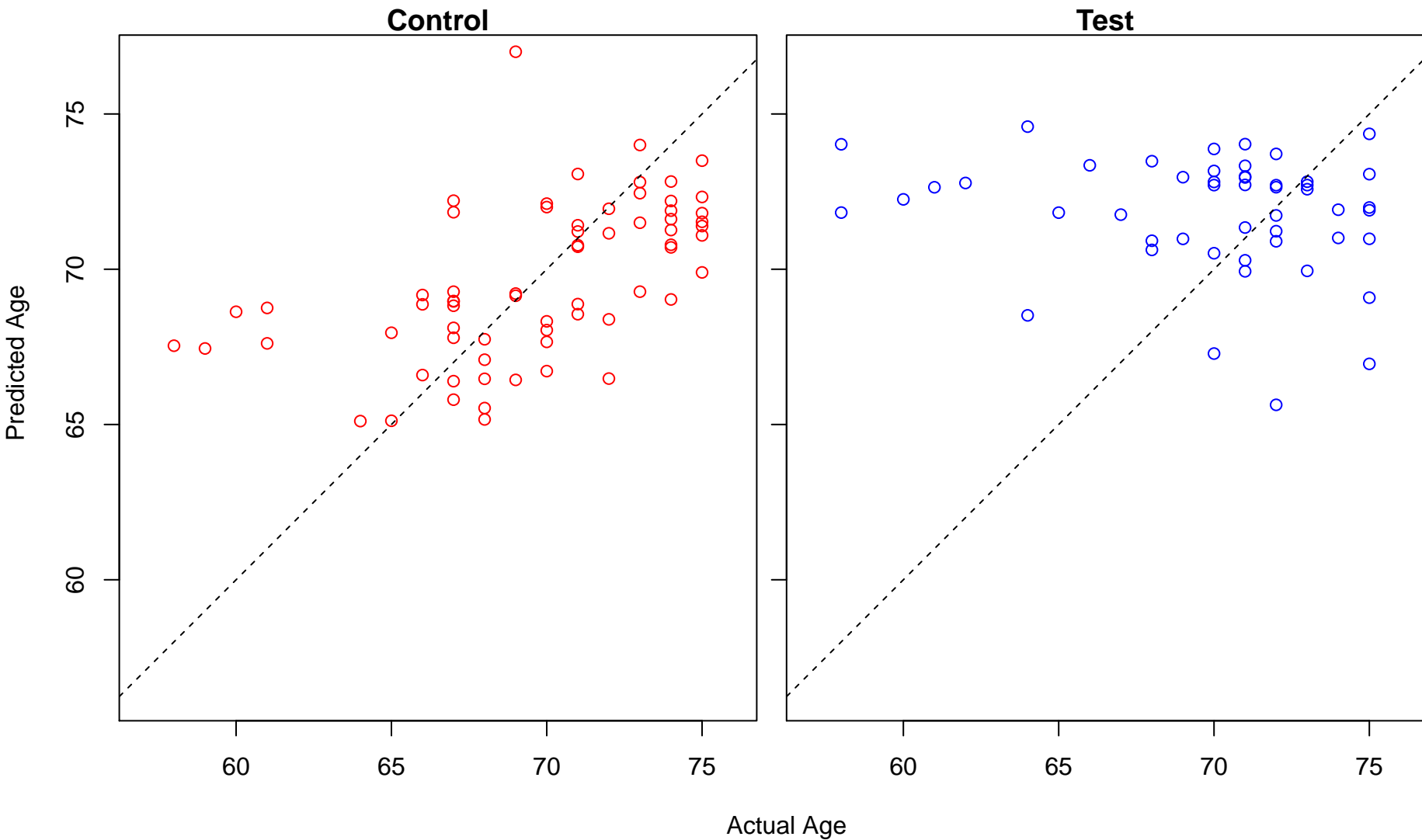
regulation of DNA endoreduplication (Score: 0.924594)



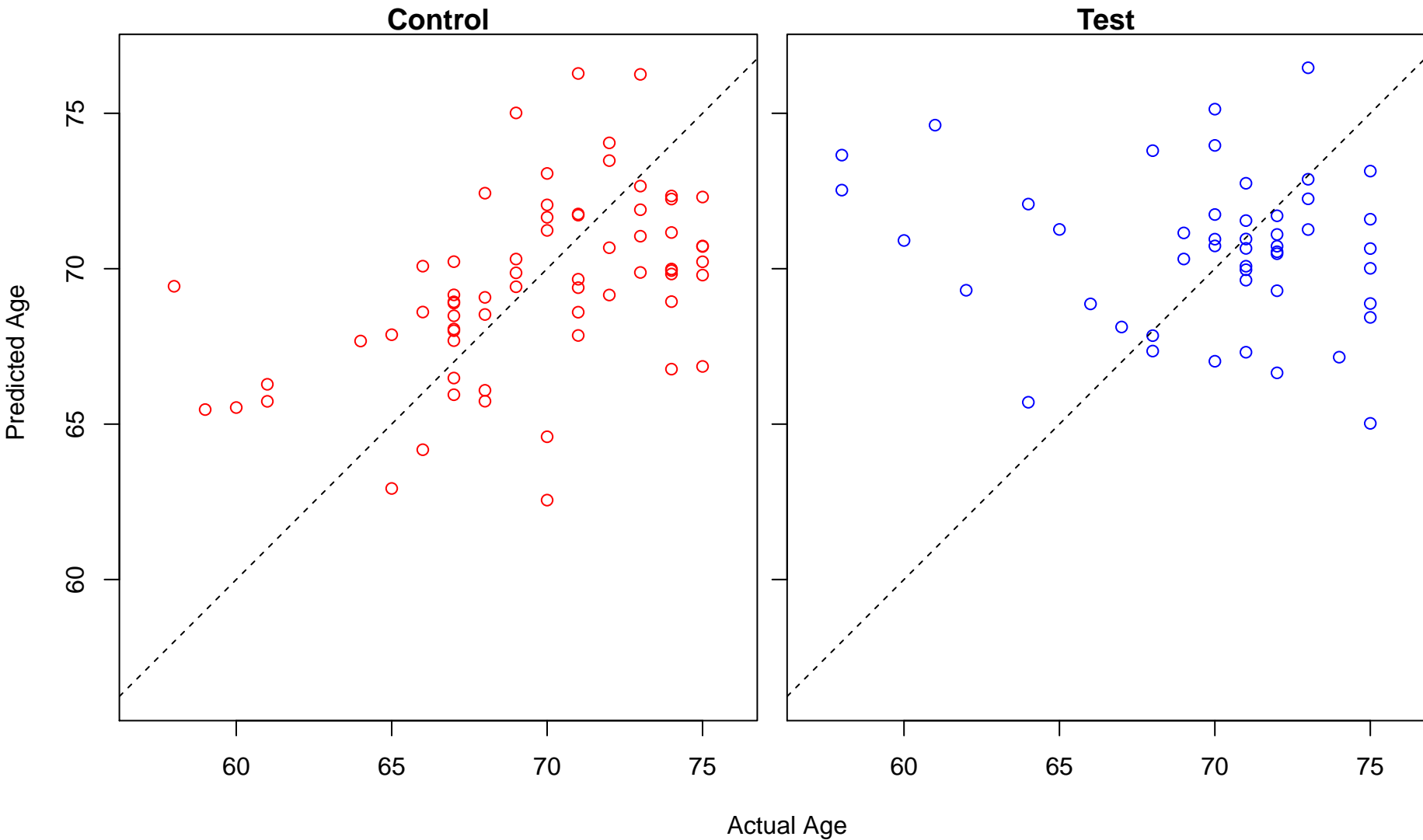
cellular ketone body metabolic process (Score: 0.924471)



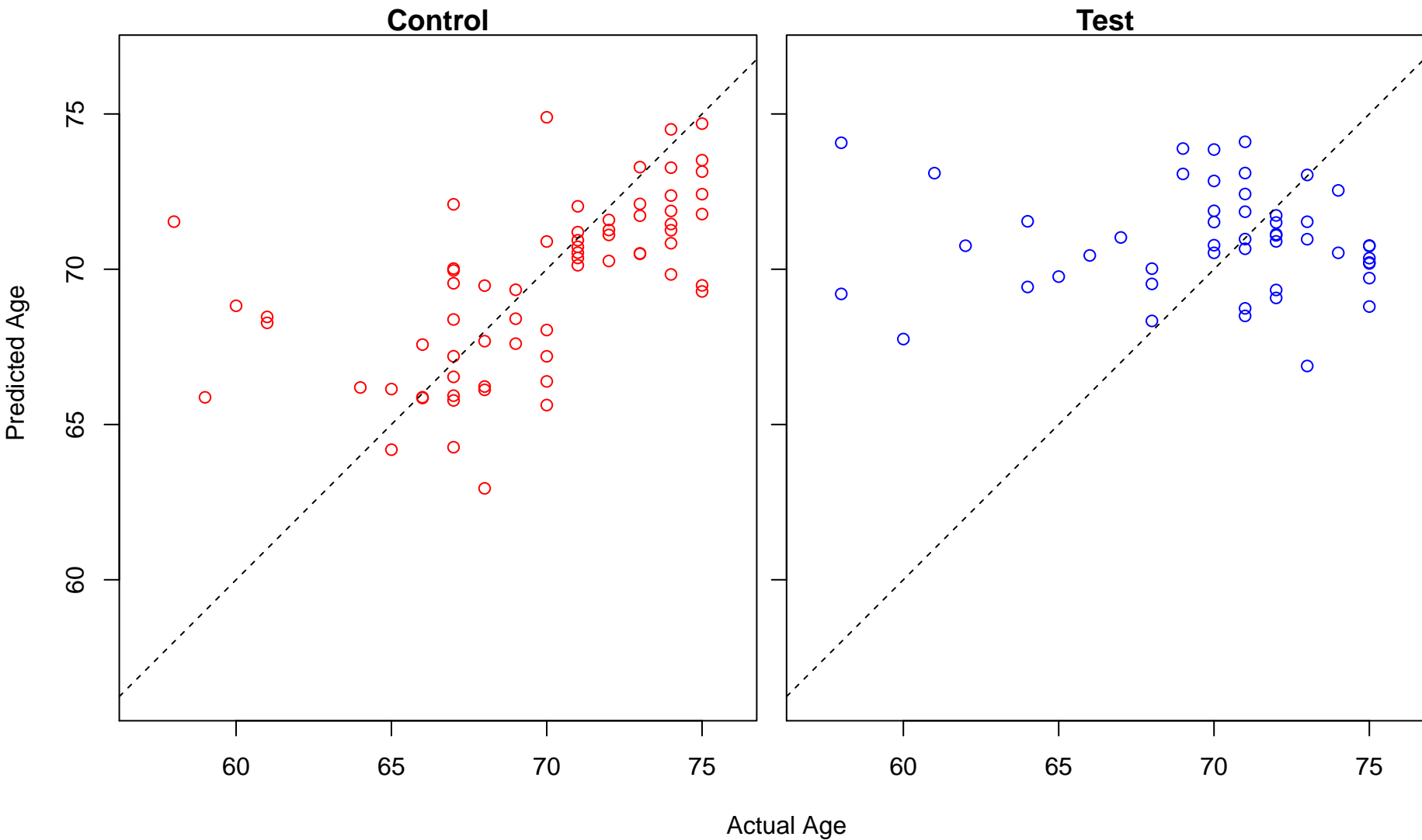
ketone body metabolic process (Score: 0.924471)



positive regulation of chemokine production (Score: 0.924024)

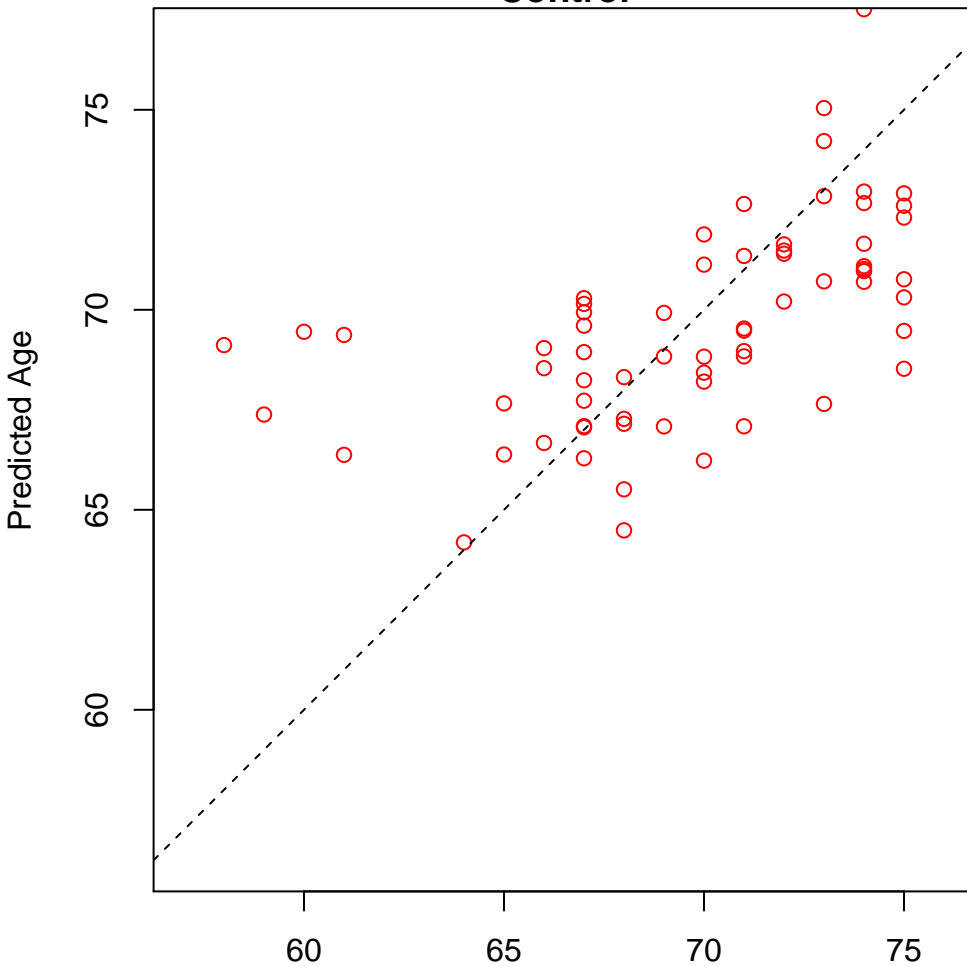


antigen processing and presentation of endogenous antigen (Score: 0.923603)

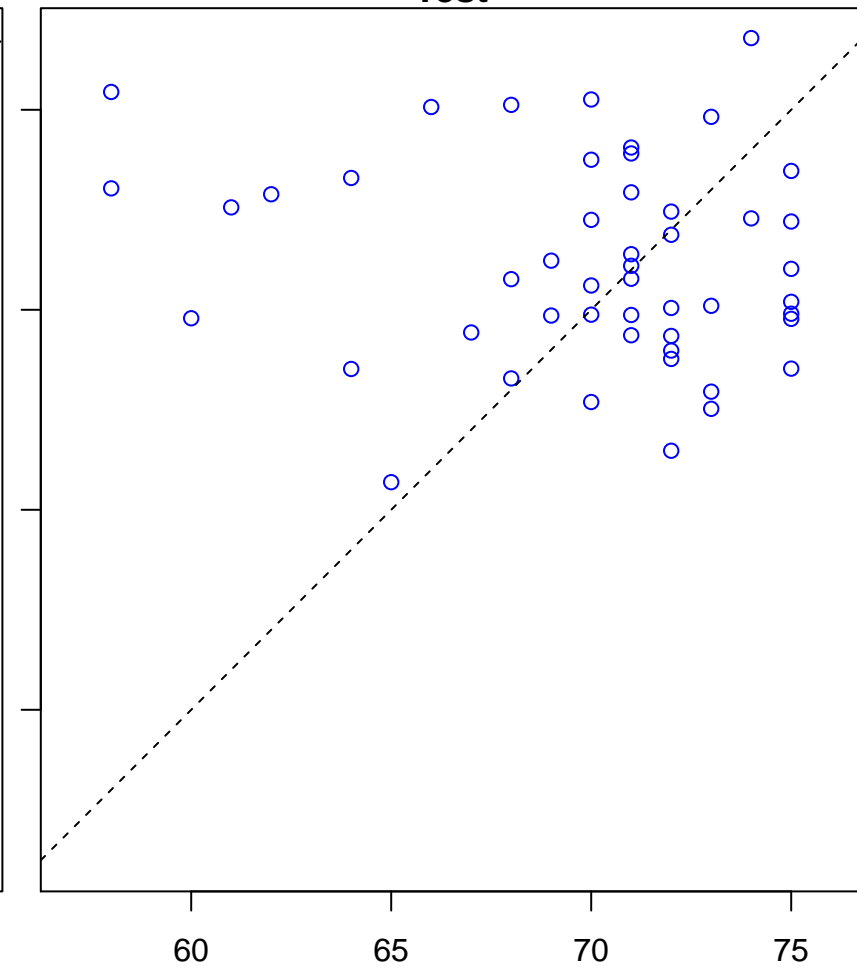


response to transition metal nanoparticle (Score: 0.923513)

Control

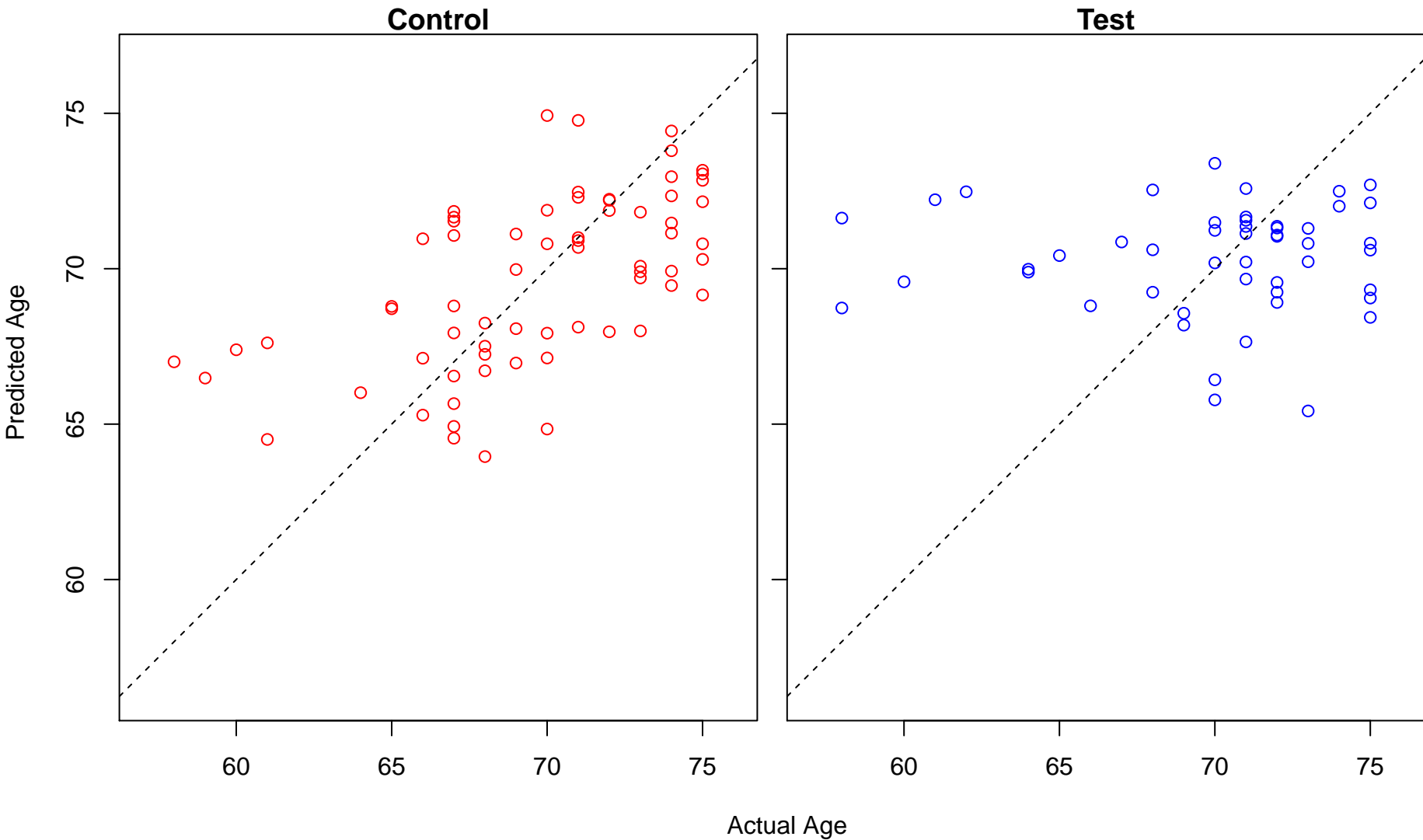


Test

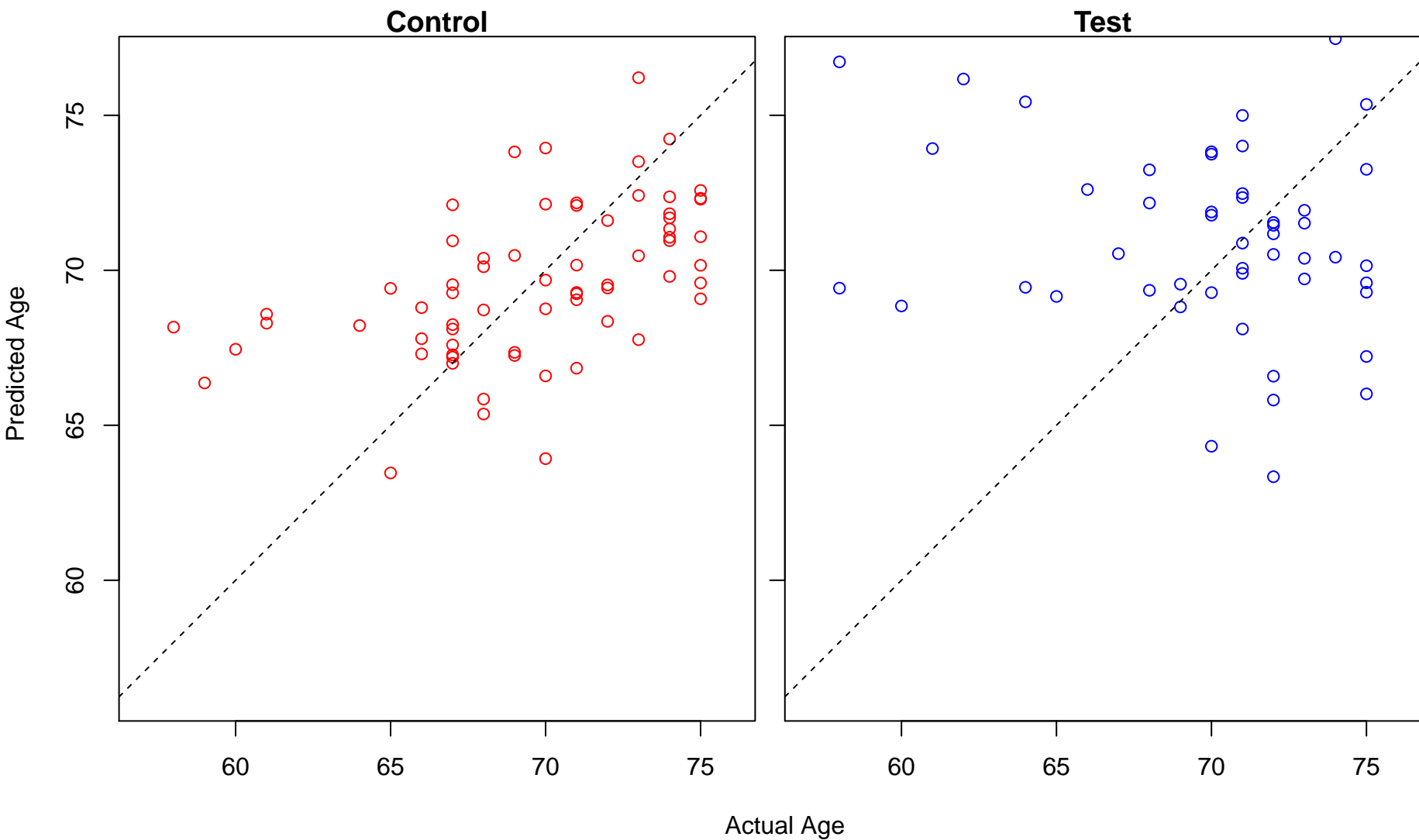


Actual Age

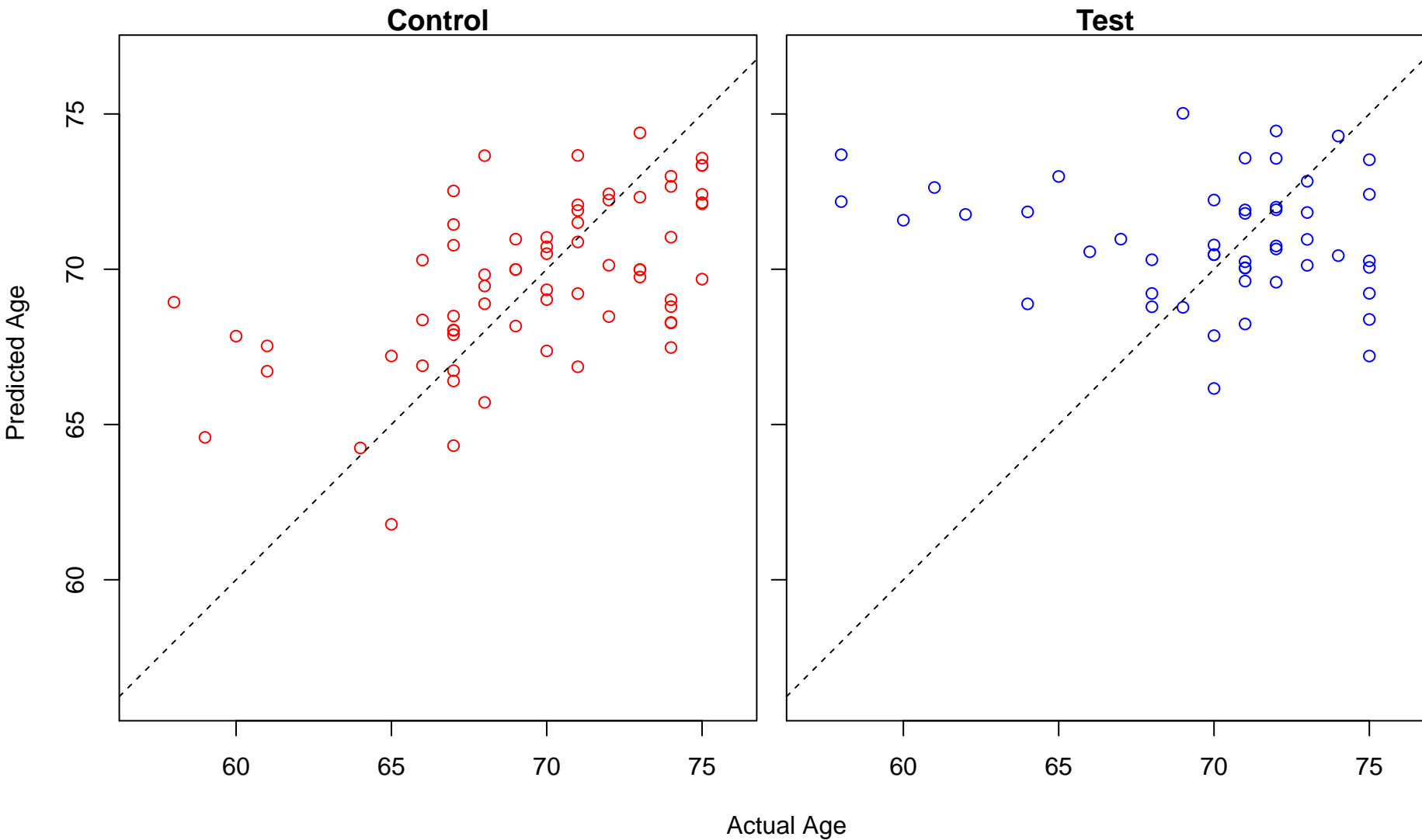
regulation of protein heterodimerization activity (Score: 0.923466)



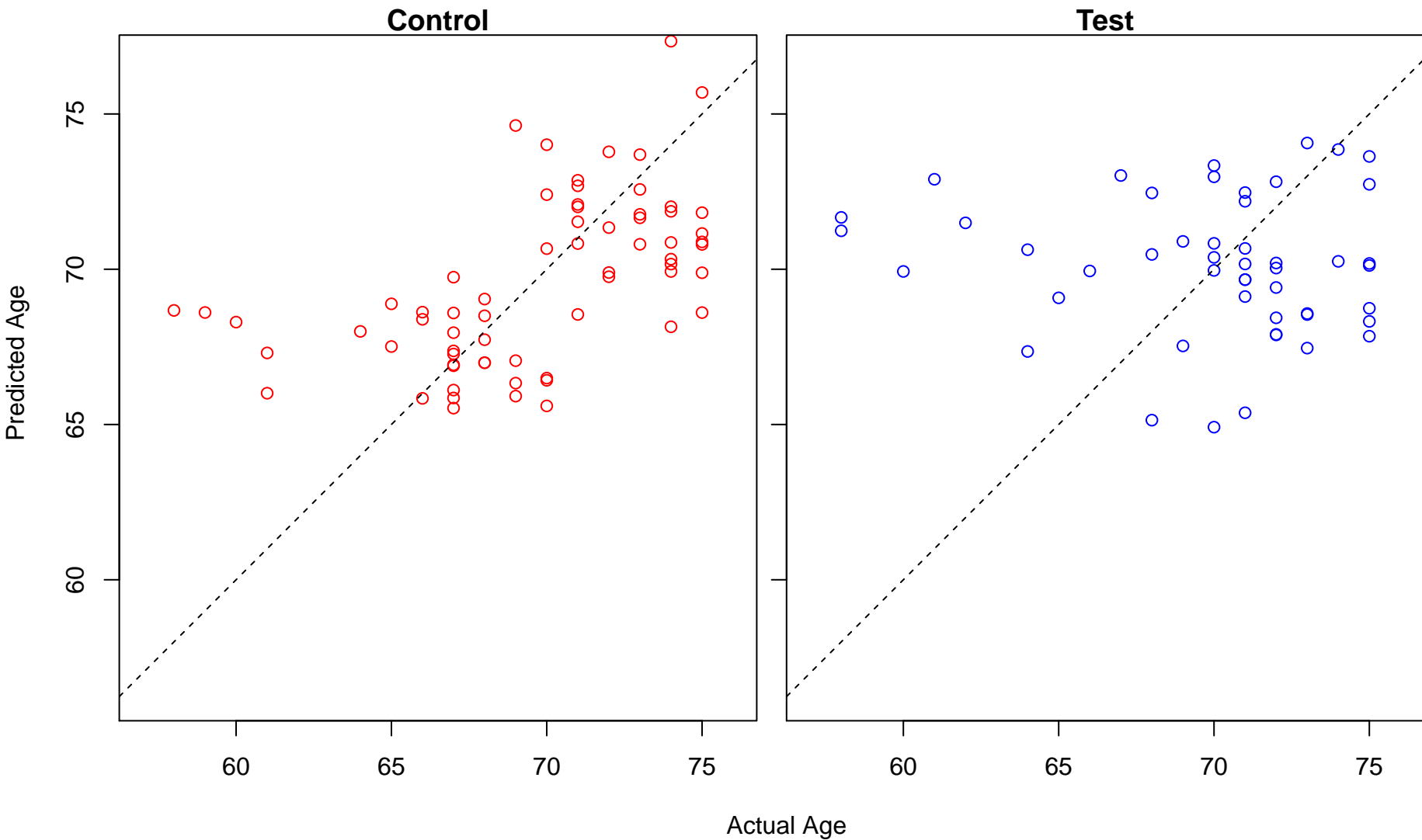
positive regulation of sequestering of calcium ion (Score: 0.923176)



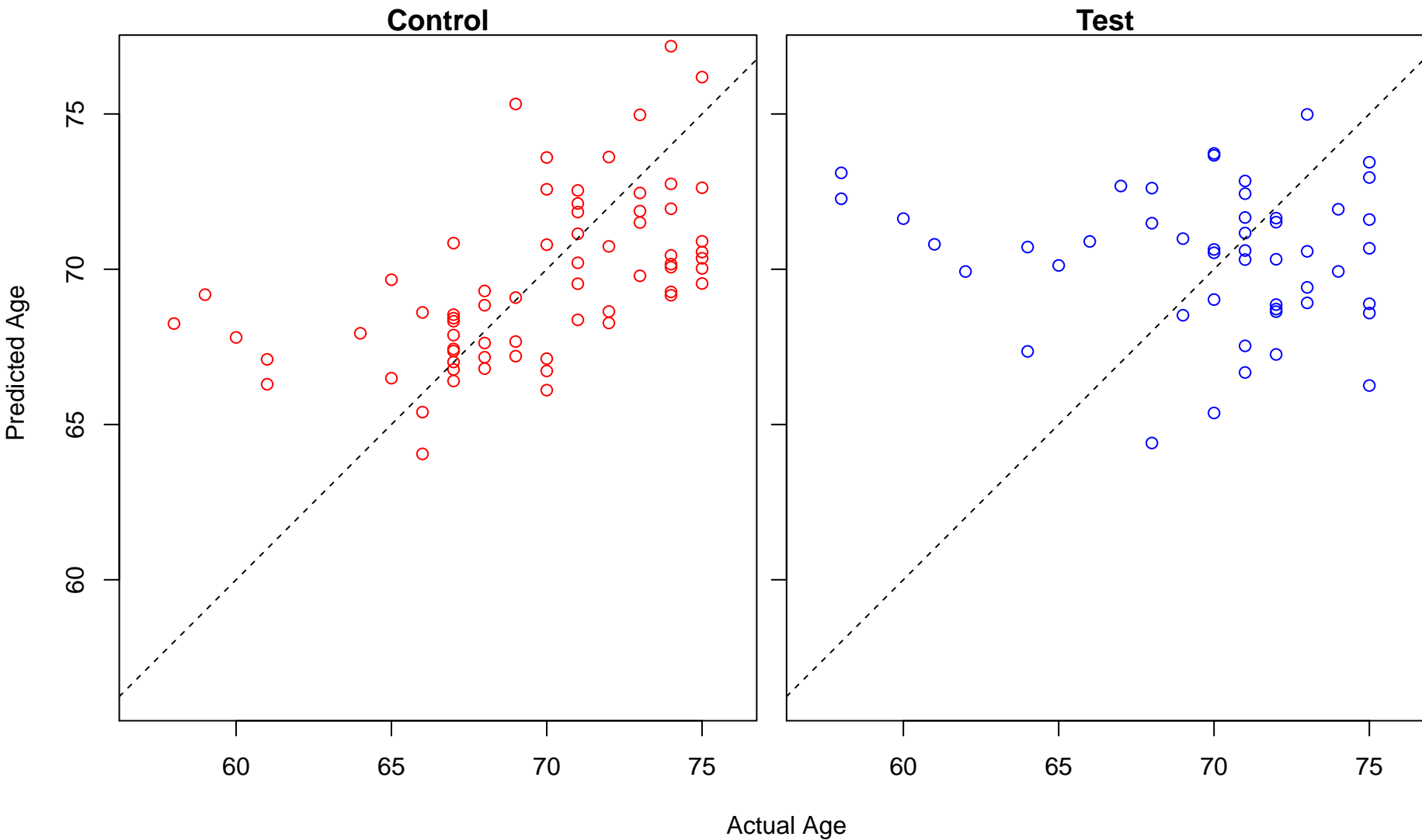
membrane to membrane docking (Score: 0.922469)



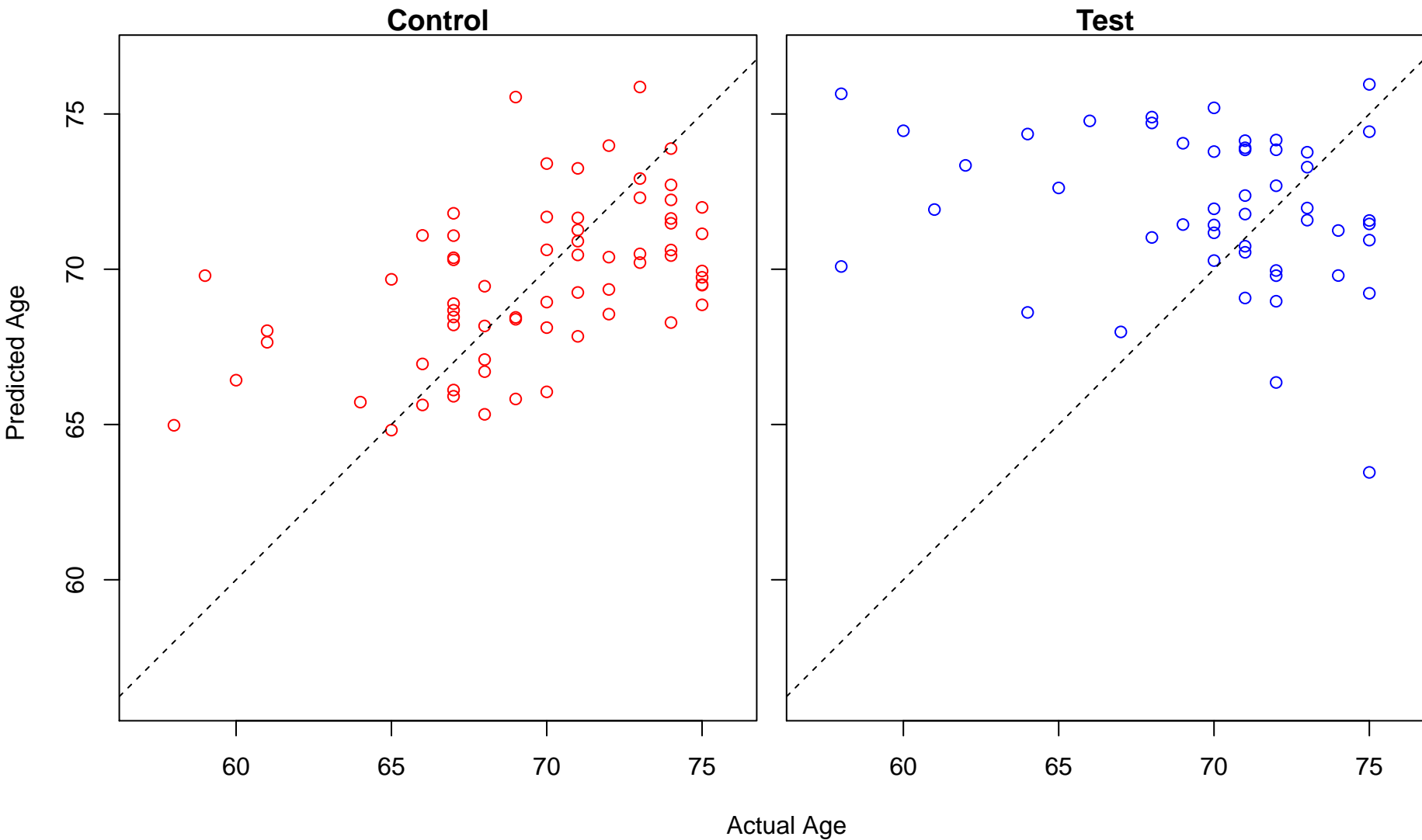
alcohol catabolic process (Score: 0.922439)



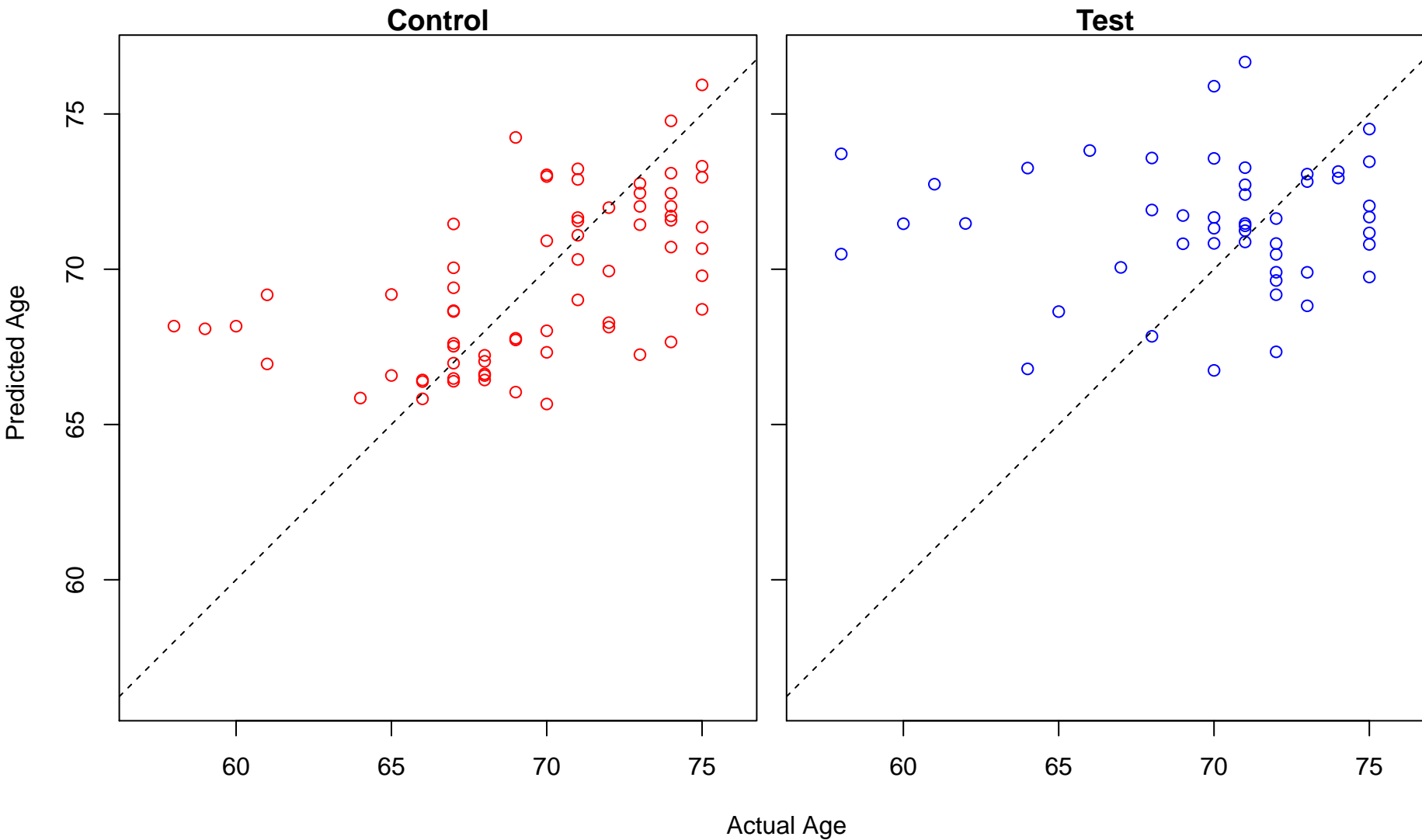
pallium development (Score: 0.922433)



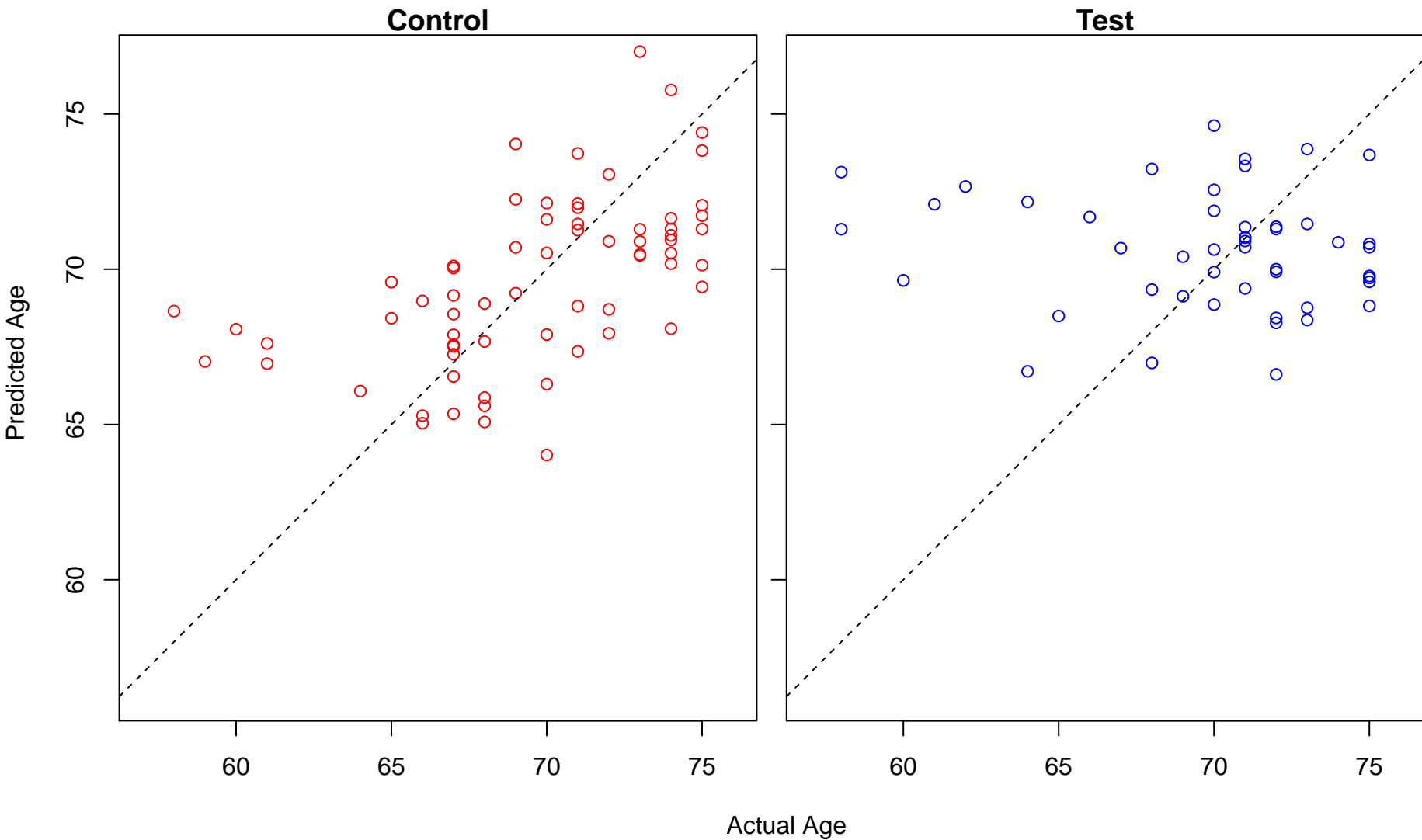
regulation of astrocyte differentiation (Score: 0.921484)



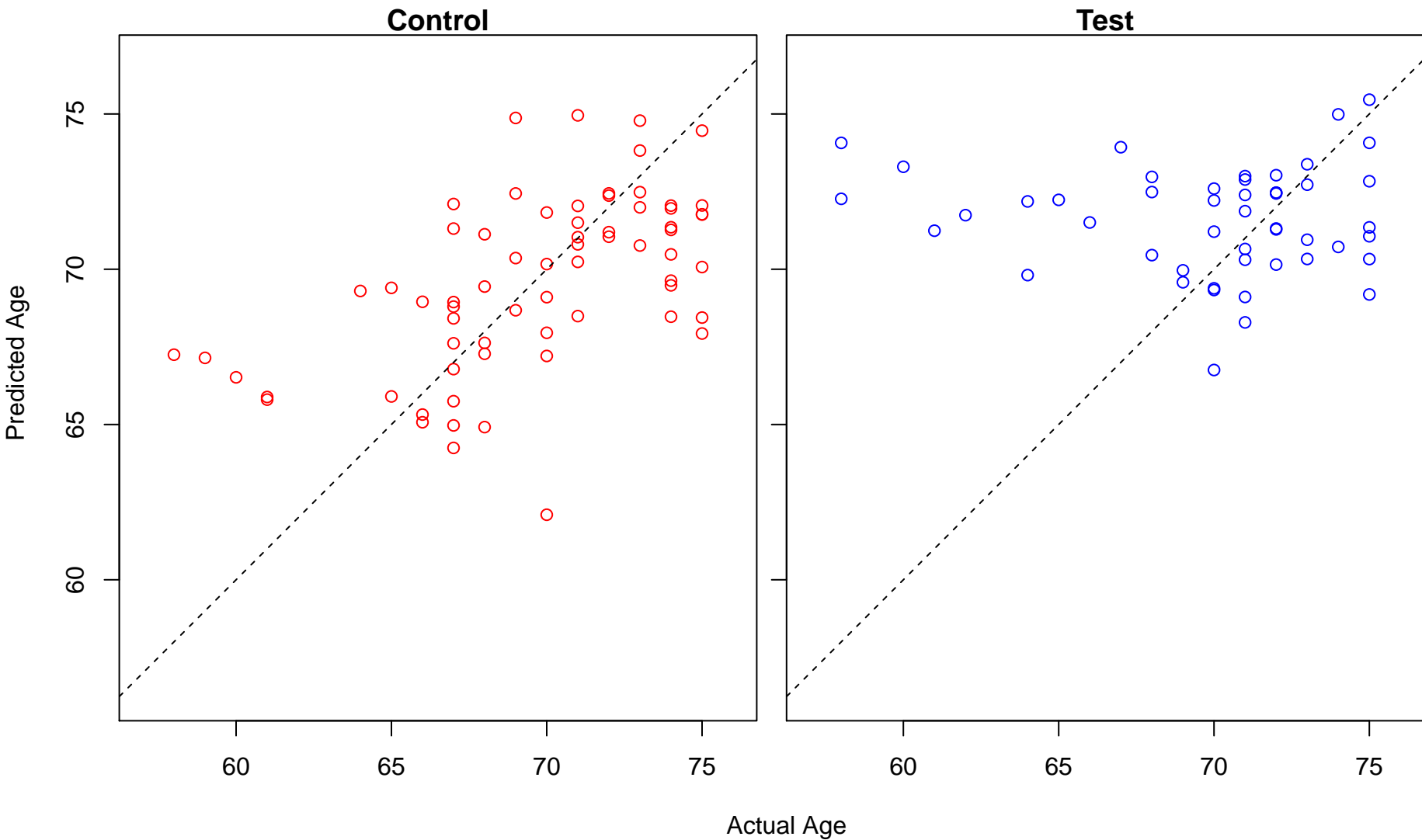
neurotransmitter transport (Score: 0.920935)



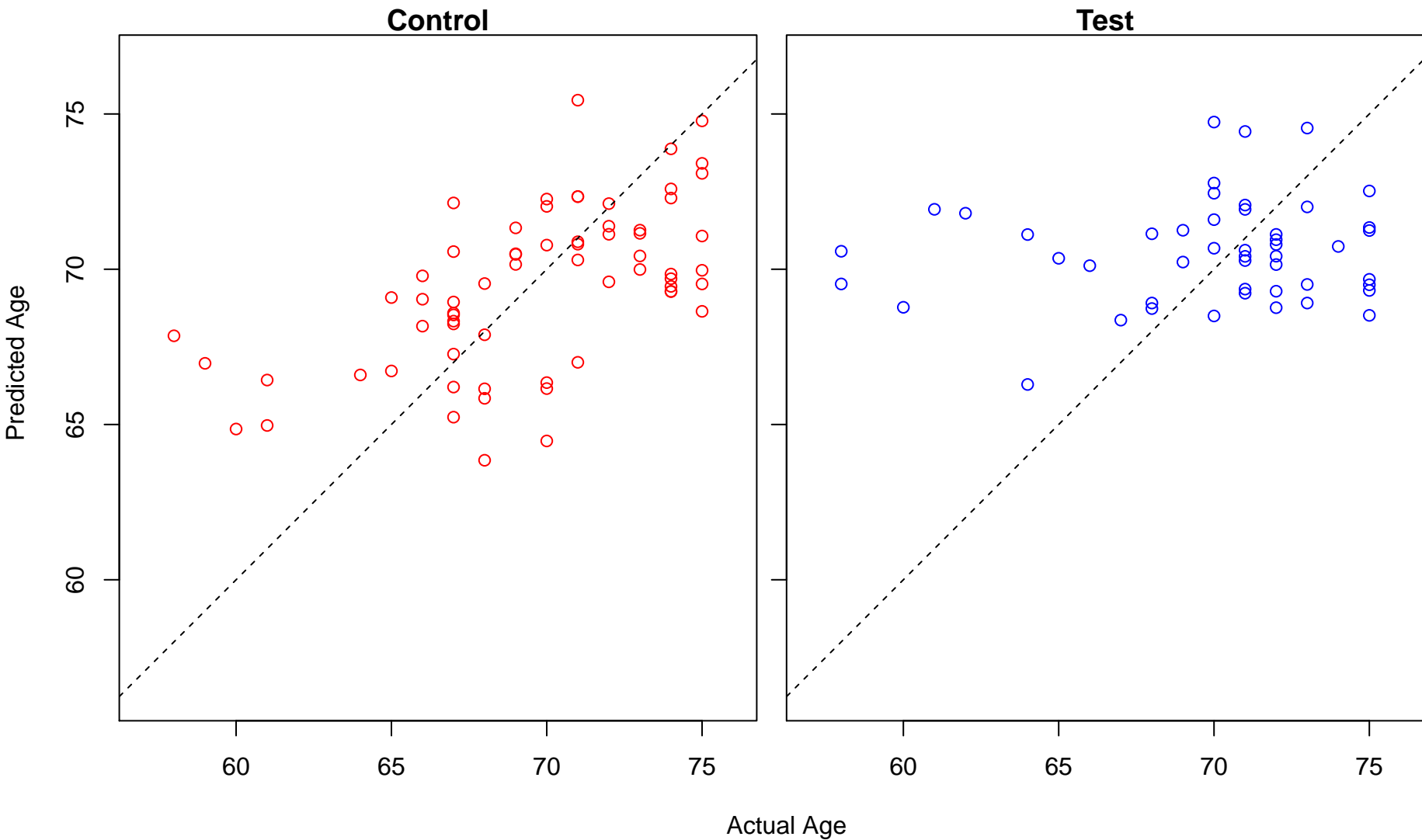
monosaccharide biosynthetic process (Score: 0.920783)



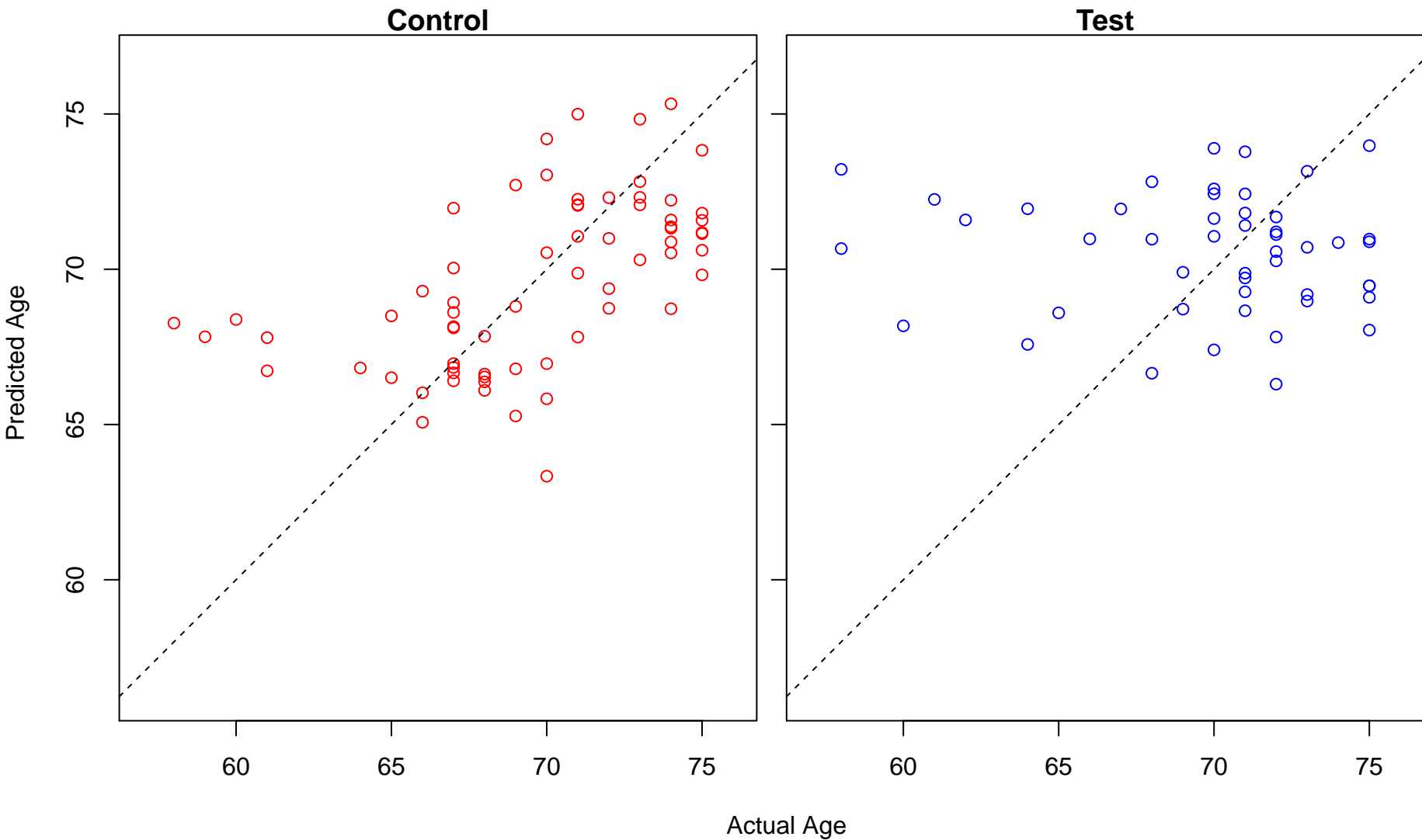
regulation of entry of bacterium into host cell (Score: 0.920612)



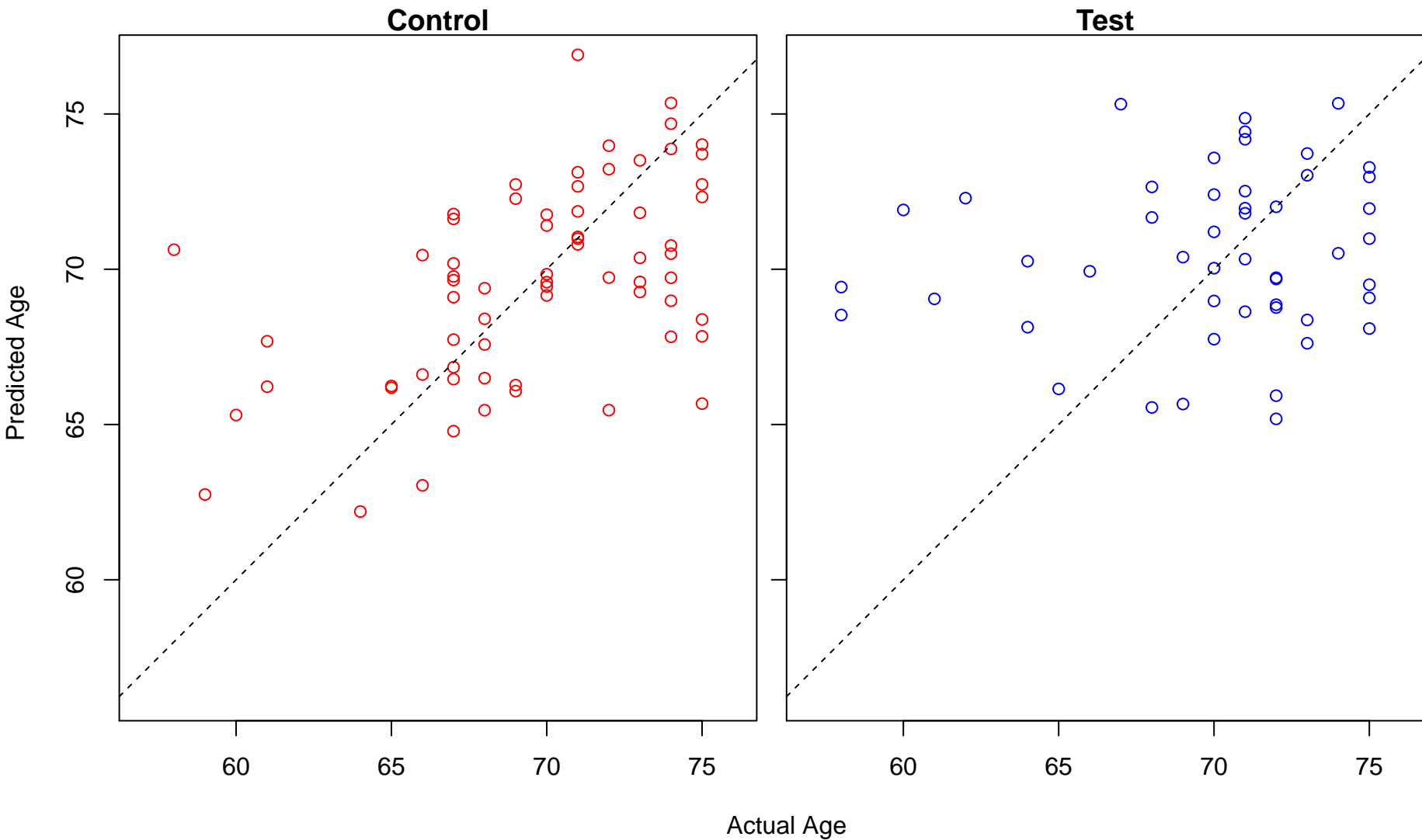
ribonucleoside diphosphate metabolic process (Score: 0.919963)



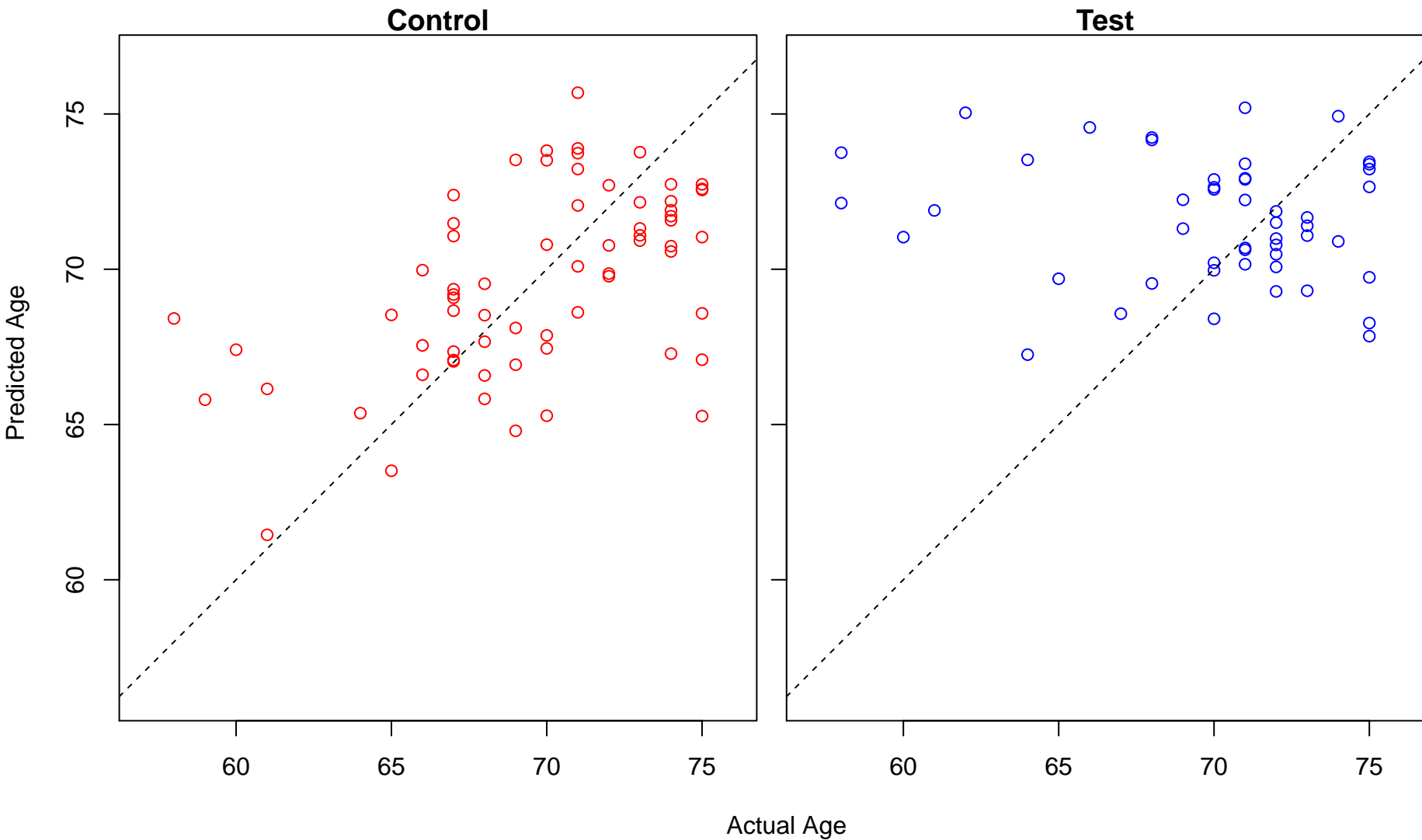
regulation of circadian rhythm (Score: 0.919669)



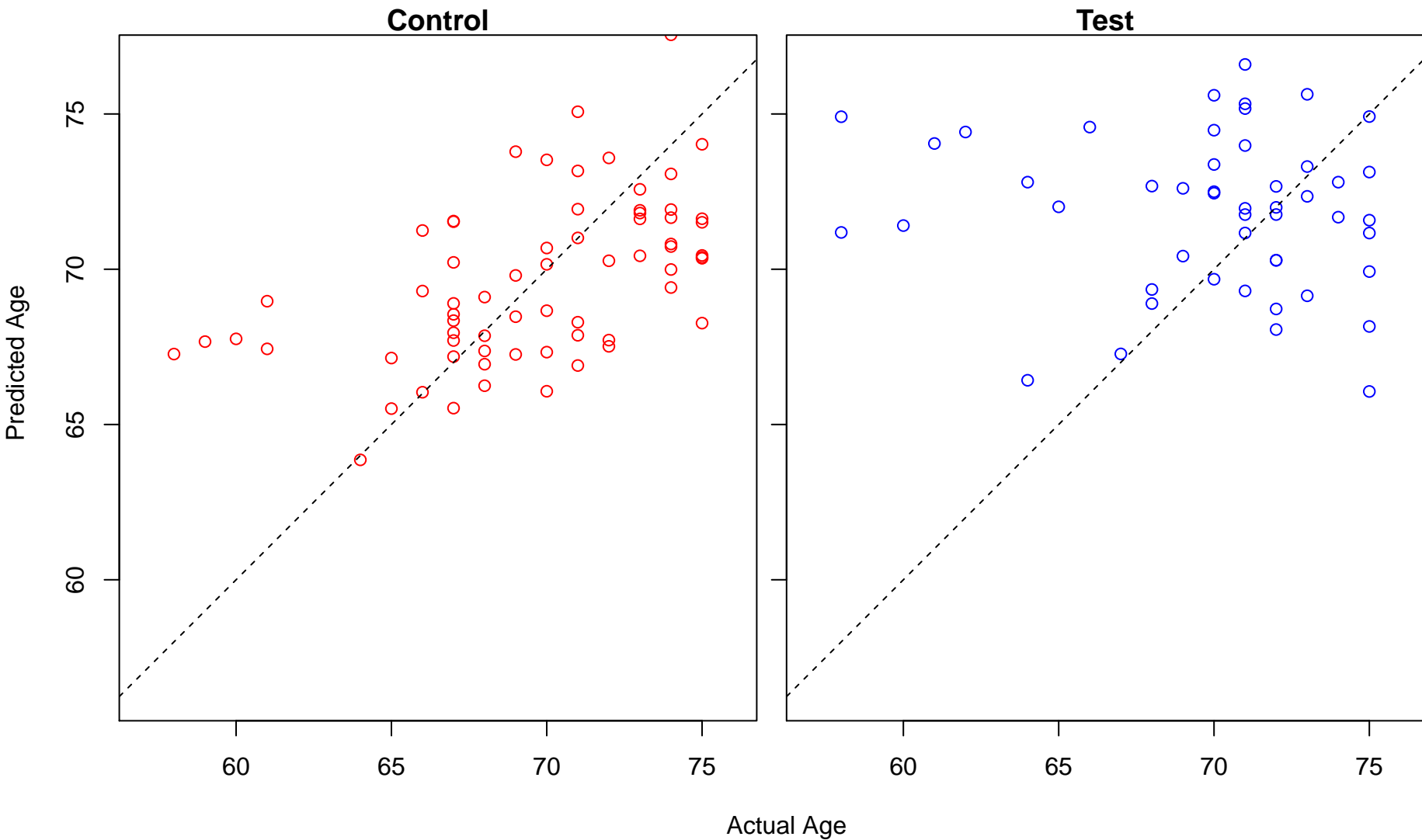
mesoderm morphogenesis (Score: 0.919633)



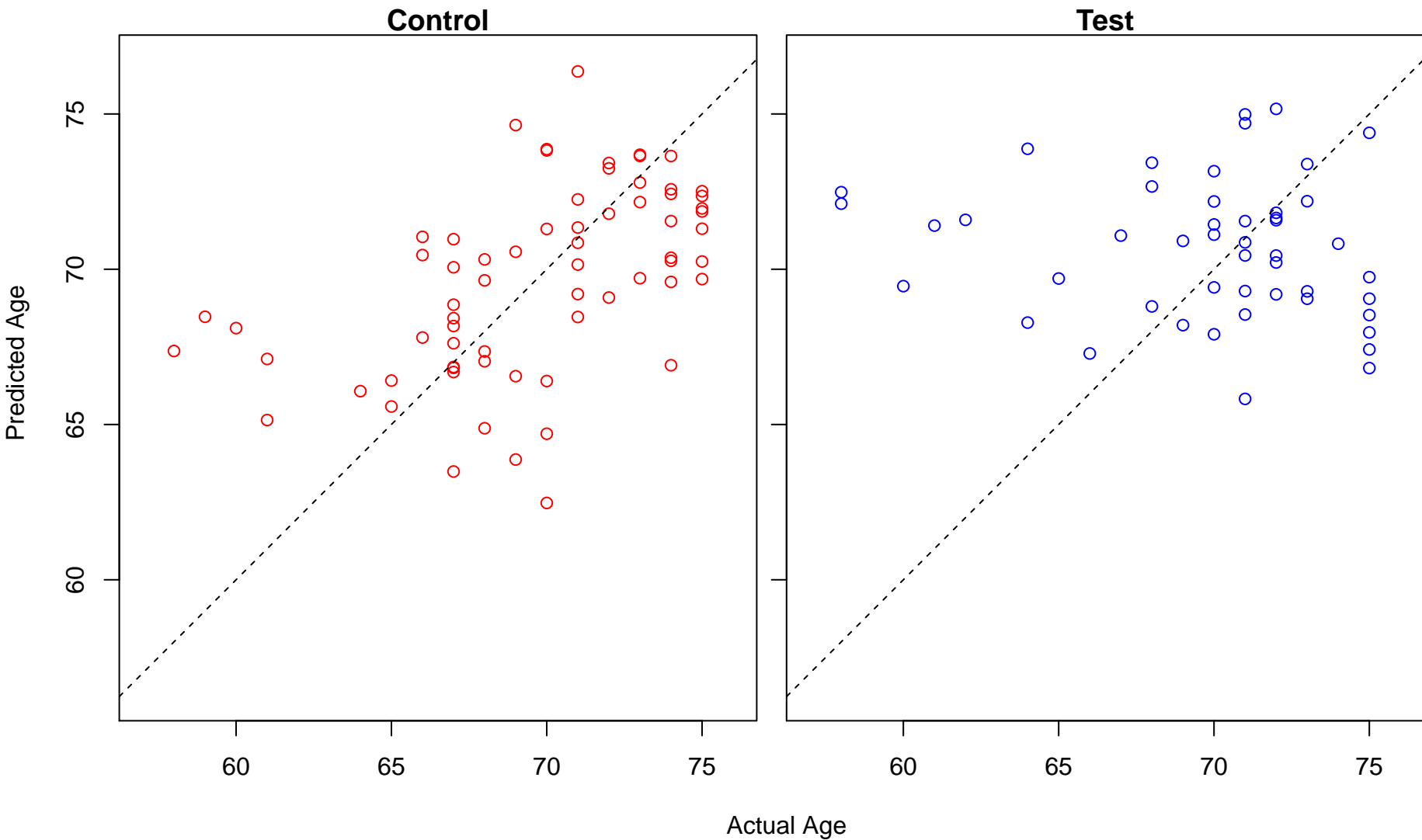
negative regulation of GTPase activity (Score: 0.919407)



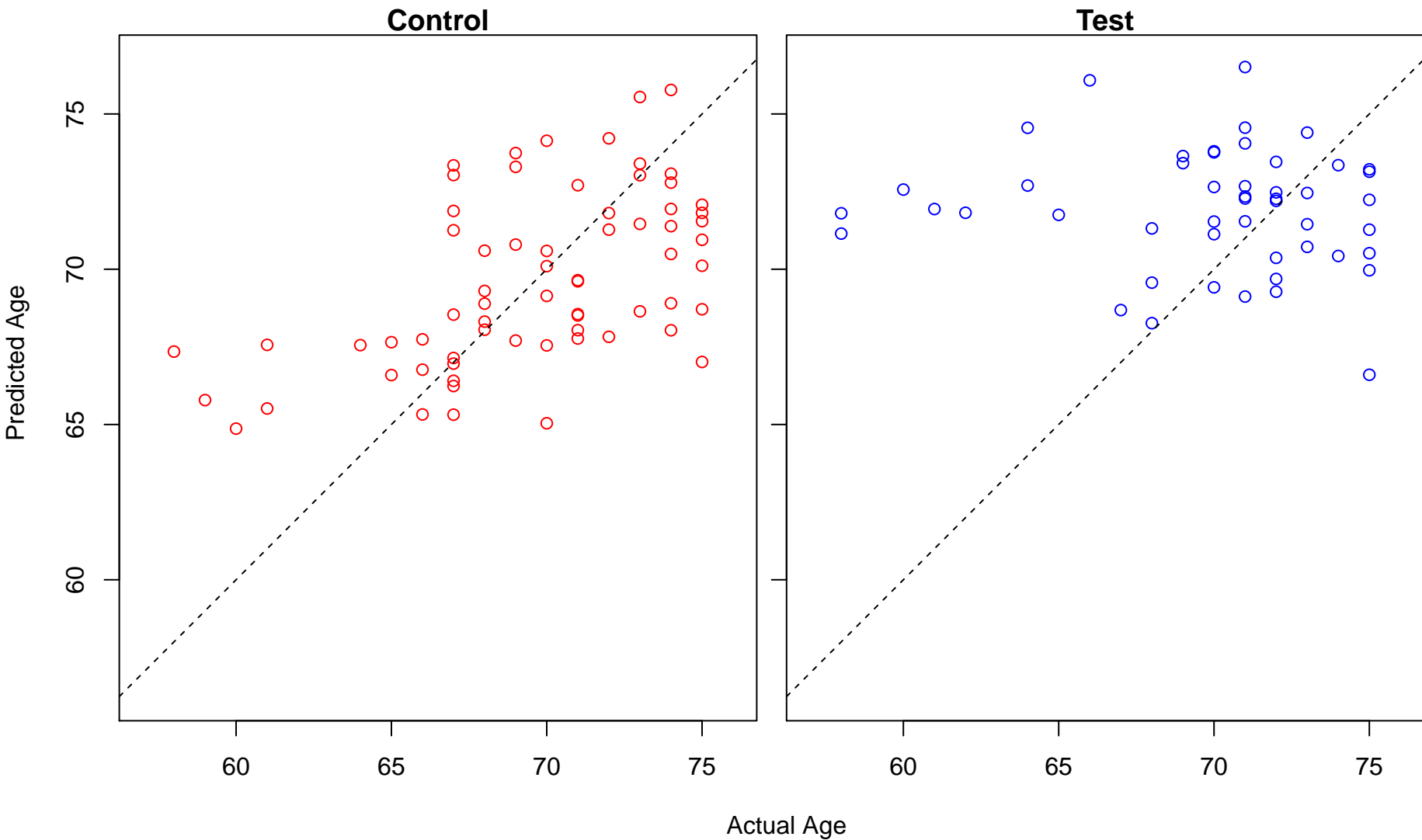
long-term memory (Score: 0.919400)



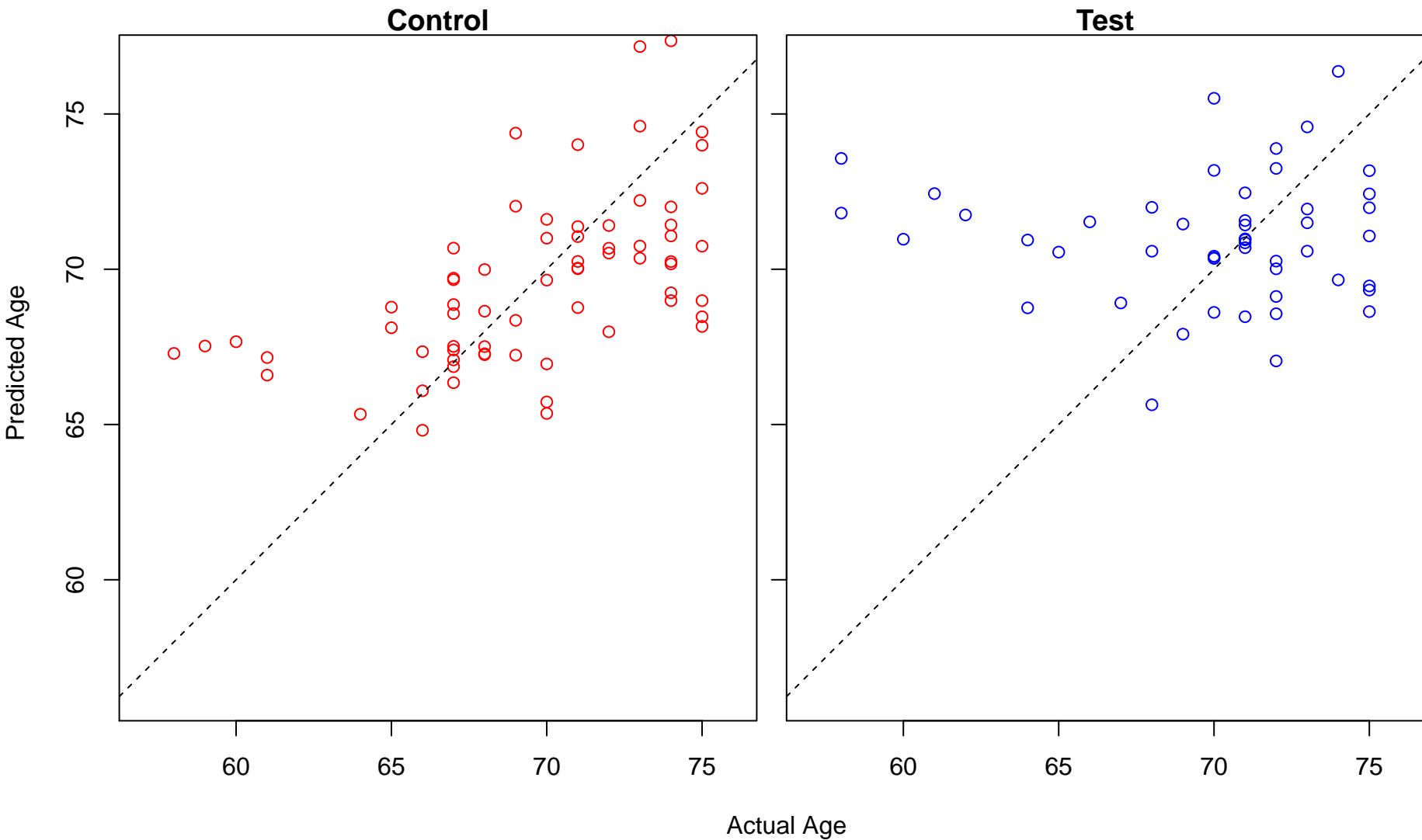
gene silencing by miRNA (Score: 0.919311)



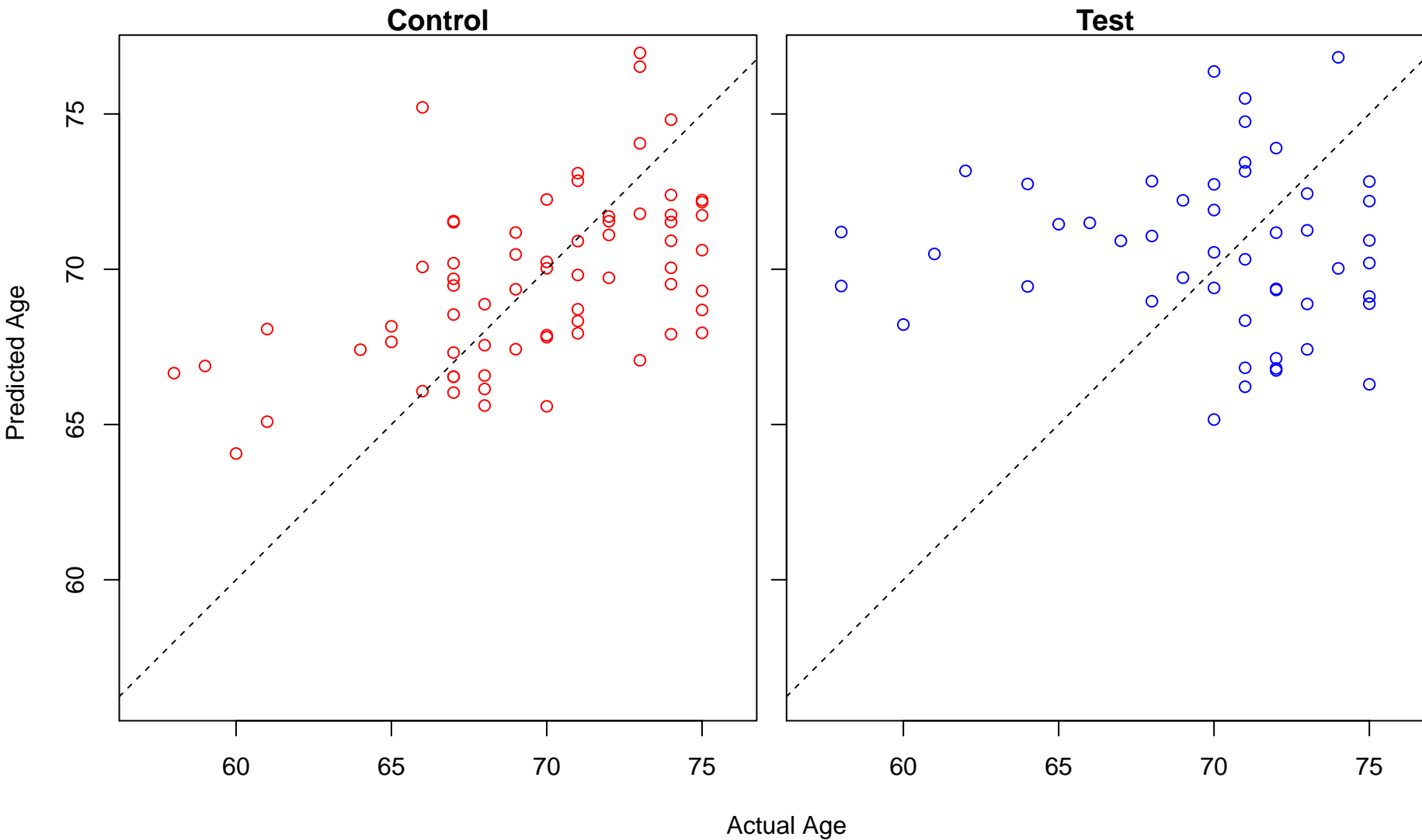
cardiolipin biosynthetic process (Score: 0.919115)



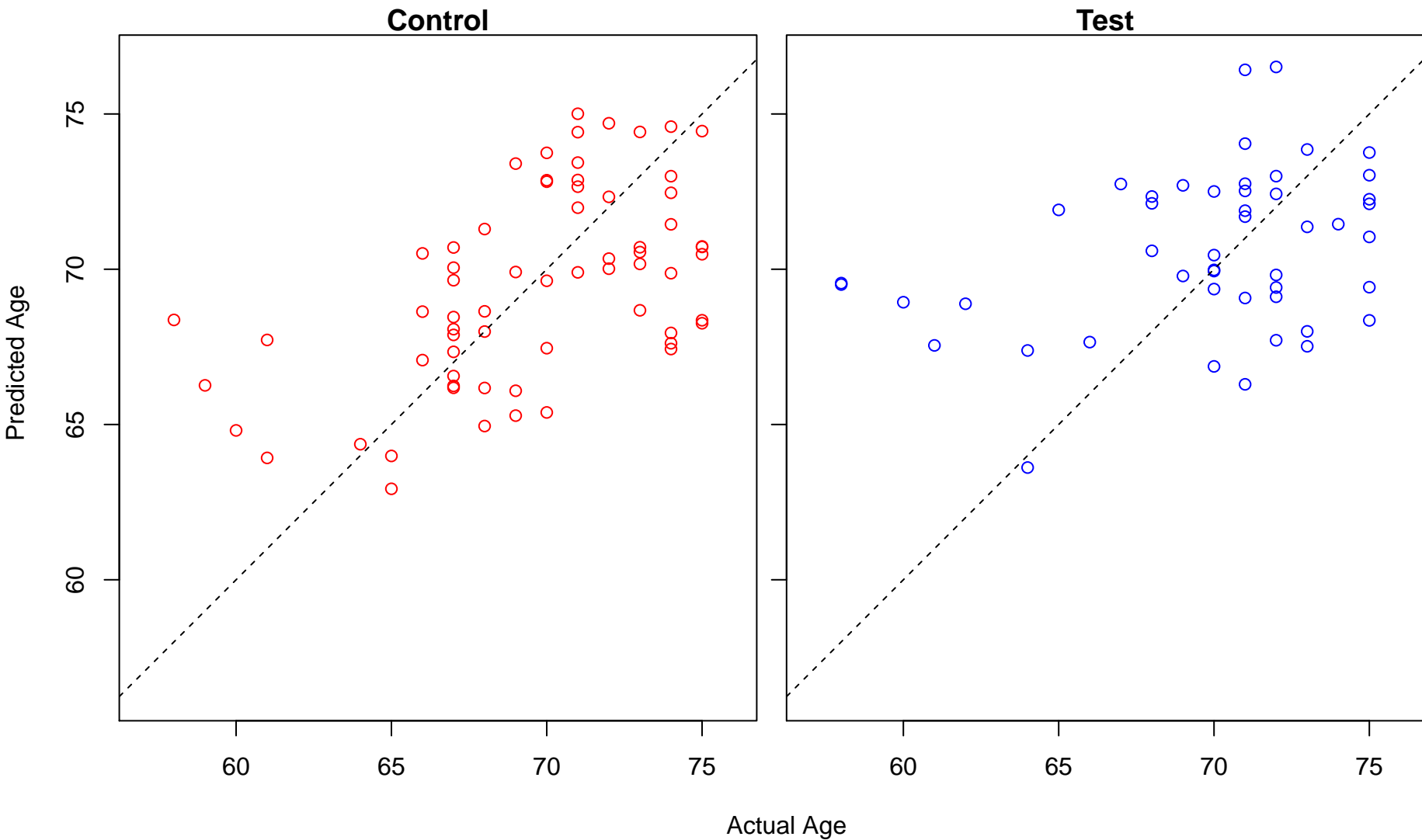
striated muscle contraction (Score: 0.918848)



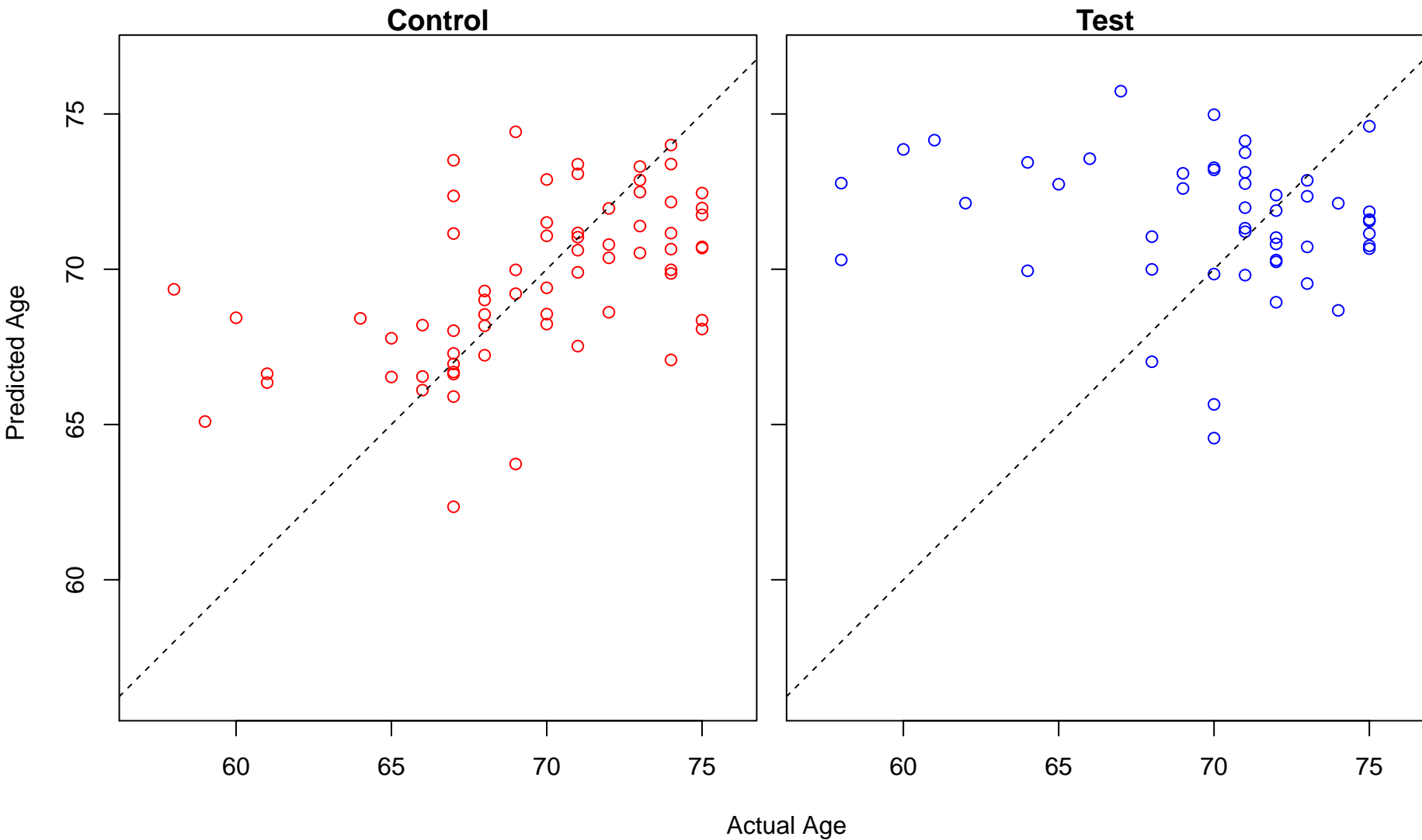
diacylglycerol metabolic process (Score: 0.918497)



response to gamma radiation (Score: 0.918497)

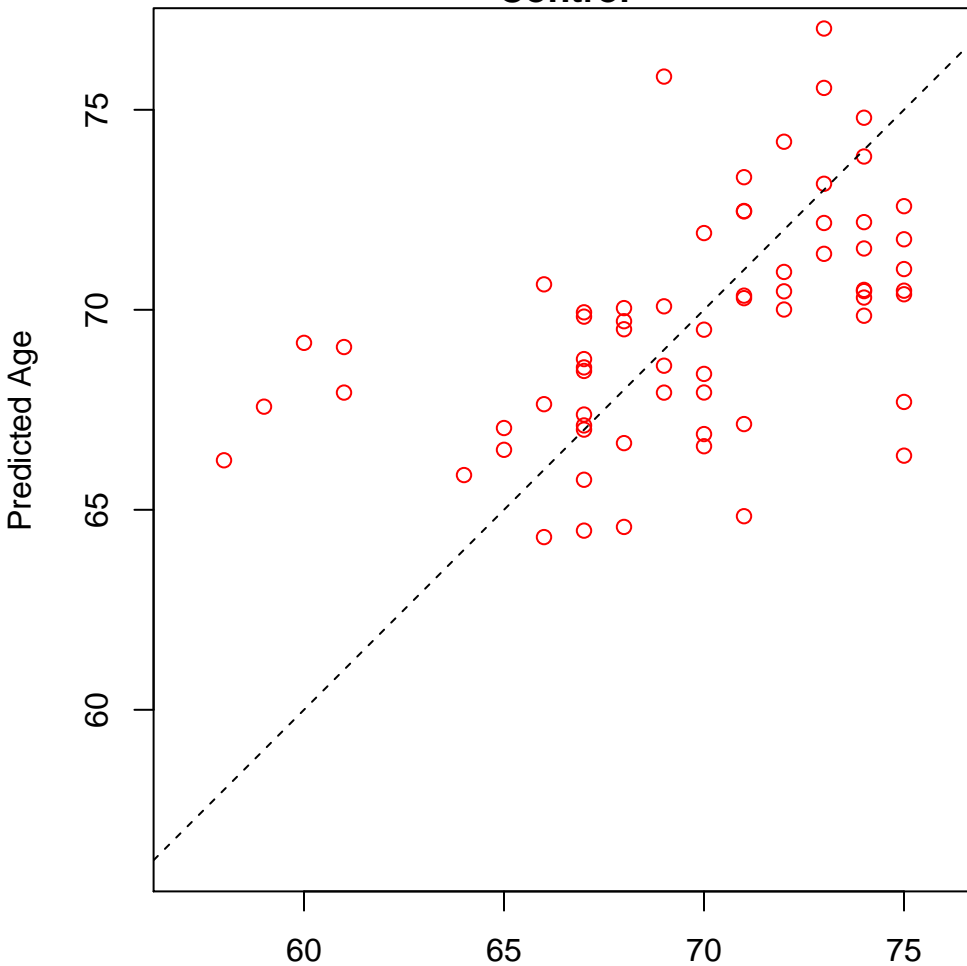


protein localization to chromatin (Score: 0.918130)

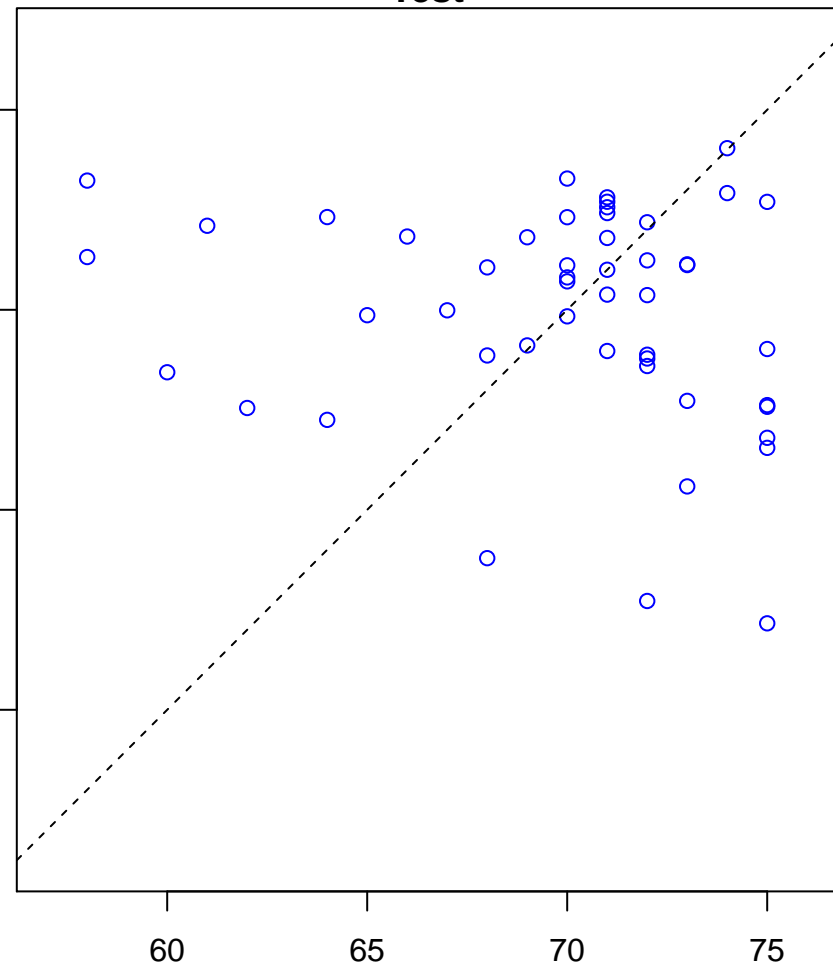


regulation of interleukin-4 production (Score: 0.917425)

Control

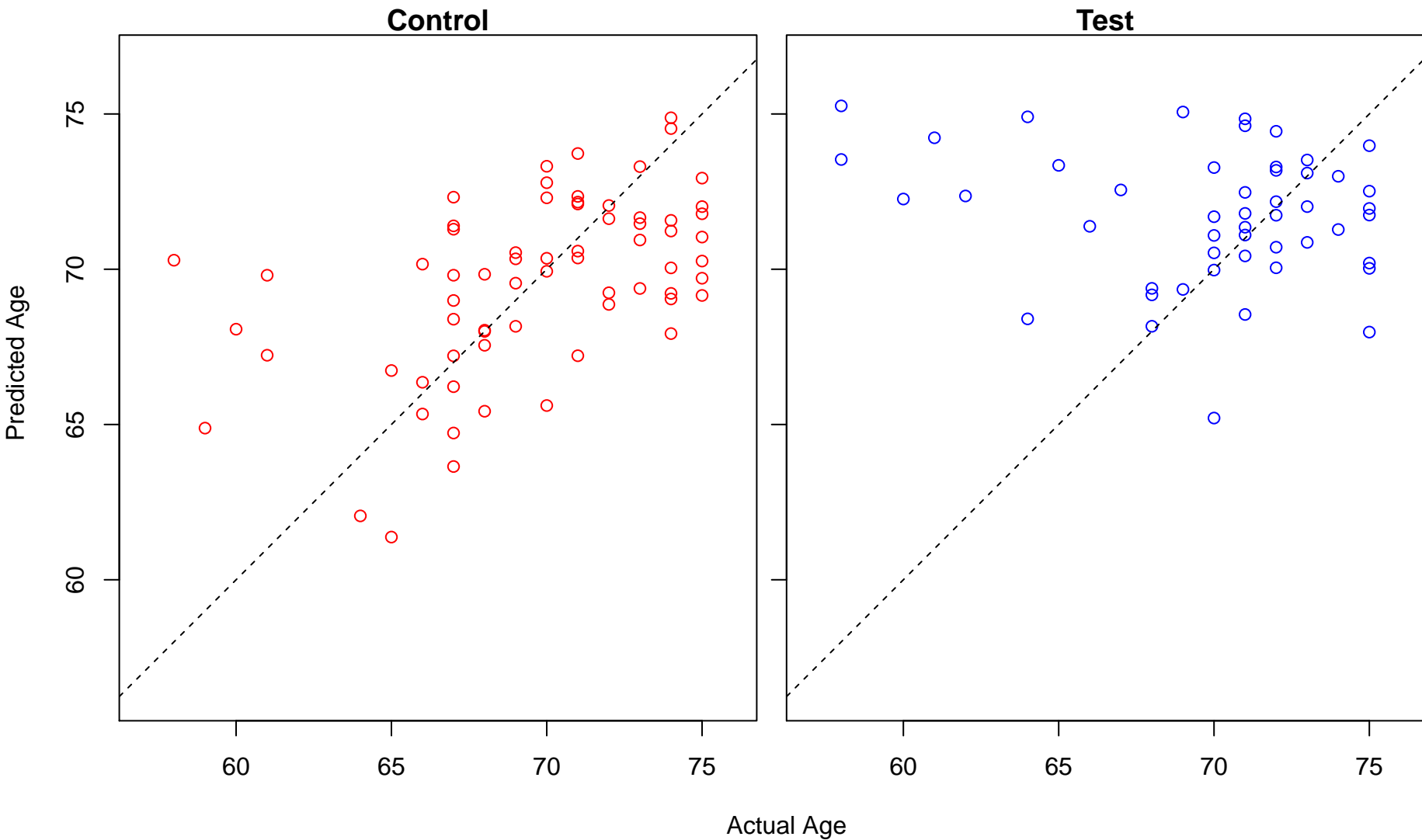


Test

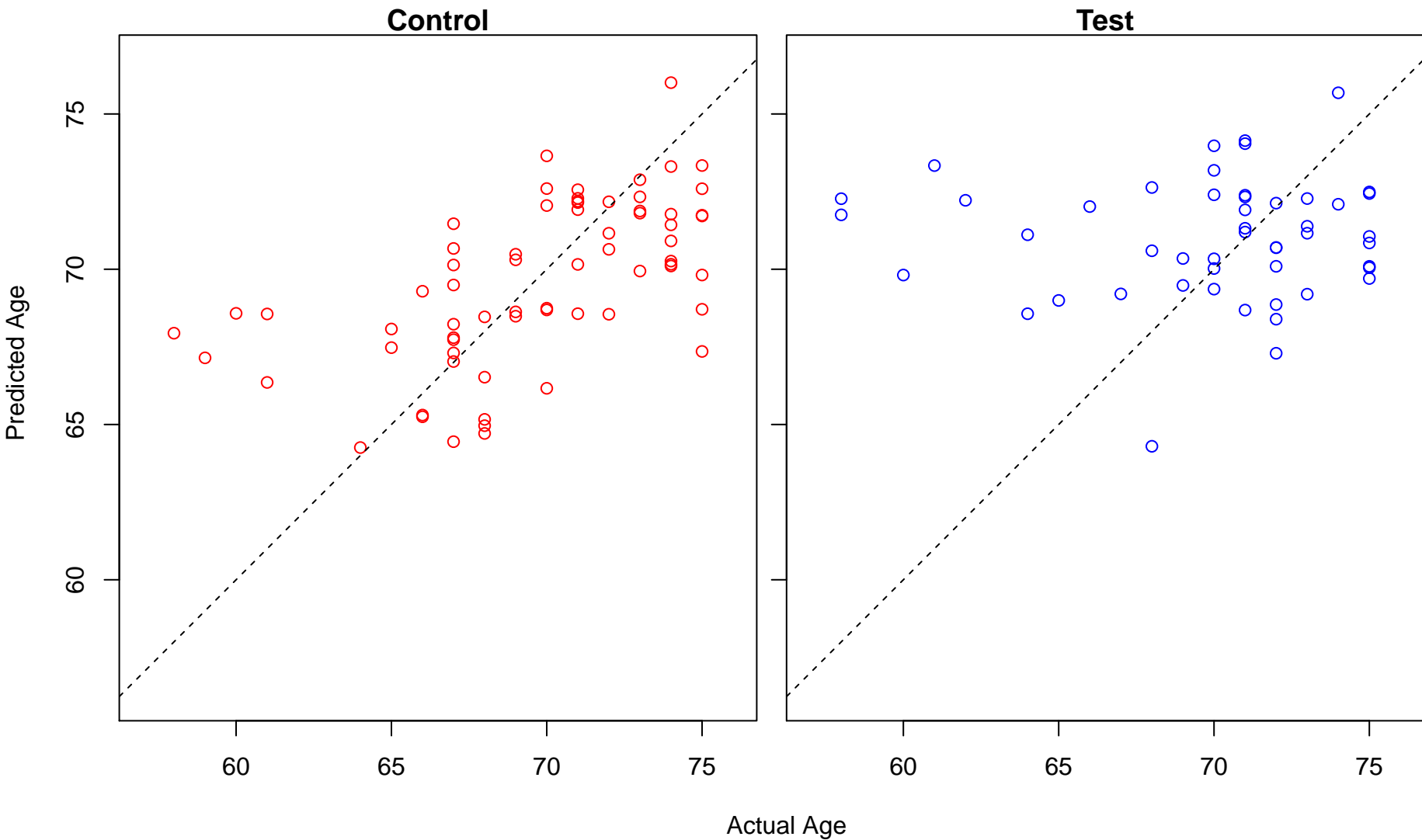


Actual Age

smooth muscle contraction (Score: 0.916945)

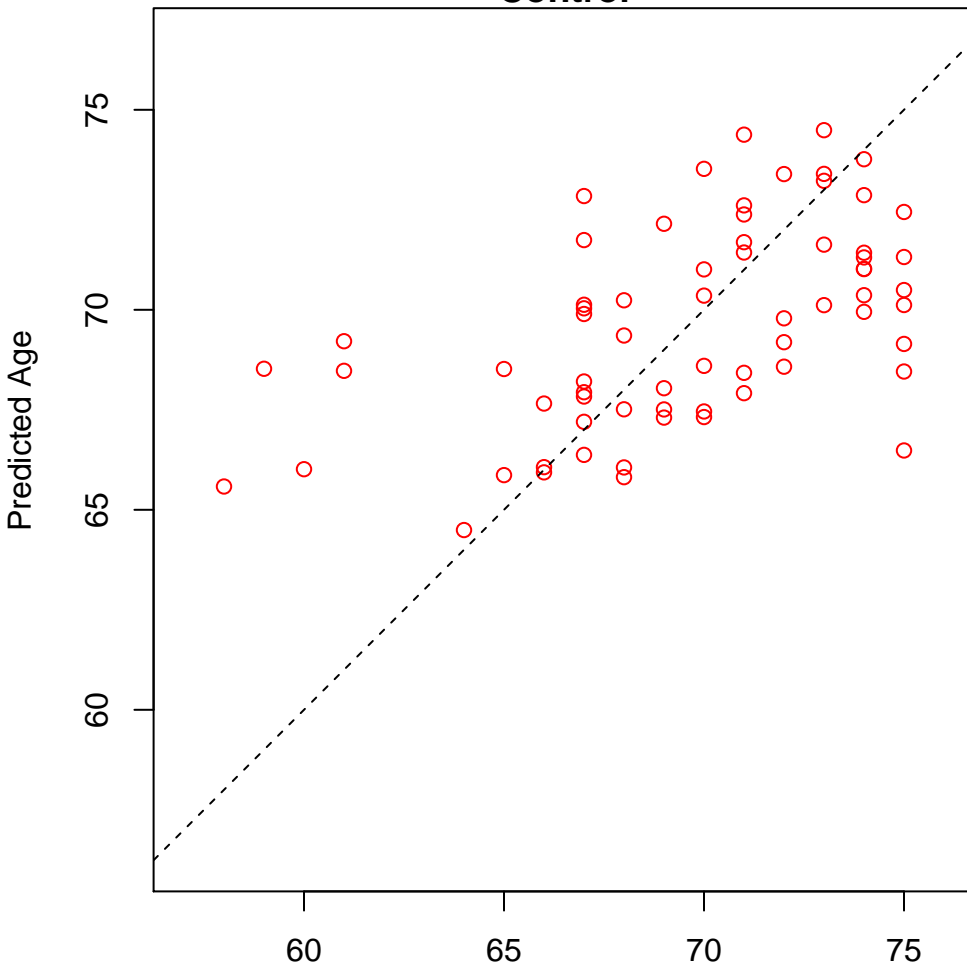


striated muscle cell differentiation (Score: 0.916506)

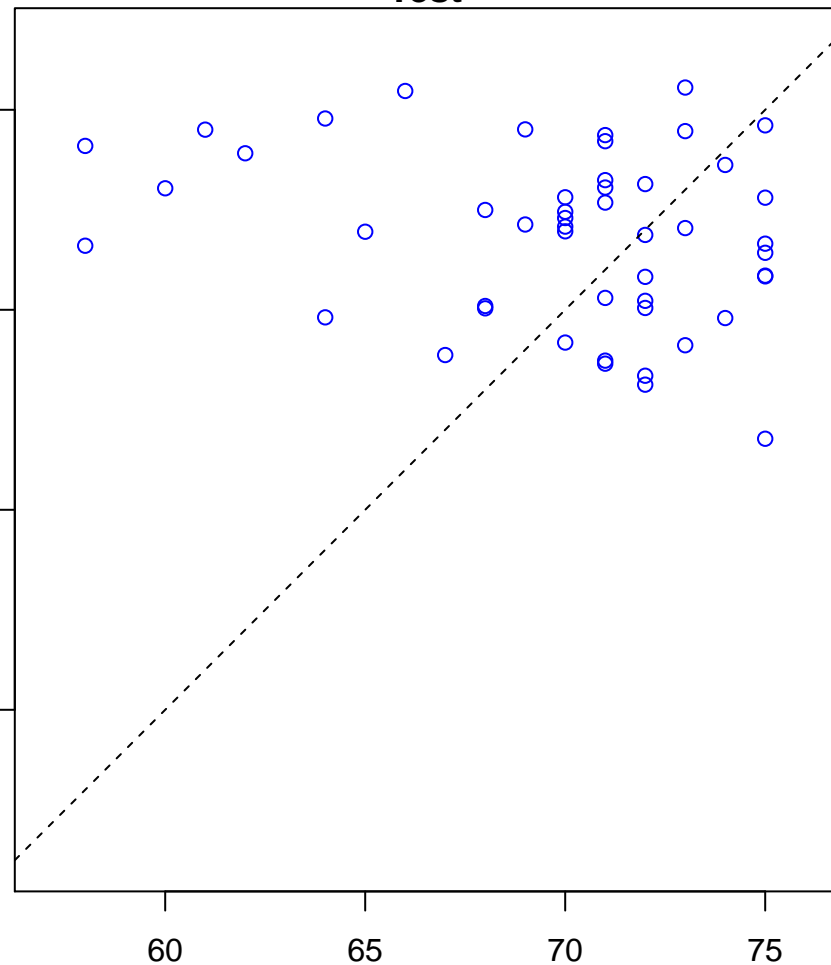


cardiac left ventricle morphogenesis (Score: 0.916395)

Control

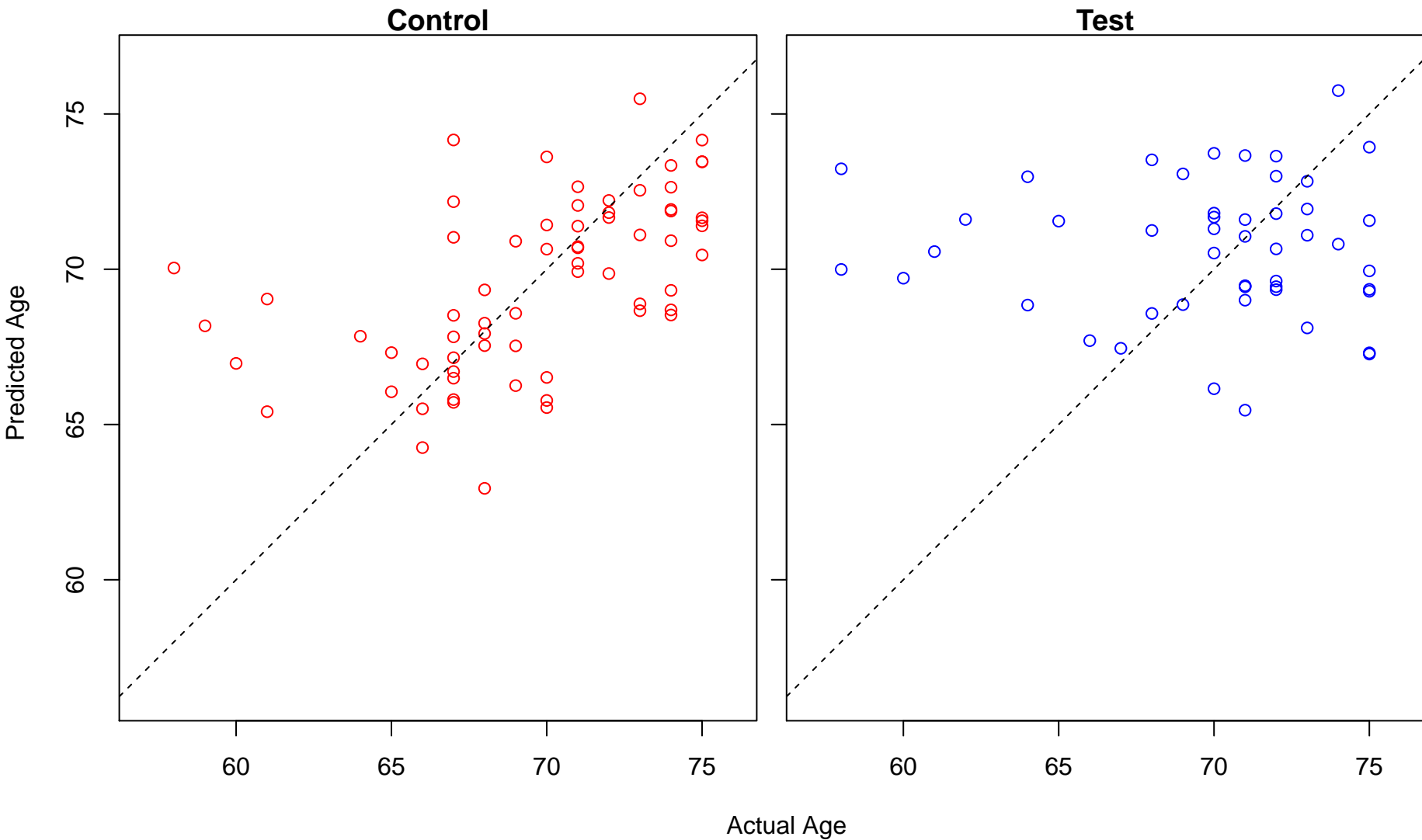


Test

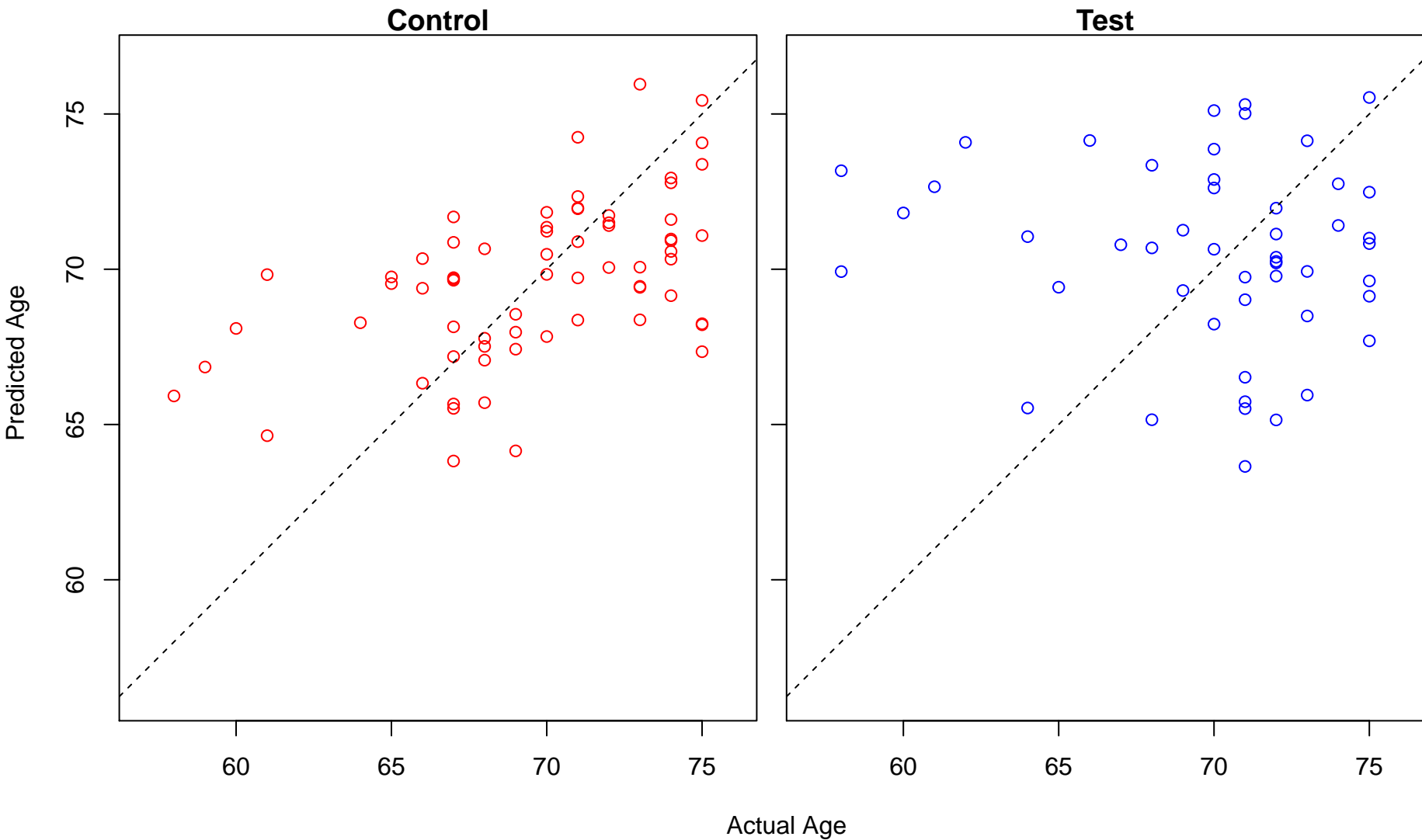


Actual Age

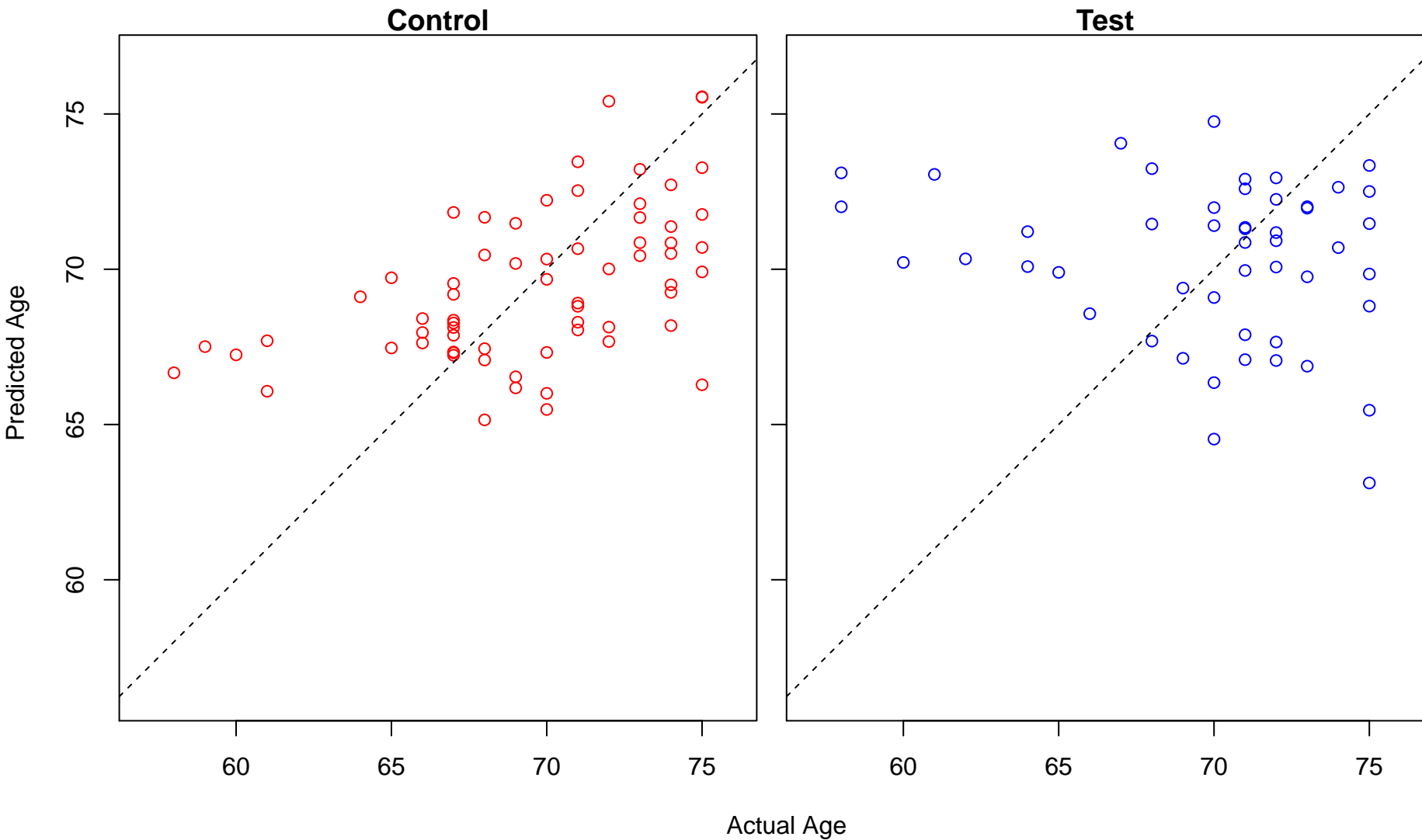
regulation of oxidative stress-induced neuron death (Score: 0.916018)



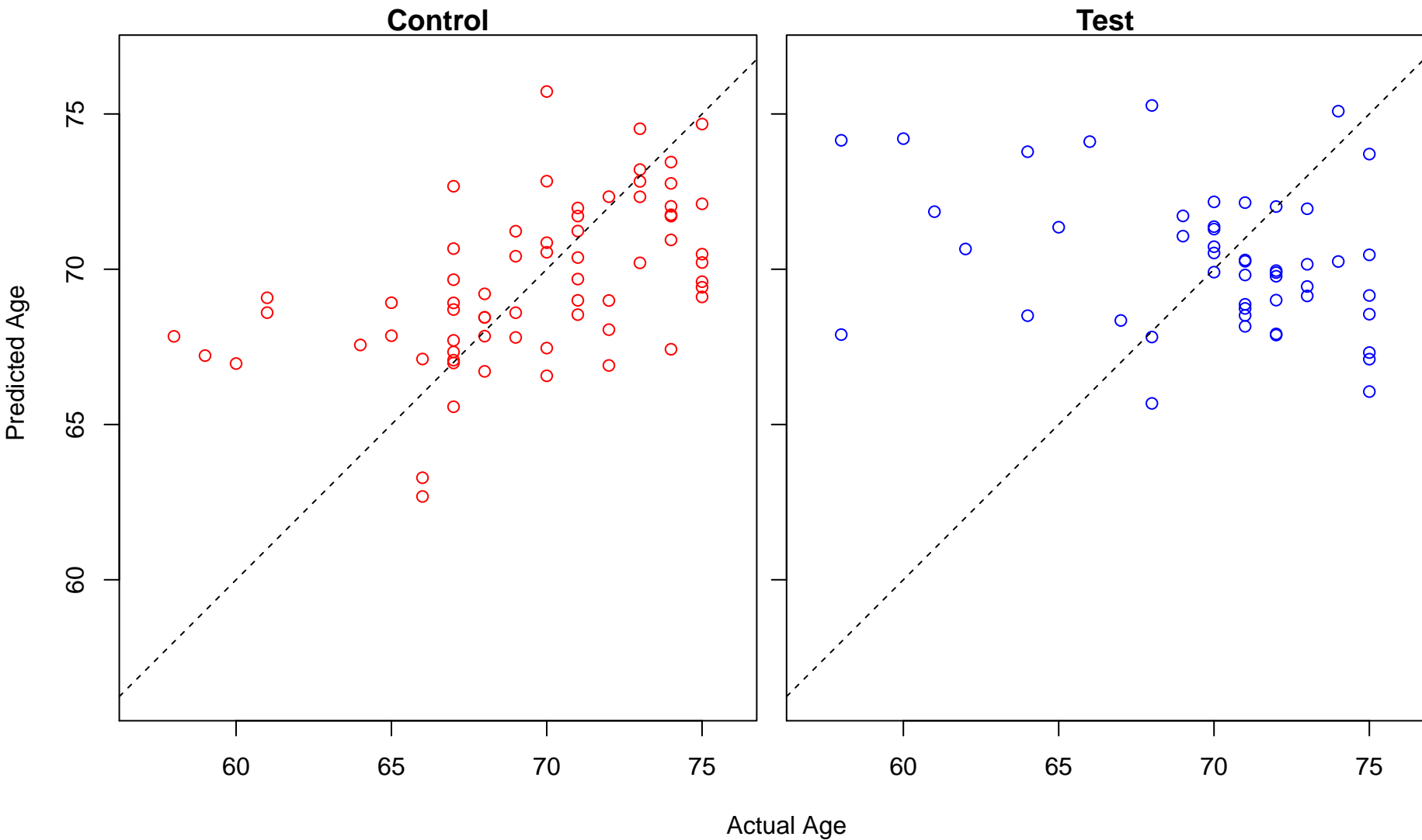
astrocyte development (Score: 0.915608)



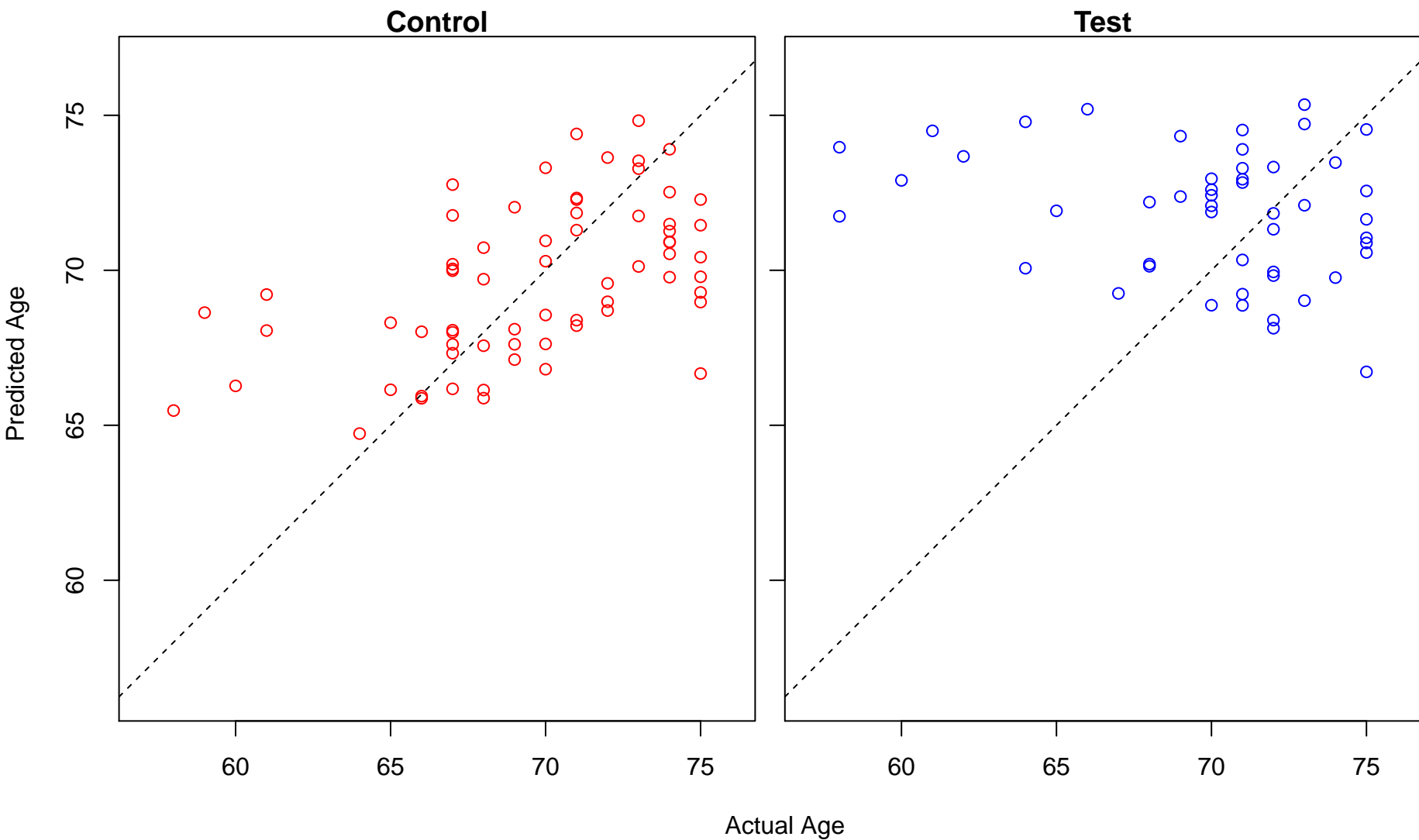
cellular response to nutrient (Score: 0.915570)



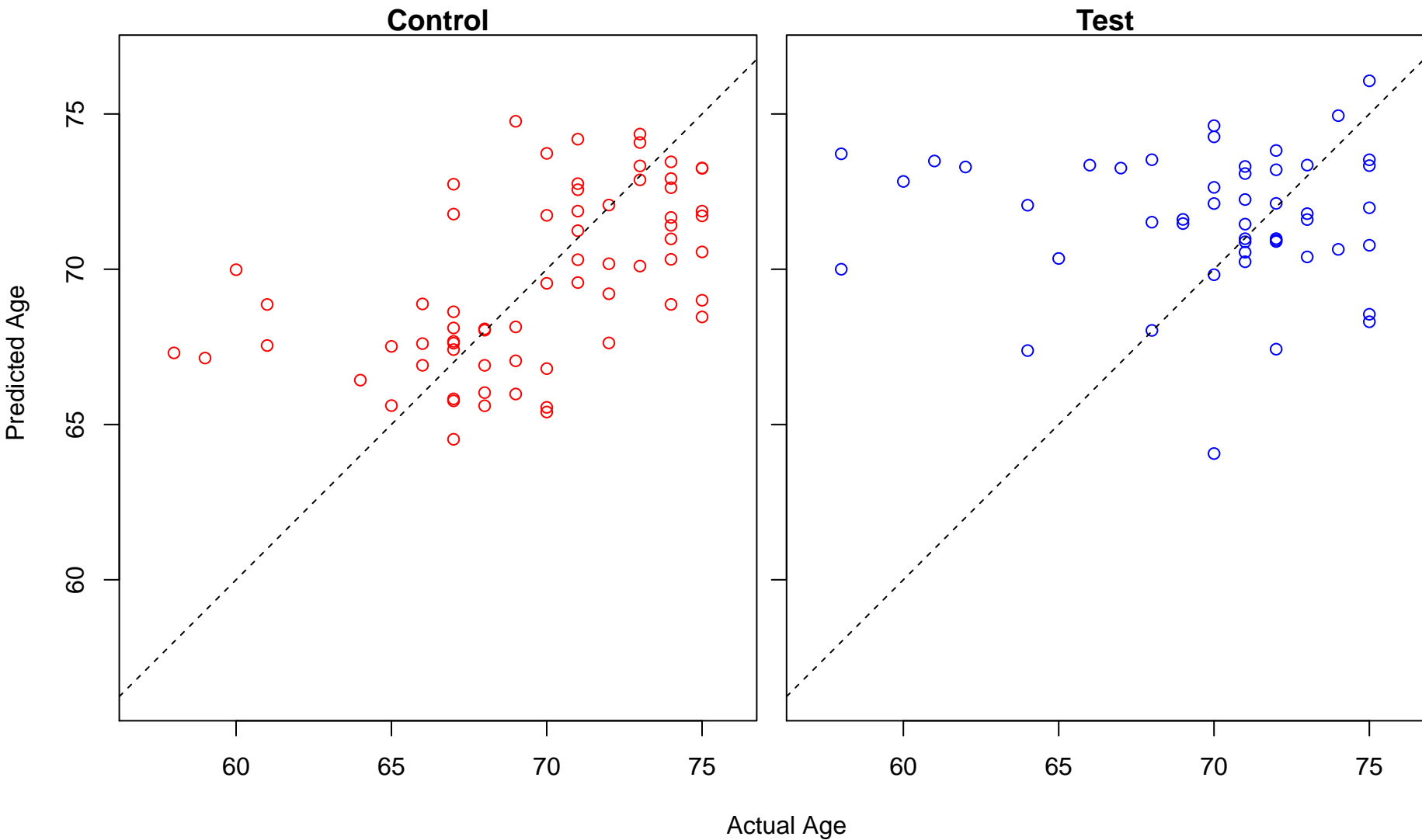
positive regulation of triglyceride biosynthetic process (Score: 0.915298)



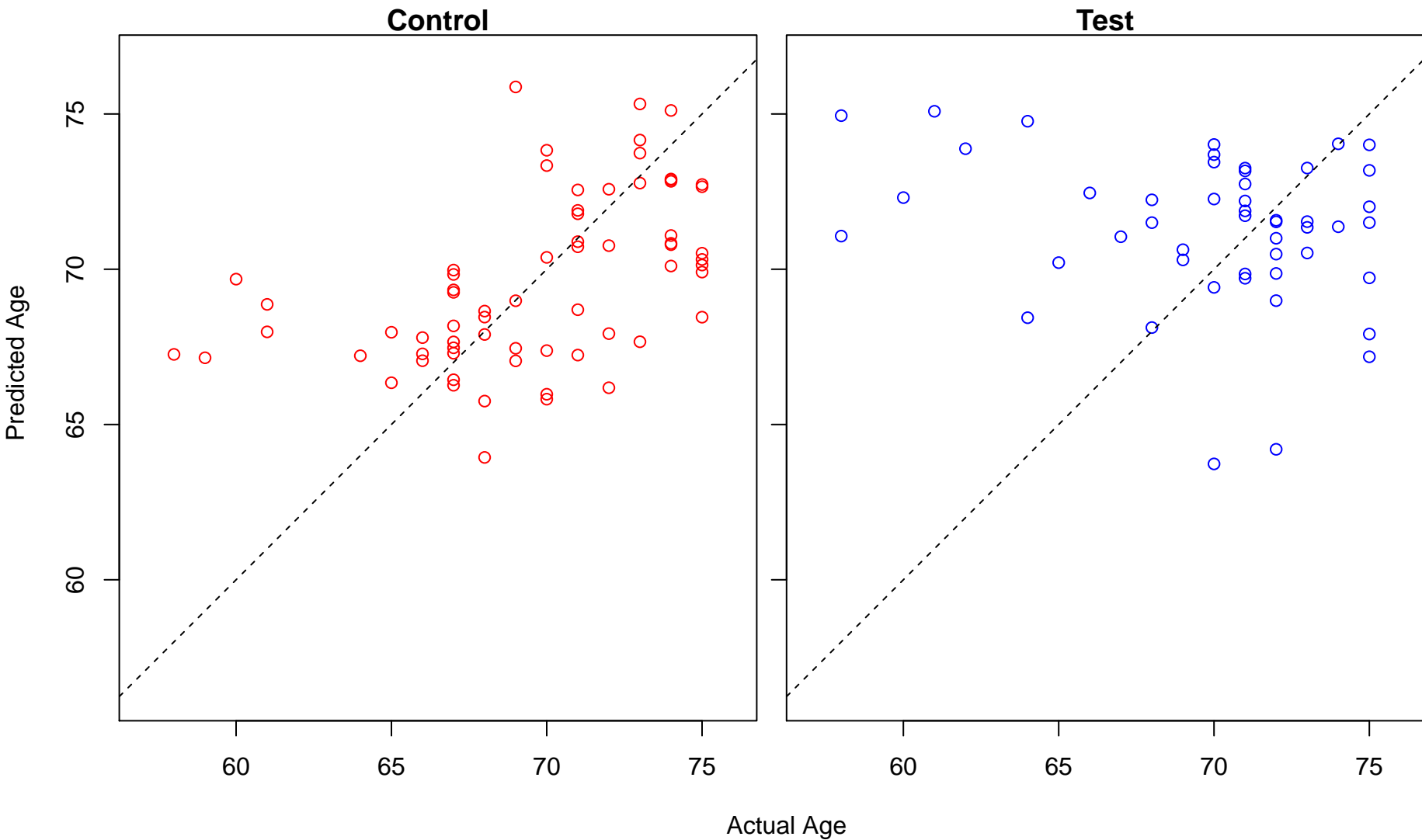
epithelial to mesenchymal transition involved in endocardial cushion formation (Score: 0.915156)



regulation of reactive oxygen species biosynthetic process (Score: 0.914852)

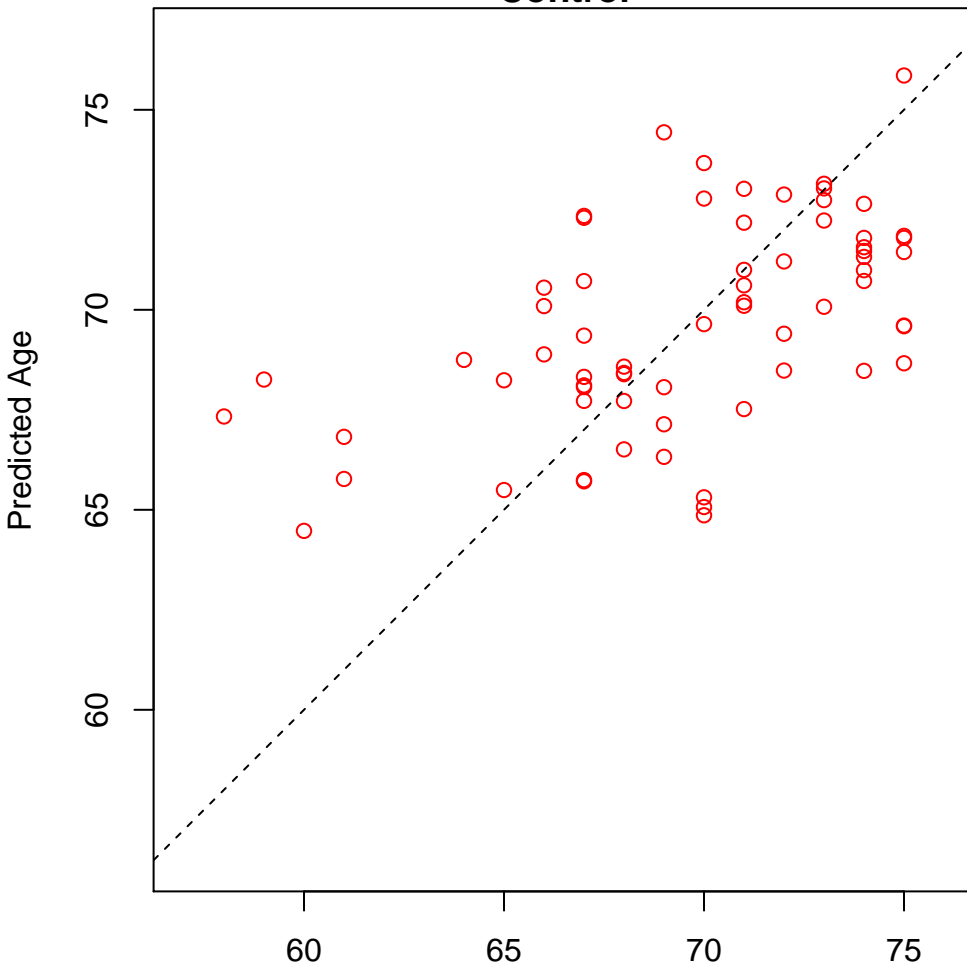


negative regulation of transmembrane transport (Score: 0.914833)

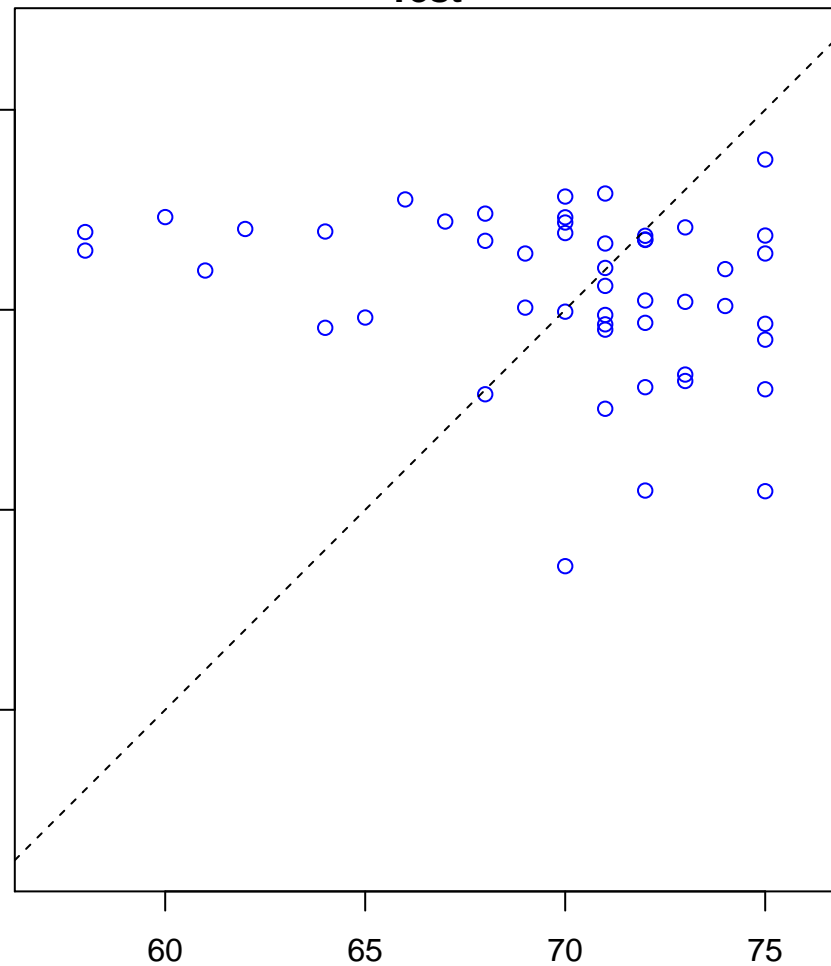


detection of external biotic stimulus (Score: 0.914545)

Control

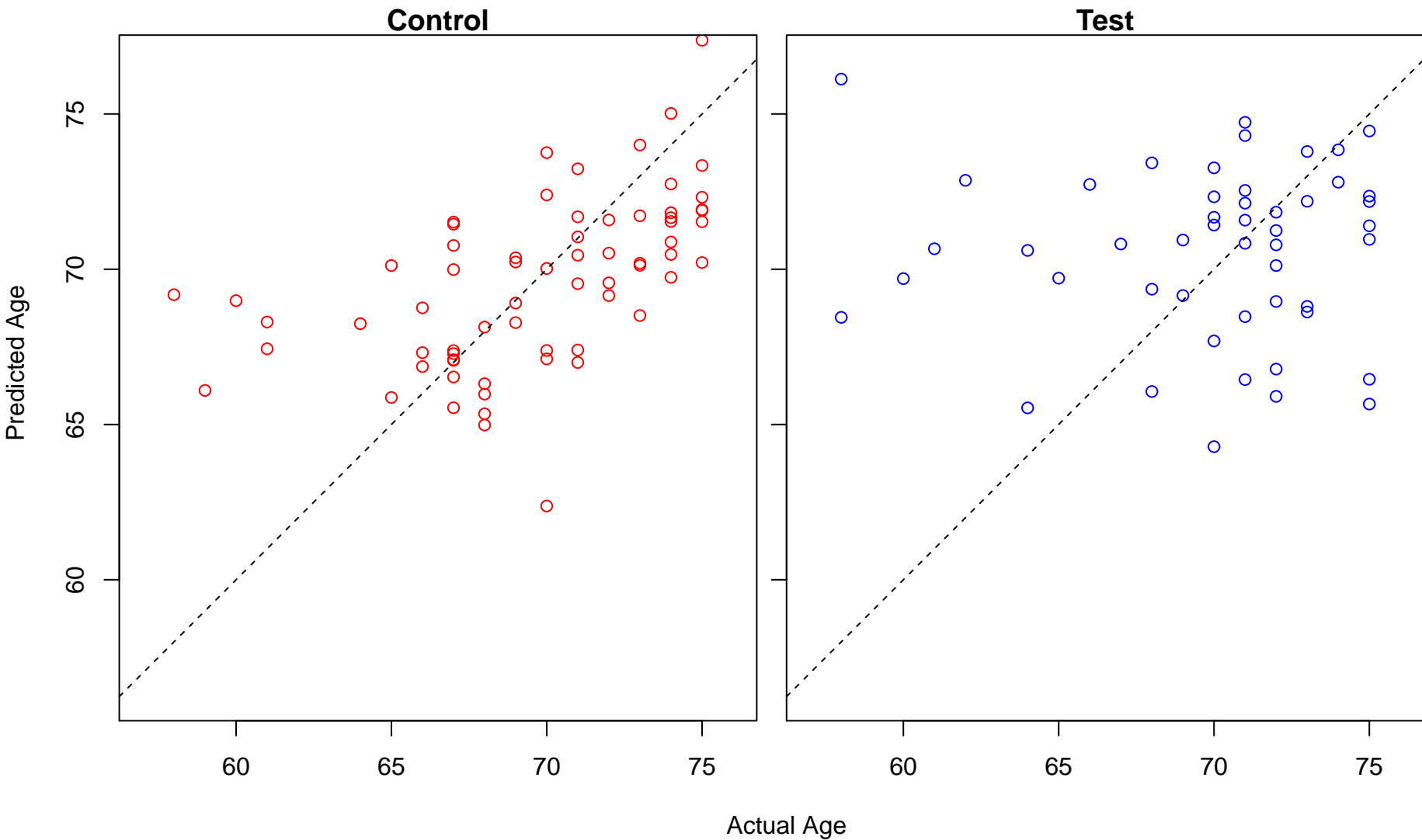


Test

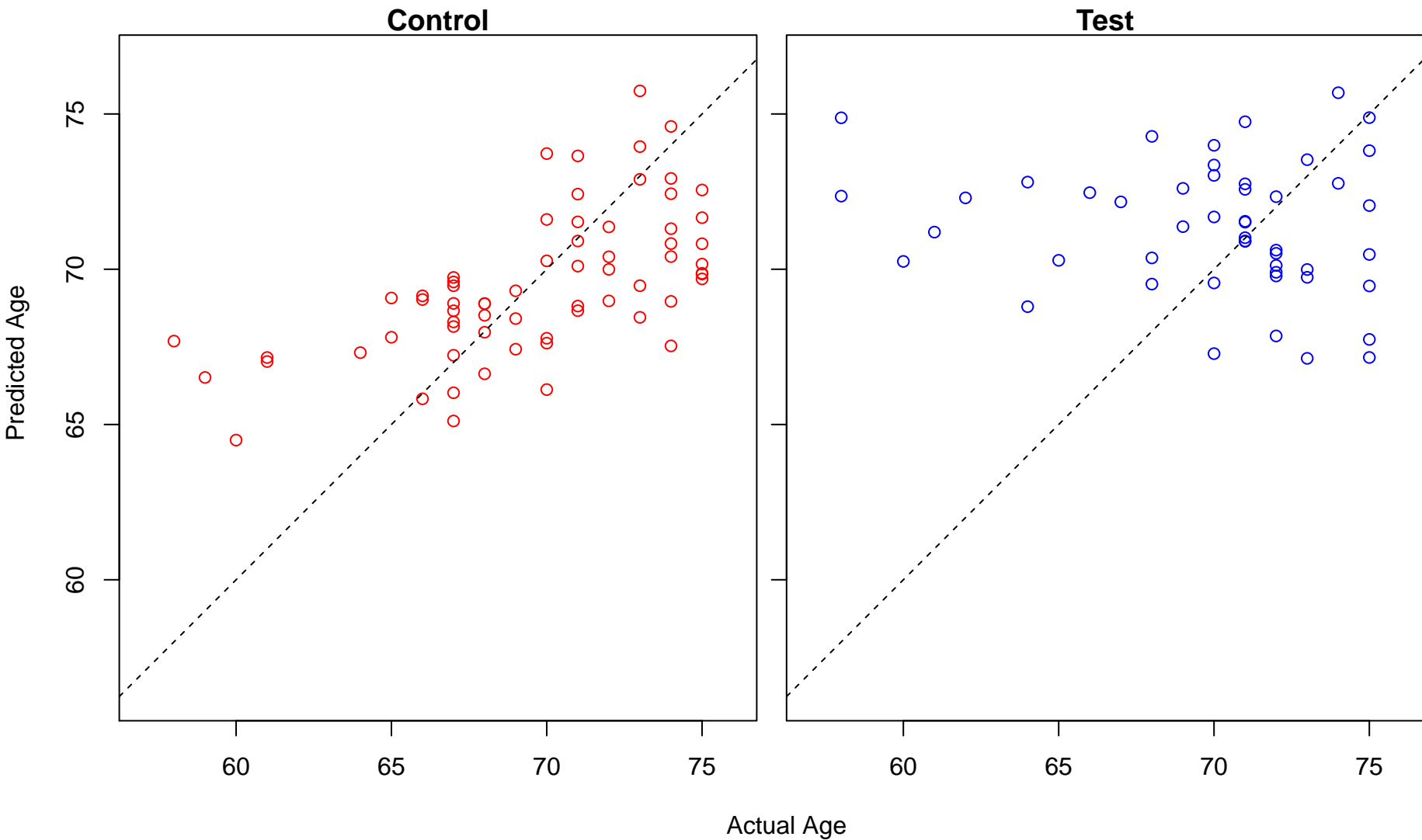


Actual Age

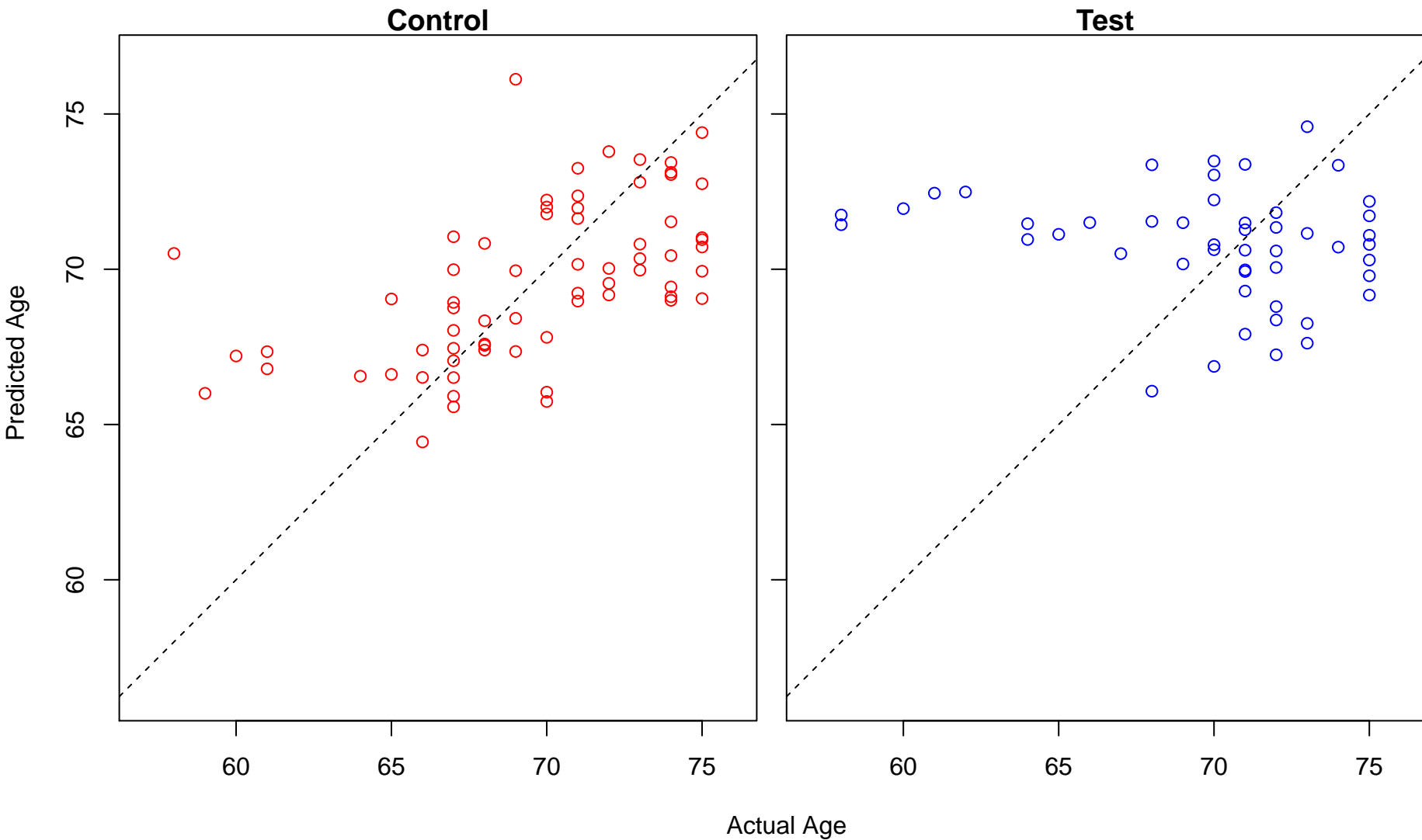
synaptic vesicle endocytosis (Score: 0.914409)



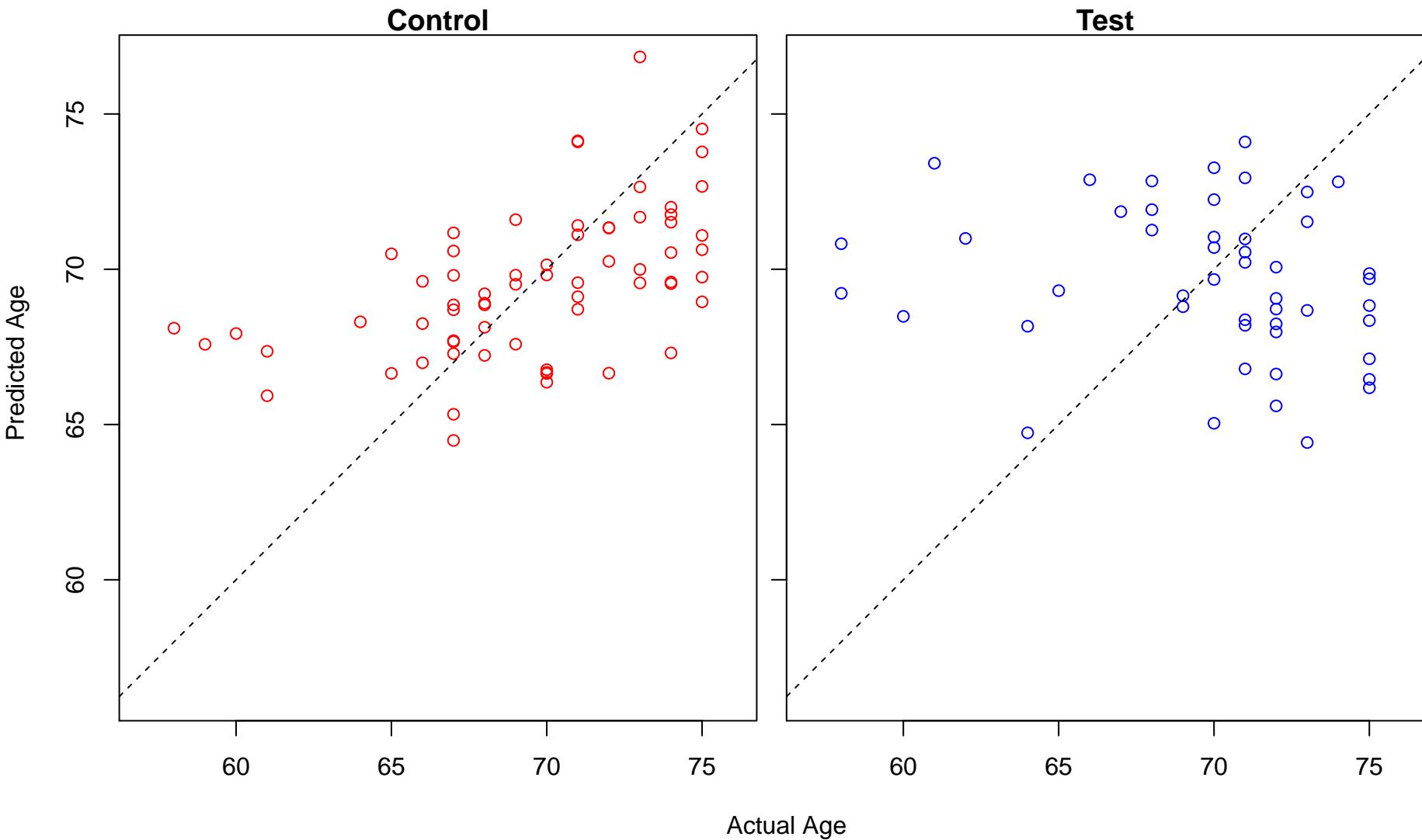
regulation of T cell mediated immunity (Score: 0.914239)



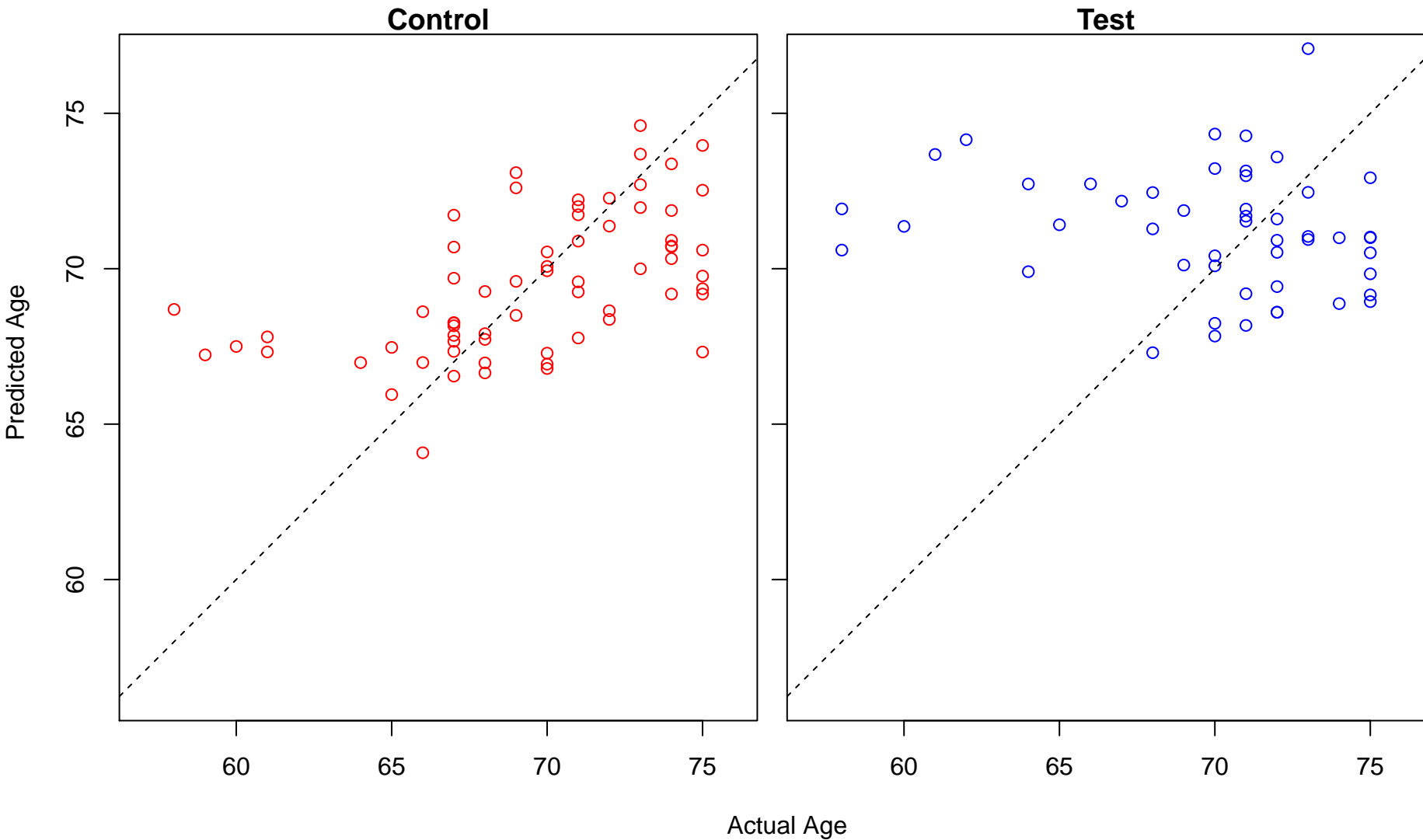
regulation of NFAT protein import into nucleus (Score: 0.914170)



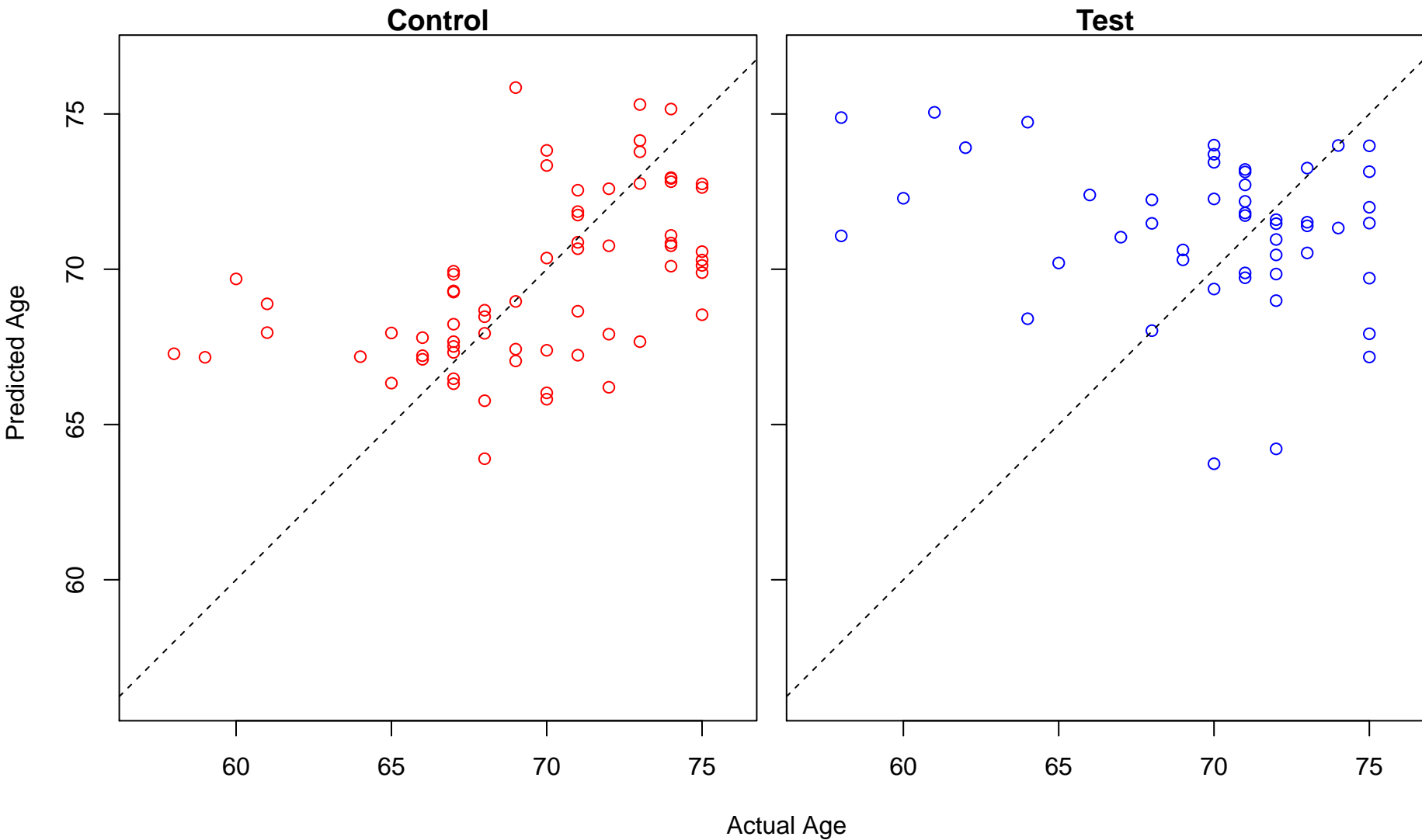
regulation of t-circle formation (Score: 0.913964)



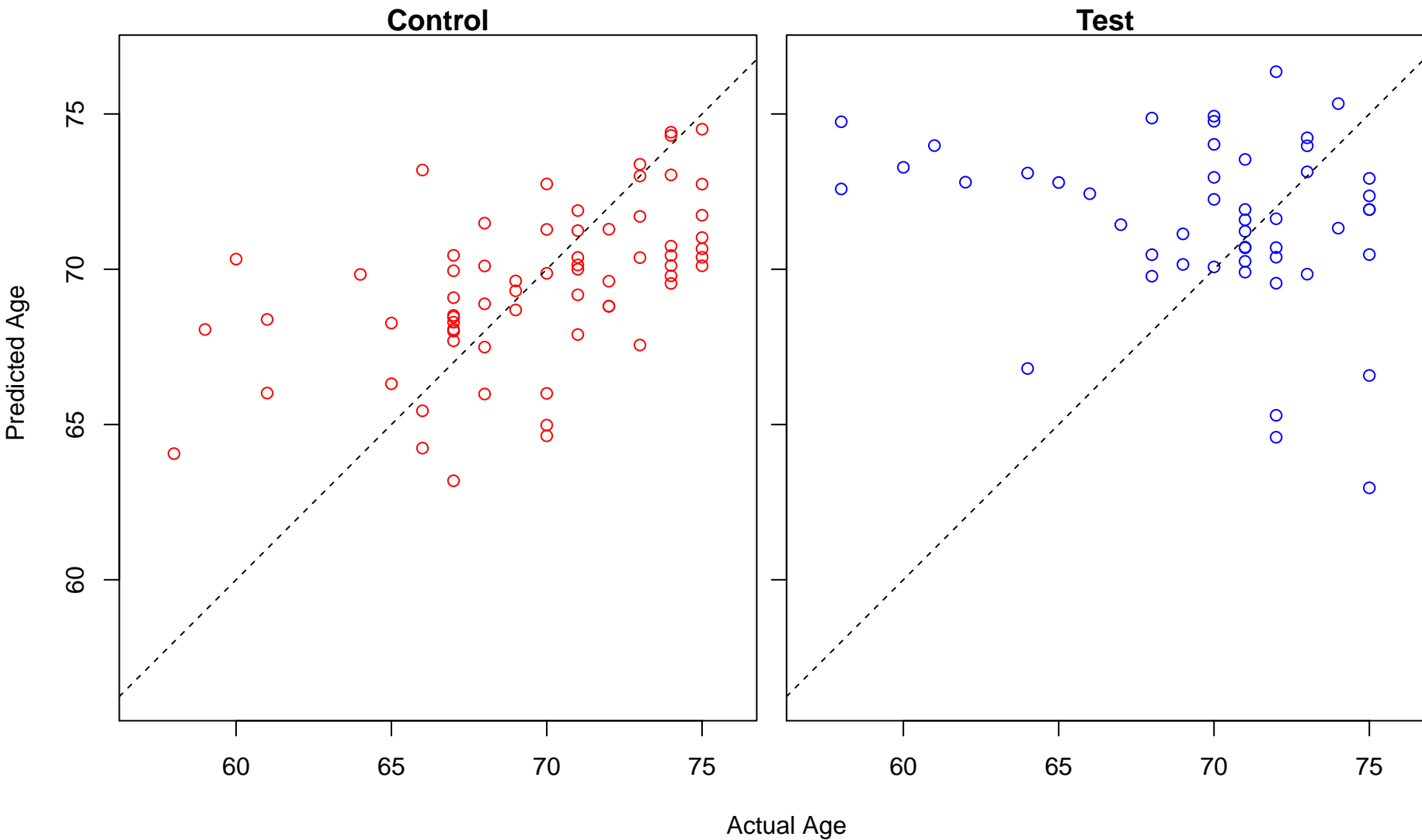
negative regulation of glycoprotein biosynthetic process (Score: 0.913910)



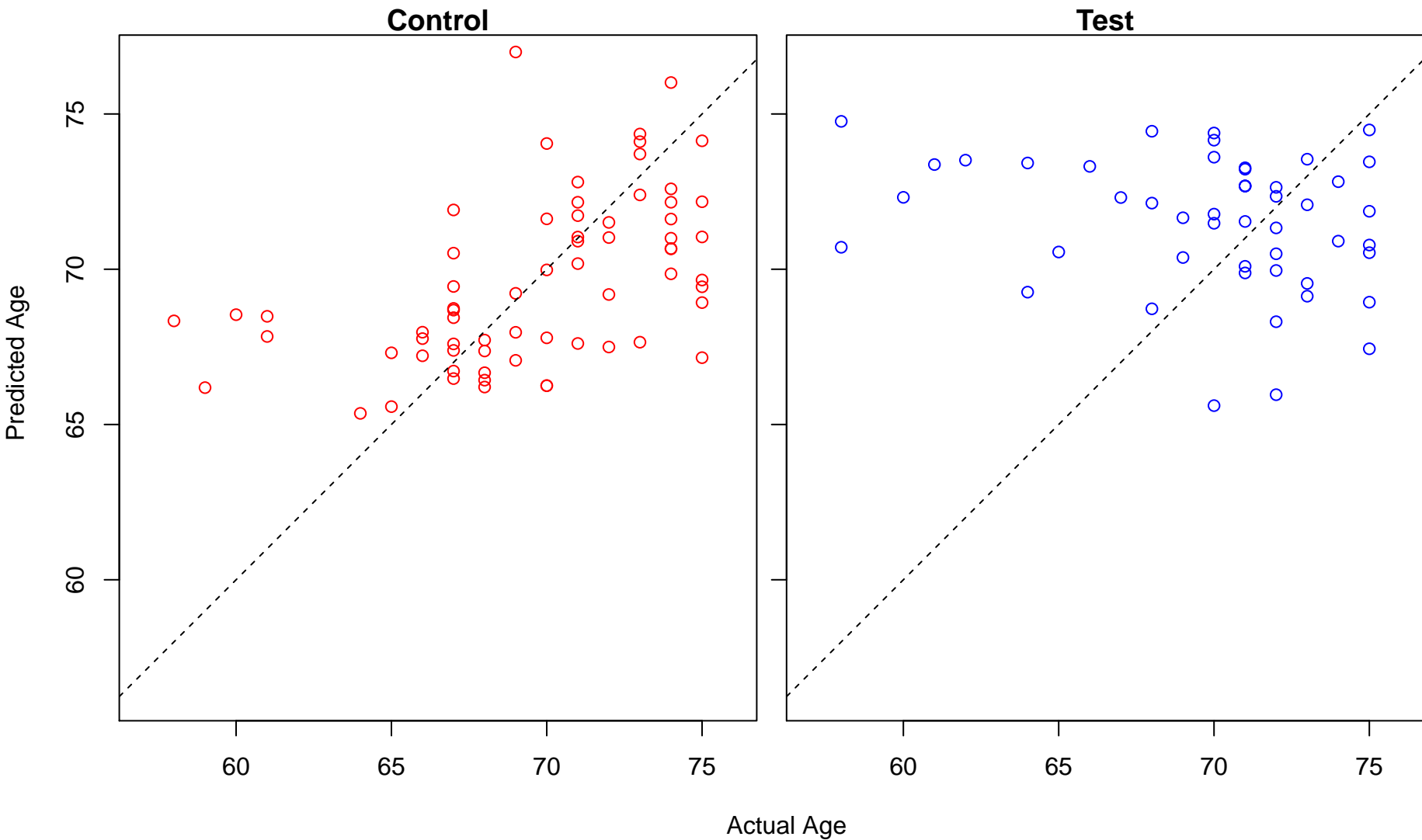
negative regulation of ion transmembrane transport (Score: 0.913707)



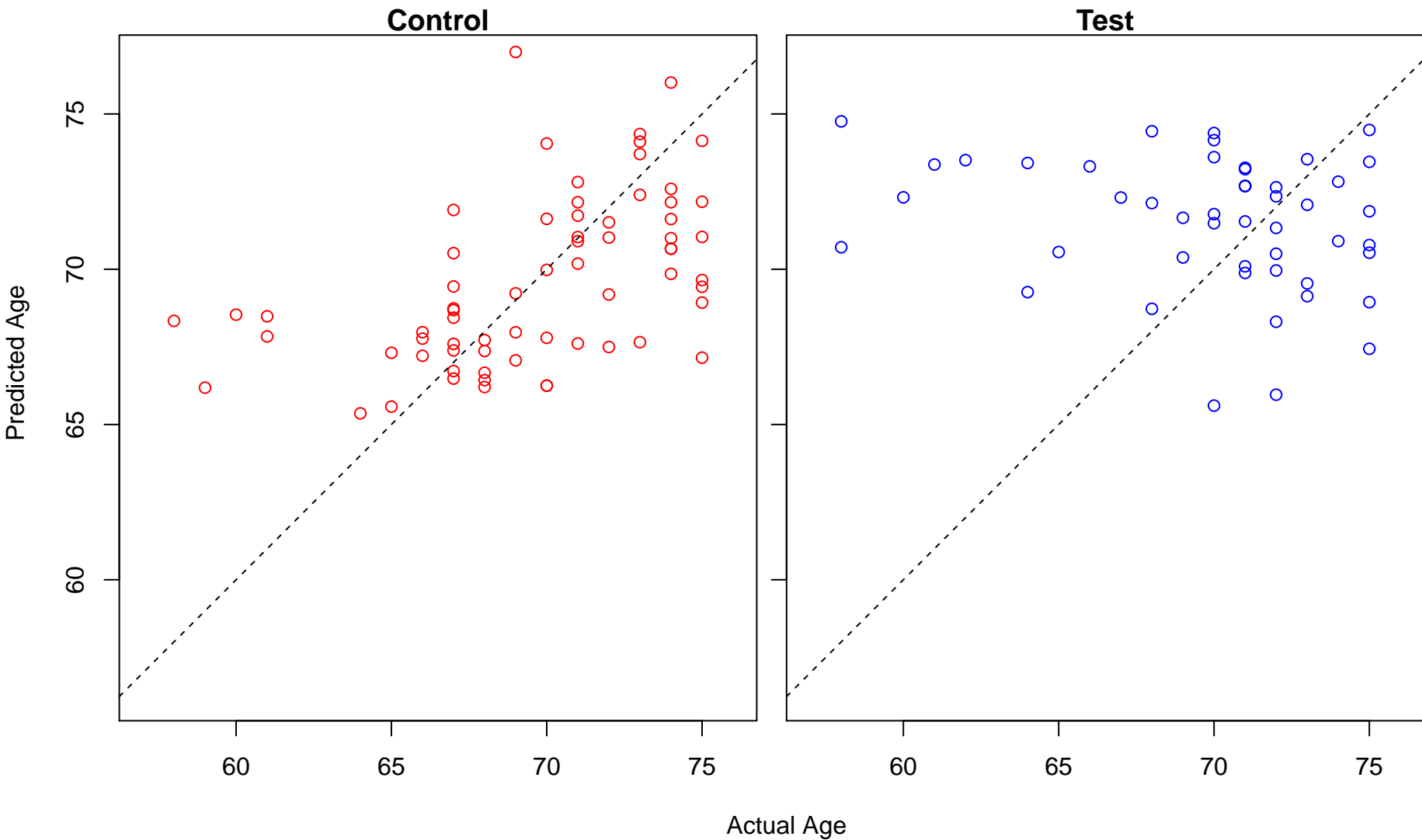
positive regulation of mitochondrial calcium ion concentration (Score: 0.913335)



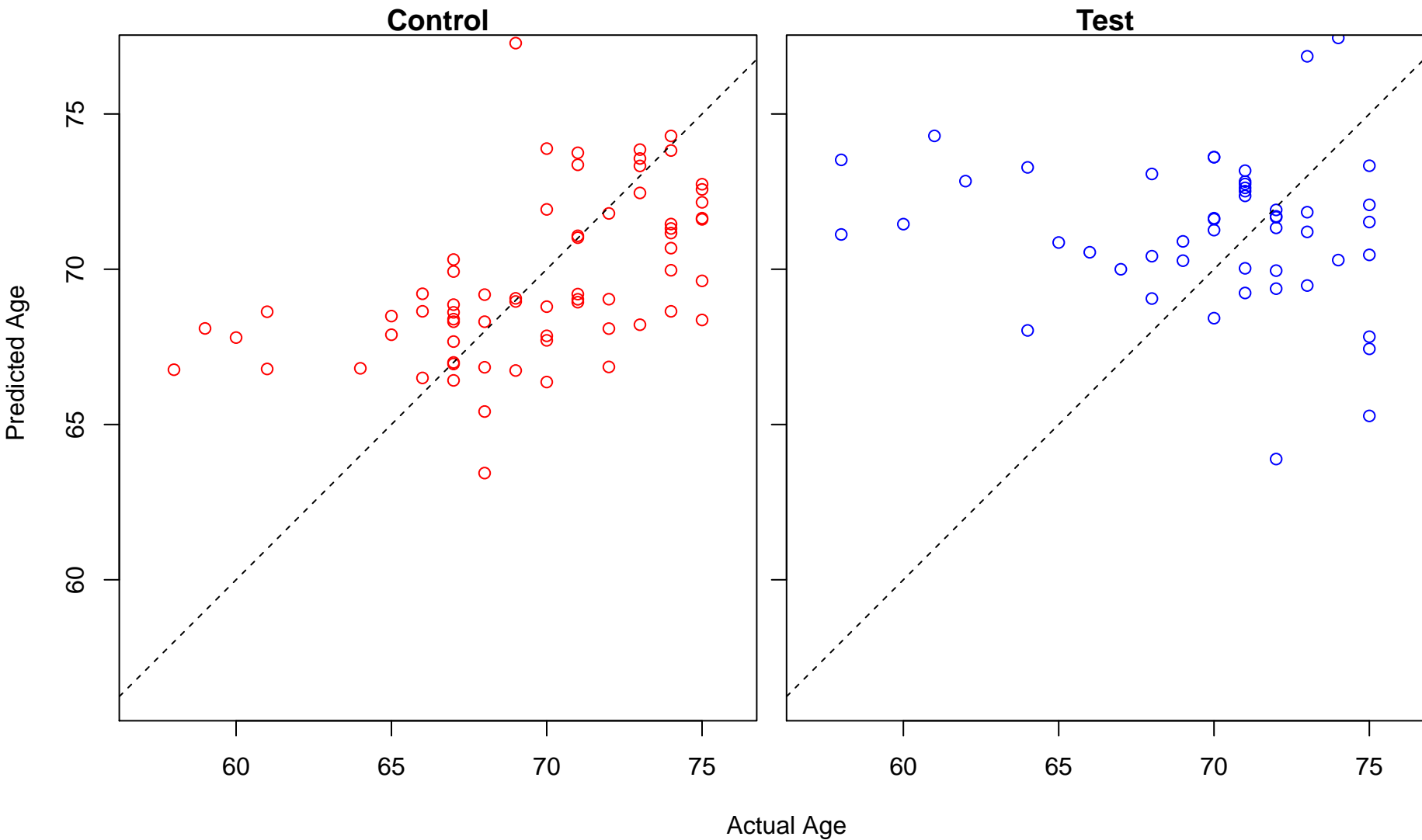
regulation of protein localization to plasma membrane (Score: 0.913233)



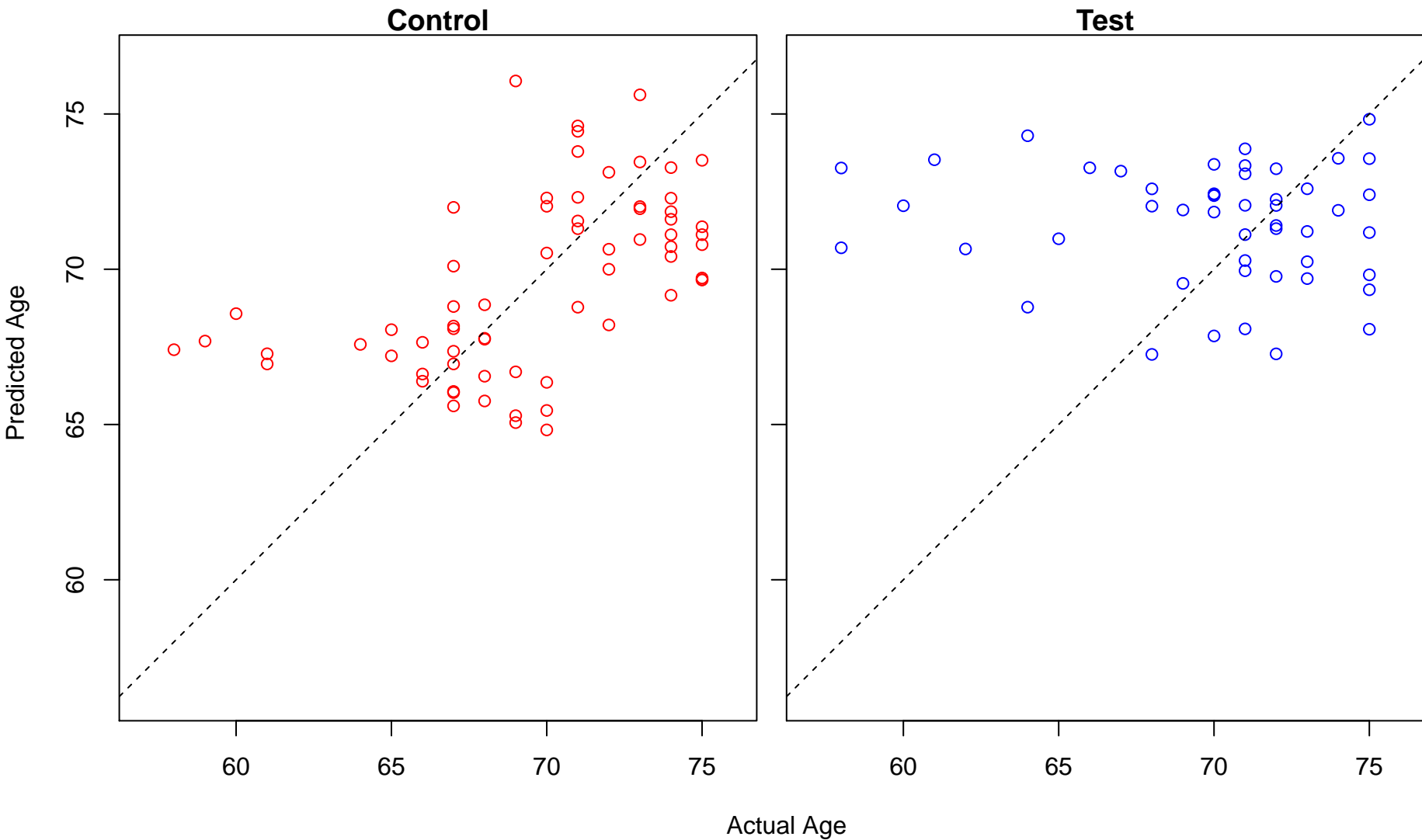
regulation of protein localization to cell periphery (Score: 0.913233)



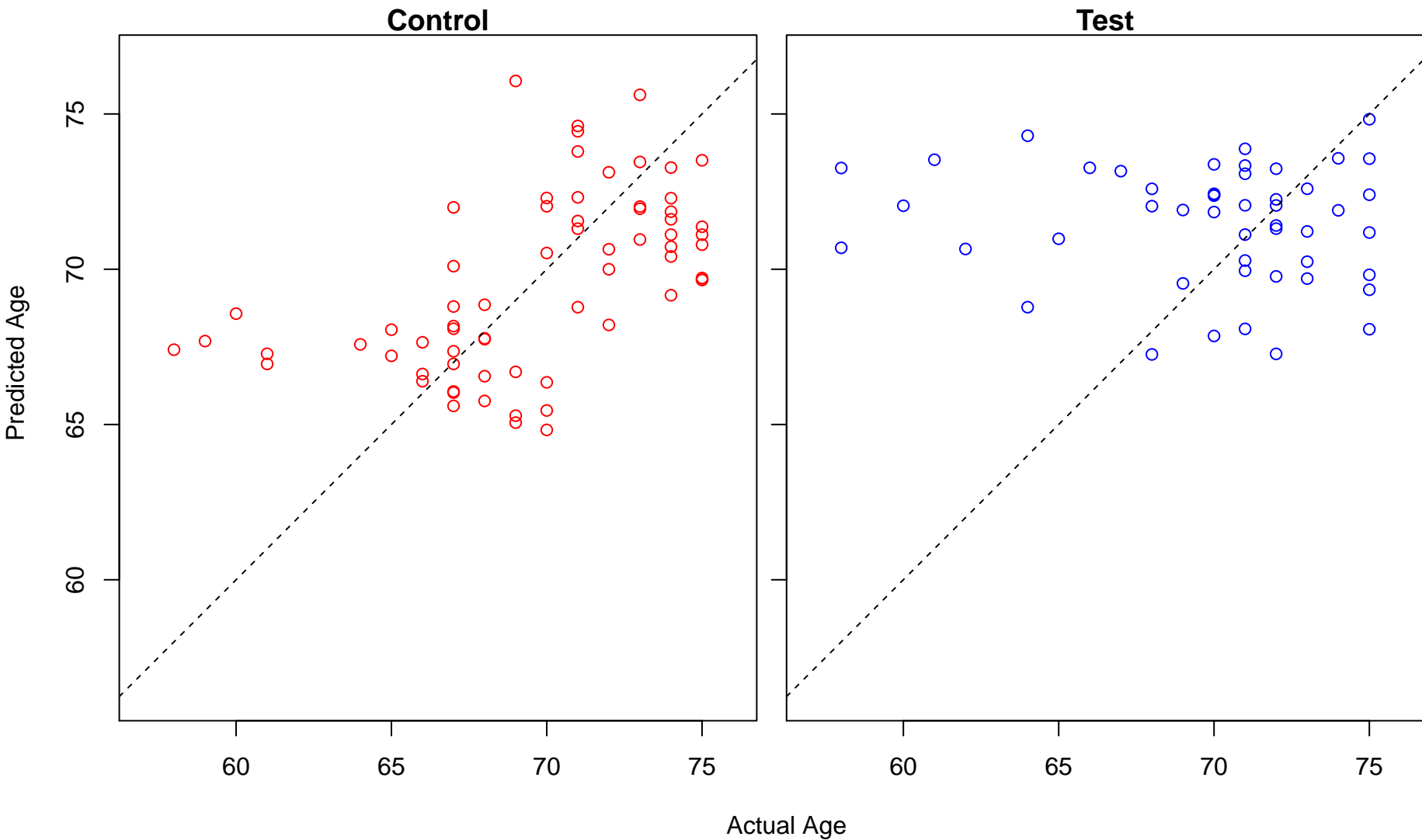
chaperone-mediated protein folding (Score: 0.913125)



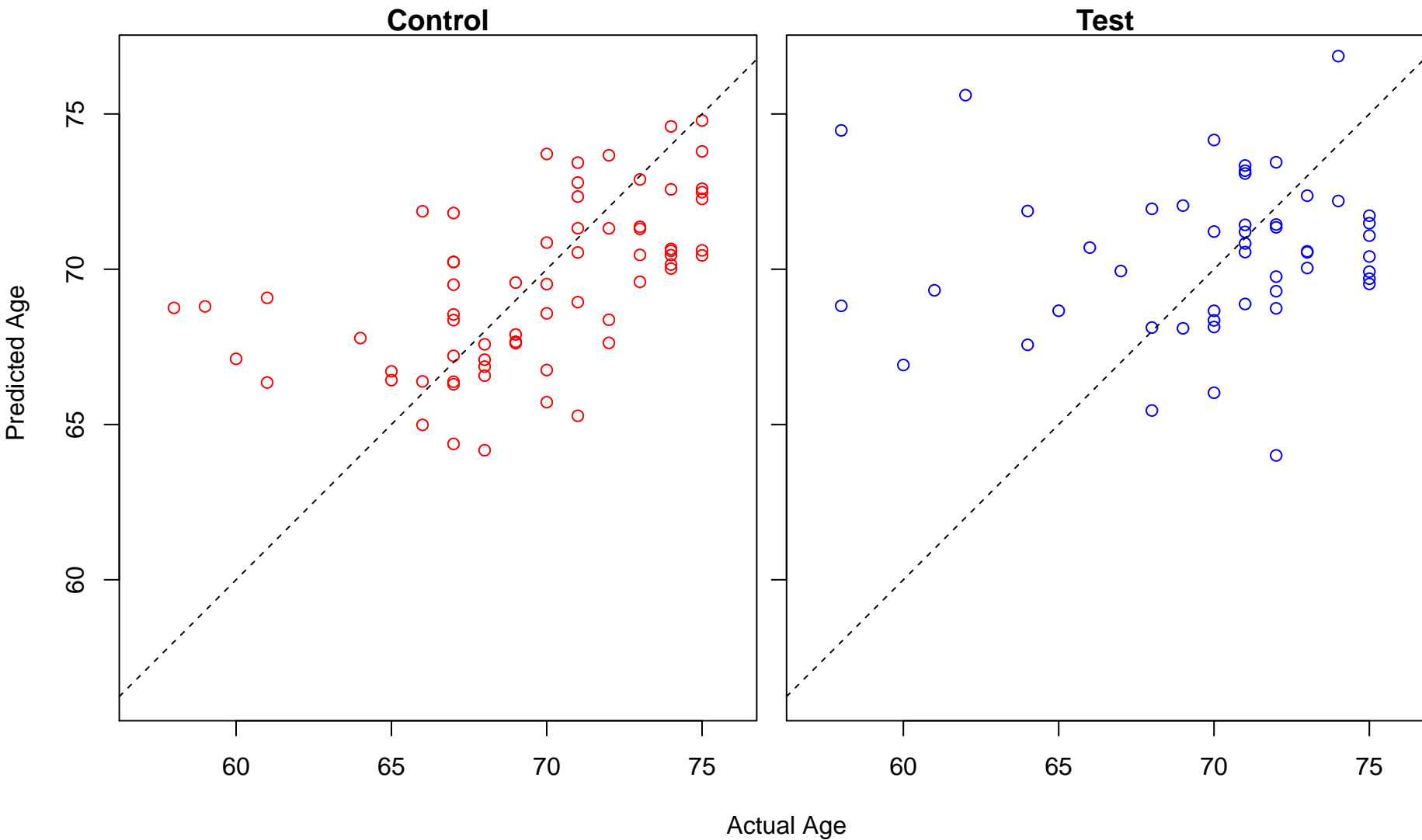
negative regulation of protein import into nucleus (Score: 0.912976)



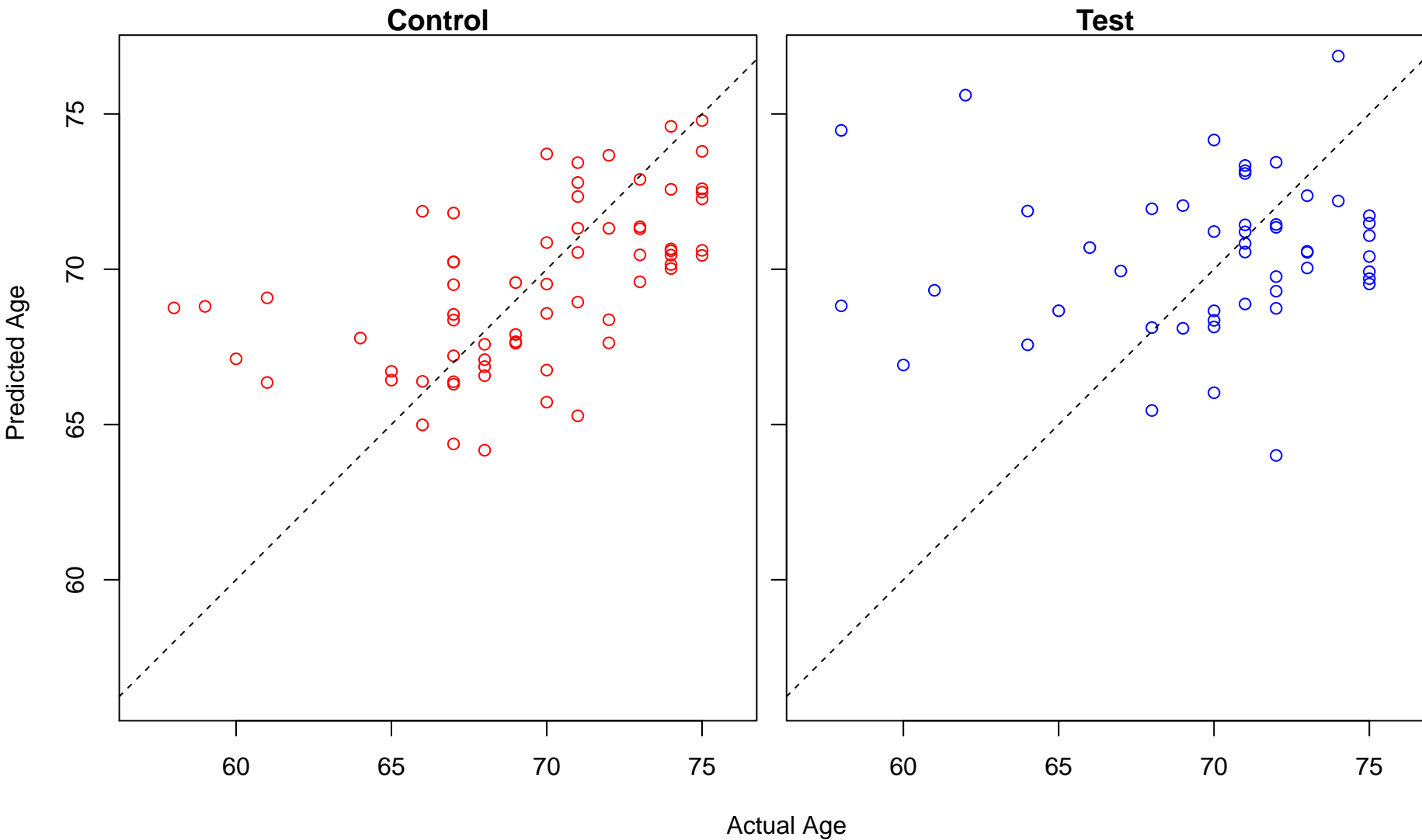
negative regulation of protein import (Score: 0.912976)



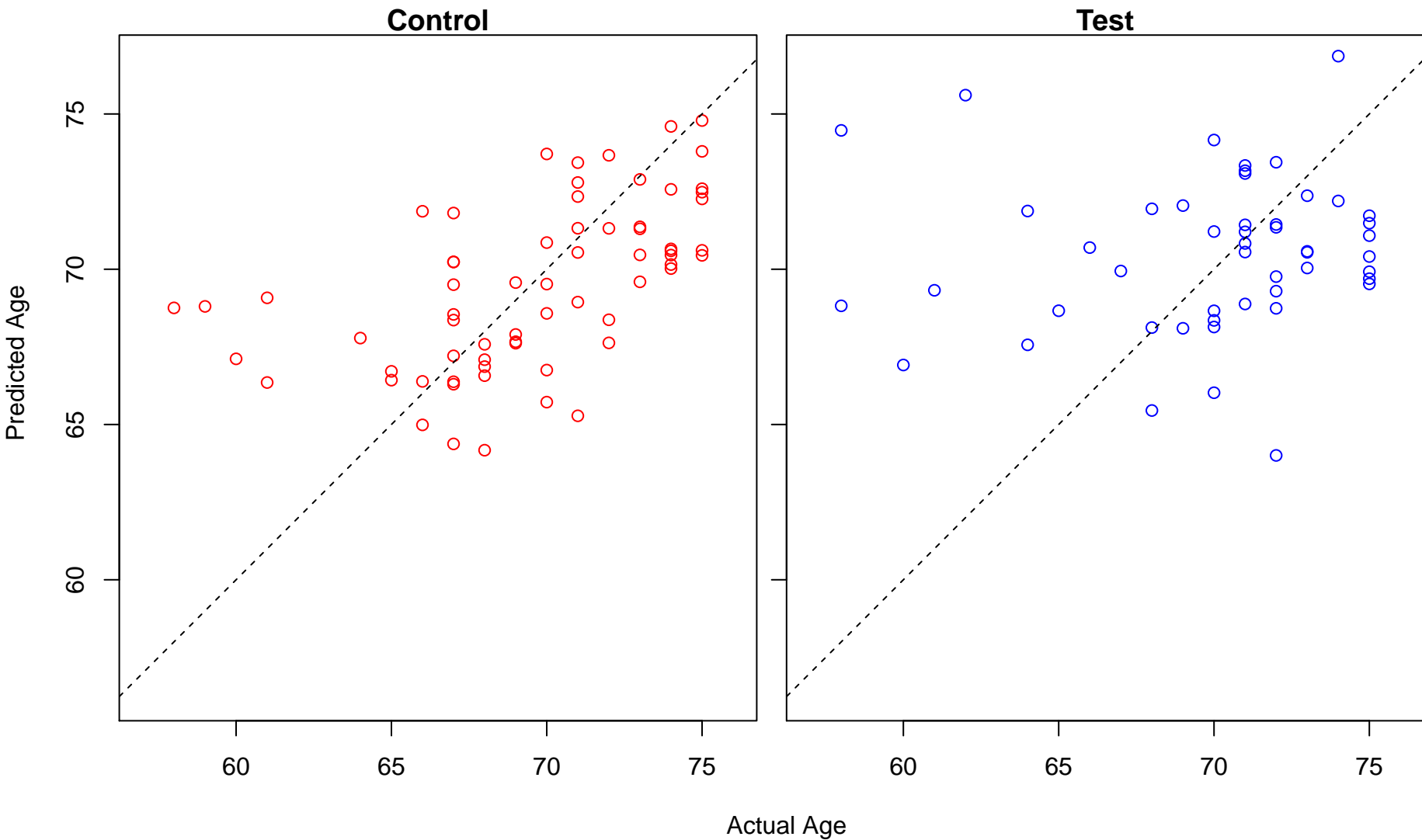
response to sterol depletion (Score: 0.912589)



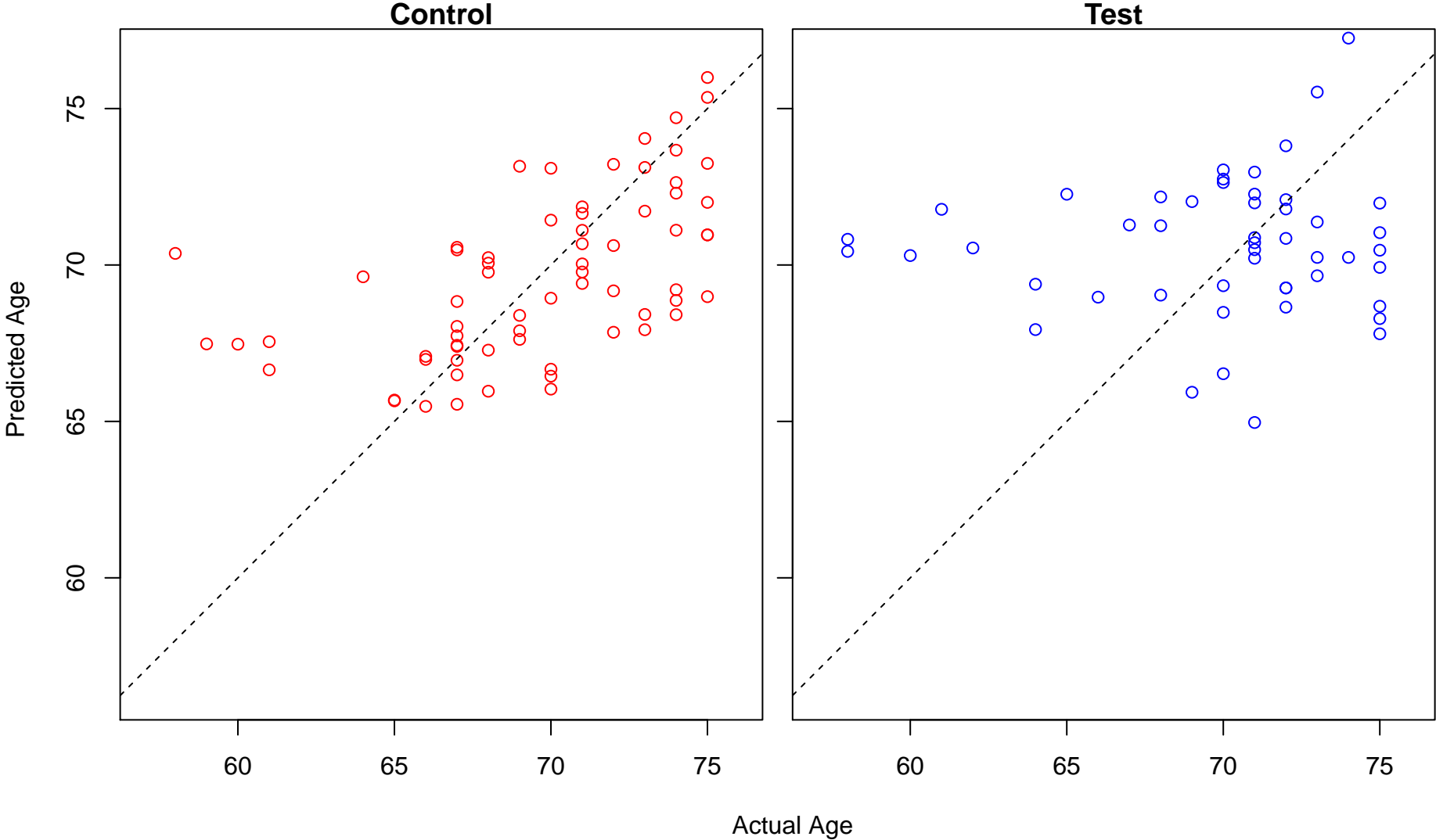
SREBP signaling pathway (Score: 0.912589)



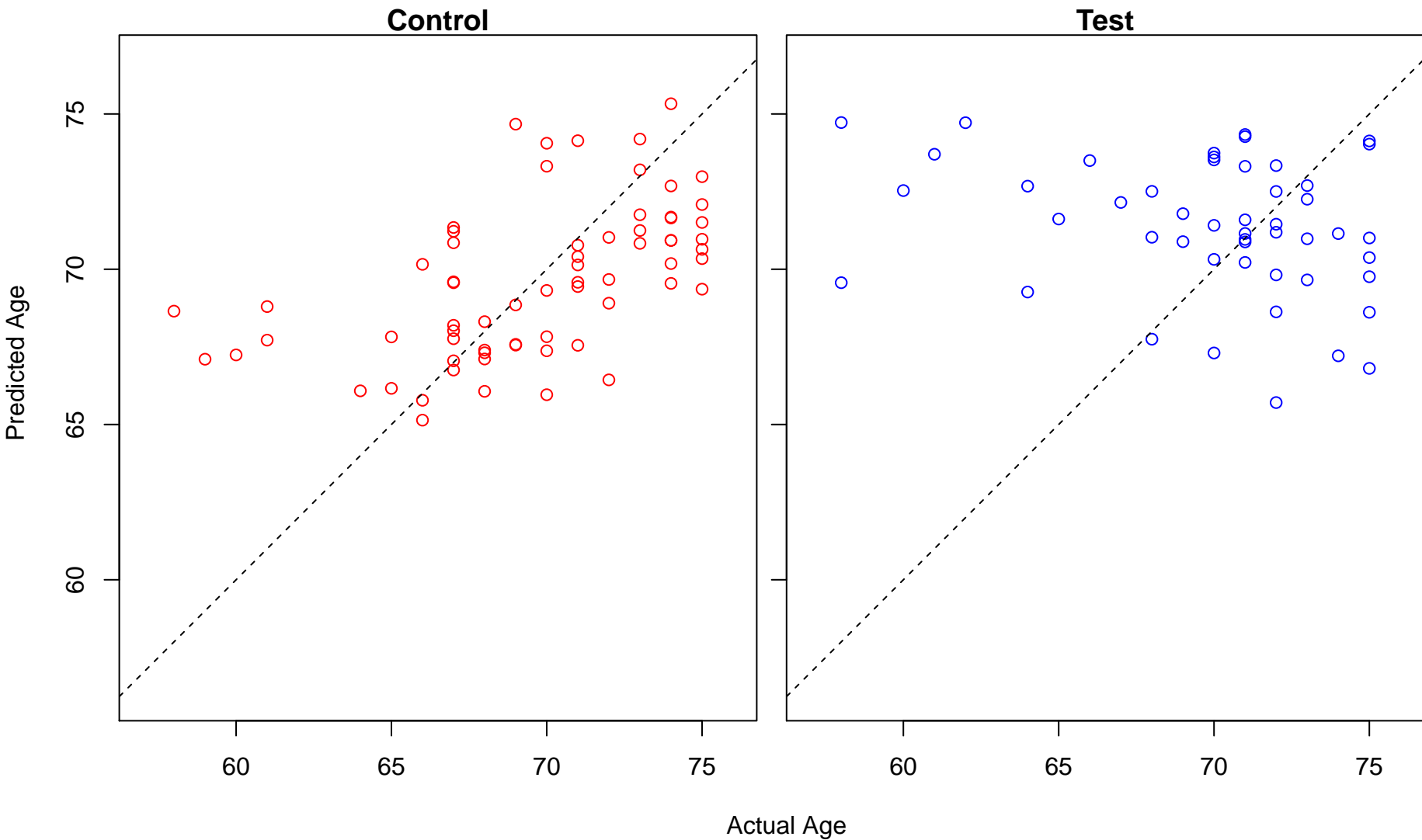
cellular response to sterol depletion (Score: 0.912589)



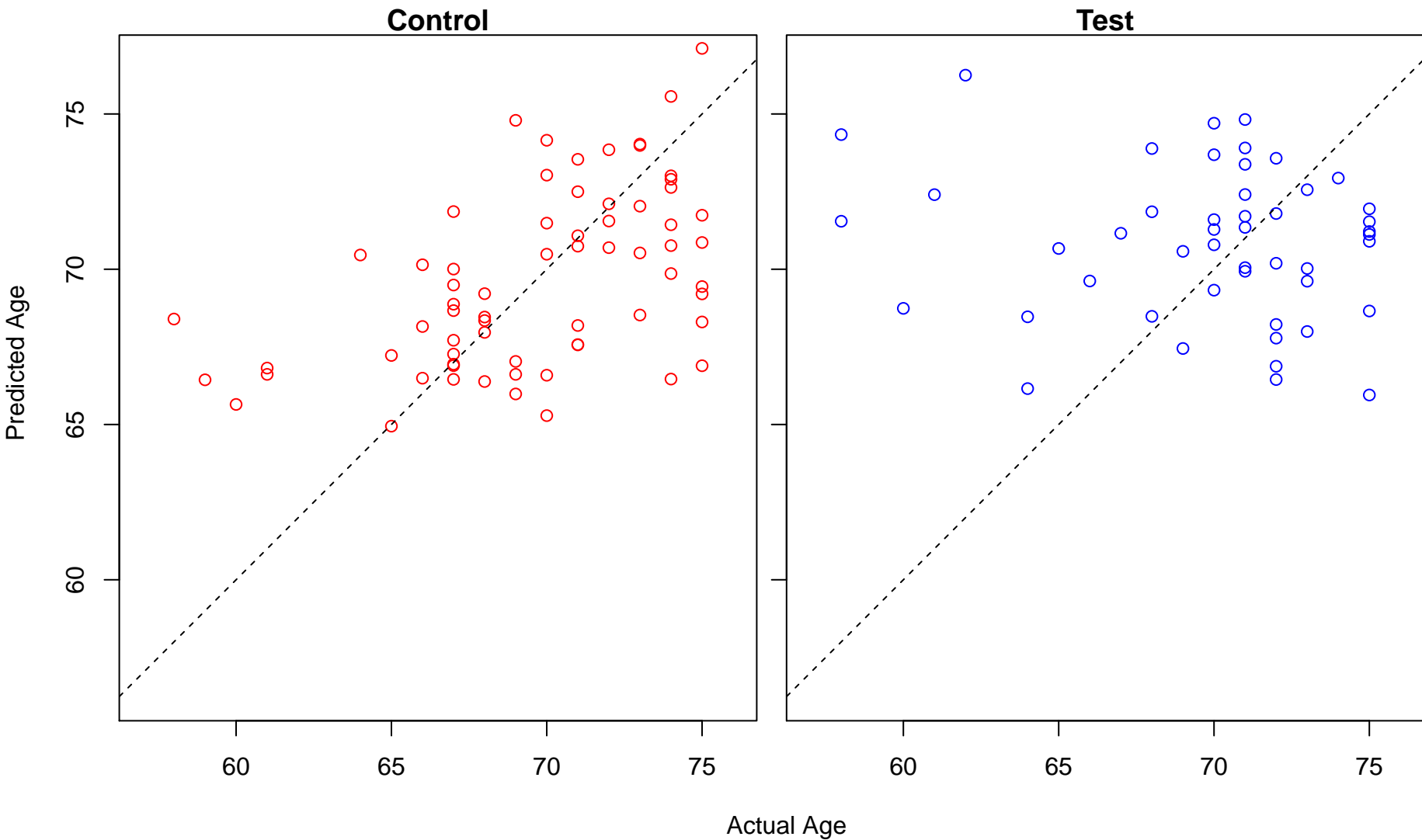
negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway (Score: 0.9125)



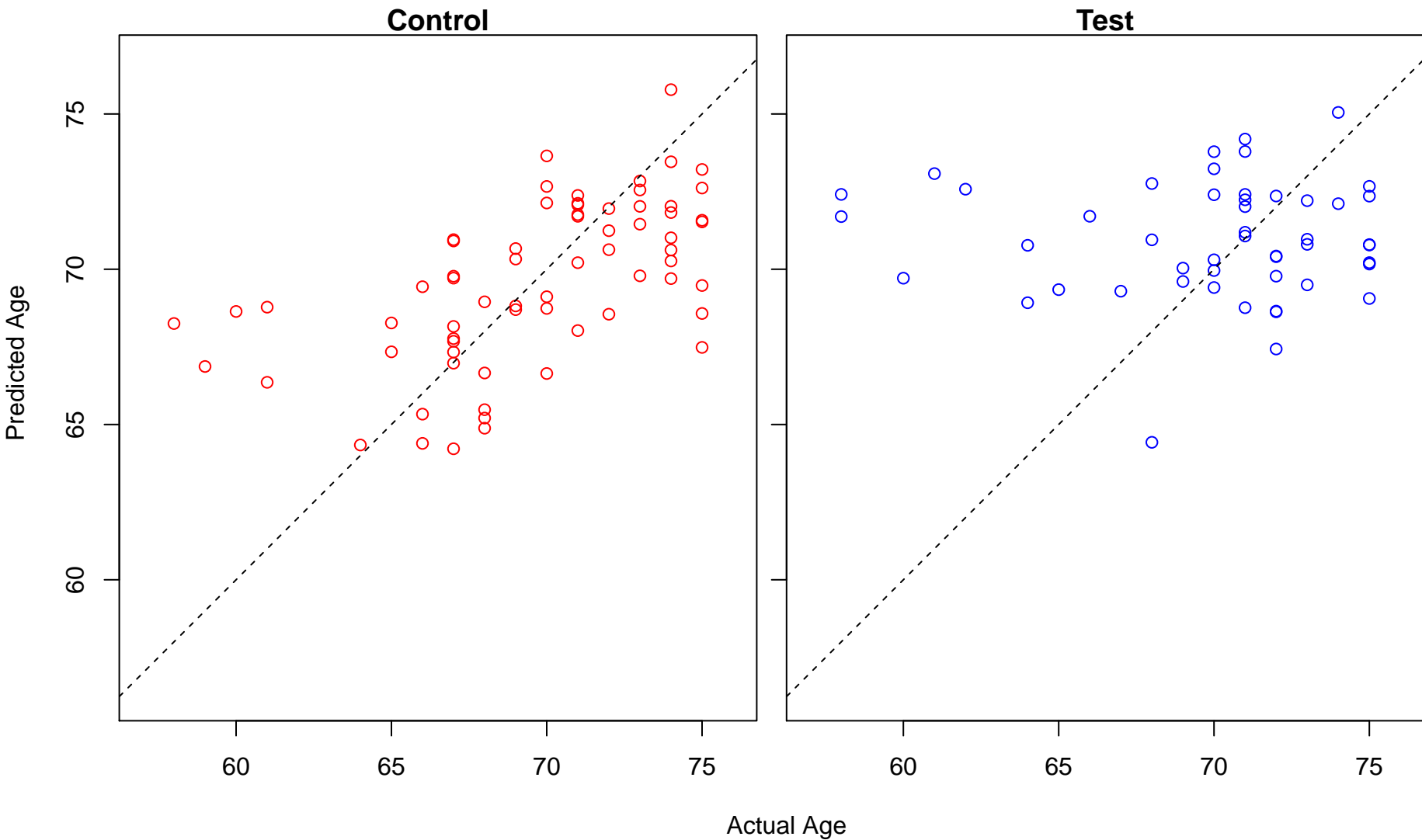
positive regulation of mast cell activation (Score: 0.912291)



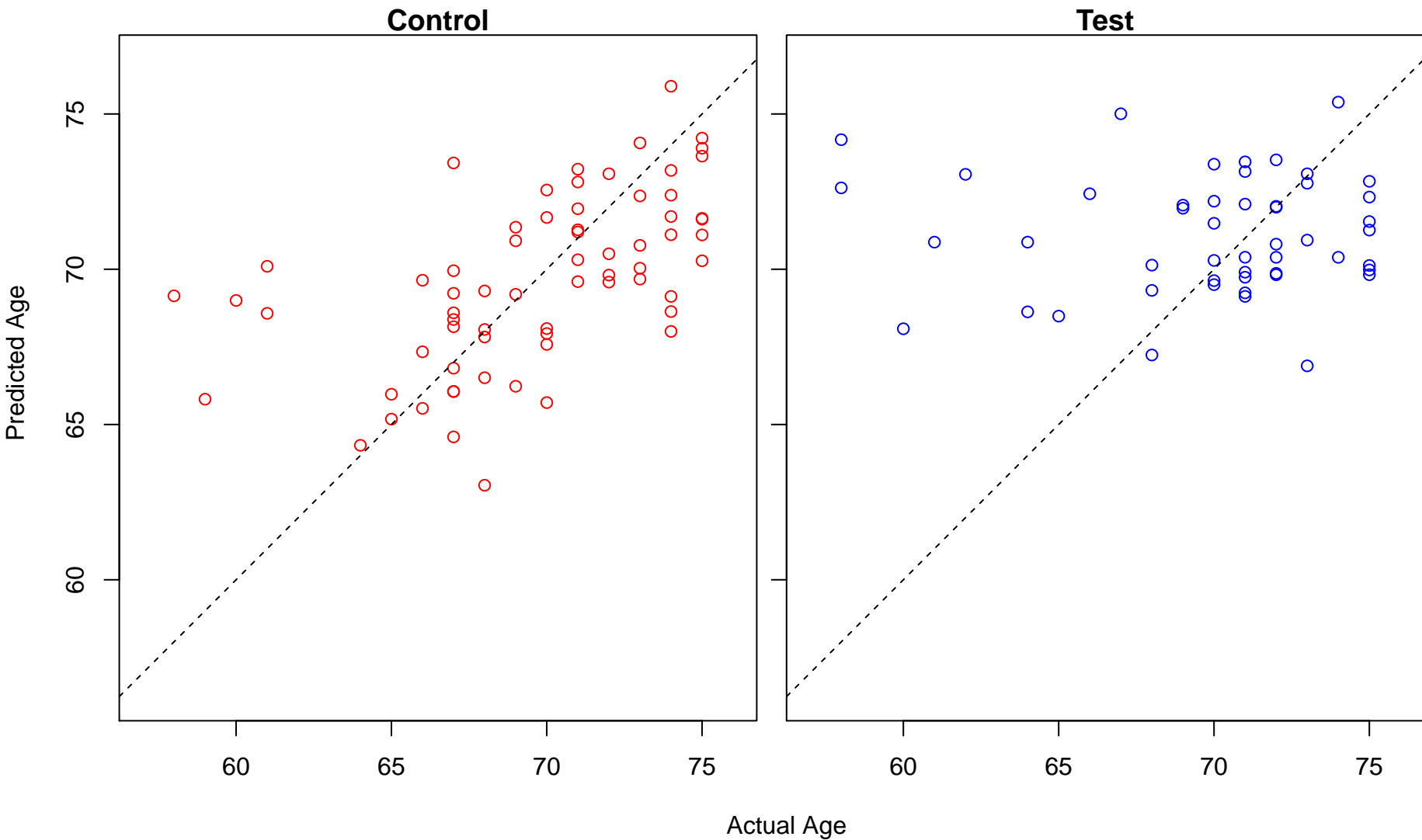
cellular response to fatty acid (Score: 0.911275)



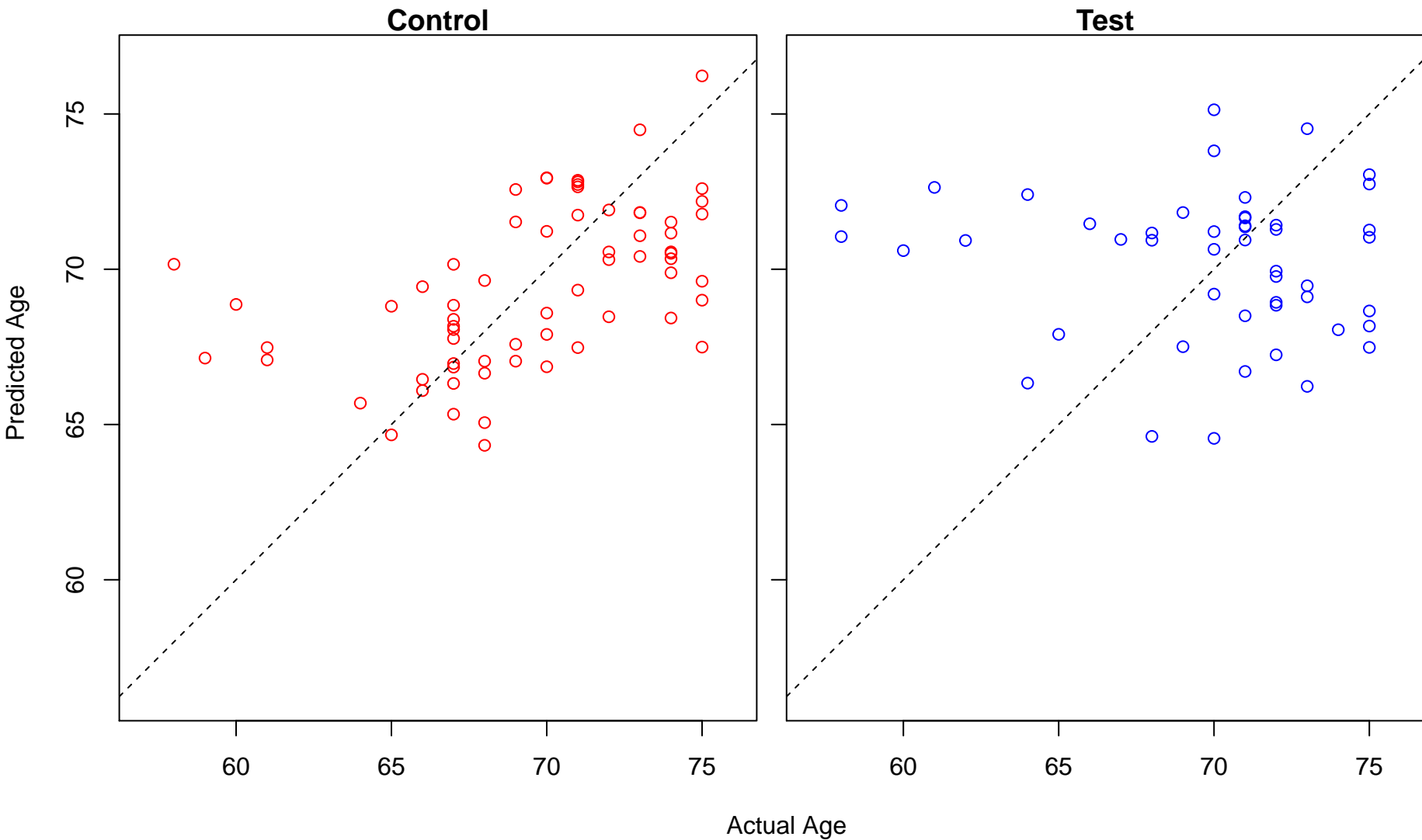
striated muscle cell development (Score: 0.911256)



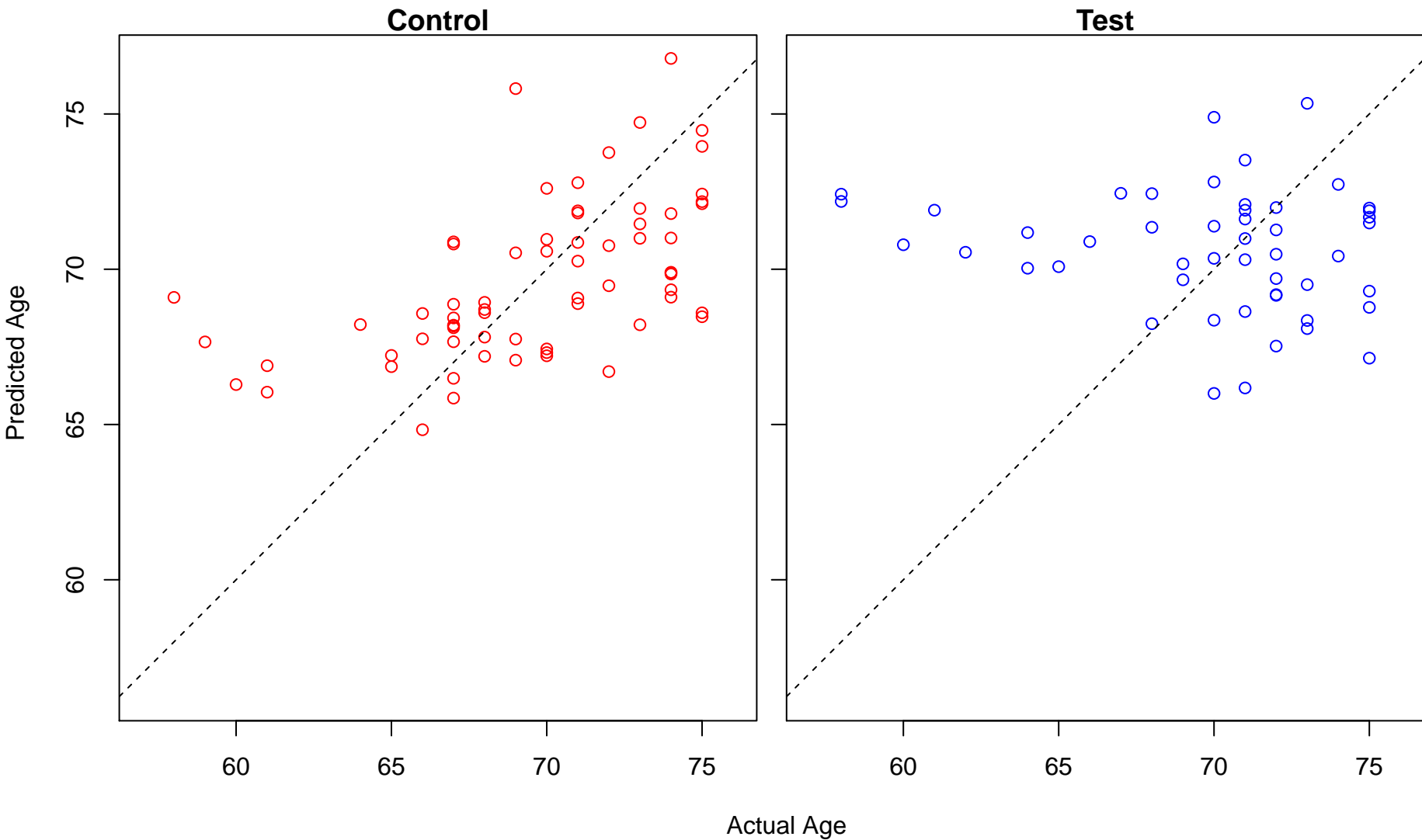
peptide transport (Score: 0.911224)



negative regulation of endocytosis (Score: 0.91122)

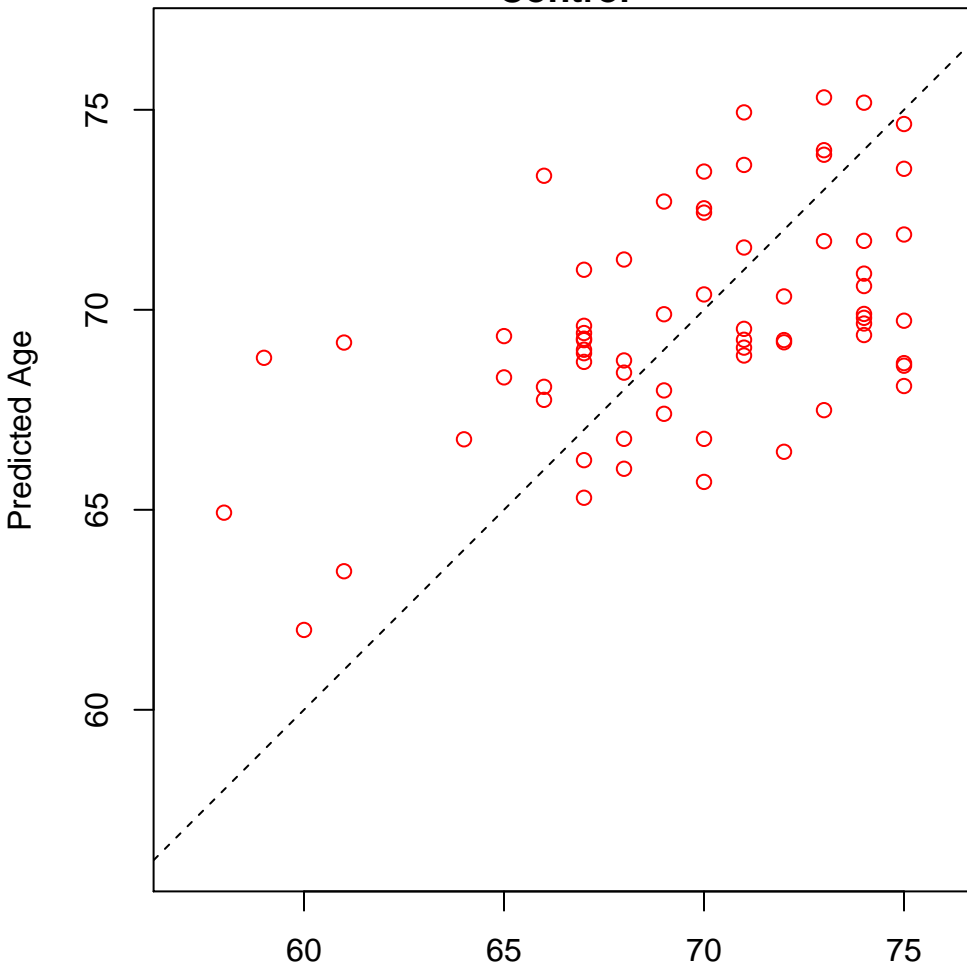


regulation of endosome size (Score: 0.910883)

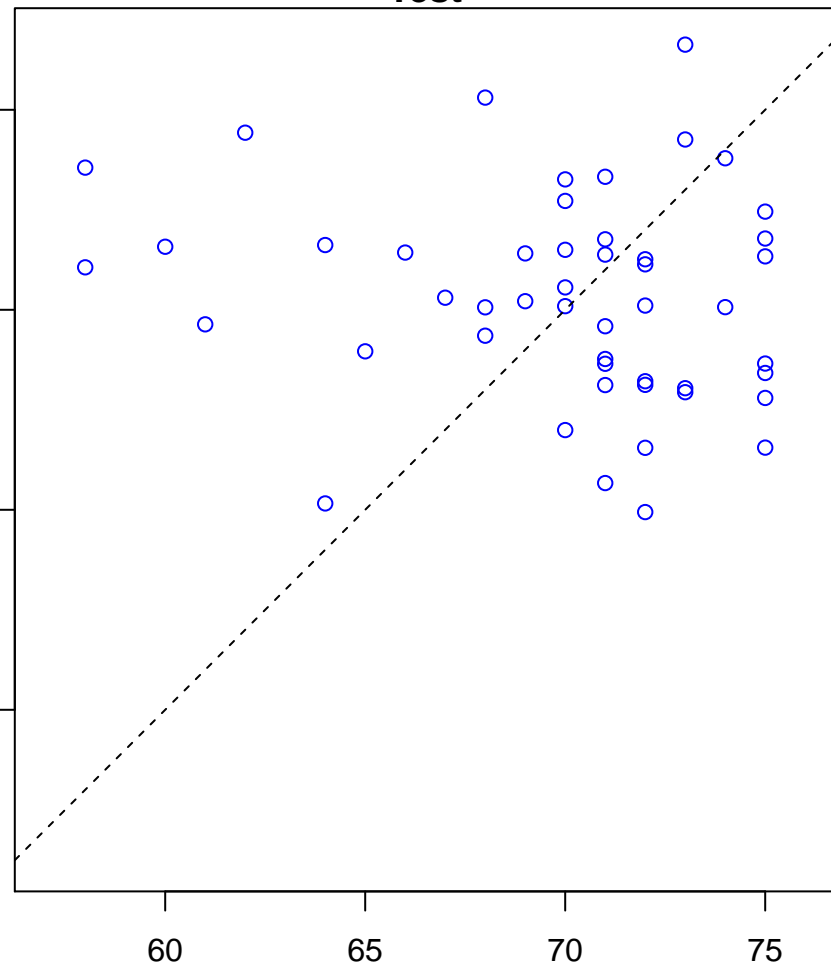


response to bacterial lipoprotein (Score: 0.910303)

Control

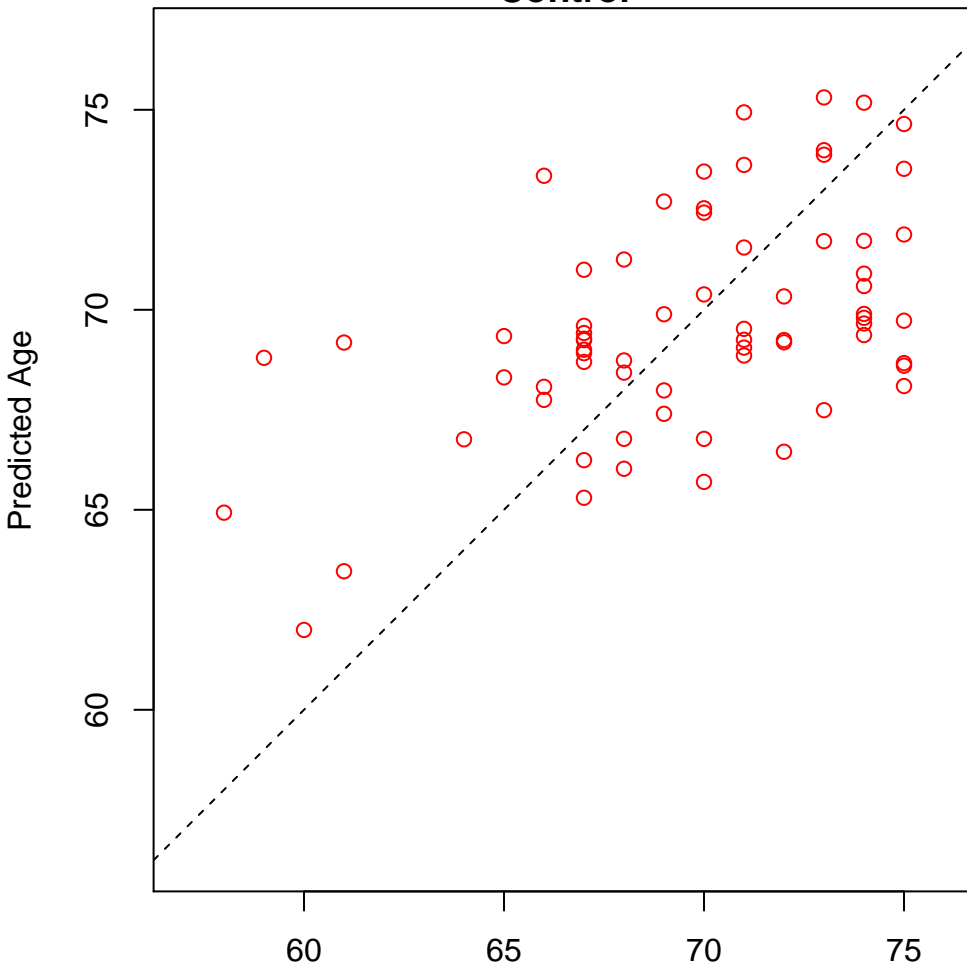


Test

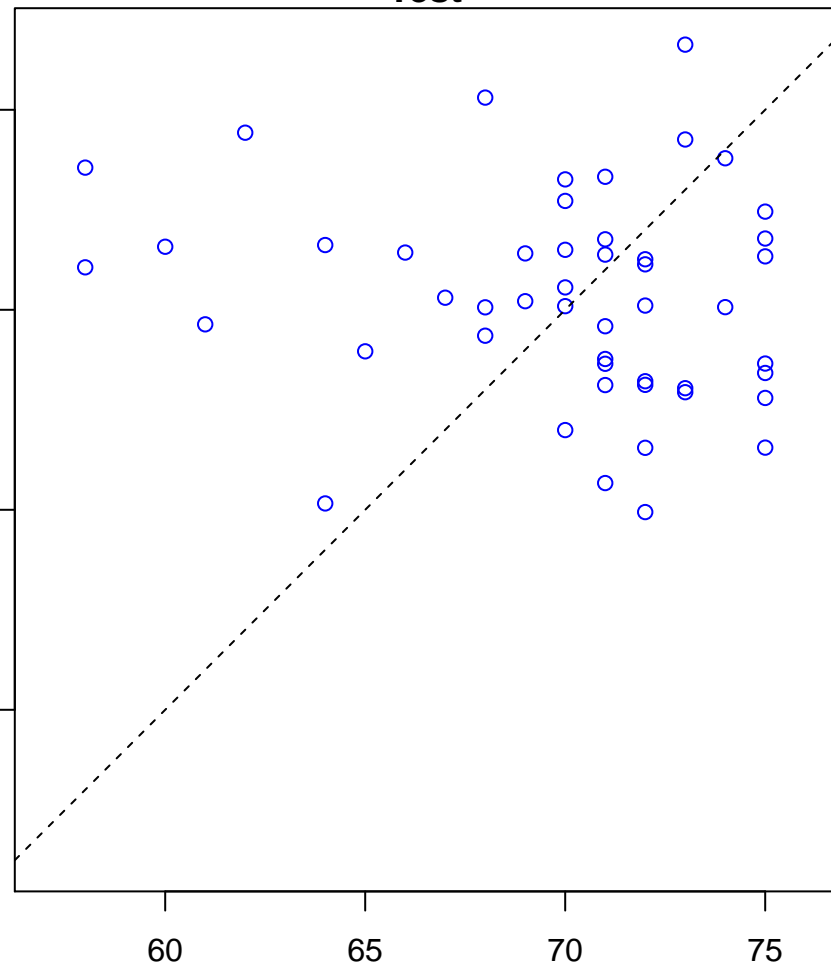


response to bacterial lipopeptide (Score: 0.910303)

Control



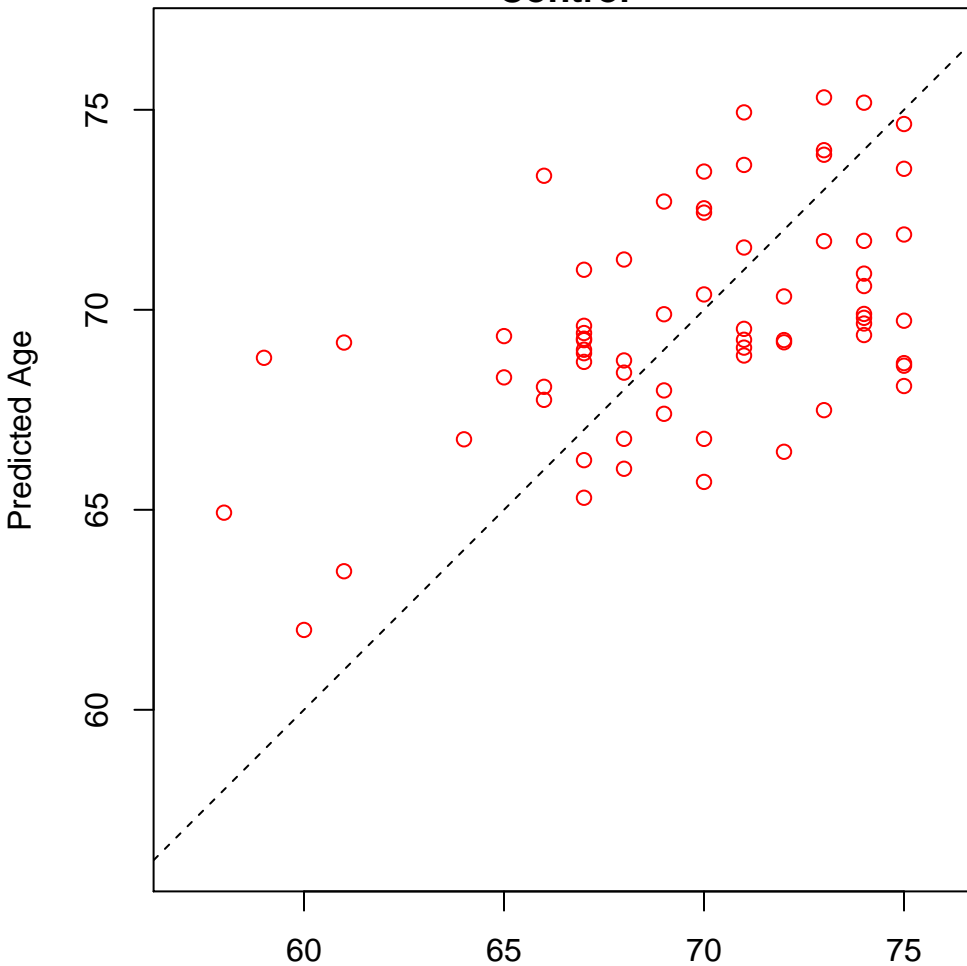
Test



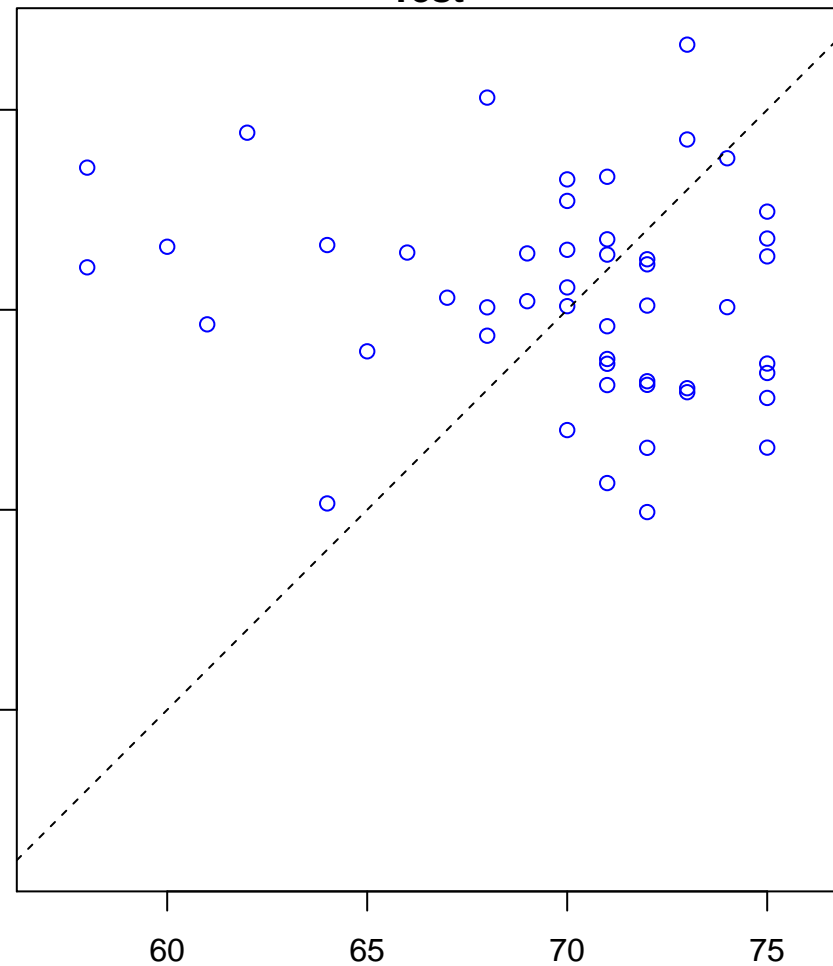
Actual Age

cellular response to bacterial lipoprotein (Score: 0.910303)

Control



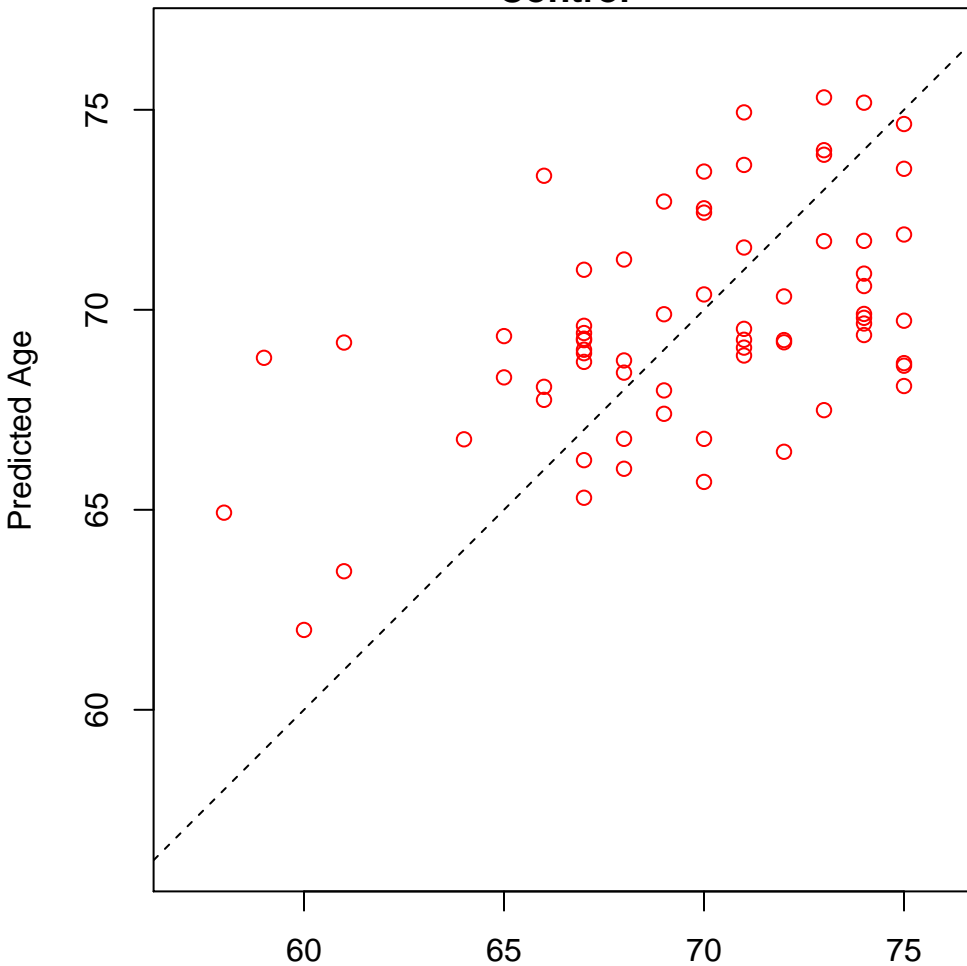
Test



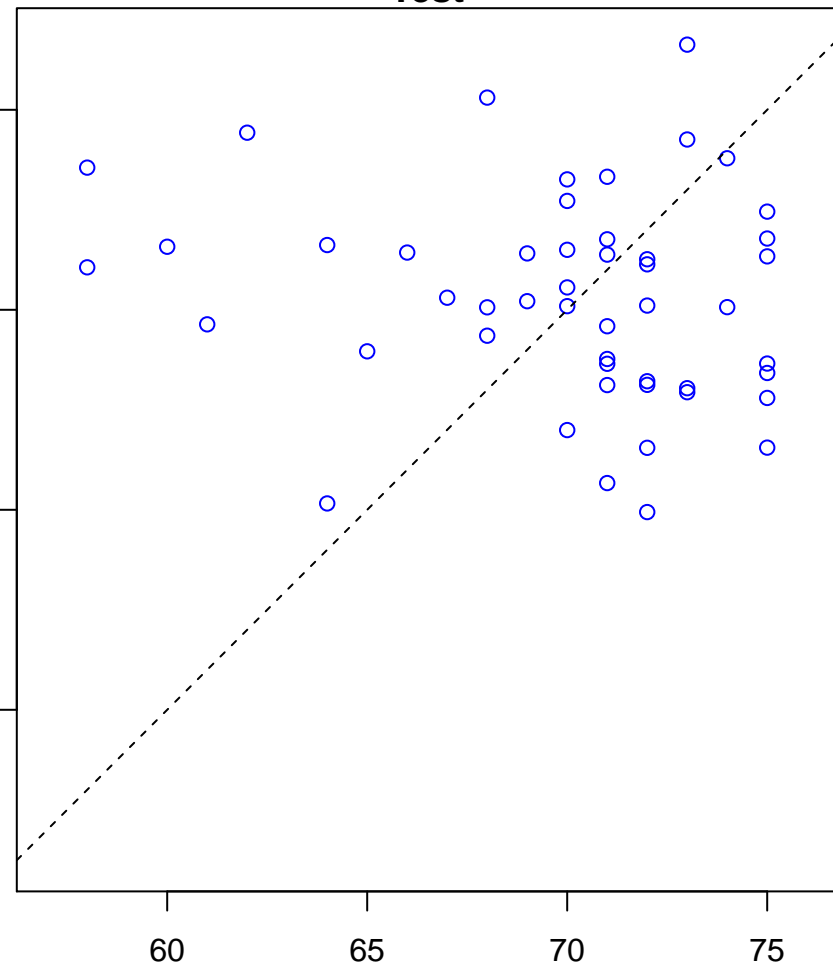
Actual Age

cellular response to bacterial lipopeptide (Score: 0.910303)

Control

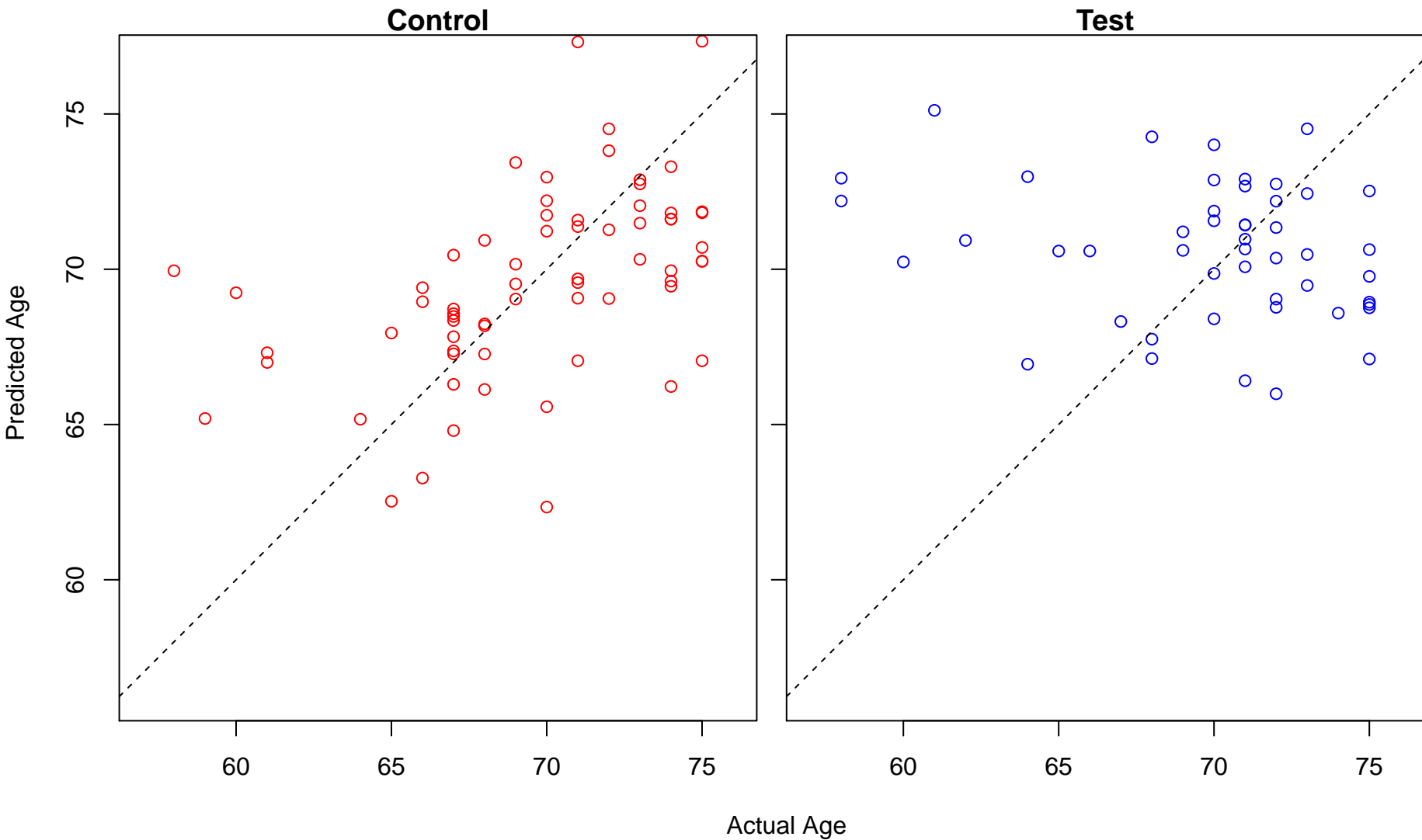


Test

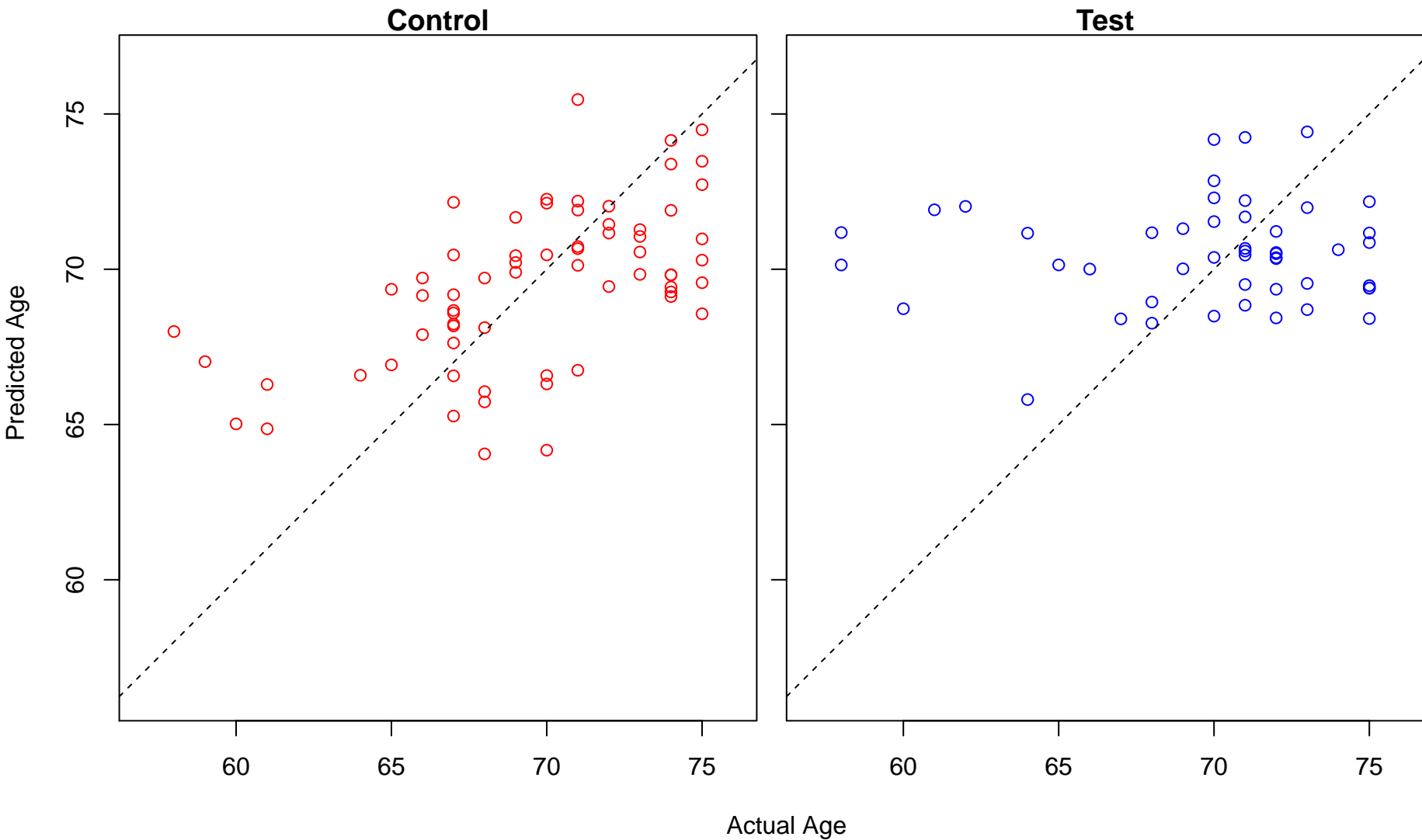


Actual Age

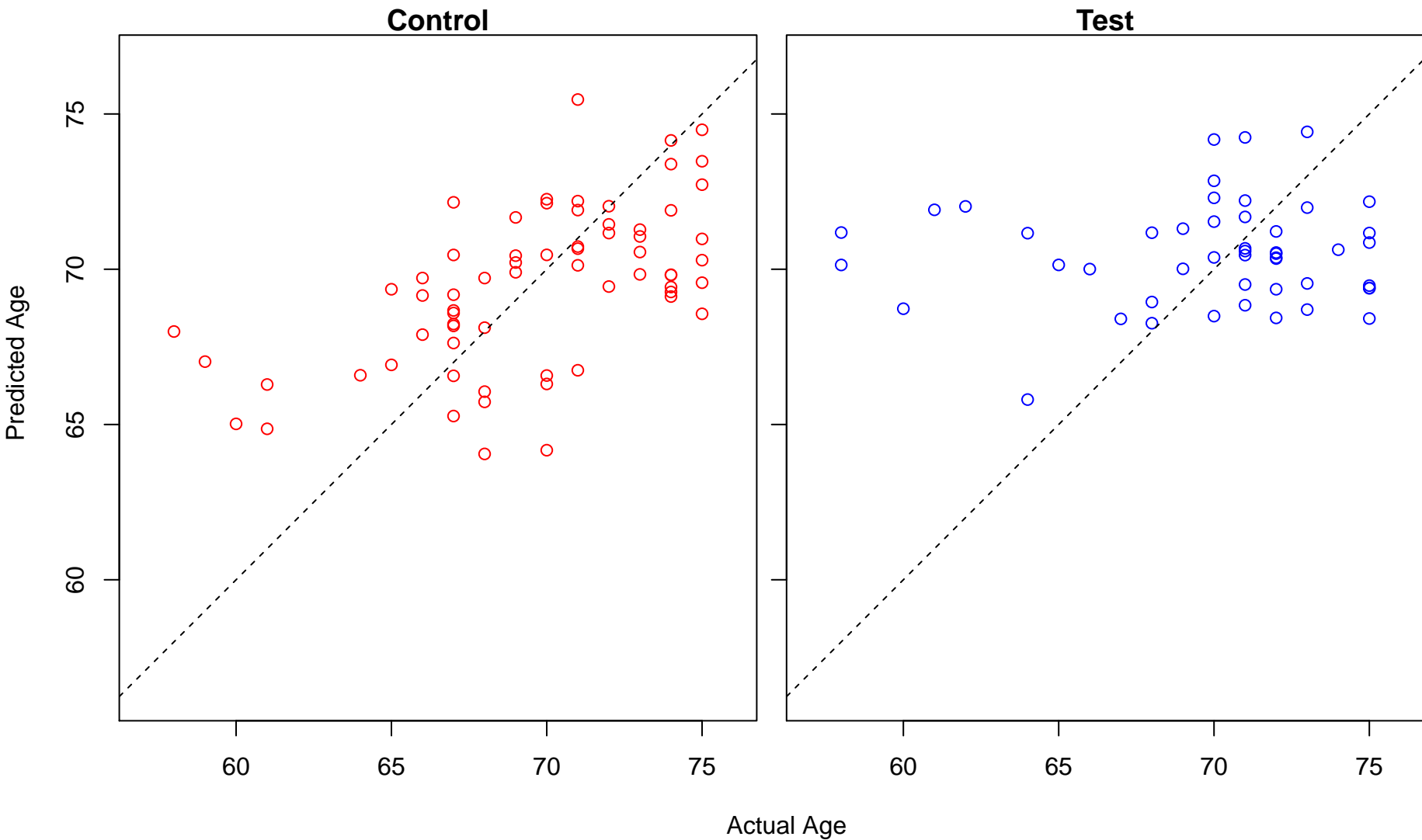
regulation of chemokine production (Score: 0.910044)



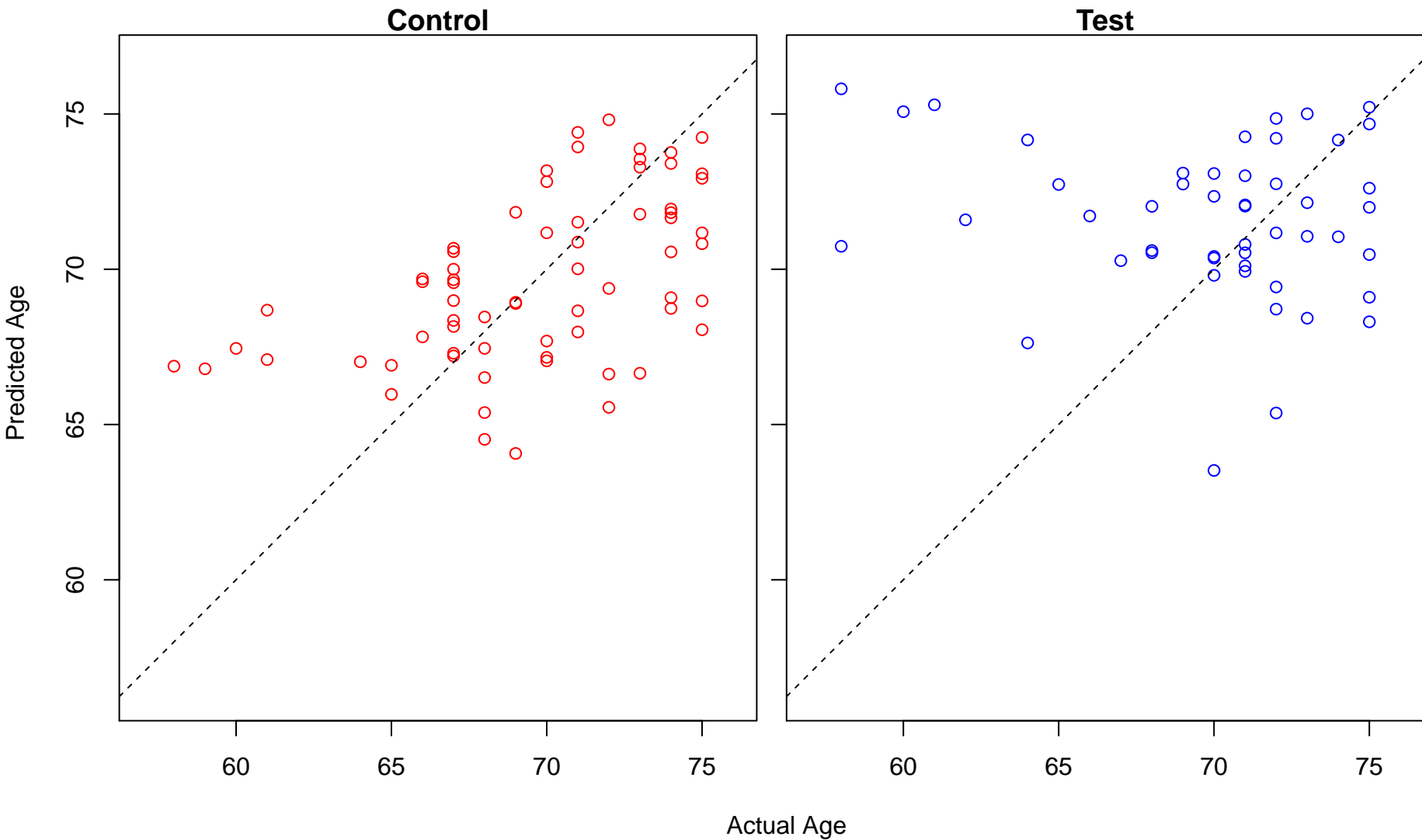
purine nucleoside diphosphate metabolic process (Score: 0.909757)



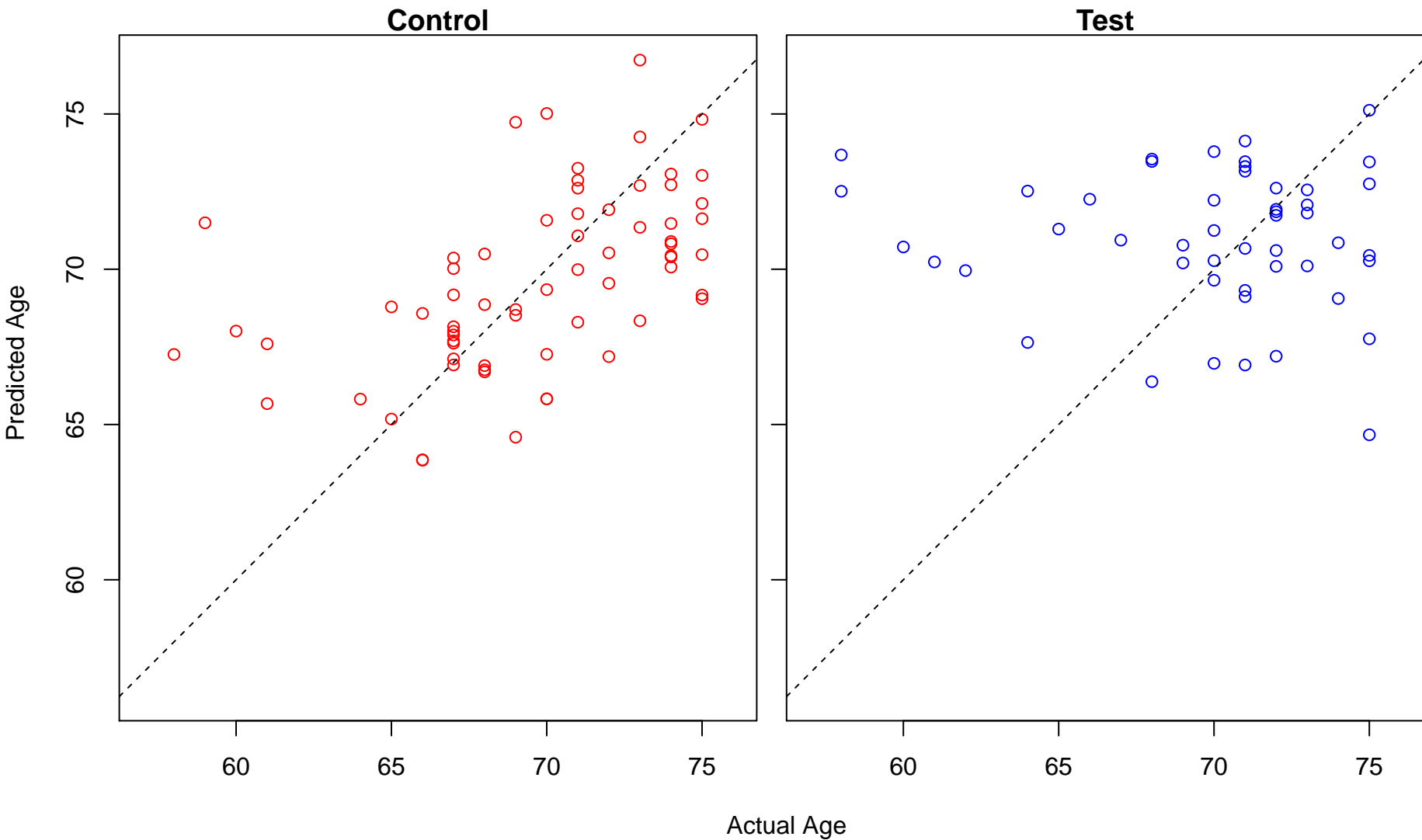
purine ribonucleoside diphosphate metabolic process (Score: 0.909757)



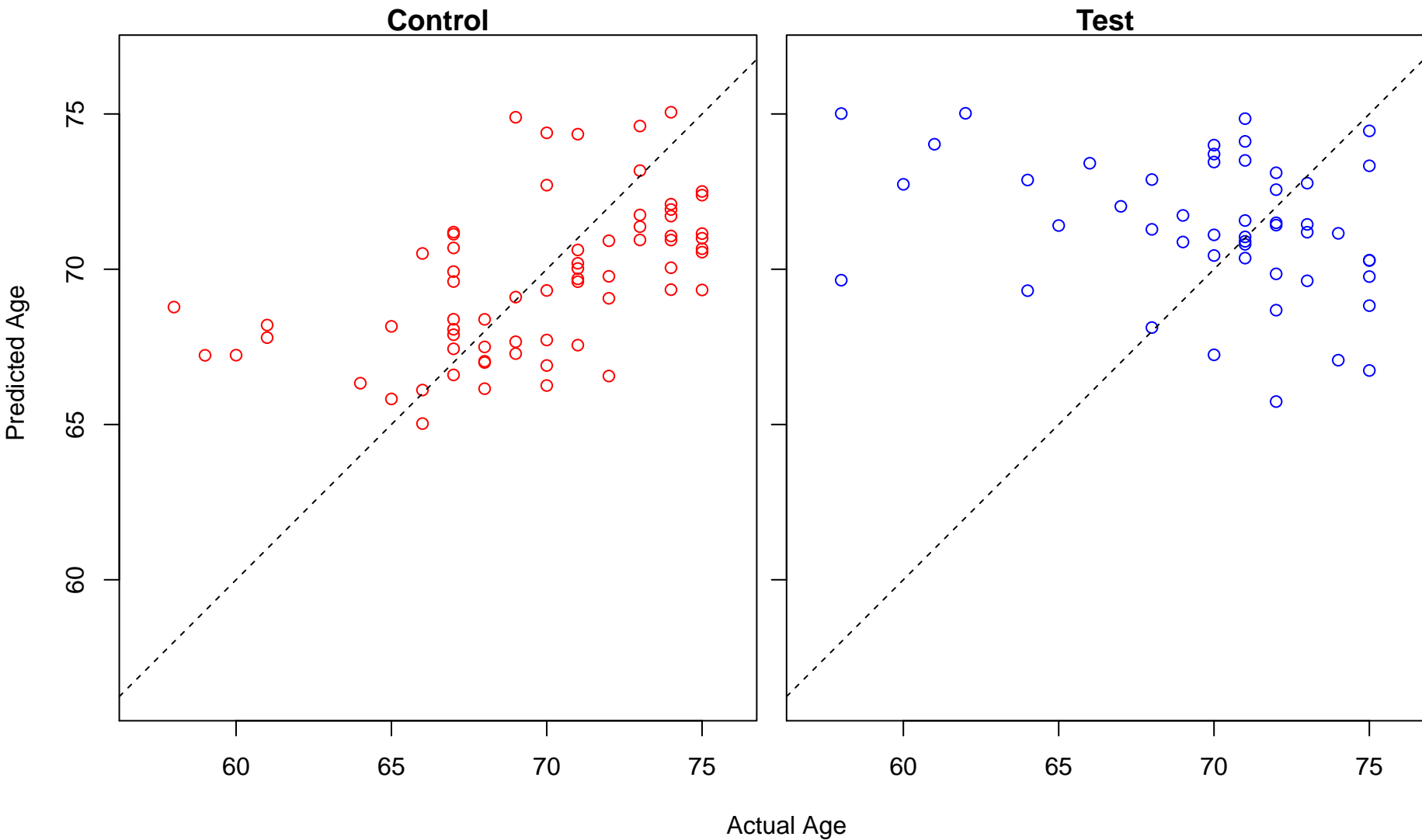
response to UV-A (Score: 0.909690)



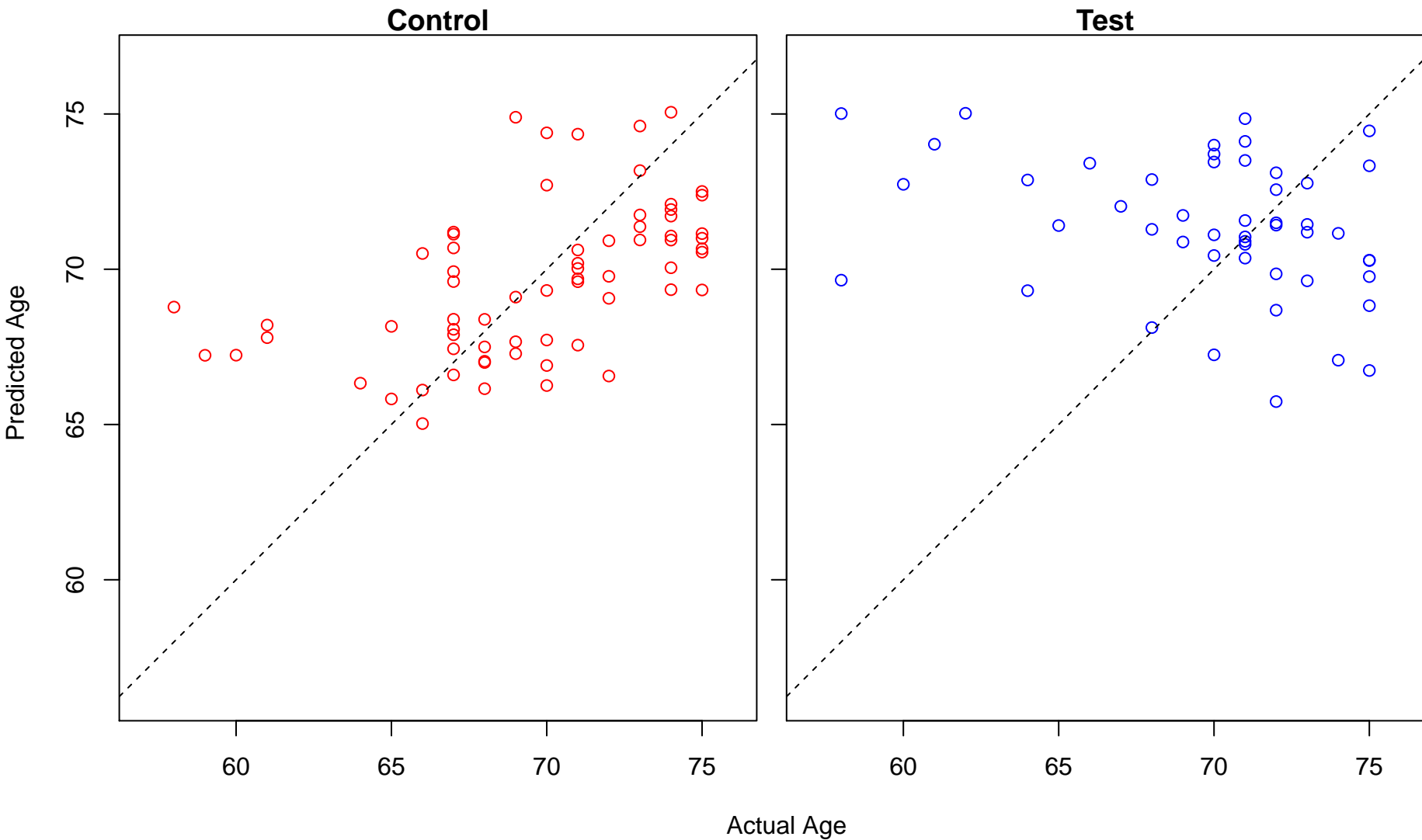
cerebral cortex development (Score: 0.909202)



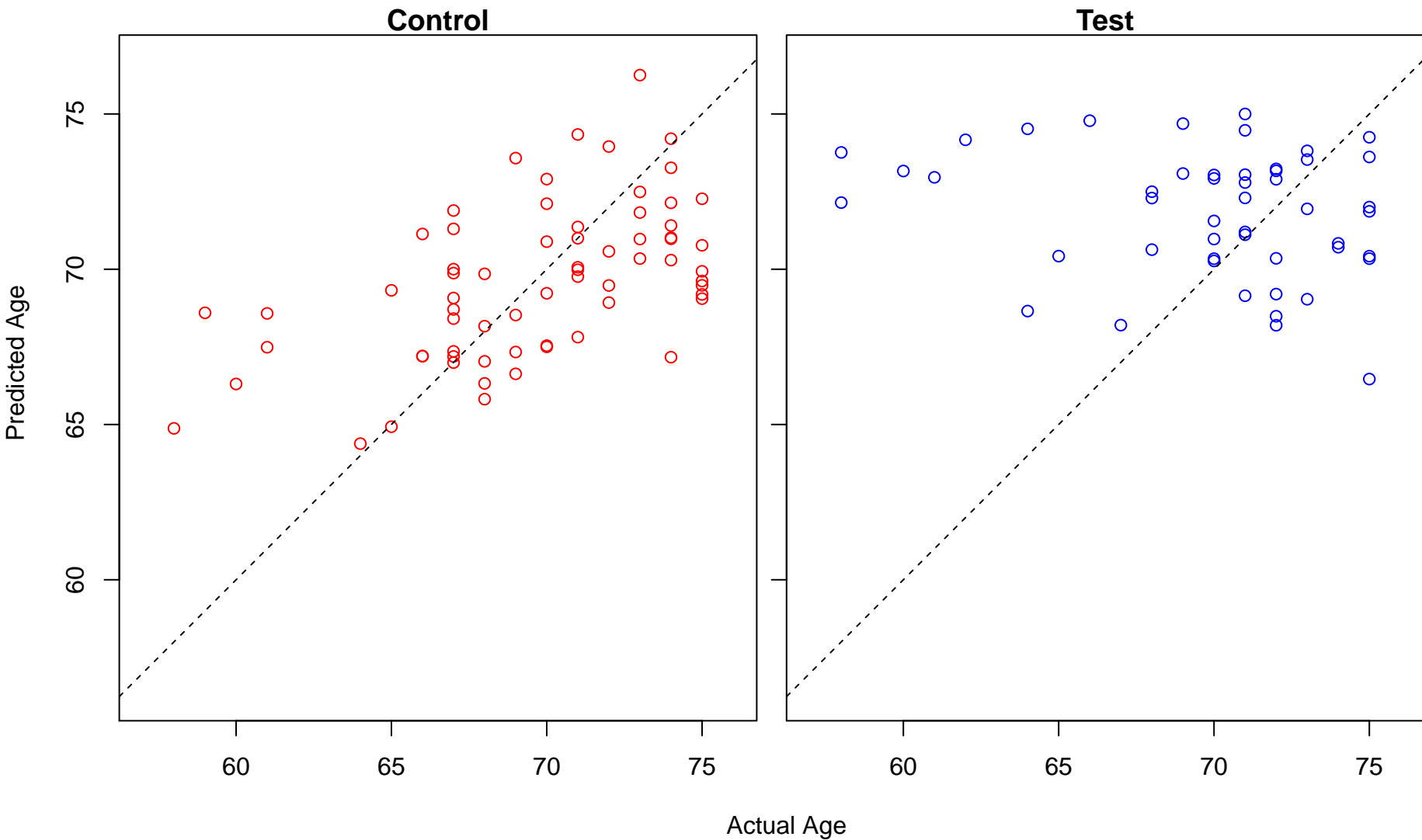
positive regulation of mast cell activation involved in immune response (Score: 0.909041)



positive regulation of mast cell degranulation (Score: 0.909041)

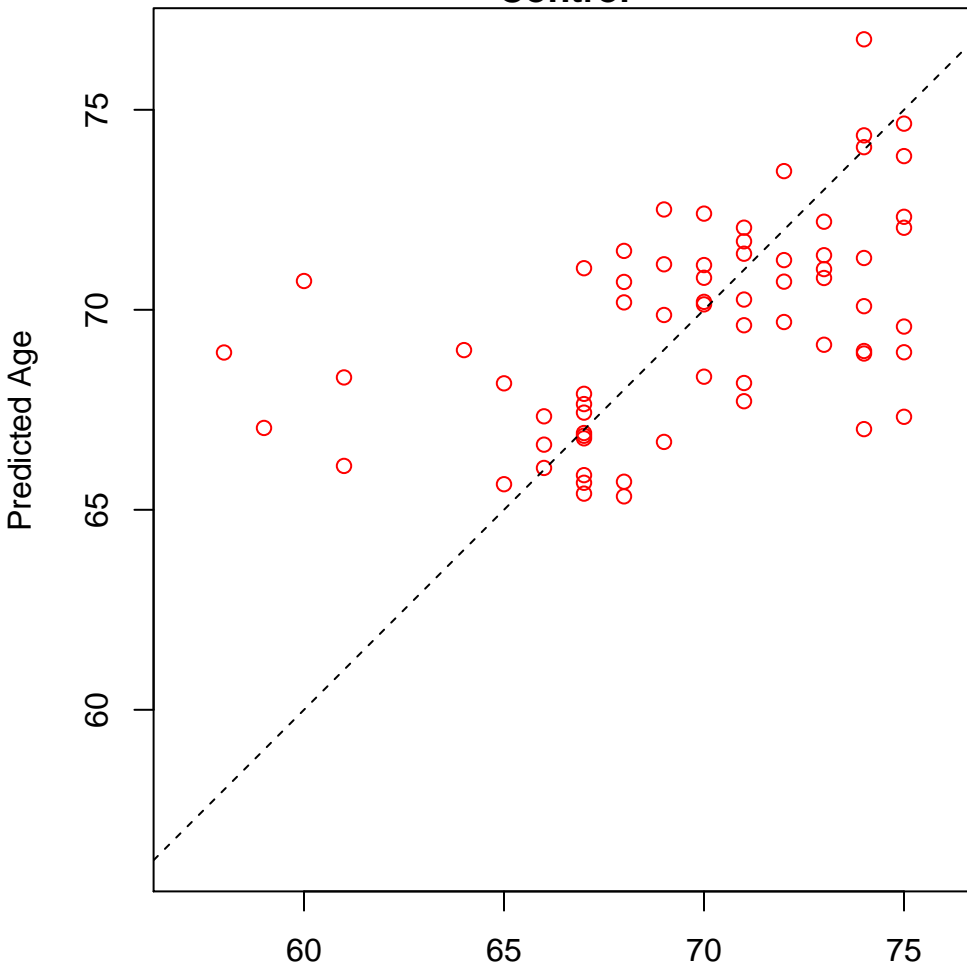


cardiac atrium development (Score: 0.908747)

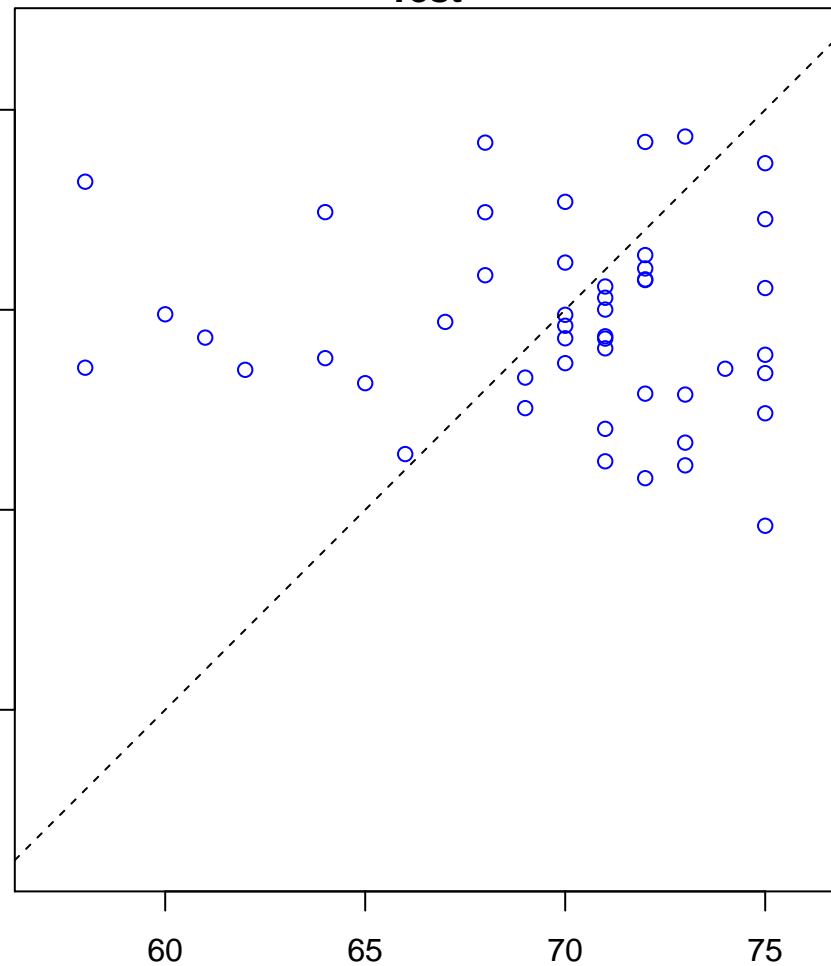


negative regulation of B cell proliferation (Score: 0.908597)

Control

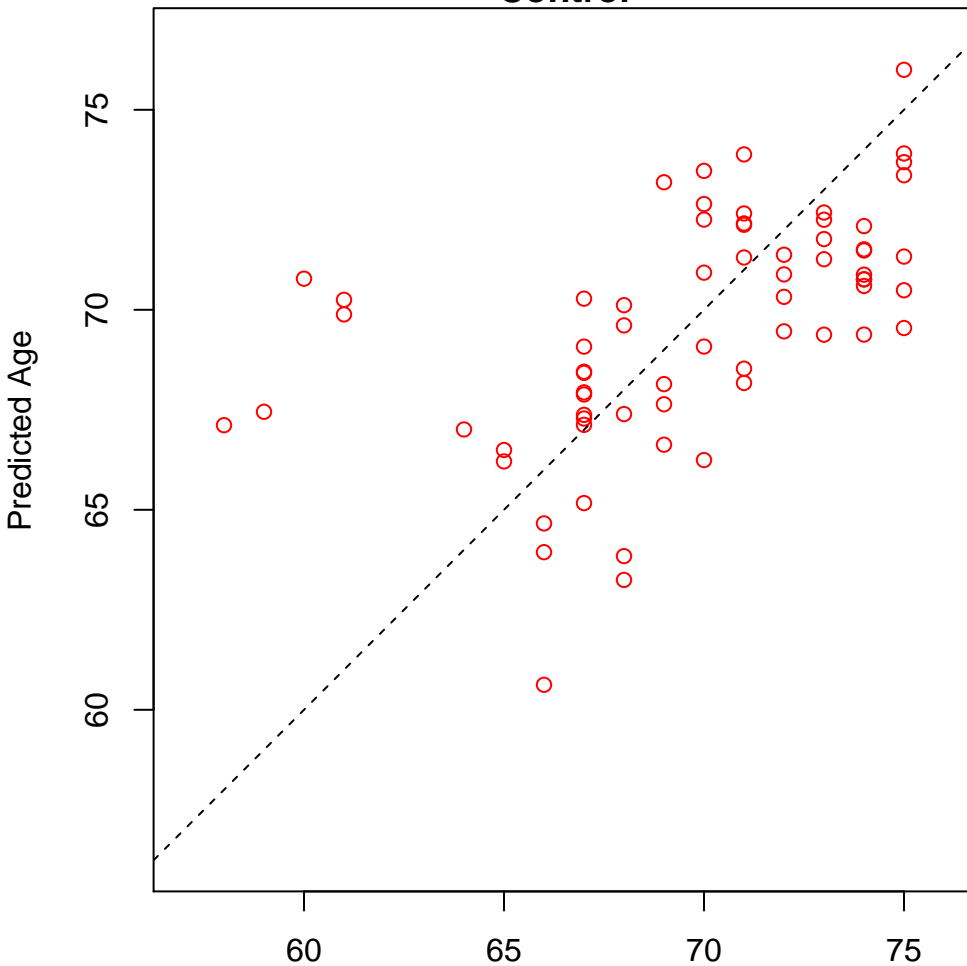


Test

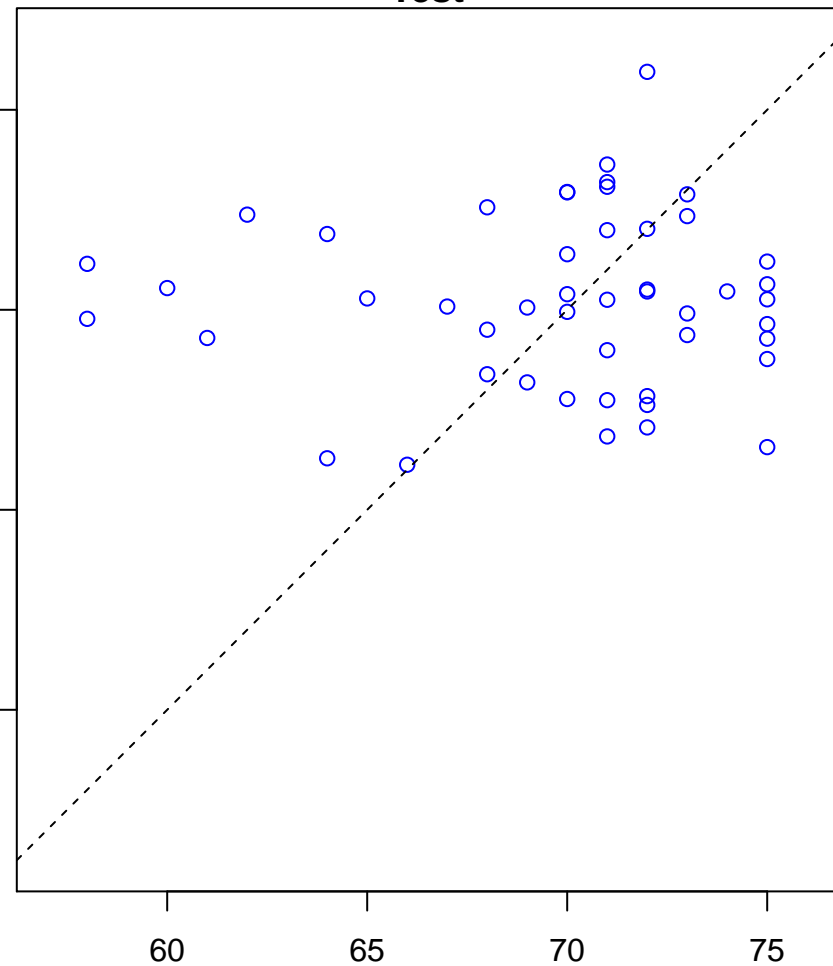


3'-UTR-mediated mRNA stabilization (Score: 0.908494)

Control

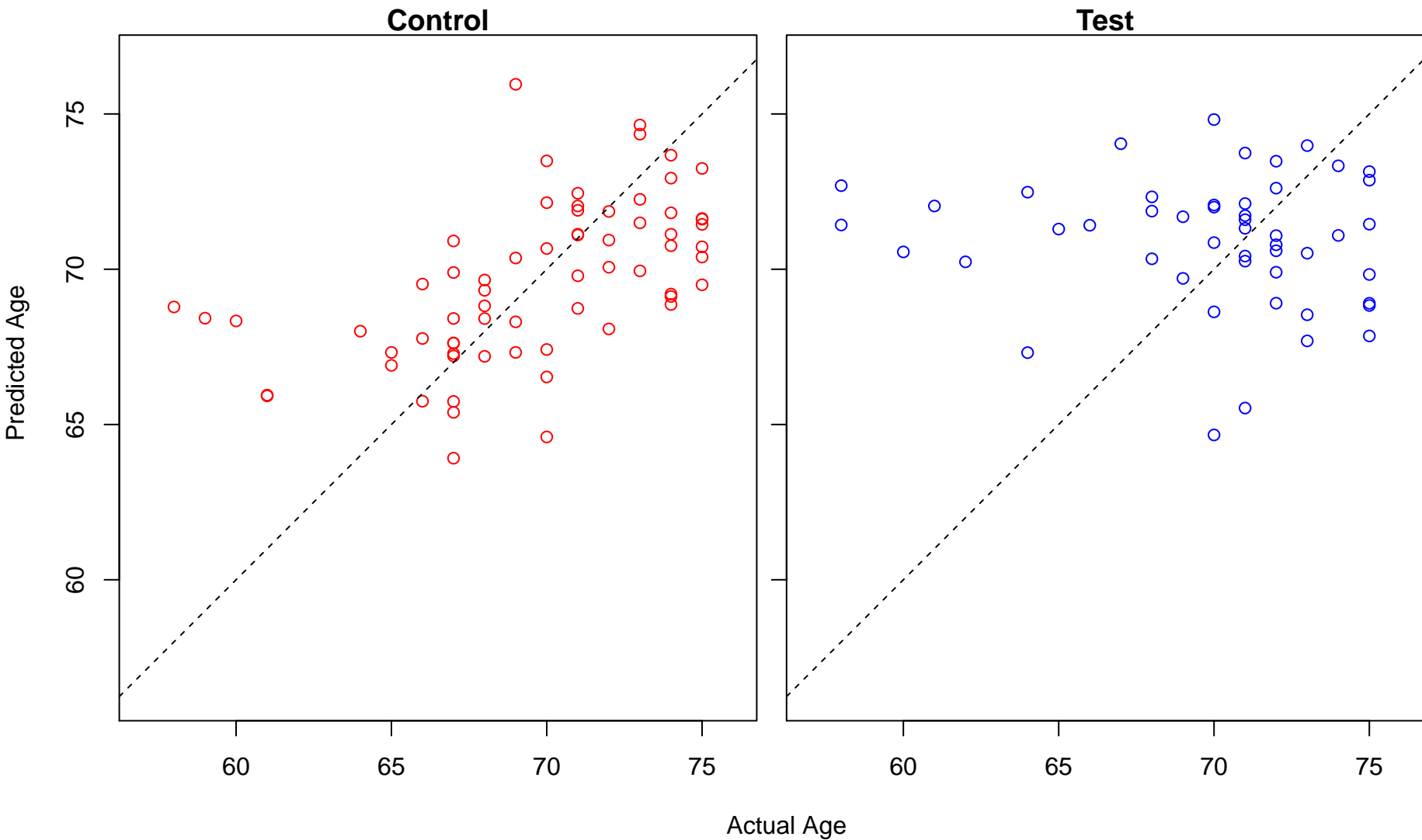


Test

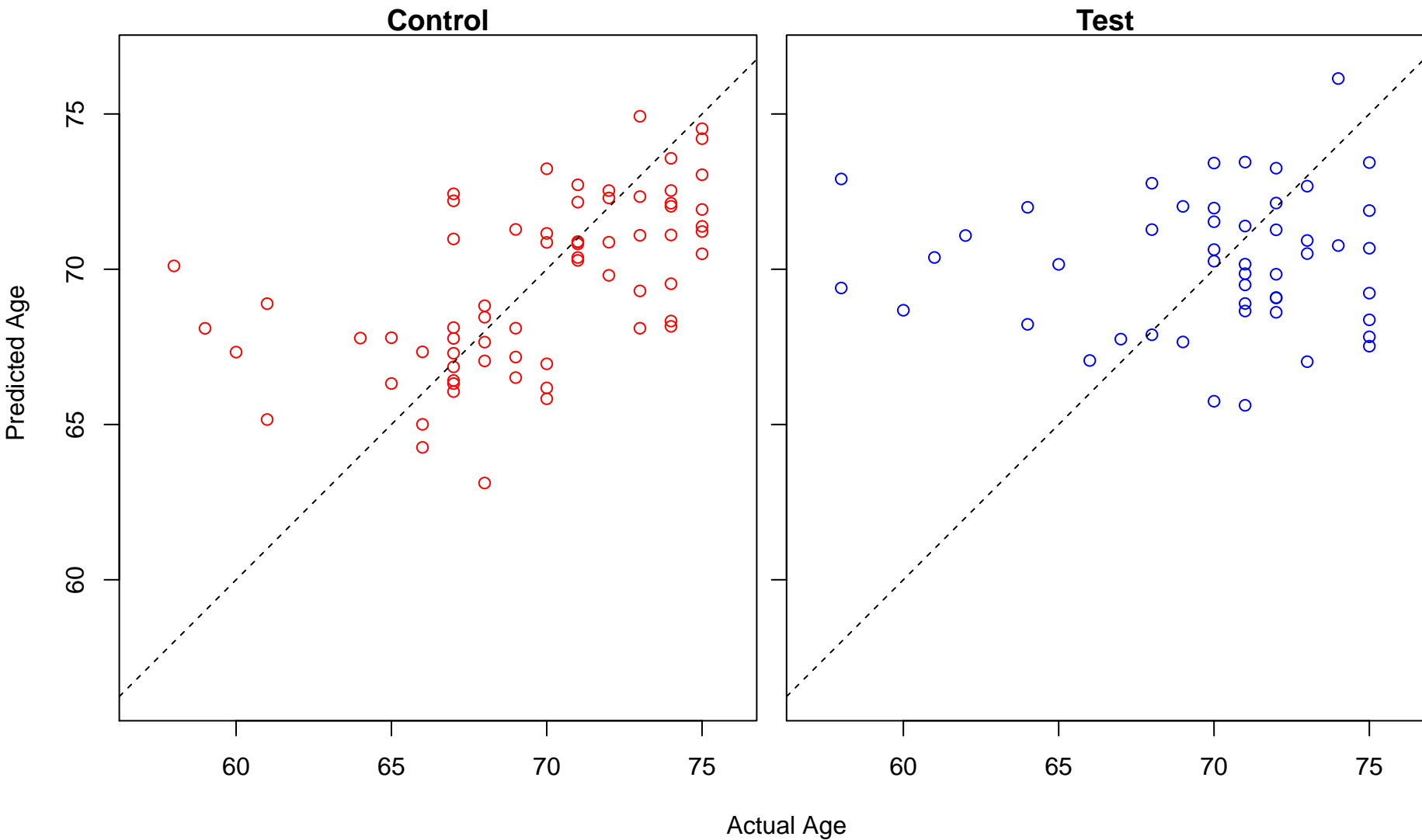


Actual Age

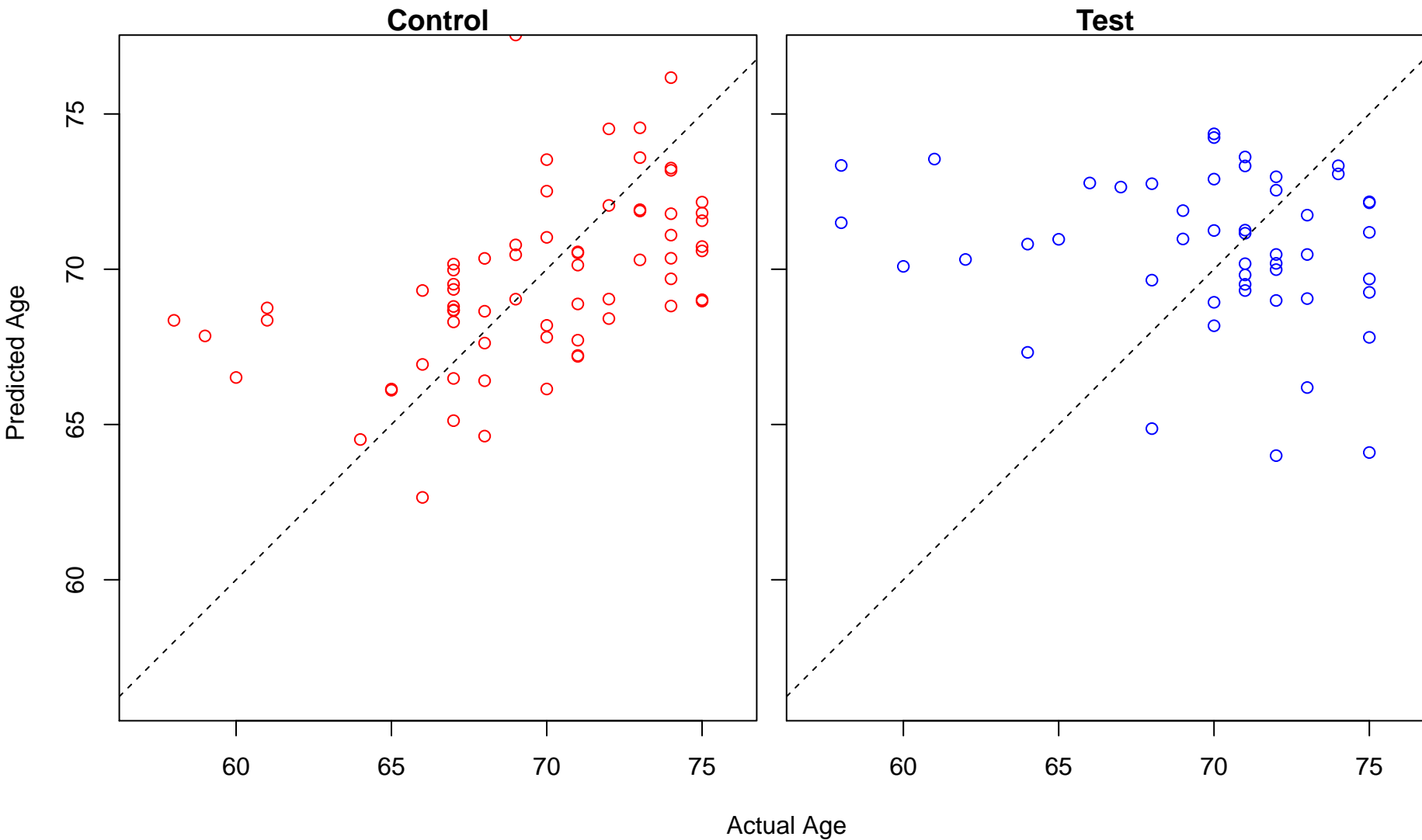
tetrahydrofolate metabolic process (Score: 0.908426)



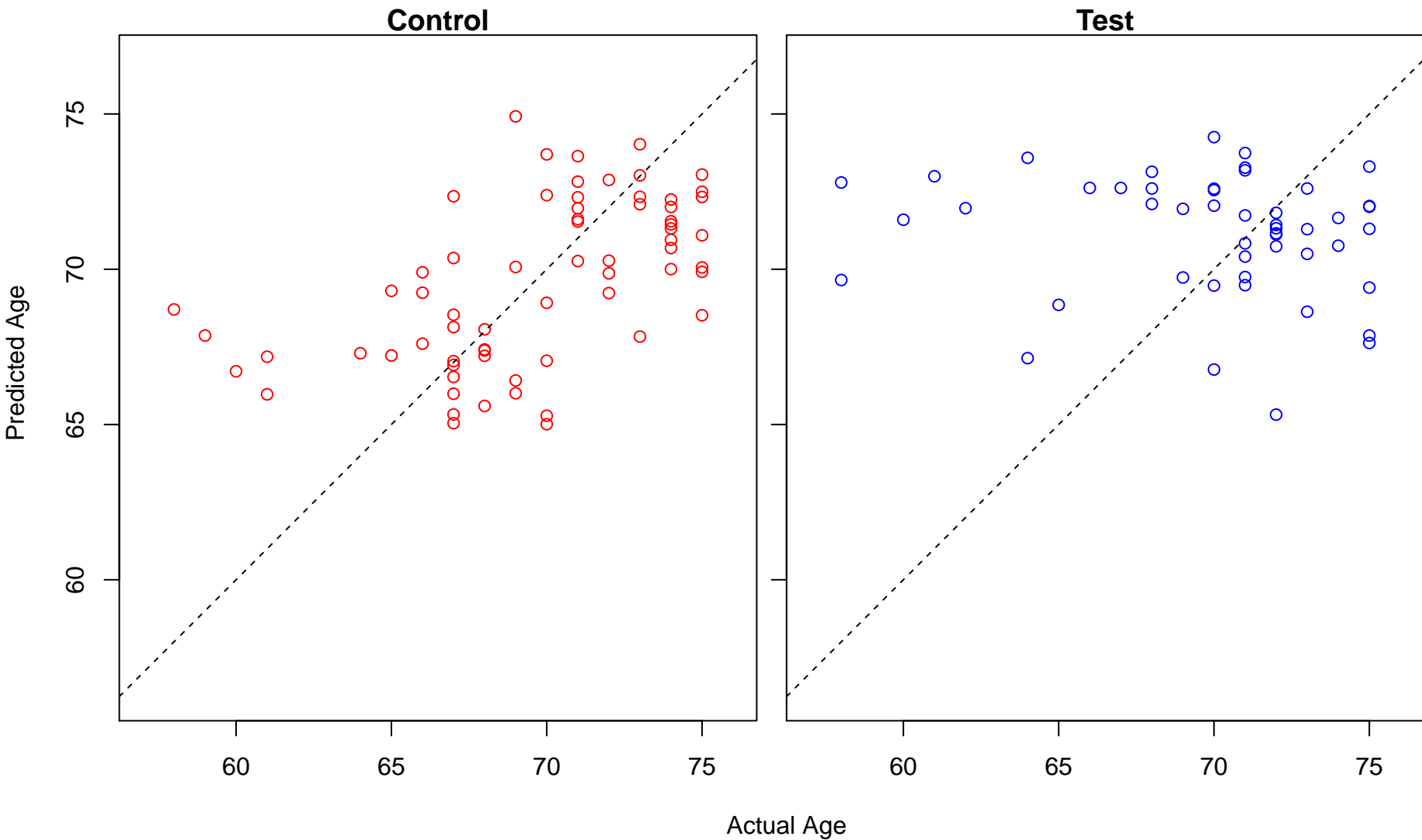
regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway (Score: 0.90815)



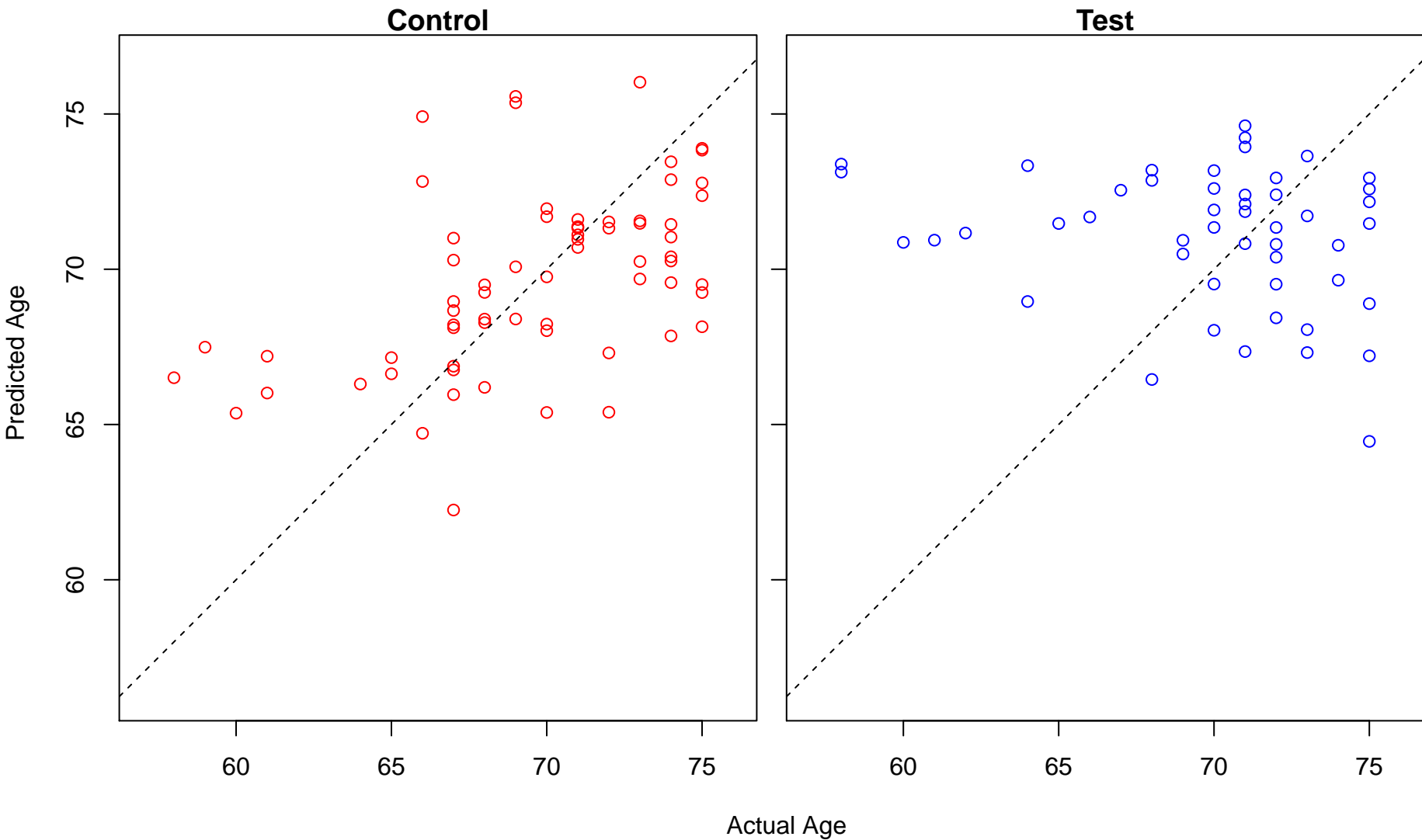
positive regulation of T cell mediated immunity (Score: 0.907822)



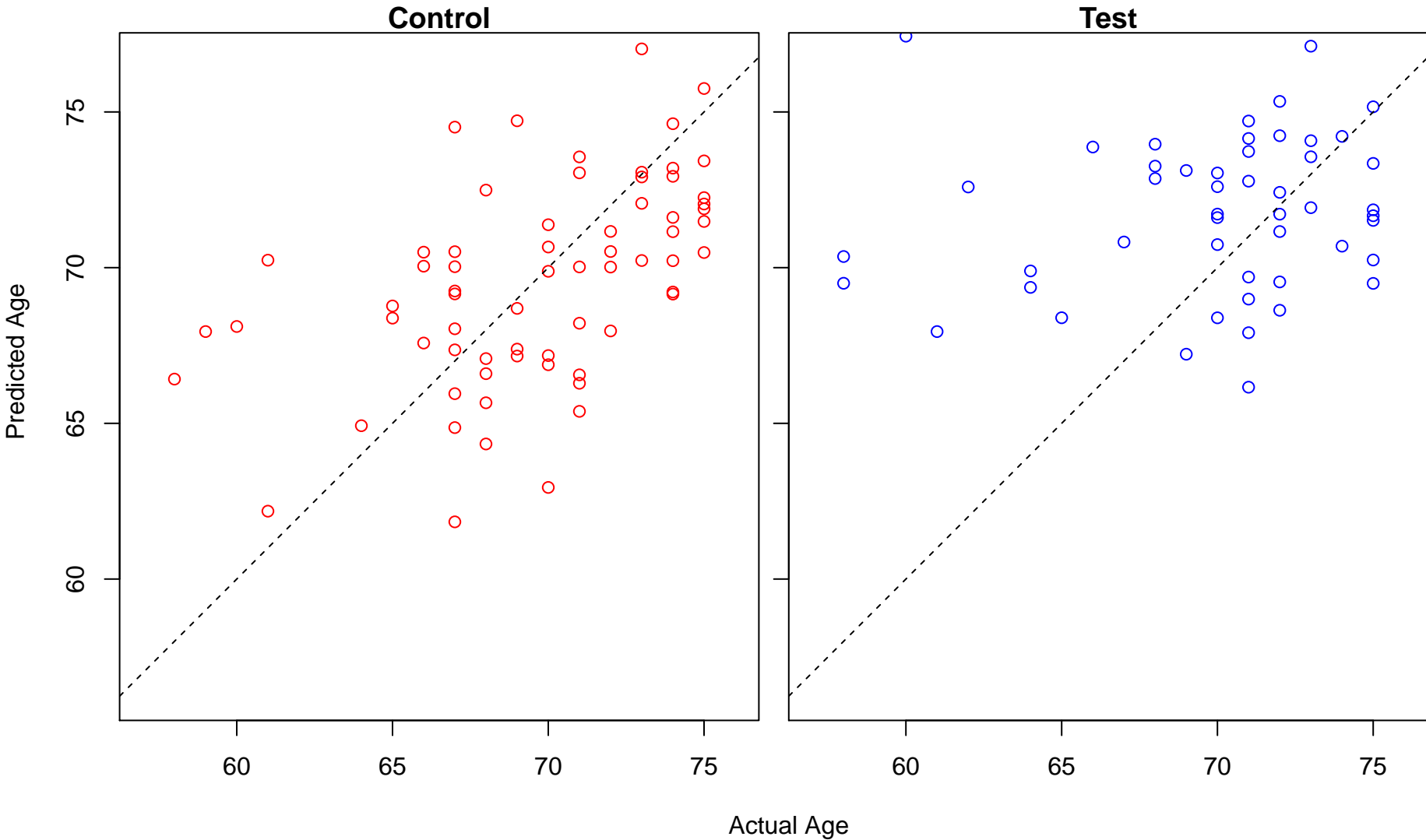
apoptotic DNA fragmentation (Score: 0.907774)



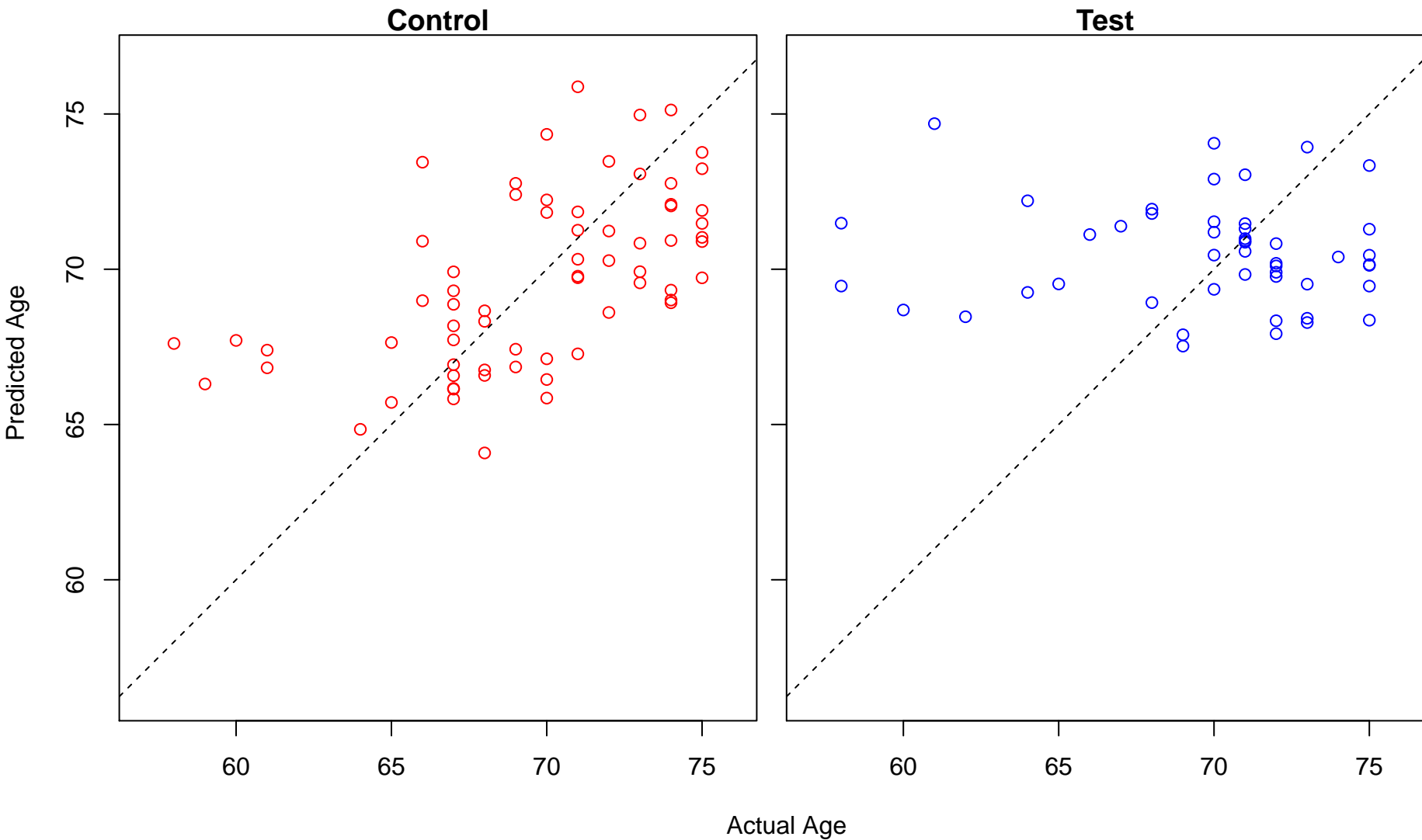
regulation of protein complex stability (Score: 0.907289)



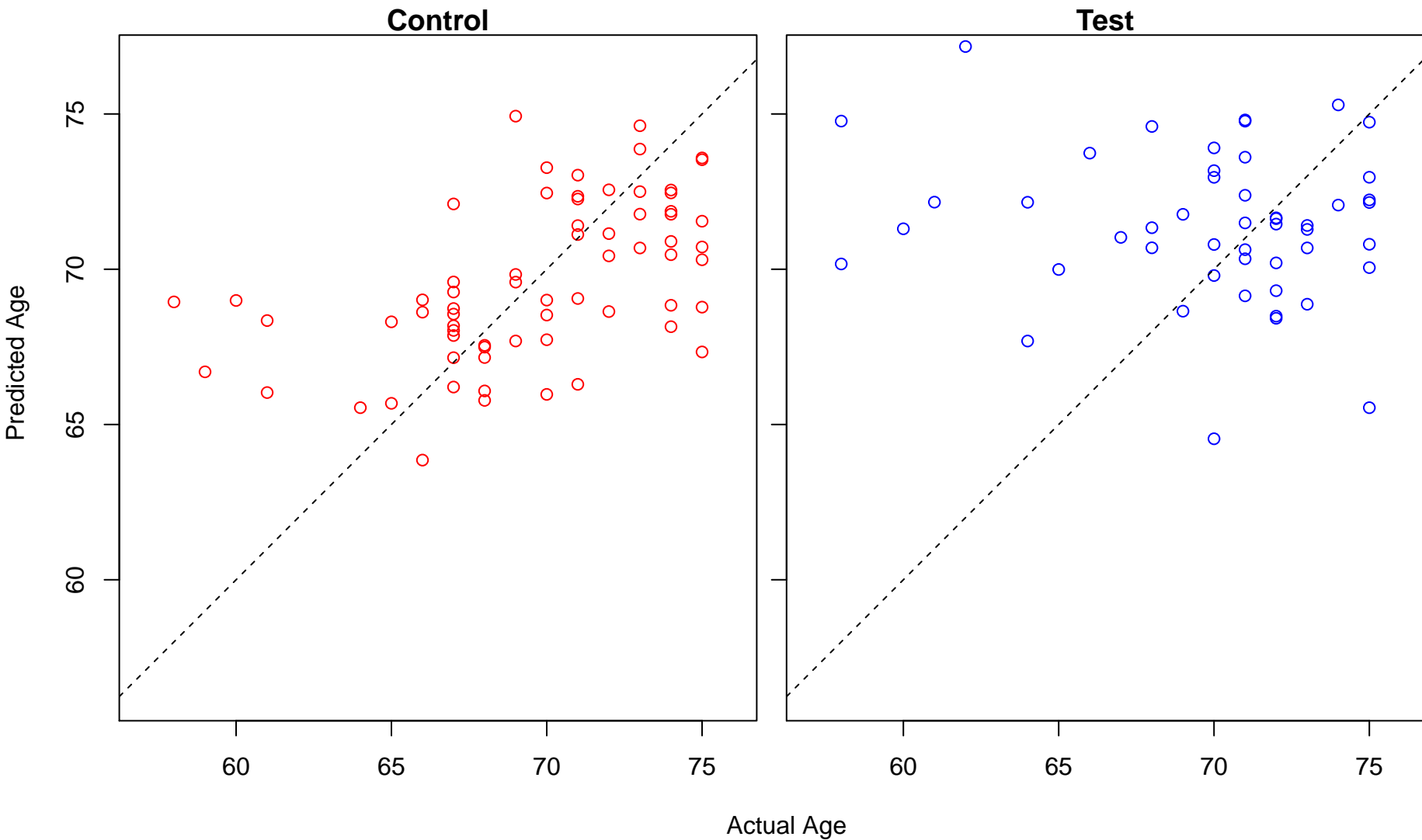
aromatic amino acid family metabolic process (Score: 0.907122)



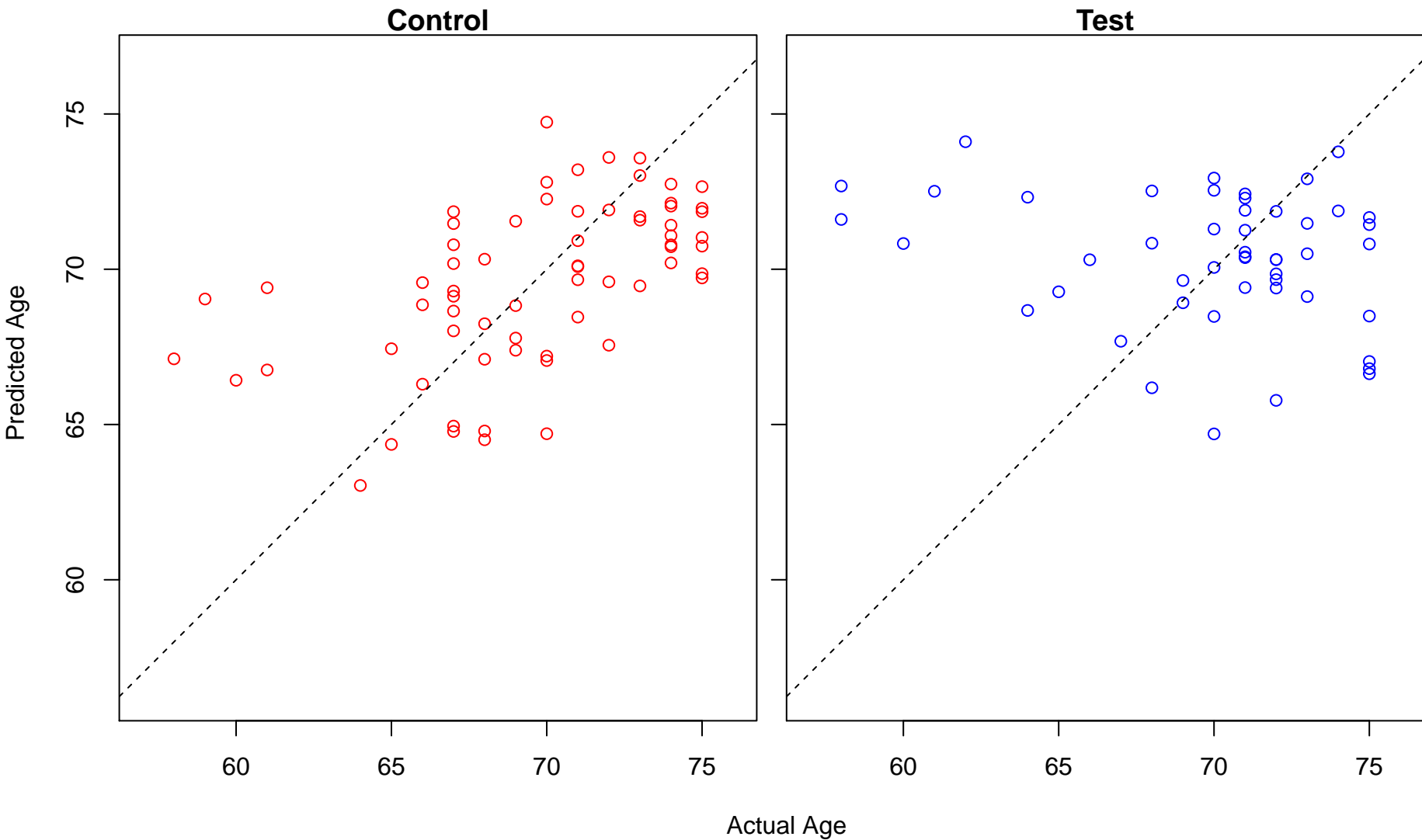
DNA demethylation (Score: 0.906798)



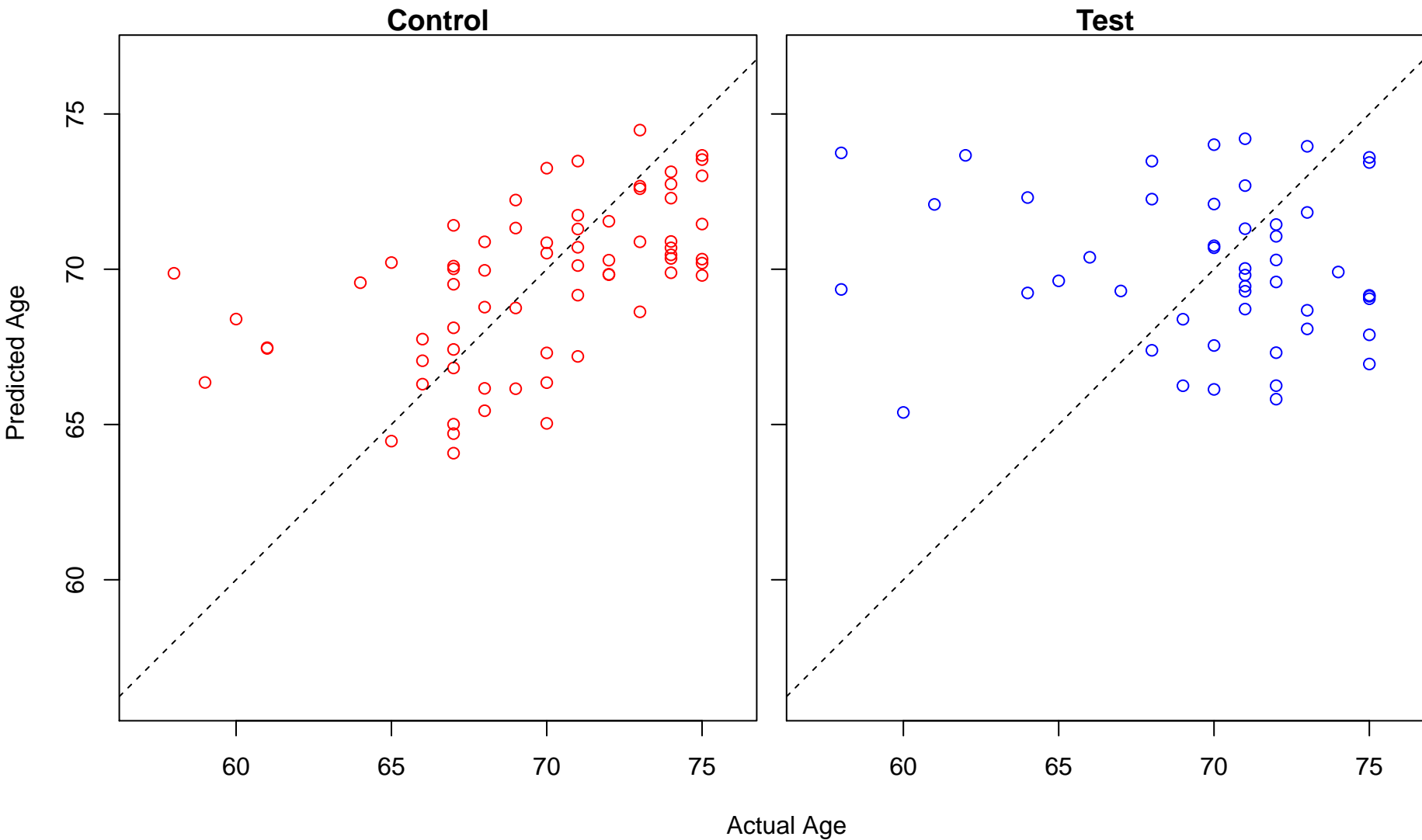
modulation by host of viral genome replication (Score: 0.906690)



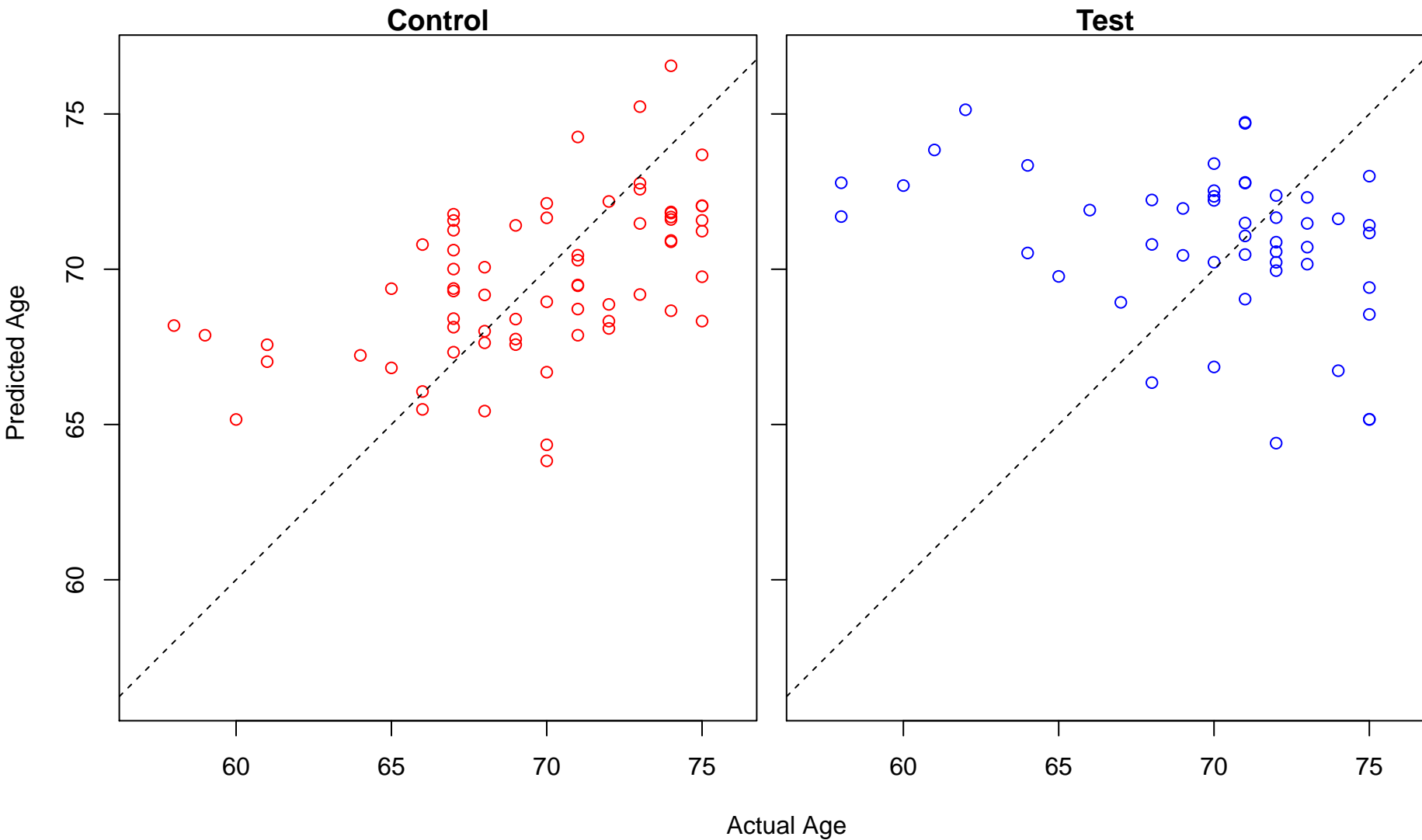
protein deglycosylation (Score: 0.906675)



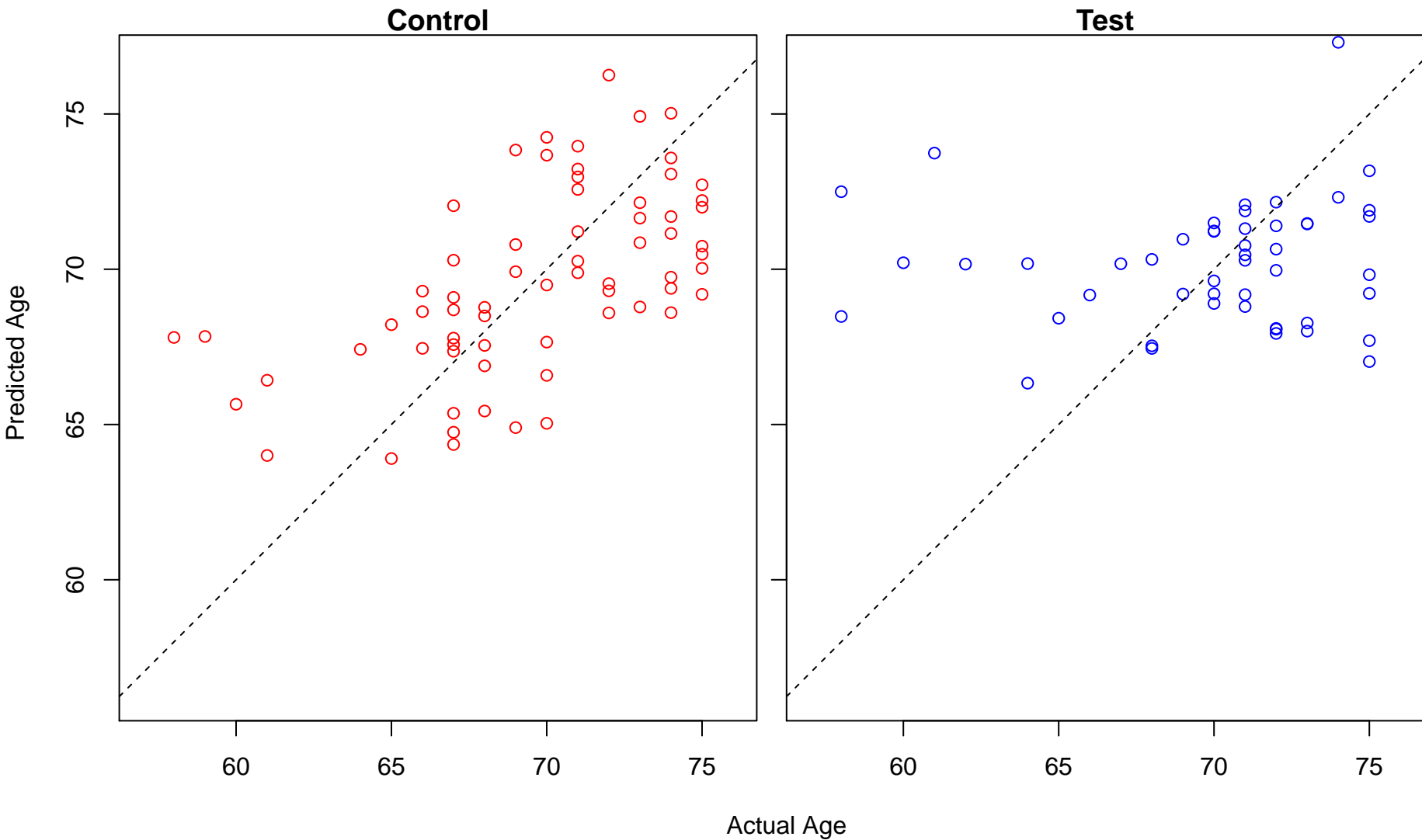
regulation of ryanodine-sensitive calcium-release channel activity (Score: 0.906550)



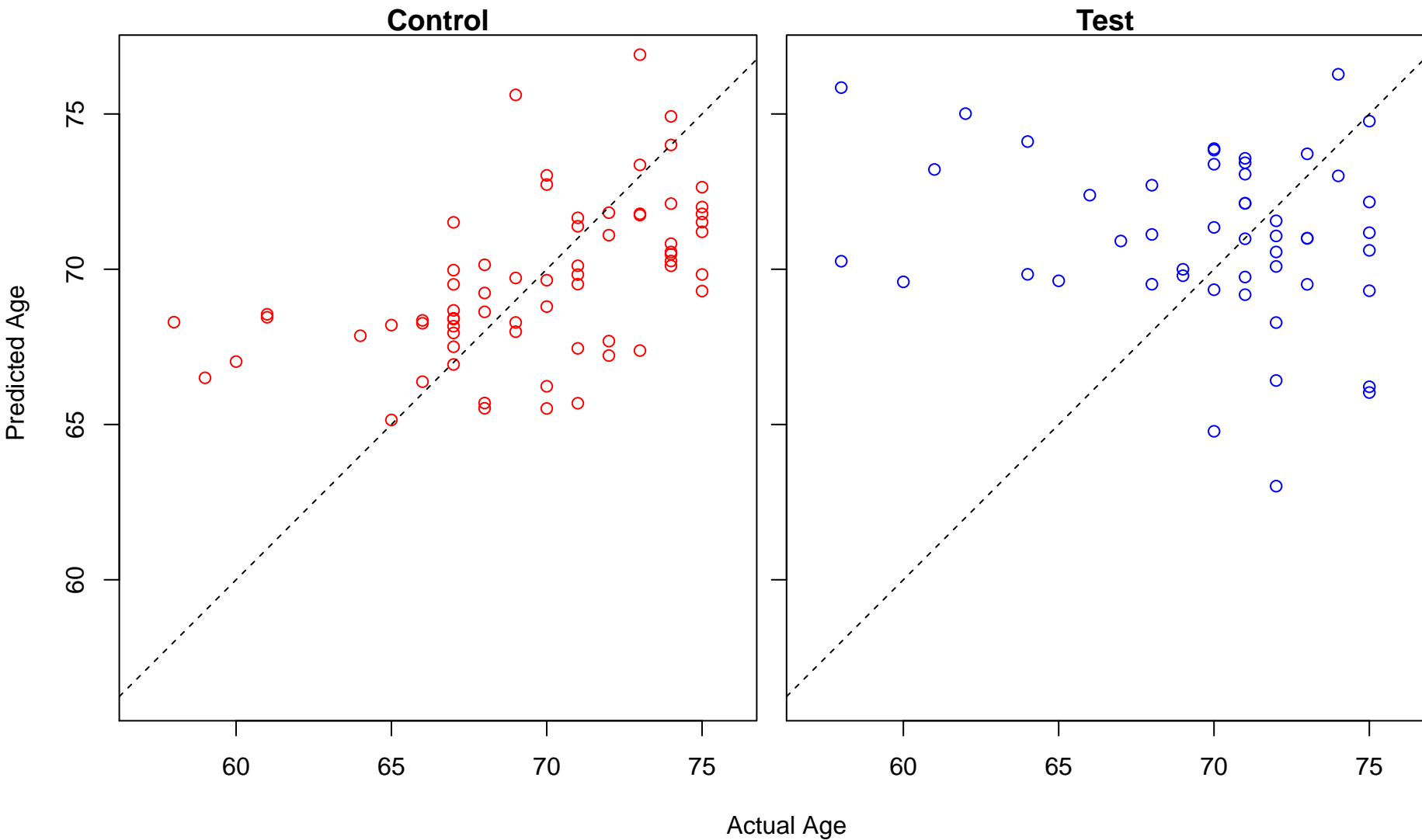
response to redox state (Score: 0.906287)



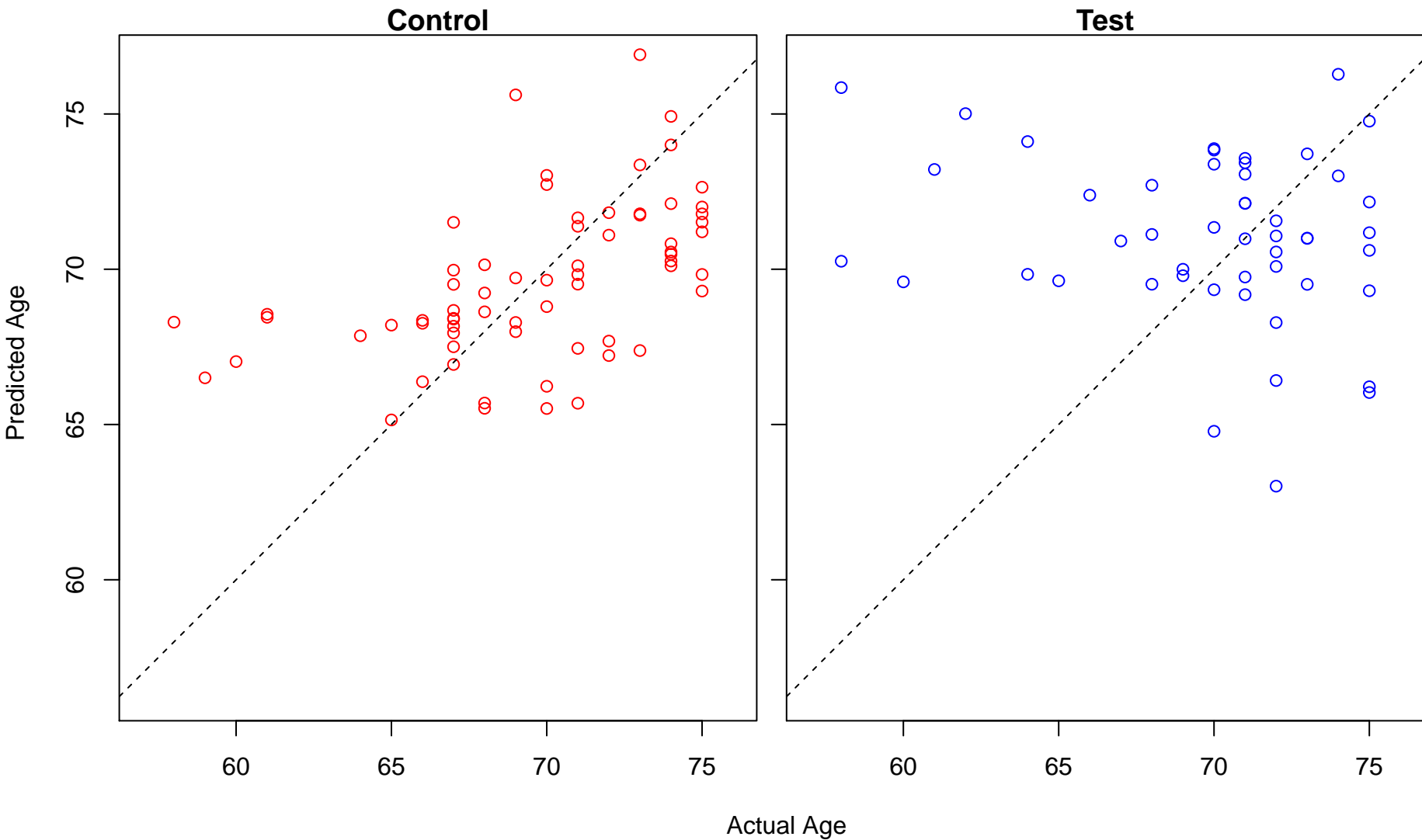
in utero embryonic development (Score: 0.906220)



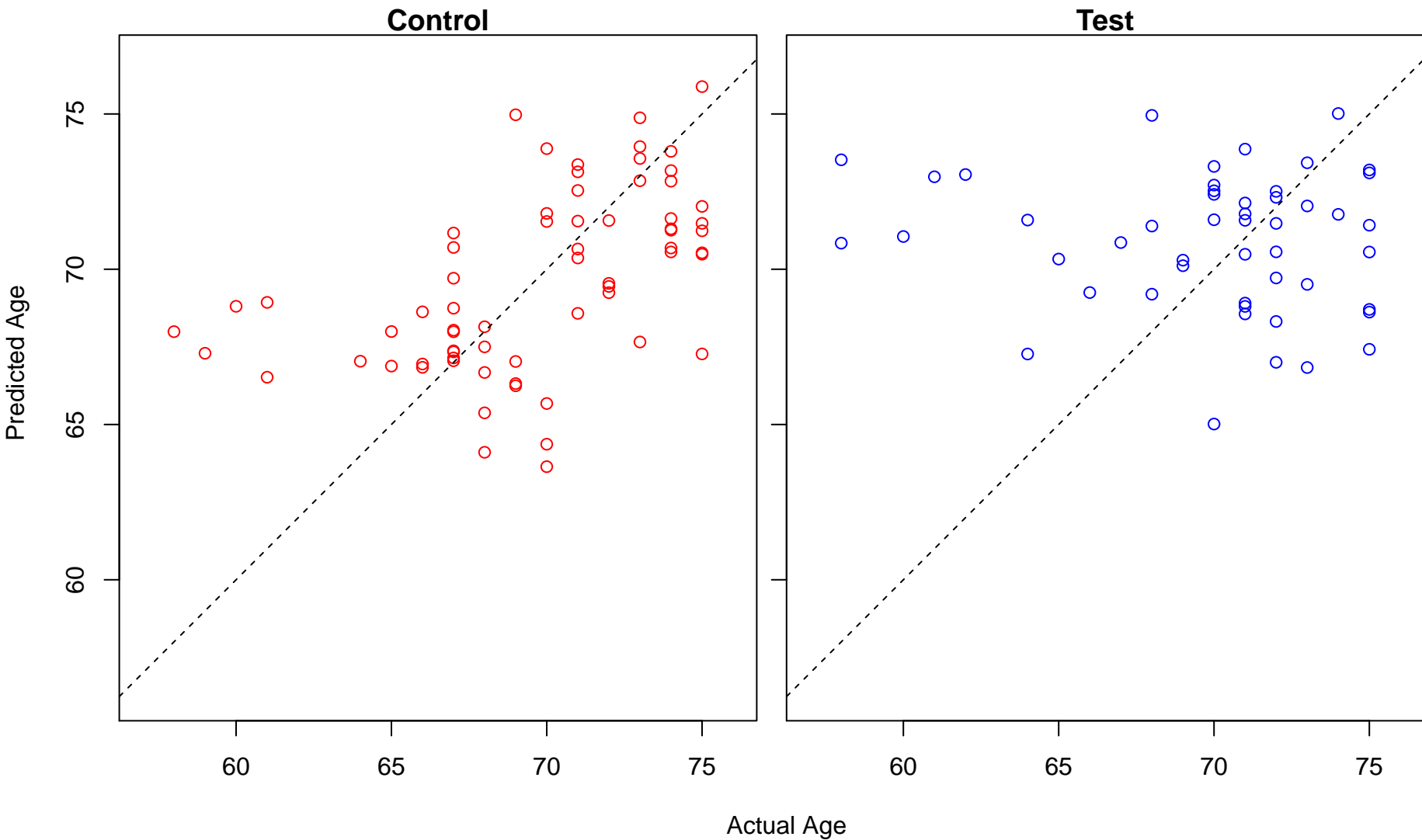
negative regulation of calcium ion transmembrane transporter activity (Score: 0.906192)



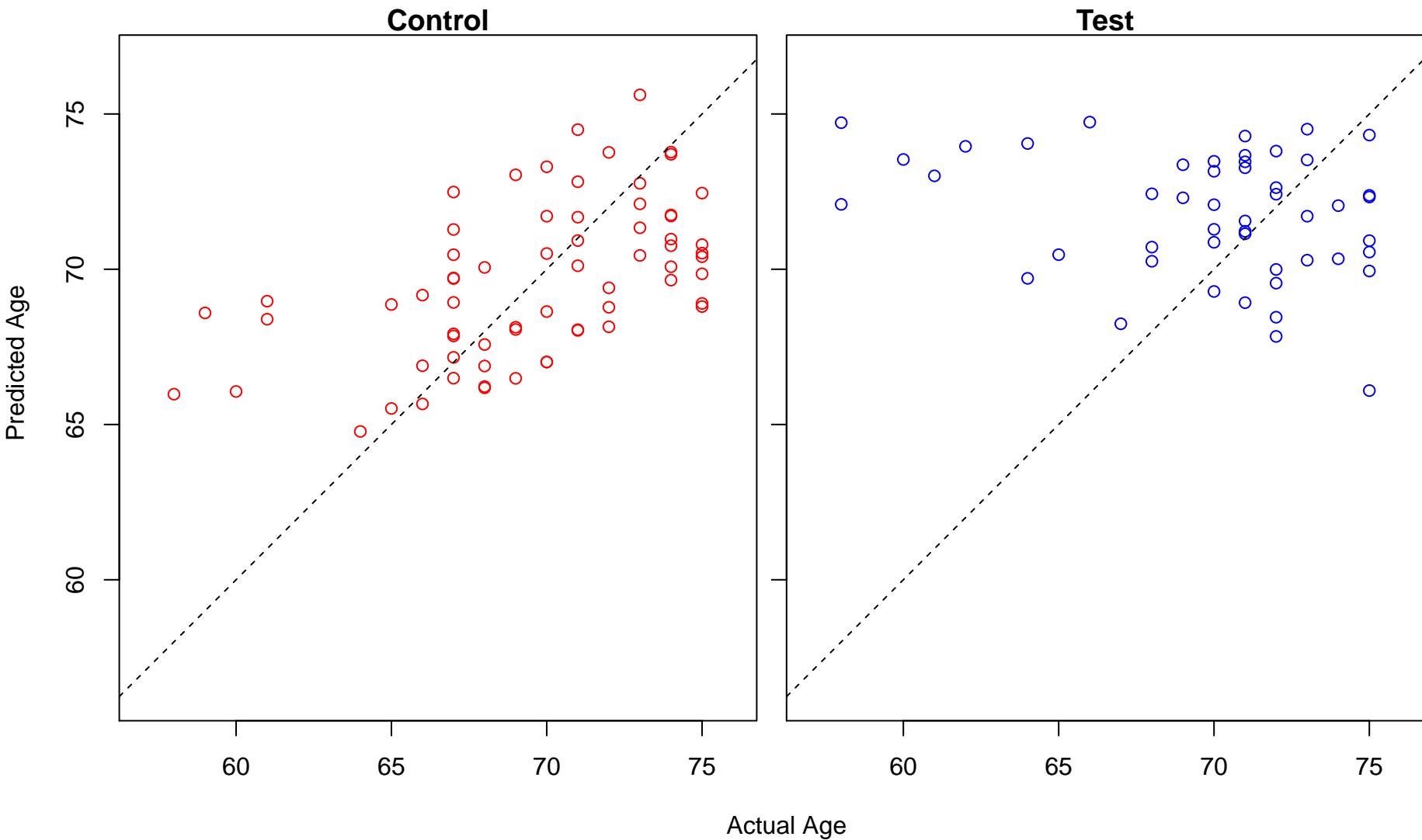
negative regulation of calcium ion transmembrane transport (Score: 0.906192)



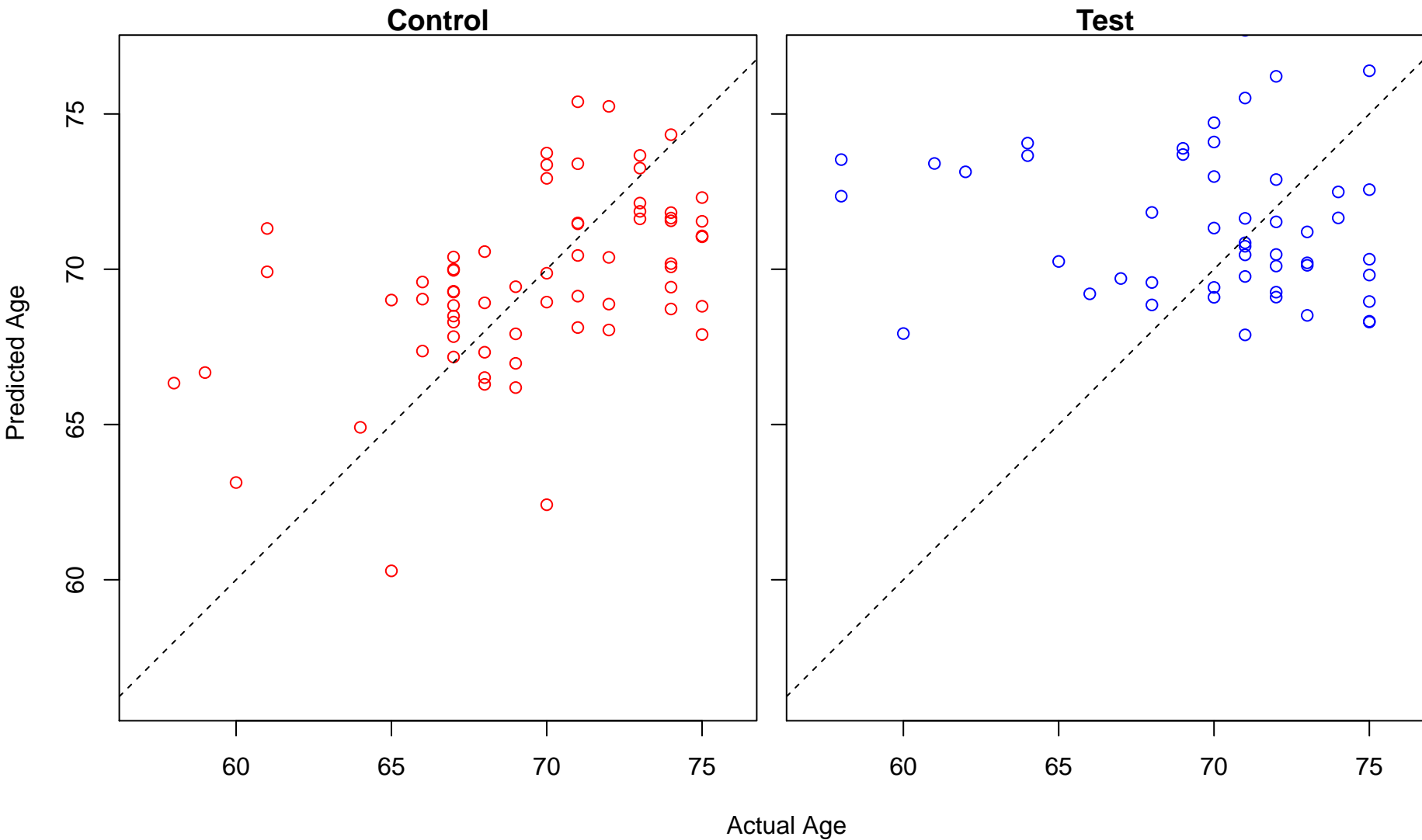
regulation of establishment of protein localization to plasma membrane (Score: 0.906154)



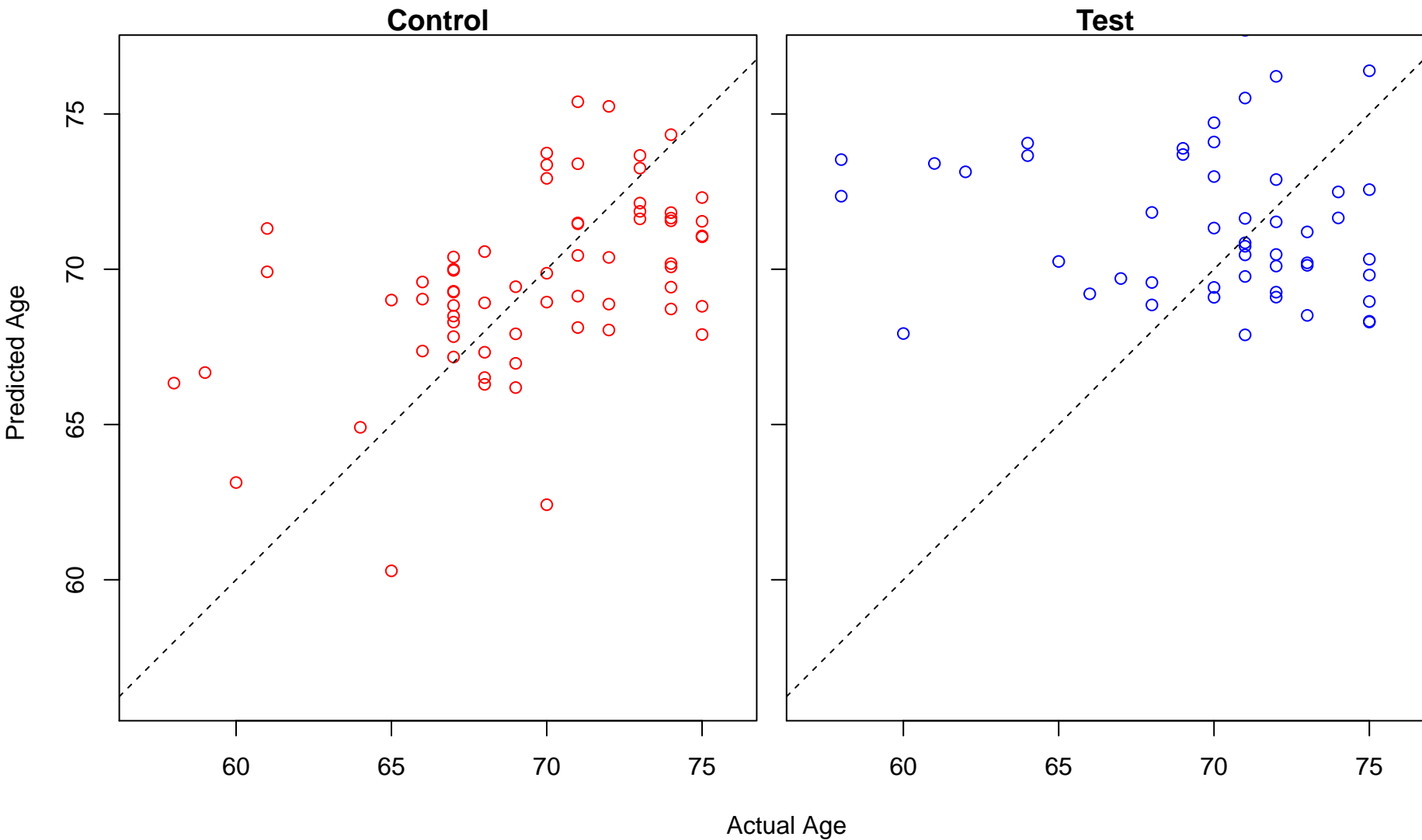
artery morphogenesis (Score: 0.905933)



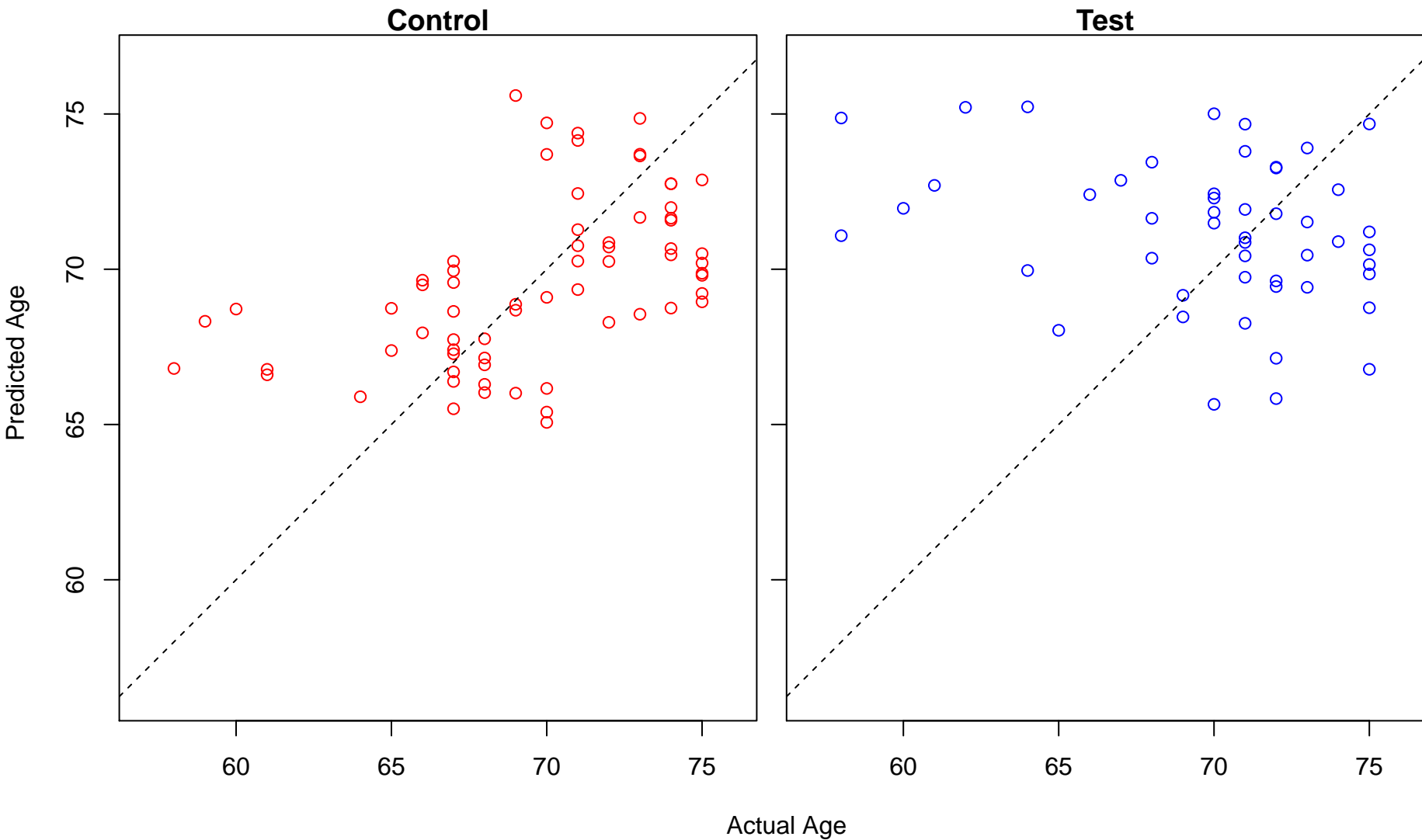
response to protozoan (Score: 0.904949)



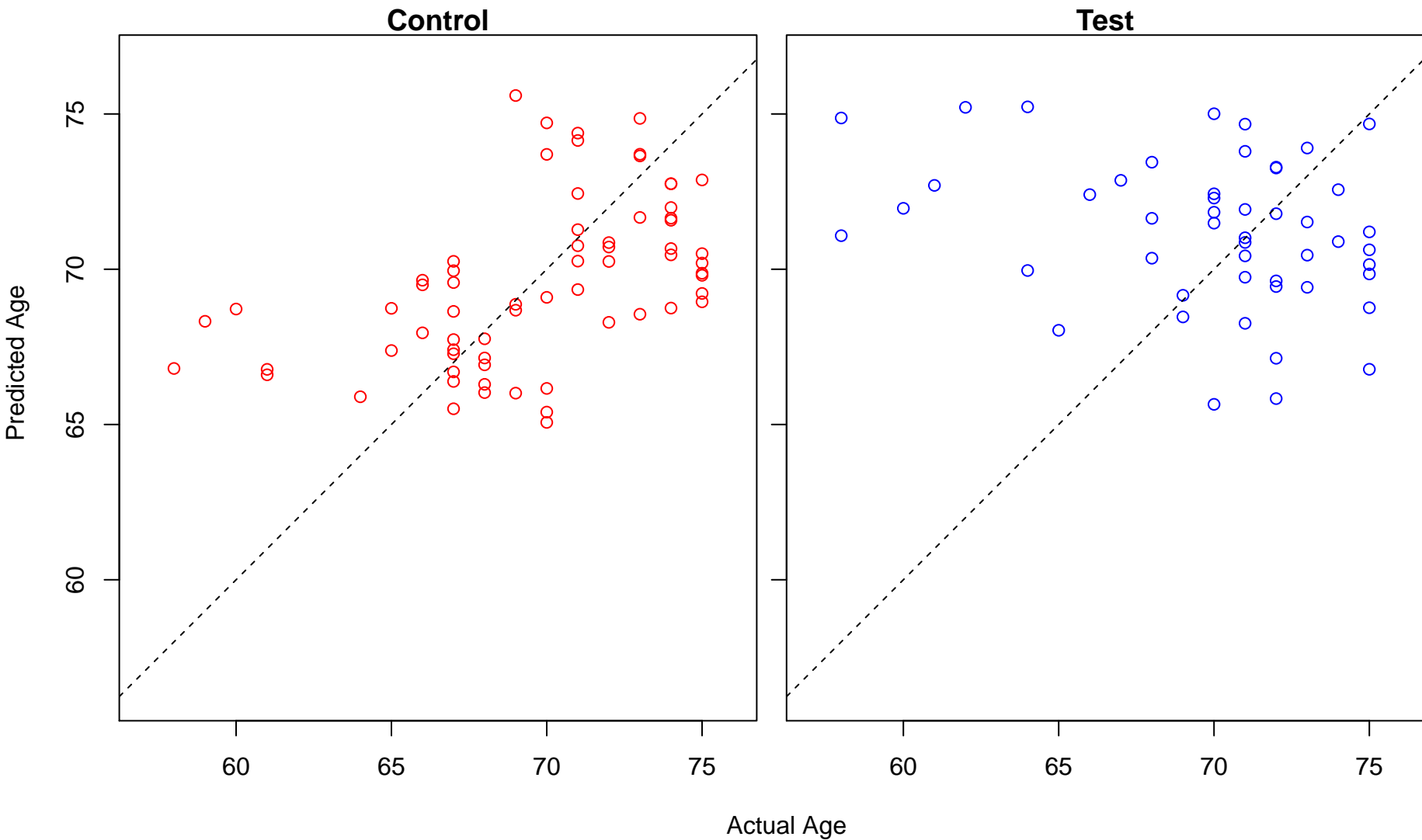
defense response to protozoan (Score: 0.904949)



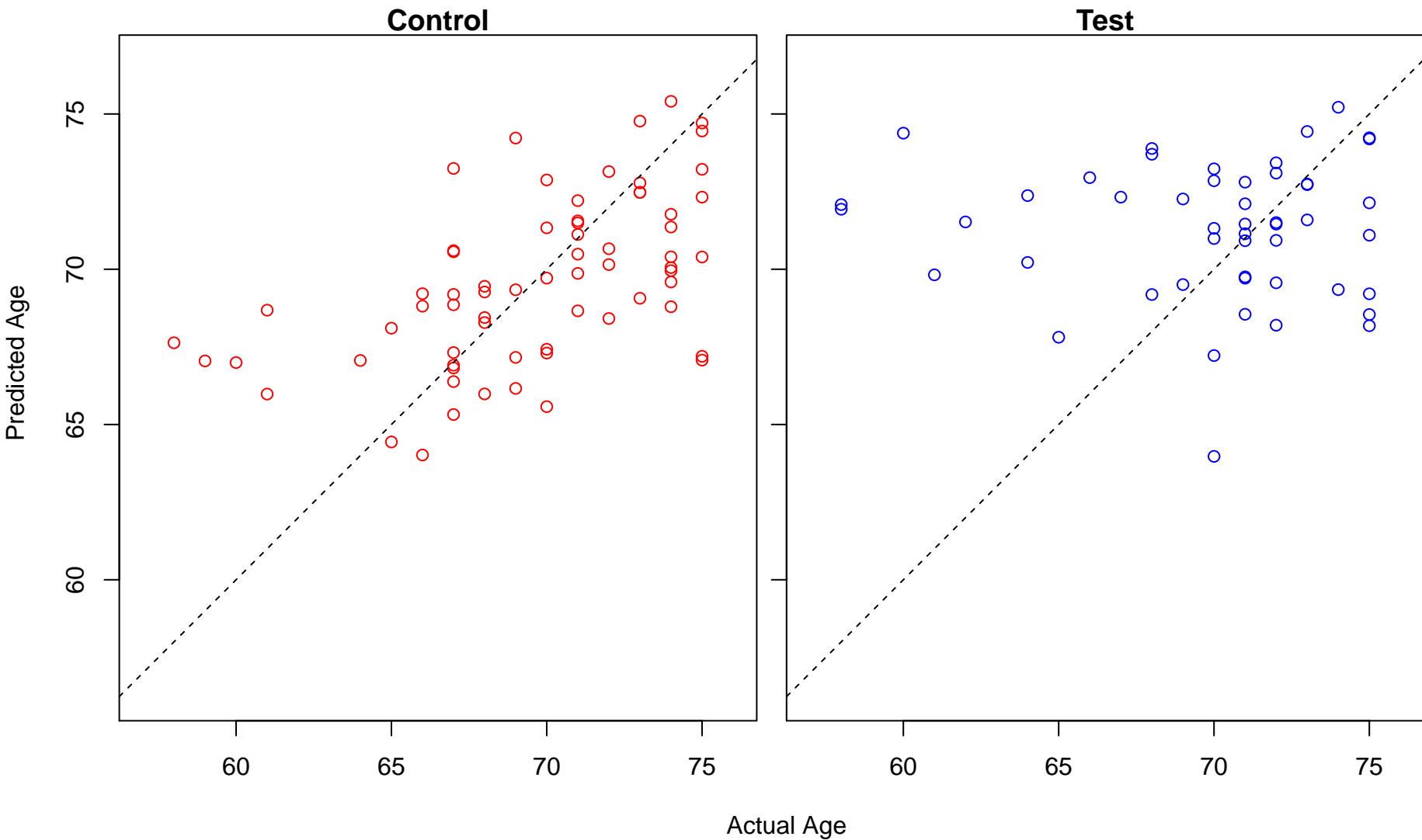
positive regulation of cardiac muscle hypertrophy (Score: 0.904464)



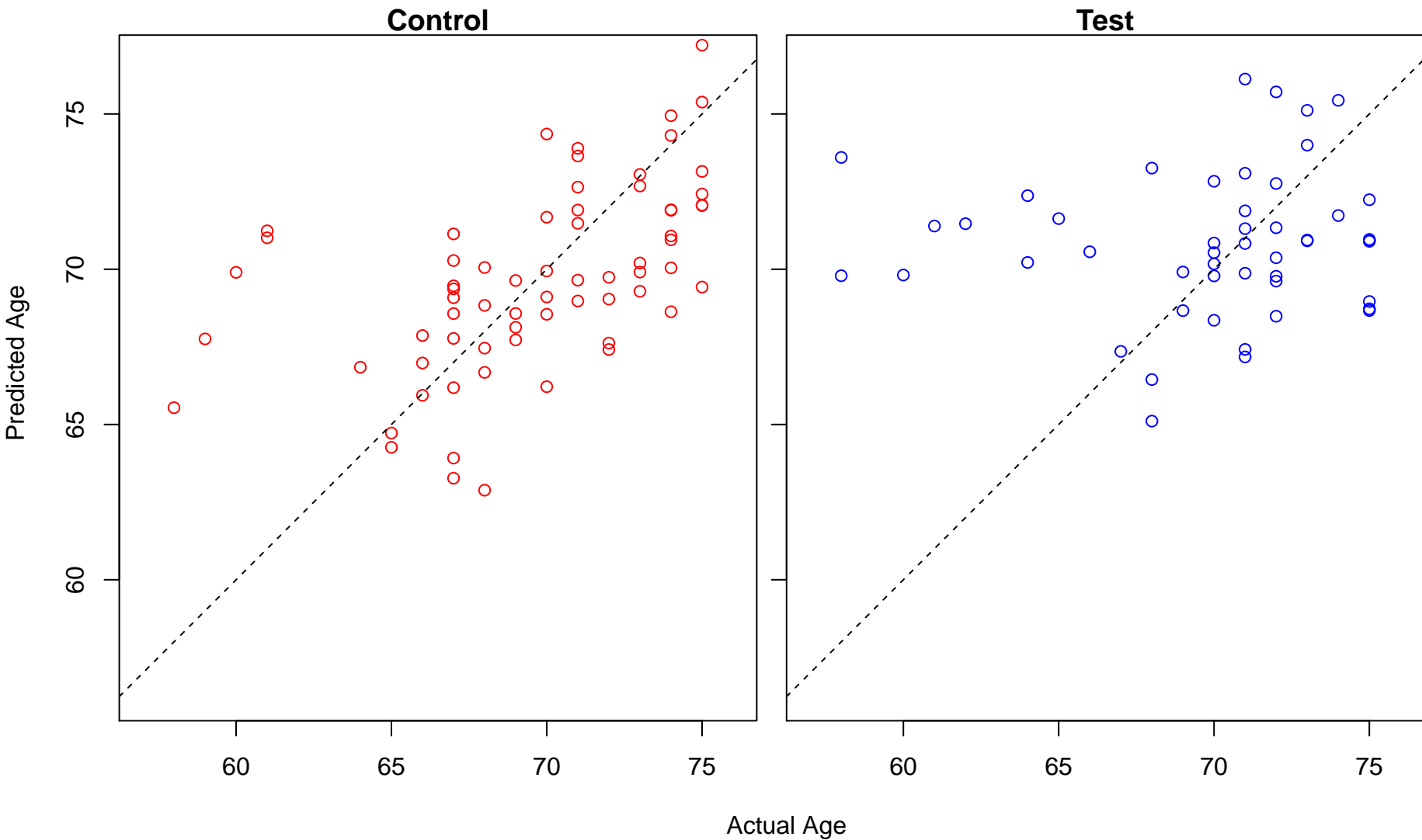
positive regulation of muscle hypertrophy (Score: 0.904464)



cellular response to laminar fluid shear stress (Score: 0.904224)

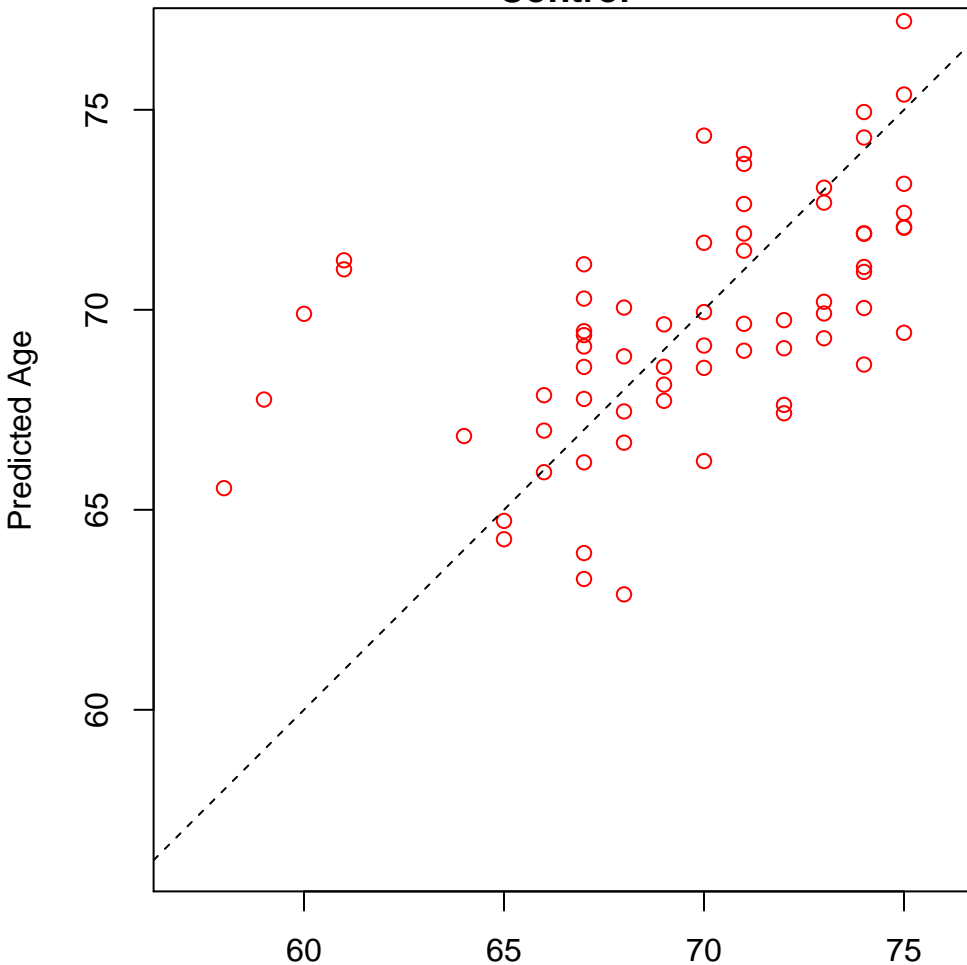


retrograde protein transport, ER to cytosol (Score: 0.903740)

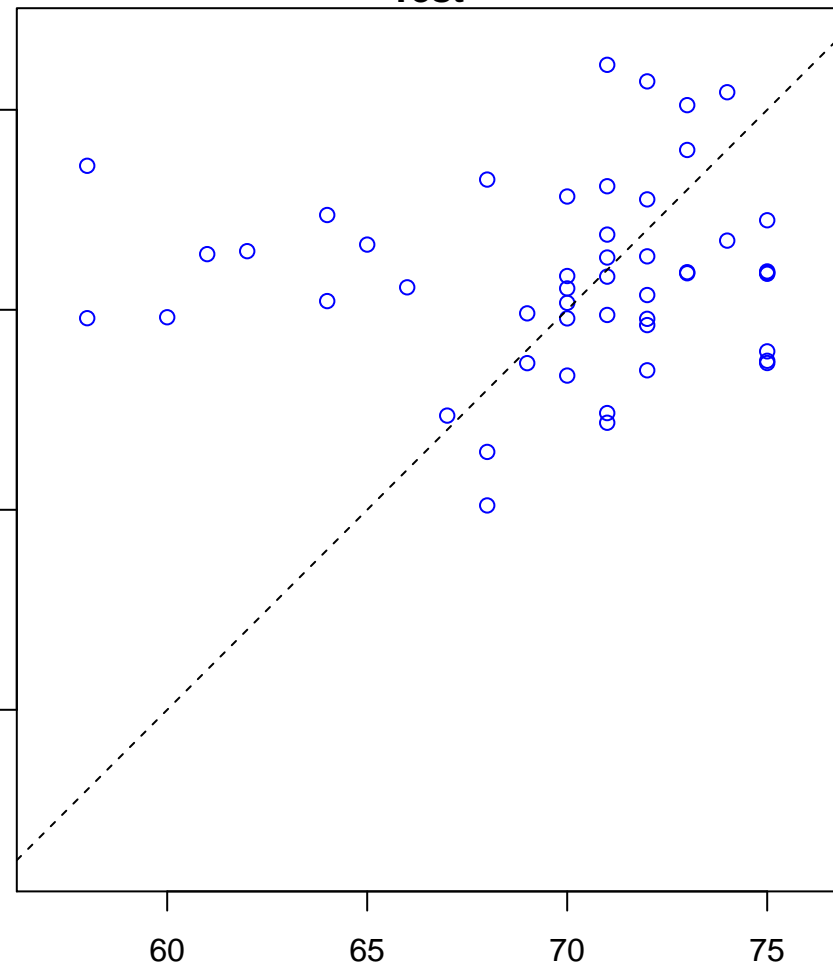


protein exit from endoplasmic reticulum (Score: 0.903740)

Control

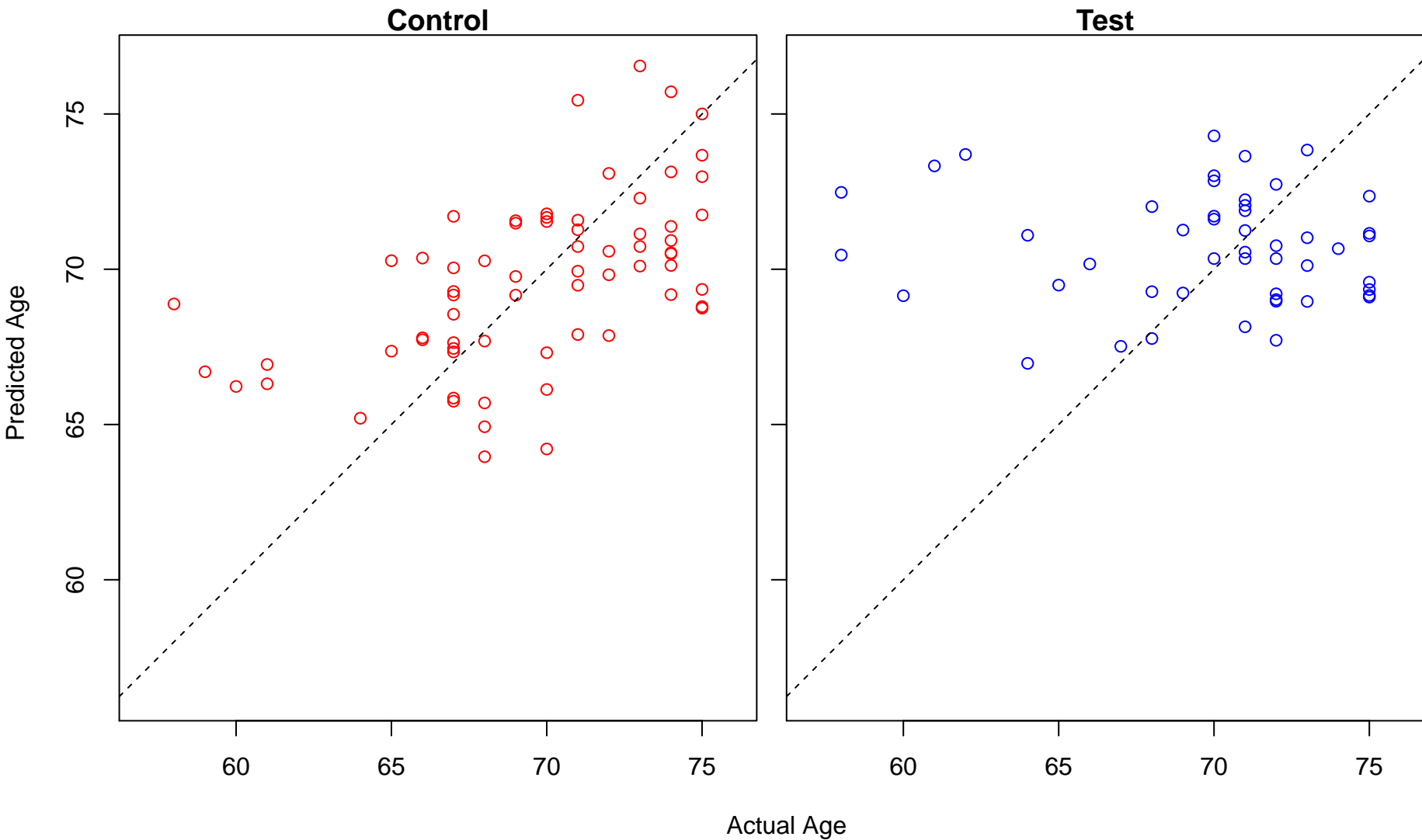


Test

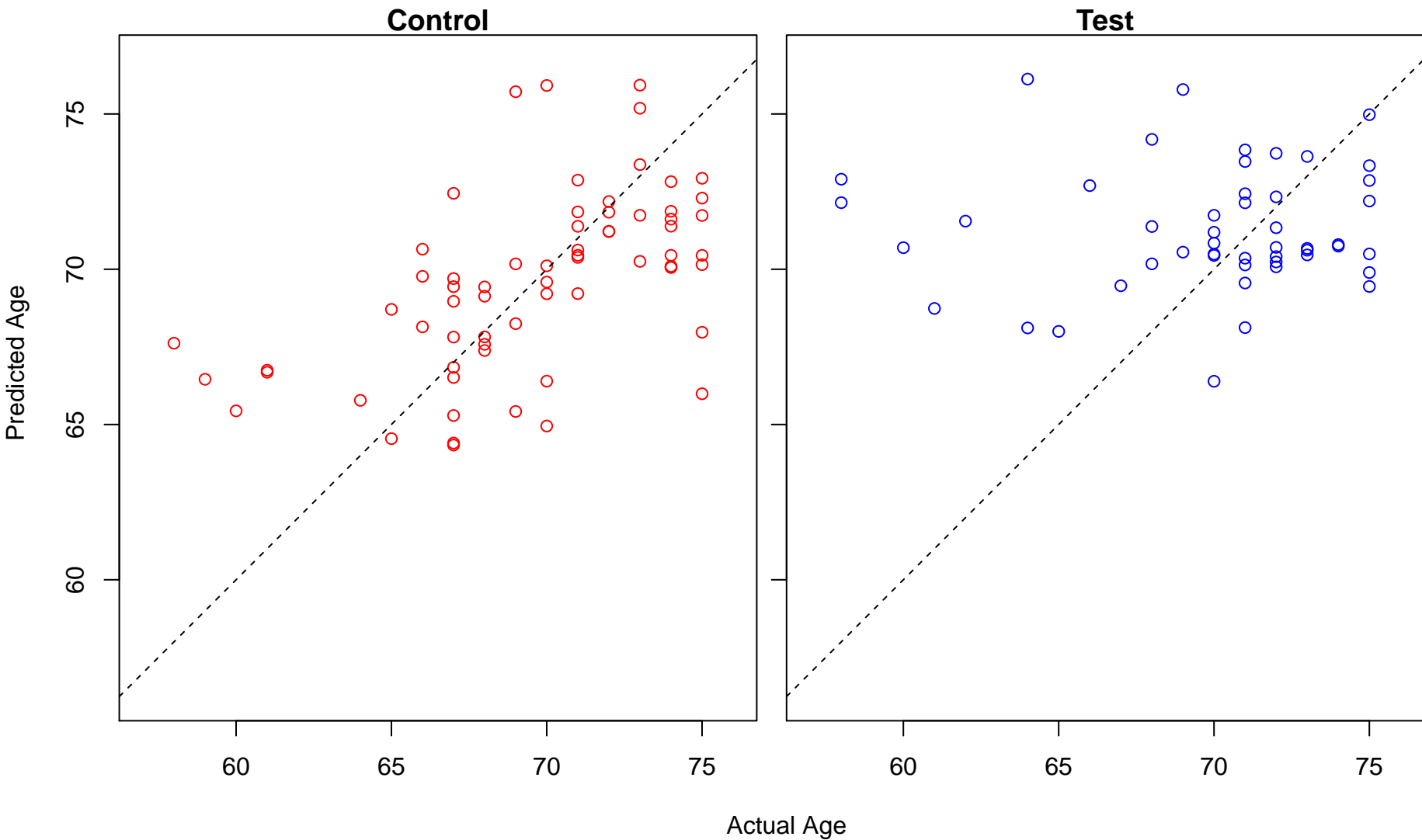


Actual Age

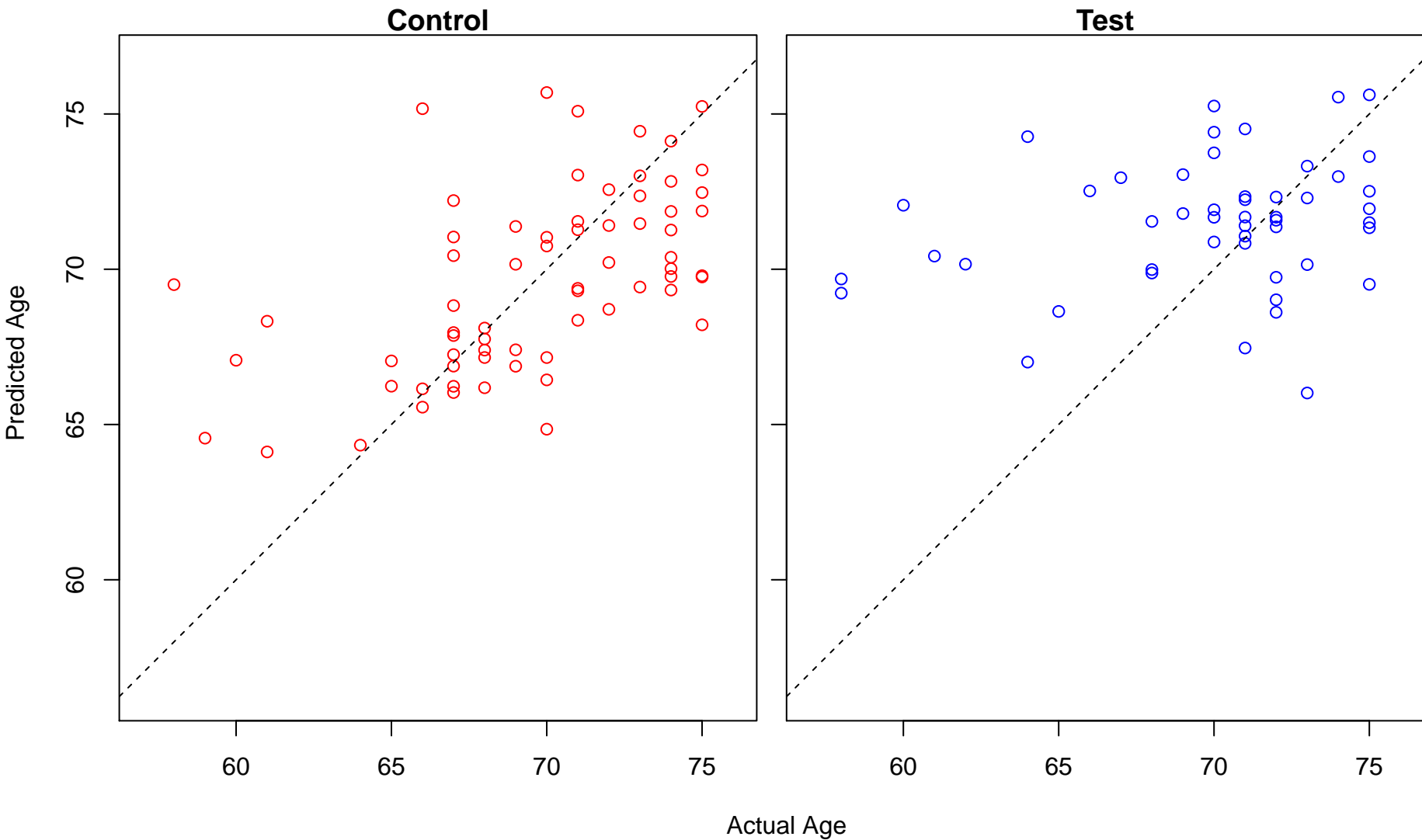
single-organism carbohydrate catabolic process (Score: 0.903653)



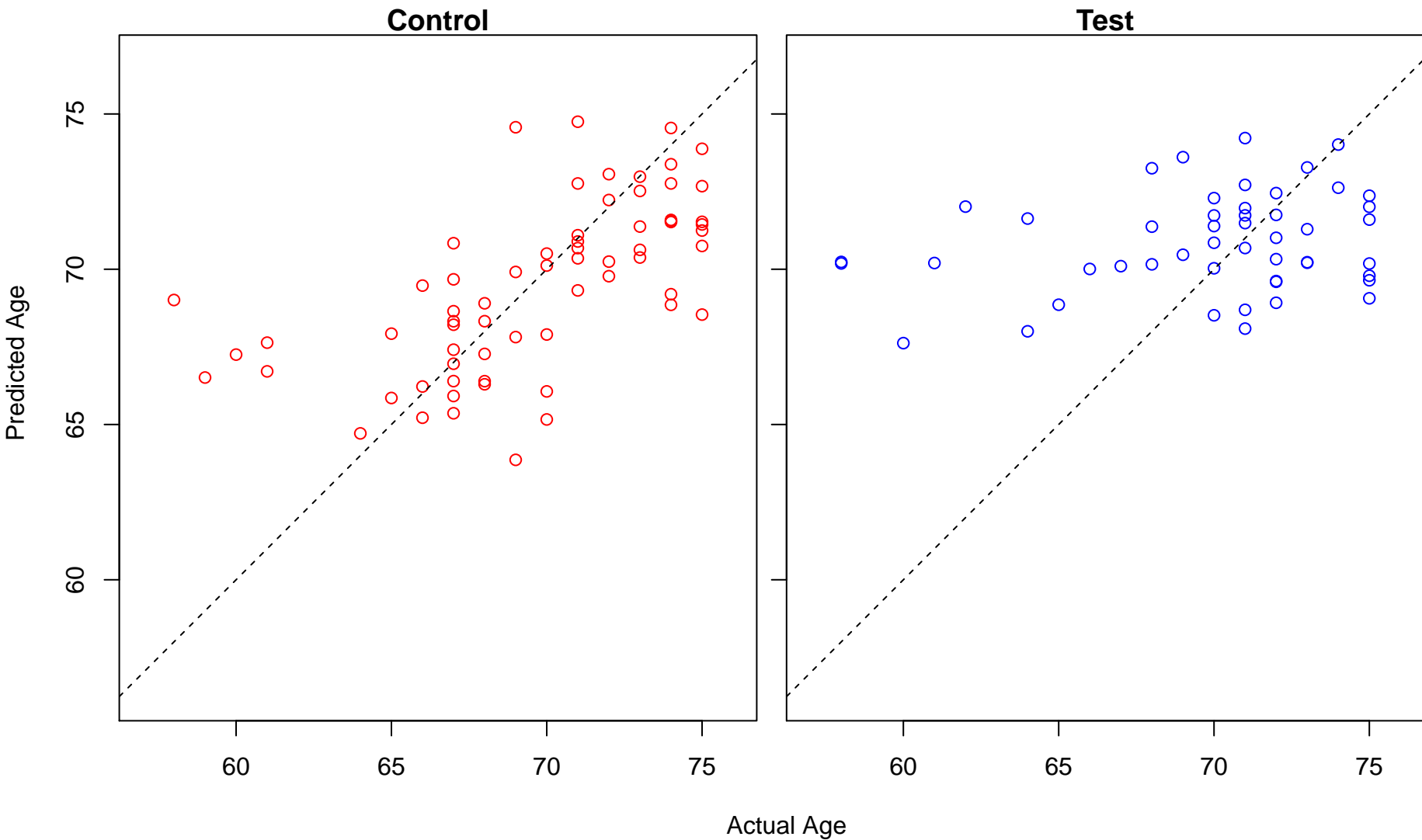
respiratory tube development (Score: 0.903555)



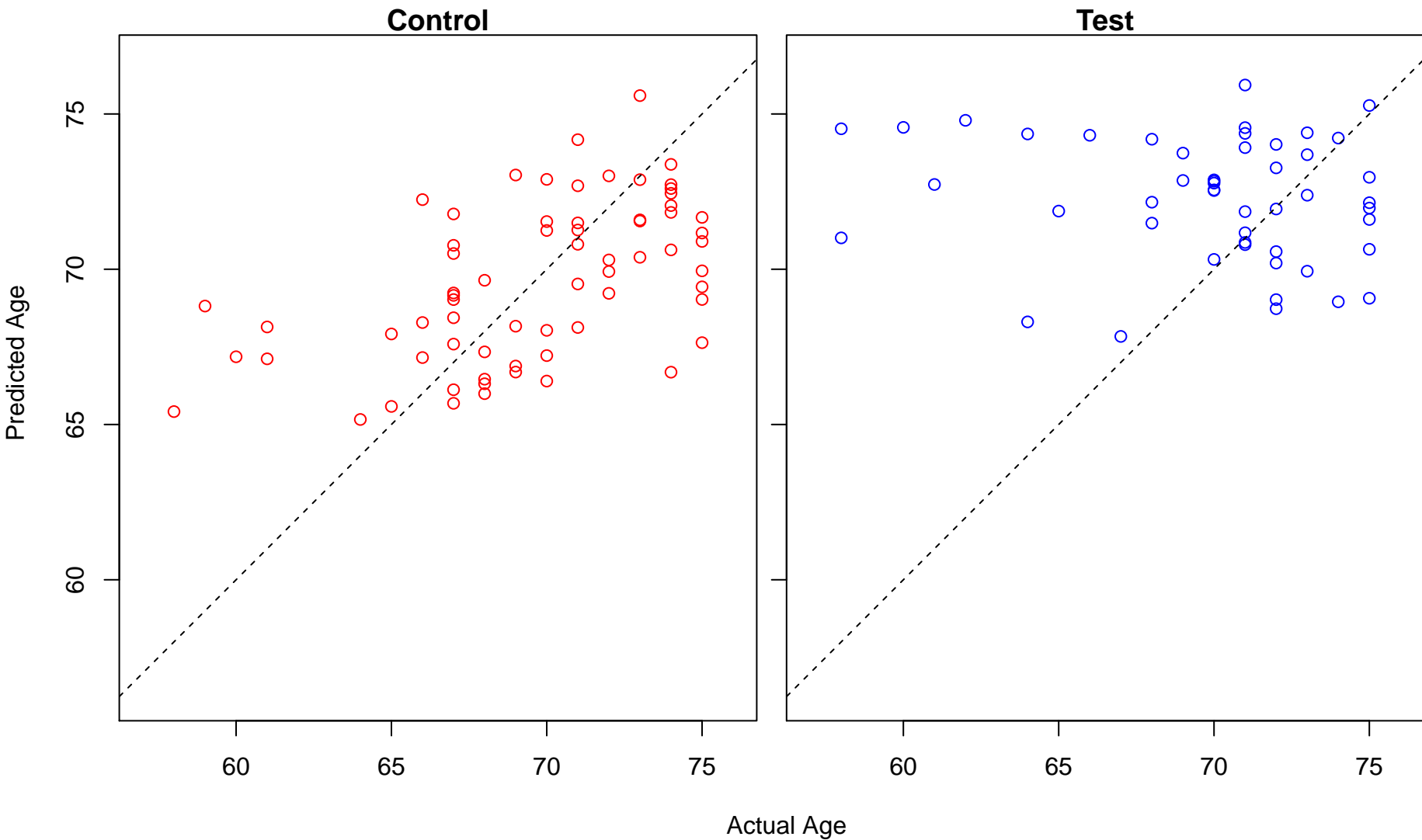
dermatan sulfate metabolic process (Score: 0.903405)



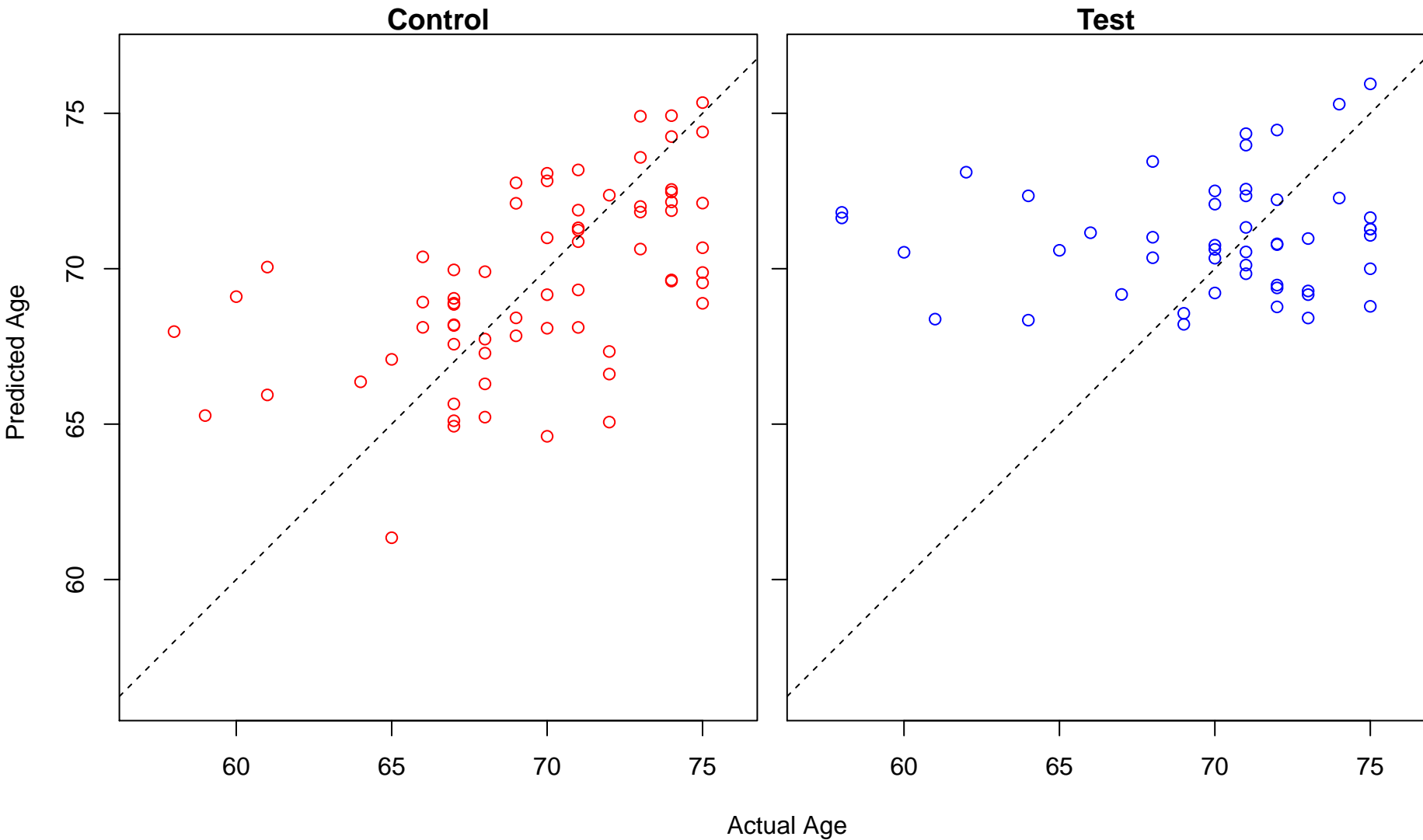
kidney morphogenesis (Score: 0.903372)



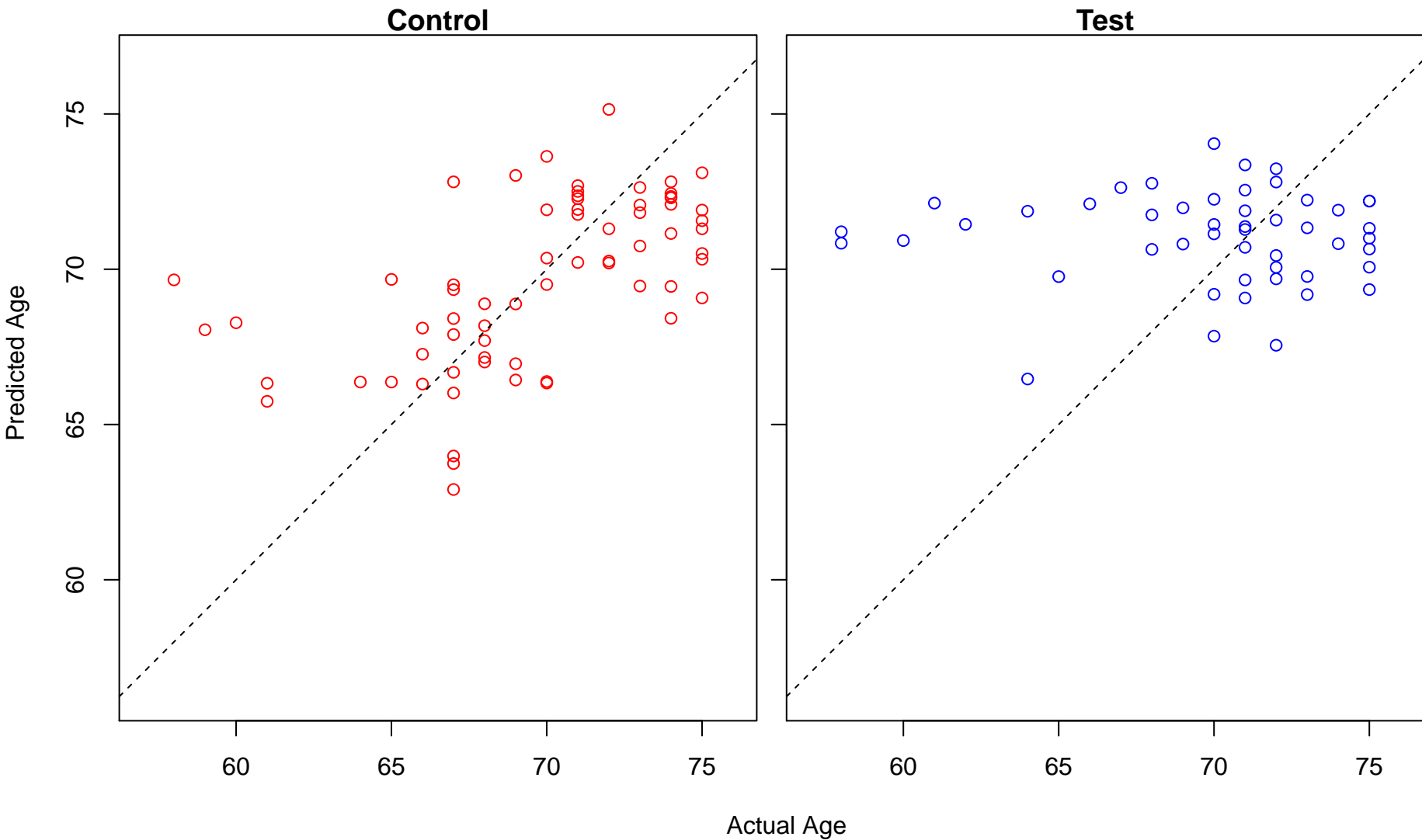
negative regulation of hematopoietic progenitor cell differentiation (Score: 0.903077)



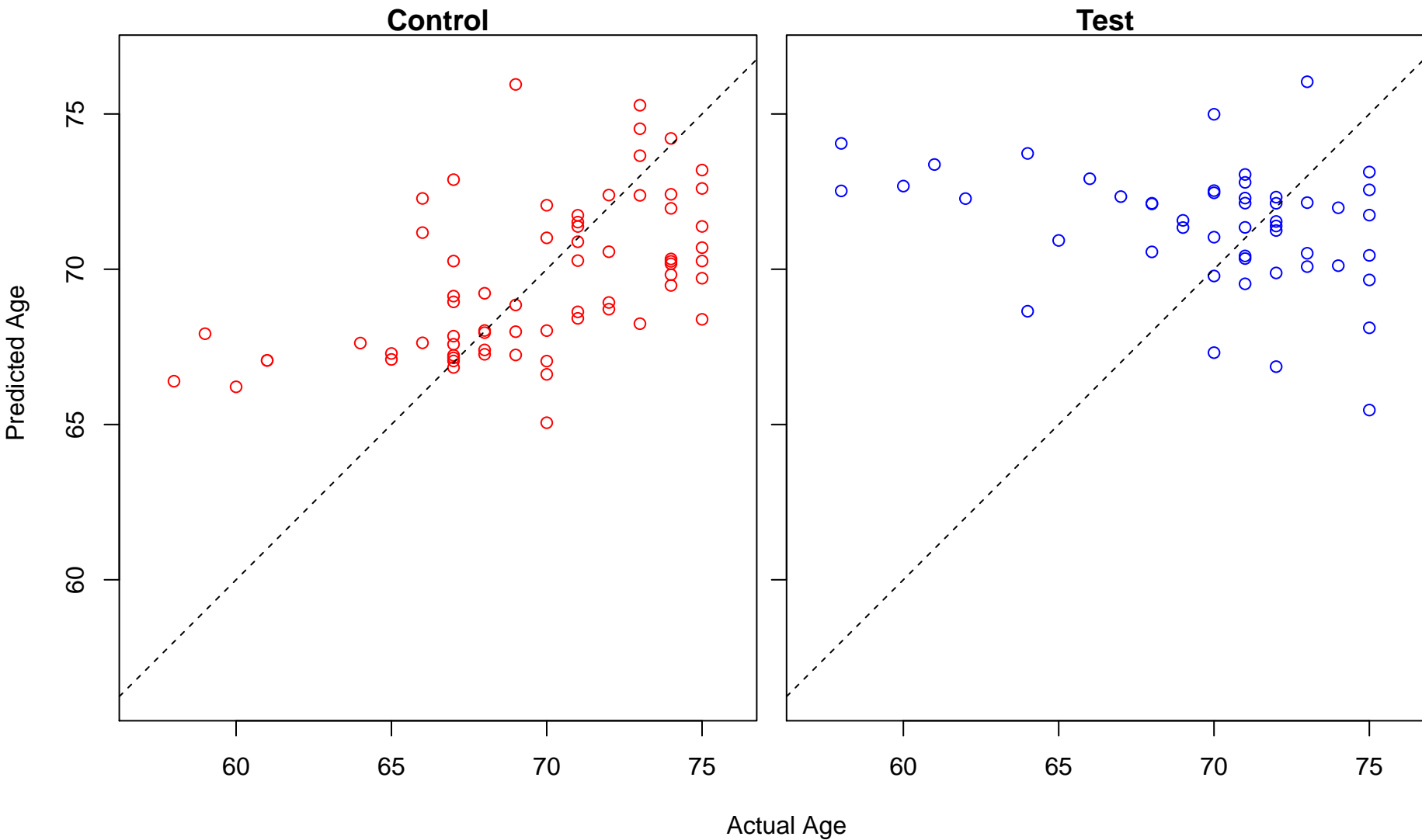
cellular response to interferon-beta (Score: 0.902626)



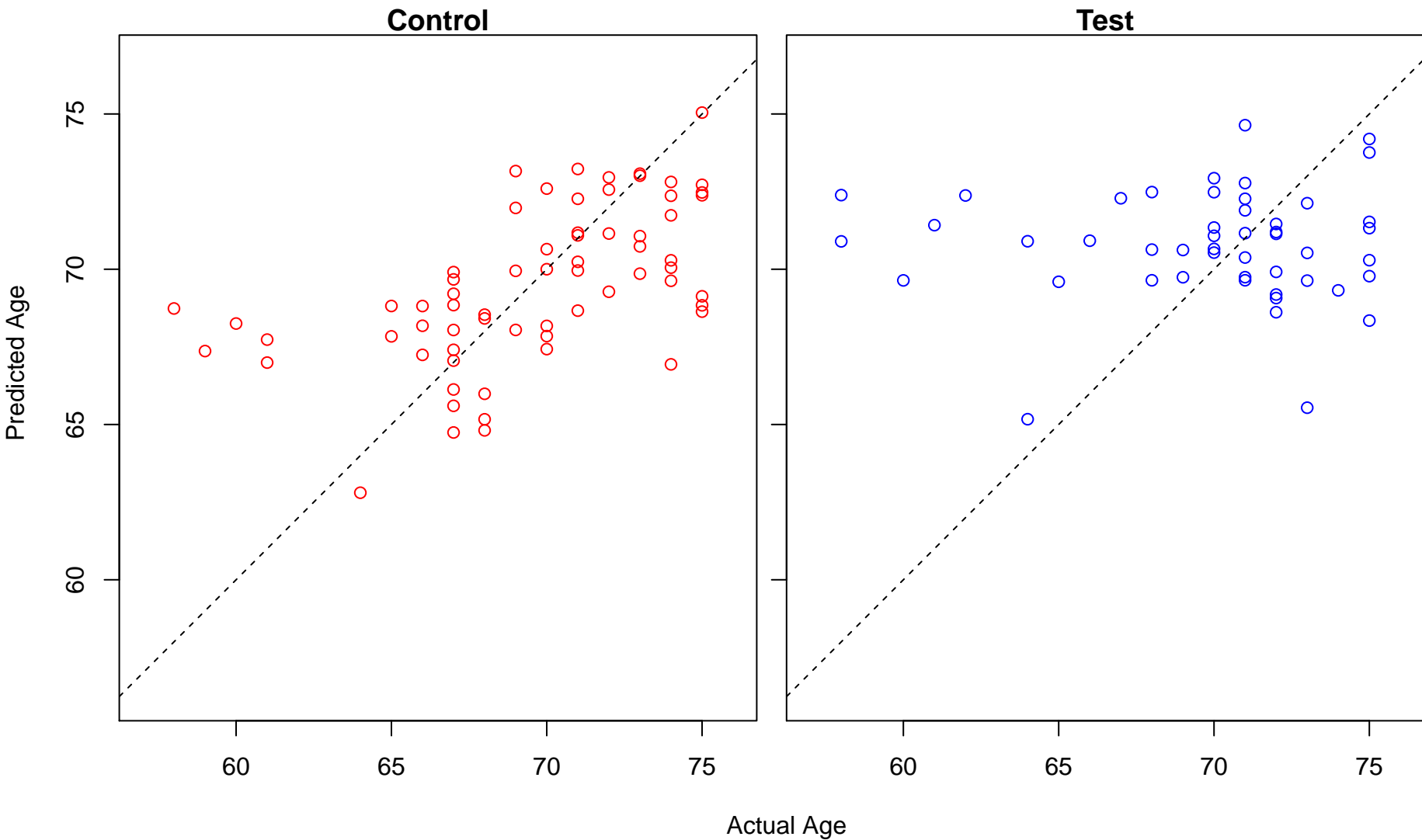
DNA ligation (Score: 0.902602)



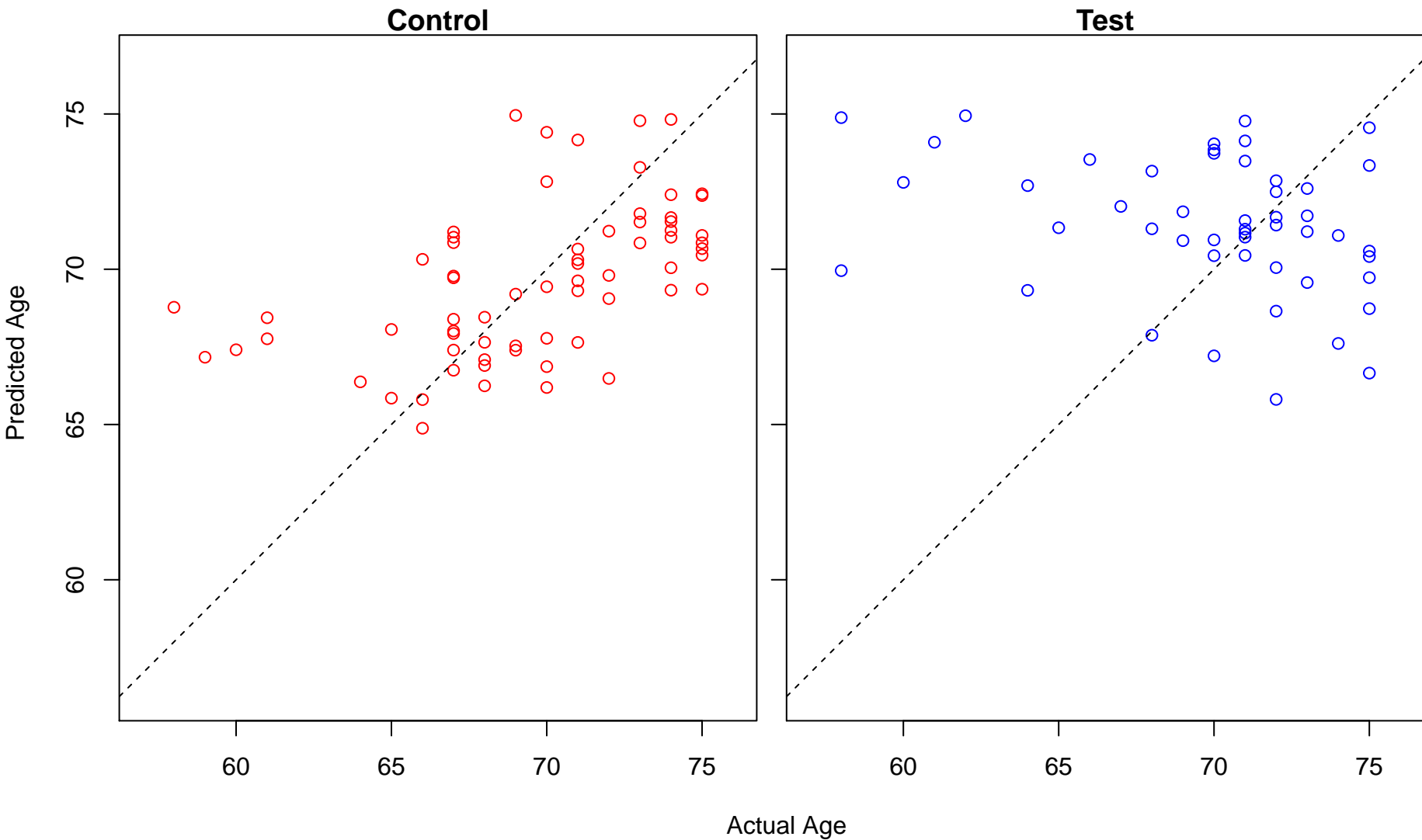
retrograde transport, endosome to plasma membrane (Score: 0.901927)



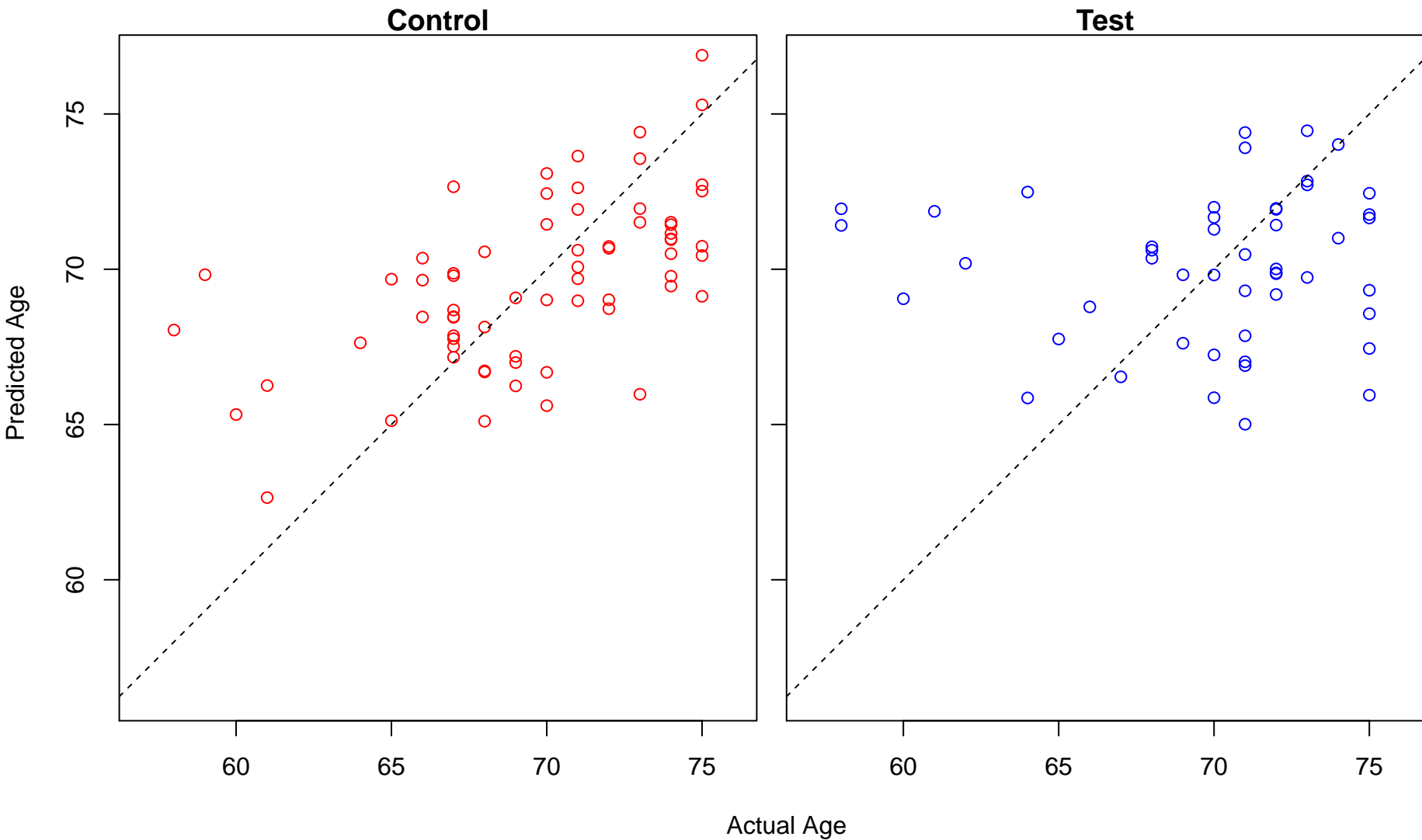
response to interleukin-6 (Score: 0.901590)



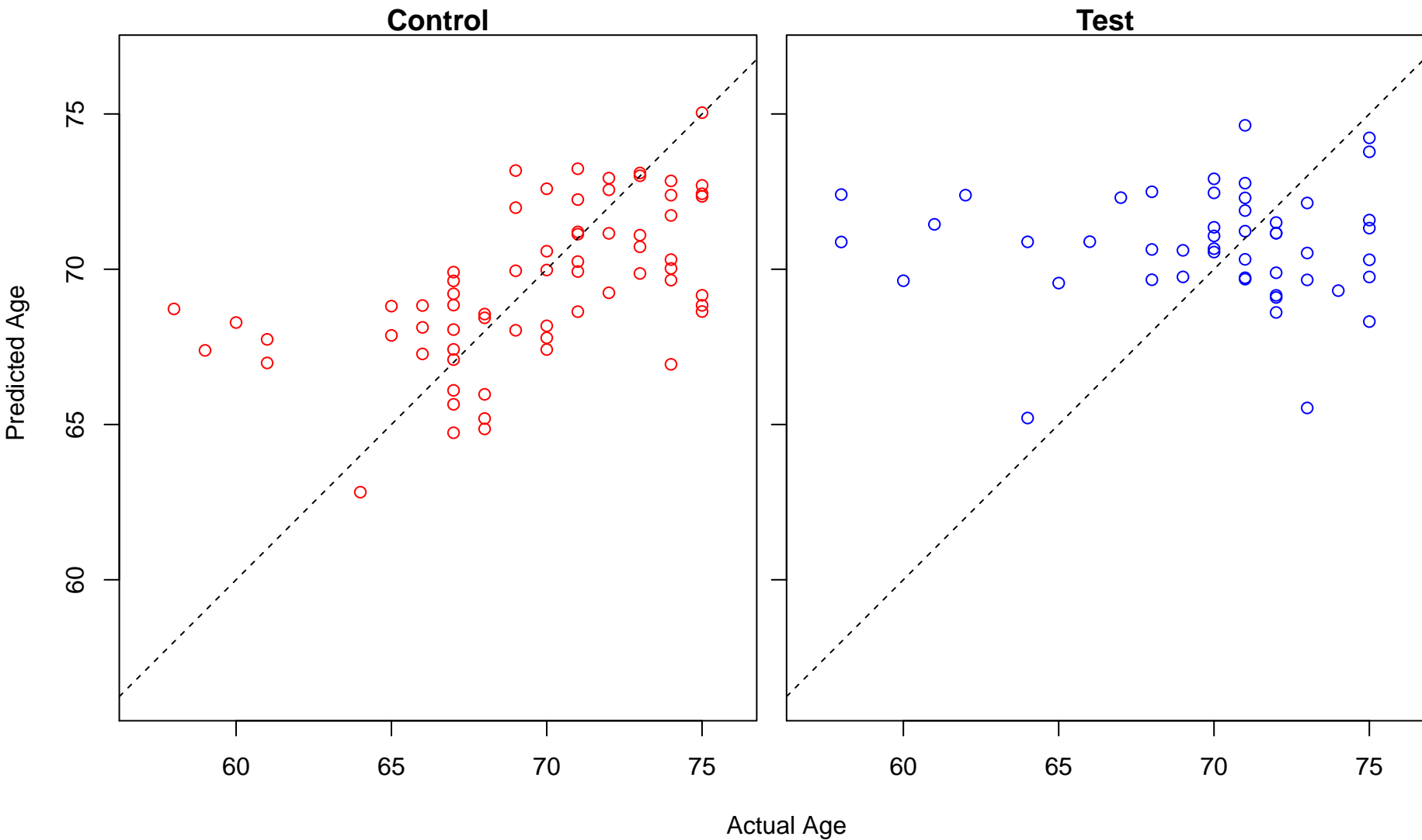
positive regulation of myeloid leukocyte mediated immunity (Score: 0.900622)



barbed-end actin filament capping (Score: 0.900518)

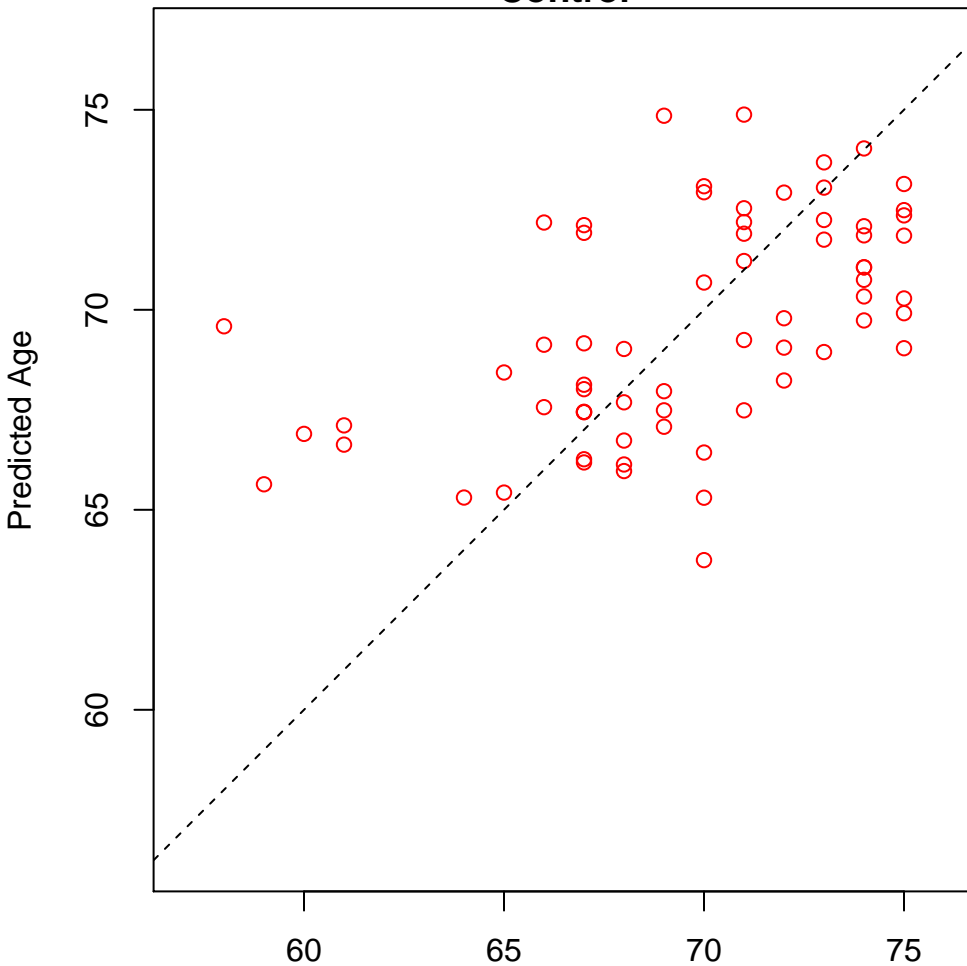


cellular response to interleukin-6 (Score: 0.899998)

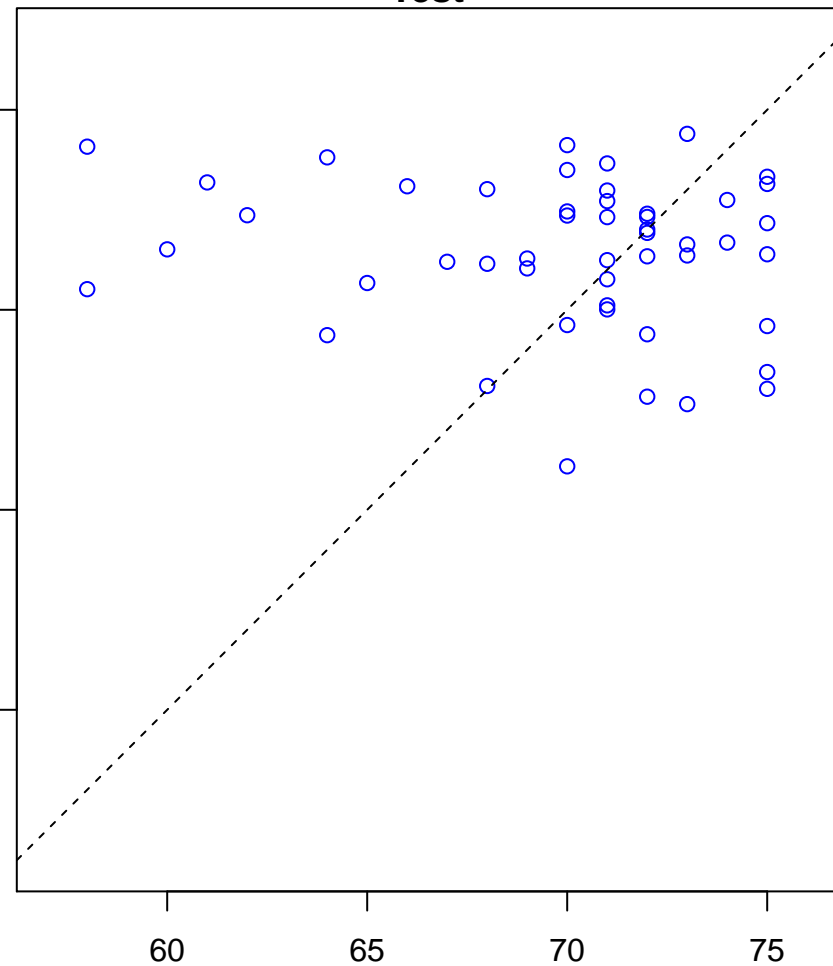


glycosaminoglycan catabolic process (Score: 0.899912)

Control

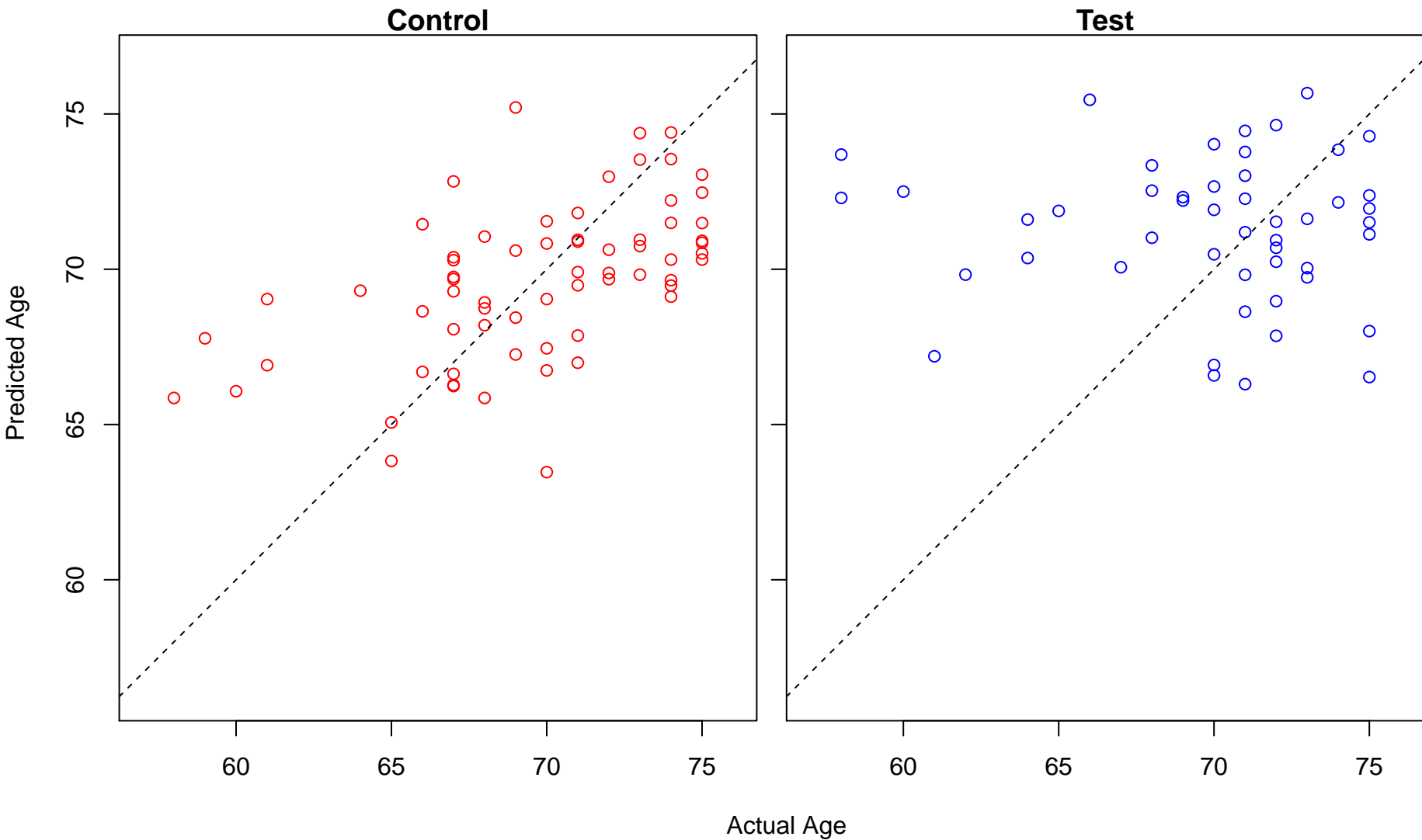


Test

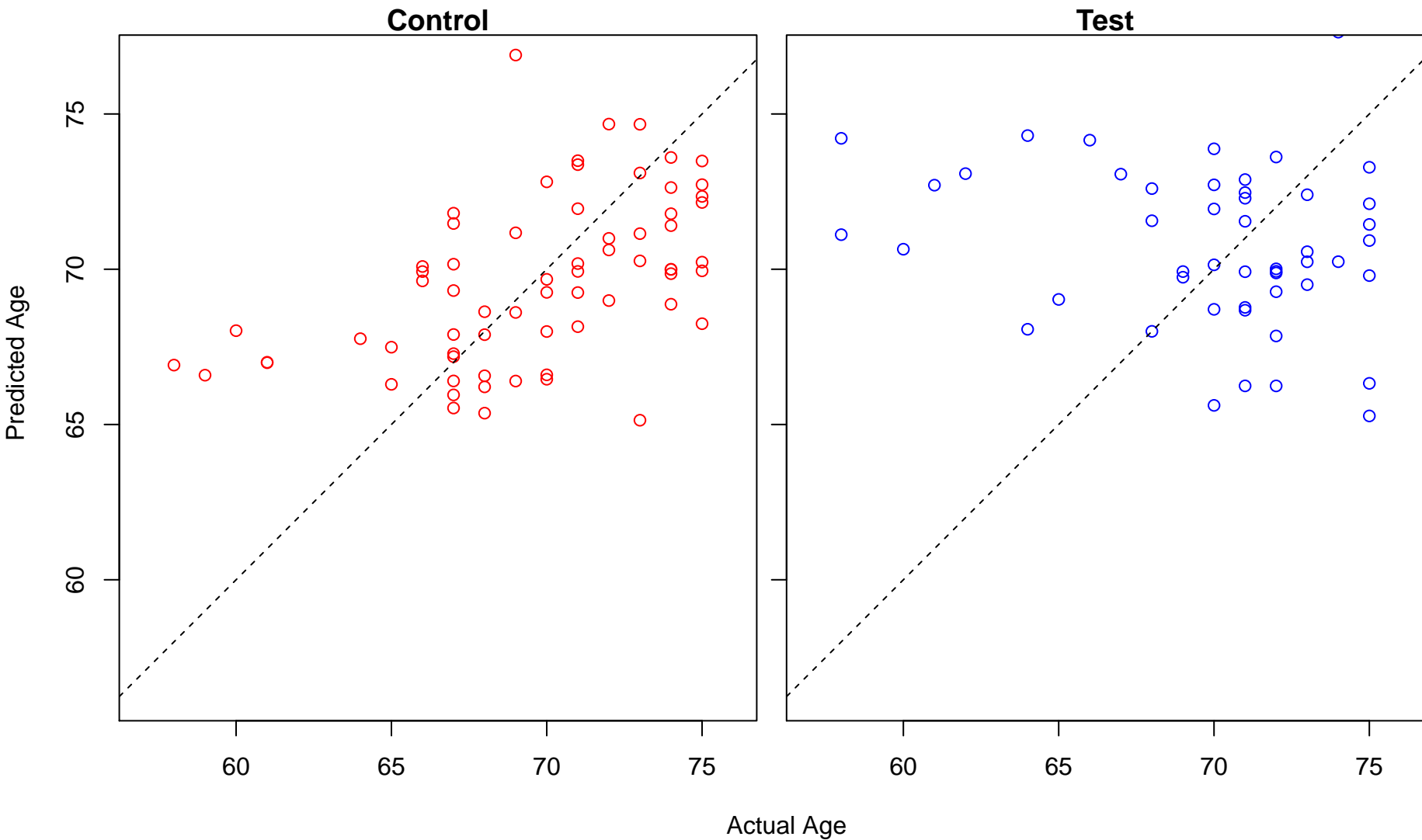


Actual Age

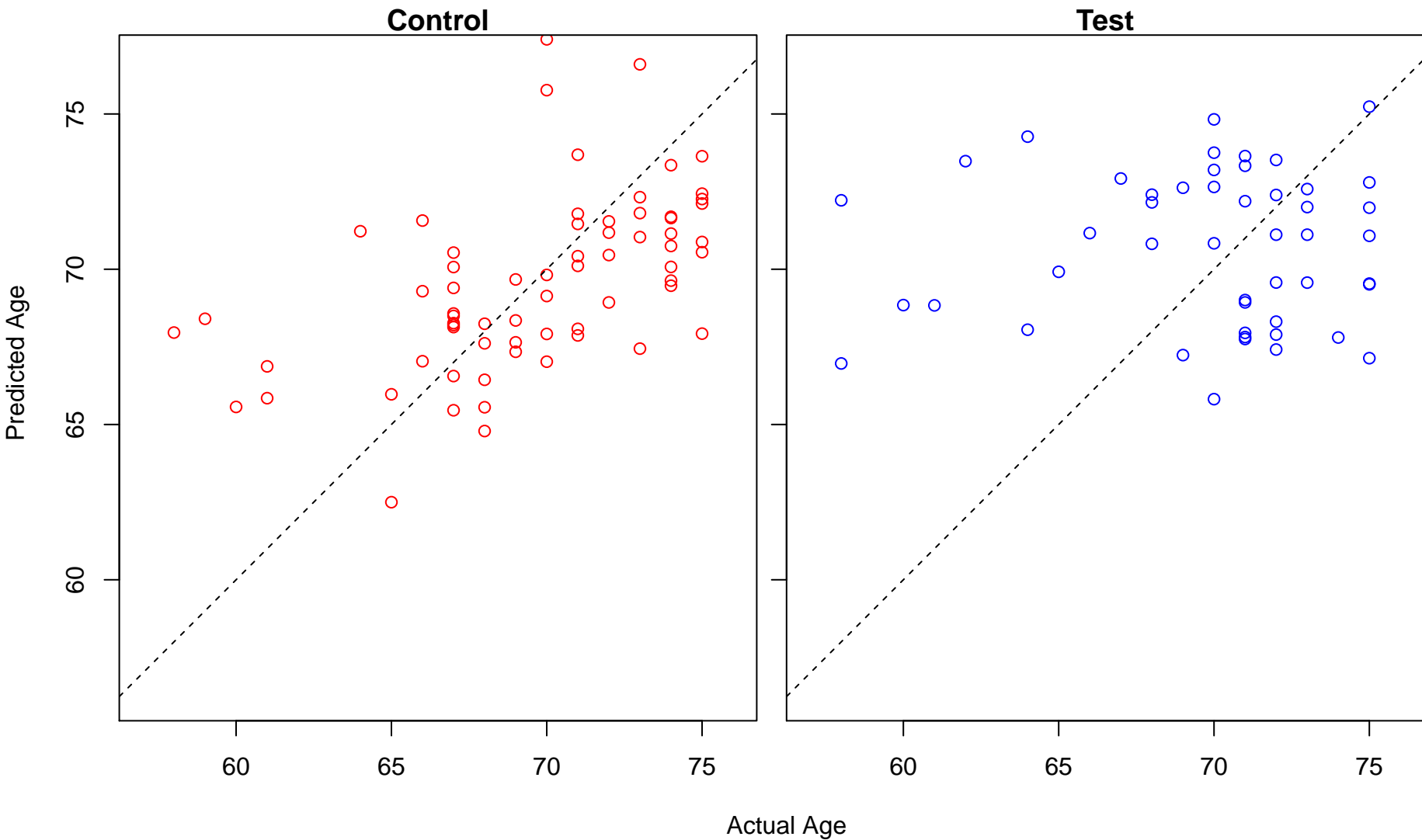
positive regulation of osteoclast differentiation (Score: 0.899690)



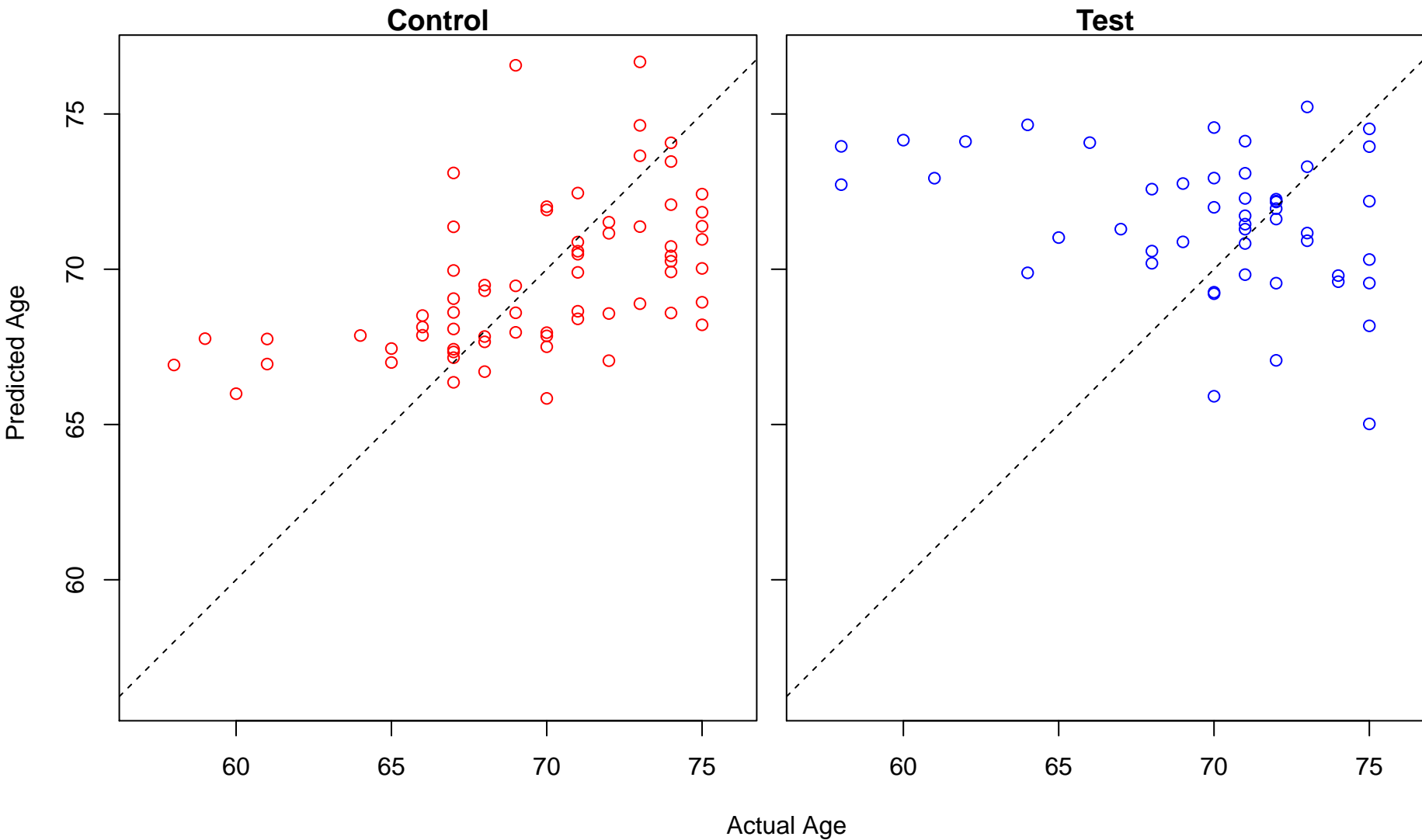
macromolecule deacylation (Score: 0.899662)



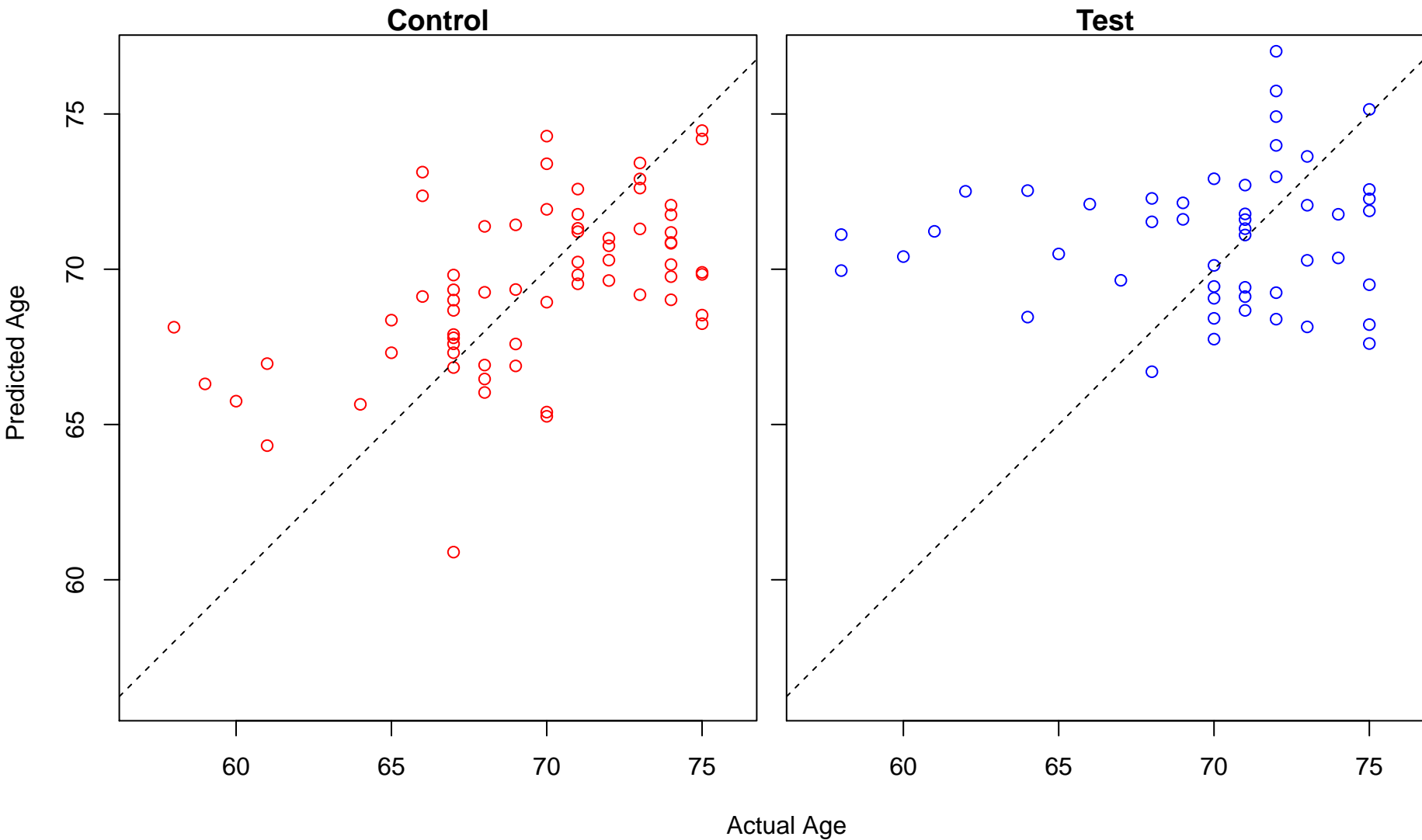
regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter (Score: 0.8



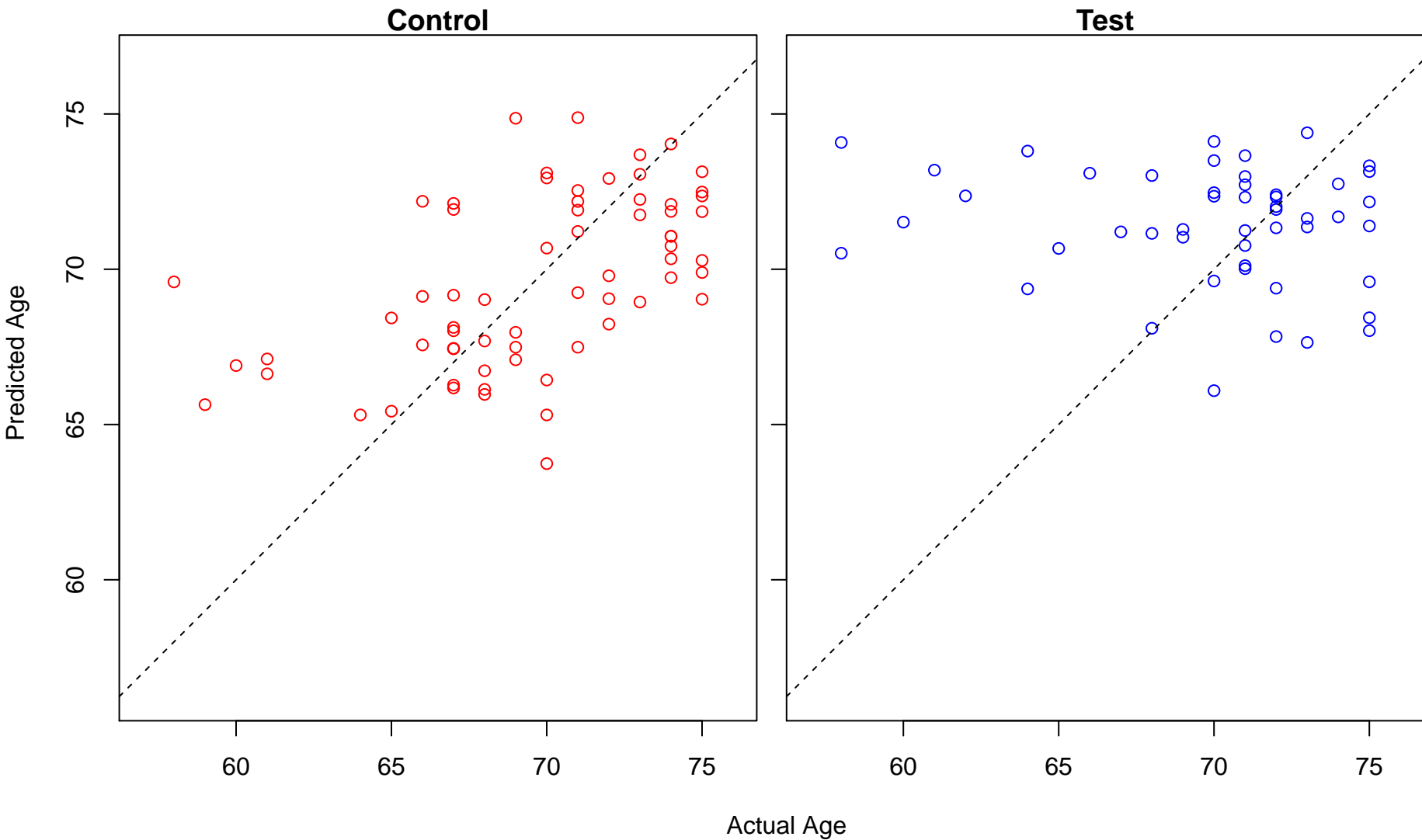
natural killer cell activation (Score: 0.899174)



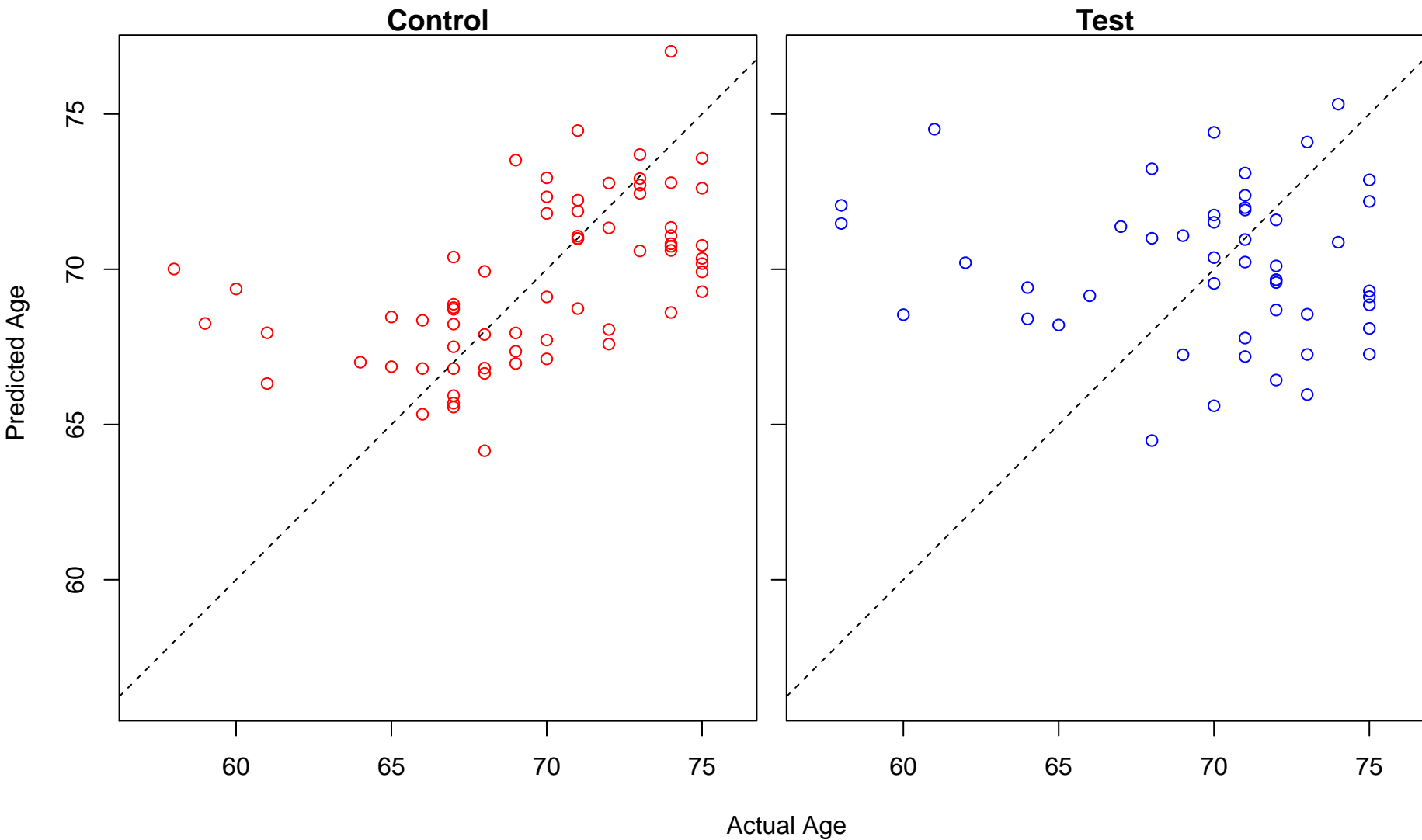
stem cell division (Score: 0.899082)



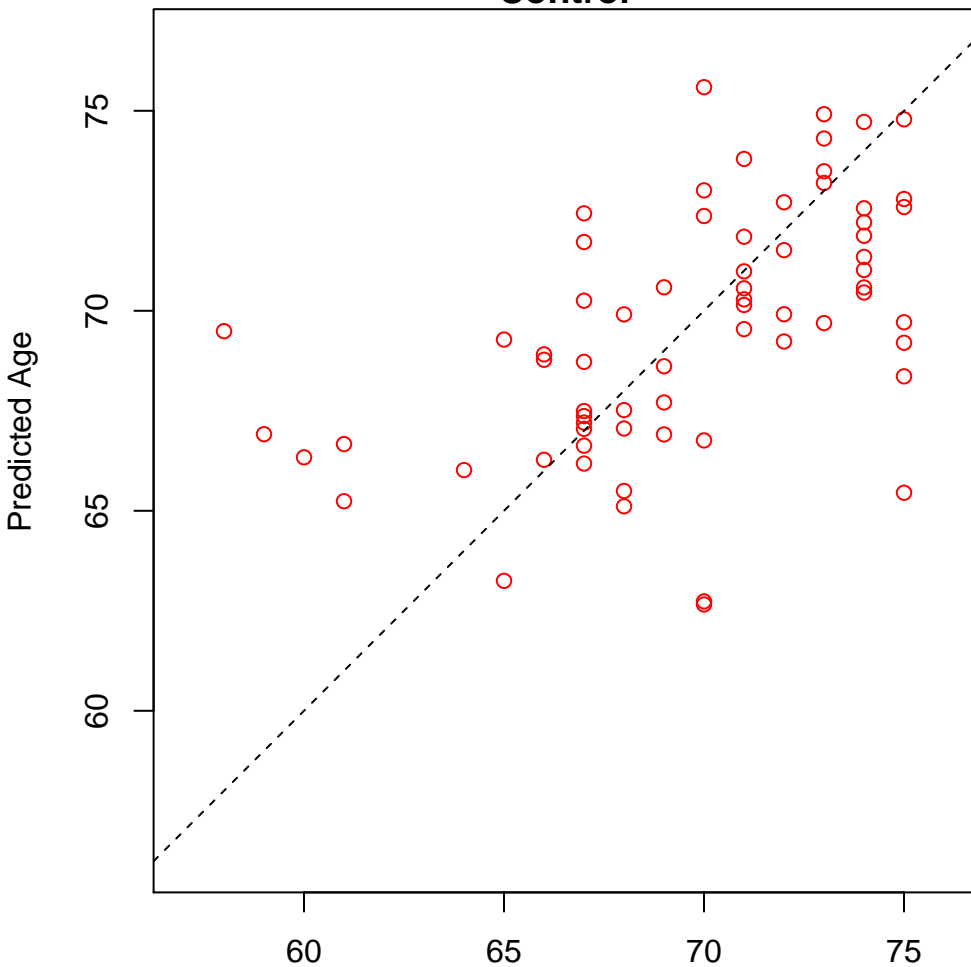
aminoglycan catabolic process (Score: 0.899042)



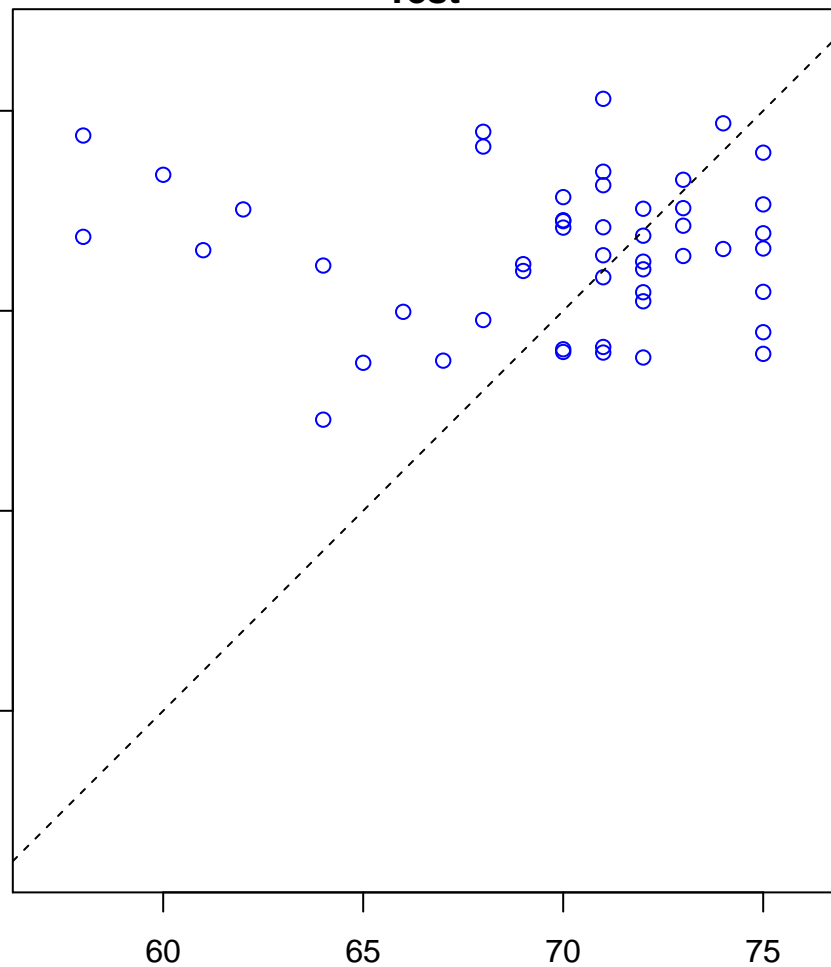
negative regulation of interferon-beta production (Score: 0.898569)



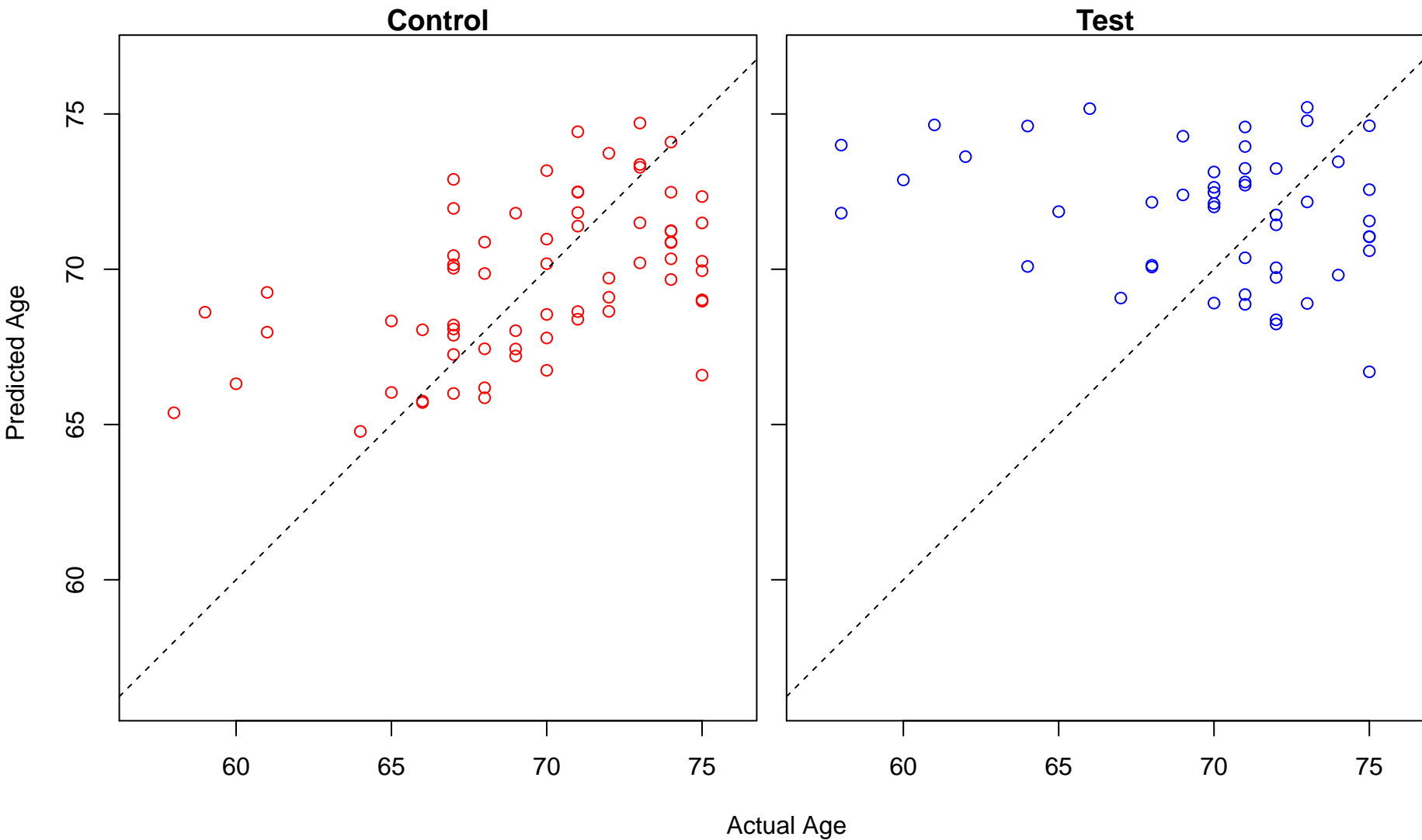
Control



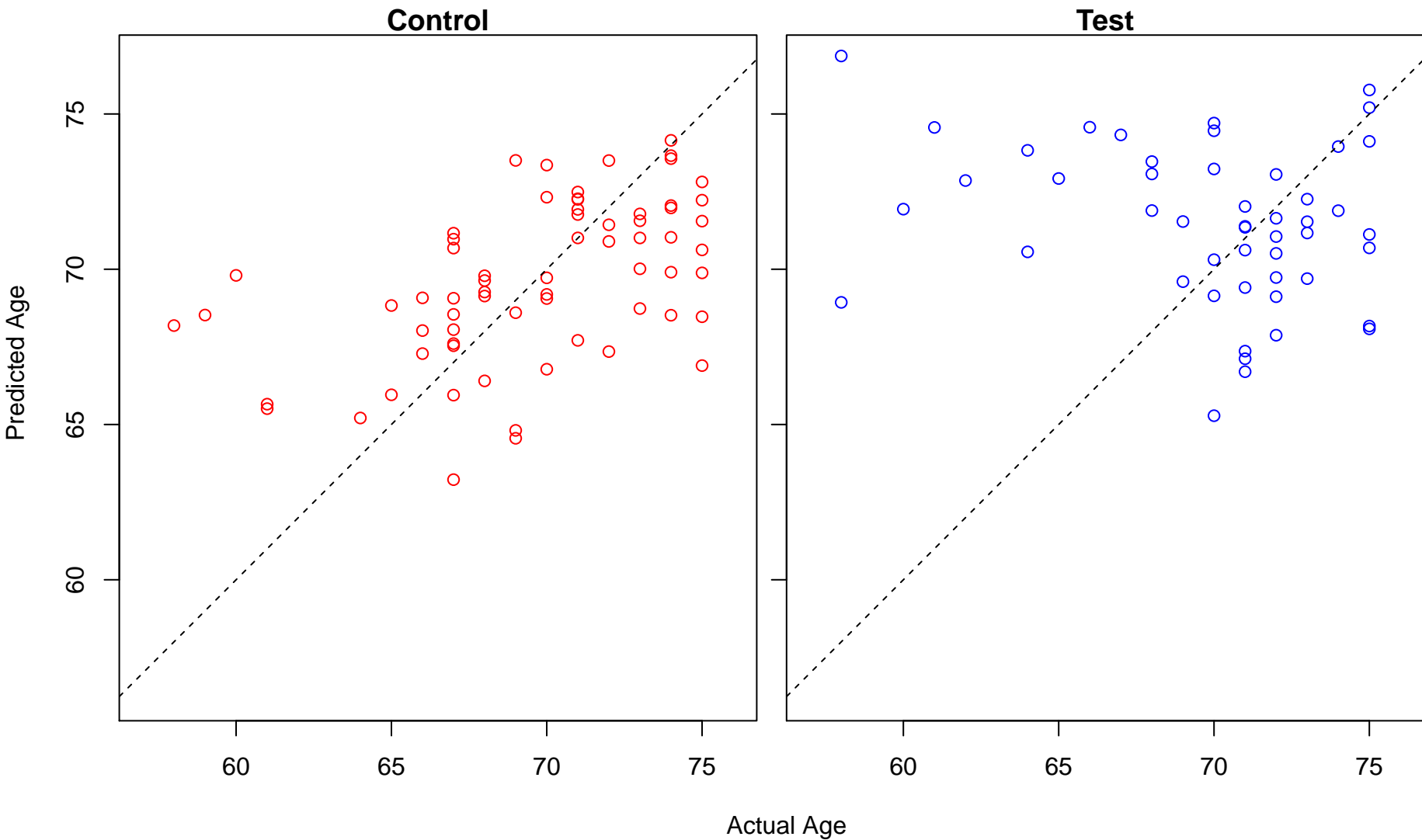
Test



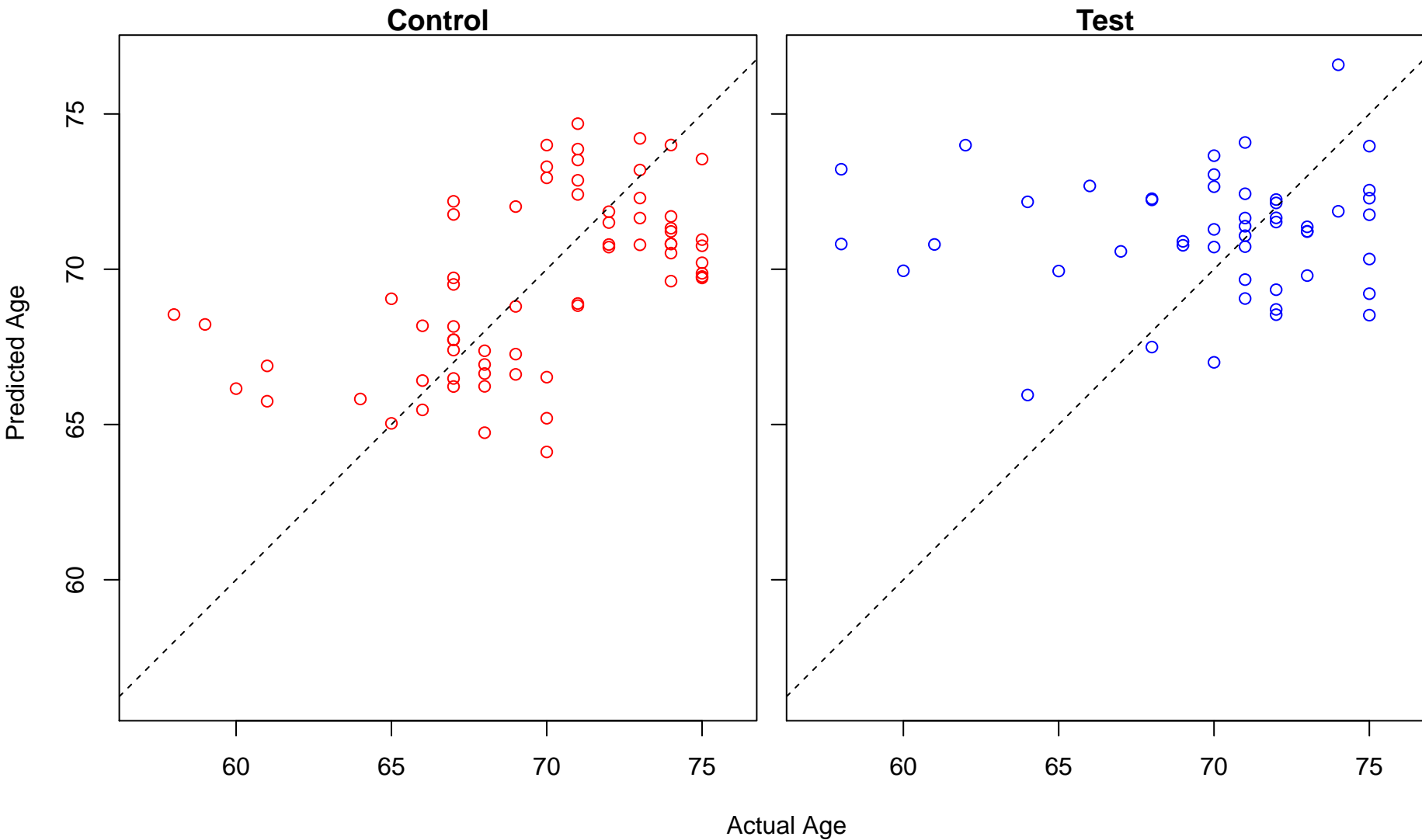
endocardial cushion formation (Score: 0.897943)



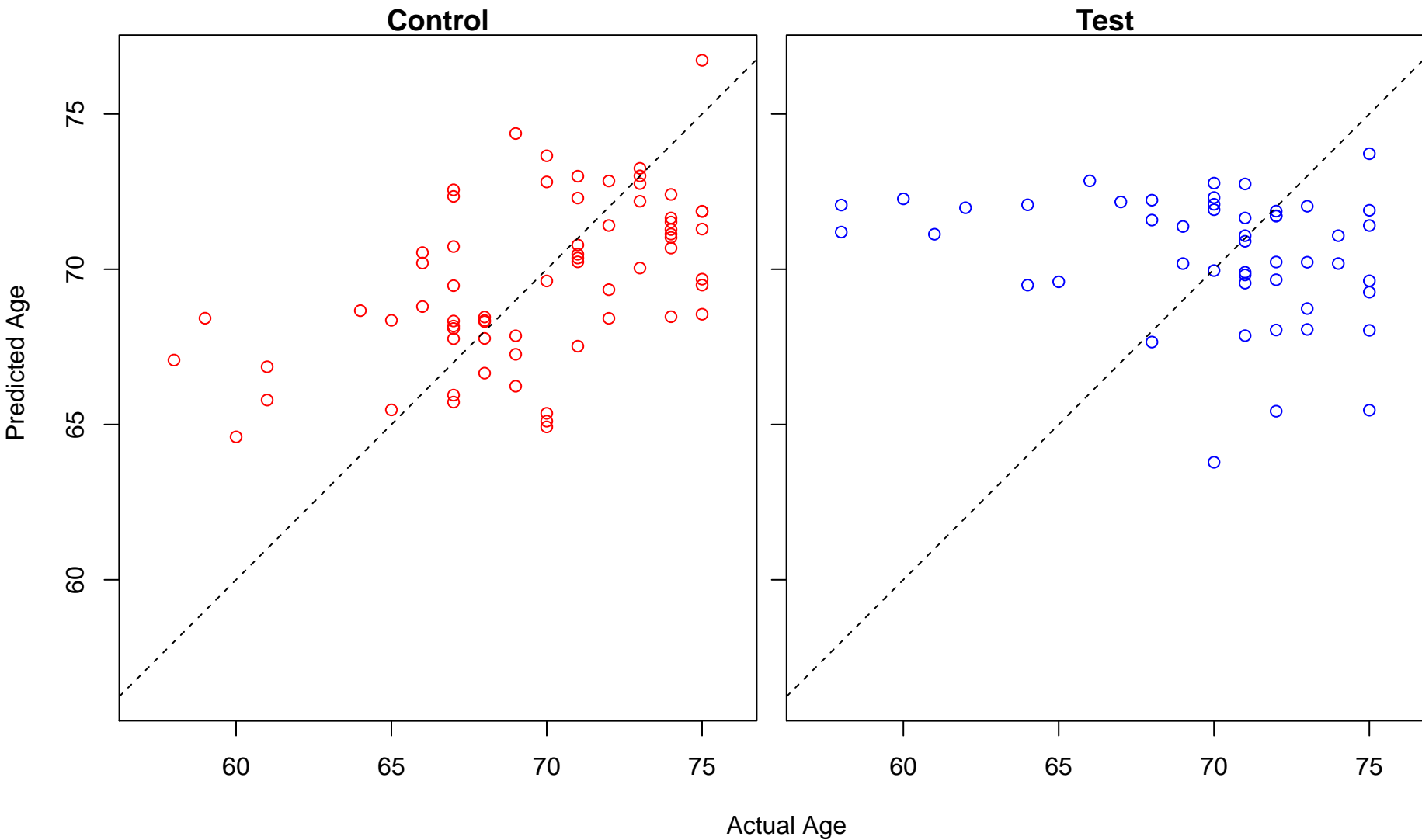
type B pancreatic cell proliferation (Score: 0.897900)



positive regulation of neurogenesis (Score: 0.897897)

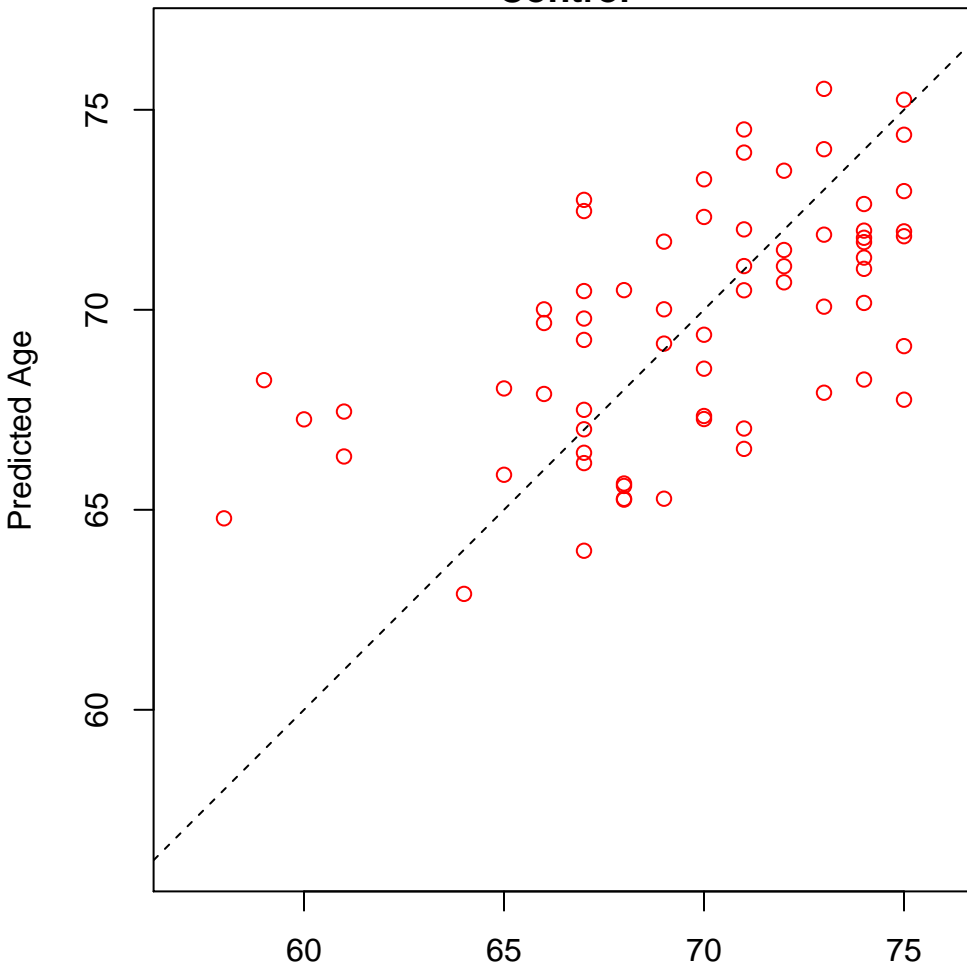


detection of biotic stimulus (Score: 0.897022)

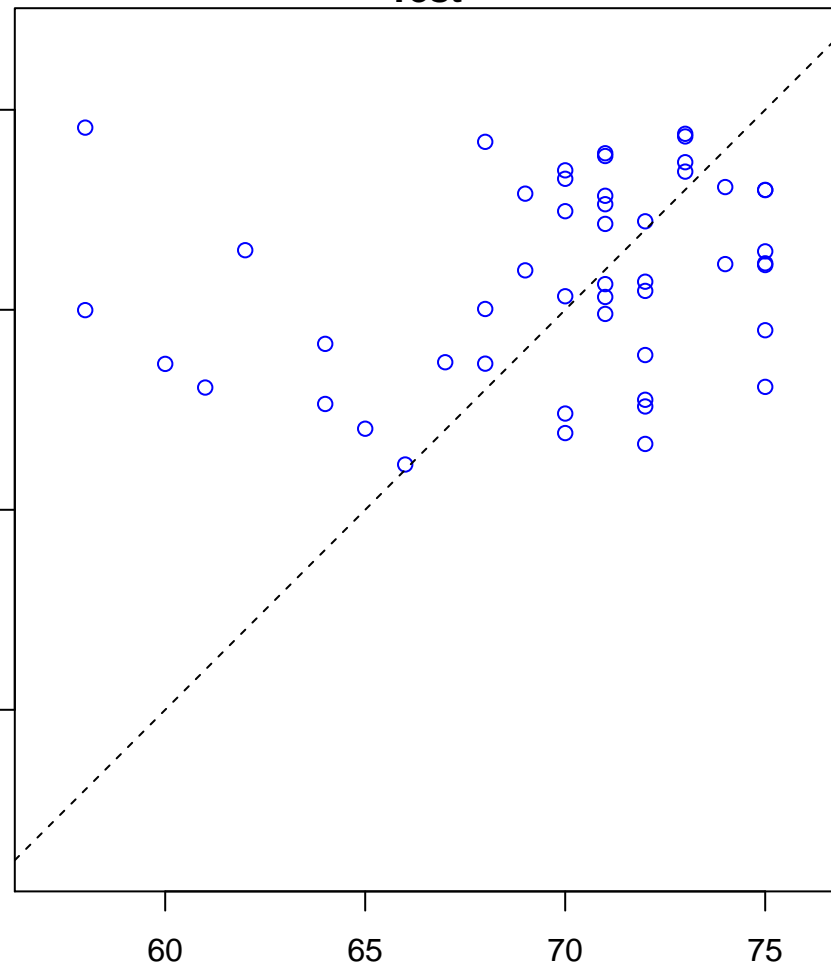


detection of mechanical stimulus (Score: 0.896155)

Control

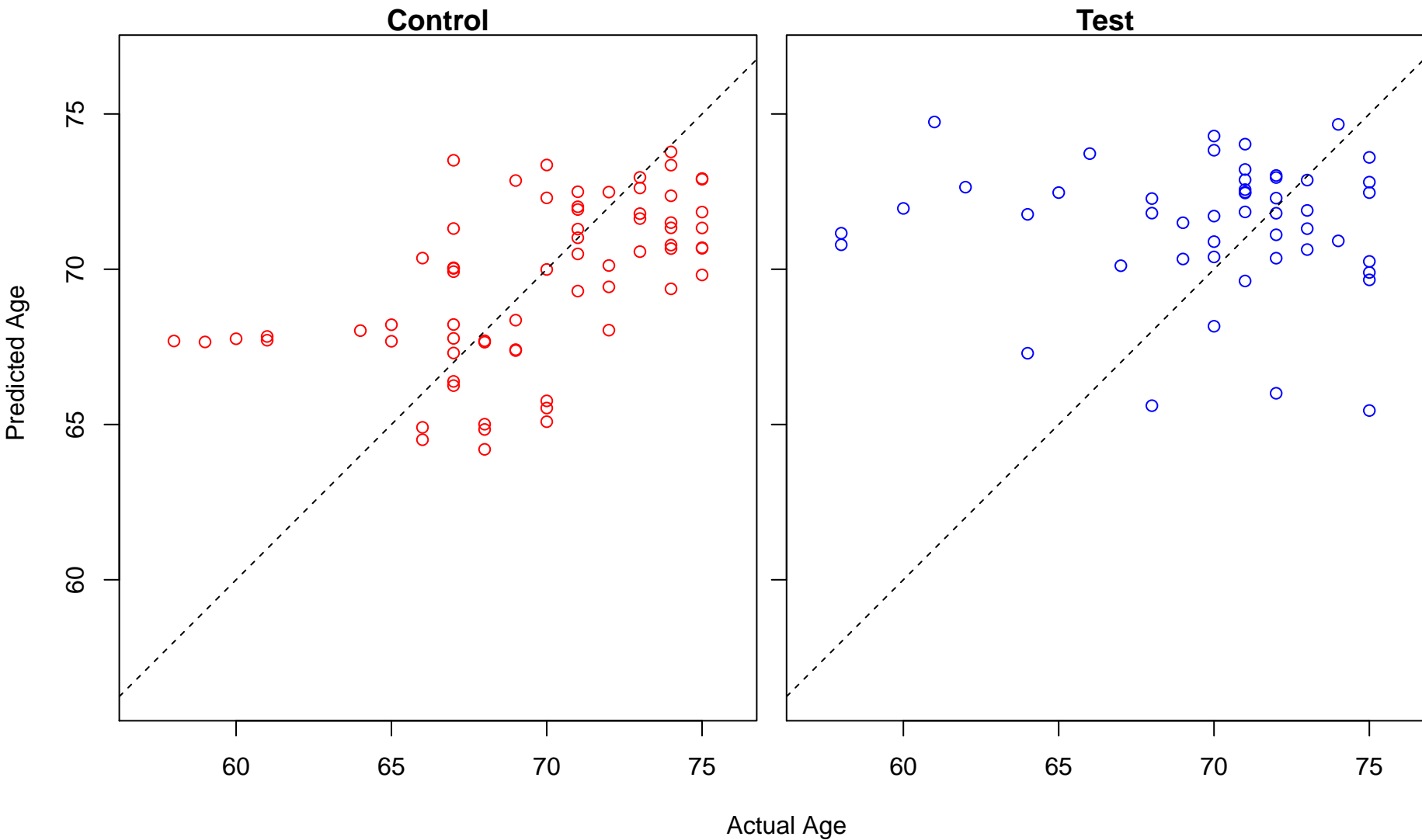


Test

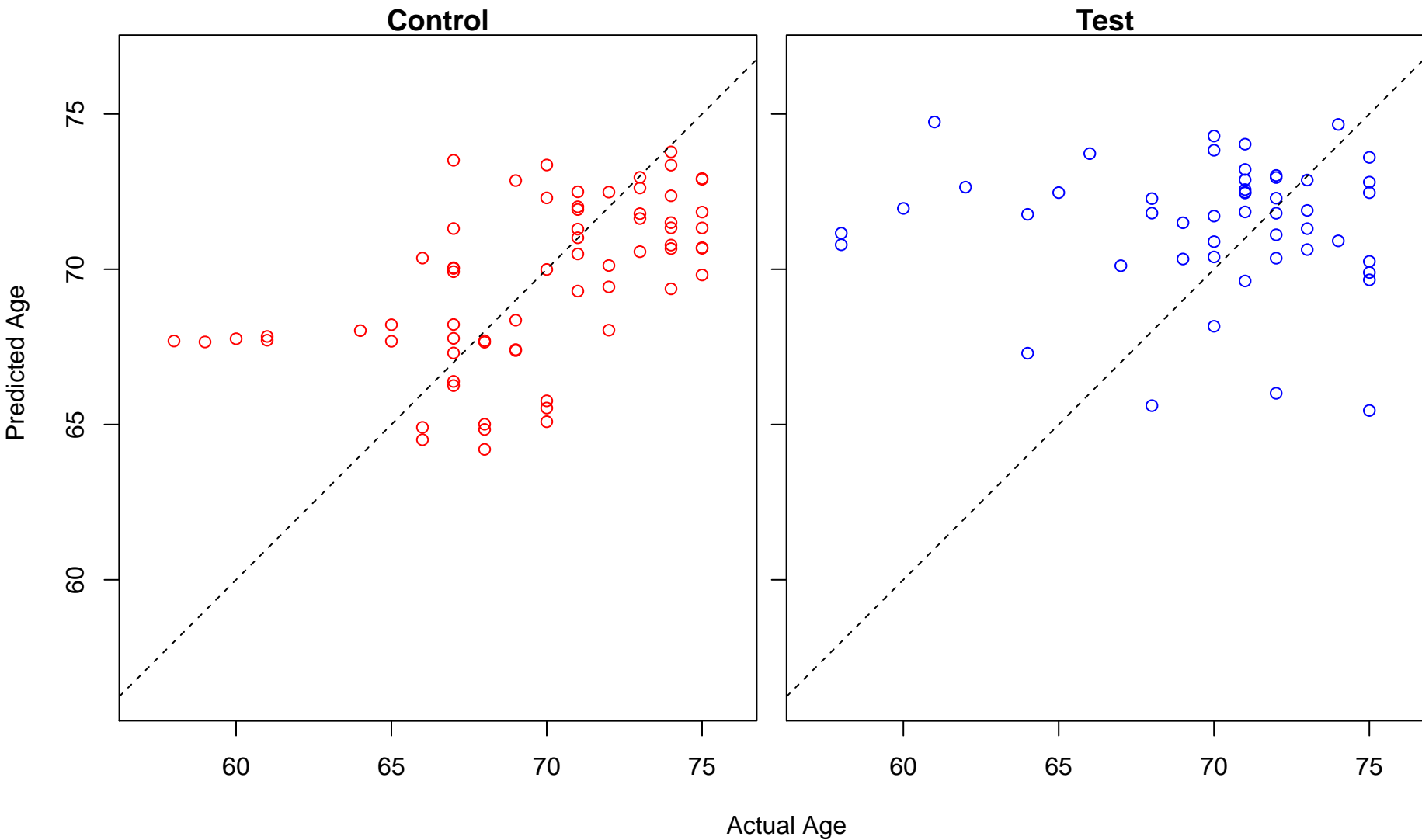


Actual Age

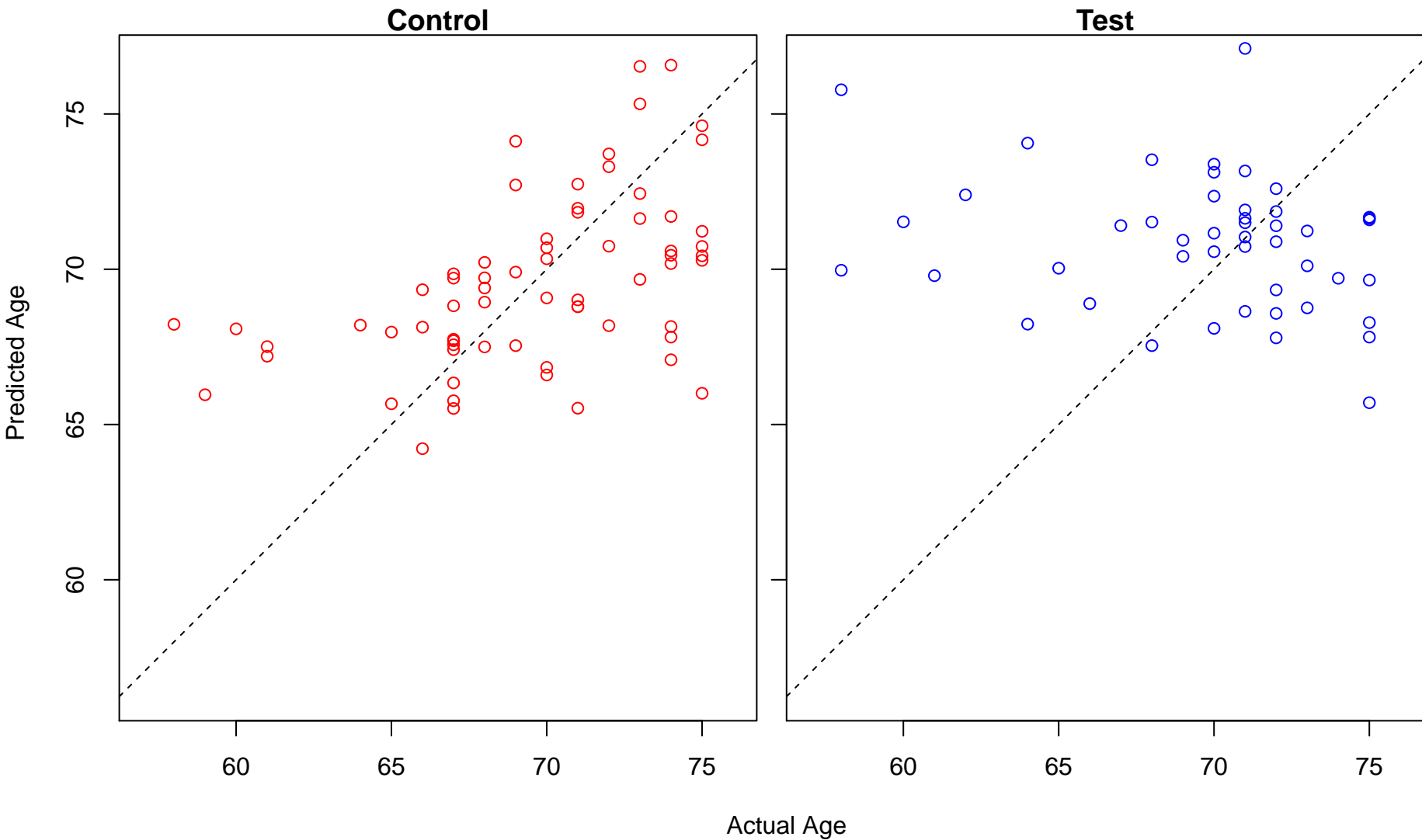
iron-sulfur cluster assembly (Score: 0.895118)



metallo-sulfur cluster assembly (Score: 0.895118)

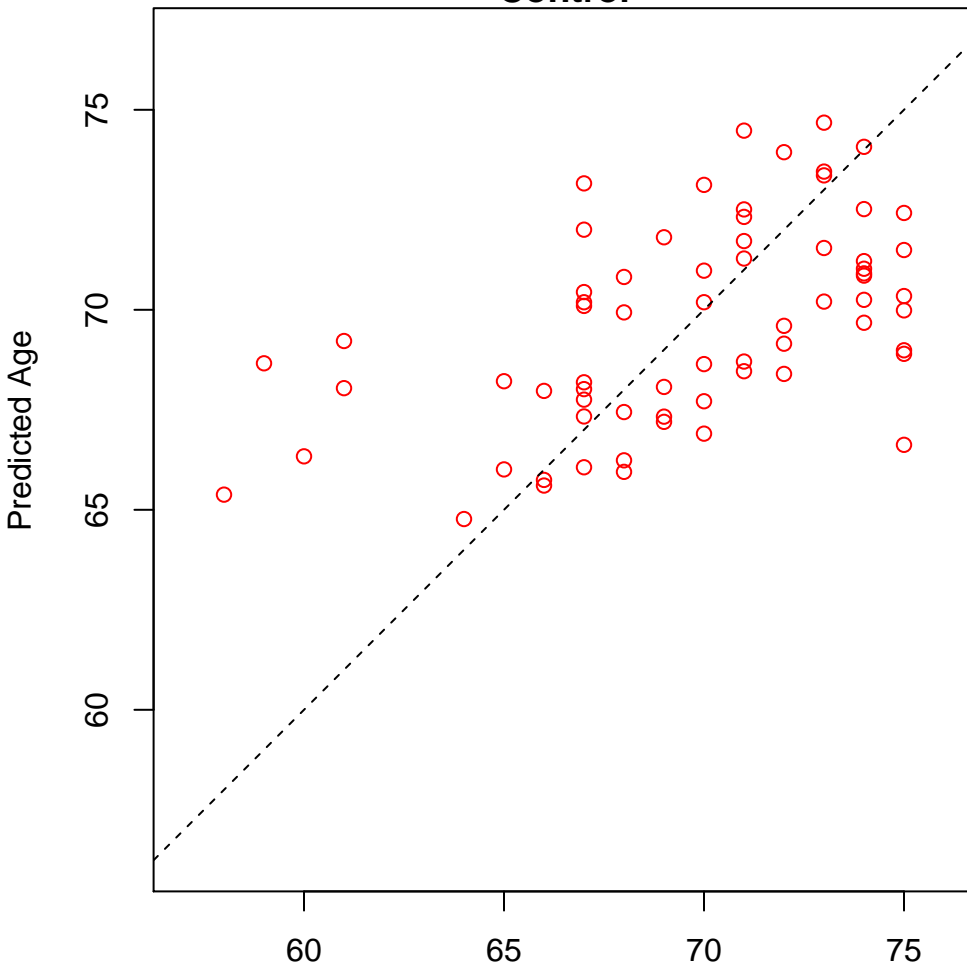


cellular response to virus (Score: 0.895019)

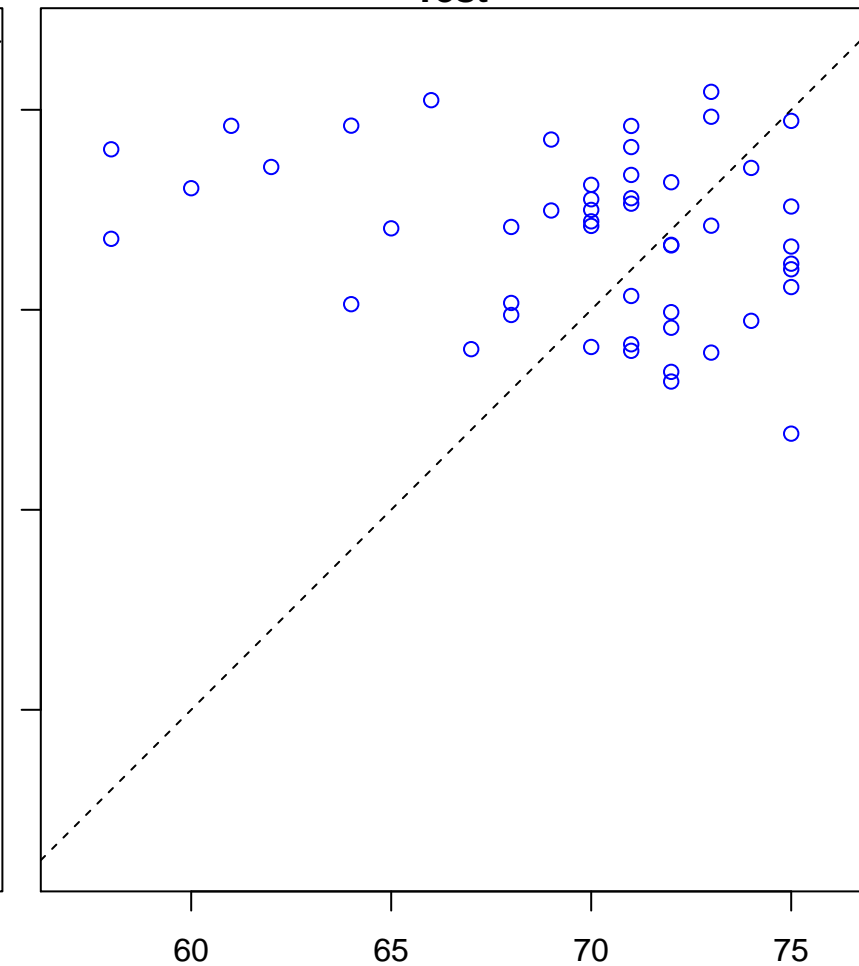


endocardial cushion morphogenesis (Score: 0.894925)

Control

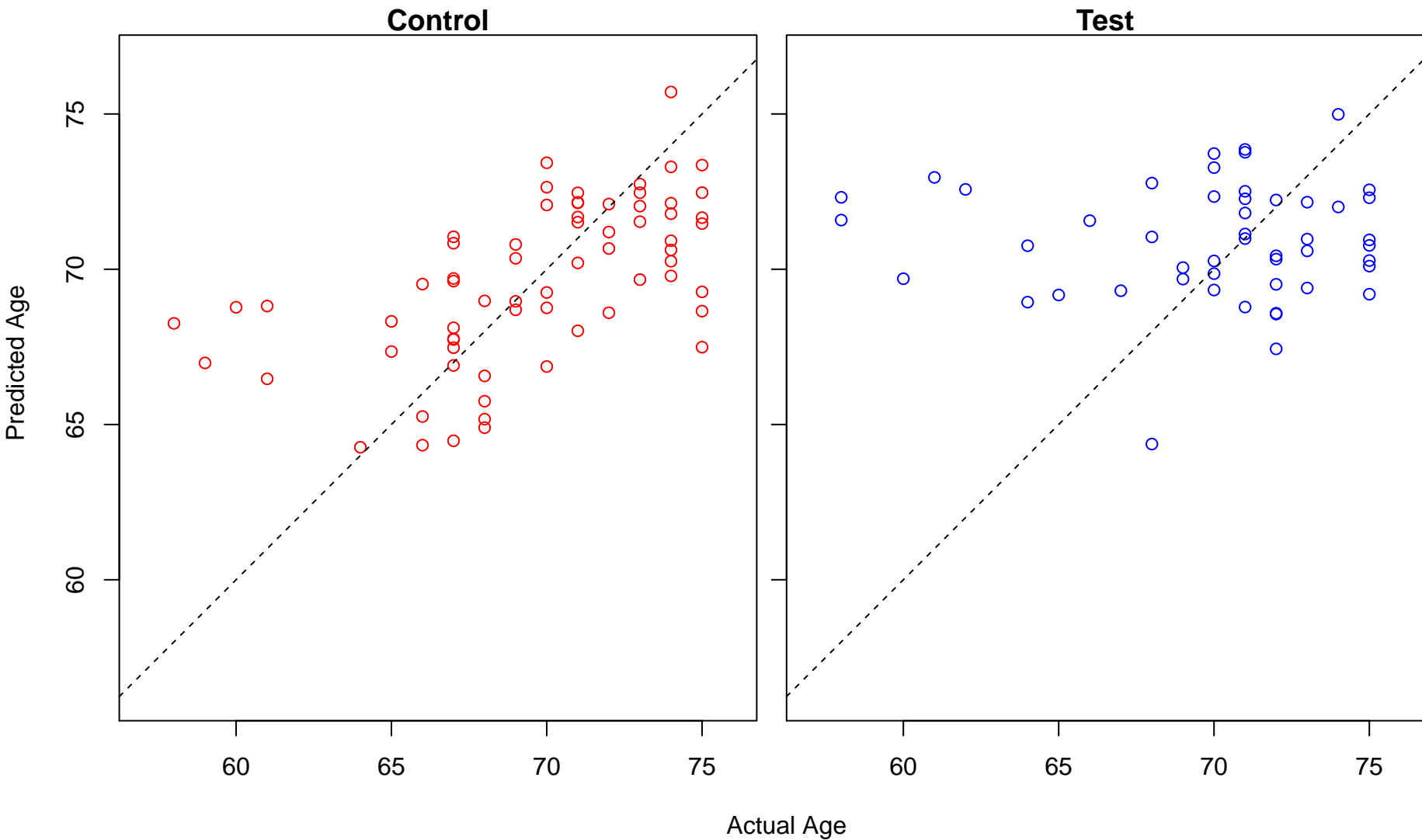


Test



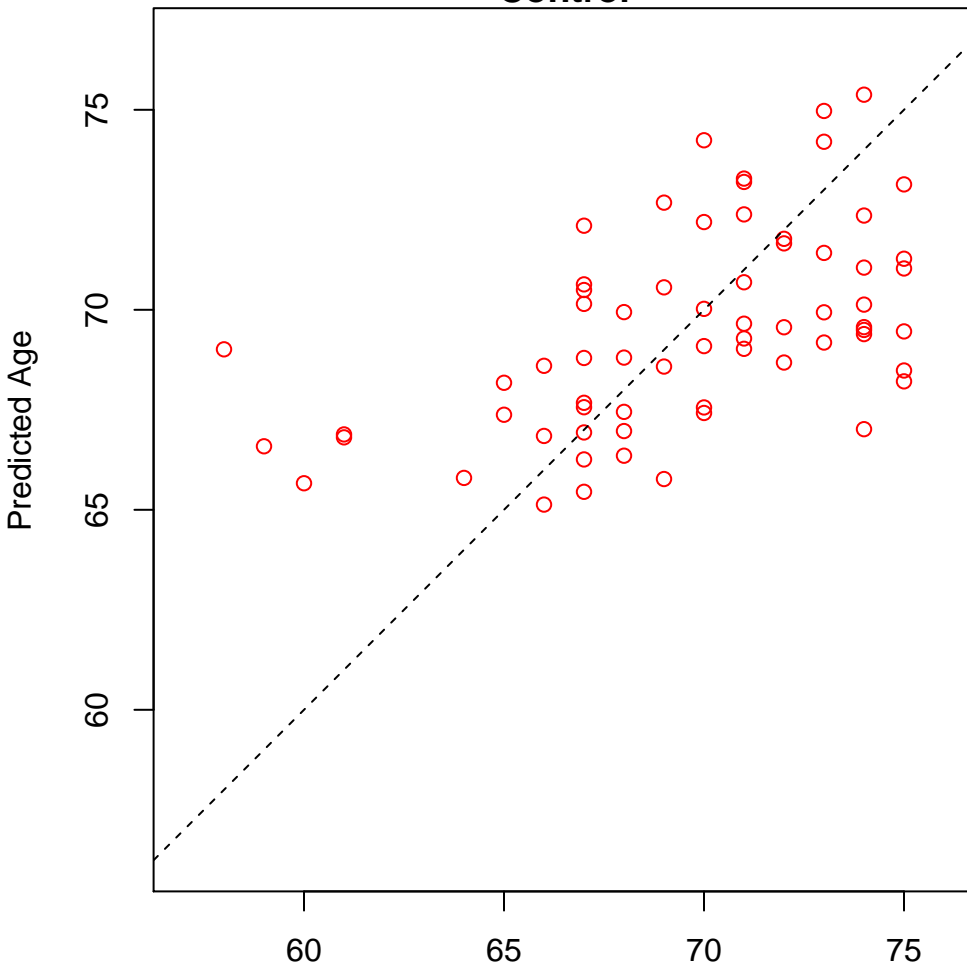
Actual Age

myofibril assembly (Score: 0.894837)

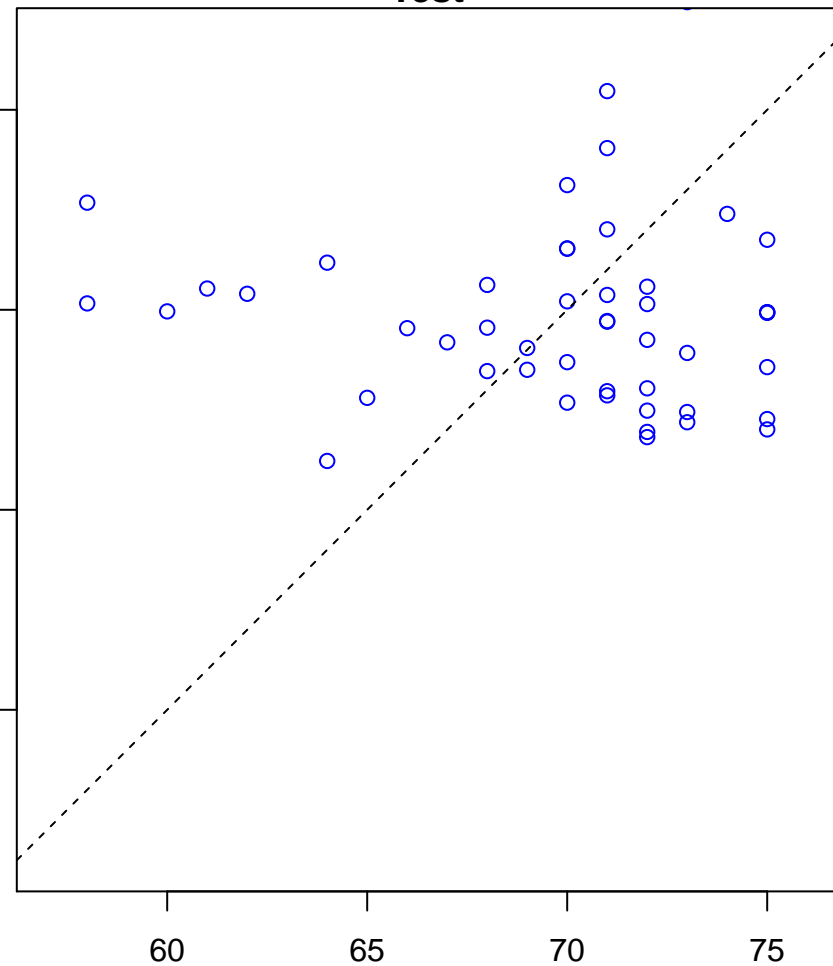


alpha-linolenic acid metabolic process (Score: 0.894801)

Control

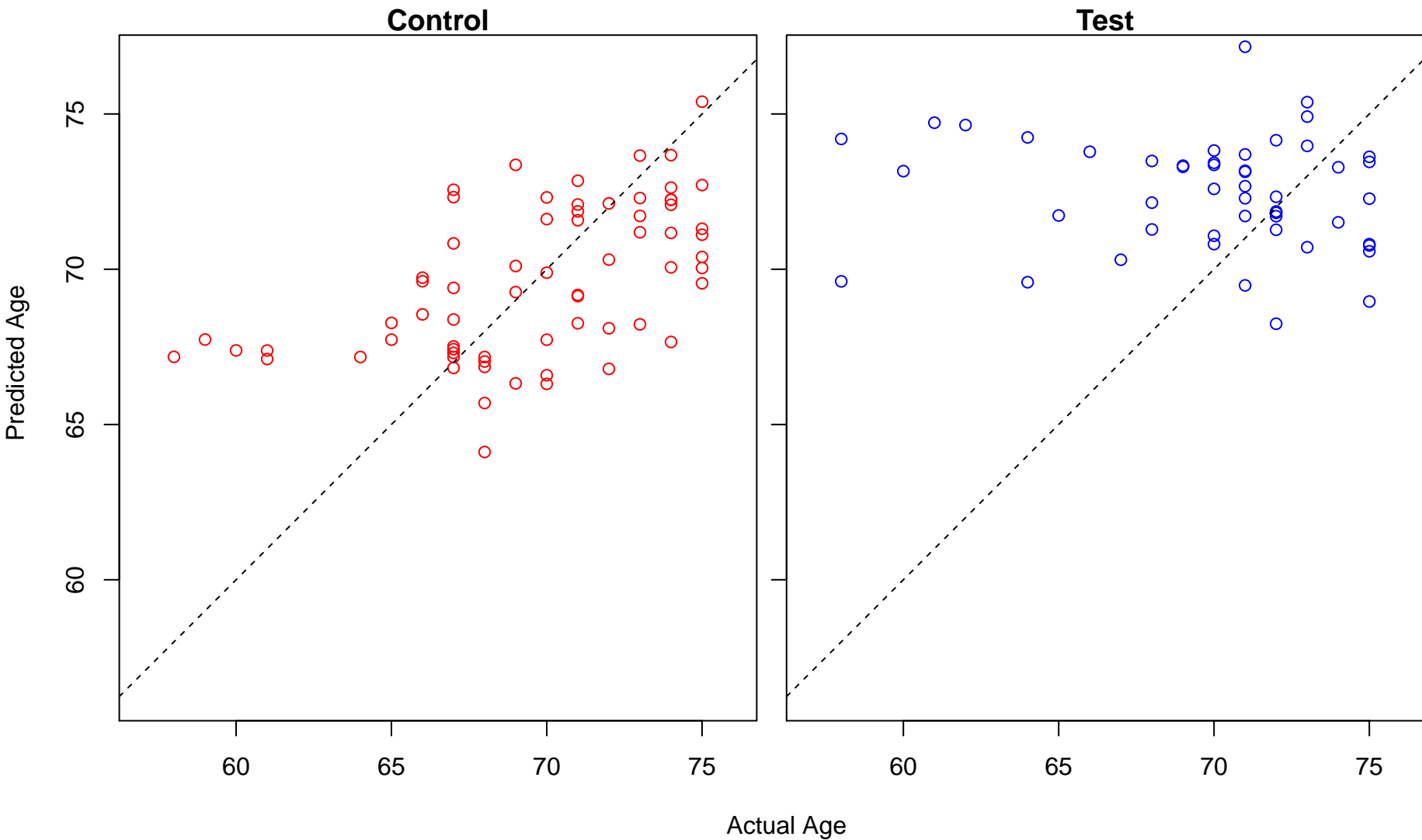


Test

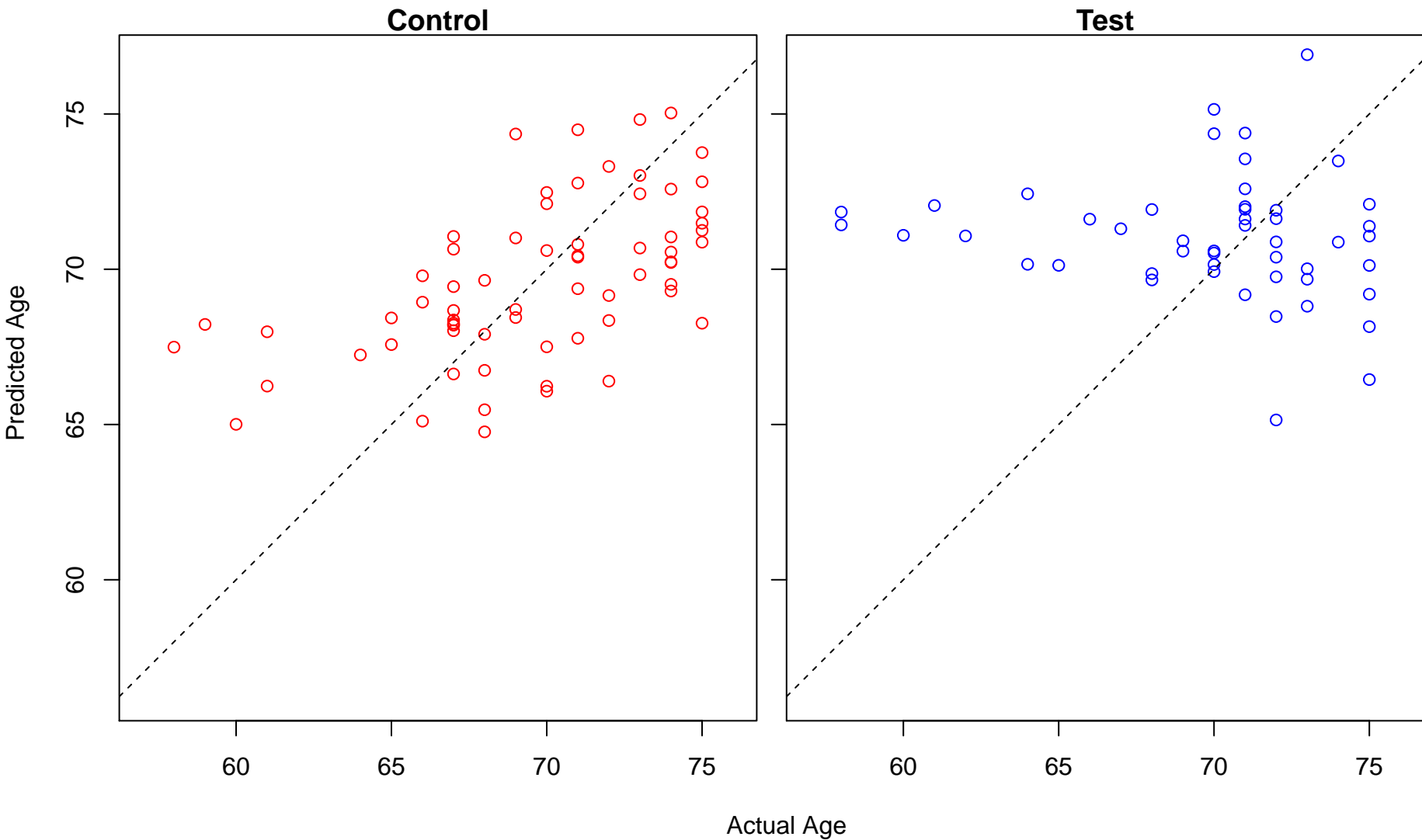


Actual Age

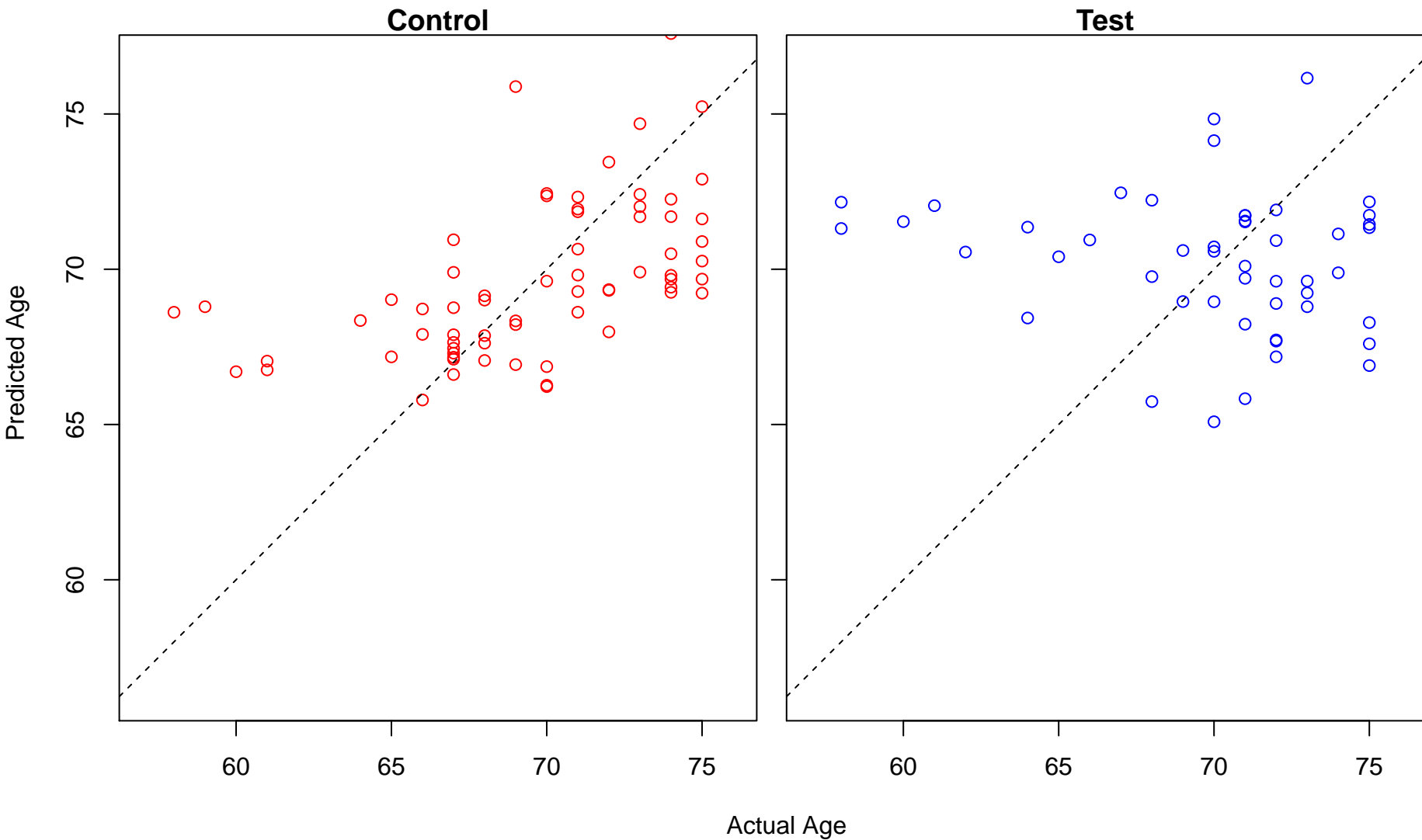
neuroepithelial cell differentiation (Score: 0.894735)



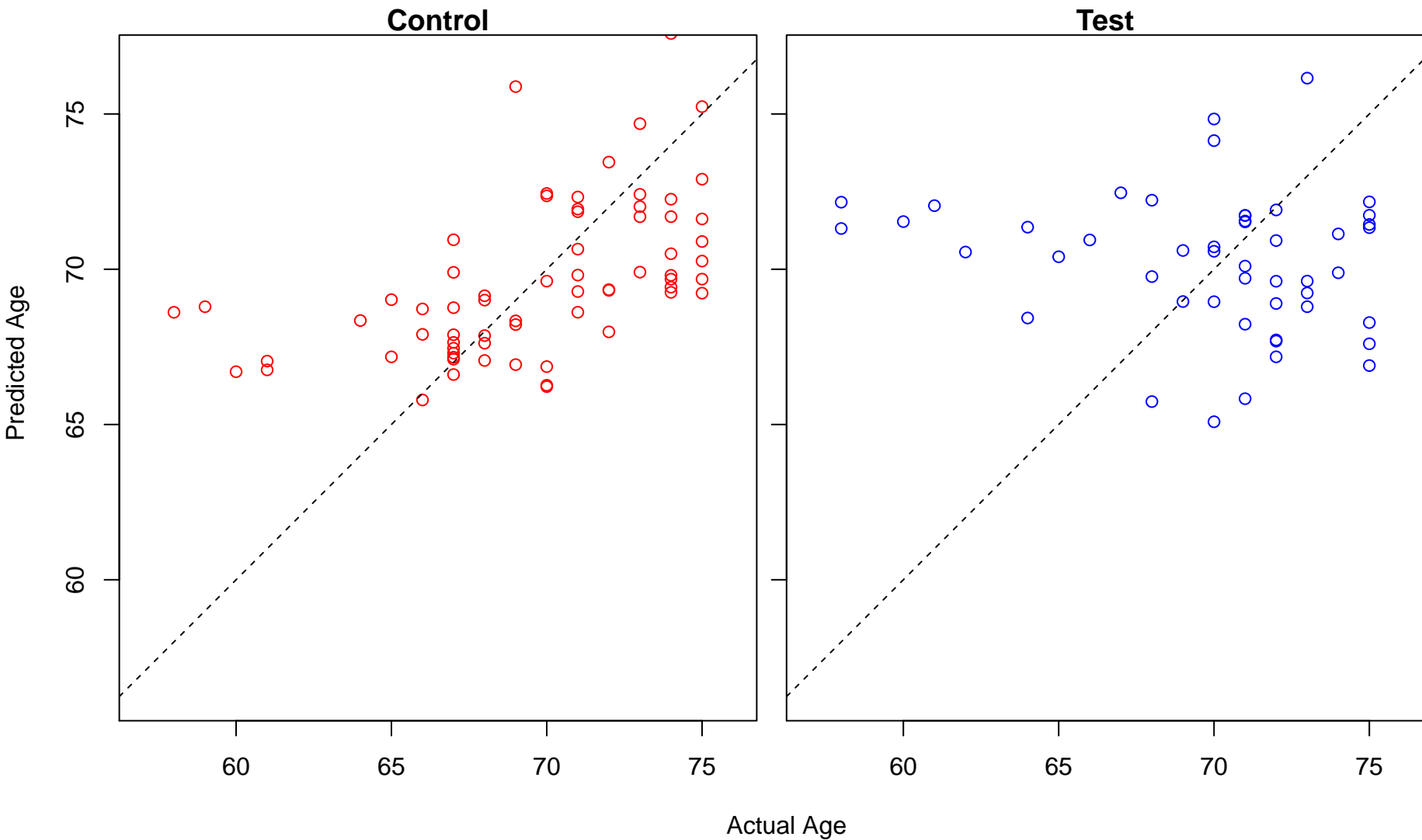
methionine metabolic process (Score: 0.894443)



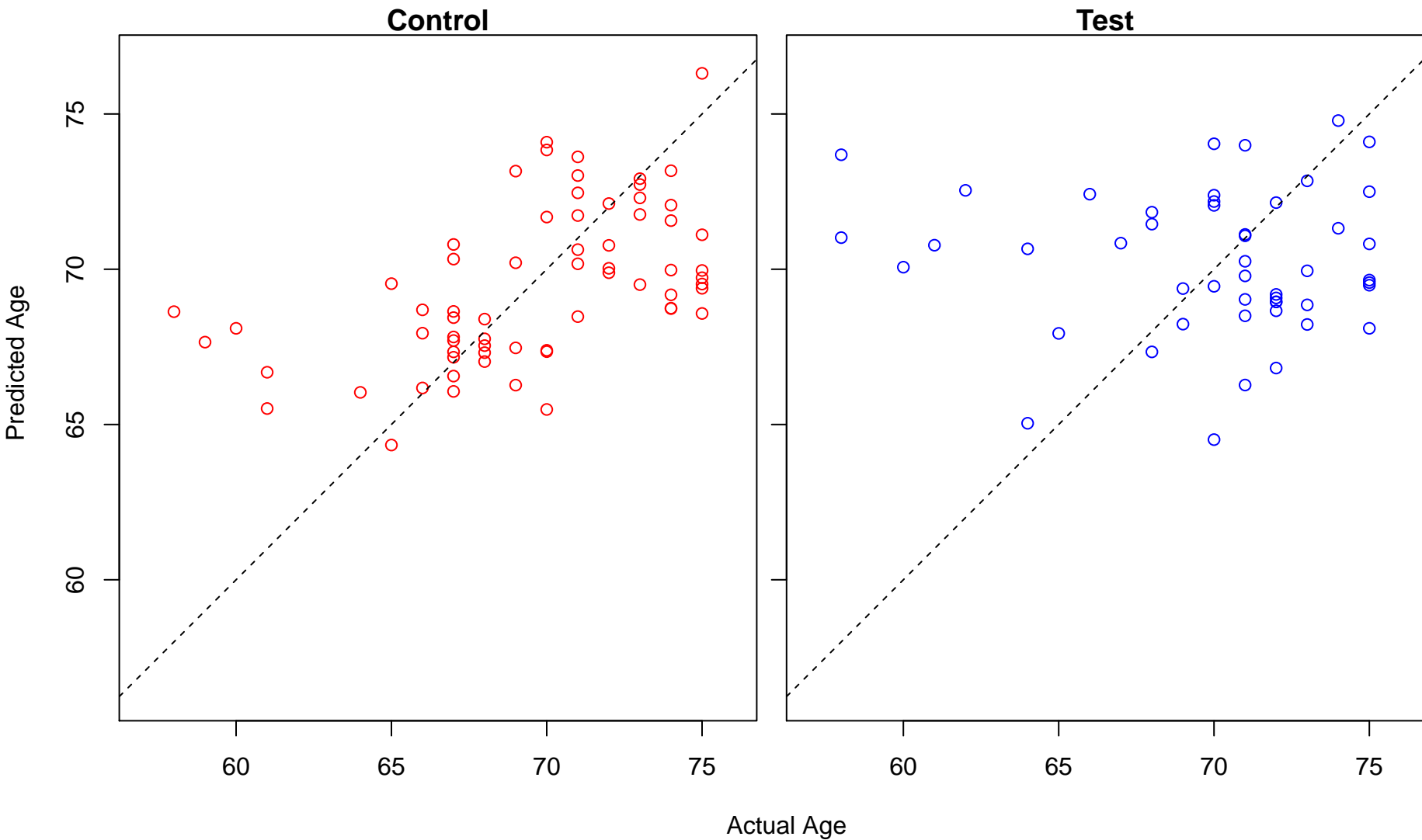
social behavior (Score: 0.894316)



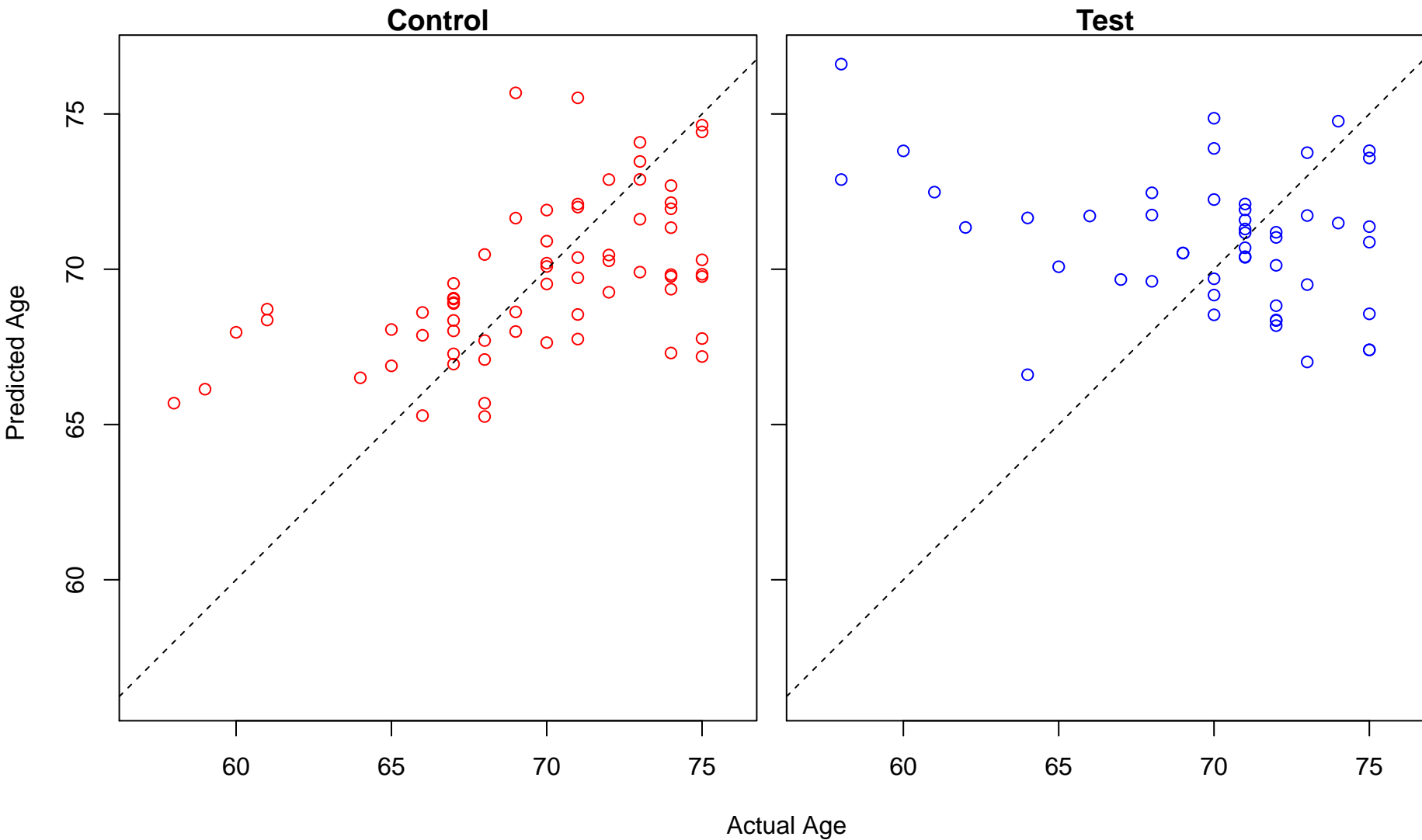
intraspecies interaction between organisms (Score: 0.894316)



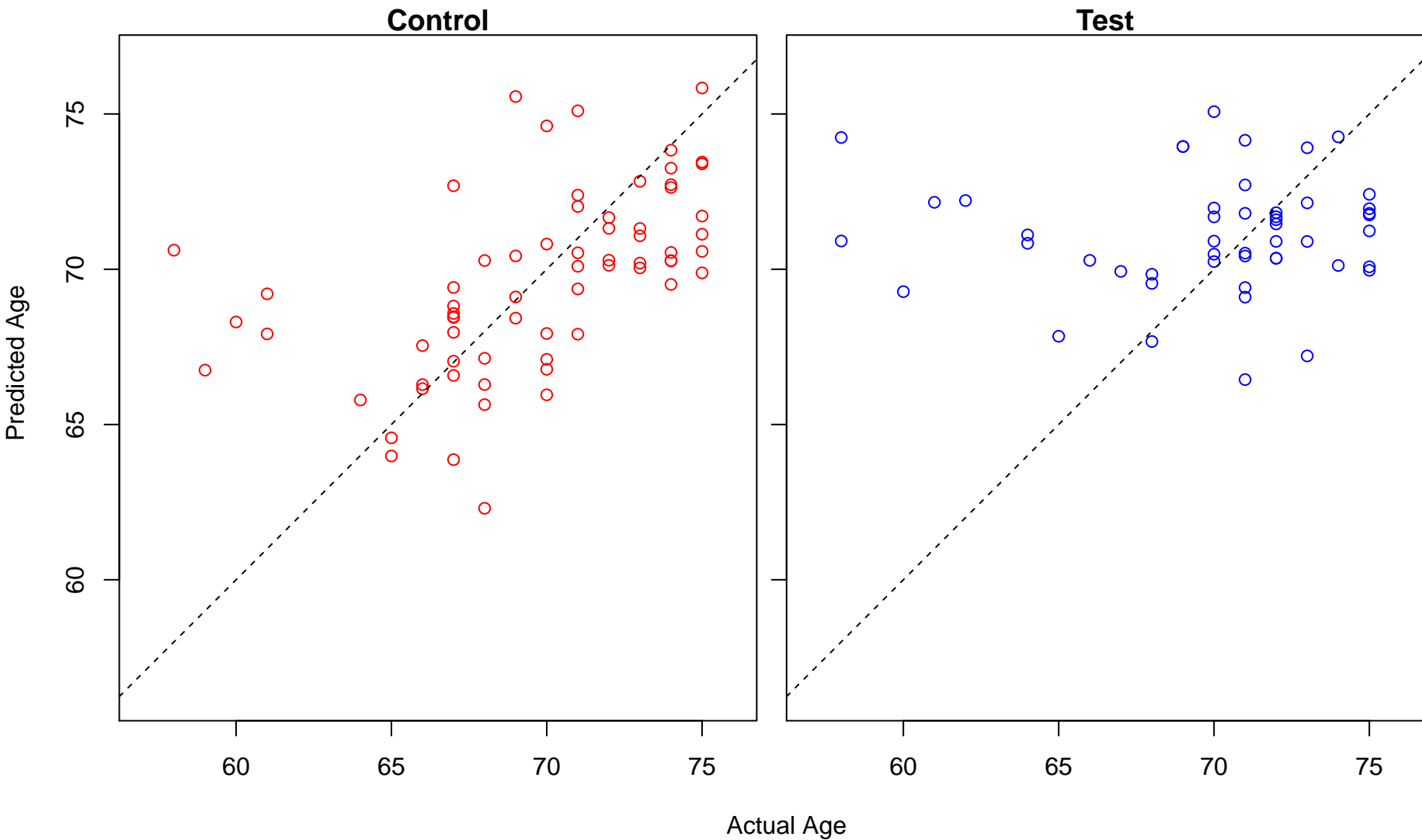
regulation of axonogenesis (Score: 0.893620)



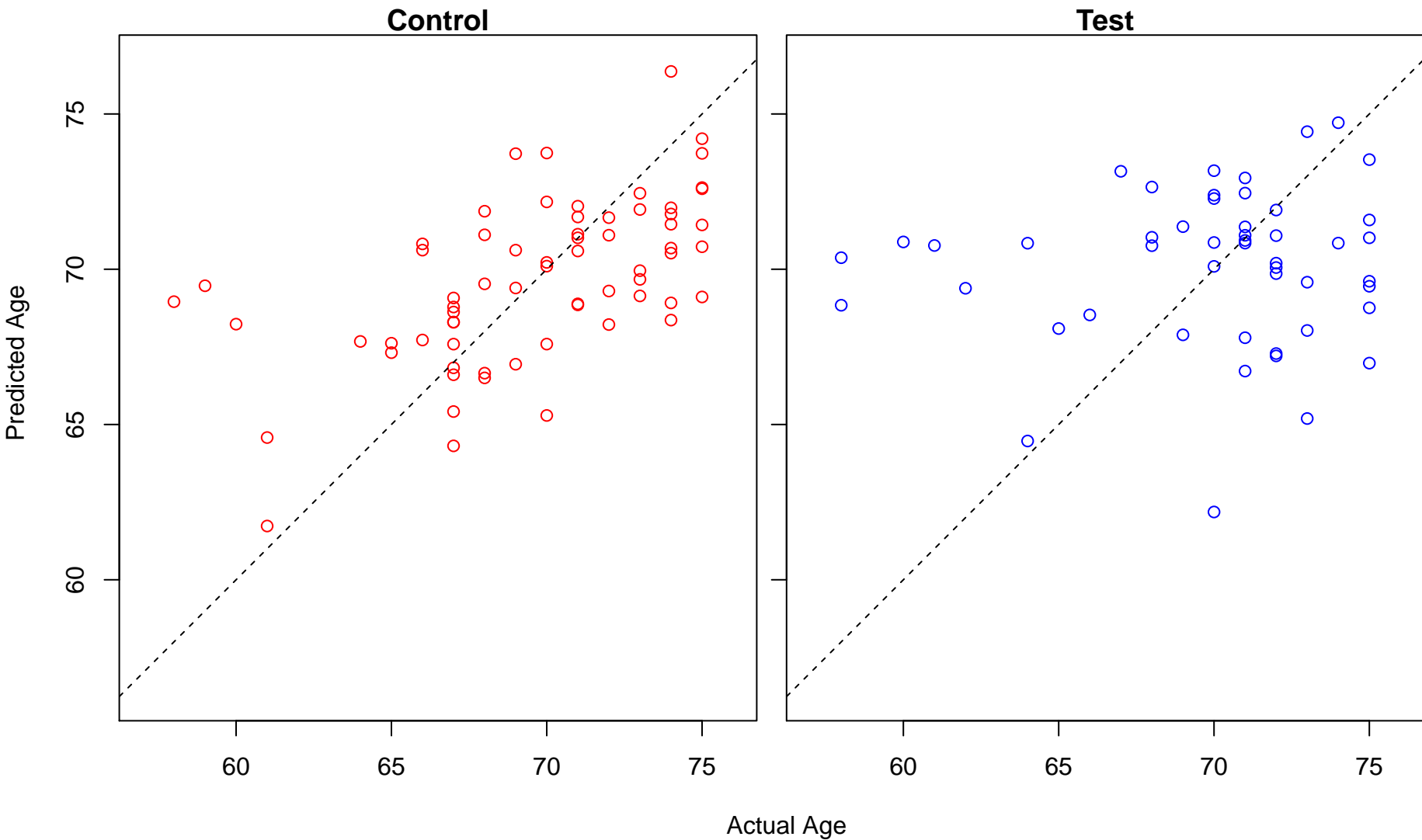
equilibrioception (Score: 0.893567)



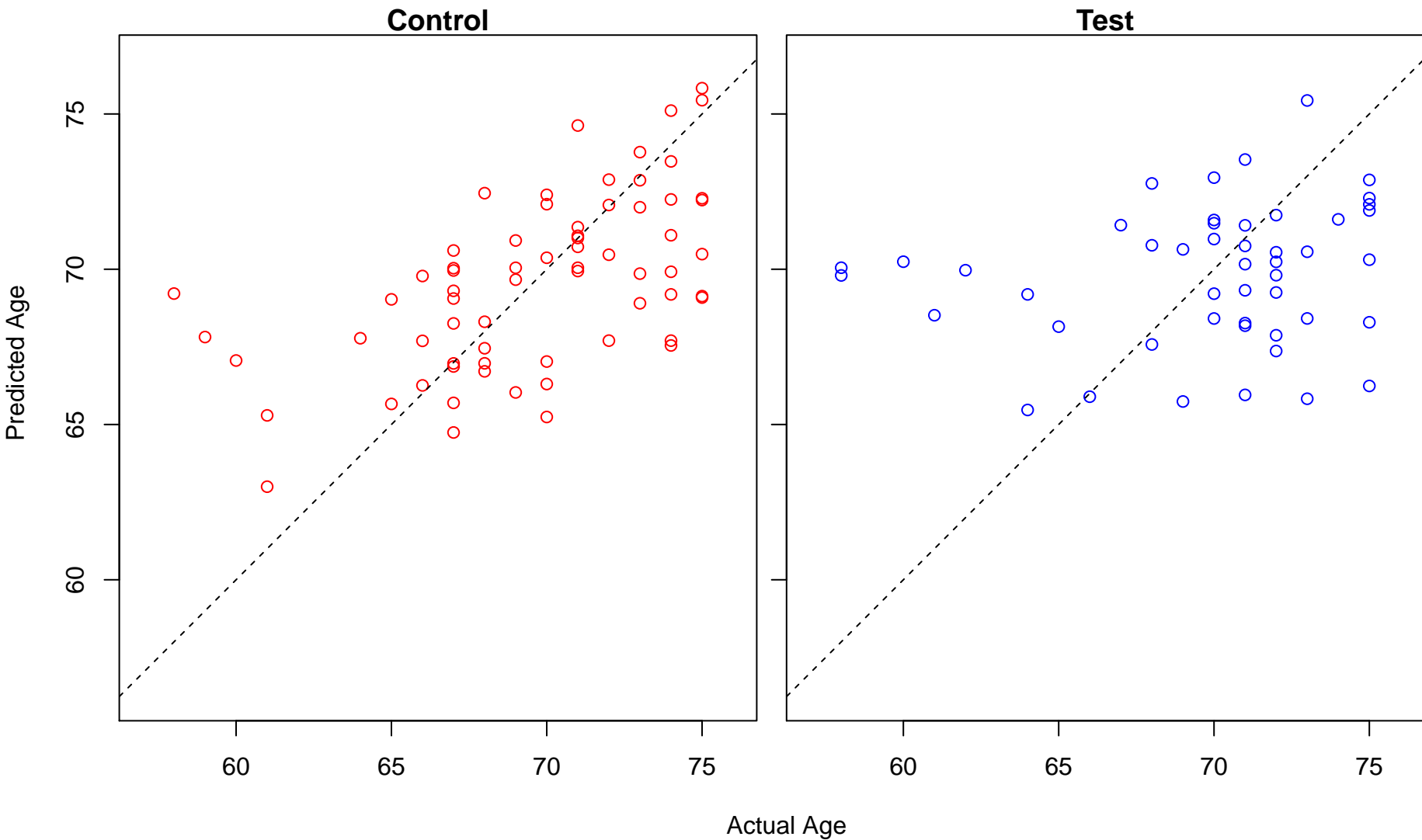
antigen processing and presentation of endogenous peptide antigen via MHC class I (Score: 0.8934)



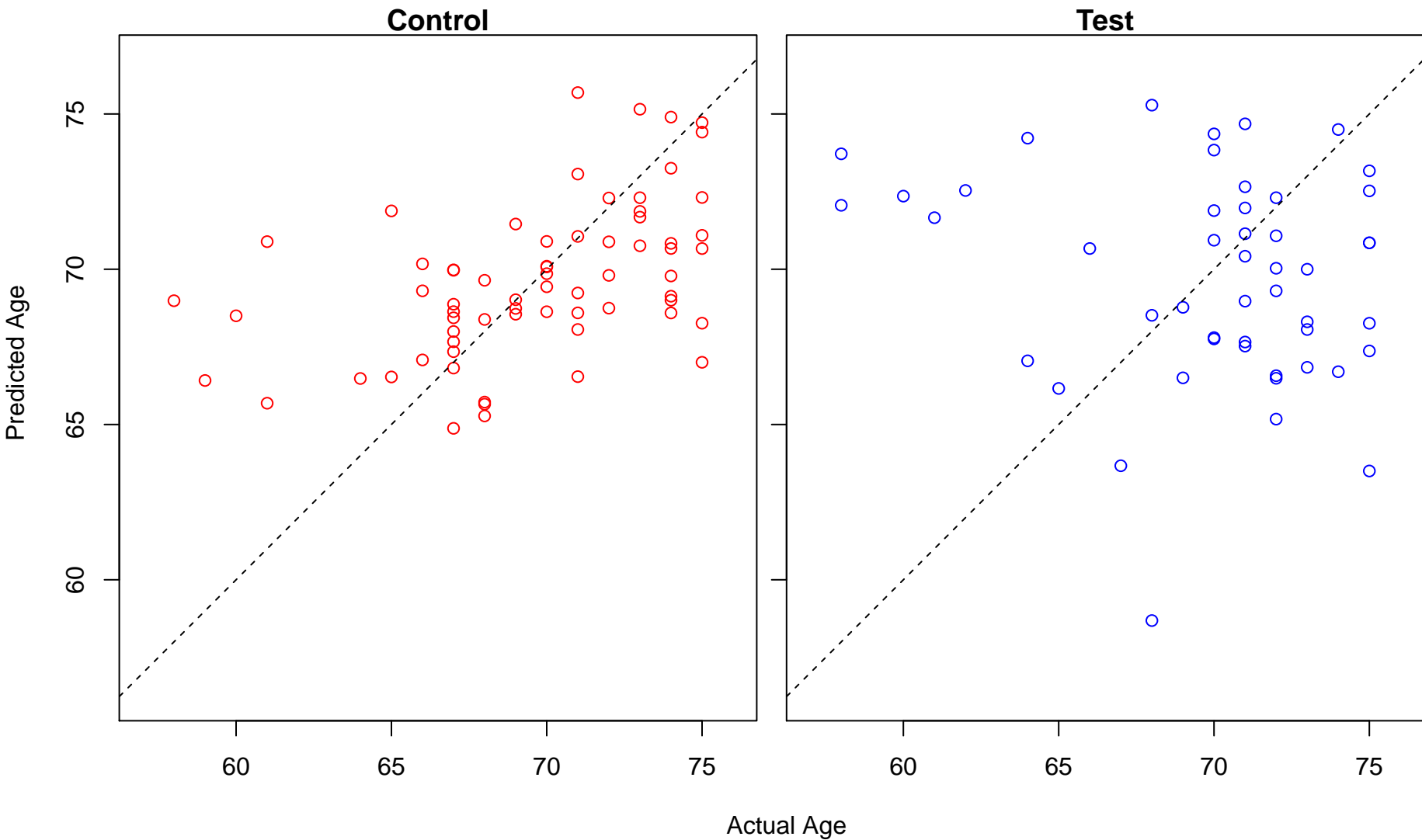
negative regulation of CREB transcription factor activity (Score: 0.893355)



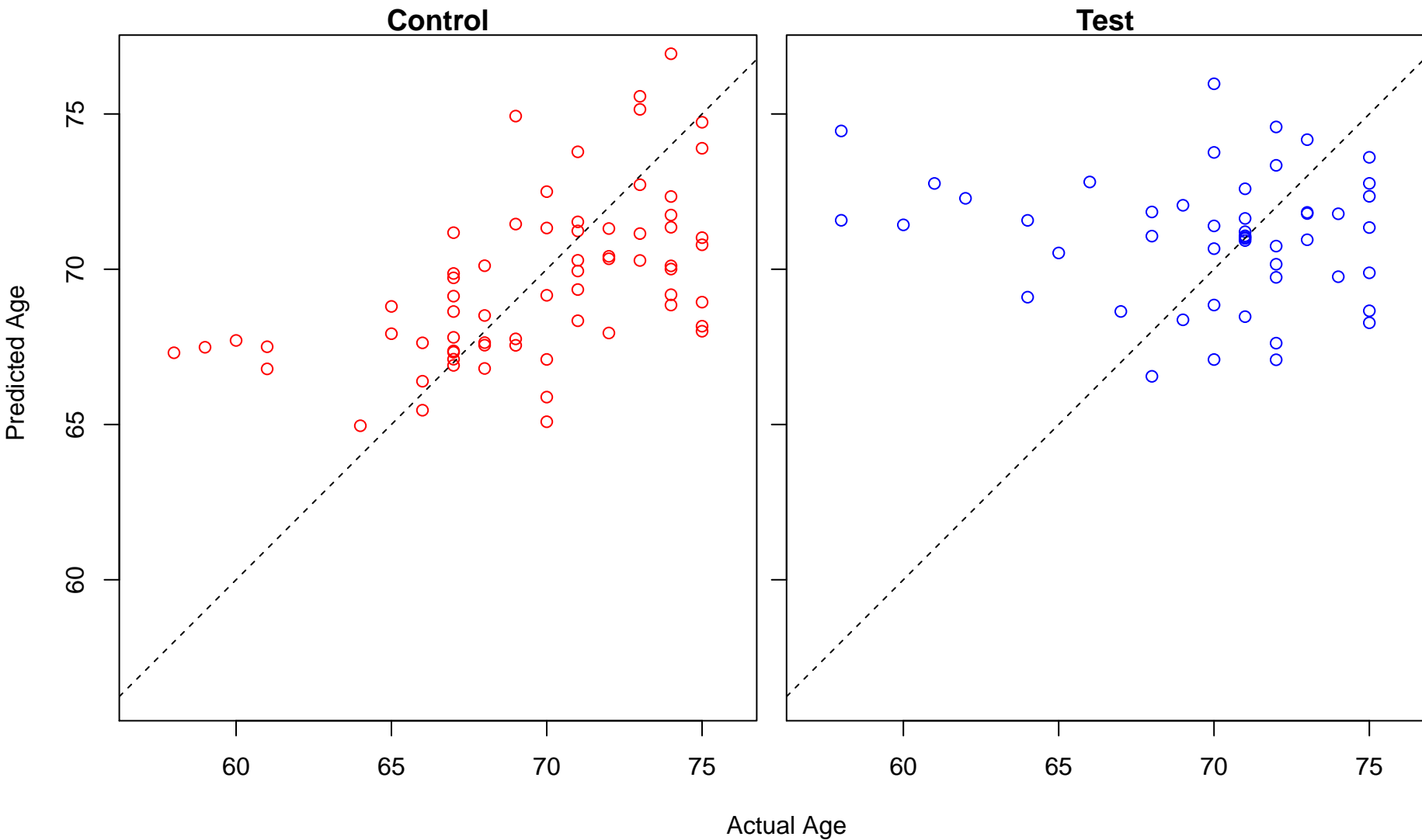
positive regulation of viral release from host cell (Score: 0.892624)



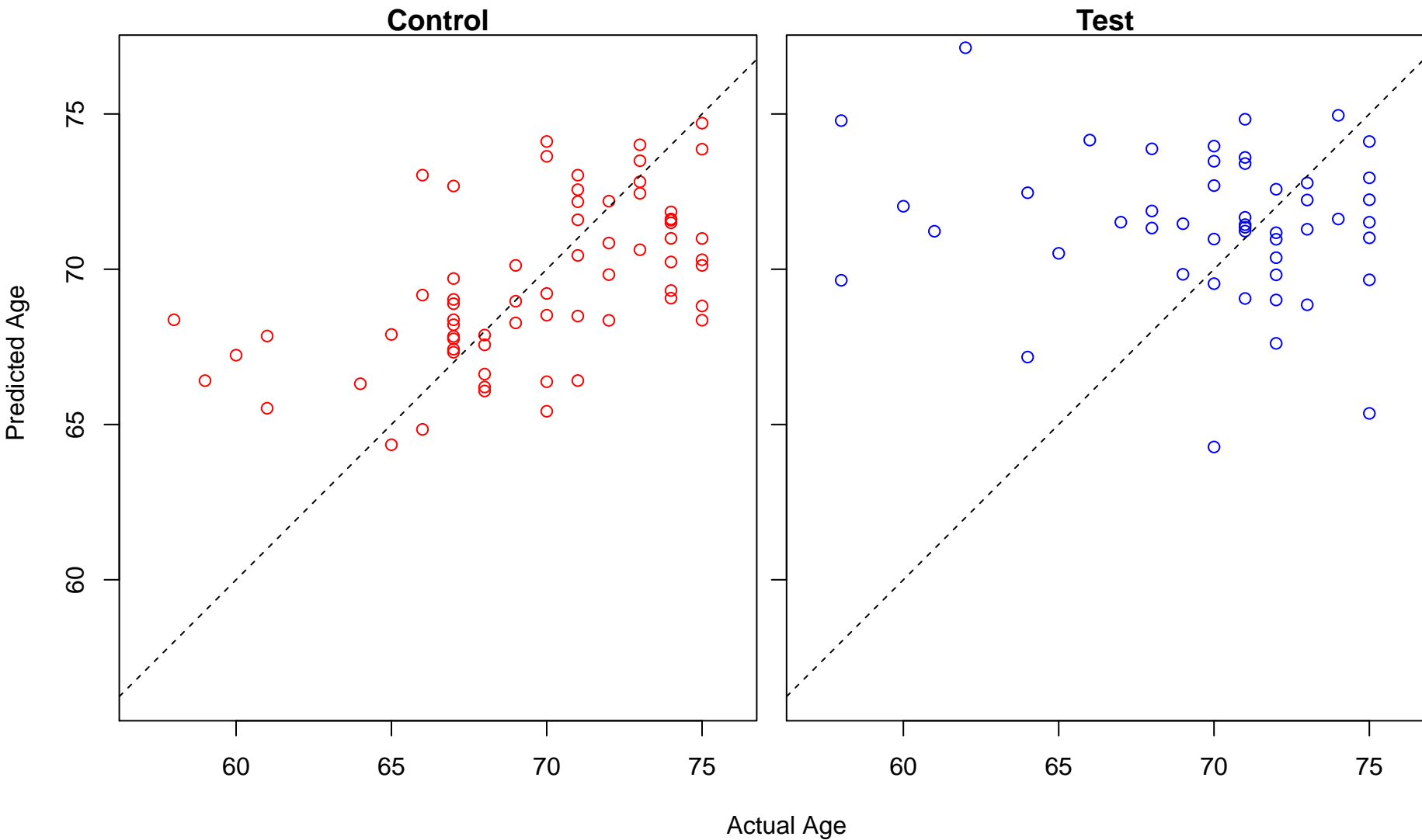
hematopoietic stem cell proliferation (Score: 0.892619)



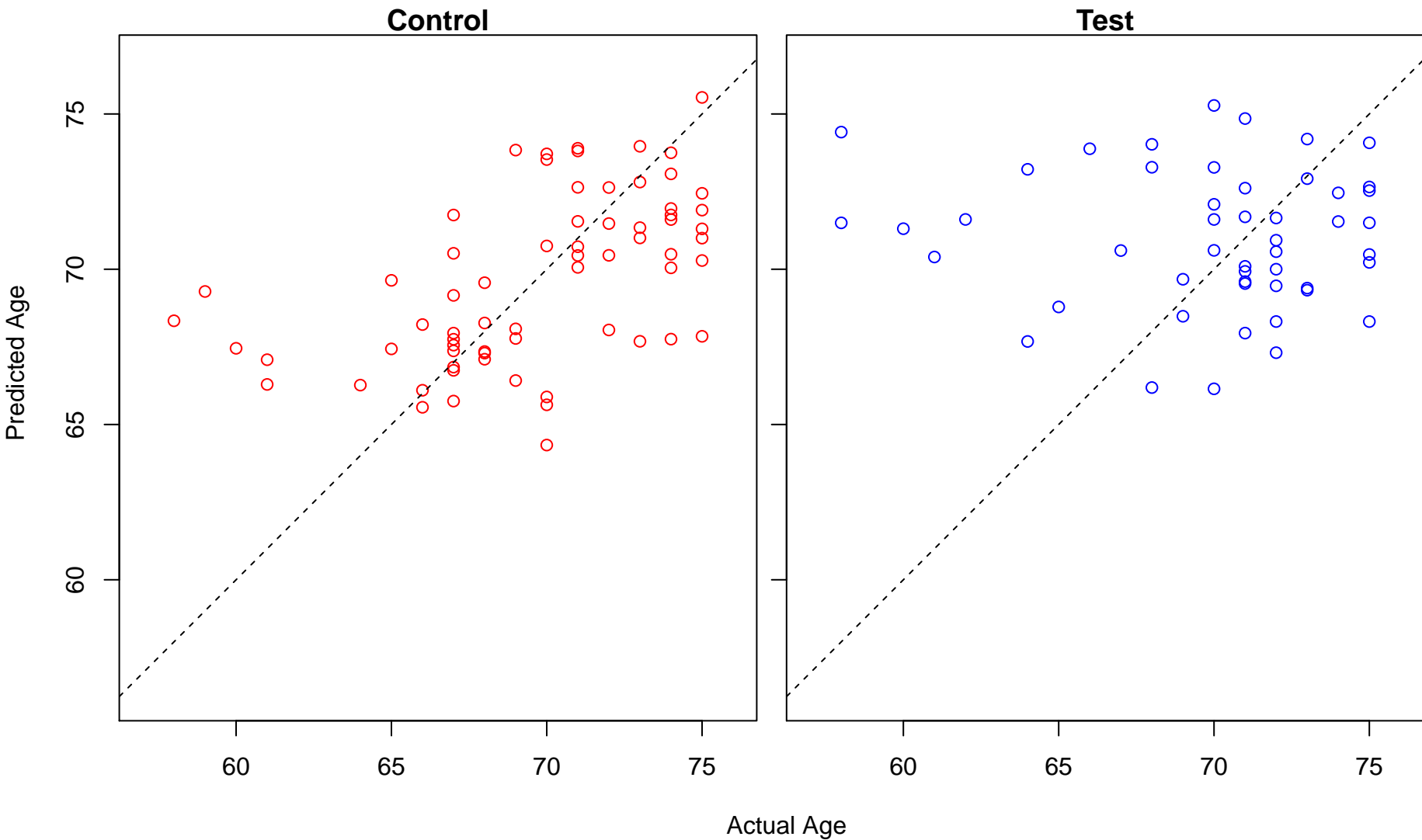
cardiac muscle contraction (Score: 0.892441)



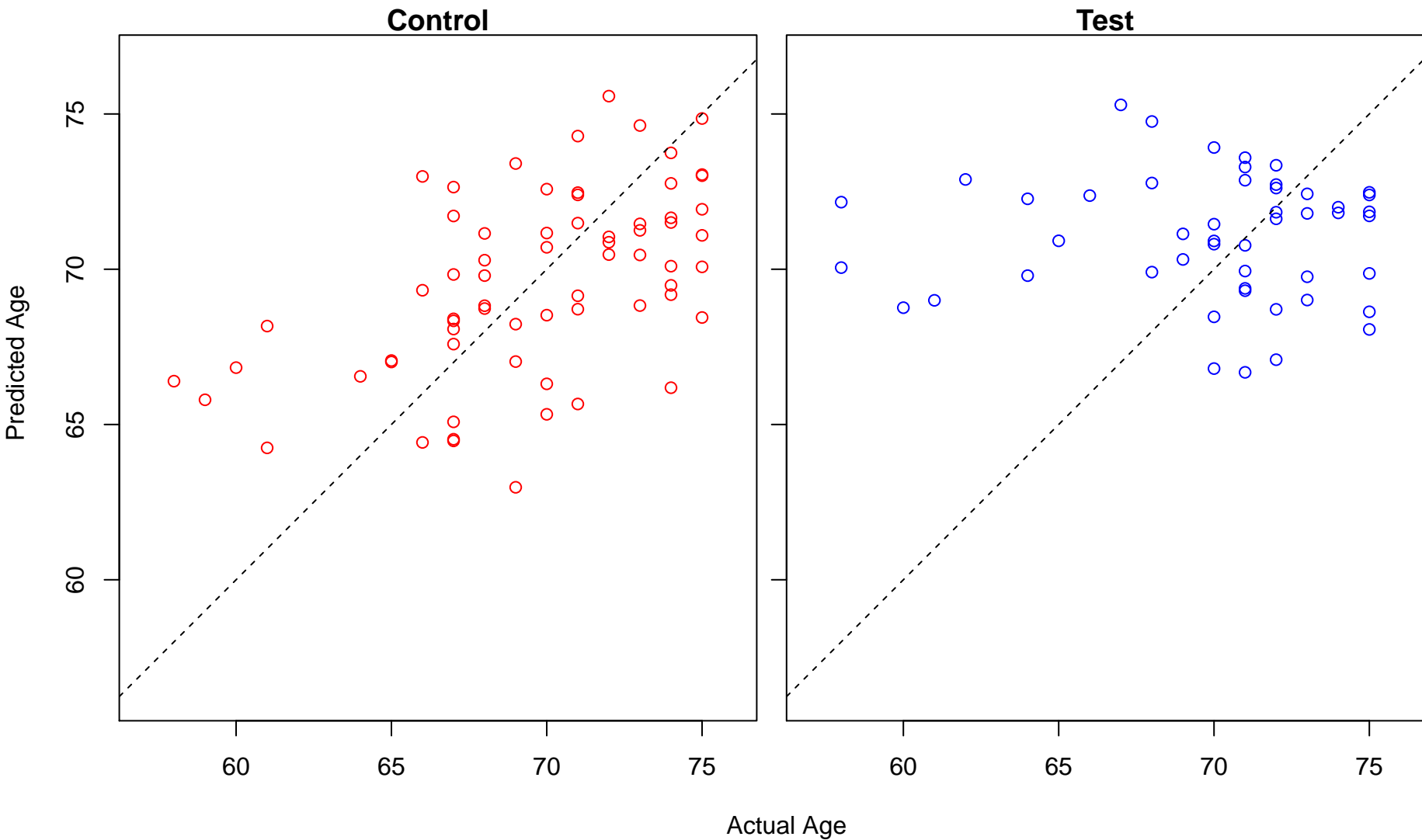
modulation by host of viral process (Score: 0.892351)



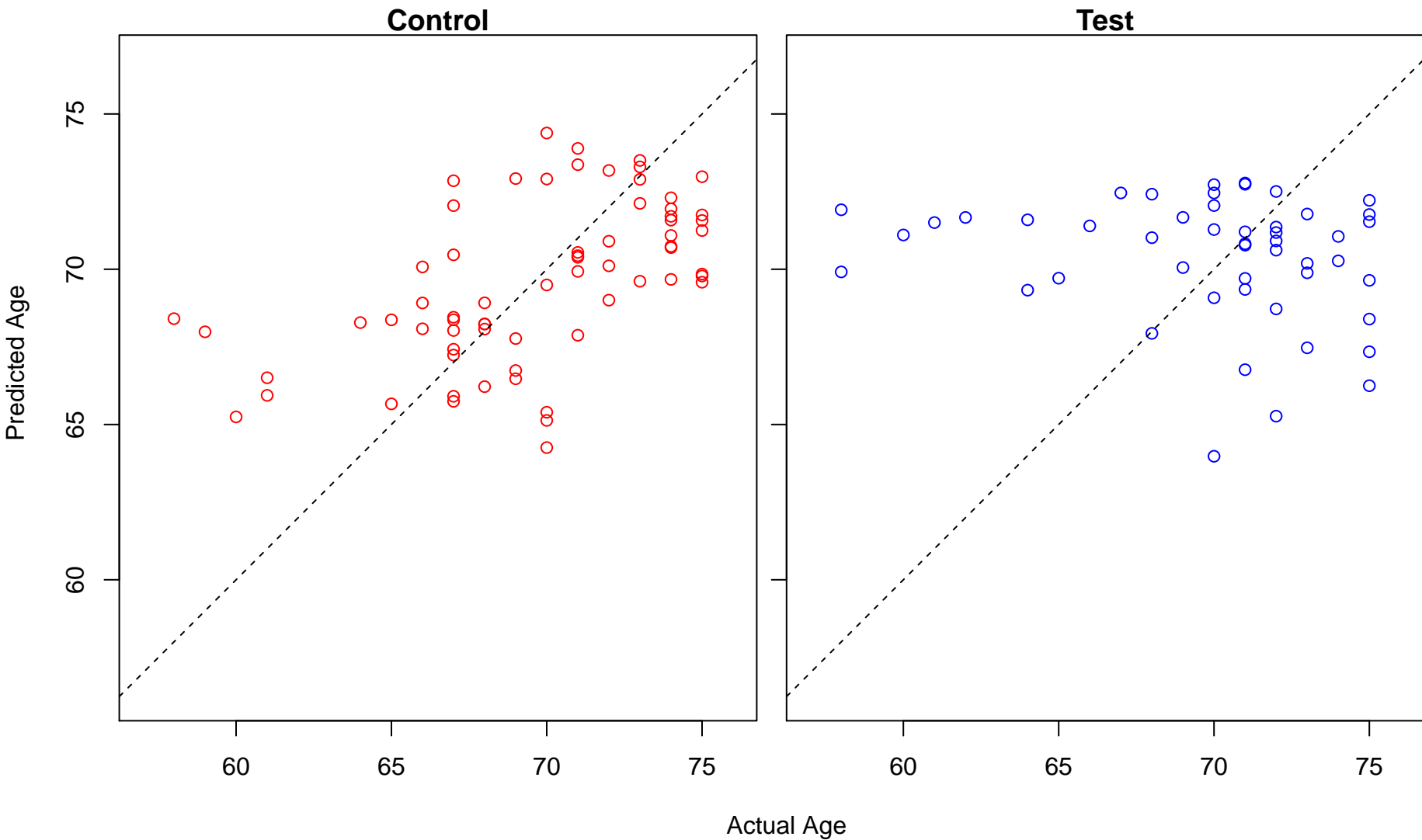
import into cell (Score: 0.892041)



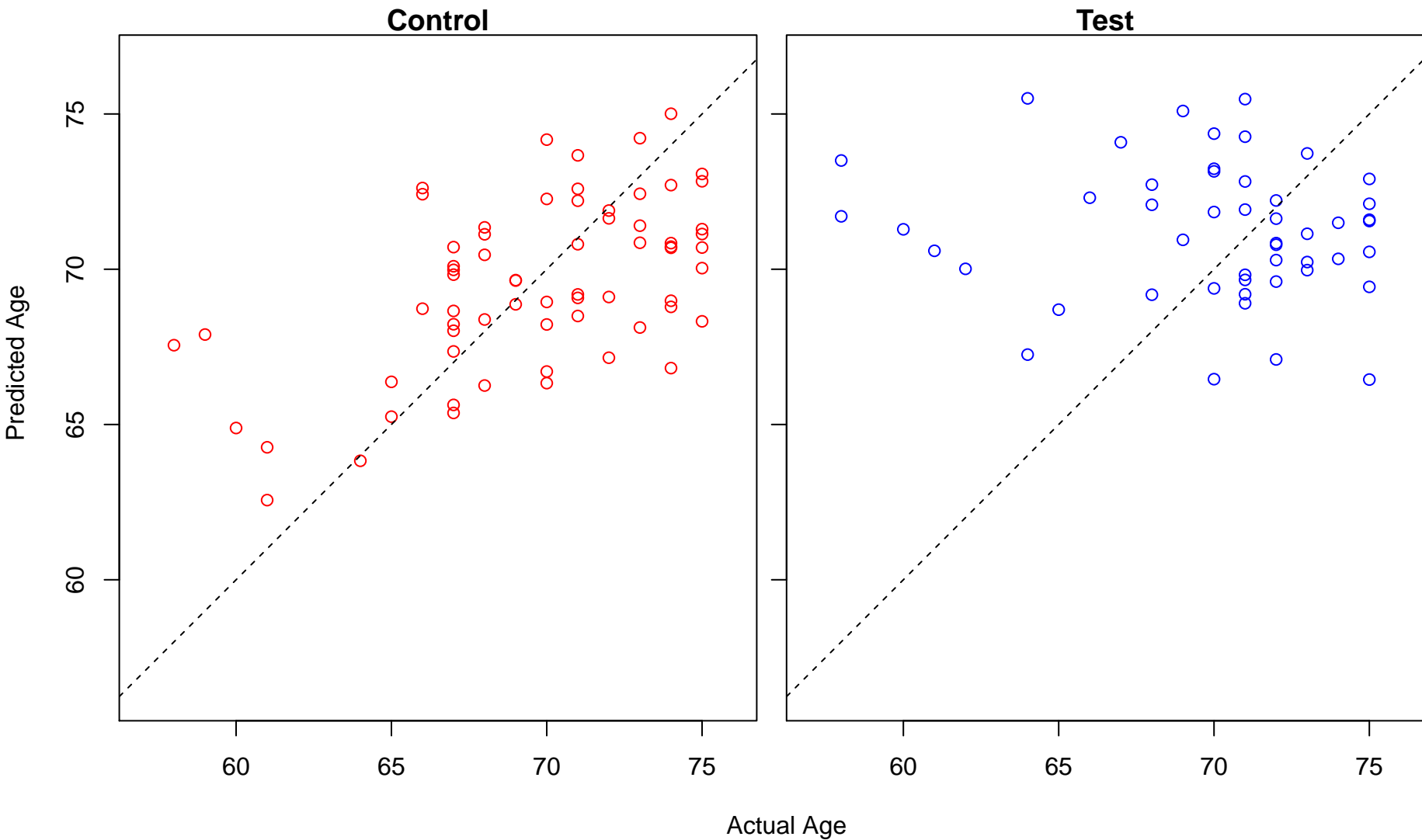
regulation of endothelial cell apoptotic process (Score: 0.891761)



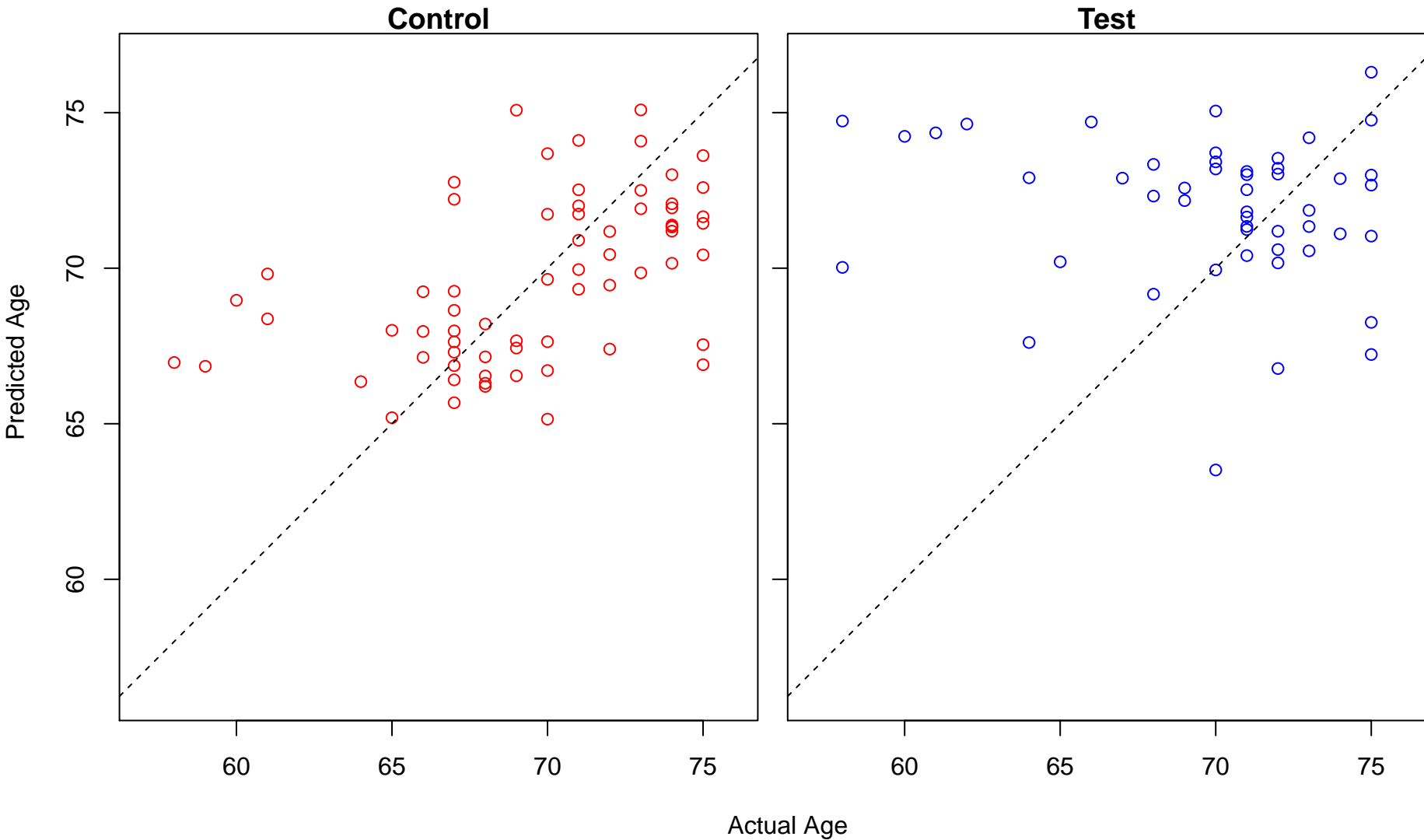
positive regulation of tumor necrosis factor production (Score: 0.891288)



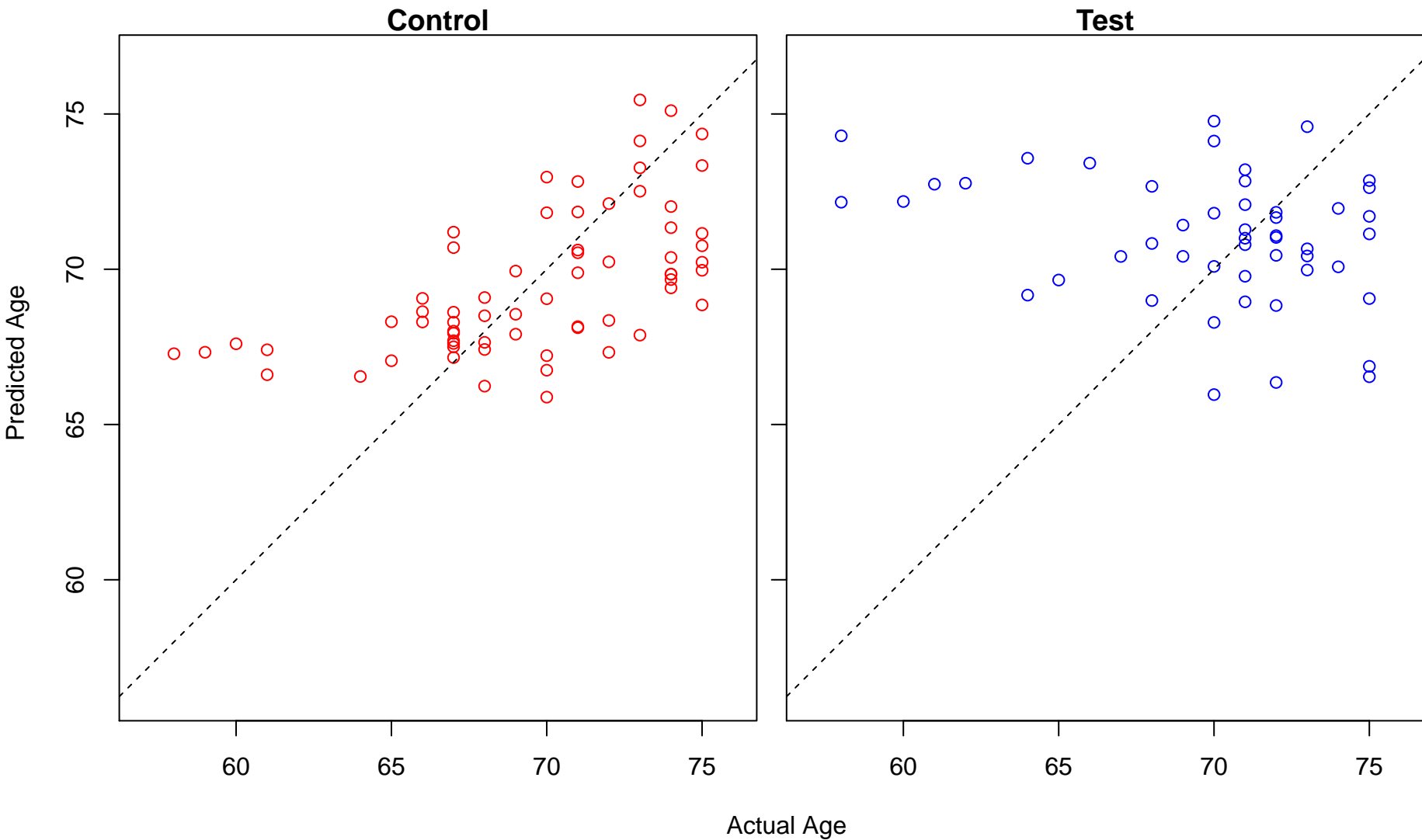
axis specification (Score: 0.890822)



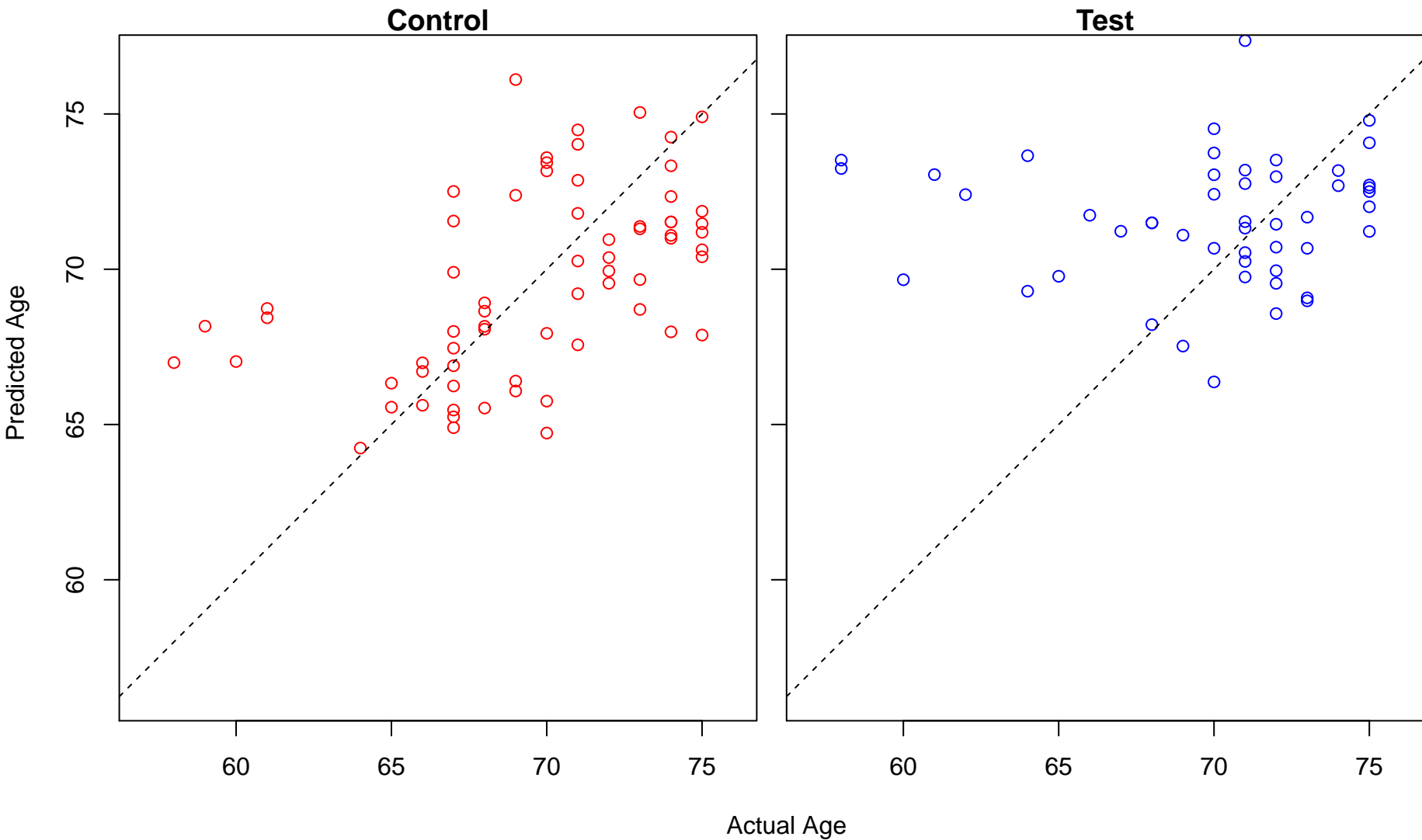
regulation of nitric oxide biosynthetic process (Score: 0.890443)



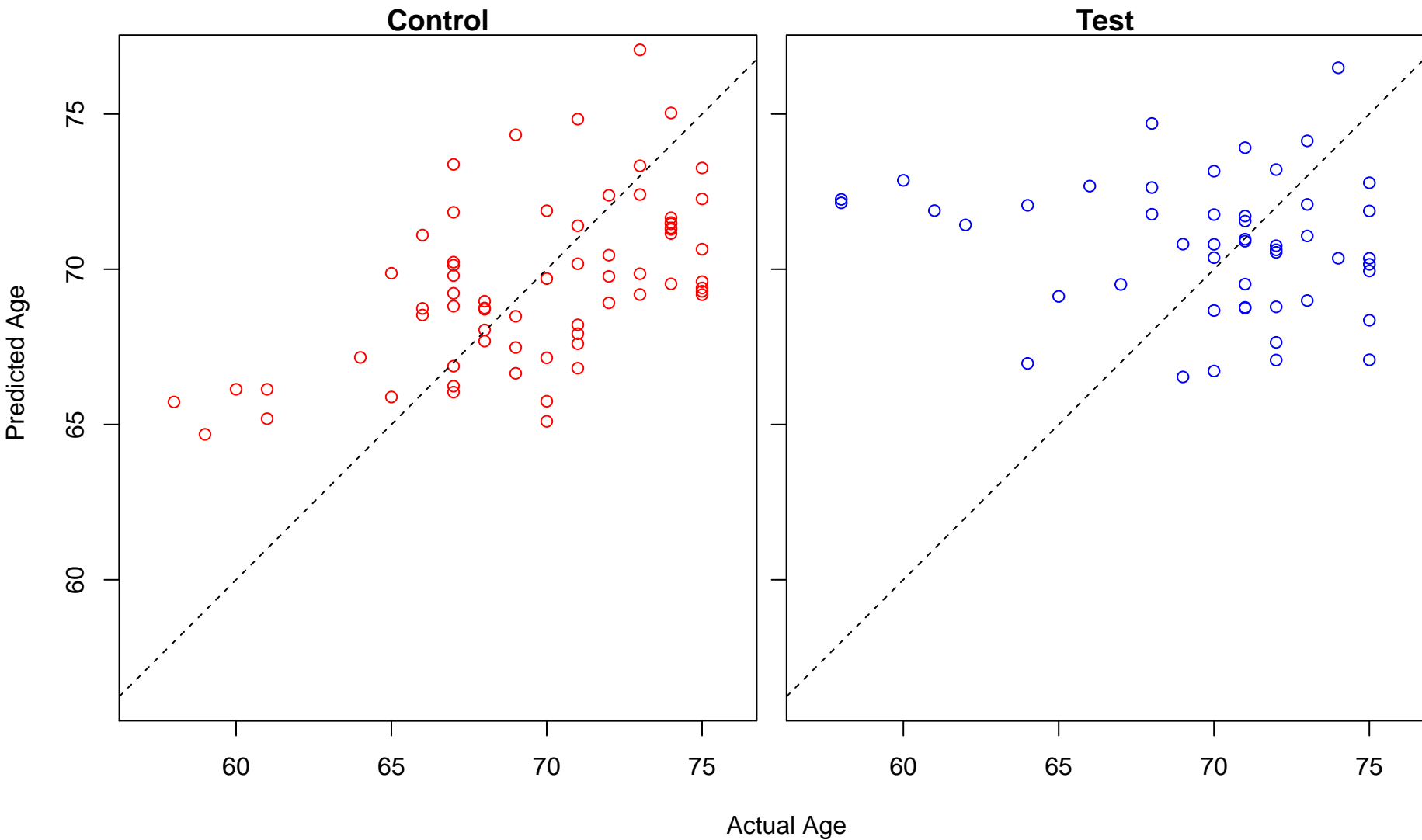
maintenance of location in cell (Score: 0.890067)



positive regulation of JUN kinase activity (Score: 0.889780)

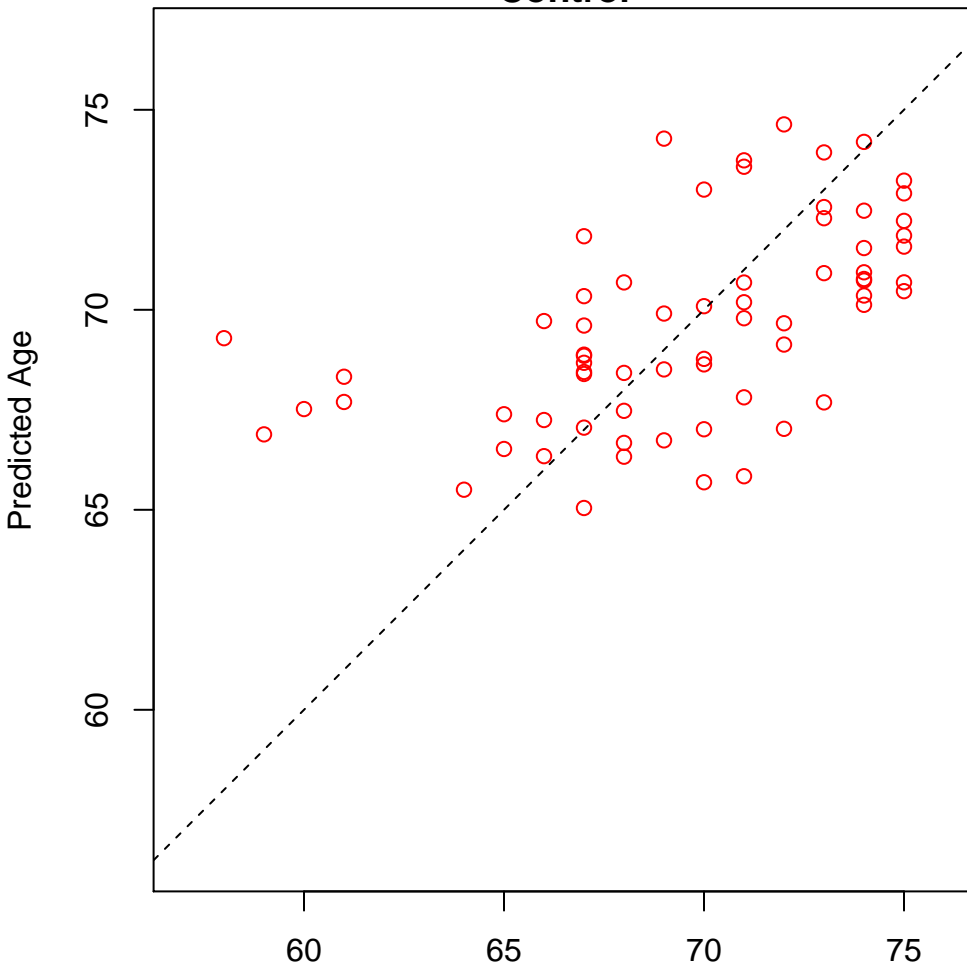


amyloid precursor protein metabolic process (Score: 0.889682)

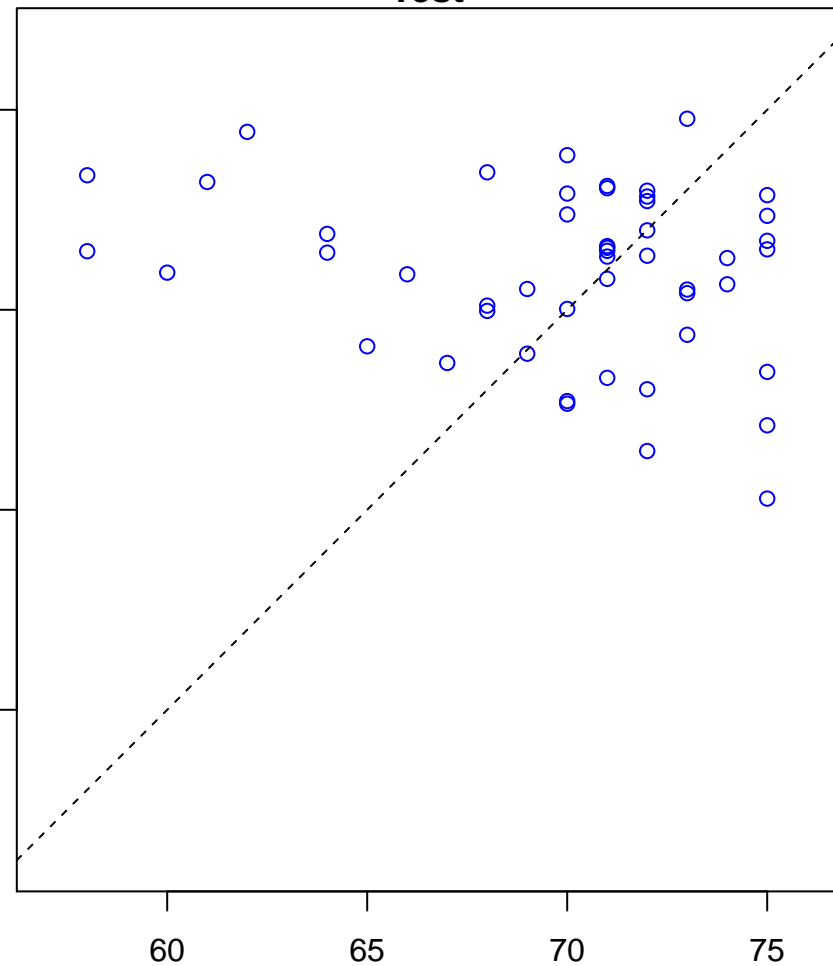


short-chain fatty acid catabolic process (Score: 0.888187)

Control

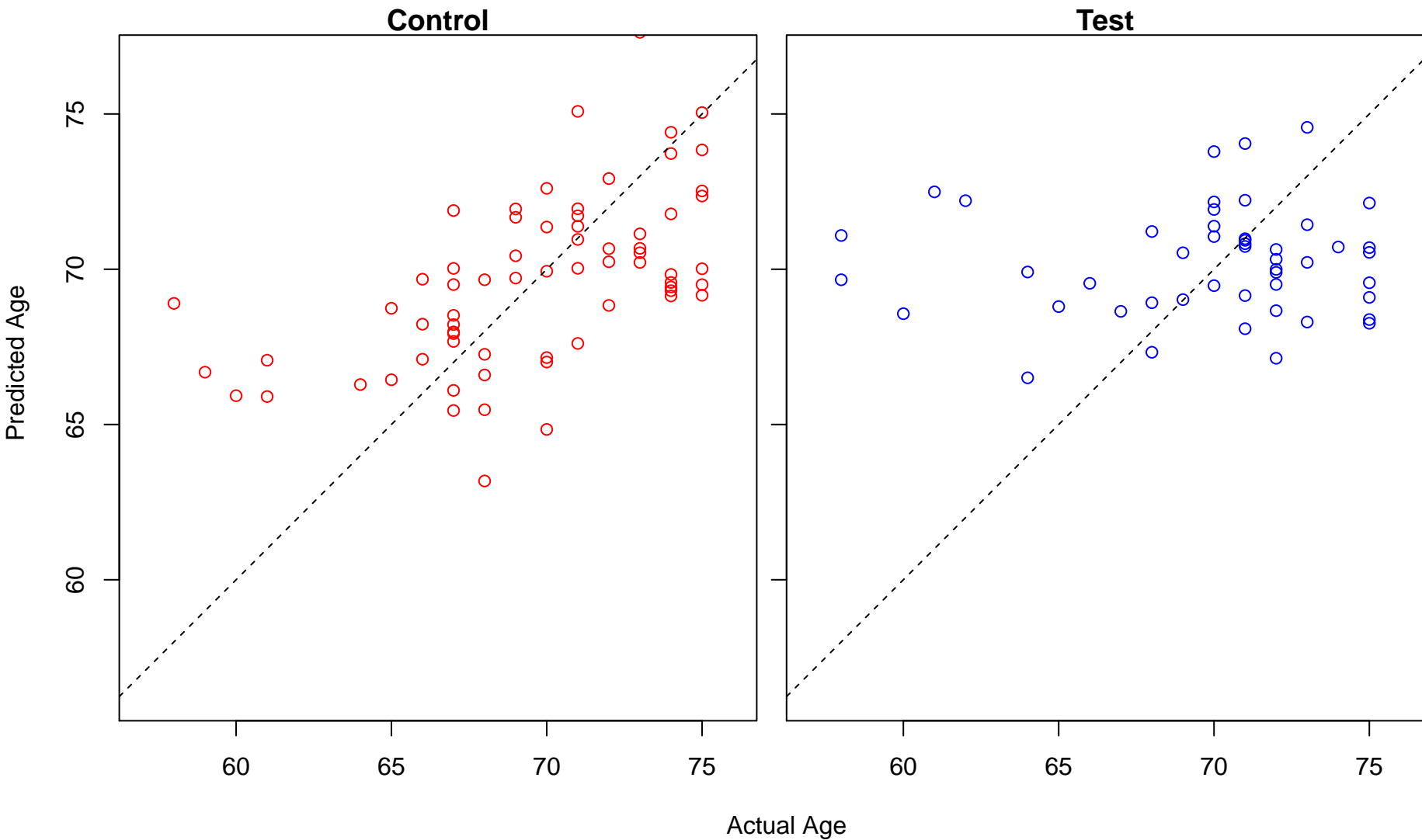


Test

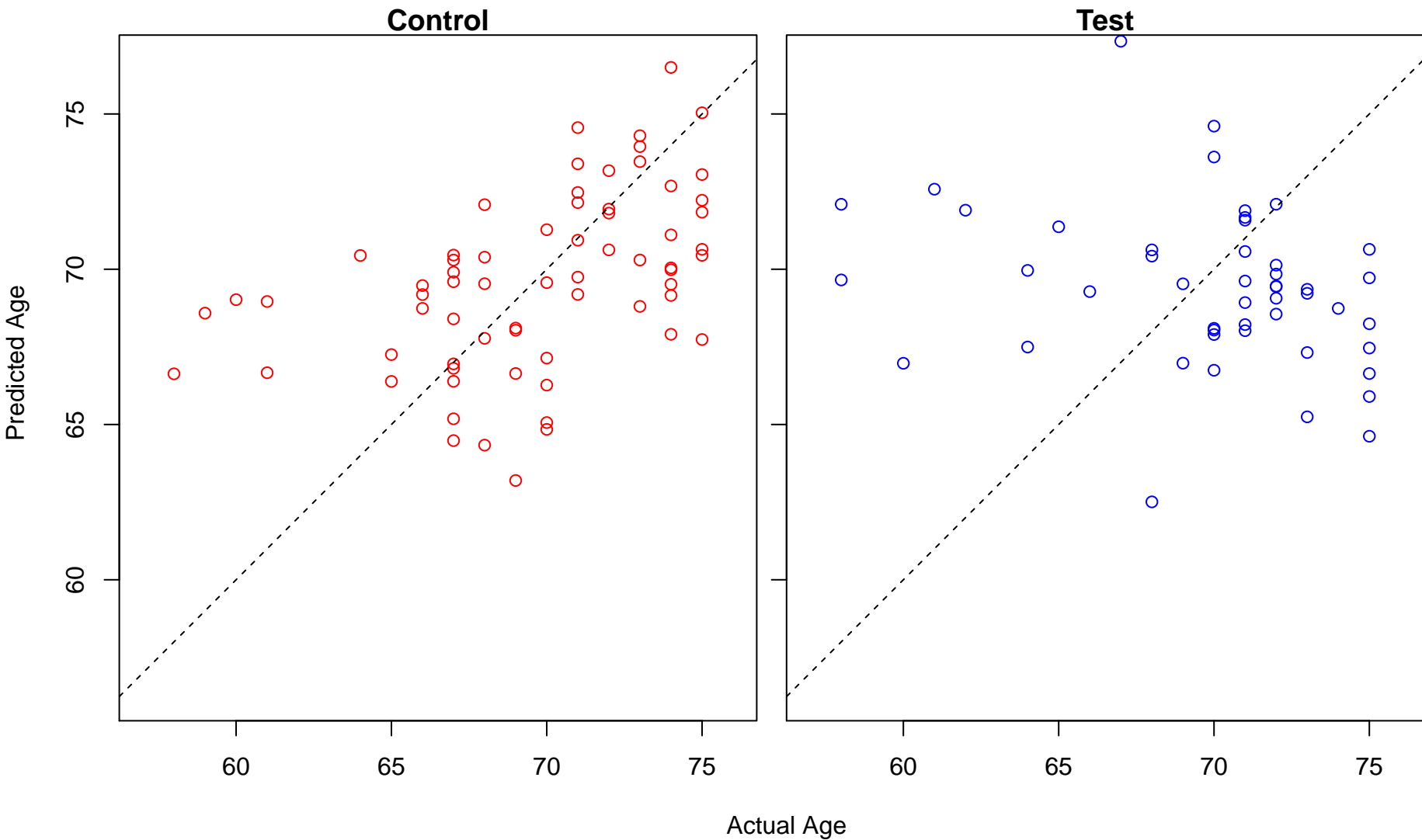


Actual Age

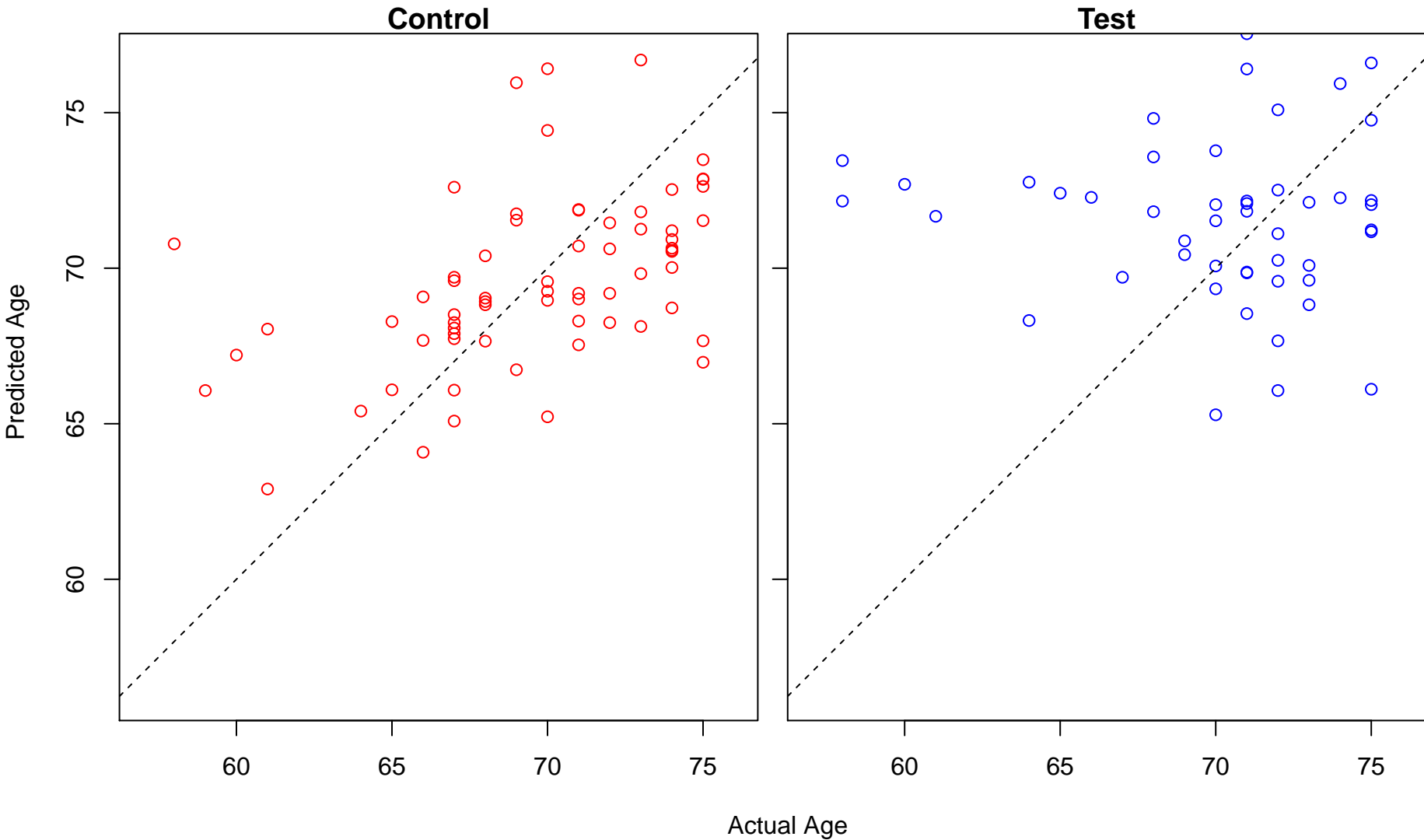
NAD metabolic process (Score: 0.888126)



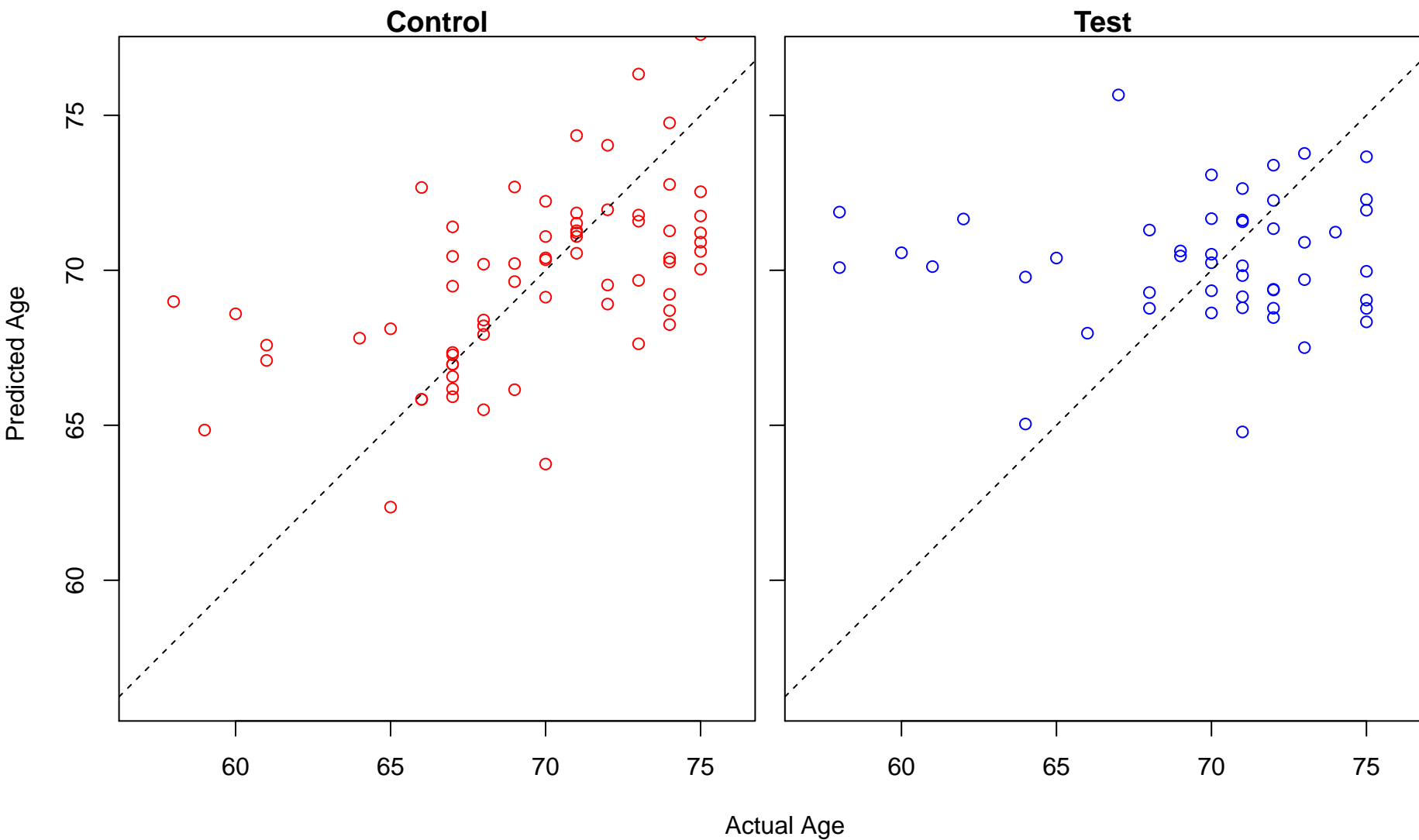
positive regulation of interleukin-6 secretion (Score: 0.887495)



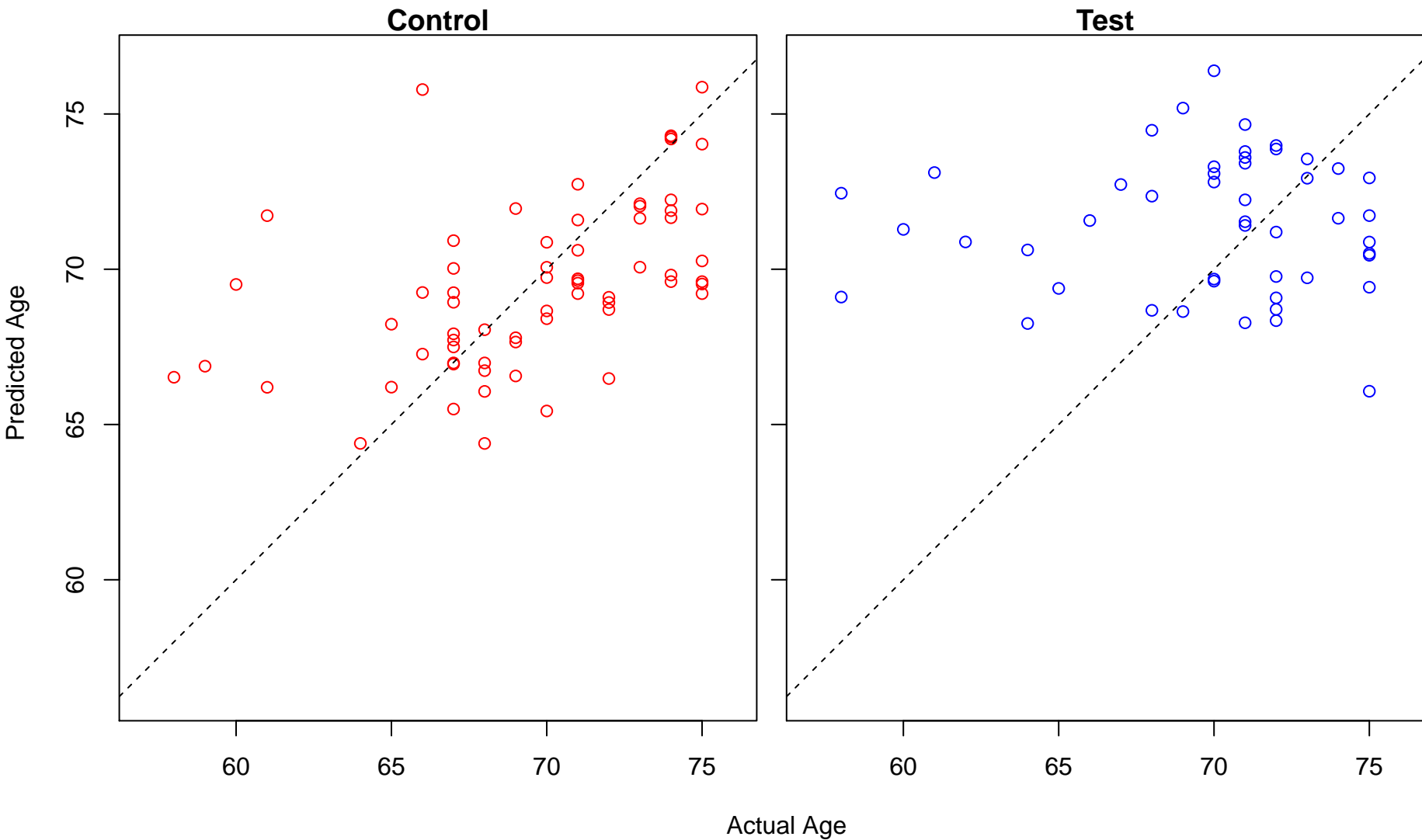
positive regulation by host of viral process (Score: 0.886824)



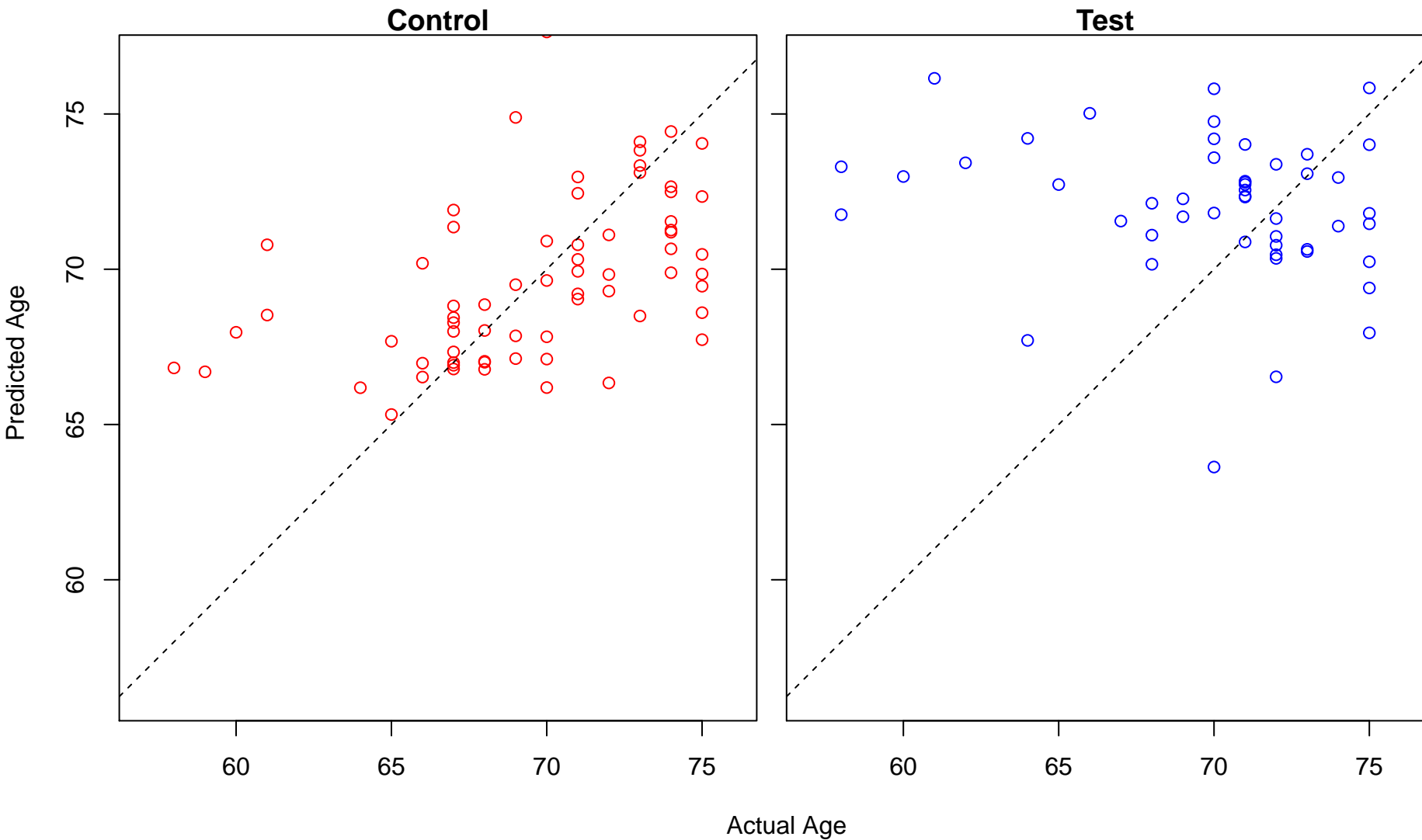
leukocyte tethering or rolling (Score: 0.886322)



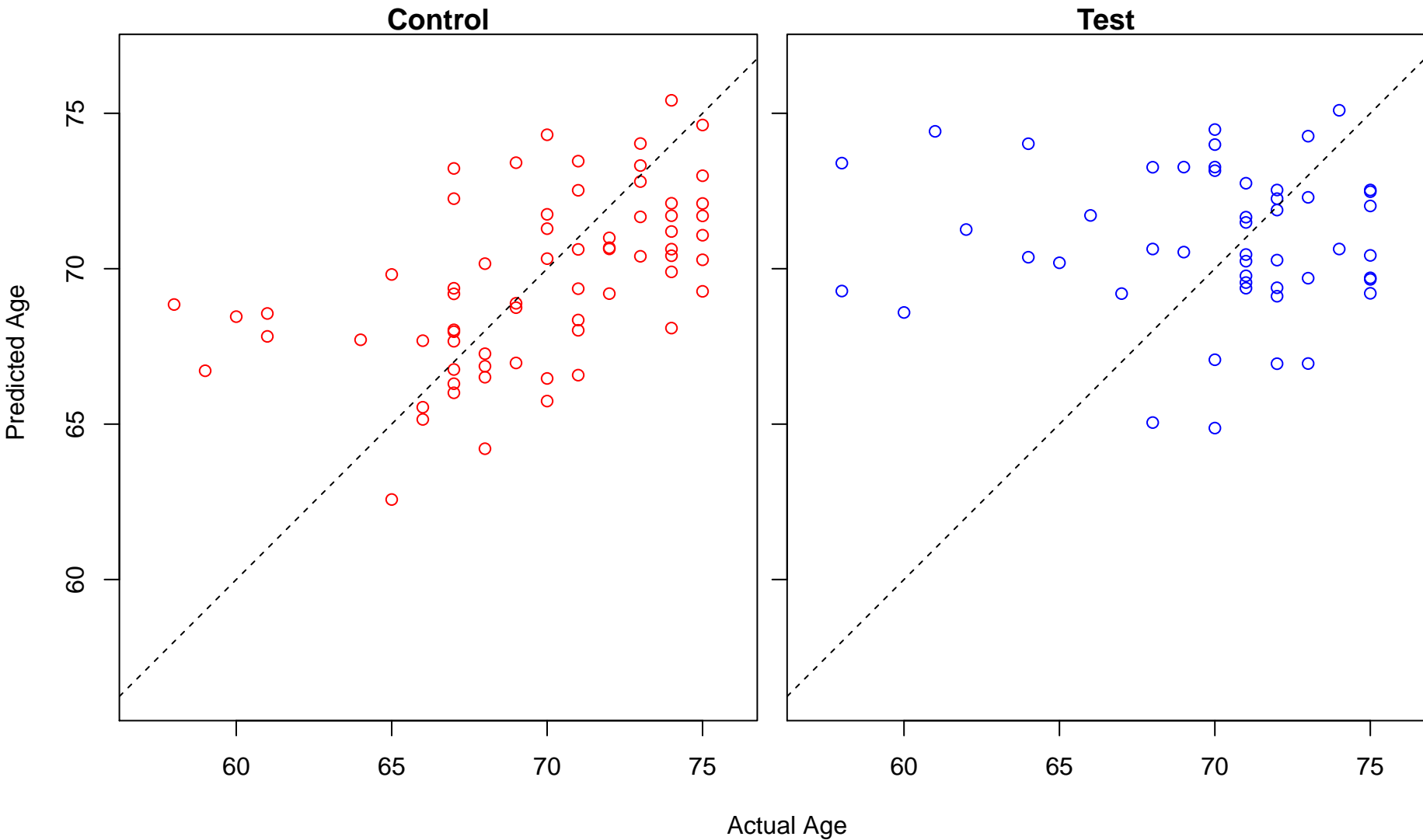
regulation of nucleobase-containing compound transport (Score: 0.886119)



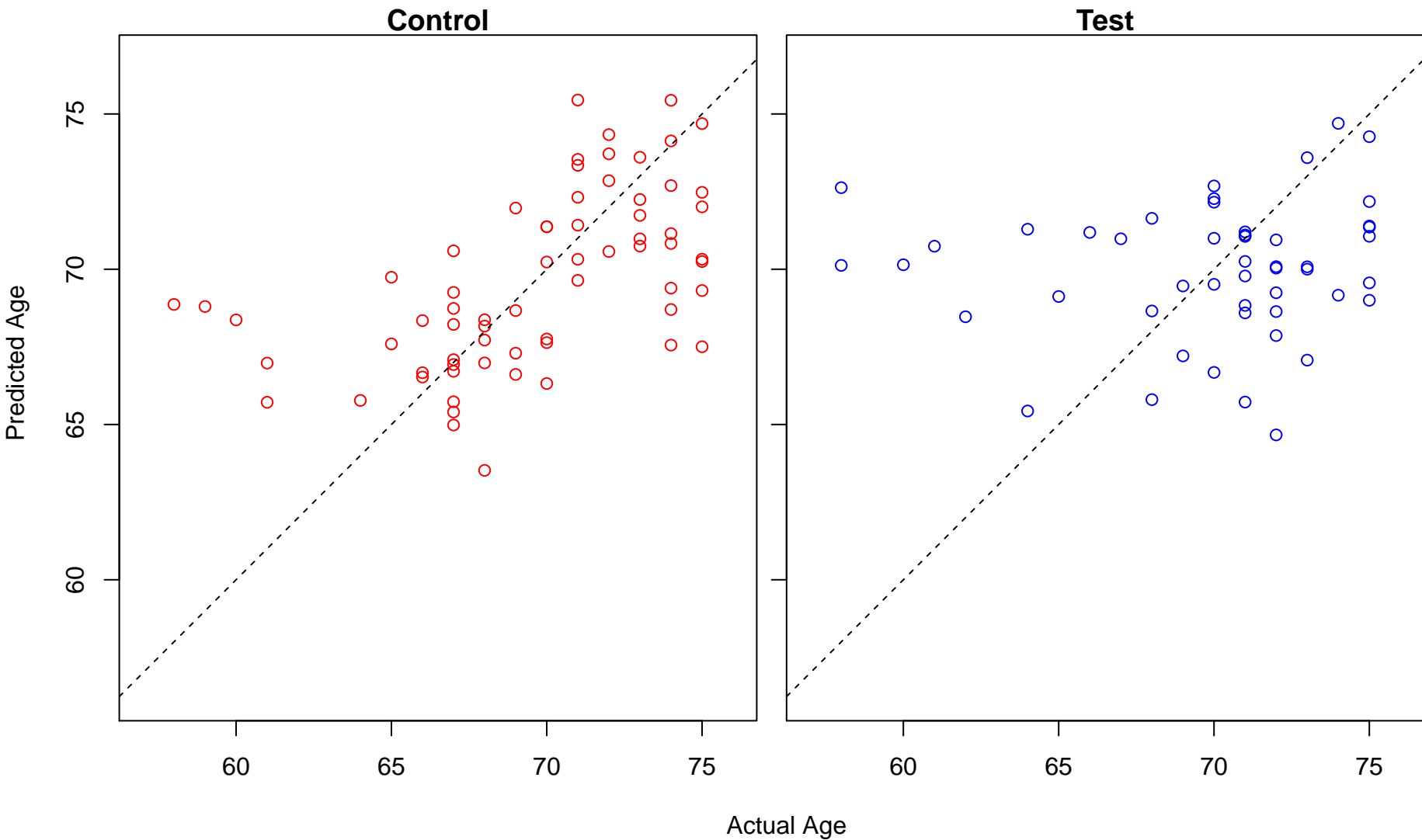
nitric oxide metabolic process (Score: 0.885884)



regulation of T cell receptor signaling pathway (Score: 0.885794)

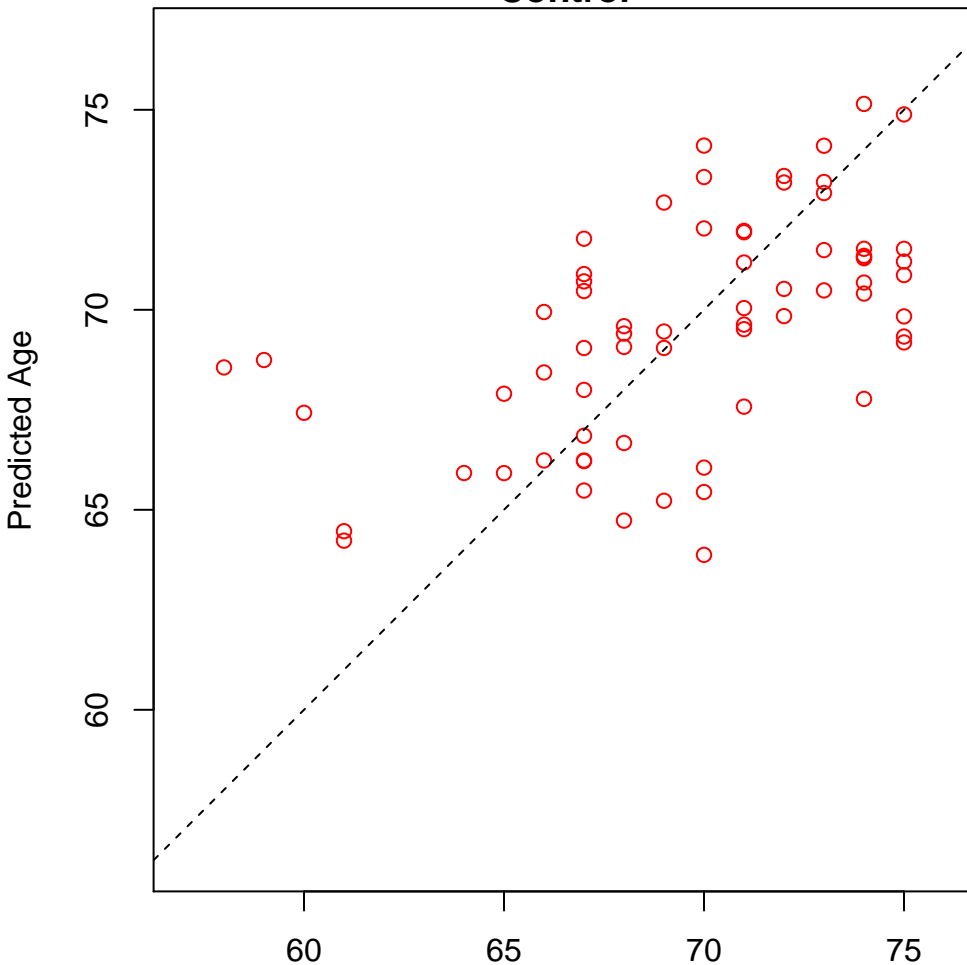


dendrite morphogenesis (Score: 0.885691)

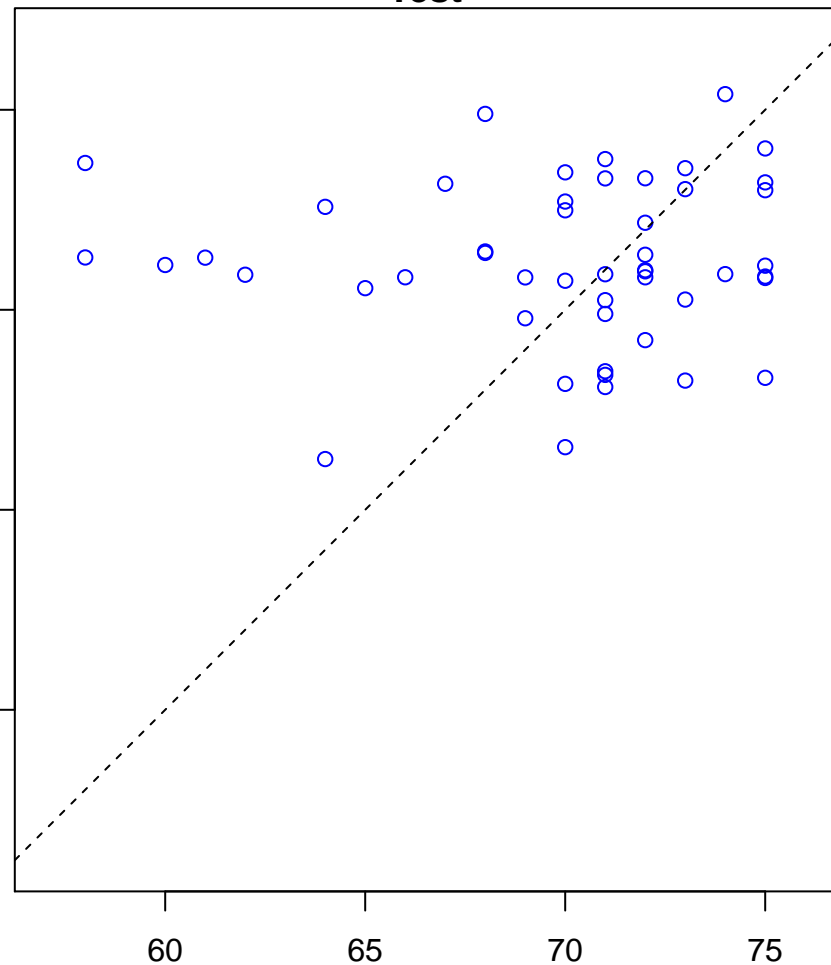


endoplasmic reticulum organization (Score: 0.885503)

Control

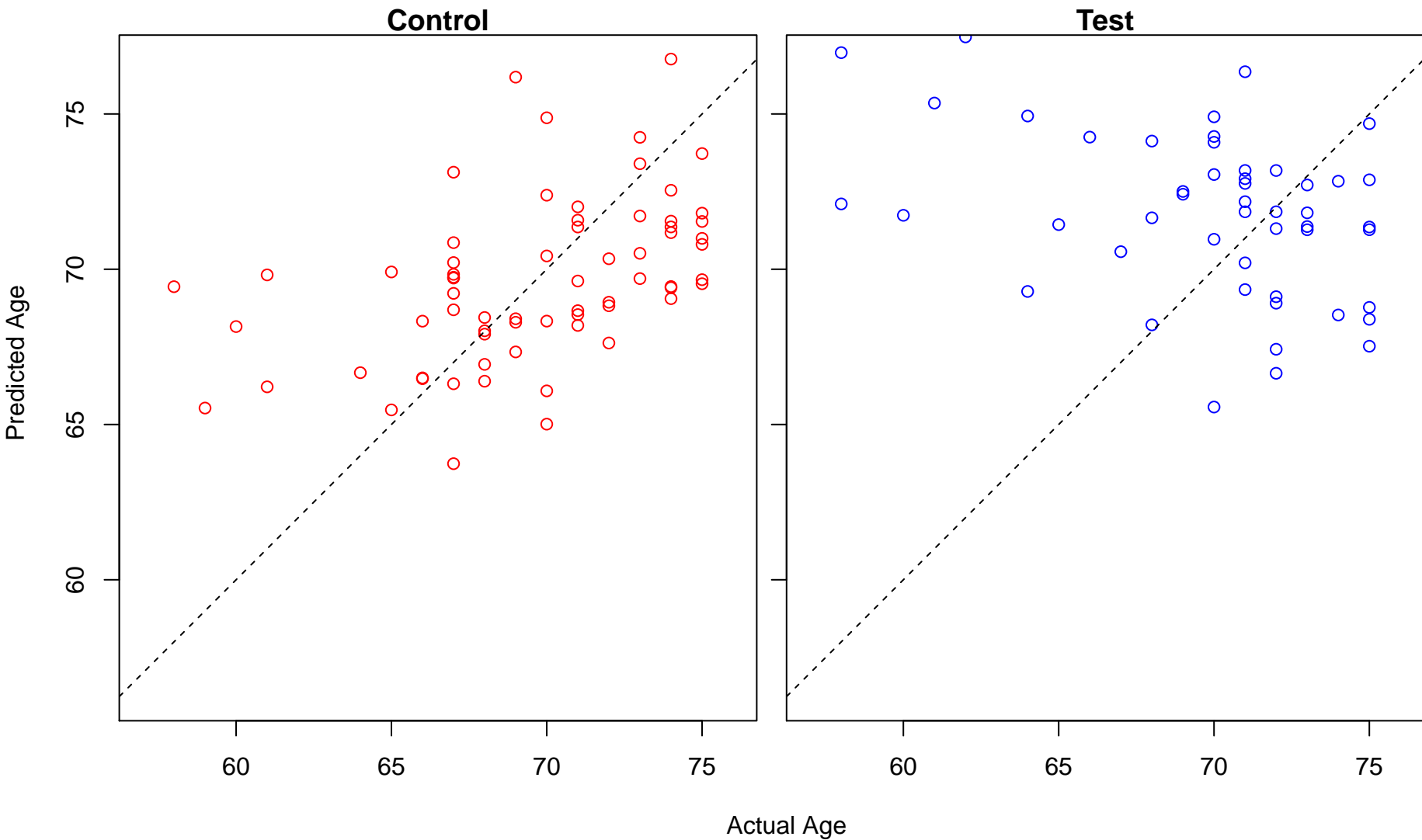


Test

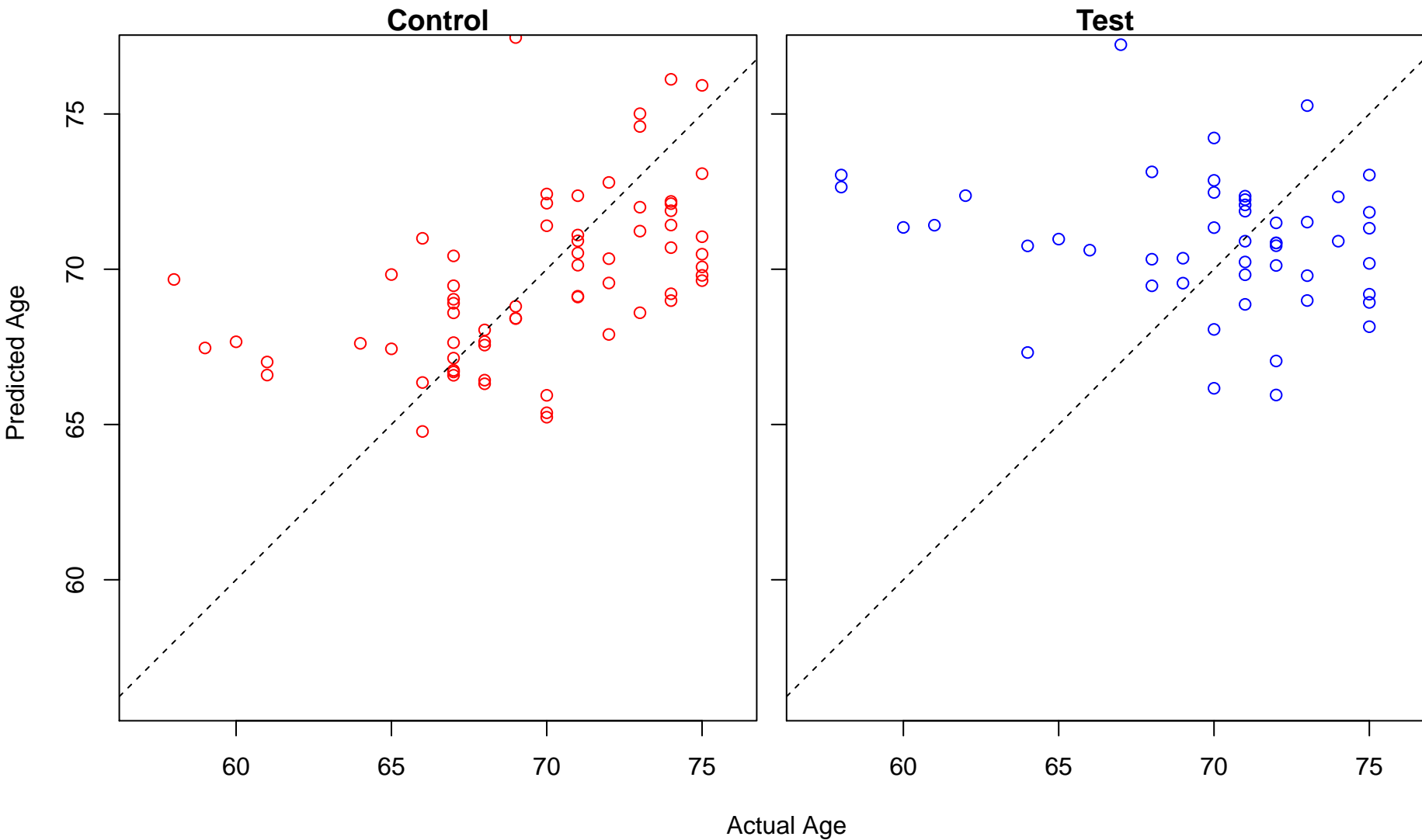


Actual Age

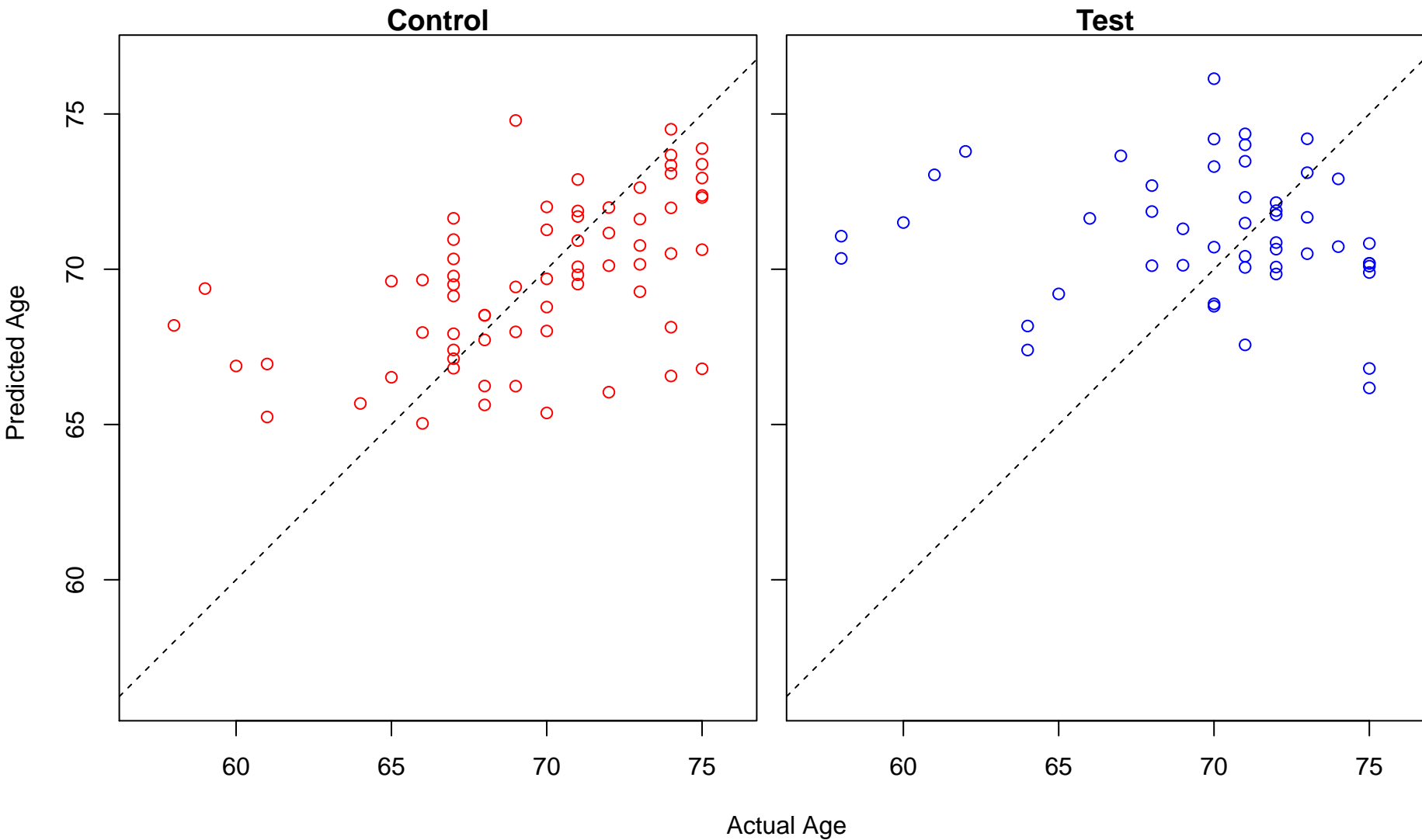
regulation of protein processing (Score: 0.885476)



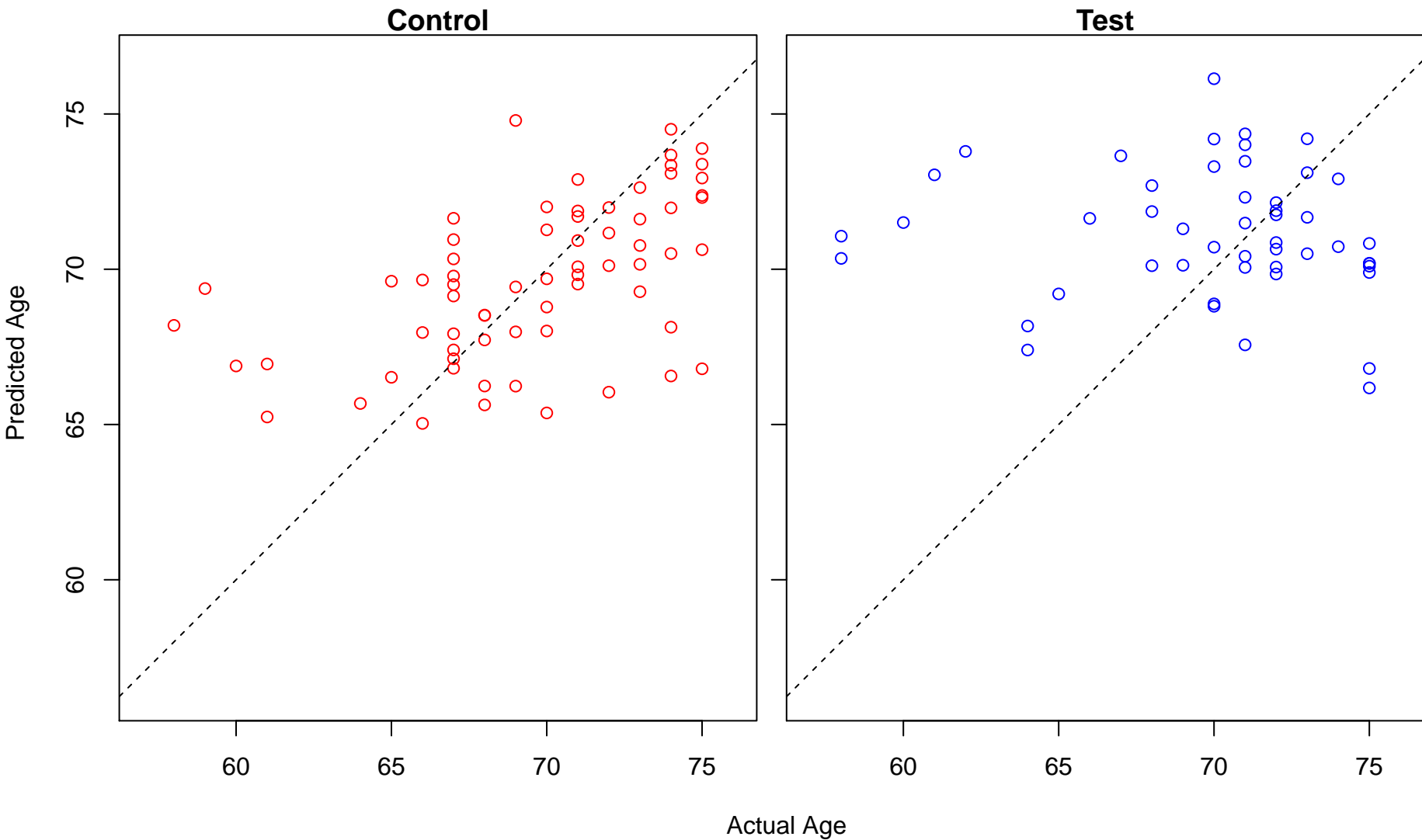
positive regulation of DNA repair (Score: 0.885415)



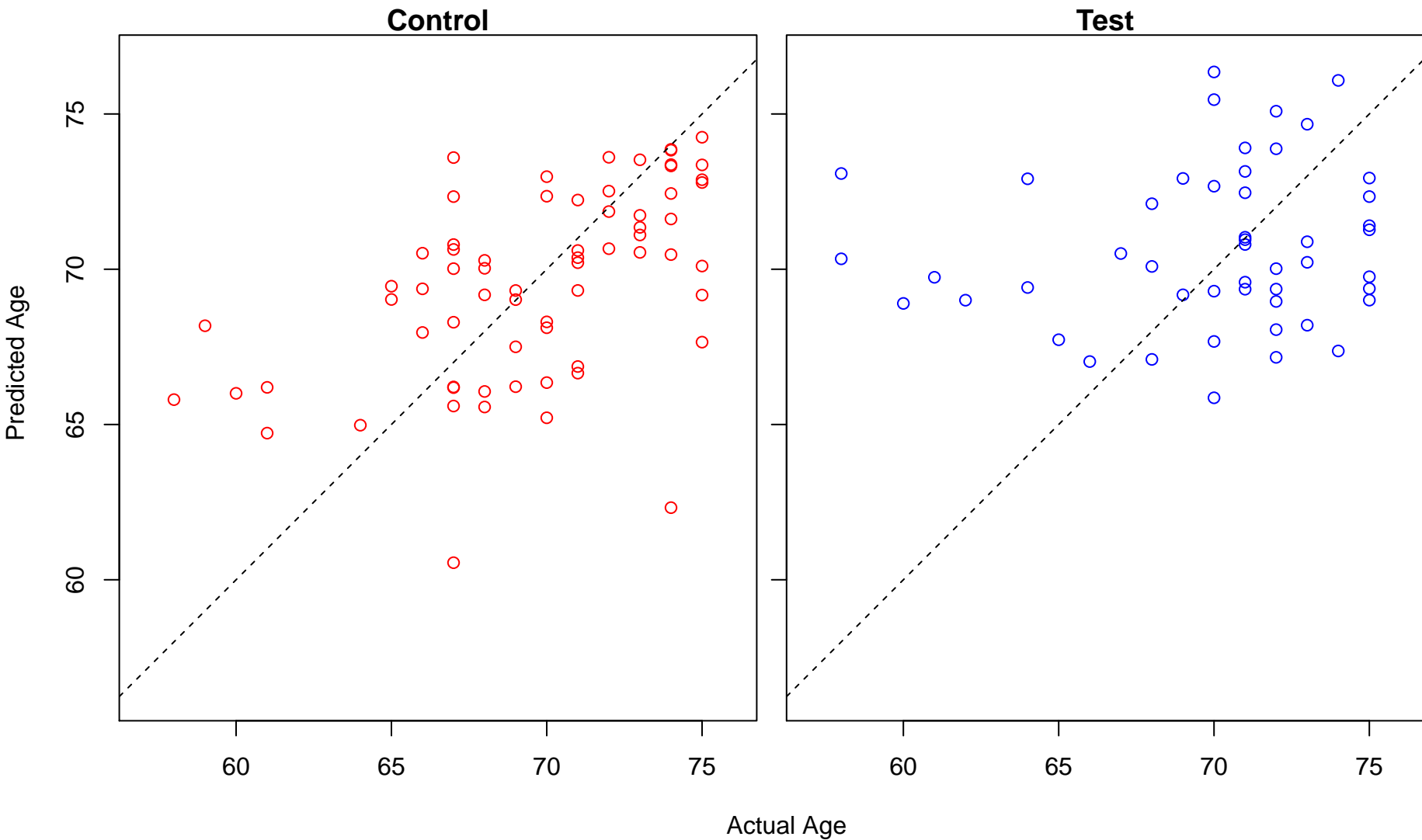
lipid translocation (Score: 0.885188)



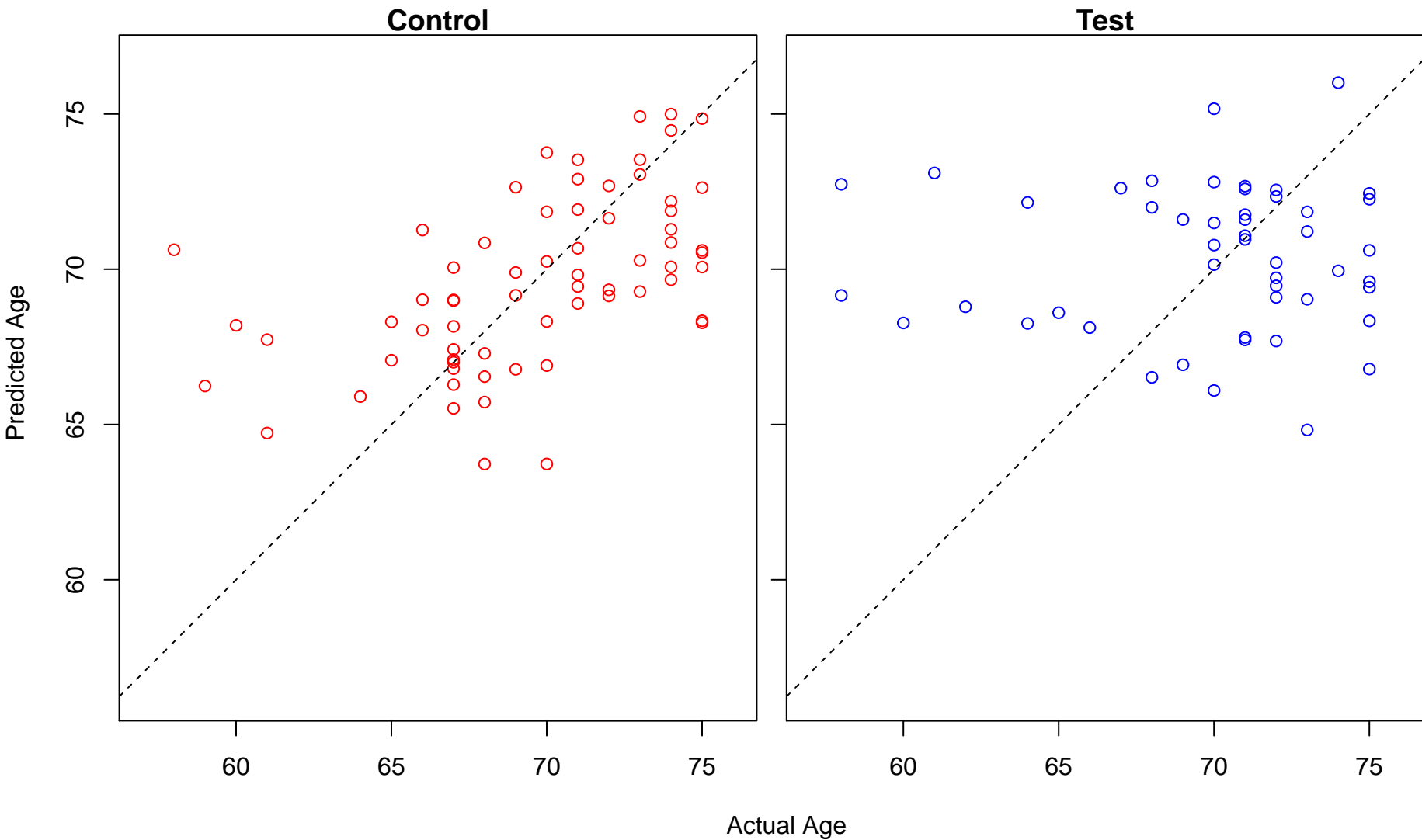
phospholipid translocation (Score: 0.885188)



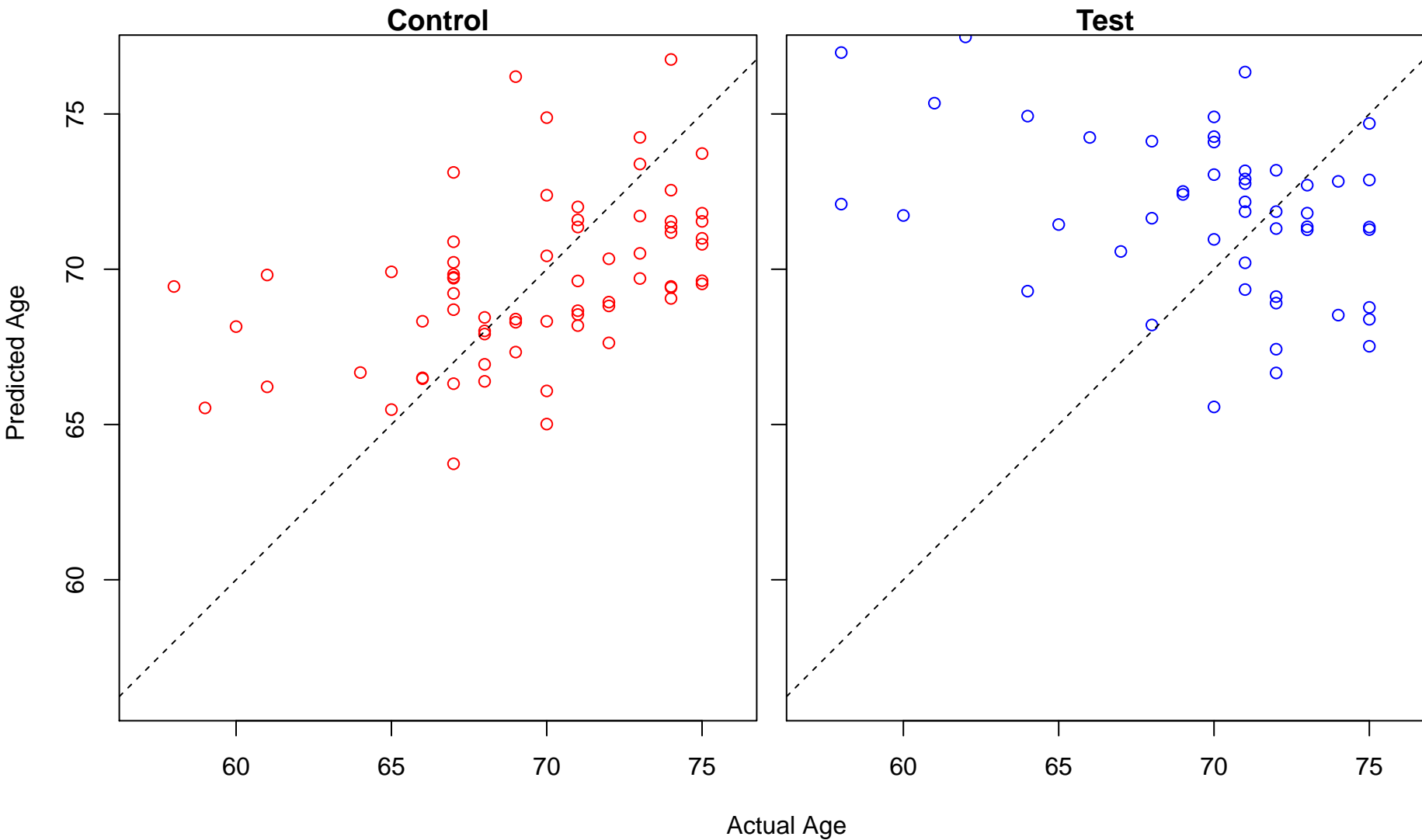
regulation of cardiac muscle cell contraction (Score: 0.885045)



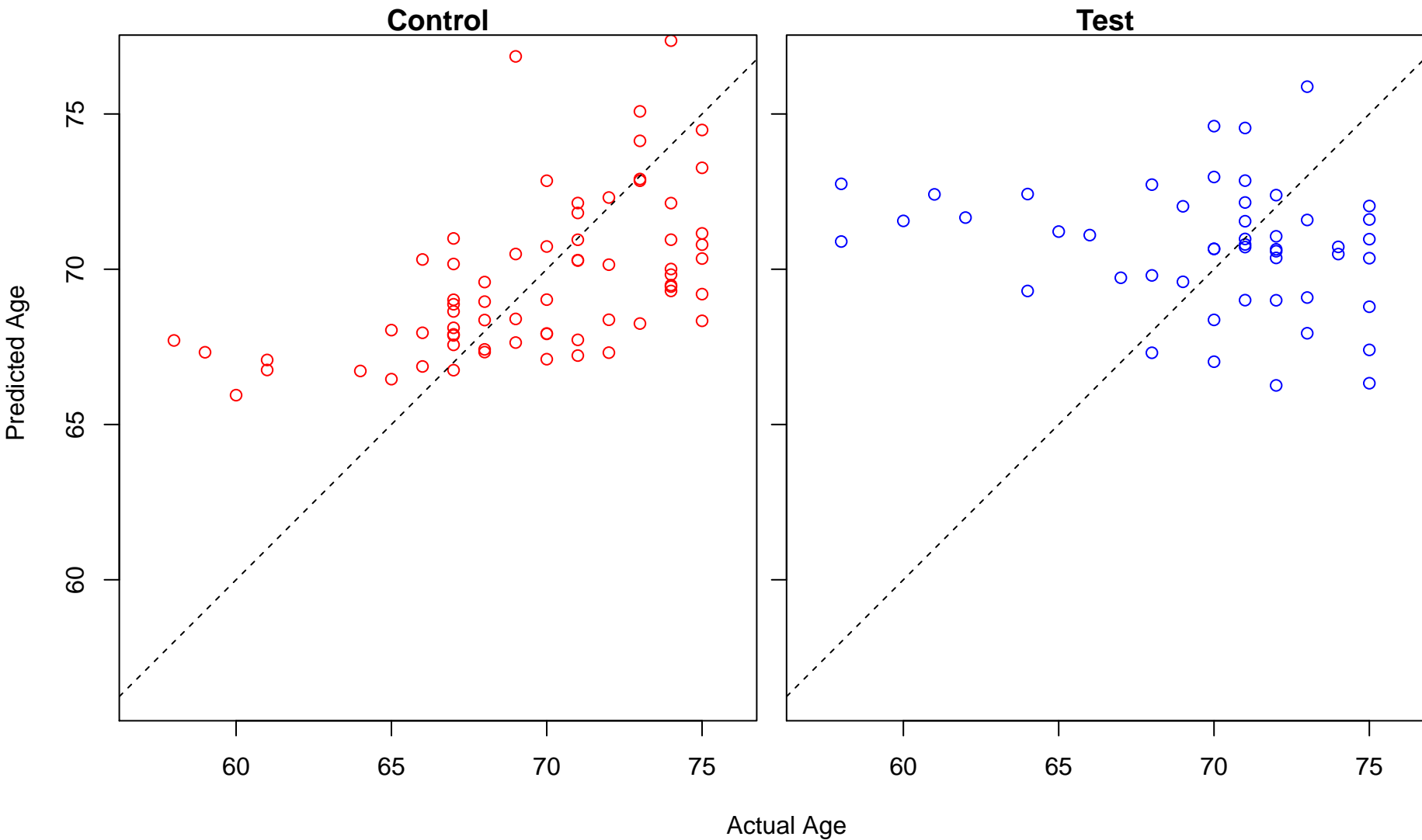
dendritic cell differentiation (Score: 0.884014)



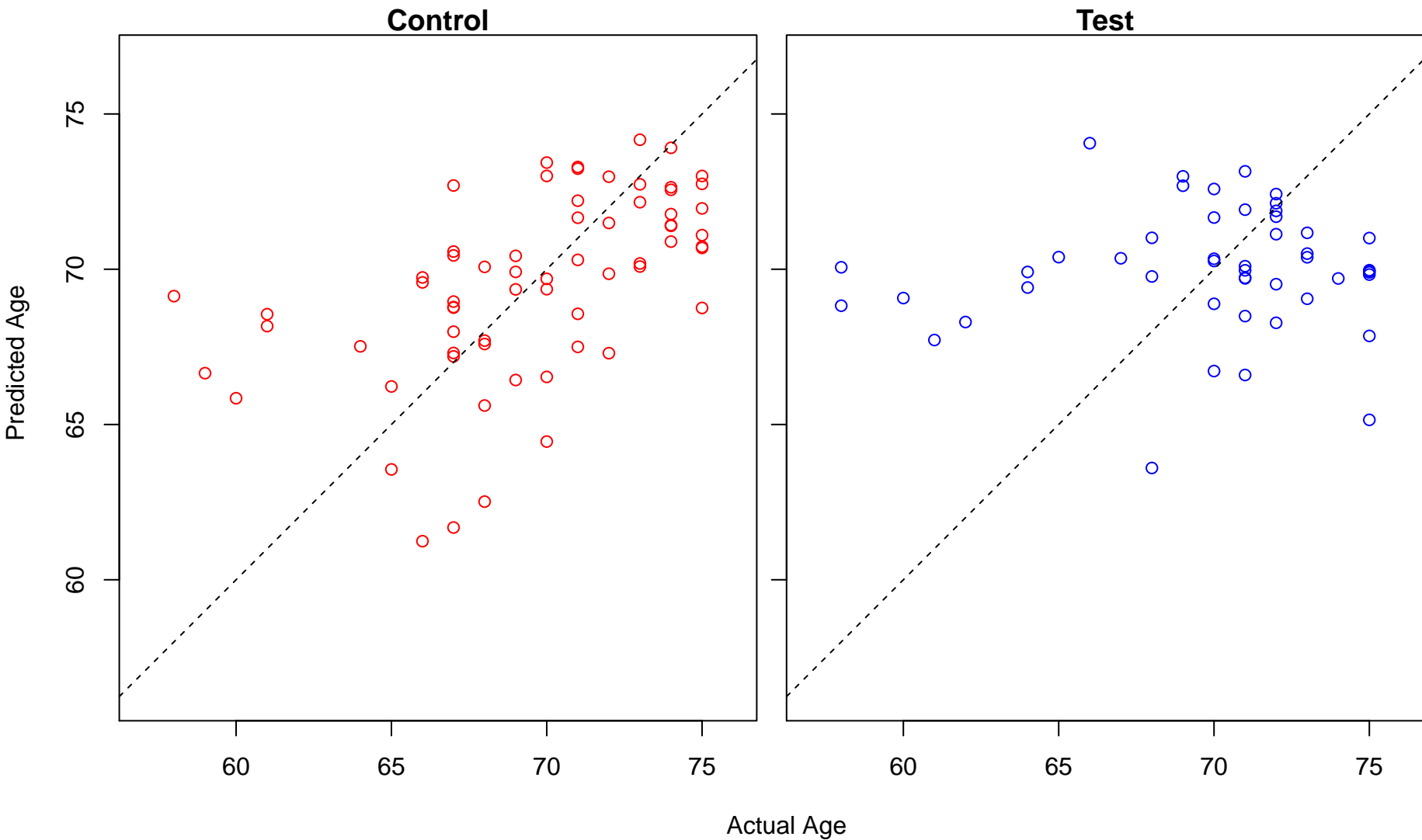
regulation of protein maturation (Score: 0.883606)



transcription from mitochondrial promoter (Score: 0.883581)

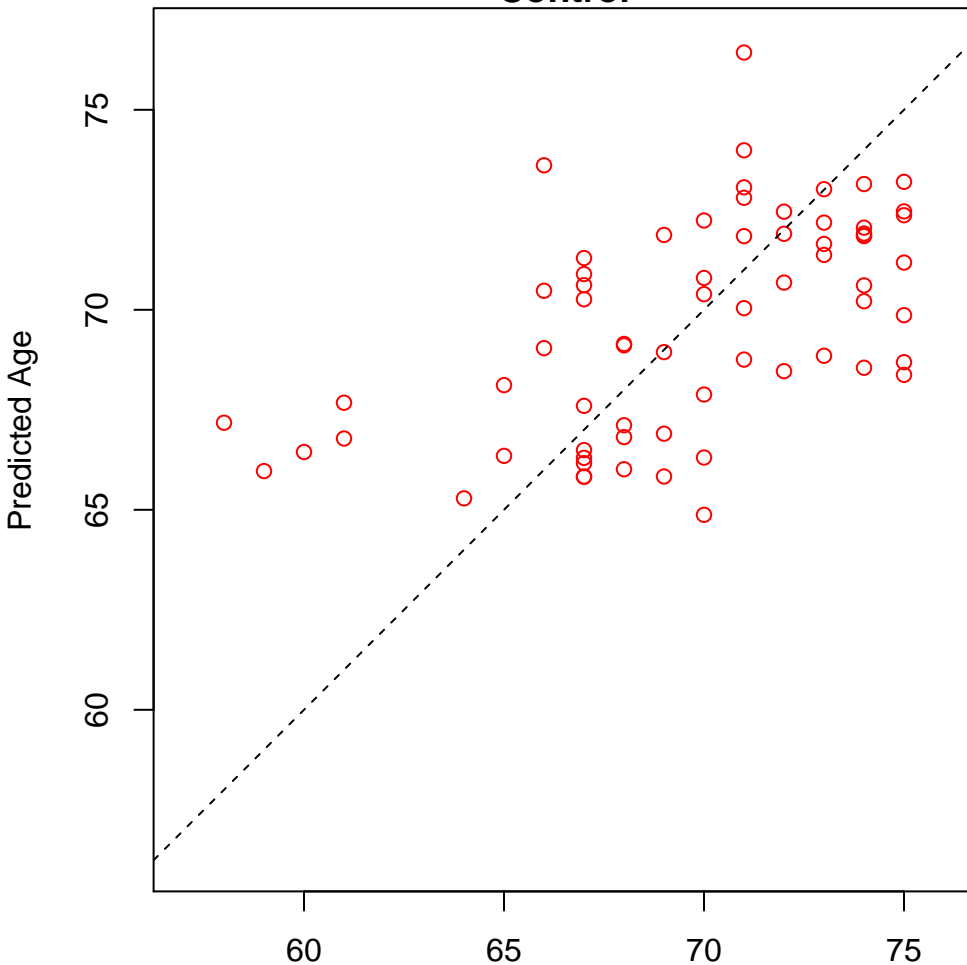


dendritic cell chemotaxis (Score: 0.883541)

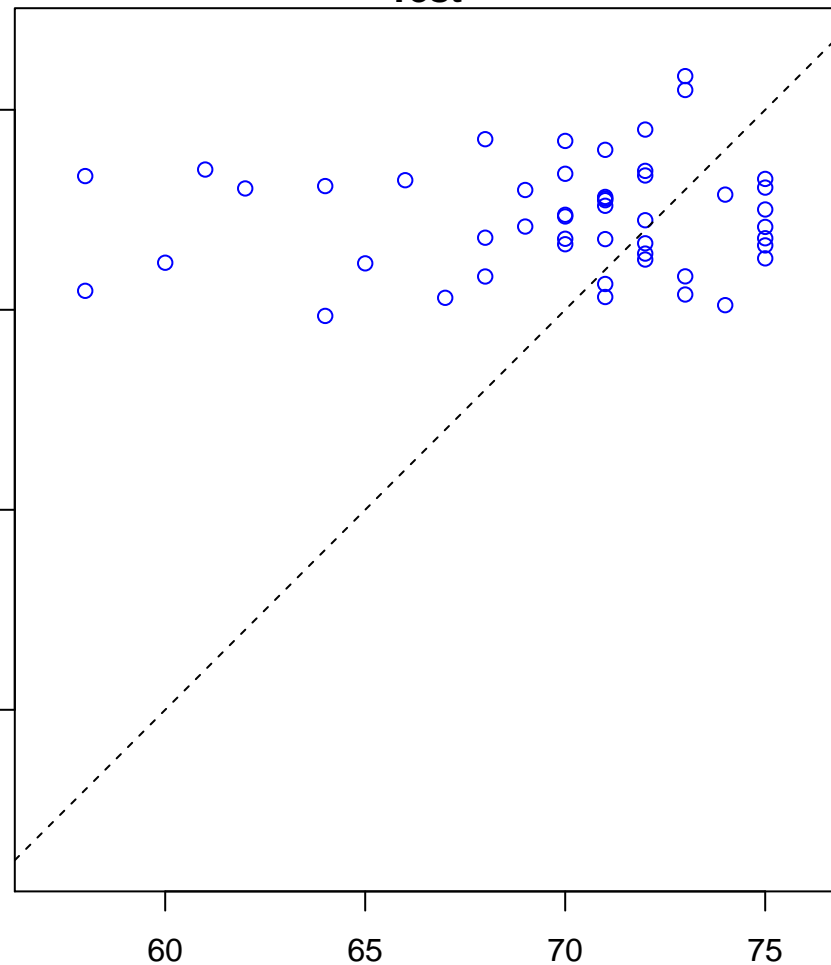


regulation of cytoplasmic translation (Score: 0.883263)

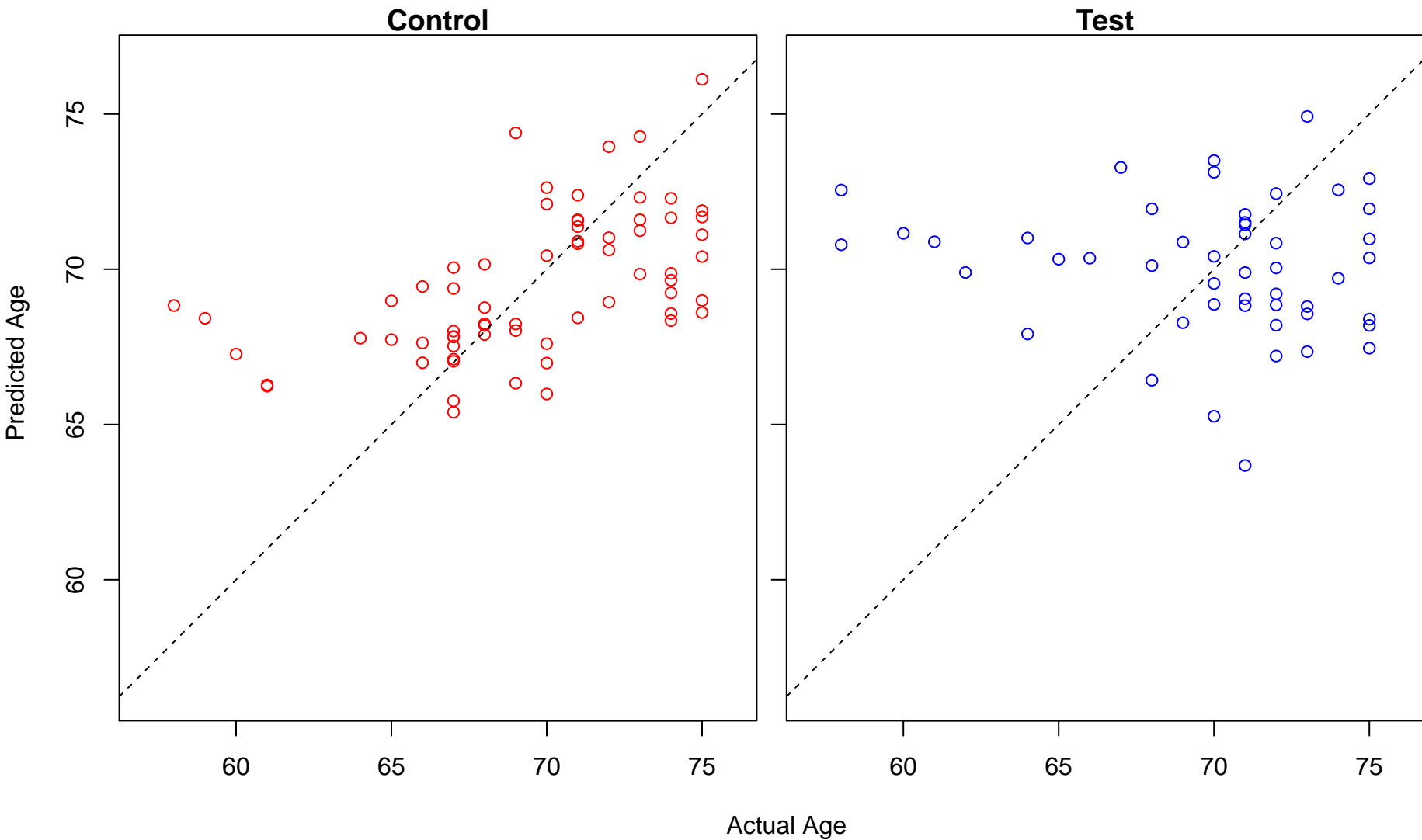
Control



Test

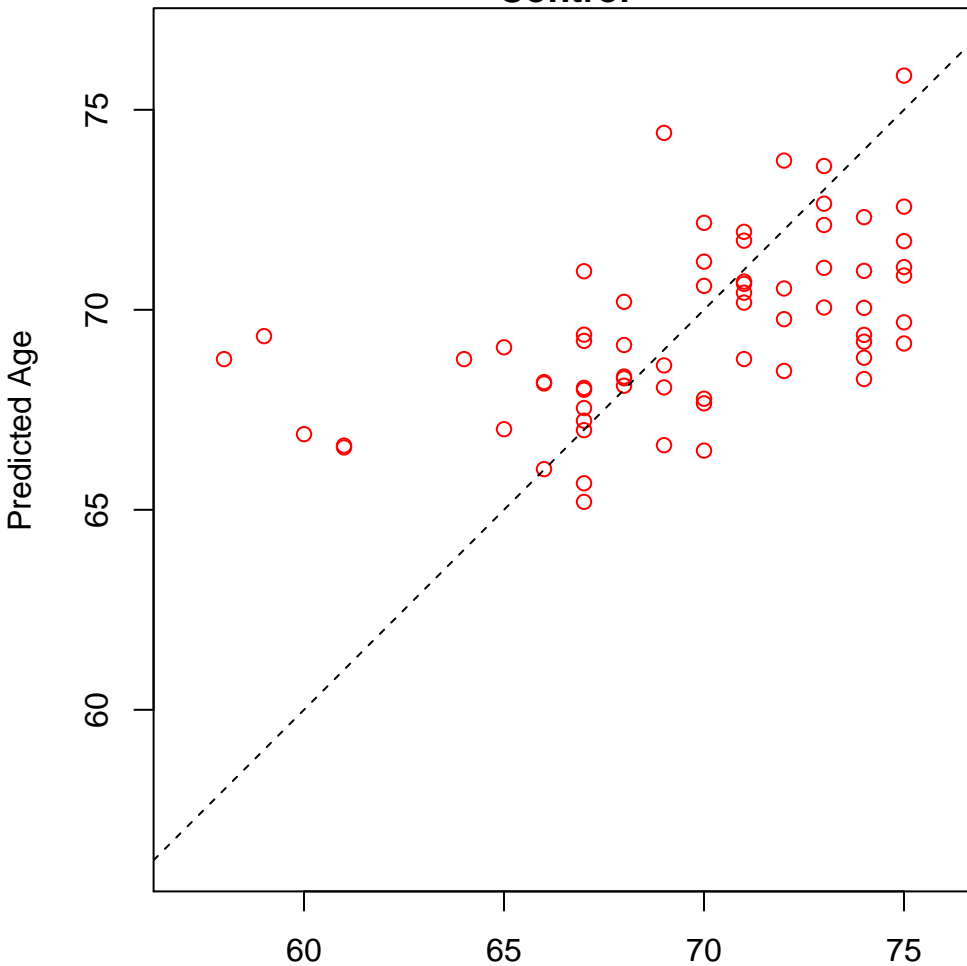


polyol catabolic process (Score: 0.882464)

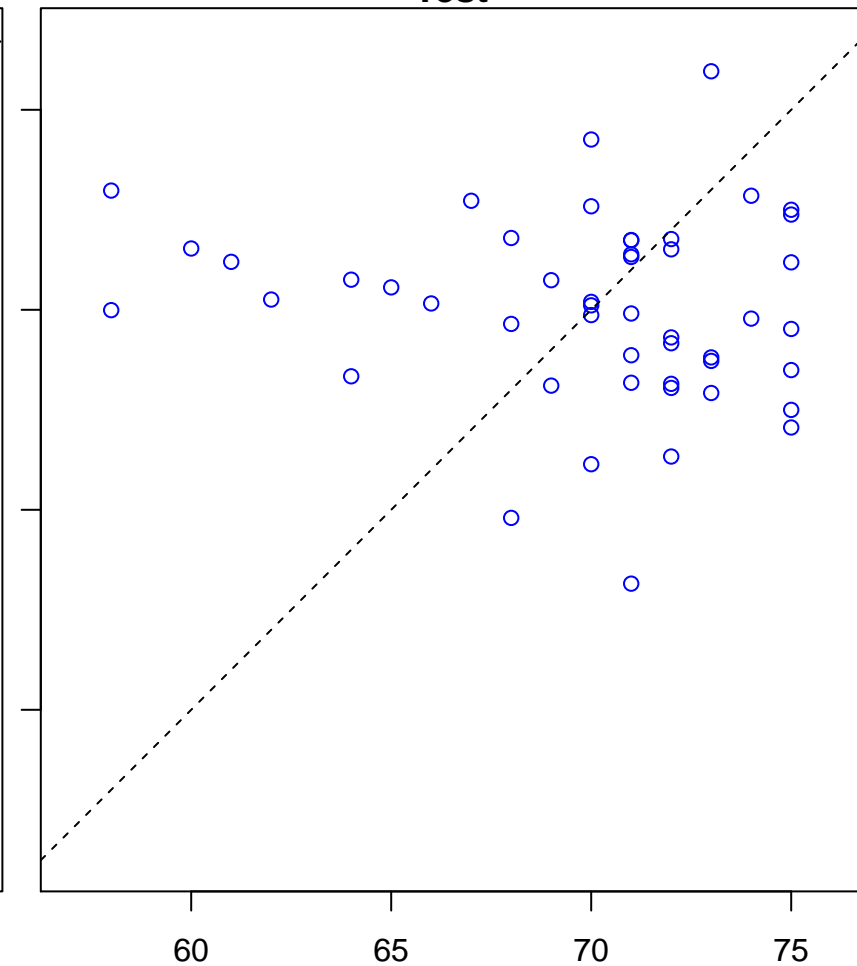


neuron–neuron synaptic transmission (Score: 0.882195)

Control

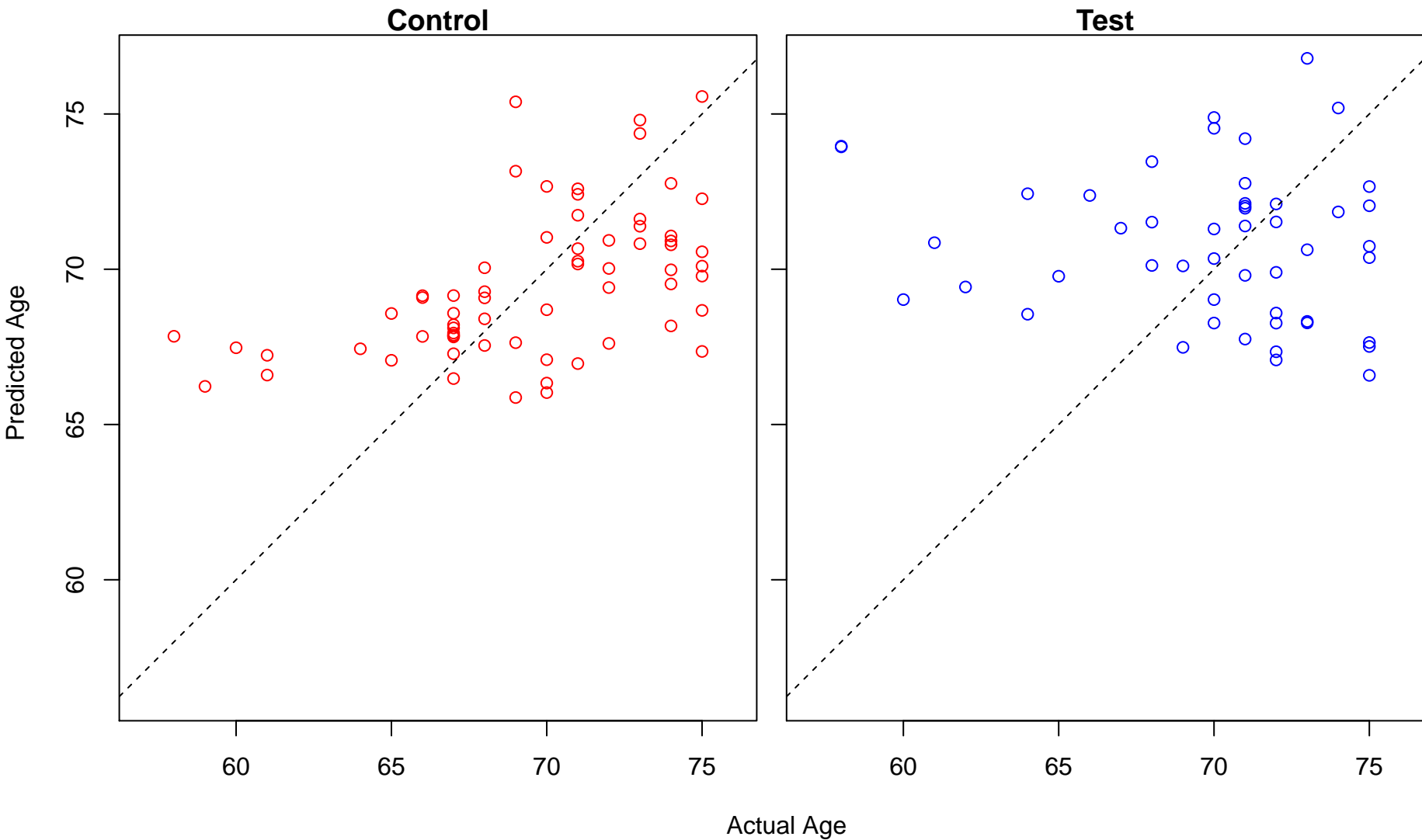


Test

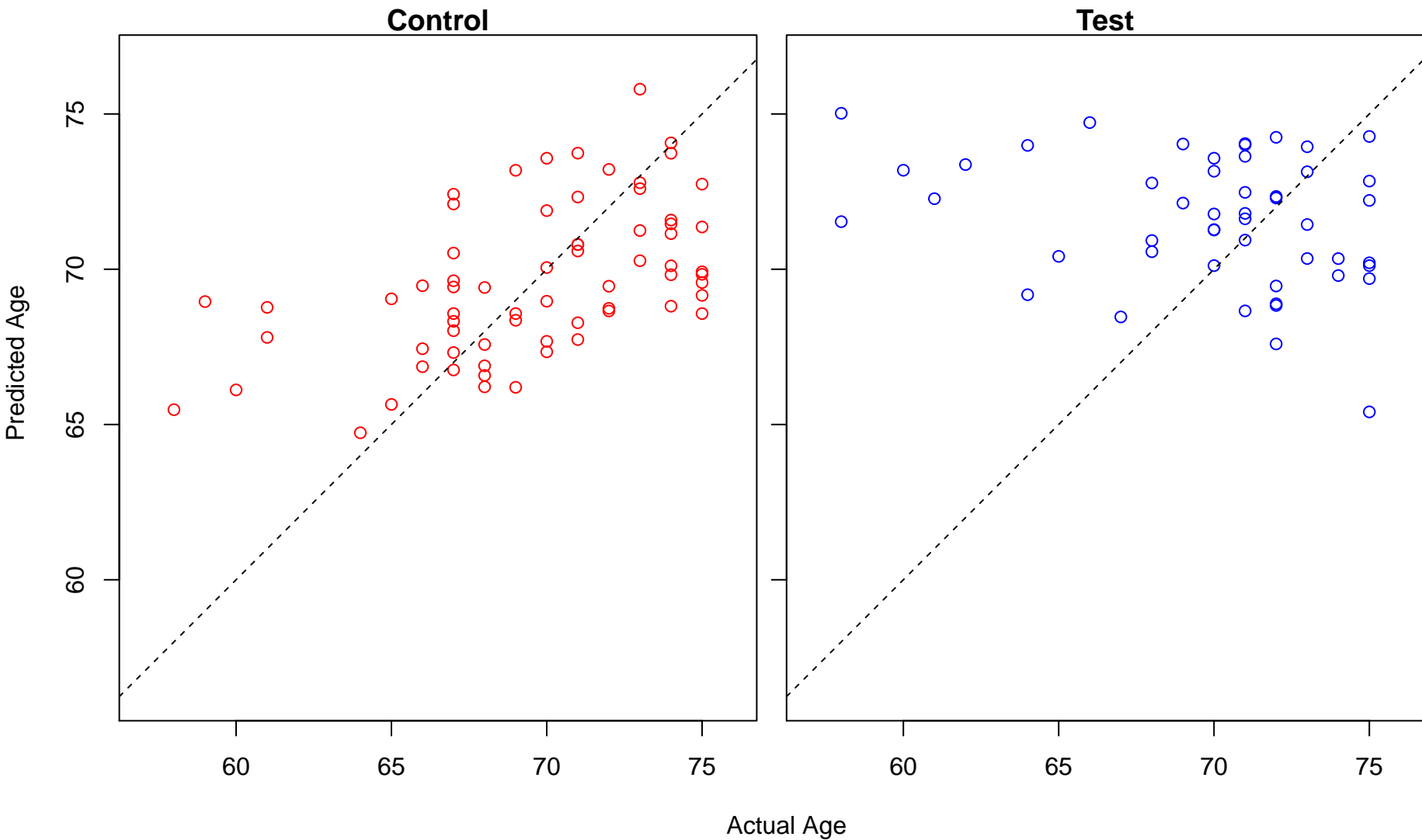


Actual Age

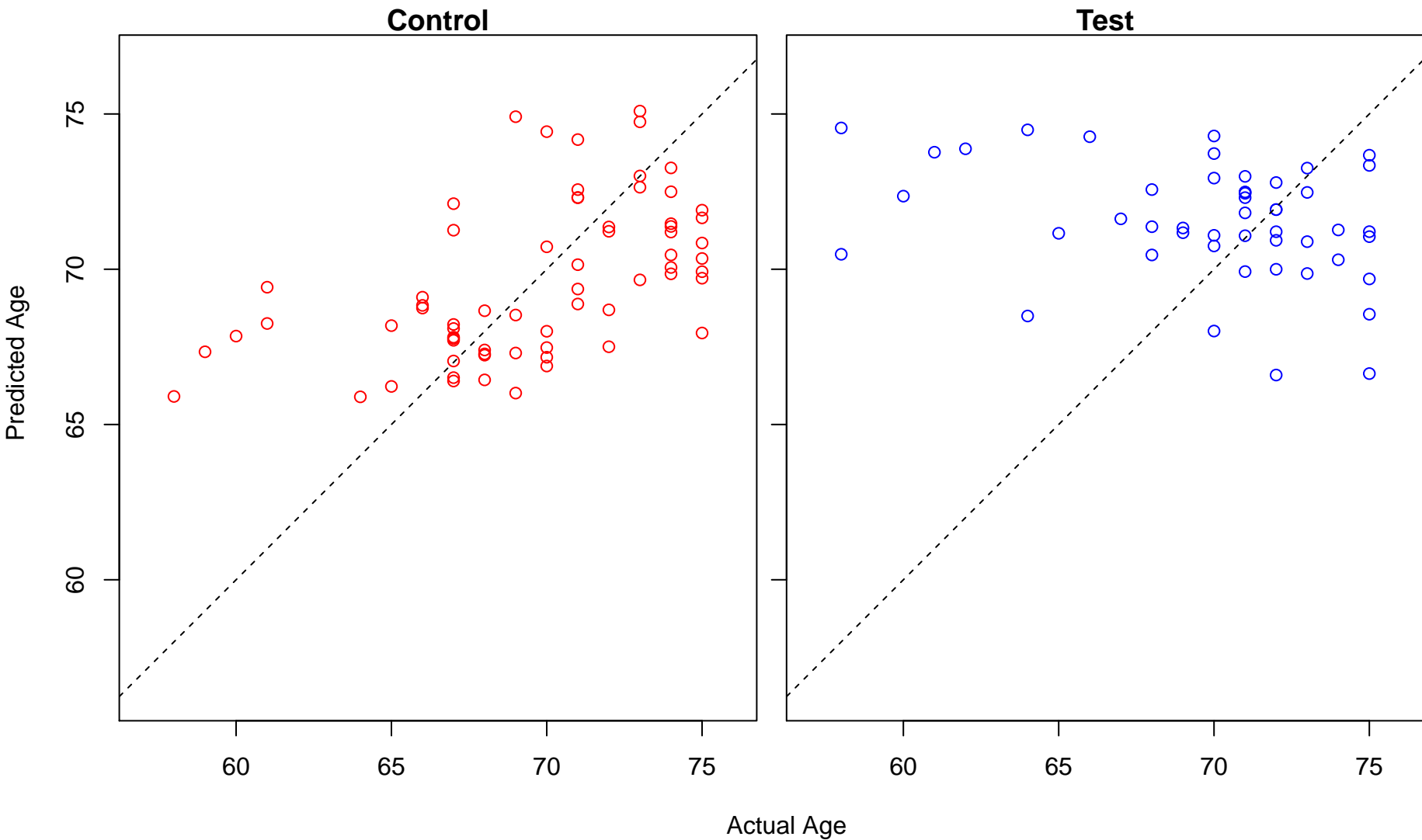
regulation of DNA recombination (Score: 0.881977)



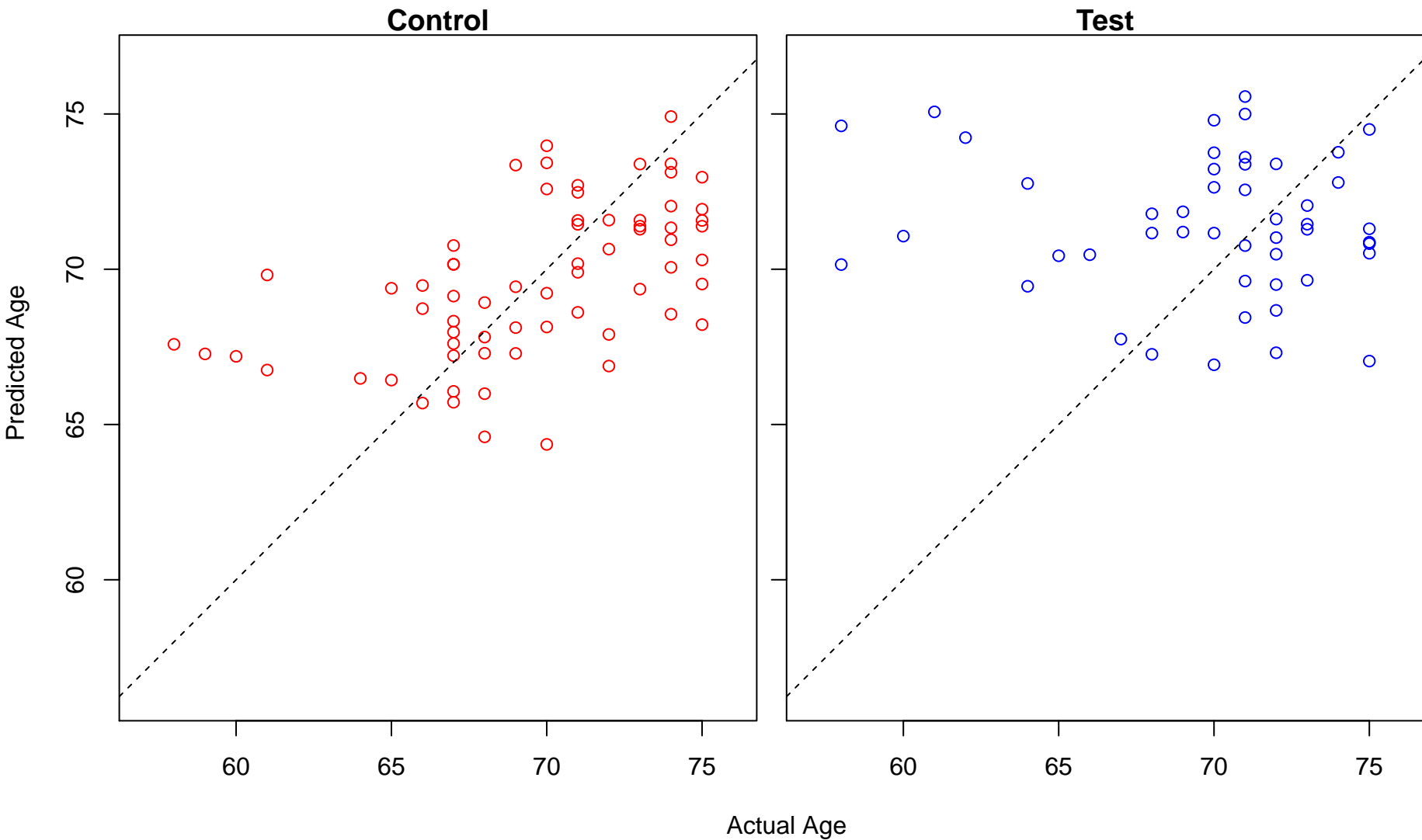
negative regulation of myoblast differentiation (Score: 0.881848)



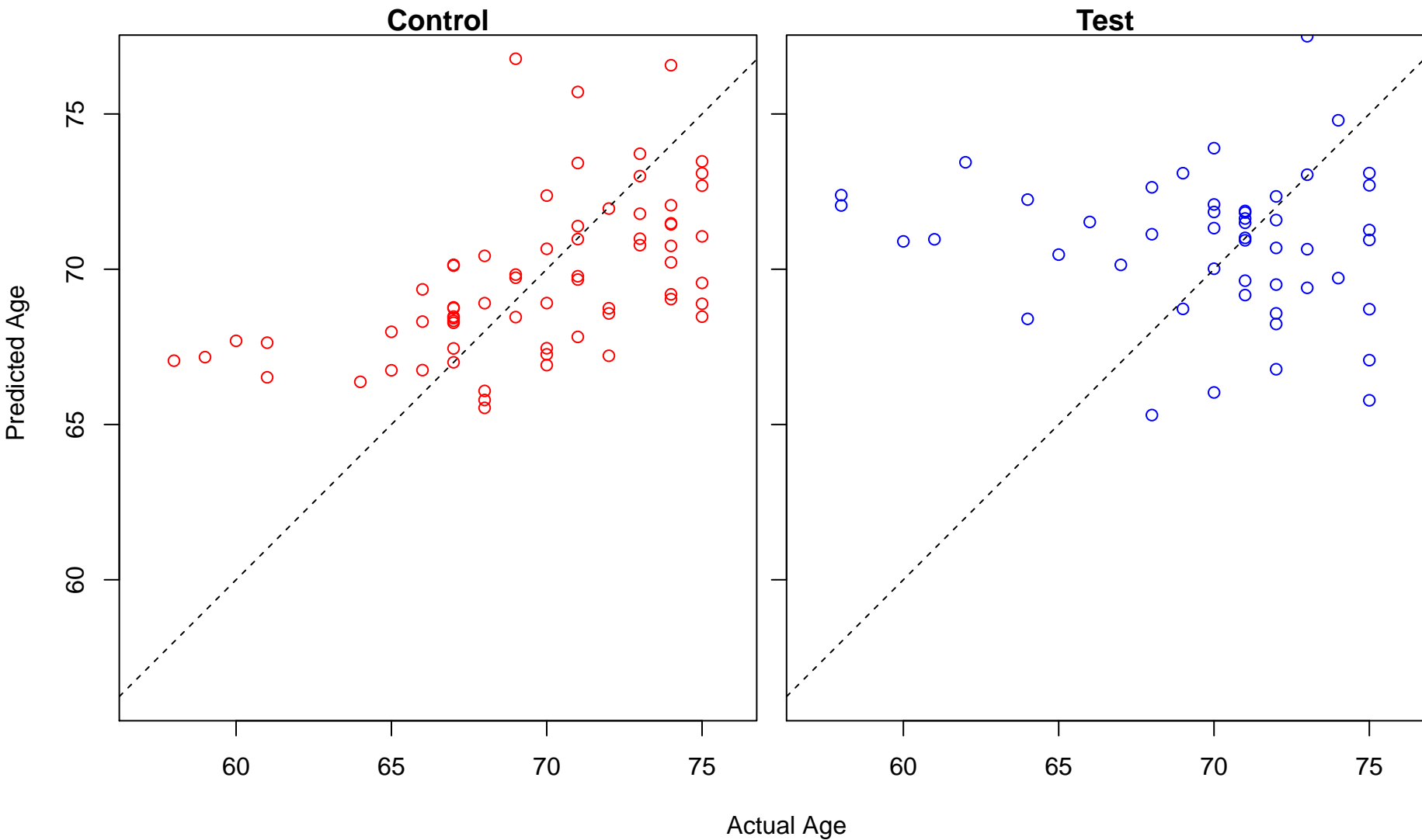
regulation of oxidoreductase activity (Score: 0.881459)



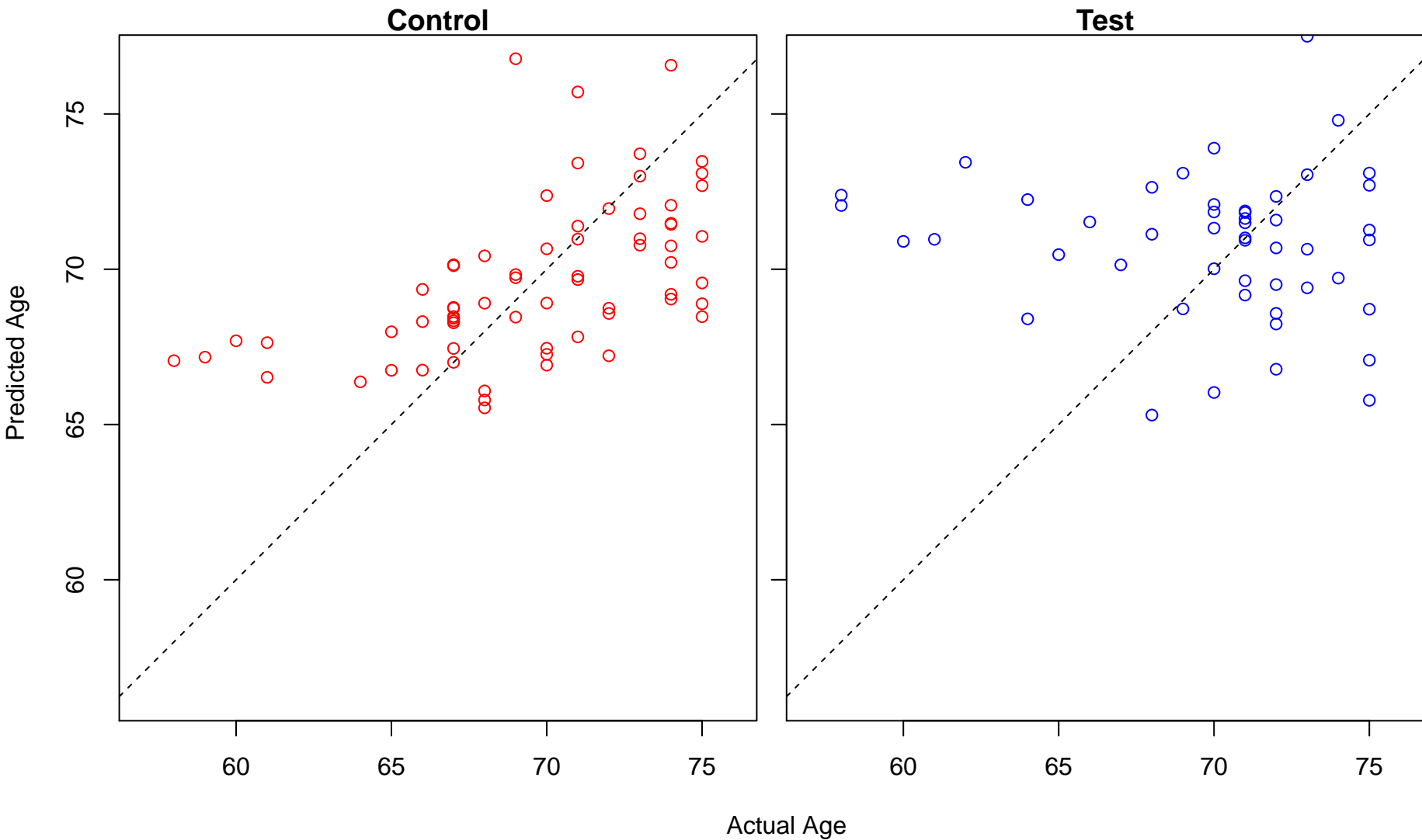
T cell proliferation (Score: 0.881282)



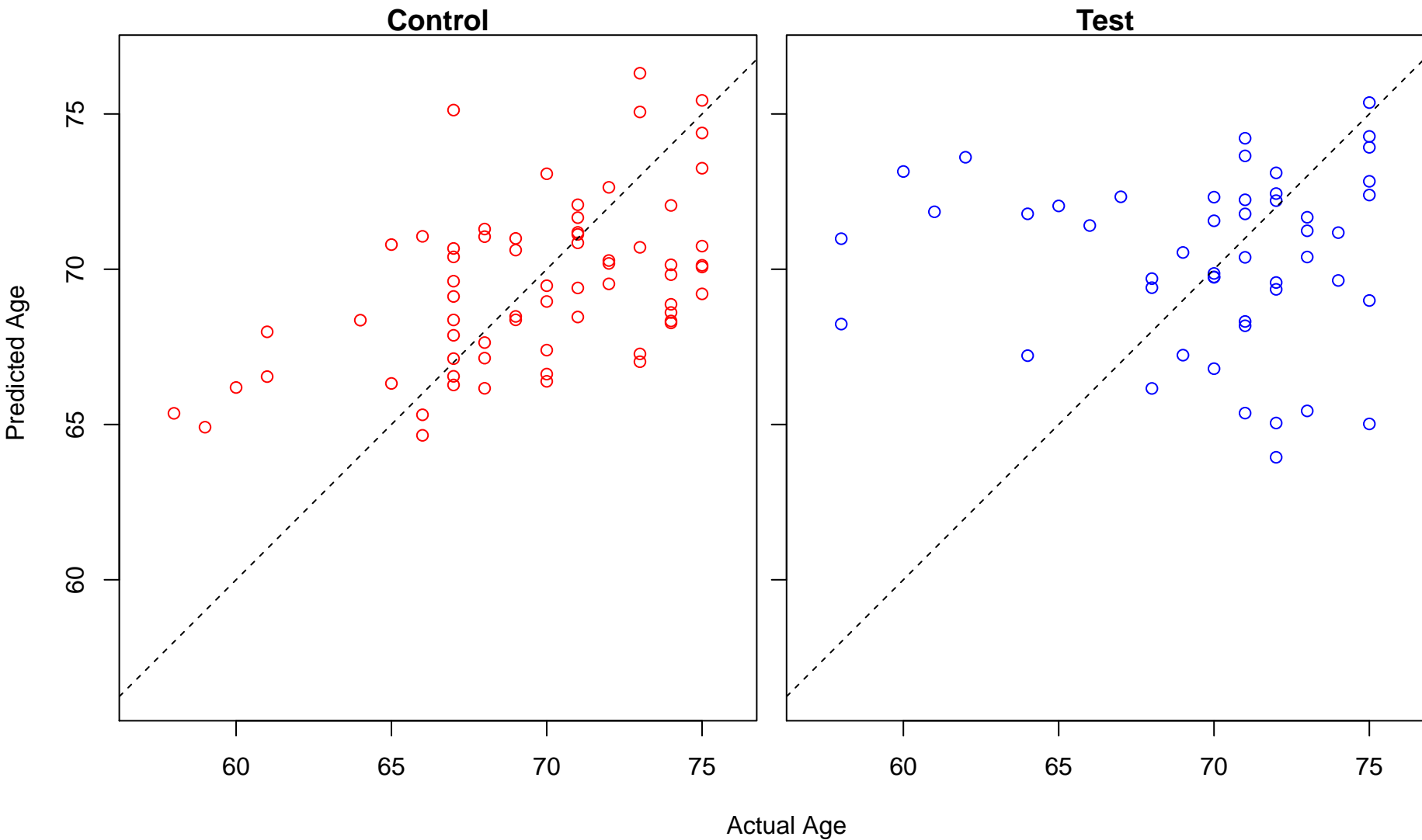
negative regulation of T cell differentiation in thymus (Score: 0.881059)



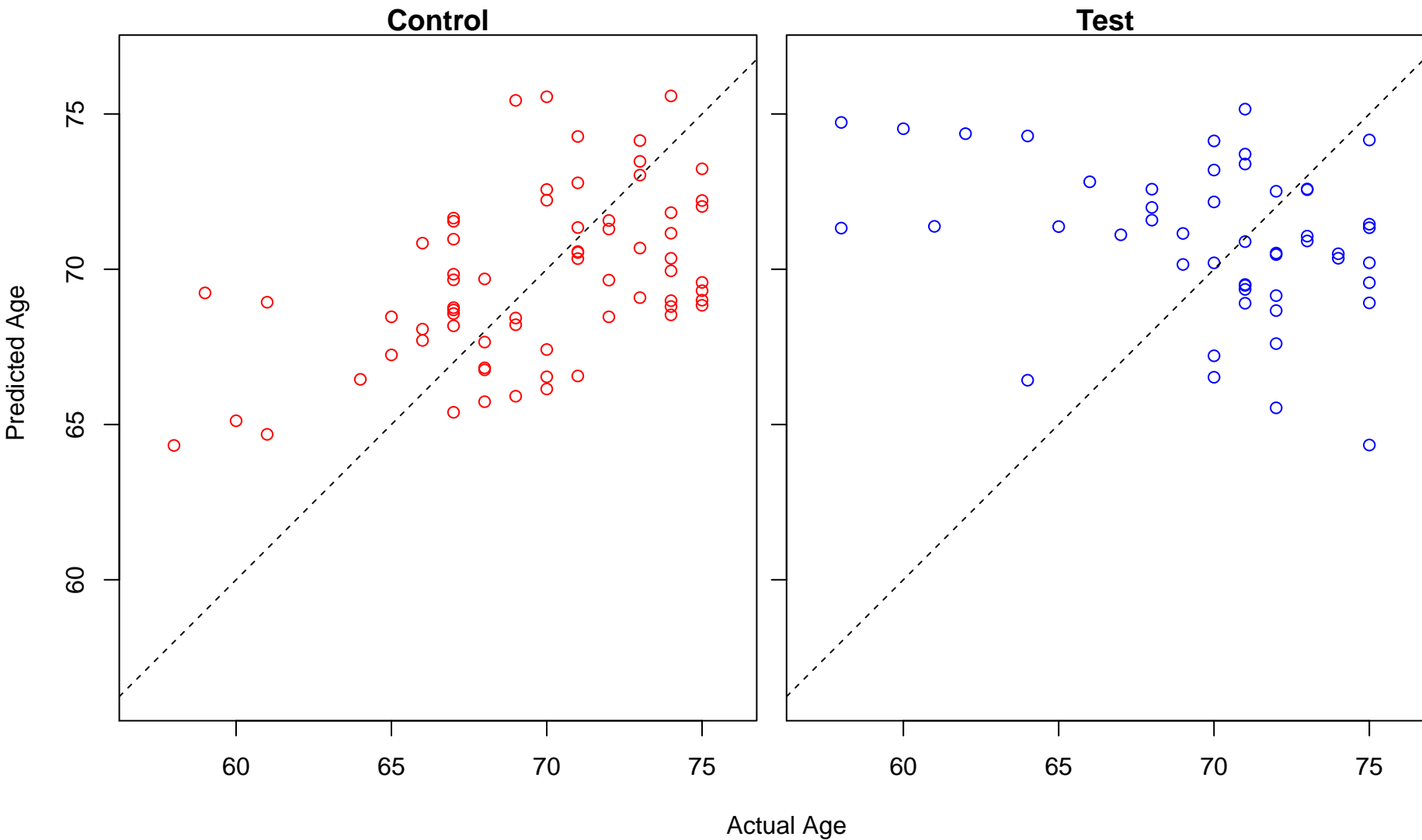
negative regulation of thymocyte aggregation (Score: 0.881059)



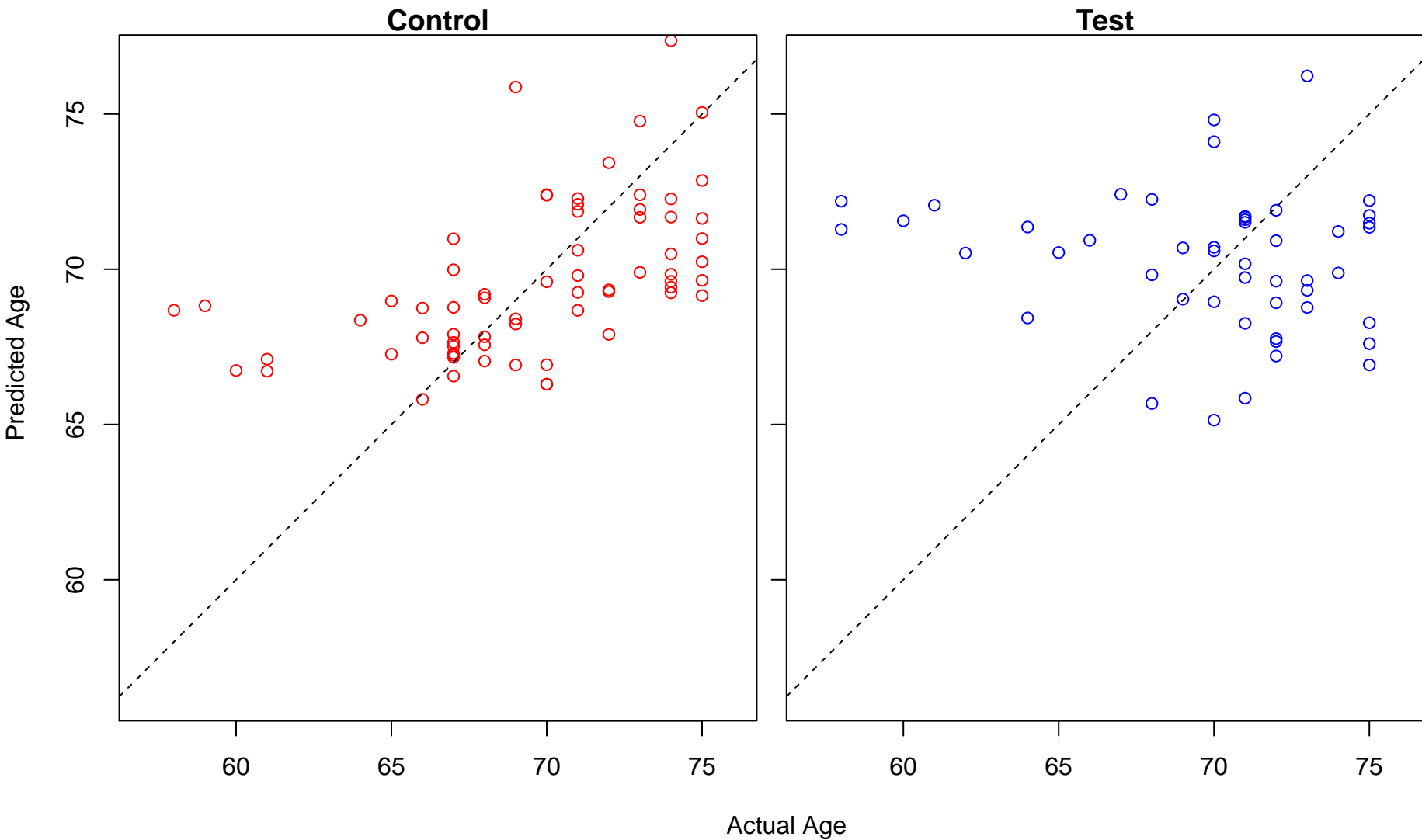
negative regulation of potassium ion transport (Score: 0.880702)



digestive system process (Score: 0.880294)

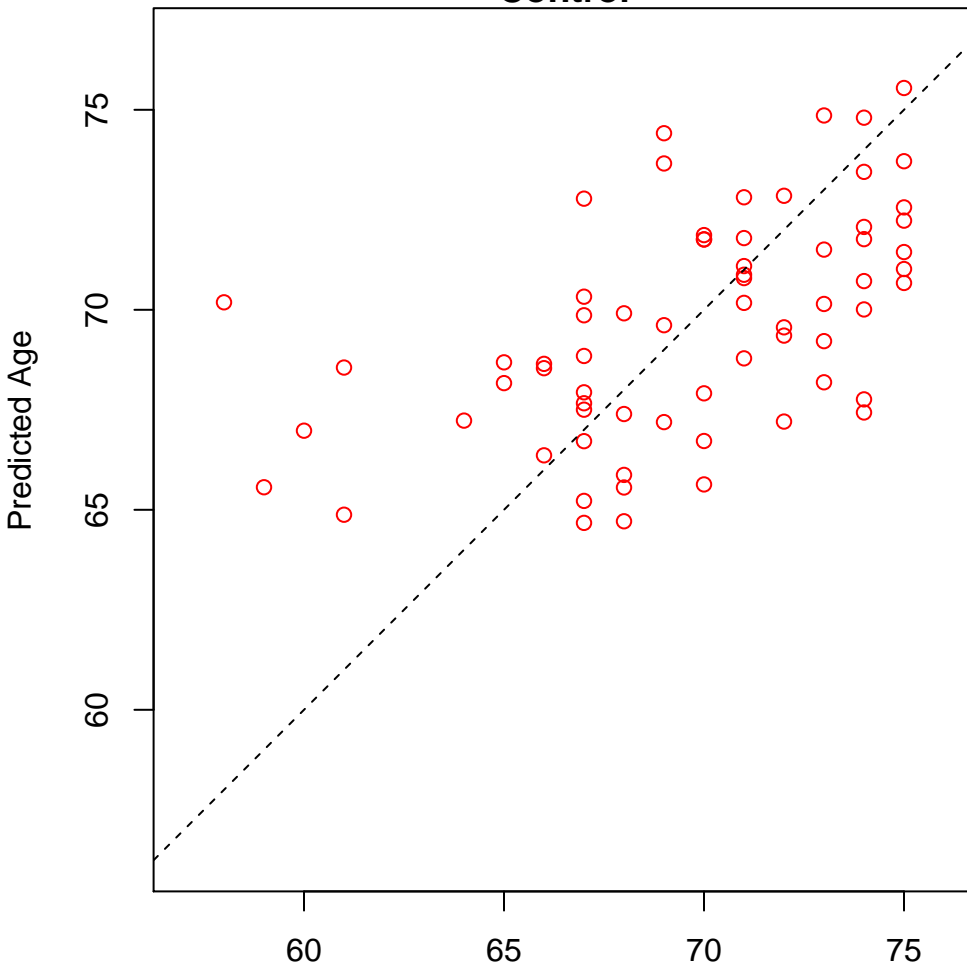


multi-organism behavior (Score: 0.880251)

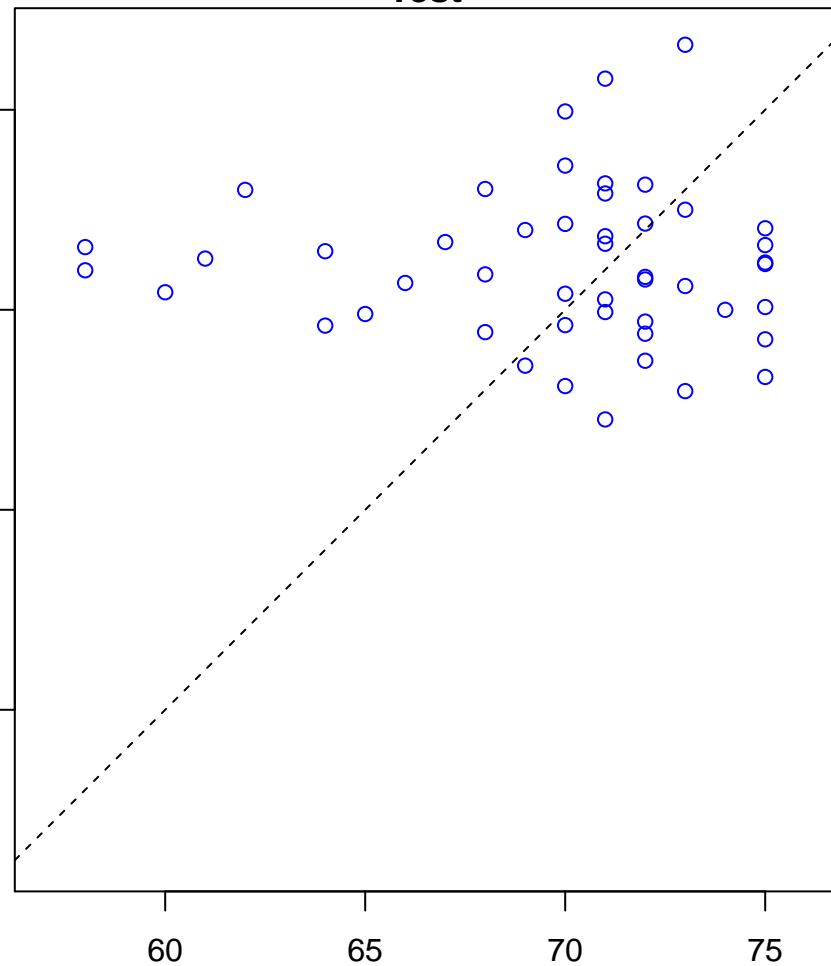


intermediate filament-based process (Score: 0.880218)

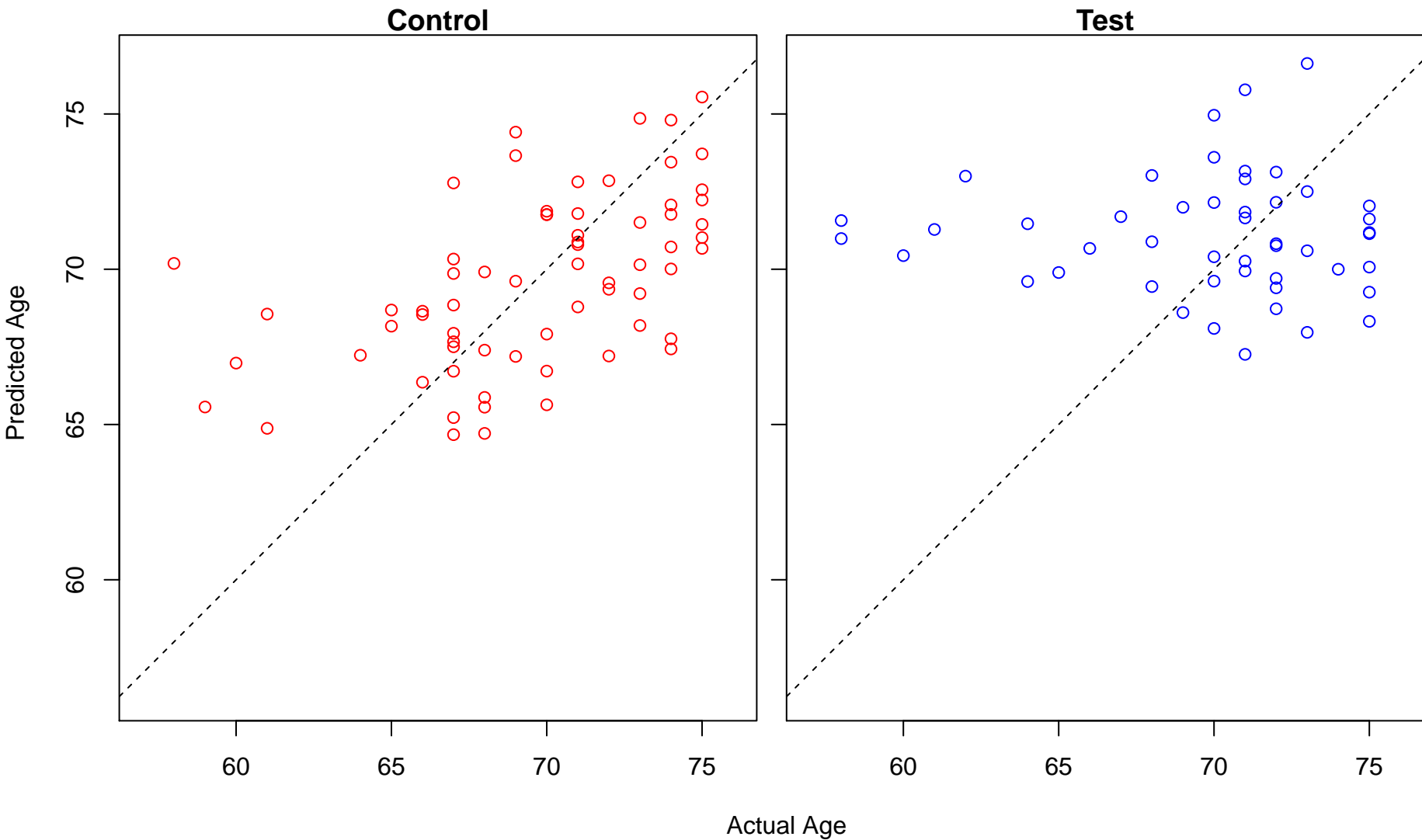
Control



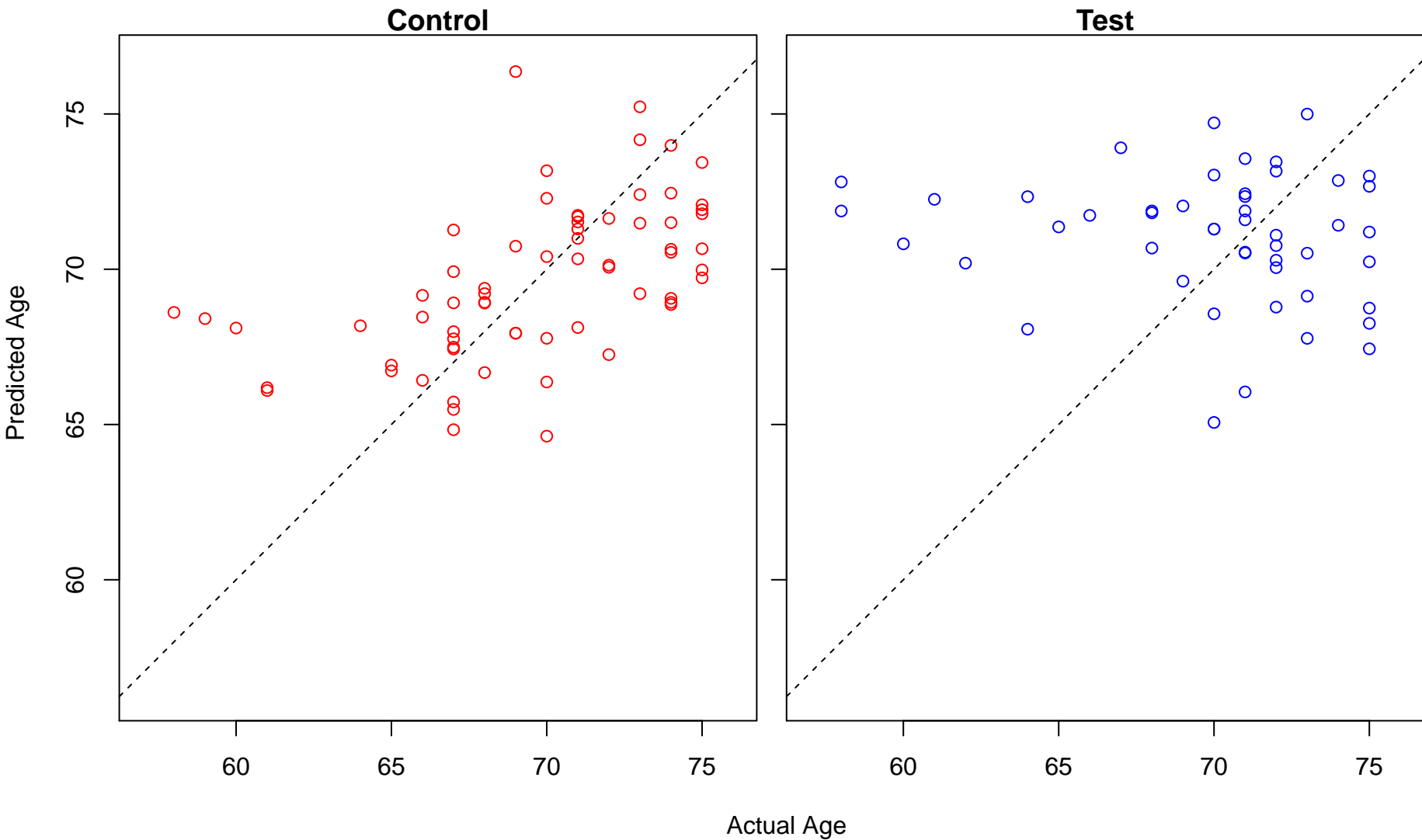
Test



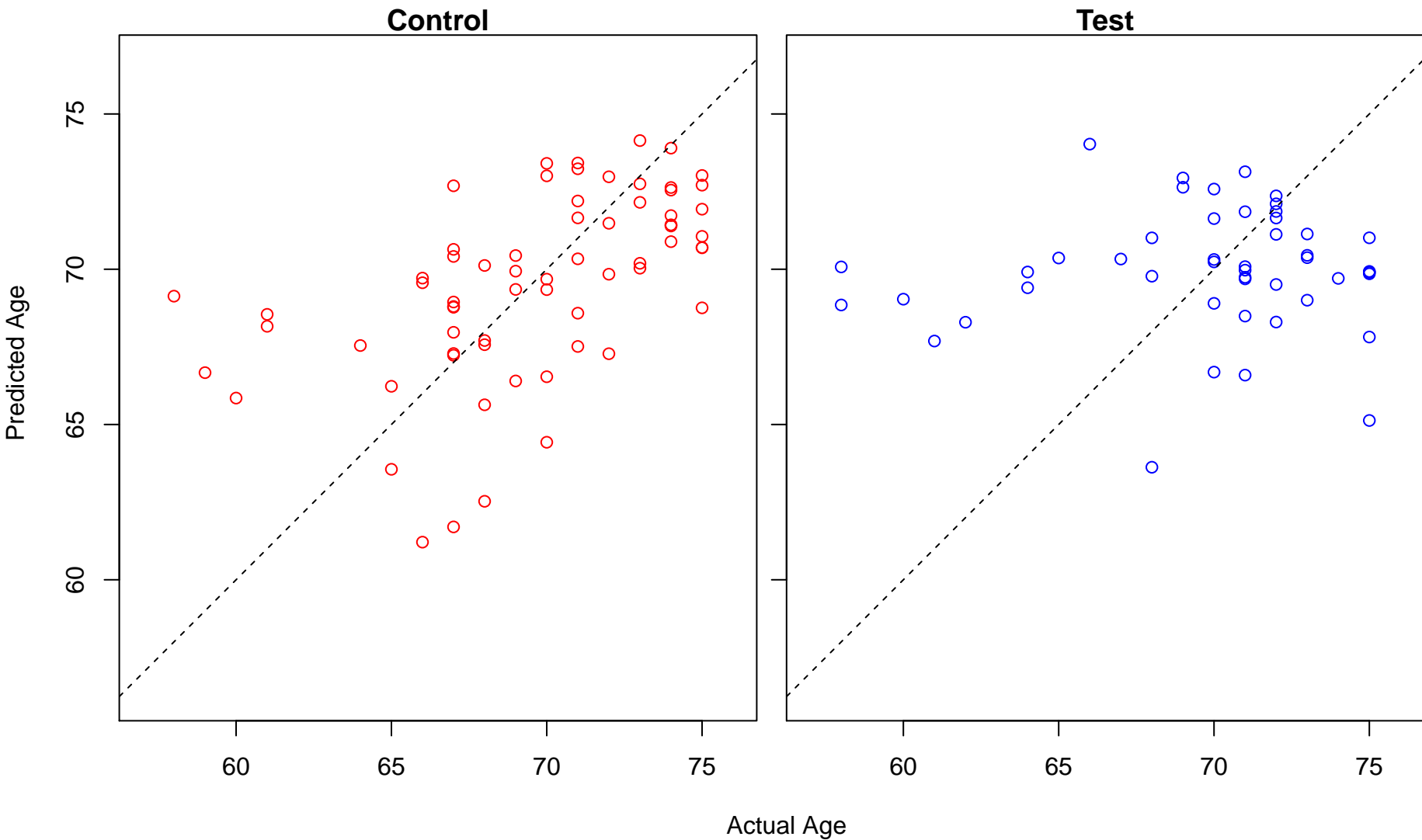
intermediate filament cytoskeleton organization (Score: 0.880218)



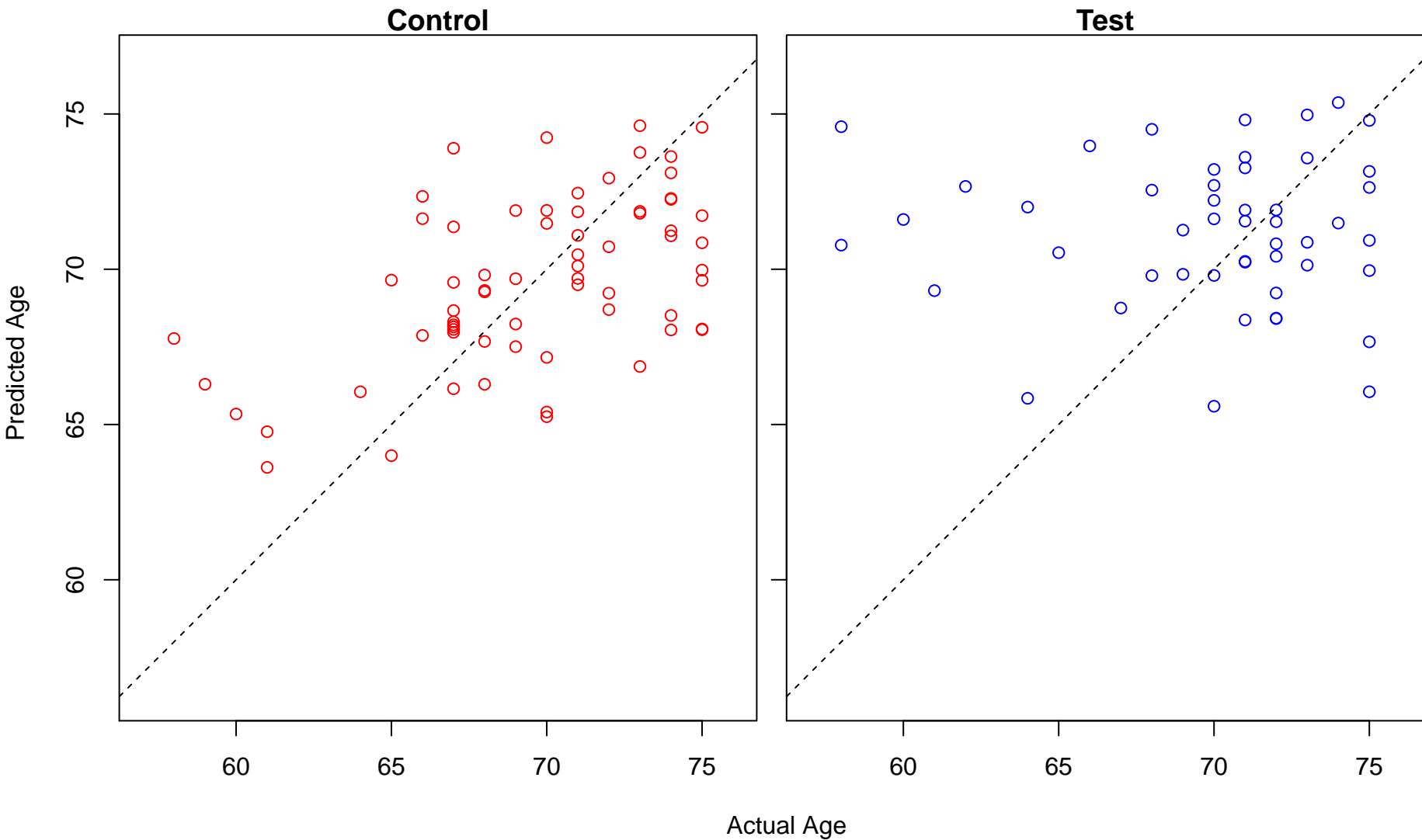
pteridine-containing compound metabolic process (Score: 0.879945)



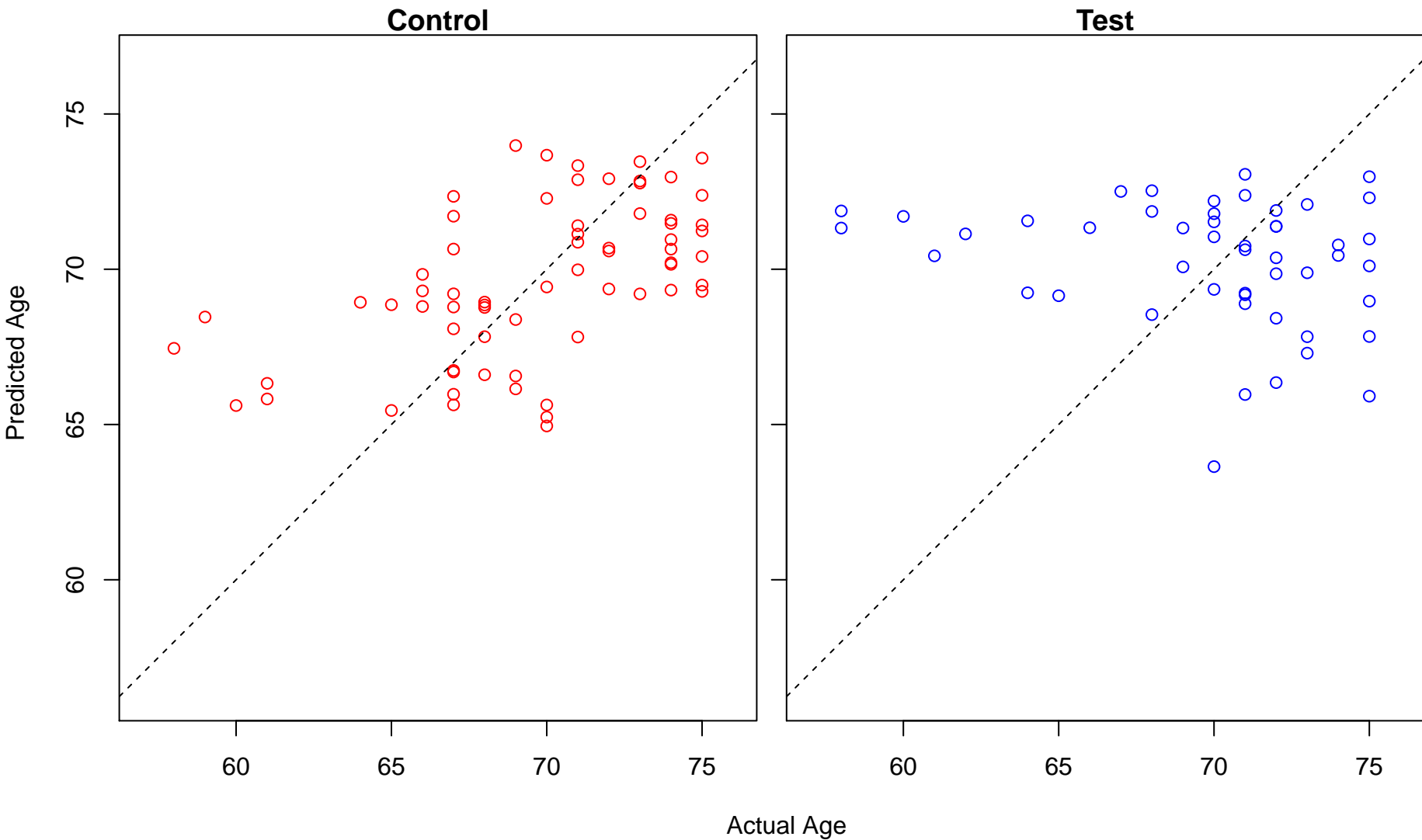
dendritic cell migration (Score: 0.879788)



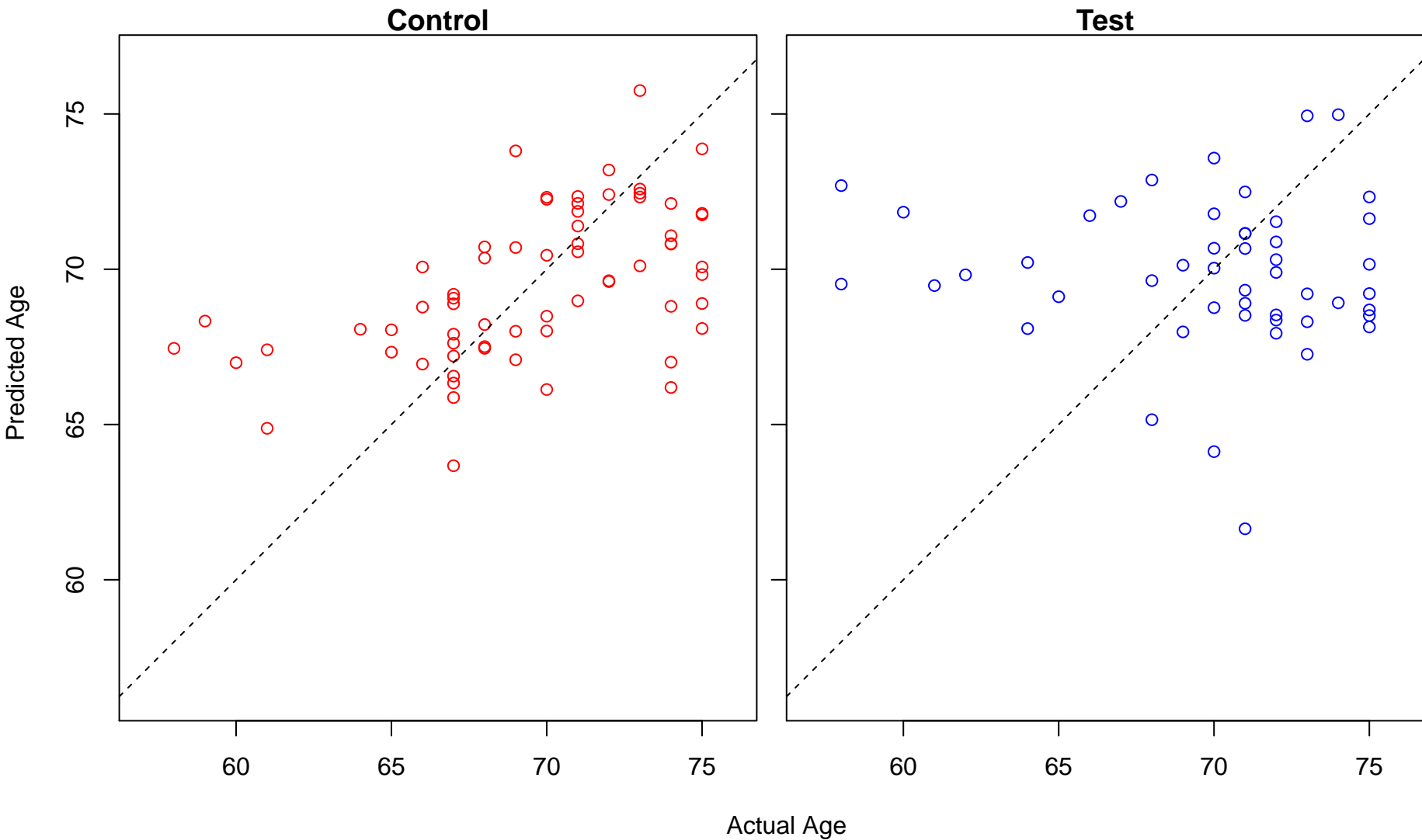
adherens junction assembly (Score: 0.879686)



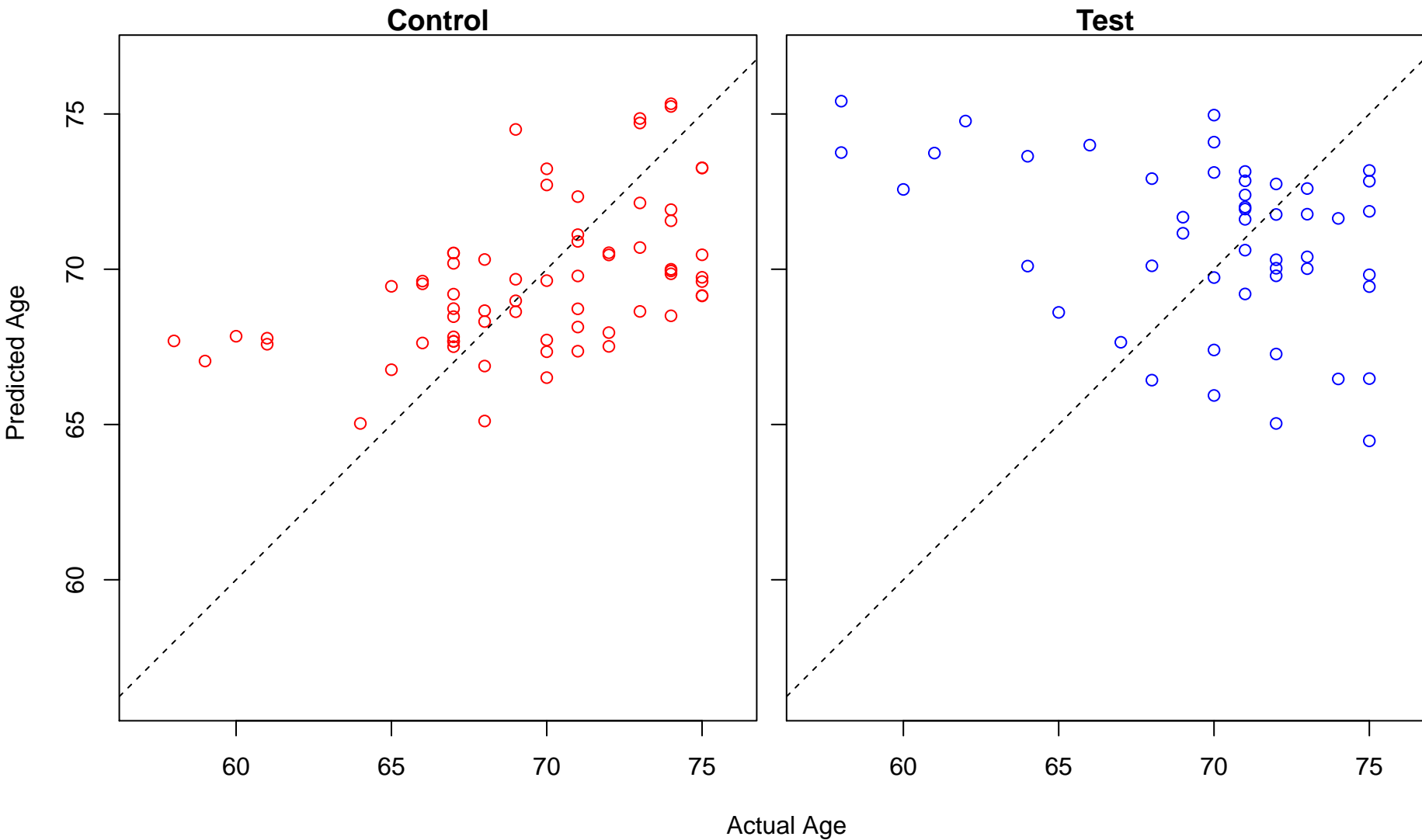
detection of chemical stimulus (Score: 0.879176)



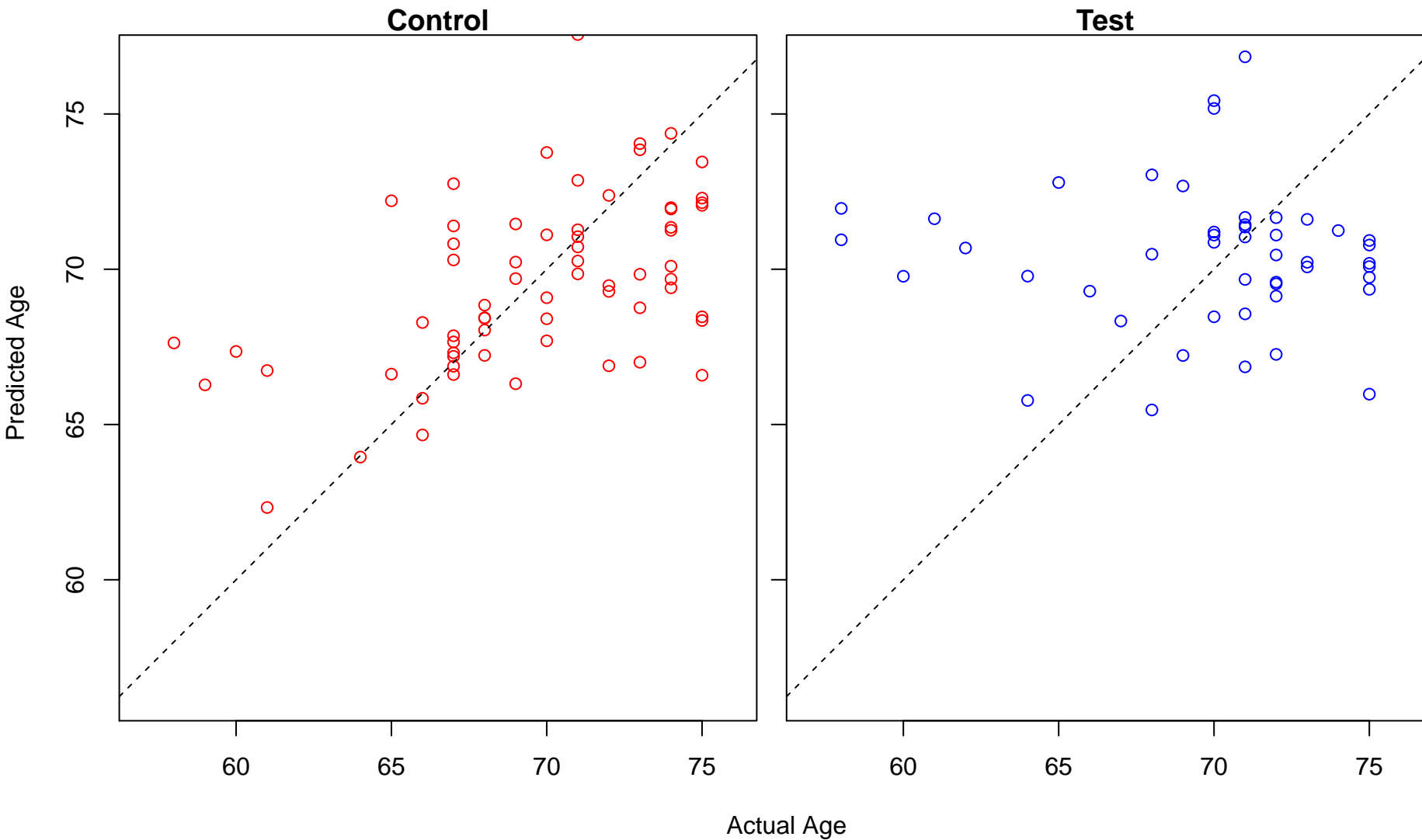
excitatory synapse assembly (Score: 0.879143)



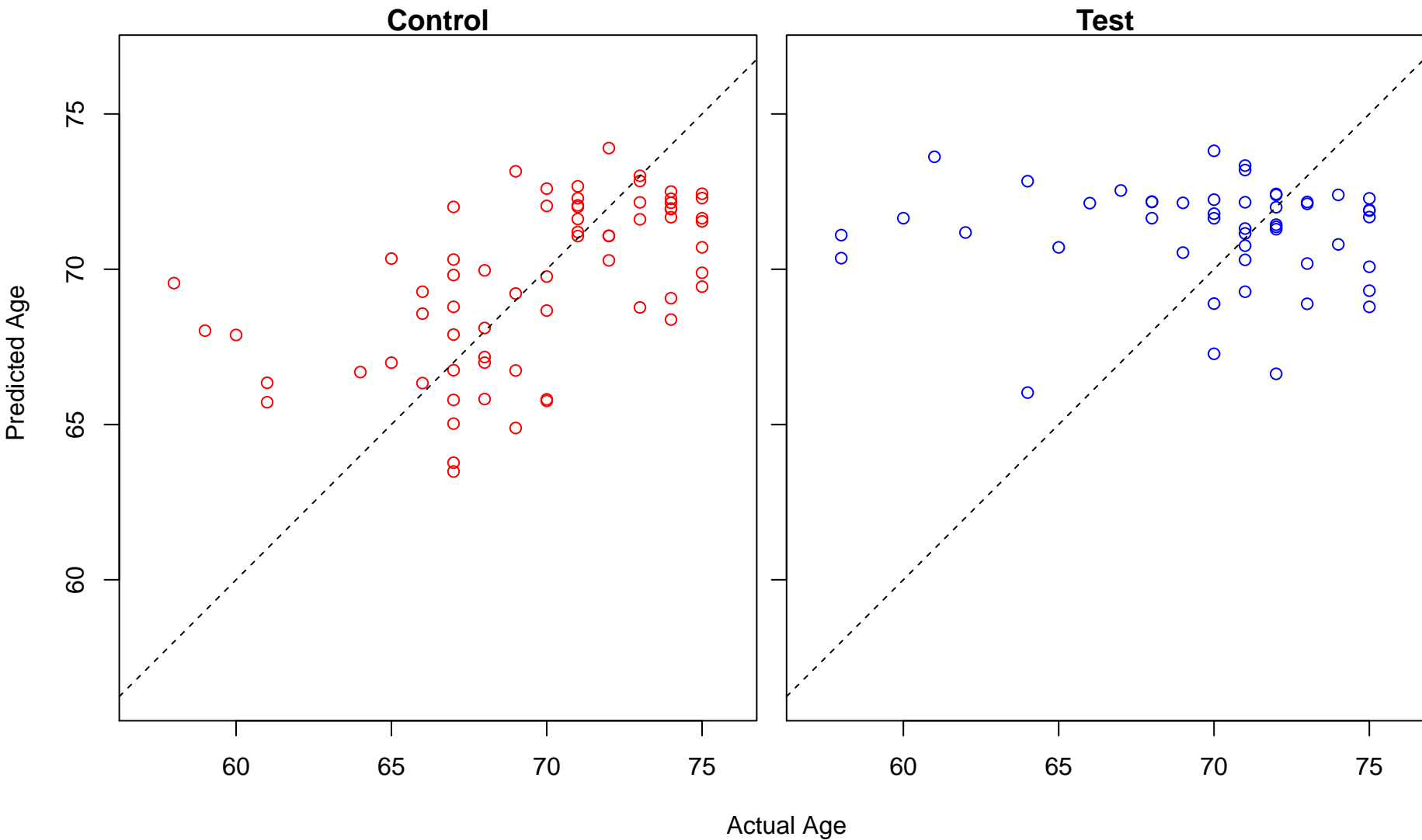
regulation of protein exit from endoplasmic reticulum (Score: 0.879120)



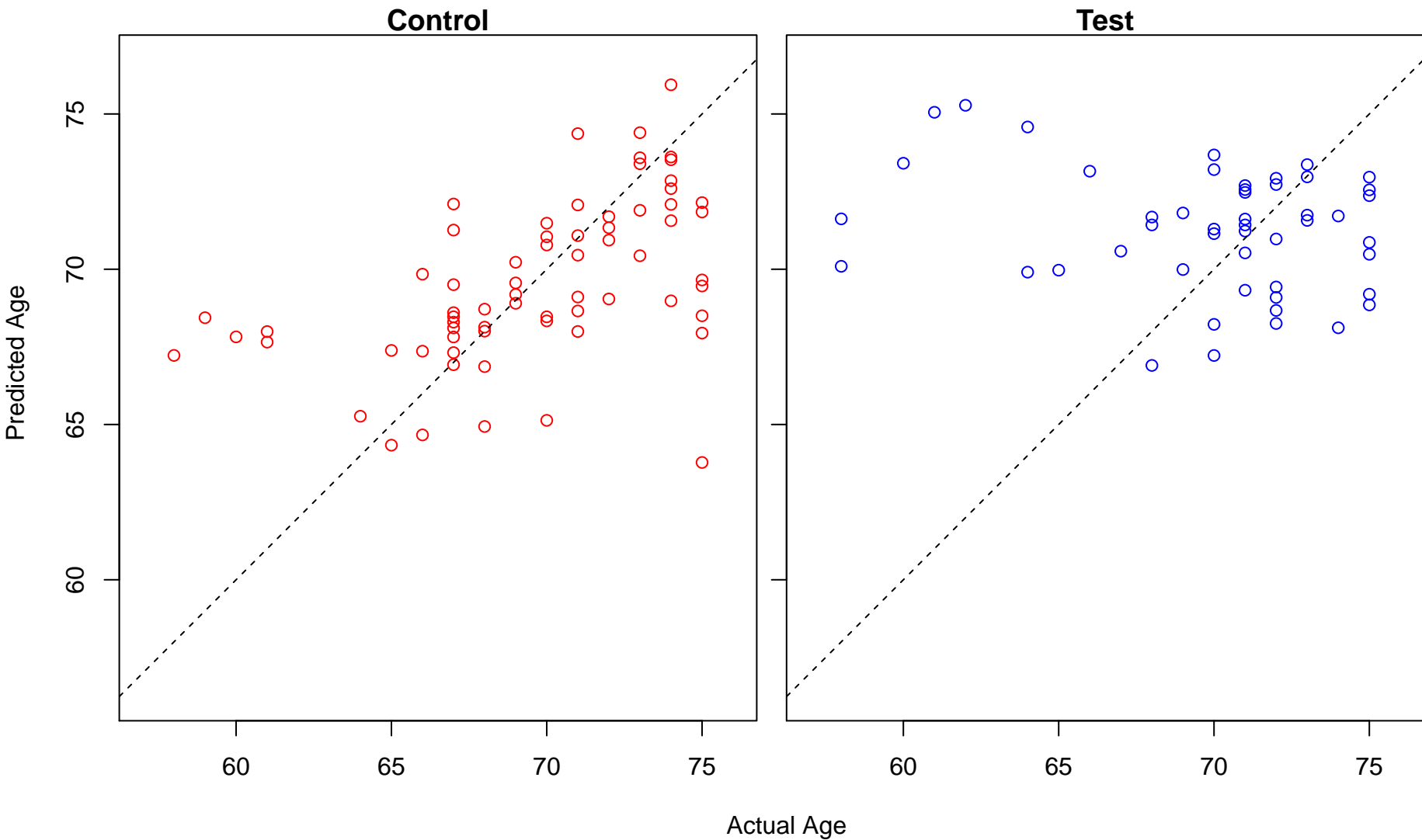
UV-damage excision repair (Score: 0.879094)



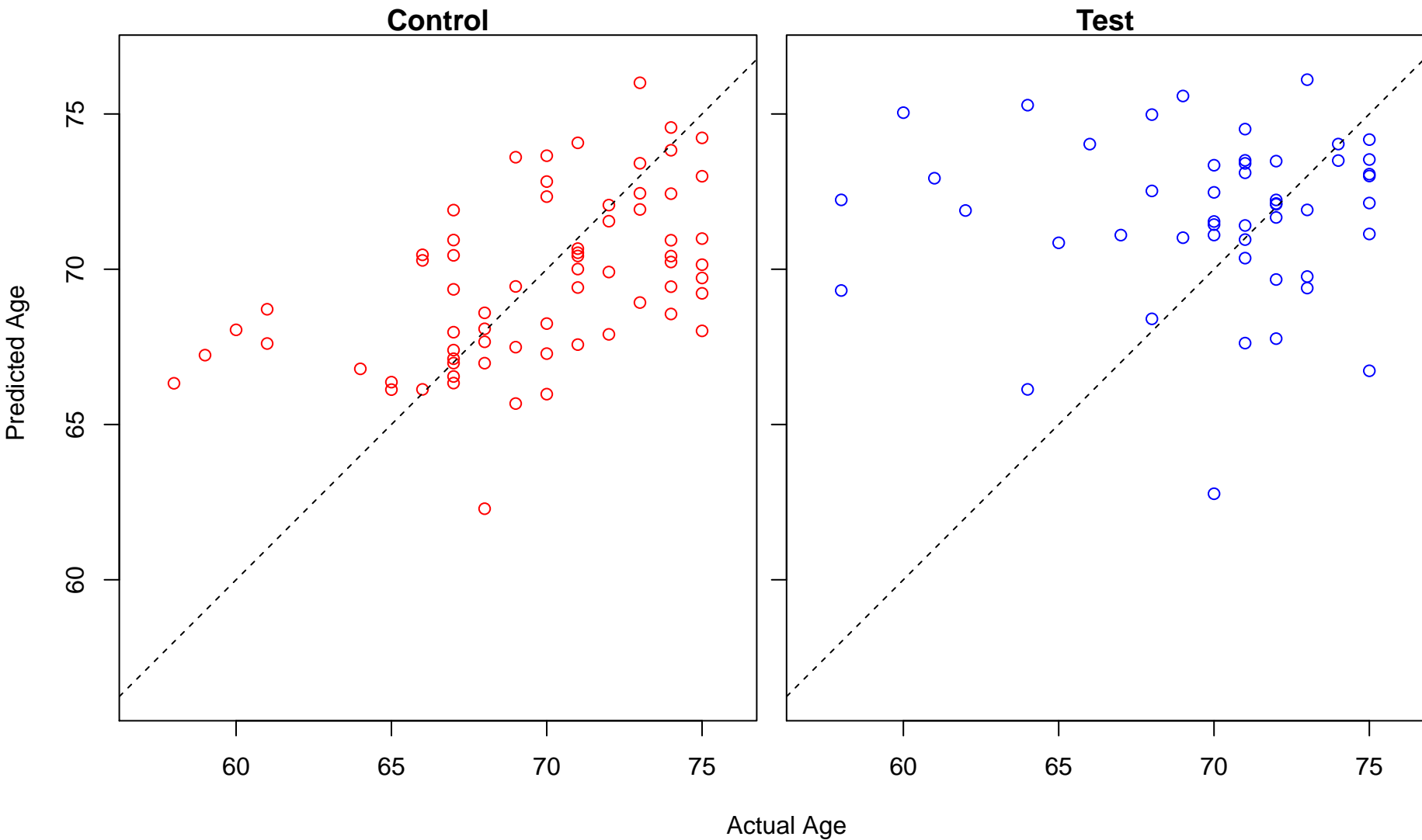
DNA ligation involved in DNA repair (Score: 0.878983)



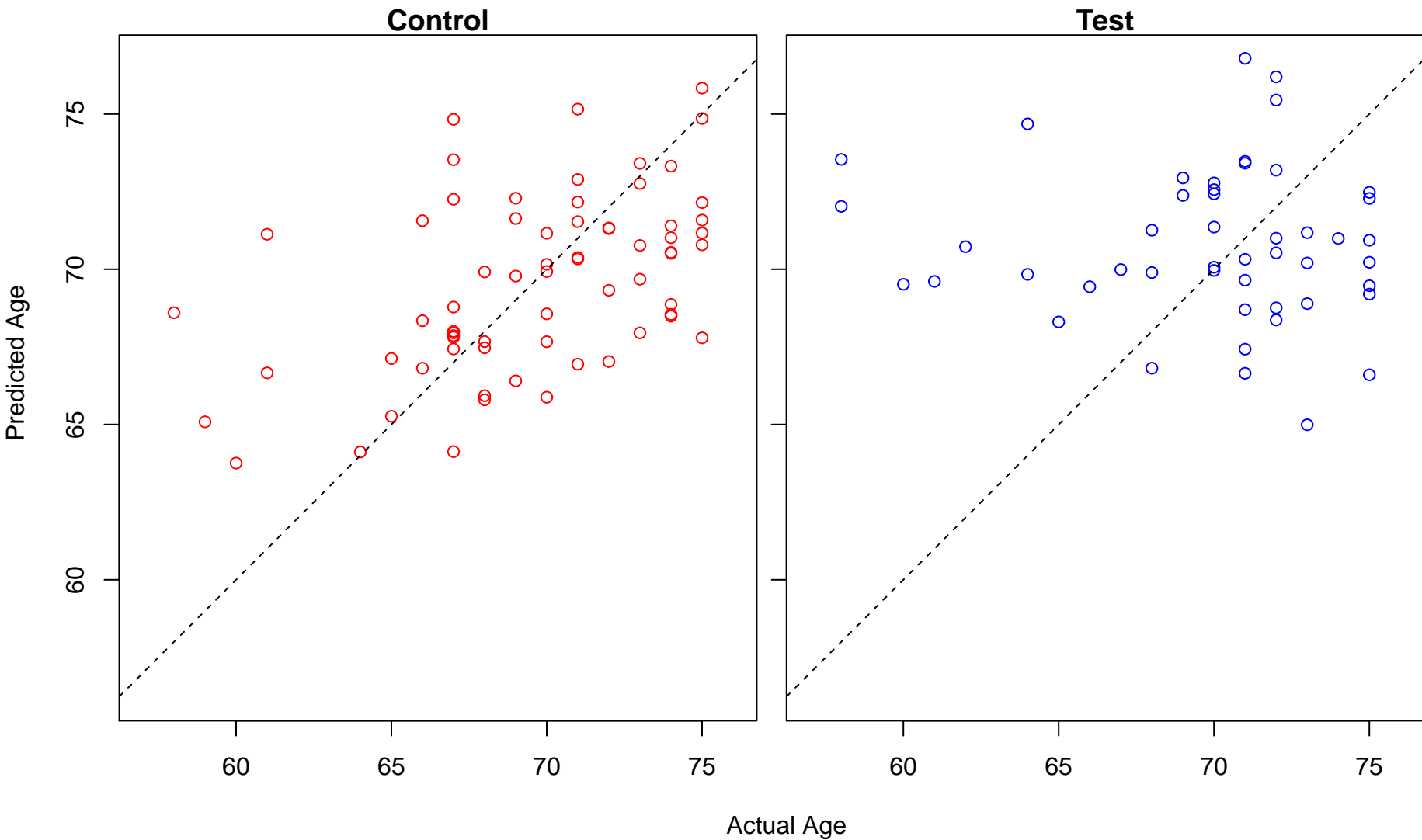
positive regulation of lipid transport (Score: 0.878777)



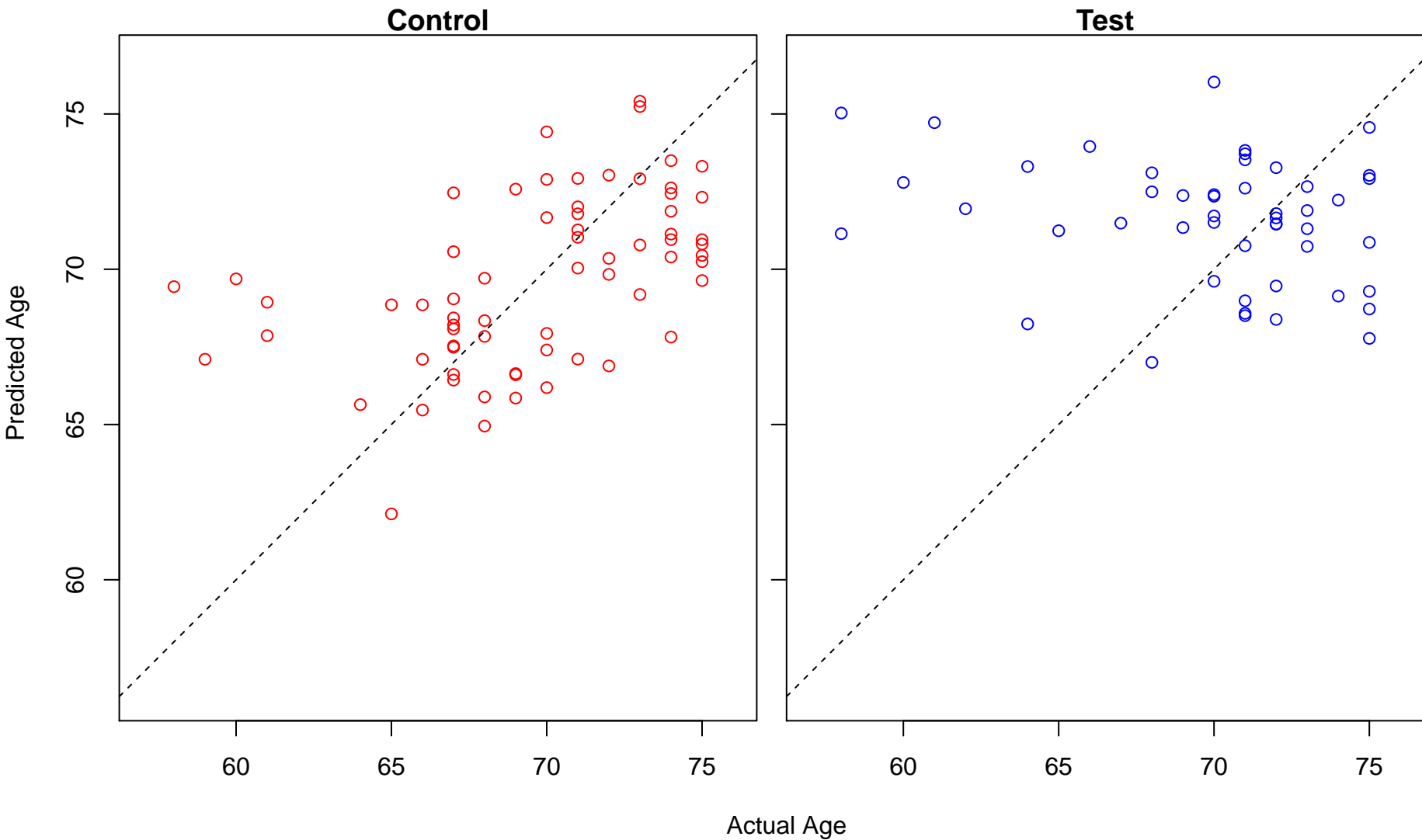
regulation of glycogen metabolic process (Score: 0.878593)



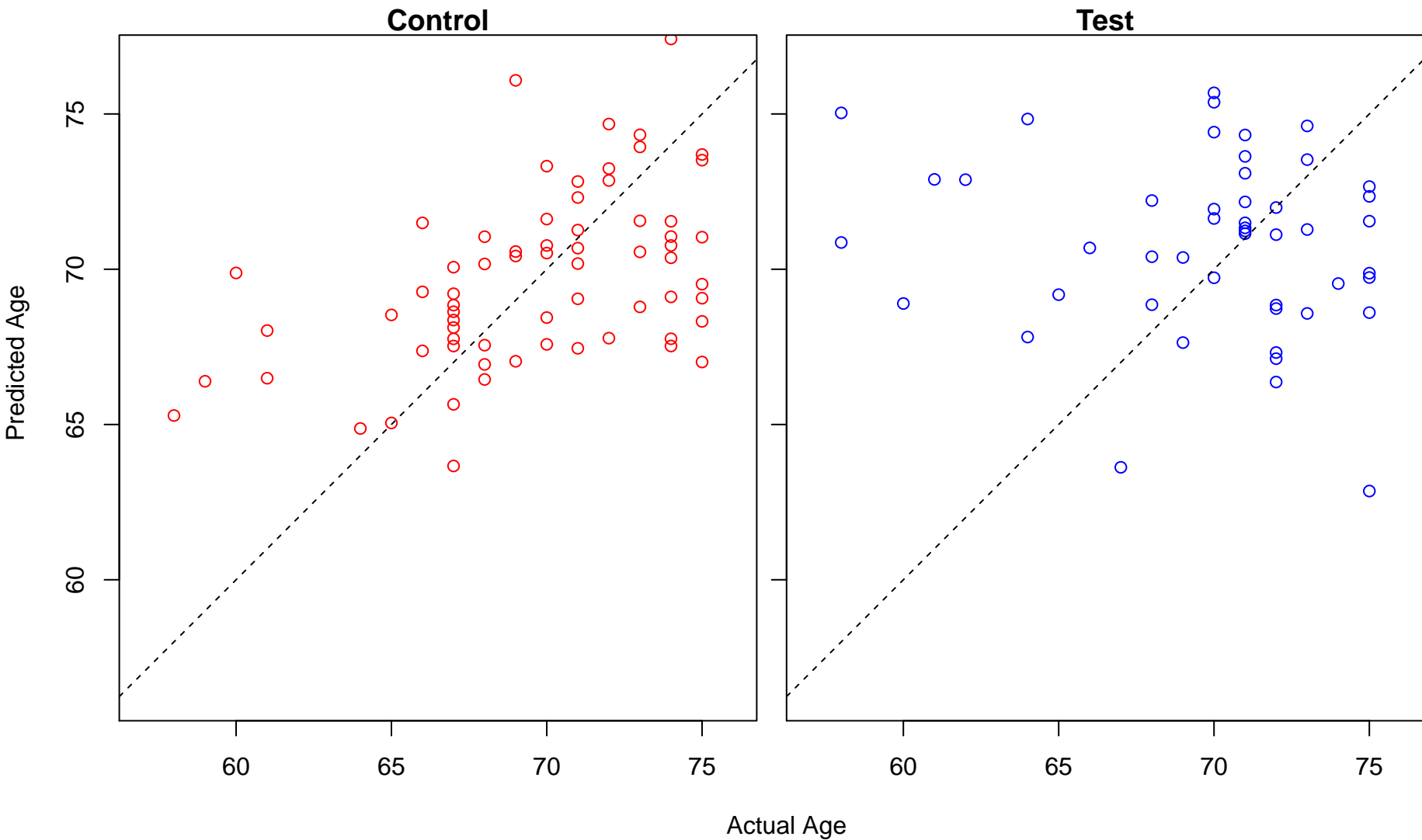
positive regulation of ERBB signaling pathway (Score: 0.878471)



positive regulation of extrinsic apoptotic signaling pathway (Score: 0.878435)

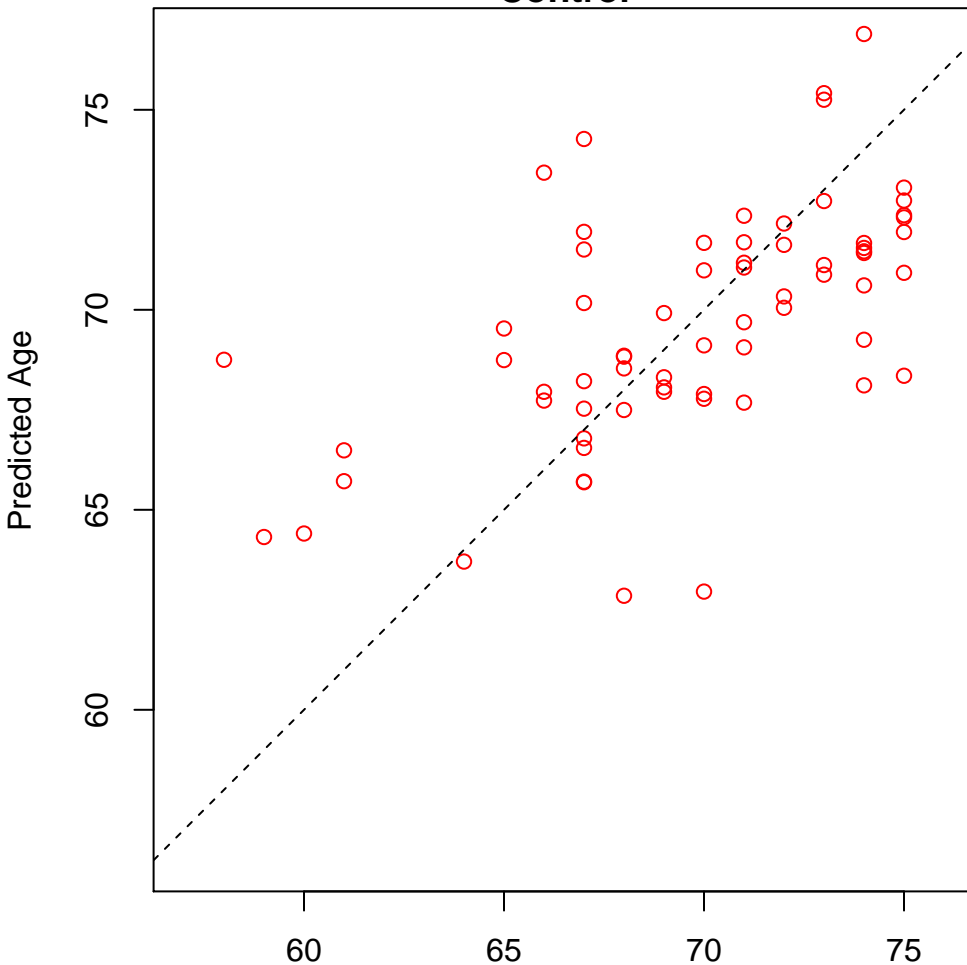


positive regulation of interleukin-12 production (Score: 0.878392)

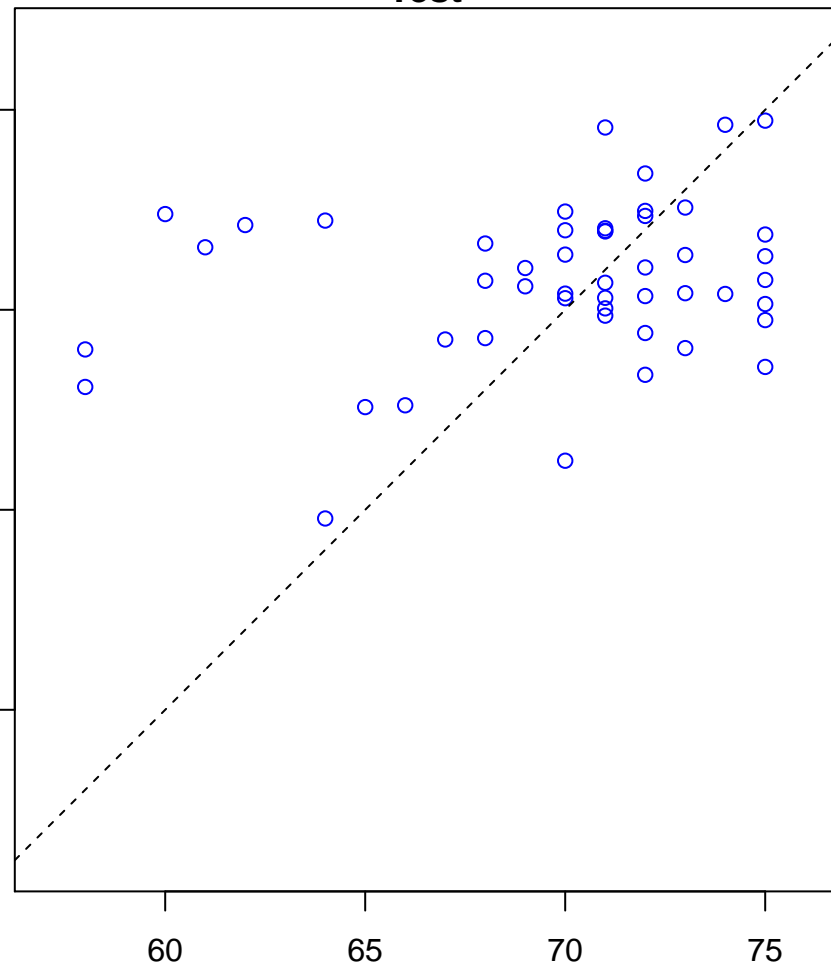


endochondral bone morphogenesis (Score: 0.876940)

Control

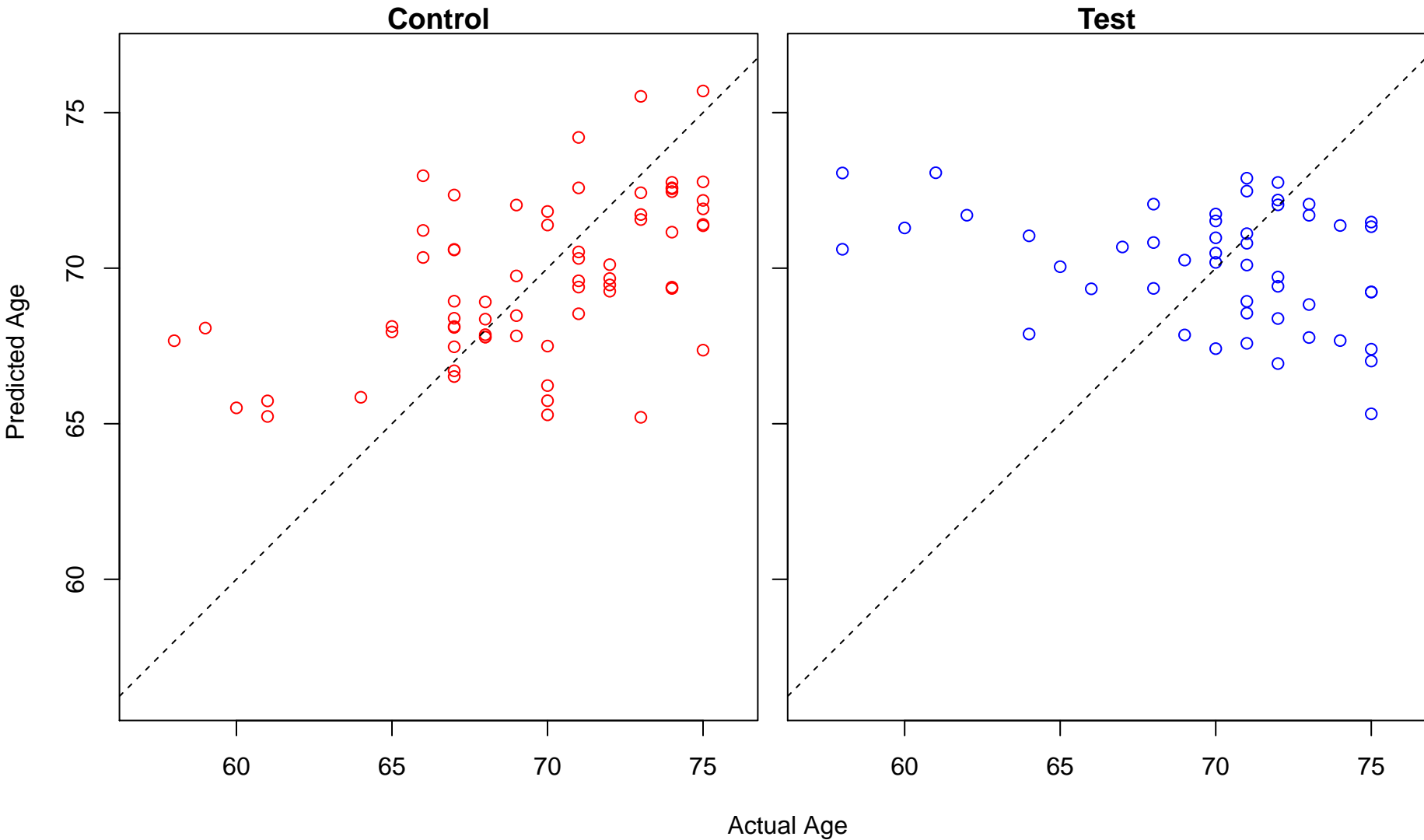


Test

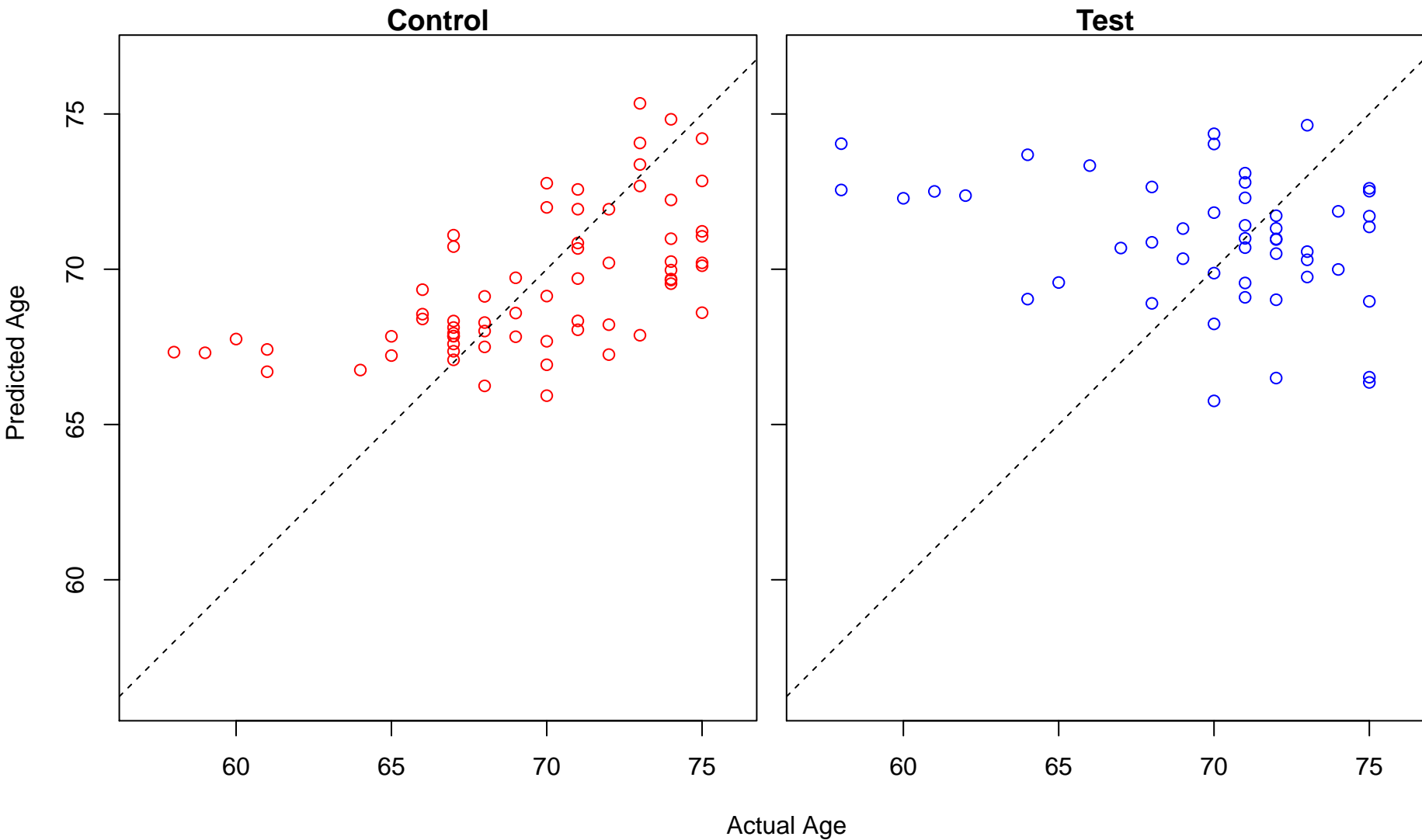


Actual Age

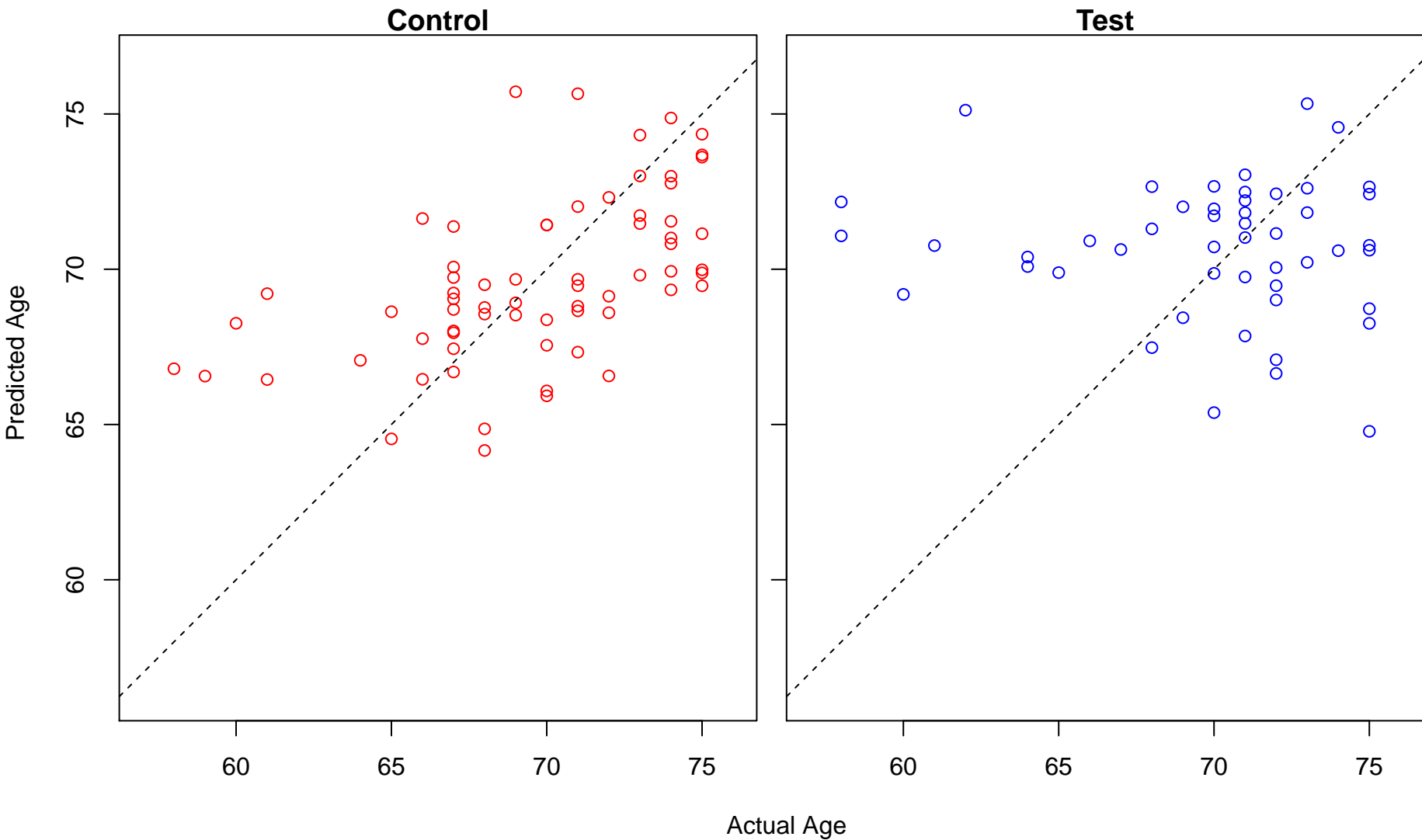
regulation of hyaluronan biosynthetic process (Score: 0.876653)



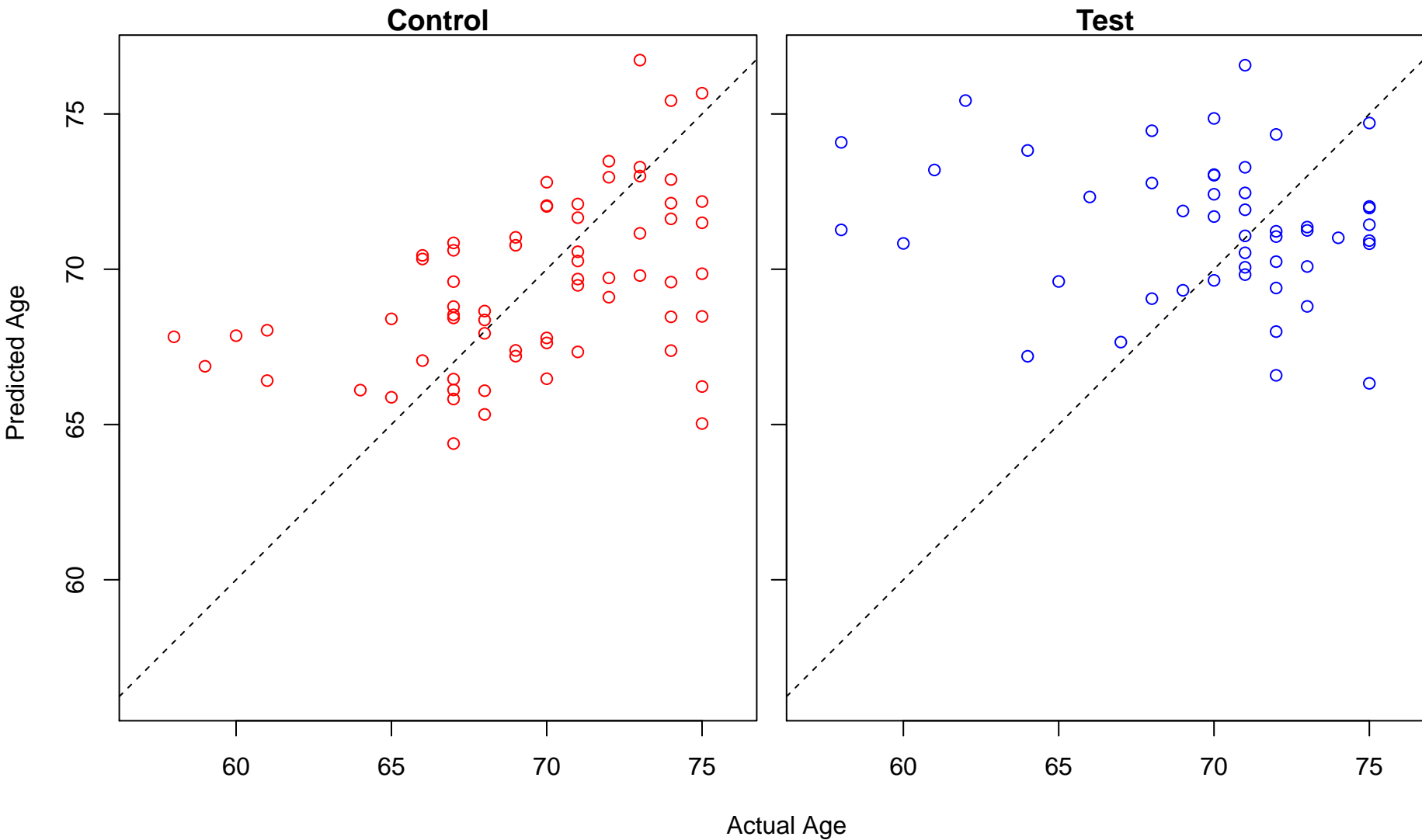
maintenance of protein location (Score: 0.876594)



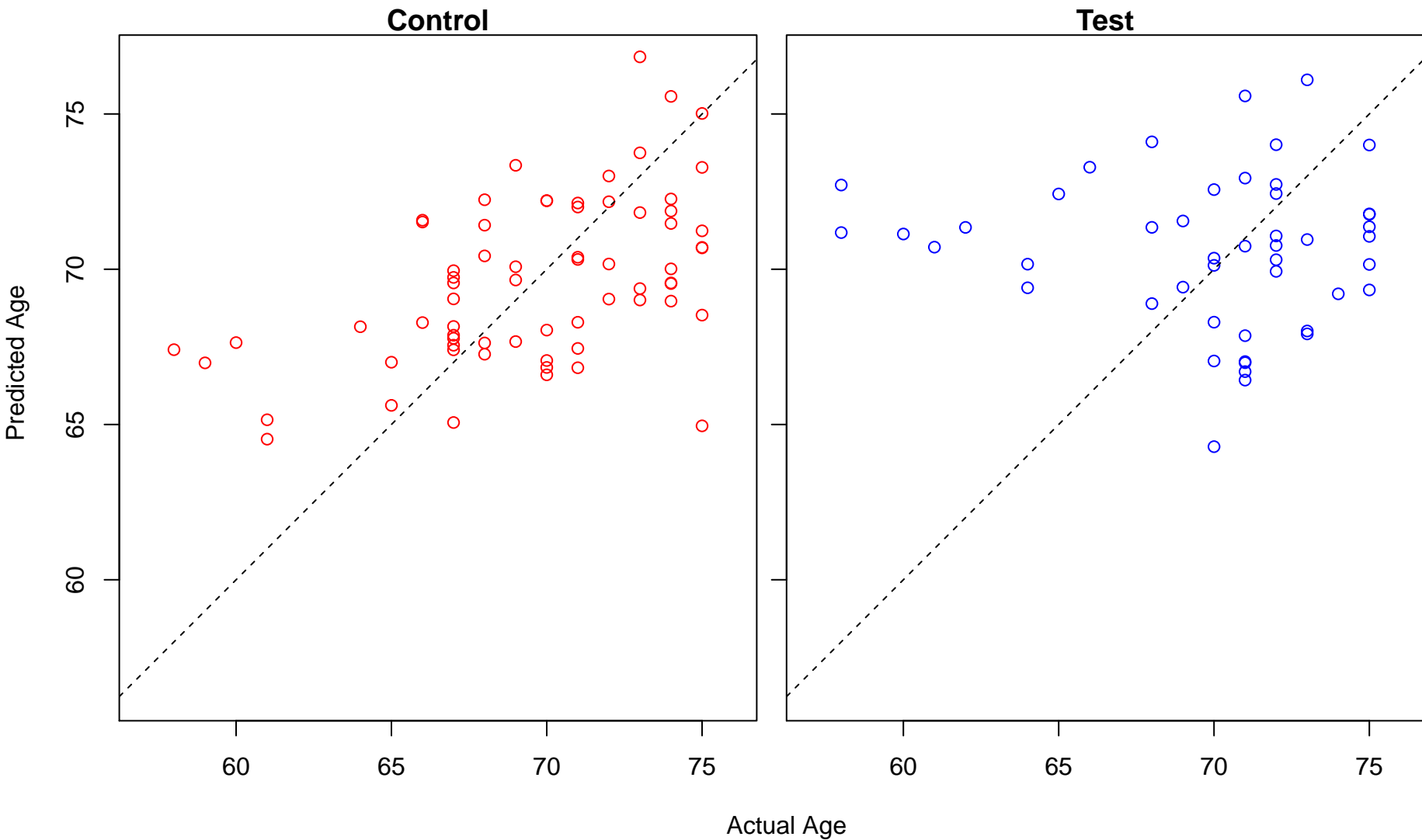
regulation of tyrosine phosphorylation of Stat1 protein (Score: 0.876165)



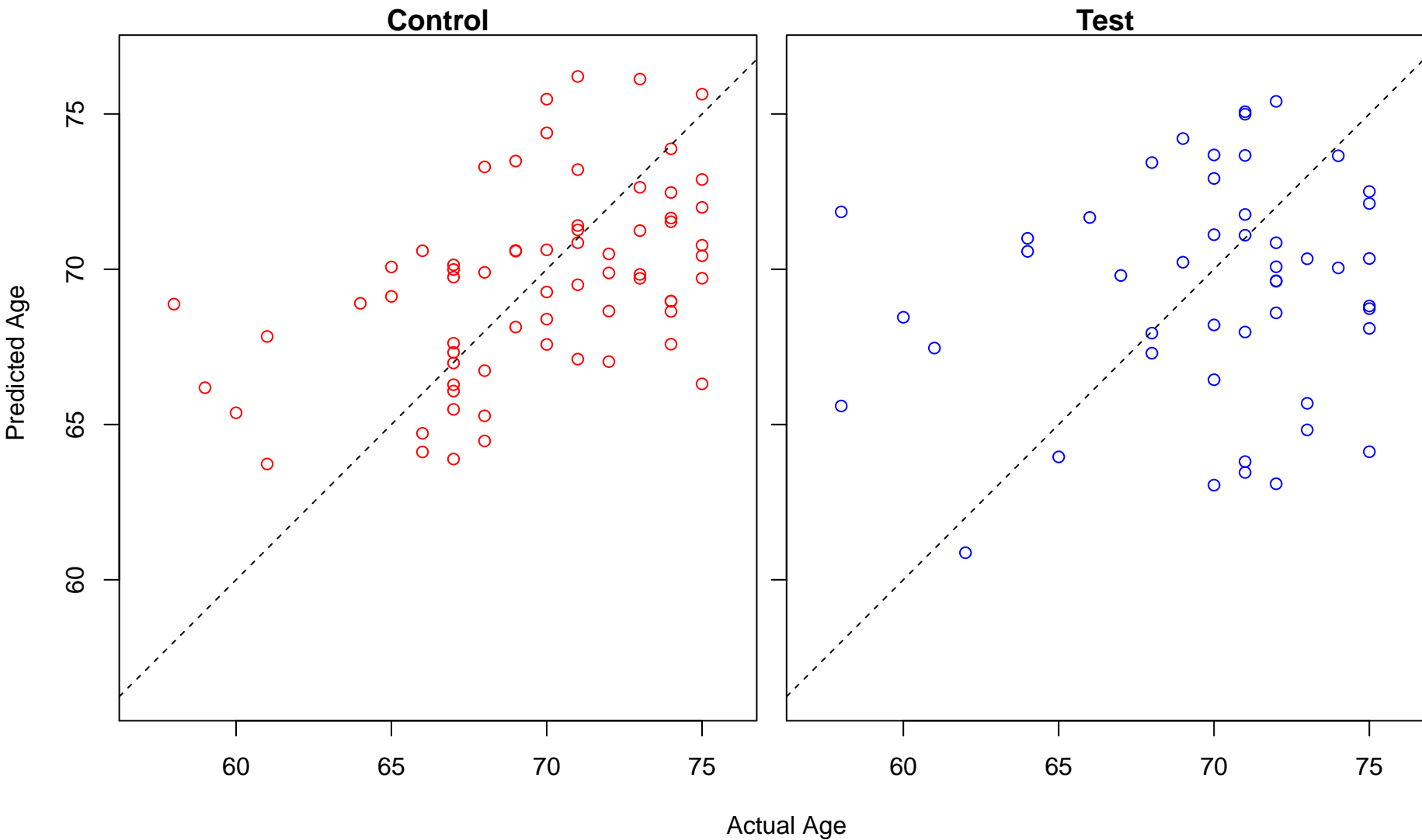
membrane raft organization (Score: 0.875953)



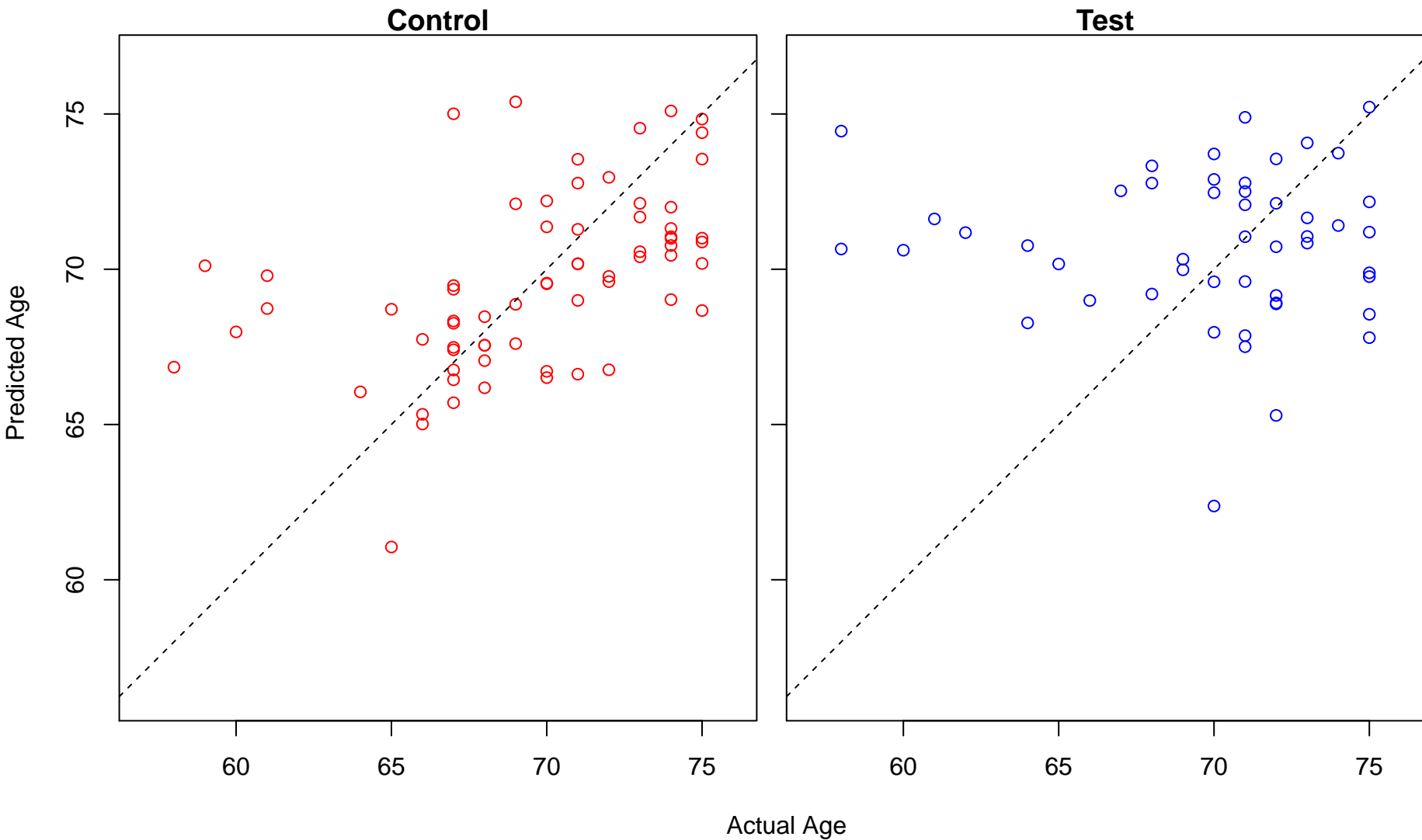
abscission (Score: 0.875758)



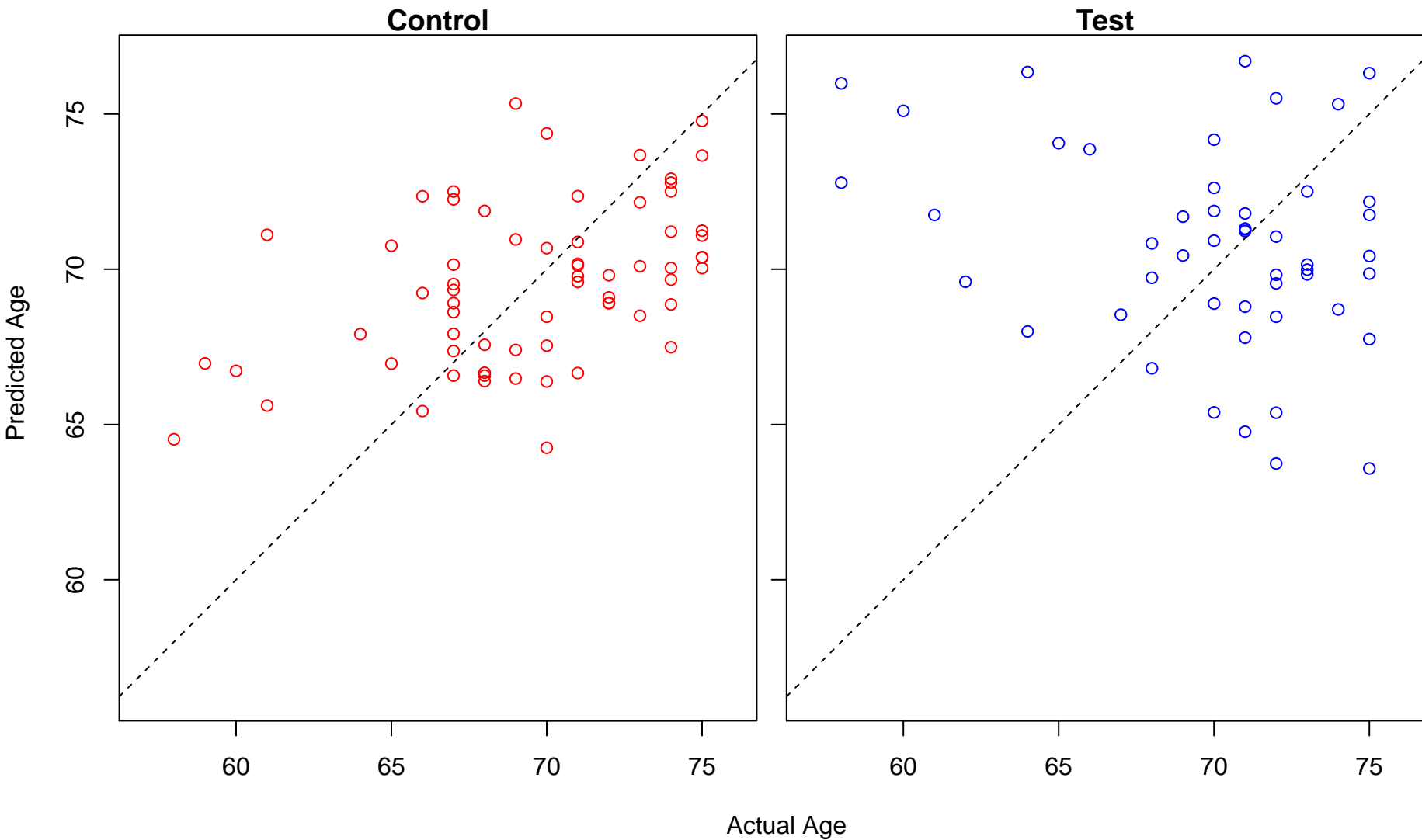
regulation of protein homooligomerization (Score: 0.874671)



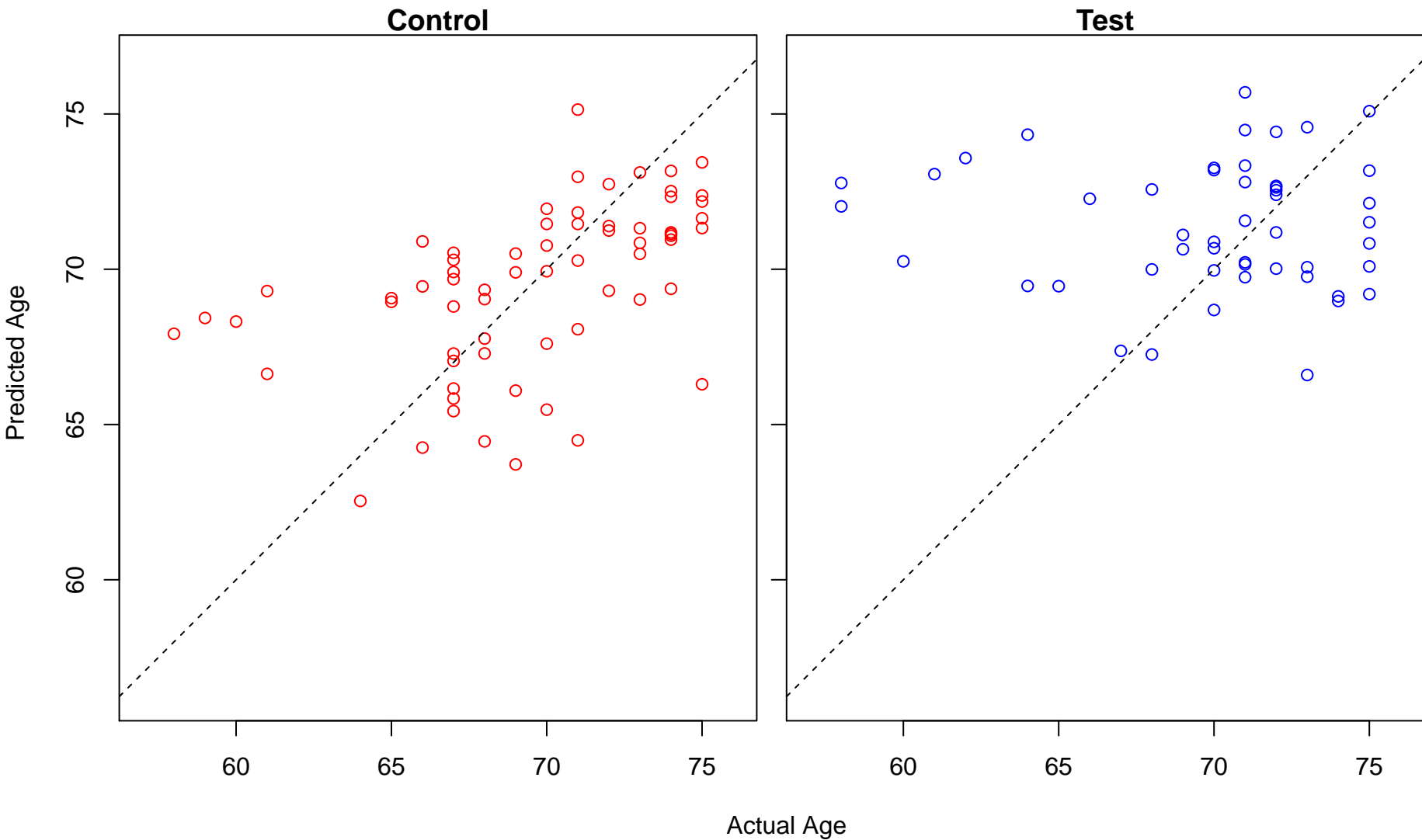
regulation of nitric-oxide synthase biosynthetic process (Score: 0.874633)



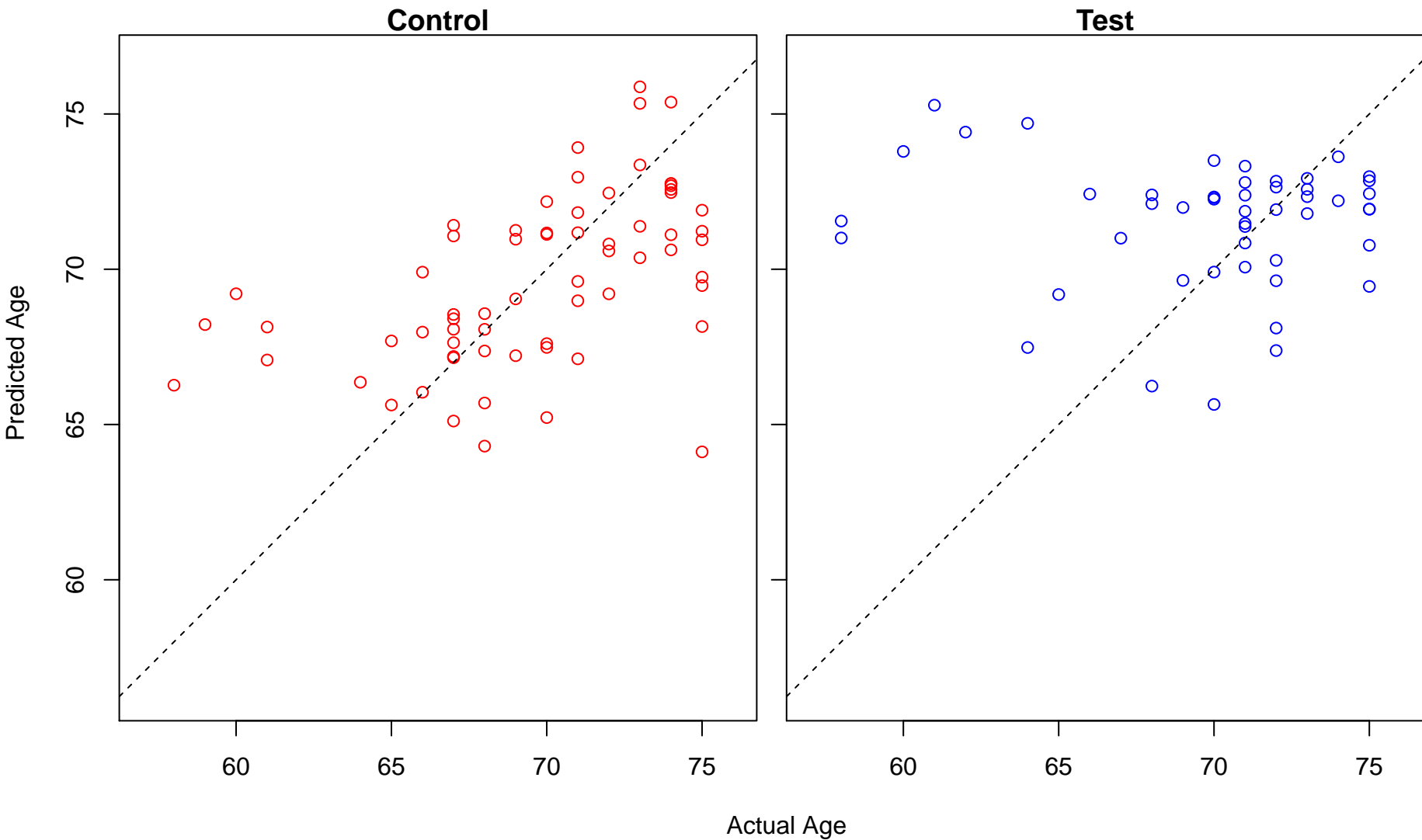
renal absorption (Score: 0.874220)



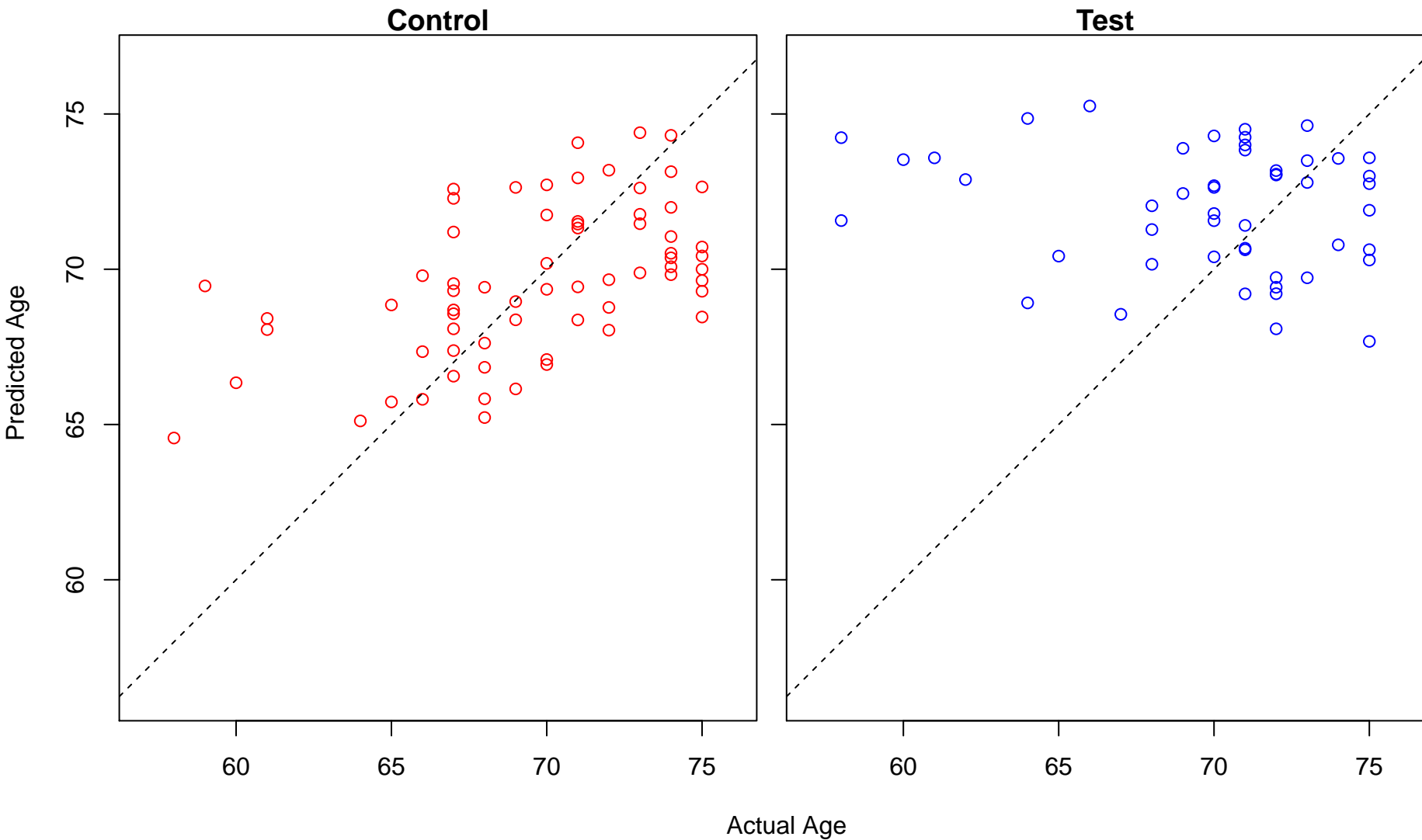
leukotriene metabolic process (Score: 0.872326)



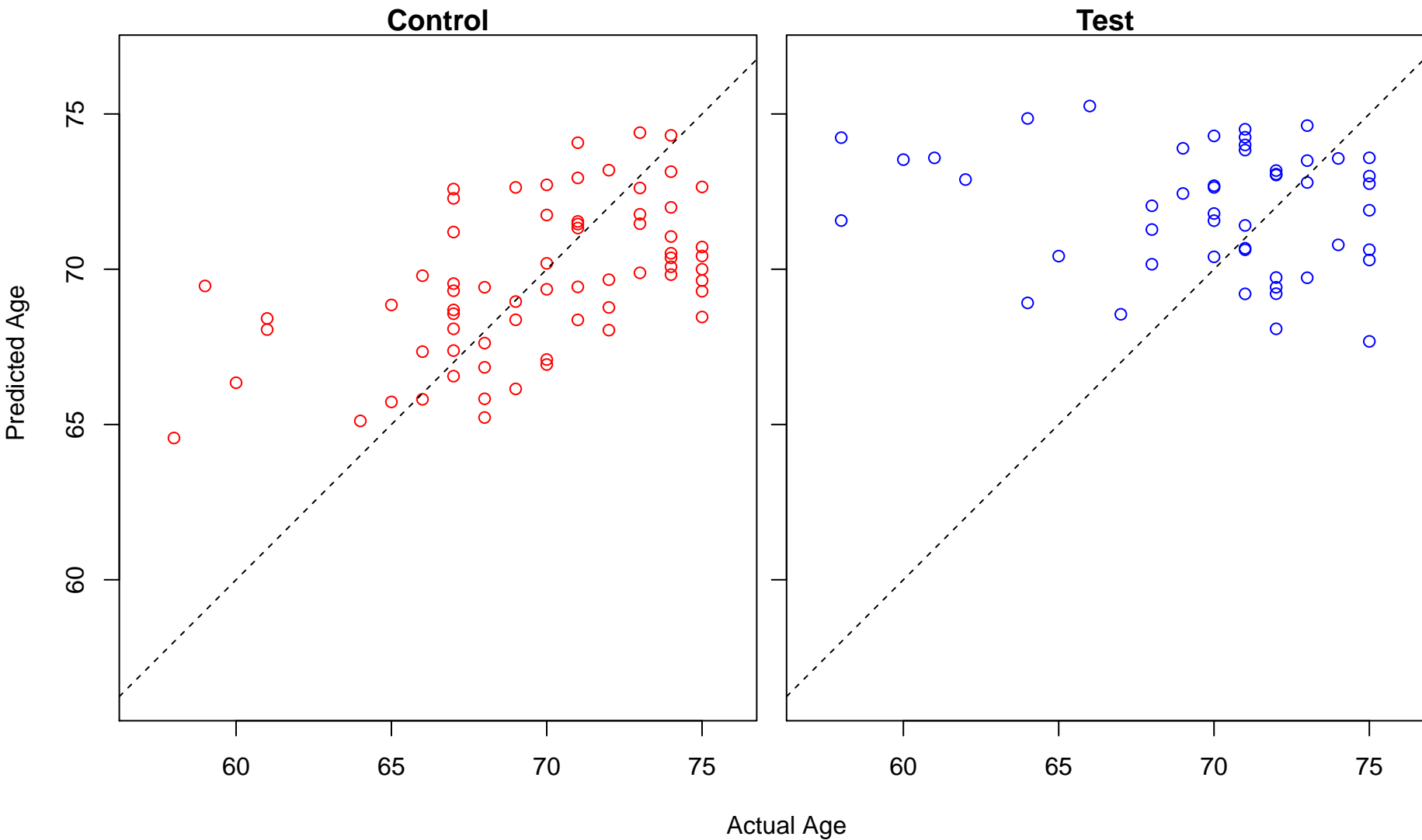
regulation of lipid transport (Score: 0.872205)



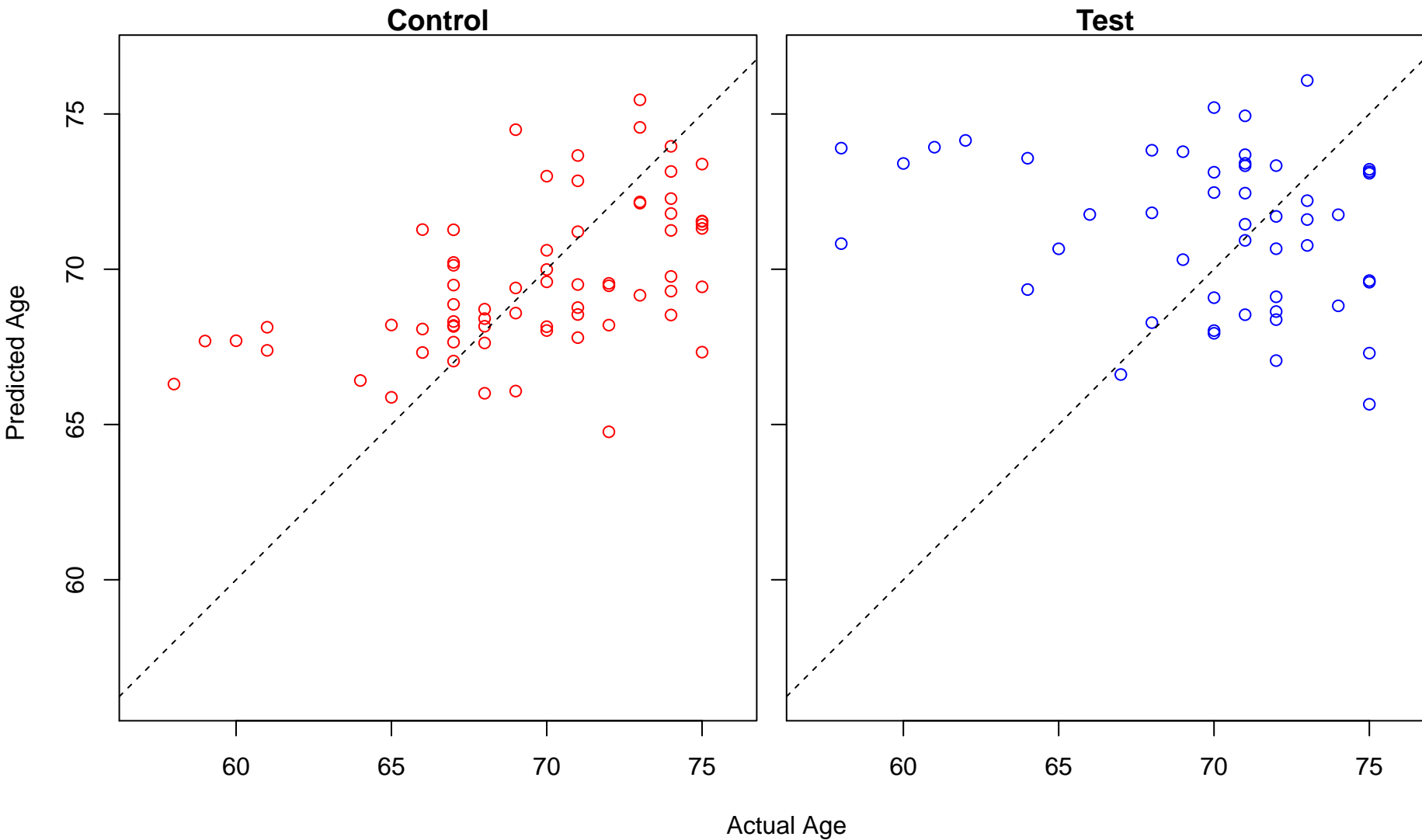
positive regulation of cardiac muscle tissue growth (Score: 0.871582)



positive regulation of cardiac muscle cell proliferation (Score: 0.871582)

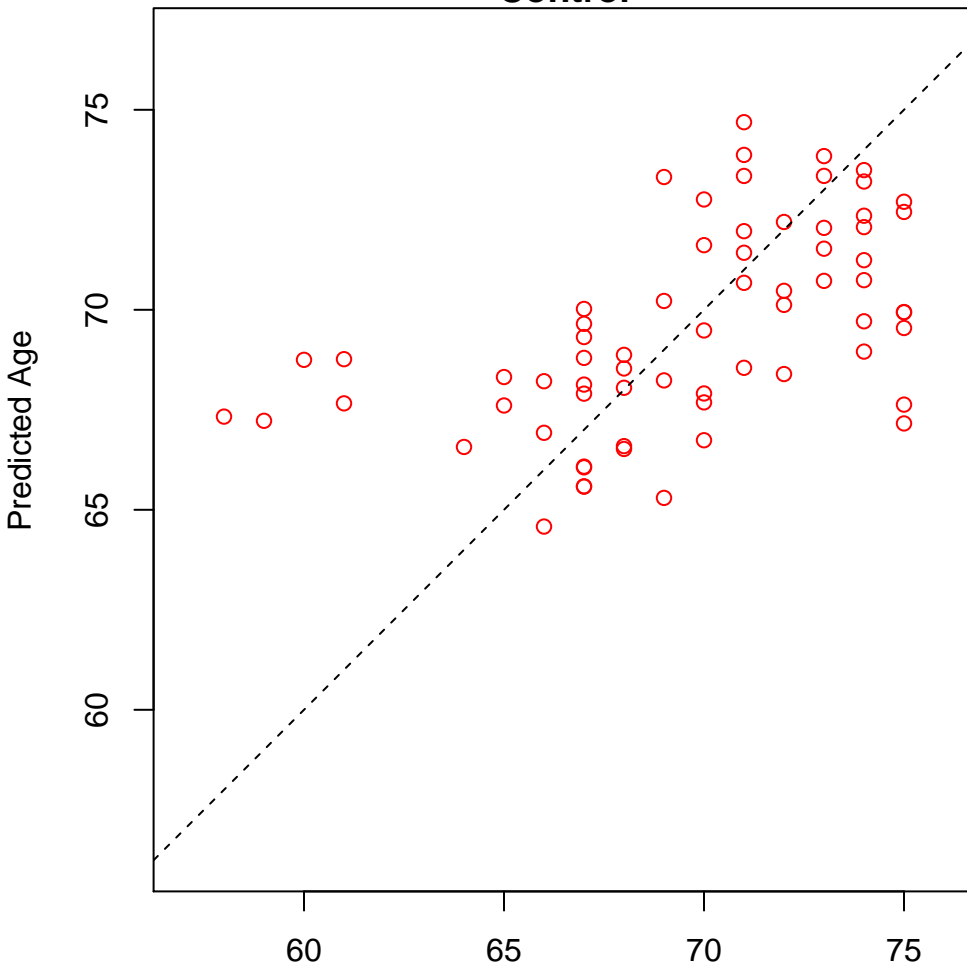


ATP synthesis coupled electron transport (Score: 0.871516)

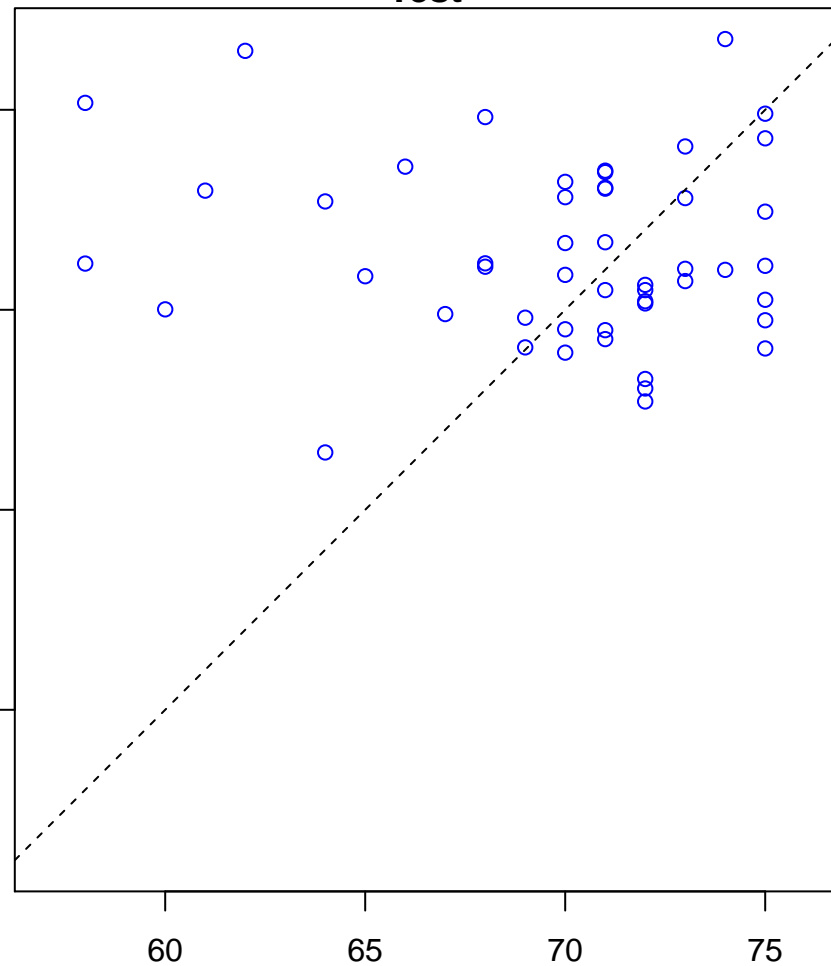


hydrogen peroxide catabolic process (Score: 0.871151)

Control

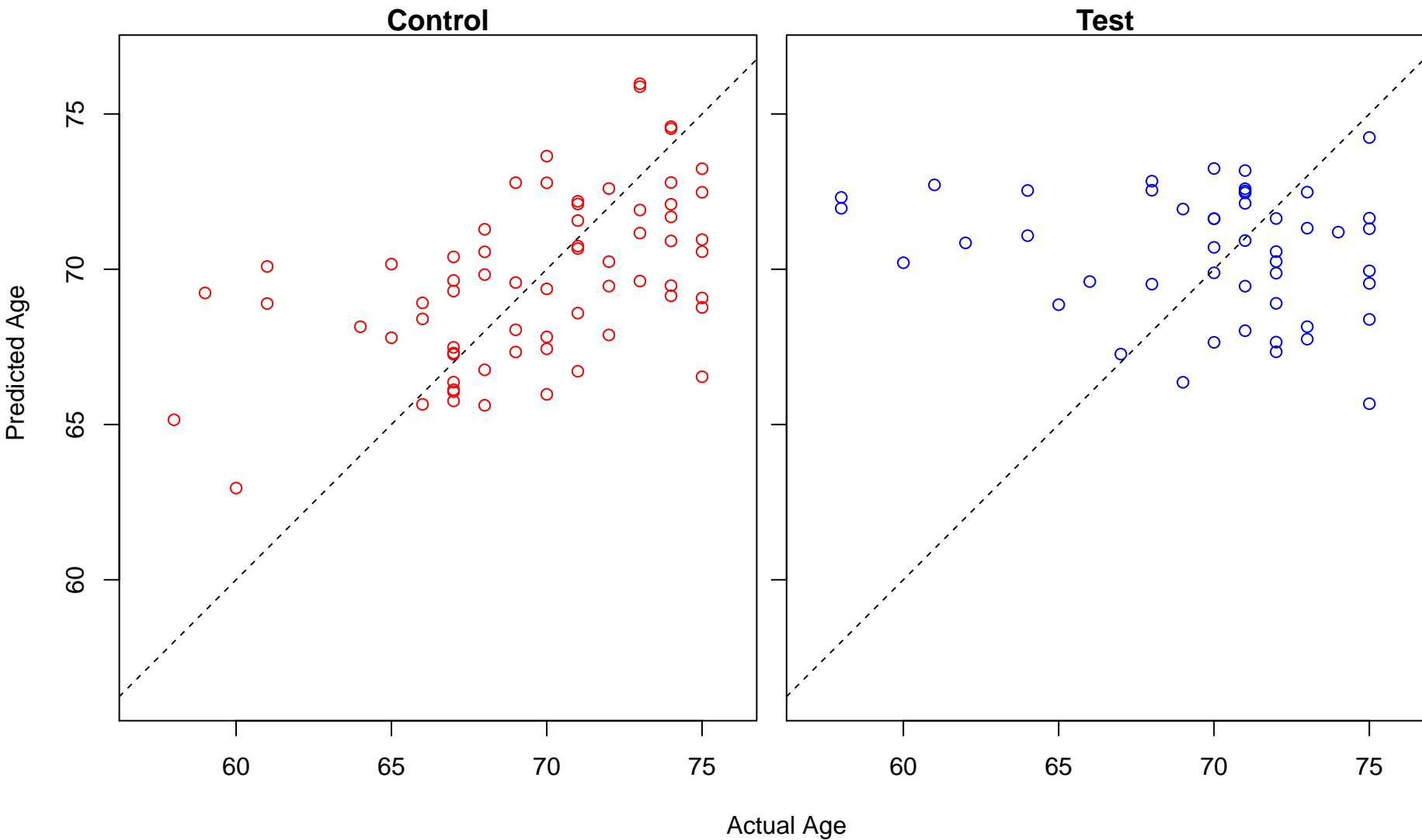


Test



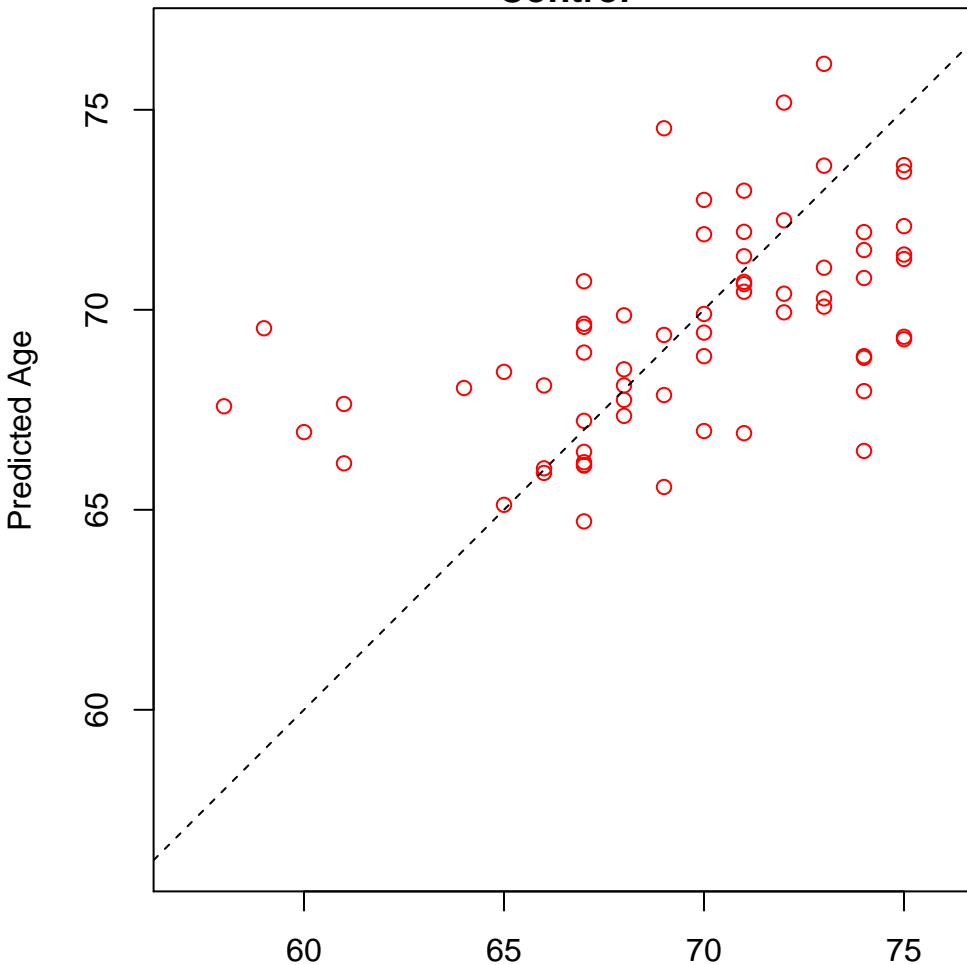
Actual Age

regulation of antigen processing and presentation (Score: 0.870882)

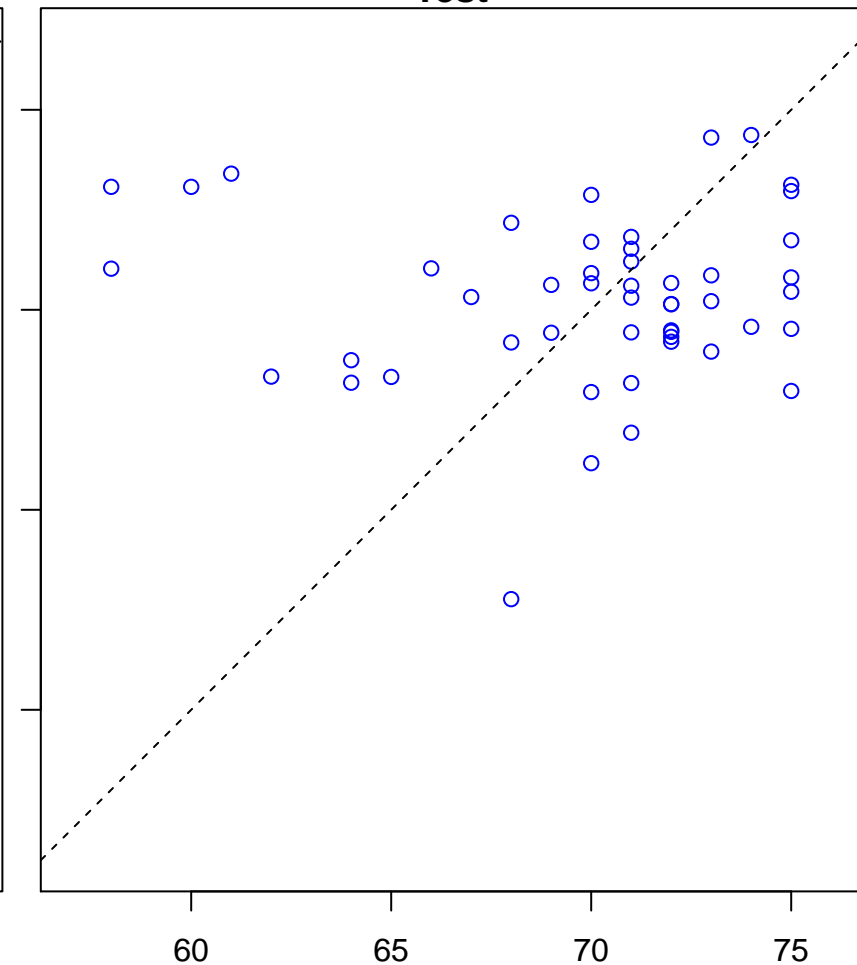


presynaptic membrane organization (Score: 0.870611)

Control

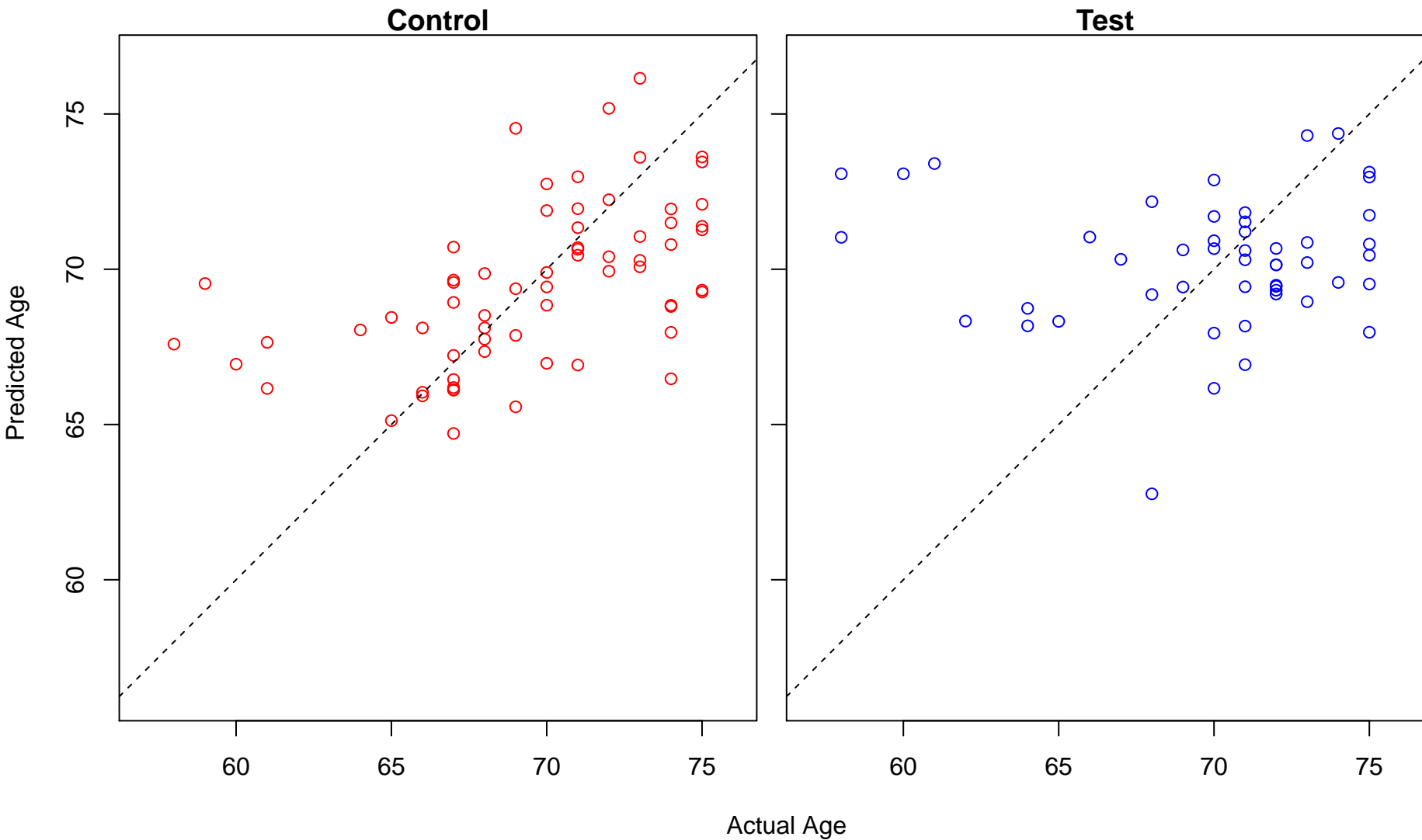


Test

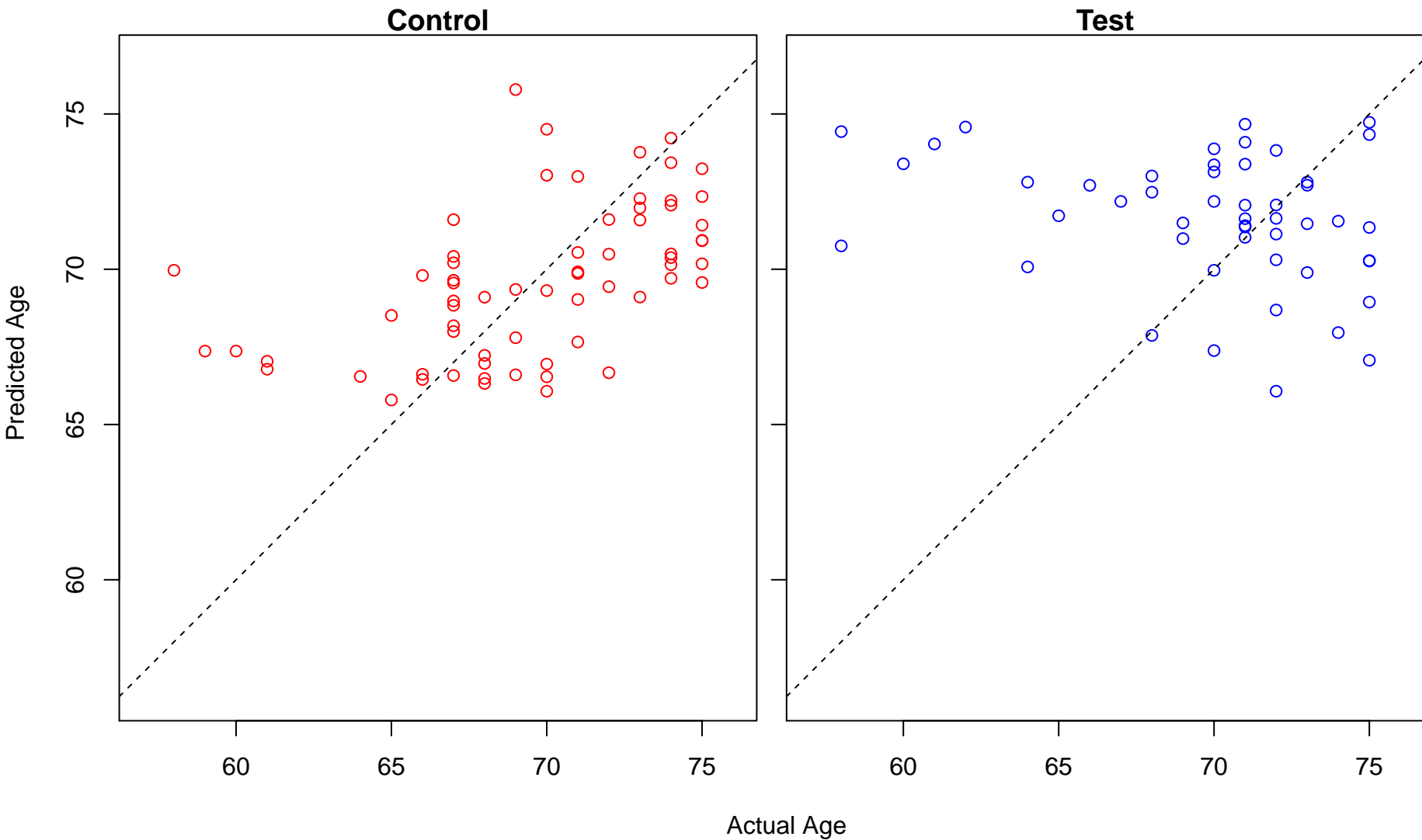


Actual Age

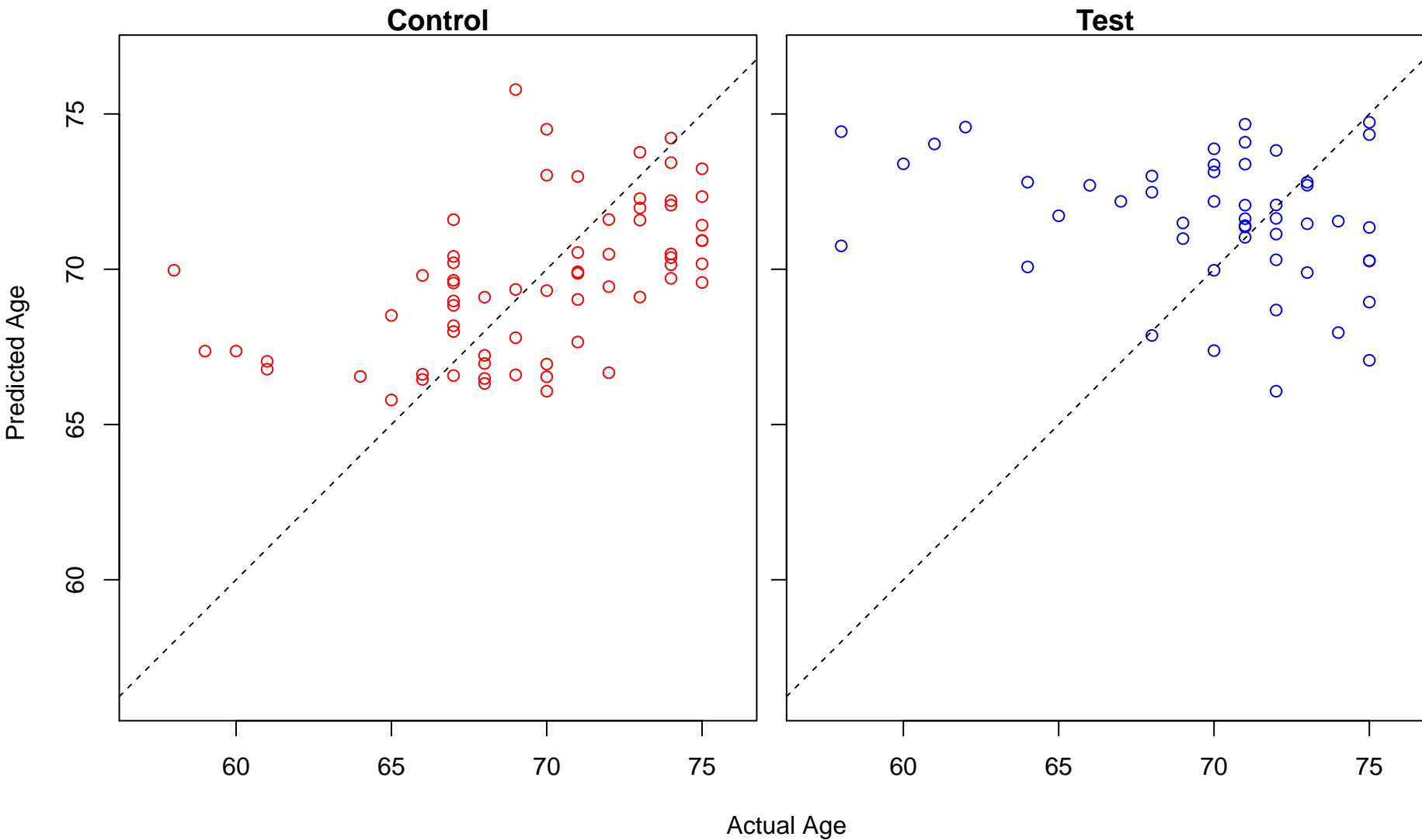
presynaptic membrane assembly (Score: 0.870611)



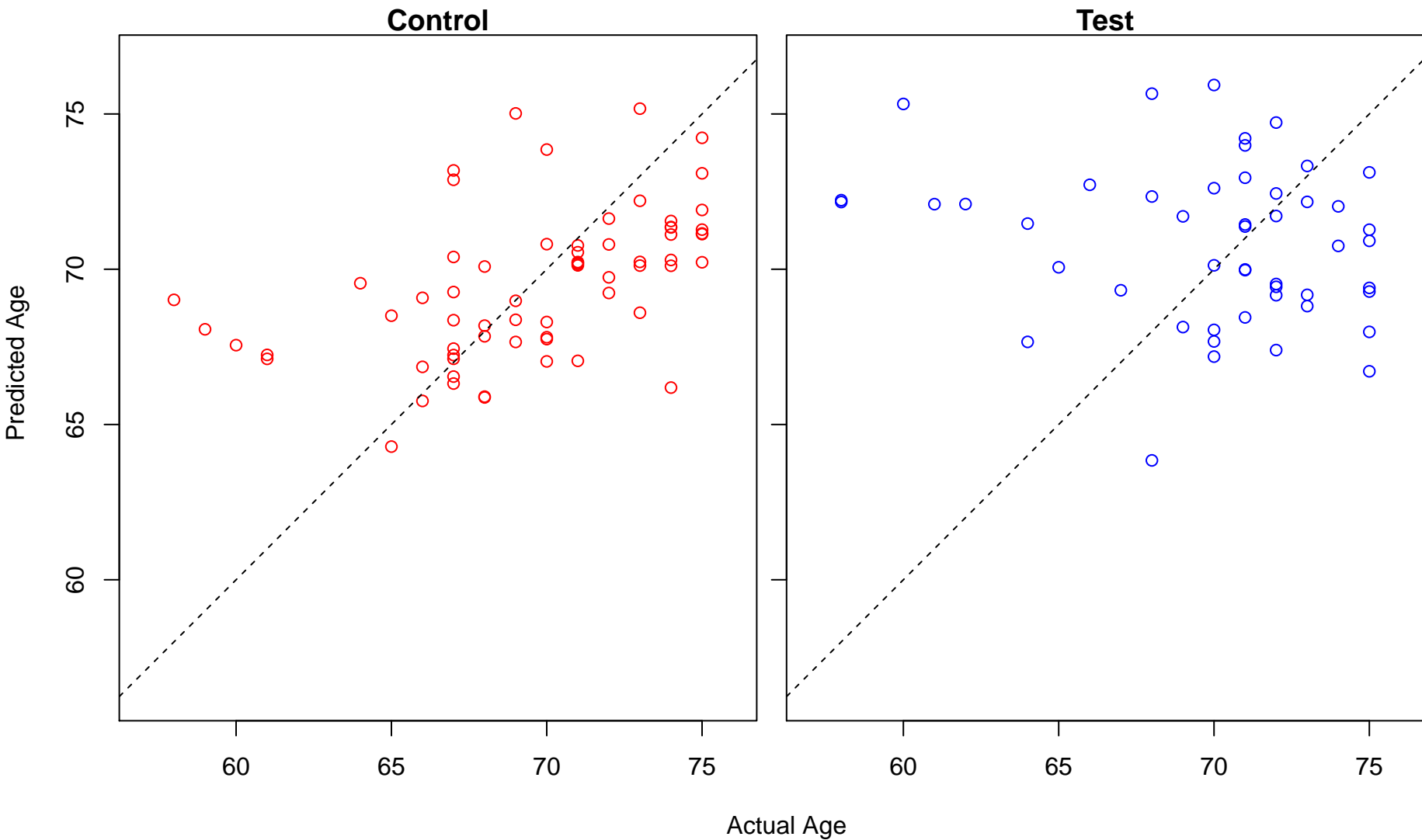
autophagosome maturation (Score: 0.870415)



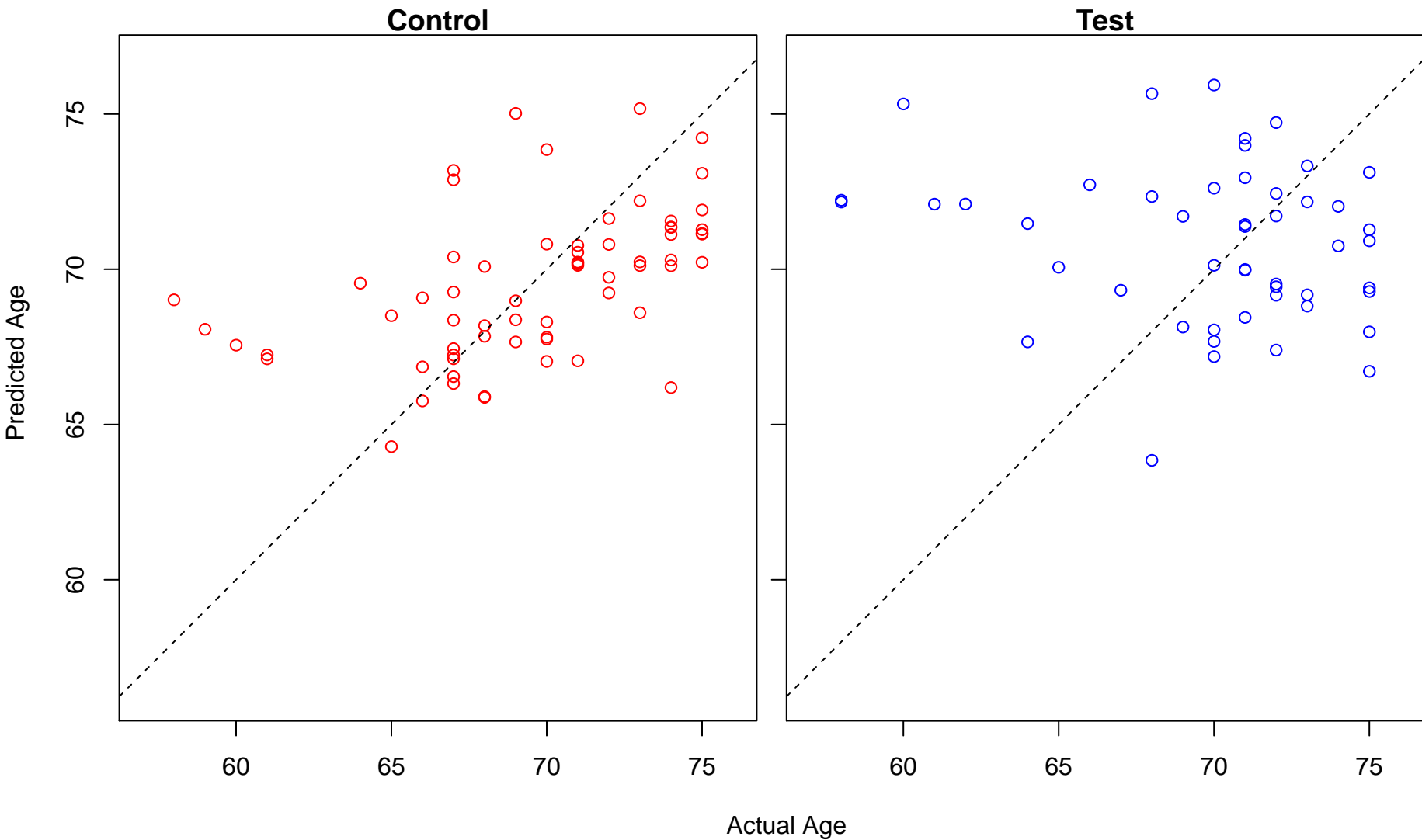
vacuole fusion (Score: 0.870415)



pH elevation (Score: 0.870216)

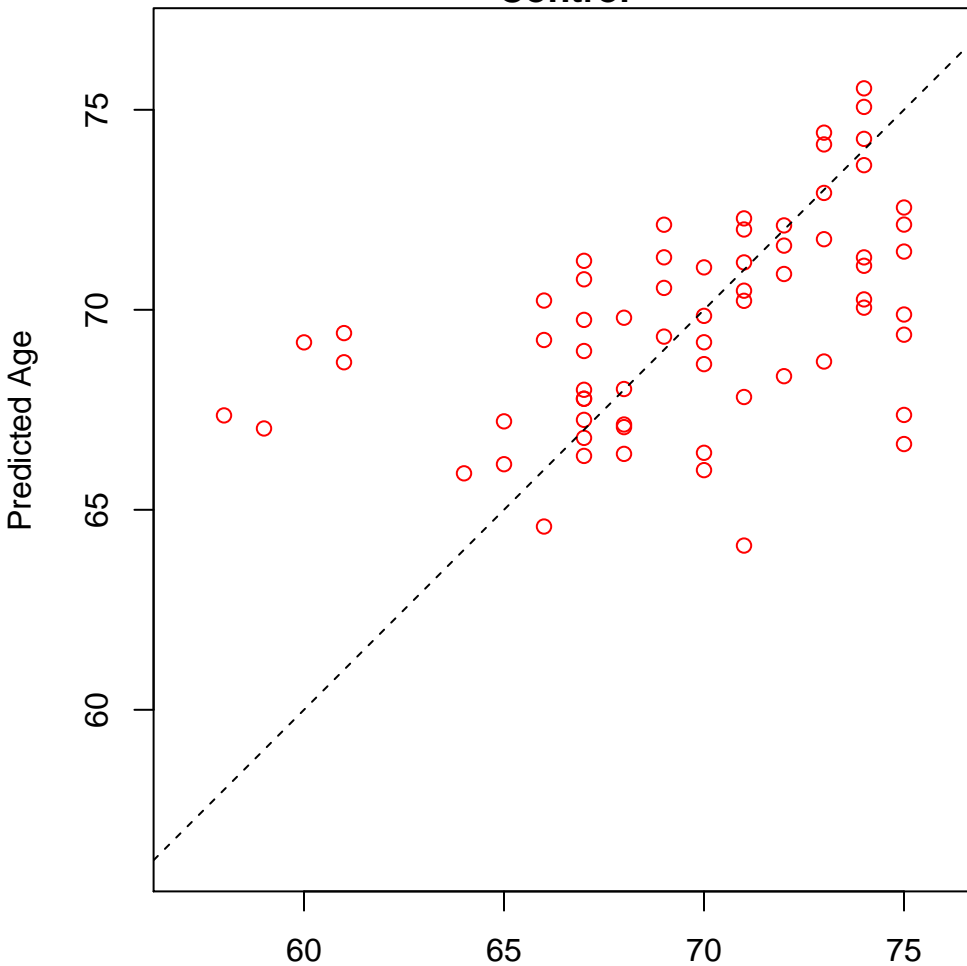


intracellular pH elevation (Score: 0.870216)

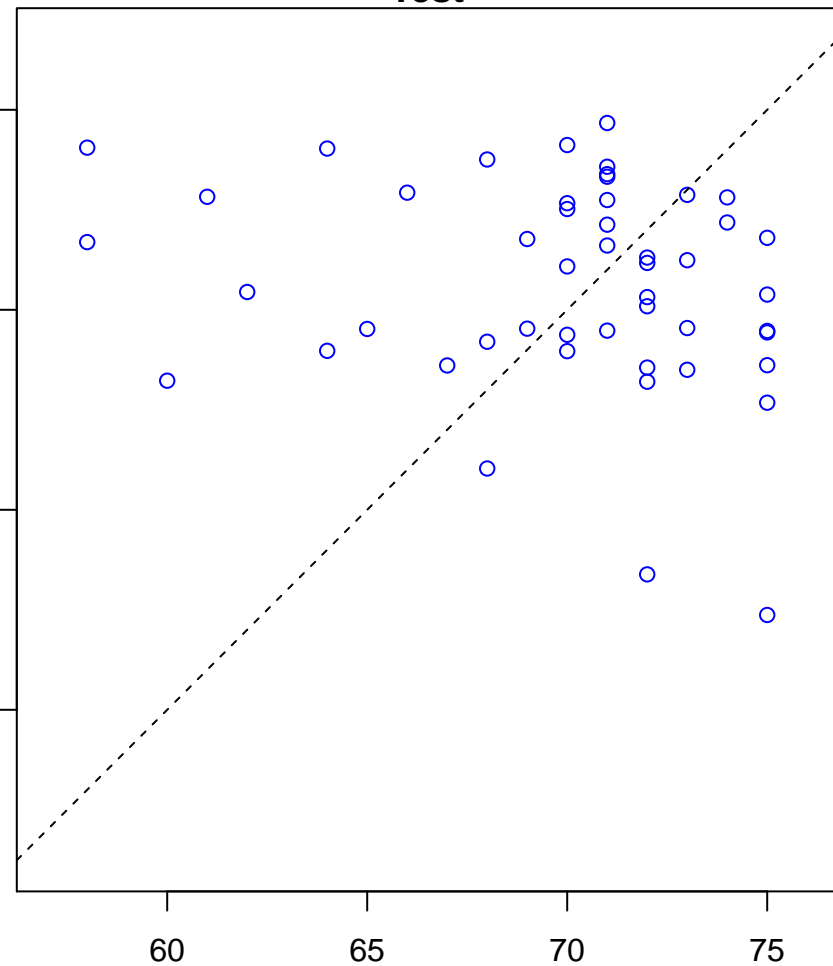


regulation of interleukin-13 production (Score: 0.869411)

Control

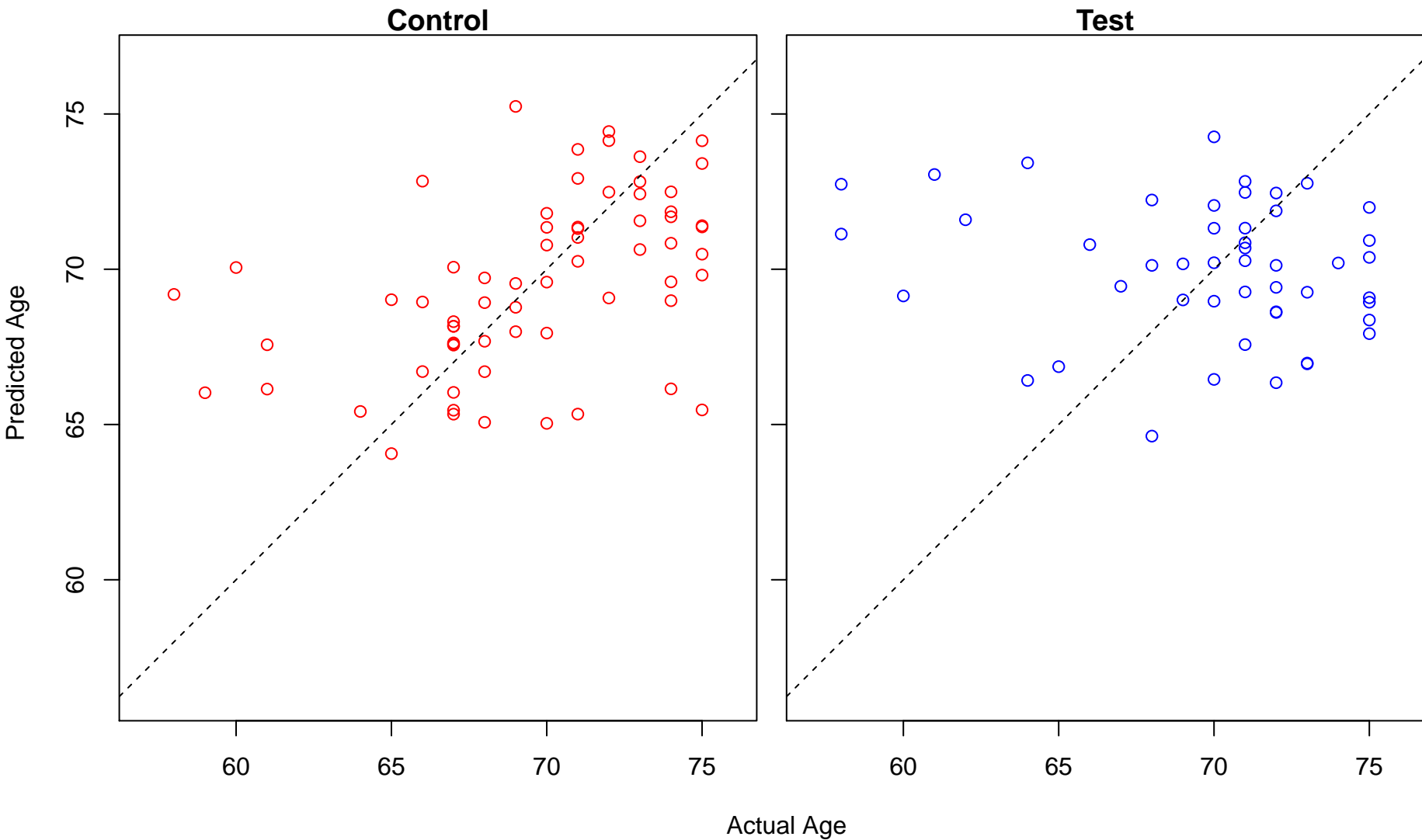


Test

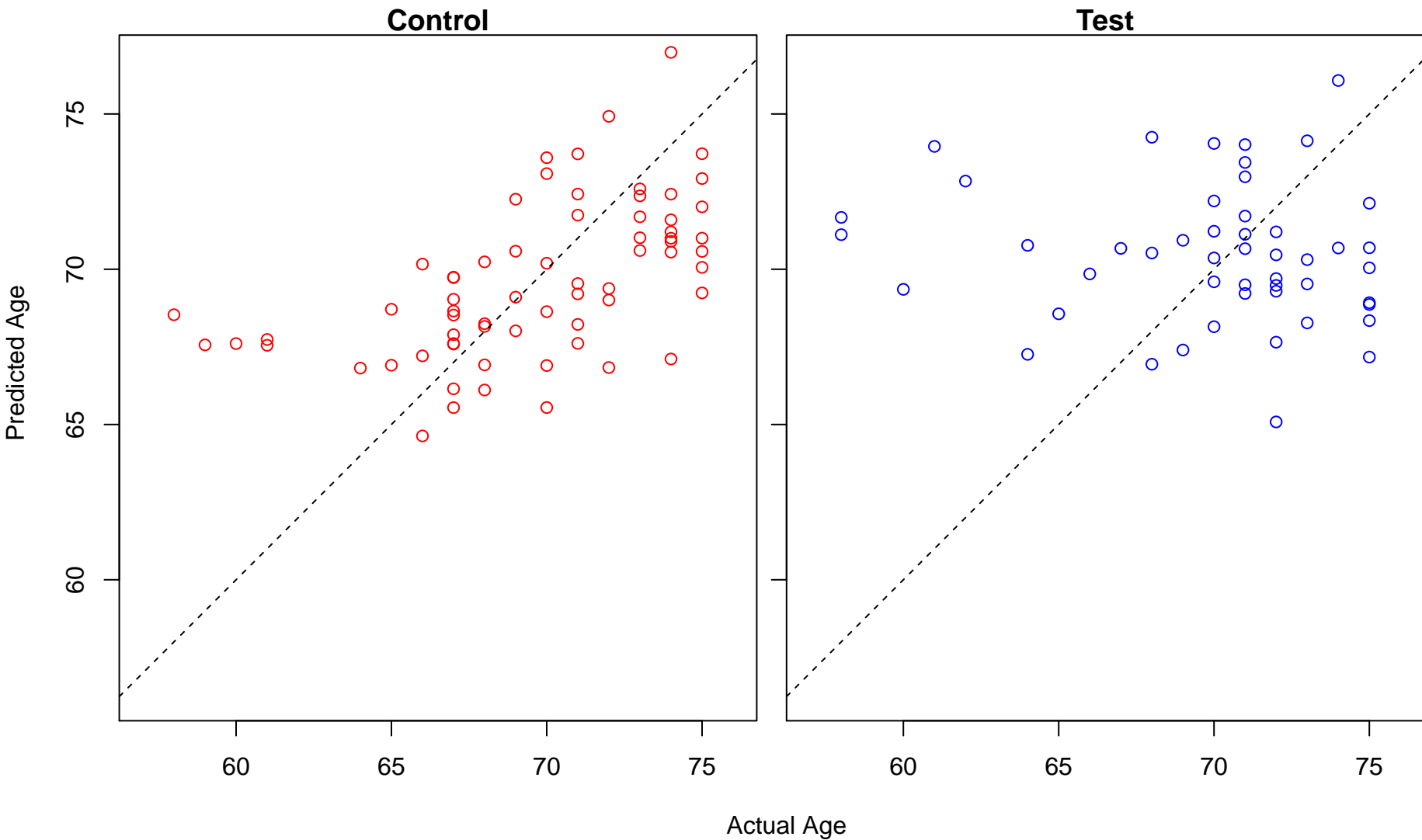


Actual Age

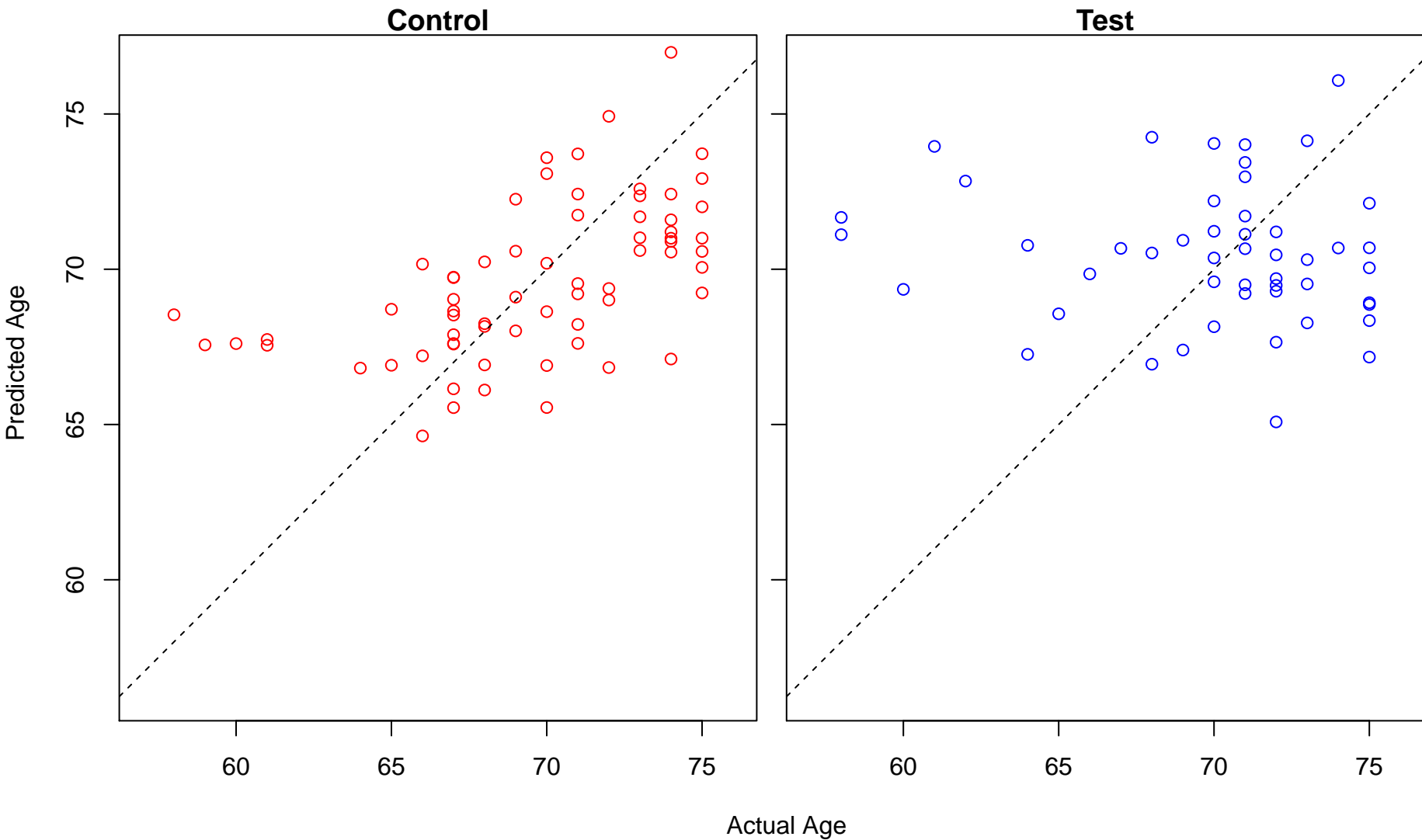
negative regulation of tumor necrosis factor superfamily cytokine production (Score: 0.868629)



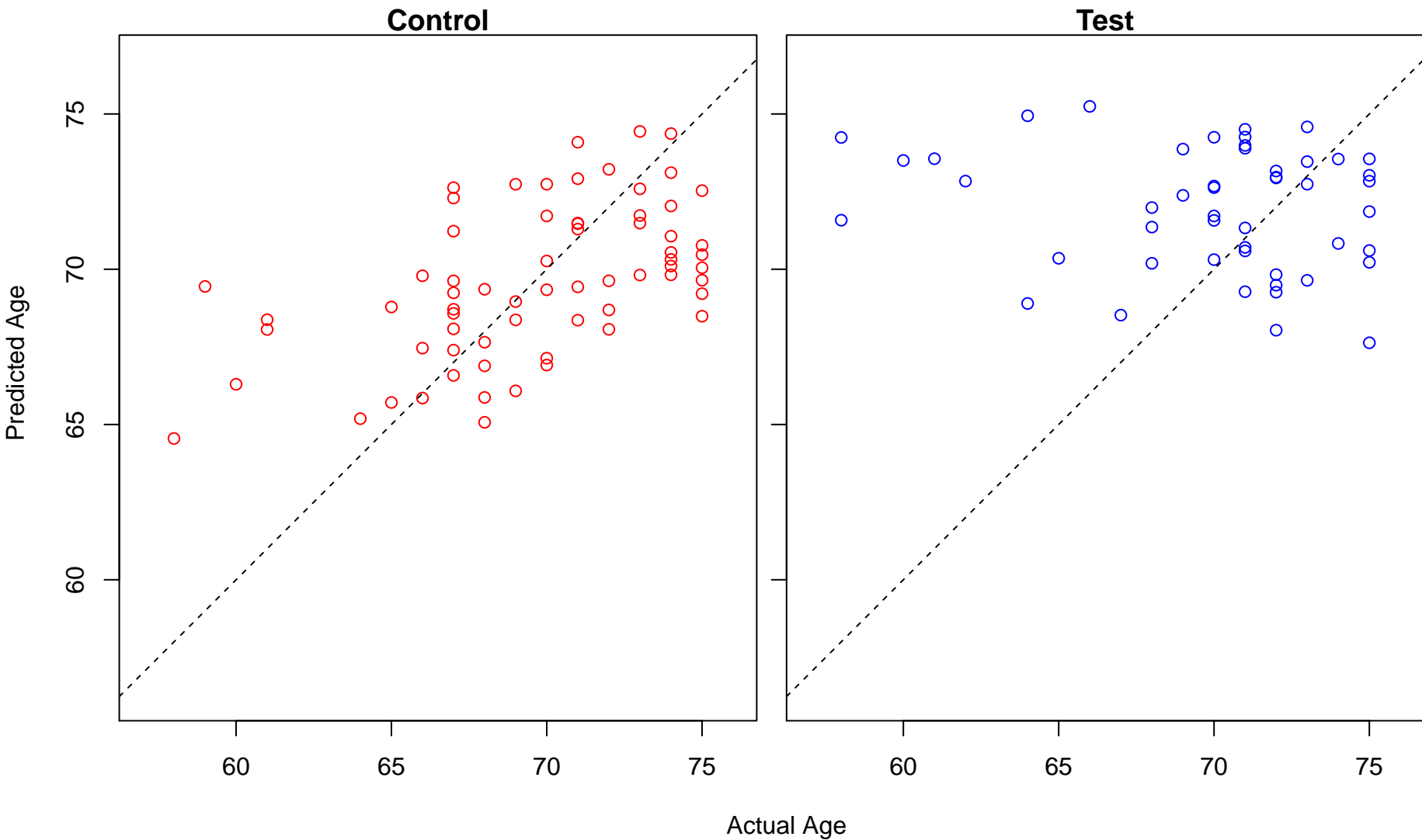
cytoplasmic translation (Score: 0.868578)



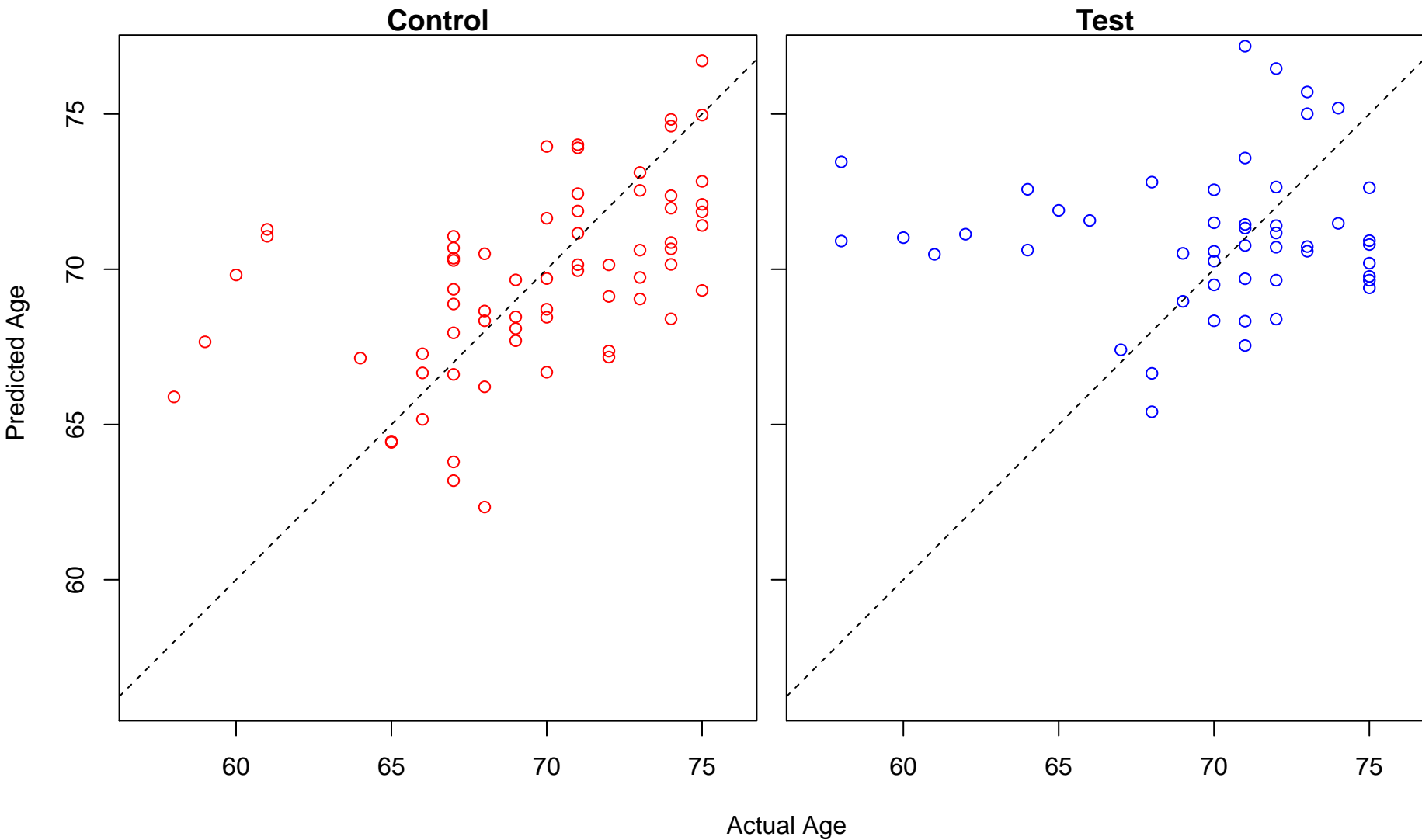
cytoplasmic translational initiation (Score: 0.868578)



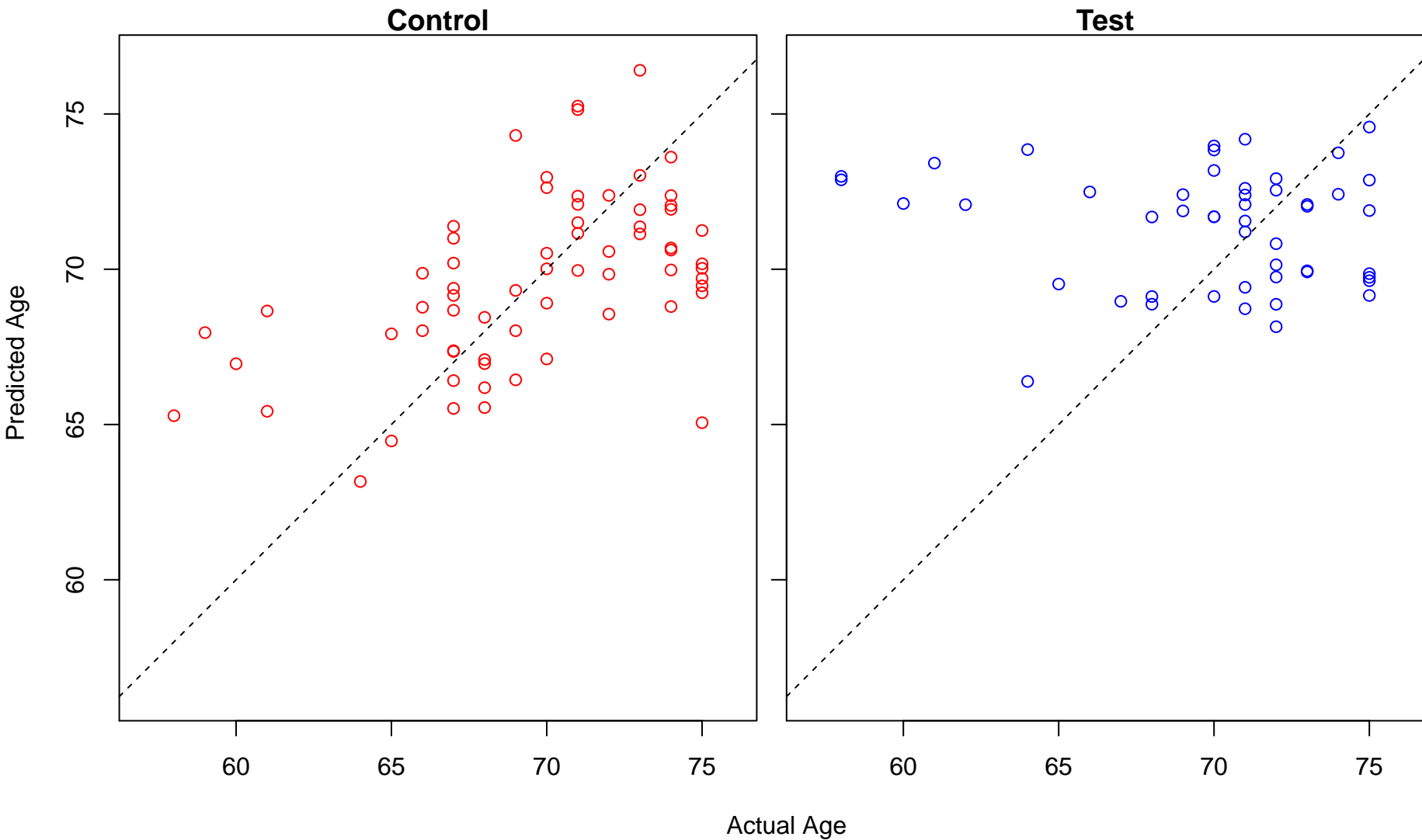
positive regulation of cardiac muscle tissue development (Score: 0.868448)



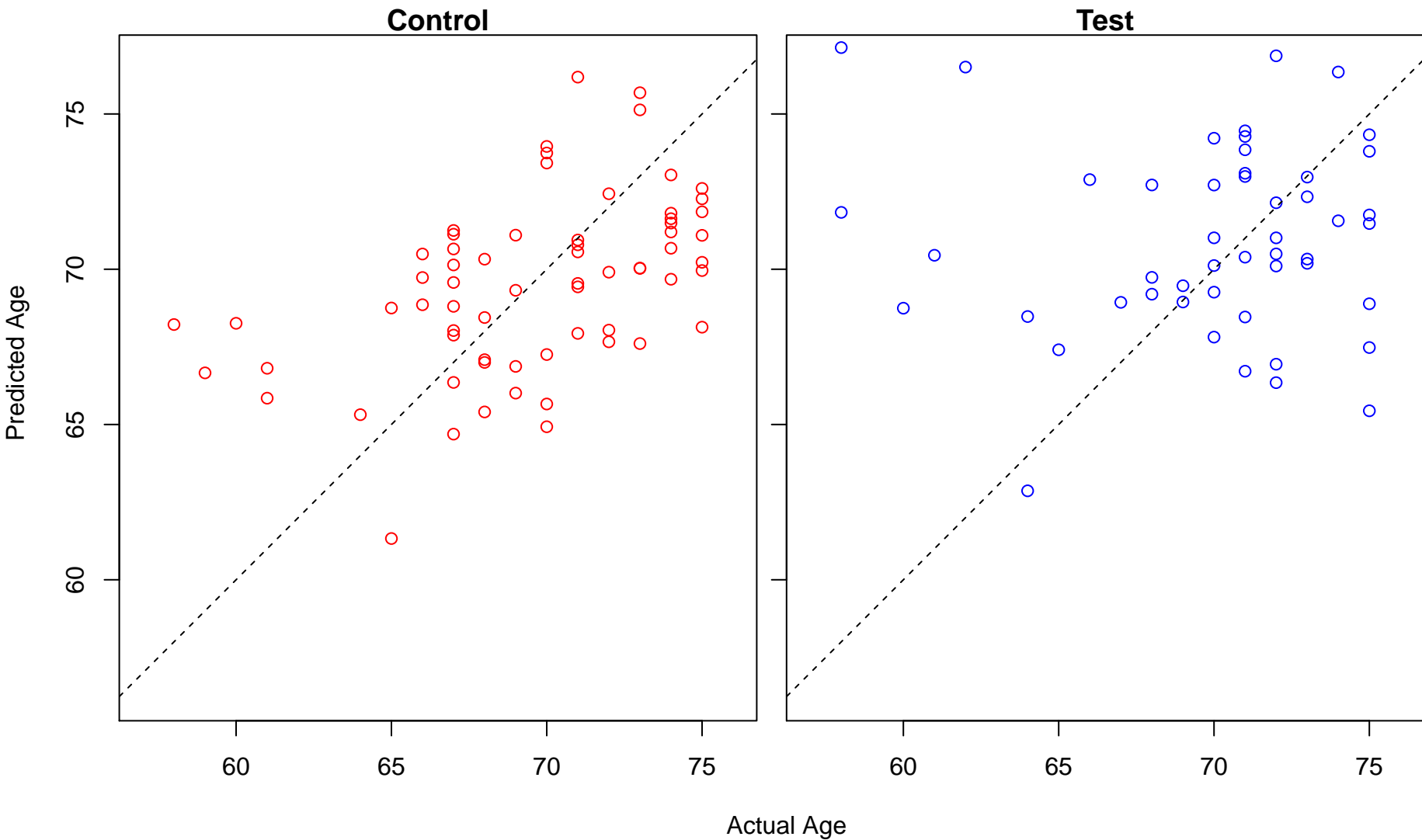
endoplasmic reticulum to cytosol transport (Score: 0.868368)



positive regulation of developmental growth (Score: 0.868120)

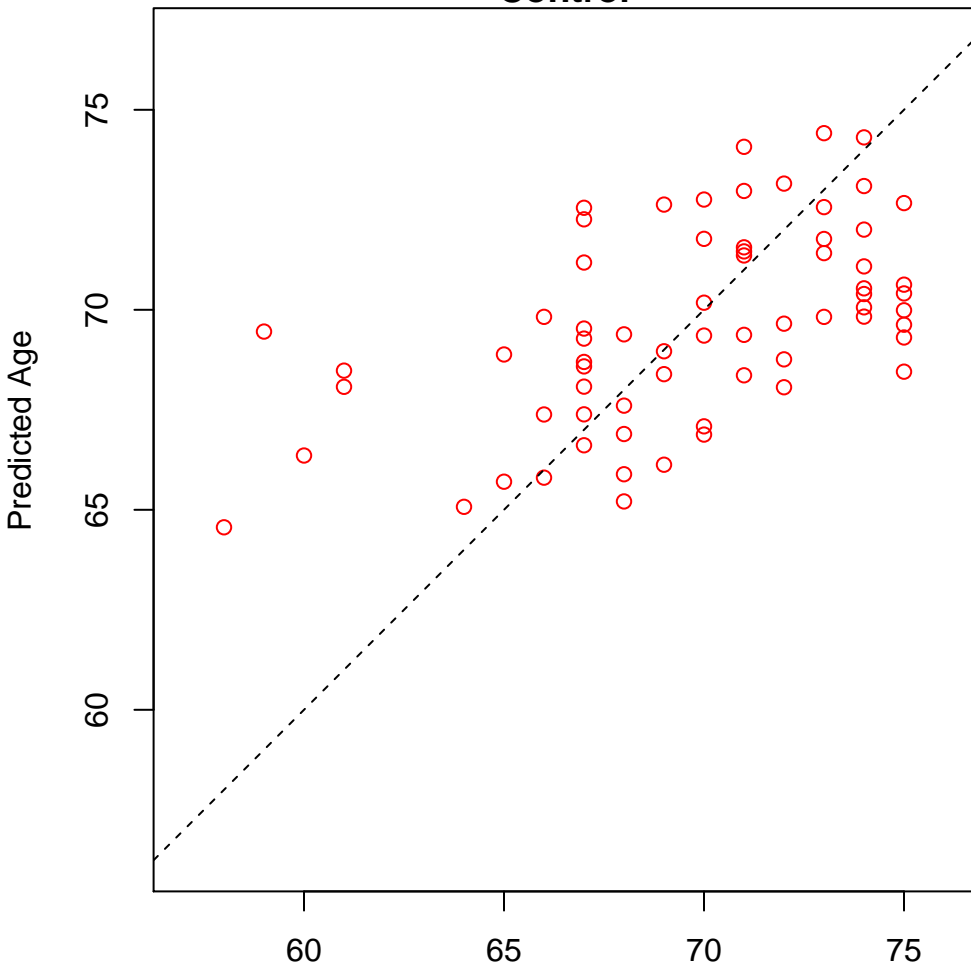


regulation of extent of cell growth (Score: 0.867805)

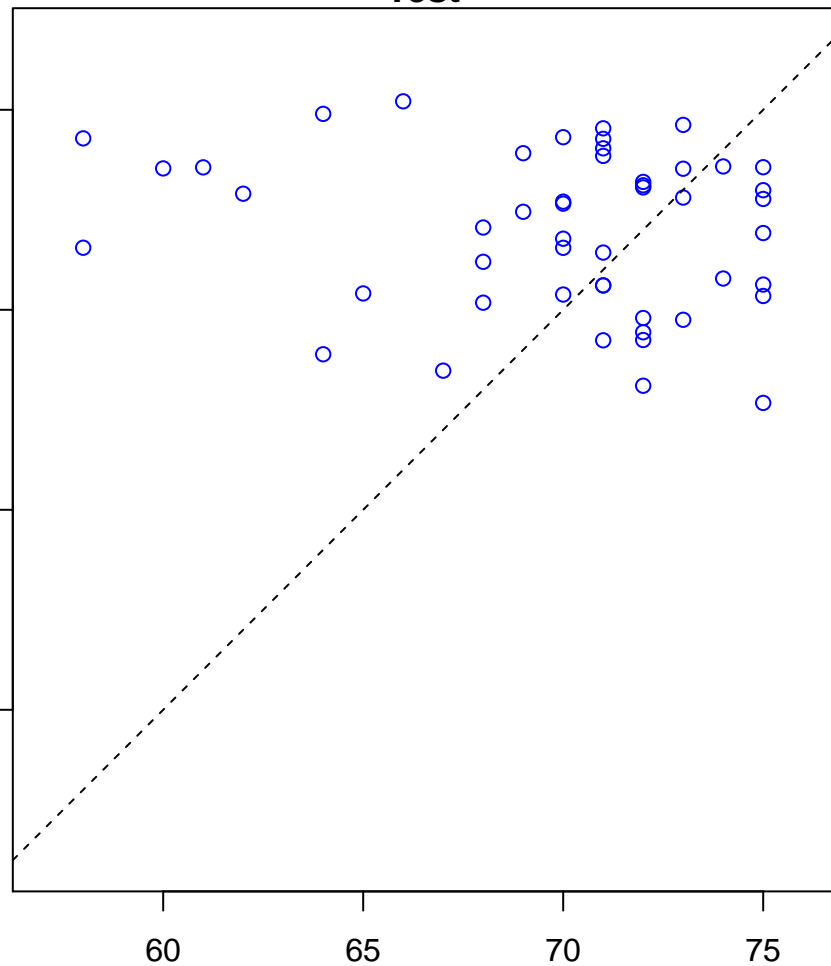


regulation of cardiac muscle tissue growth (Score: 0.866595)

Control

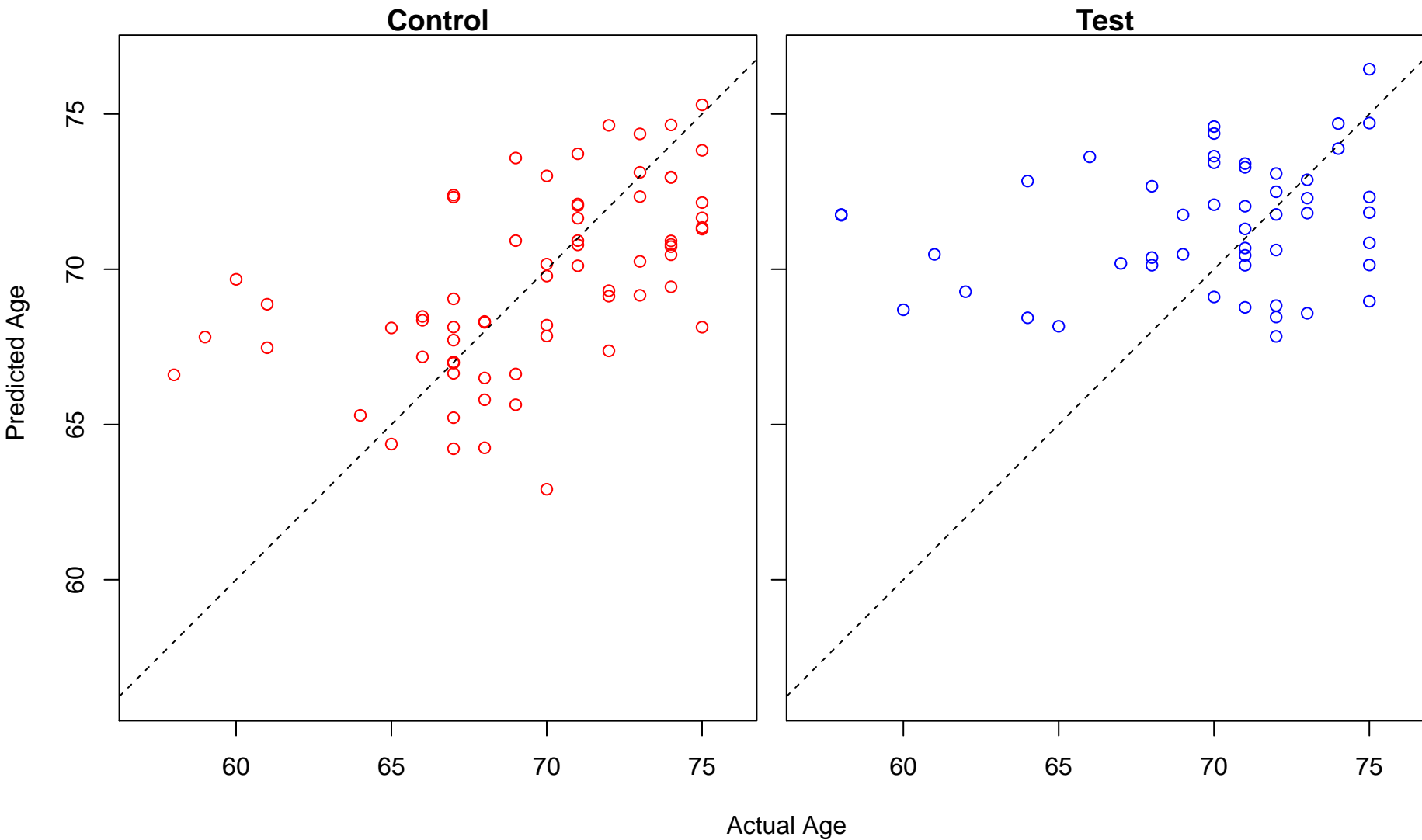


Test

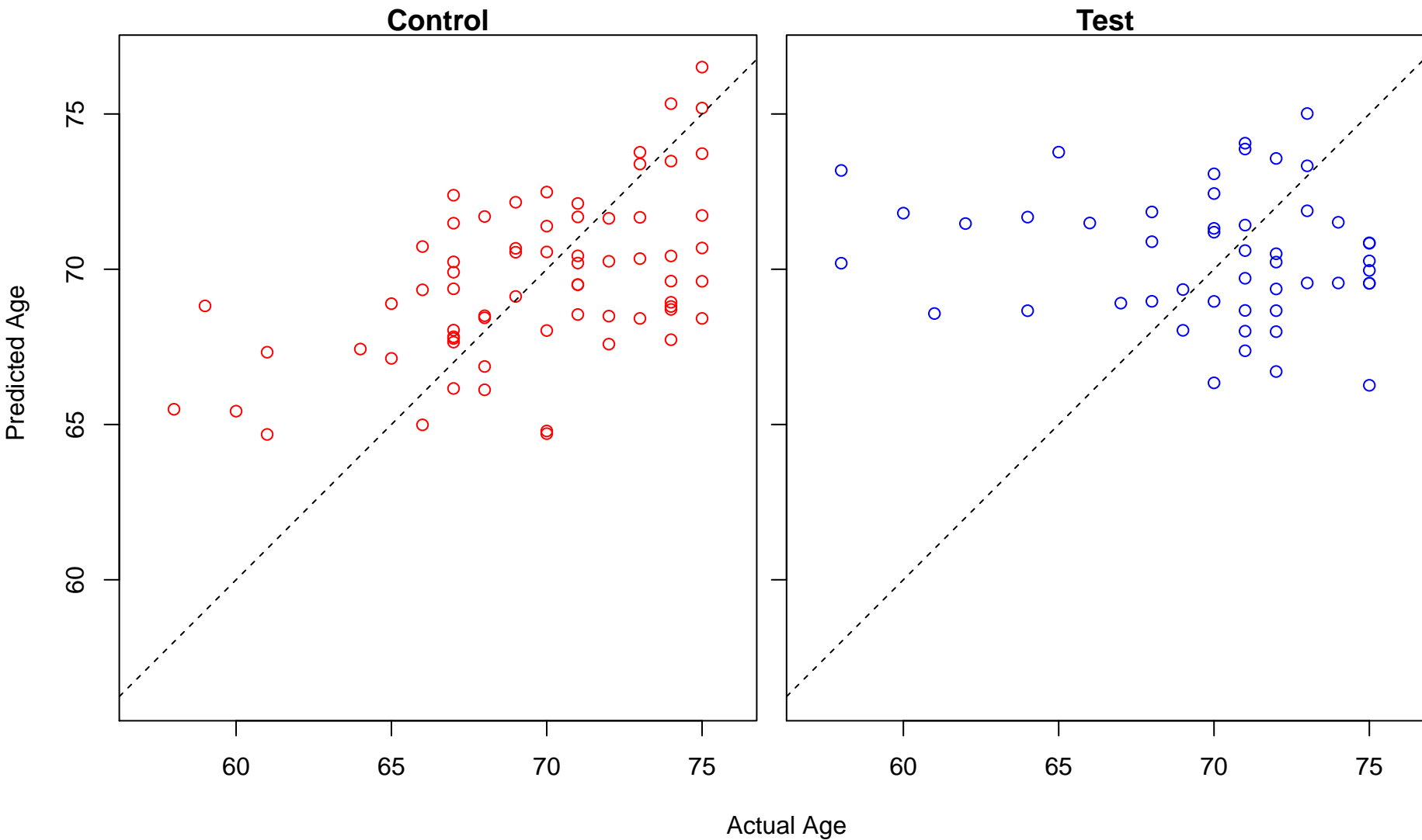


Actual Age

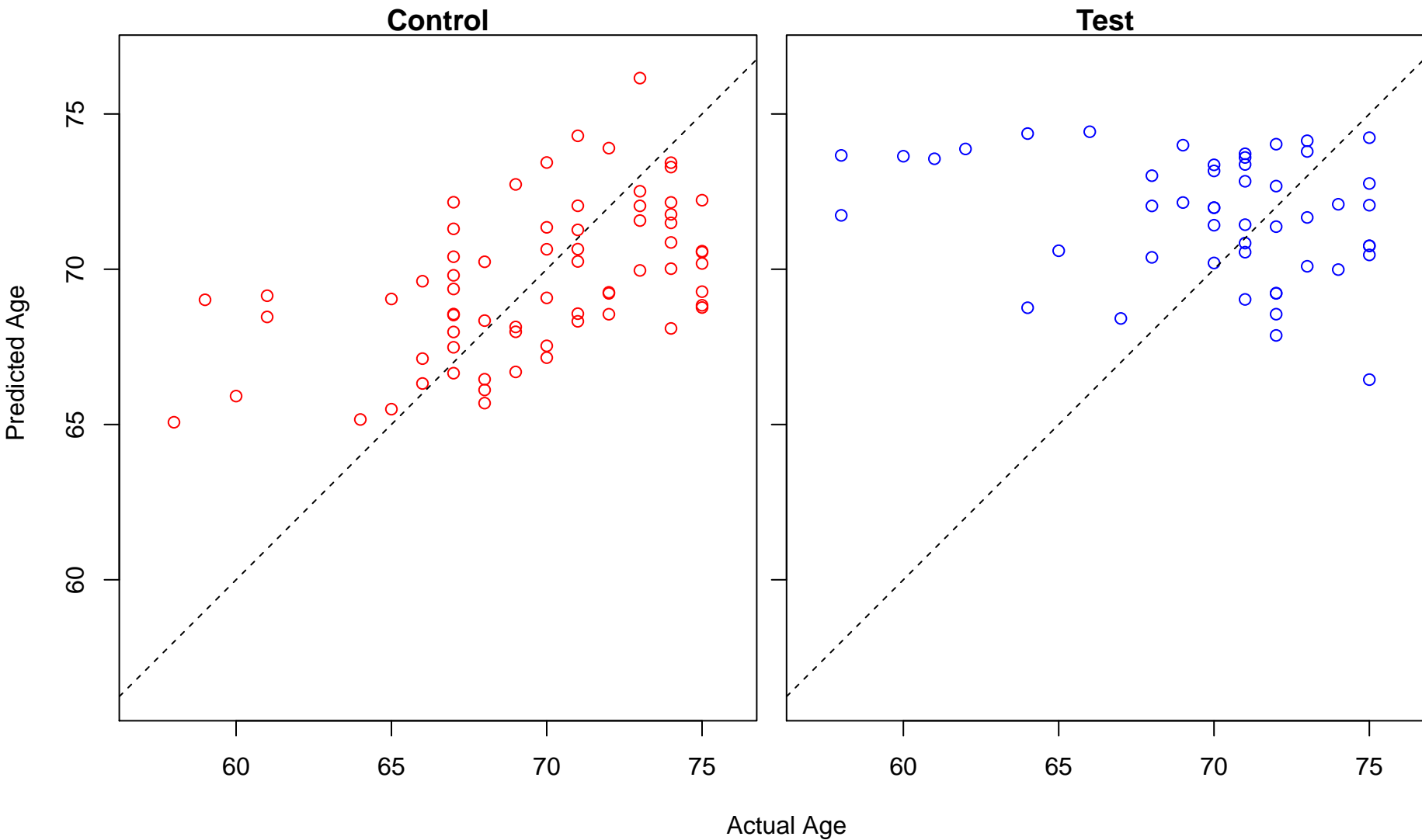
cartilage development (Score: 0.866358)



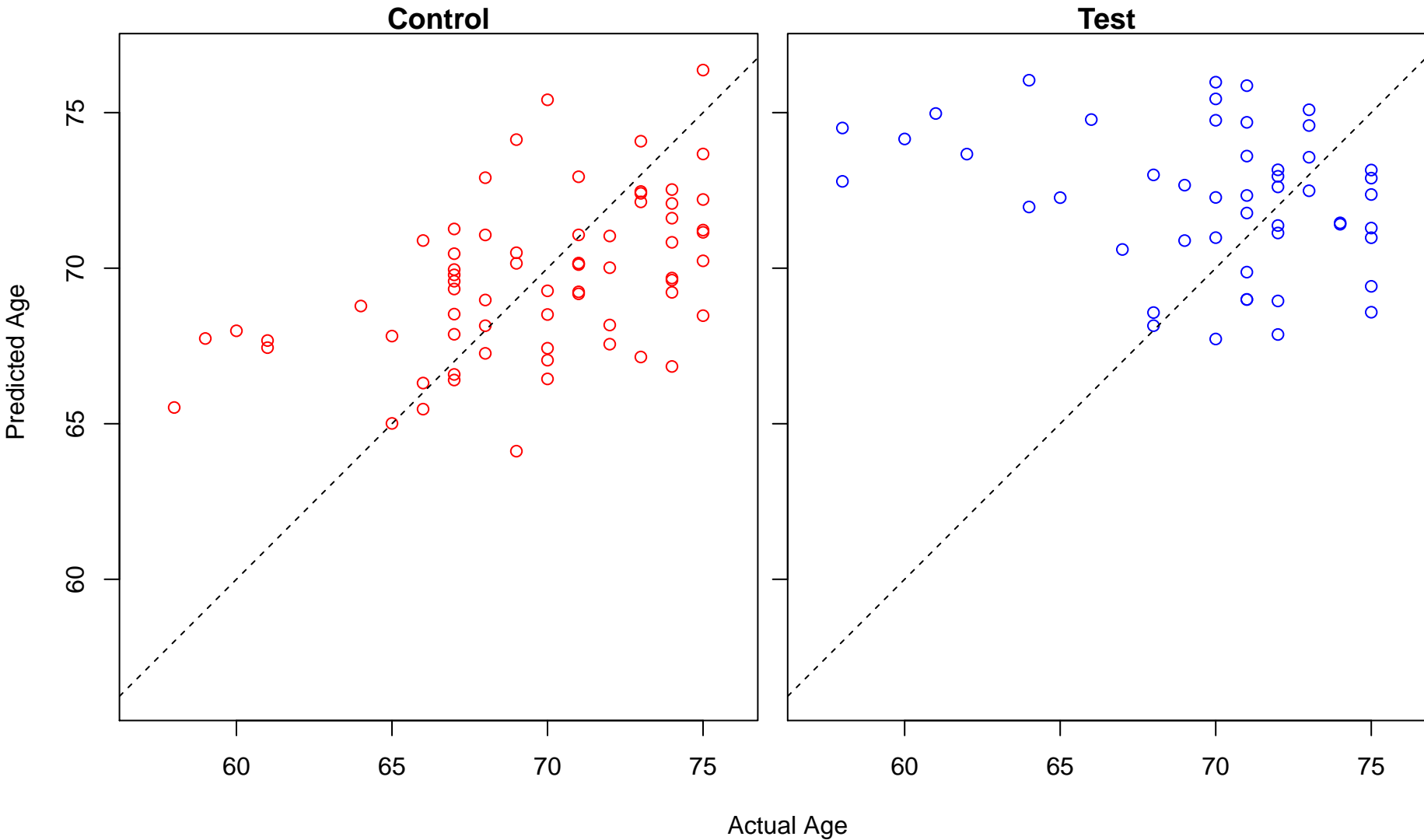
amyloid fibril formation (Score: 0.866297)



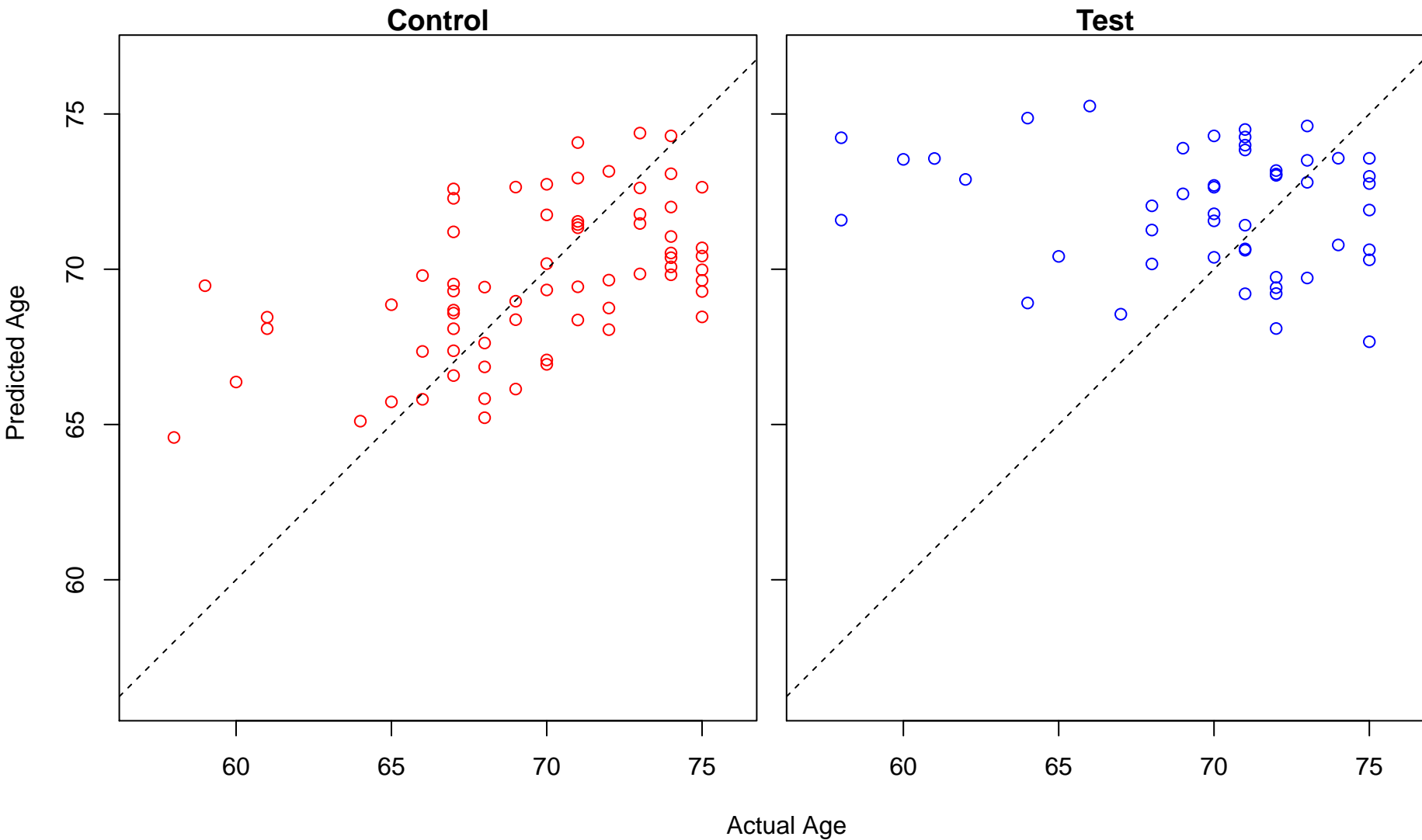
endocardial cushion development (Score: 0.866244)



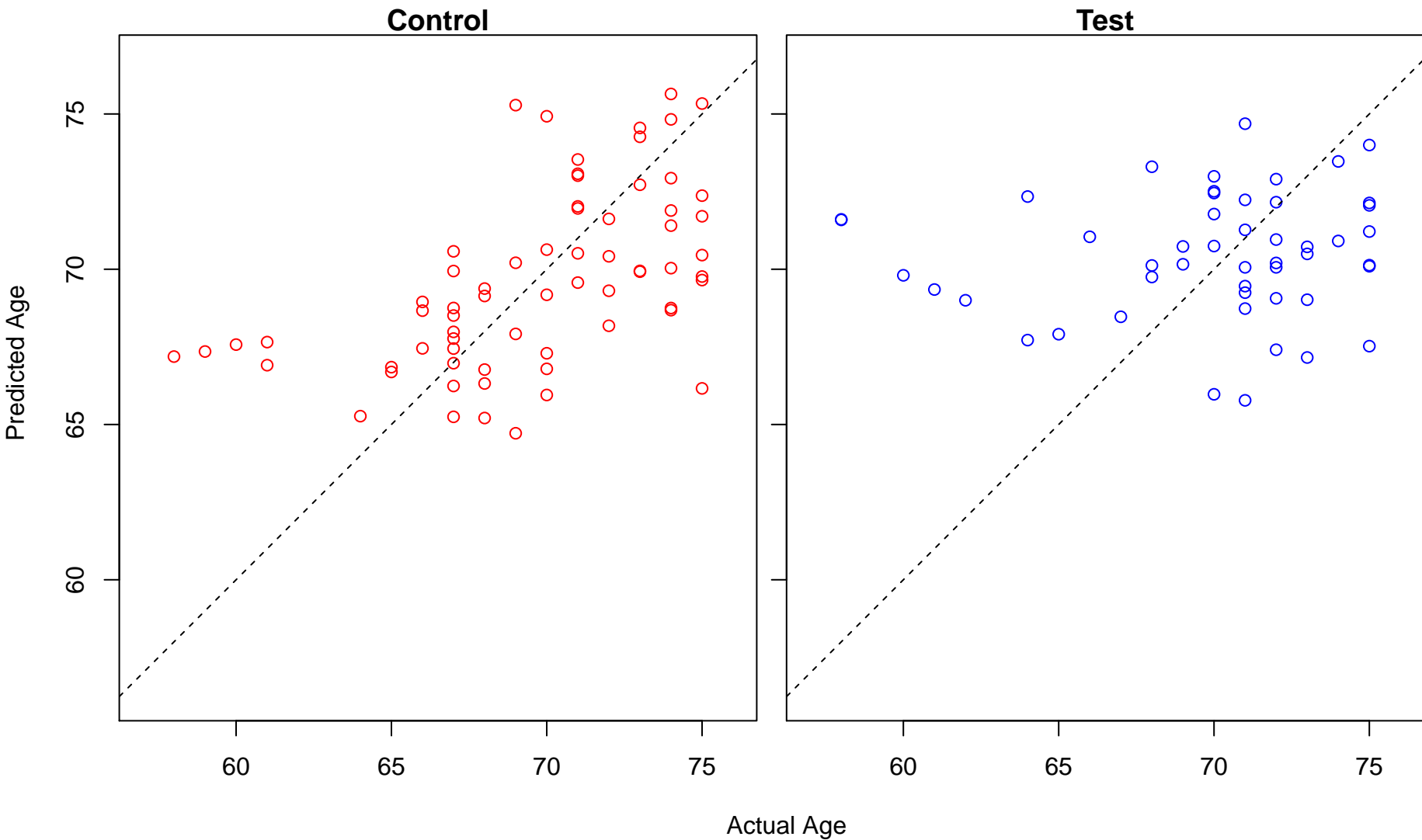
acetyl-CoA biosynthetic process from pyruvate (Score: 0.865893)



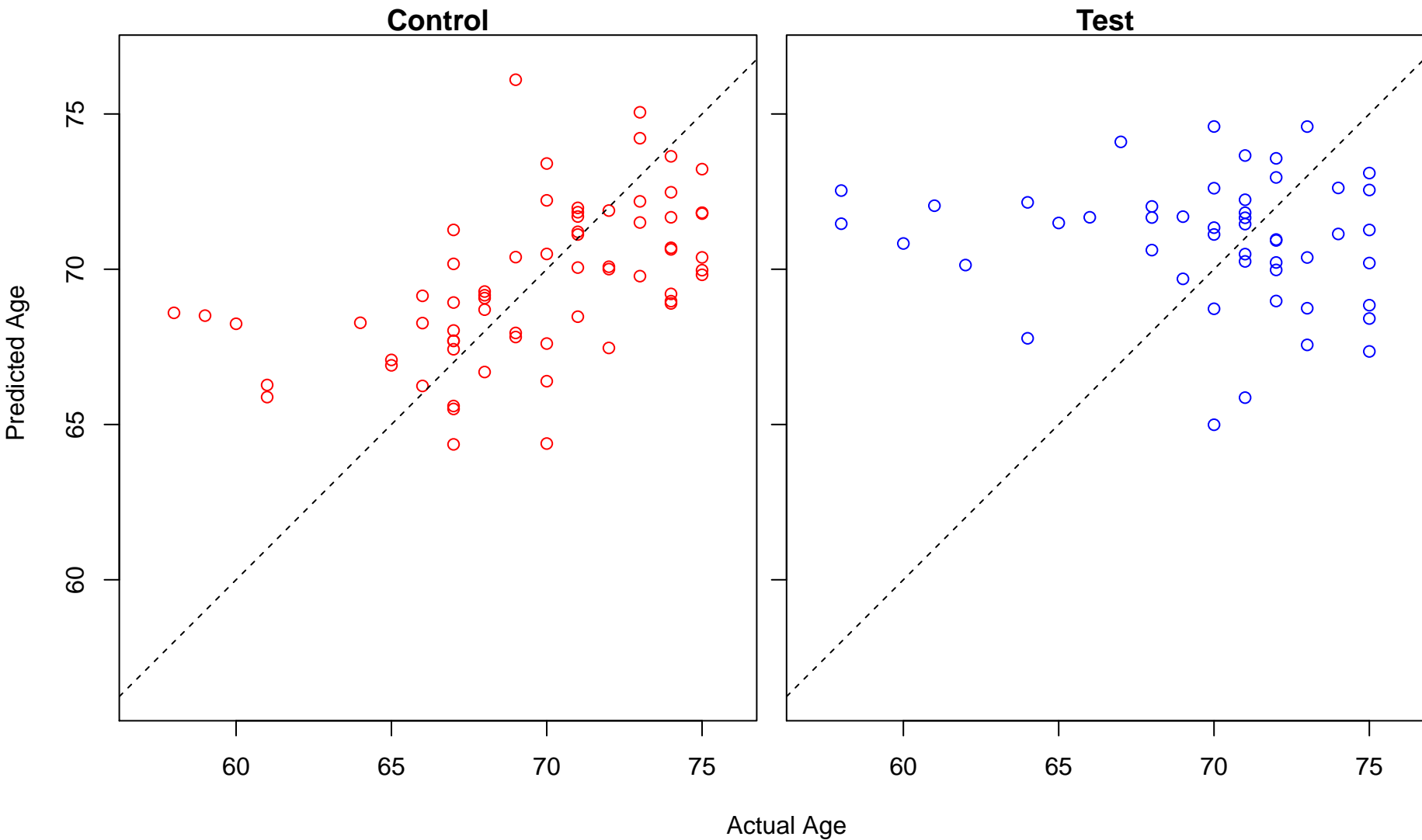
regulation of cardiac muscle cell proliferation (Score: 0.865857)



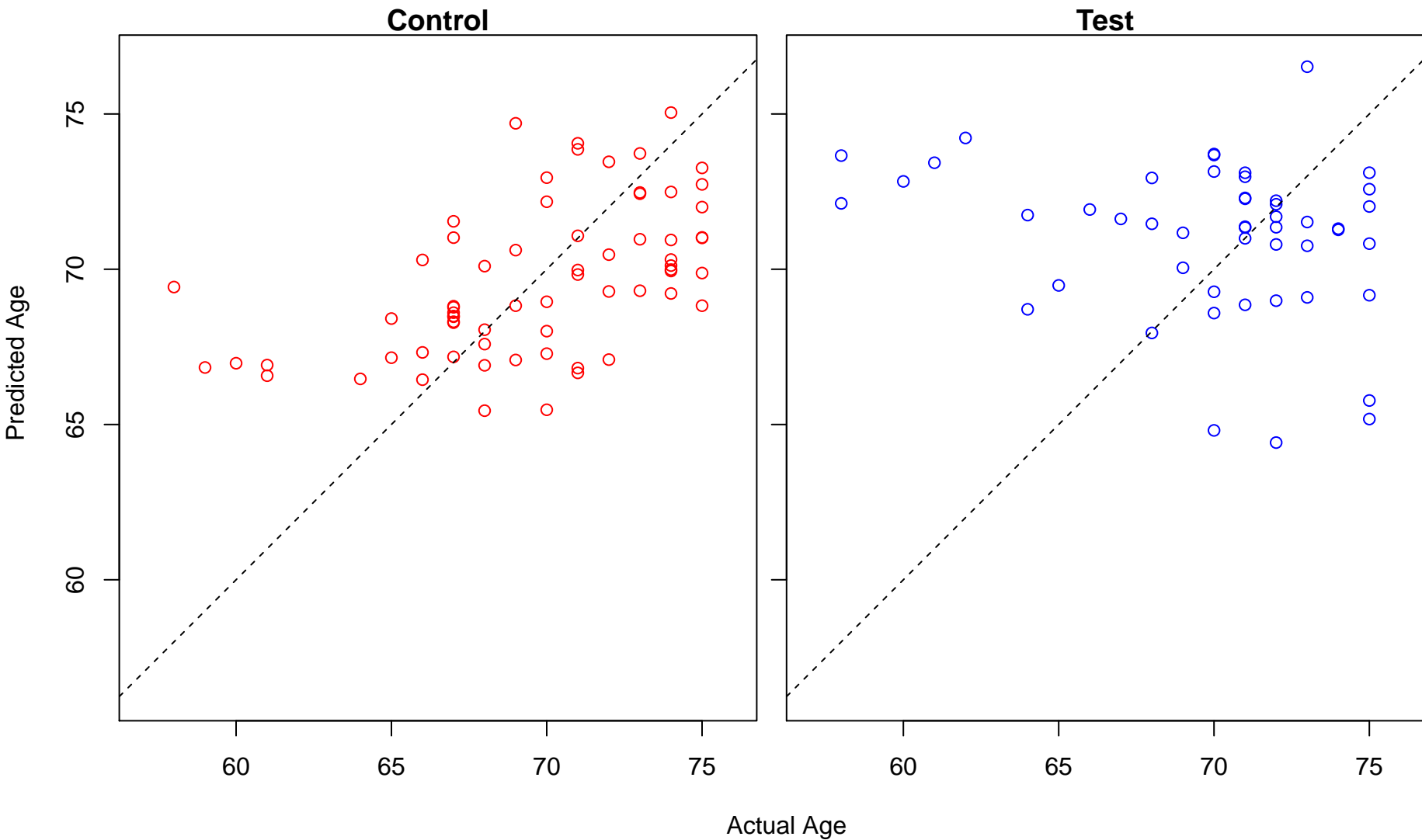
renal tubule development (Score: 0.865528)



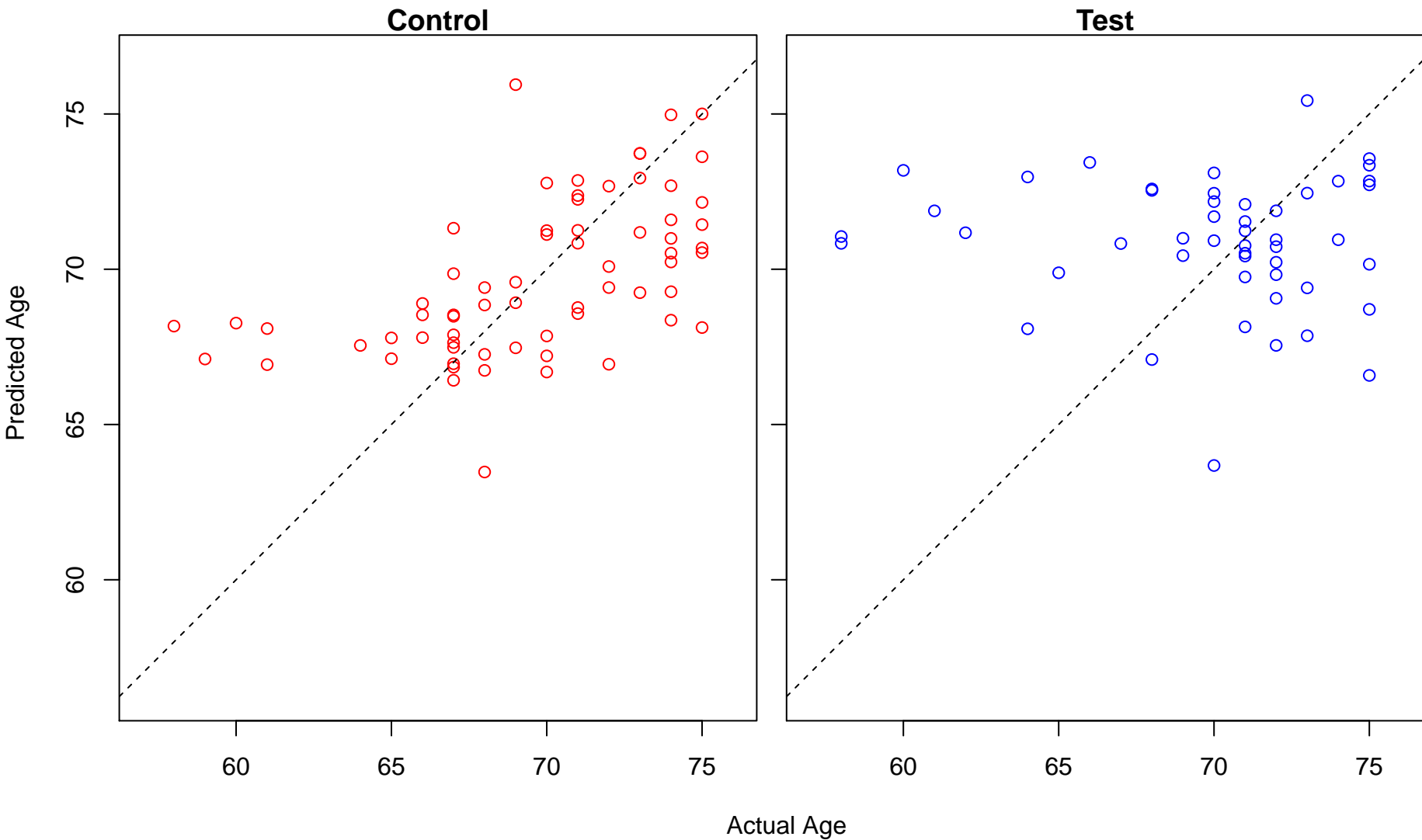
folic acid-containing compound metabolic process (Score: 0.864697)



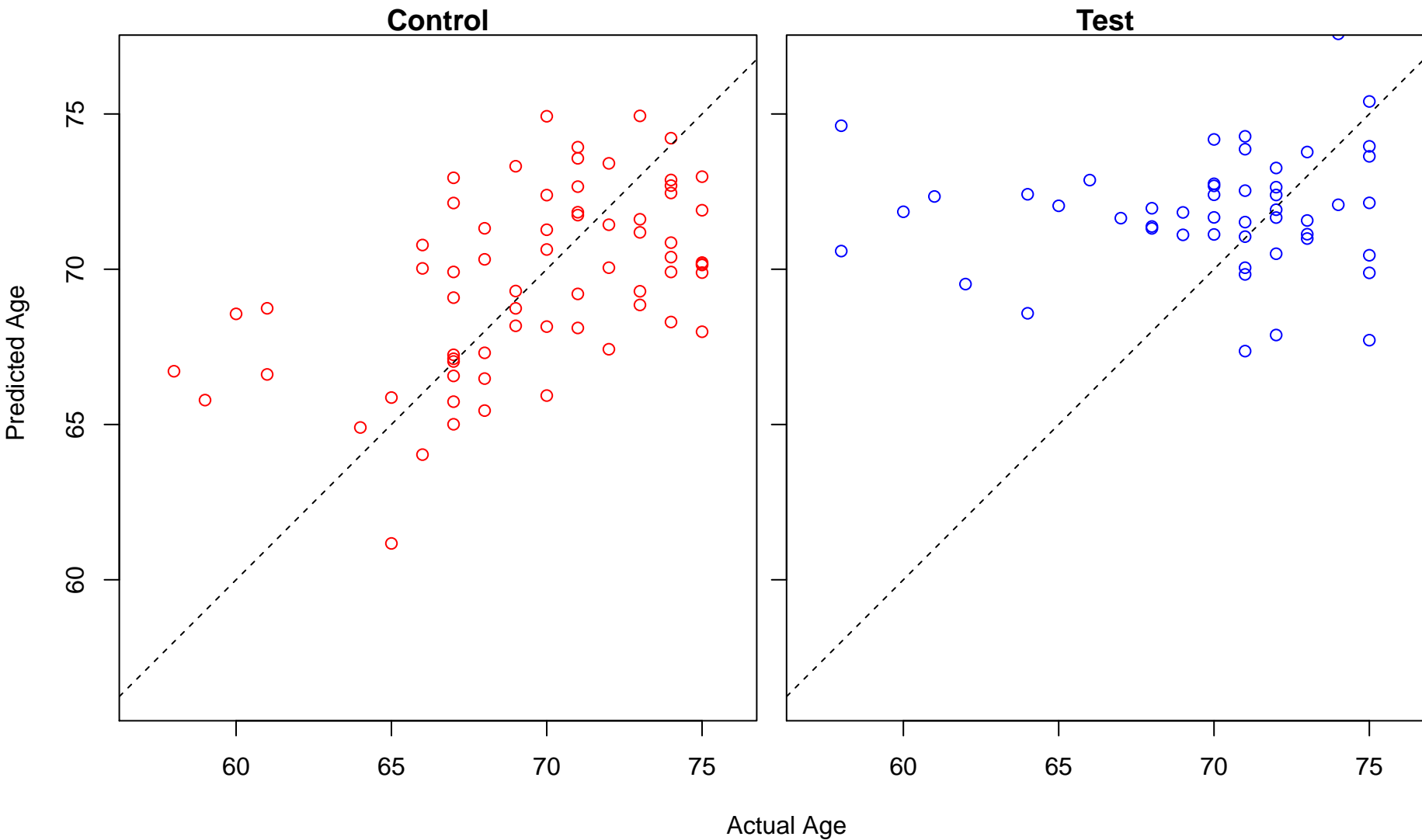
coenzyme A metabolic process (Score: 0.864107)



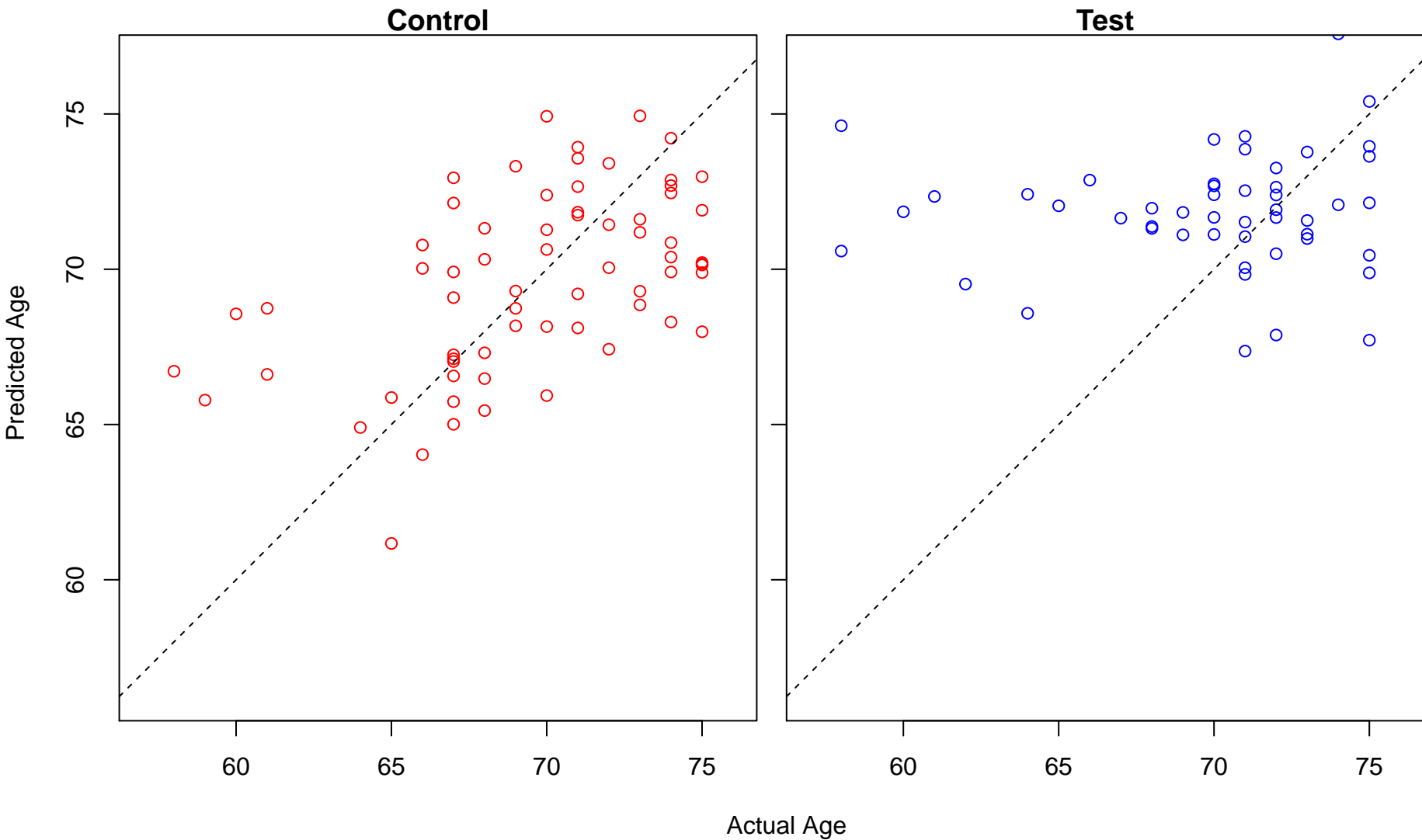
positive regulation of cellular carbohydrate metabolic process (Score: 0.863991)



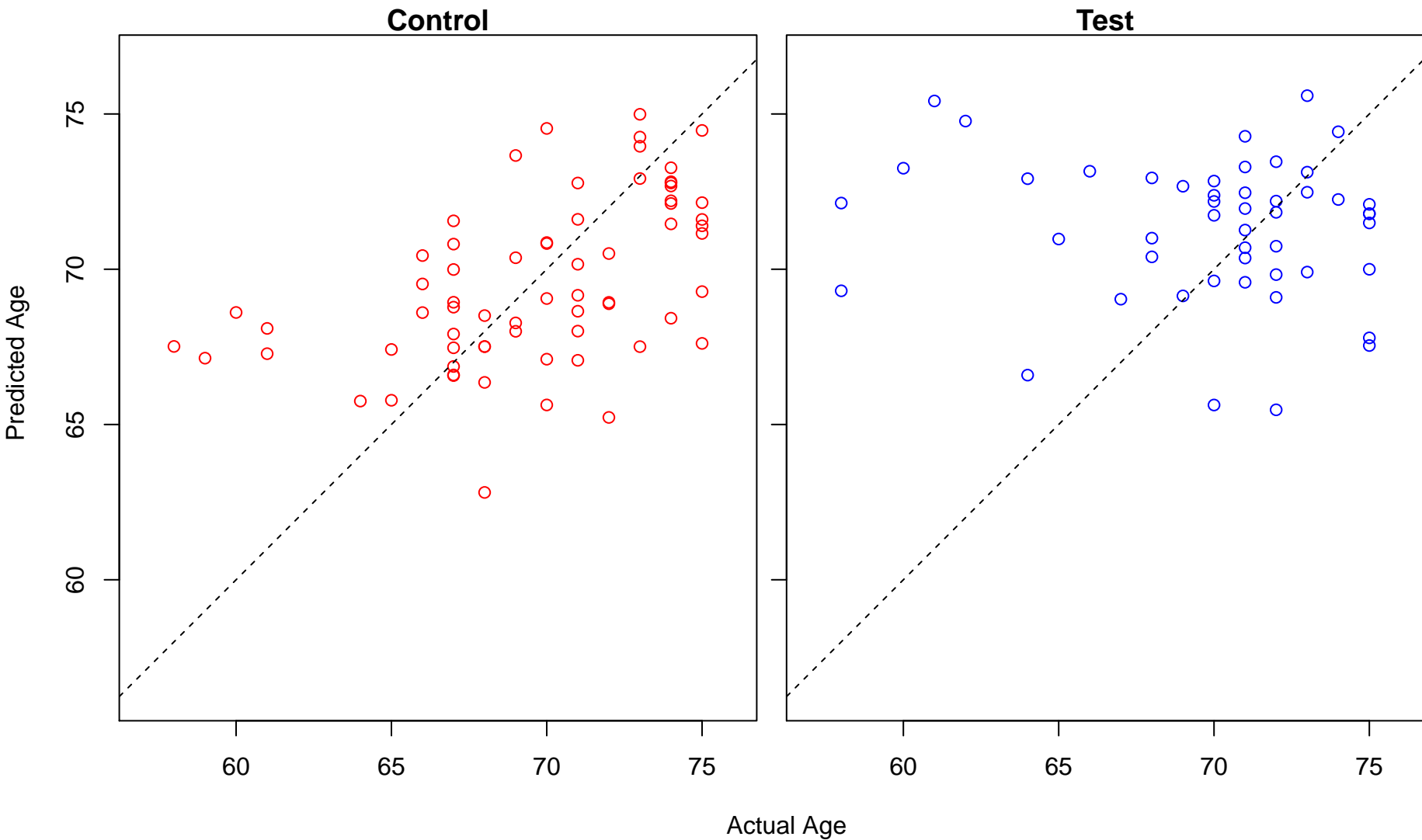
prostaglandin biosynthetic process (Score: 0.863638)



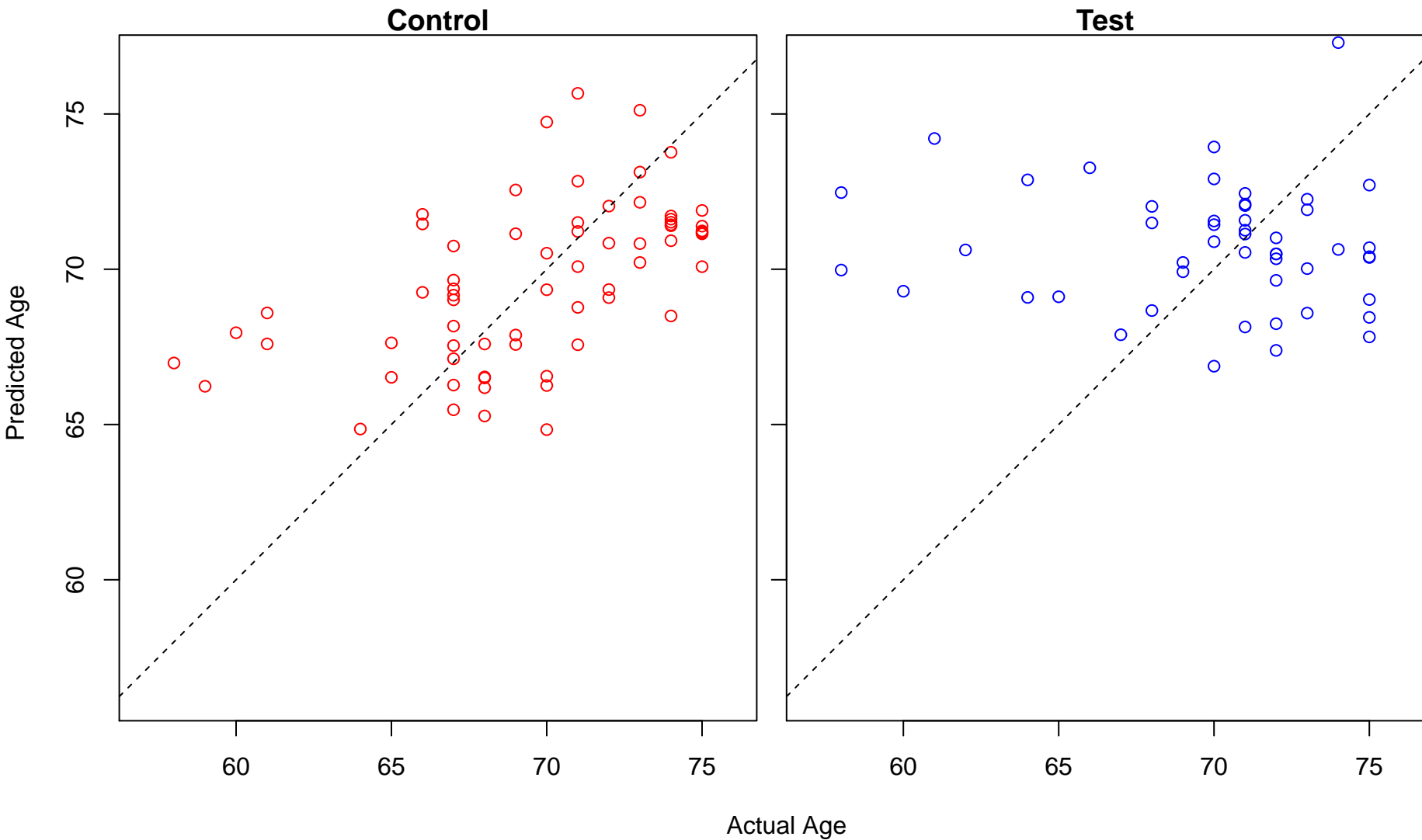
prostanoid biosynthetic process (Score: 0.863638)



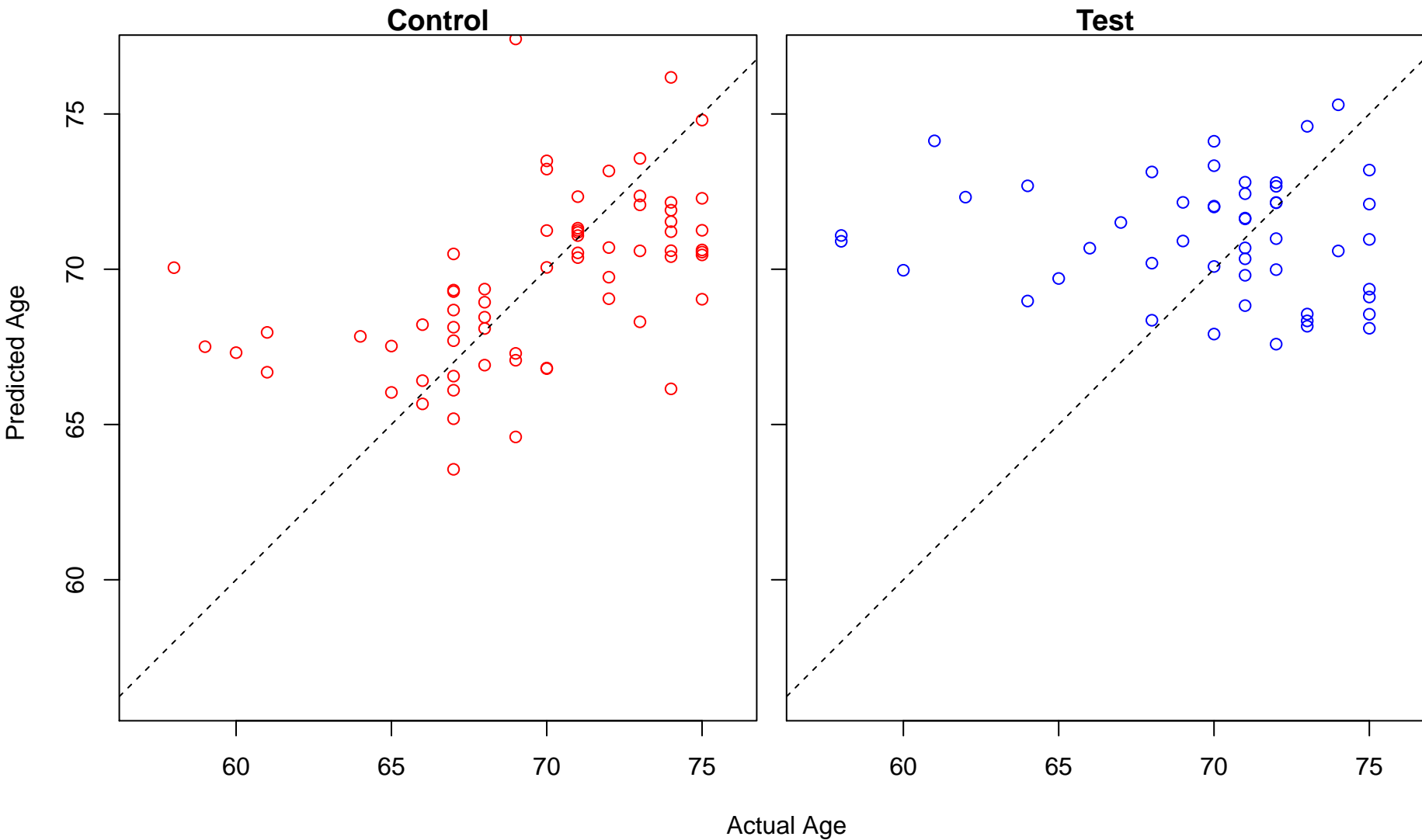
reactive oxygen species biosynthetic process (Score: 0.863475)



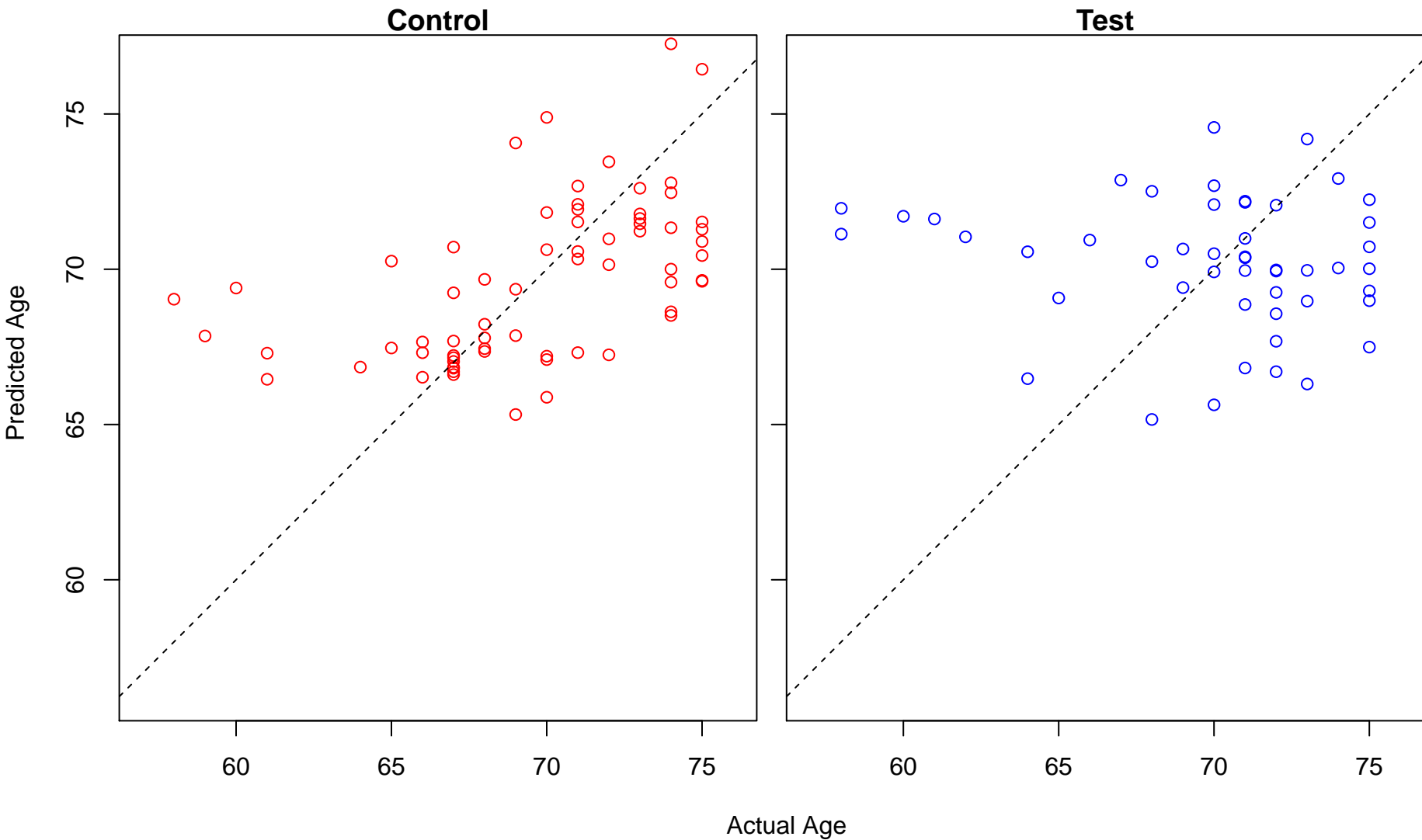
ribonucleoside catabolic process (Score: 0.863464)



androgen metabolic process (Score: 0.863260)

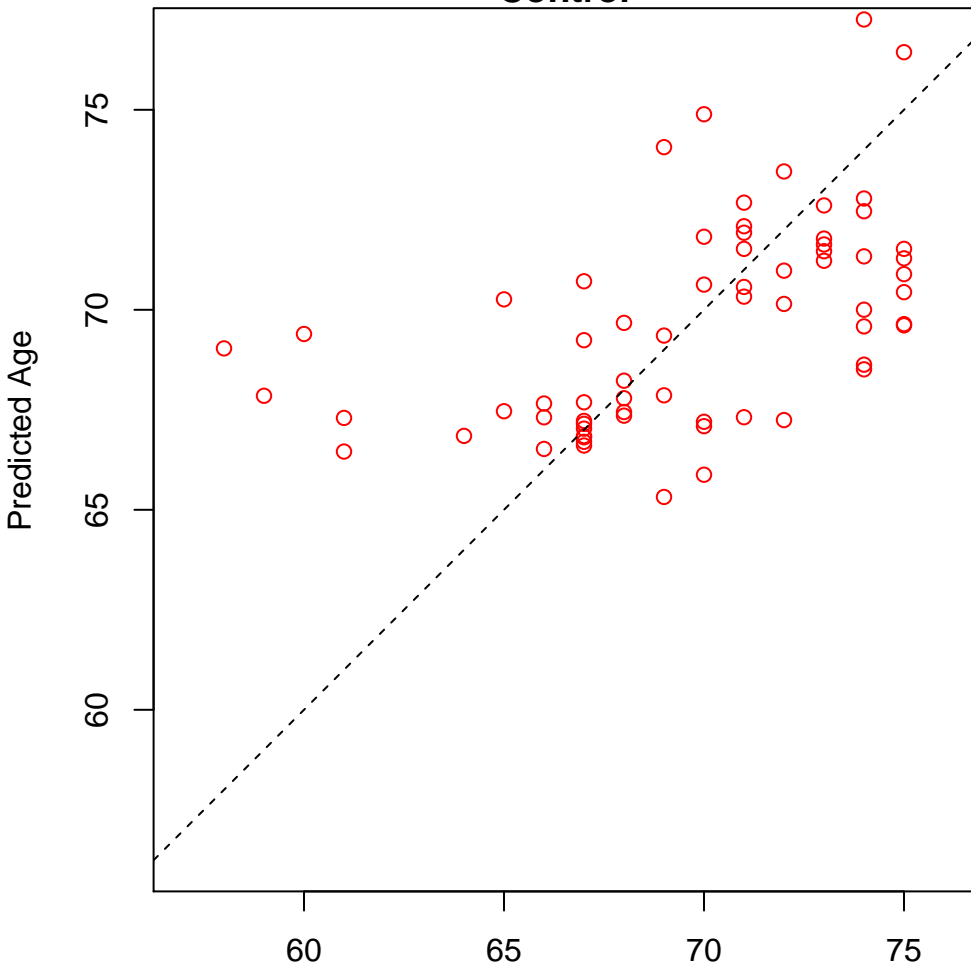


phosphorylated carbohydrate dephosphorylation (Score: 0.862835)

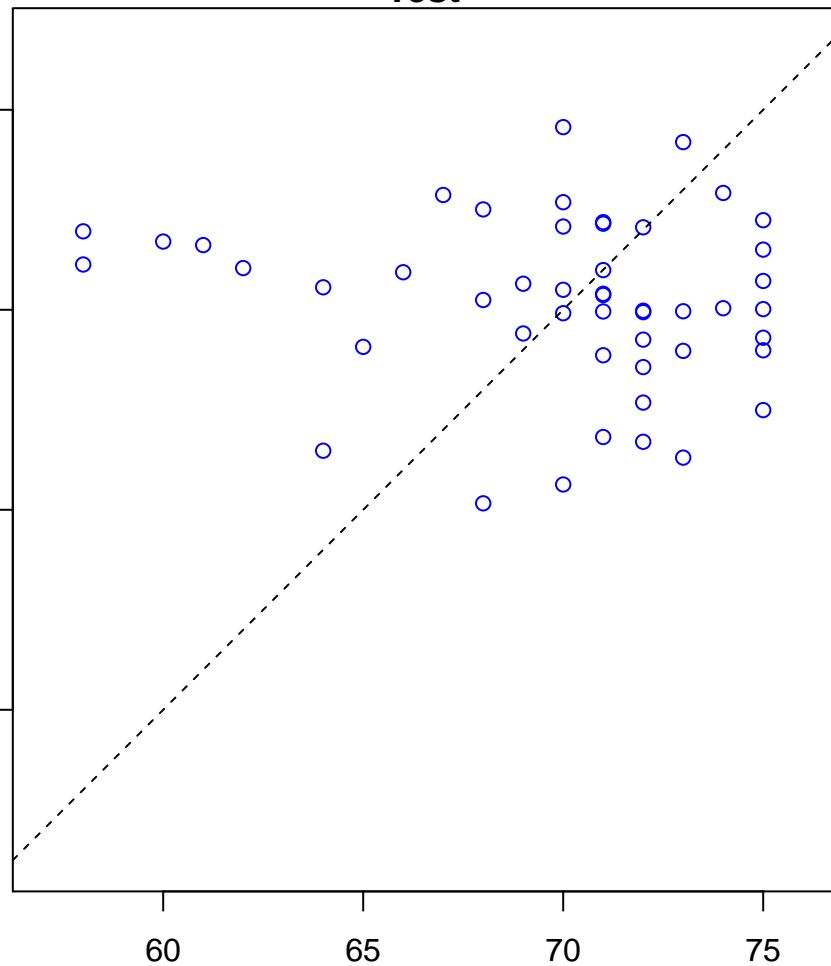


inositol phosphate dephosphorylation (Score: 0.862835)

Control

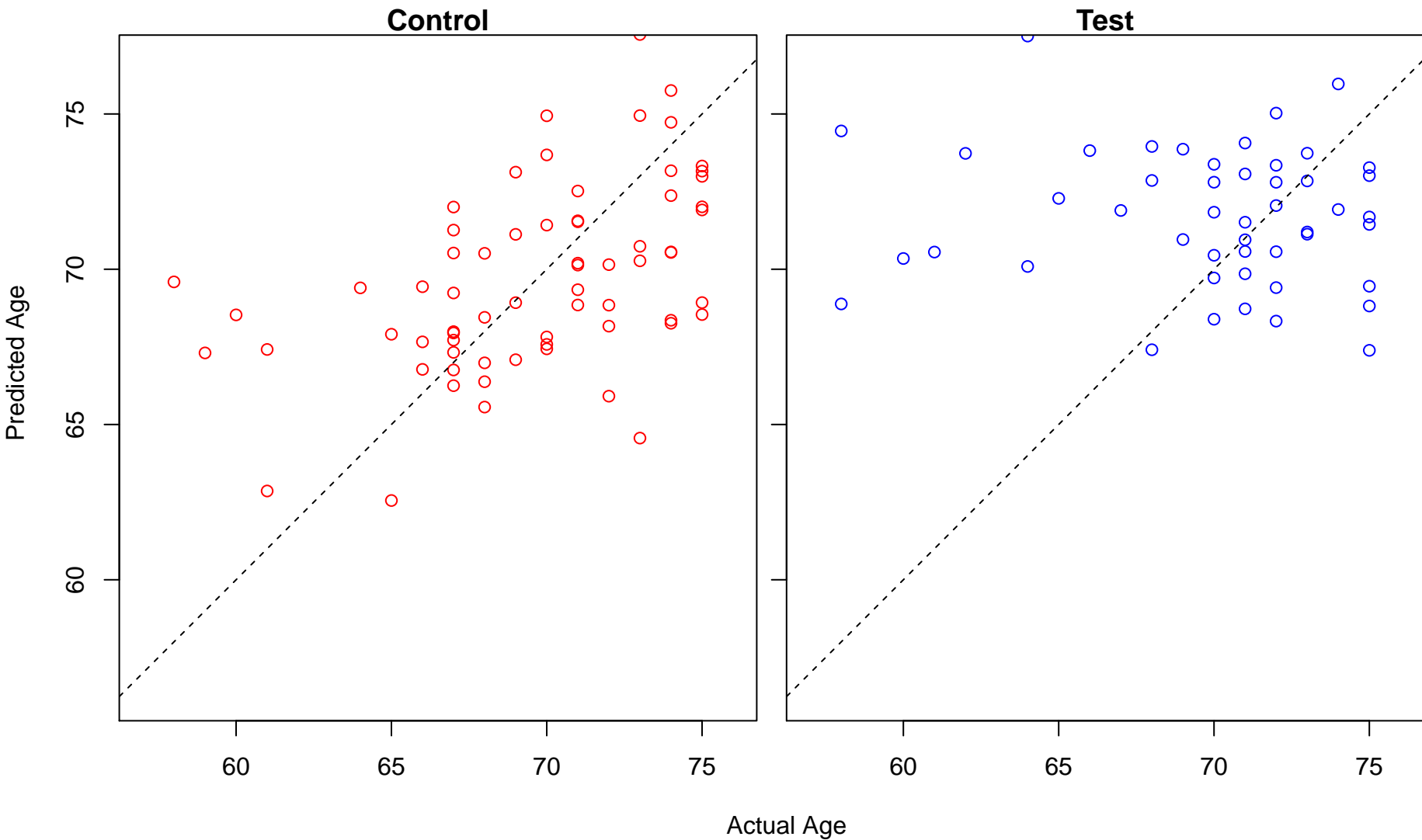


Test

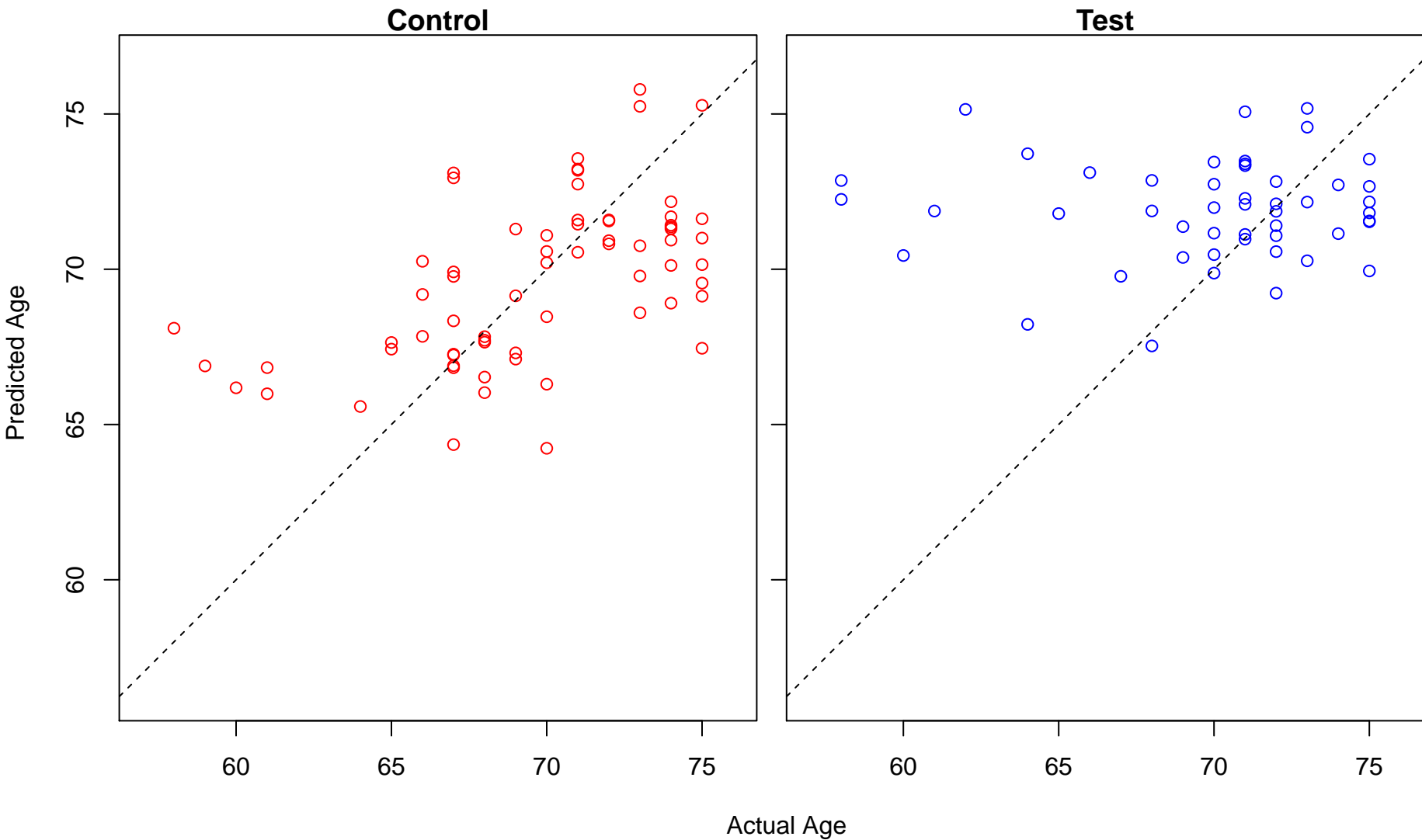


Actual Age

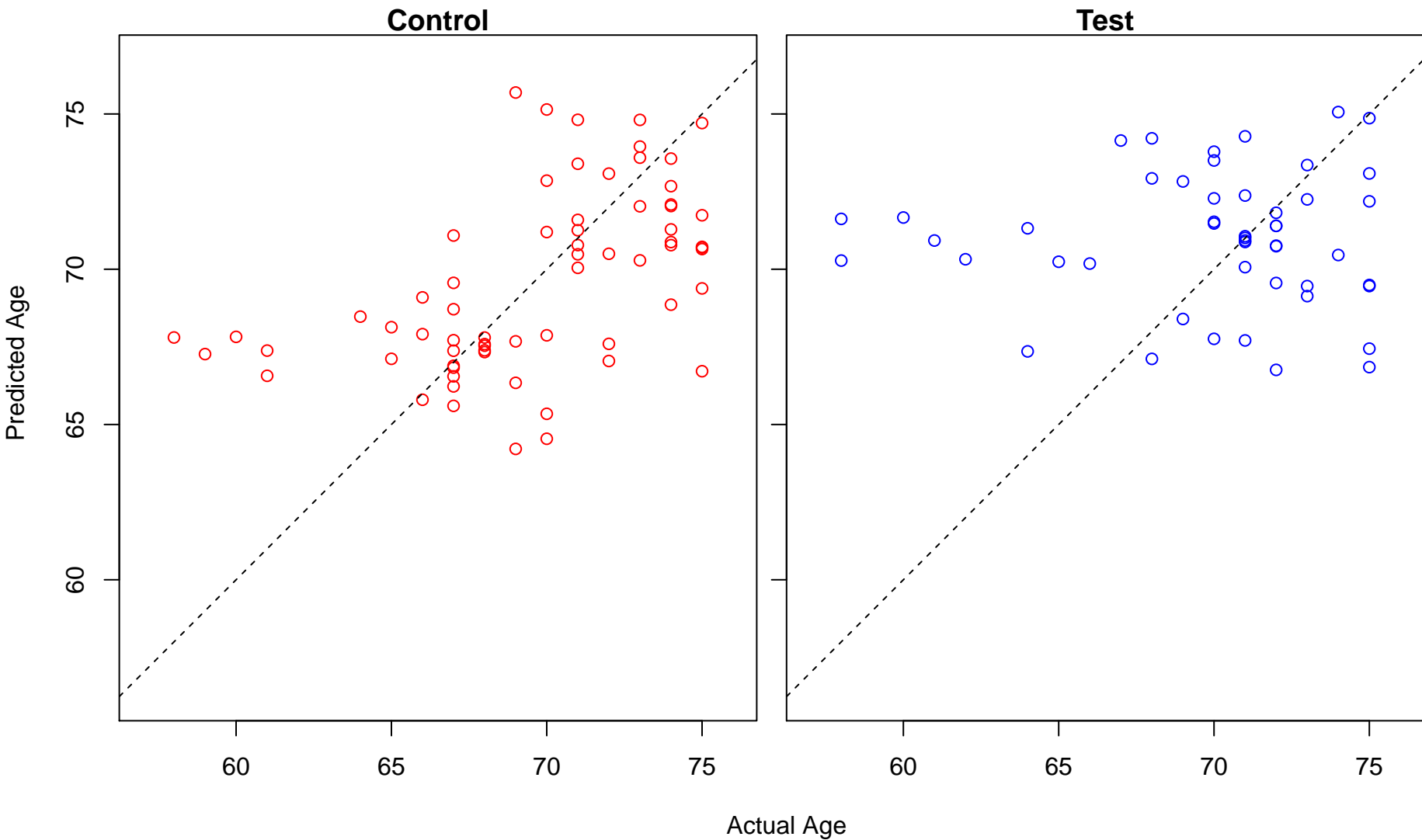
purine deoxyribonucleotide catabolic process (Score: 0.862630)



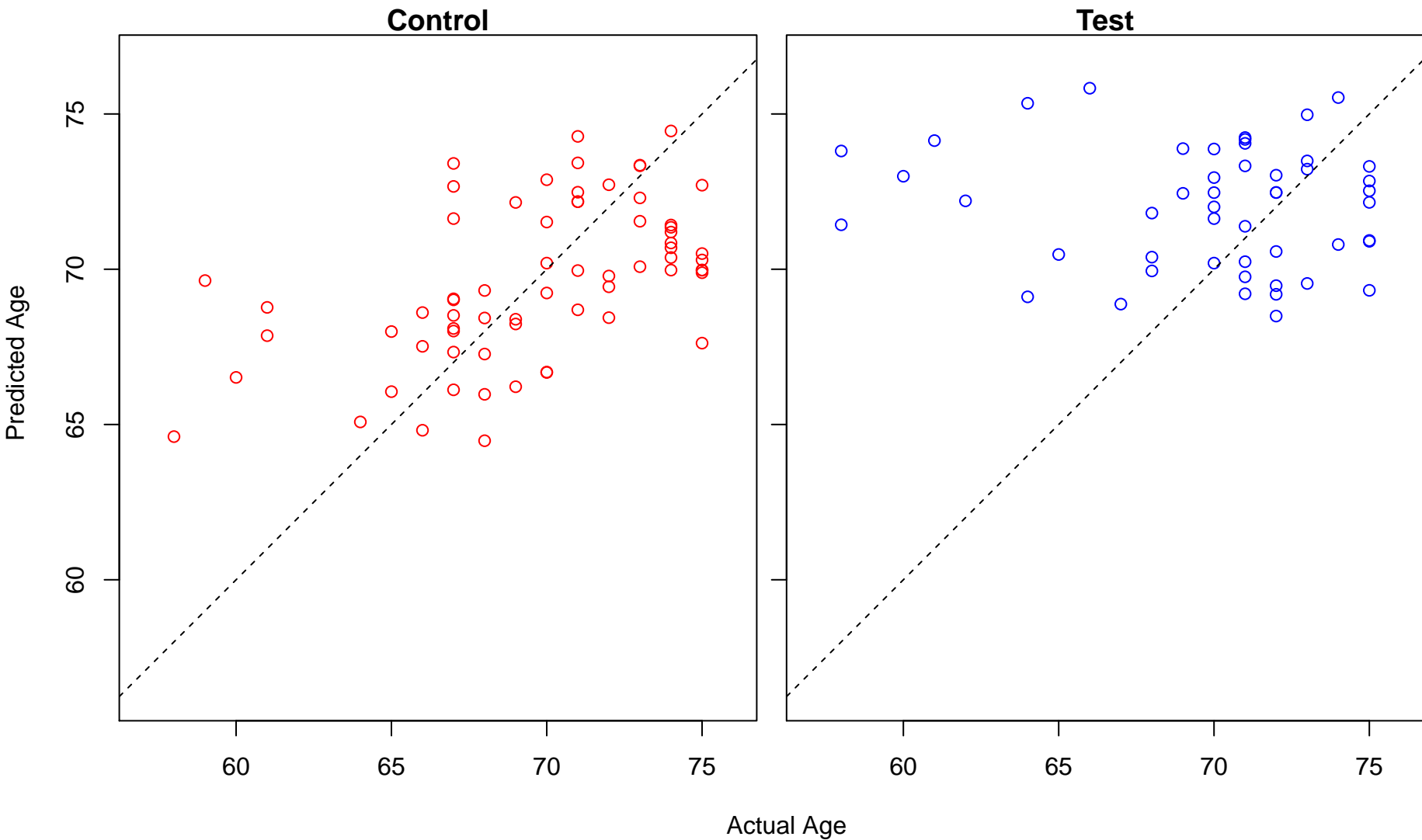
cellular response to osmotic stress (Score: 0.862360)



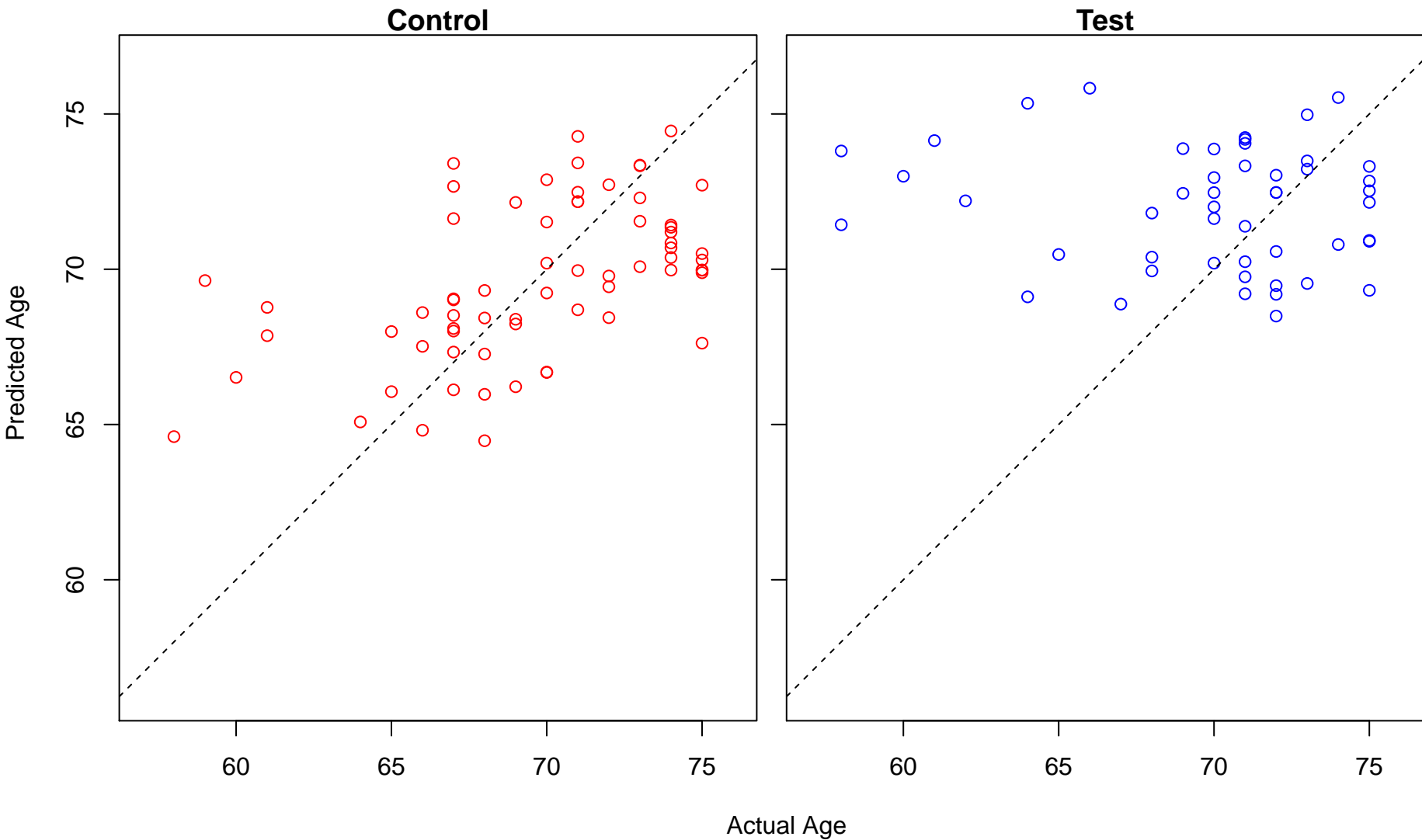
detection of visible light (Score: 0.862348)



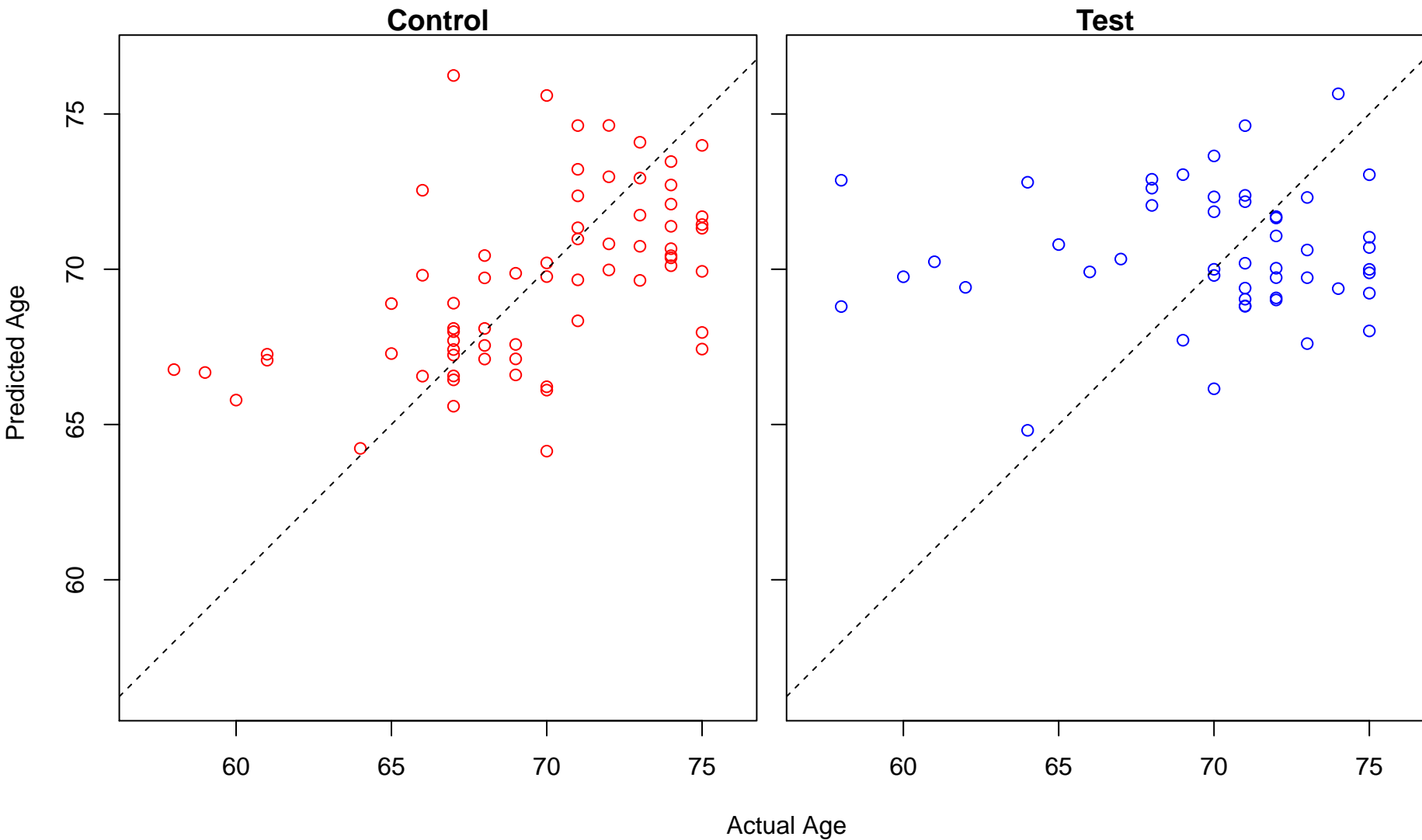
positive regulation of organ growth (Score: 0.861926)



positive regulation of heart growth (Score: 0.861926)

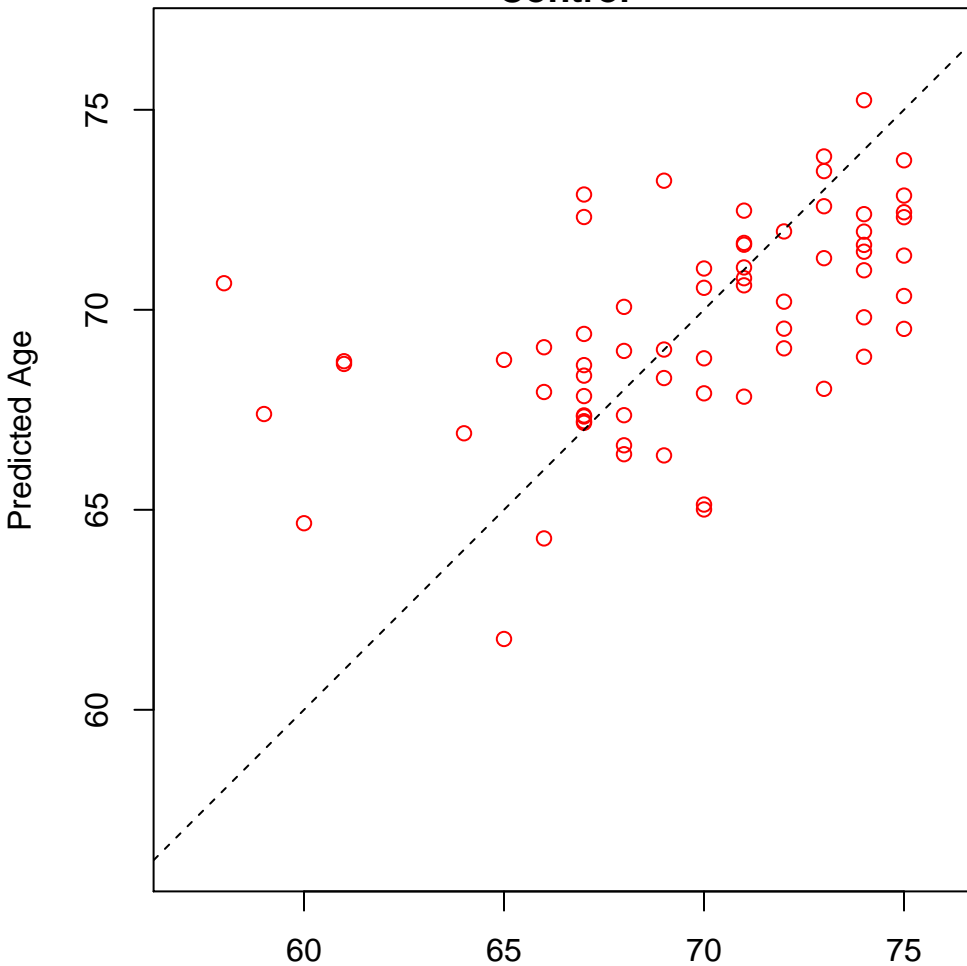


membrane protein intracellular domain proteolysis (Score: 0.861847)

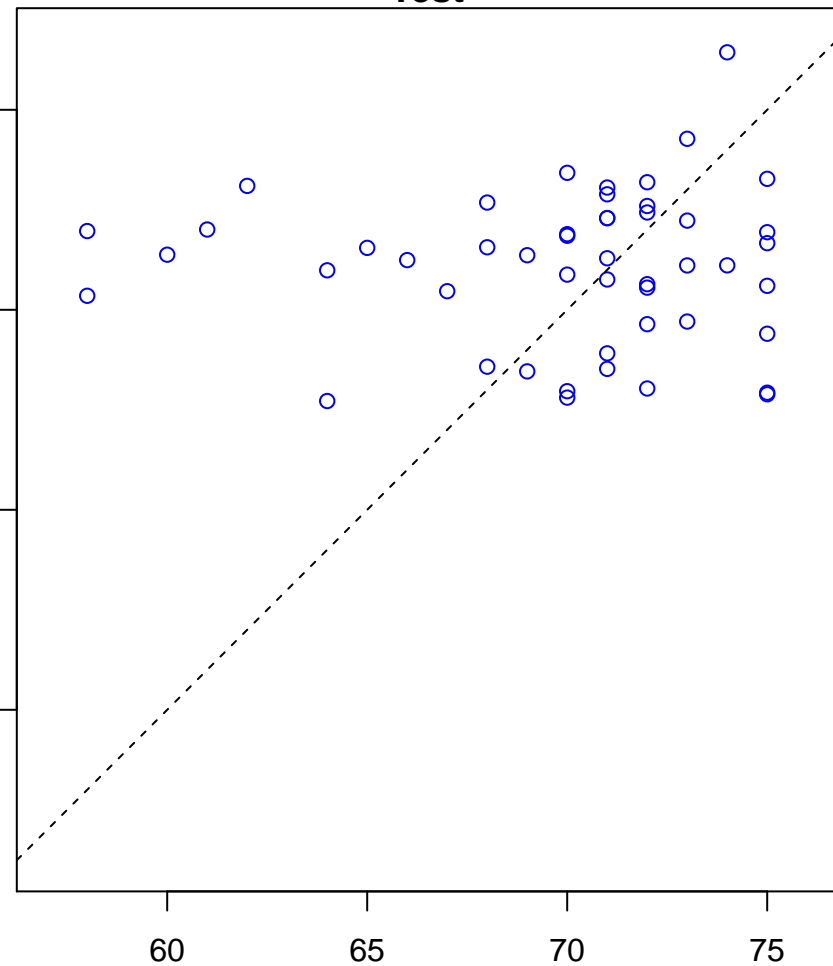


cellular response to muramyl dipeptide (Score: 0.861793)

Control

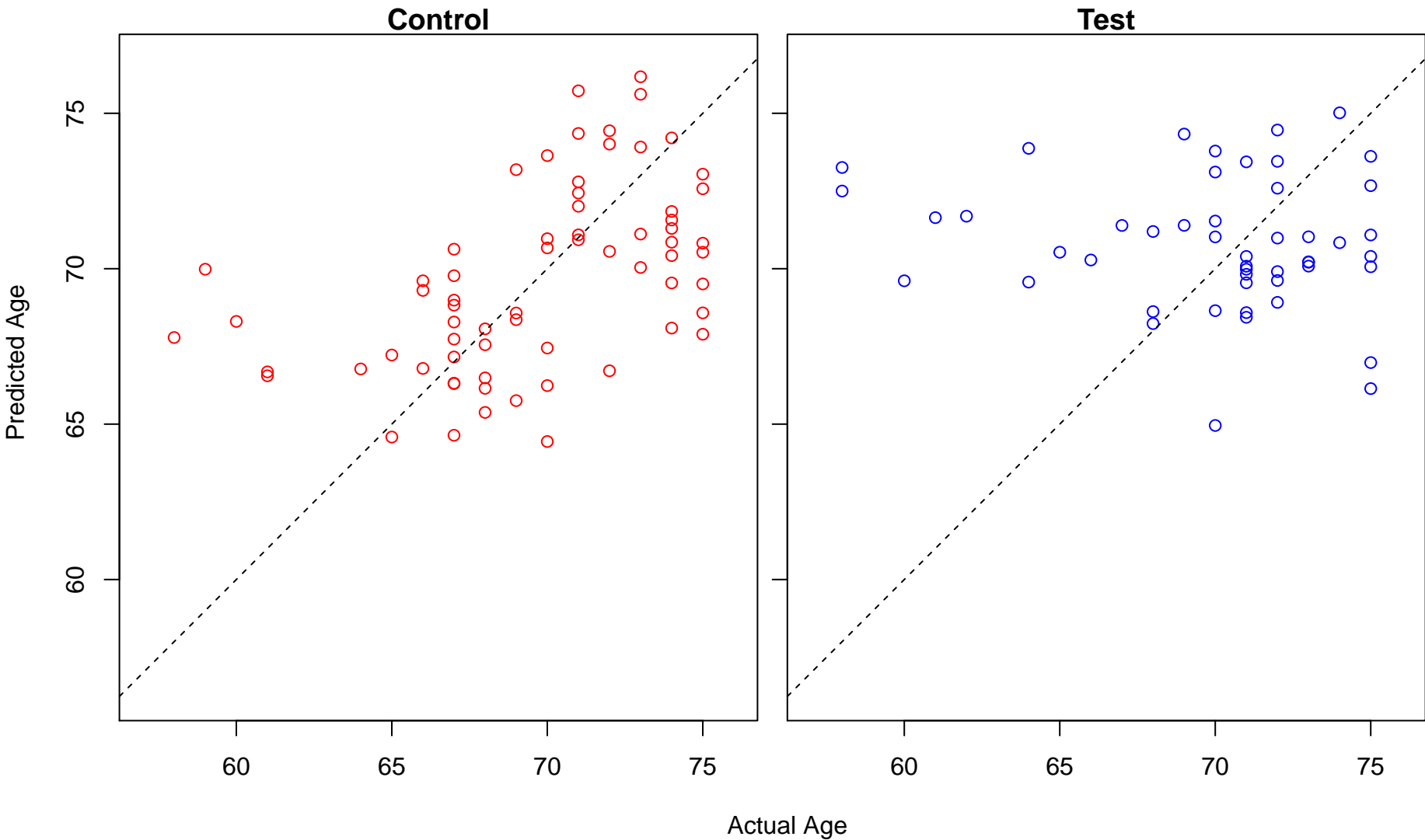


Test

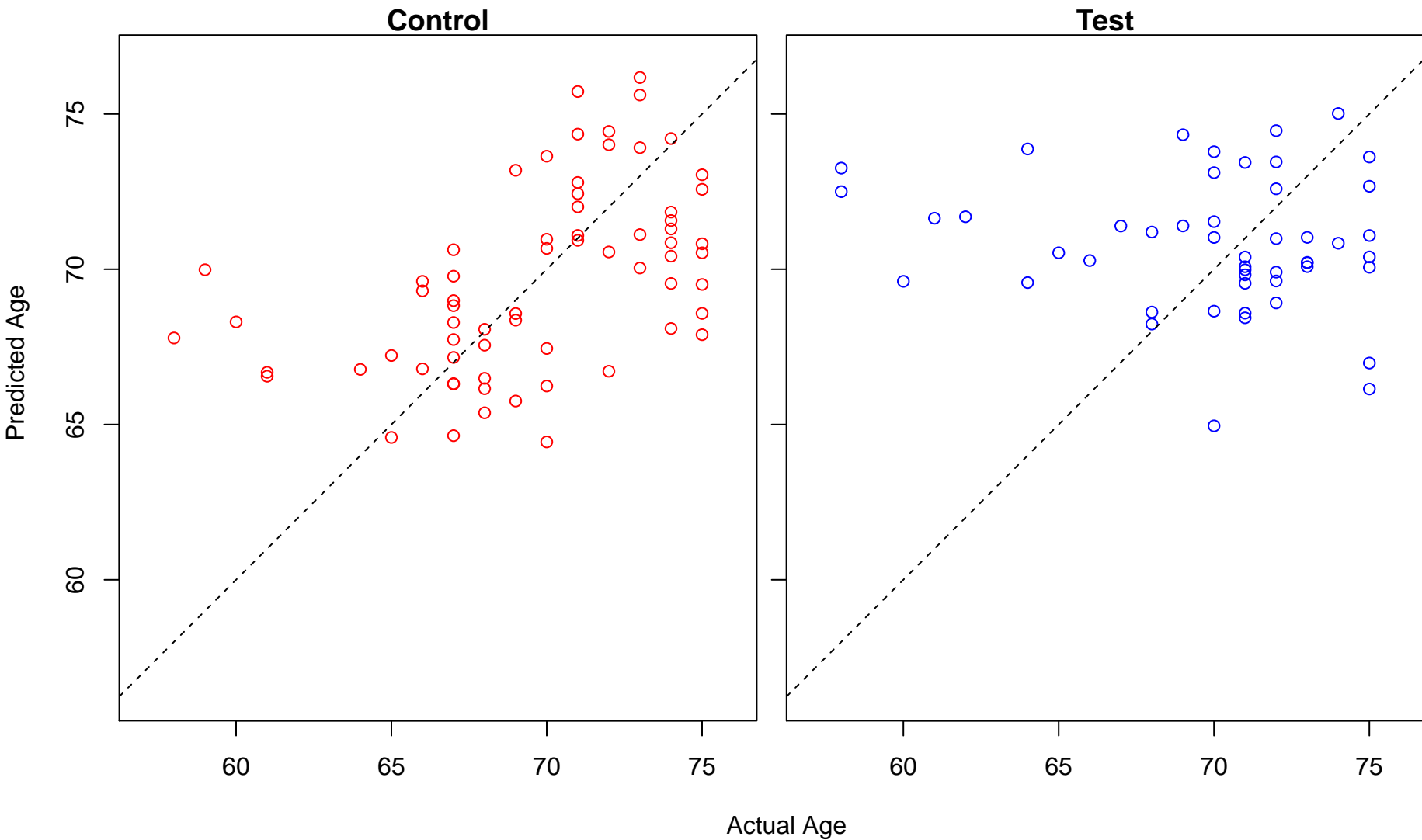


Actual Age

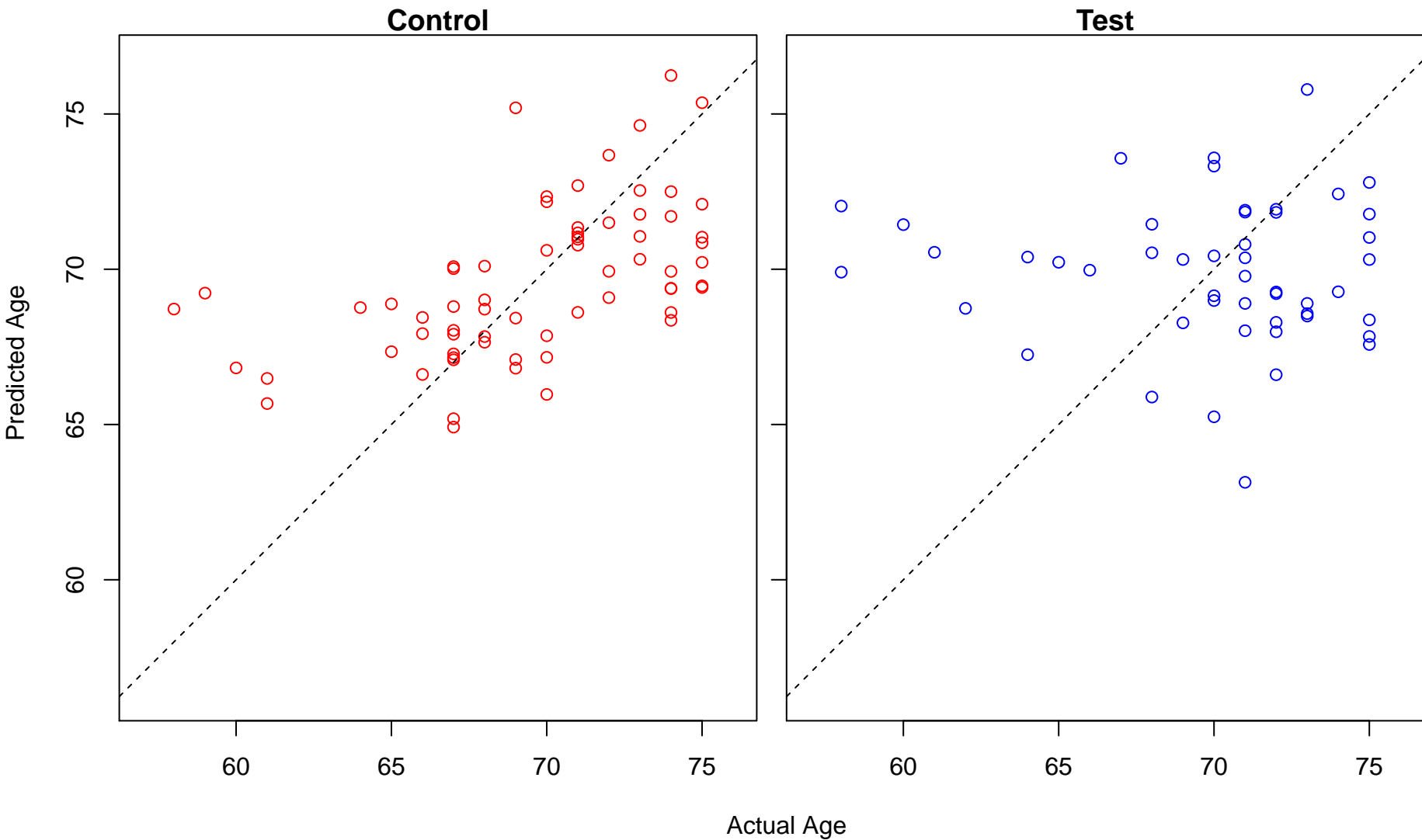
CD4-positive, alpha-beta T cell differentiation involved in immune response (Score: 0.861758)



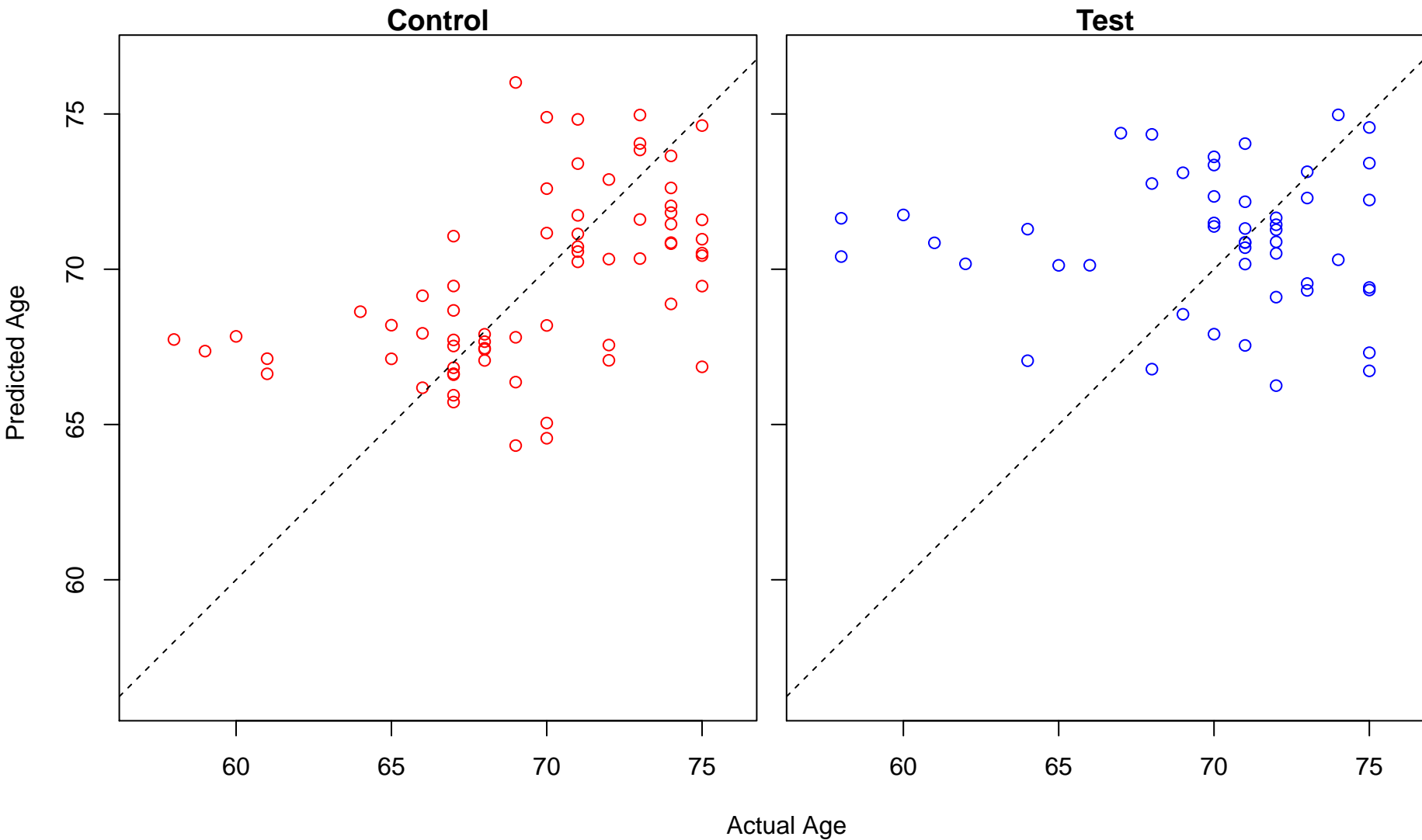
T-helper cell differentiation (Score: 0.861758)



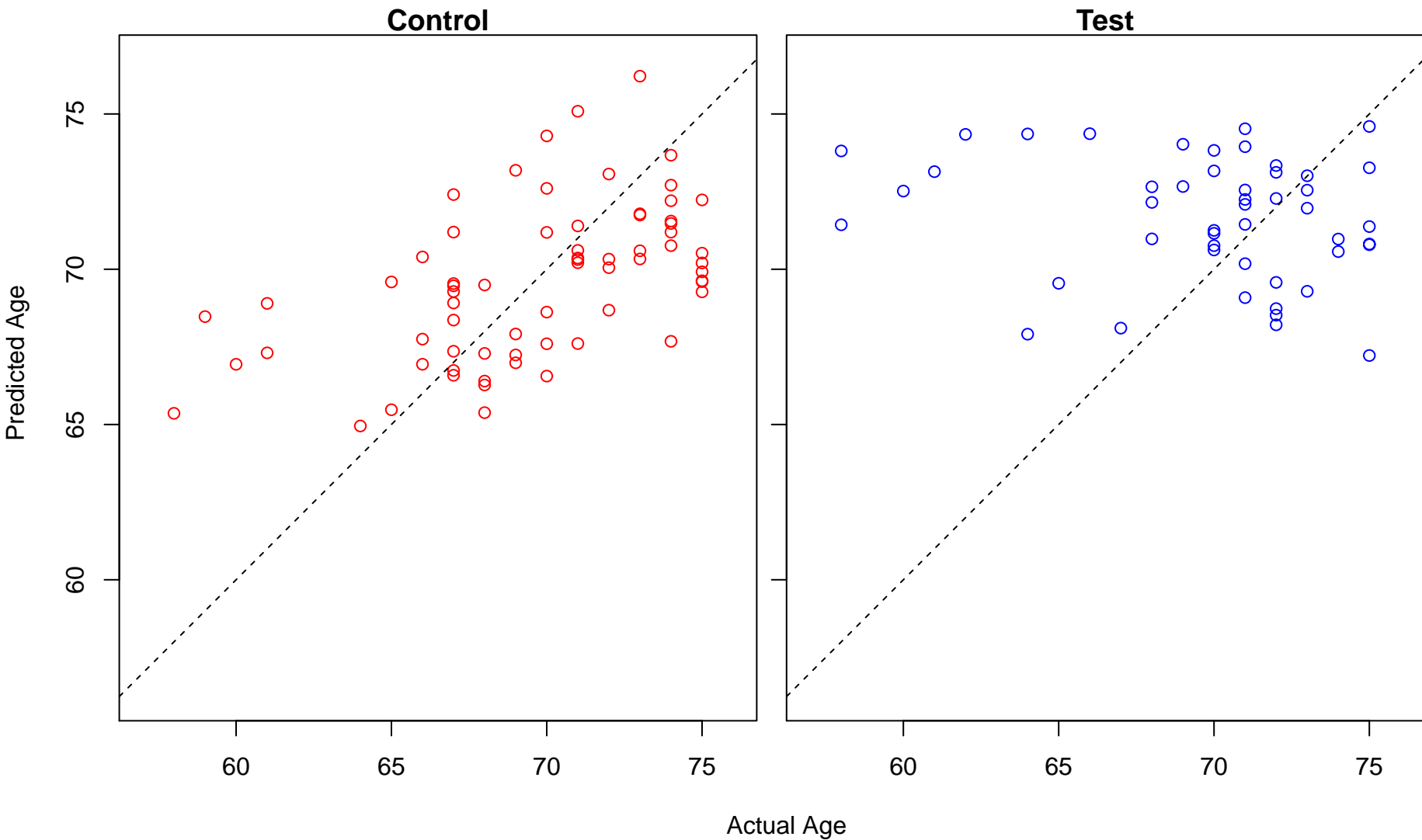
hippocampus development (Score: 0.861743)



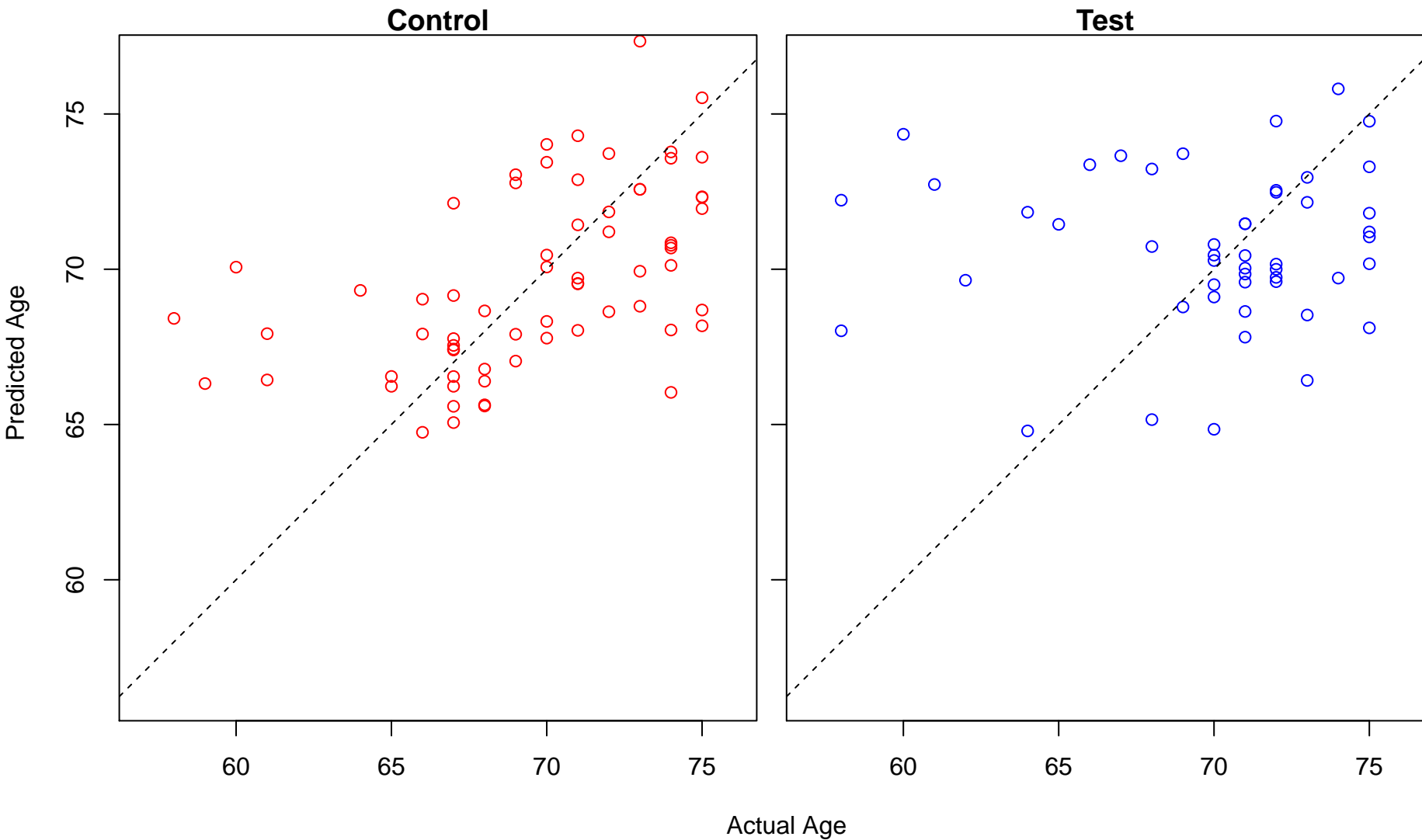
phototransduction, visible light (Score: 0.861628)



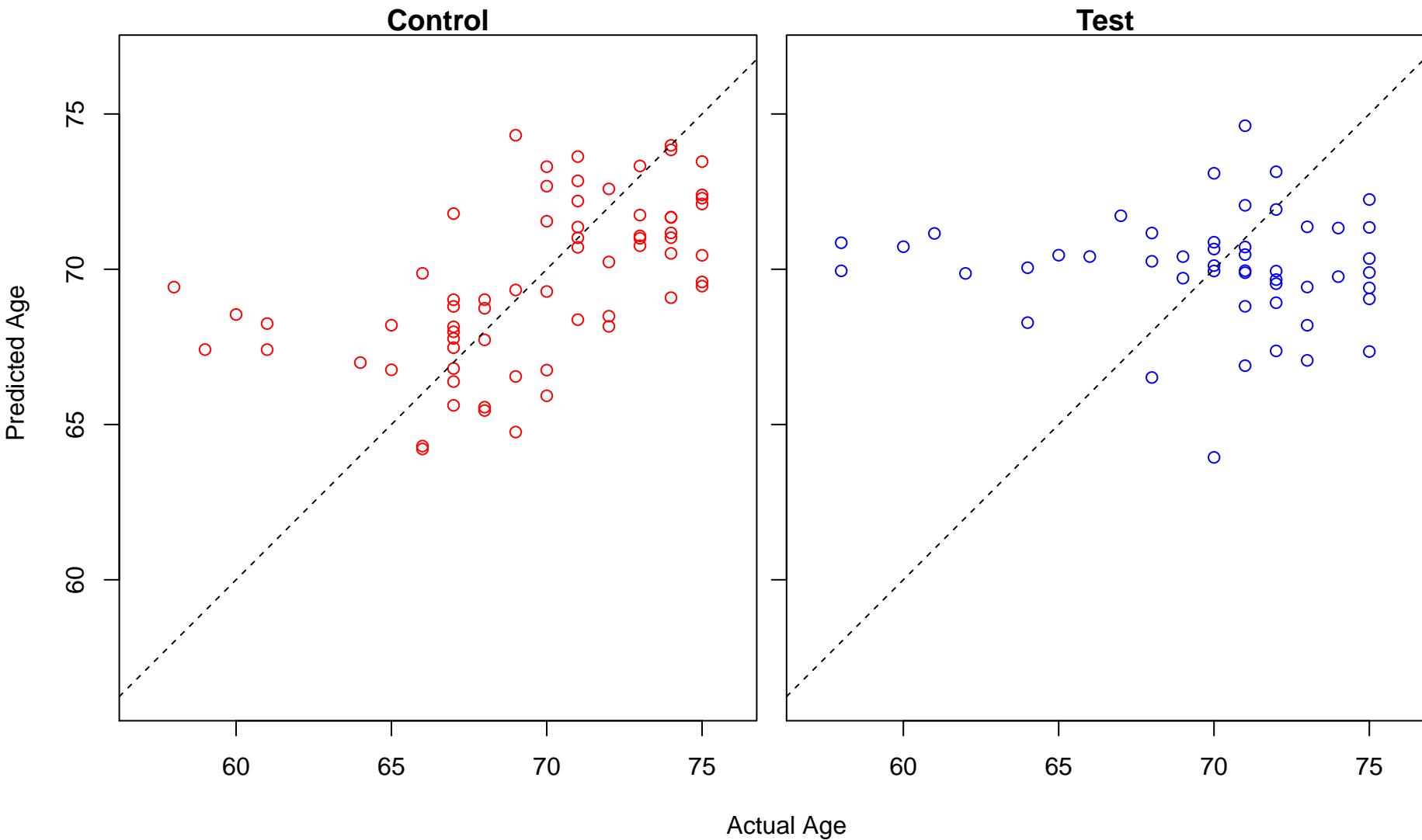
cardiac septum development (Score: 0.861615)



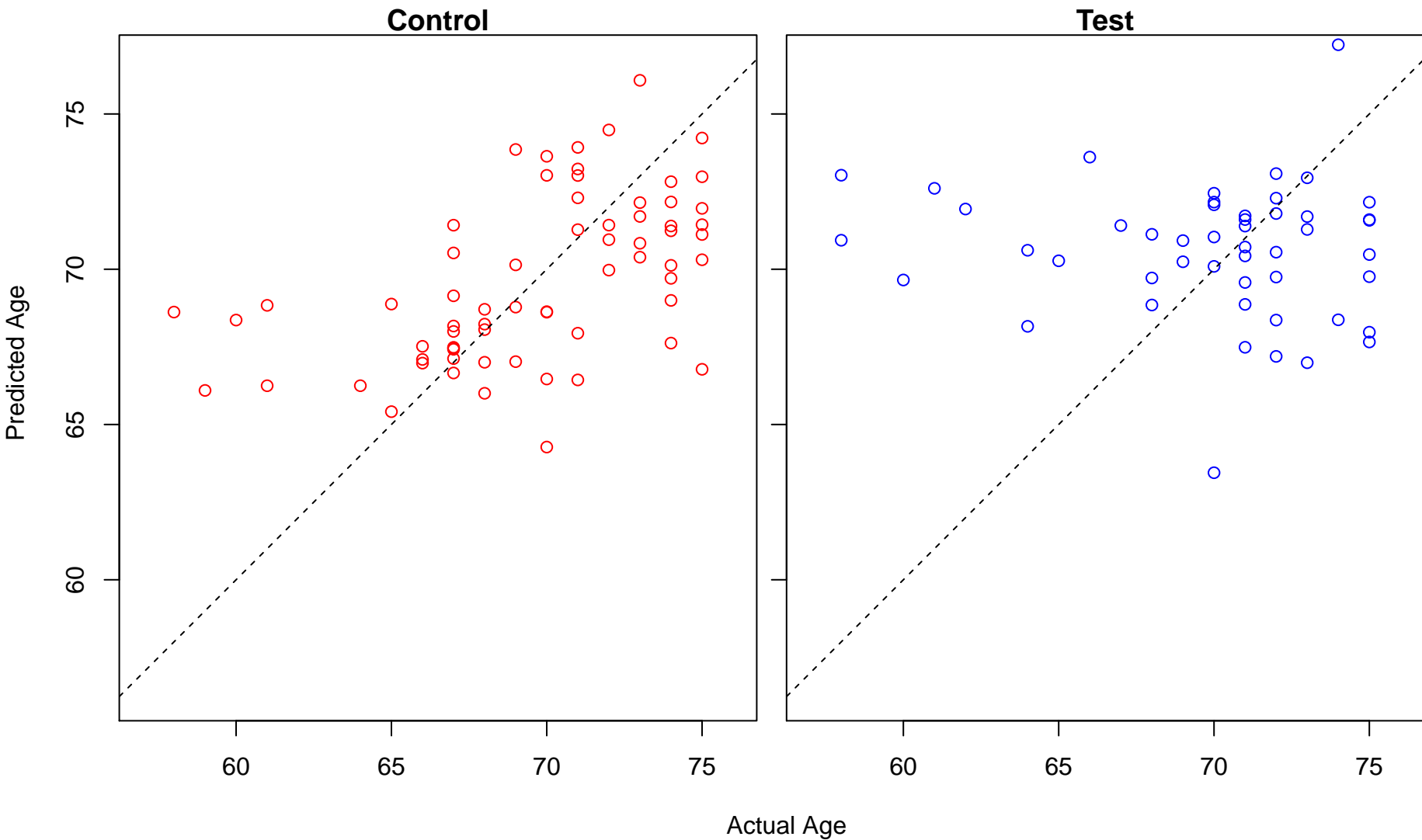
endocrine system development (Score: 0.861499)



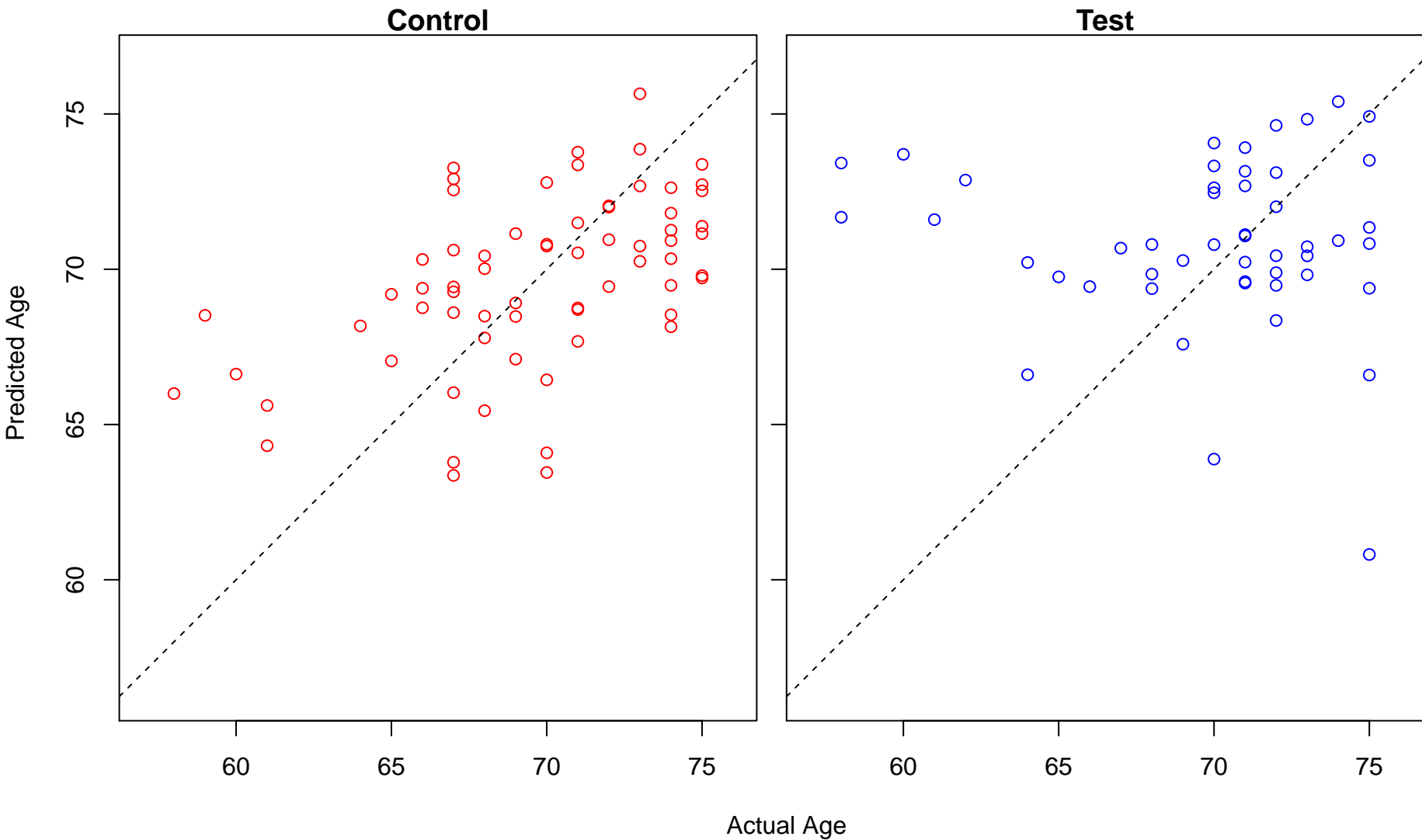
negative regulation of epithelial cell differentiation (Score: 0.860258)



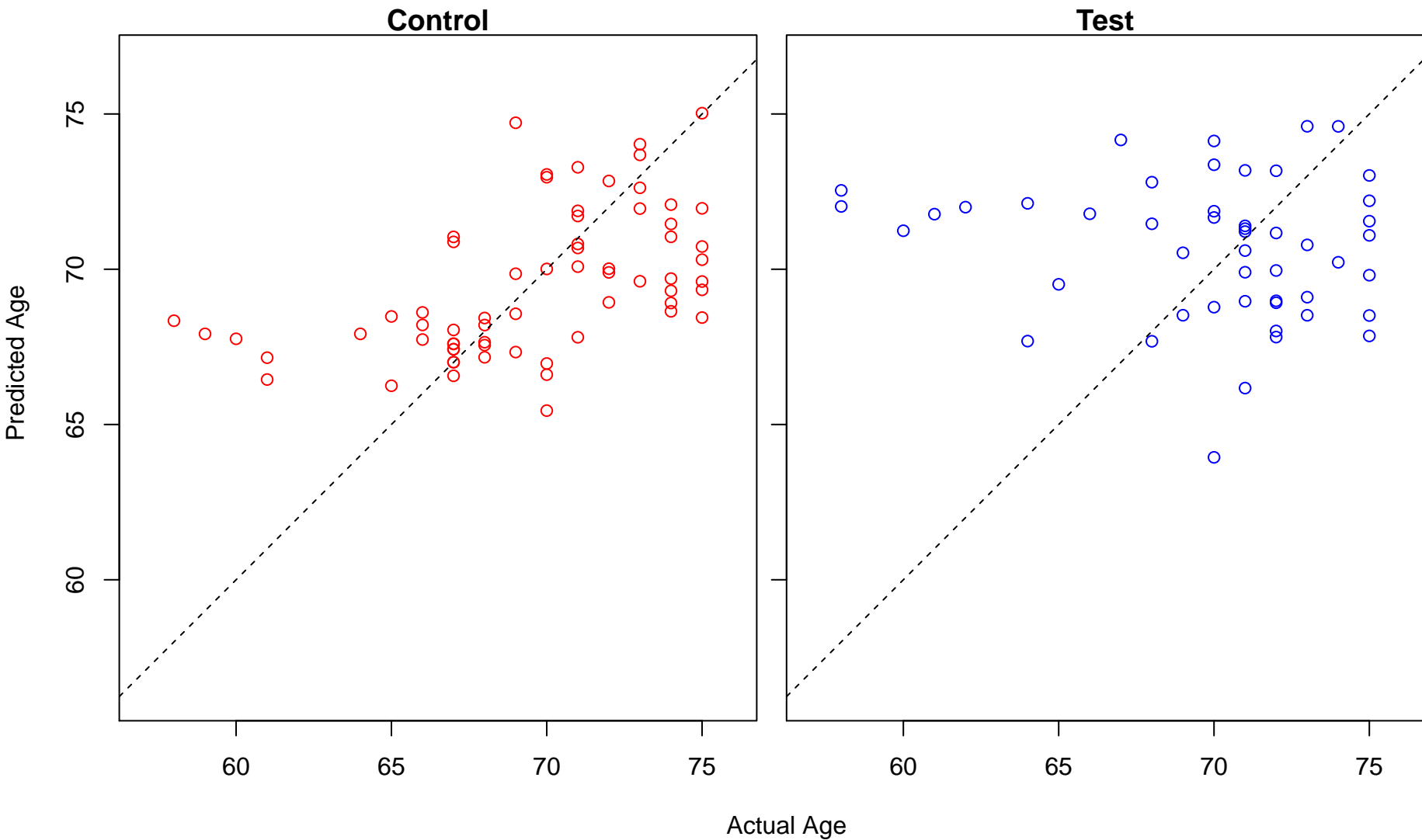
positive regulation of tyrosine phosphorylation of STAT protein (Score: 0.859815)



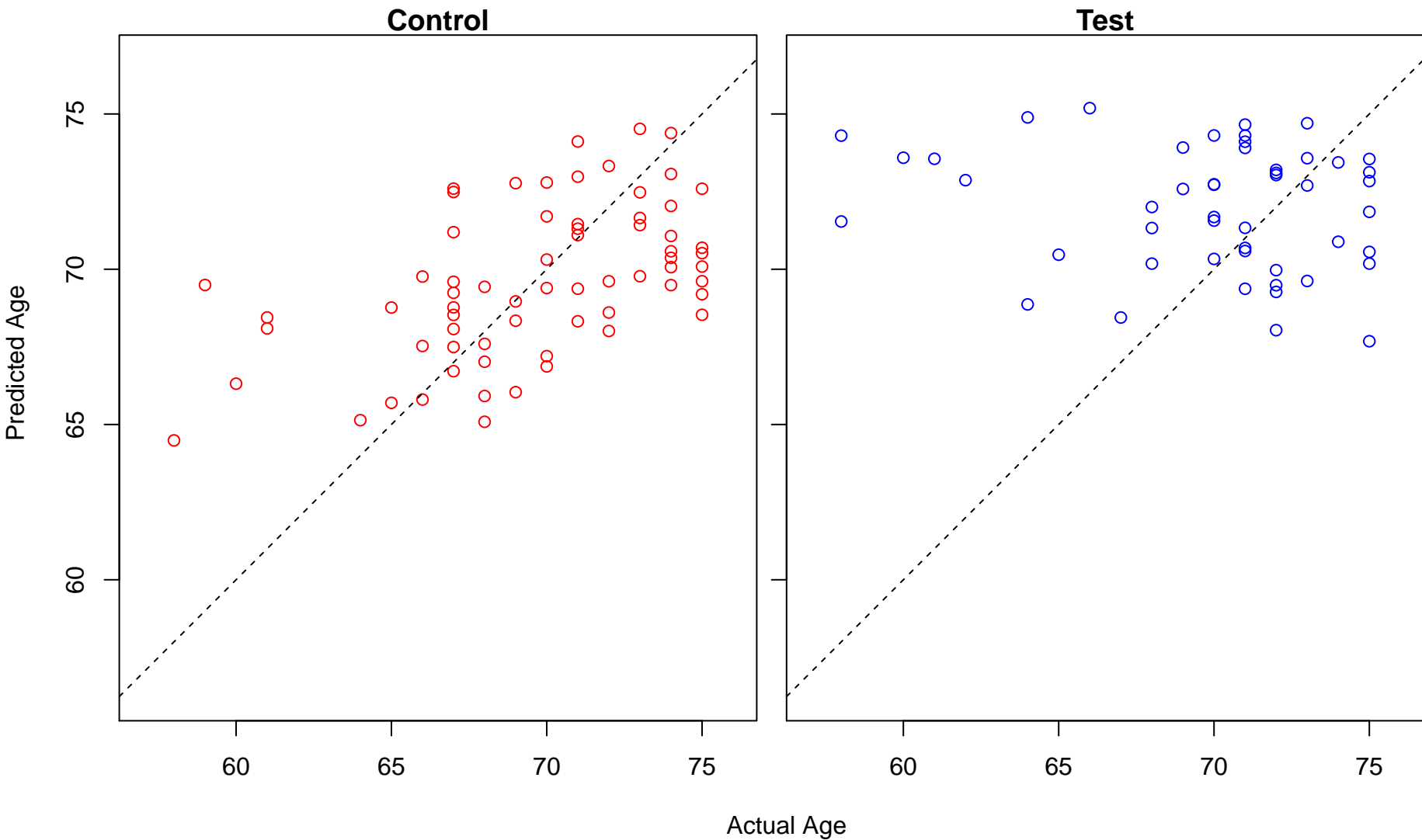
cellular response to cAMP (Score: 0.859628)



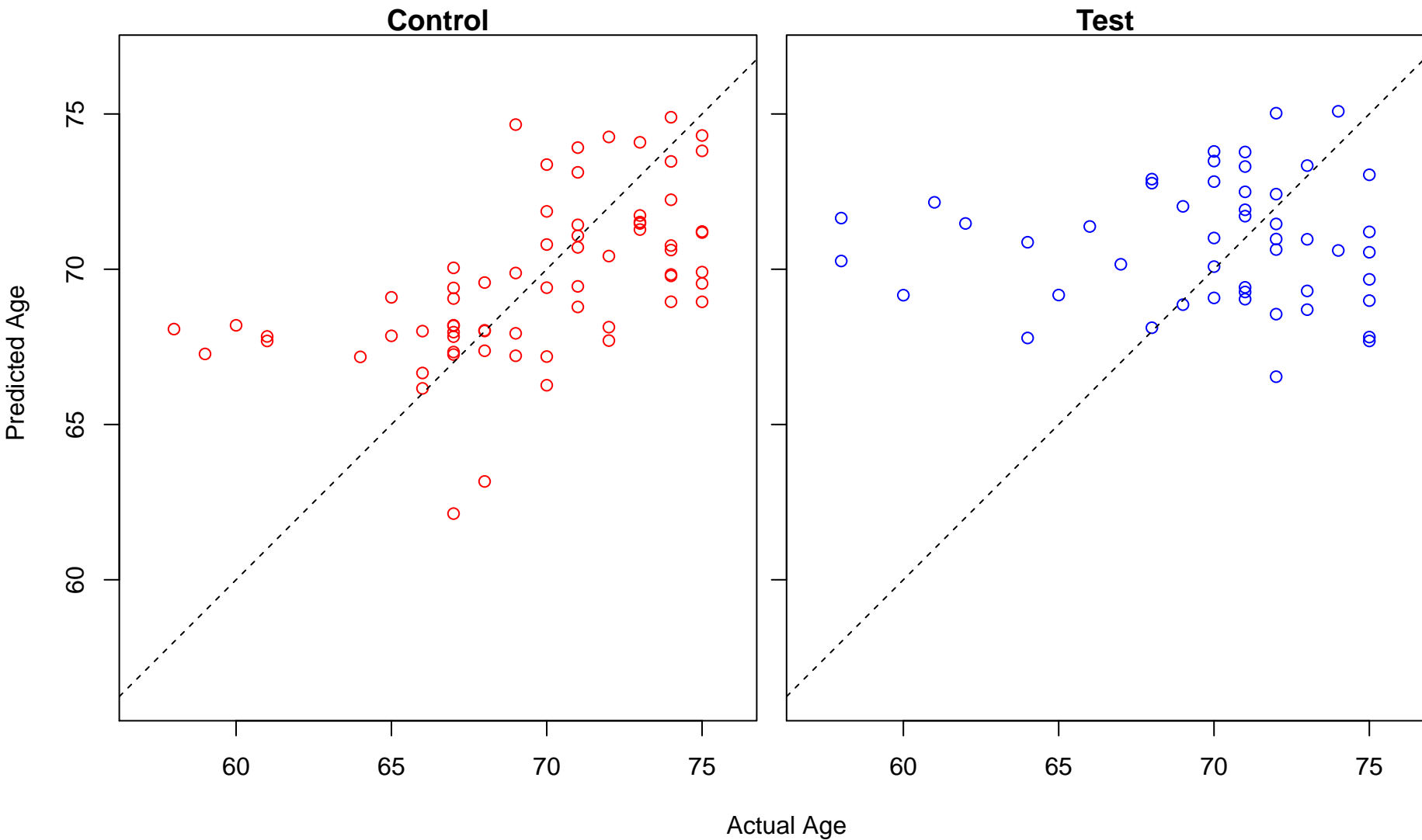
negative regulation of cell projection organization (Score: 0.859430)



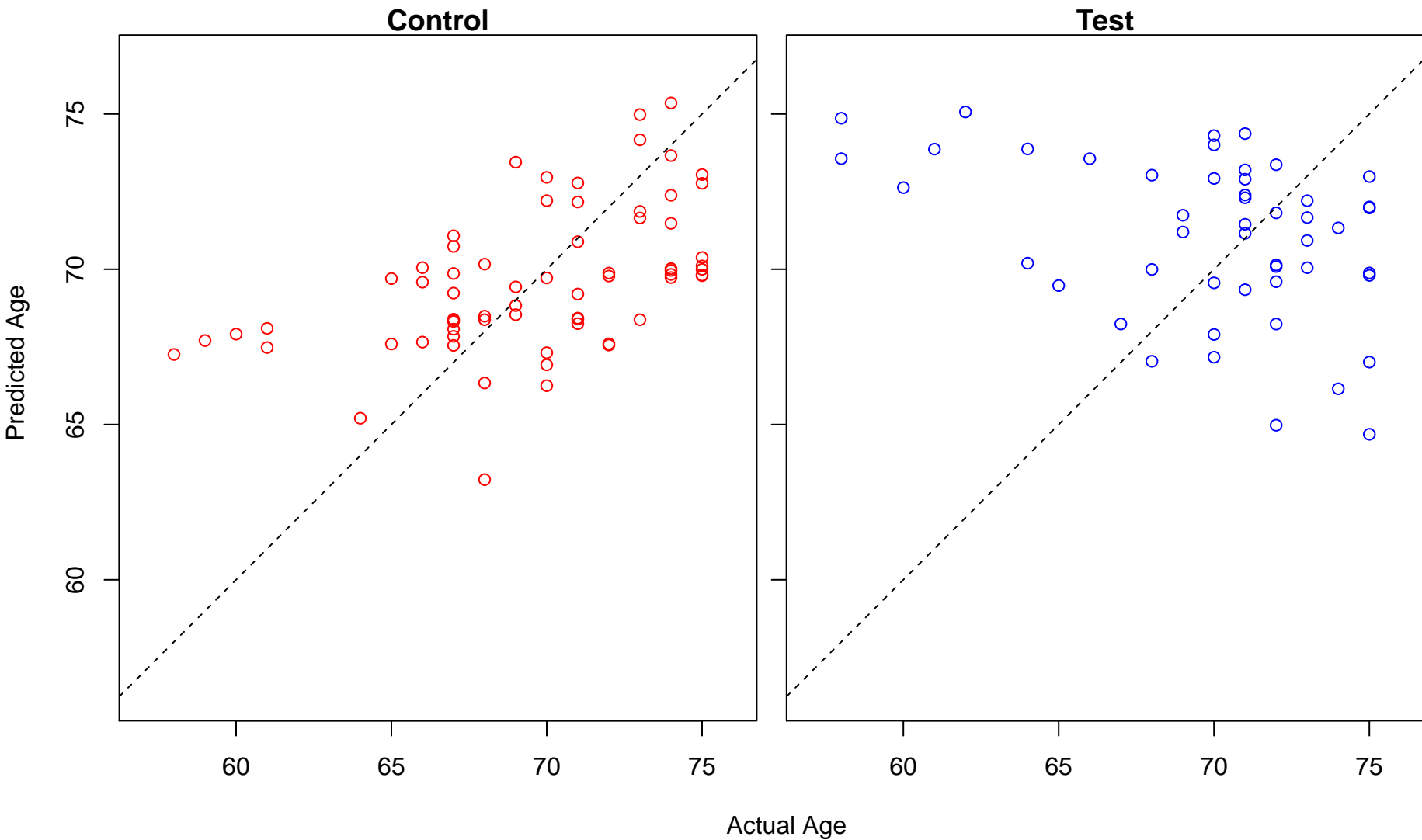
regulation of cardiac muscle tissue development (Score: 0.858928)



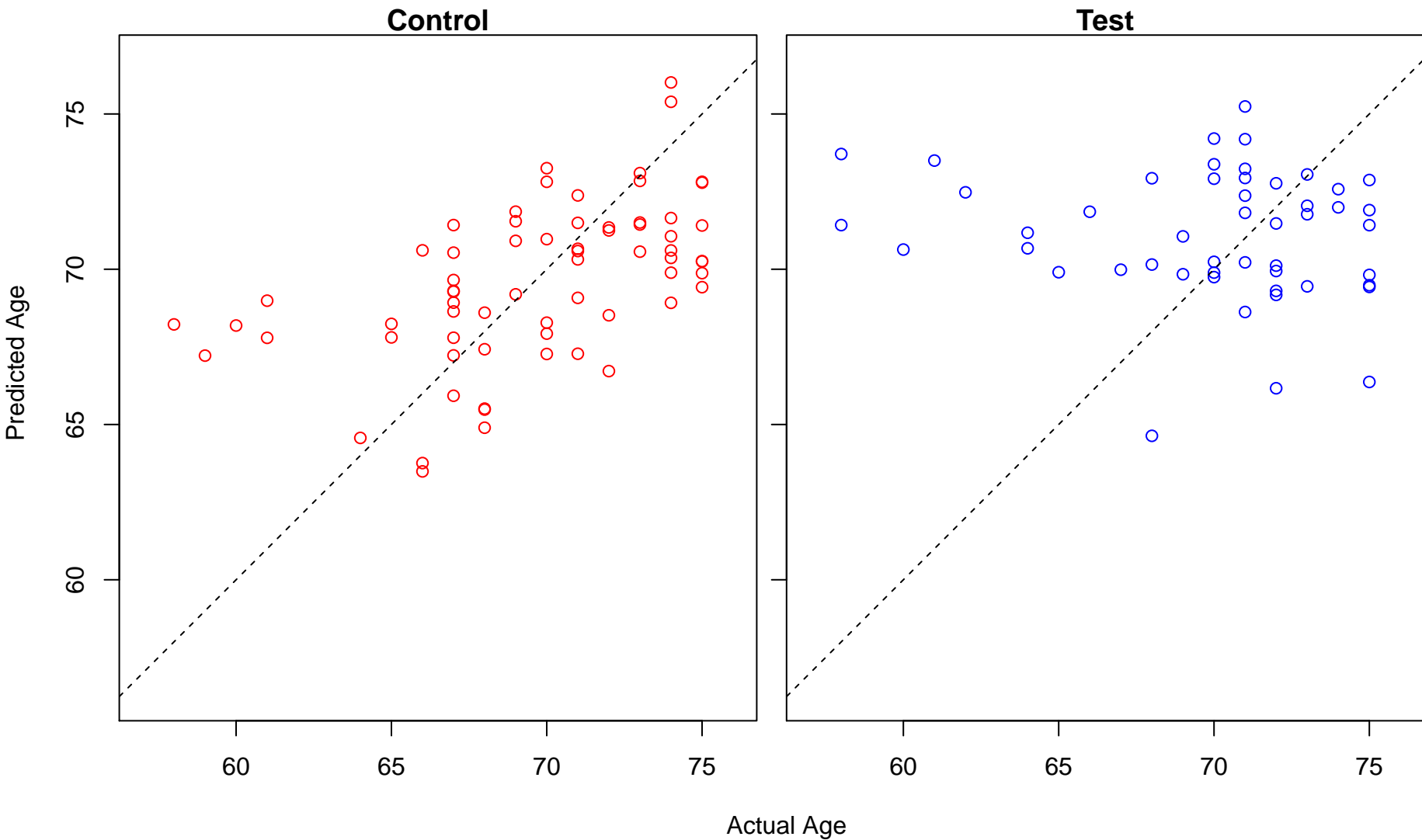
bile acid biosynthetic process (Score: 0.858801)



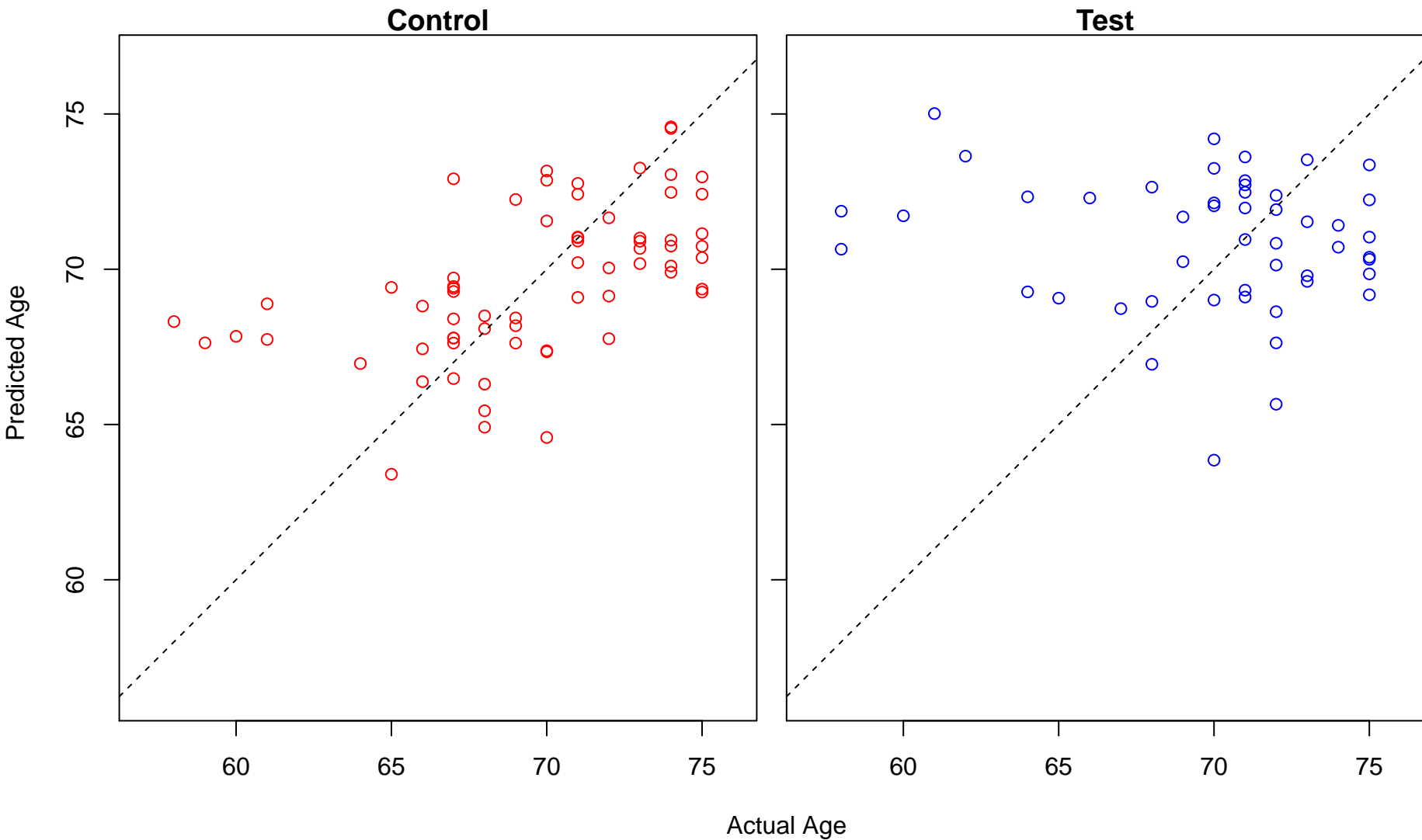
negative regulation of protein oligomerization (Score: 0.858800)



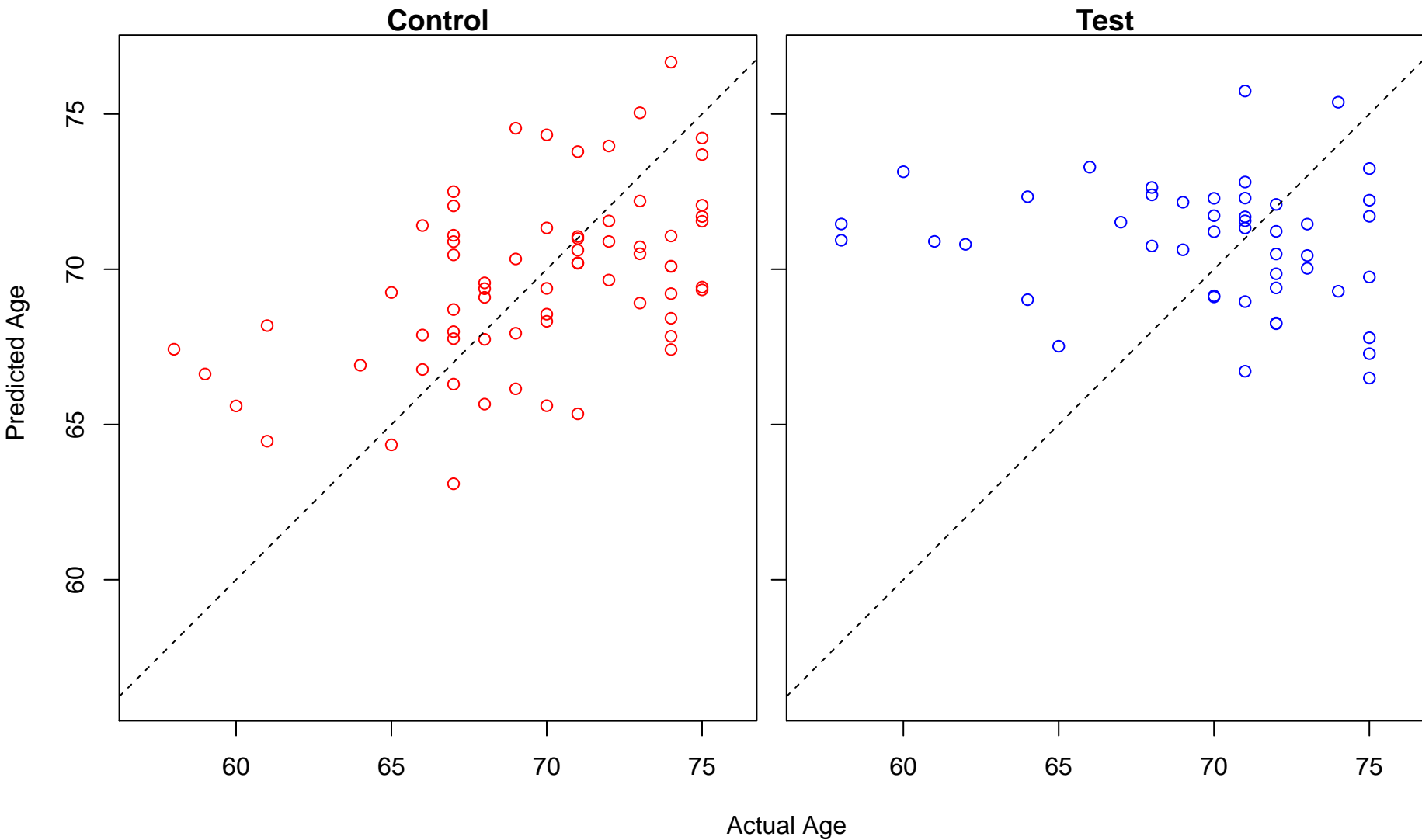
striated muscle adaptation (Score: 0.858733)



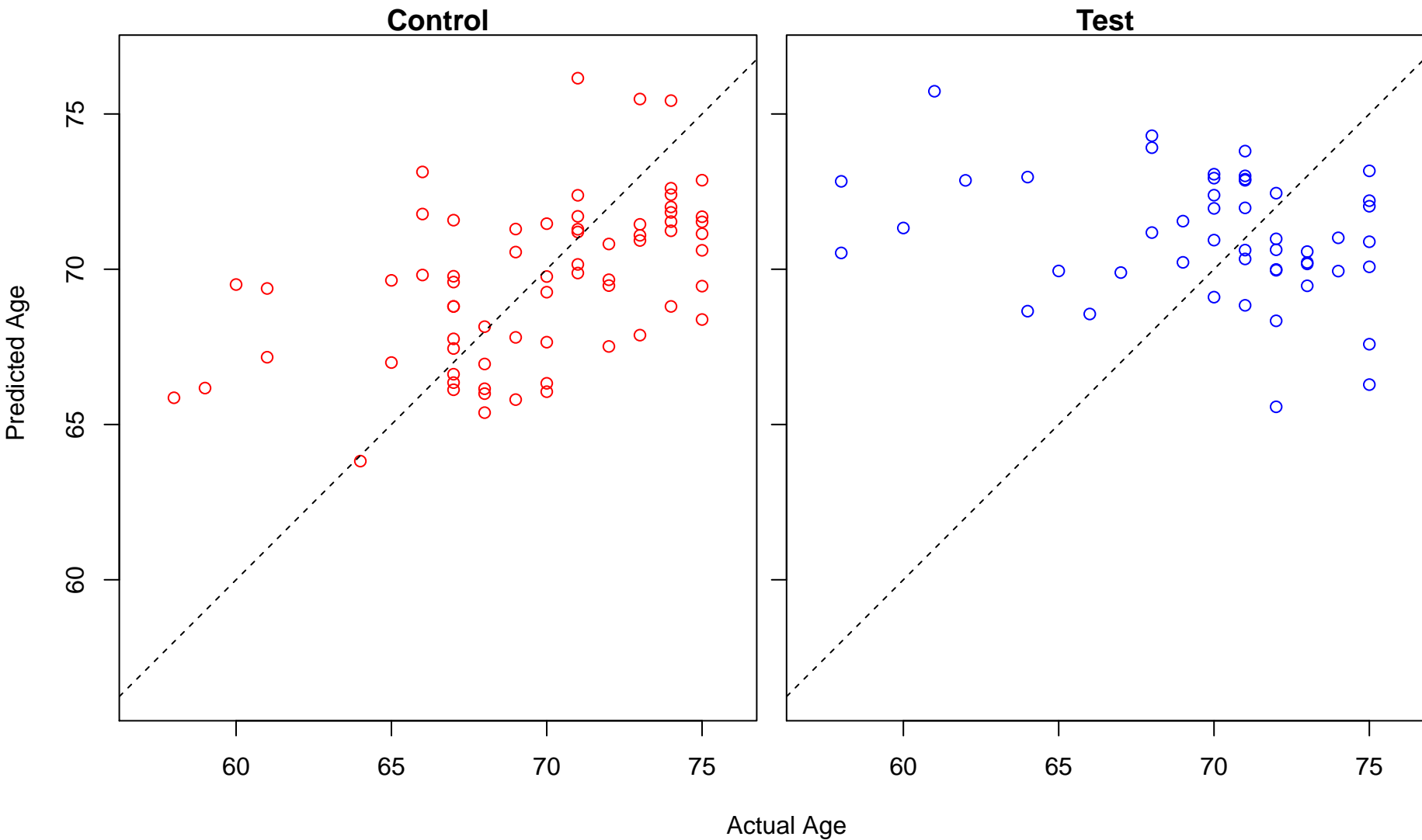
T cell chemotaxis (Score: 0.858710)



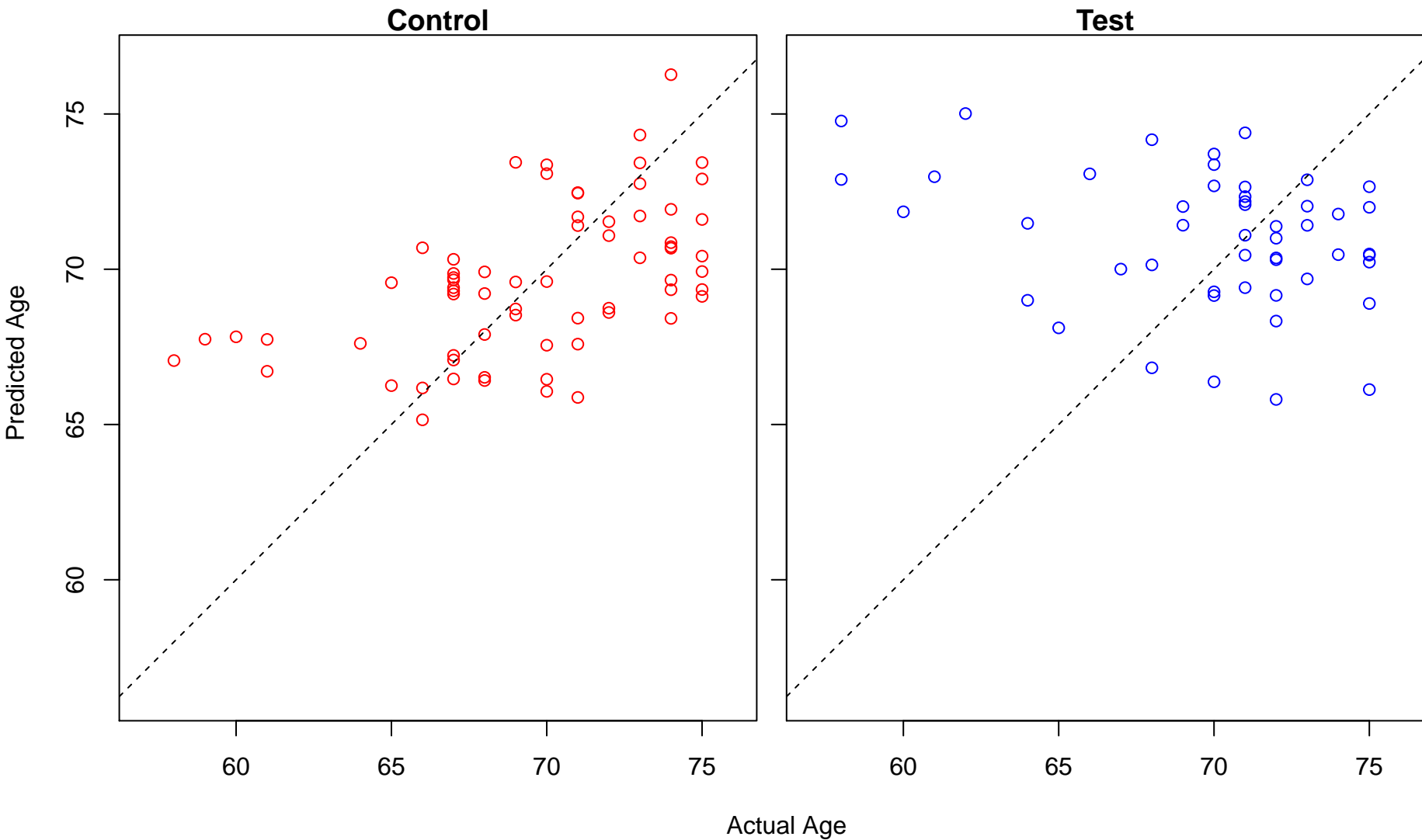
regulation of cardiac muscle cell membrane potential (Score: 0.858679)



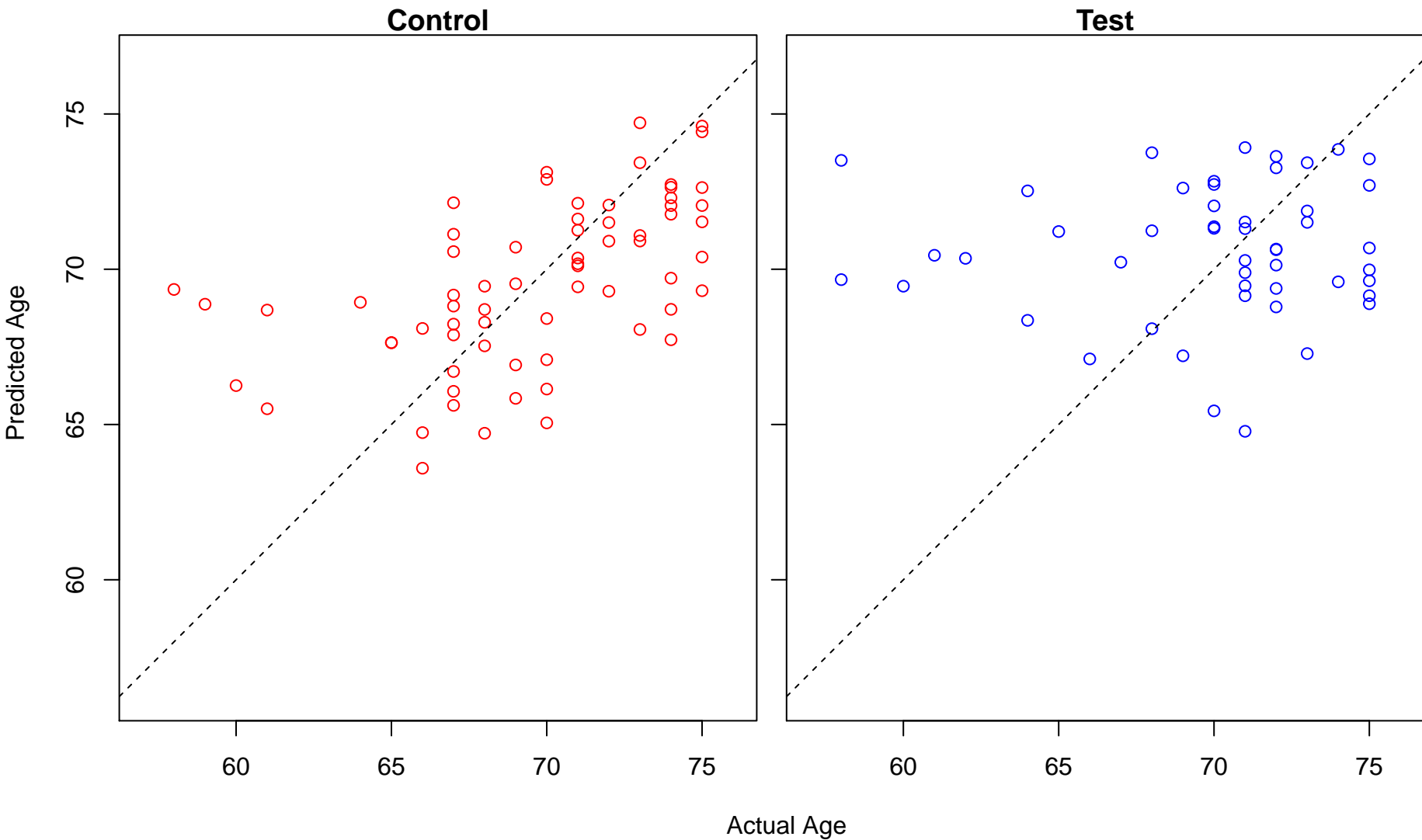
valine metabolic process (Score: 0.858391)



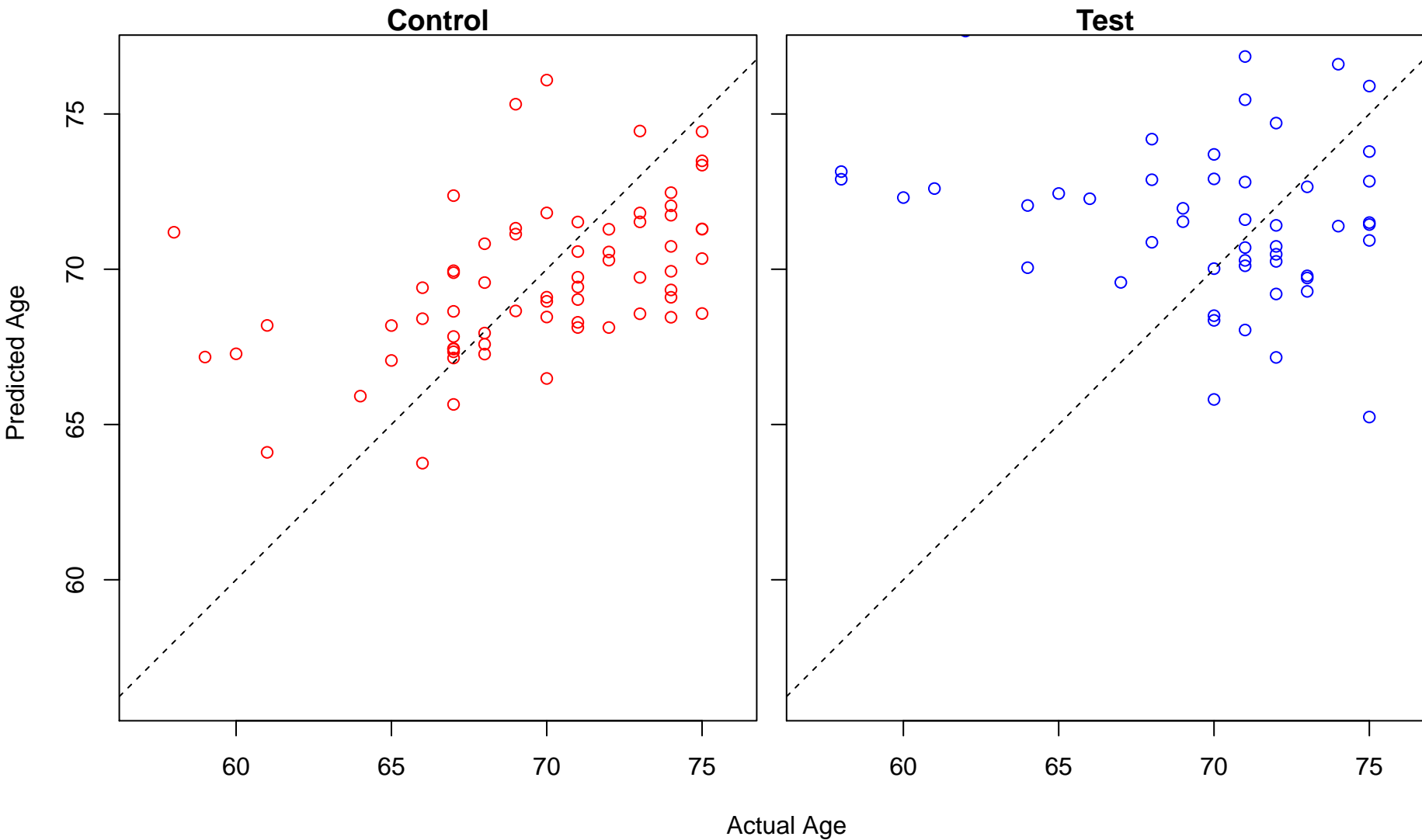
positive regulation of vascular endothelial growth factor receptor signaling pathway (Score: 0.85825)



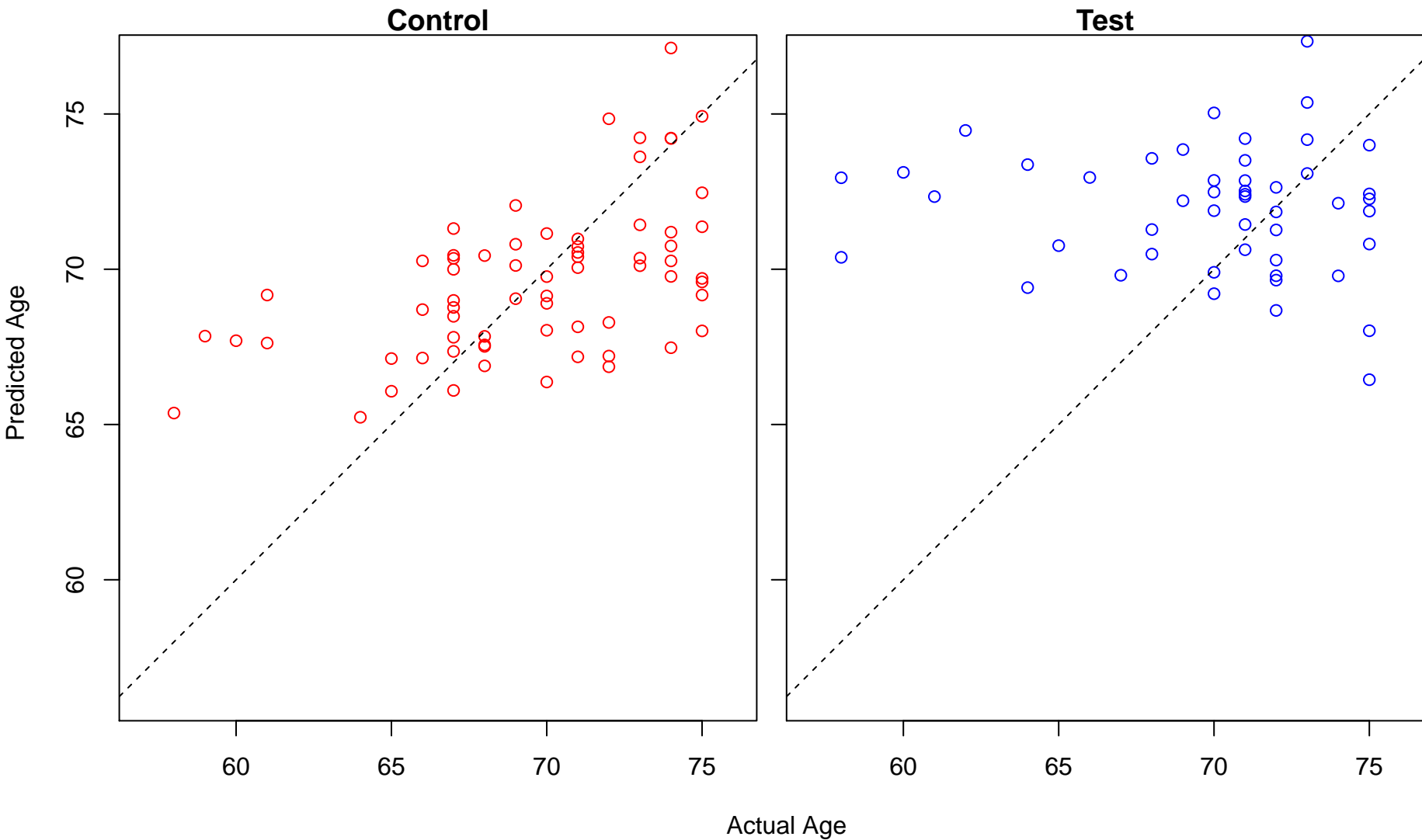
negative regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway (Score: 0.8)



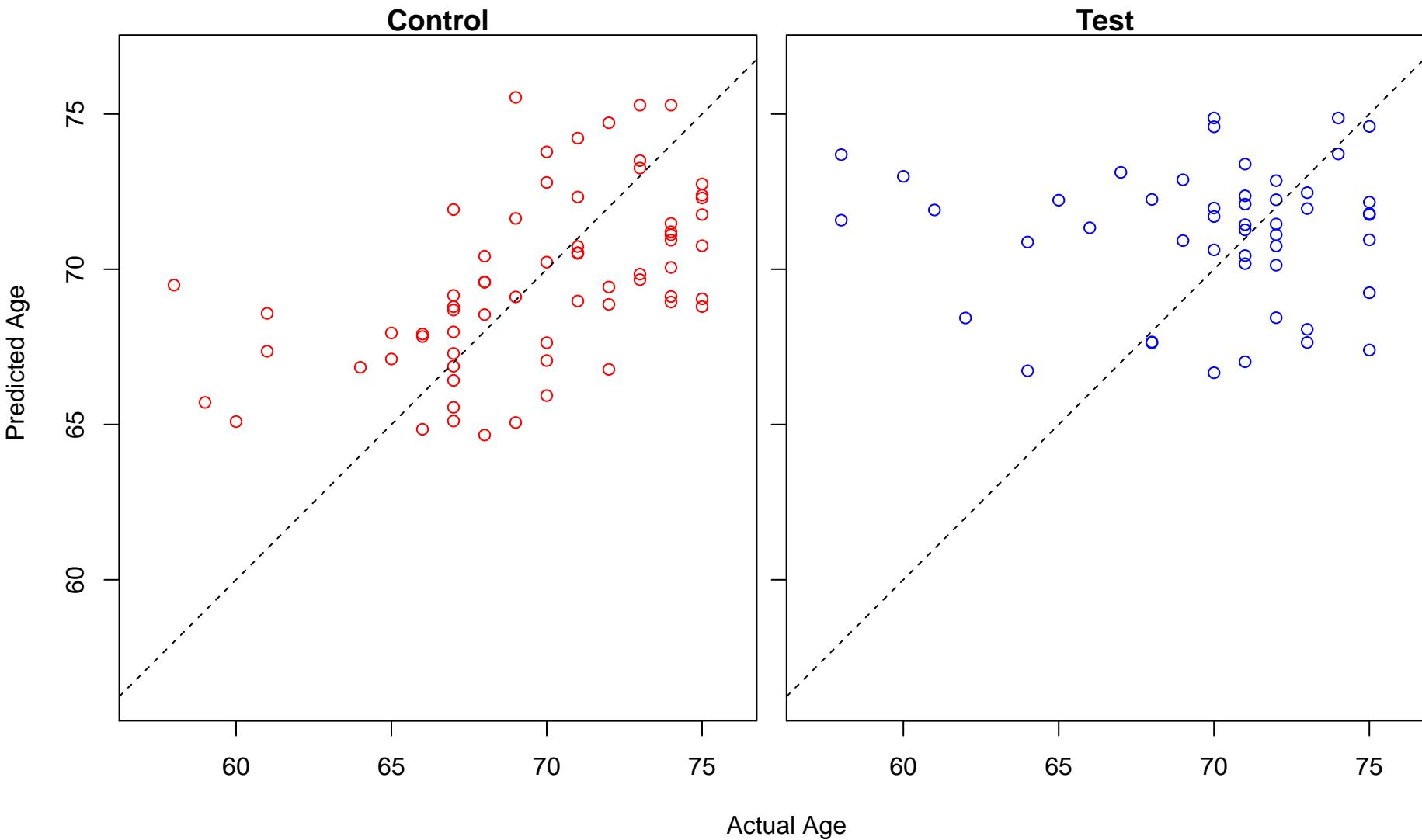
positive regulation by host of viral genome replication (Score: 0.857876)



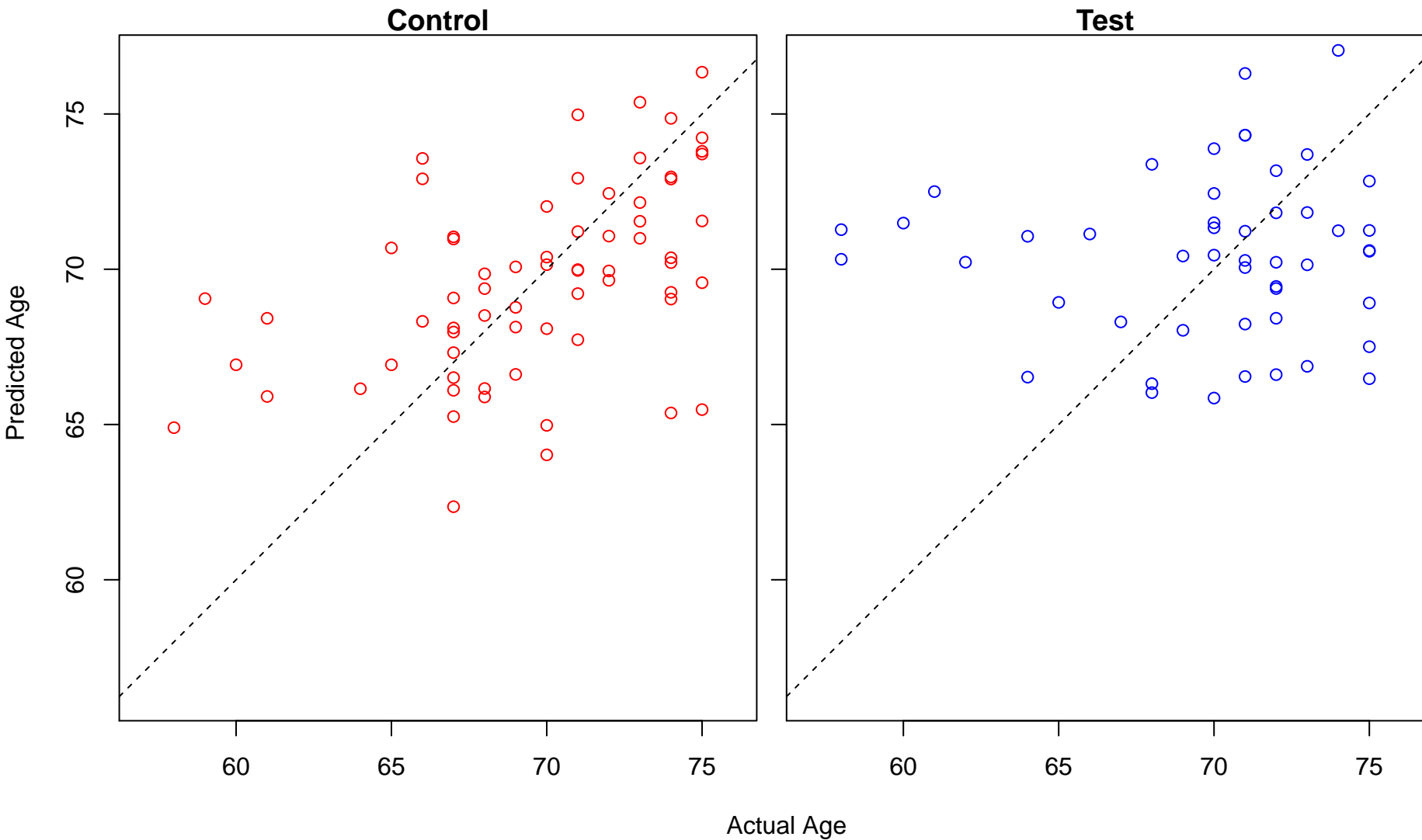
regulation of plasma lipoprotein particle levels (Score: 0.857849)



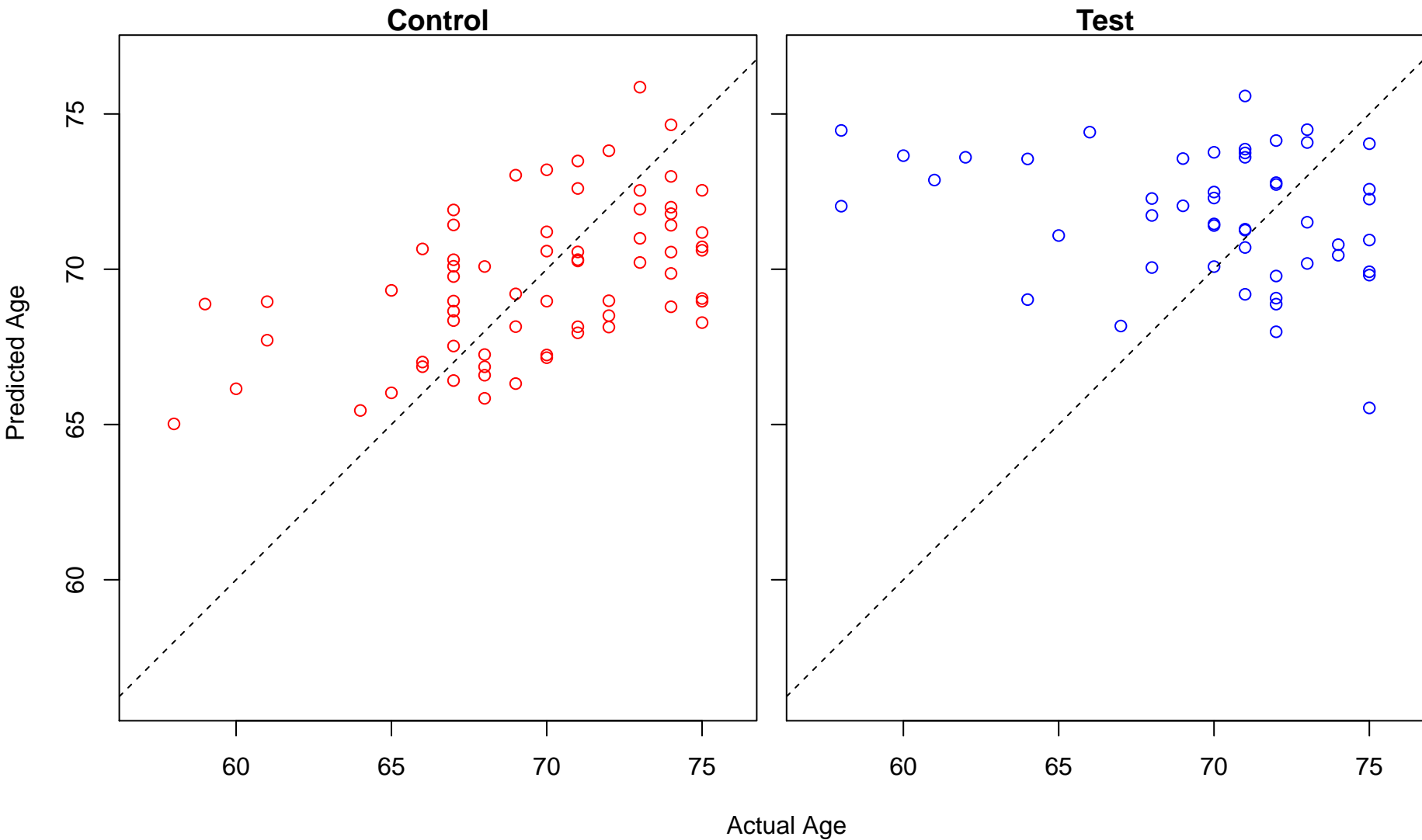
cell recognition (Score: 0.857718)



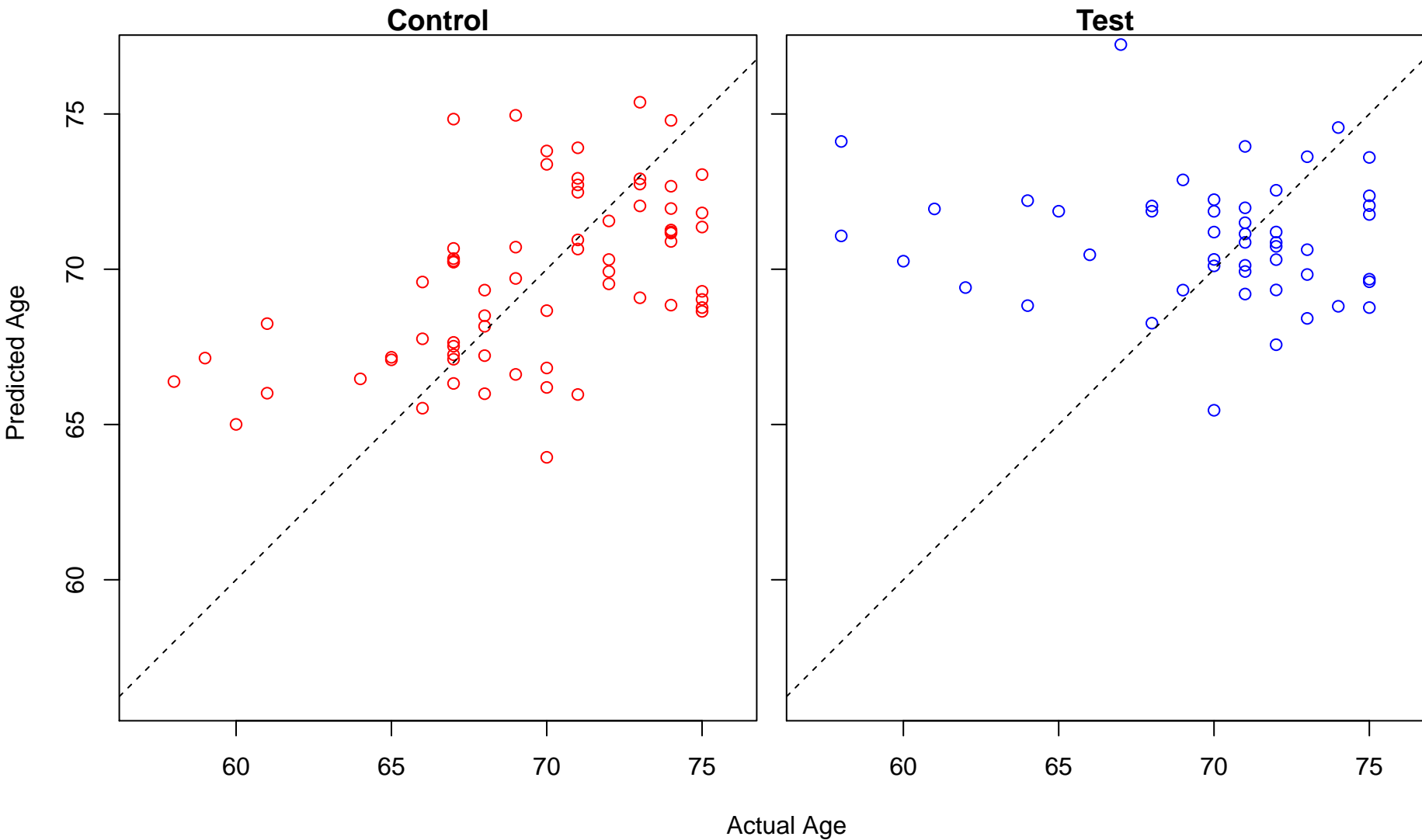
regulation of synapse assembly (Score: 0.857696)



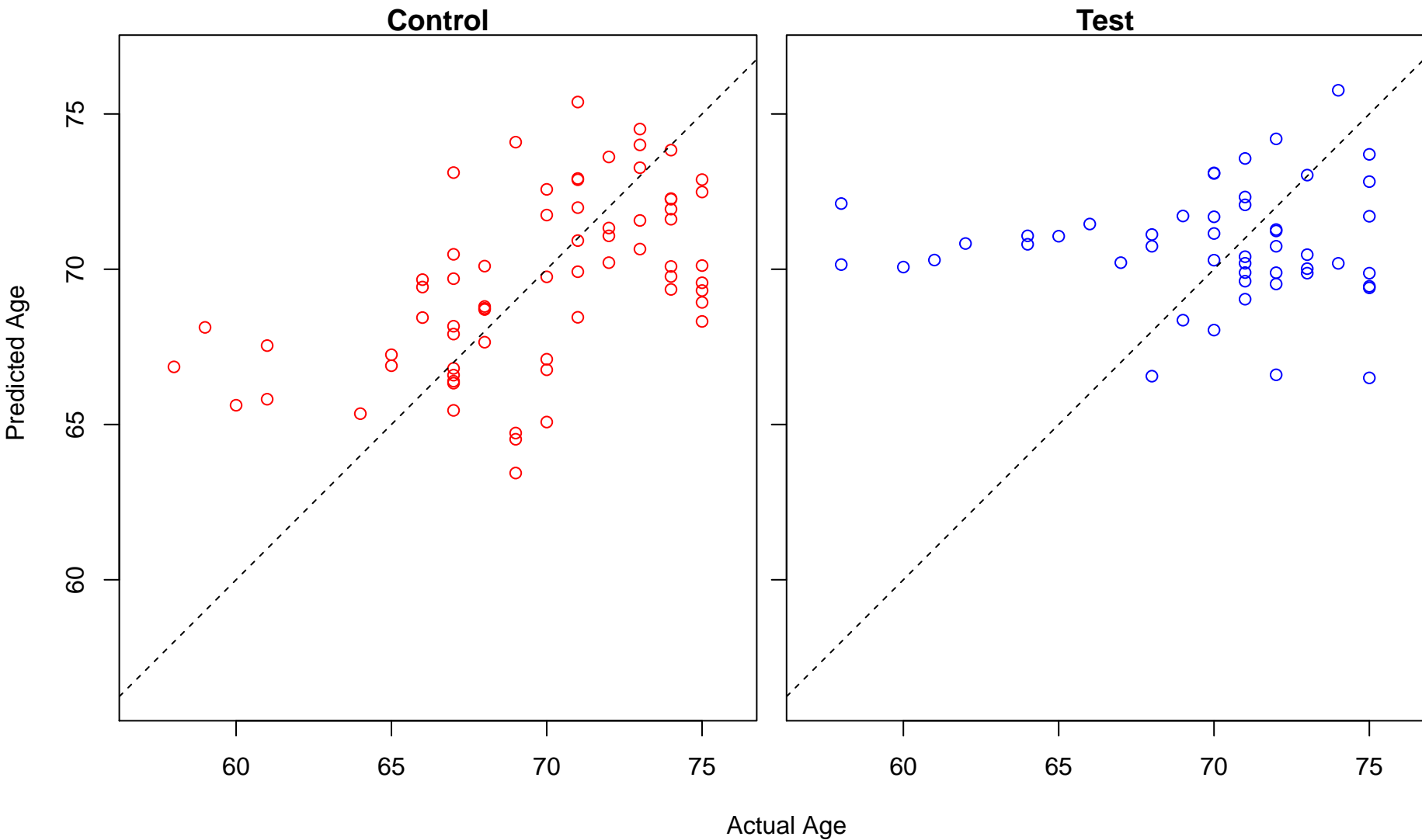
cardiac cell development (Score: 0.857686)



nucleobase biosynthetic process (Score: 0.857665)

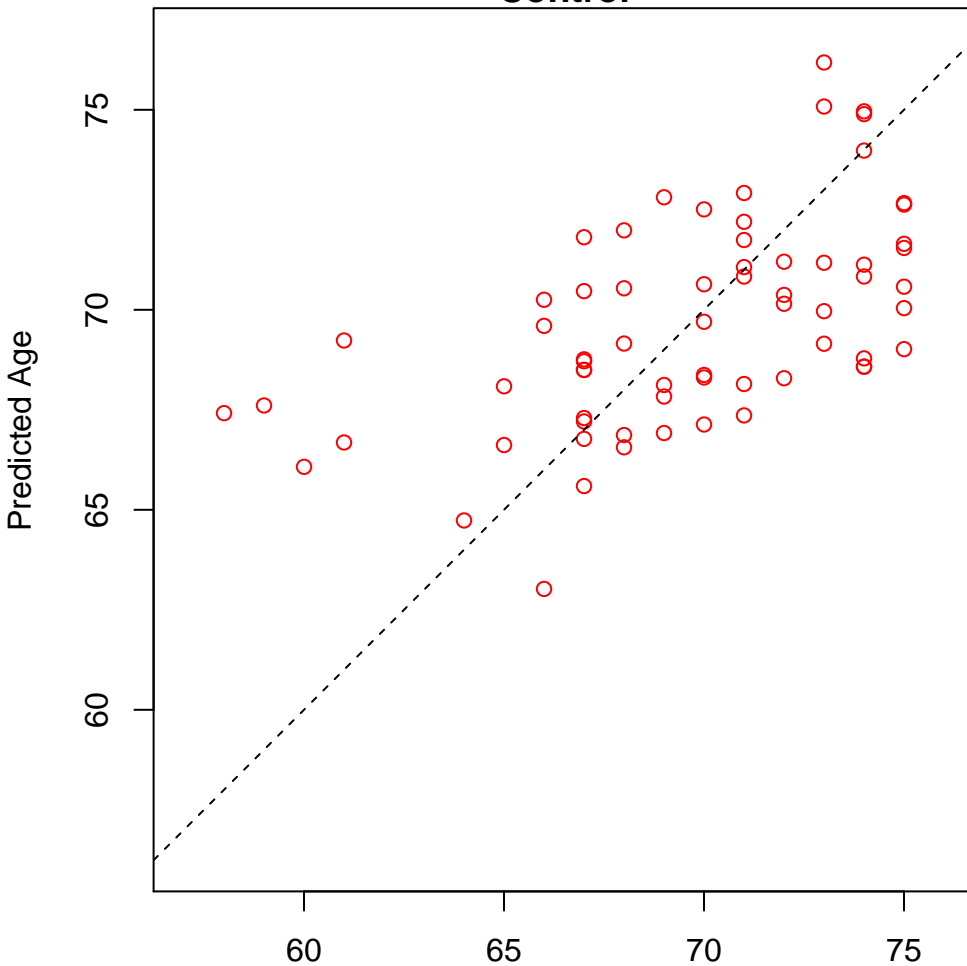


Golgi ribbon formation (Score: 0.857360)

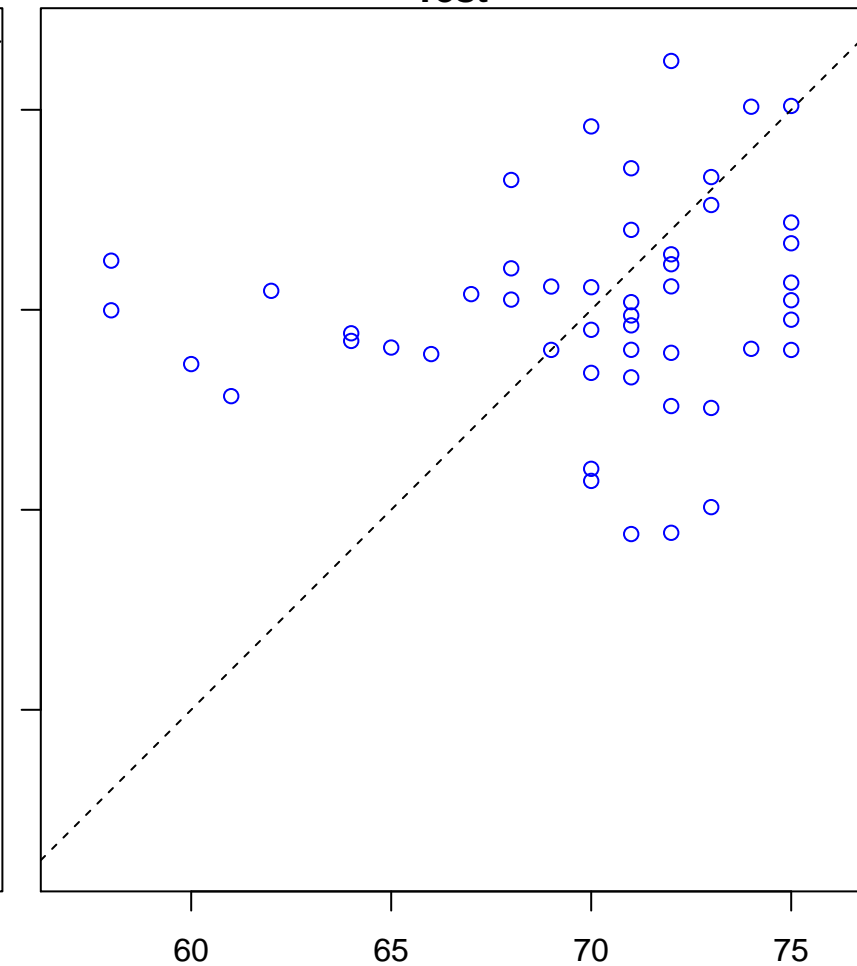


regulation of phospholipase A2 activity (Score: 0.857217)

Control

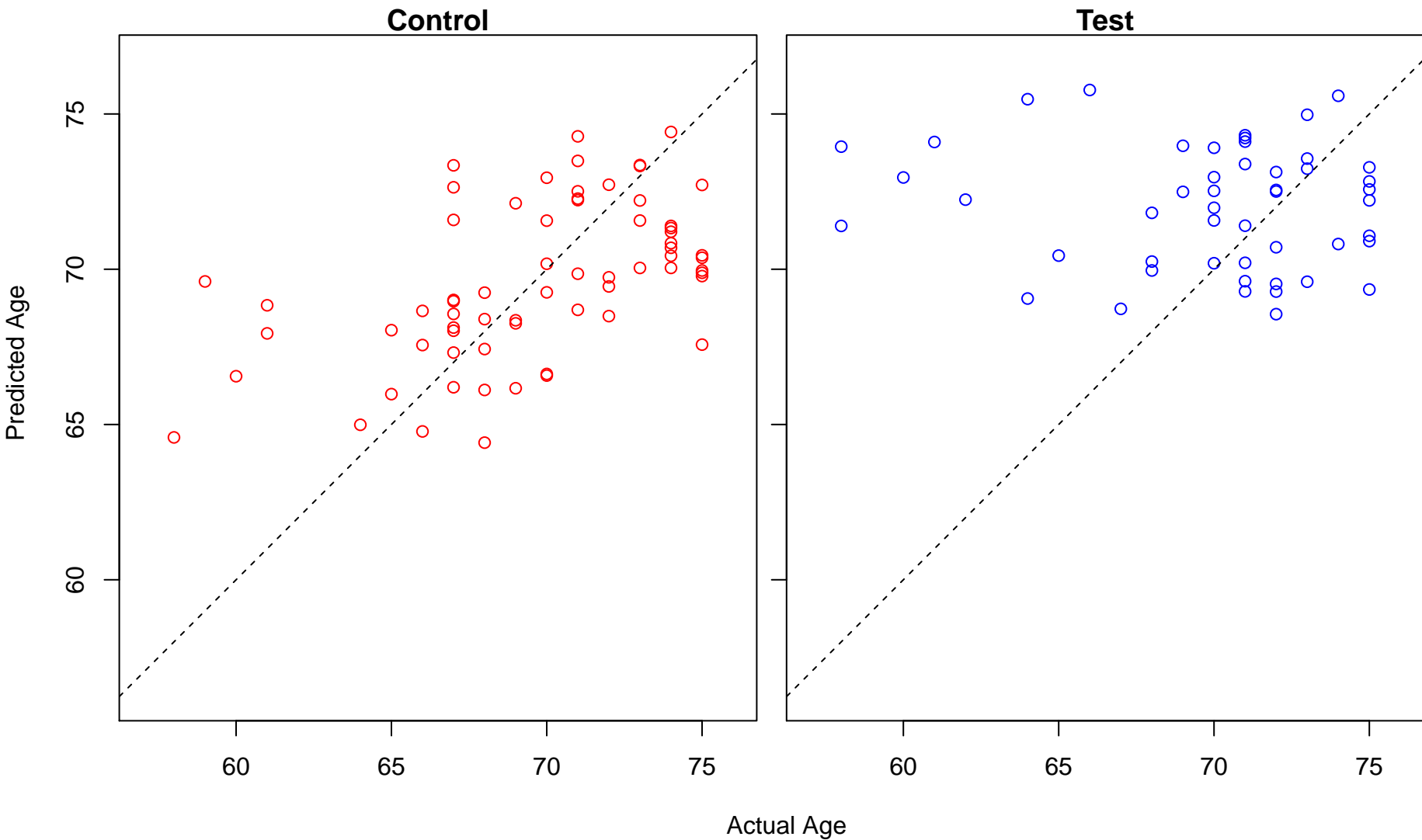


Test

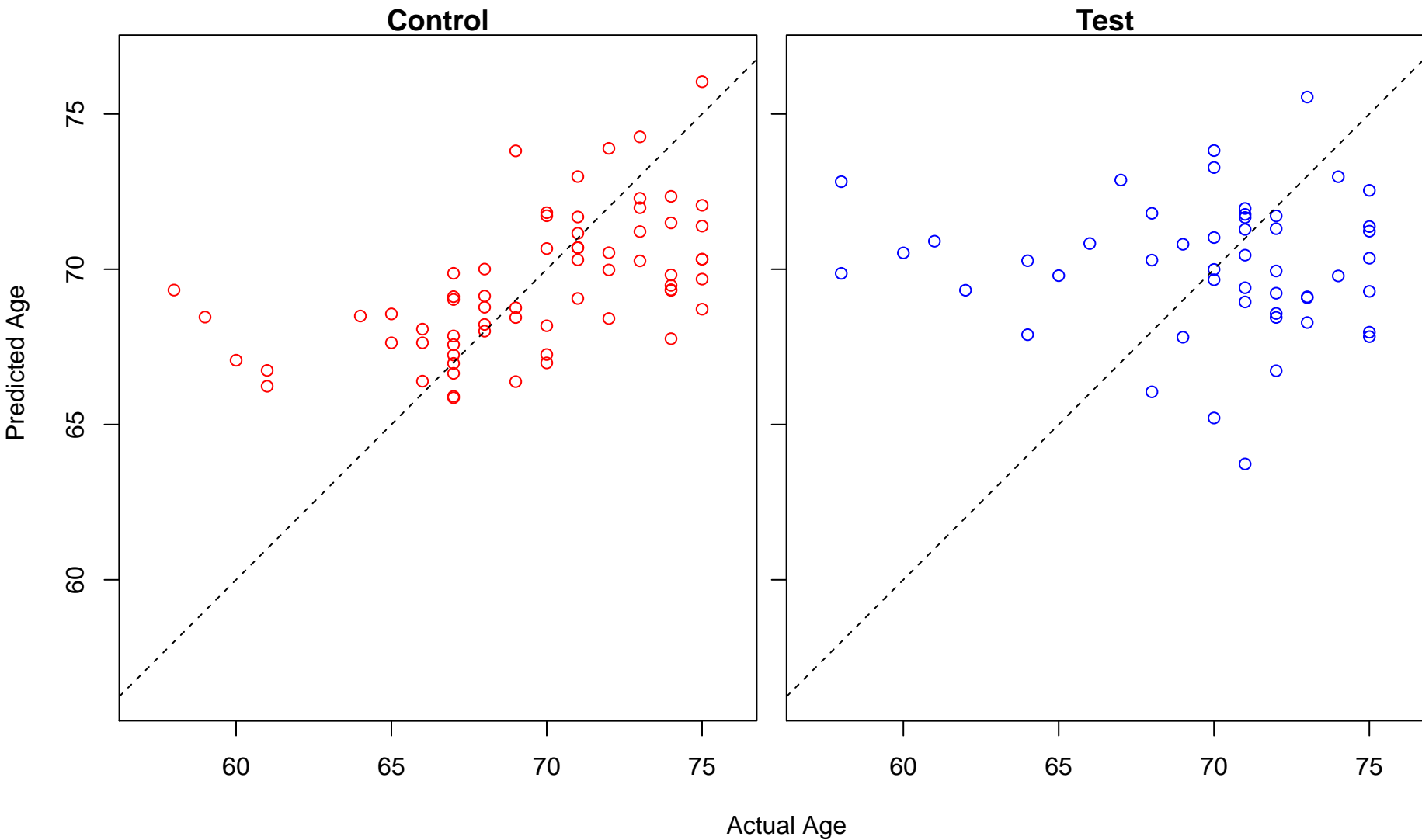


Actual Age

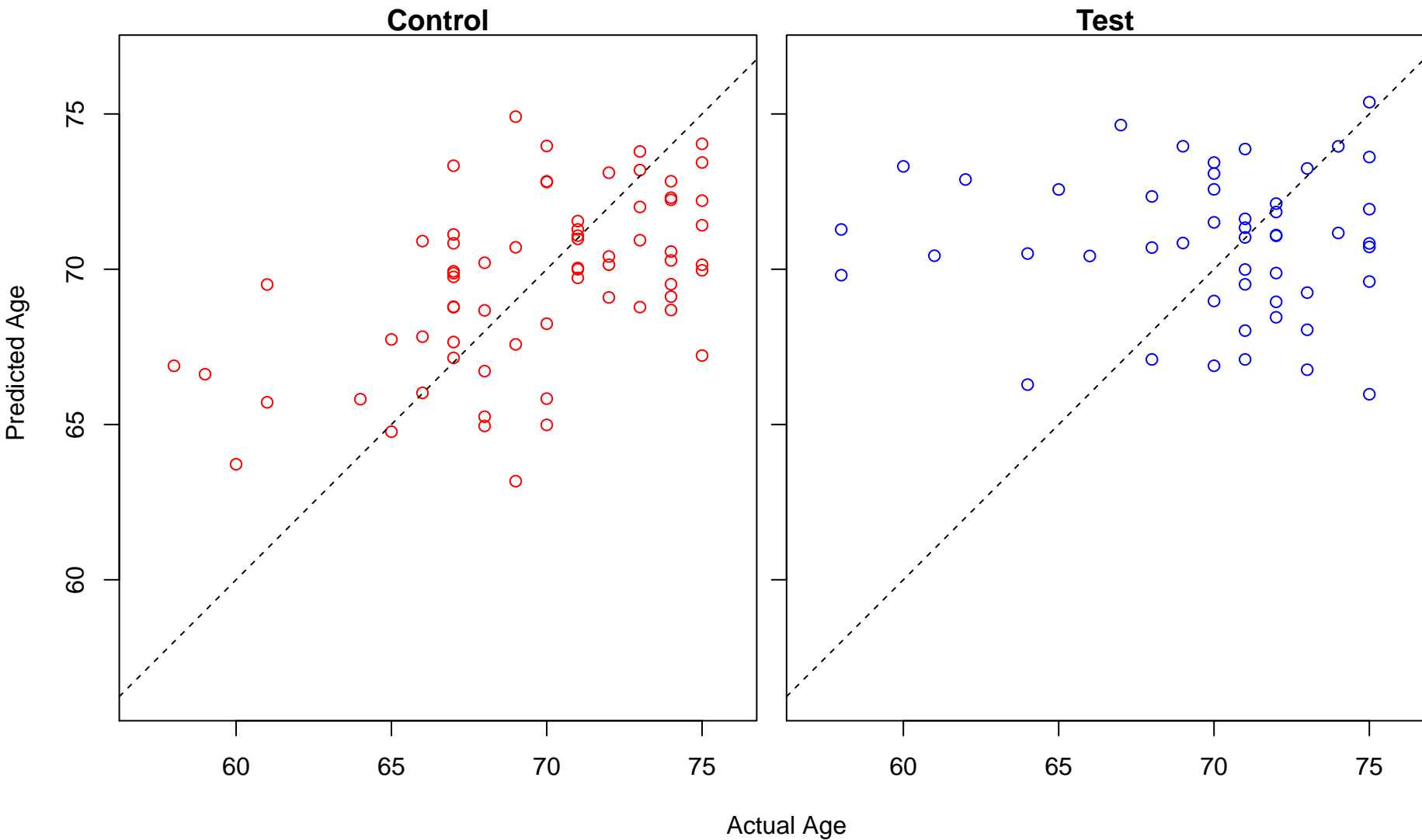
regulation of heart growth (Score: 0.856795)



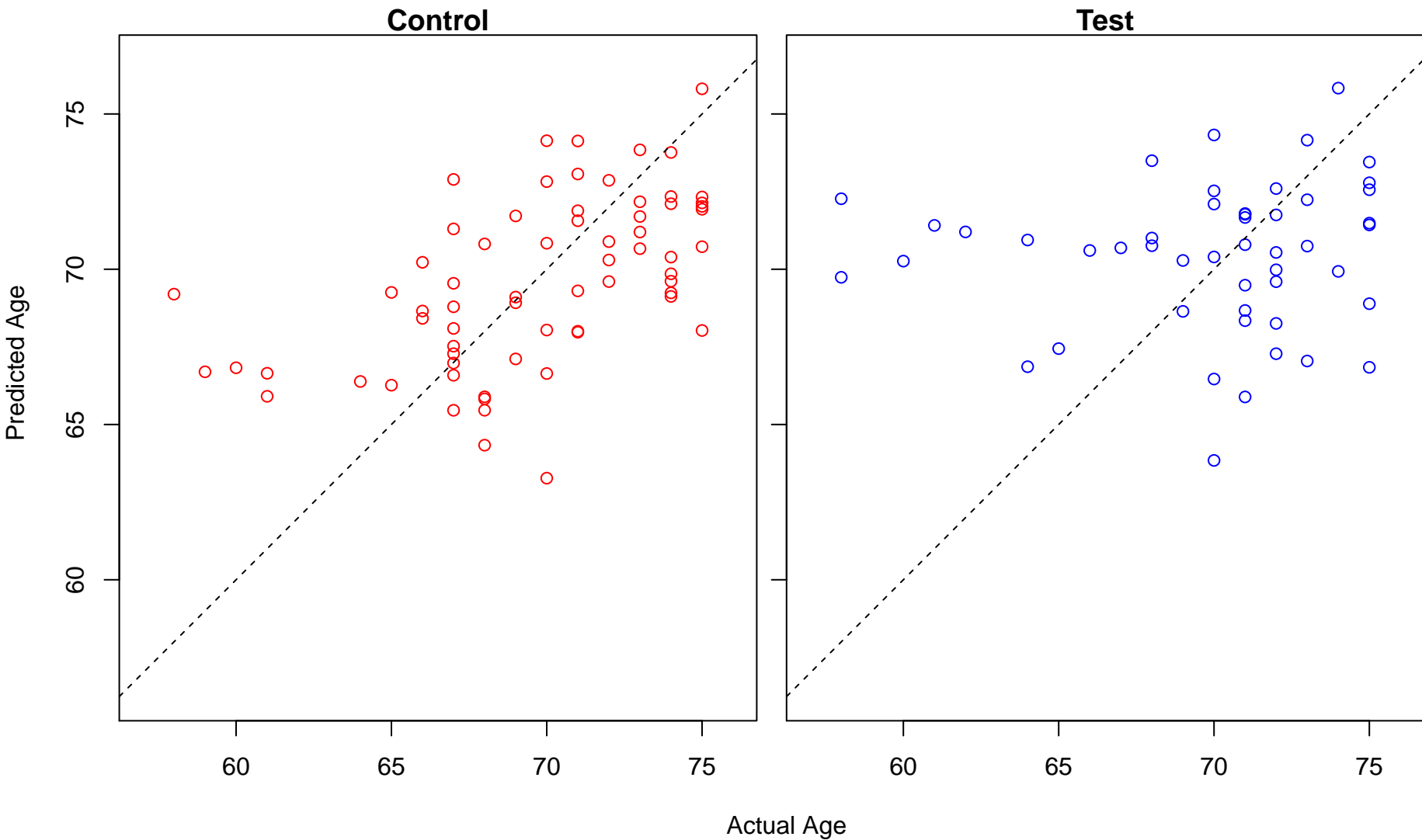
negative regulation of dendrite morphogenesis (Score: 0.856638)



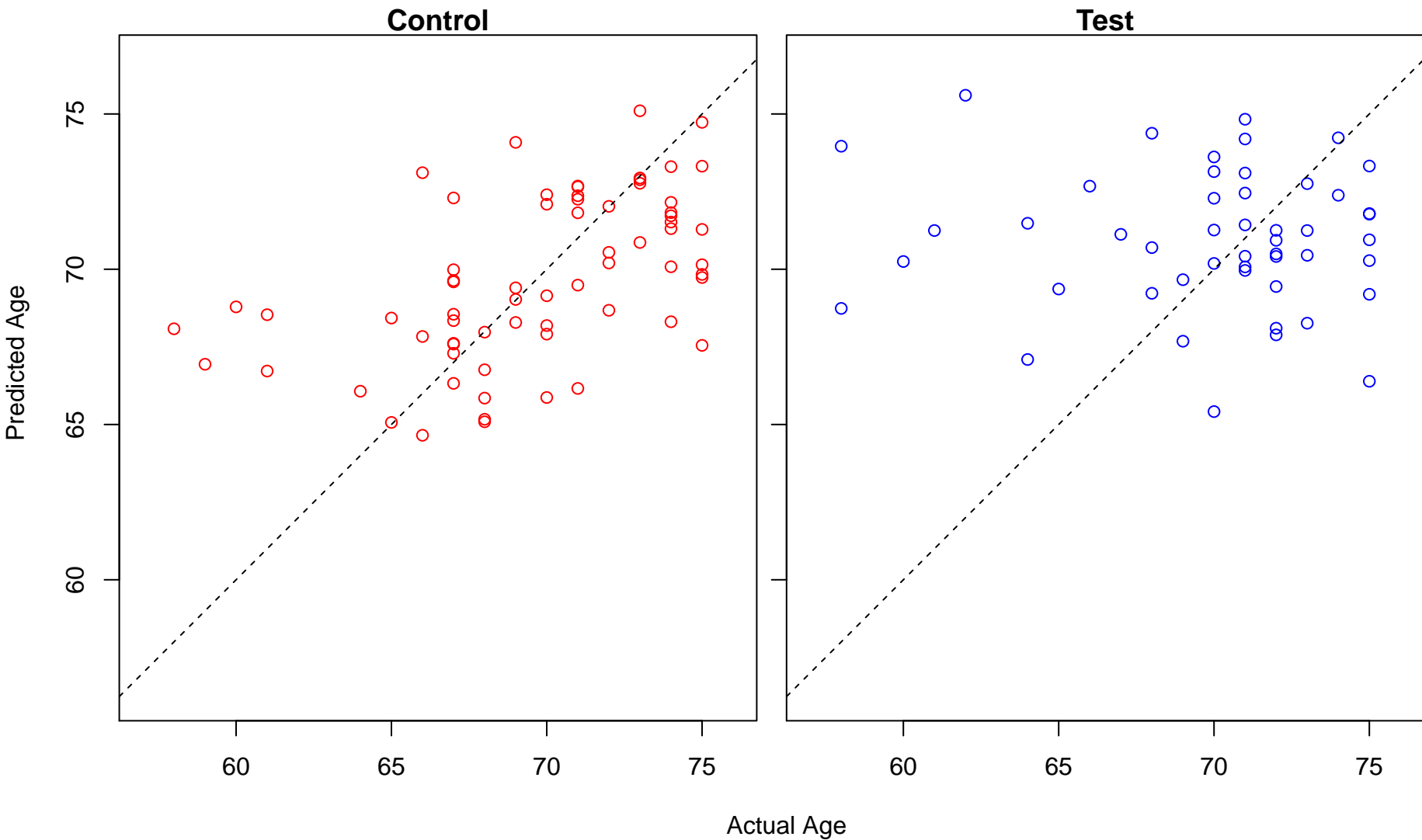
positive regulation of phospholipid metabolic process (Score: 0.855955)



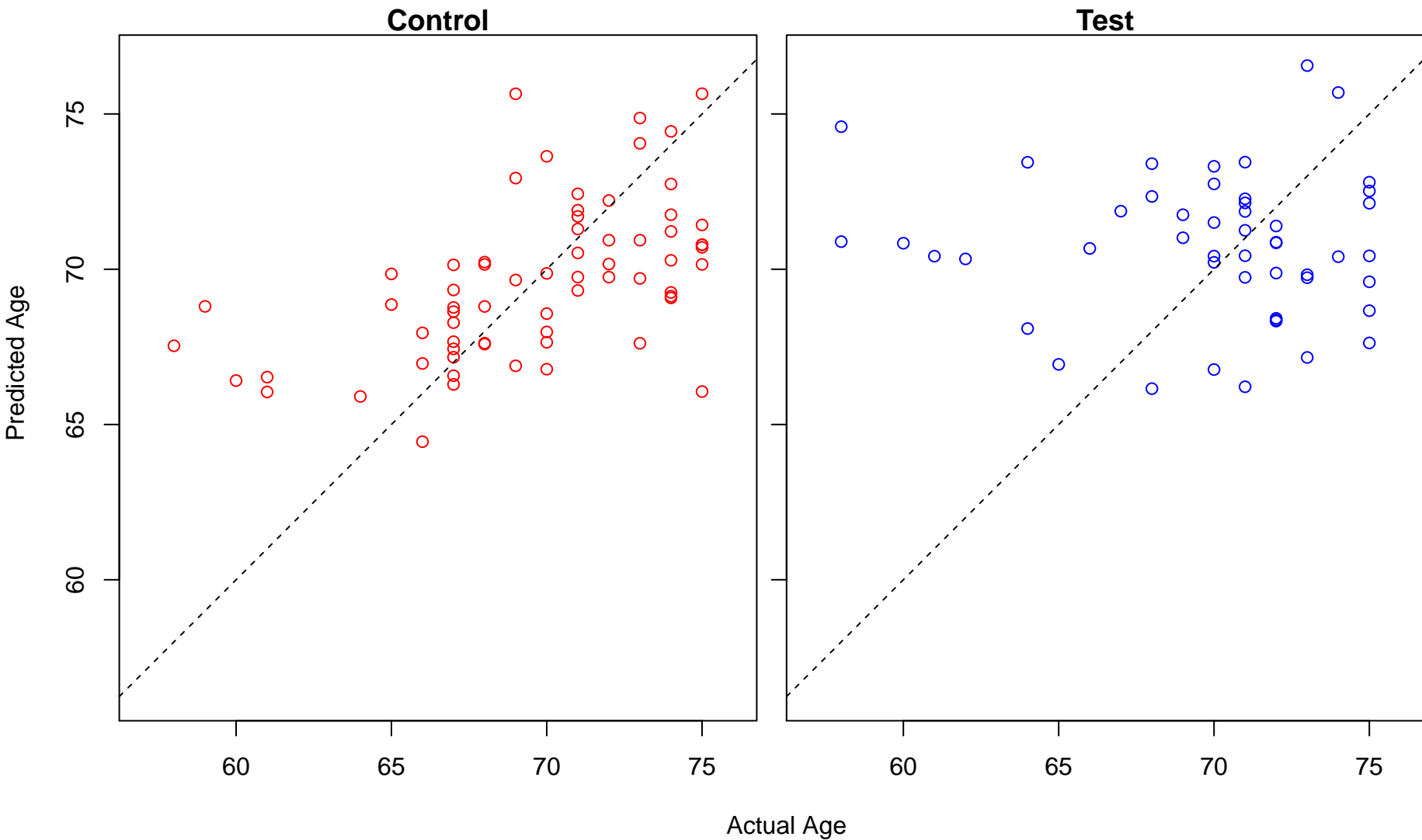
neural tube development (Score: 0.855942)



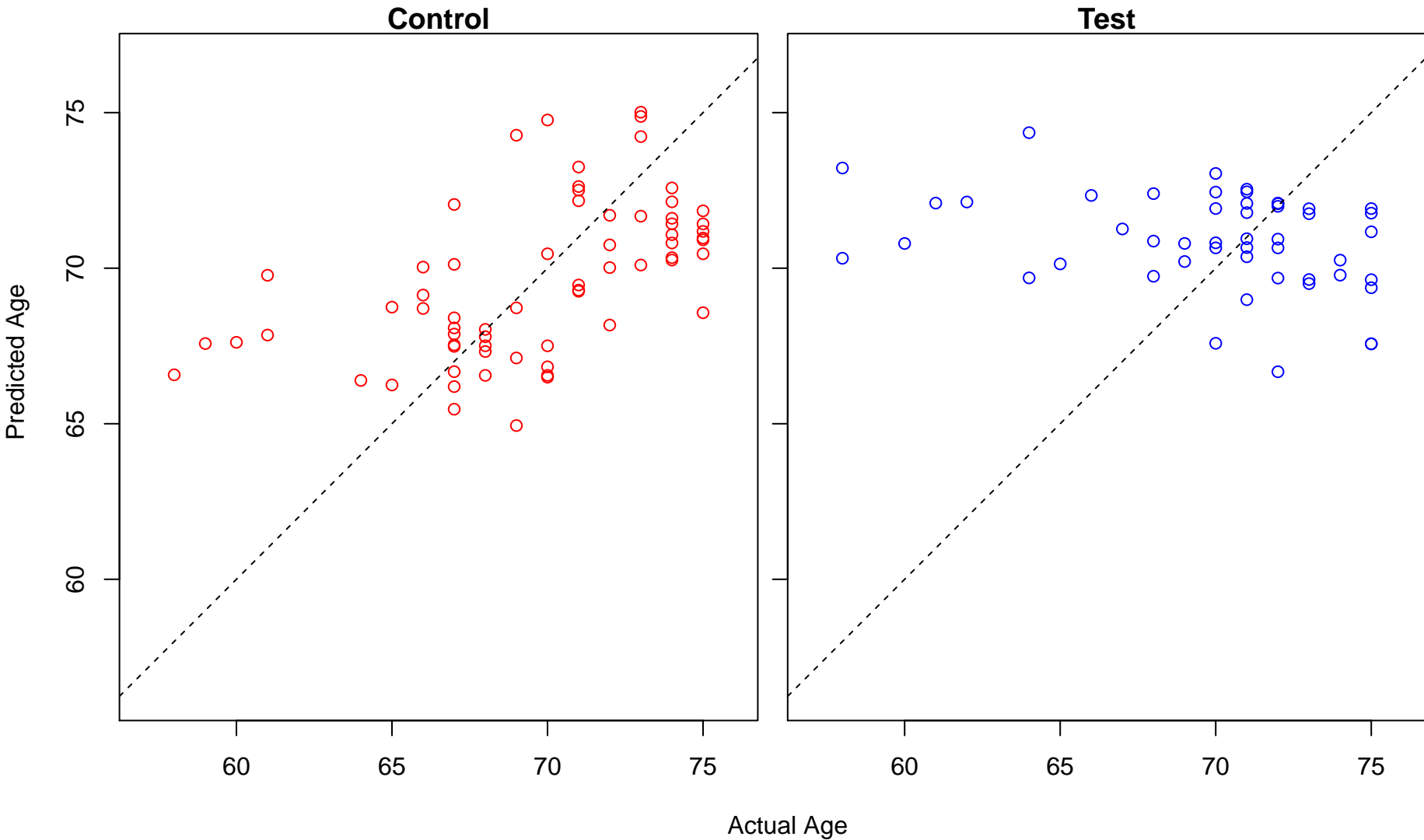
negative regulation by host of viral process (Score: 0.855784)



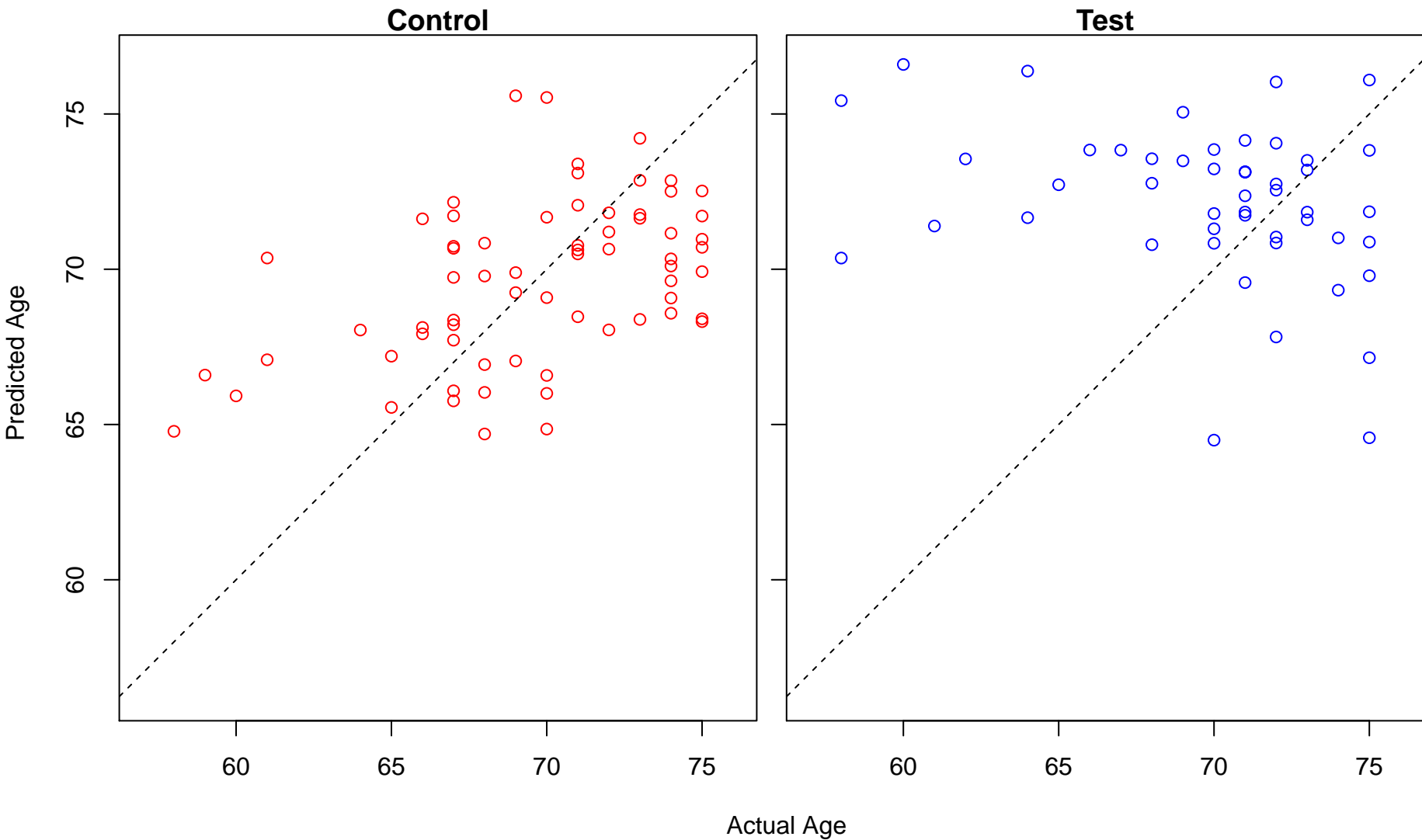
heparan sulfate proteoglycan biosynthetic process (Score: 0.855564)



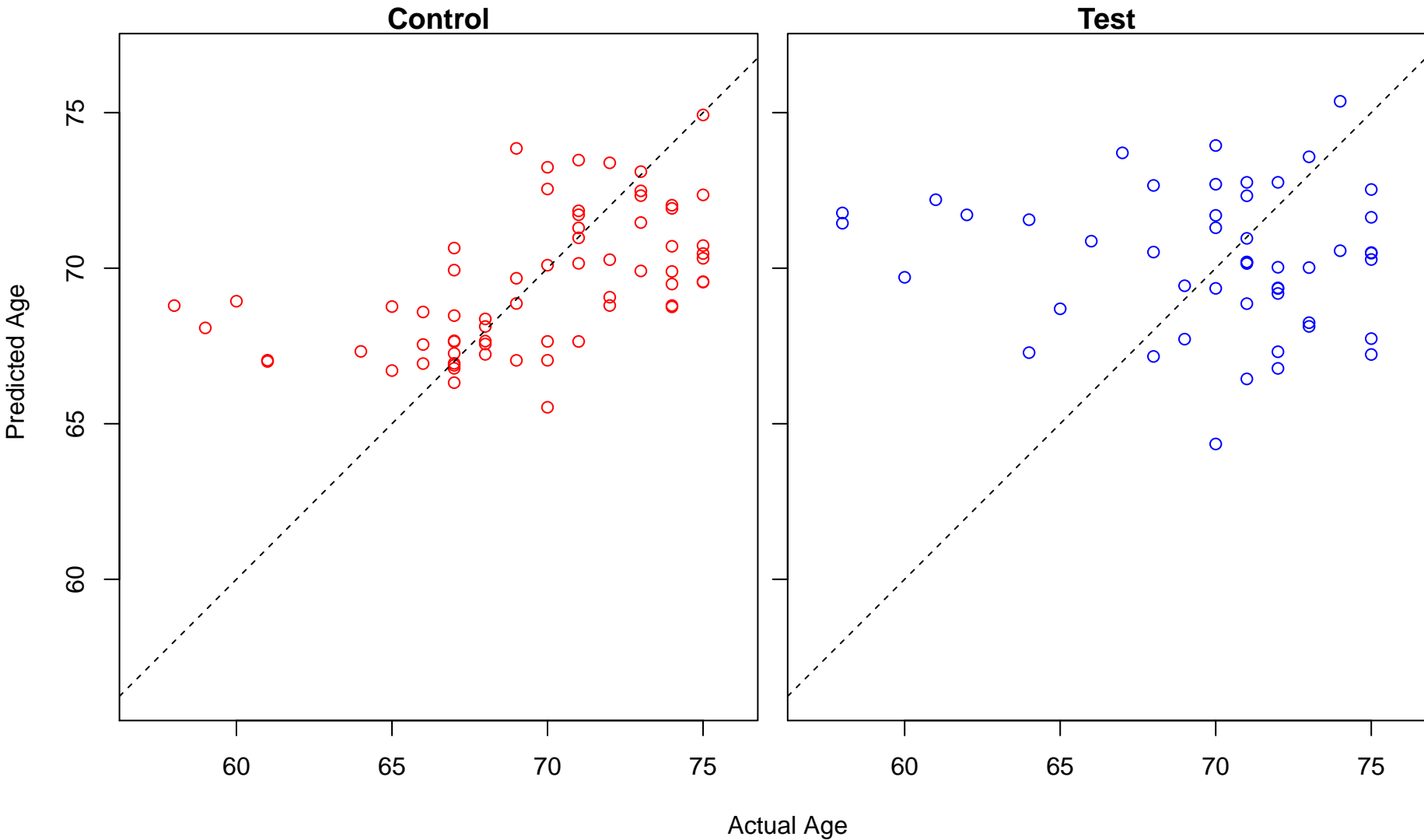
negative regulation of DNA binding (Score: 0.855467)



regulation of translational termination (Score: 0.855250)

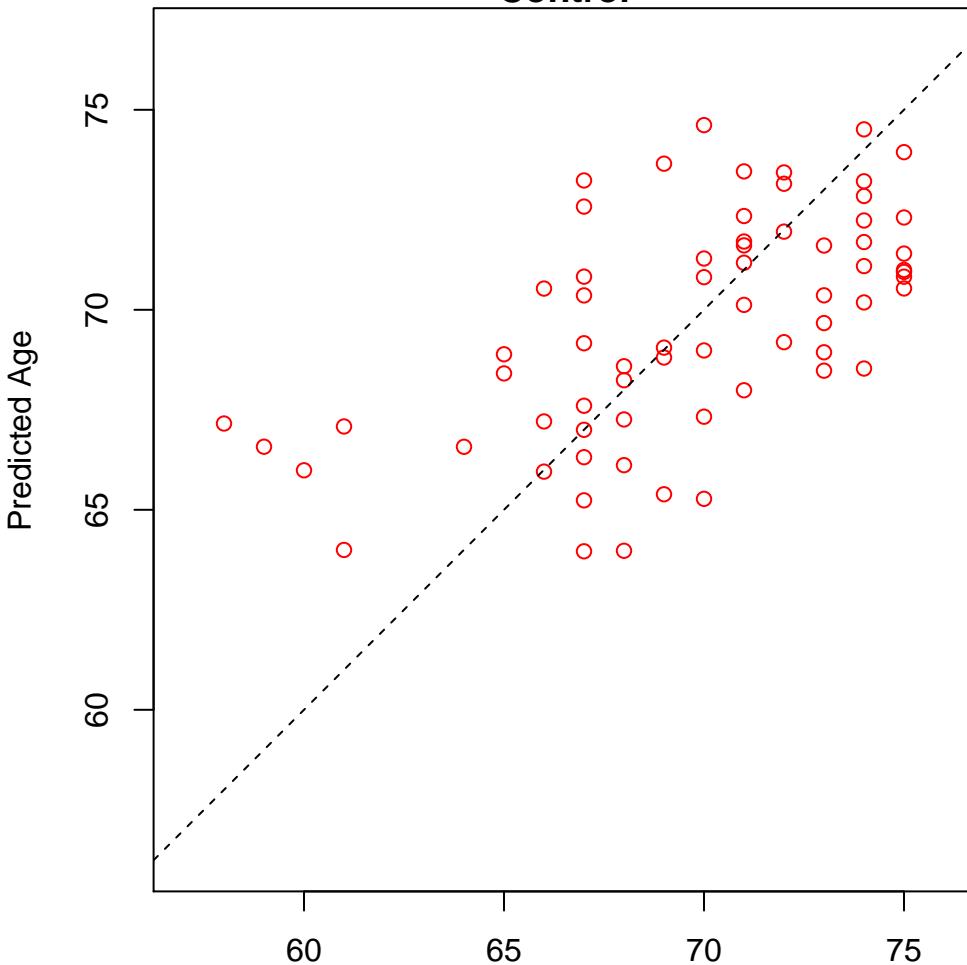


negative regulation of neuron differentiation (Score: 0.854784)

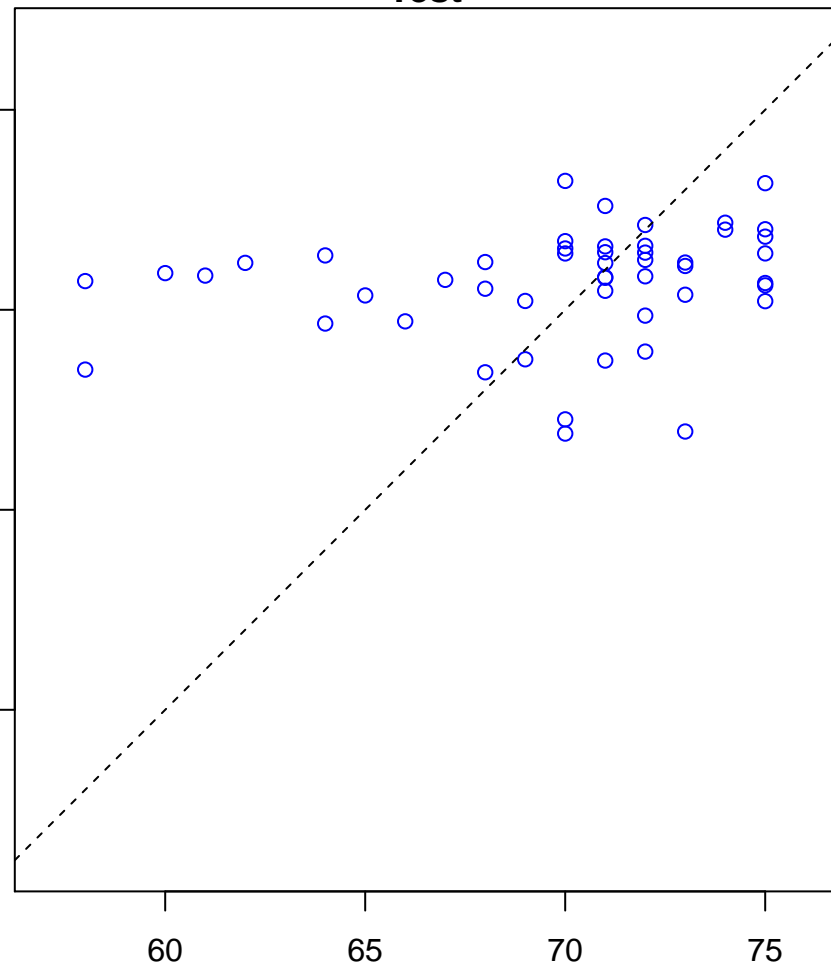


transformed cell apoptotic process (Score: 0.854377)

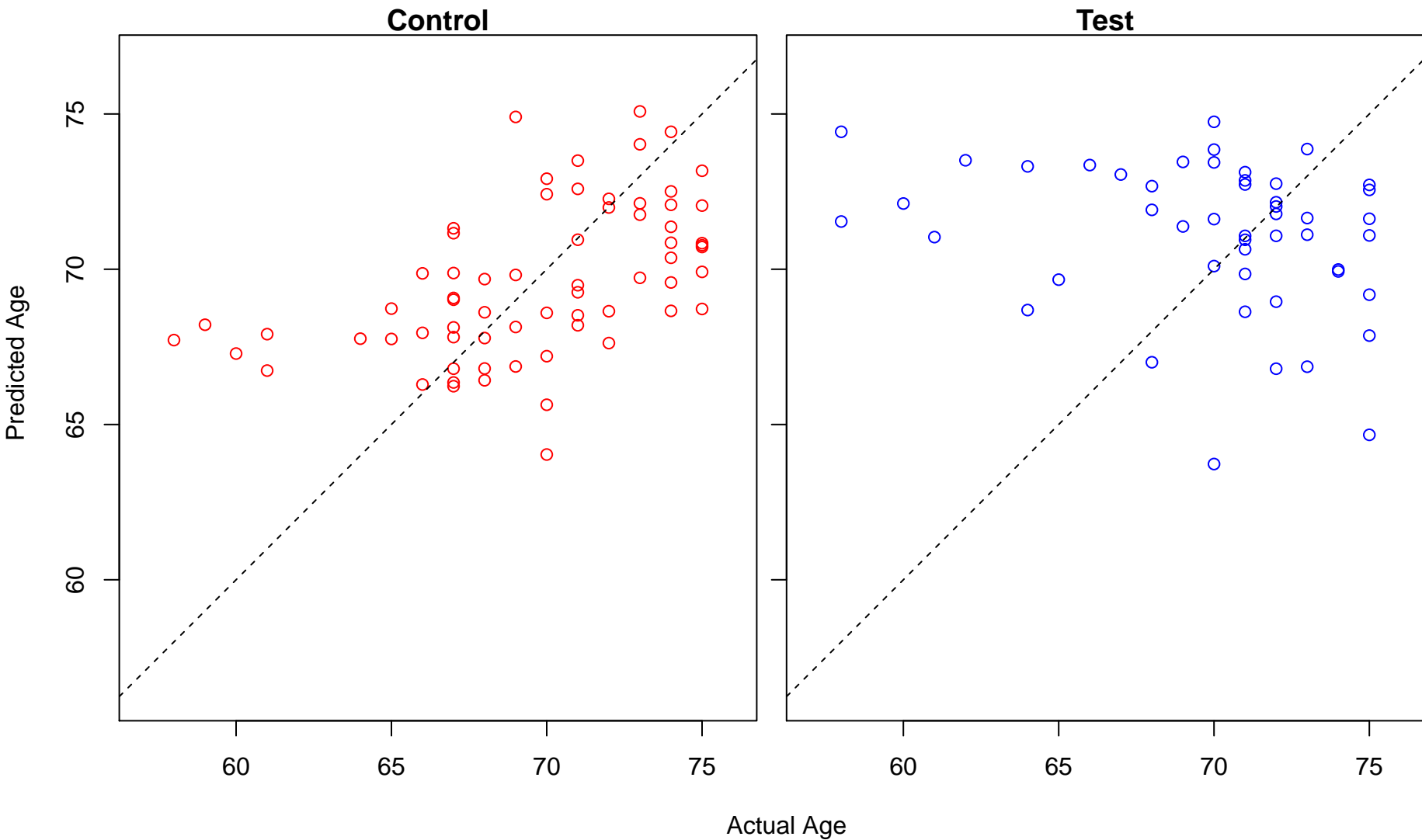
Control



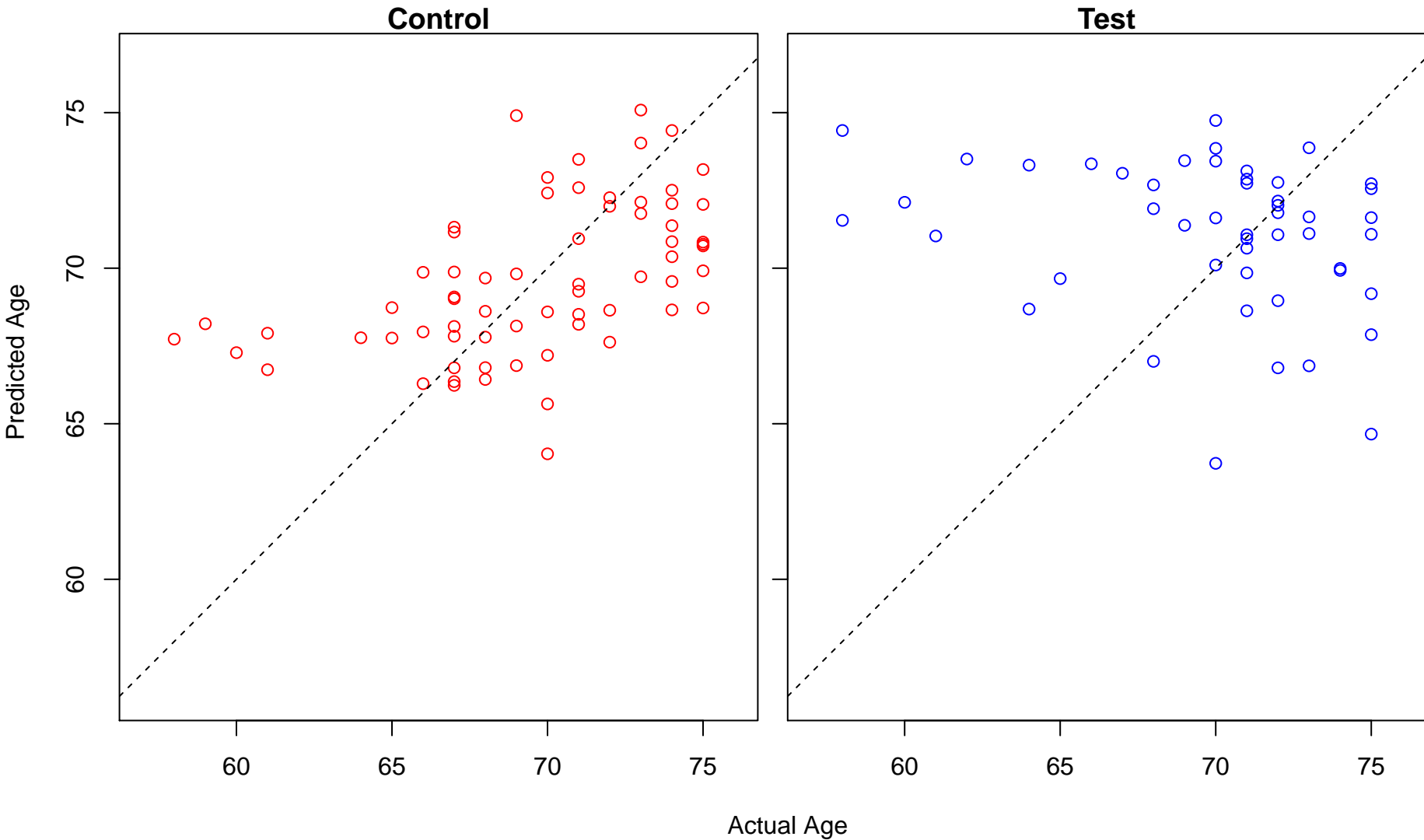
Test



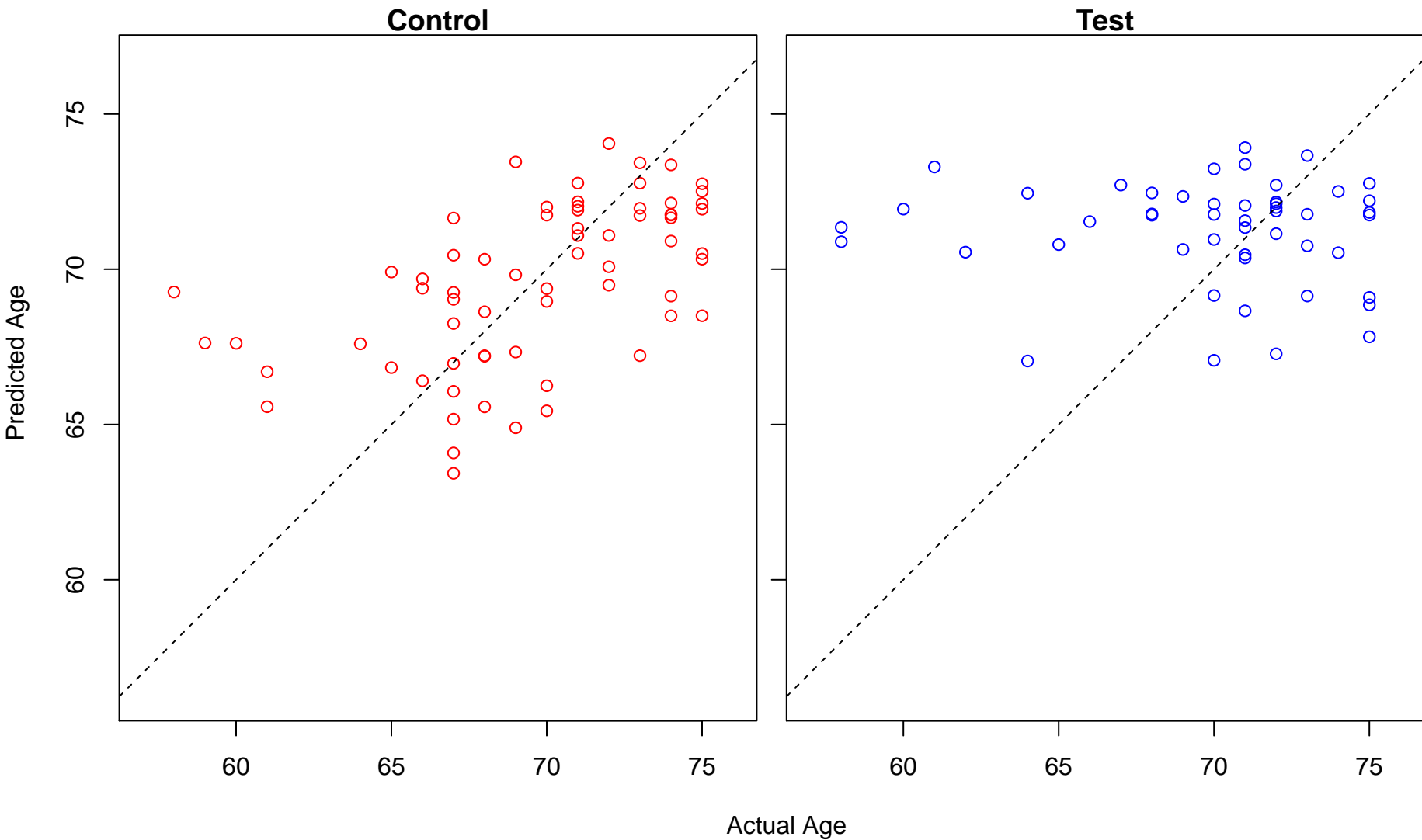
regulation of sphingolipid biosynthetic process (Score: 0.854221)



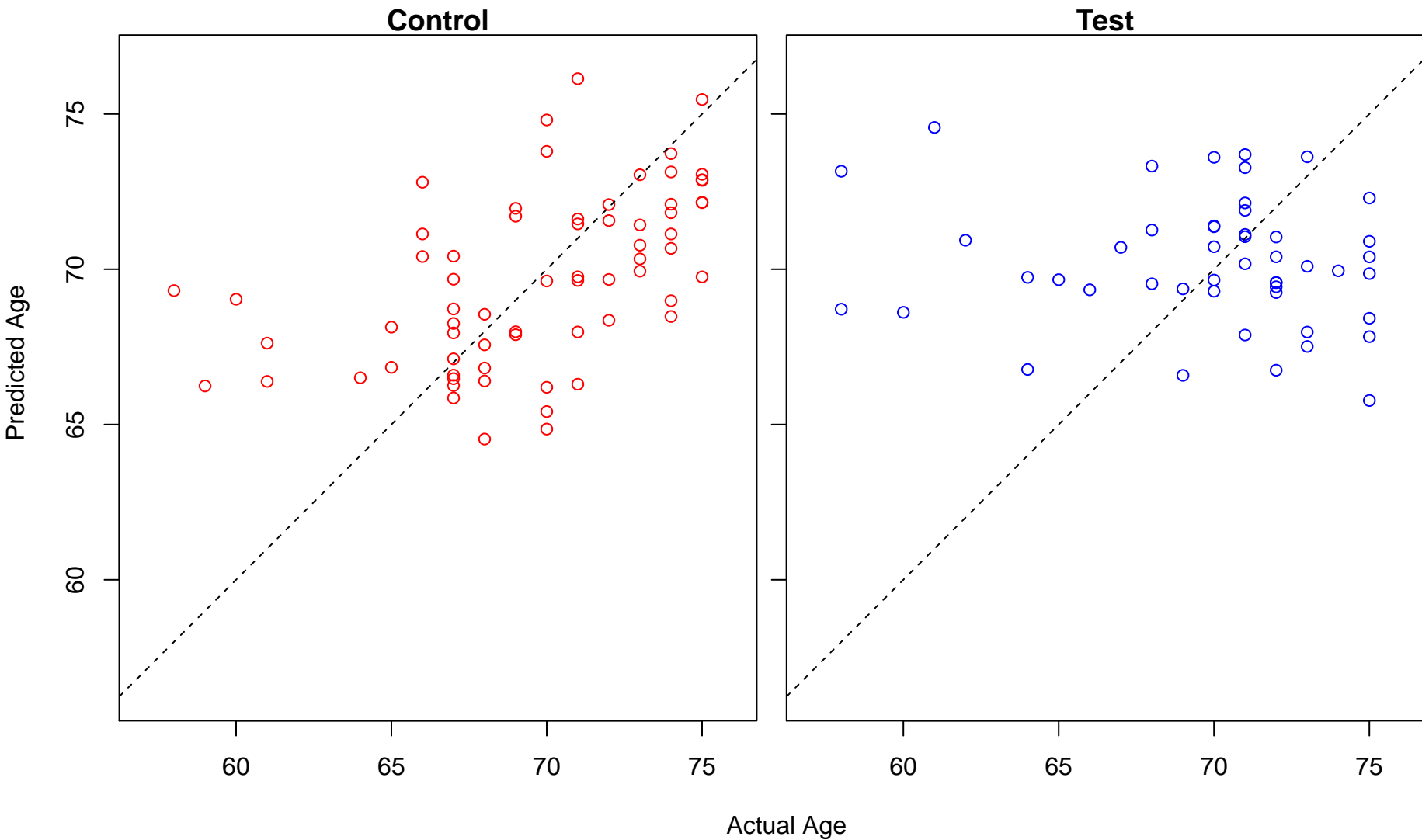
regulation of ceramide biosynthetic process (Score: 0.854221)



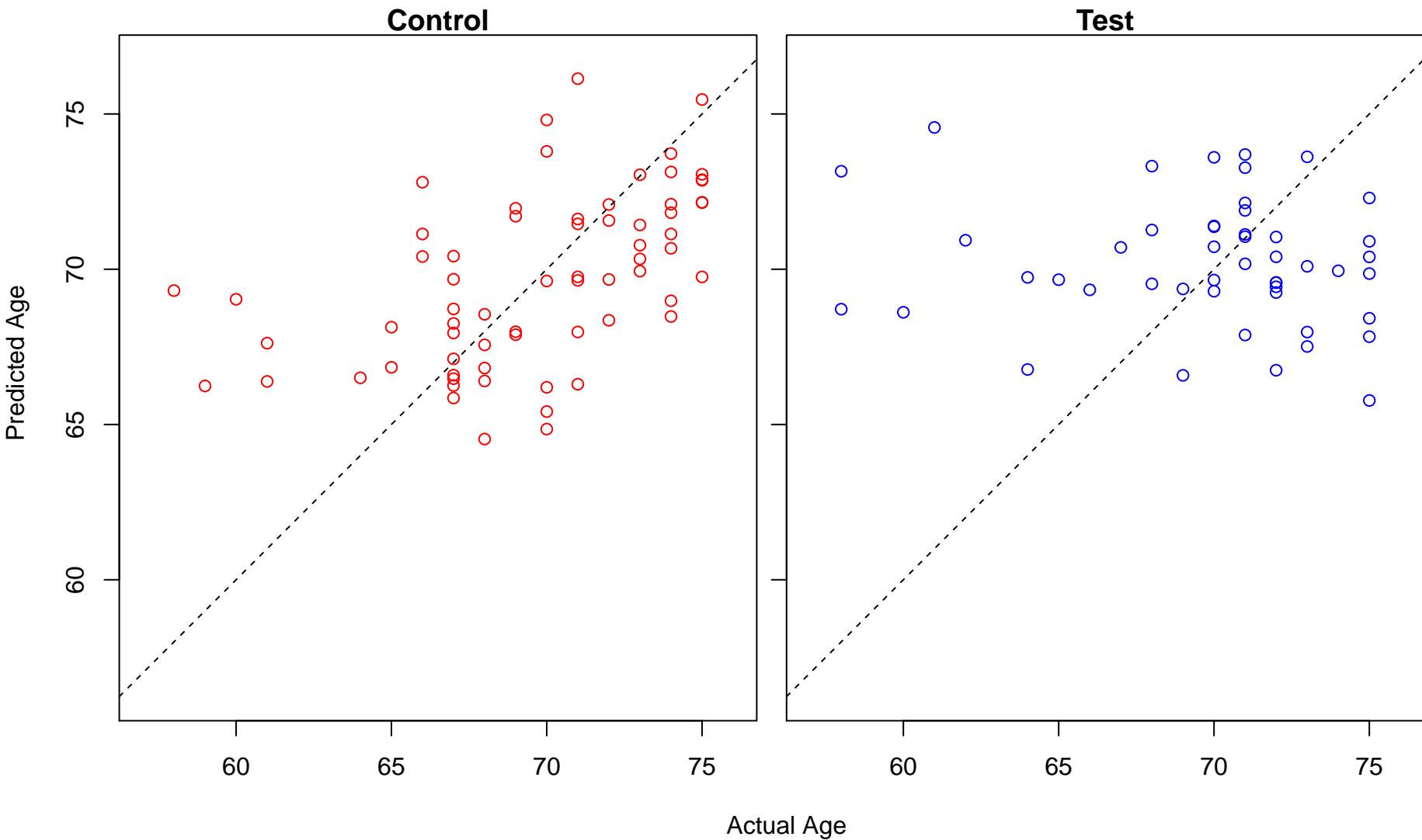
positive regulation of megakaryocyte differentiation (Score: 0.854179)



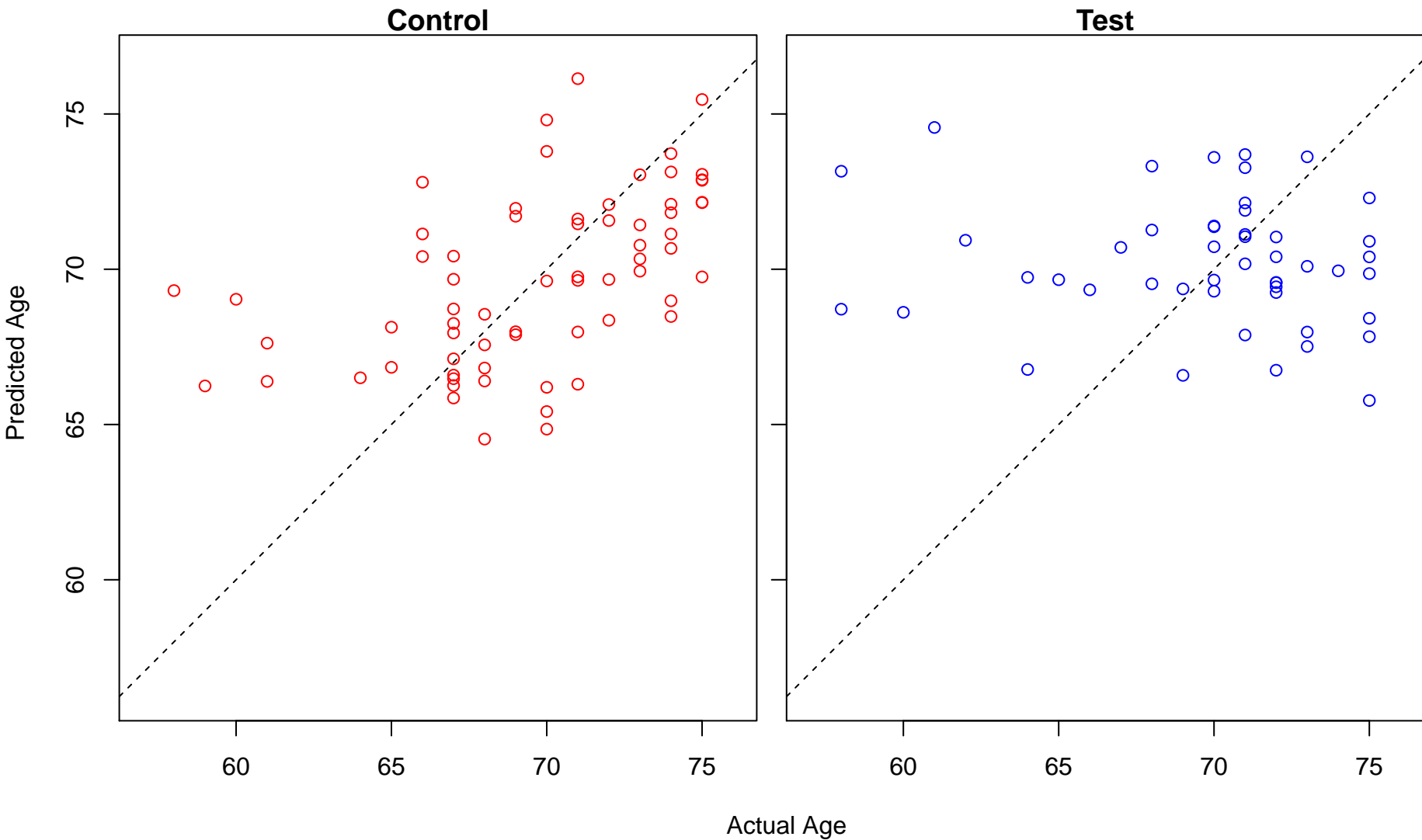
cytidine catabolic process (Score: 0.854107)



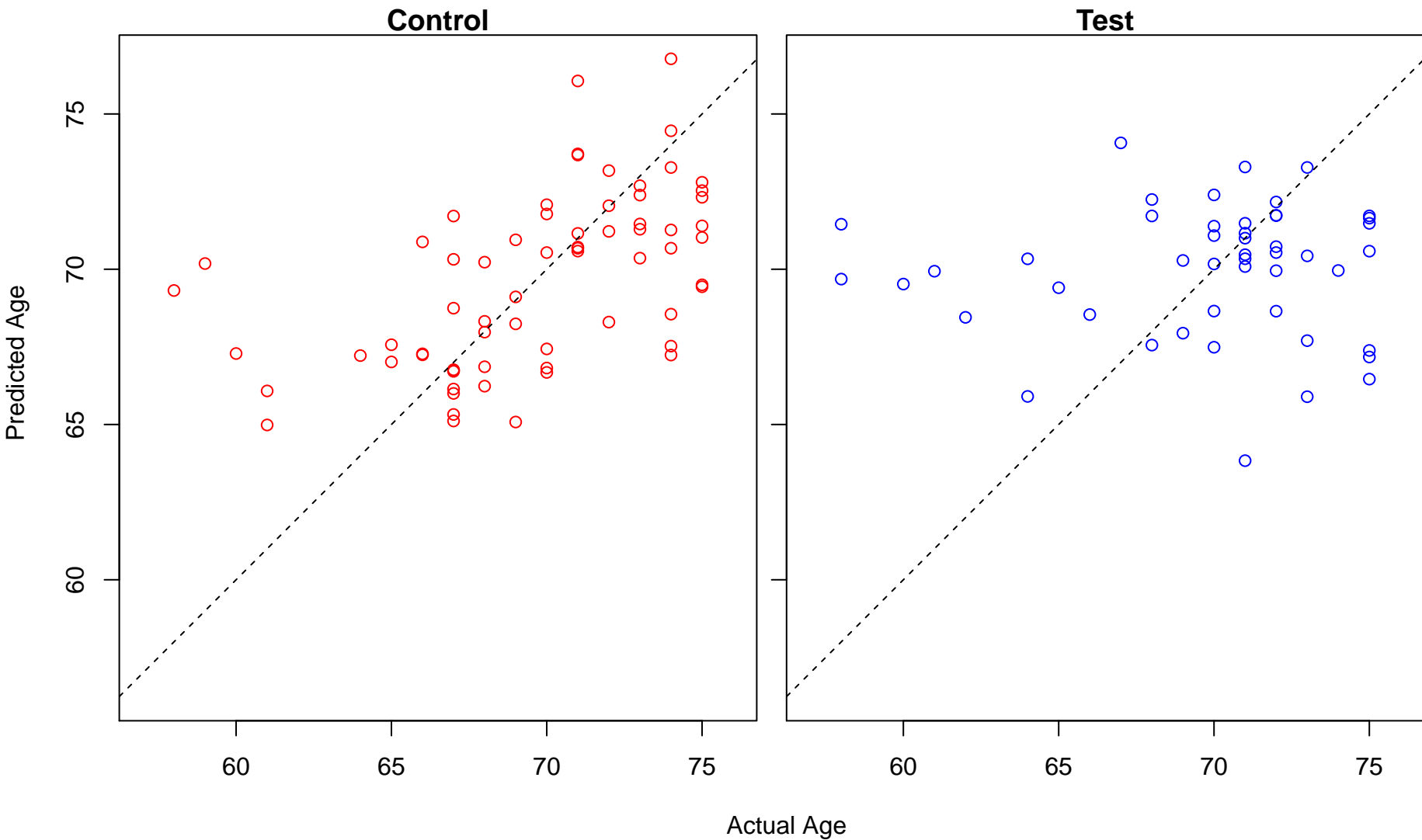
cytidine deamination (Score: 0.854107)



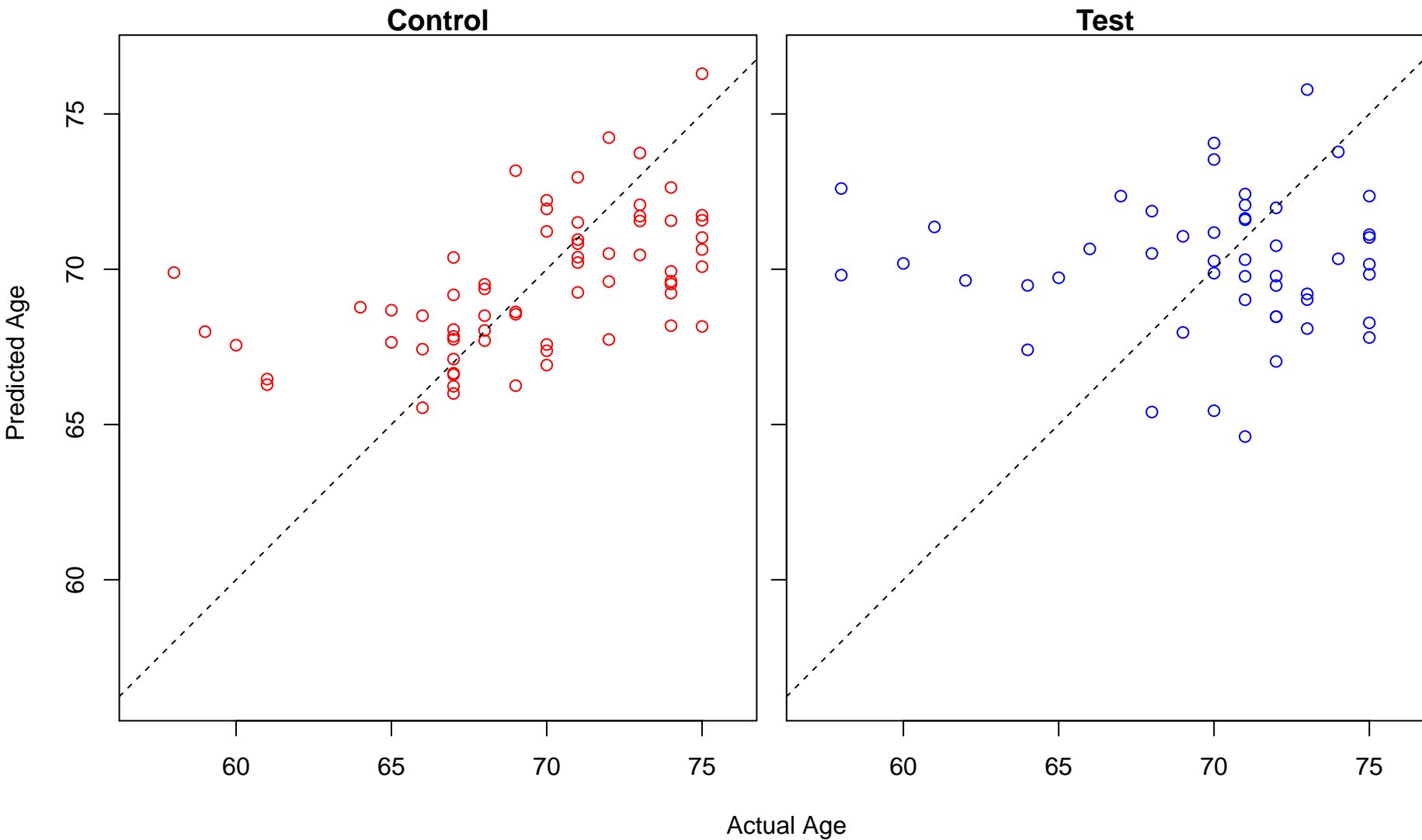
cytidine metabolic process (Score: 0.854107)



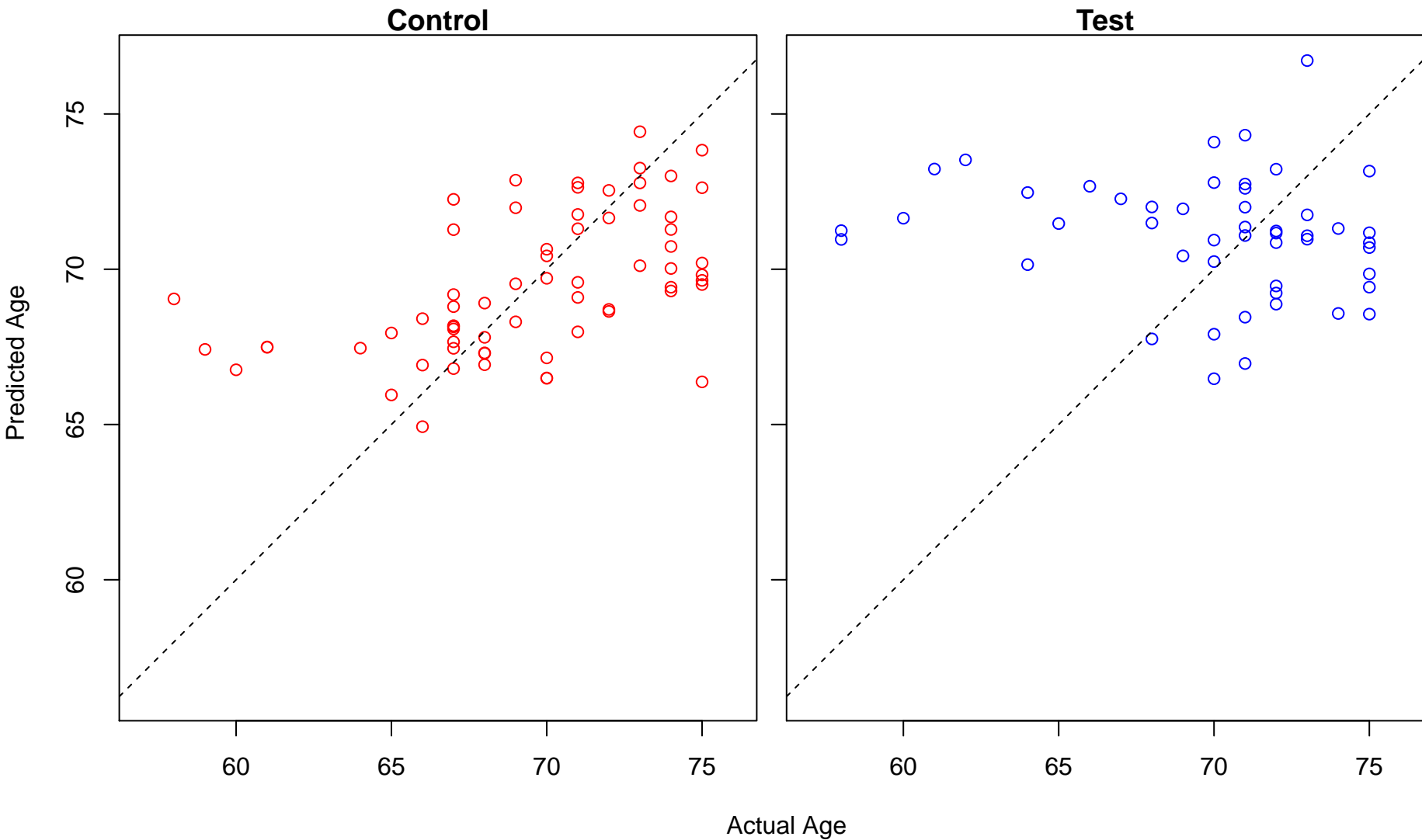
regulation of translational initiation in response to stress (Score: 0.853902)



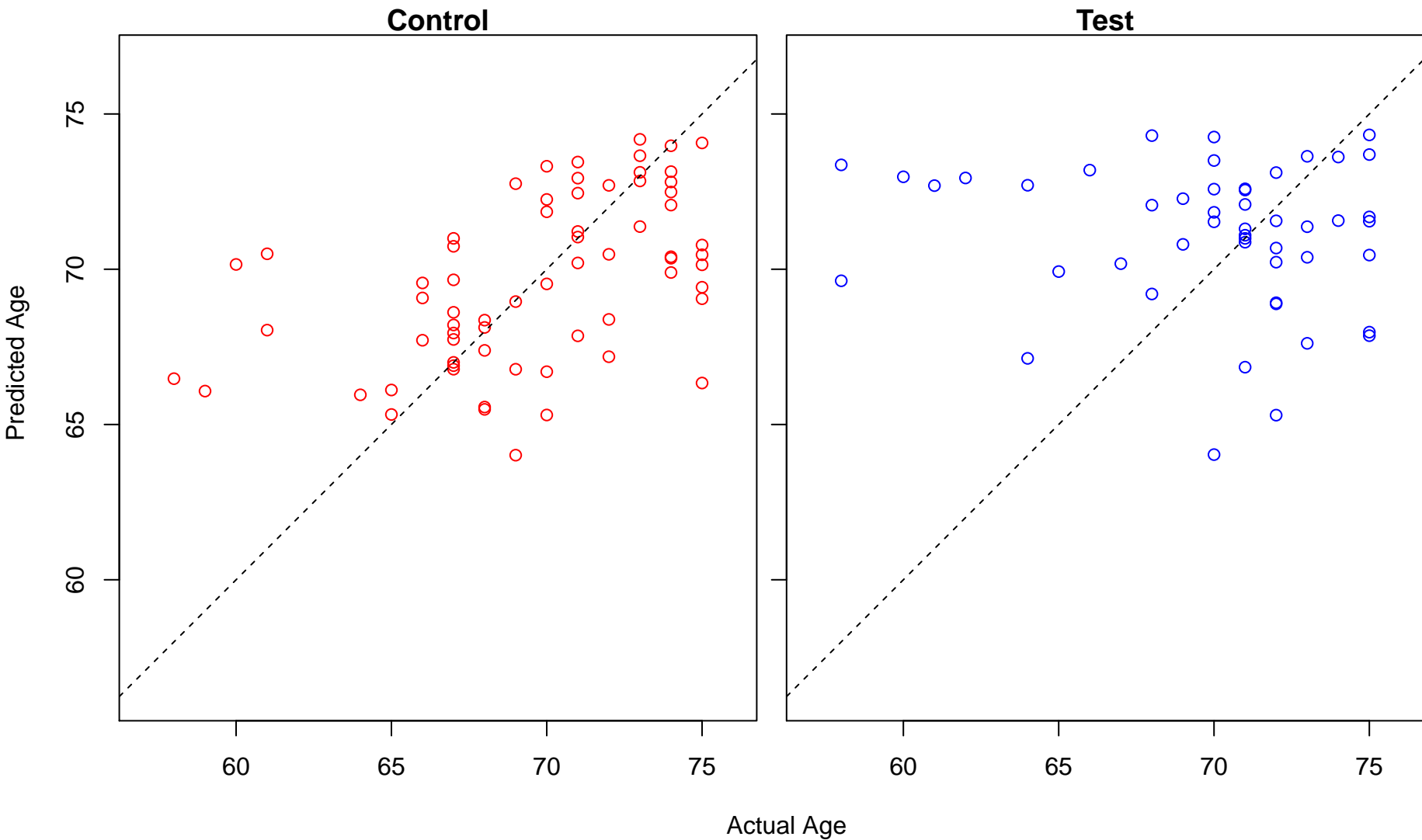
negative regulation of dendrite development (Score: 0.853720)



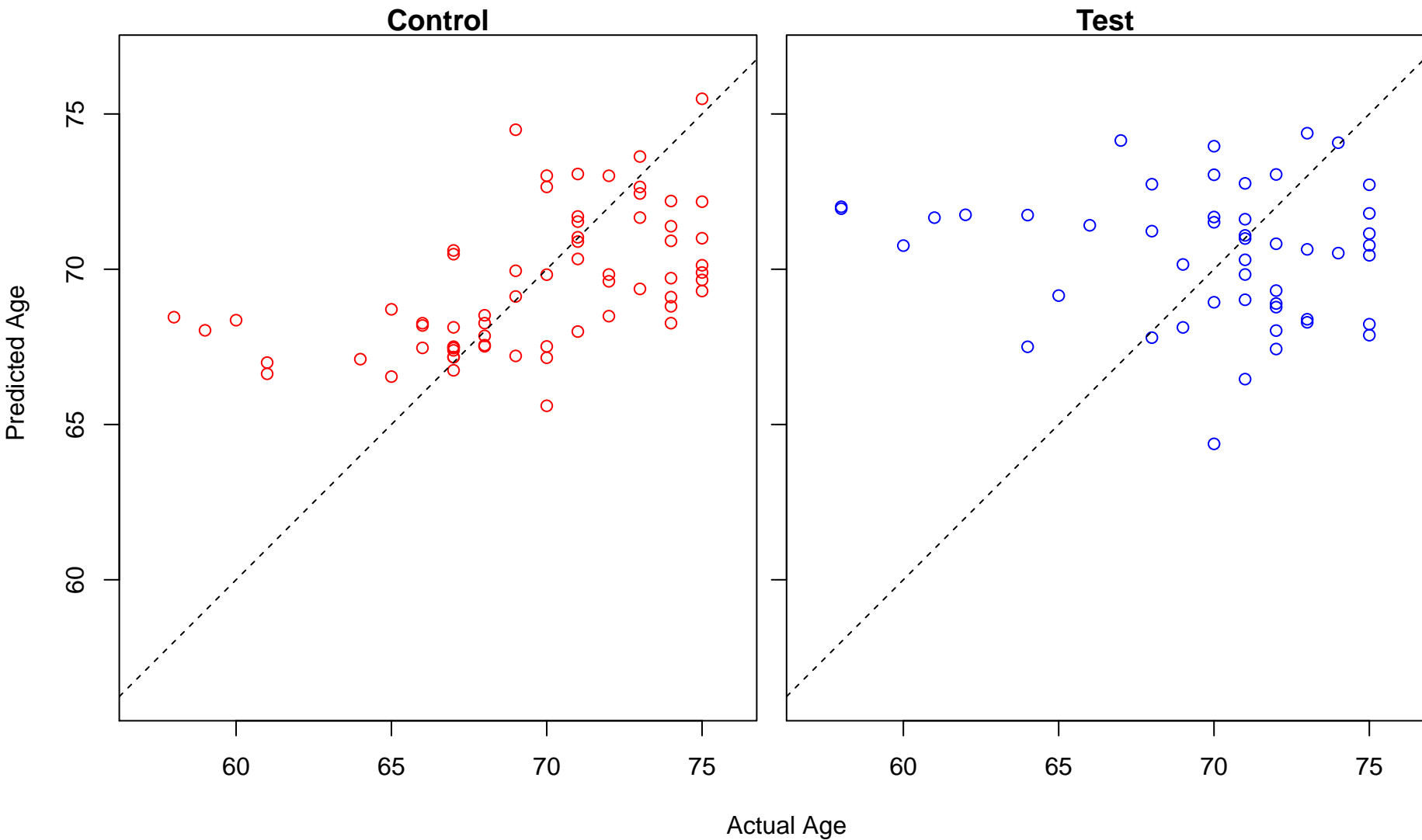
negative regulation of glycoprotein metabolic process (Score: 0.853686)



positive regulation of establishment of protein localization to plasma membrane (Score: 0.853652)

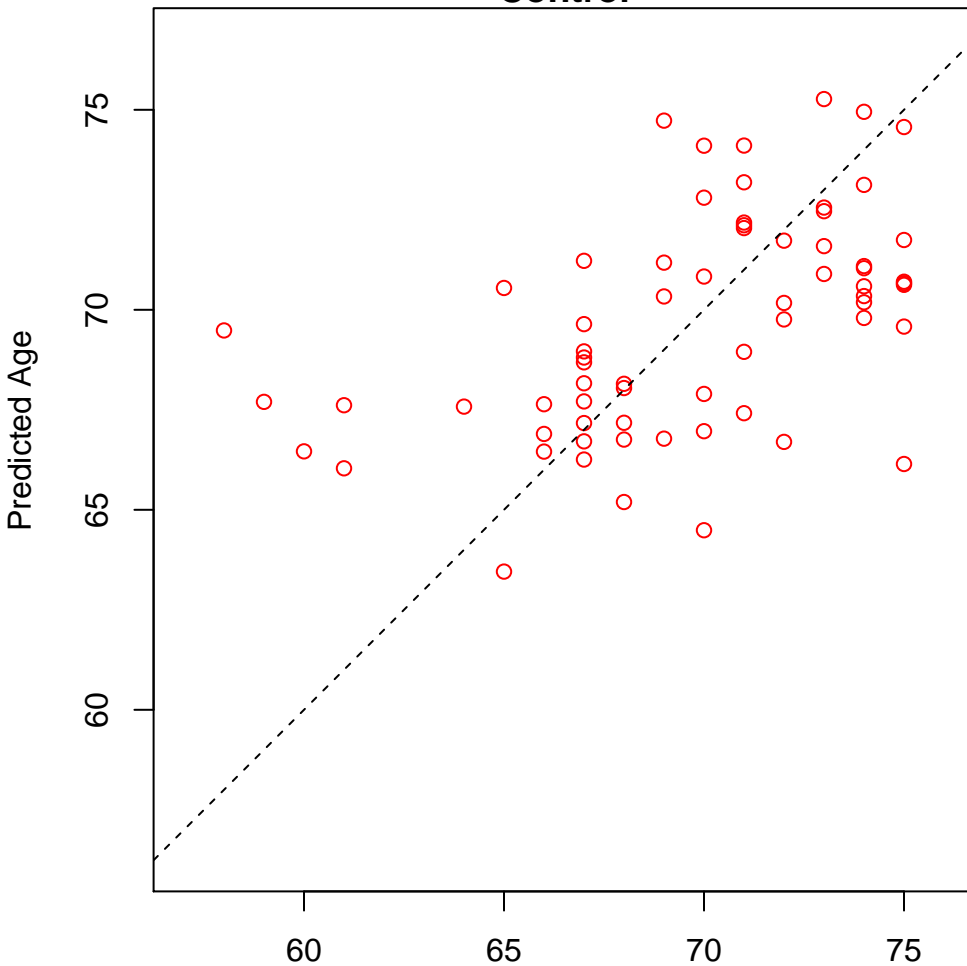


negative regulation of neuron projection development (Score: 0.852838)

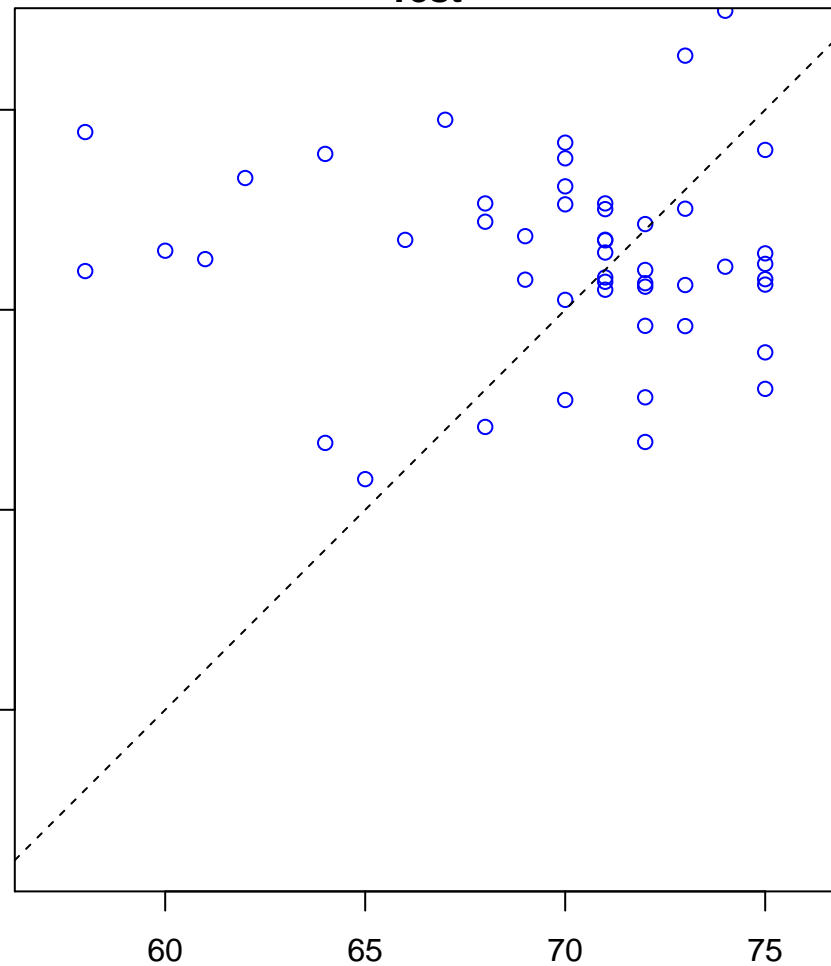


cellular amino acid biosynthetic process (Score: 0.852557)

Control



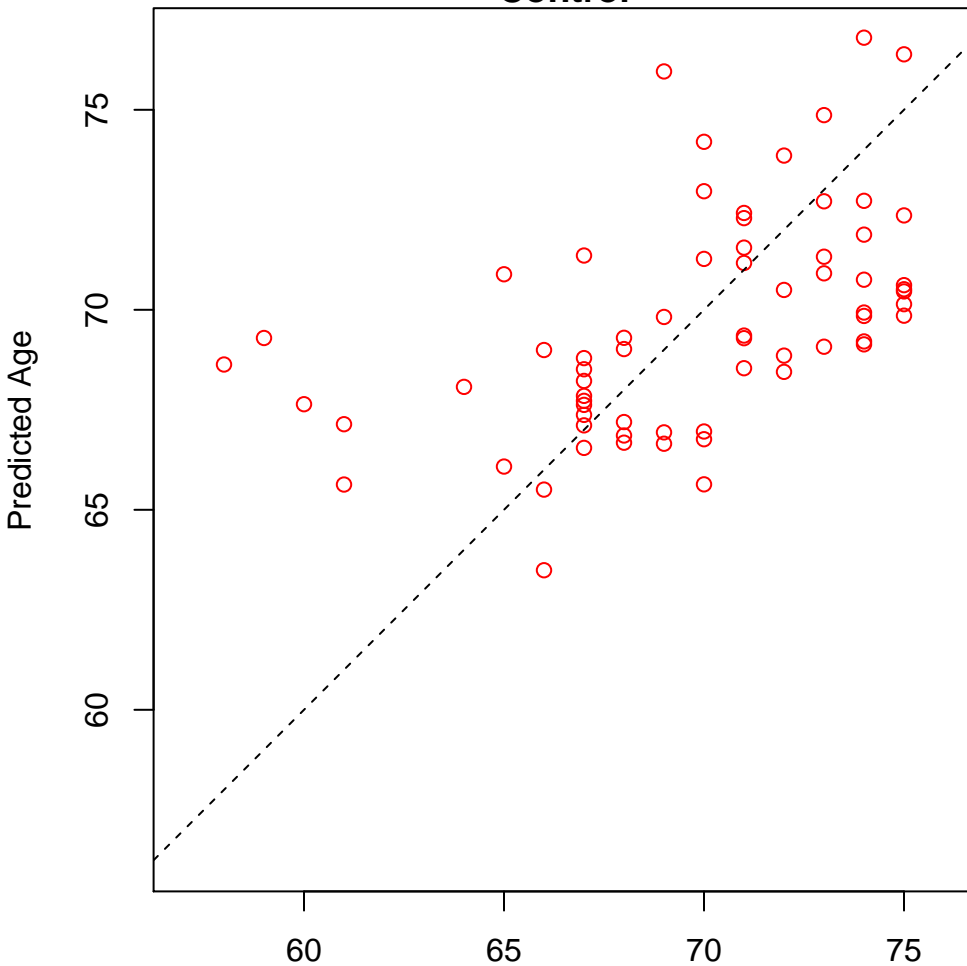
Test



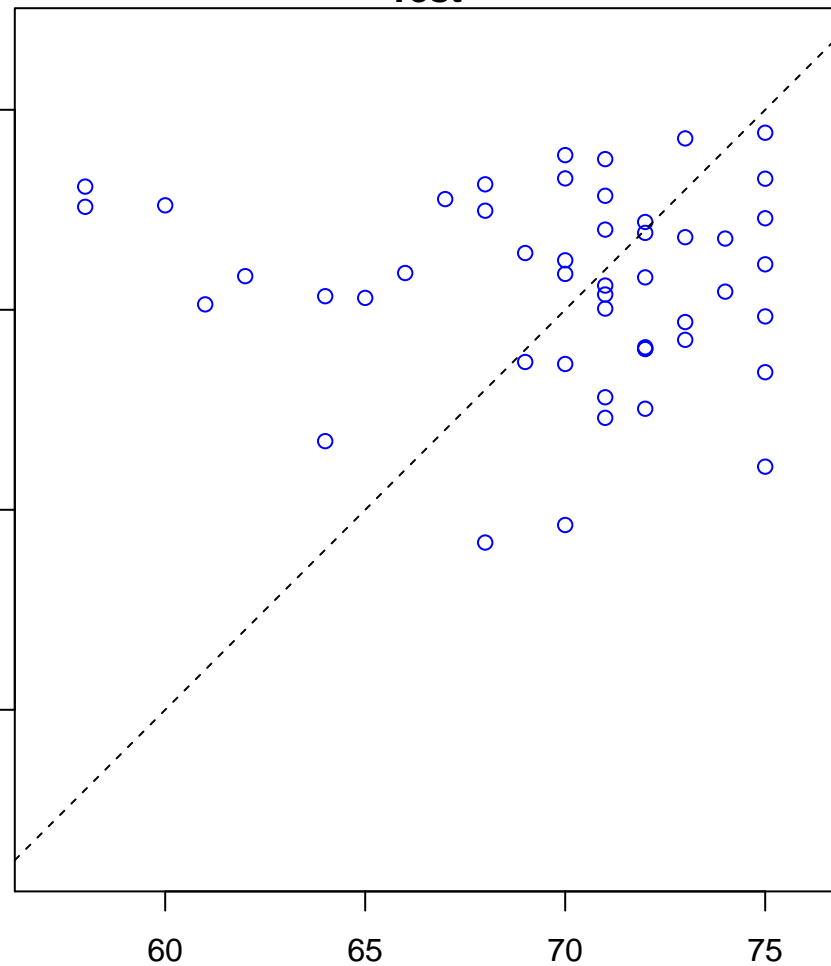
Actual Age

telencephalon development (Score: 0.851817)

Control

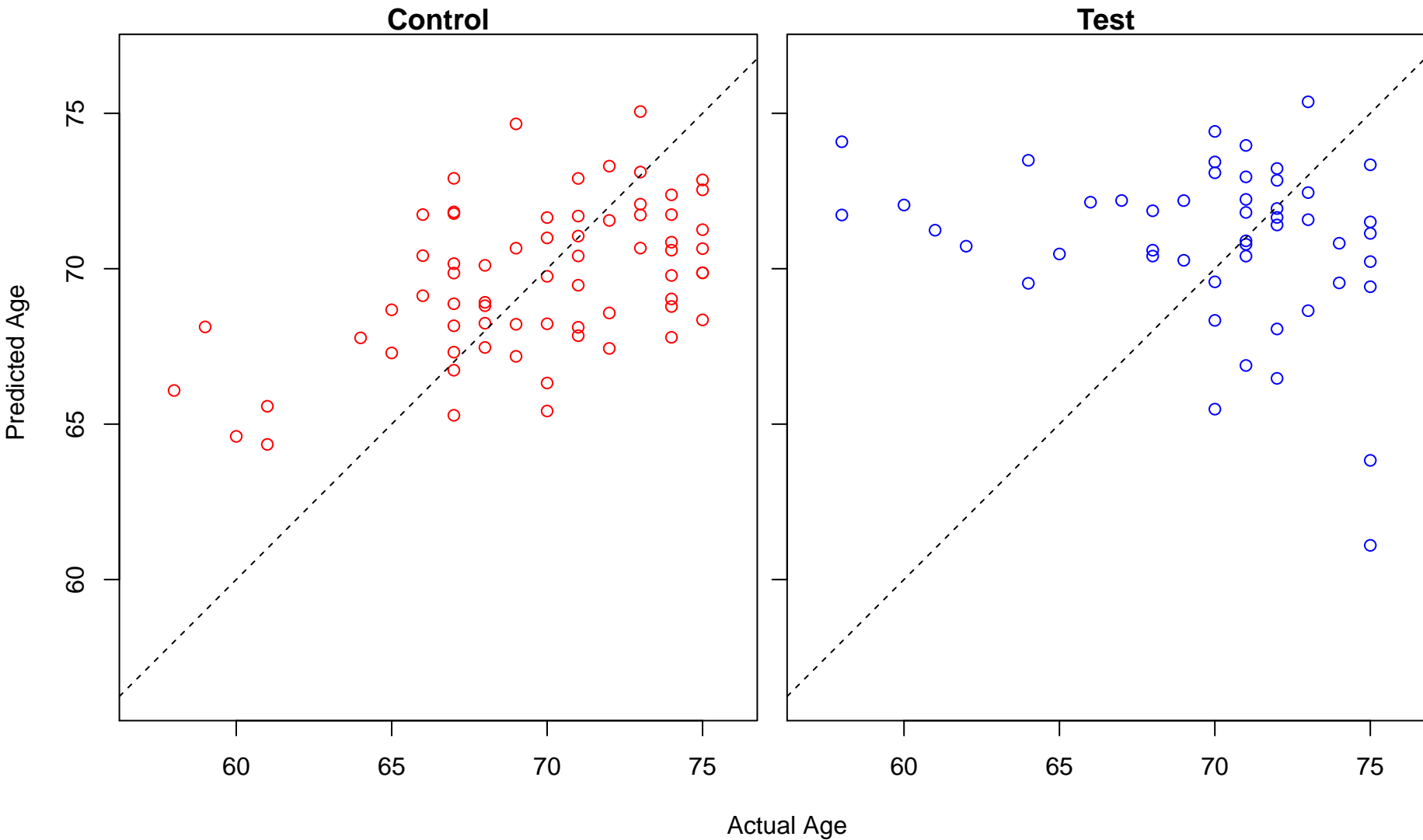


Test

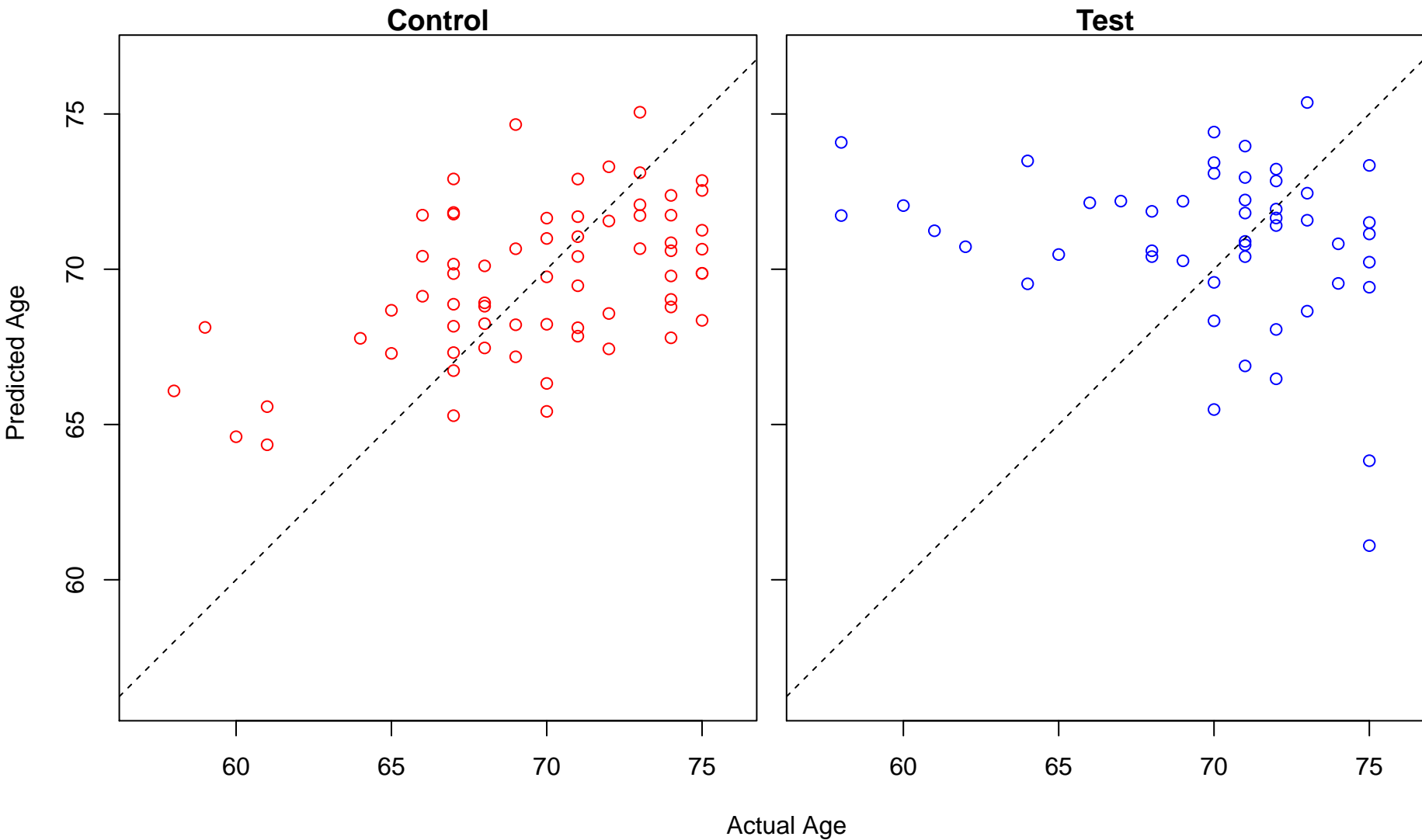


Actual Age

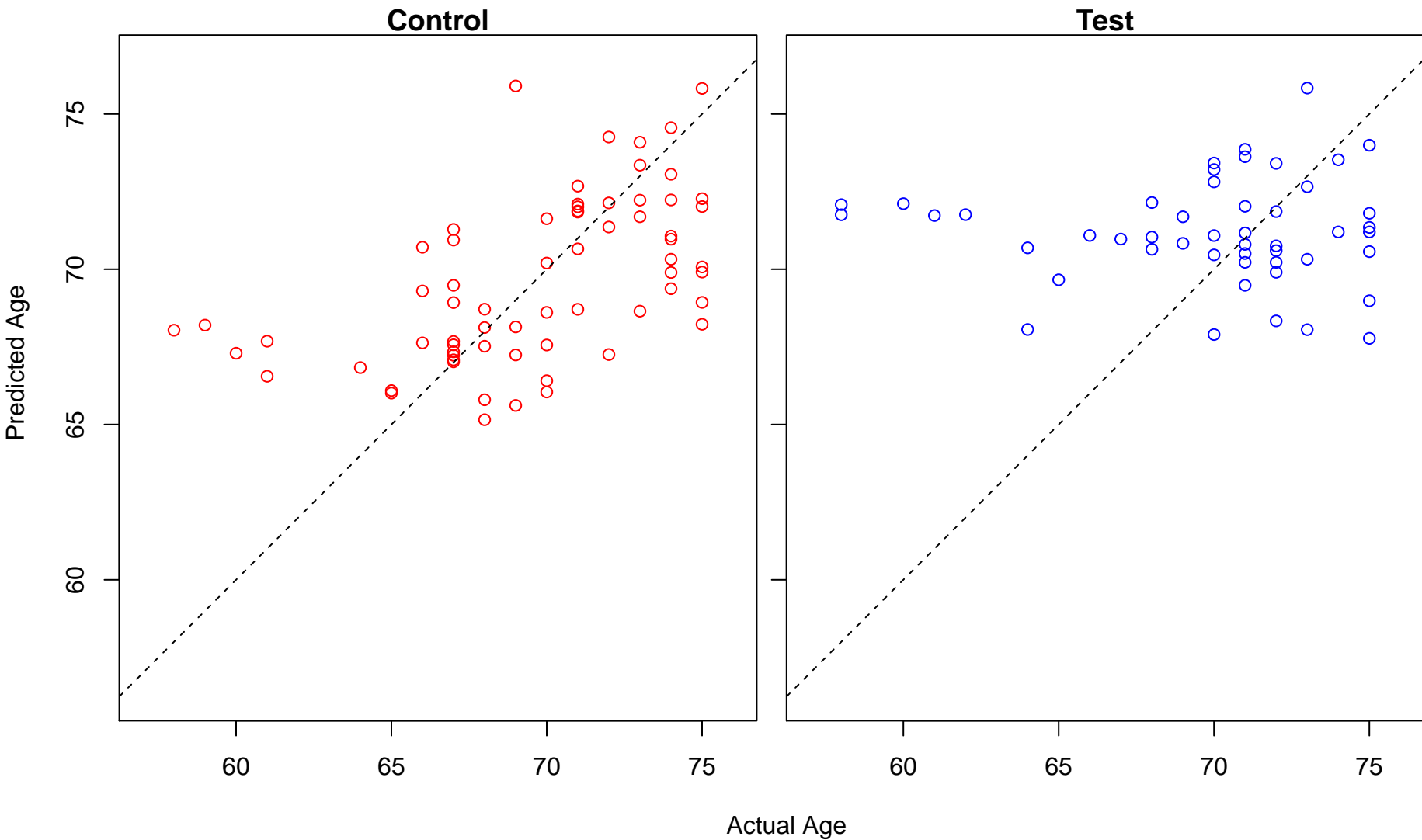
positive regulation of delayed rectifier potassium channel activity (Score: 0.850976)



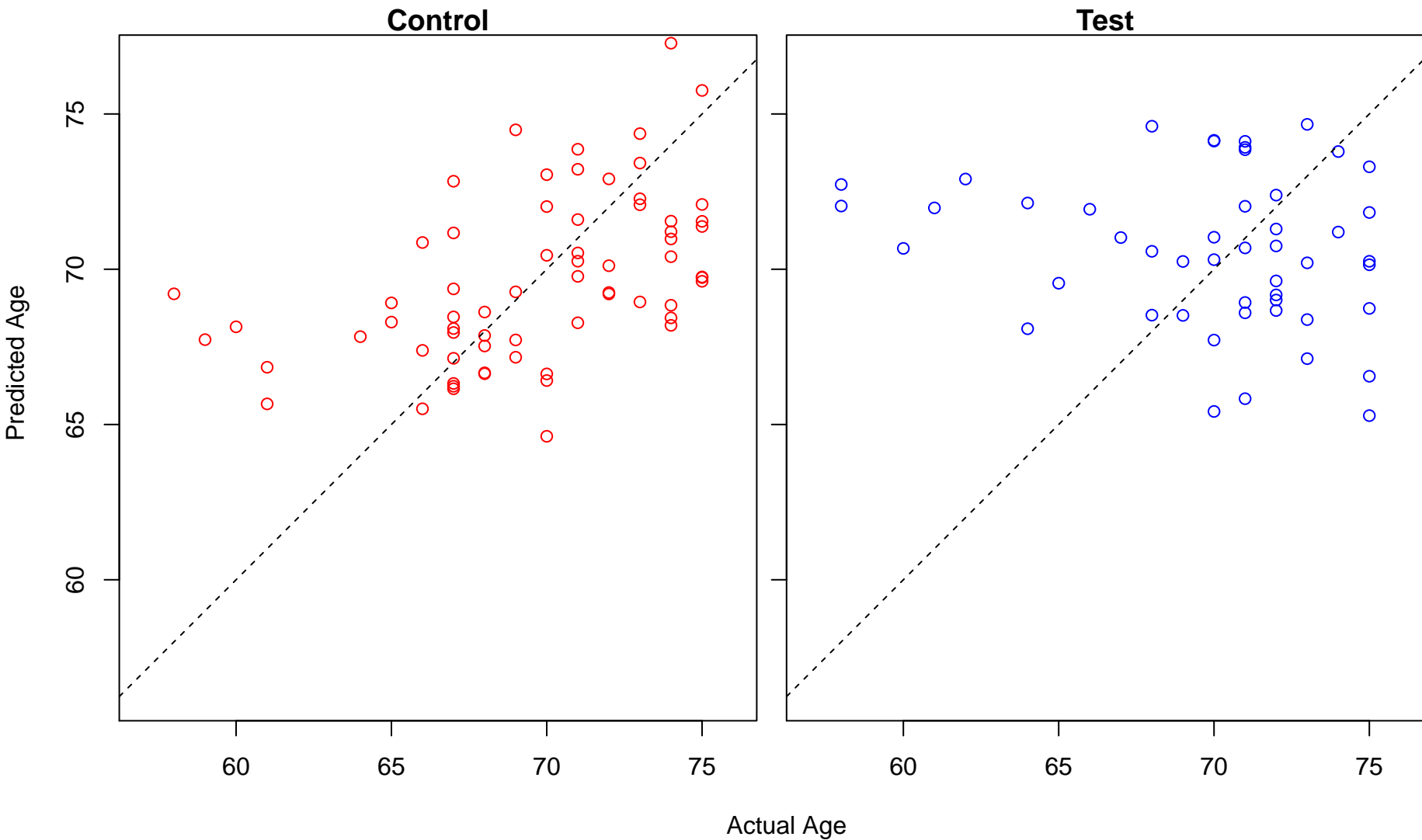
positive regulation of voltage-gated potassium channel activity (Score: 0.850976)



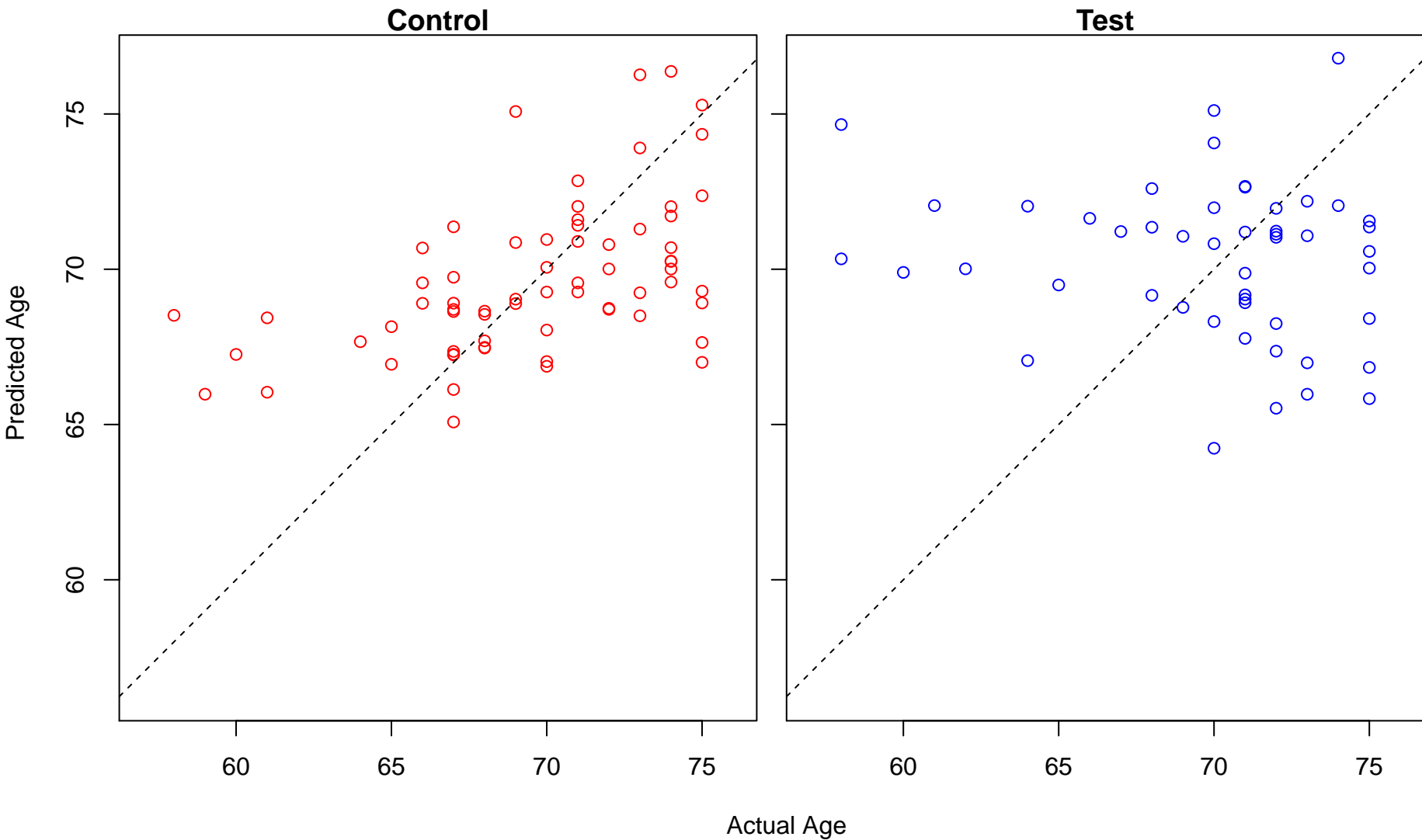
positive regulation of gene silencing by miRNA (Score: 0.850717)



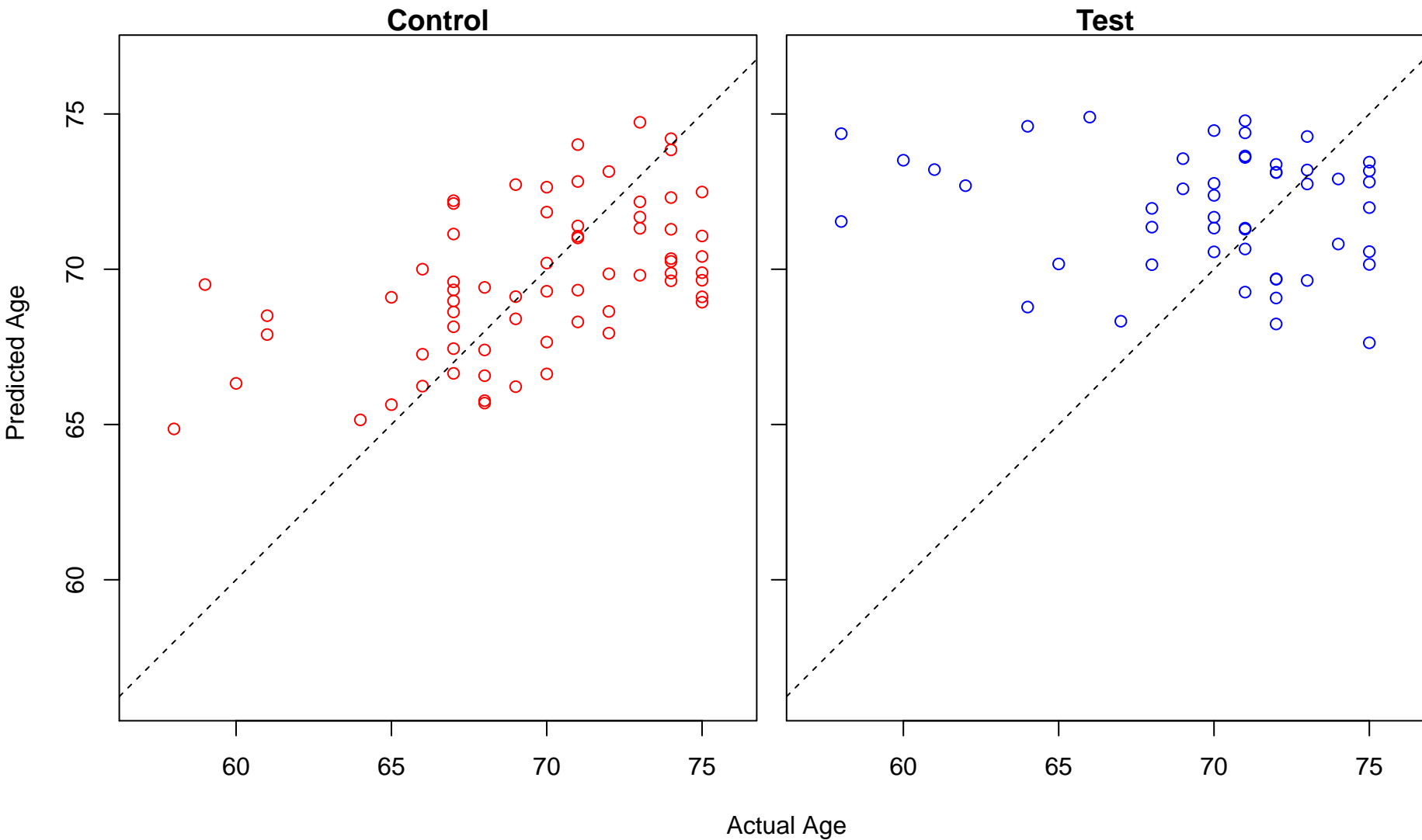
neuron apoptotic process (Score: 0.850546)



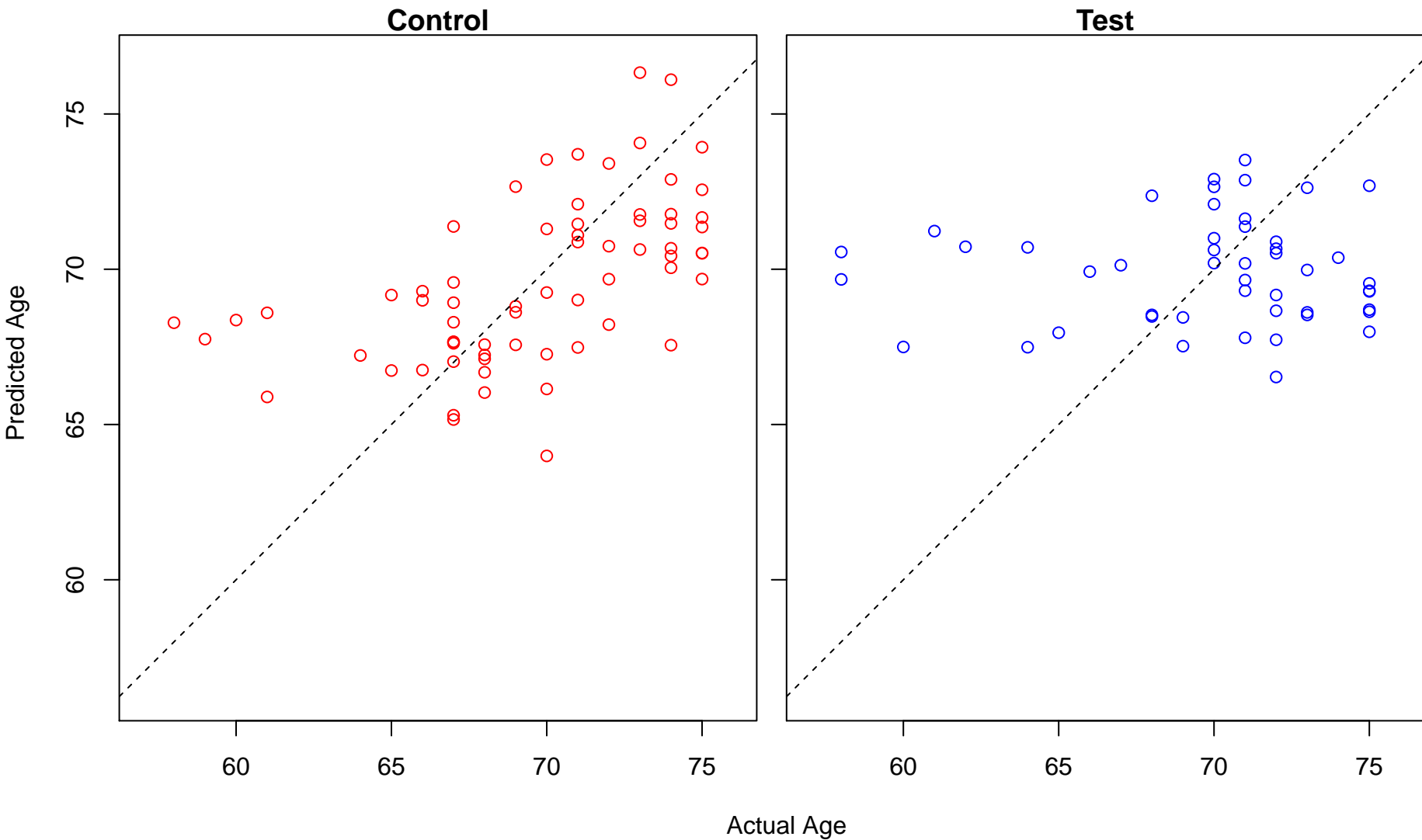
protein localization to chromosome, telomeric region (Score: 0.850416)



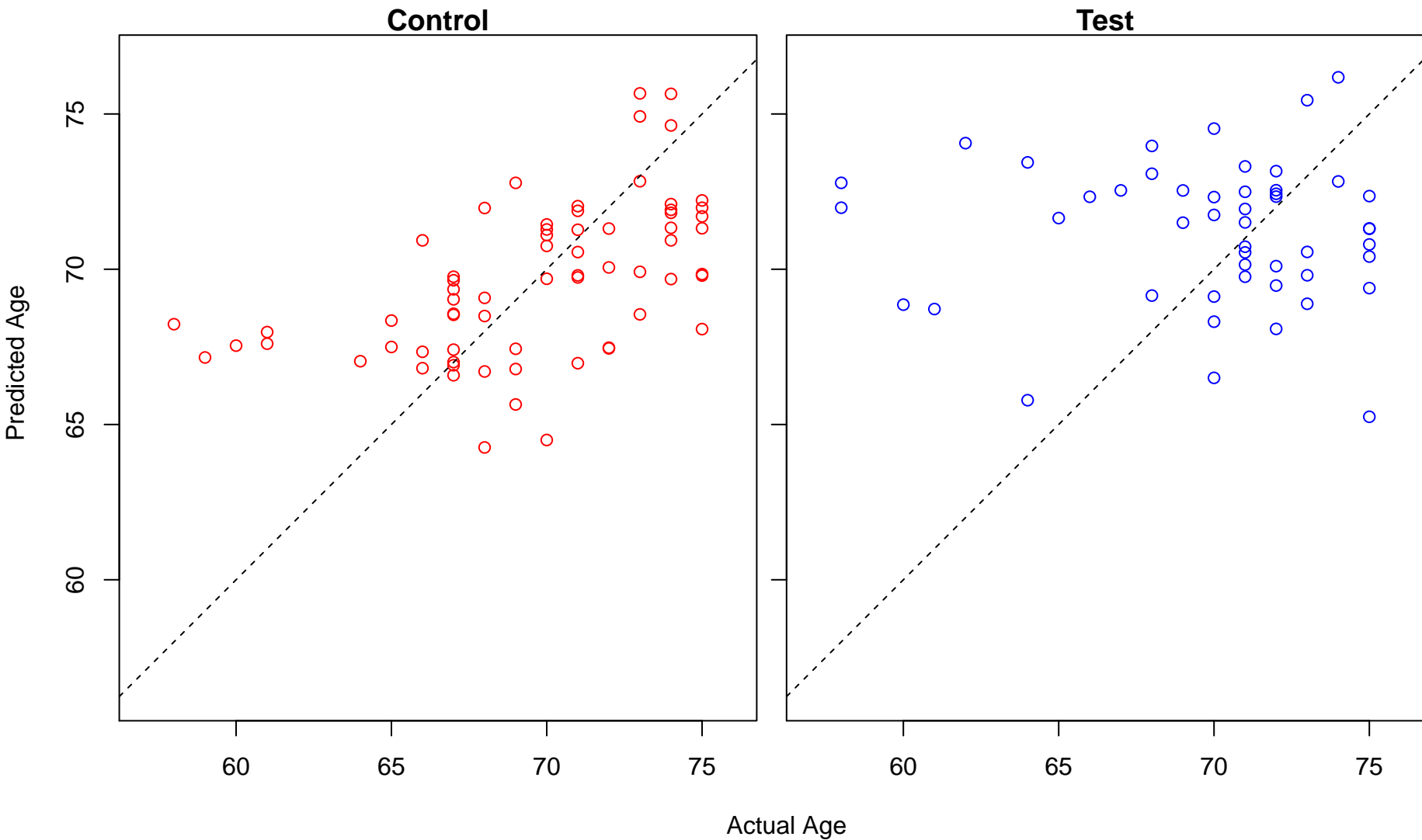
cardiac chamber formation (Score: 0.850397)



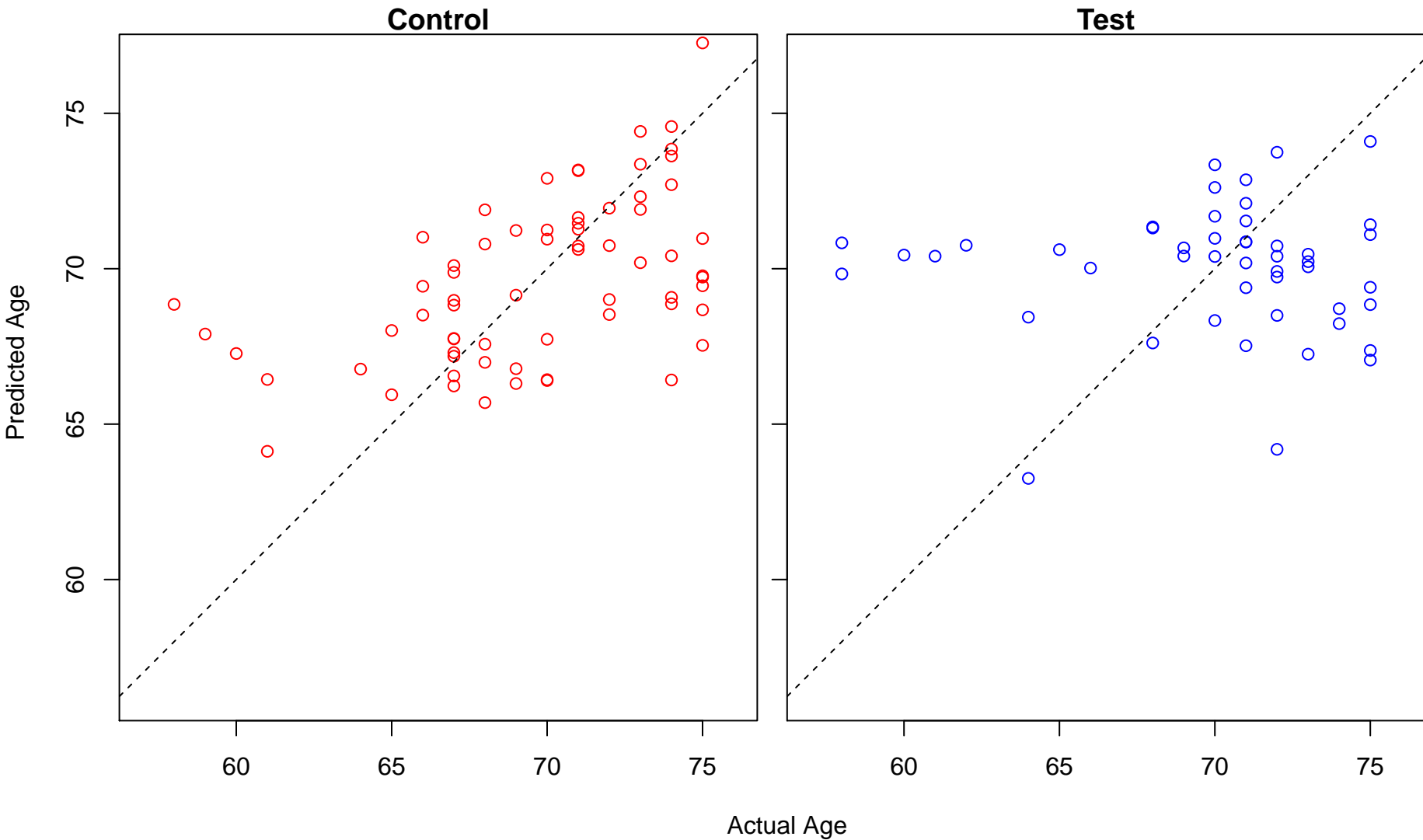
entrainment of circadian clock by photoperiod (Score: 0.850071)



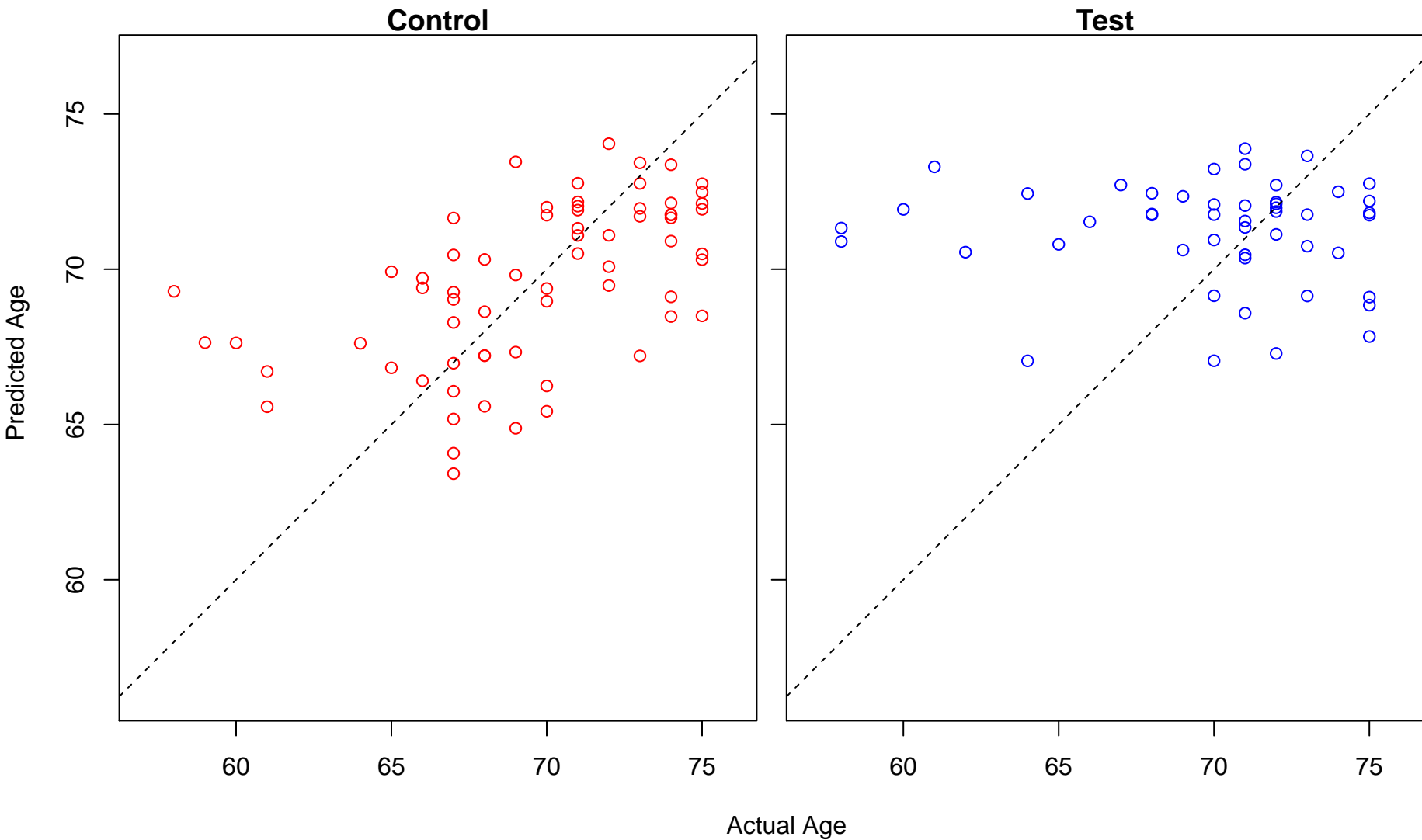
response to manganese ion (Score: 0.849984)



regulation of transcription involved in G1/S transition of mitotic cell cycle (Score: 0.849594)

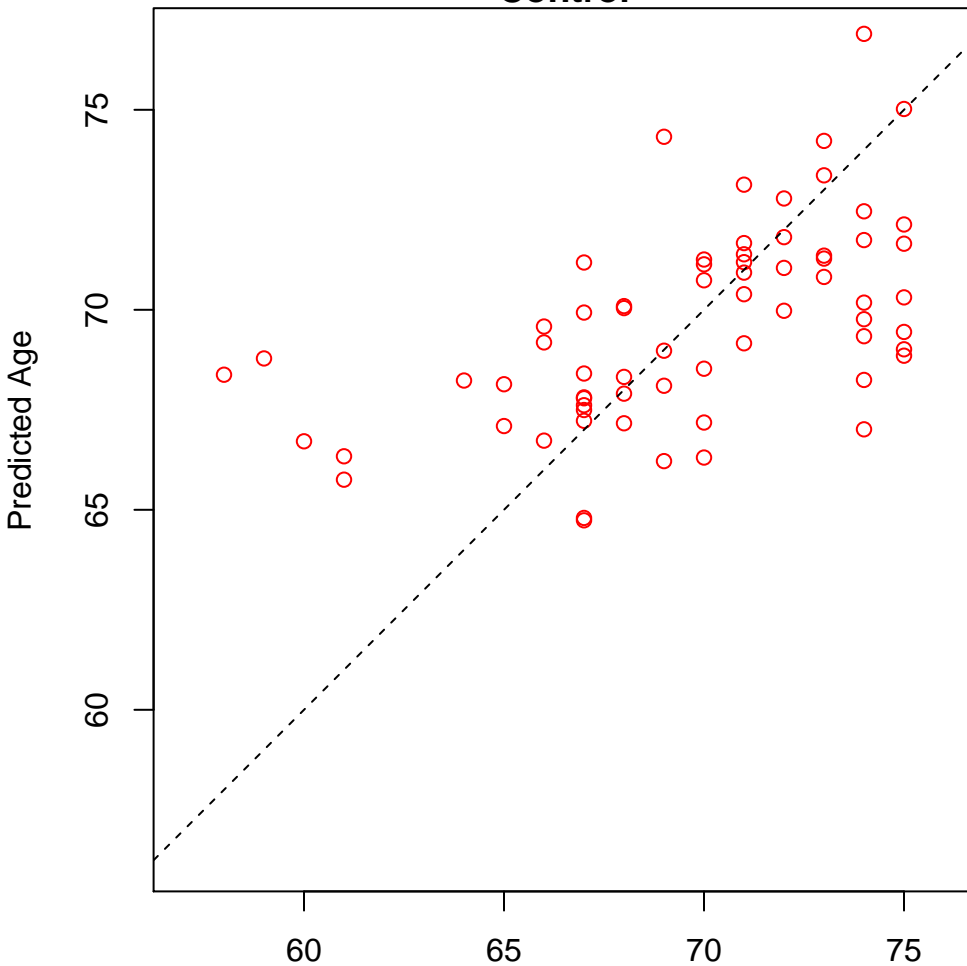


positive regulation of hematopoietic progenitor cell differentiation (Score: 0.849419)

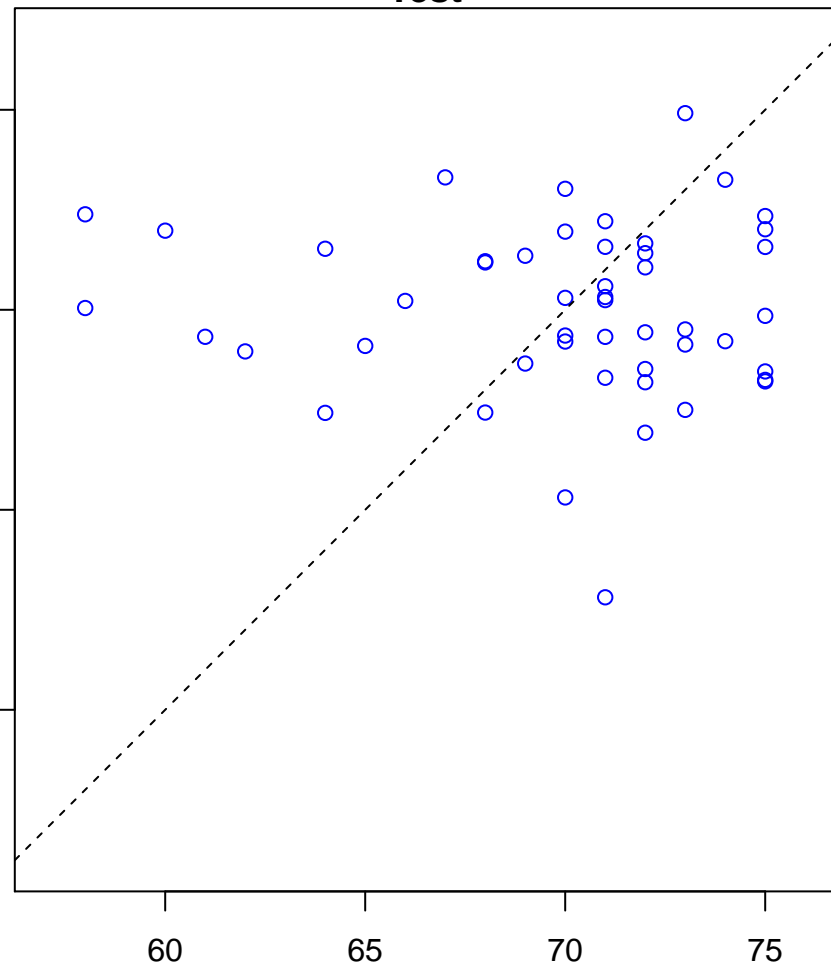


oligodendrocyte differentiation (Score: 0.849079)

Control

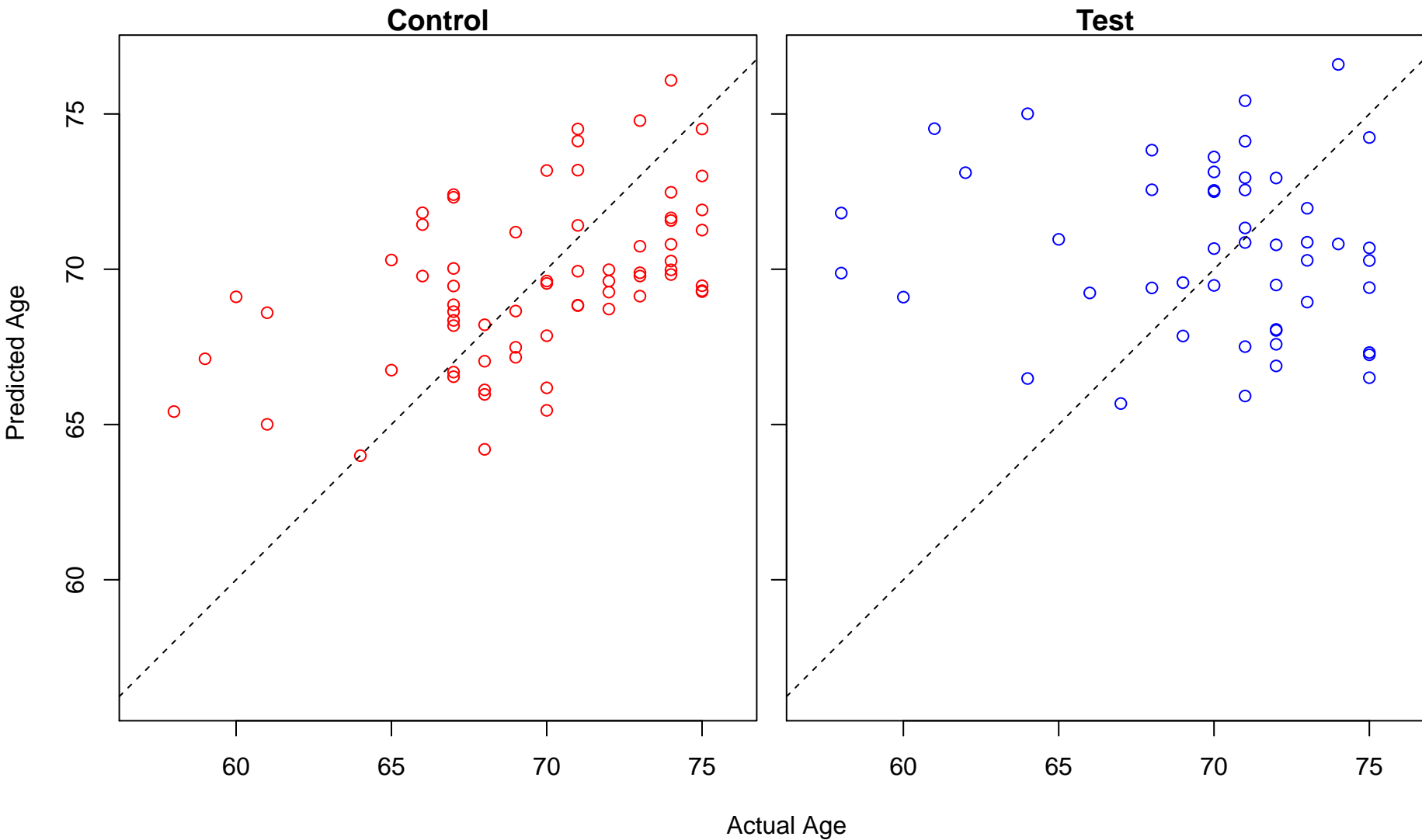


Test

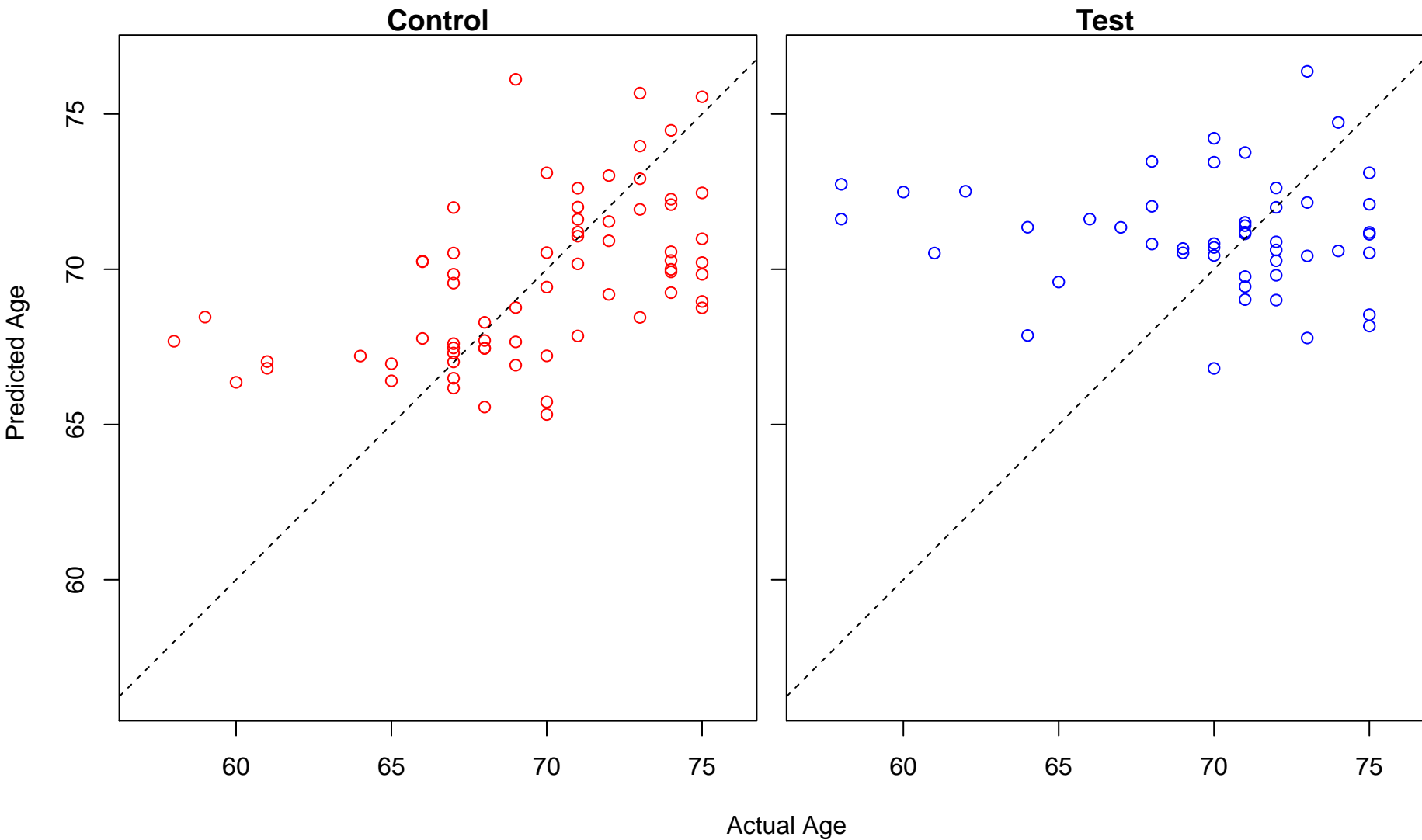


Actual Age

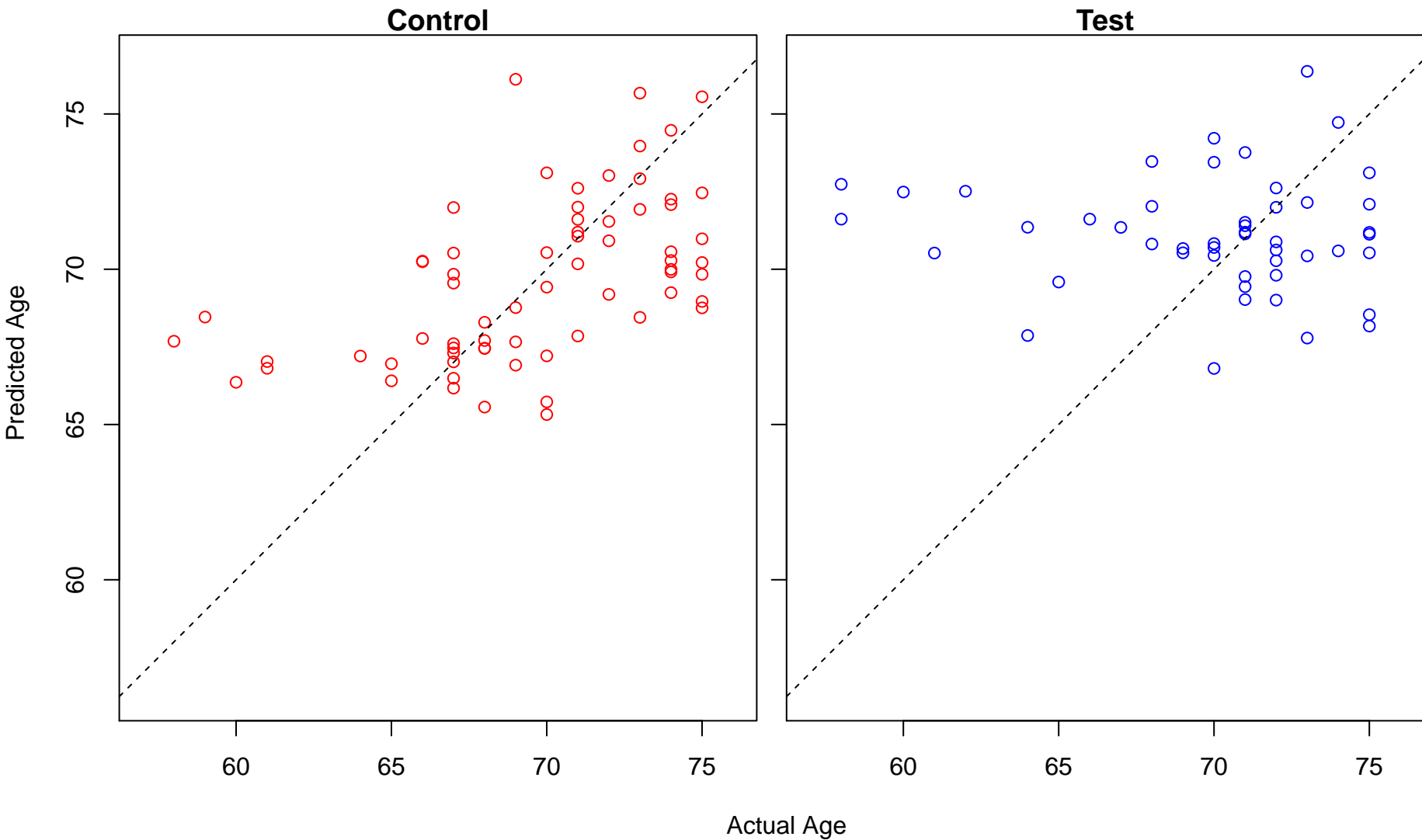
succinate metabolic process (Score: 0.848947)



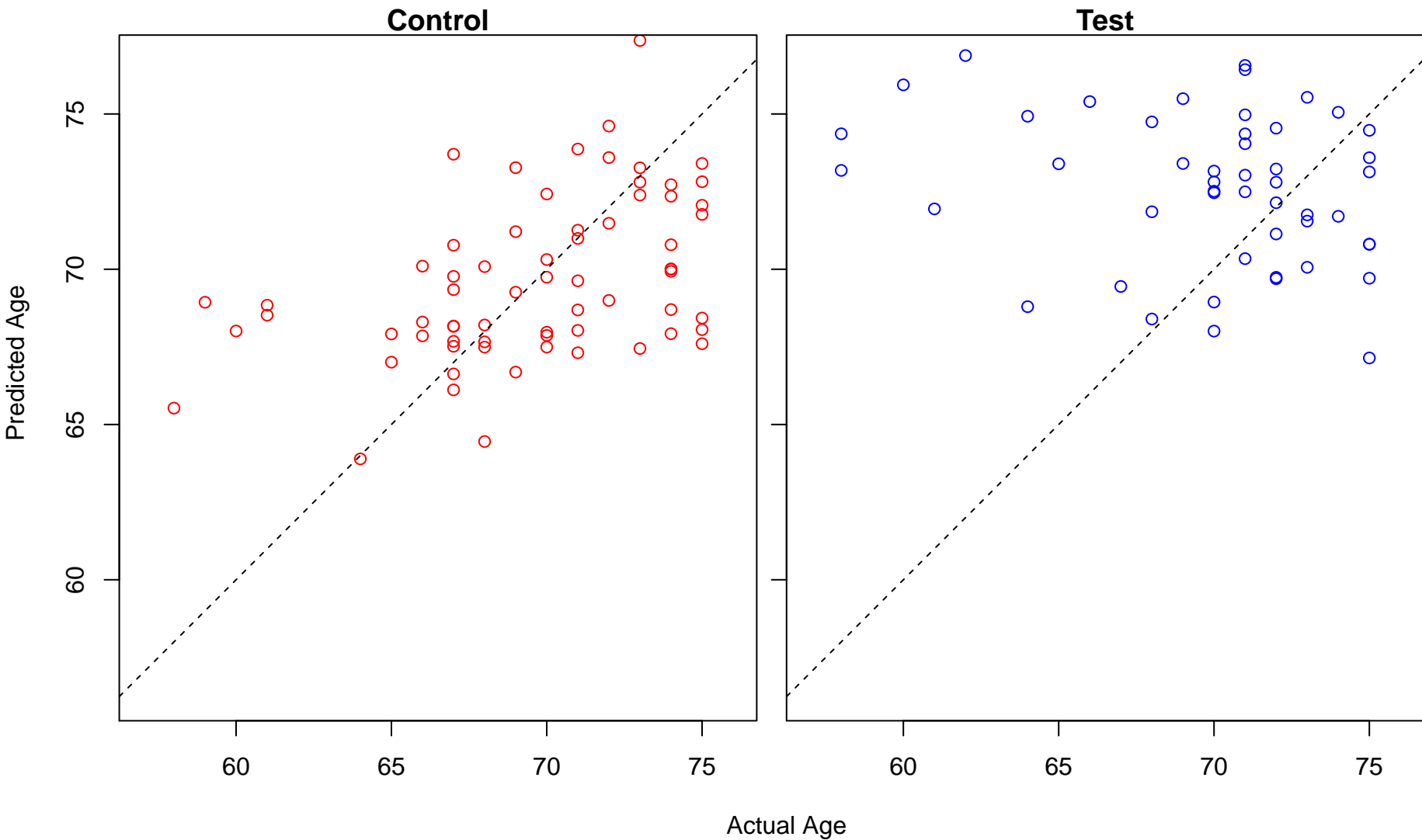
regulation of posttranscriptional gene silencing (Score: 0.848500)



regulation of gene silencing by RNA (Score: 0.848500)

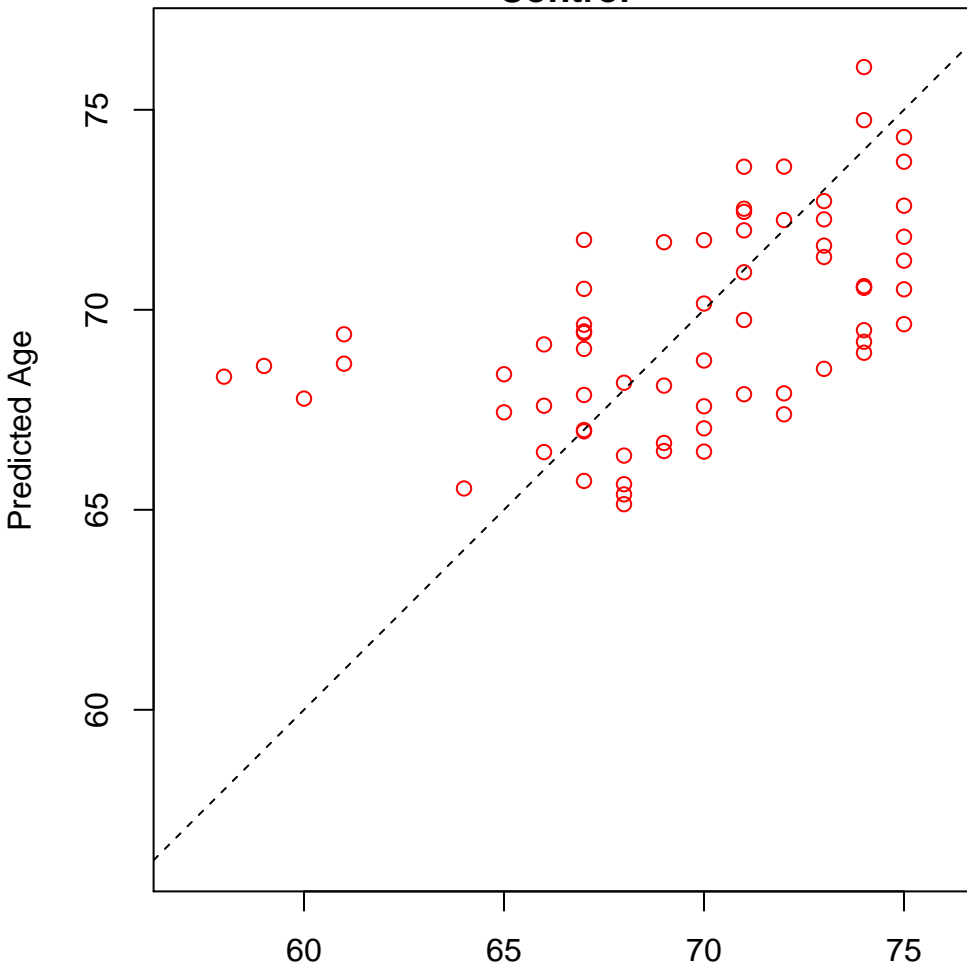


transepithelial transport (Score: 0.847975)

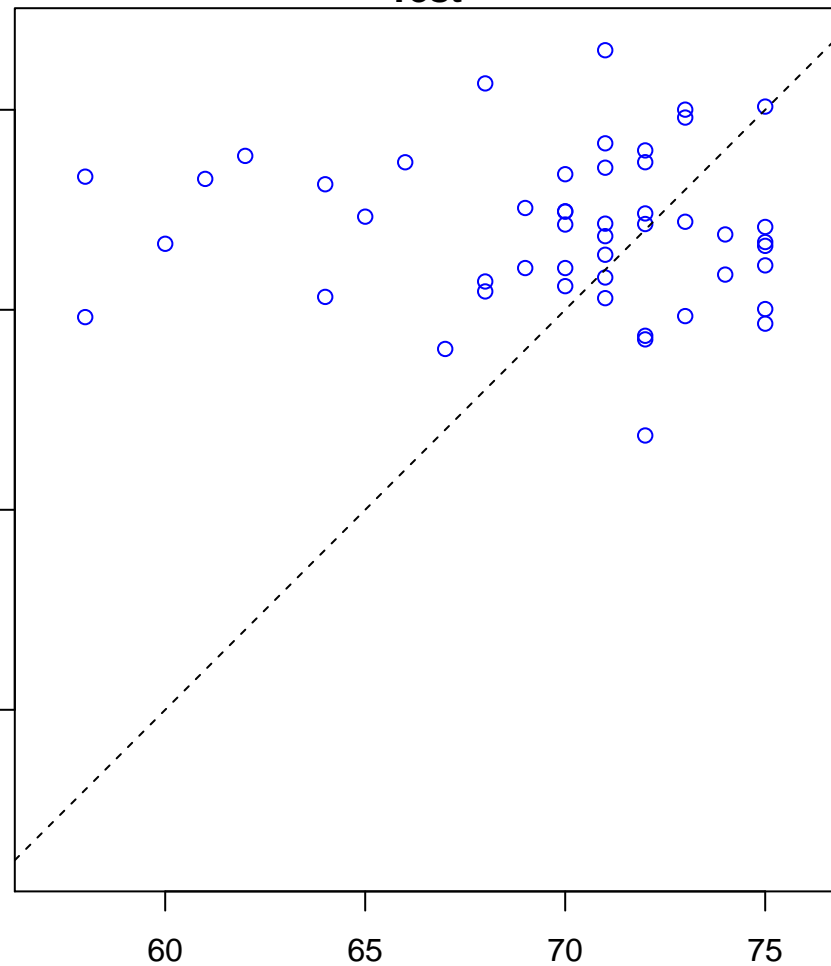


regulation of muscle tissue development (Score: 0.847548)

Control

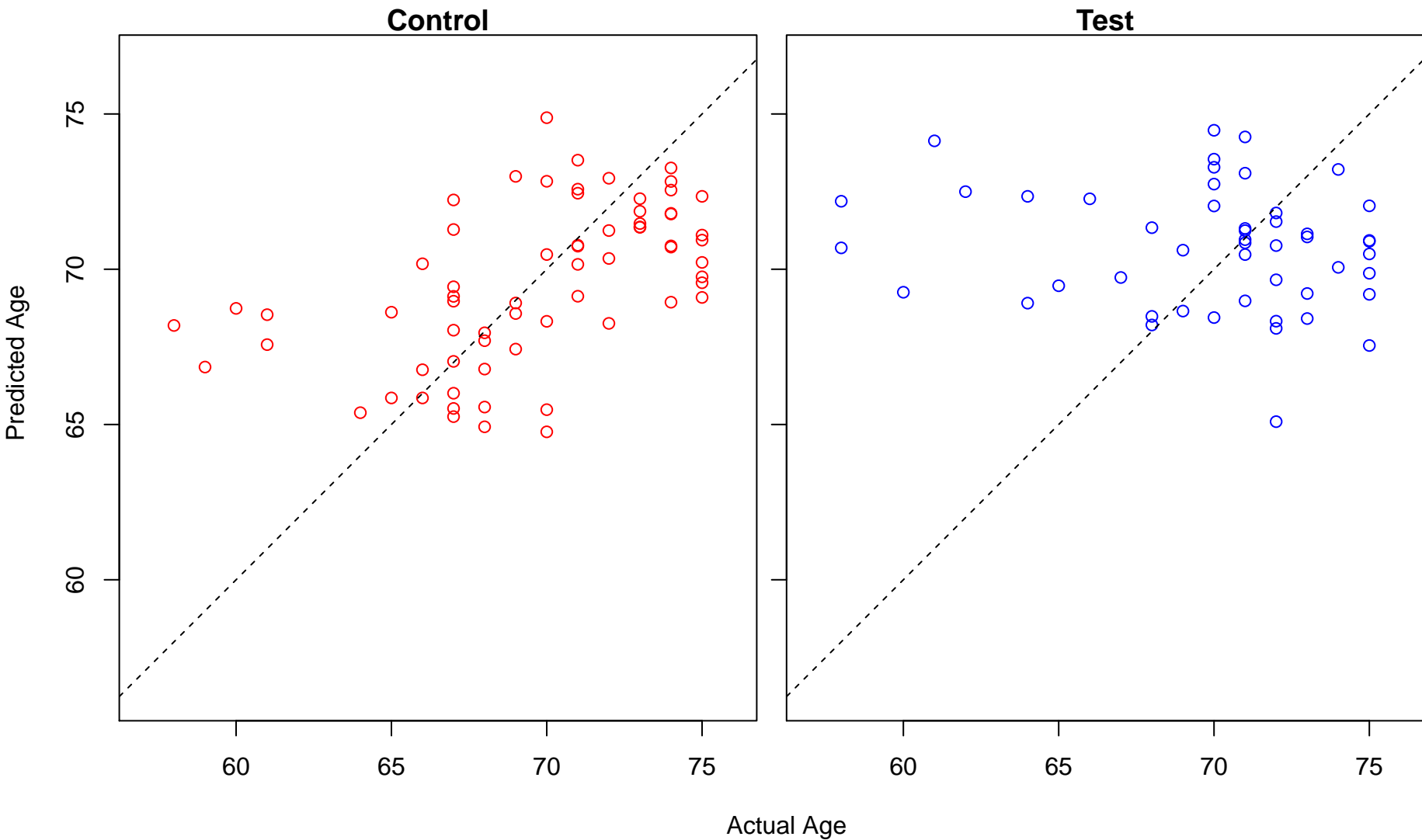


Test

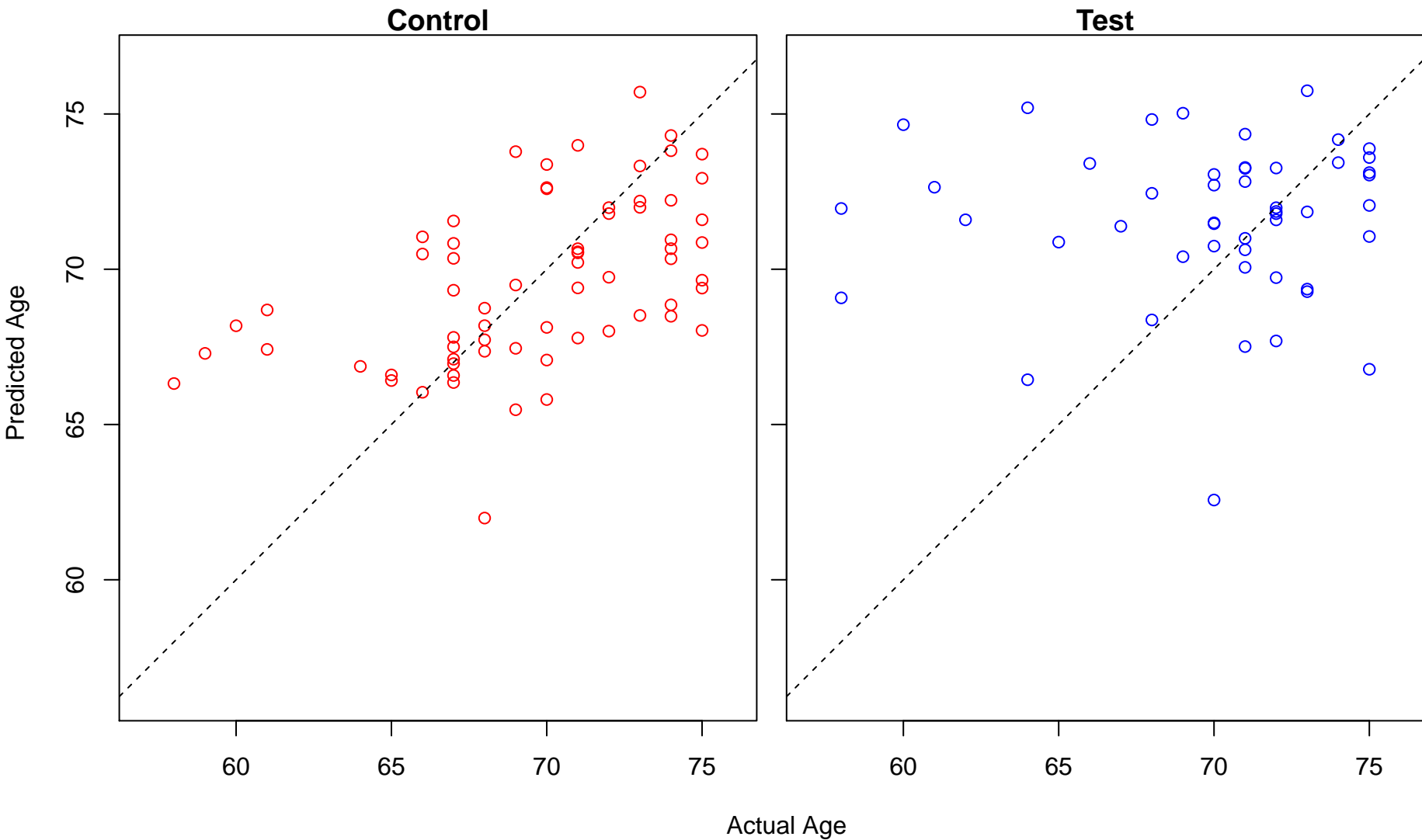


Actual Age

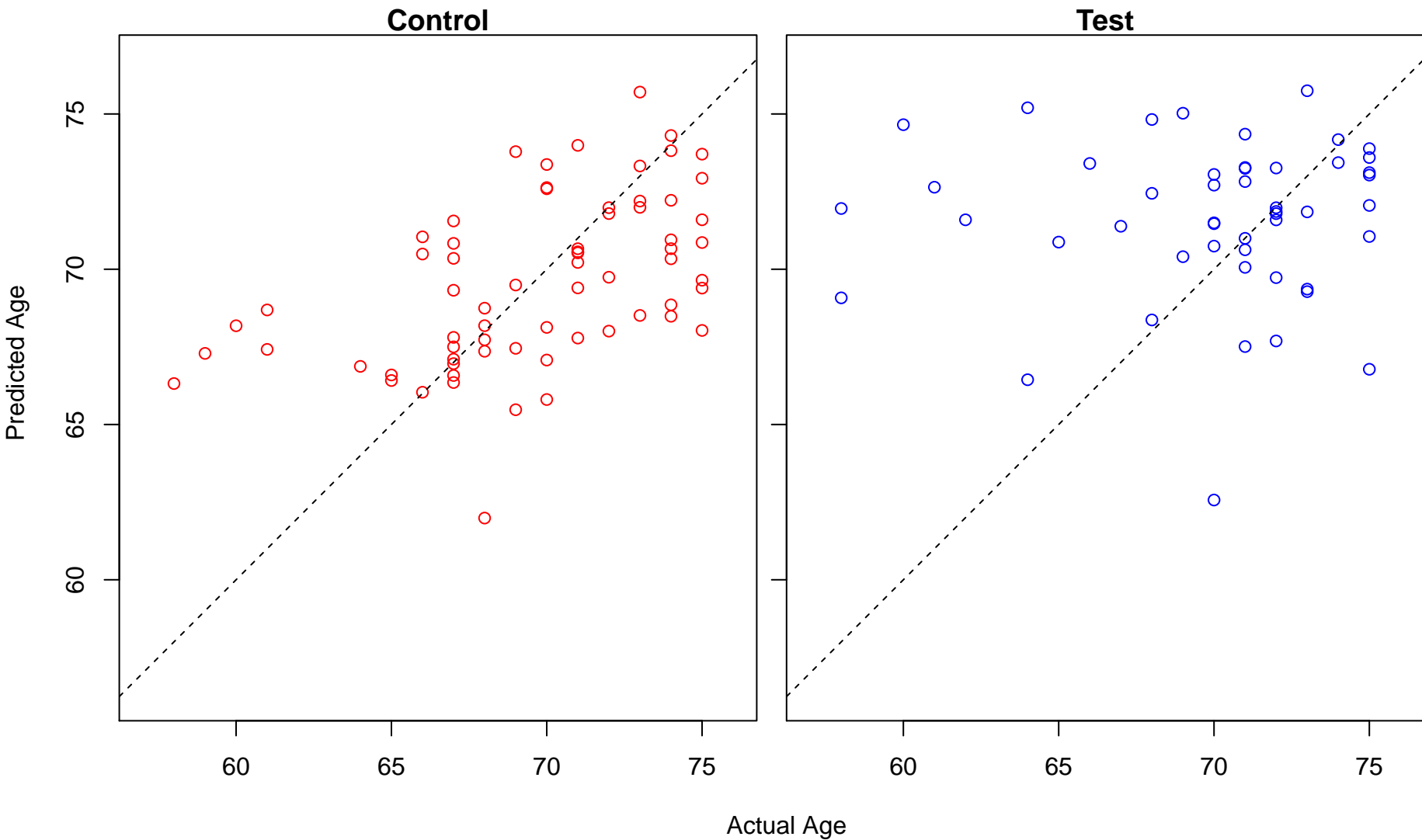
regulation of cytokine biosynthetic process (Score: 0.847257)



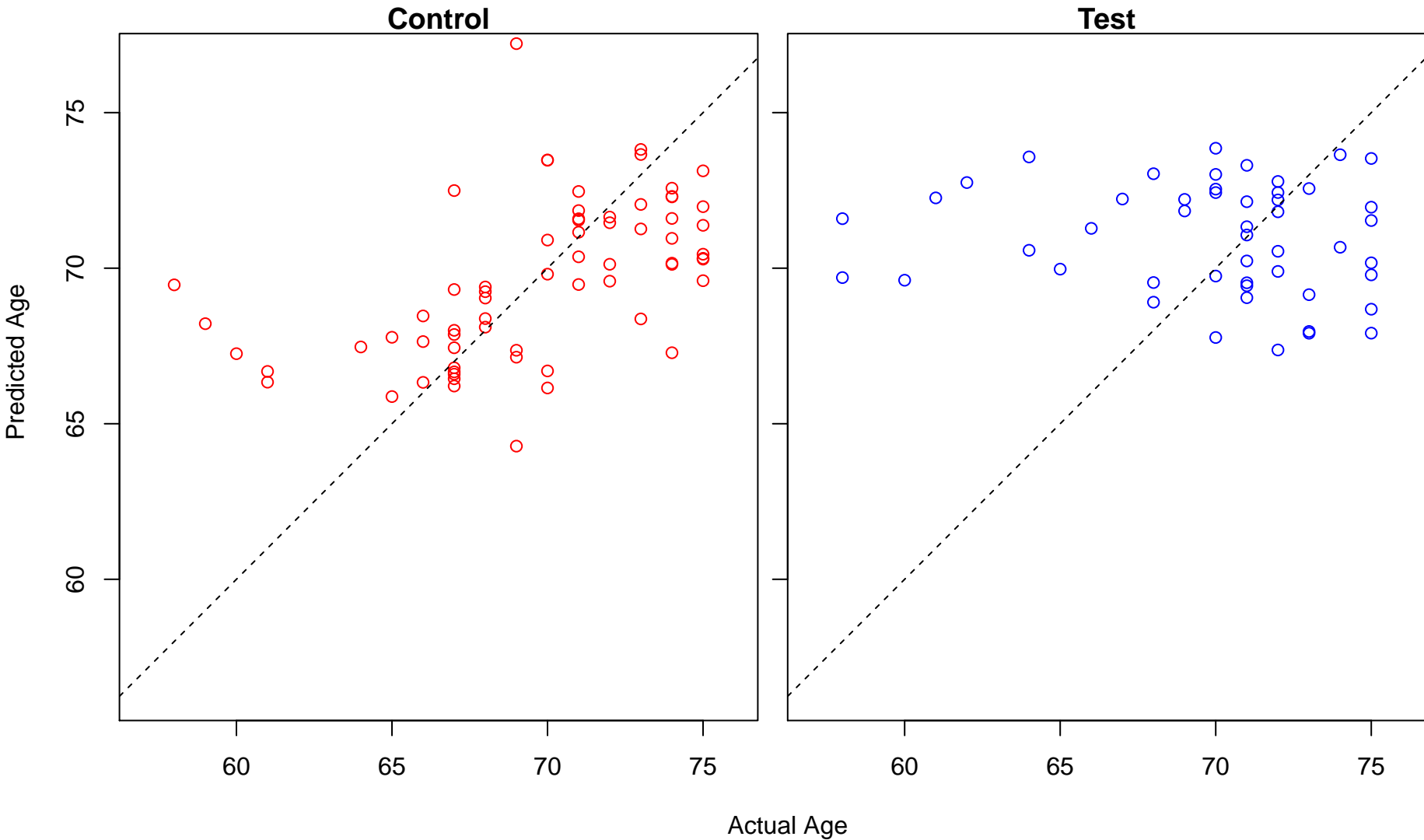
regulation of glycogen biosynthetic process (Score: 0.846950)



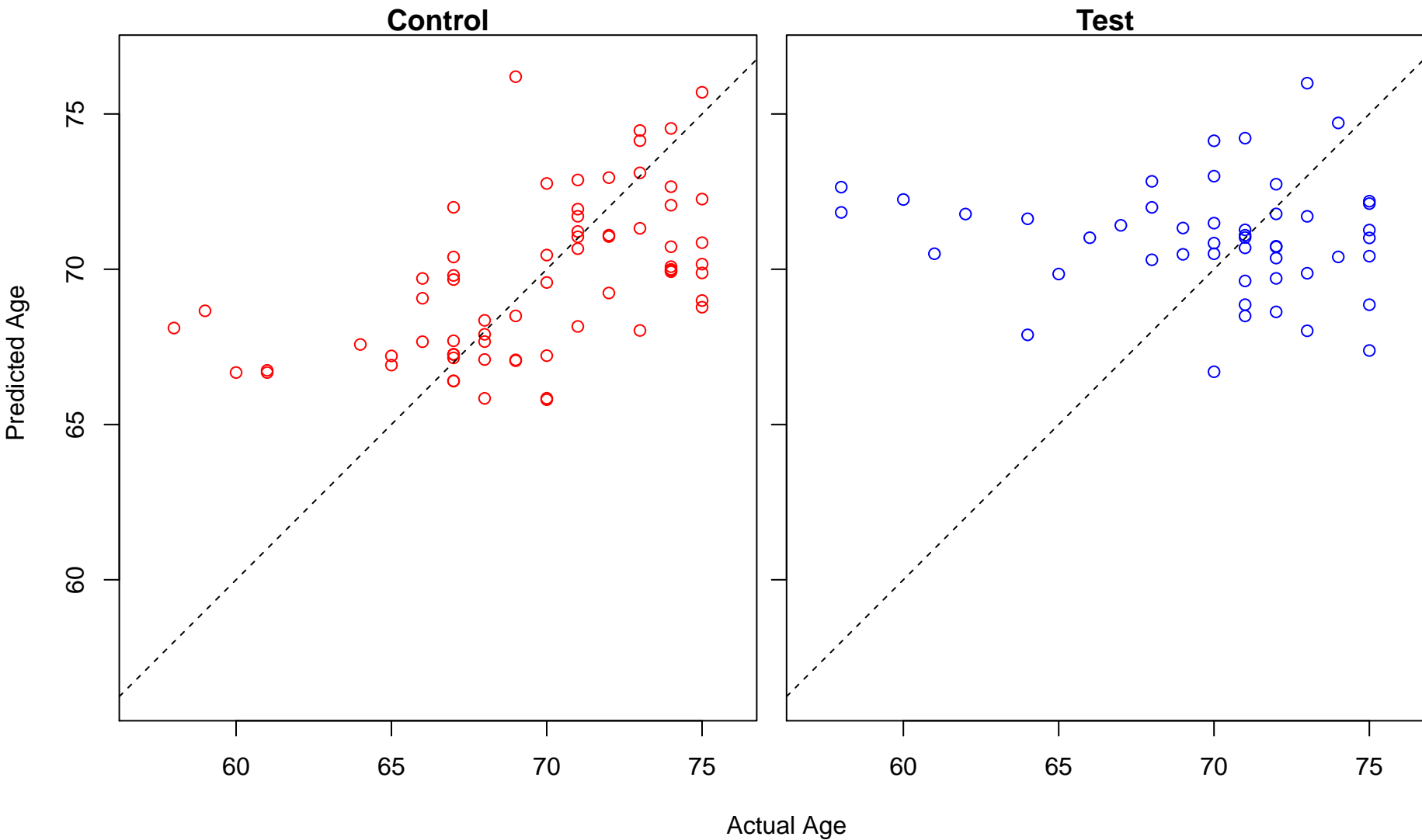
regulation of glucan biosynthetic process (Score: 0.846950)



cellular hormone metabolic process (Score: 0.846898)

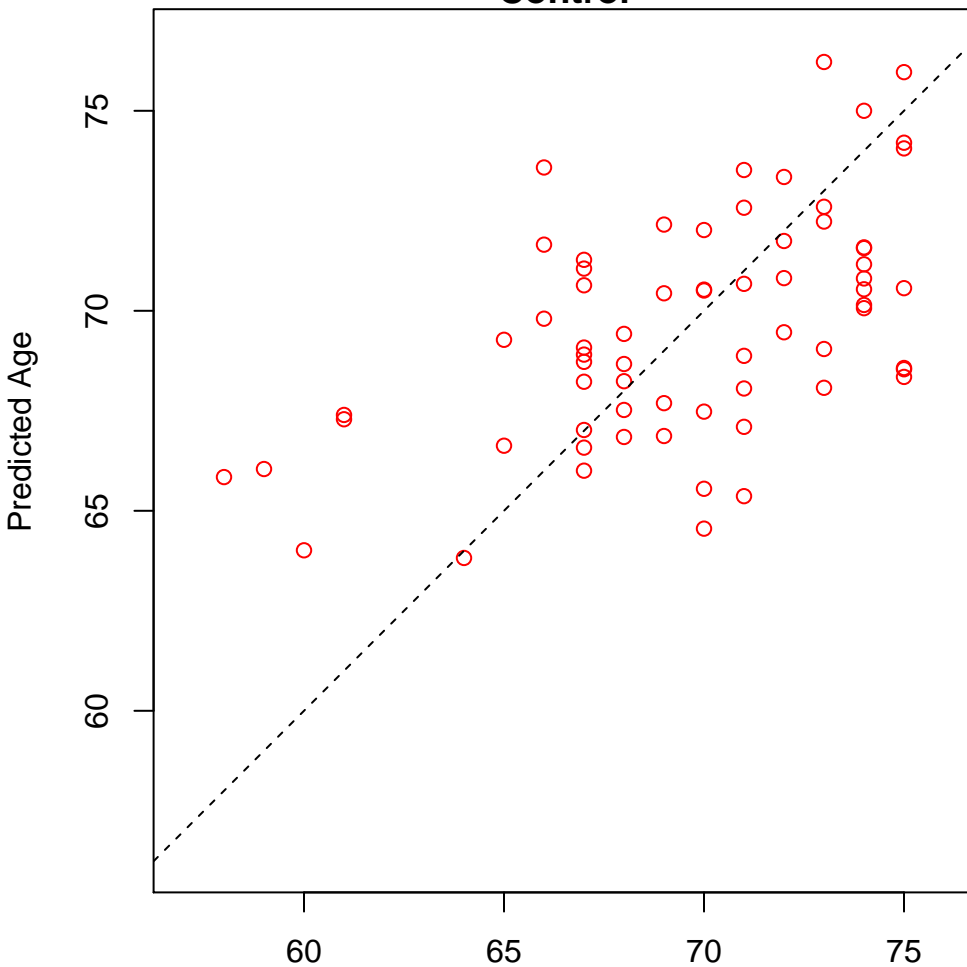


positive regulation of posttranscriptional gene silencing (Score: 0.846888)

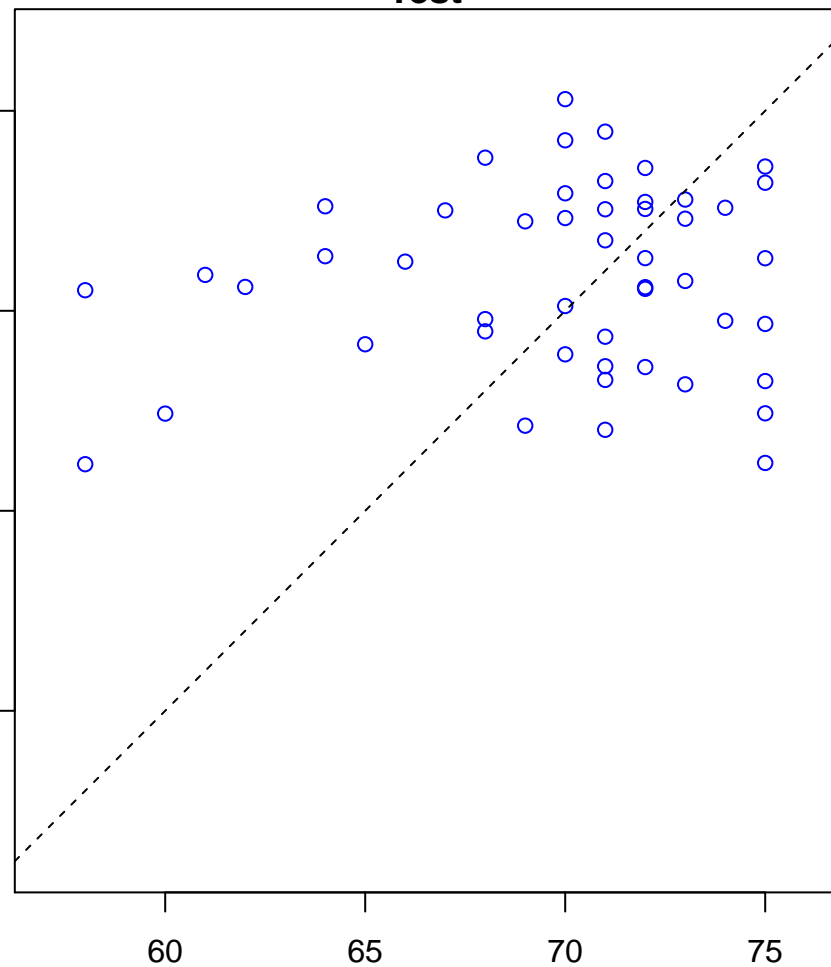


regulation of glial cell apoptotic process (Score: 0.846833)

Control

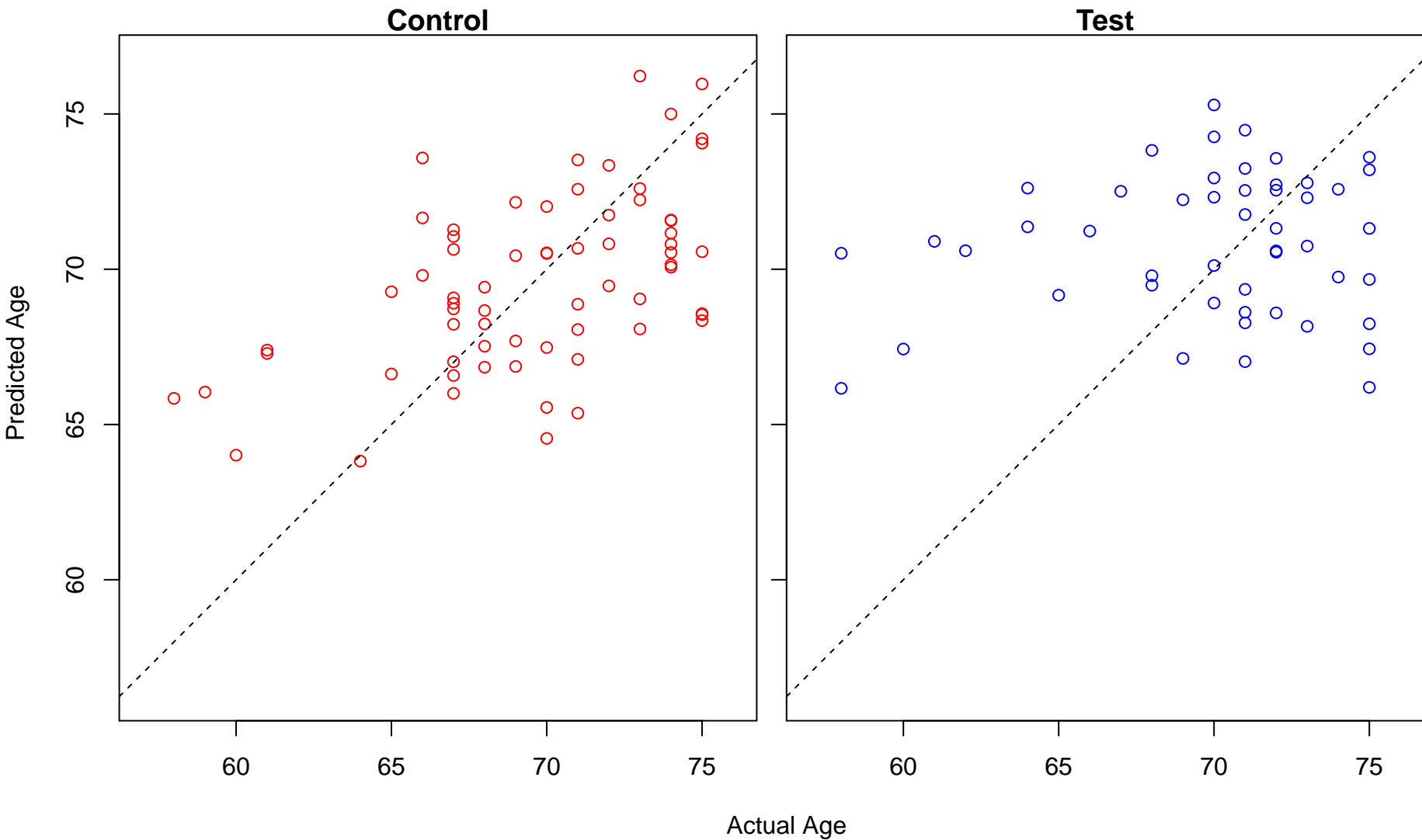


Test

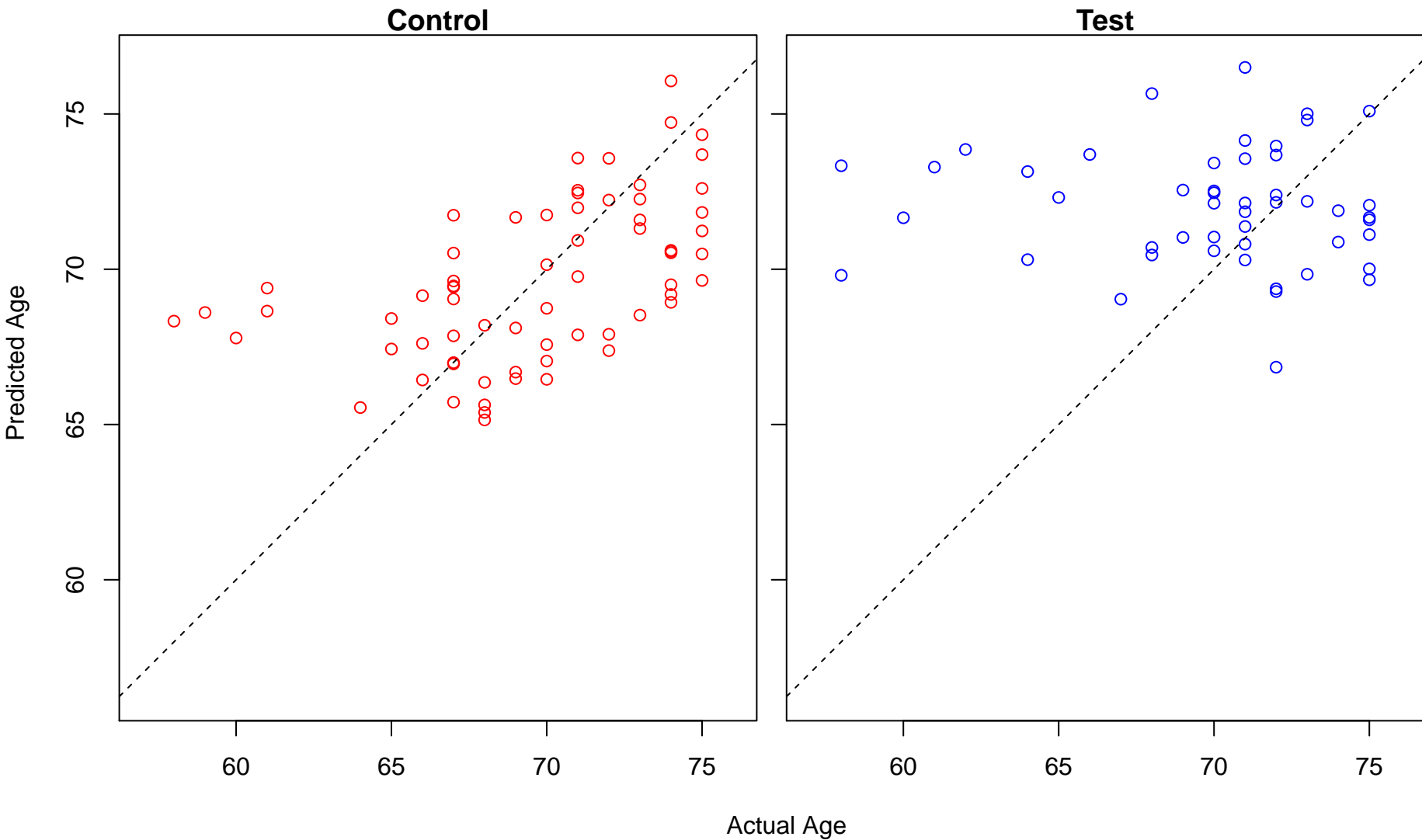


Actual Age

negative regulation of glial cell apoptotic process (Score: 0.846833)

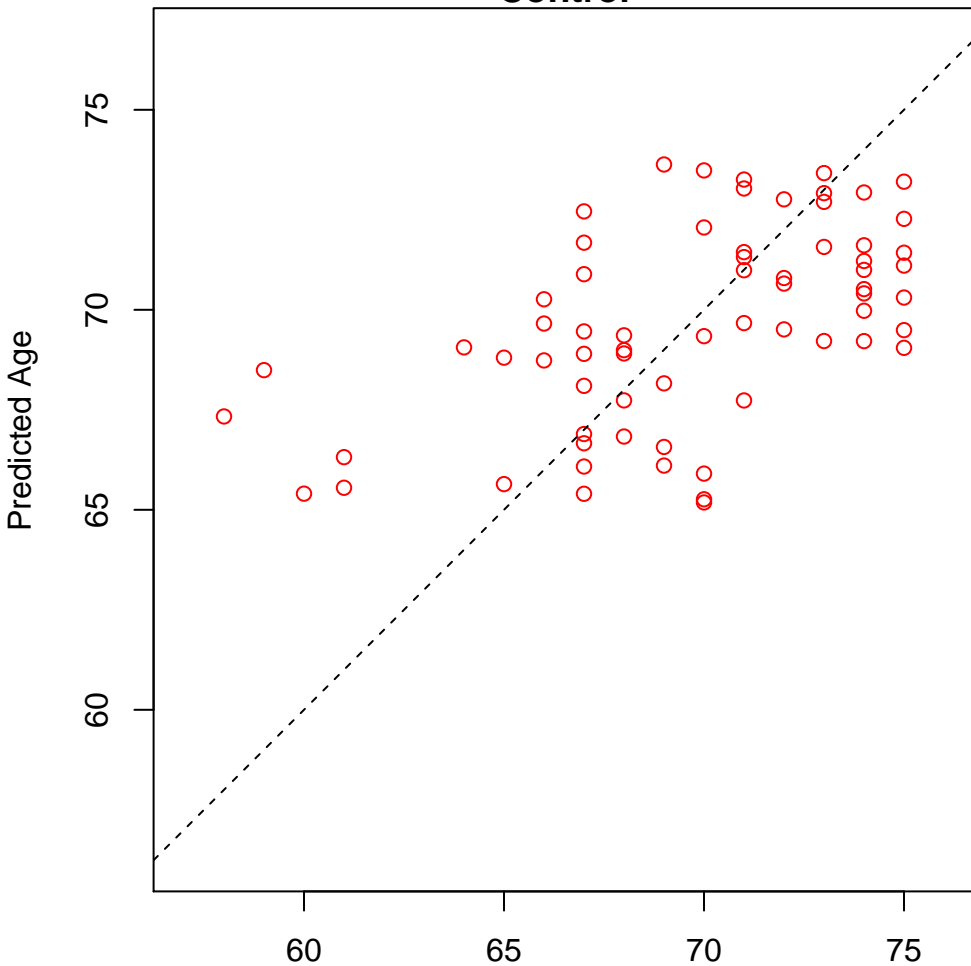


regulation of striated muscle tissue development (Score: 0.846313)

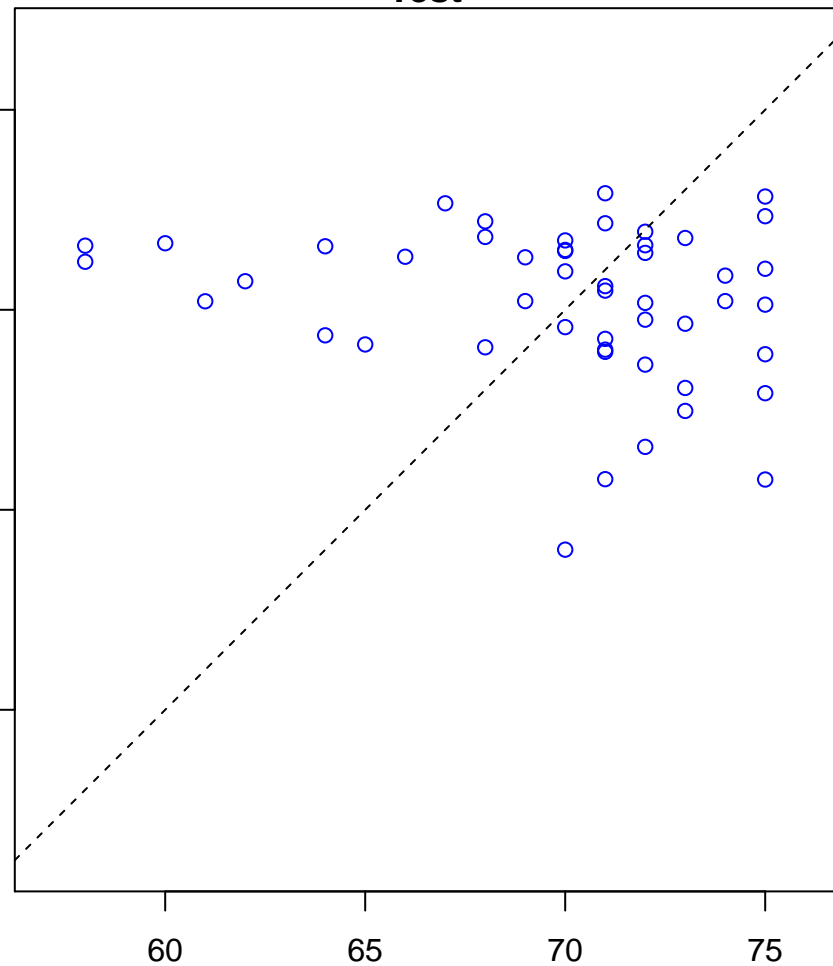


detection of molecule of bacterial origin (Score: 0.846251)

Control

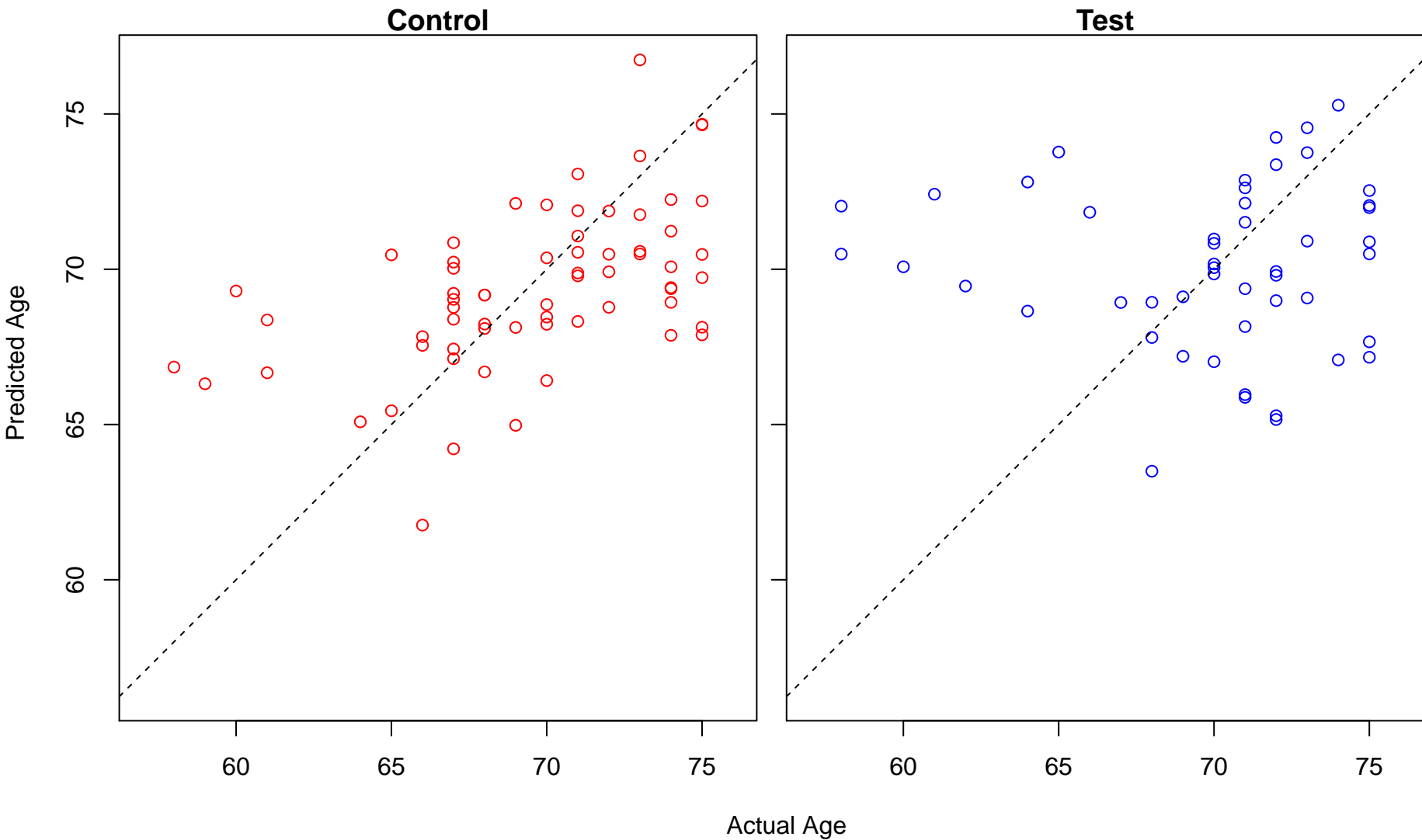


Test

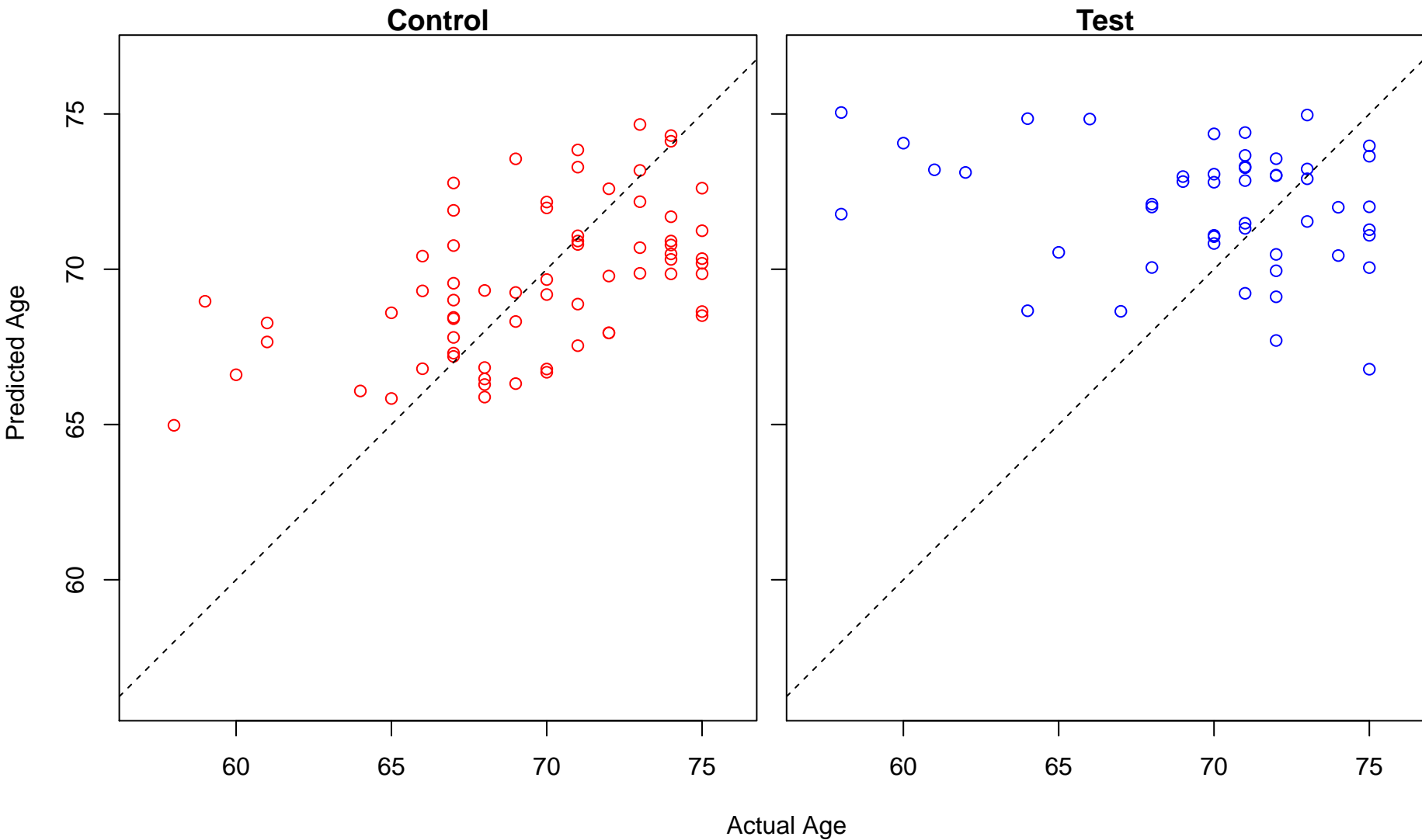


Actual Age

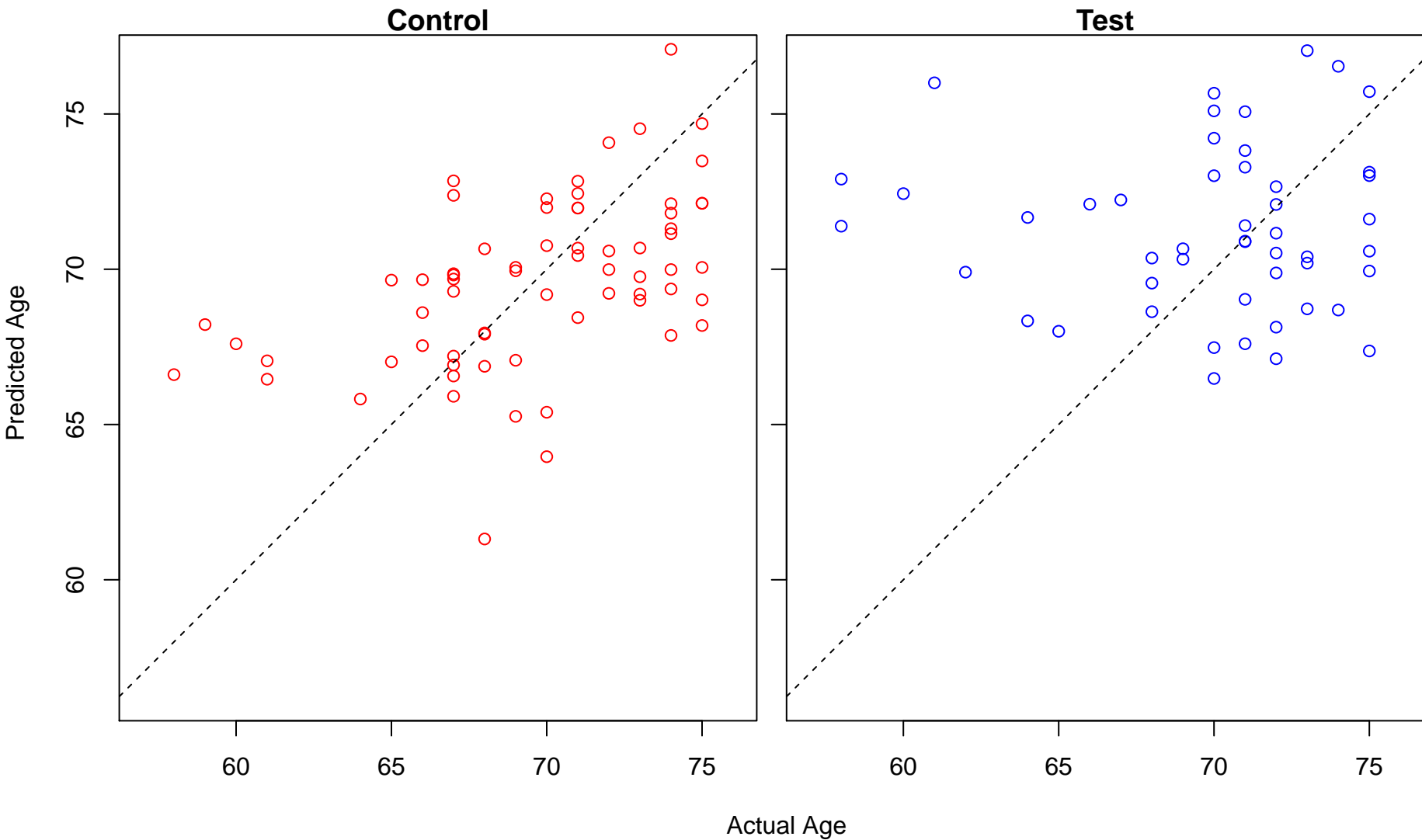
cardiac muscle cell contraction (Score: 0.845858)



smooth muscle cell differentiation (Score: 0.845550)

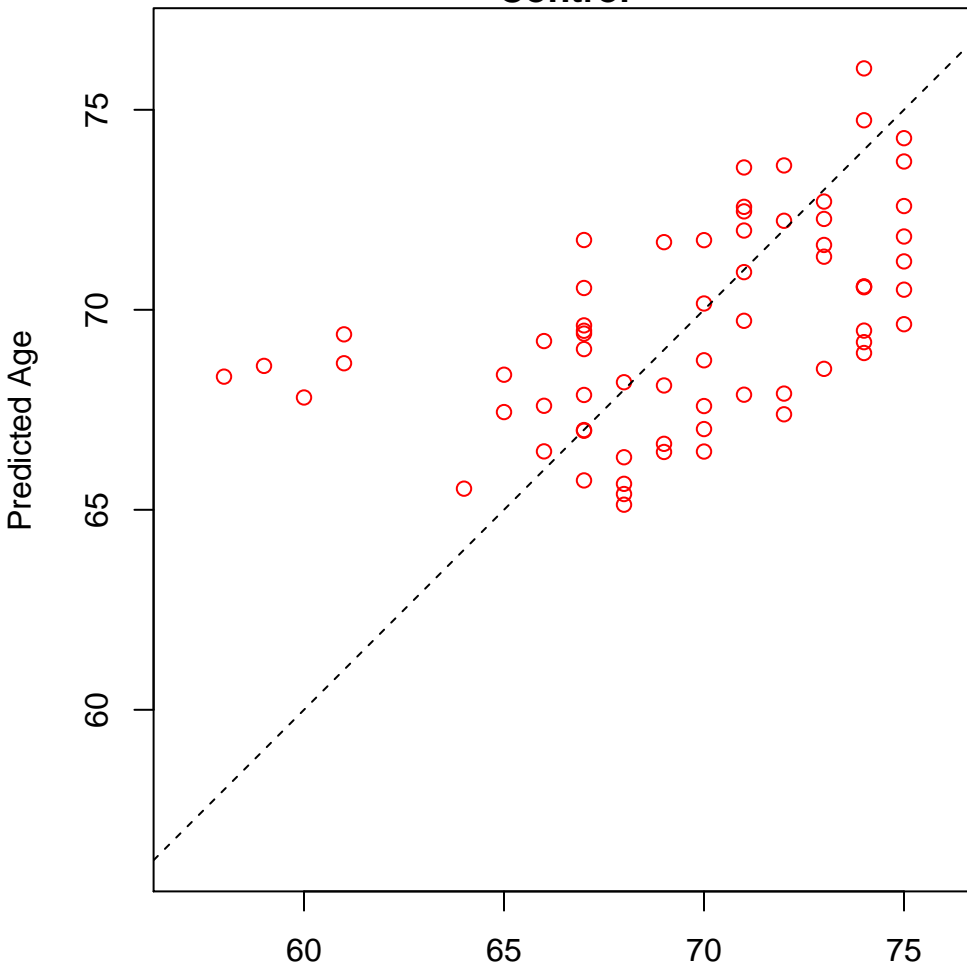


positive regulation of heart rate (Score: 0.845117)

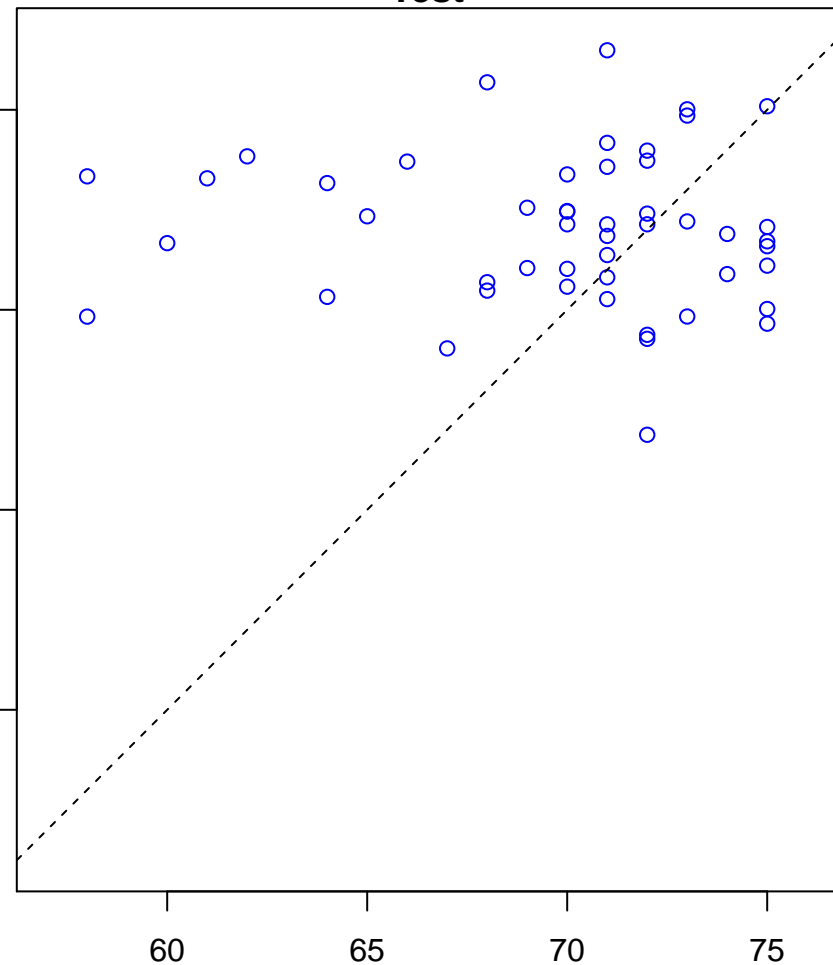


regulation of muscle organ development (Score: 0.845093)

Control

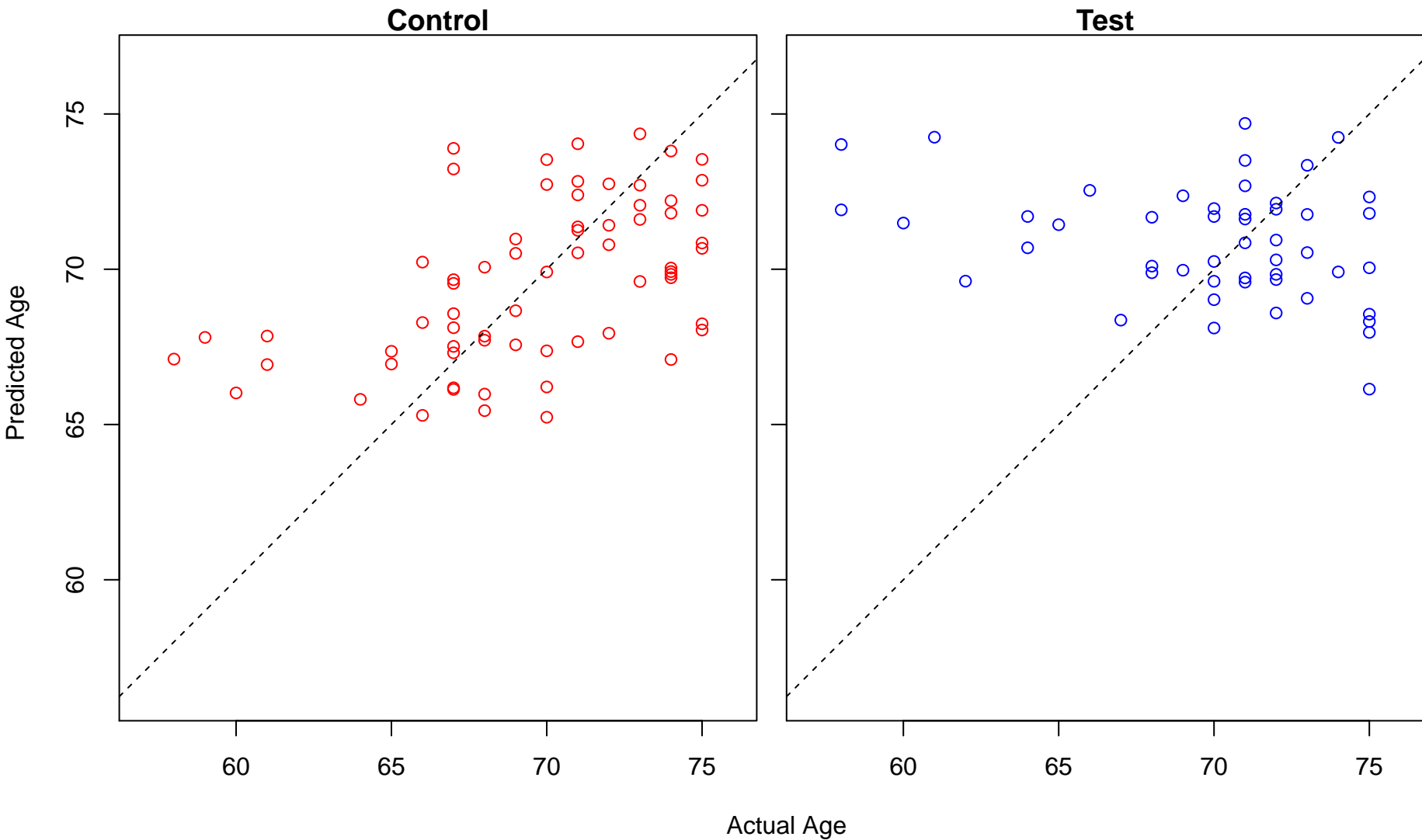


Test

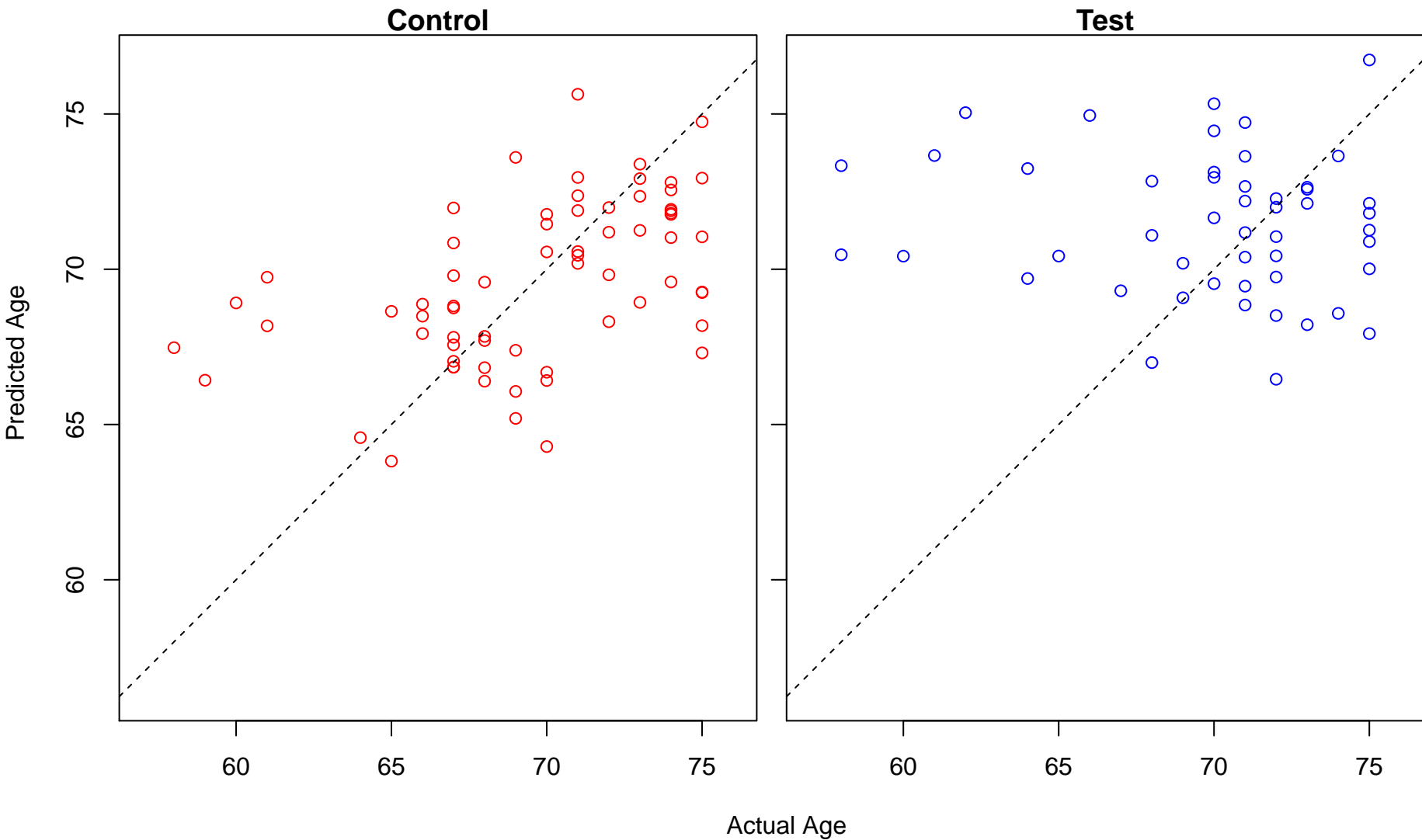


Actual Age

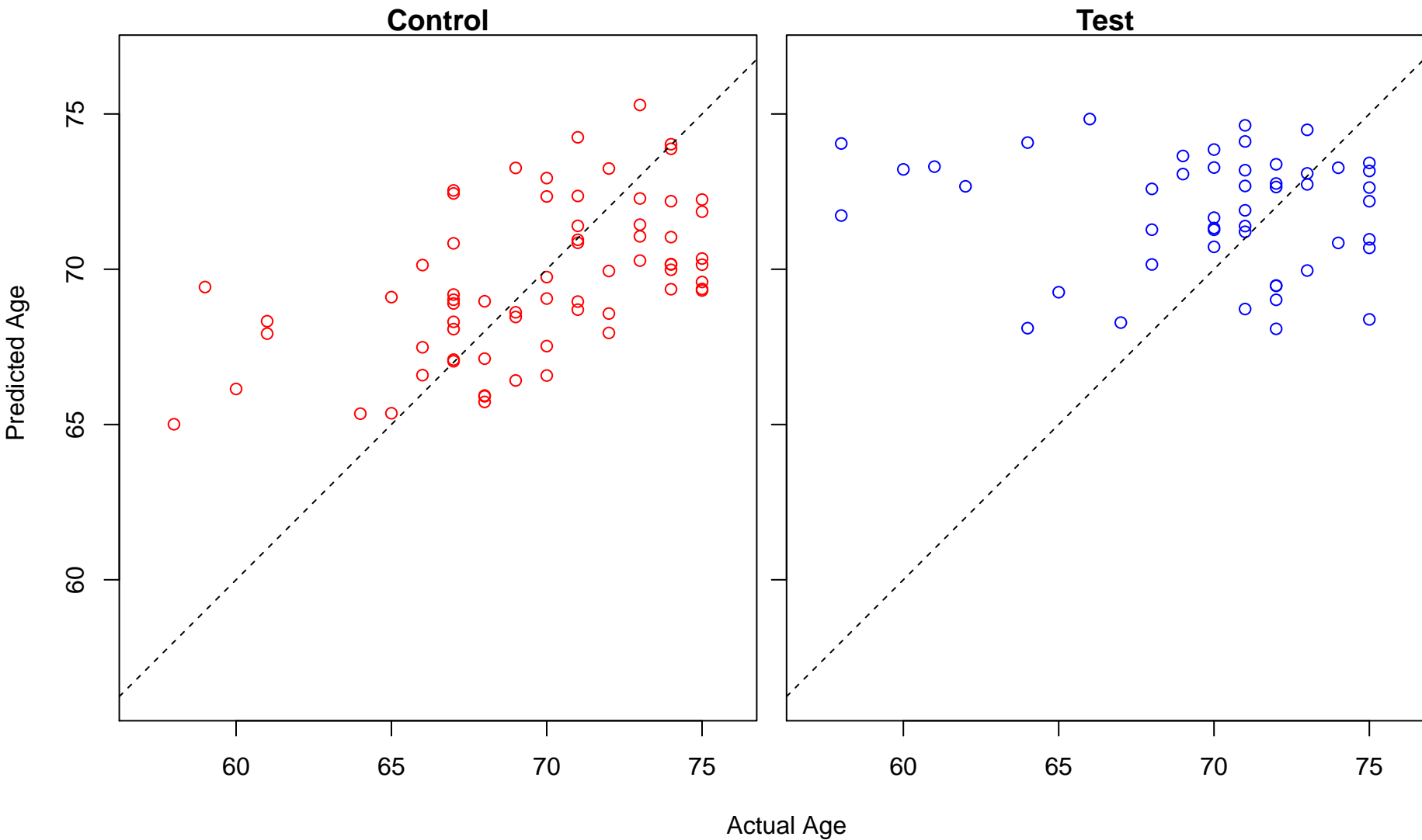
collagen metabolic process (Score: 0.844568)



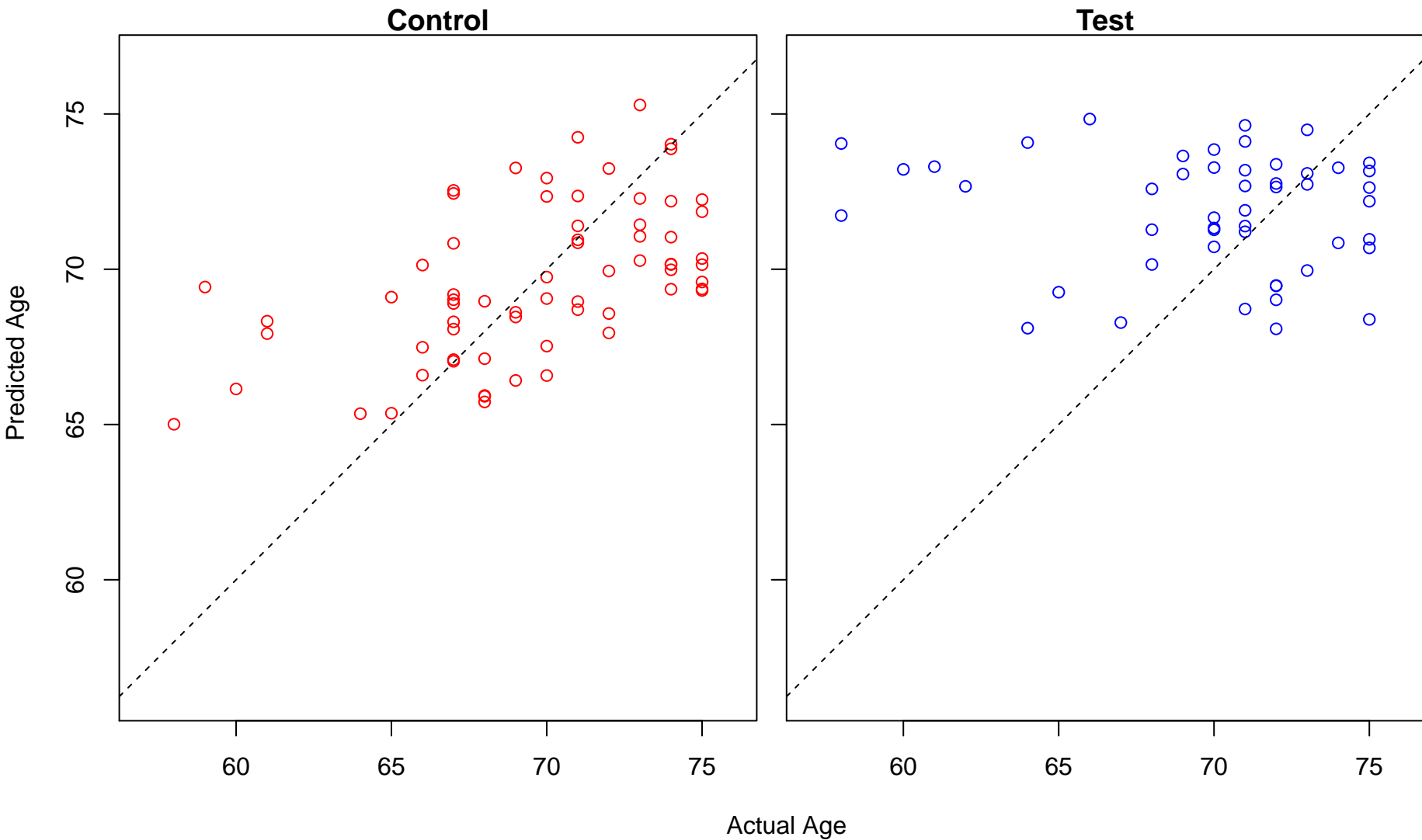
hyaluronan metabolic process (Score: 0.844204)



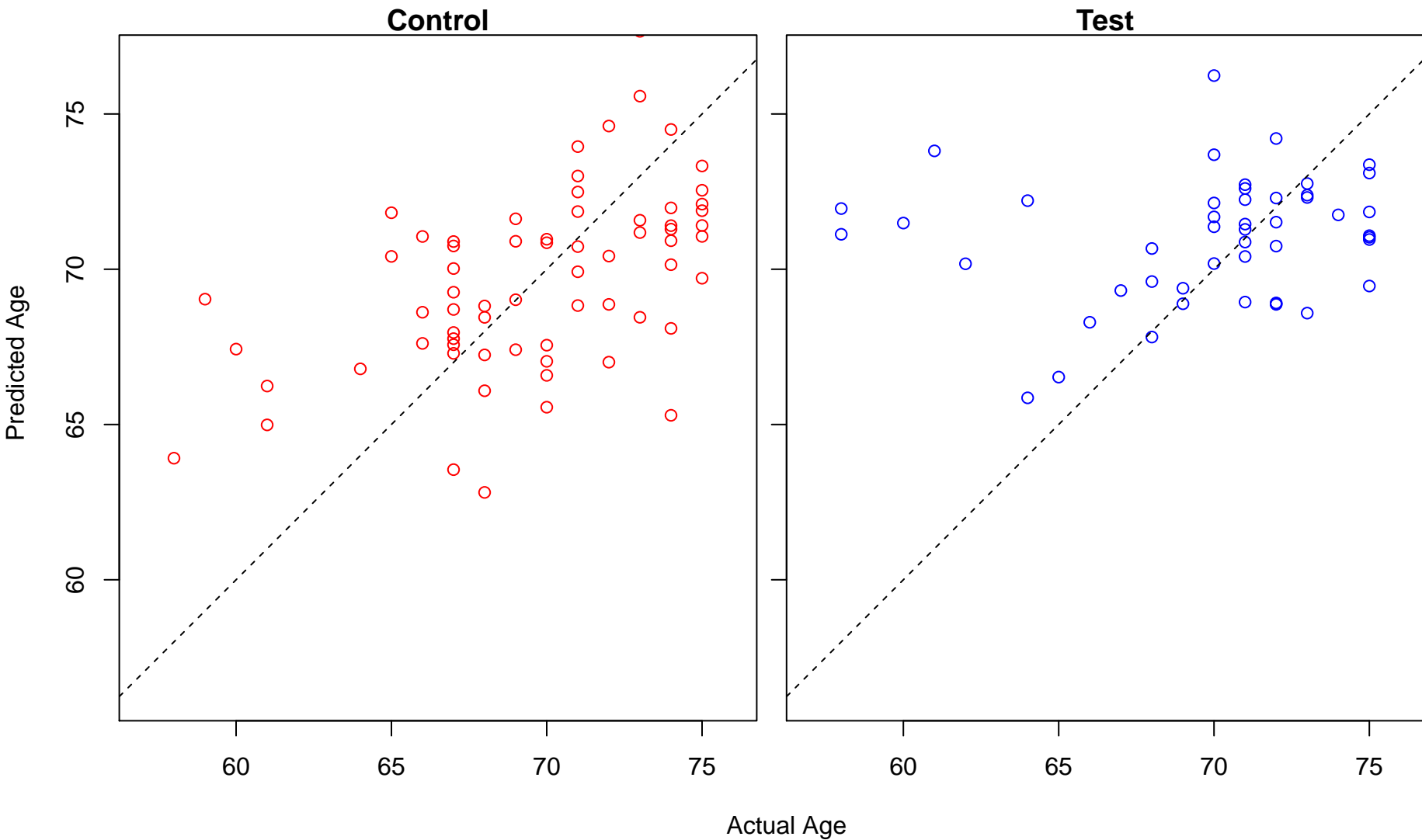
heart valve development (Score: 0.843888)



heart valve morphogenesis (Score: 0.843888)

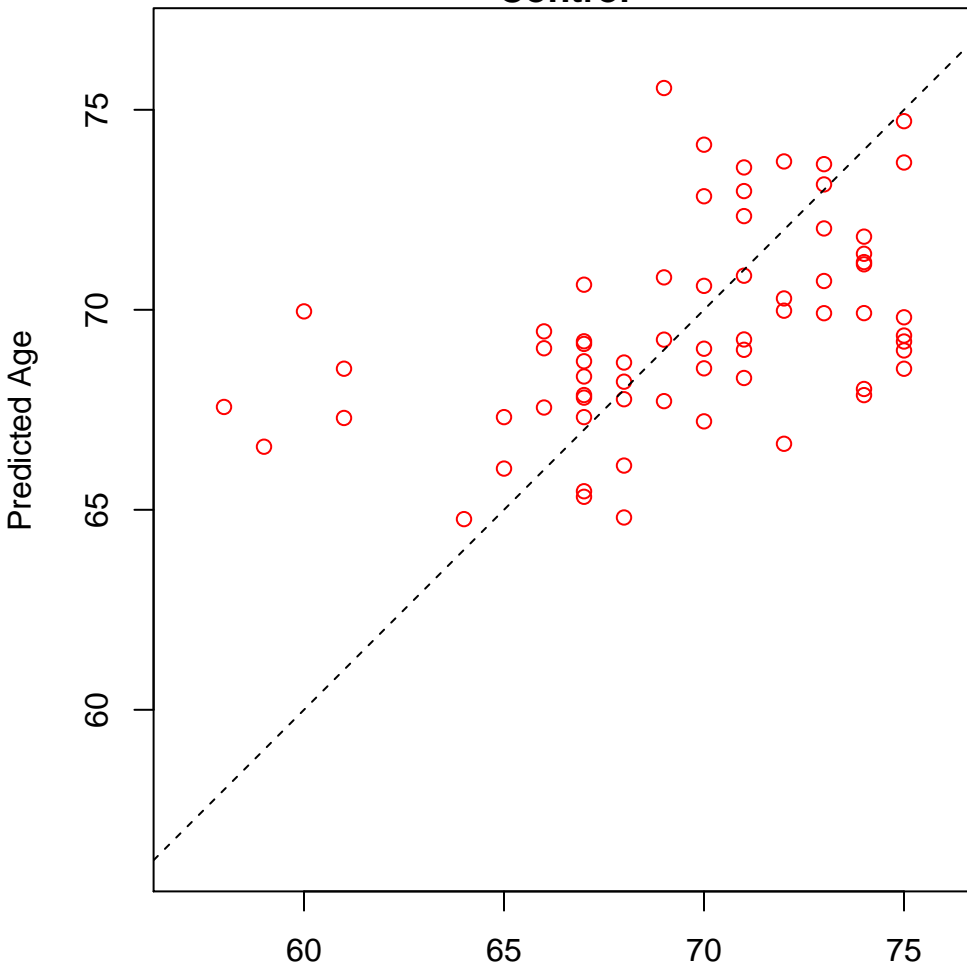


chemical synaptic transmission, postsynaptic (Score: 0.843788)

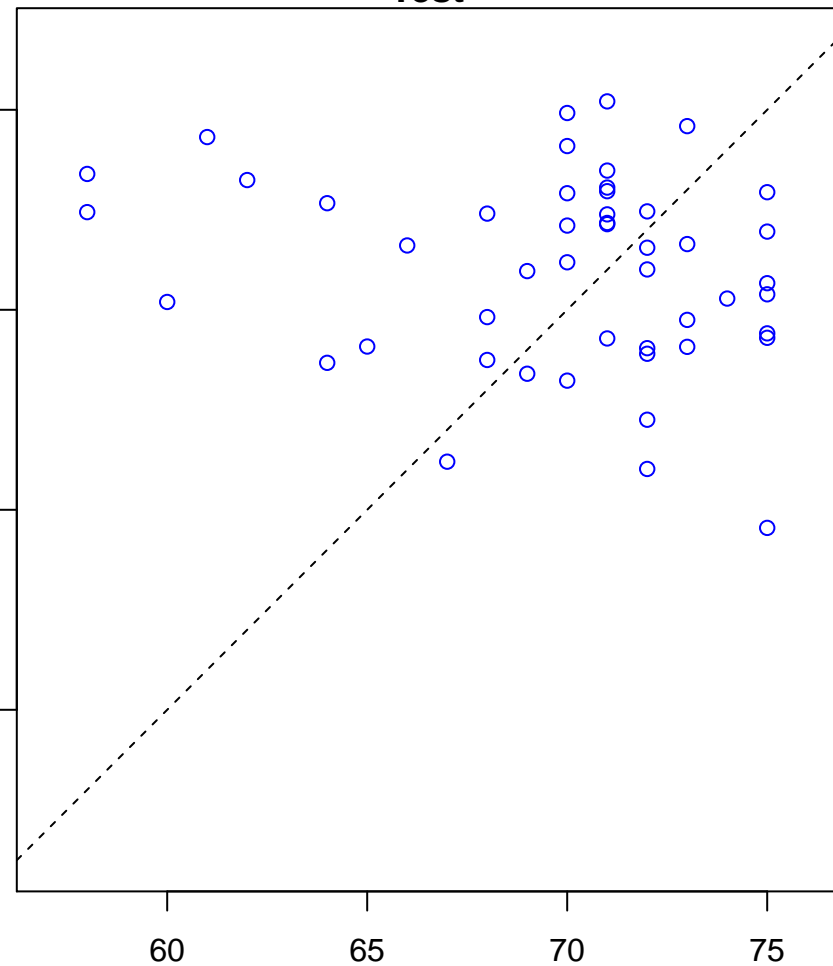


regulation of interleukin-12 production (Score: 0.843725)

Control



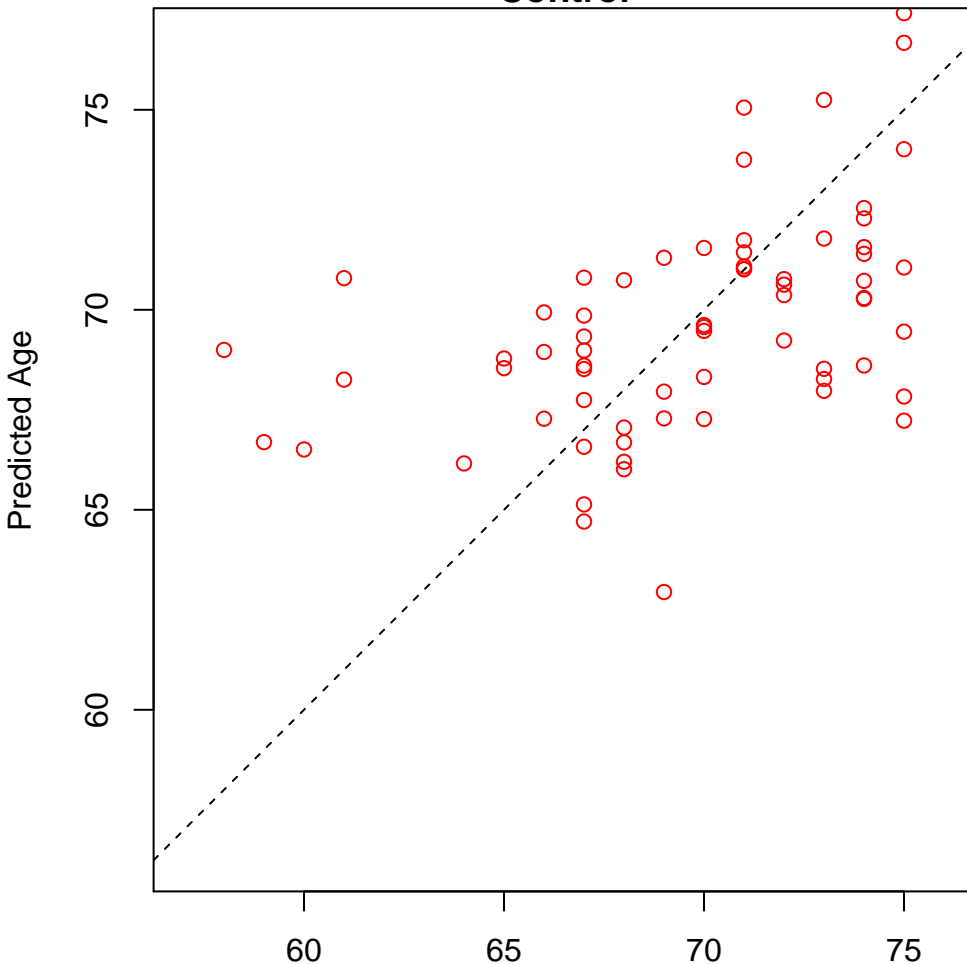
Test



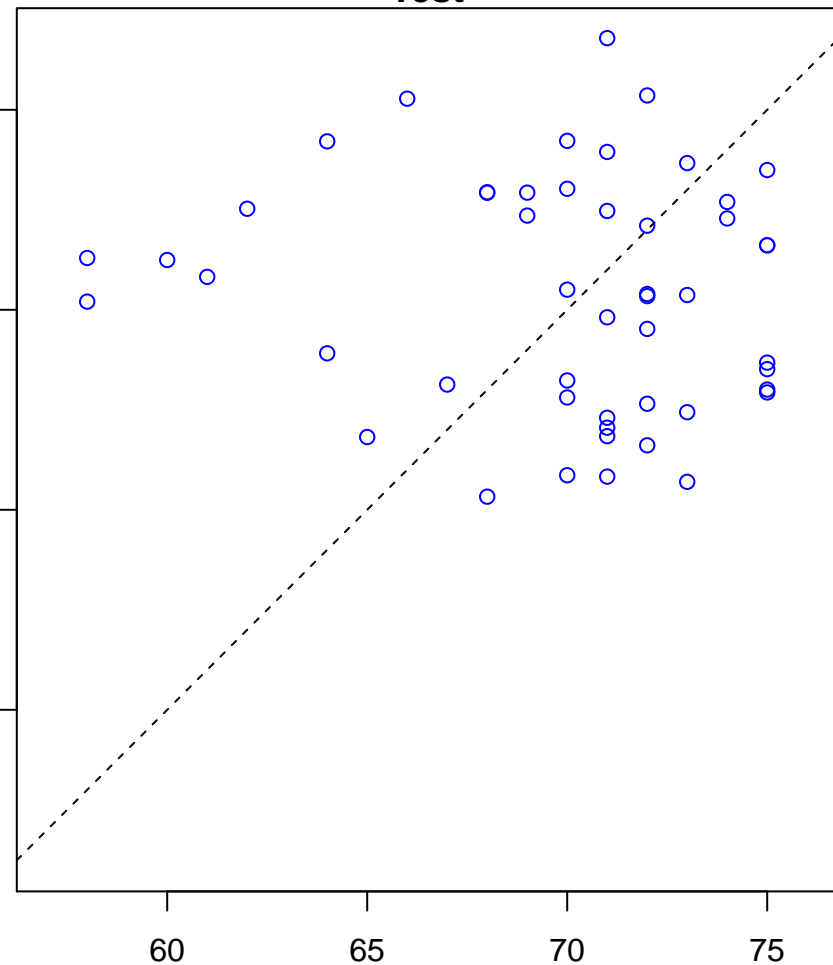
Actual Age

smooth muscle tissue development (Score: 0.843495)

Control

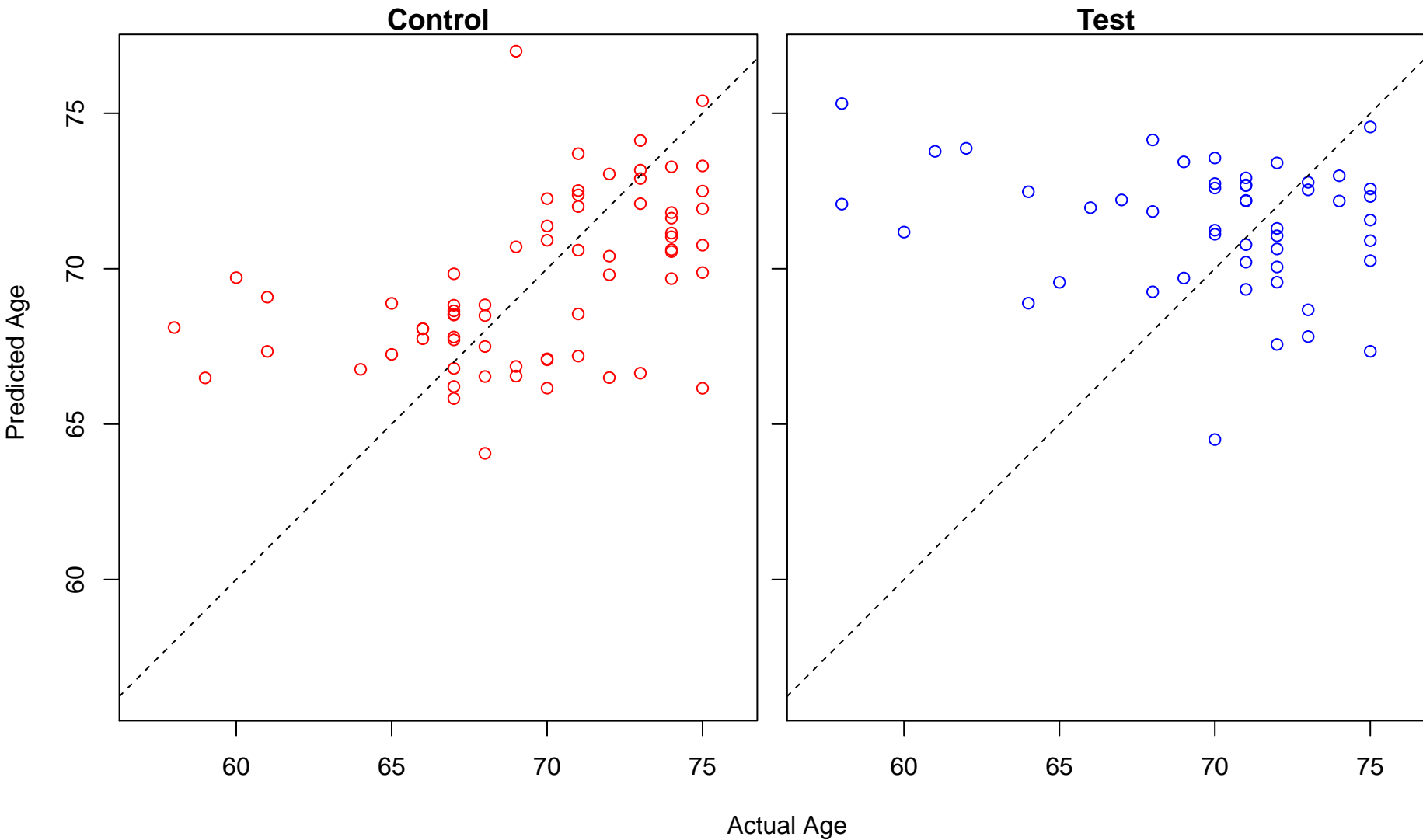


Test



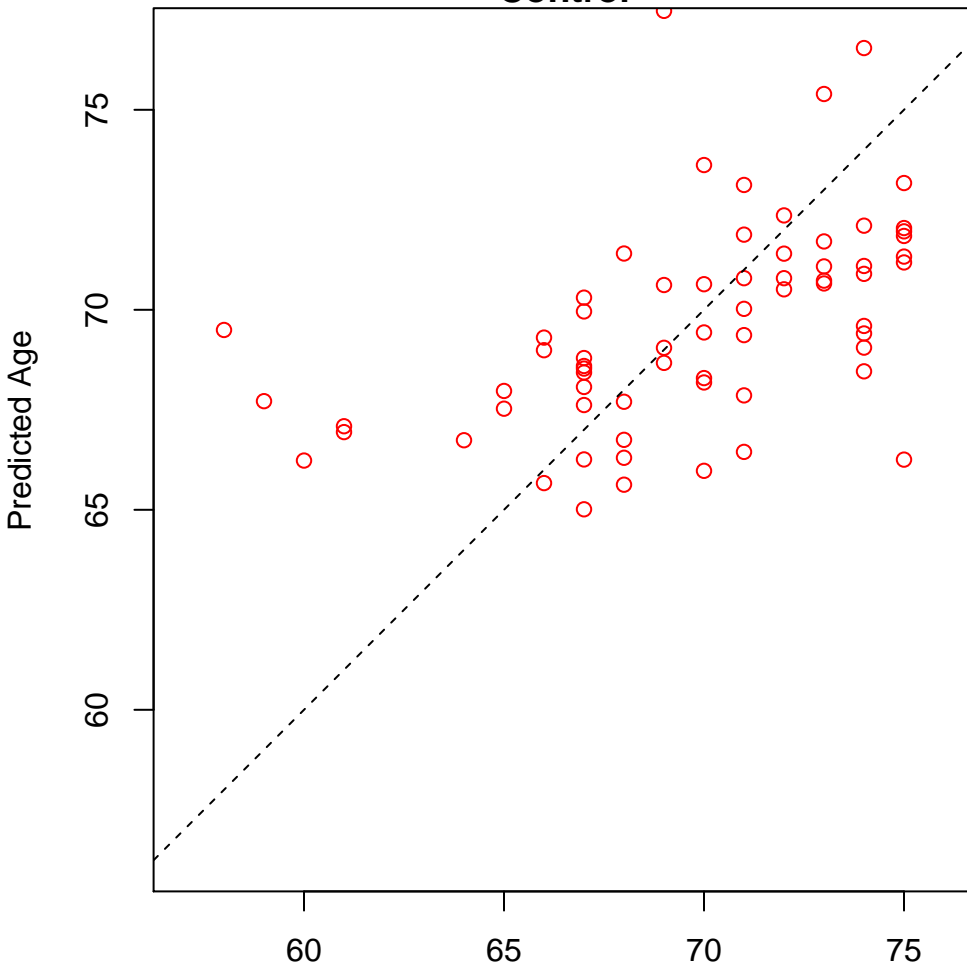
Actual Age

positive regulation of fat cell differentiation (Score: 0.843363)

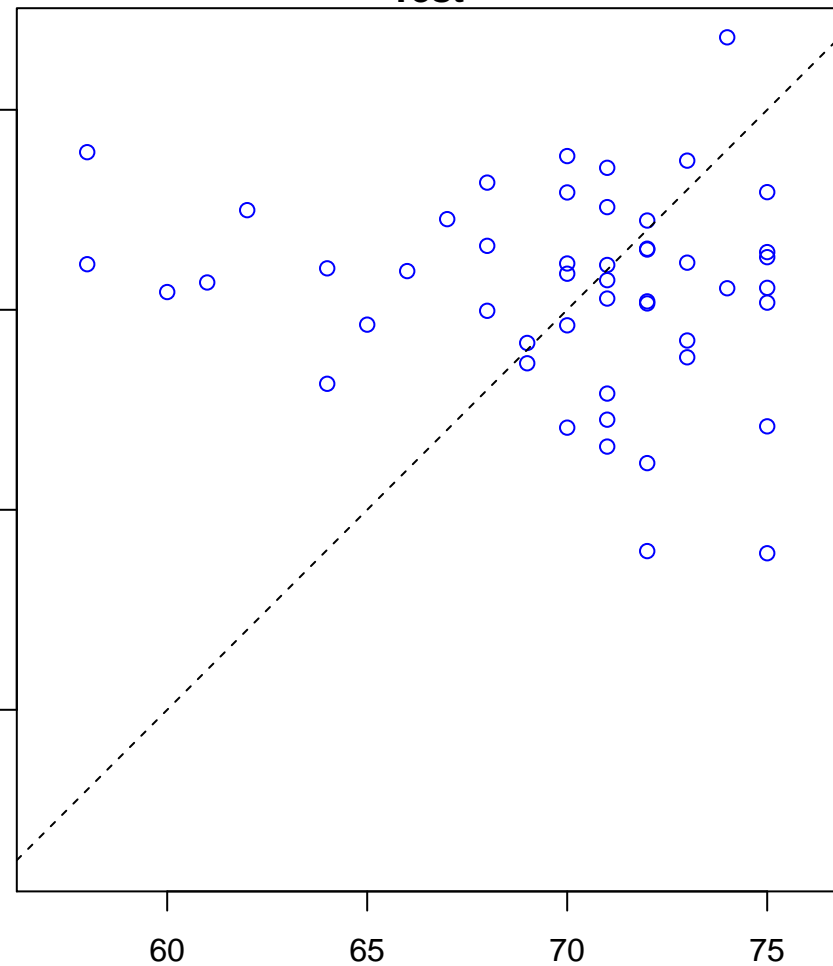


regulation of natural killer cell activation (Score: 0.843022)

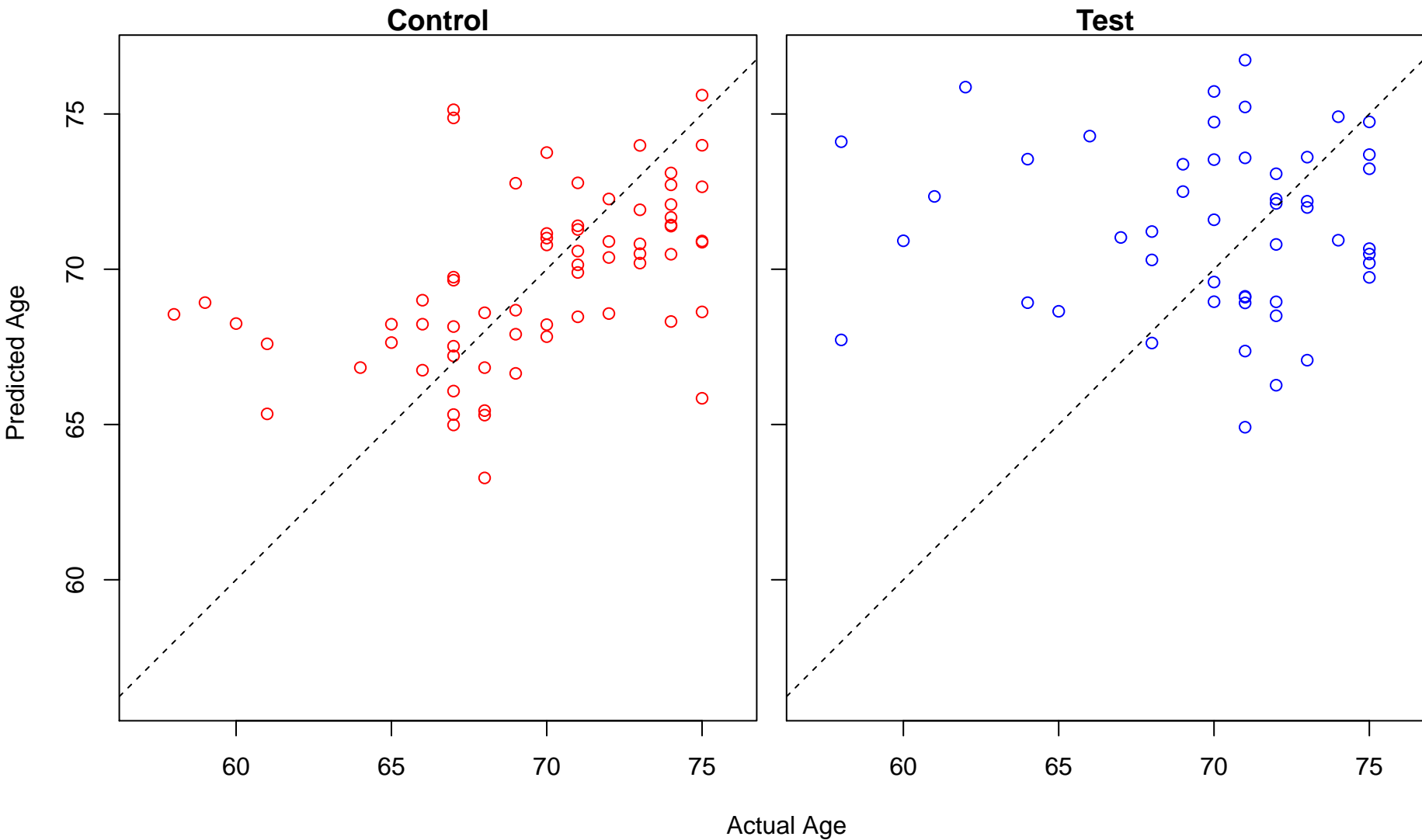
Control



Test

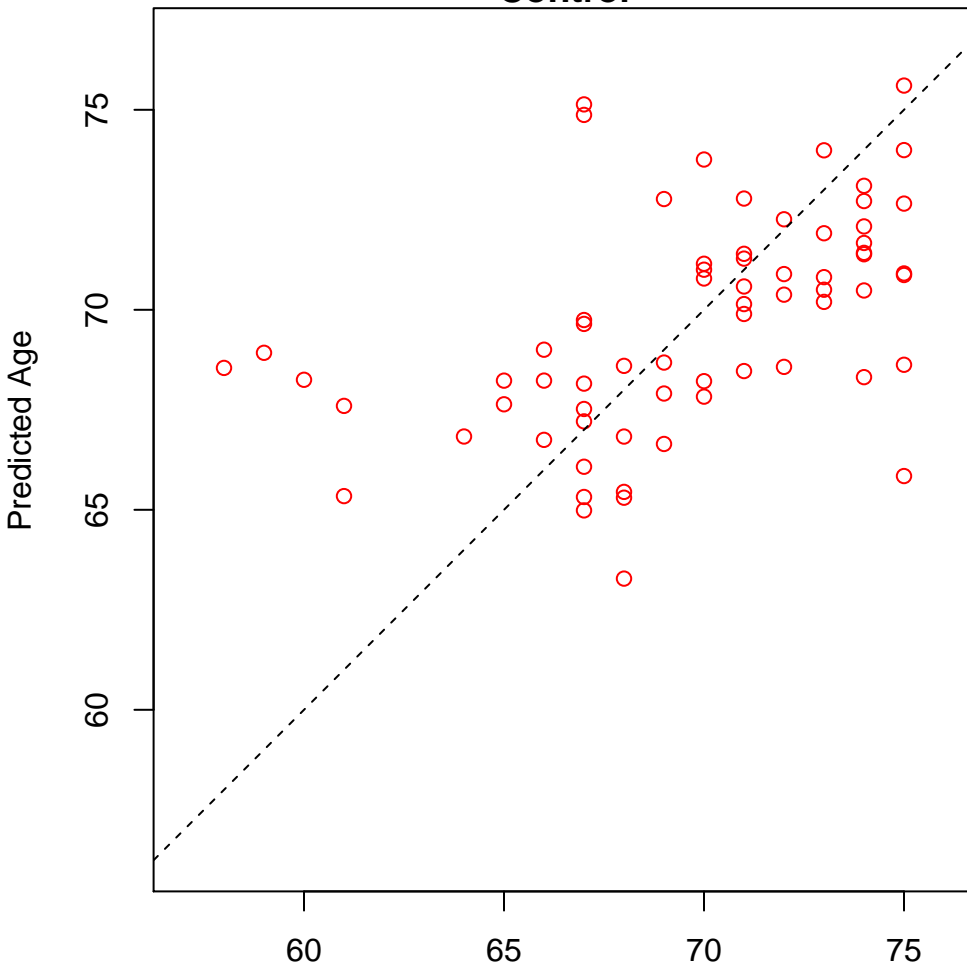


Schwann cell development (Score: 0.842749)

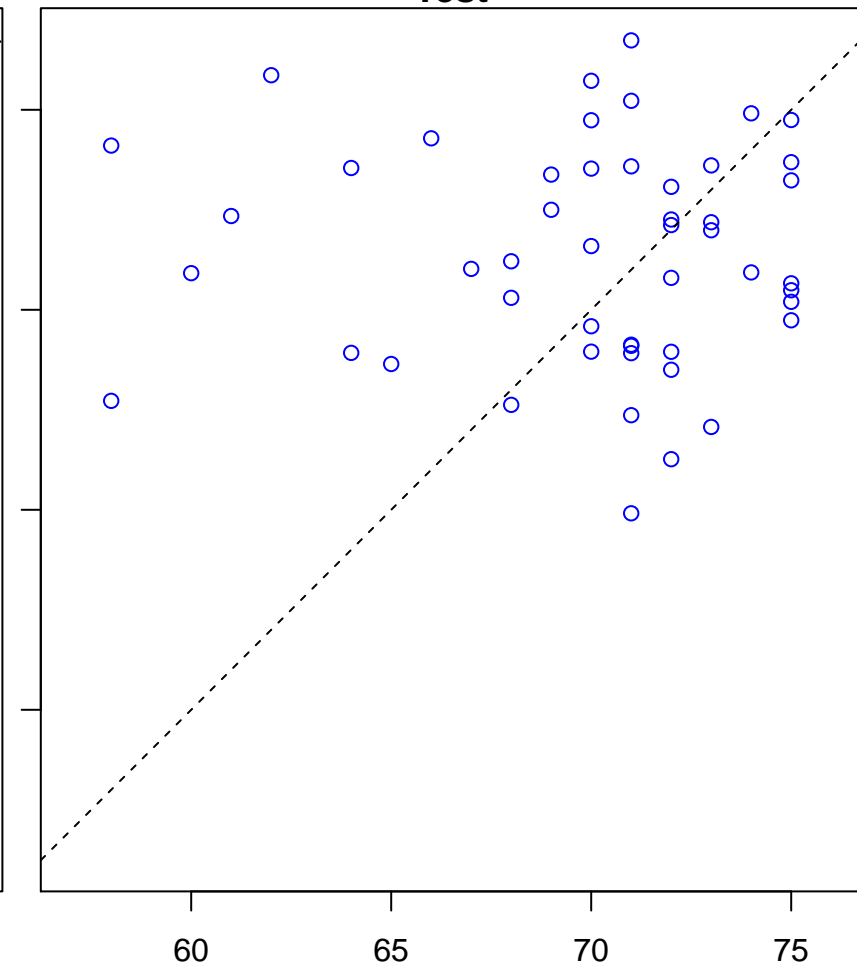


myelination in peripheral nervous system (Score: 0.842749)

Control

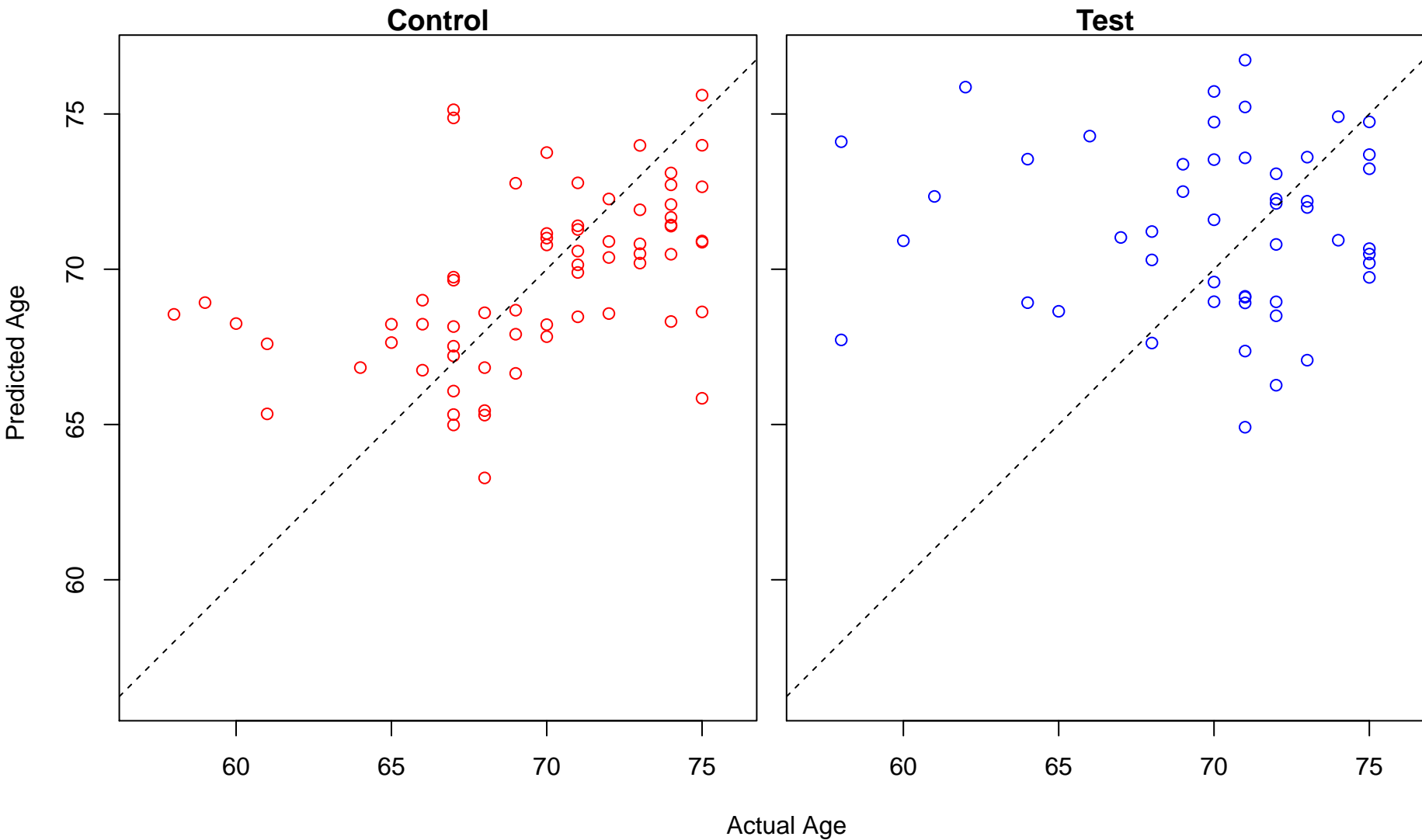


Test

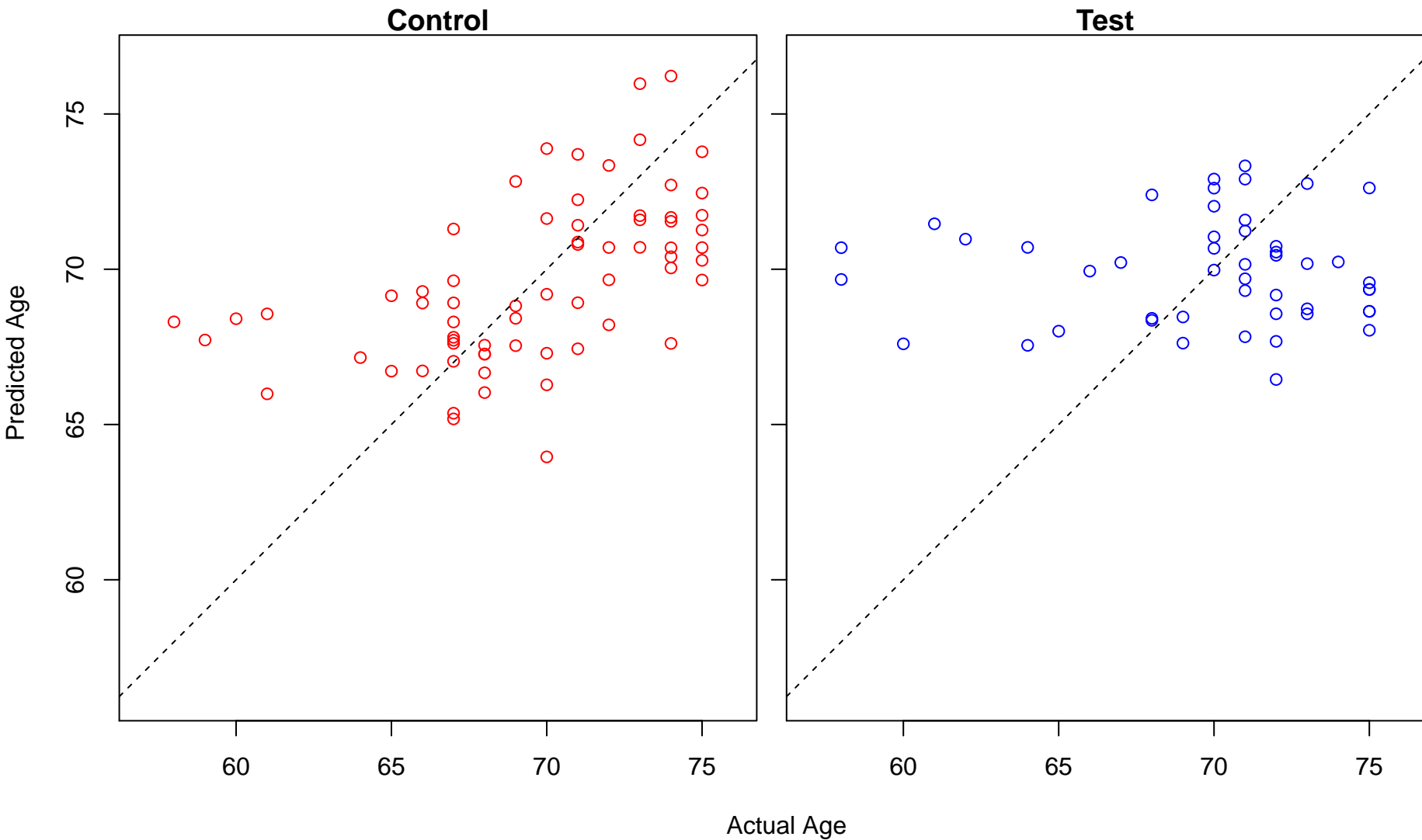


Actual Age

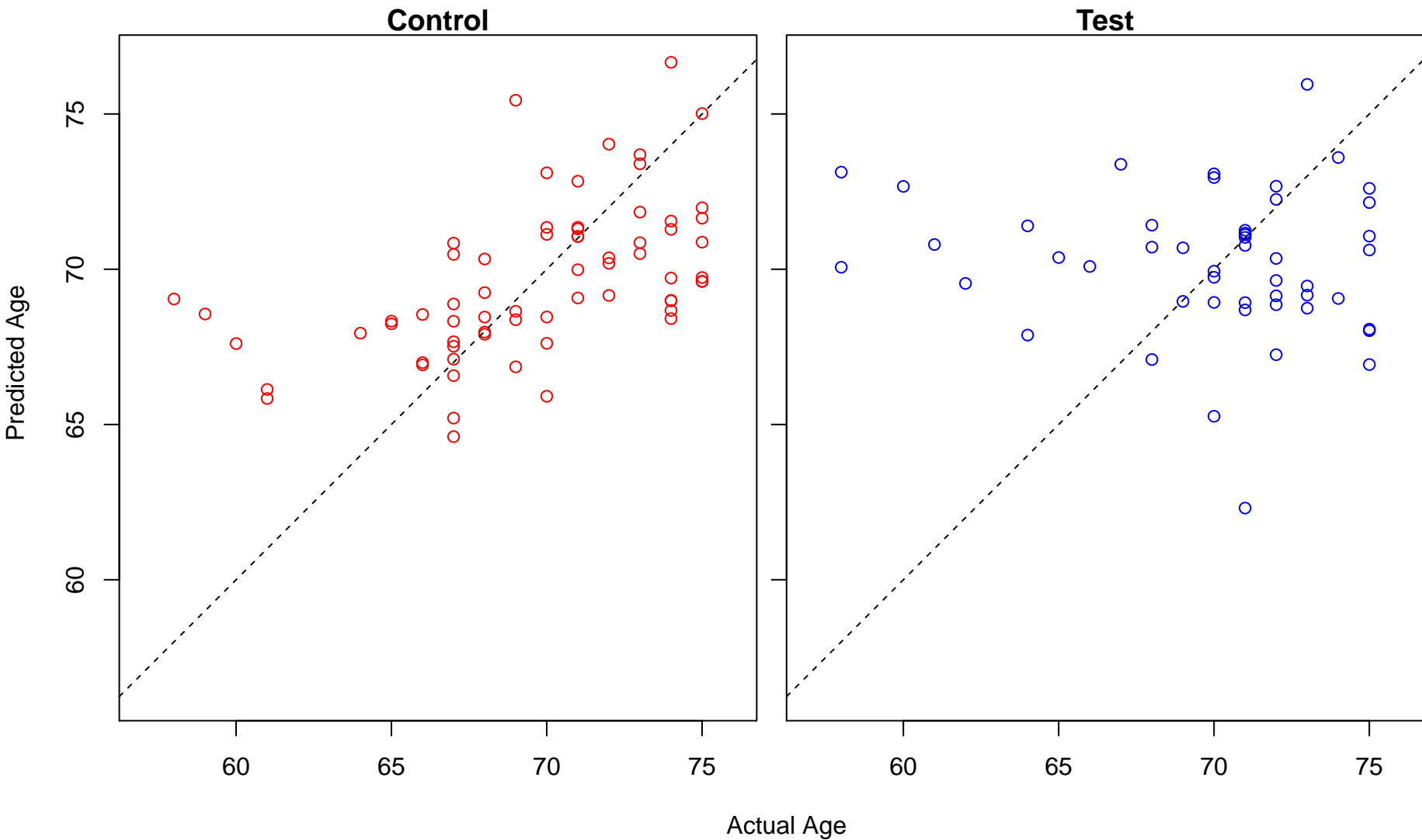
peripheral nervous system axon ensheathment (Score: 0.842749)



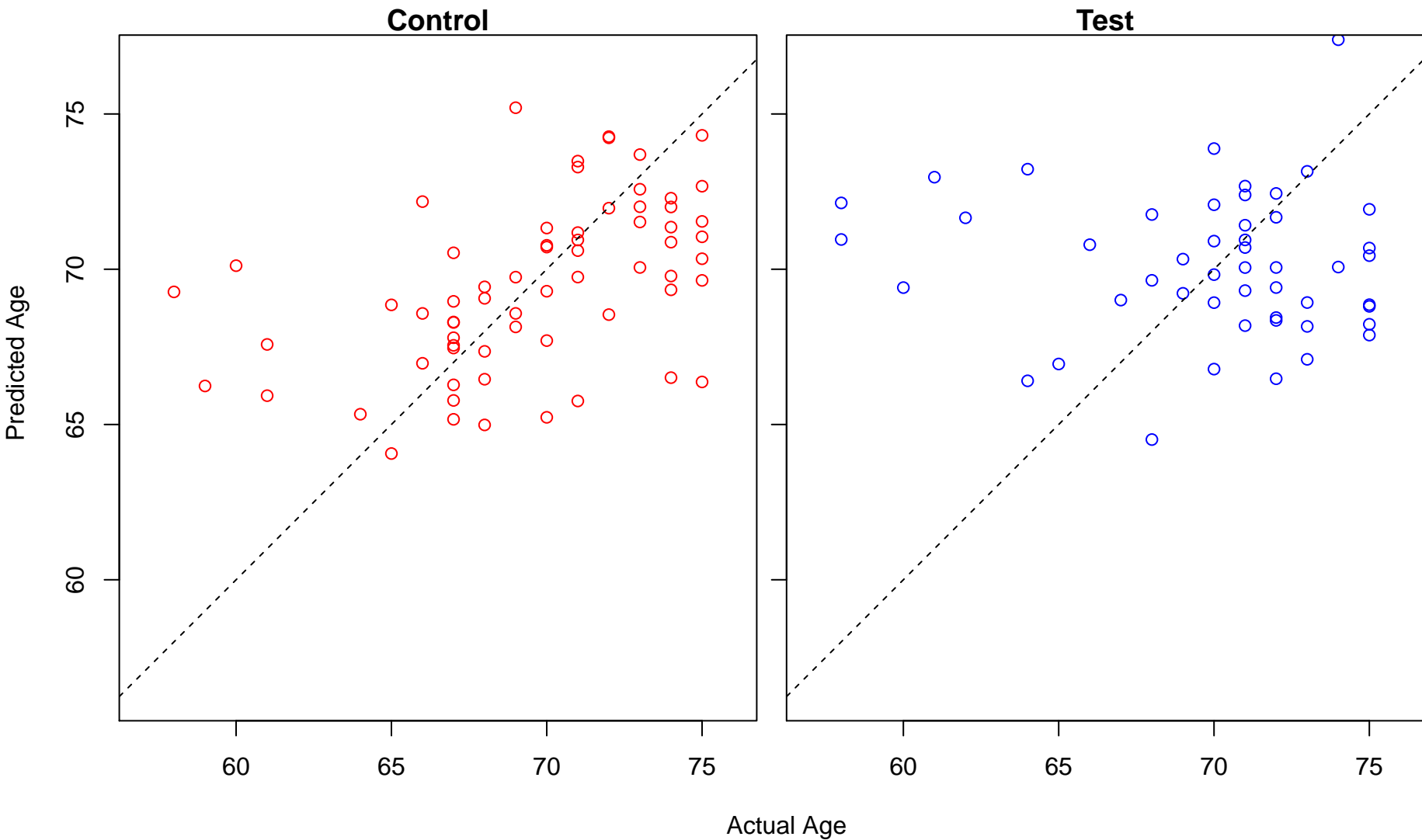
photoperiodism (Score: 0.842647)



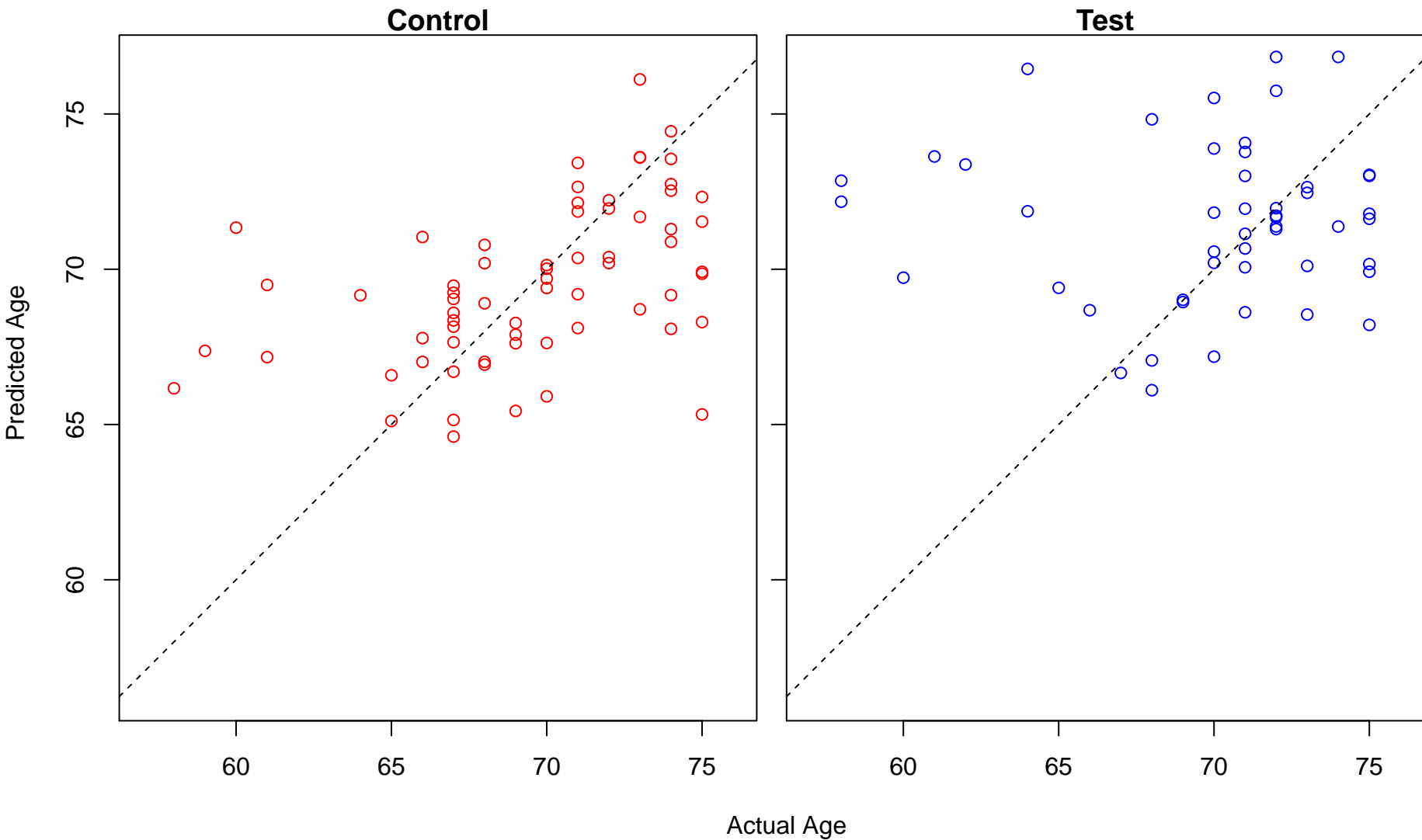
negative regulation of cell junction assembly (Score: 0.841711)



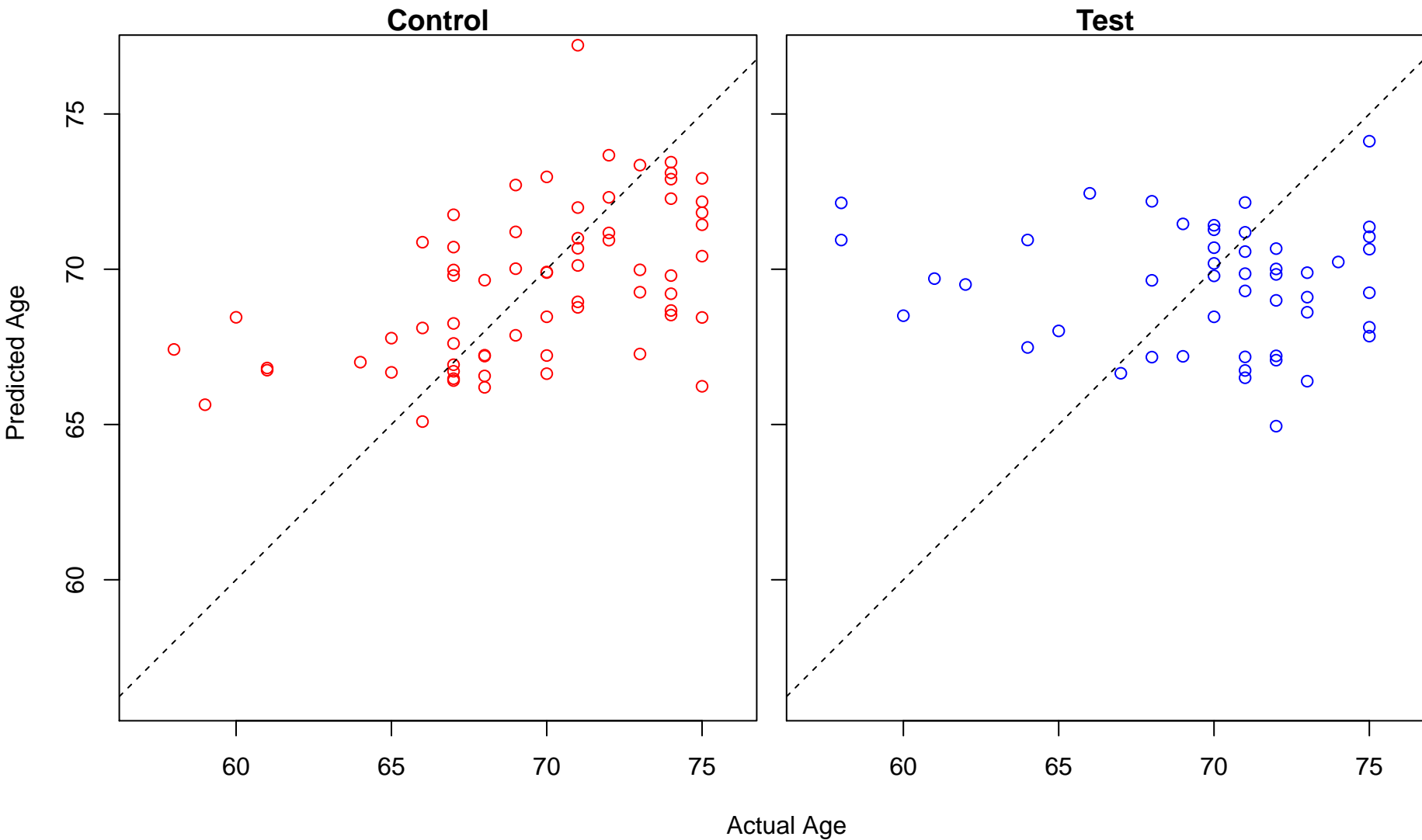
negative regulation of tumor necrosis factor production (Score: 0.841438)



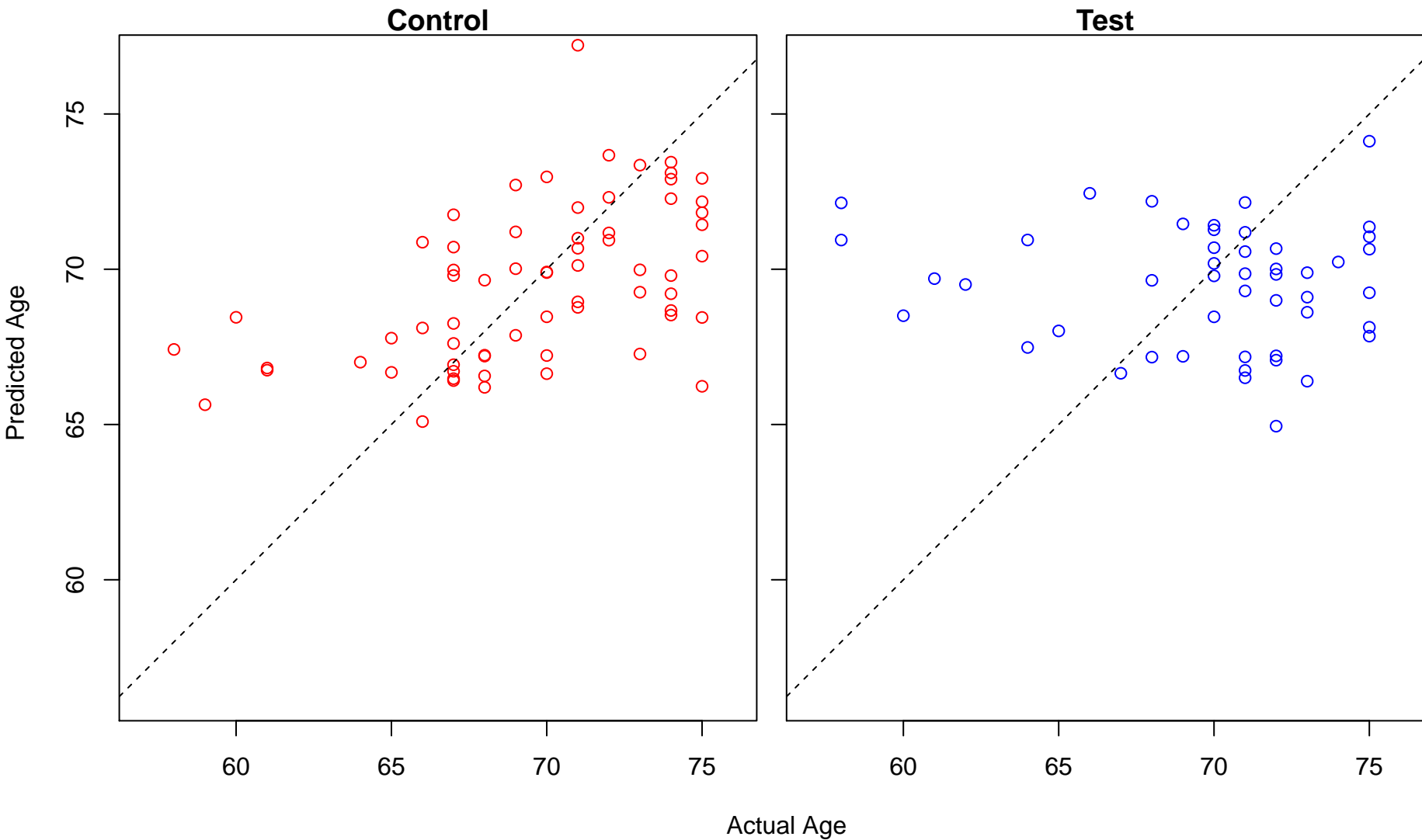
biotin metabolic process (Score: 0.841140)



extracellular regulation of signal transduction (Score: 0.840972)

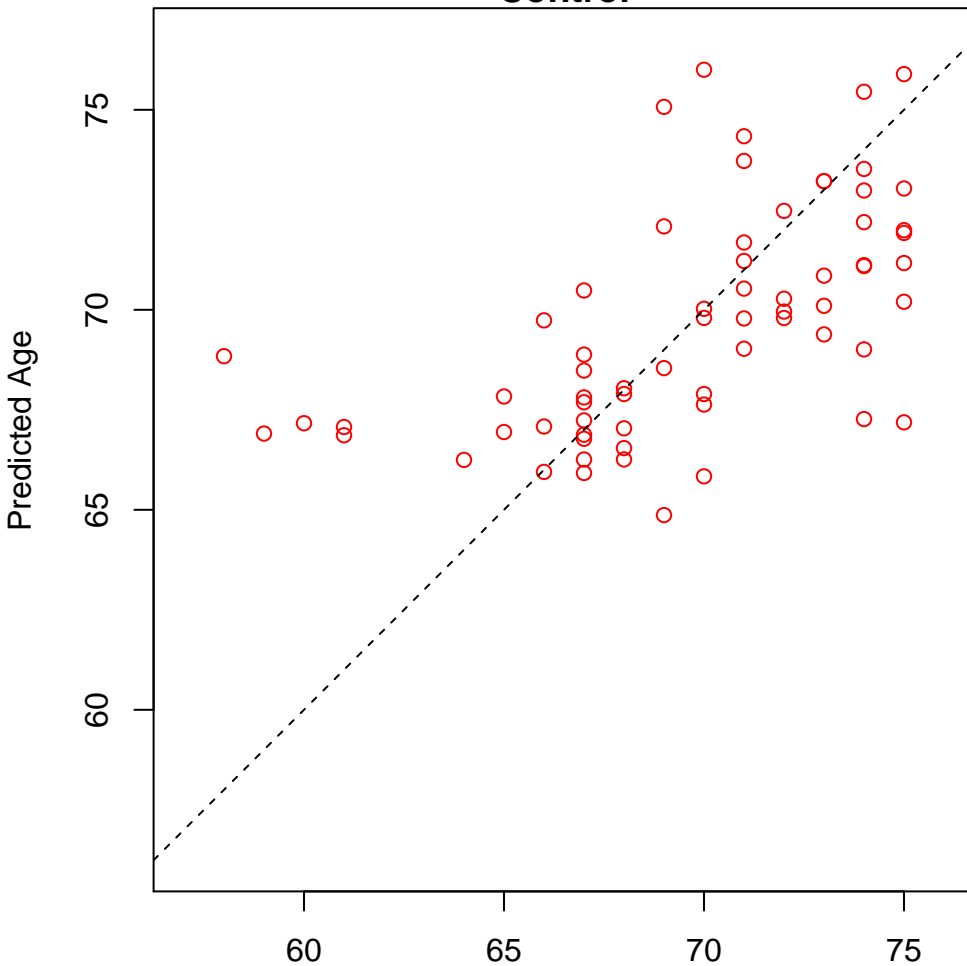


extracellular negative regulation of signal transduction (Score: 0.840972)

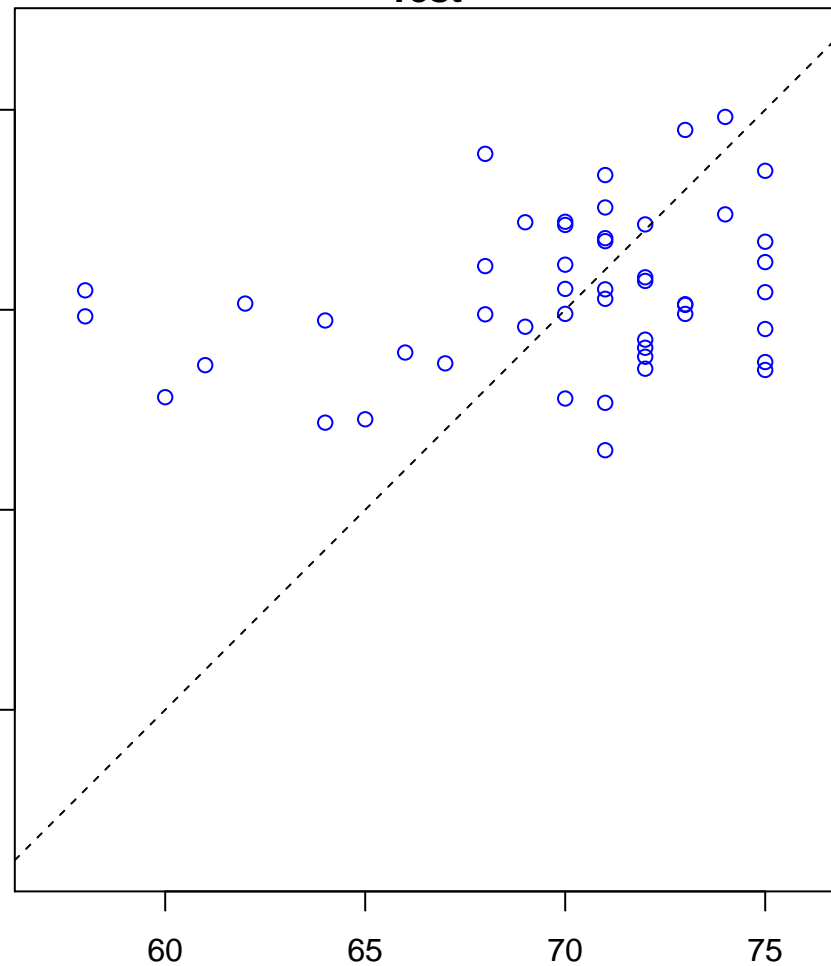


mesonephric epithelium development (Score: 0.840918)

Control



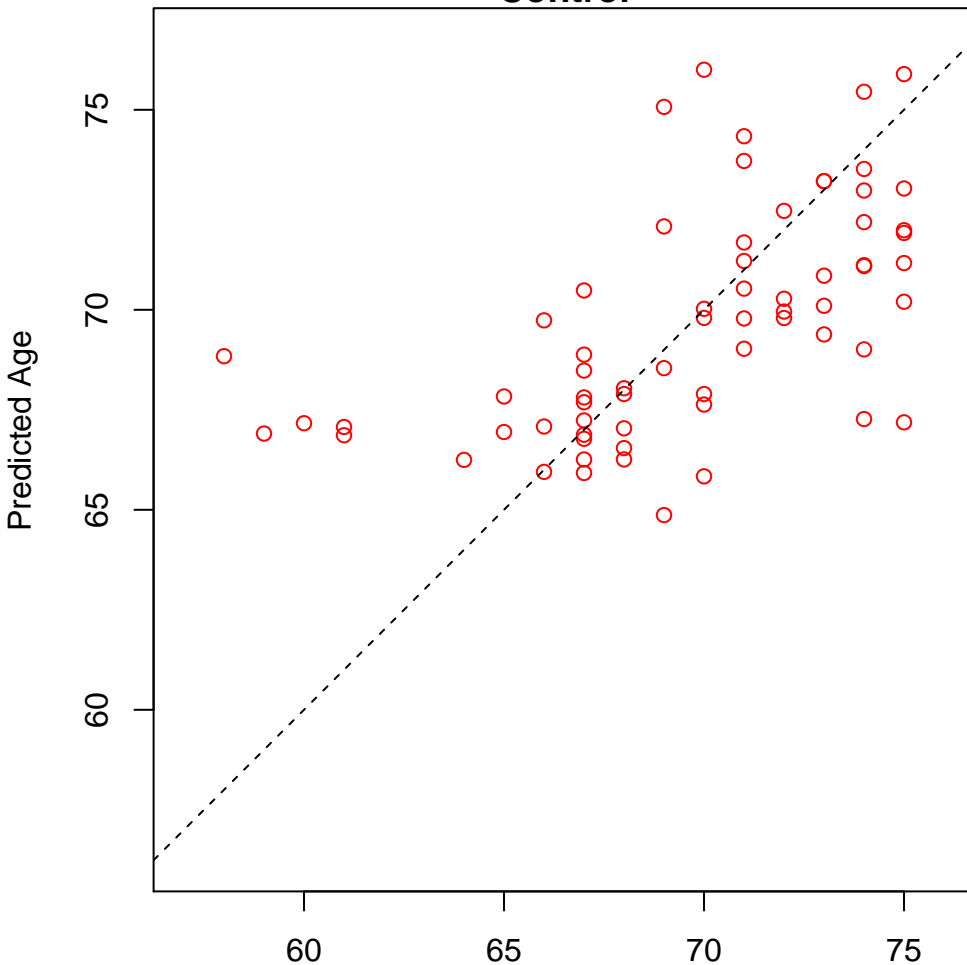
Test



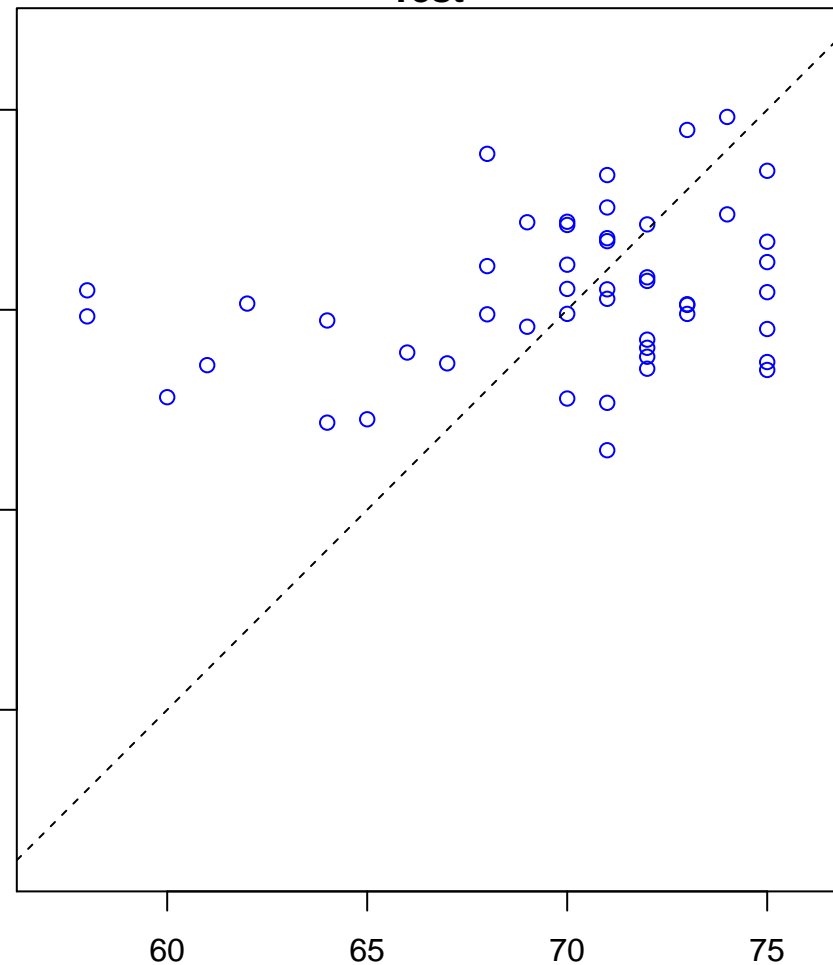
Actual Age

mesonephric tubule development (Score: 0.840918)

Control

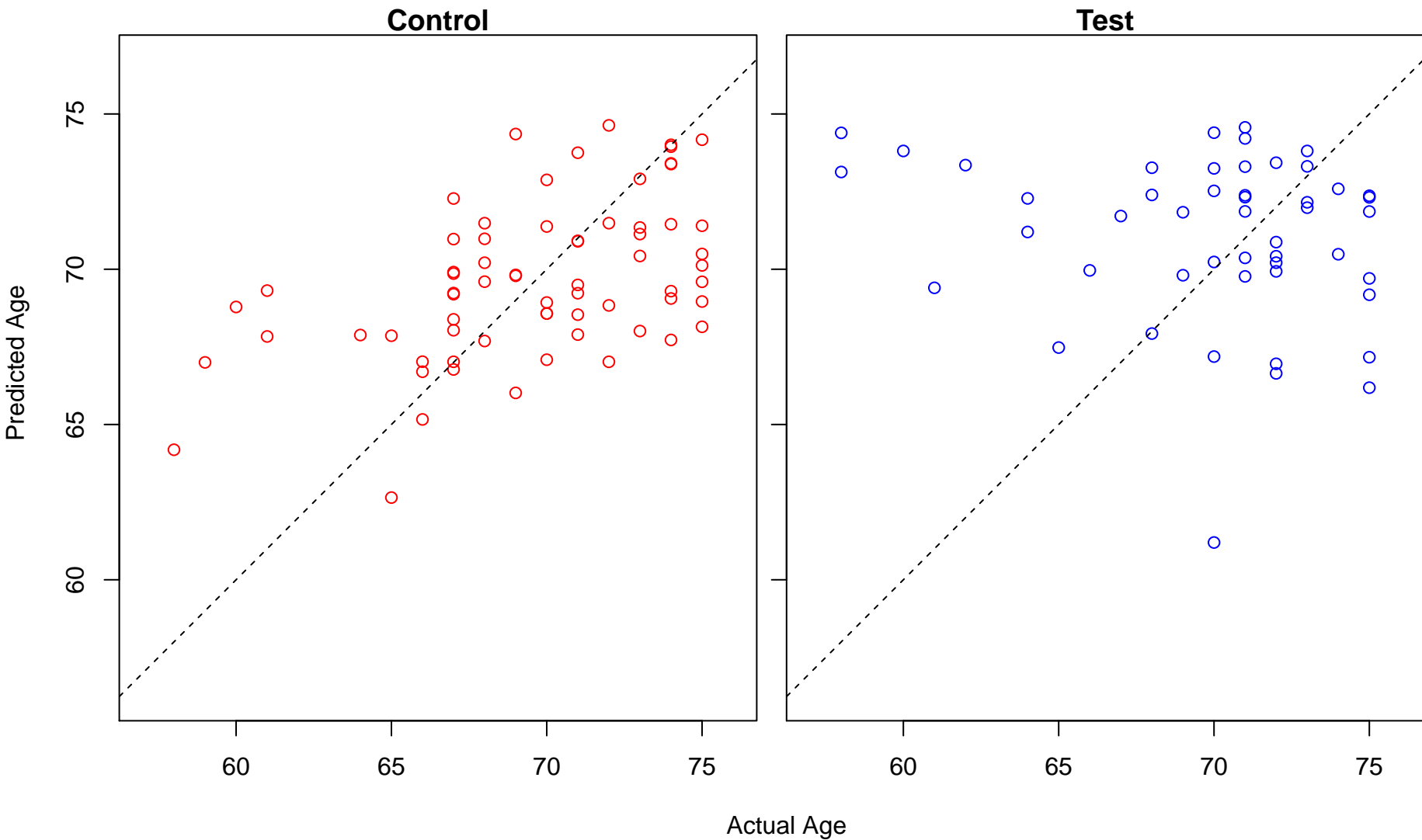


Test

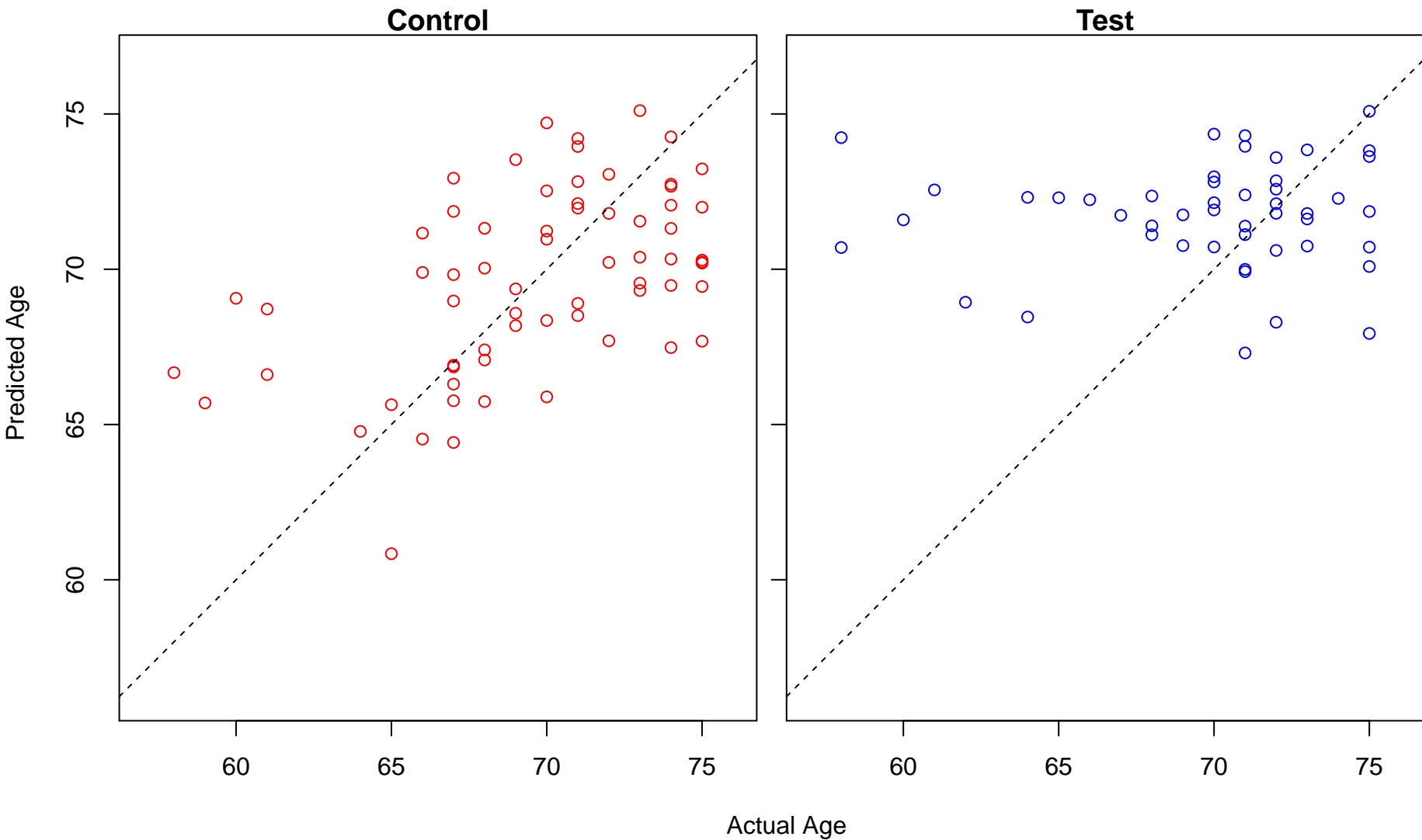


Actual Age

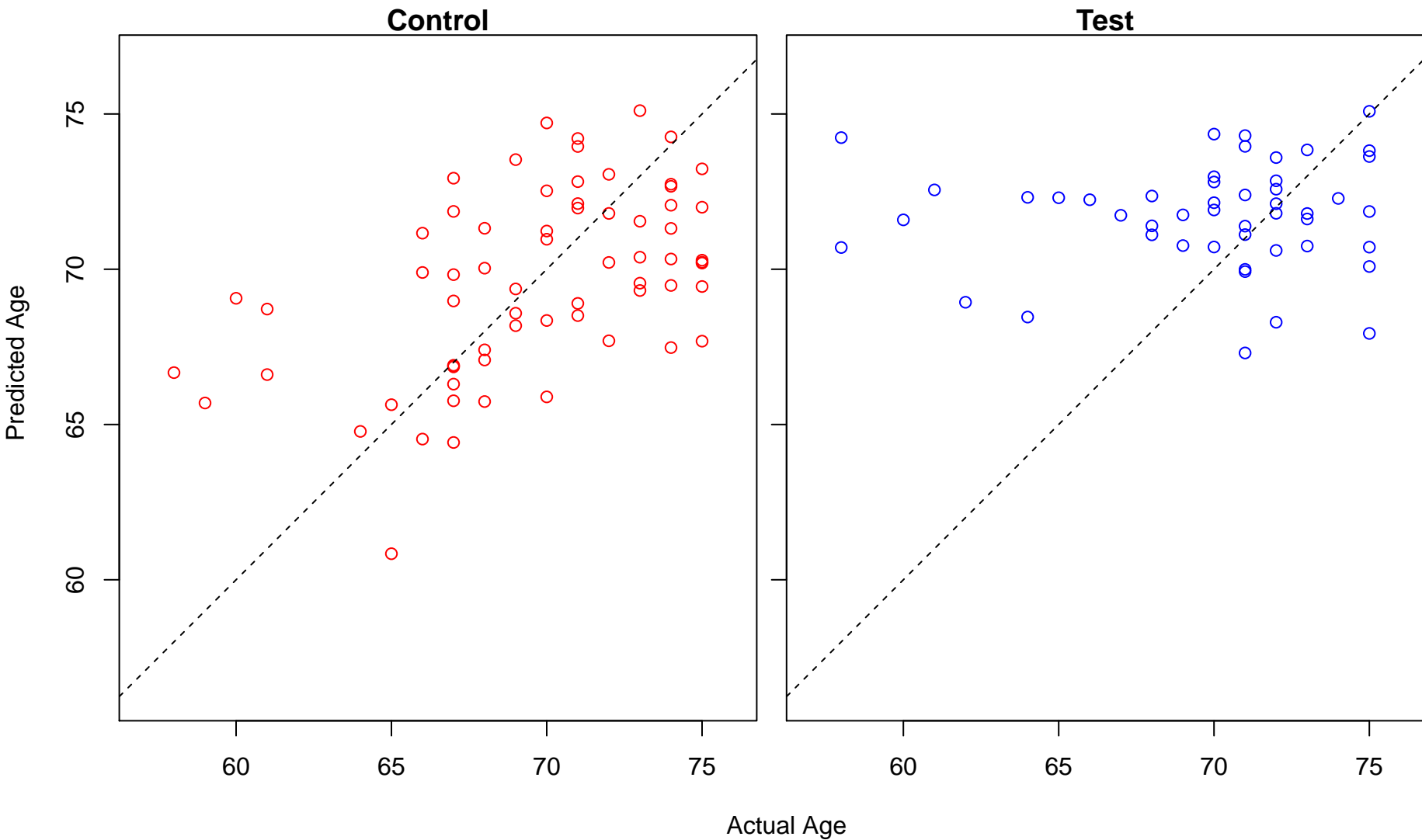
positive regulation of tyrosine phosphorylation of Stat5 protein (Score: 0.840622)



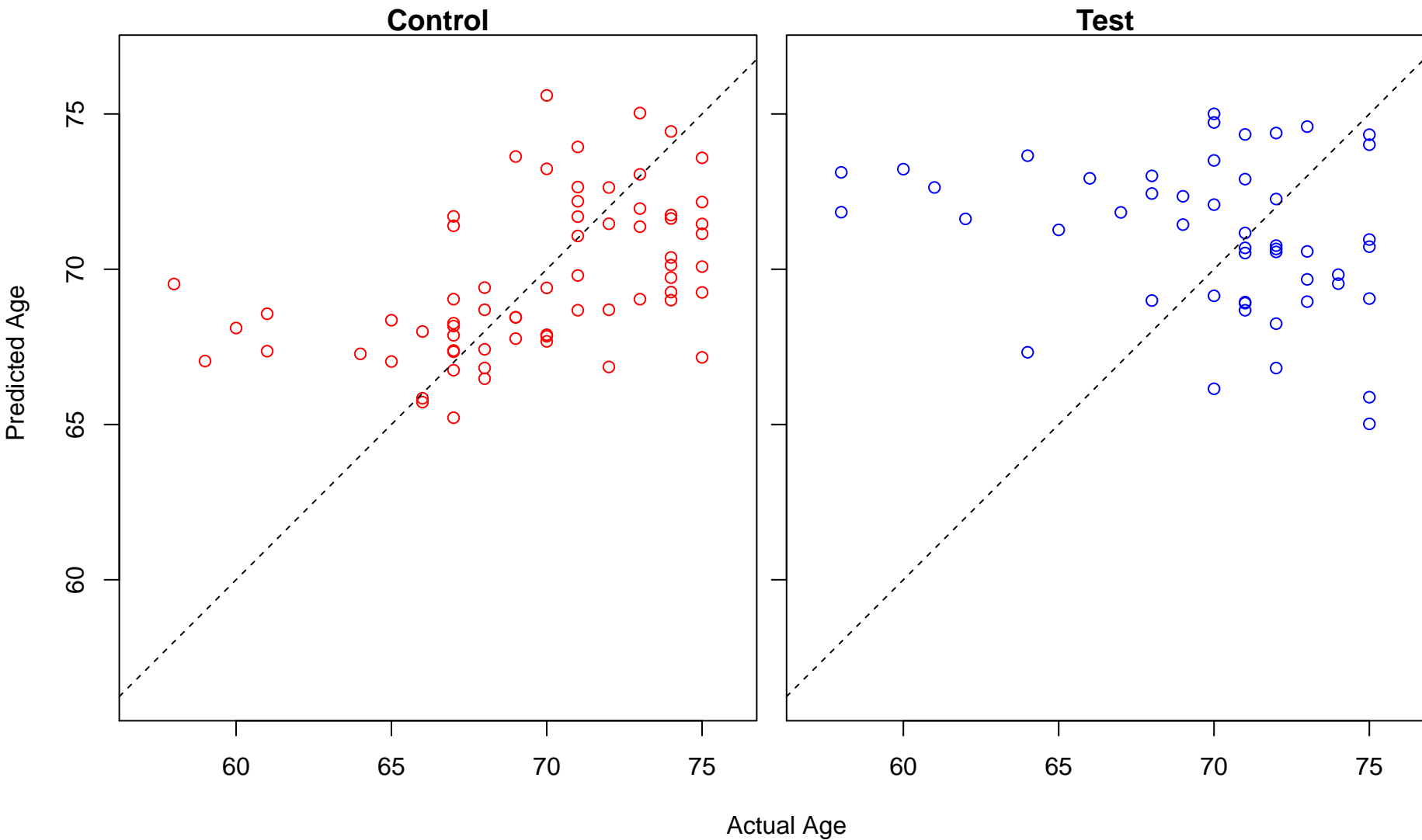
prostanoid metabolic process (Score: 0.840163)



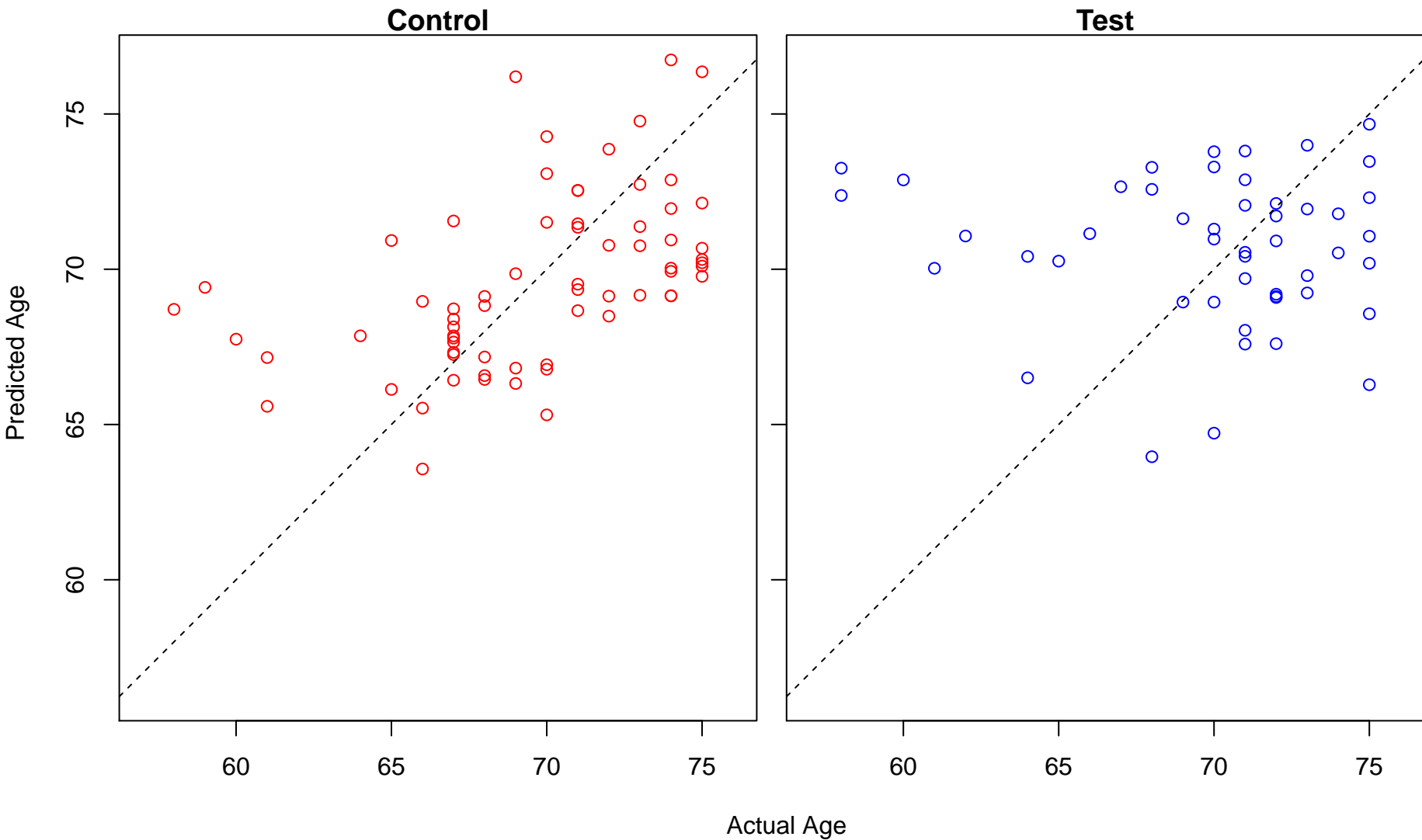
prostaglandin metabolic process (Score: 0.840163)



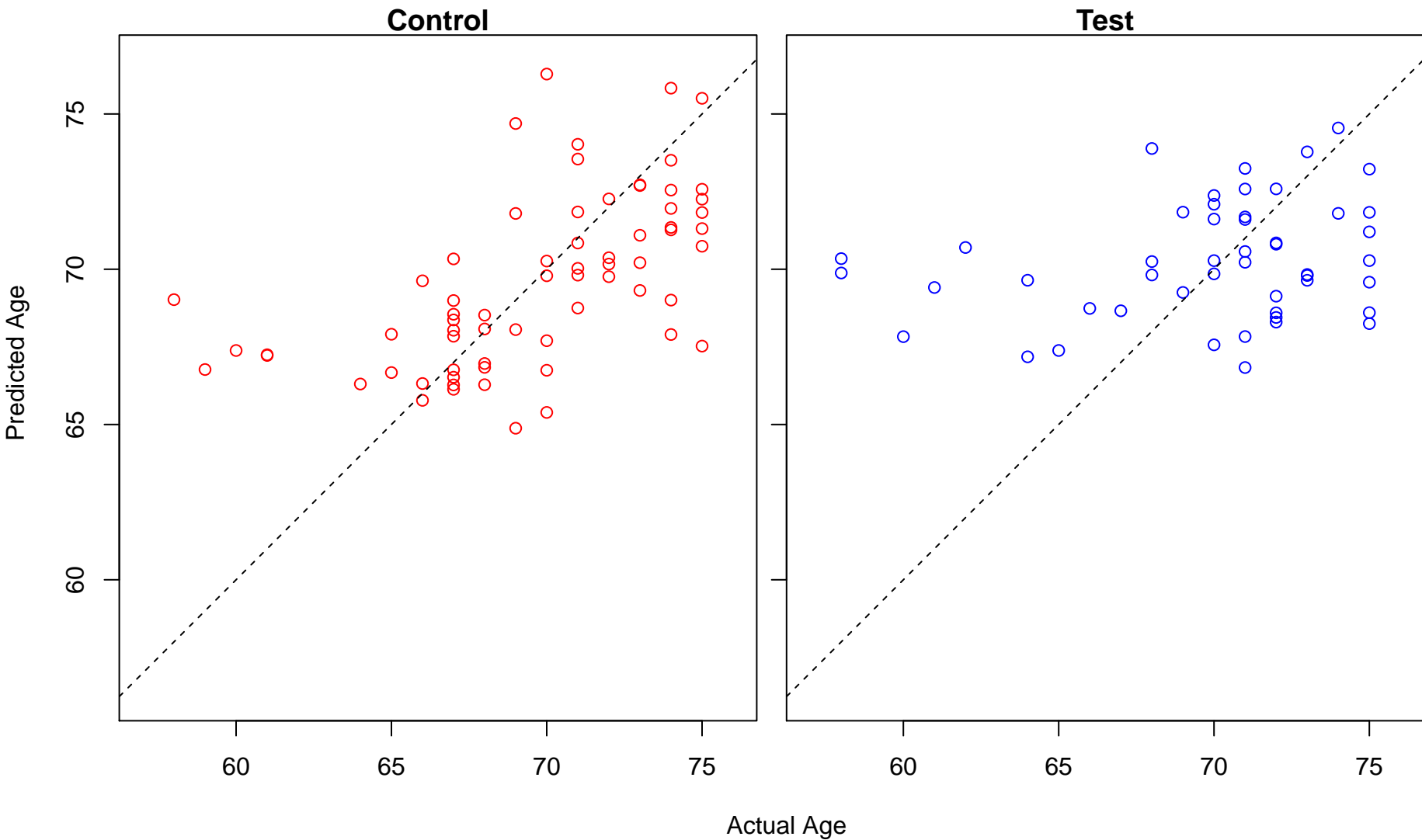
maturation of 5.8S rRNA (Score: 0.839687)



forebrain development (Score: 0.839555)

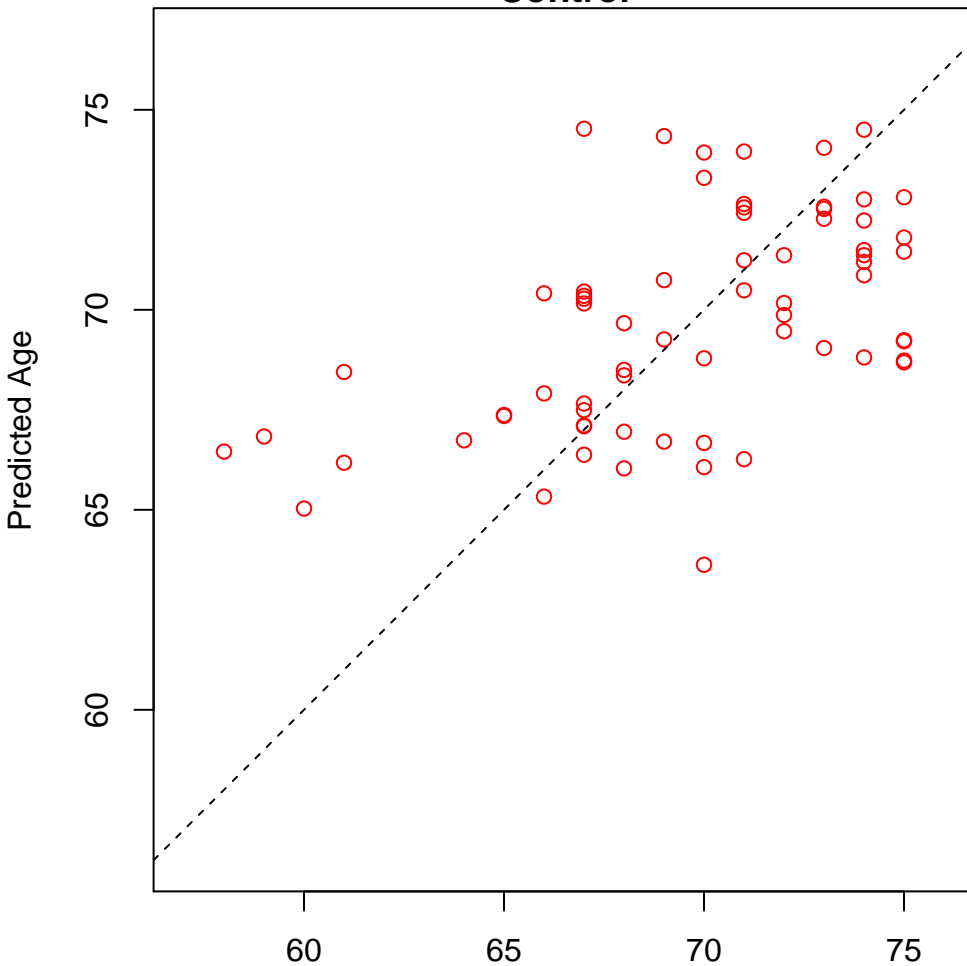


nephron tubule morphogenesis (Score: 0.839388)

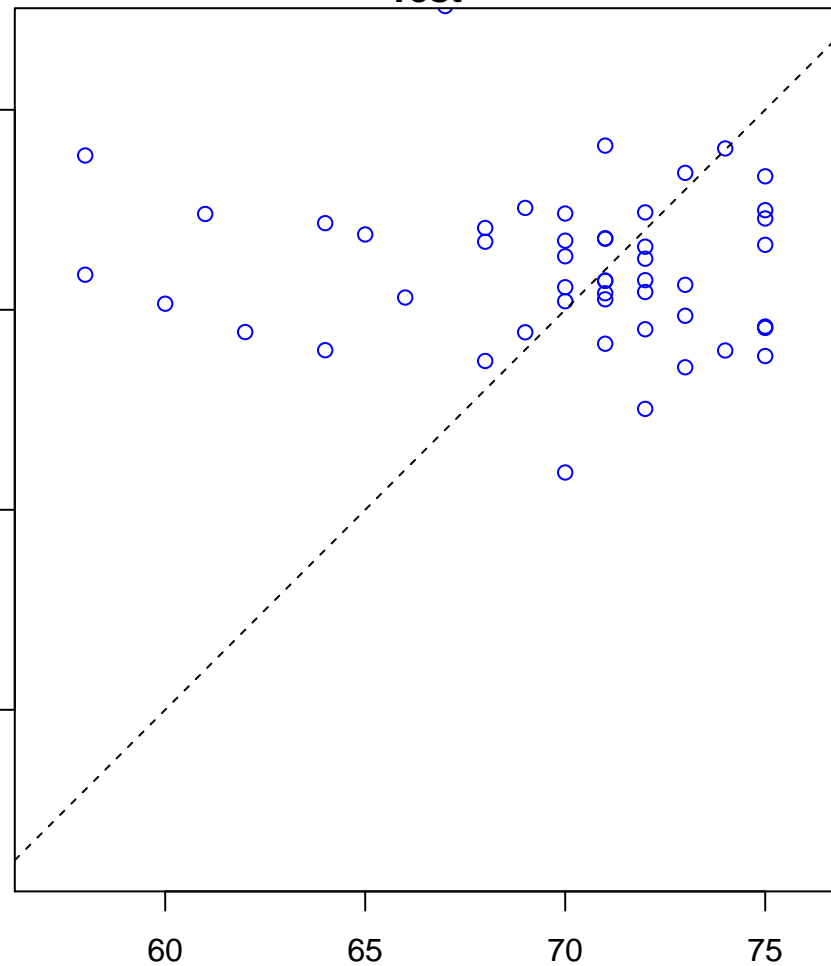


purine nucleobase biosynthetic process (Score: 0.839243)

Control

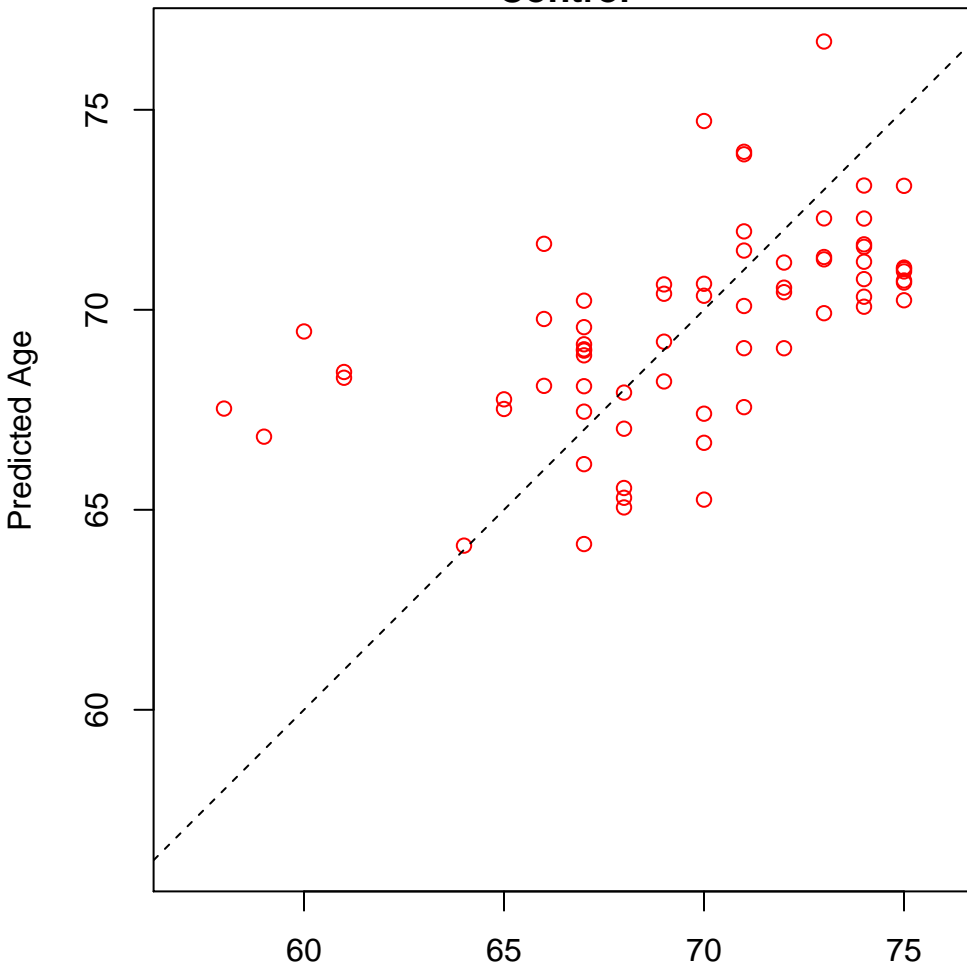


Test

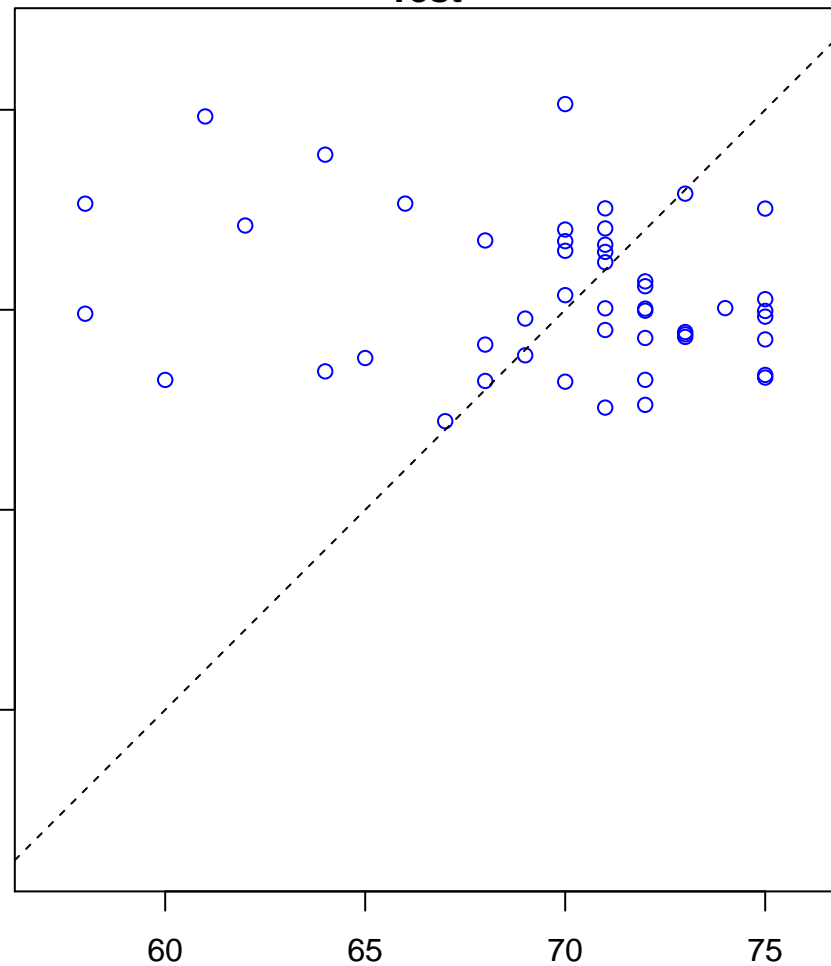


base conversion or substitution editing (Score: 0.838595)

Control

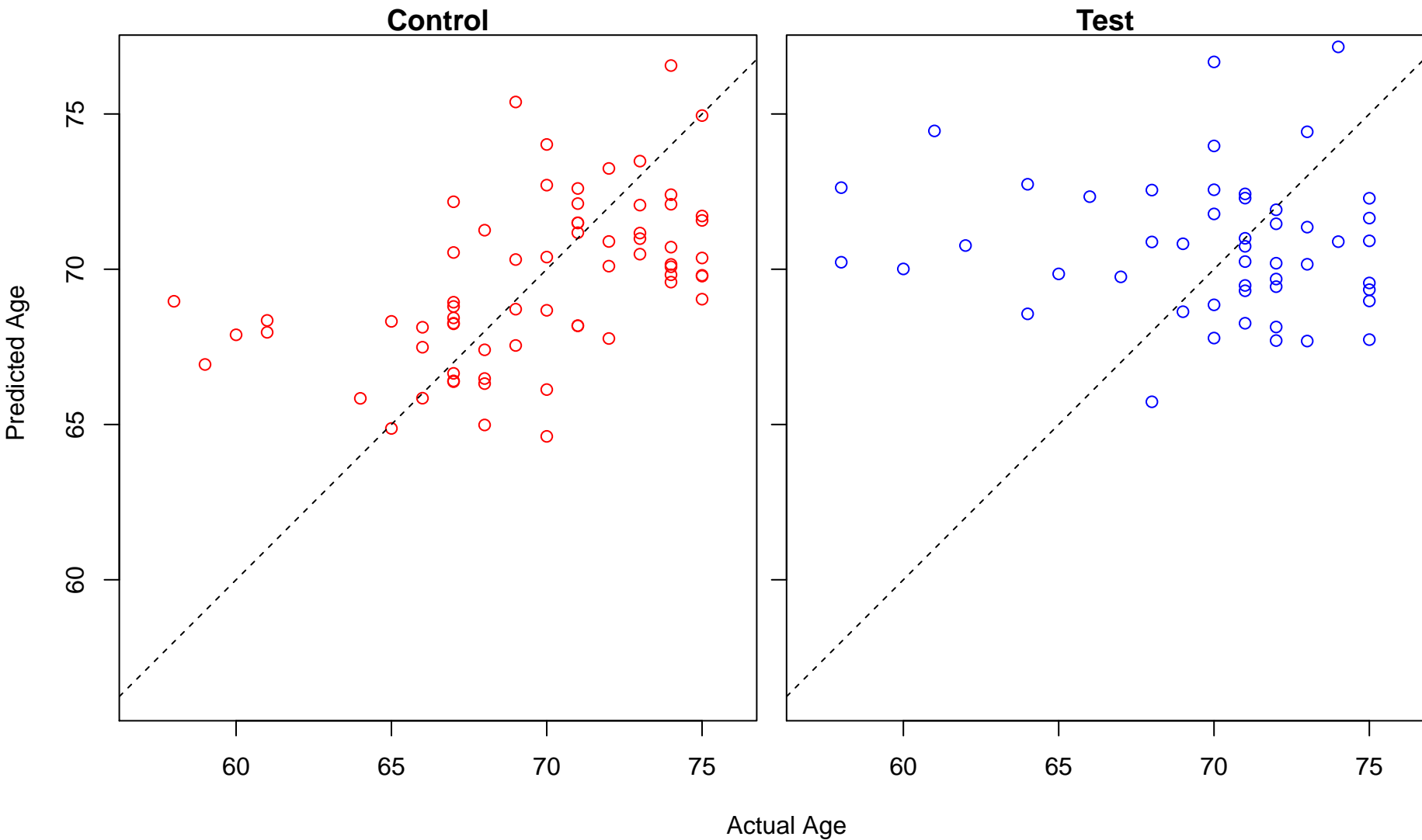


Test

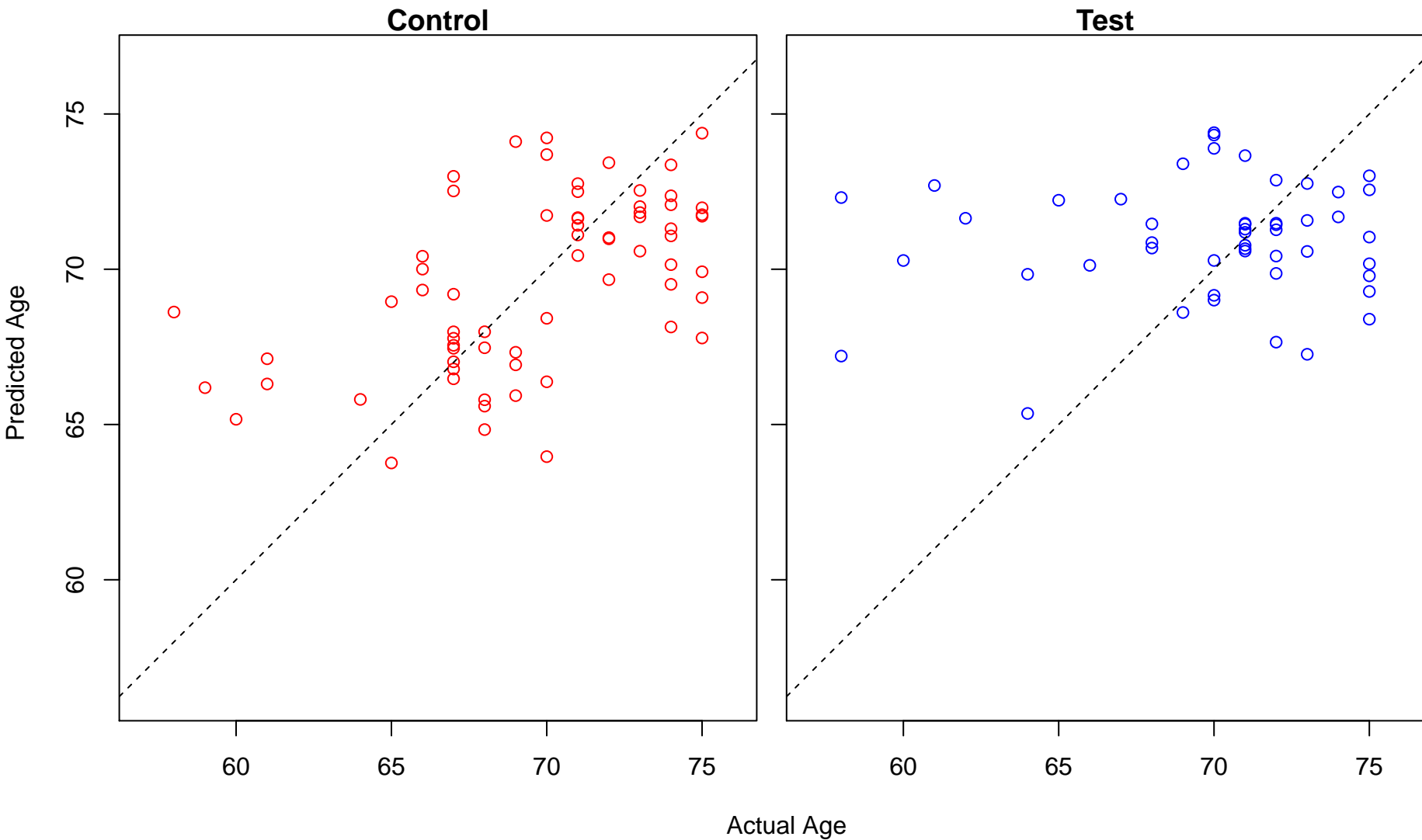


Actual Age

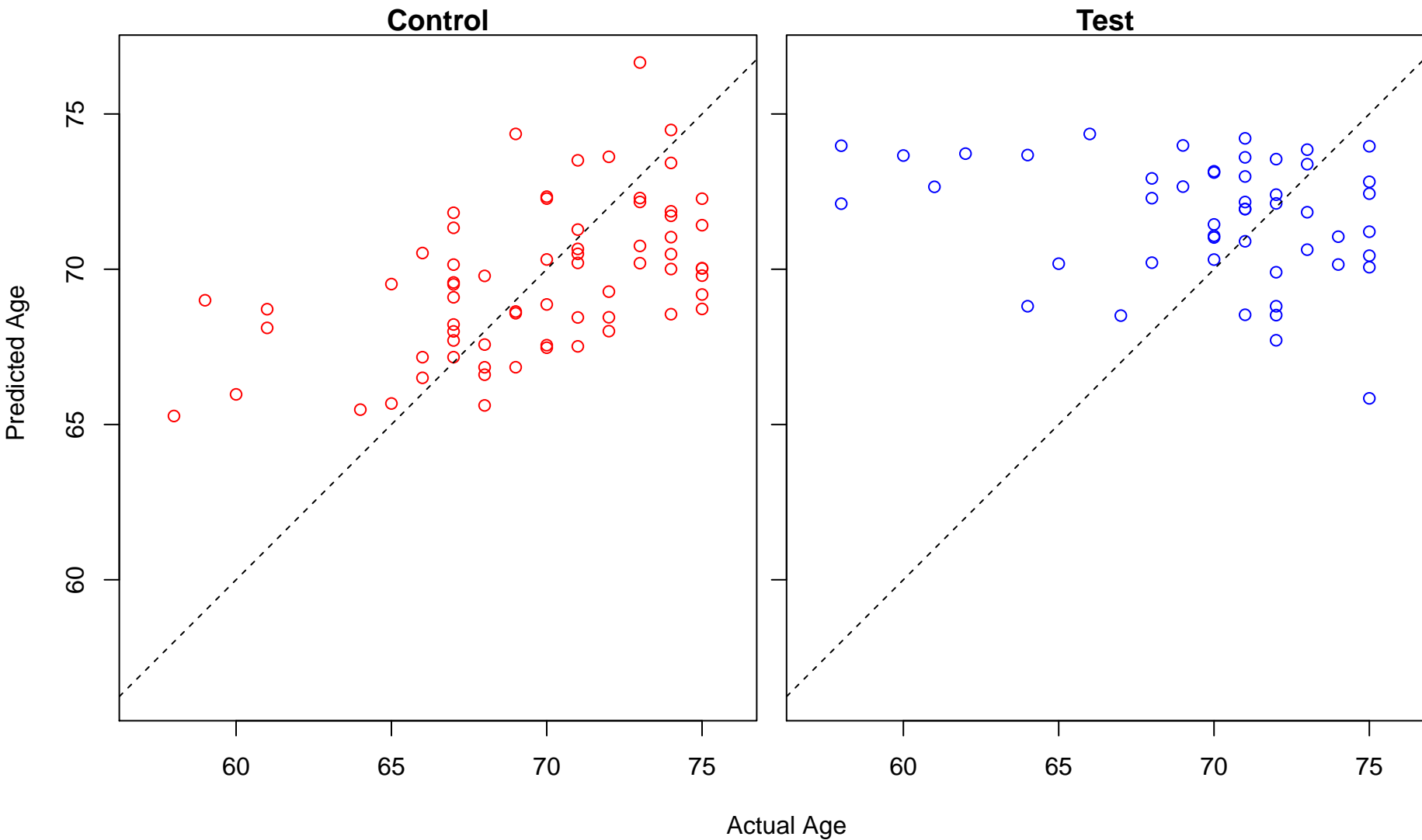
negative regulation of ERK1 and ERK2 cascade (Score: 0.838551)



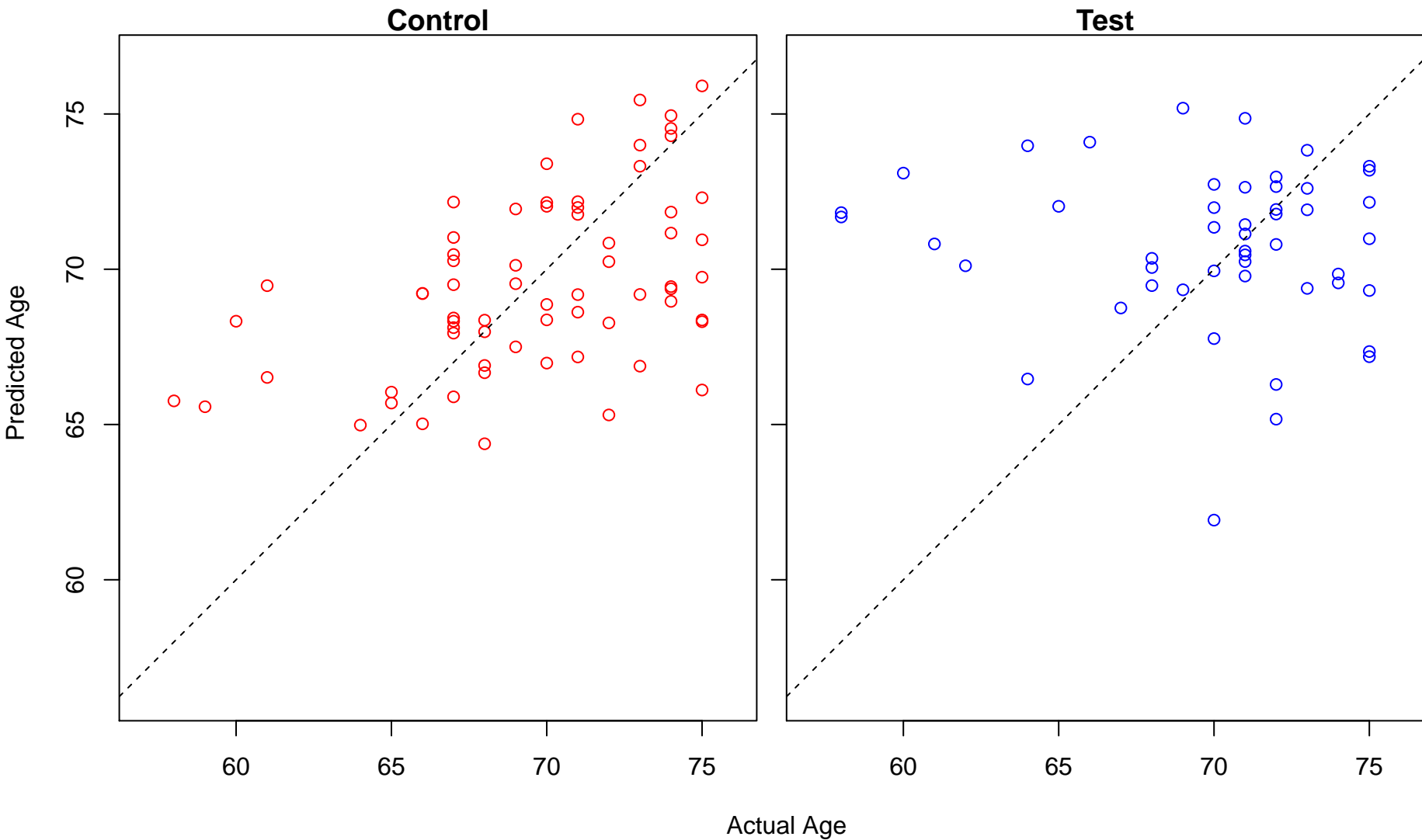
carbohydrate phosphorylation (Score: 0.838206)



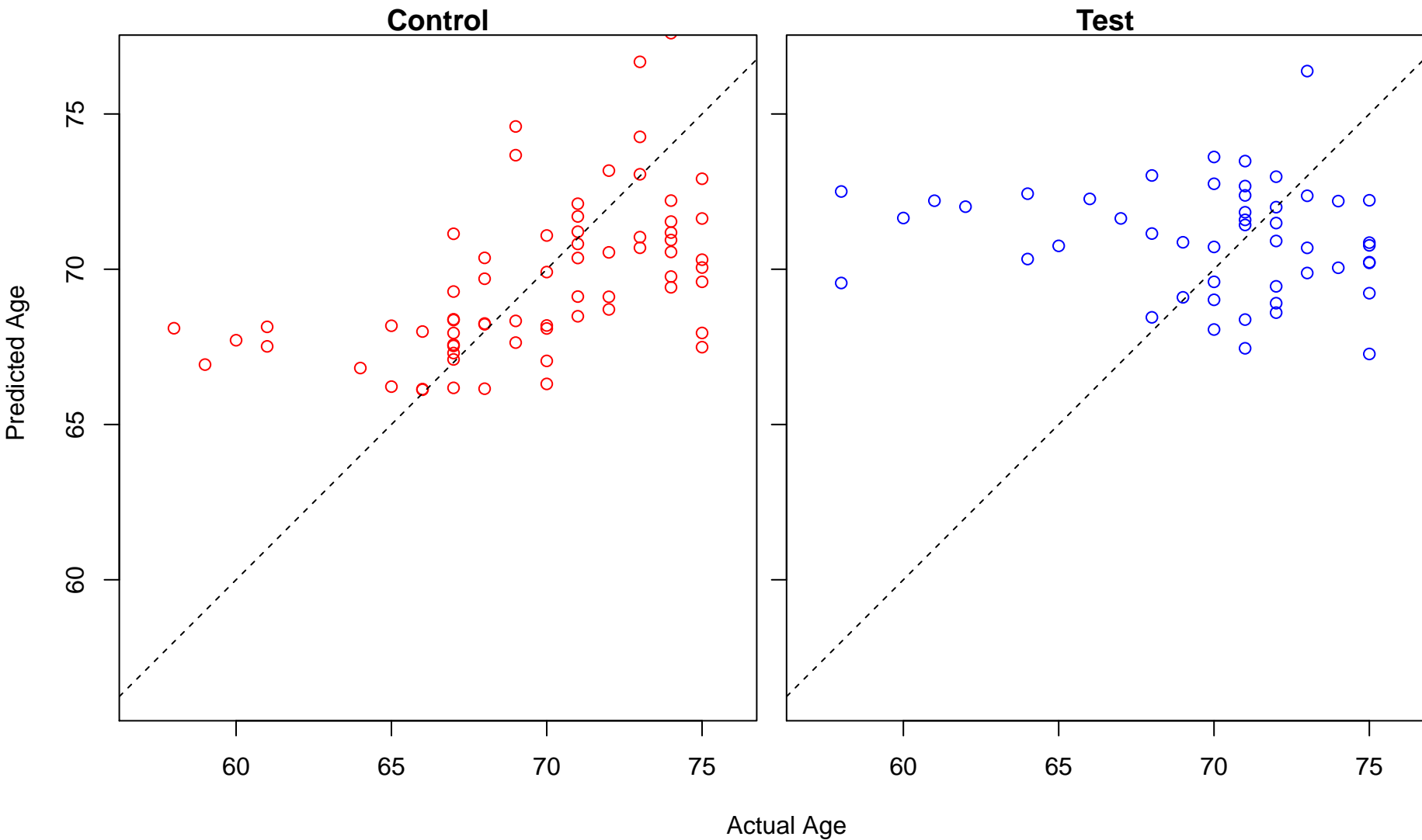
mitral valve morphogenesis (Score: 0.836136)



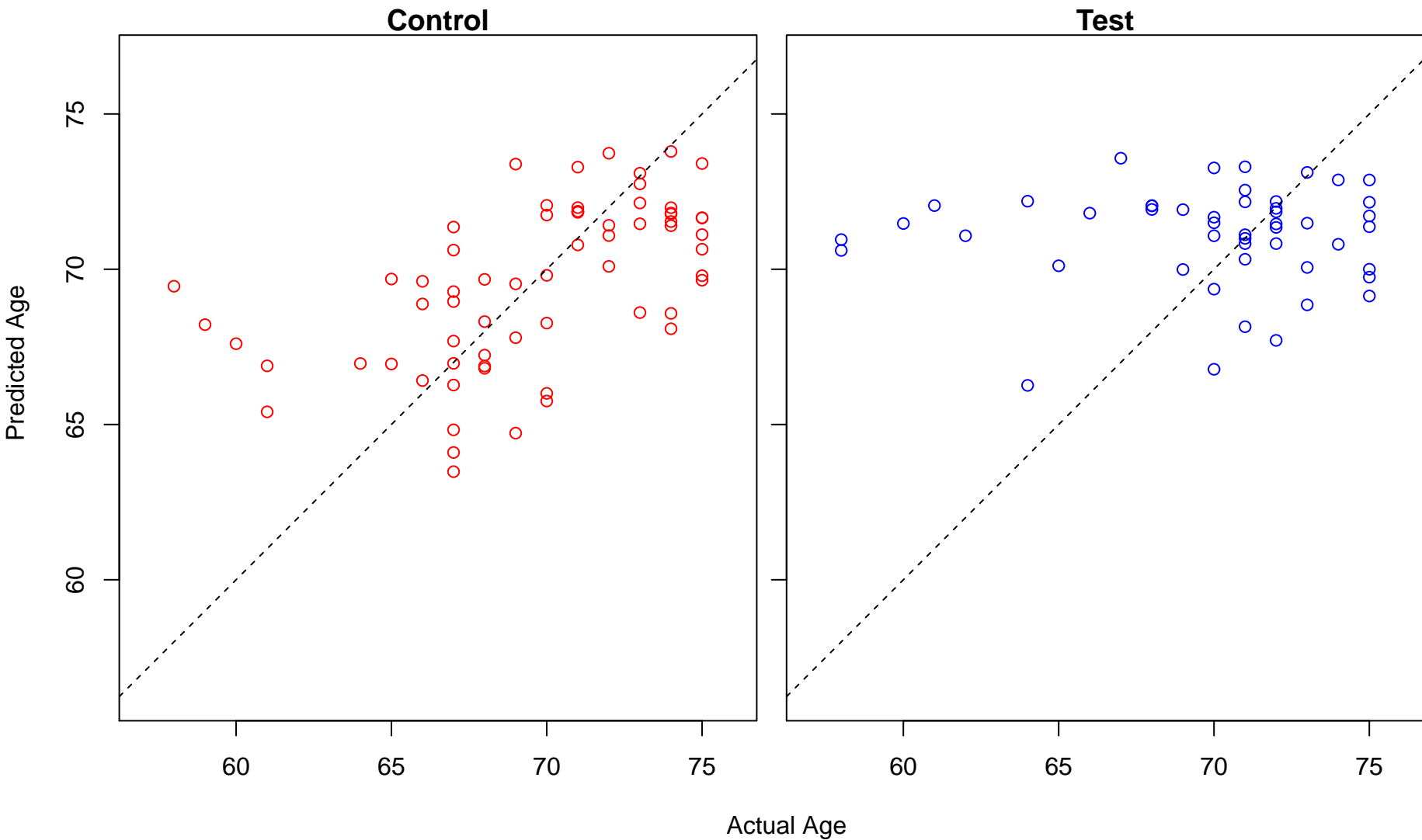
nitric oxide biosynthetic process (Score: 0.835541)



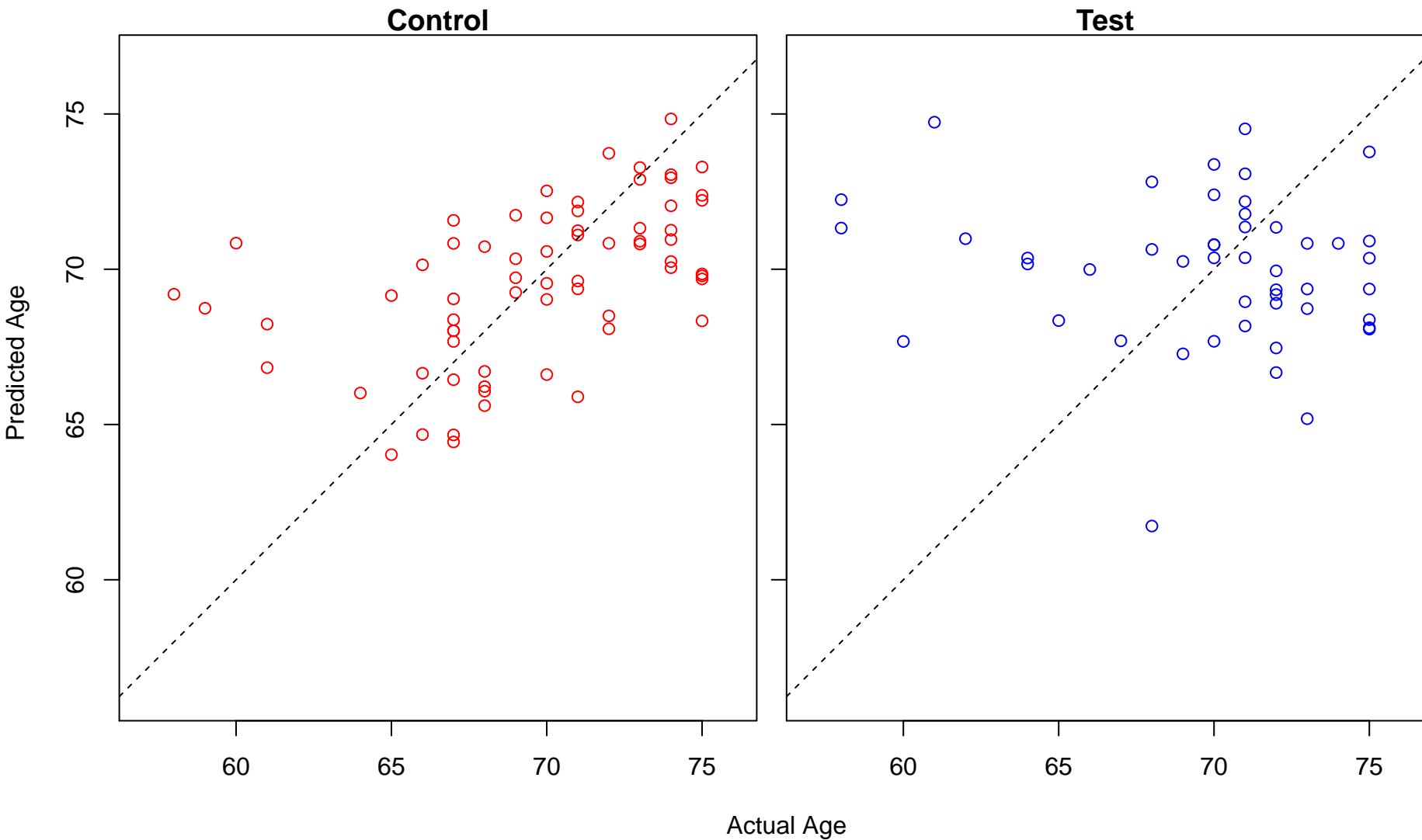
regulation of glycoprotein biosynthetic process (Score: 0.834552)



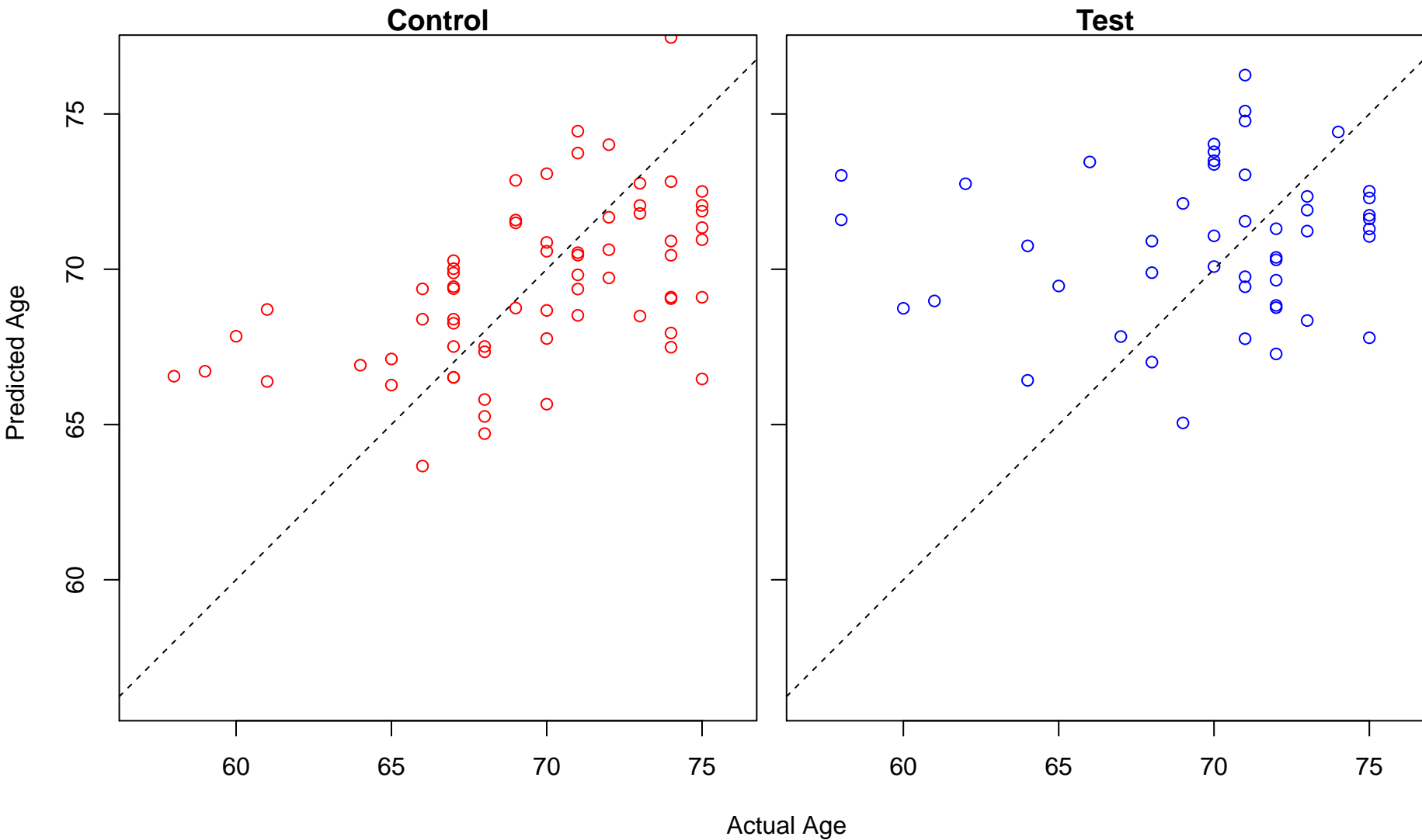
V(D)J recombination (Score: 0.834319)



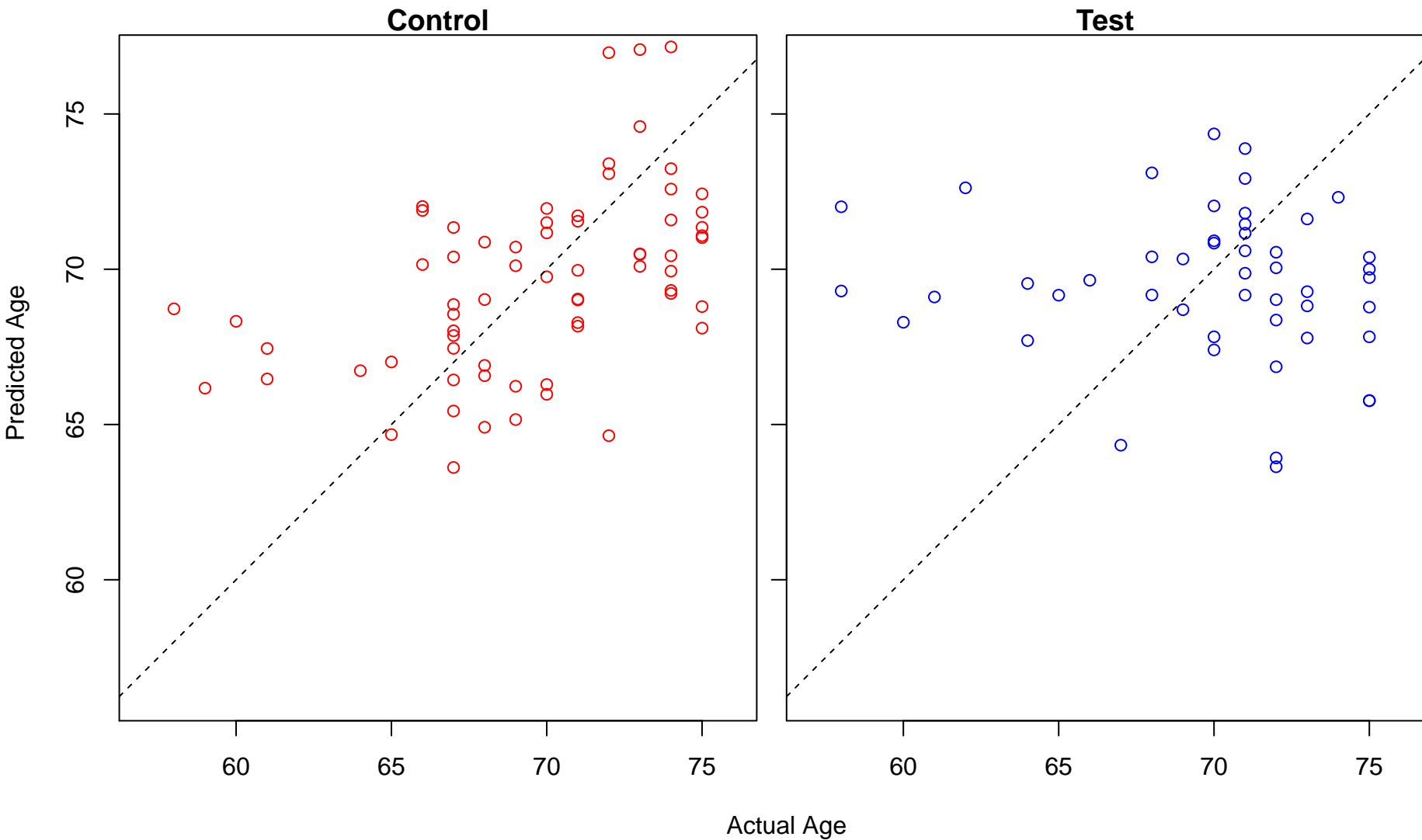
regulation of interleukin-10 secretion (Score: 0.834068)



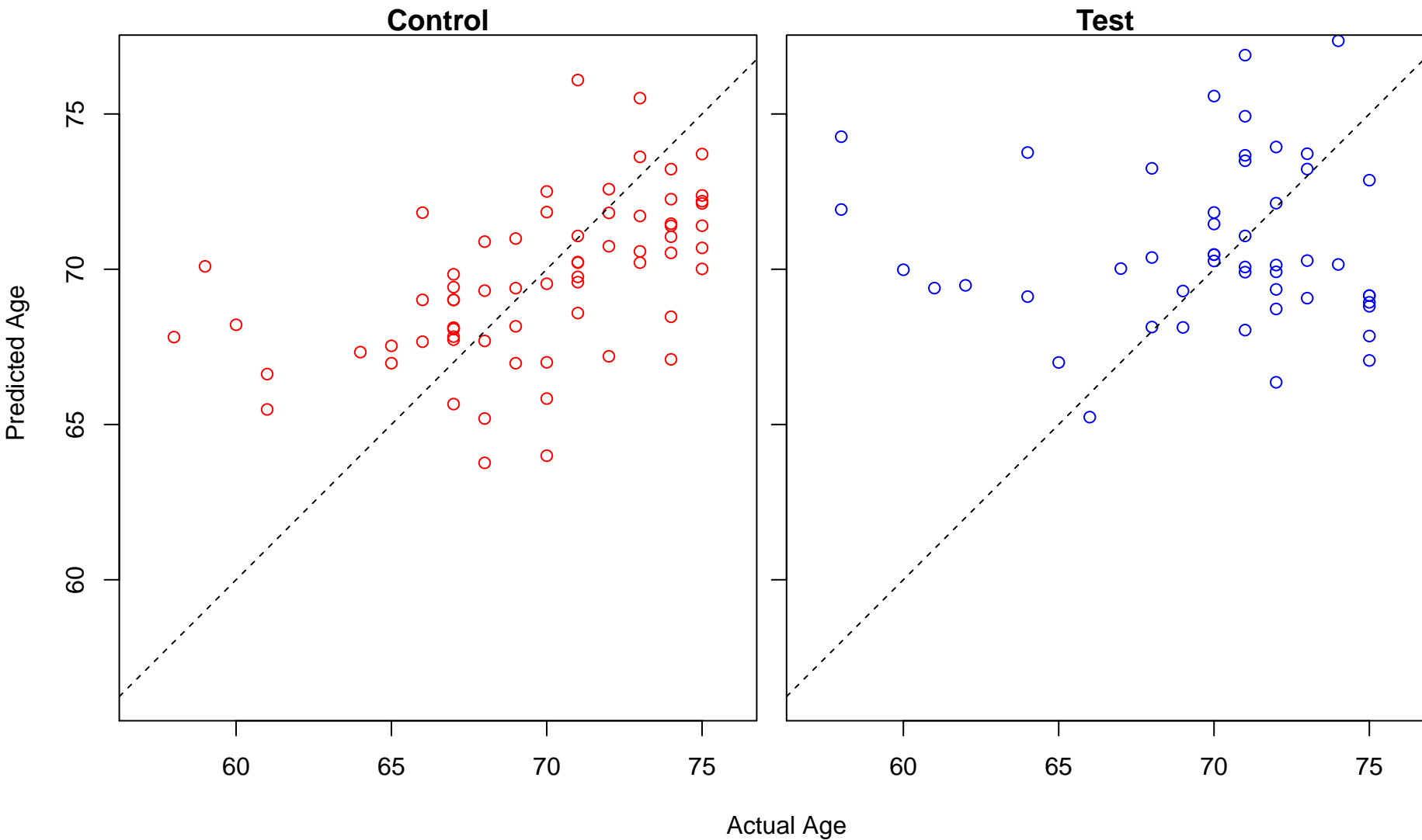
acute inflammatory response (Score: 0.832453)



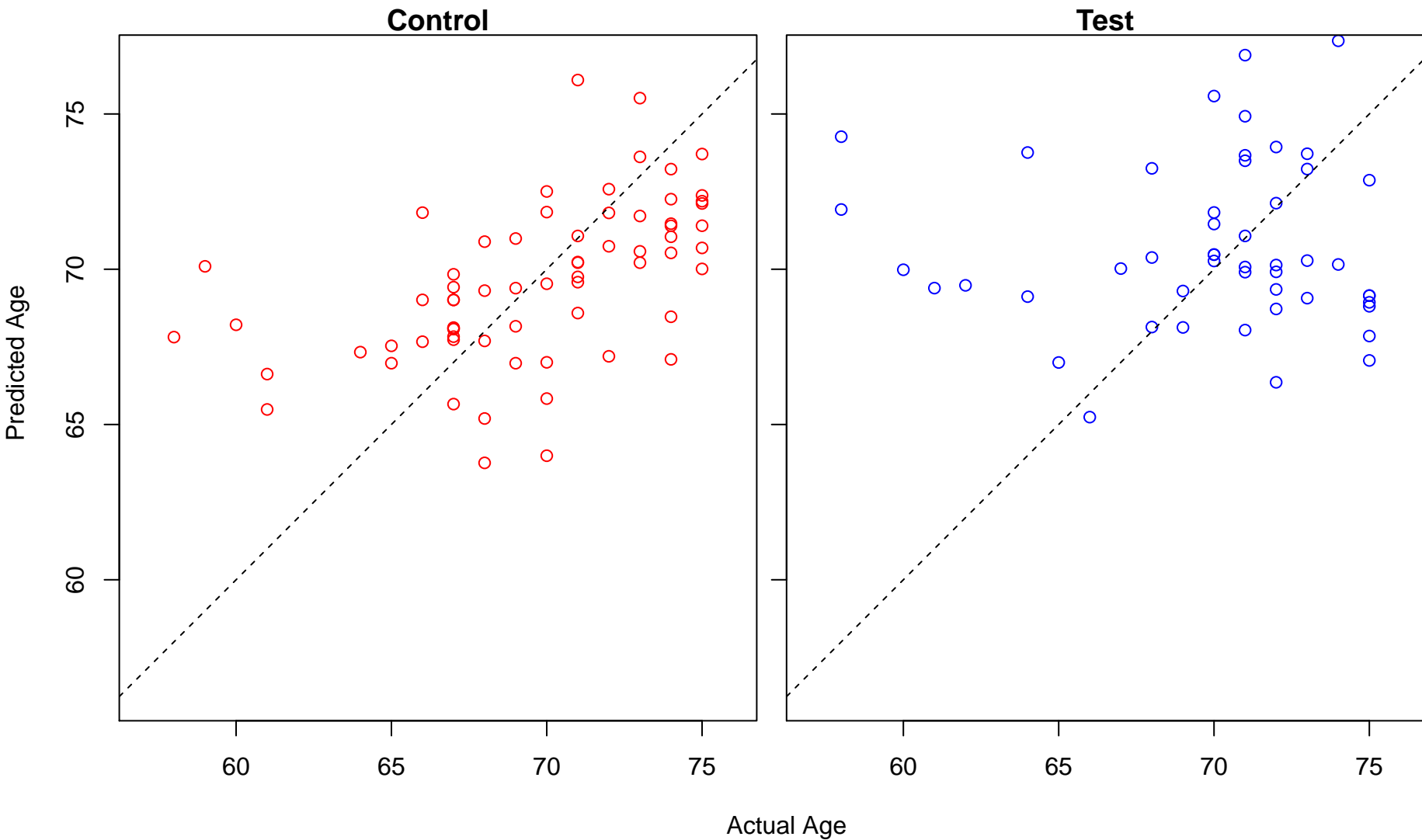
regulation of regulatory T cell differentiation (Score: 0.832412)



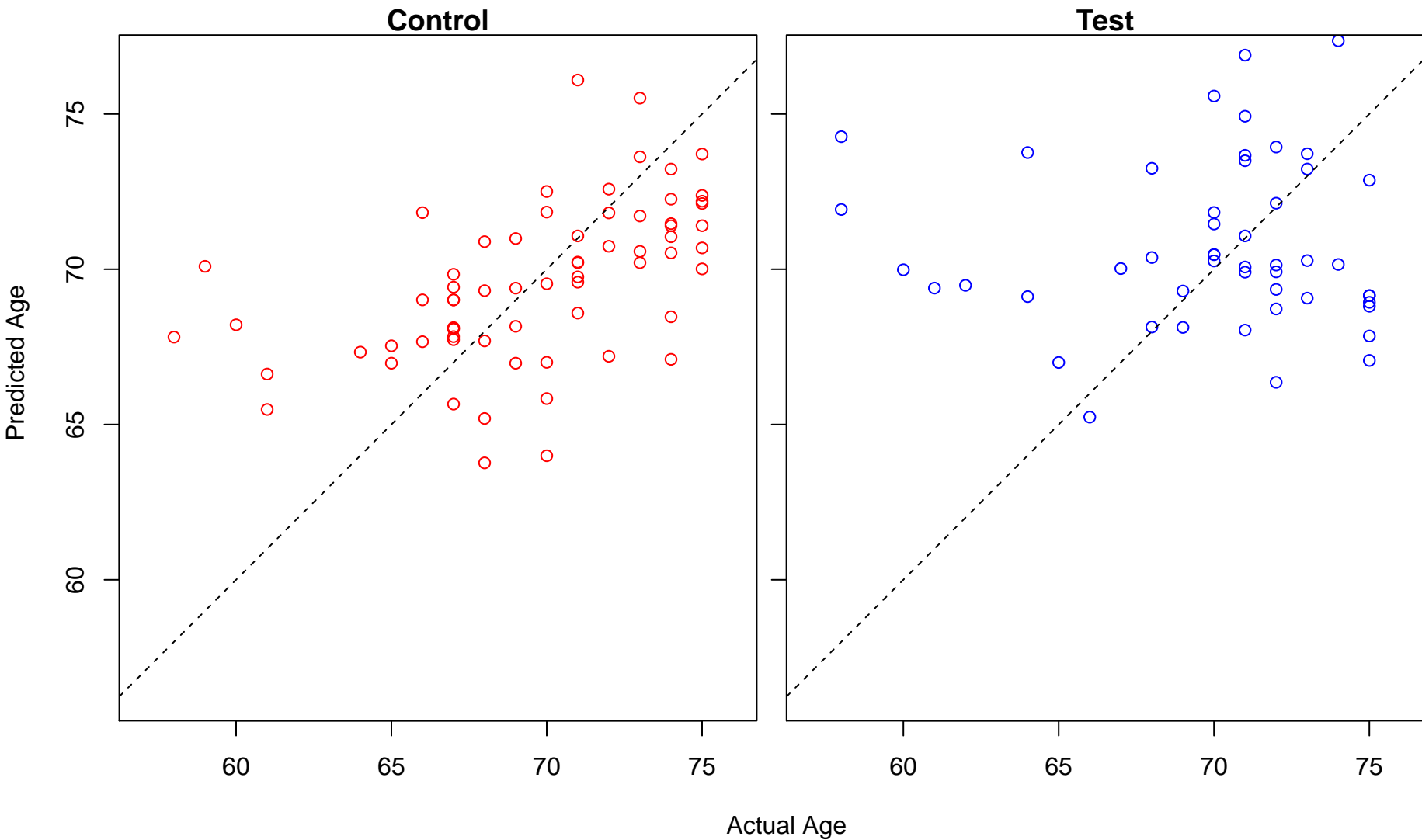
miRNA mediated inhibition of translation (Score: 0.832337)



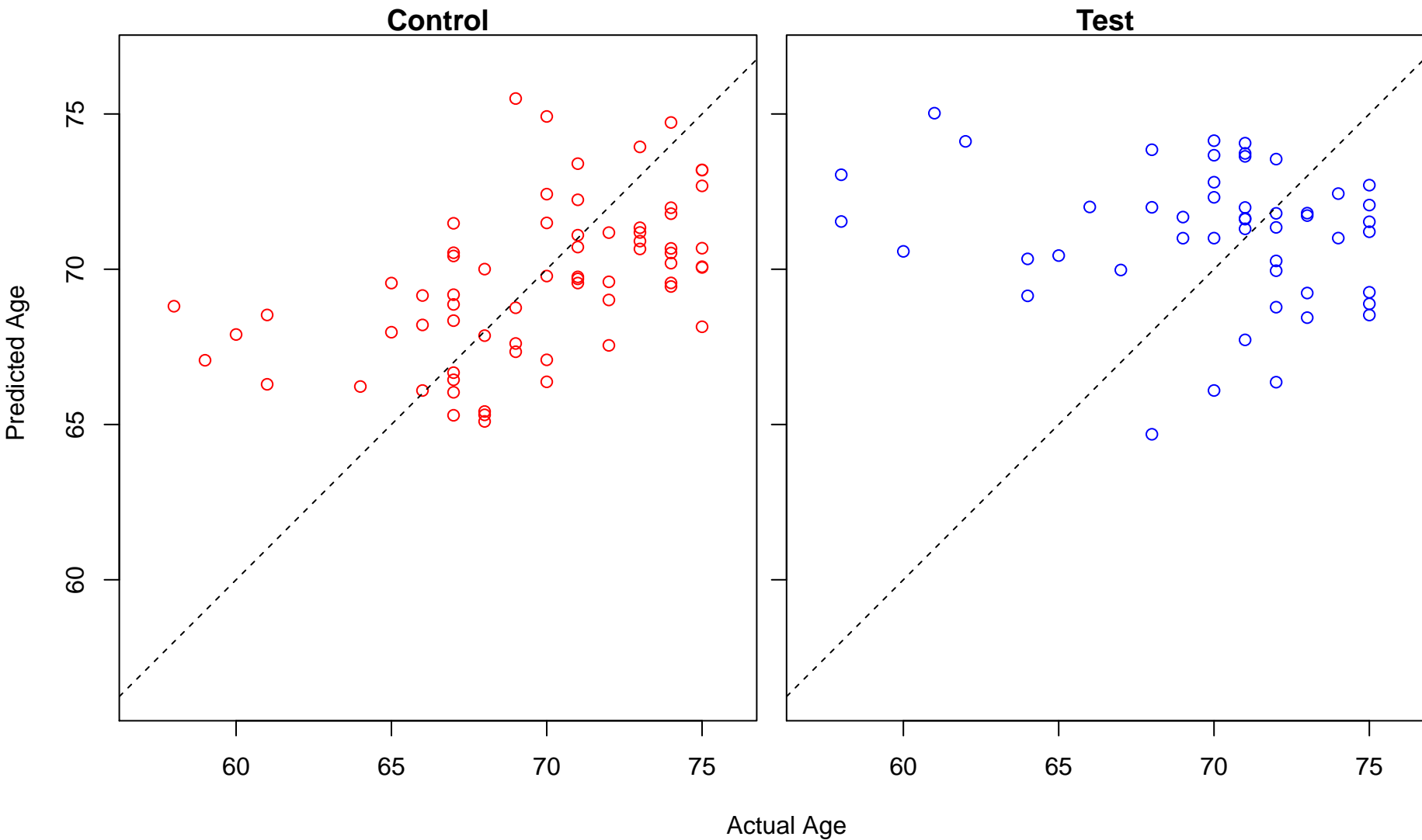
negative regulation of translation, ncRNA-mediated (Score: 0.832337)



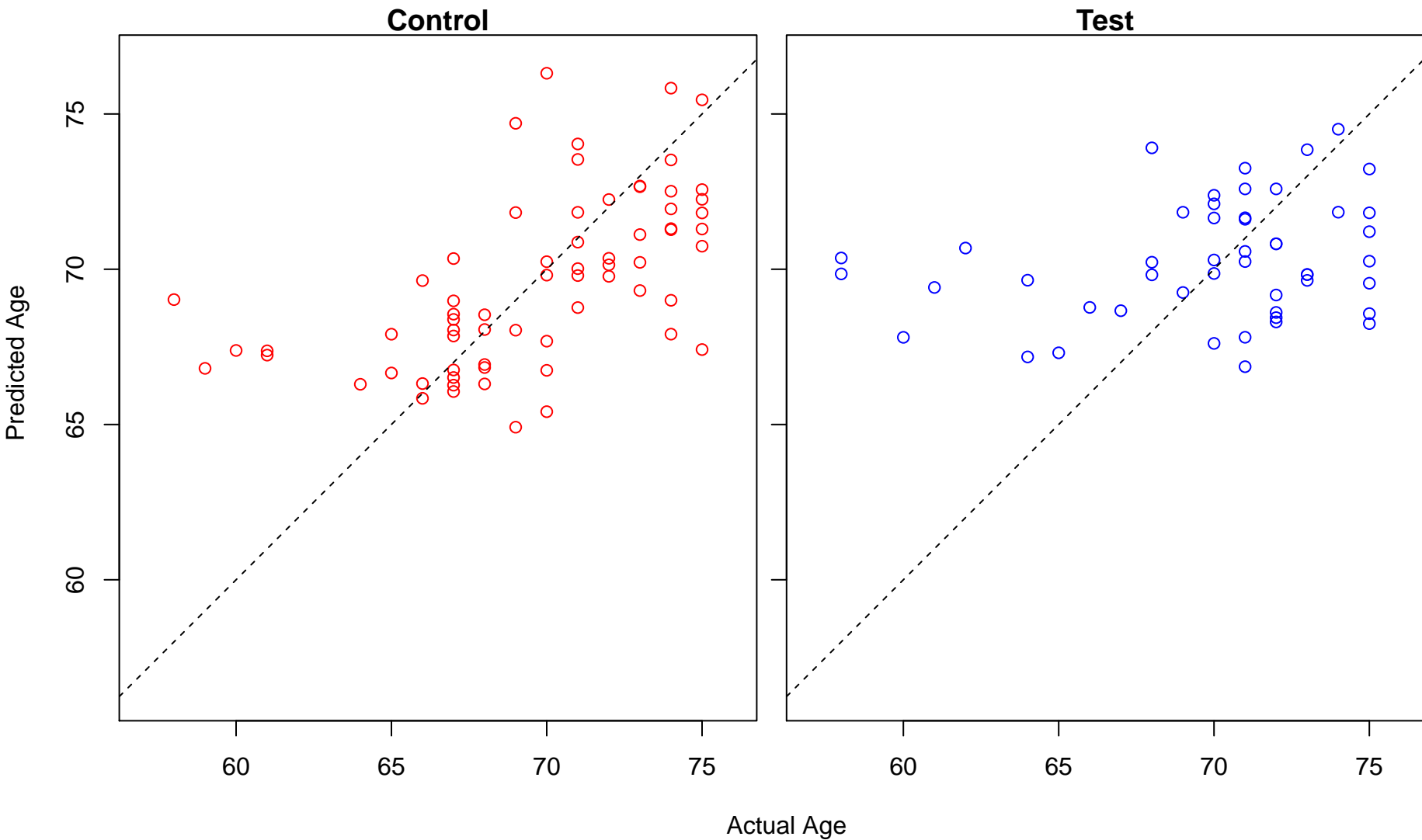
regulation of translation, ncRNA-mediated (Score: 0.832337)



regulation of interferon-gamma biosynthetic process (Score: 0.832243)

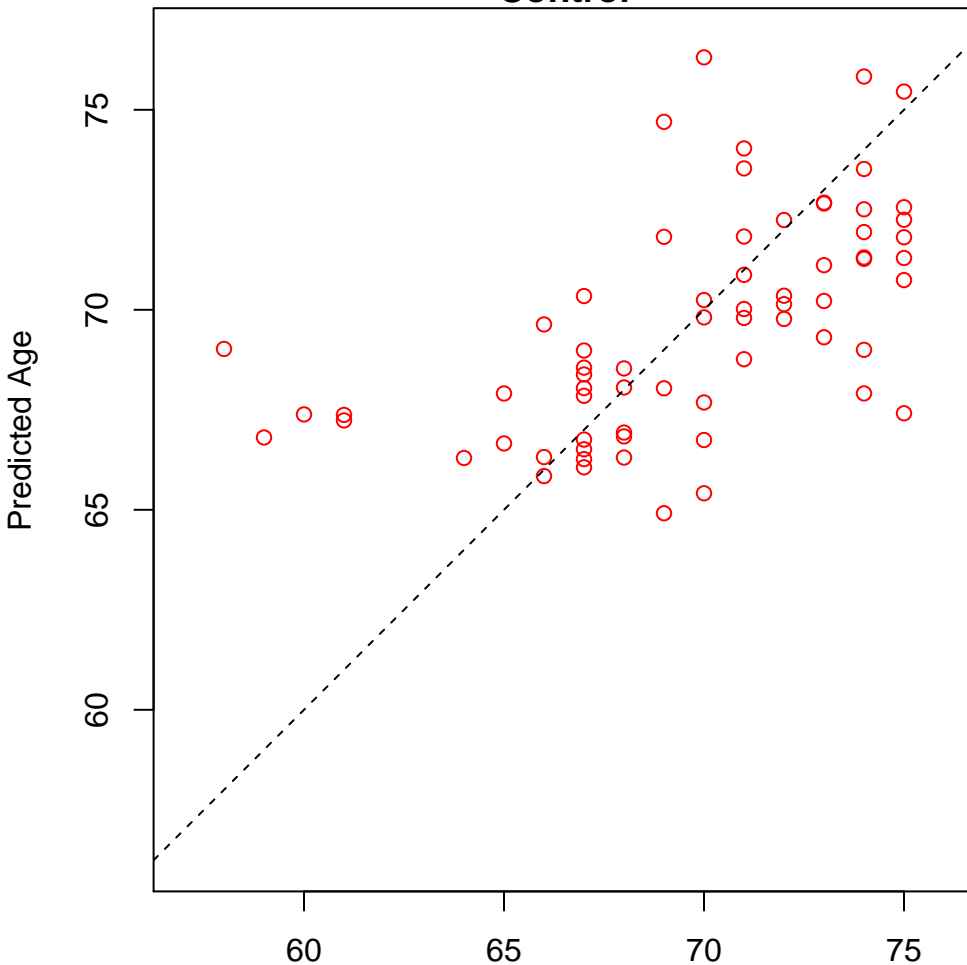


nephron morphogenesis (Score: 0.831987)

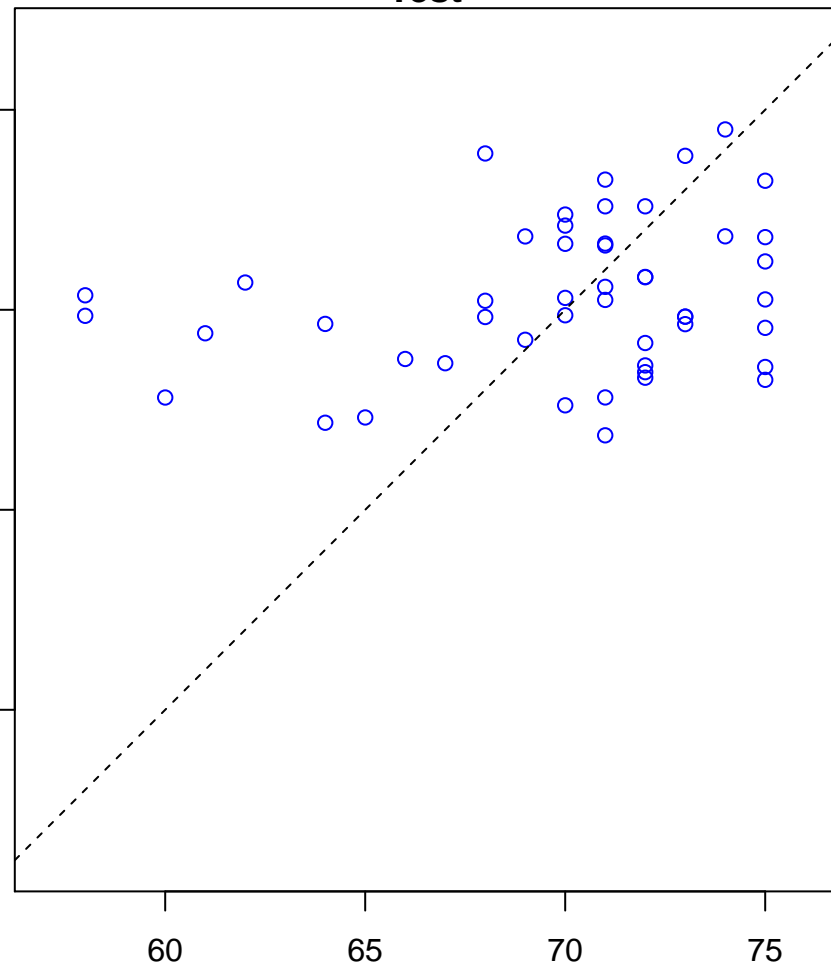


nephron epithelium morphogenesis (Score: 0.831987)

Control



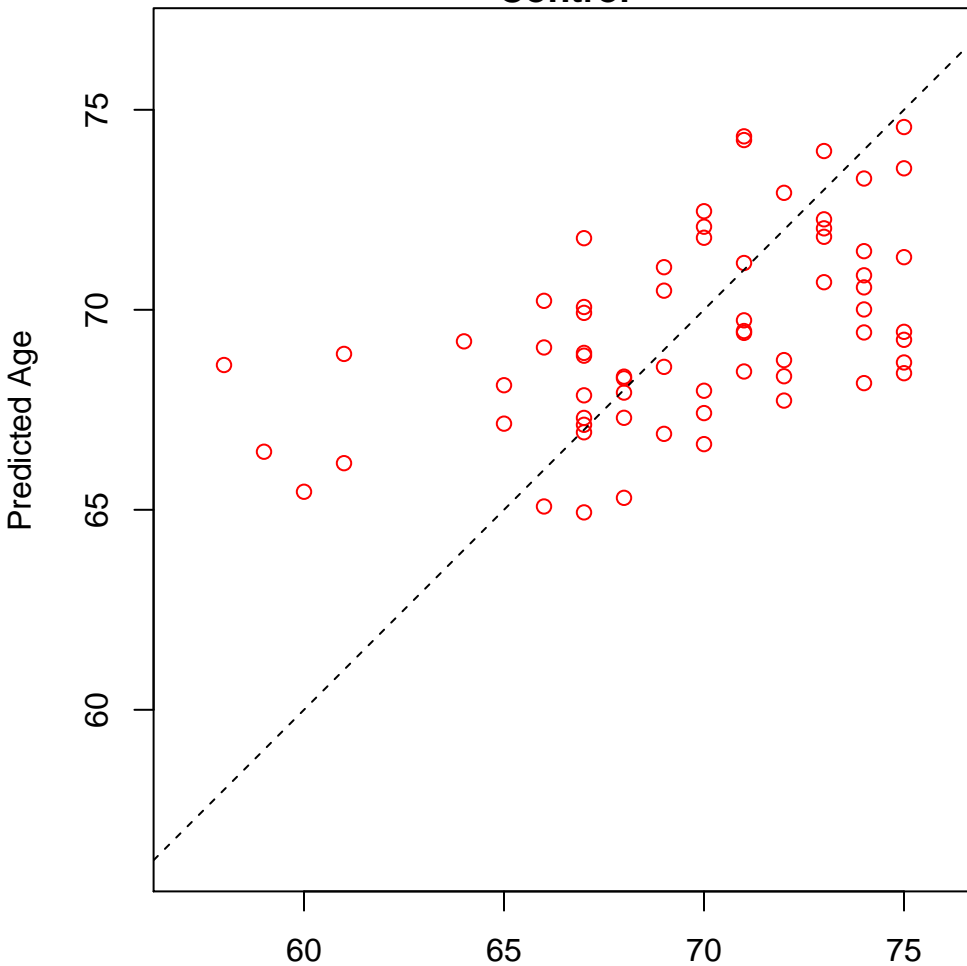
Test



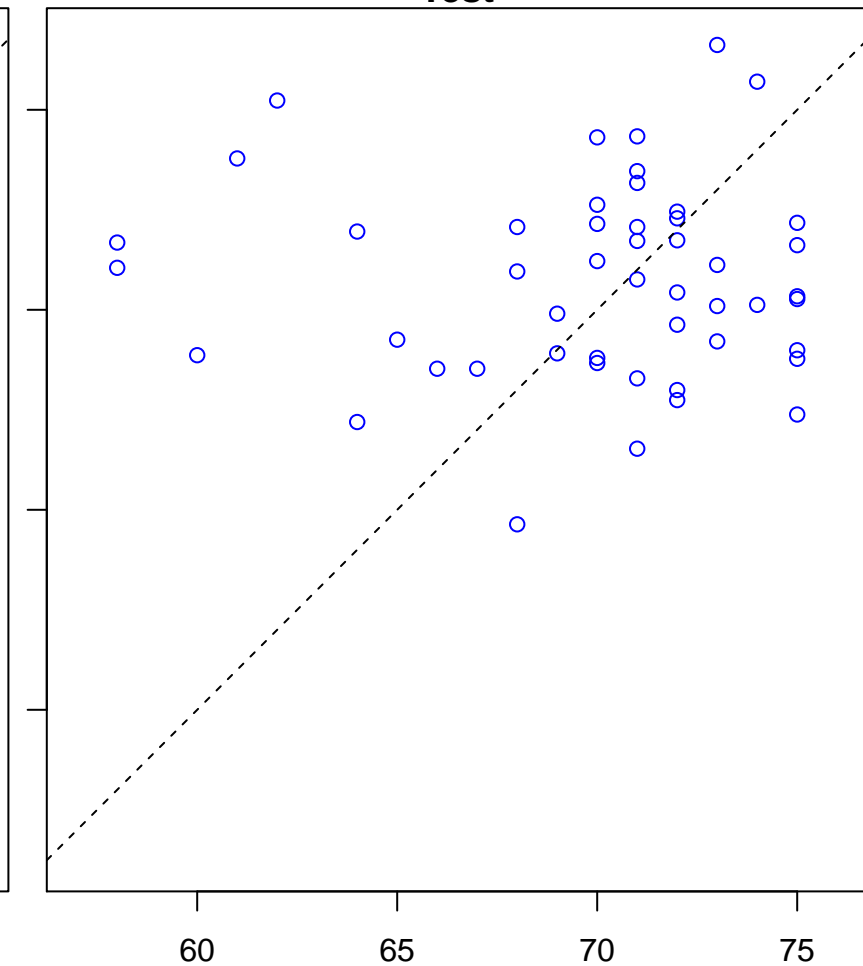
Actual Age

quaternary ammonium group transport (Score: 0.831983)

Control

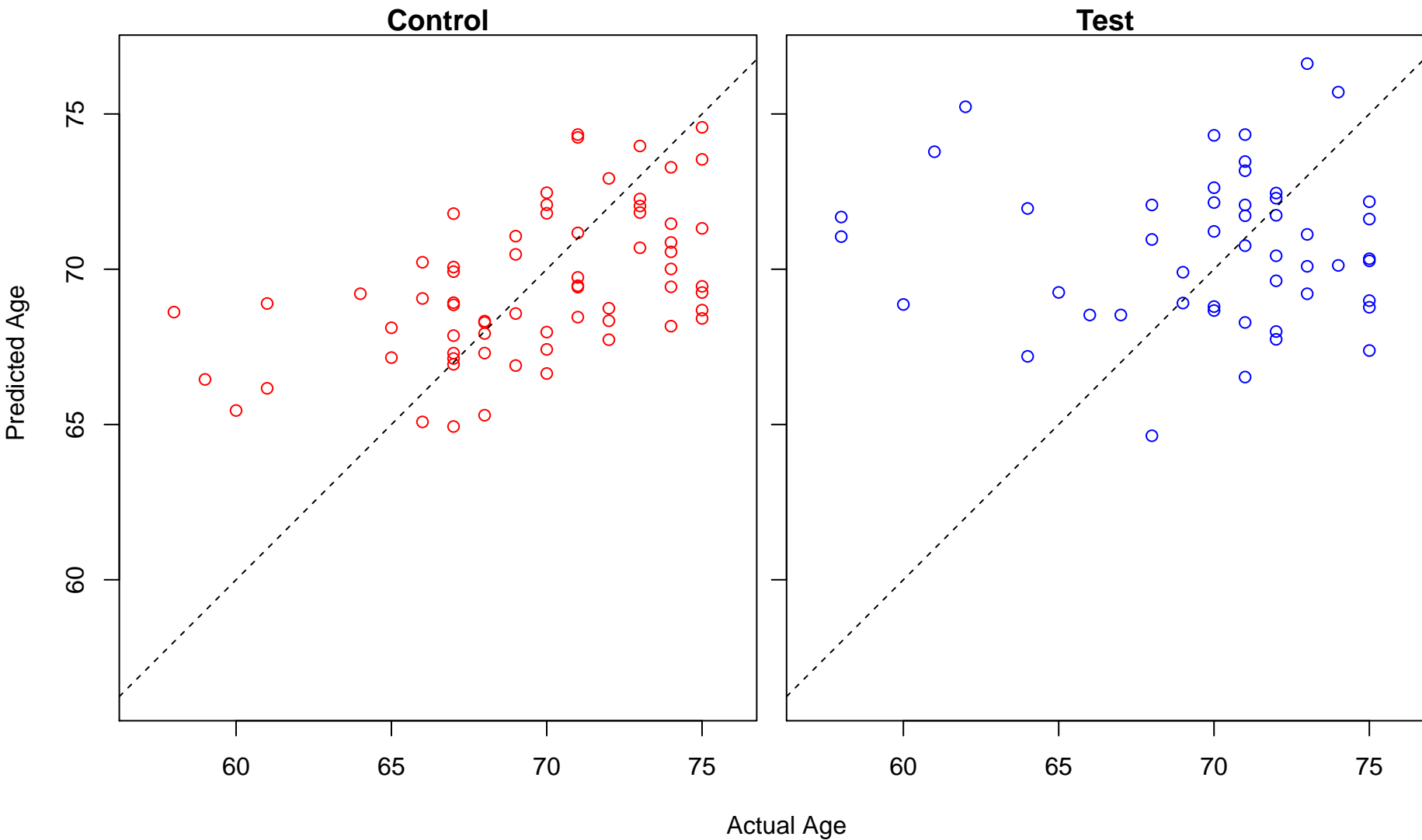


Test

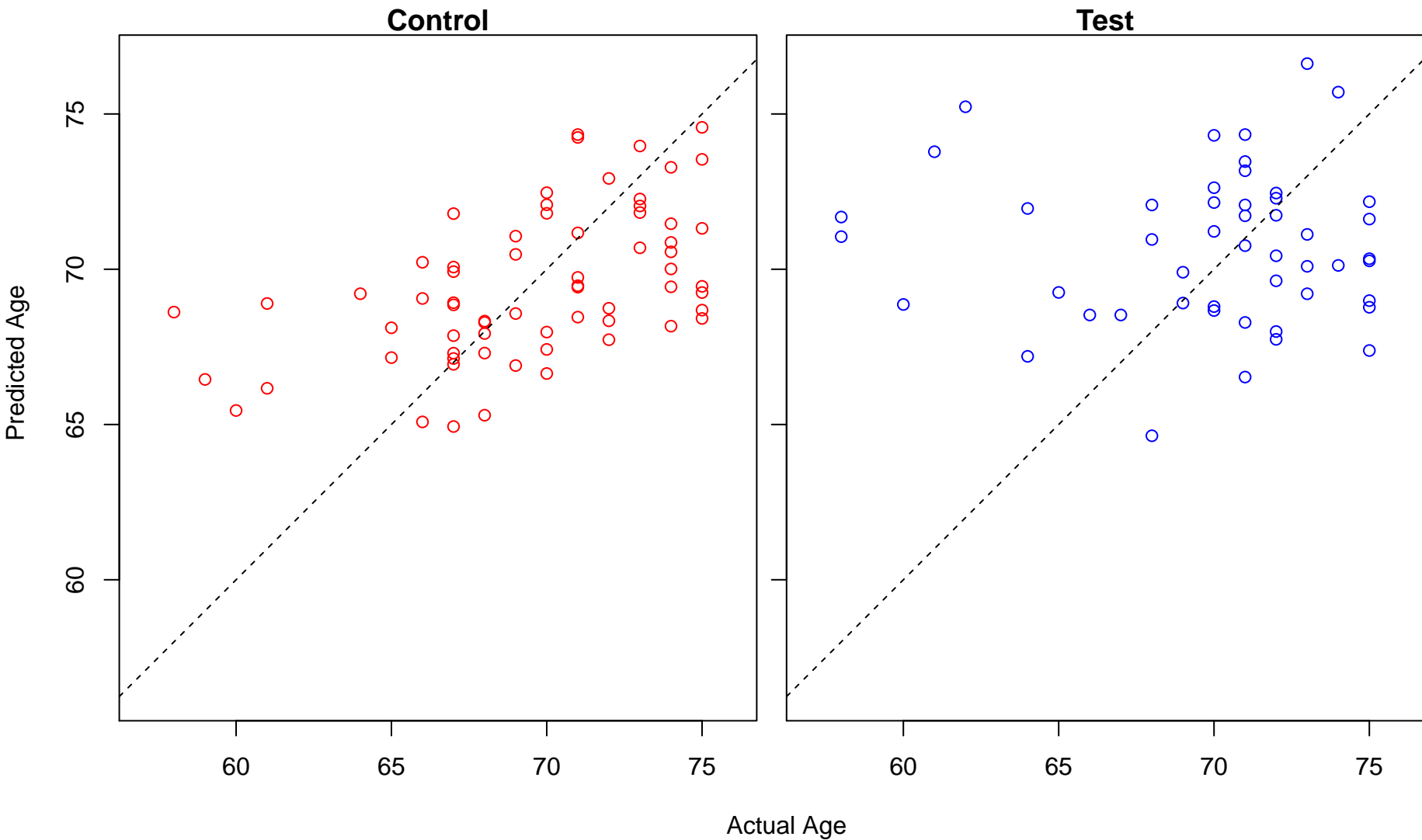


Actual Age

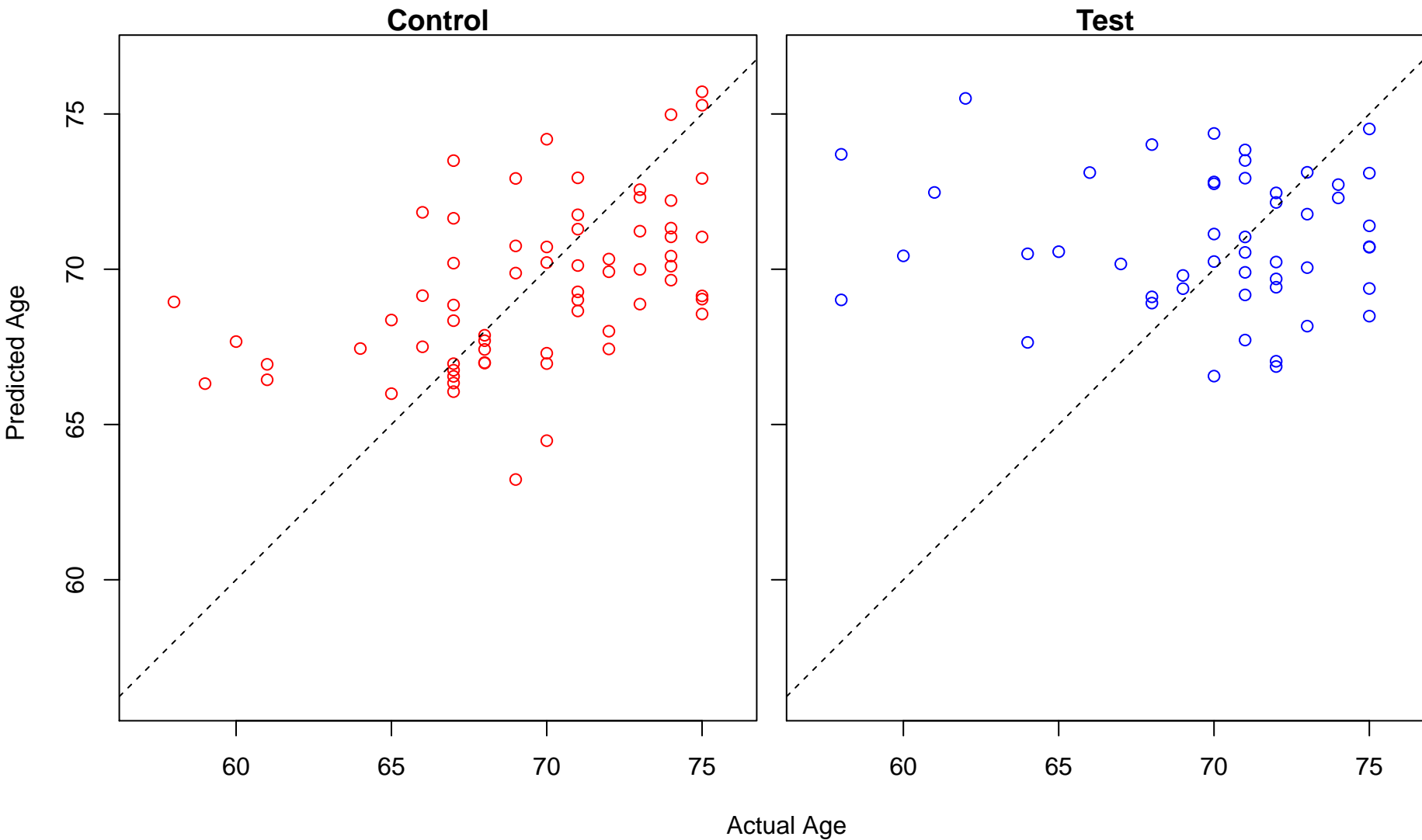
amino-acid betaine transport (Score: 0.831983)



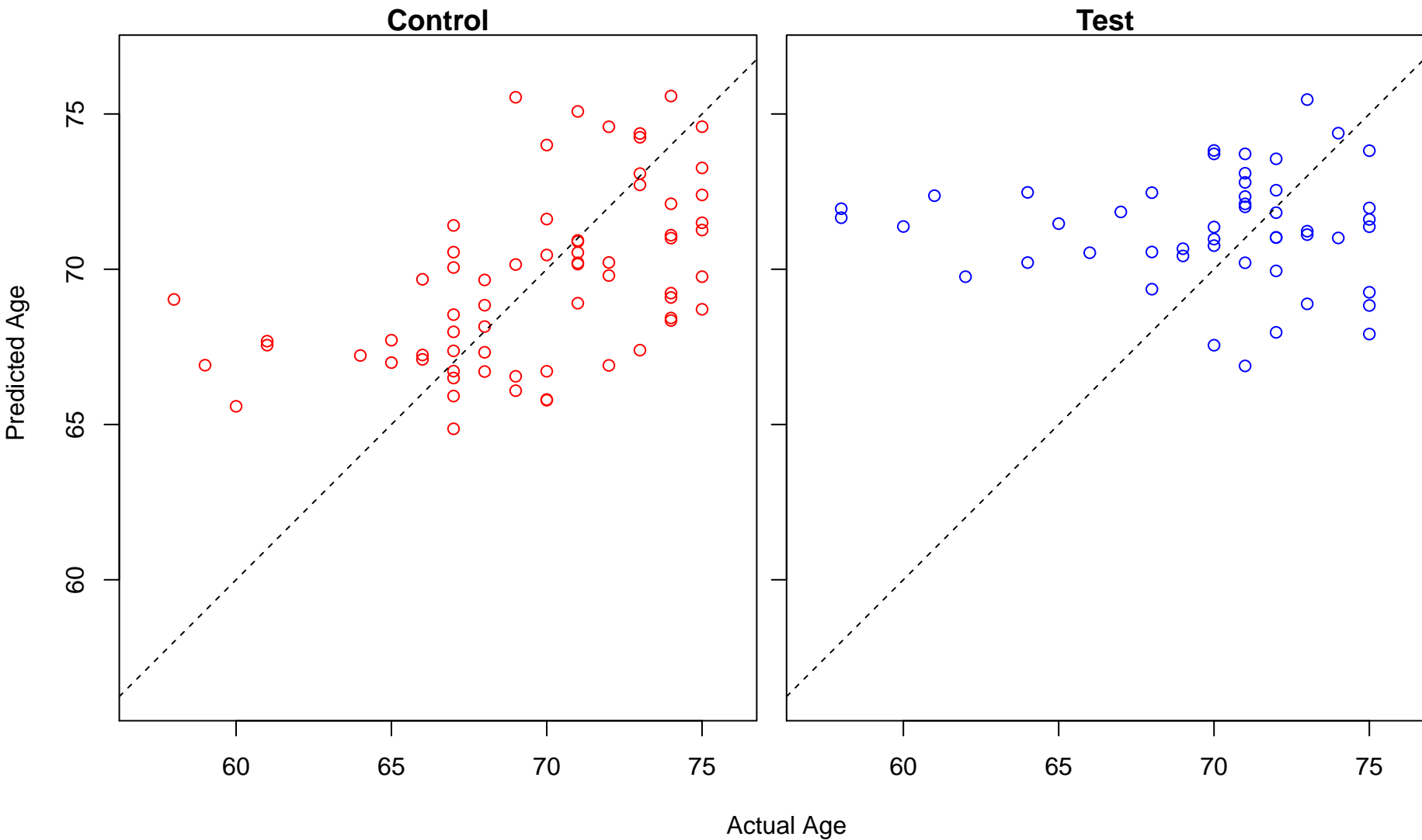
carnitine transport (Score: 0.831983)



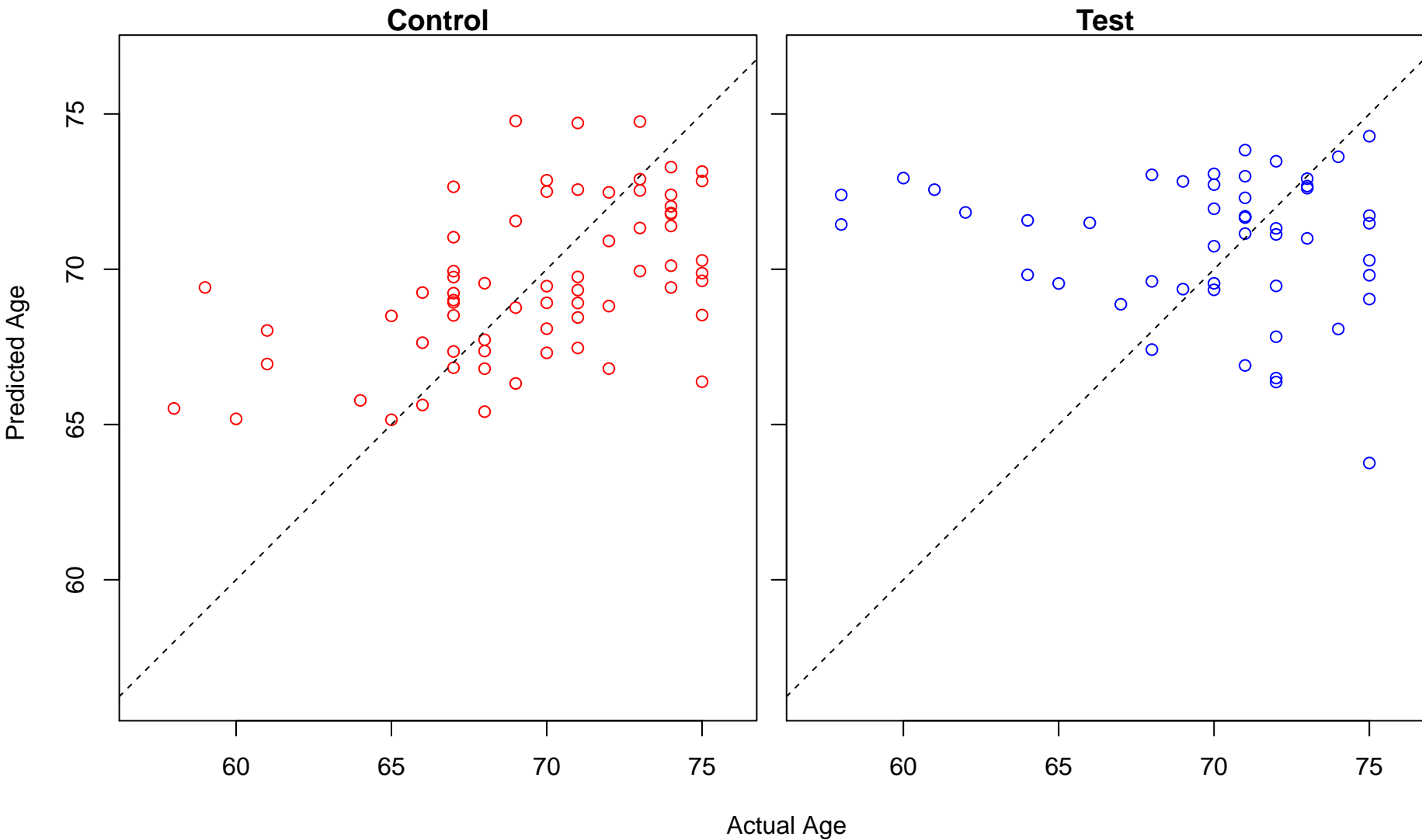
regulation of alcohol biosynthetic process (Score: 0.831766)



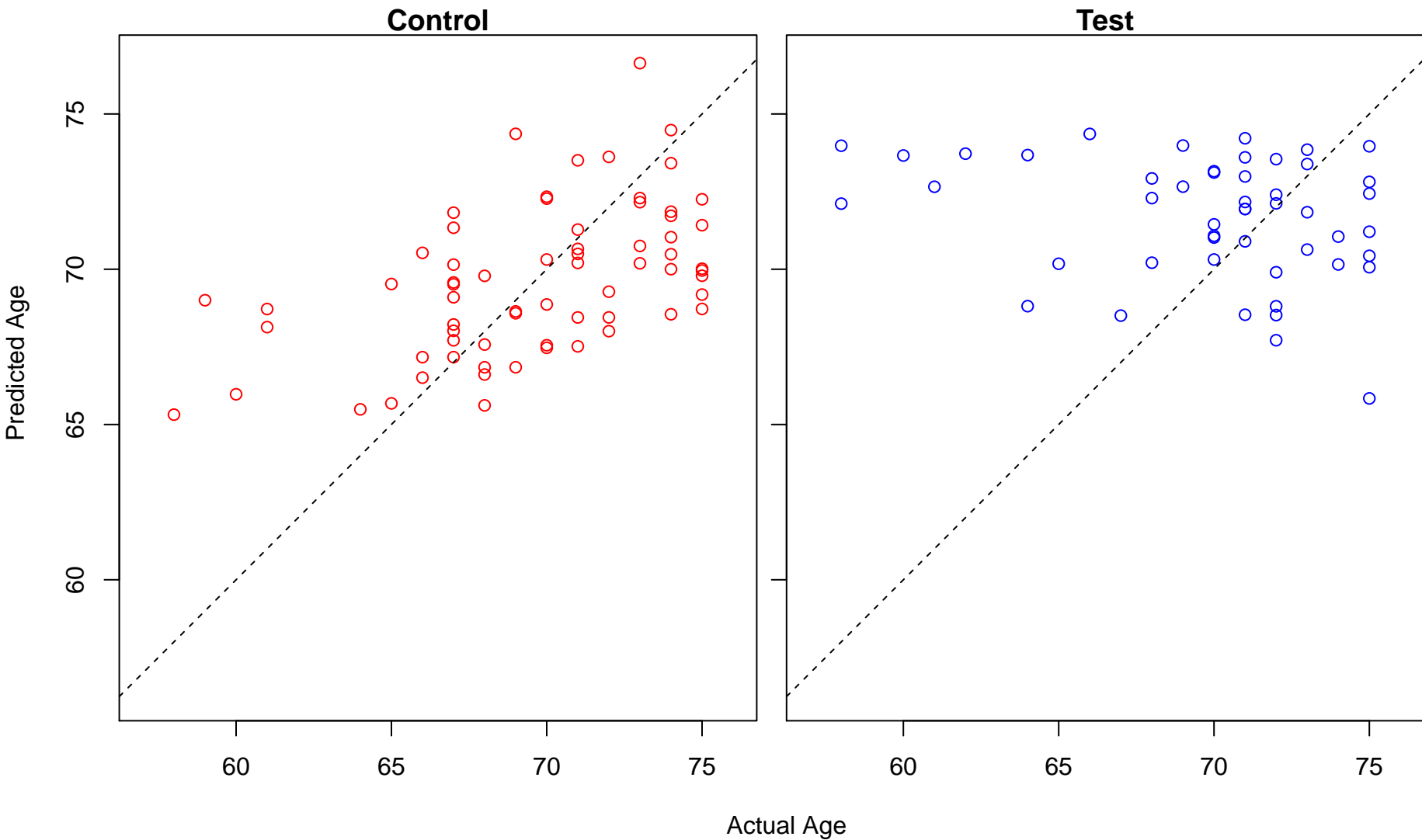
glycosaminoglycan biosynthetic process (Score: 0.831757)



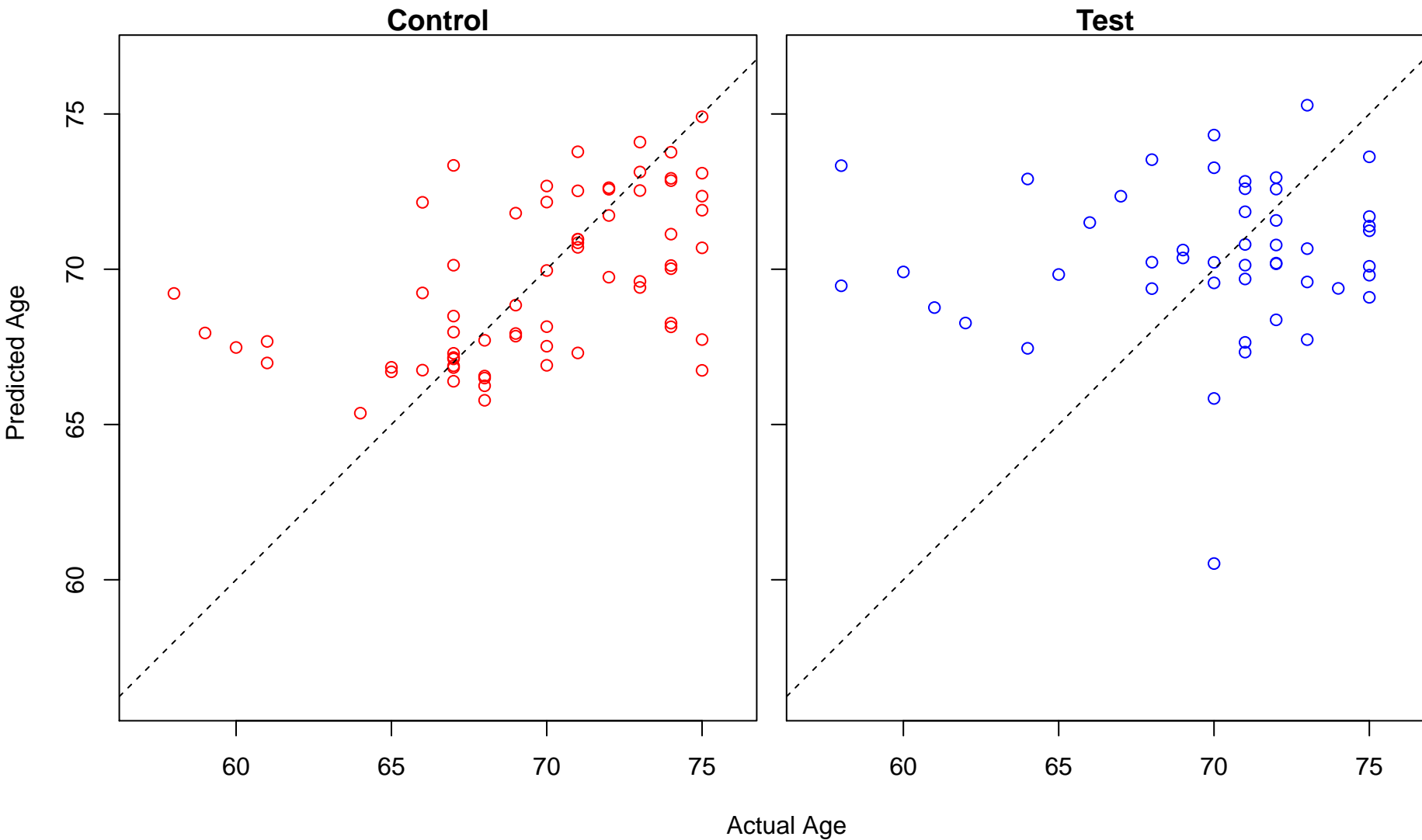
negative regulation of glial cell proliferation (Score: 0.831527)



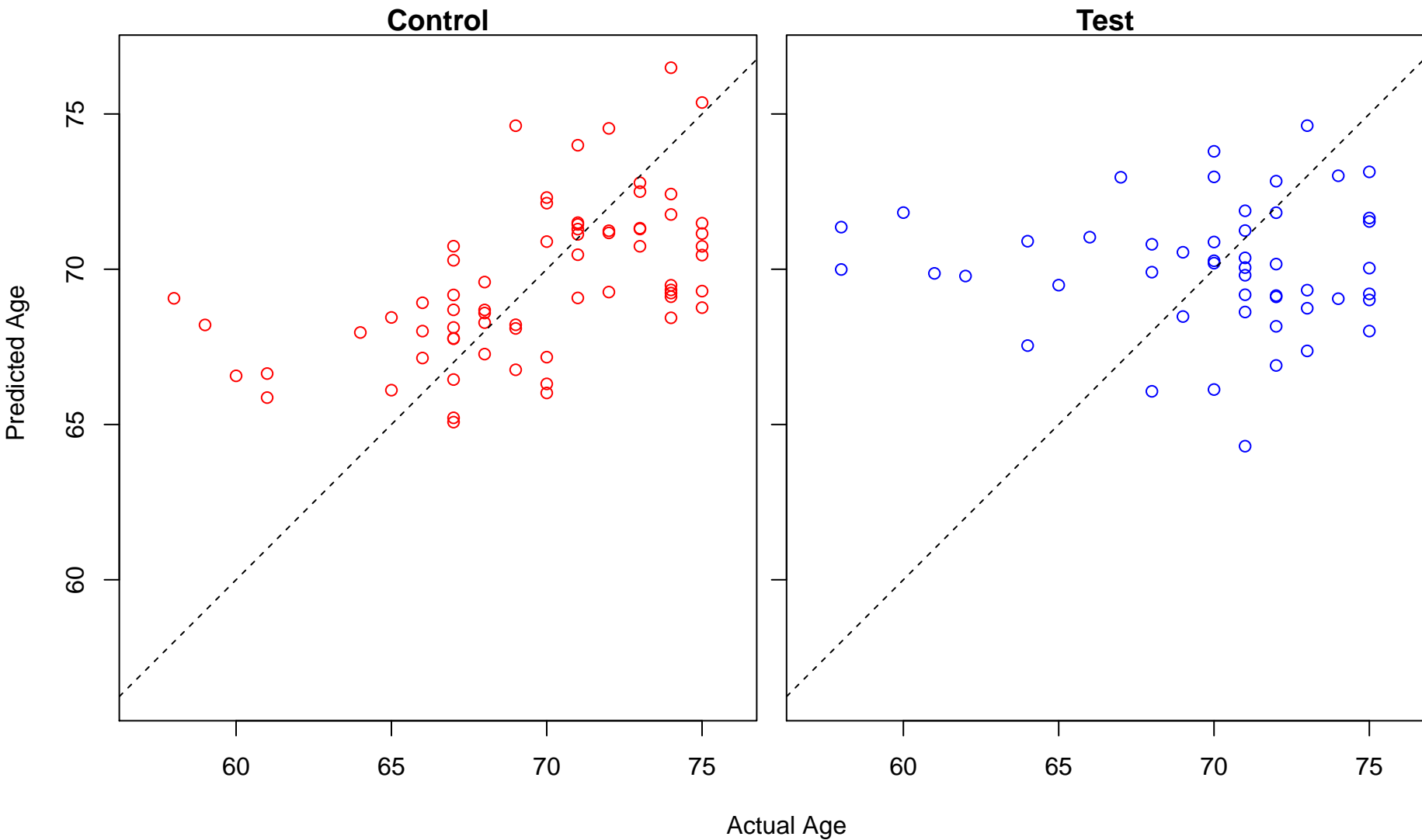
mitral valve development (Score: 0.830837)



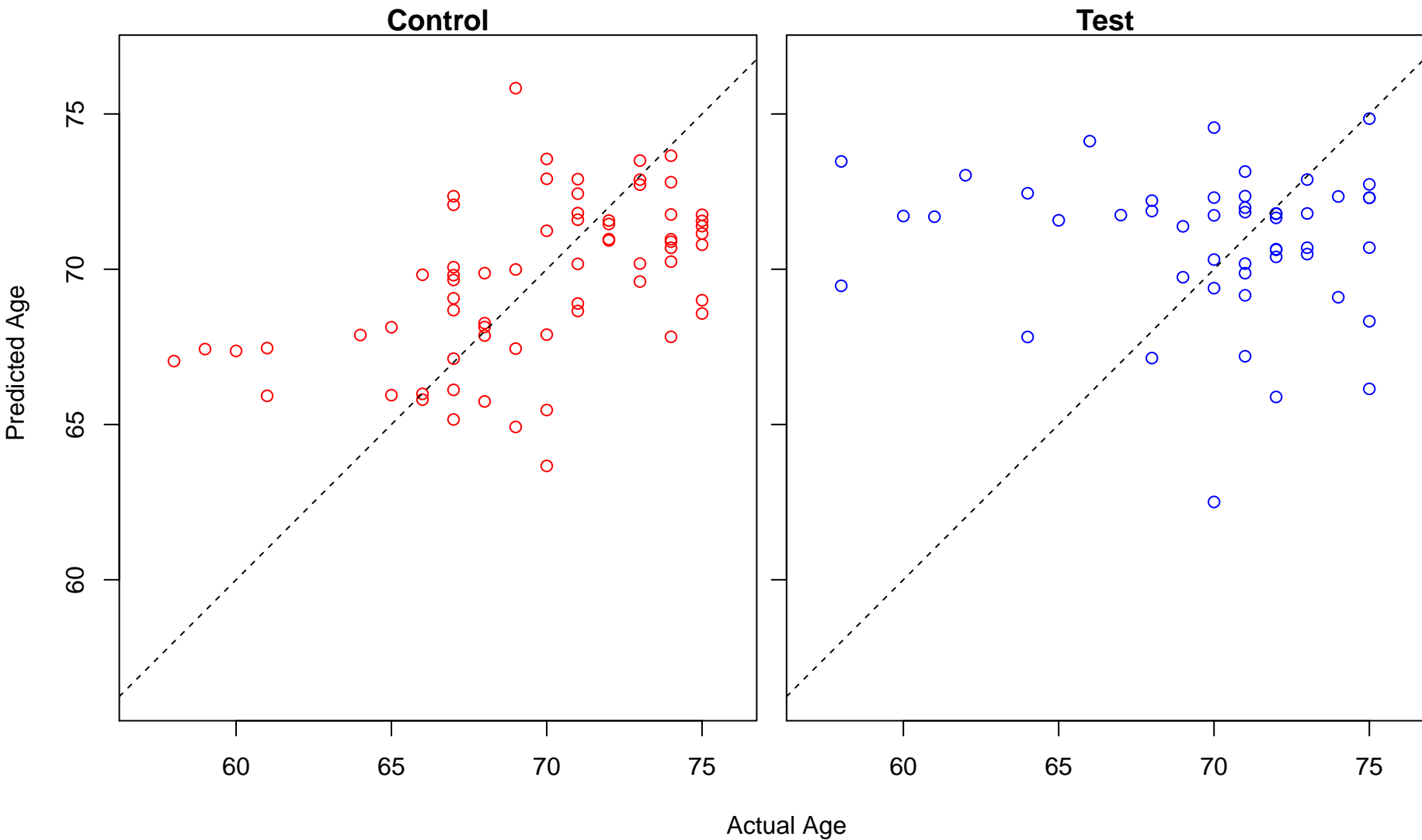
postsynaptic membrane organization (Score: 0.830818)



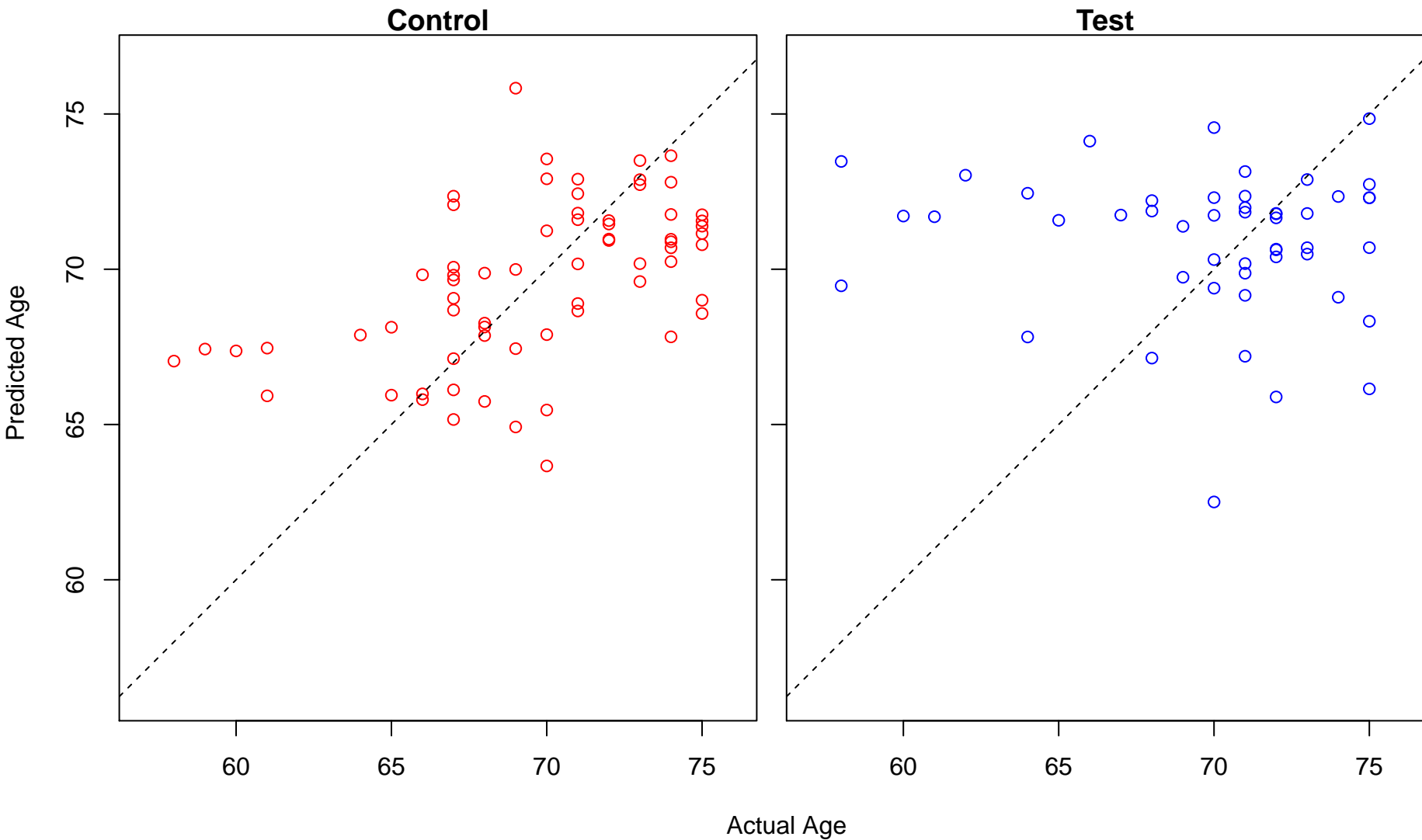
negative regulation of cyclin–dependent protein serine/threonine kinase activity (Score: 0.830730)



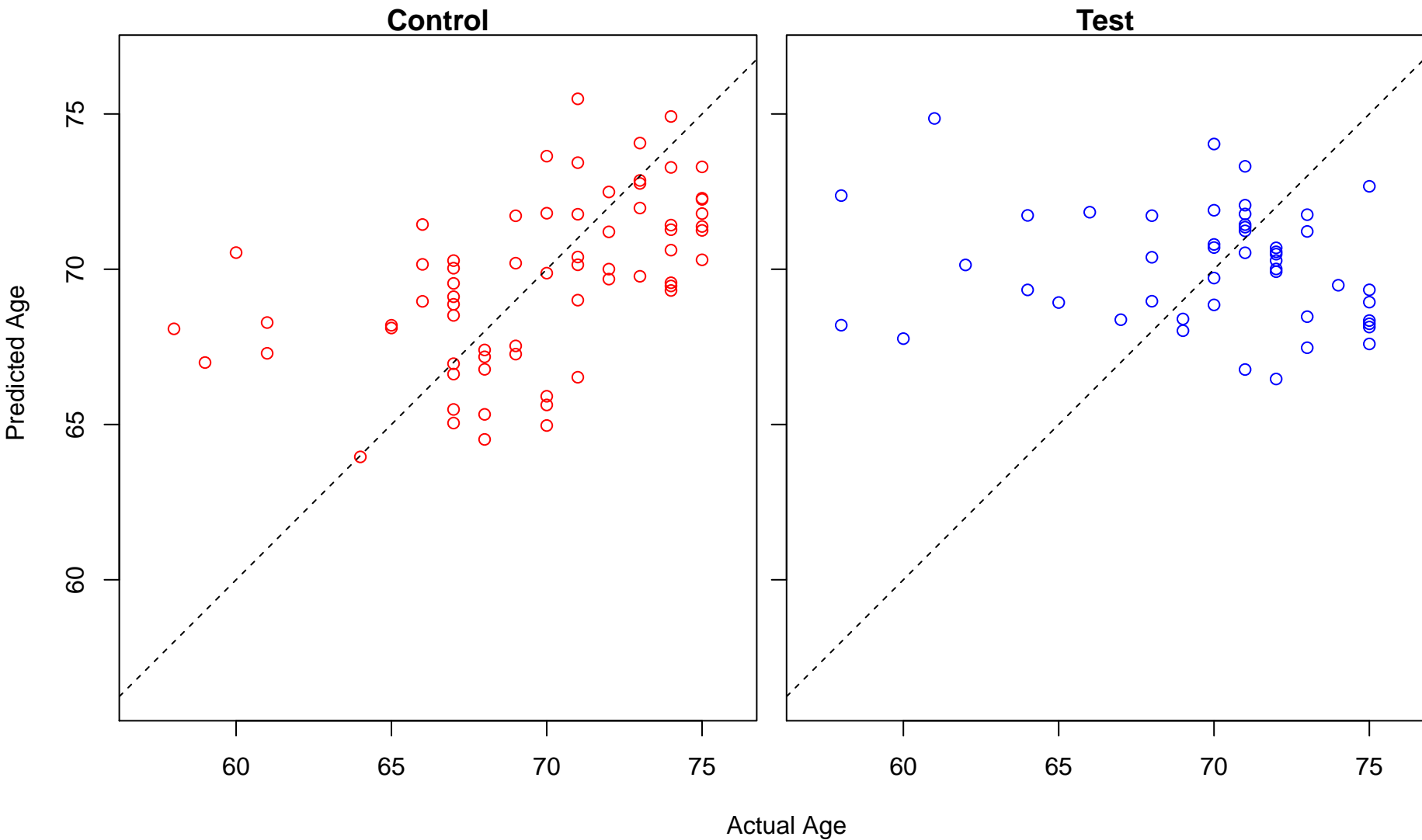
melanosome organization (Score: 0.830475)



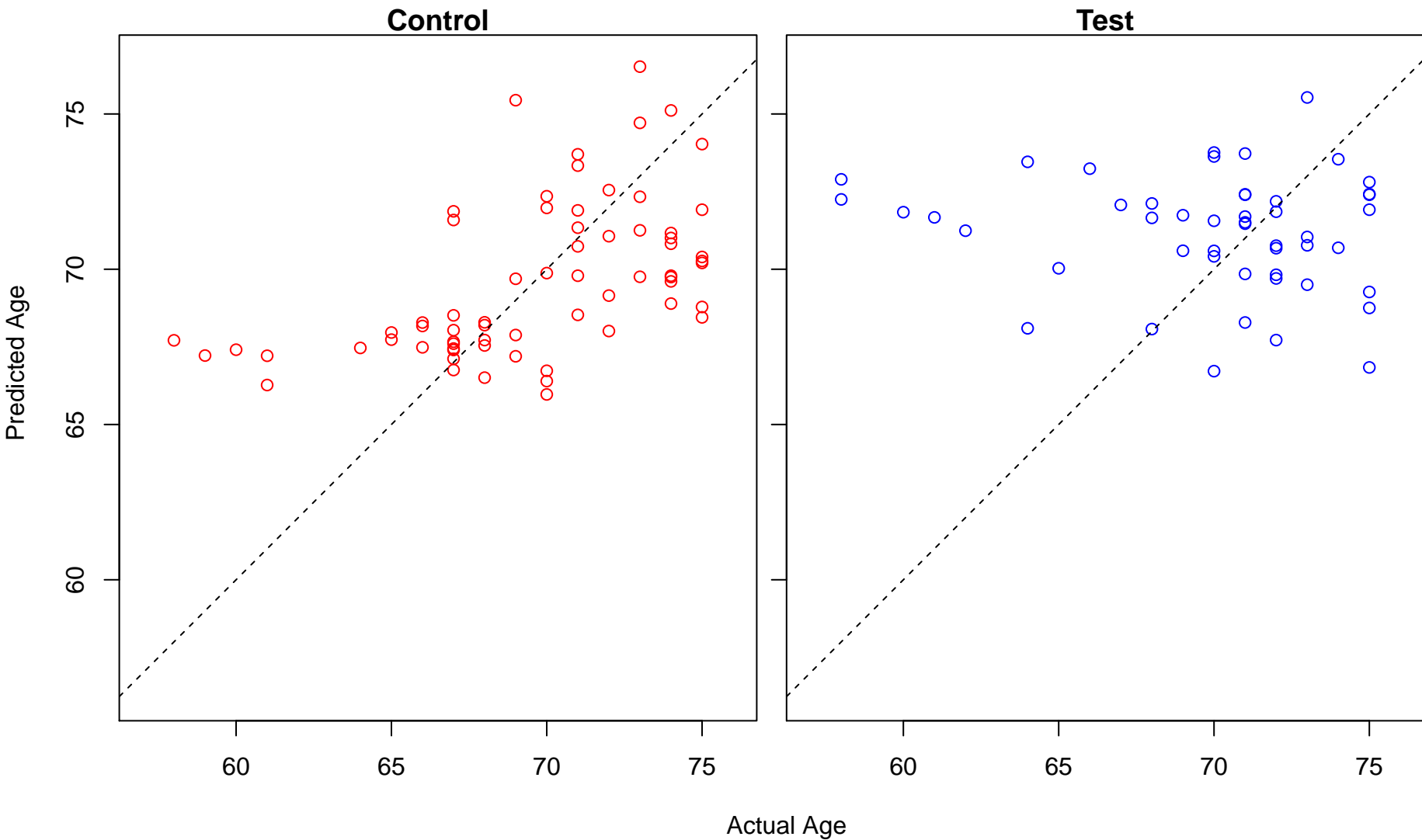
pigment granule organization (Score: 0.830475)



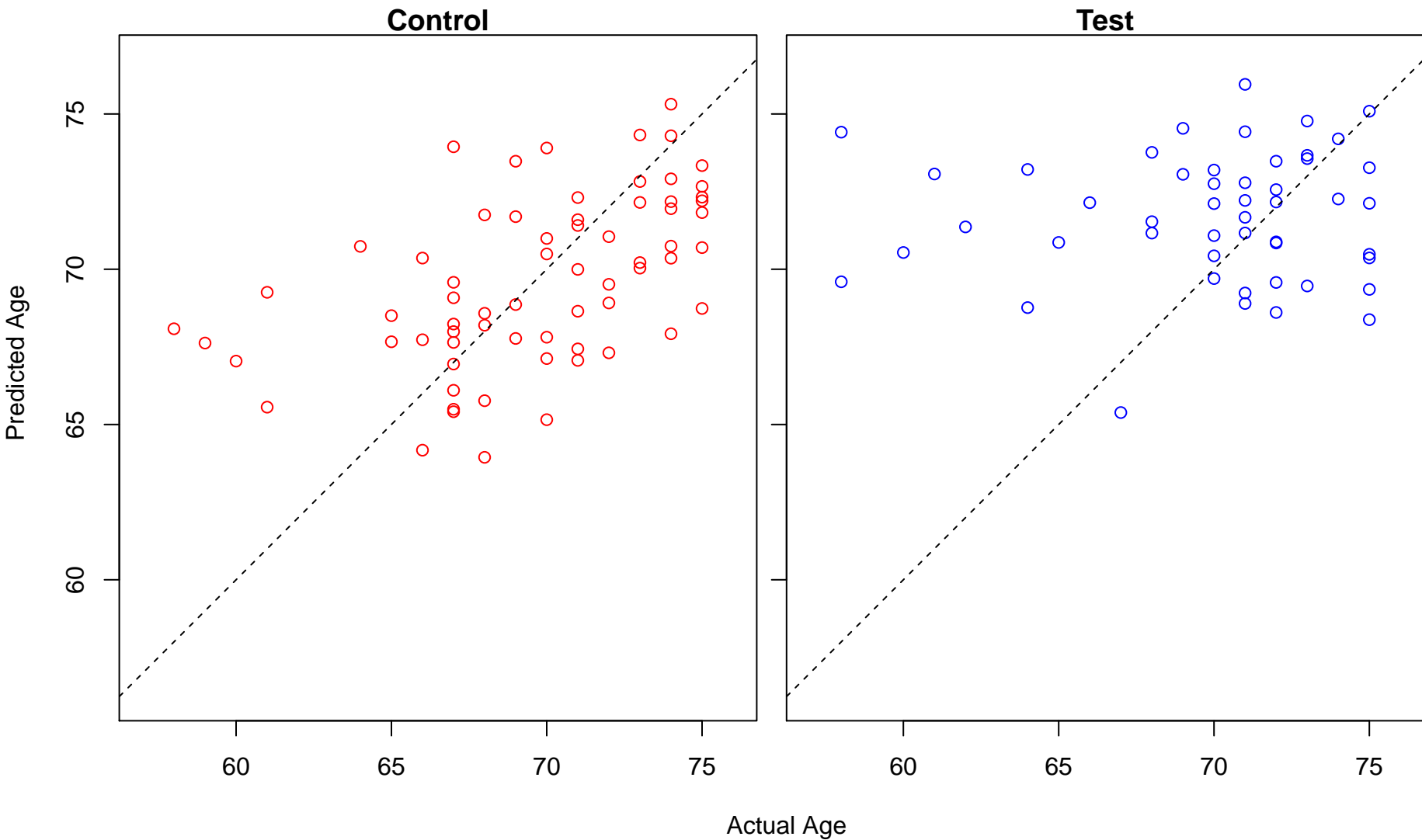
pyrimidine ribonucleoside metabolic process (Score: 0.829424)



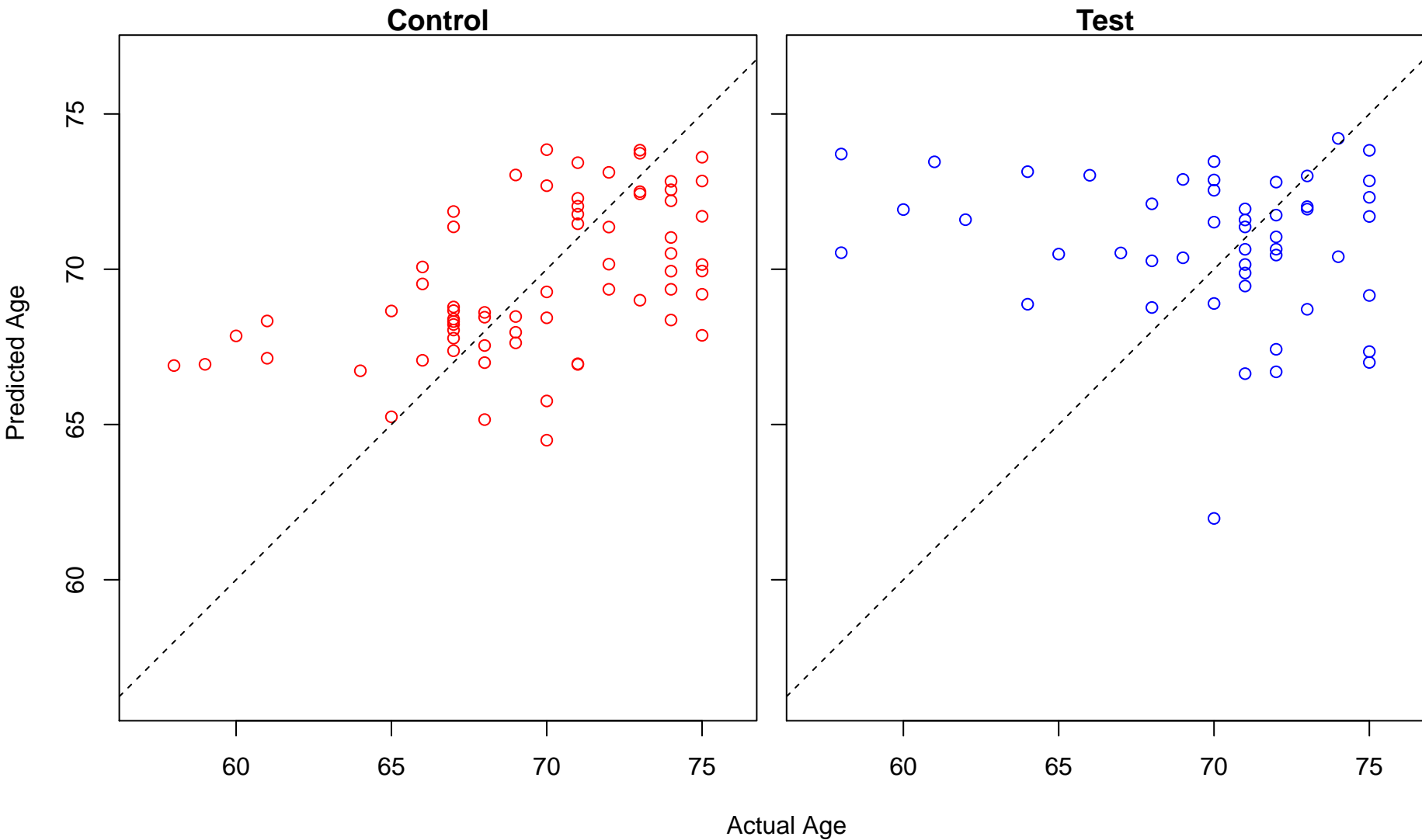
negative regulation of nucleocytoplasmic transport (Score: 0.829106)



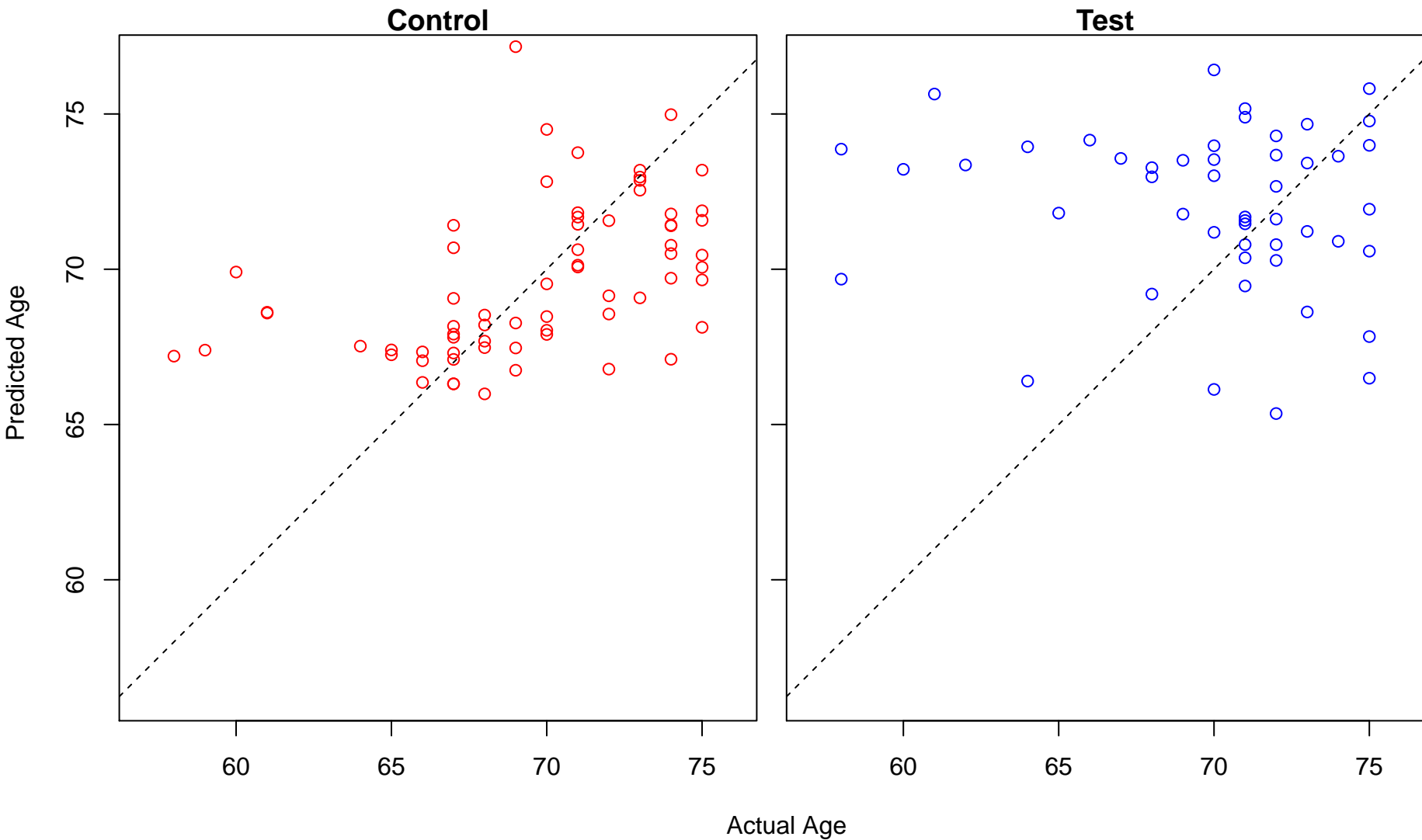
embryo implantation (Score: 0.828969)



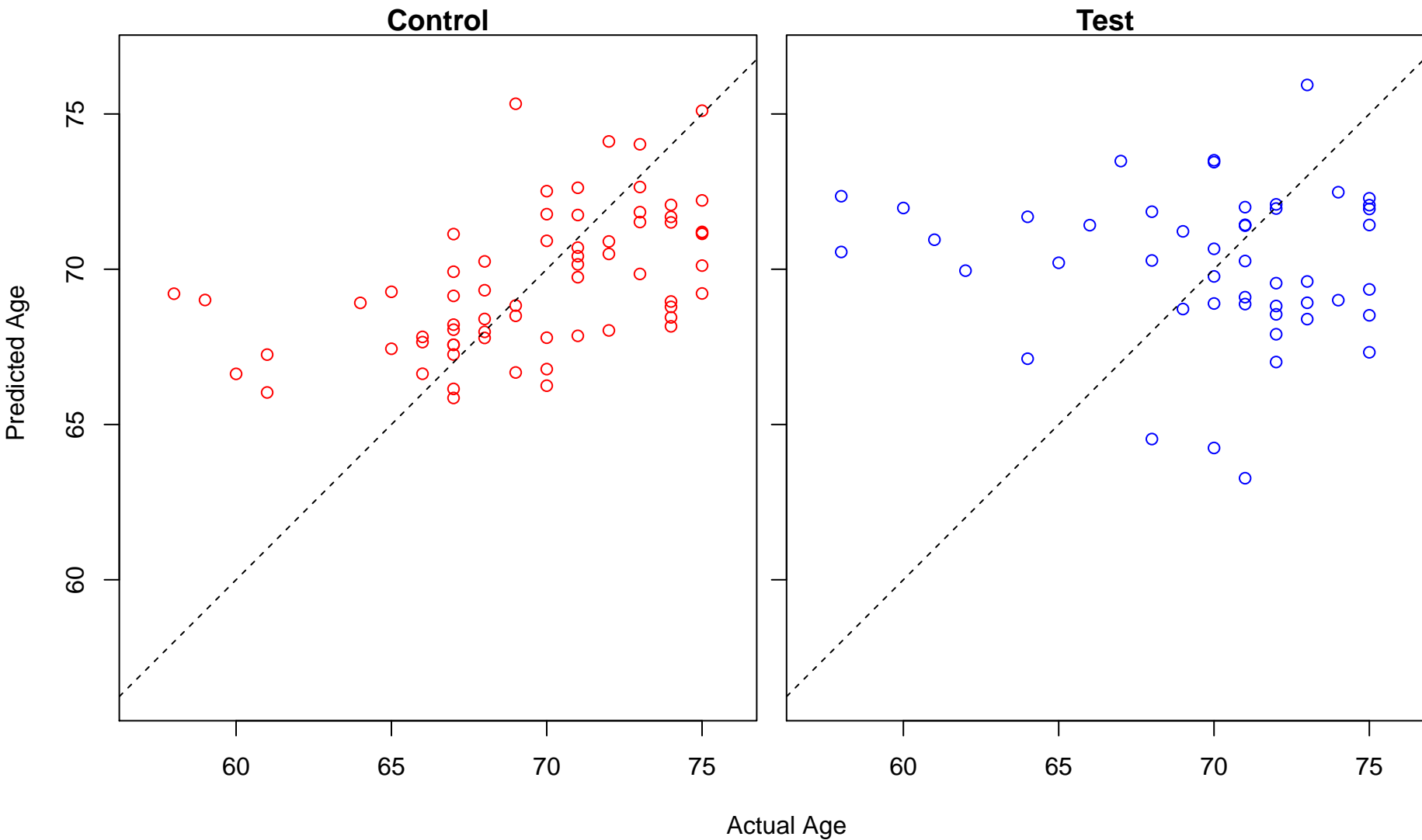
mammary gland development (Score: 0.828729)



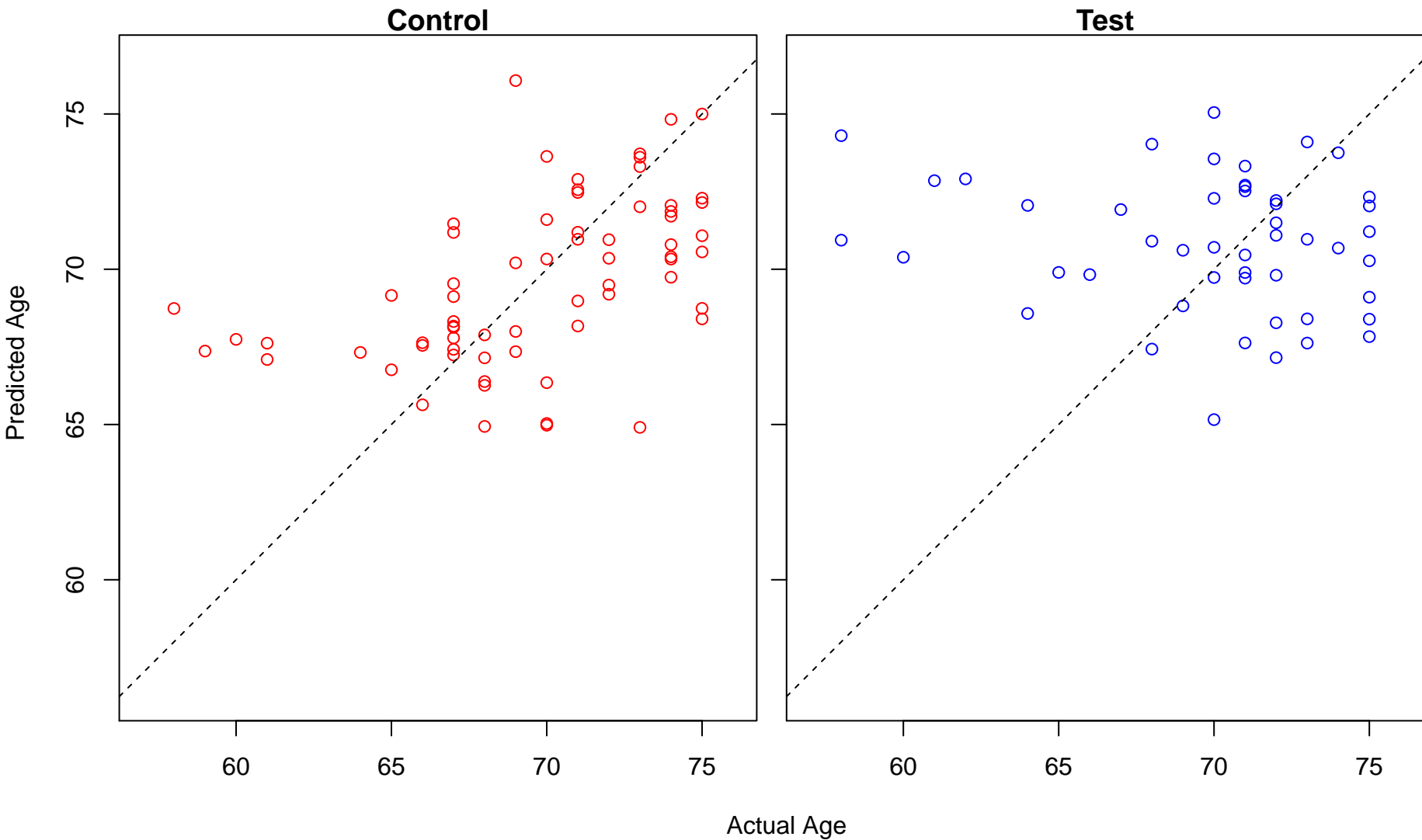
response to antibiotic (Score: 0.828681)



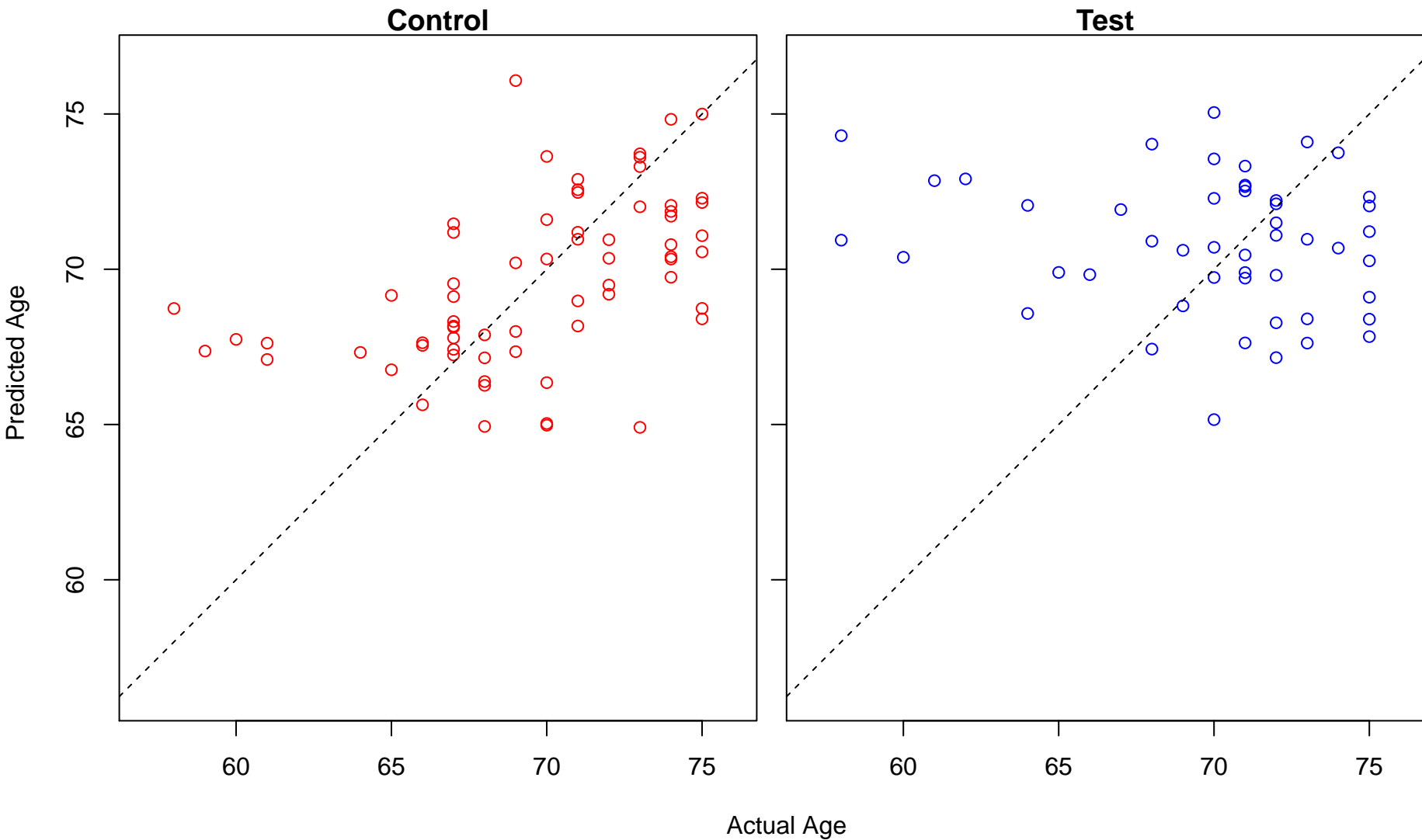
negative regulation of synaptic transmission (Score: 0.828606)



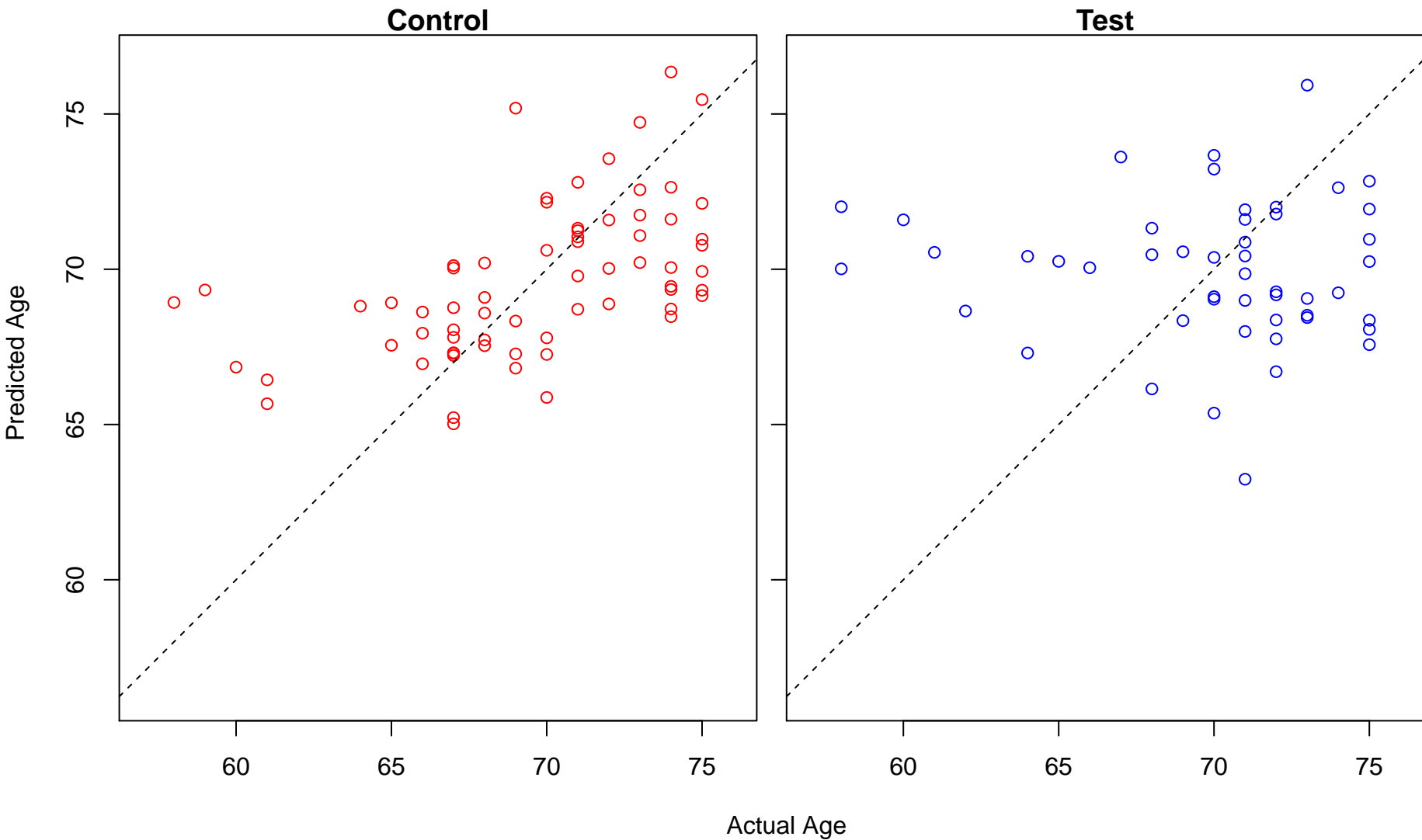
negative regulation of protein localization to plasma membrane (Score: 0.828546)



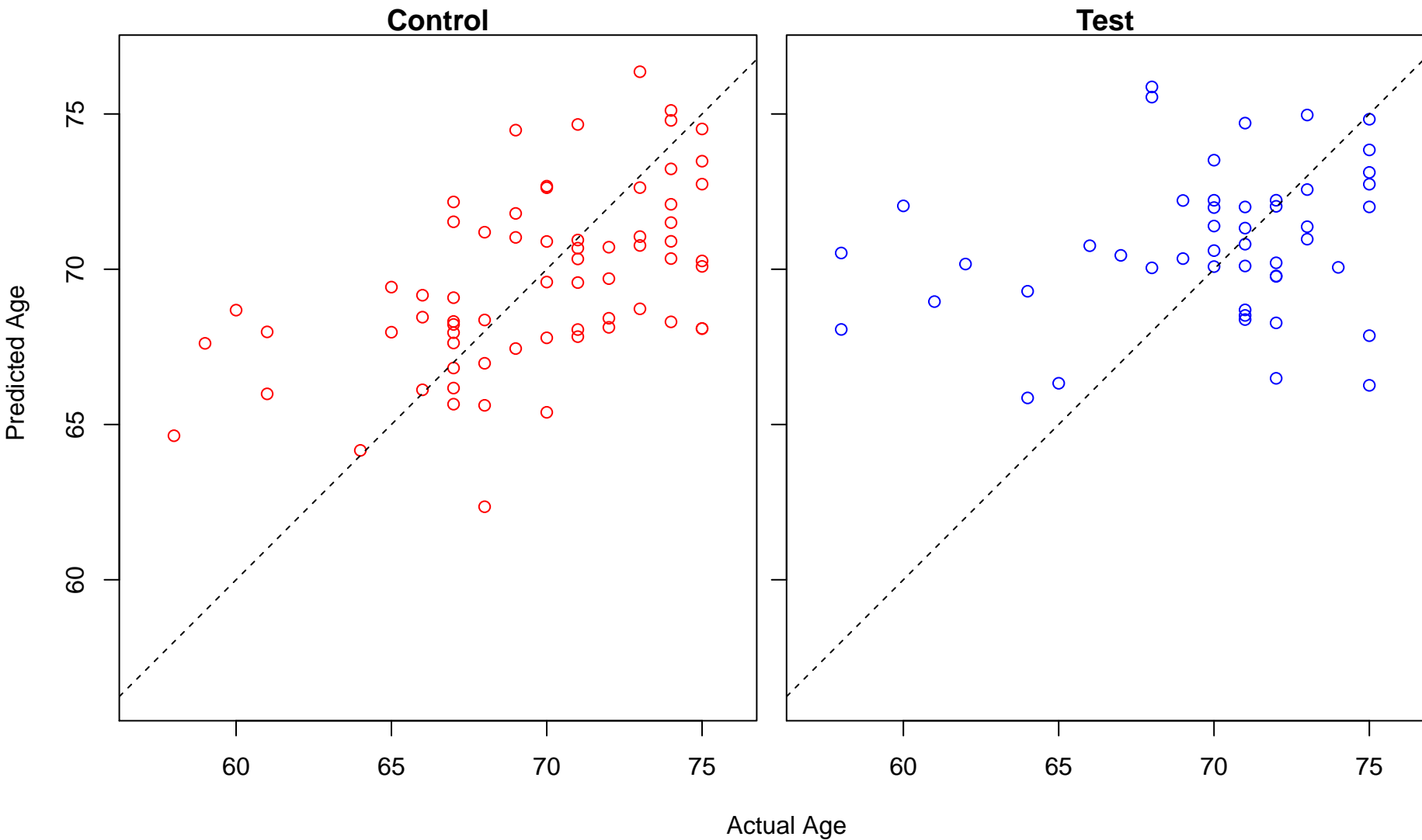
negative regulation of protein localization to cell periphery (Score: 0.828546)



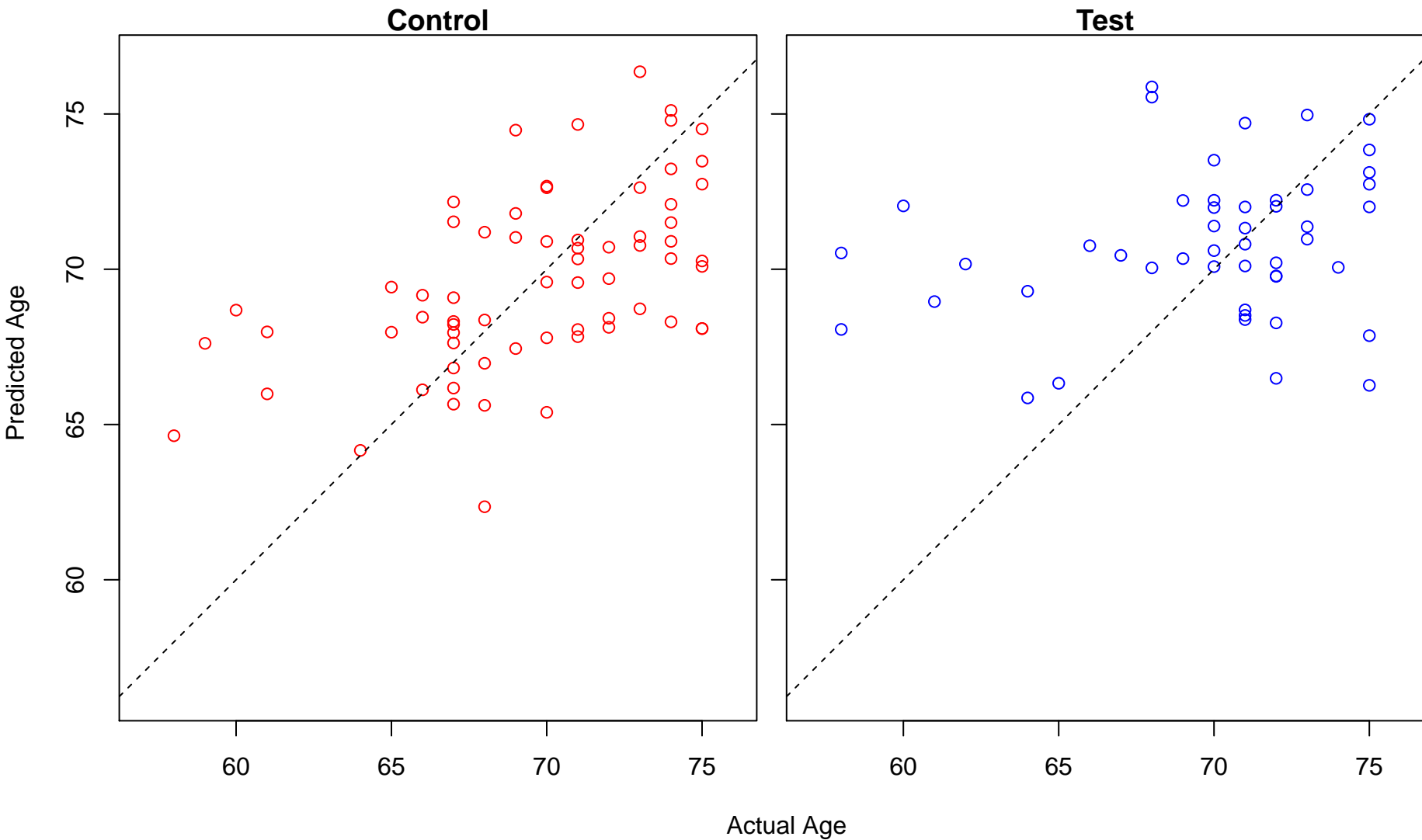
limbic system development (Score: 0.828466)



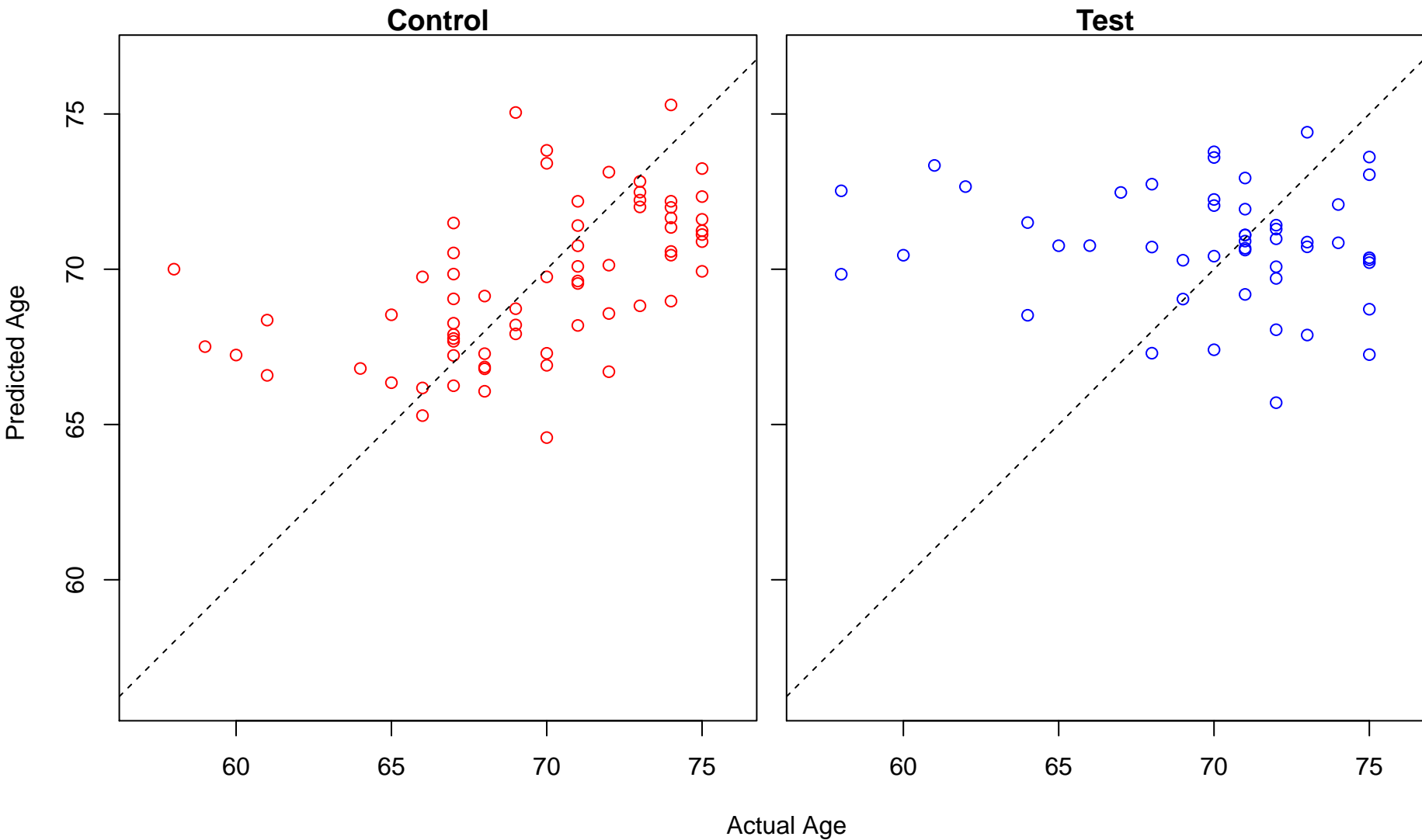
intracellular sterol transport (Score: 0.828445)



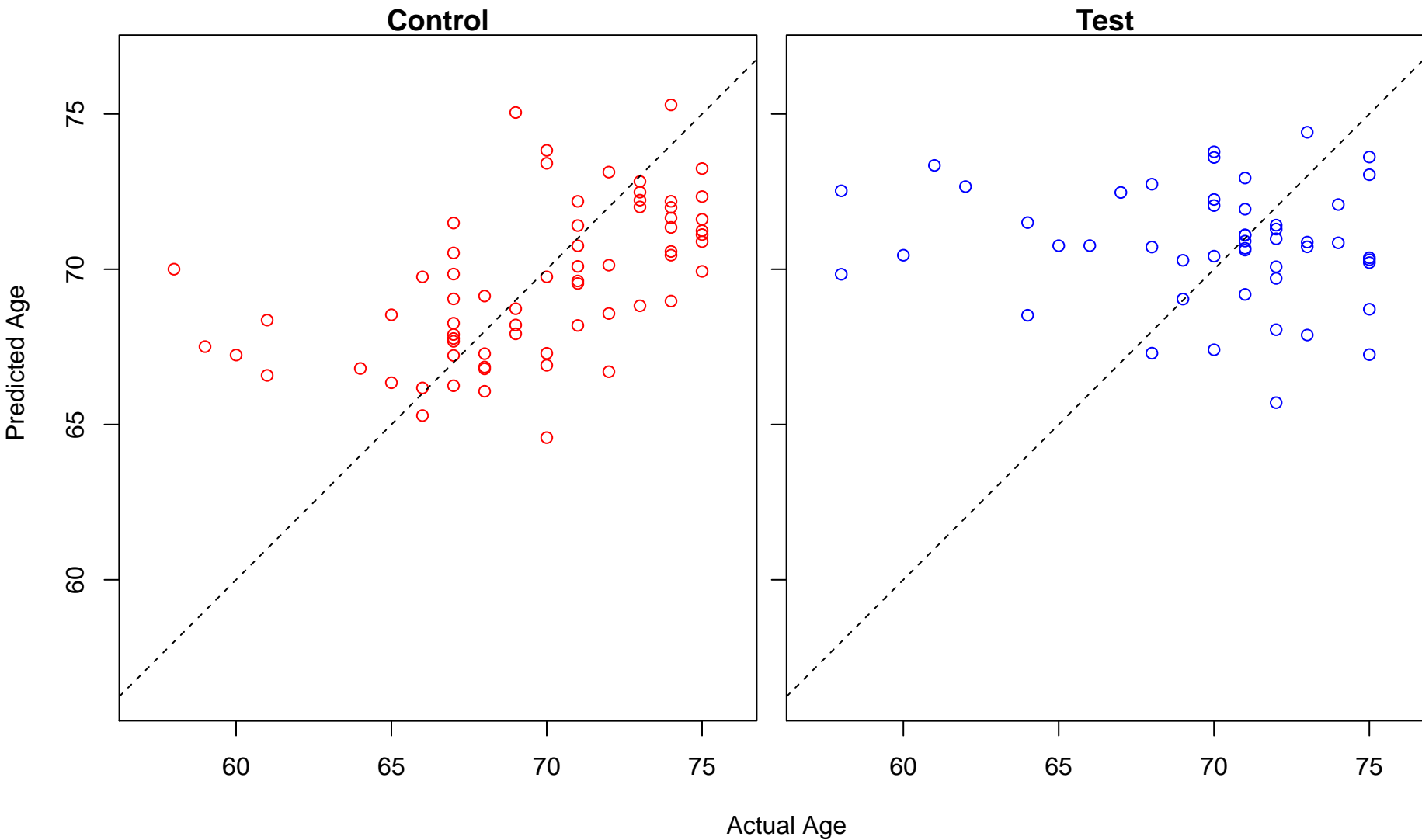
intracellular cholesterol transport (Score: 0.828445)



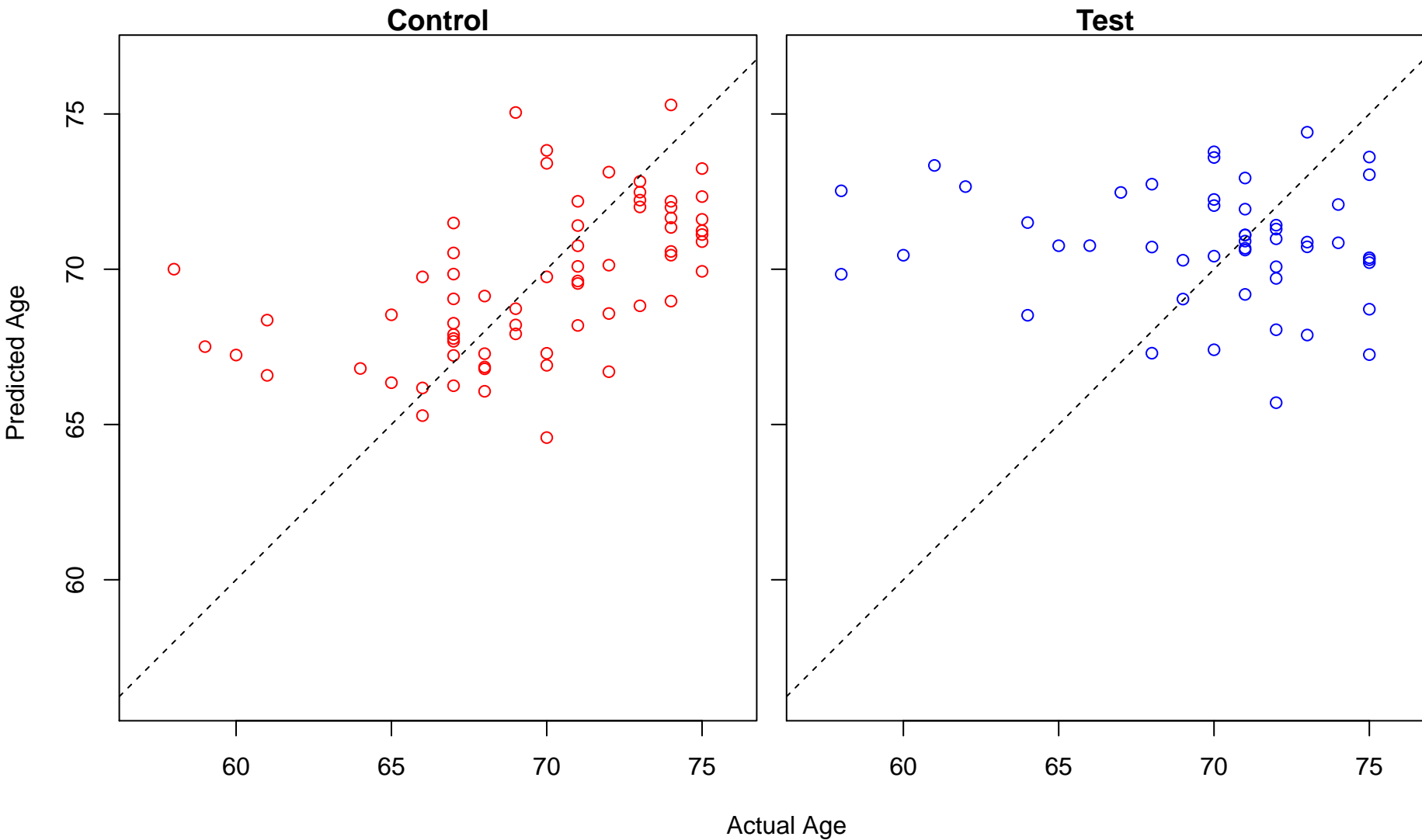
entry into host cell (Score: 0.827921)



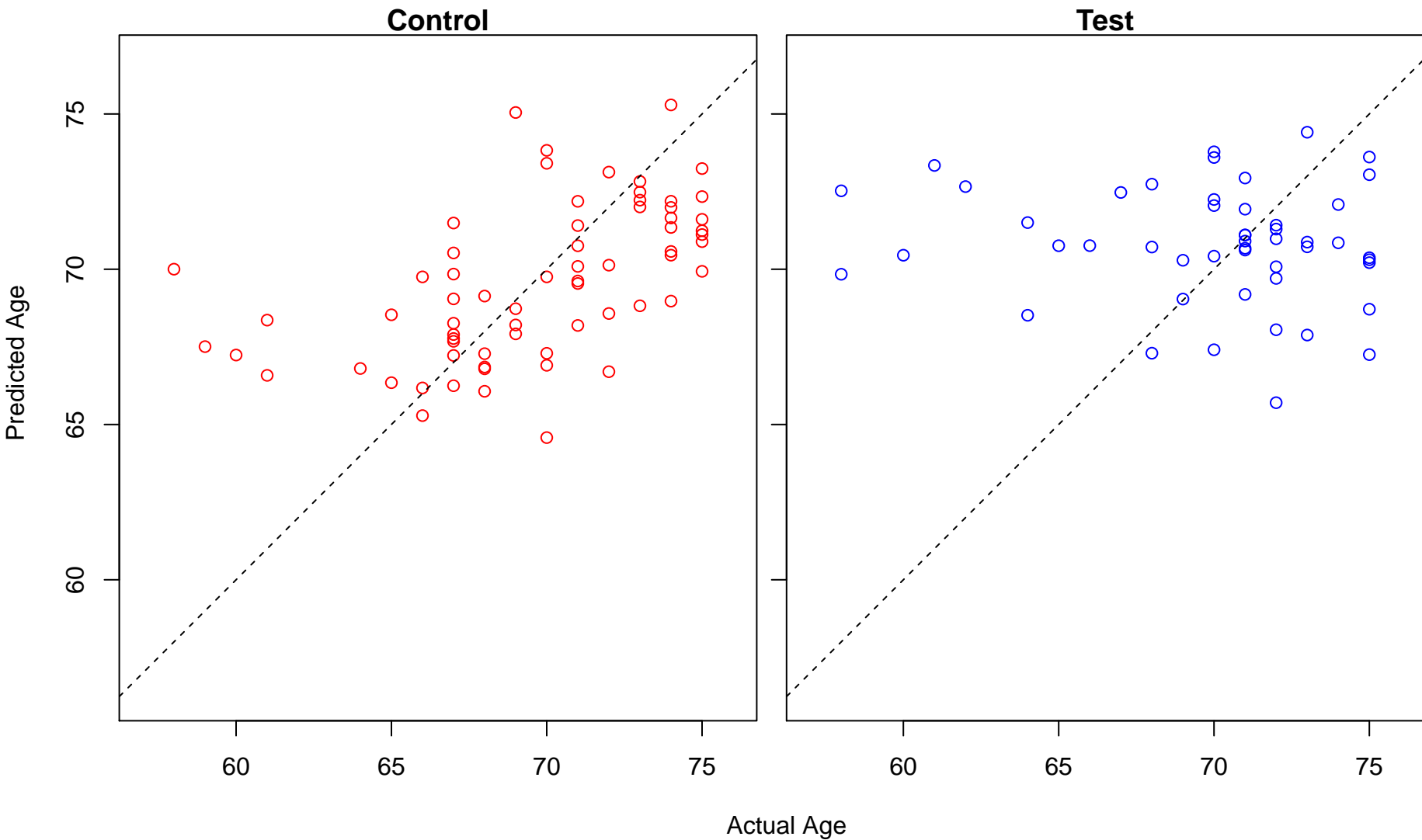
entry into host (Score: 0.827921)



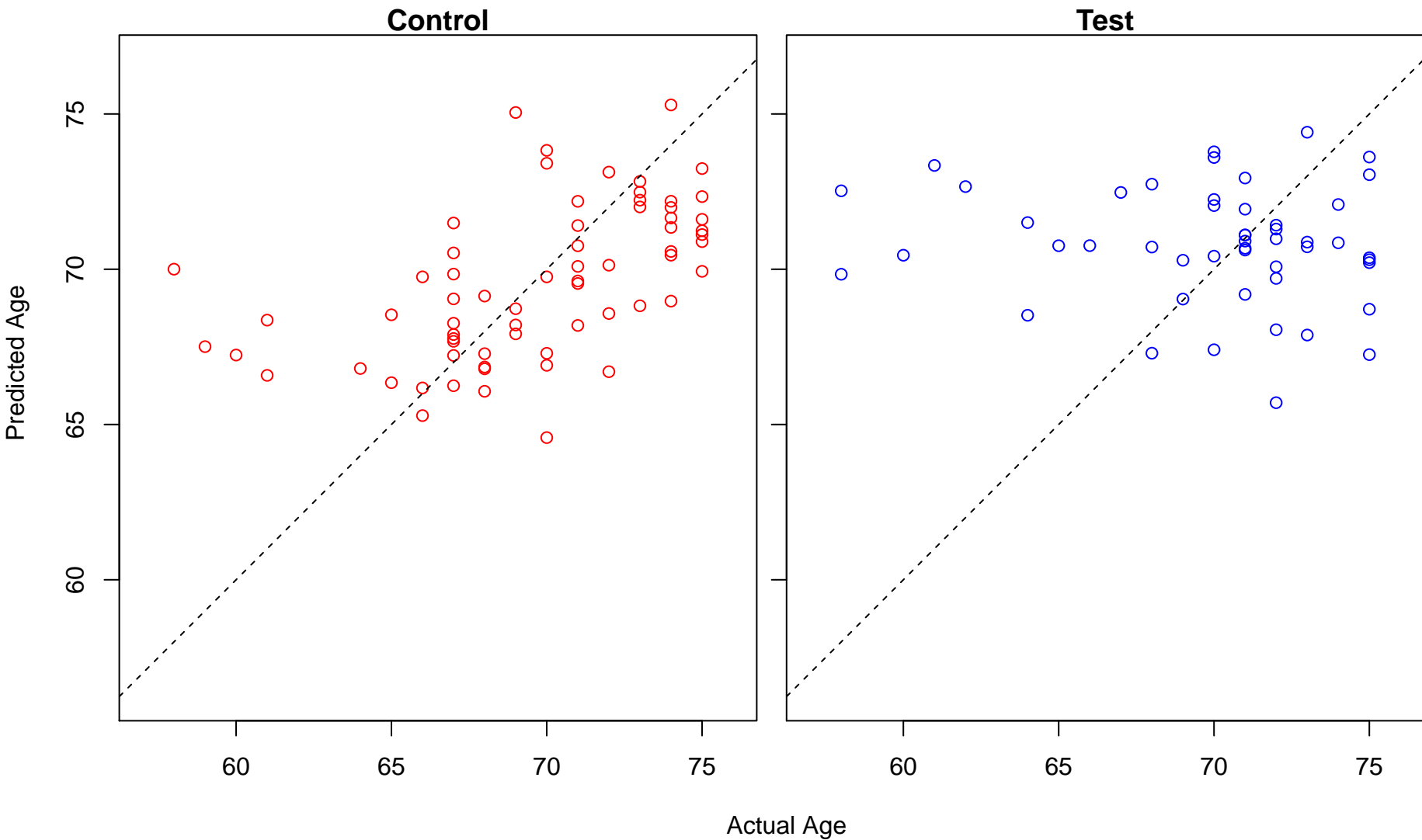
entry into cell of other organism involved in symbiotic interaction (Score: 0.827921)



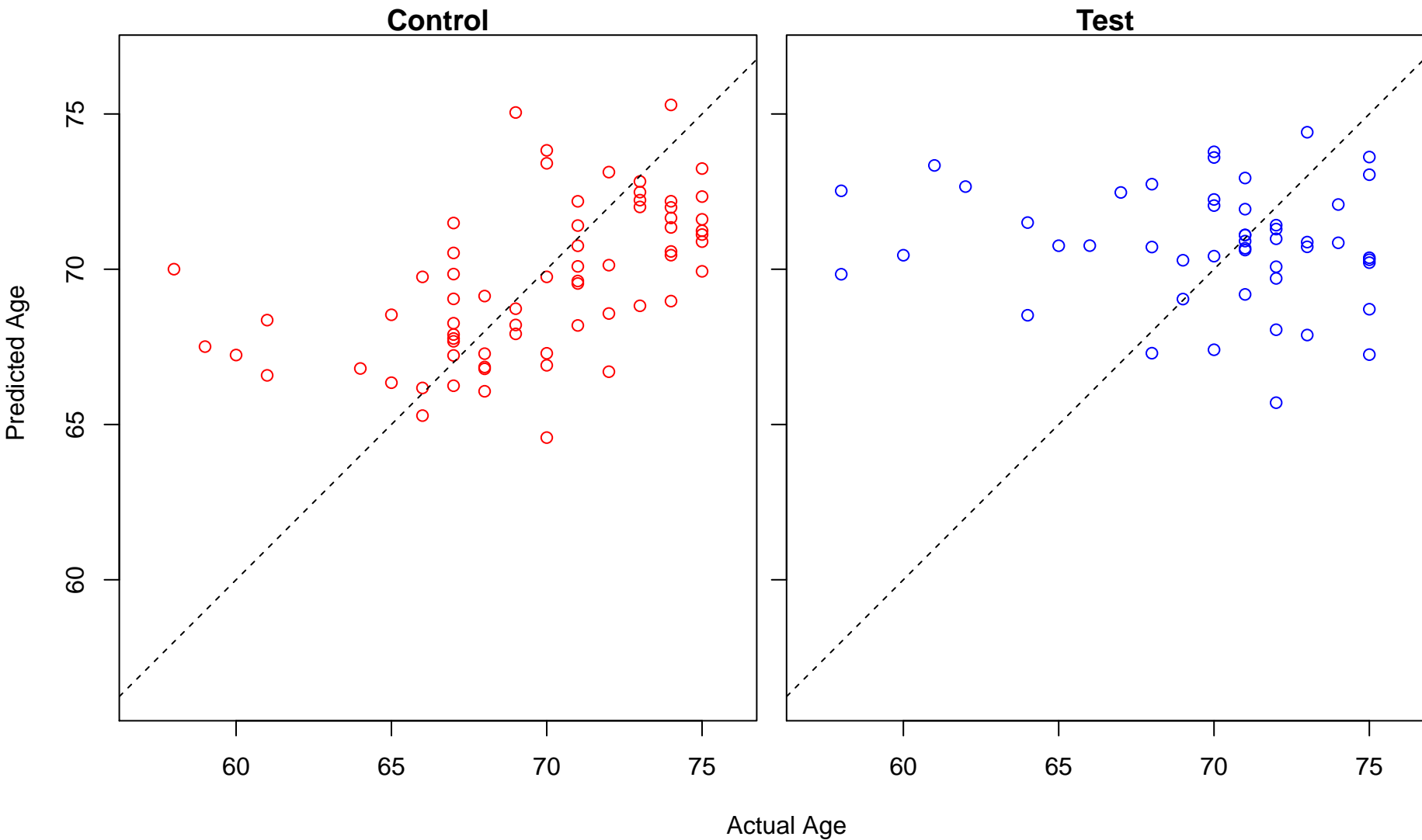
entry into other organism involved in symbiotic interaction (Score: 0.827921)



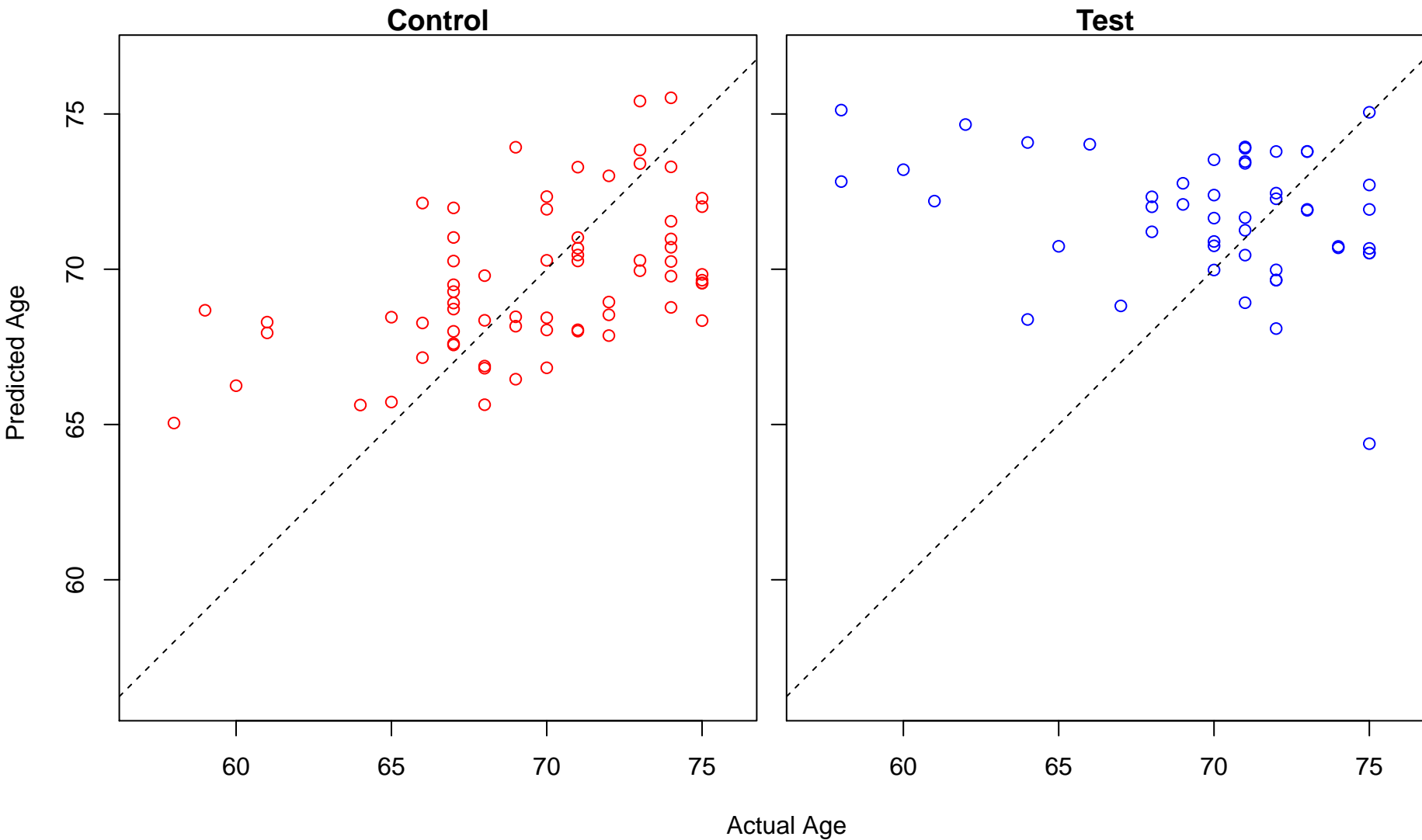
movement in host environment (Score: 0.827921)



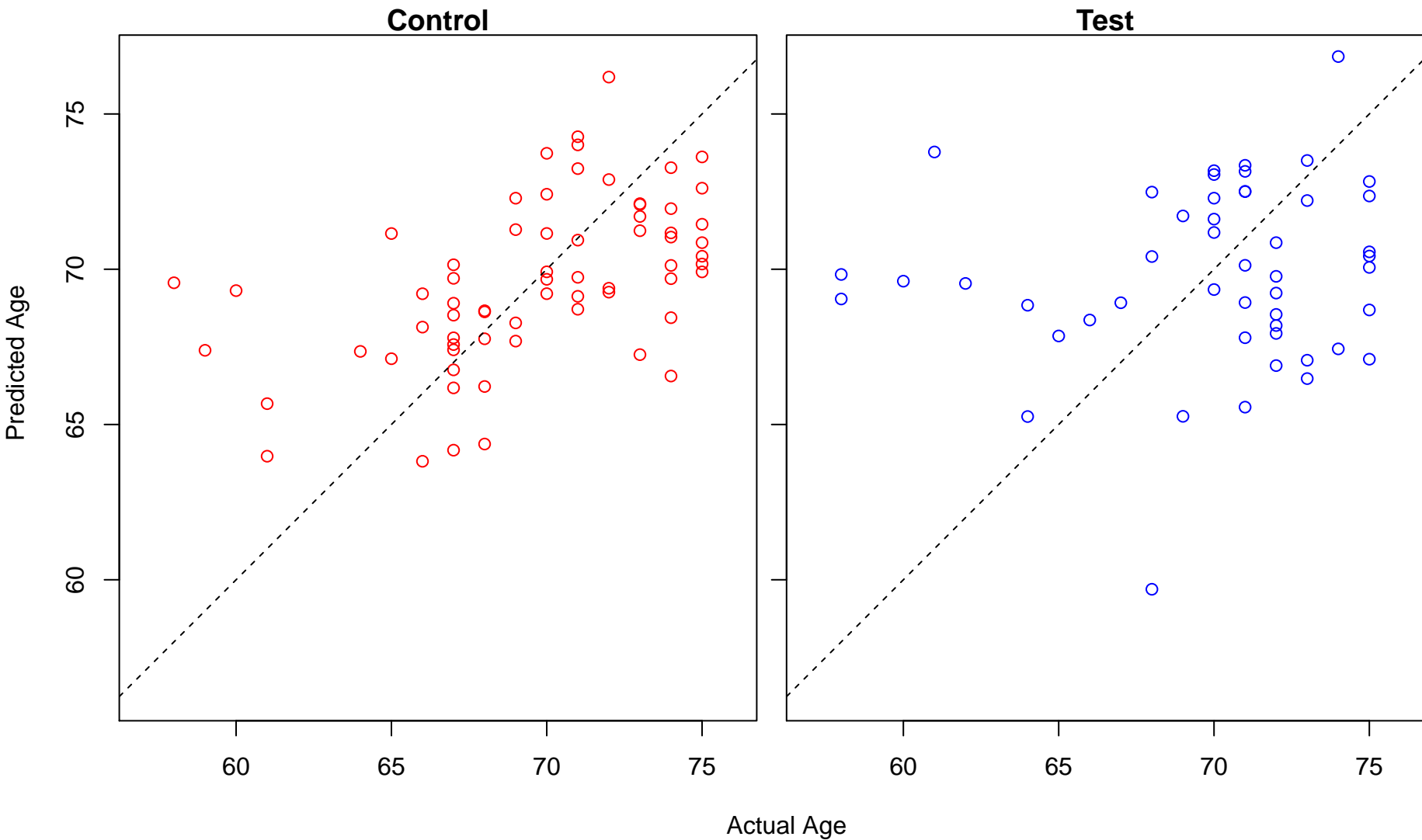
movement in environment of other organism involved in symbiotic interaction (Score: 0.827921)



negative regulation of osteoblast differentiation (Score: 0.827719)

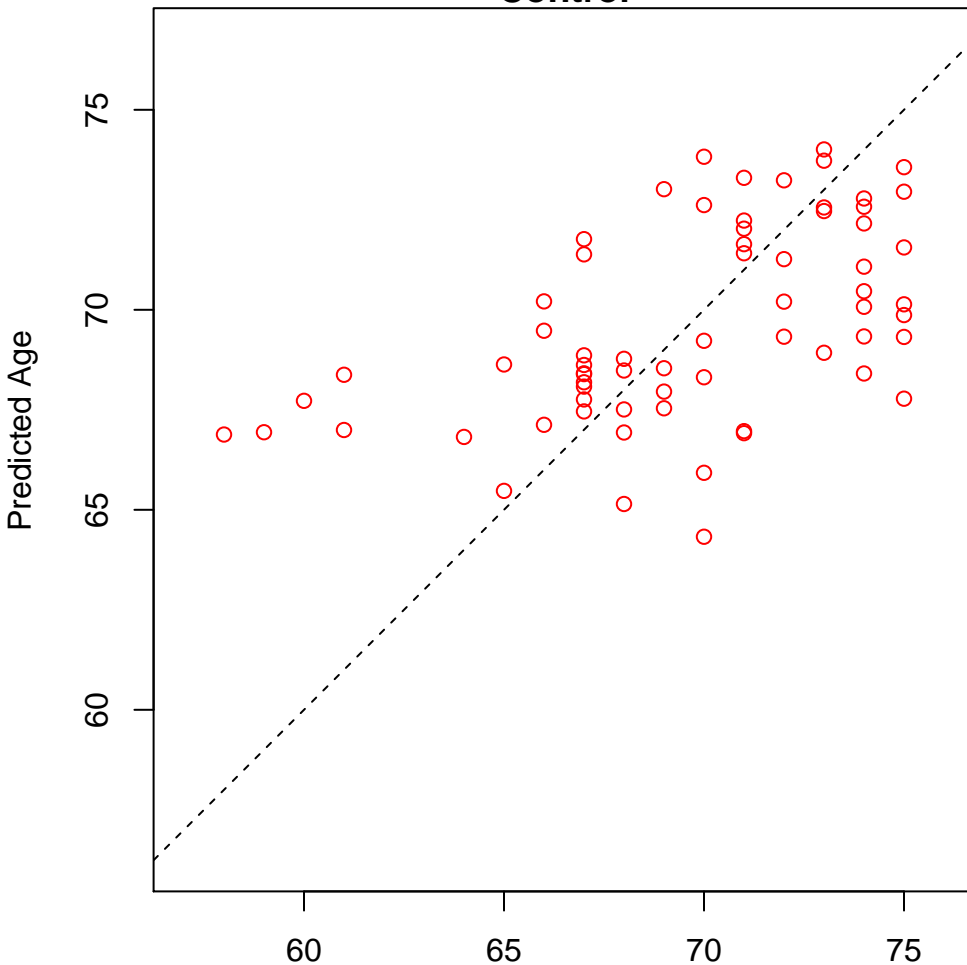


negative regulation of cytokine secretion involved in immune response (Score: 0.827685)

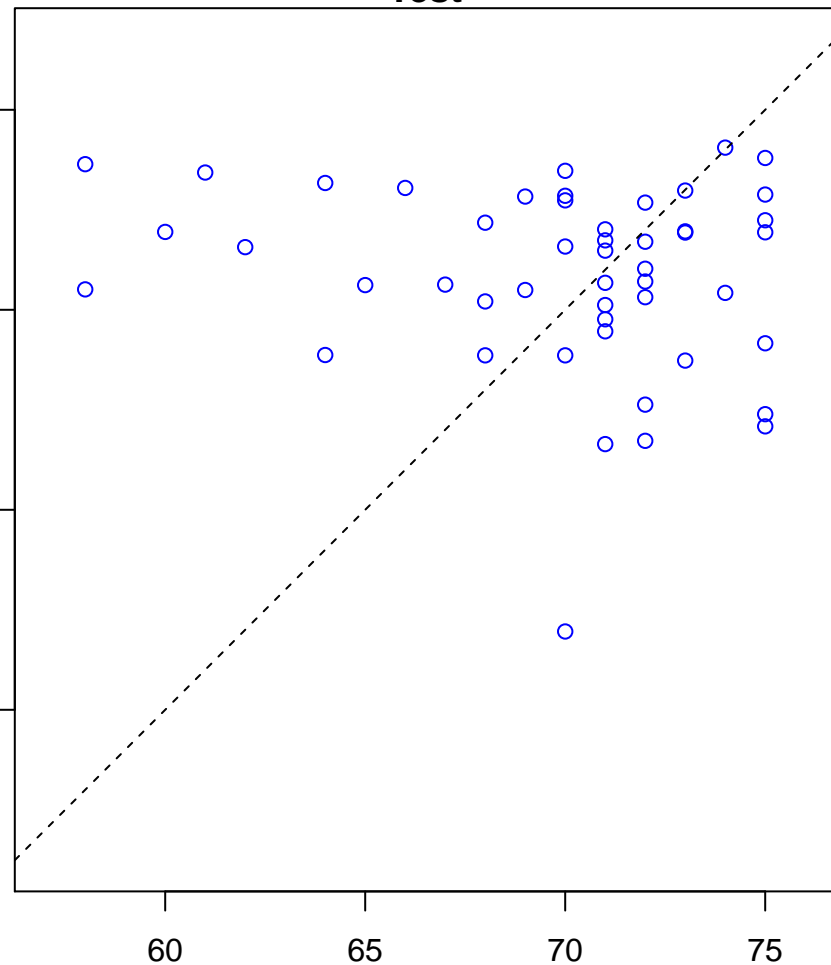


mammary gland epithelium development (Score: 0.827139)

Control

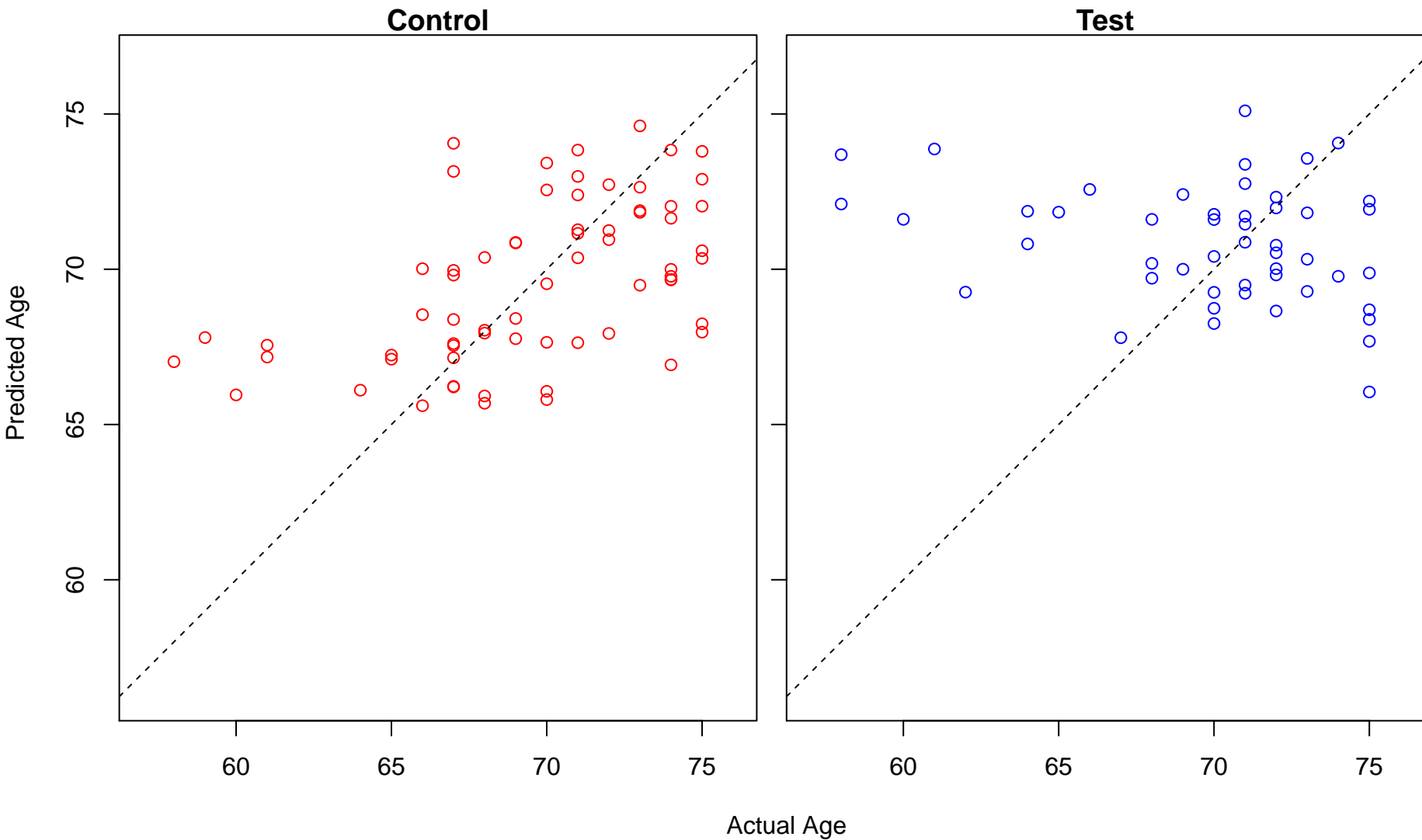


Test

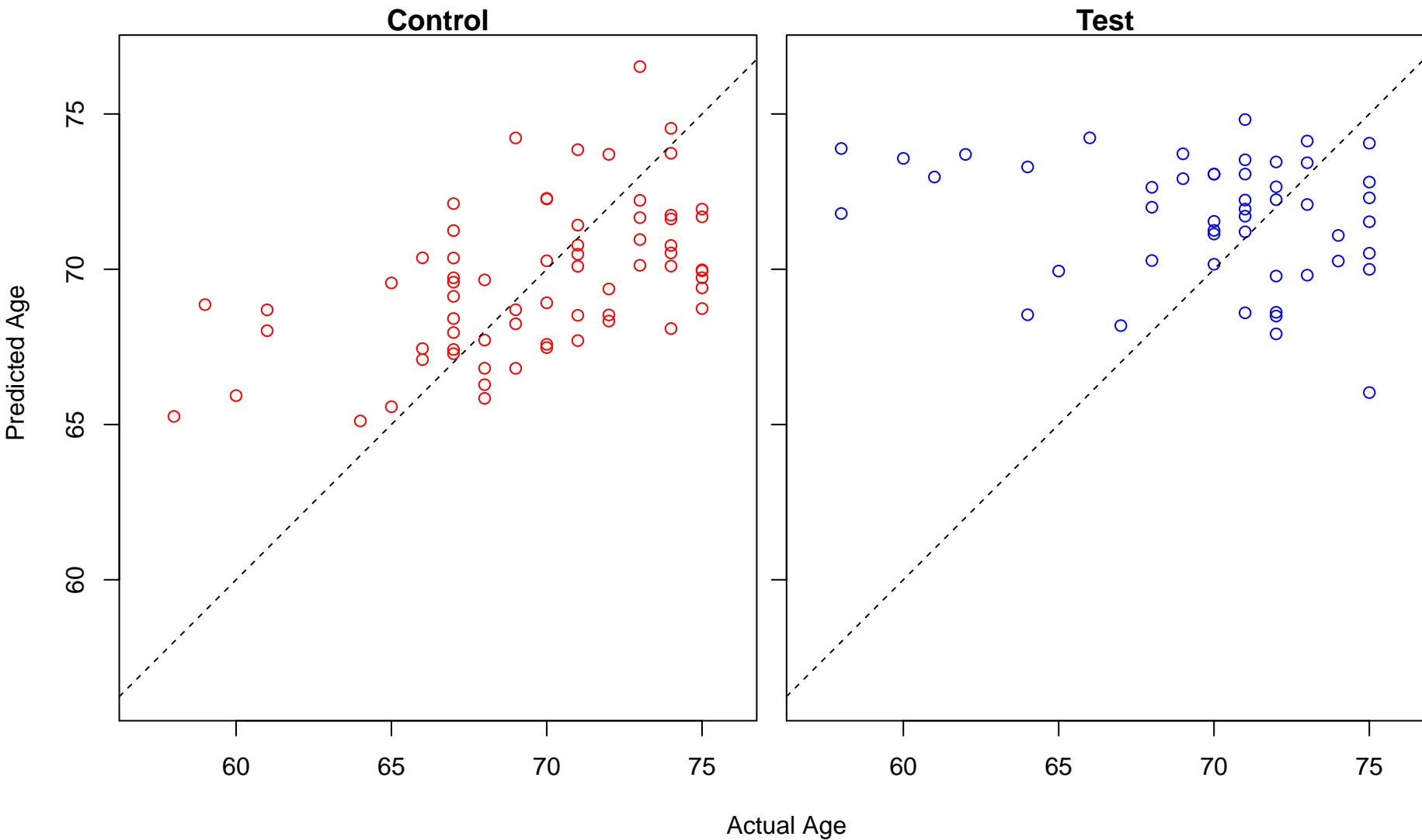


Actual Age

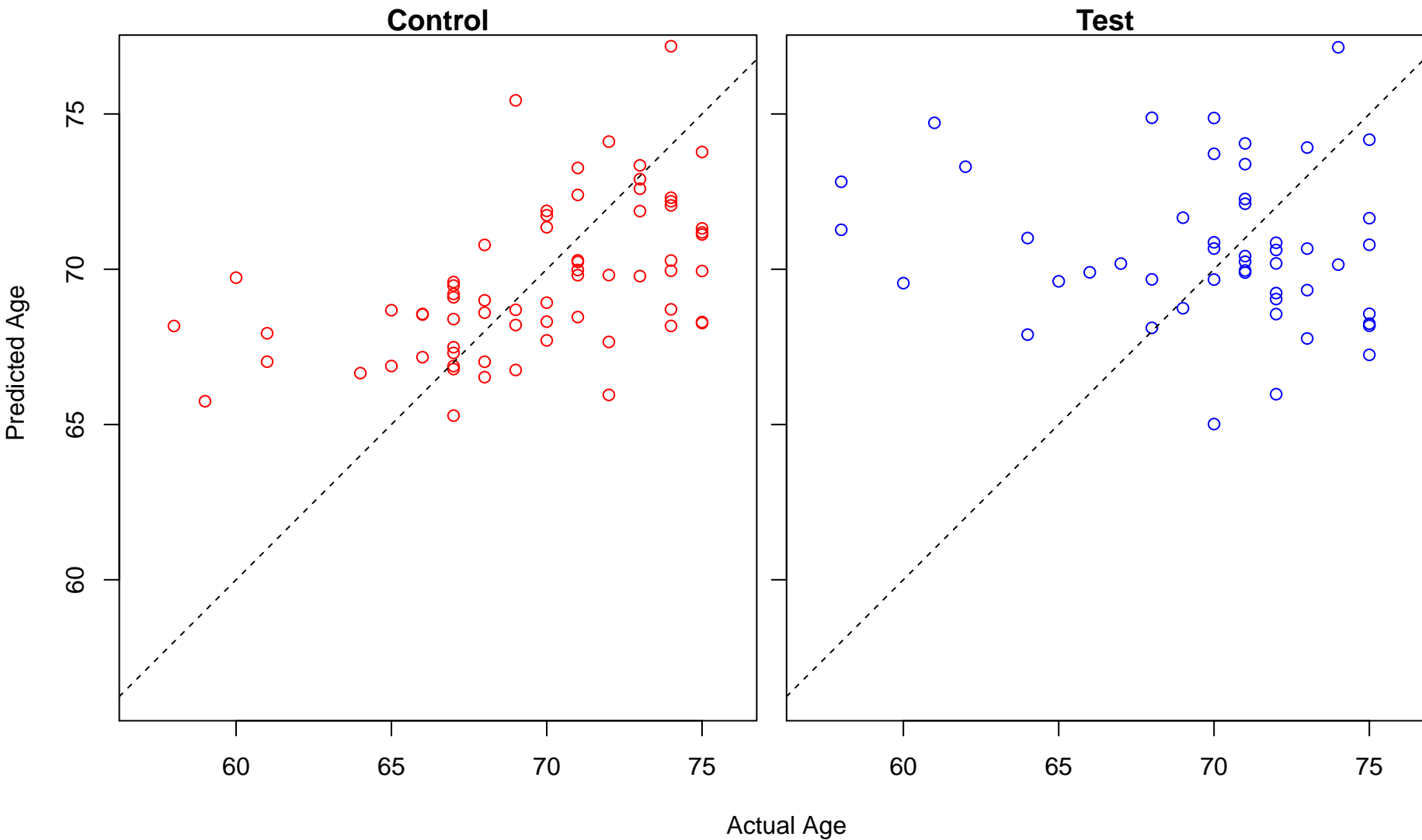
collagen catabolic process (Score: 0.826593)



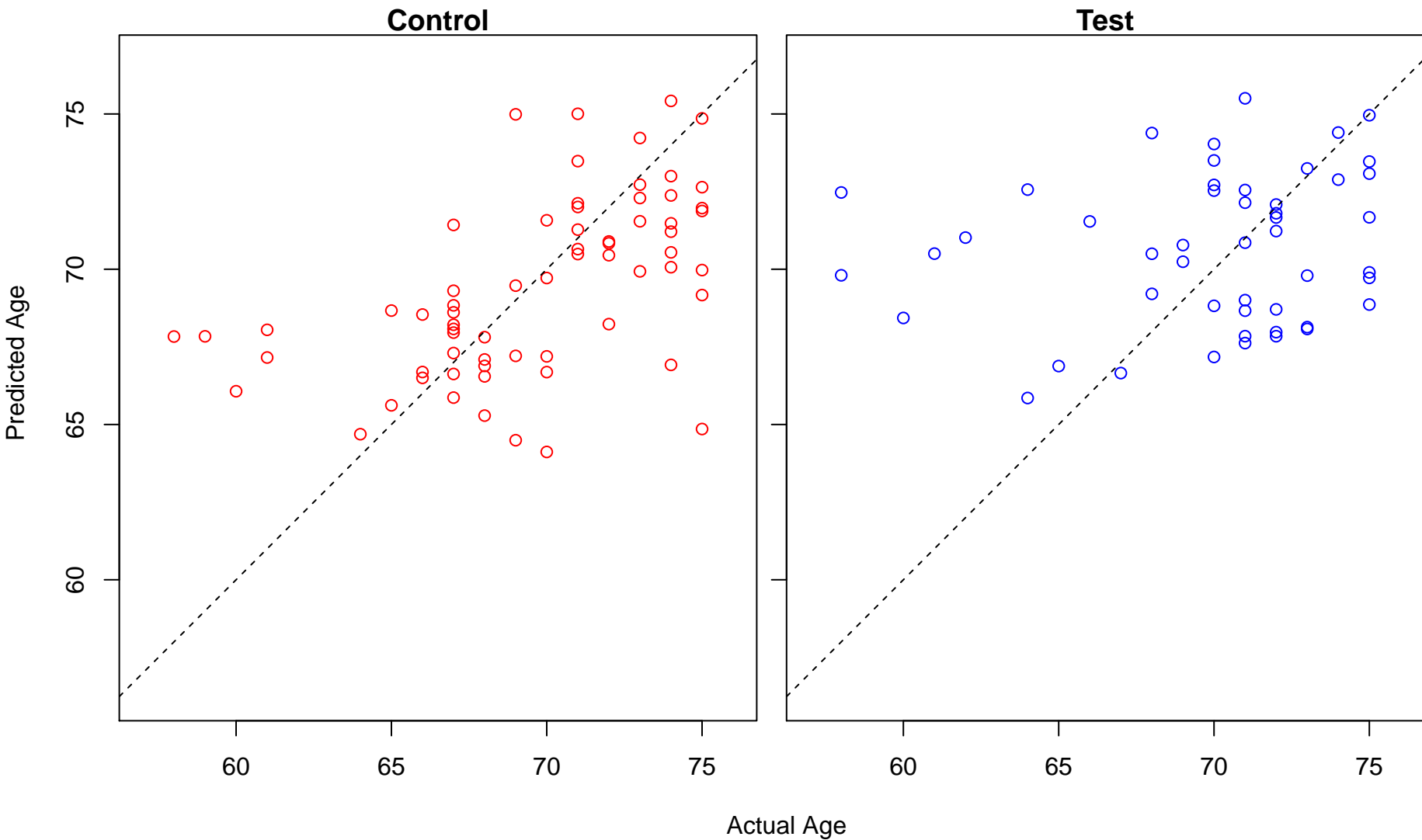
cardiac atrium morphogenesis (Score: 0.826321)



bicellular tight junction assembly (Score: 0.825853)

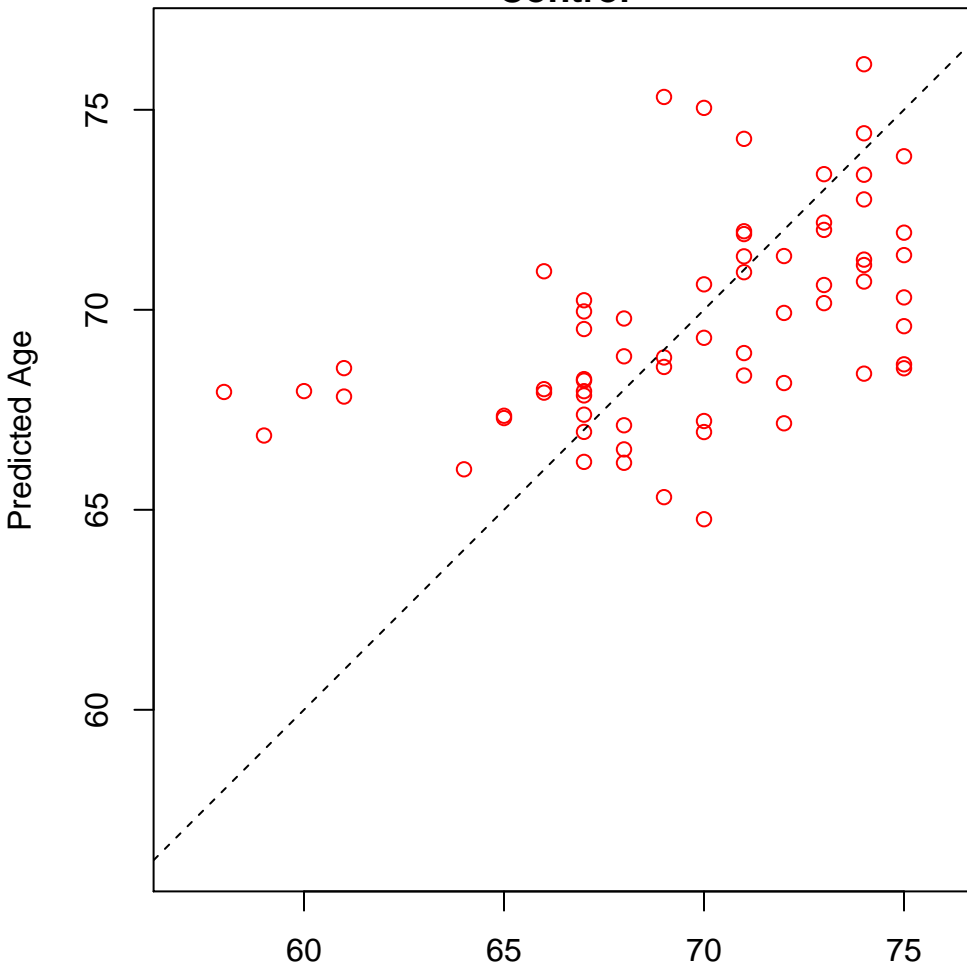


nephron epithelium development (Score: 0.825738)

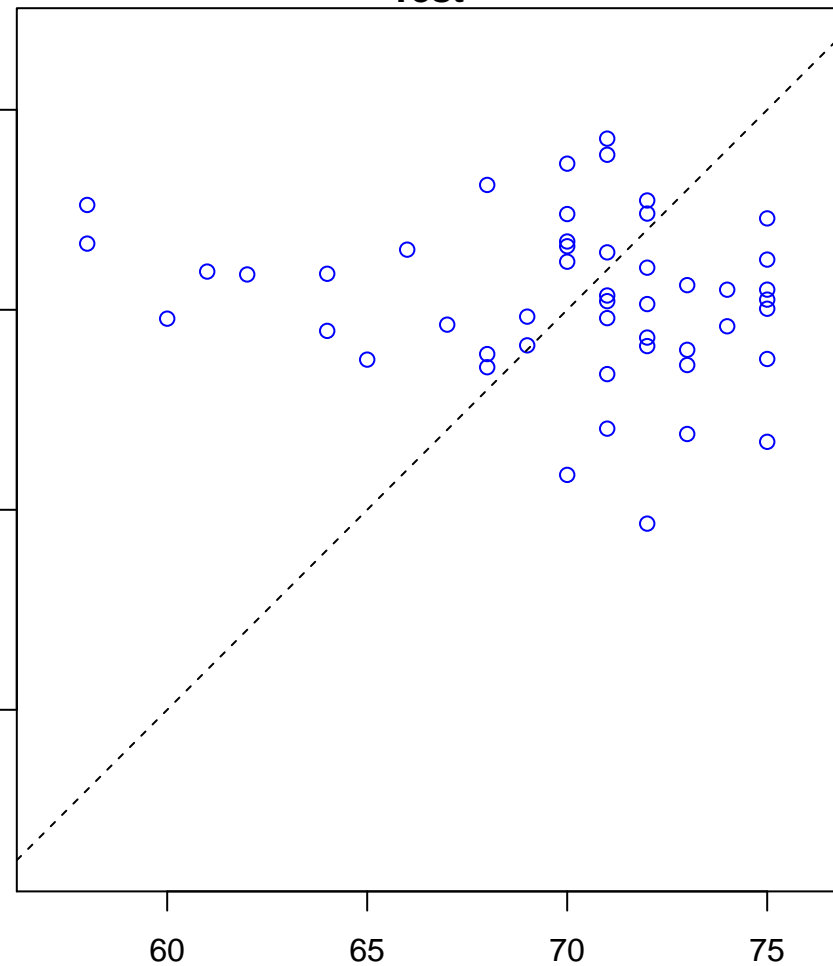


regulation of metanephros development (Score: 0.825465)

Control

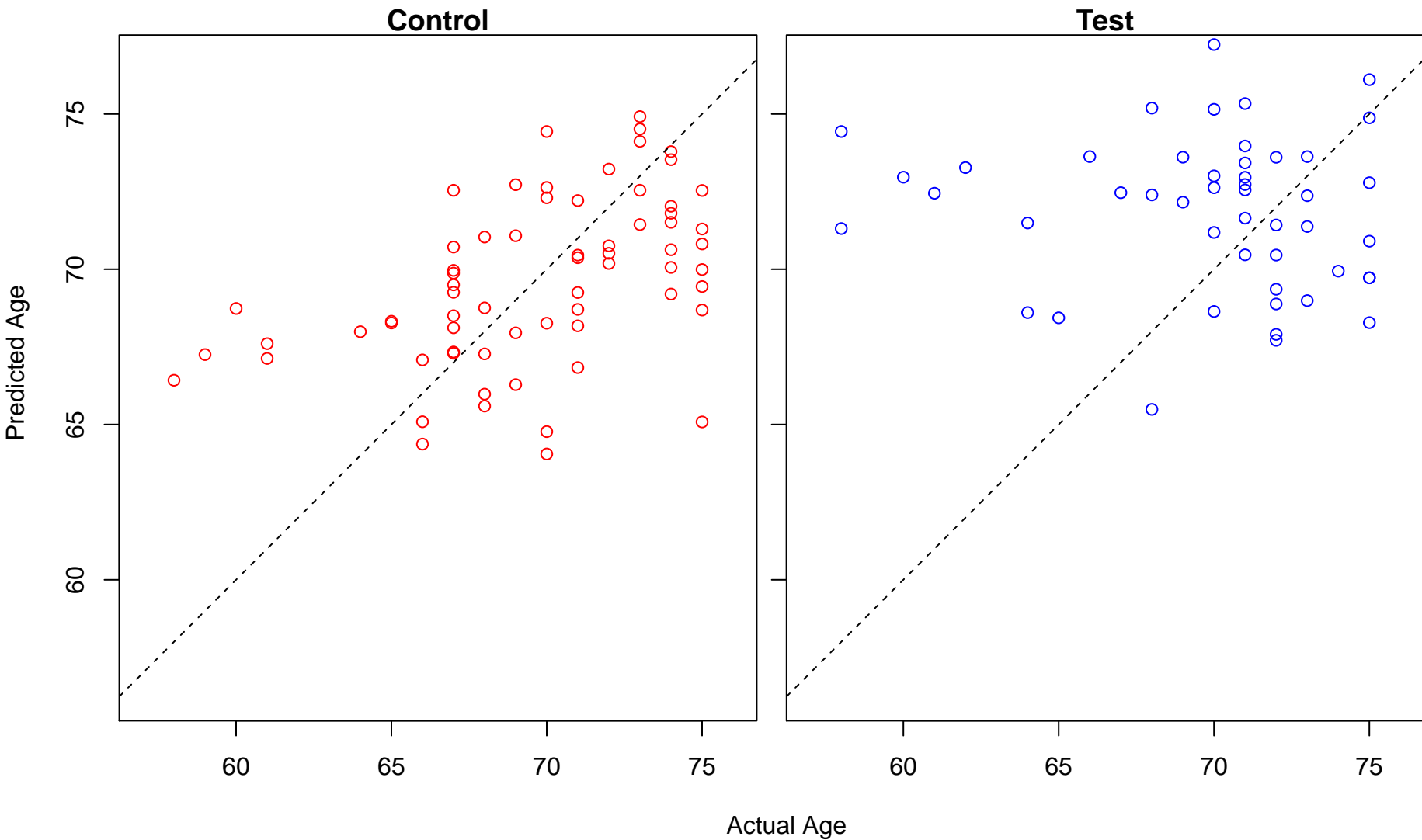


Test

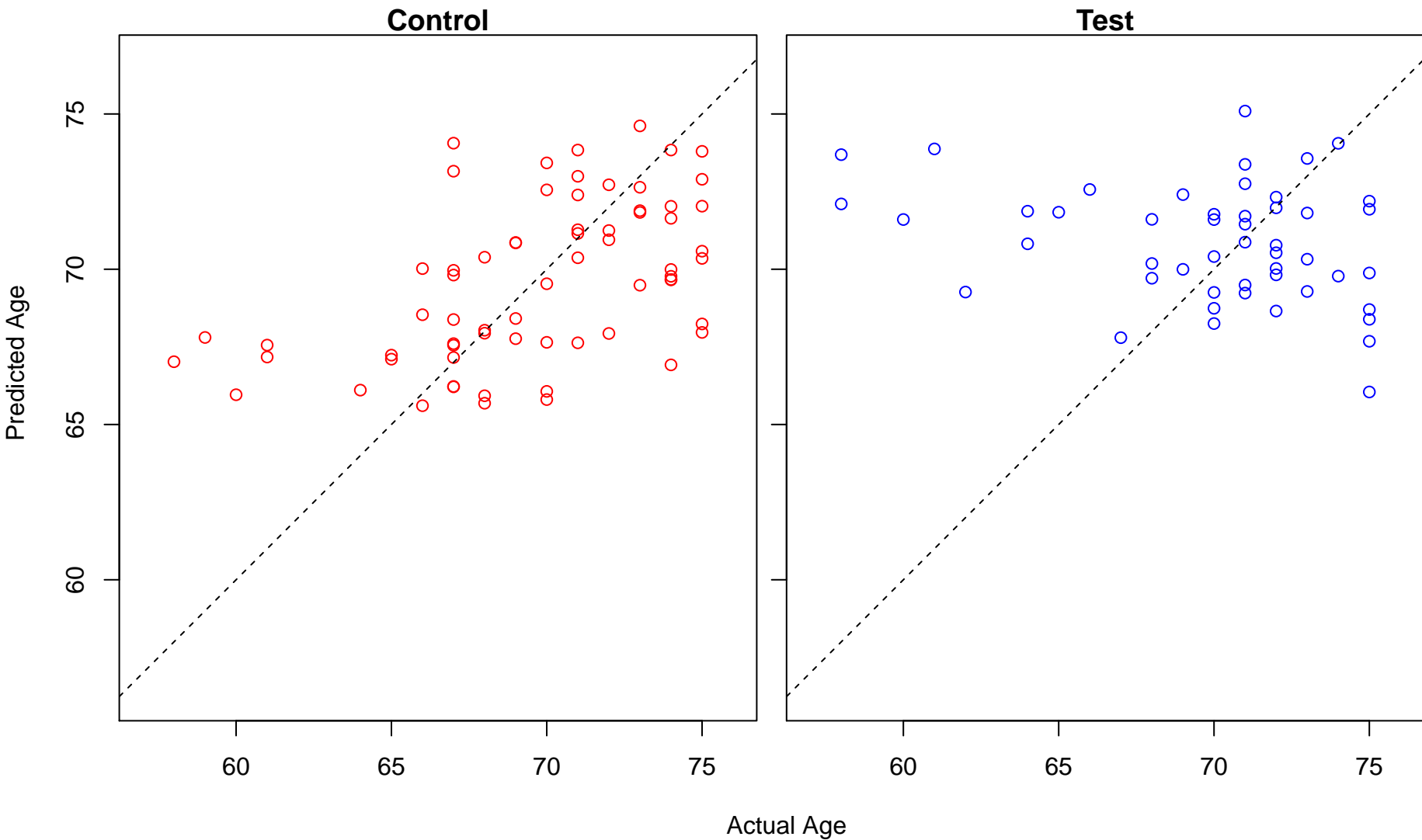


Actual Age

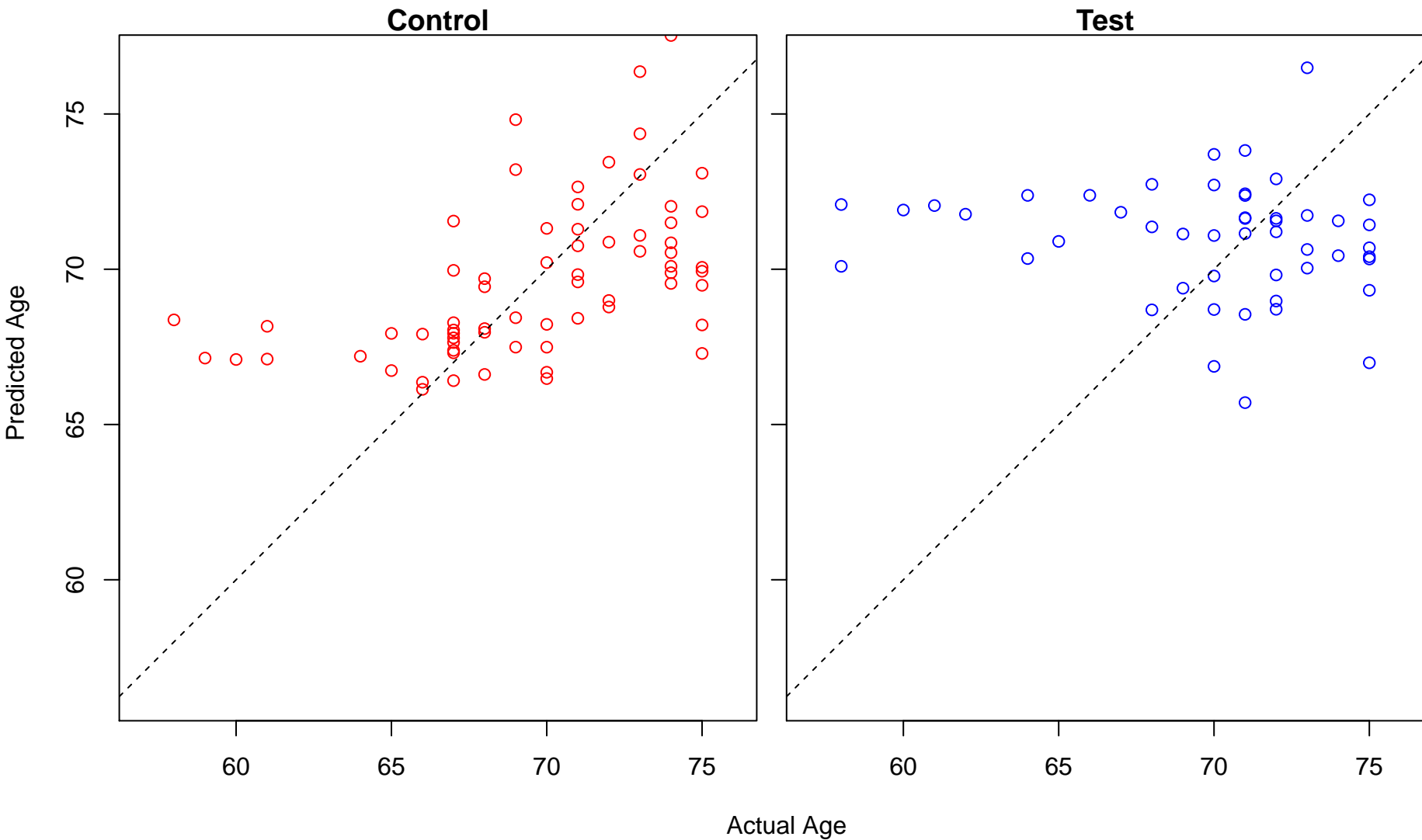
response to hydroperoxide (Score: 0.825326)



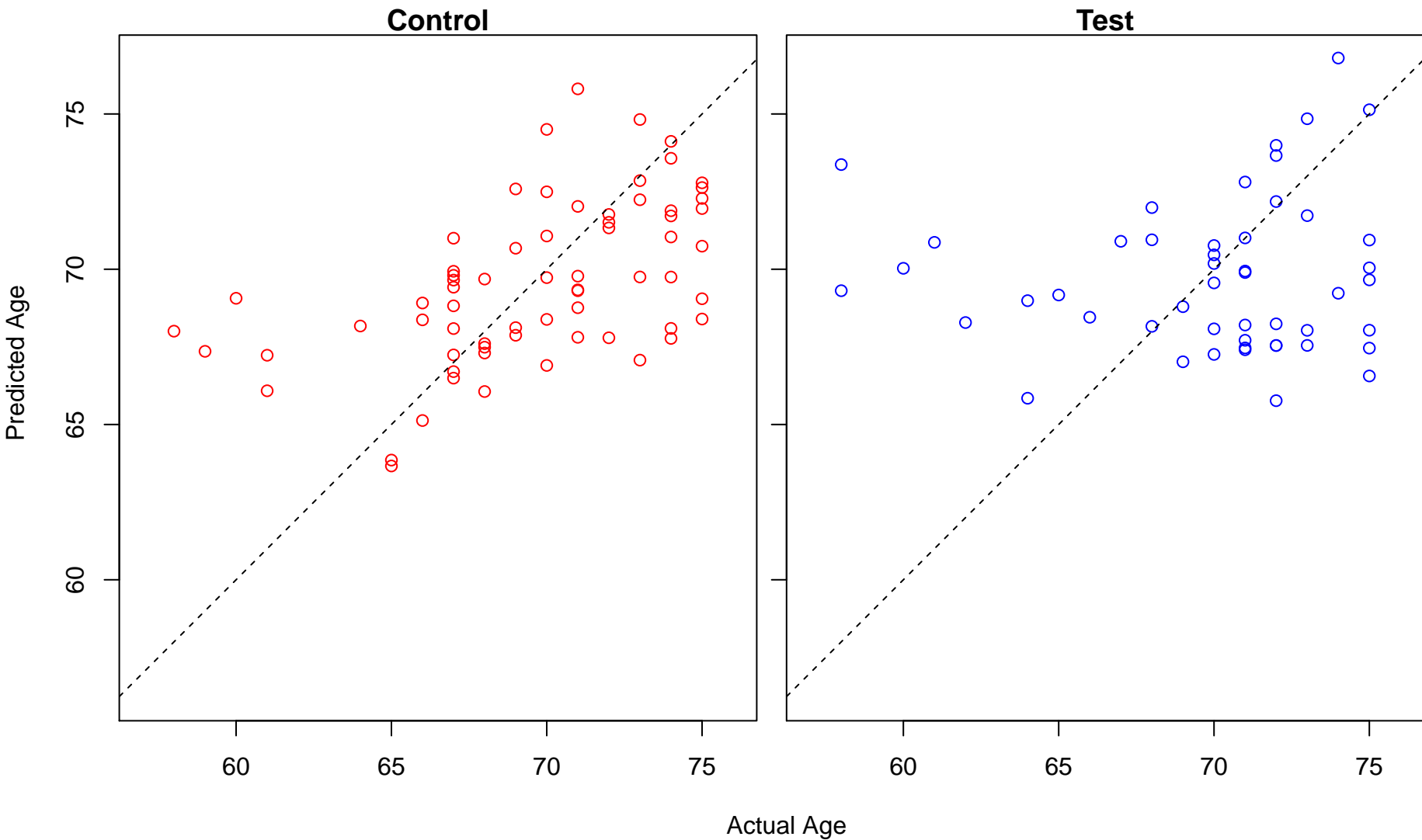
multicellular organismal catabolic process (Score: 0.825238)



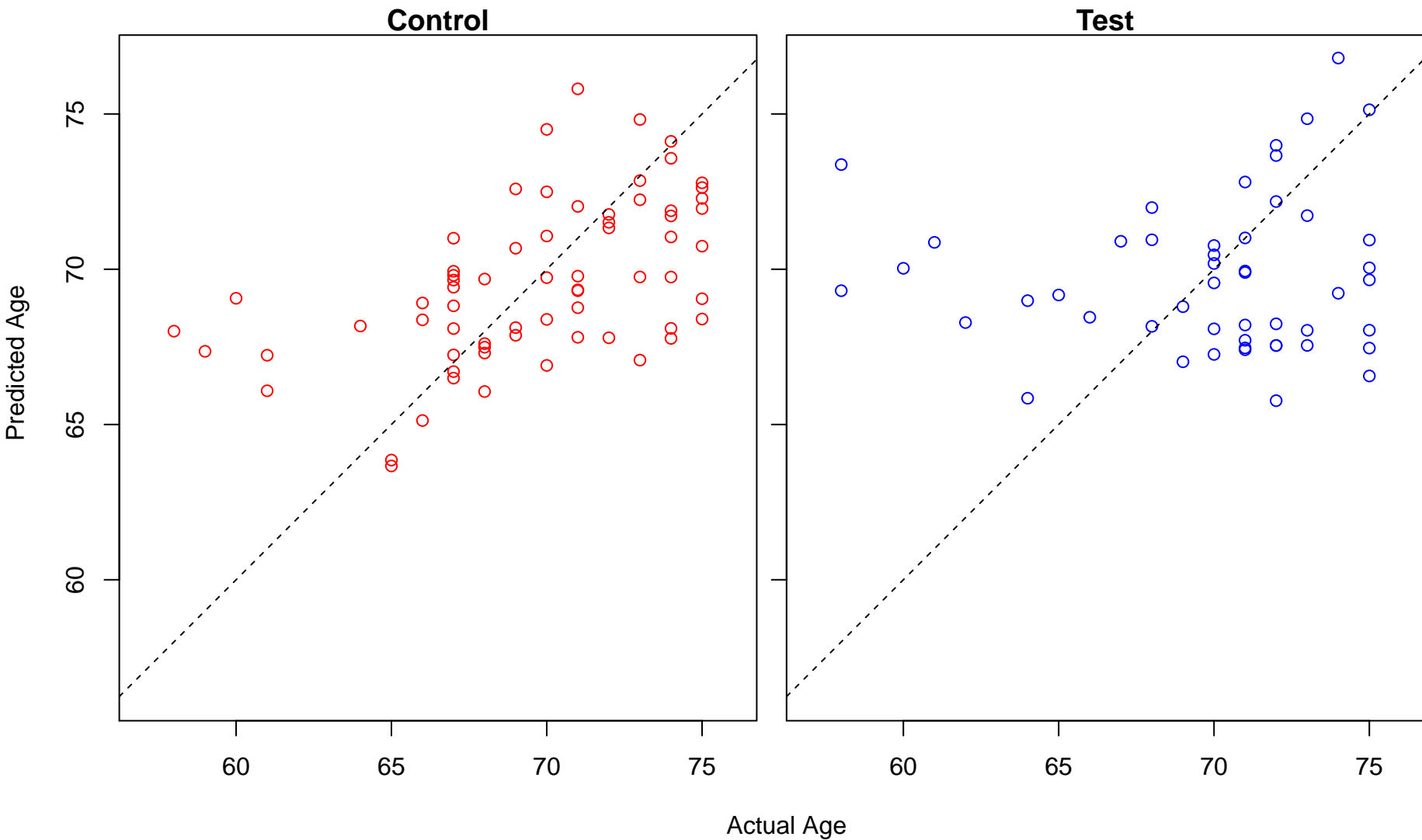
regulation of glycoprotein metabolic process (Score: 0.824925)



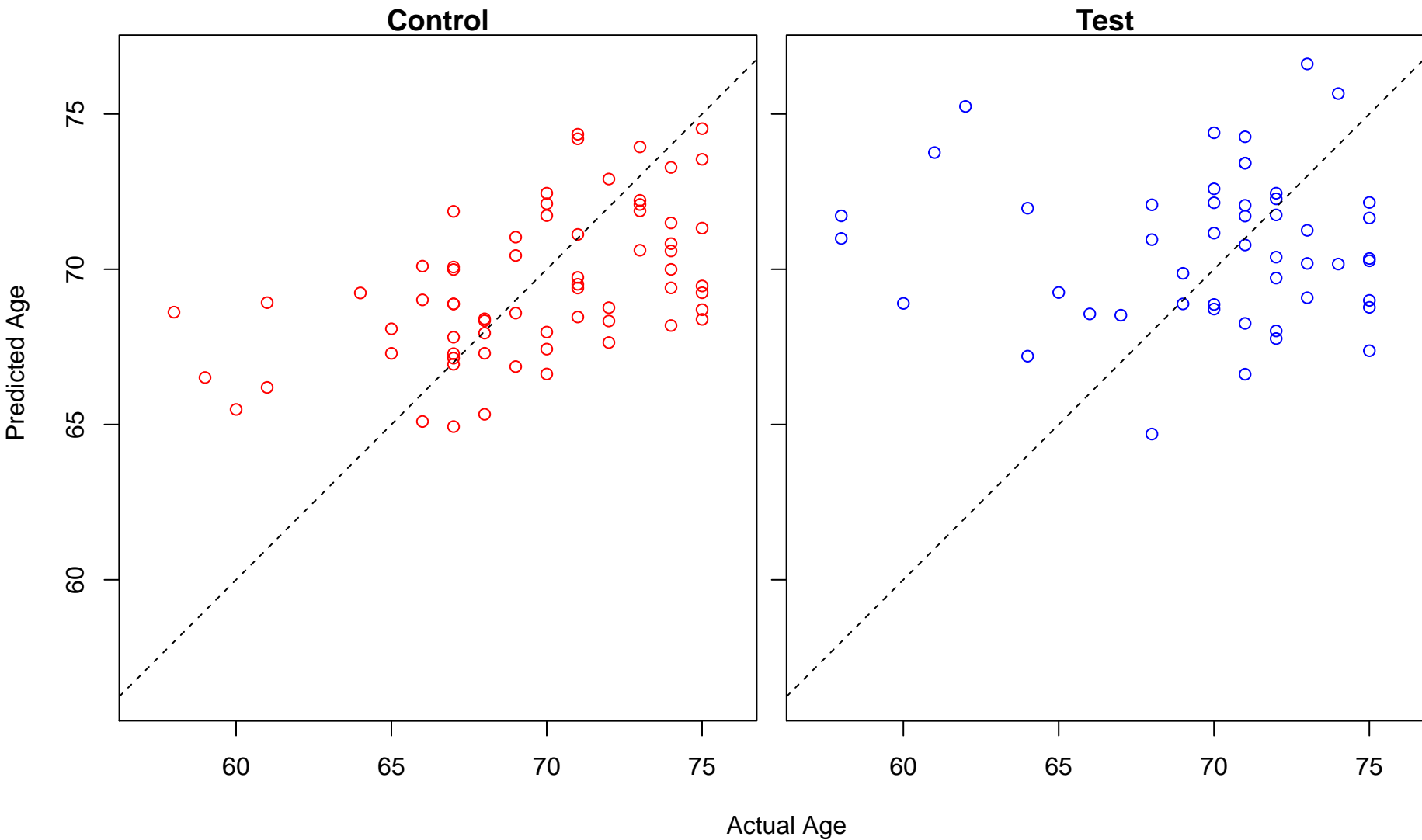
regulation of mitochondrial fusion (Score: 0.824825)



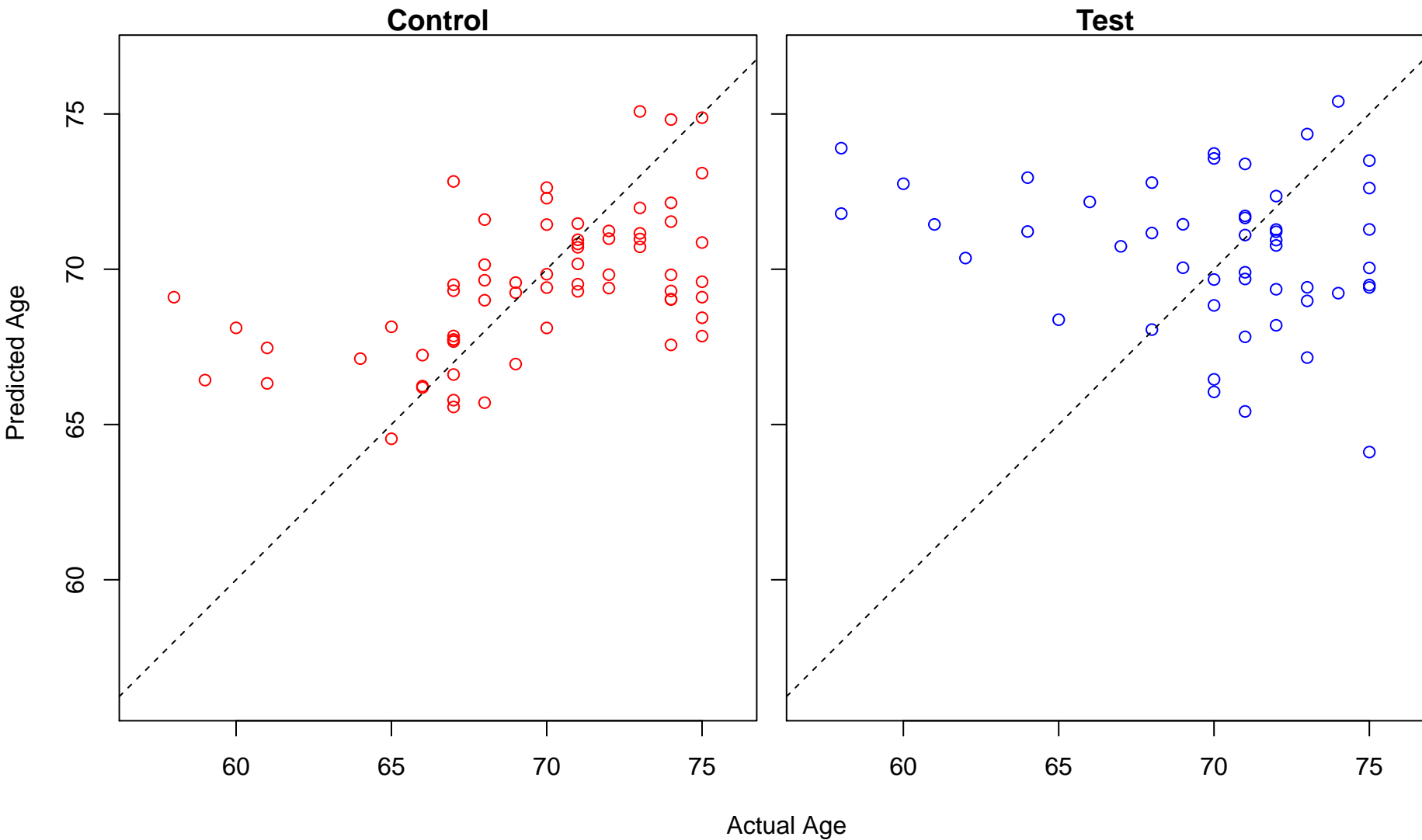
negative regulation of mitochondrial fusion (Score: 0.824825)



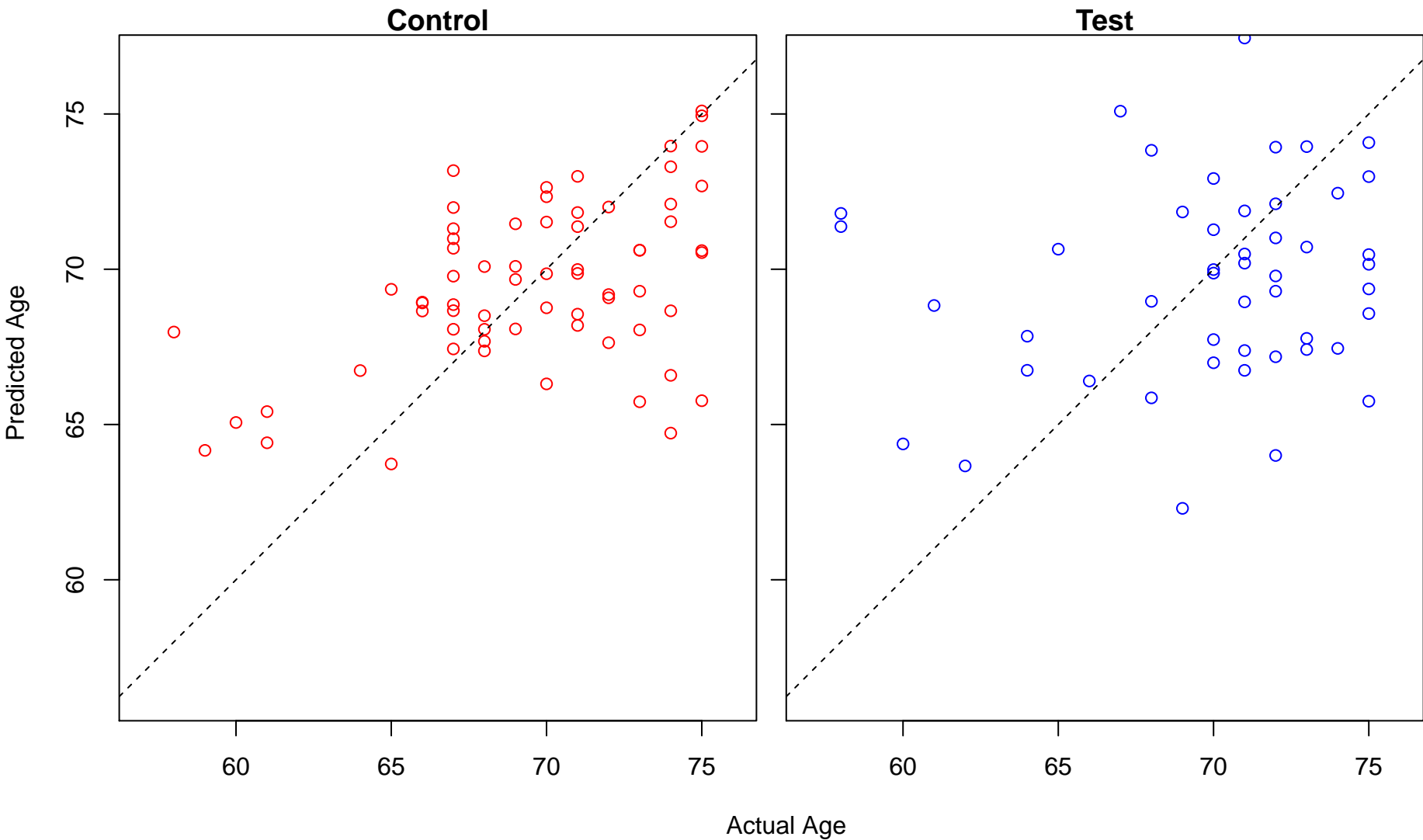
carnitine transmembrane transport (Score: 0.824661)



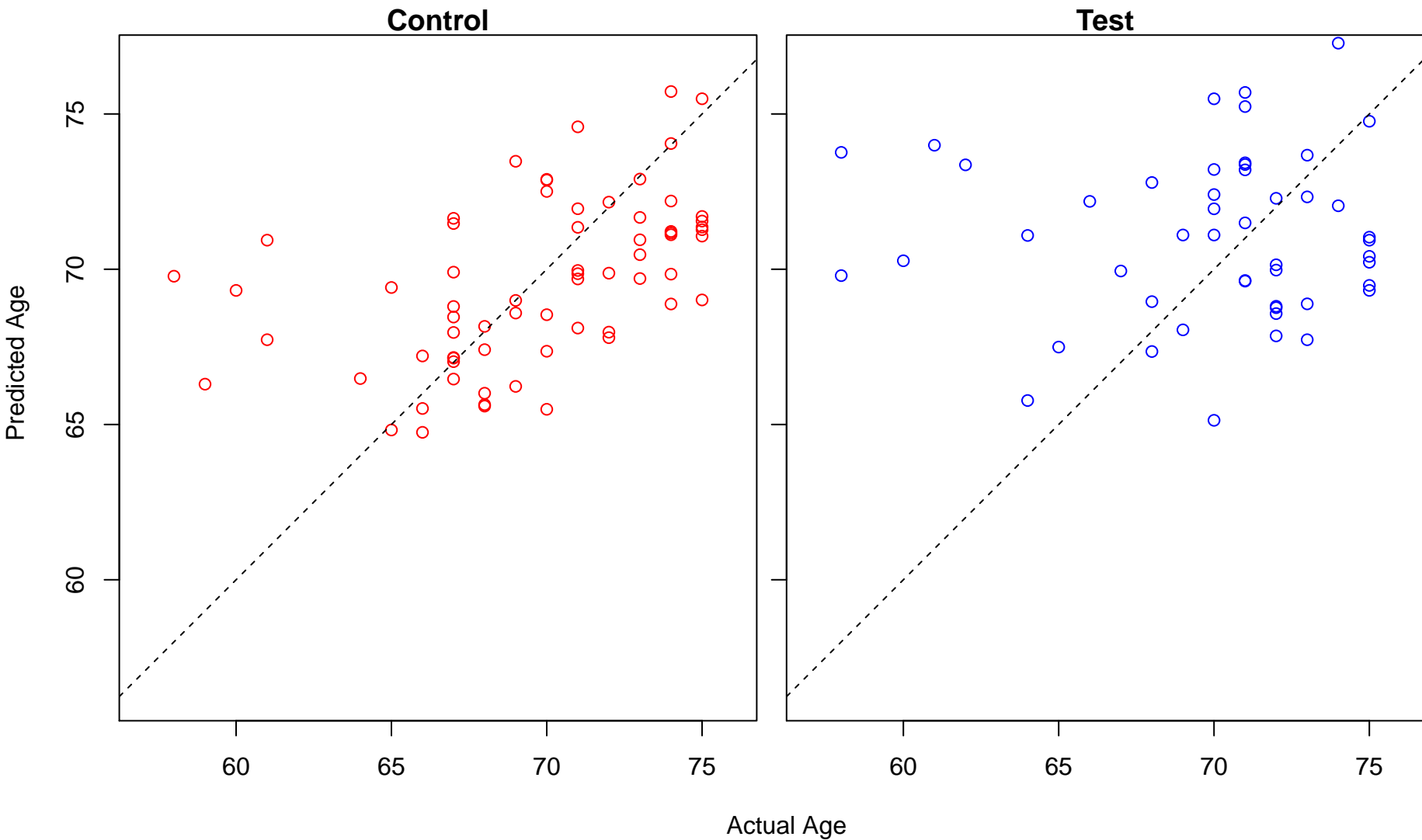
camera-type eye morphogenesis (Score: 0.824470)



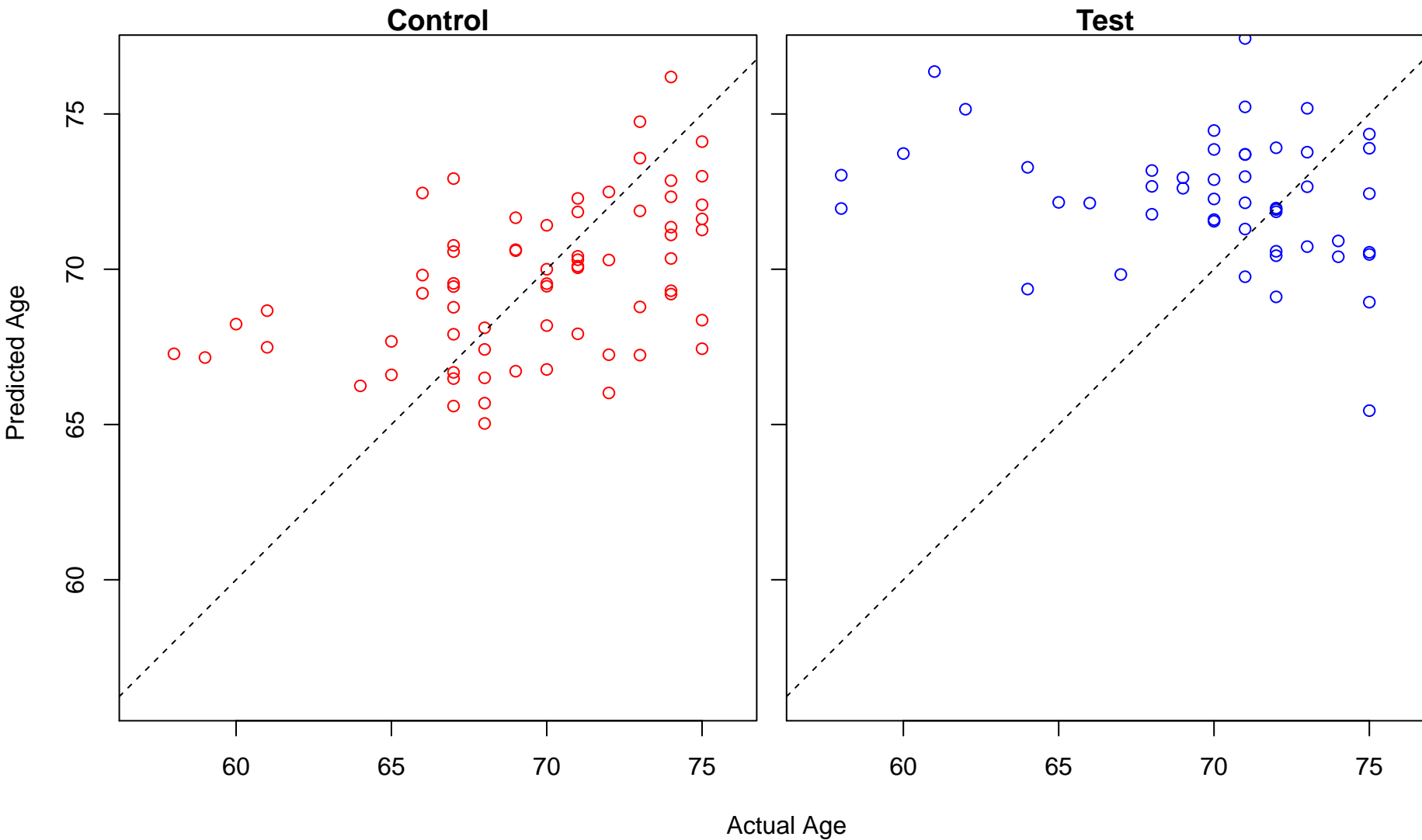
regulation of macrophage activation (Score: 0.824250)



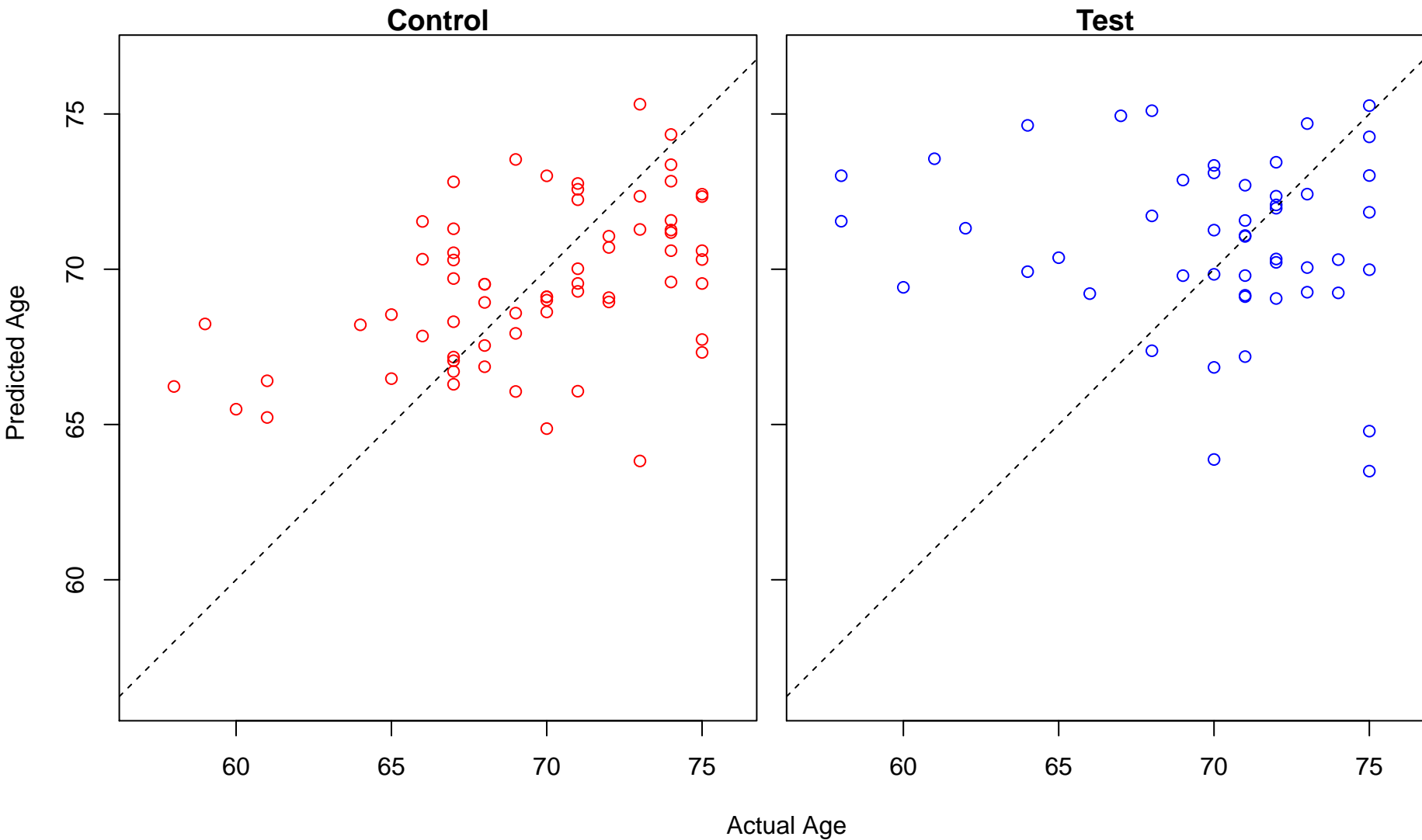
signal release (Score: 0.823999)



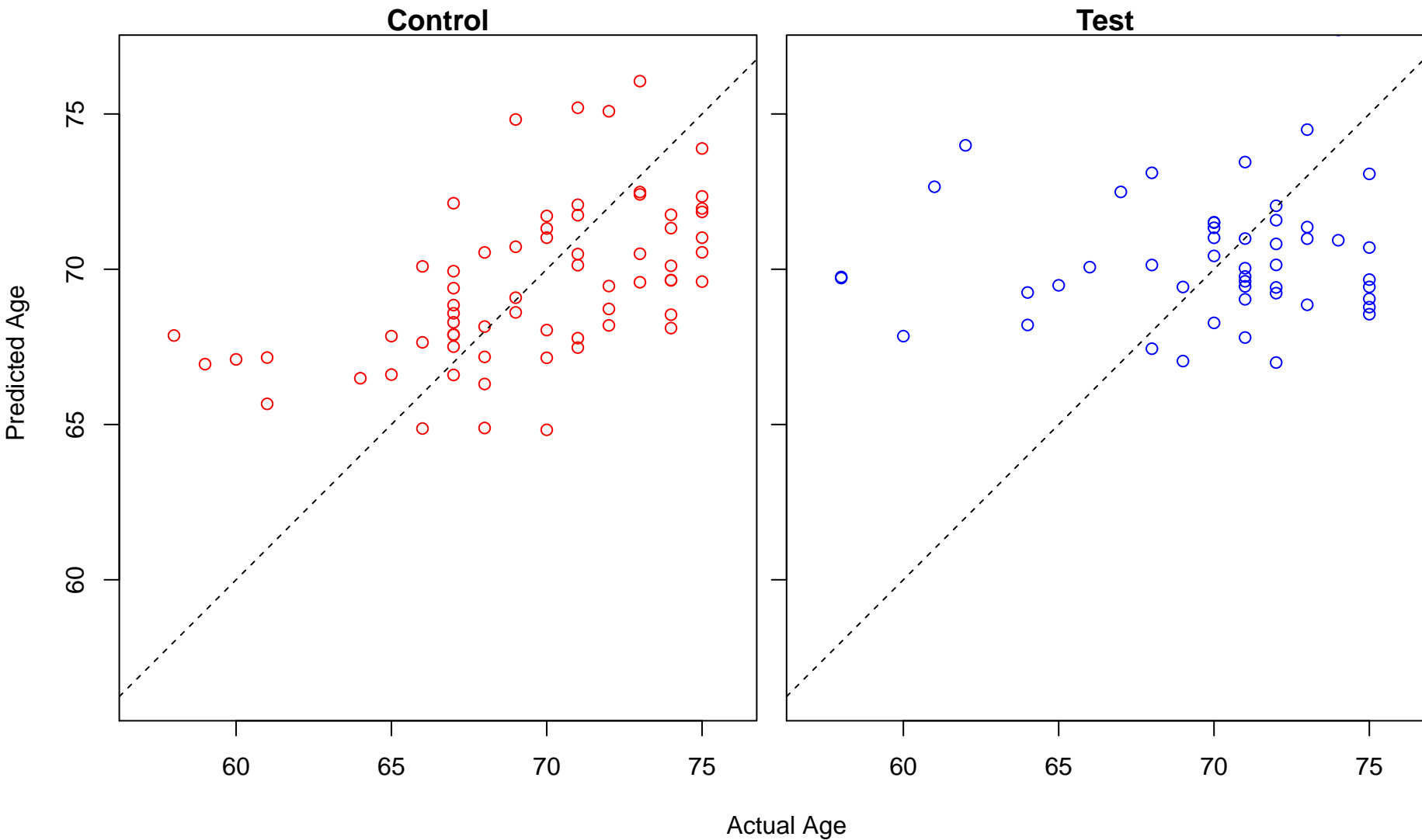
regulation of multicellular organism growth (Score: 0.823950)



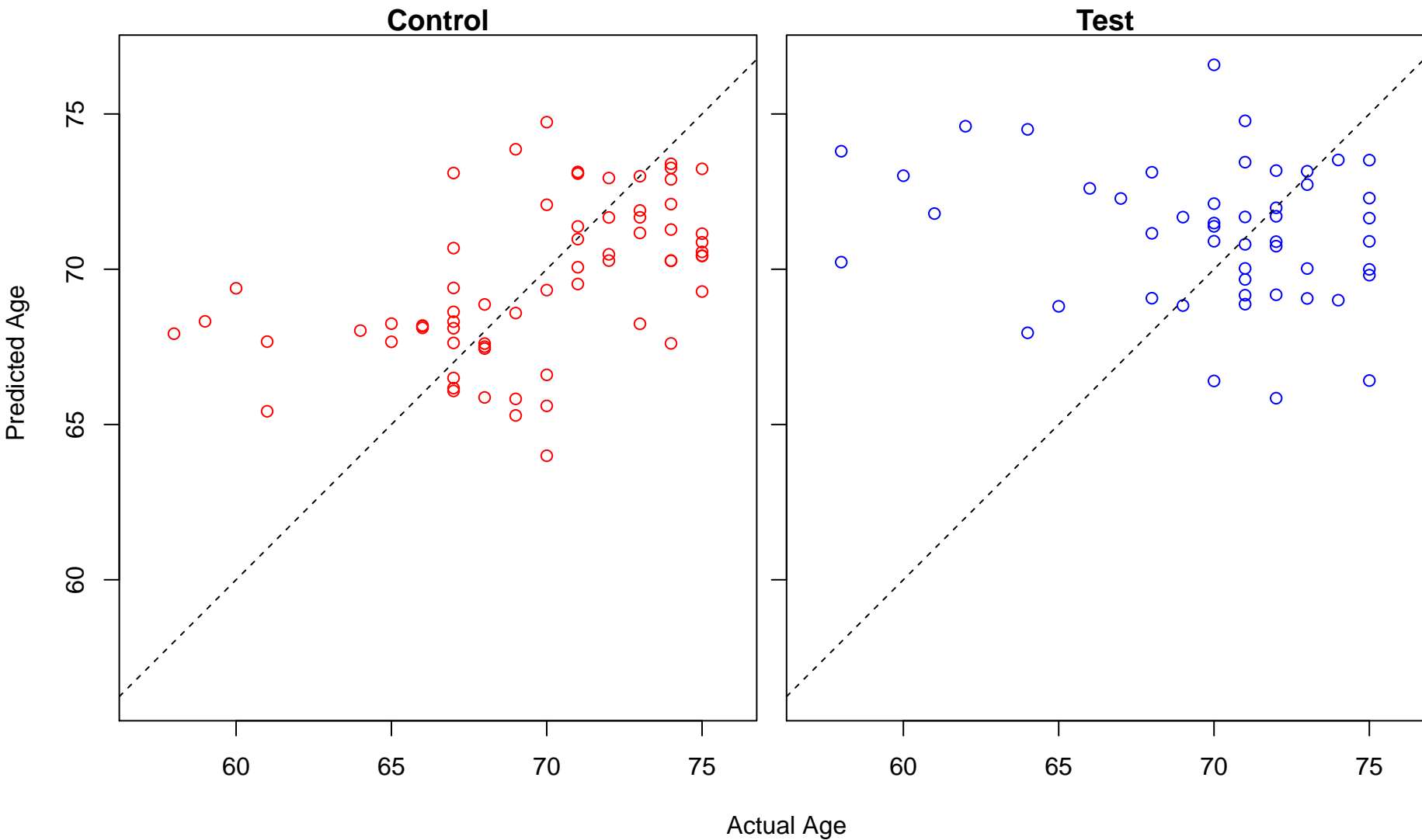
positive regulation of sodium ion transmembrane transporter activity (Score: 0.822798)



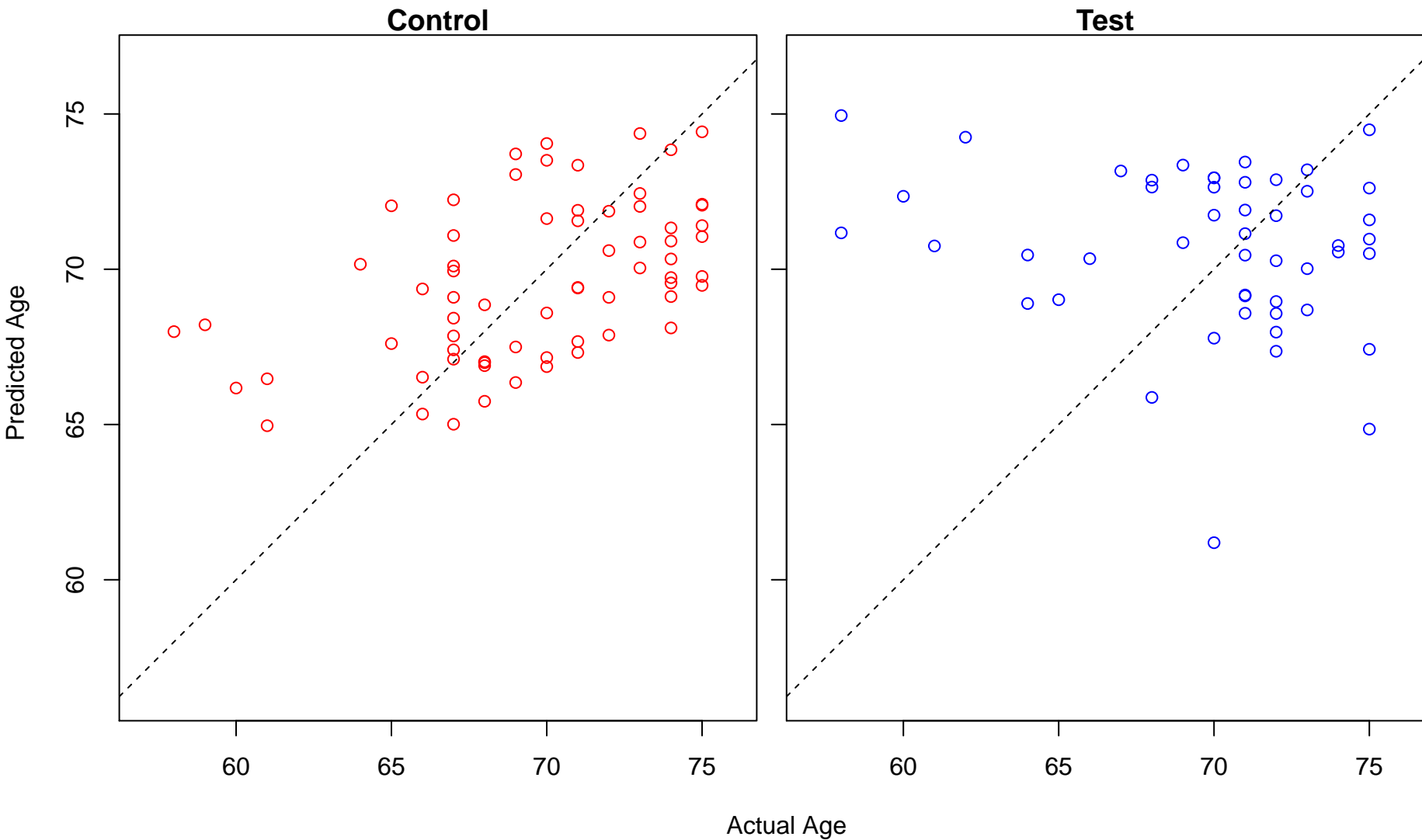
negative regulation of tumor necrosis factor–mediated signaling pathway (Score: 0.822420)



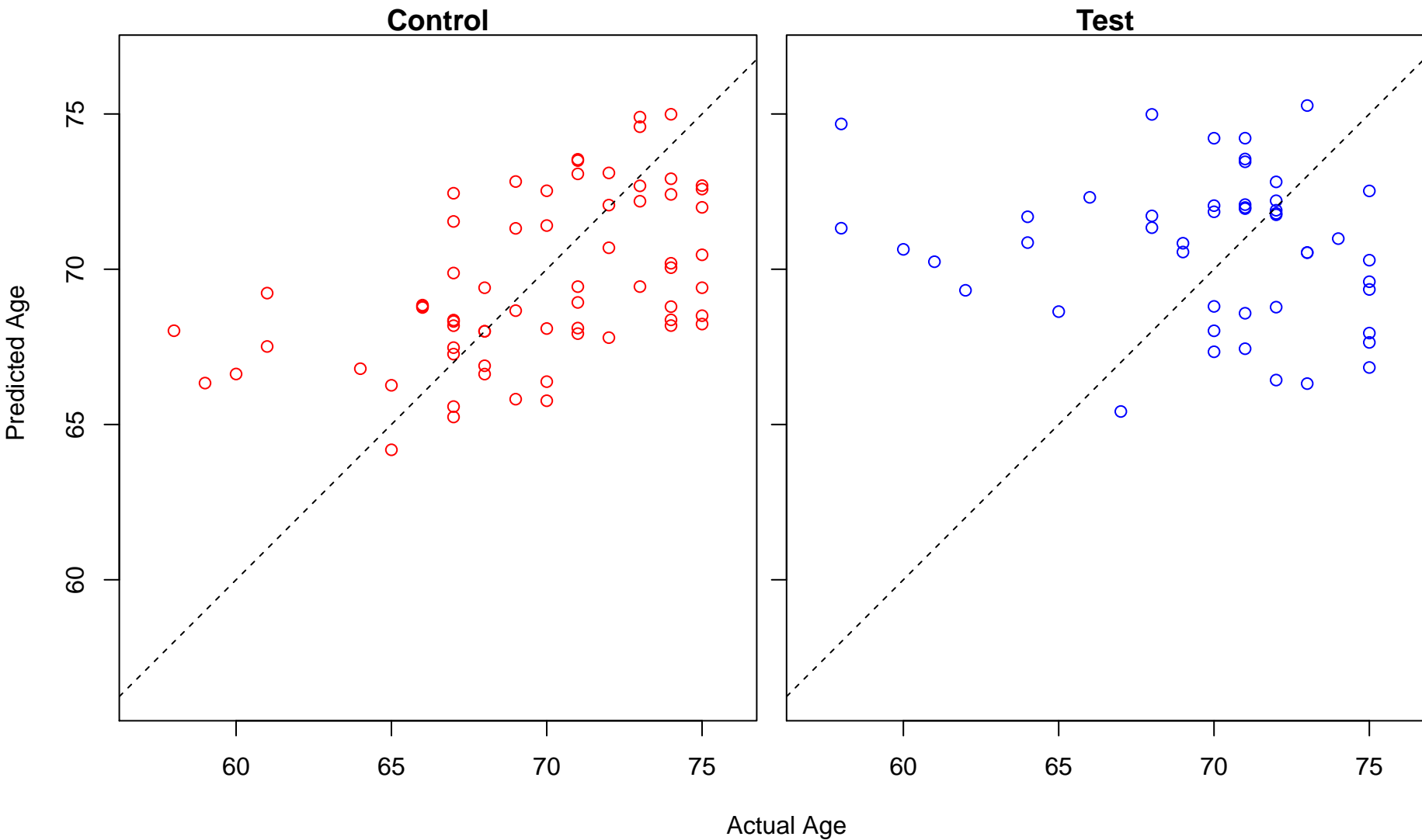
regulation of muscle adaptation (Score: 0.821705)



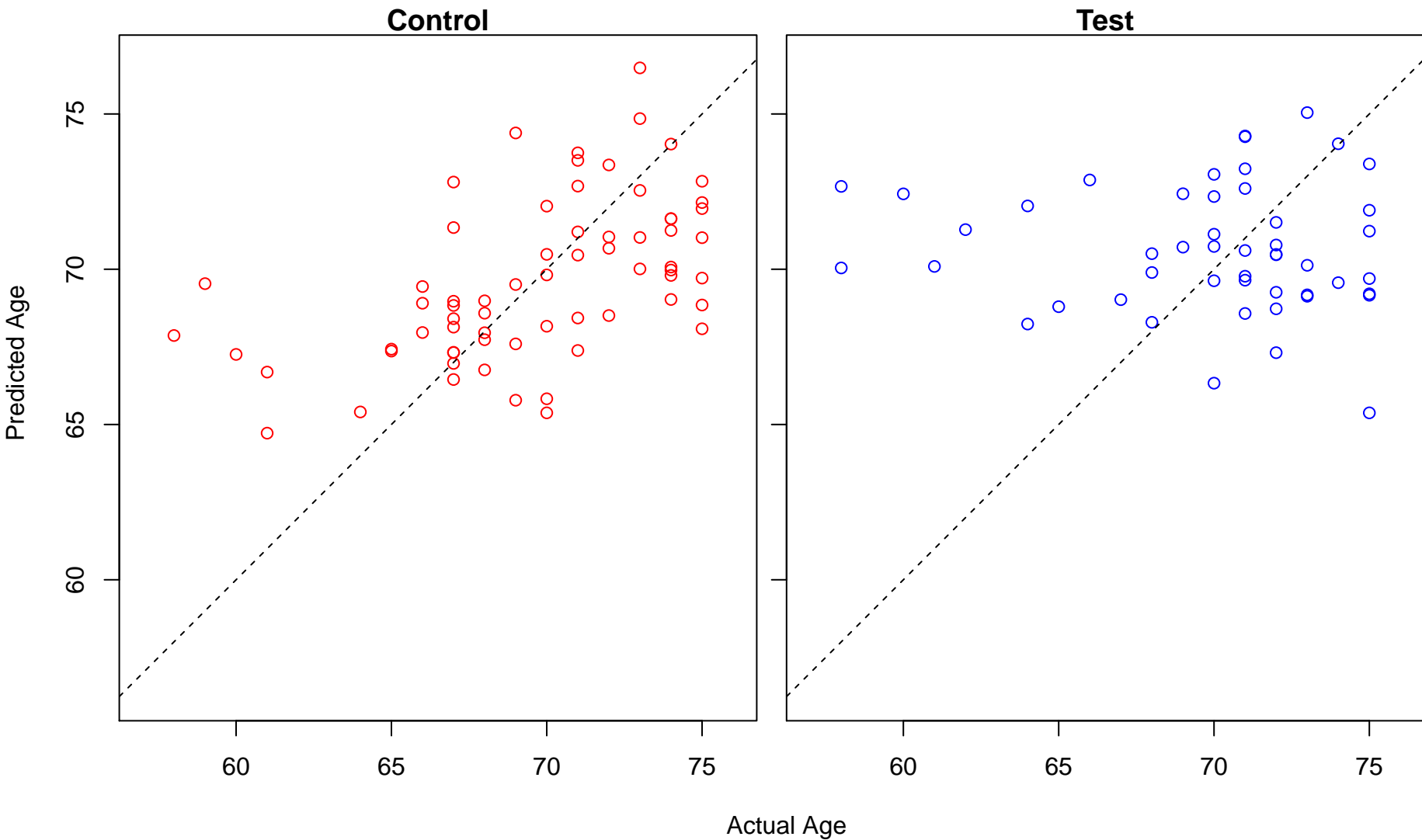
positive regulation of antigen receptor-mediated signaling pathway (Score: 0.821462)



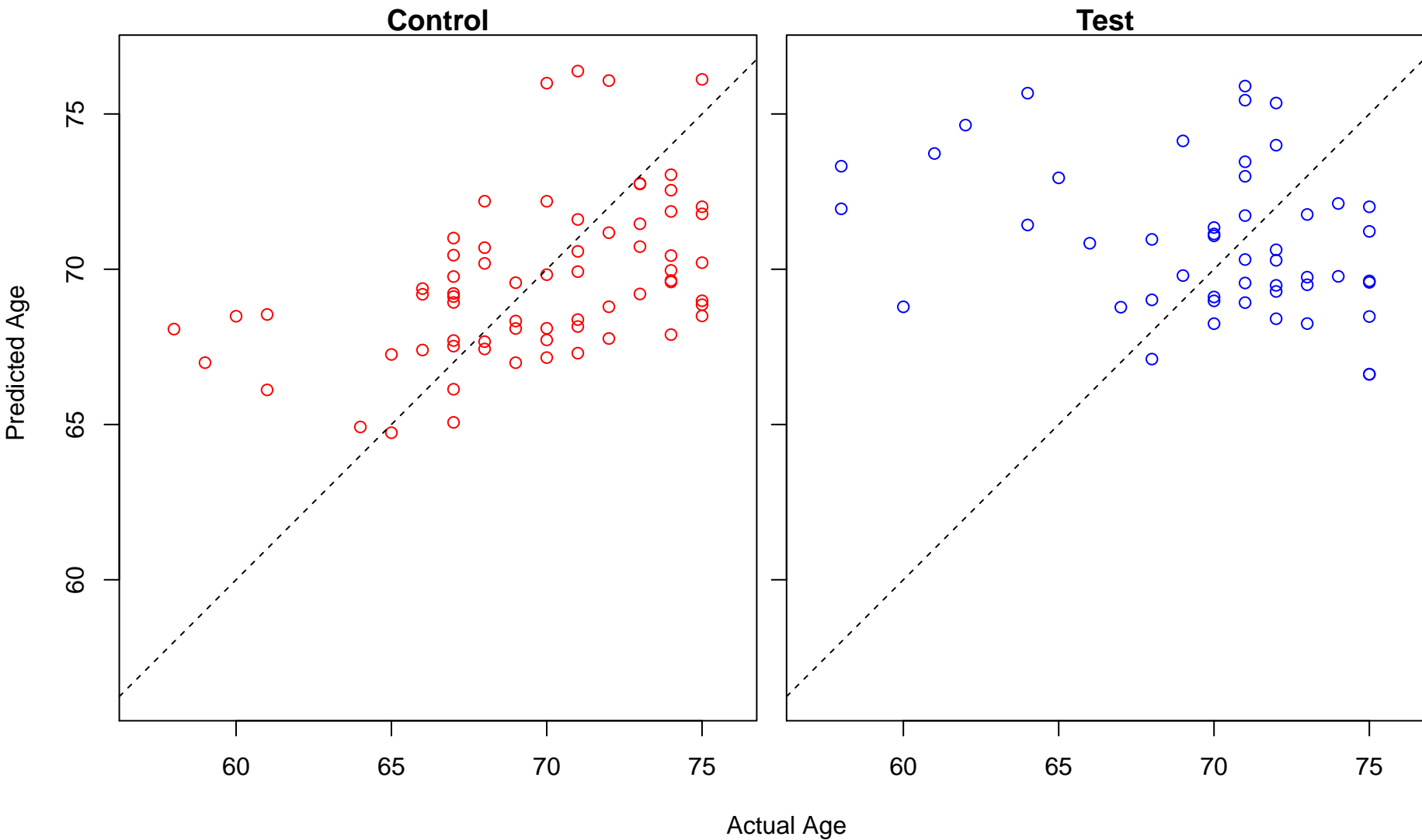
protein complex localization (Score: 0.821342)



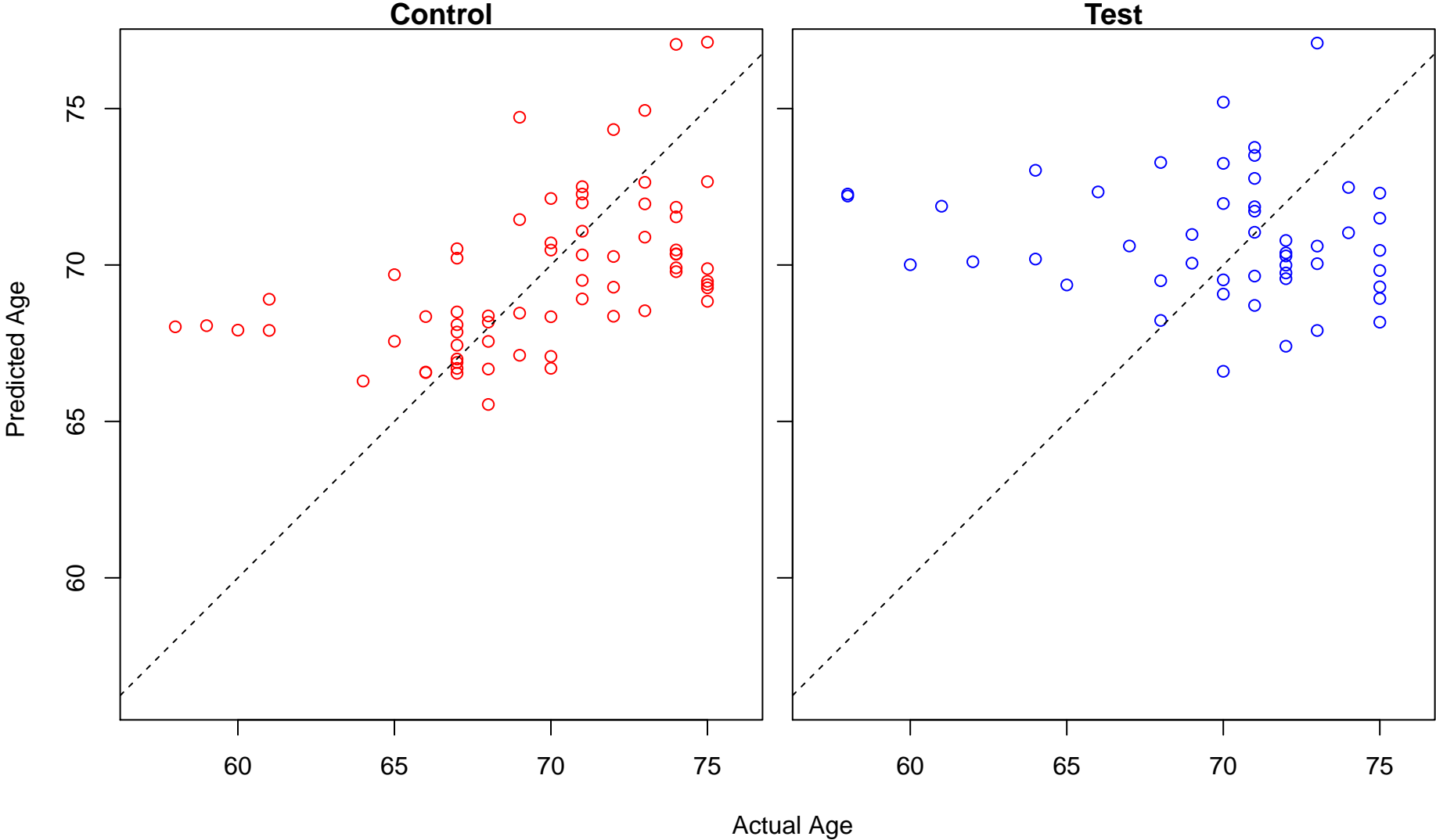
regulation of cytoplasmic mRNA processing body assembly (Score: 0.820885)



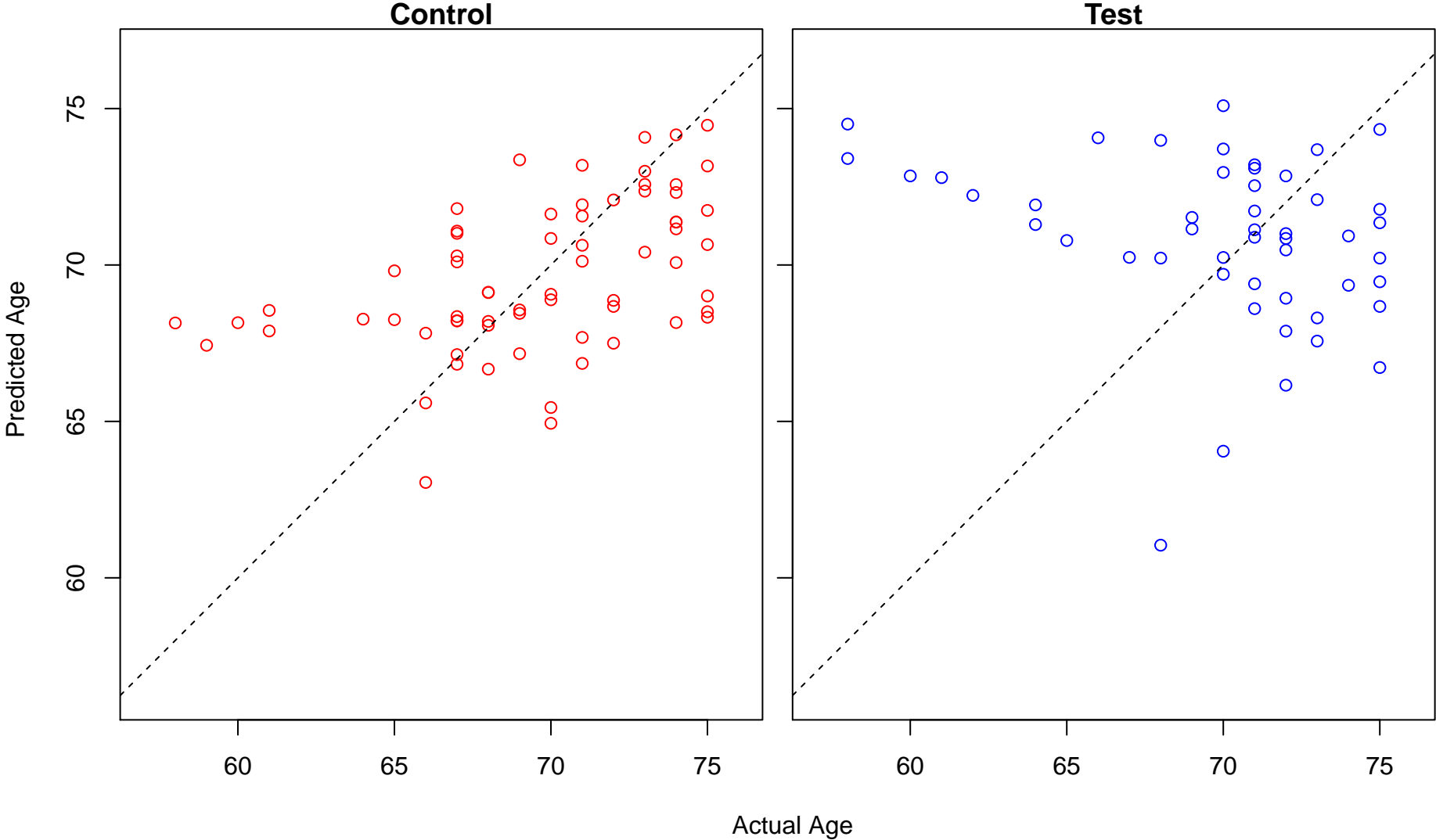
regulation of non-canonical Wnt signaling pathway (Score: 0.820719)



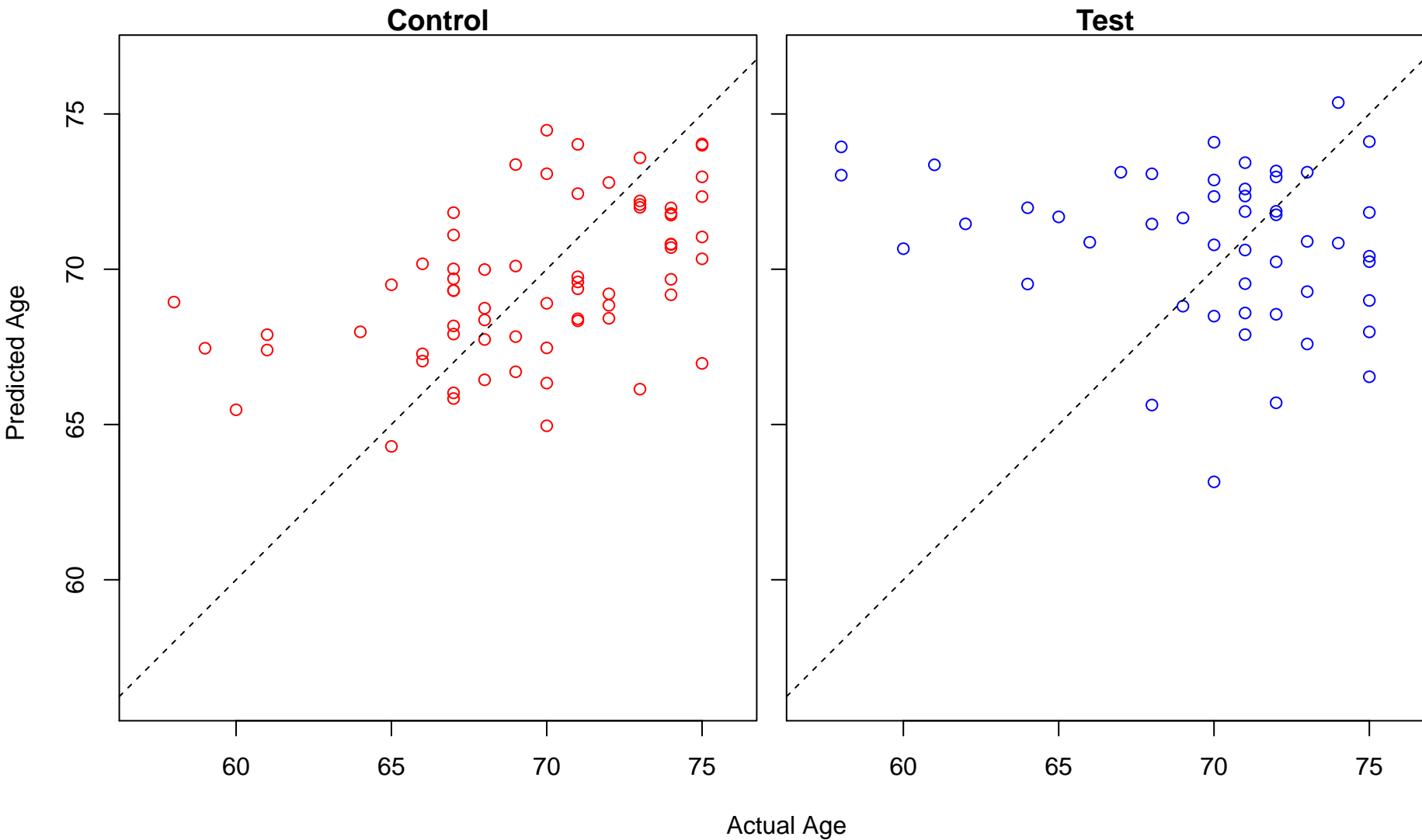
negative regulation of transcription from RNA polymerase II promoter in response to stress (Score: 0.8)



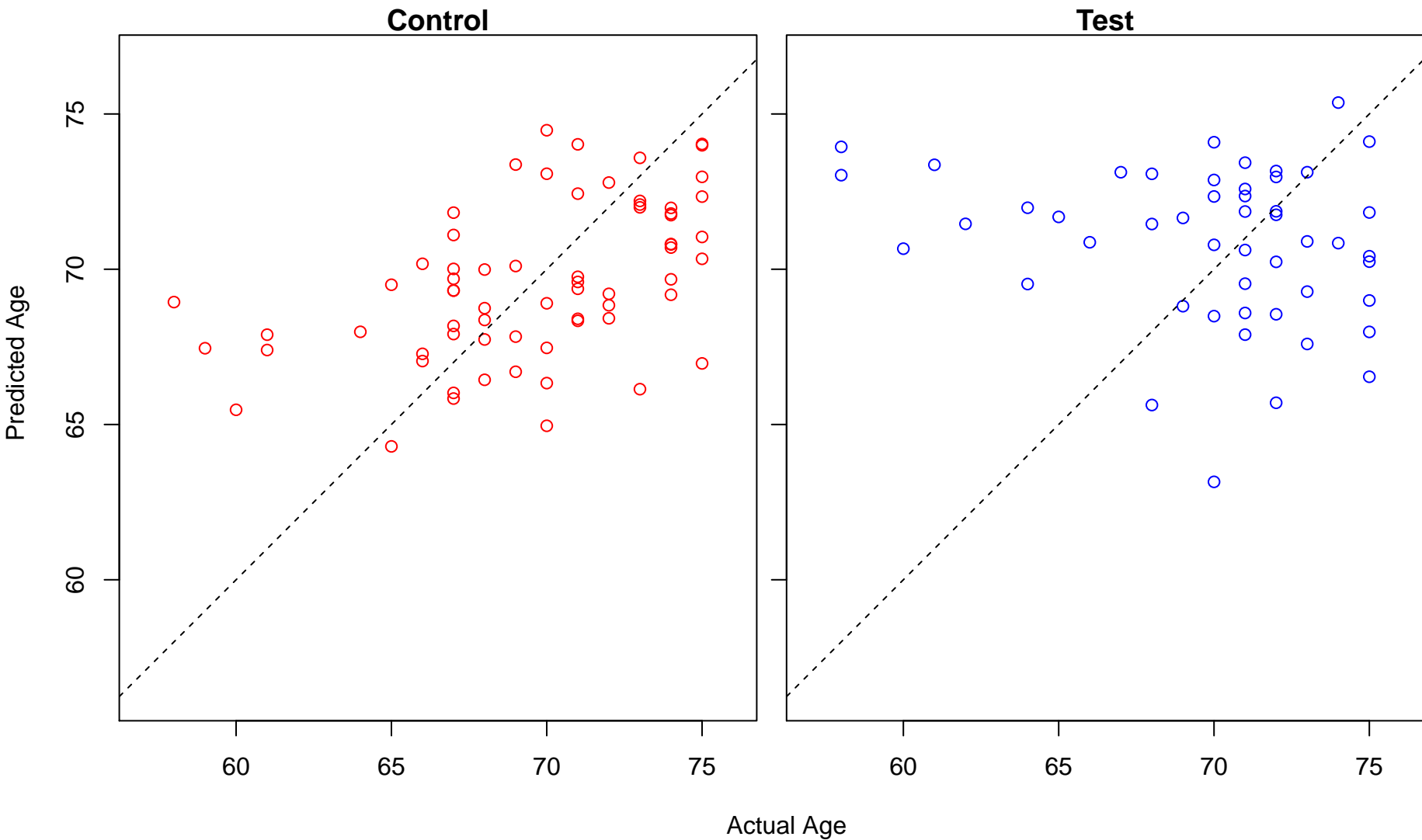
positive regulation of insulin secretion involved in cellular response to glucose stimulus (Score: 0.819)



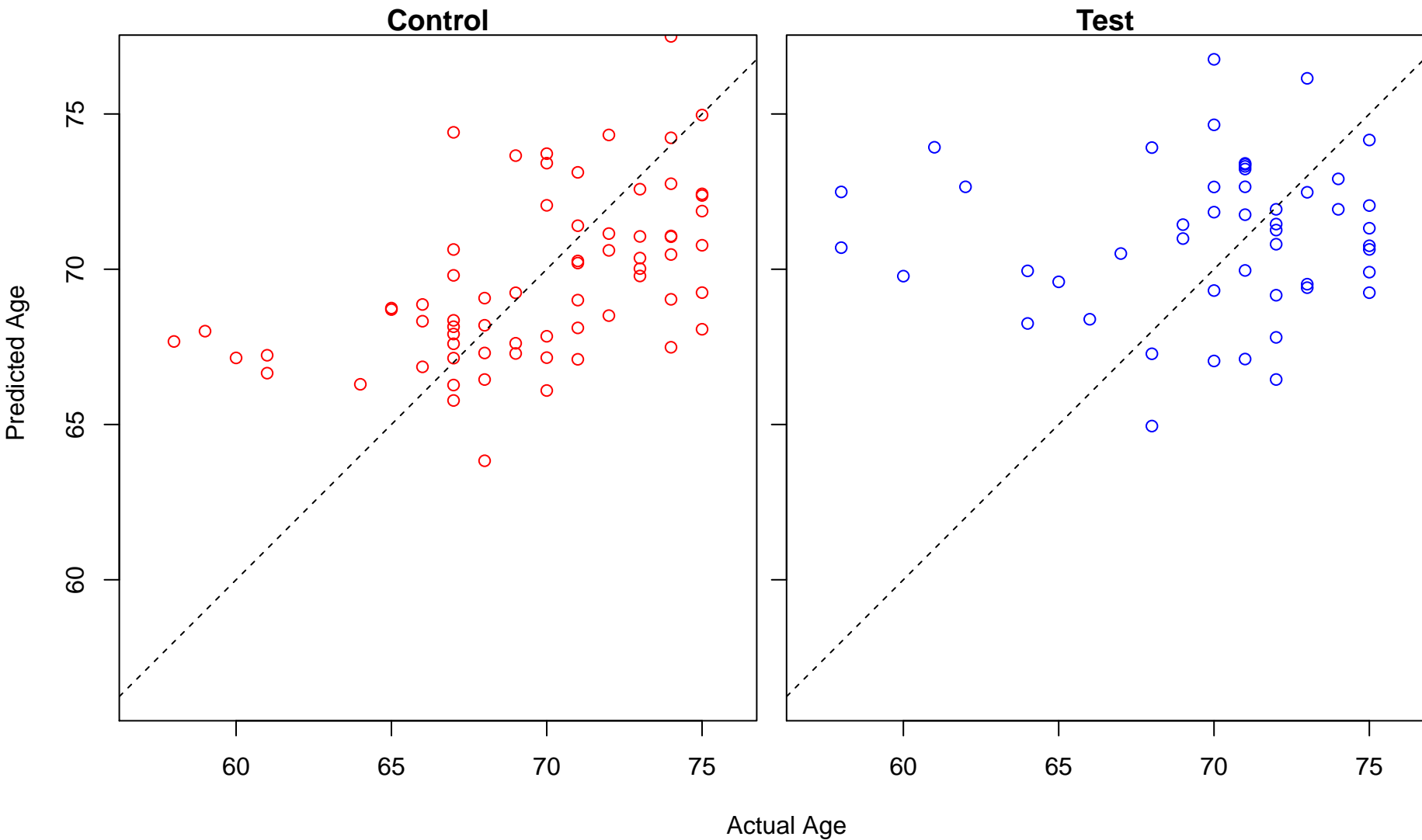
long-chain fatty-acyl-CoA biosynthetic process (Score: 0.819378)



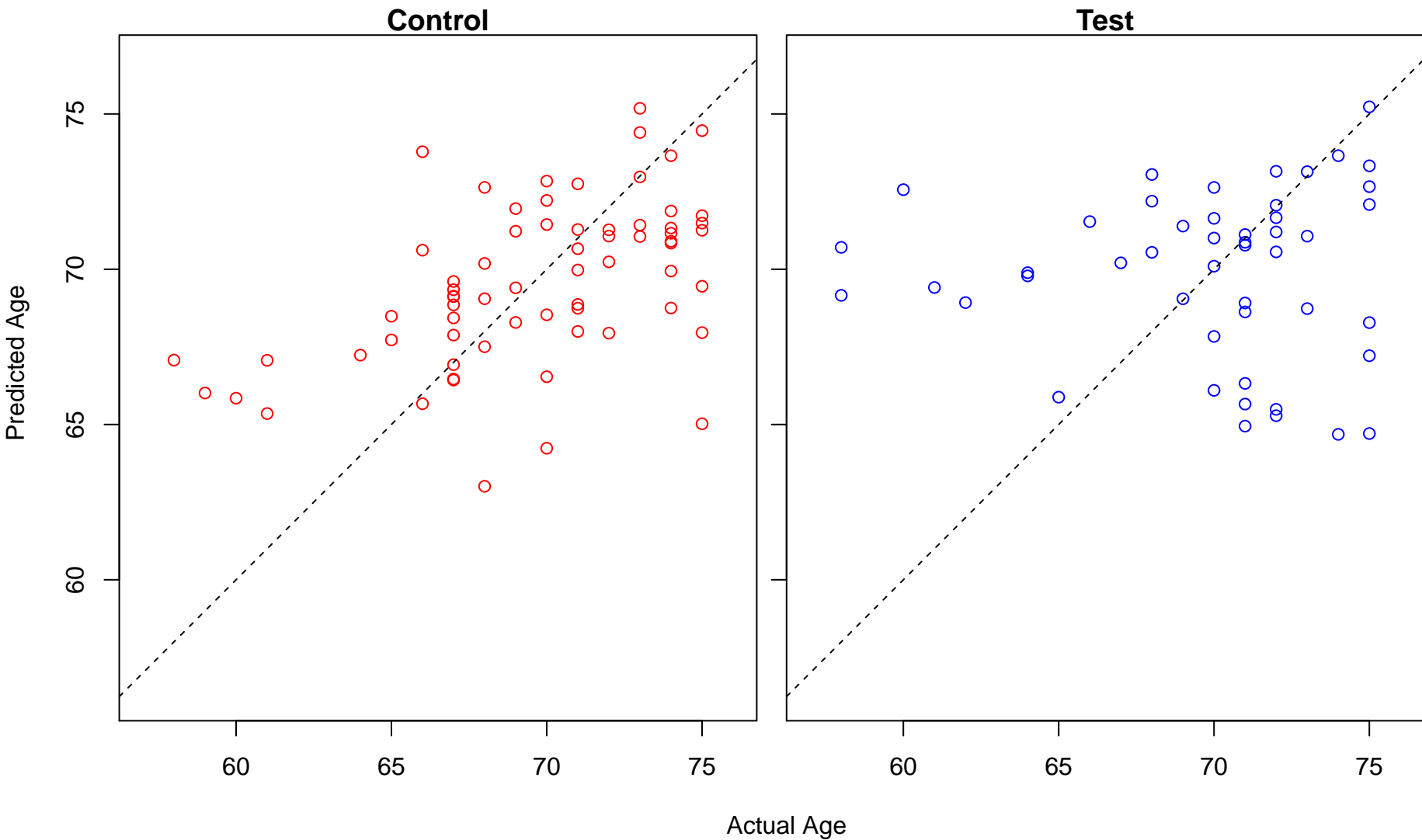
fatty-acyl-CoA biosynthetic process (Score: 0.819378)



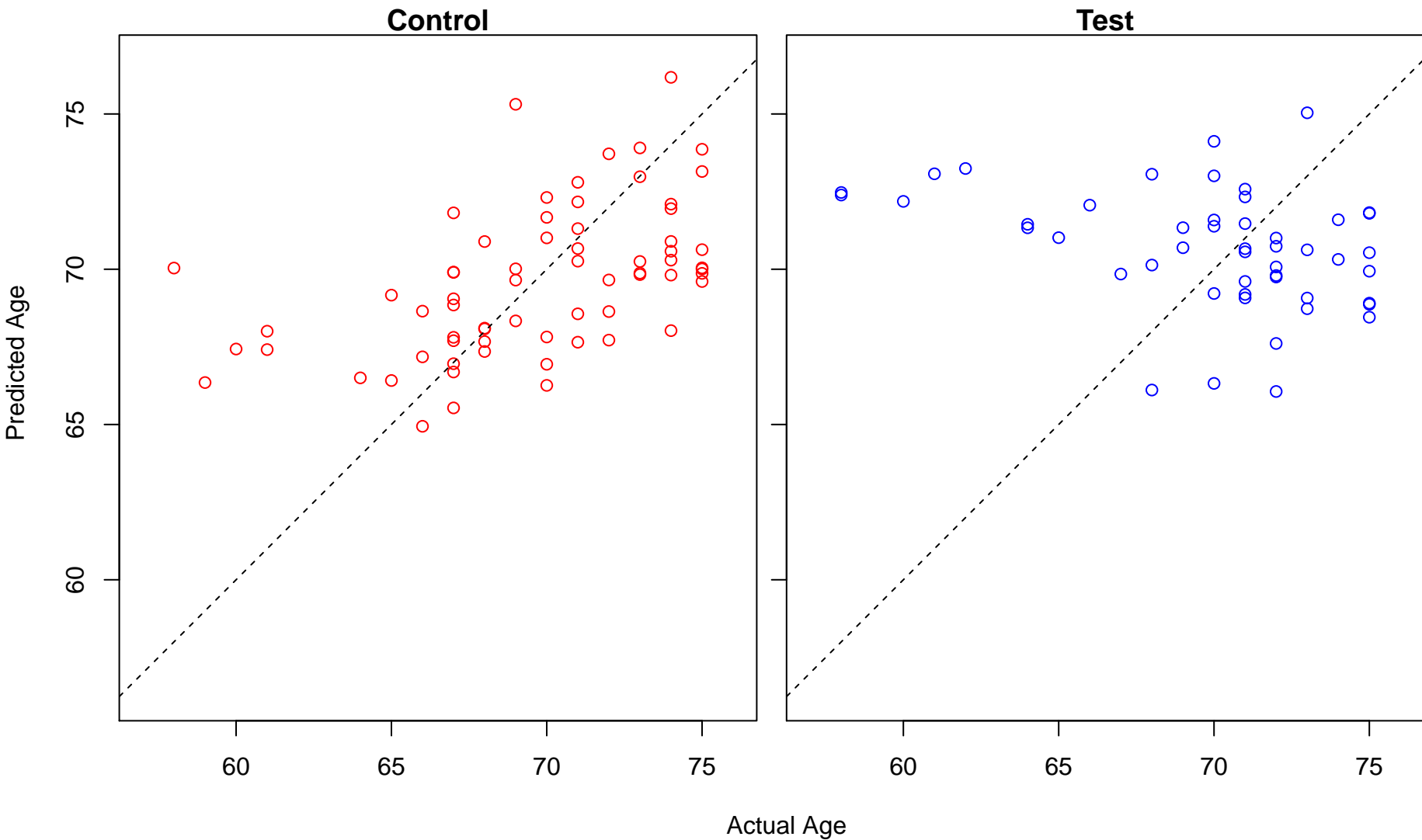
regulation of cardiac muscle contraction (Score: 0.819344)



negative regulation of cilium assembly (Score: 0.818651)

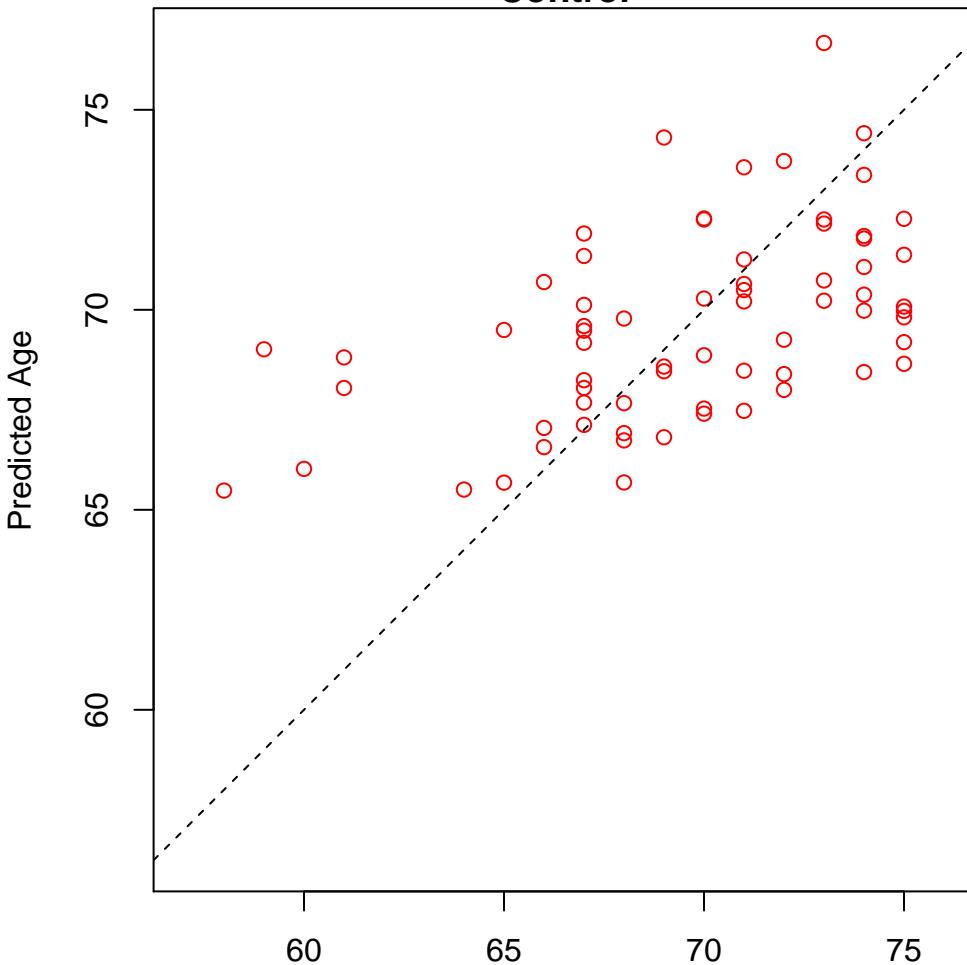


positive regulation of NFAT protein import into nucleus (Score: 0.818644)

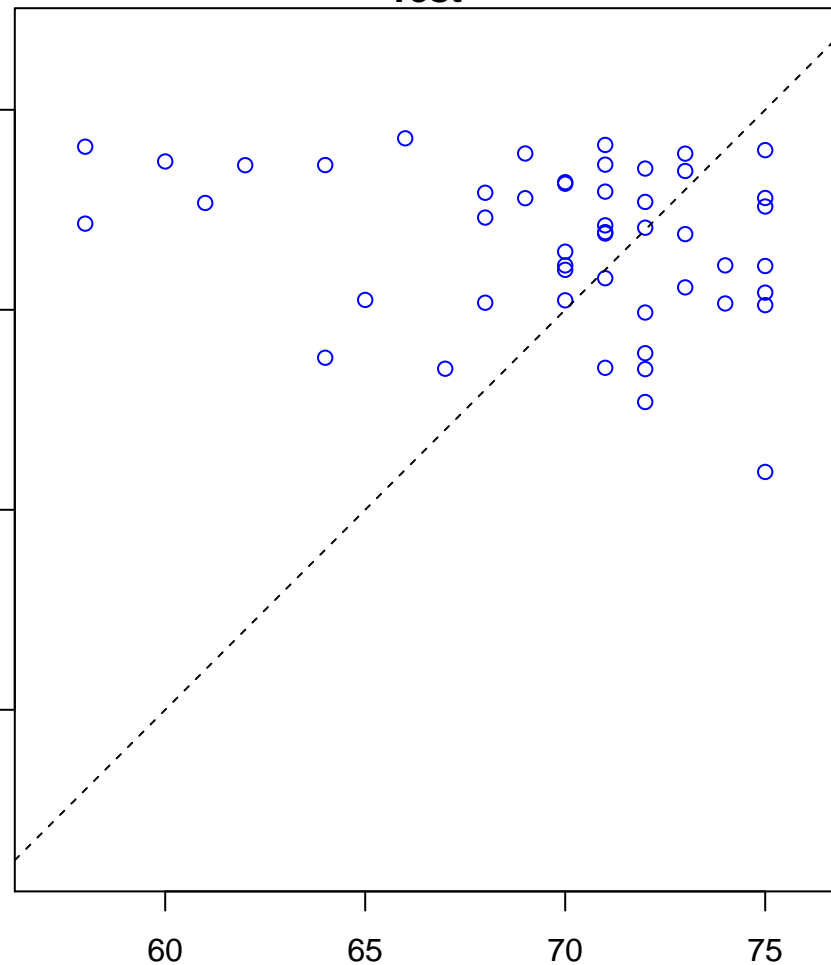


atrioventricular valve morphogenesis (Score: 0.817567)

Control

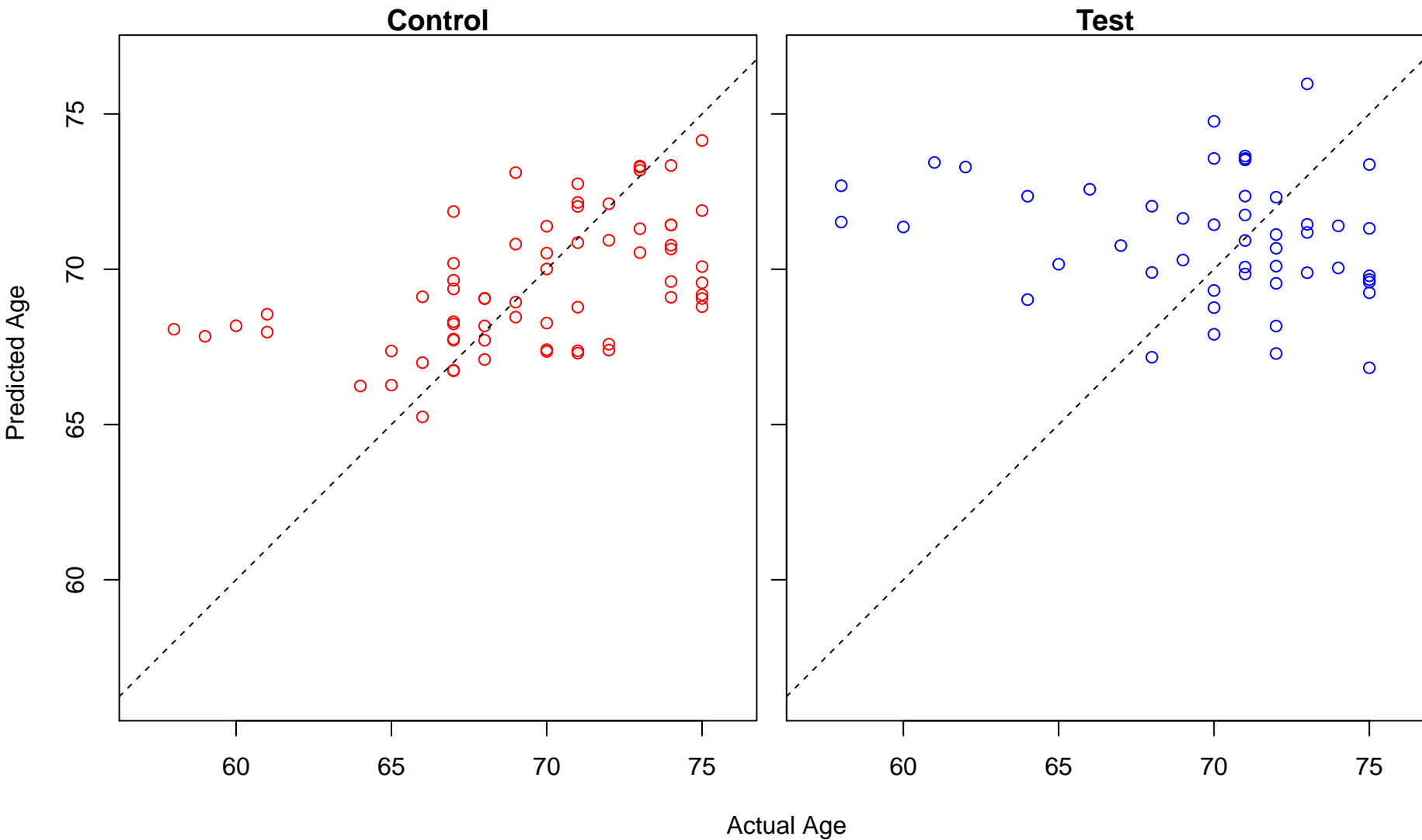


Test



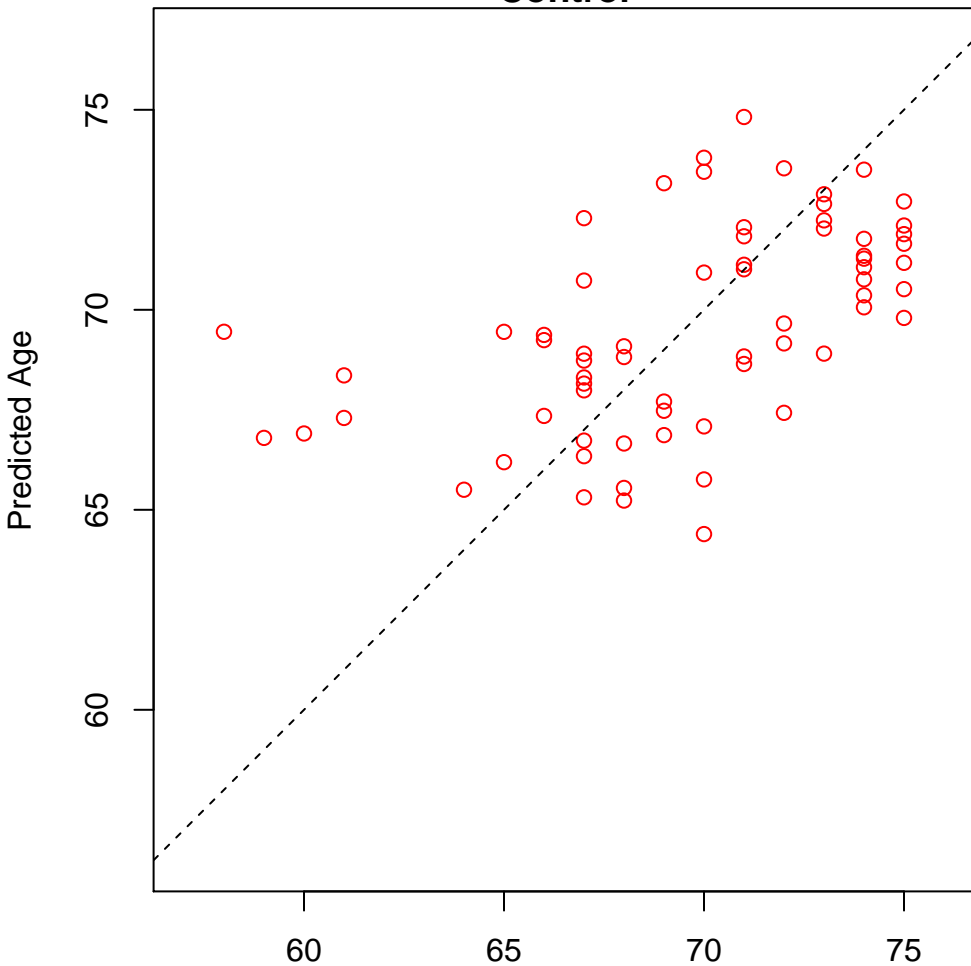
Actual Age

memory (Score: 0.816983)

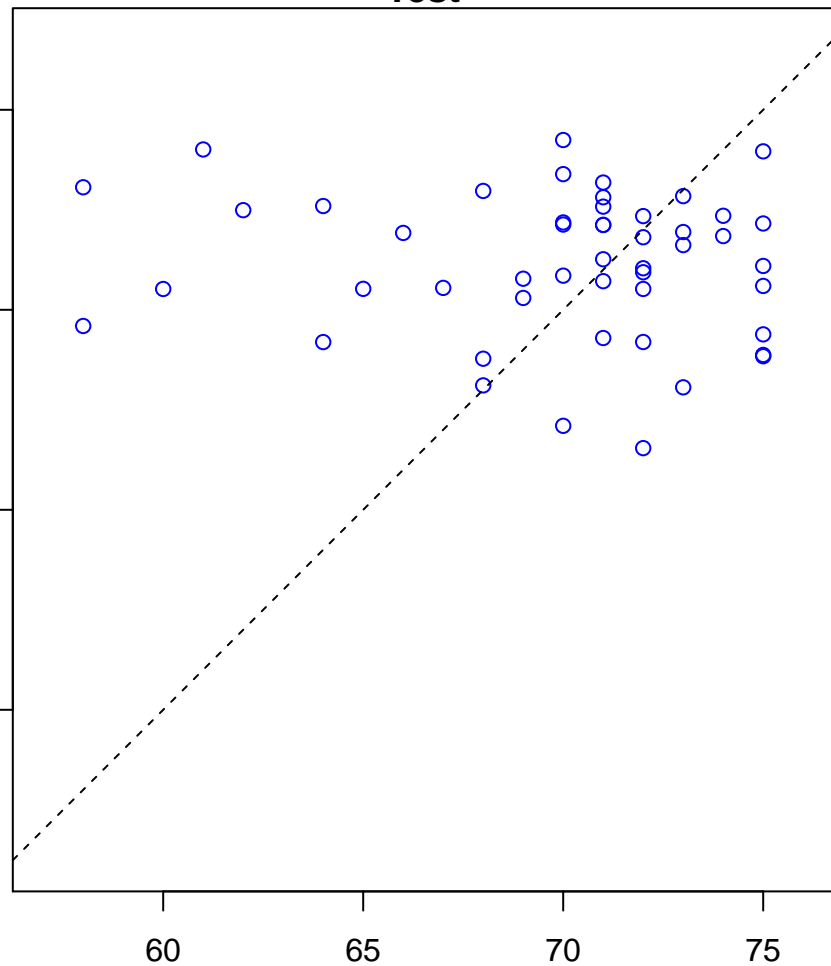


glycosaminoglycan metabolic process (Score: 0.816900)

Control

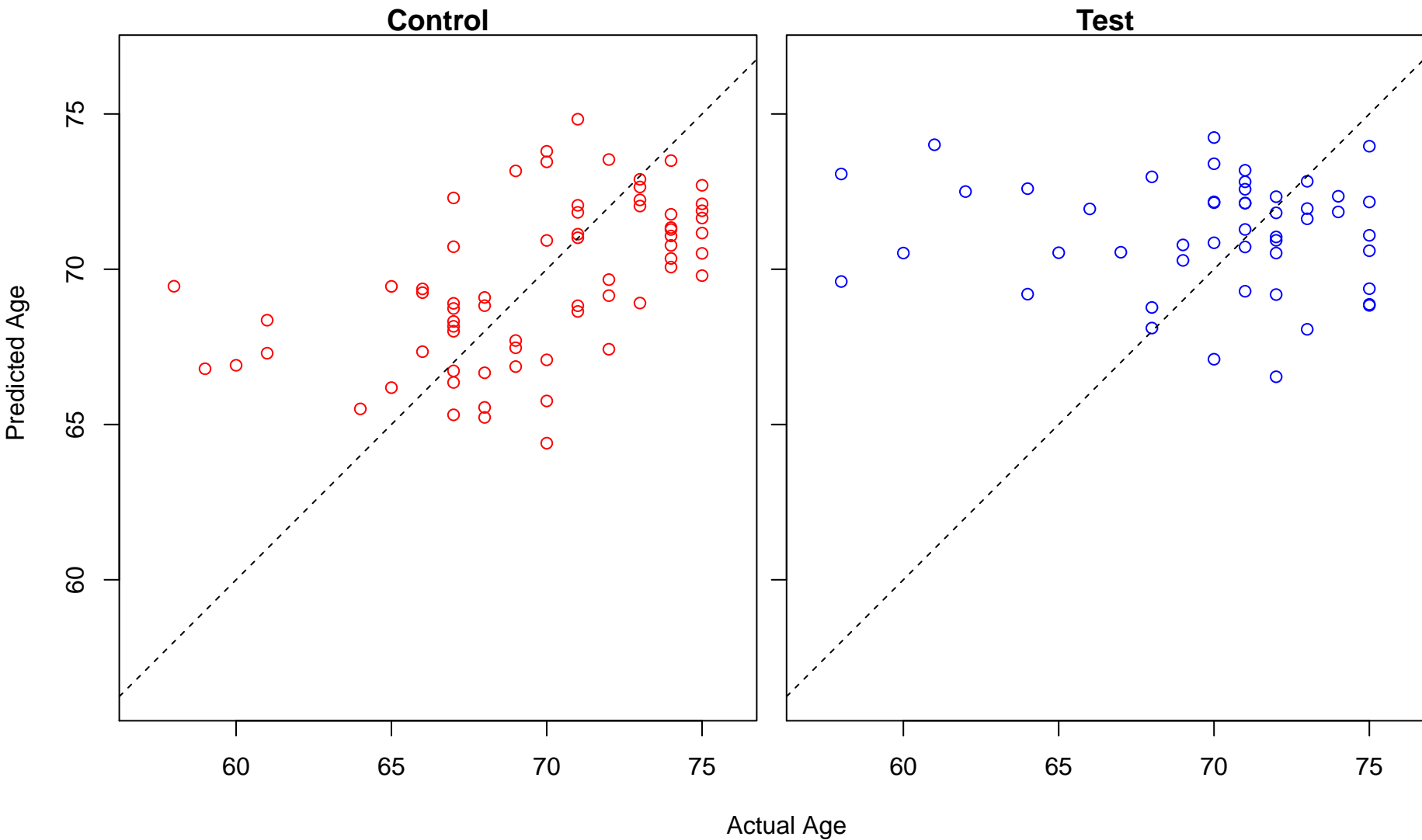


Test

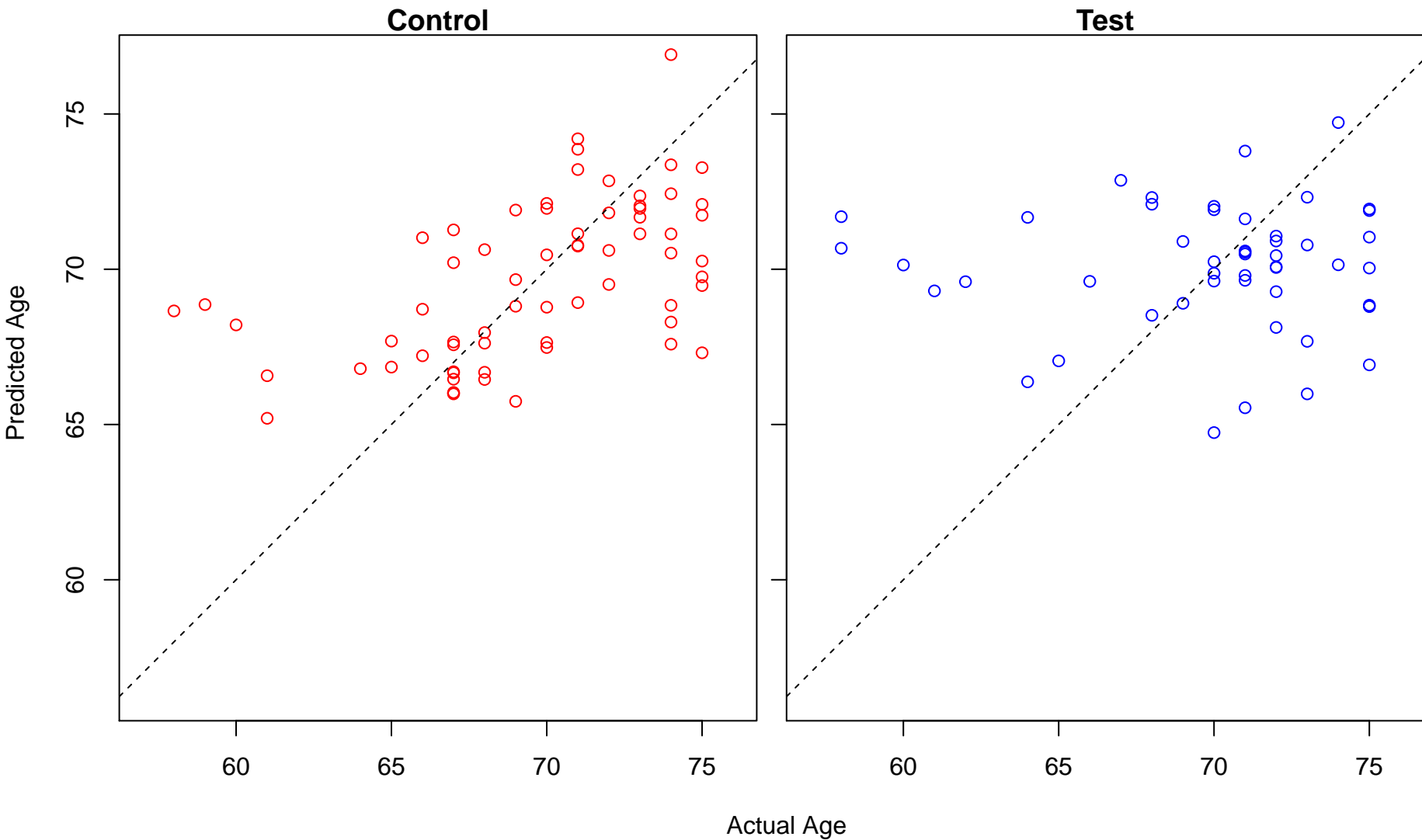


Actual Age

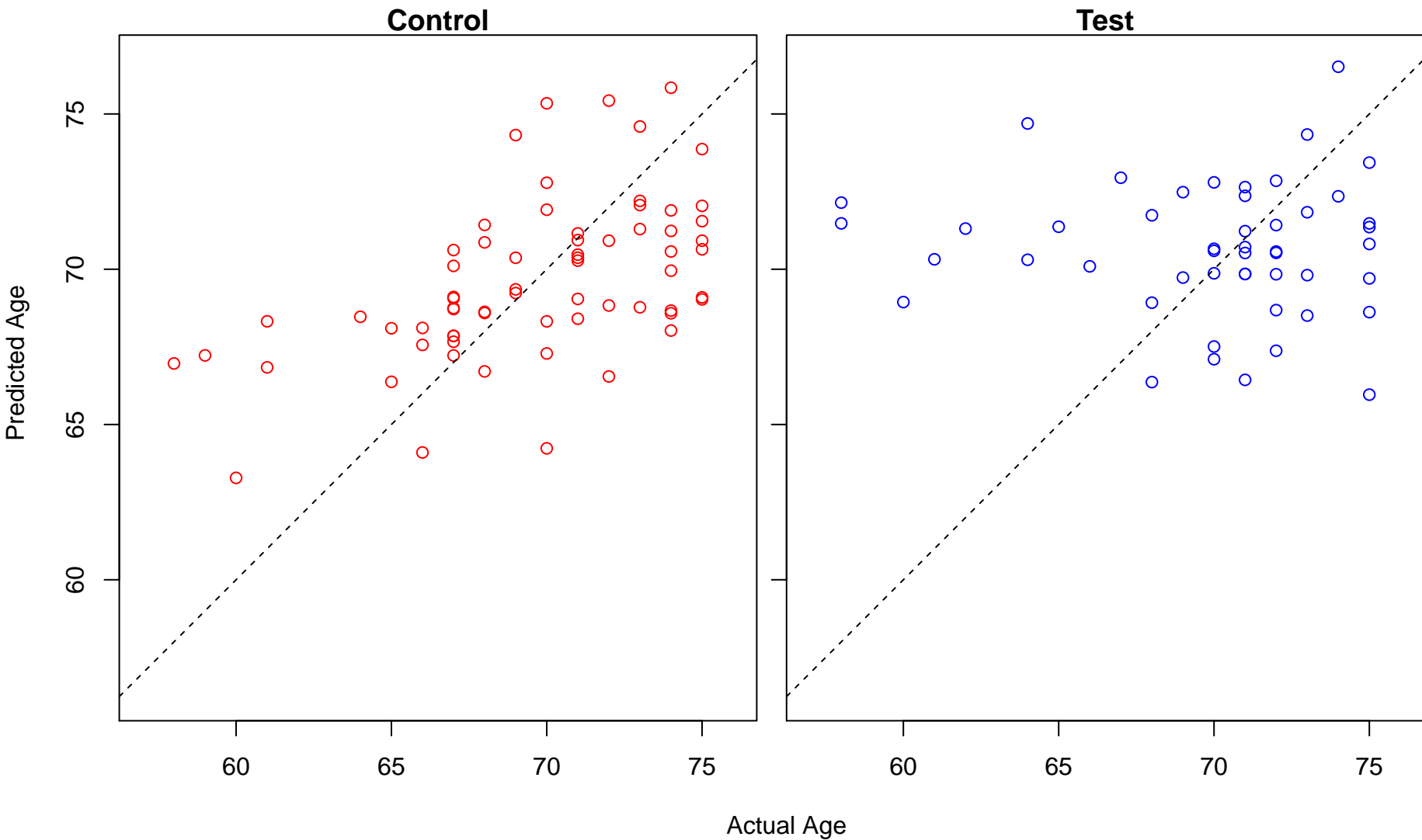
aminoglycan metabolic process (Score: 0.816514)



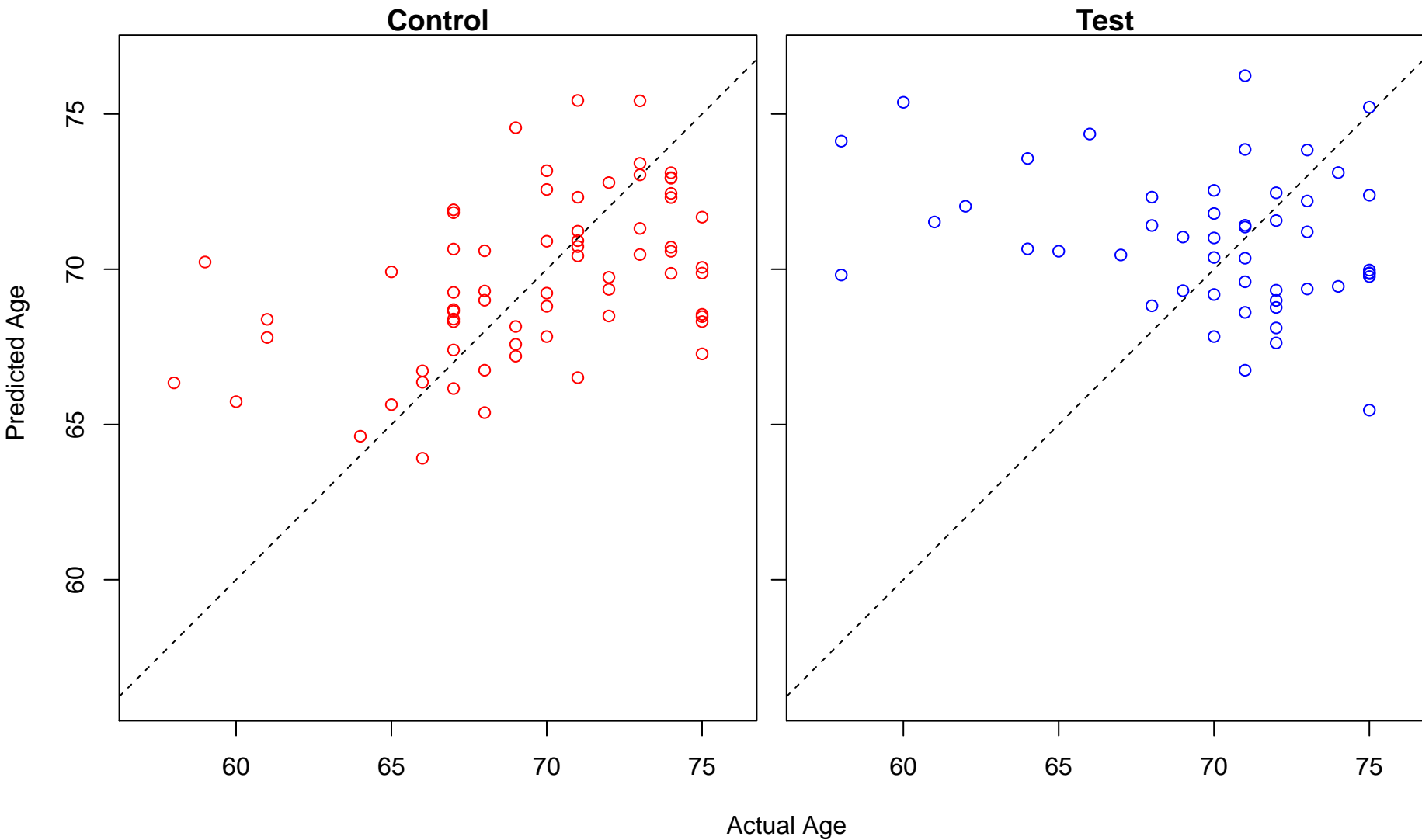
negative regulation of translational initiation in response to stress (Score: 0.816351)



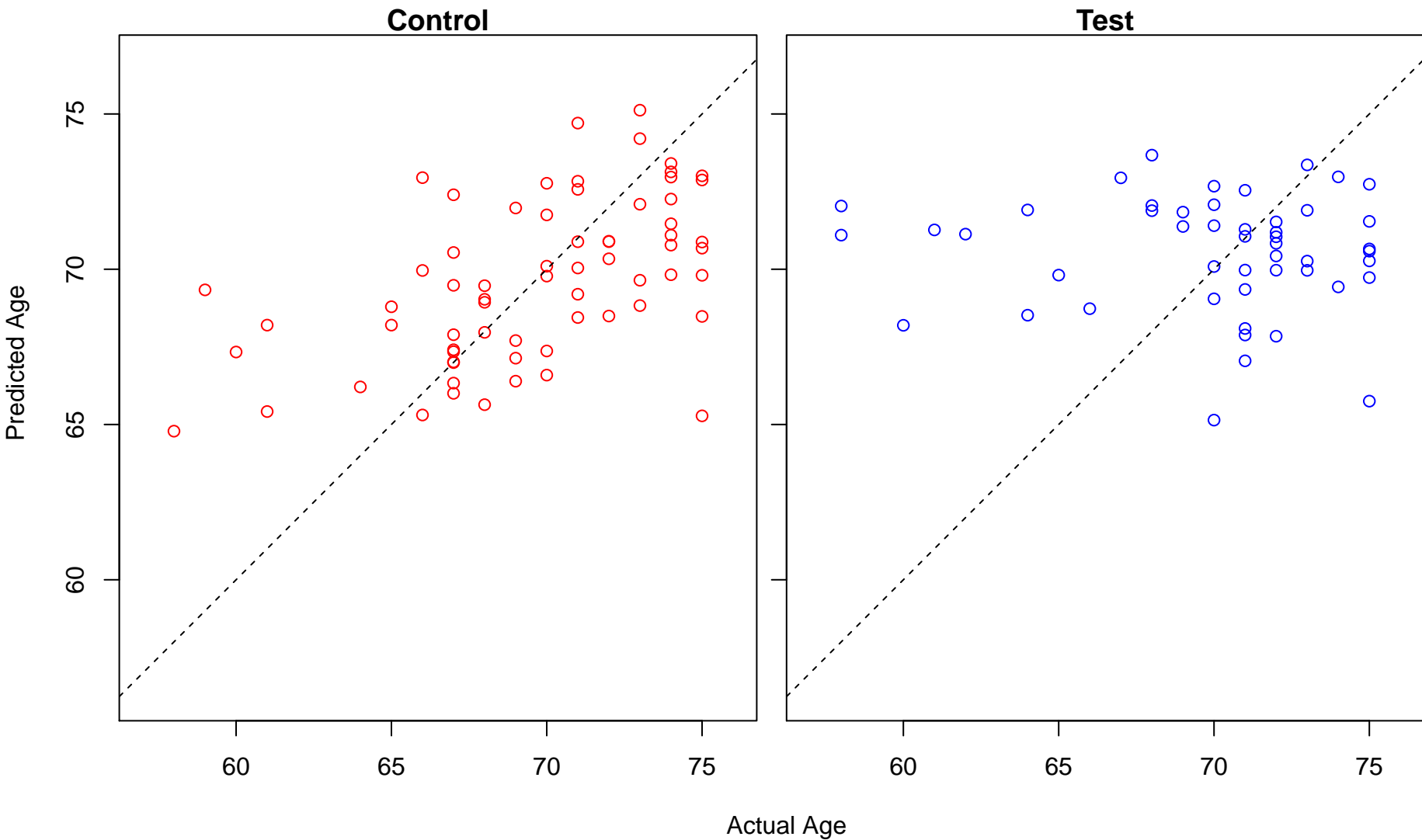
amino acid import (Score: 0.816008)



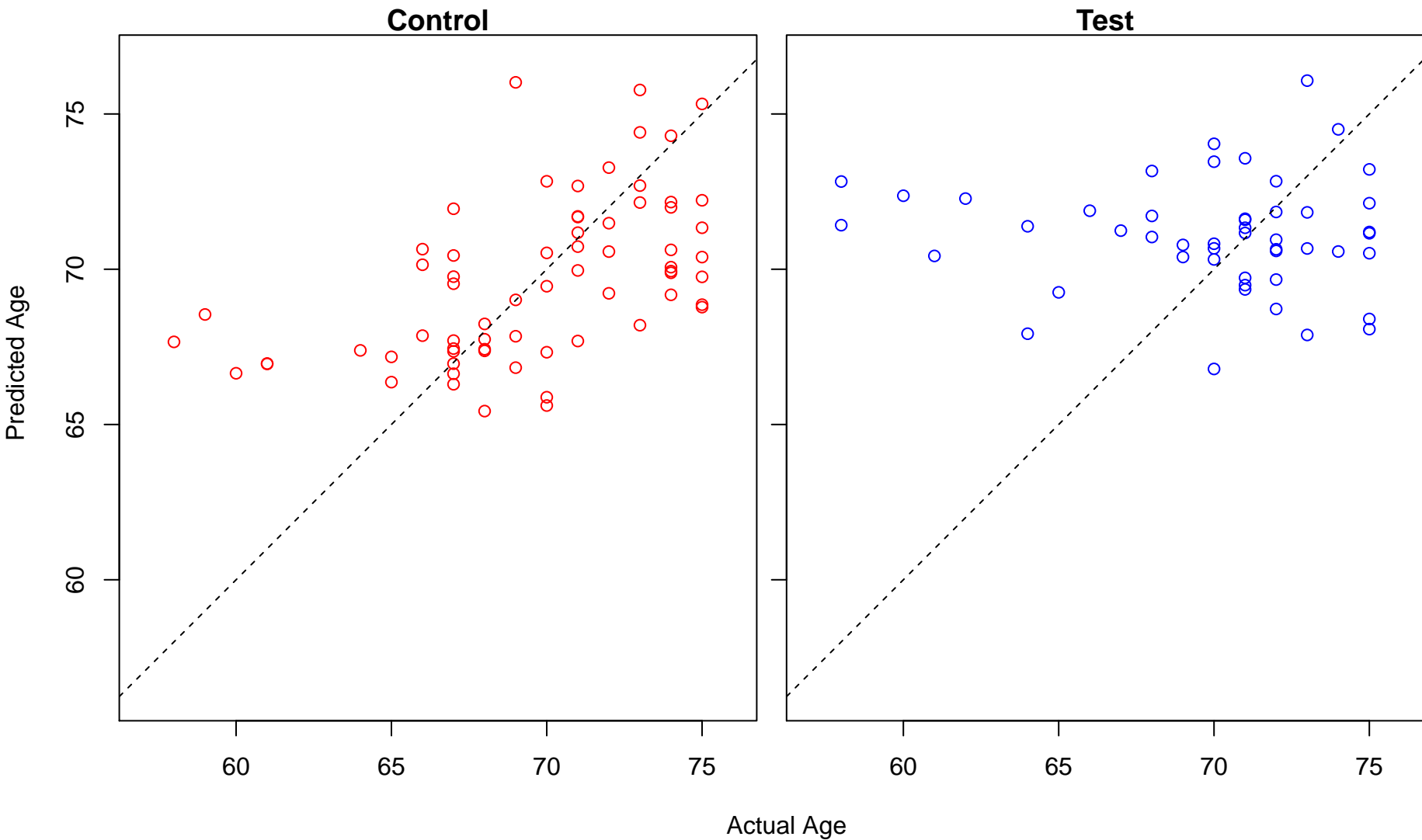
regulation of pro-B cell differentiation (Score: 0.815977)



positive regulation of membrane potential (Score: 0.815597)

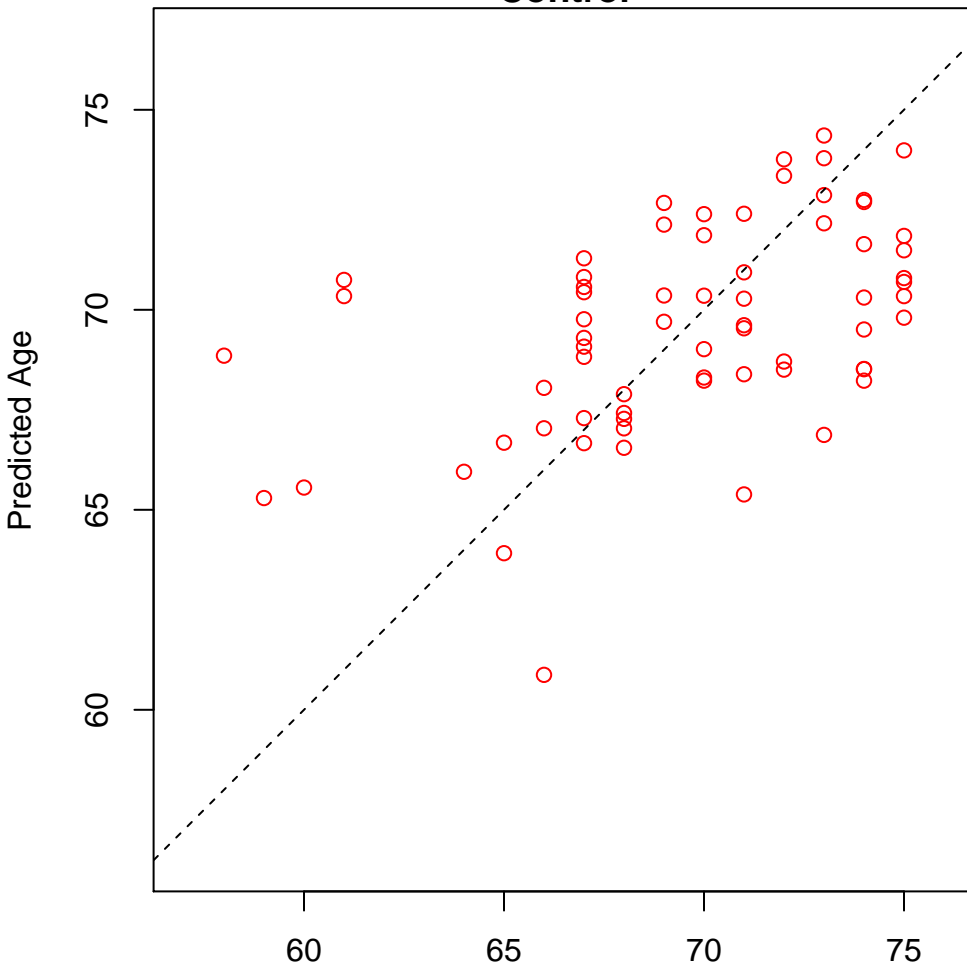


regulation of gene silencing by miRNA (Score: 0.815456)

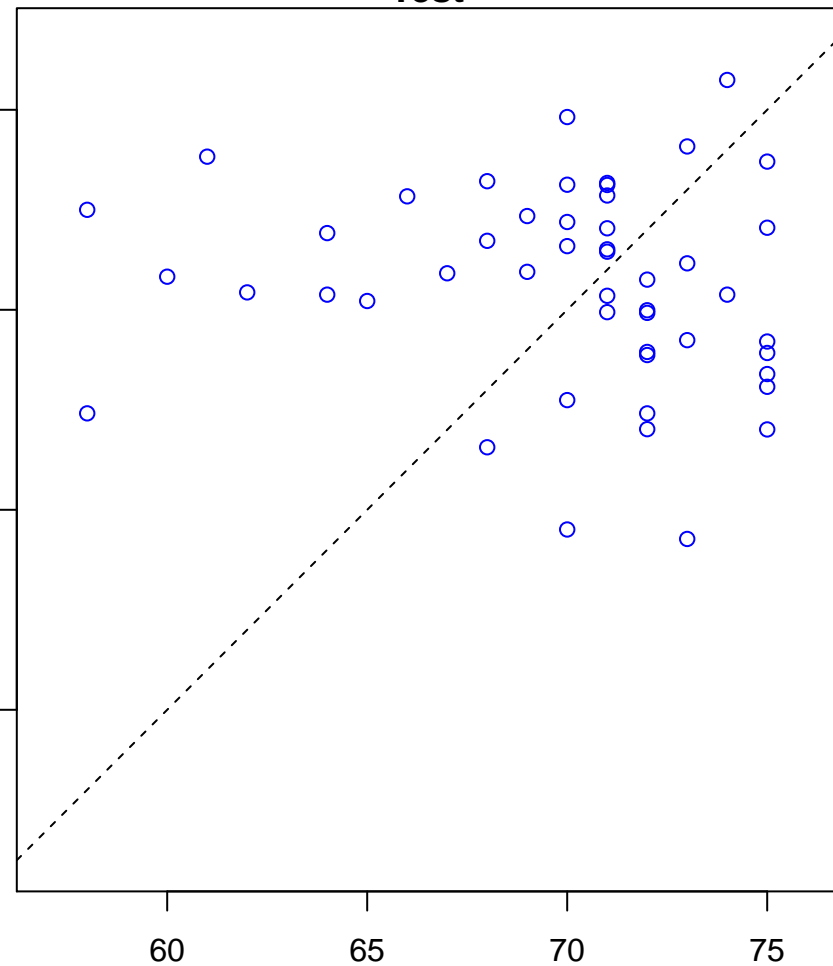


regulation of MDA-5 signaling pathway (Score: 0.815425)

Control

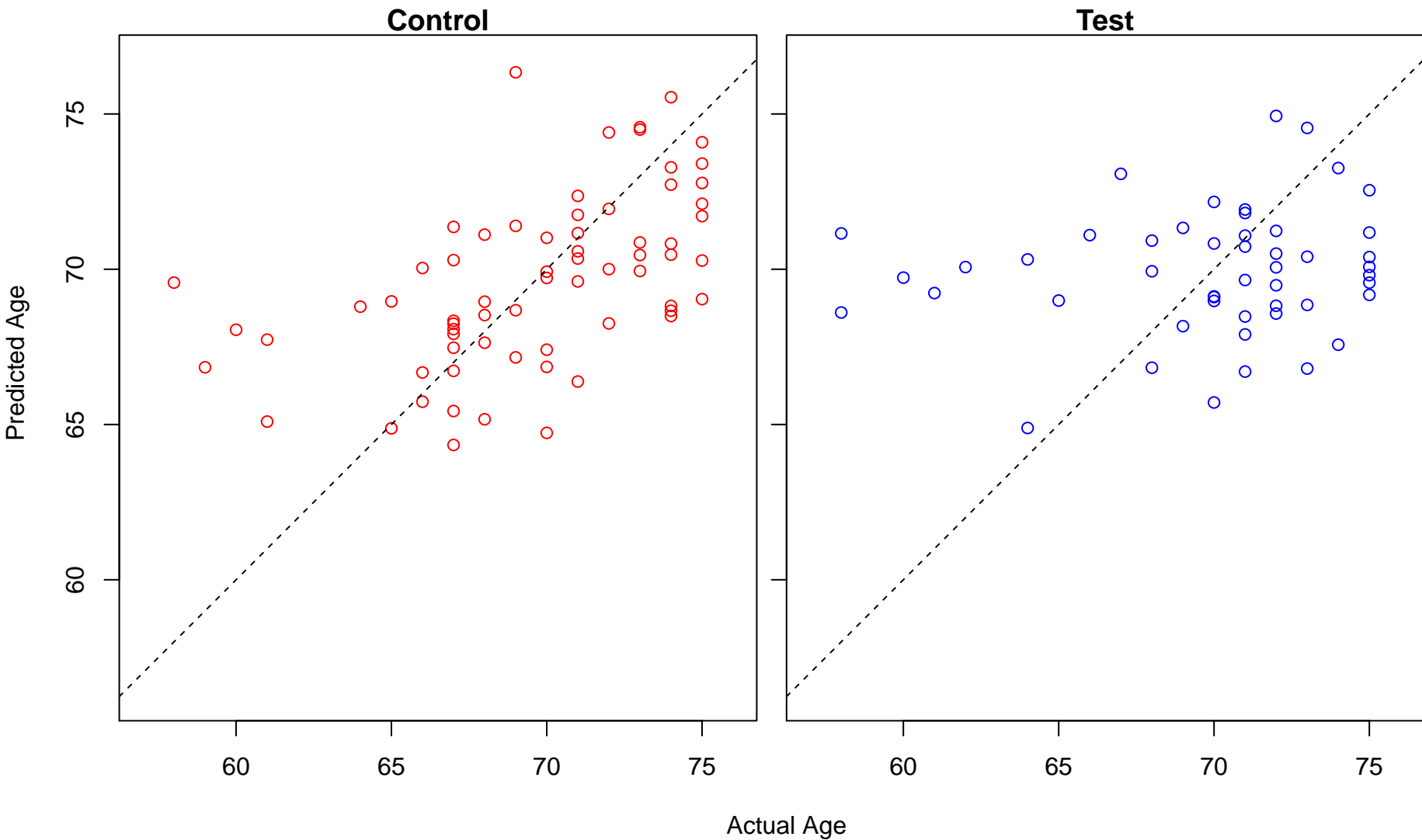


Test

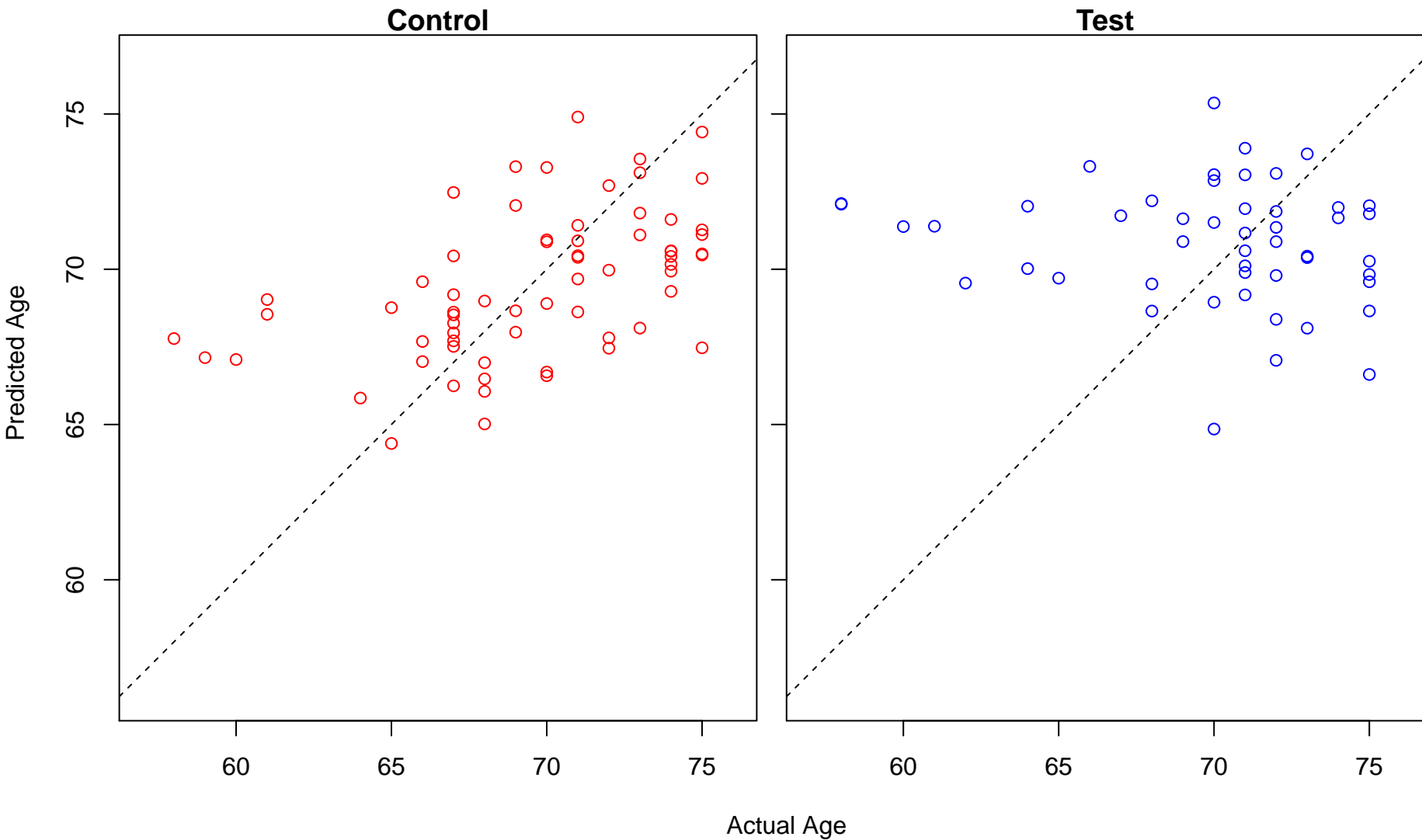


Actual Age

neutrophil mediated immunity (Score: 0.815387)

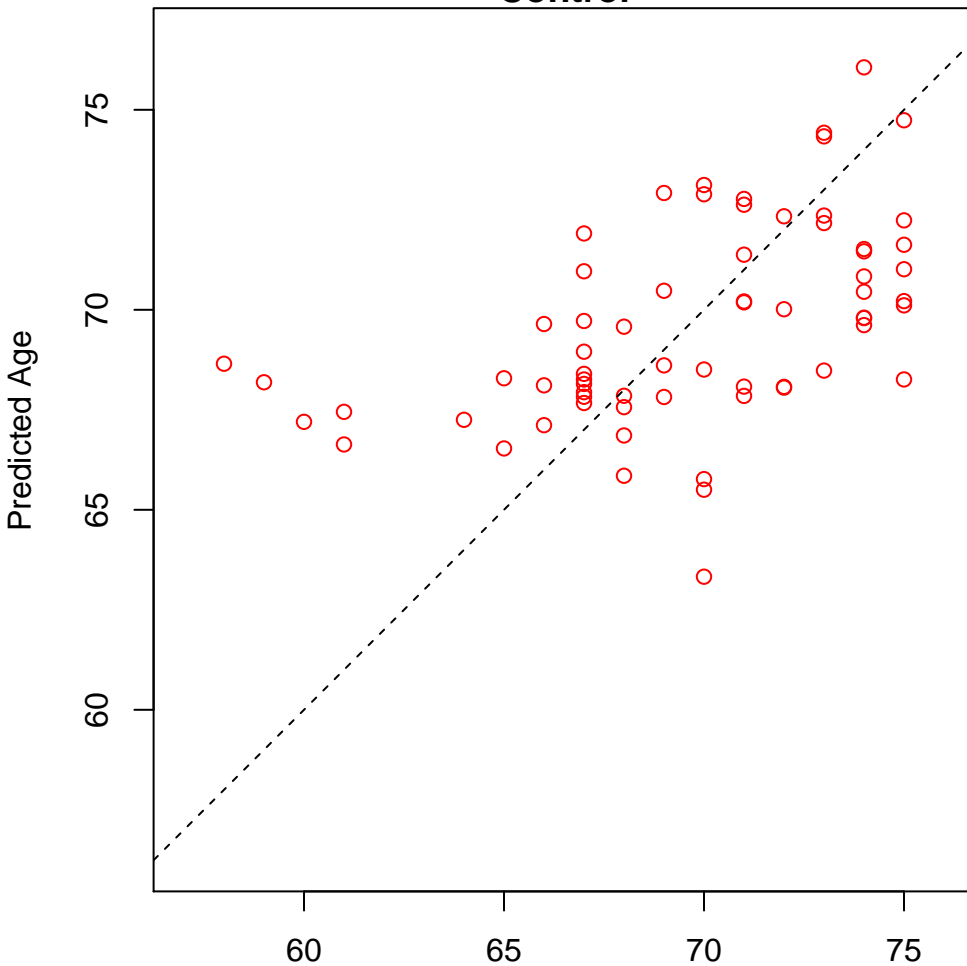


metanephros development (Score: 0.815269)

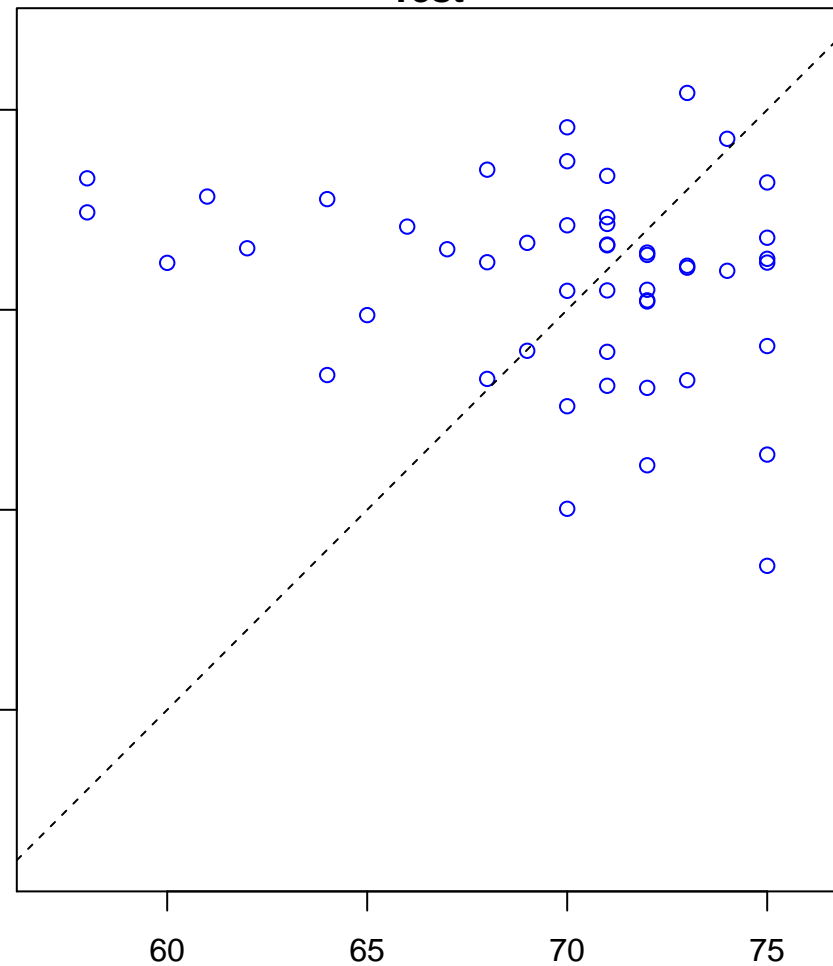


regulation of mRNA 3'-end processing (Score: 0.814594)

Control

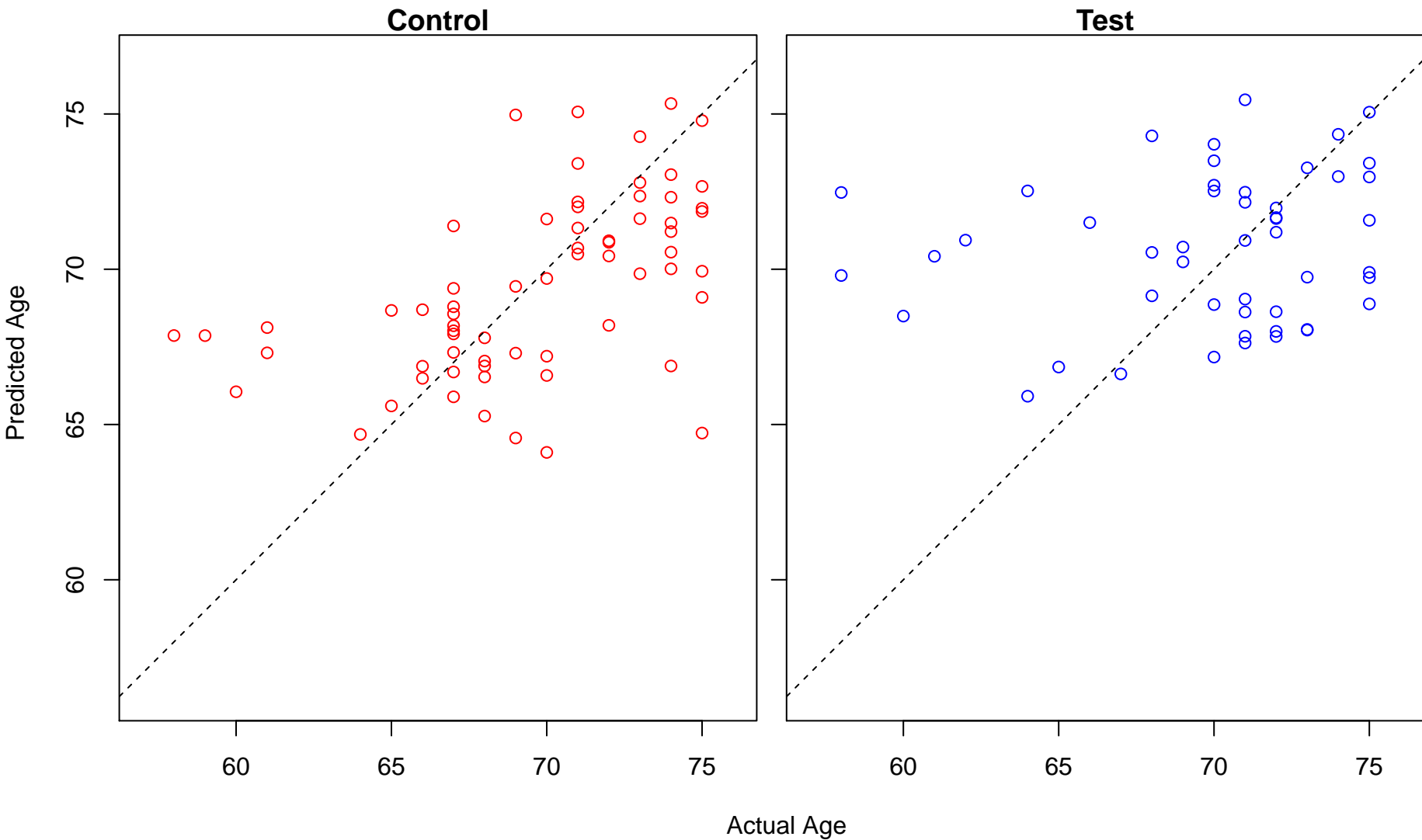


Test

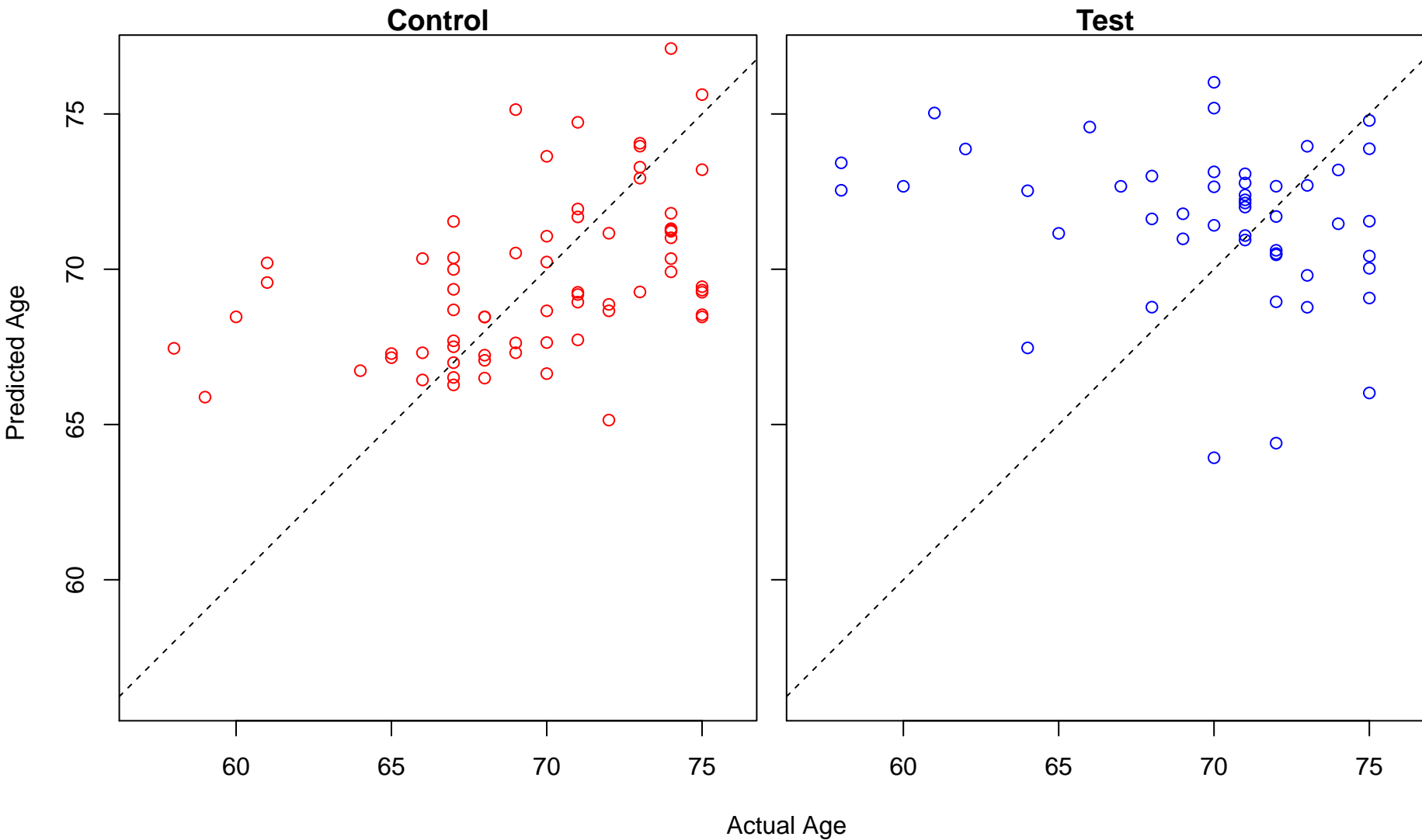


Actual Age

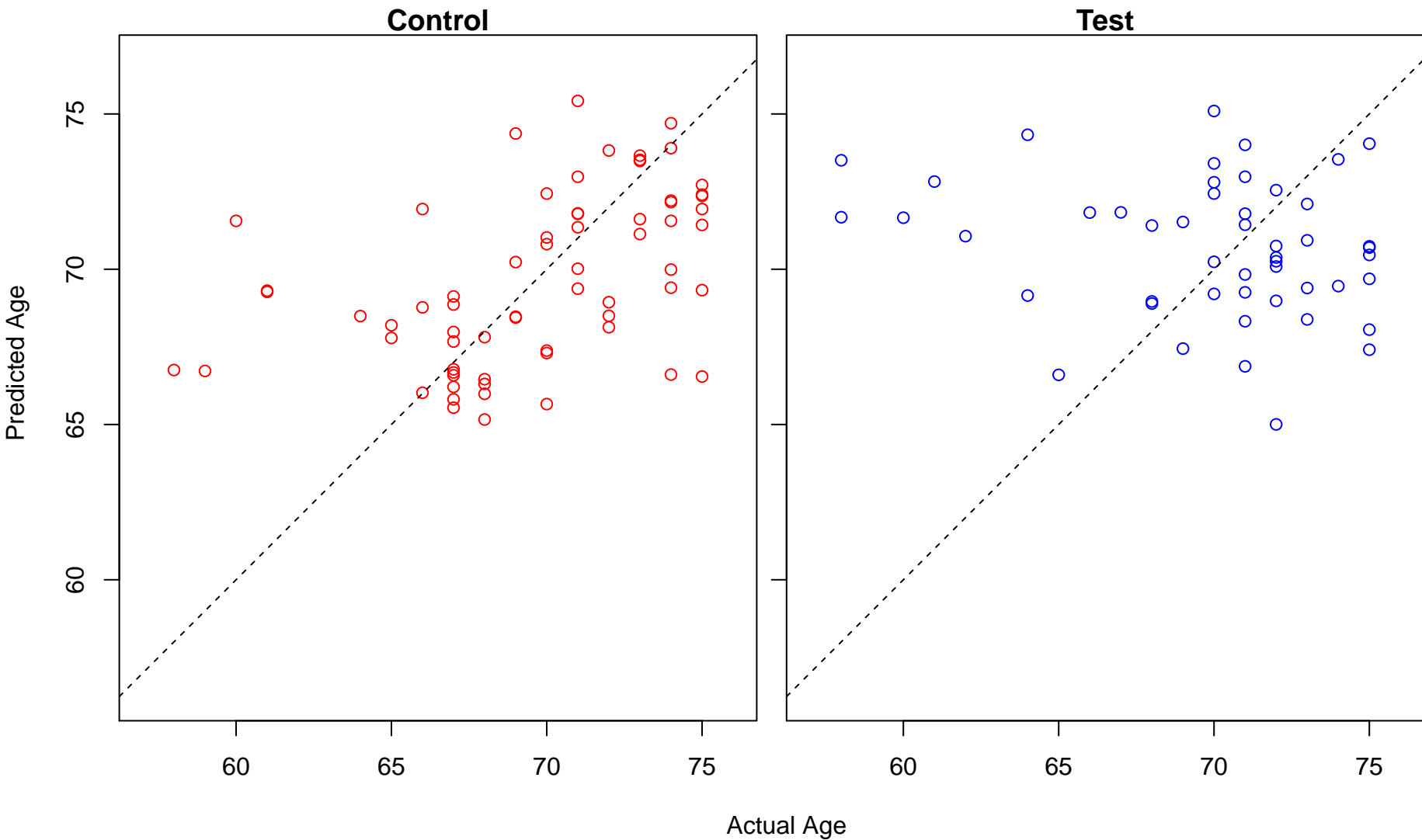
kidney epithelium development (Score: 0.813733)



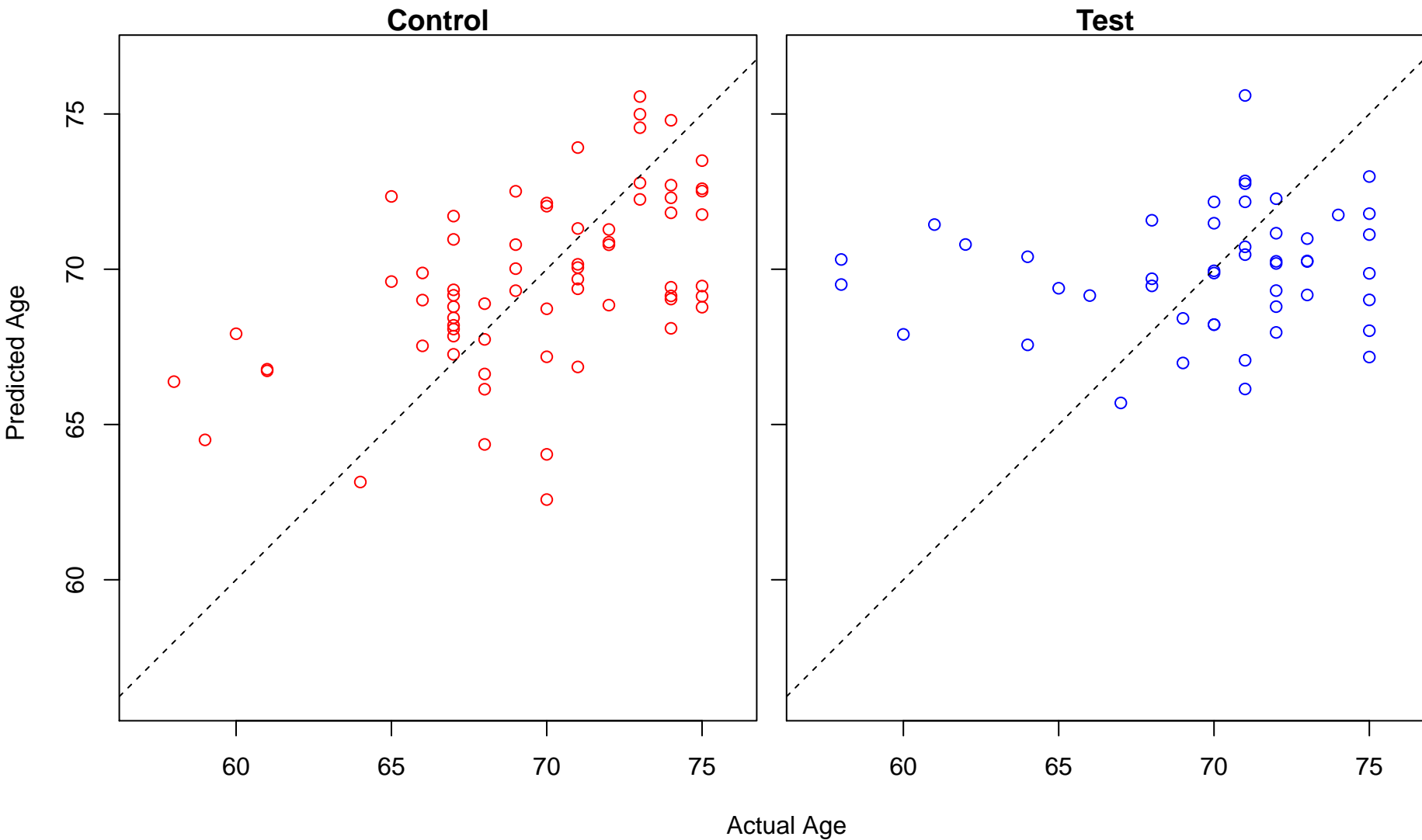
regulation of nitric-oxide synthase activity (Score: 0.812936)



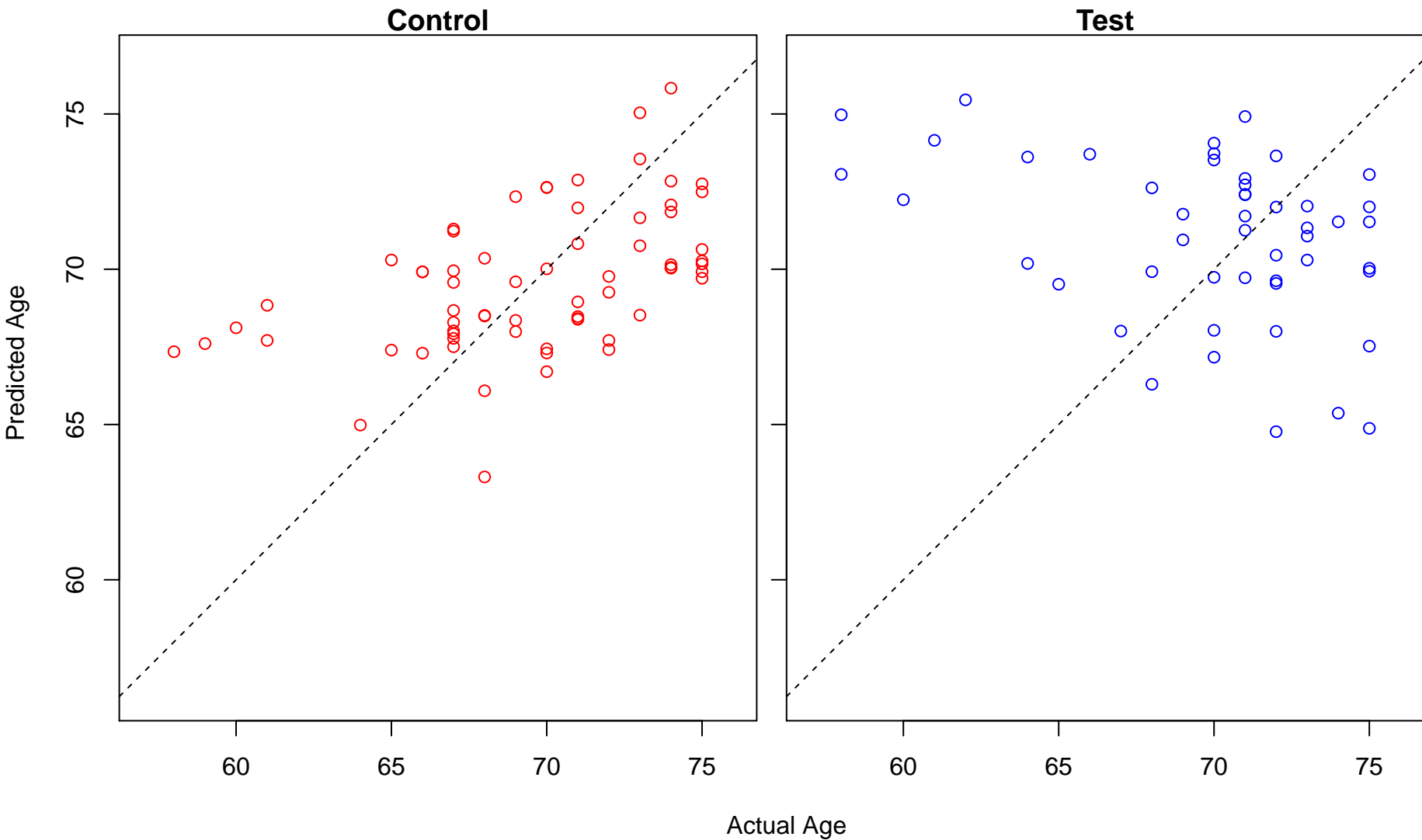
palate development (Score: 0.812729)



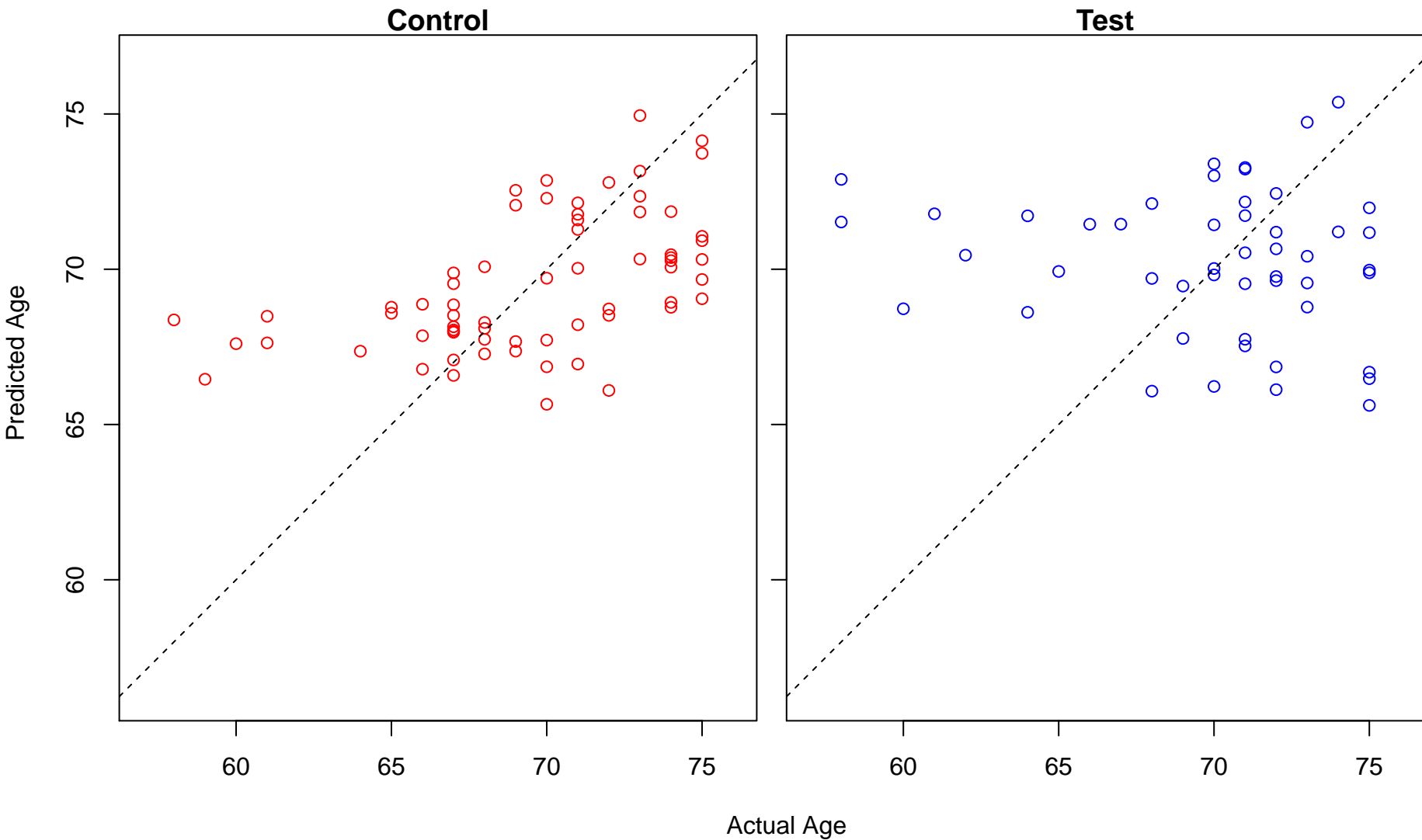
copper ion transport (Score: 0.812348)



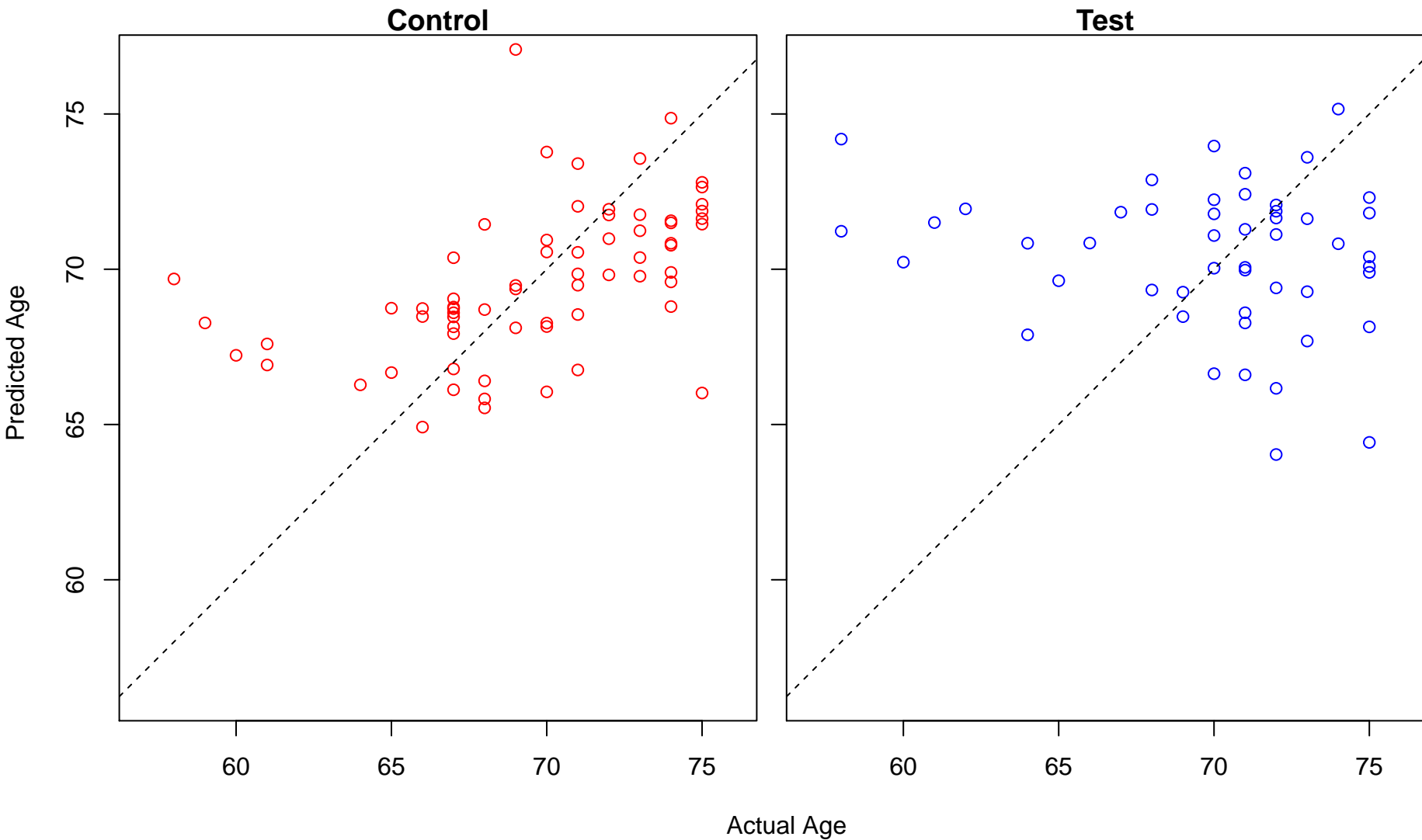
regulation of metalloendopeptidase activity (Score: 0.812081)



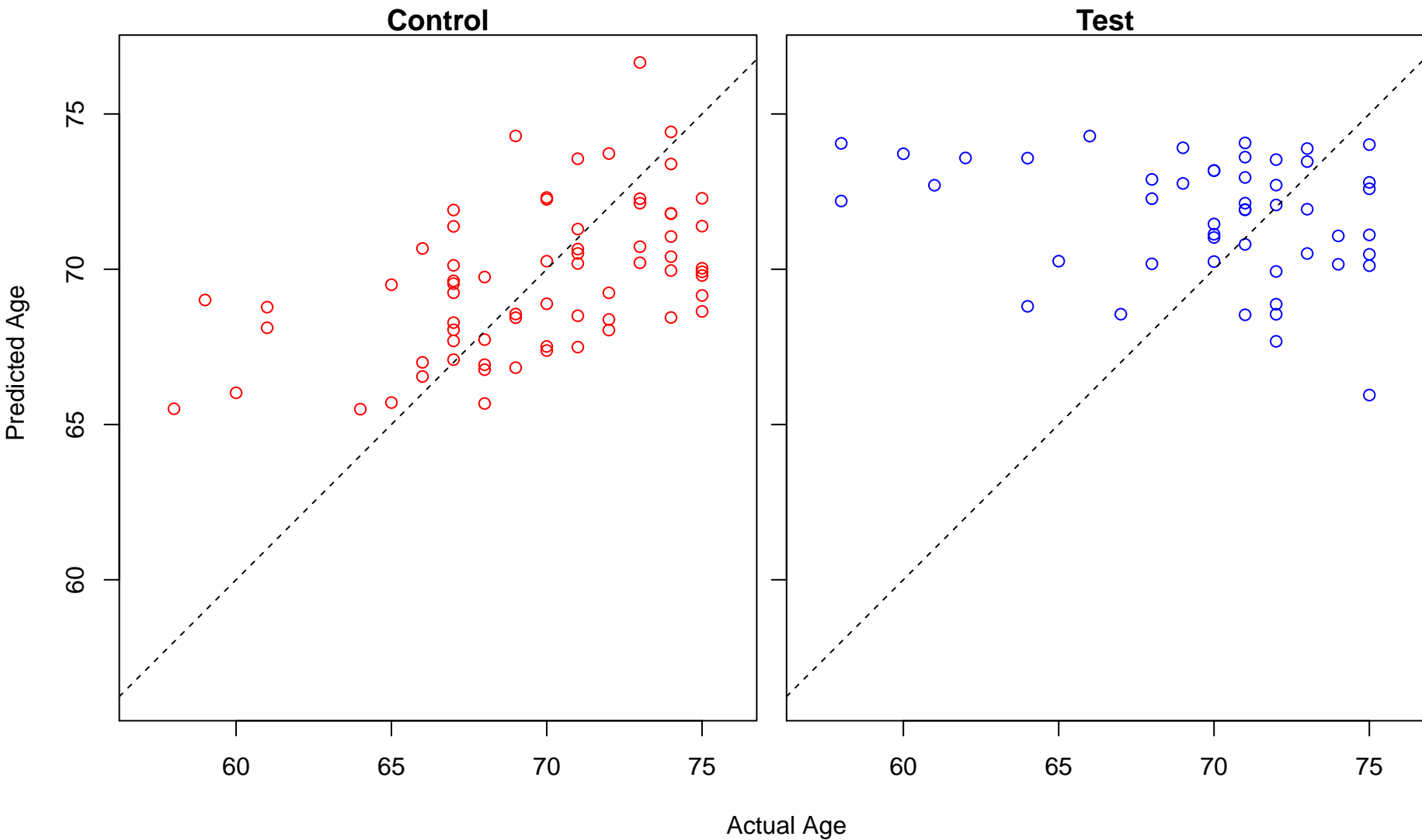
negative regulation of DNA recombination (Score: 0.811973)



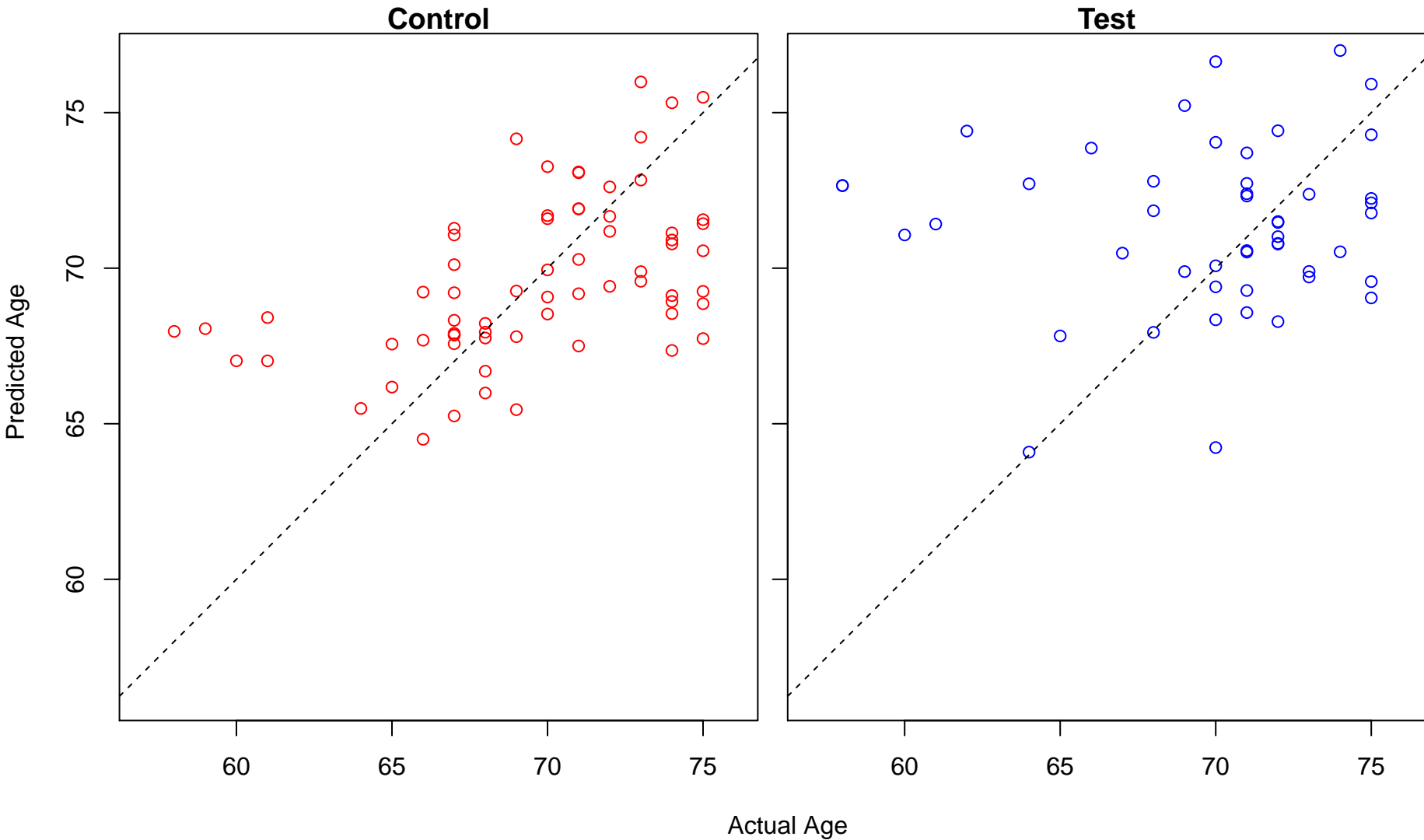
positive regulation of natural killer cell activation (Score: 0.811845)



atrioventricular valve development (Score: 0.811778)

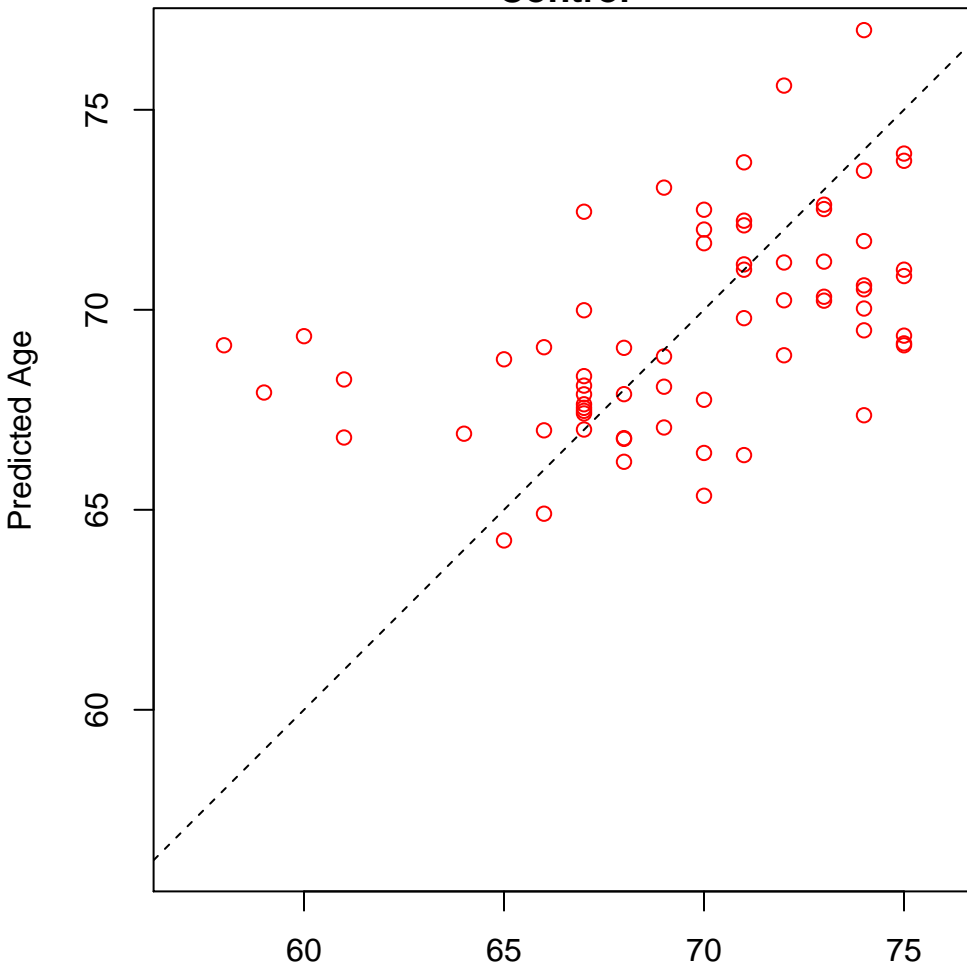


regulation of smoothened signaling pathway (Score: 0.811731)

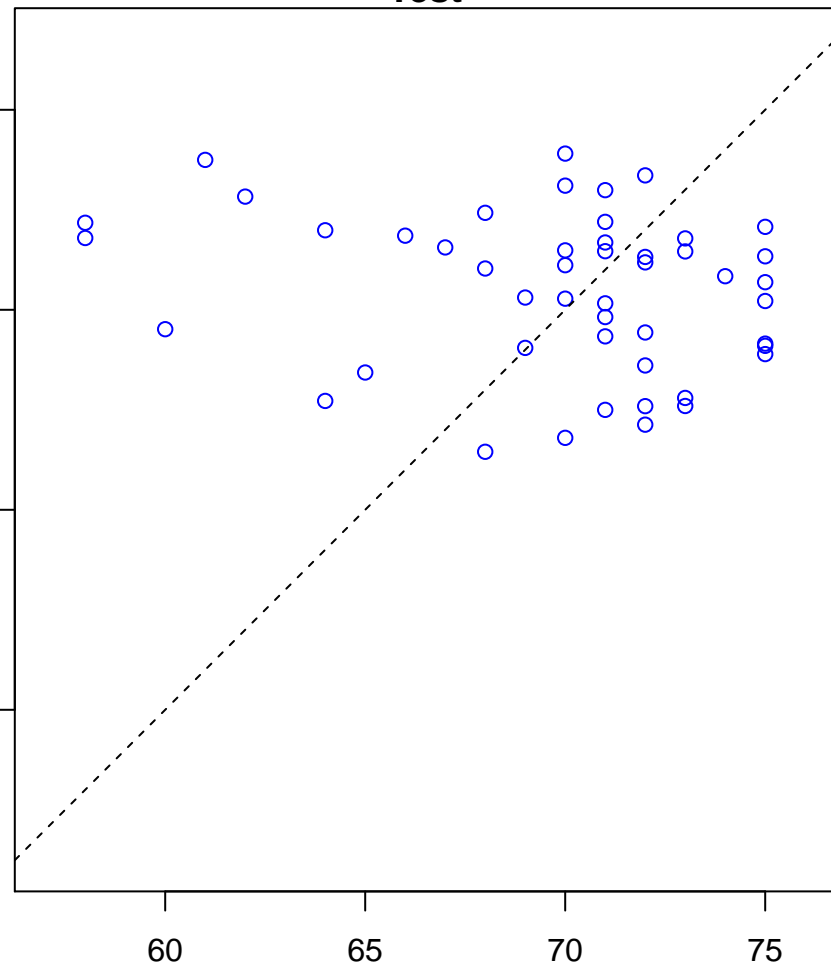


regulation of interleukin-6 production (Score: 0.811241)

Control

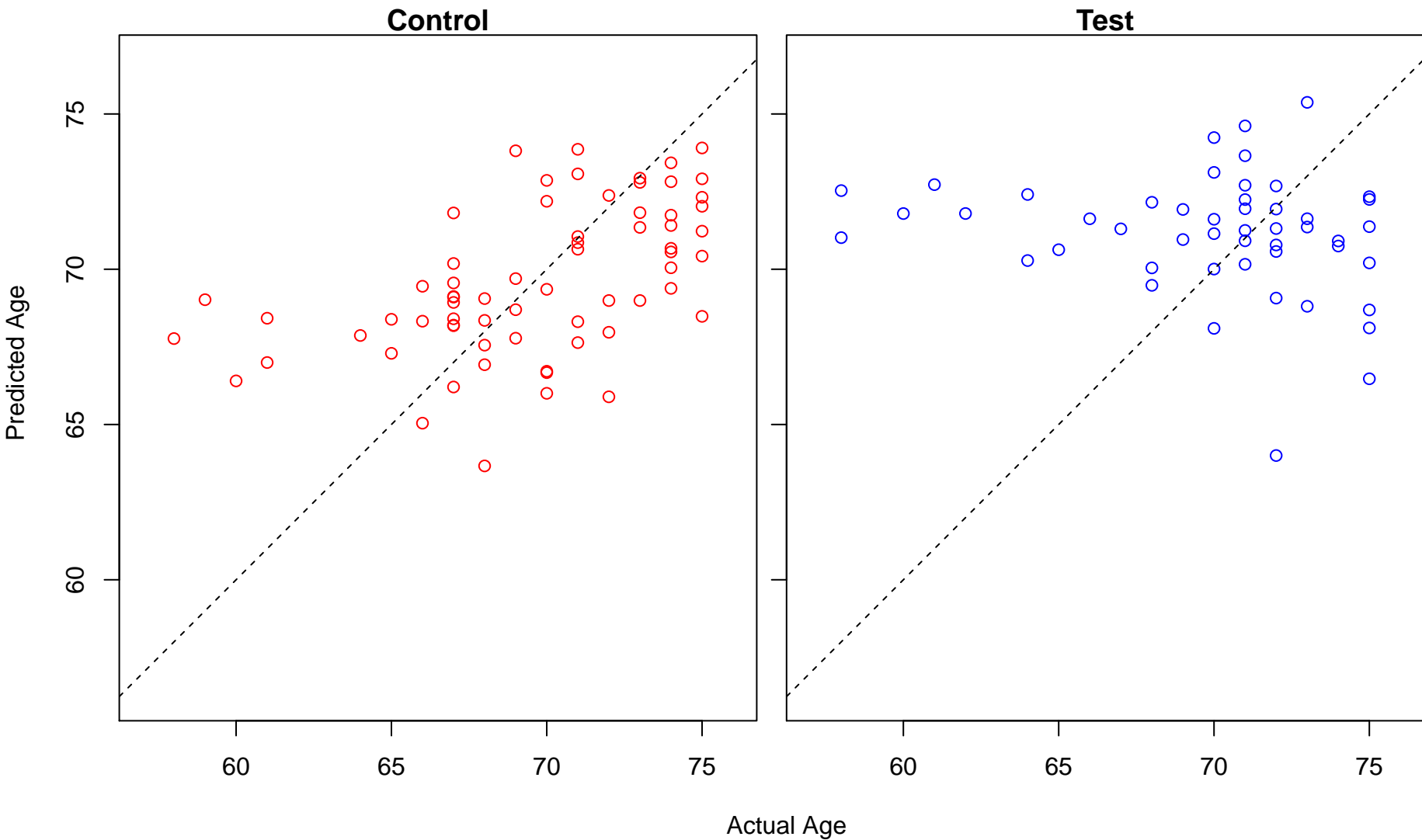


Test

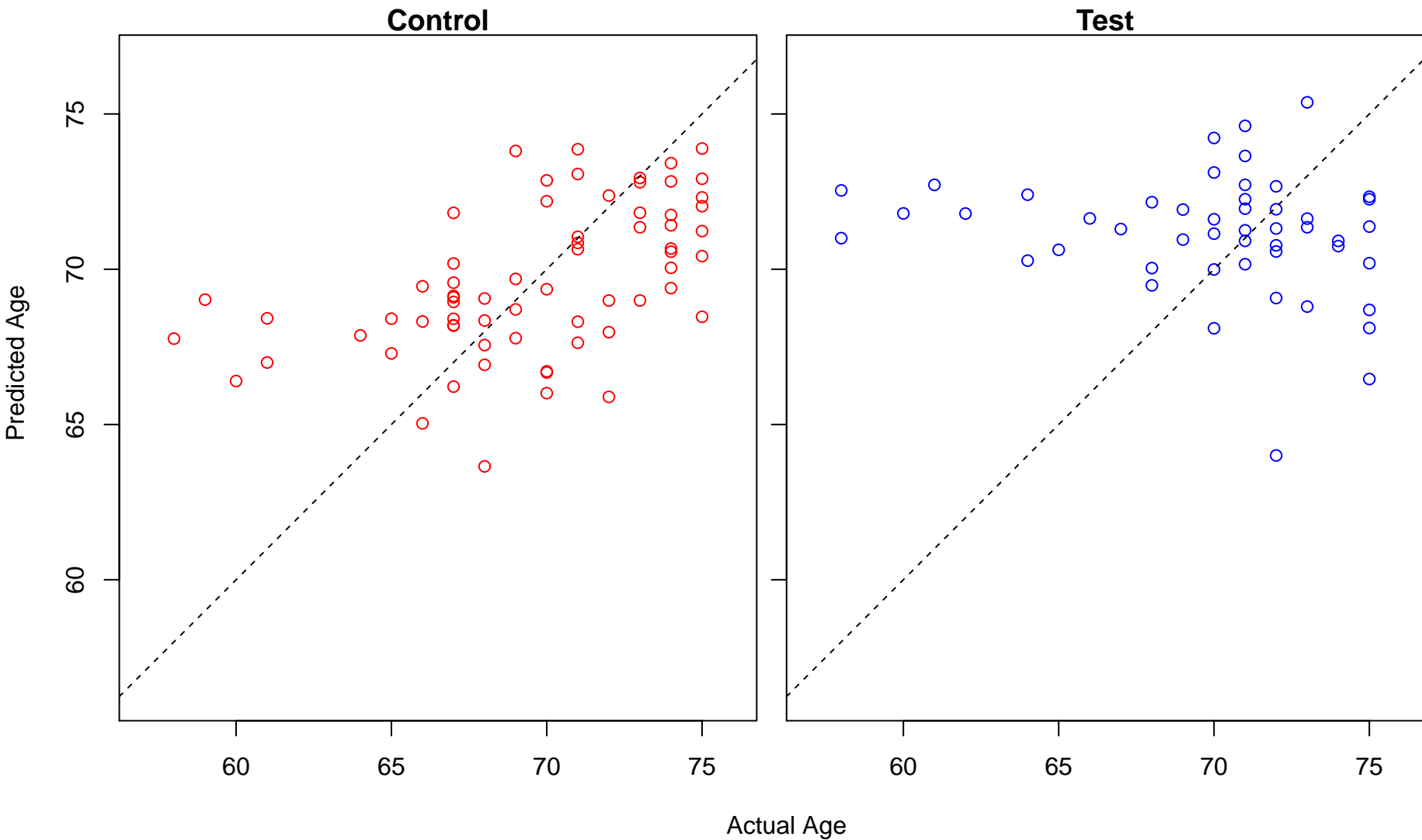


Actual Age

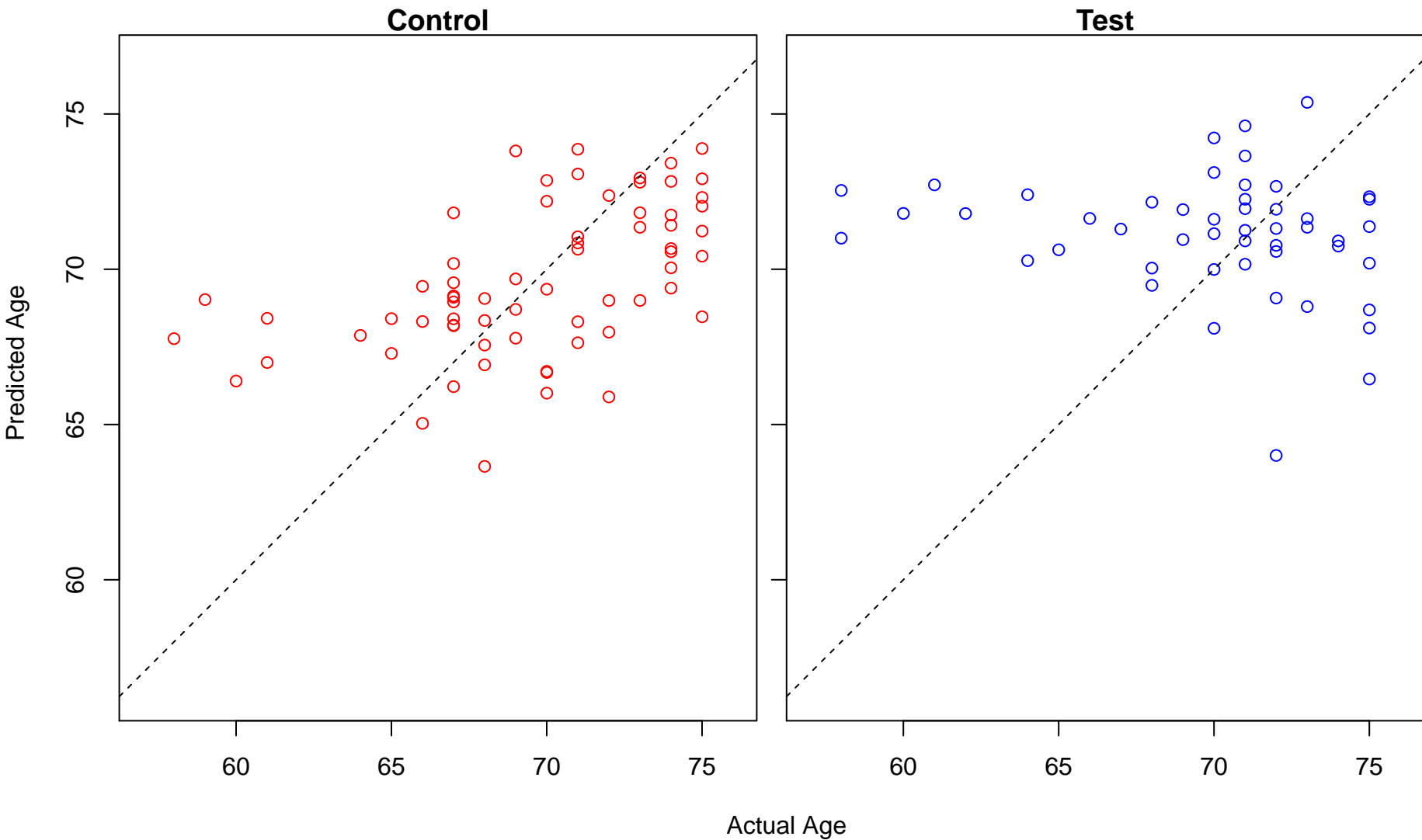
L-methionine biosynthetic process from methylthioadenosine (Score: 0.811096)



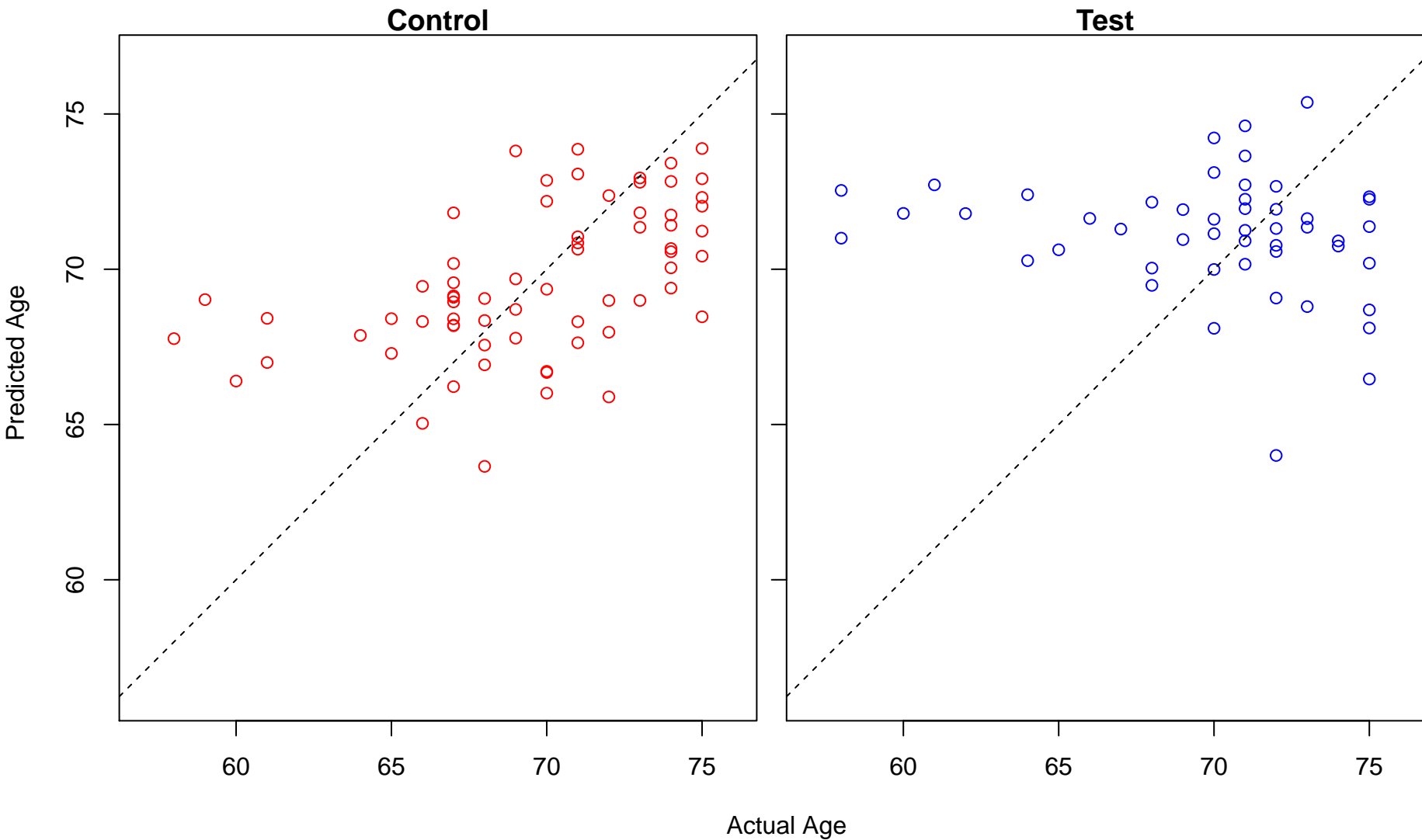
amino acid salvage (Score: 0.810630)



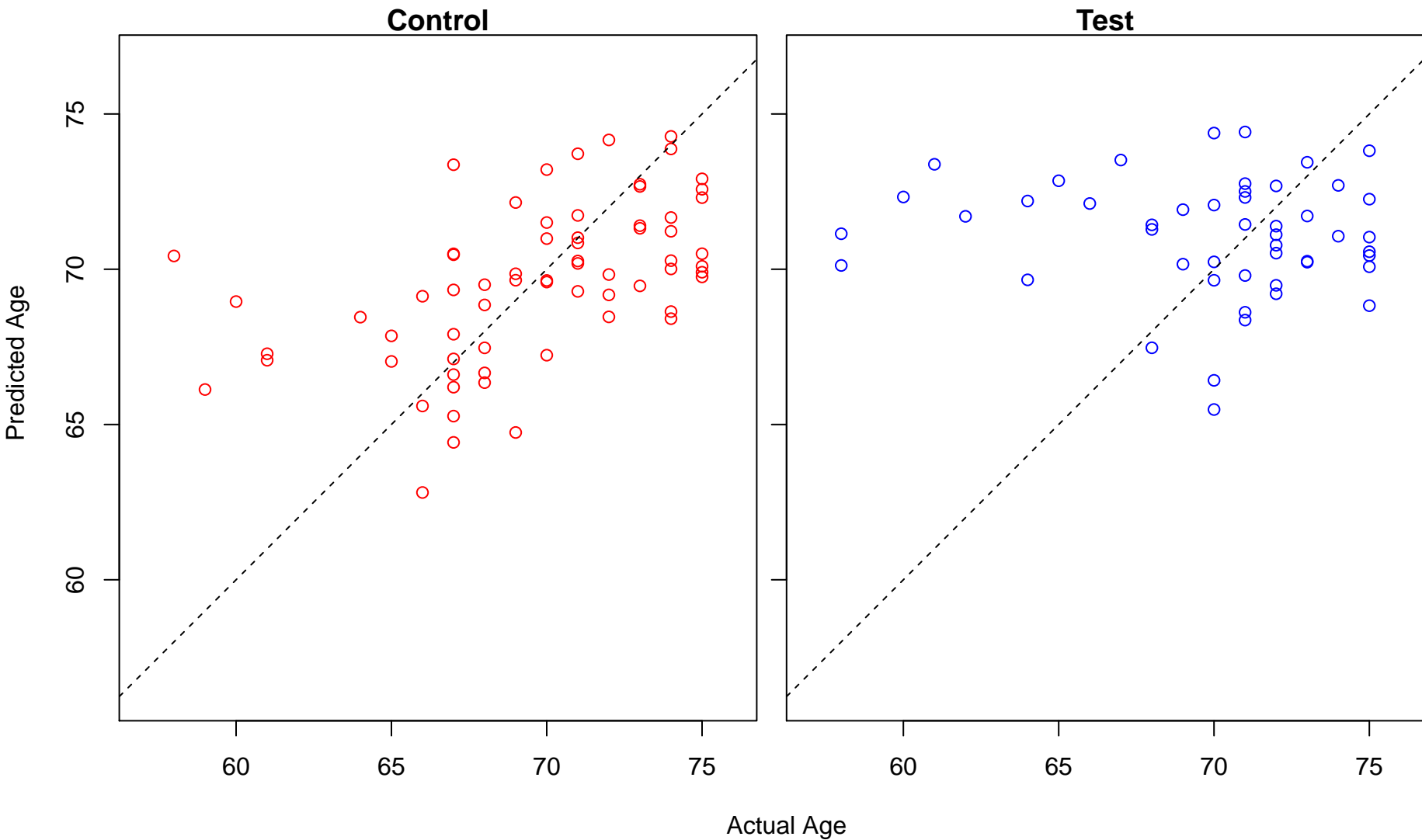
L-methionine biosynthetic process (Score: 0.810630)



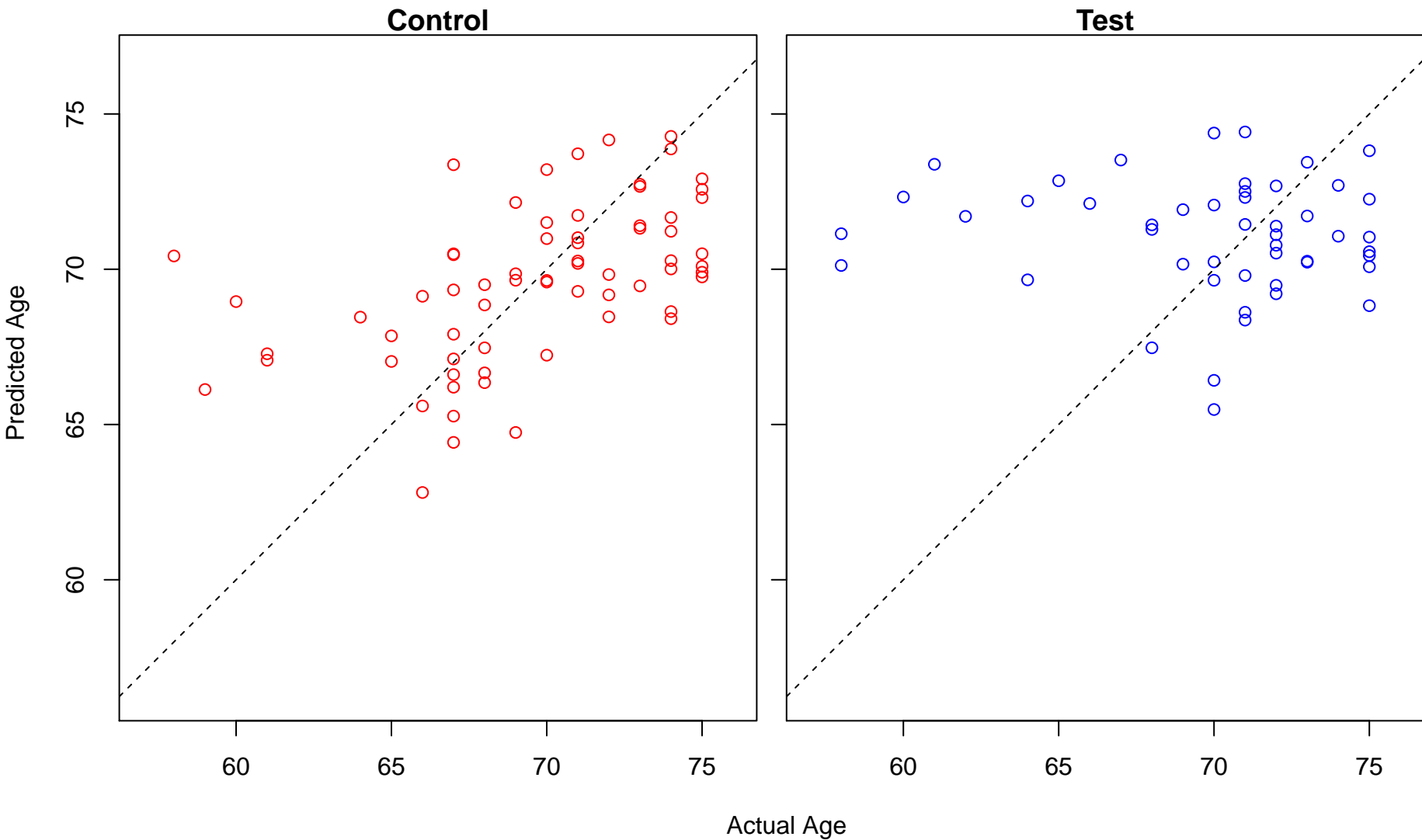
L-methionine salvage (Score: 0.810630)



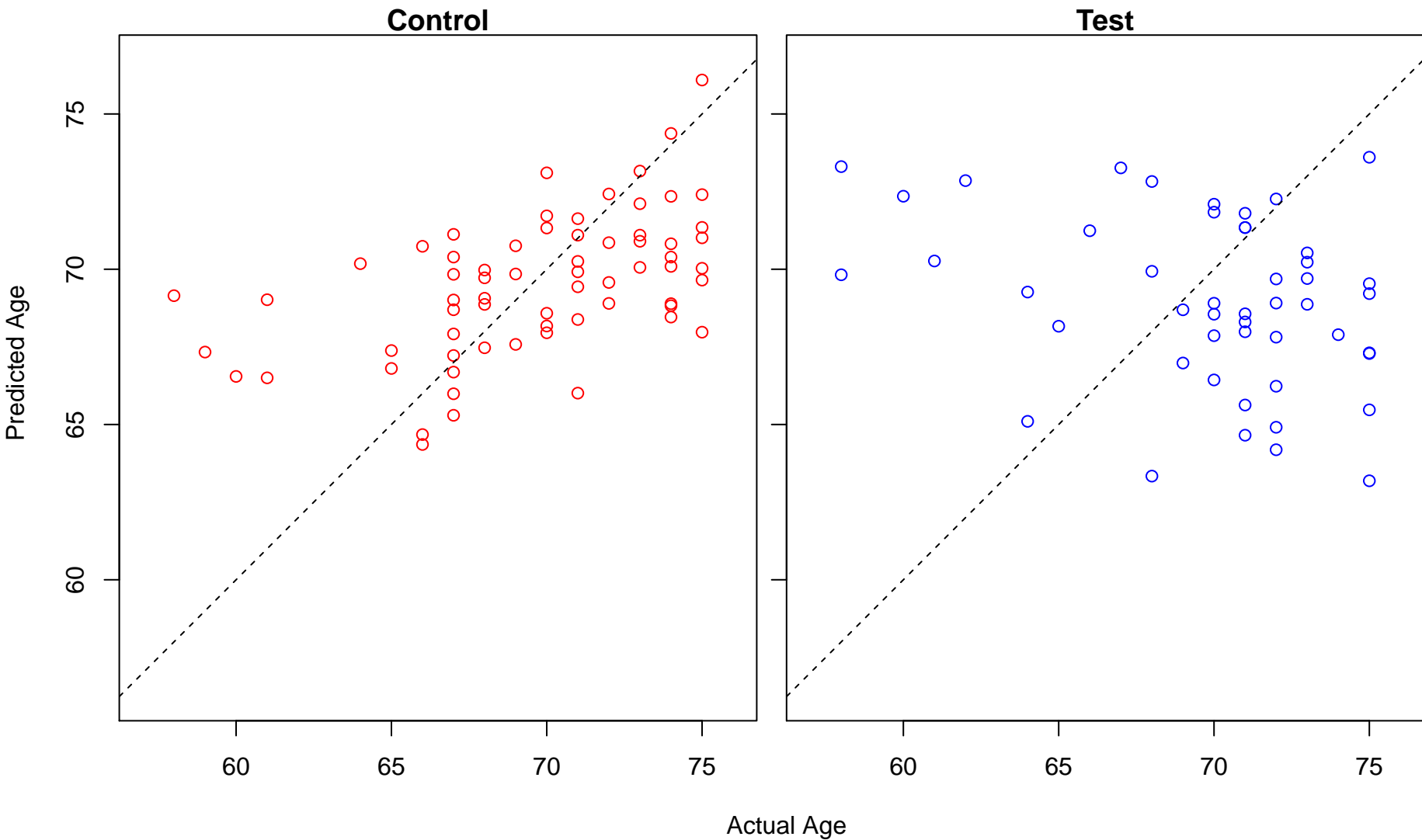
reciprocal meiotic recombination (Score: 0.810426)



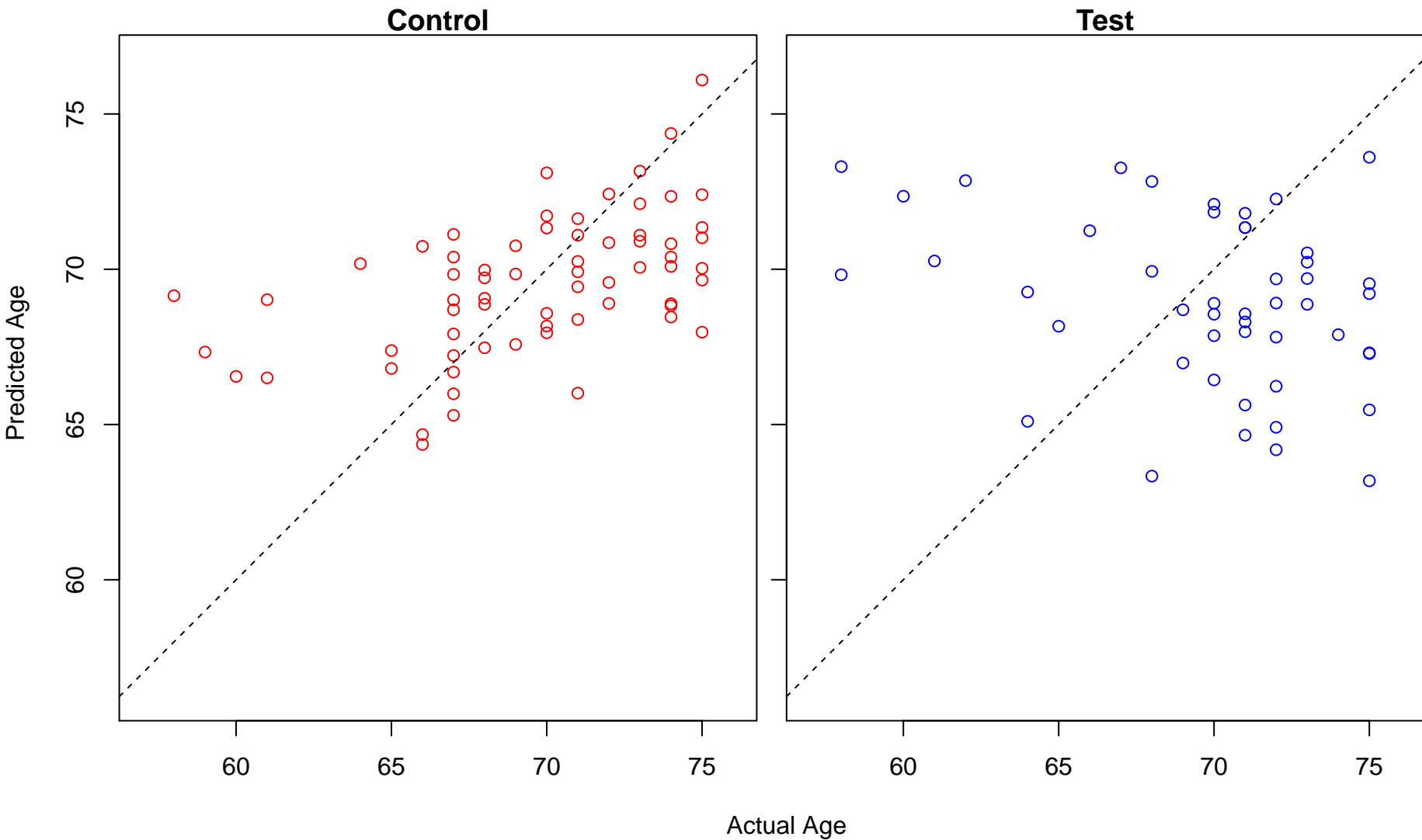
reciprocal DNA recombination (Score: 0.810426)



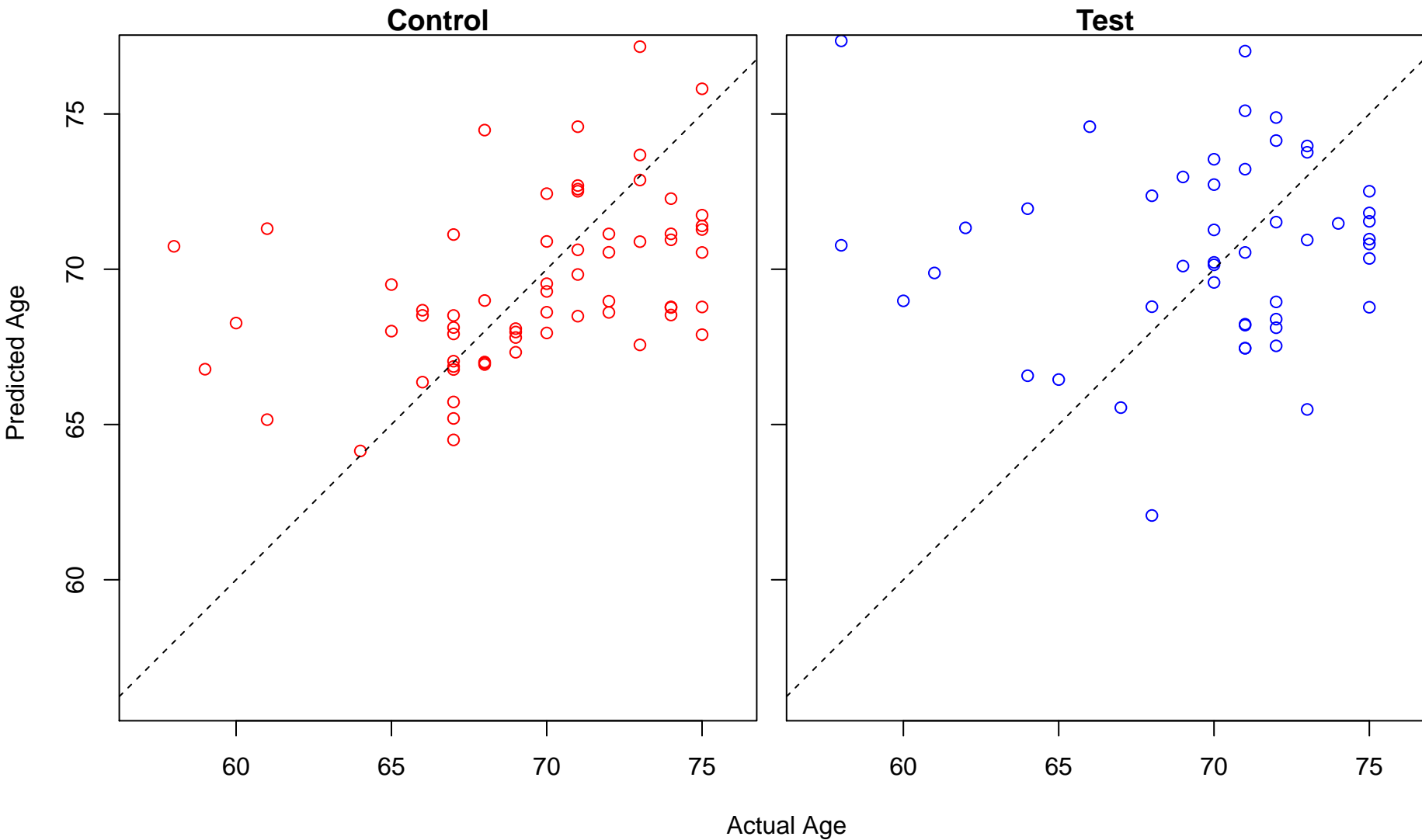
MHC protein complex assembly (Score: 0.809754)



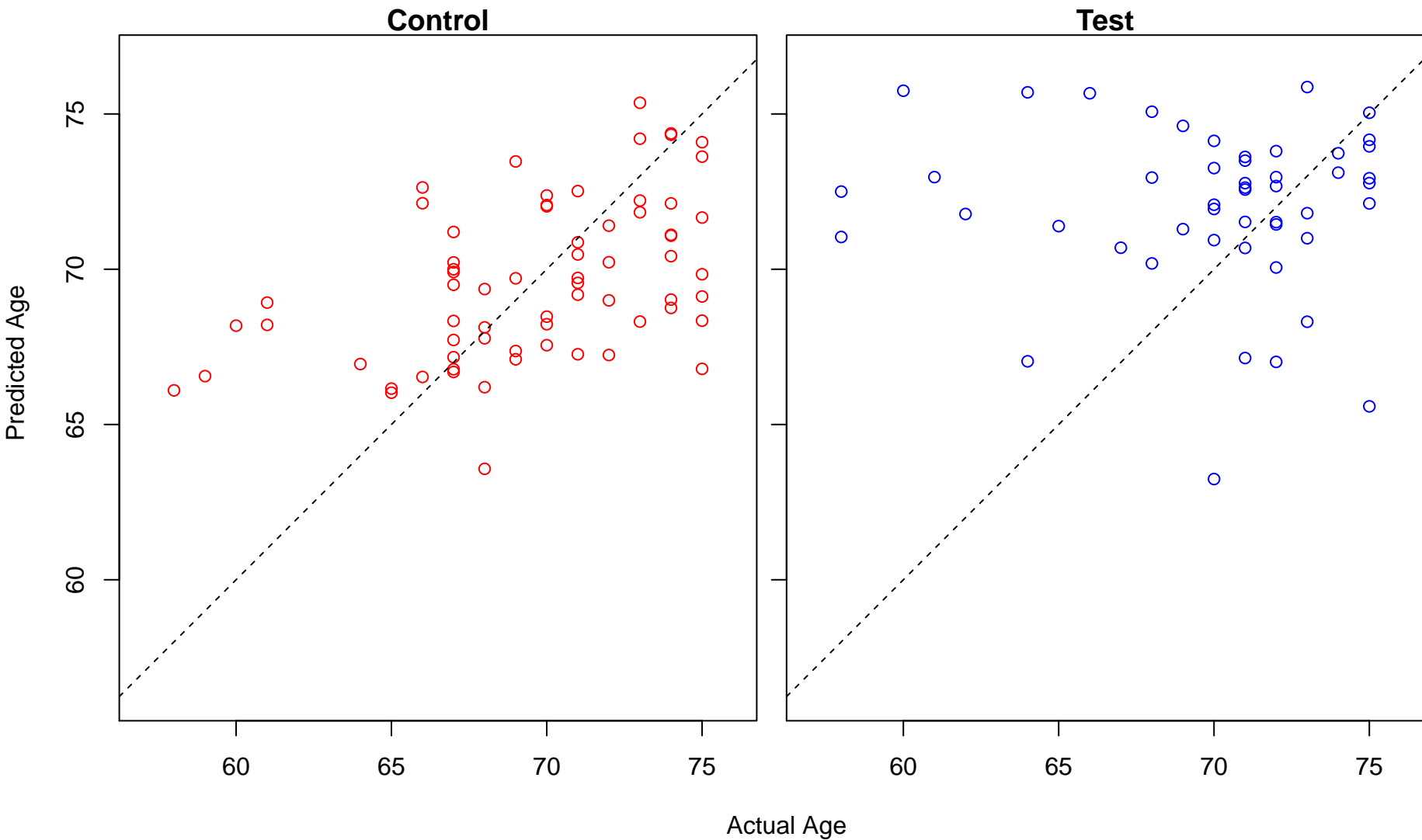
peptide antigen assembly with MHC protein complex (Score: 0.809754)



regulation of neuroblast proliferation (Score: 0.809248)

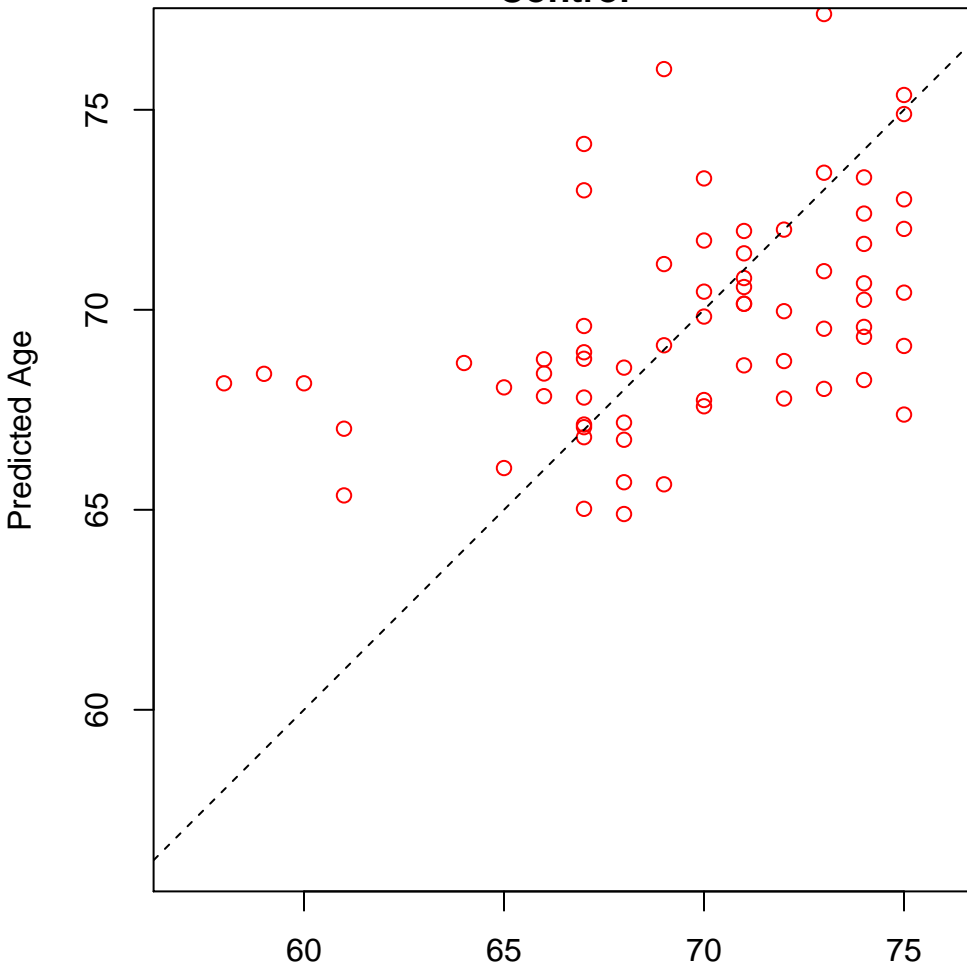


positive regulation of glycogen metabolic process (Score: 0.808925)

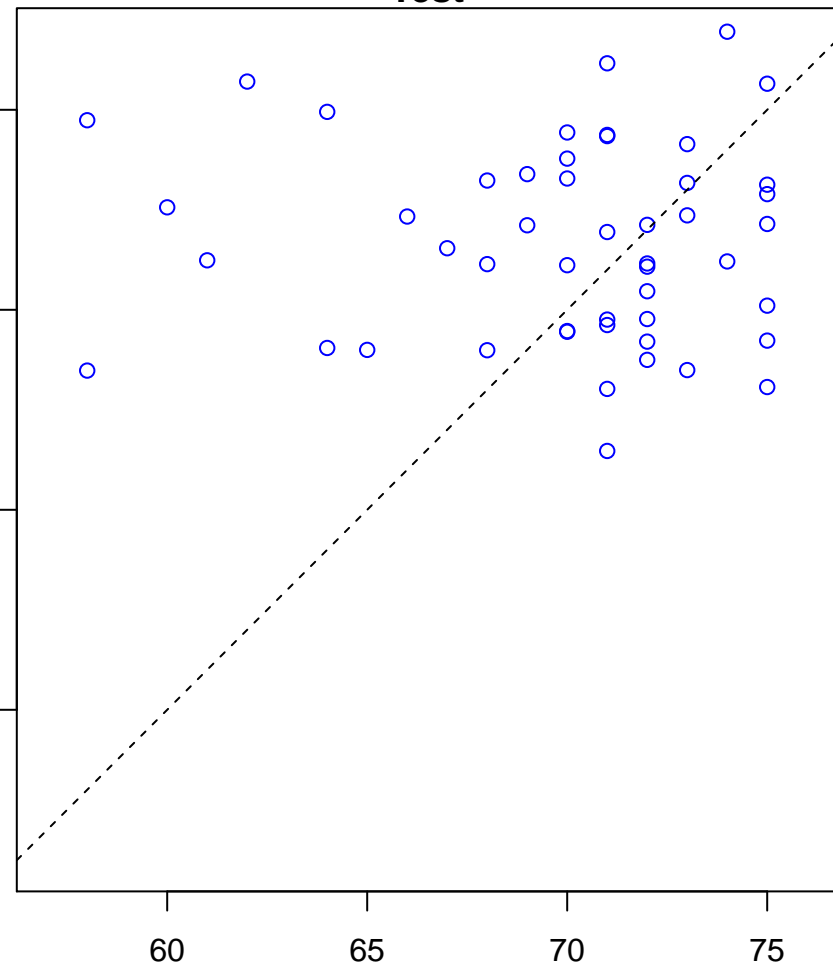


peripheral nervous system development (Score: 0.808674)

Control

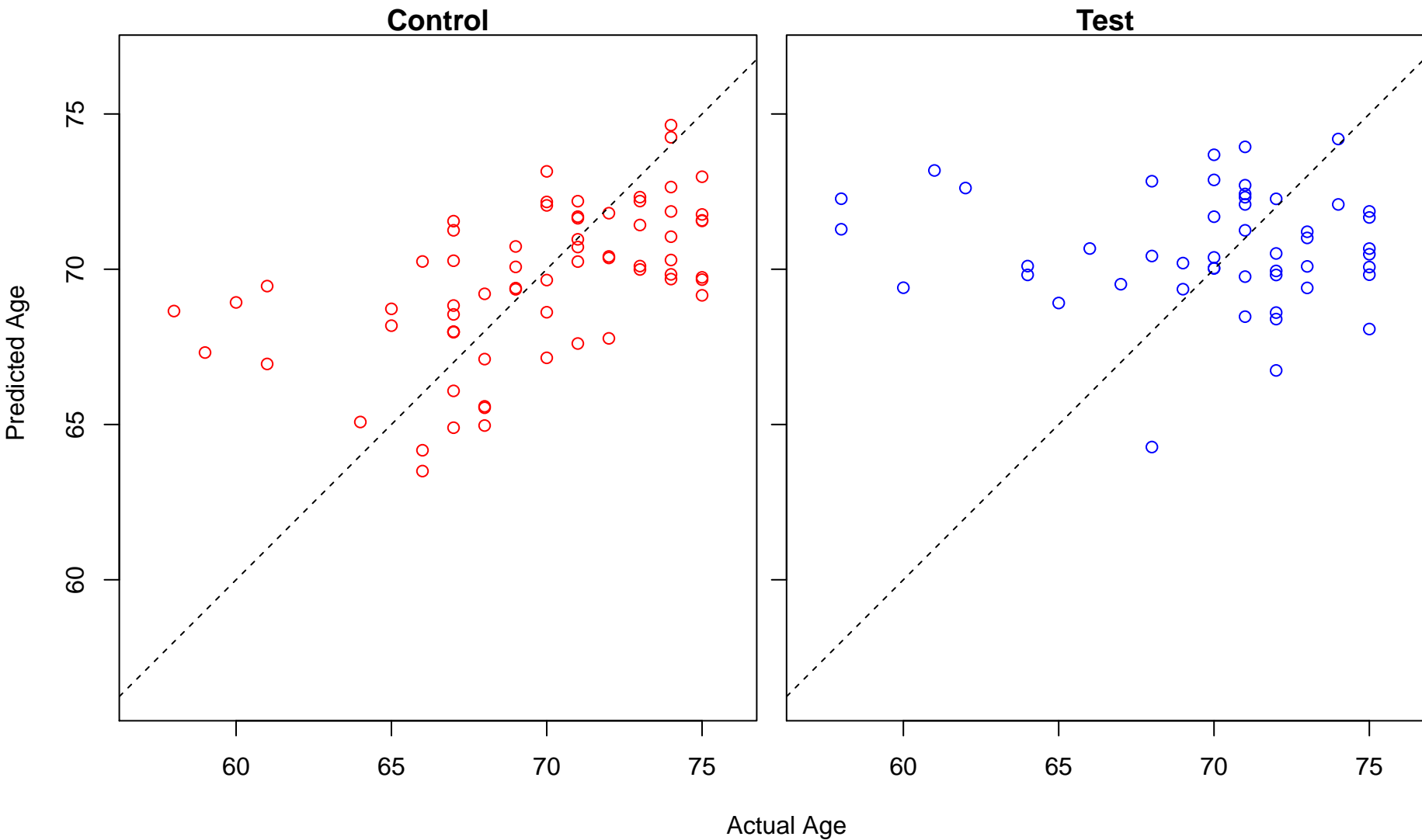


Test

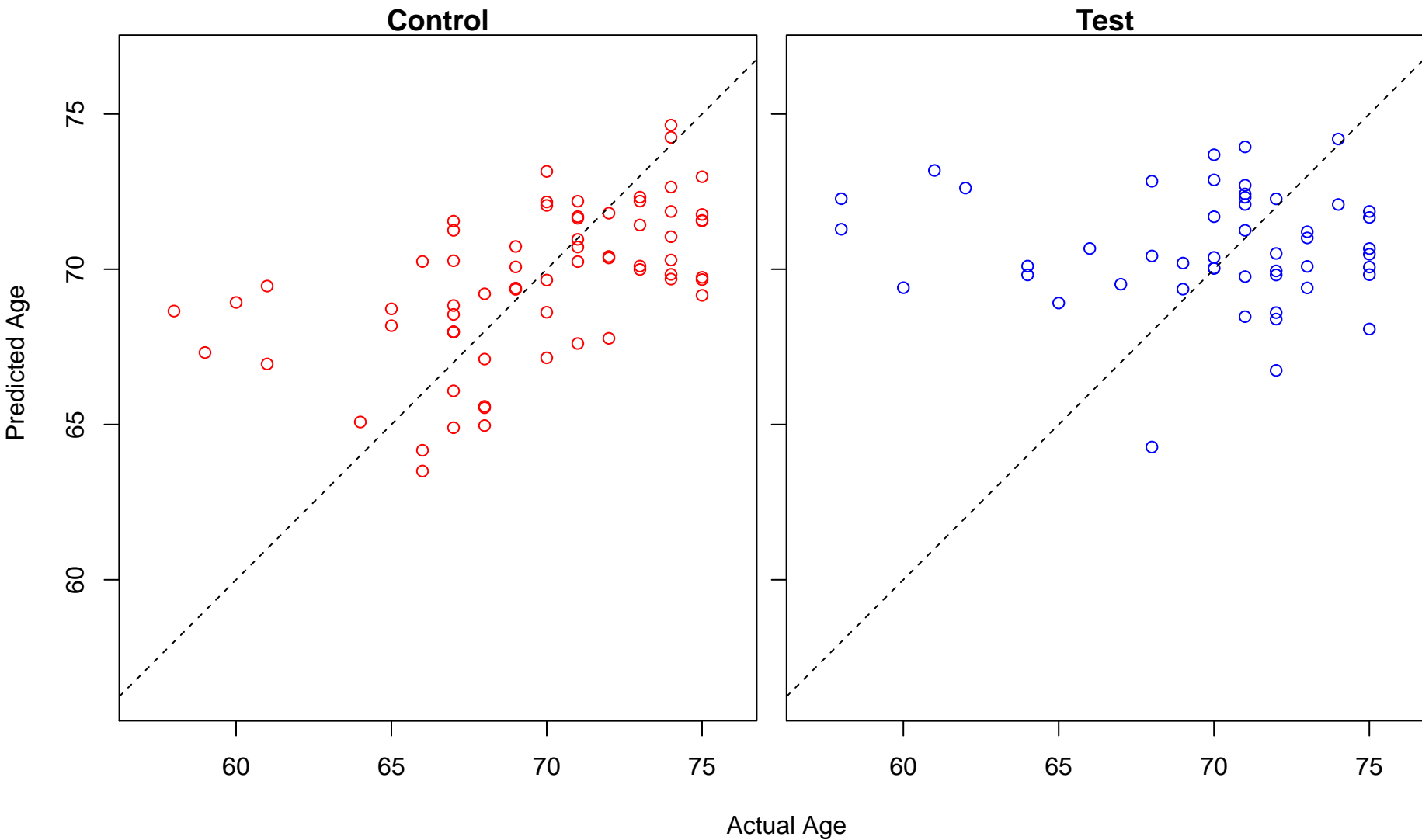


Actual Age

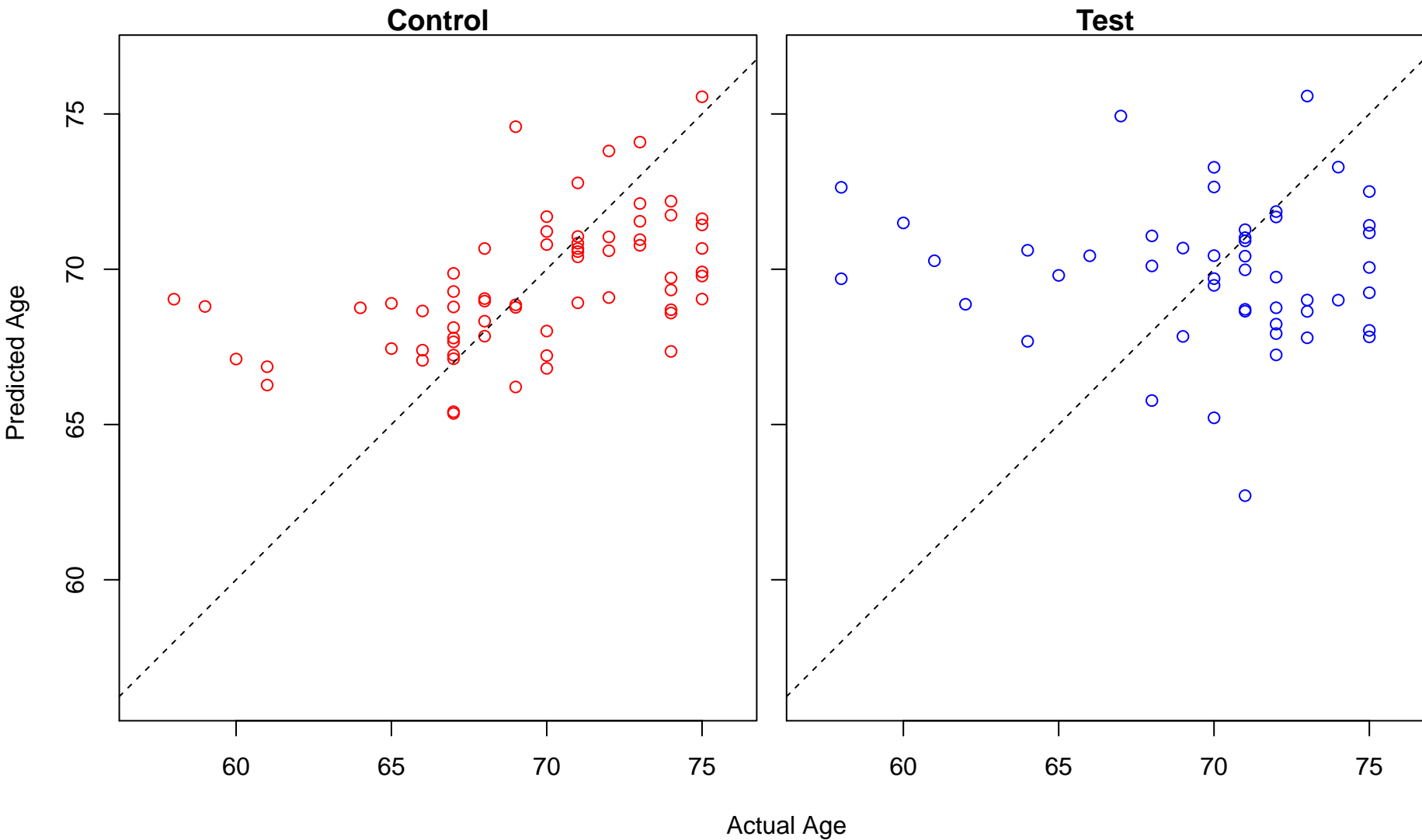
regulation of skeletal muscle satellite cell proliferation (Score: 0.807917)



regulation of skeletal muscle cell proliferation (Score: 0.807917)

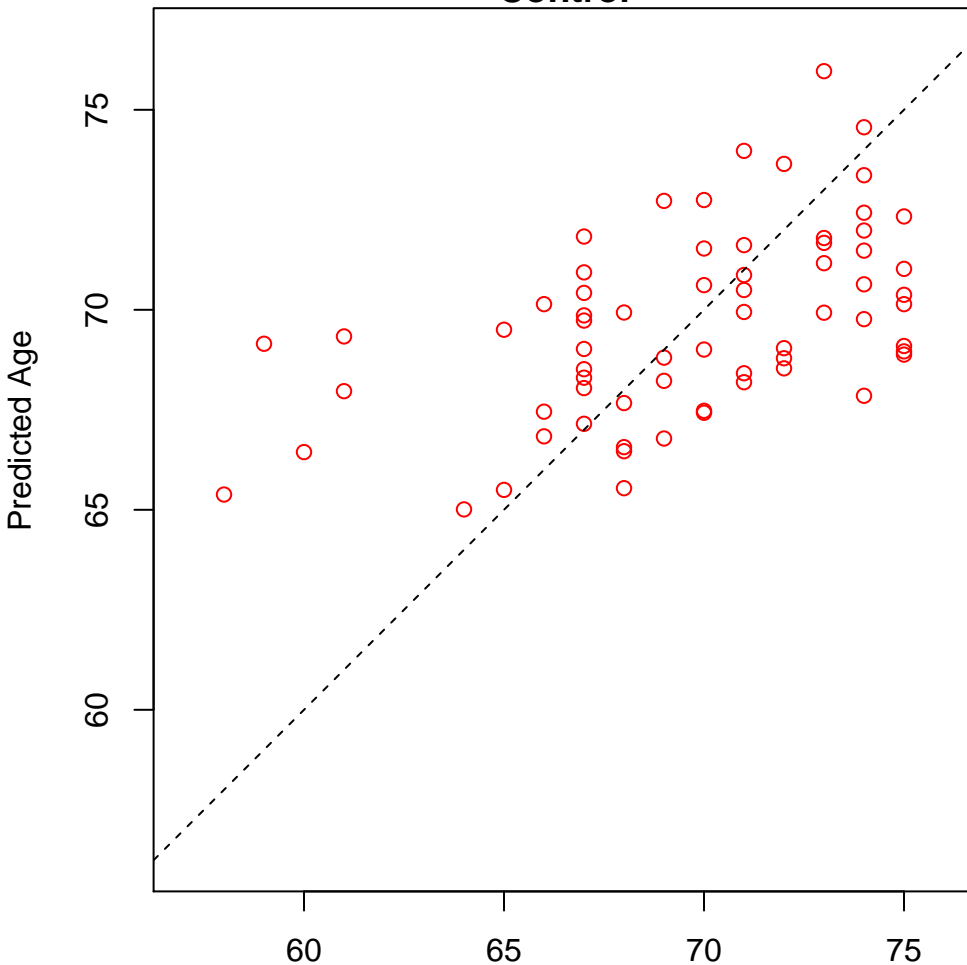


activation of anaphase-promoting complex activity (Score: 0.807572)

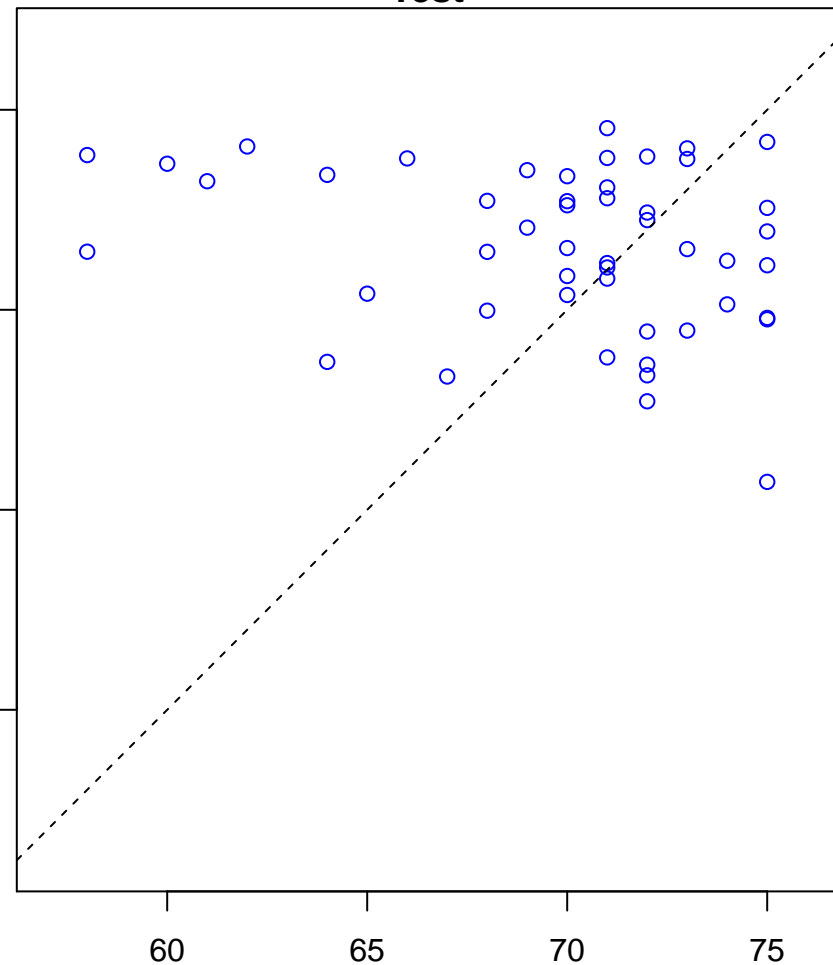


cardiac endothelial cell differentiation (Score: 0.807024)

Control

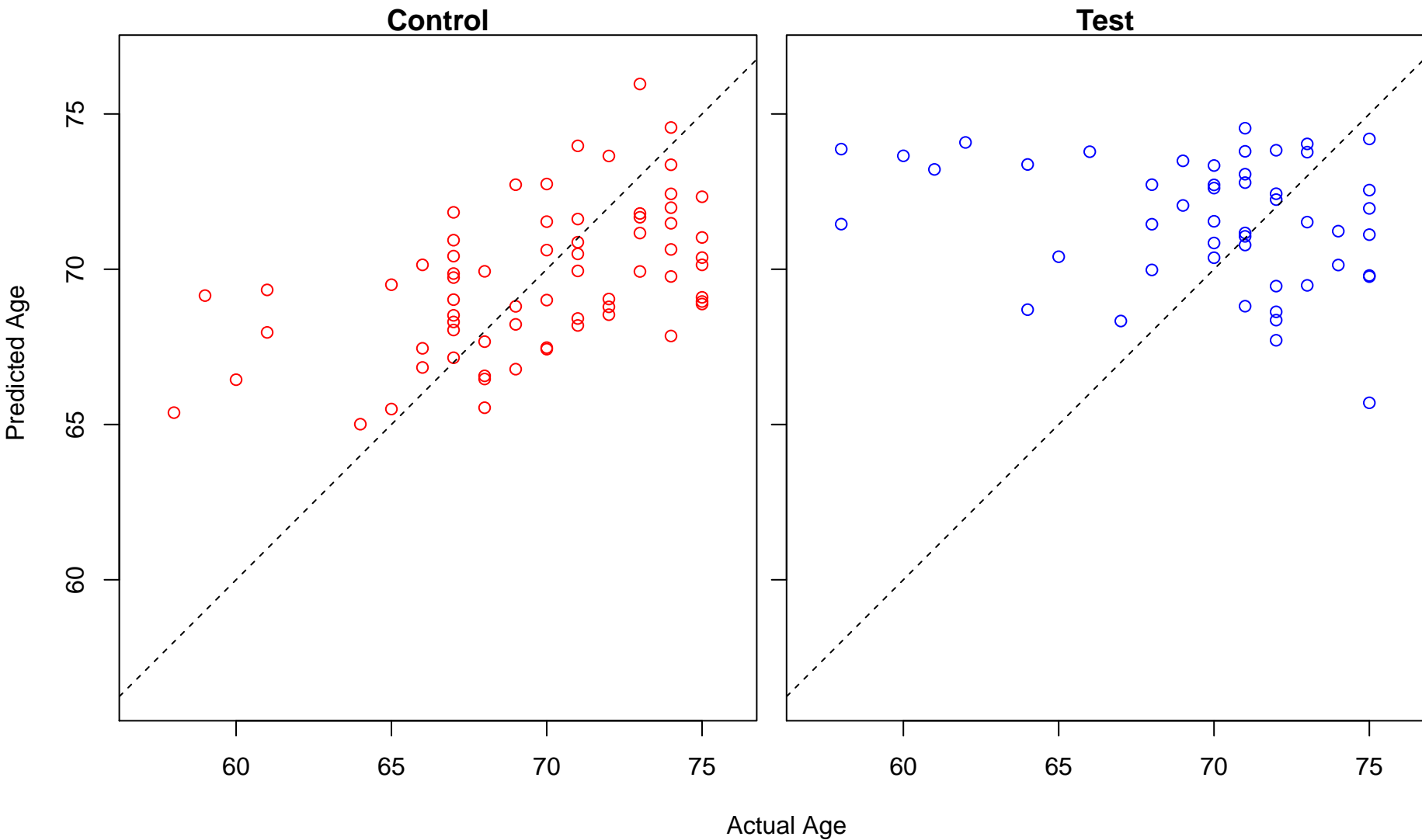


Test

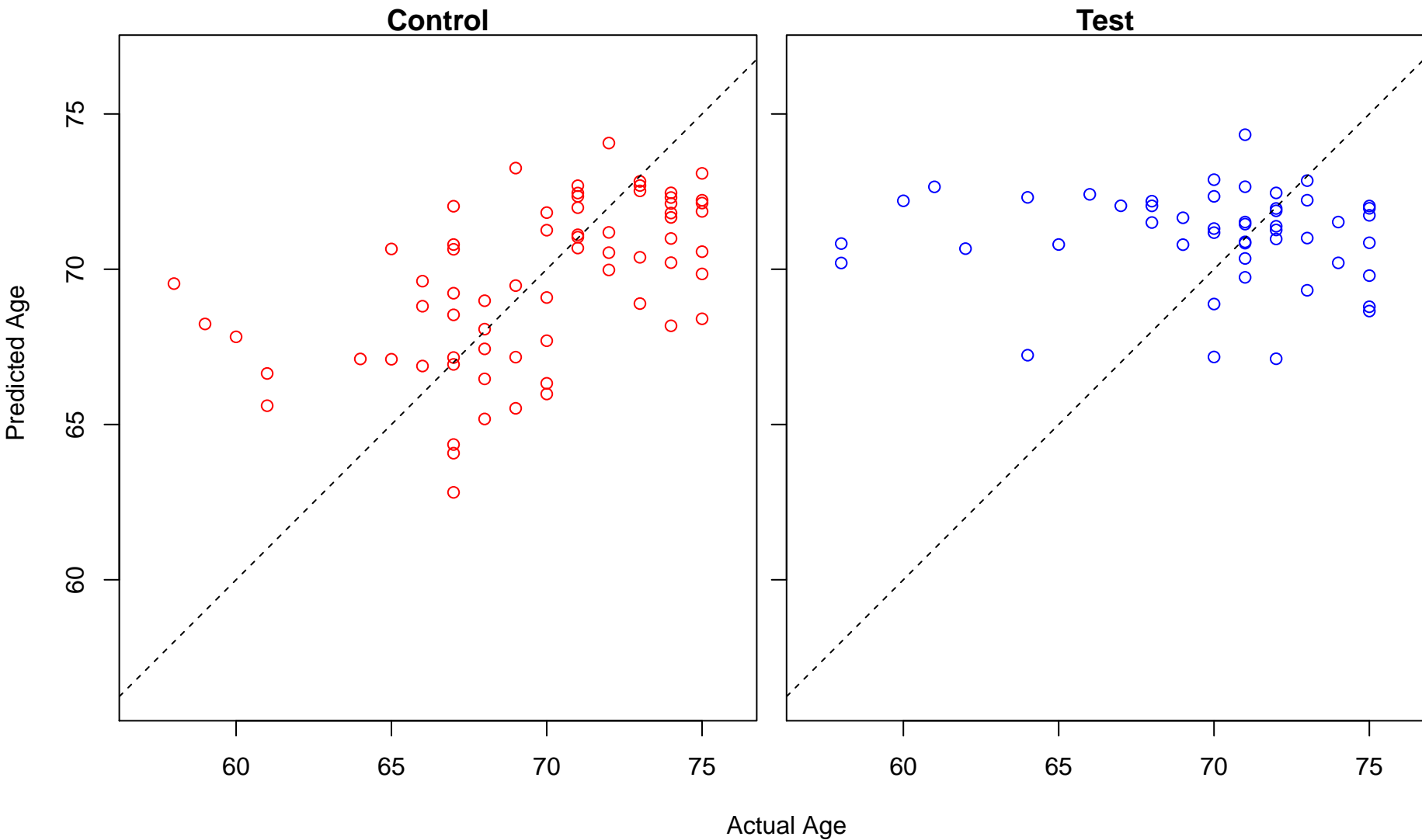


Actual Age

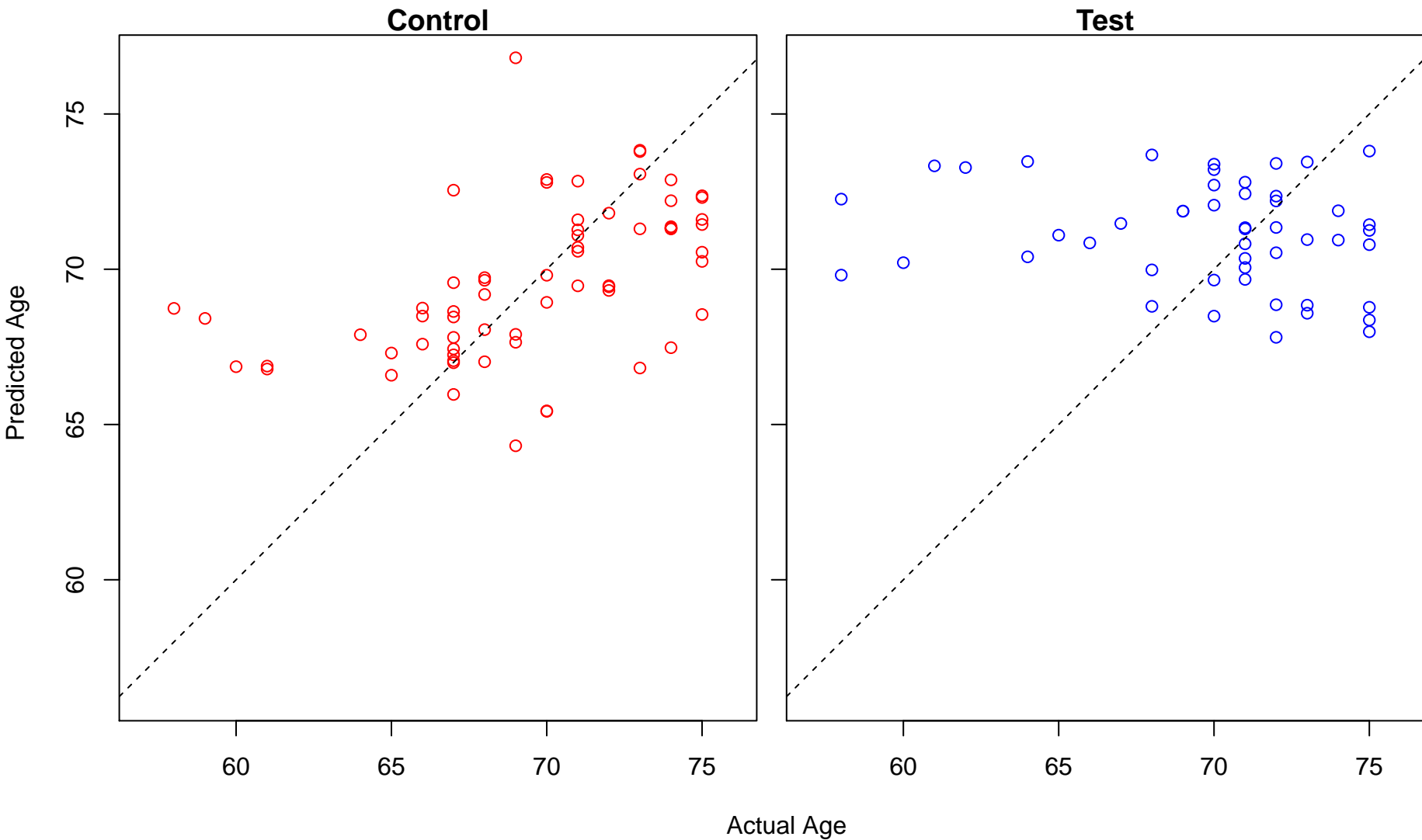
endocardial cell differentiation (Score: 0.807024)



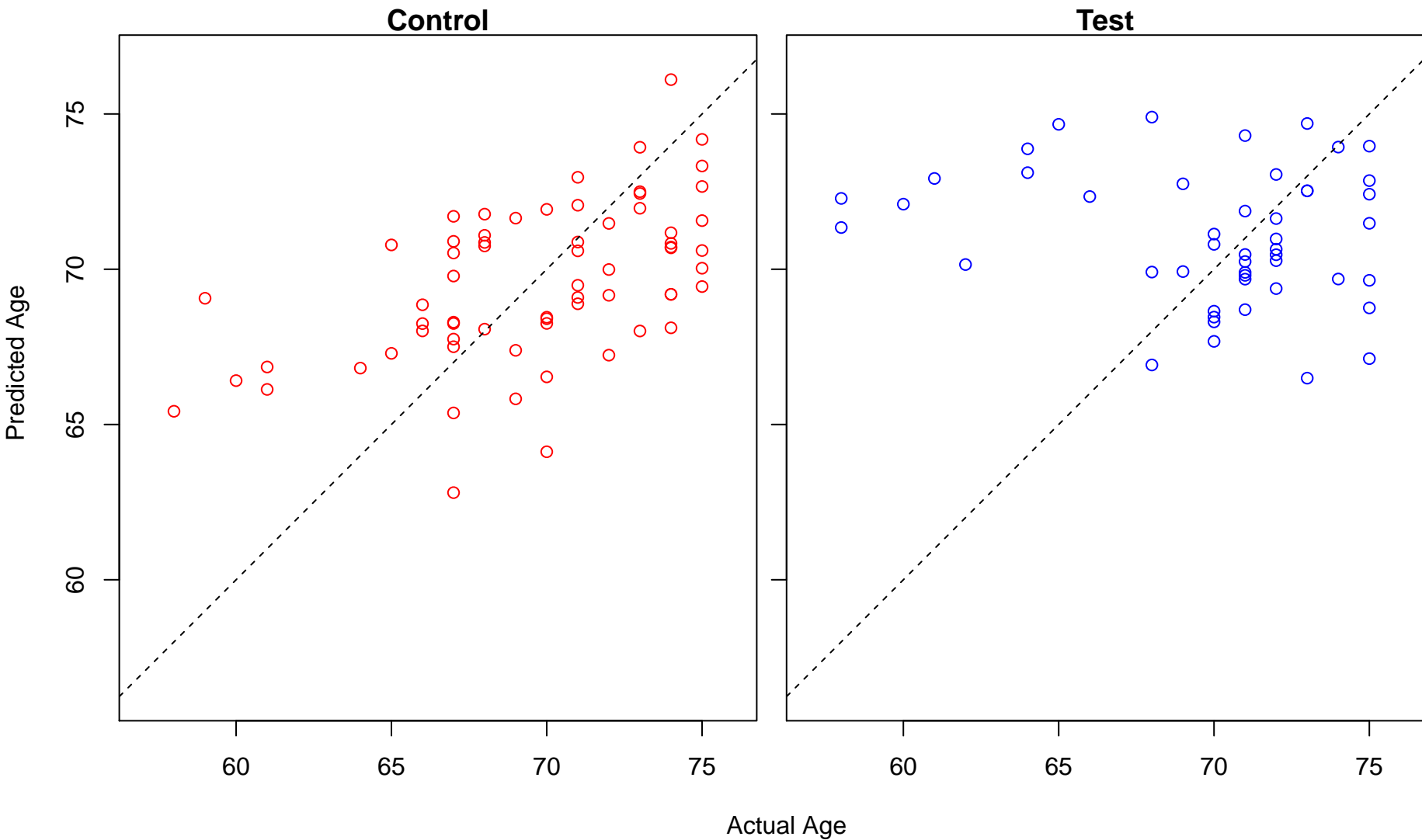
inflammatory response to antigenic stimulus (Score: 0.806809)



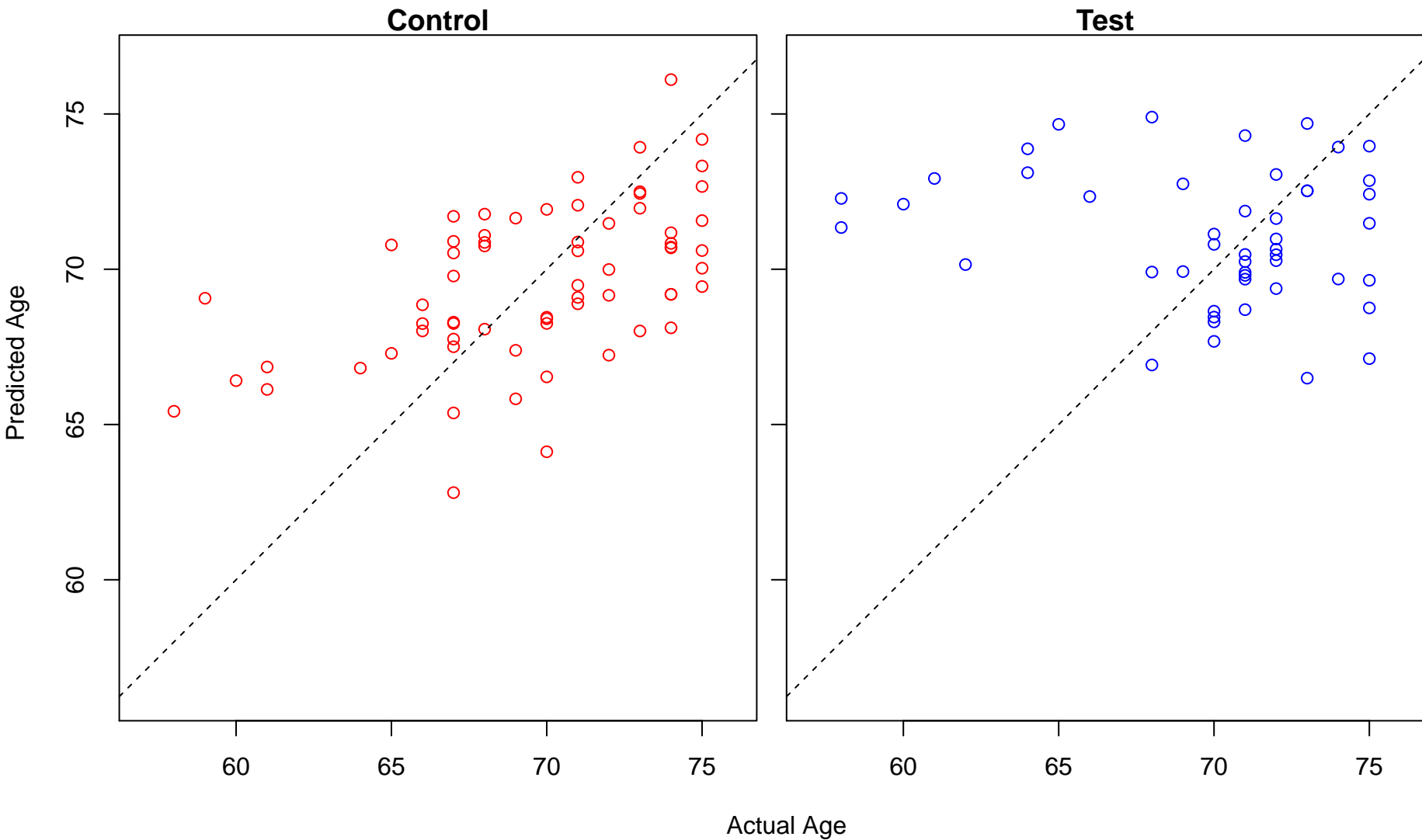
cellular ketone metabolic process (Score: 0.806789)



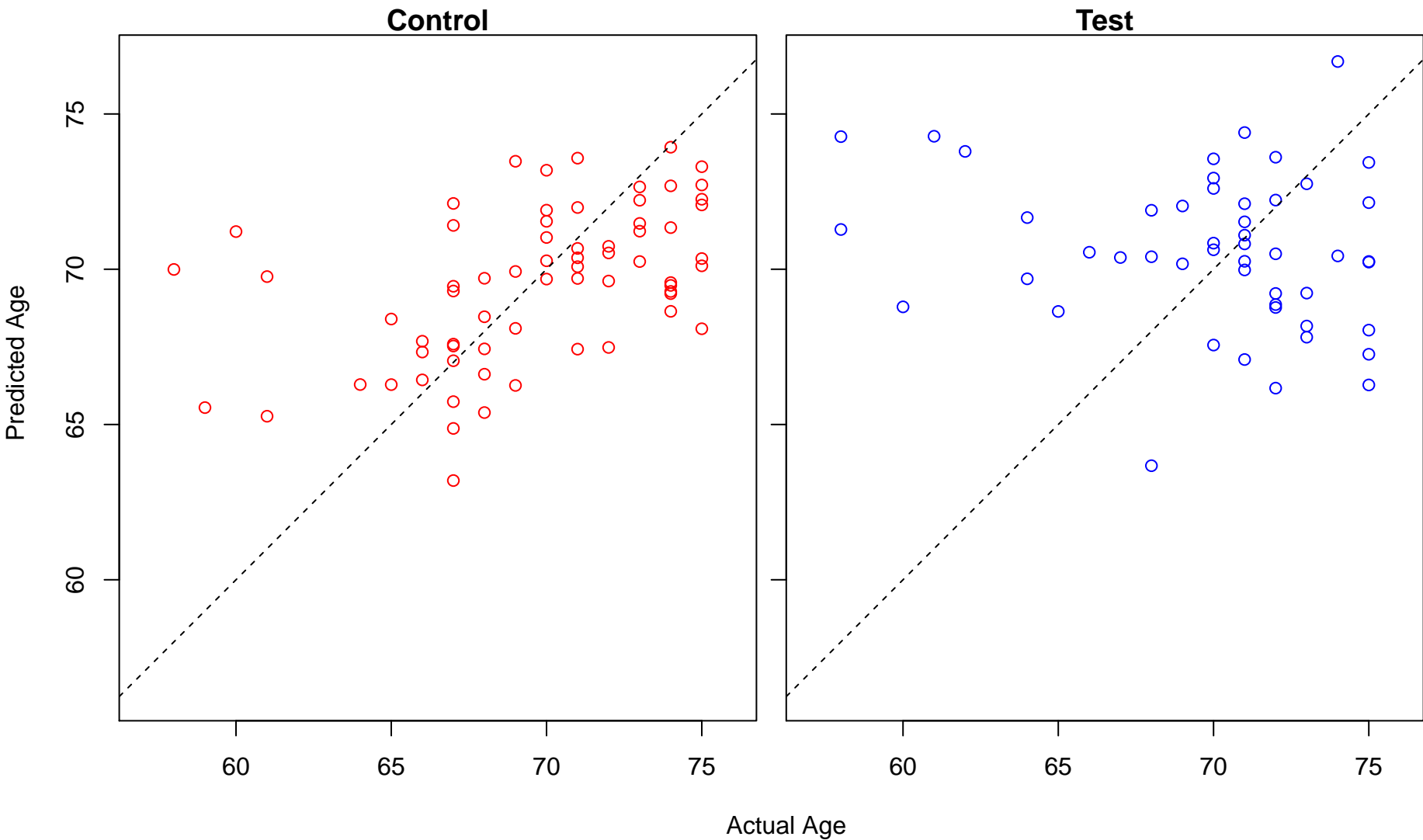
lysine metabolic process (Score: 0.806760)



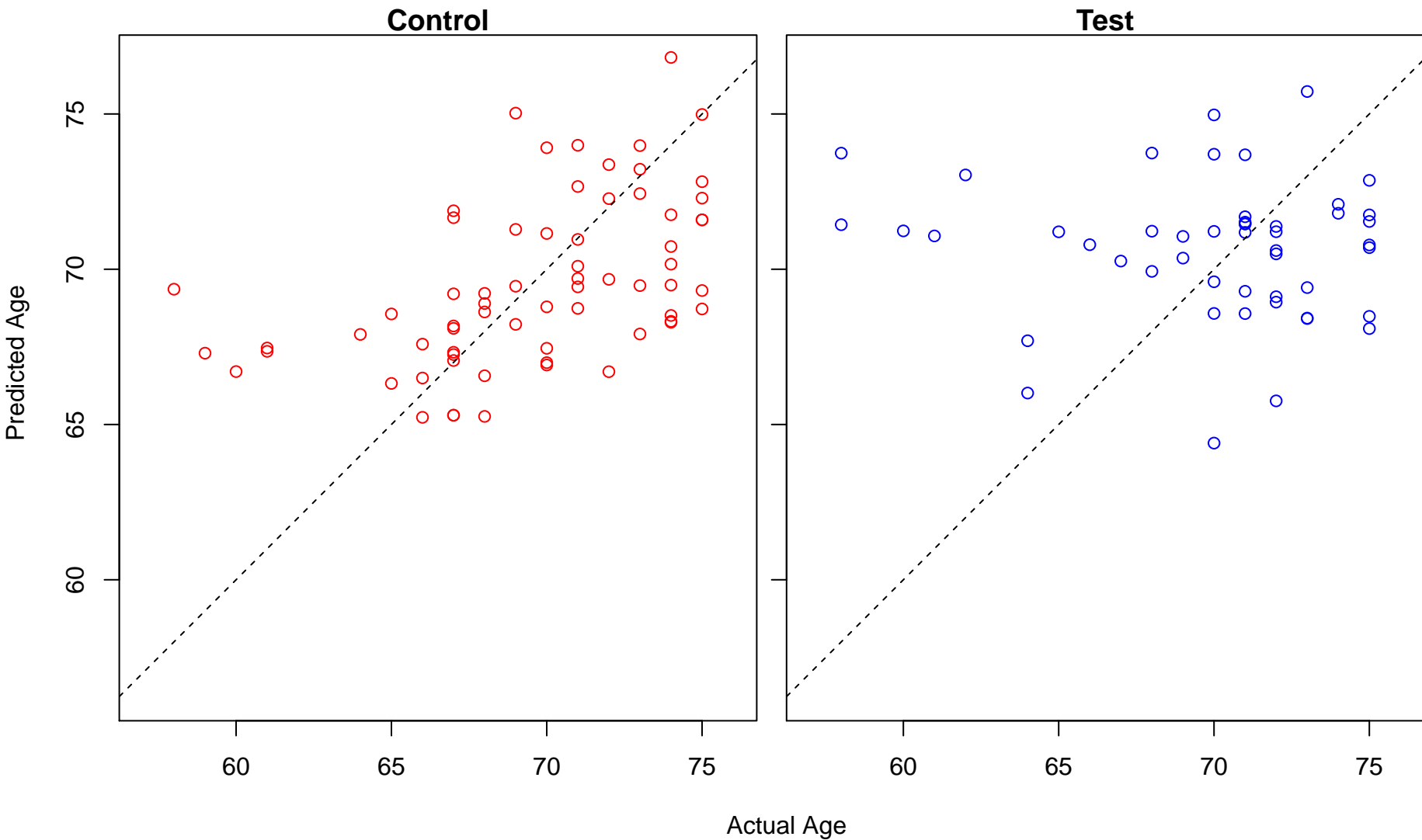
lysine catabolic process (Score: 0.806760)



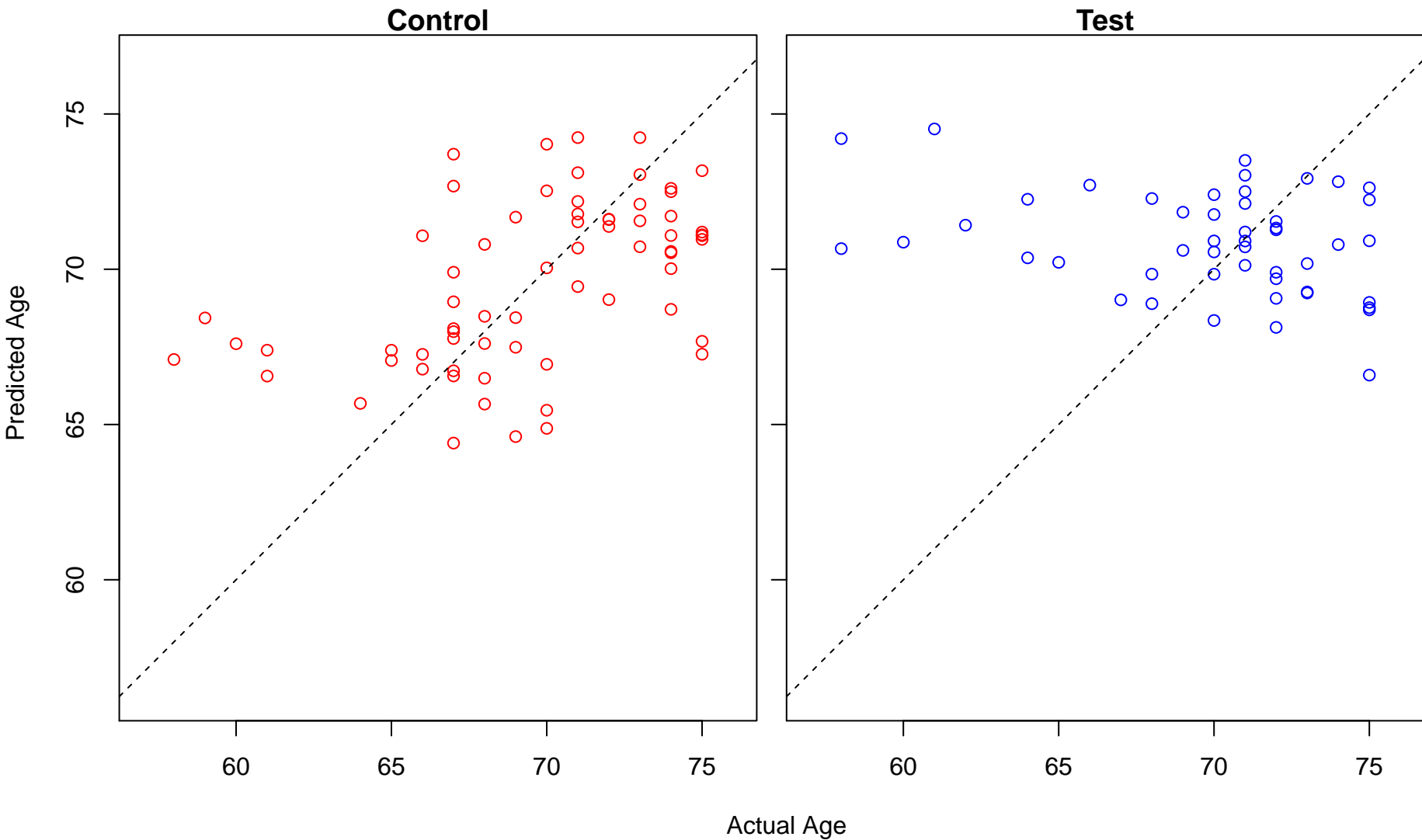
ive immune response based on somatic recombination of immune receptors built from immunoglobulin su



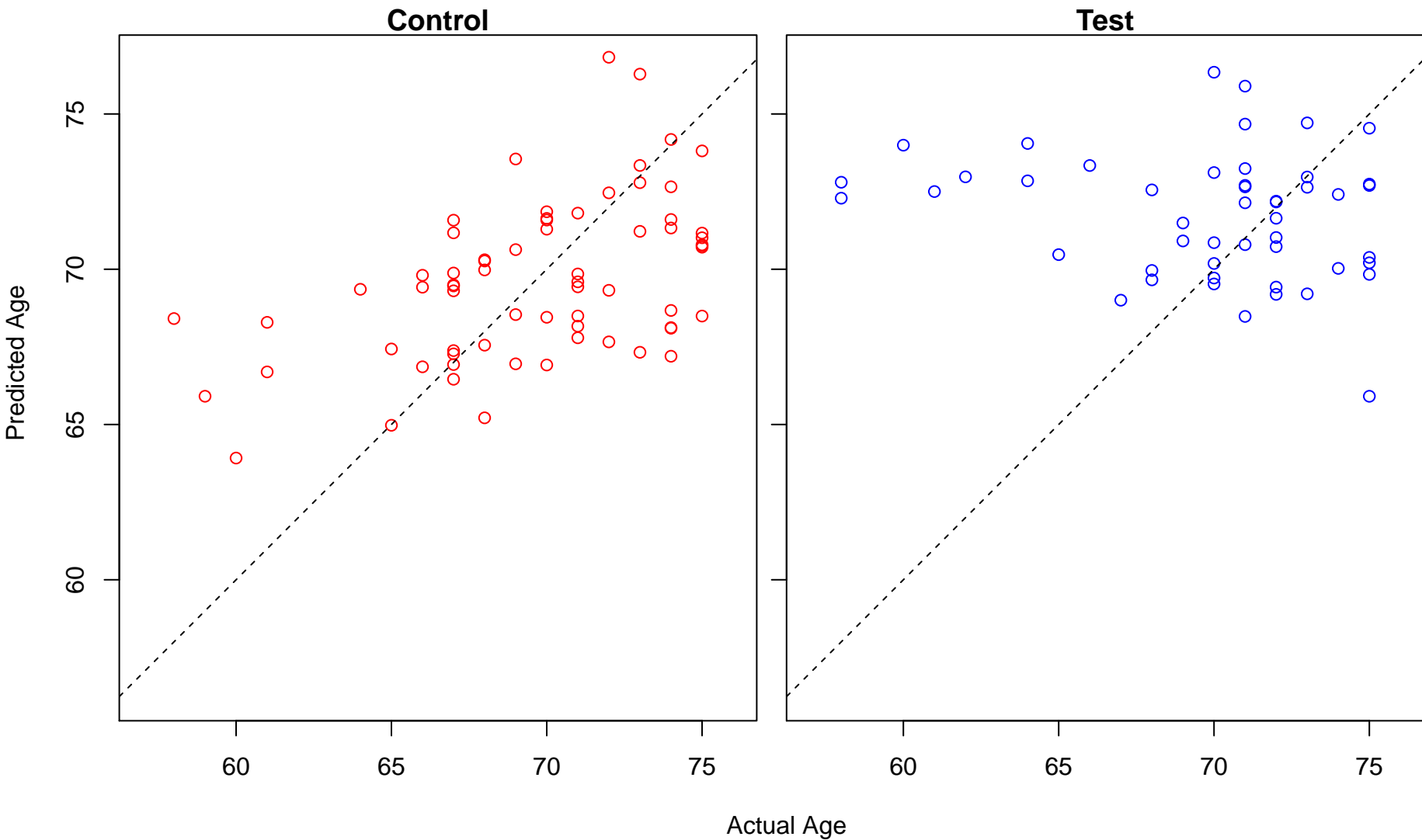
biomineral tissue development (Score: 0.806387)



multicellular organismal metabolic process (Score: 0.805488)

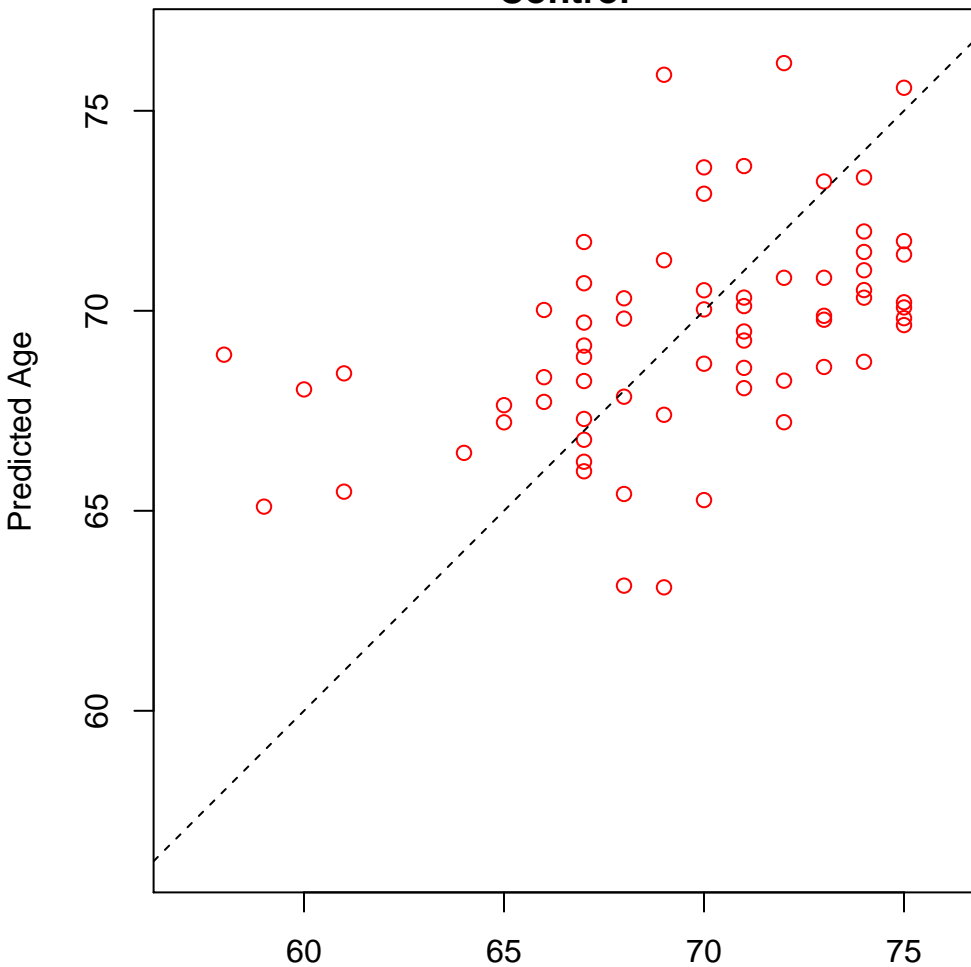


basic amino acid transport (Score: 0.805288)

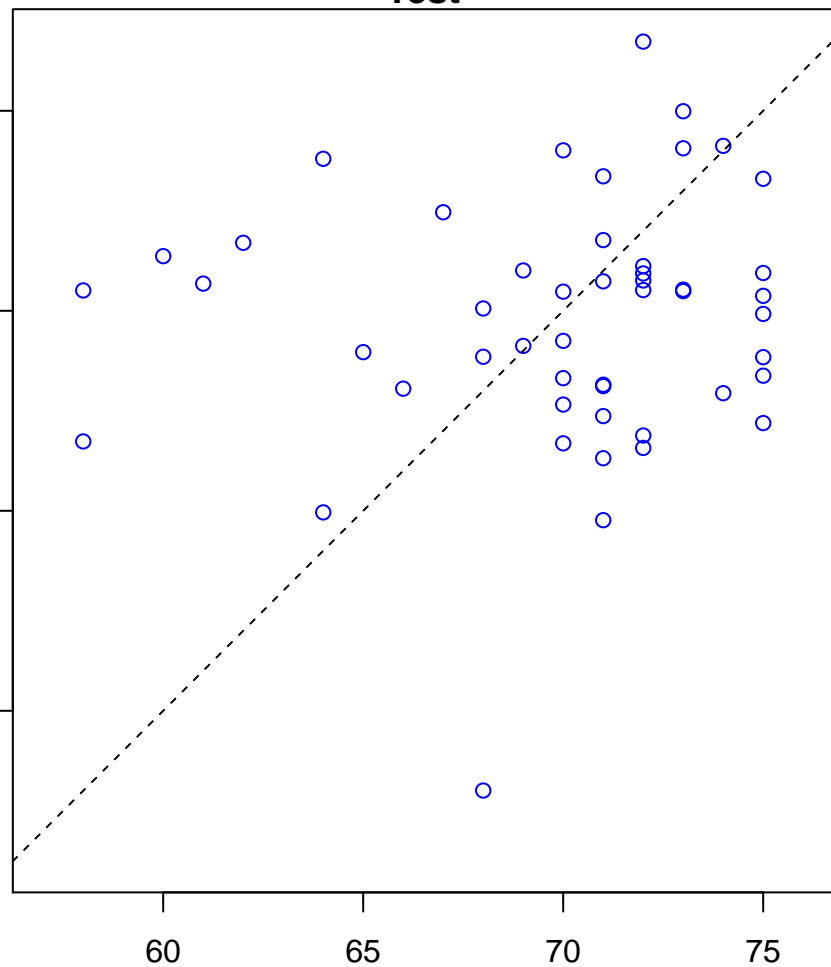


DNA dealkylation involved in DNA repair (Score: 0.804616)

Control

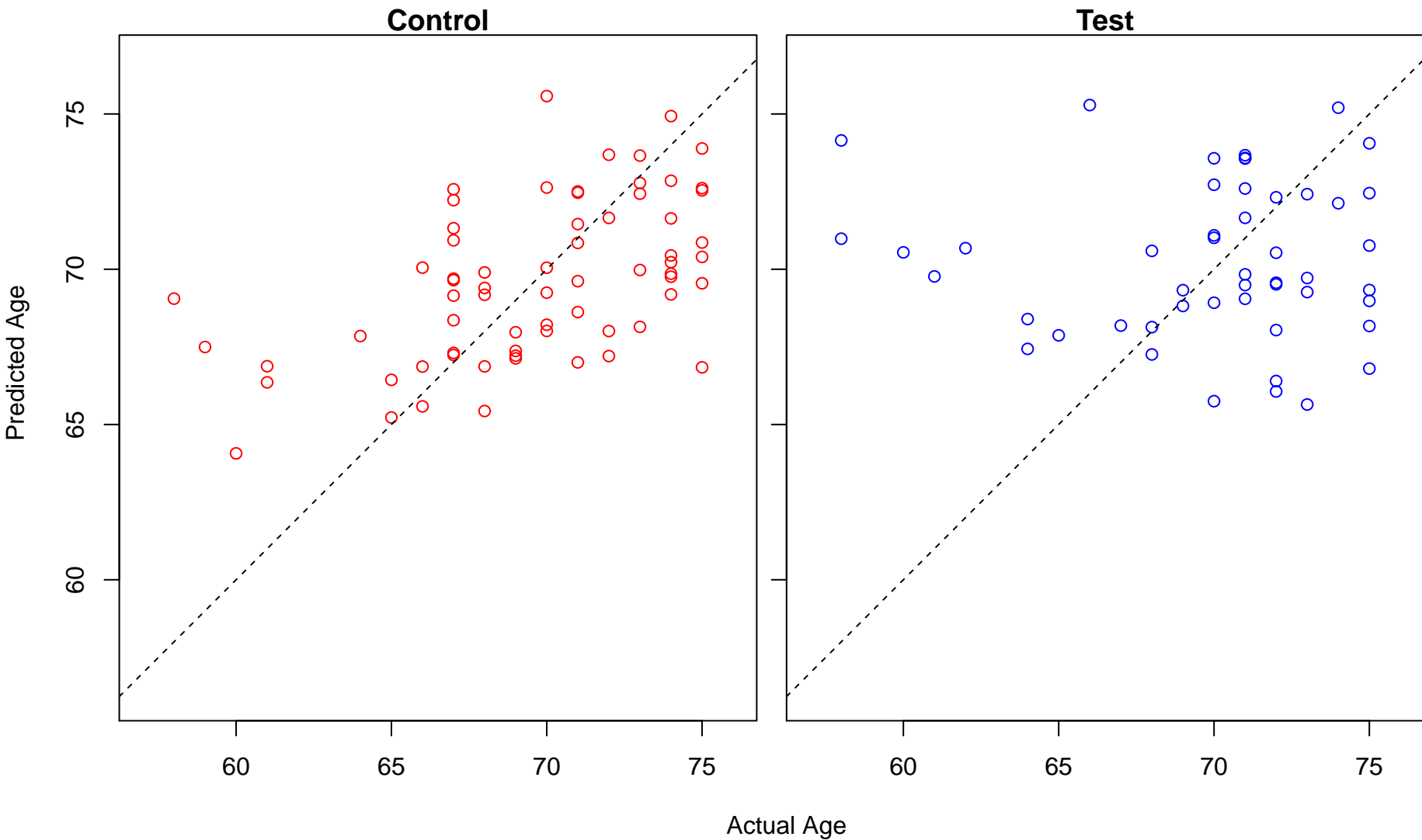


Test

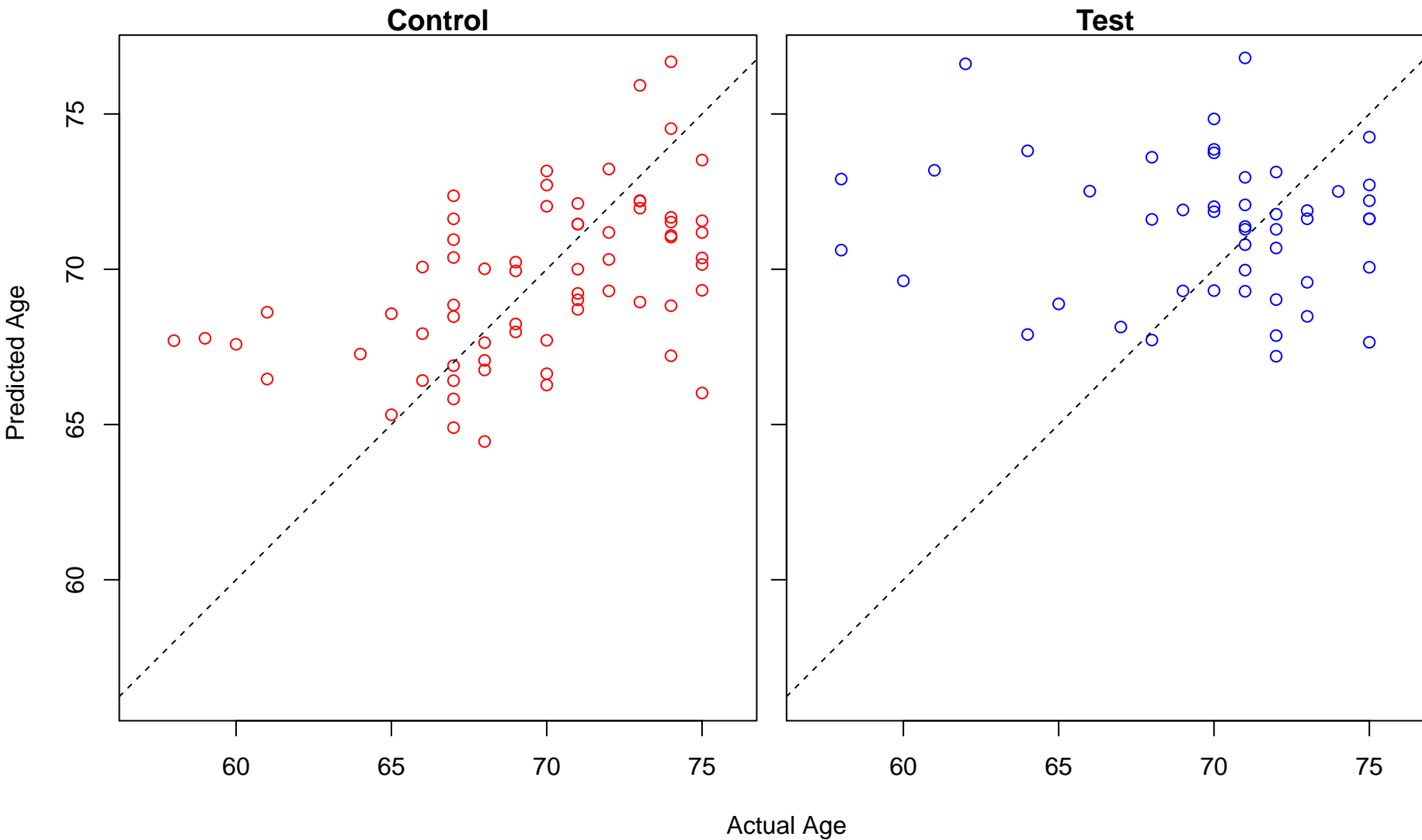


Actual Age

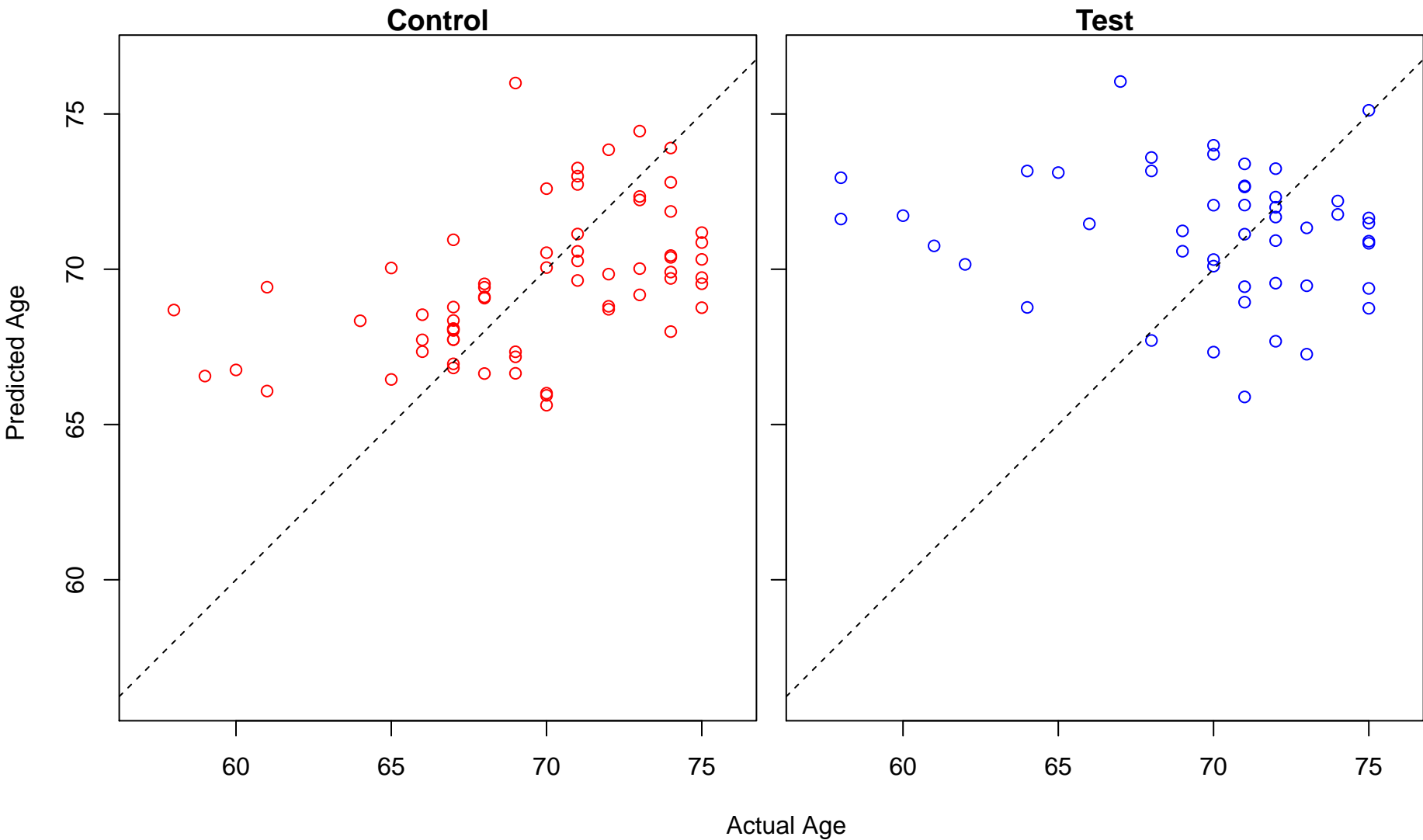
linoleic acid metabolic process (Score: 0.804007)



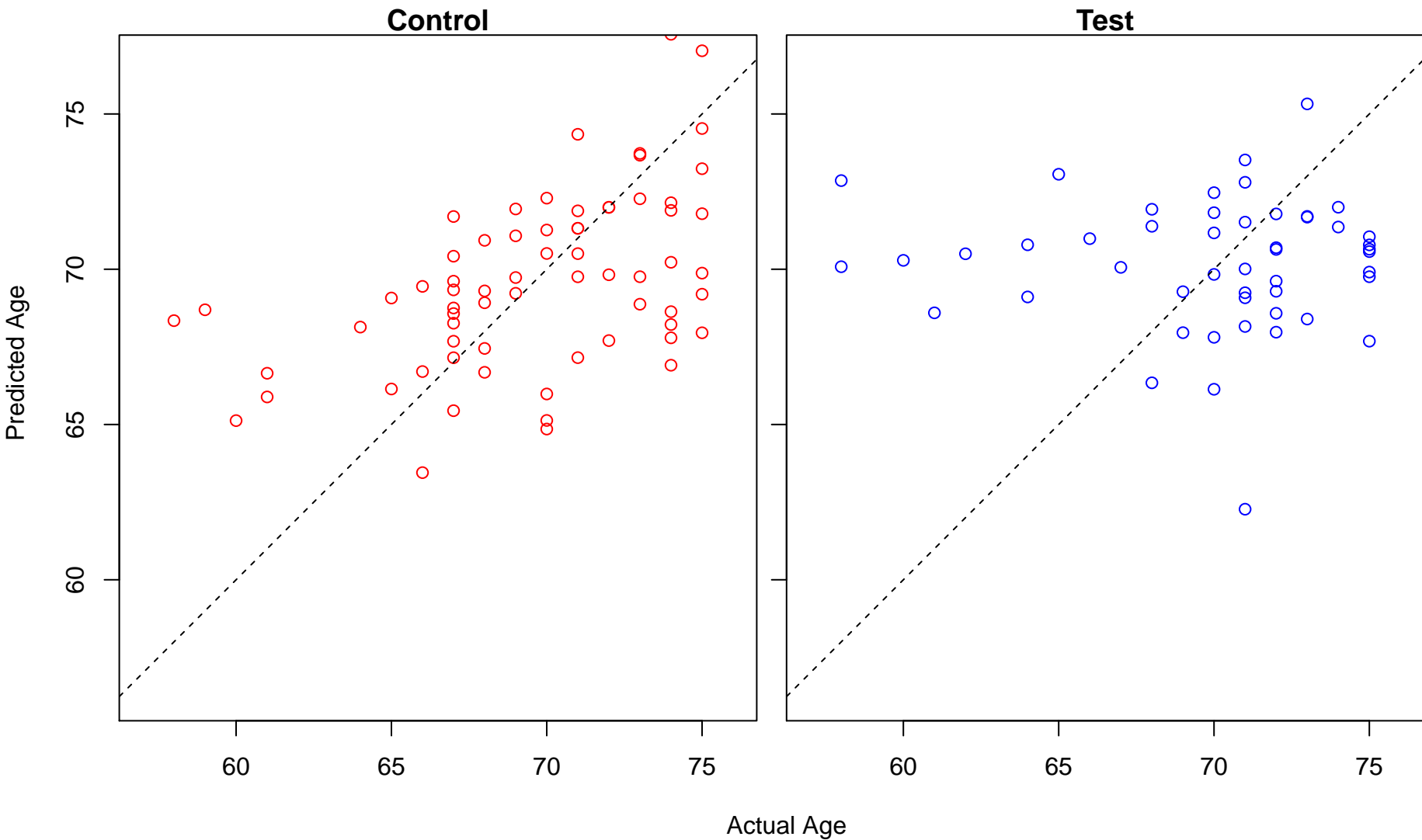
membrane raft assembly (Score: 0.804003)



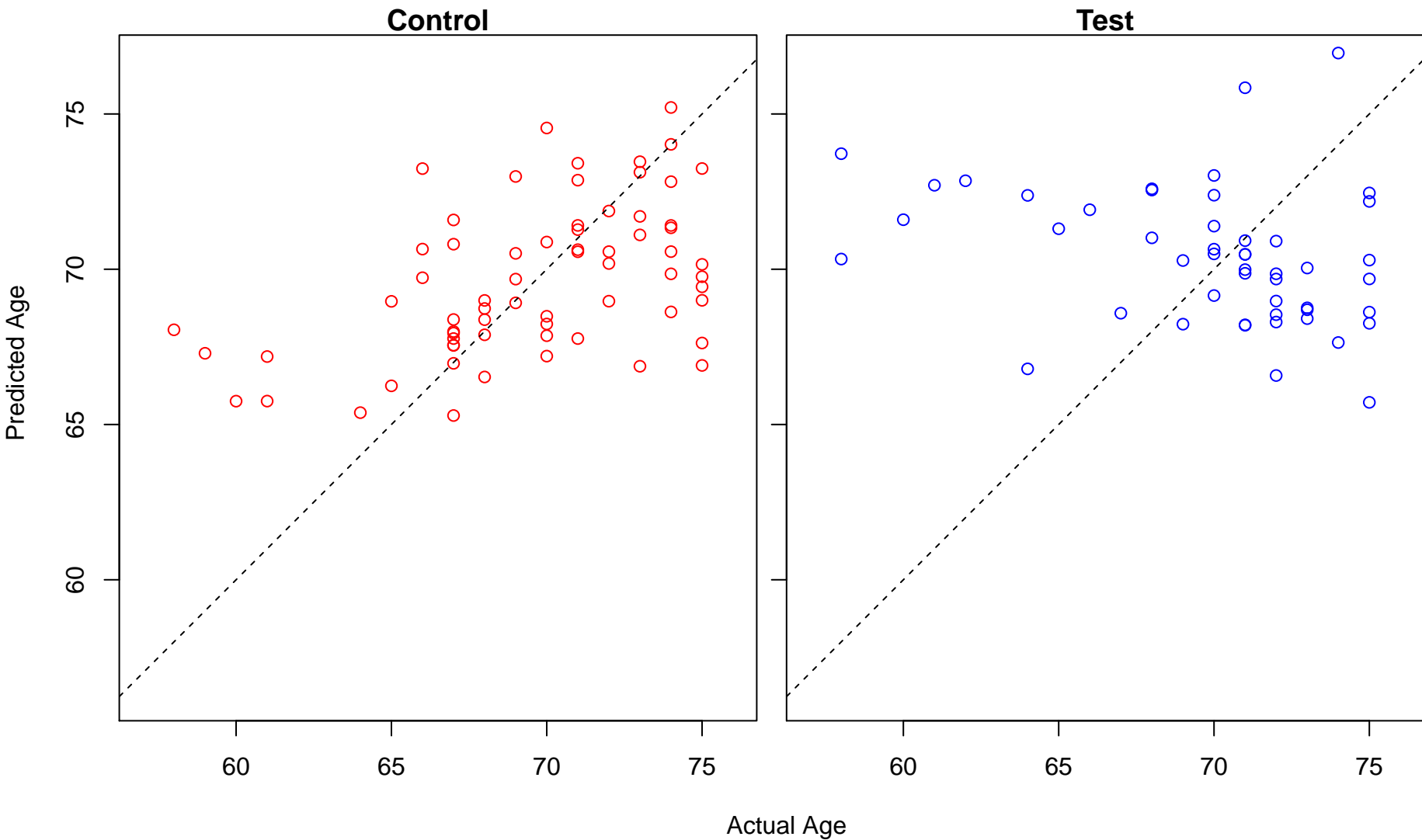
negative regulation of endoplasmic reticulum unfolded protein response (Score: 0.803691)



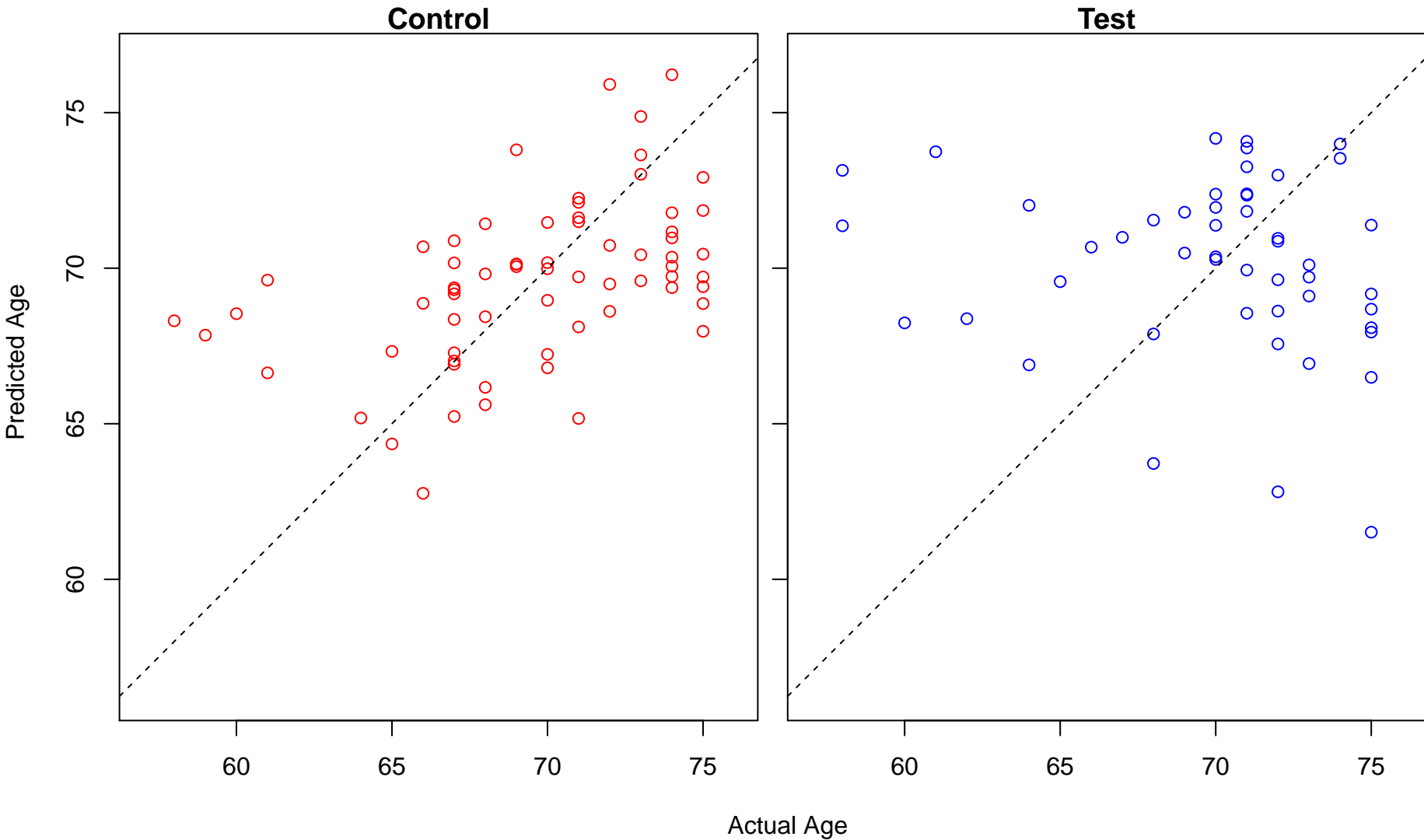
fibril organization (Score: 0.803688)



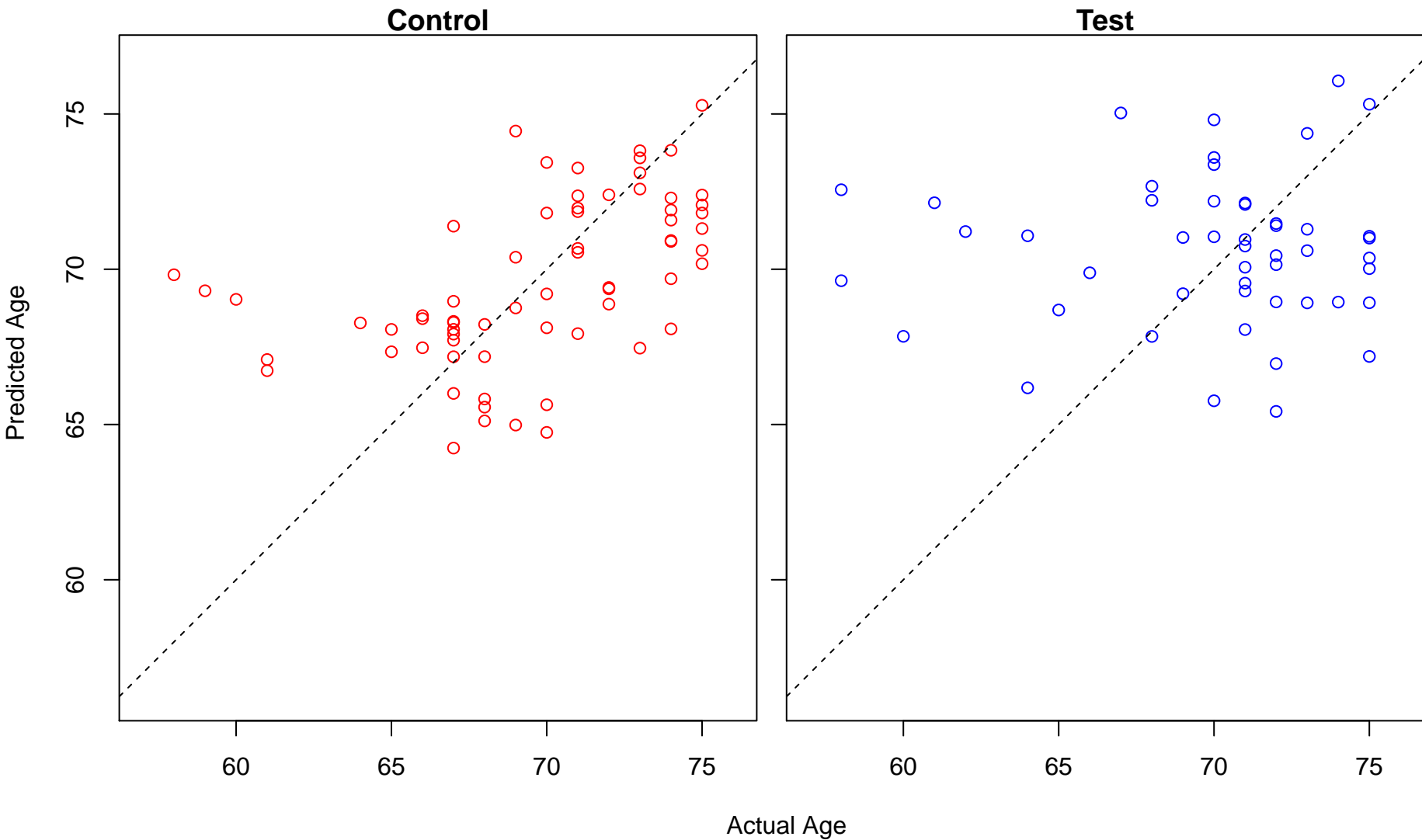
cellular response to alkaloid (Score: 0.803360)



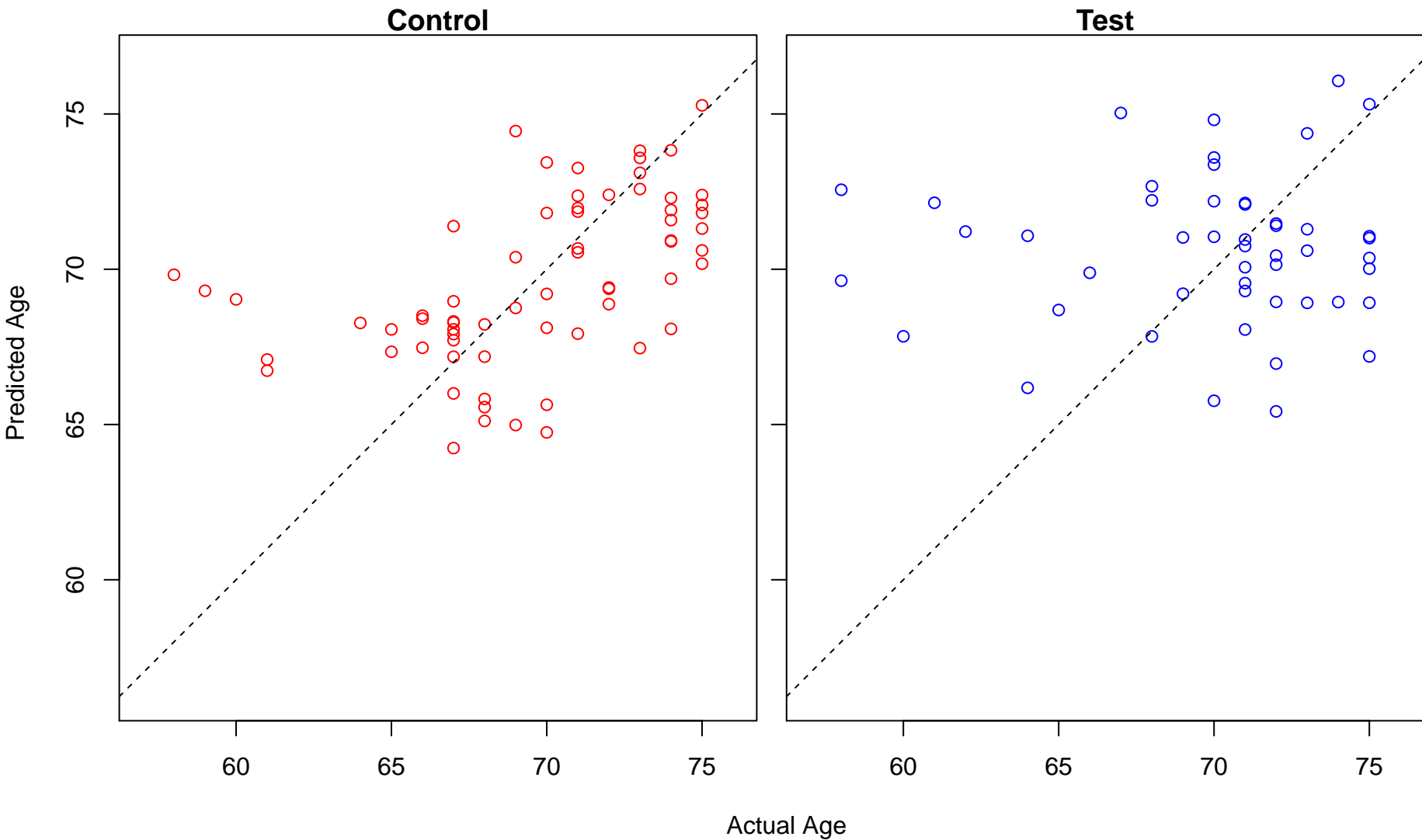
positive regulation of interleukin-4 production (Score: 0.802594)



nucleosome disassembly (Score: 0.802510)

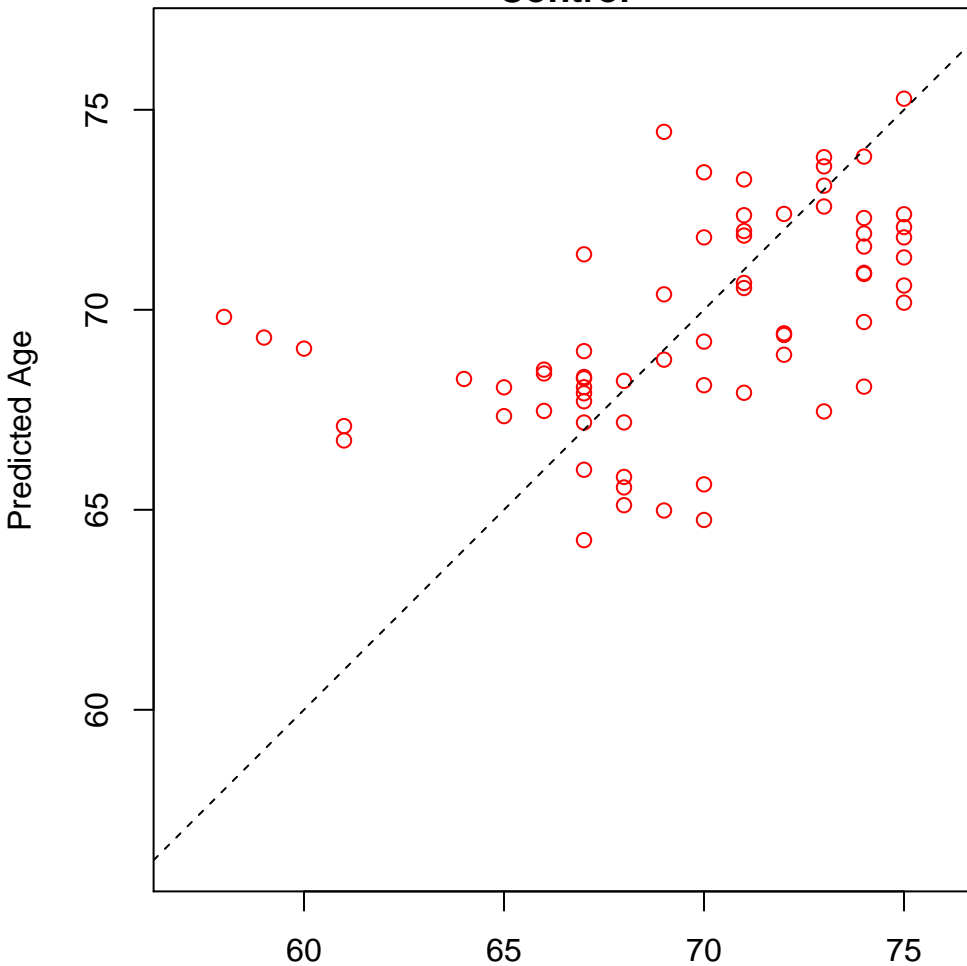


chromatin disassembly (Score: 0.802510)

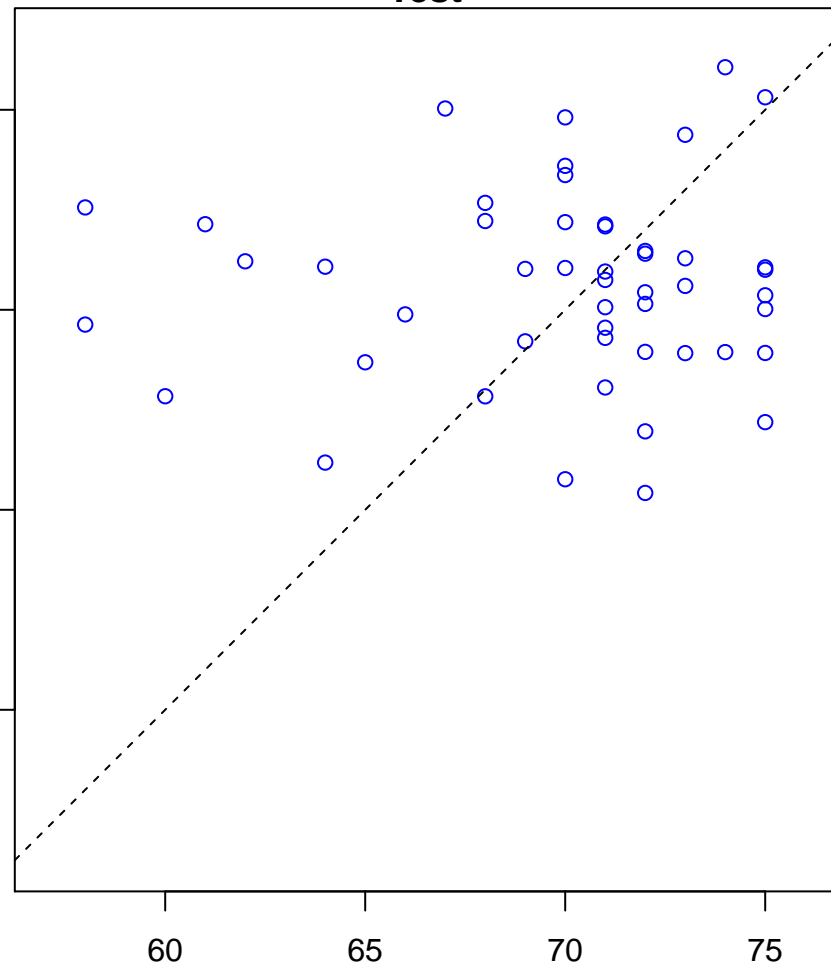


protein-DNA complex disassembly (Score: 0.802510)

Control

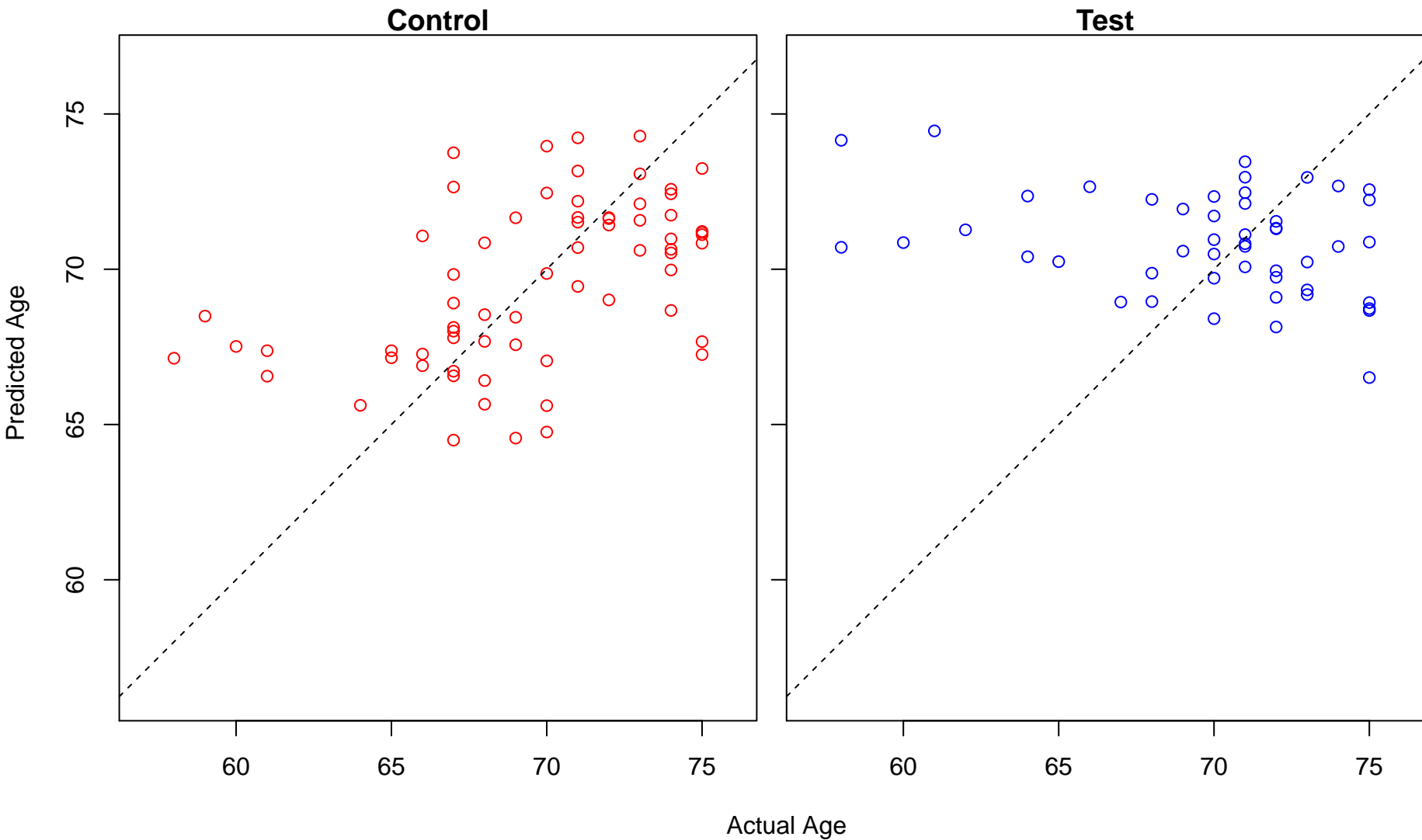


Test

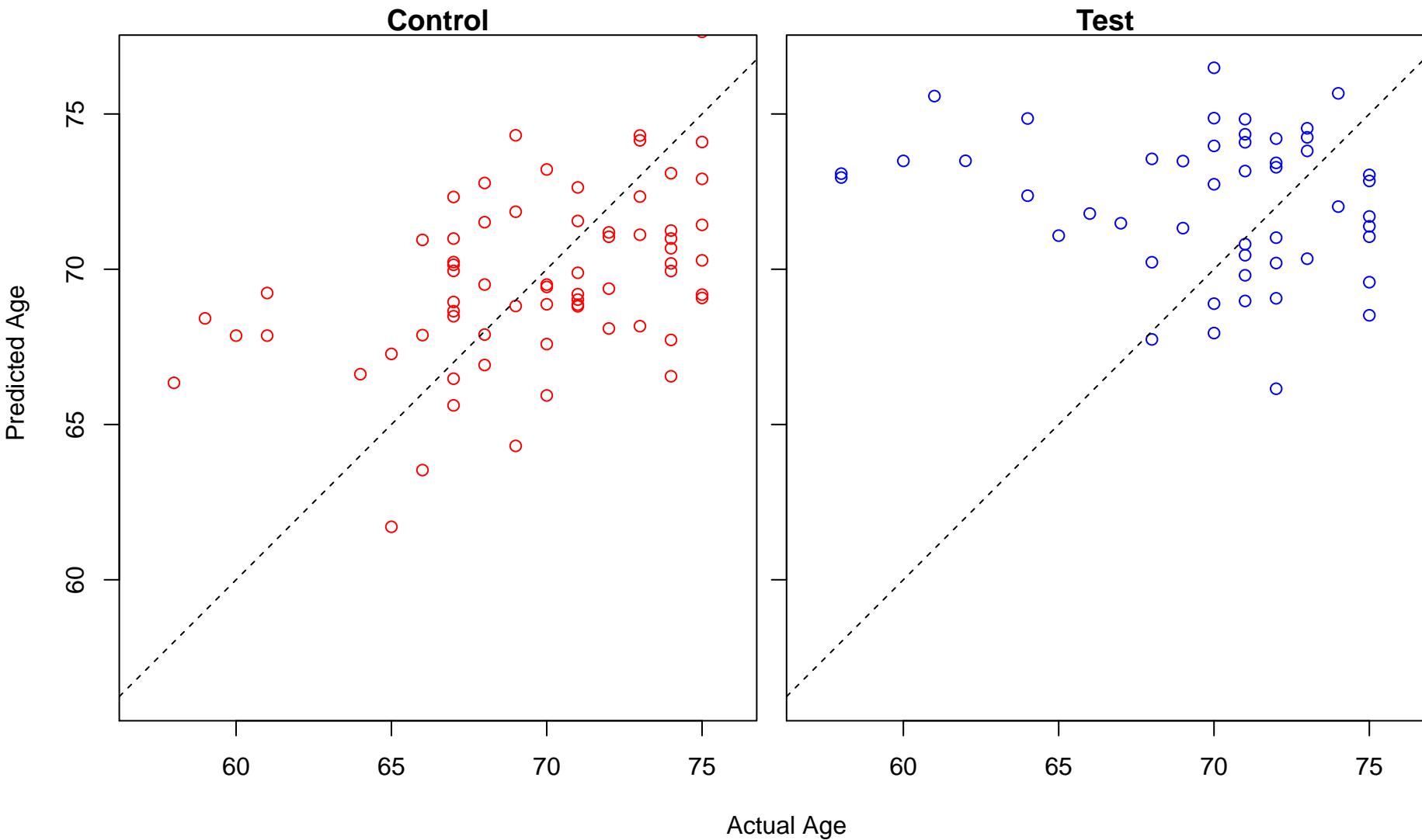


Actual Age

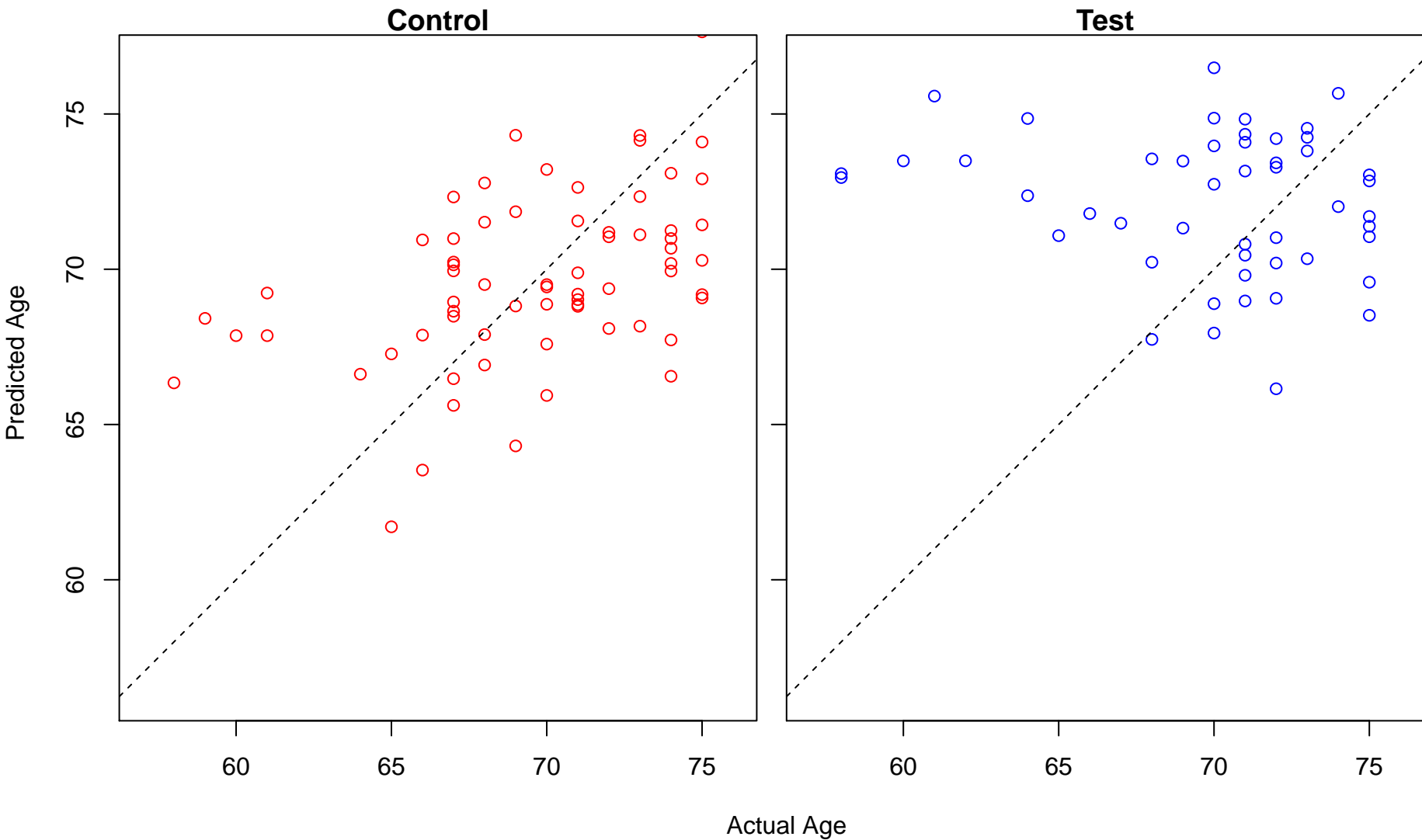
multicellular organismal macromolecule metabolic process (Score: 0.802302)



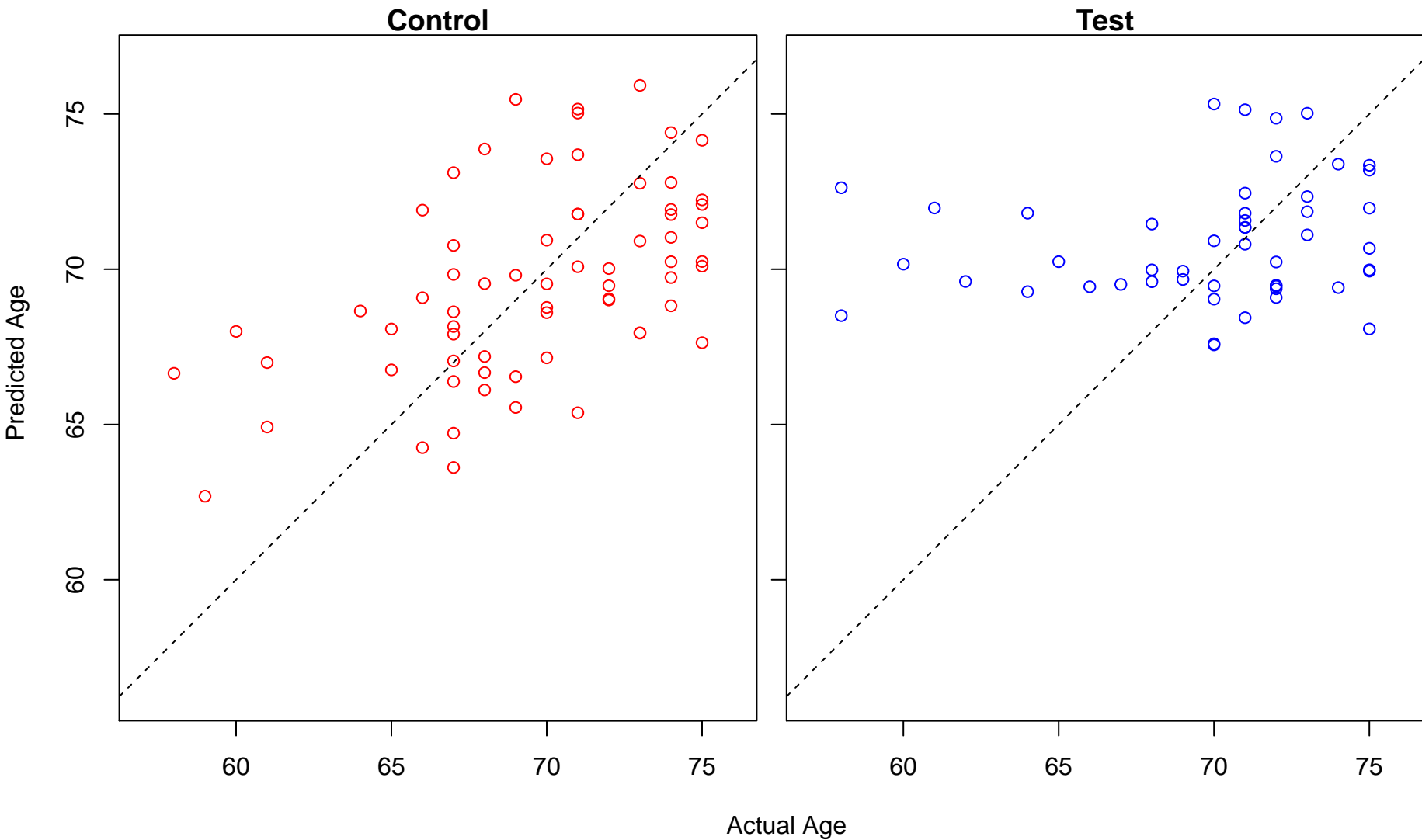
regulation of acetyl-CoA biosynthetic process from pyruvate (Score: 0.802011)



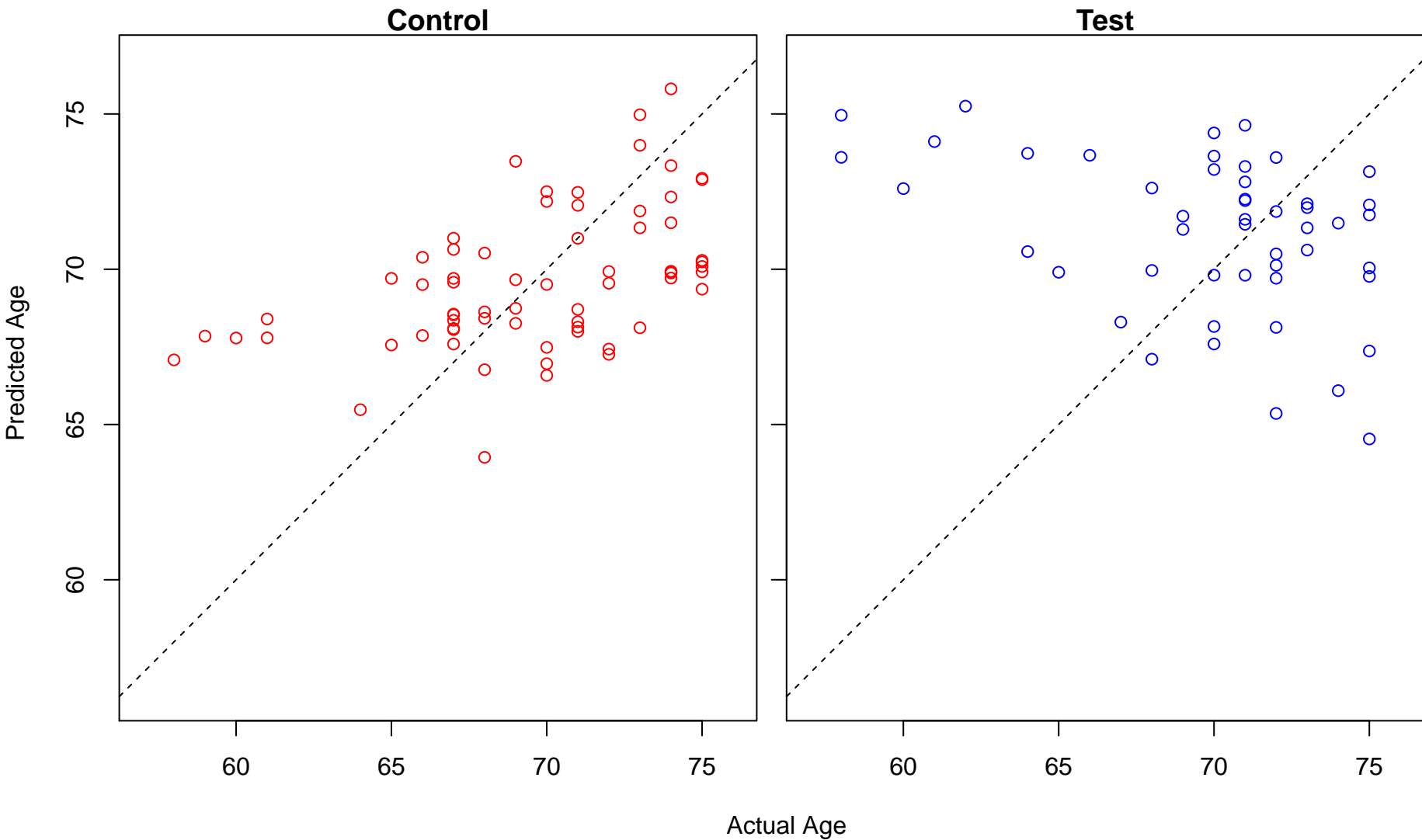
regulation of acyl-CoA biosynthetic process (Score: 0.802011)



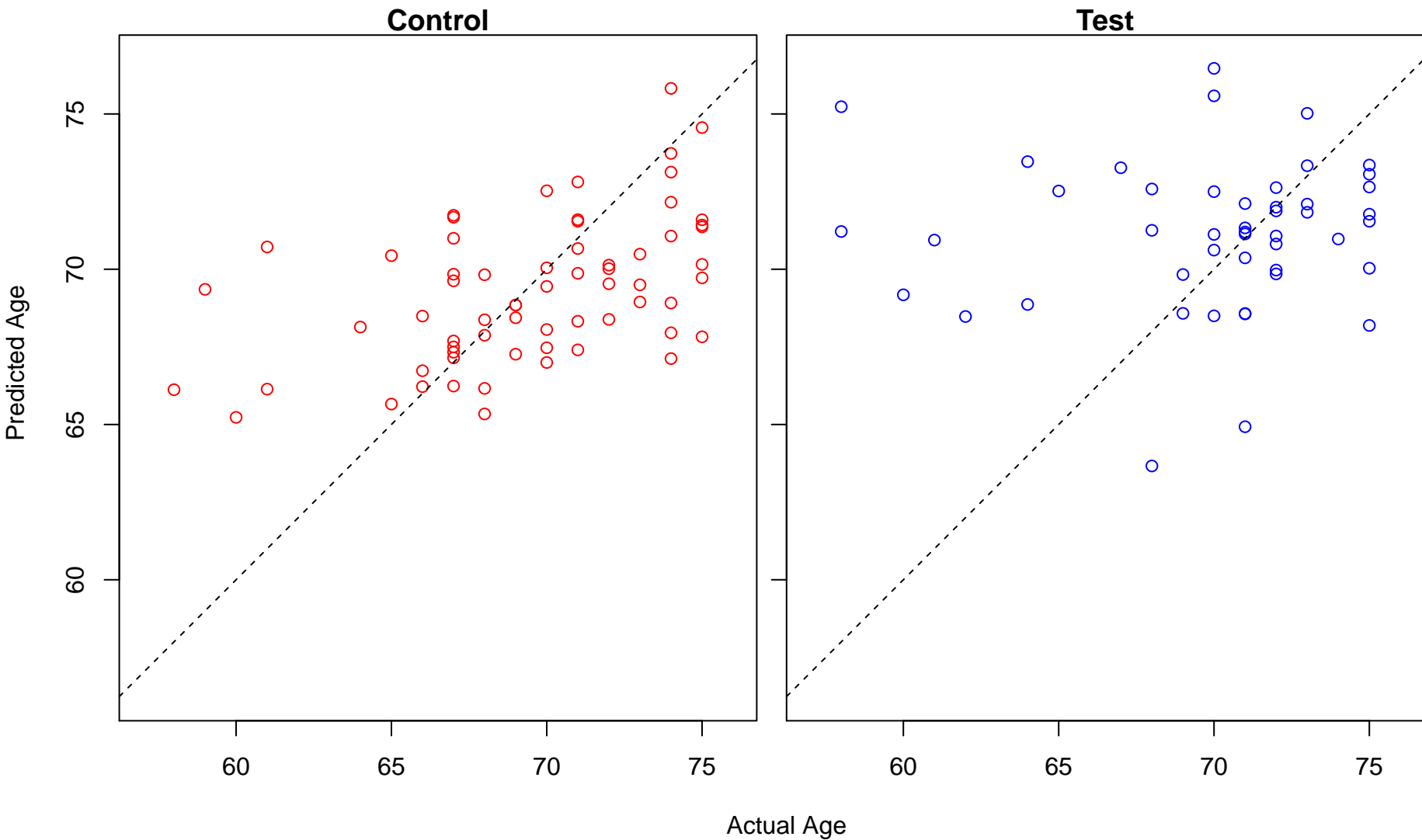
response to misfolded protein (Score: 0.801946)



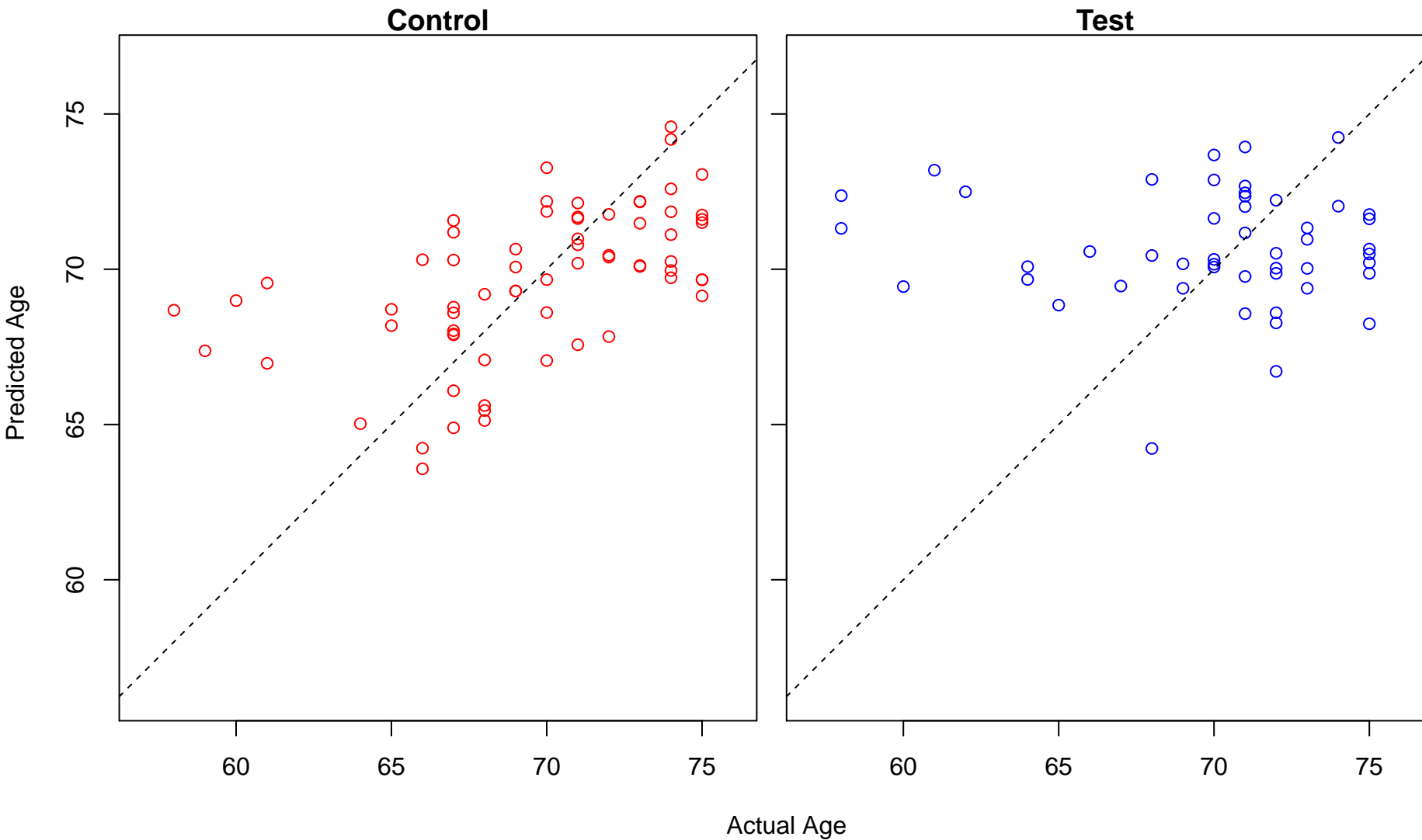
regulation of endocytic recycling (Score: 0.801921)



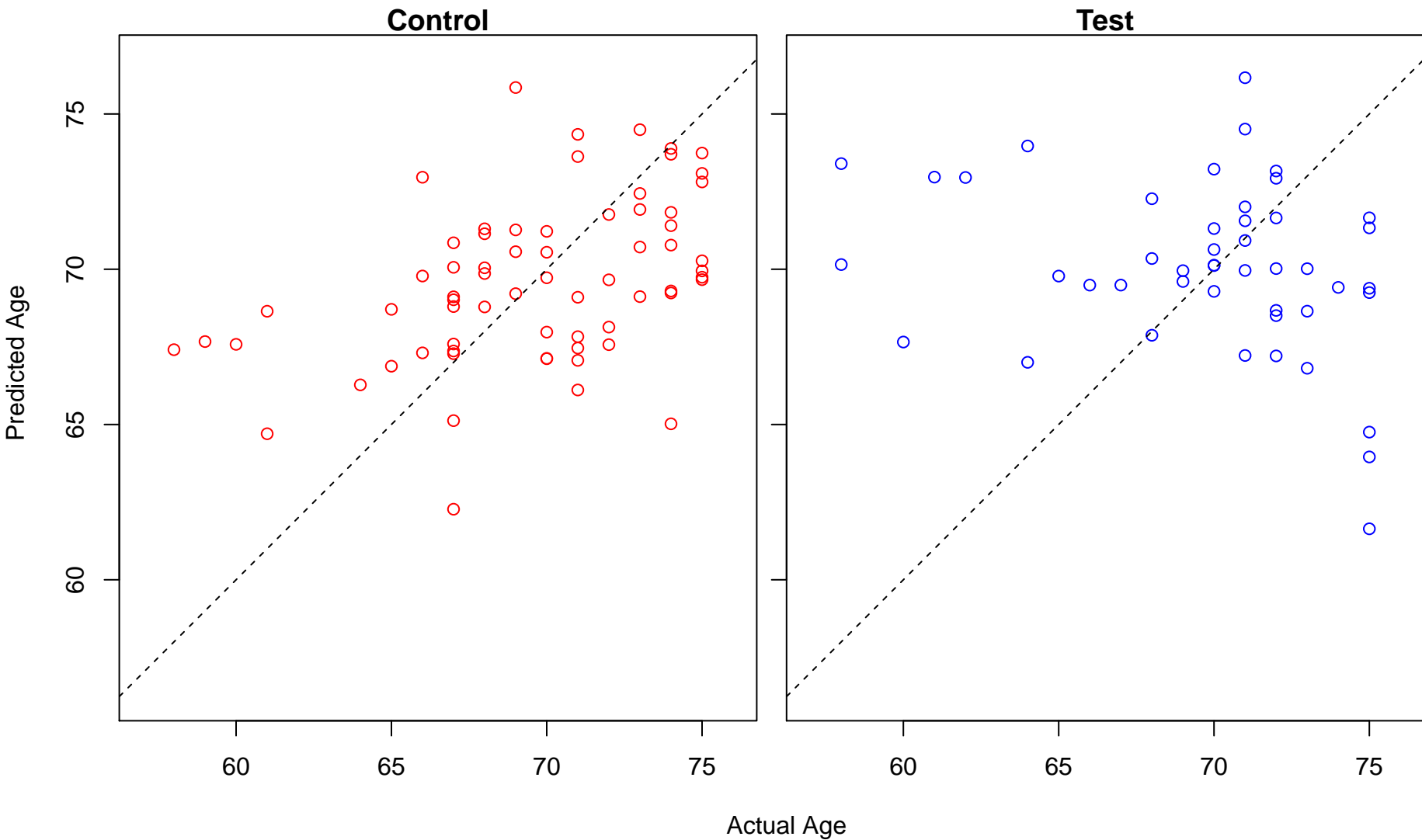
regulation of respiratory burst (Score: 0.801882)



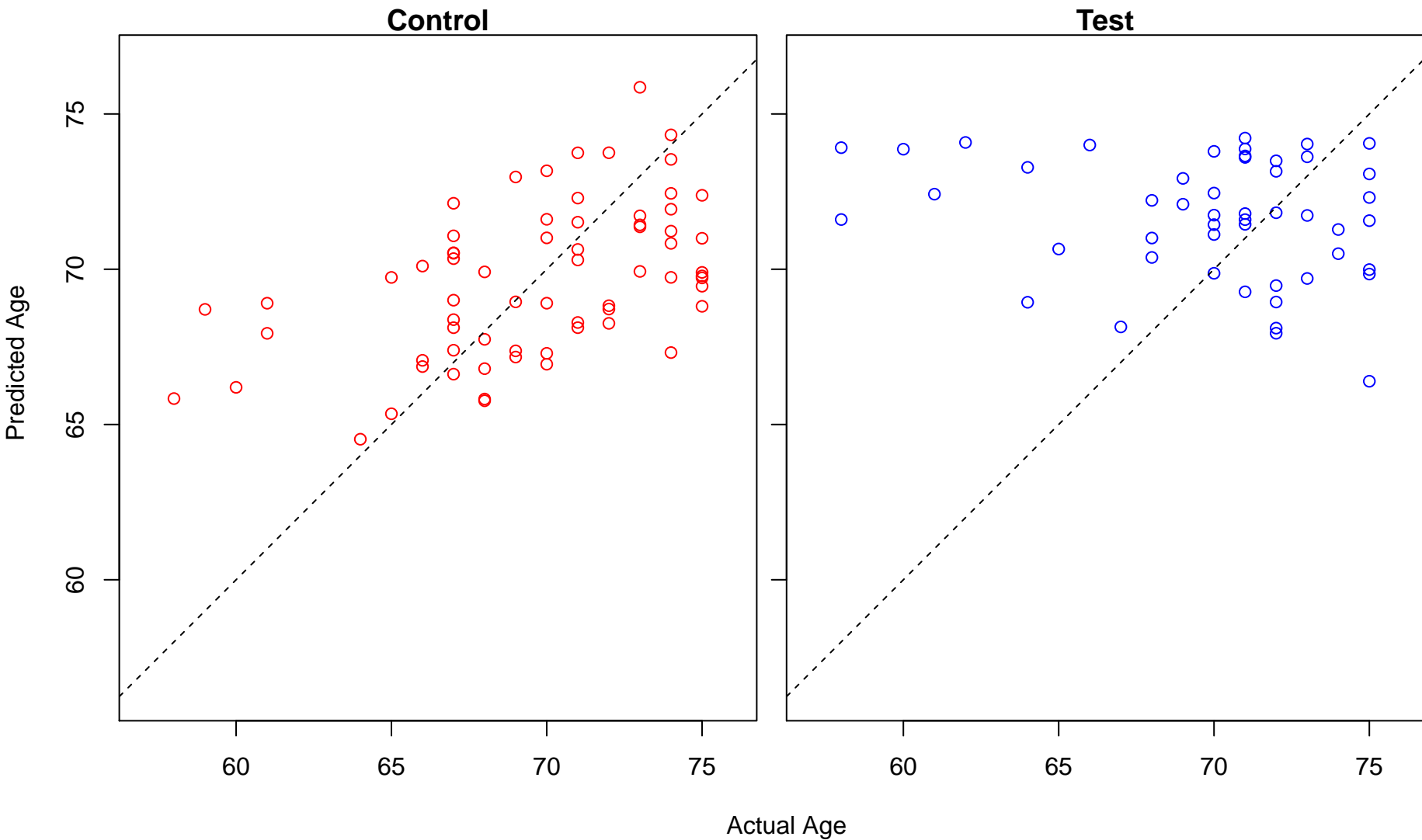
skeletal myofibril assembly (Score: 0.801781)



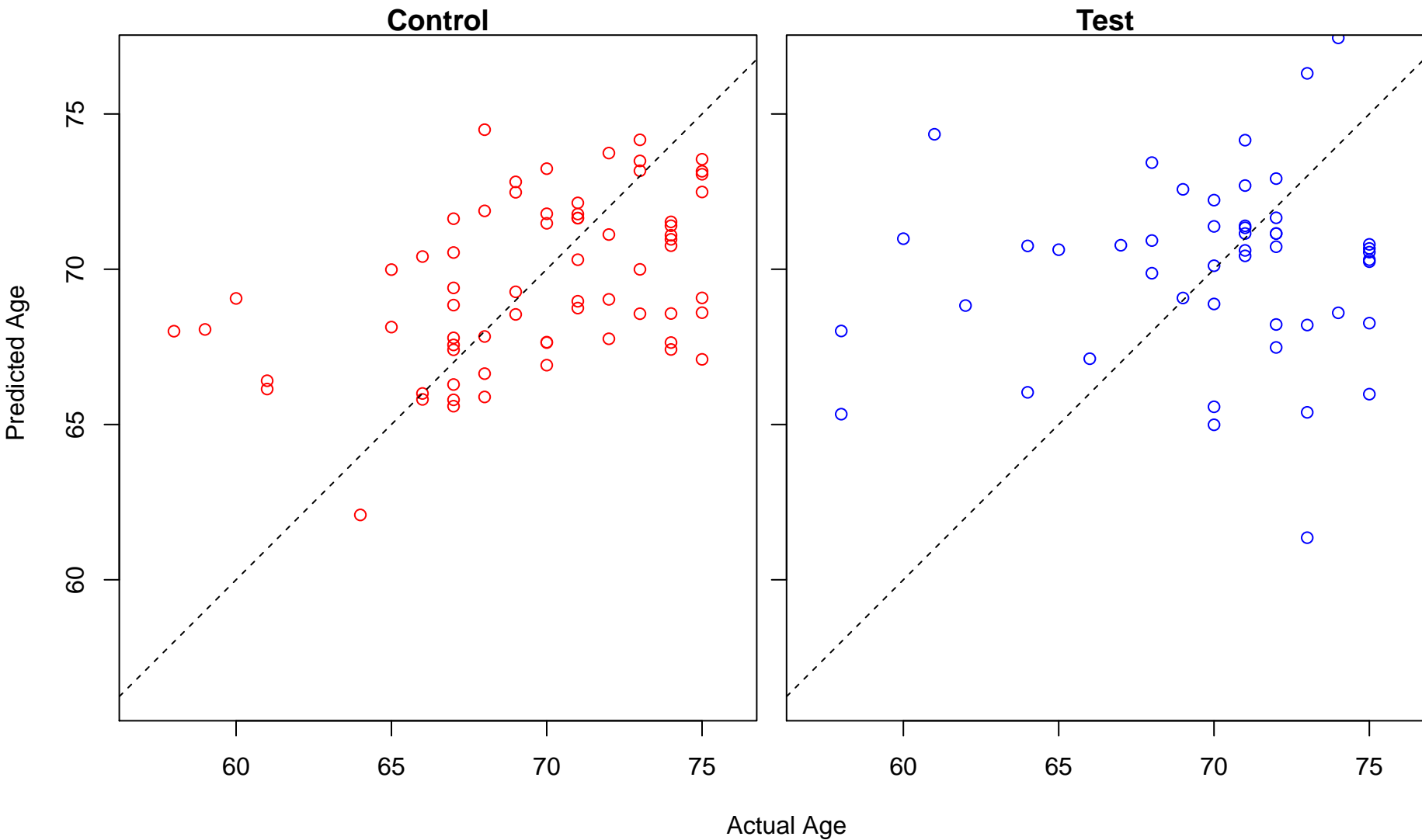
regulation of transforming growth factor beta production (Score: 0.800944)



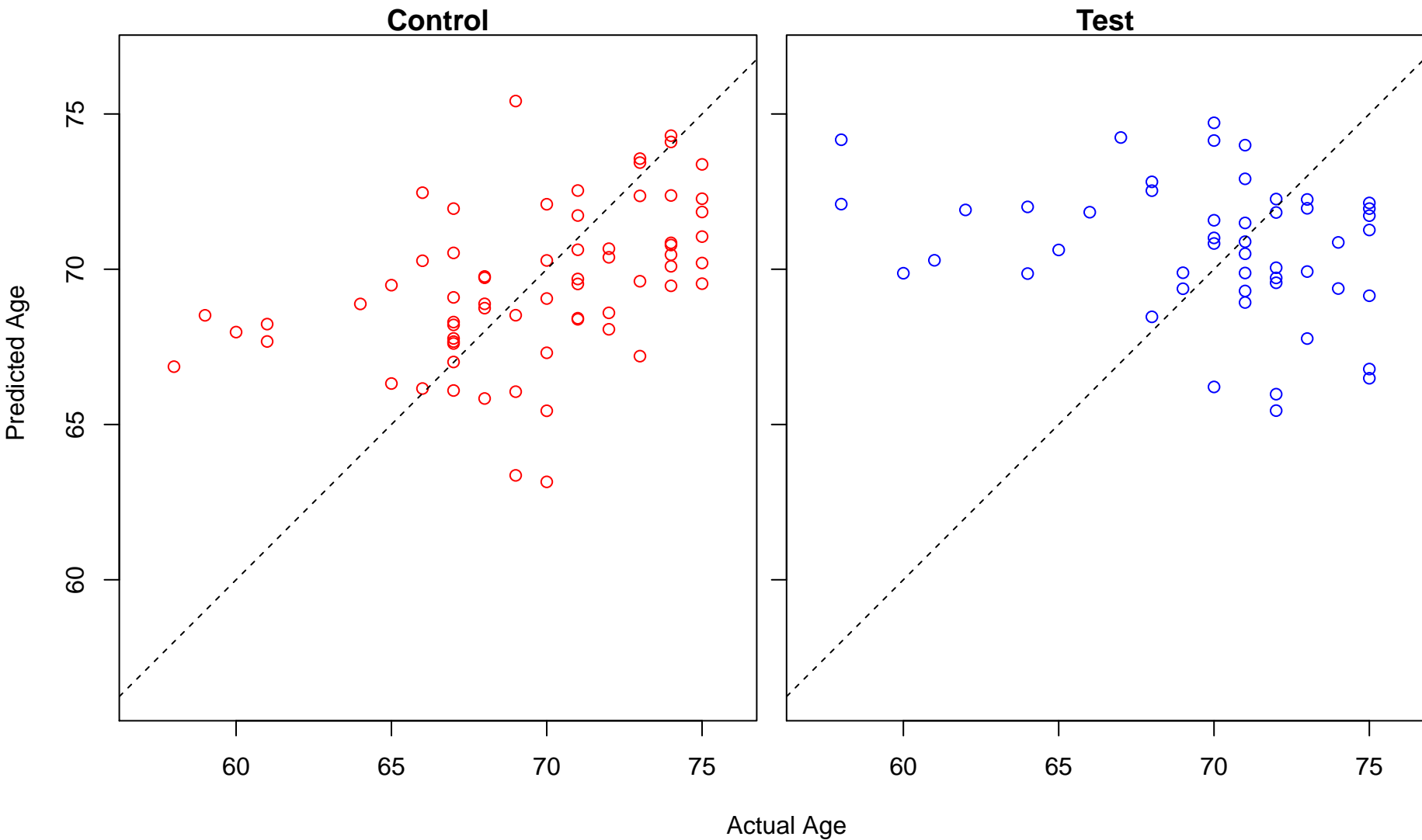
venous blood vessel development (Score: 0.800526)



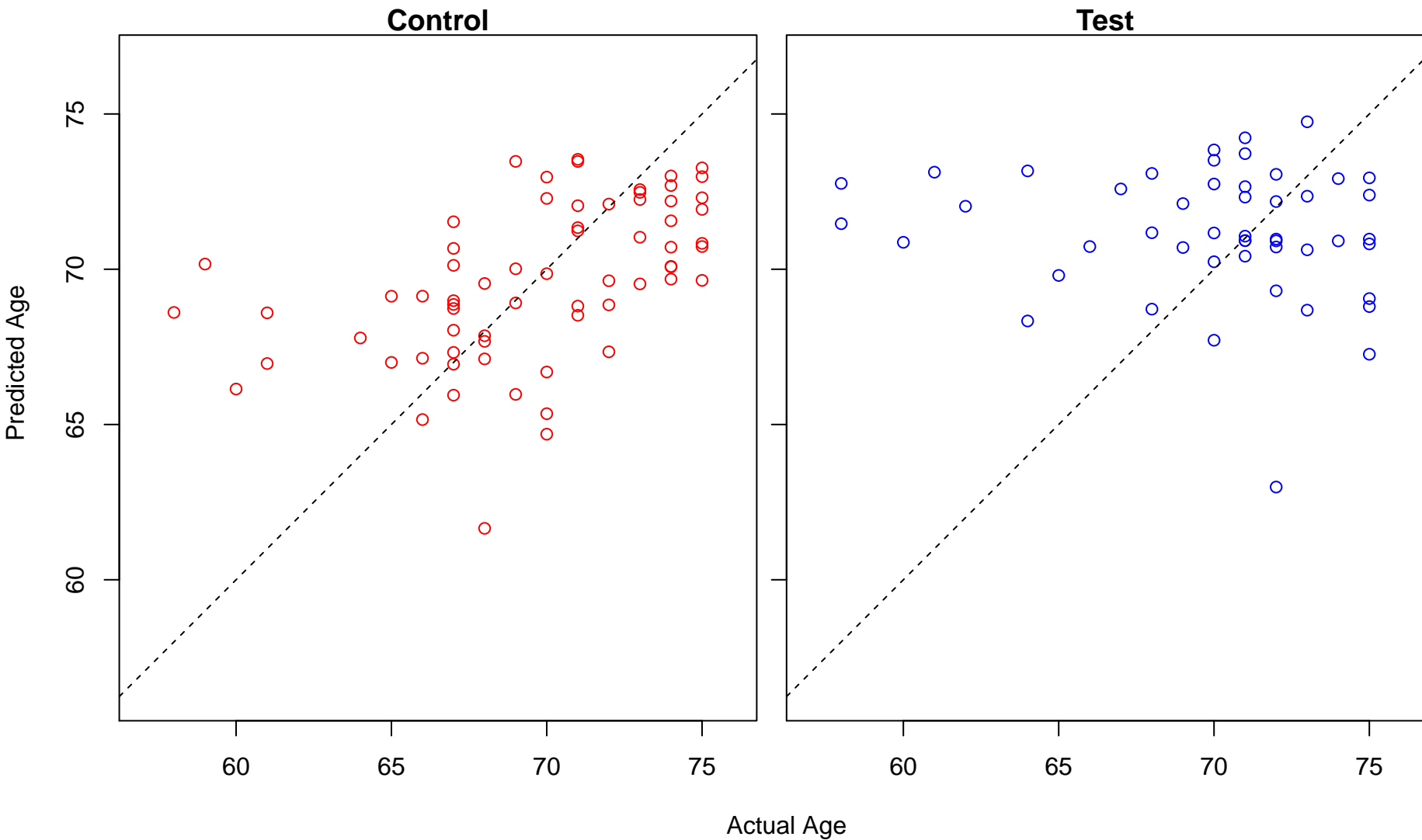
neurotransmitter biosynthetic process (Score: 0.800443)



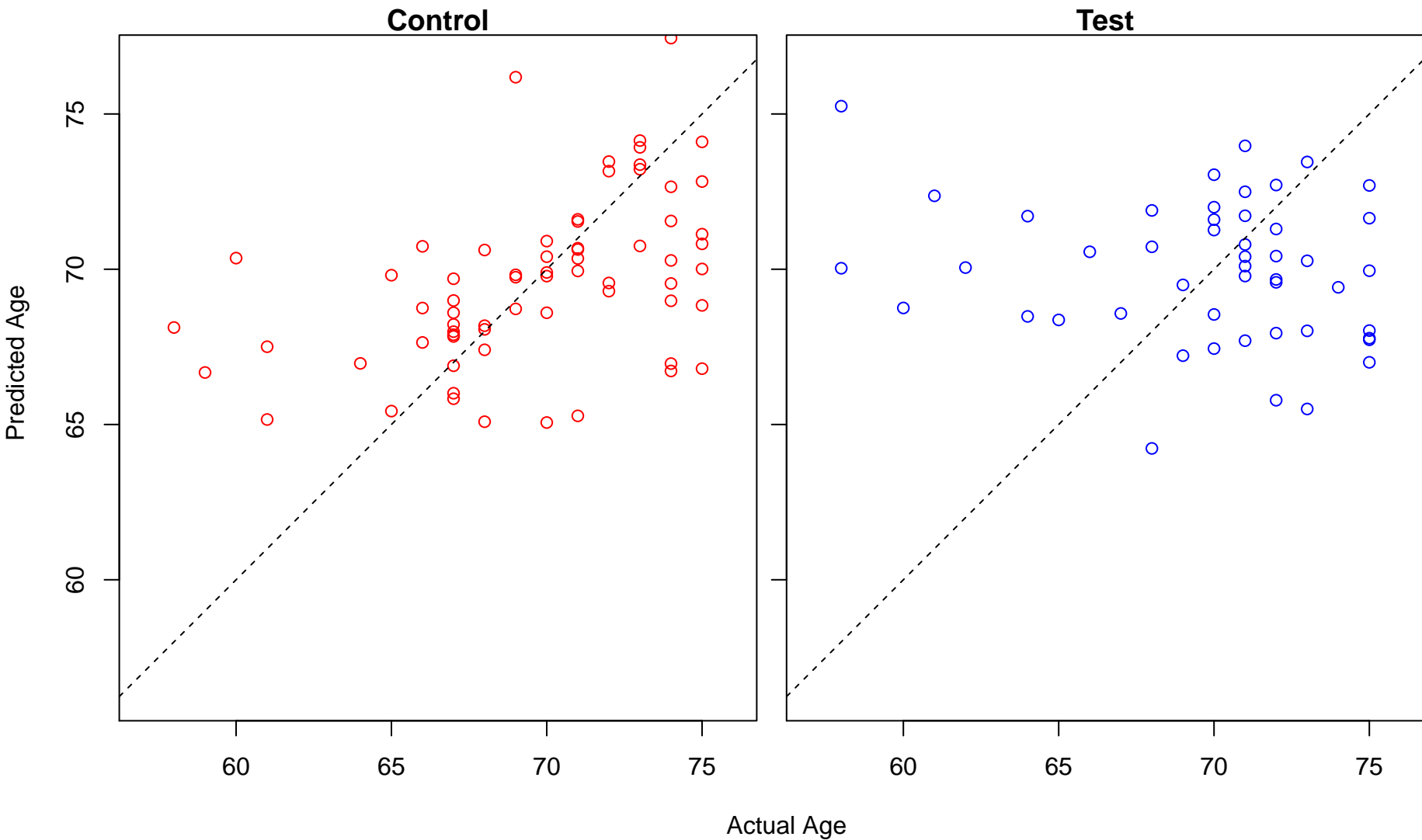
positive regulation of epithelial cell apoptotic process (Score: 0.798799)



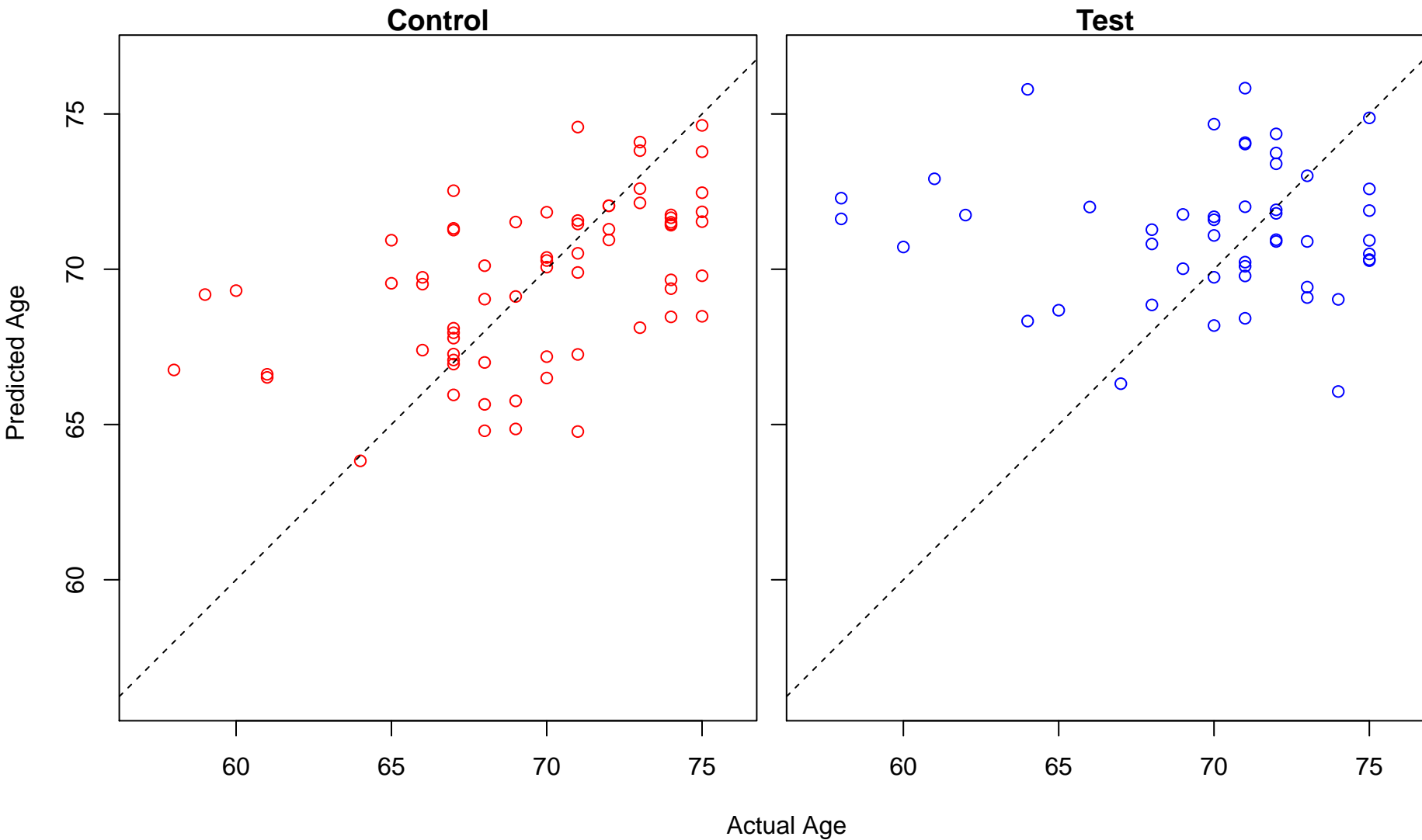
sulfur amino acid biosynthetic process (Score: 0.798588)



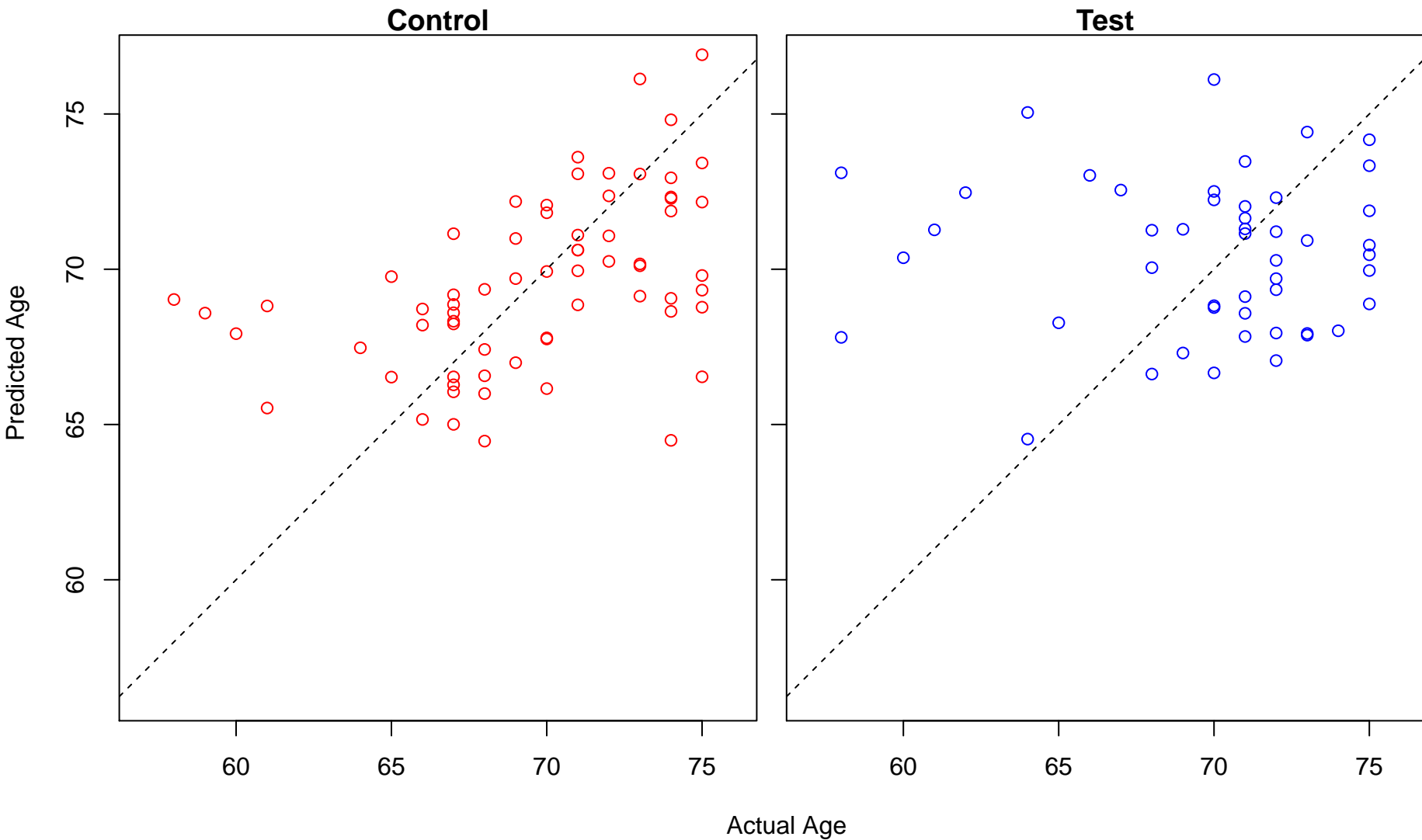
negative regulation of interferon-gamma production (Score: 0.797291)



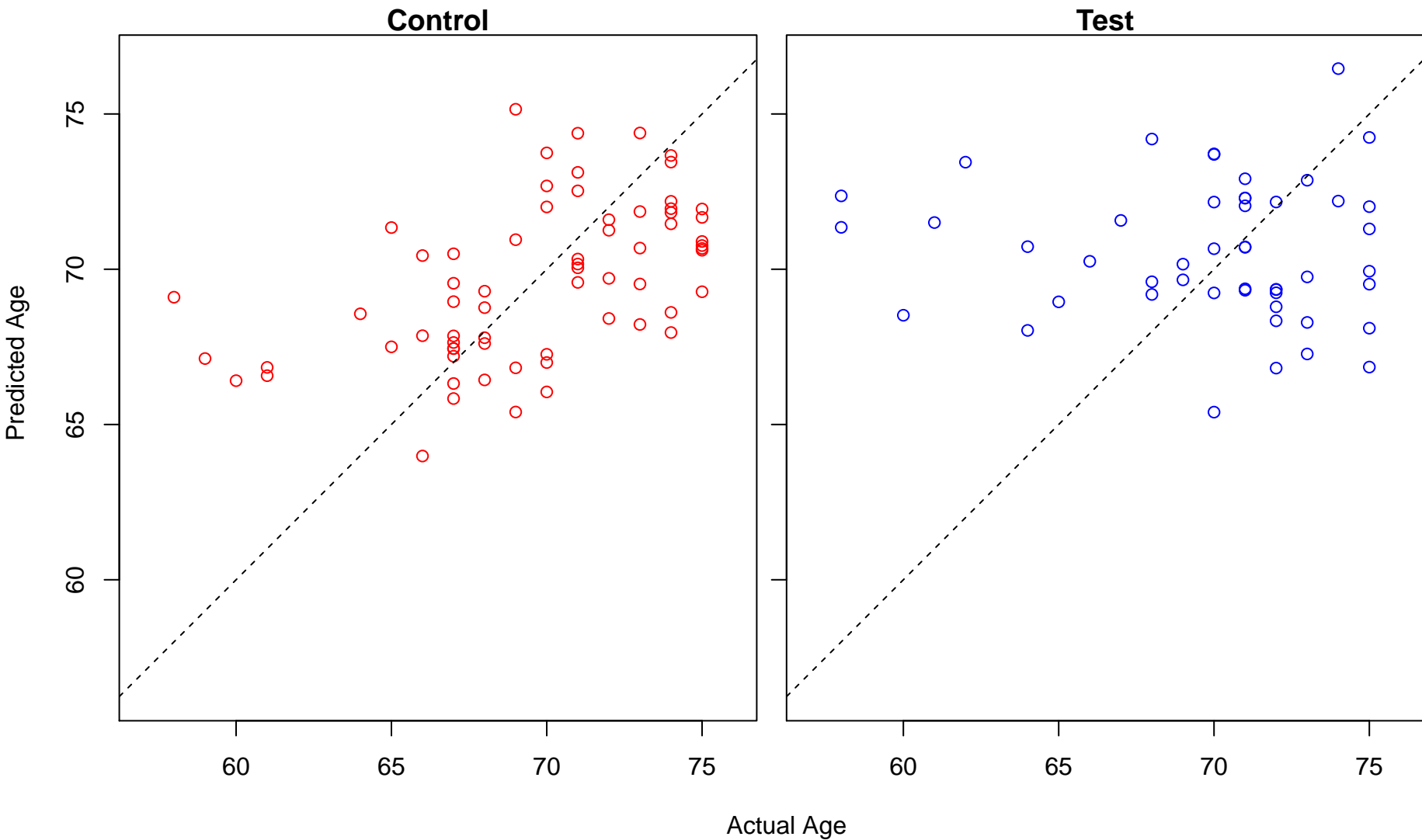
leukotriene biosynthetic process (Score: 0.797247)



regulation of receptor internalization (Score: 0.797140)

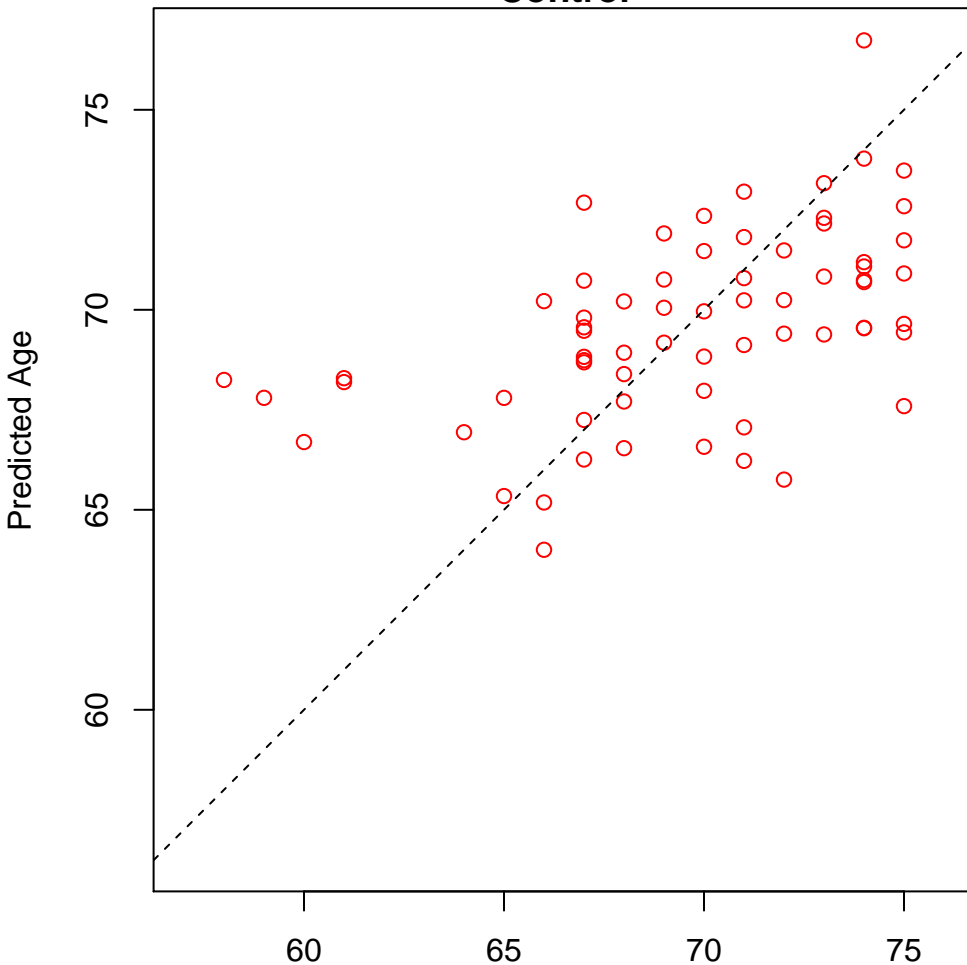


regulation of tolerance induction (Score: 0.797118)

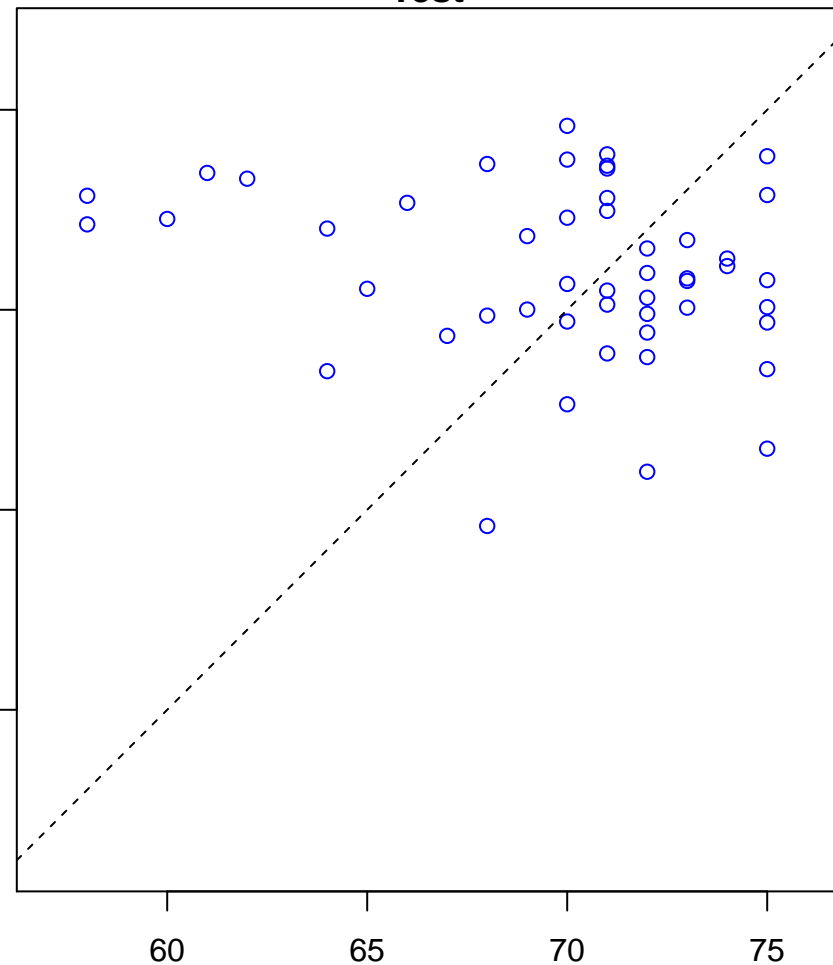


long-term synaptic potentiation (Score: 0.796606)

Control



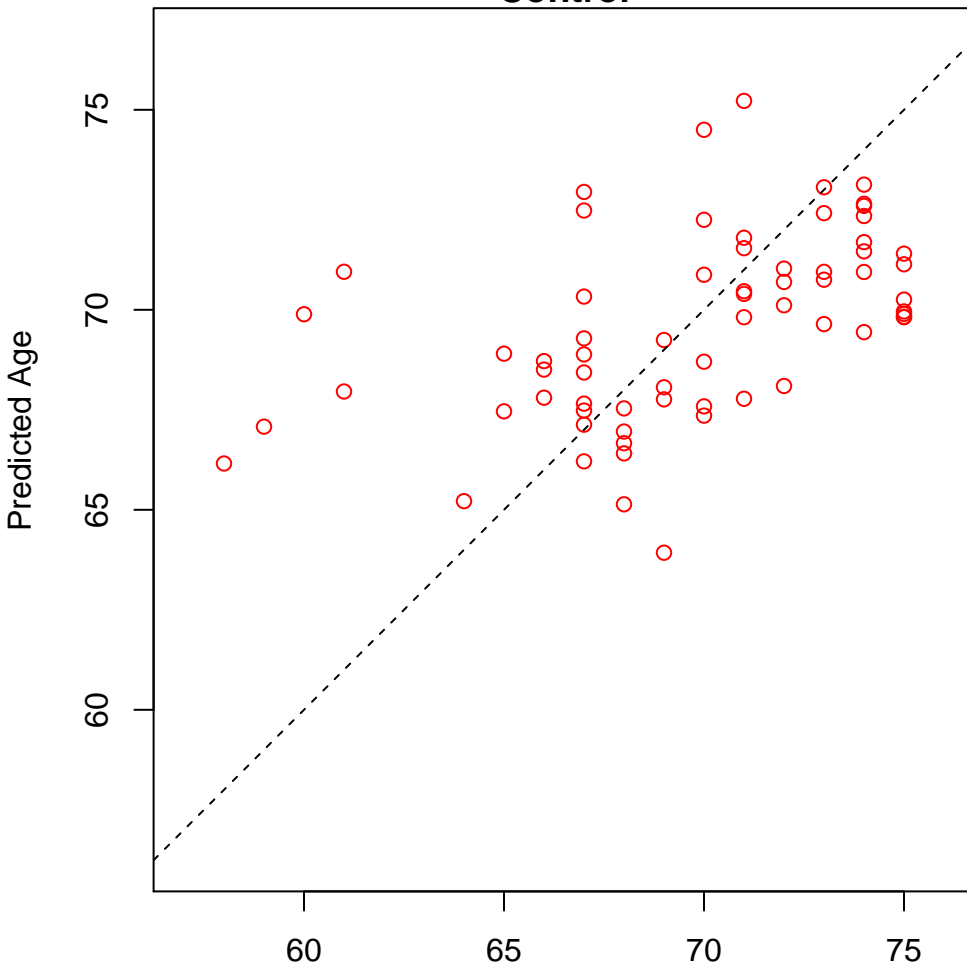
Test



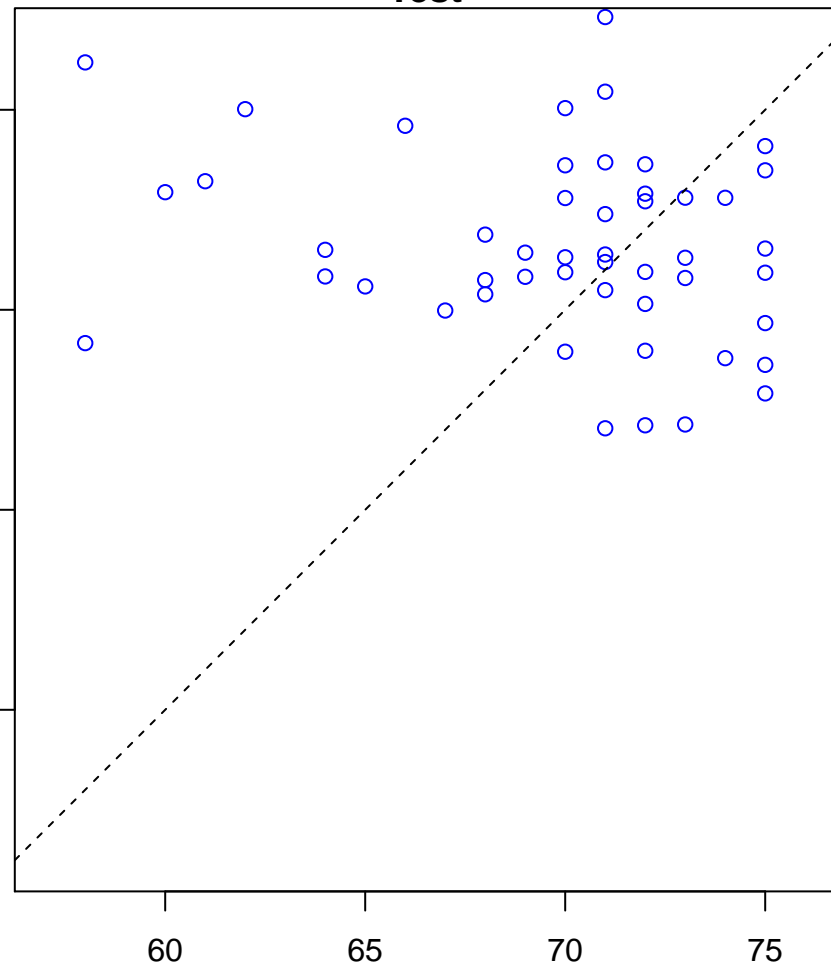
Actual Age

sulfur amino acid catabolic process (Score: 0.796591)

Control

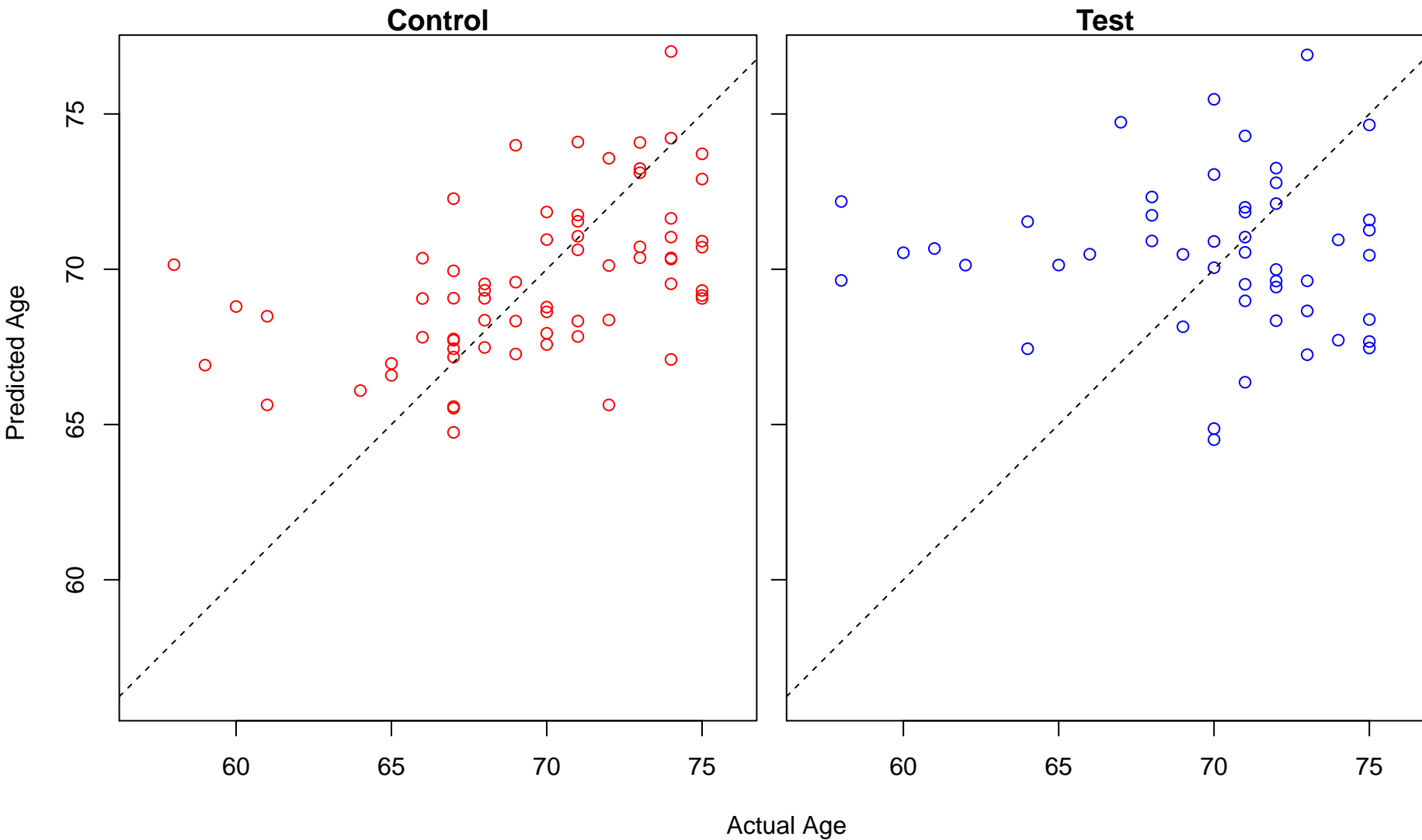


Test

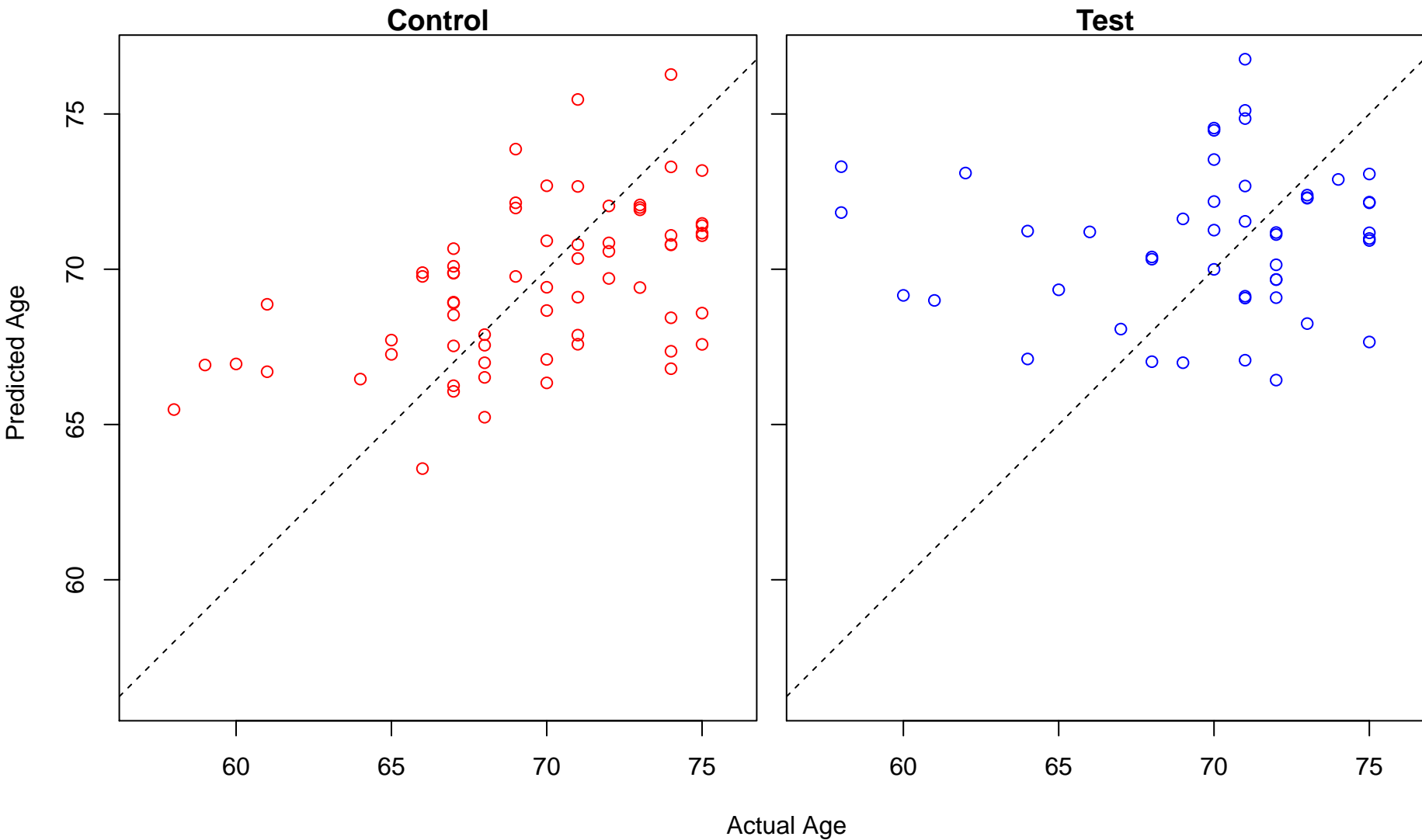


Actual Age

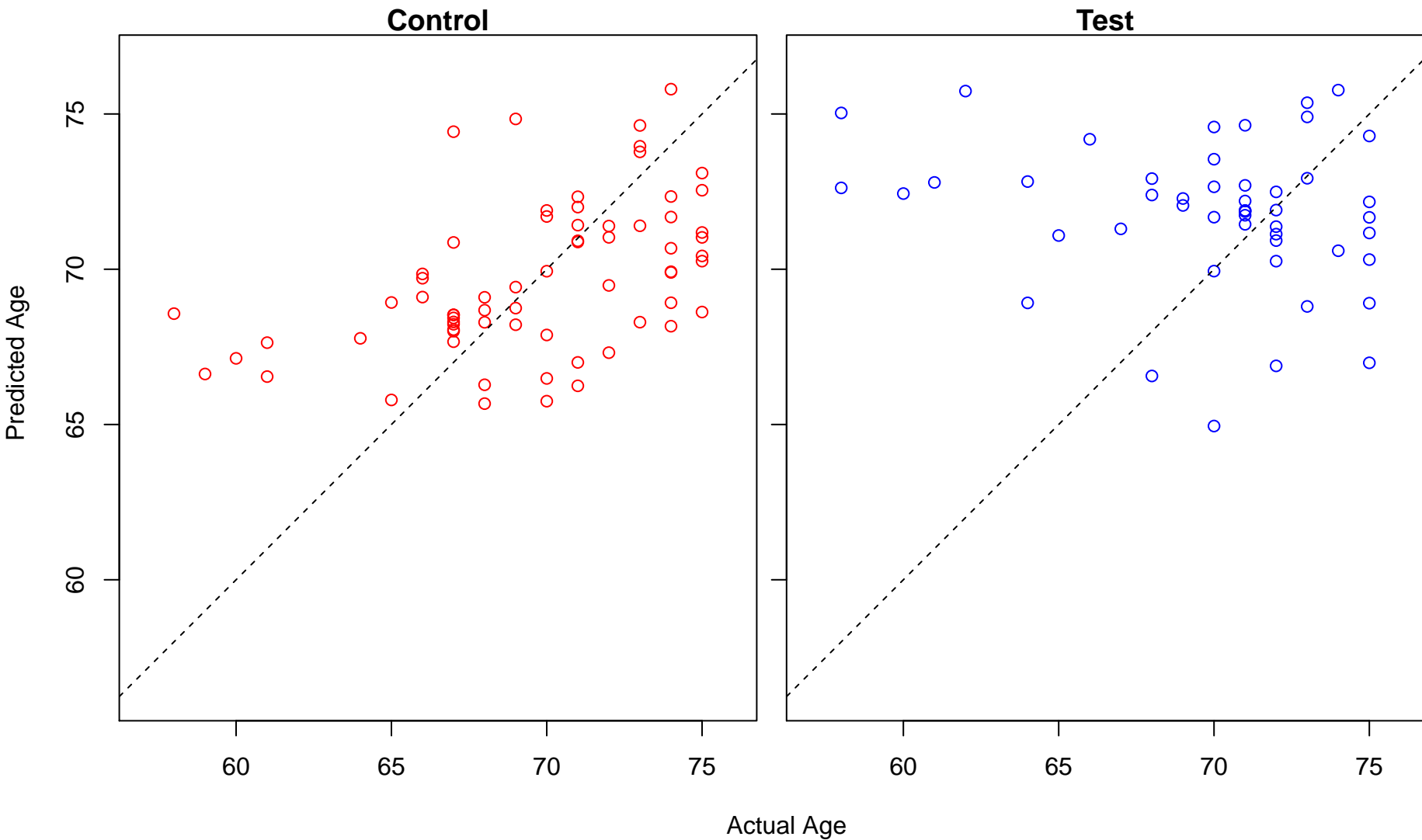
mRNA methylation (Score: 0.795894)



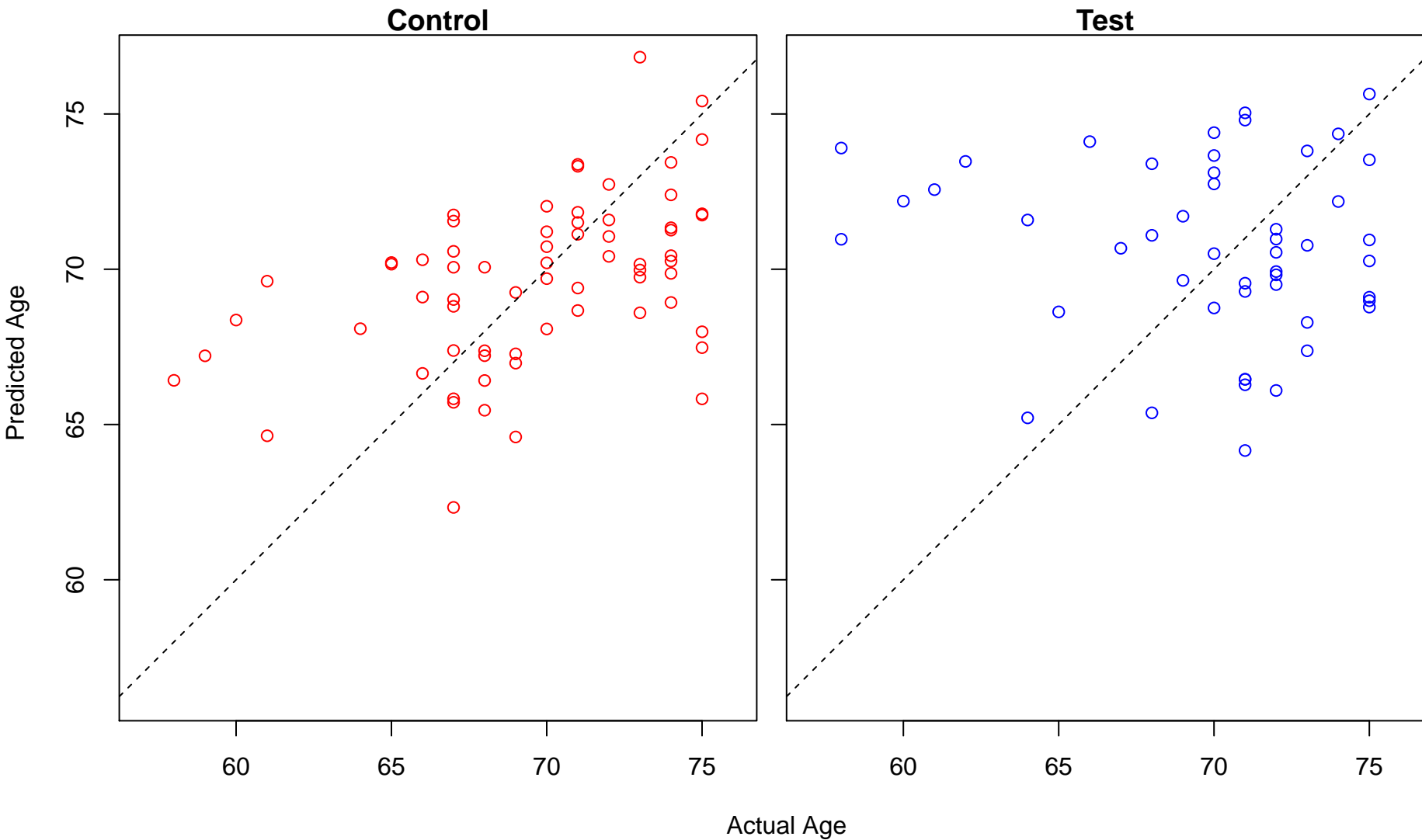
acute-phase response (Score: 0.795514)



regulation of microtubule polymerization or depolymerization (Score: 0.795078)

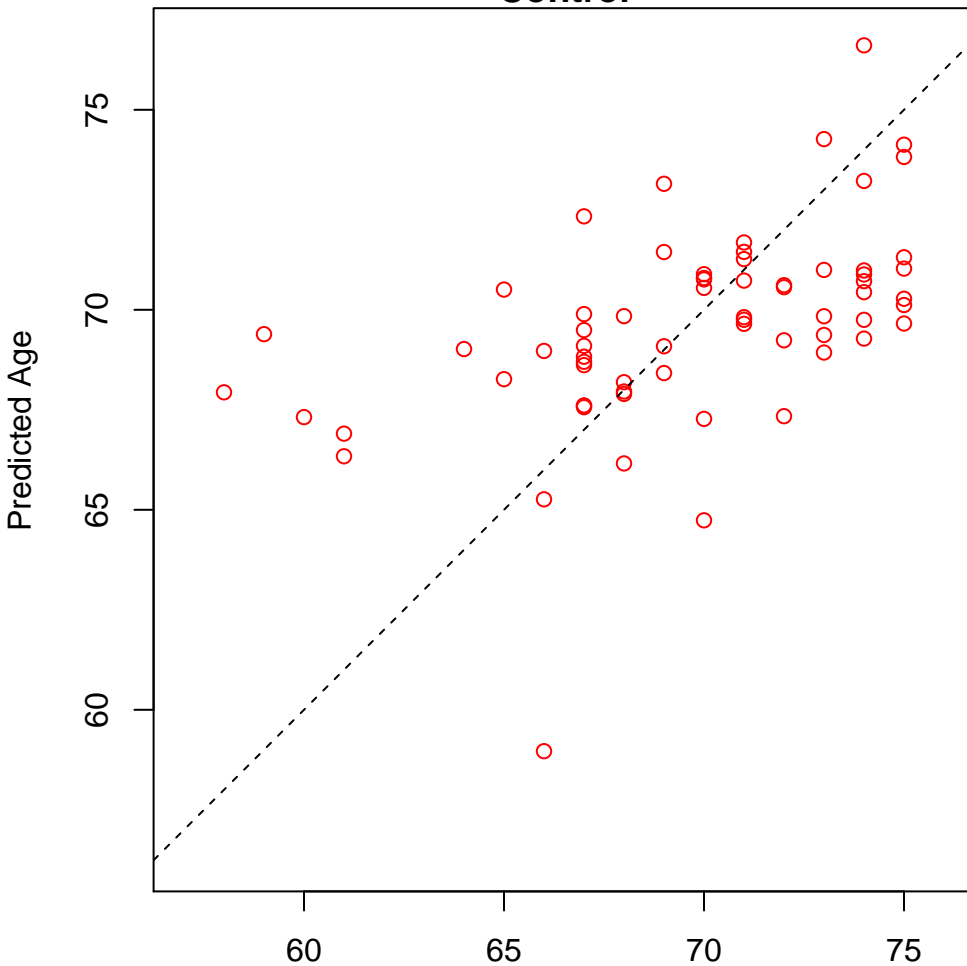


astrocyte differentiation (Score: 0.794927)

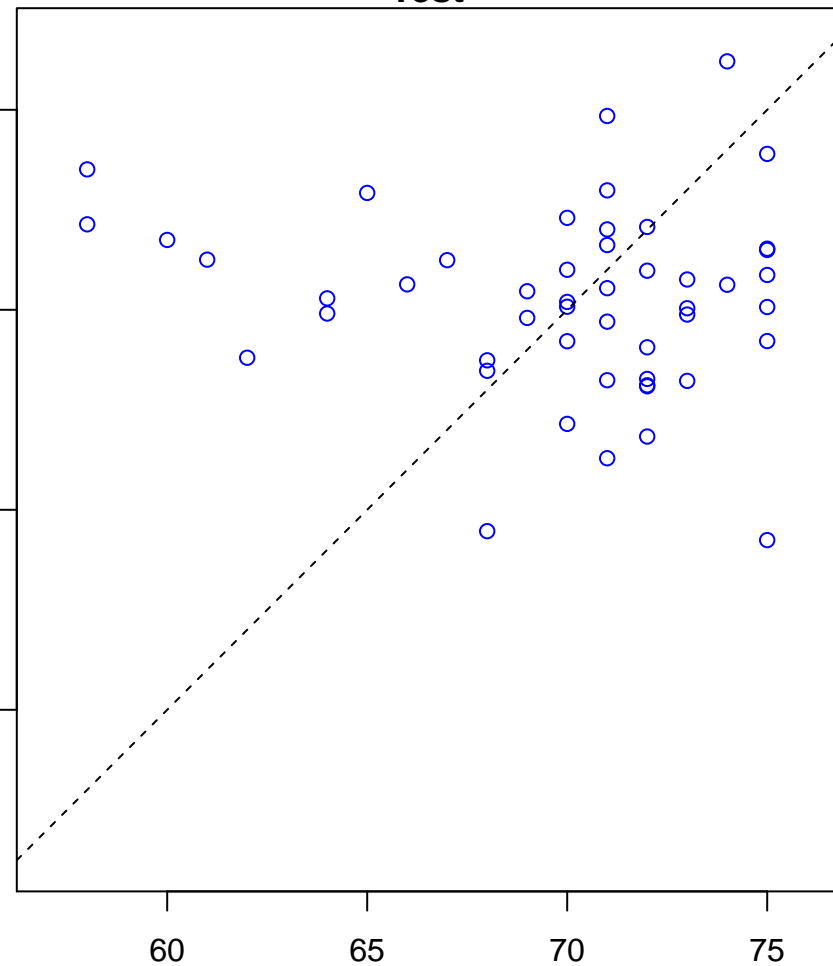


regulation of digestive system process (Score: 0.794794)

Control



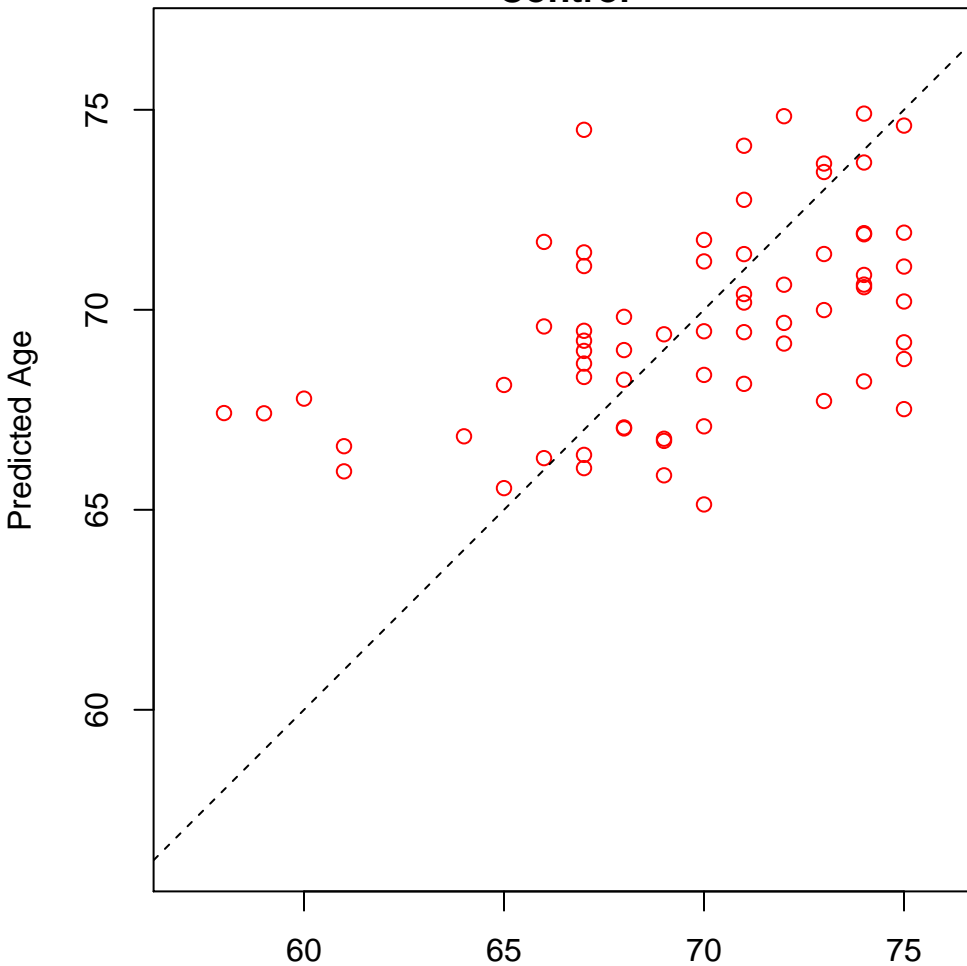
Test



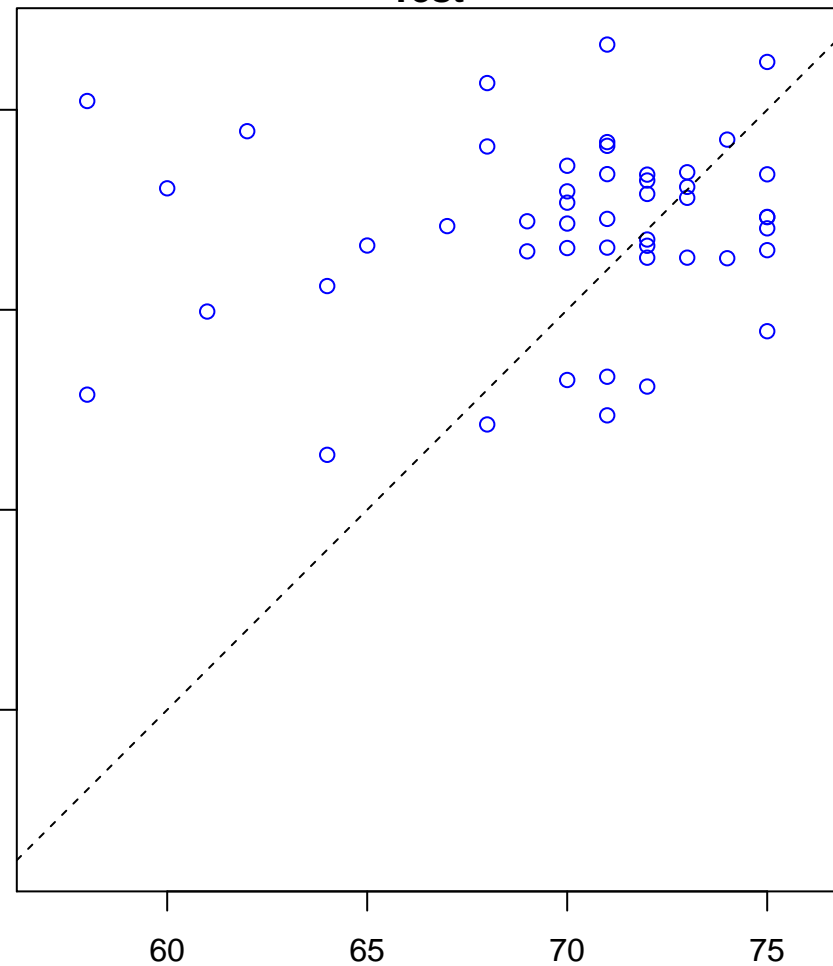
Actual Age

regulation of smooth muscle contraction (Score: 0.794764)

Control

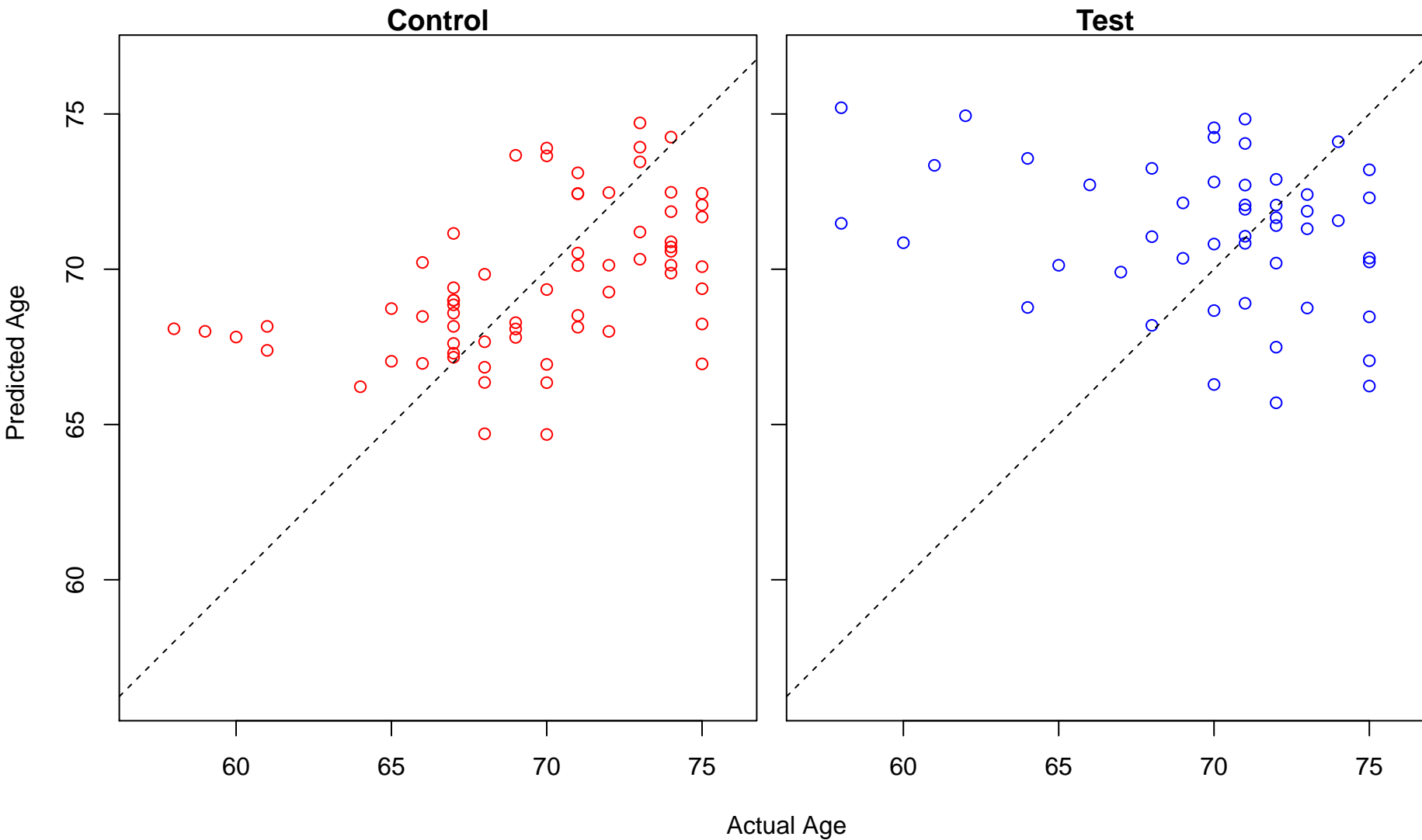


Test

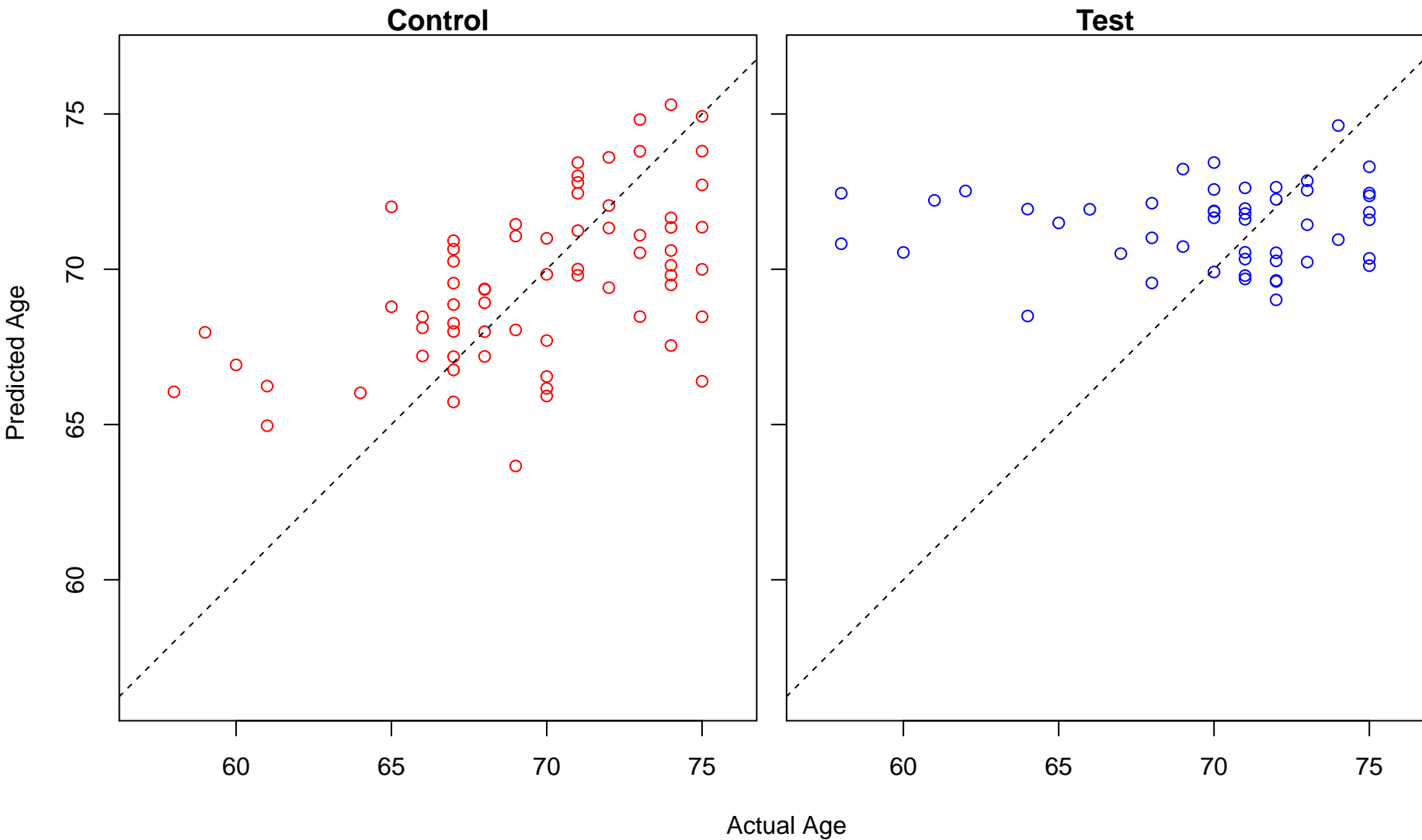


Actual Age

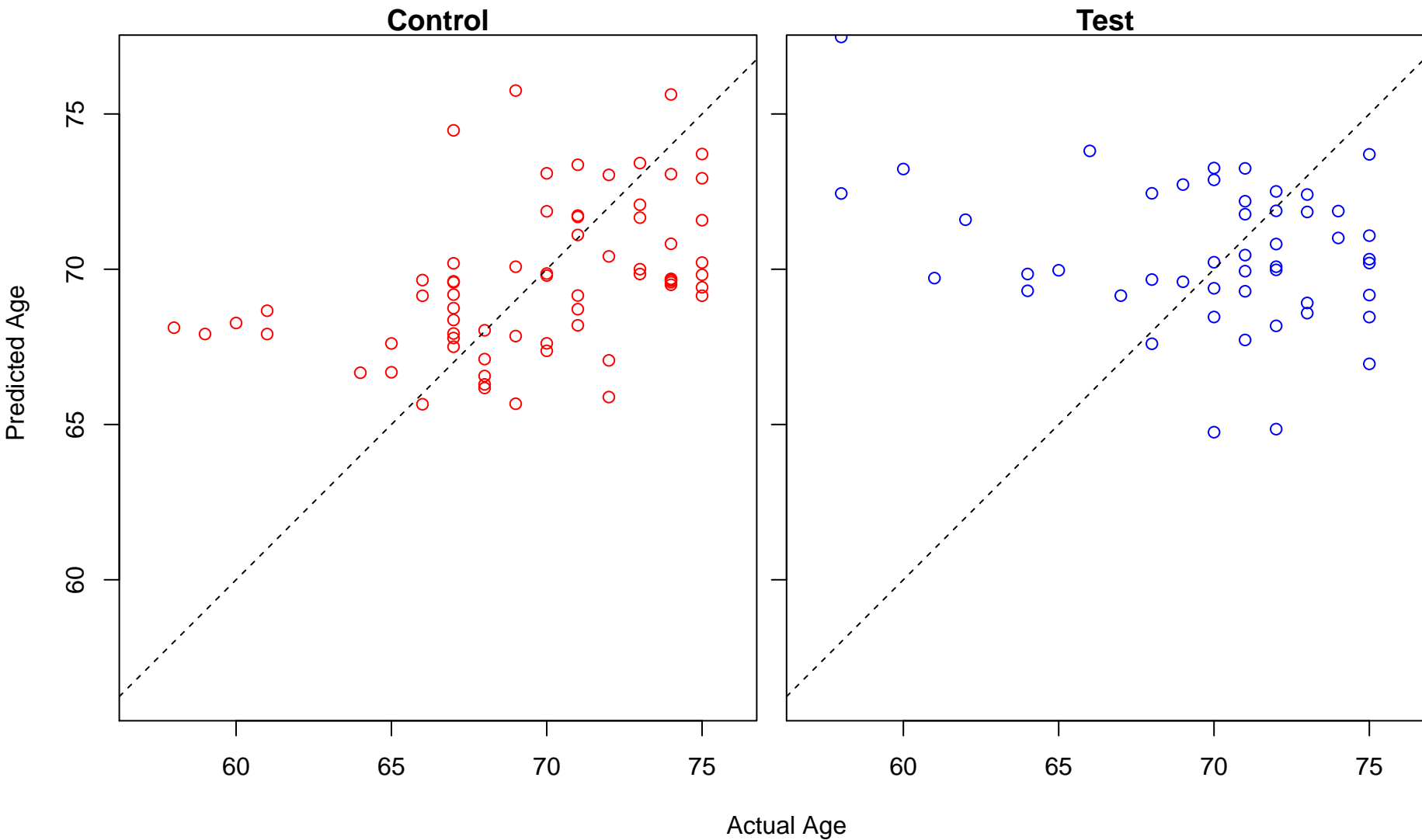
regulation of mRNA catabolic process (Score: 0.794747)



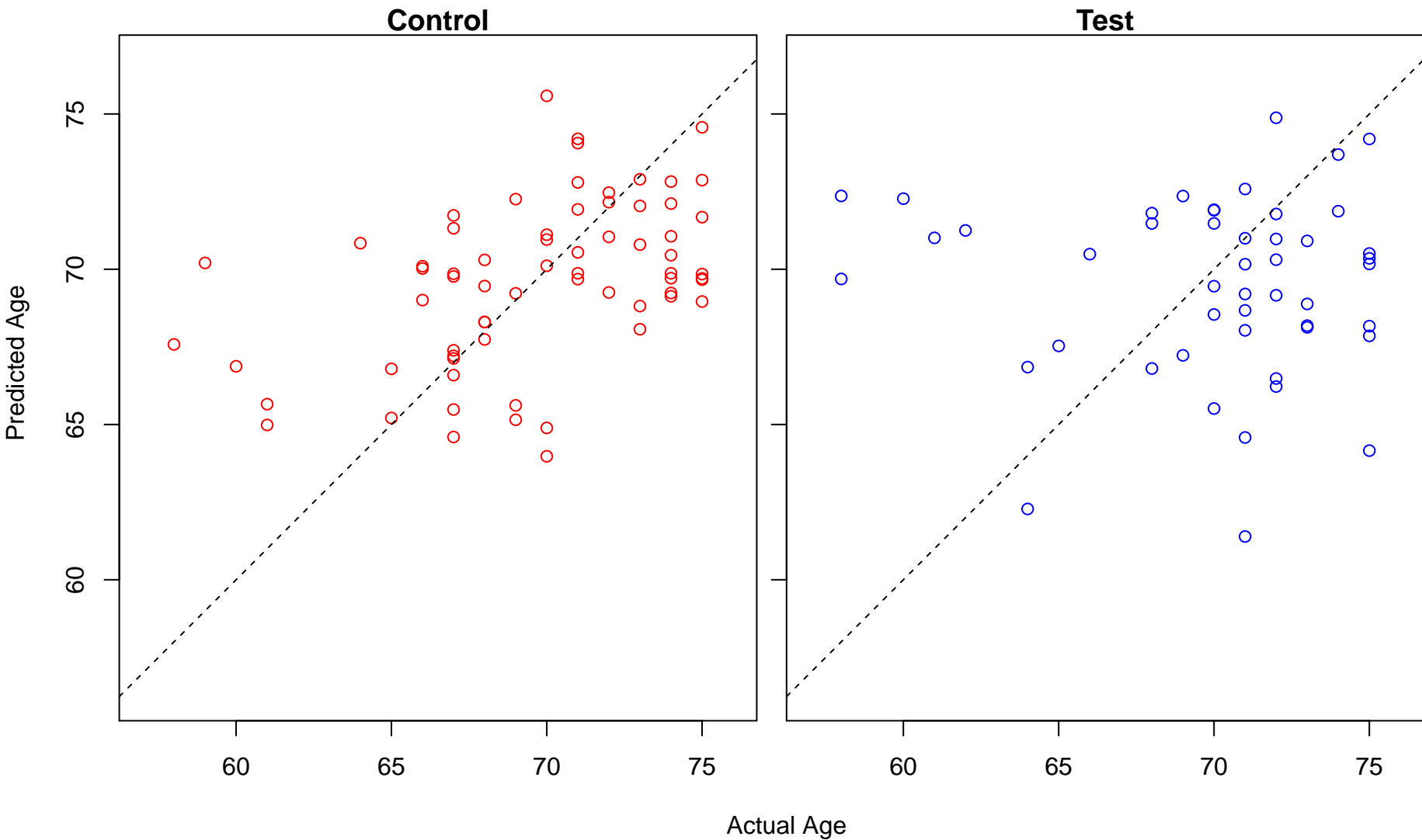
skeletal muscle contraction (Score: 0.794733)



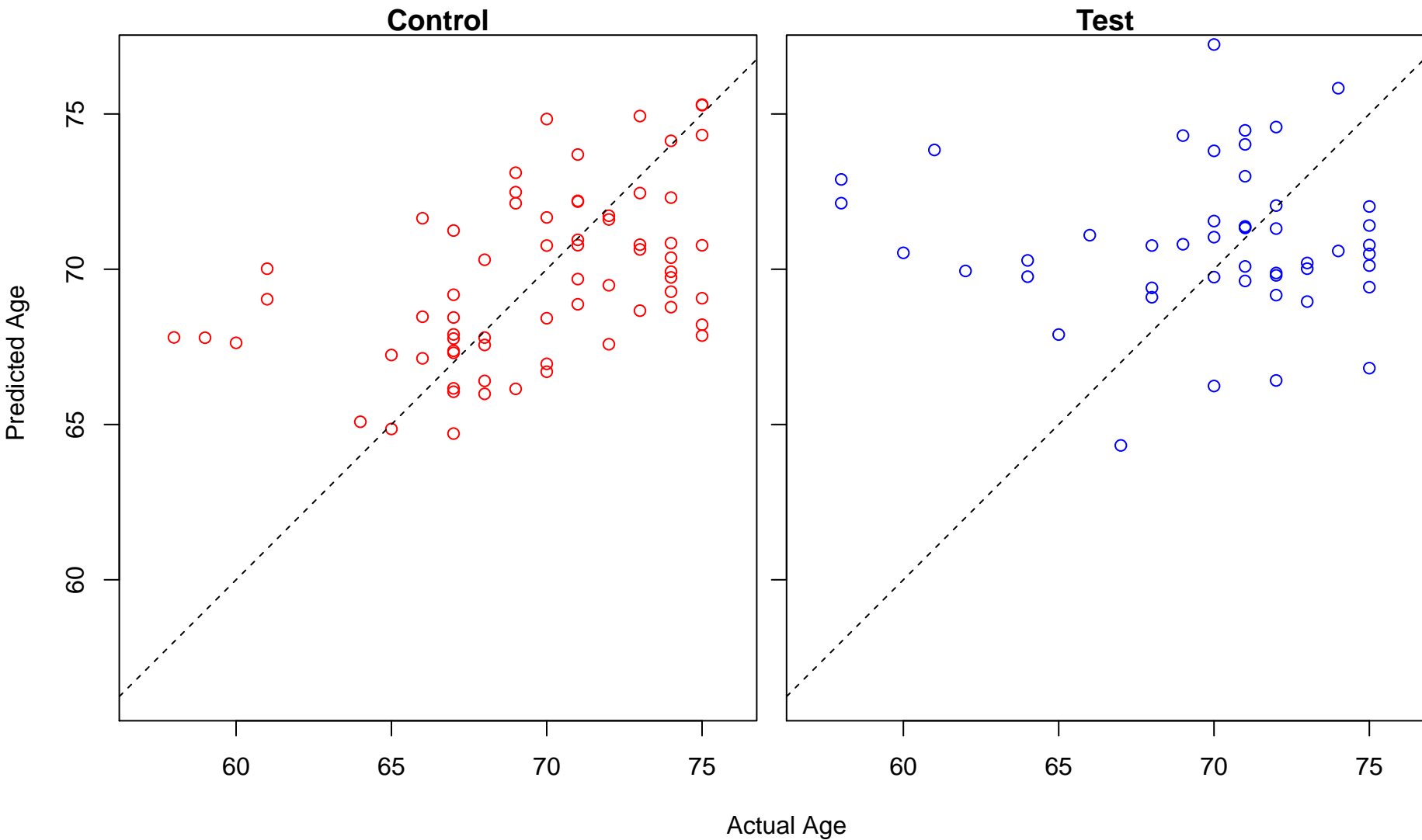
cell proliferation involved in kidney development (Score: 0.794173)



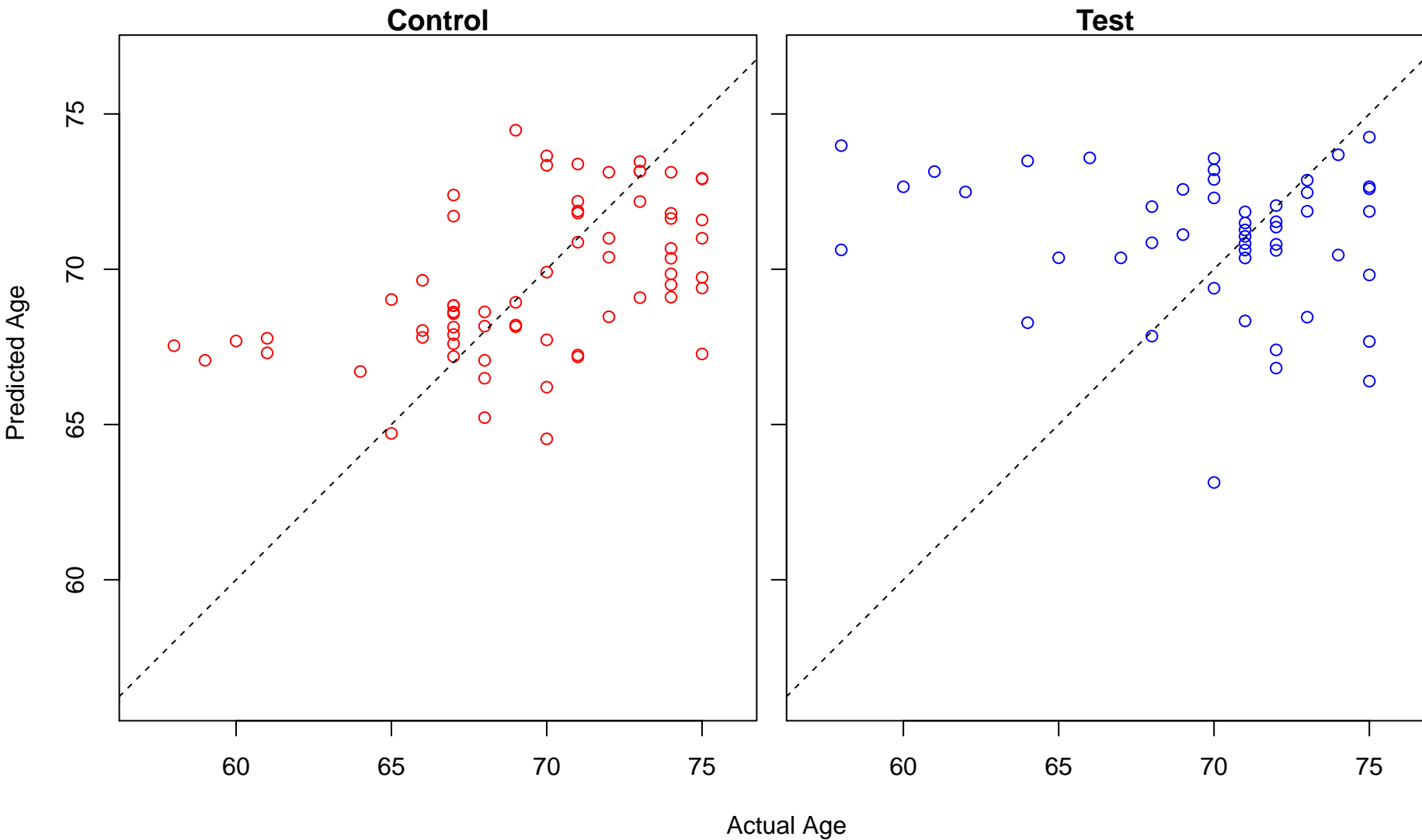
regulation of retinoic acid receptor signaling pathway (Score: 0.794092)



GDP-mannose metabolic process (Score: 0.793967)

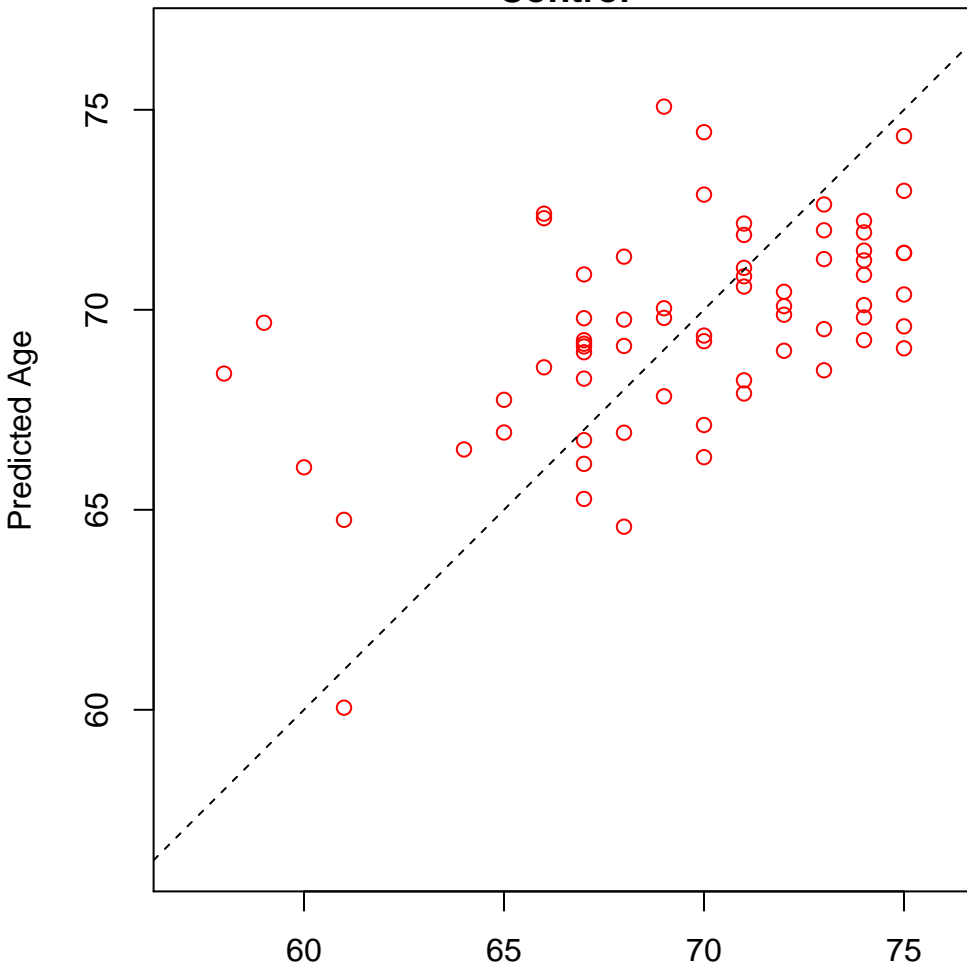


gland development (Score: 0.792982)

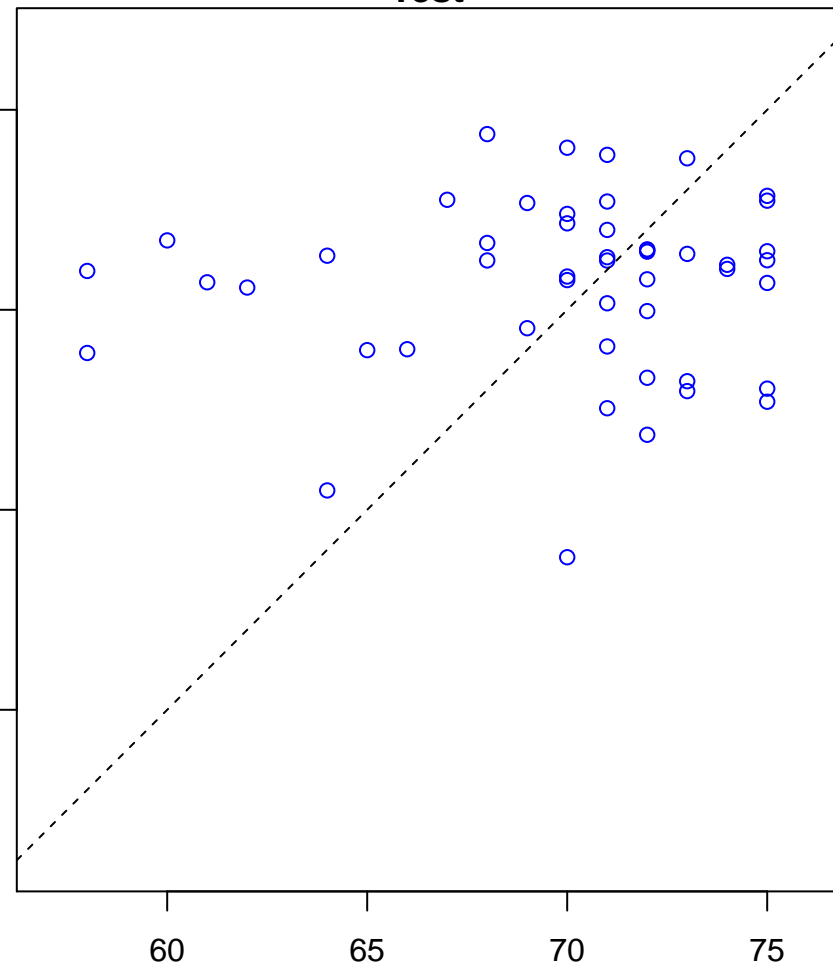


anterior/posterior axis specification (Score: 0.792398)

Control

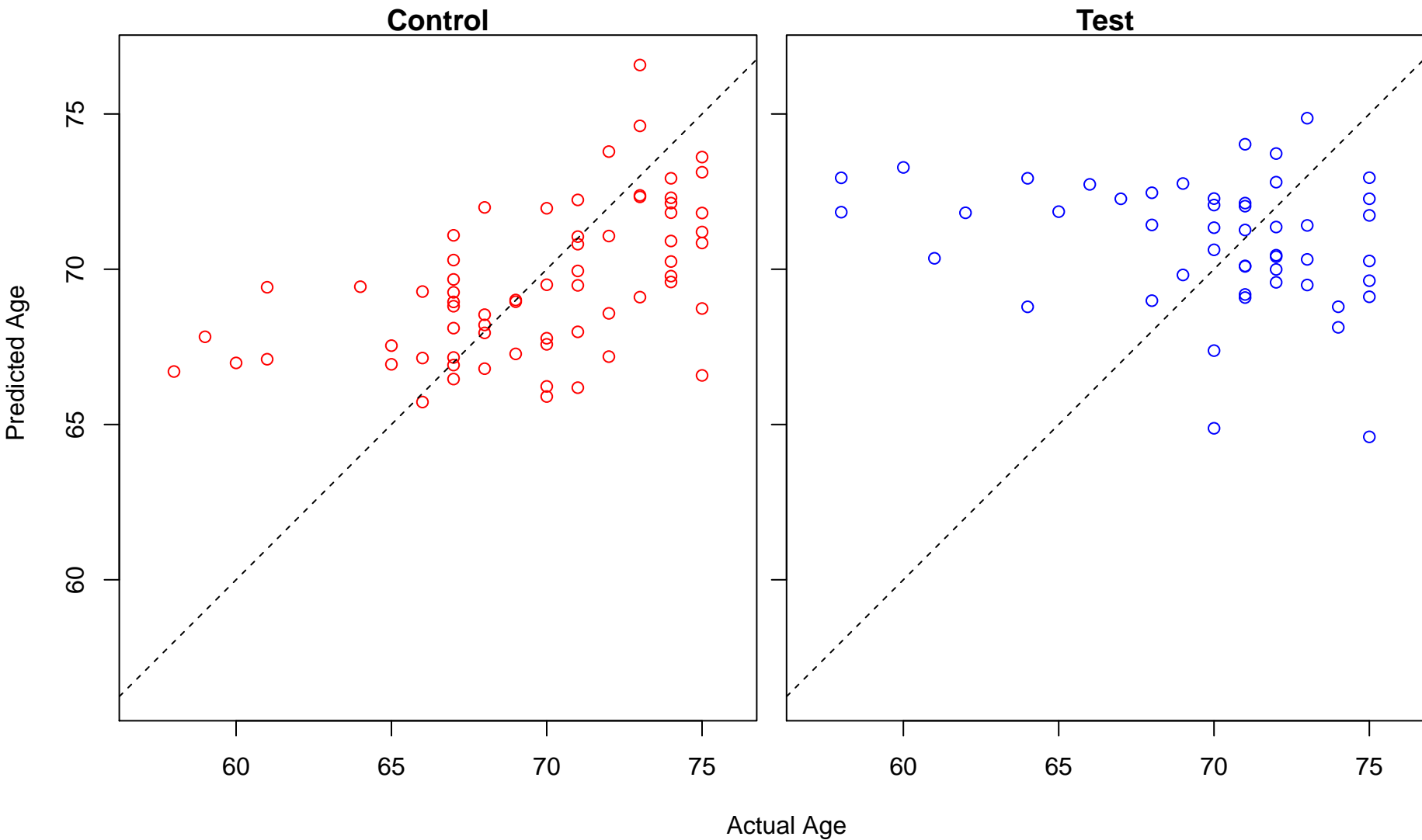


Test

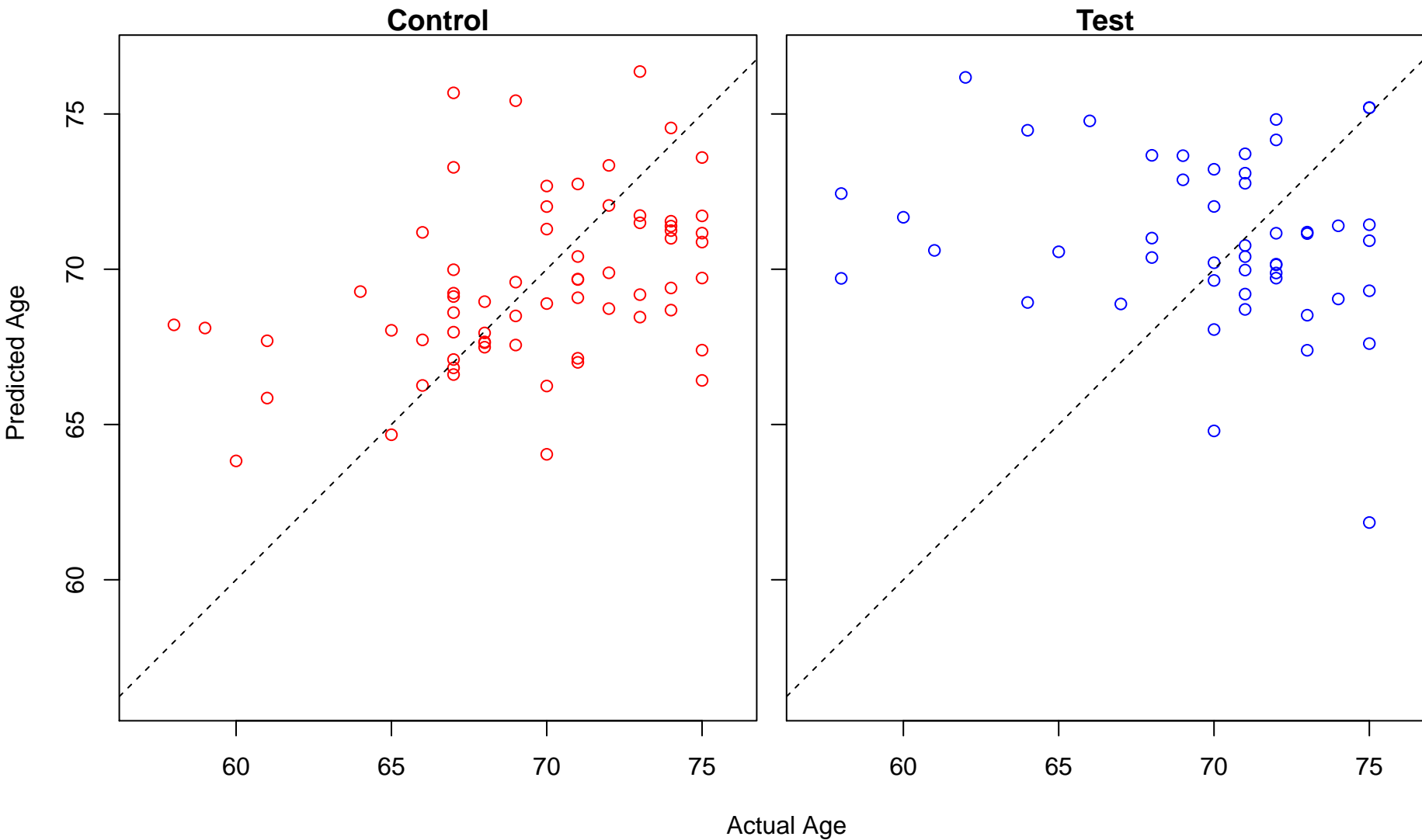


Actual Age

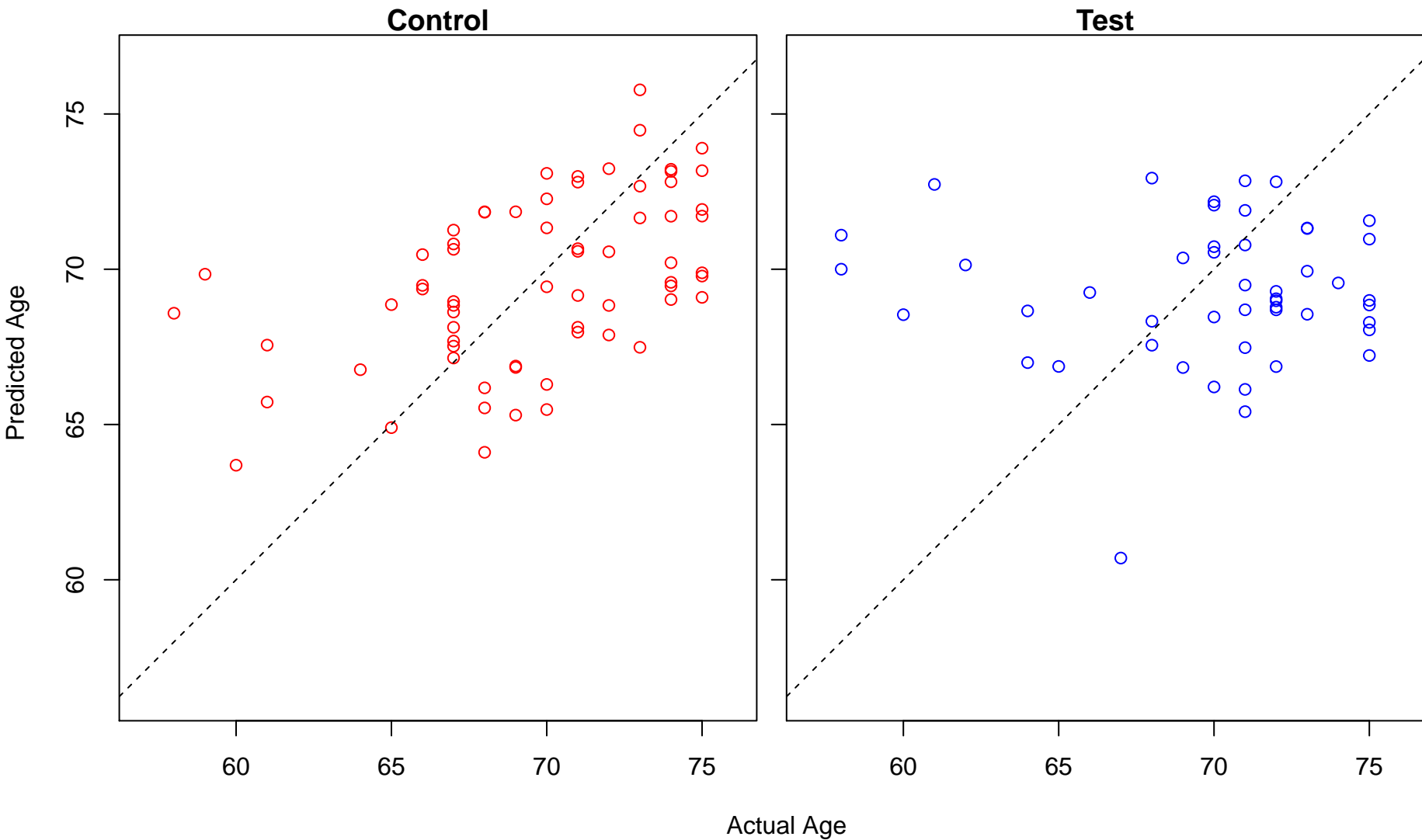
neutrophil activation involved in immune response (Score: 0.792372)



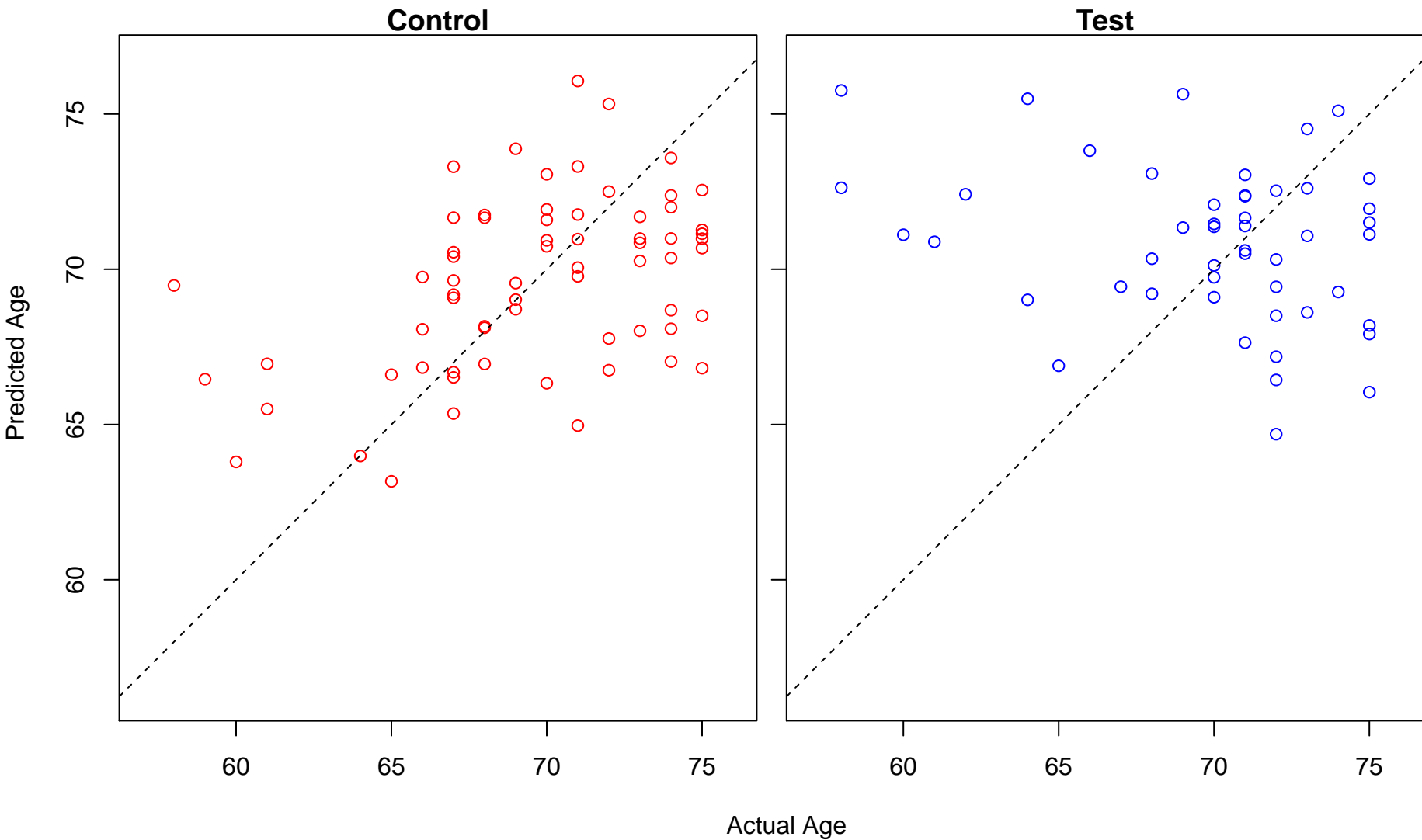
sprouting angiogenesis (Score: 0.792244)



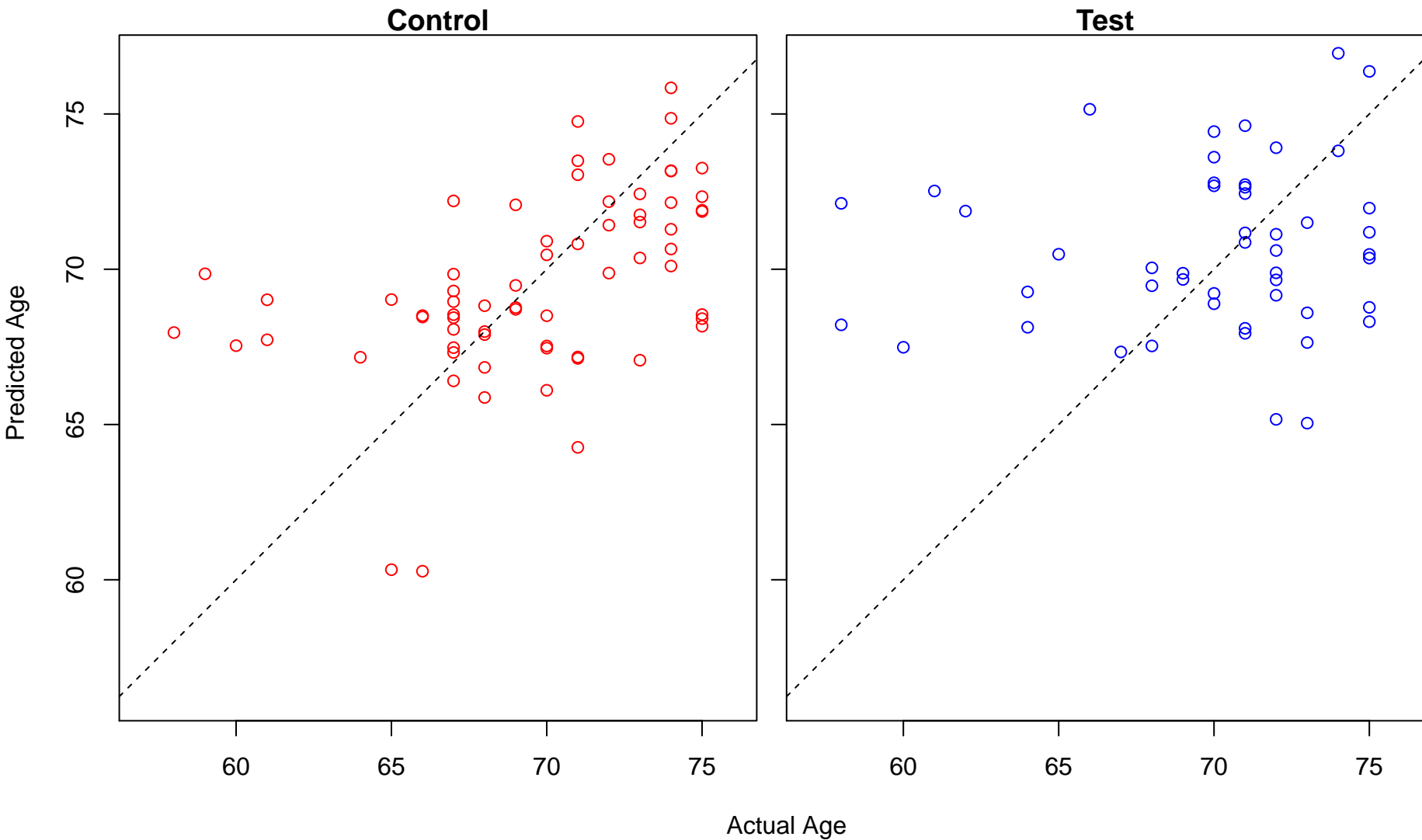
pinocytosis (Score: 0.792053)



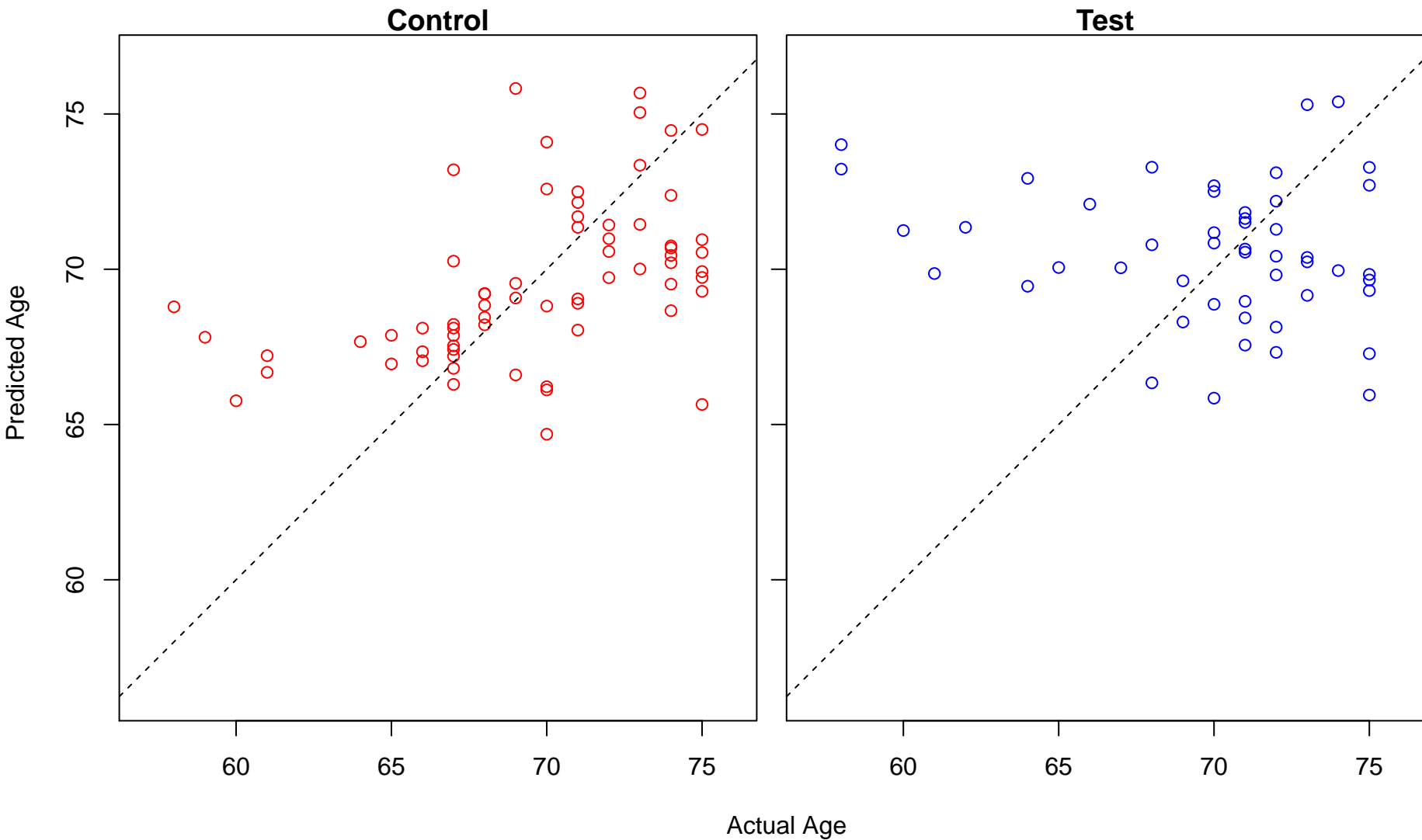
protein localization to centrosome (Score: 0.791484)



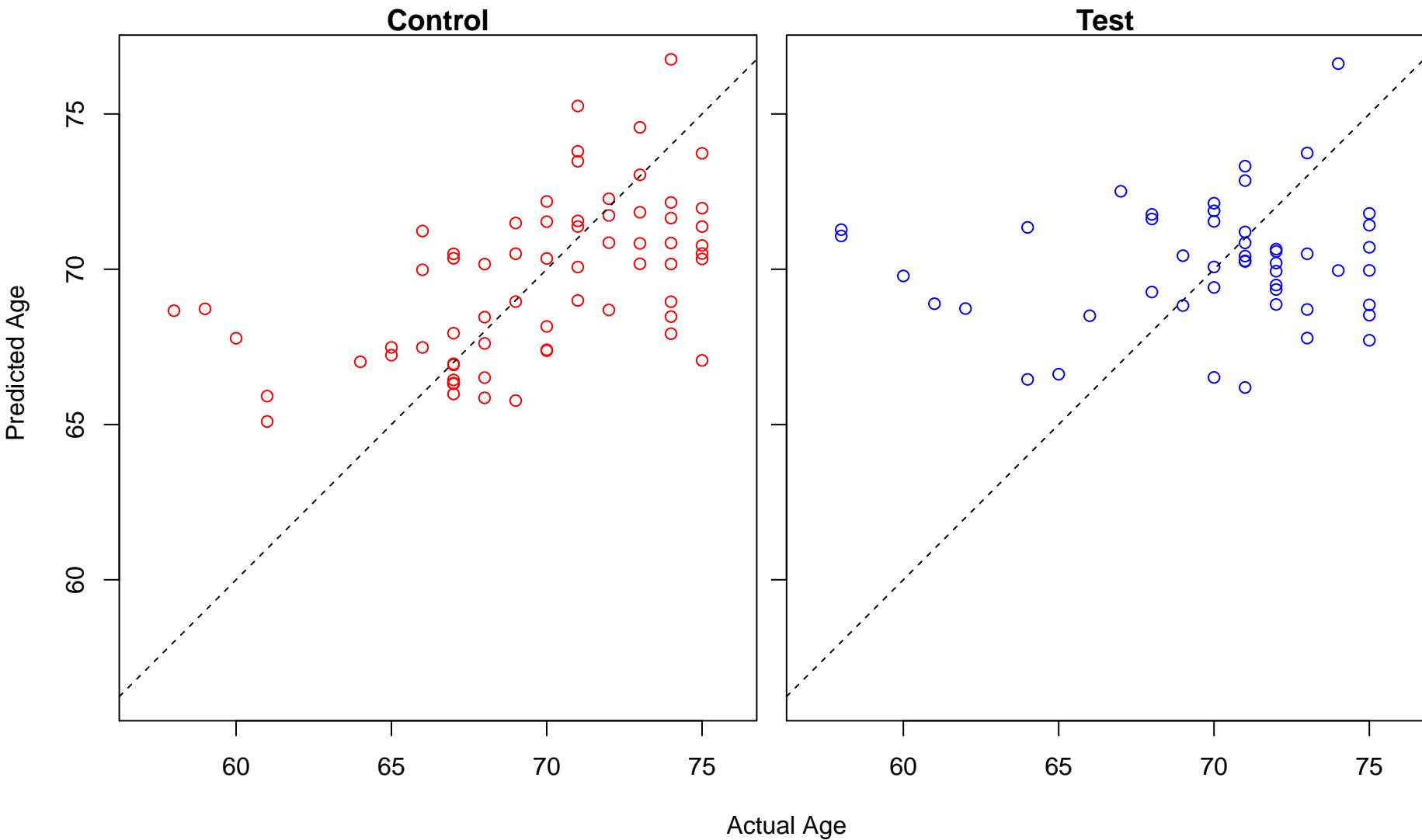
positive regulation of type 2 immune response (Score: 0.791432)



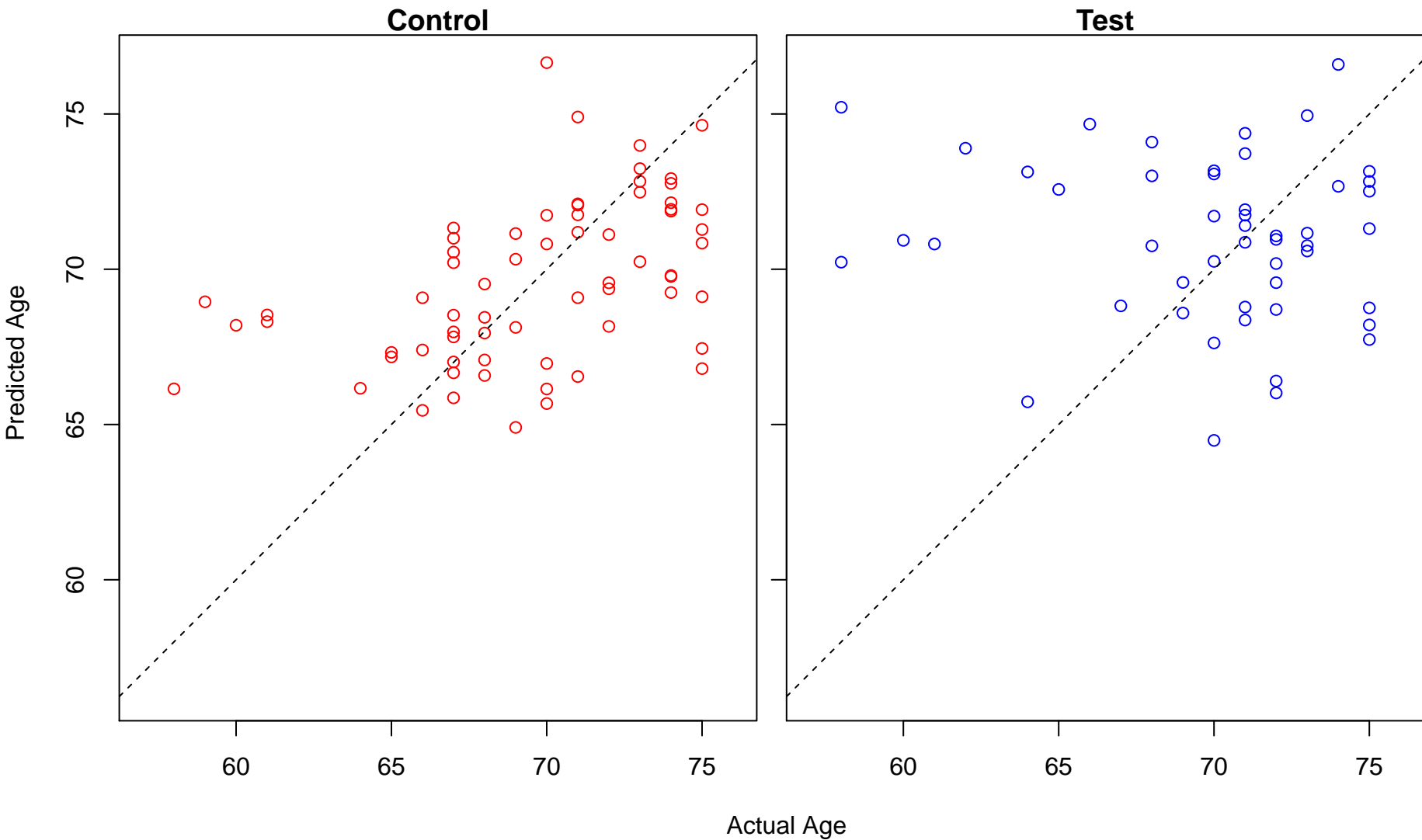
sodium ion transport (Score: 0.791229)



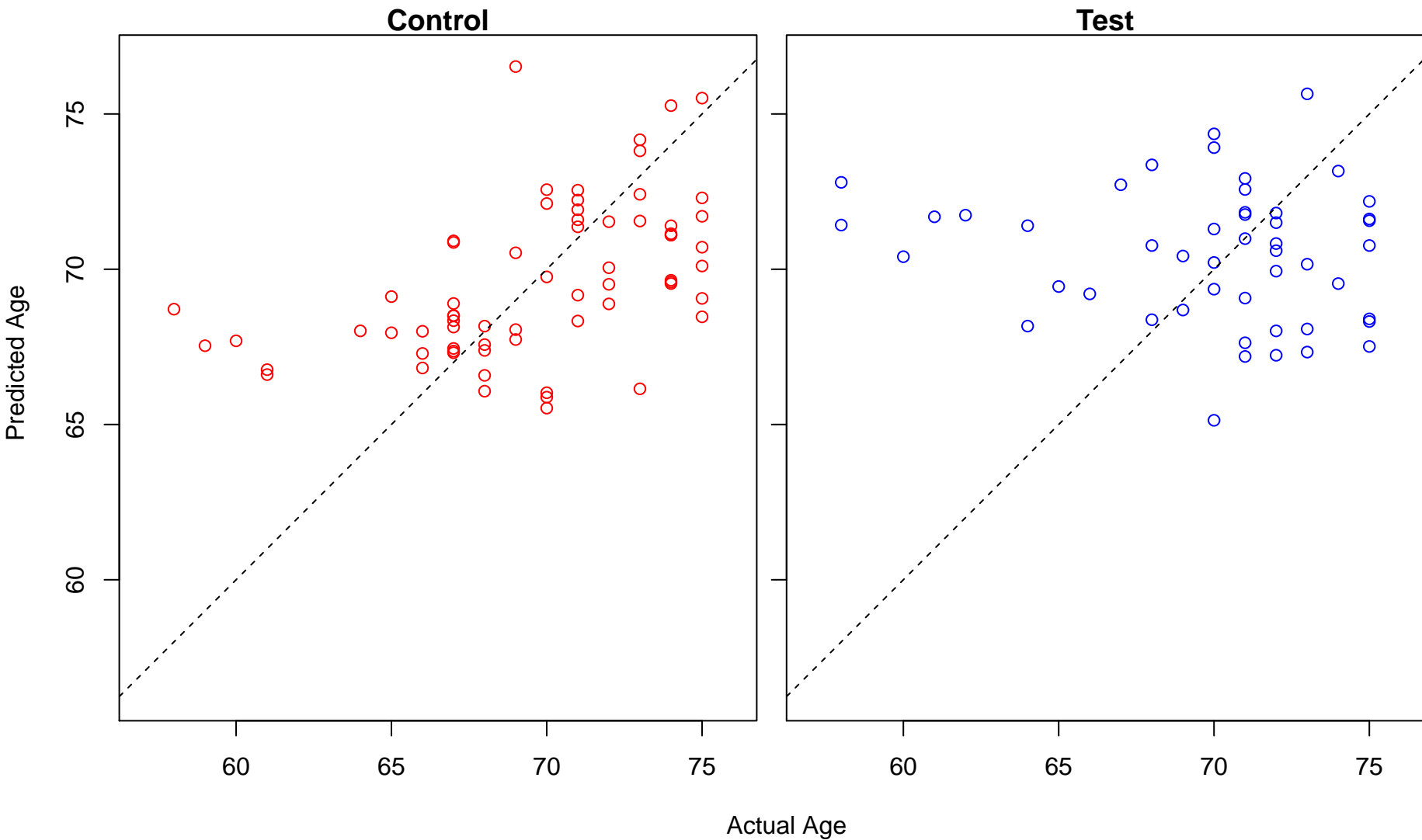
negative regulation of translation in response to stress (Score: 0.790959)



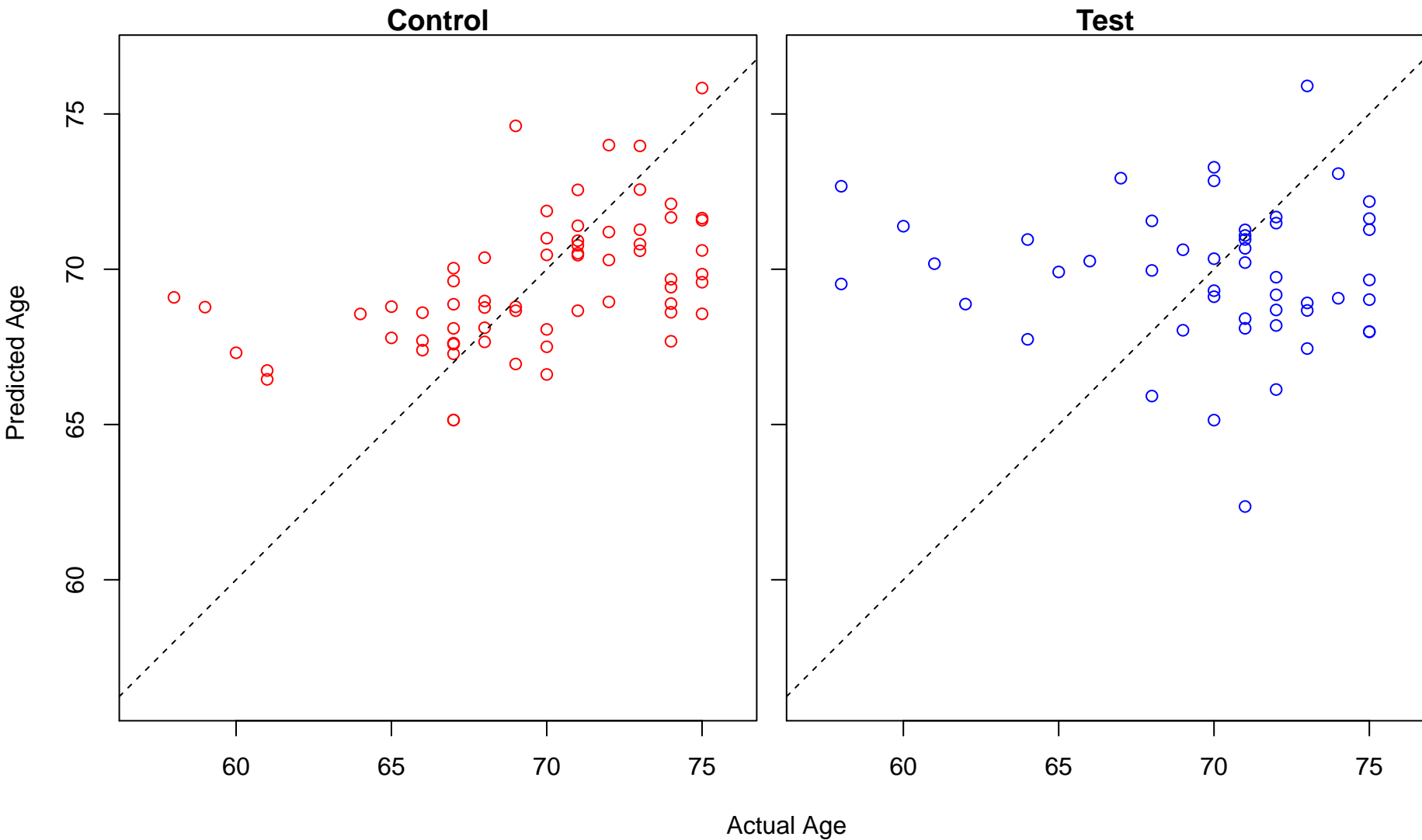
NADP metabolic process (Score: 0.790807)



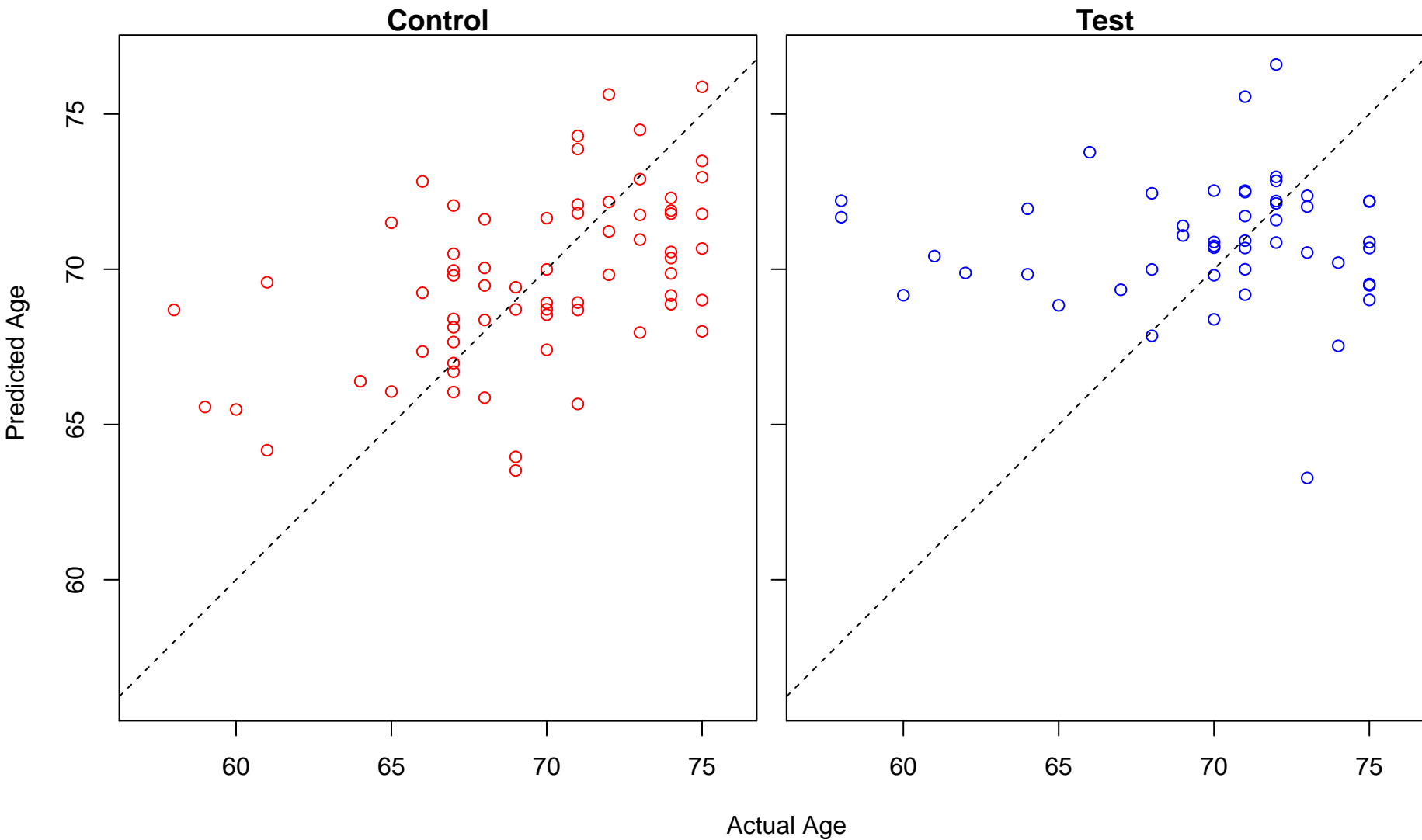
negative regulation of establishment of protein localization to plasma membrane (Score: 0.790698)



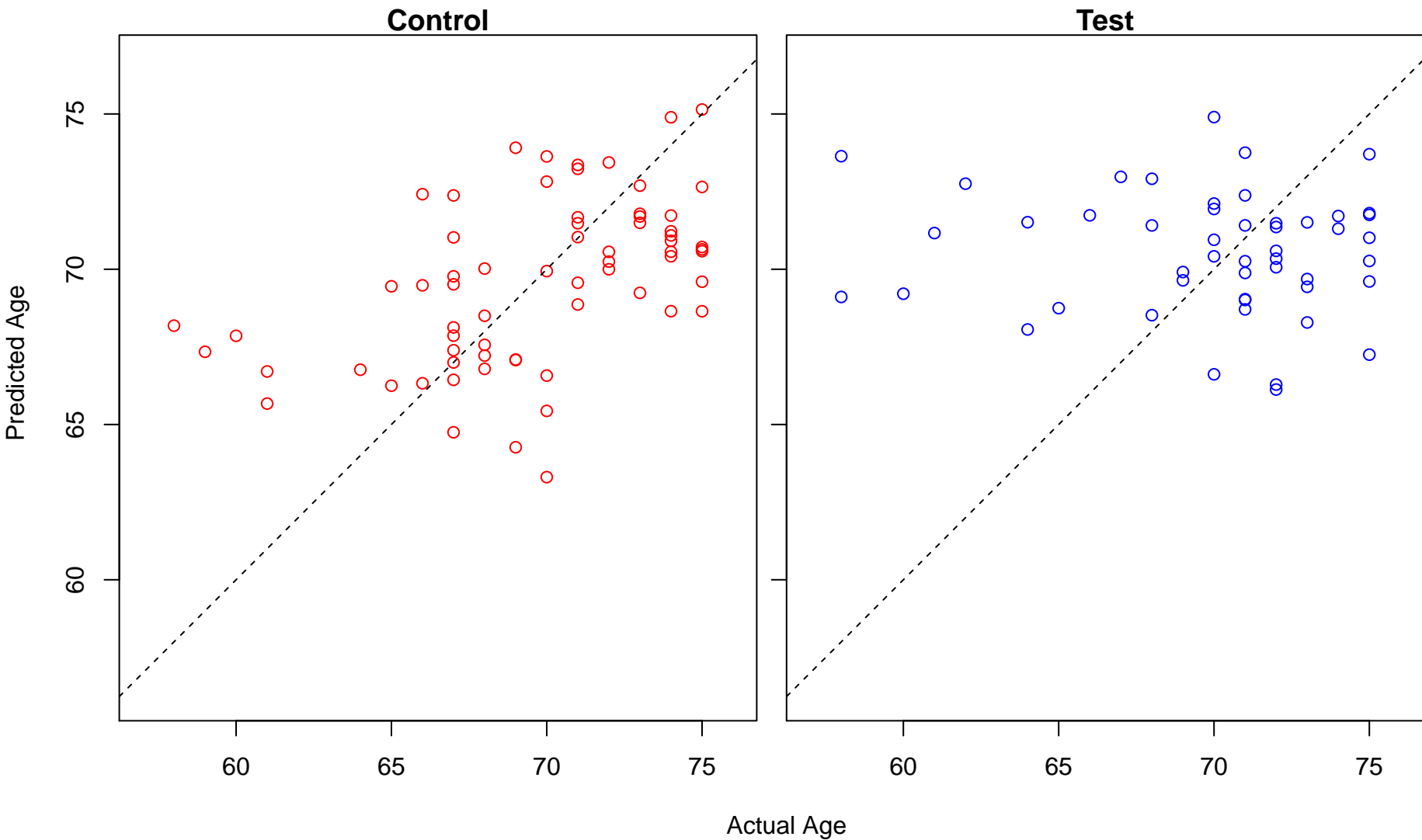
dendritic spine morphogenesis (Score: 0.790545)



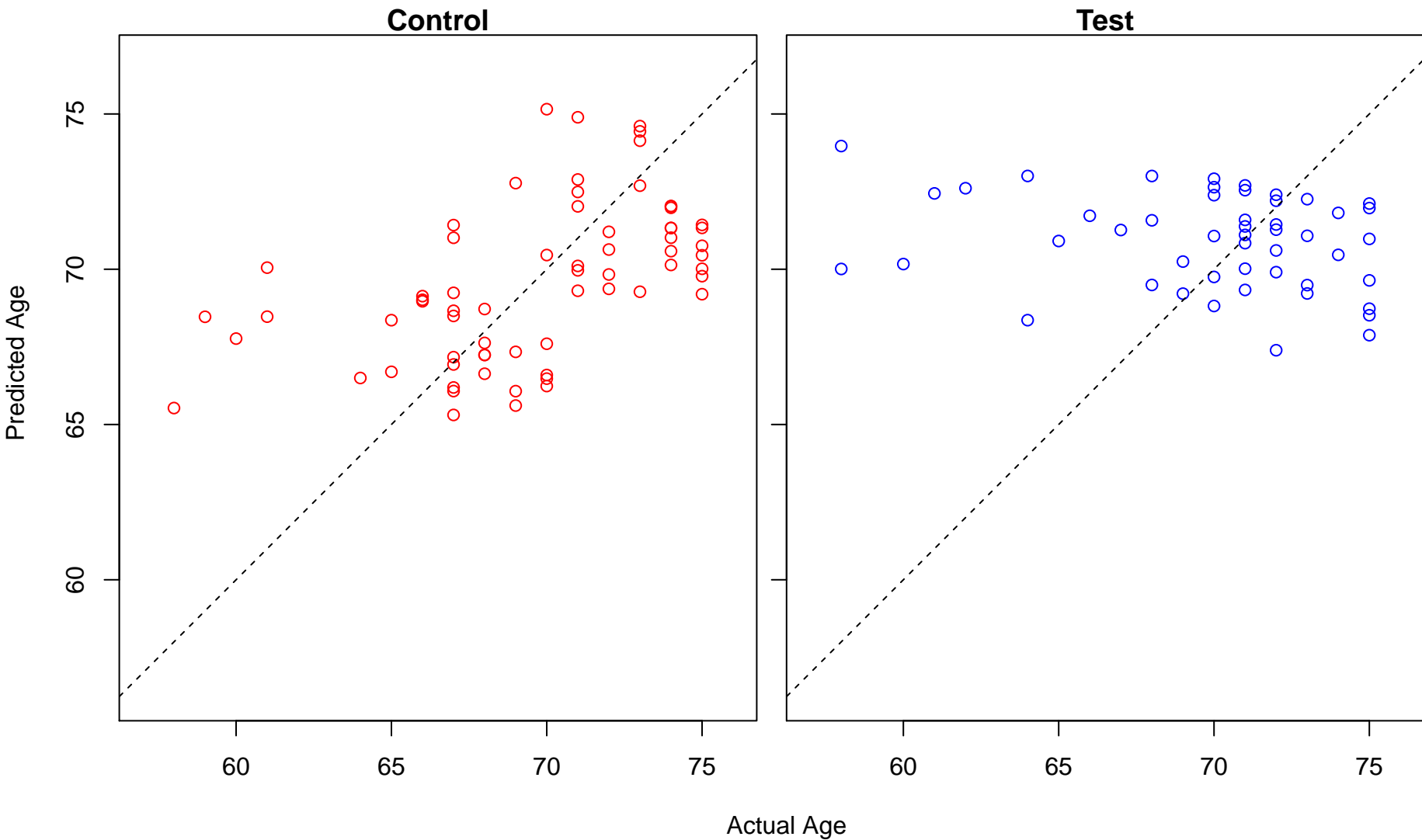
lipoxin metabolic process (Score: 0.790344)



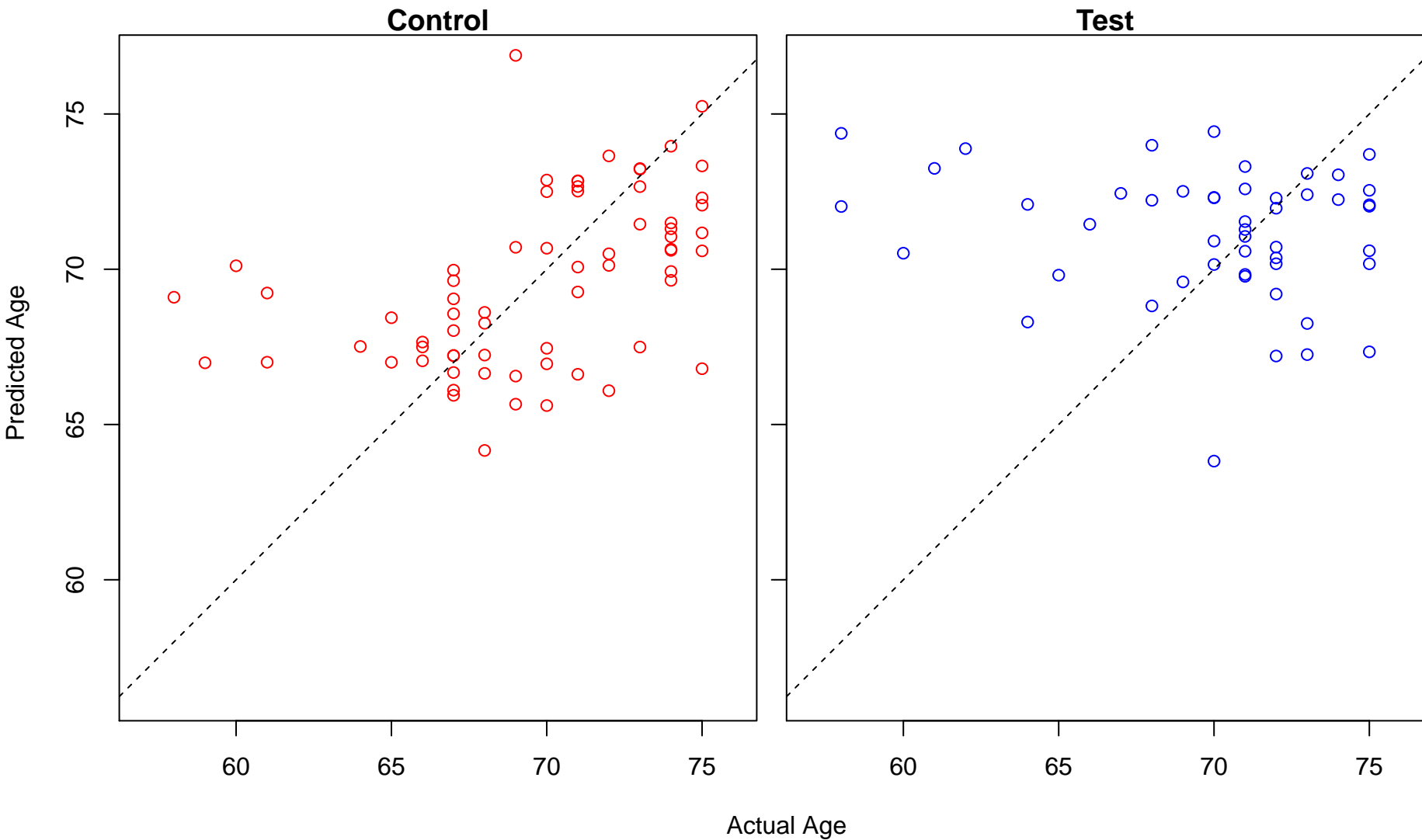
regulation of epithelial cell apoptotic process (Score: 0.790226)



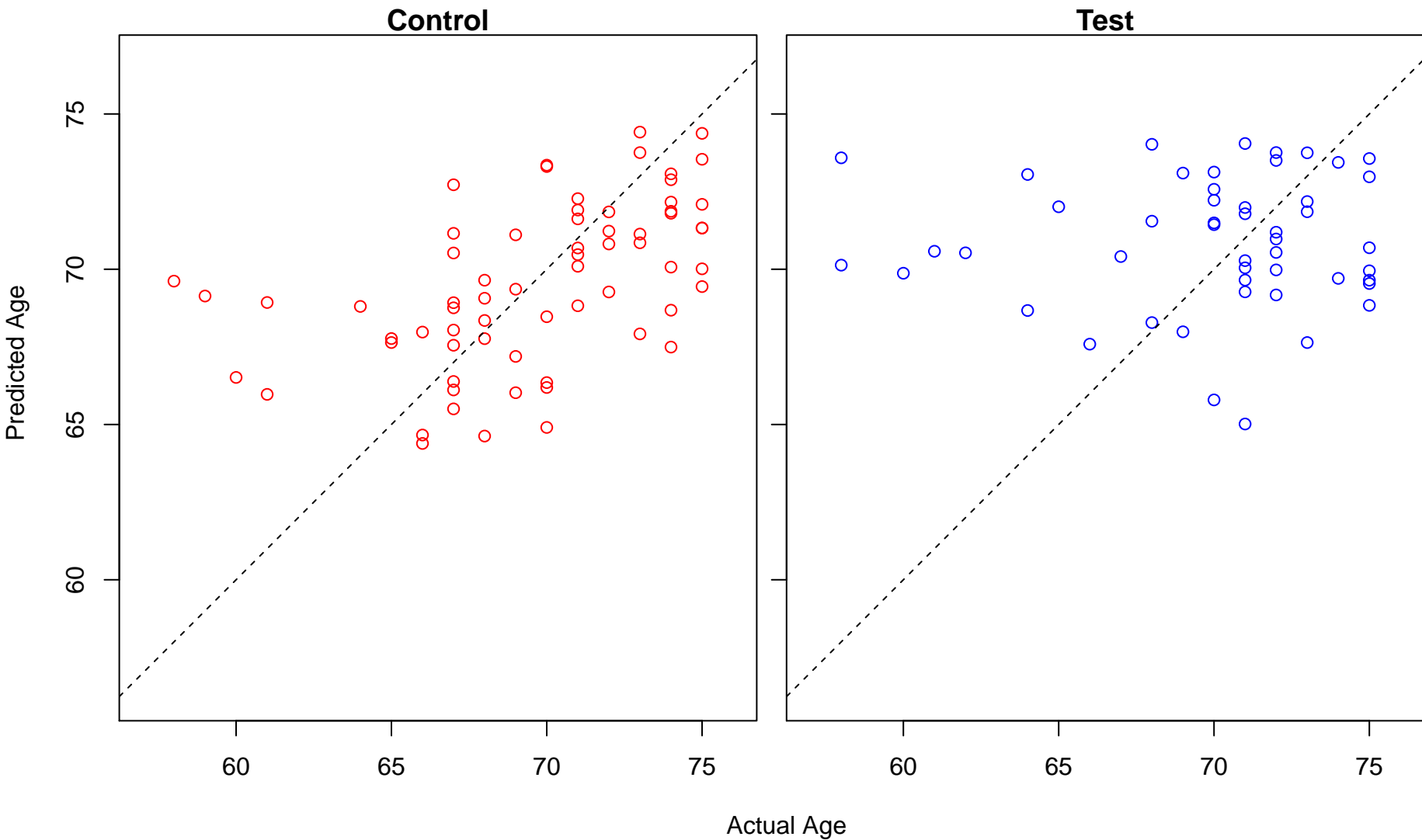
negative regulation of oxidoreductase activity (Score: 0.790128)



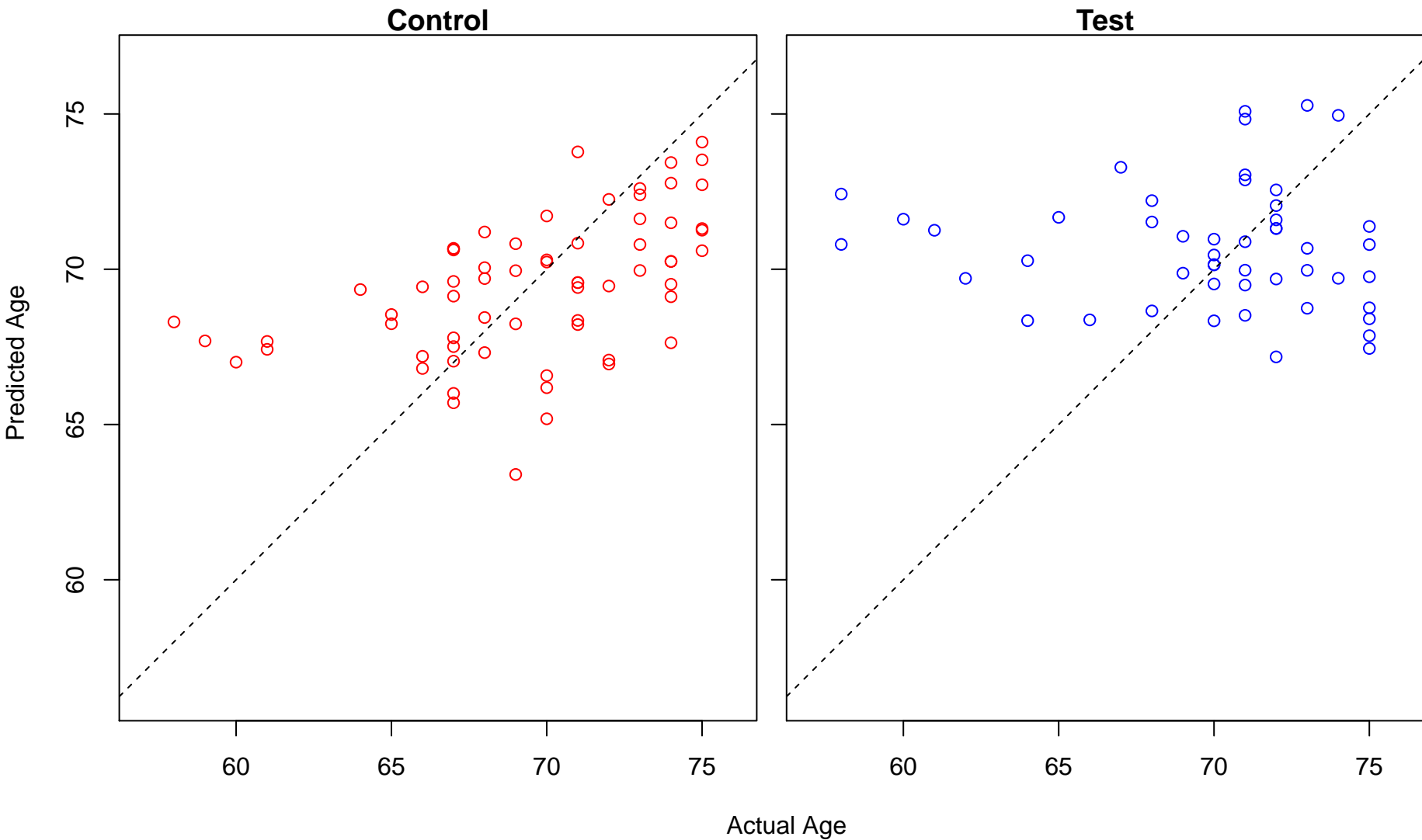
regulation of fat cell differentiation (Score: 0.789423)



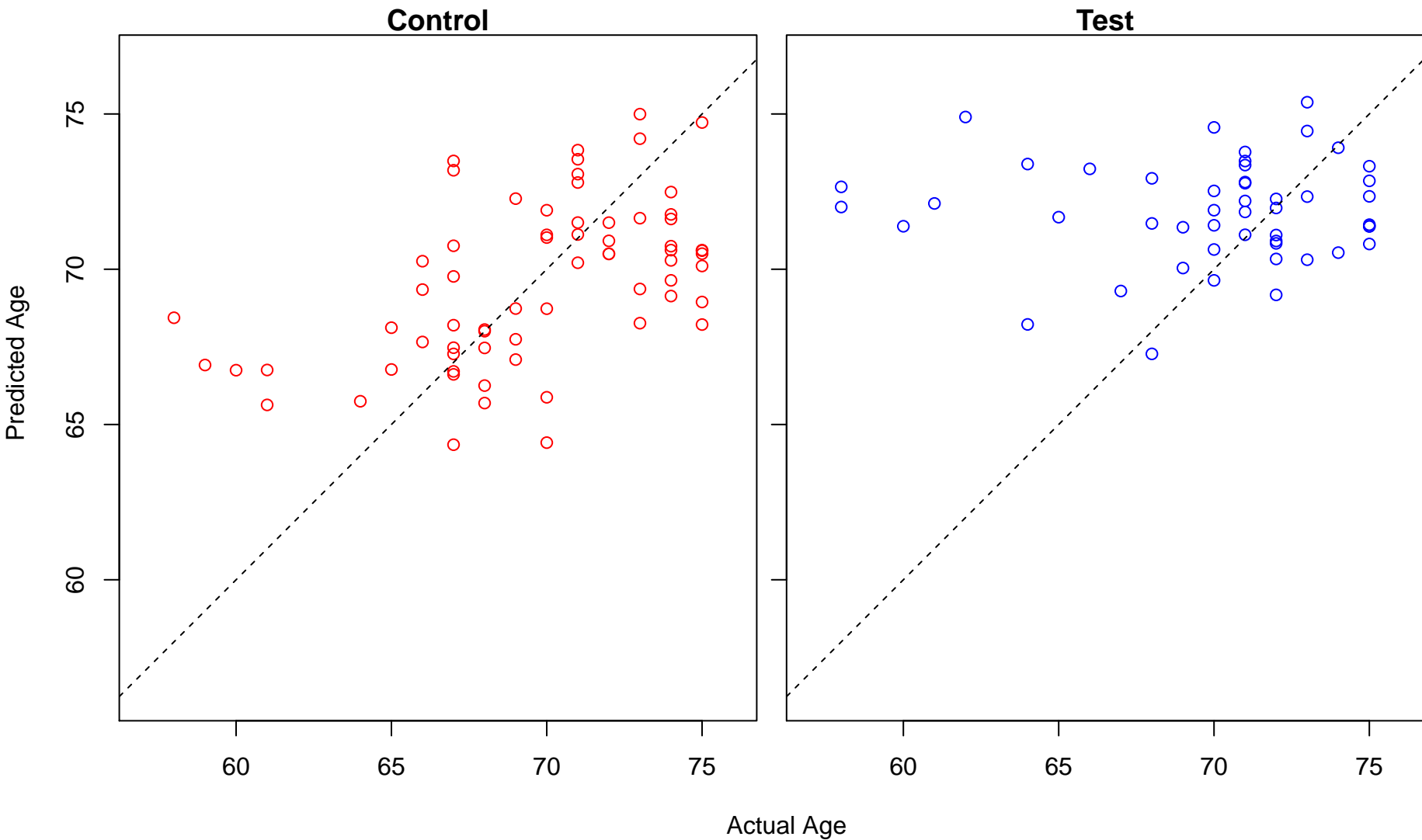
negative regulation of oxidative stress-induced neuron death (Score: 0.788561)



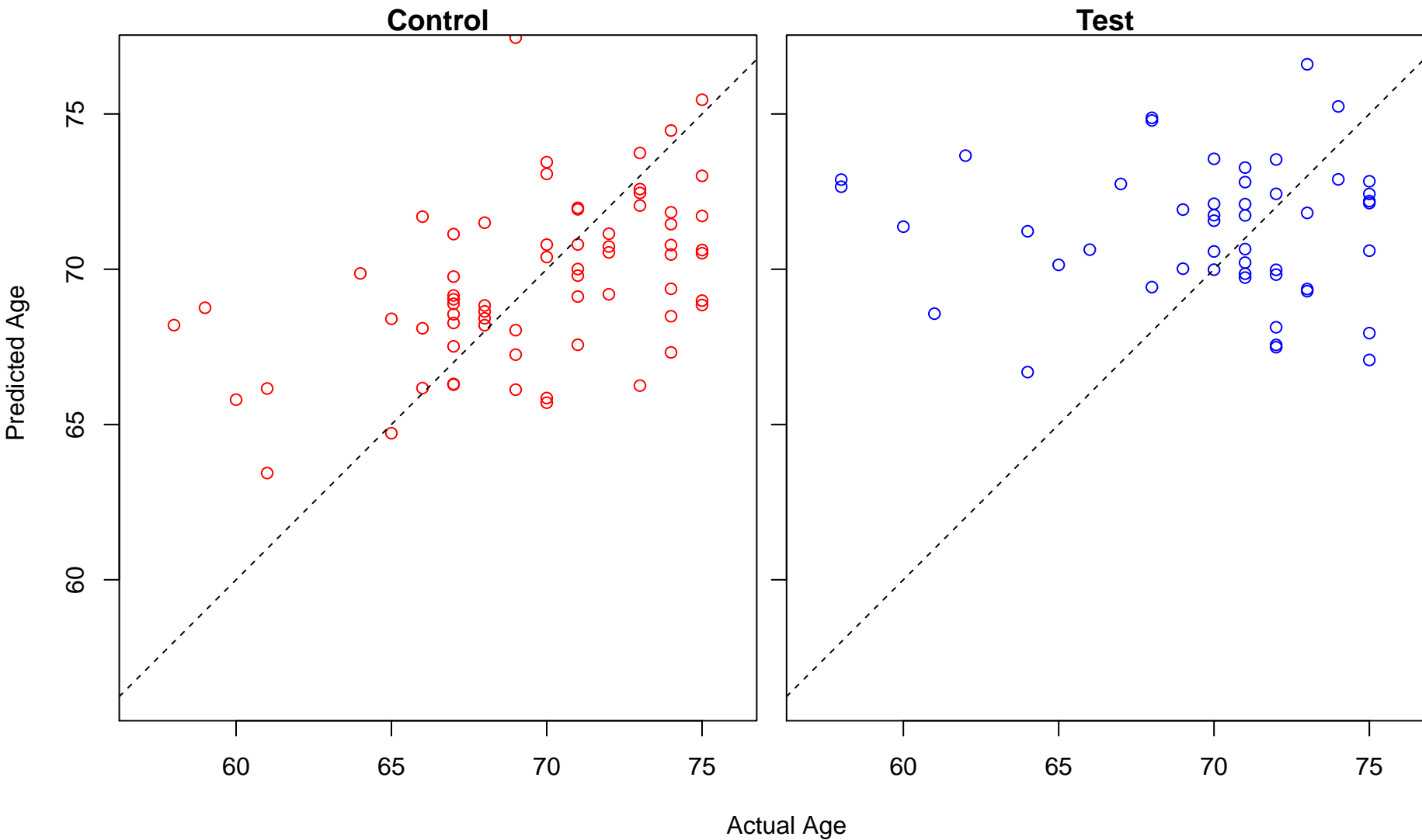
regulation of sequestering of triglyceride (Score: 0.788056)



response to osmotic stress (Score: 0.787976)

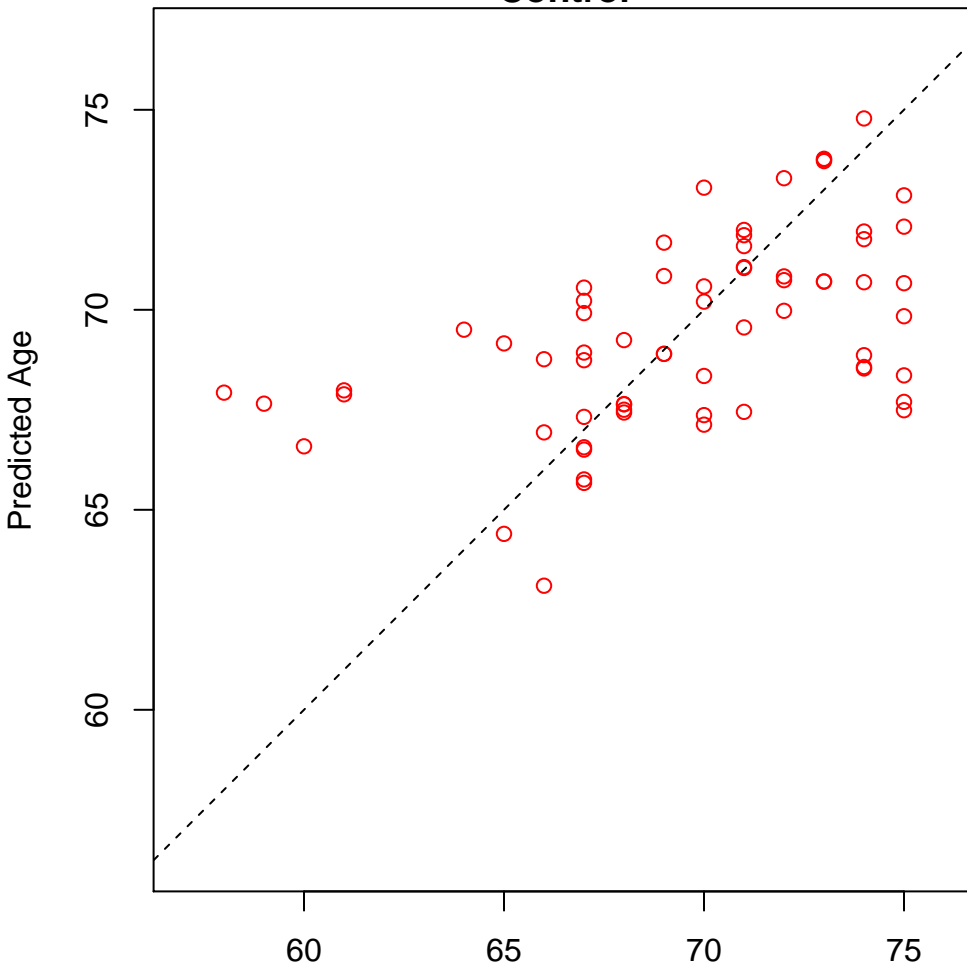


response to fatty acid (Score: 0.787927)

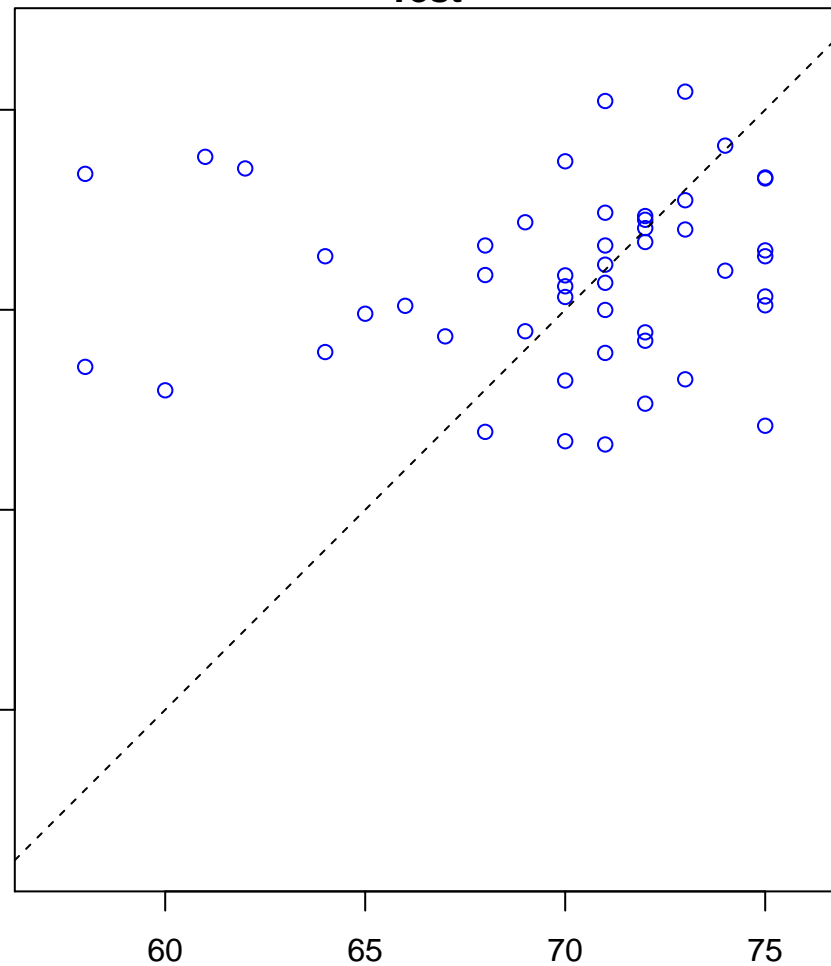


regulation of phagocytosis, engulfment (Score: 0.787902)

Control



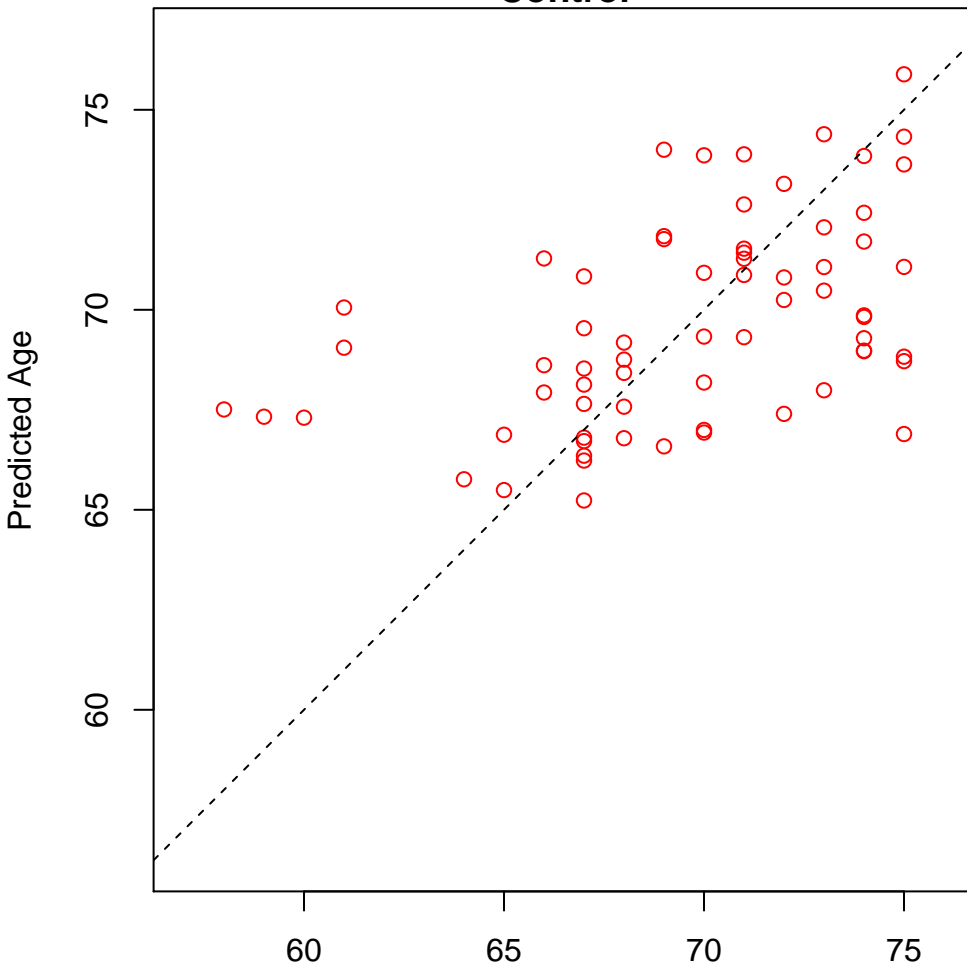
Test



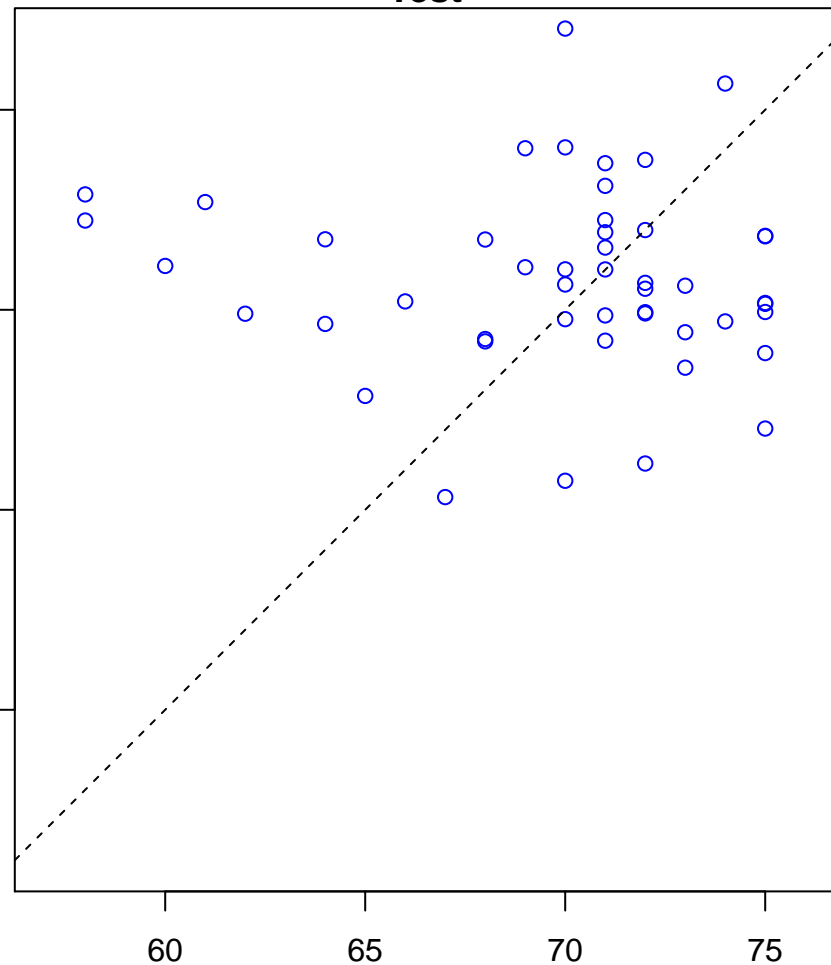
Actual Age

GDP-mannose biosynthetic process (Score: 0.787688)

Control

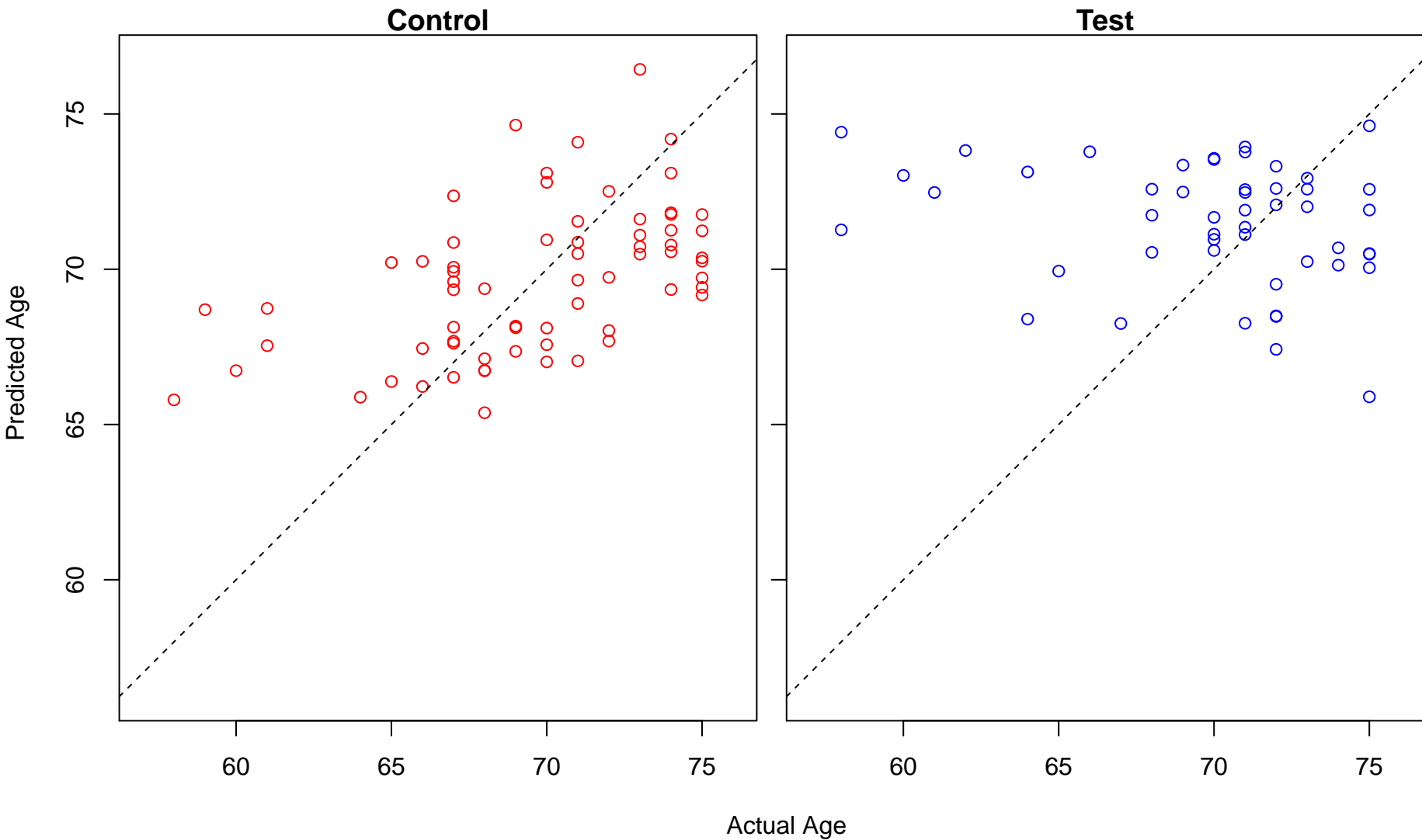


Test

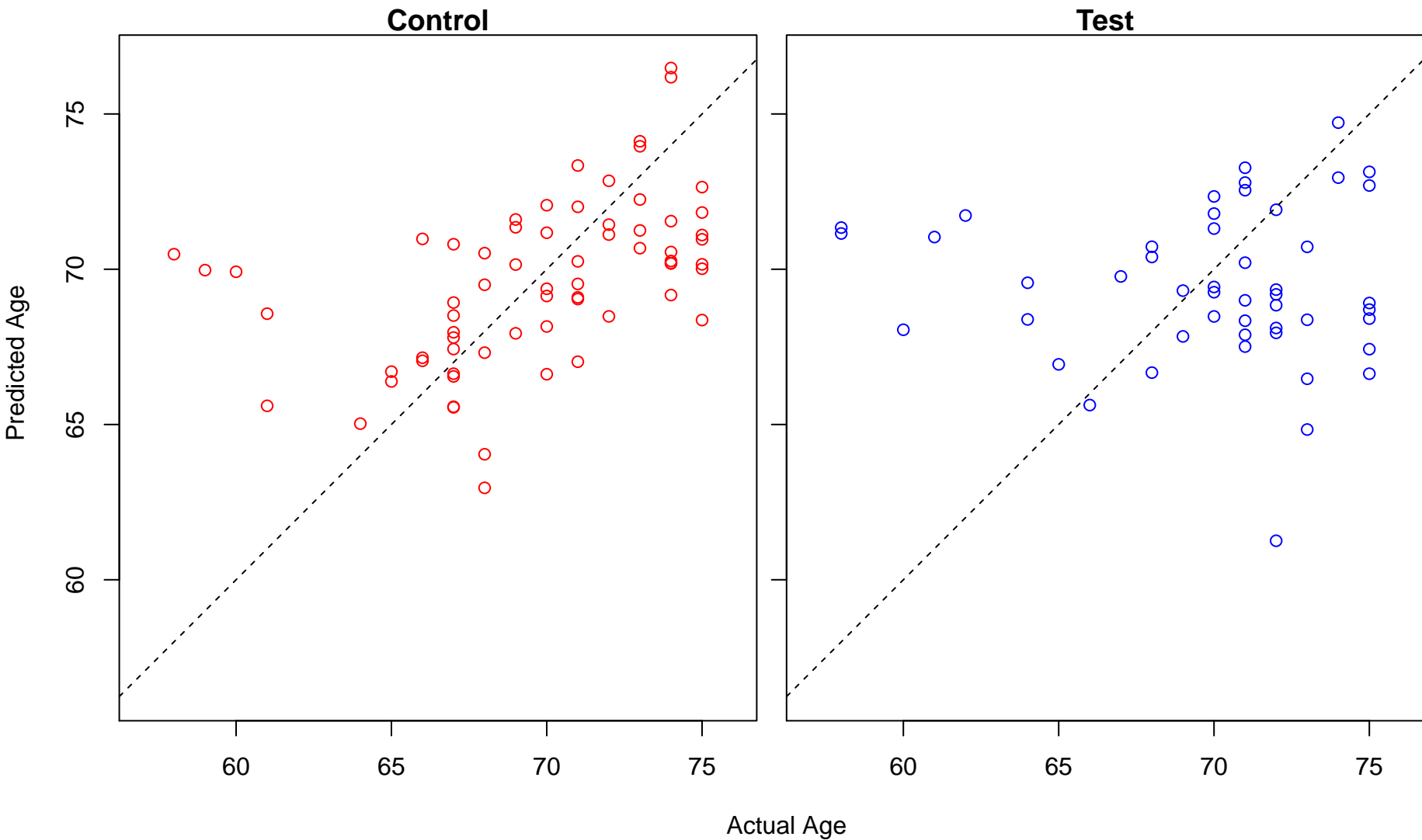


Actual Age

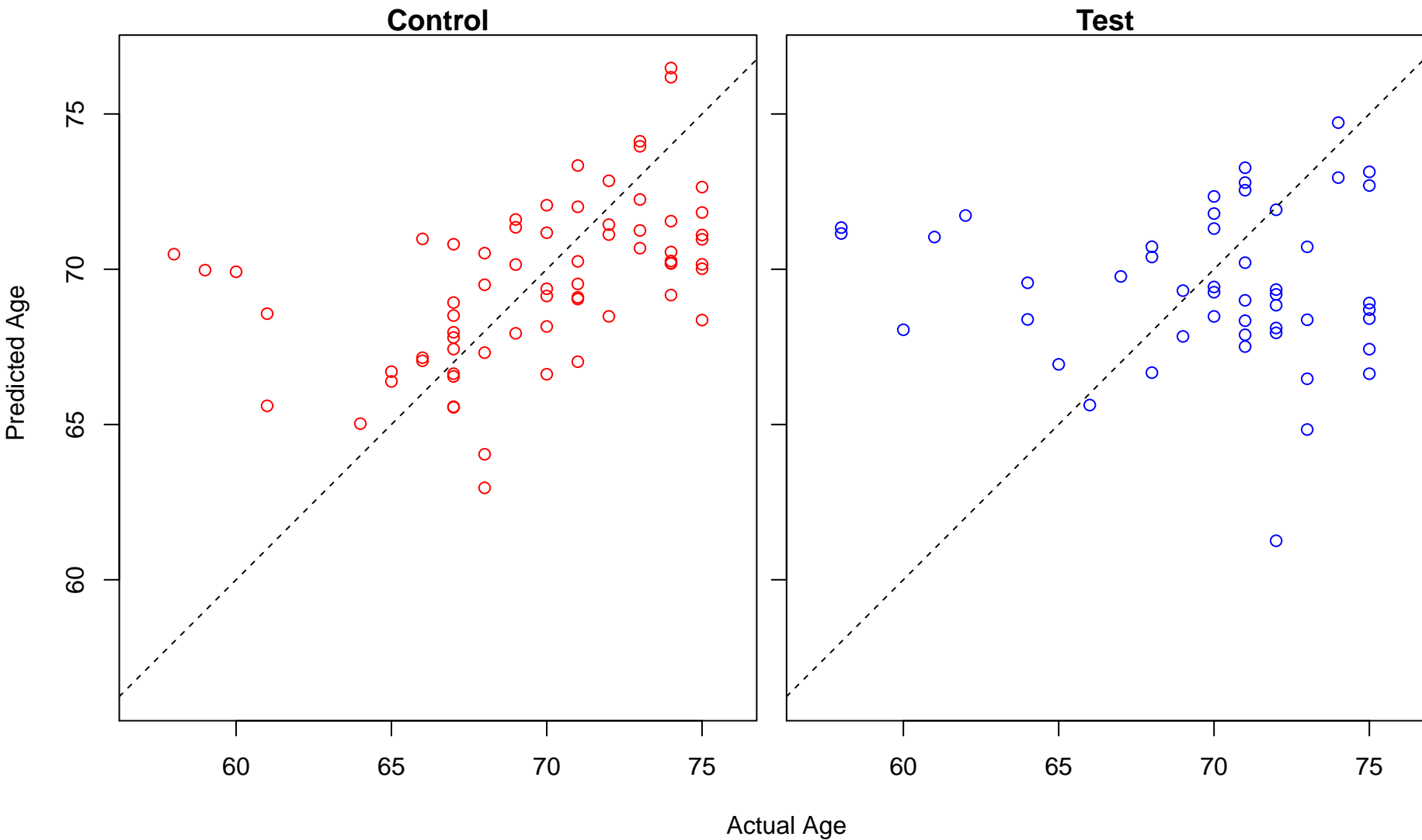
ventricular septum morphogenesis (Score: 0.787371)



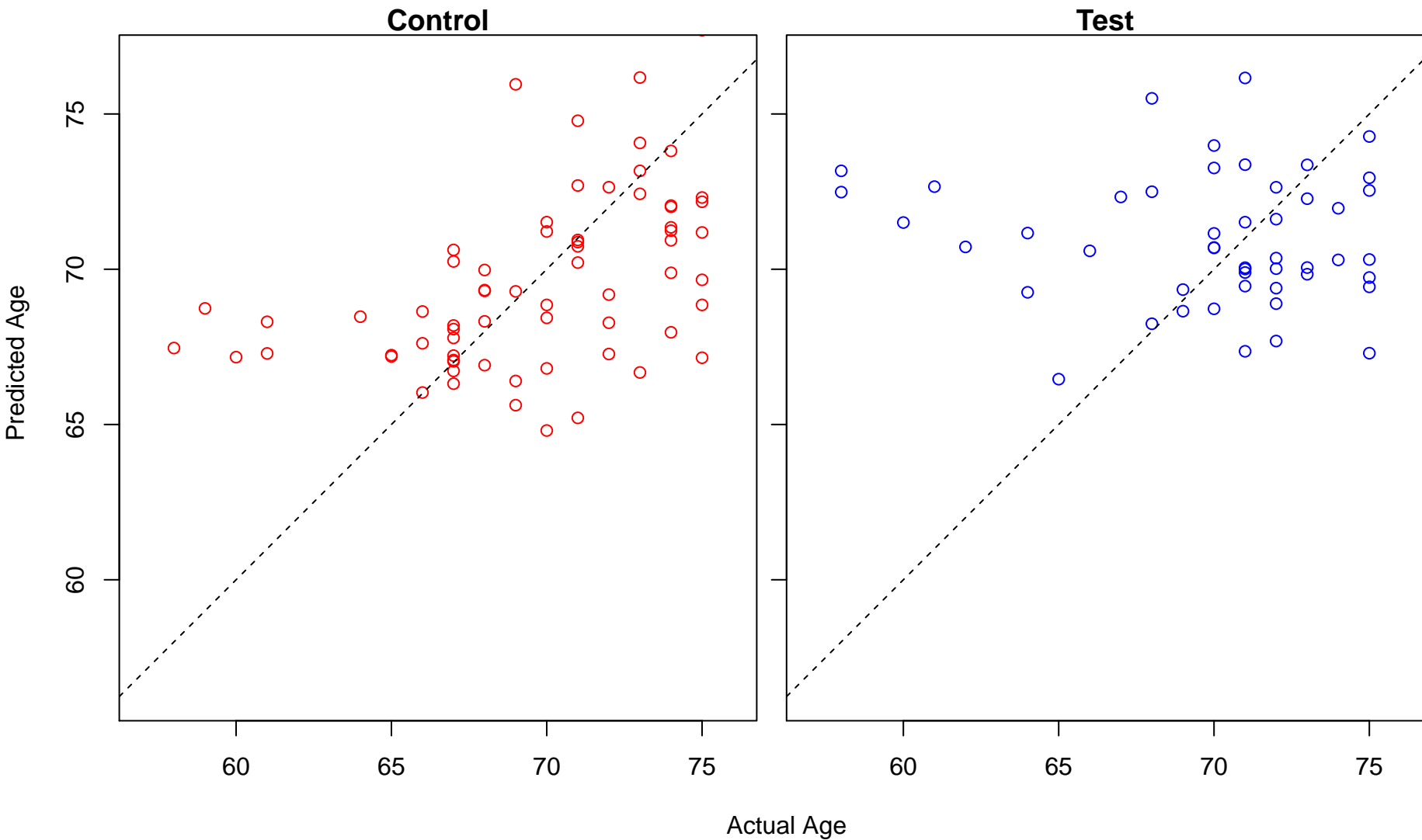
immune response-inhibiting signal transduction (Score: 0.786549)



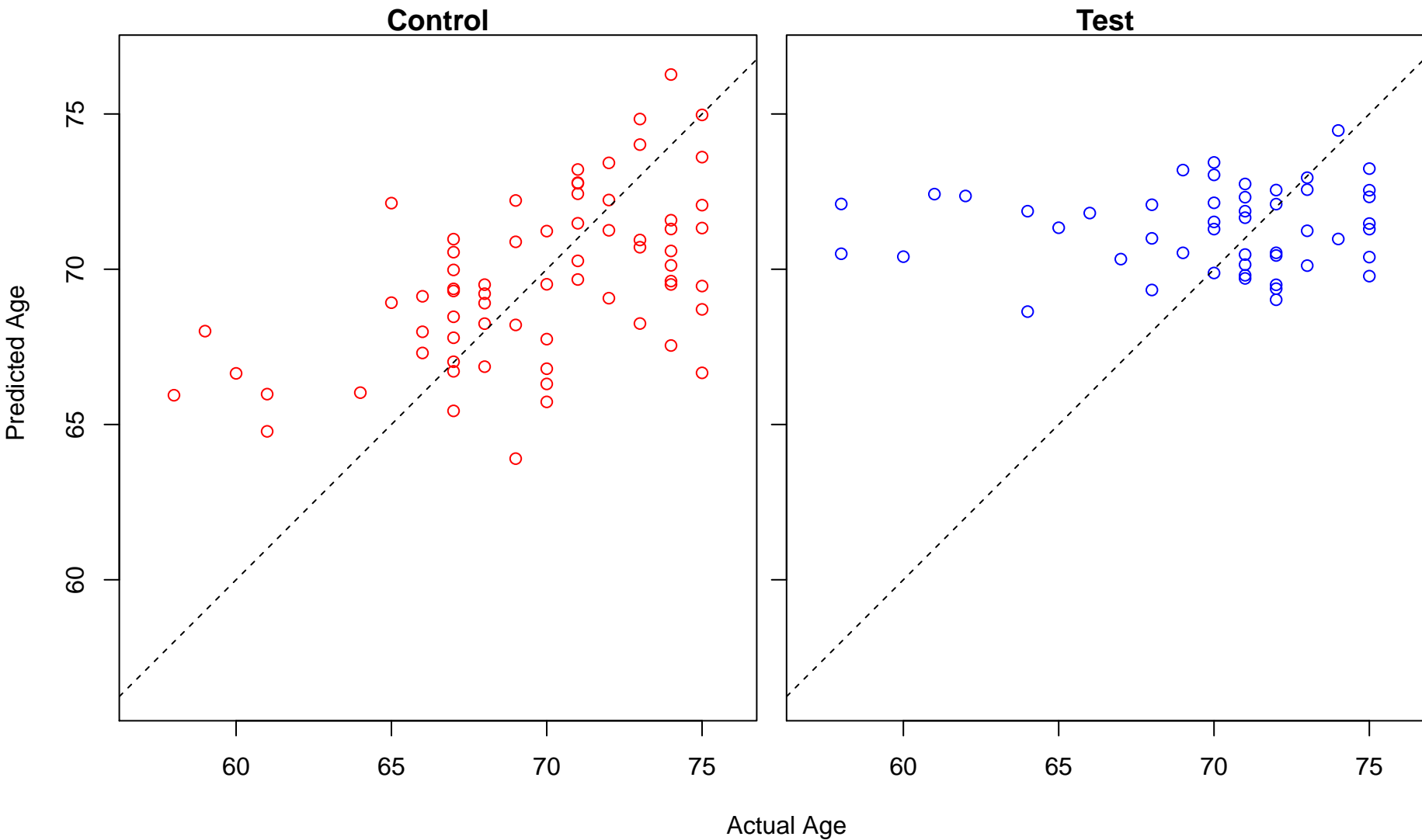
immune response–inhibiting cell surface receptor signaling pathway (Score: 0.786549)



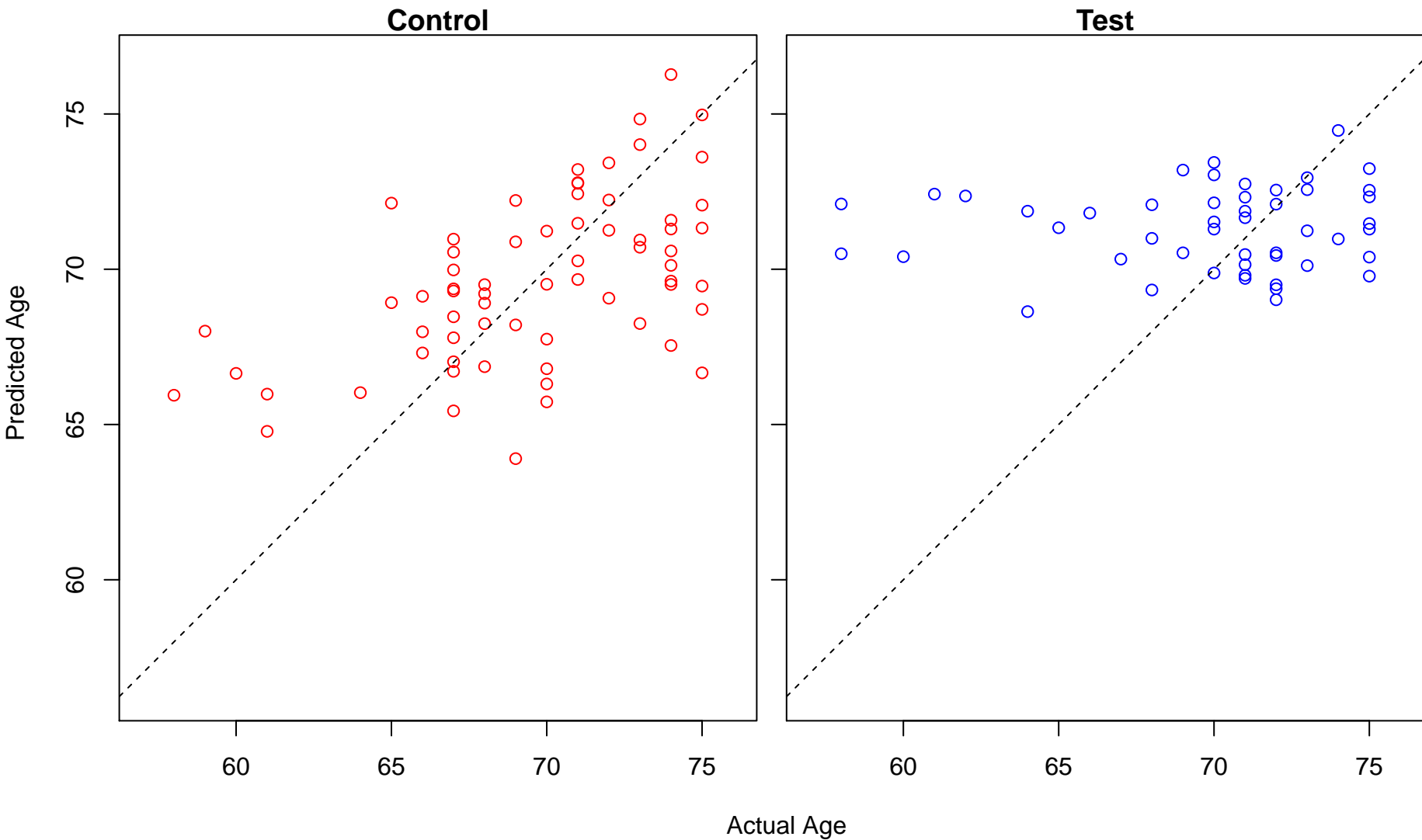
O-glycan processing (Score: 0.786463)



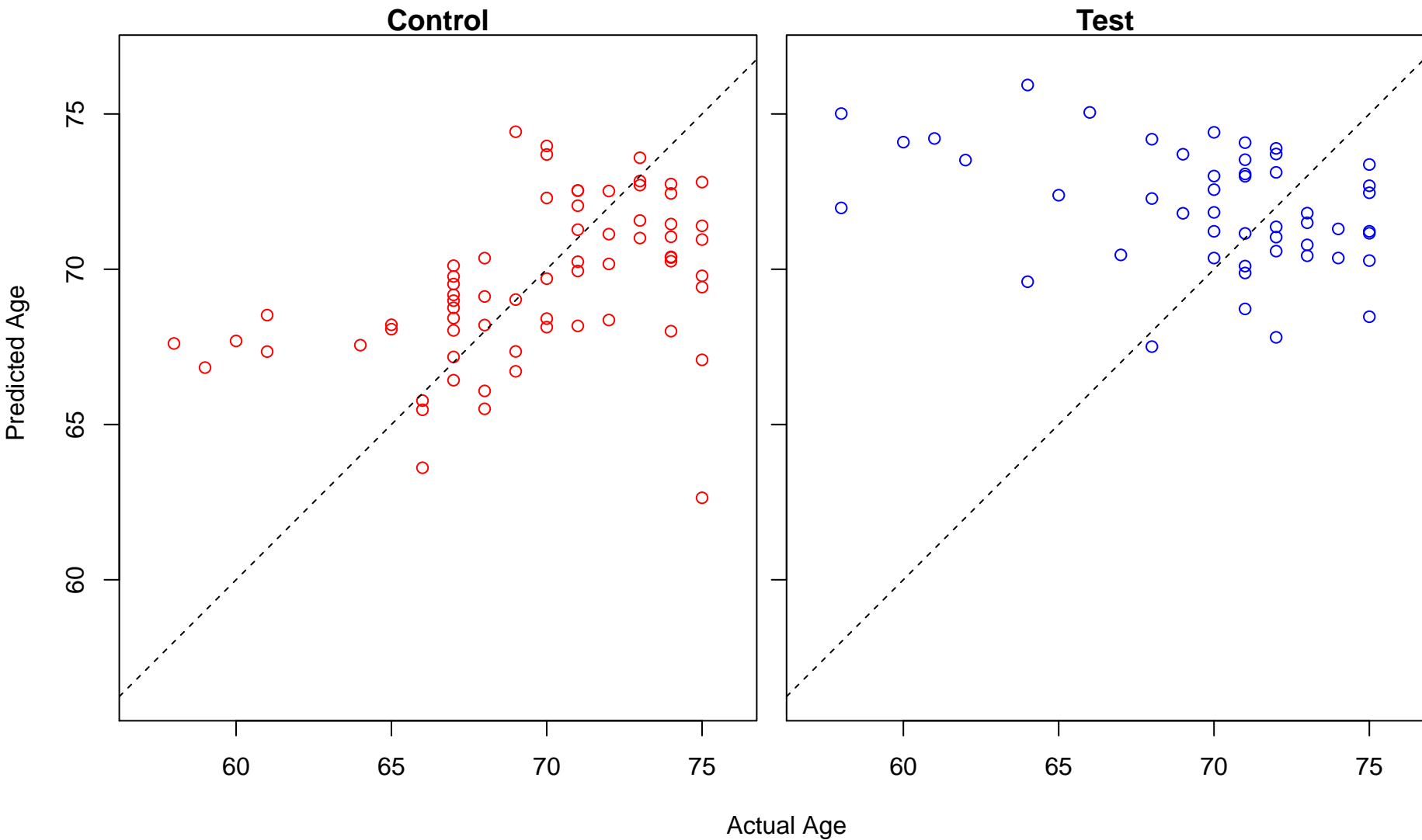
multicellular organismal movement (Score: 0.786406)



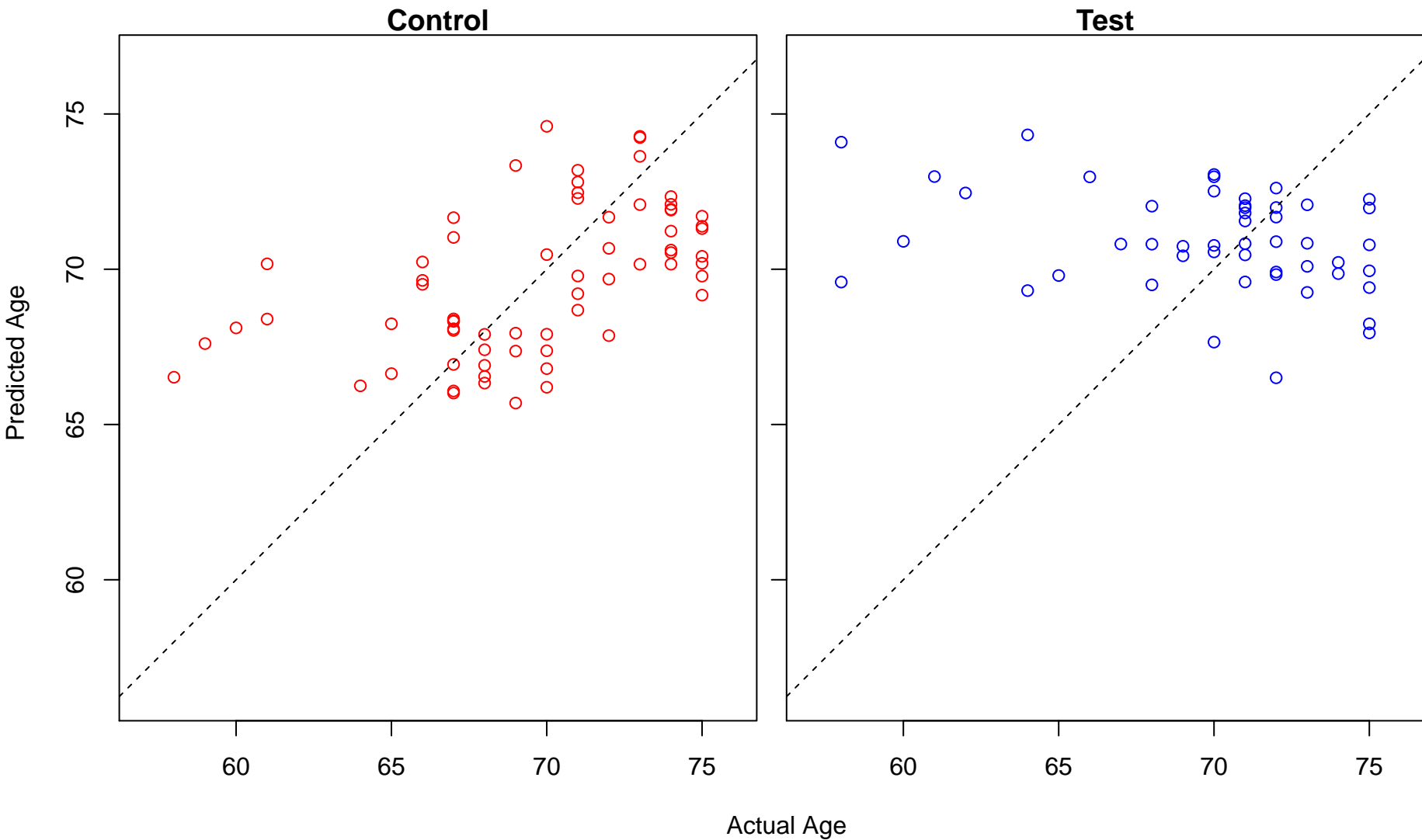
musculoskeletal movement (Score: 0.786406)



mitotic cell cycle arrest (Score: 0.785538)

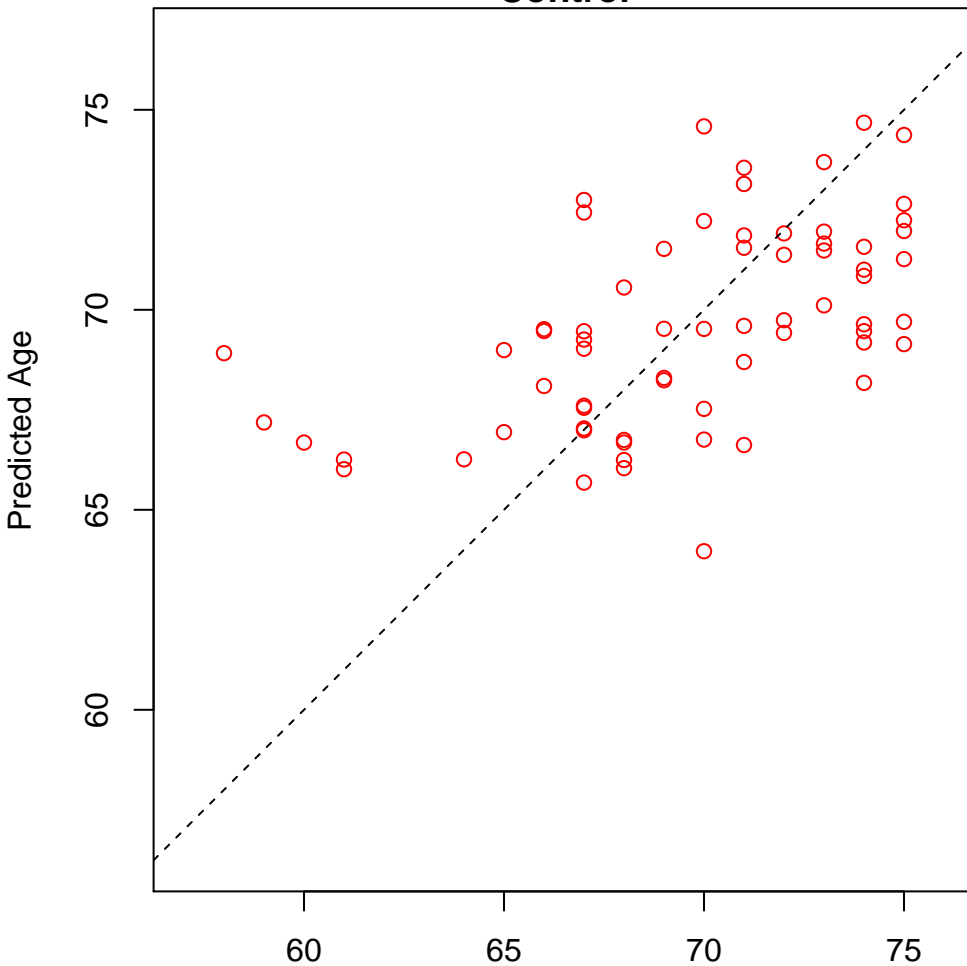


regulation of endodeoxyribonuclease activity (Score: 0.785000)

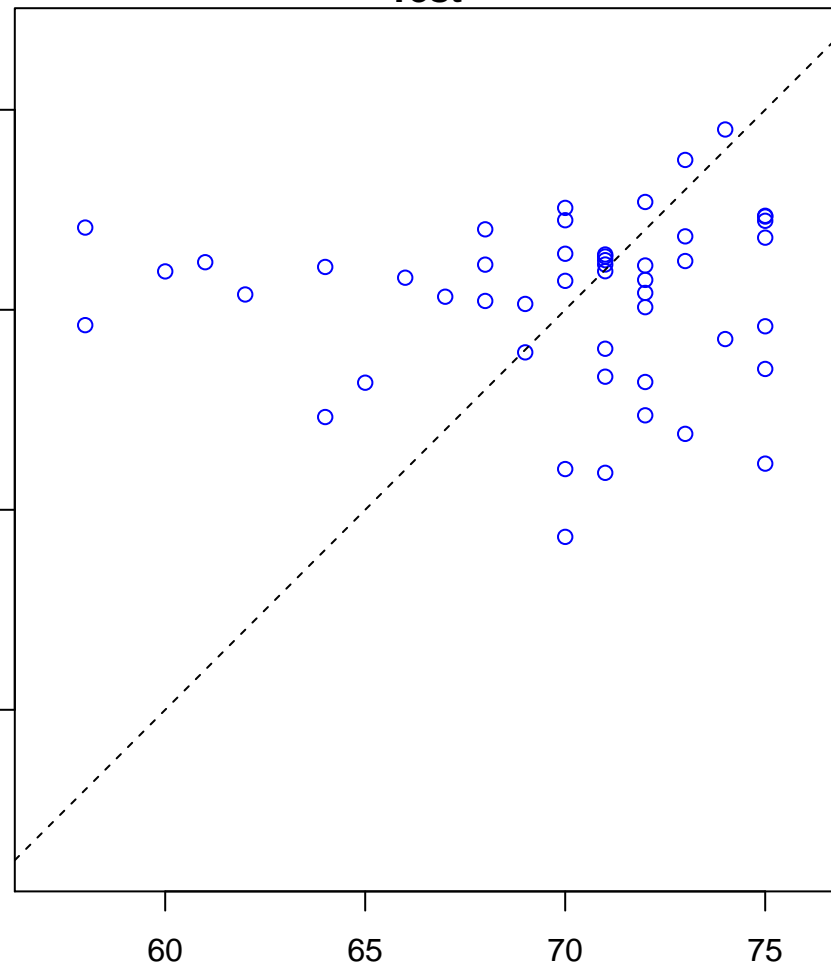


embryonic epithelial tube formation (Score: 0.784605)

Control

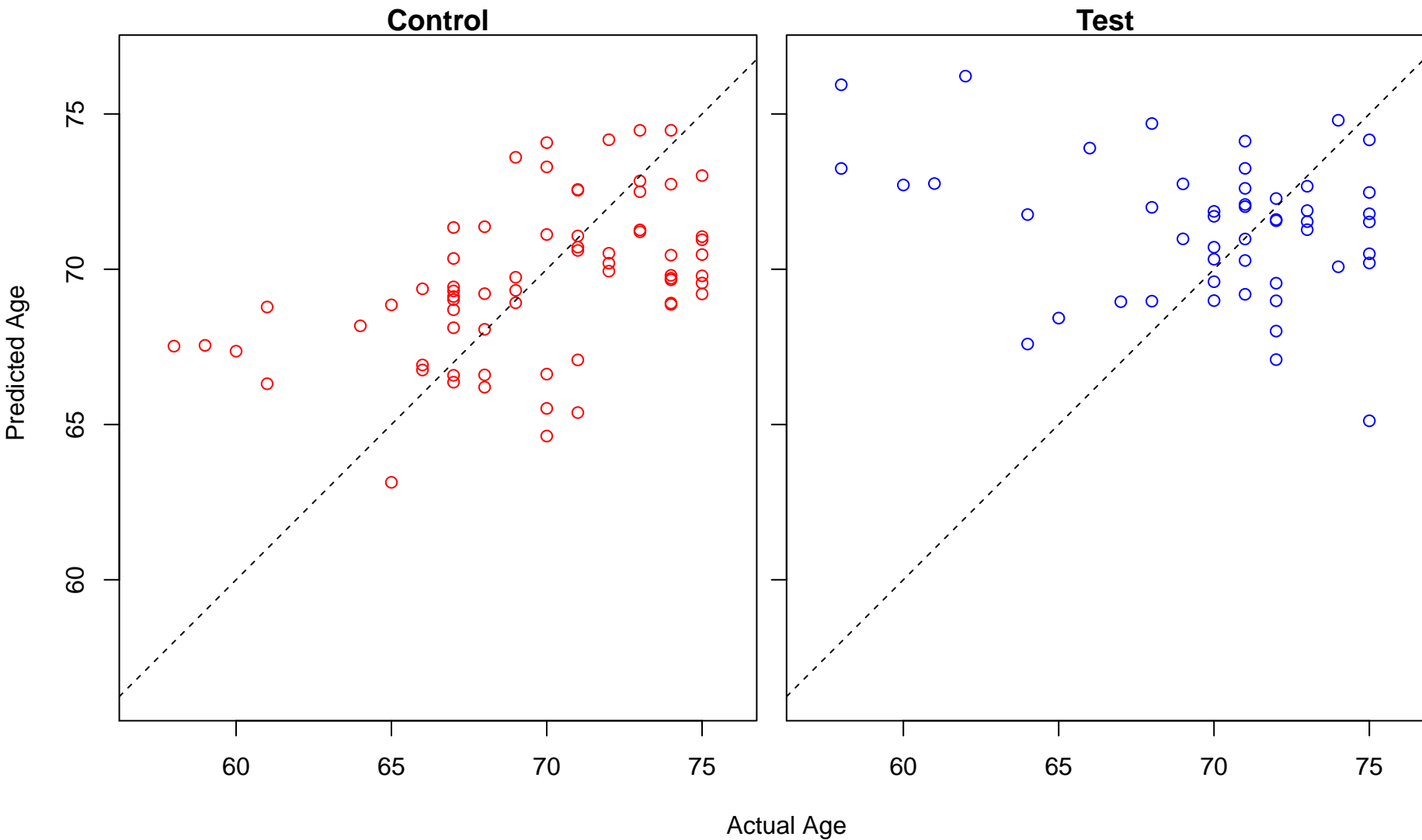


Test

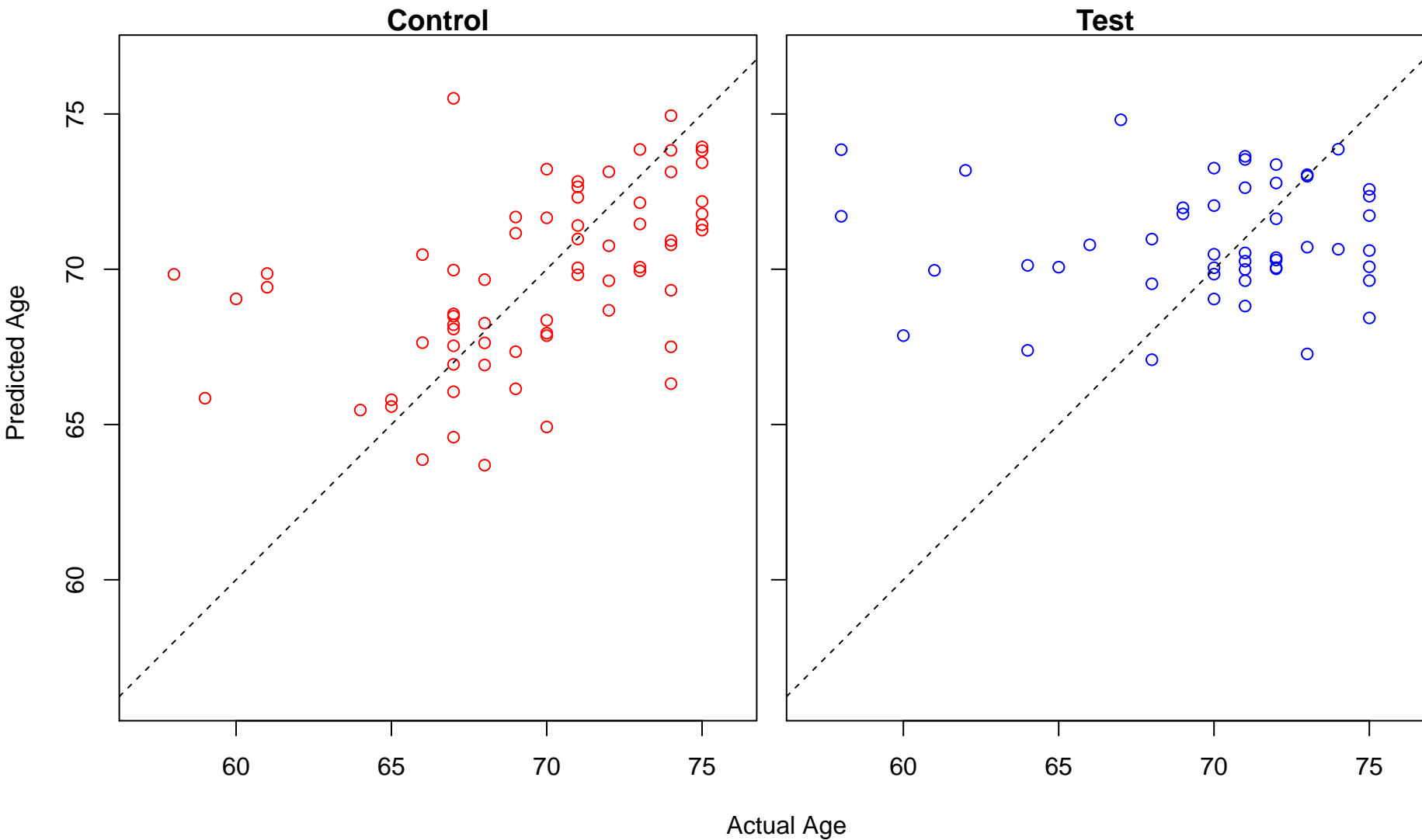


Actual Age

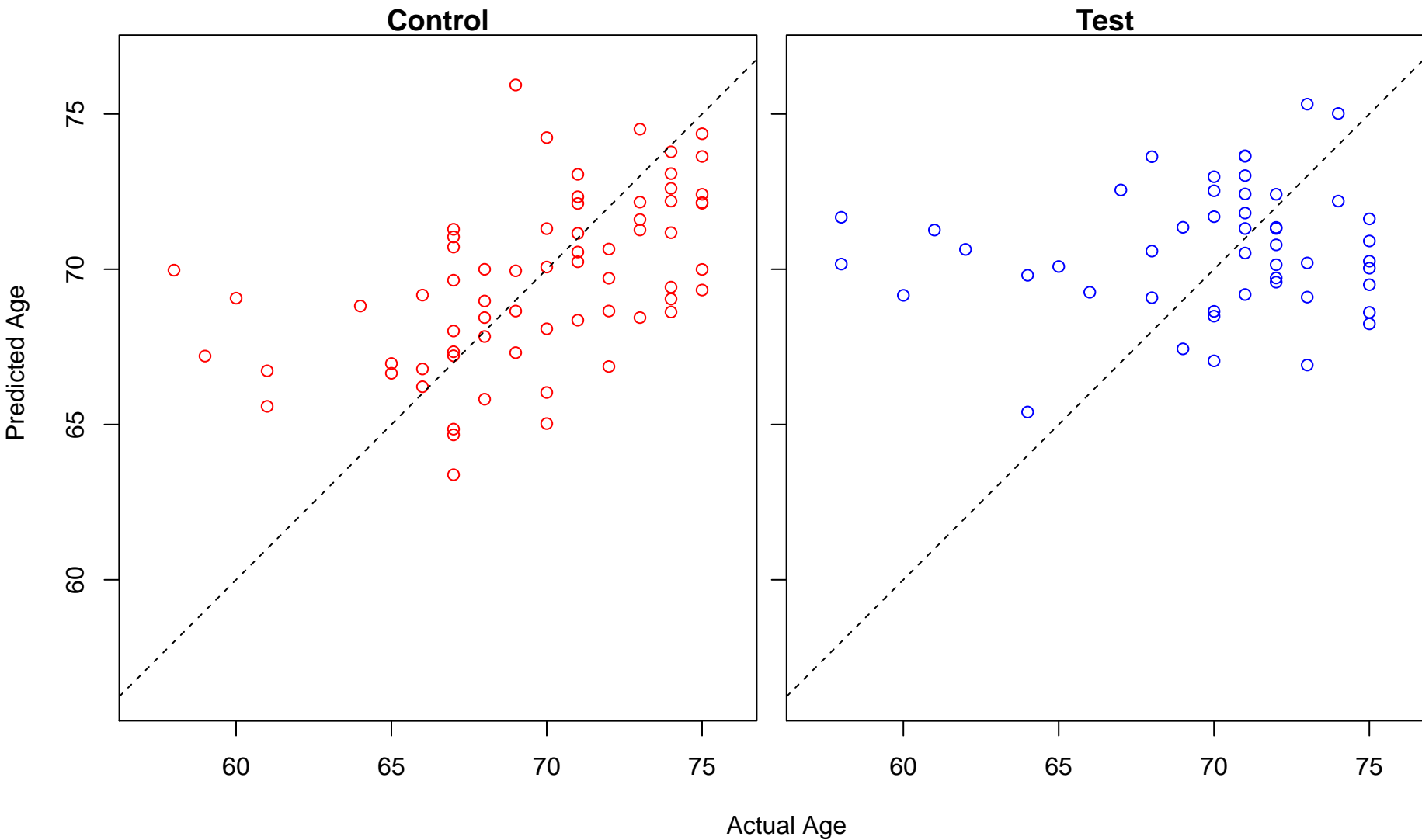
positive regulation of sprouting angiogenesis (Score: 0.784303)



amide transport (Score: 0.783905)

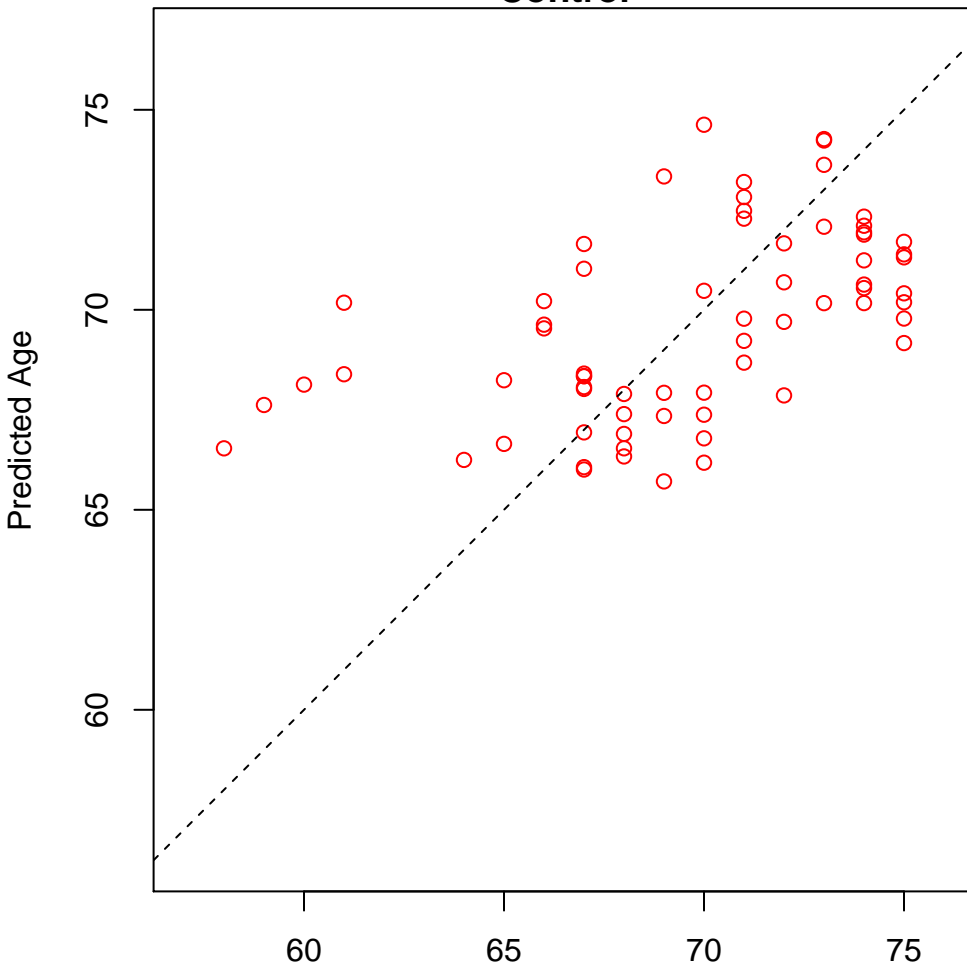


glutamine family amino acid metabolic process (Score: 0.783881)

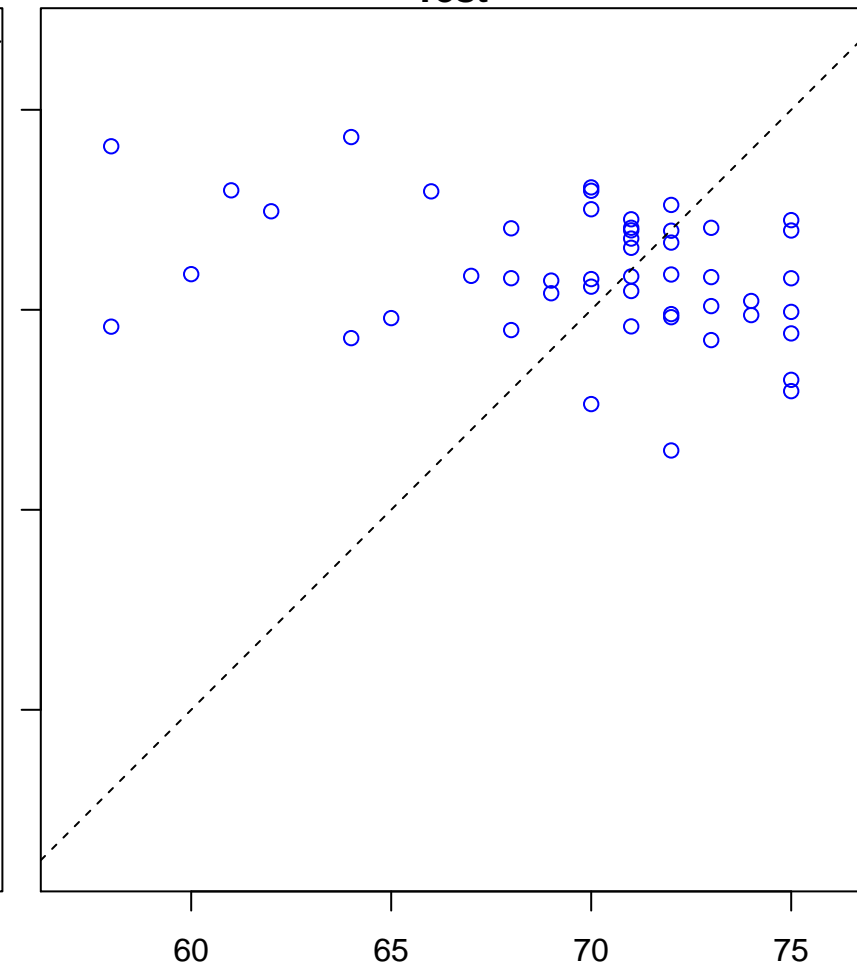


regulation of deoxyribonuclease activity (Score: 0.783874)

Control

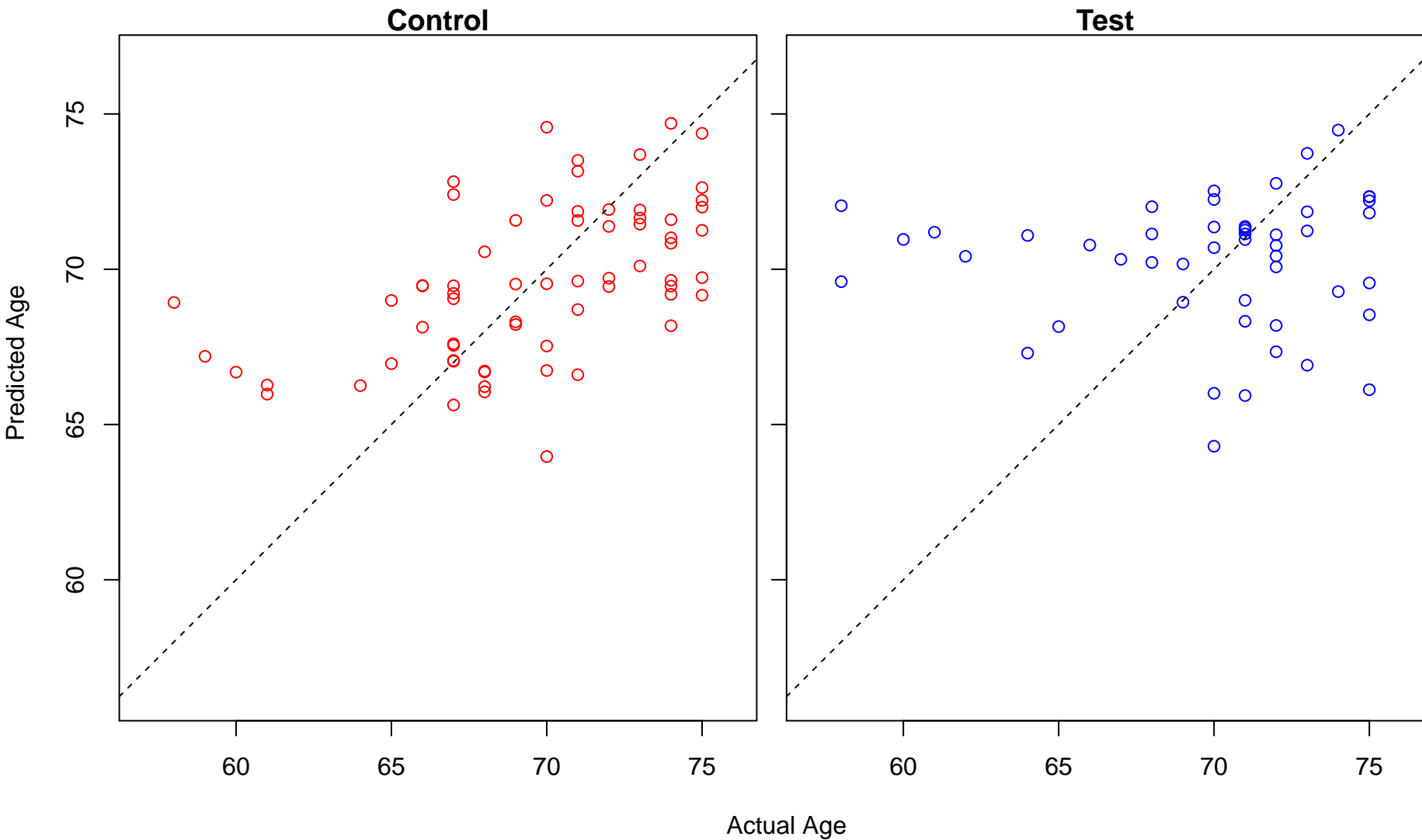


Test

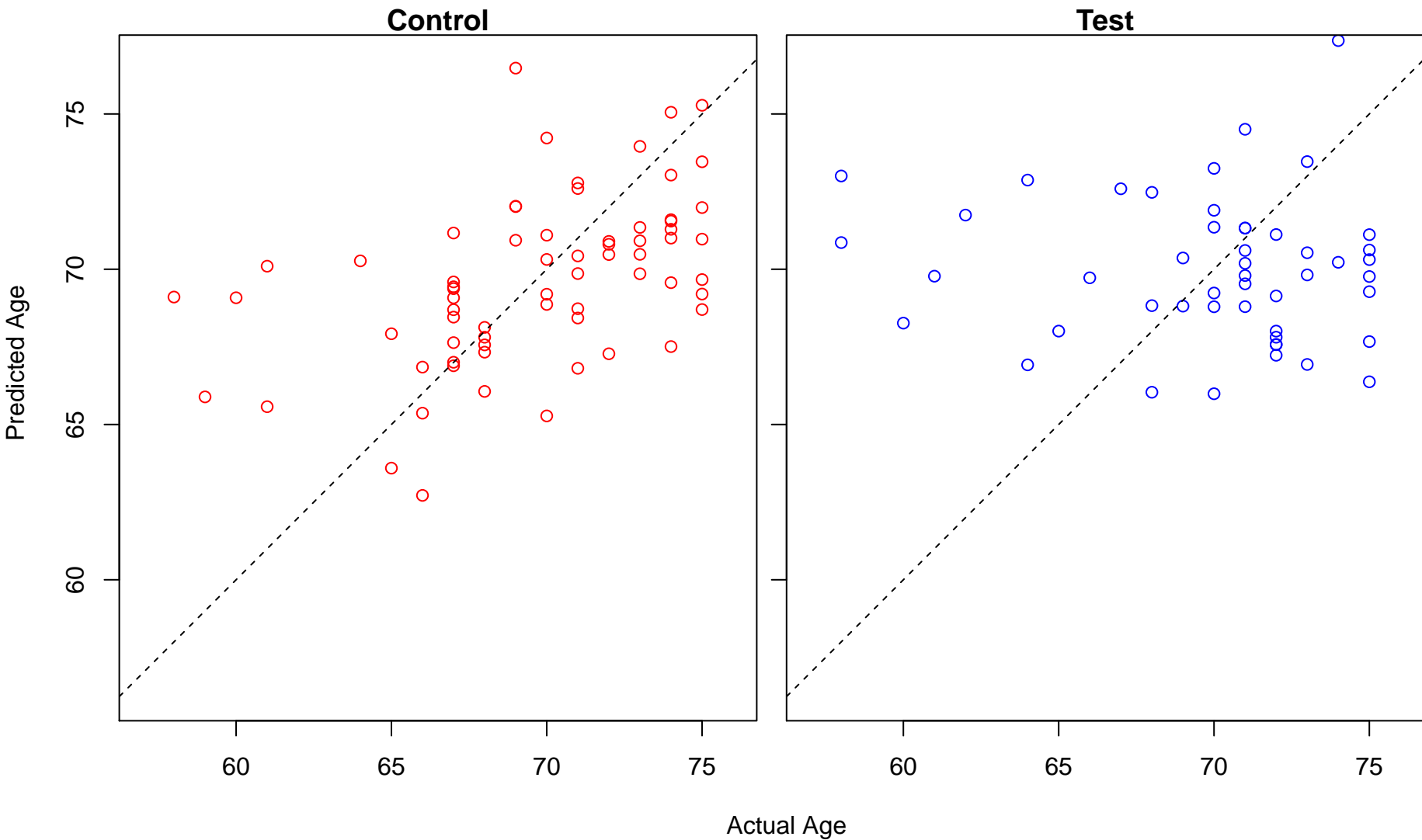


Actual Age

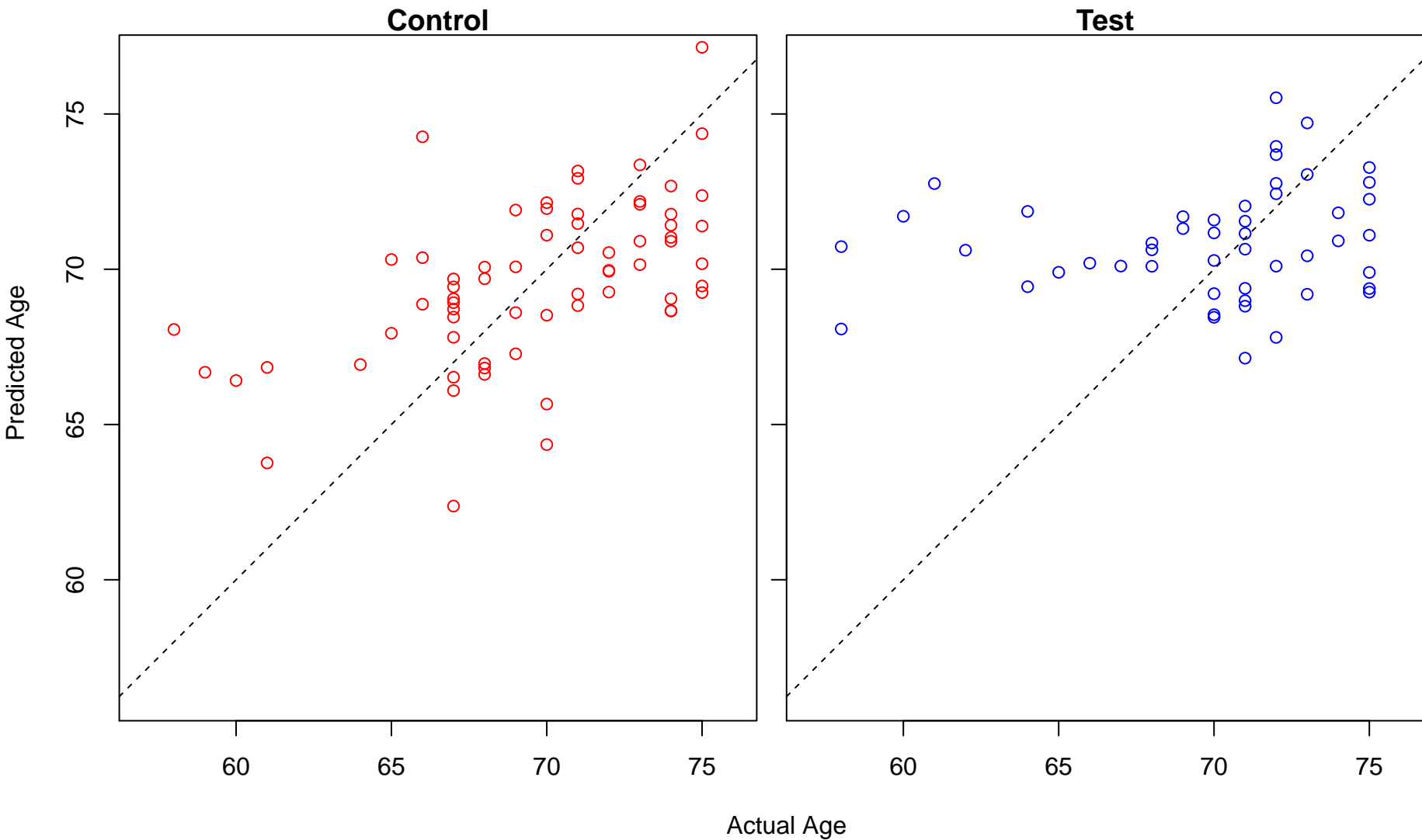
epithelial tube formation (Score: 0.783827)



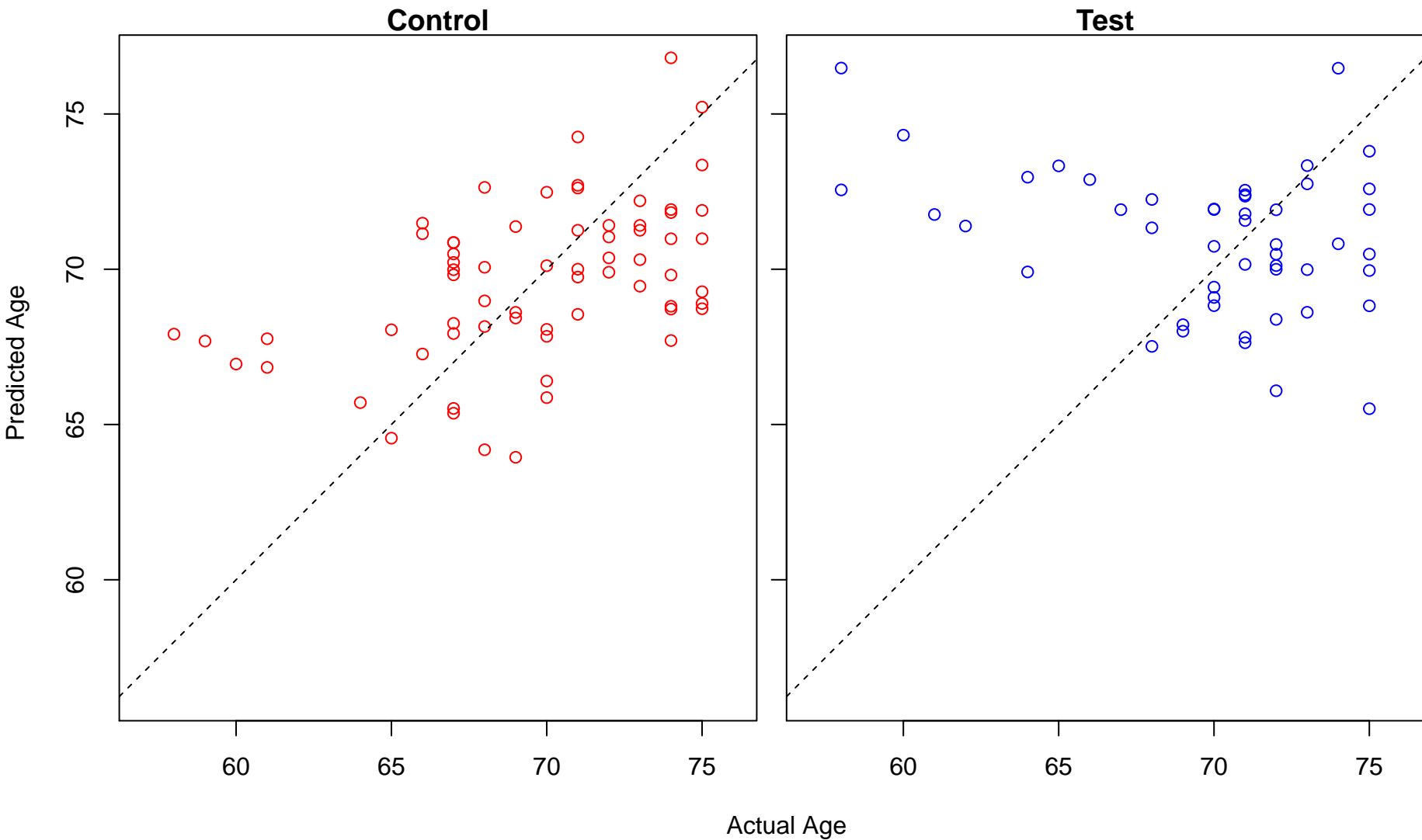
glutamine family amino acid catabolic process (Score: 0.783374)



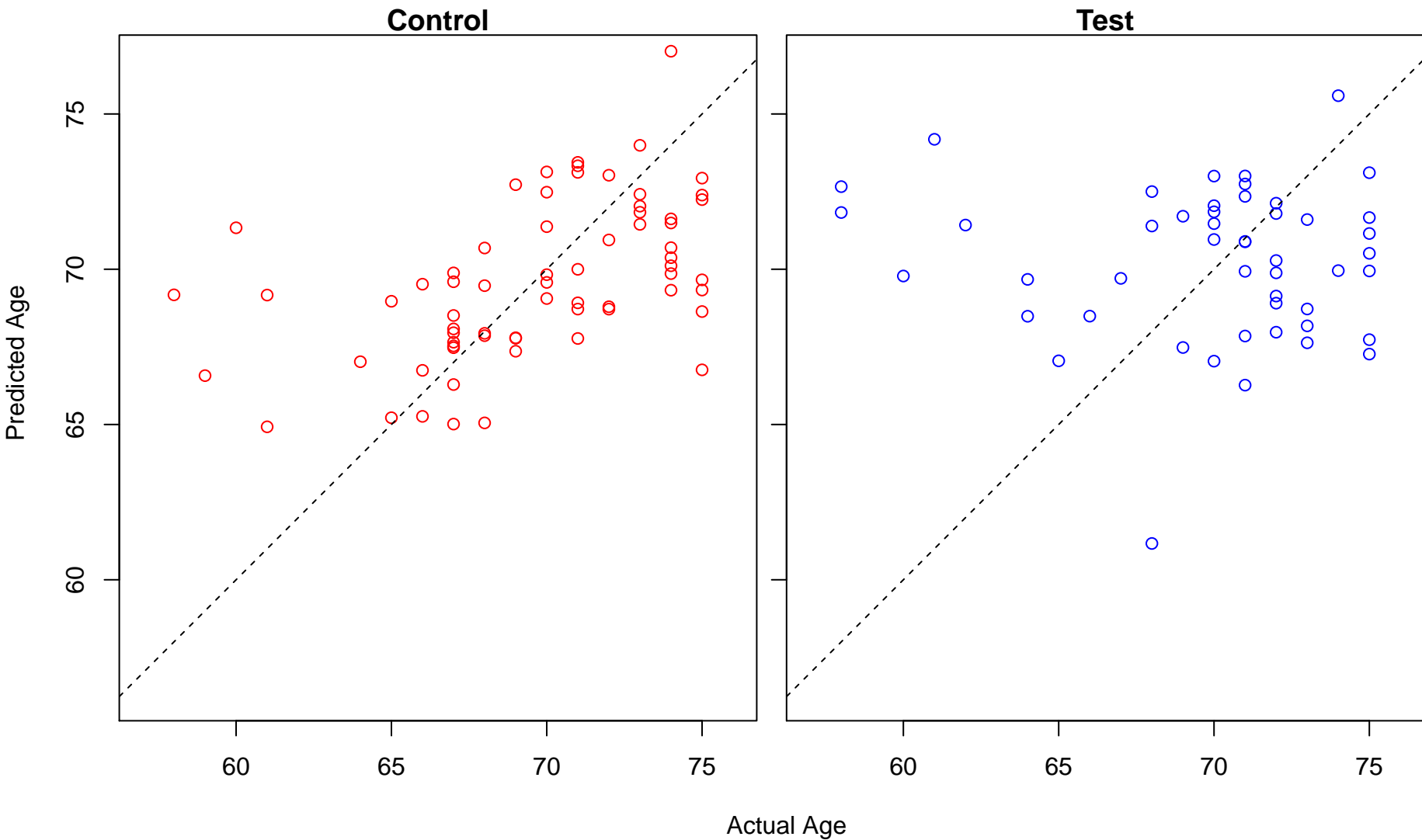
asymmetric stem cell division (Score: 0.782450)



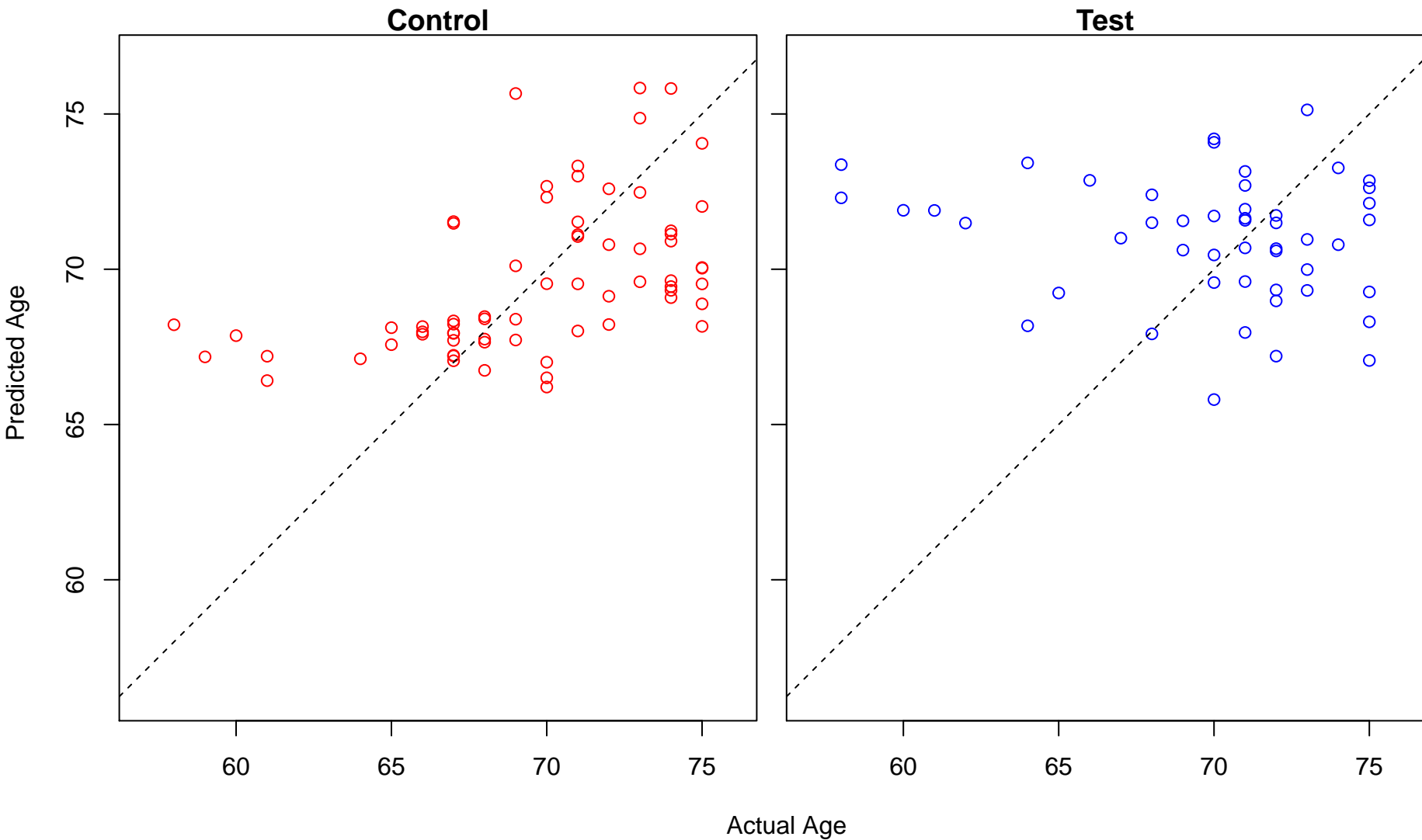
Golgi disassembly (Score: 0.782197)



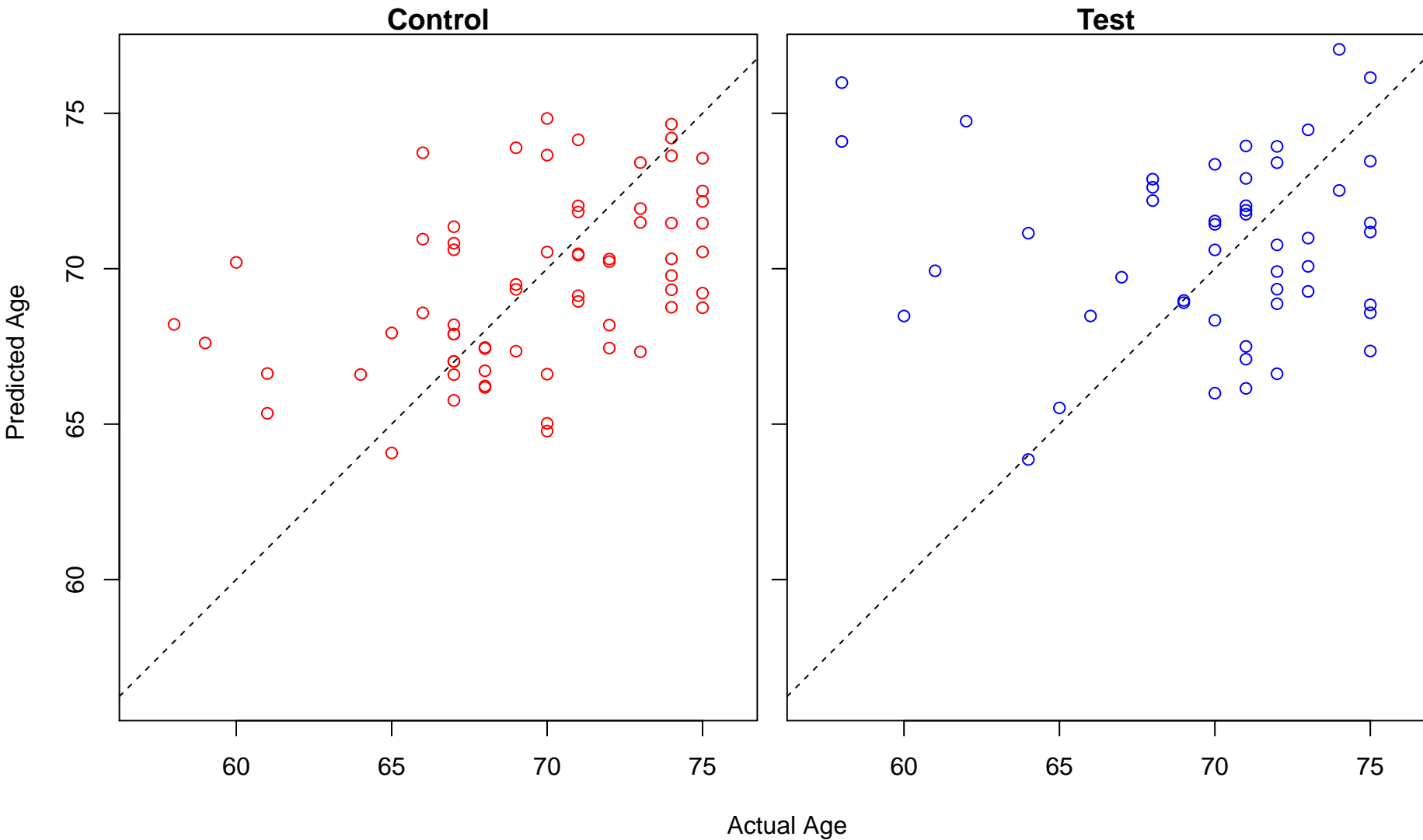
negative regulation of interleukin-10 production (Score: 0.782181)



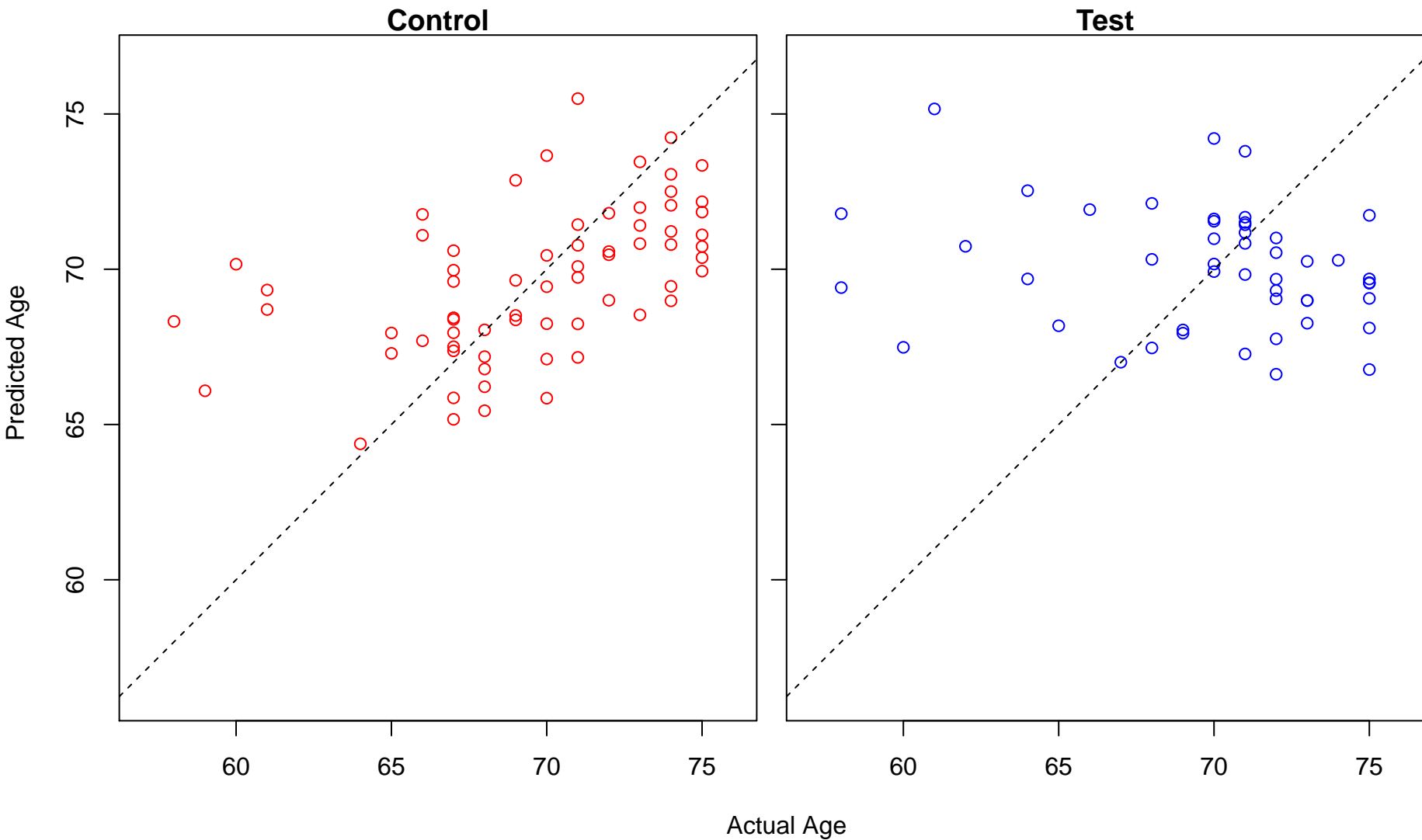
negative regulation of intracellular protein transport (Score: 0.782078)



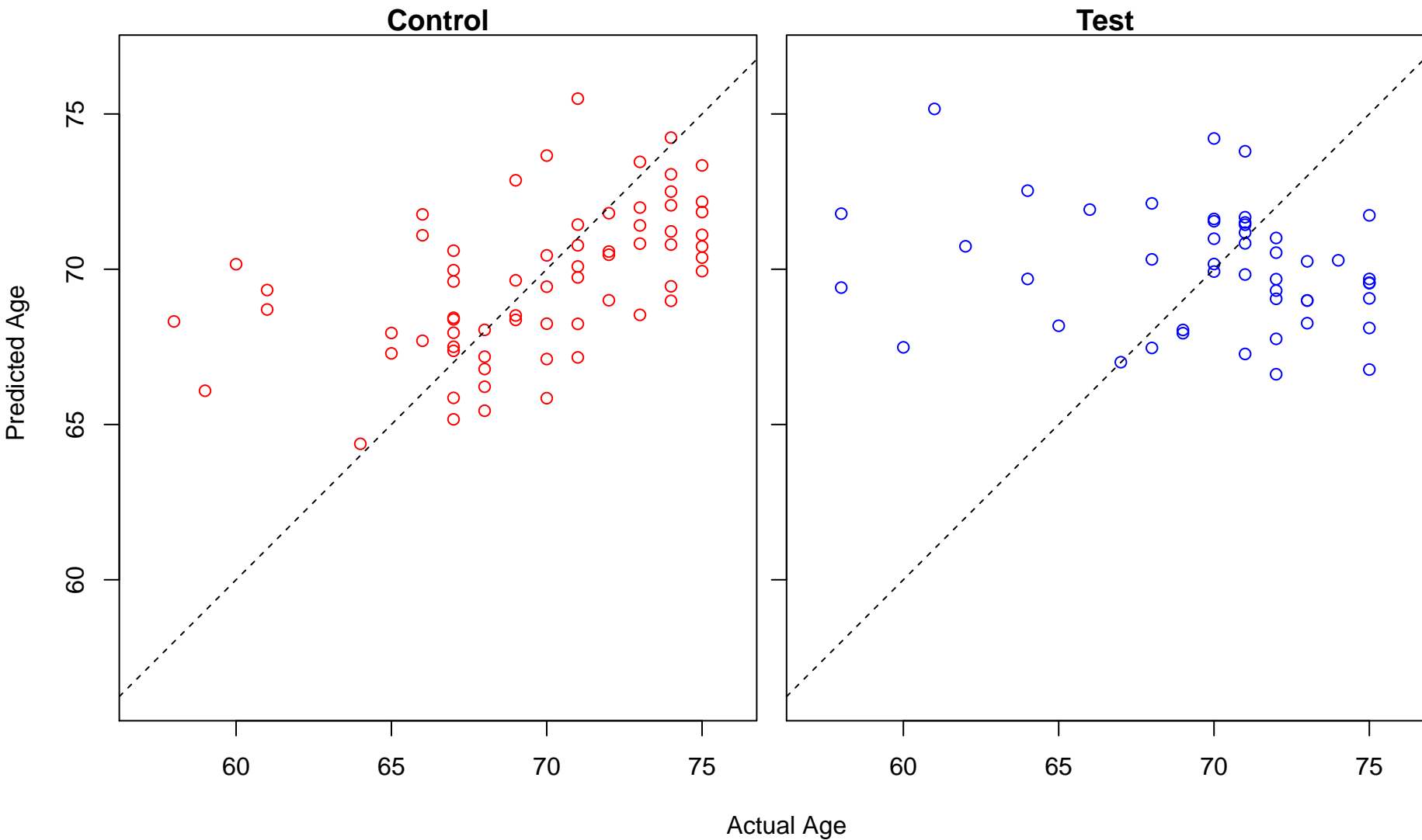
positive regulation of axonogenesis (Score: 0.780963)



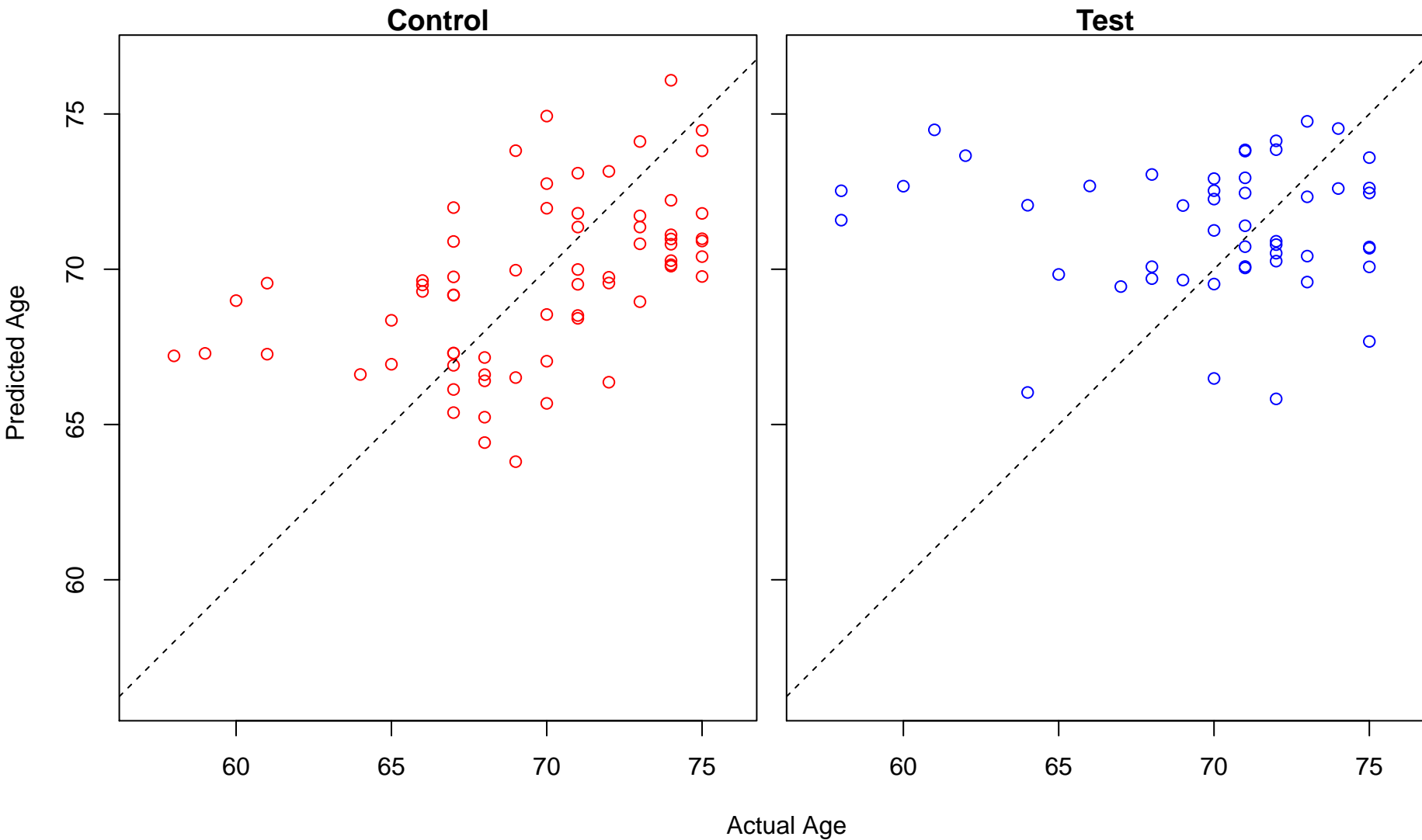
regulation of transposition (Score: 0.780571)



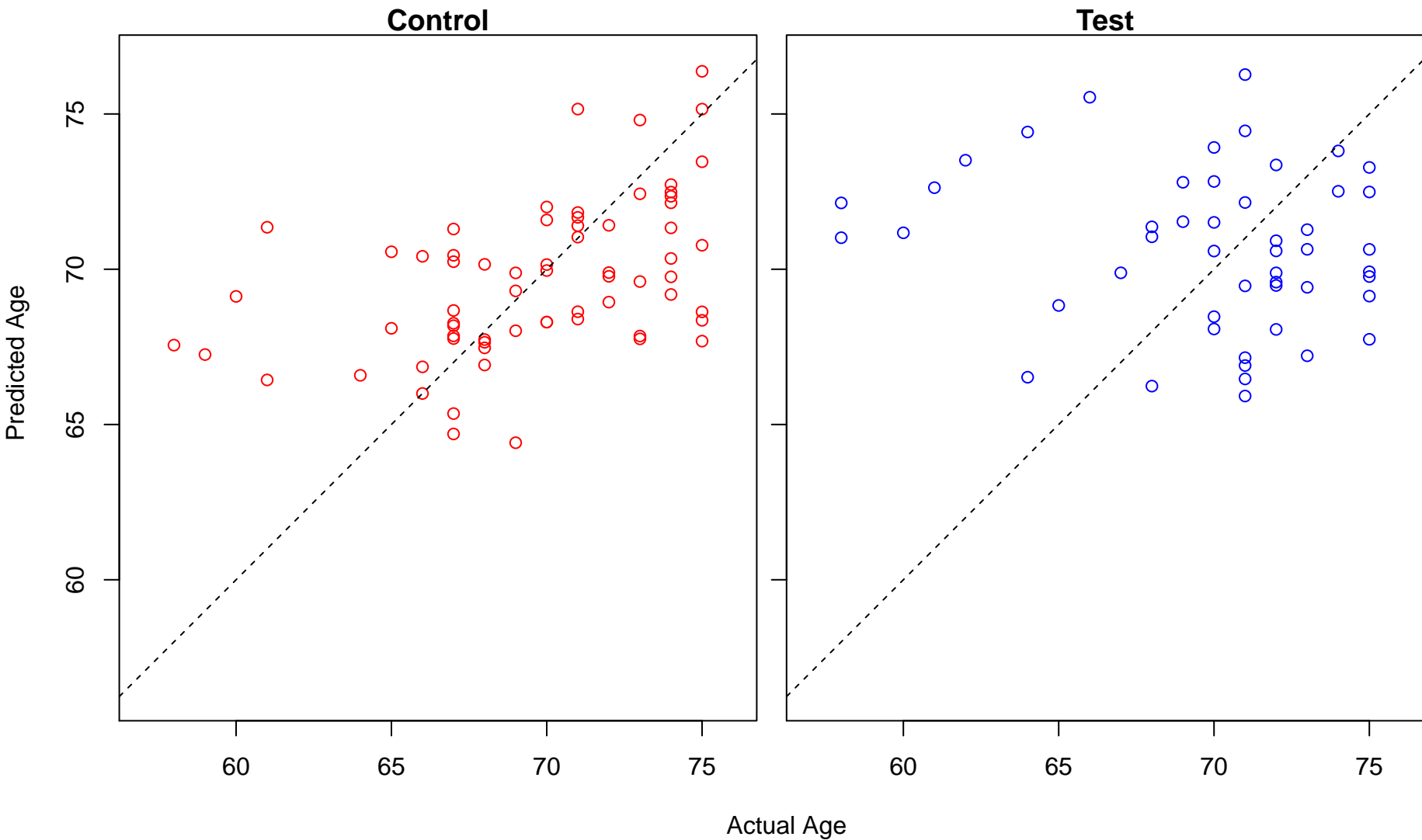
negative regulation of transposition (Score: 0.780571)



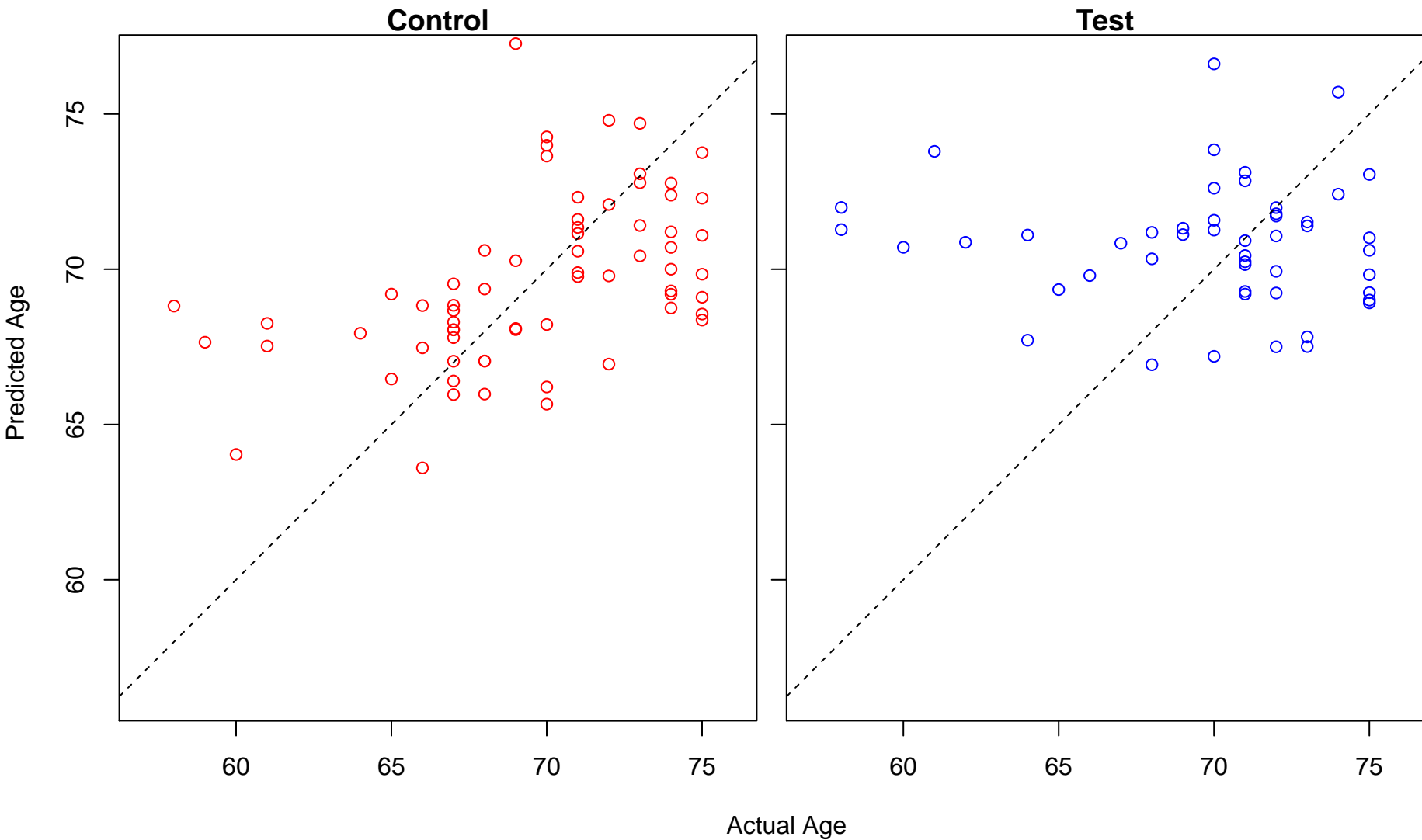
regulation of glucose import (Score: 0.780491)



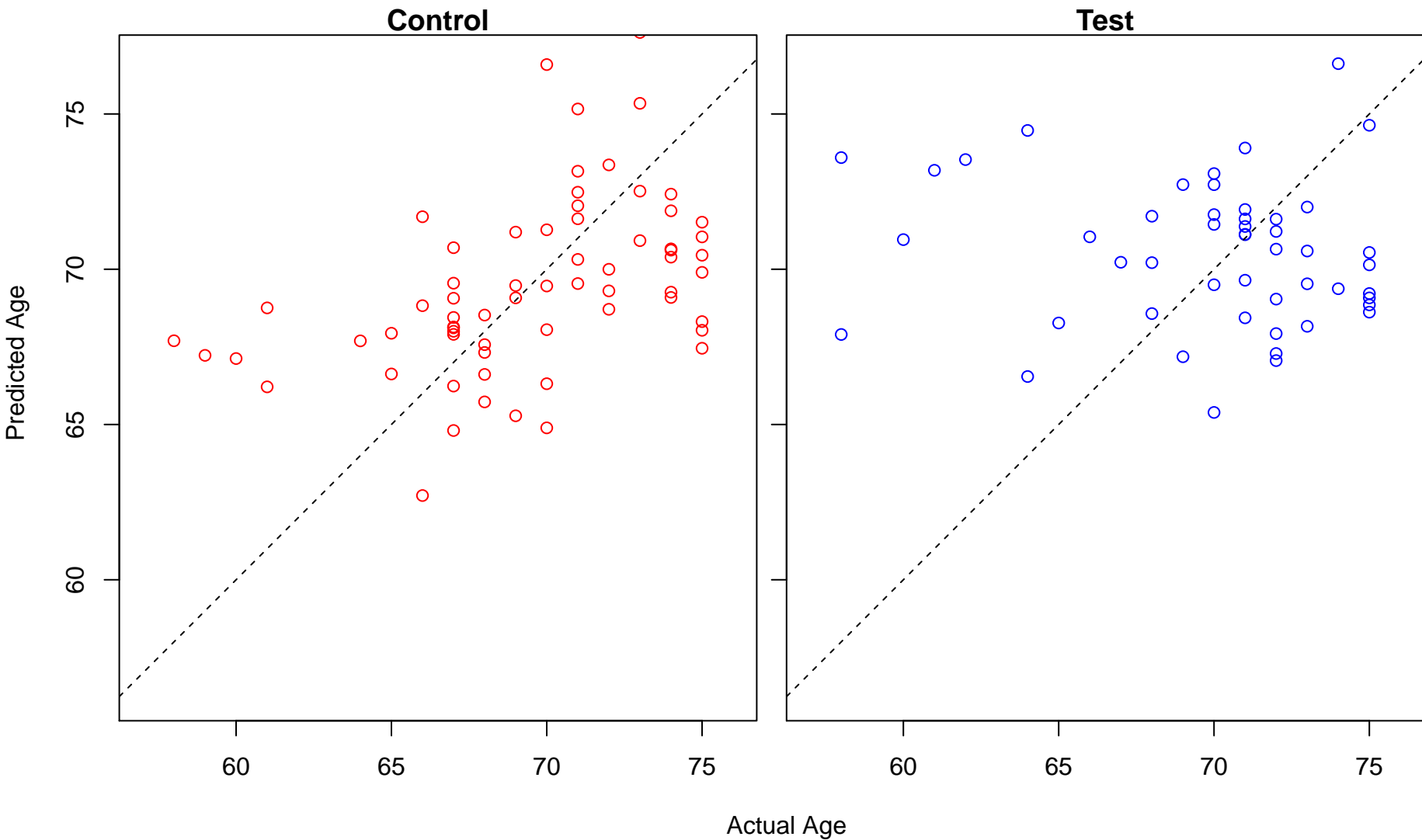
negative regulation of stem cell proliferation (Score: 0.780357)



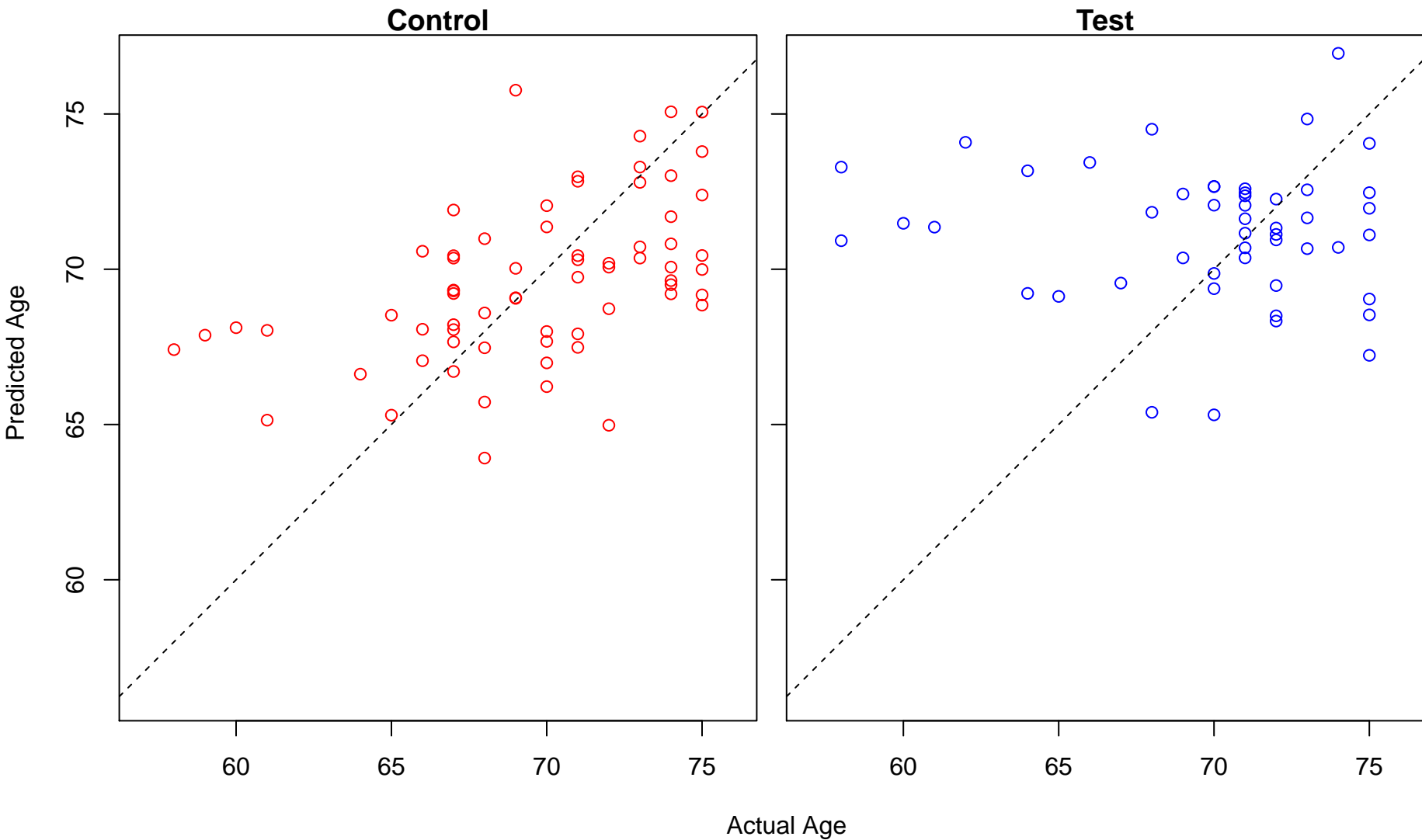
positive regulation of interferon-gamma production (Score: 0.780226)



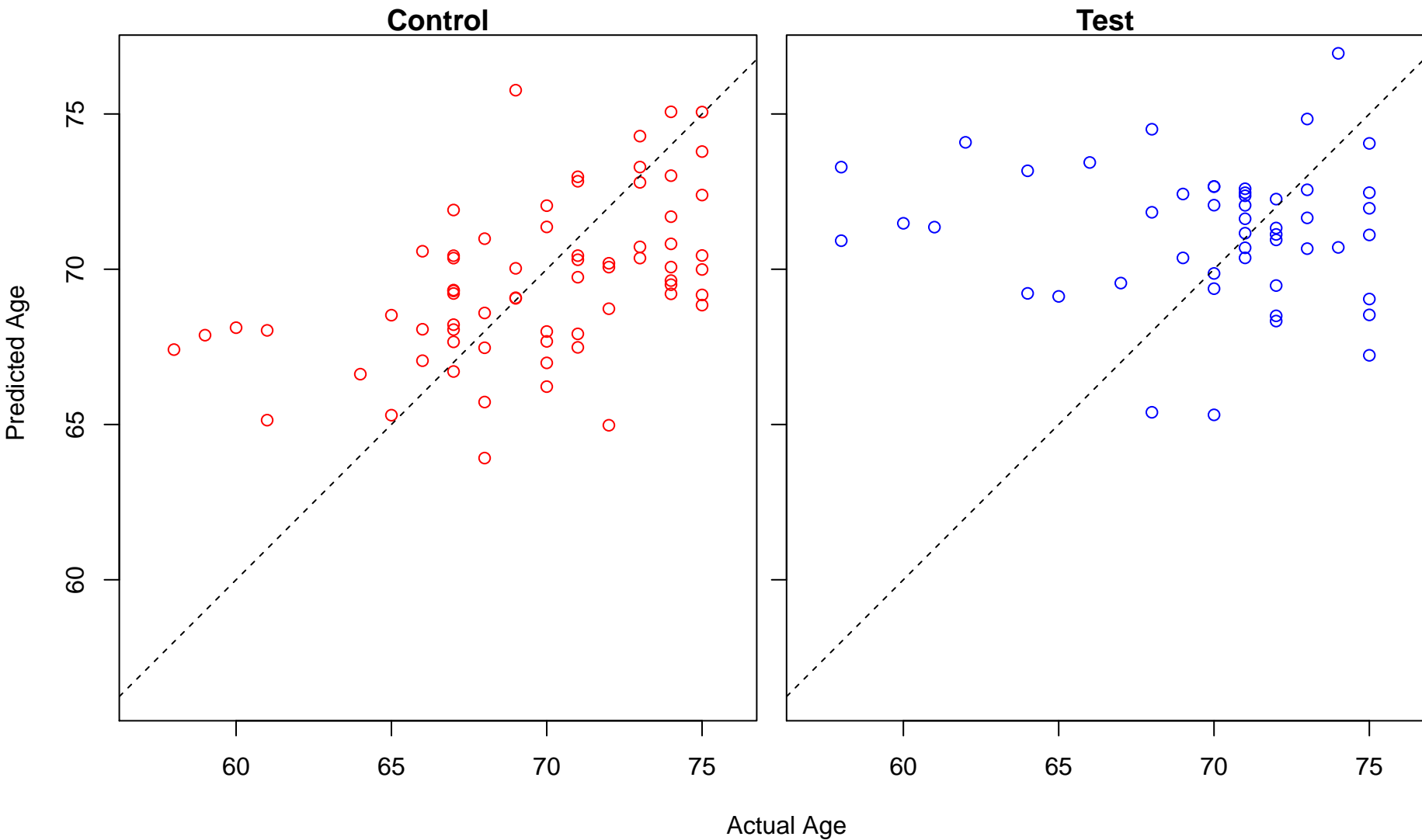
regulation of endocrine process (Score: 0.780166)



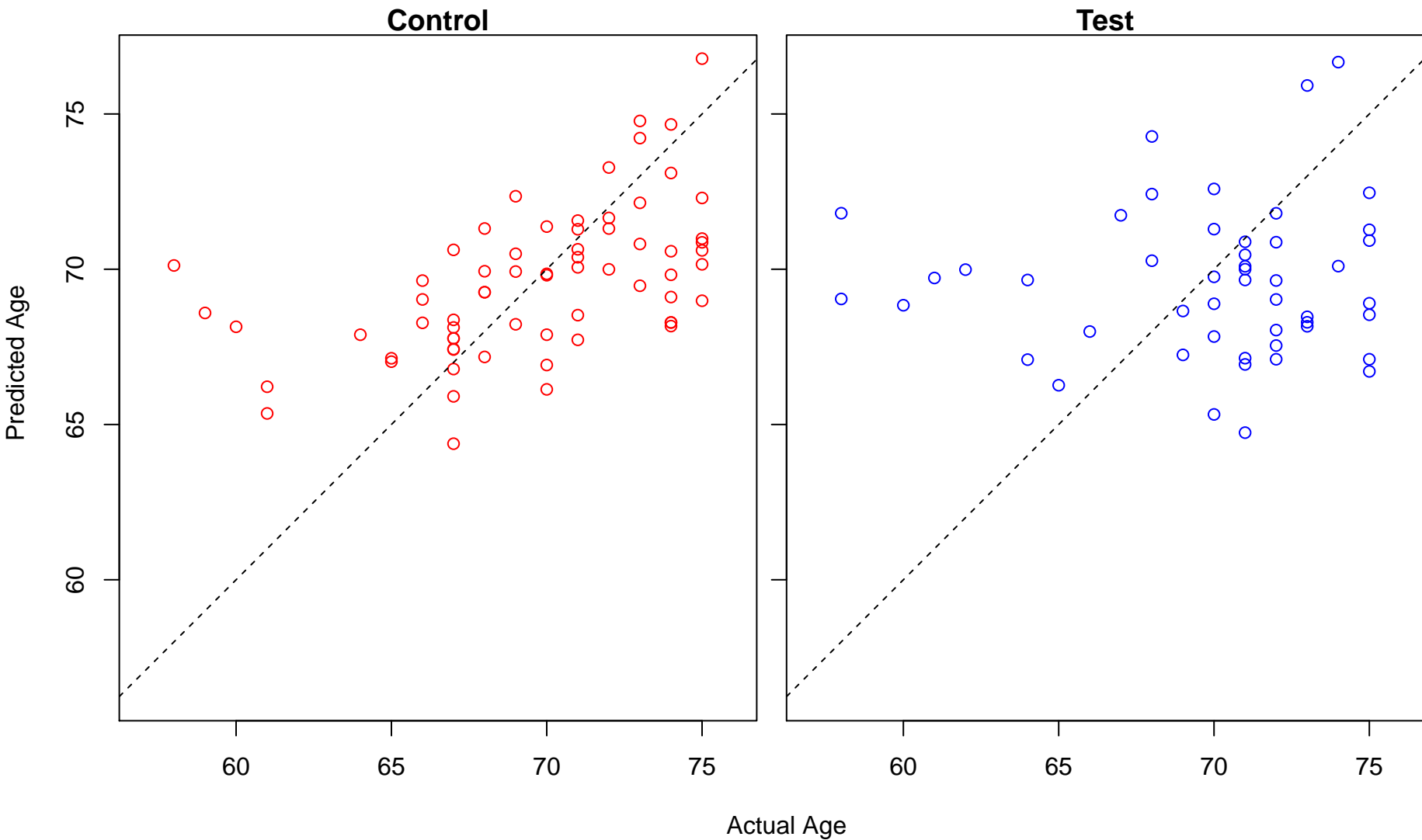
negative regulation of JAK-STAT cascade (Score: 0.779581)



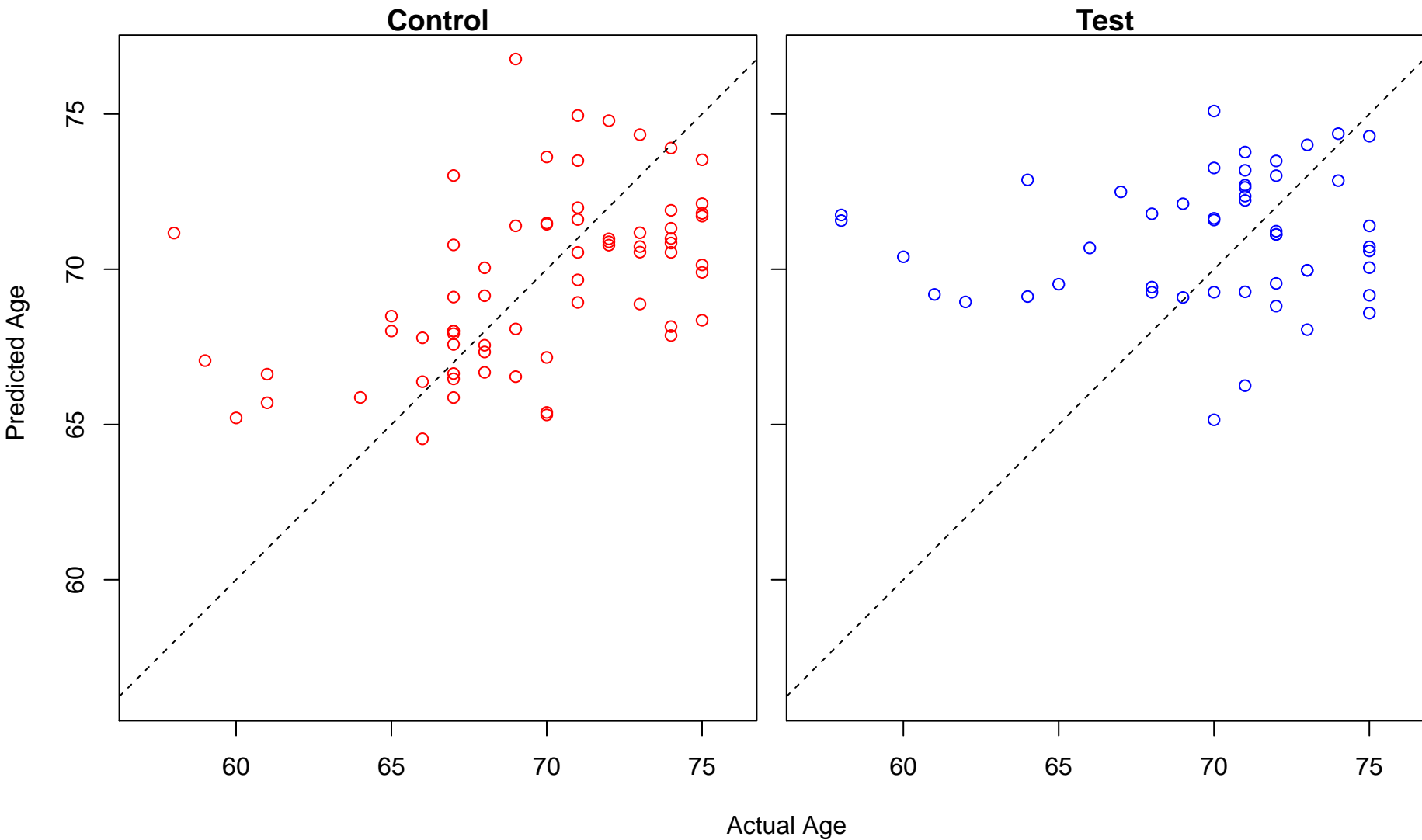
negative regulation of STAT cascade (Score: 0.779581)



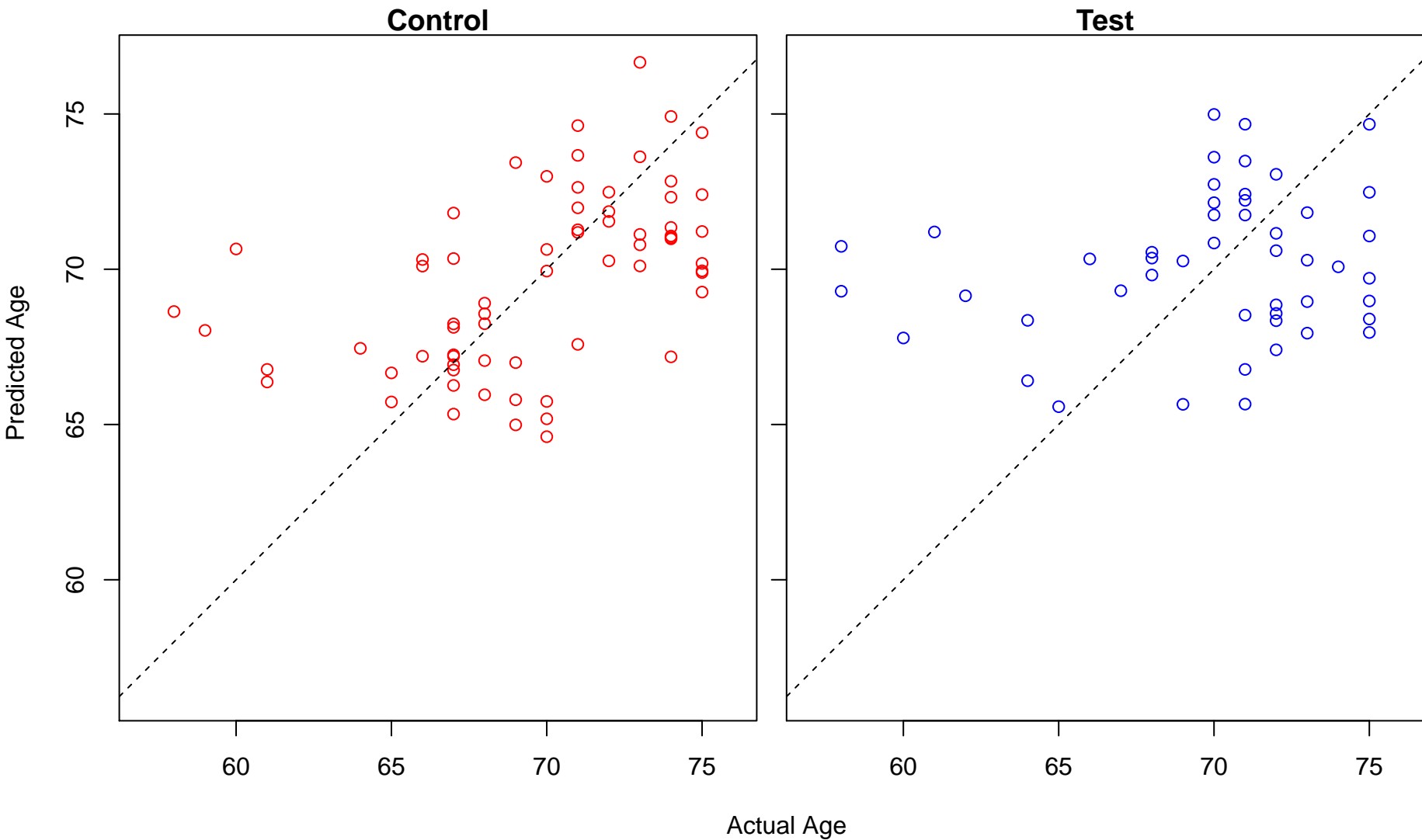
negative regulation of DNA-templated transcription, elongation (Score: 0.779501)



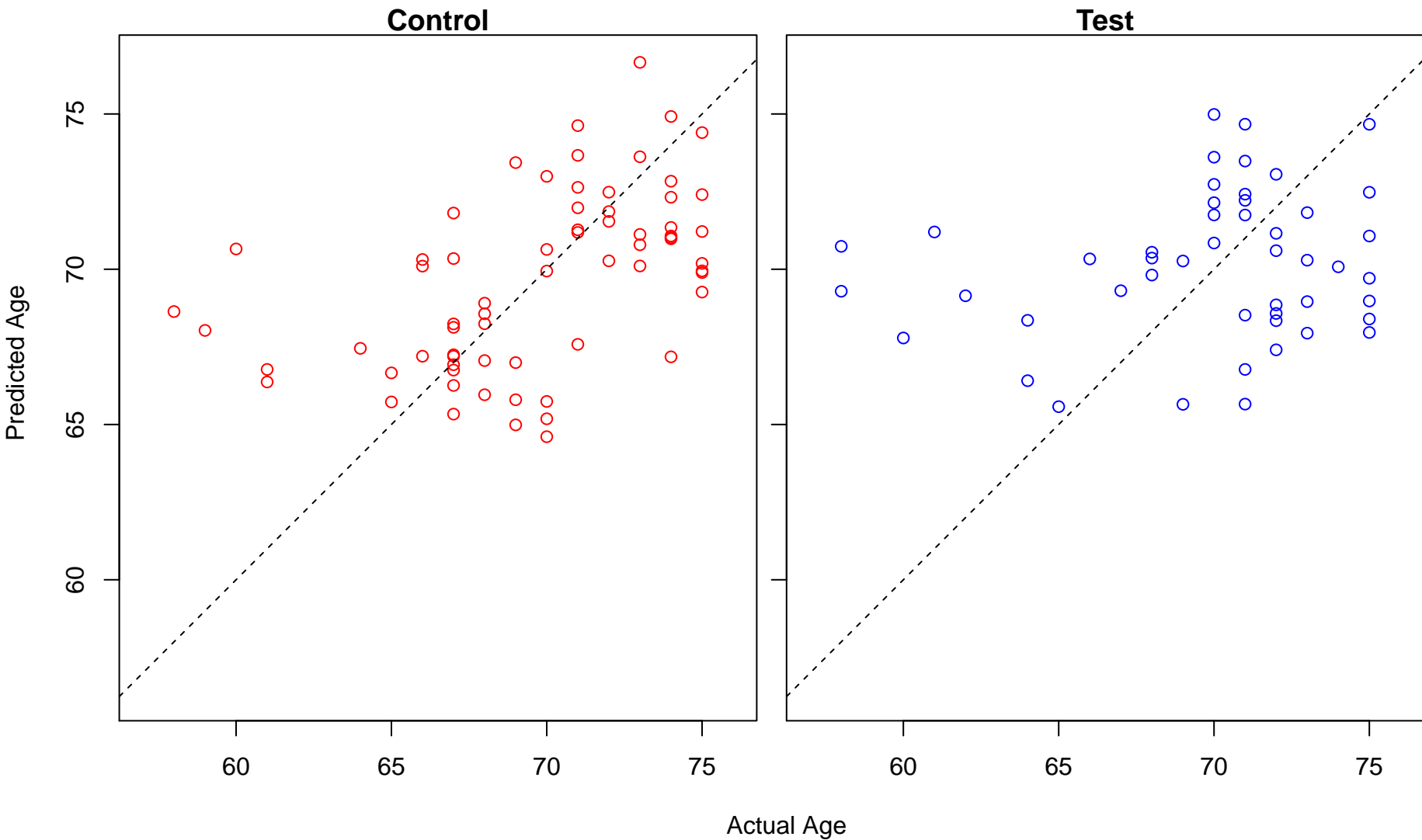
chondroitin sulfate proteoglycan biosynthetic process (Score: 0.779487)



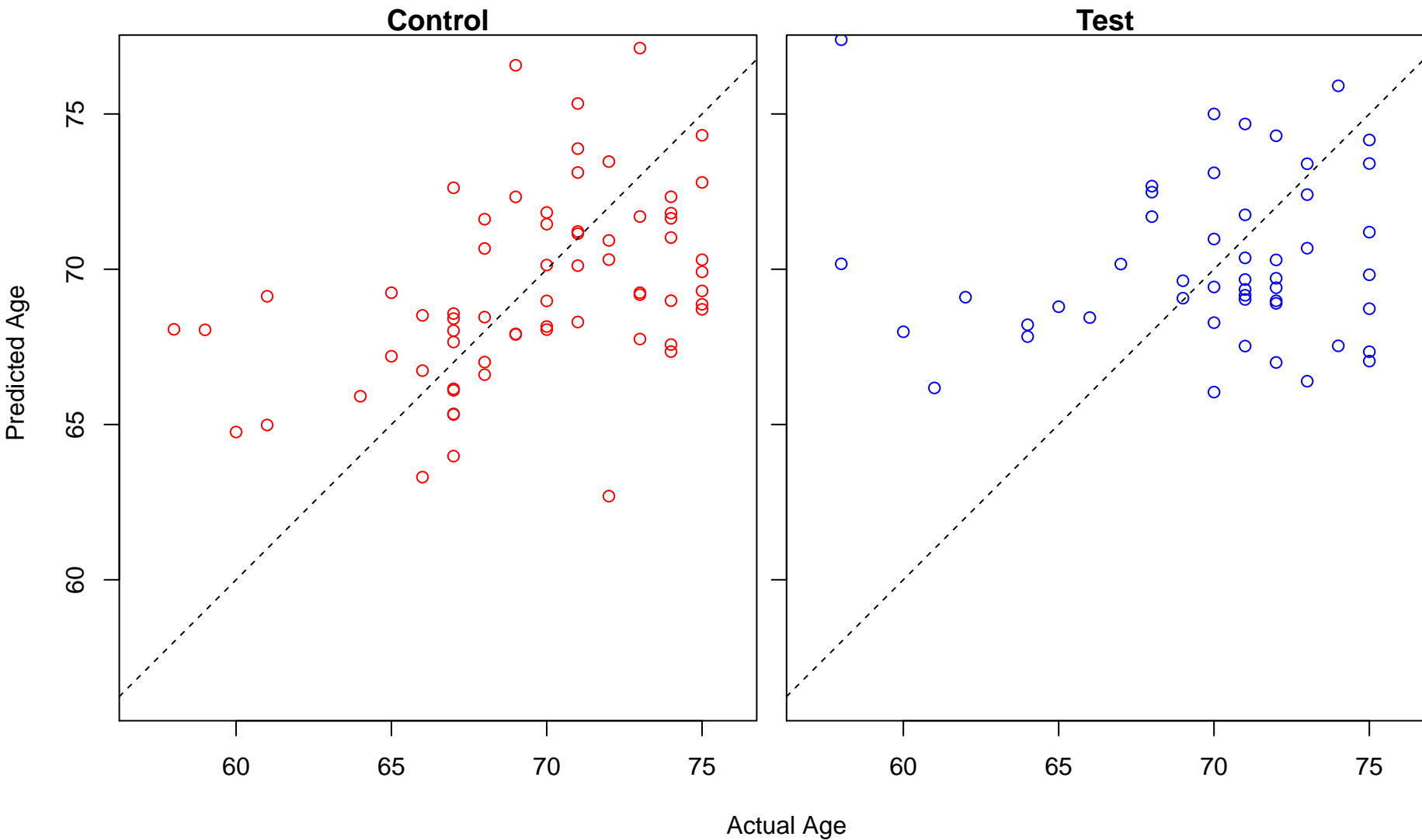
regulation of blood coagulation (Score: 0.779123)



regulation of hemostasis (Score: 0.779123)

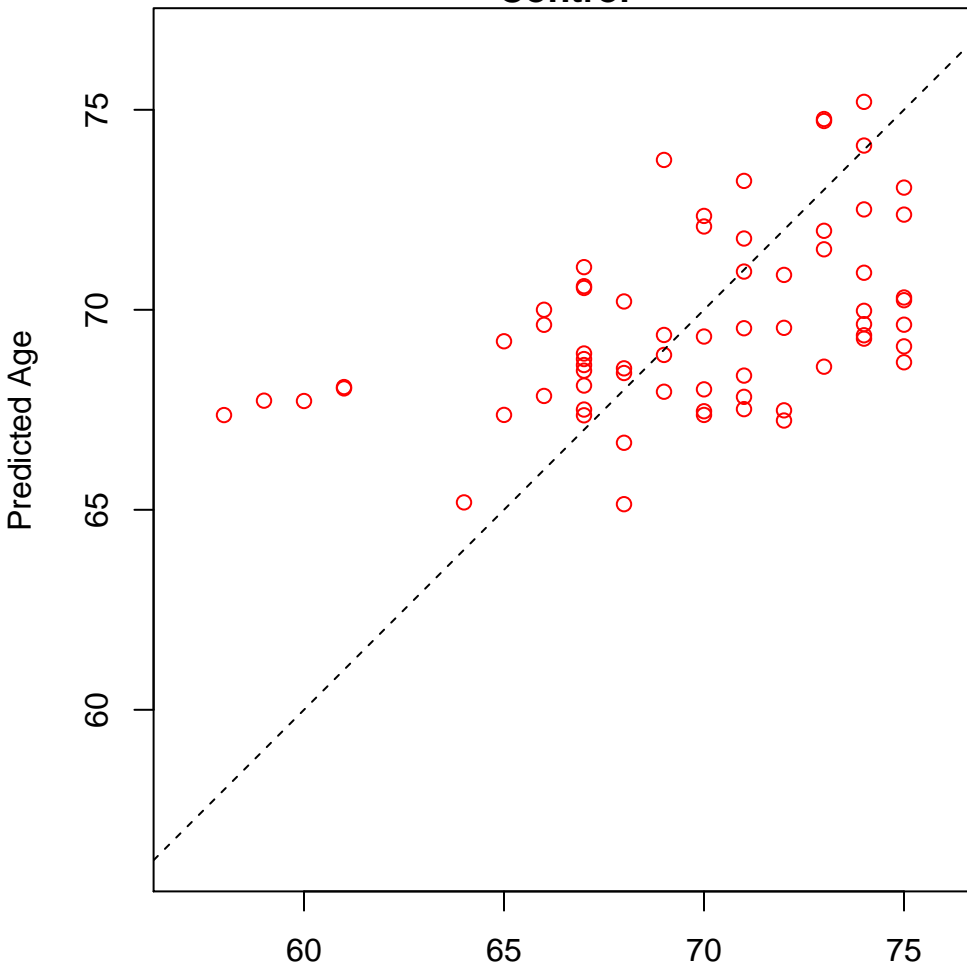


apoptotic cell clearance (Score: 0.778583)

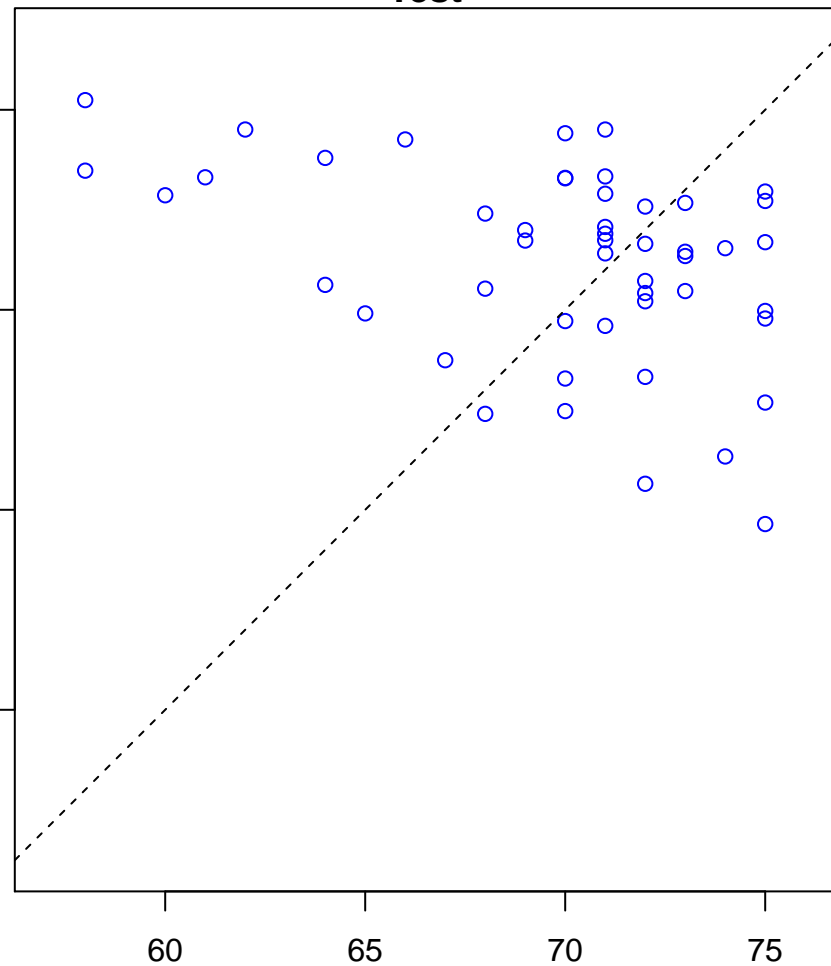


protein localization to Golgi apparatus (Score: 0.778533)

Control

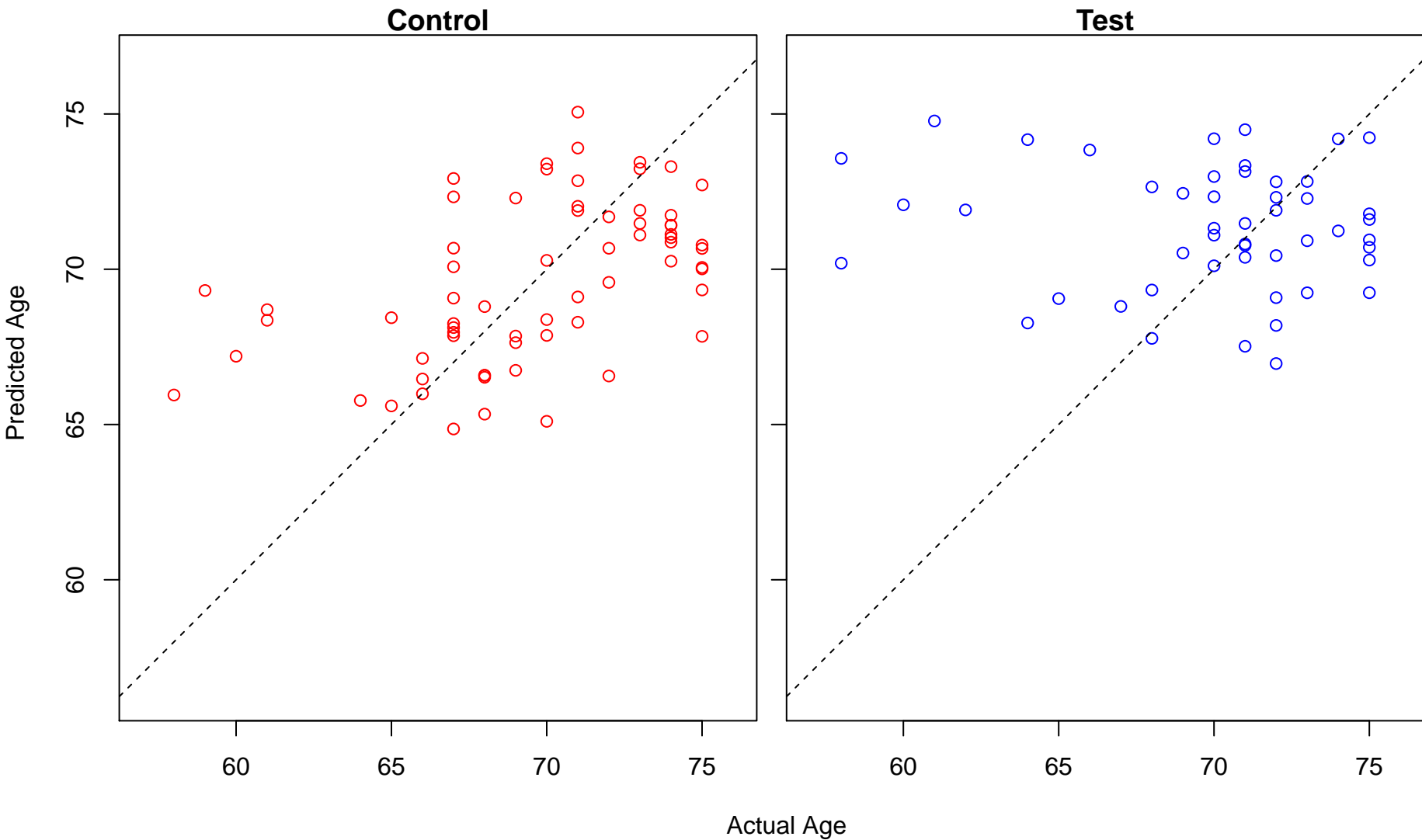


Test



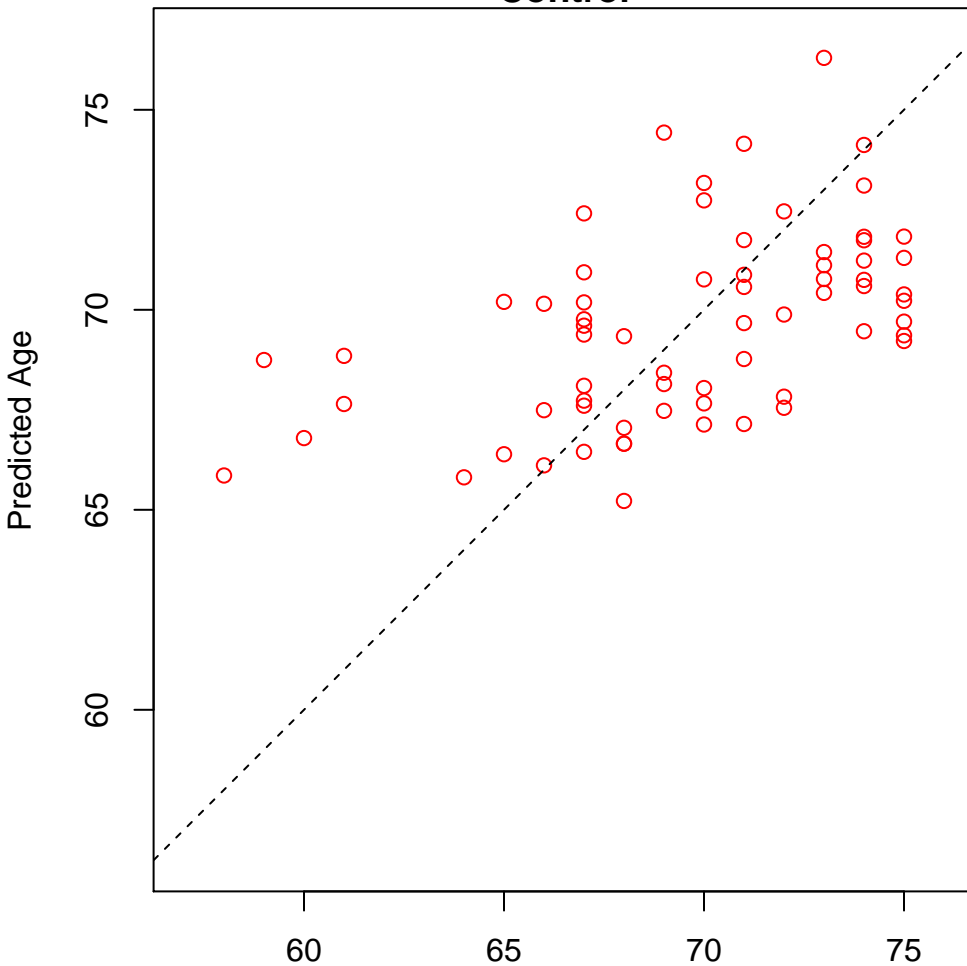
Actual Age

positive regulation of muscle tissue development (Score: 0.778432)

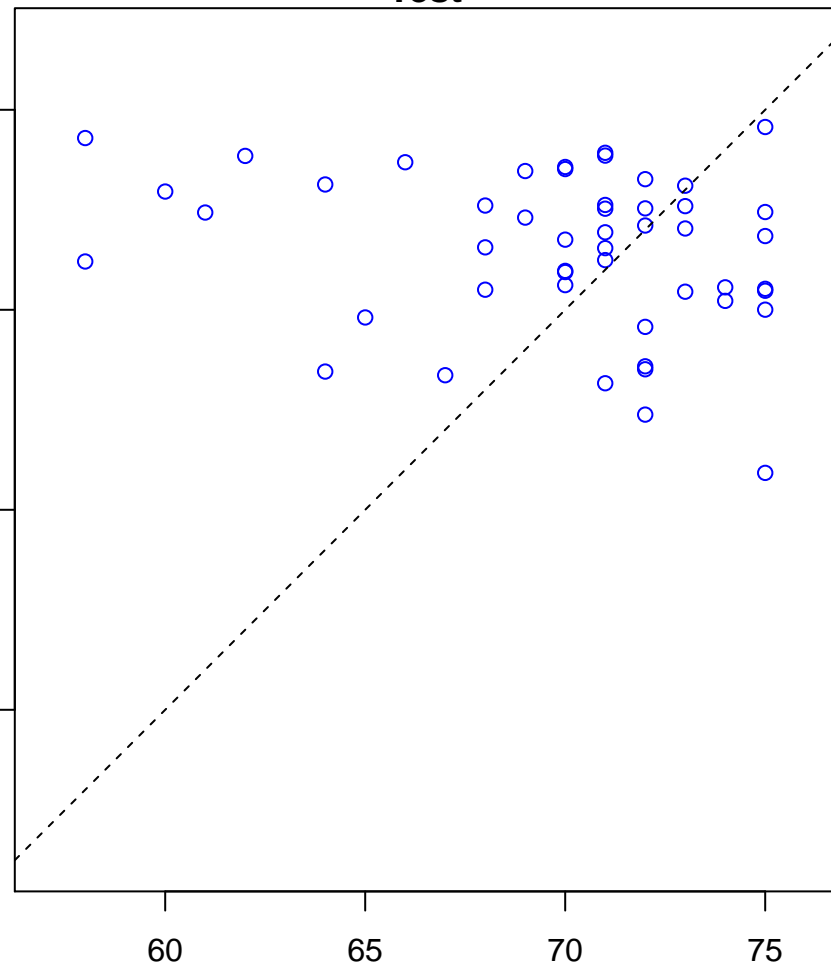


ventricular septum development (Score: 0.778375)

Control

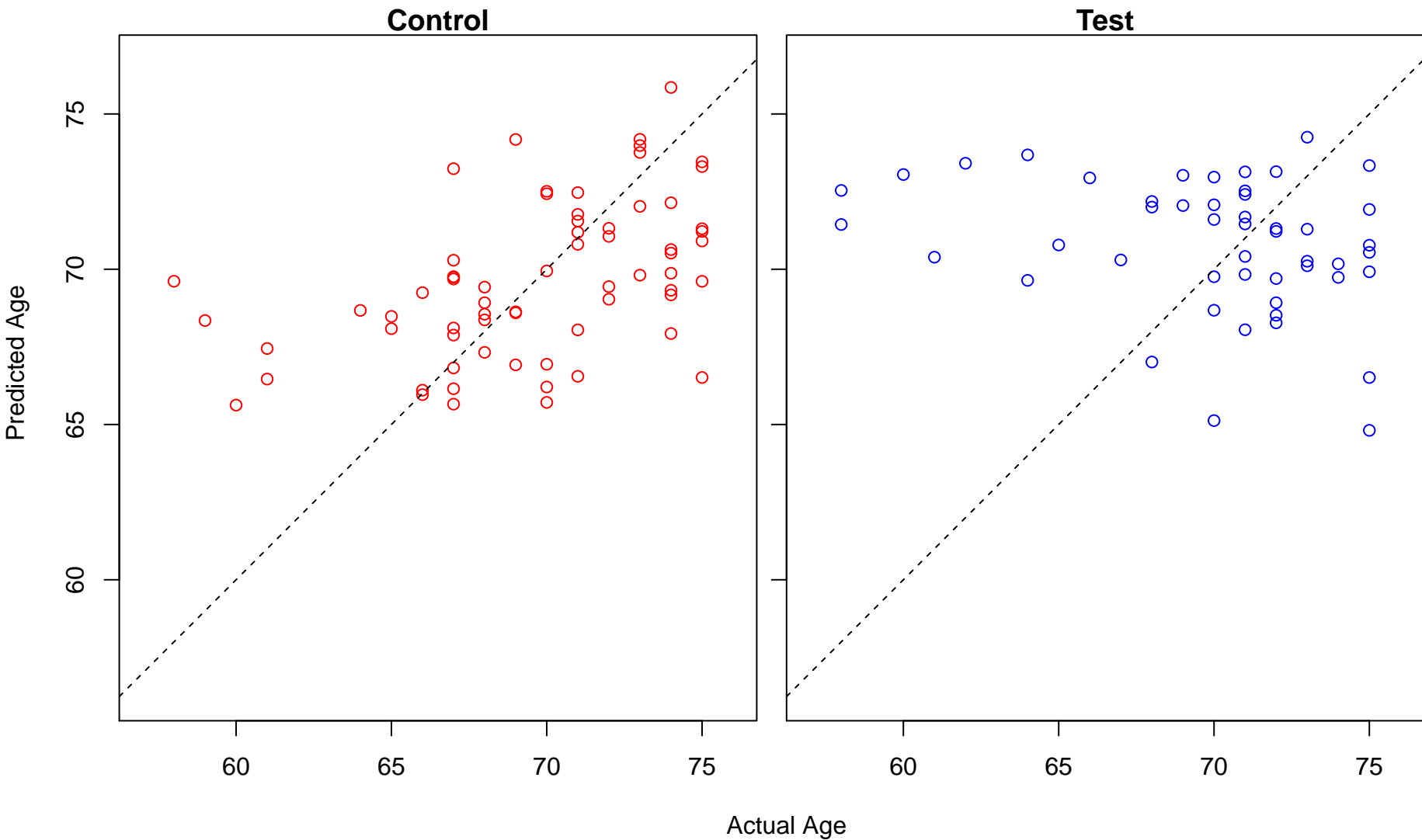


Test

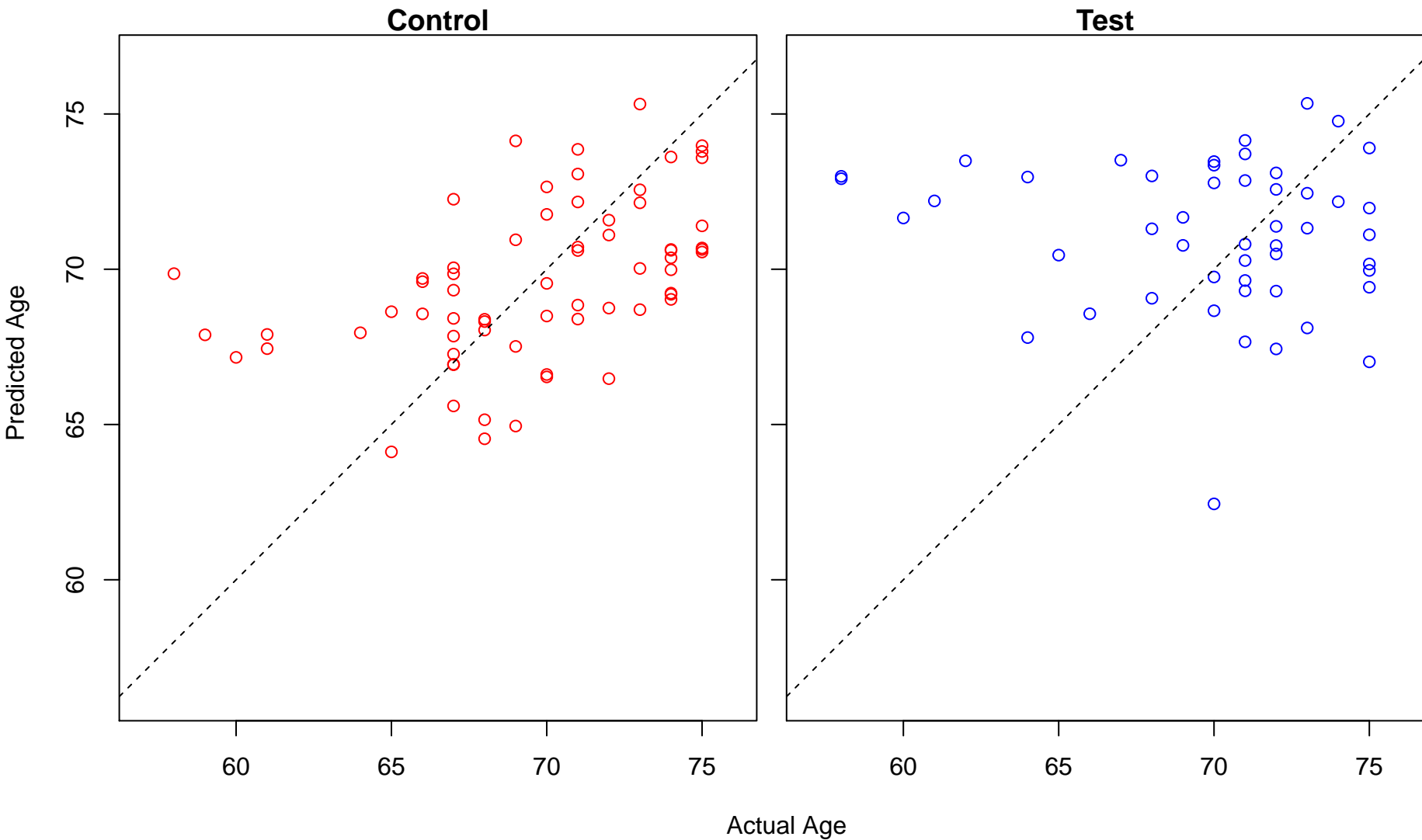


Actual Age

developmental cell growth (Score: 0.777746)

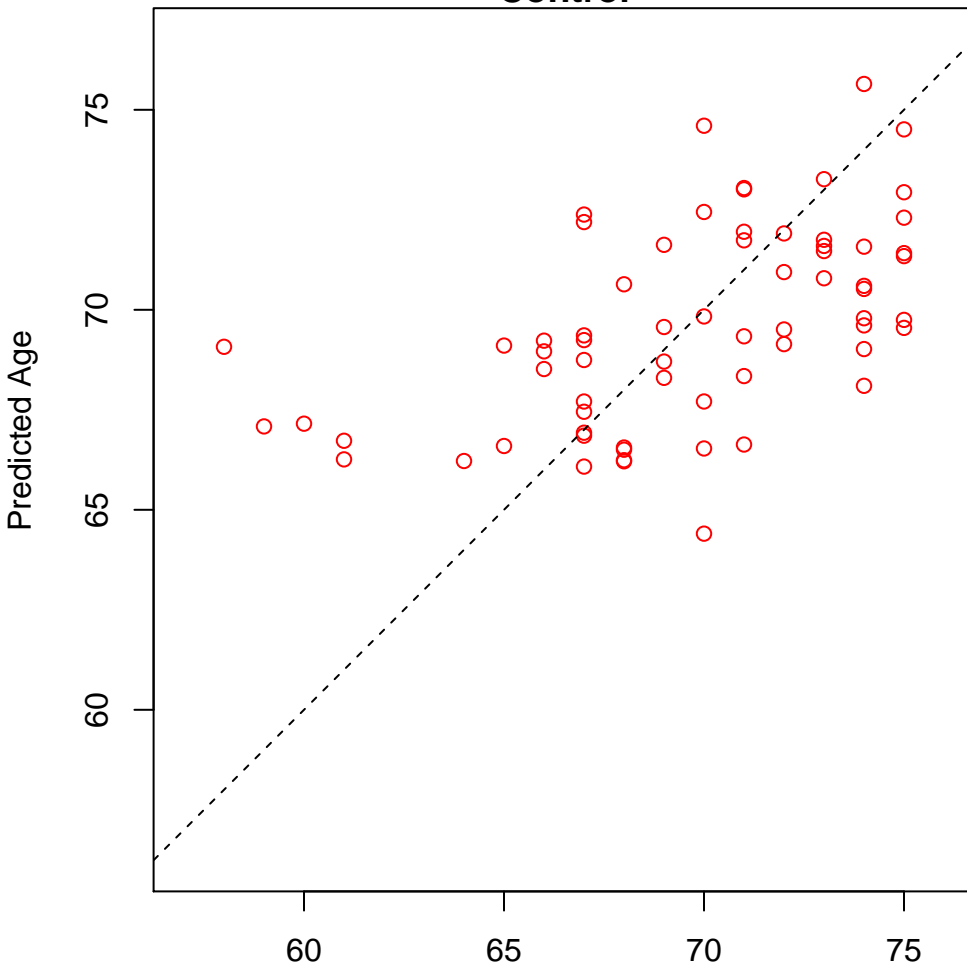


response to sterol (Score: 0.777490)

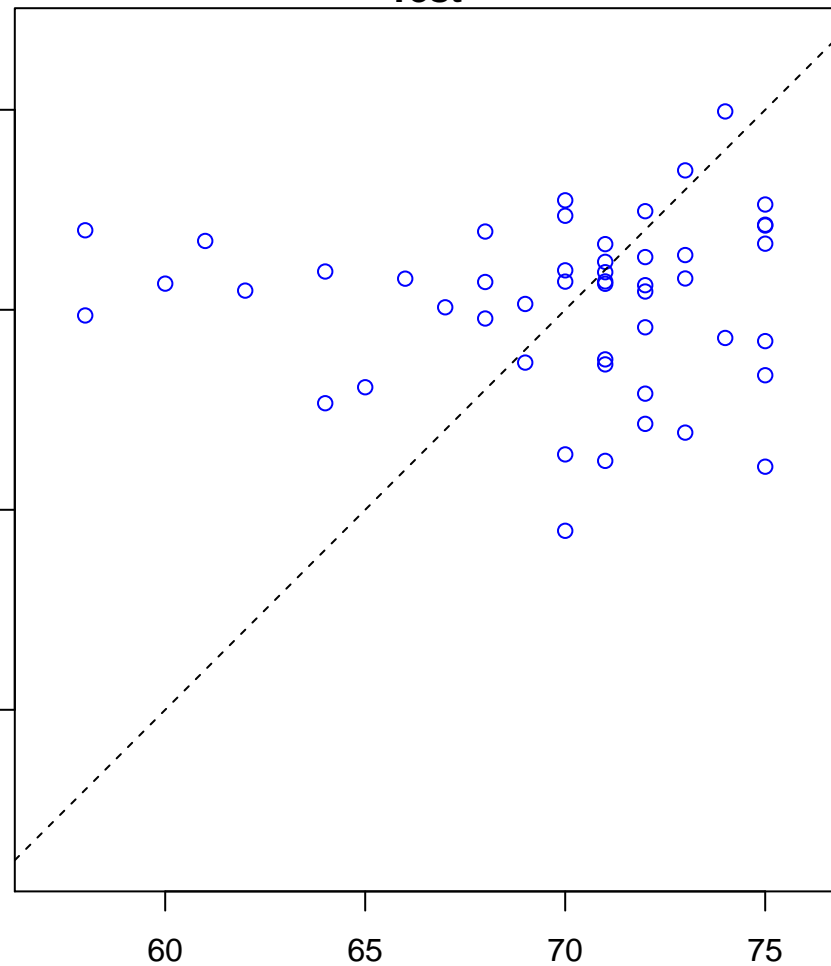


morphogenesis of embryonic epithelium (Score: 0.777476)

Control

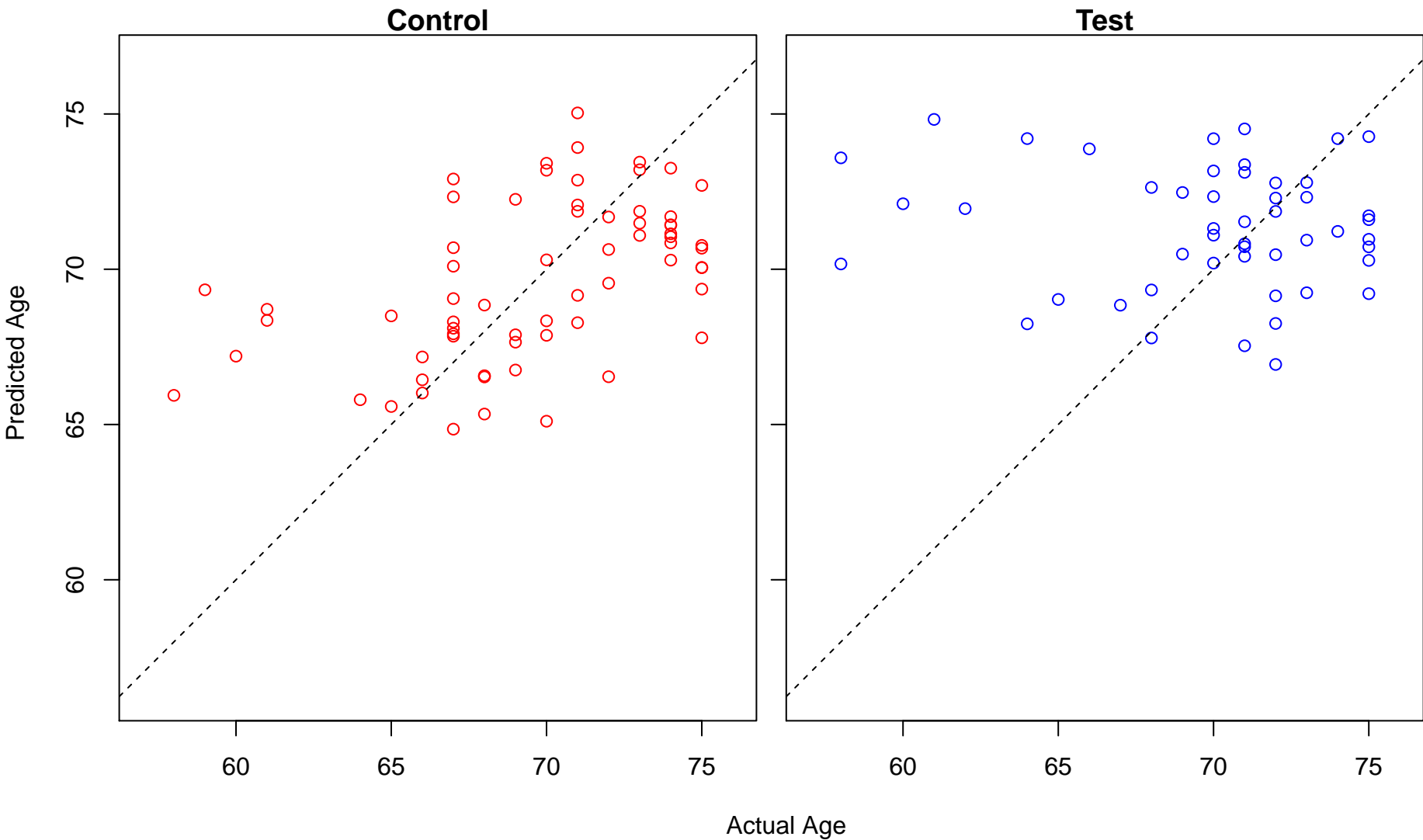


Test

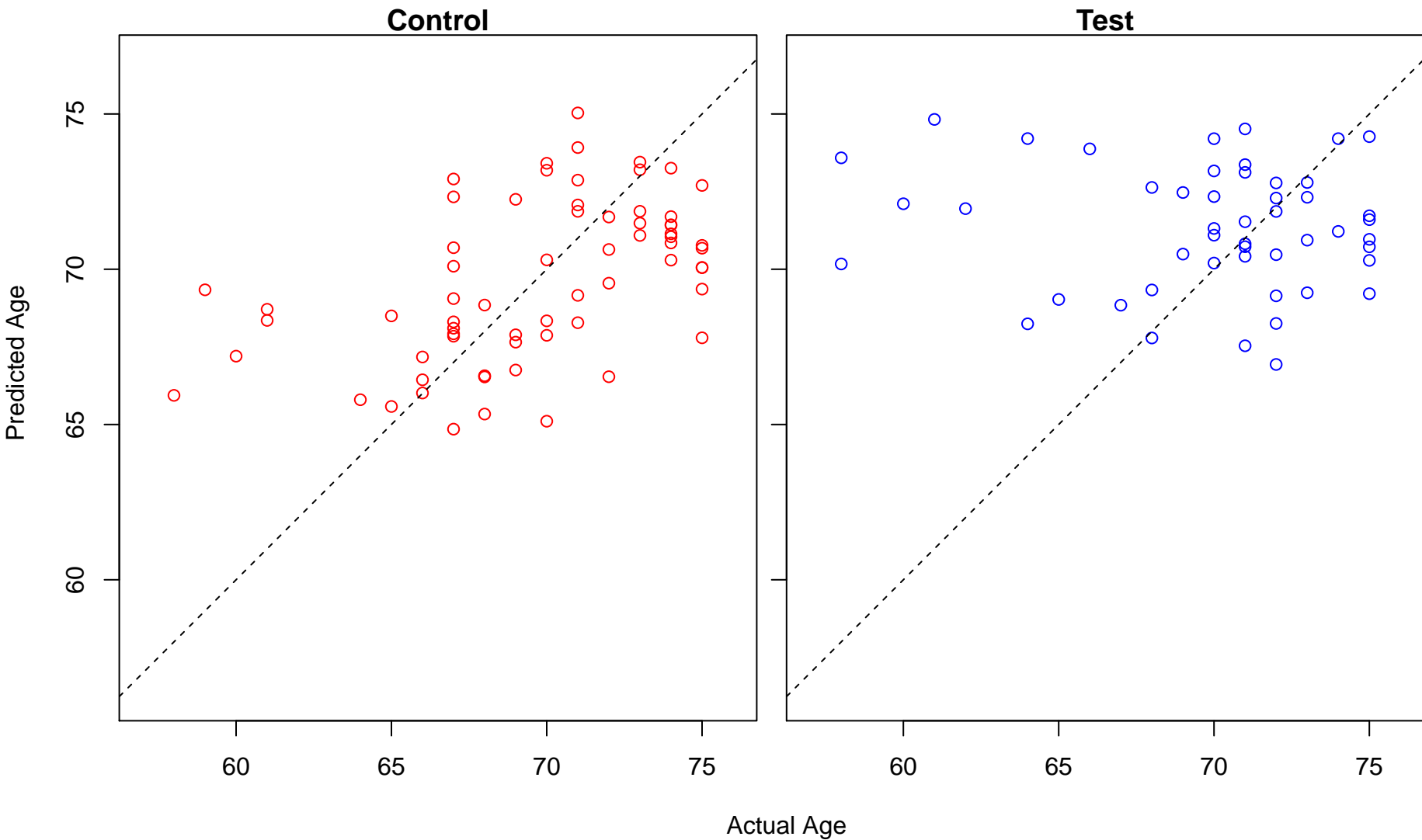


Actual Age

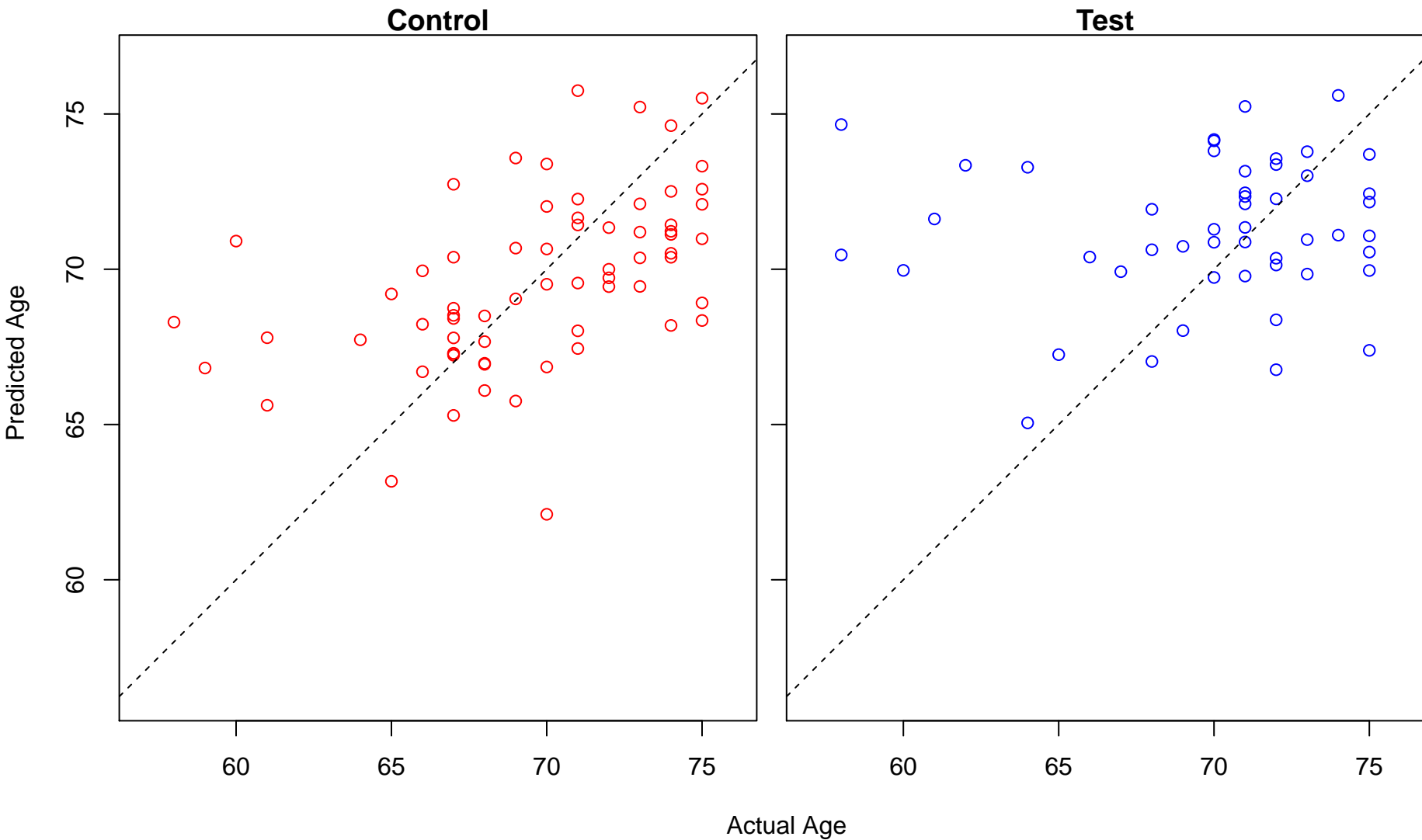
positive regulation of striated muscle tissue development (Score: 0.777461)



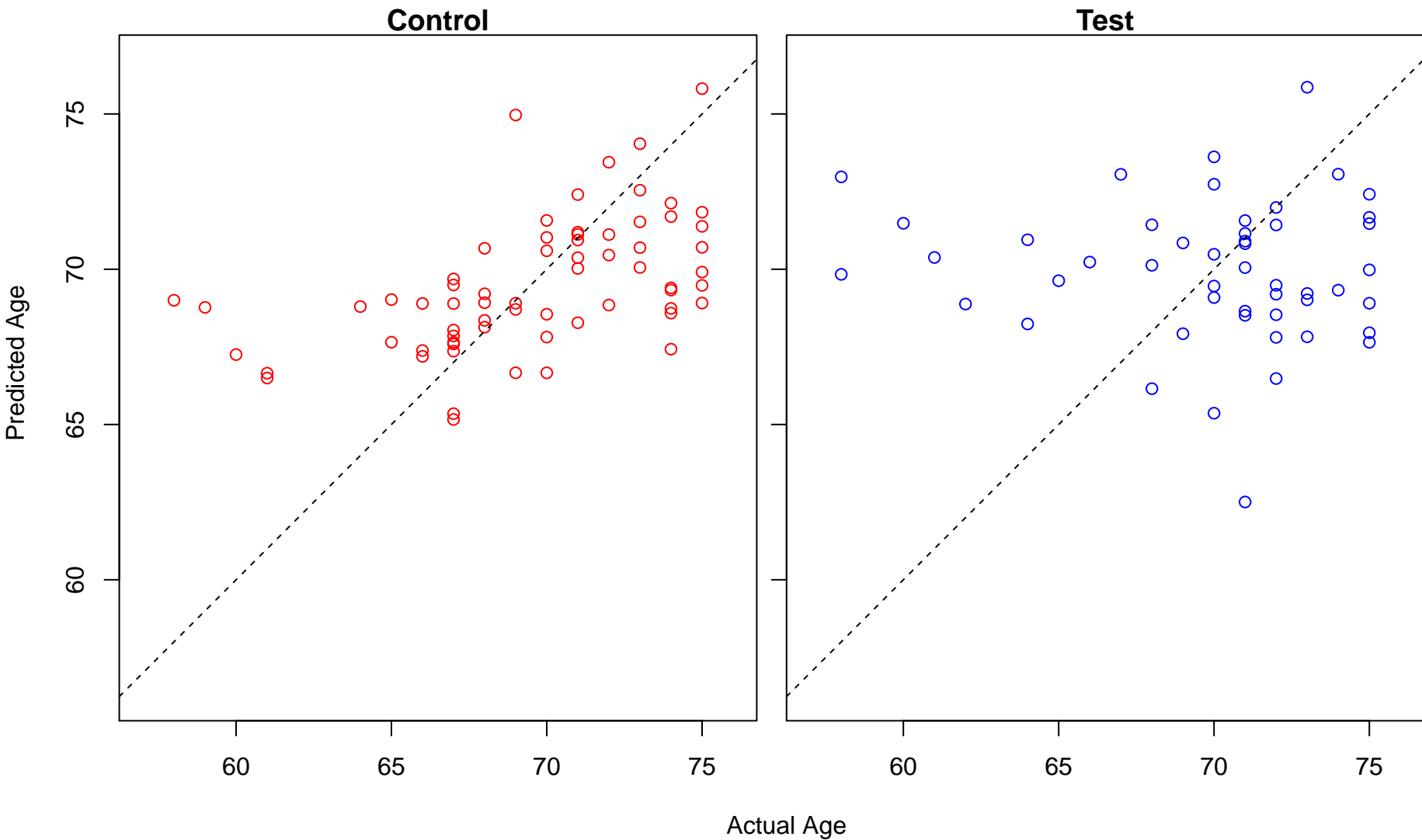
positive regulation of muscle organ development (Score: 0.777461)



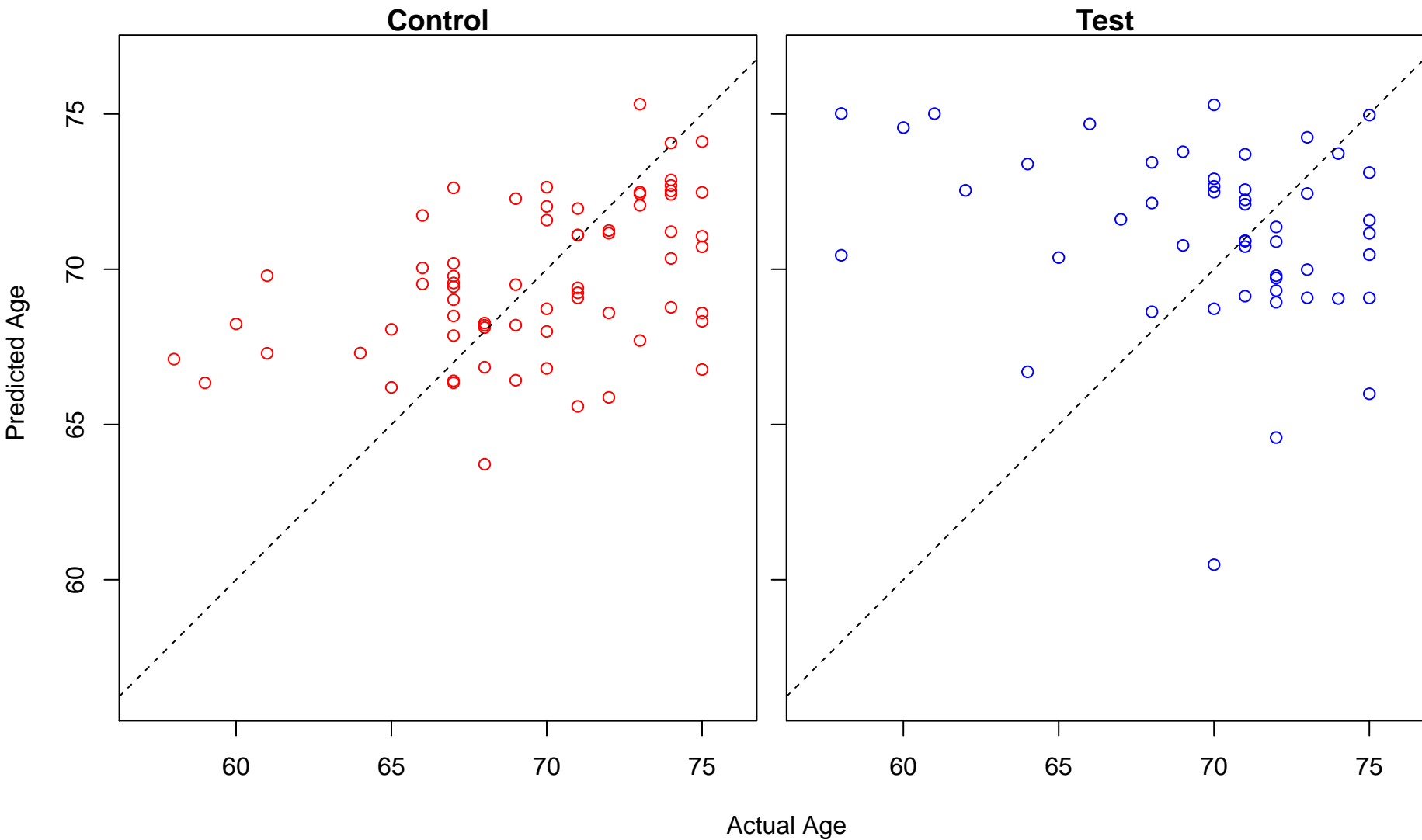
negative regulation of histone acetylation (Score: 0.777072)



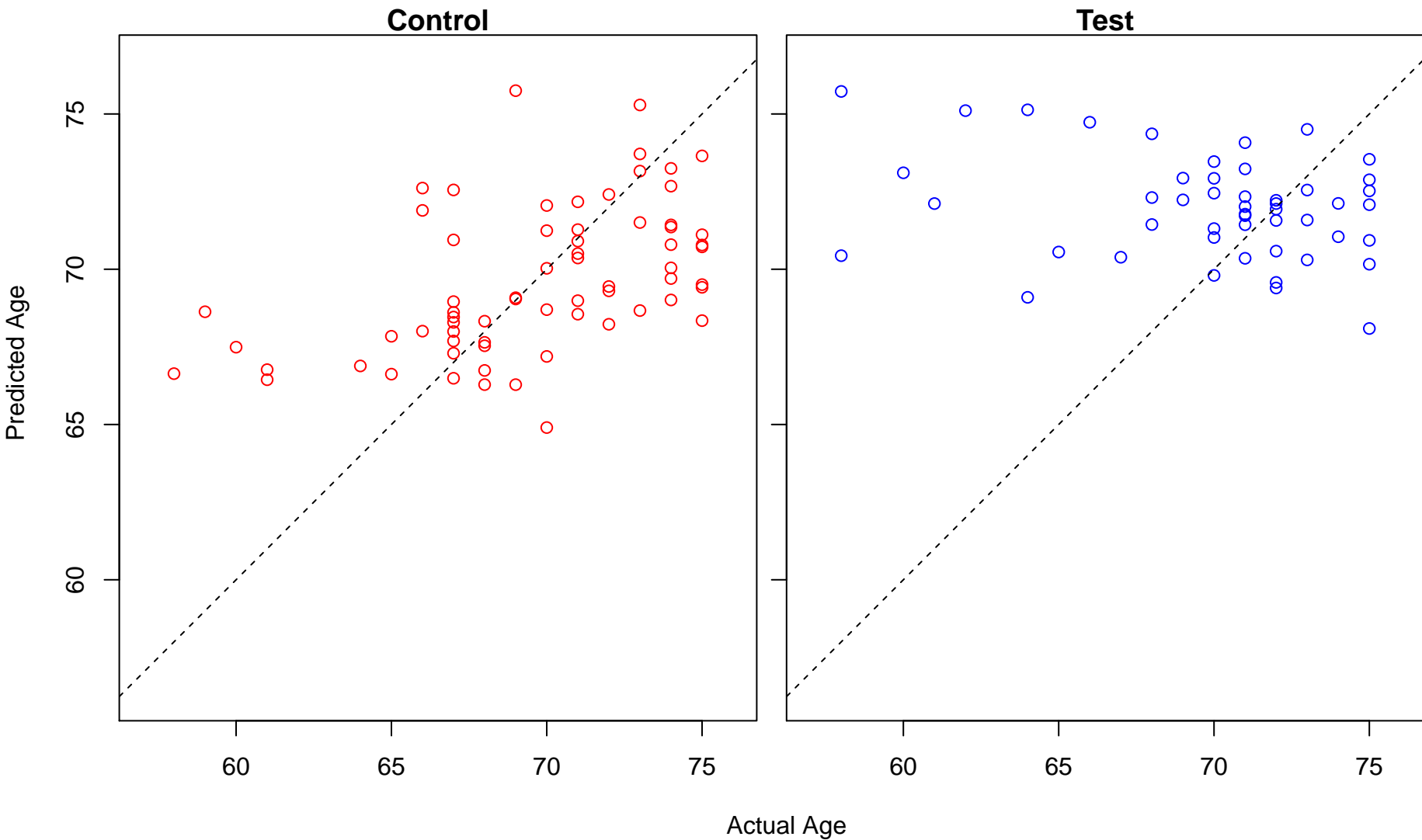
multicellular organismal response to stress (Score: 0.777029)



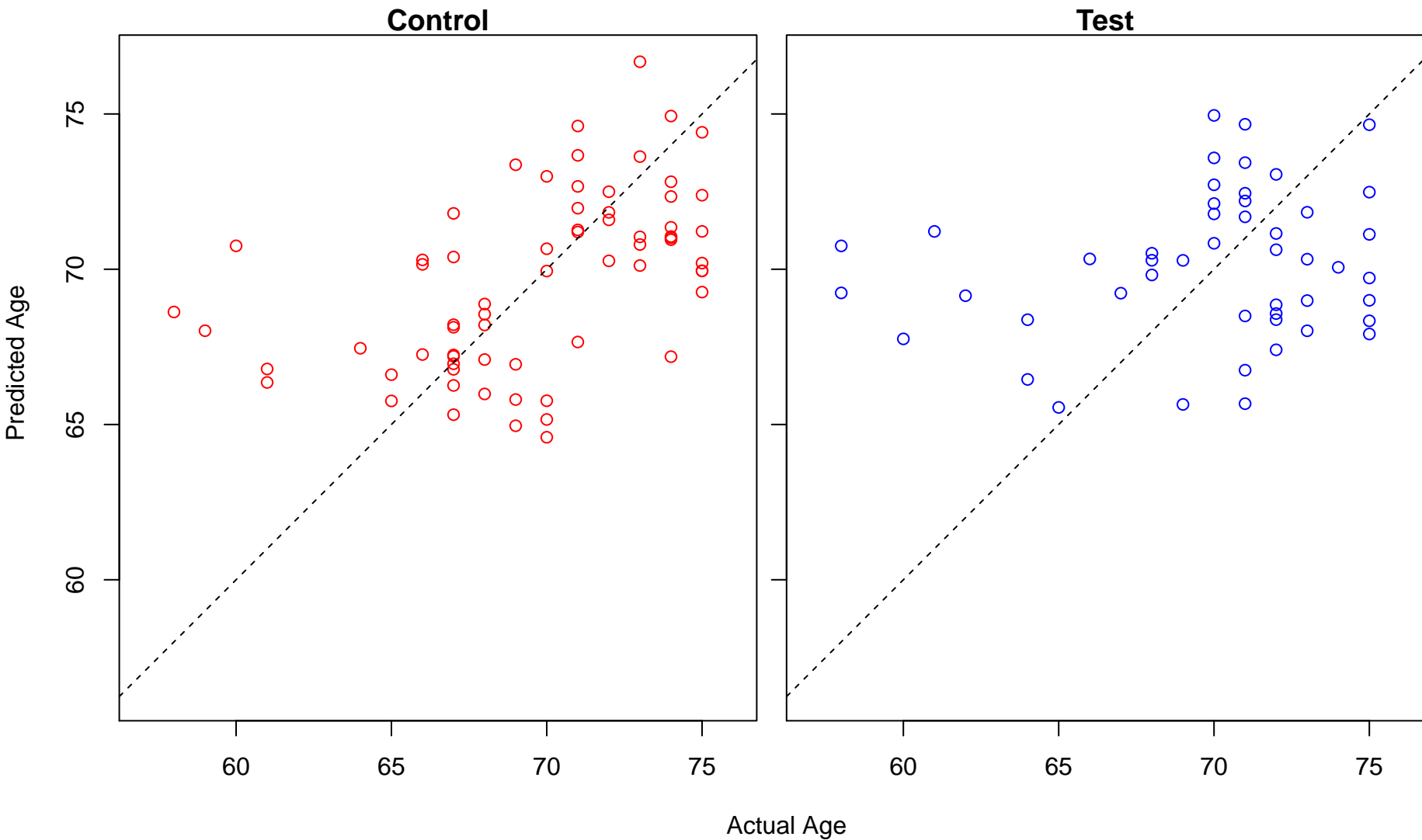
positive regulation of nitric-oxide synthase activity (Score: 0.776945)



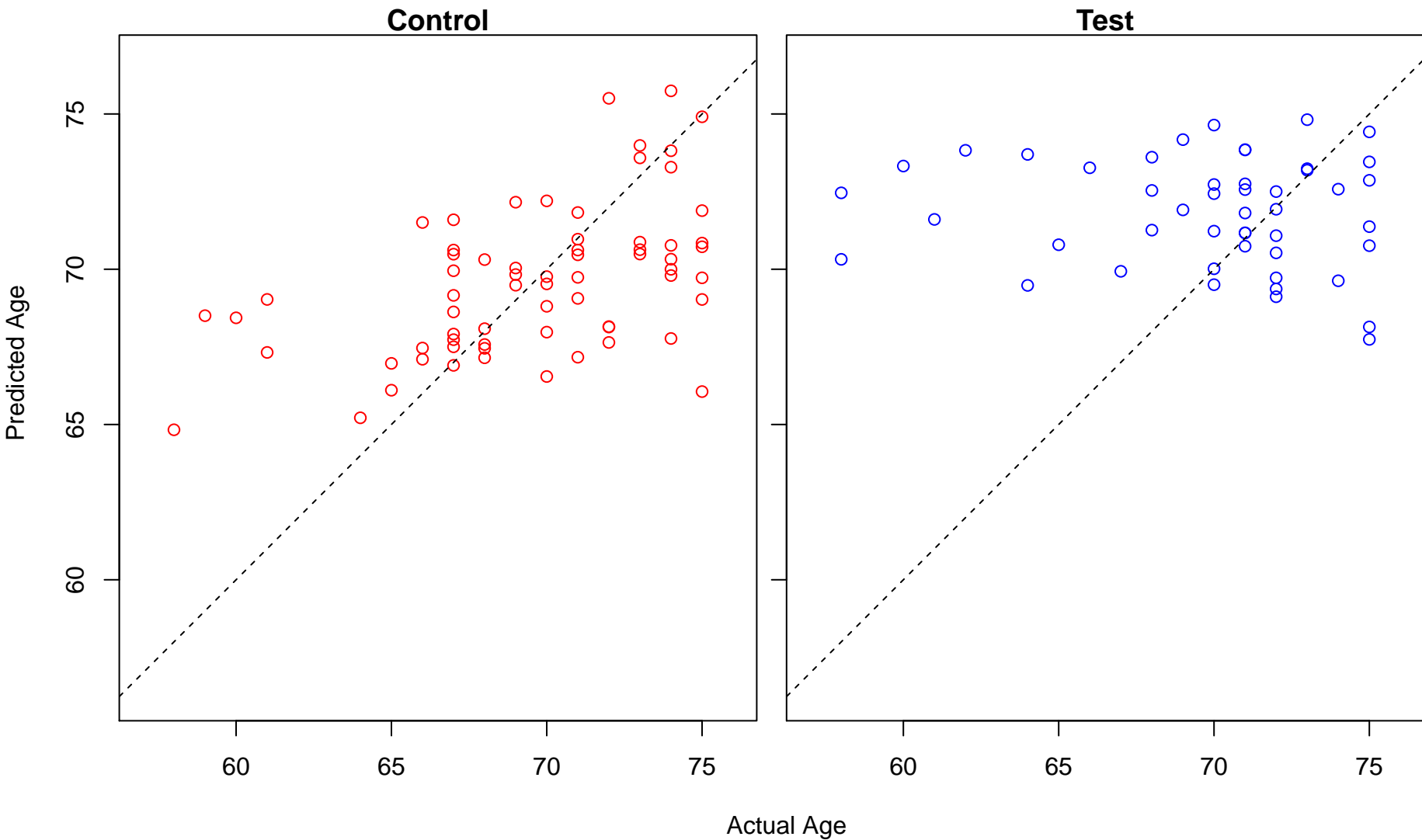
anterograde axonal transport (Score: 0.776531)



regulation of coagulation (Score: 0.776132)

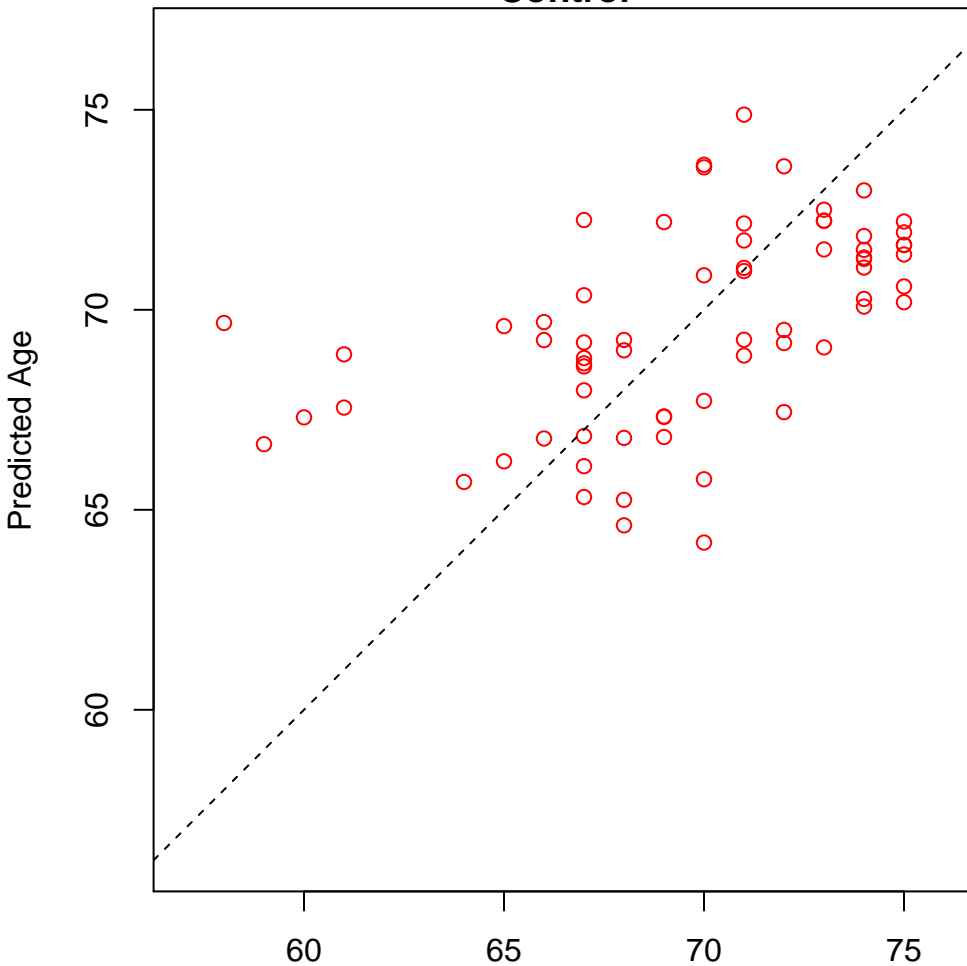


cholesterol transport (Score: 0.776128)

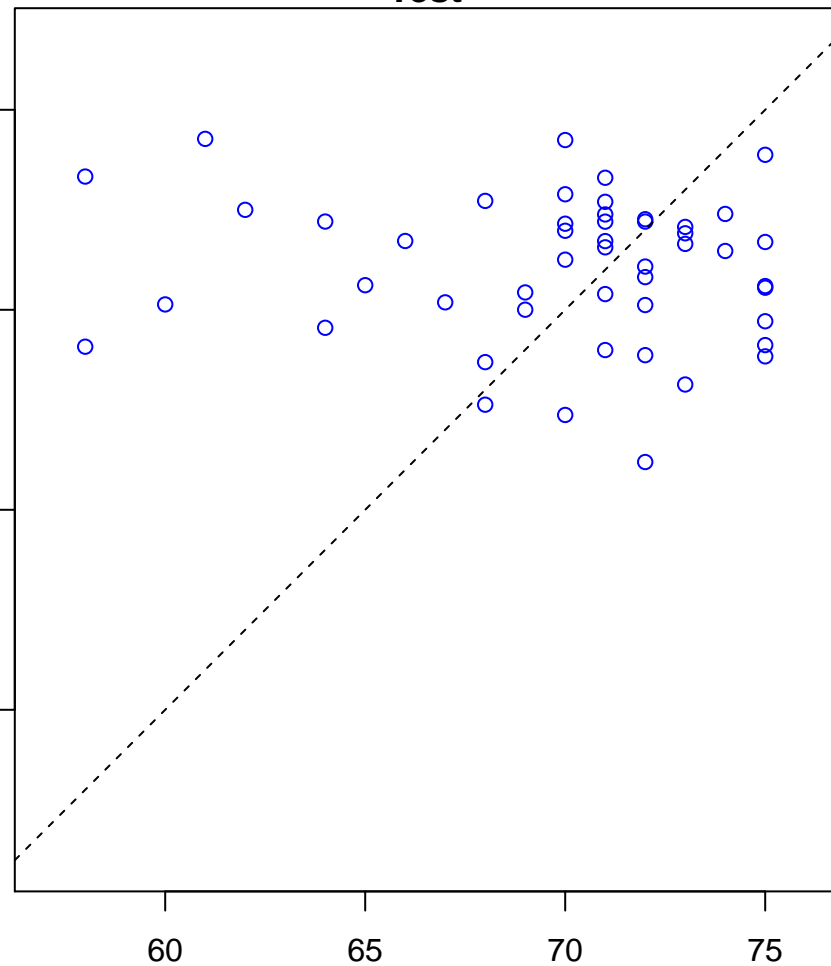


mucopolysaccharide metabolic process (Score: 0.775827)

Control



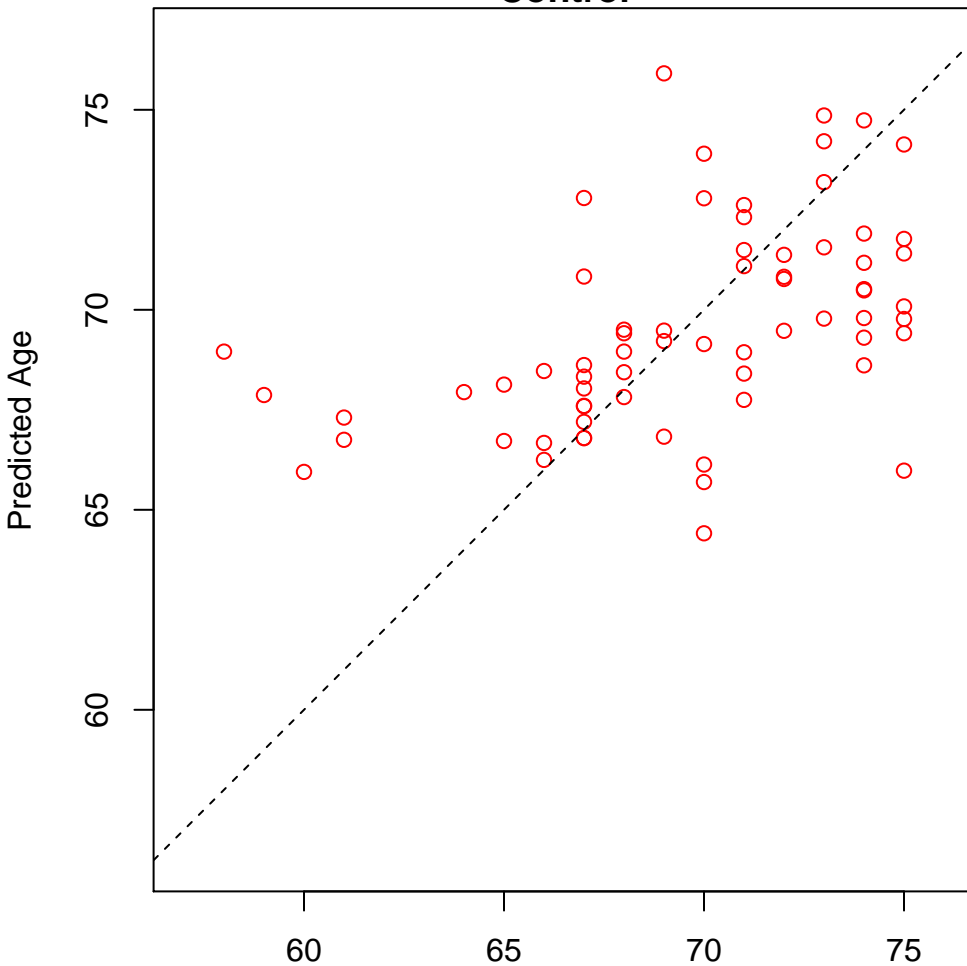
Test



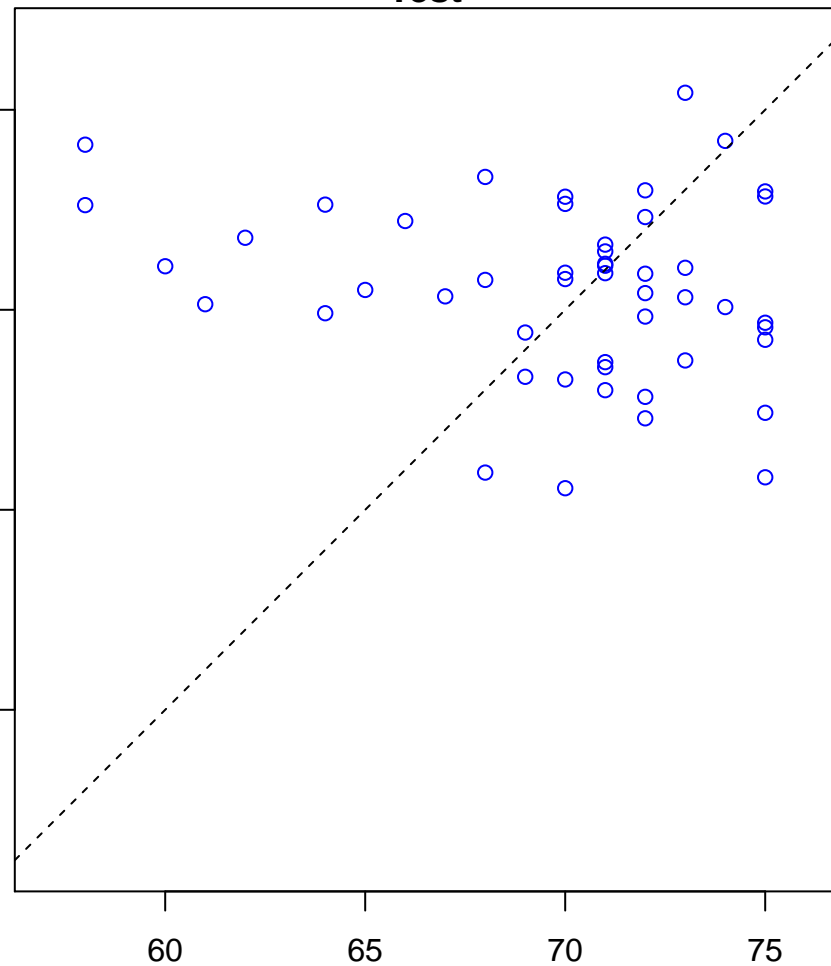
Actual Age

sodium ion transmembrane transport (Score: 0.775435)

Control

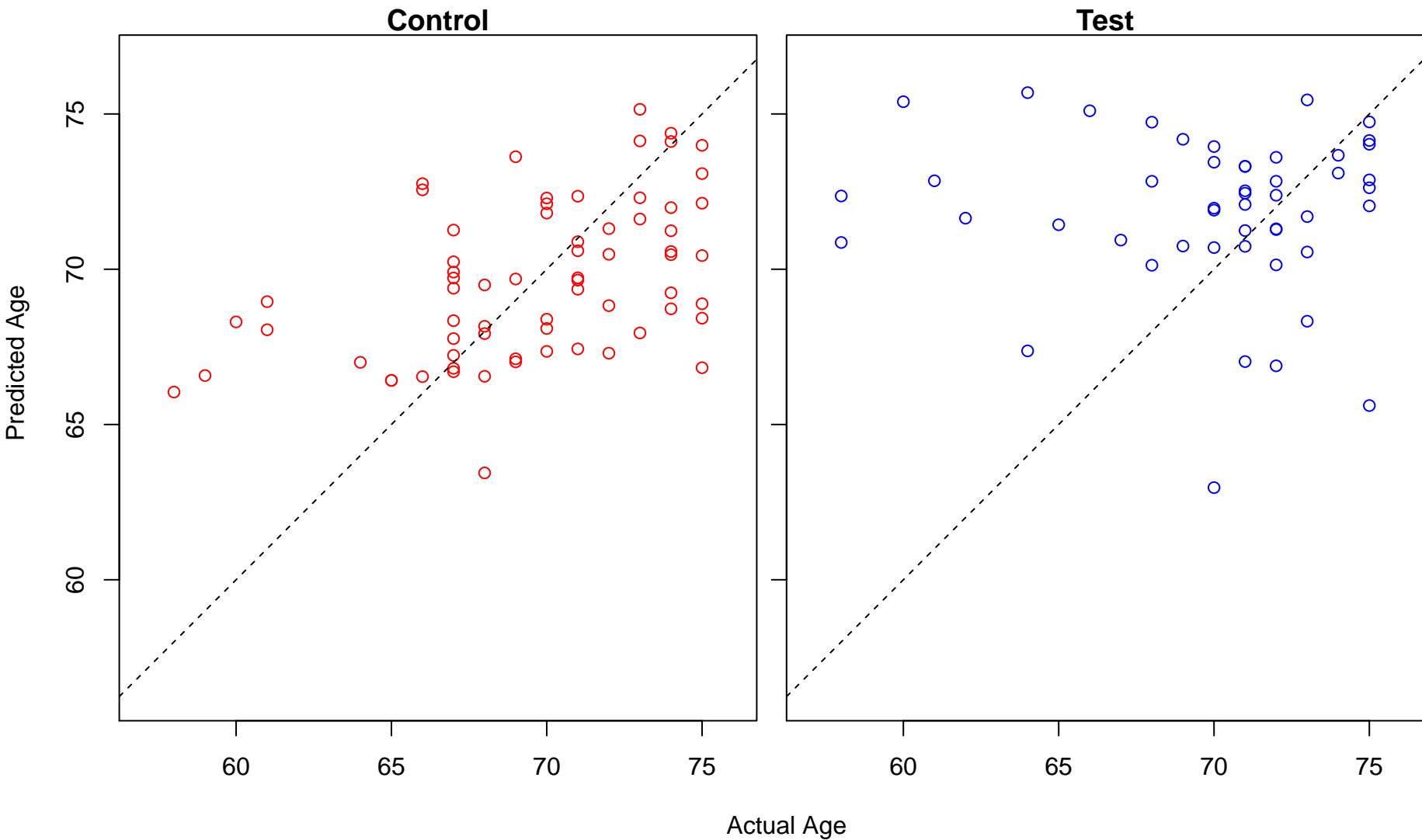


Test

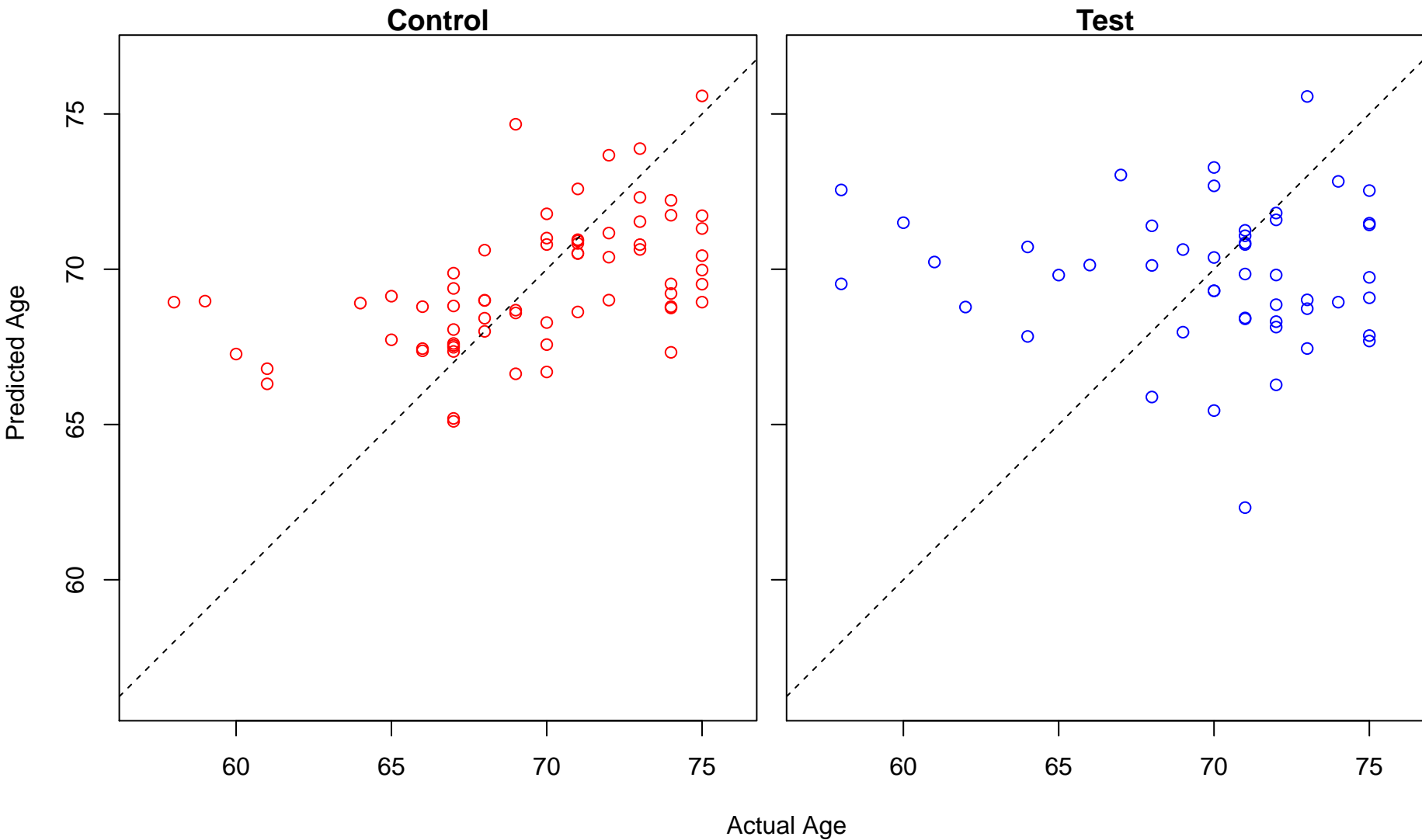


Actual Age

positive regulation of glycogen biosynthetic process (Score: 0.775237)

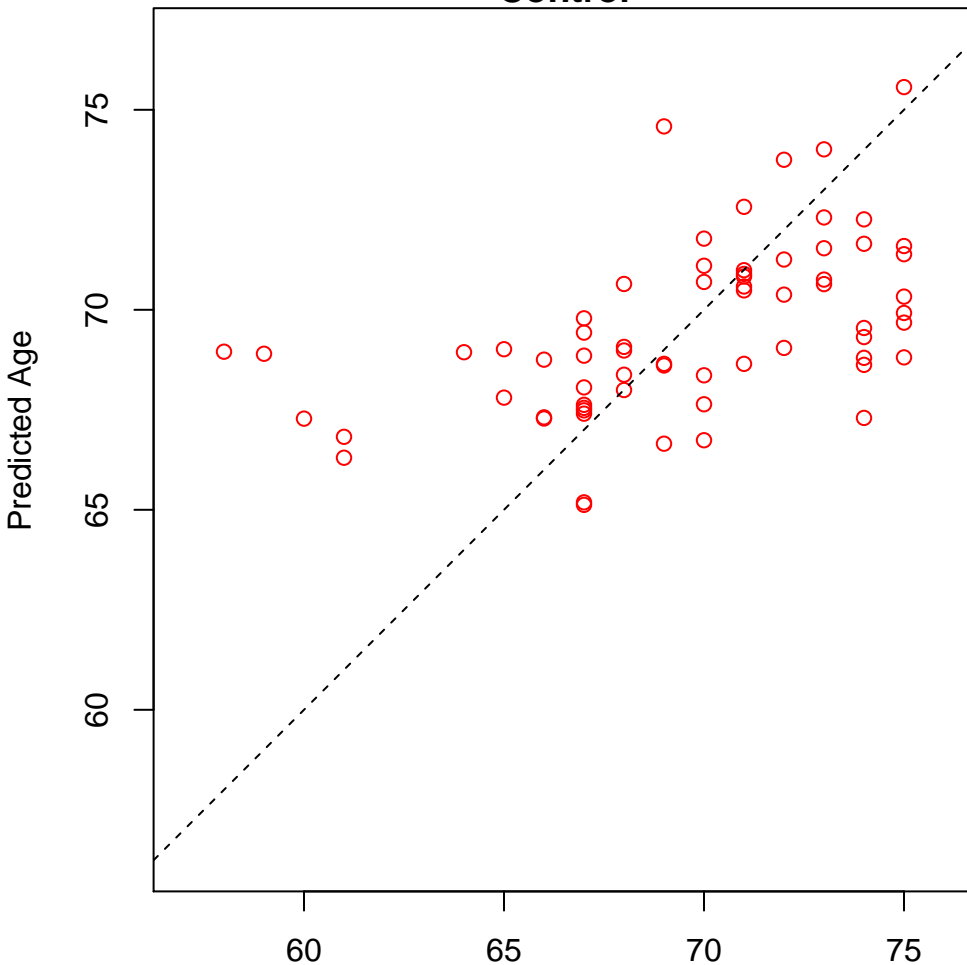


startle response (Score: 0.774620)

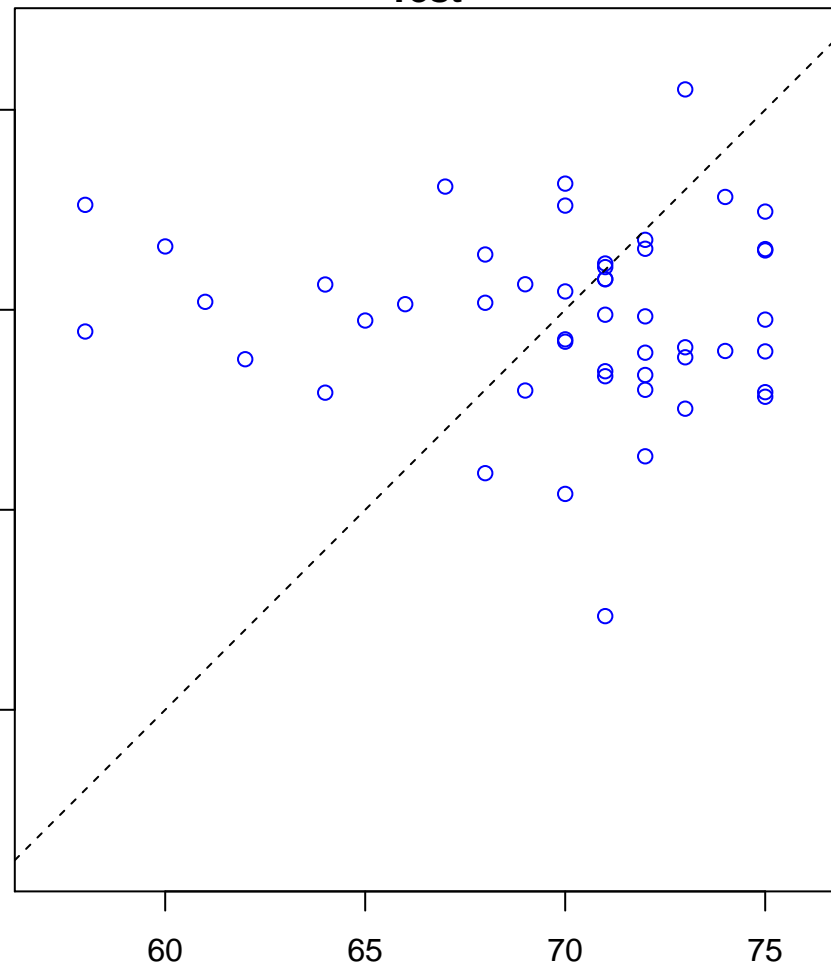


postsynaptic density organization (Score: 0.774608)

Control

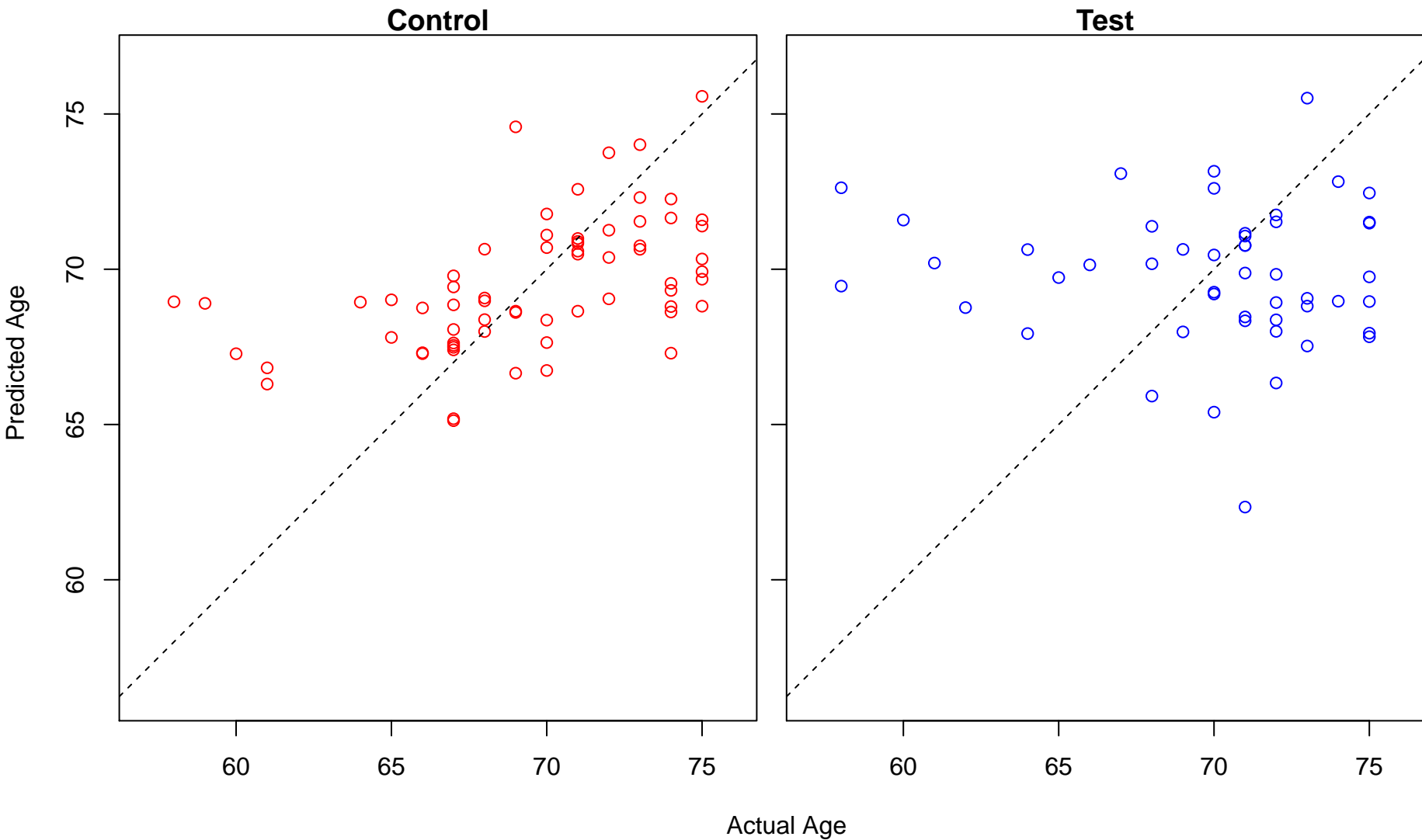


Test

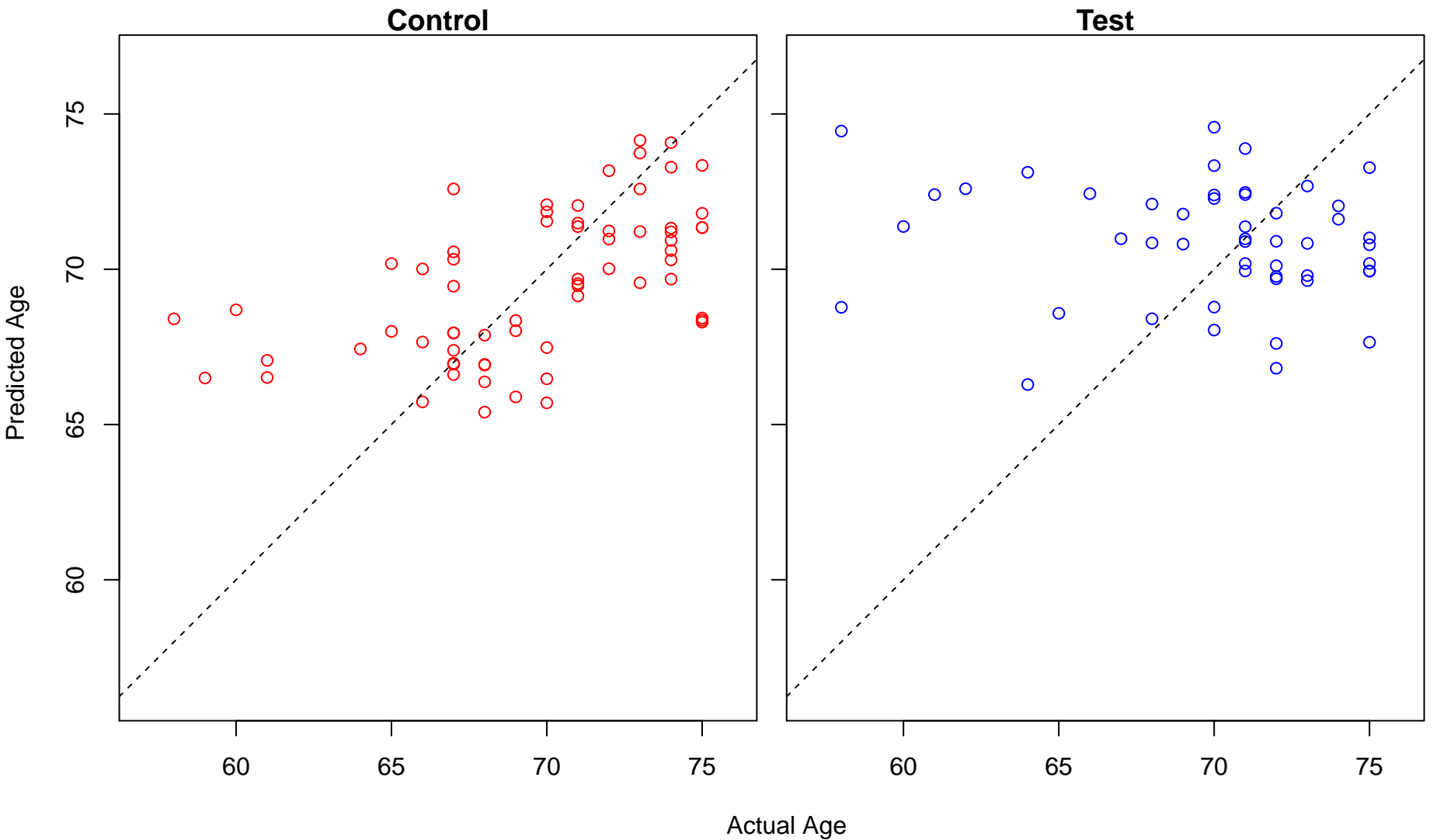


Actual Age

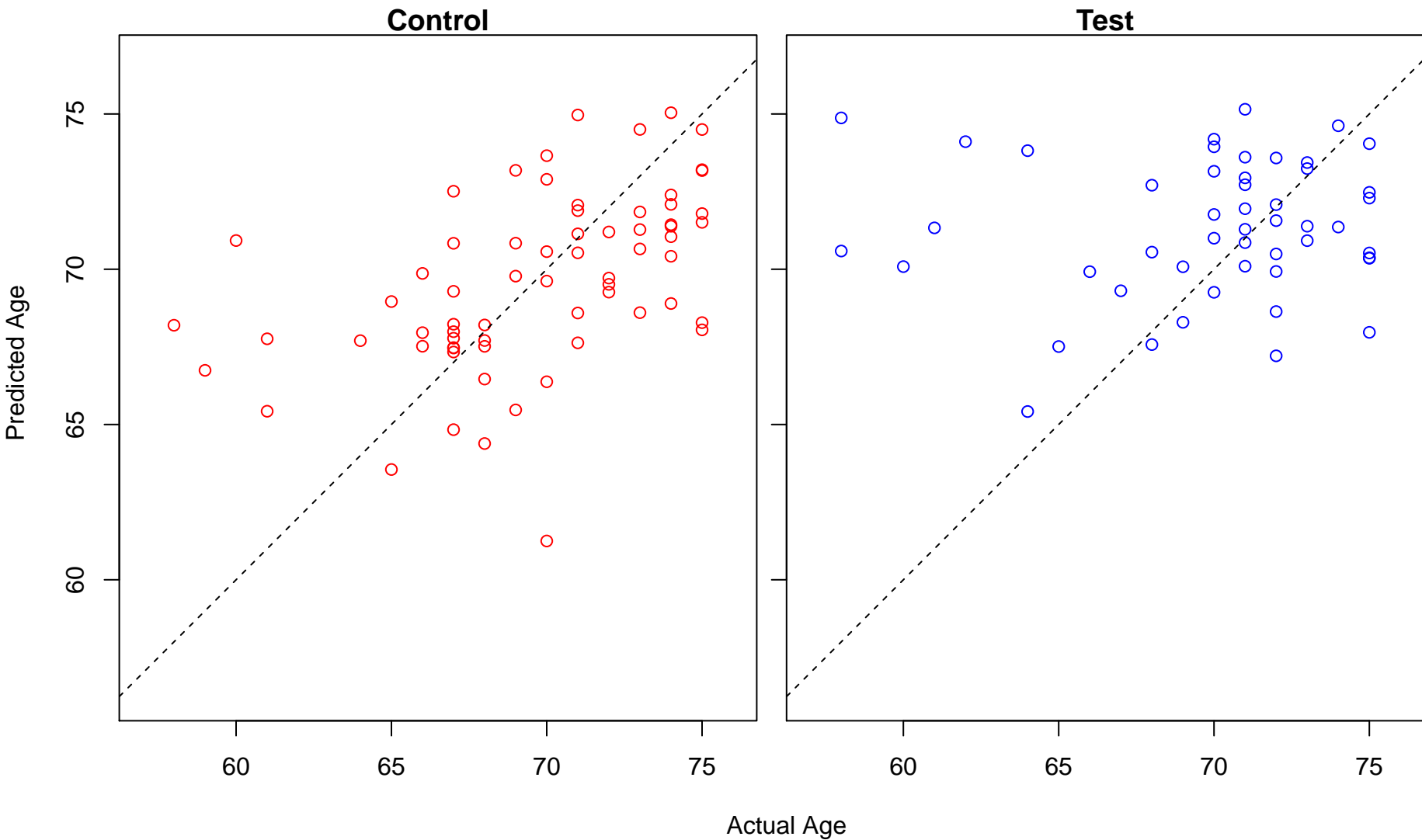
postsynaptic density assembly (Score: 0.774608)



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

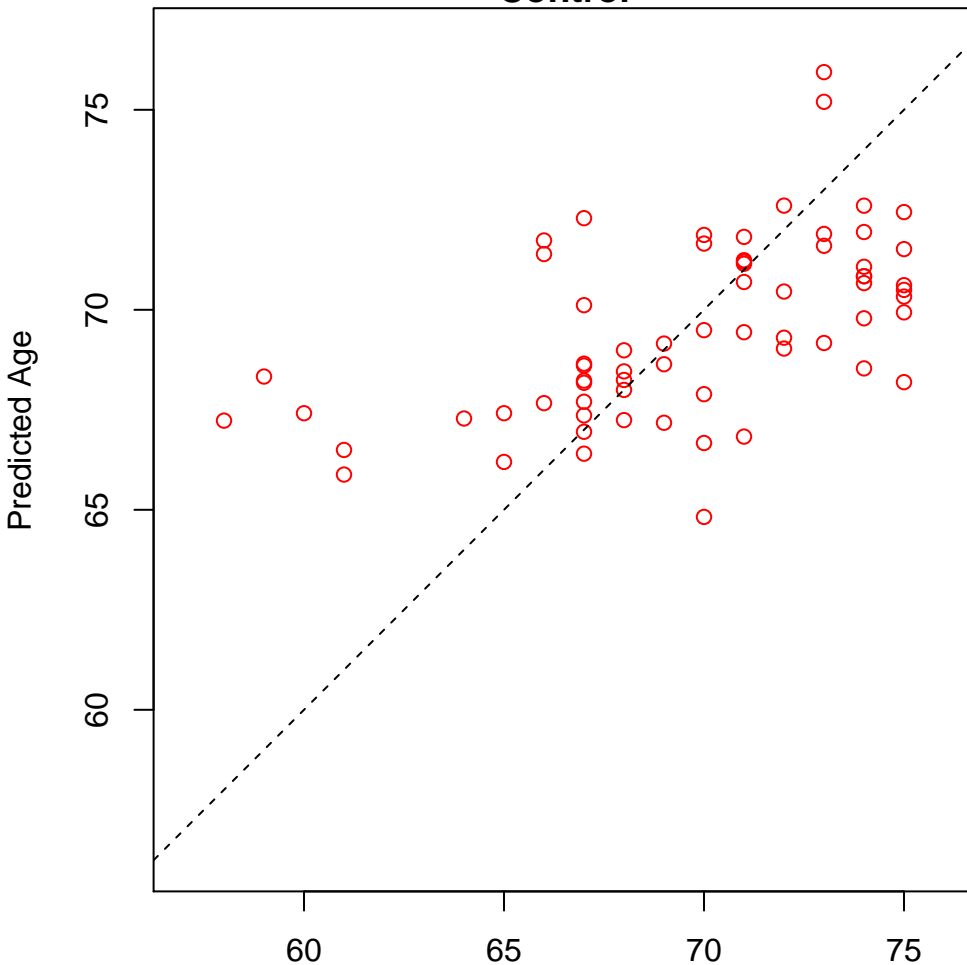


negative regulation of protein acetylation (Score: 0.774267)

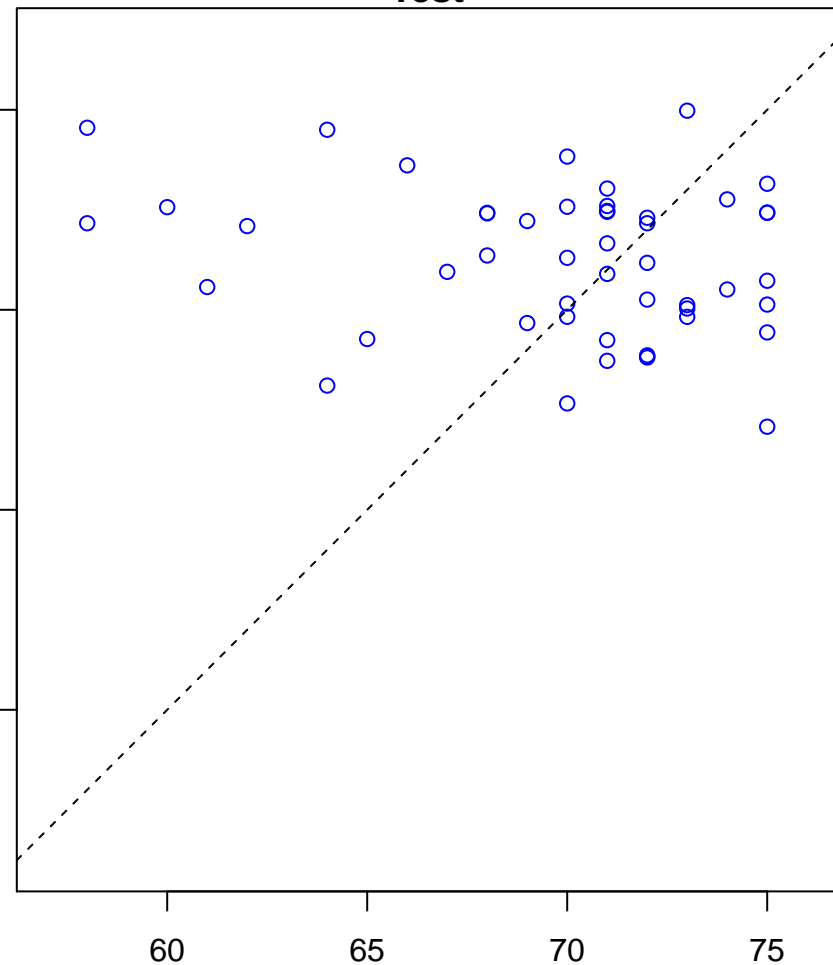


vesicle transport along microtubule (Score: 0.773934)

Control

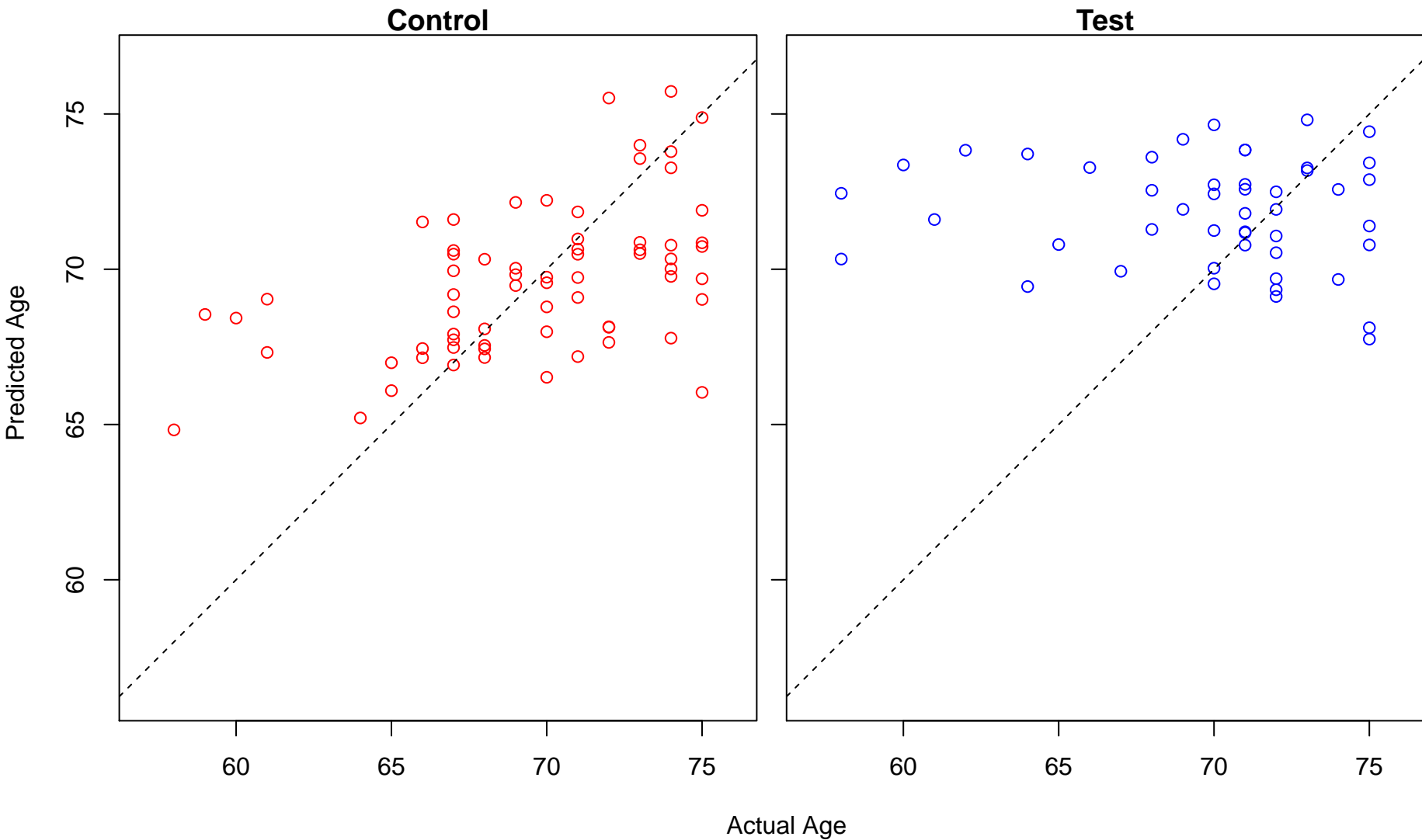


Test

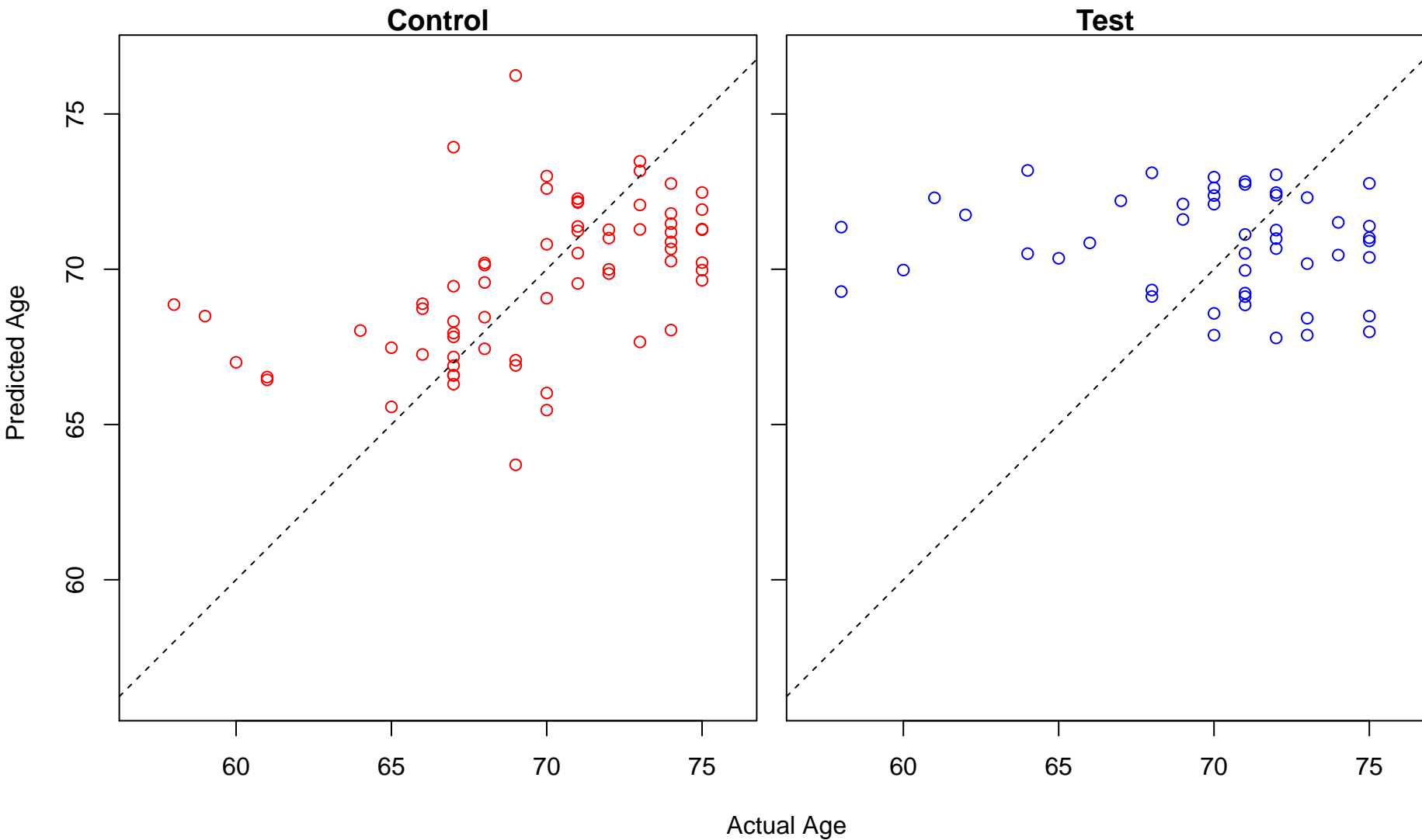


Actual Age

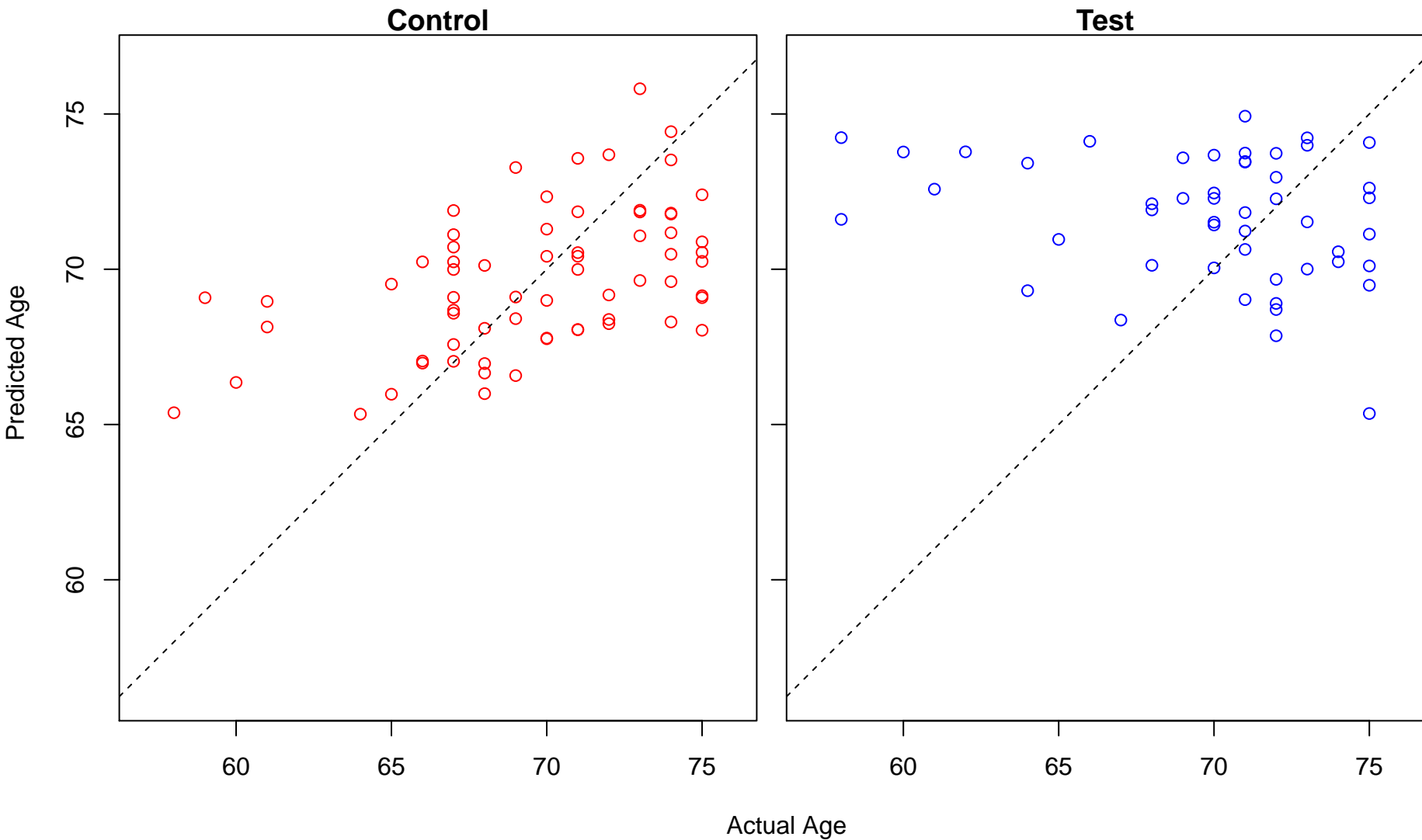
sterol transport (Score: 0.773858)



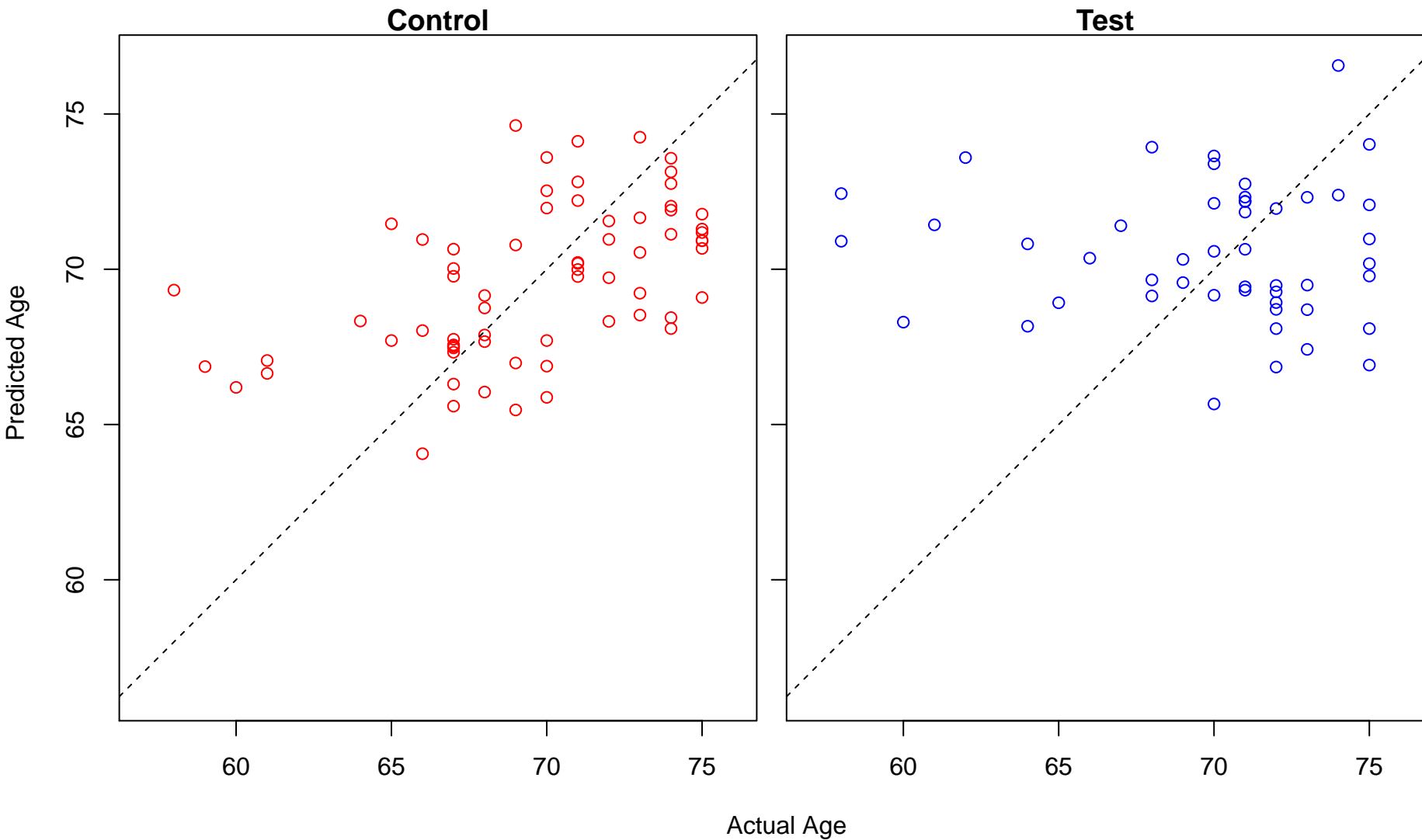
terpenoid metabolic process (Score: 0.773448)



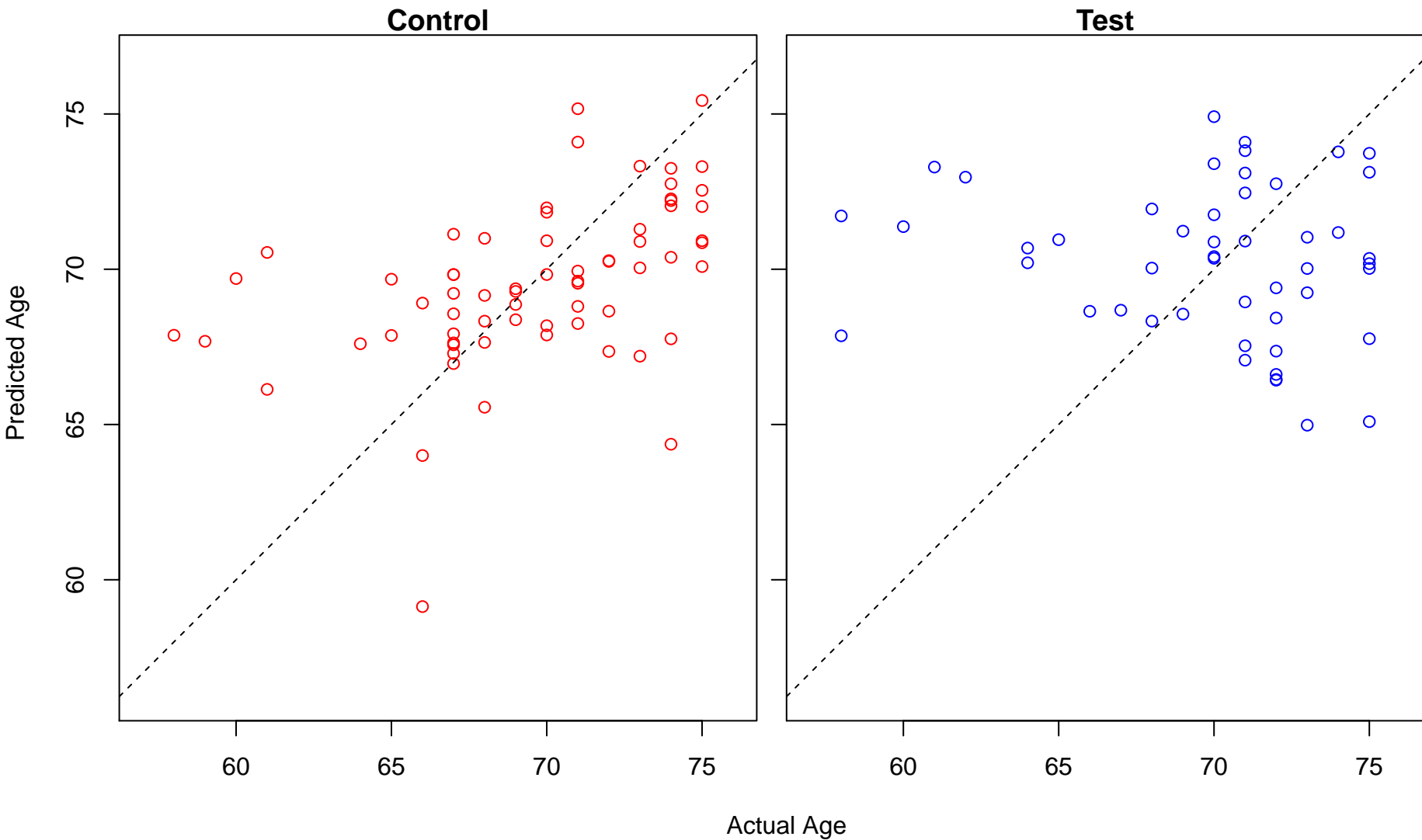
pericardium development (Score: 0.773346)



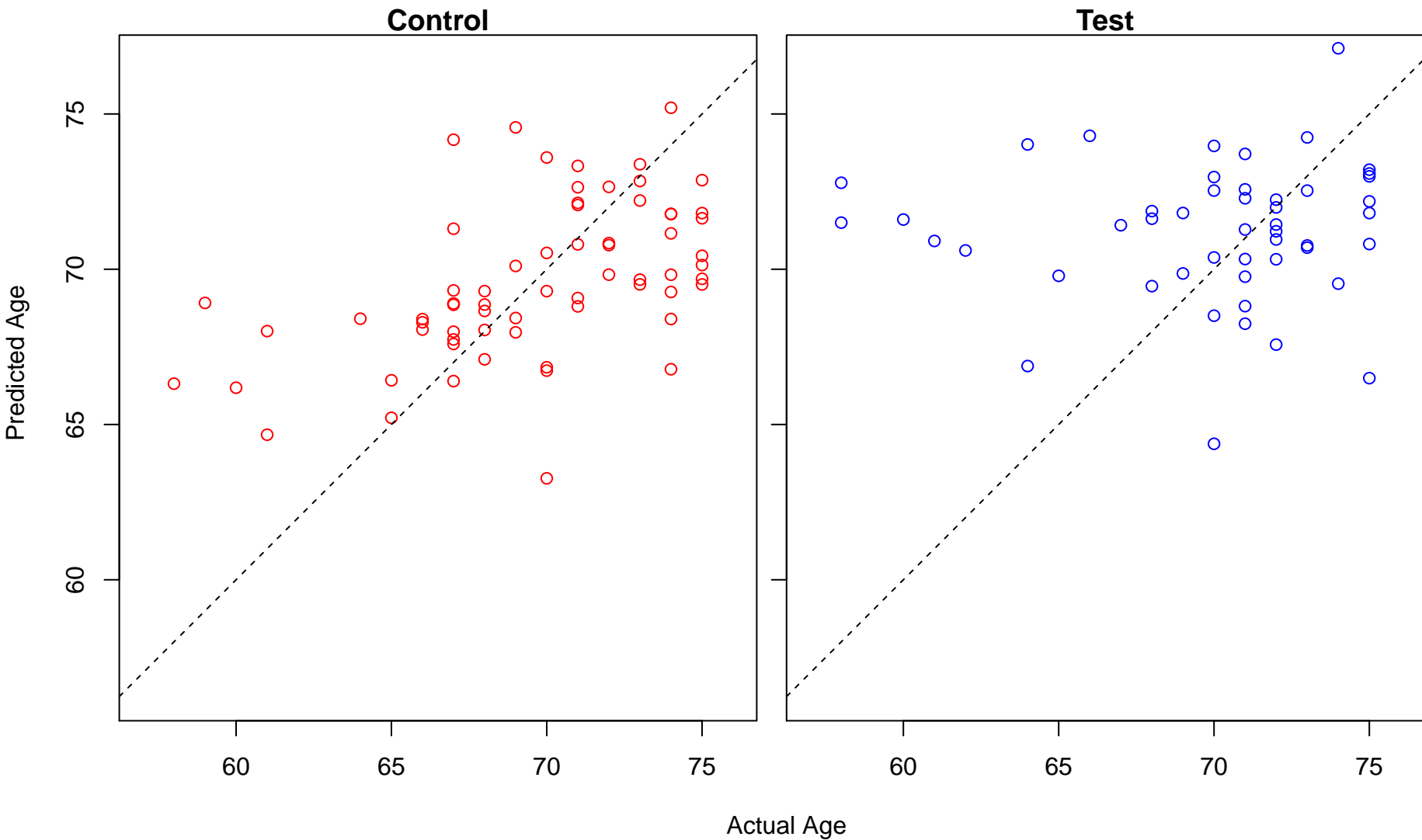
regulation of T cell tolerance induction (Score: 0.772646)



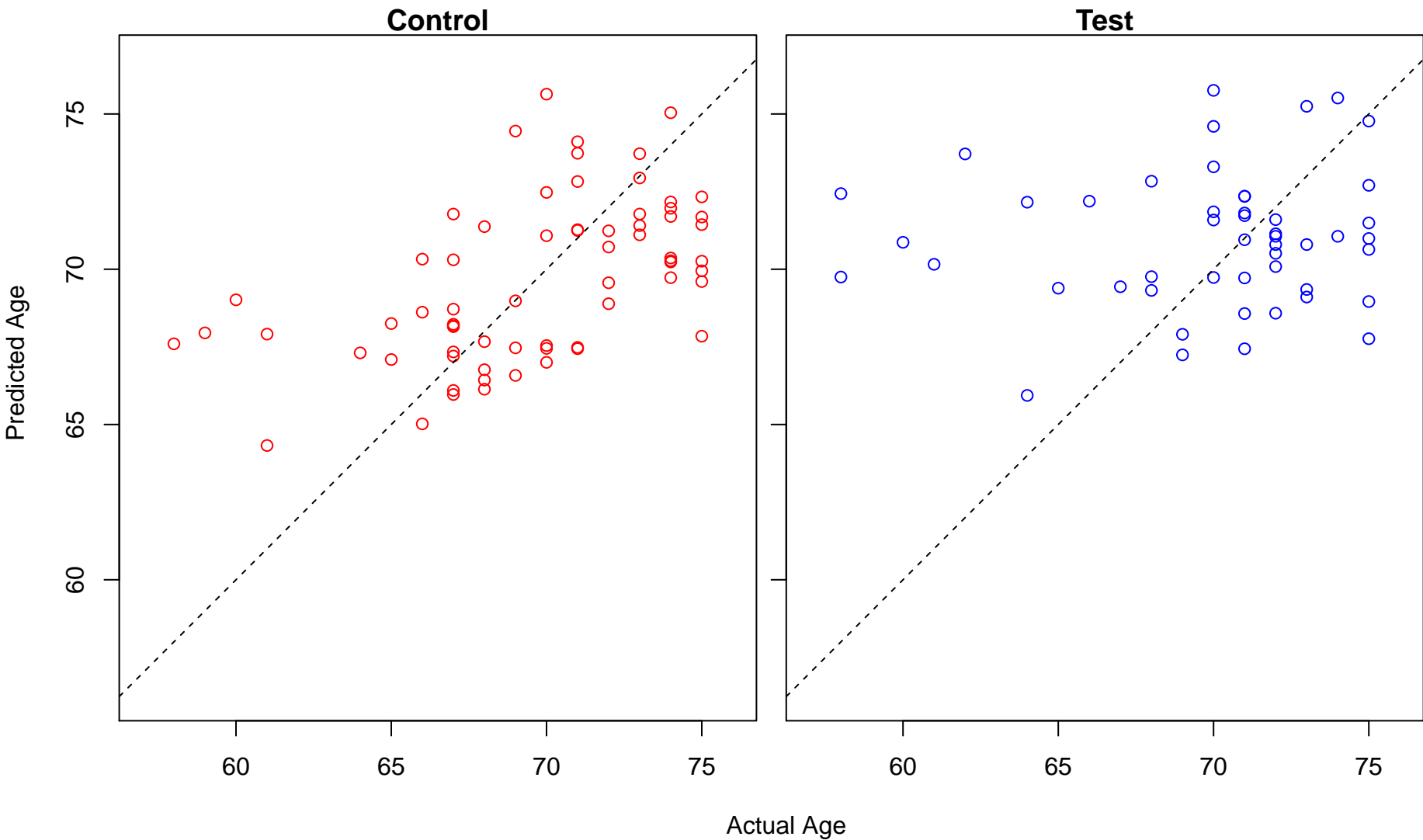
regulation of insulin-like growth factor receptor signaling pathway (Score: 0.772492)



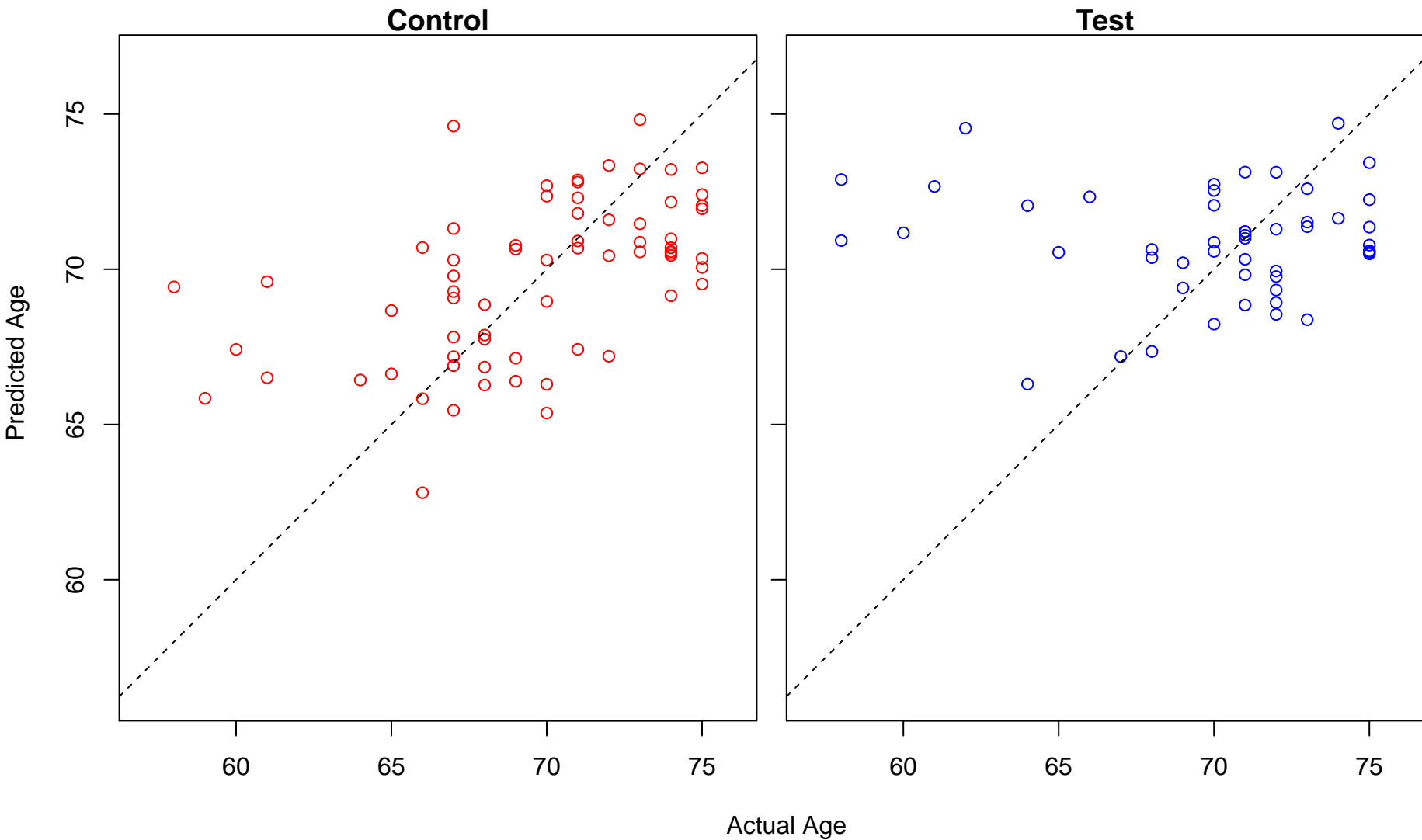
pigment cell differentiation (Score: 0.772297)



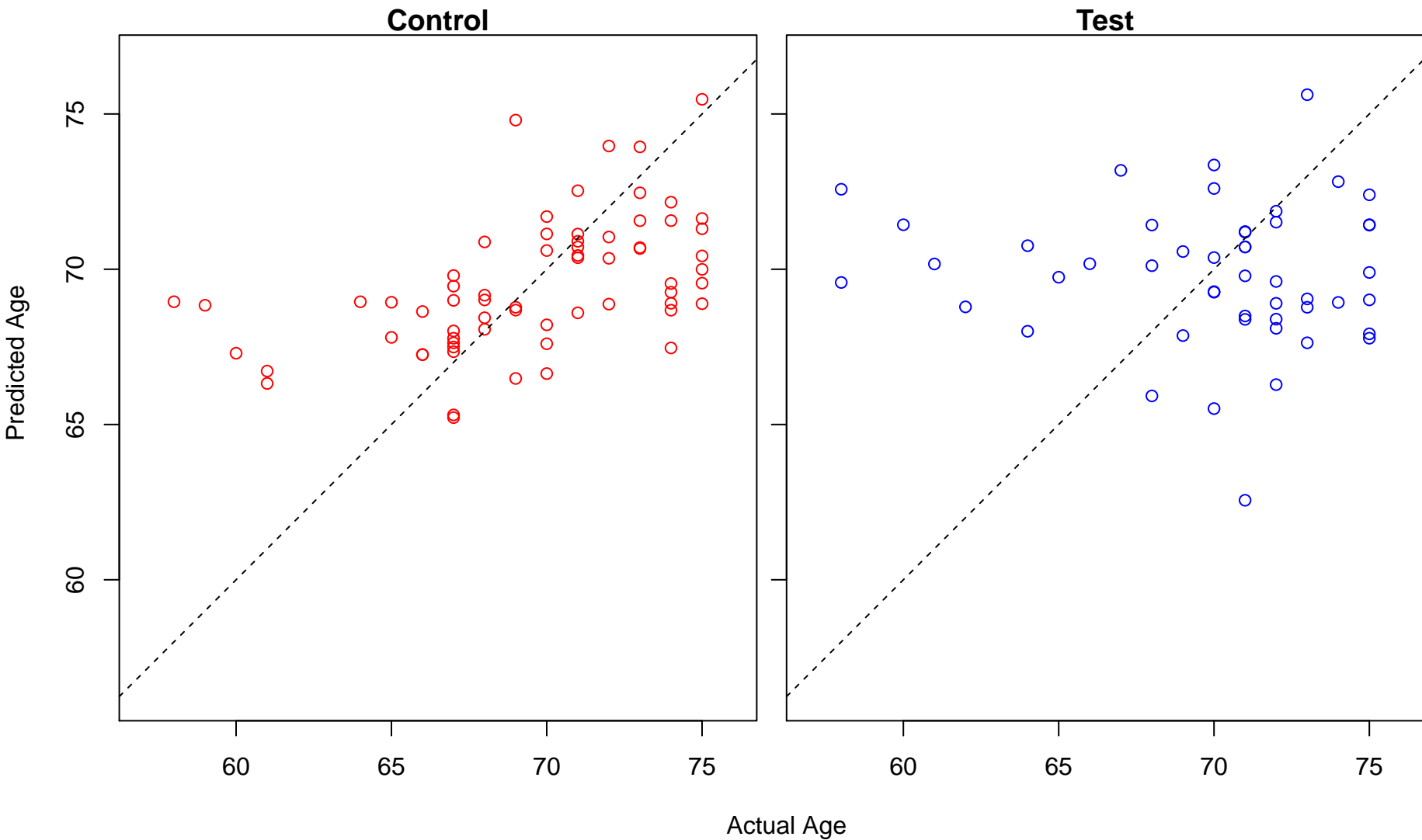
negative regulation of vascular endothelial growth factor receptor signaling pathway (Score: 0.7718)



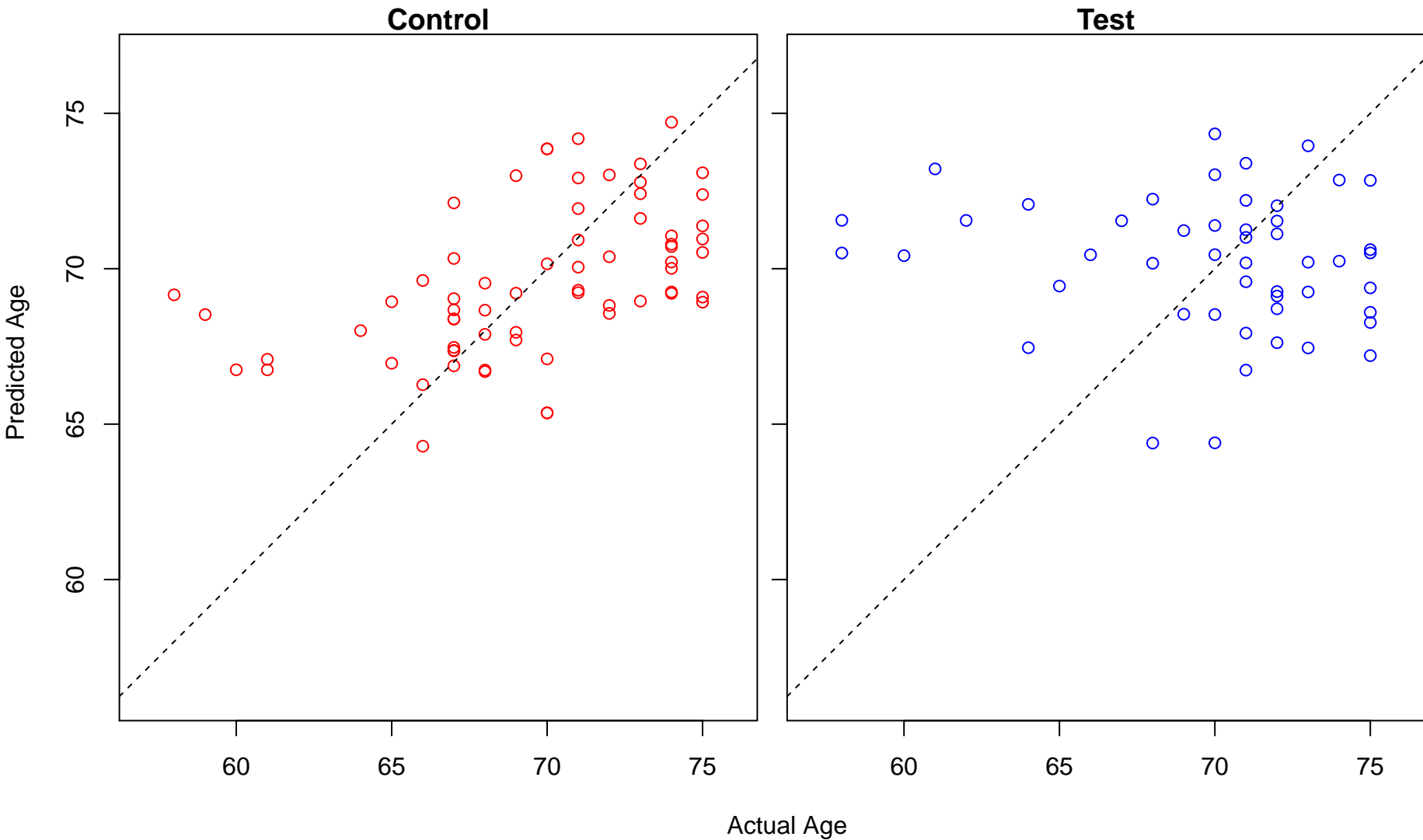
drug metabolic process (Score: 0.771755)



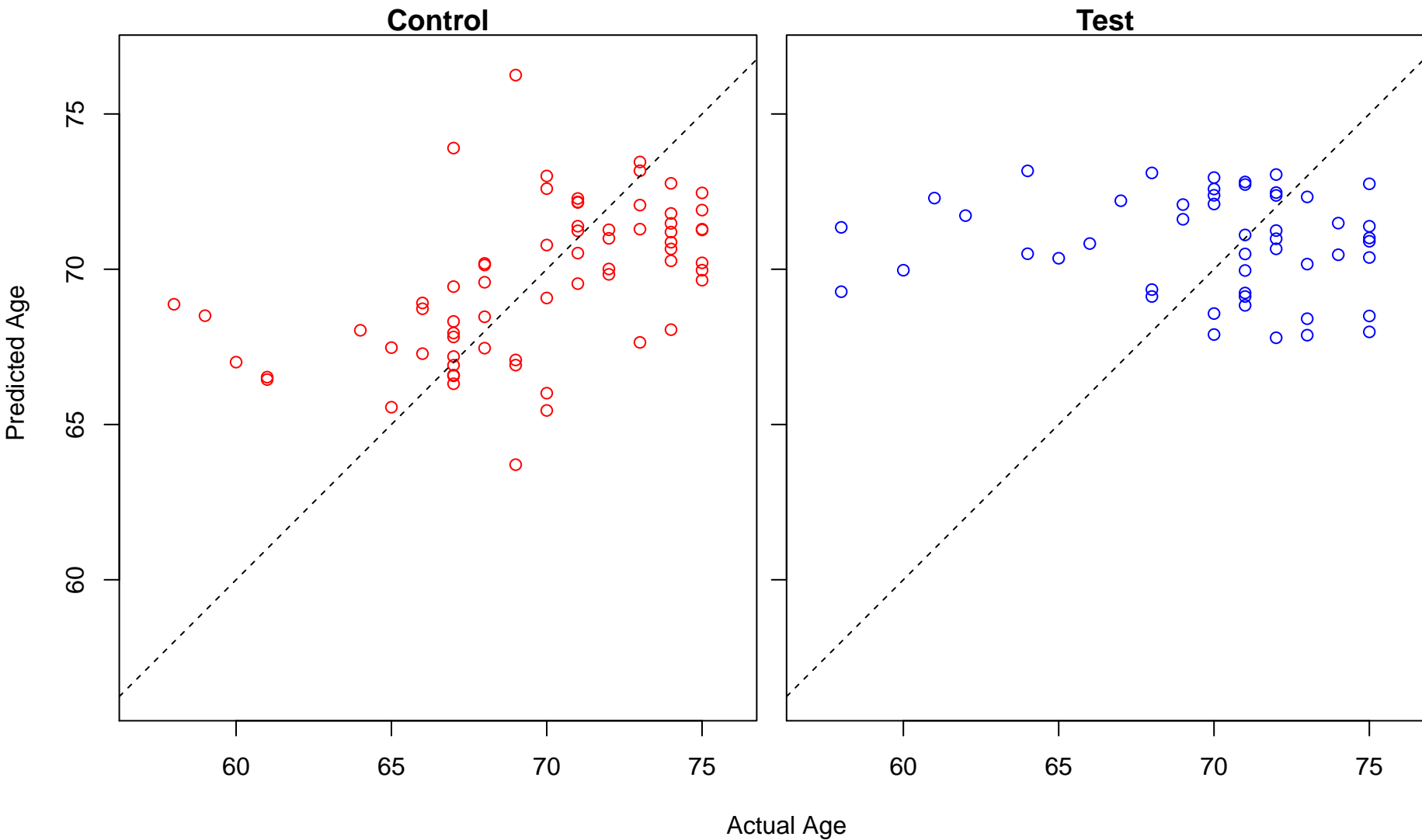
negative regulation of cell size (Score: 0.771602)



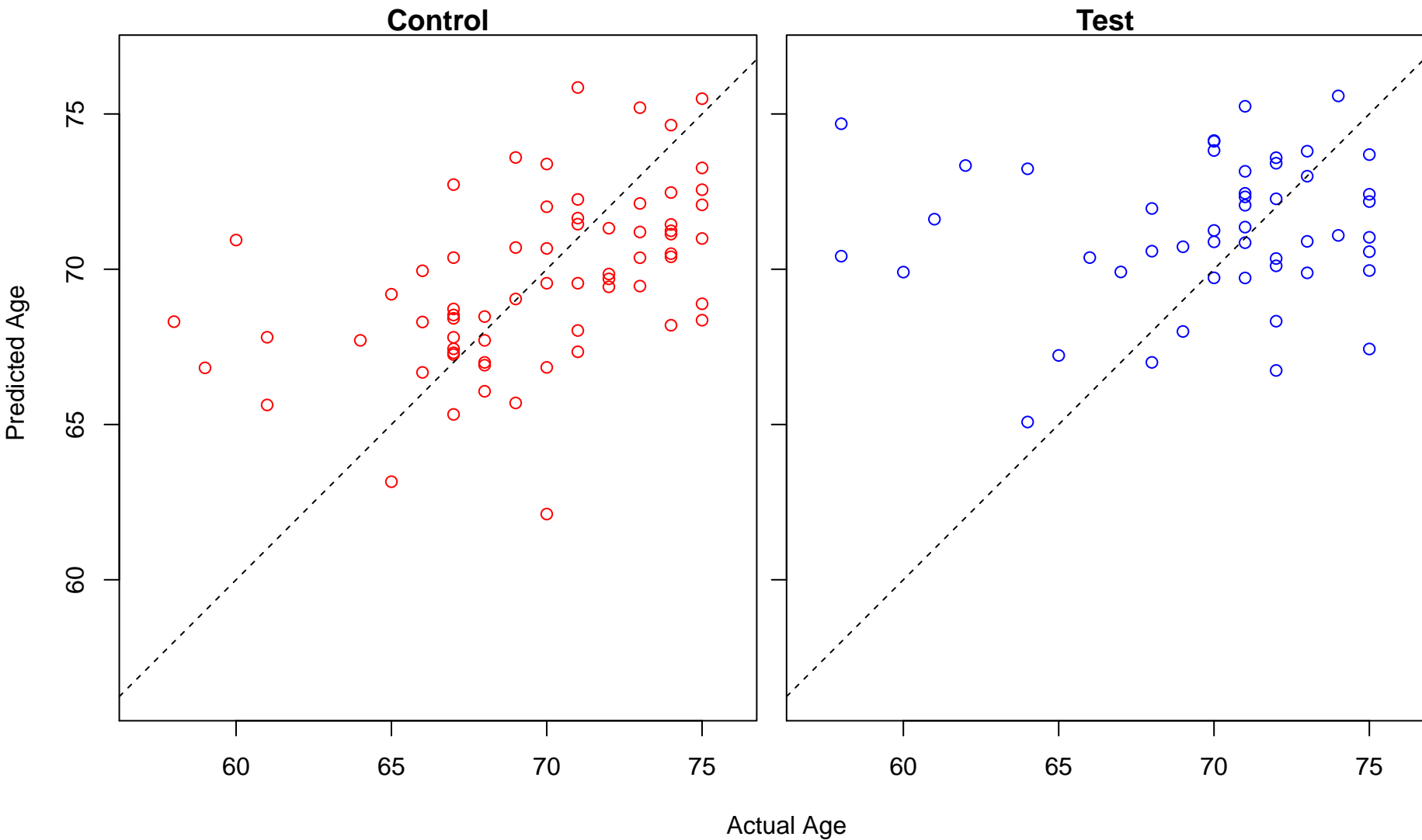
protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score: 0.771252)



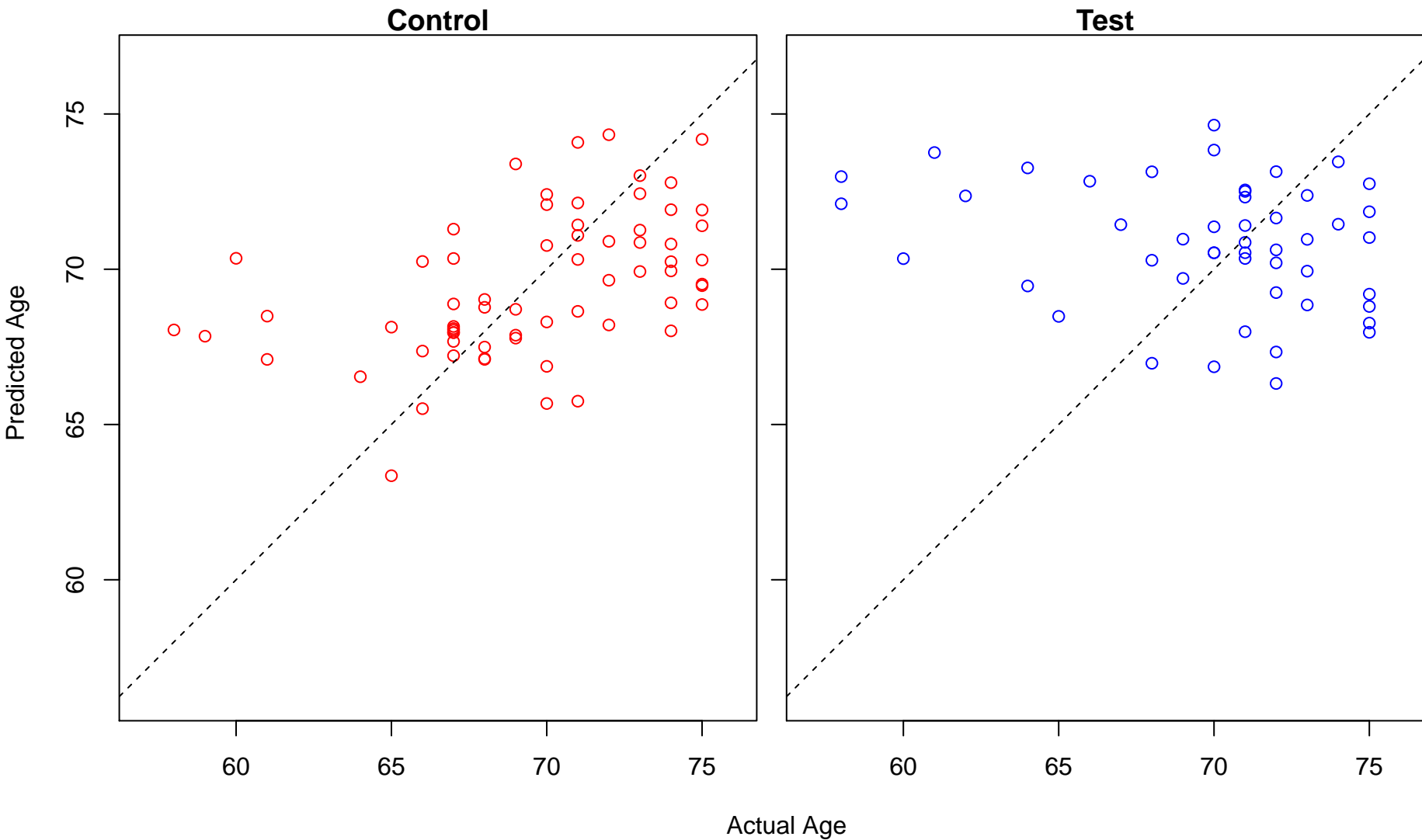
diterpenoid metabolic process (Score: 0.771150)



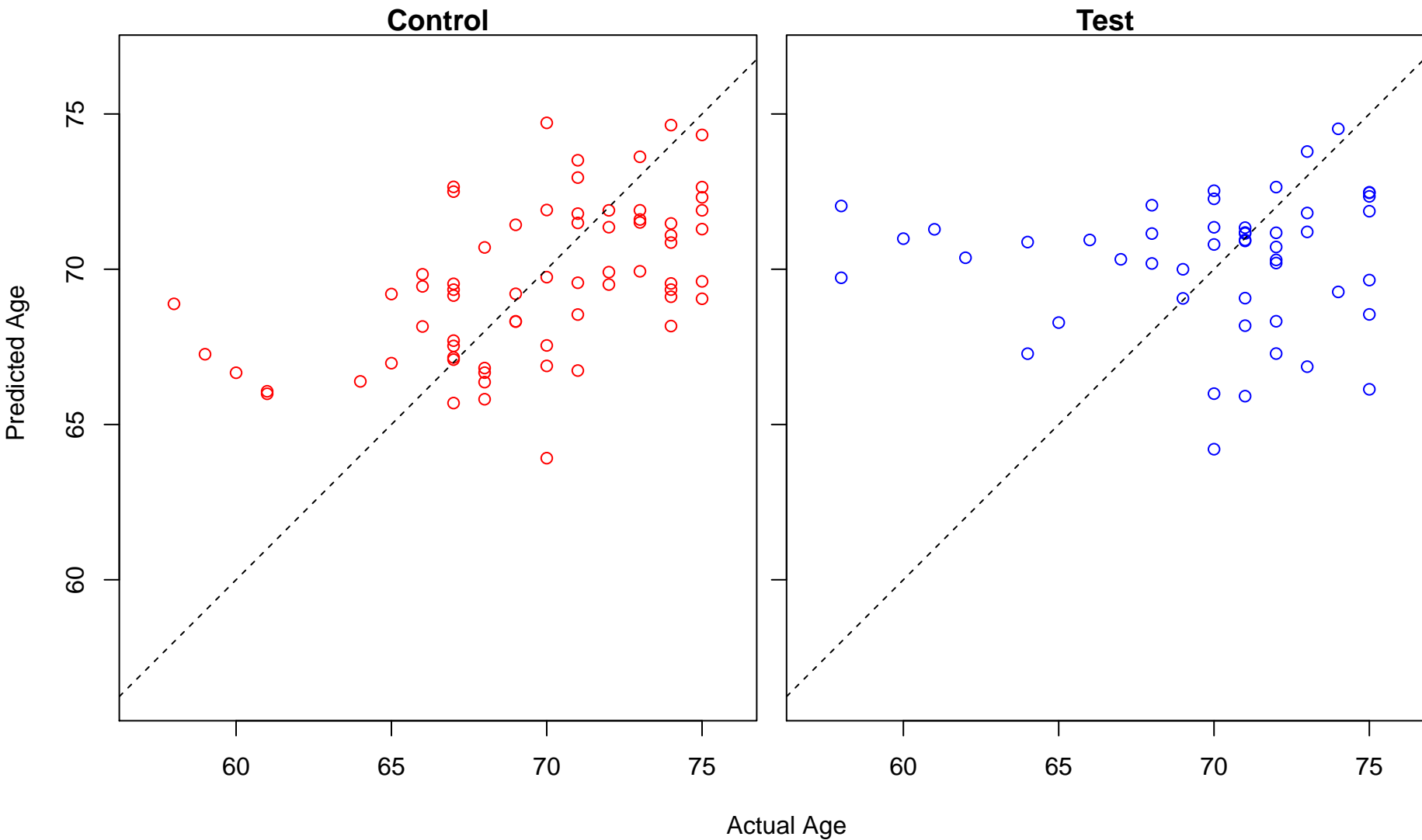
negative regulation of peptidyl-lysine acetylation (Score: 0.770328)



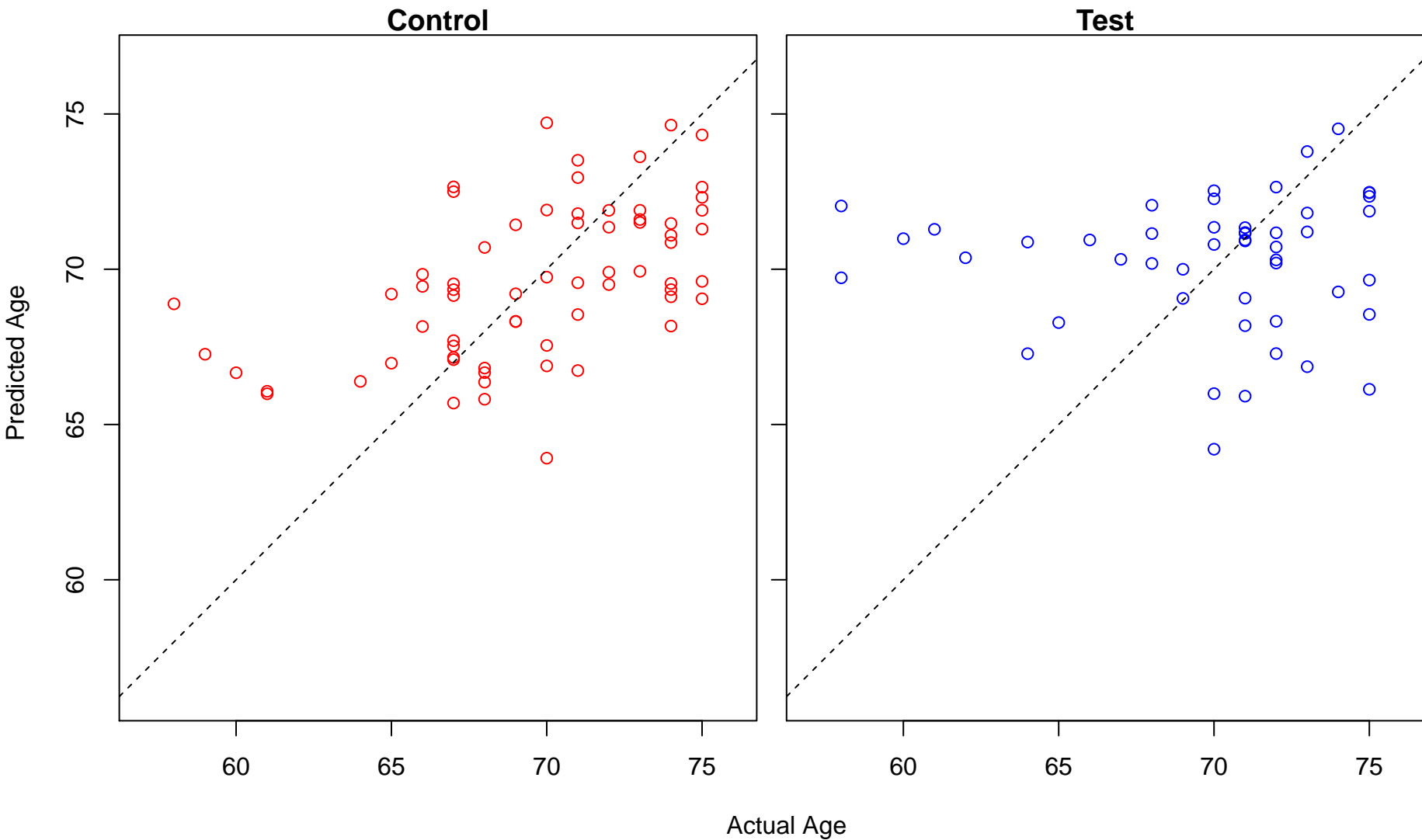
negative regulation of interleukin-6 production (Score: 0.770292)



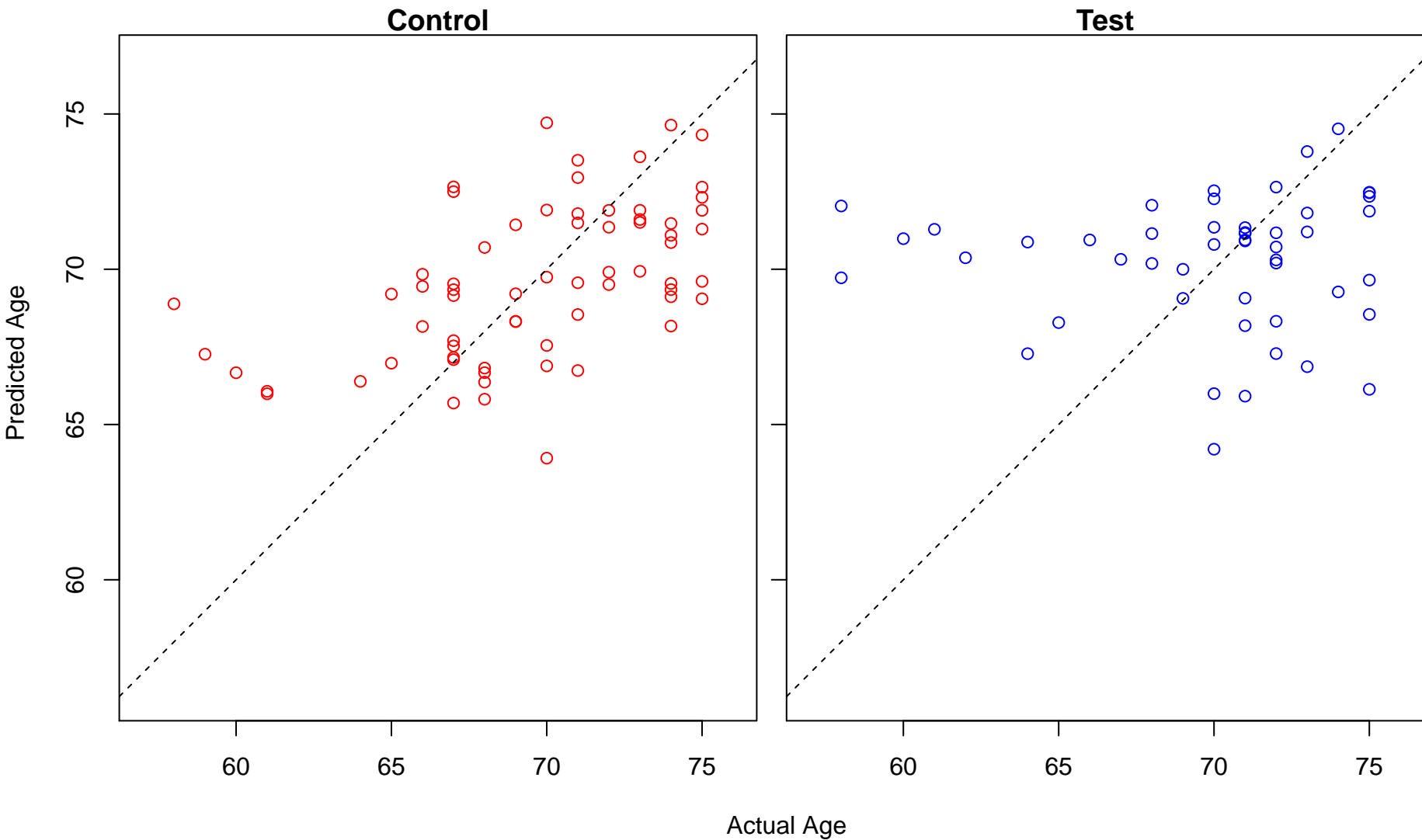
neural tube closure (Score: 0.769897)



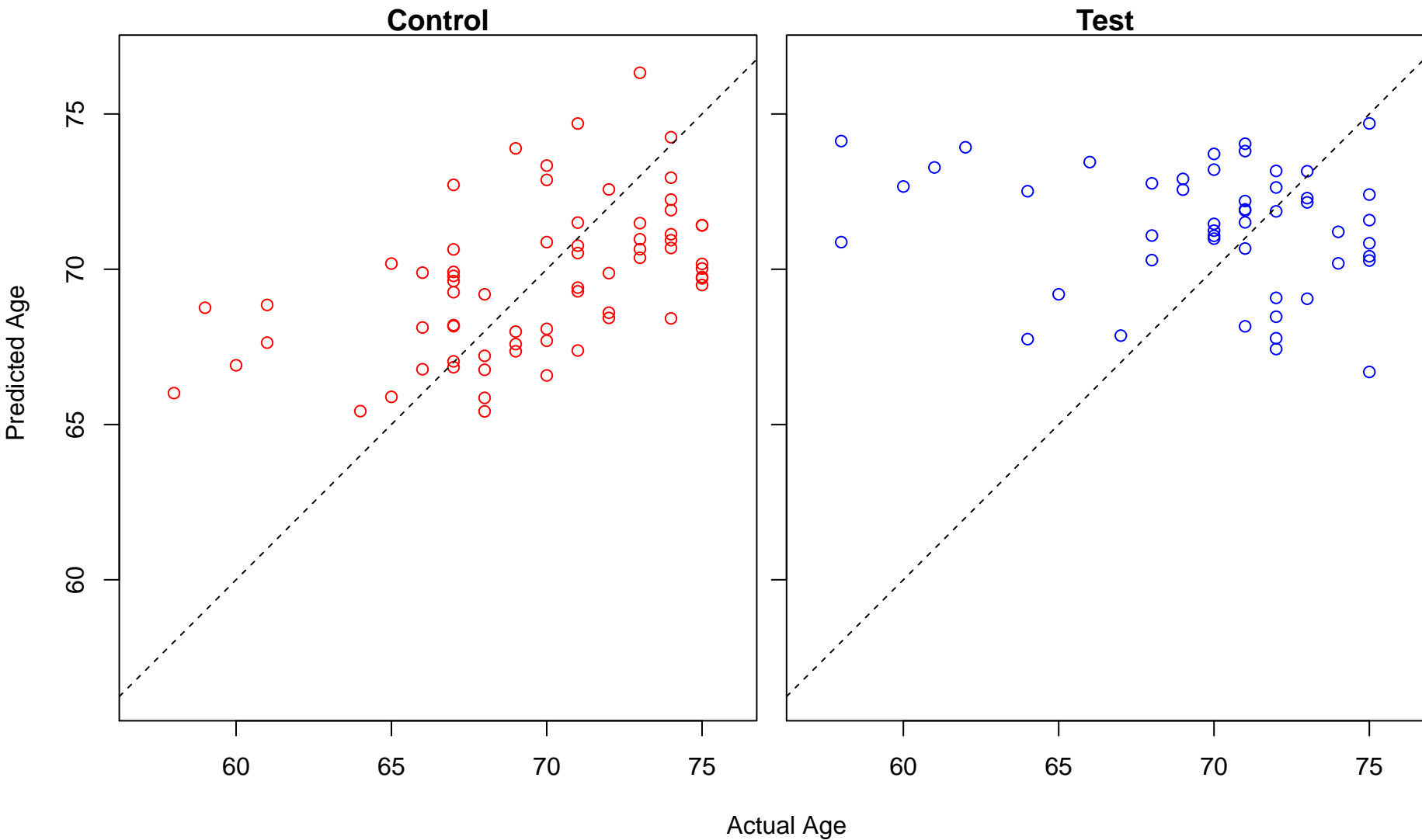
primary neural tube formation (Score: 0.769897)



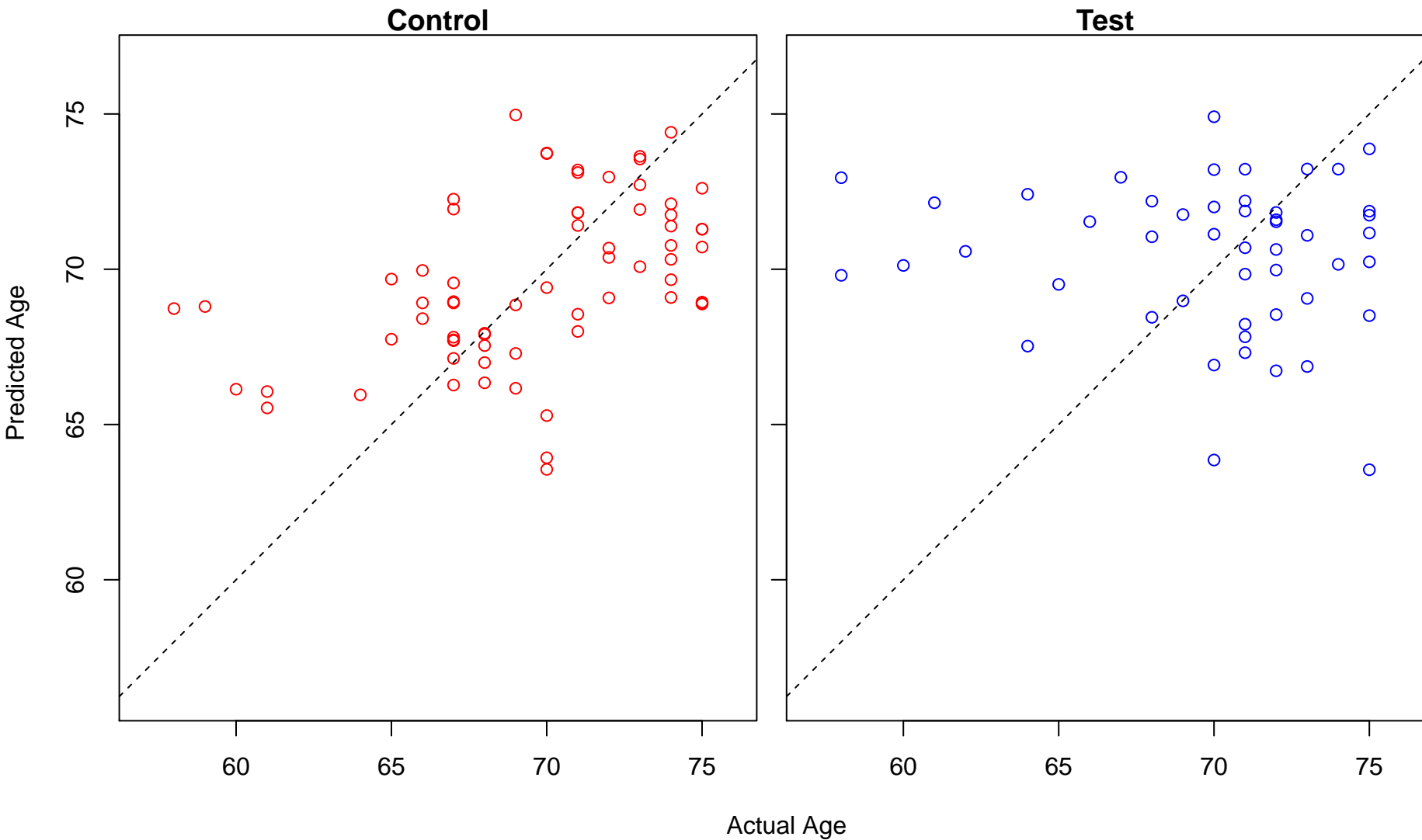
tube closure (Score: 0.769897)



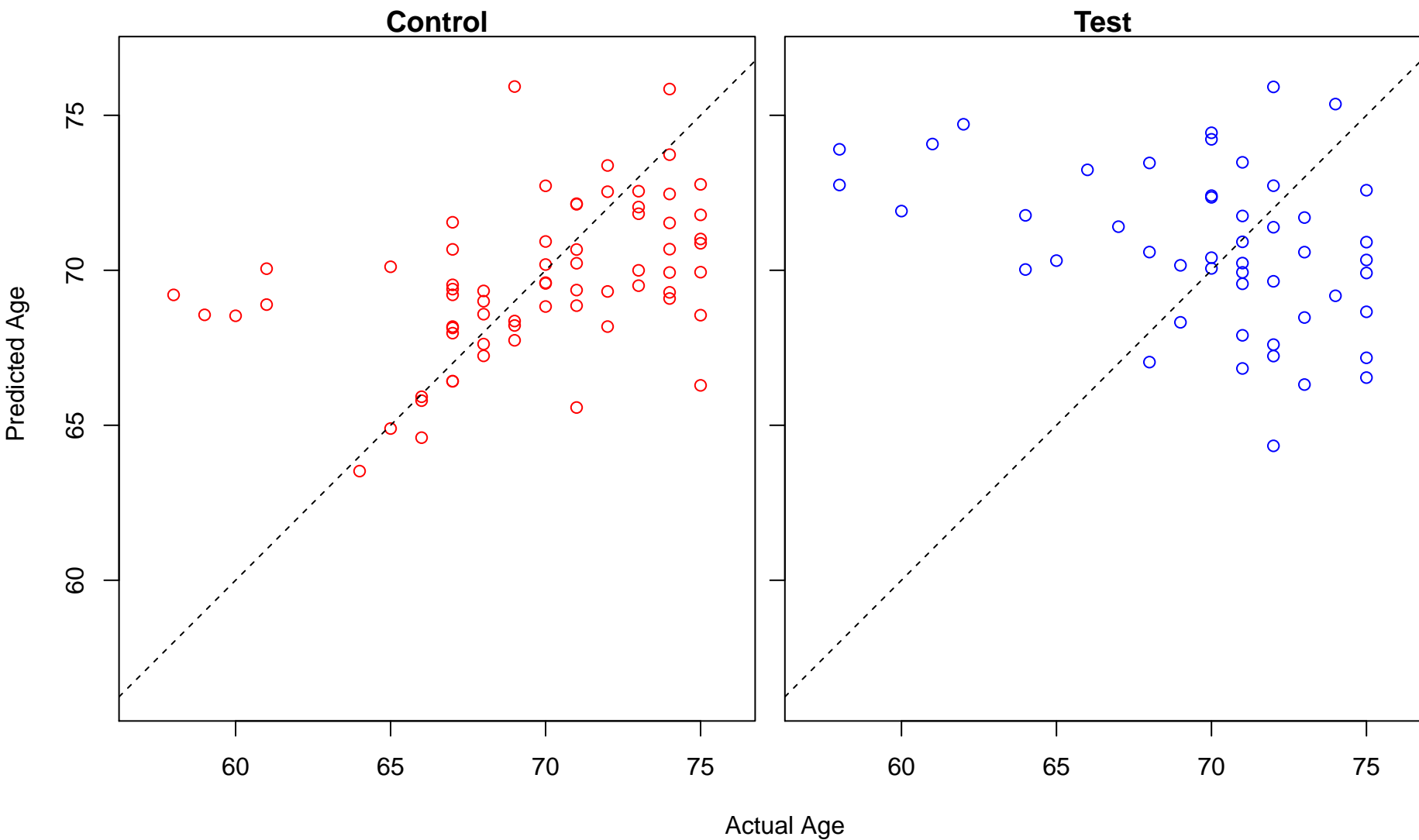
cardiac septum morphogenesis (Score: 0.769808)



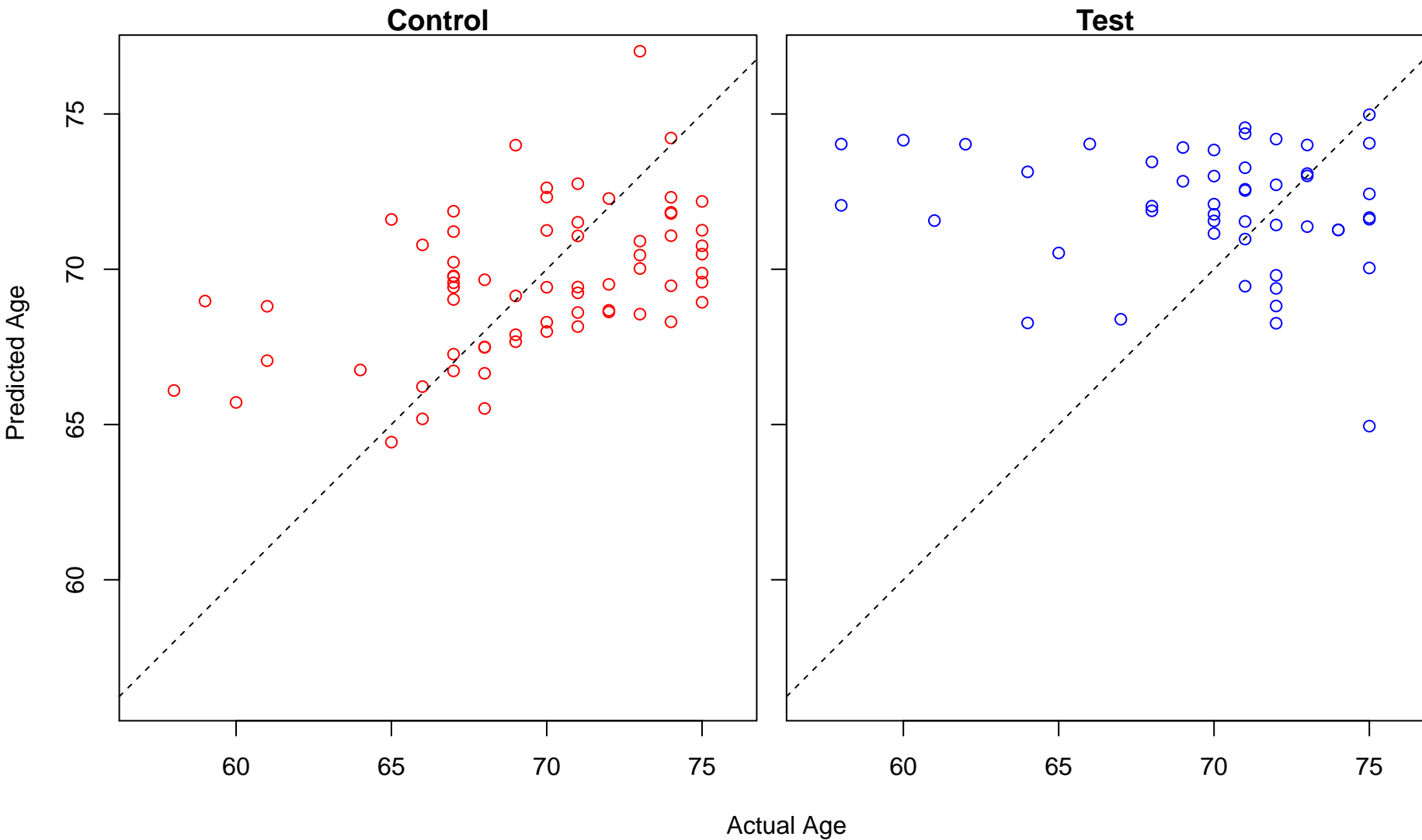
nuclear-transcribed mRNA poly(A) tail shortening (Score: 0.769668)



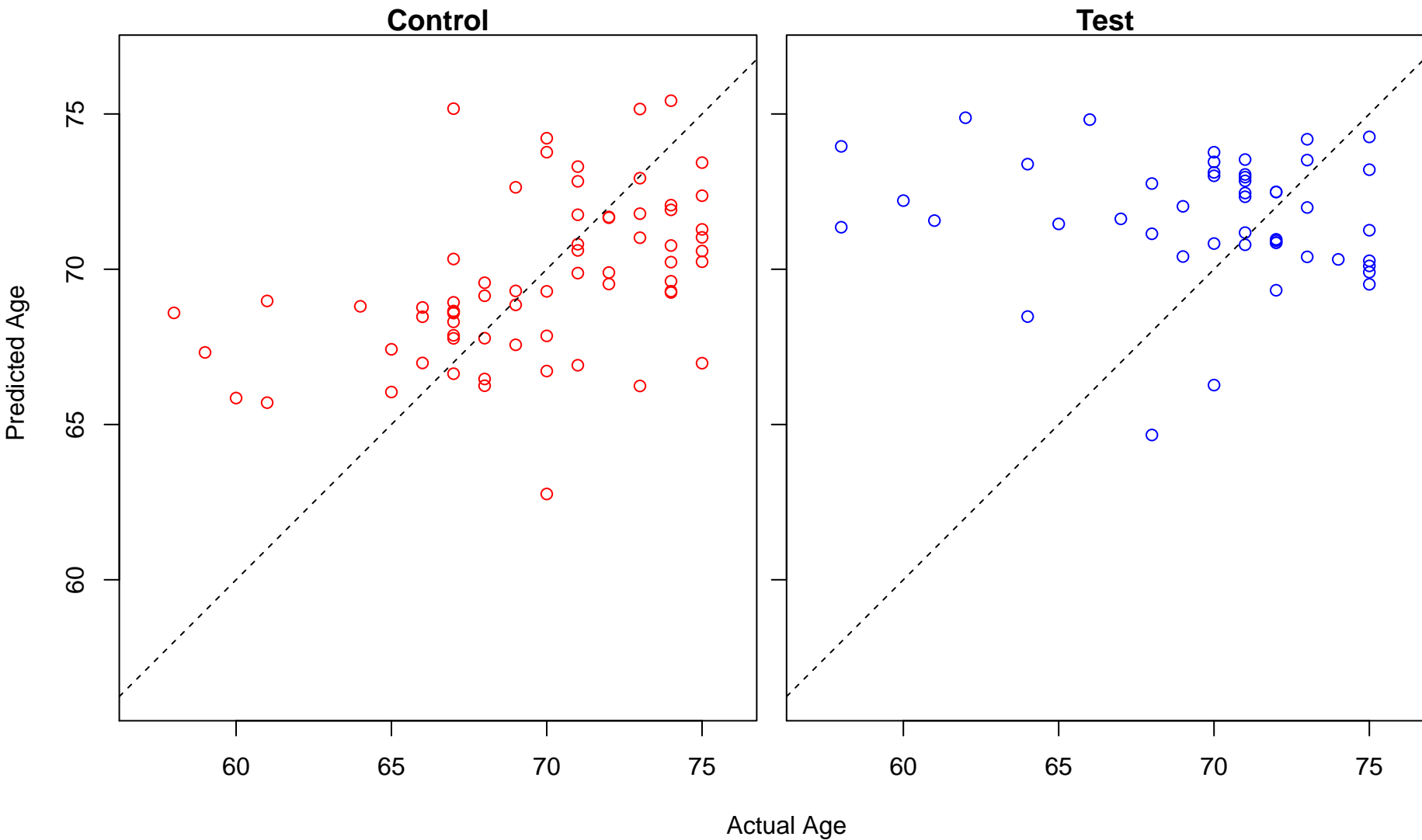
positive regulation of granulocyte macrophage colony-stimulating factor production (Score: 0.7692)



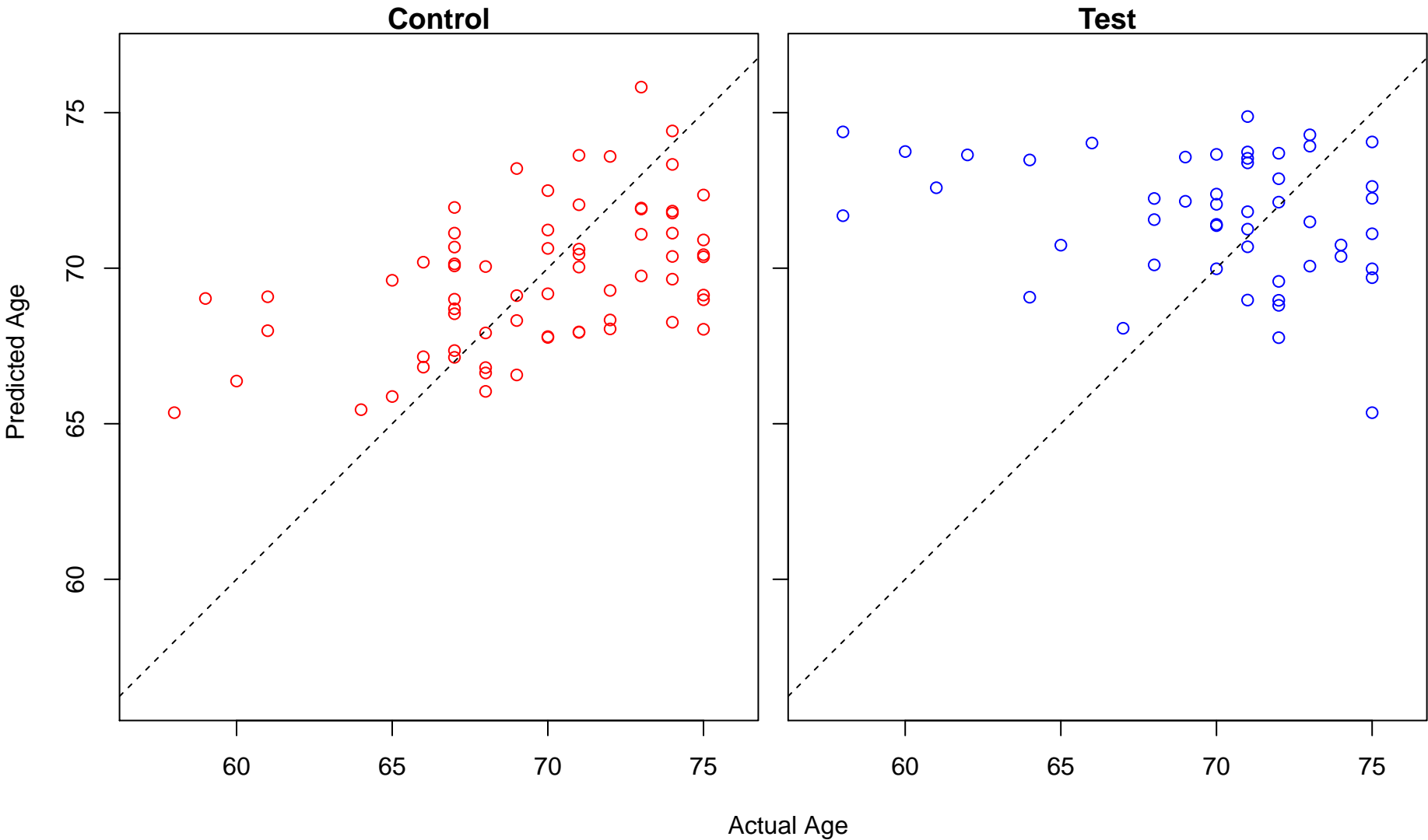
response to gonadotropin (Score: 0.768974)



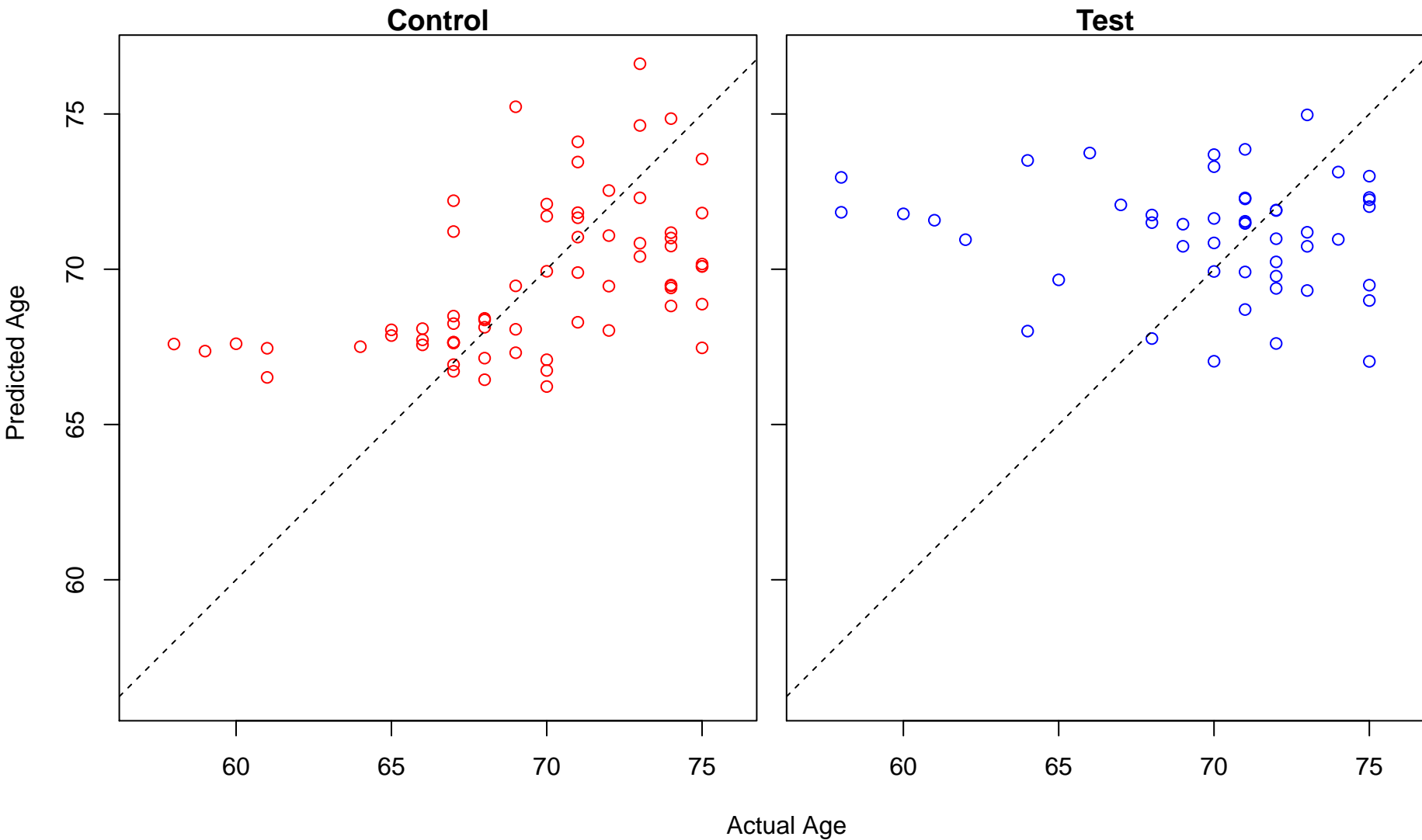
negative regulation of microtubule depolymerization (Score: 0.768805)



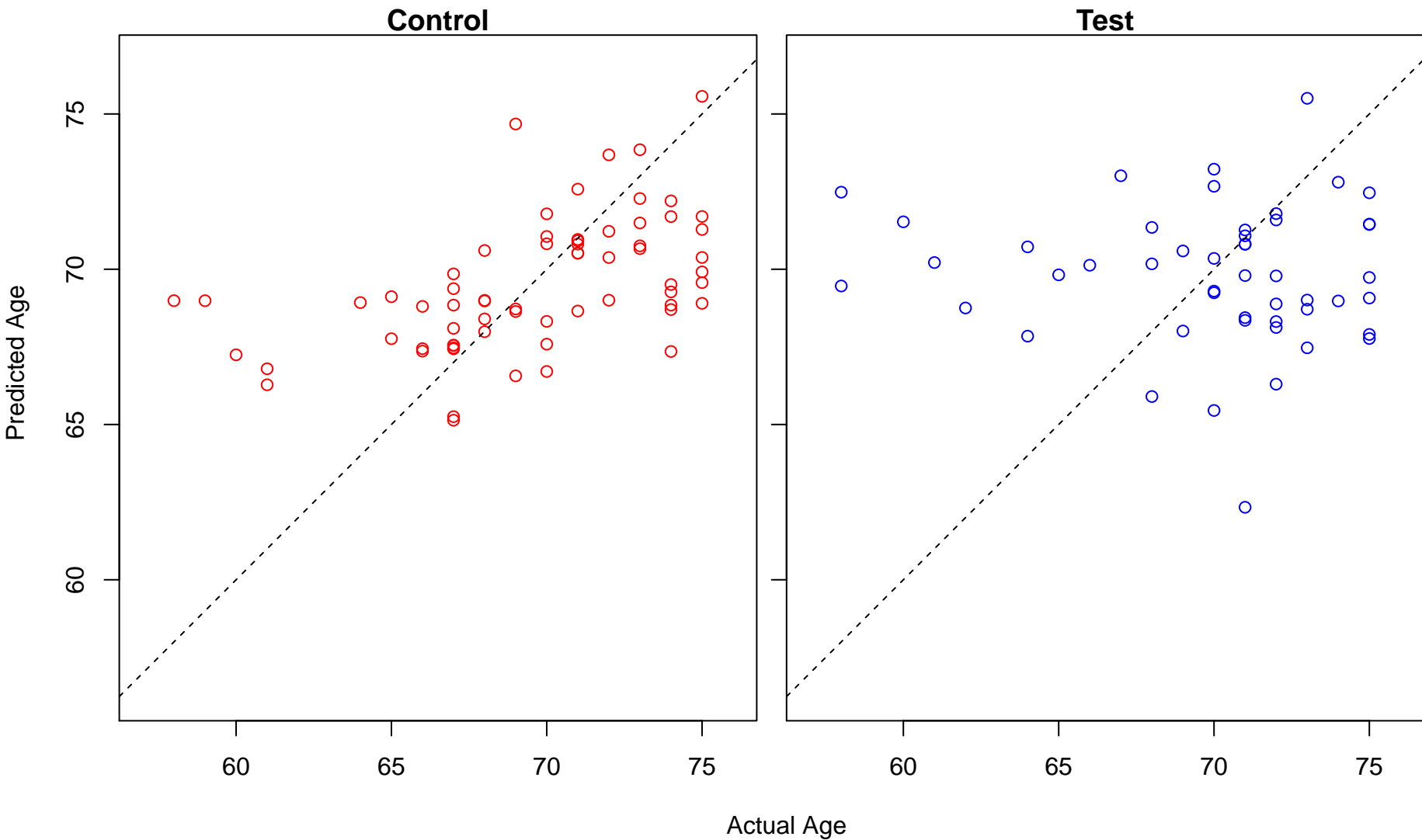
cell surface receptor signaling pathway involved in heart development (Score: 0.768466)



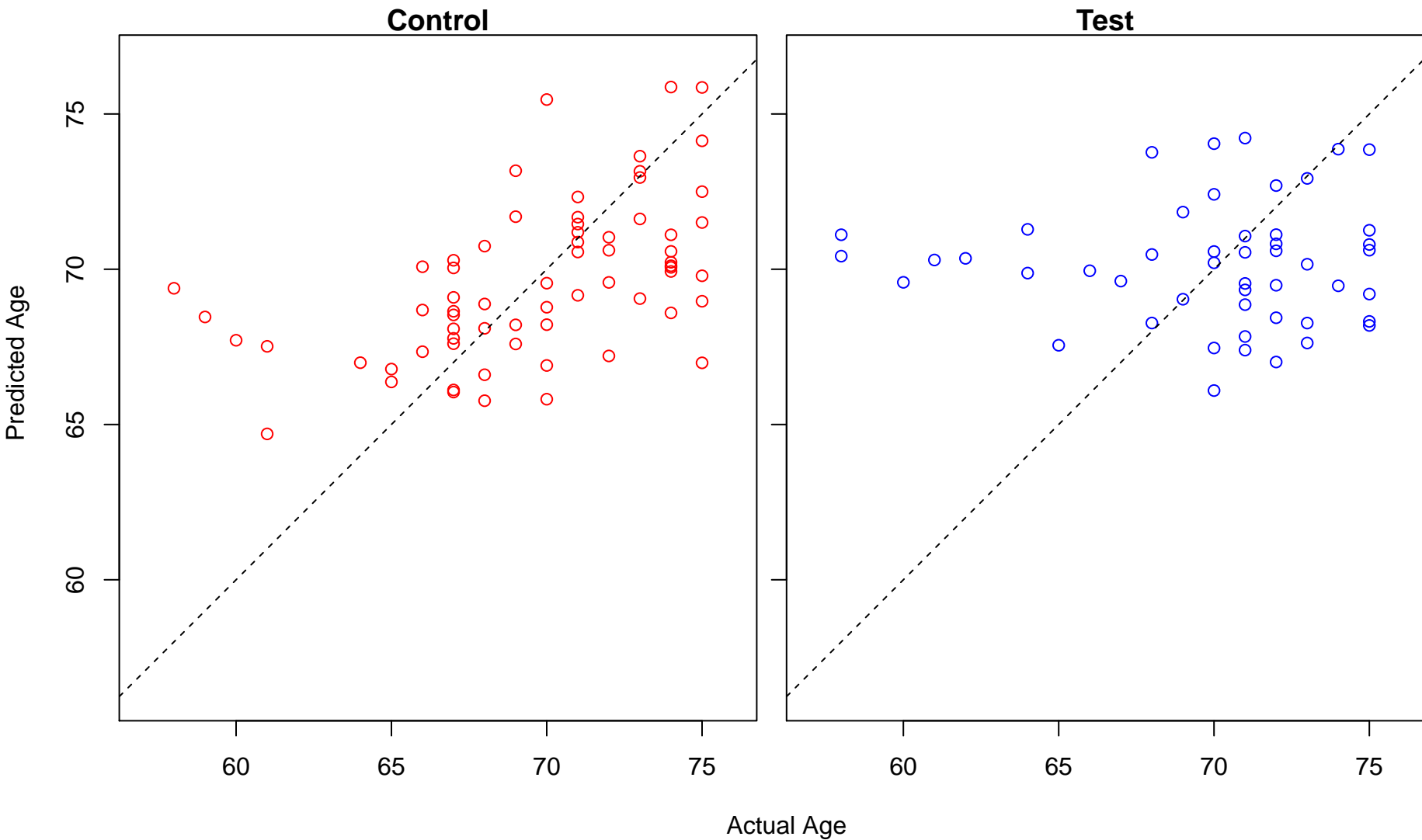
negative regulation of protein localization to nucleus (Score: 0.768367)



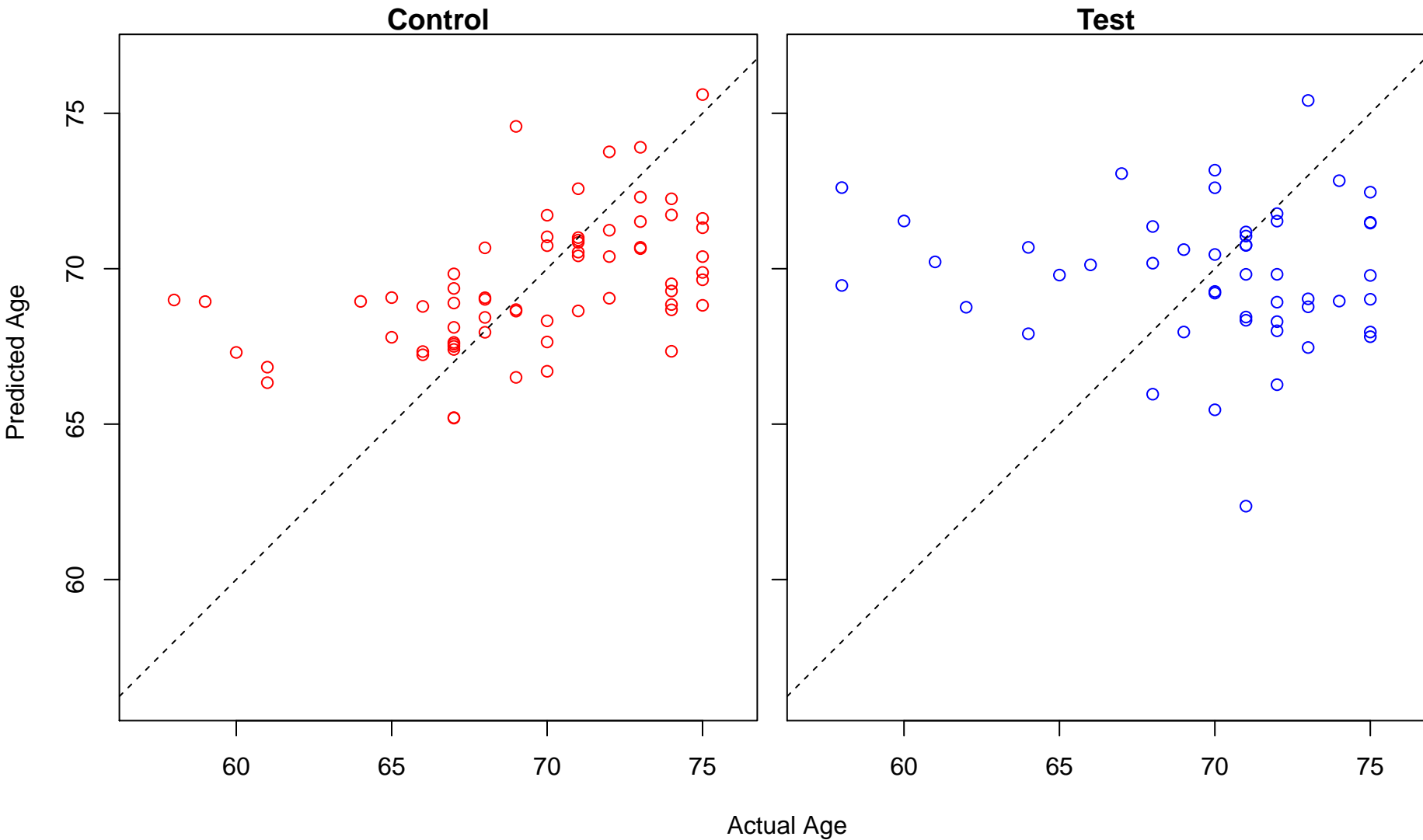
prepulse inhibition (Score: 0.768258)



cristae formation (Score: 0.767606)

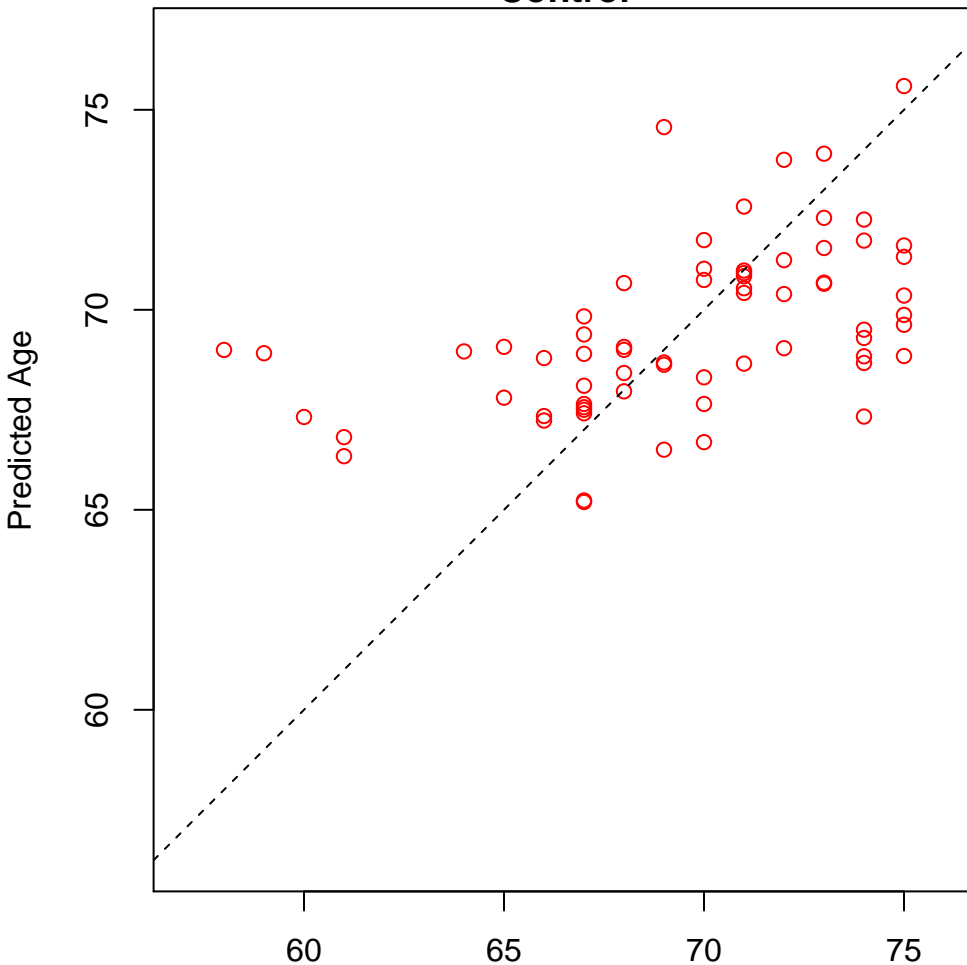


negative regulation of dendritic spine development (Score: 0.767121)

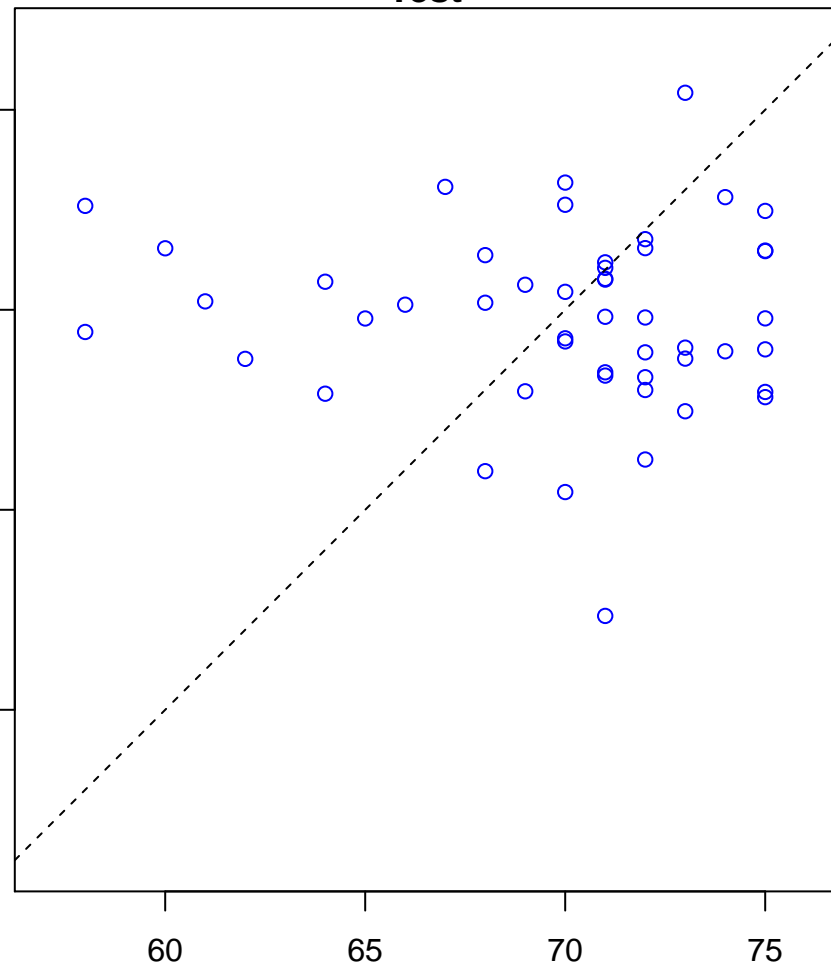


central nervous system myelination (Score: 0.766361)

Control

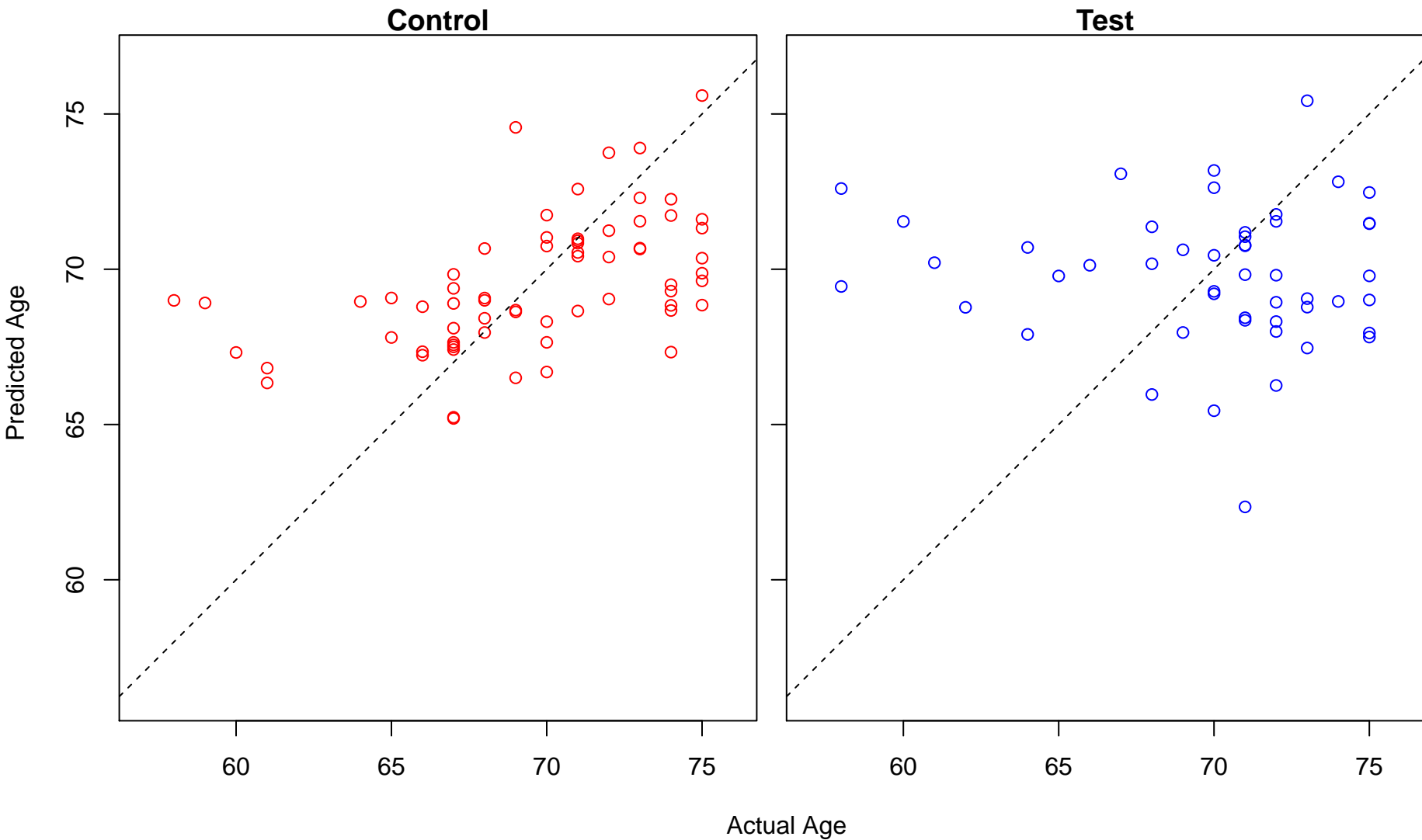


Test

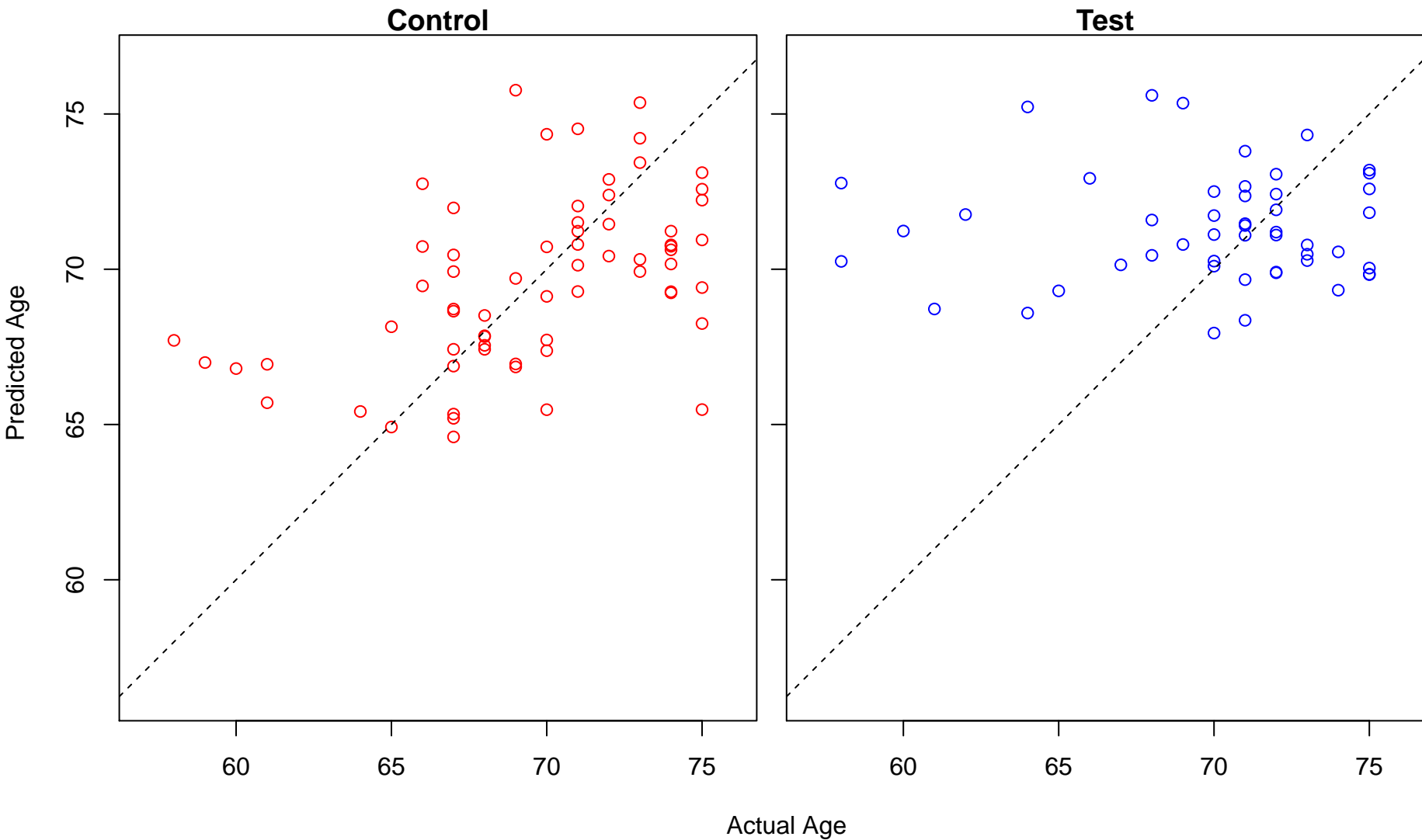


Actual Age

axon ensheathment in central nervous system (Score: 0.766361)

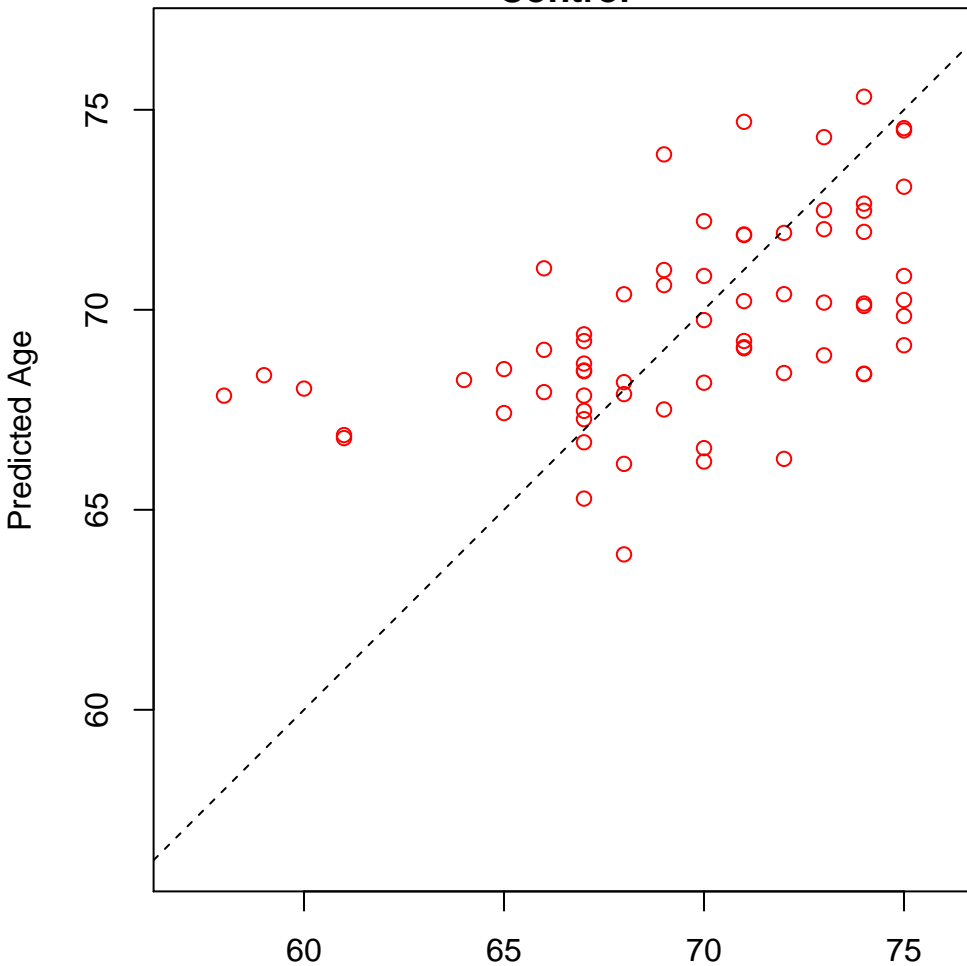


lung development (Score: 0.766161)

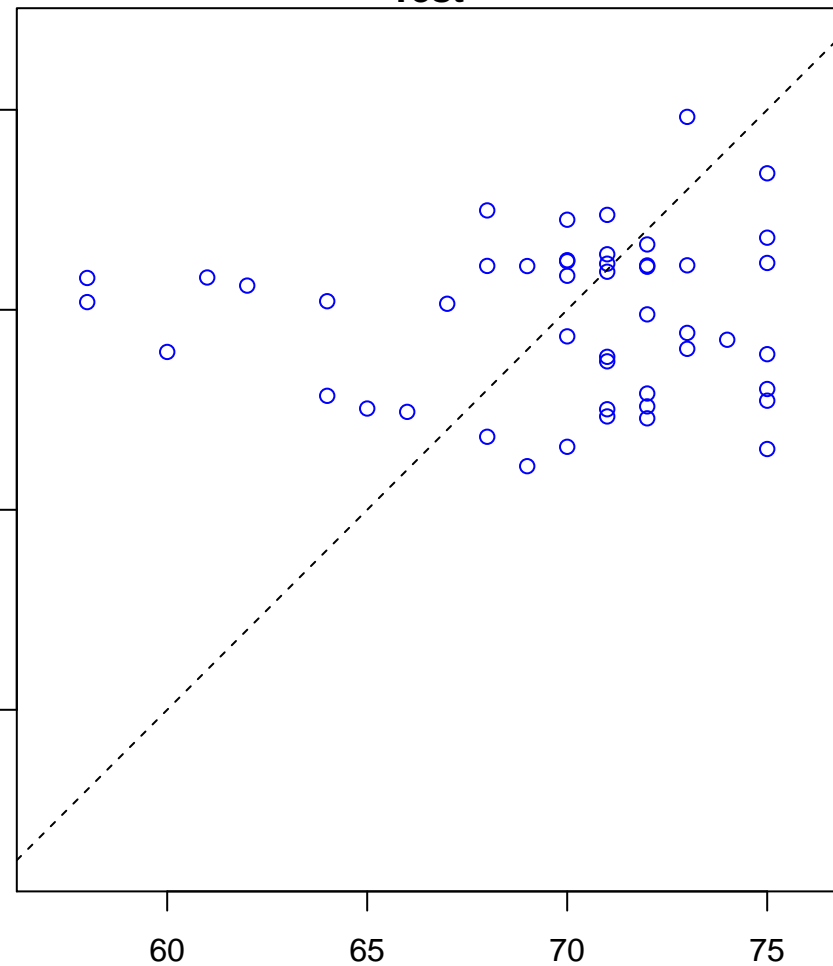


regulation of macrophage differentiation (Score: 0.765522)

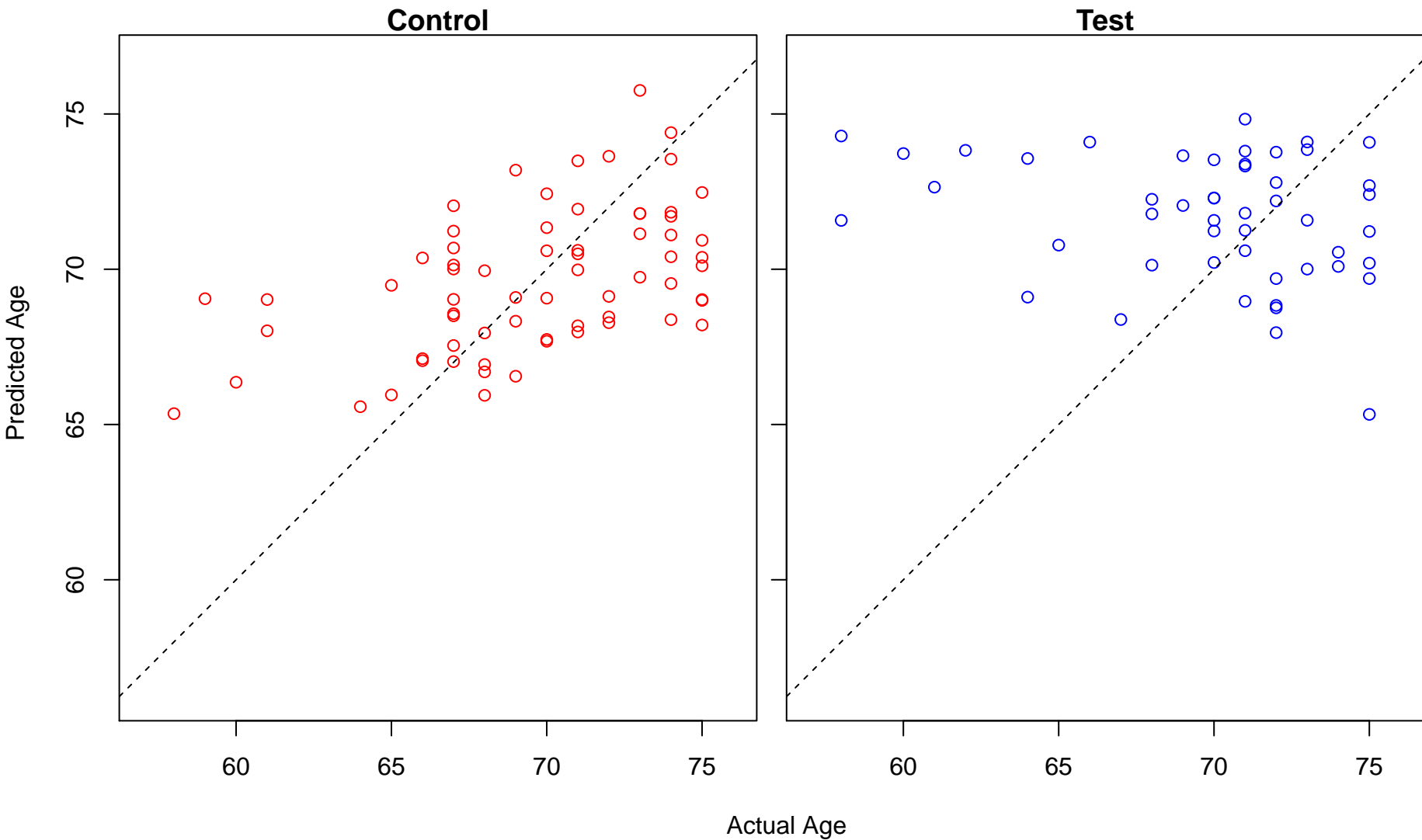
Control



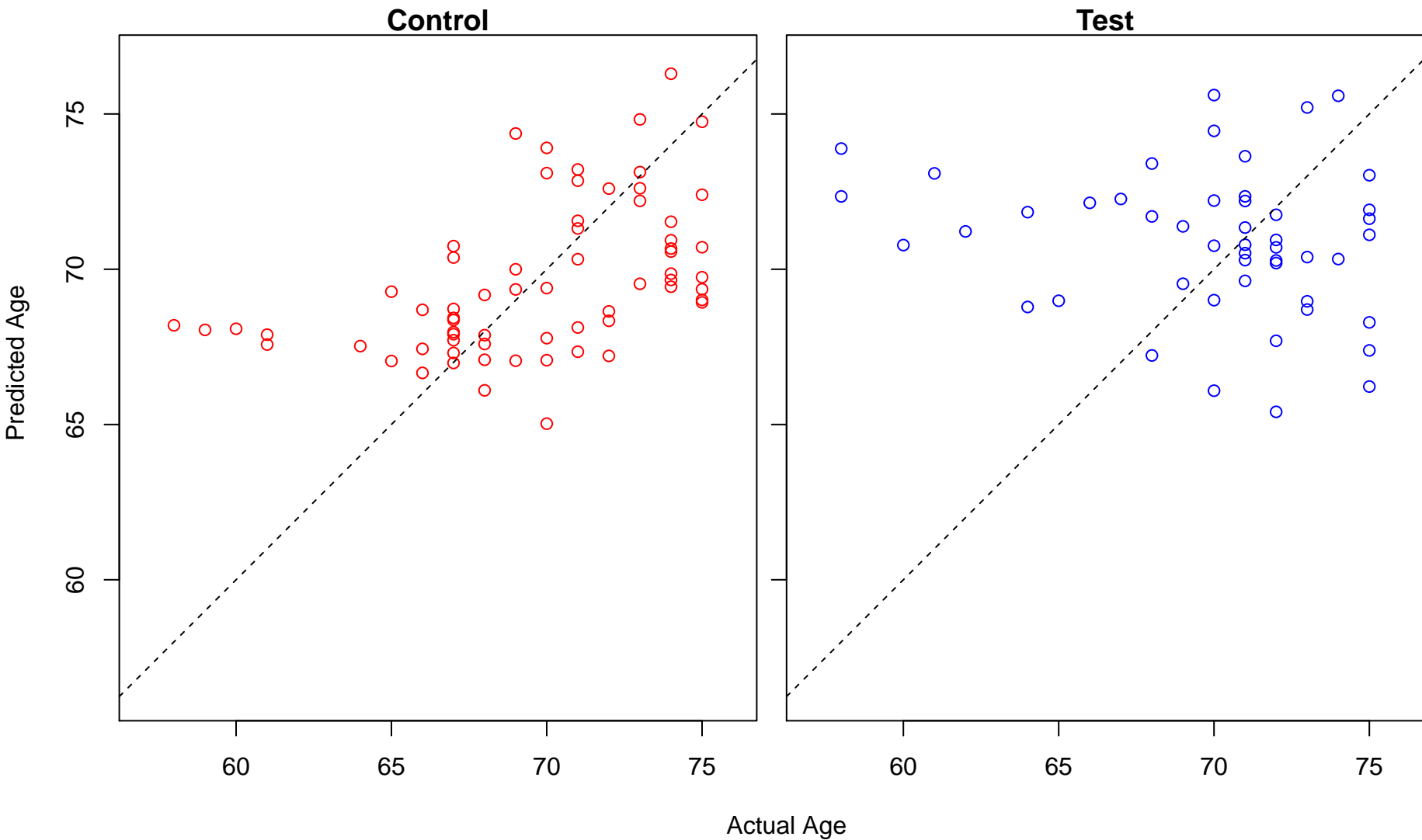
Test



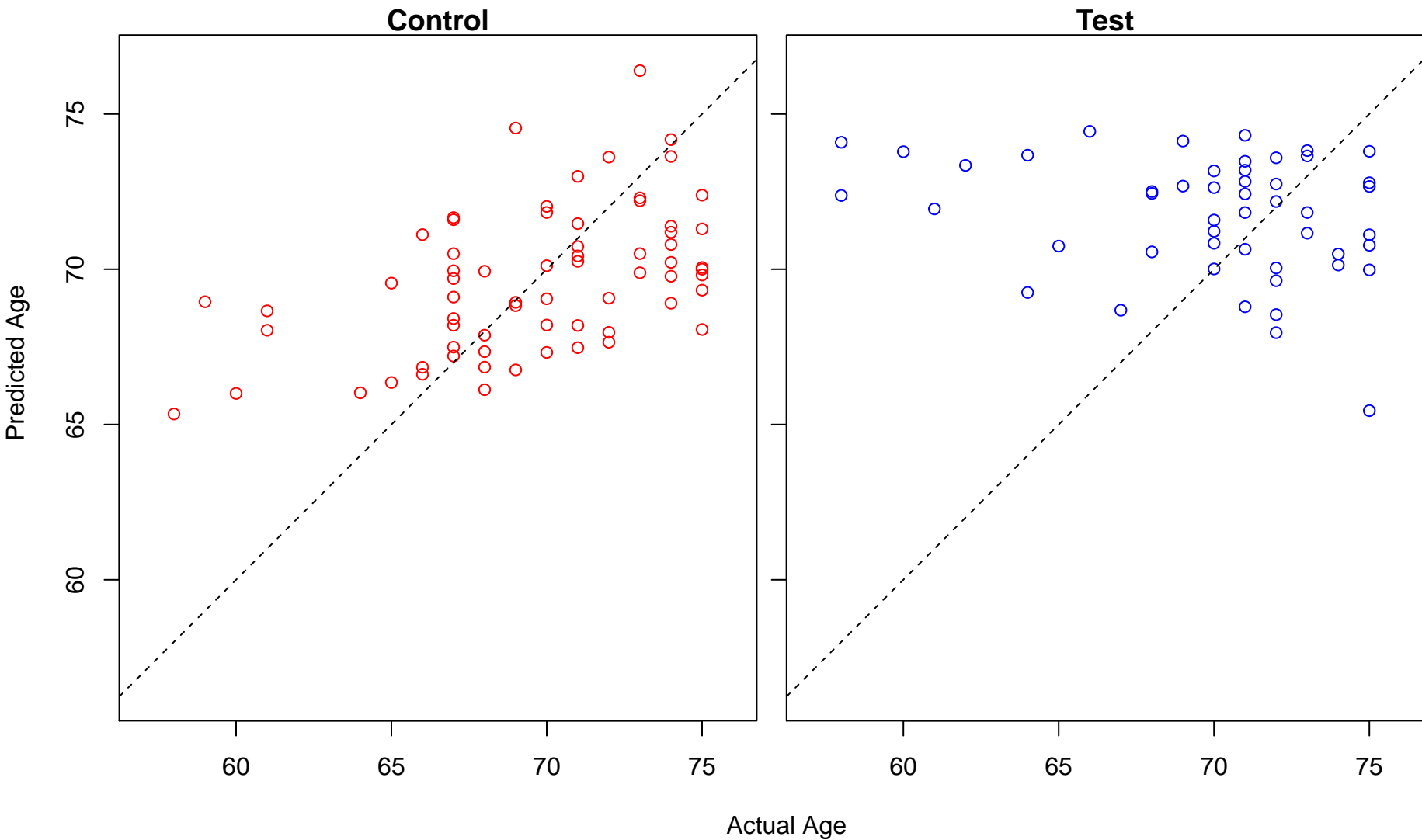
neuronal stem cell population maintenance (Score: 0.765490)



mRNA polyadenylation (Score: 0.764922)

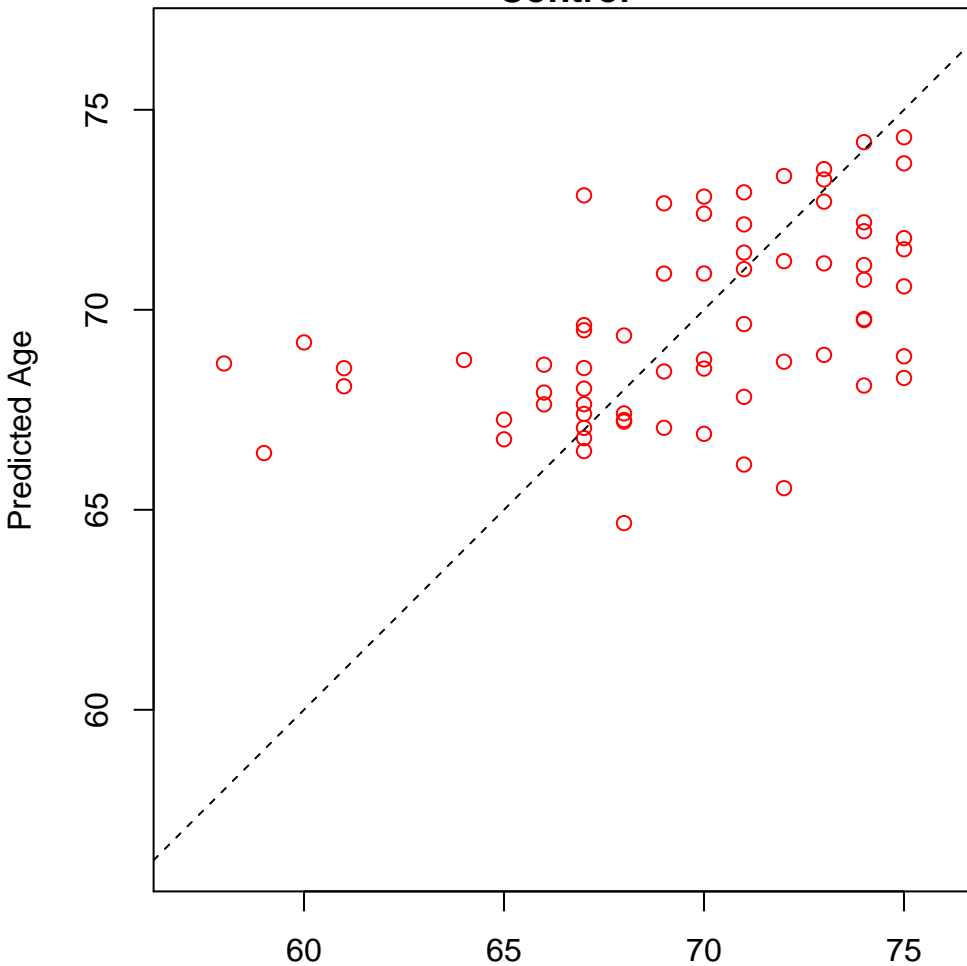


atrioventricular valve formation (Score: 0.764863)

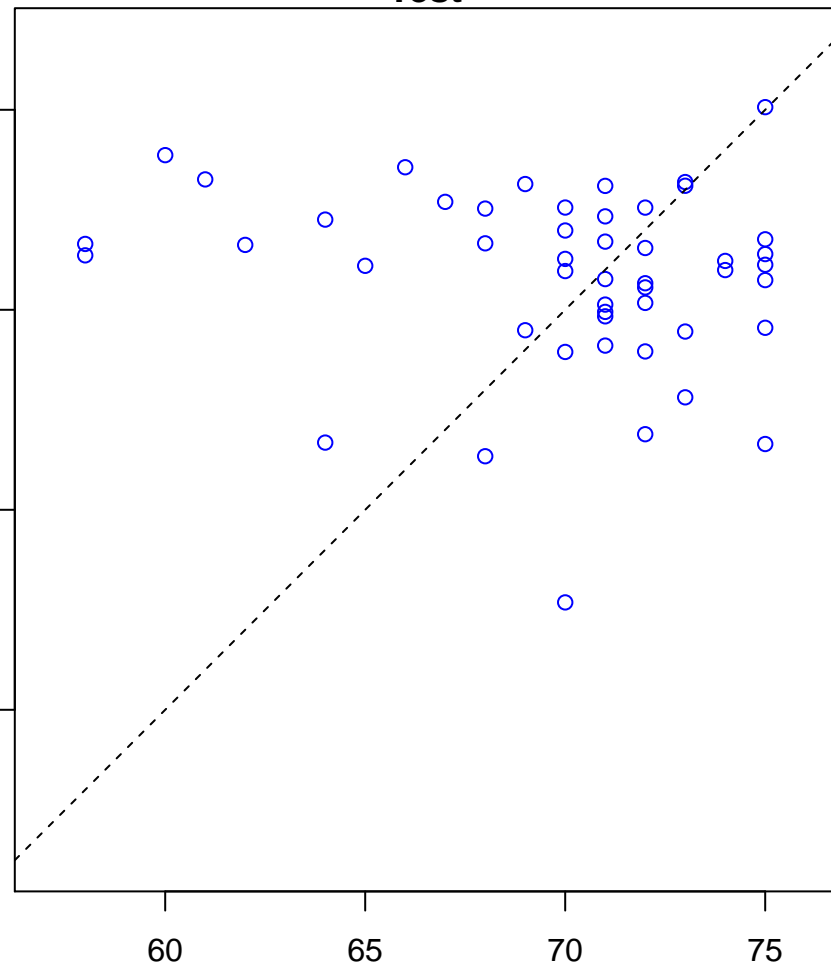


endocrine pancreas development (Score: 0.764585)

Control

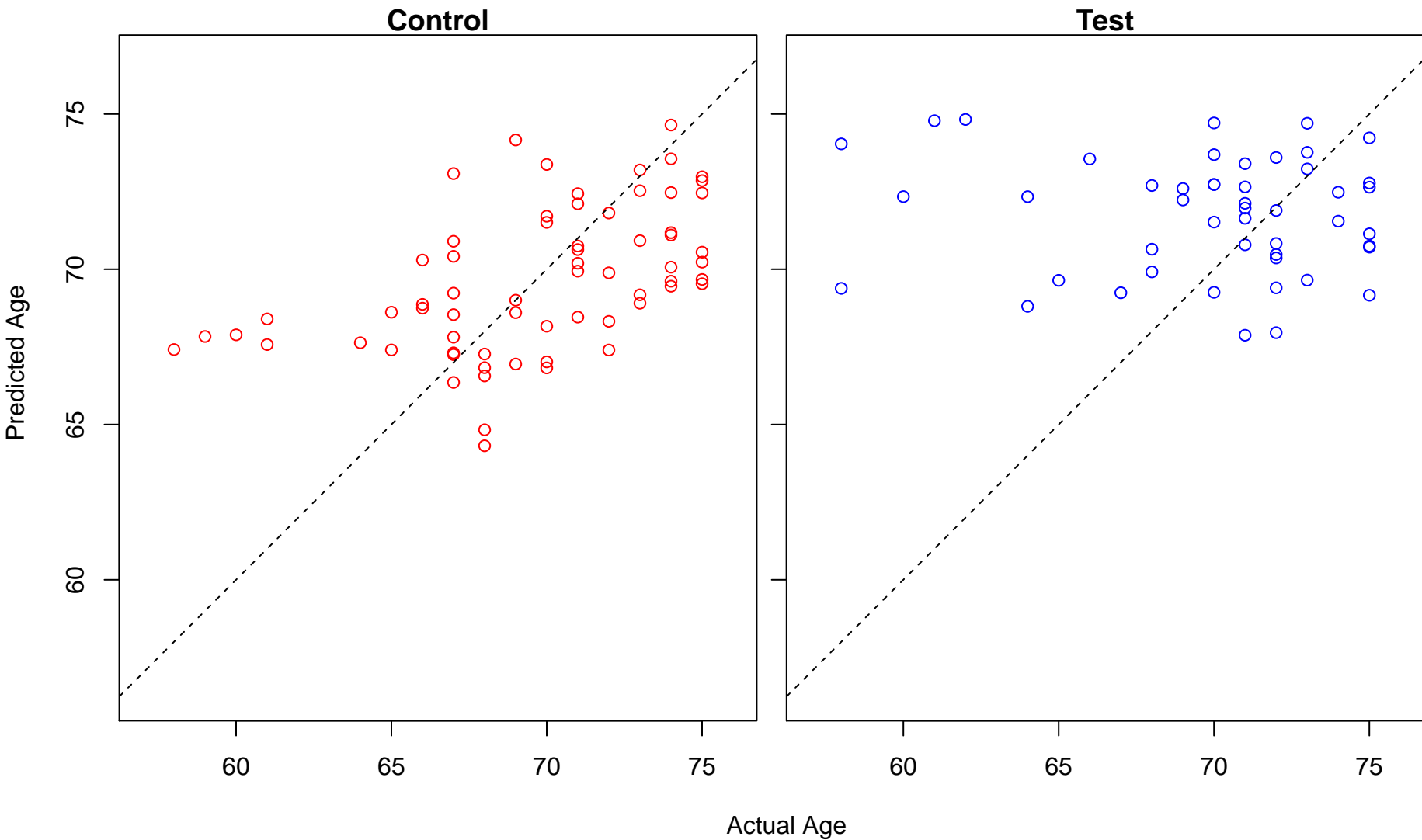


Test

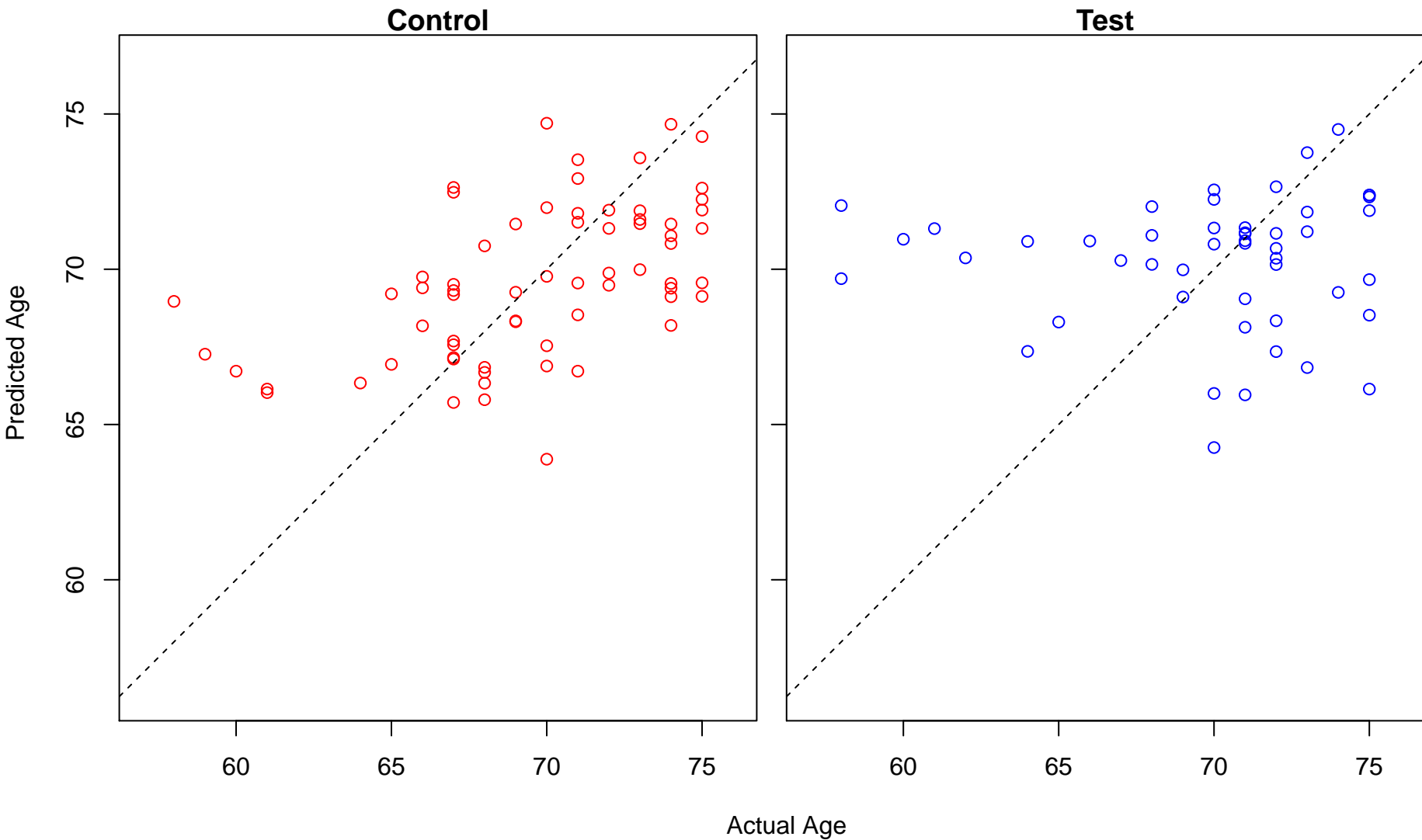


Actual Age

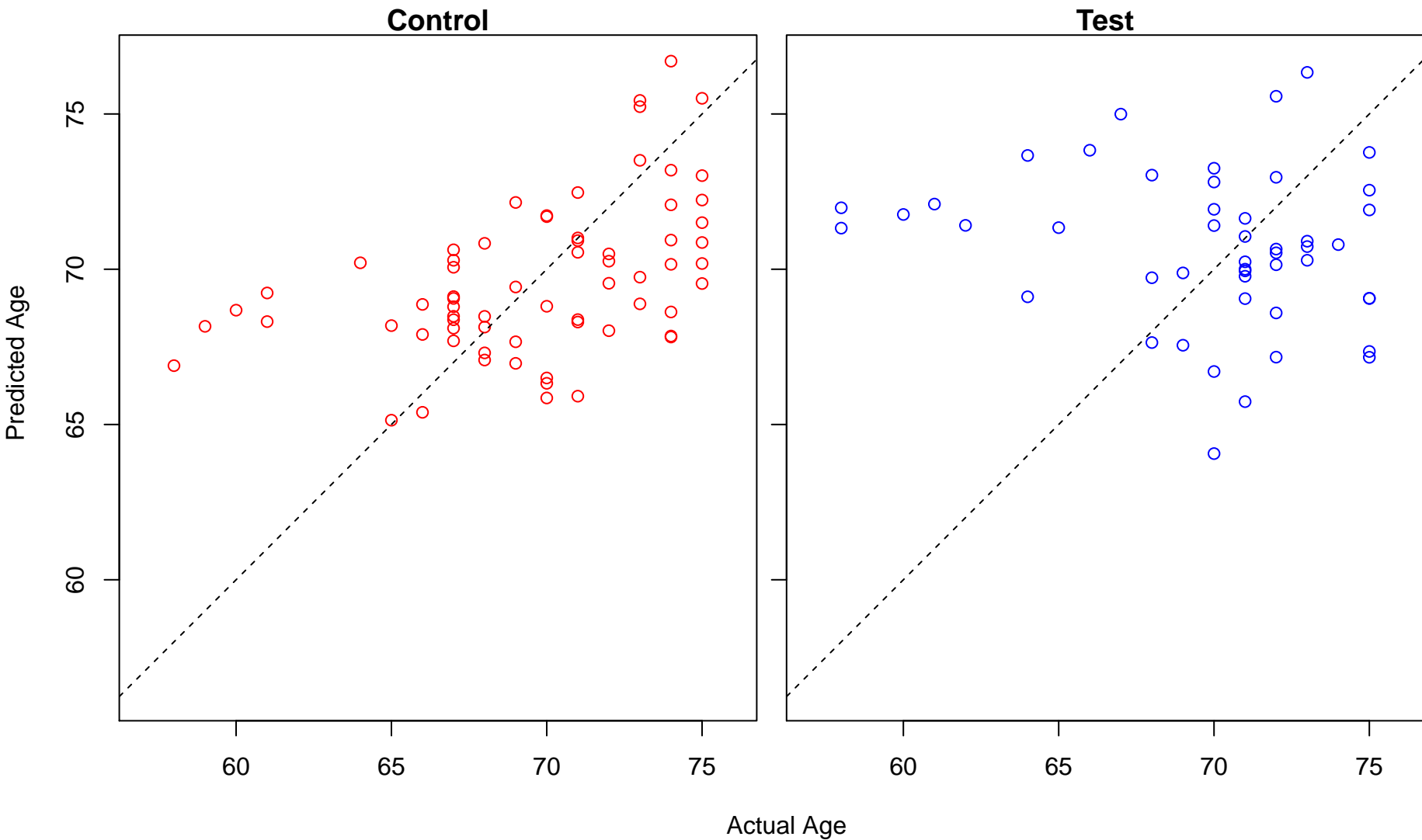
negative regulation of muscle contraction (Score: 0.764308)



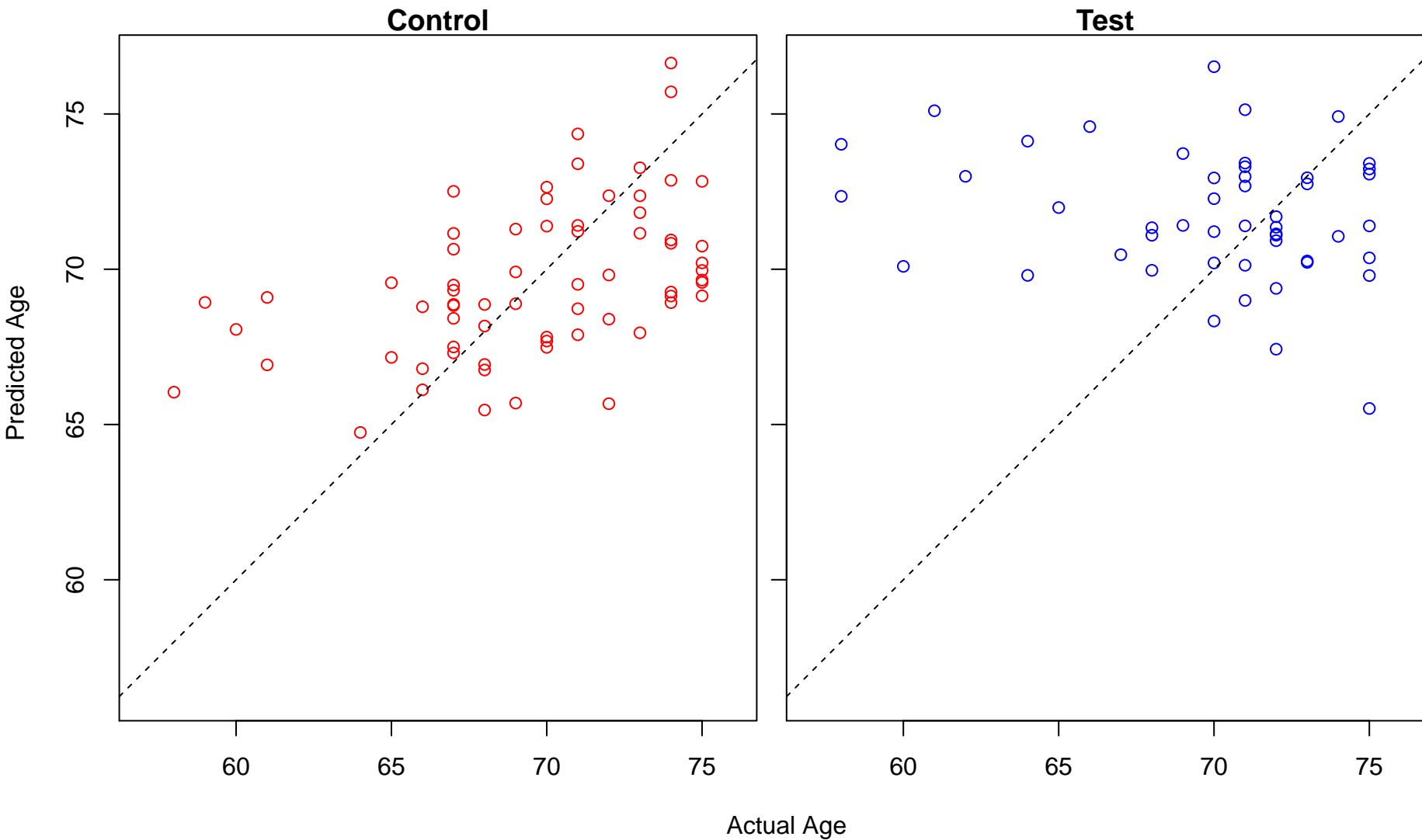
neural tube formation (Score: 0.764091)



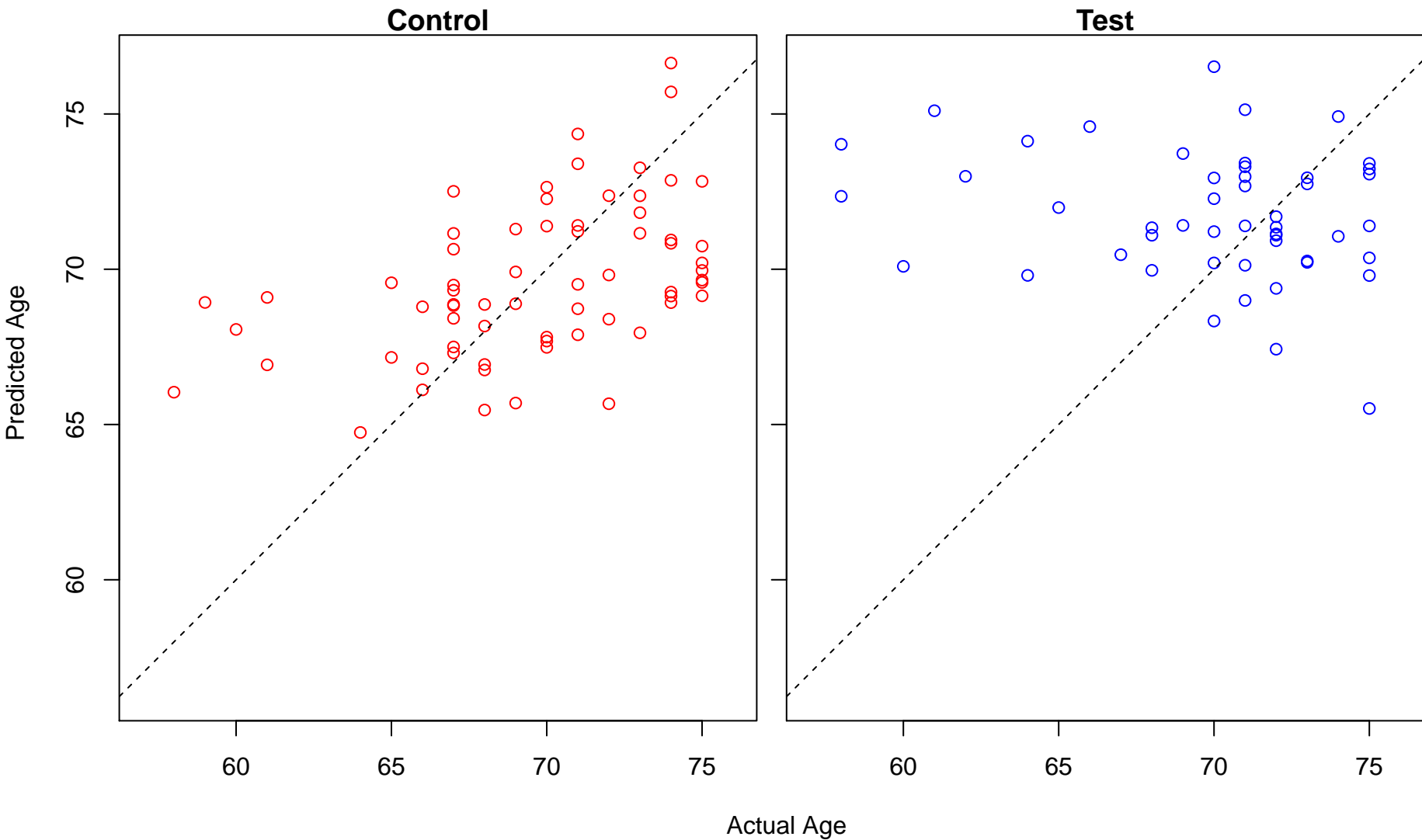
establishment or maintenance of monopolar cell polarity (Score: 0.763913)



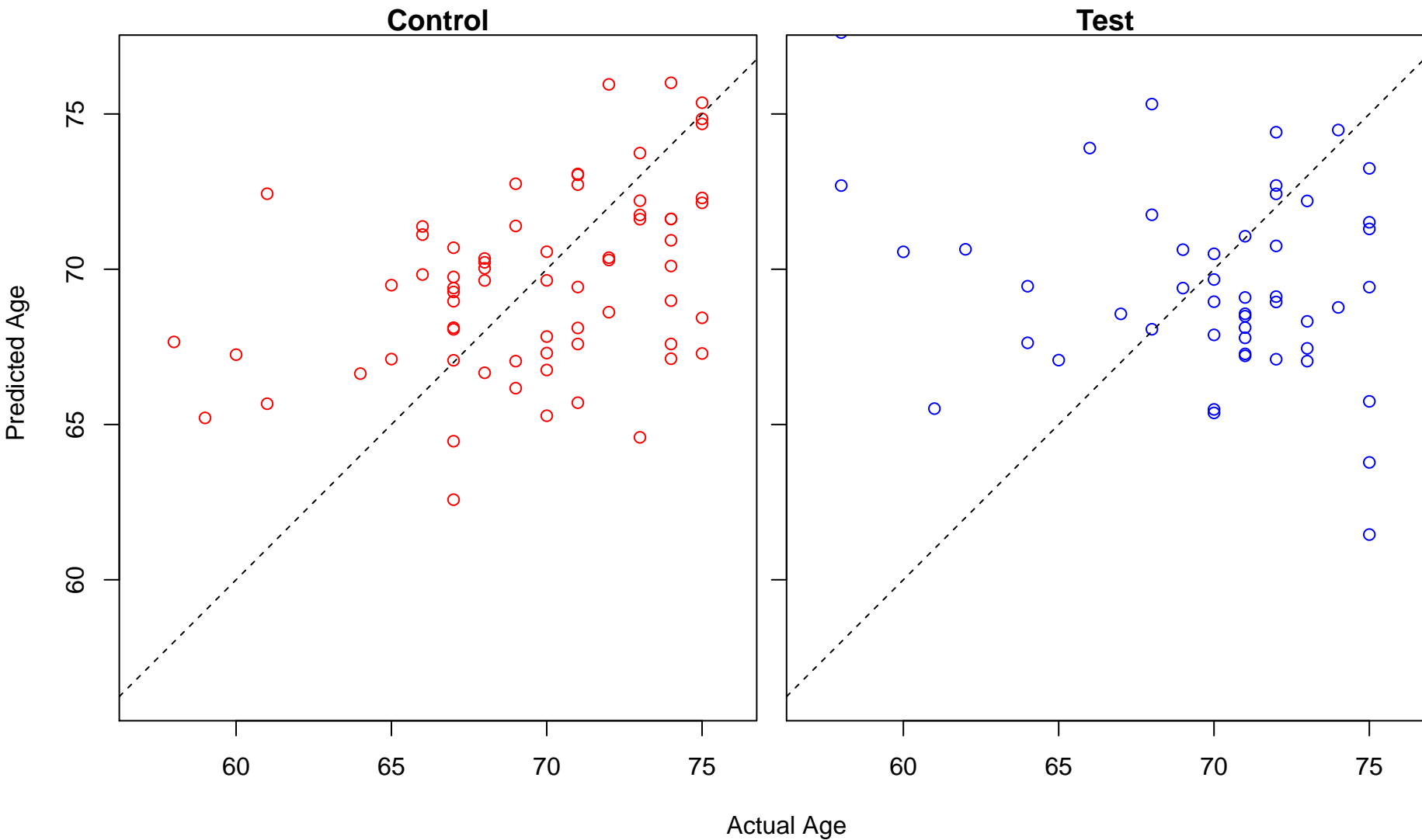
regulation of MHC class I biosynthetic process (Score: 0.763827)



positive regulation of MHC class I biosynthetic process (Score: 0.763827)

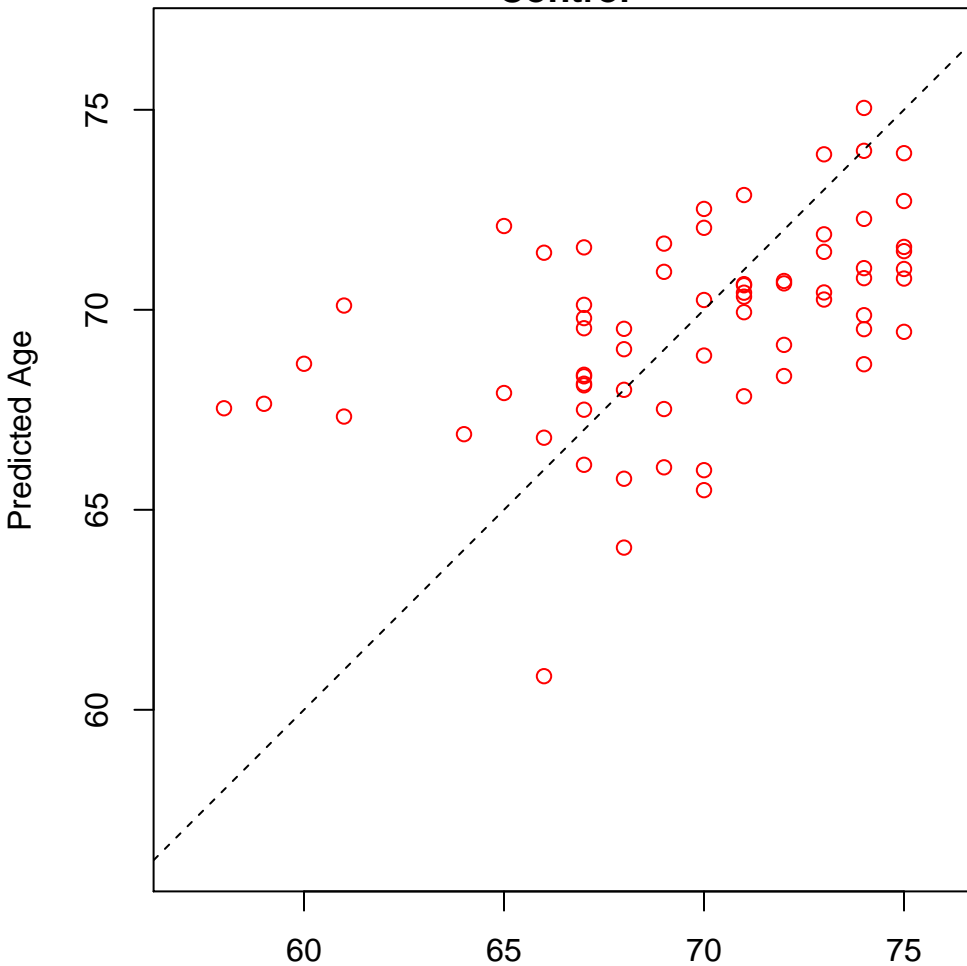


negative regulation of granulocyte differentiation (Score: 0.763685)

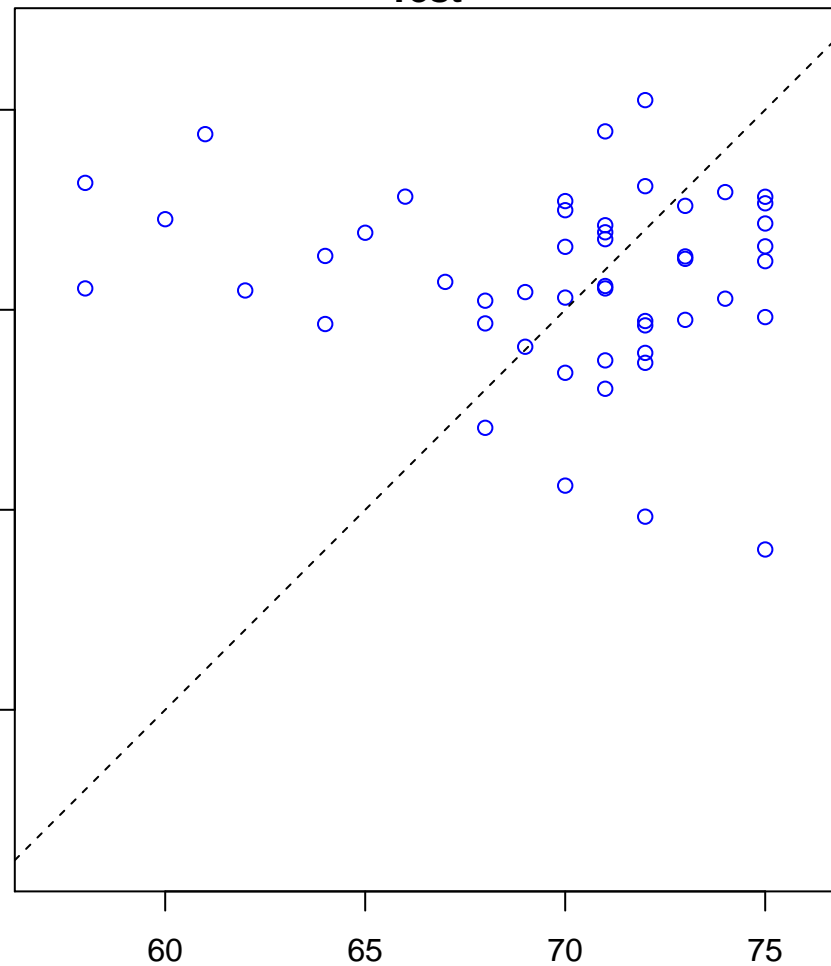


atrial cardiac muscle cell action potential (Score: 0.762709)

Control

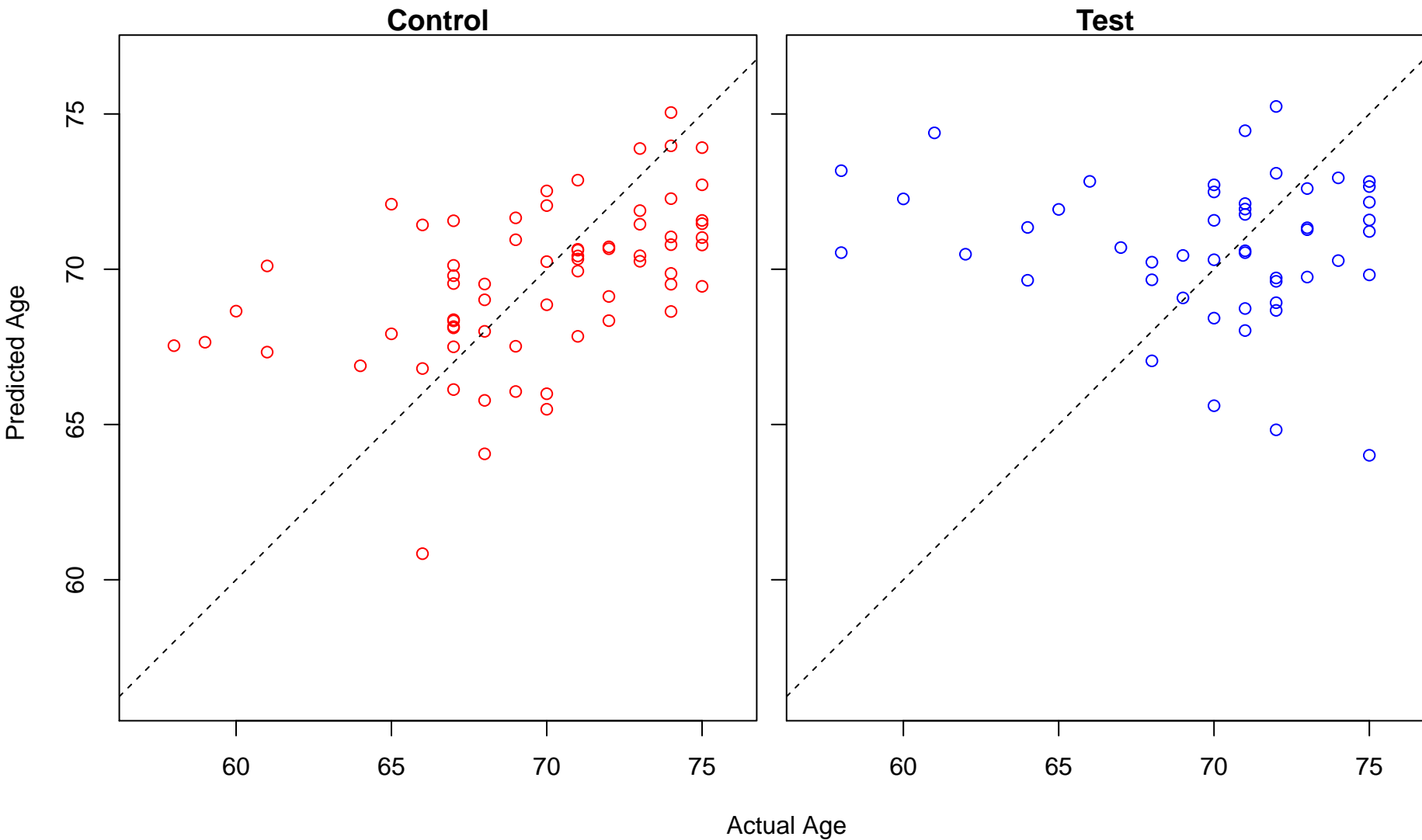


Test

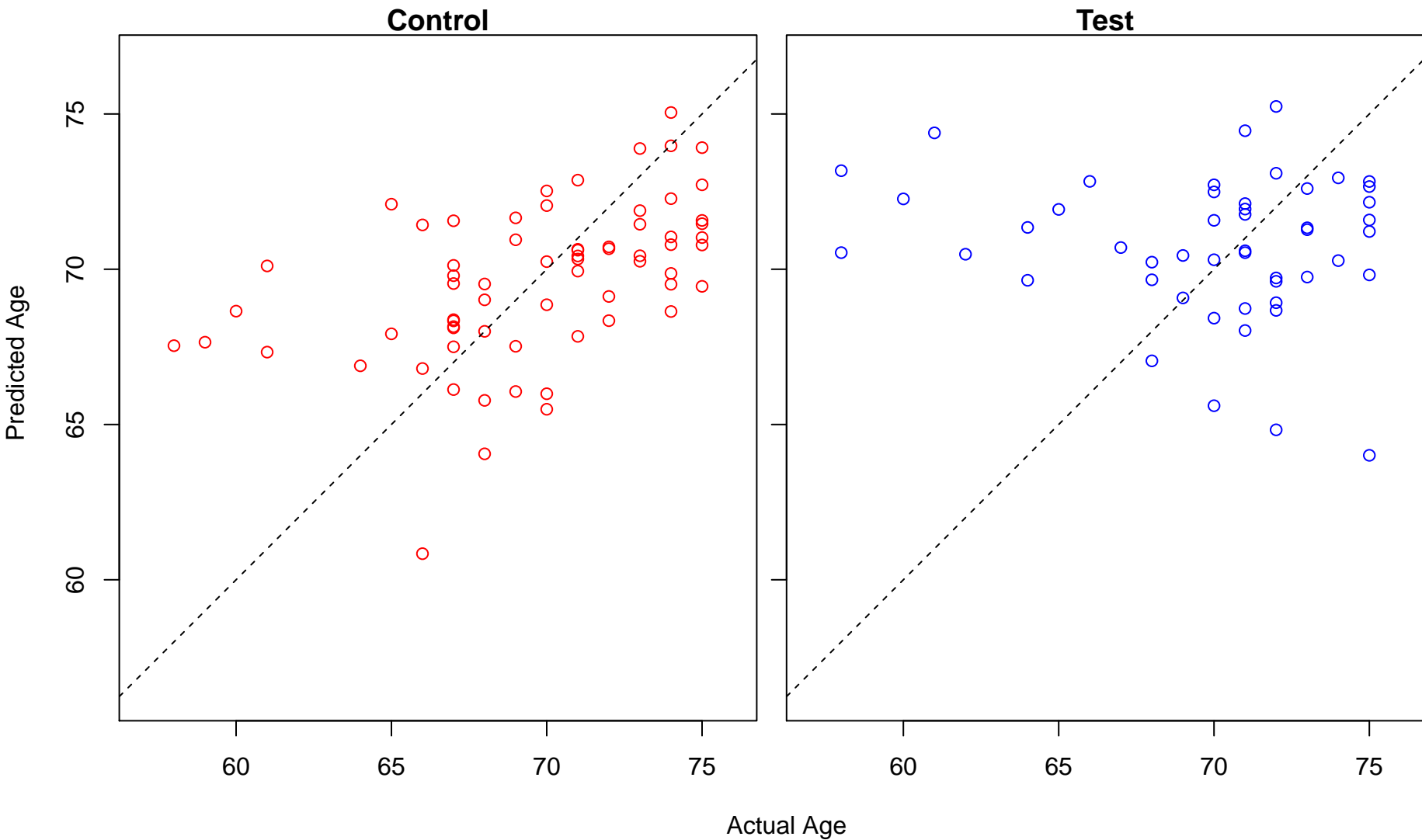


Actual Age

atrial cardiac muscle cell to AV node cell signaling (Score: 0.762709)

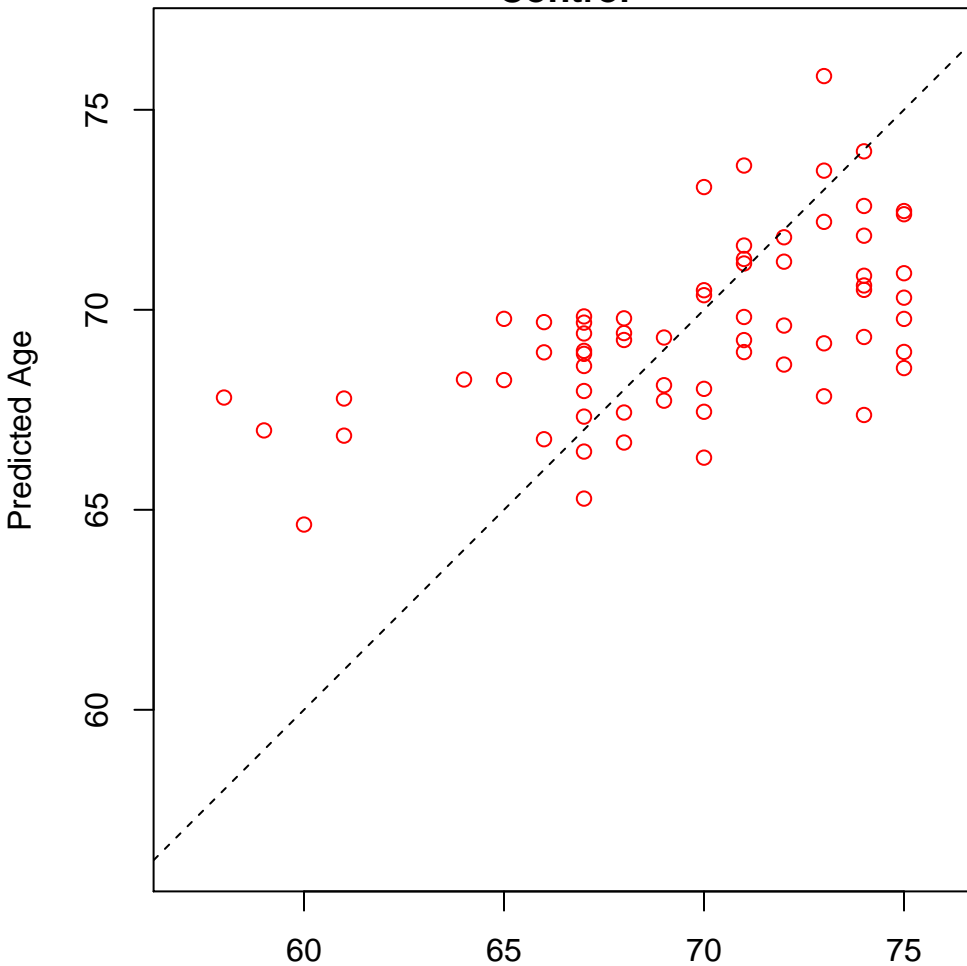


atrial cardiac muscle cell to AV node cell communication (Score: 0.762709)

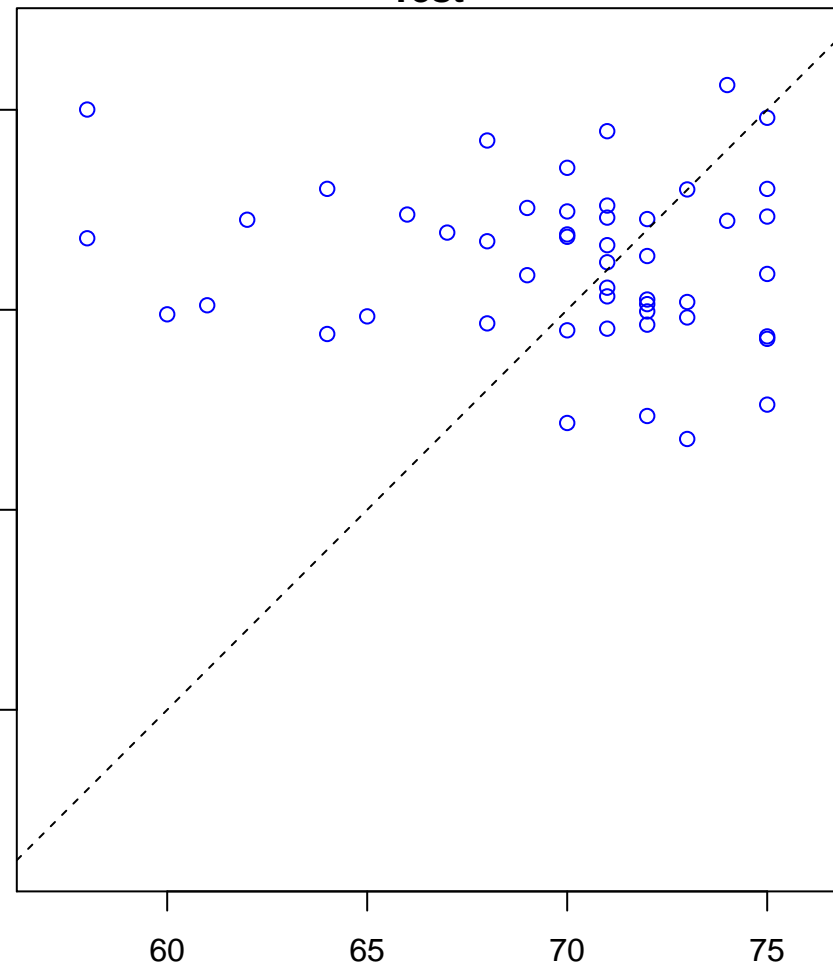


regulation of T cell cytokine production (Score: 0.762455)

Control

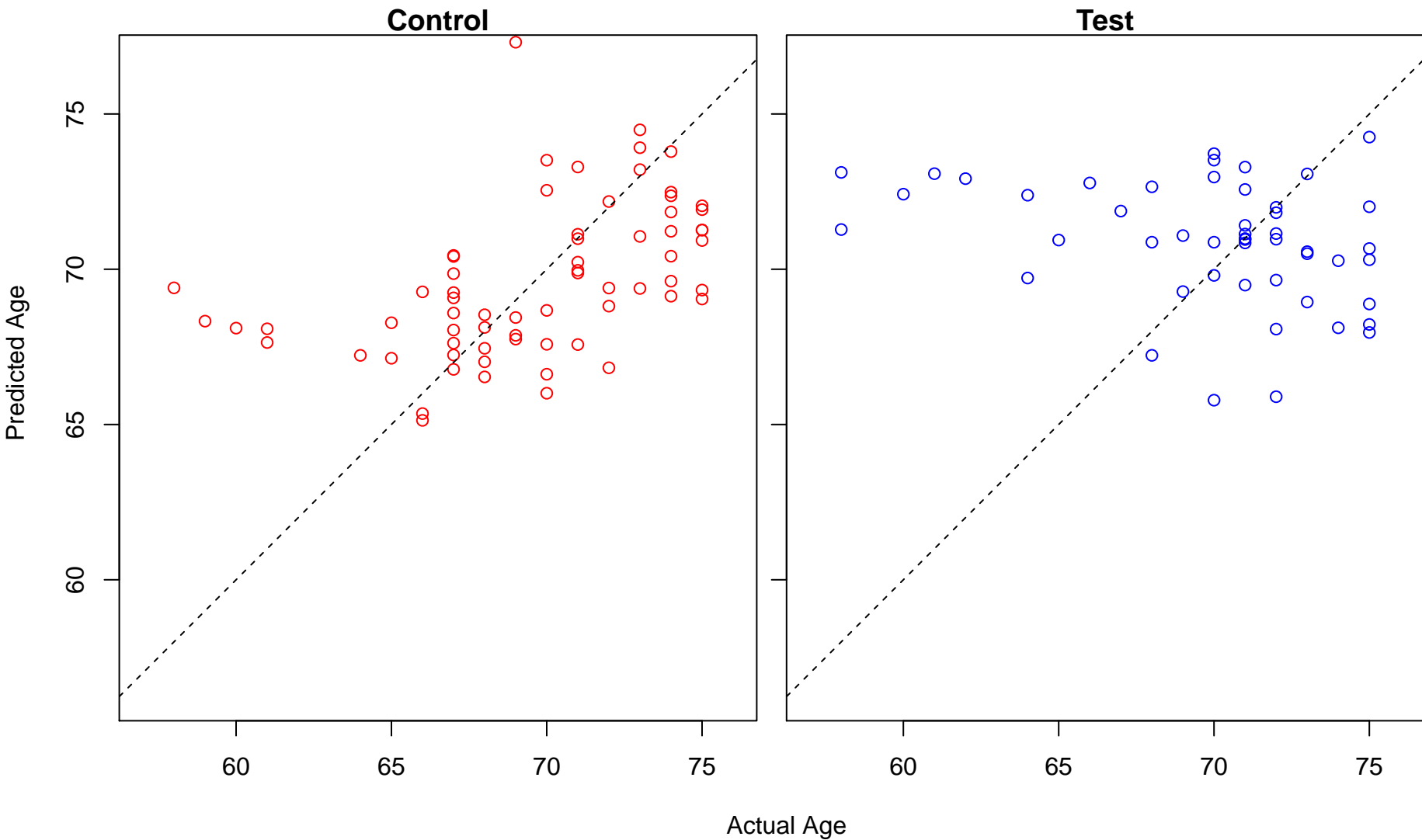


Test

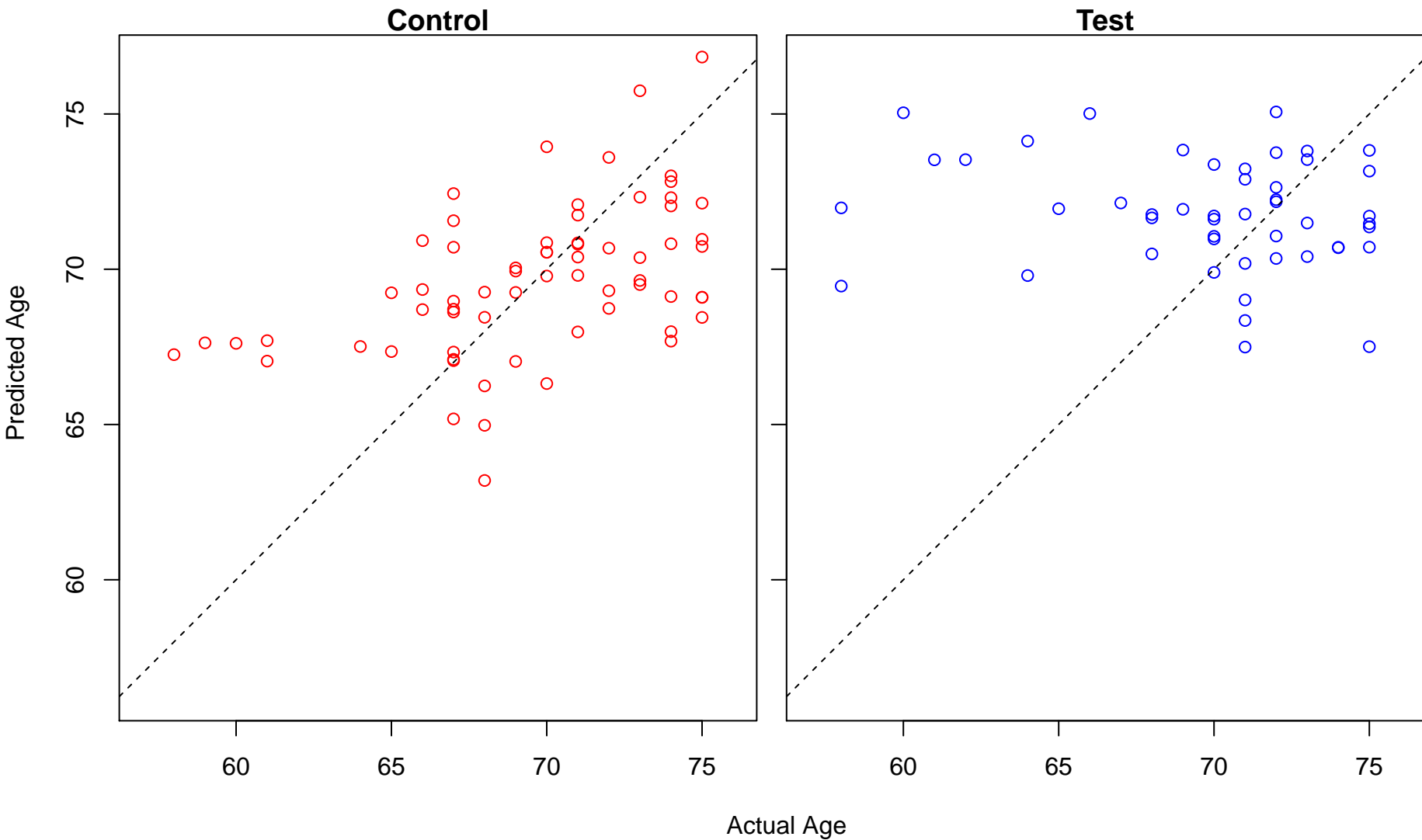


Actual Age

positive regulation of hormone secretion (Score: 0.762373)

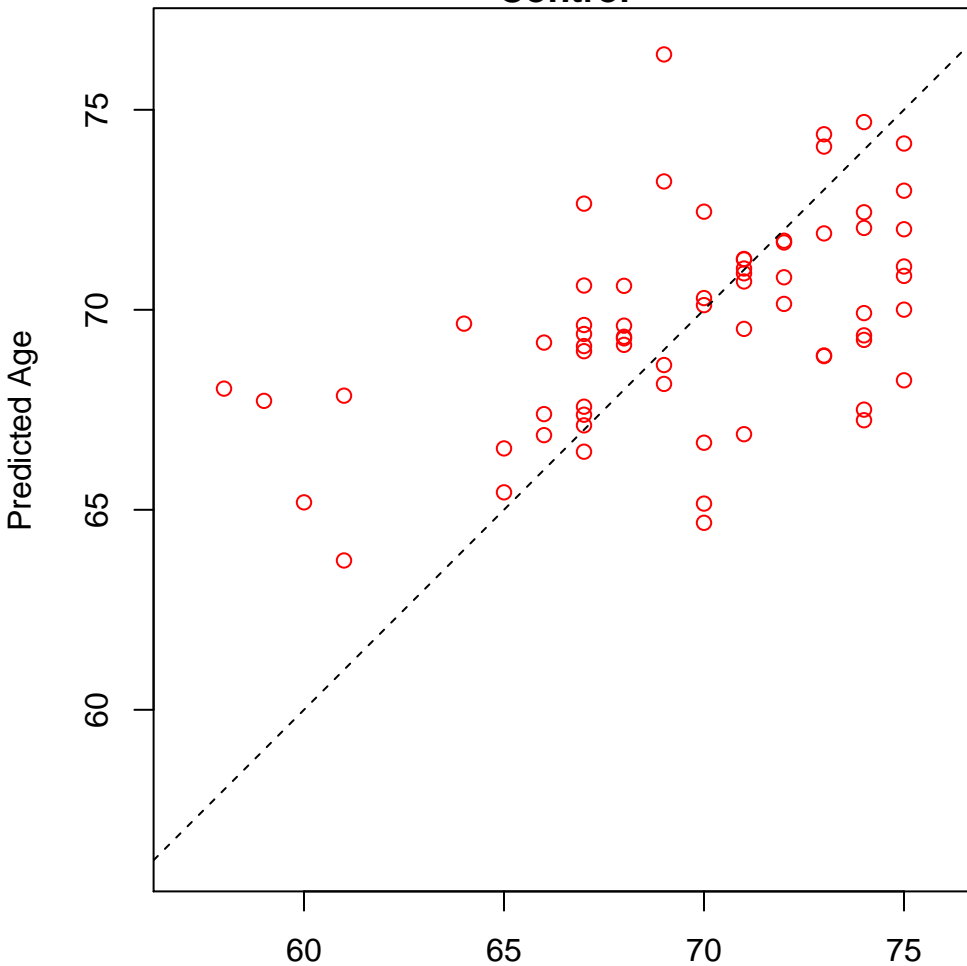


columnar/cuboidal epithelial cell development (Score: 0.761448)

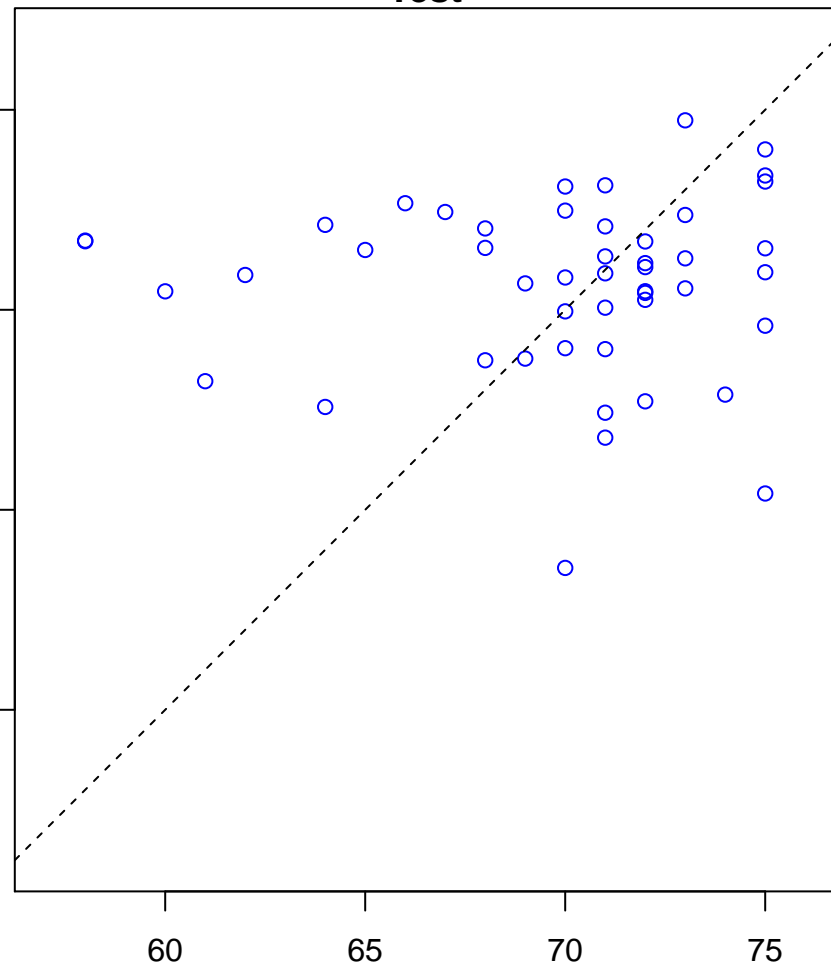


endosome to melanosome transport (Score: 0.760908)

Control



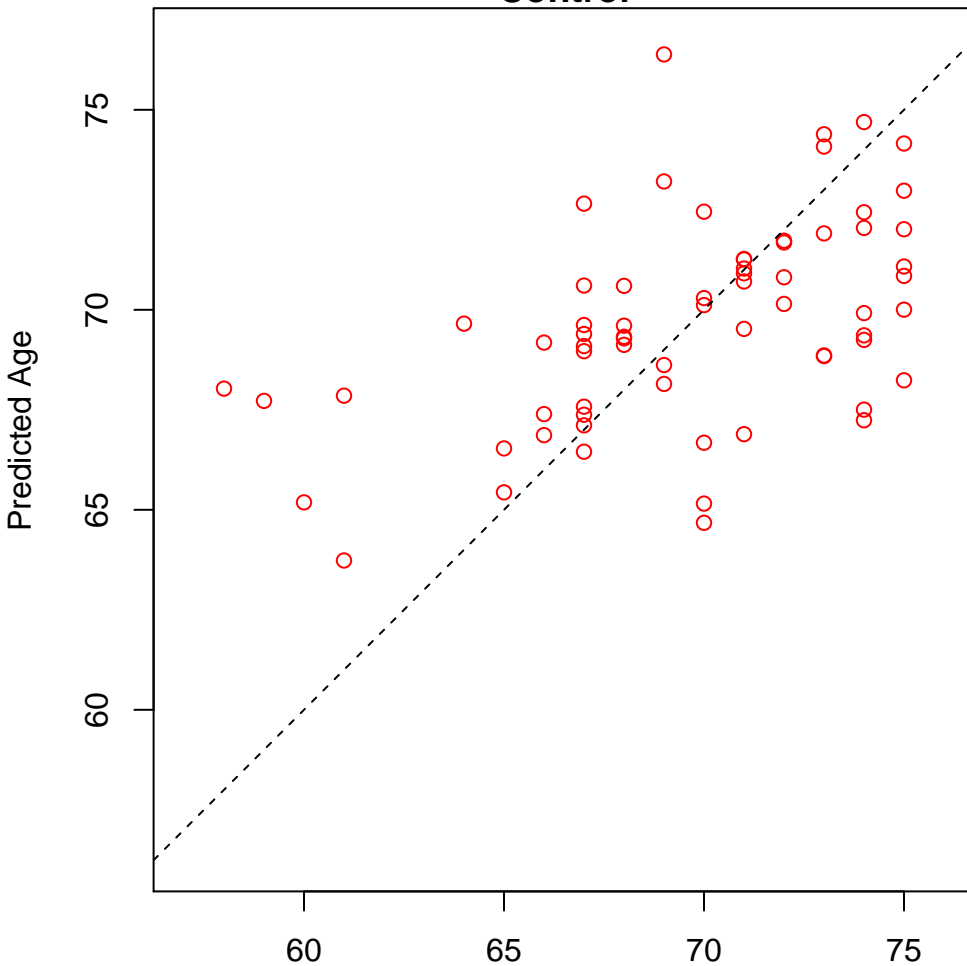
Test



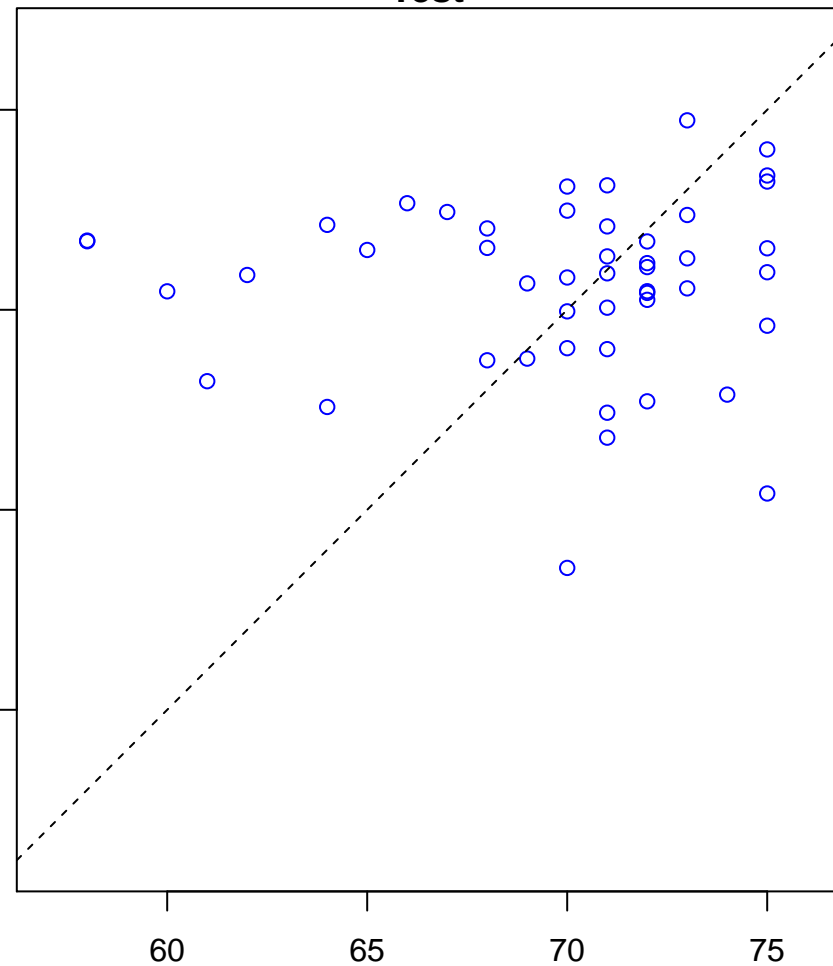
Actual Age

endosome to pigment granule transport (Score: 0.760908)

Control



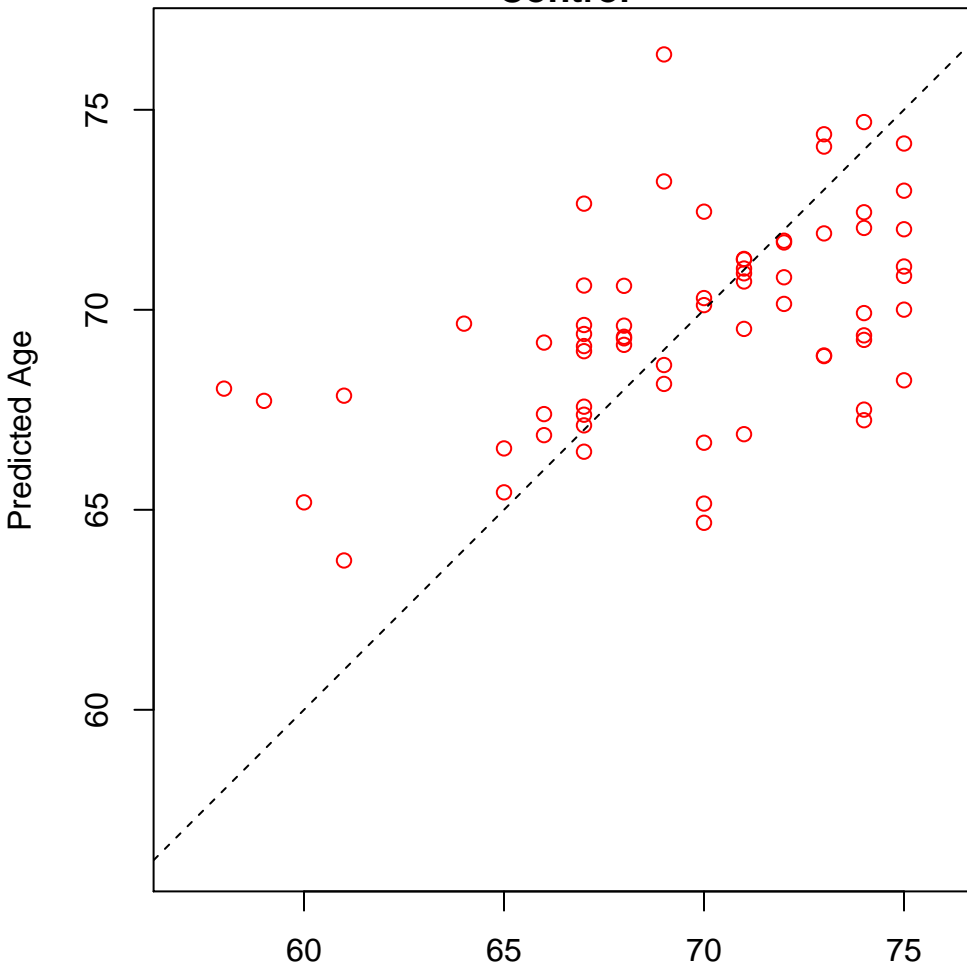
Test



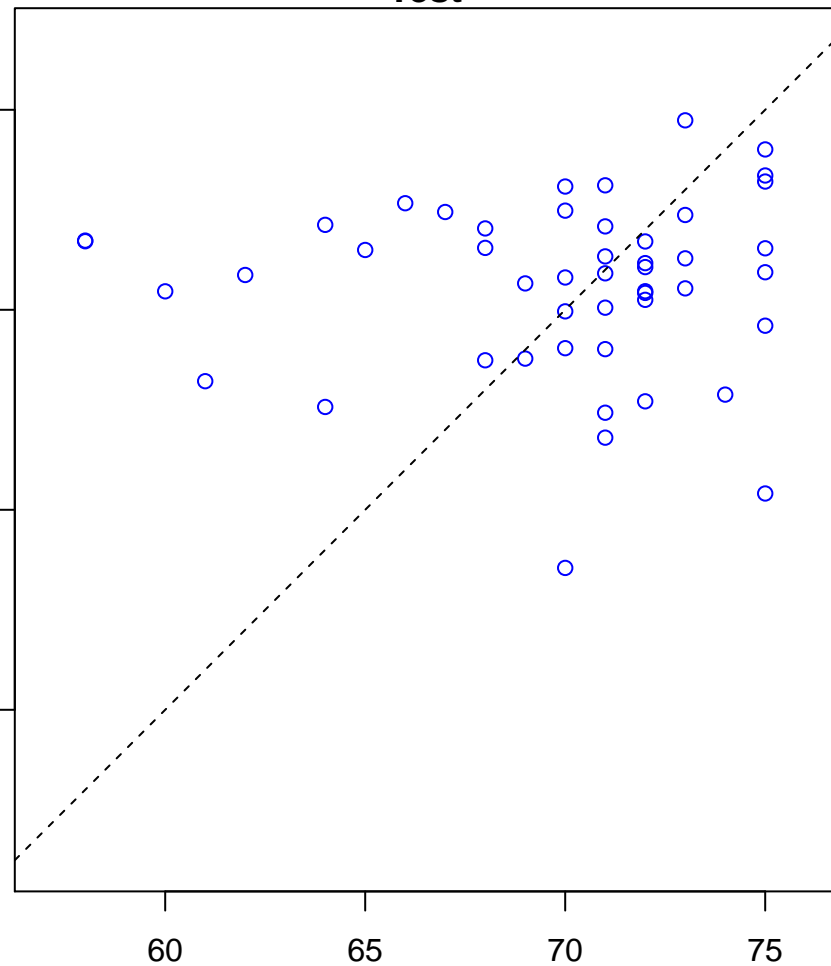
Actual Age

pigment granule maturation (Score: 0.760908)

Control

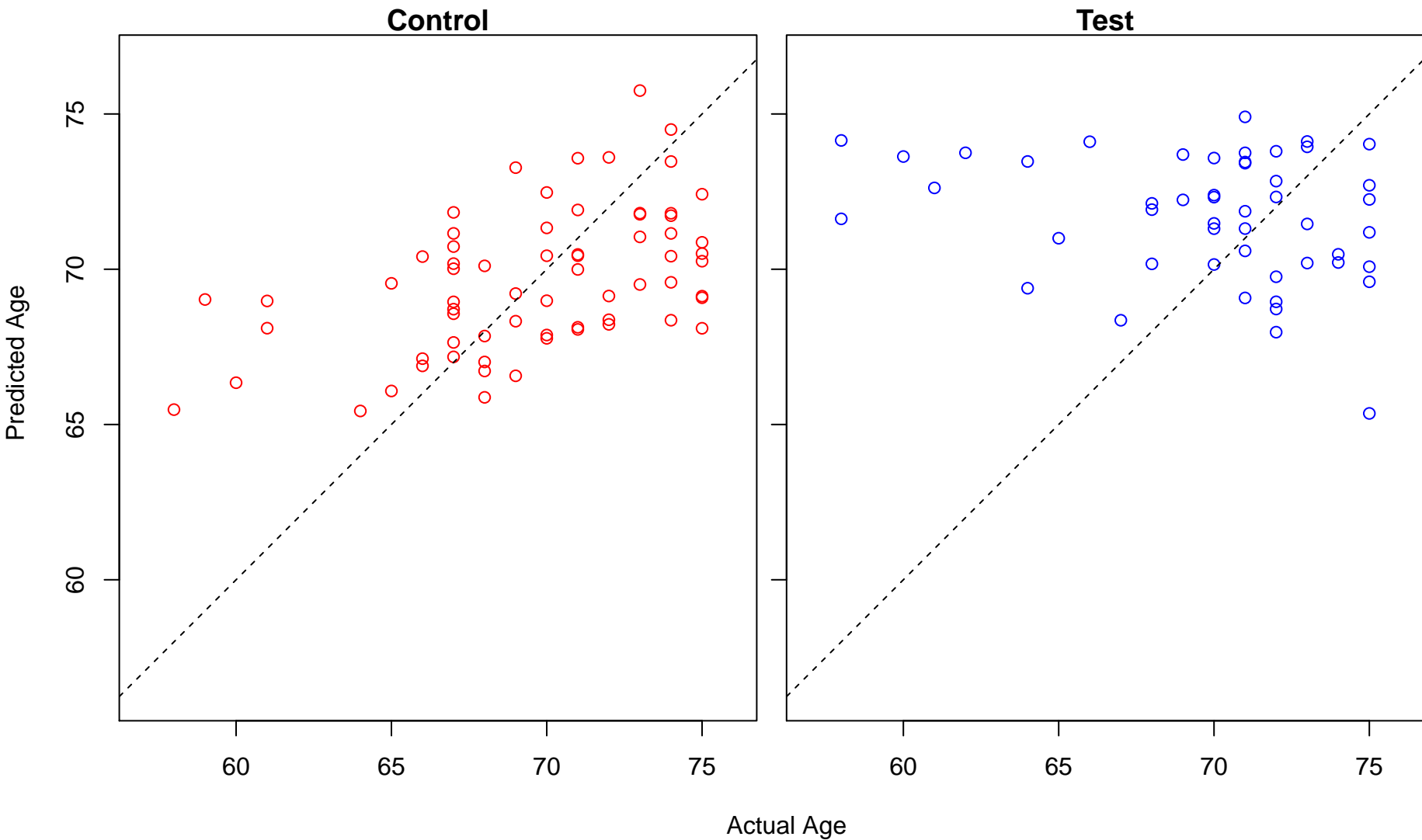


Test



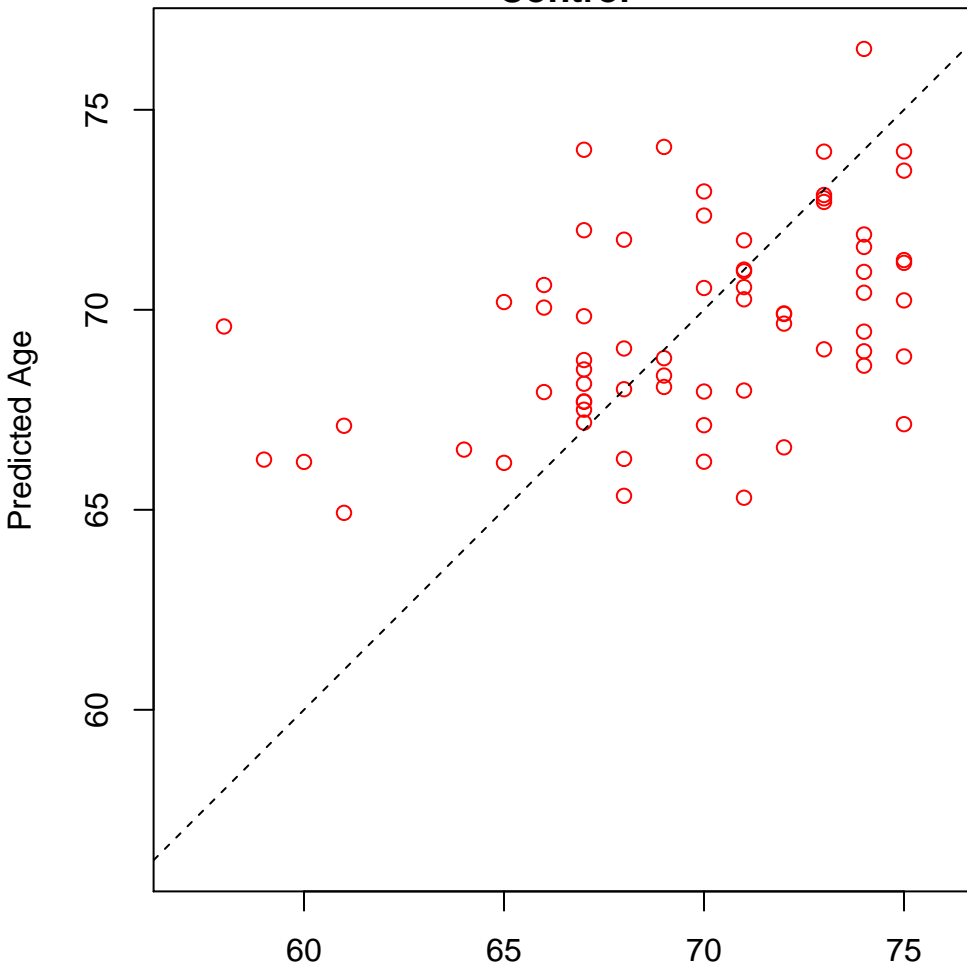
Actual Age

cellular response to gonadotropin stimulus (Score: 0.760688)

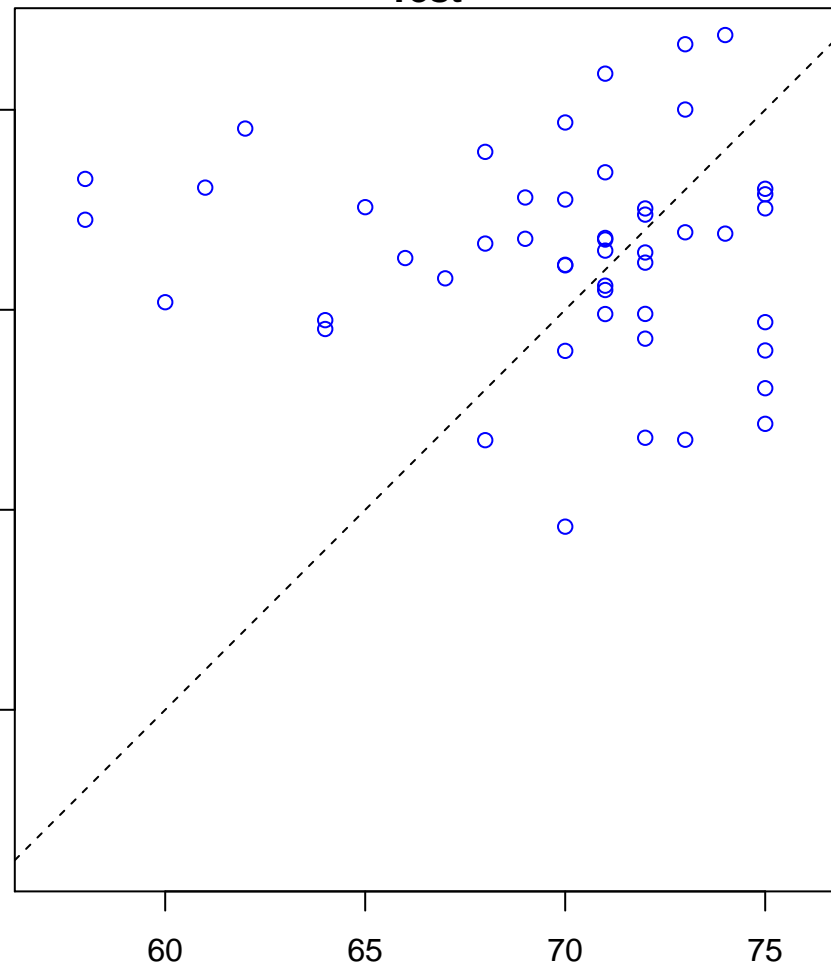


regulation of microtubule polymerization (Score: 0.760667)

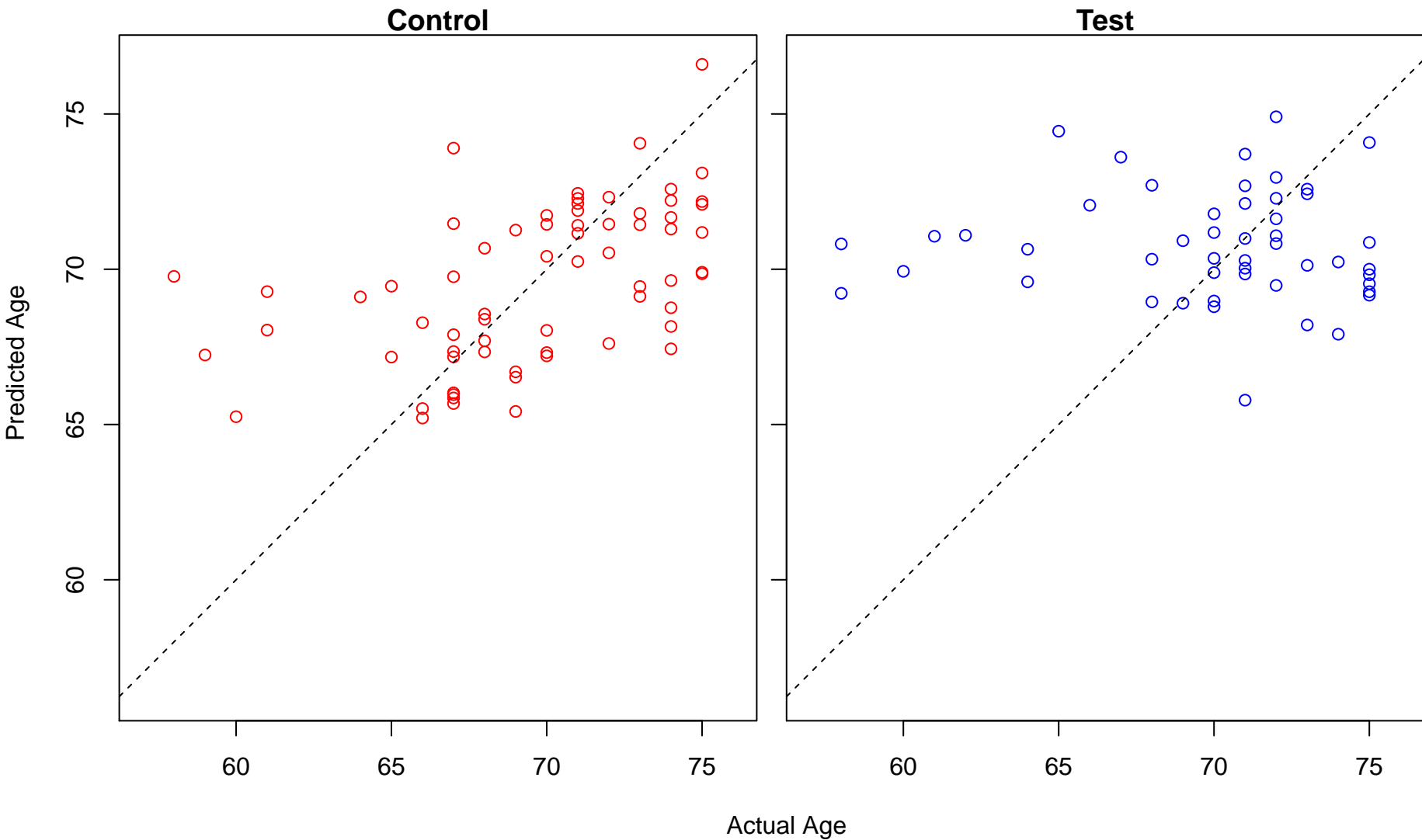
Control



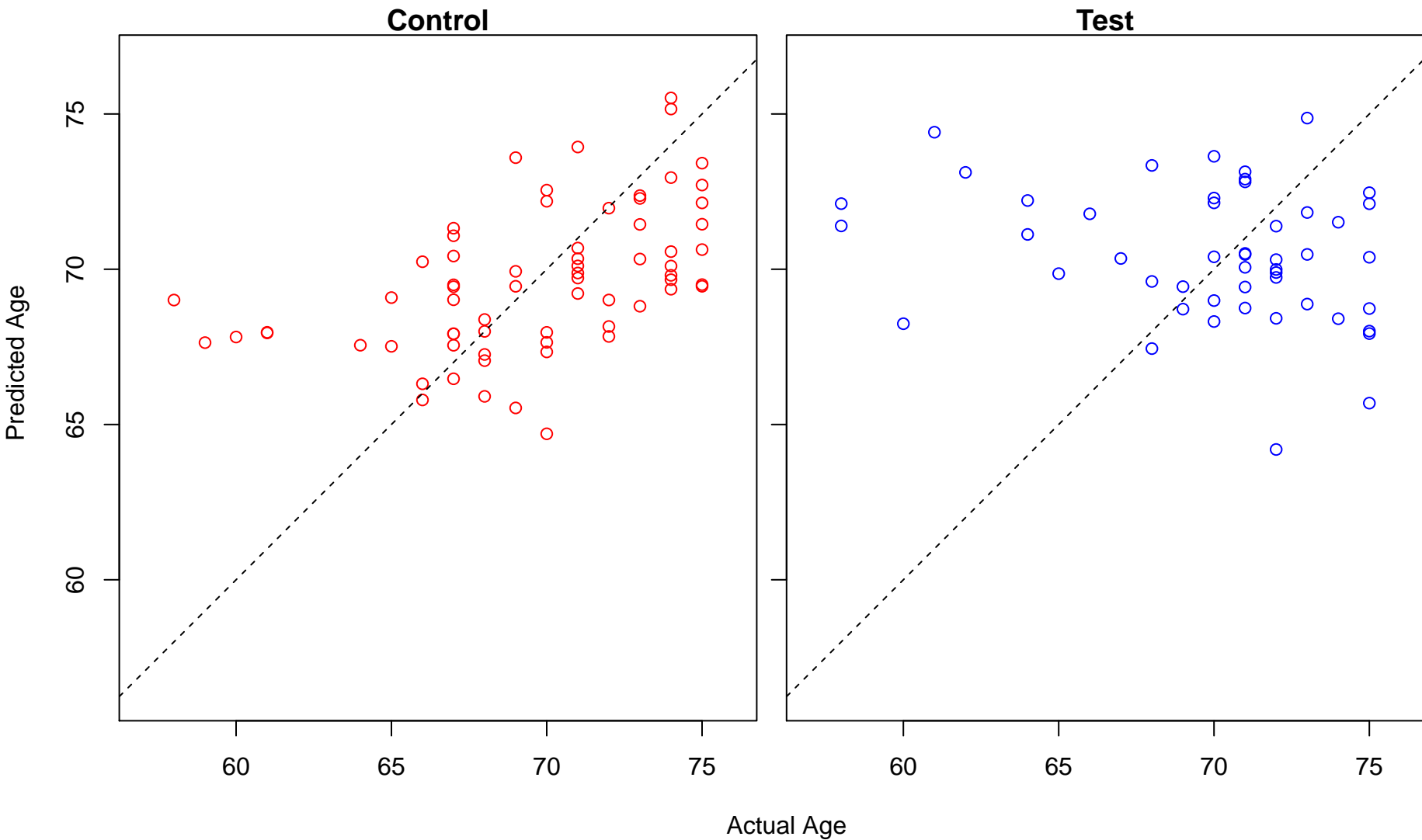
Test



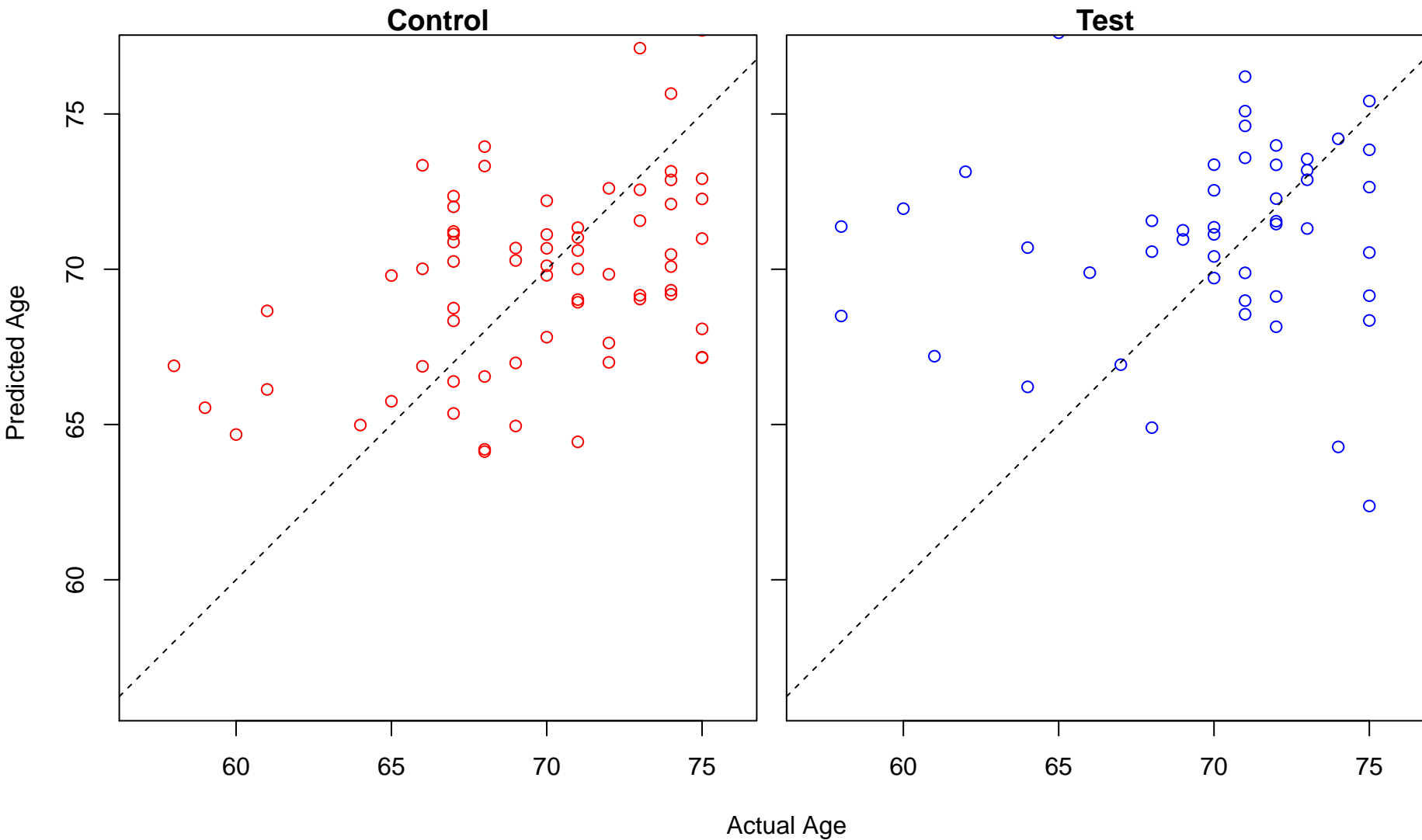
cellular glucose homeostasis (Score: 0.760310)



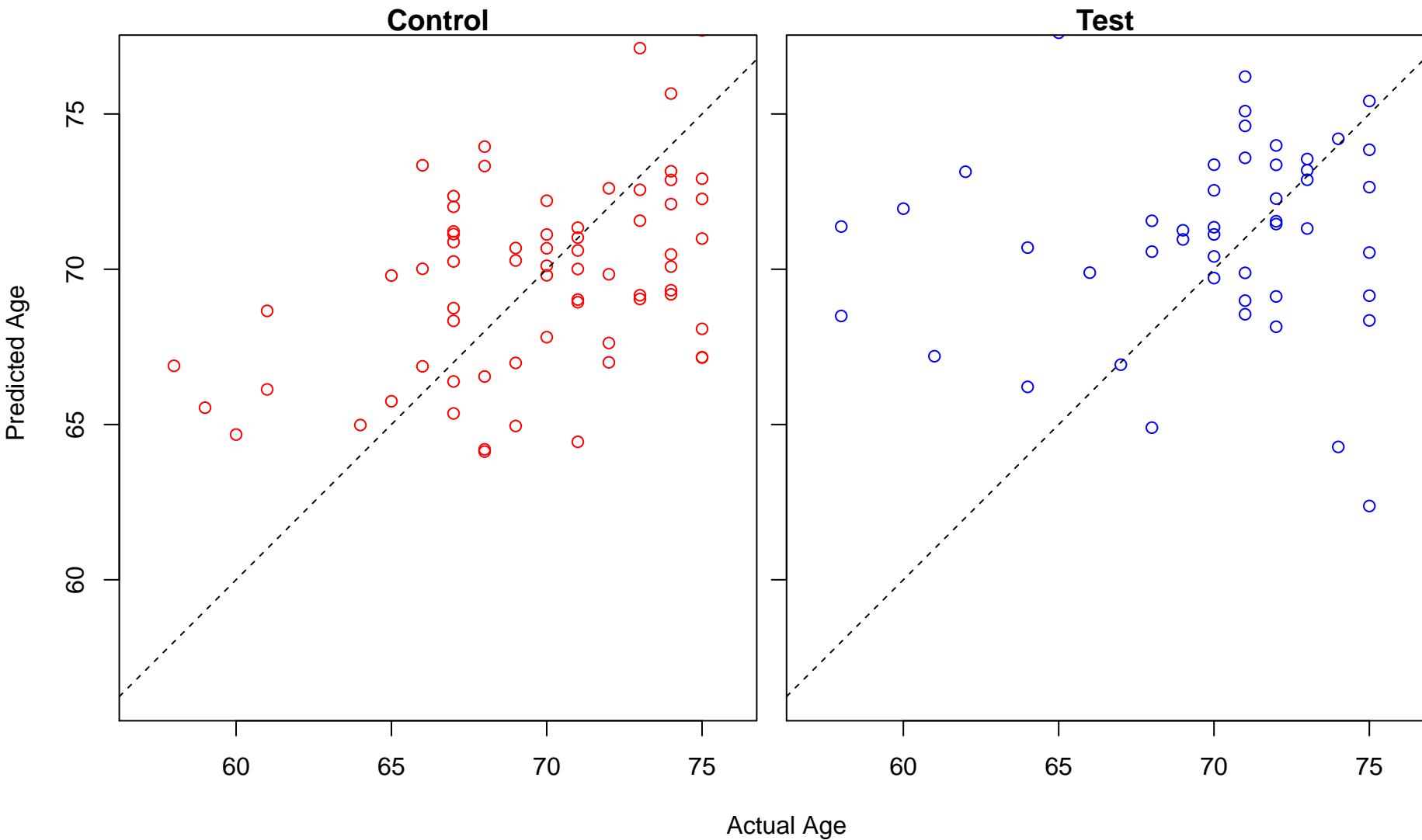
peptidyl-lysine dimethylation (Score: 0.760257)



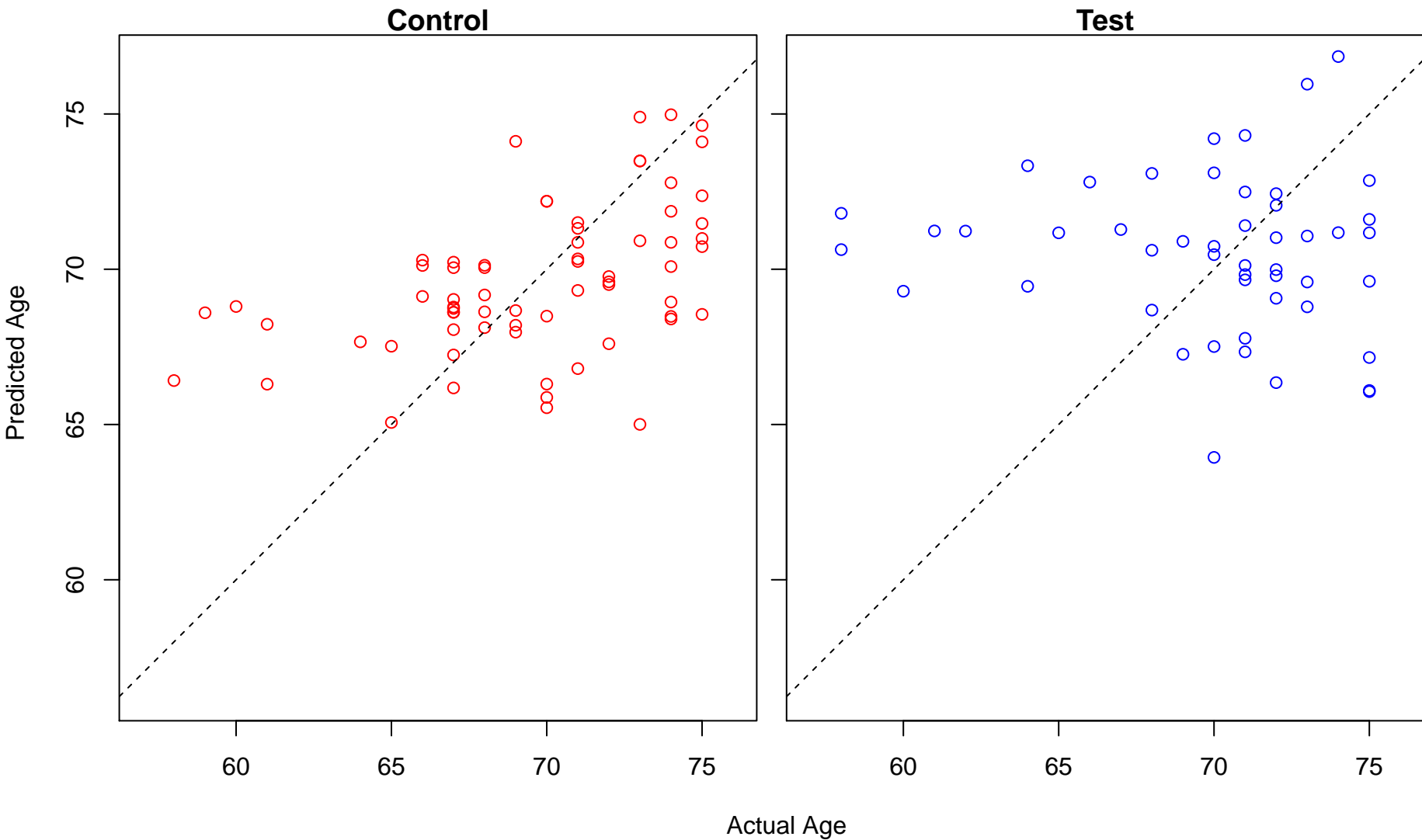
catecholamine metabolic process (Score: 0.760087)



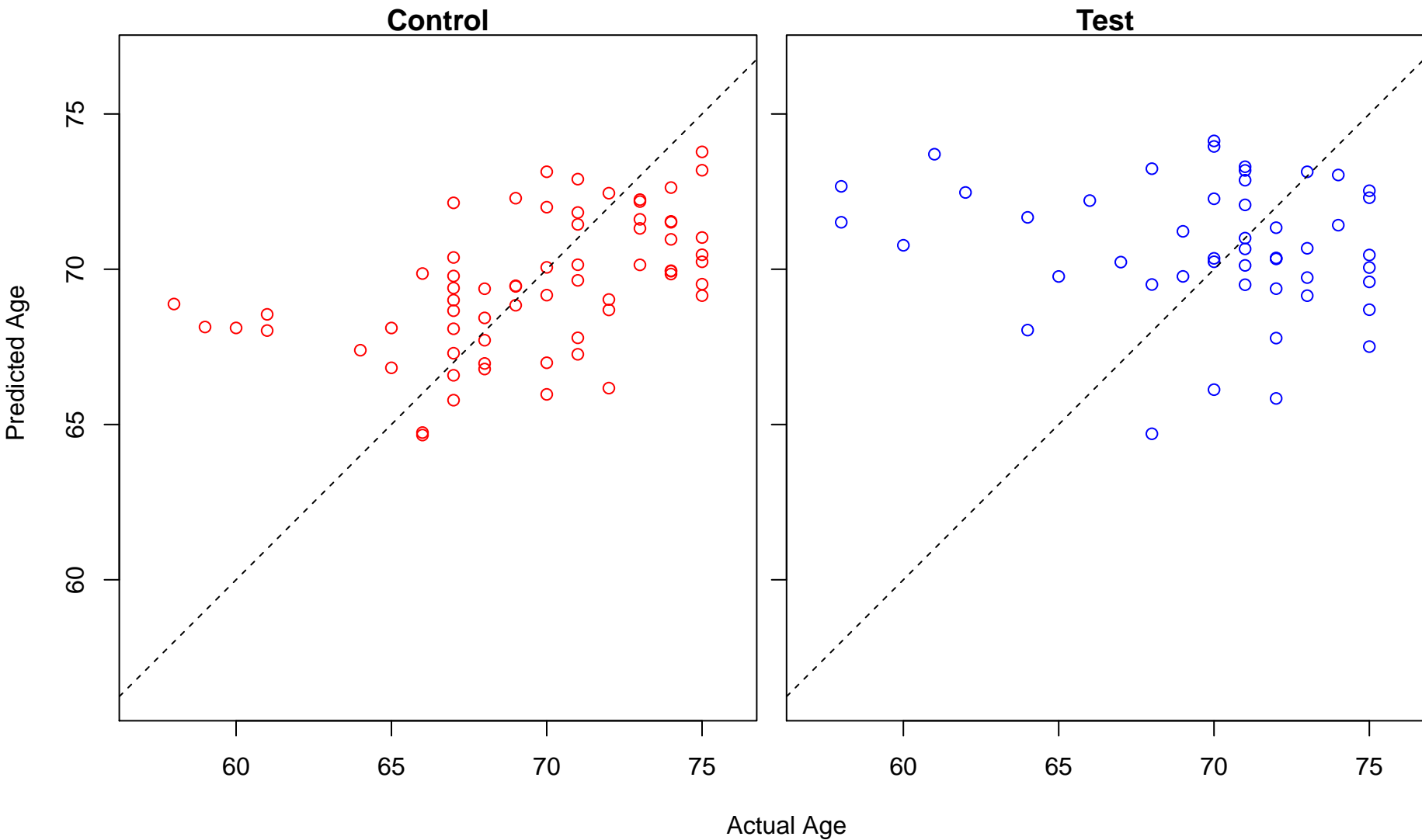
catechol-containing compound metabolic process (Score: 0.760087)



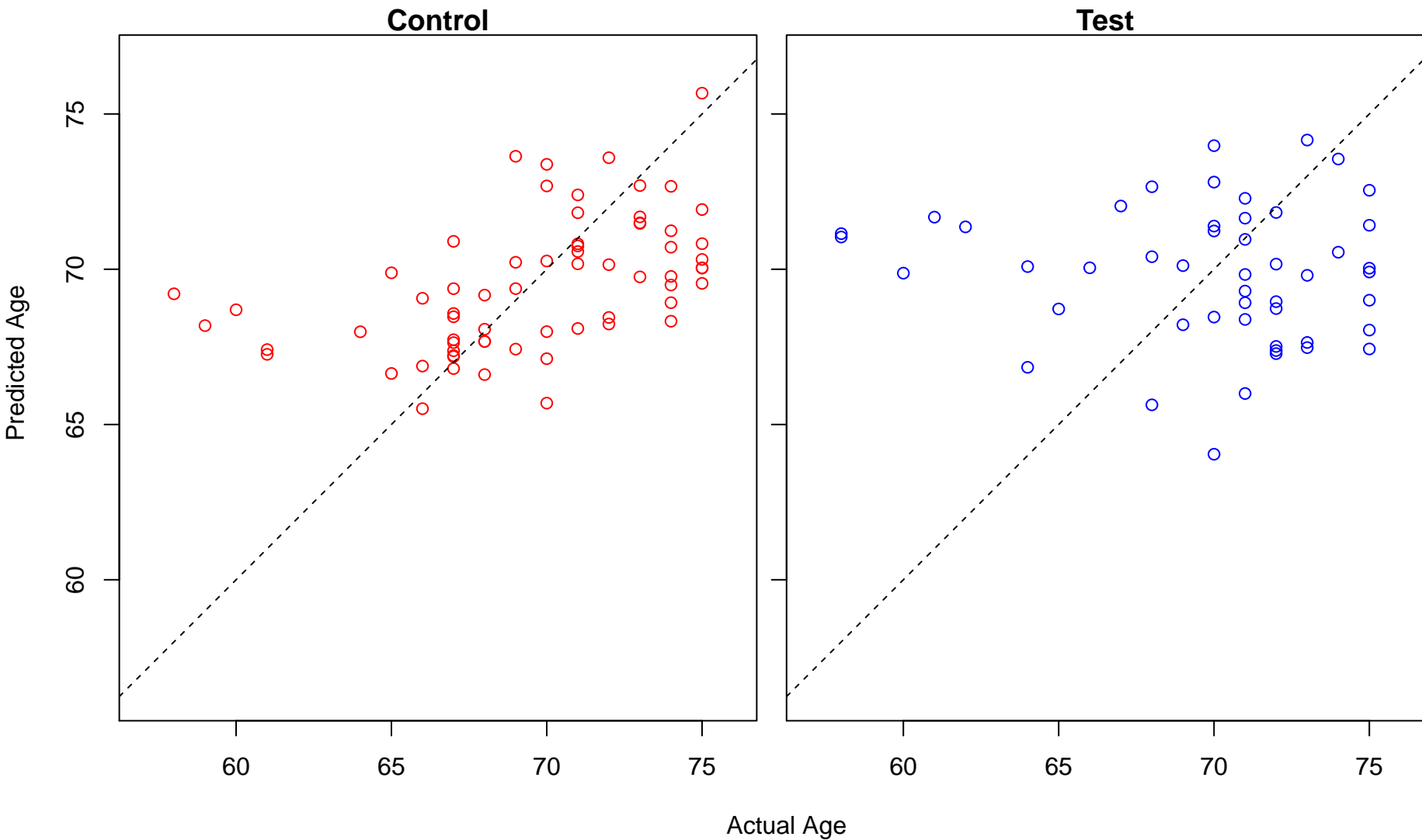
positive regulation of extracellular matrix organization (Score: 0.760082)



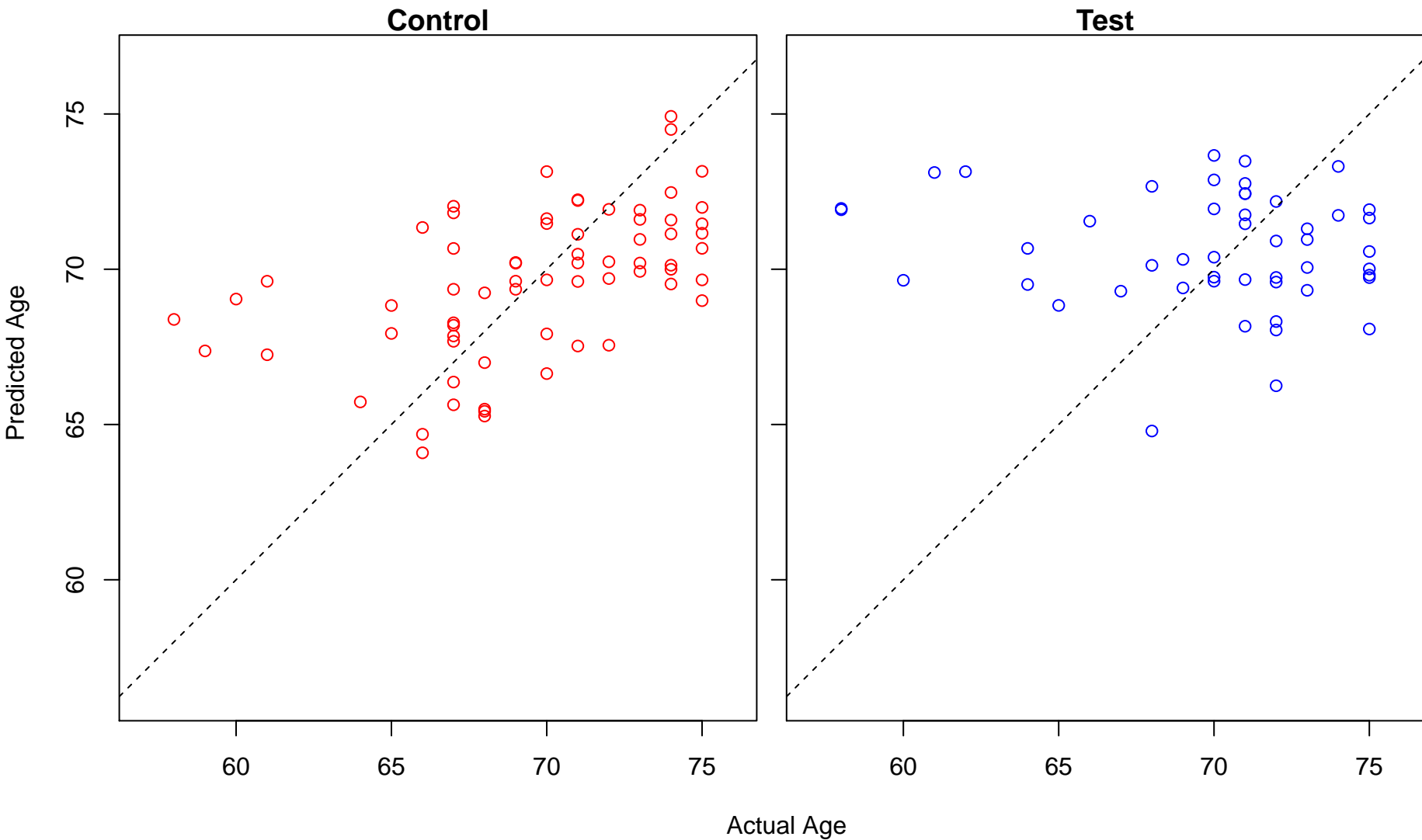
regulation of synaptic plasticity (Score: 0.759226)



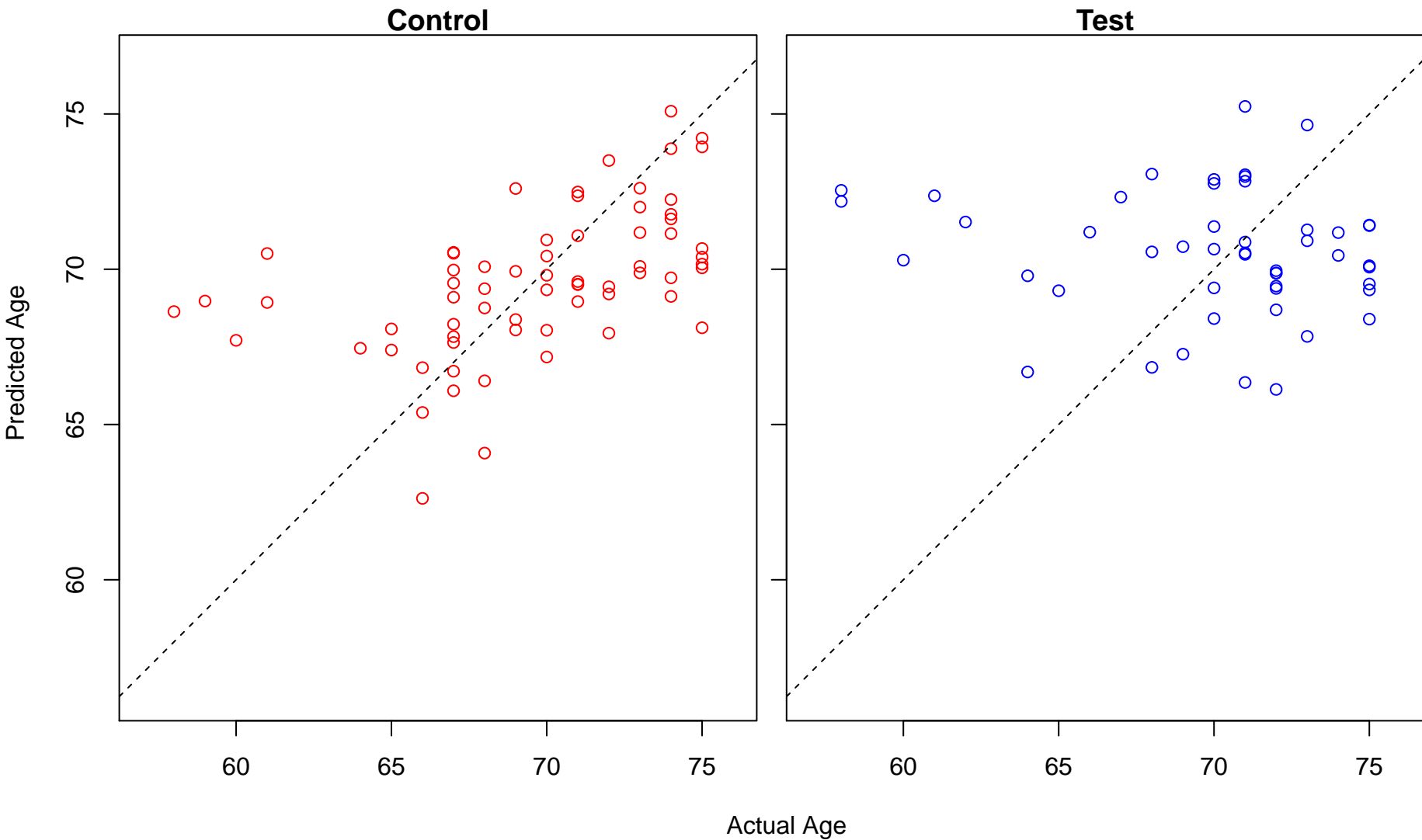
negative regulation of axonogenesis (Score: 0.758899)



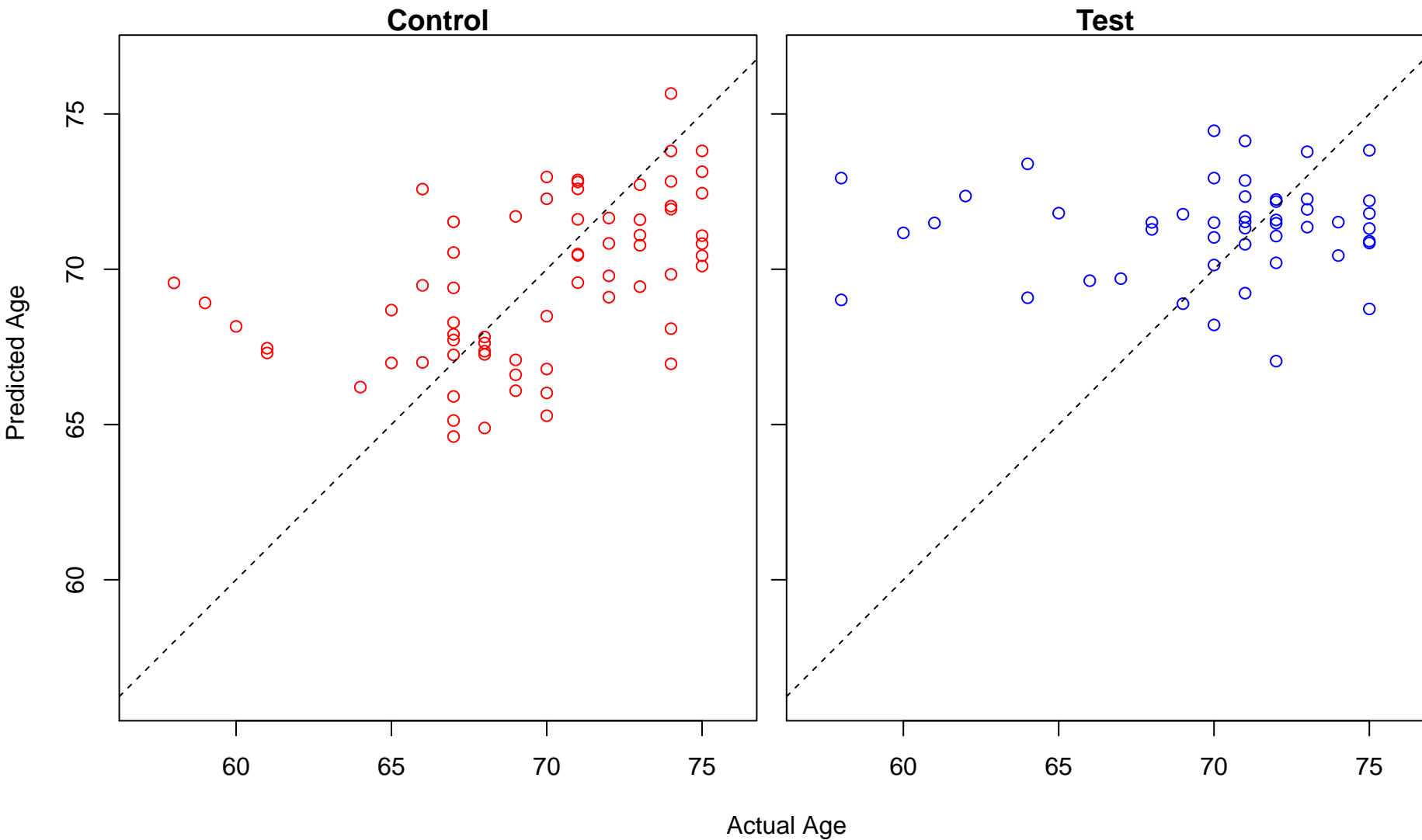
muscle adaptation (Score: 0.758238)



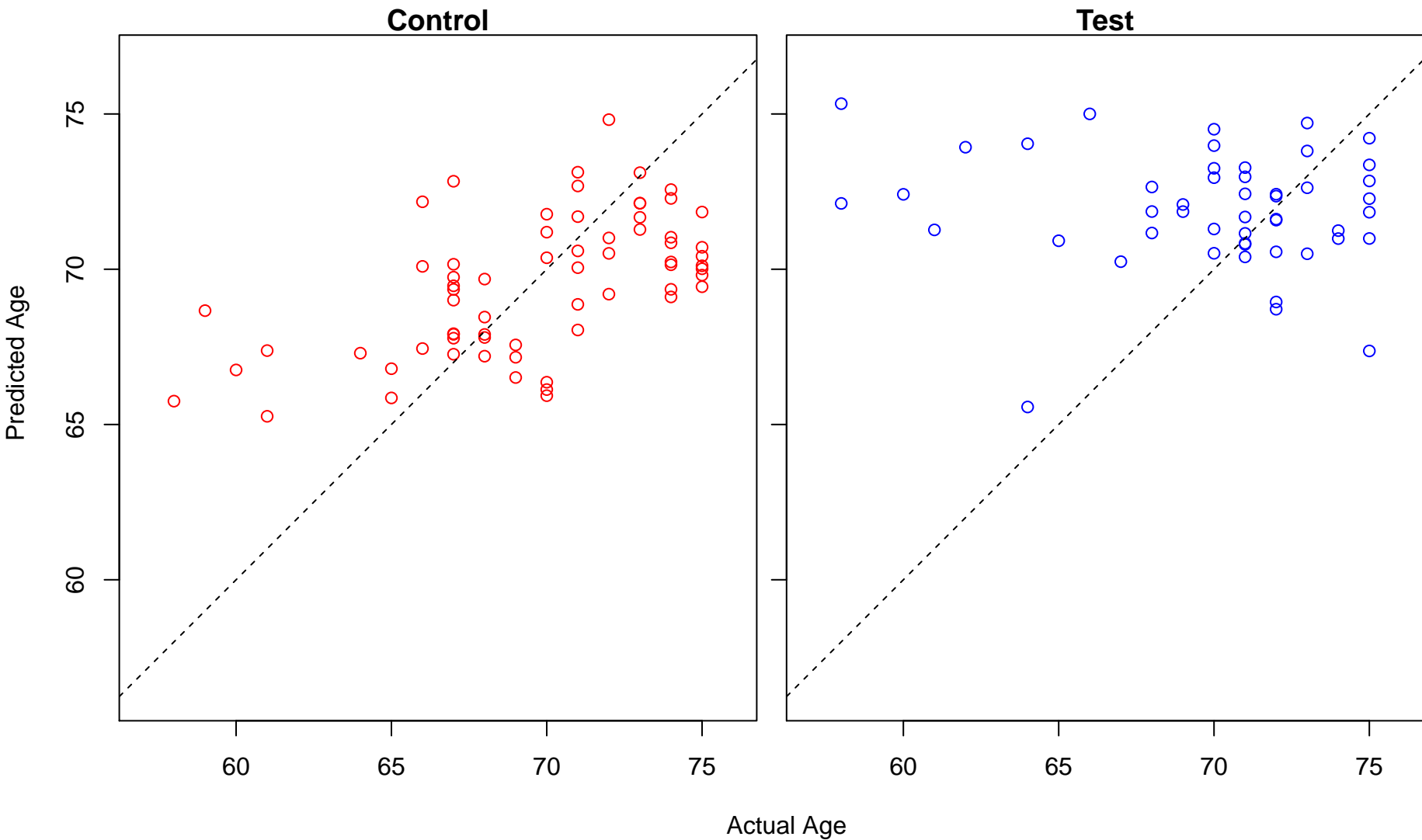
thiamine-containing compound metabolic process (Score: 0.758236)



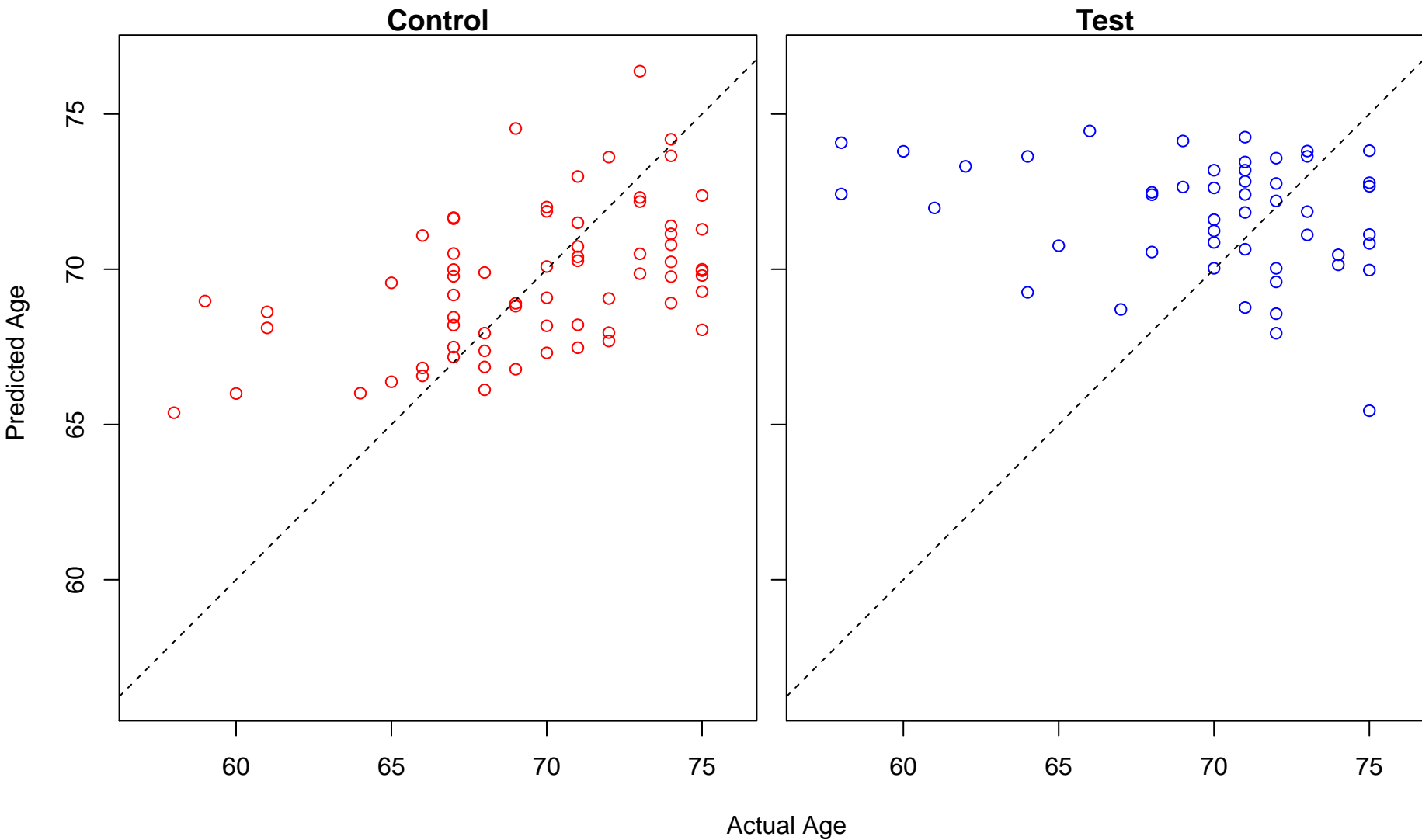
positive regulation of intracellular steroid hormone receptor signaling pathway (Score: 0.757775)



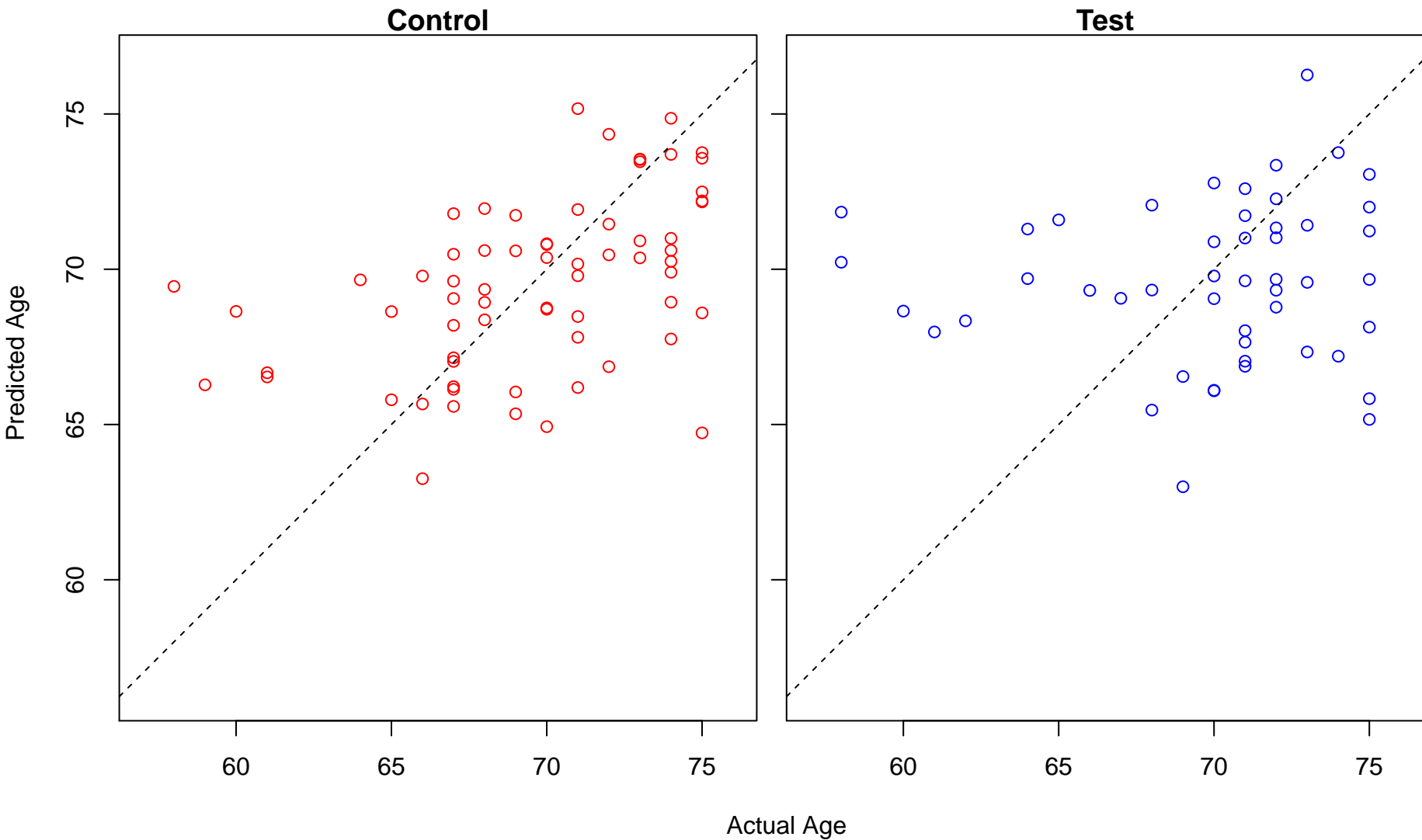
platelet-derived growth factor receptor signaling pathway (Score: 0.757543)



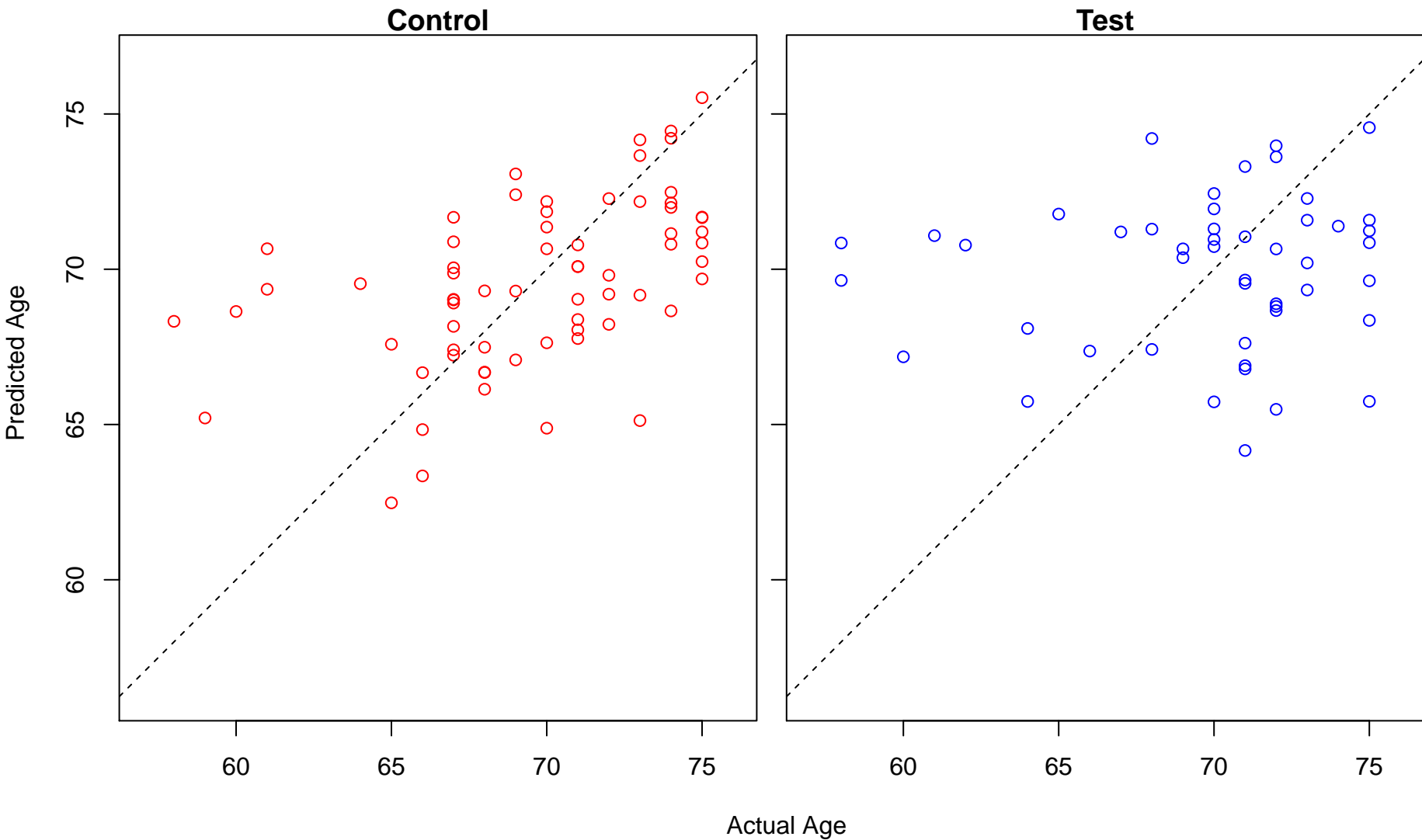
heart valve formation (Score: 0.756828)



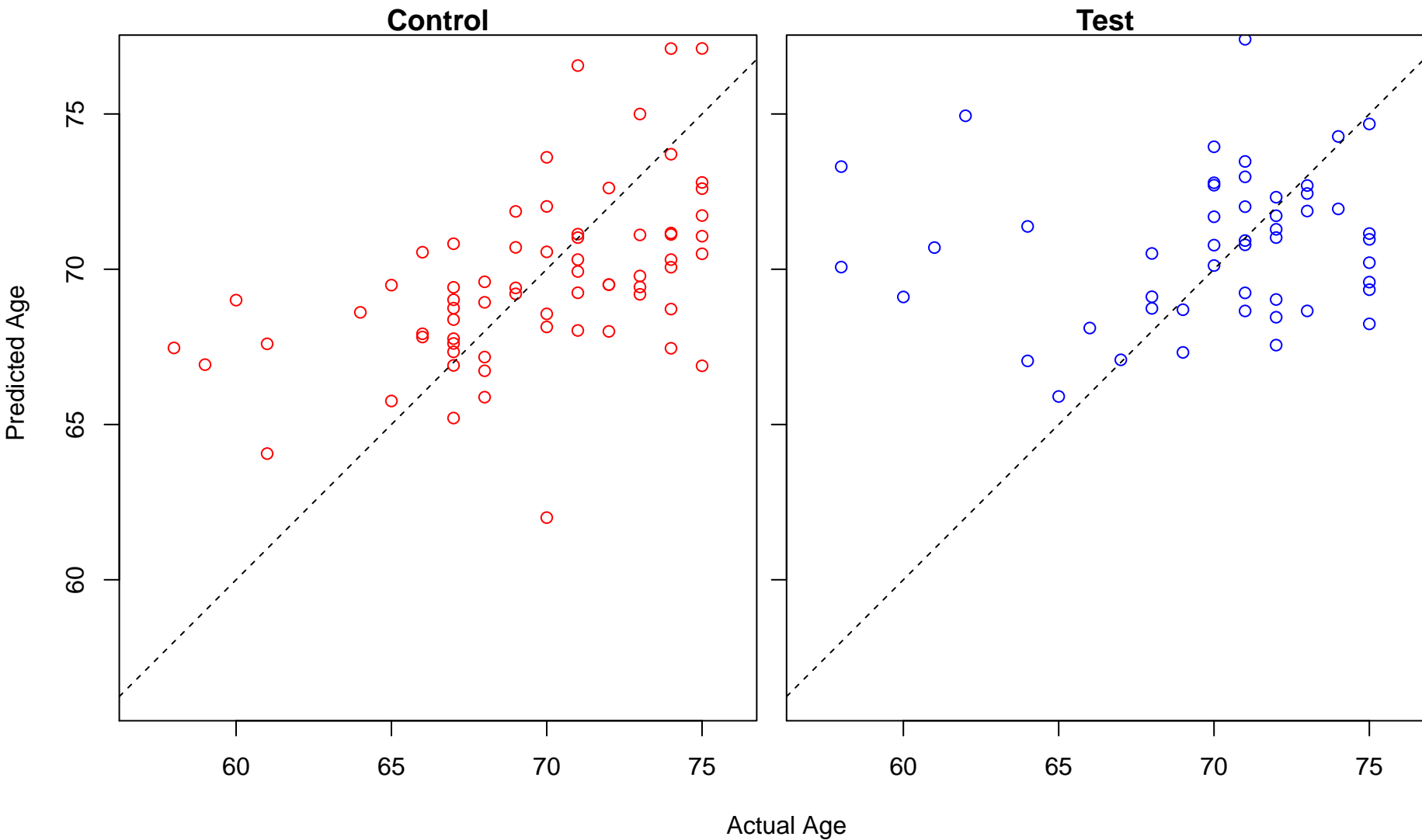
cell communication by electrical coupling involved in cardiac conduction (Score: 0.755968)



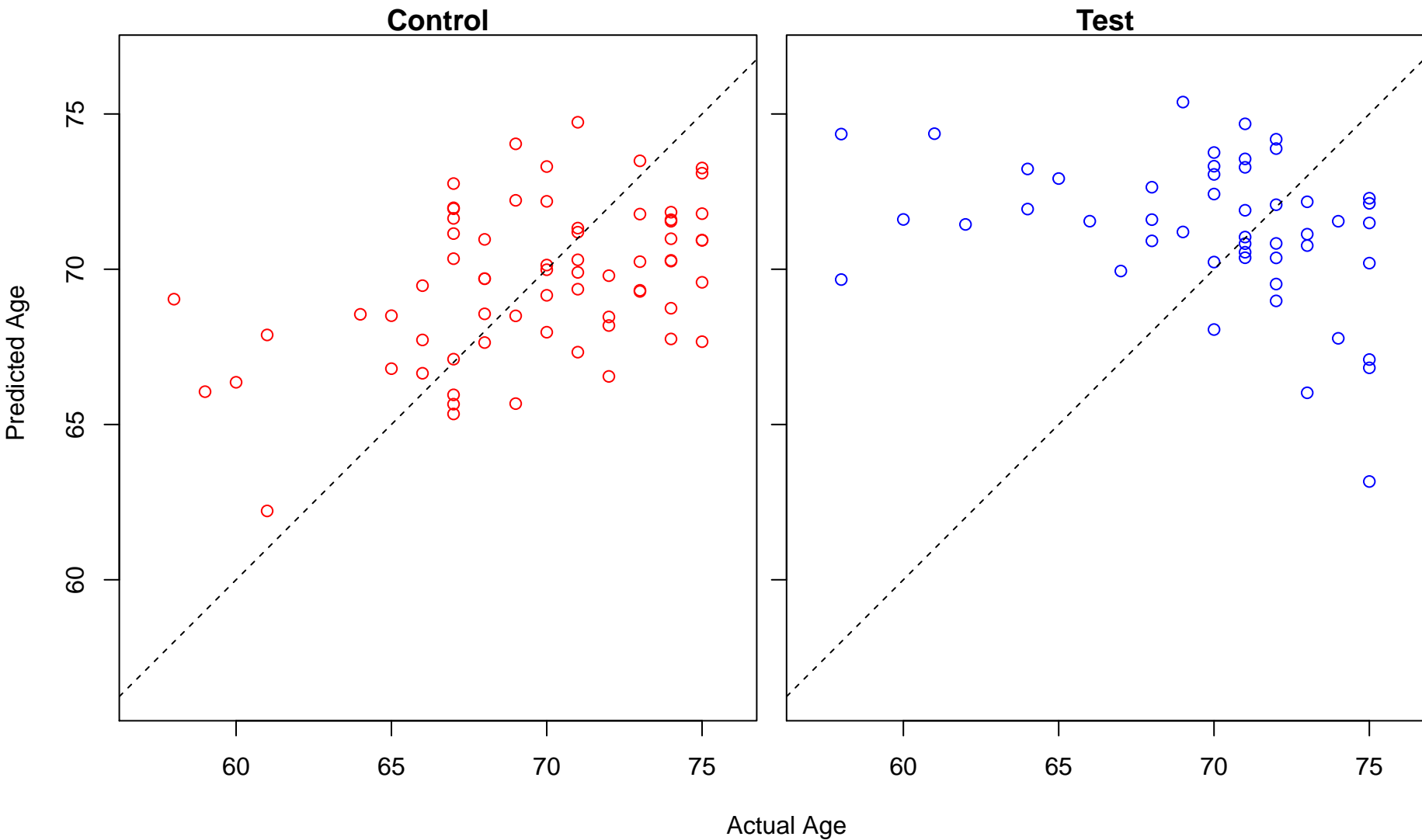
Age response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator



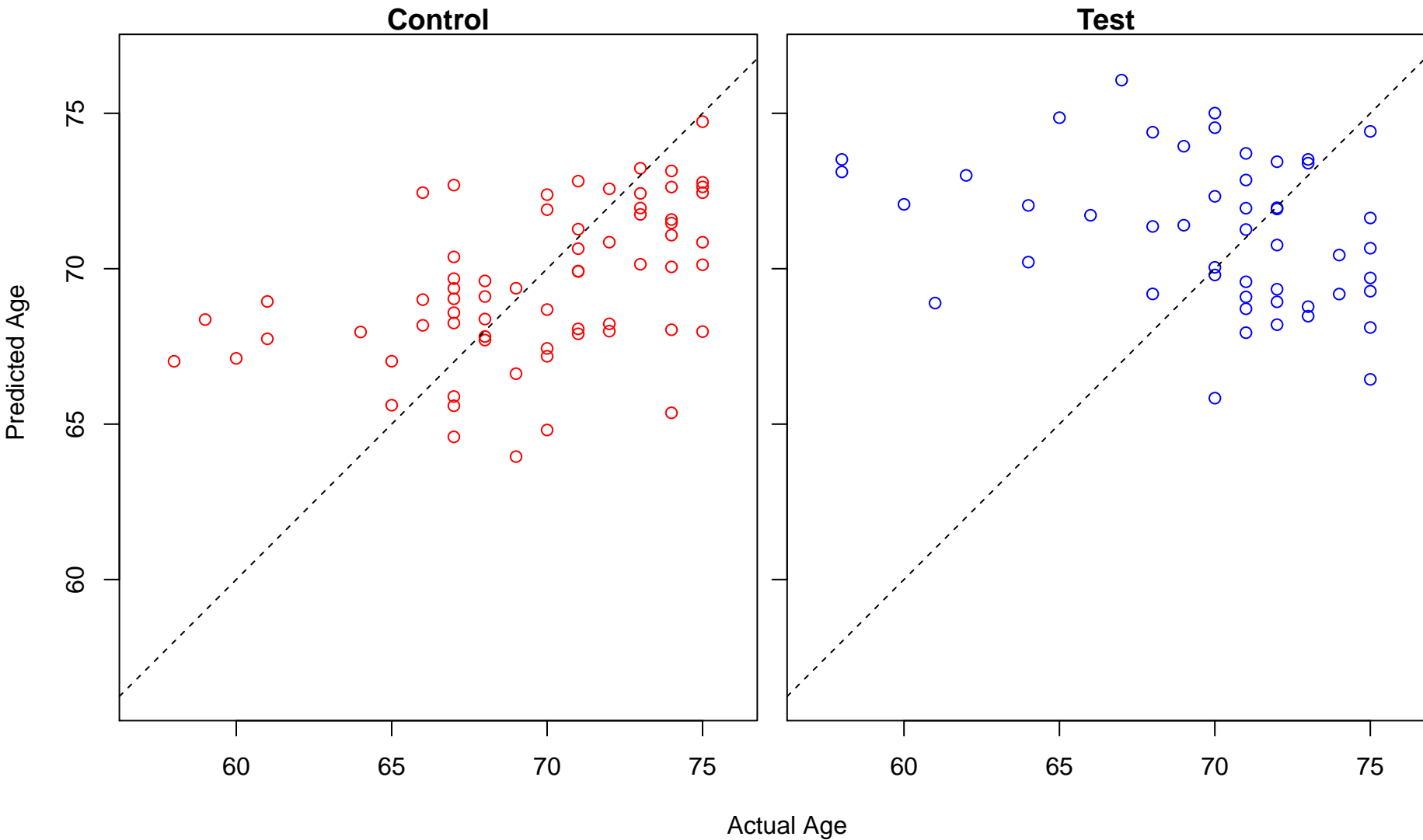
positive regulation of histone deacetylation (Score: 0.755861)



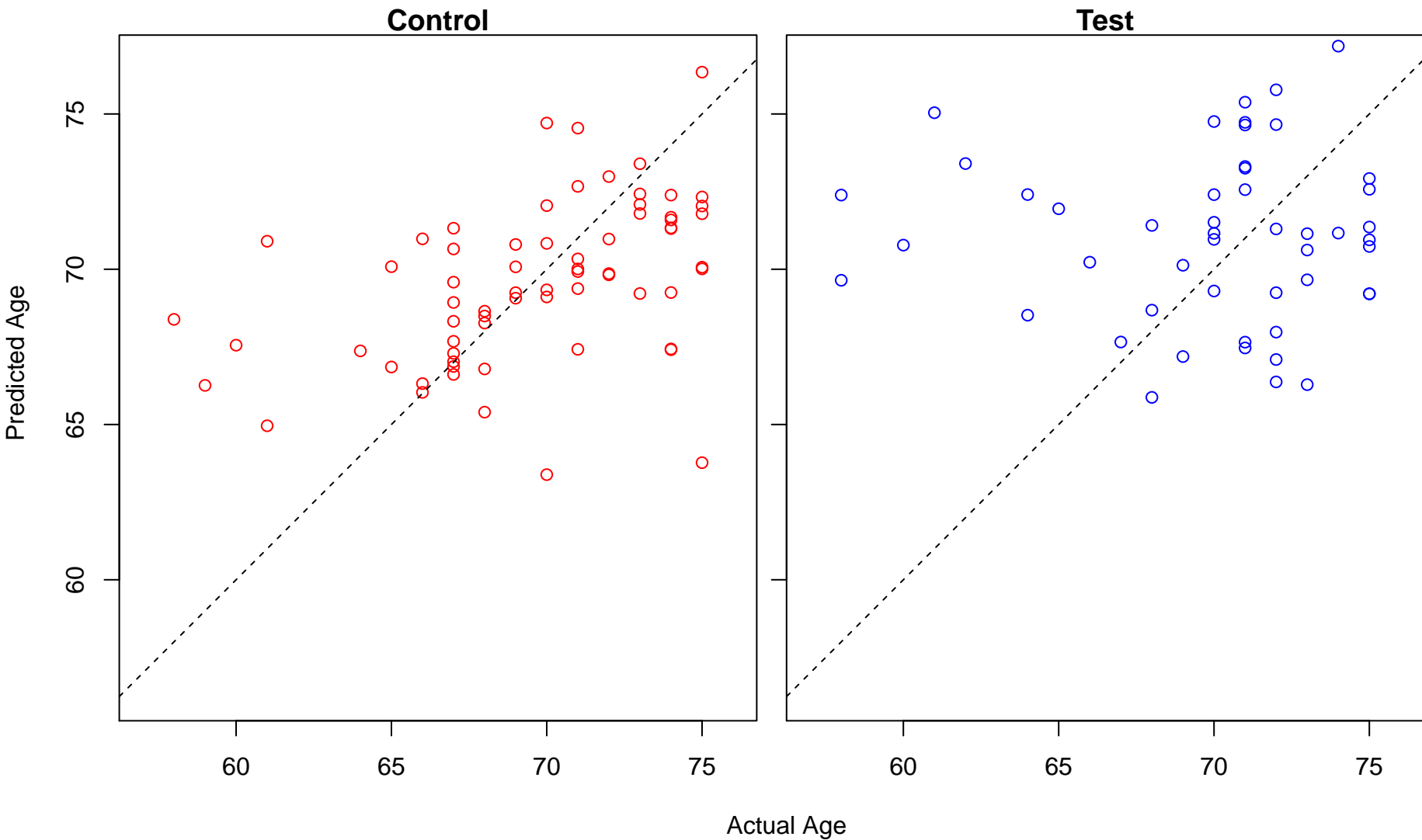
mitochondrial tRNA processing (Score: 0.755600)



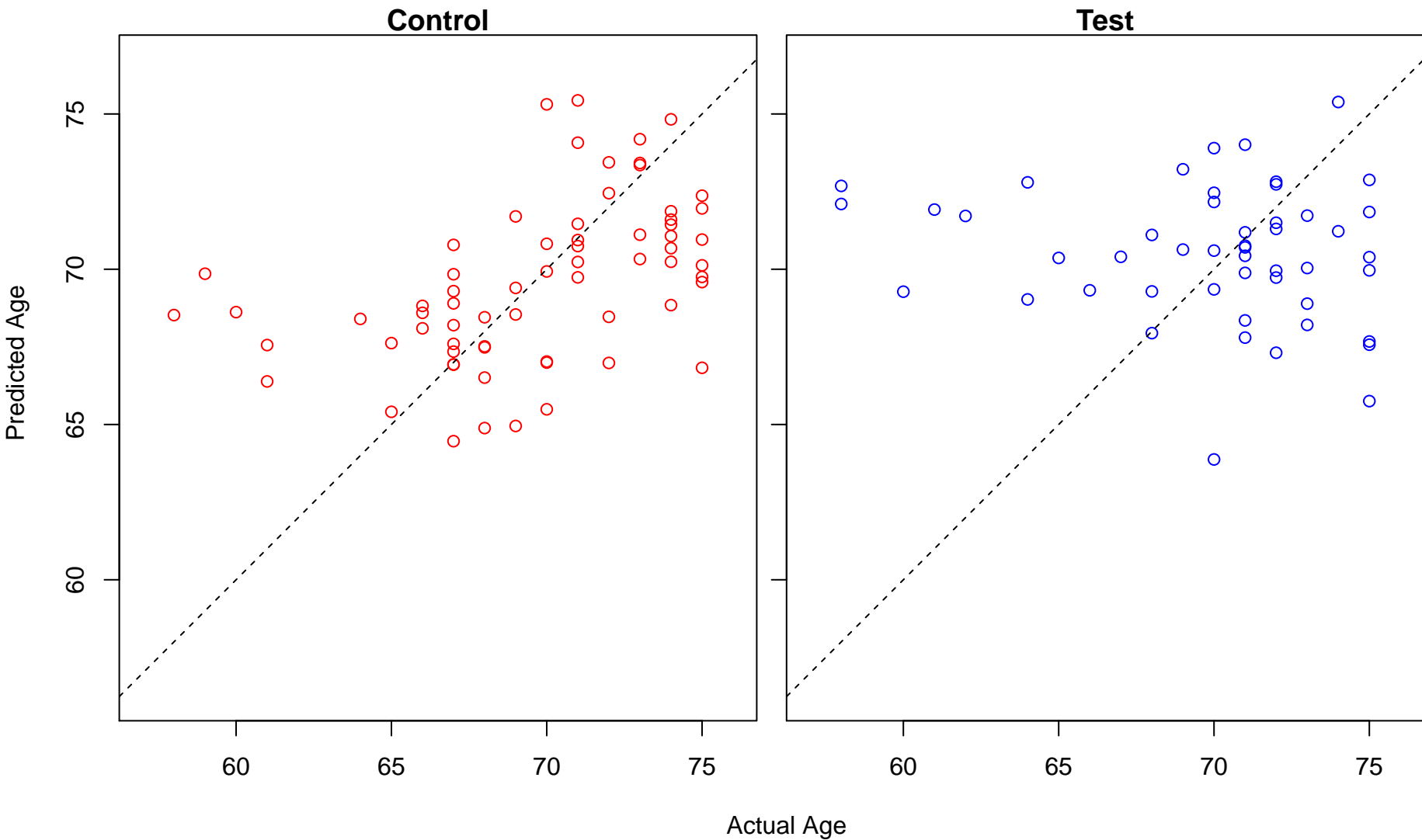
positive regulation of reproductive process (Score: 0.755481)



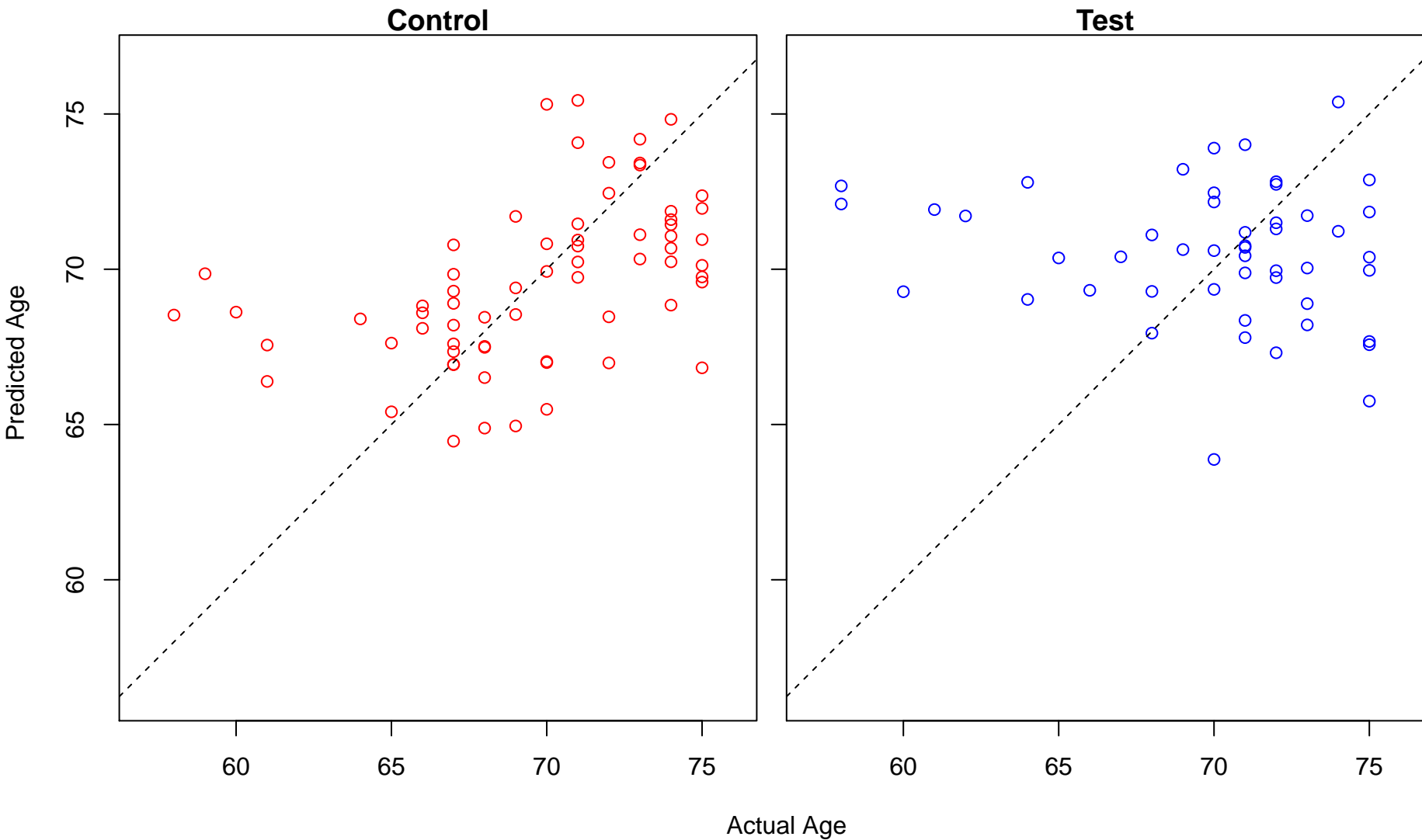
histone H4-R3 methylation (Score: 0.754949)



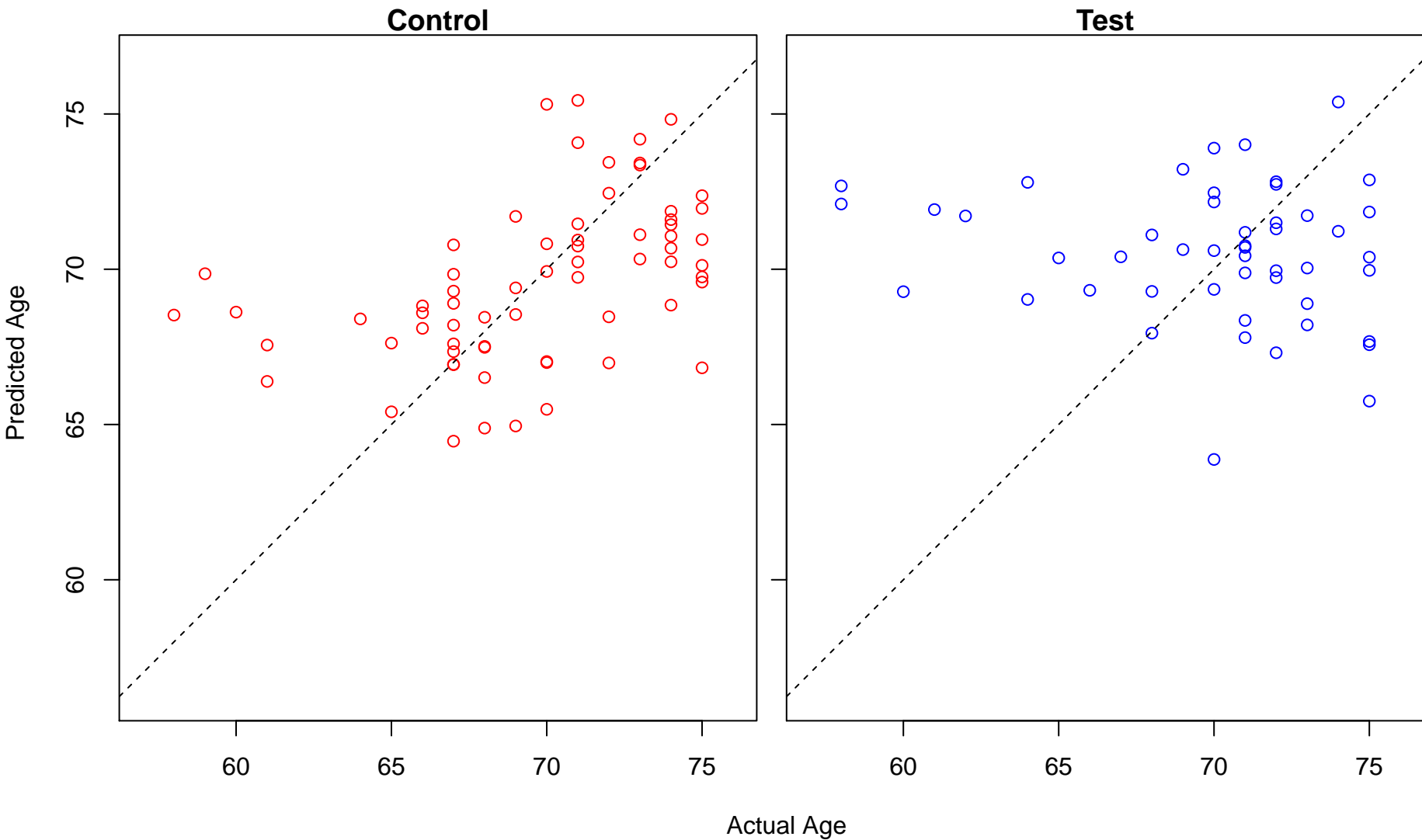
alpha-beta T cell activation involved in immune response (Score: 0.754156)



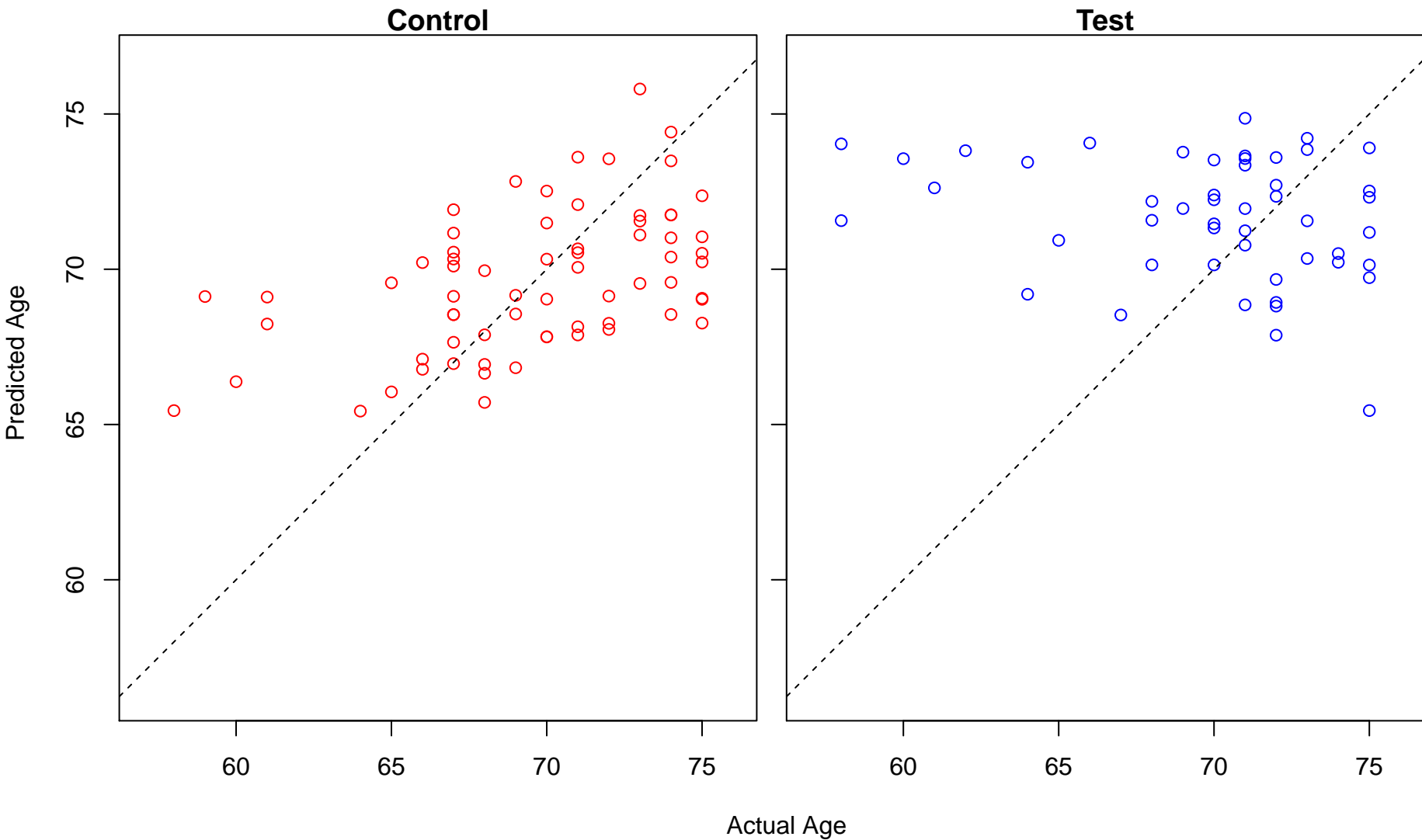
T cell differentiation involved in immune response (Score: 0.754156)



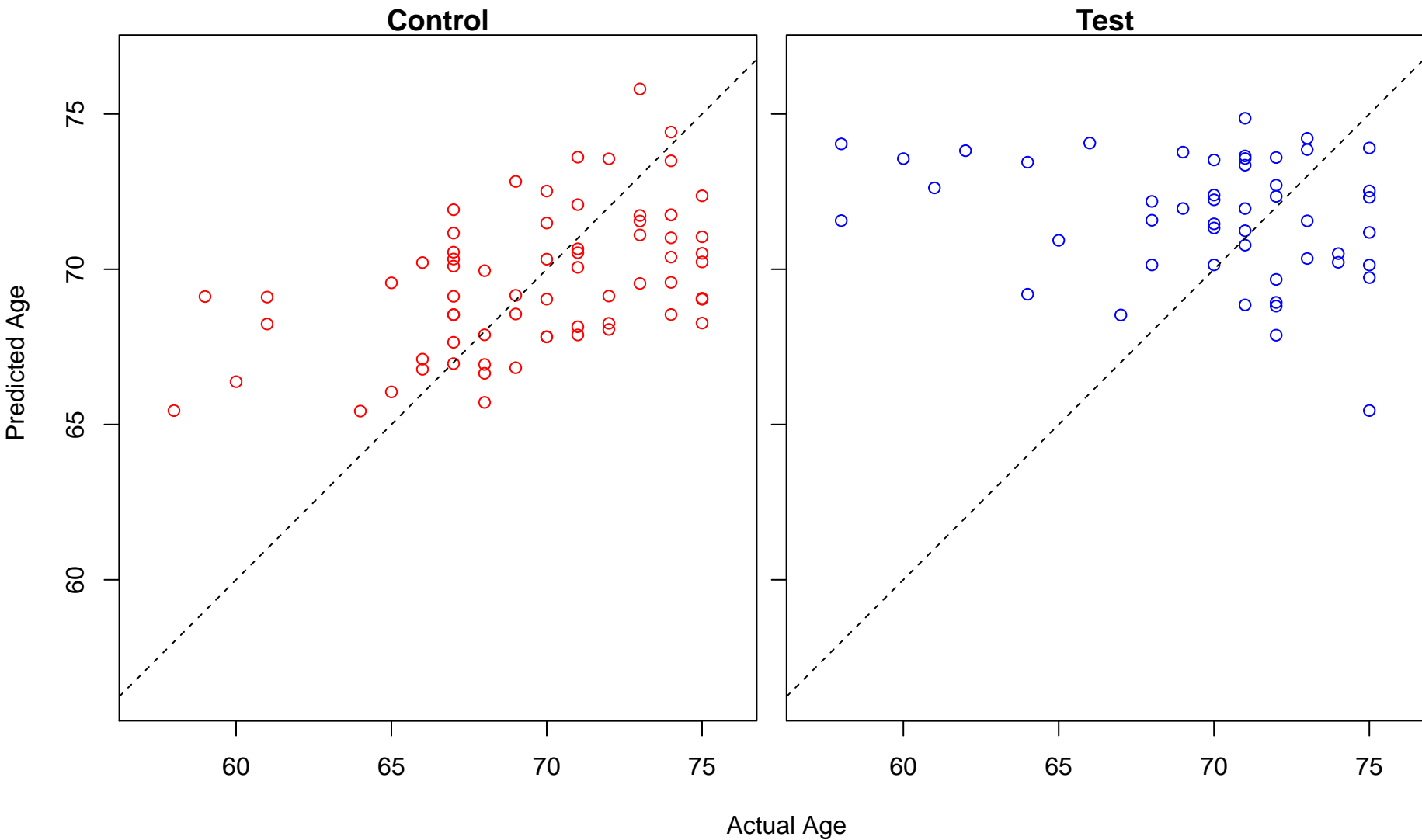
alpha-beta T cell differentiation involved in immune response (Score: 0.754156)



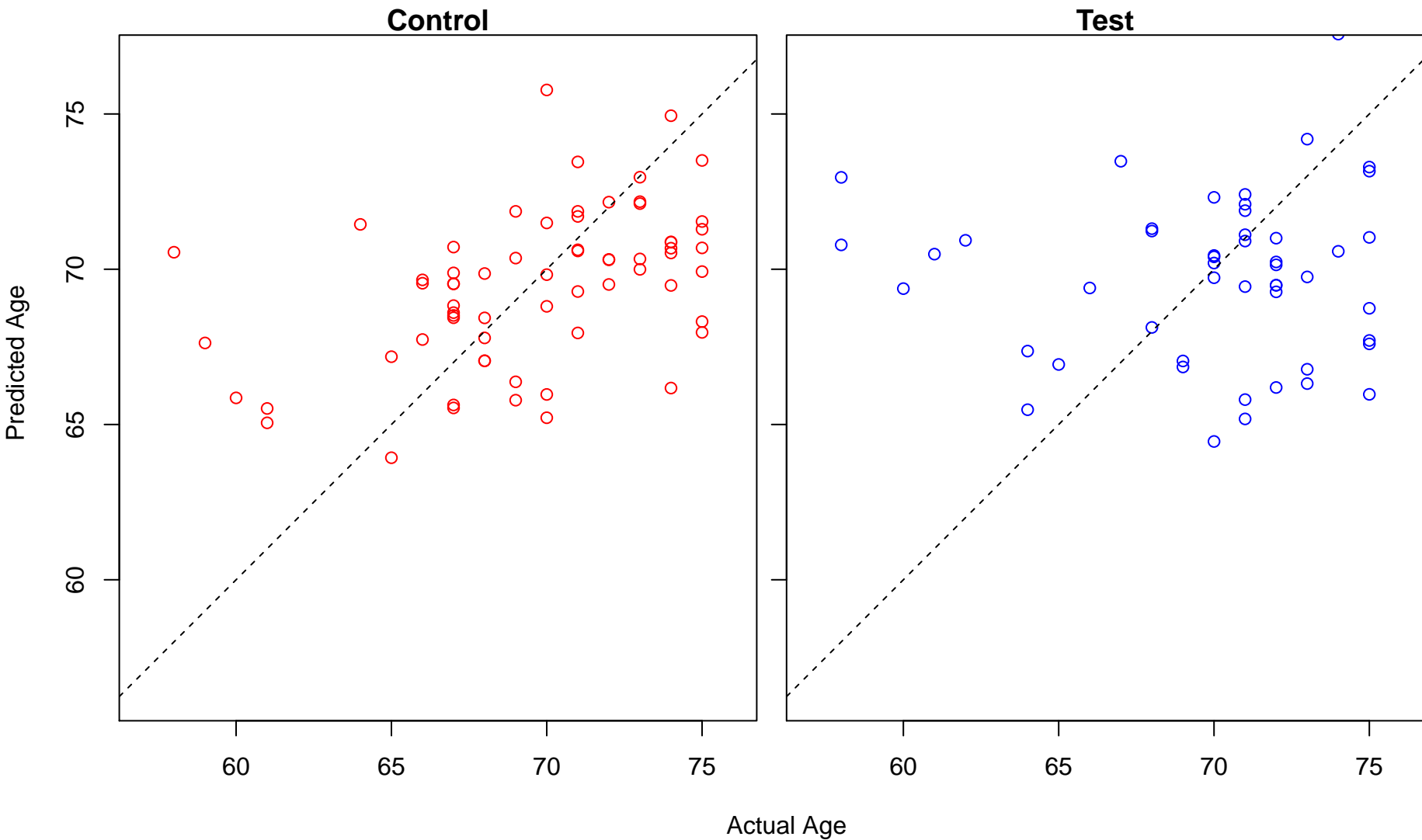
aortic valve development (Score: 0.753359)



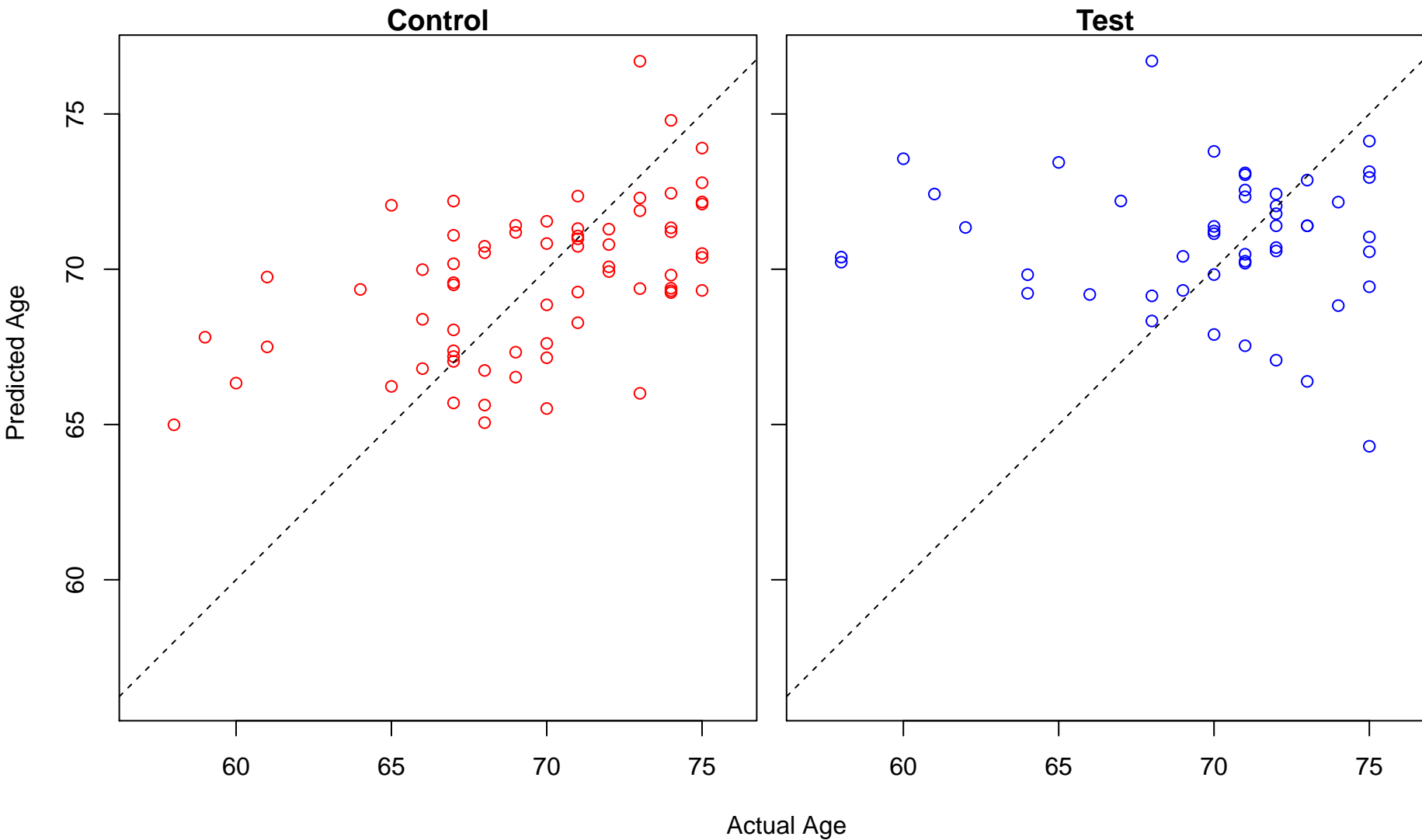
aortic valve morphogenesis (Score: 0.753359)



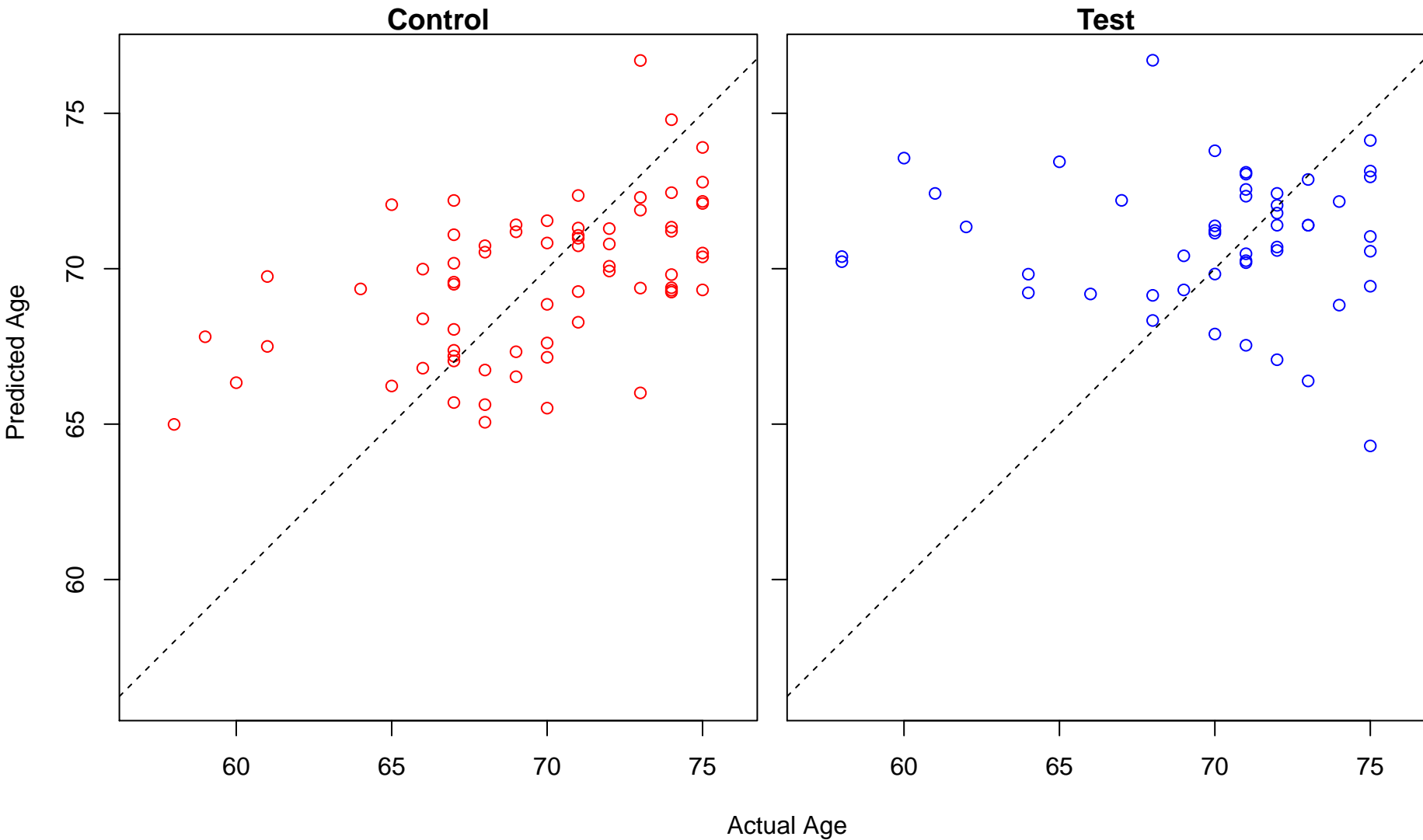
positive regulation of substrate adhesion-dependent cell spreading (Score: 0.753078)



negative regulation of delayed rectifier potassium channel activity (Score: 0.753037)

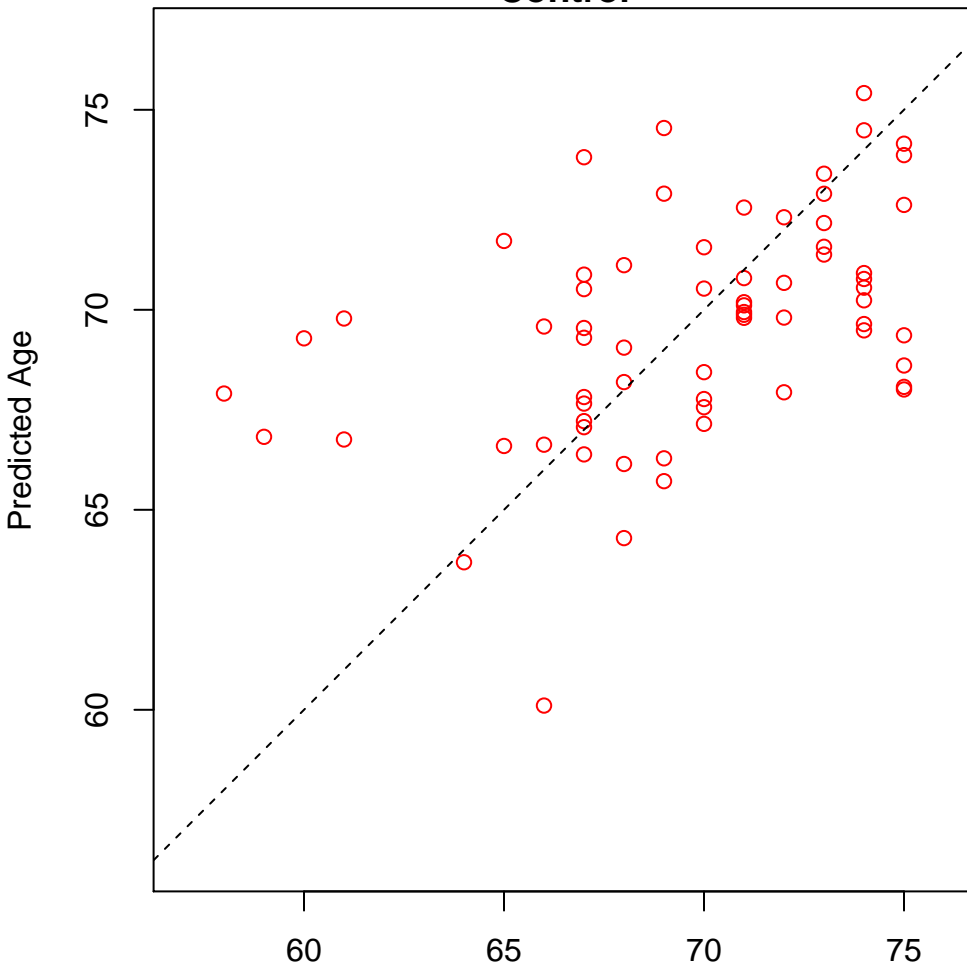


negative regulation of voltage-gated potassium channel activity (Score: 0.753037)

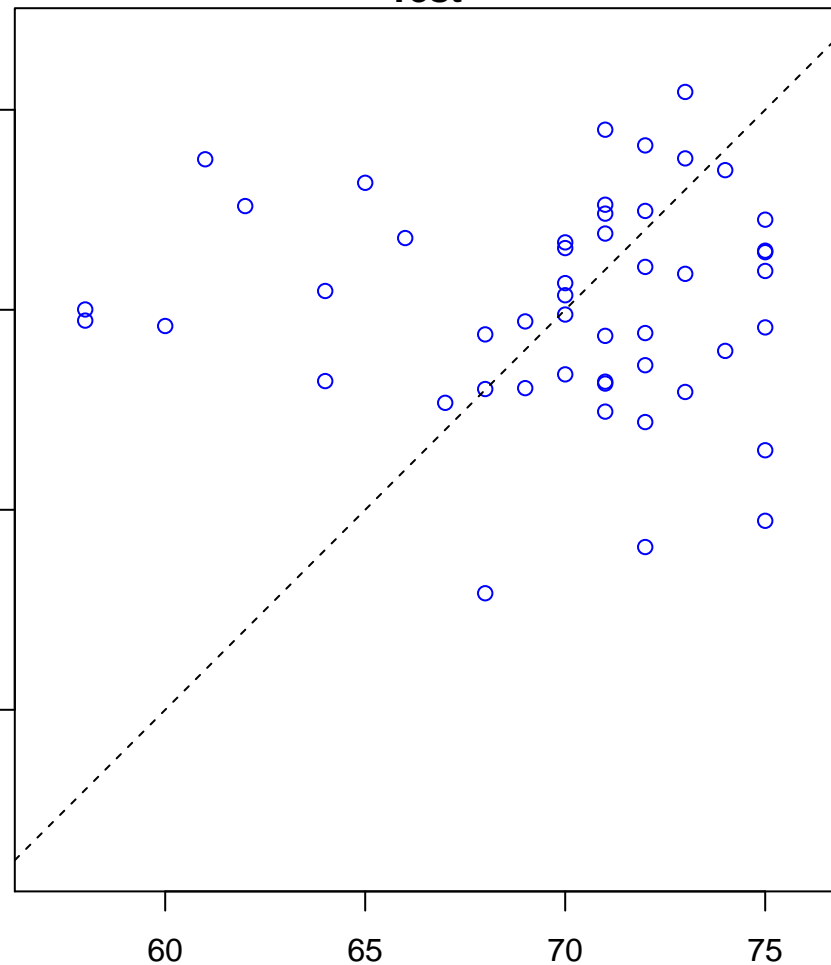


cardiac muscle cell action potential (Score: 0.752984)

Control

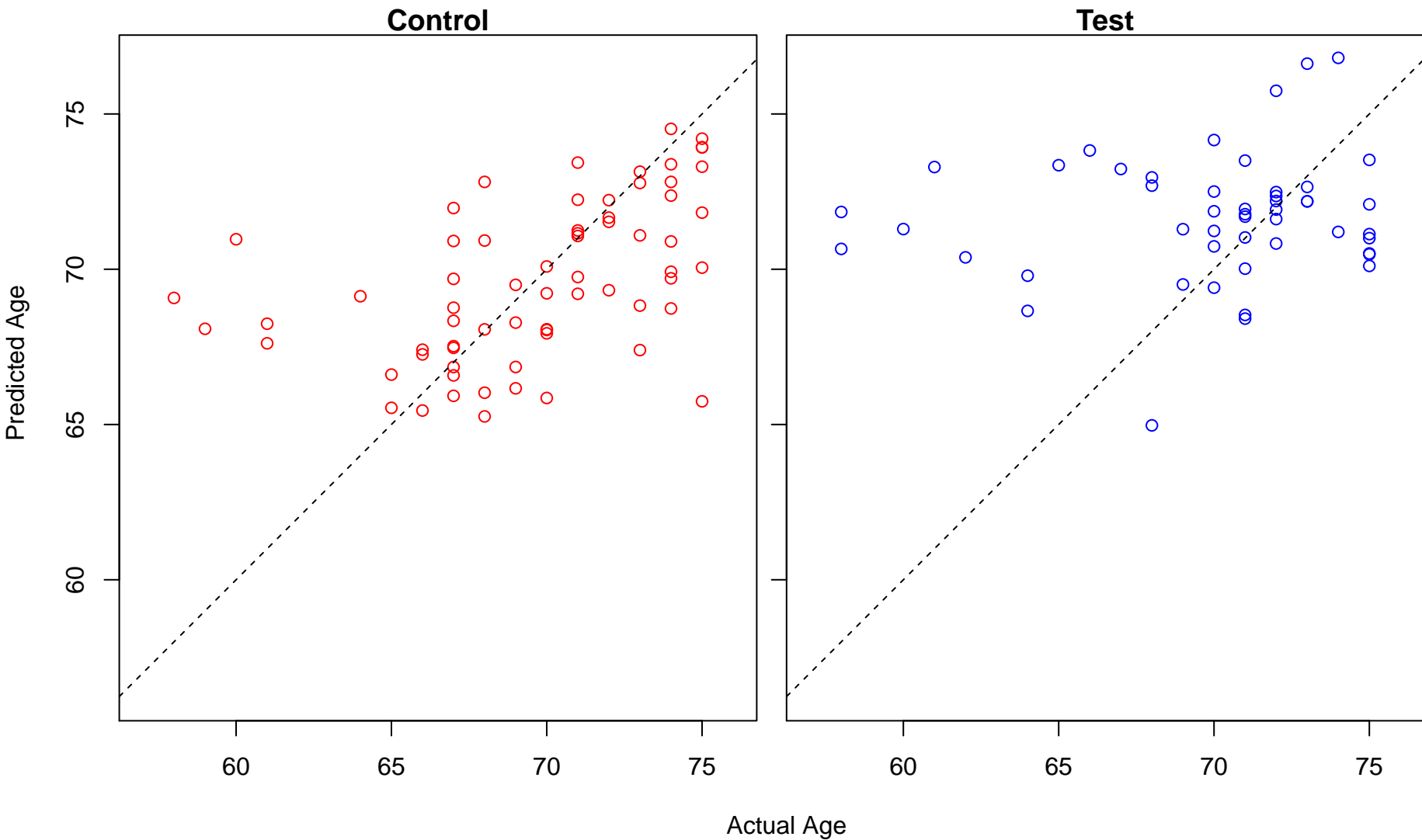


Test



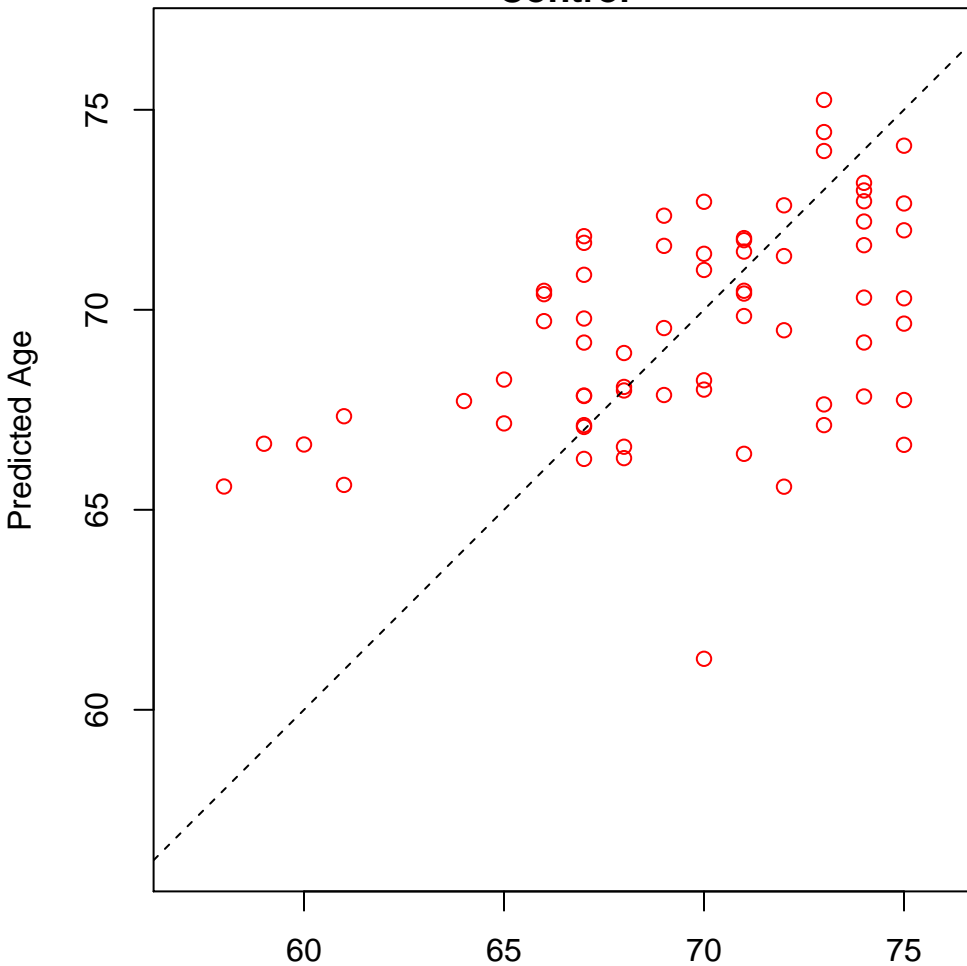
Actual Age

oxygen homeostasis (Score: 0.751962)

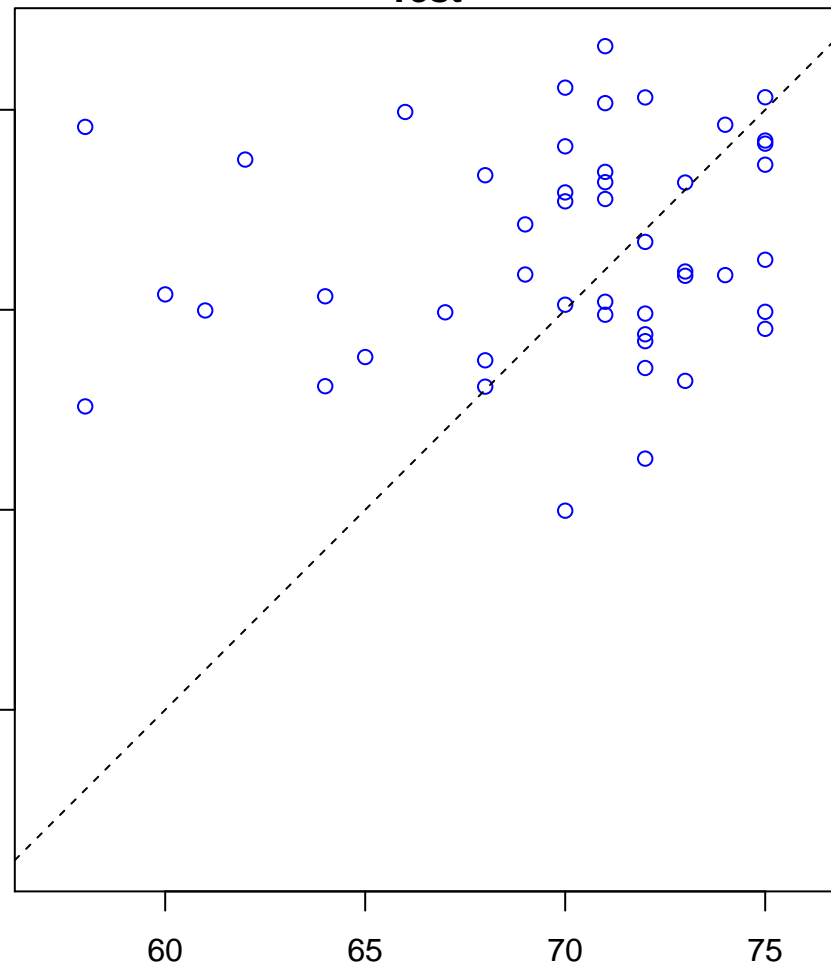


protein localization to membrane raft (Score: 0.751650)

Control

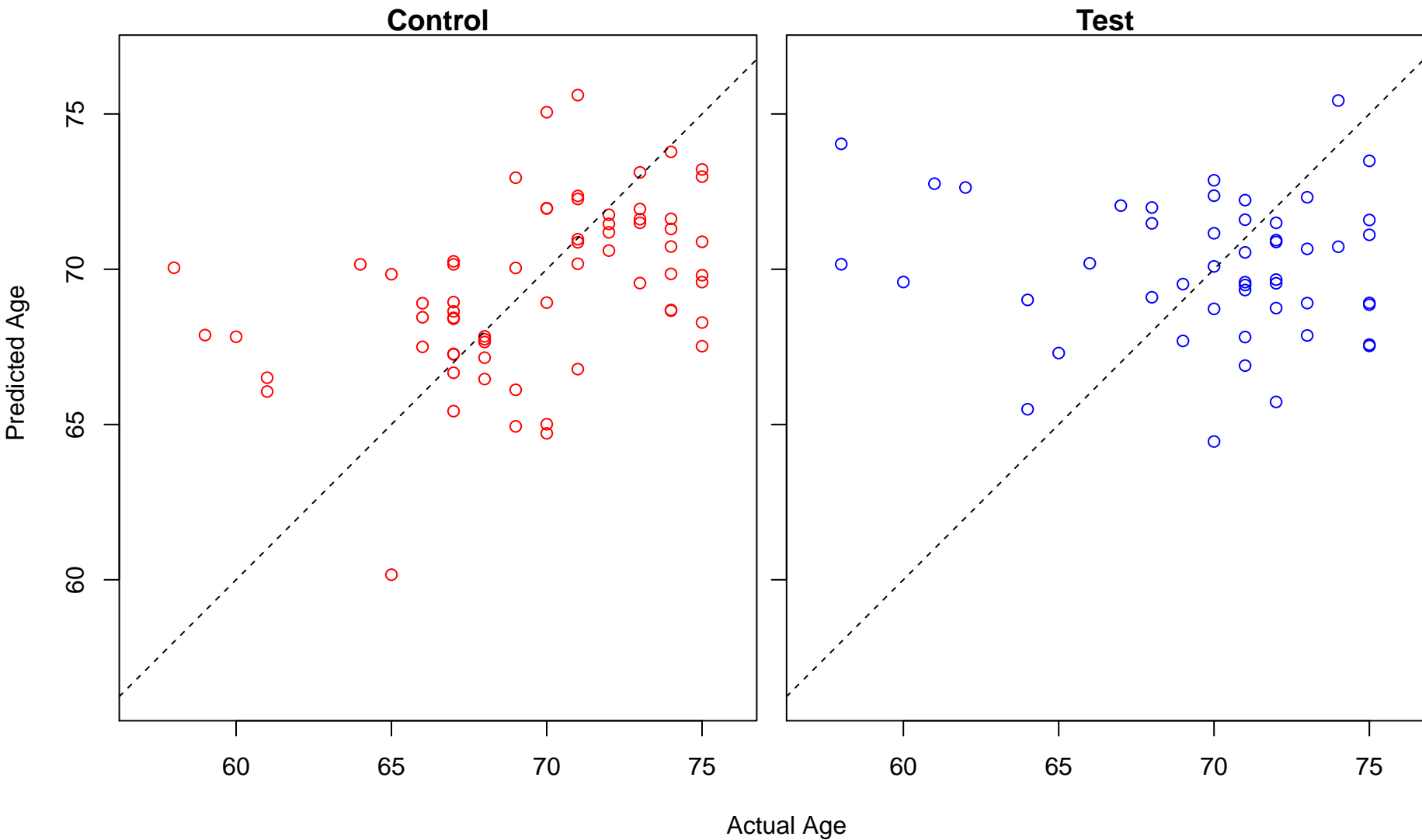


Test

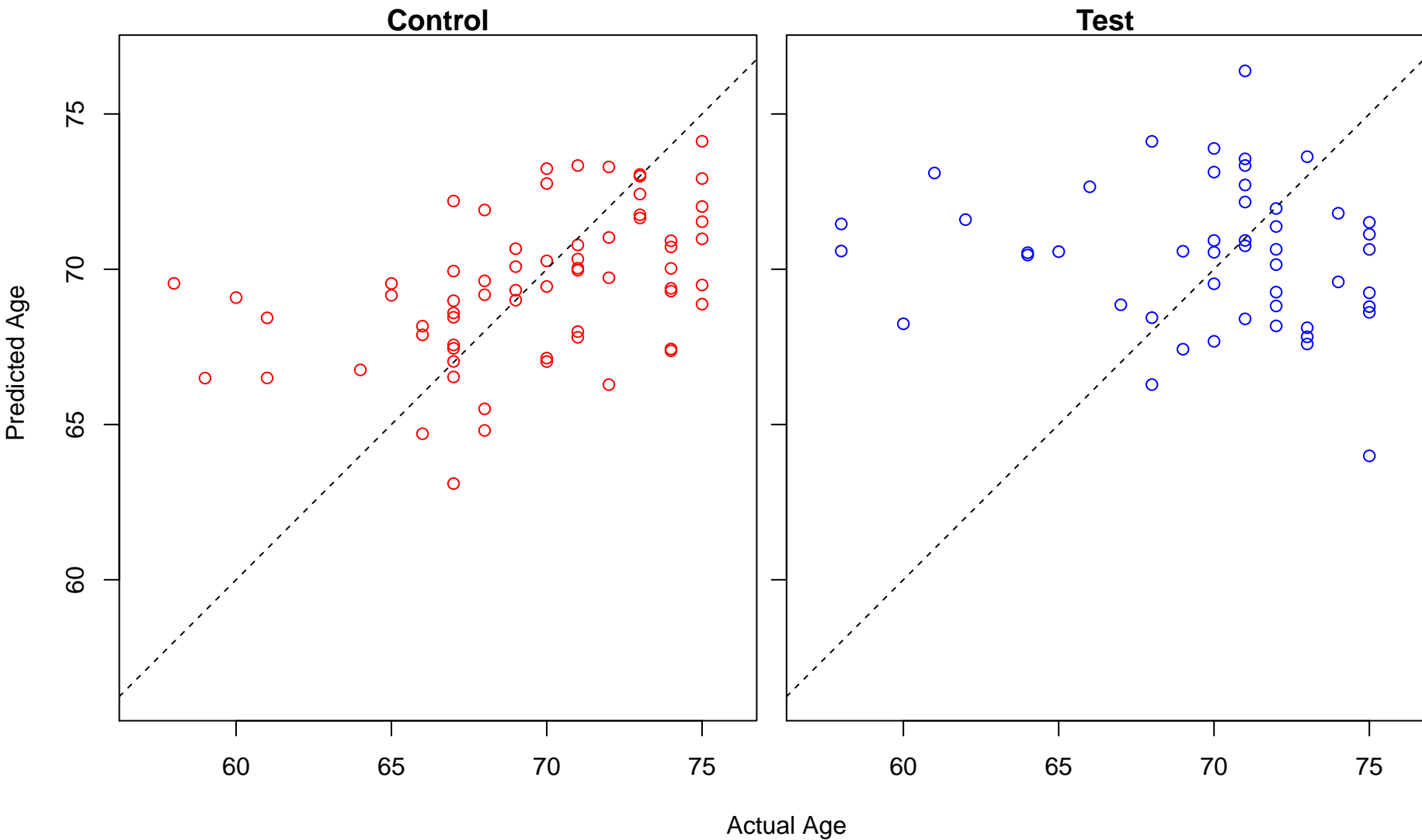


Actual Age

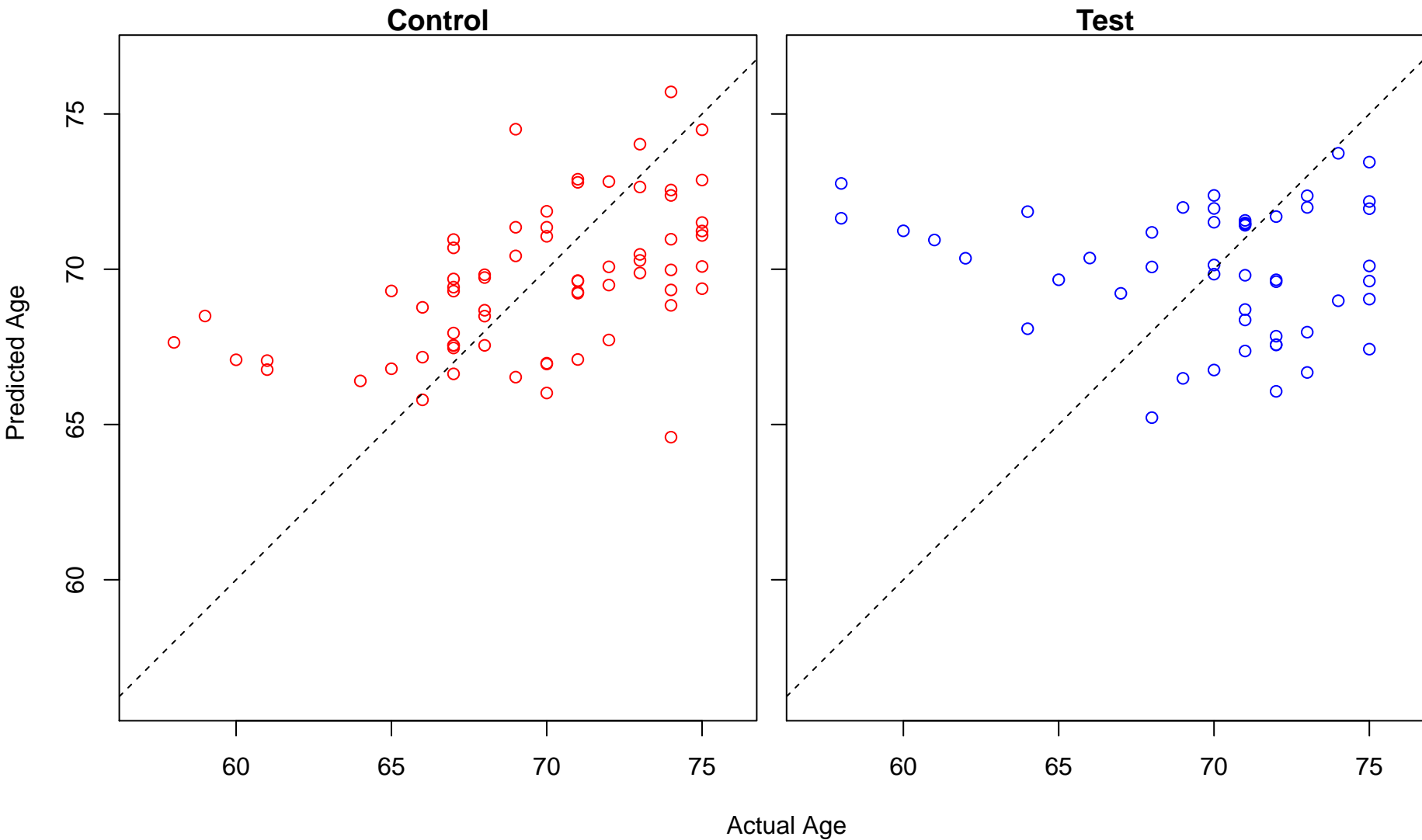
regulation of substrate adhesion-dependent cell spreading (Score: 0.751360)



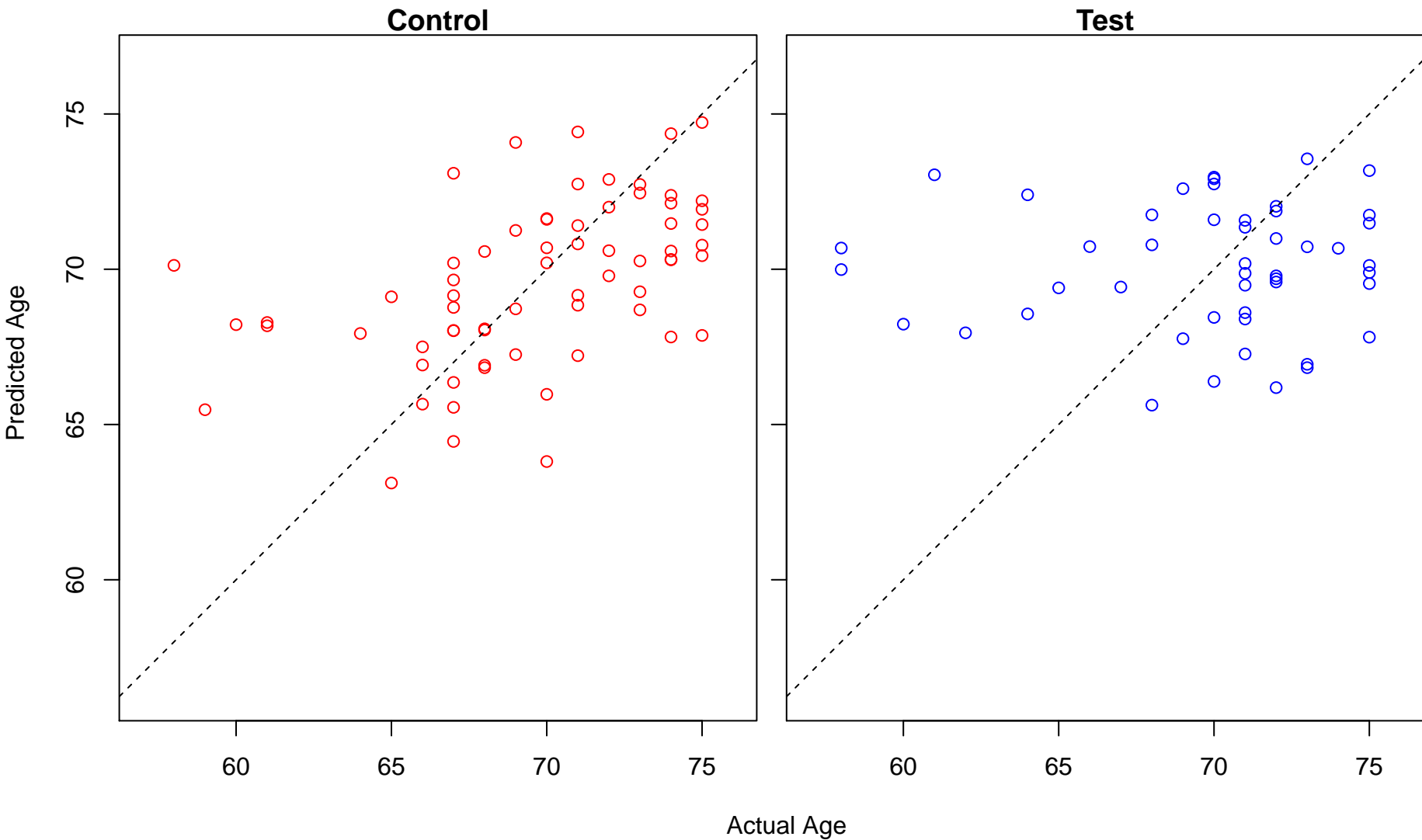
protein trimerization (Score: 0.750649)



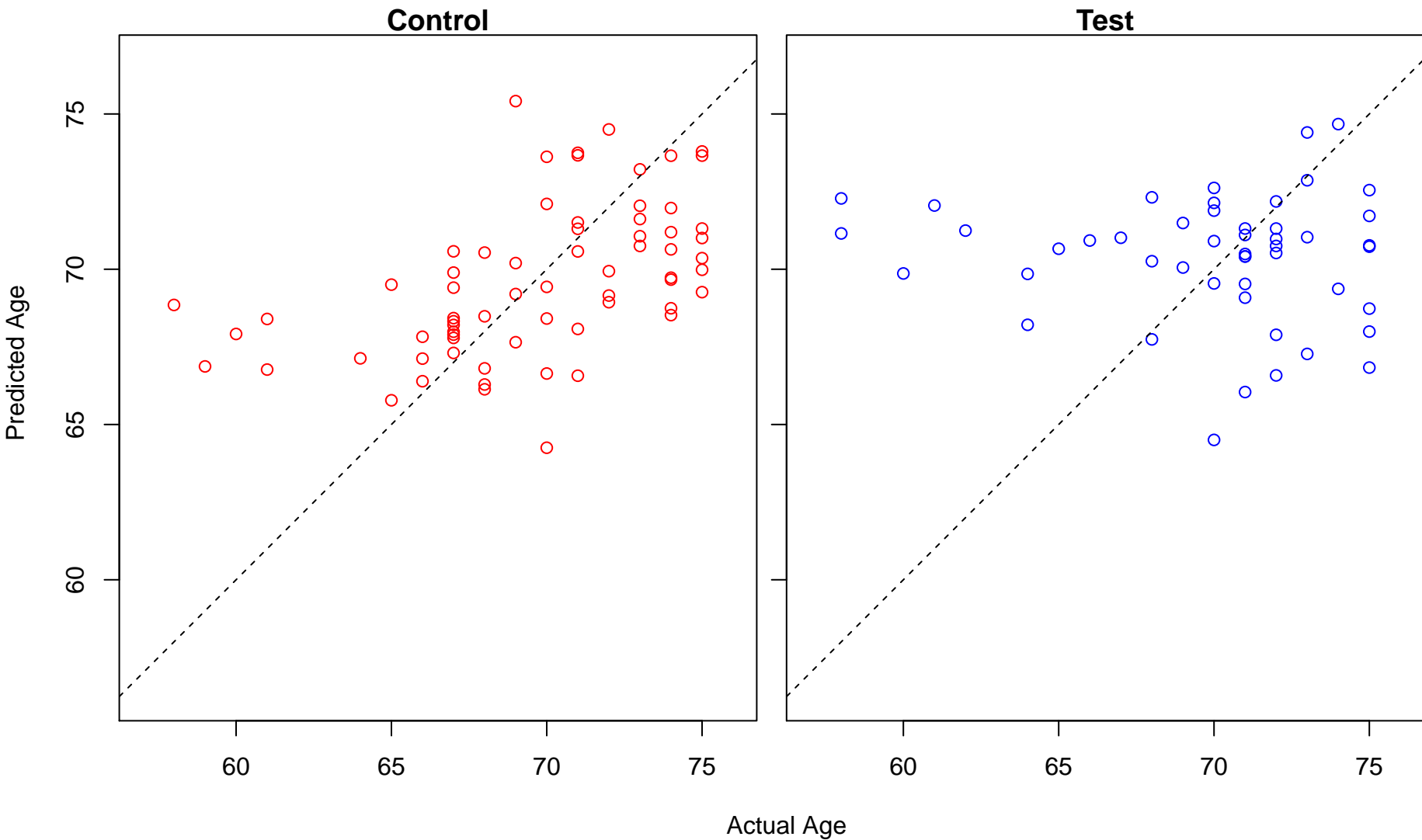
histone-threonine phosphorylation (Score: 0.750348)



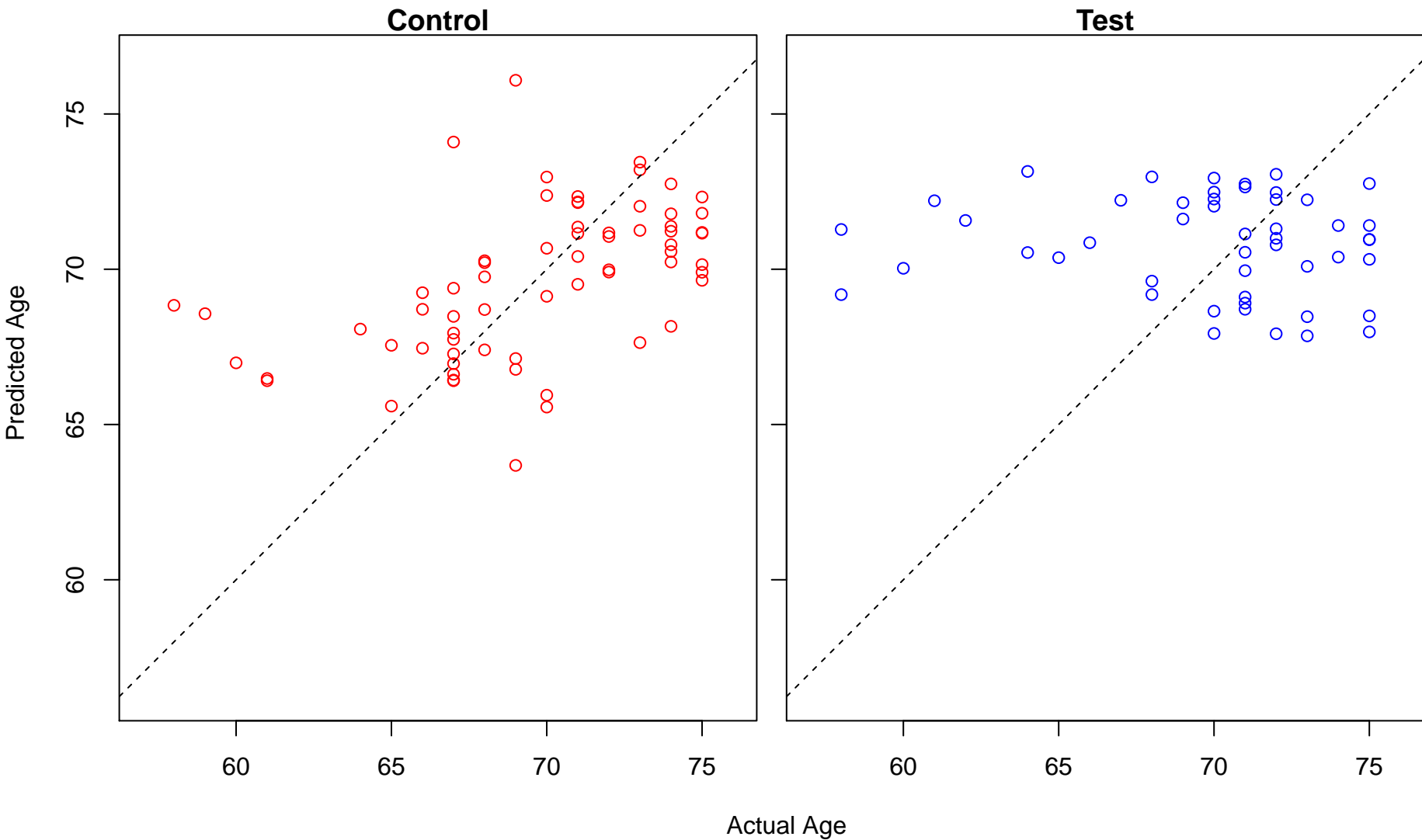
negative regulation of antigen receptor-mediated signaling pathway (Score: 0.749710)



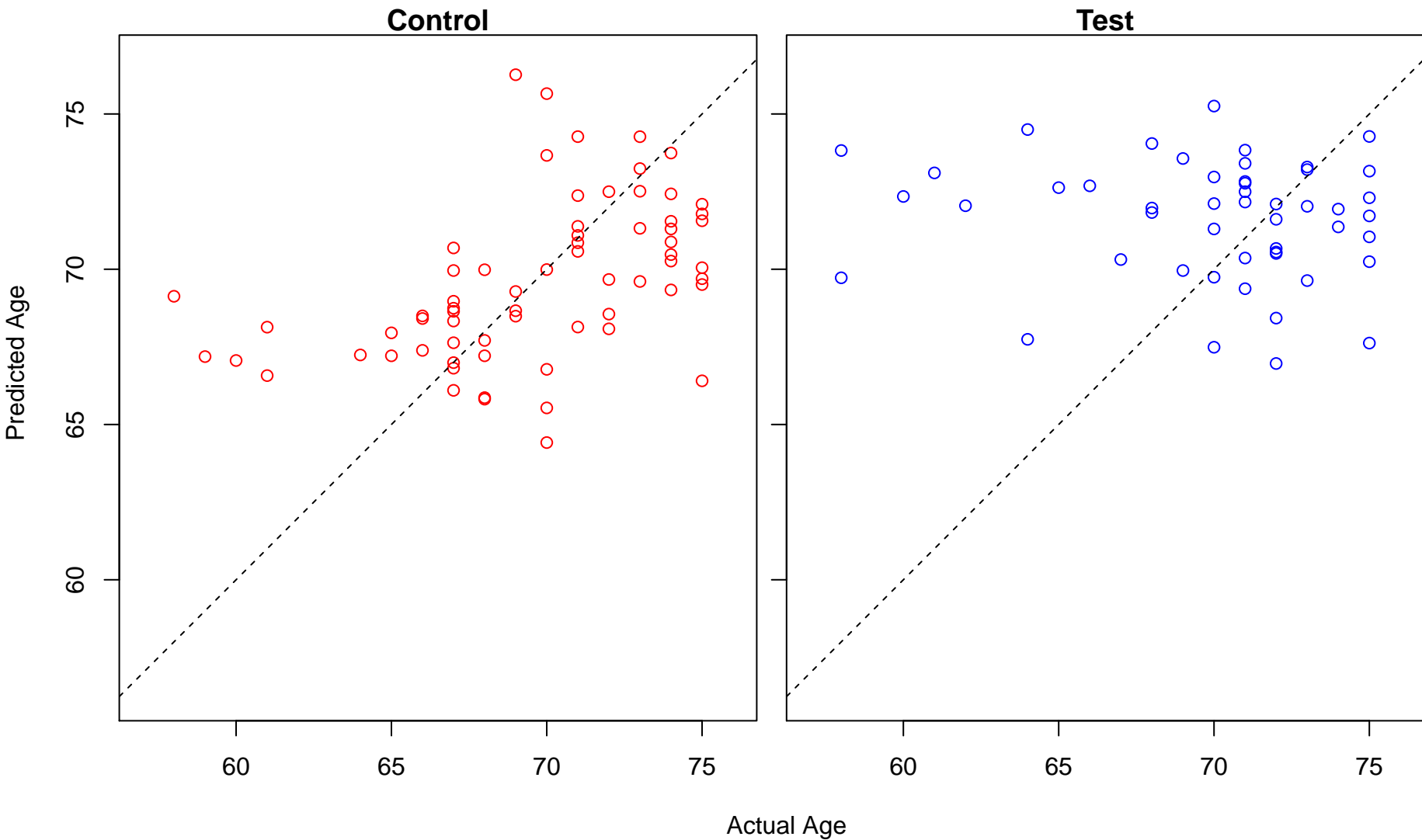
regulation of tyrosine phosphorylation of Stat3 protein (Score: 0.749564)



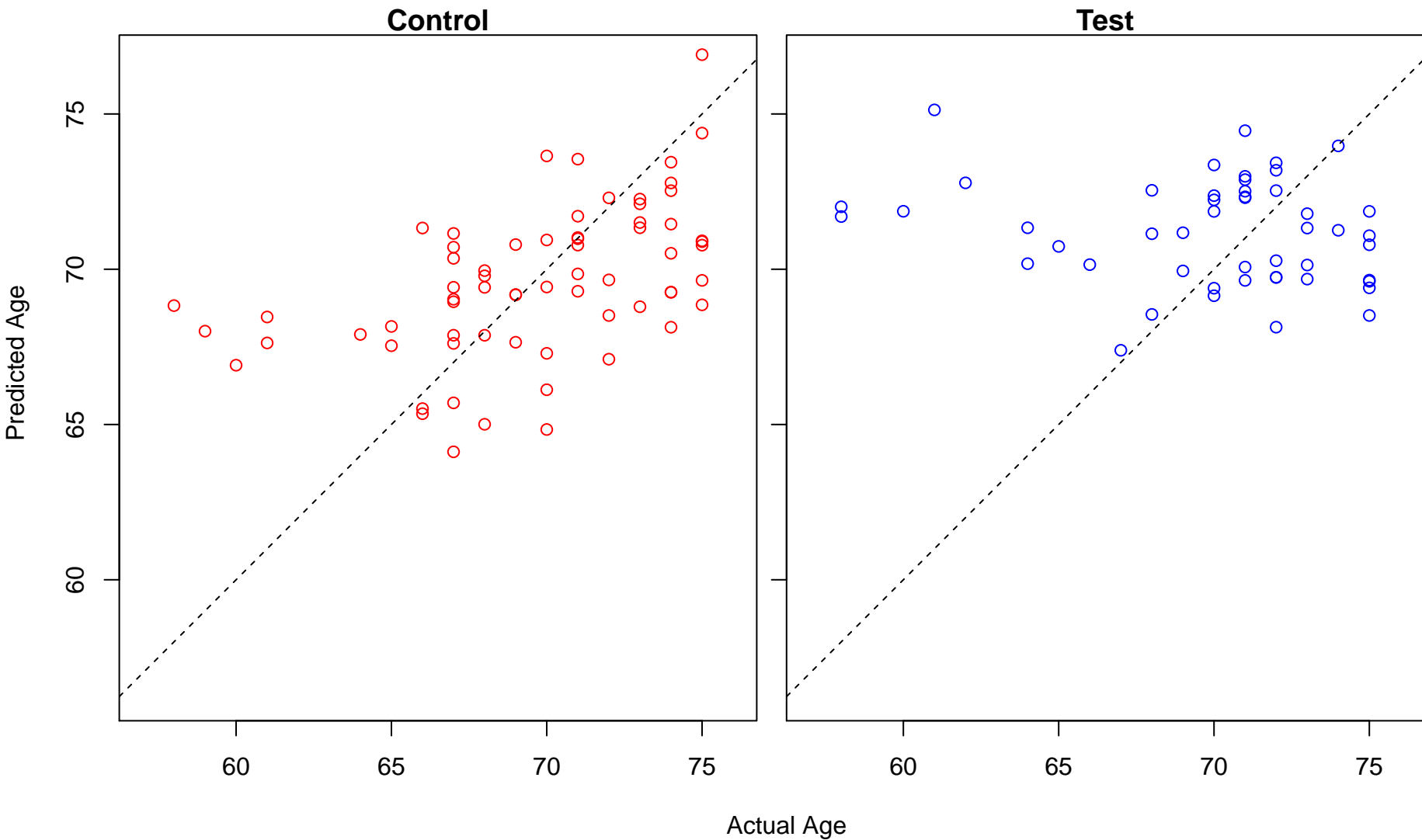
retinoid metabolic process (Score: 0.749502)



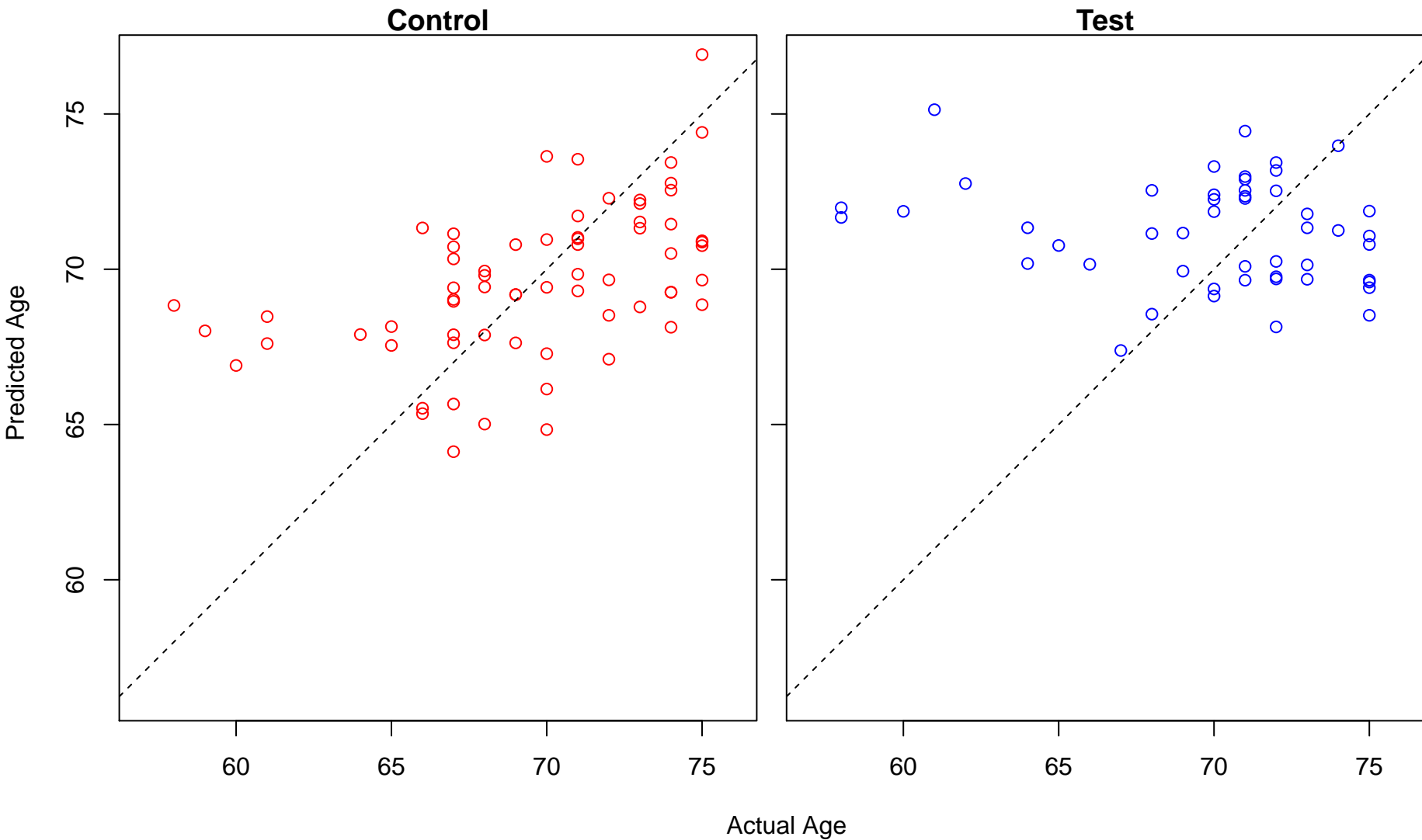
viral mRNA export from host cell nucleus (Score: 0.749289)



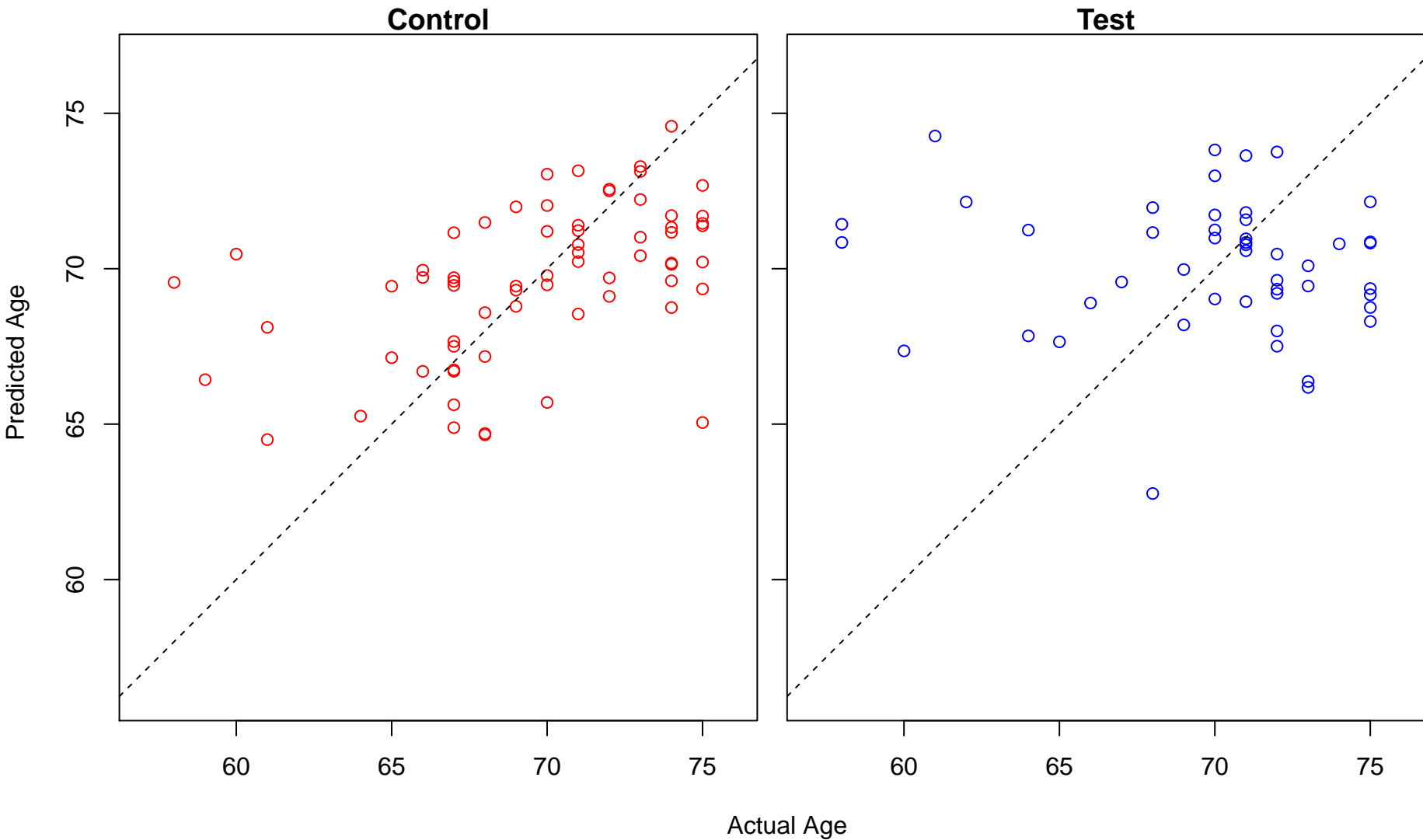
peptidyl-arginine methylation (Score: 0.749226)



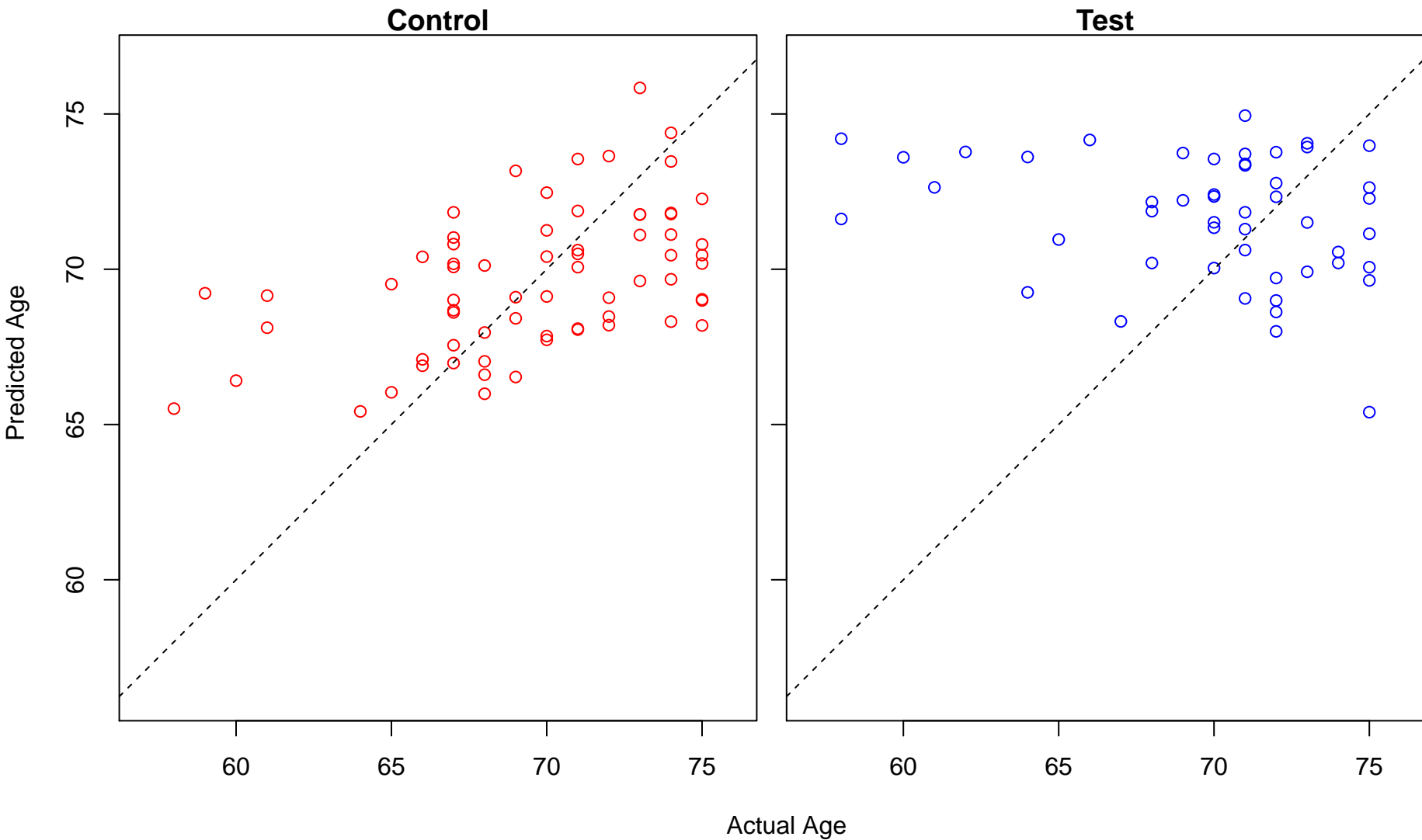
peptidyl-arginine N-methylation (Score: 0.748767)



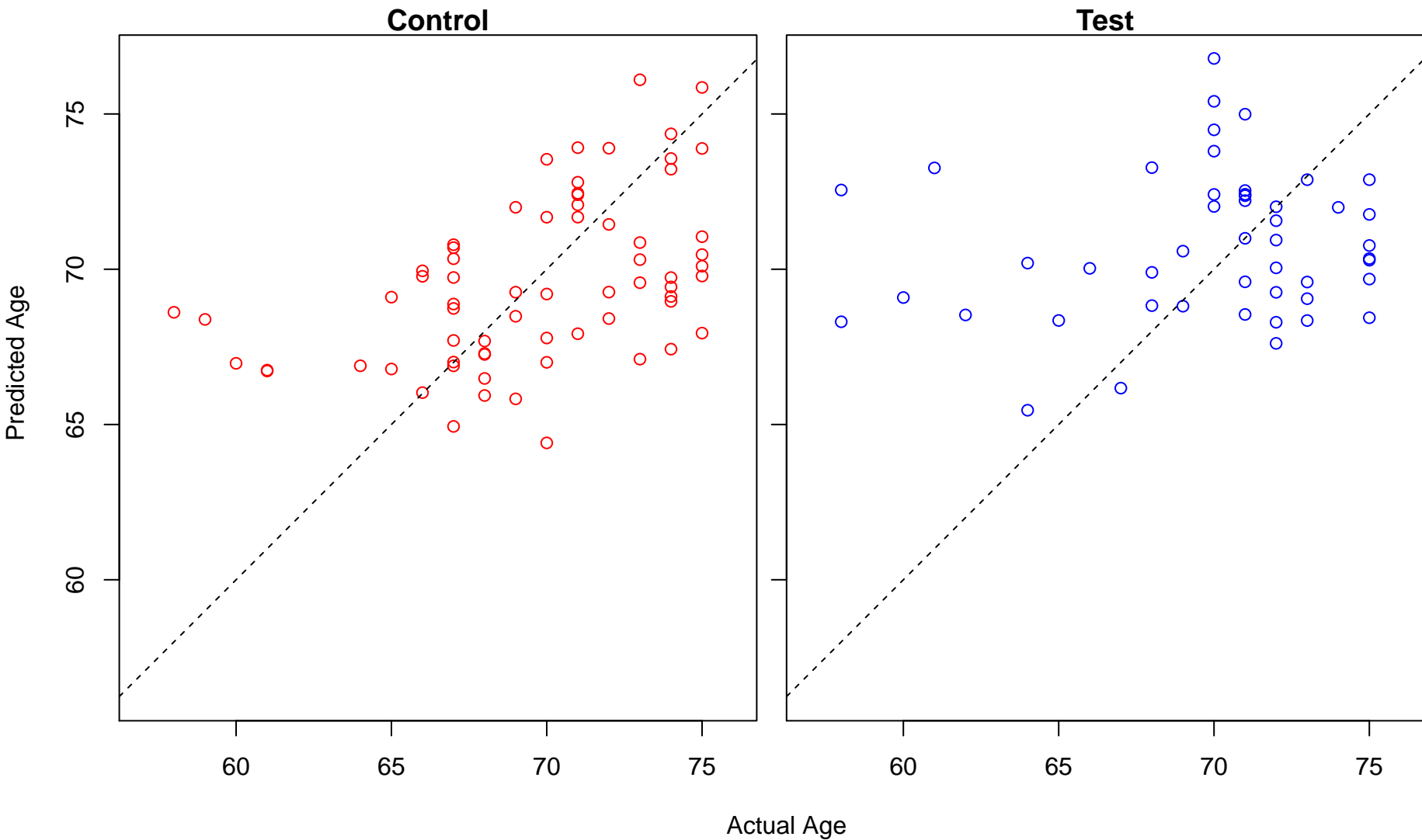
regulation of dendritic cell apoptotic process (Score: 0.748354)



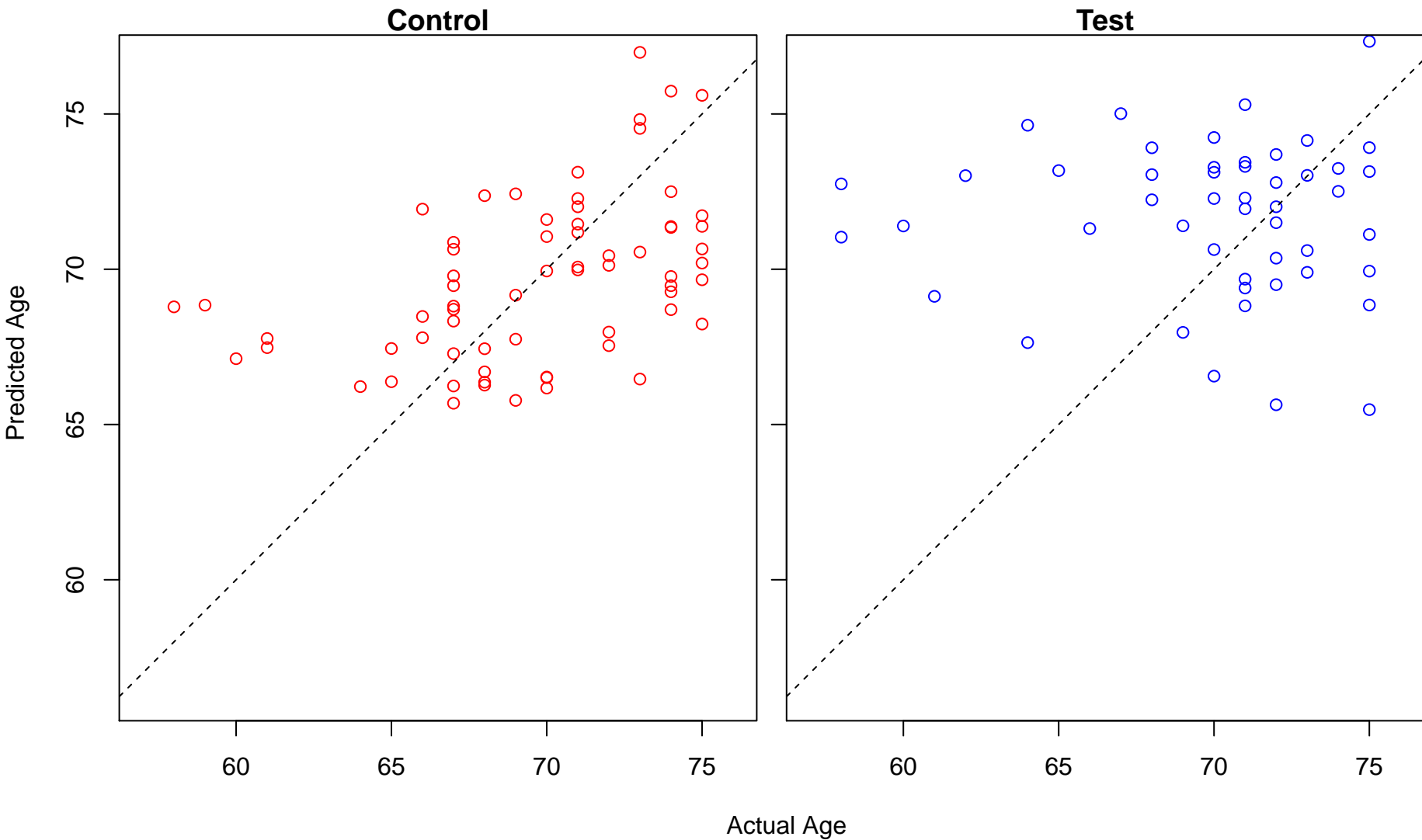
cell migration involved in heart development (Score: 0.748327)



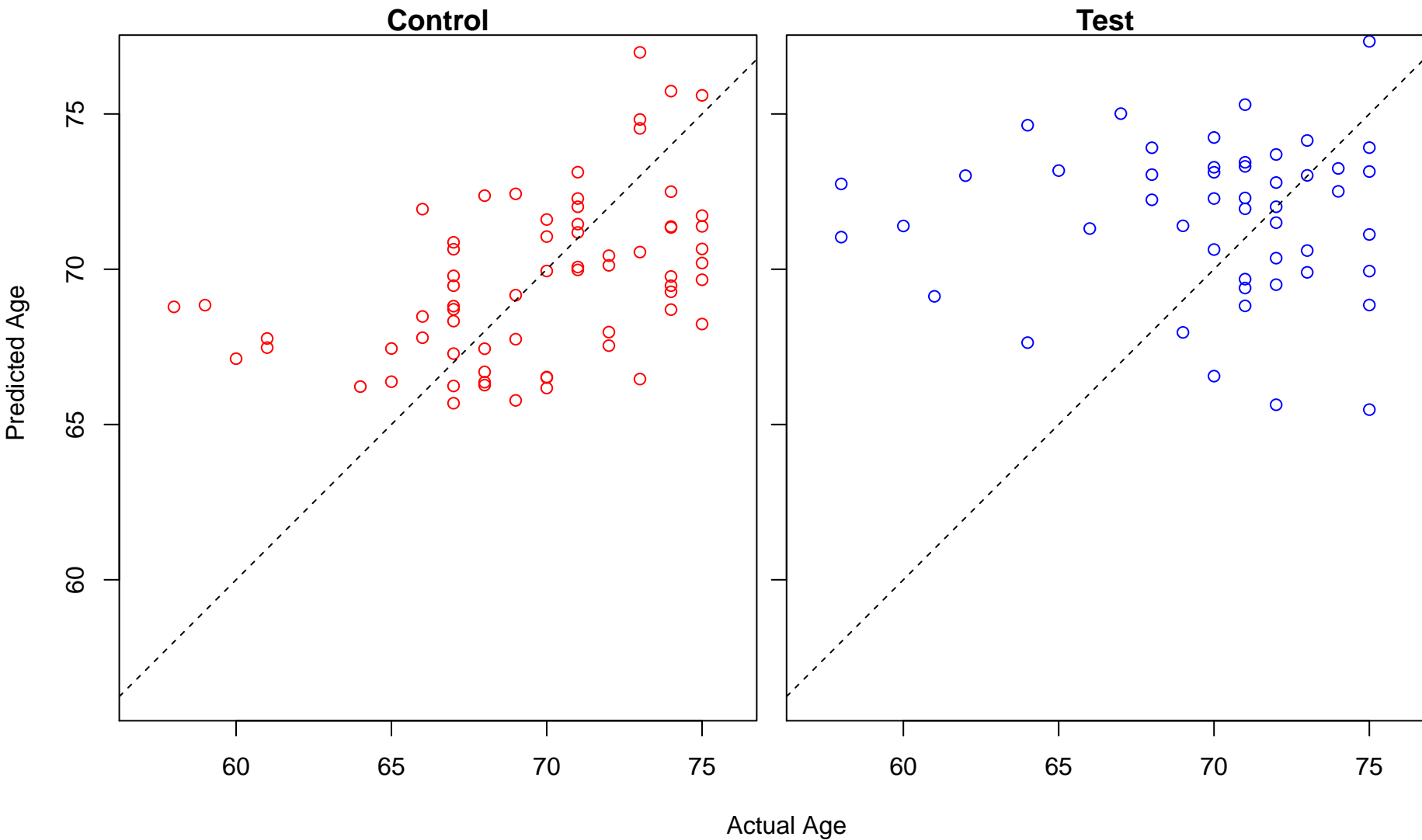
B cell proliferation (Score: 0.748107)



cellular response to lipoprotein particle stimulus (Score: 0.747347)

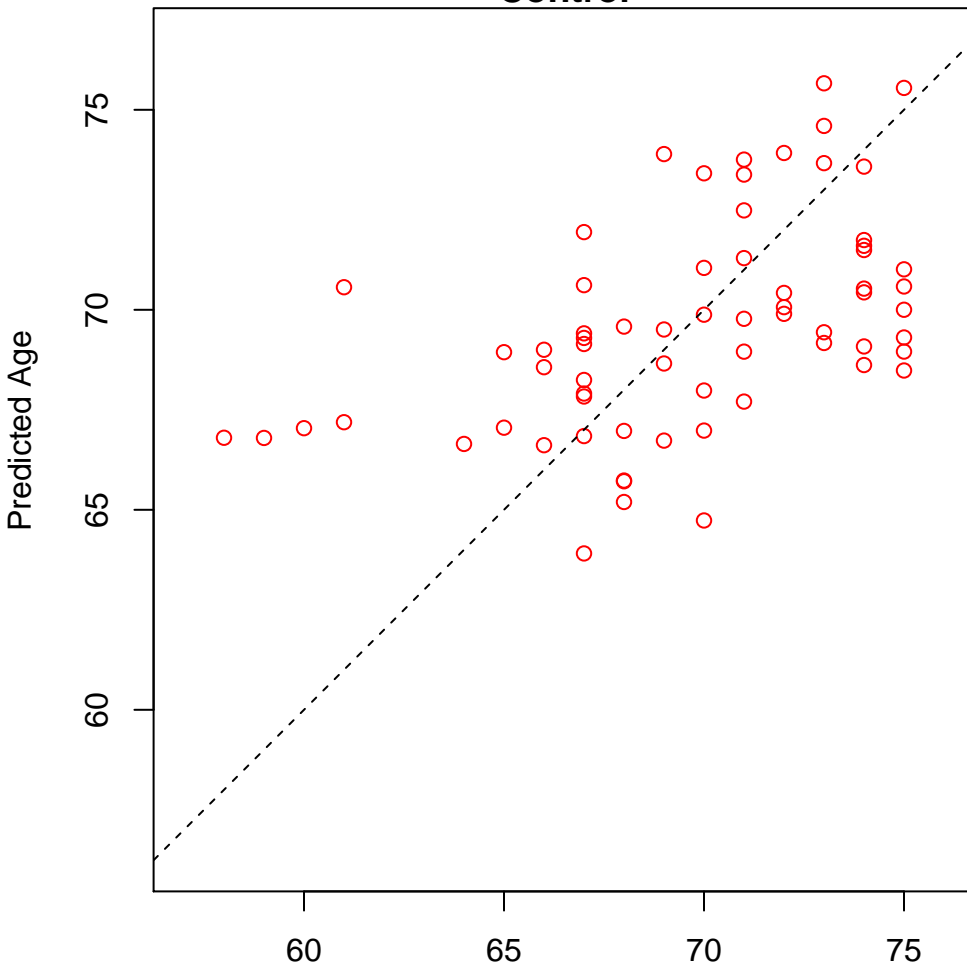


cellular response to low-density lipoprotein particle stimulus (Score: 0.747347)

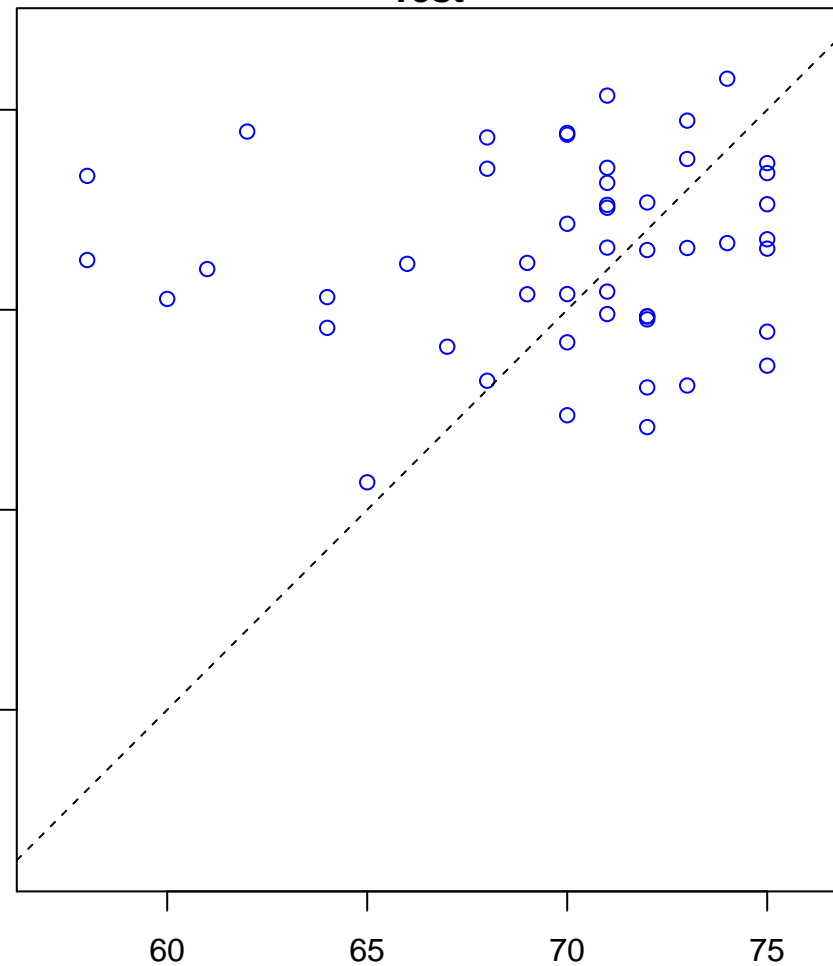


negative regulation of heart contraction (Score: 0.746909)

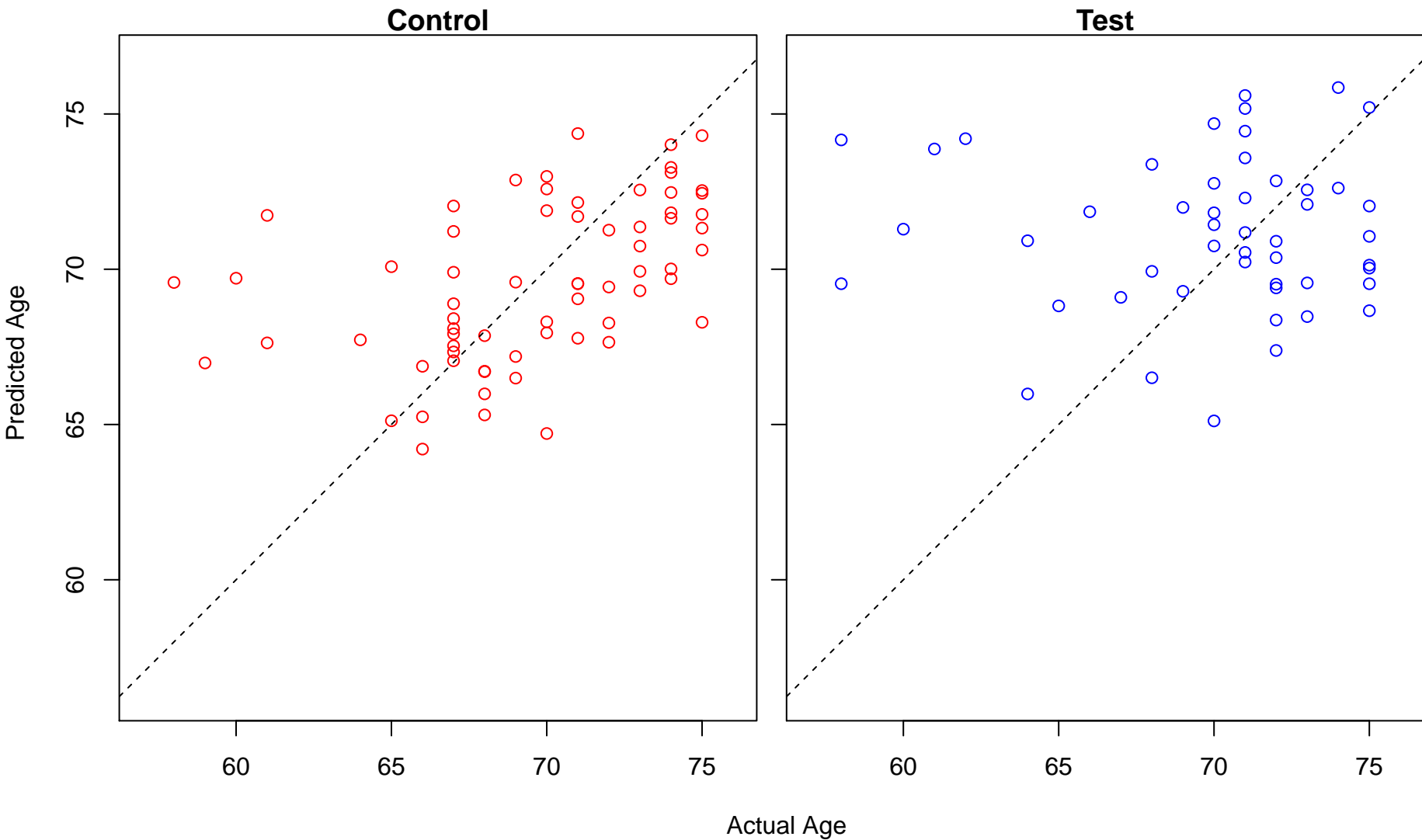
Control



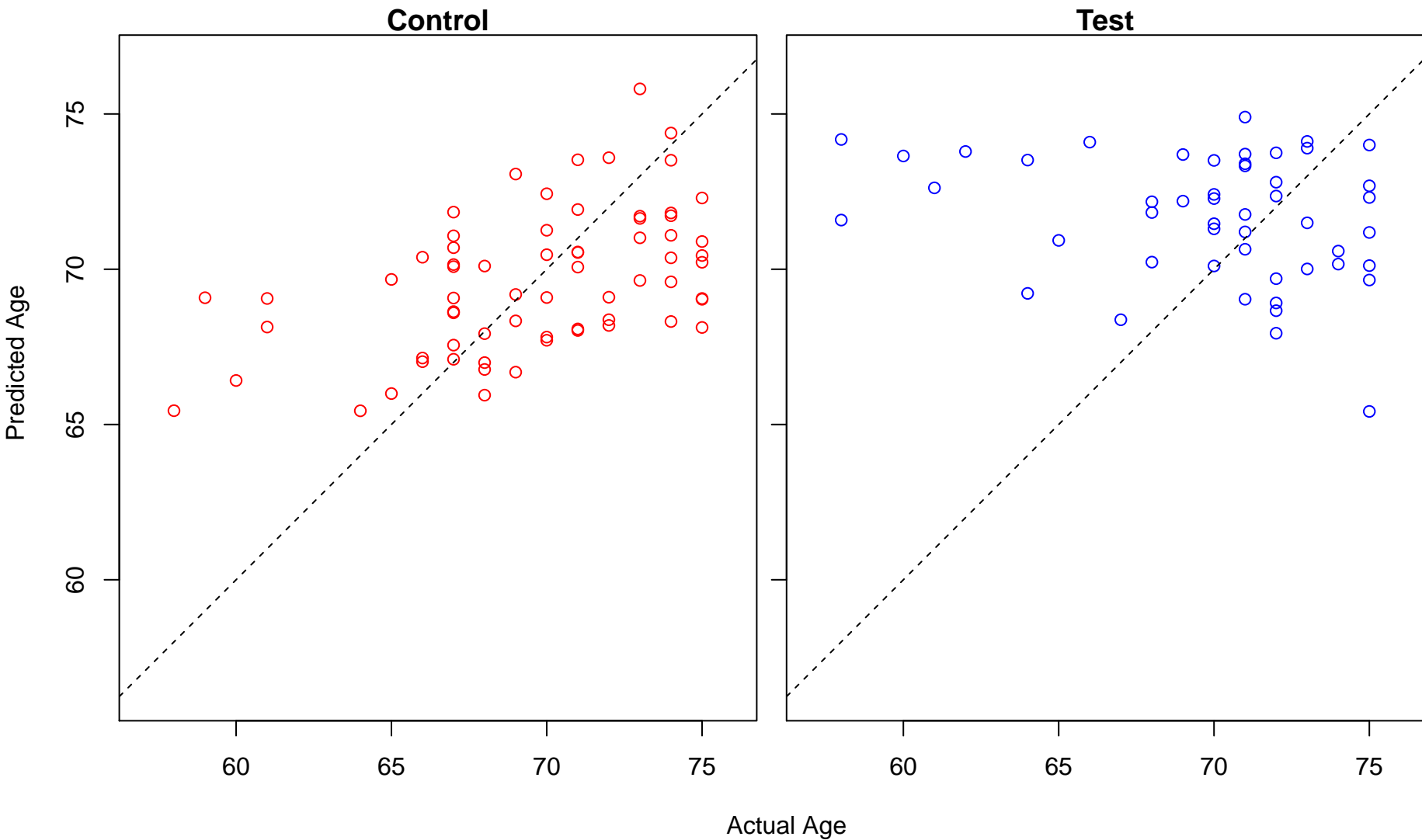
Test



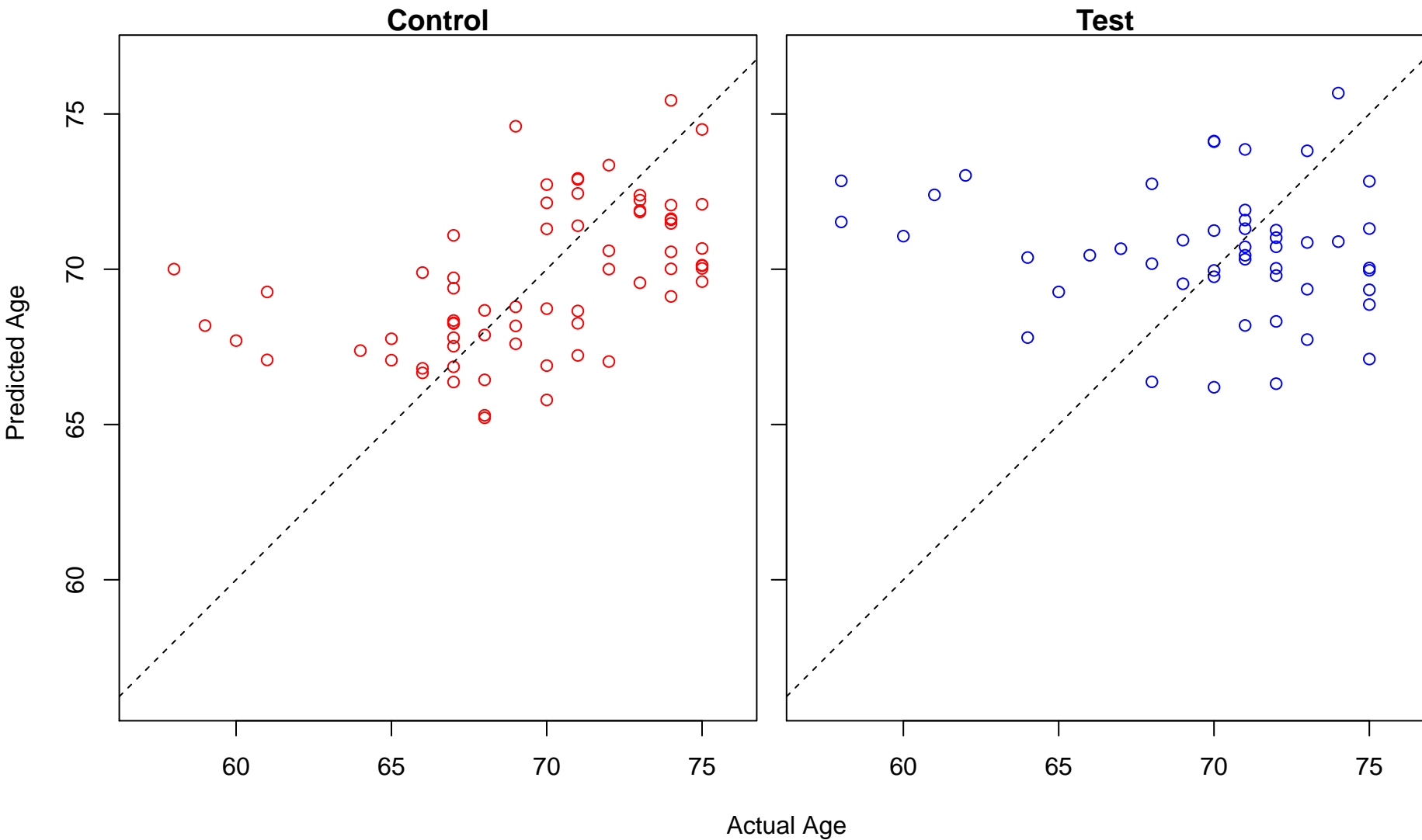
neurotransmitter secretion (Score: 0.746734)



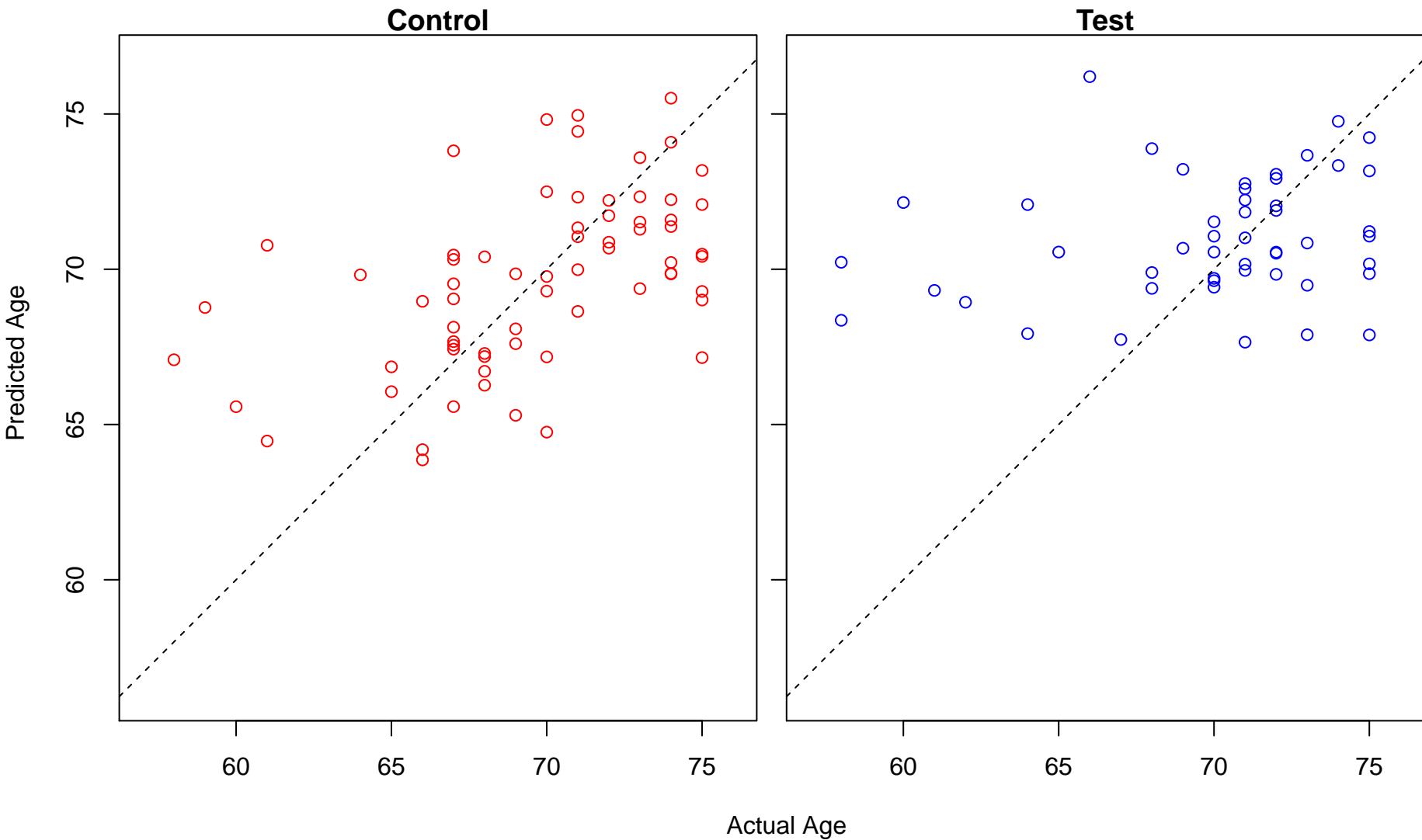
negative regulation of endothelial cell chemotaxis (Score: 0.746727)



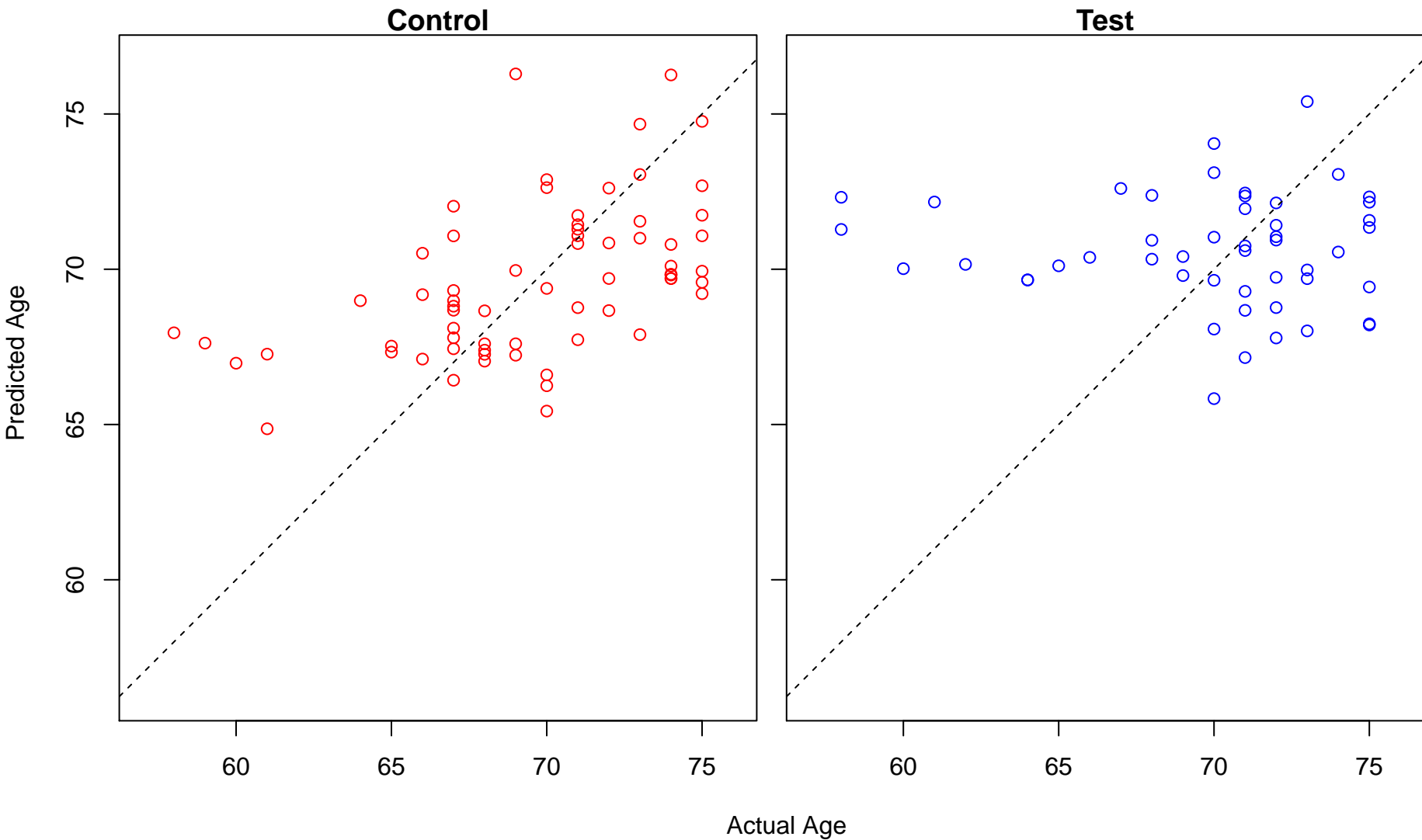
adult behavior (Score: 0.746663)



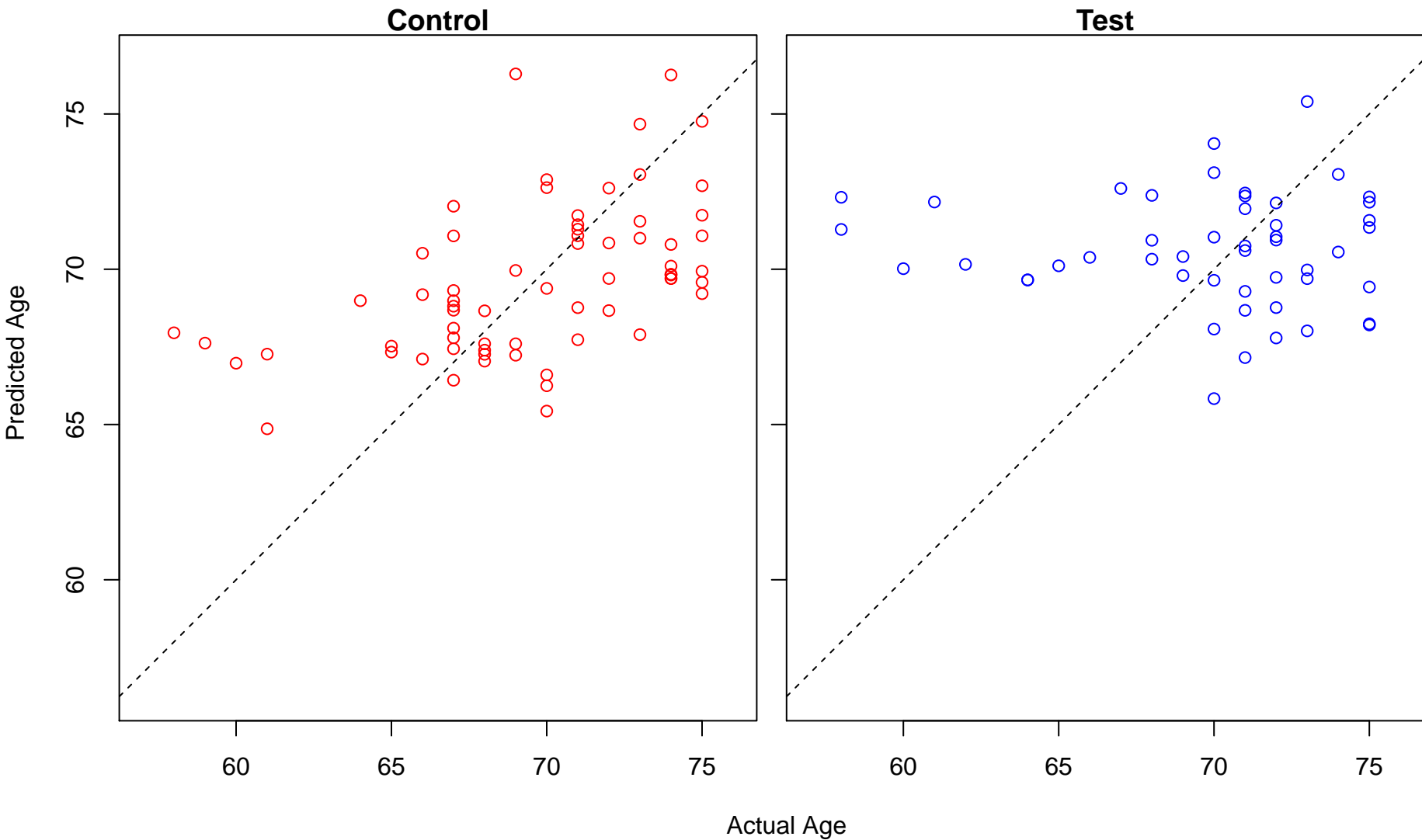
centromere complex assembly (Score: 0.746579)



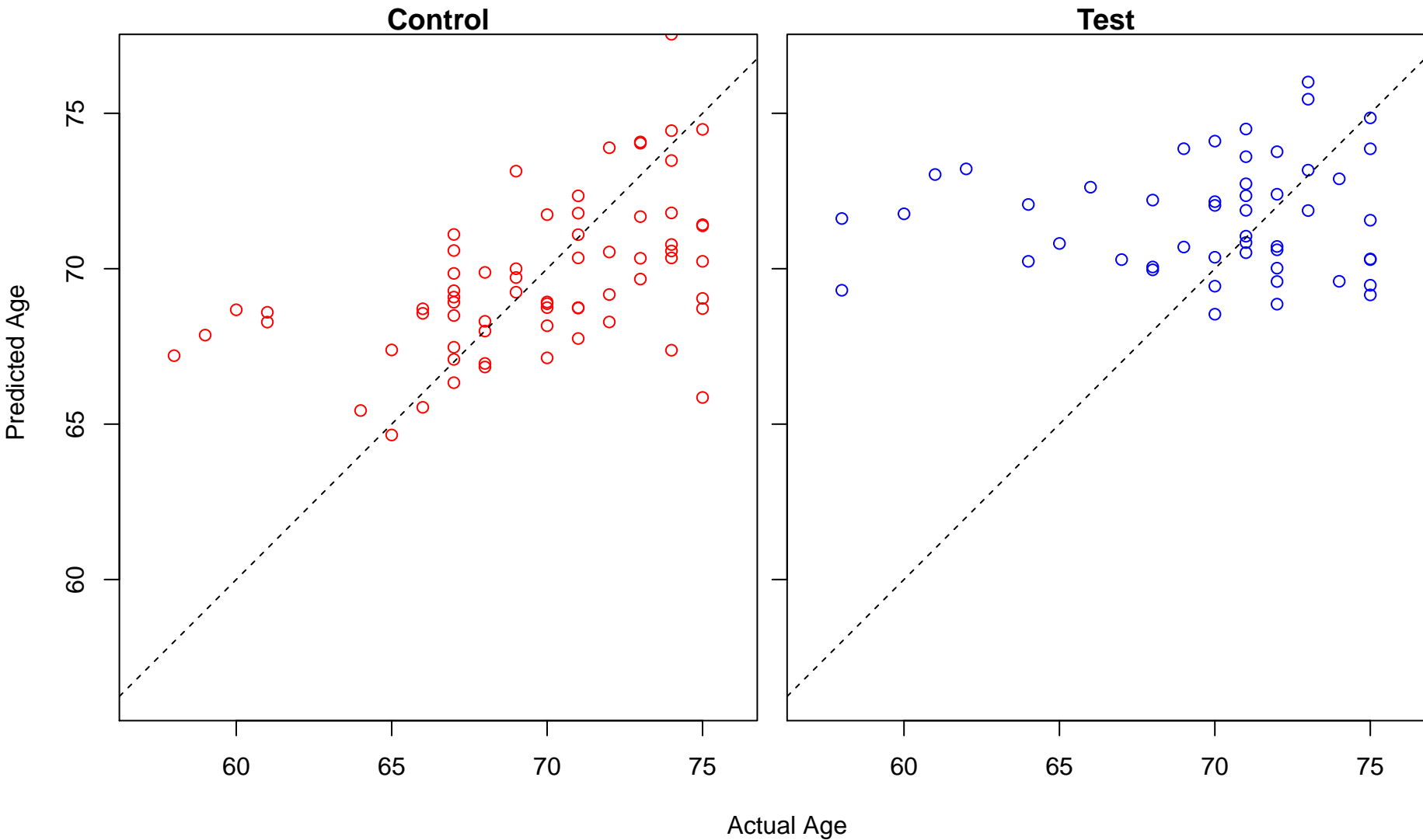
positive regulation of dephosphorylation (Score: 0.746273)



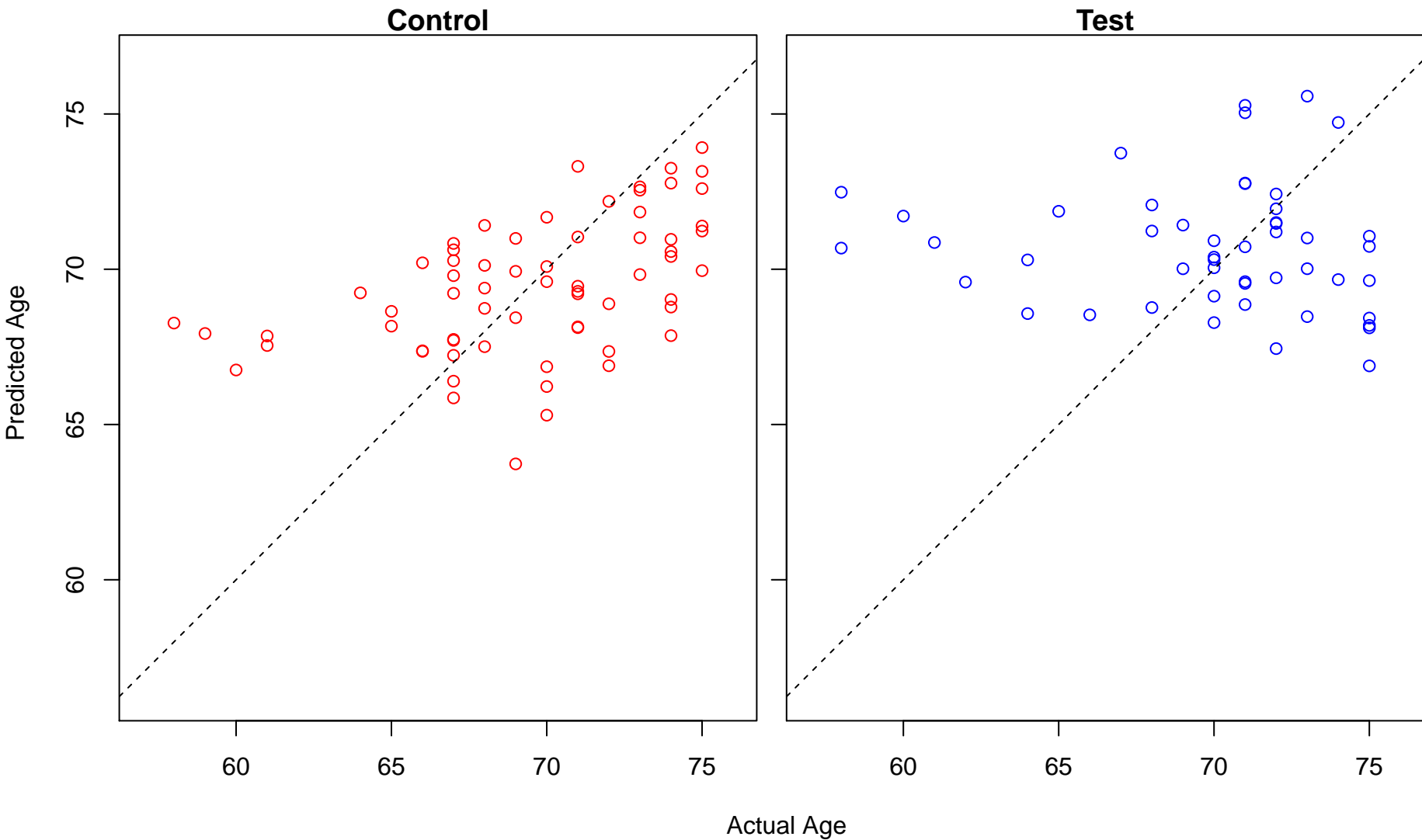
positive regulation of protein dephosphorylation (Score: 0.746273)



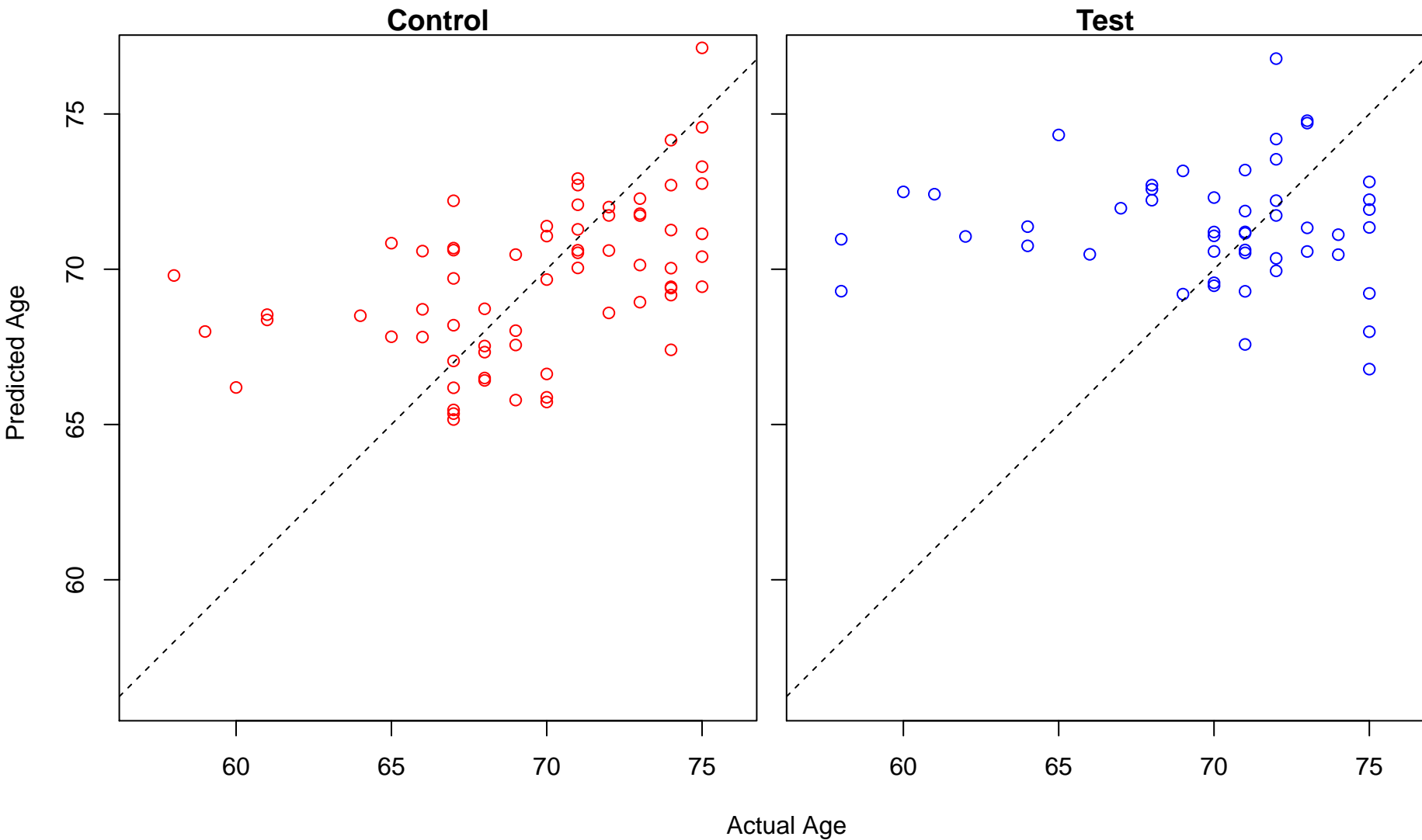
plasma lipoprotein particle assembly (Score: 0.746069)



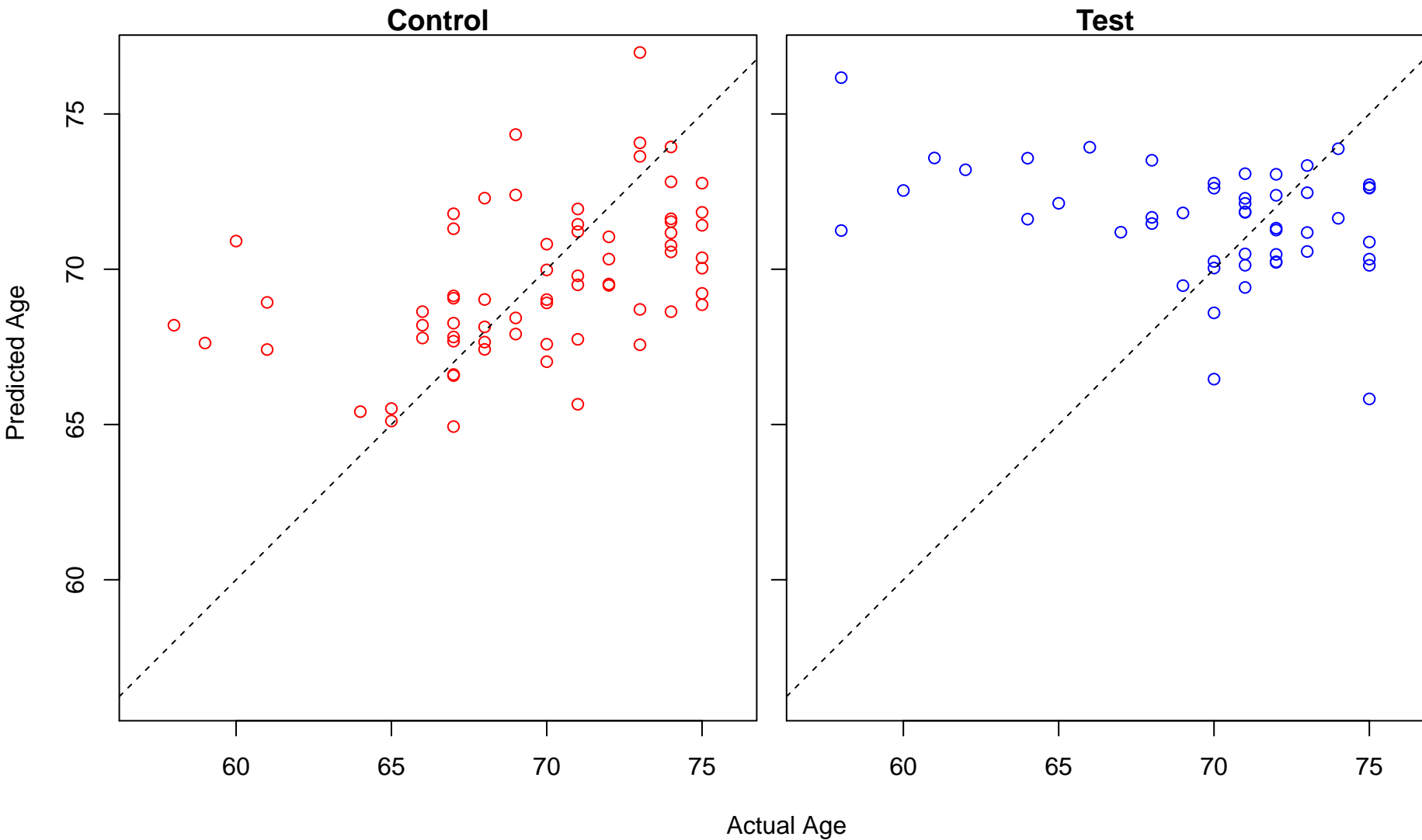
negative regulation of sequestering of triglyceride (Score: 0.745926)



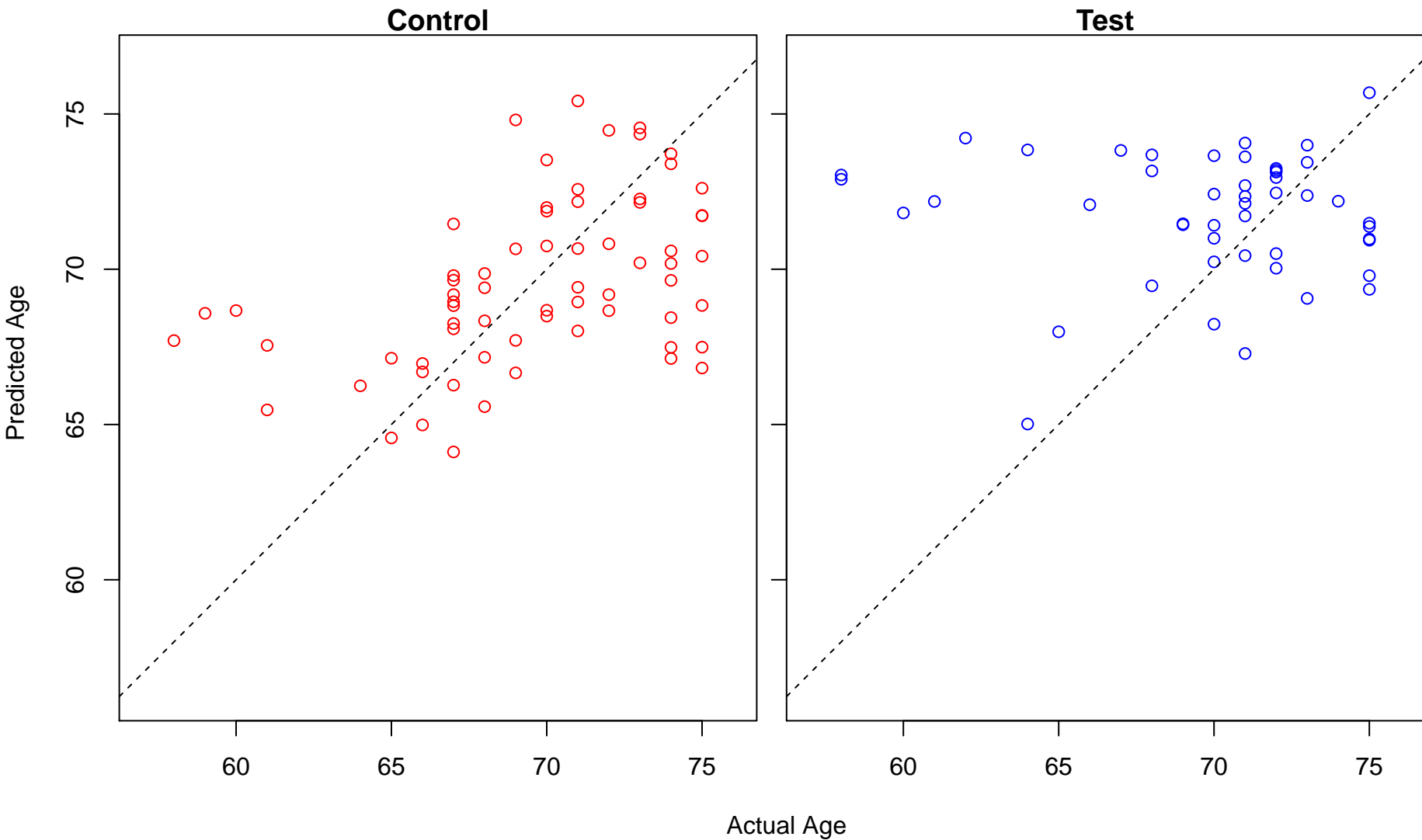
phosphatidylinositol-3-phosphate biosynthetic process (Score: 0.745914)



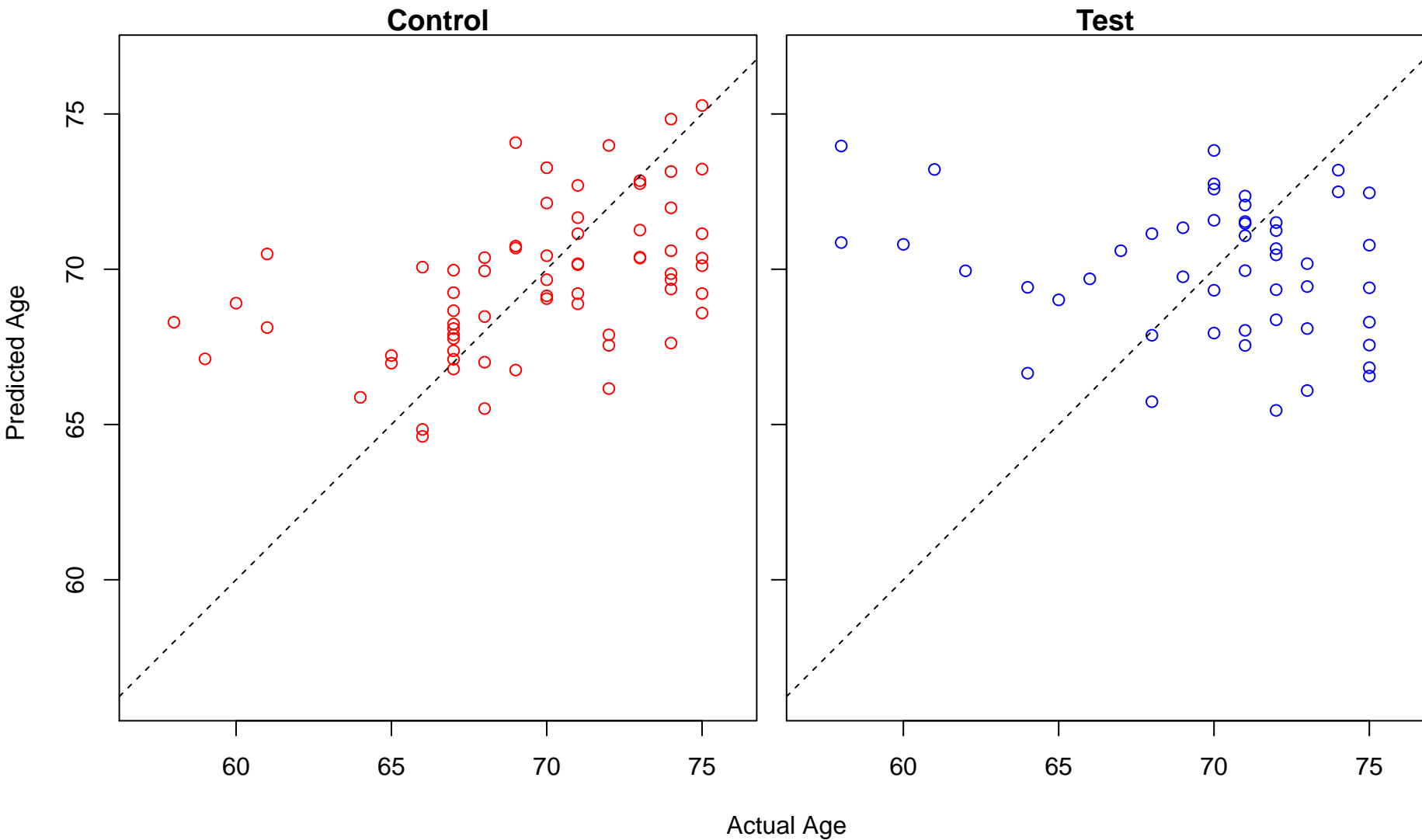
negative regulation of Rho protein signal transduction (Score: 0.745907)



protein heterooligomerization (Score: 0.745500)

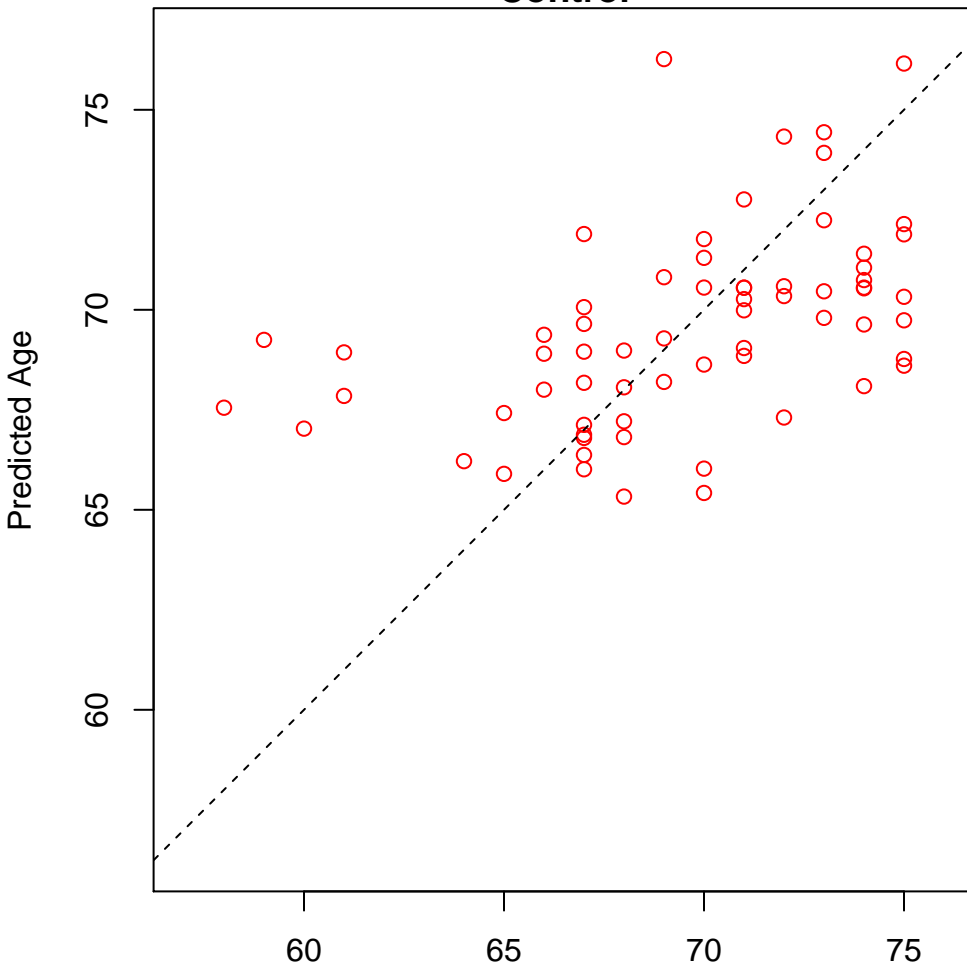


female gamete generation (Score: 0.745379)

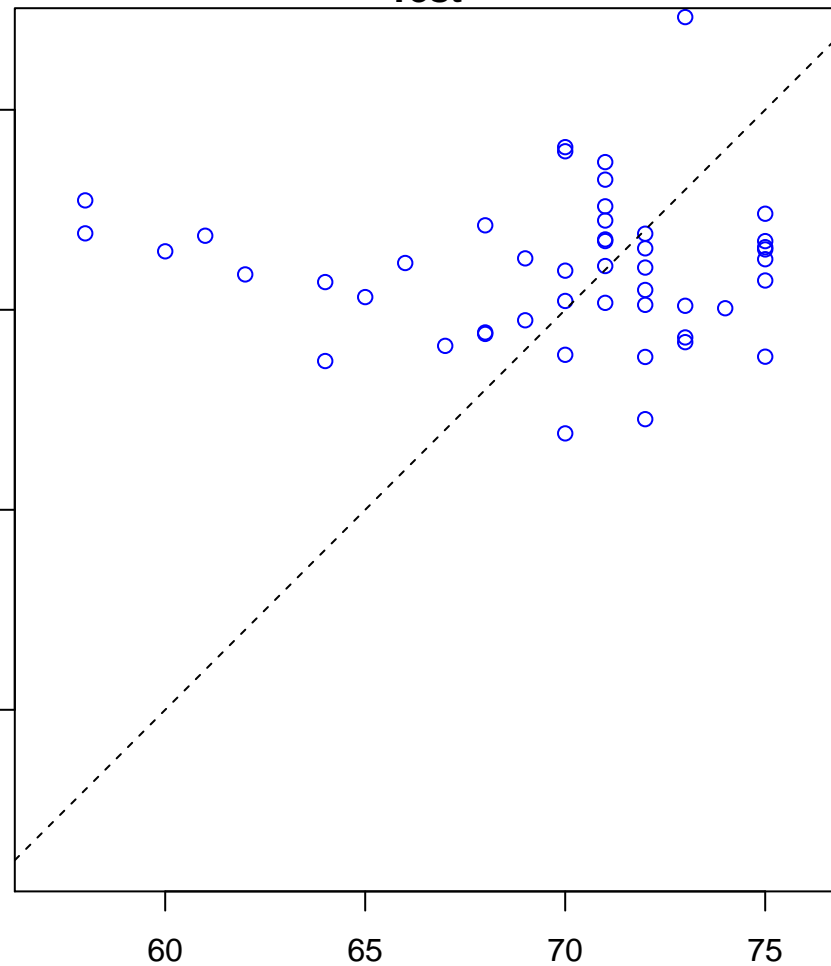


nucleotide-sugar metabolic process (Score: 0.745192)

Control

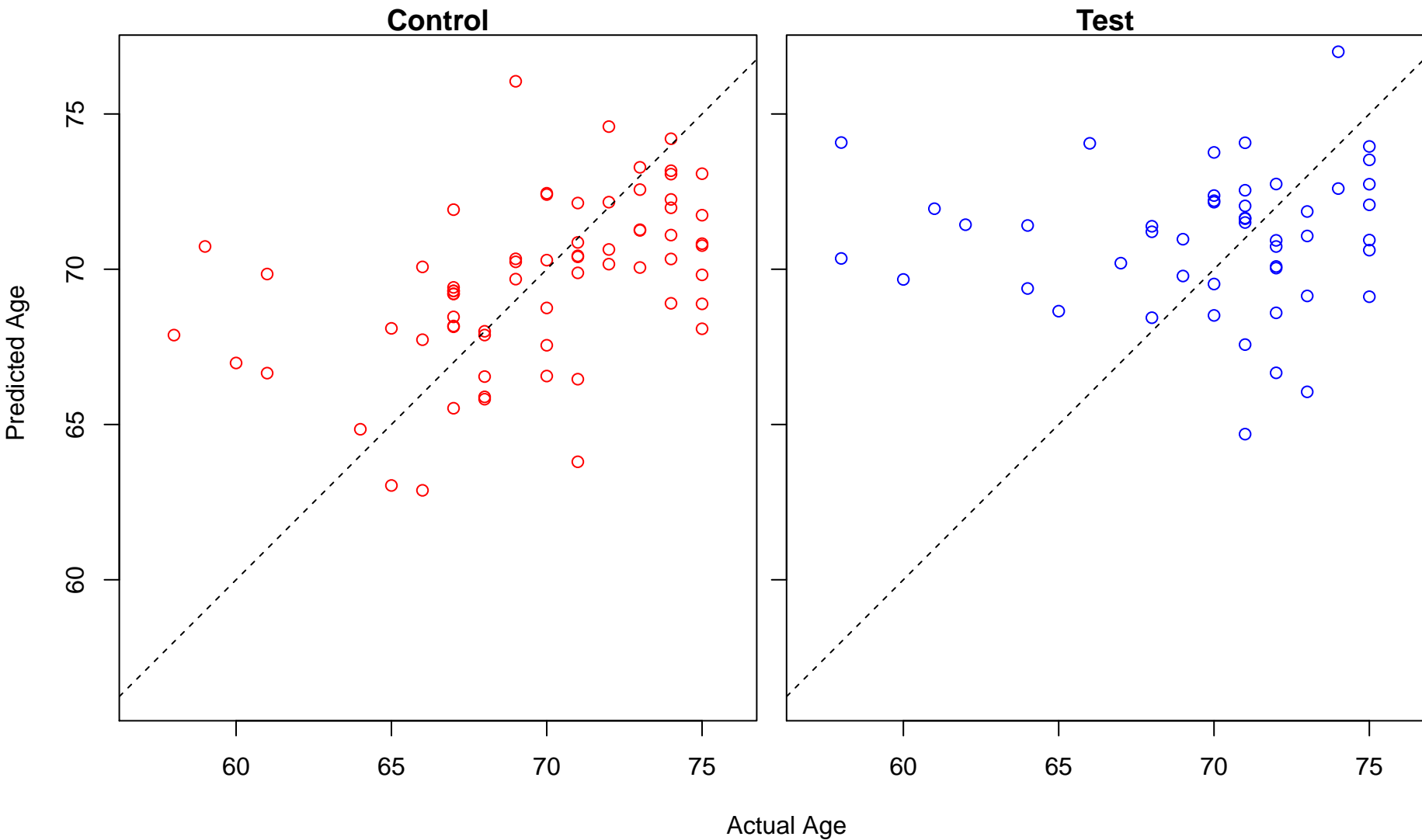


Test

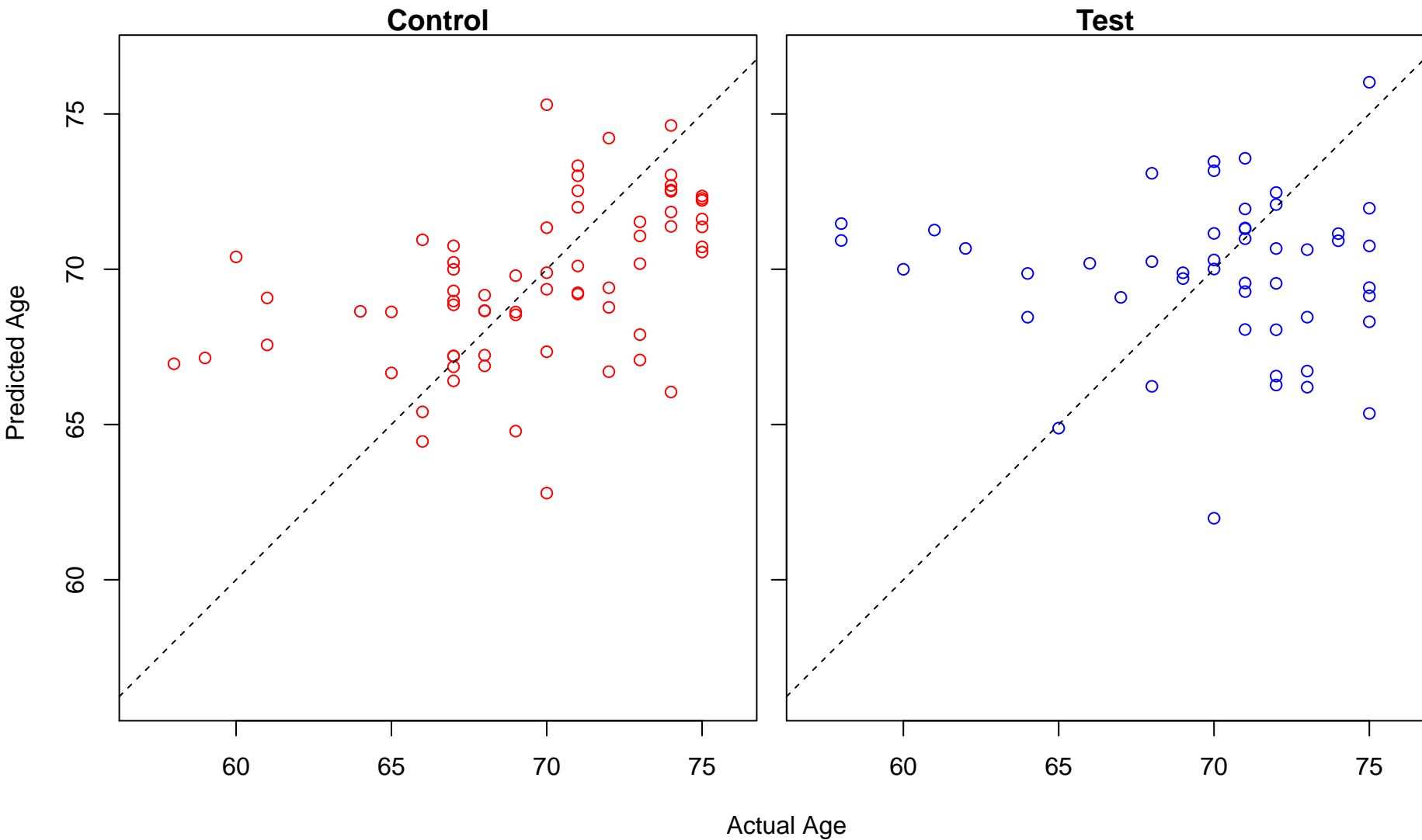


Actual Age

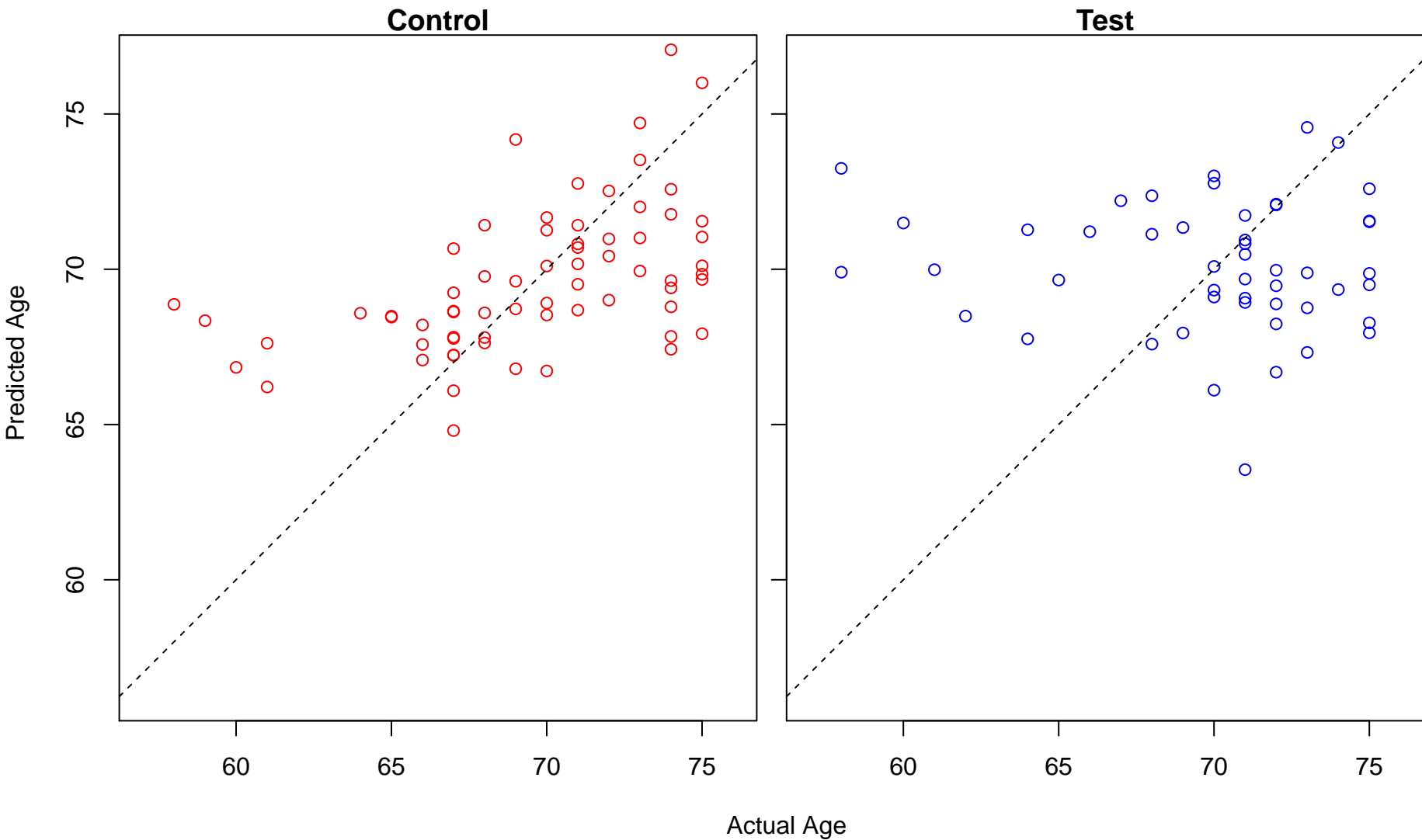
positive regulation of T cell cytokine production (Score: 0.745178)



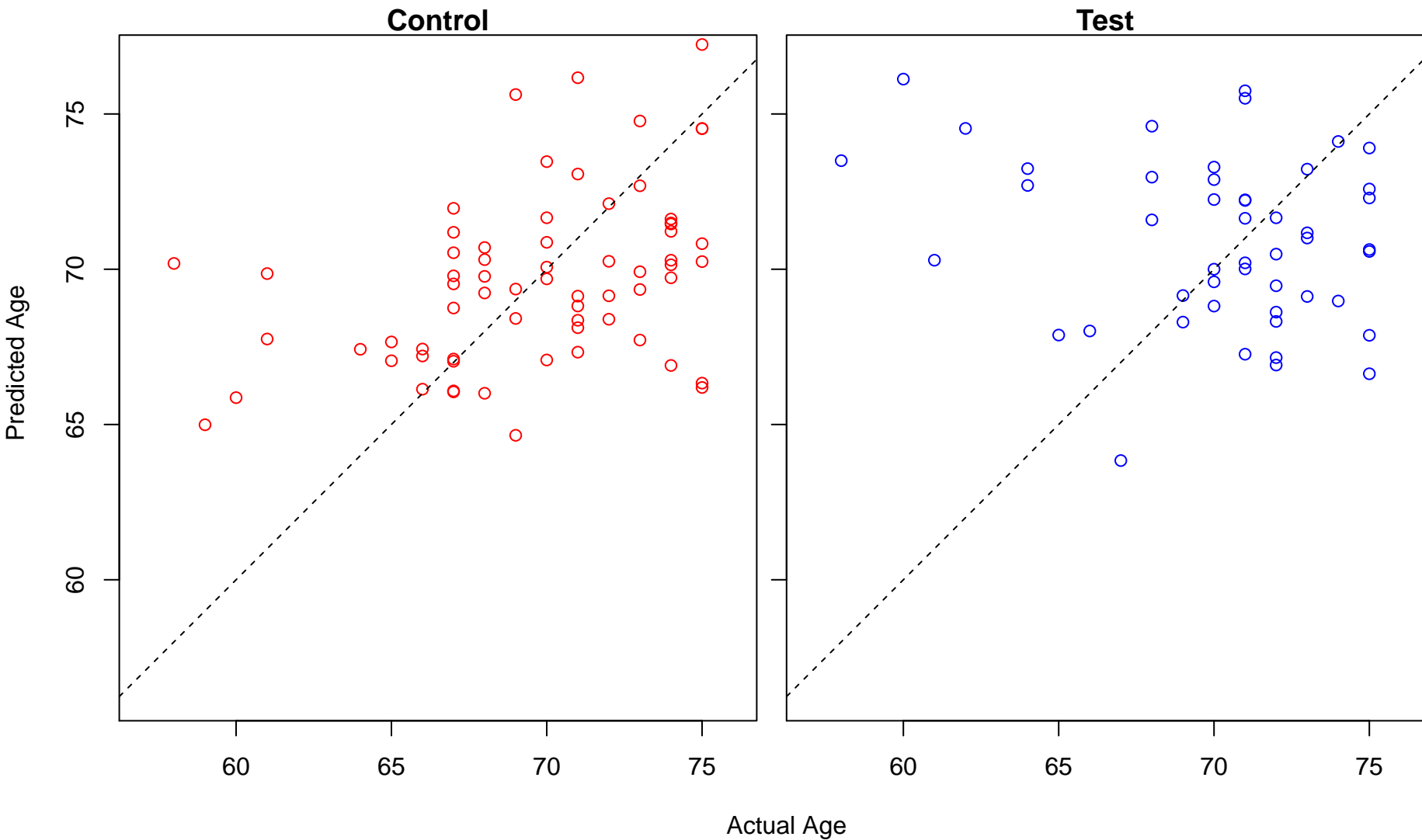
type 2 immune response (Score: 0.745061)



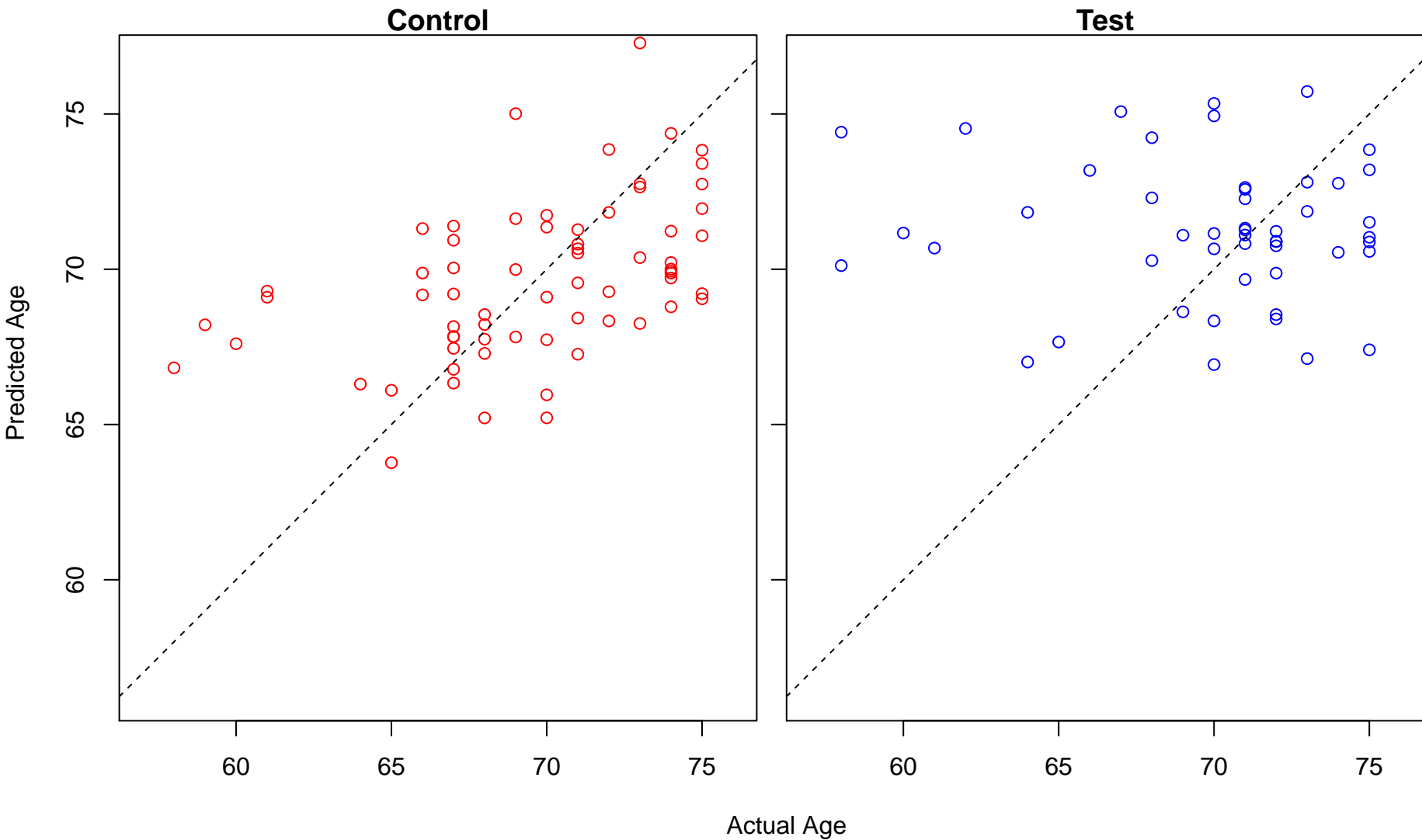
negative regulation of phosphatidylinositol 3-kinase signaling (Score: 0.744994)



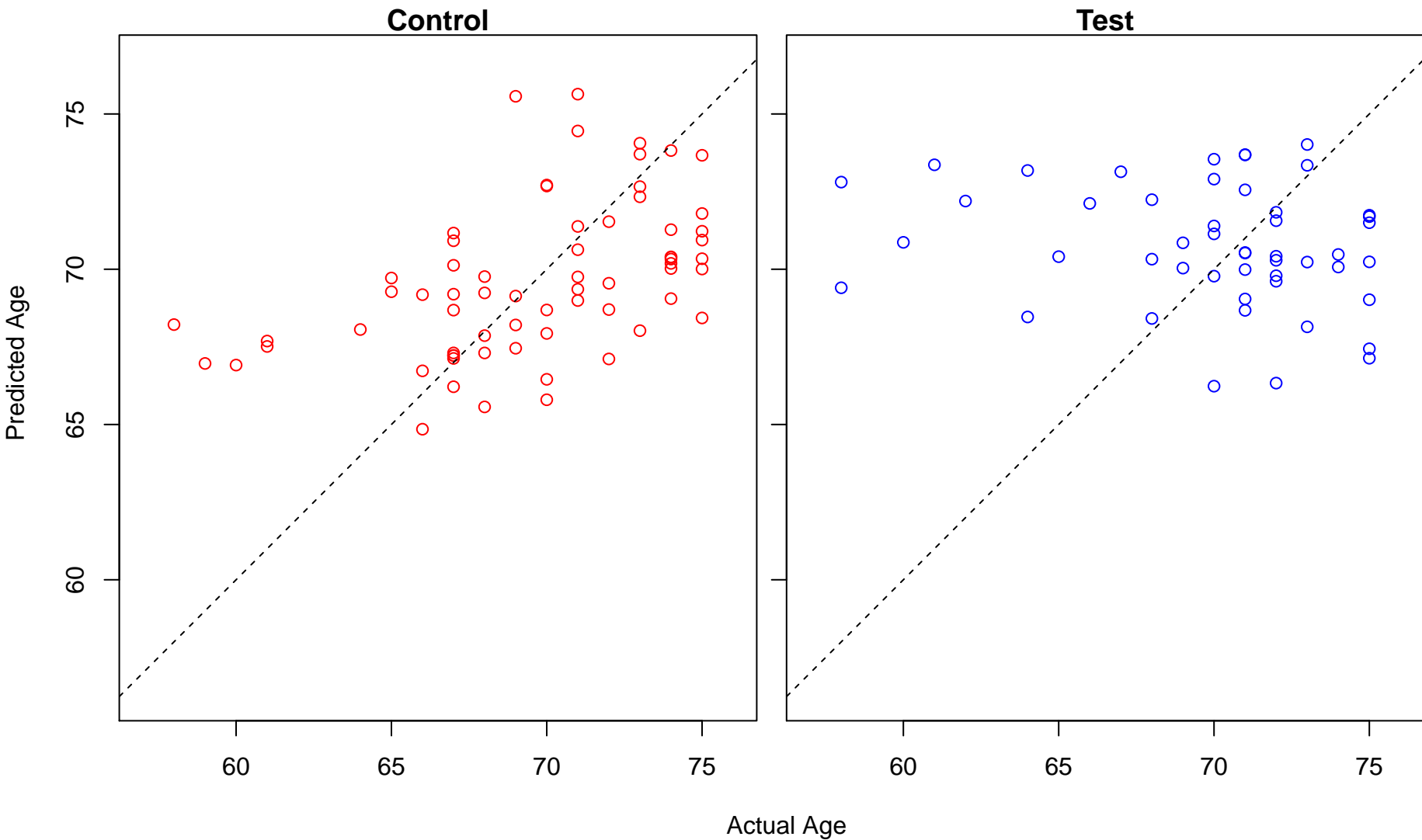
cellular response to ATP (Score: 0.744197)



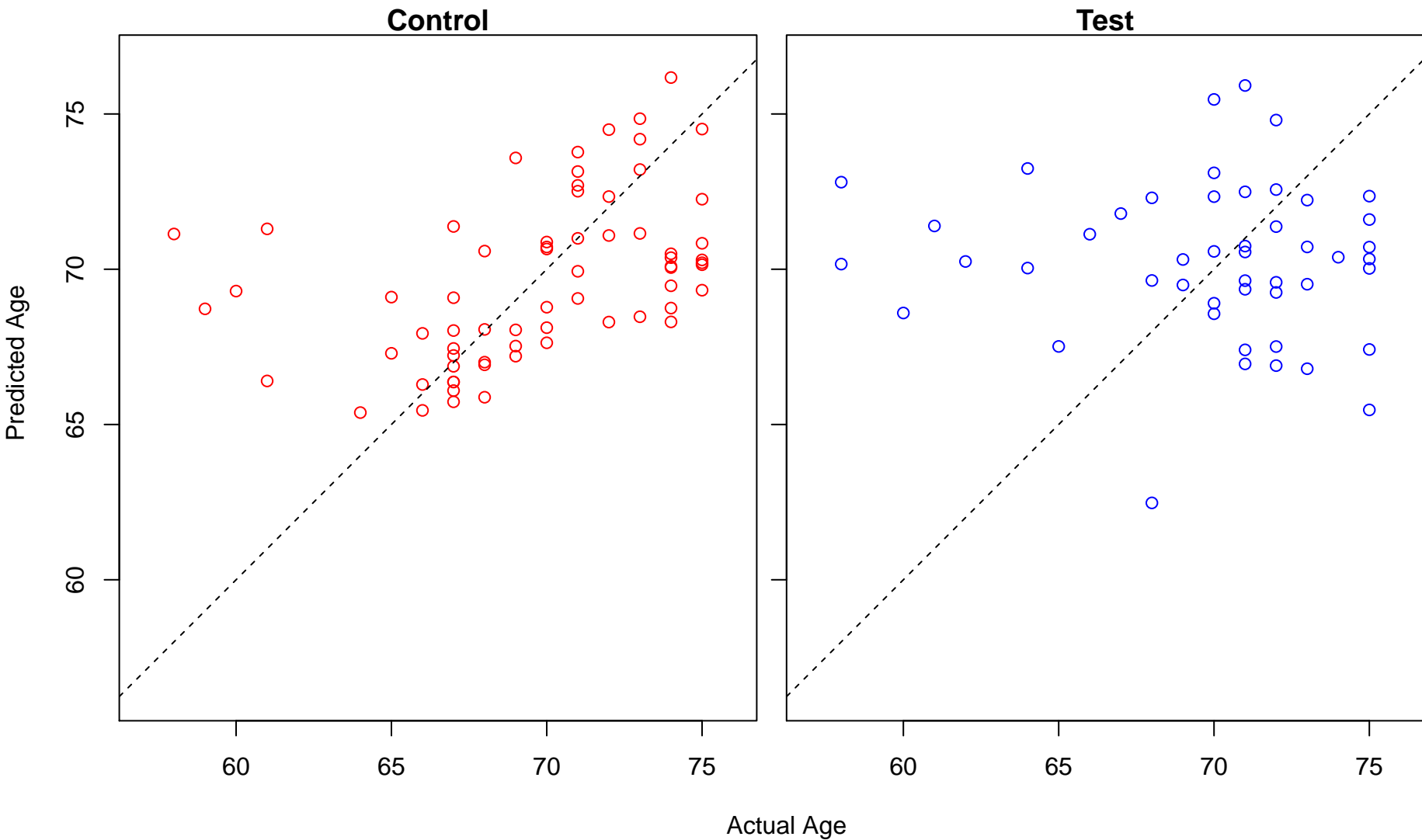
negative regulation of gene silencing (Score: 0.744169)



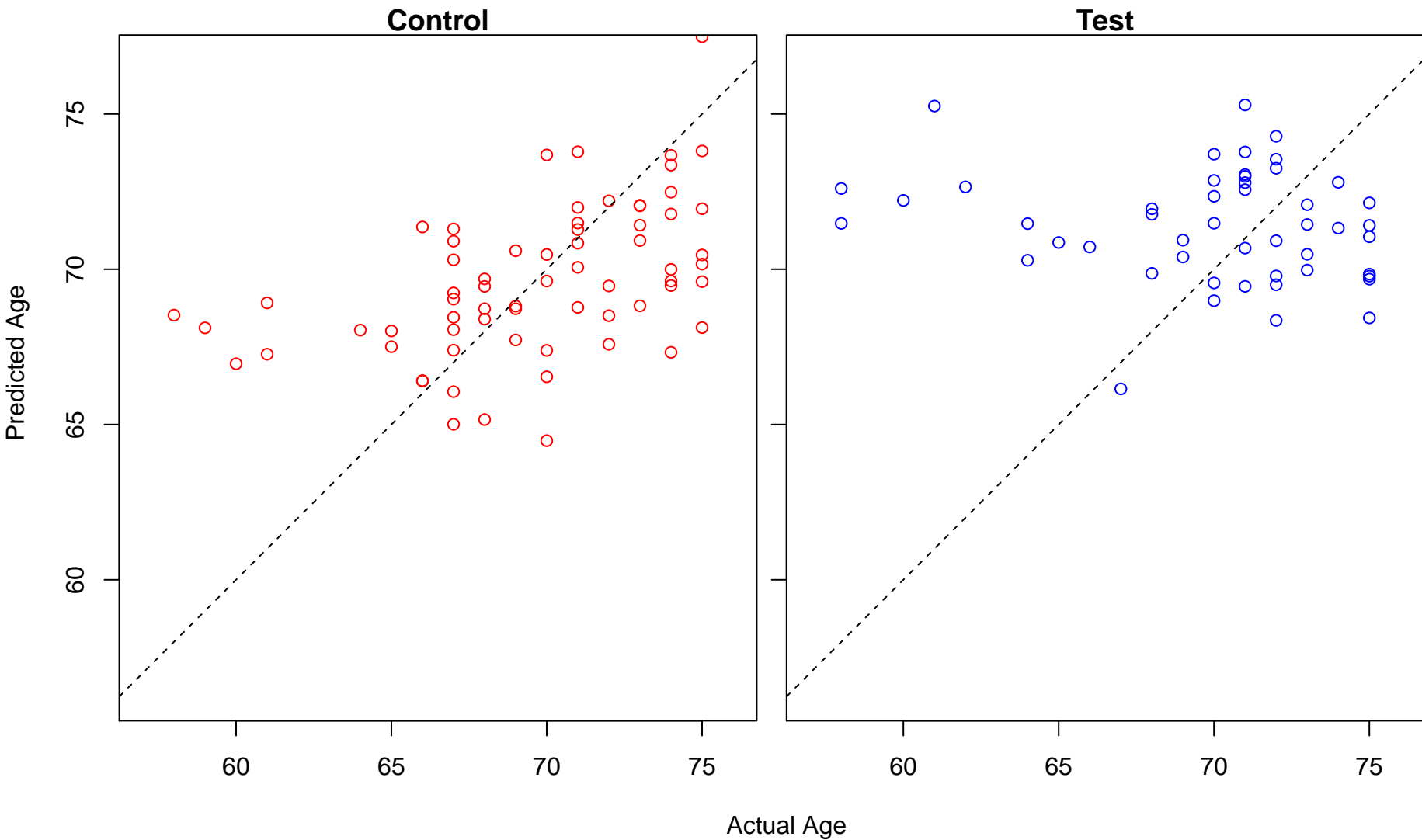
regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway (Score: 0.74)



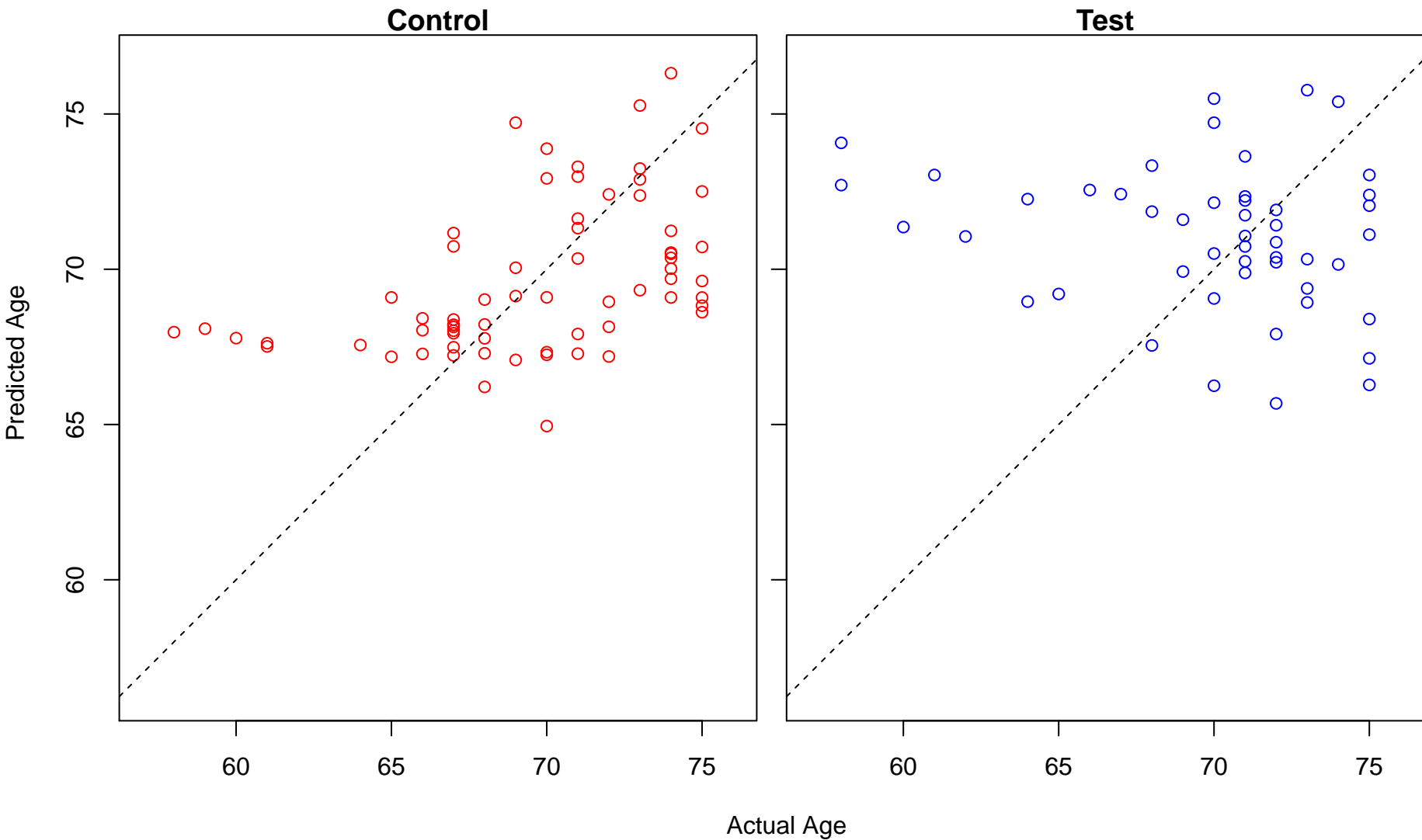
regulation of neural precursor cell proliferation (Score: 0.743902)



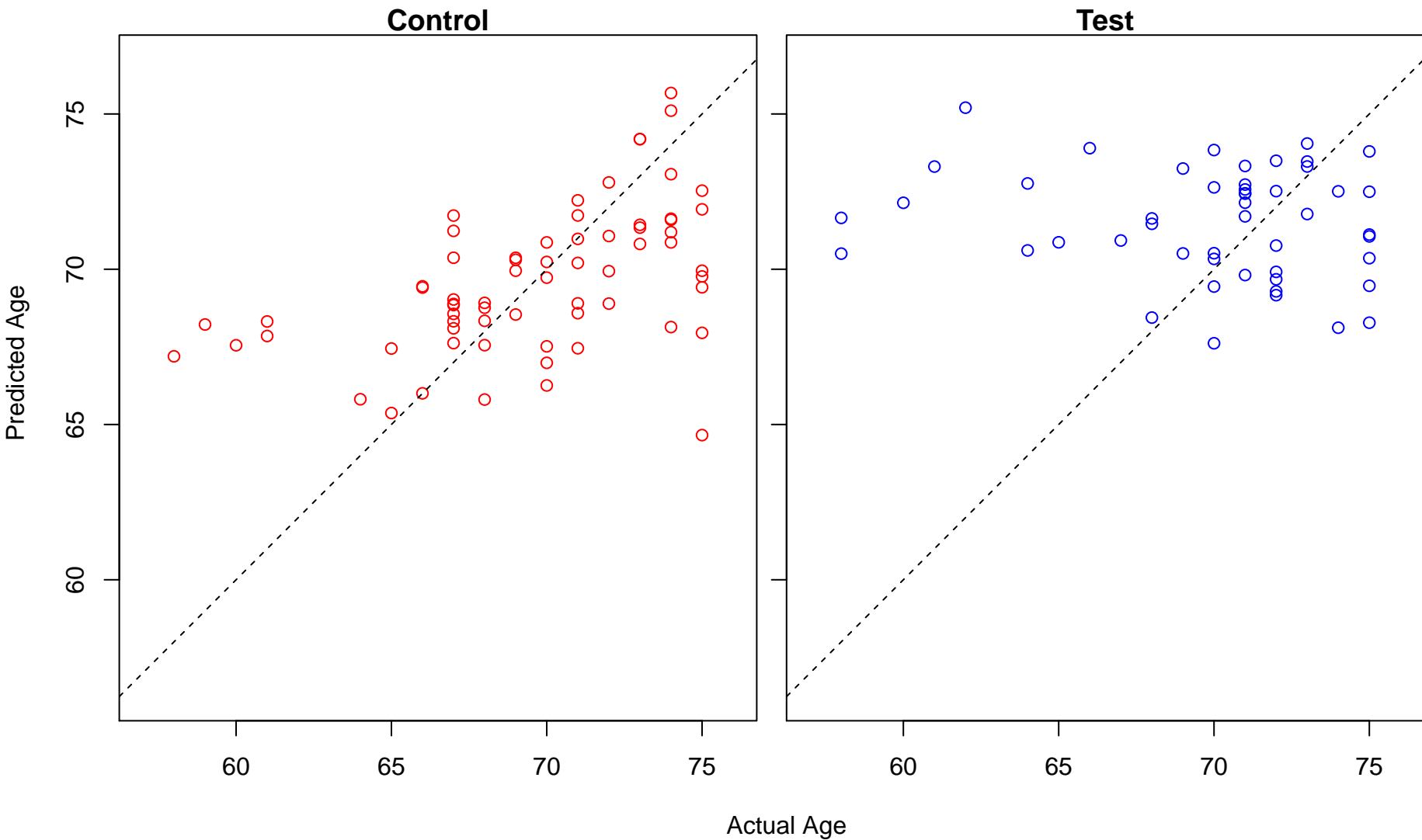
histone arginine methylation (Score: 0.743852)



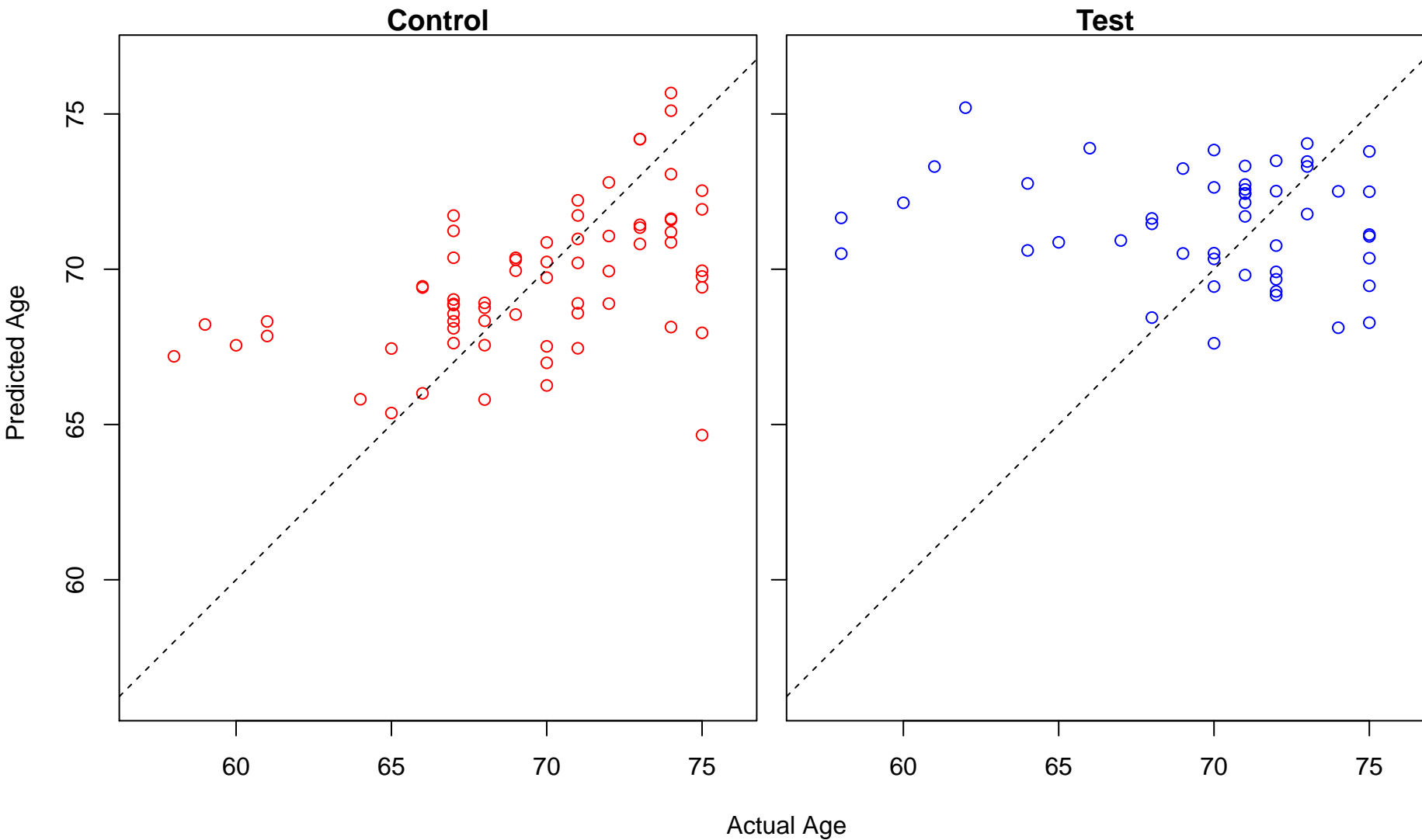
RNA polyadenylation (Score: 0.743816)



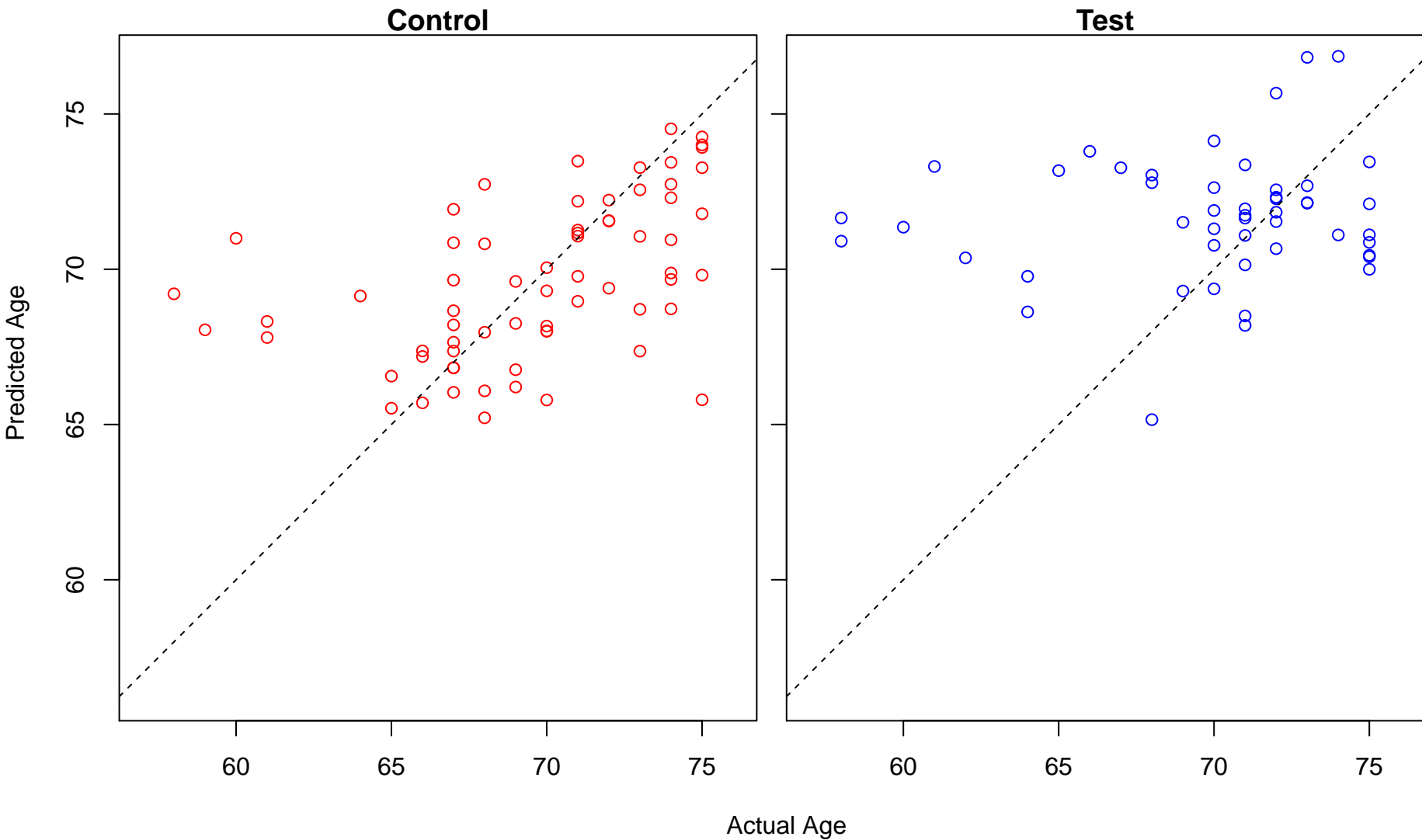
regulation of phospholipid transport (Score: 0.743215)



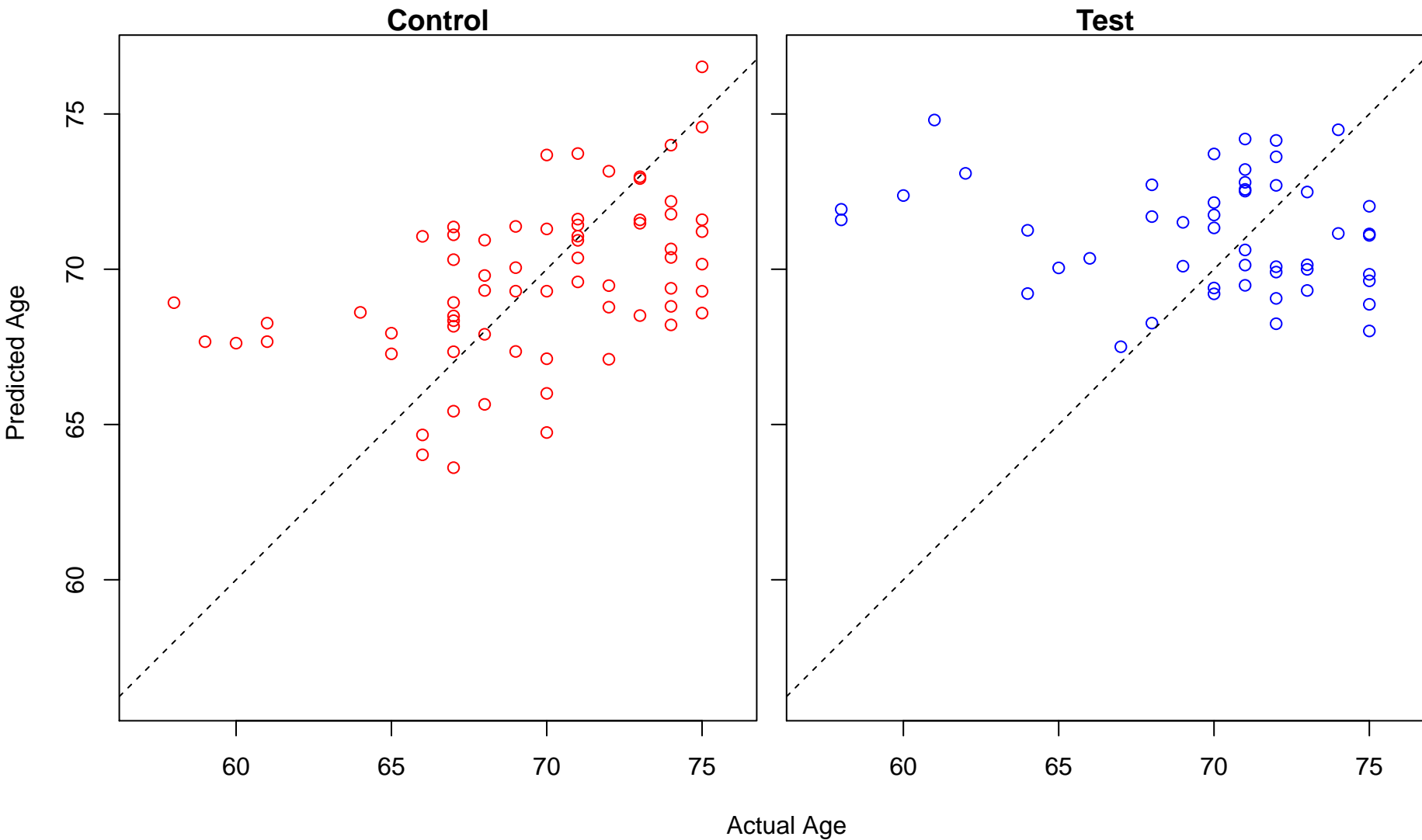
positive regulation of phospholipid transport (Score: 0.743215)



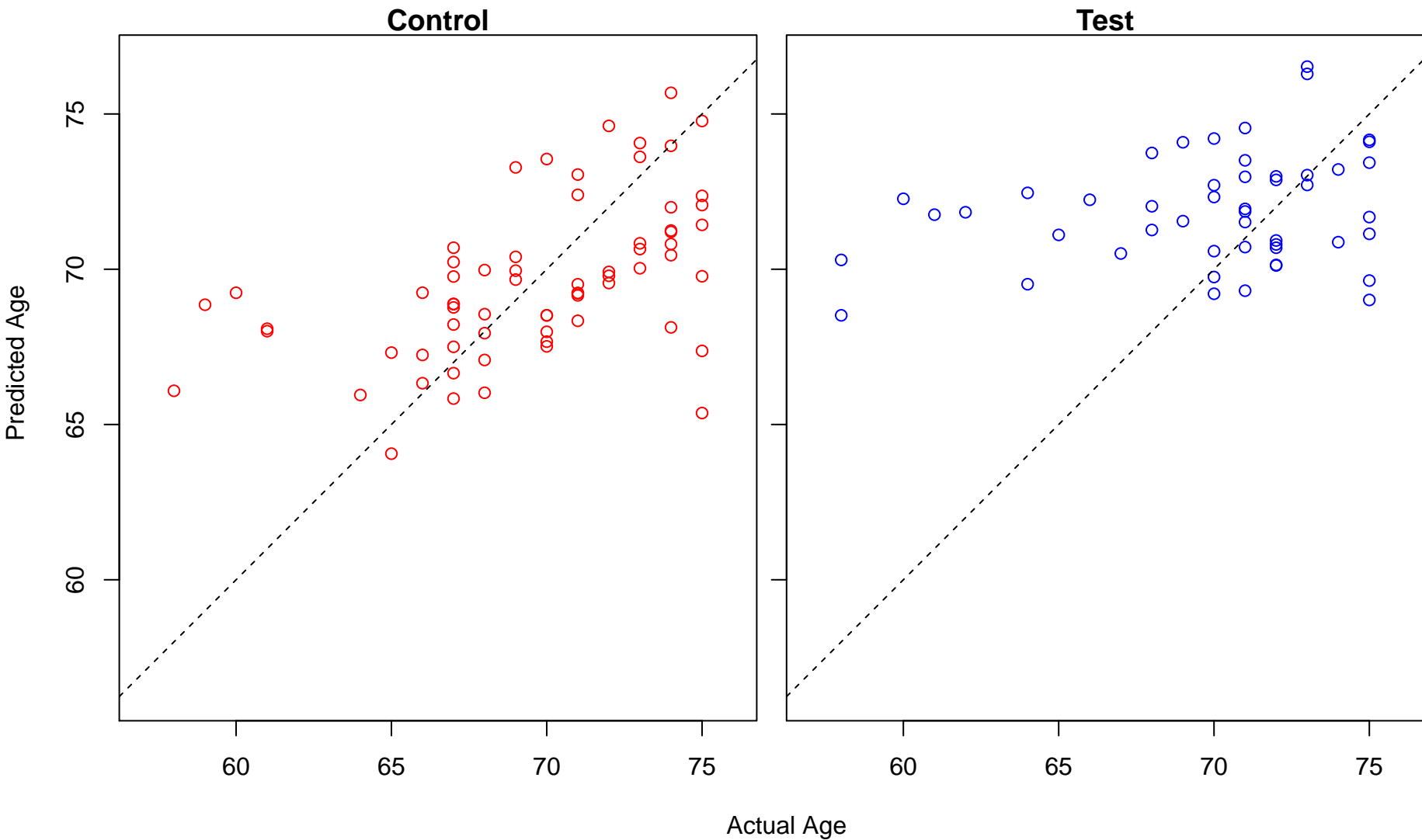
gas homeostasis (Score: 0.742695)



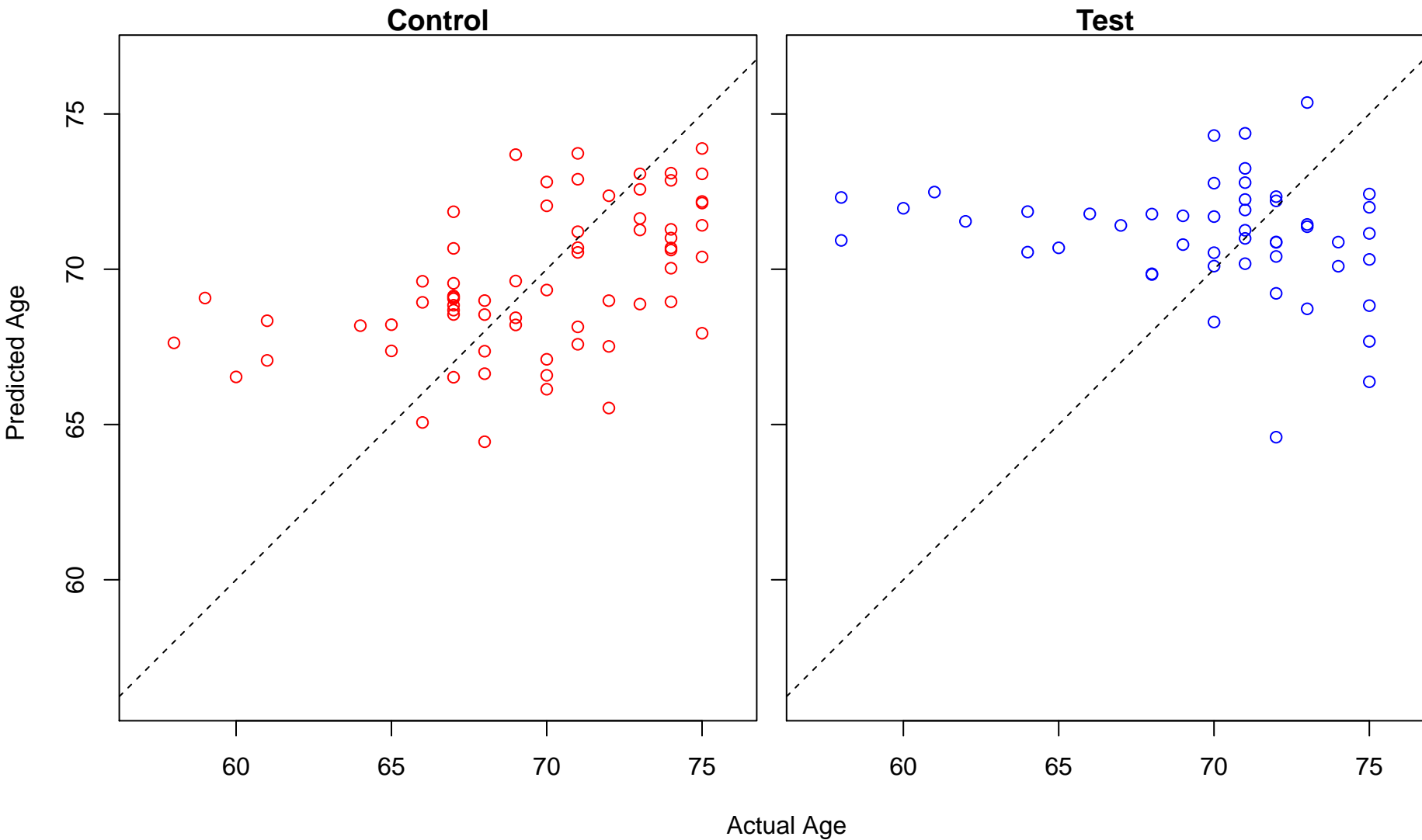
peptidyl-arginine modification (Score: 0.741604)



protein-lipid complex assembly (Score: 0.741132)

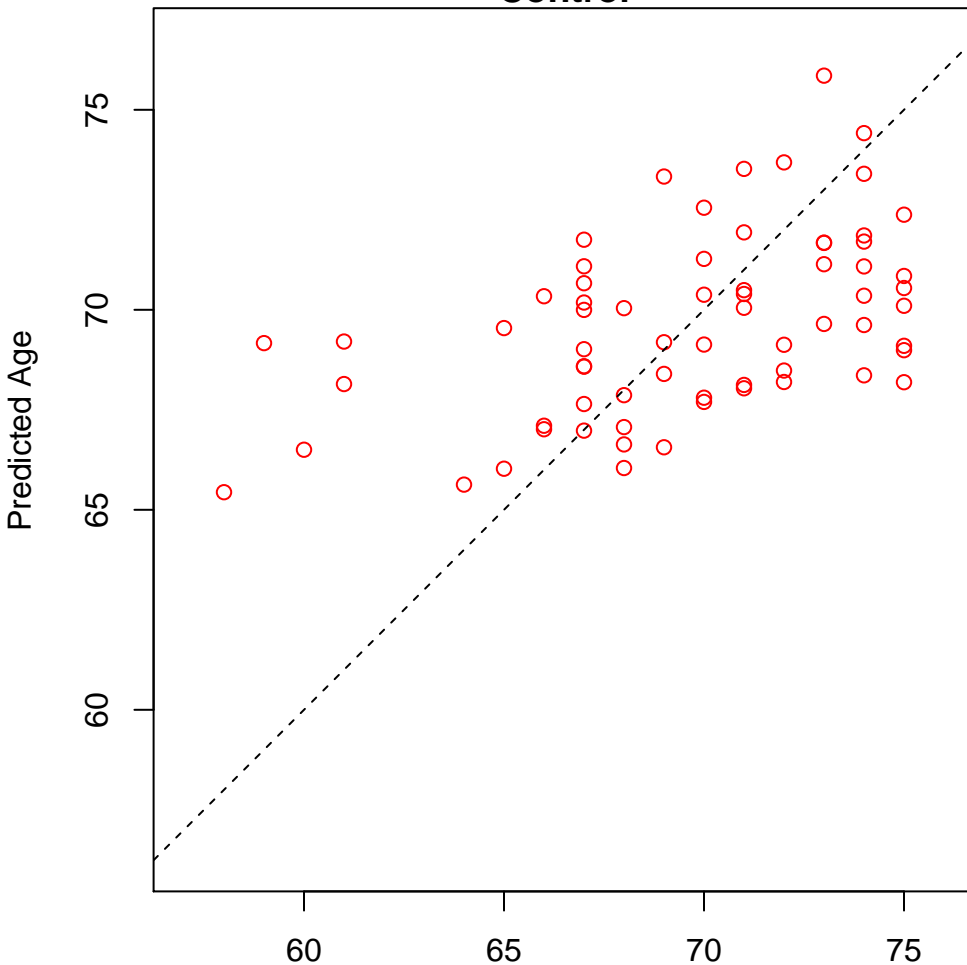


methionine biosynthetic process (Score: 0.741003)

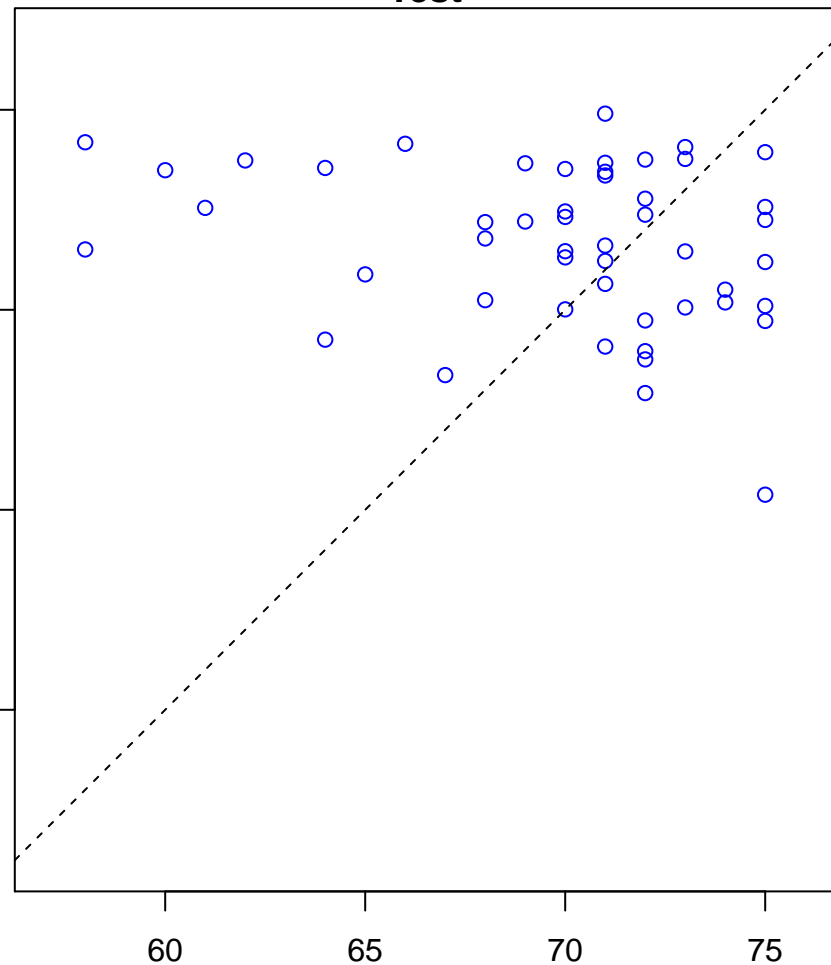


coronary vasculature morphogenesis (Score: 0.740366)

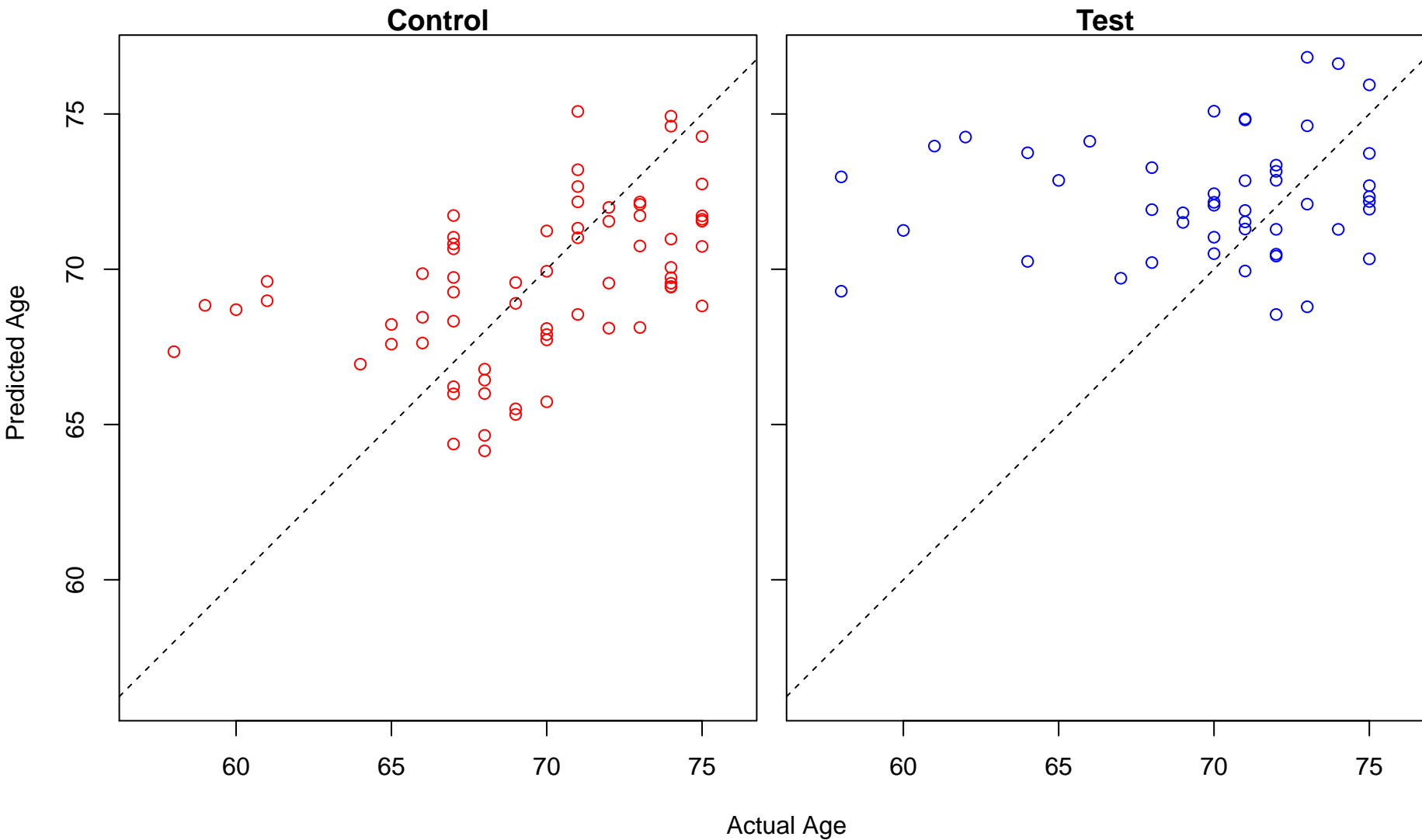
Control



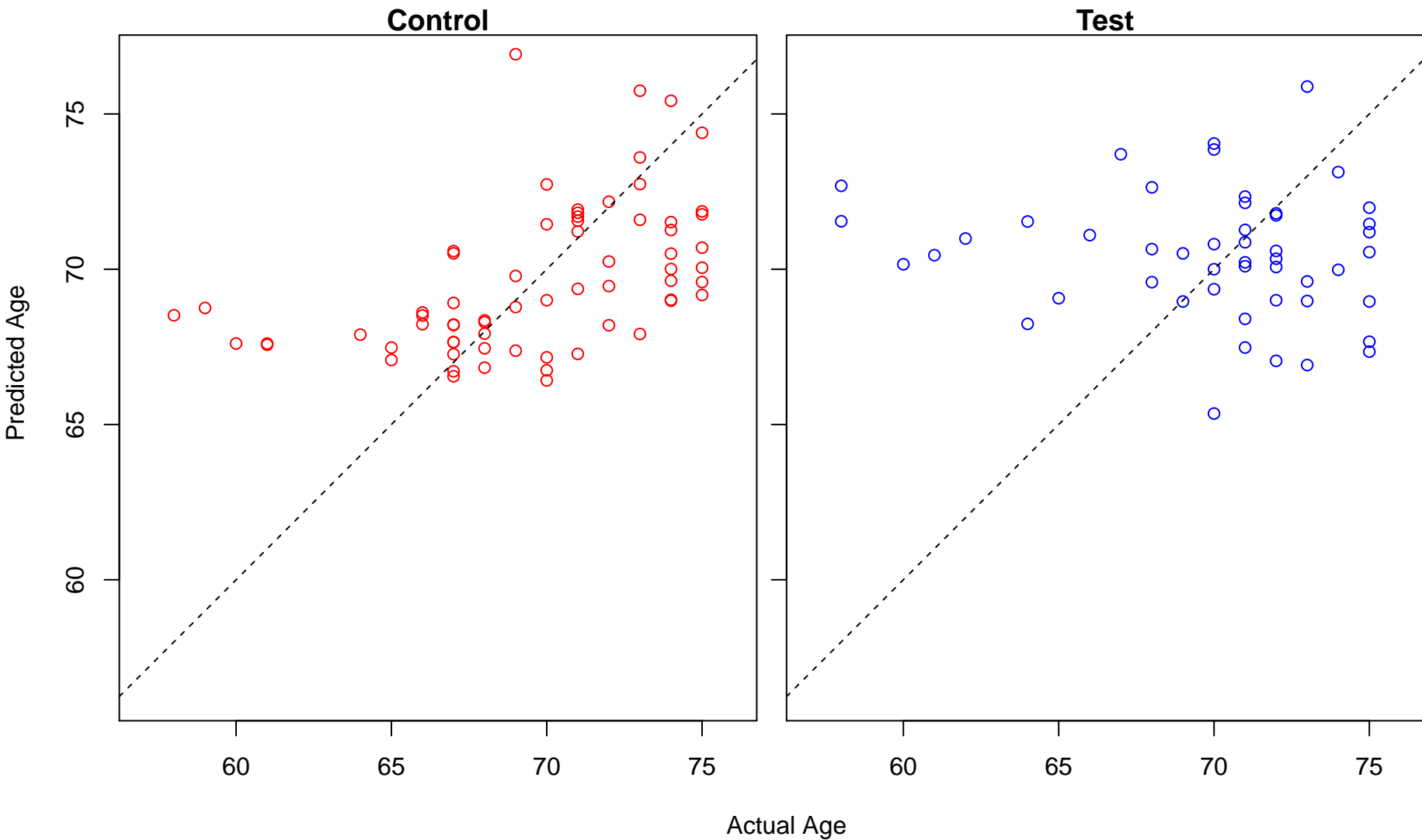
Test



regulation of skeletal muscle tissue development (Score: 0.738868)

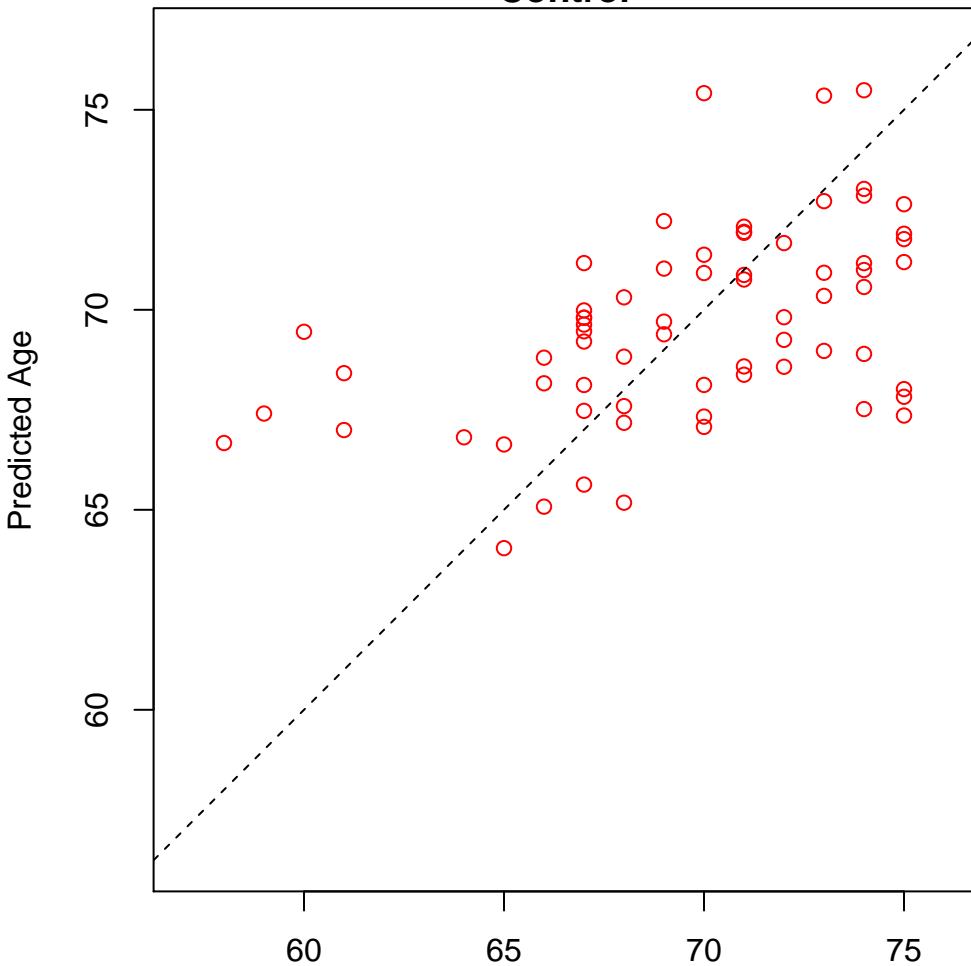


regulation of gene silencing (Score: 0.738748)

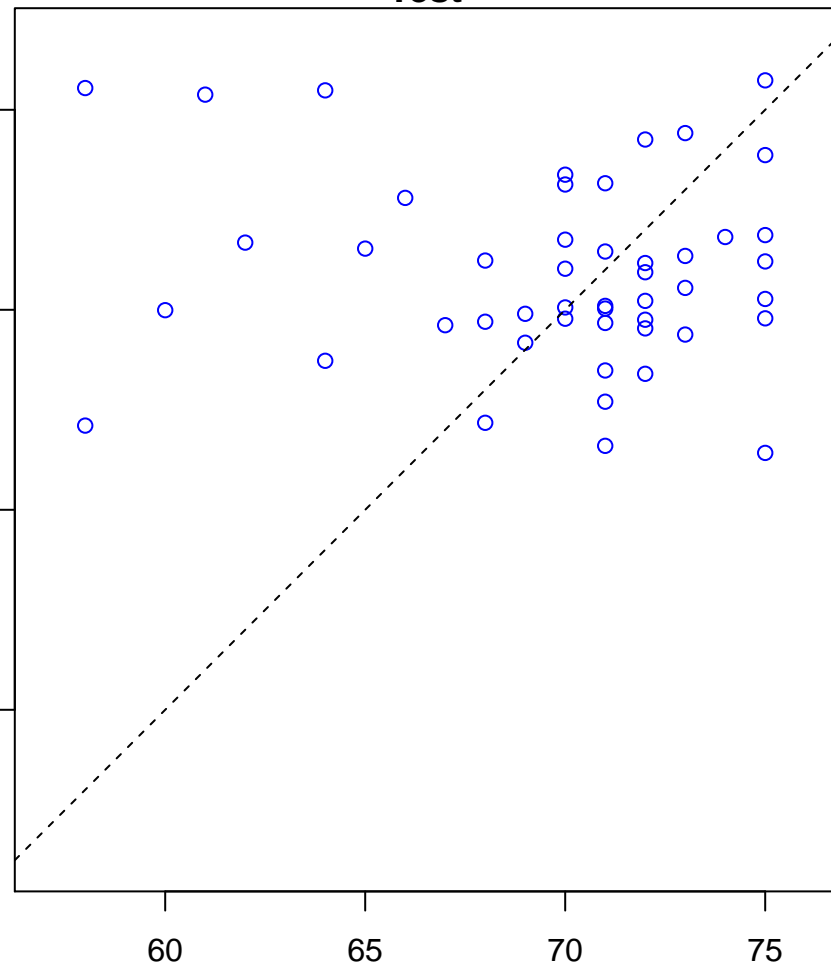


negative regulation of peptide secretion (Score: 0.738651)

Control

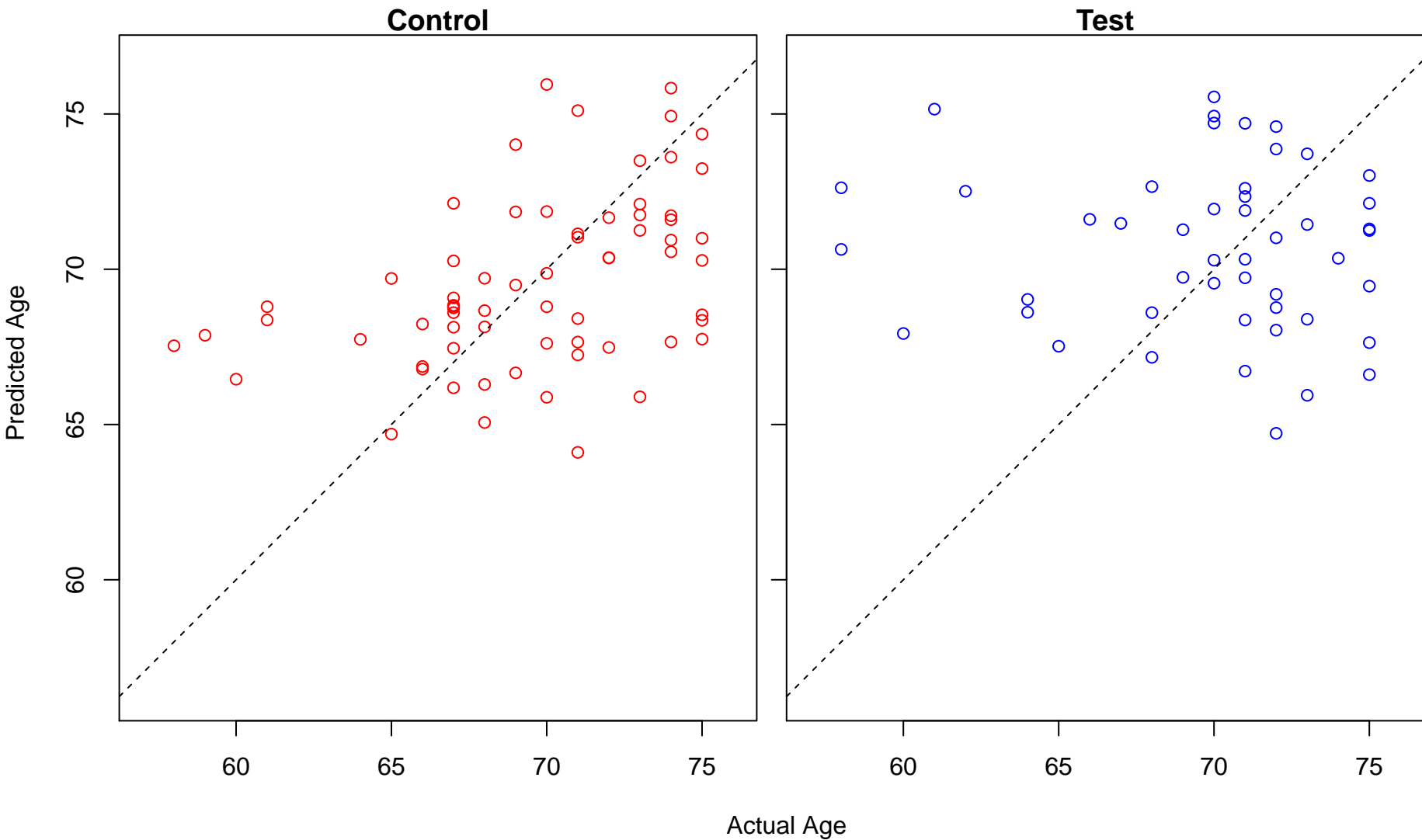


Test

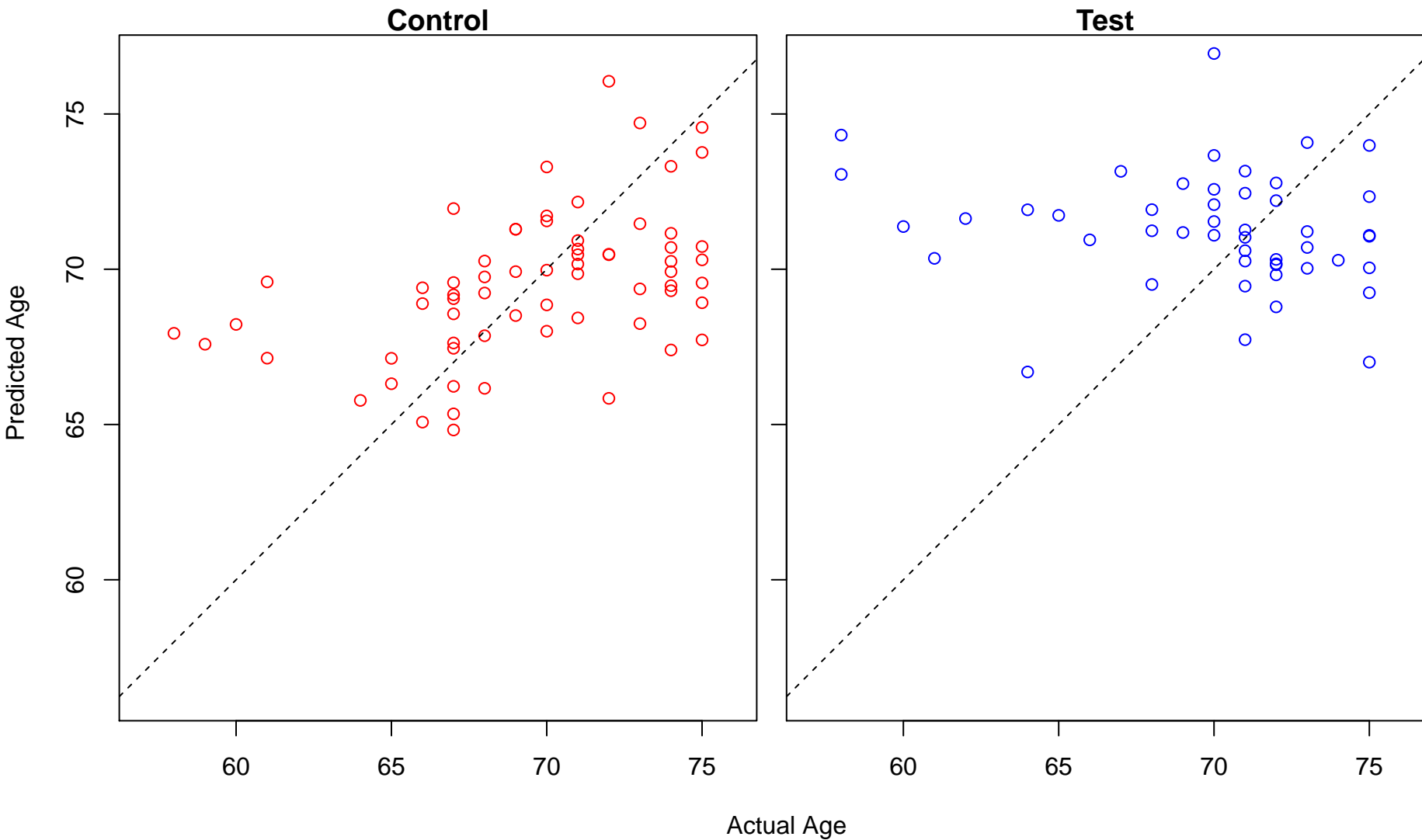


Actual Age

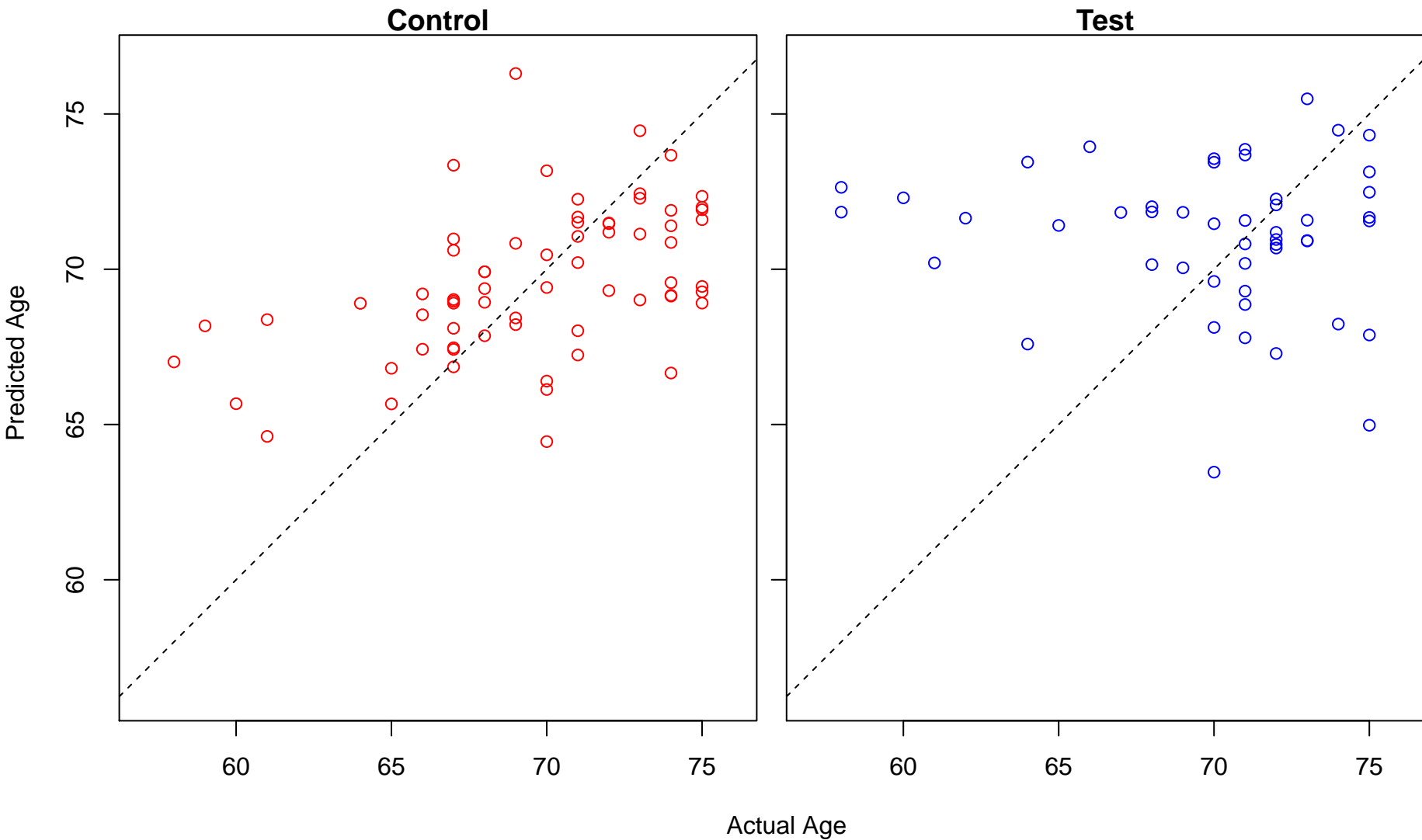
positive regulation of toll-like receptor signaling pathway (Score: 0.738319)



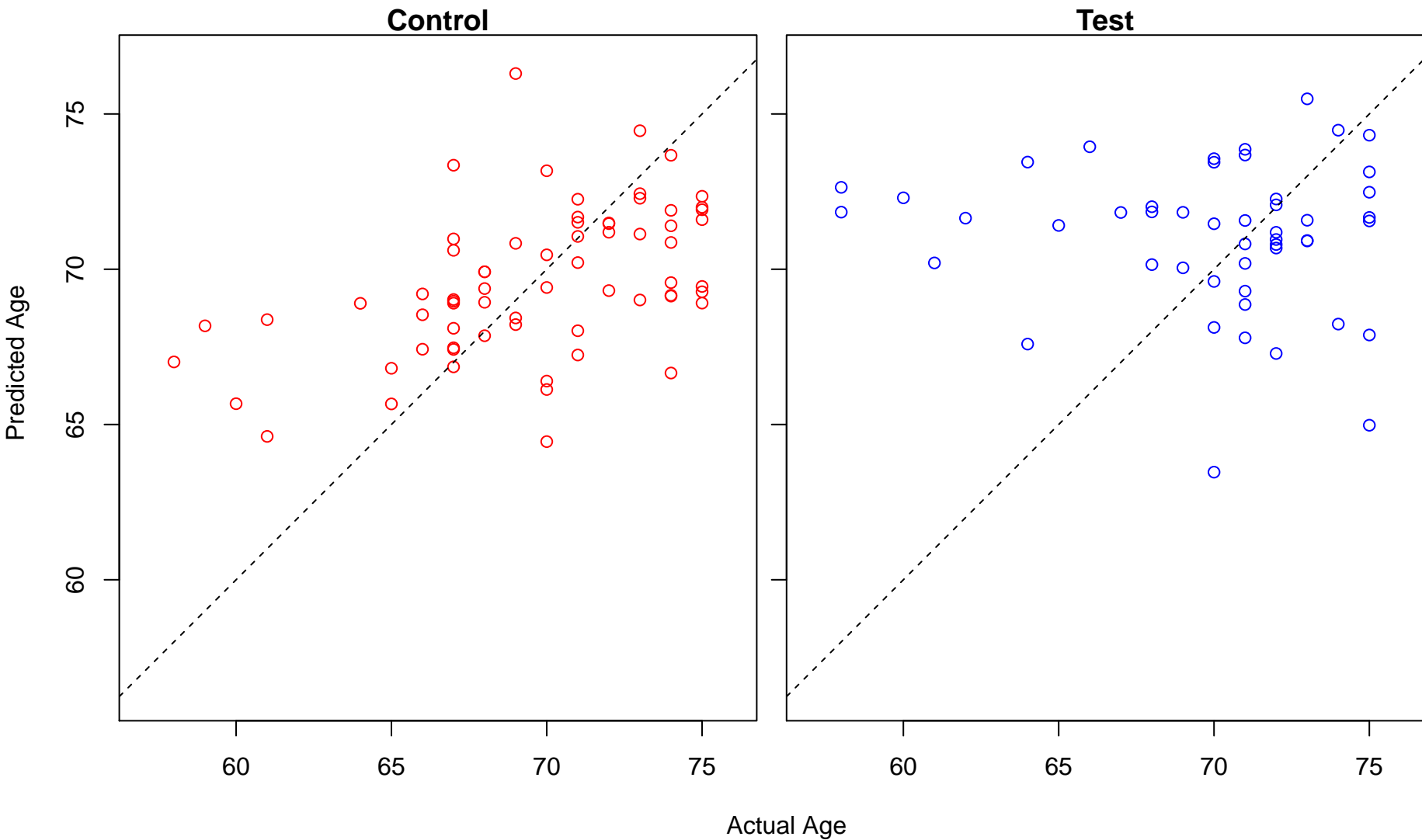
feeding behavior (Score: 0.738139)



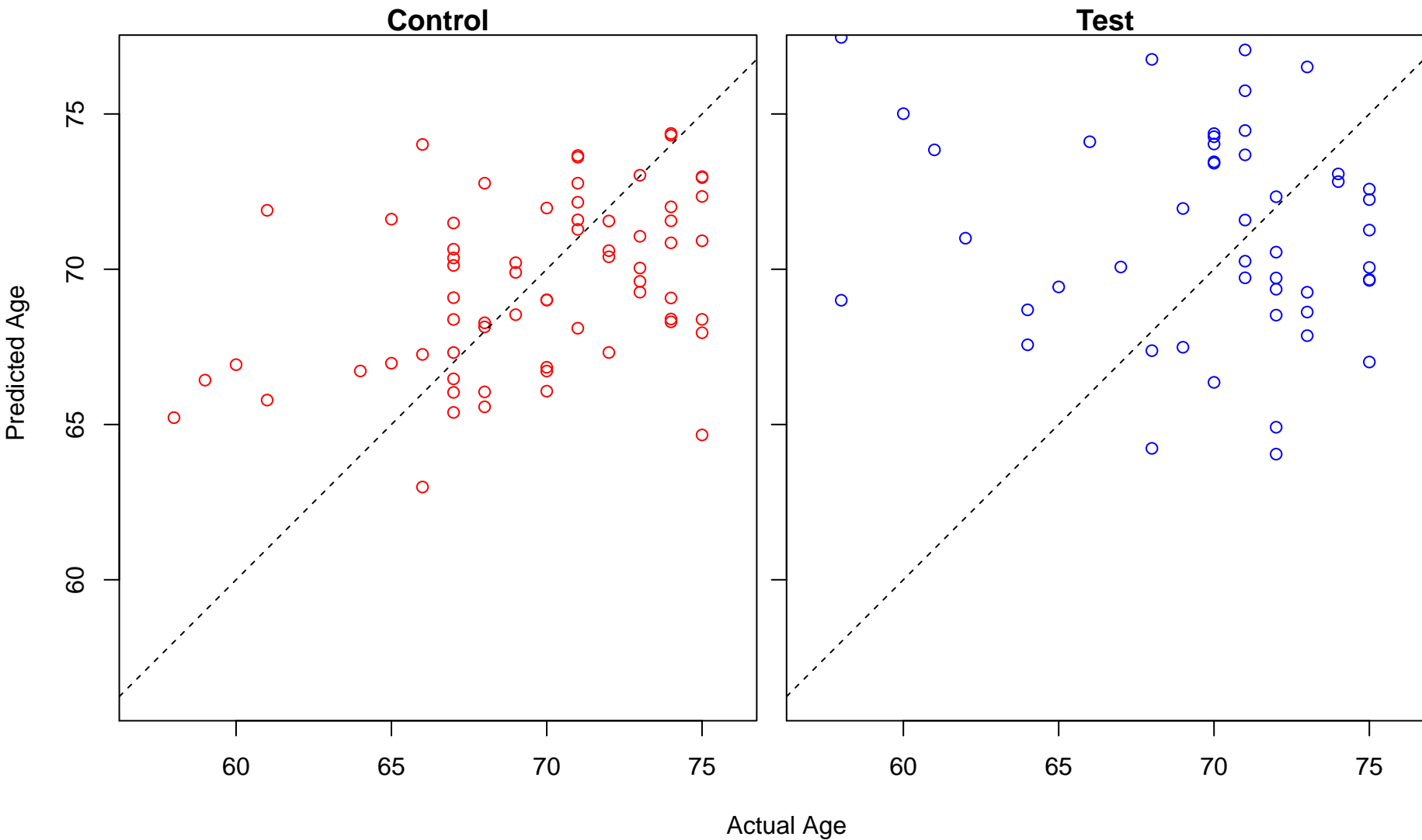
pigment accumulation (Score: 0.737991)



cellular pigment accumulation (Score: 0.737991)

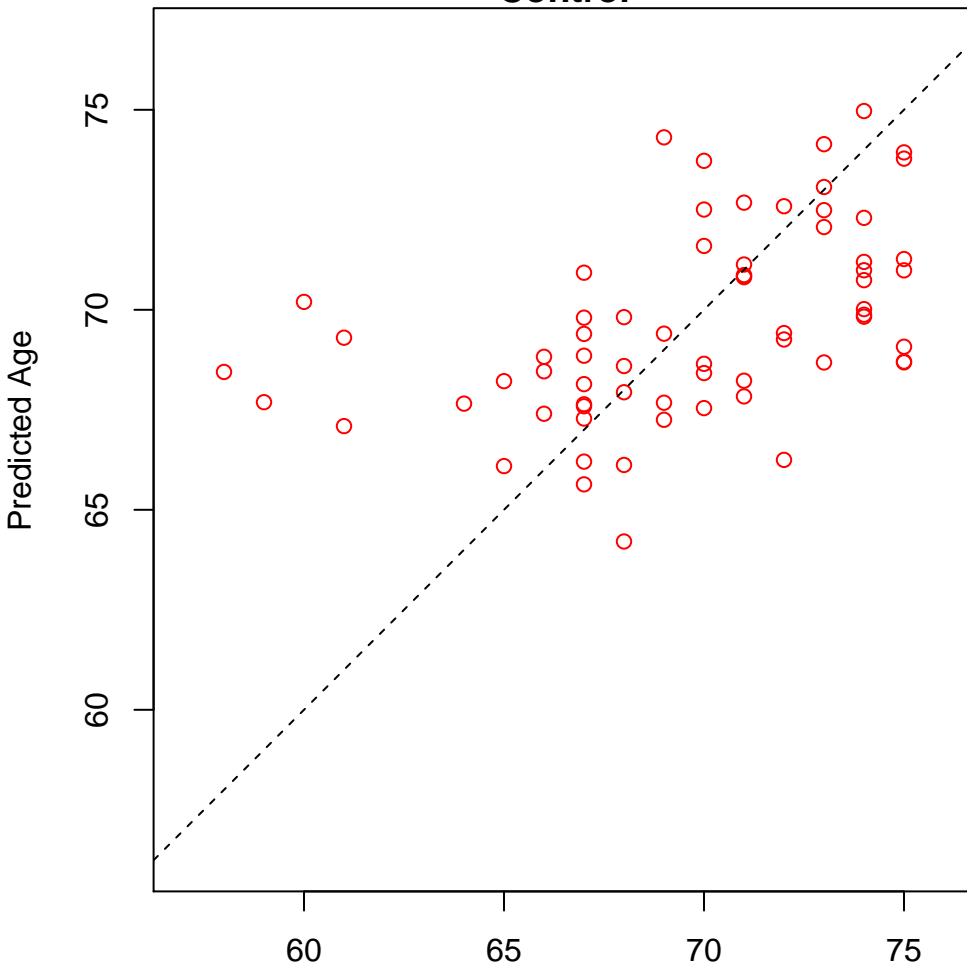


neuron recognition (Score: 0.737765)

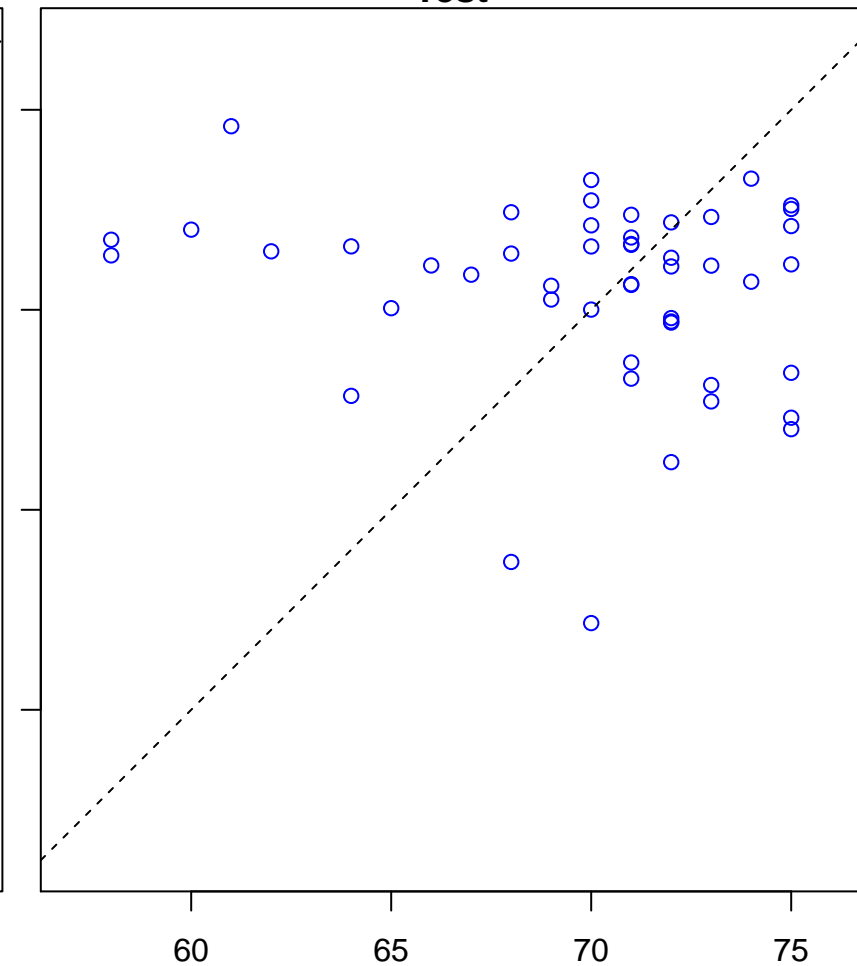


negative regulation of anion transport (Score: 0.737478)

Control

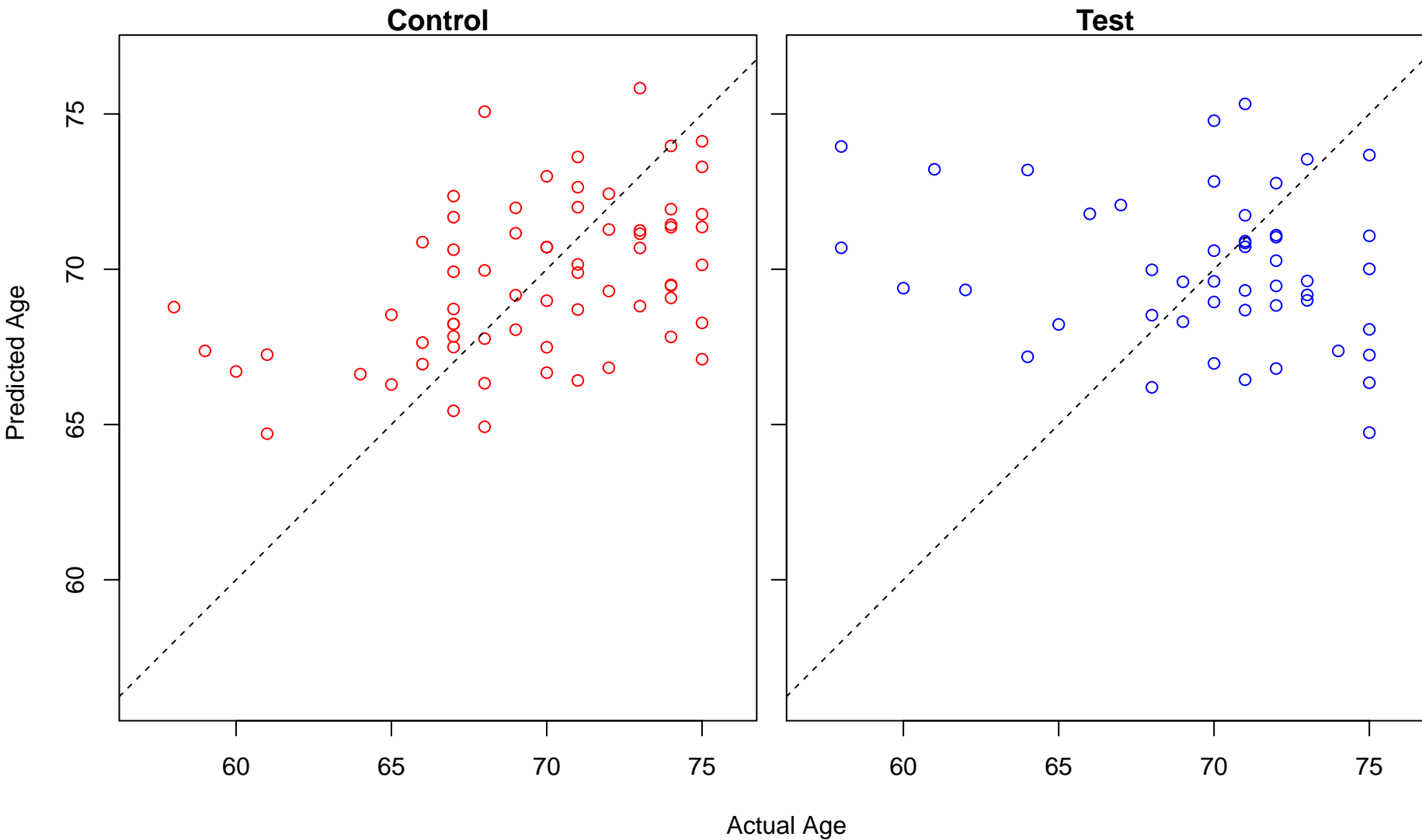


Test

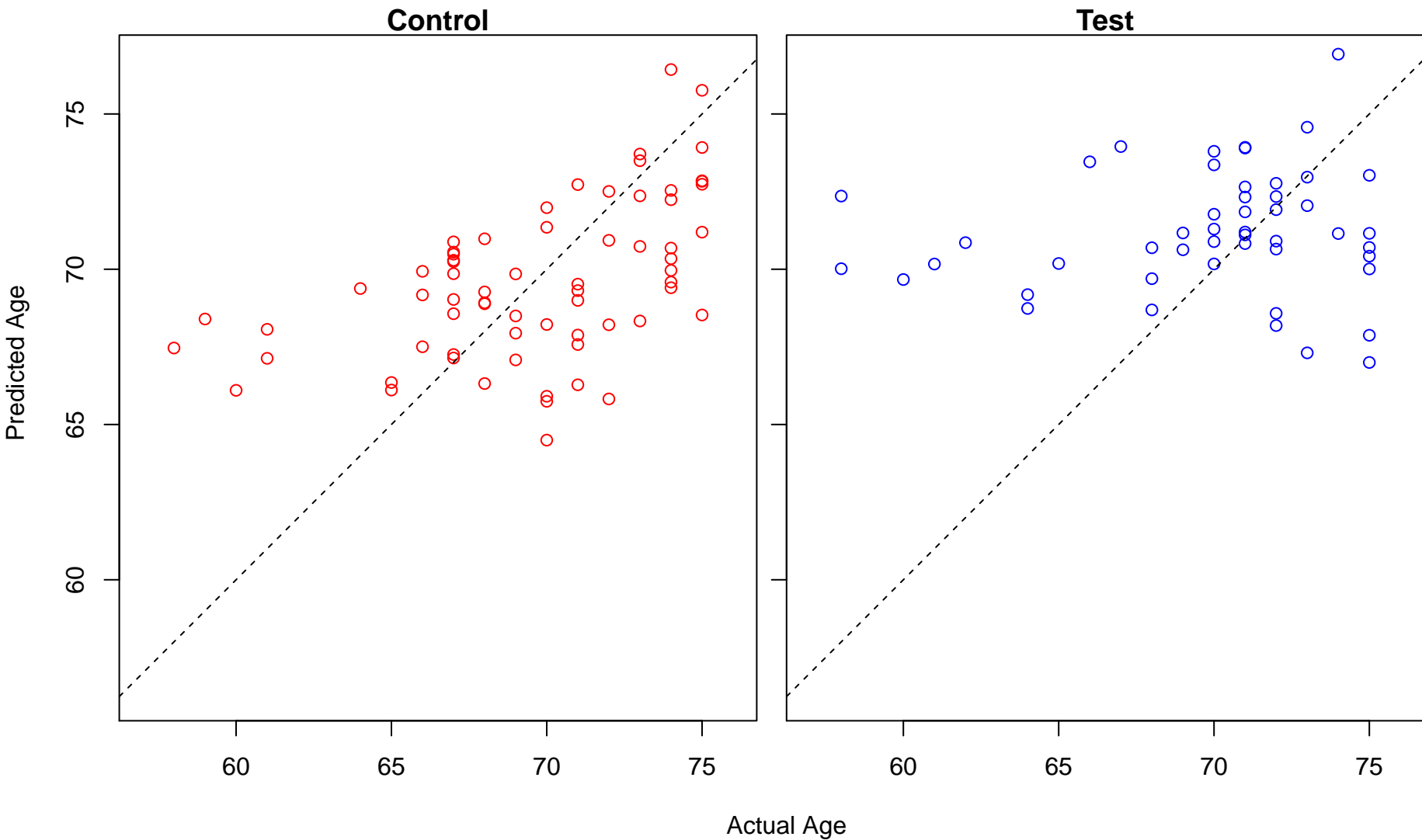


Actual Age

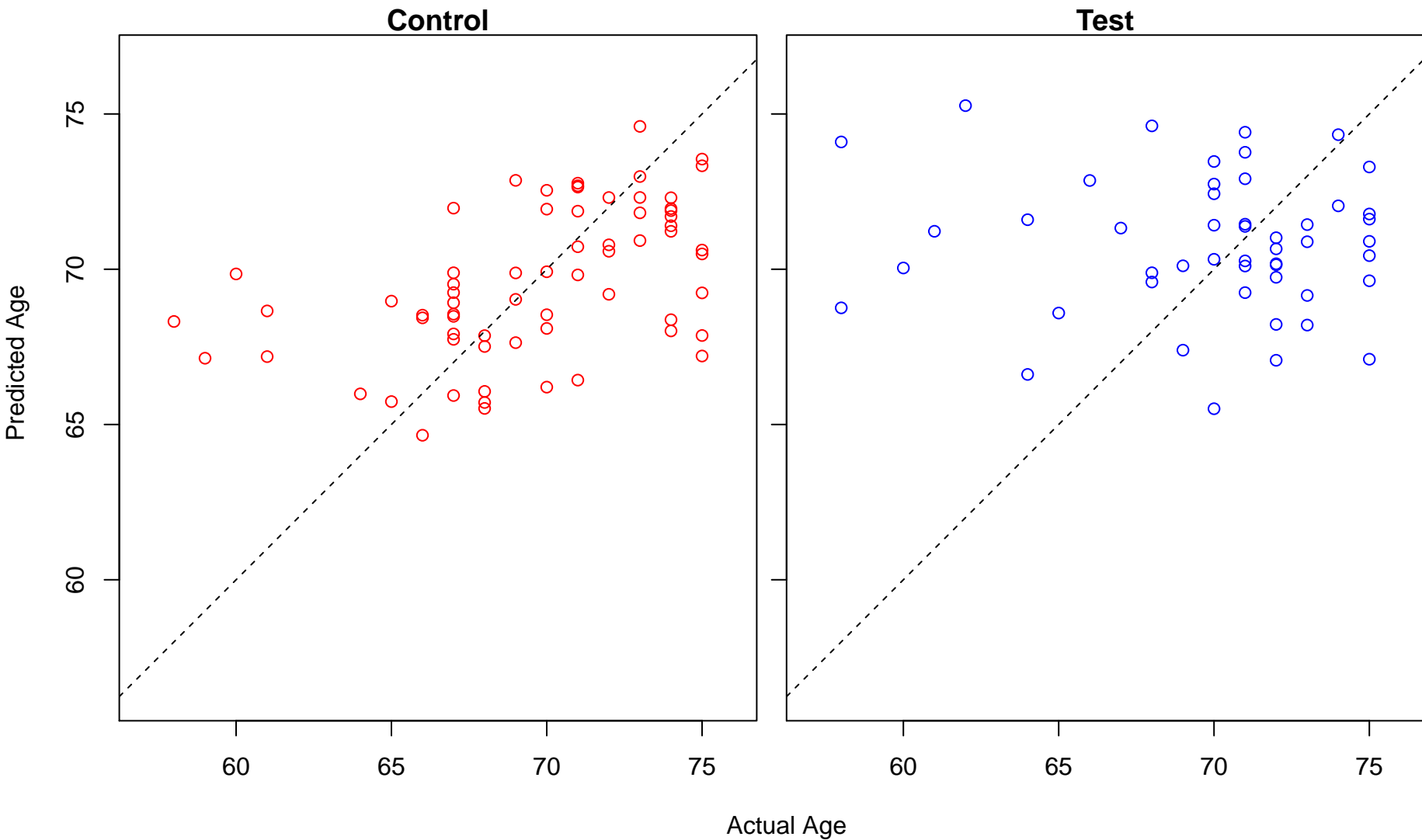
positive regulation of receptor biosynthetic process (Score: 0.737224)



acylglycerol acyl-chain remodeling (Score: 0.736990)

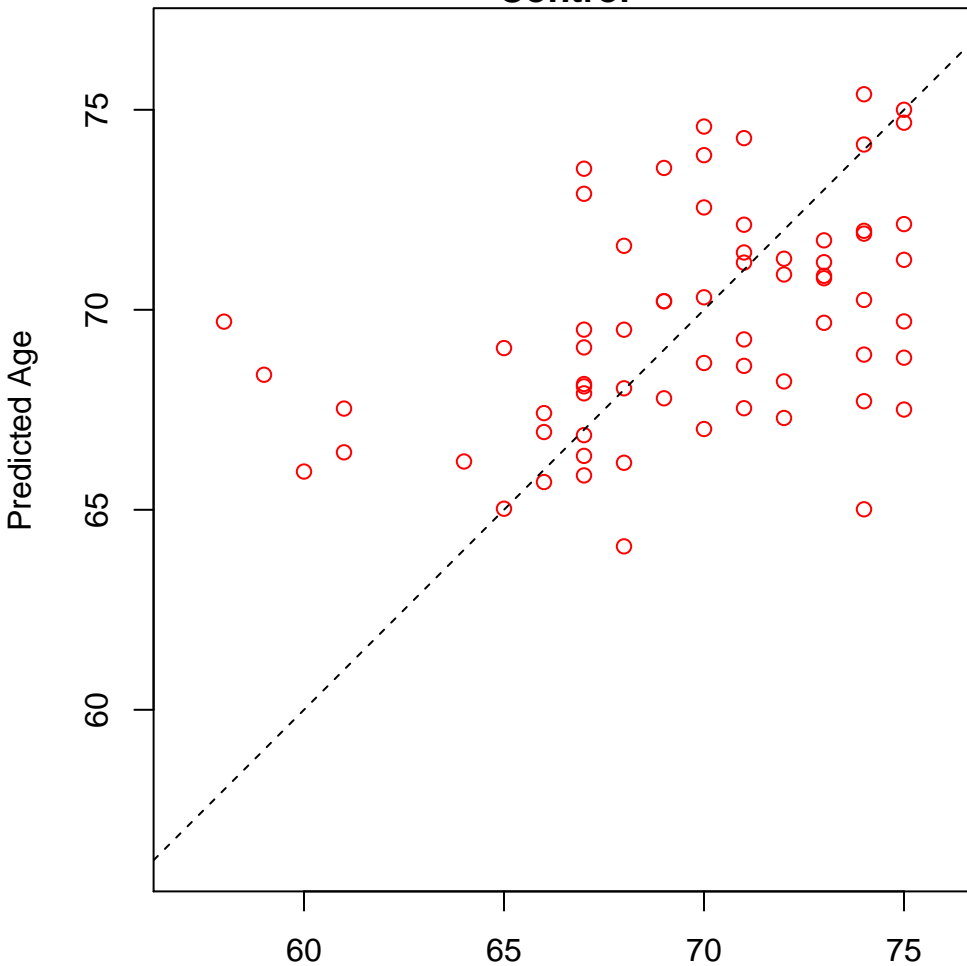


negative regulation by host of viral genome replication (Score: 0.736951)

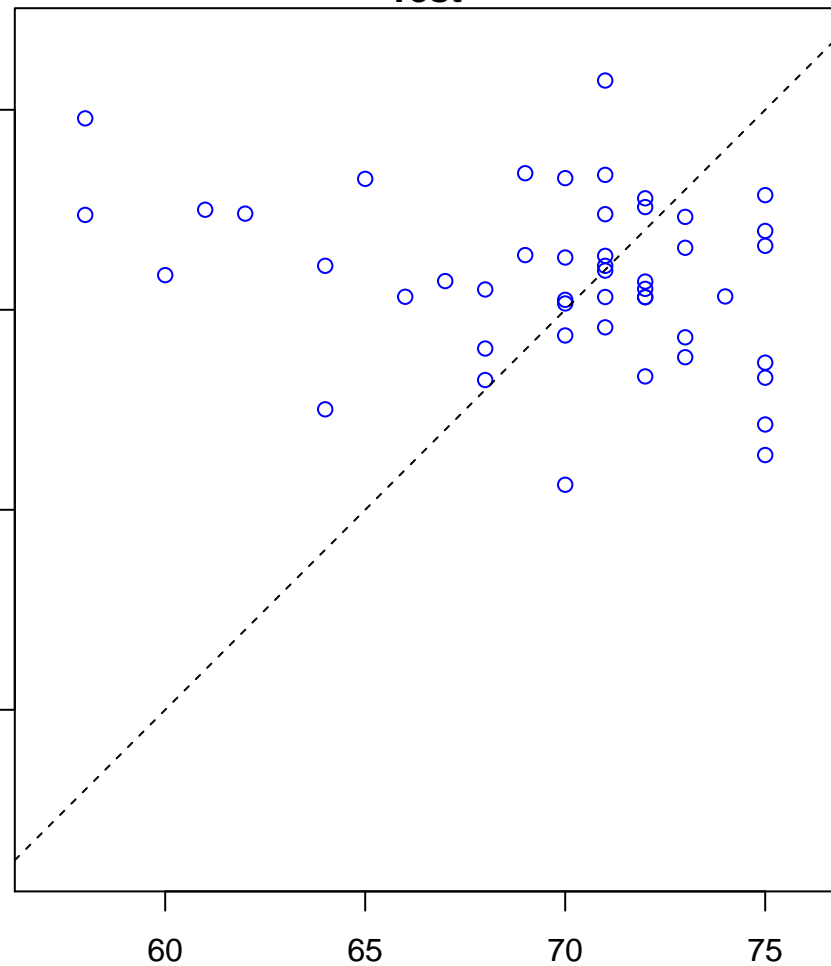


regulation of cholesterol homeostasis (Score: 0.736862)

Control

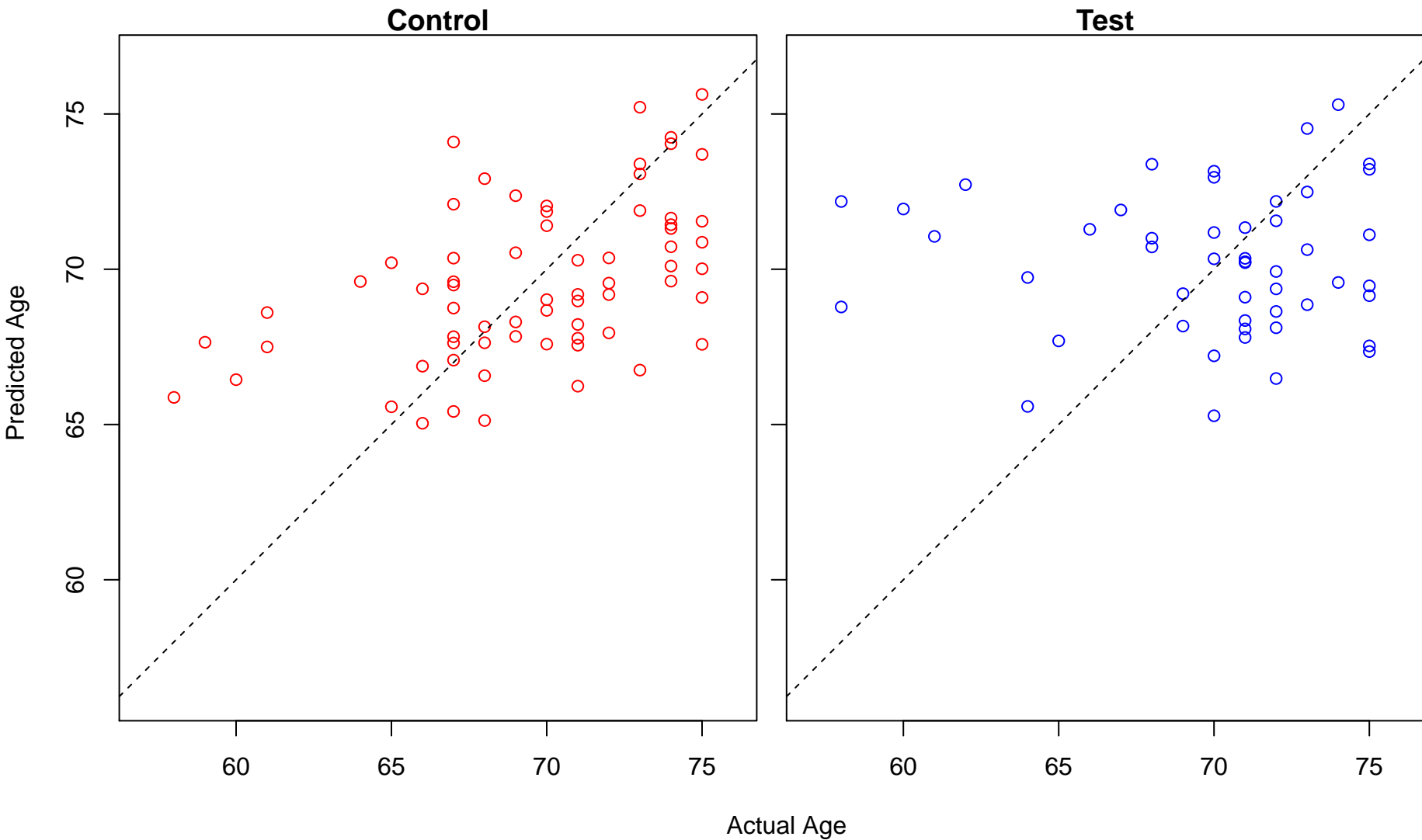


Test

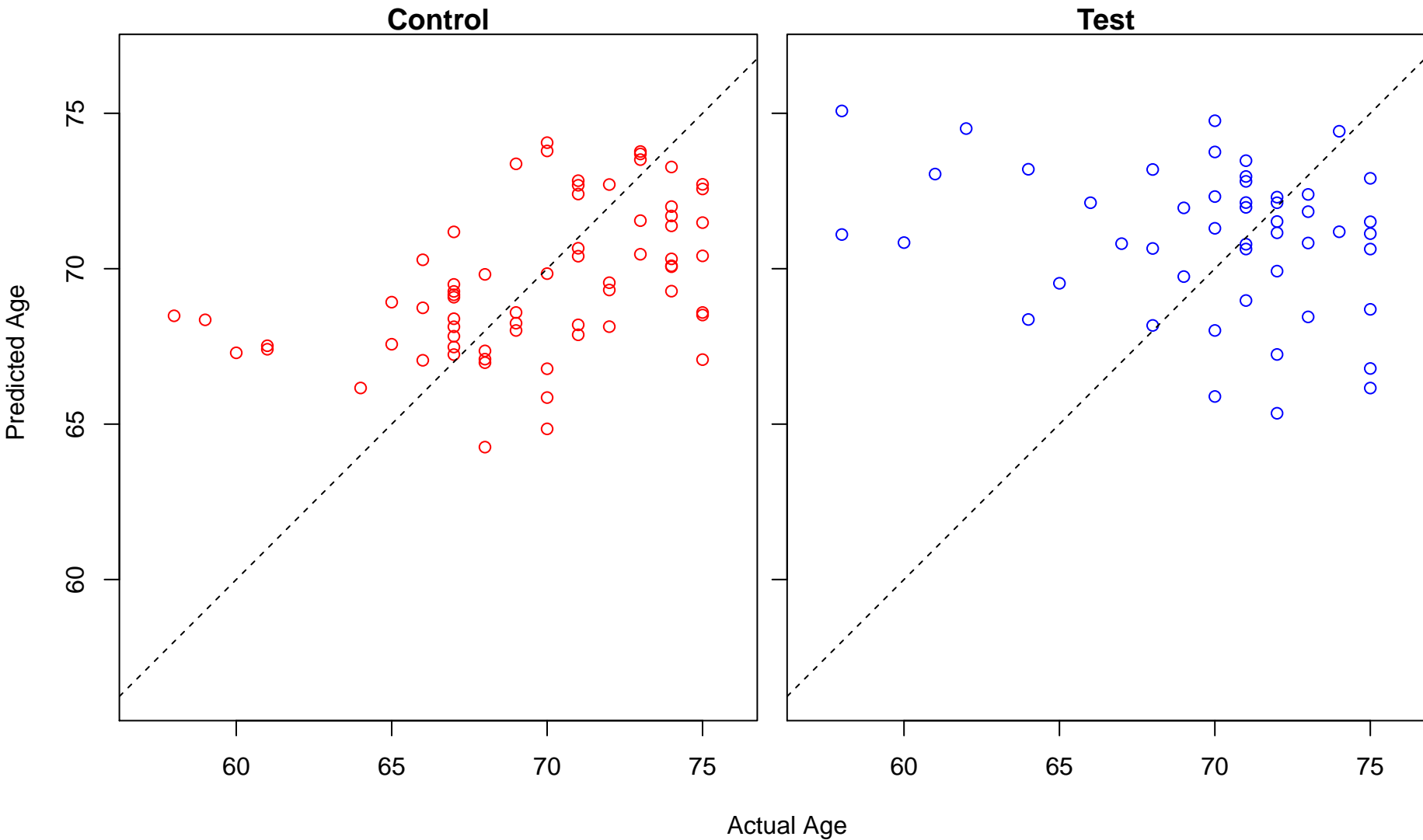


Actual Age

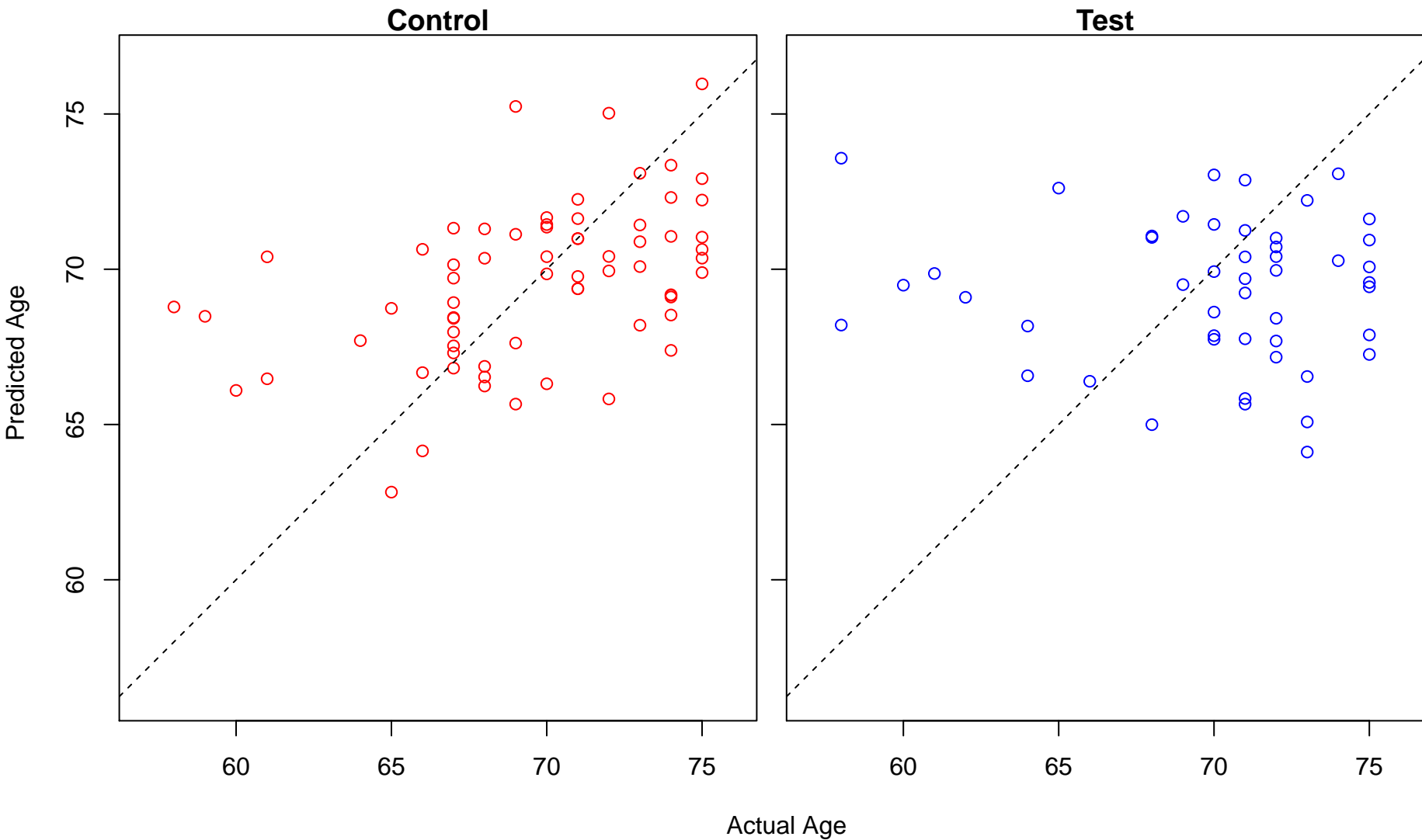
toxin transport (Score: 0.736445)



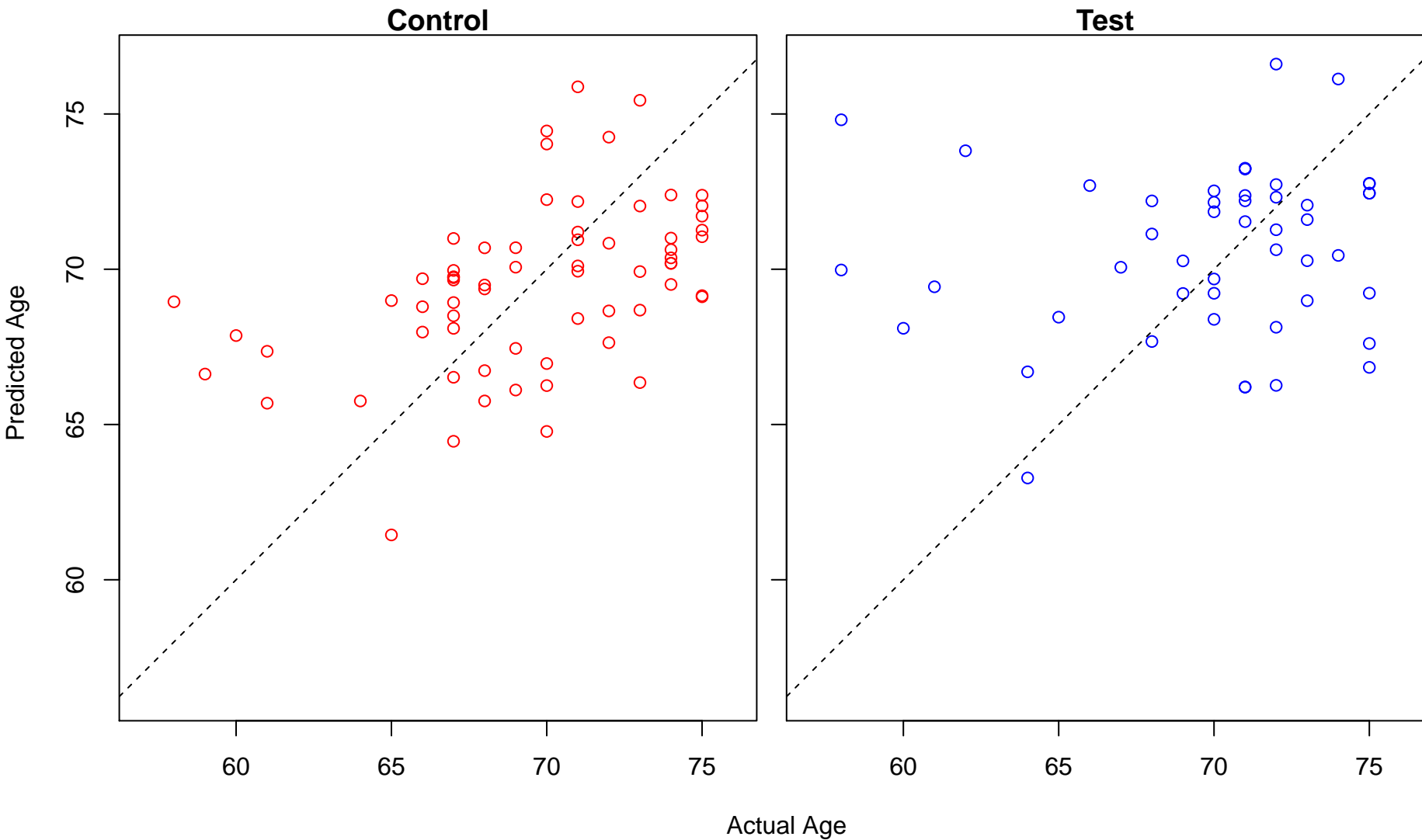
positive regulation of mRNA catabolic process (Score: 0.736095)



positive regulation of phospholipid biosynthetic process (Score: 0.735763)

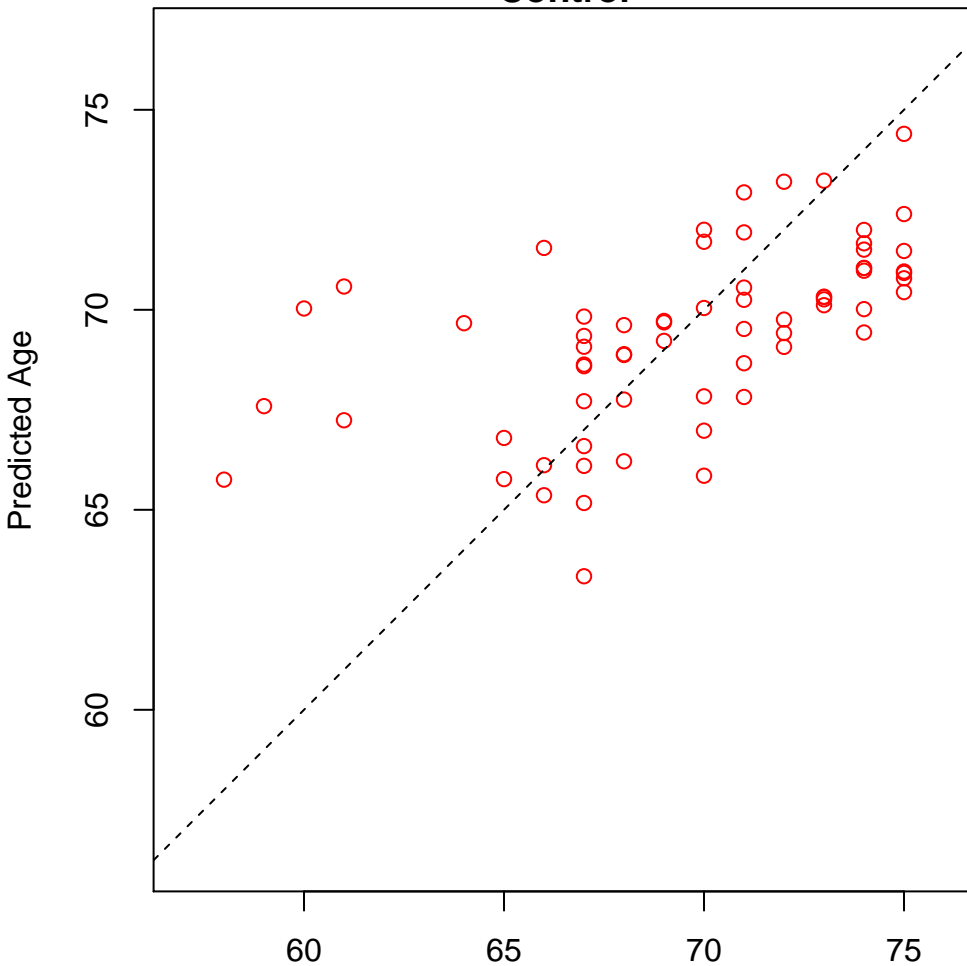


regulation of axon extension (Score: 0.735722)

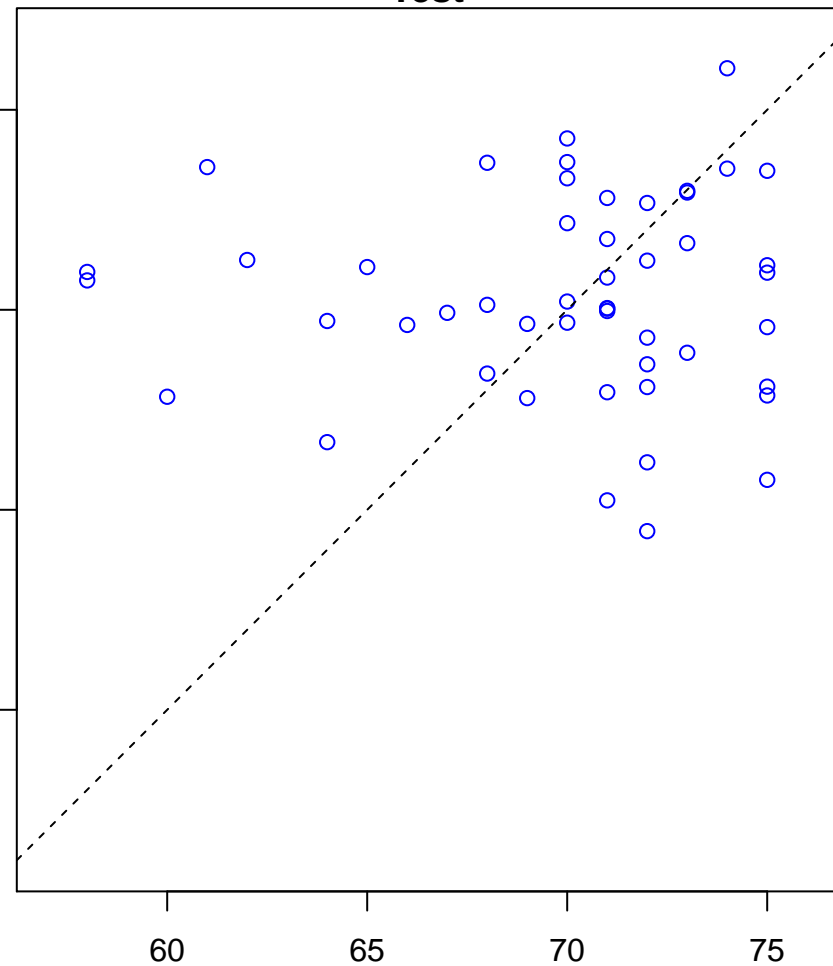


mitochondrial calcium ion homeostasis (Score: 0.734465)

Control

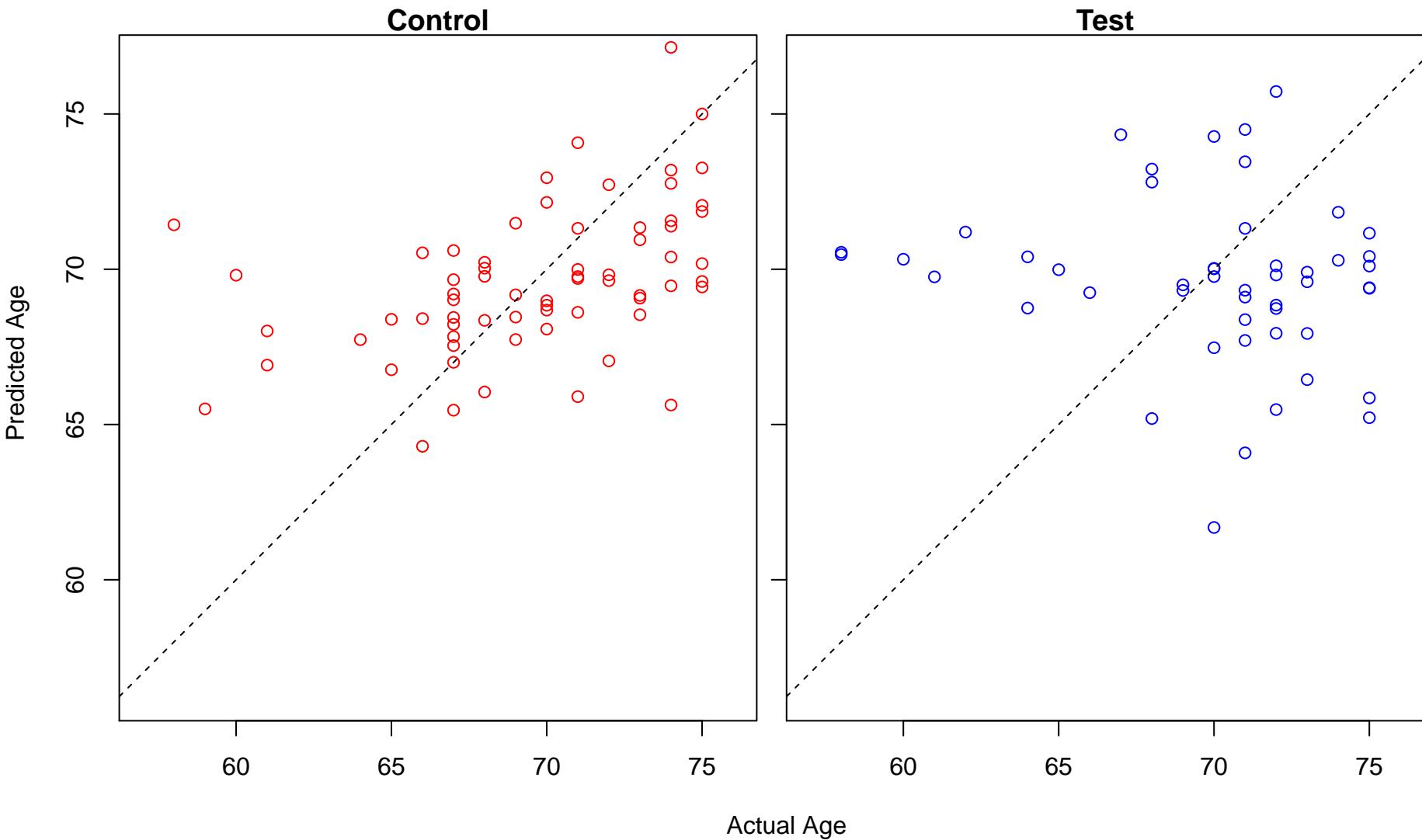


Test

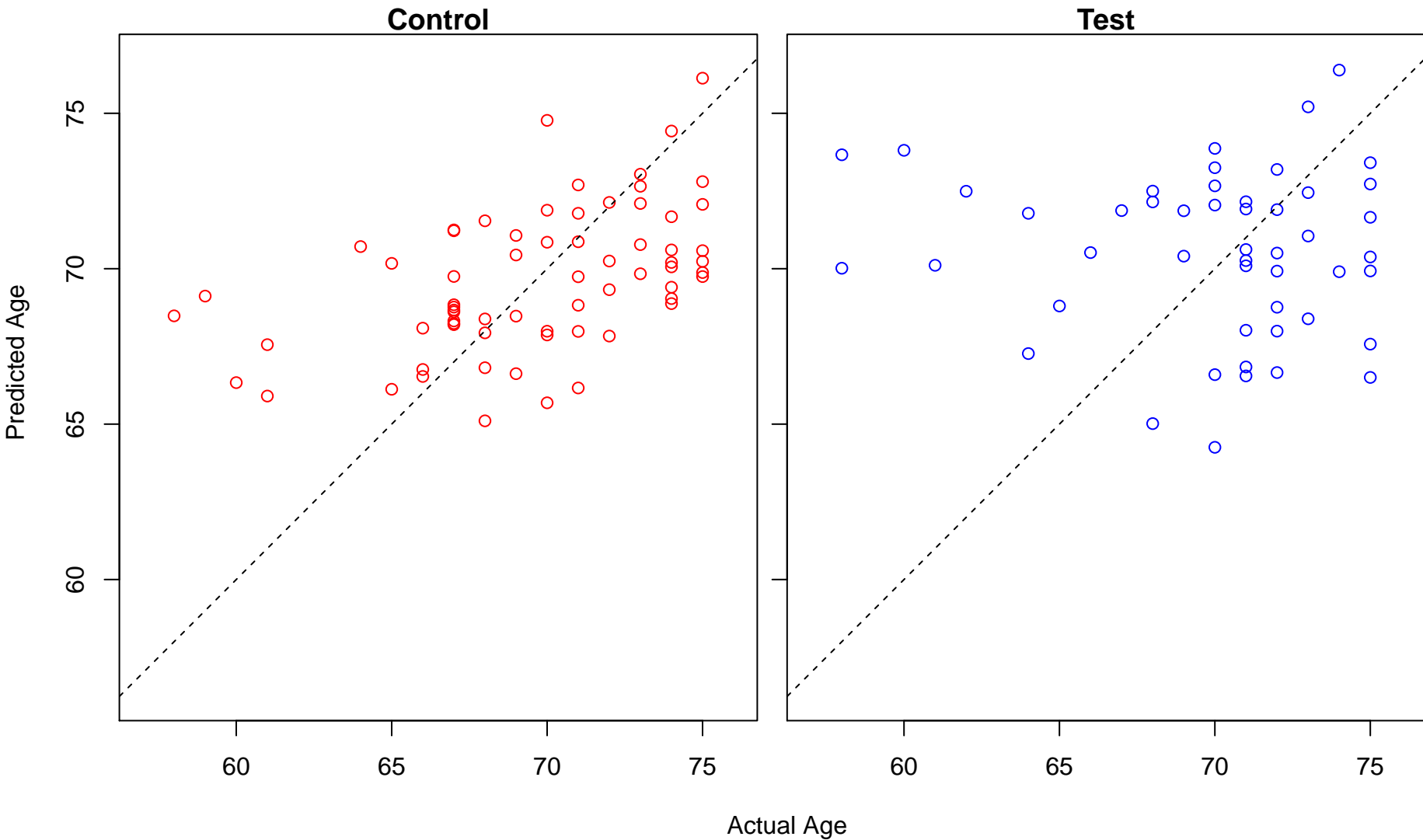


Actual Age

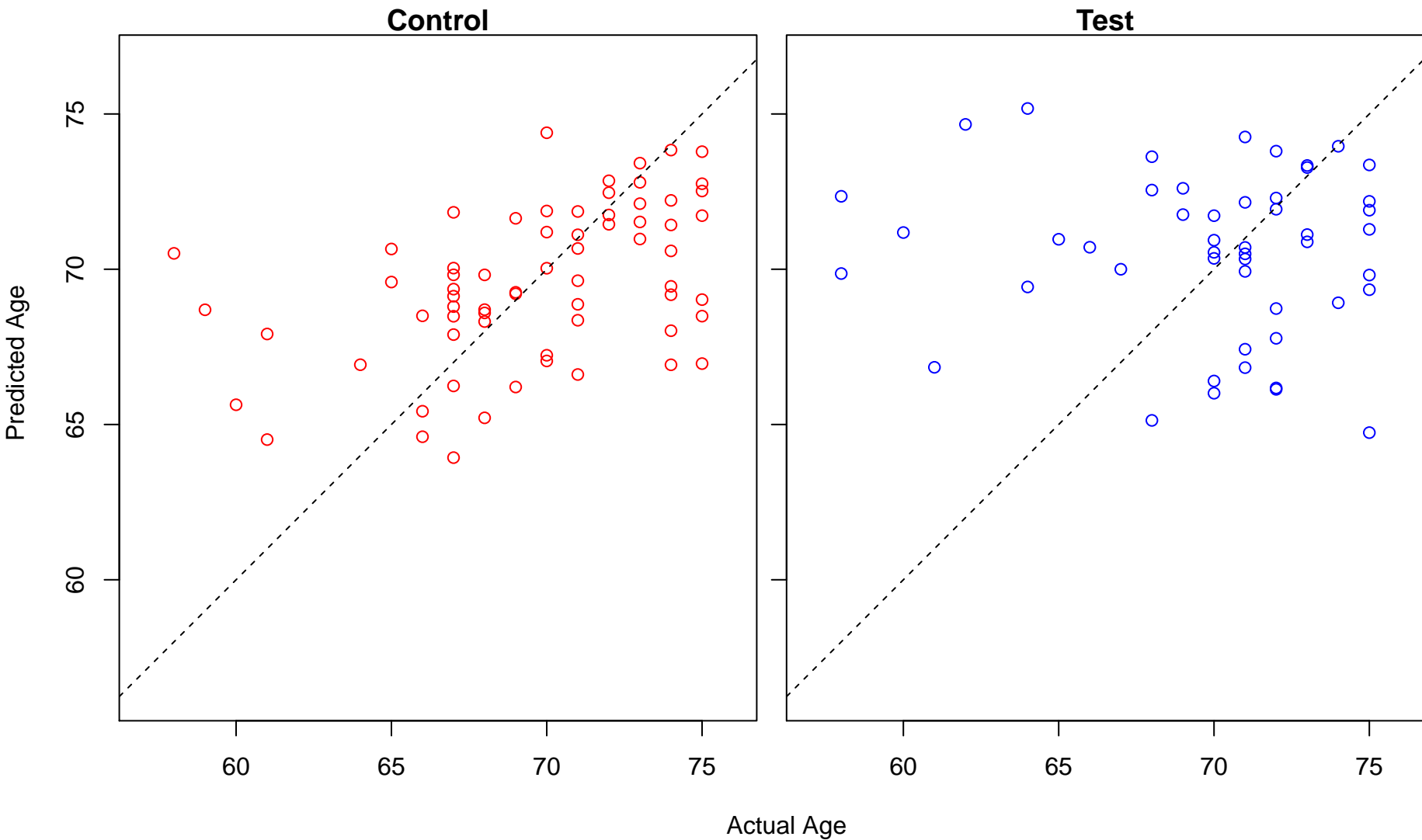
regulation of MHC class II biosynthetic process (Score: 0.734447)



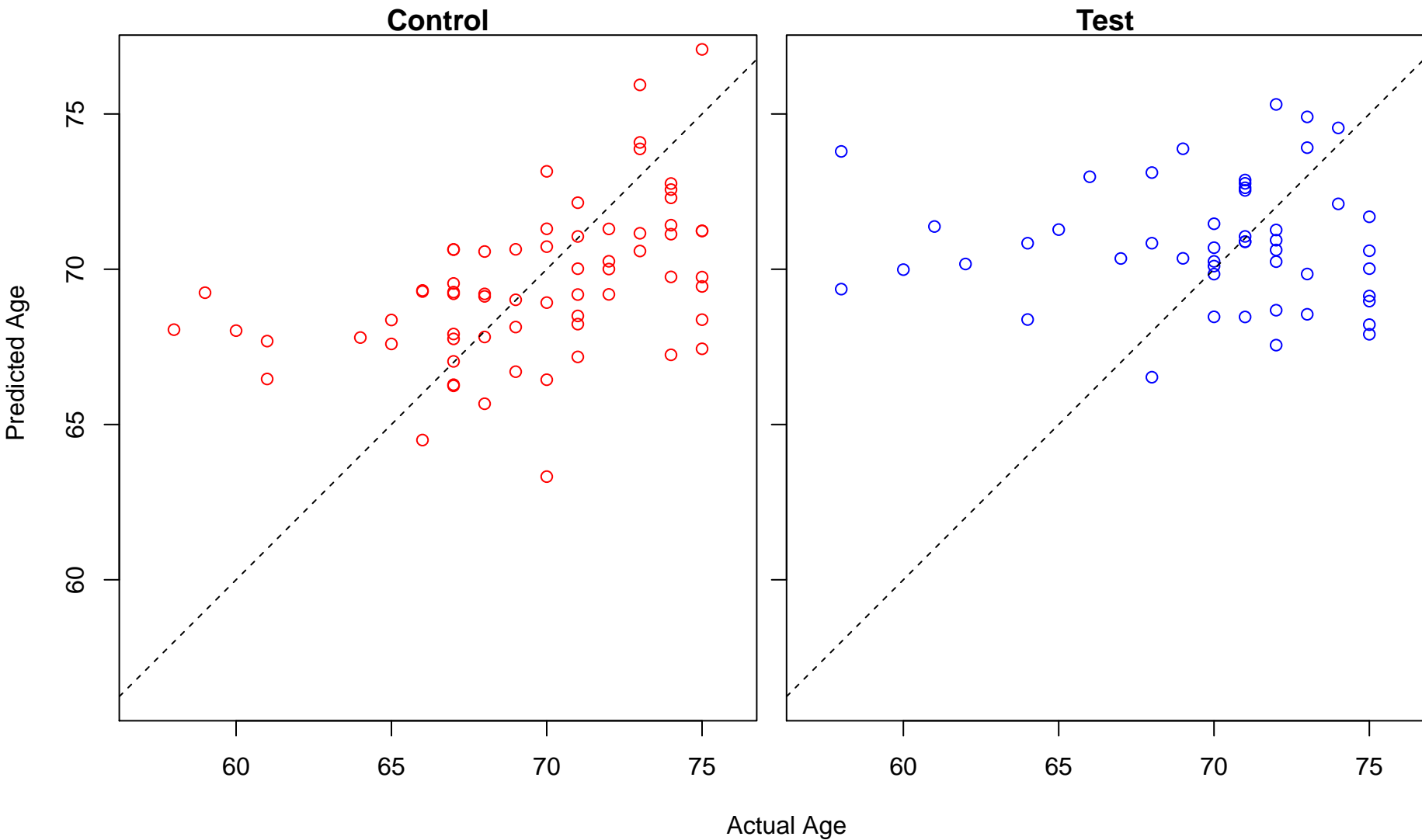
apoptotic process involved in development (Score: 0.734240)



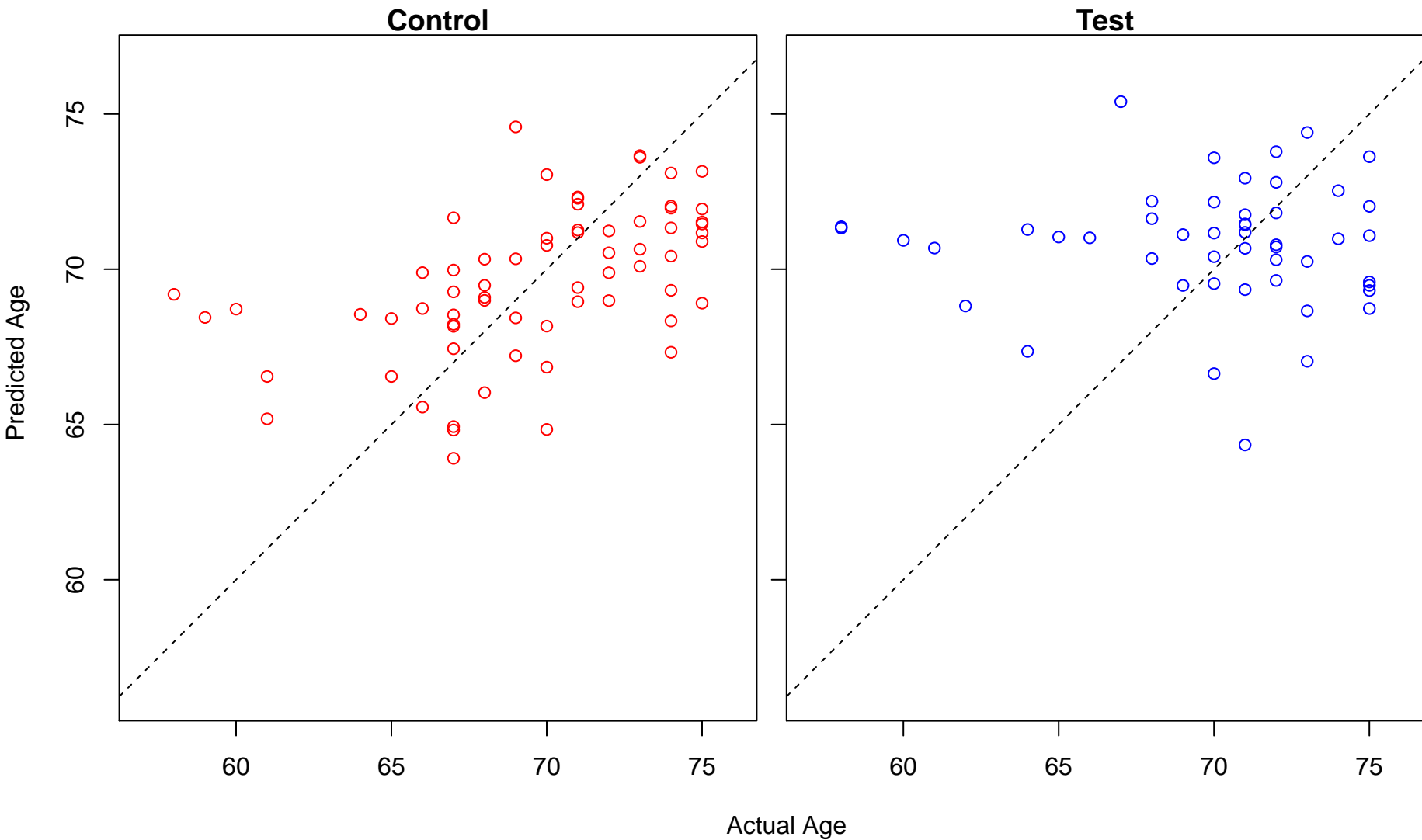
negative regulation of NIK/NF-kappaB signaling (Score: 0.733724)



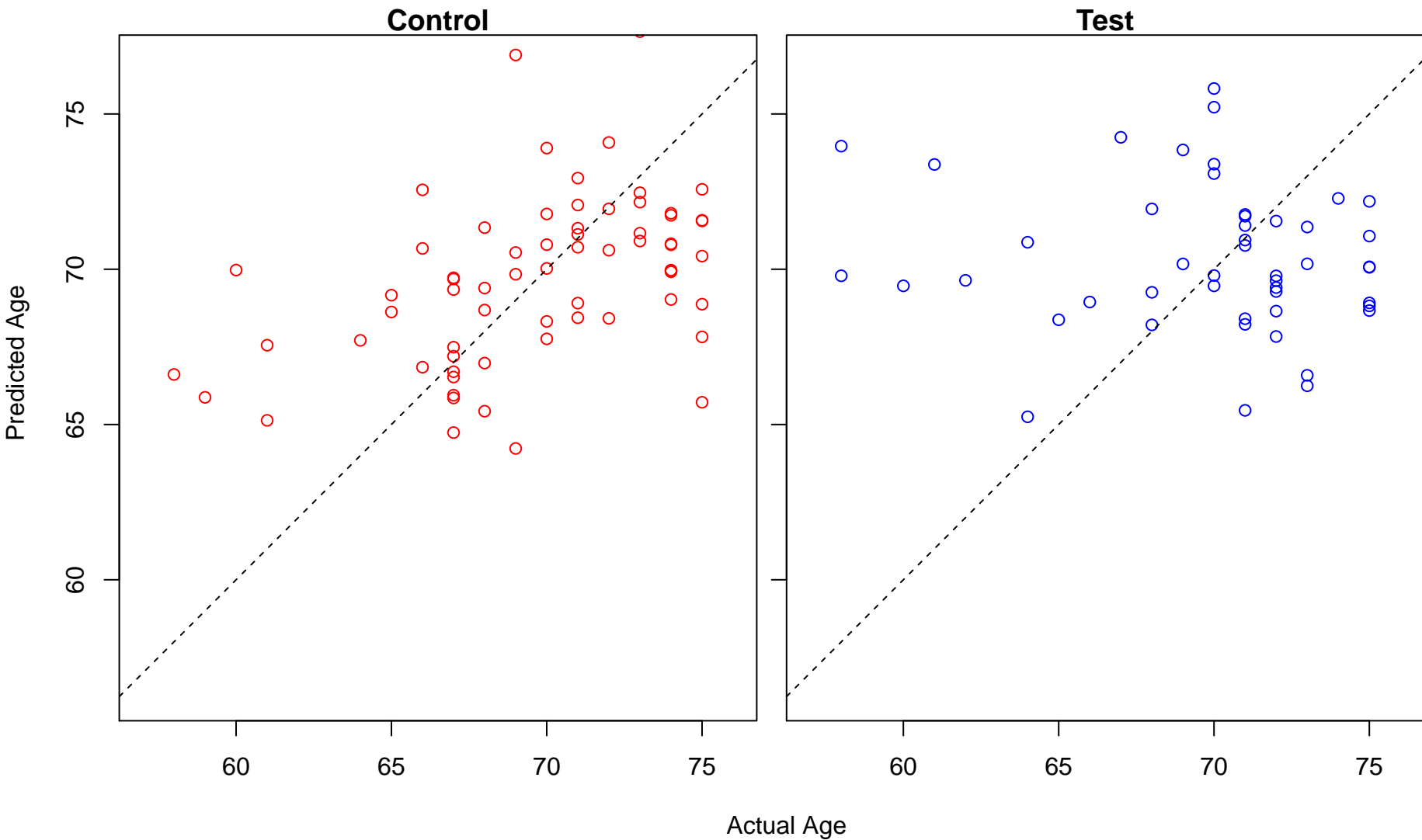
muscle hypertrophy (Score: 0.733432)



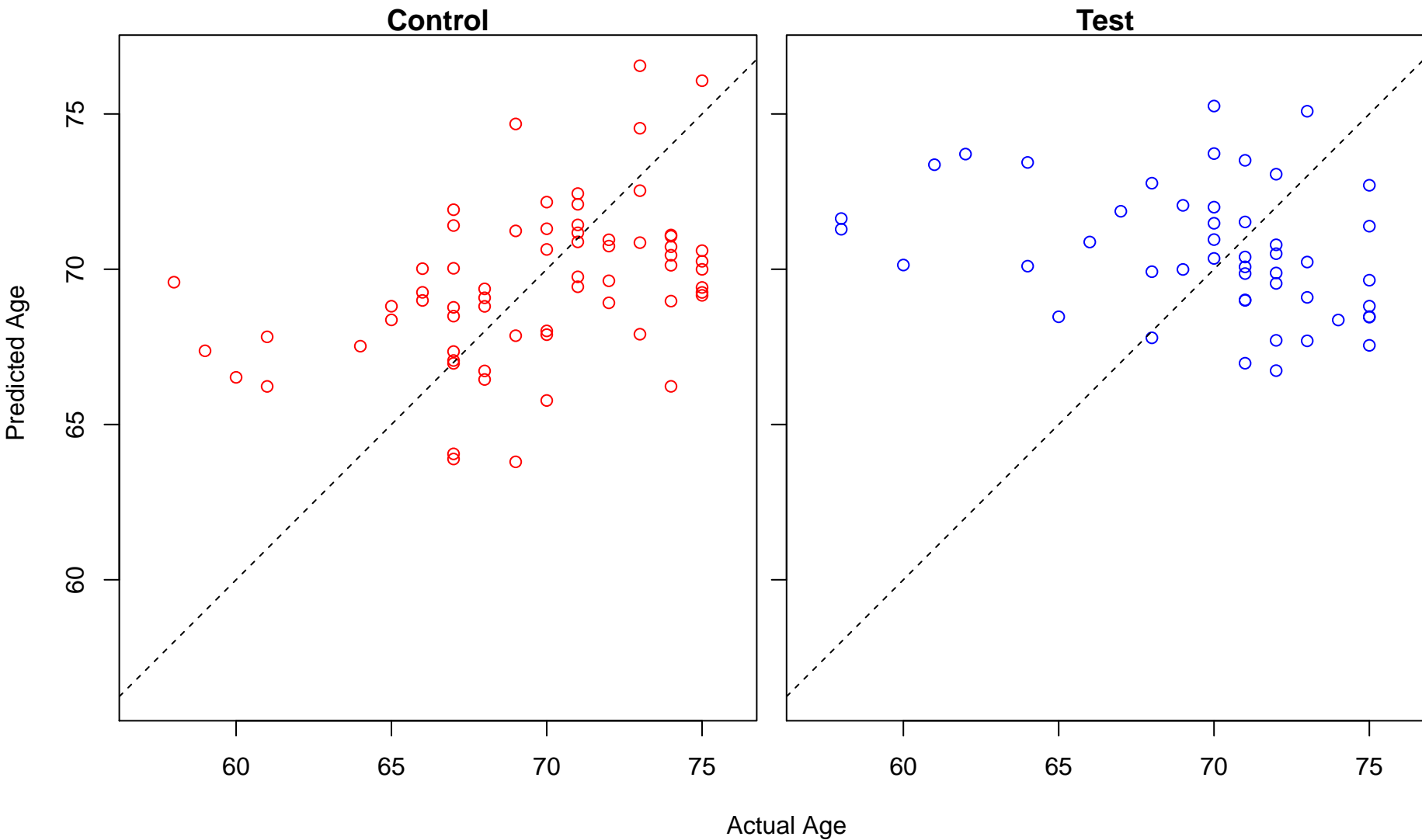
folic acid metabolic process (Score: 0.733162)



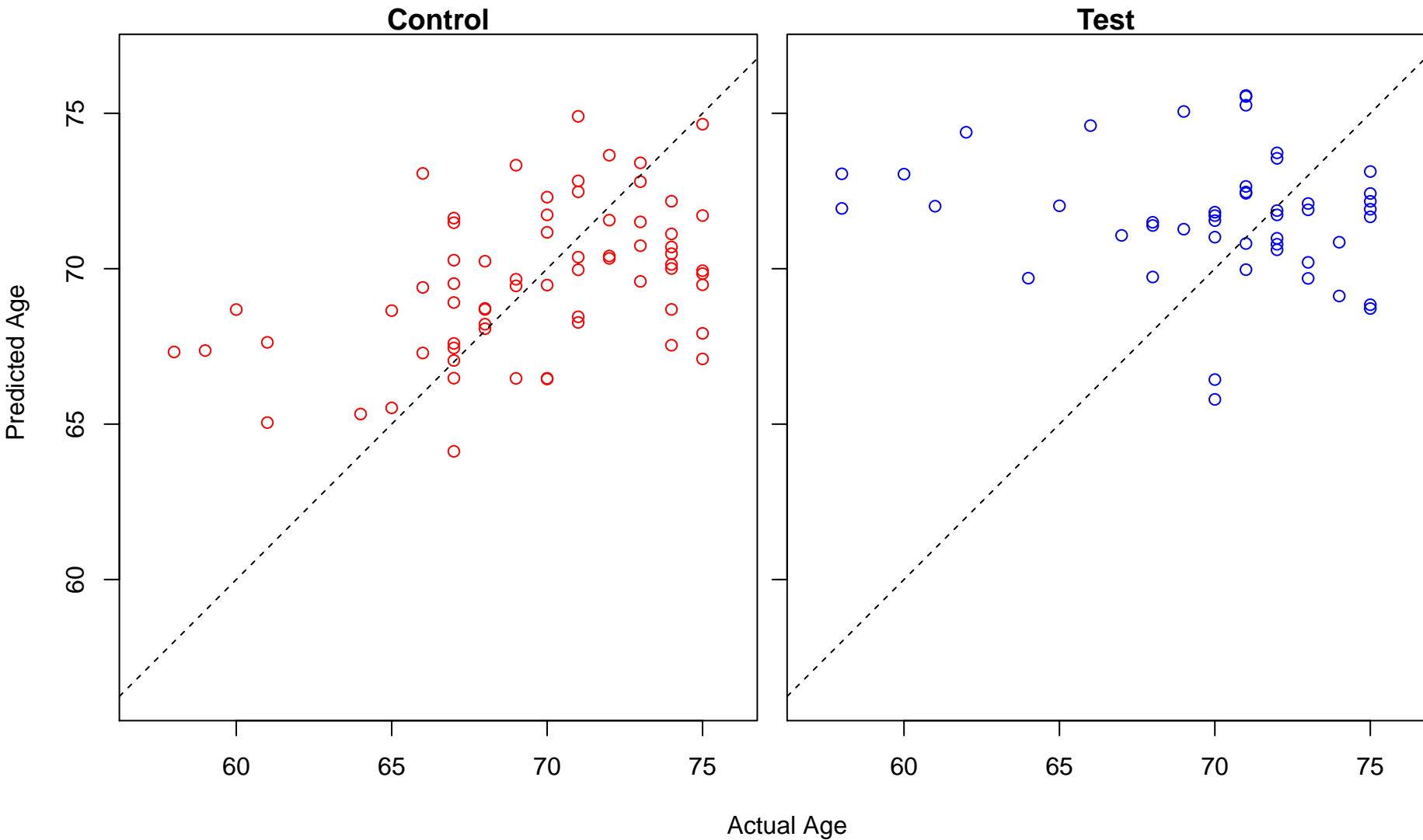
fertilization (Score: 0.733105)



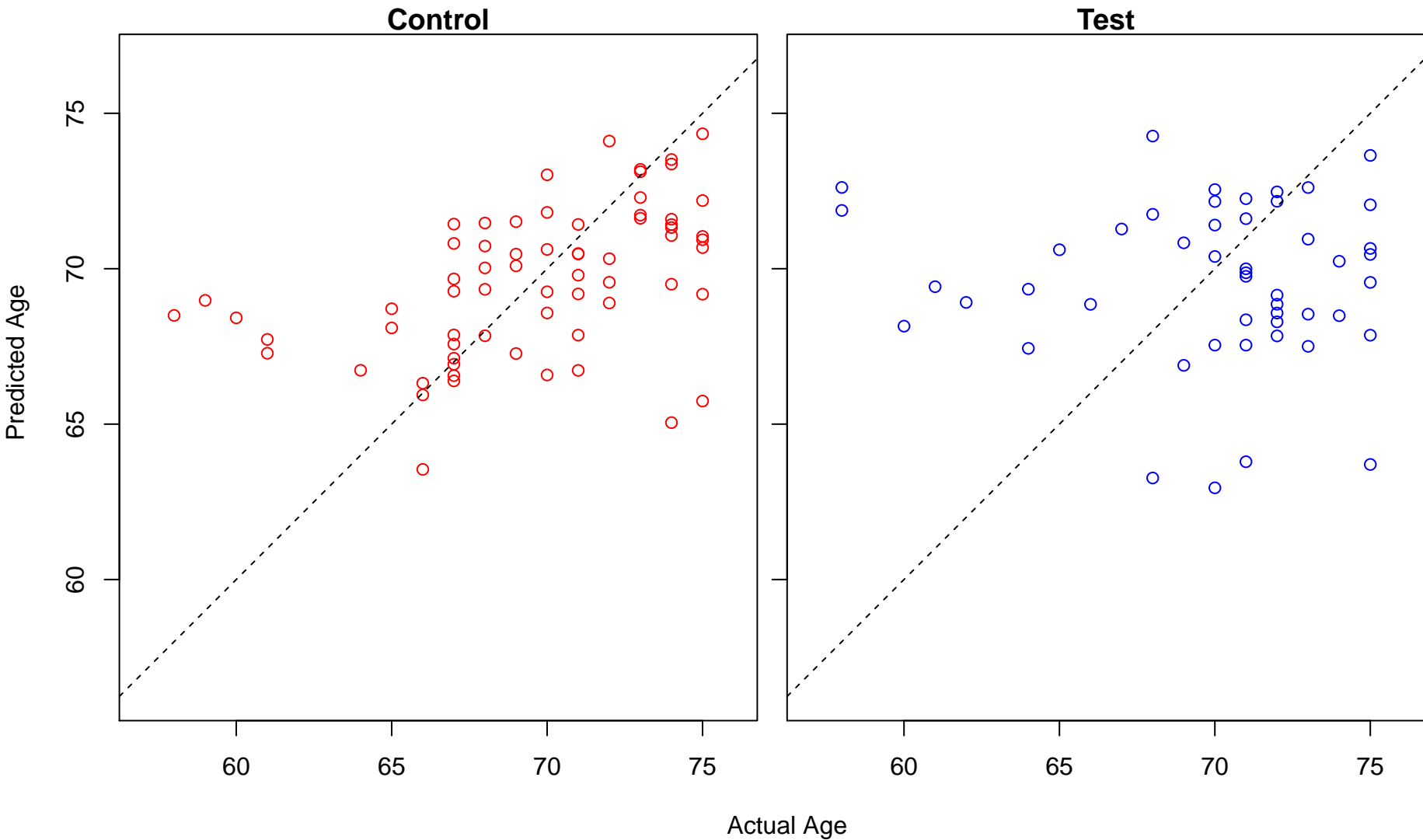
hormone biosynthetic process (Score: 0.732671)



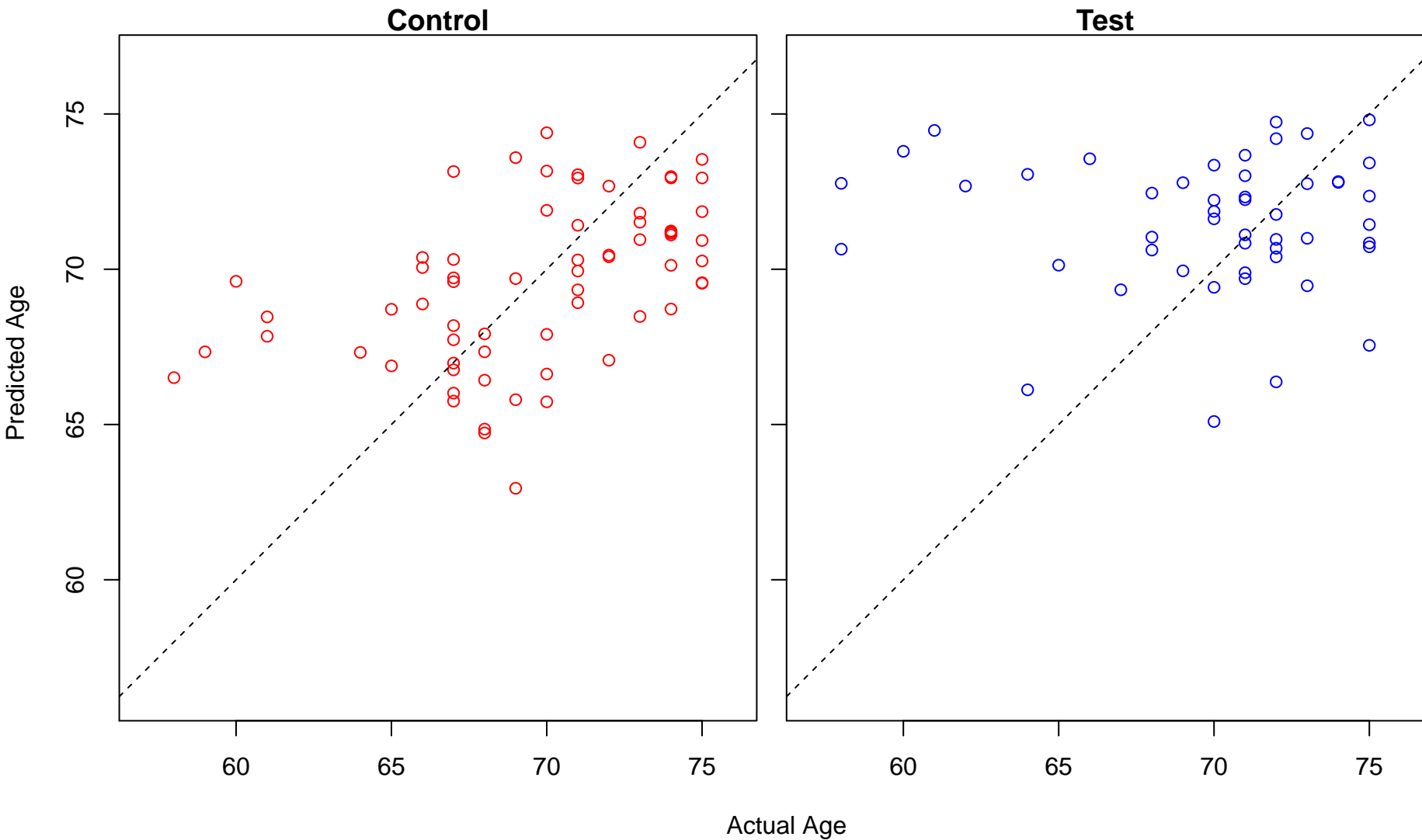
regulation of establishment of planar polarity (Score: 0.732590)



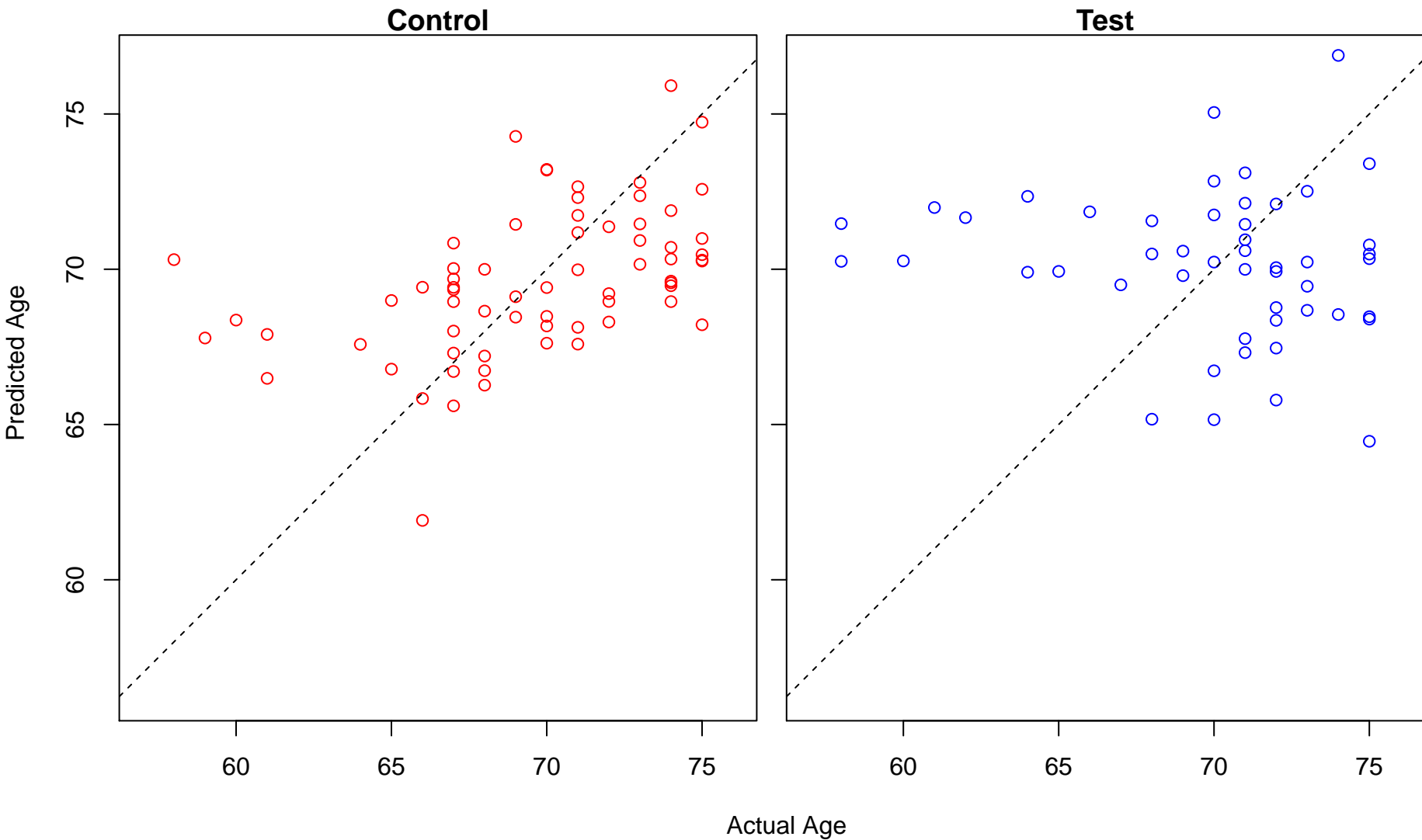
cell communication involved in cardiac conduction (Score: 0.732211)



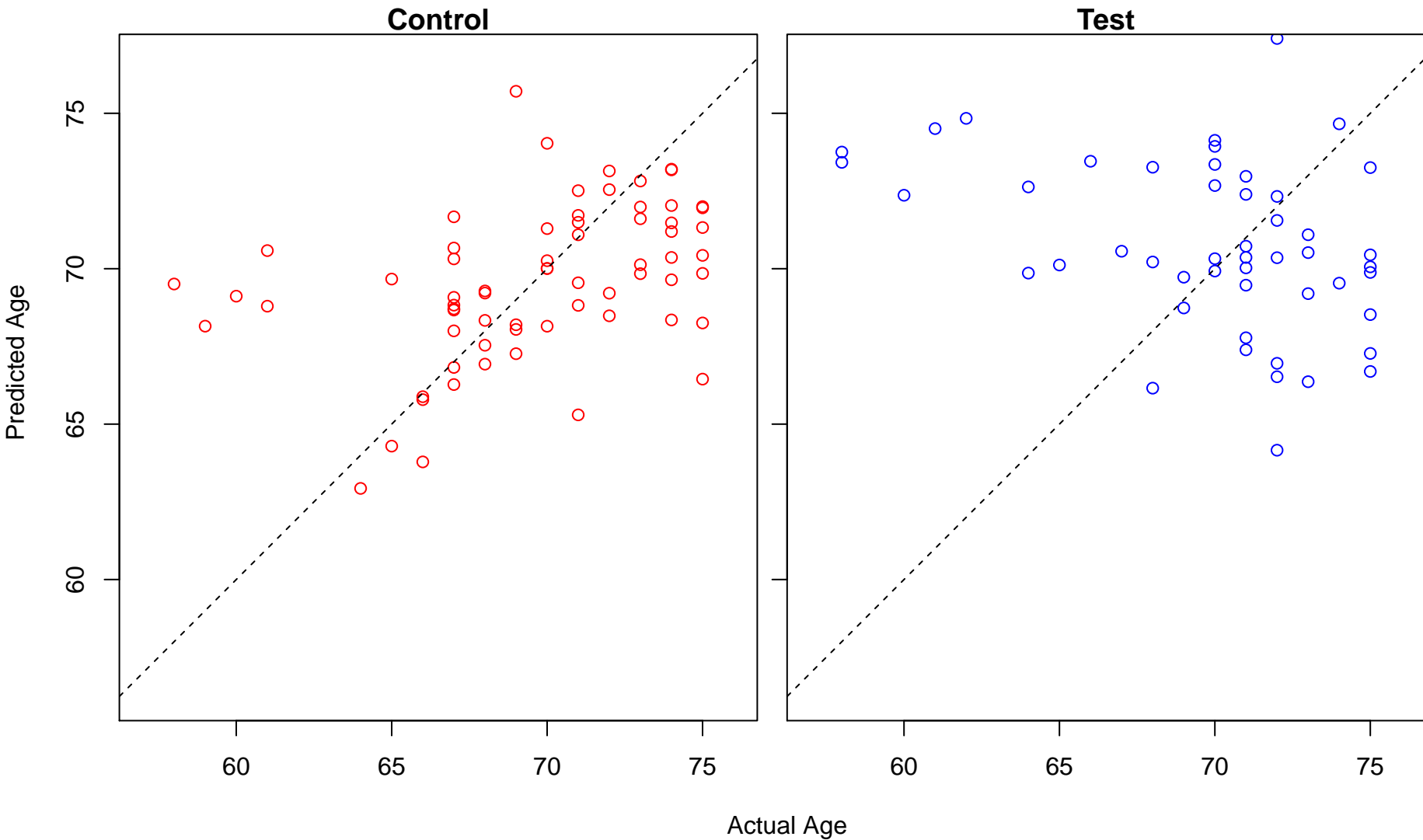
positive regulation of glucose import (Score: 0.730929)



neural retina development (Score: 0.730547)

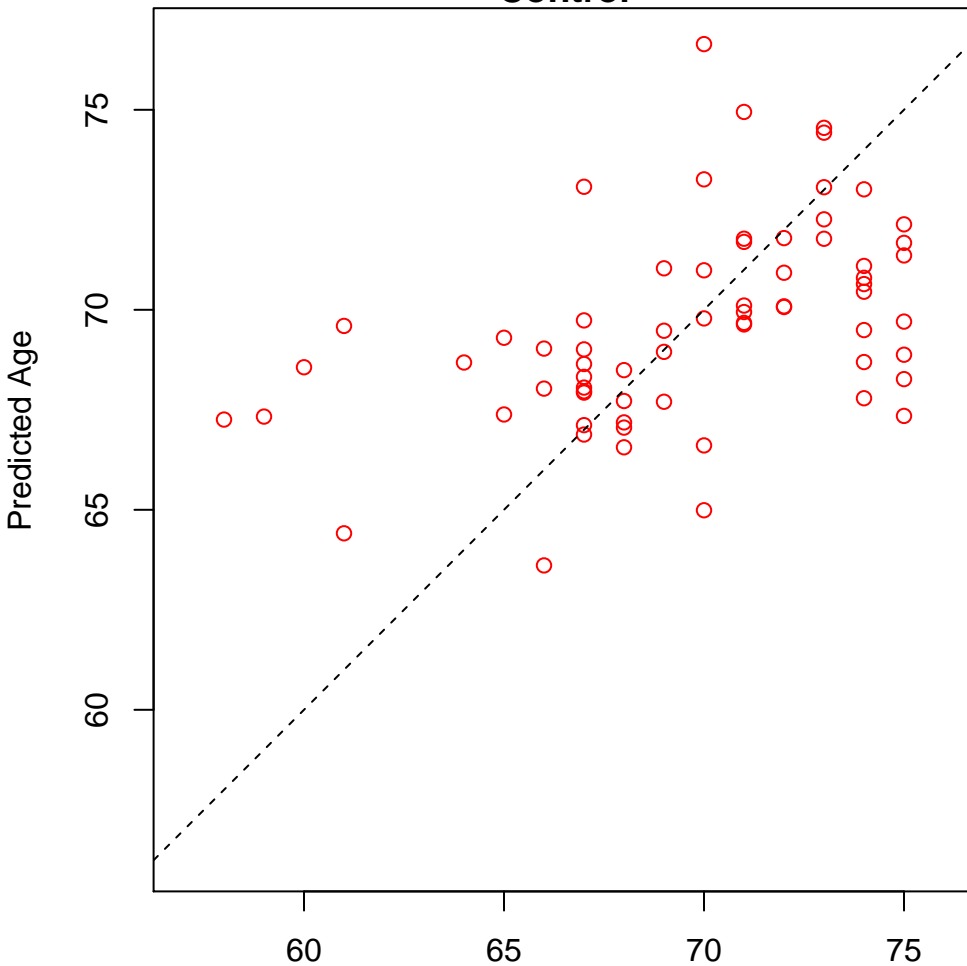


regulation of granulocyte macrophage colony-stimulating factor production (Score: 0.730517)

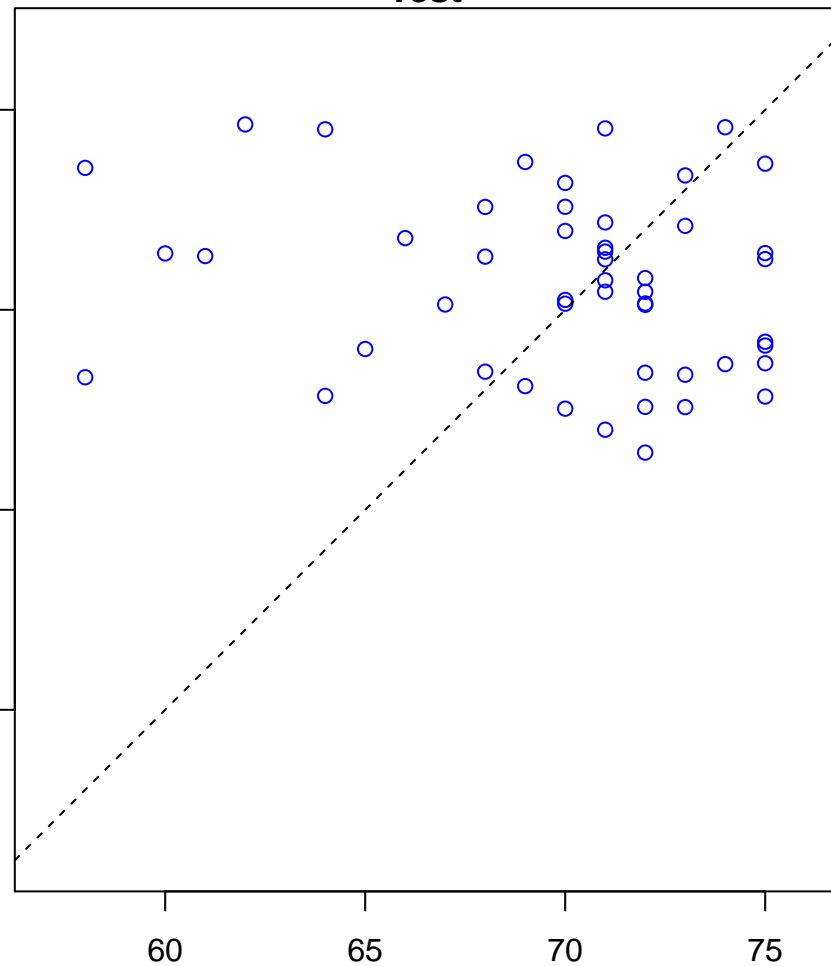


regulation of adiponectin secretion (Score: 0.730301)

Control



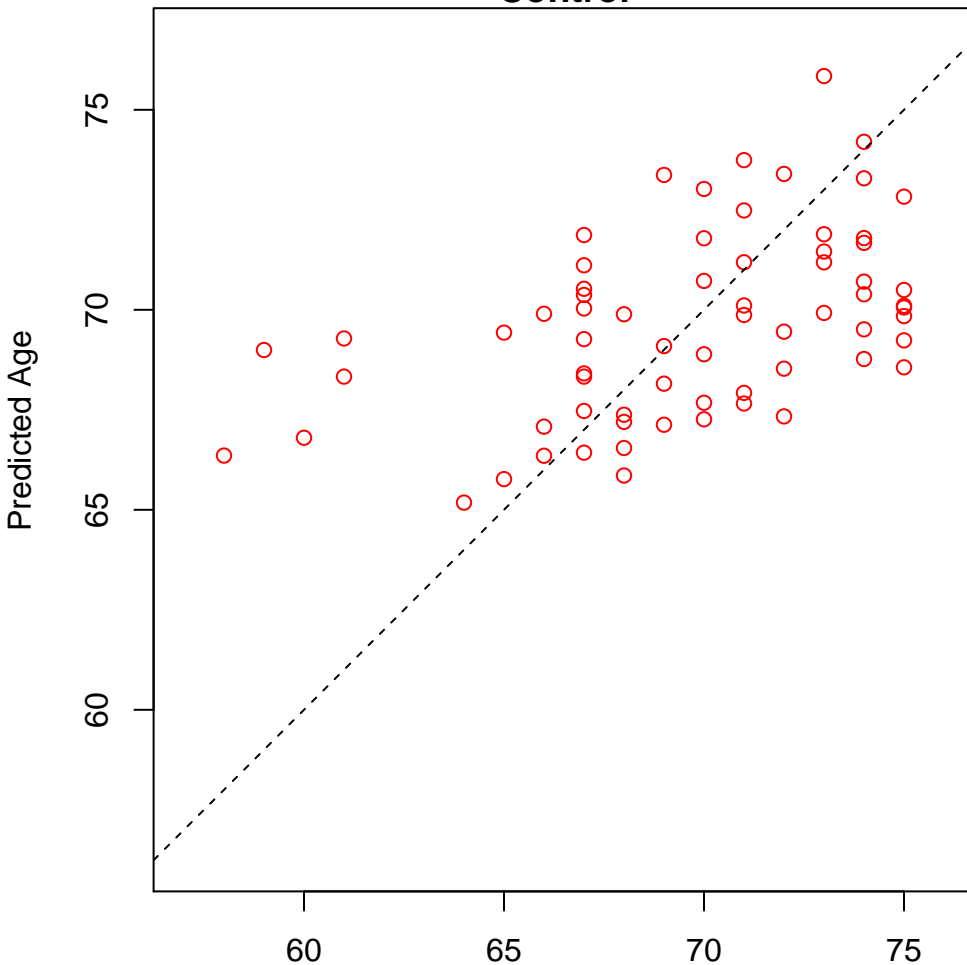
Test



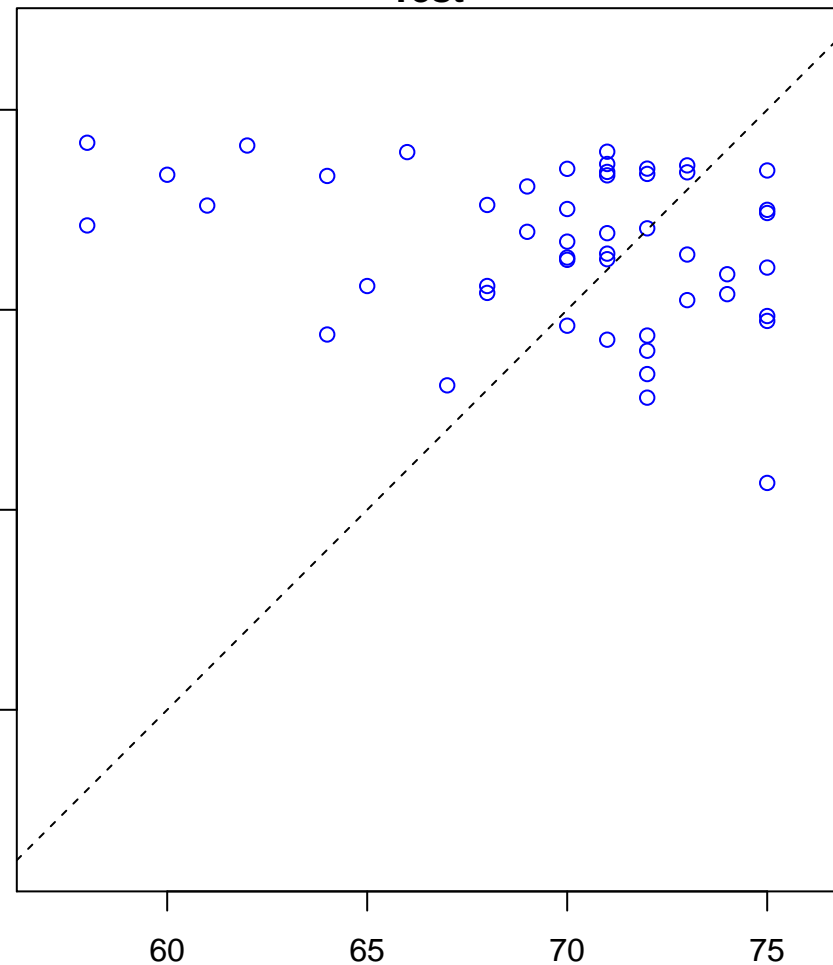
Actual Age

venous blood vessel morphogenesis (Score: 0.728763)

Control

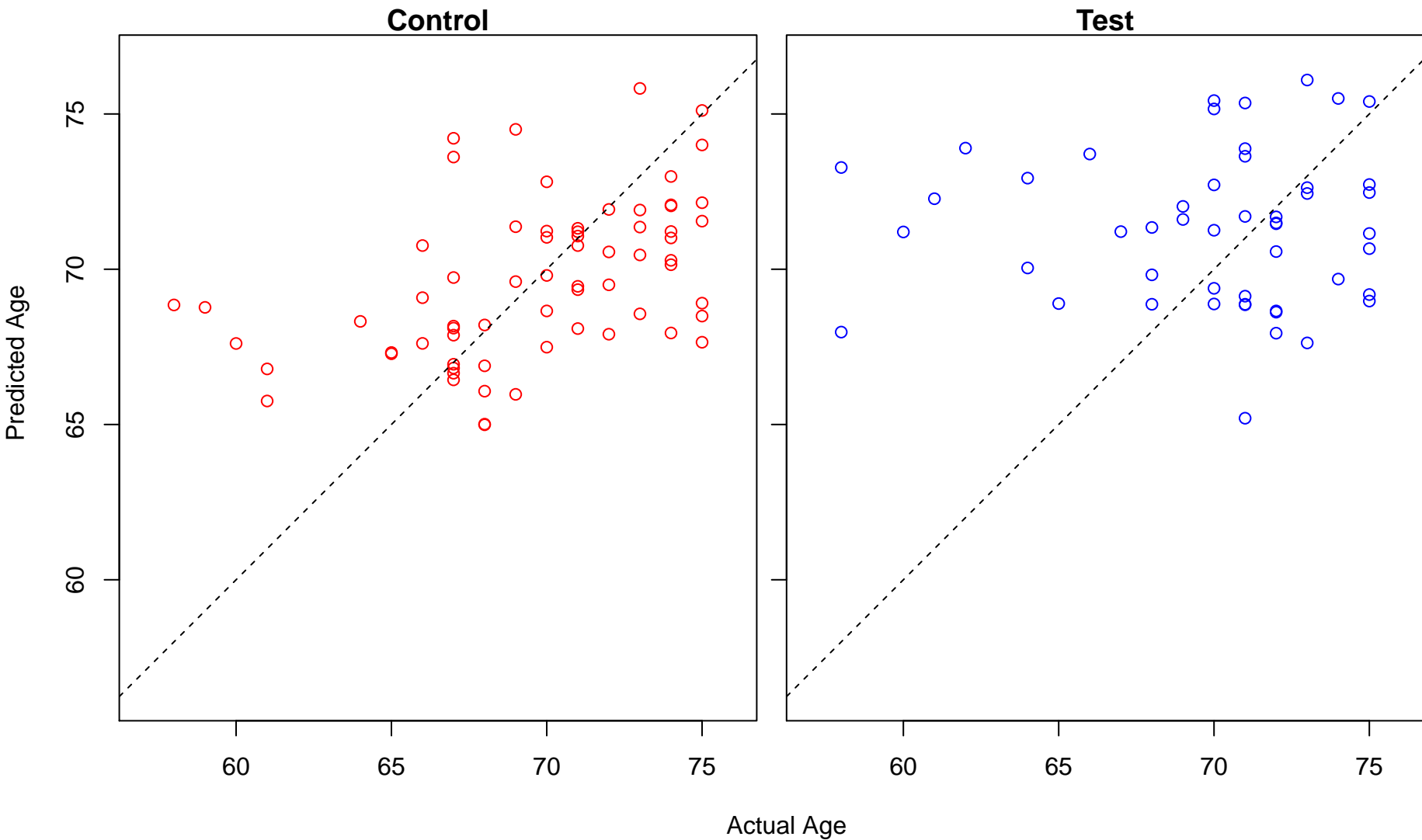


Test

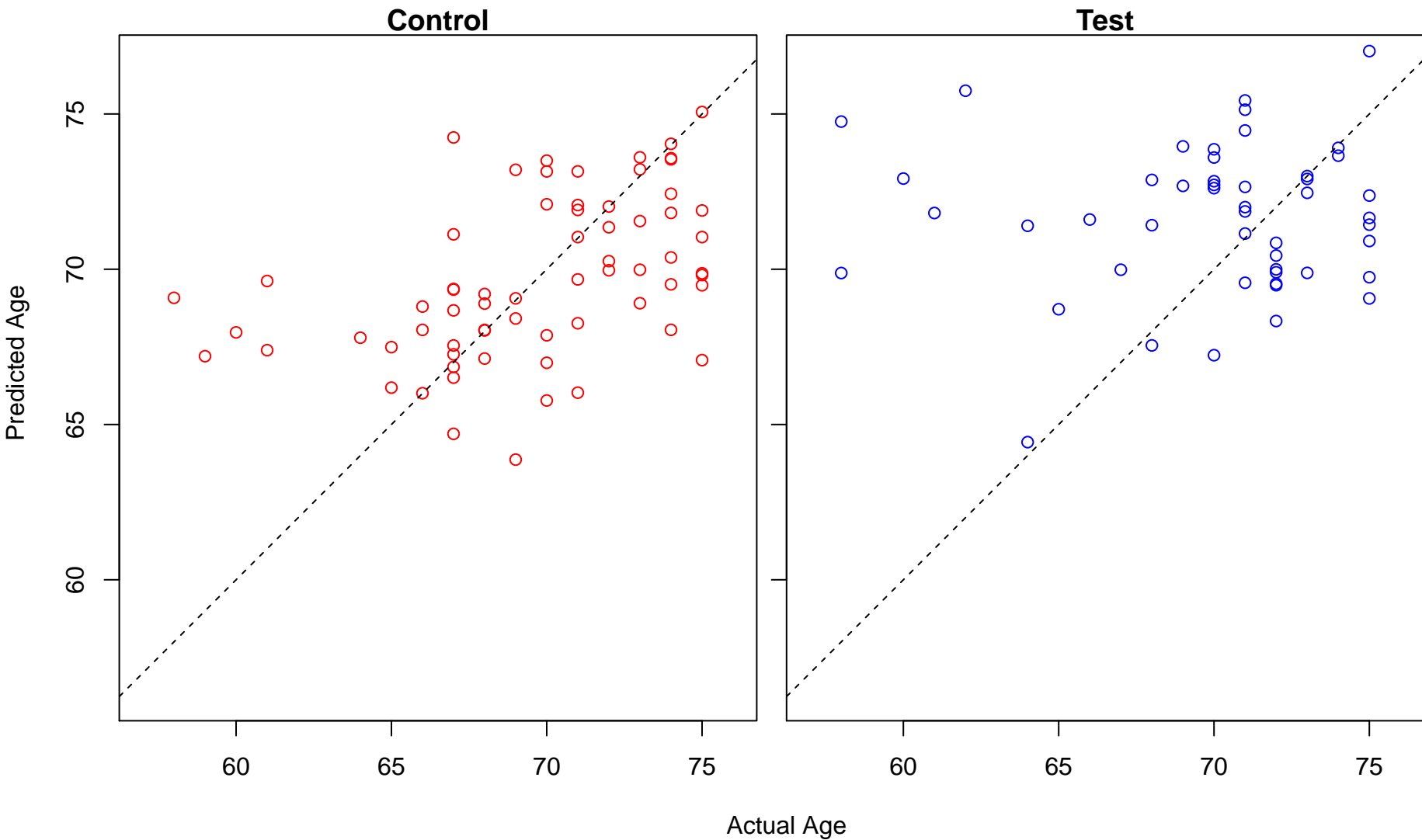


Actual Age

Schwann cell differentiation (Score: 0.728420)

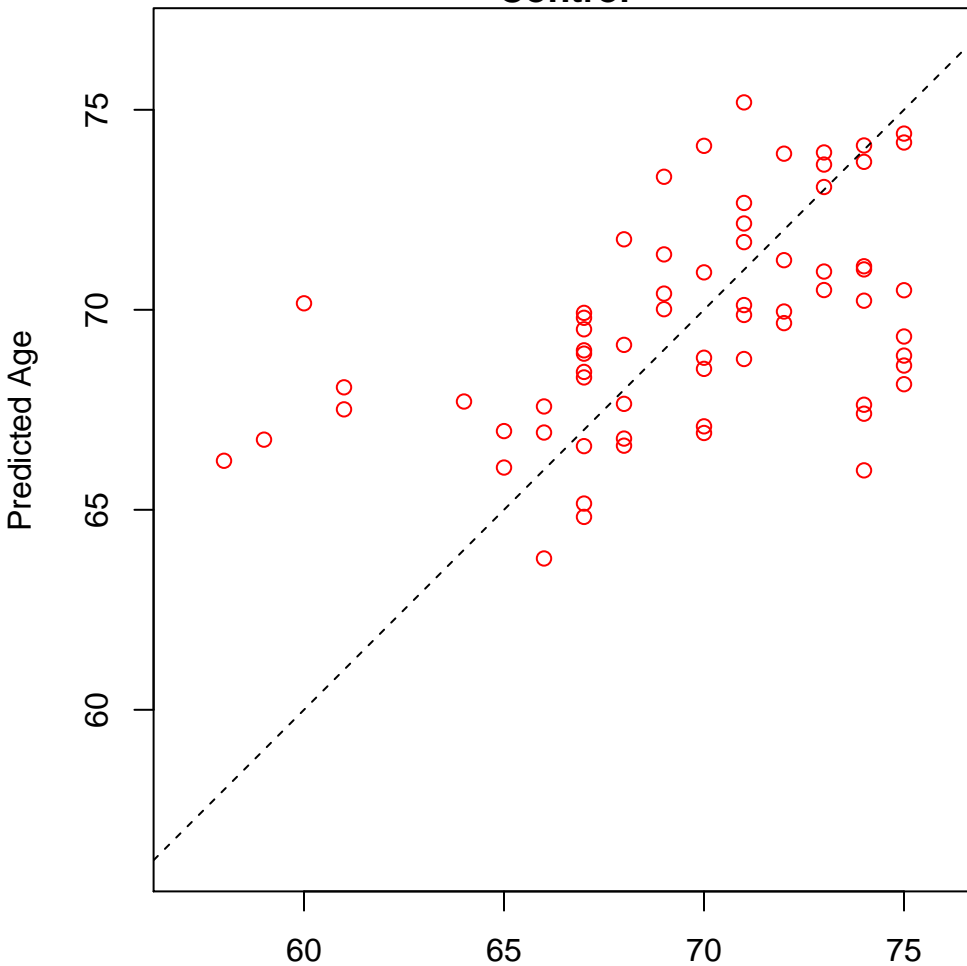


dicarboxylic acid transport (Score: 0.728419)

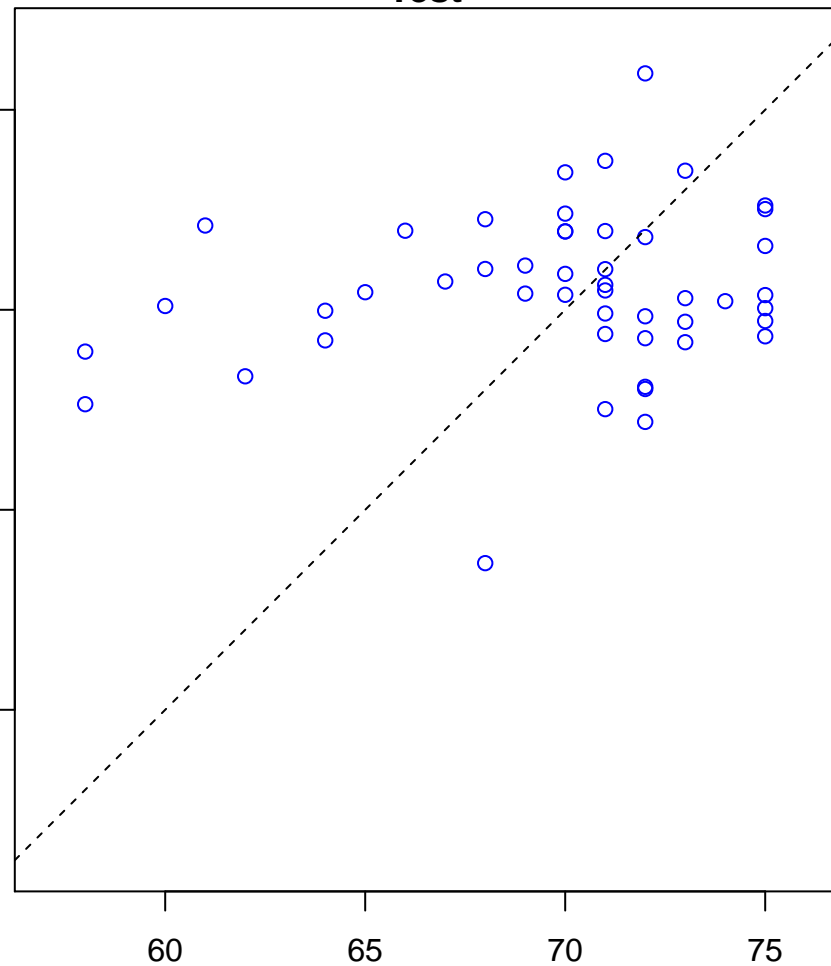


pyrimidine nucleotide catabolic process (Score: 0.728392)

Control

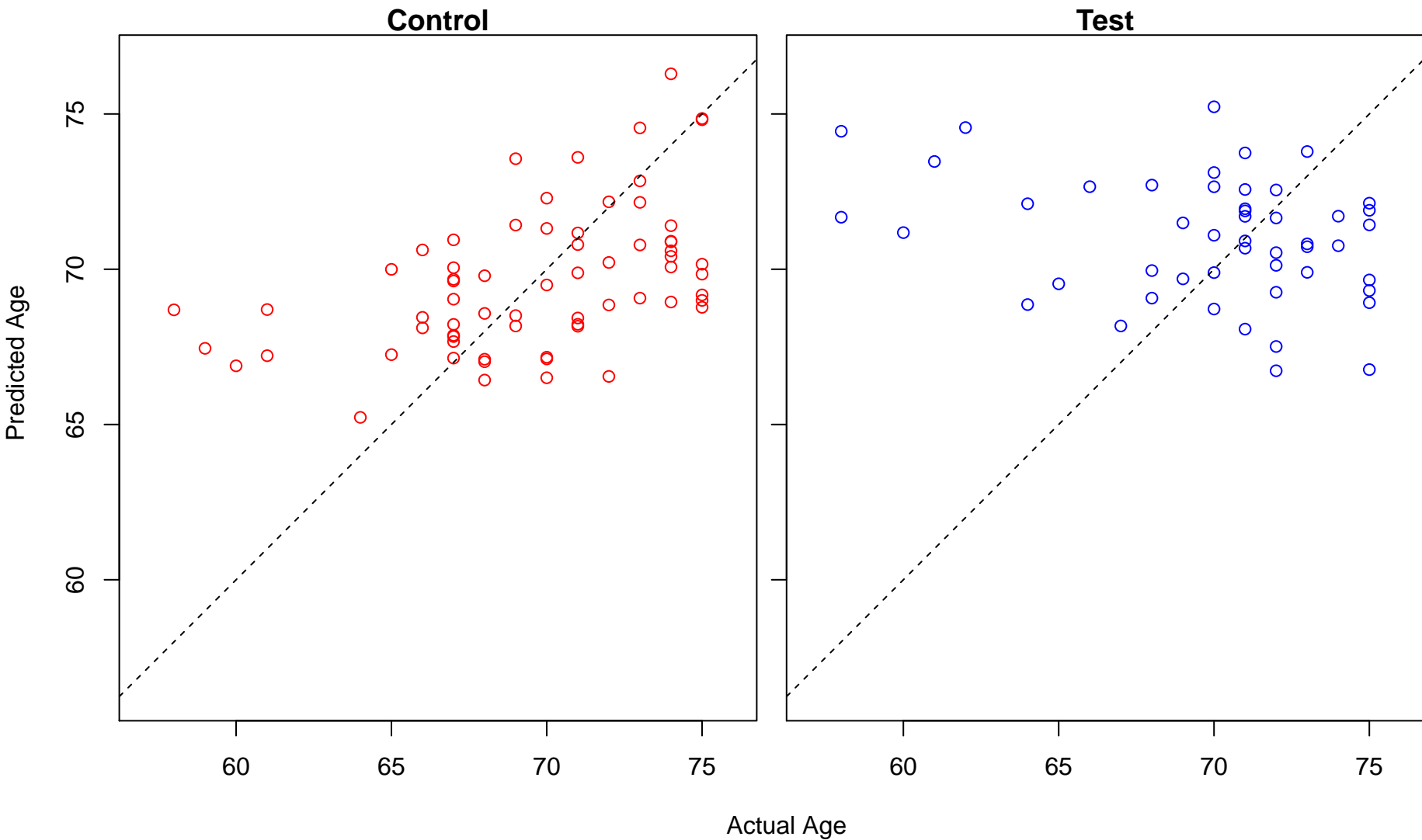


Test

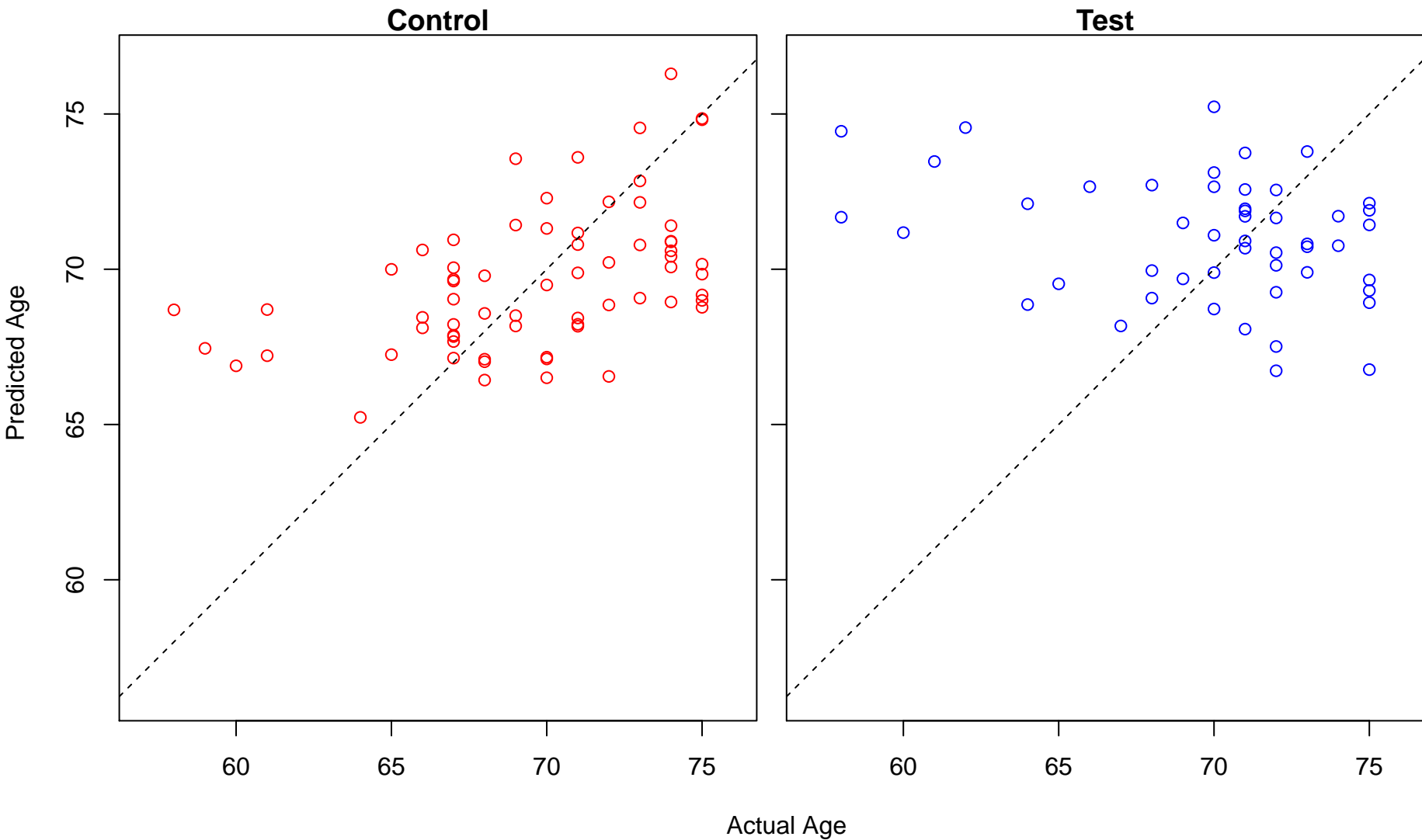


Actual Age

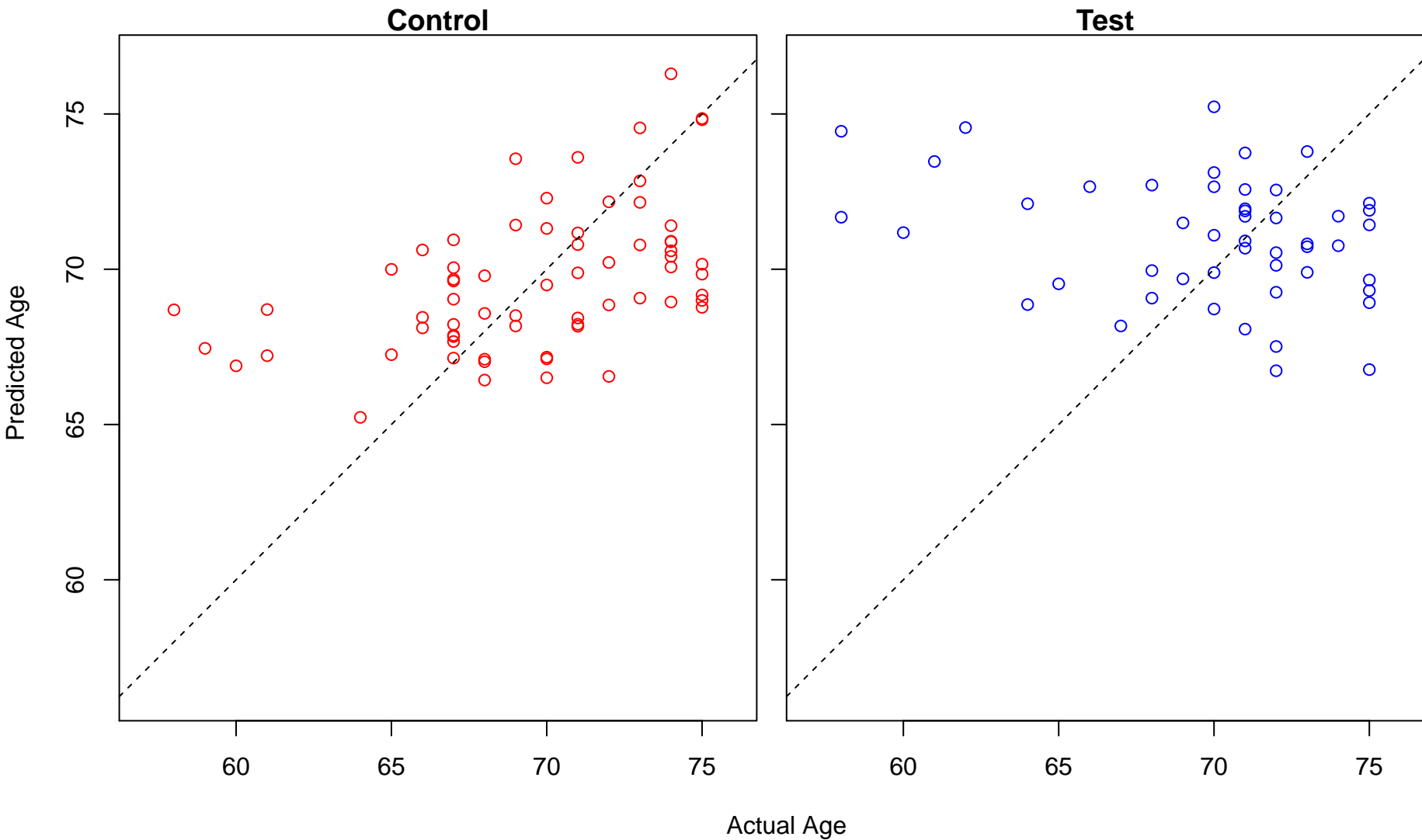
polysaccharide catabolic process (Score: 0.728246)



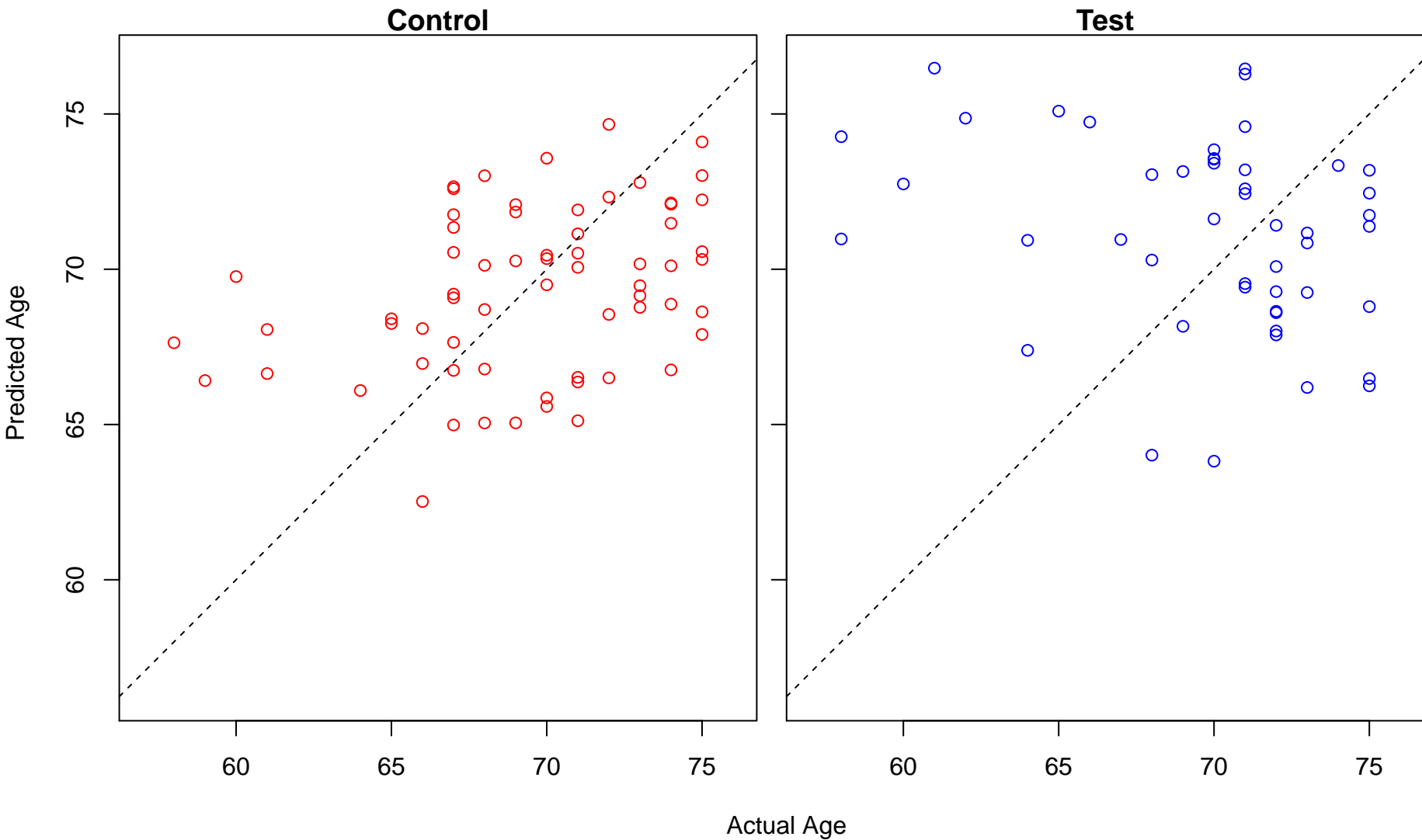
glucan catabolic process (Score: 0.728246)



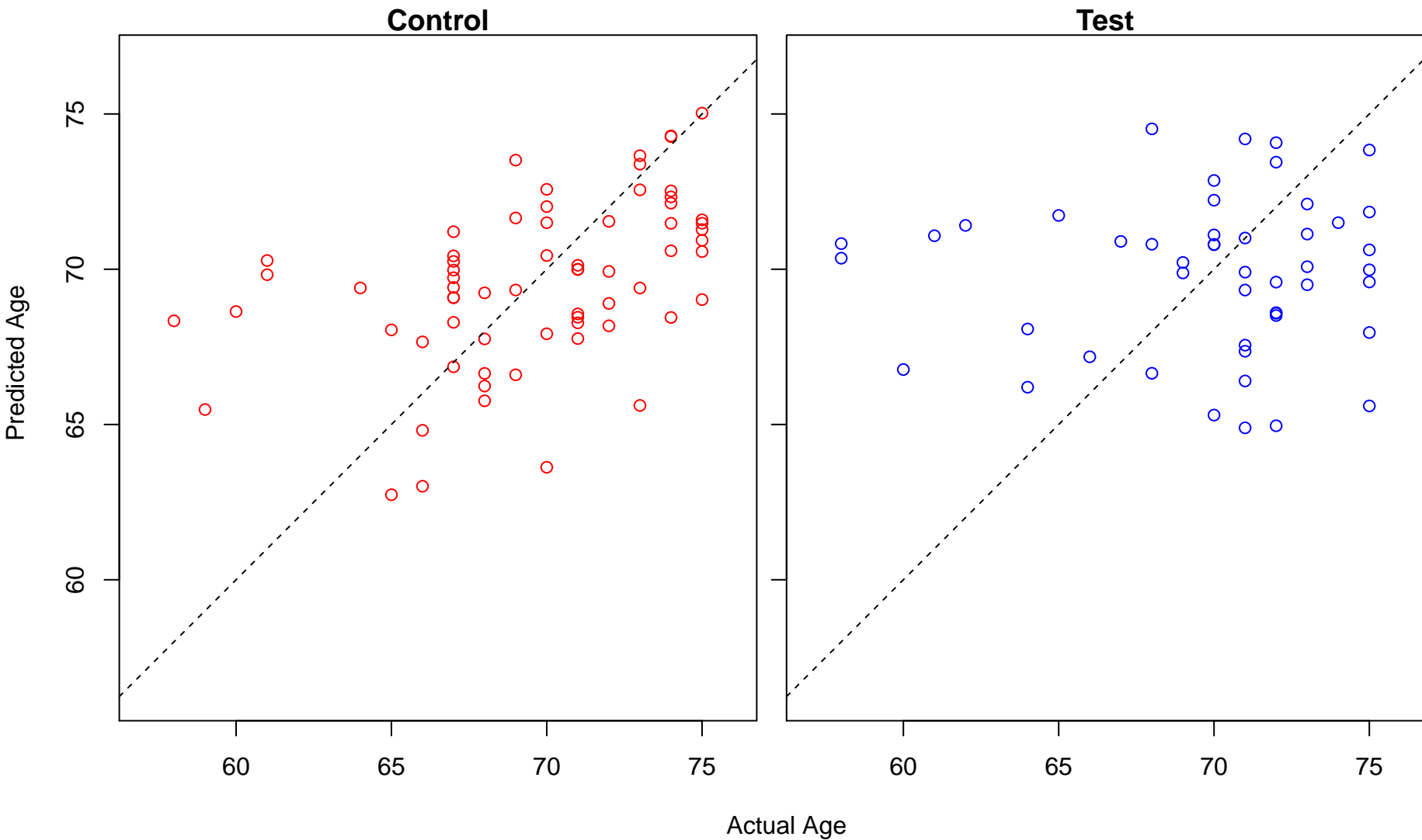
cellular polysaccharide catabolic process (Score: 0.728246)



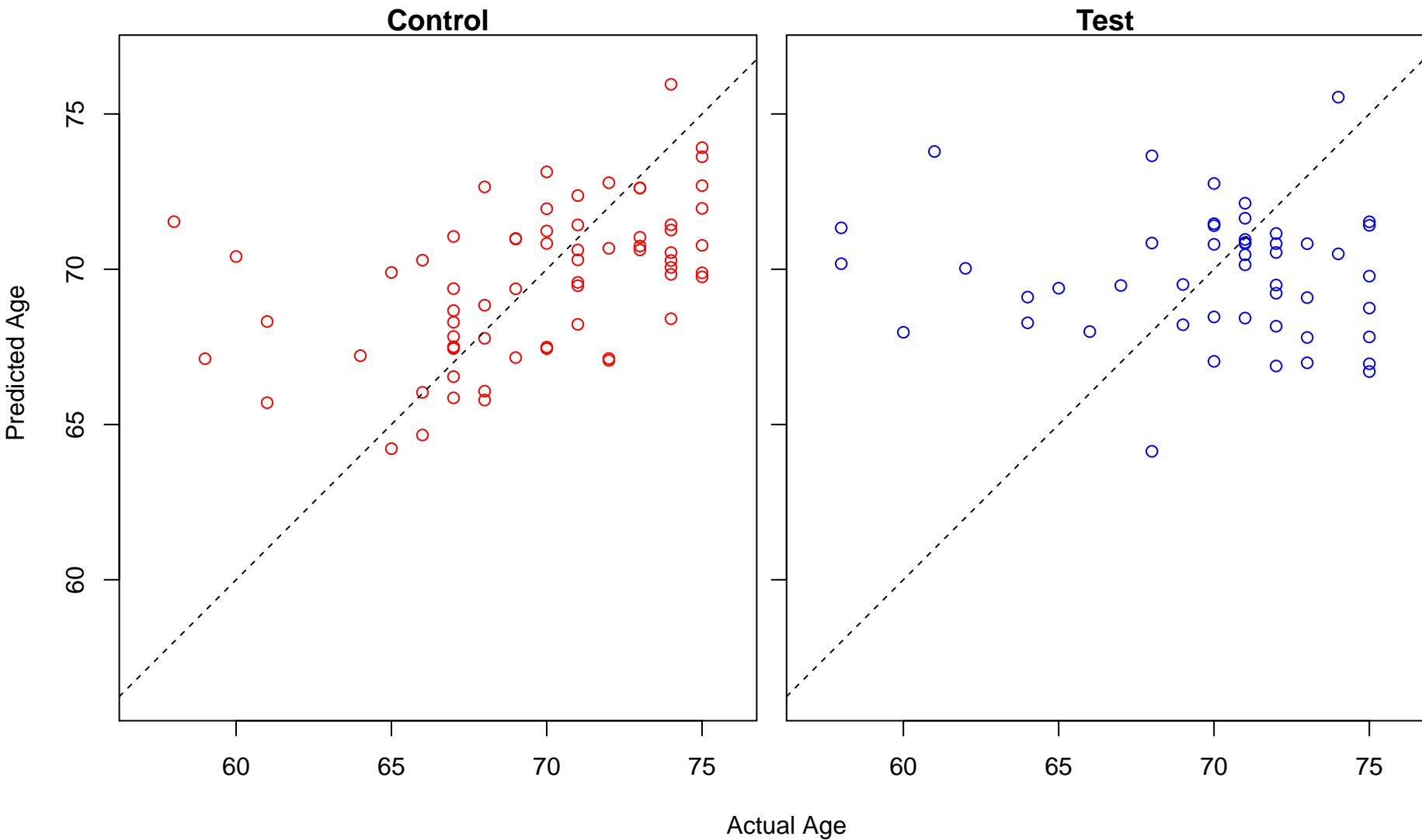
bicarbonate transport (Score: 0.728224)



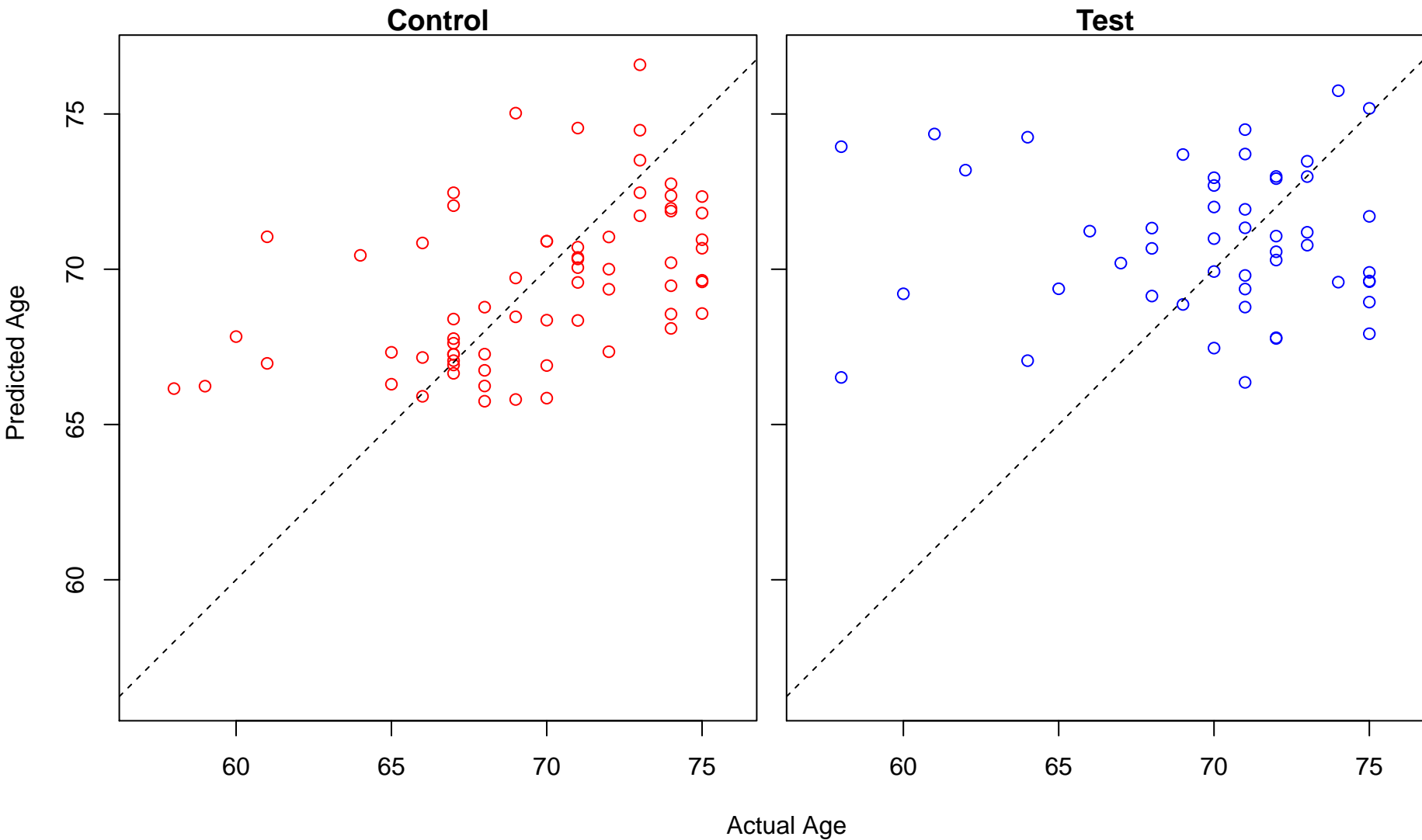
DNA damage response, signal transduction resulting in transcription (Score: 0.728224)



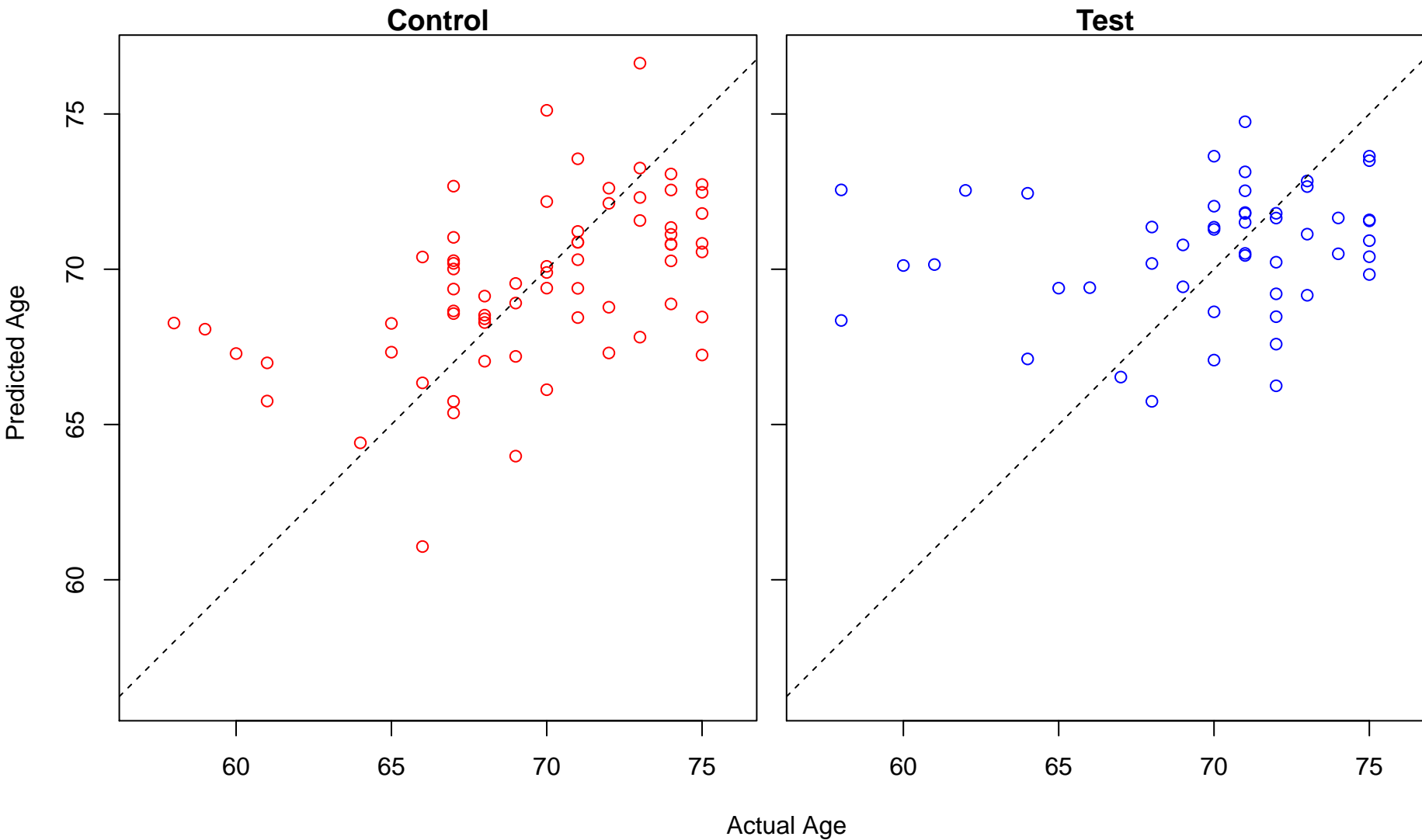
regulation of CD8-positive, alpha-beta T cell activation (Score: 0.727490)



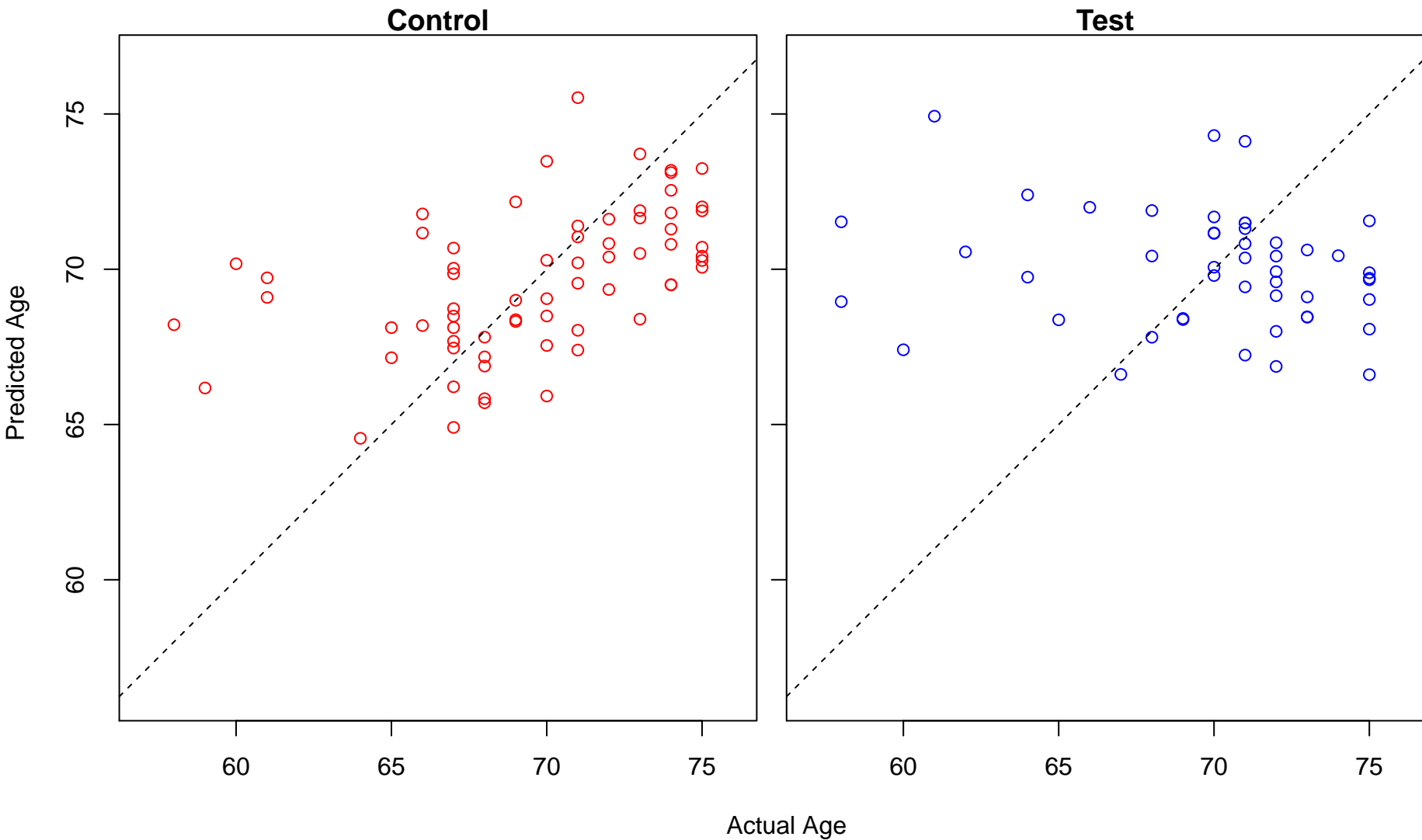
negative regulation of hormone secretion (Score: 0.727310)



negative regulation of protein localization to cell surface (Score: 0.727085)

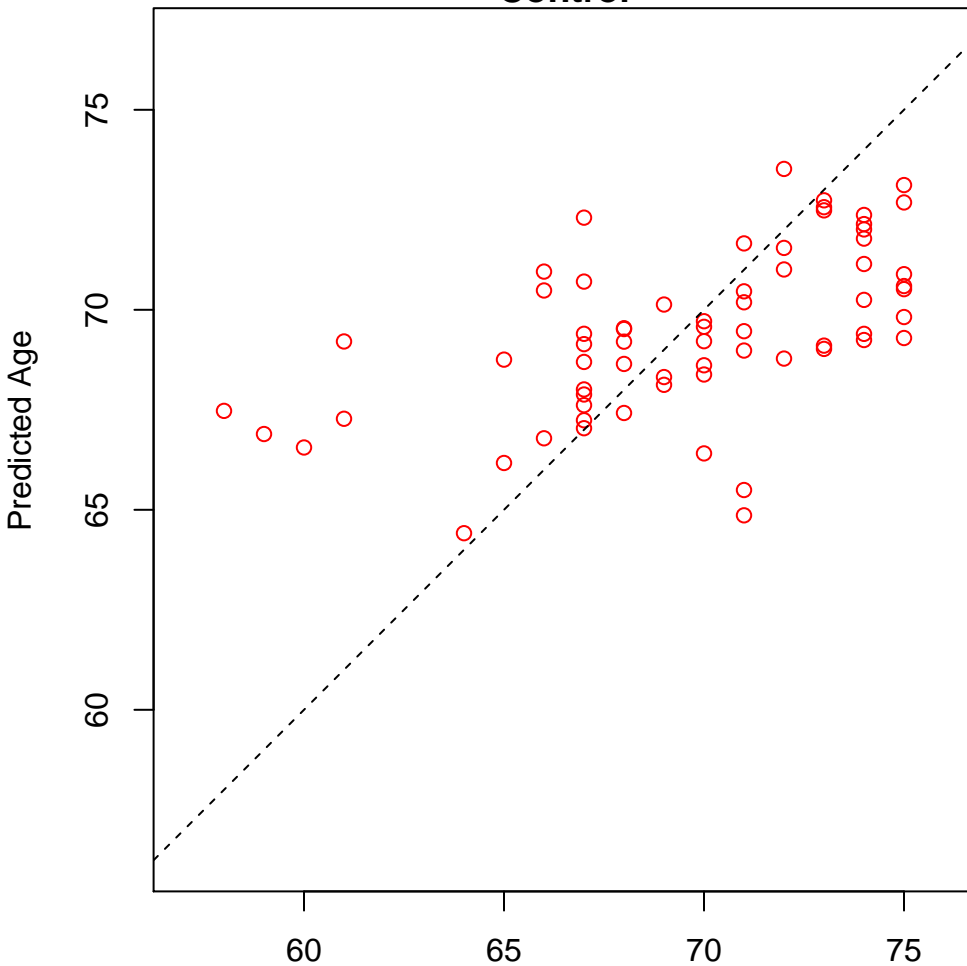


DNA cytosine deamination (Score: 0.725383)

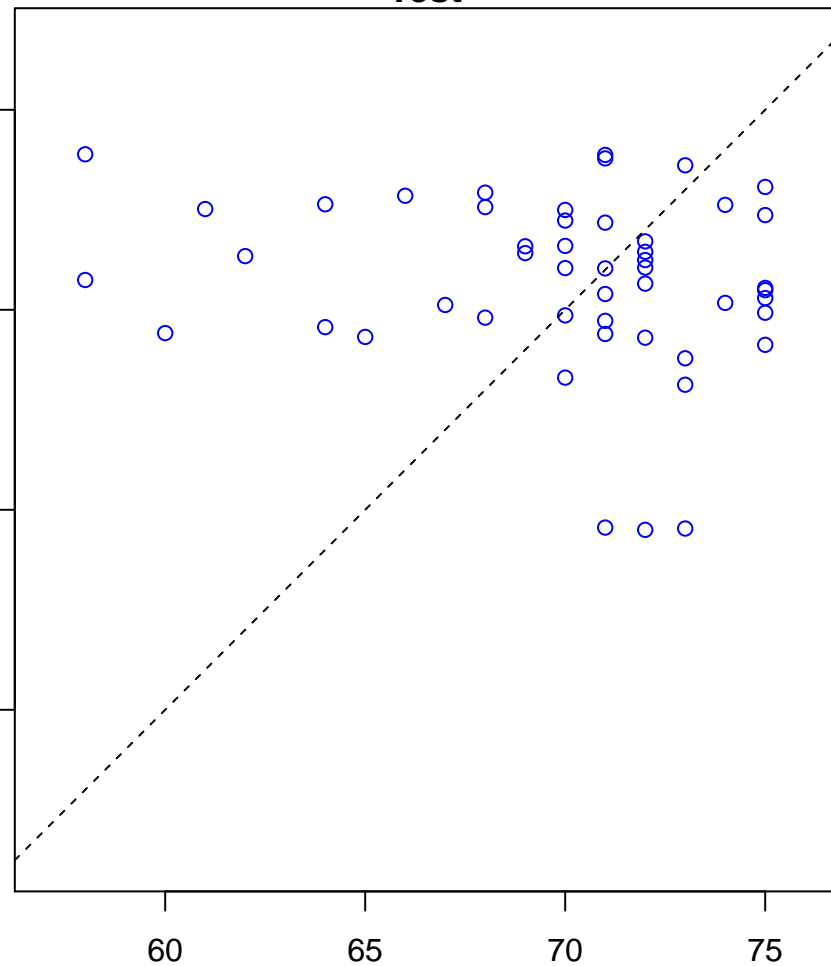


regulation of membrane depolarization (Score: 0.725167)

Control



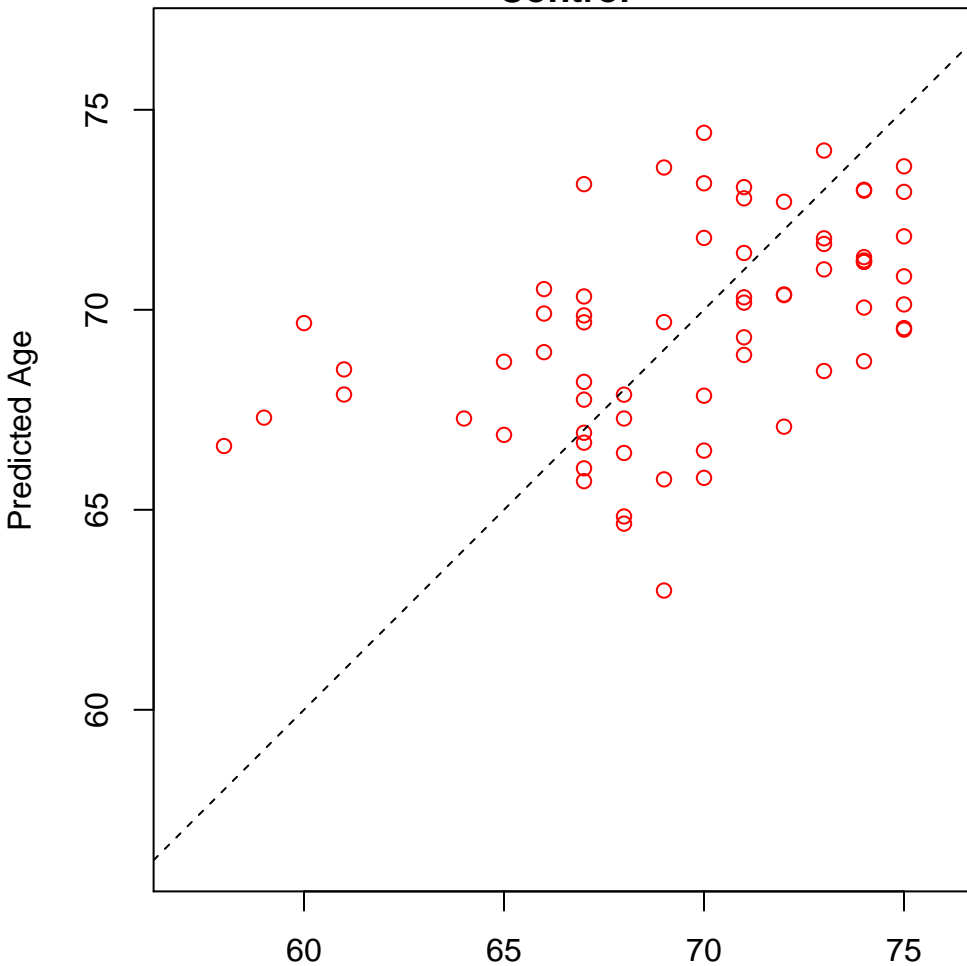
Test



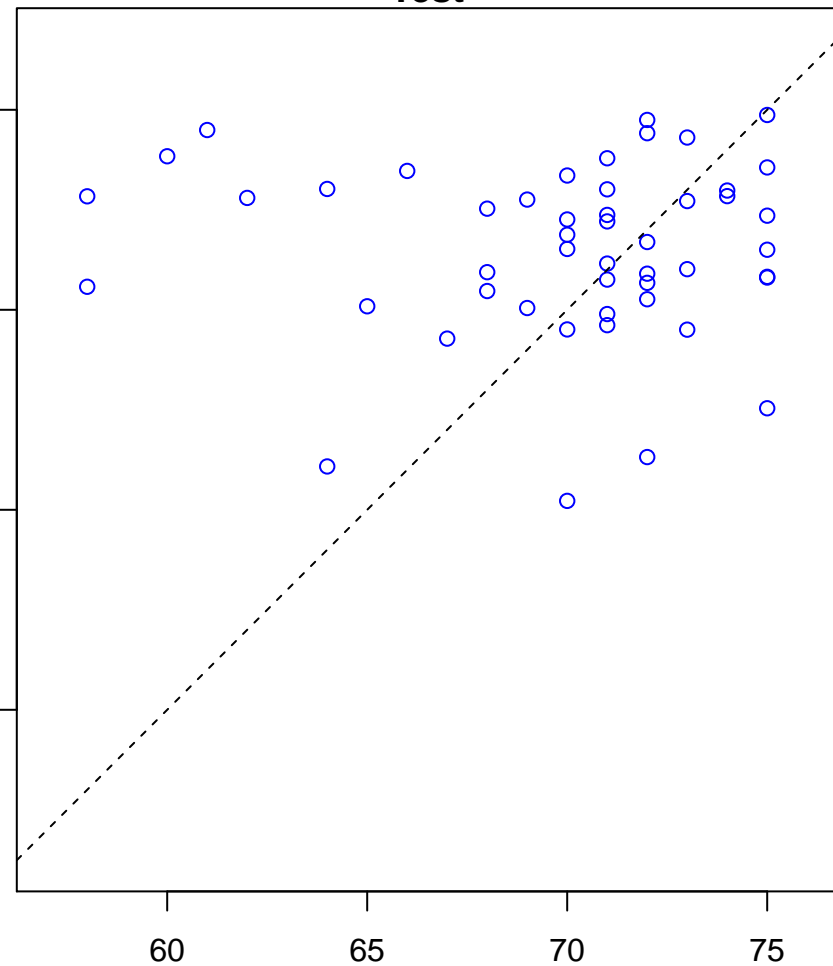
Actual Age

positive regulation of glucose transport (Score: 0.725137)

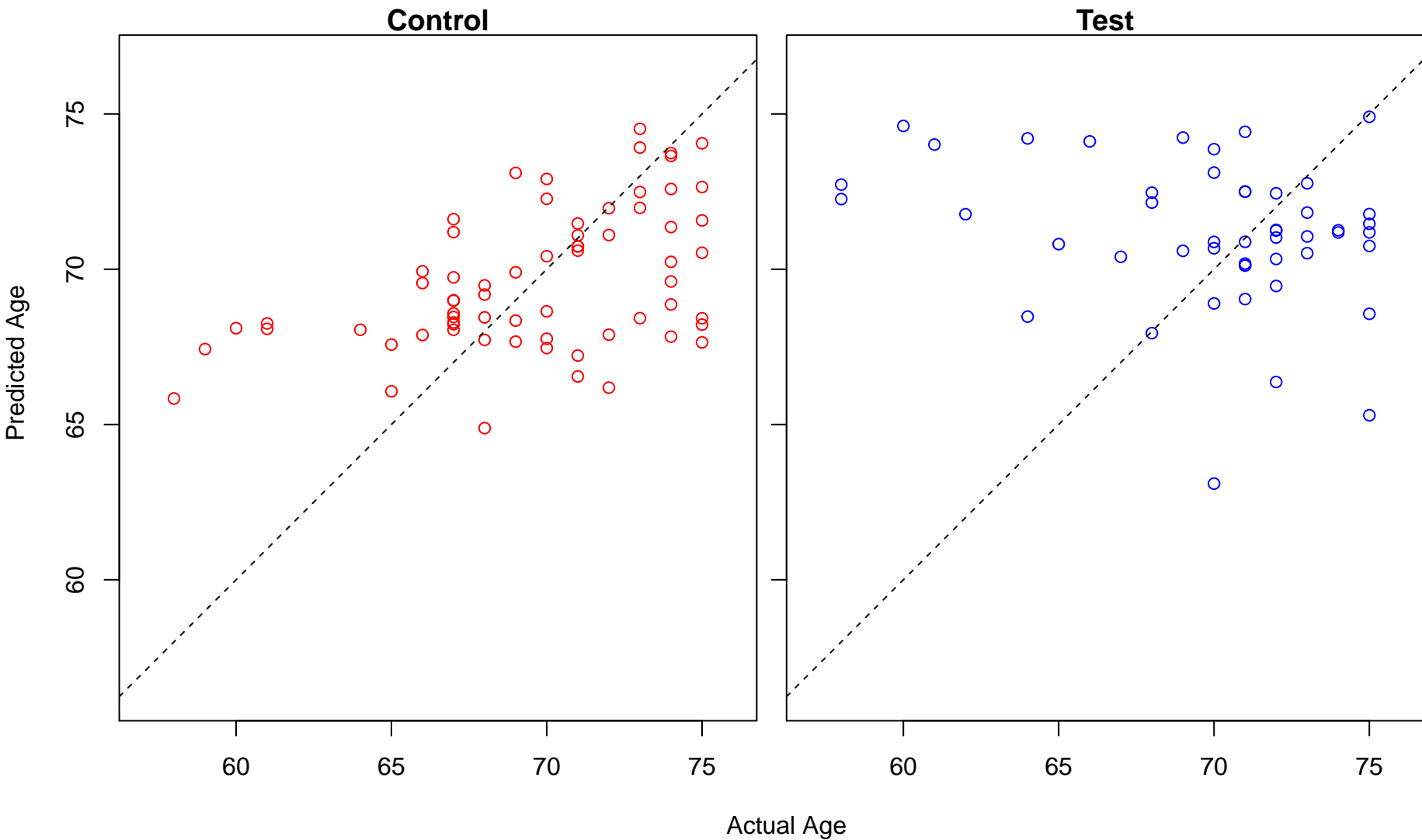
Control



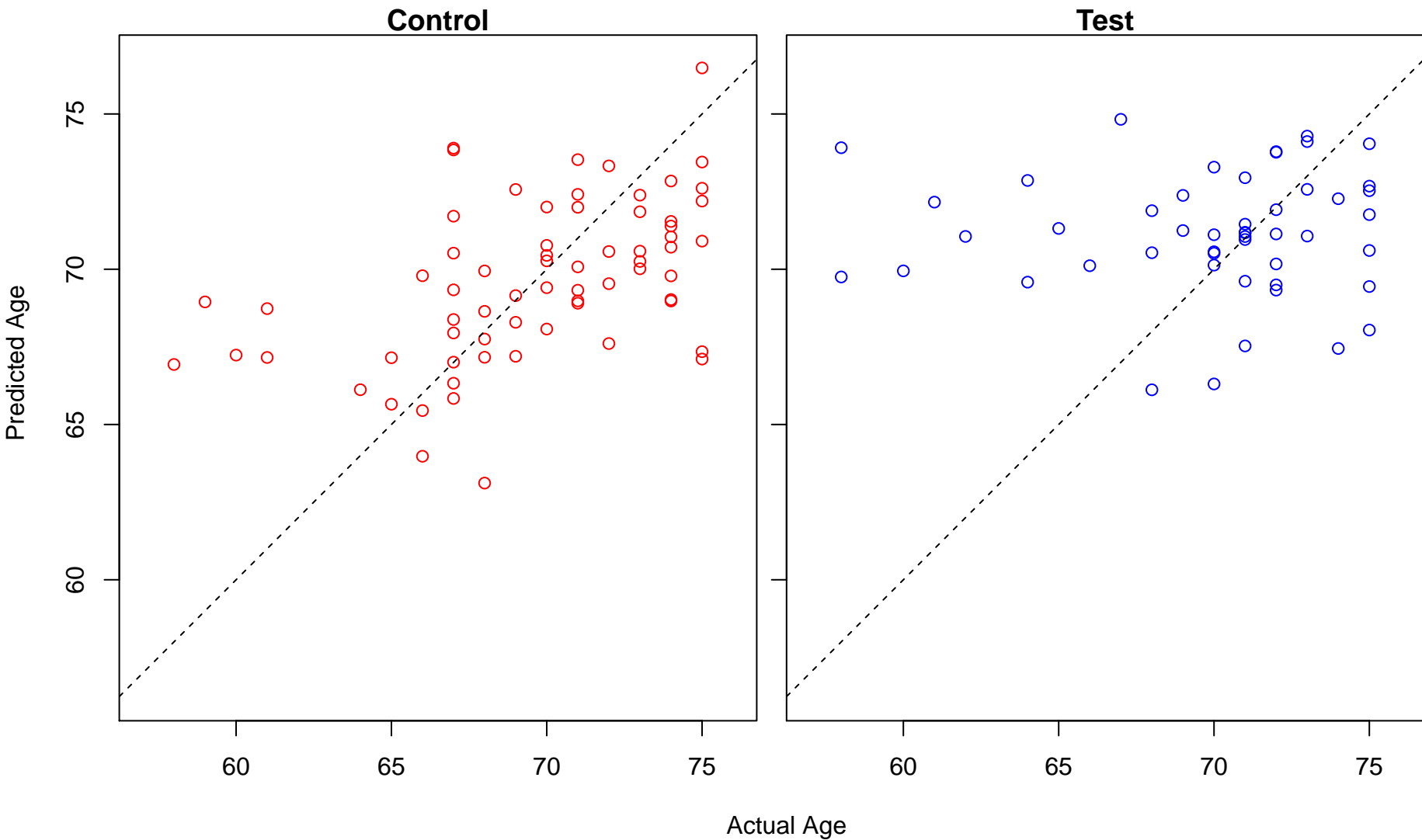
Test



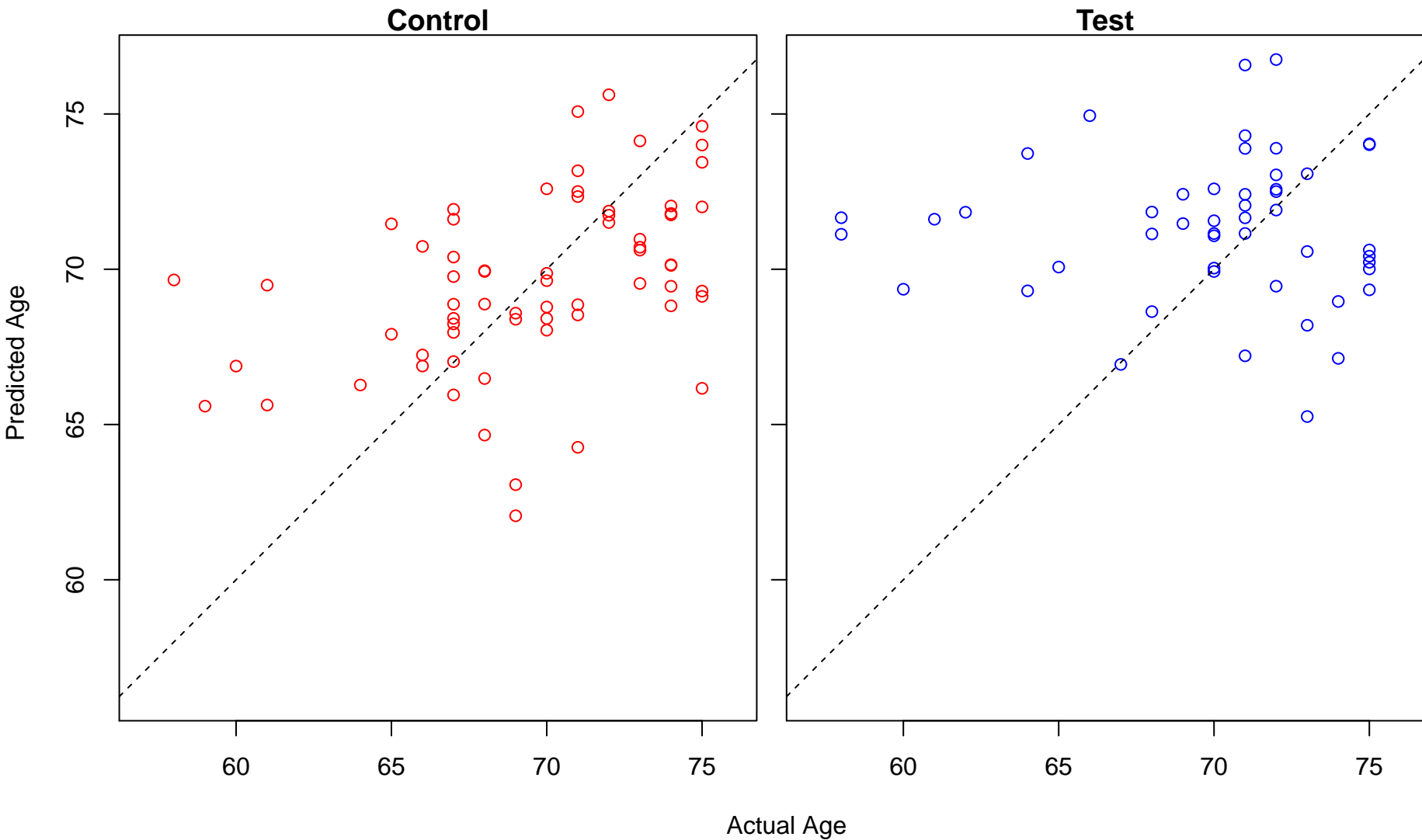
T cell homeostasis (Score: 0.724521)



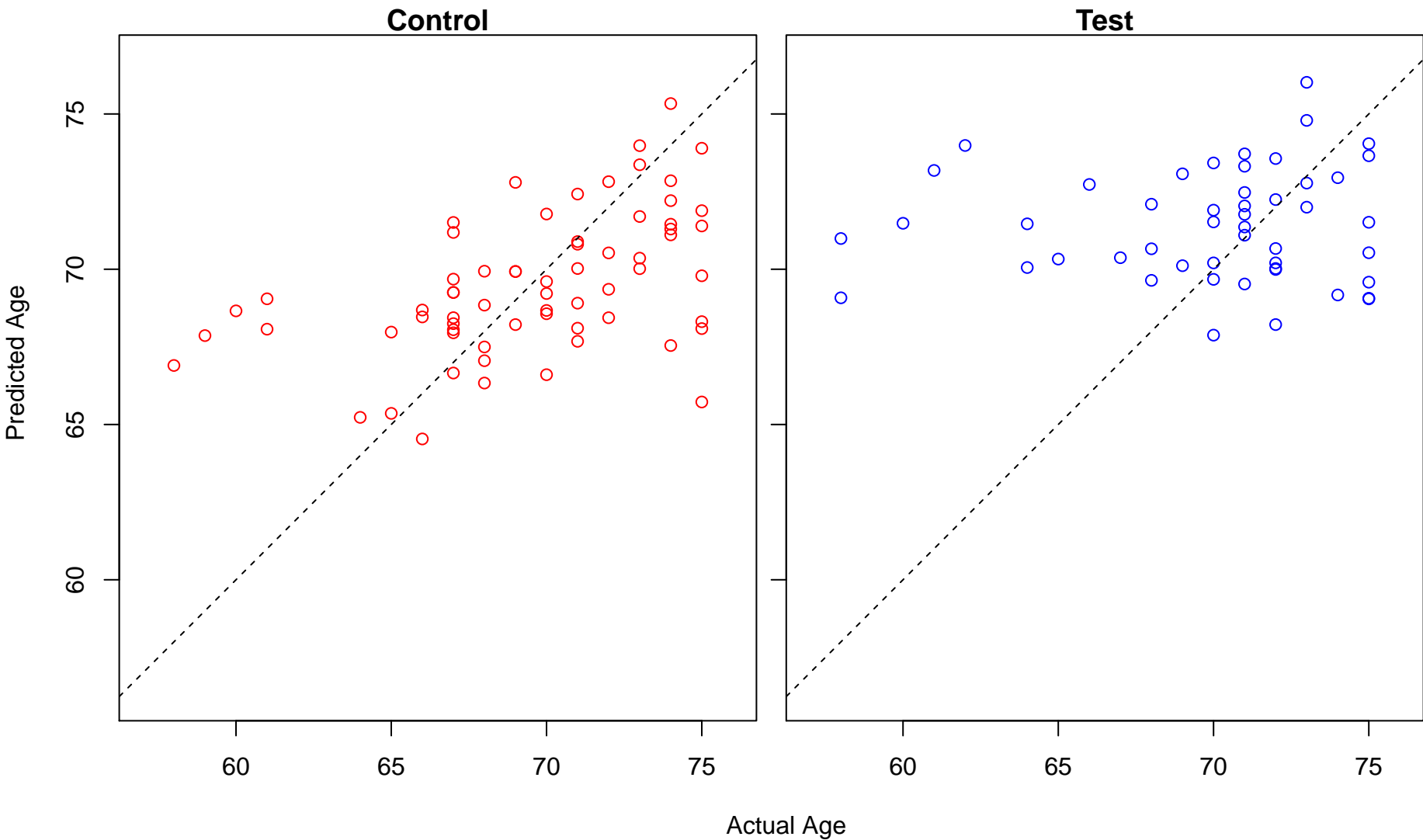
cellular response to UV-B (Score: 0.724406)



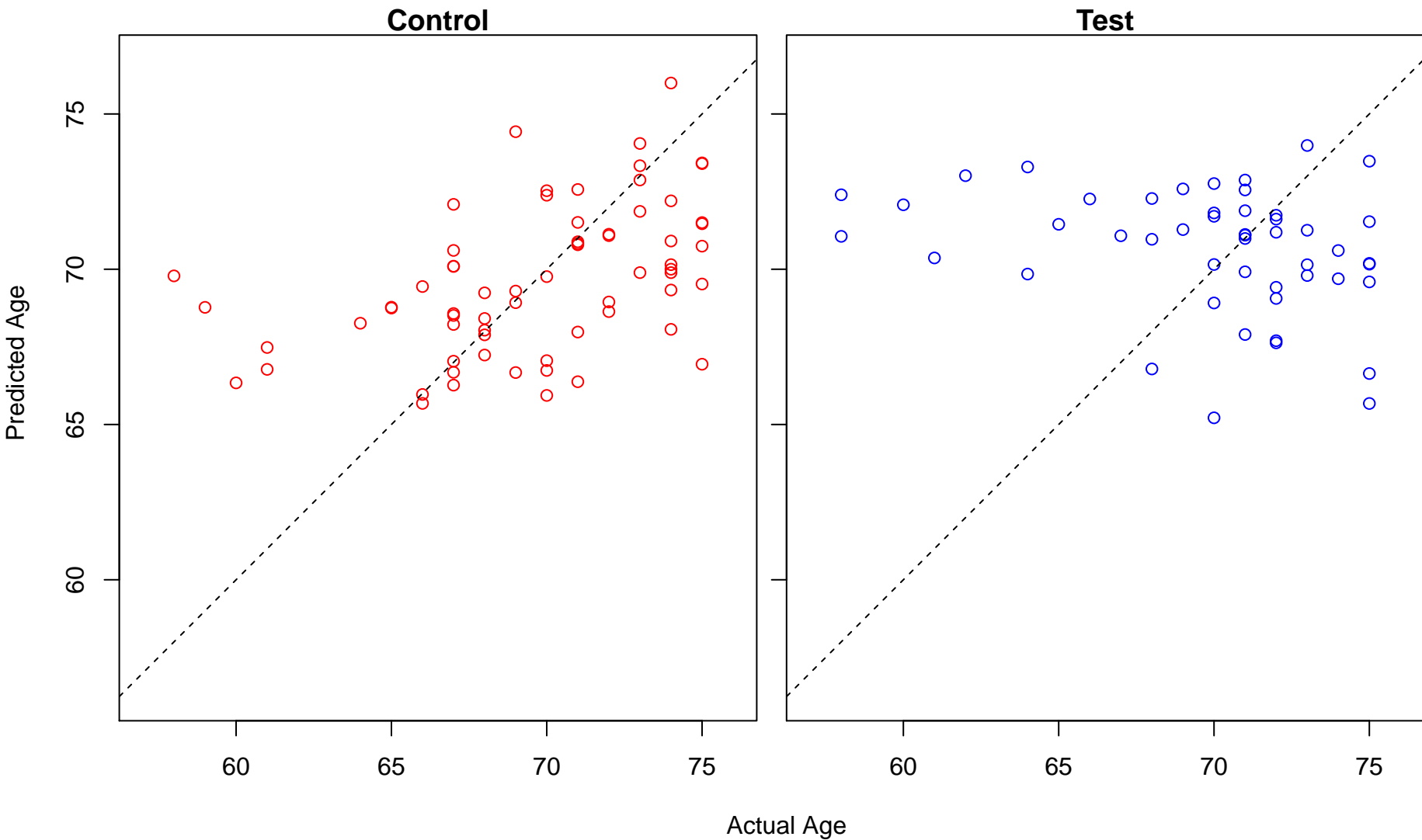
lipoxxygenase pathway (Score: 0.724371)



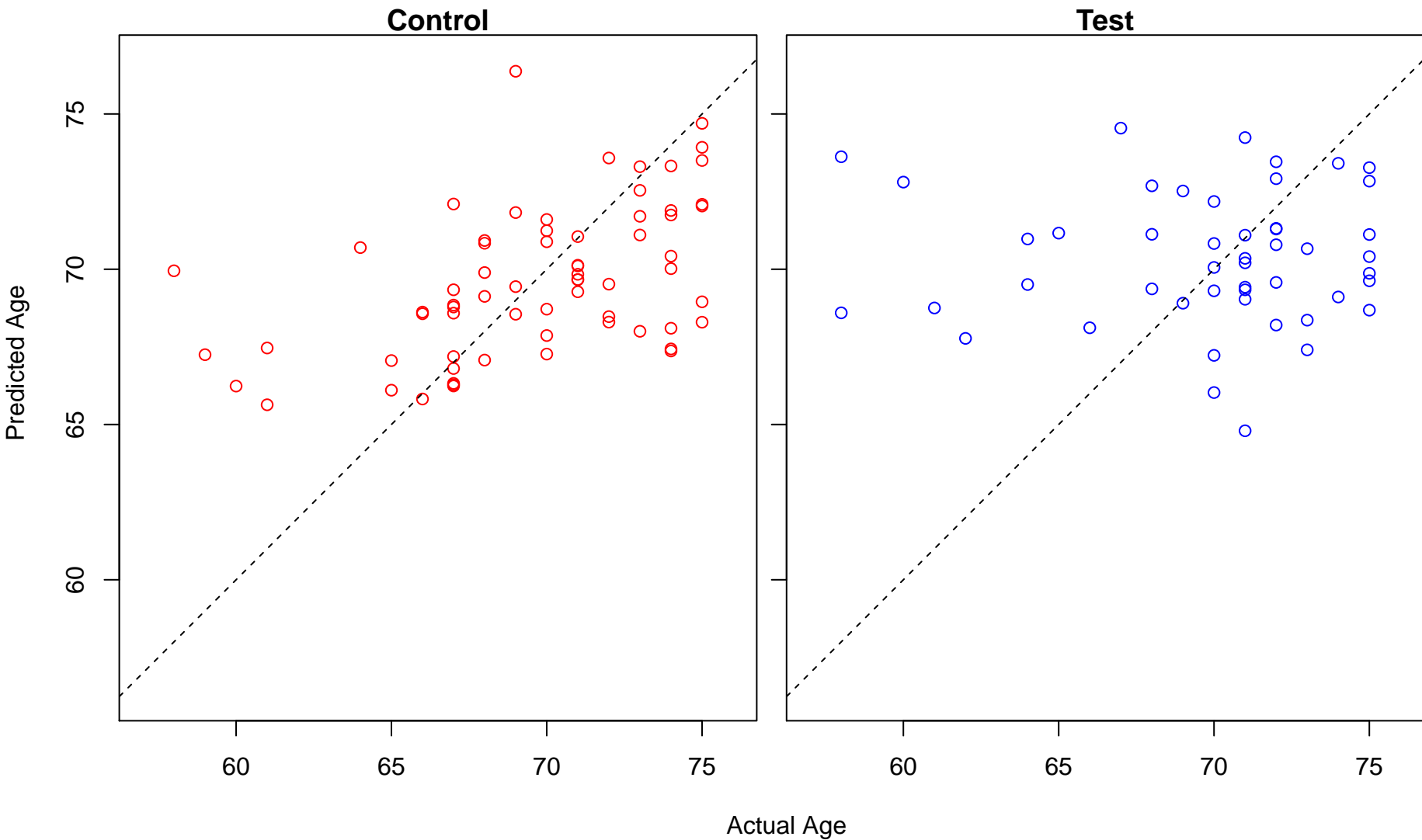
phospholipid efflux (Score: 0.722323)



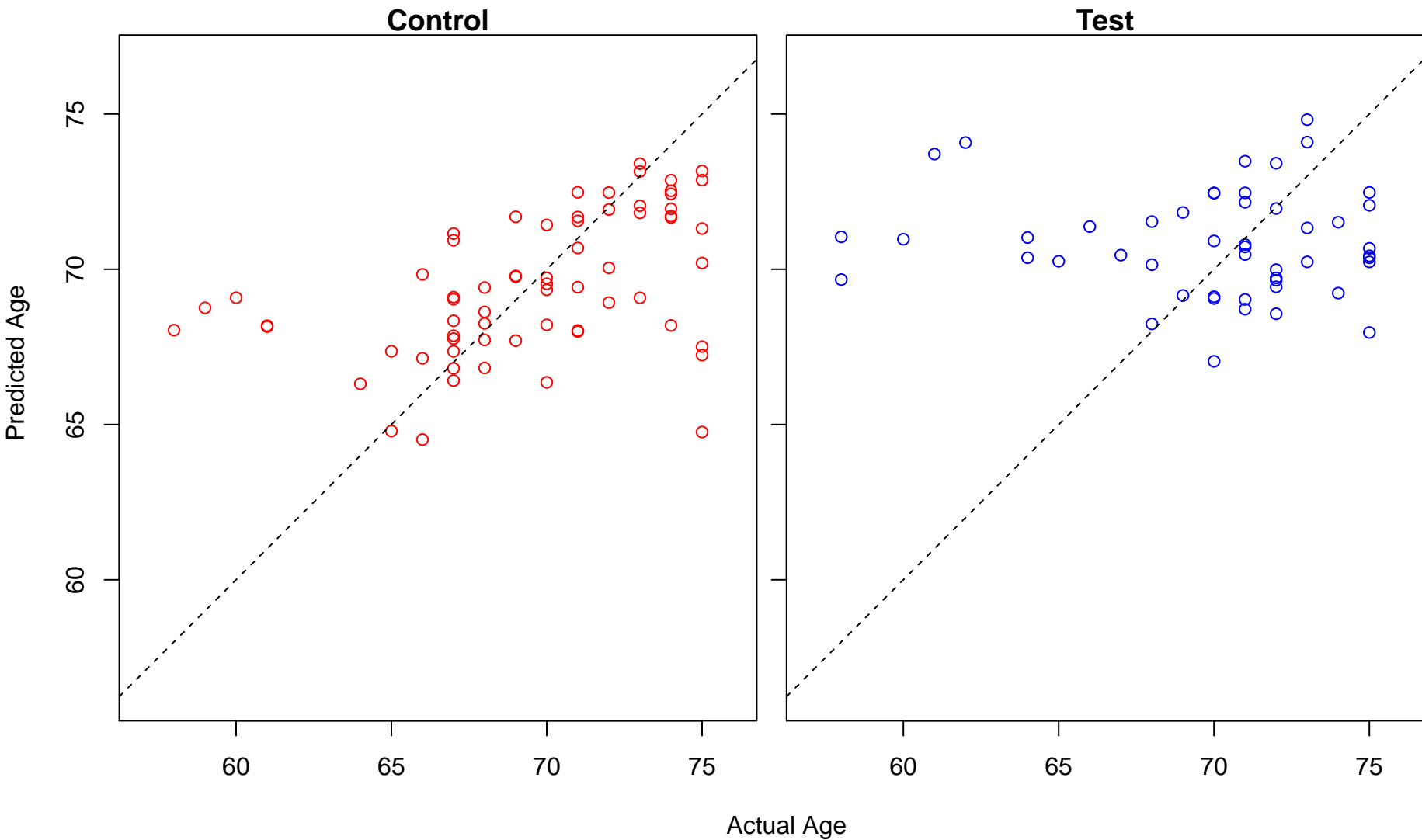
neuron projection extension (Score: 0.722294)



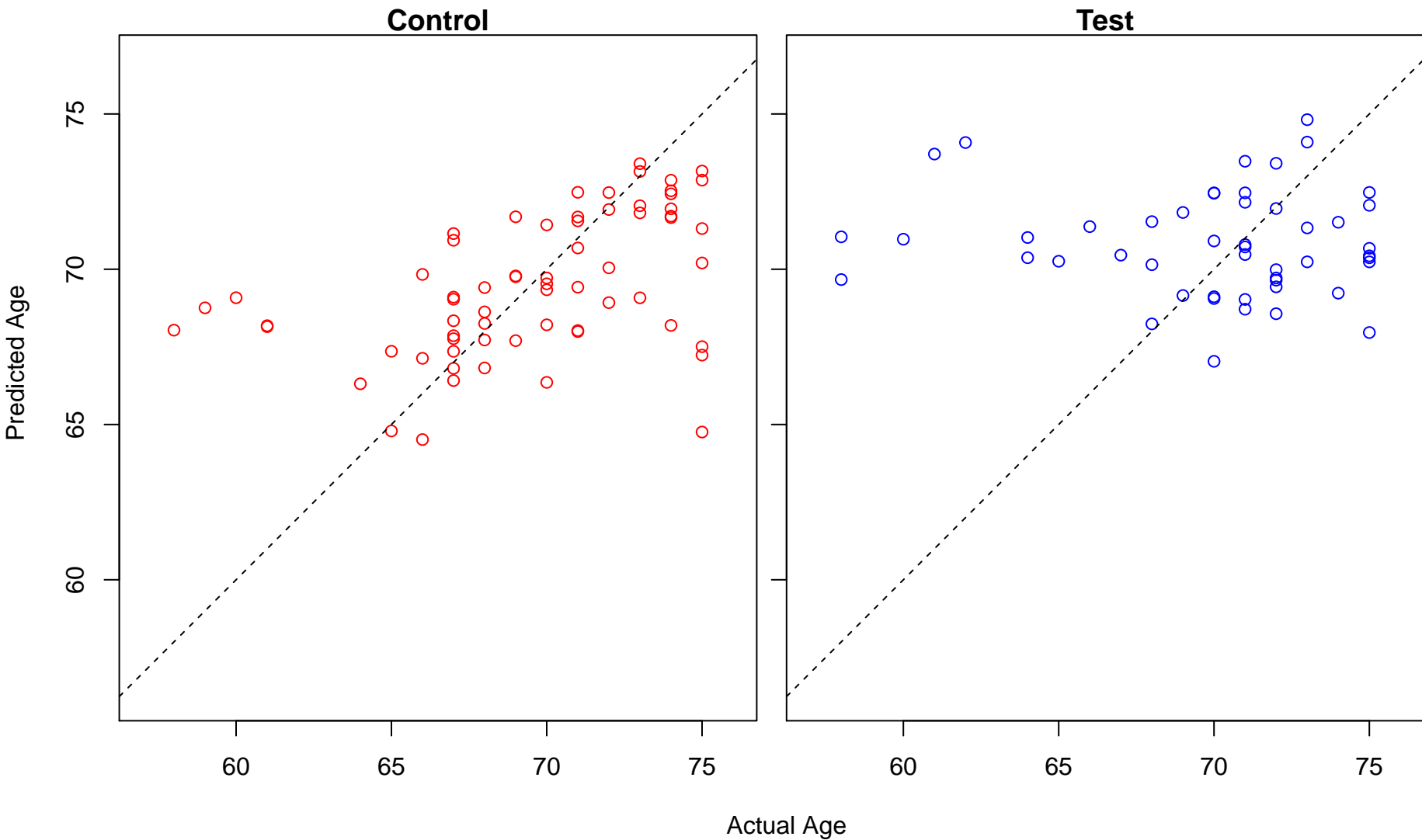
ganglioside biosynthetic process (Score: 0.722179)



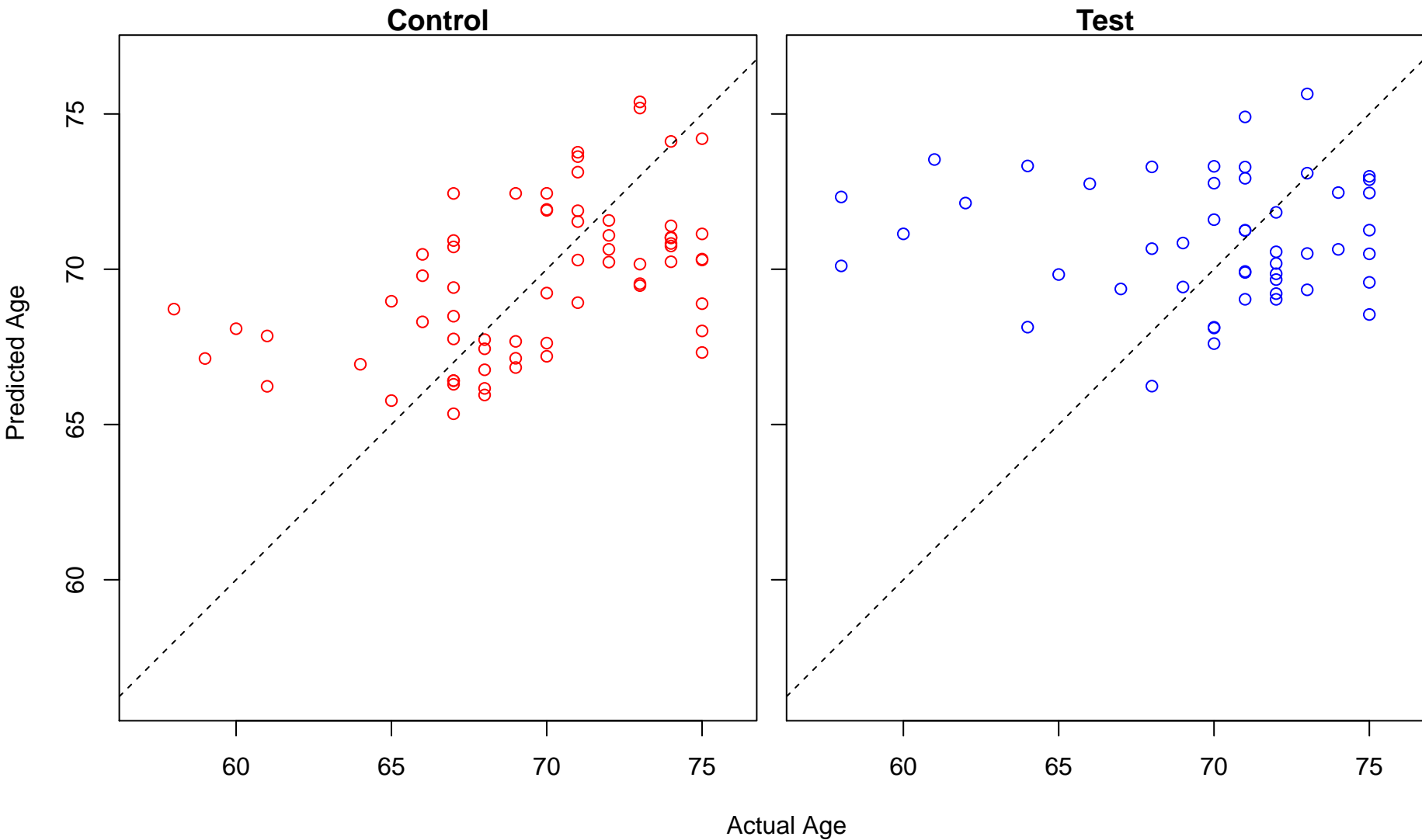
positive regulation of sterol transport (Score: 0.722159)



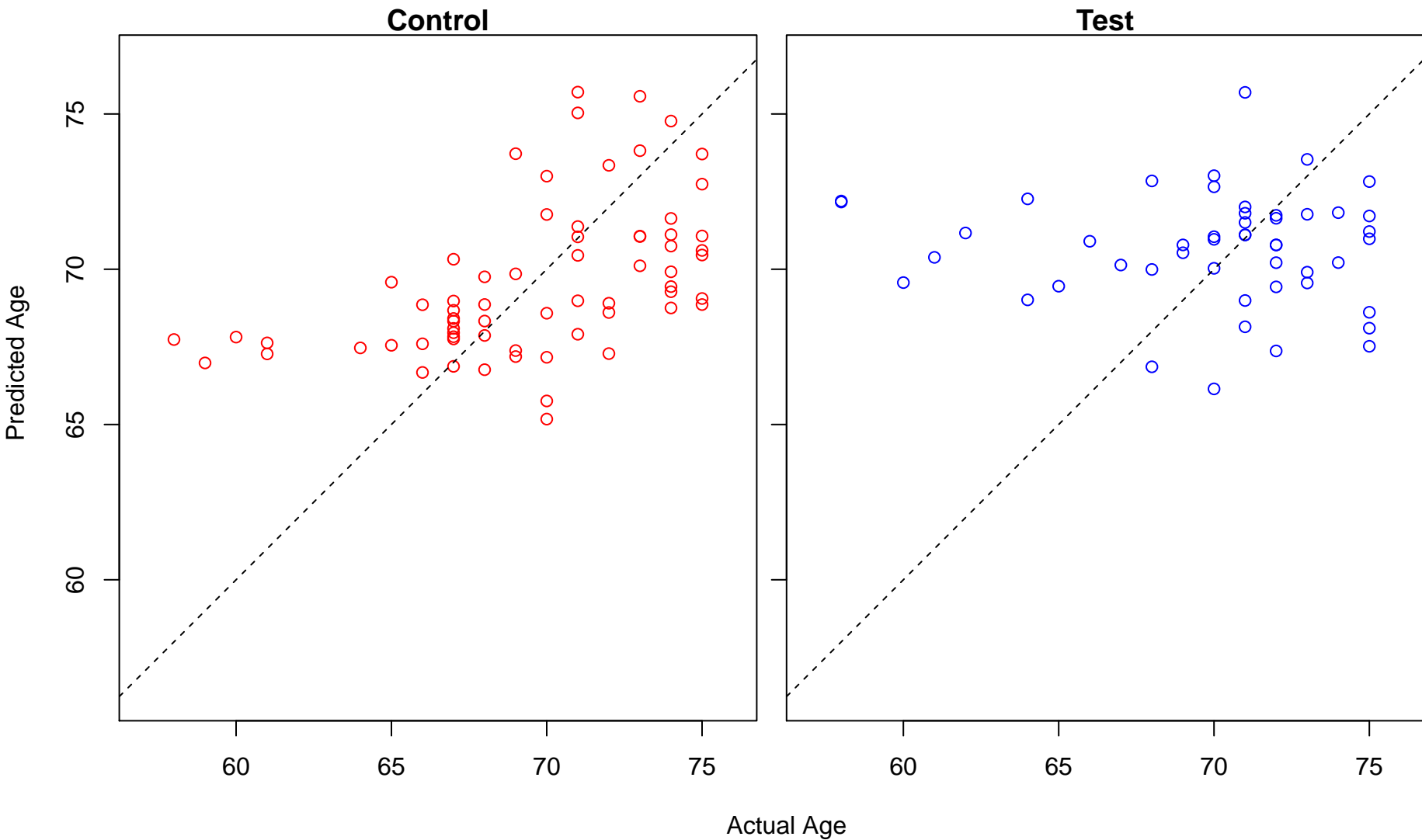
positive regulation of cholesterol transport (Score: 0.722159)



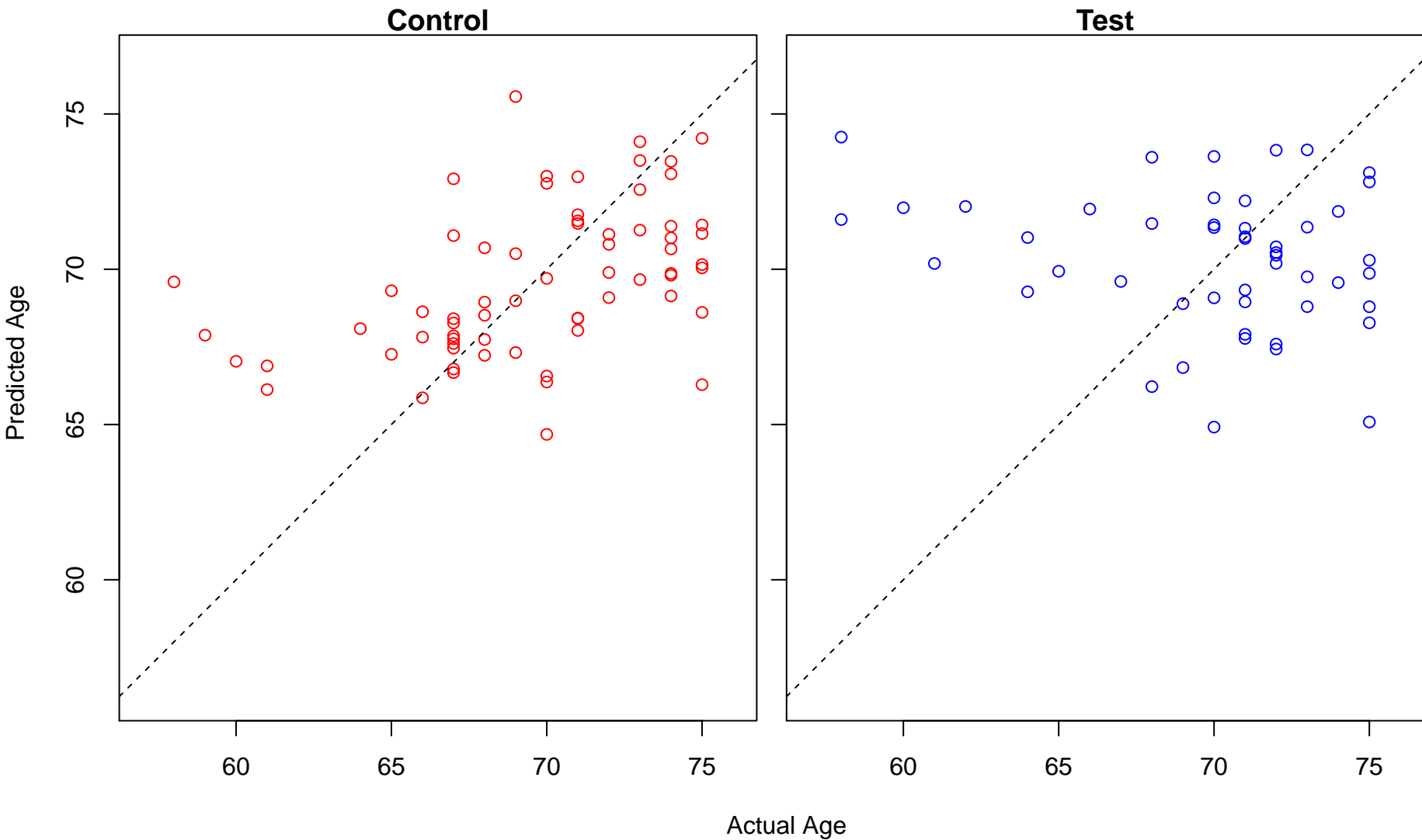
response to salt stress (Score: 0.721904)



negative regulation of fibroblast proliferation (Score: 0.721401)

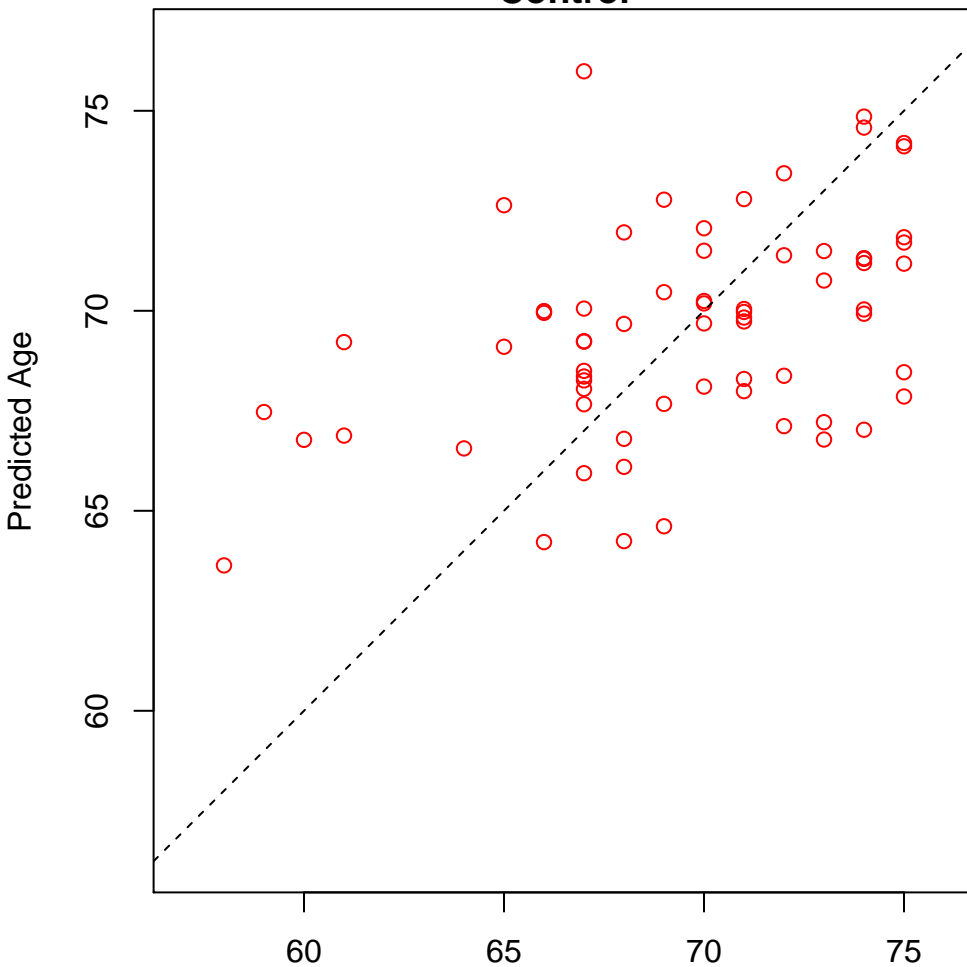


sodium ion export (Score: 0.720967)

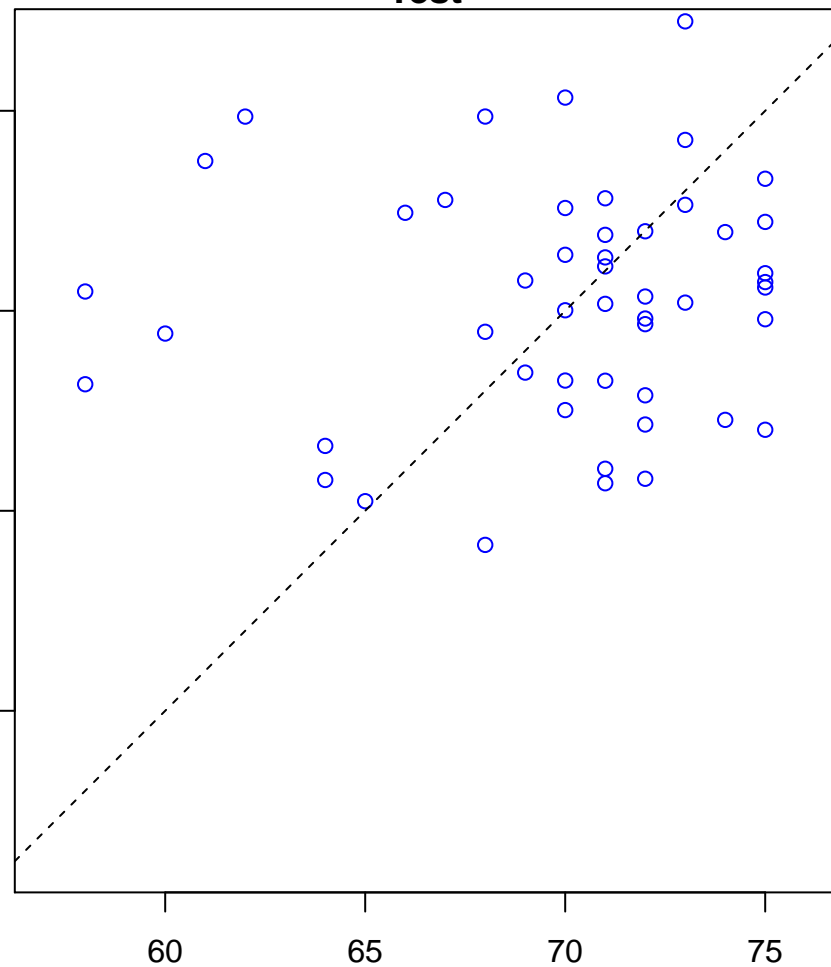


regulation of cholesterol esterification (Score: 0.720815)

Control

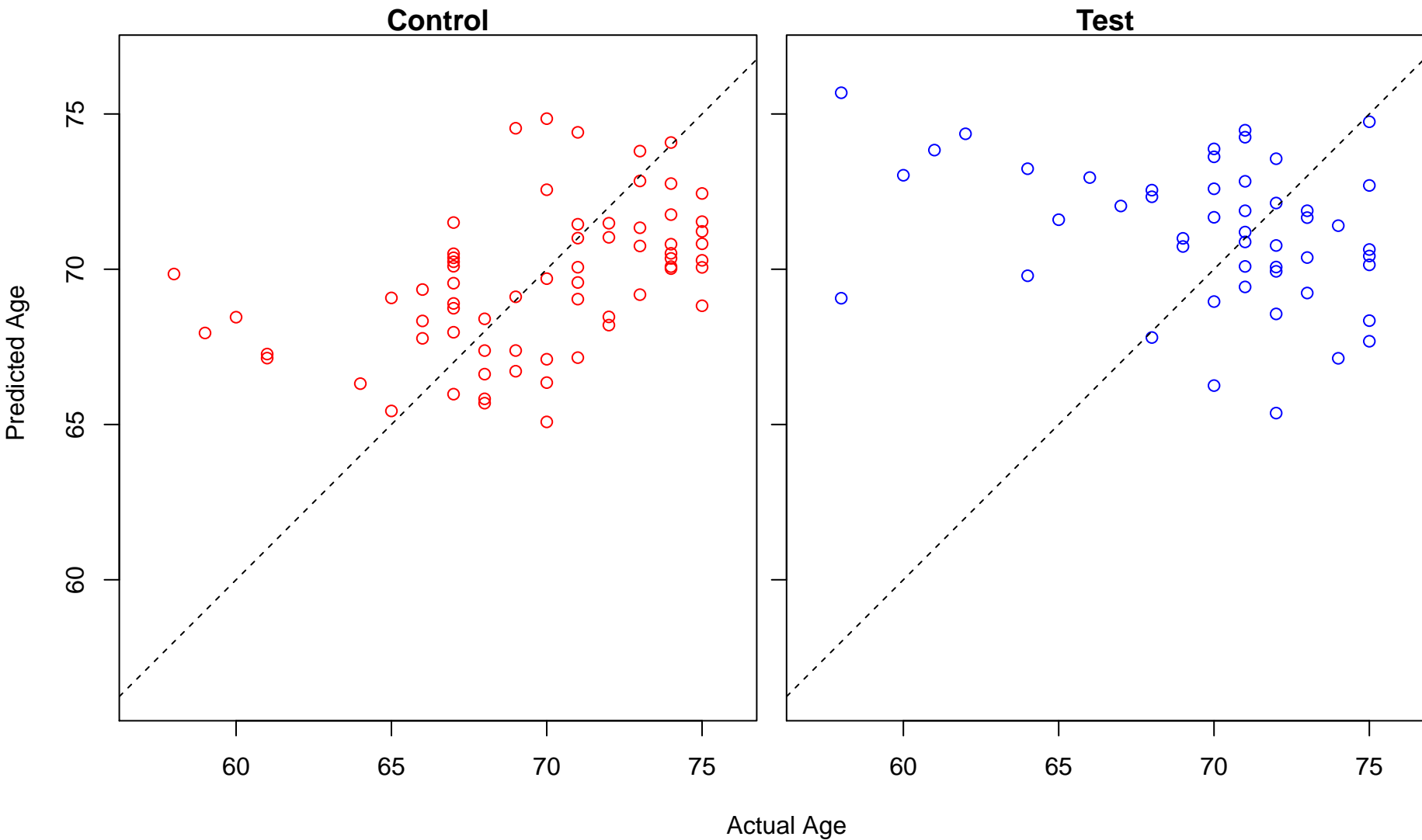


Test

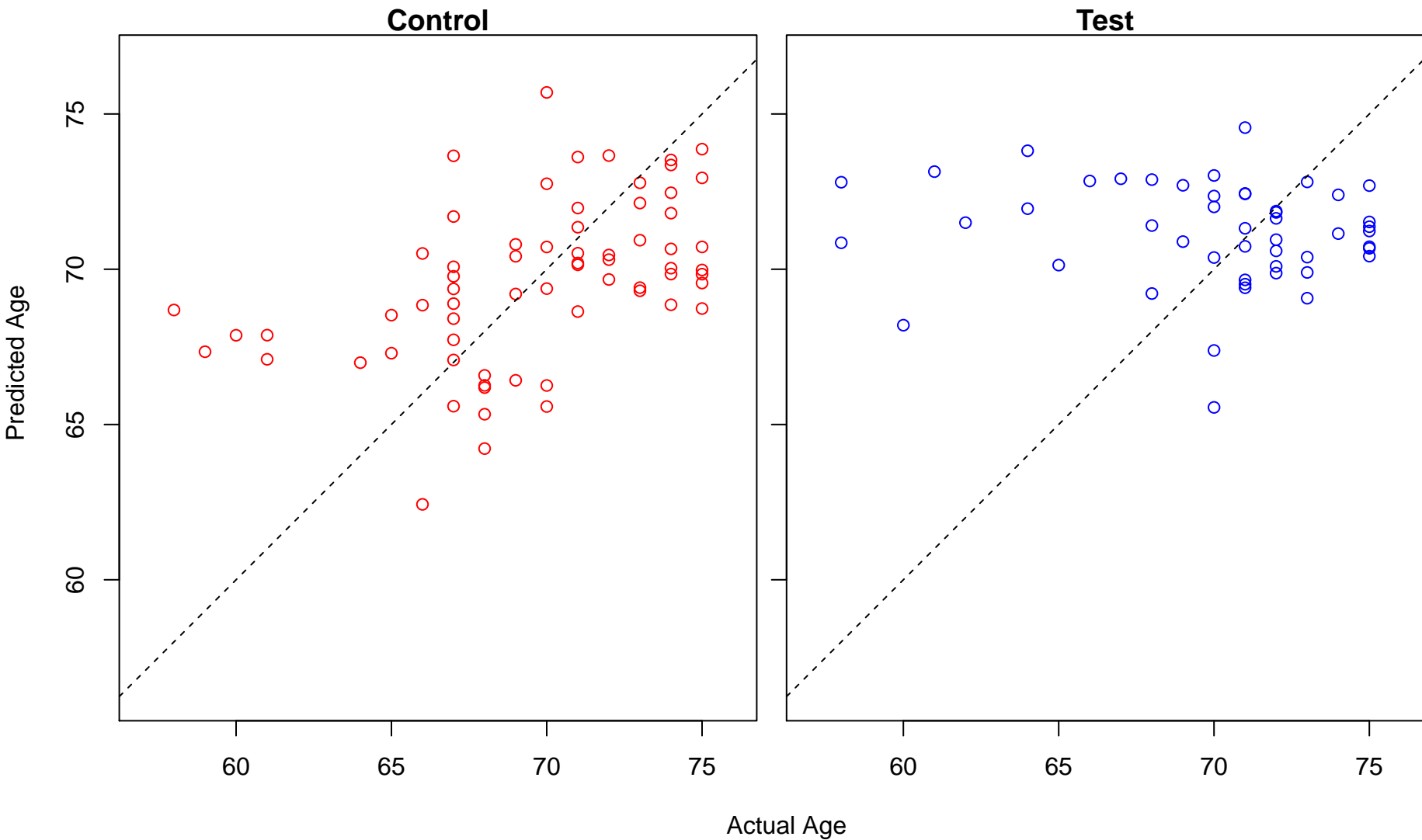


Actual Age

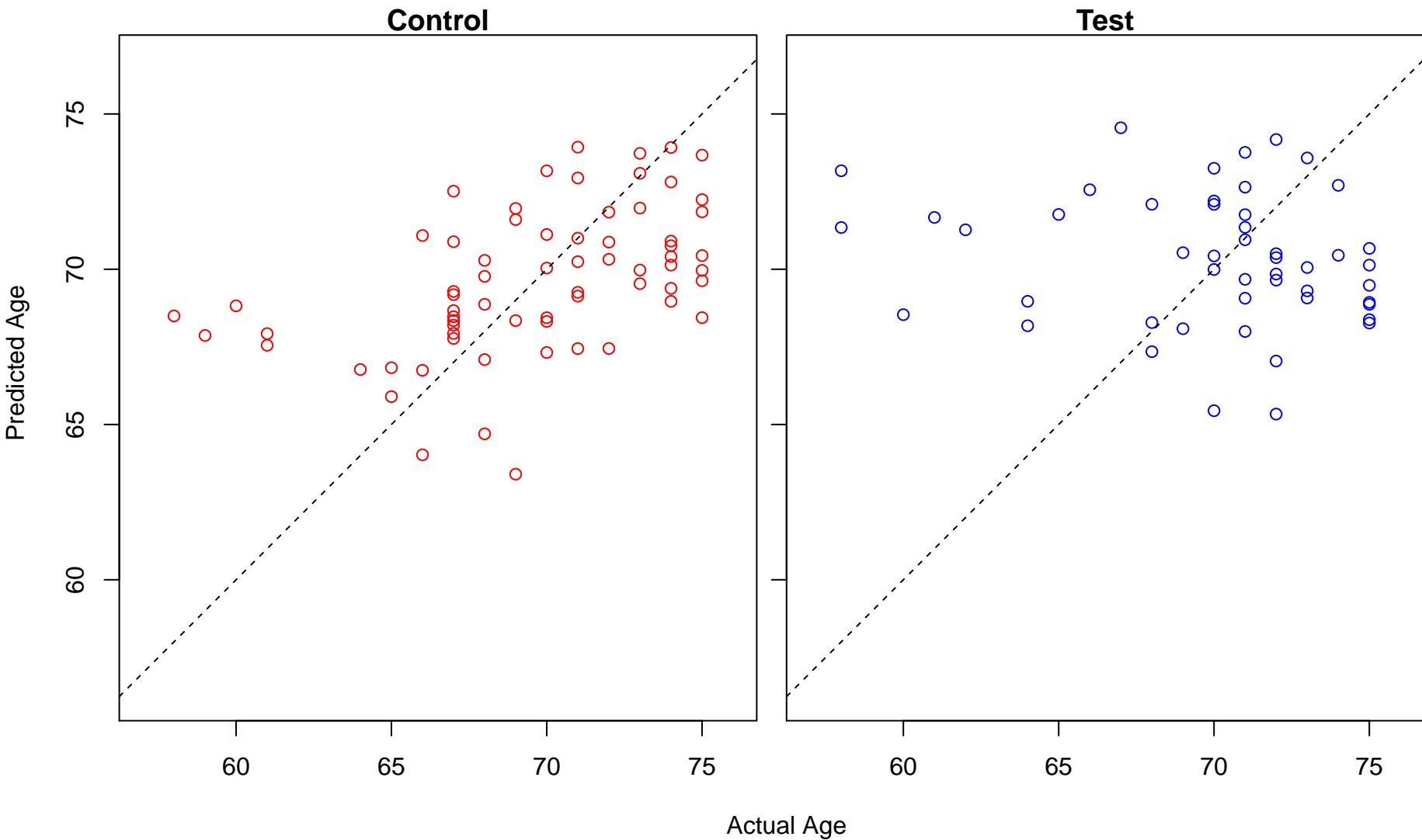
body fluid secretion (Score: 0.720565)



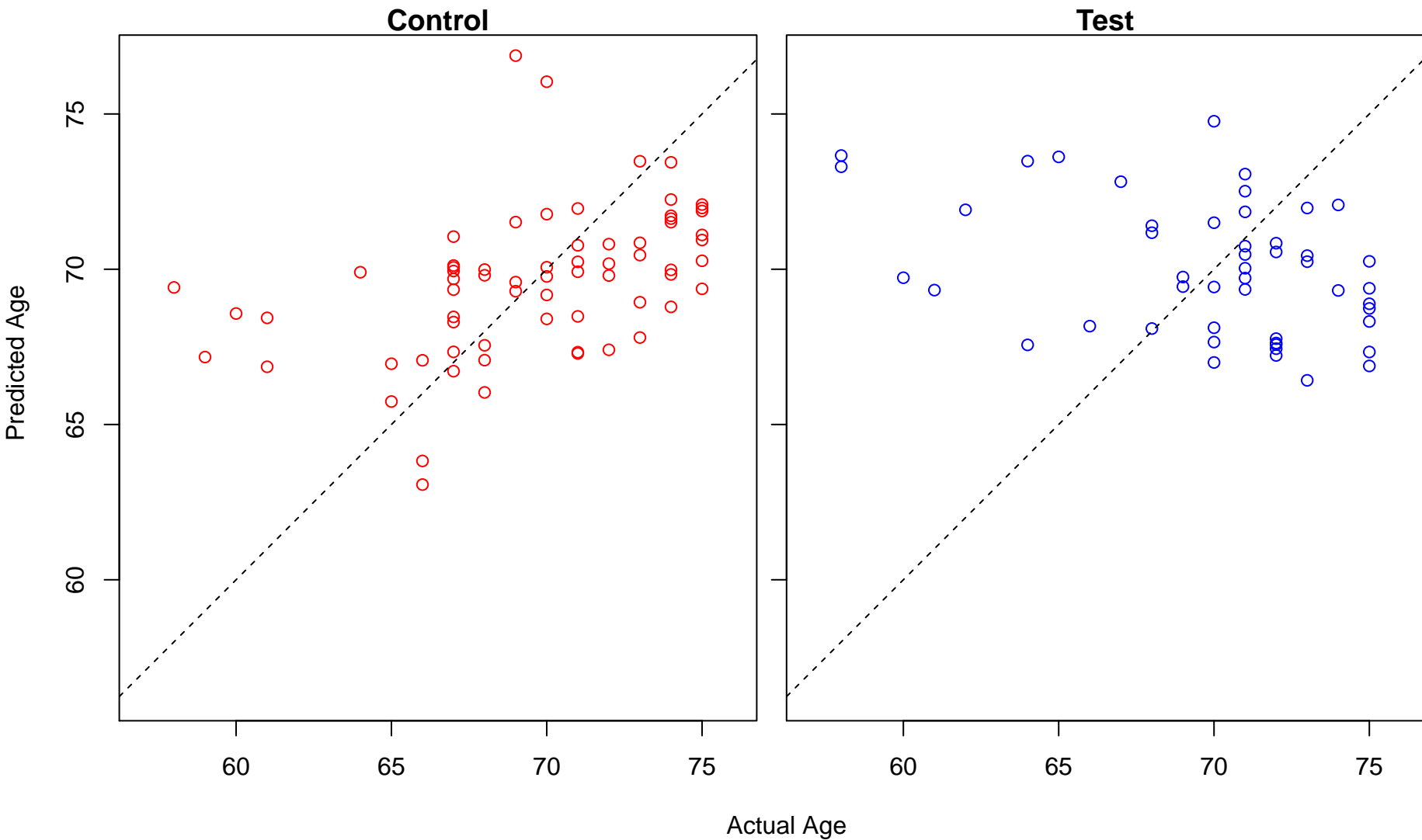
positive regulation of circadian rhythm (Score: 0.720430)



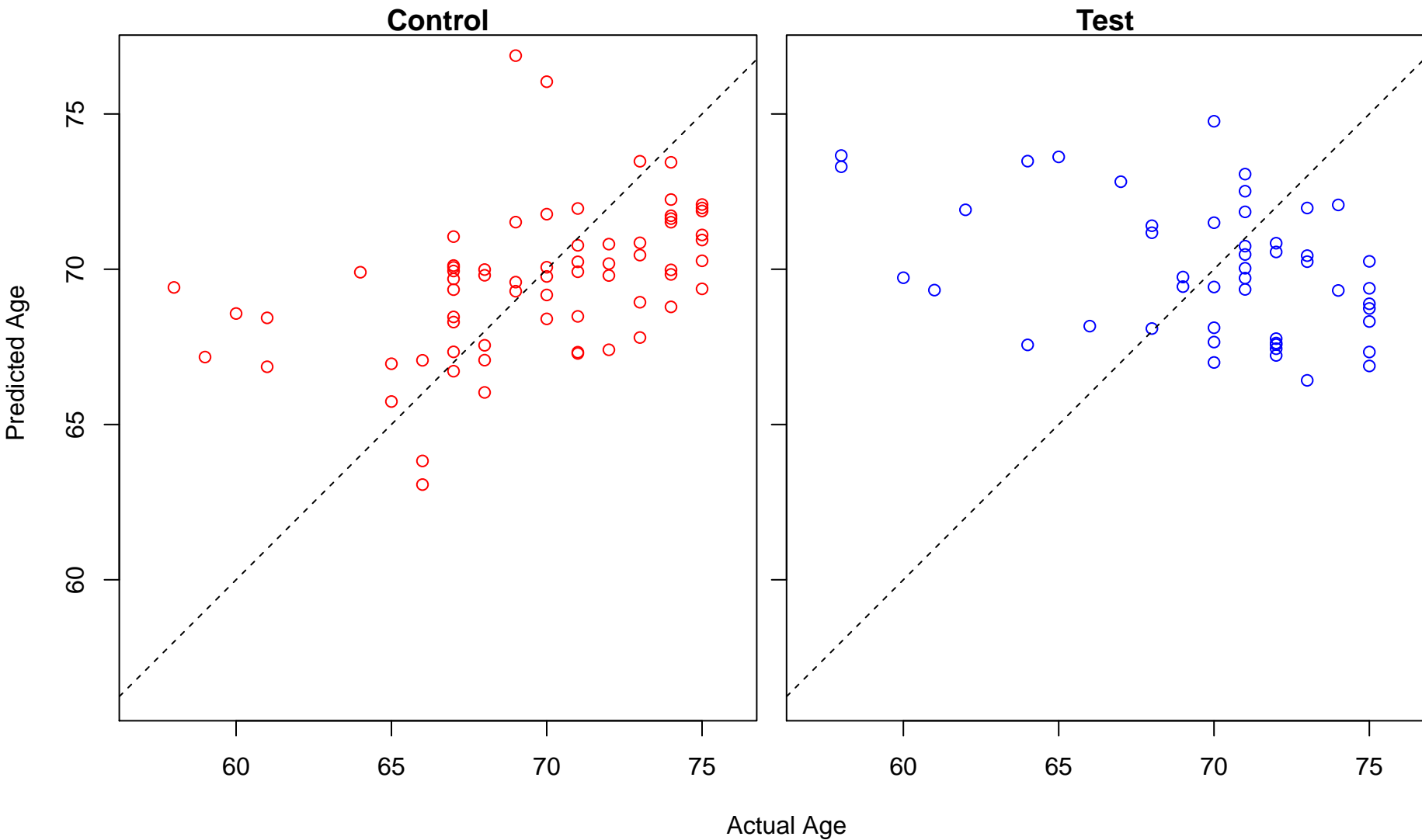
cleavage furrow formation (Score: 0.719290)



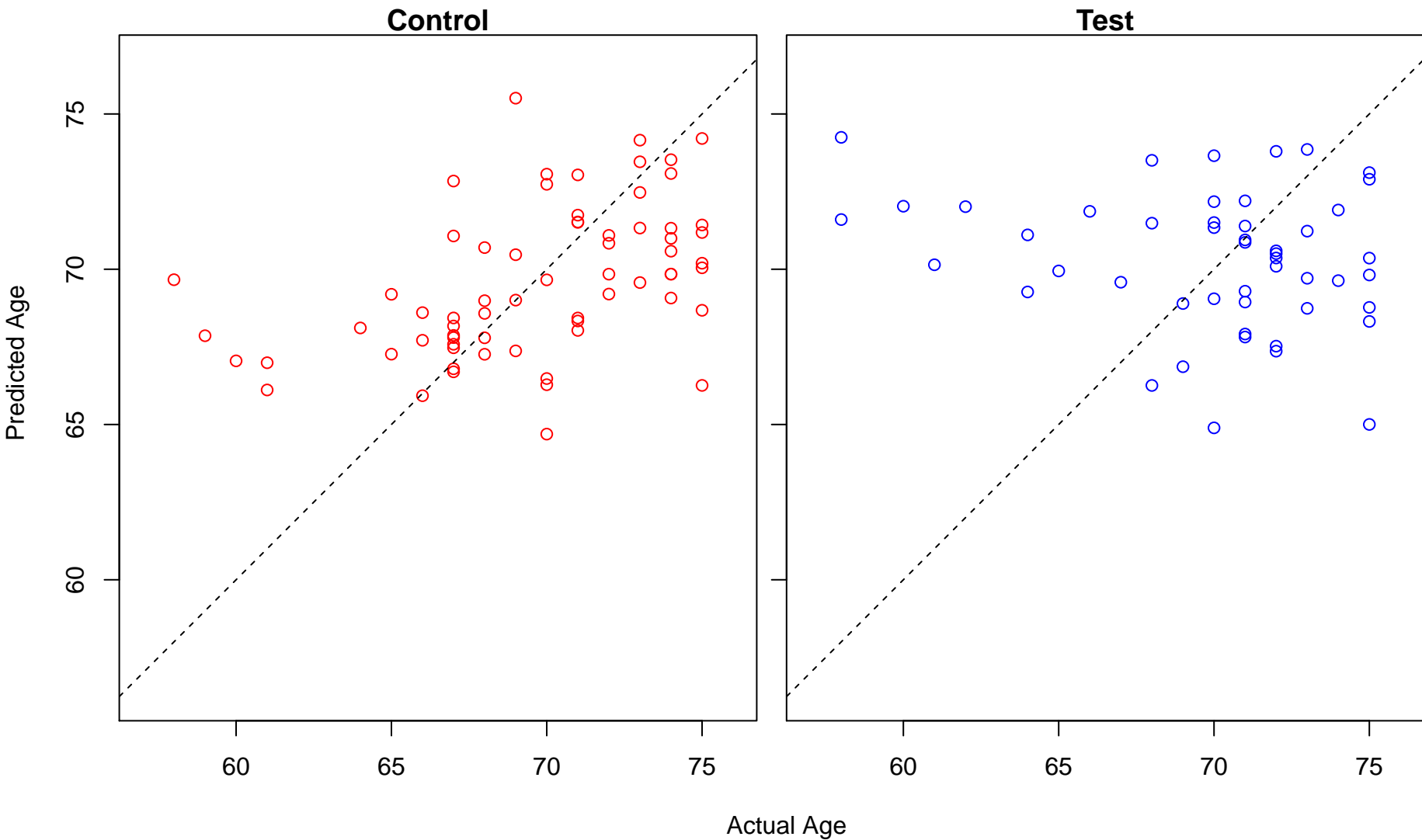
arginine metabolic process (Score: 0.718891)



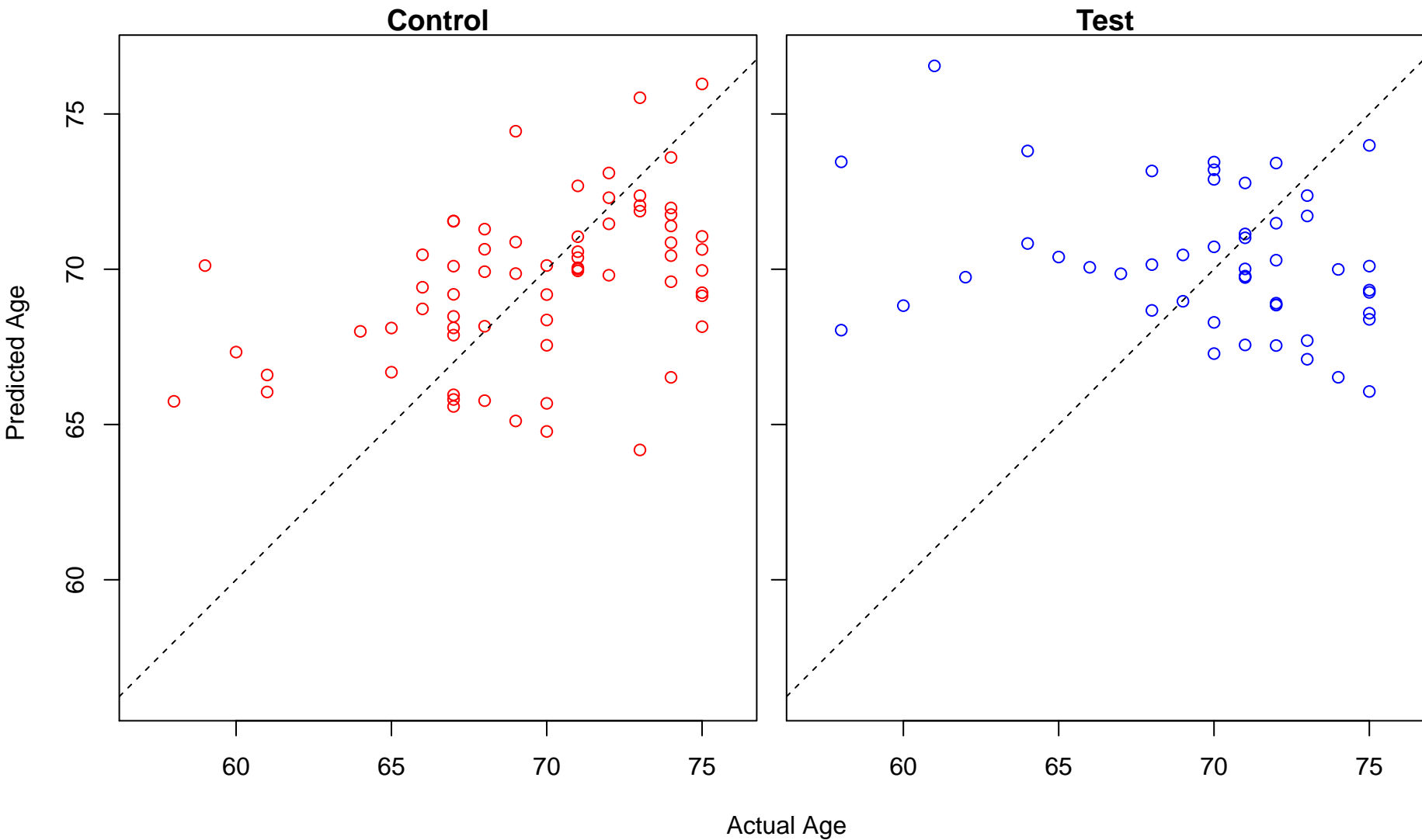
arginine catabolic process (Score: 0.718891)



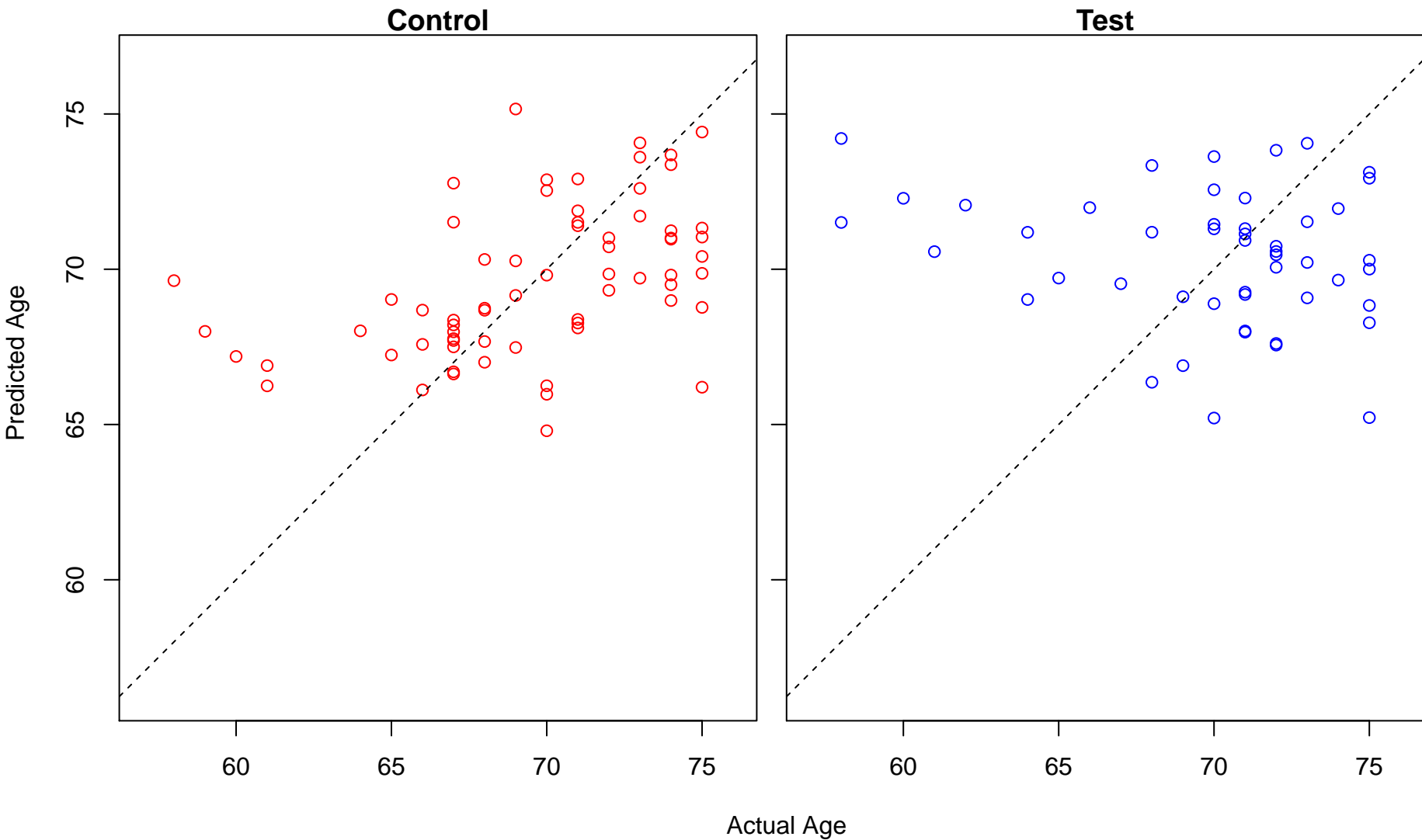
cellular sodium ion homeostasis (Score: 0.718814)



isoprenoid catabolic process (Score: 0.718784)

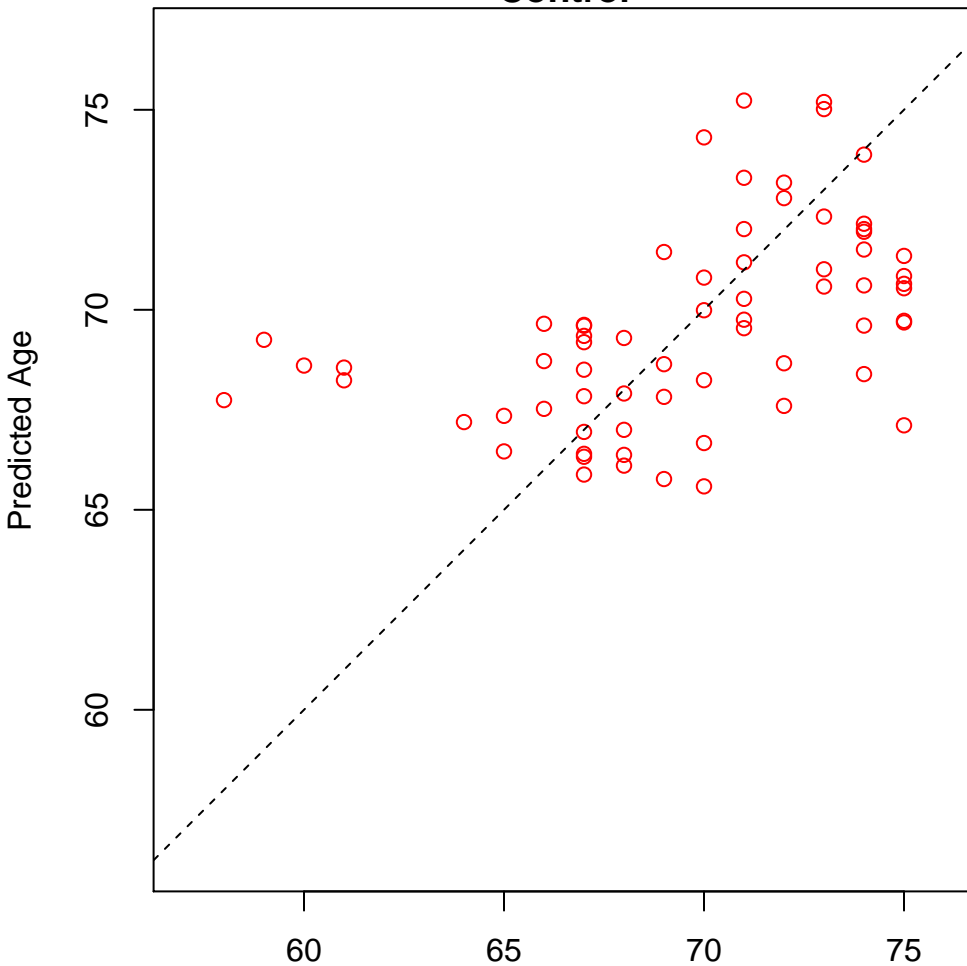


sodium ion homeostasis (Score: 0.718690)

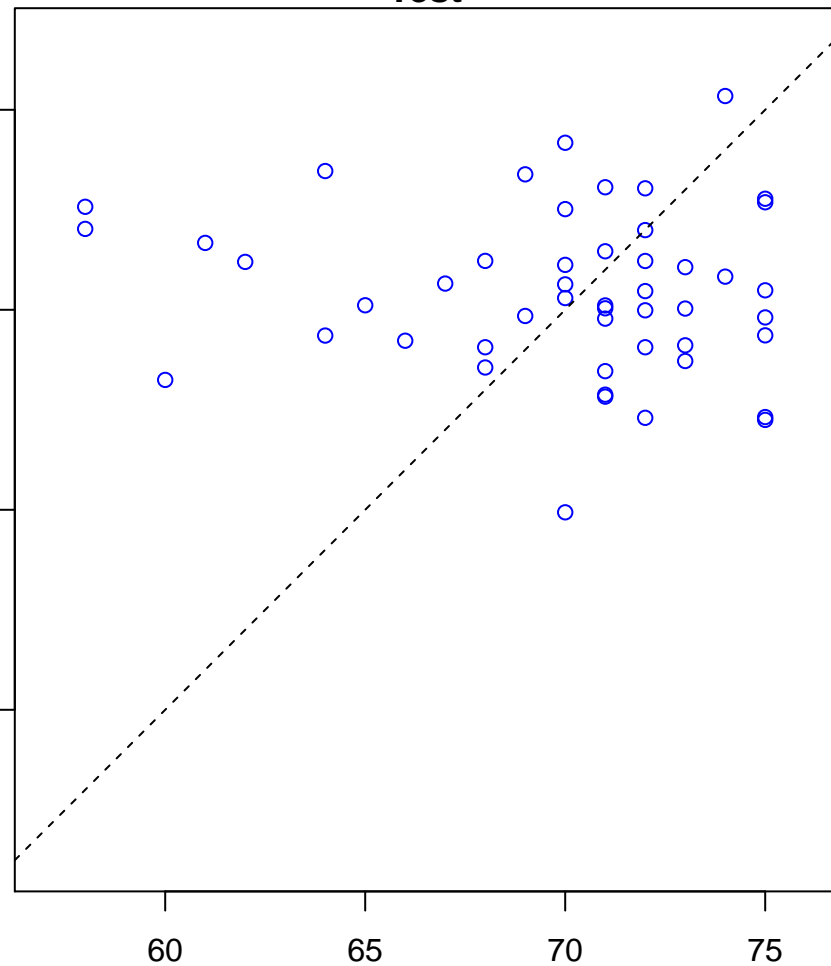


T-helper 17 type immune response (Score: 0.718052)

Control

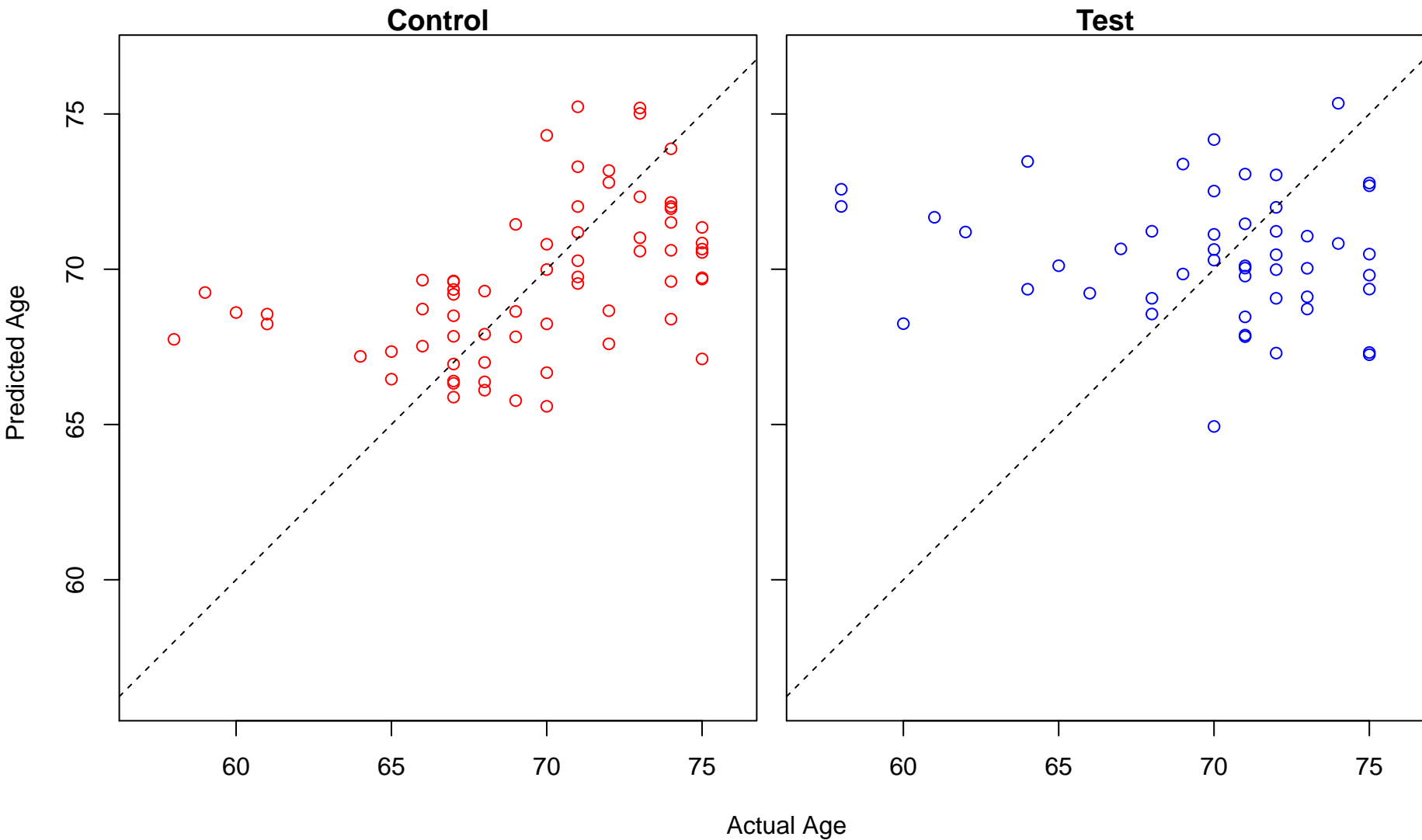


Test

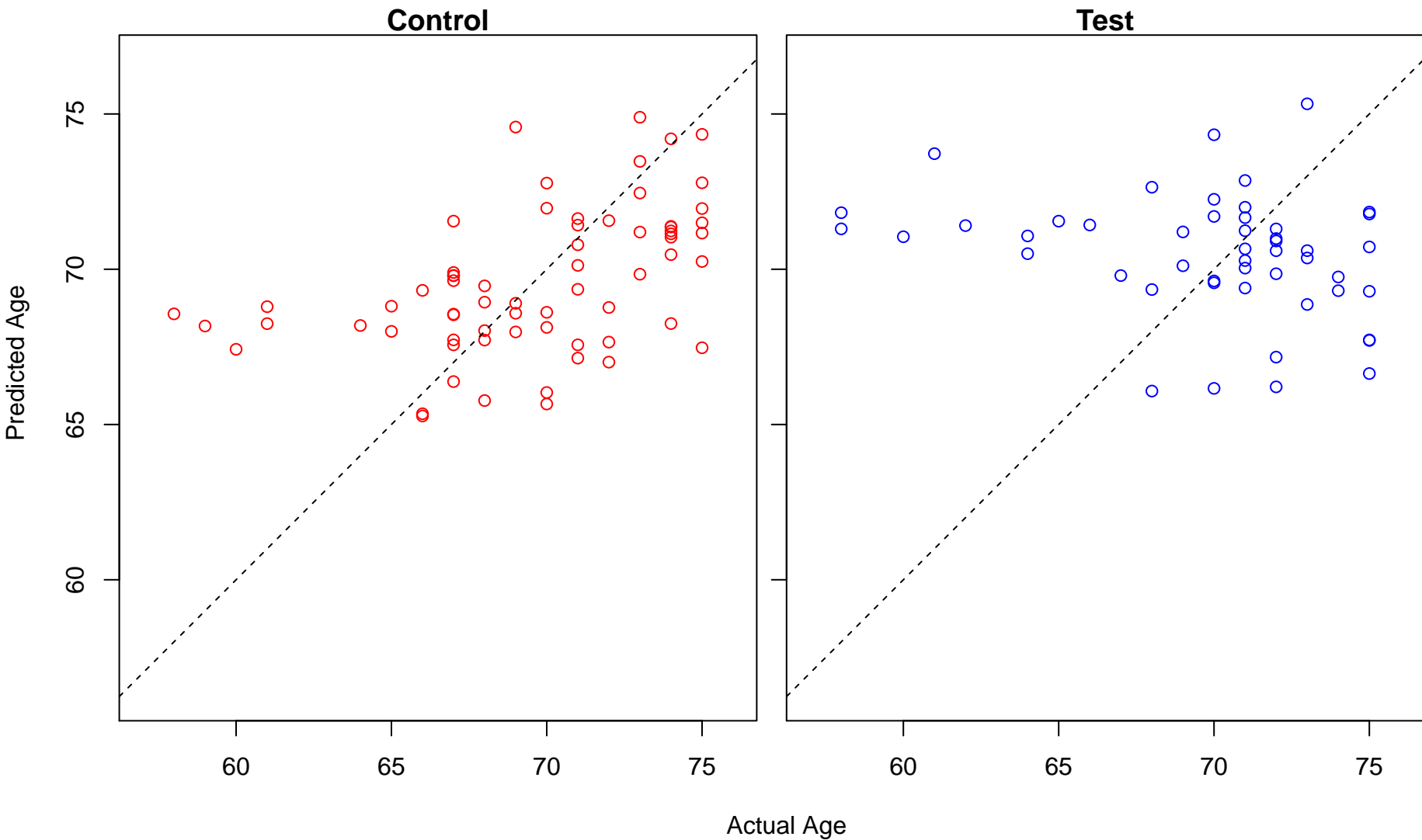


Actual Age

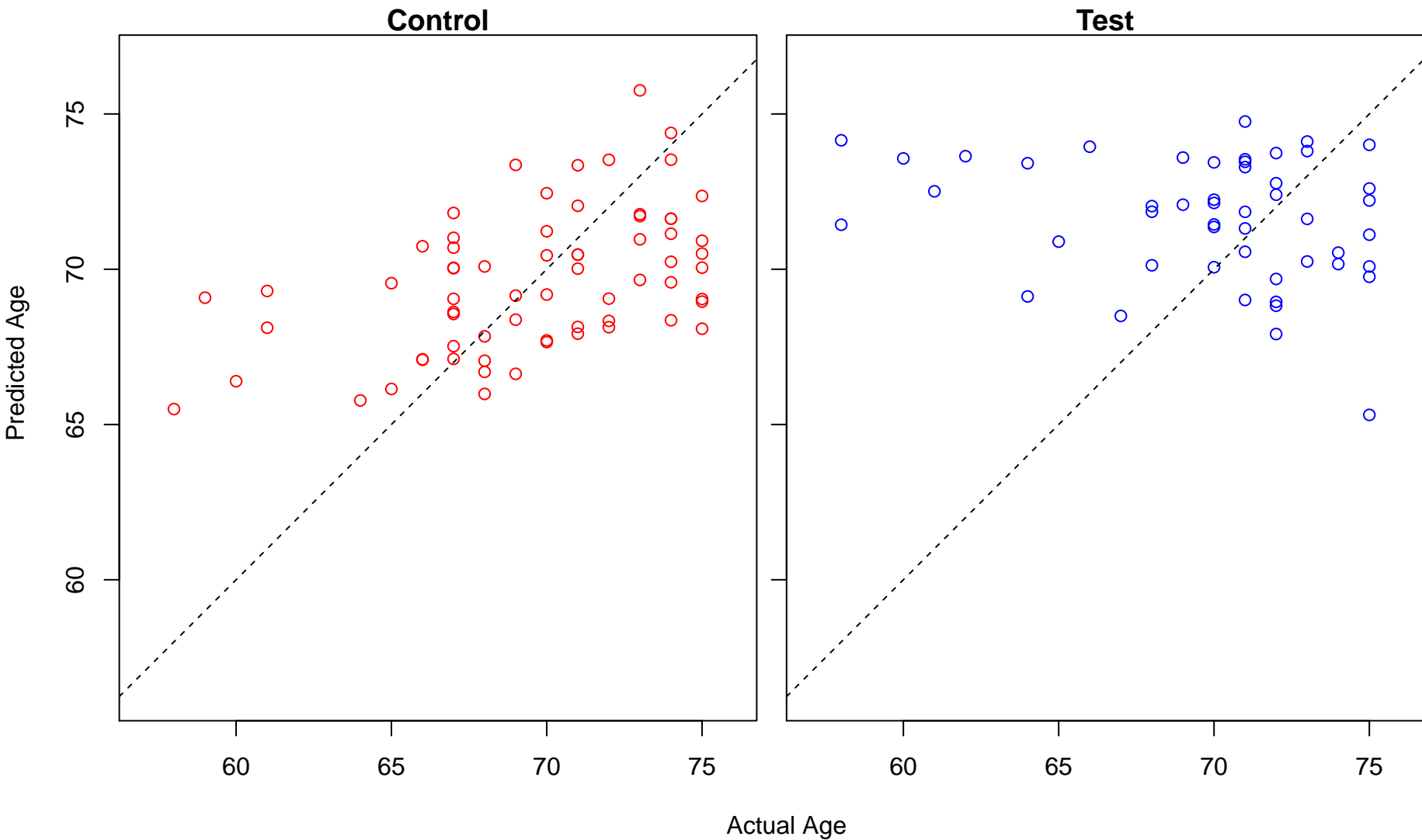
T-helper 17 cell differentiation (Score: 0.718052)



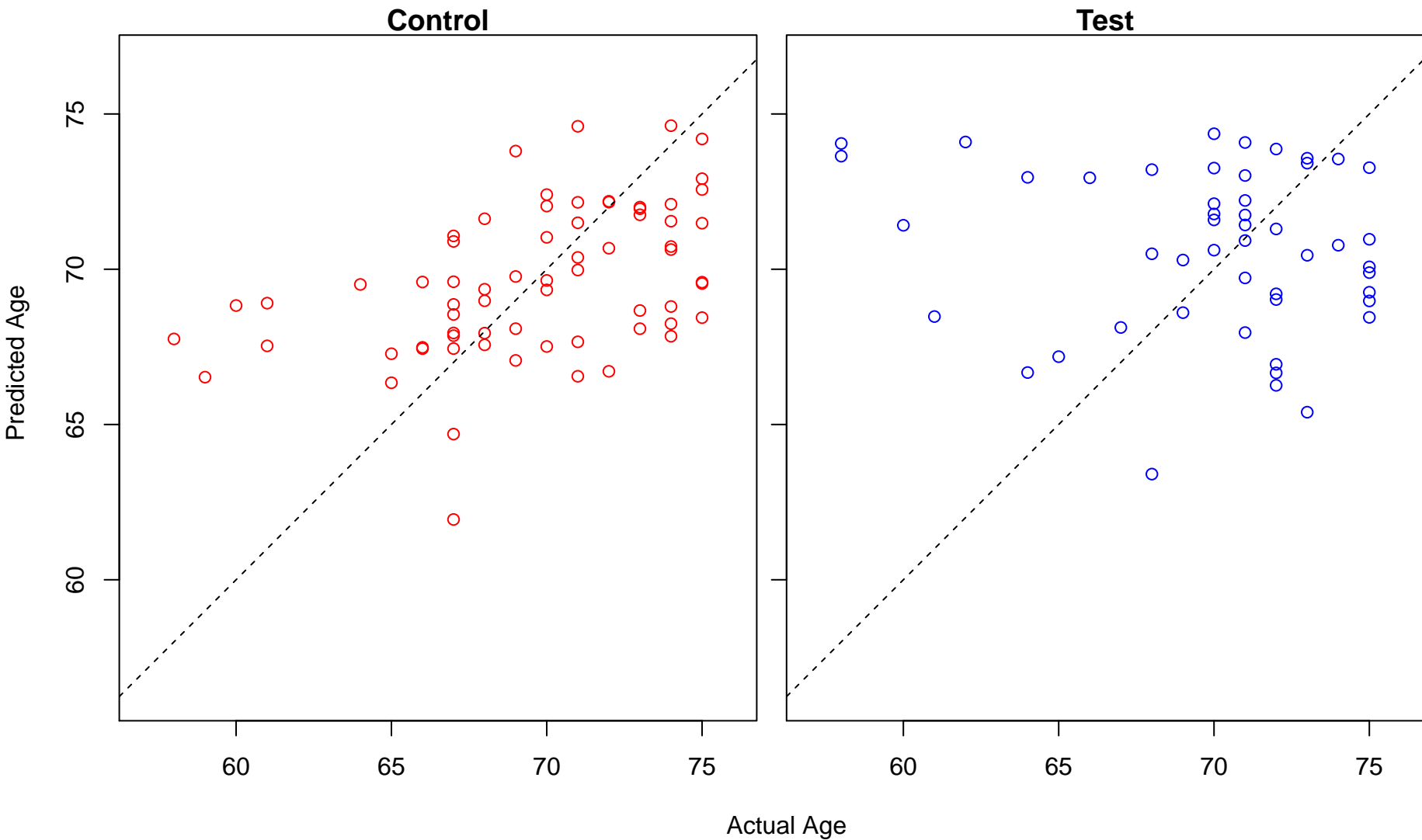
regulation of insulin secretion involved in cellular response to glucose stimulus (Score: 0.718000)



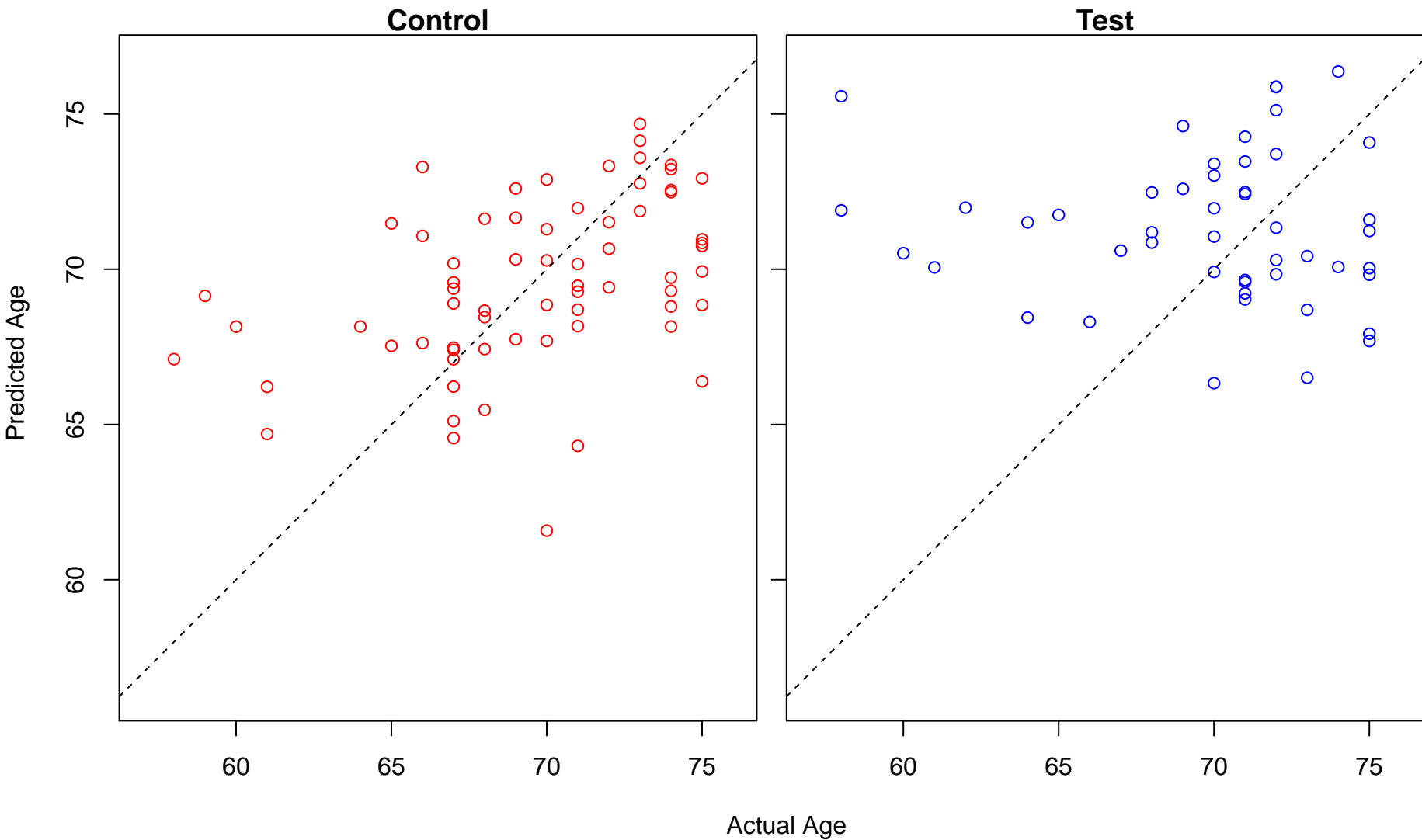
vascular smooth muscle cell differentiation (Score: 0.717204)



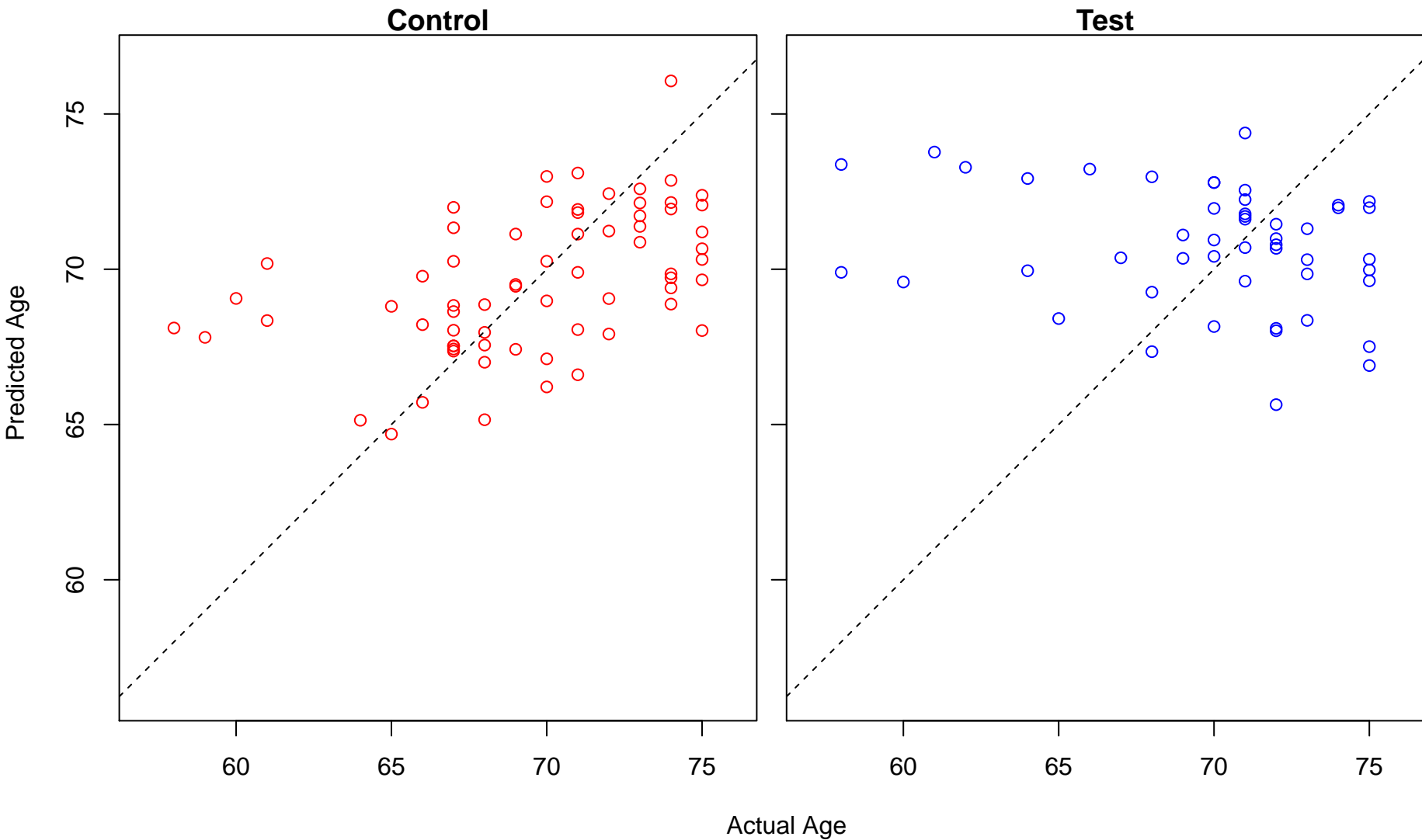
ether metabolic process (Score: 0.716896)



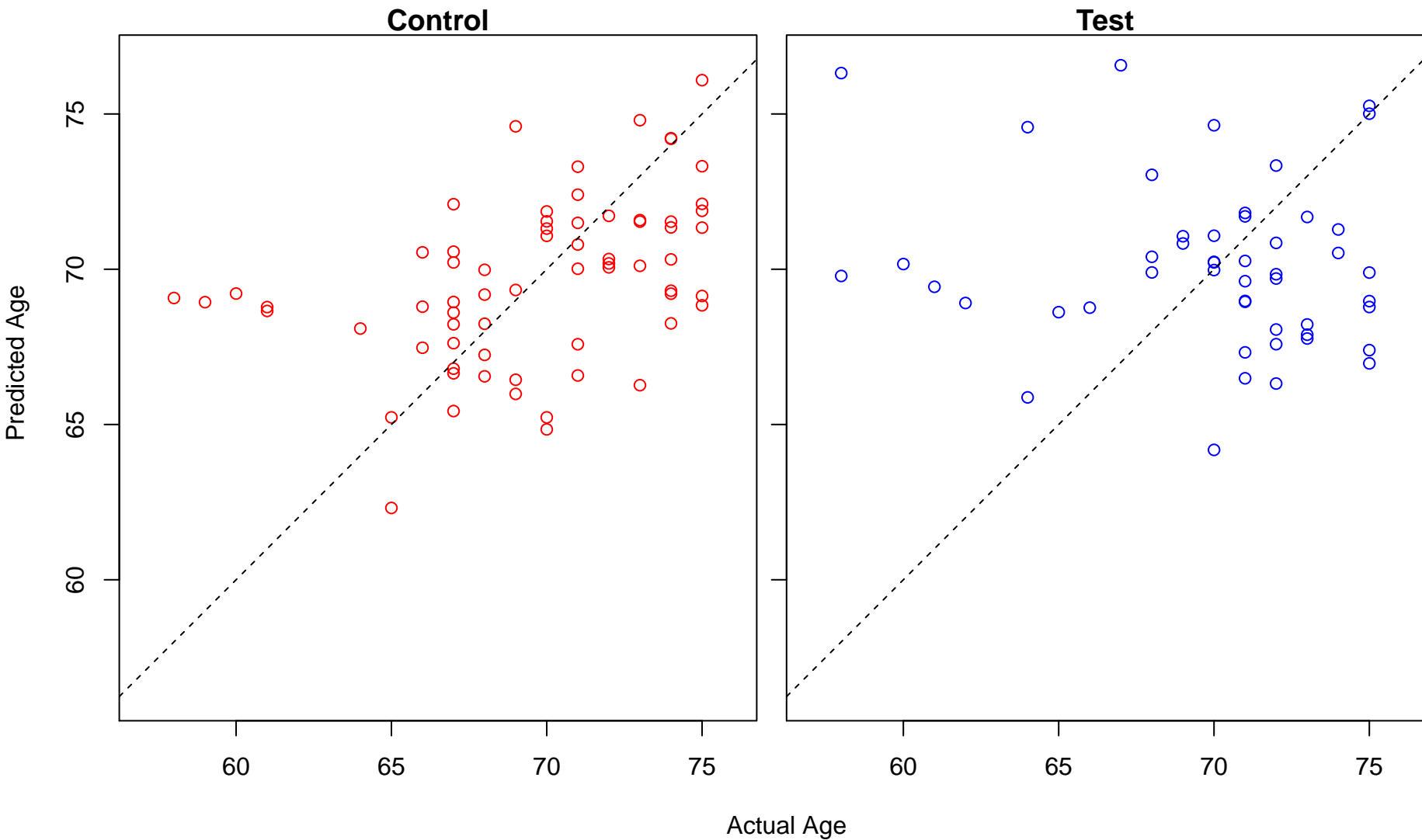
negative regulation of protein tyrosine kinase activity (Score: 0.716608)



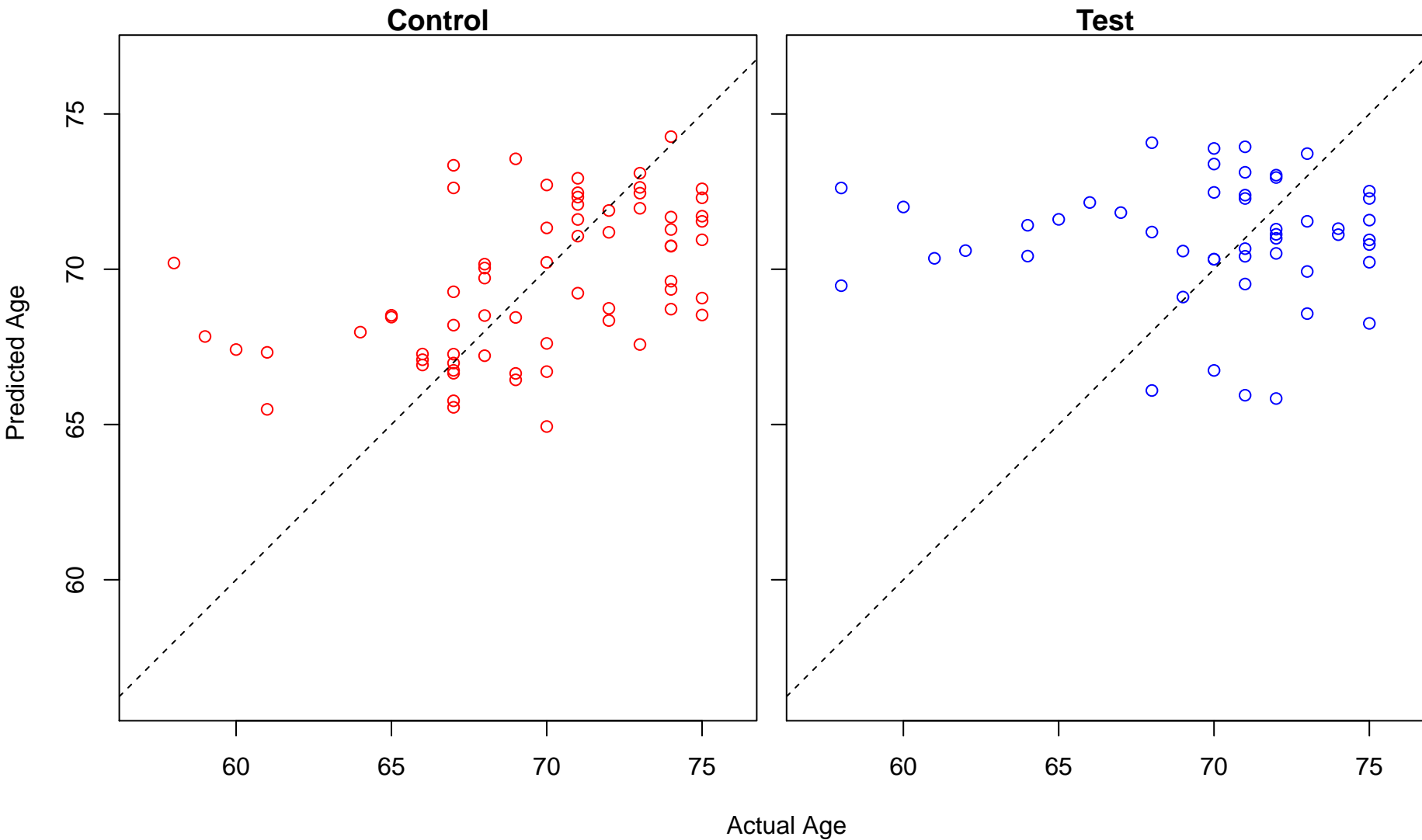
negative regulation of interleukin-1 production (Score: 0.716506)



regulation of chromatin silencing (Score: 0.716440)

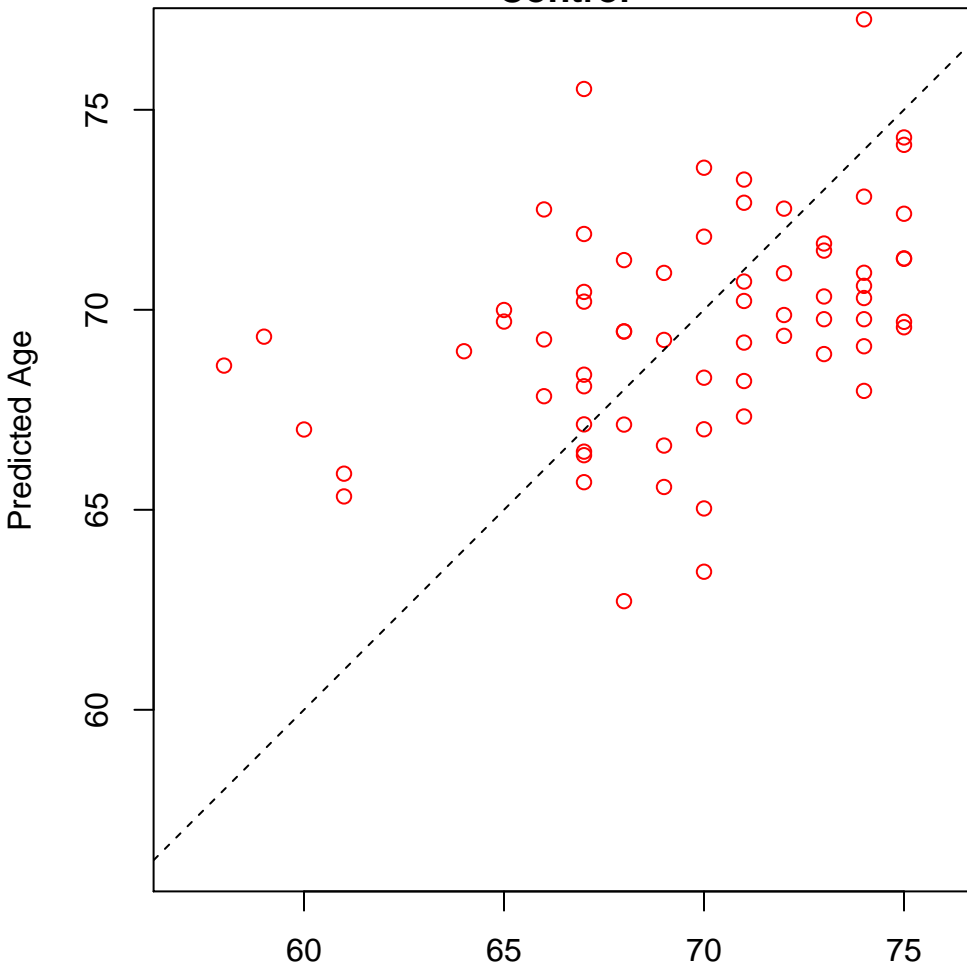


mRNA cis splicing, via spliceosome (Score: 0.715596)

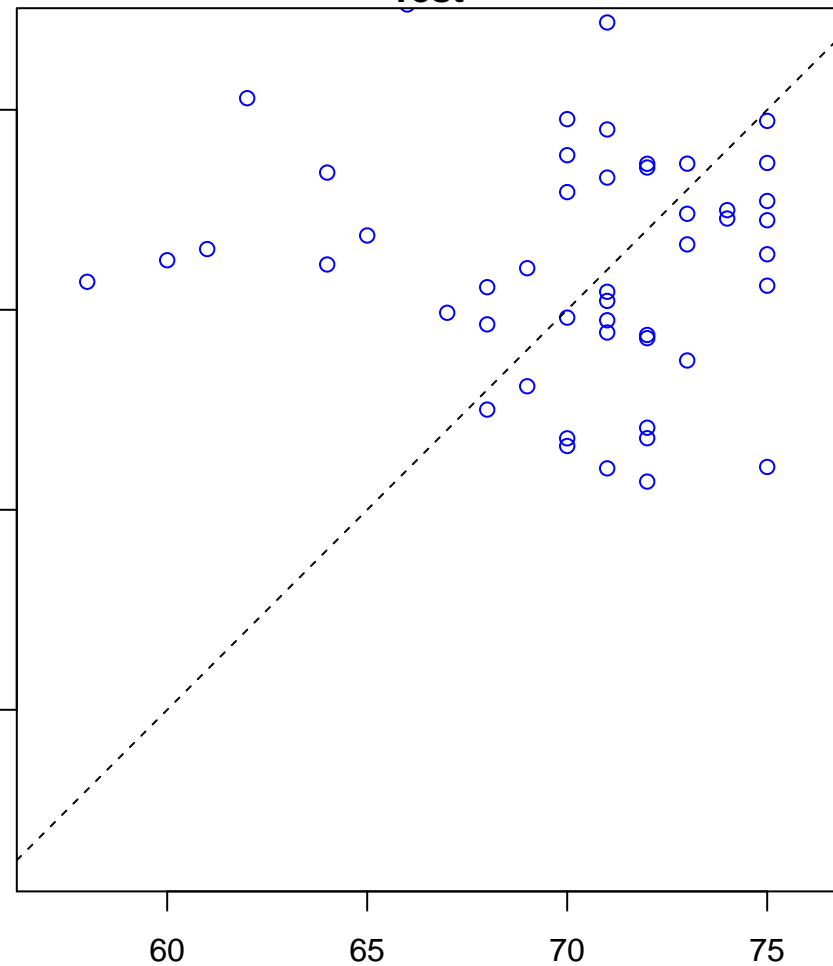


response to epinephrine (Score: 0.714770)

Control



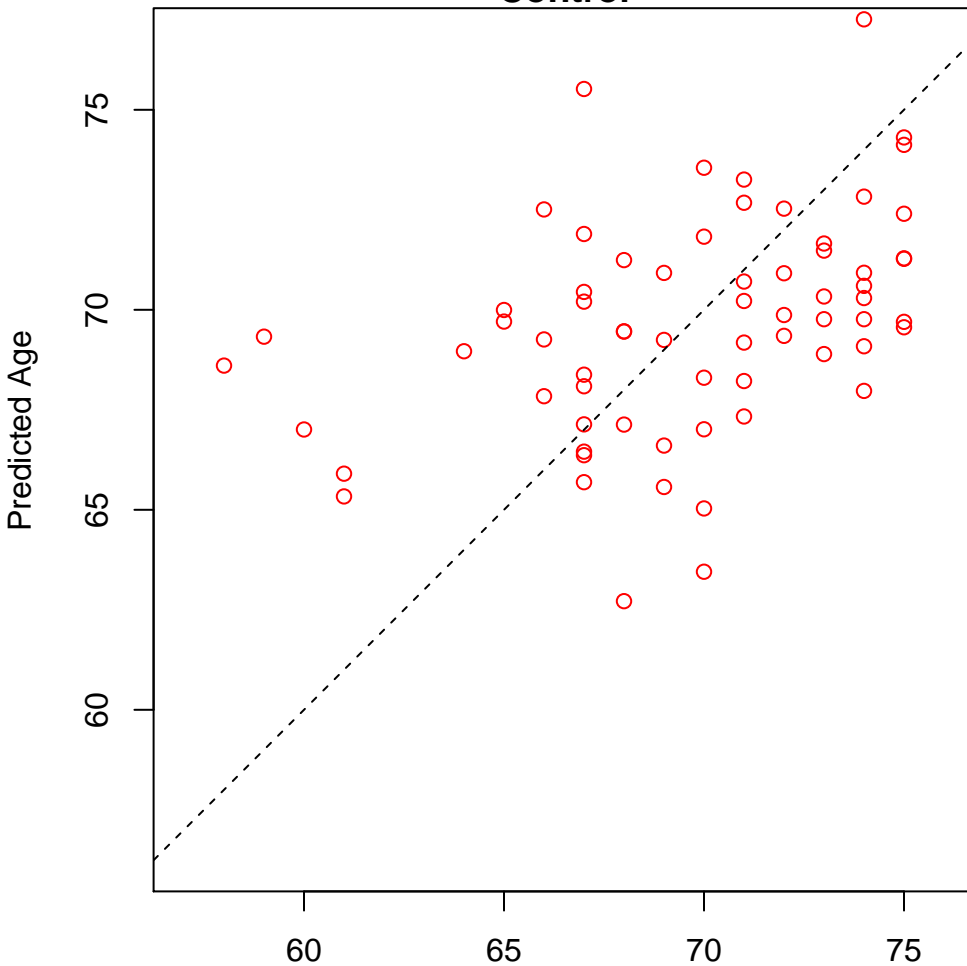
Test



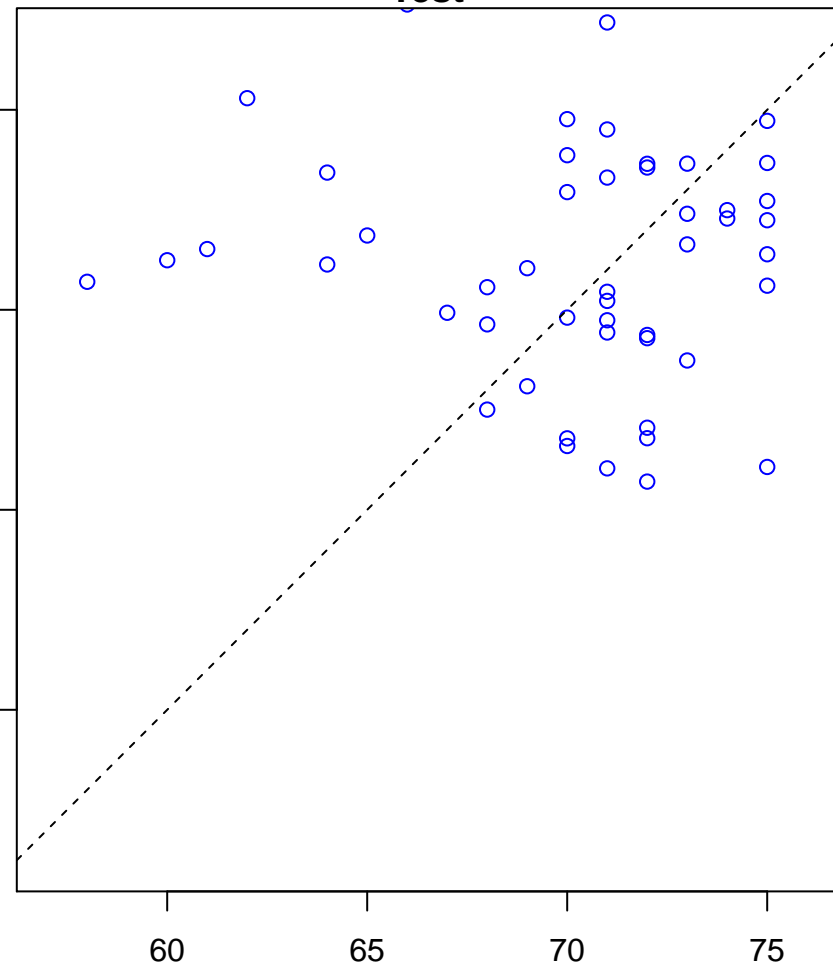
Actual Age

cellular response to epinephrine stimulus (Score: 0.714770)

Control

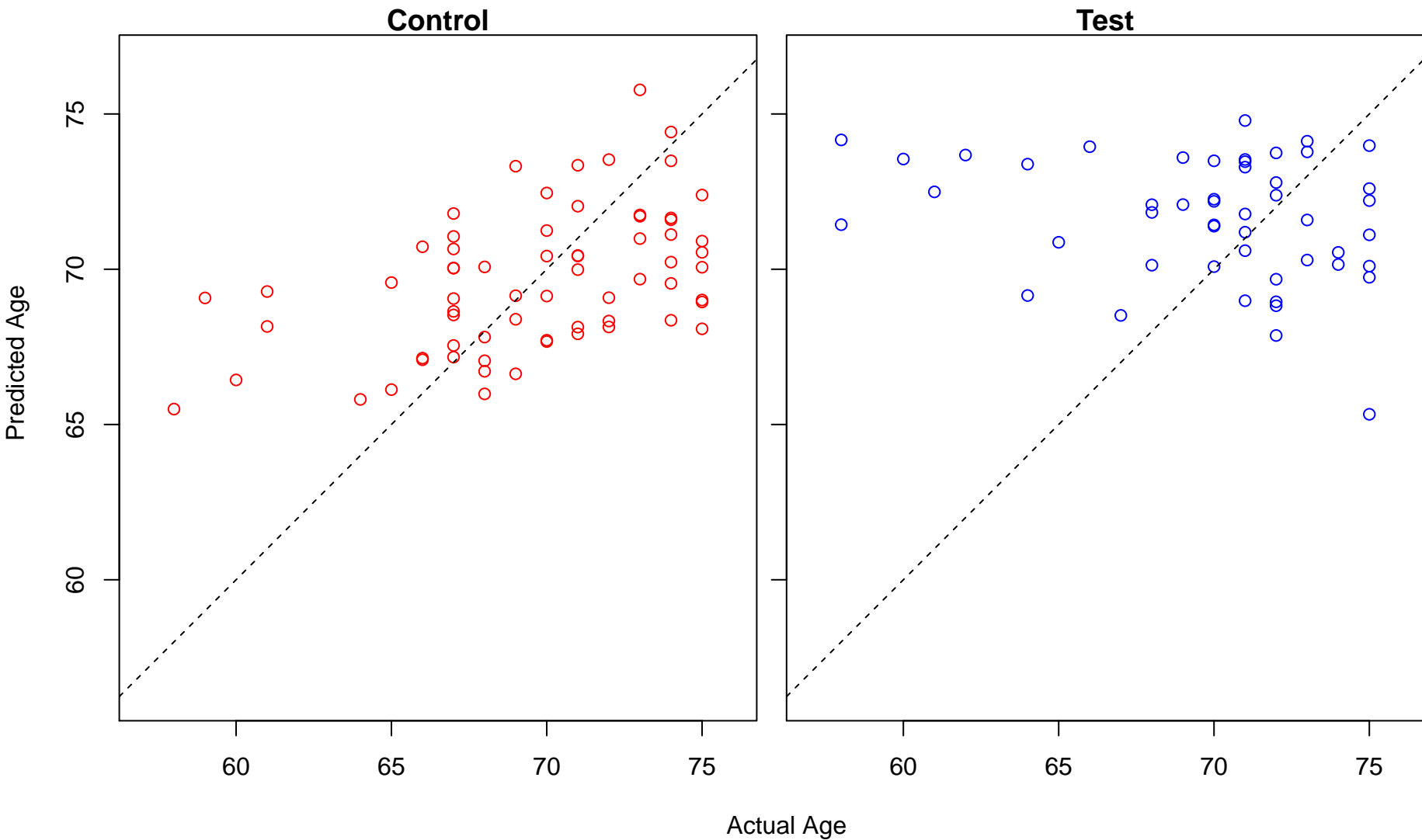


Test

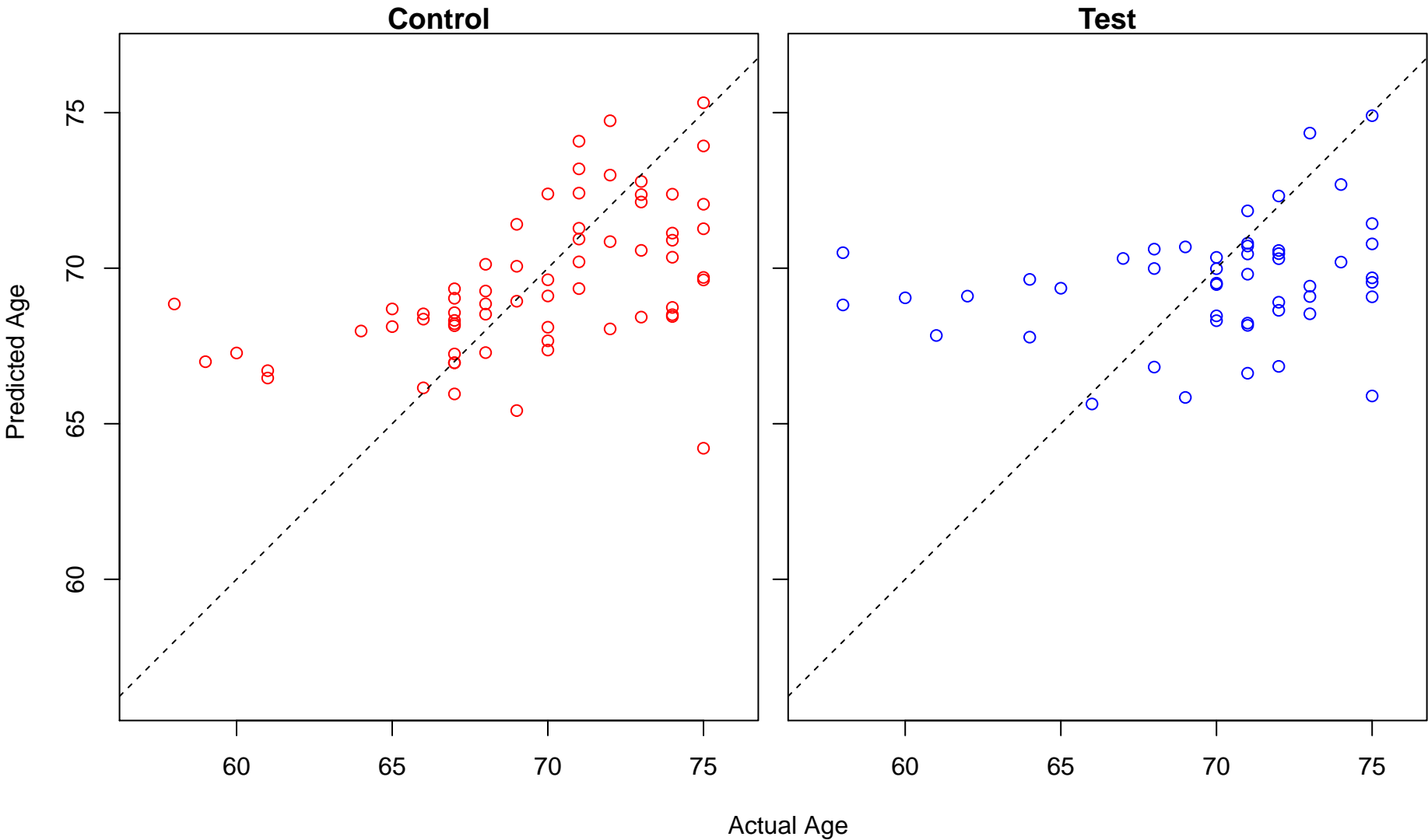


Actual Age

vascular smooth muscle cell development (Score: 0.714624)

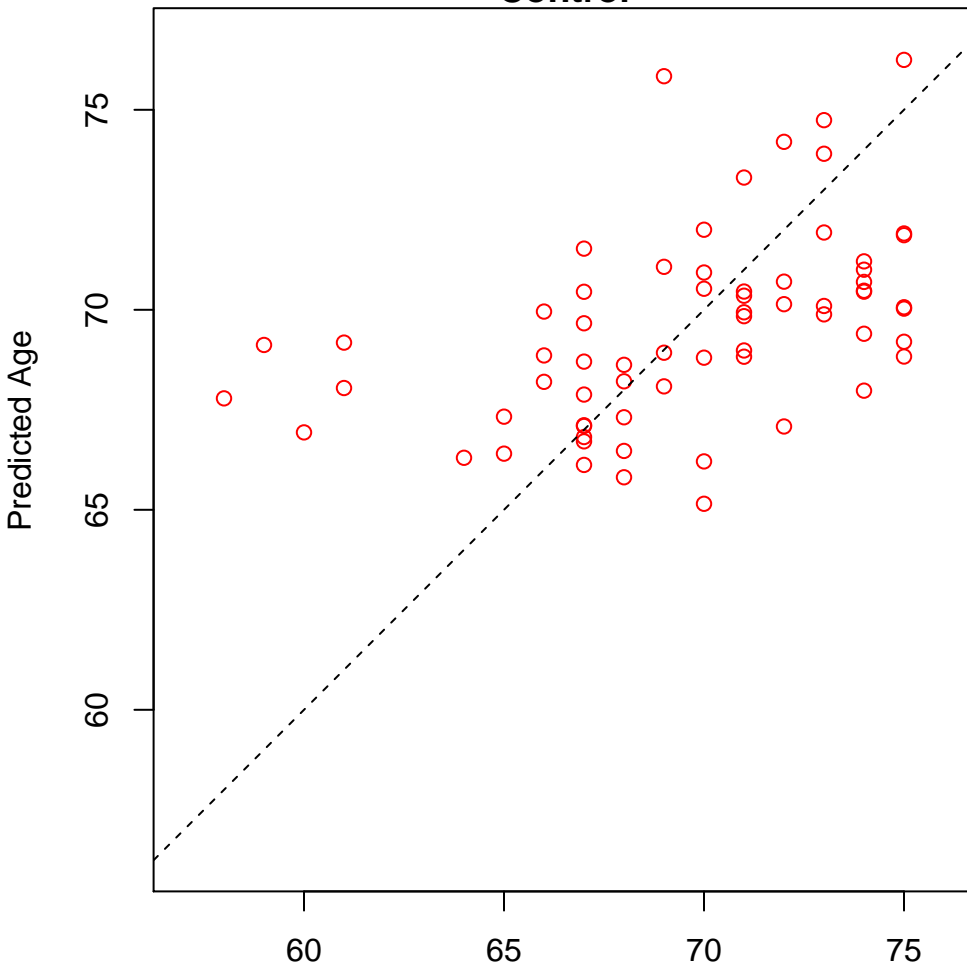


ubiquitin-independent protein catabolic process via the multivesicular body sorting pathway (Score: 0.7

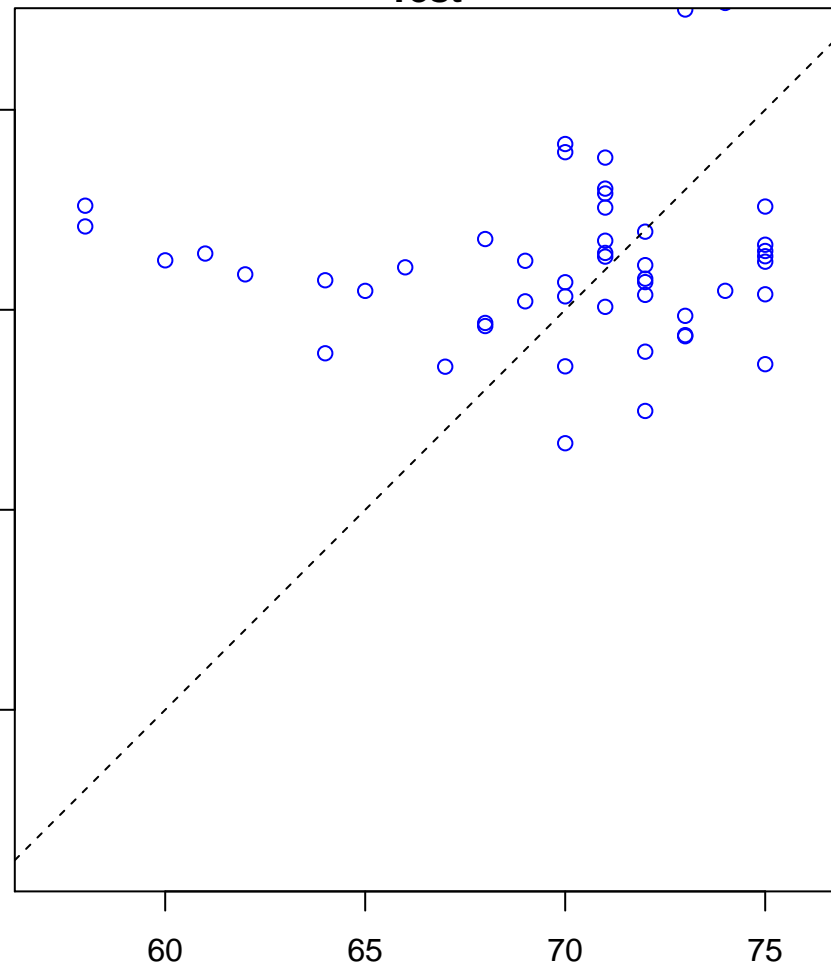


nucleotide-sugar biosynthetic process (Score: 0.714295)

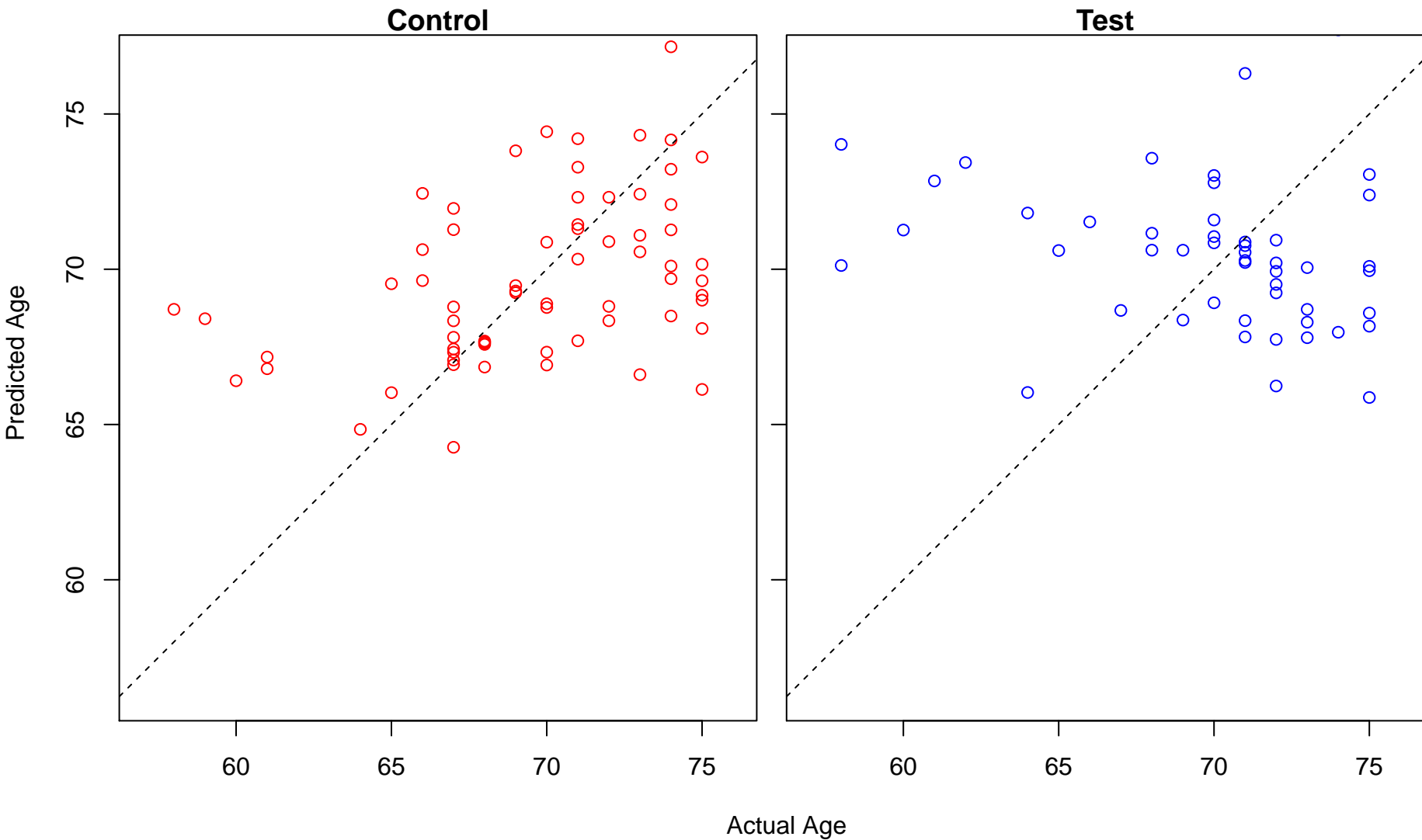
Control



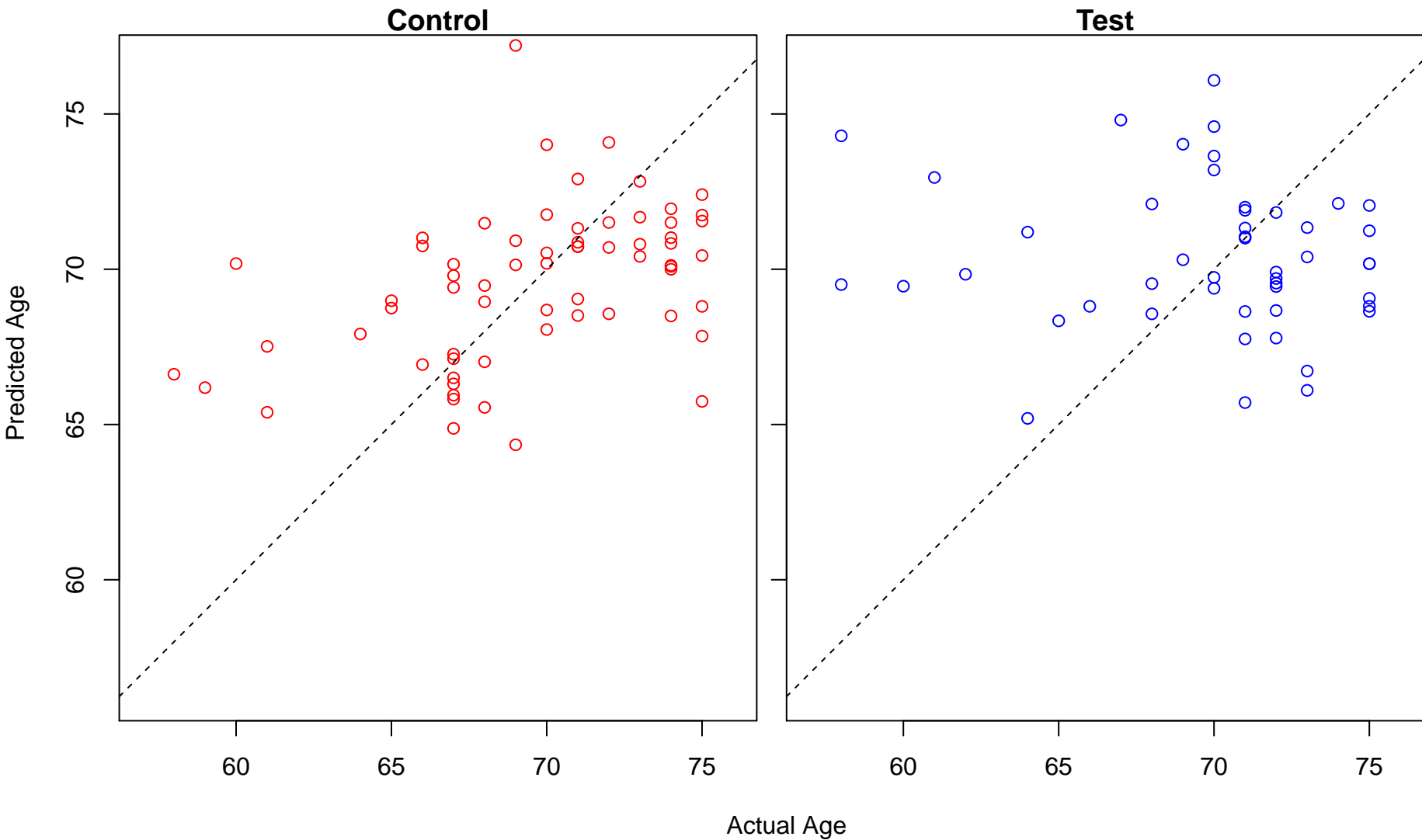
Test



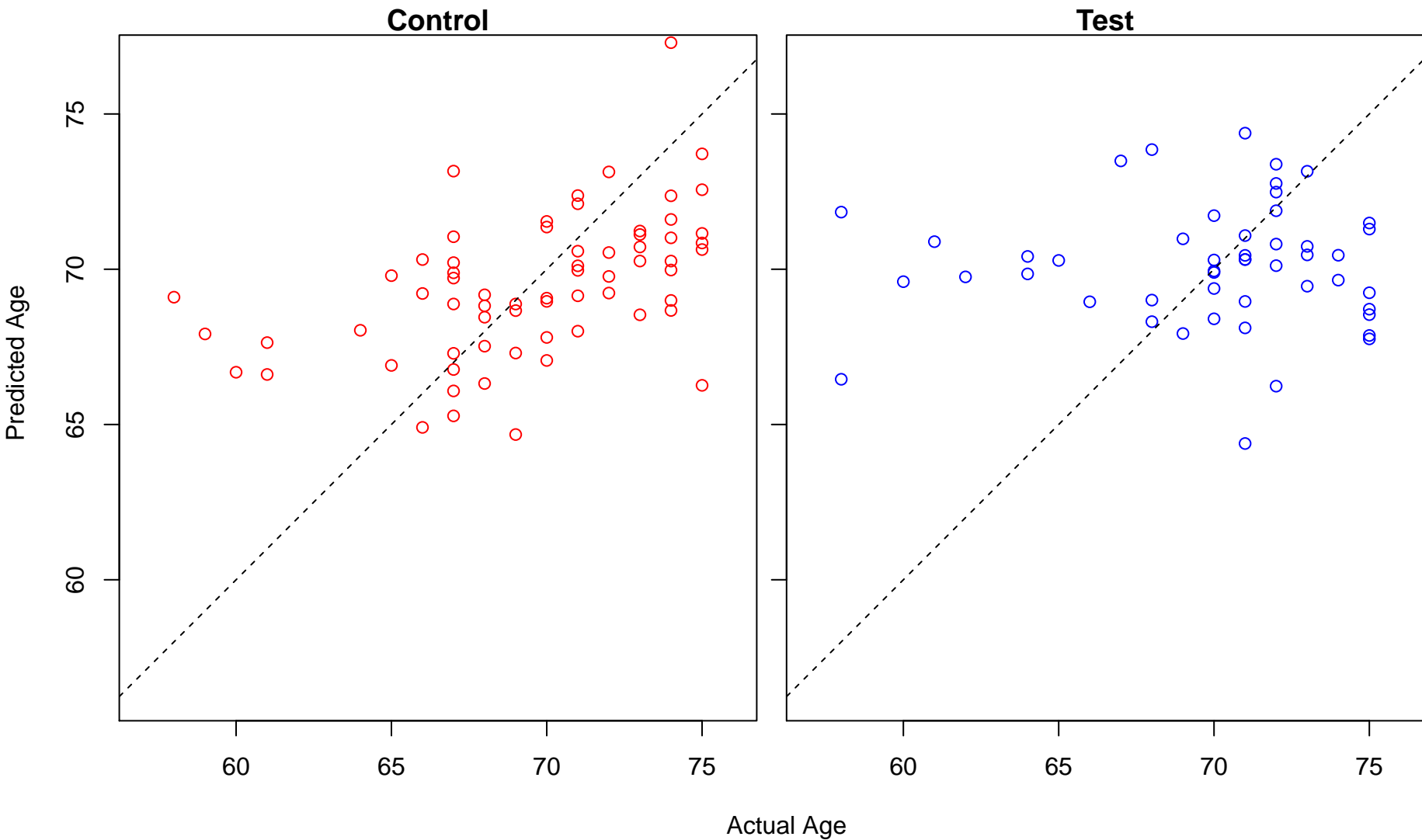
response to alkaloid (Score: 0.714225)



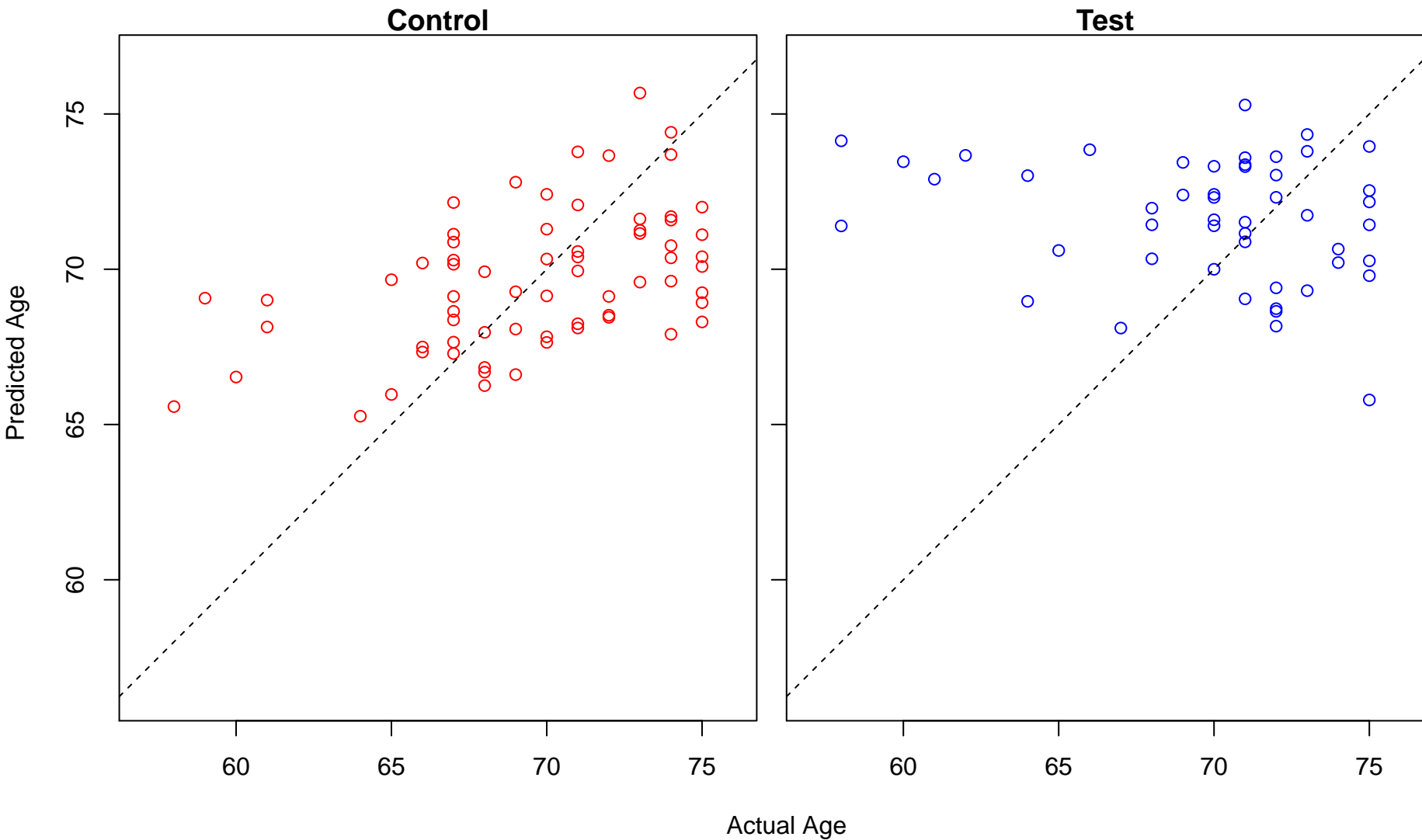
single fertilization (Score: 0.714201)



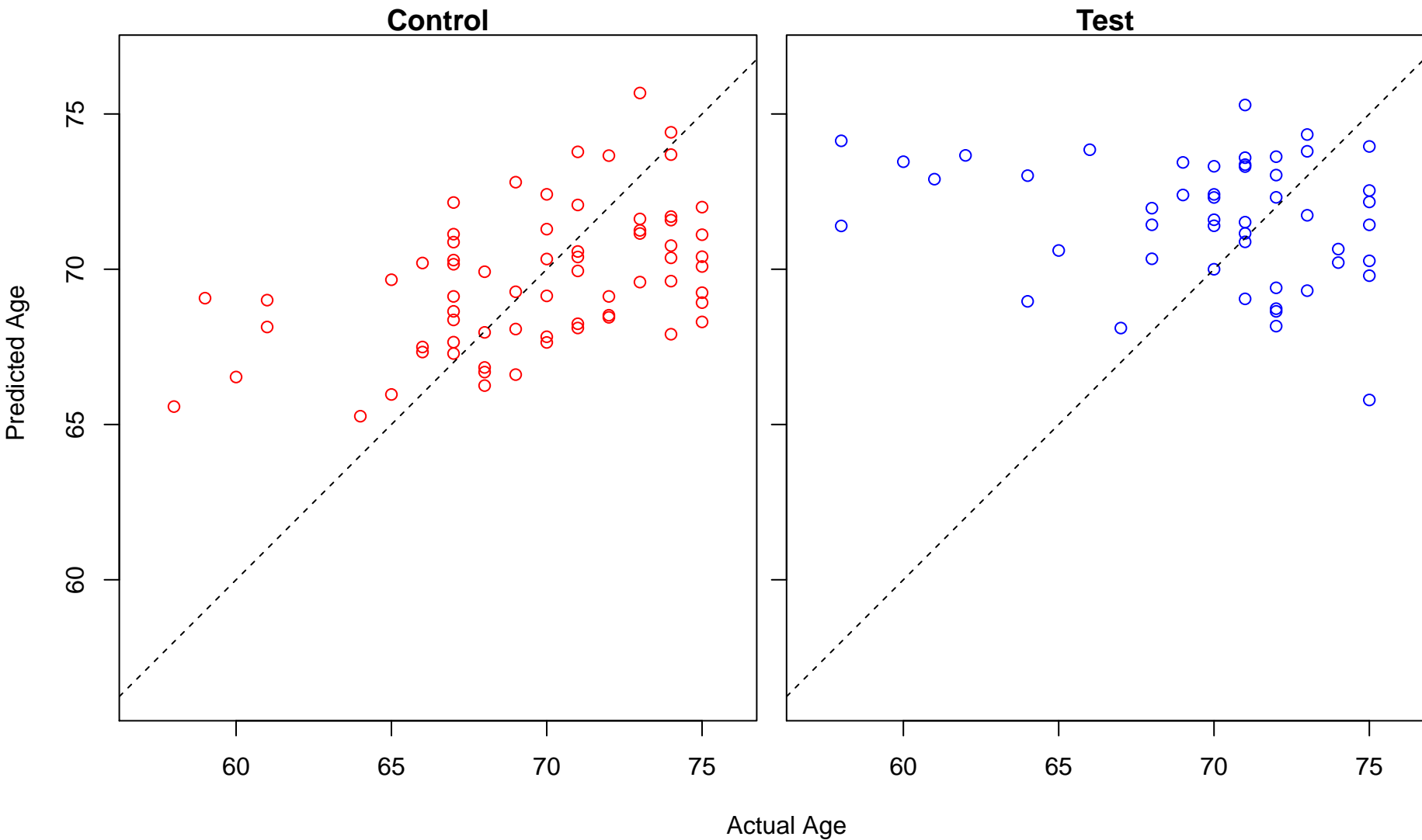
regulation of TORC1 signaling (Score: 0.713708)



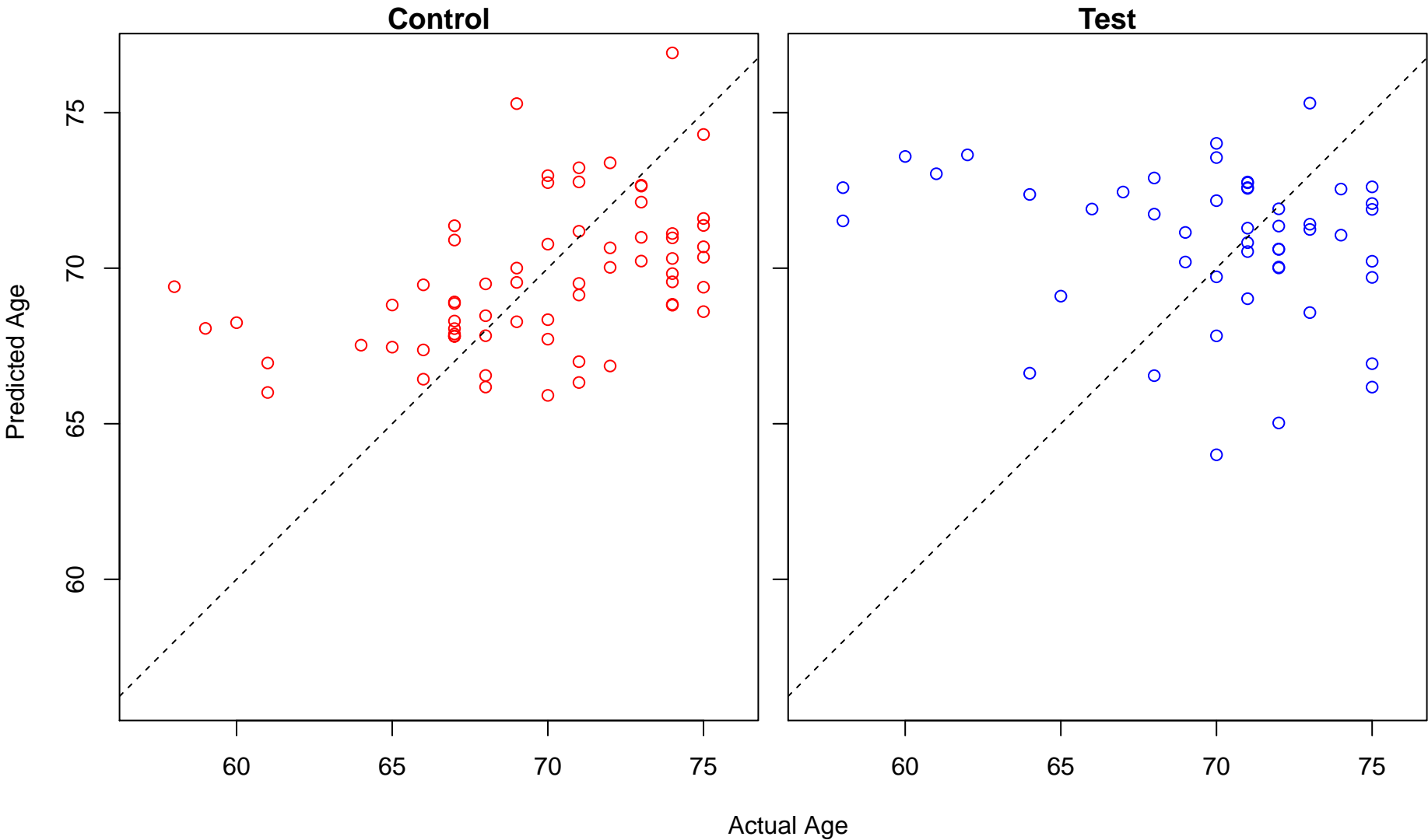
pulmonary valve development (Score: 0.713673)



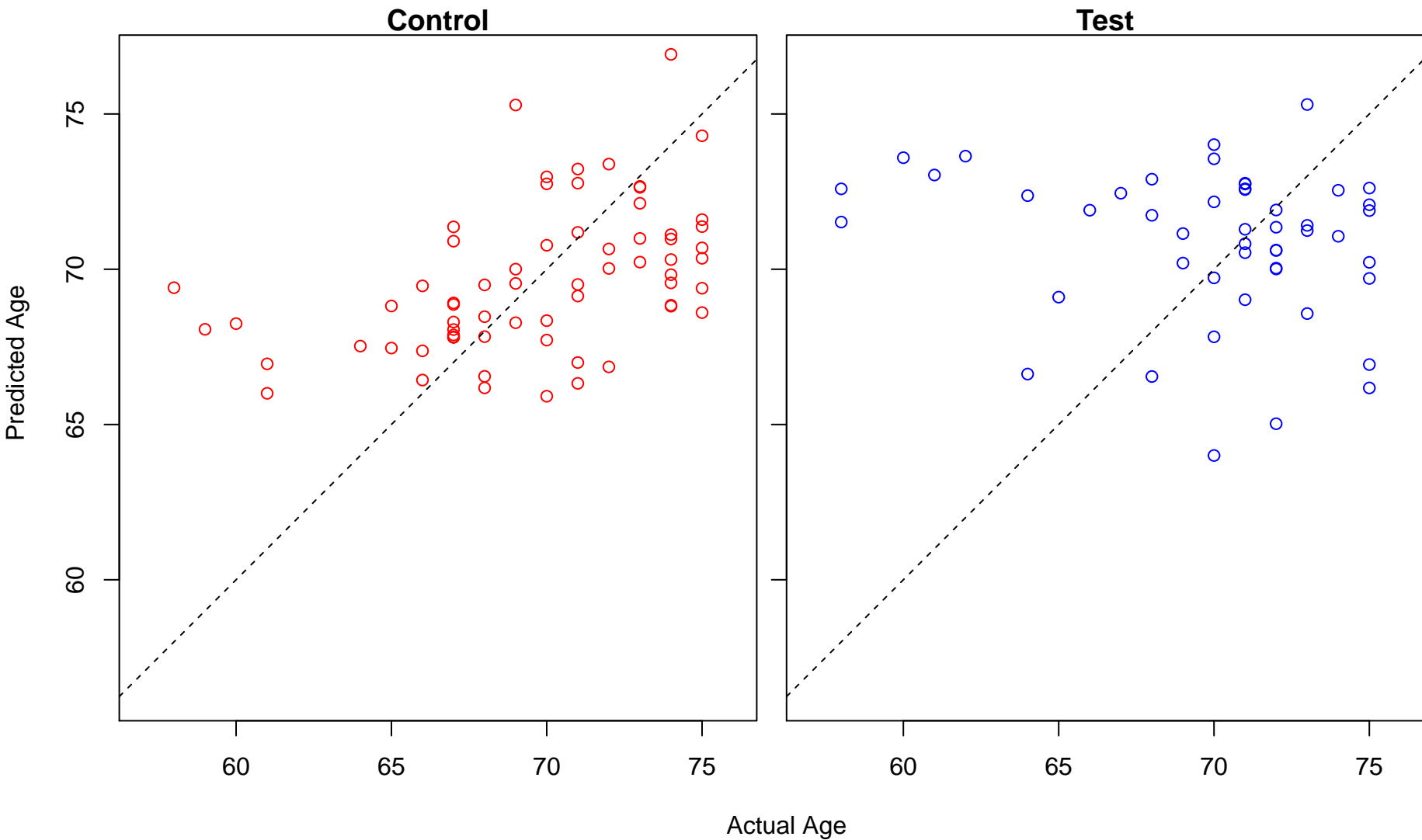
pulmonary valve morphogenesis (Score: 0.713673)



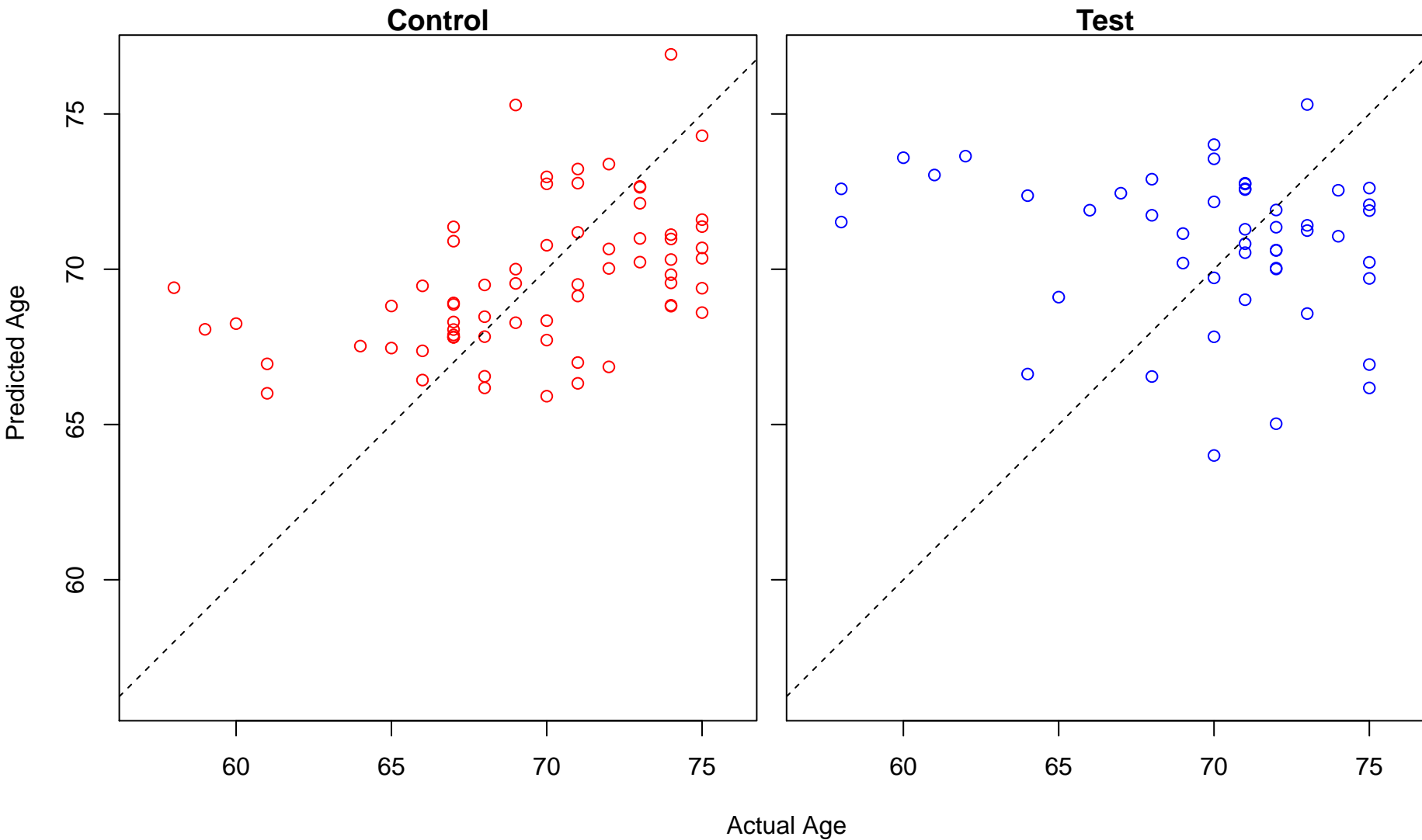
nucleoside bisphosphate biosynthetic process (Score: 0.713391)



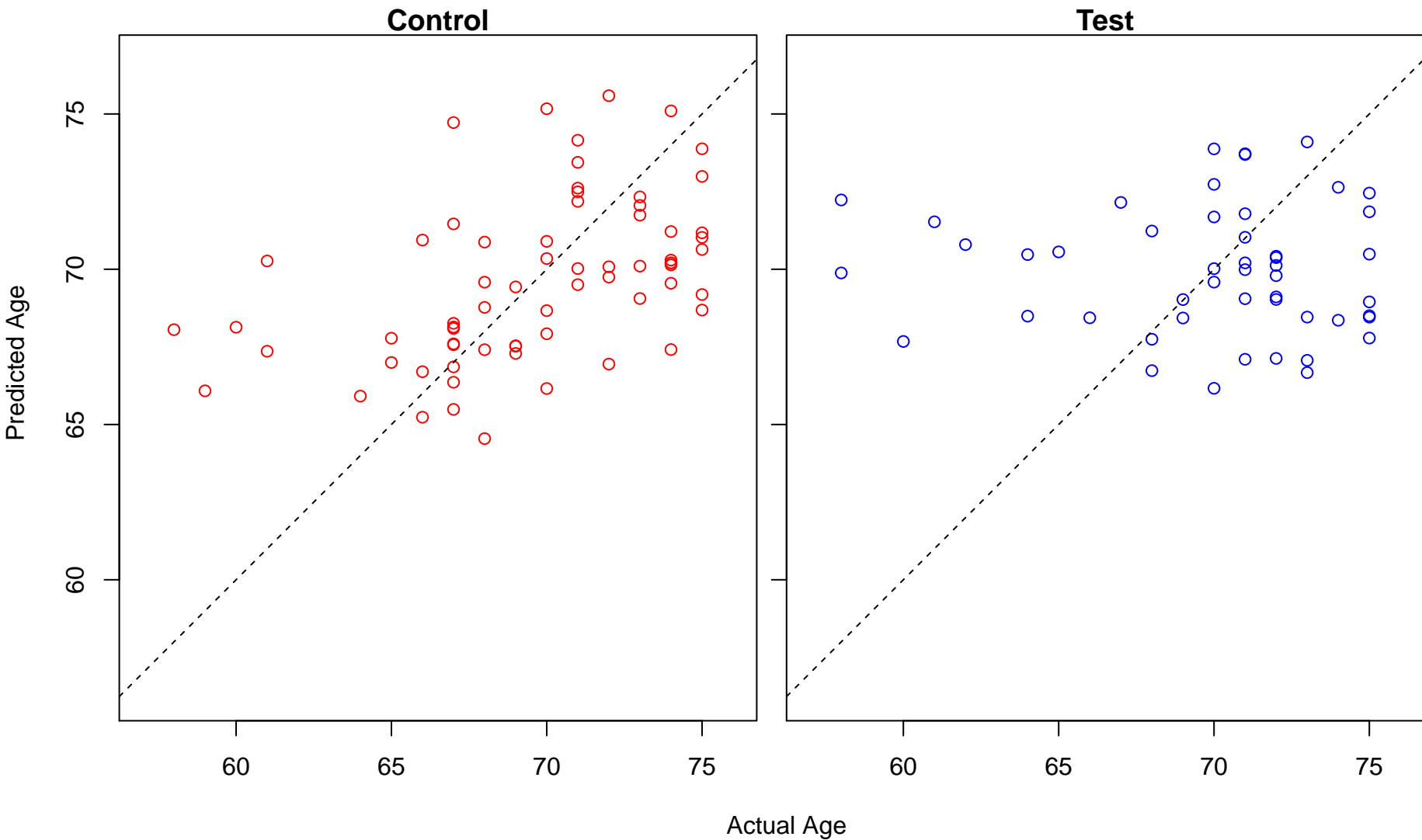
ribonucleoside bisphosphate biosynthetic process (Score: 0.713391)



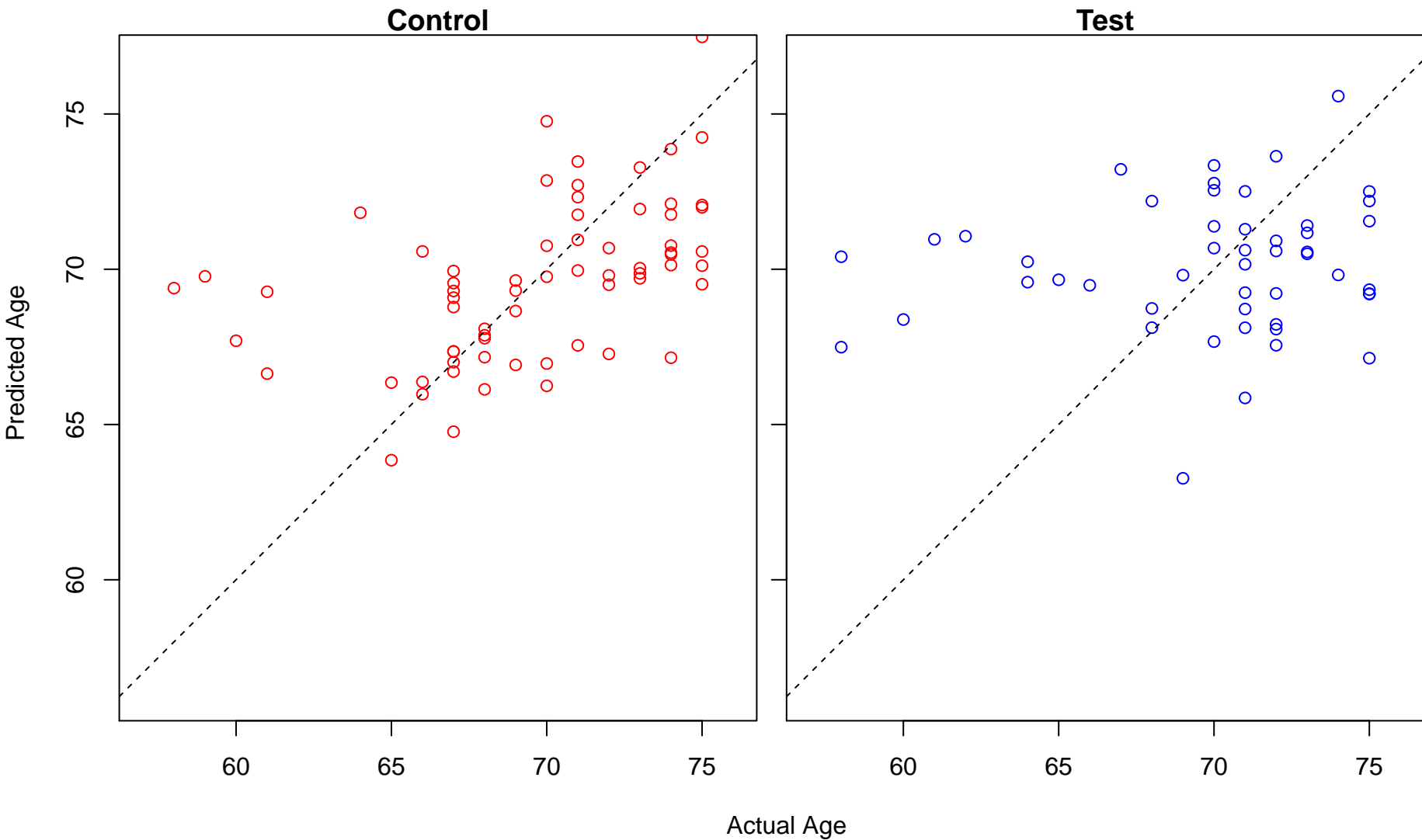
purine nucleoside bisphosphate biosynthetic process (Score: 0.713391)



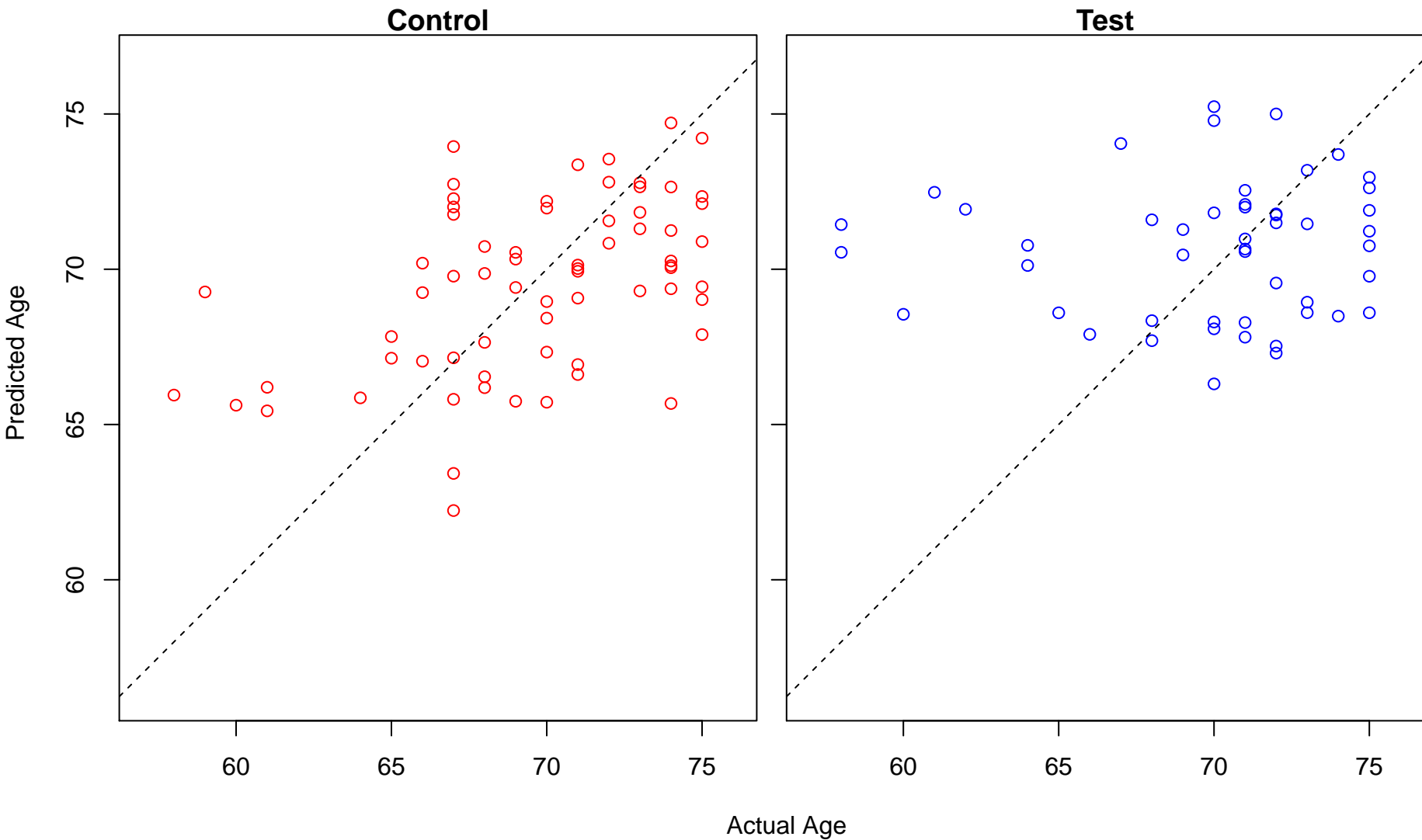
endosome transport via multivesicular body sorting pathway (Score: 0.713212)



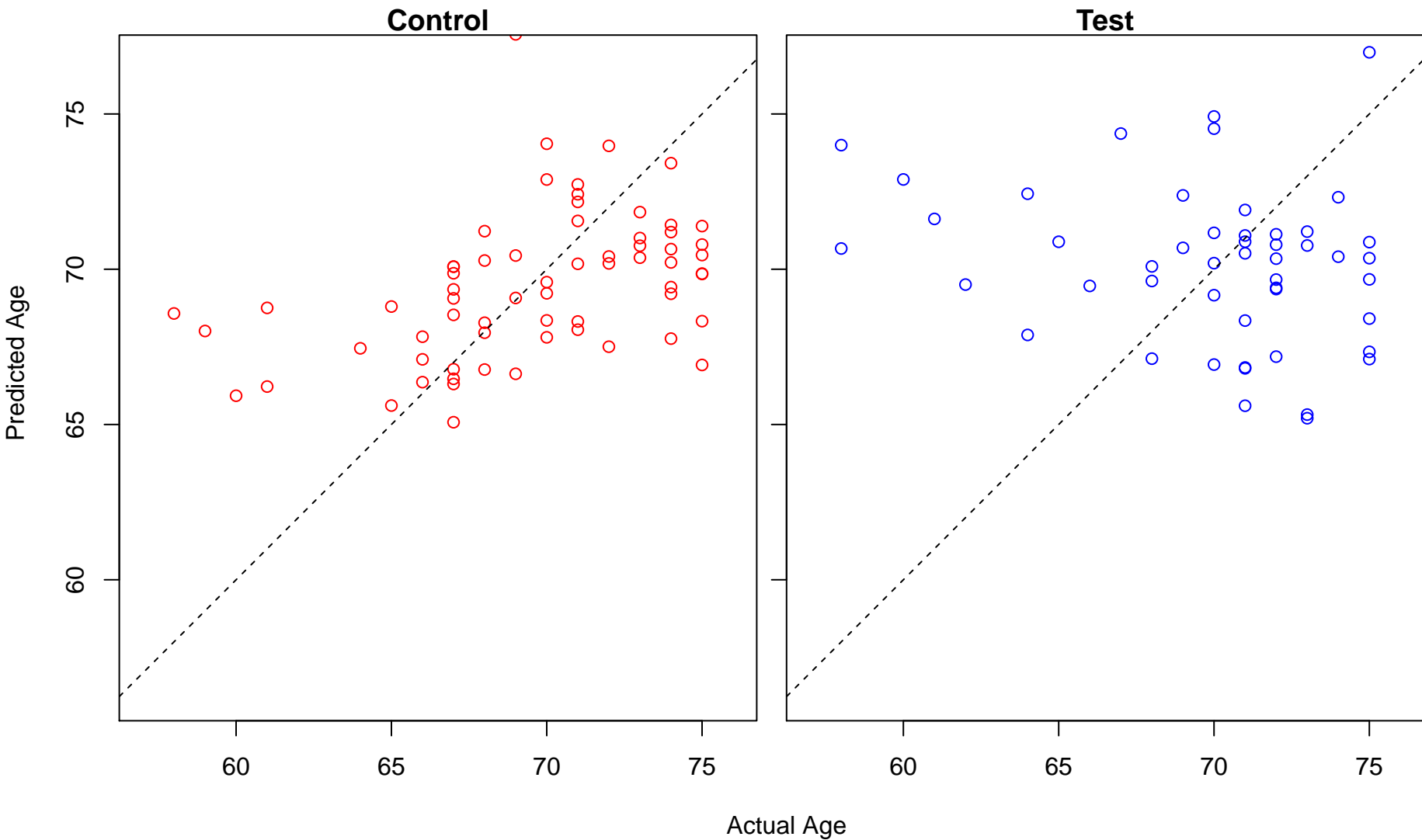
positive regulation of histone H4 acetylation (Score: 0.712996)



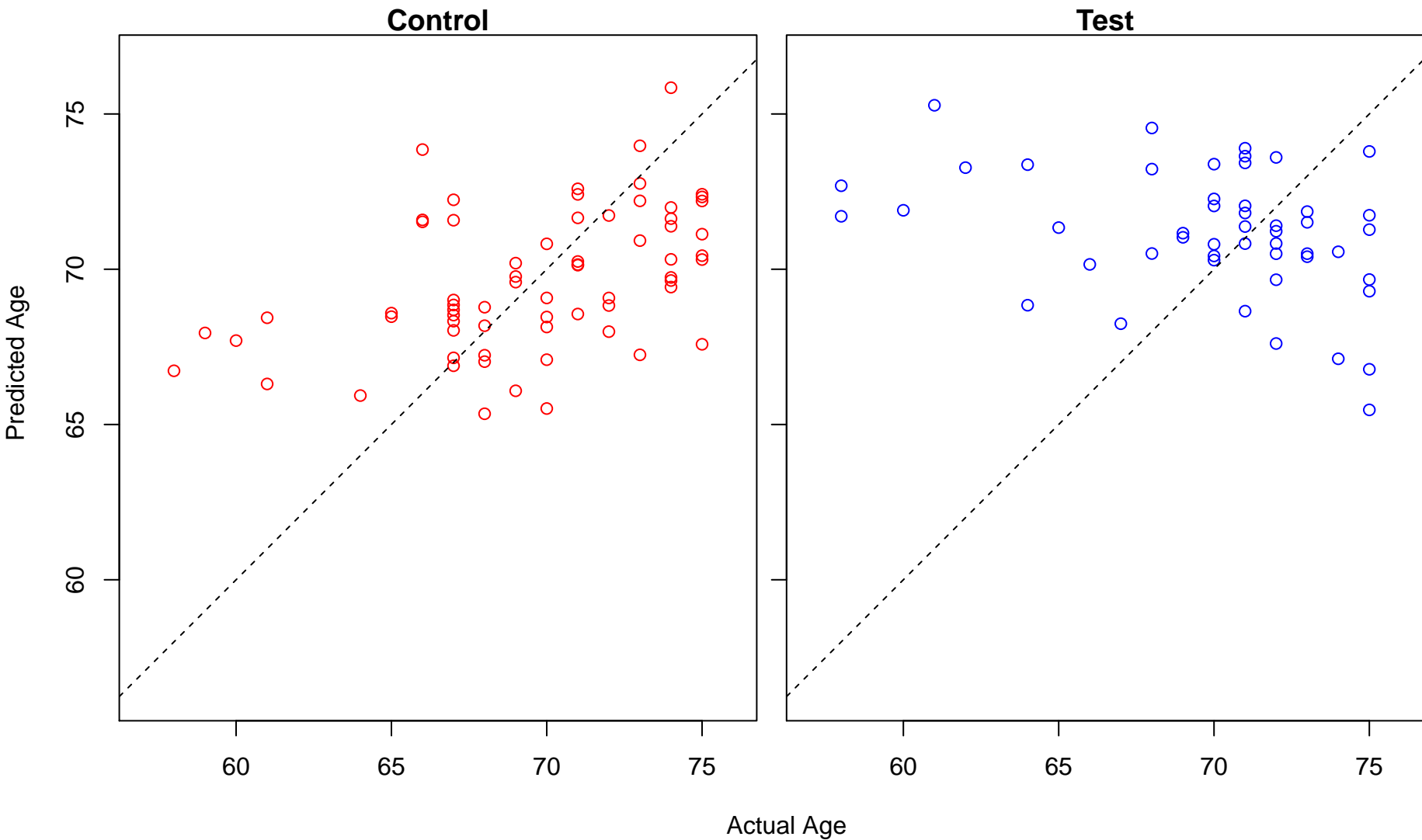
regulation of action potential (Score: 0.712917)



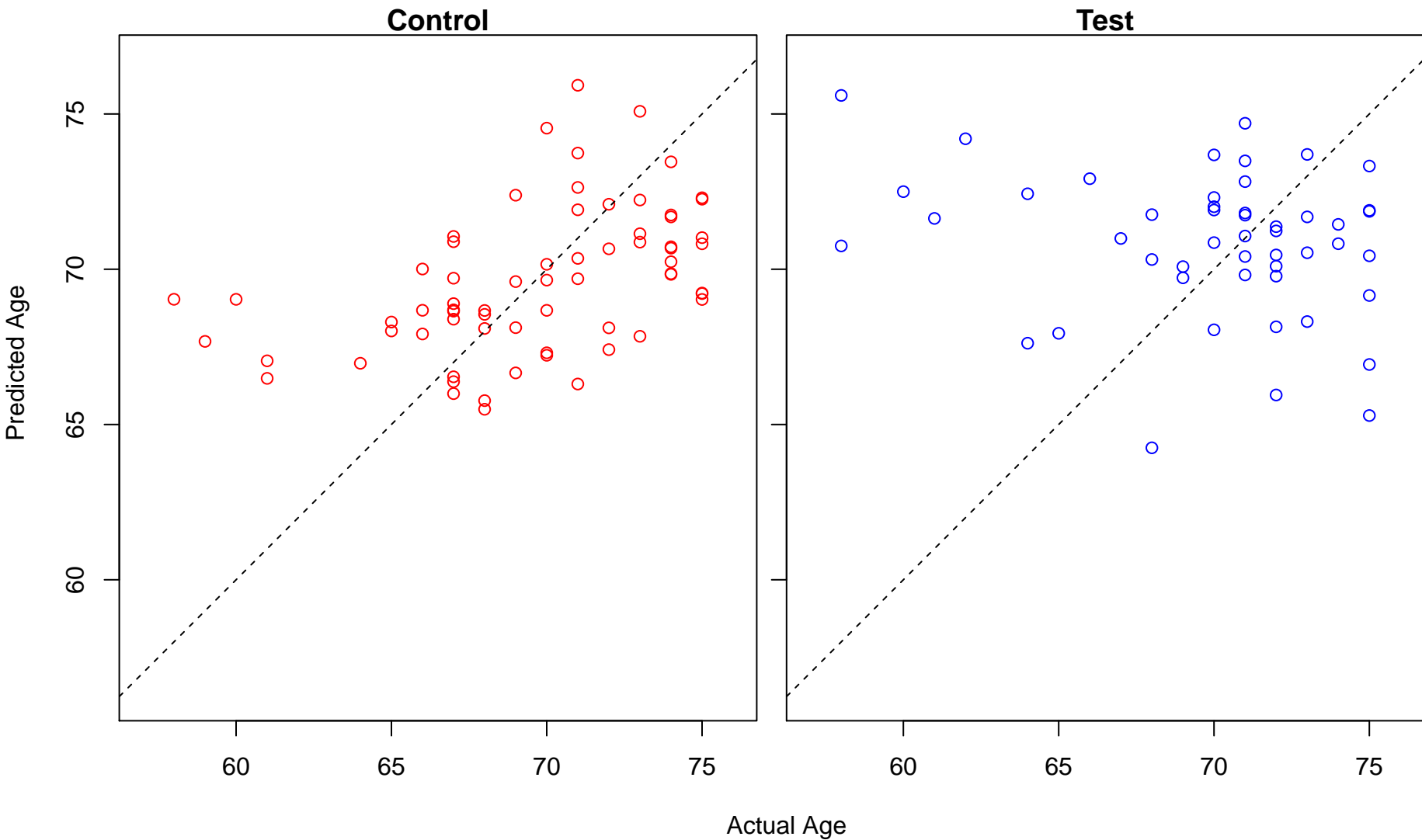
regulation of reproductive process (Score: 0.712816)



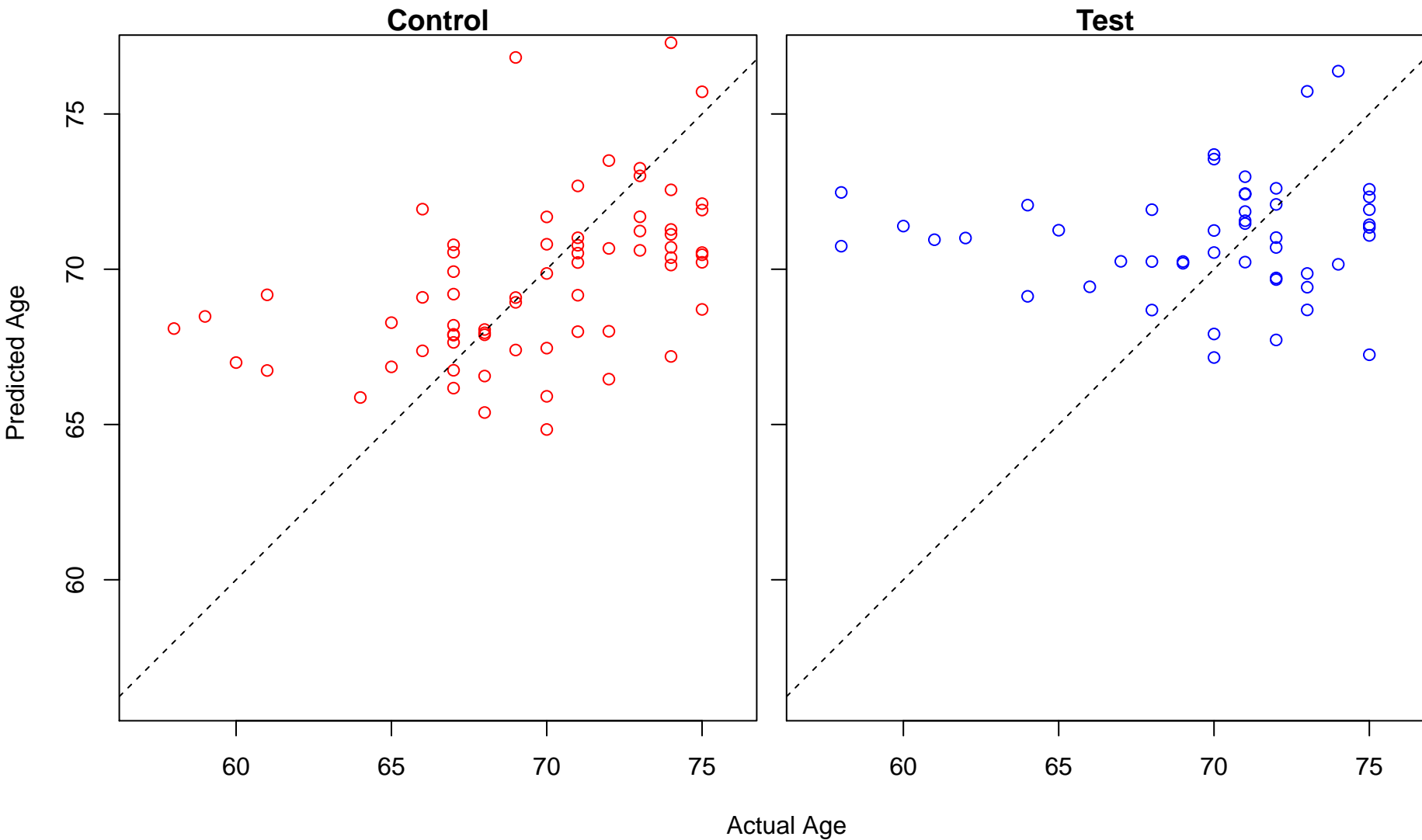
oxaloacetate metabolic process (Score: 0.712156)



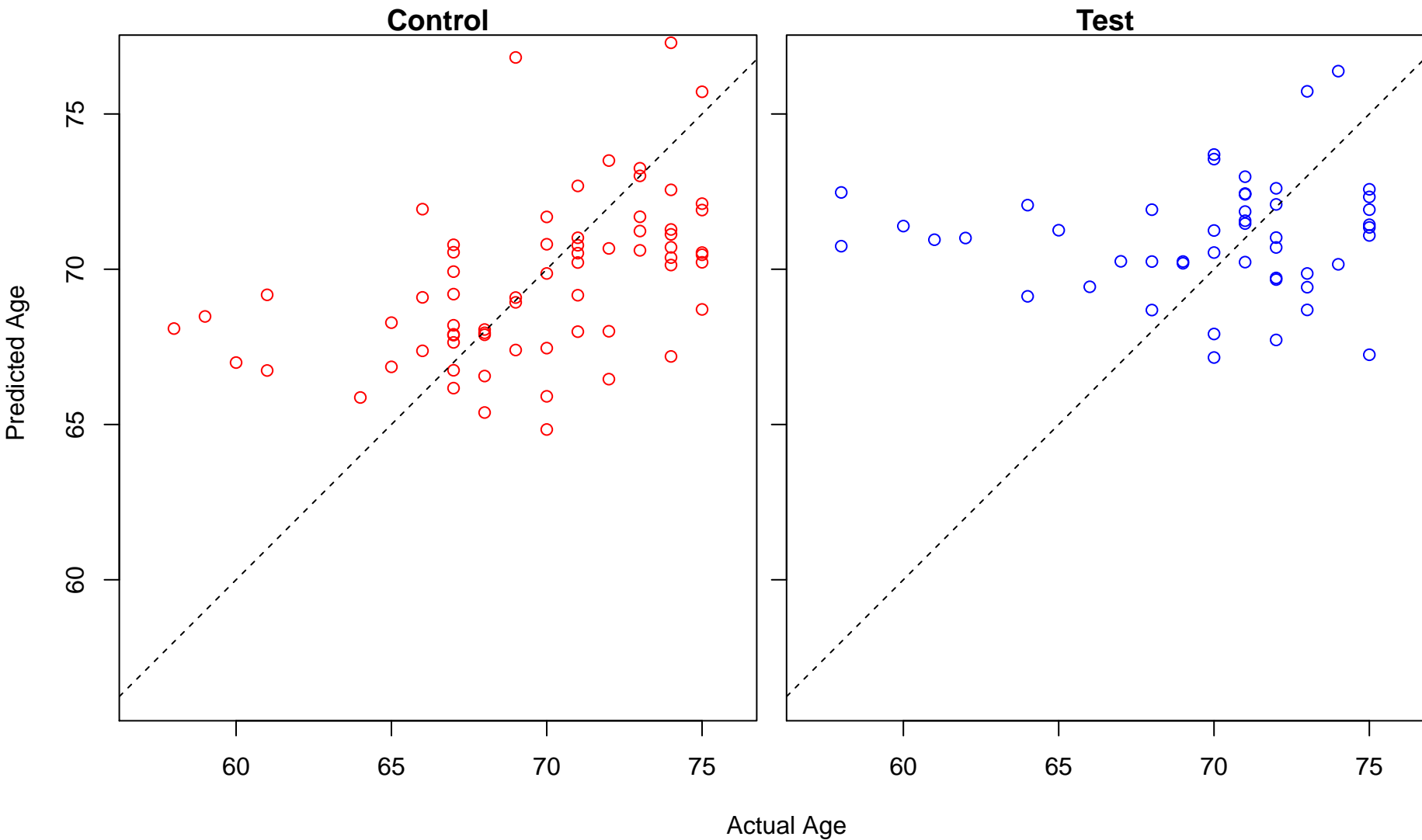
regulation of pinocytosis (Score: 0.711898)



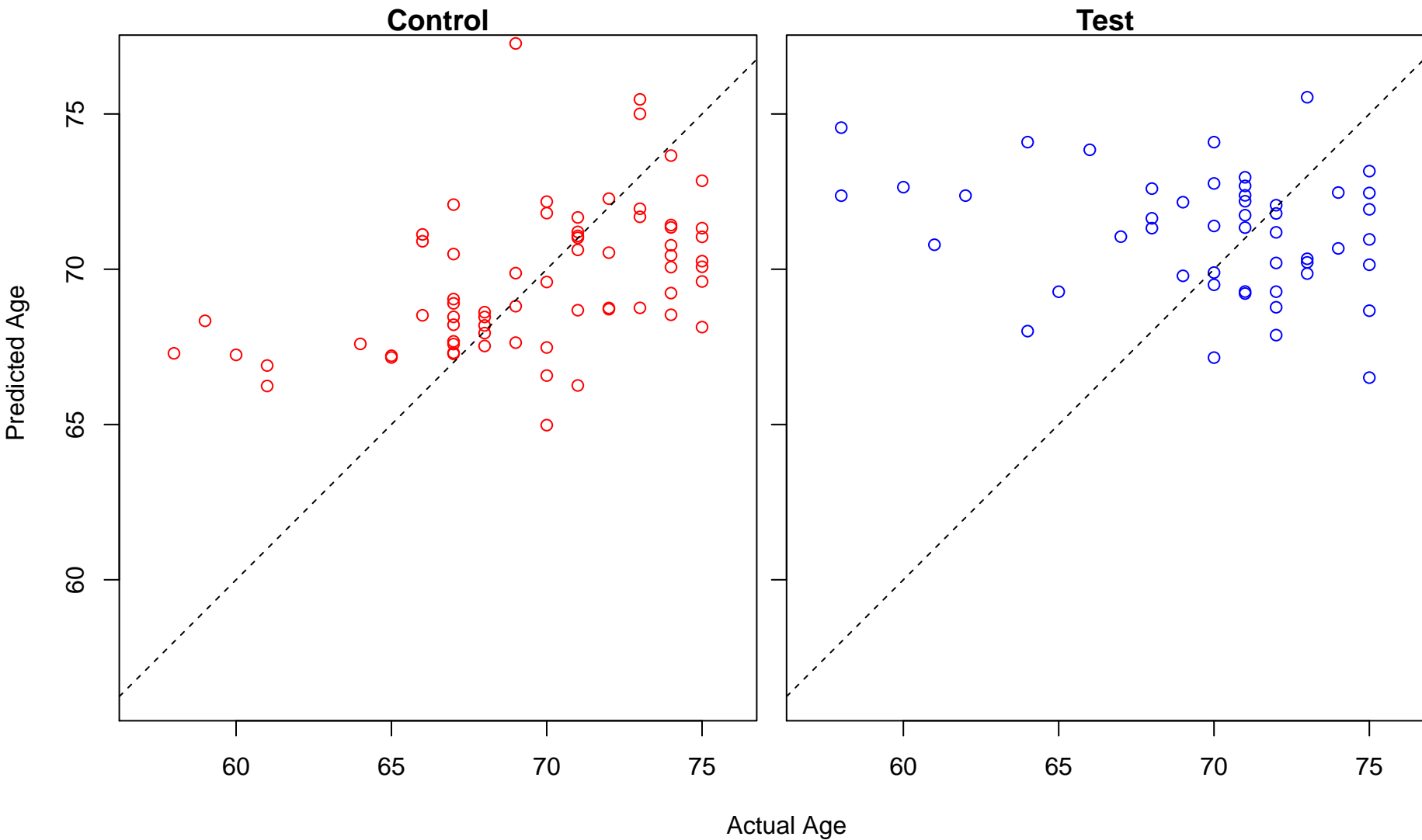
uronic acid metabolic process (Score: 0.711826)



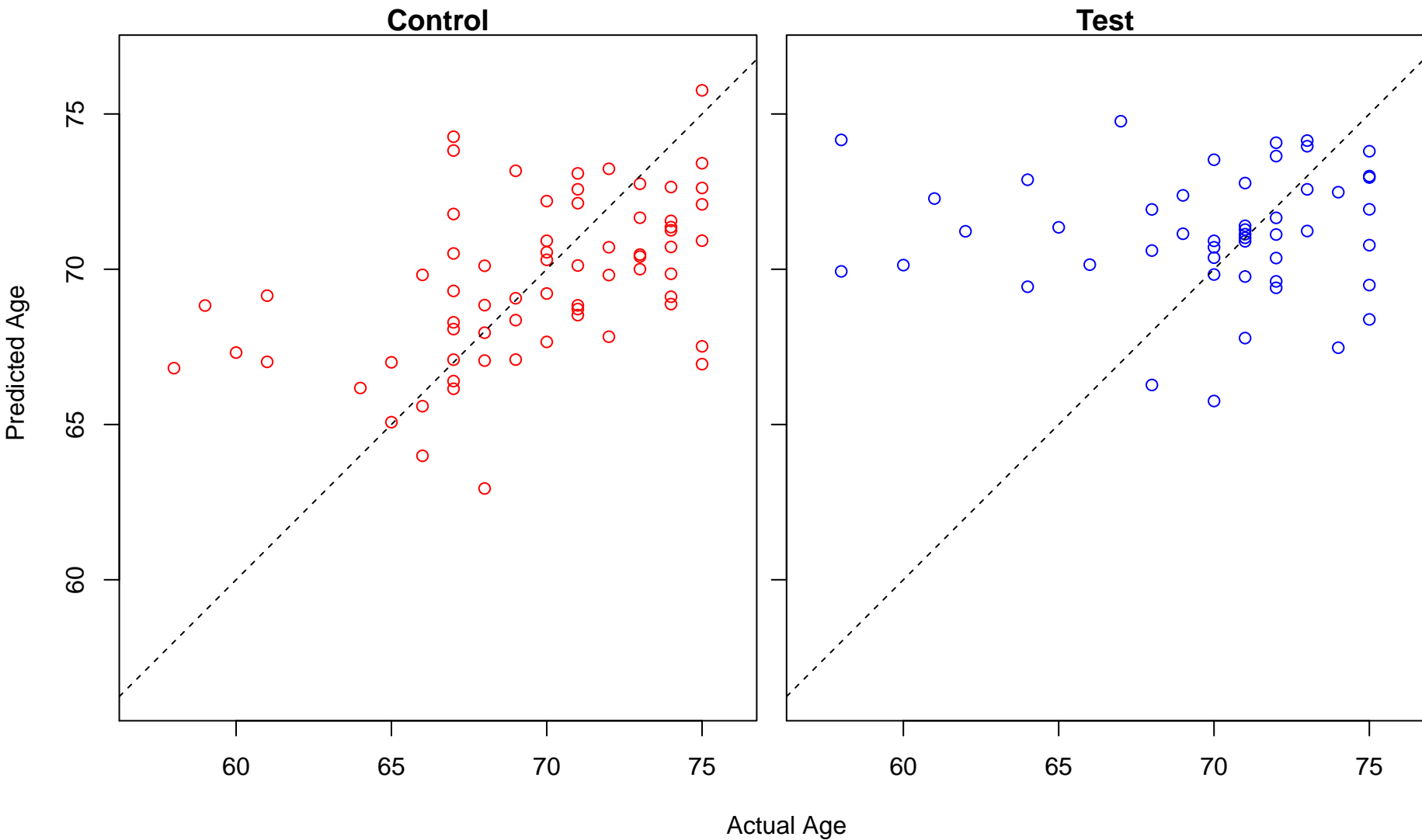
glucuronate metabolic process (Score: 0.711826)



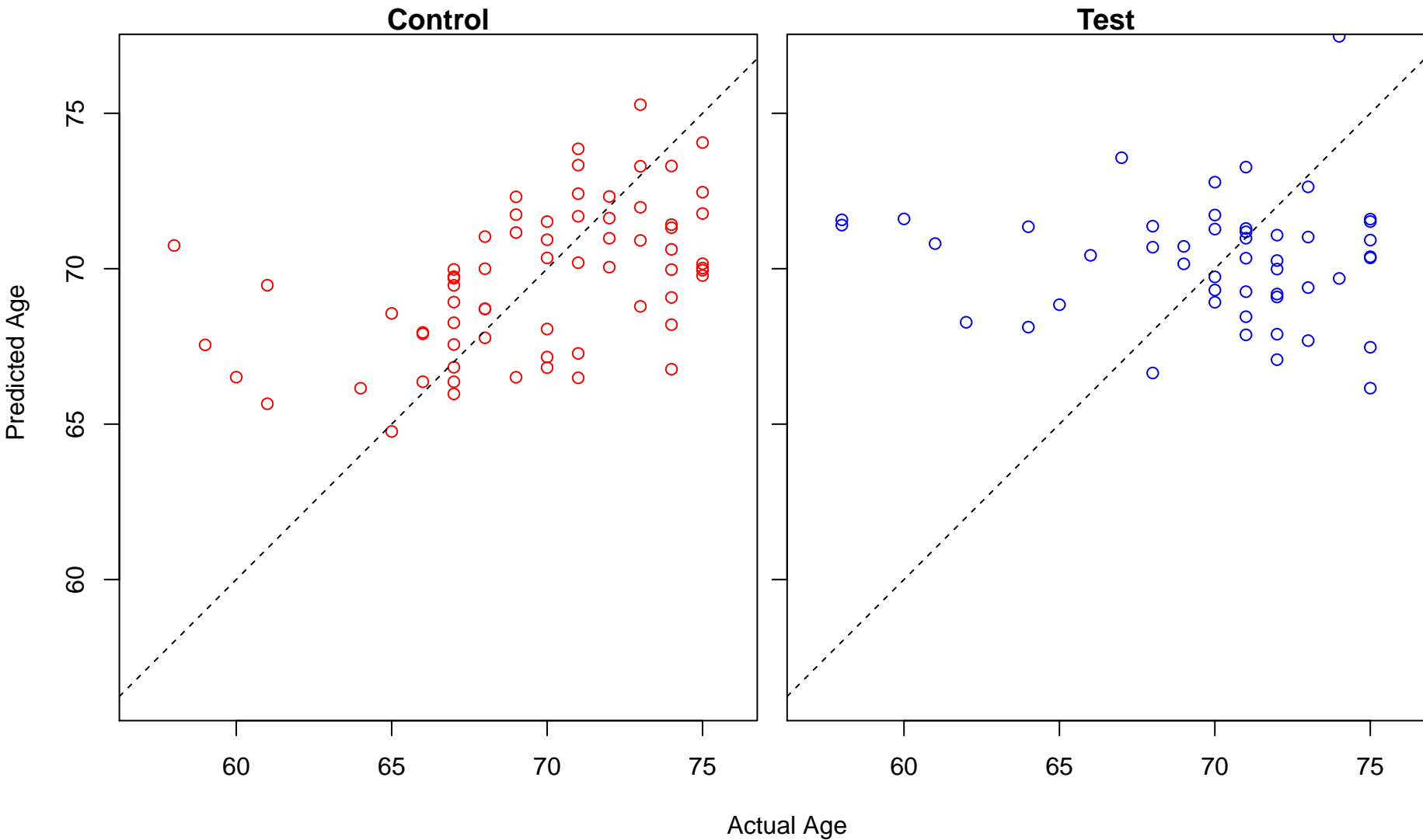
vesicle cytoskeletal trafficking (Score: 0.711404)



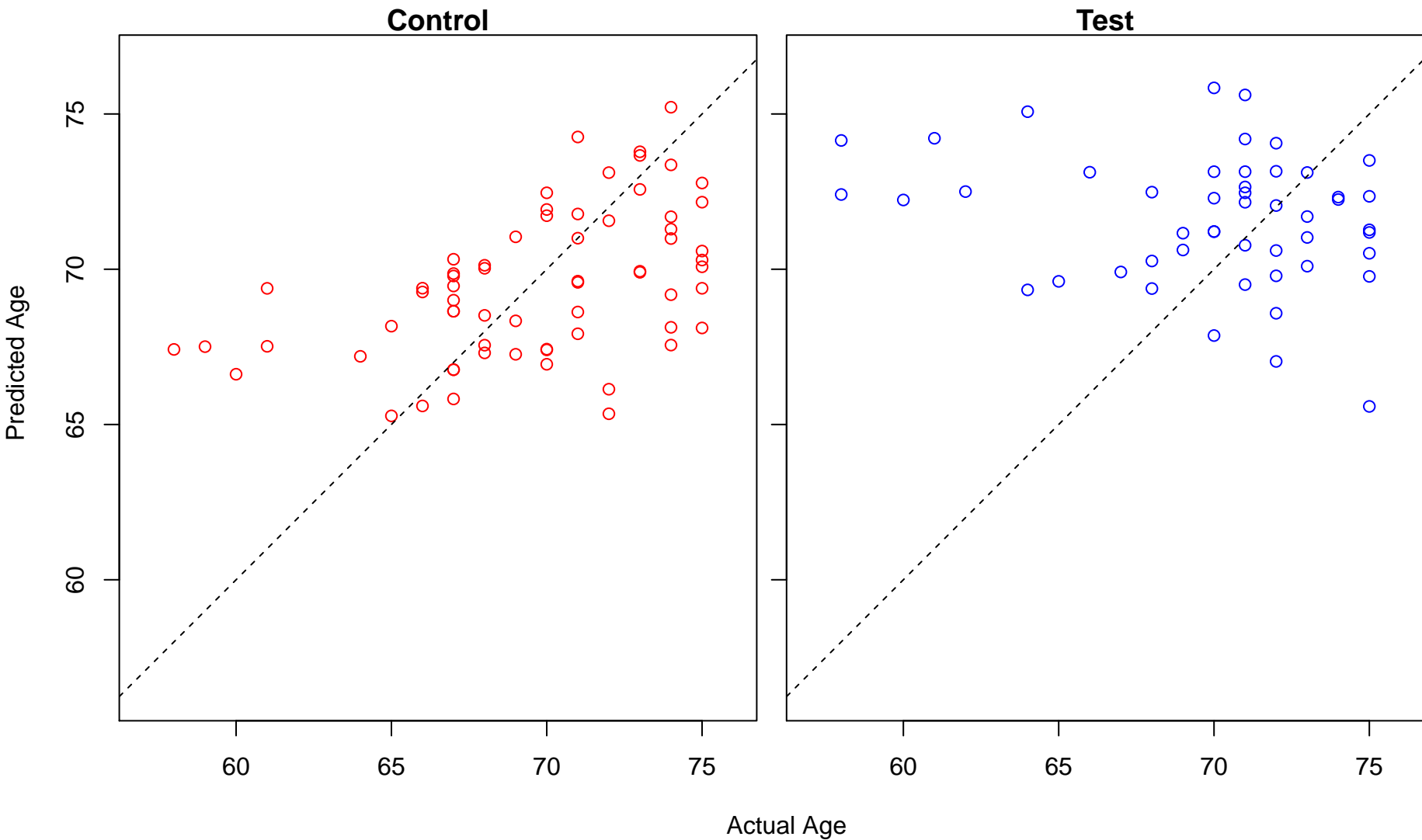
response to UV-B (Score: 0.711035)



attachment of GPI anchor to protein (Score: 0.710600)

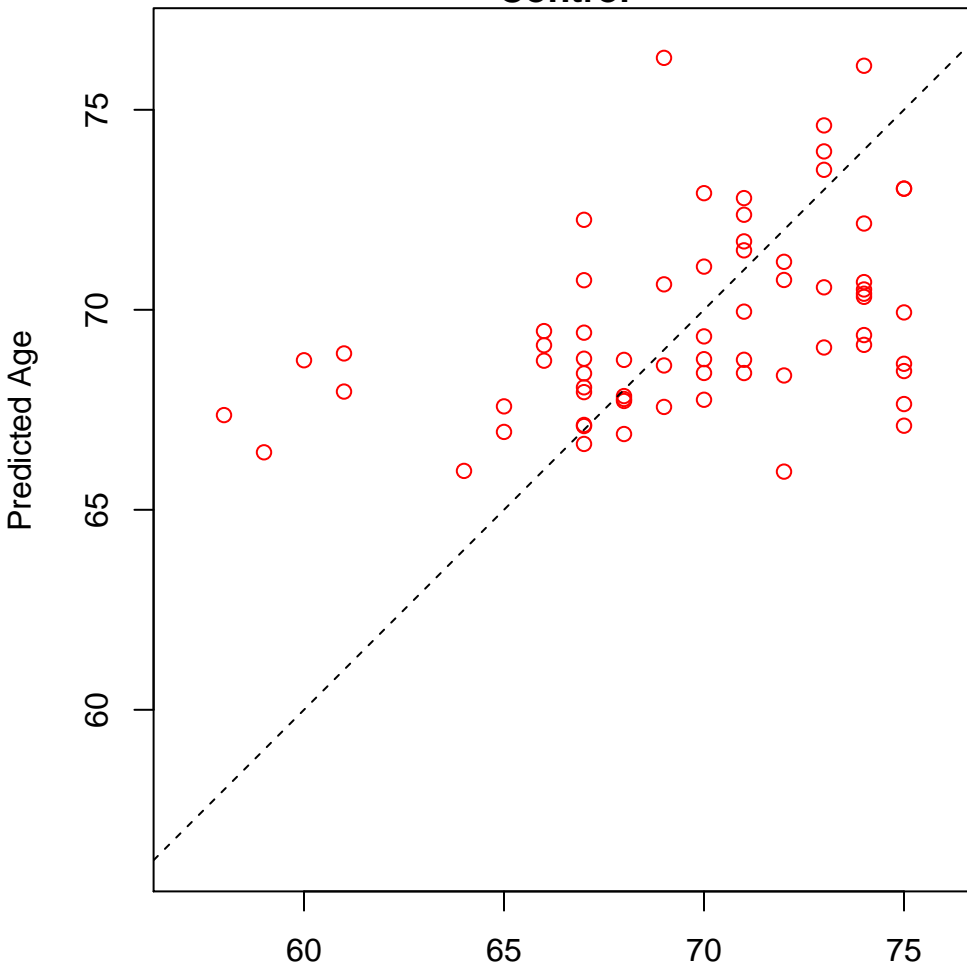


macrophage activation (Score: 0.709606)

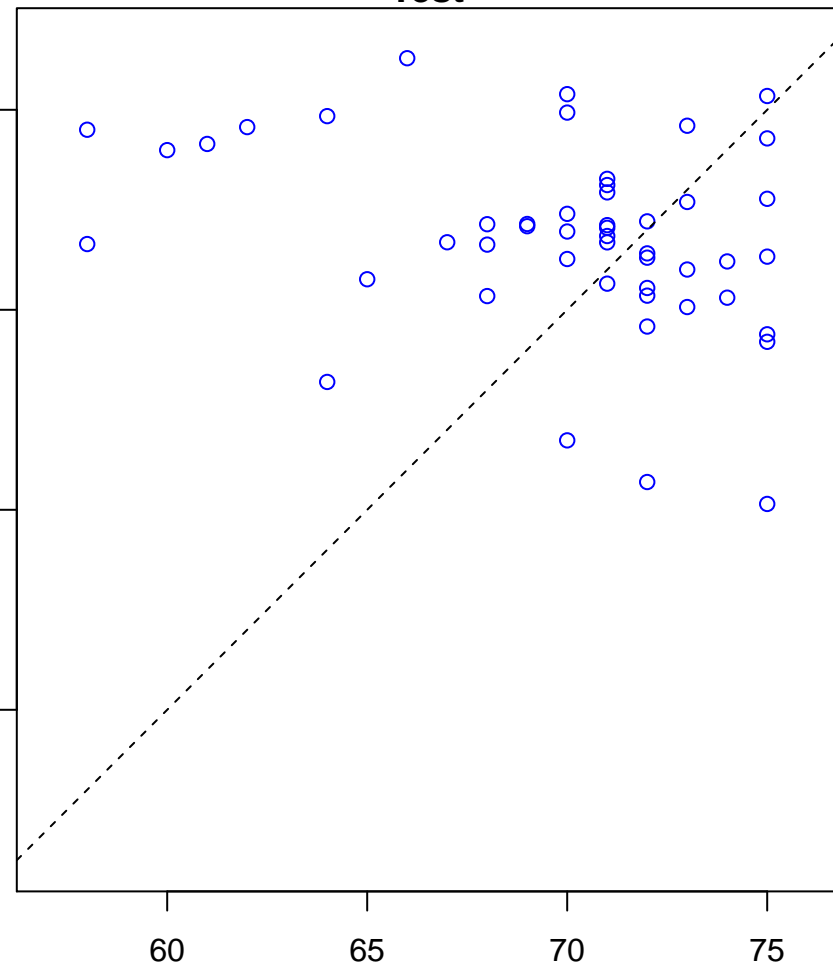


regulation of monooxygenase activity (Score: 0.708461)

Control

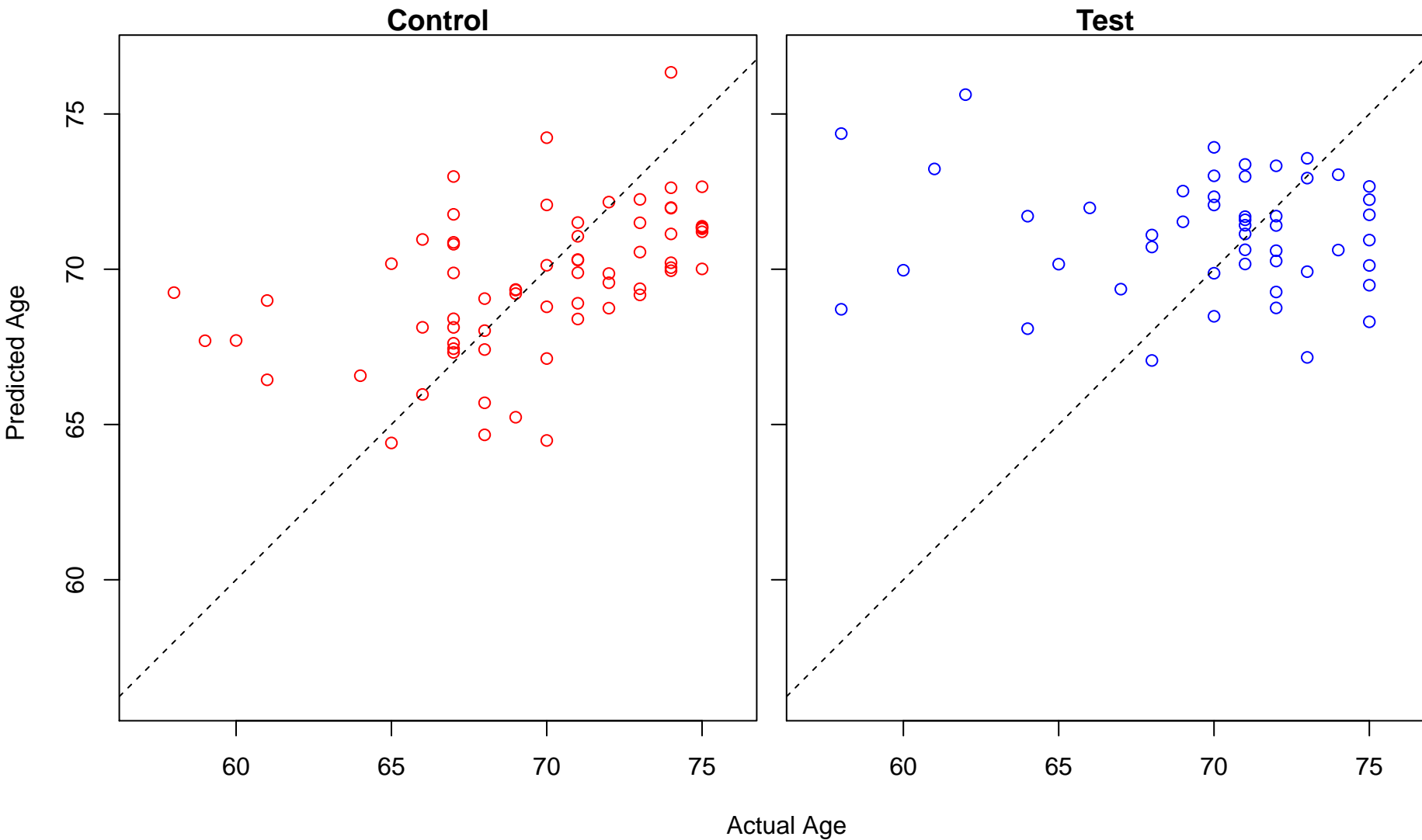


Test

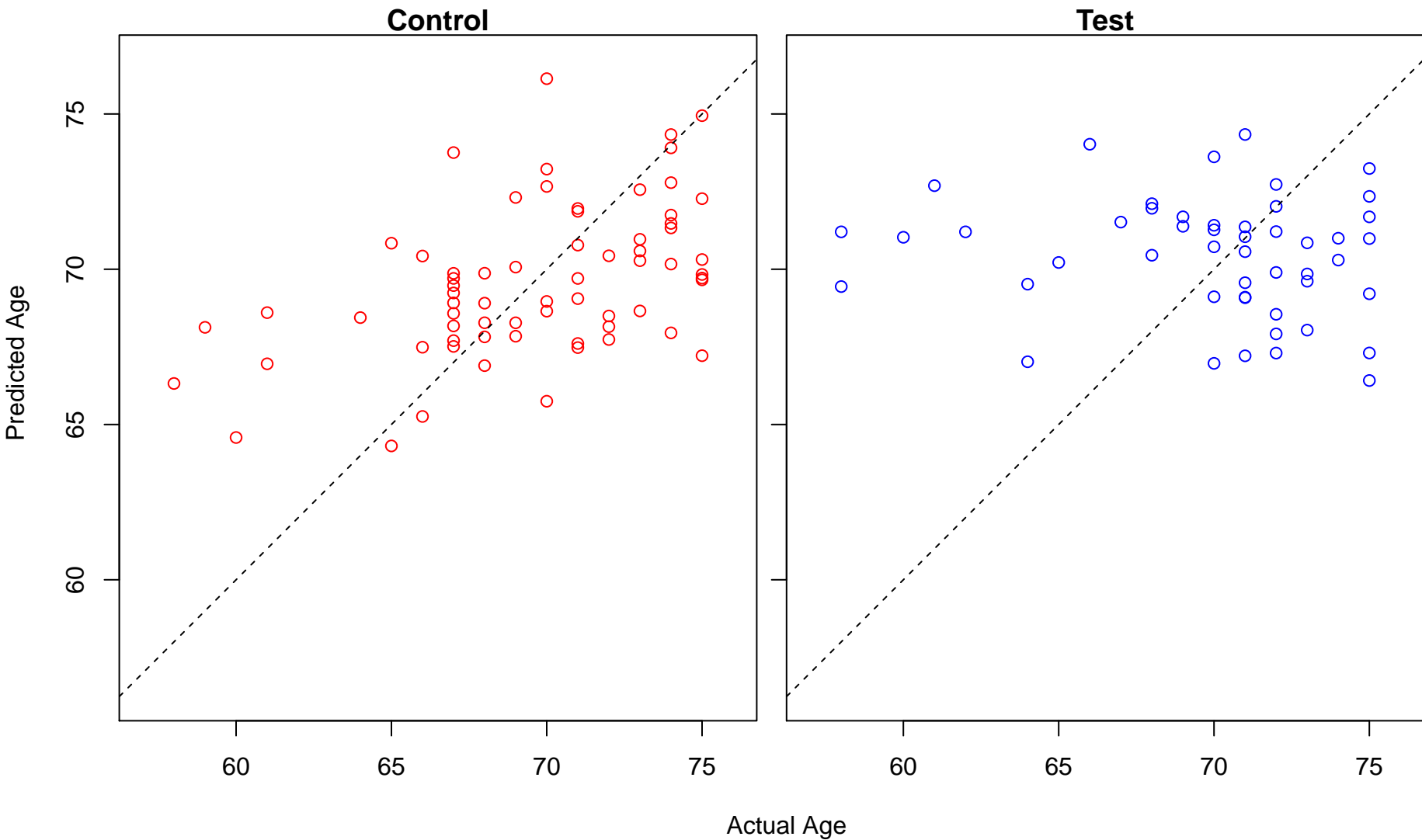


Actual Age

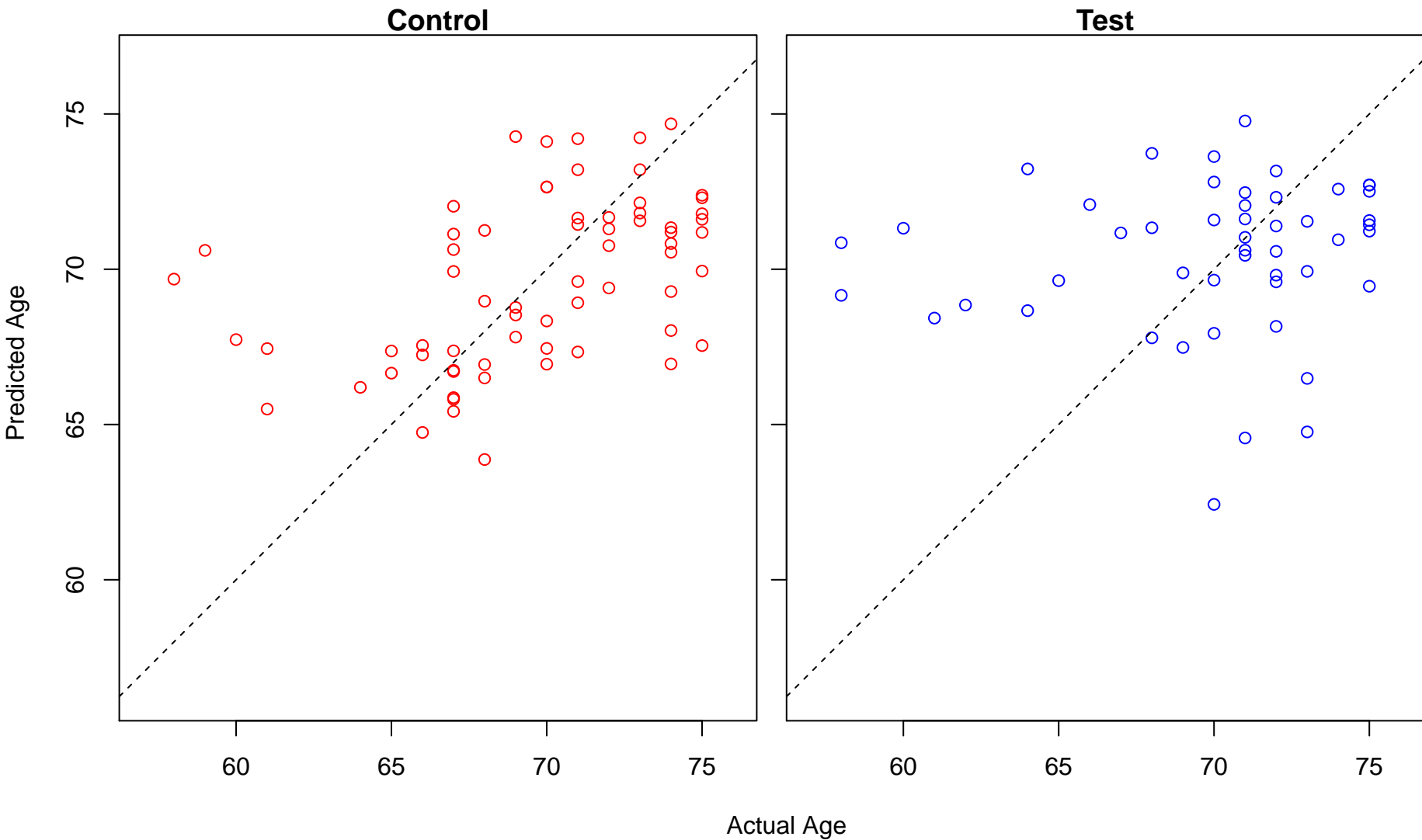
ectoderm development (Score: 0.708081)



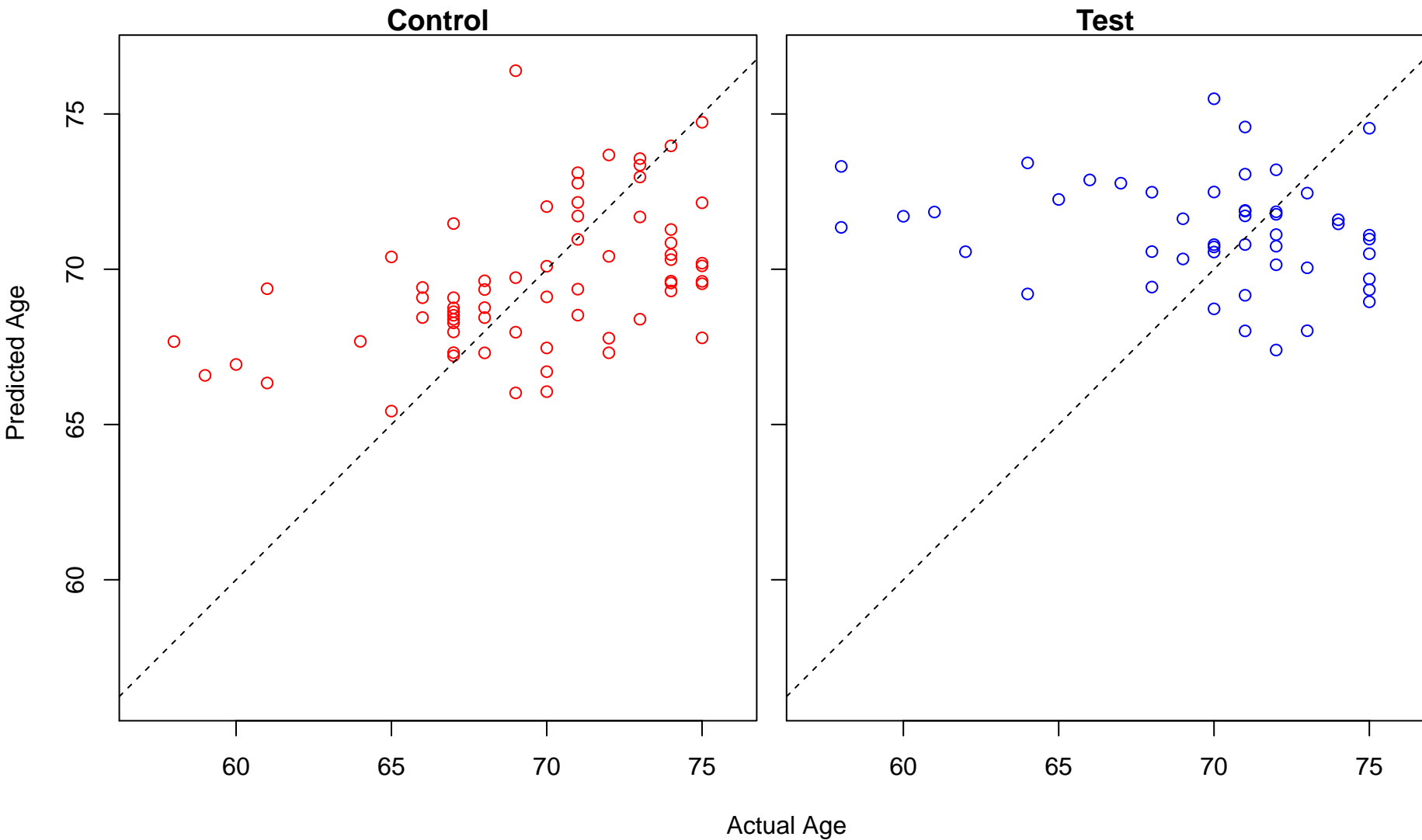
beta-amyloid metabolic process (Score: 0.707949)



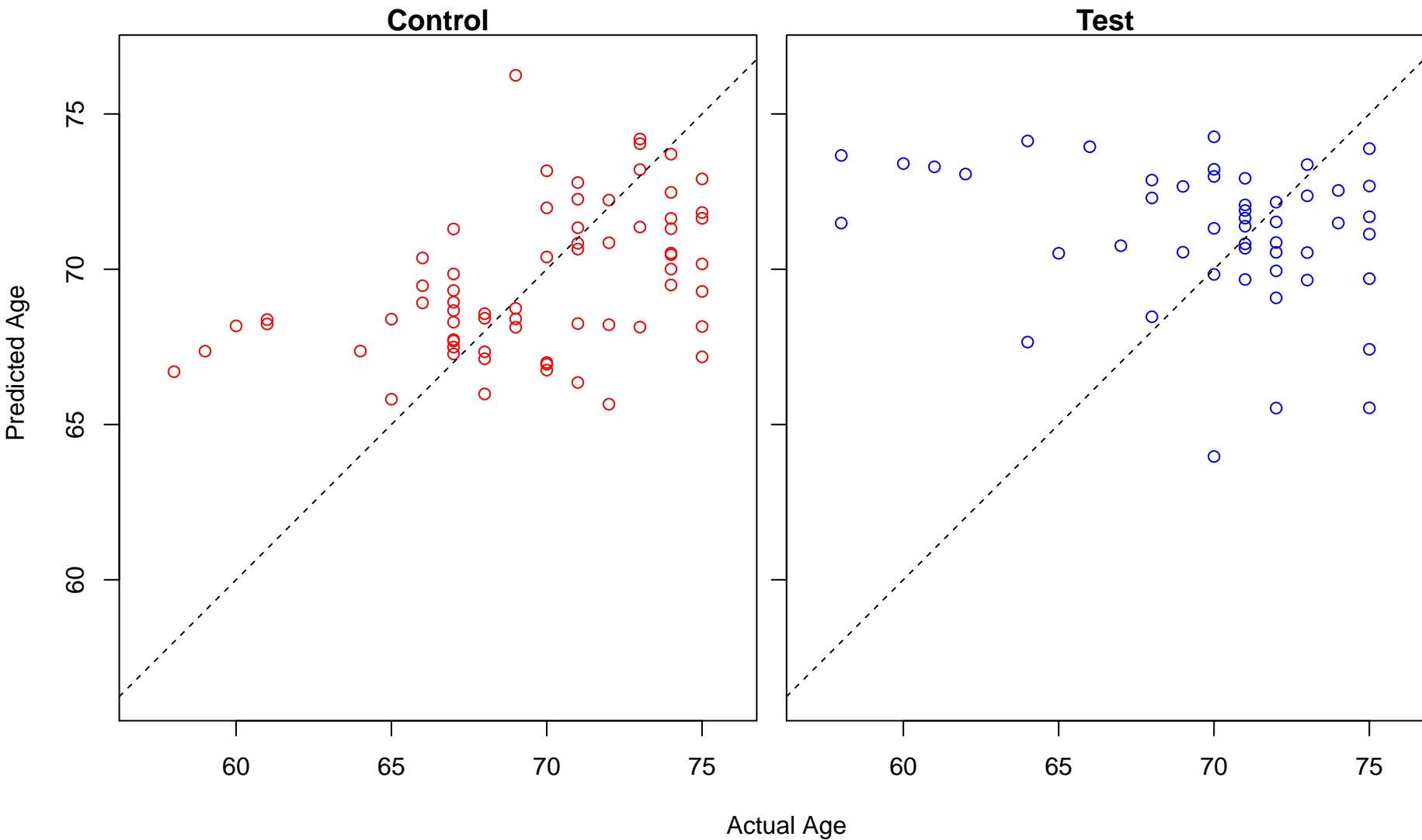
I-kappaB phosphorylation (Score: 0.707668)



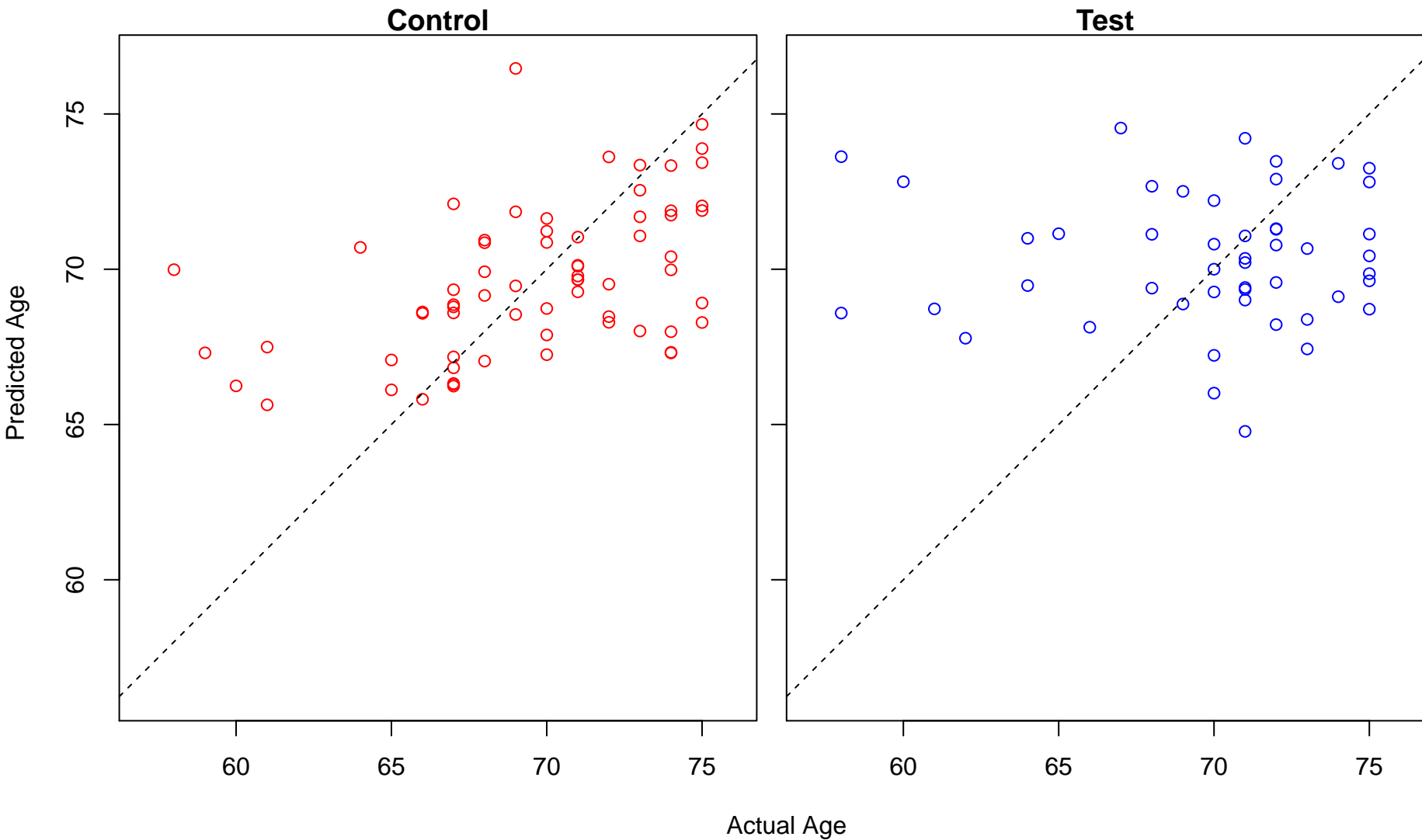
regulation of PERK-mediated unfolded protein response (Score: 0.707042)



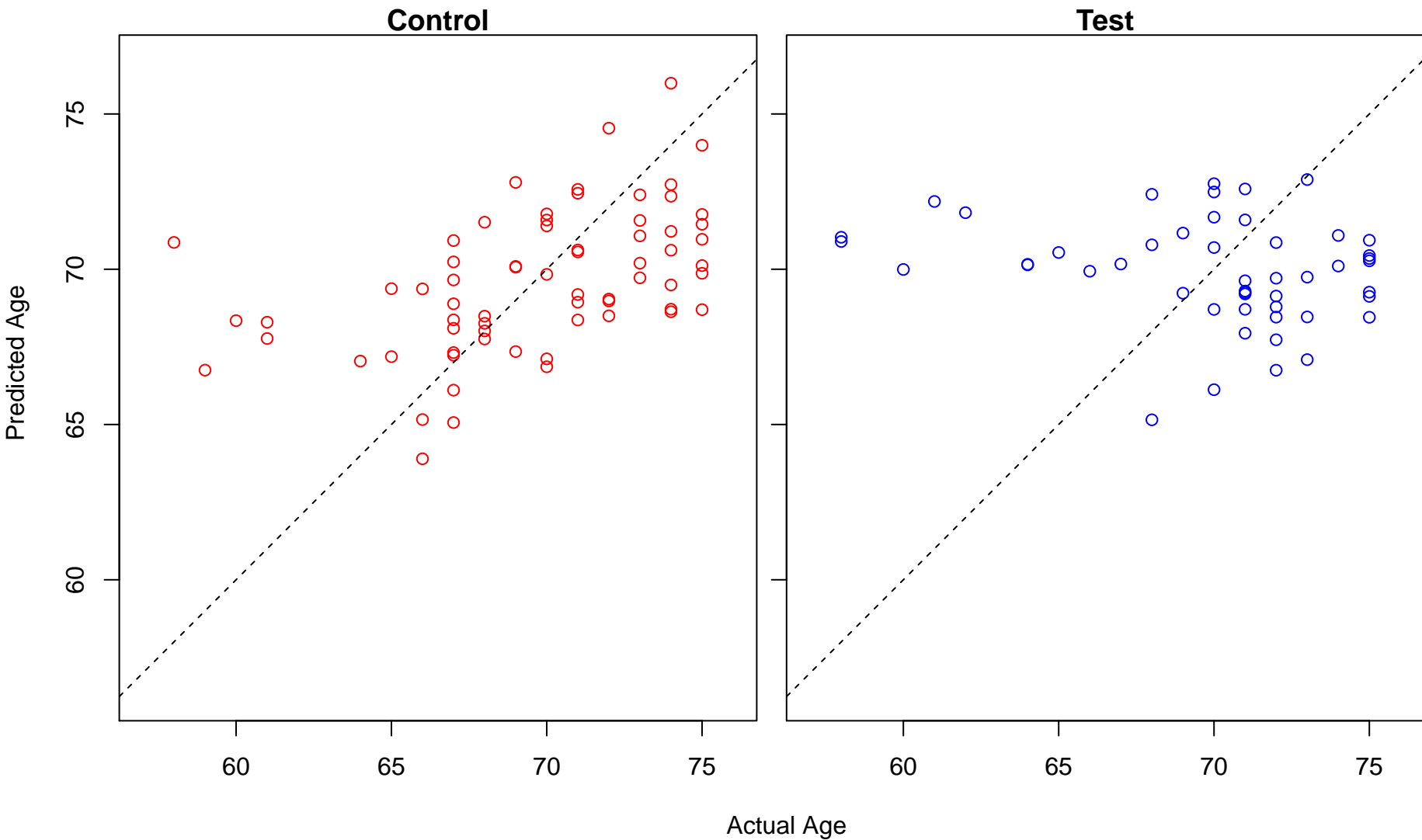
negative regulation of release of cytochrome c from mitochondria (Score: 0.706963)



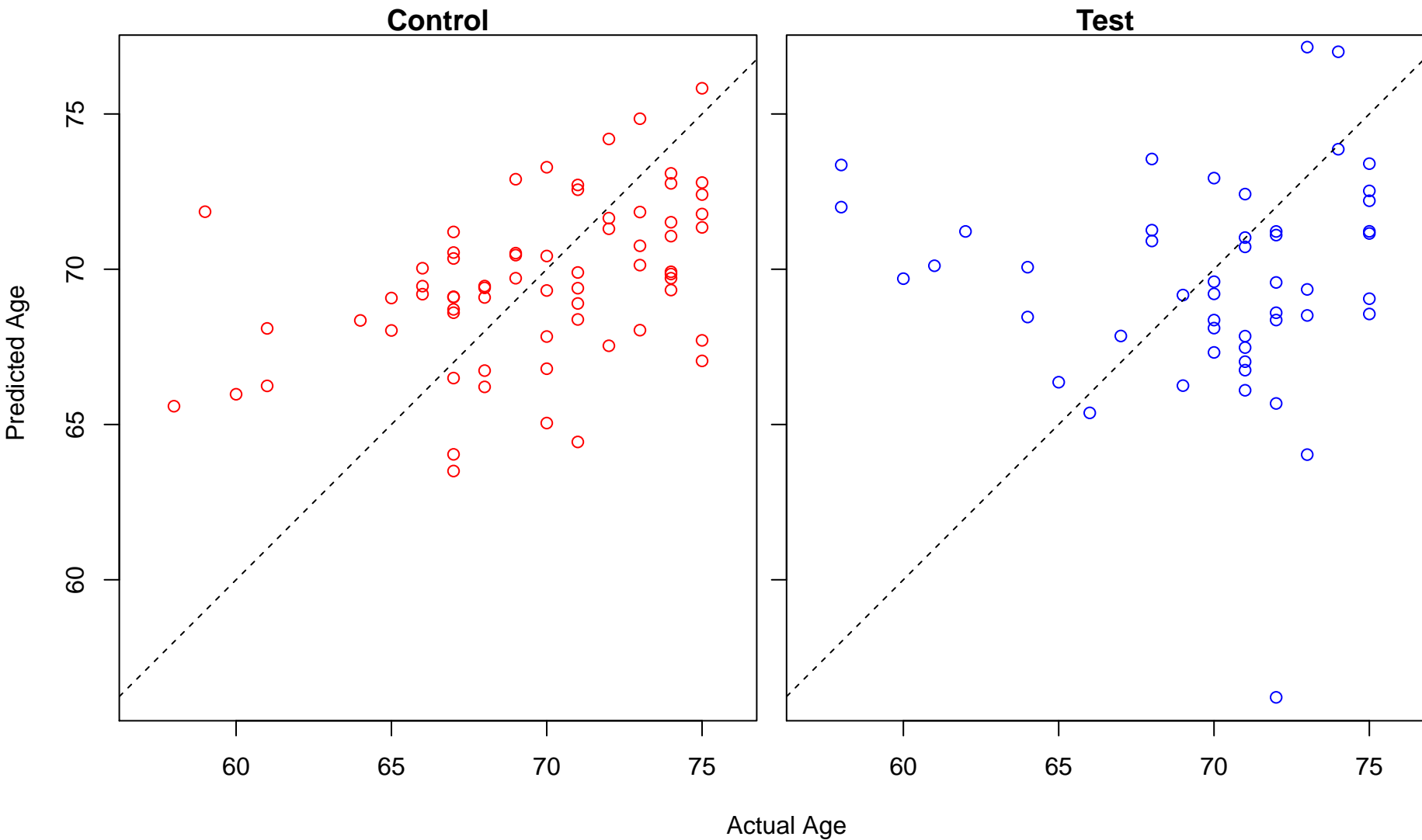
ganglioside metabolic process (Score: 0.706736)



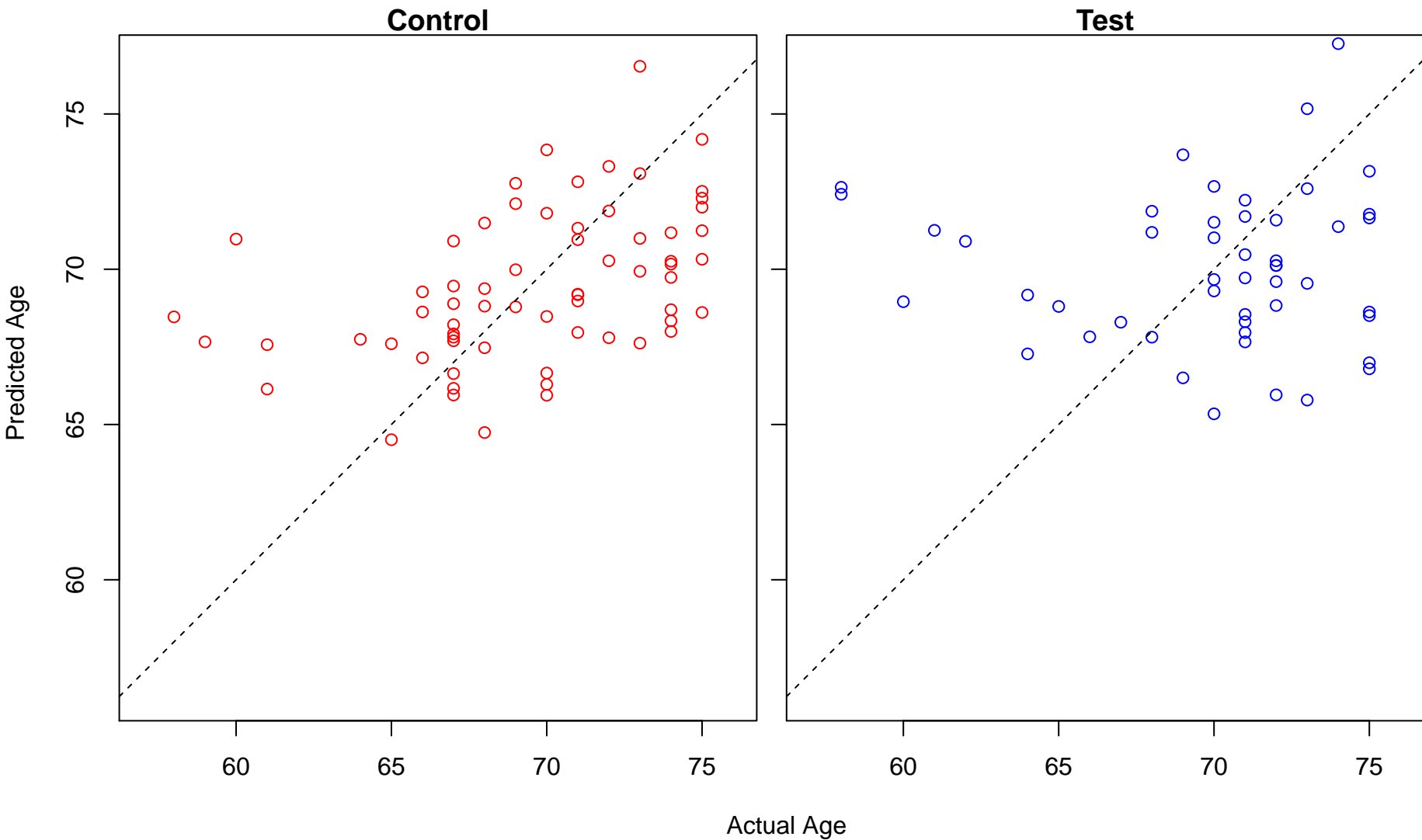
calcineurin-NFAT signaling cascade (Score: 0.706465)



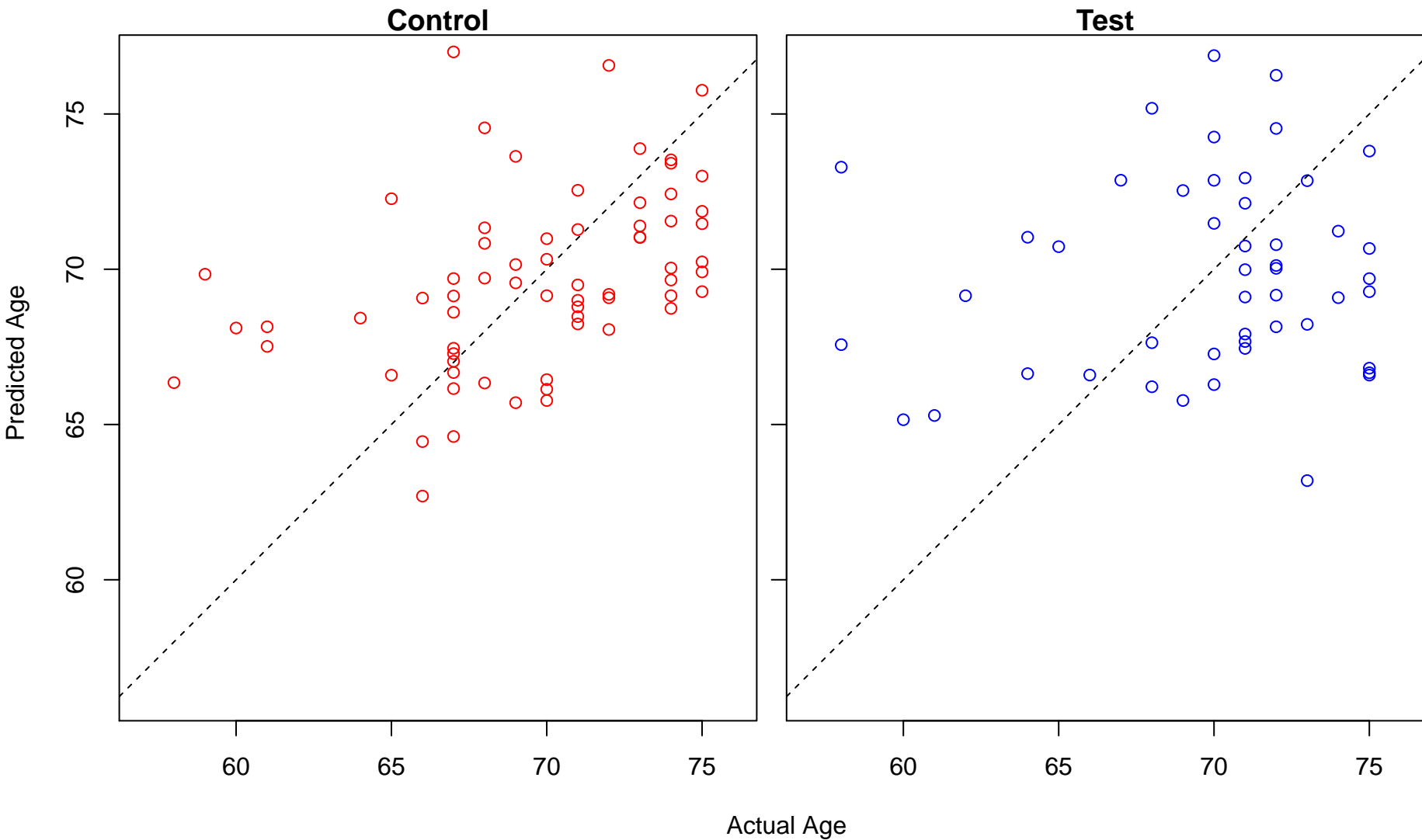
negative regulation of antigen processing and presentation (Score: 0.706389)



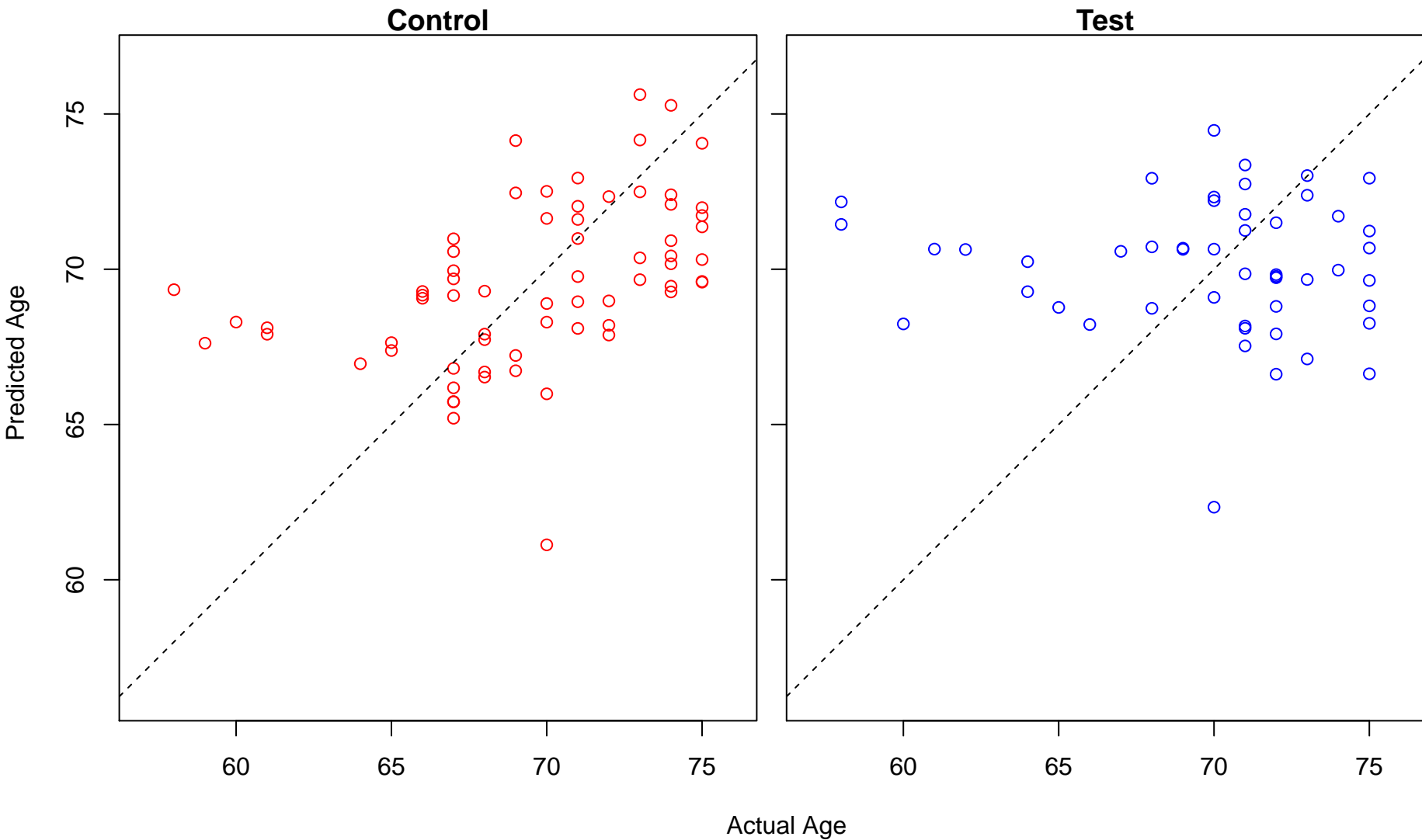
regulation of embryonic development (Score: 0.706388)



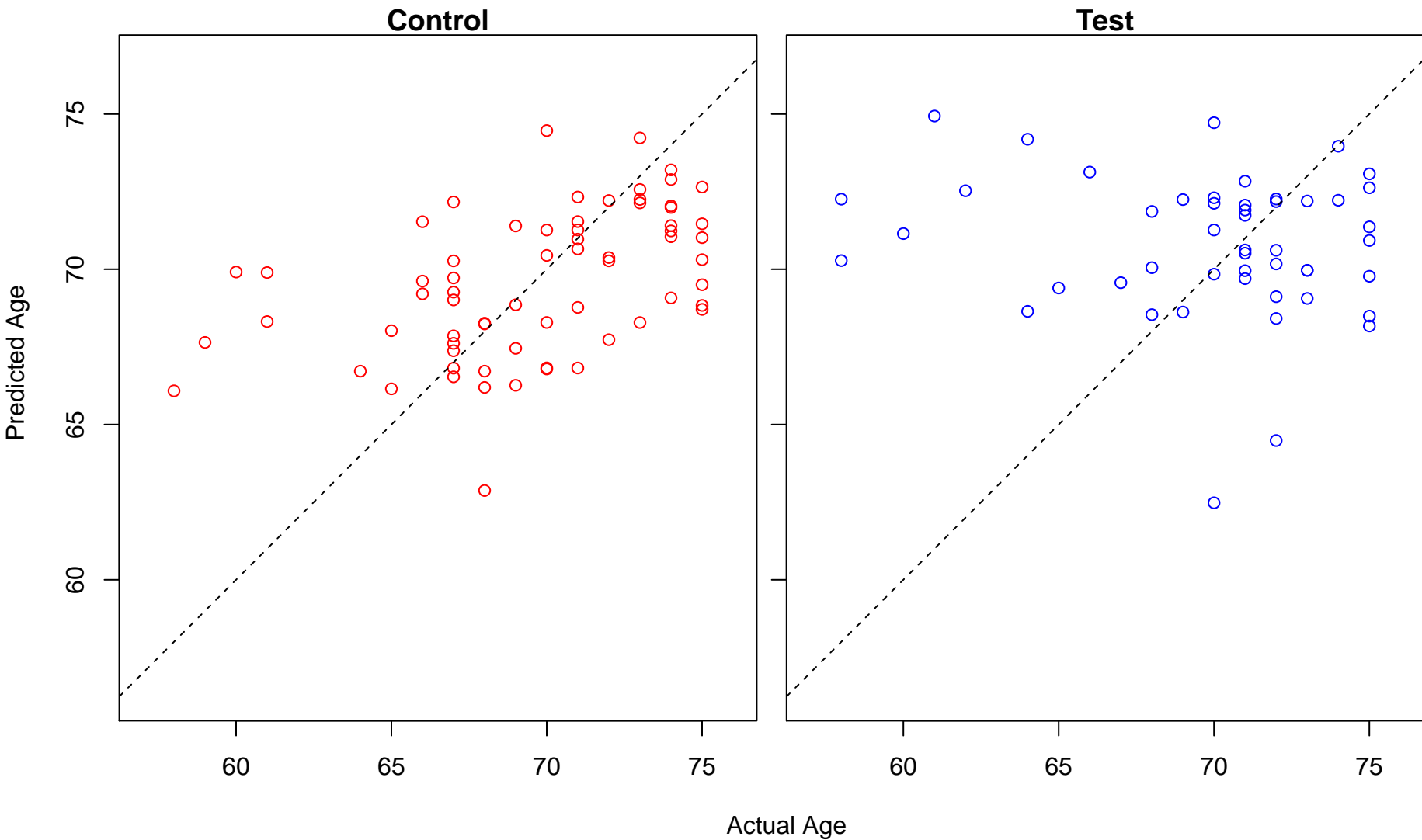
regulation of meiotic cell cycle (Score: 0.706351)



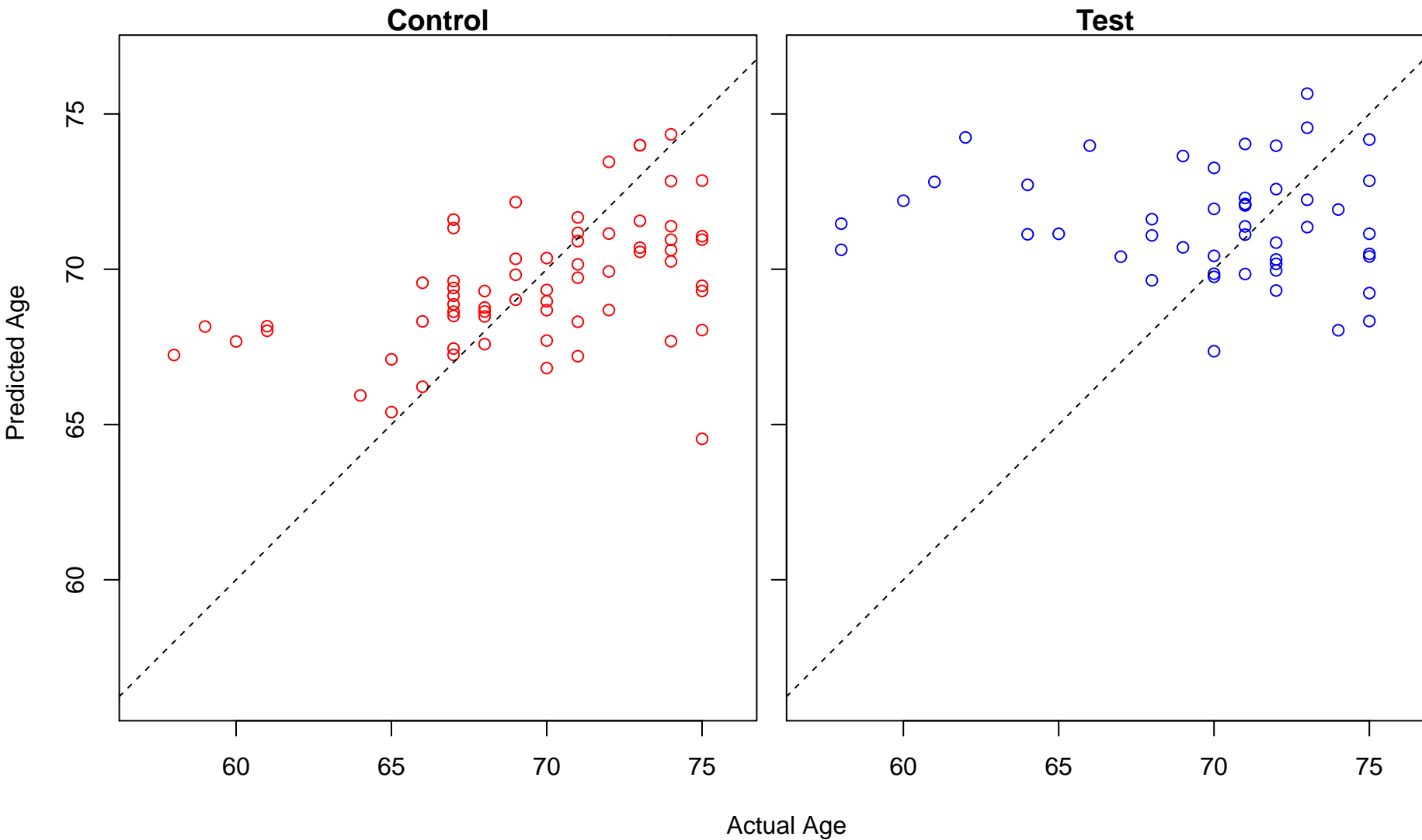
hematopoietic progenitor cell differentiation (Score: 0.705666)



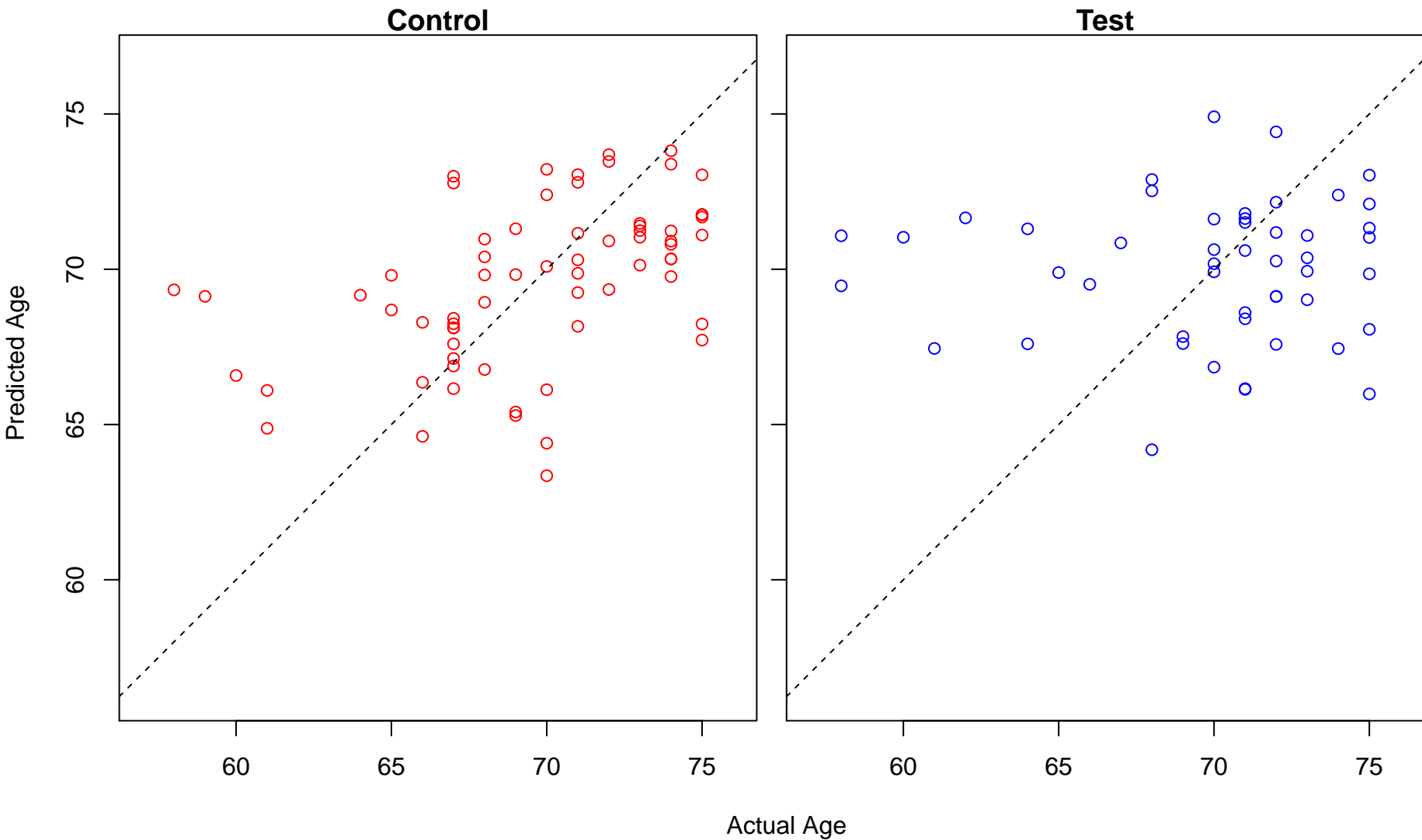
mammary gland epithelial cell differentiation (Score: 0.705645)



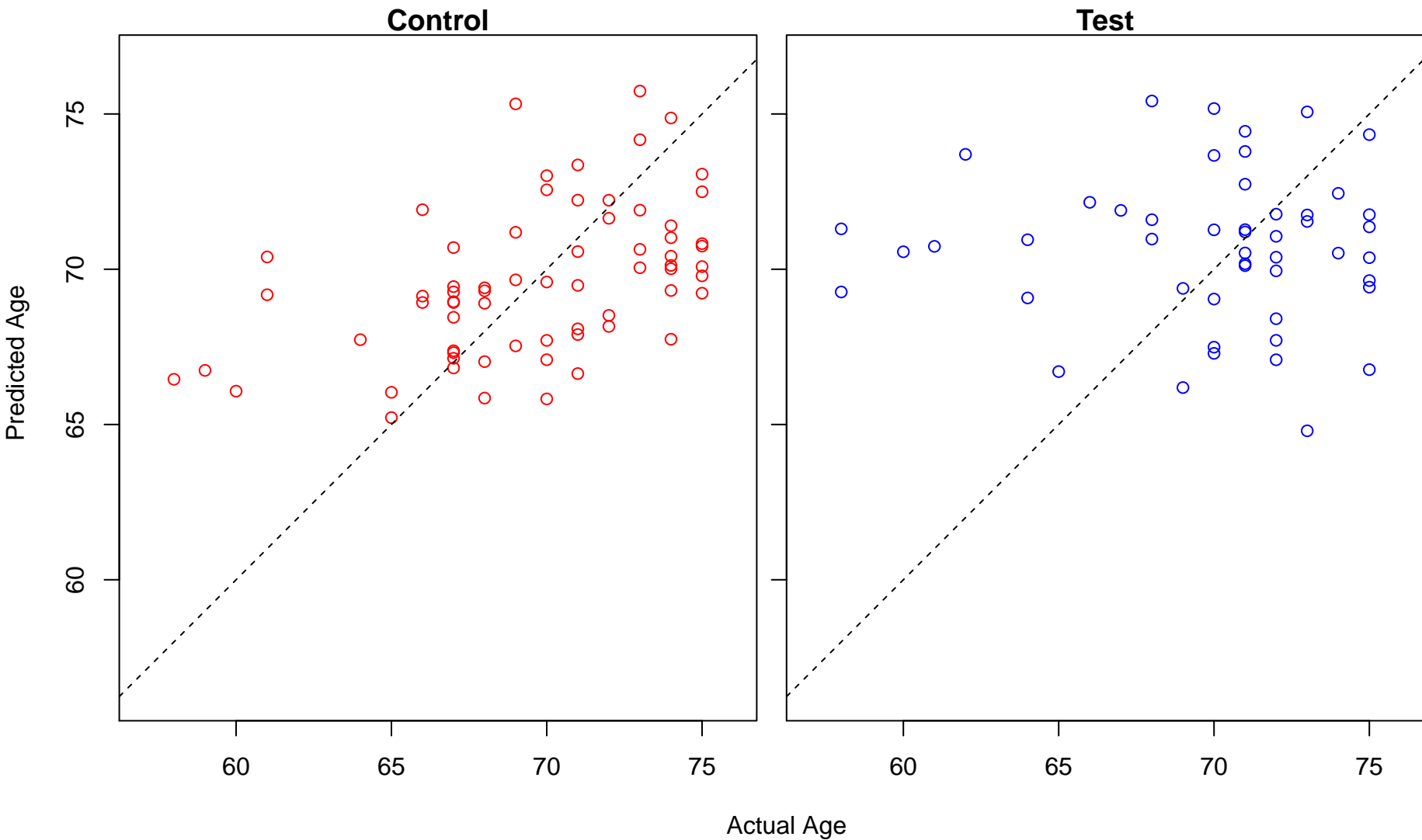
regulation of beta-amyloid clearance (Score: 0.705417)



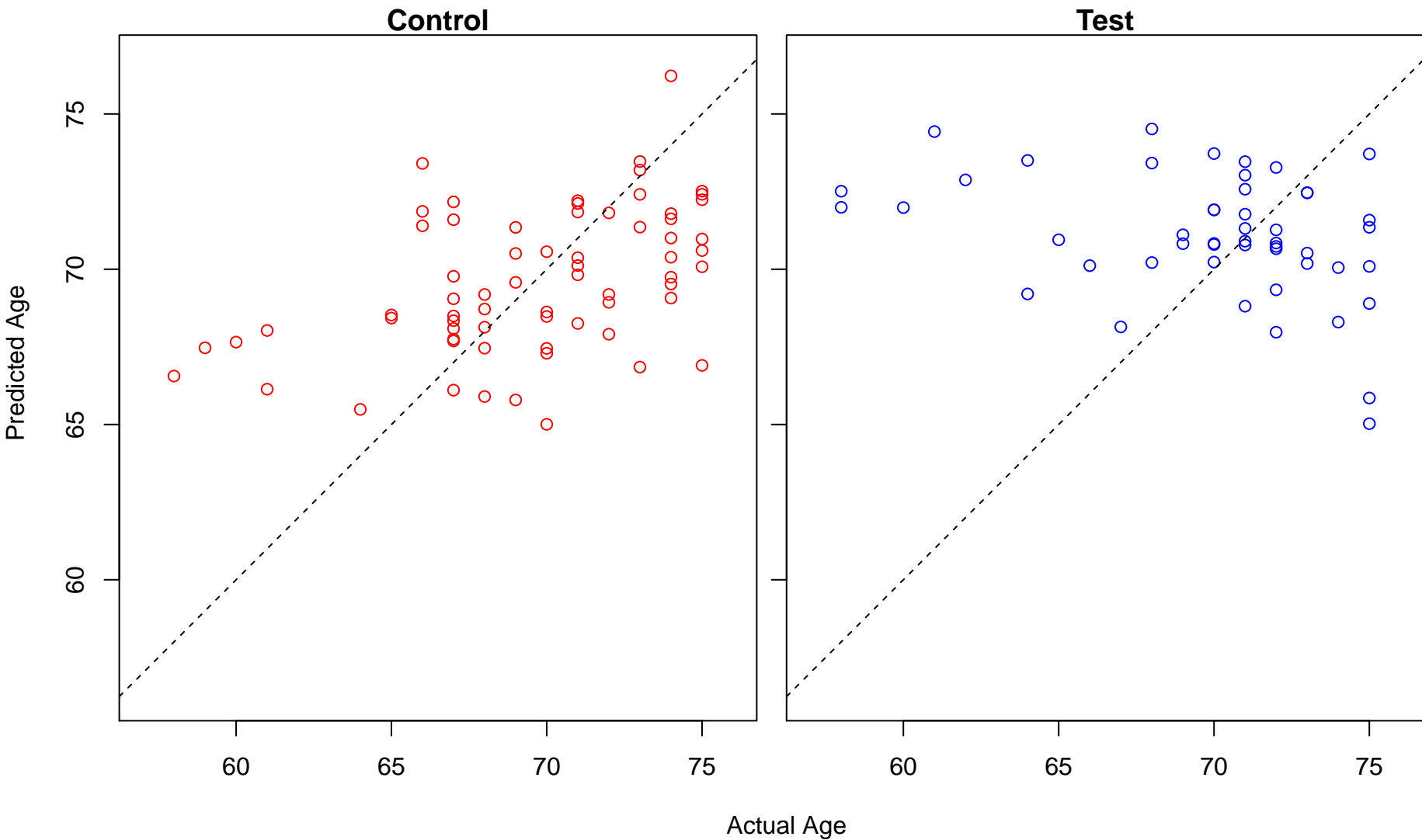
relaxation of cardiac muscle (Score: 0.705375)



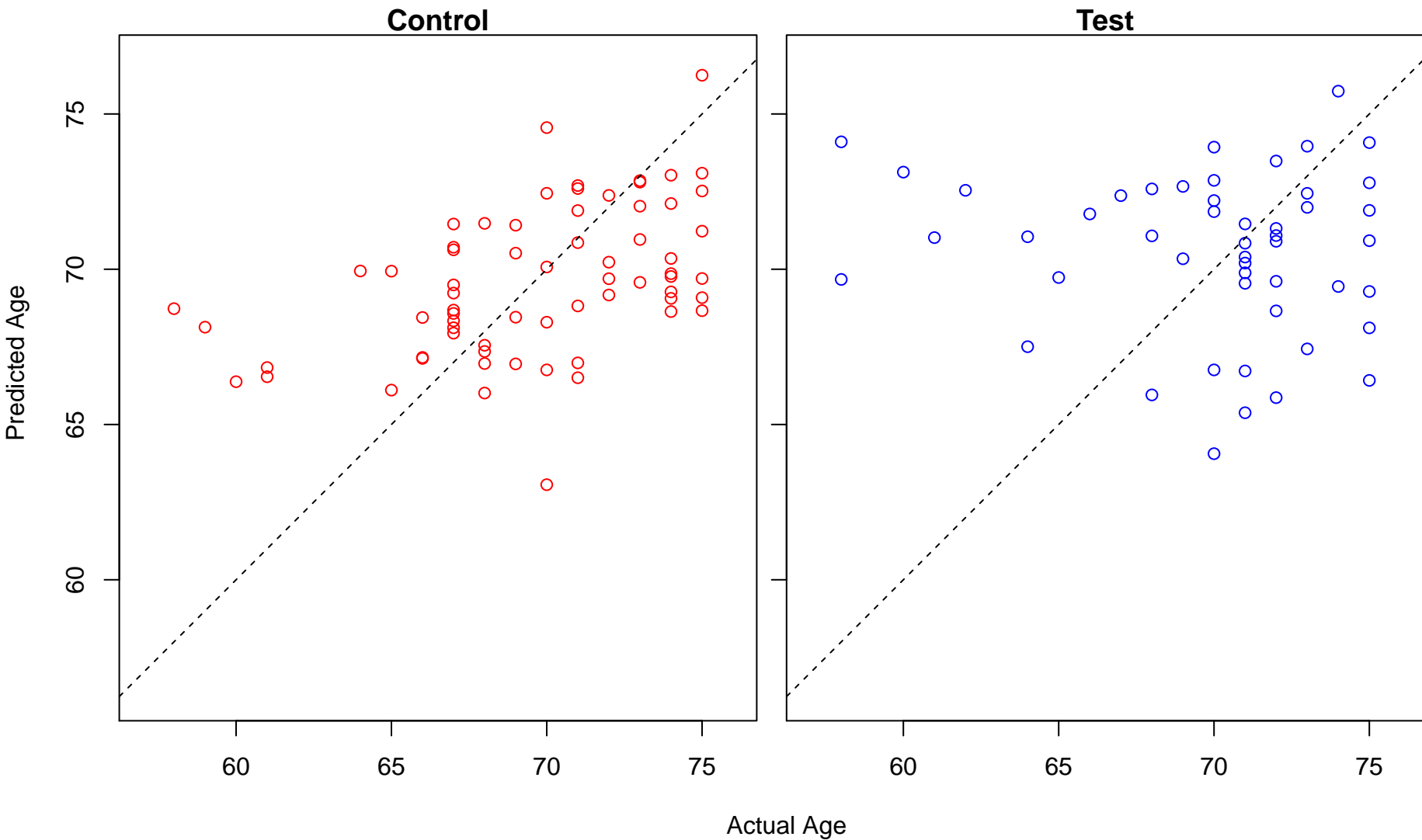
regulation of production of small RNA involved in gene silencing by RNA (Score: 0.705110)



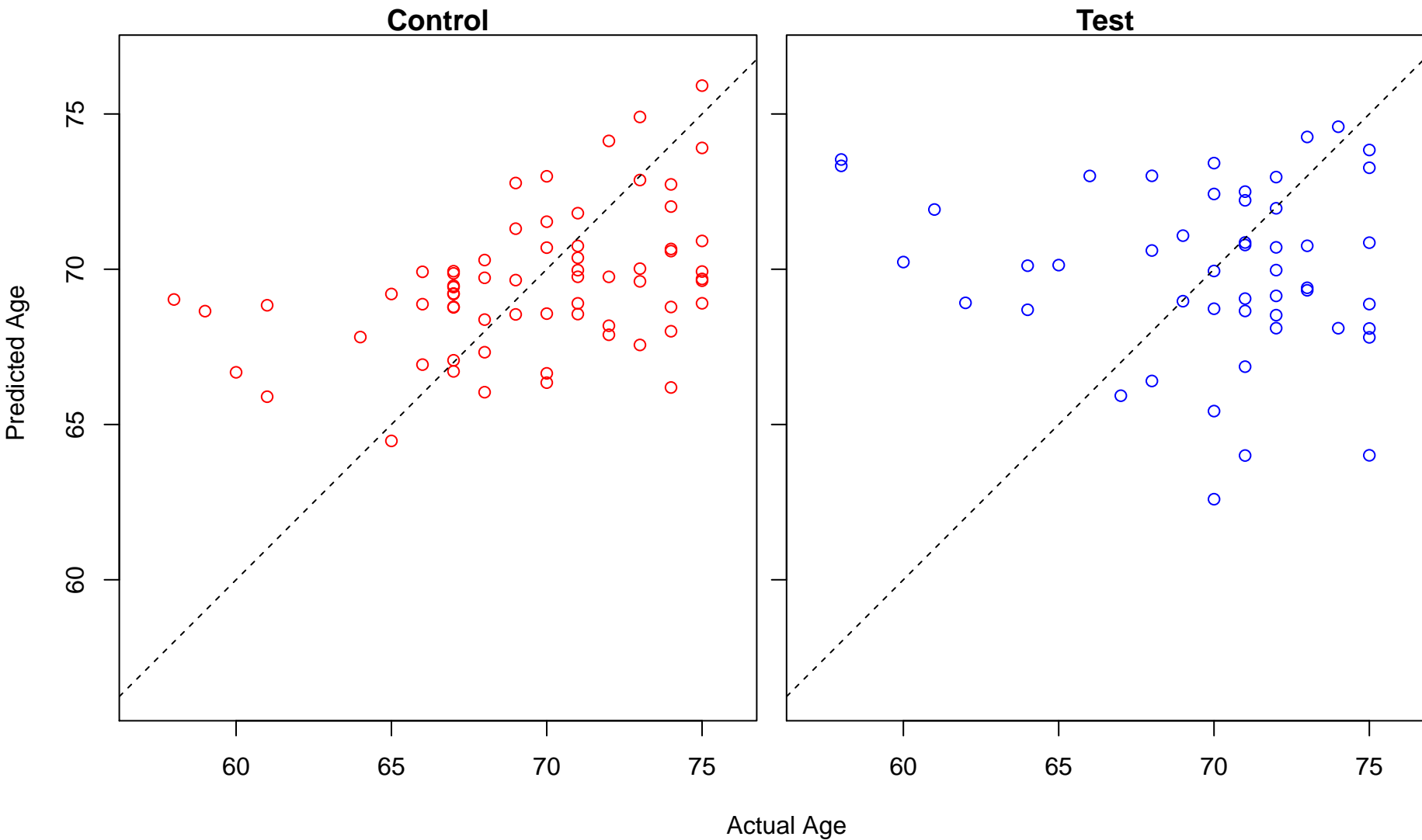
creatine metabolic process (Score: 0.705047)



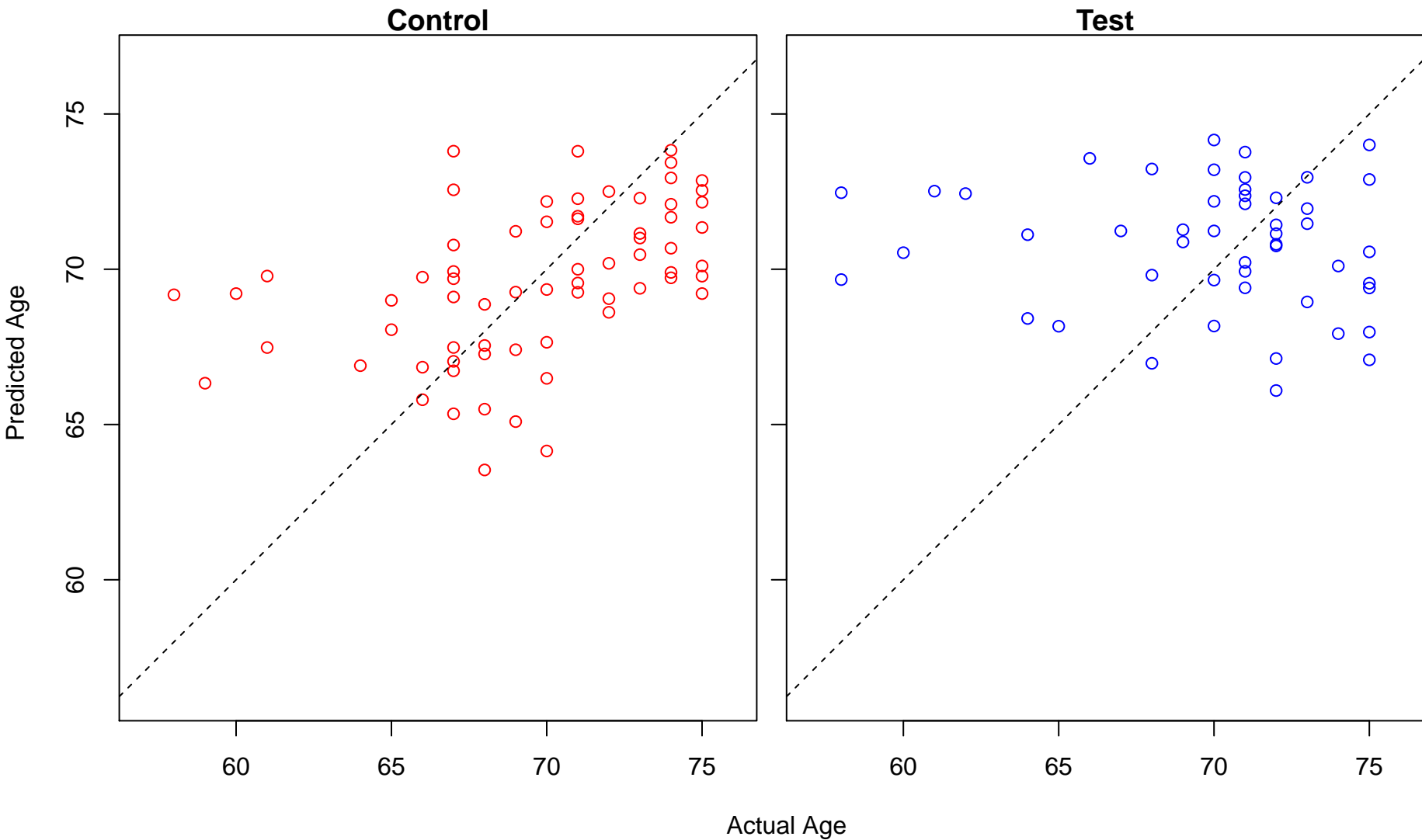
mammary gland morphogenesis (Score: 0.704859)



negative regulation of ERAD pathway (Score: 0.704187)

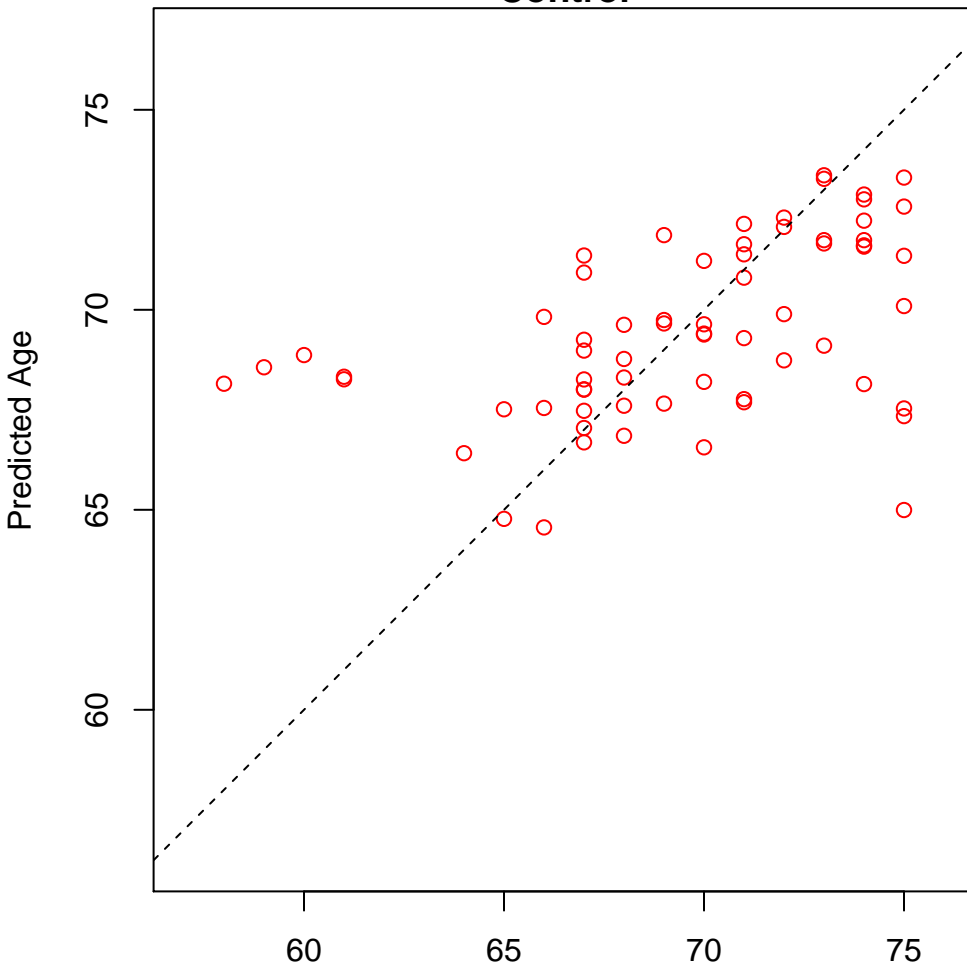


attachment of spindle microtubules to kinetochore (Score: 0.704094)

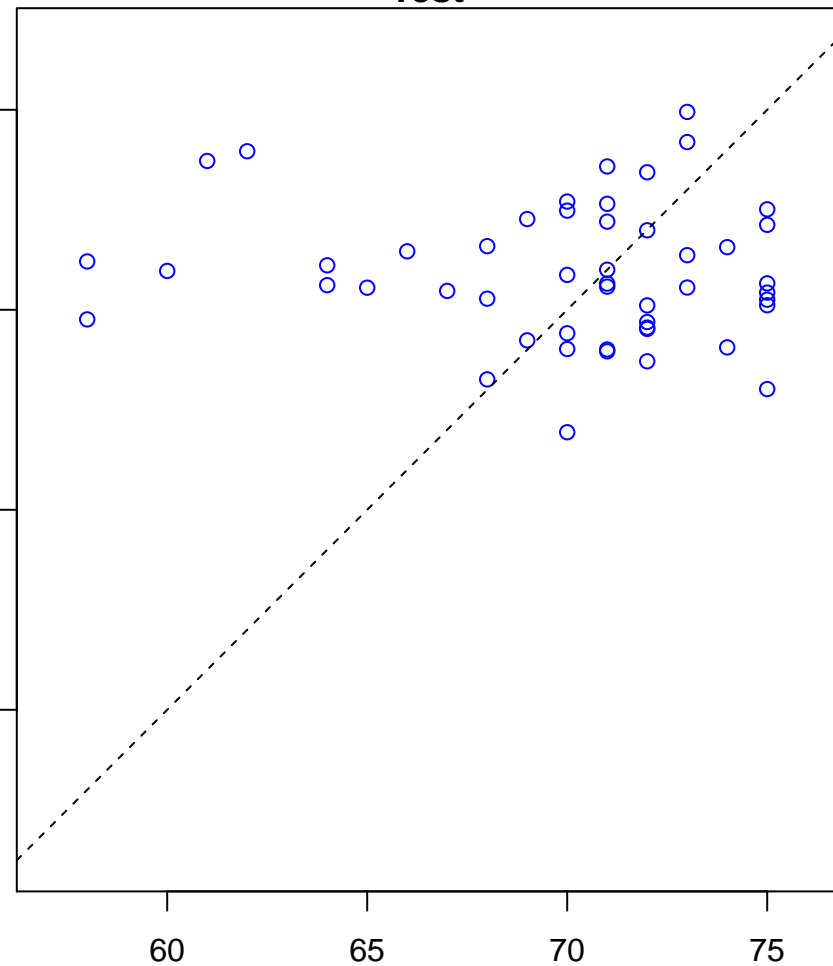


positive regulation of cholesterol efflux (Score: 0.703706)

Control

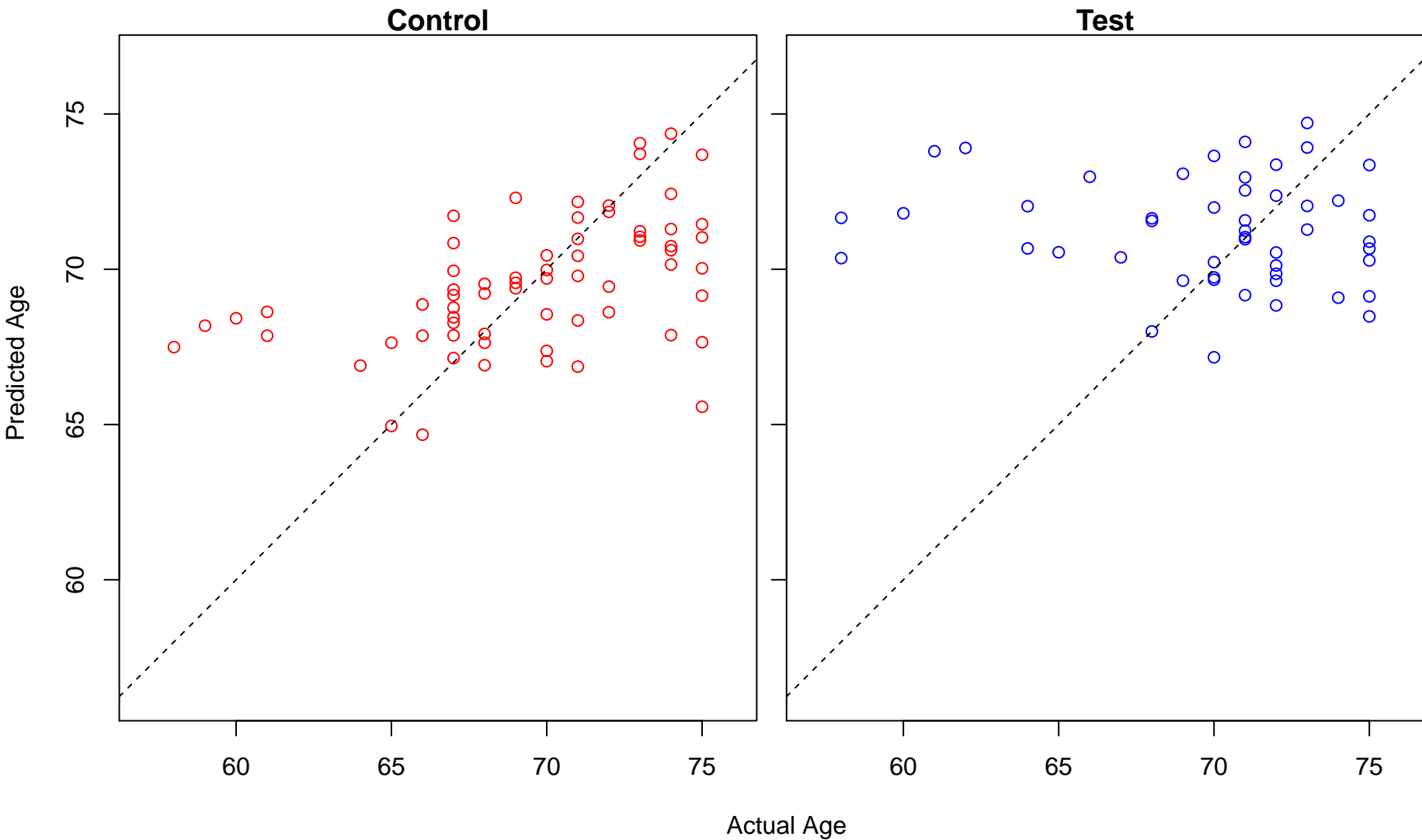


Test

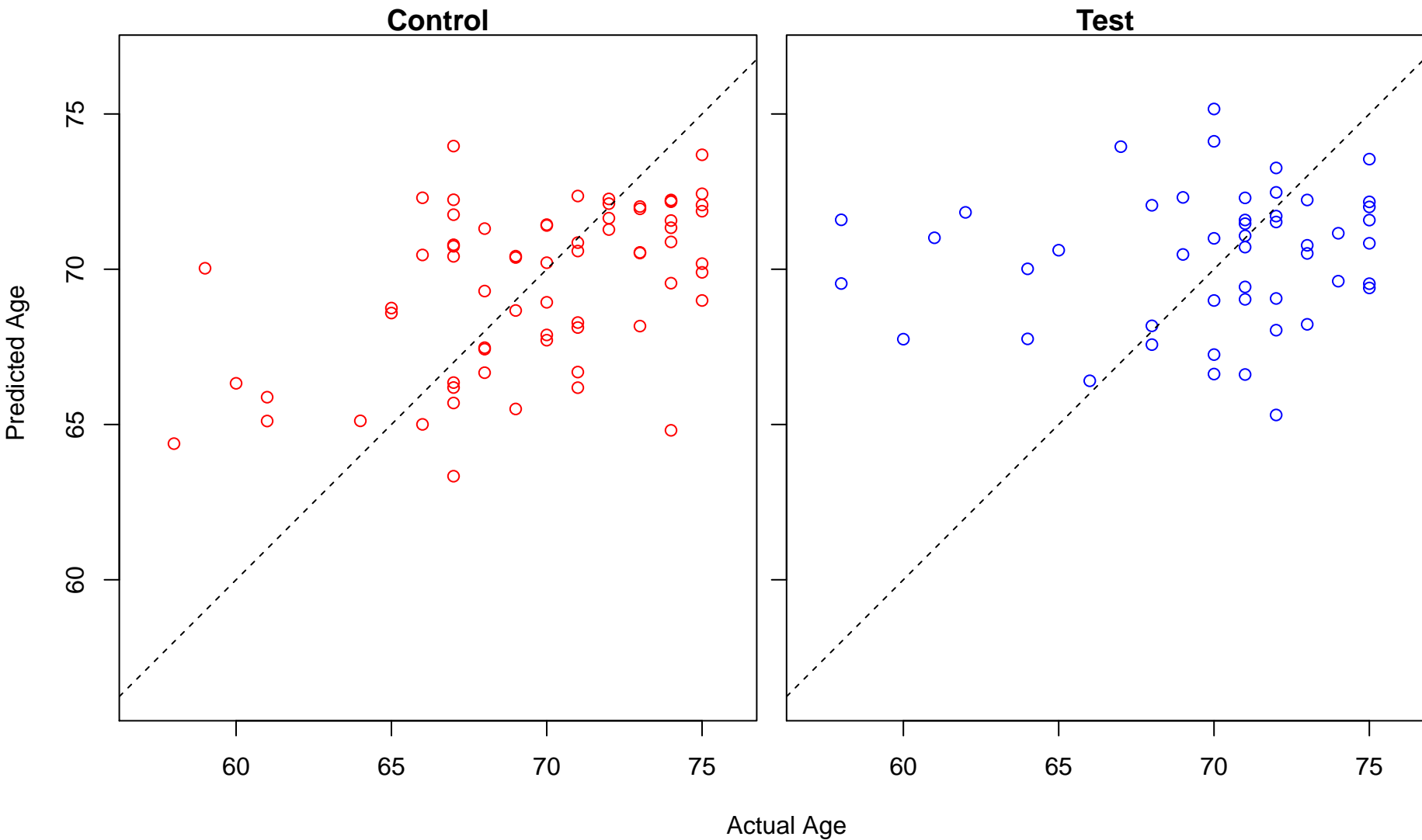


Actual Age

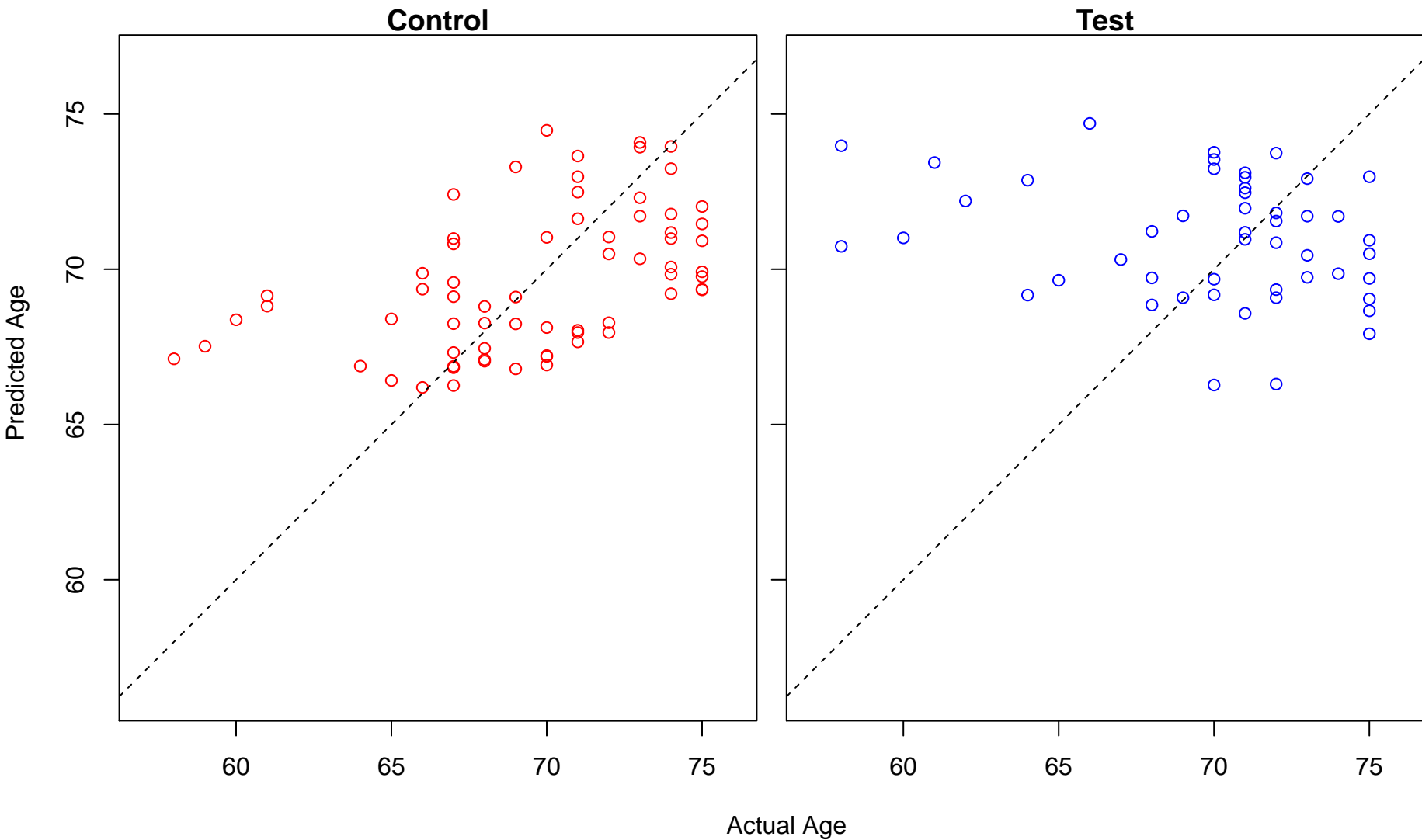
positive regulation of phagocytosis, engulfment (Score: 0.703299)



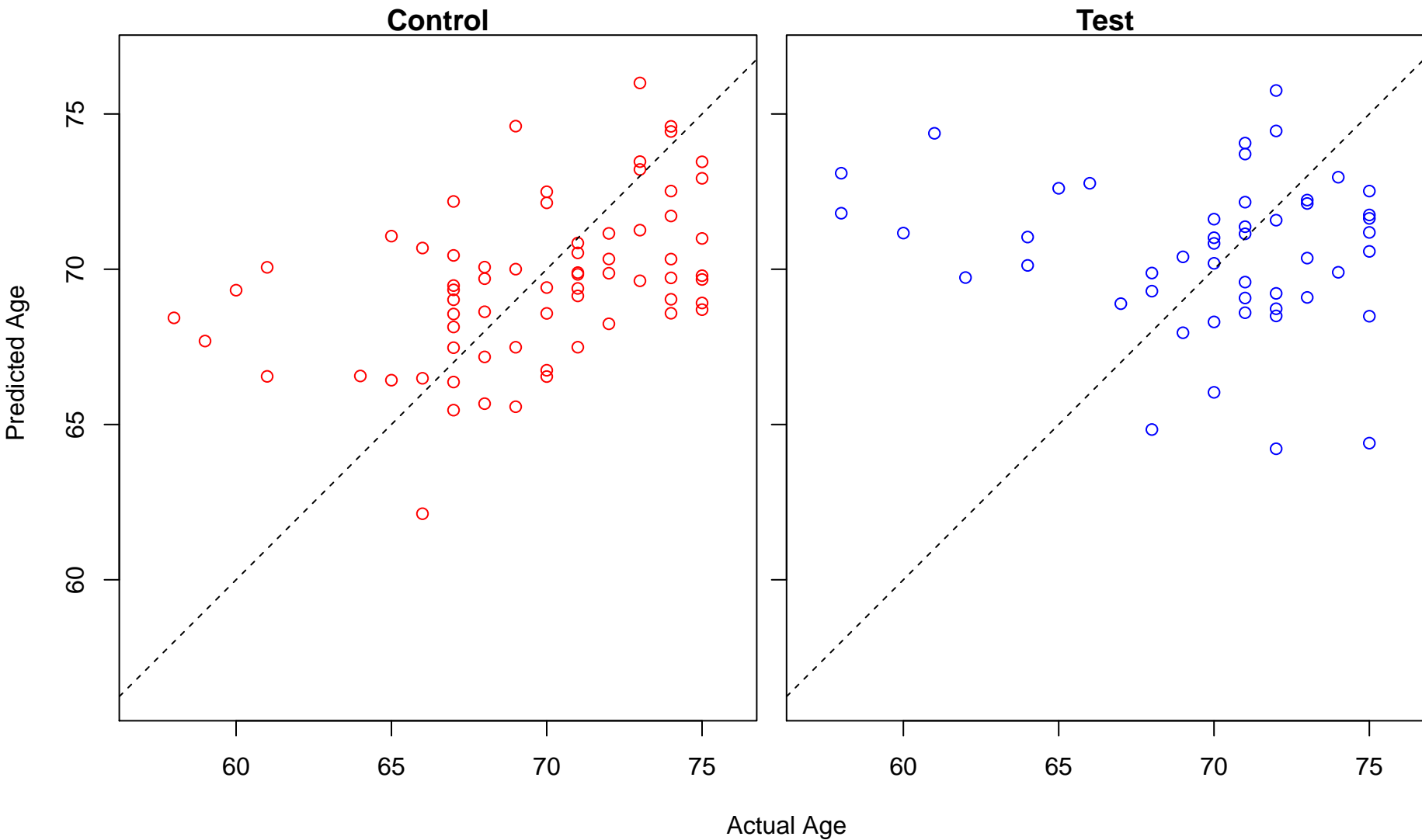
regulation of cardiac muscle cell action potential (Score: 0.702417)



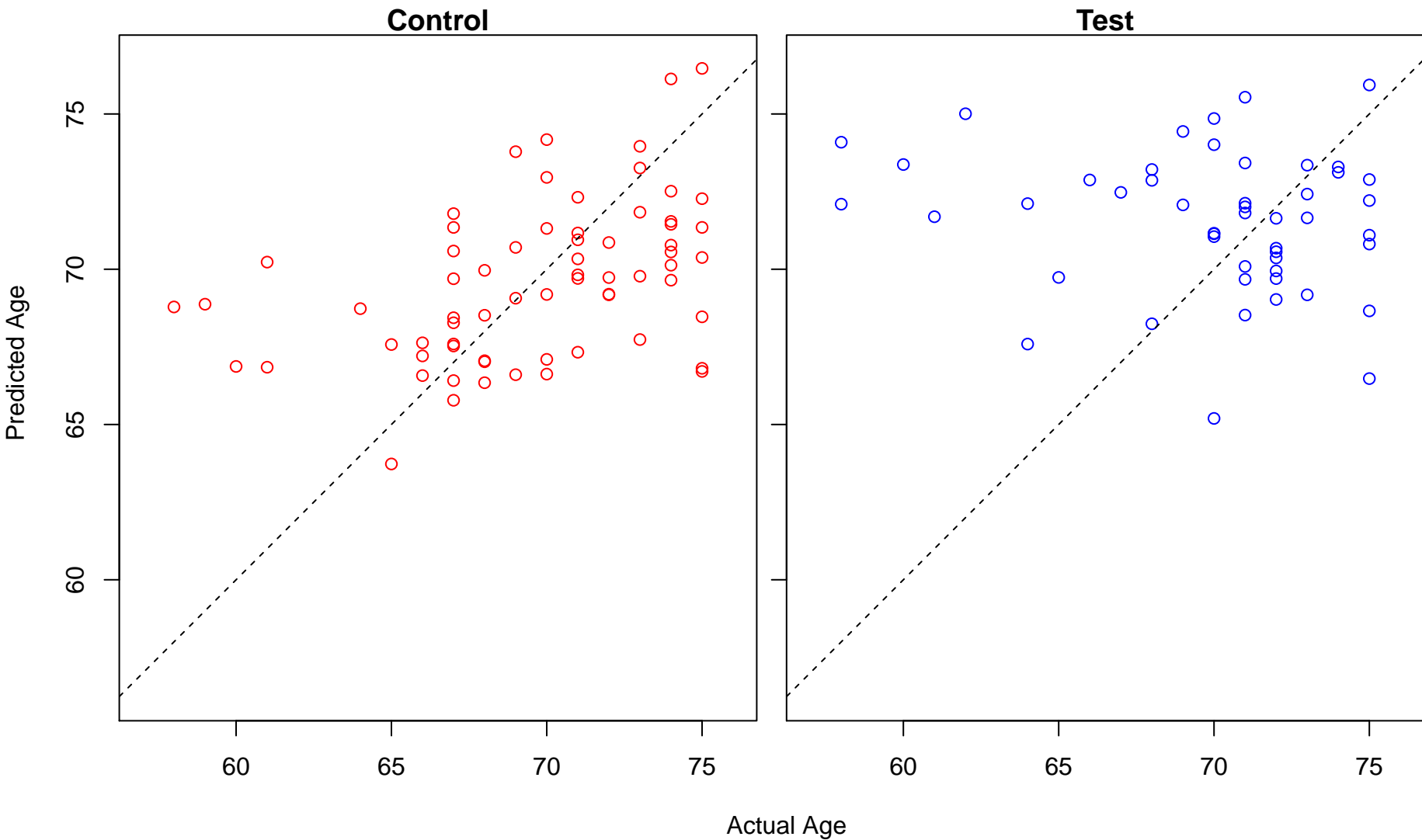
granulocyte activation (Score: 0.702120)



cell-cell signaling involved in cardiac conduction (Score: 0.701557)

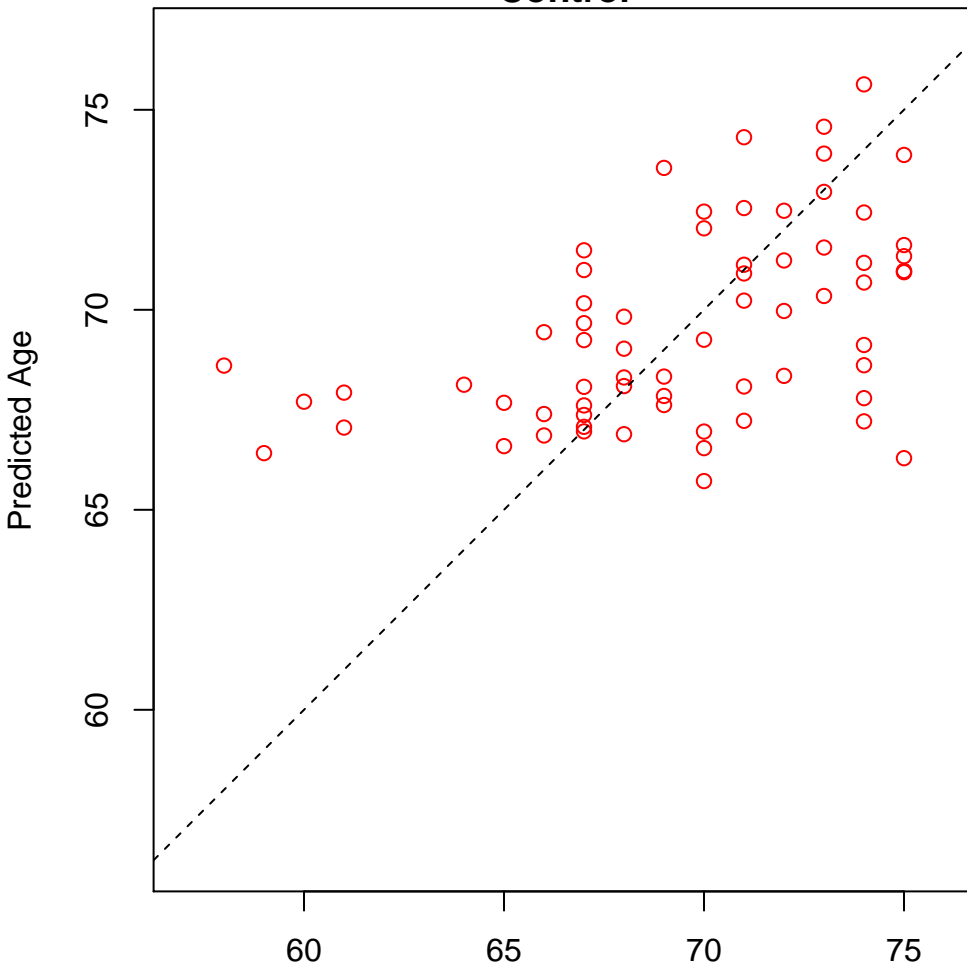


acid secretion (Score: 0.700707)

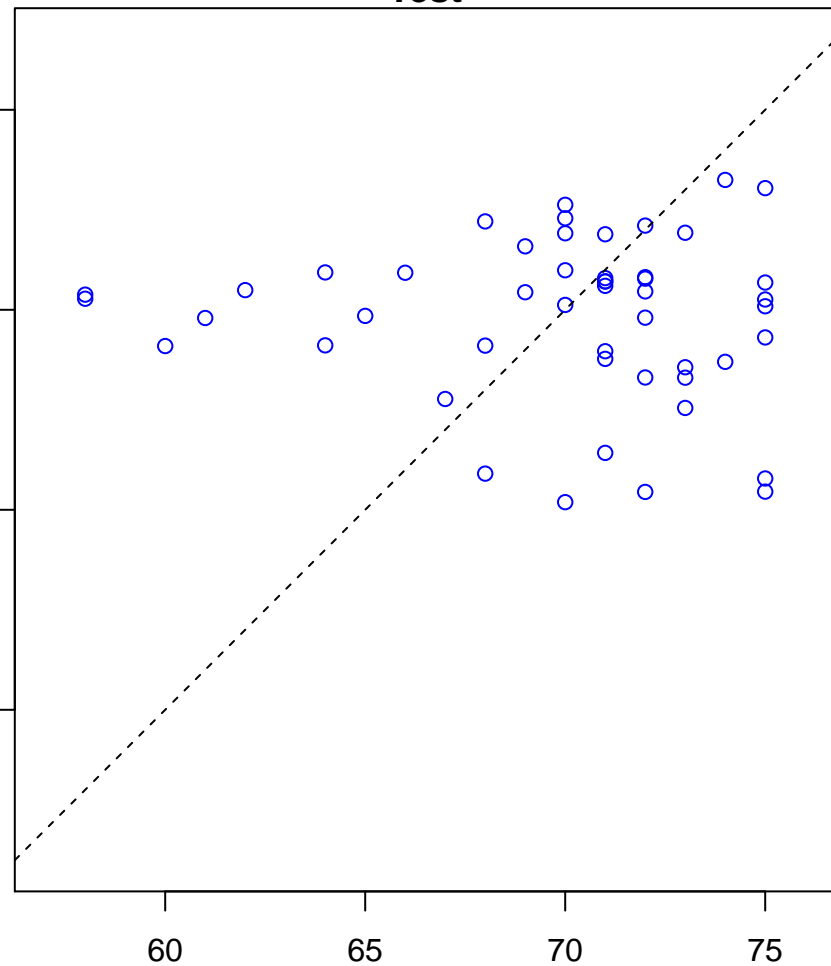


peptidyl-L-cysteine S-palmitoylation (Score: 0.700400)

Control

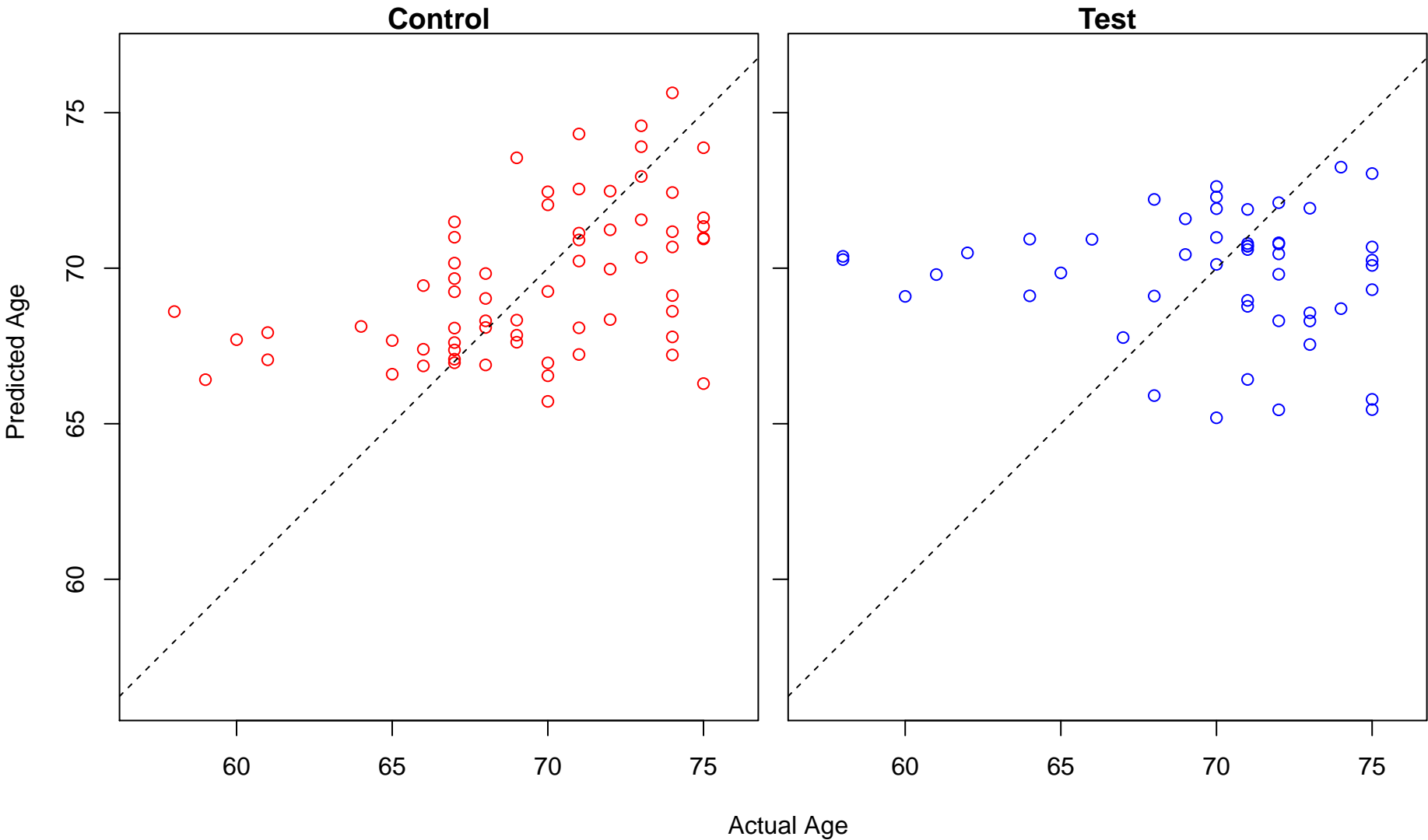


Test

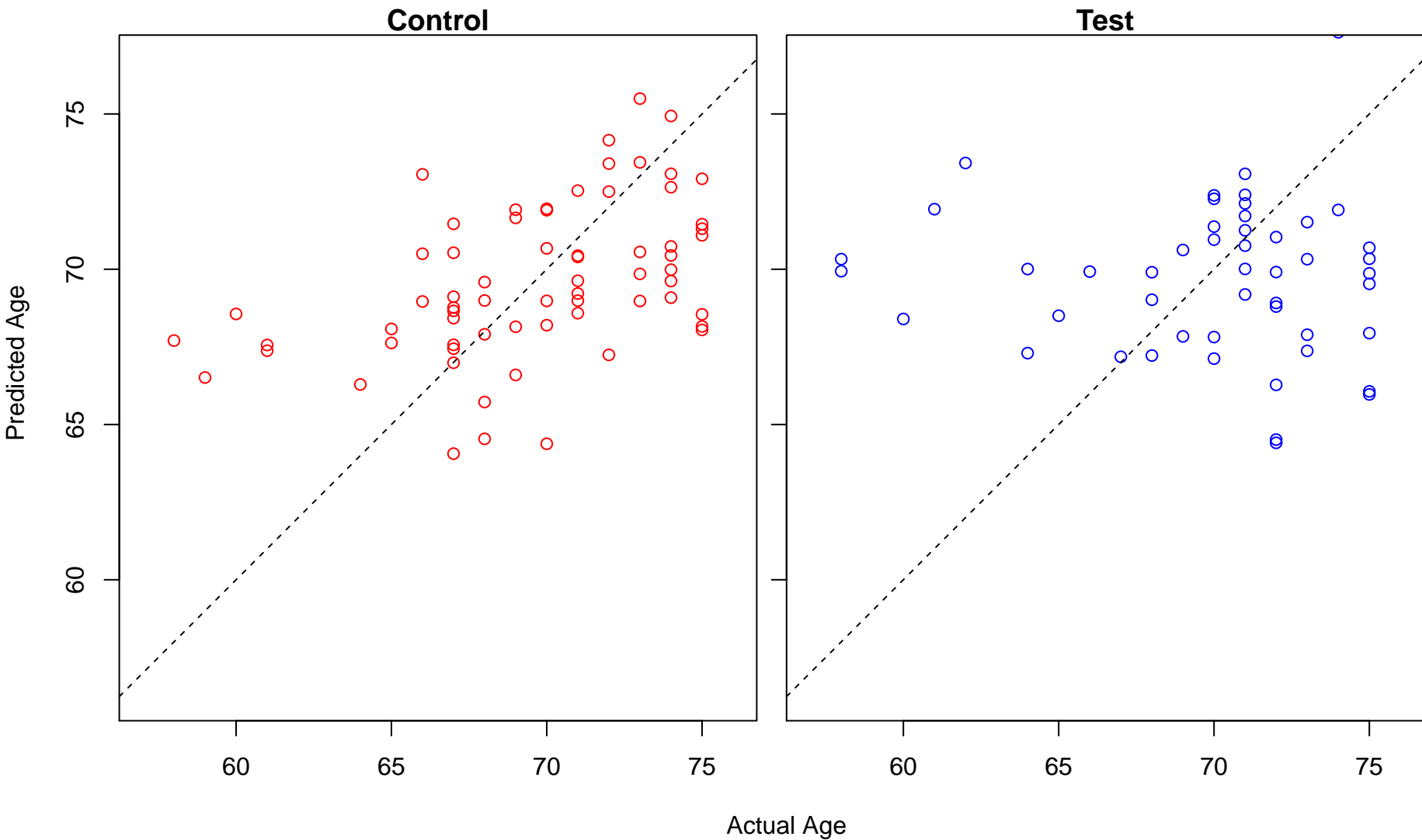


Actual Age

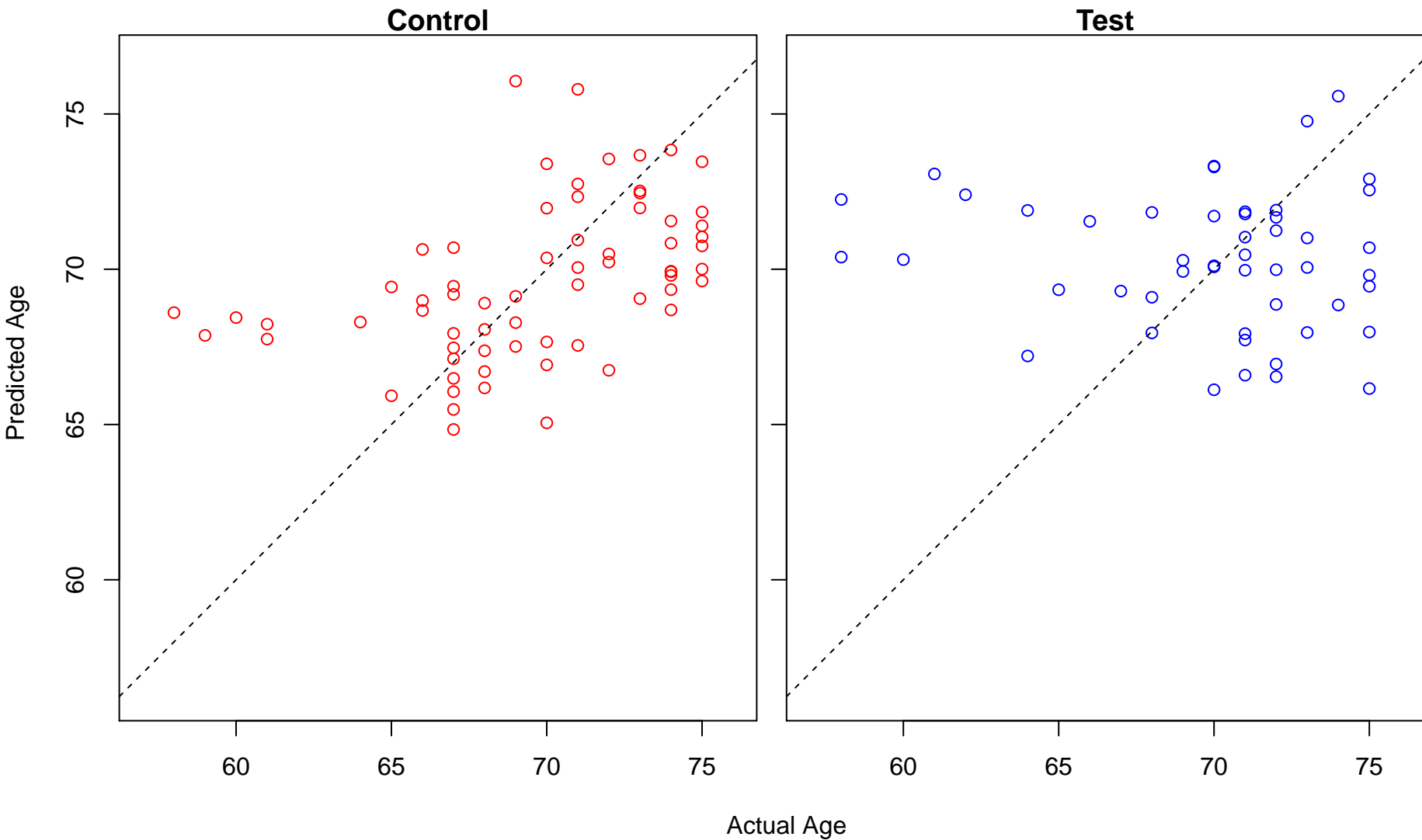
peptidyl-S-diacylglycerol-L-cysteine biosynthetic process from peptidyl-cysteine (Score: 0.70040)



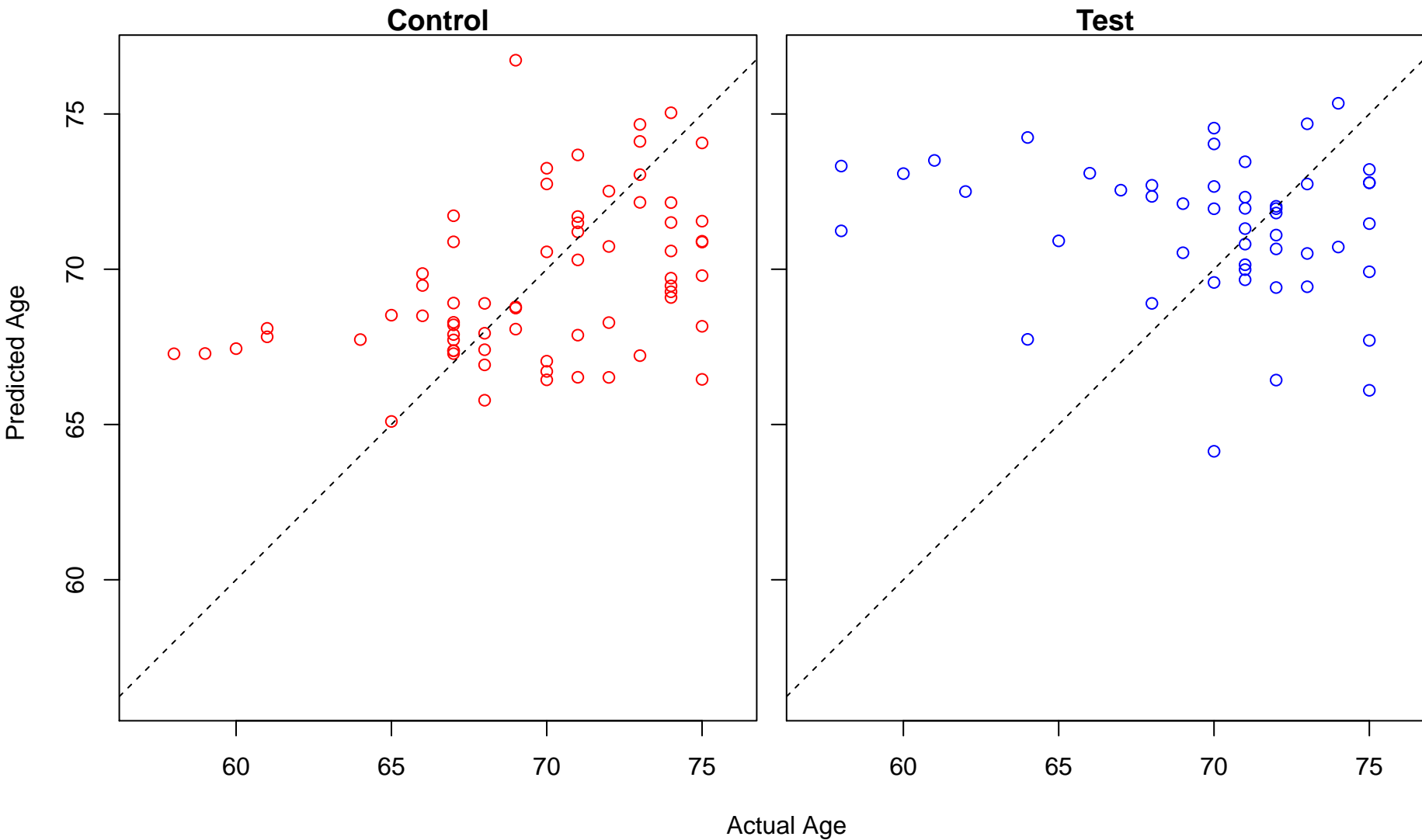
positive regulation of regulatory T cell differentiation (Score: 0.699935)



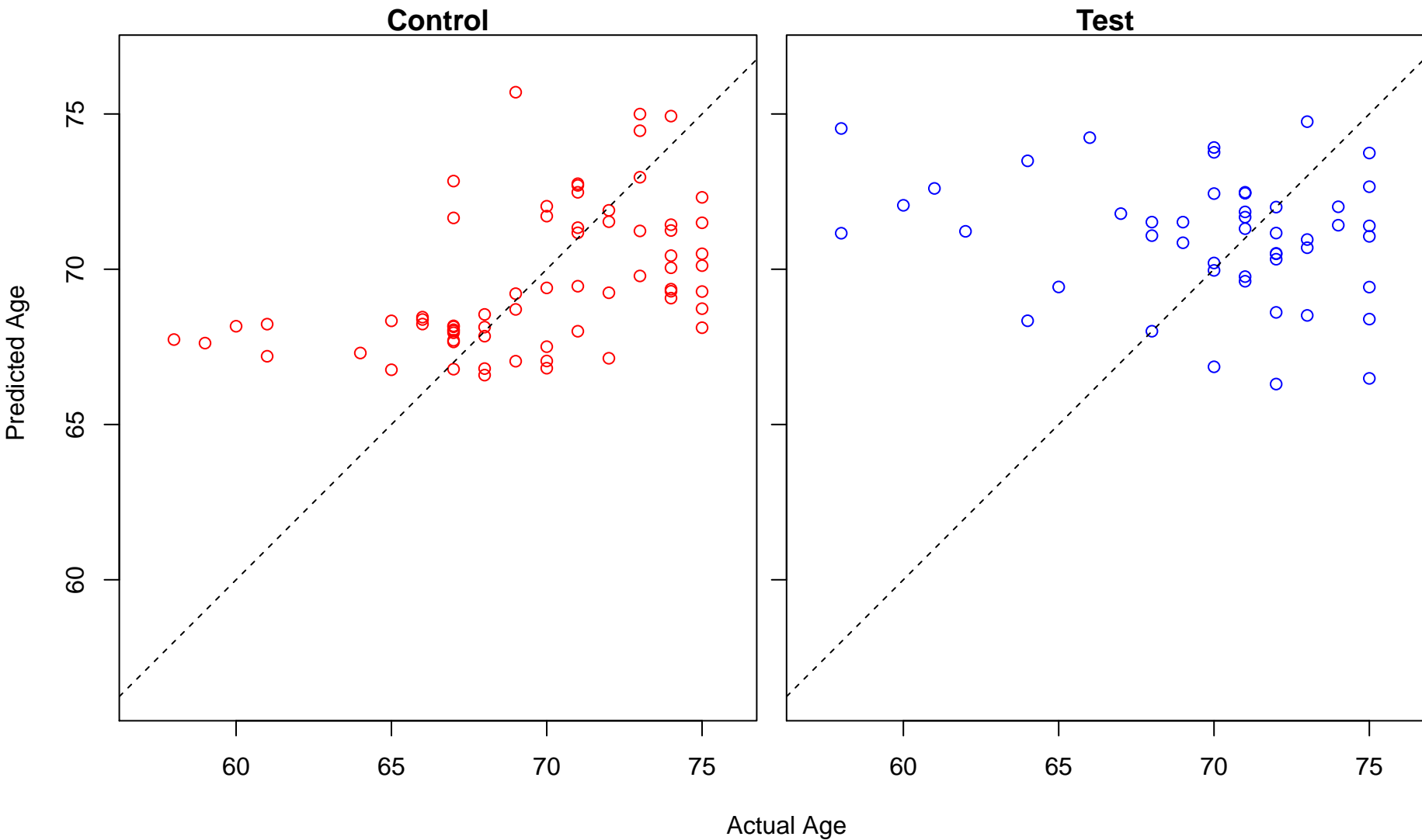
cytoplasmic sequestering of transcription factor (Score: 0.698812)



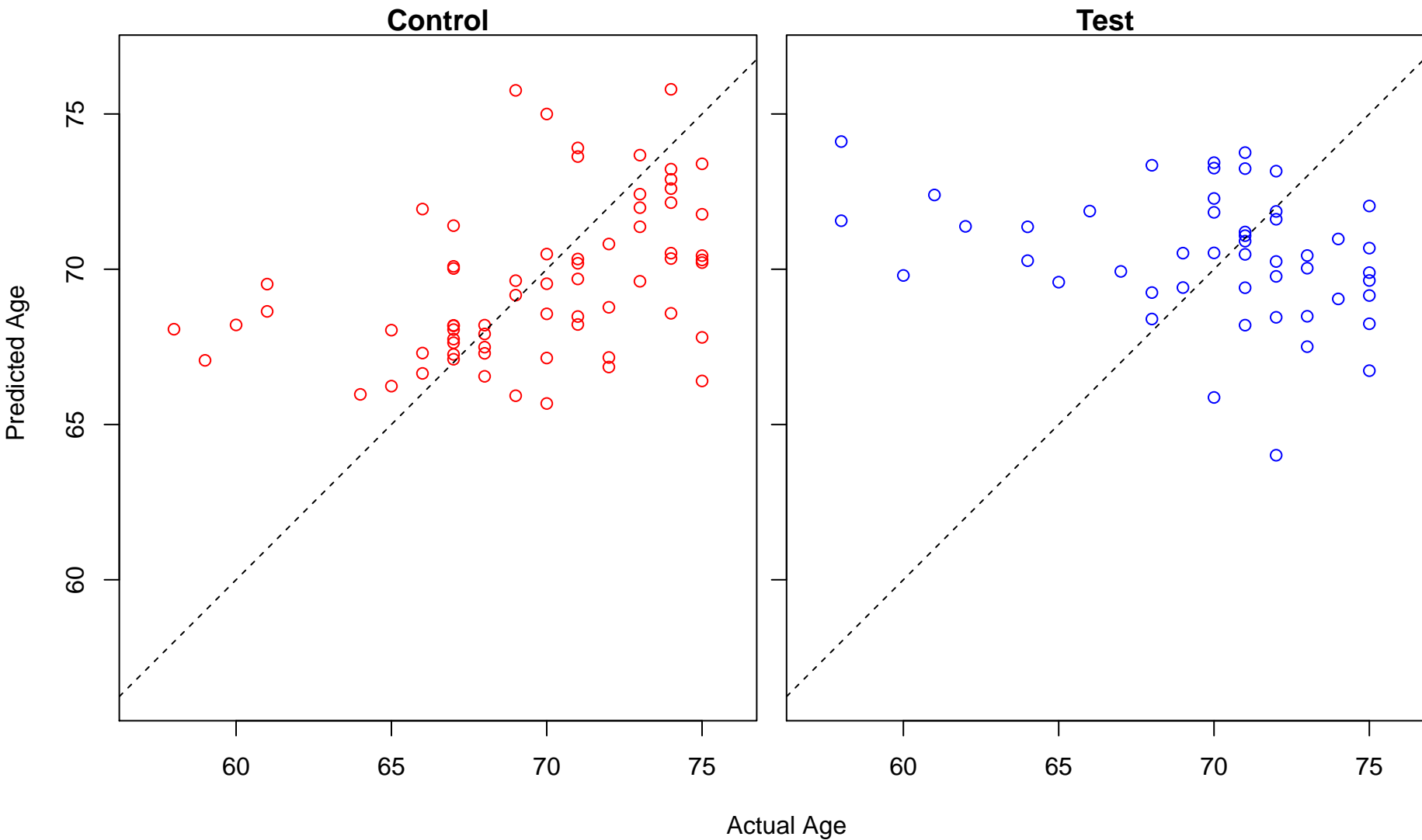
negative regulation of mitochondrion organization (Score: 0.698771)



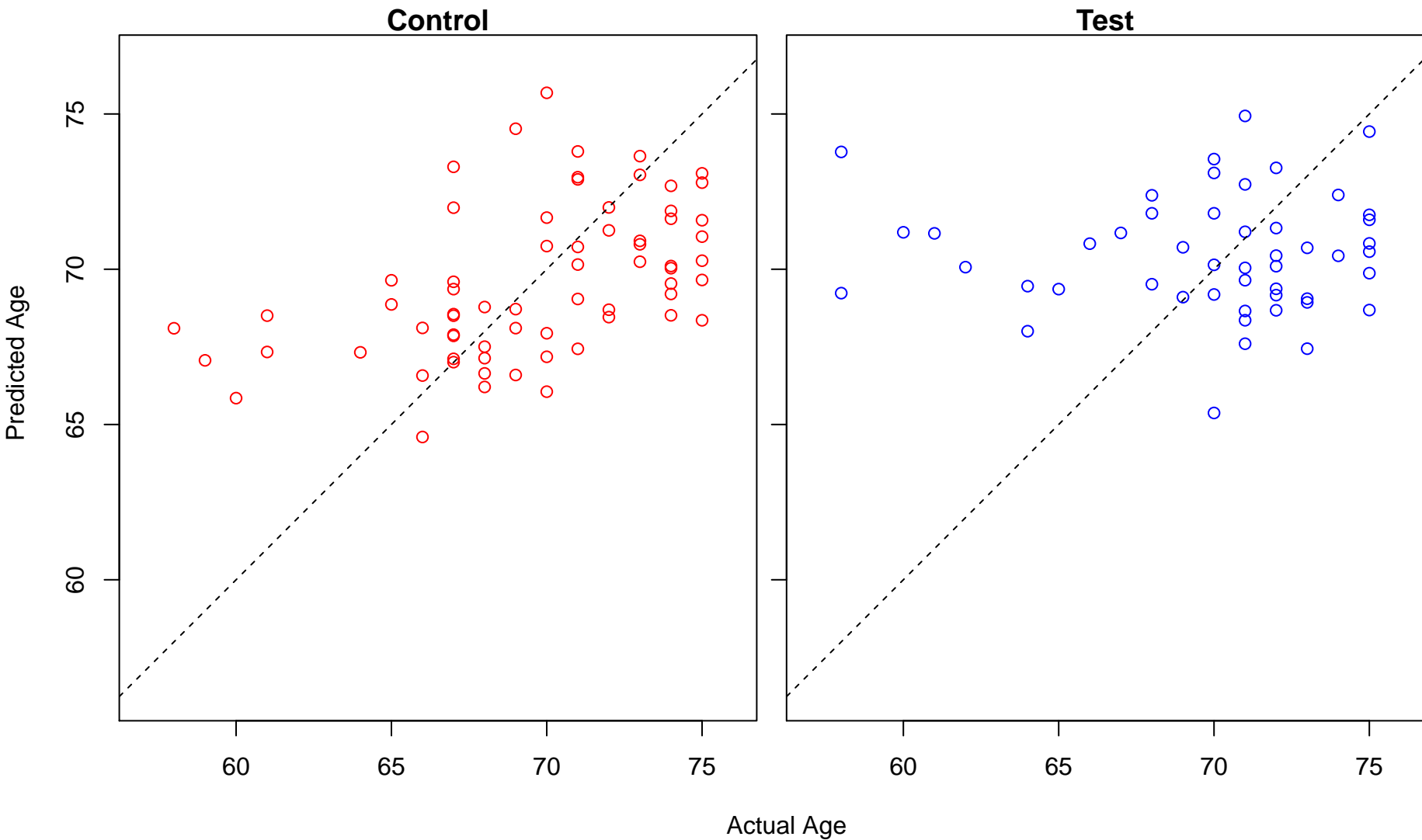
negative regulation of NF-kappaB import into nucleus (Score: 0.698563)



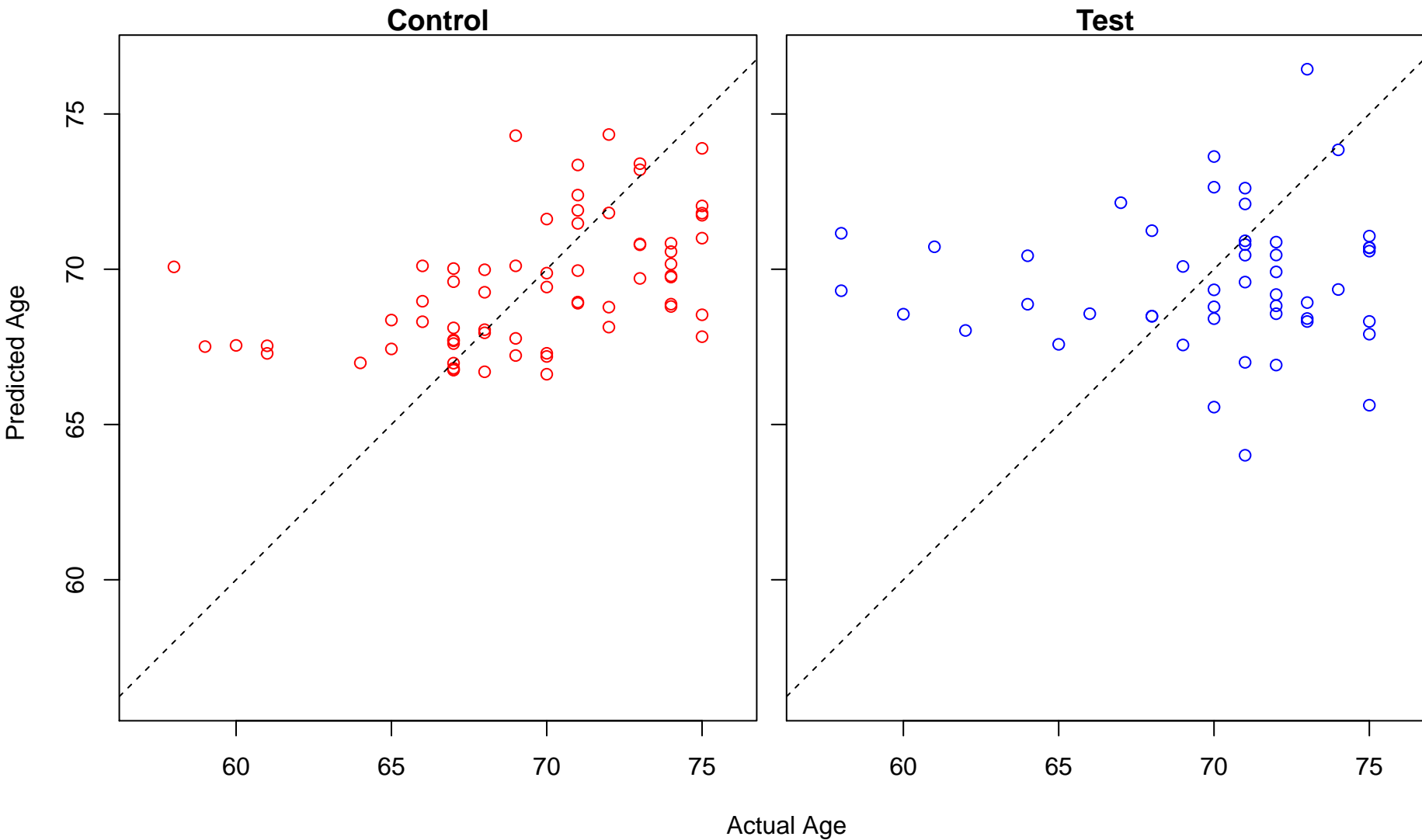
regulation of kidney development (Score: 0.698215)



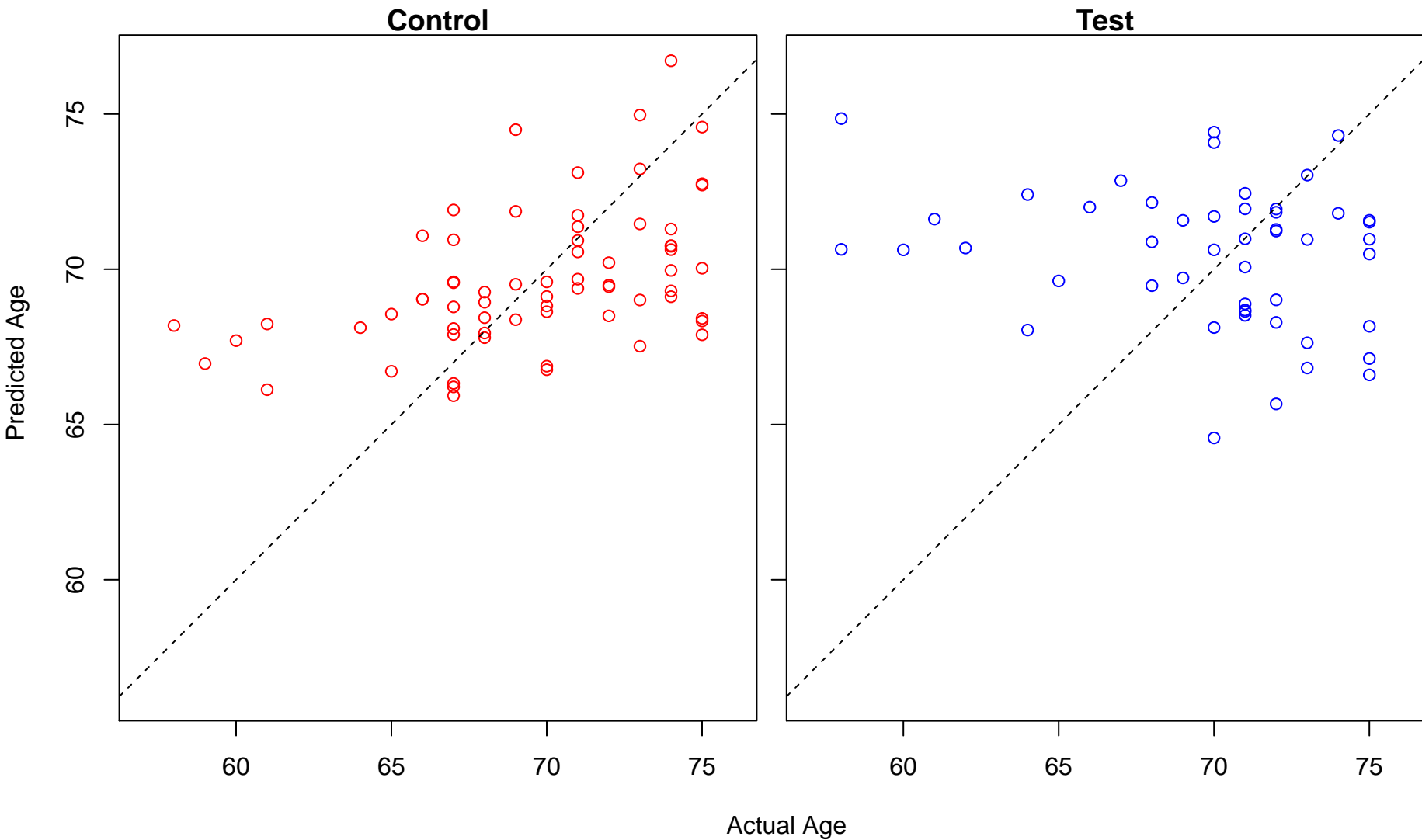
regulation of lipid kinase activity (Score: 0.697824)



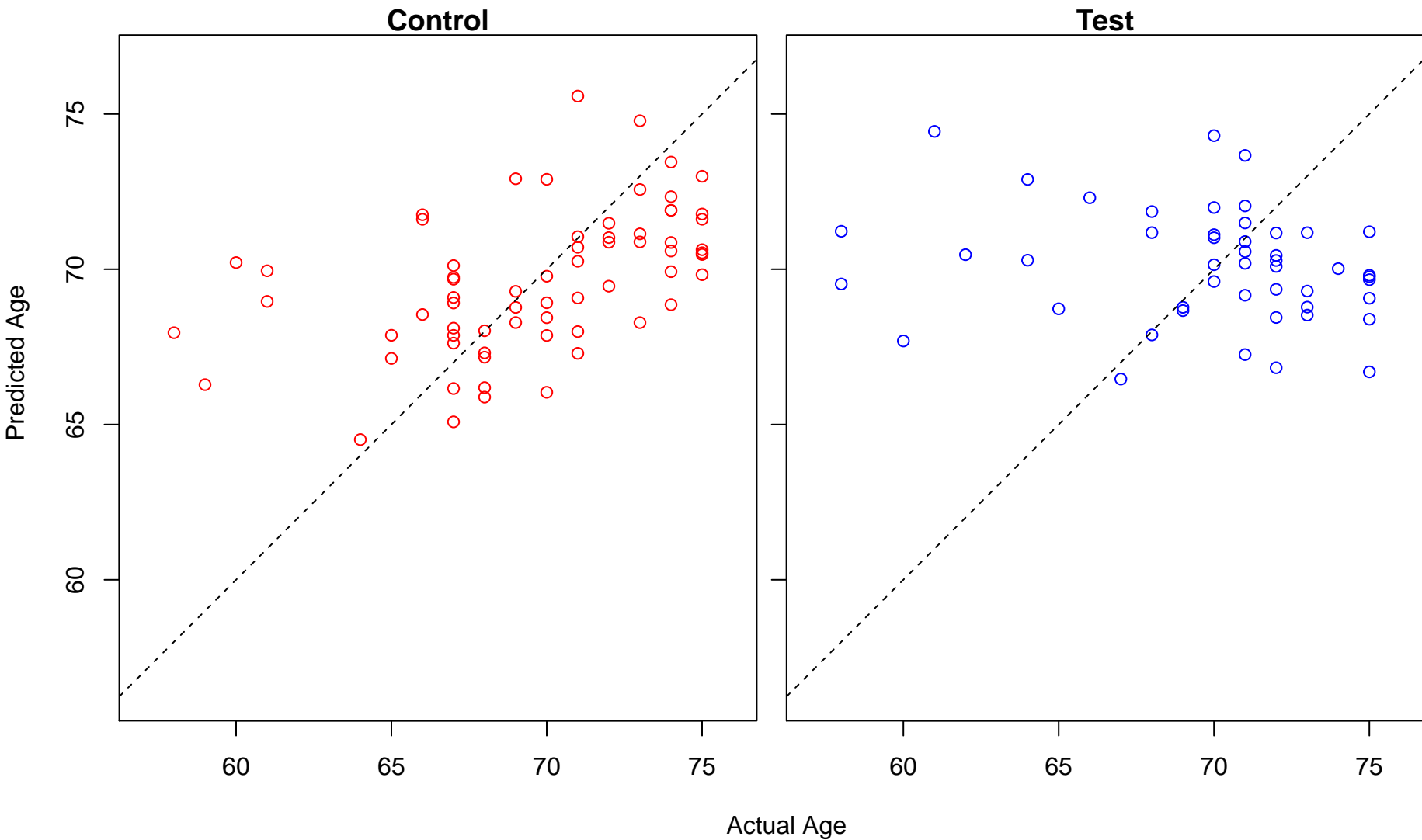
regulation of peptidyl–threonine phosphorylation (Score: 0.697045)



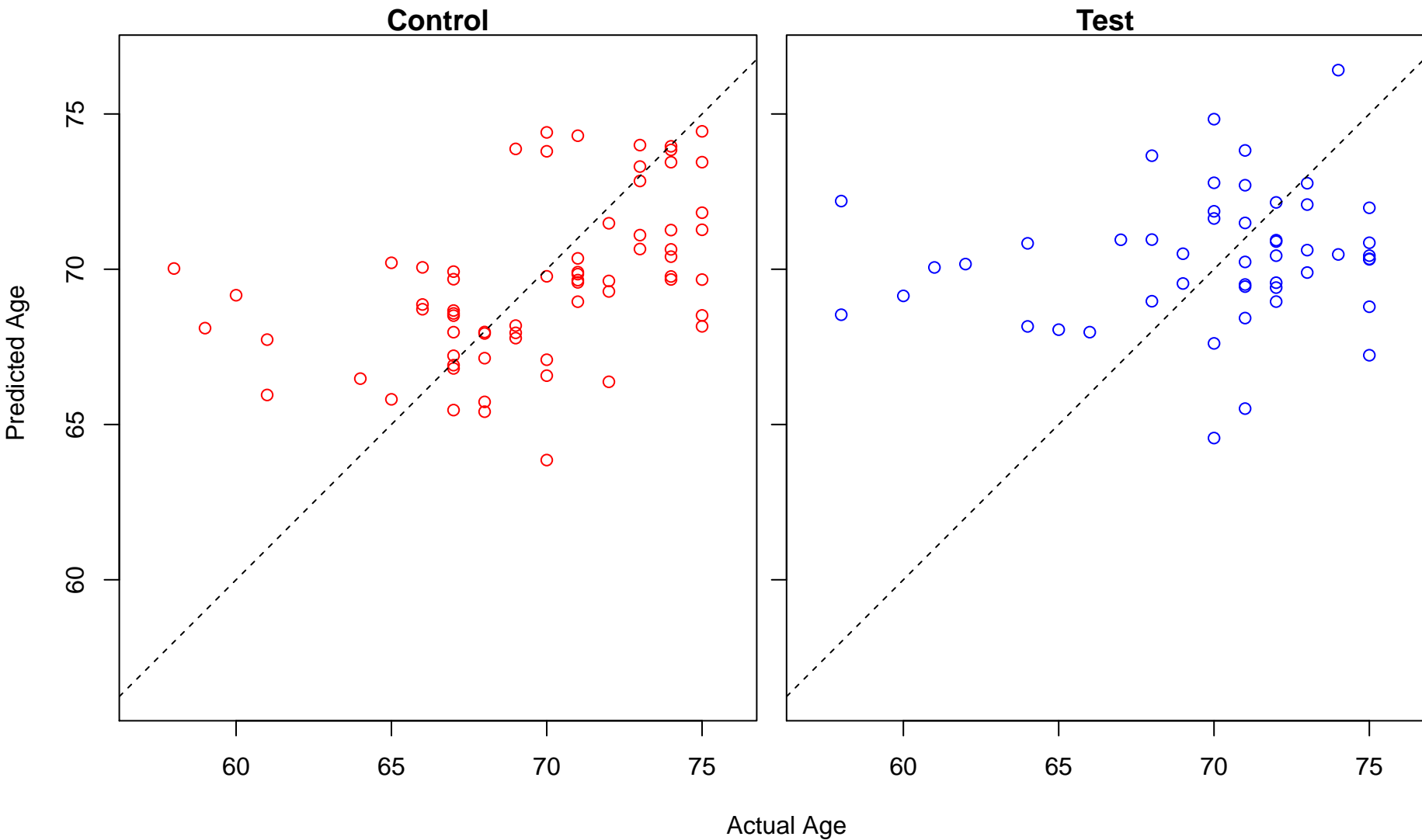
telomere maintenance in response to DNA damage (Score: 0.696187)



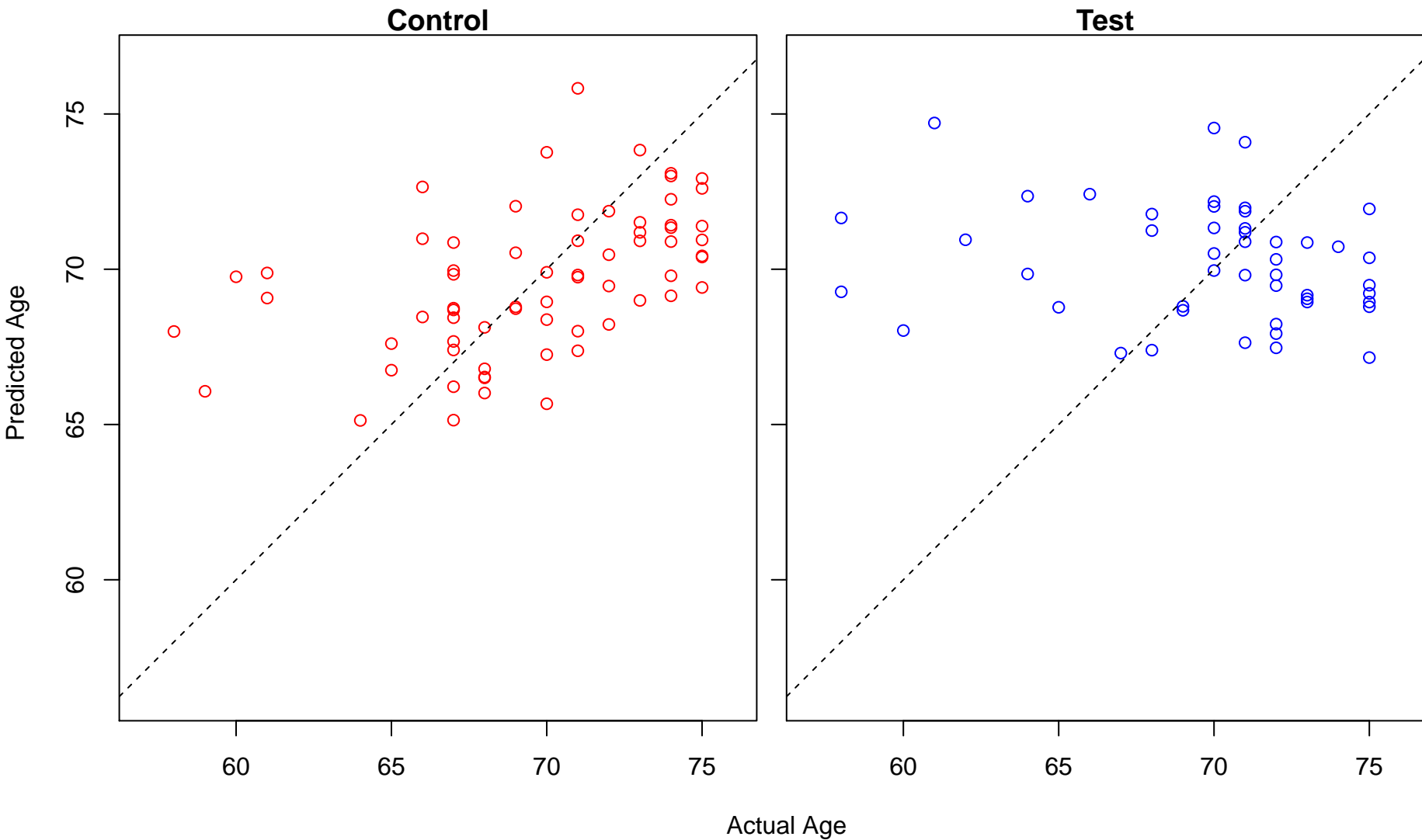
Negative regulation of single stranded viral RNA replication via double stranded DNA intermediate (Score: 0.00)



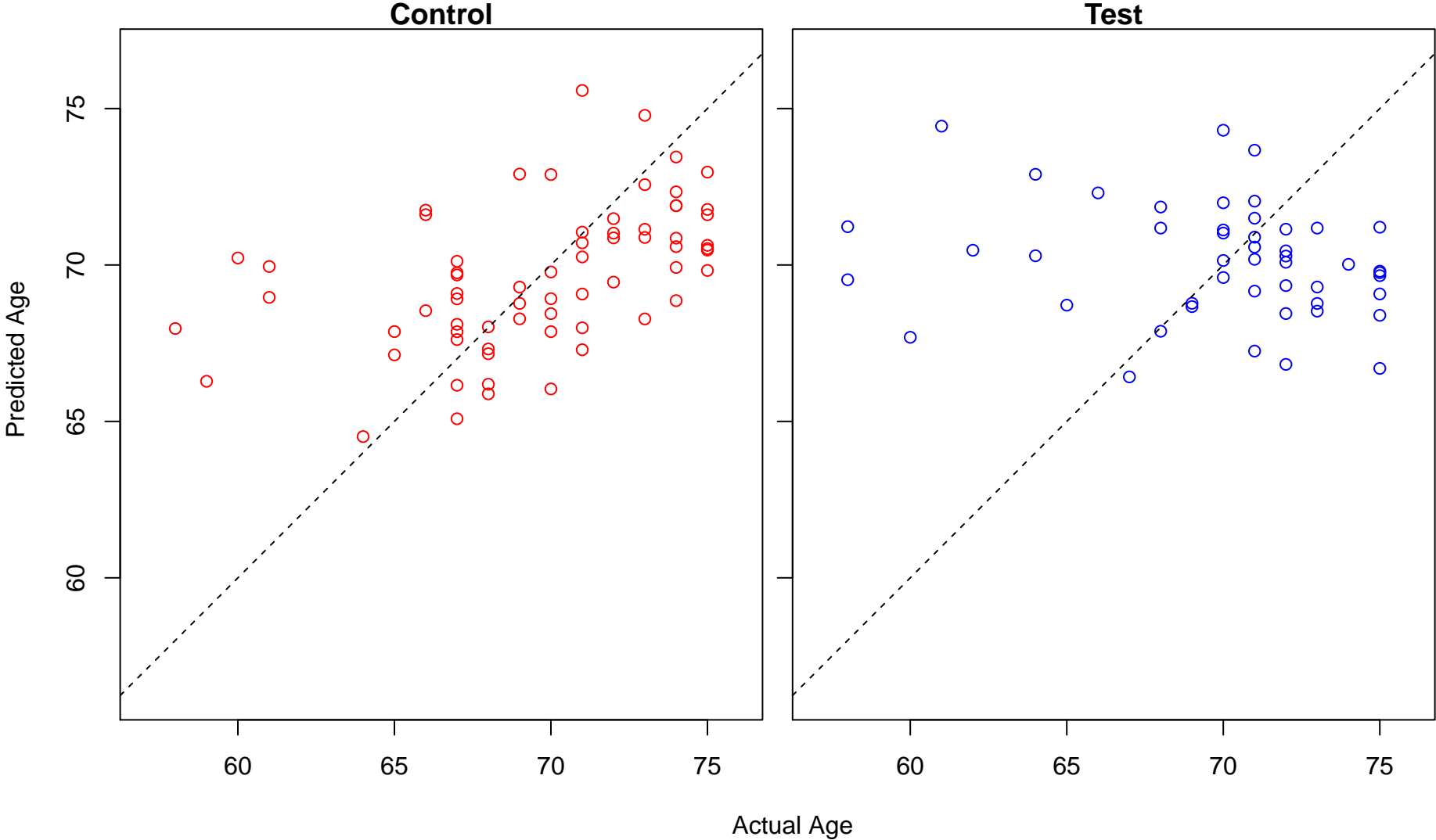
somatic stem cell population maintenance (Score: 0.694667)



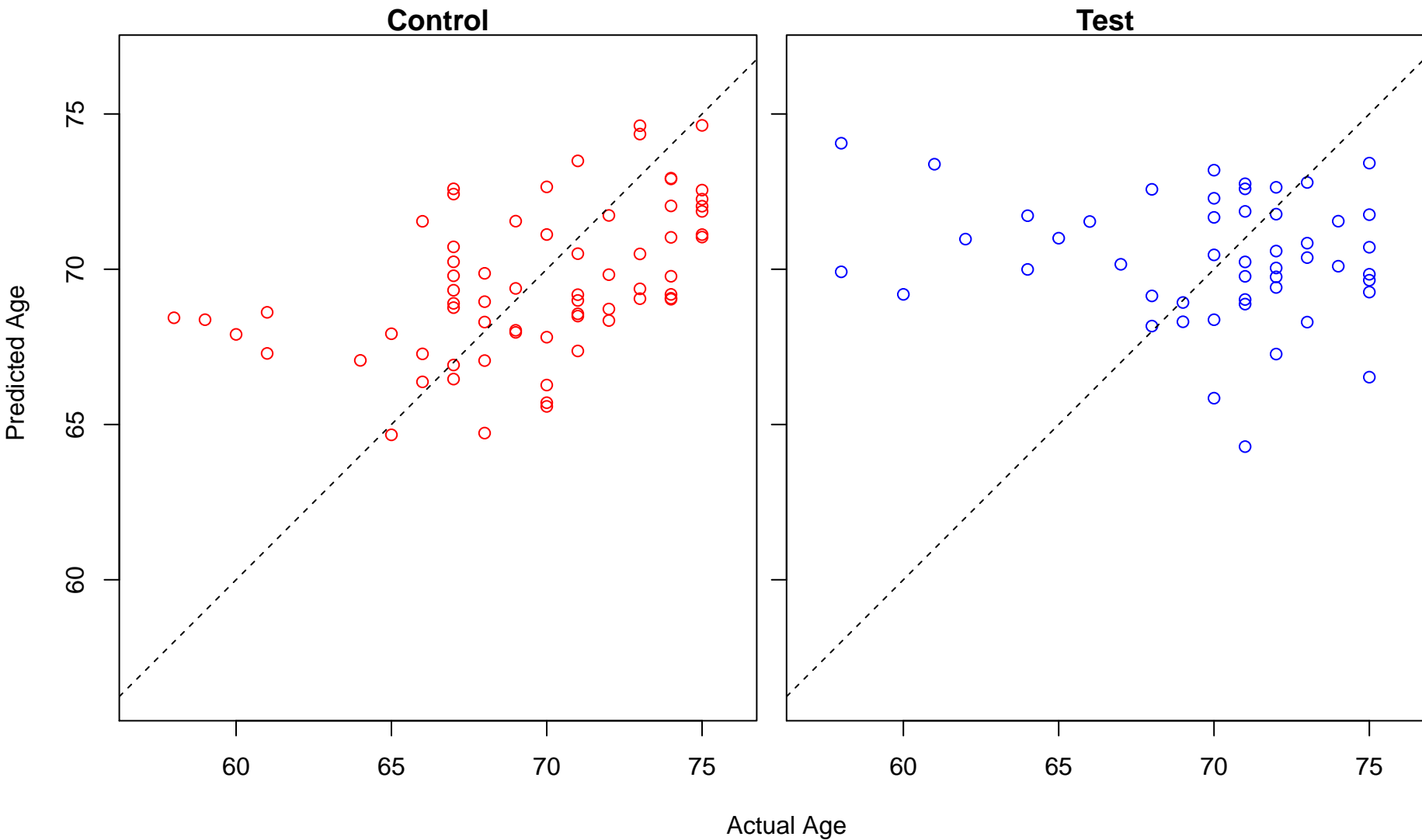
pyrimidine ribonucleoside catabolic process (Score: 0.694305)



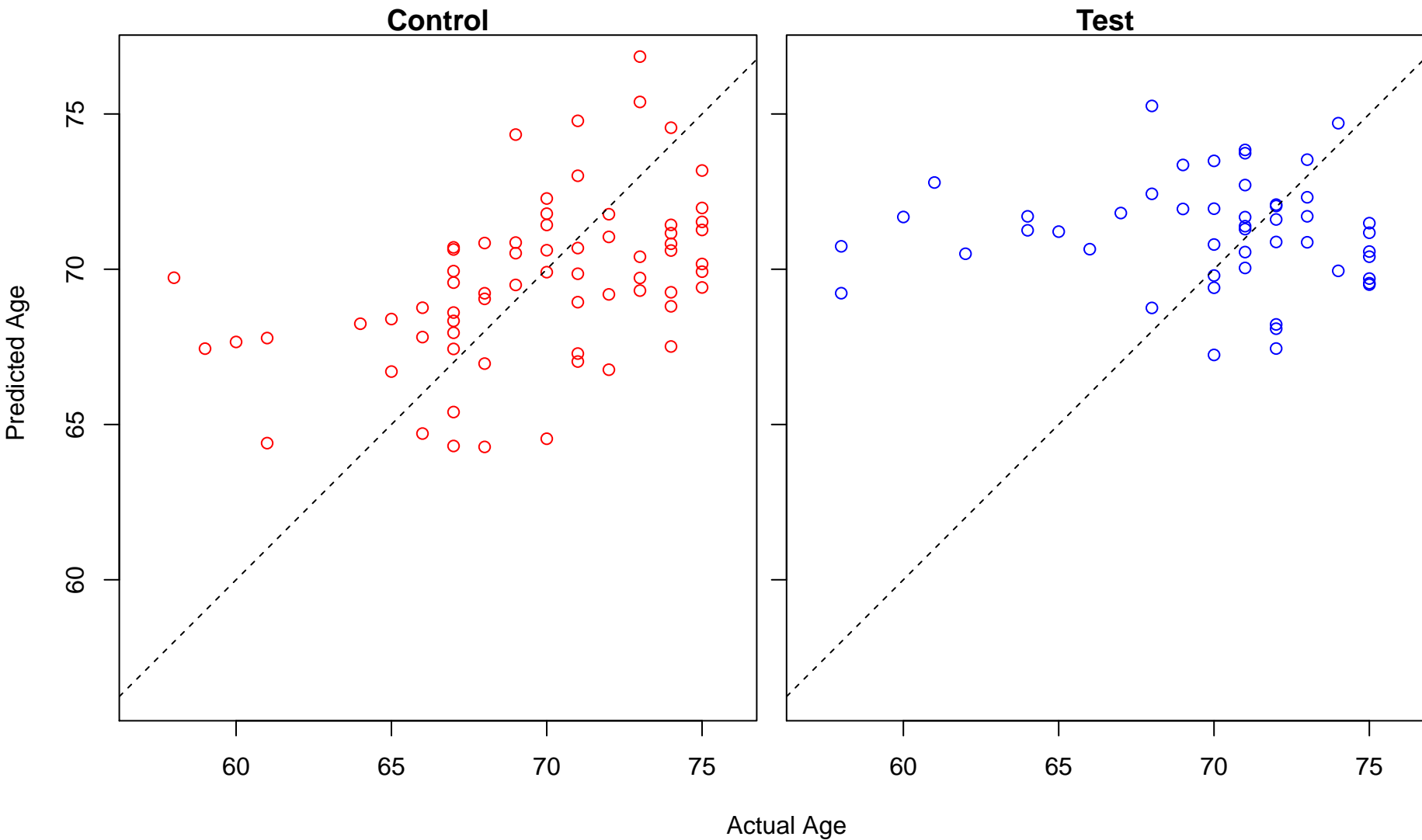
regulation of single stranded viral RNA replication via double stranded DNA intermediate (Score: 0.694)



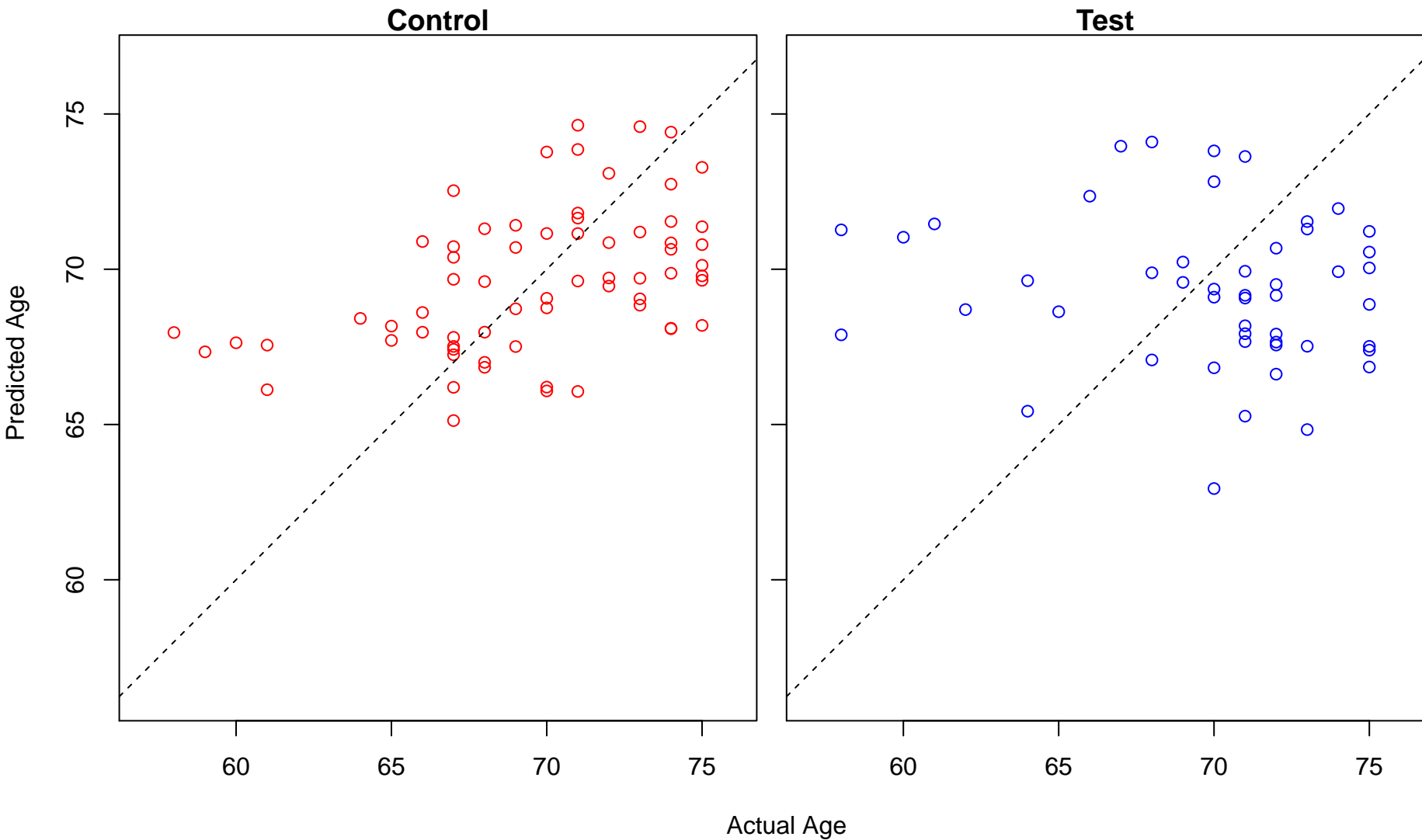
negative regulation of viral entry into host cell (Score: 0.693973)



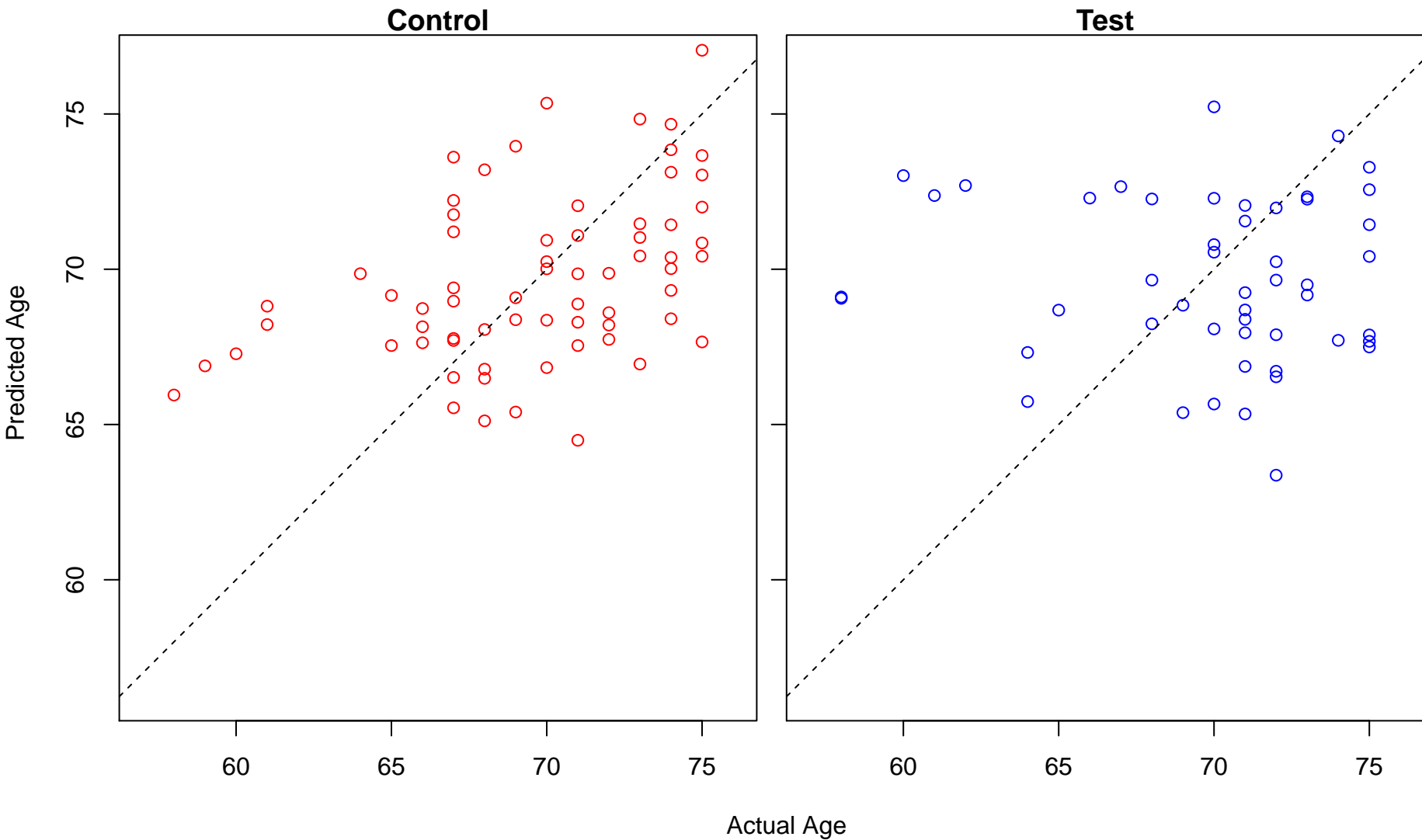
rRNA transcription (Score: 0.693546)



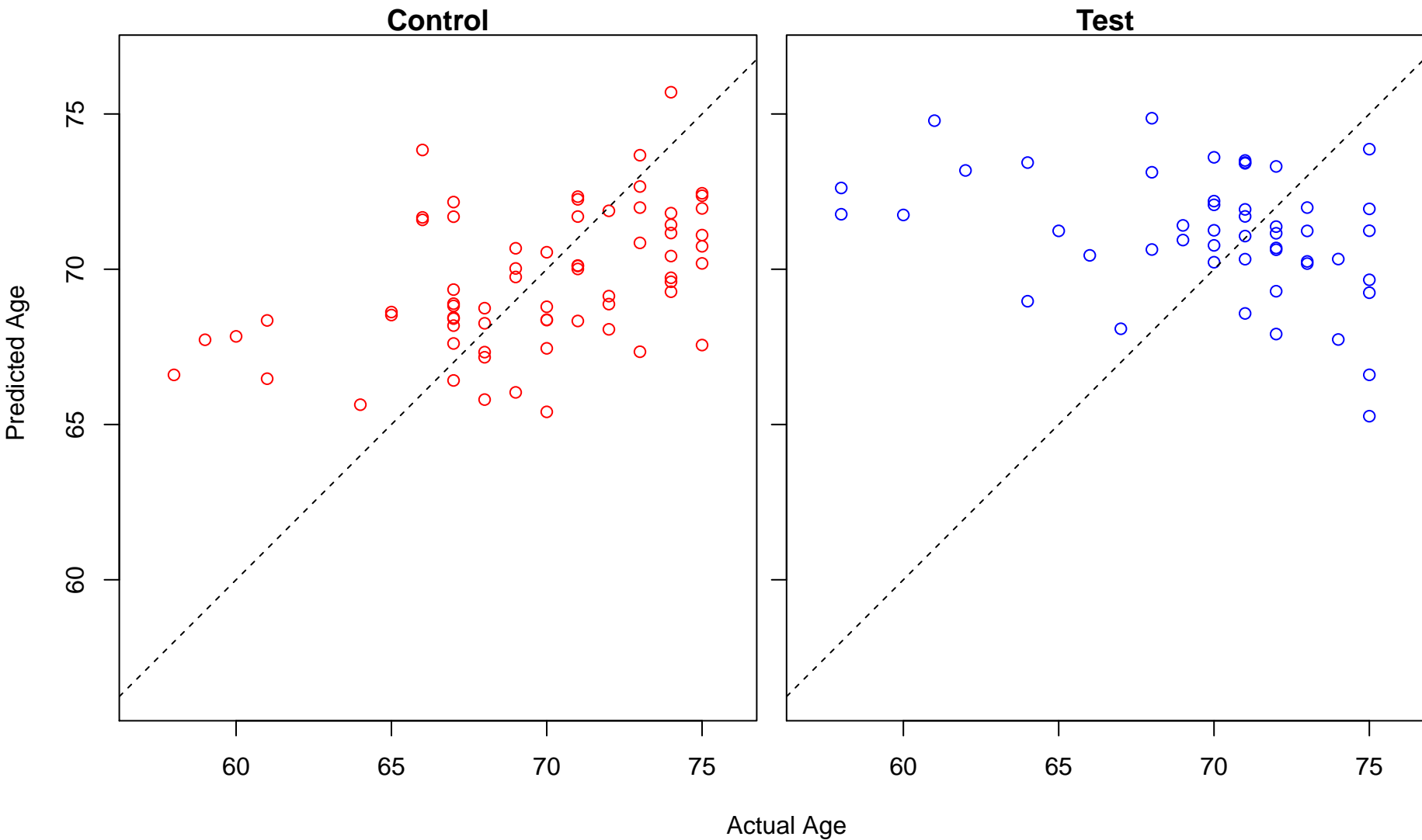
negative regulation of cellular senescence (Score: 0.693434)



positive regulation of steroid metabolic process (Score: 0.693321)

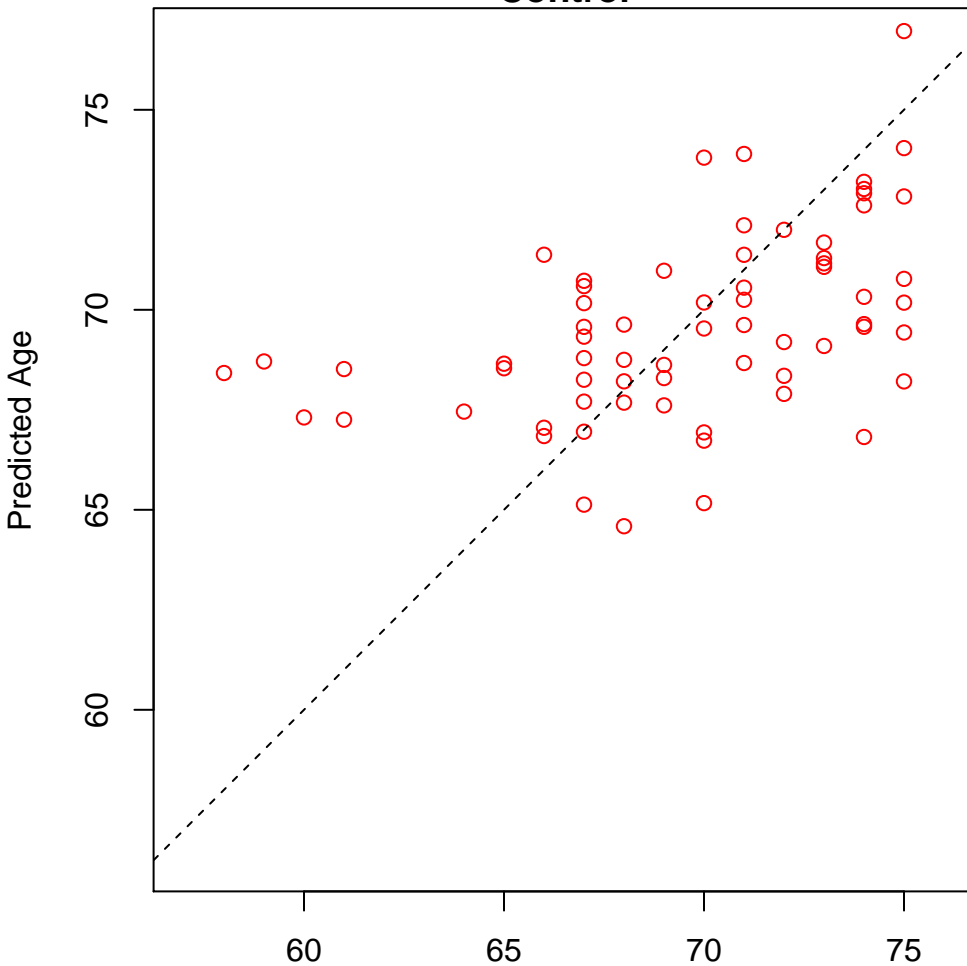


taurine metabolic process (Score: 0.692408)

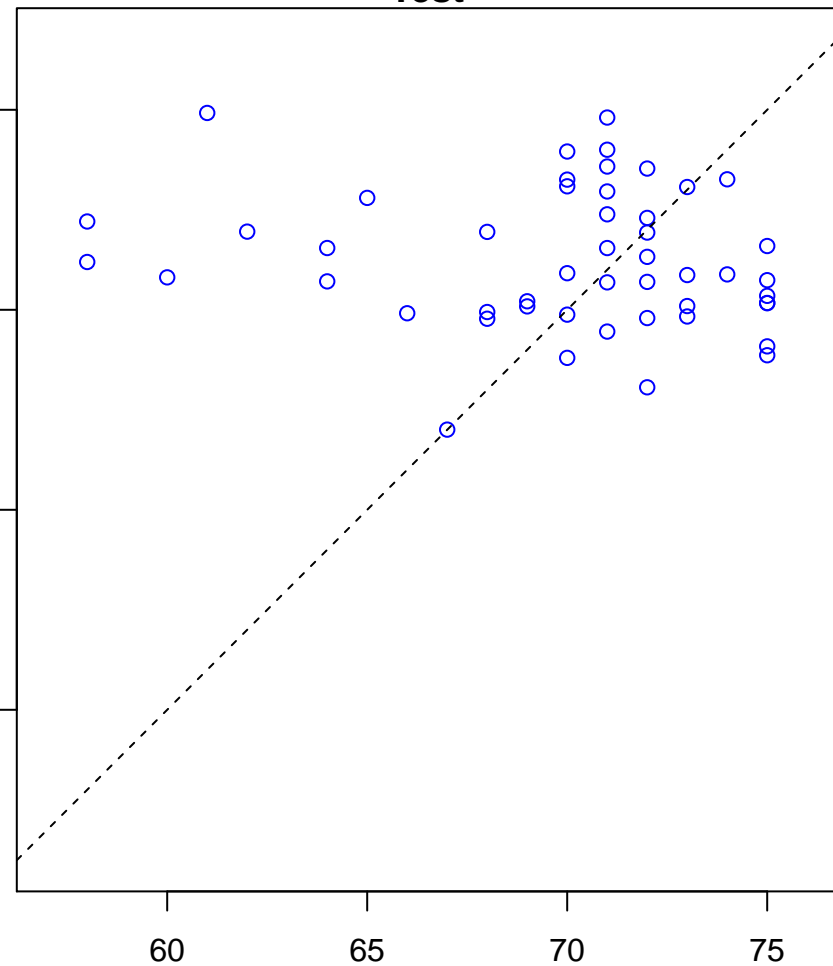


peptidyl-arginine omega-N-methylation (Score: 0.692244)

Control

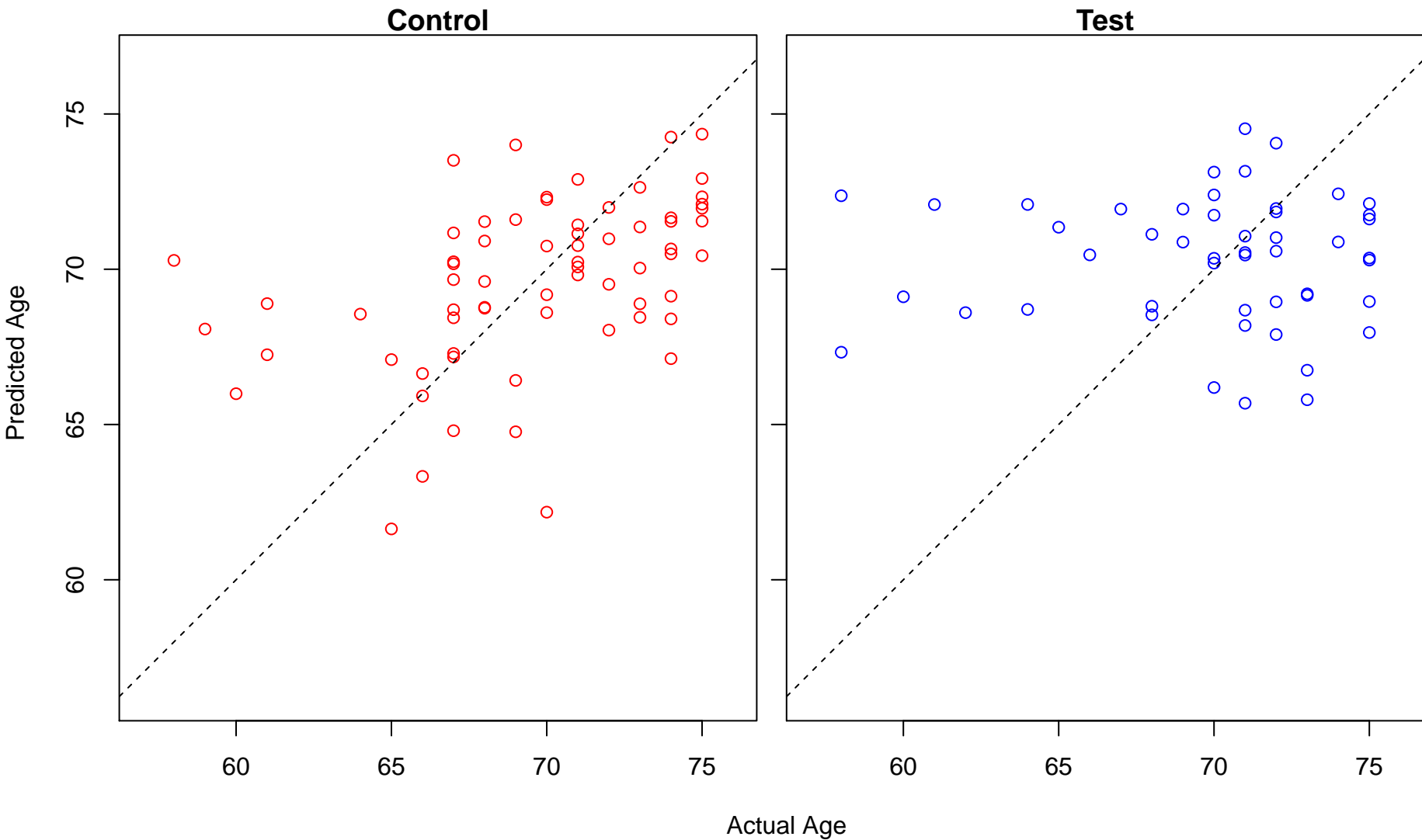


Test

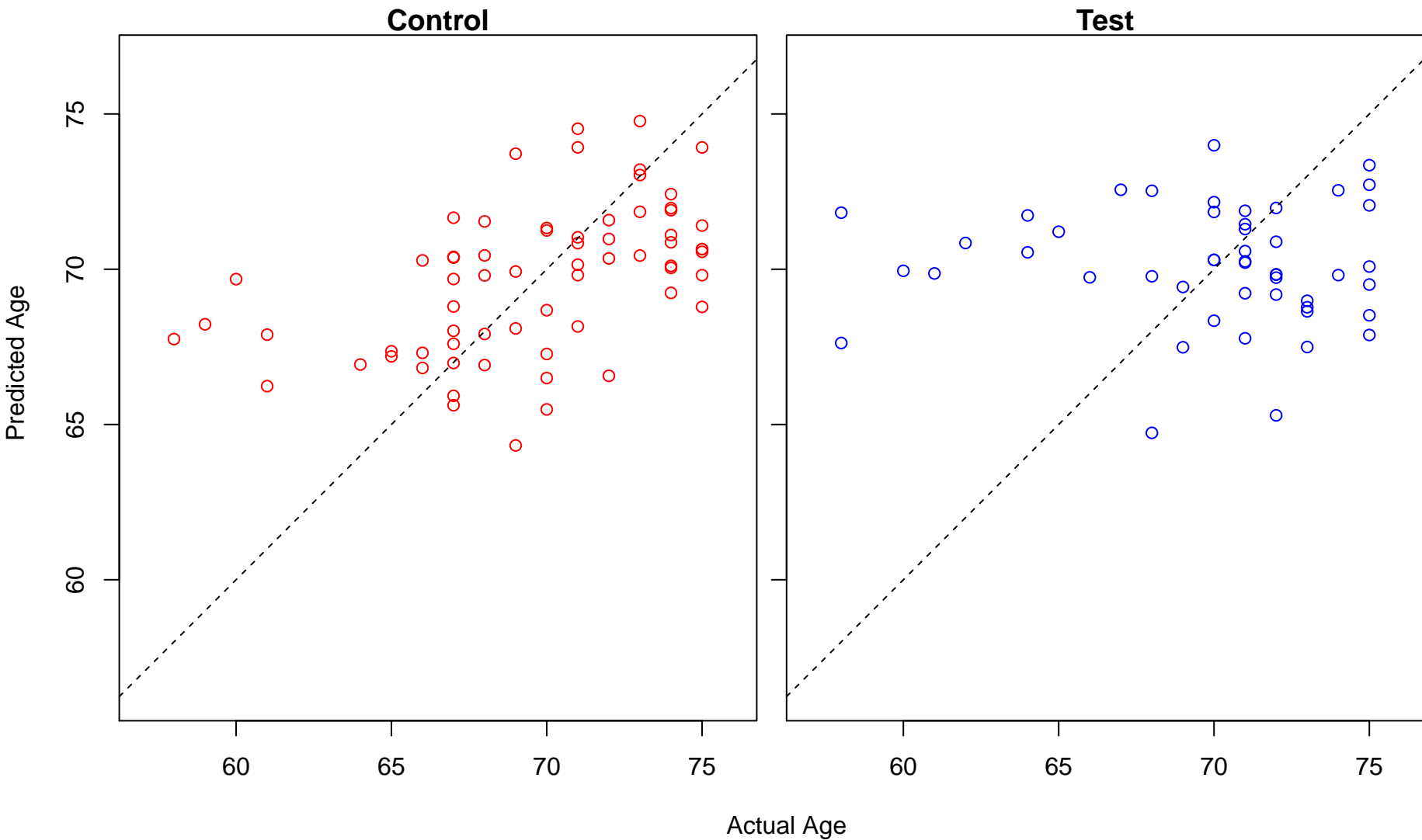


Actual Age

retinoic acid metabolic process (Score: 0.691093)

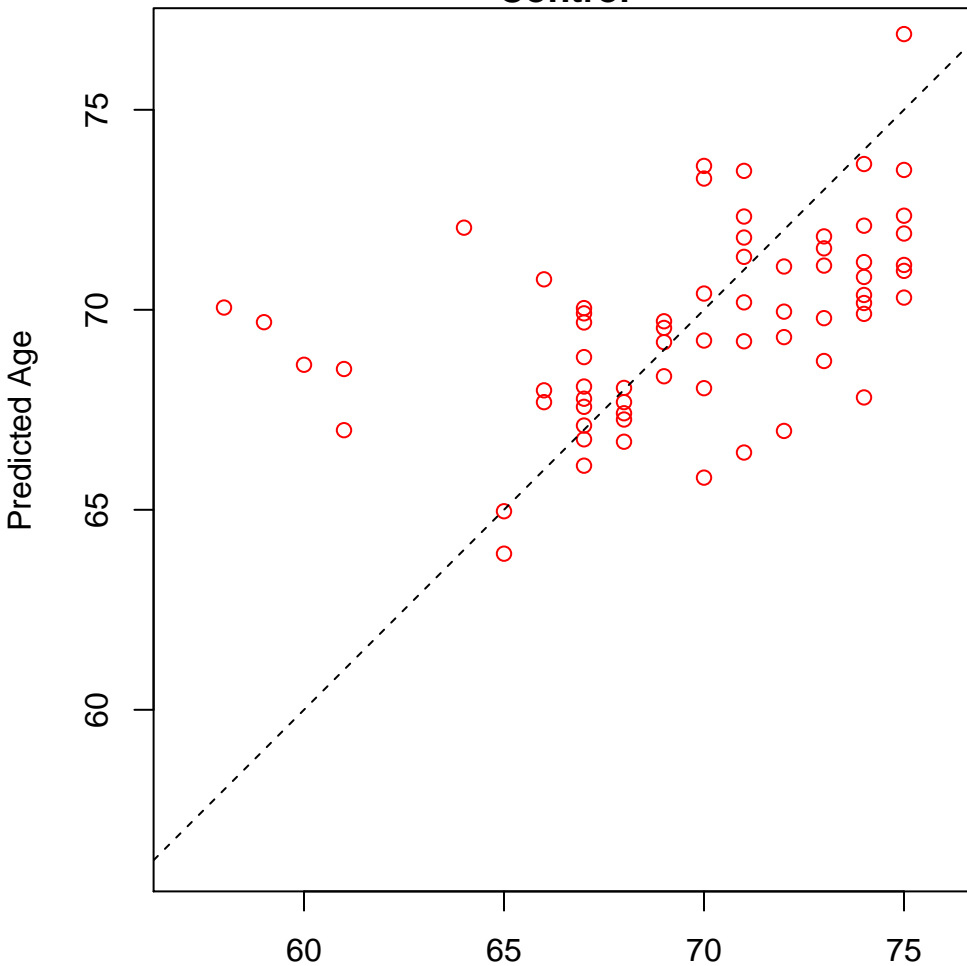


retinal metabolic process (Score: 0.690935)

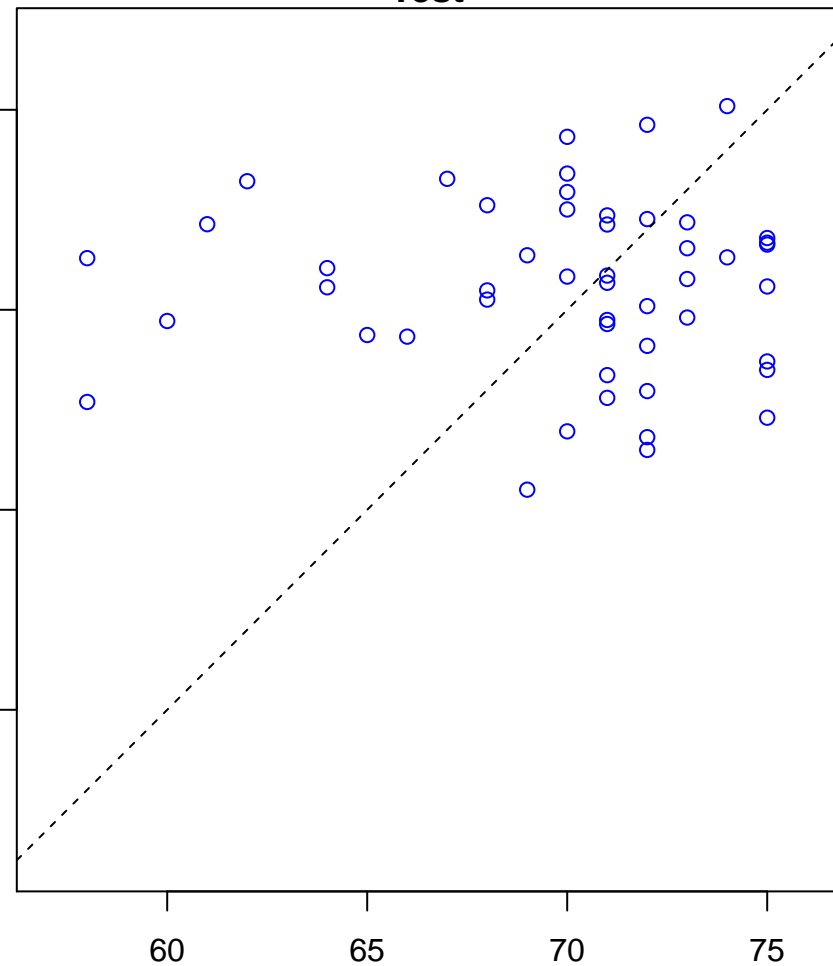


regulation of histone H3–K9 acetylation (Score: 0.690744)

Control

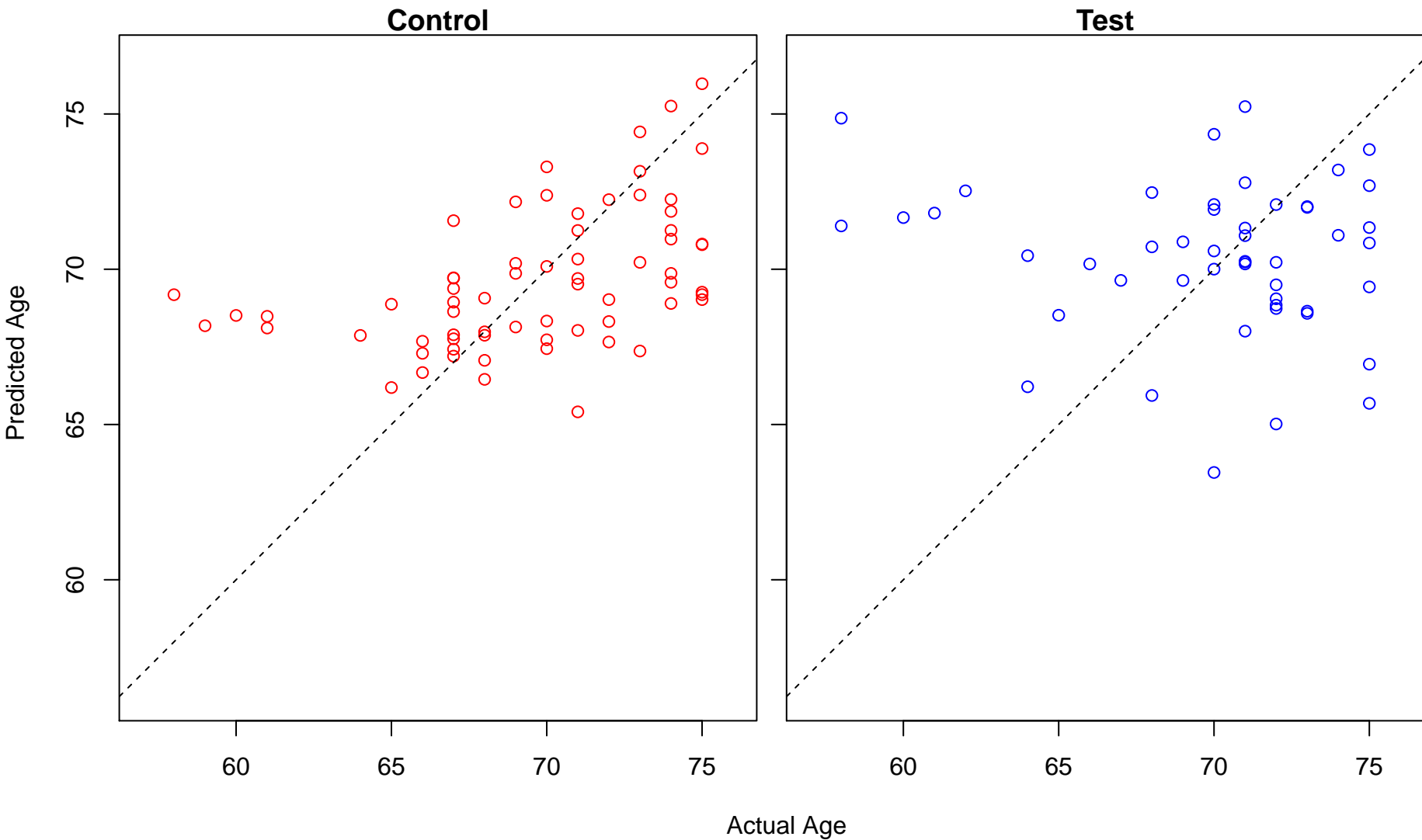


Test

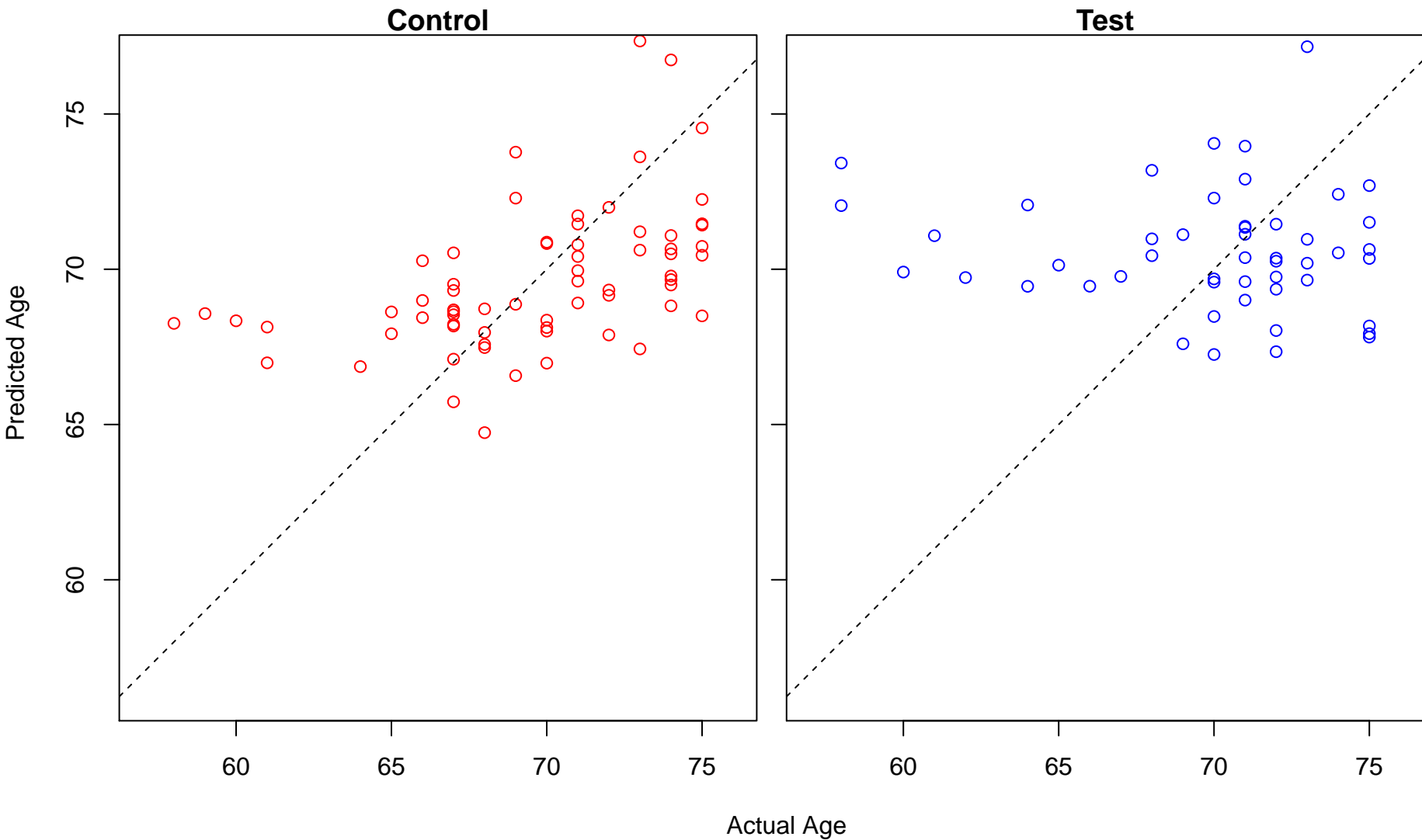


Actual Age

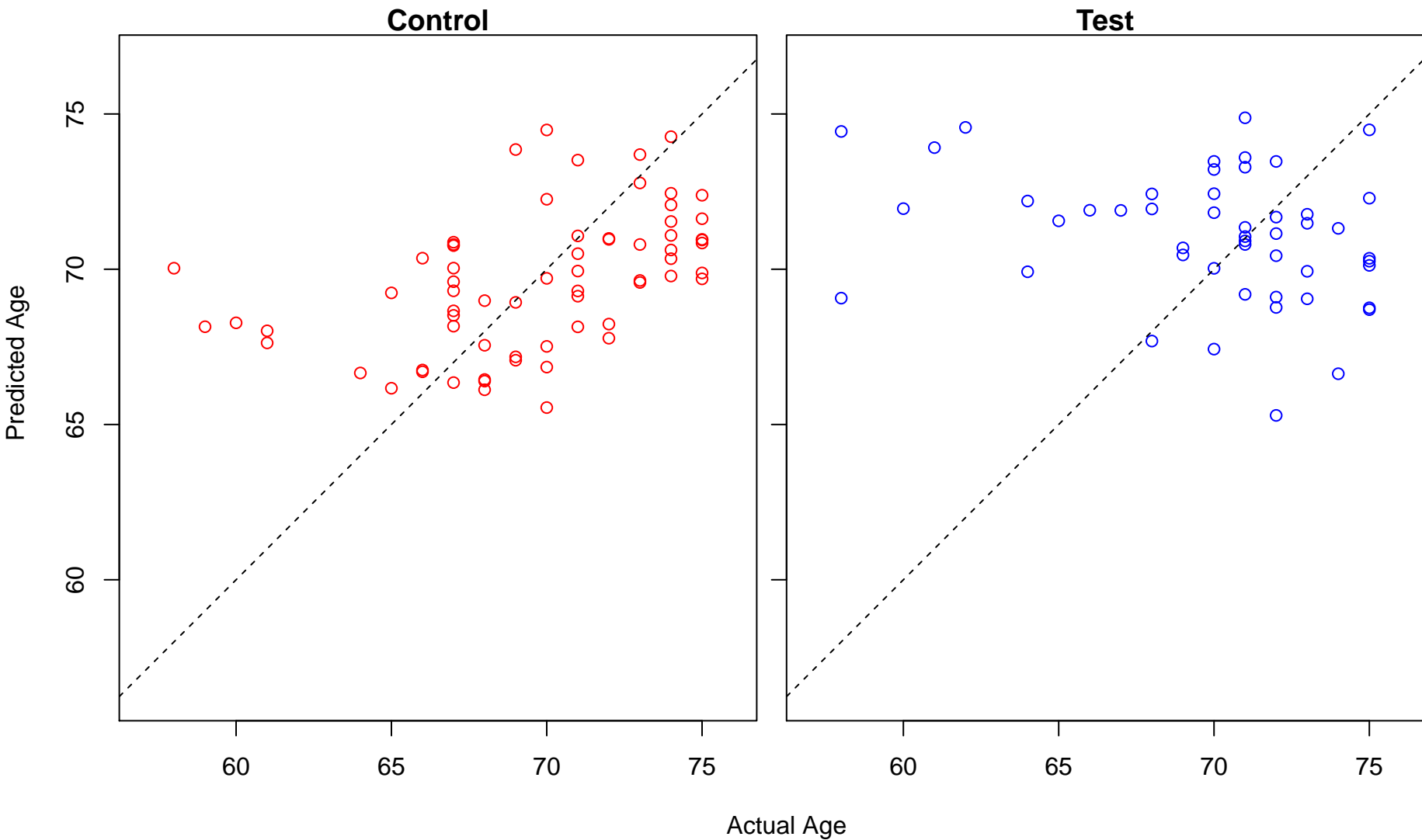
synaptic vesicle exocytosis (Score: 0.690706)



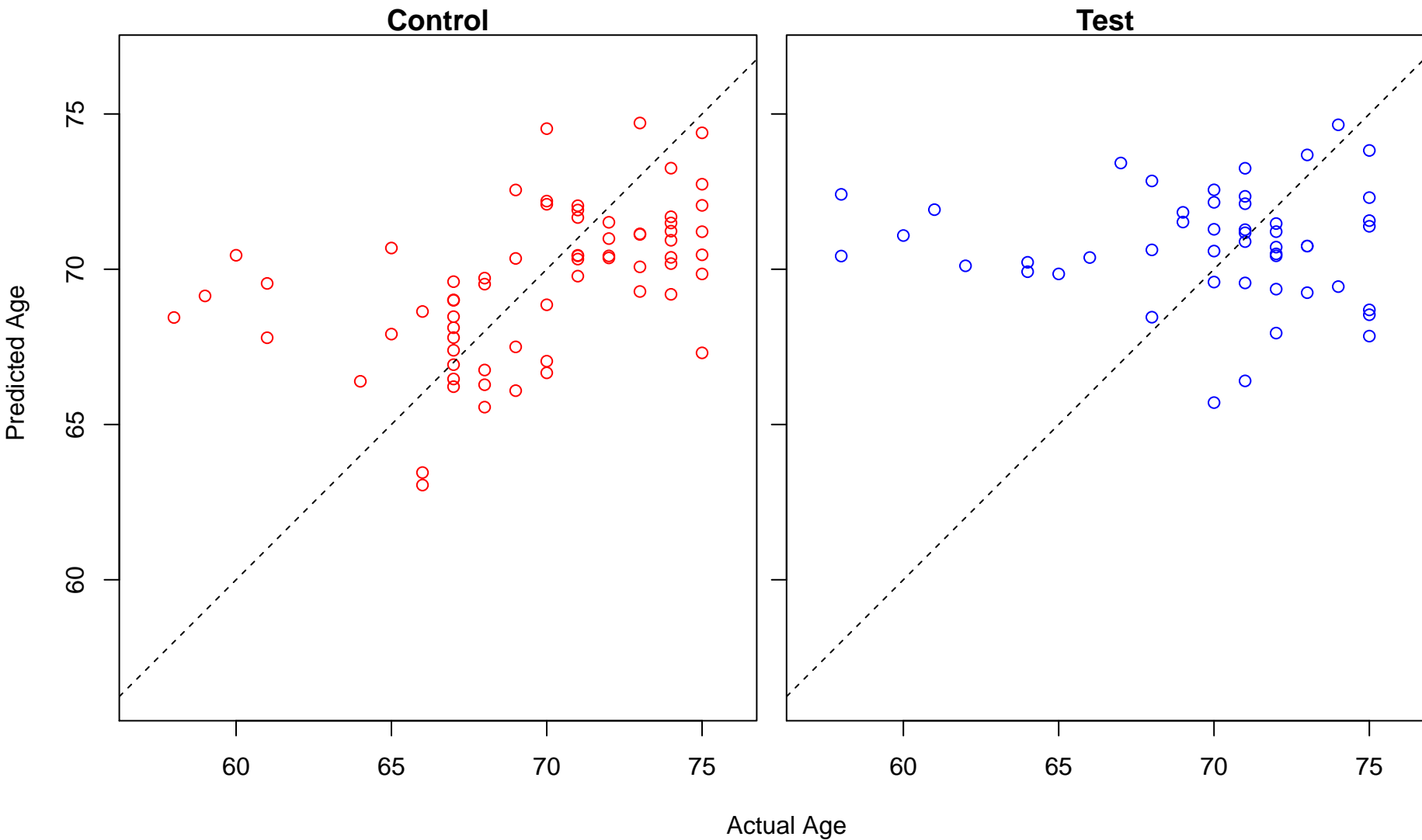
negative regulation of protein sumoylation (Score: 0.688811)



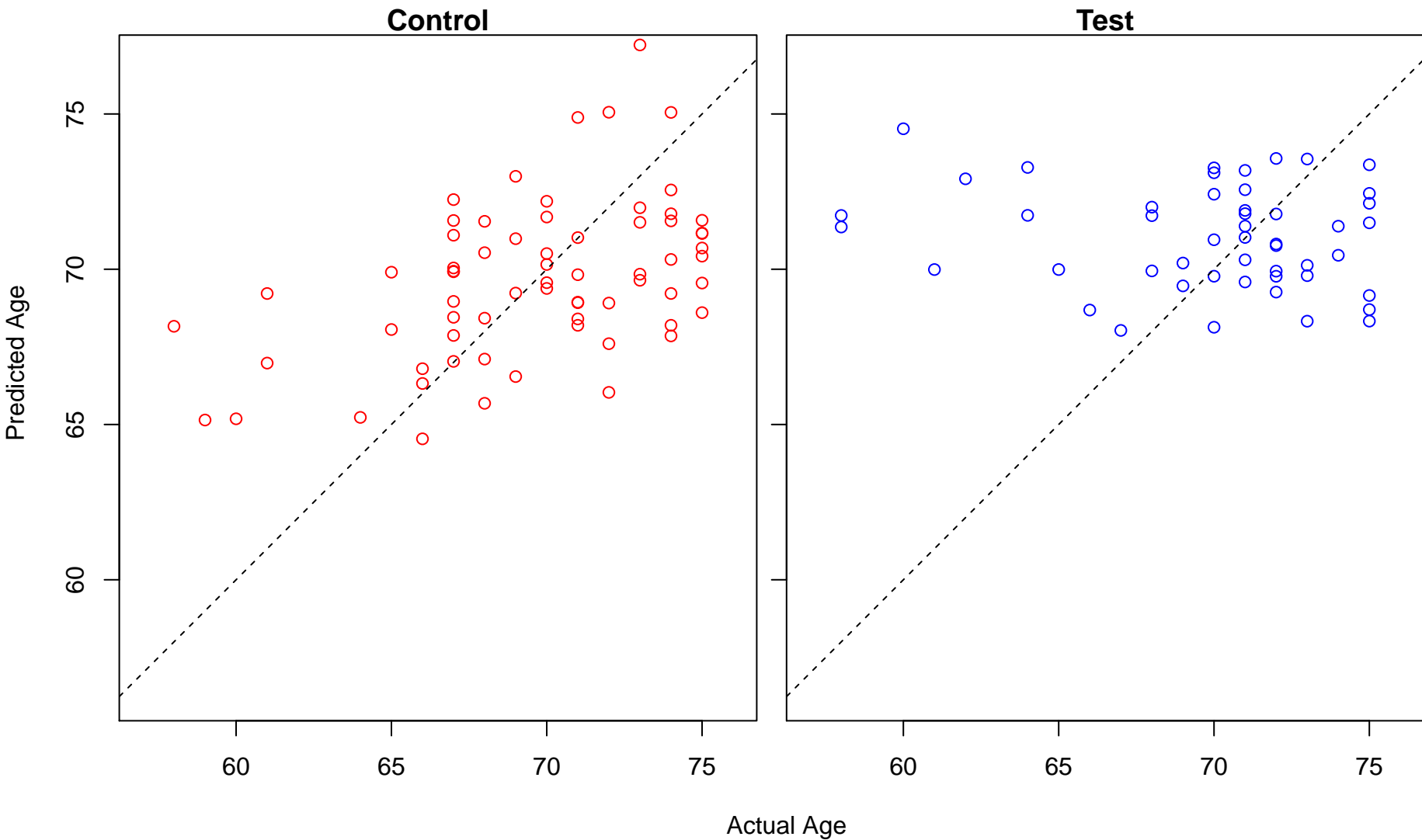
secretion by tissue (Score: 0.688076)



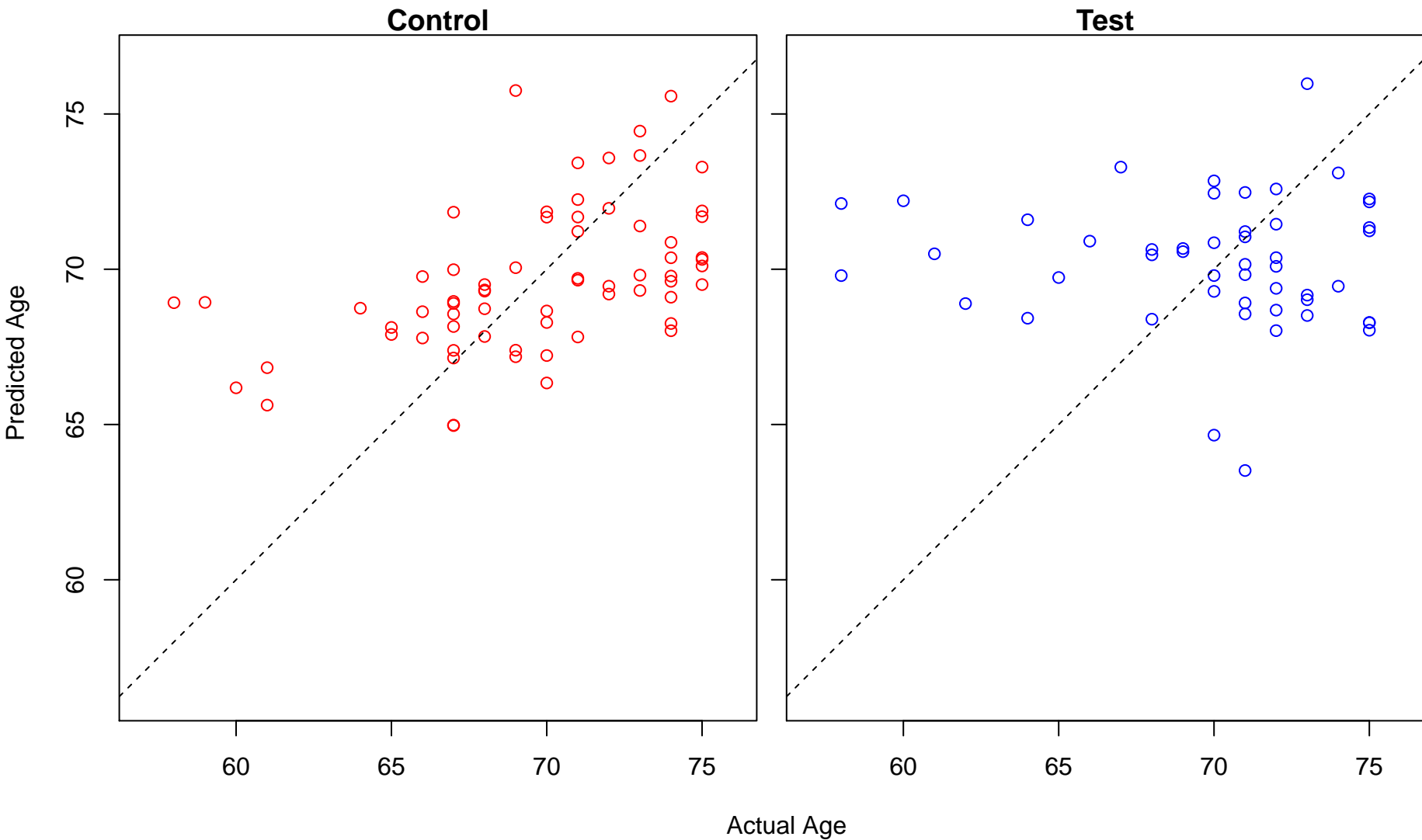
sulfation (Score: 0.687538)



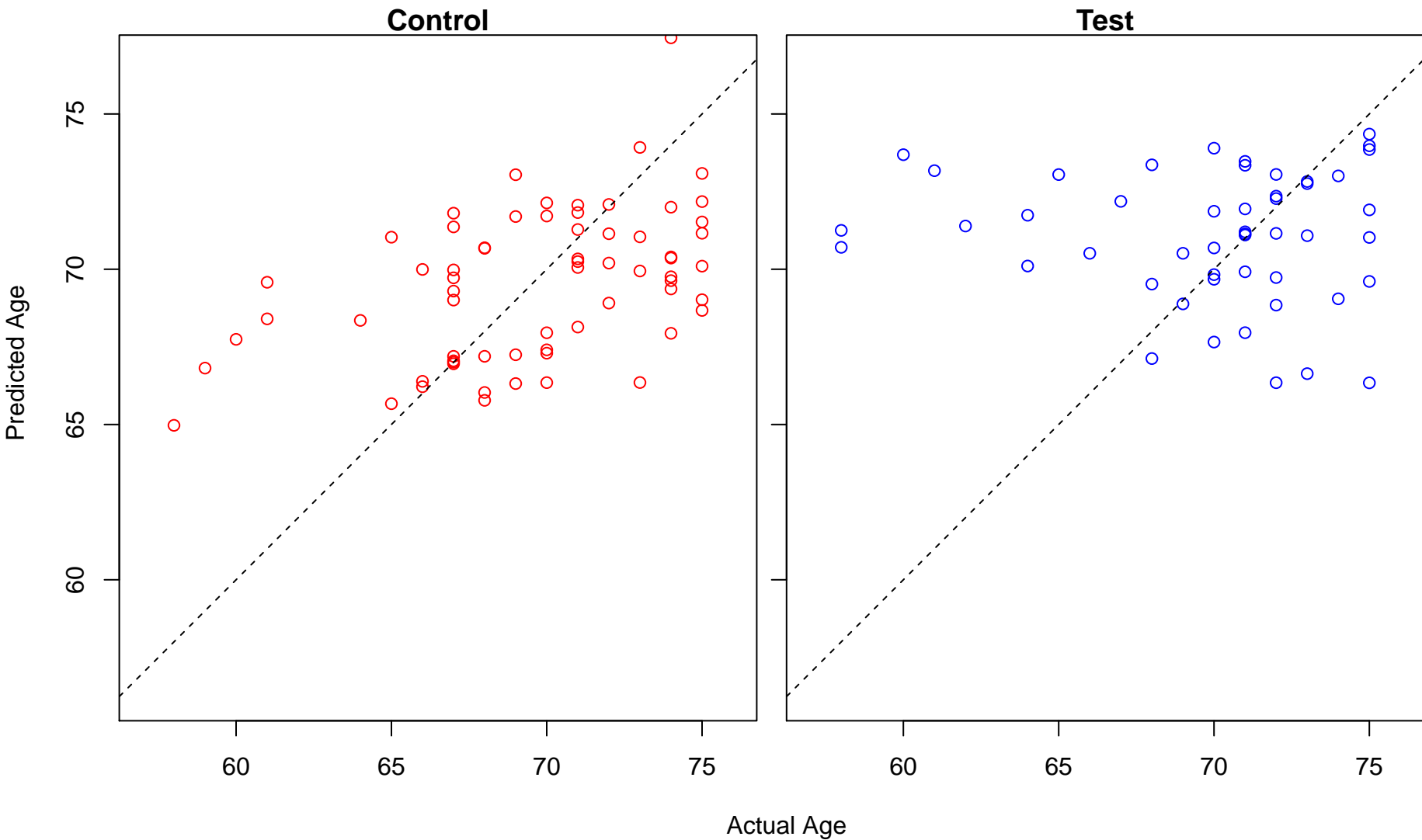
purinergic receptor signaling pathway (Score: 0.687253)



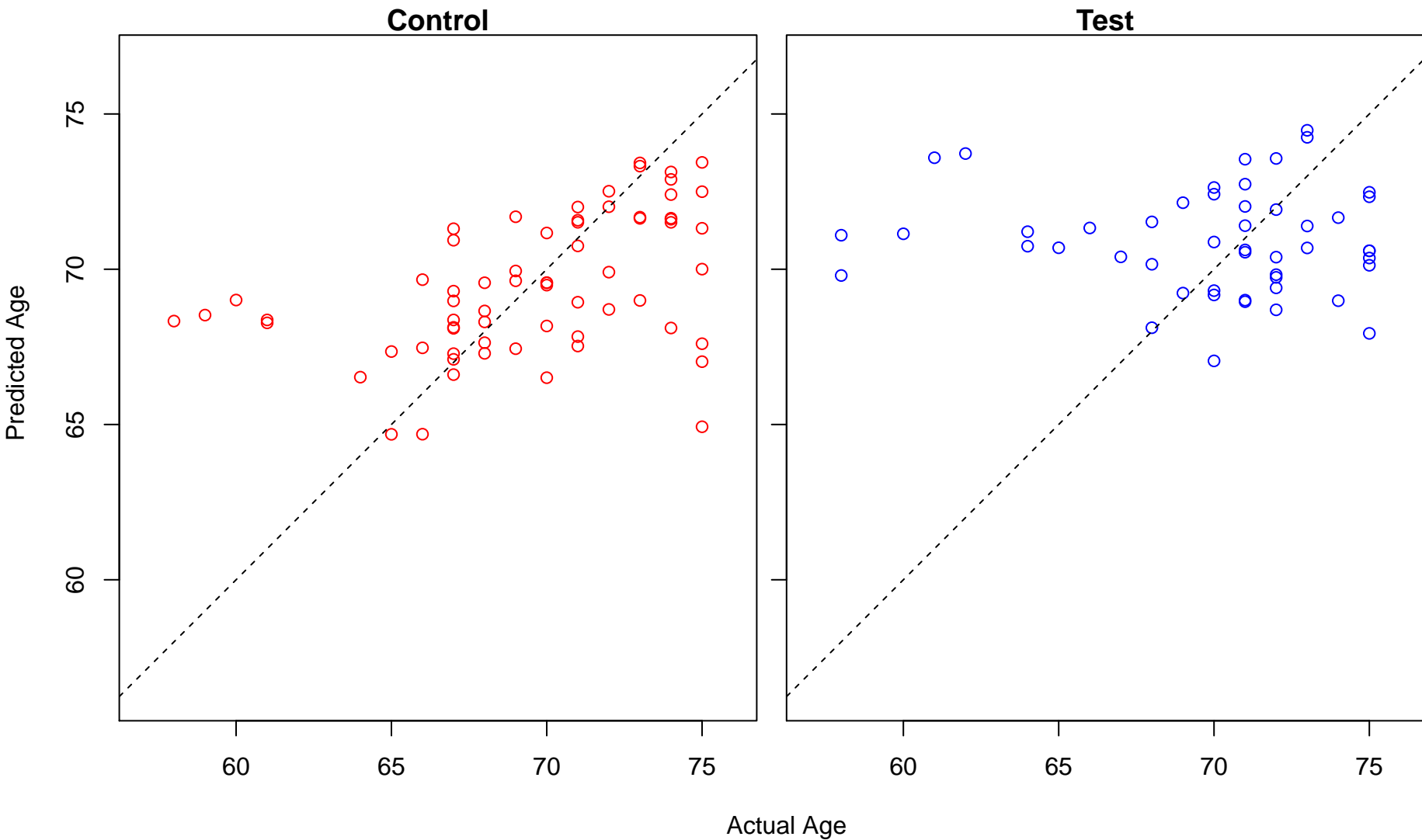
negative regulation of cell-matrix adhesion (Score: 0.686297)



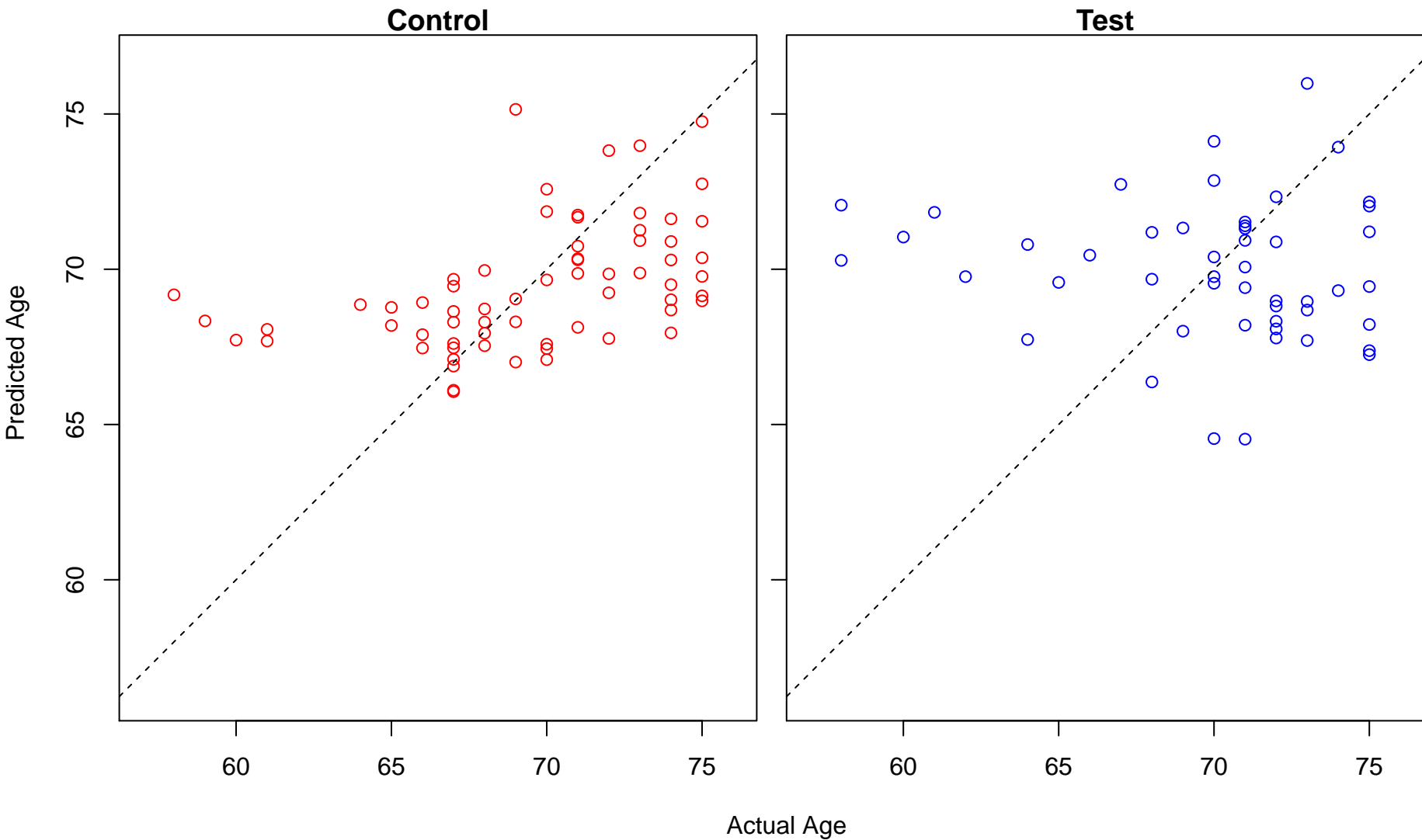
negative regulation of potassium ion transmembrane transporter activity (Score: 0.686192)



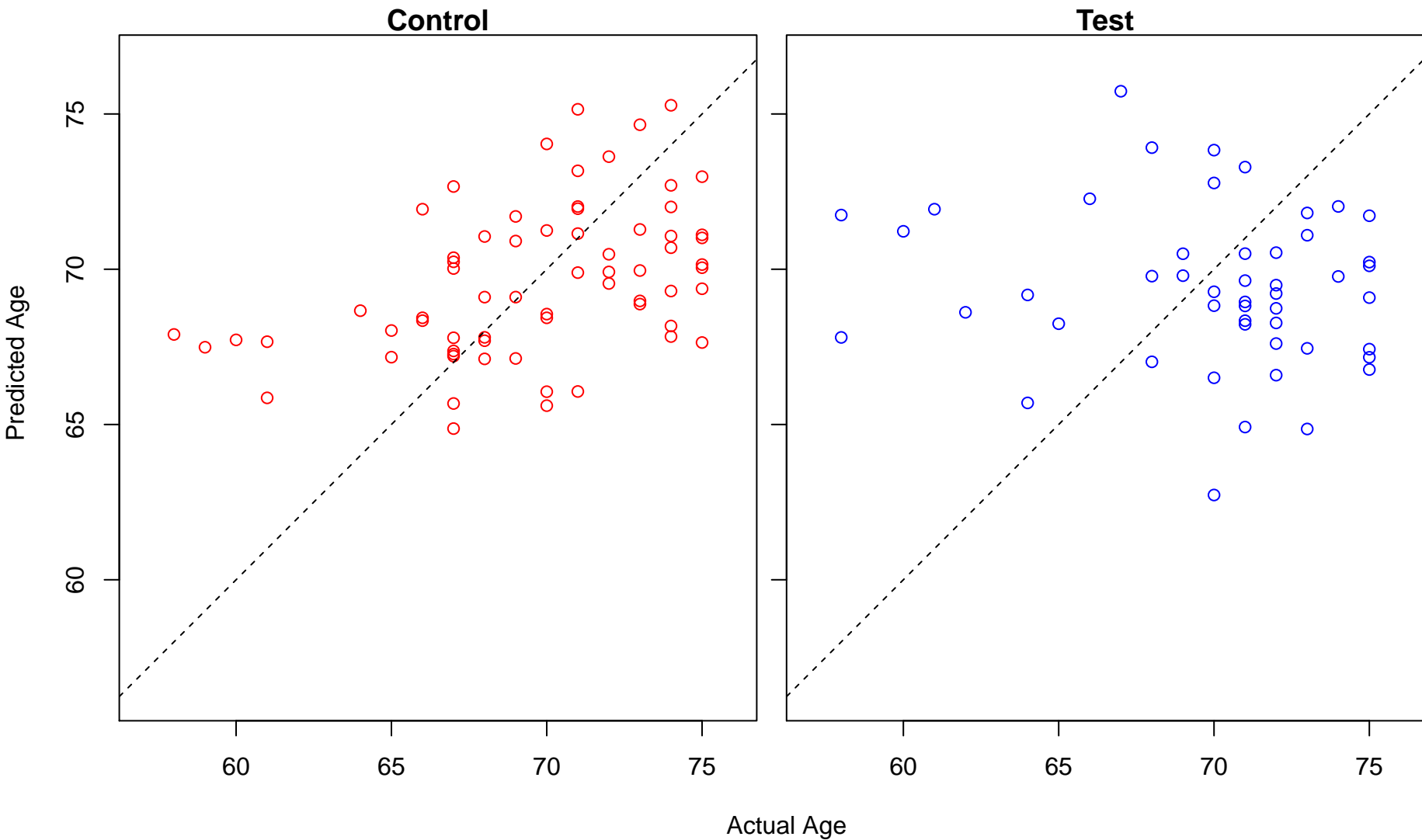
regulation of cholesterol efflux (Score: 0.686022)



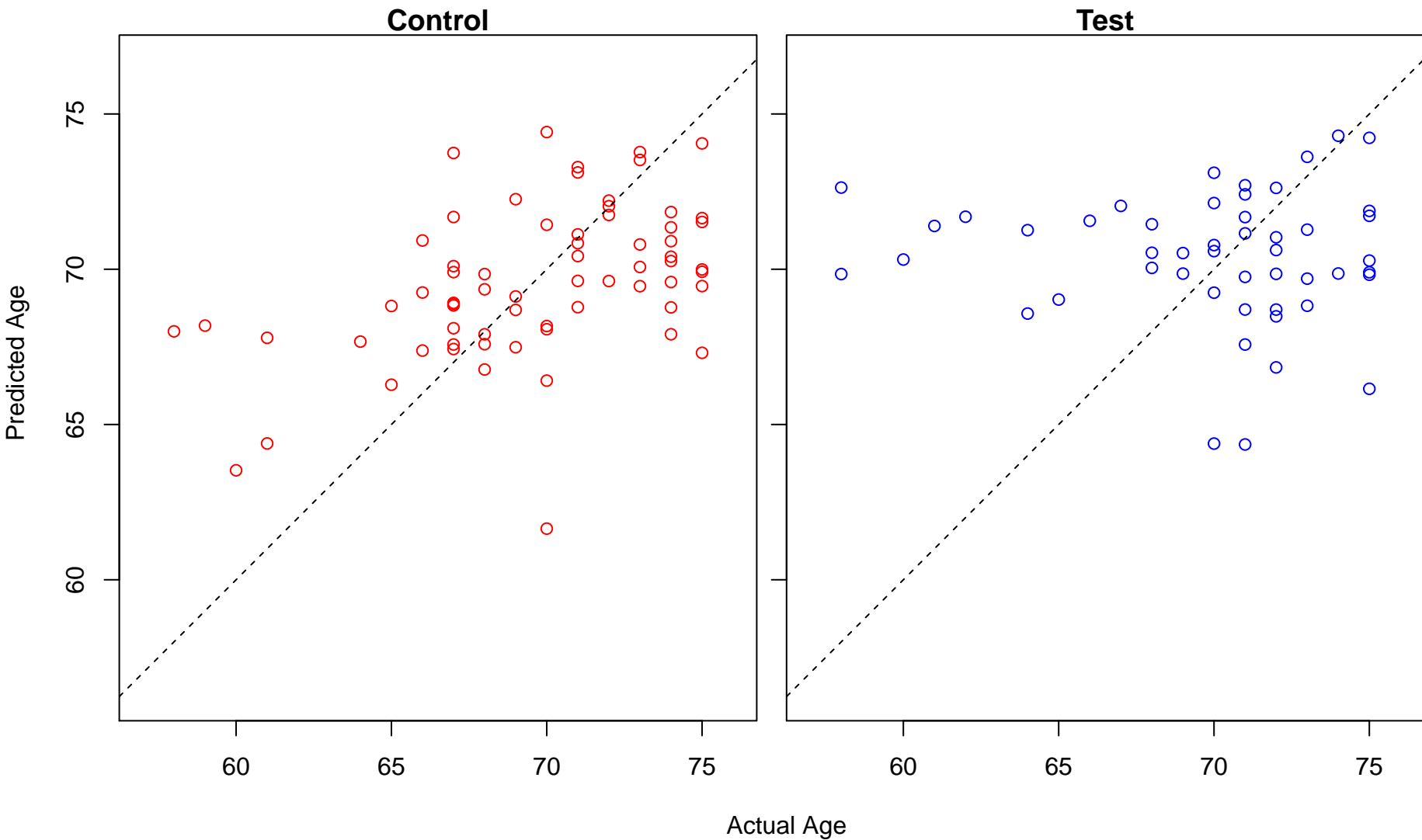
synapse assembly (Score: 0.685678)



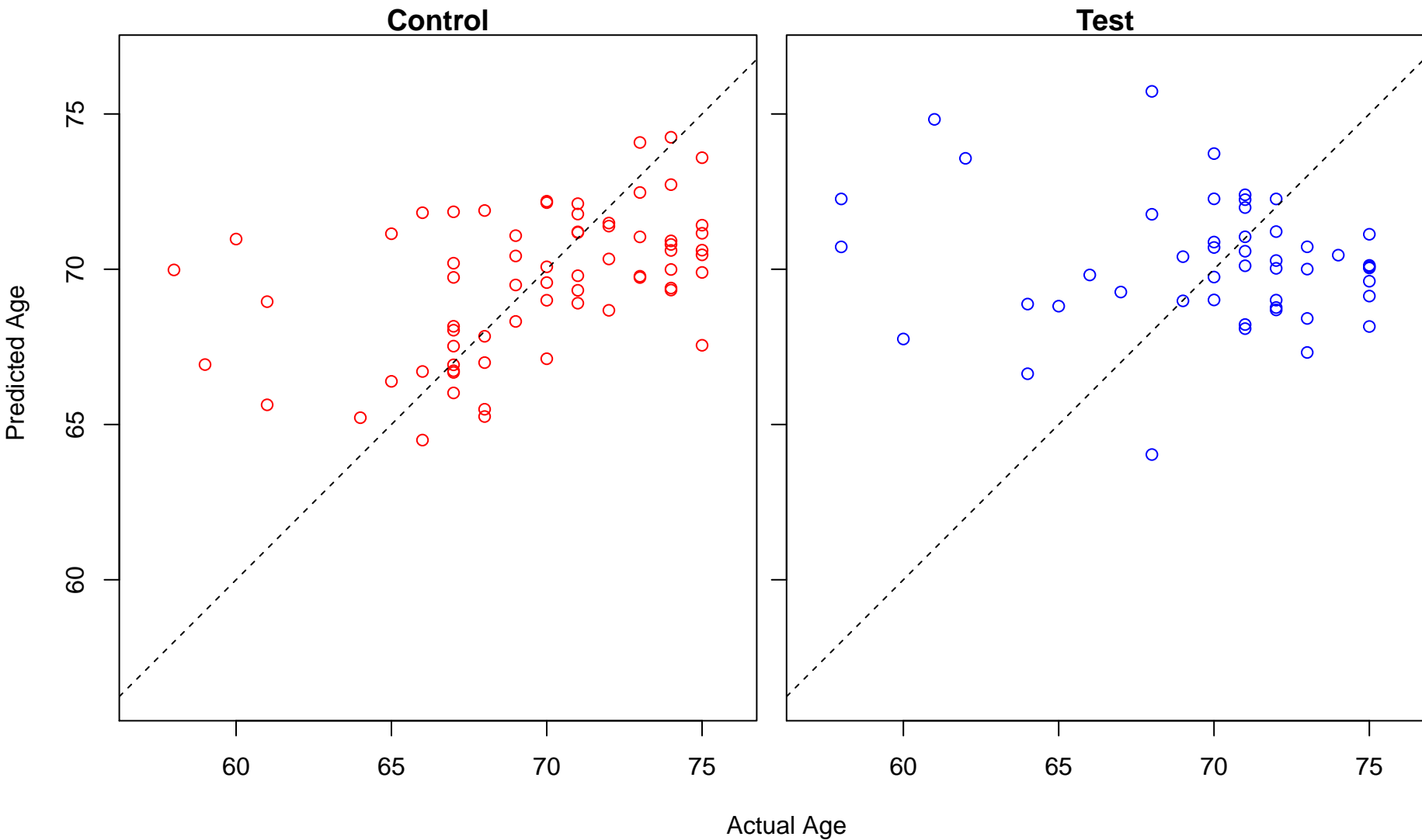
negative regulation of cell aging (Score: 0.685582)



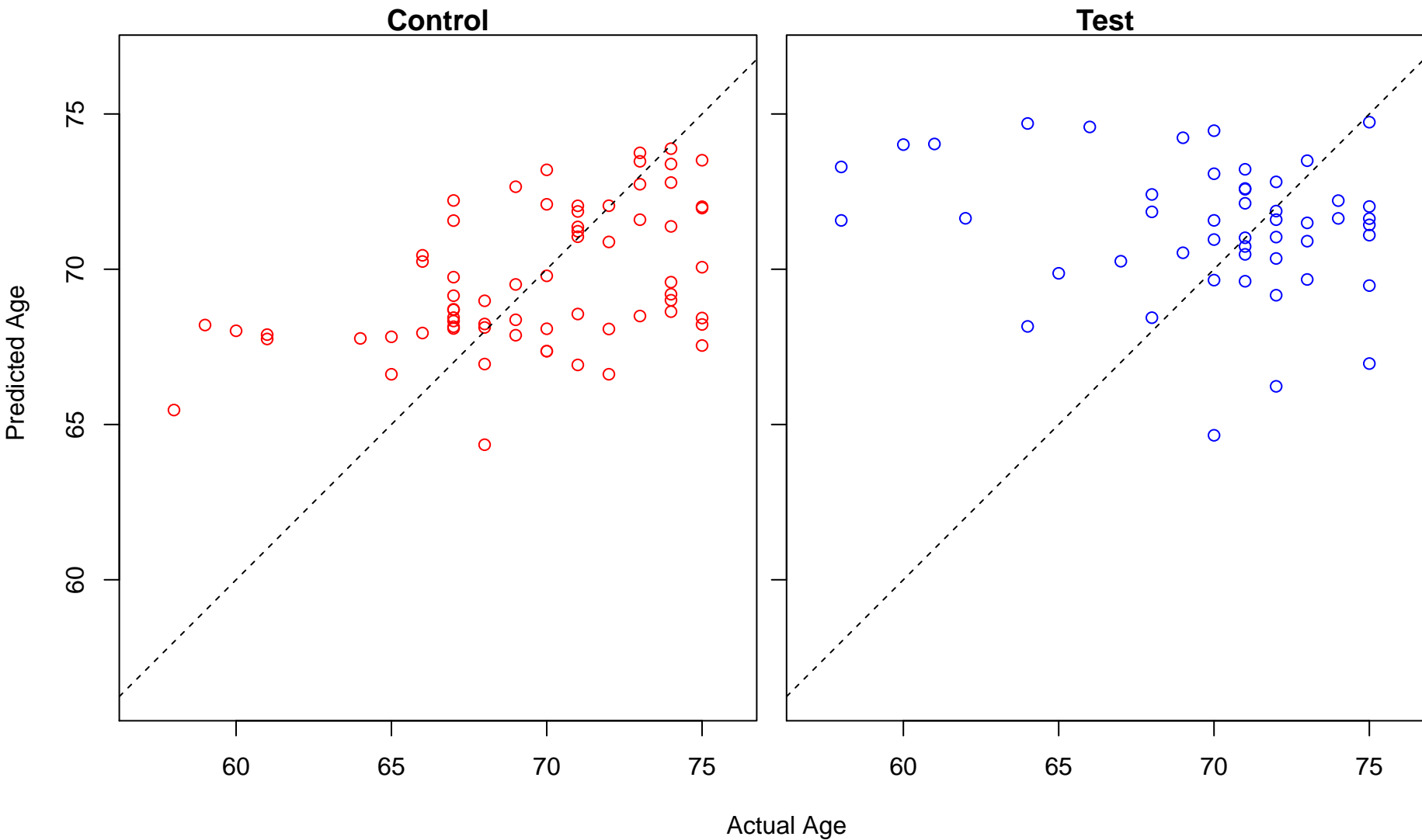
macrophage differentiation (Score: 0.684294)



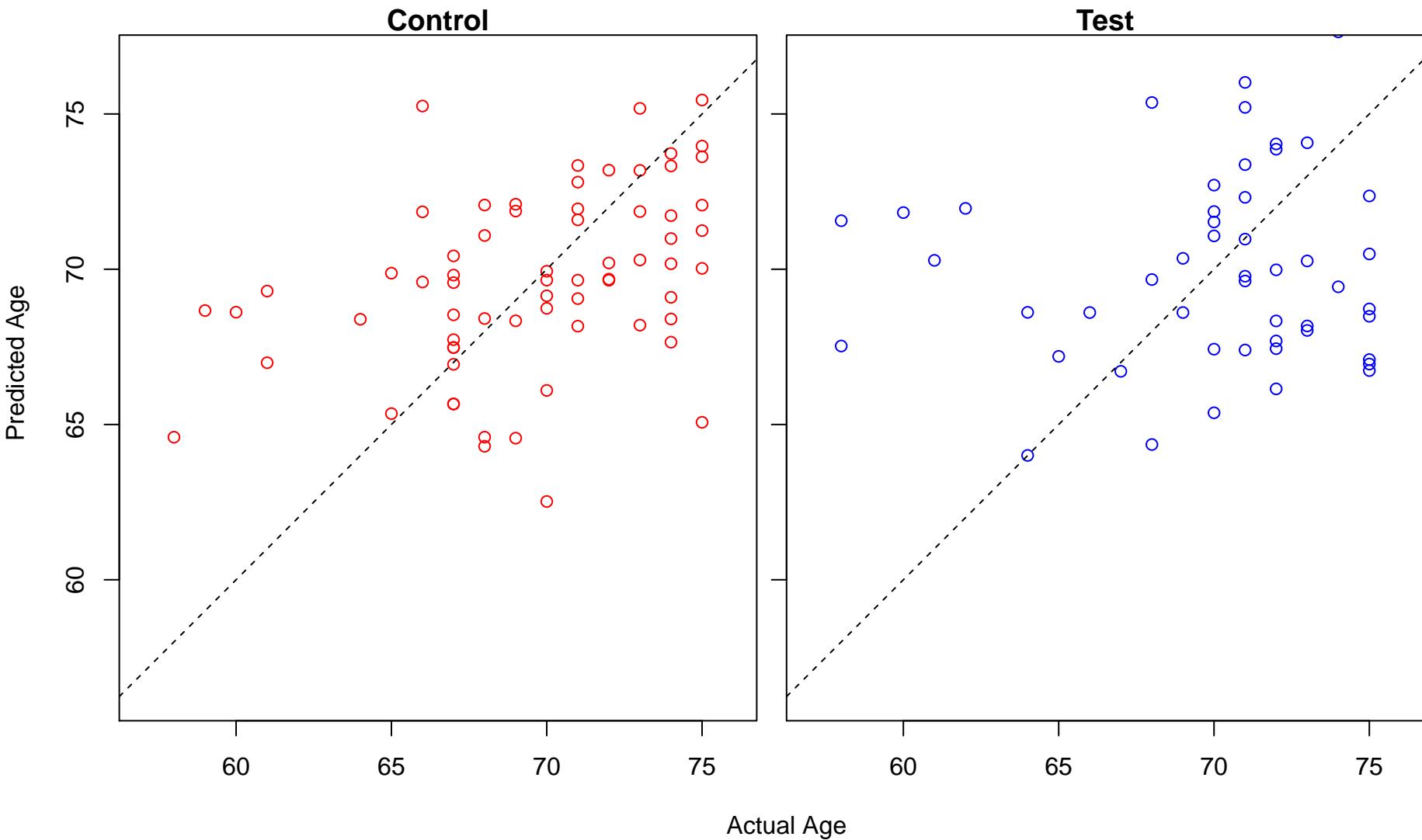
interferon-gamma secretion (Score: 0.684002)



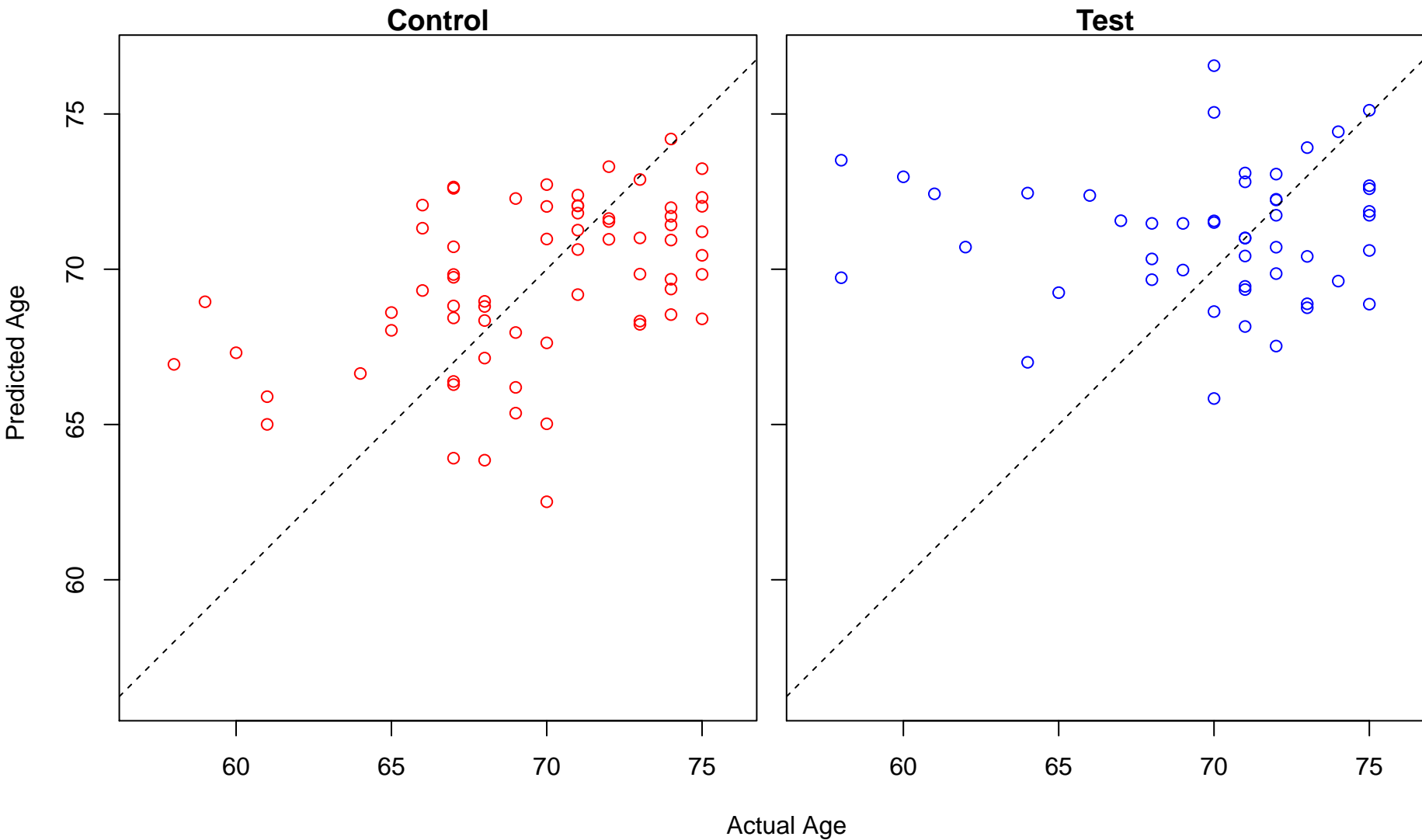
lymphocyte homeostasis (Score: 0.683990)



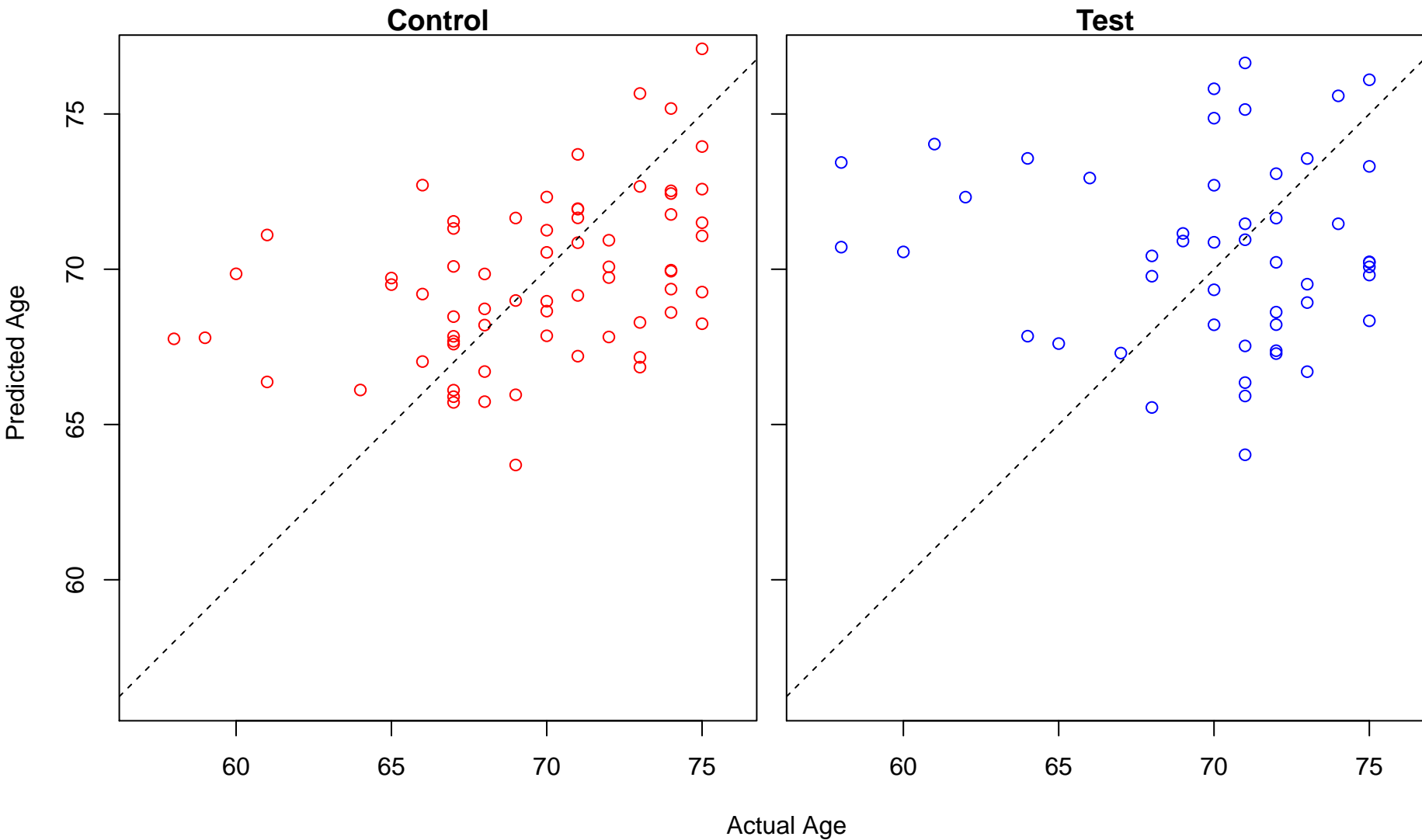
positive regulation of synapse assembly (Score: 0.683544)



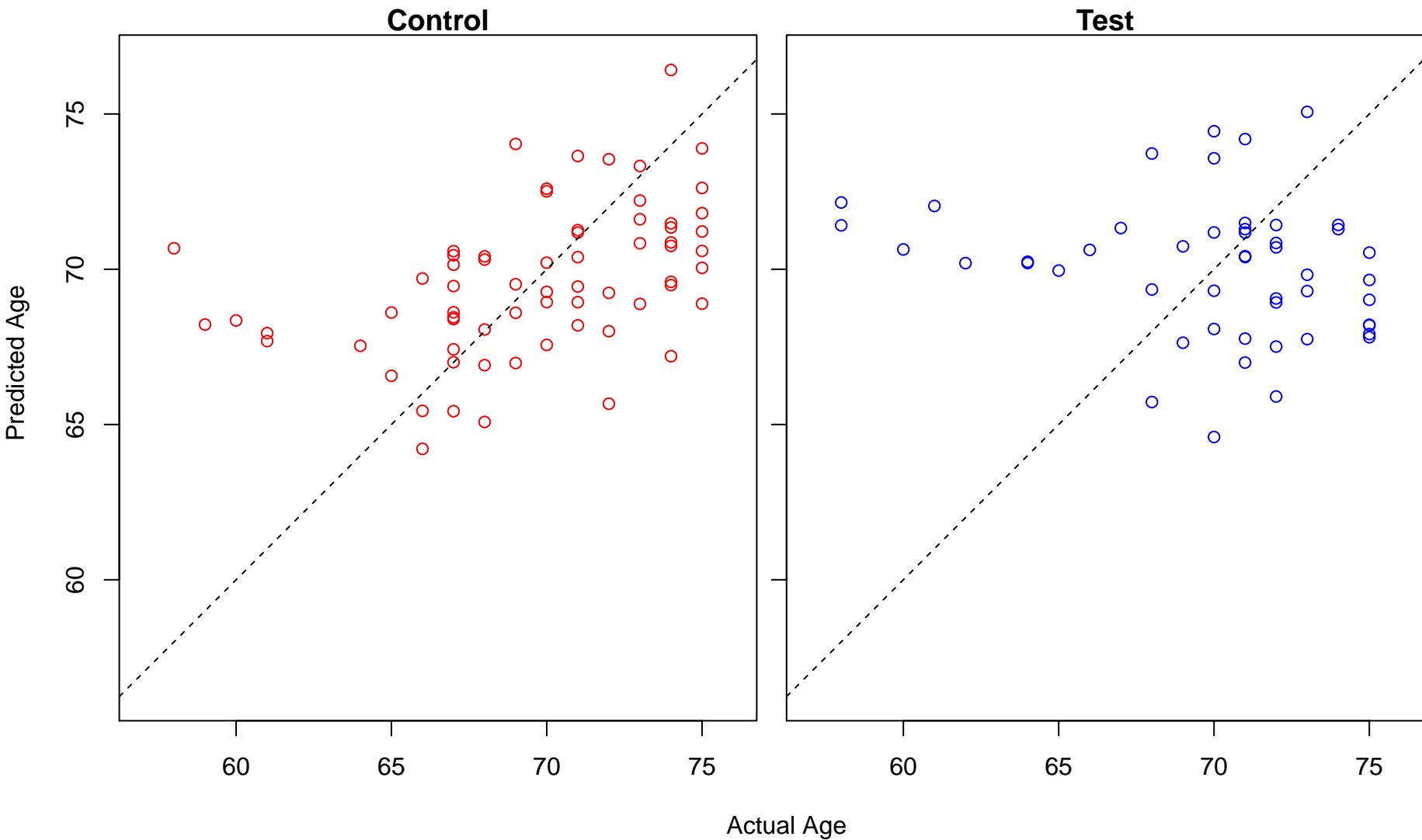
positive regulation of heart contraction (Score: 0.683274)



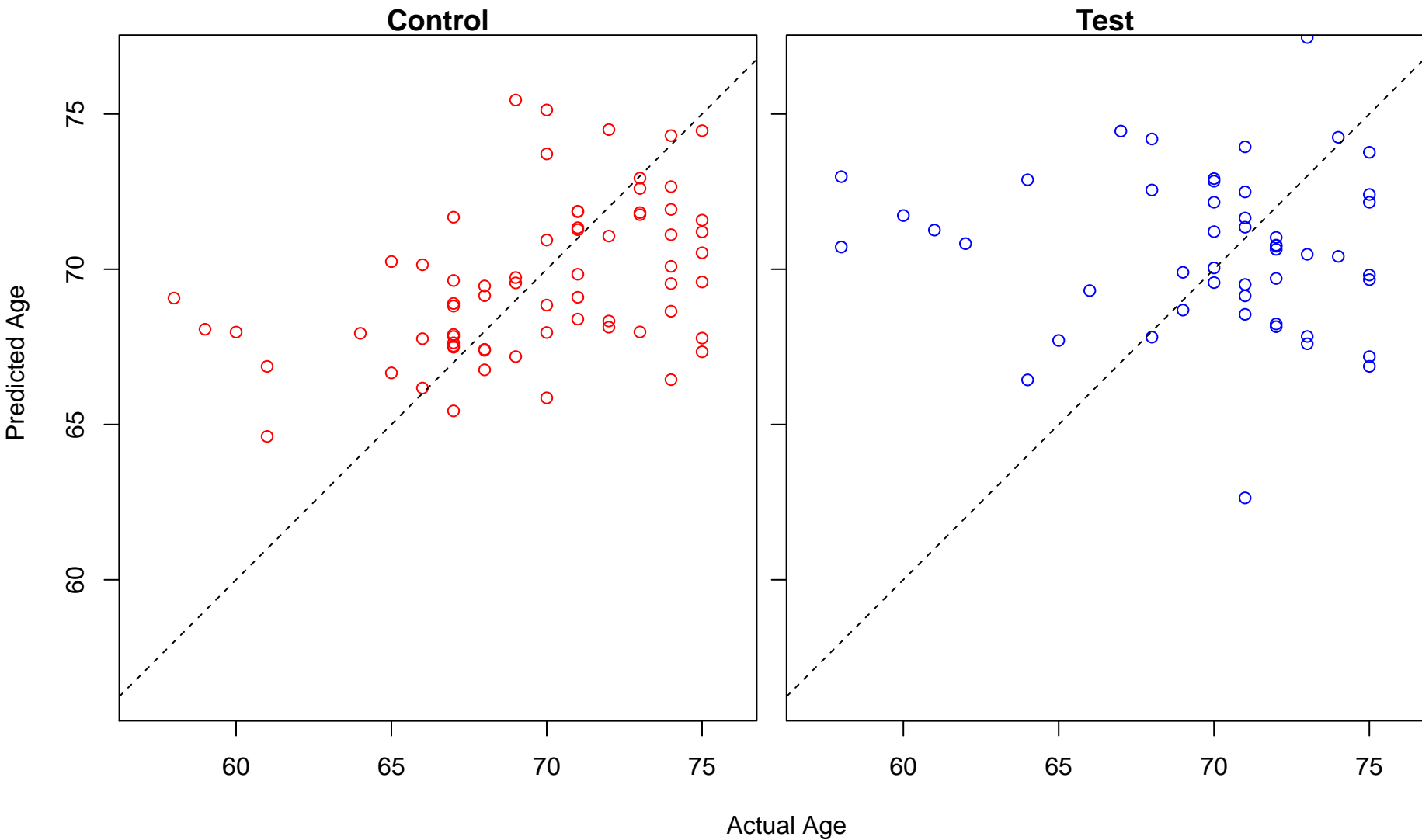
adrenal gland development (Score: 0.682806)



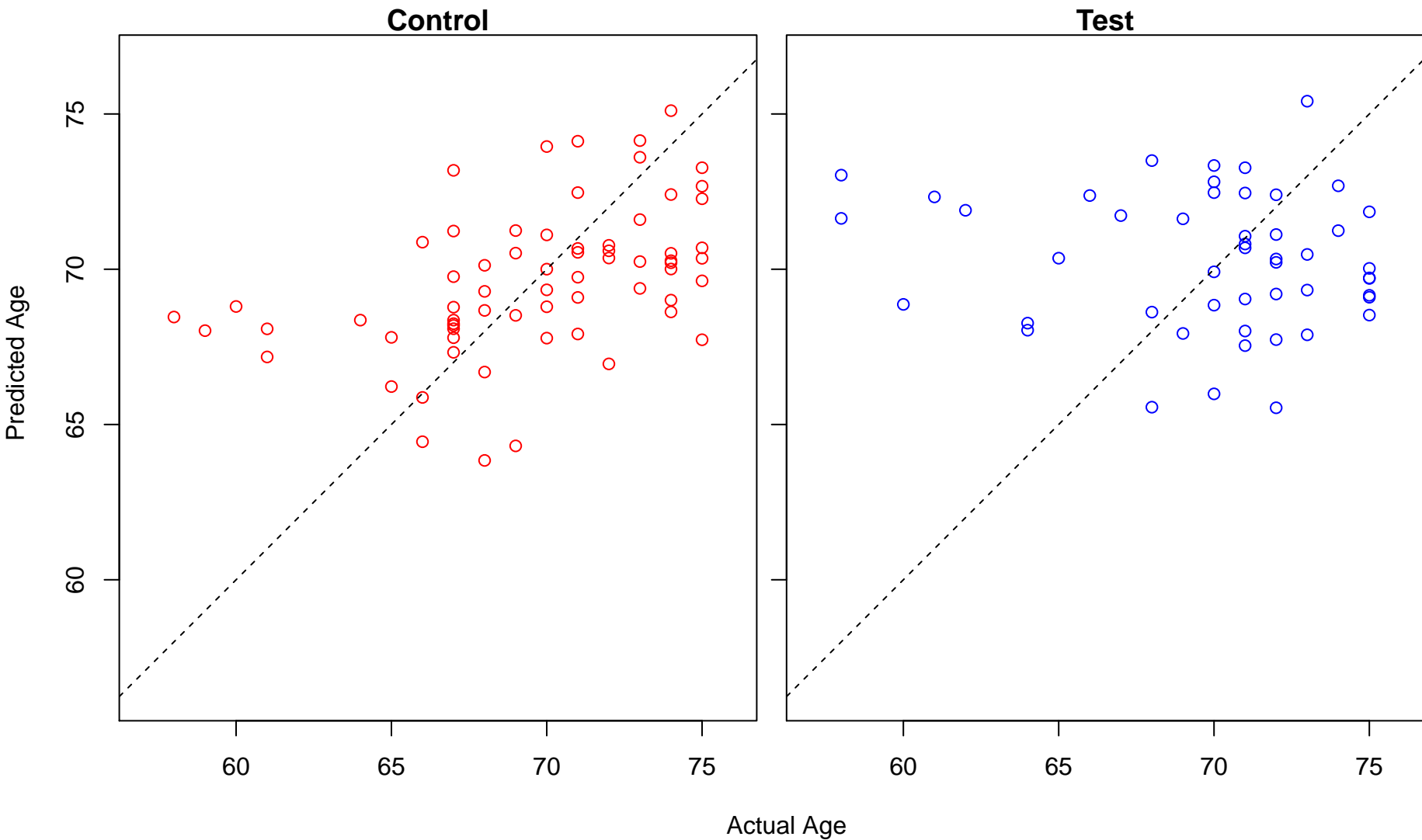
negative regulation of epithelial to mesenchymal transition (Score: 0.682296)



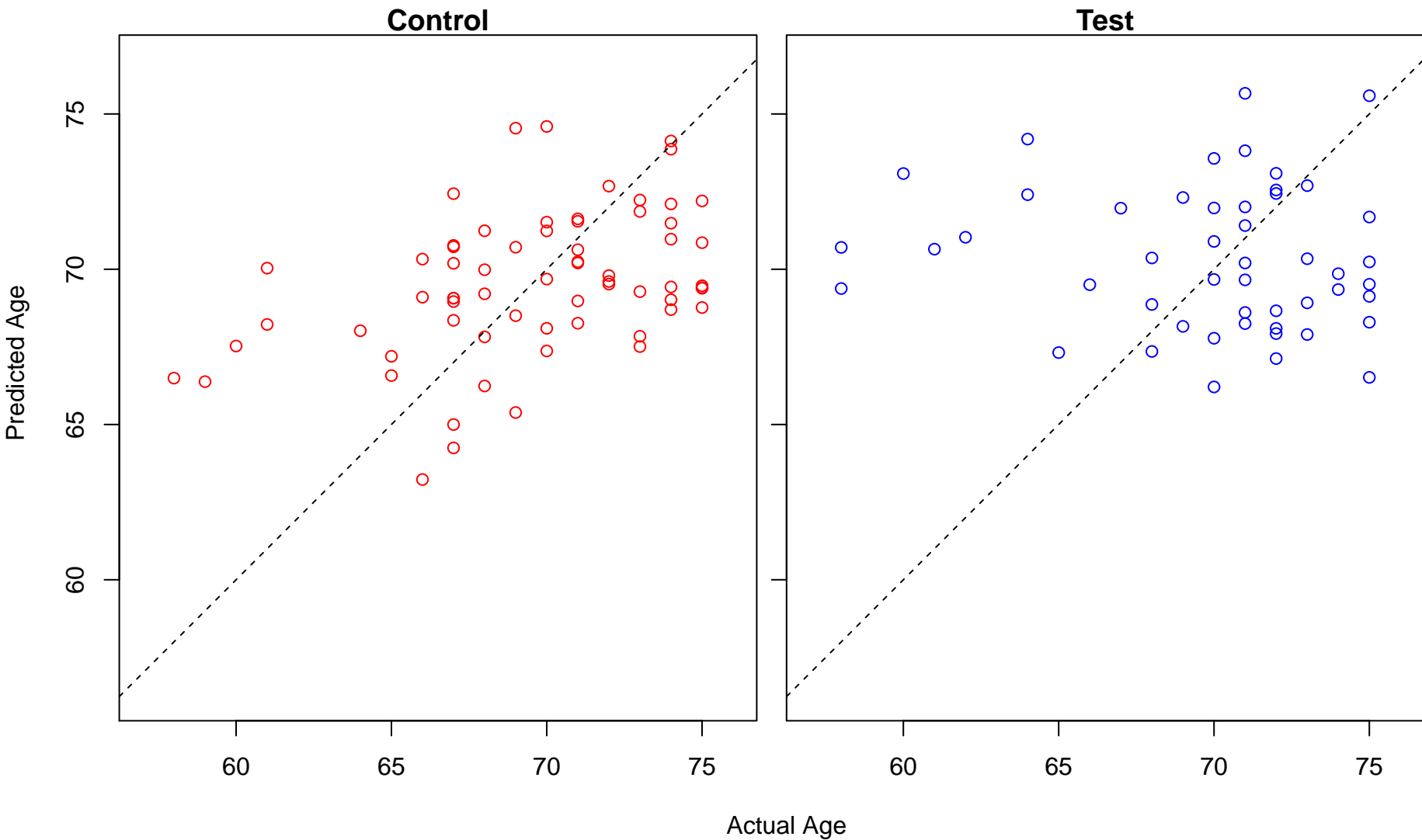
response to ketone (Score: 0.681776)



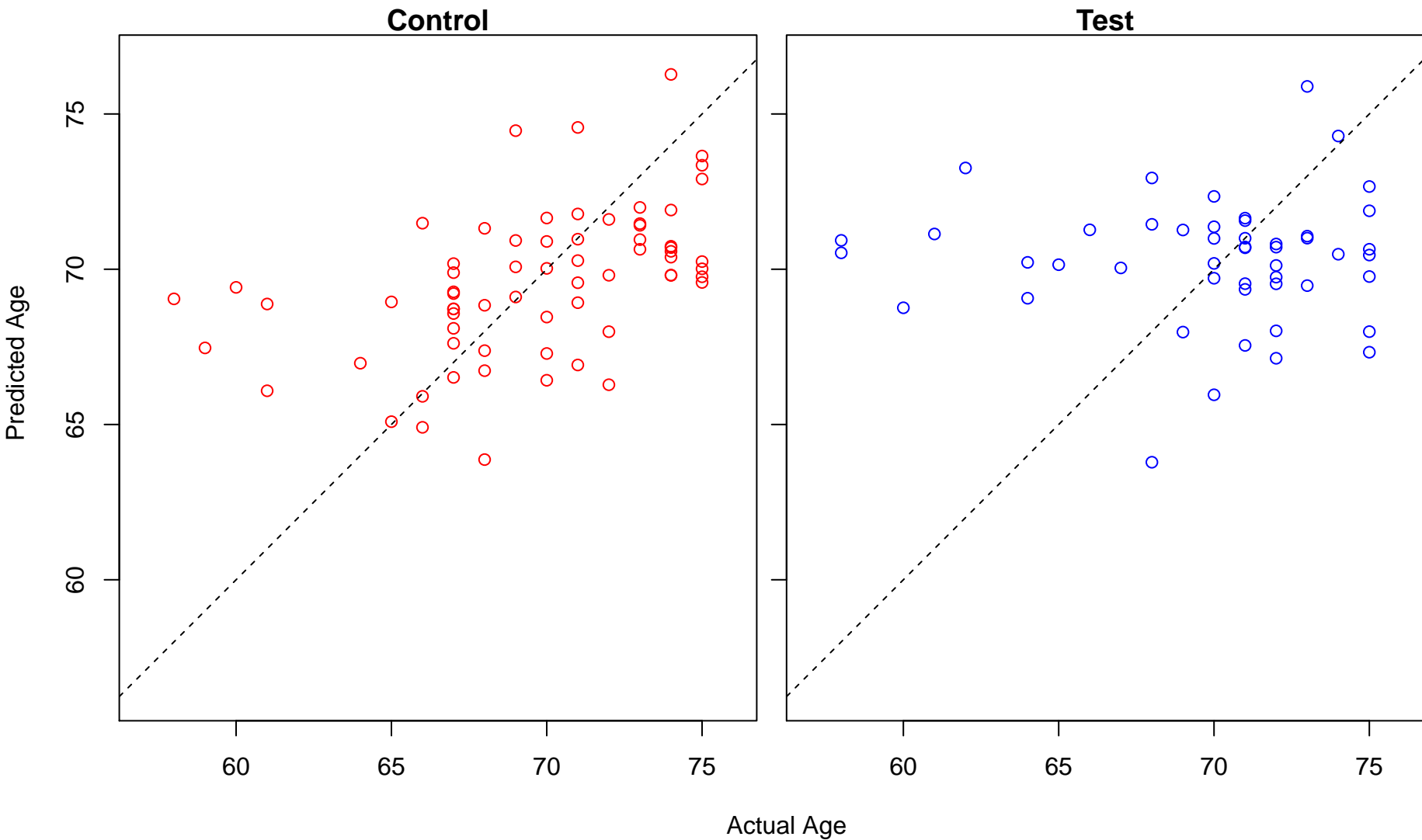
cytokinetic process (Score: 0.680468)



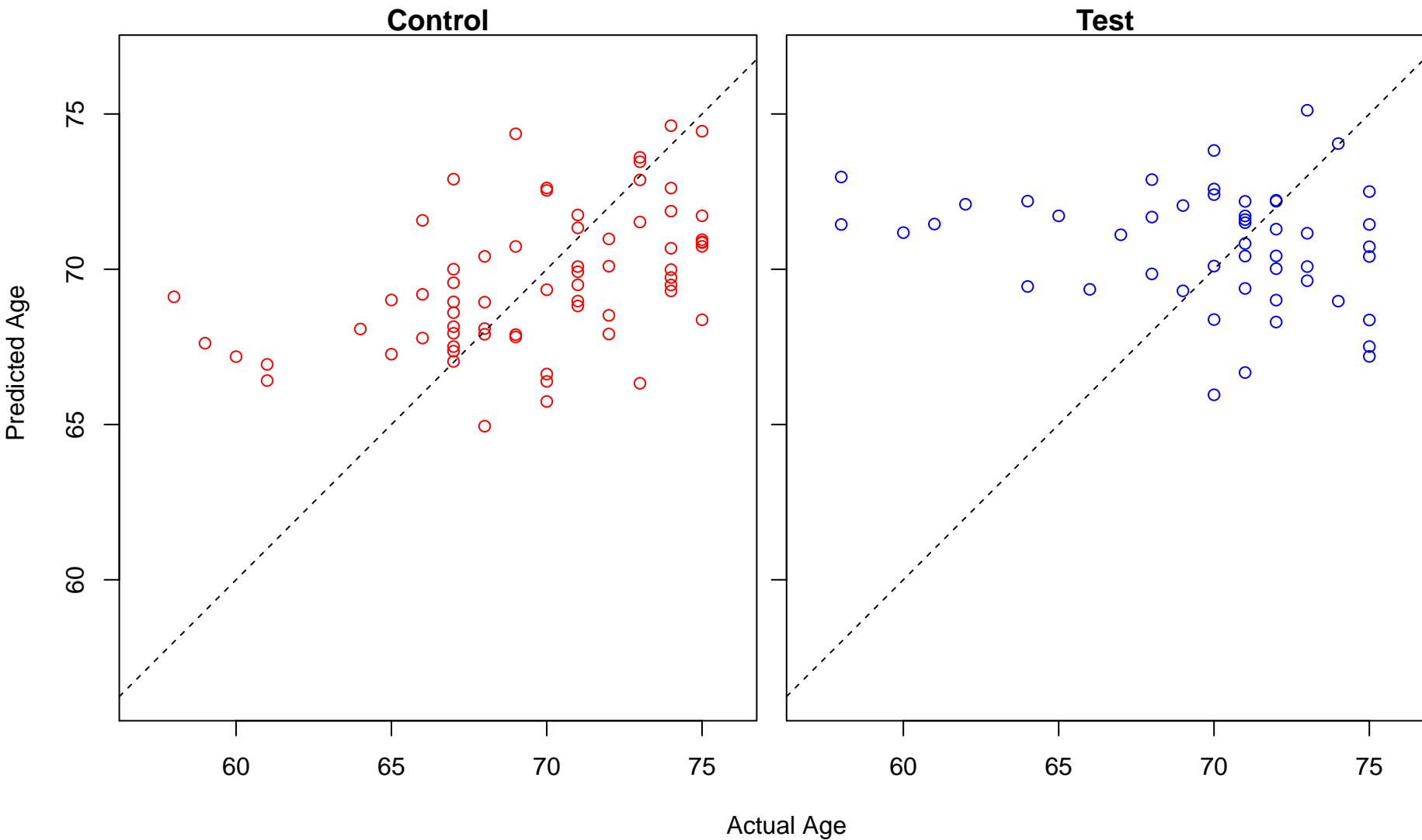
negative regulation of epidermis development (Score: 0.680055)



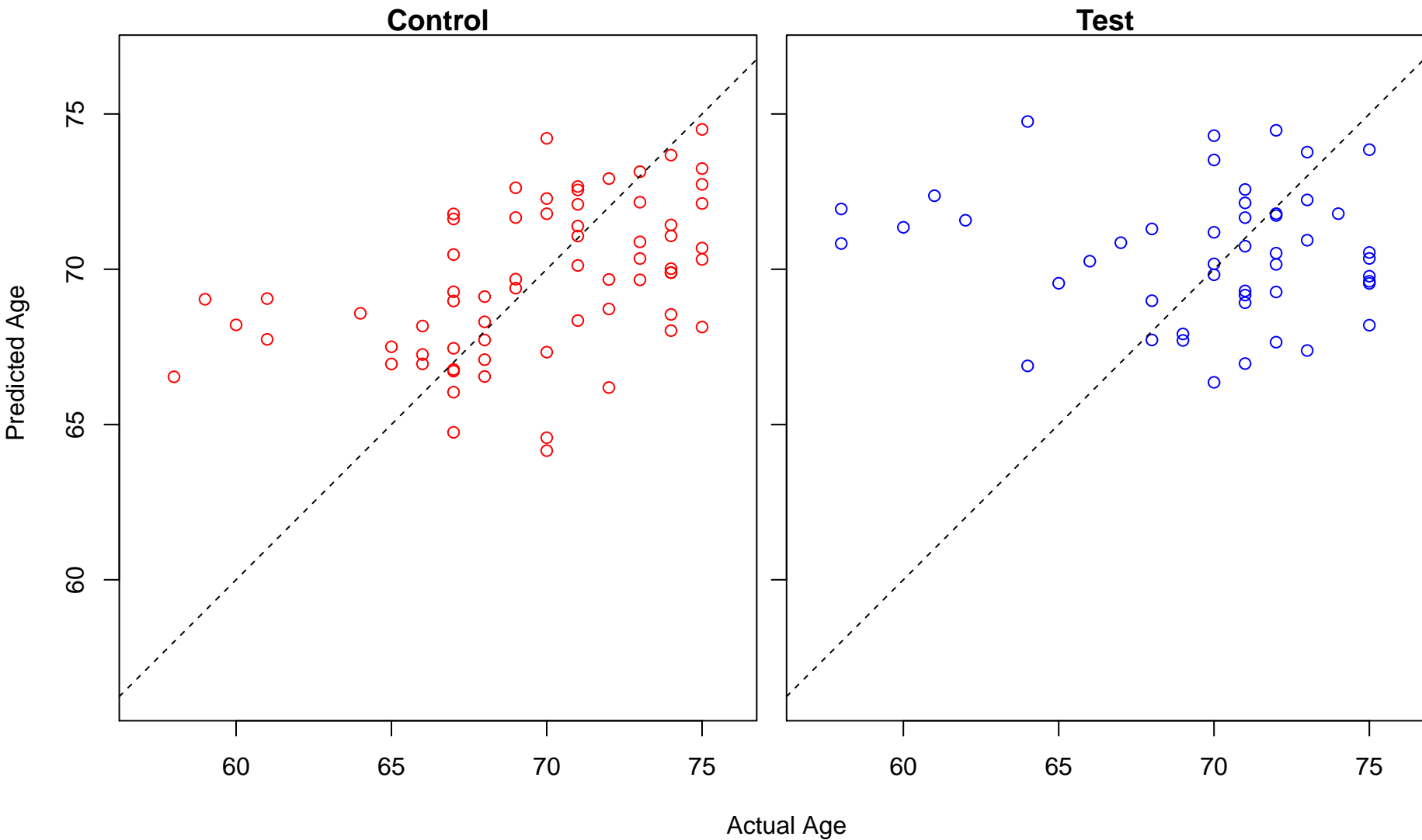
regulation of platelet-derived growth factor receptor signaling pathway (Score: 0.679806)



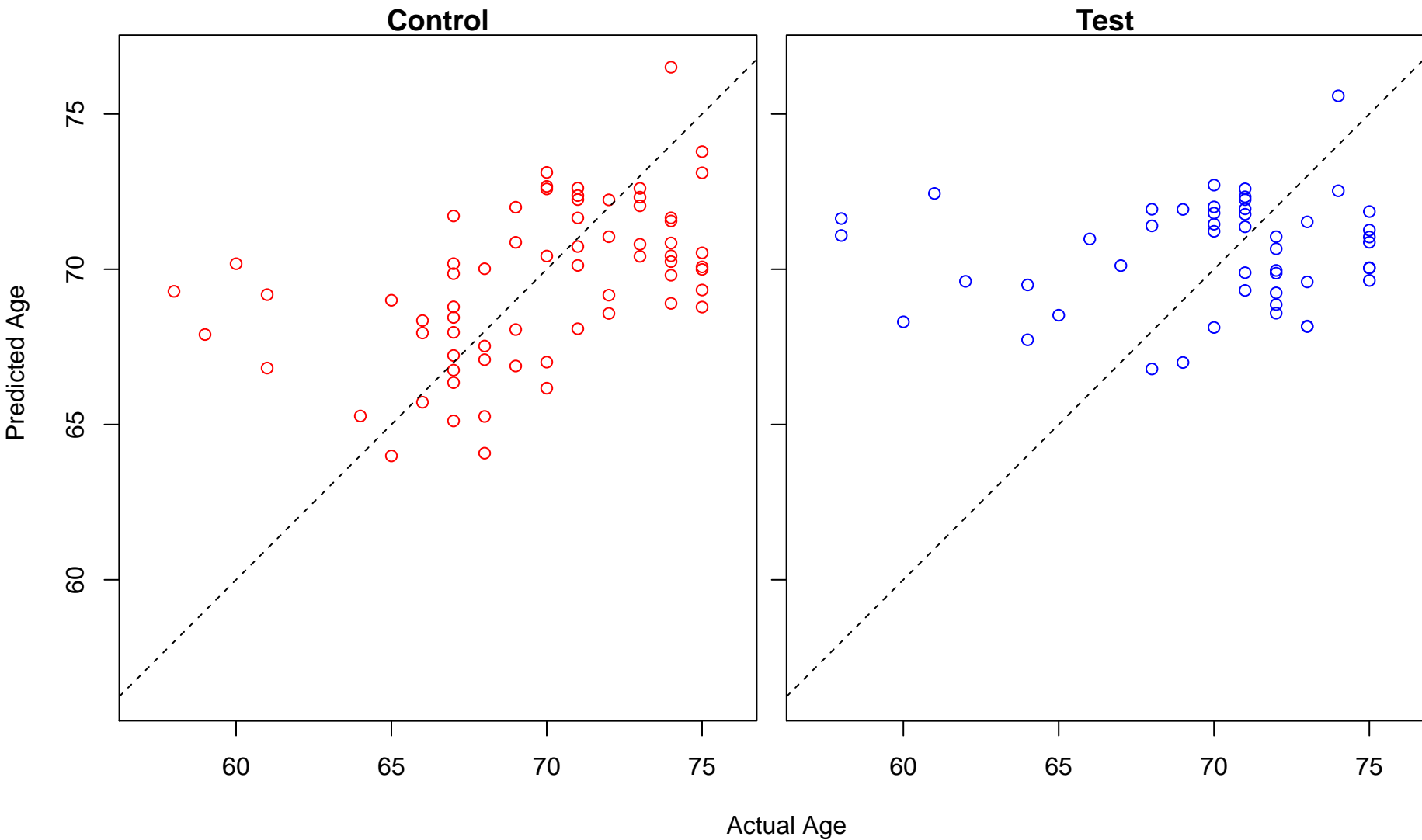
negative regulation of protein export from nucleus (Score: 0.679240)



positive regulation of striated muscle cell differentiation (Score: 0.679210)

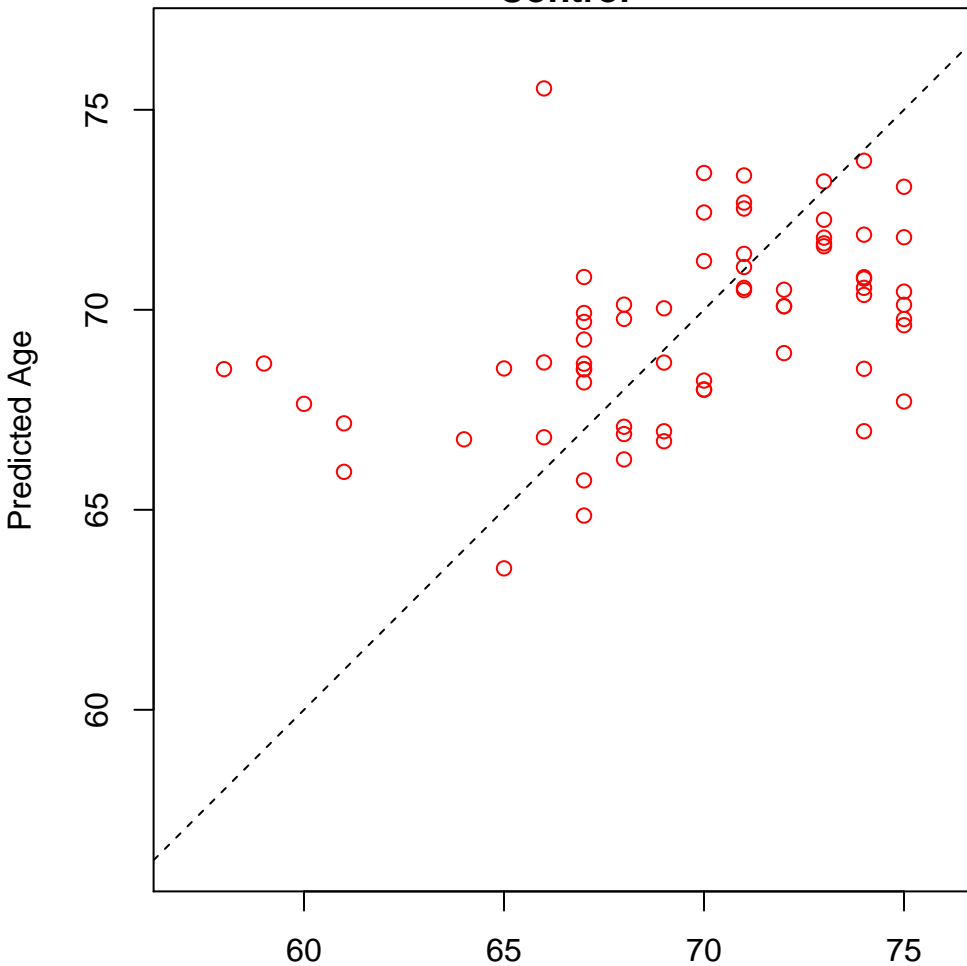


negative regulation of cytokine biosynthetic process (Score: 0.678817)

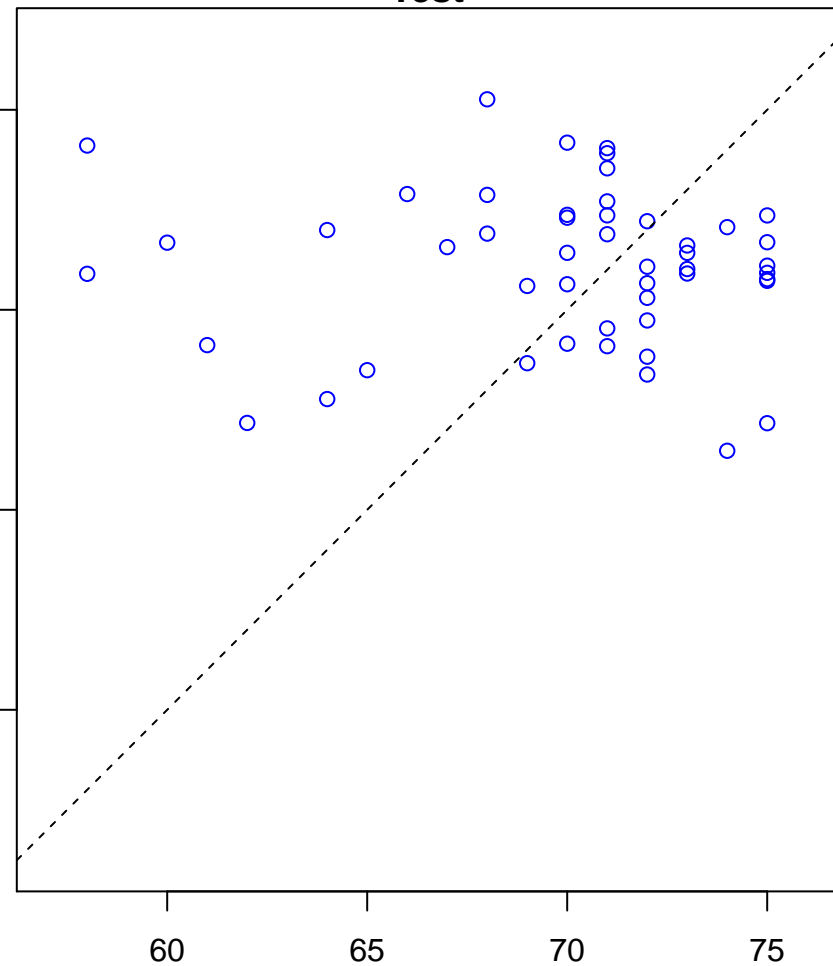


N-terminal protein amino acid acetylation (Score: 0.677640)

Control

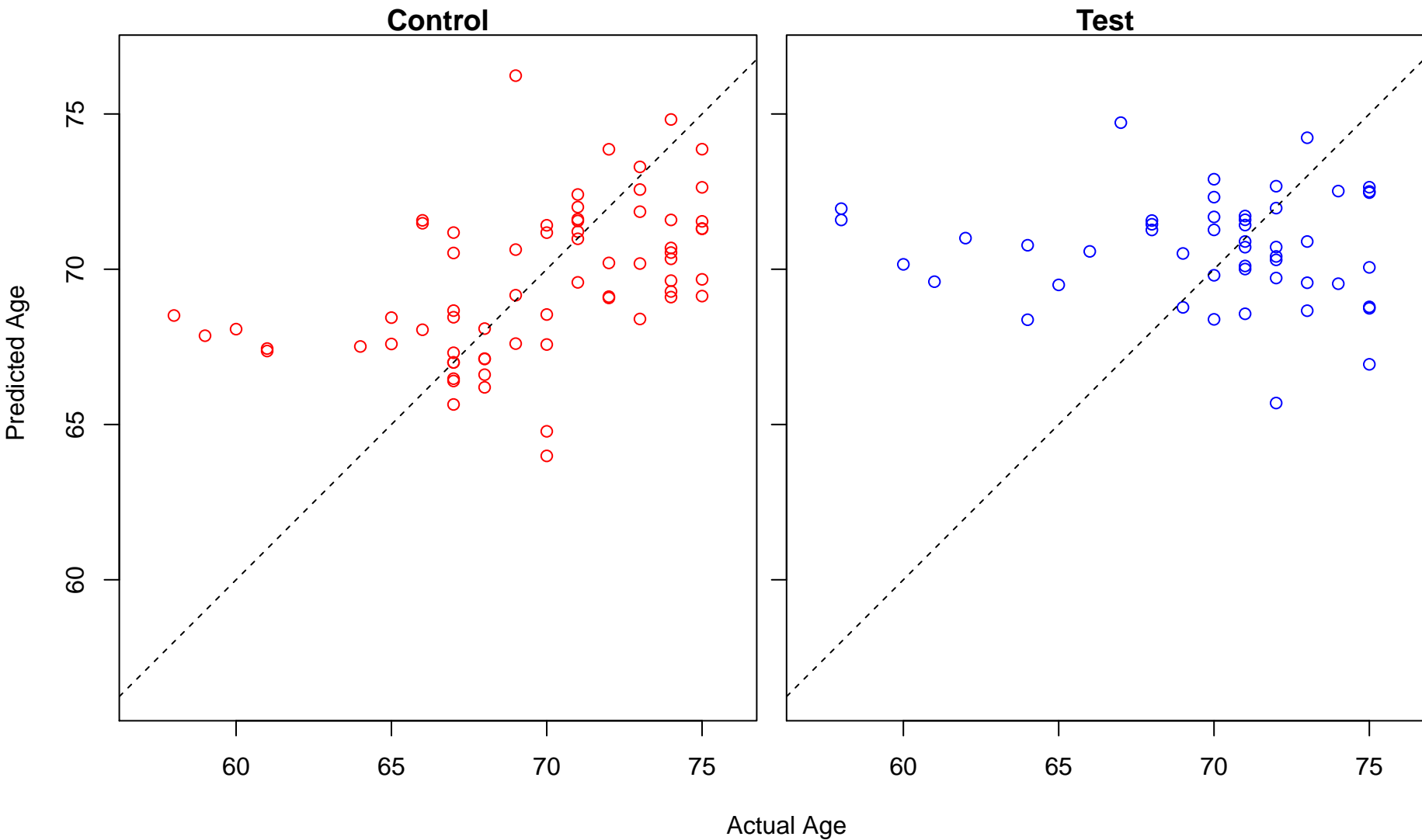


Test

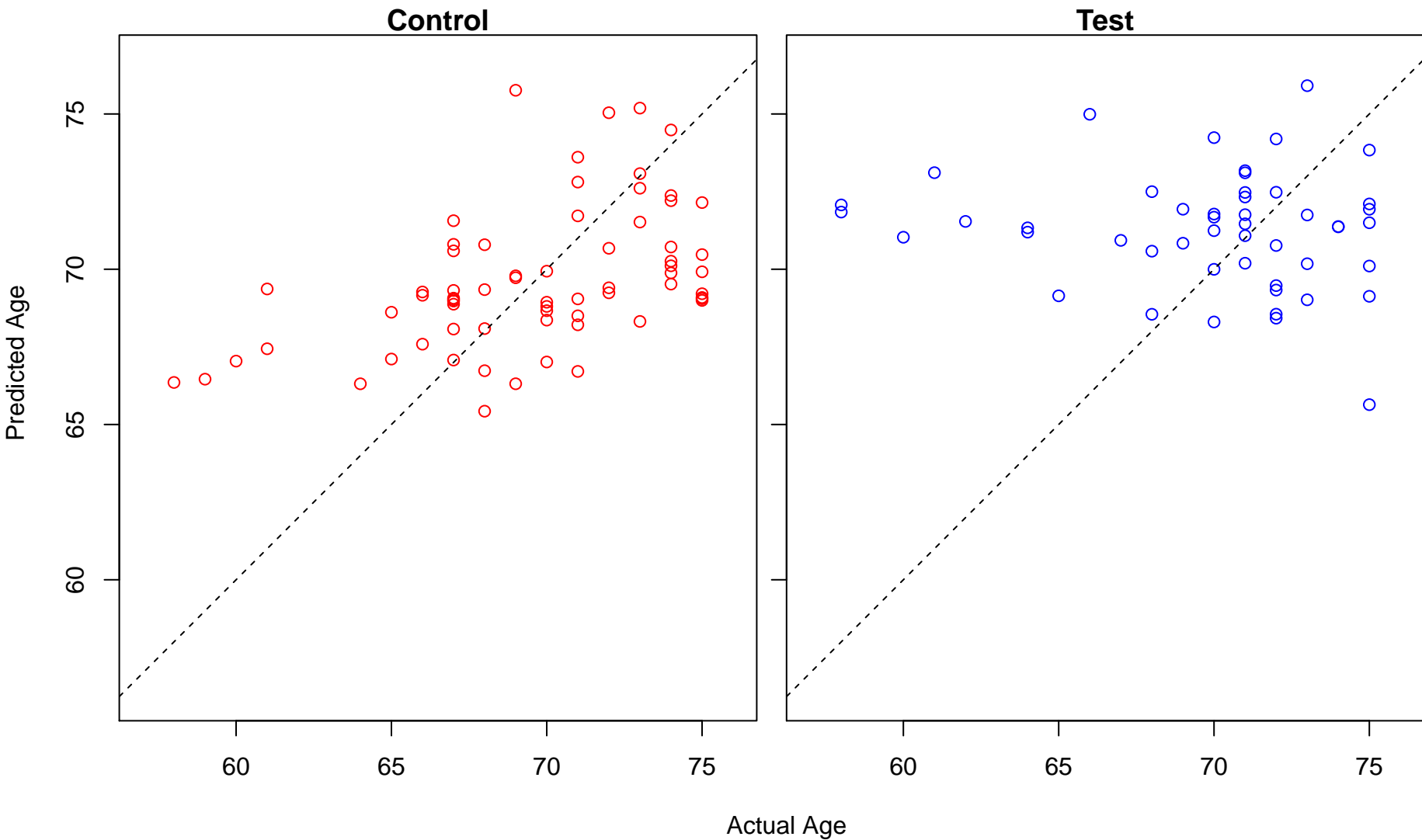


Actual Age

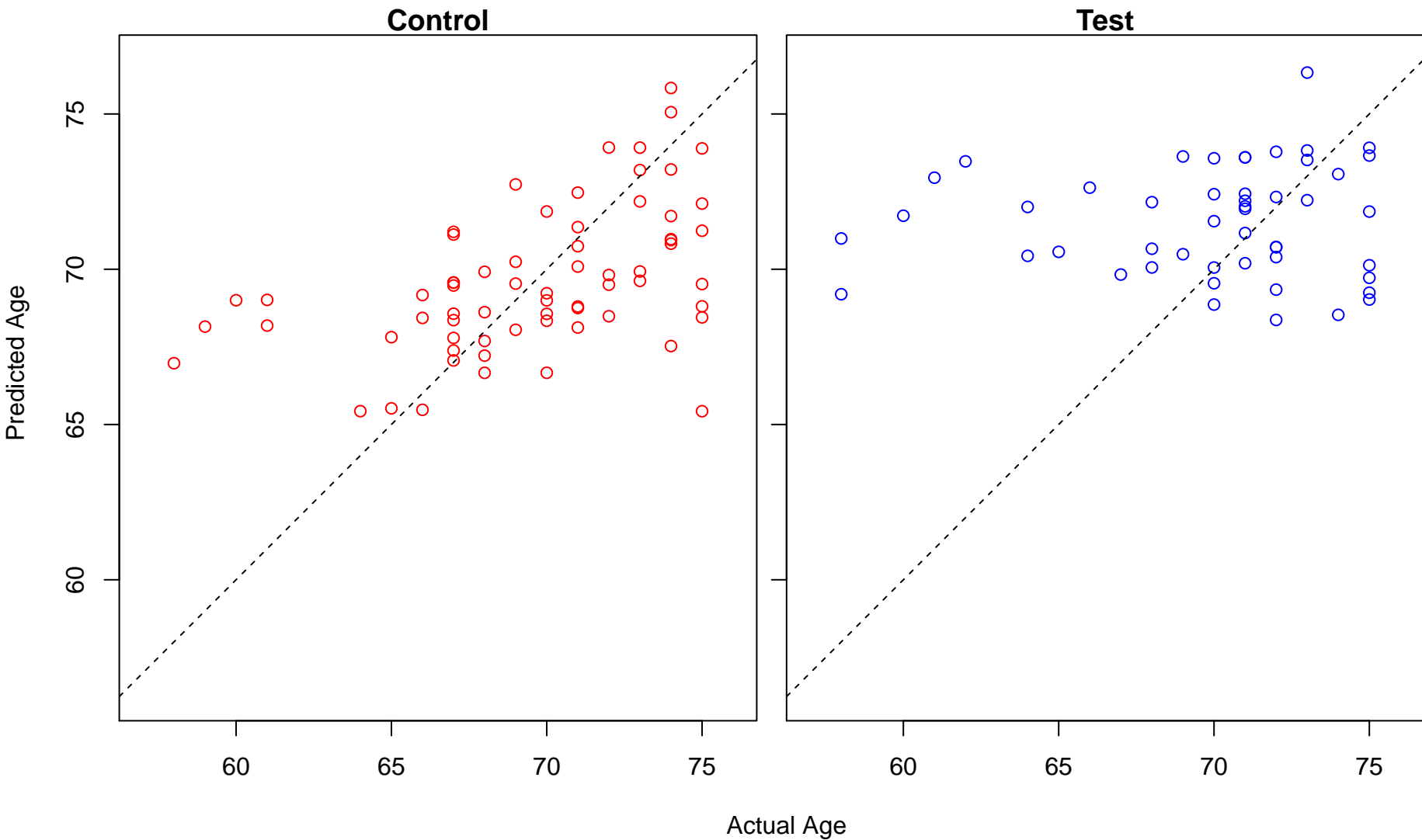
positive regulation of cell aging (Score: 0.677474)



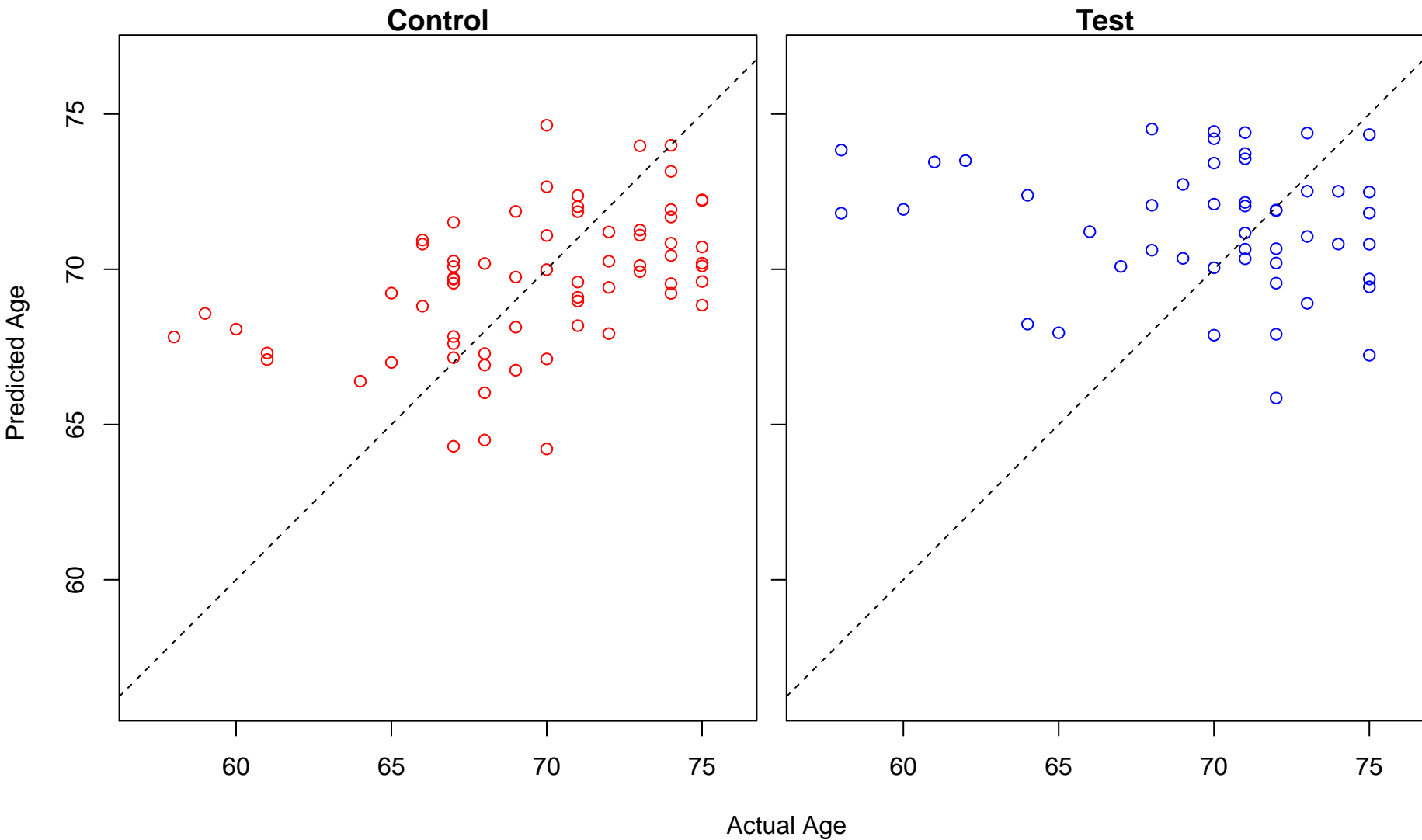
opioid receptor signaling pathway (Score: 0.676668)



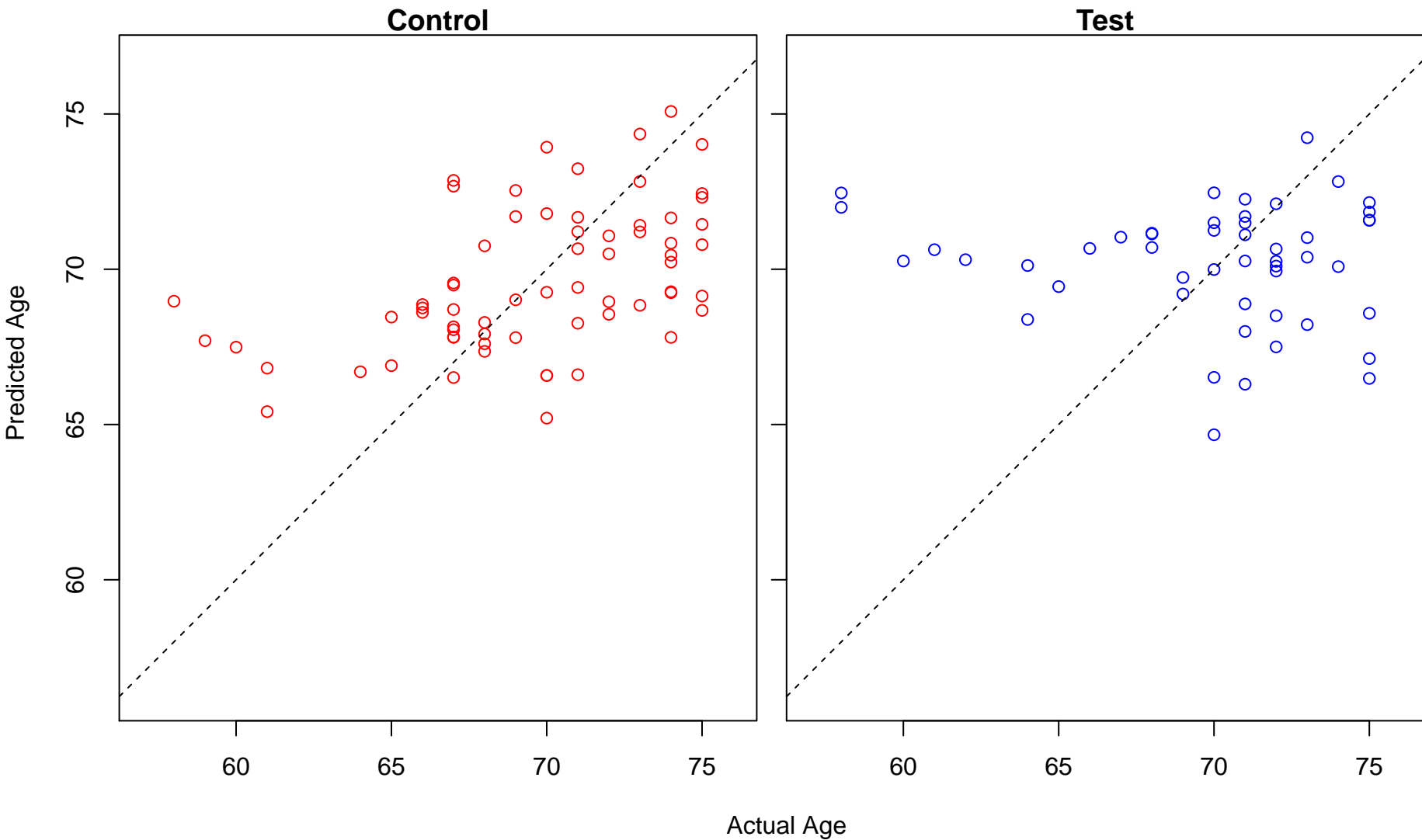
high-density lipoprotein particle assembly (Score: 0.675508)



microtubule anchoring (Score: 0.675431)

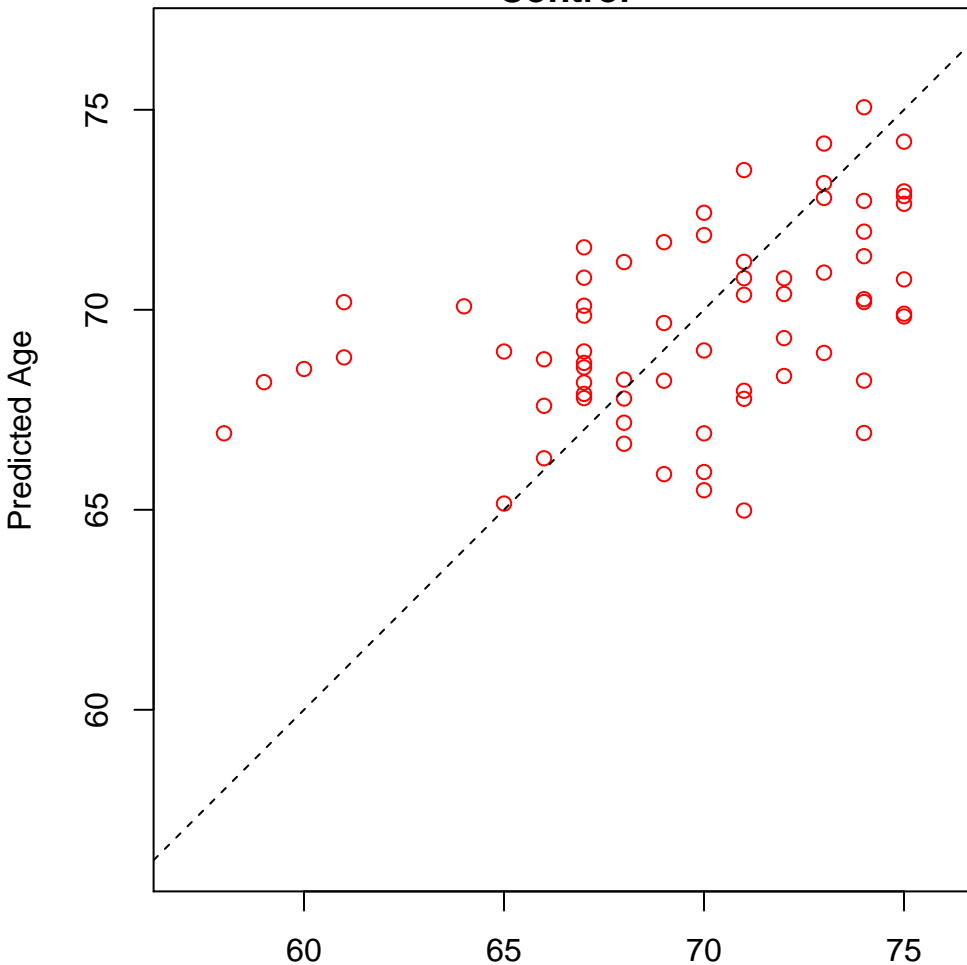


semaphorin-plexin signaling pathway (Score: 0.674866)

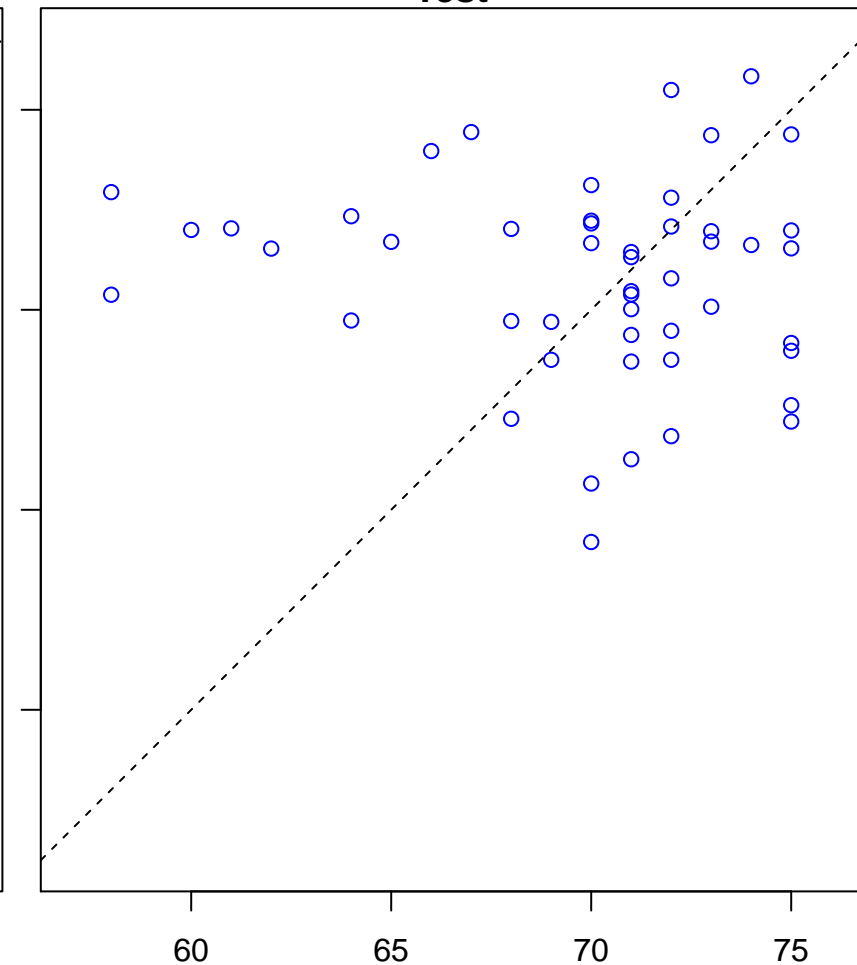


establishment of monopolar cell polarity (Score: 0.674193)

Control

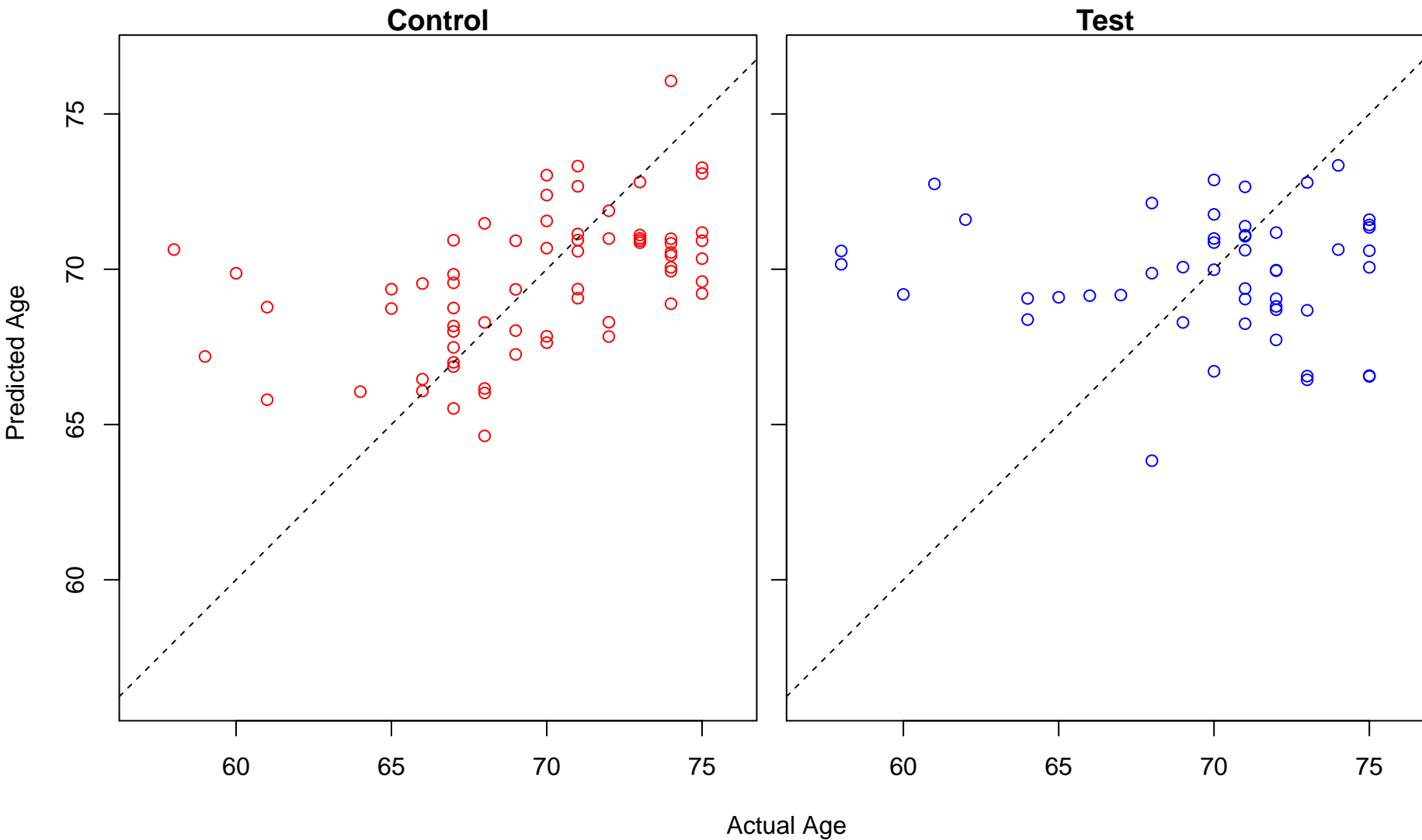


Test

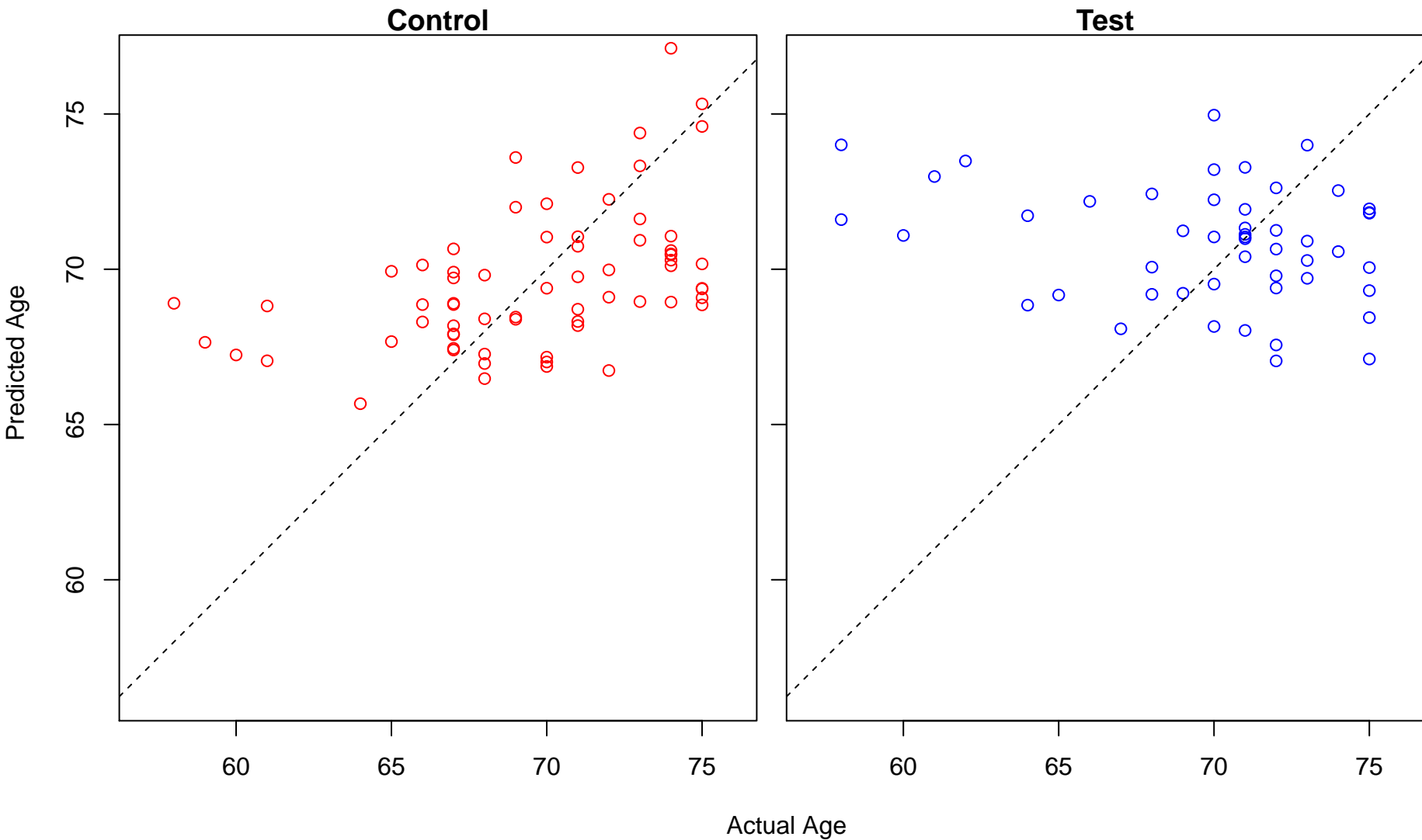


Actual Age

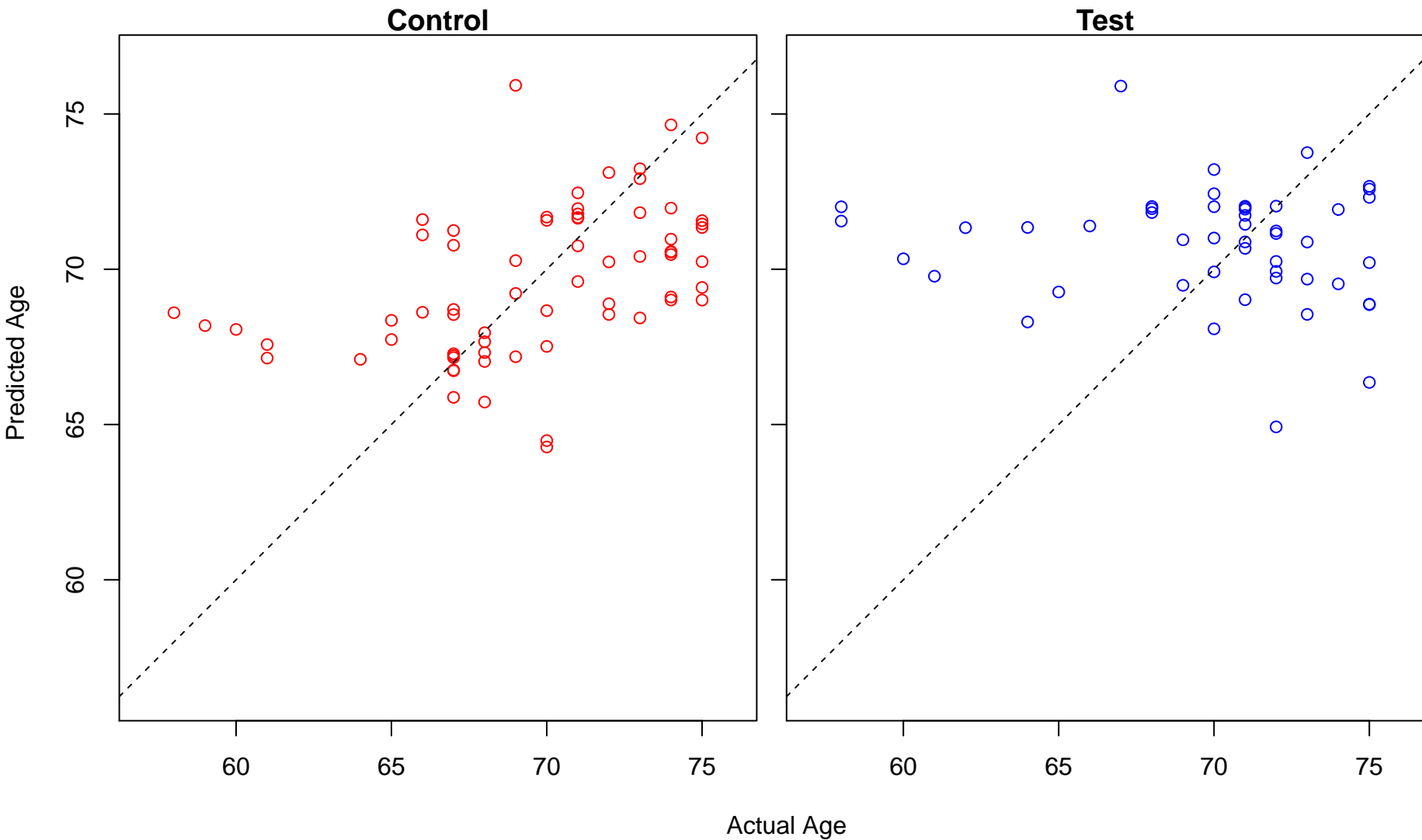
regulation of cytolysis (Score: 0.673655)



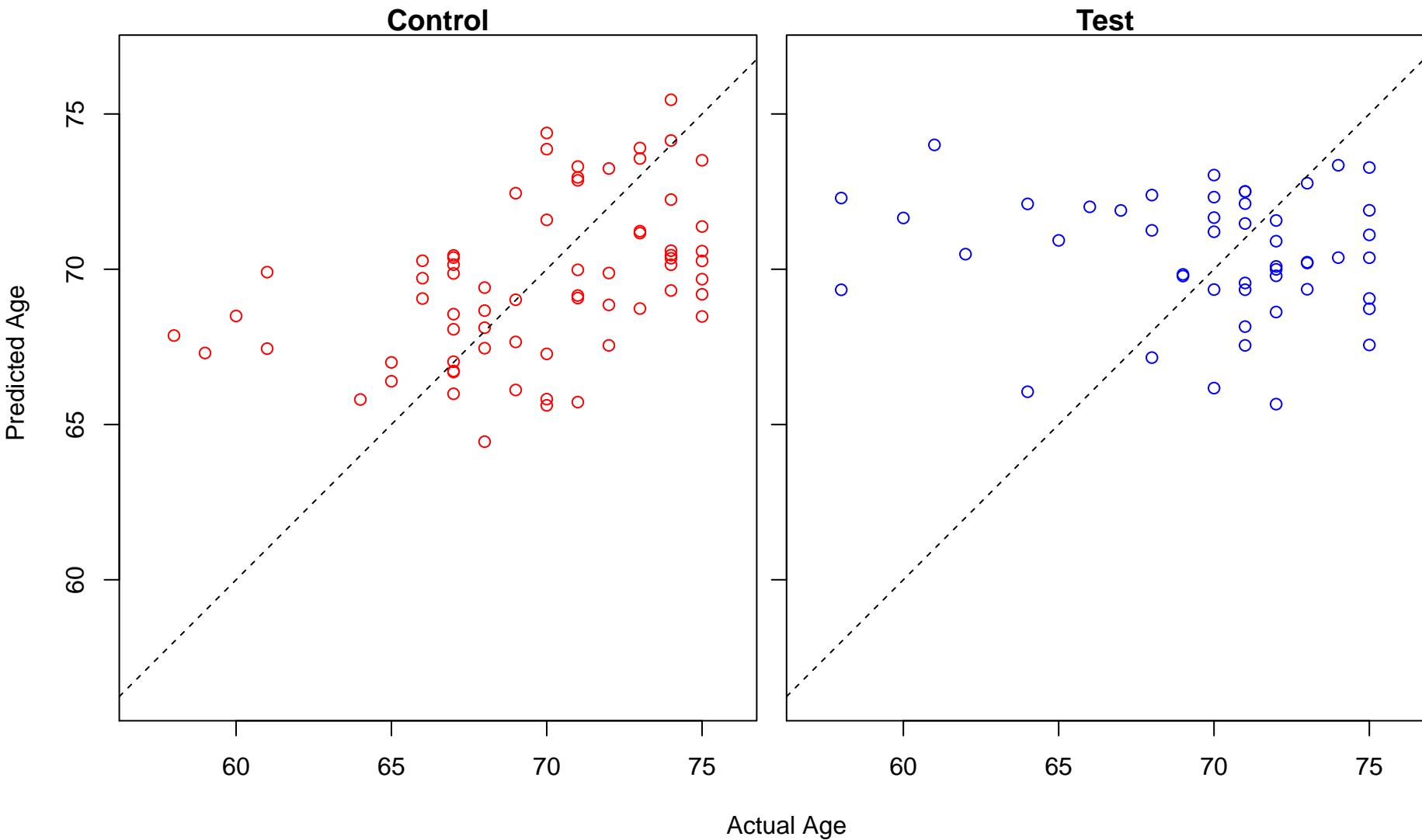
glycogen catabolic process (Score: 0.673432)



positive regulation of cellular senescence (Score: 0.672920)

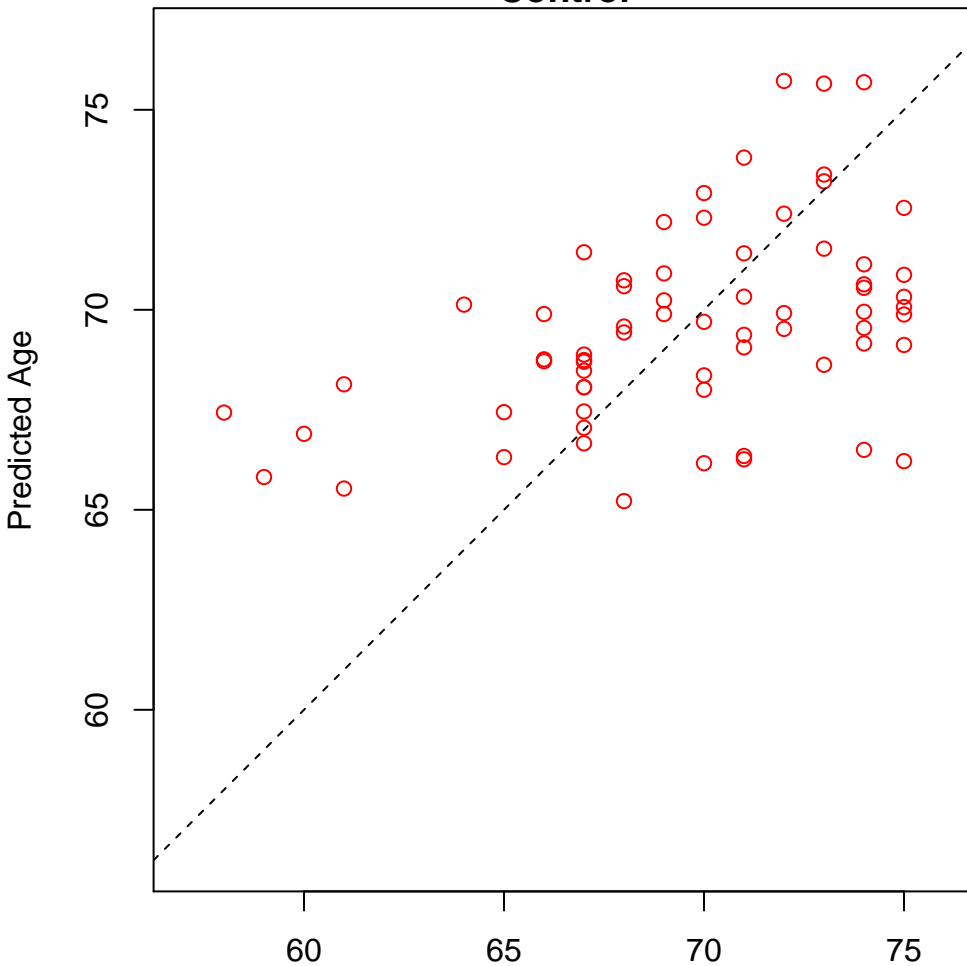


regulation of cell cycle checkpoint (Score: 0.672801)

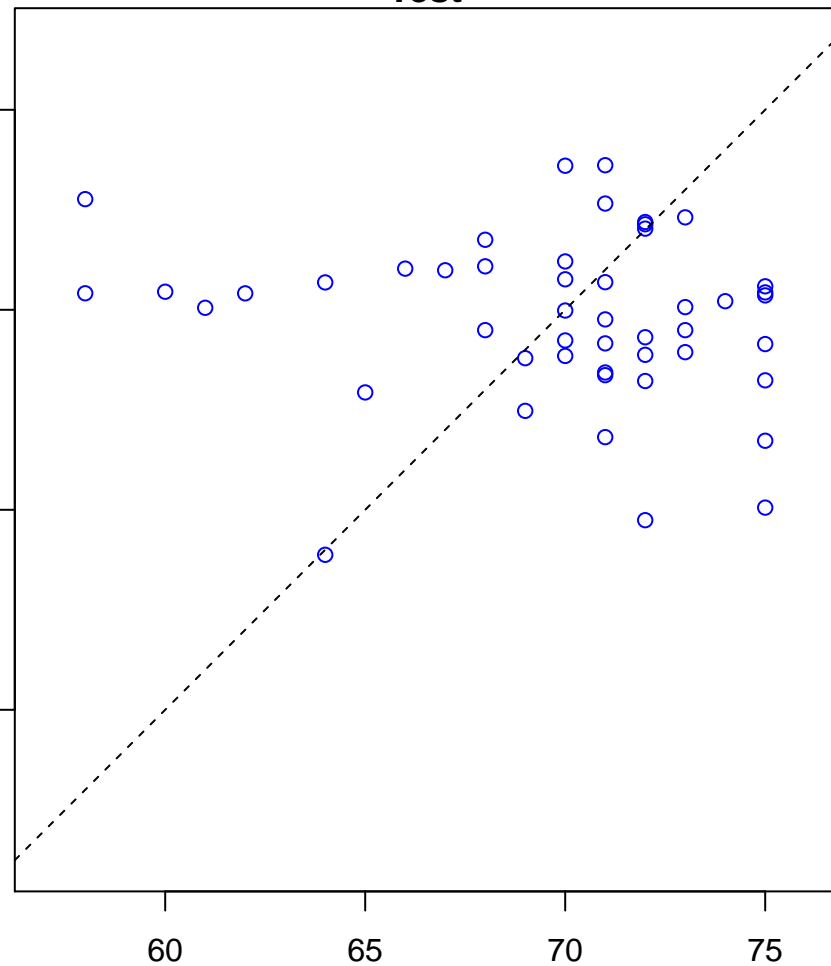


regulation of dendritic cell chemotaxis (Score: 0.672743)

Control

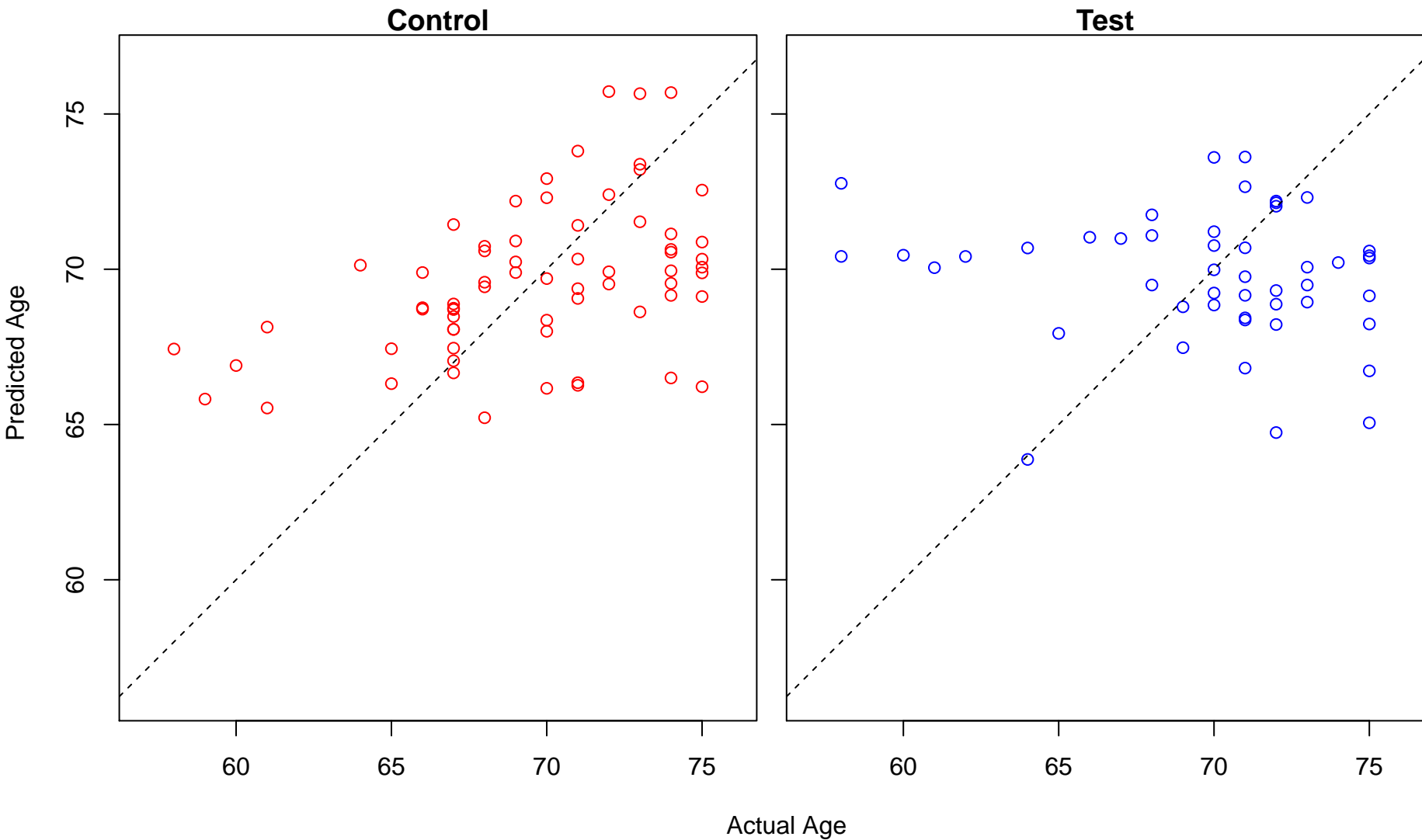


Test

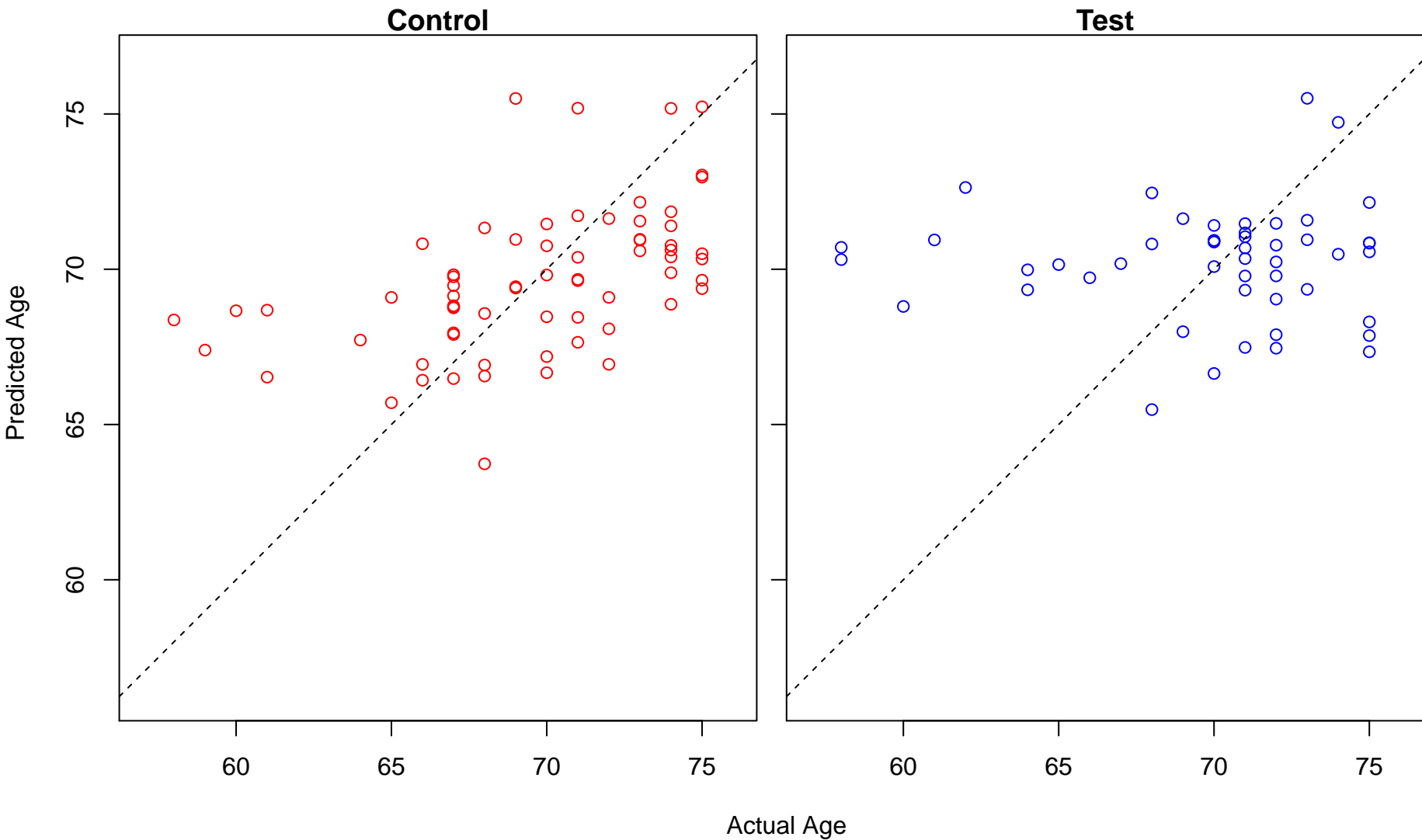


Actual Age

positive regulation of dendritic cell chemotaxis (Score: 0.672743)

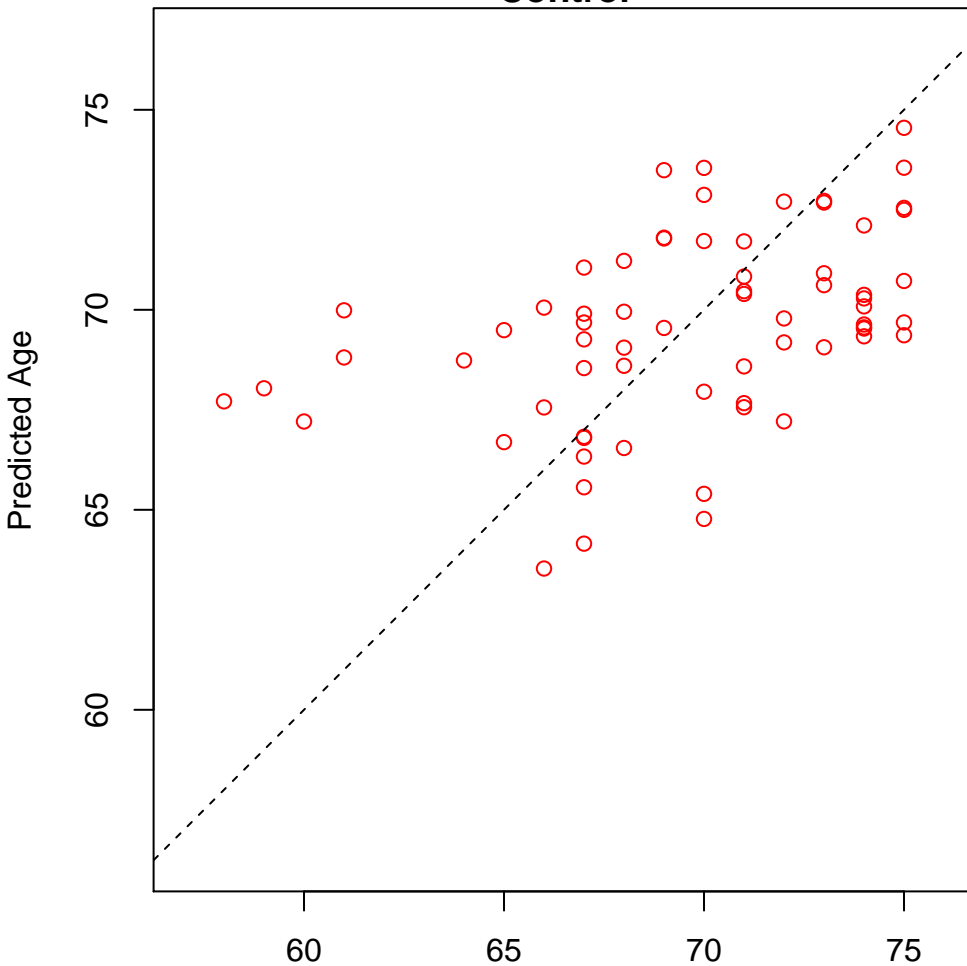


negative regulation of macrophage differentiation (Score: 0.672738)

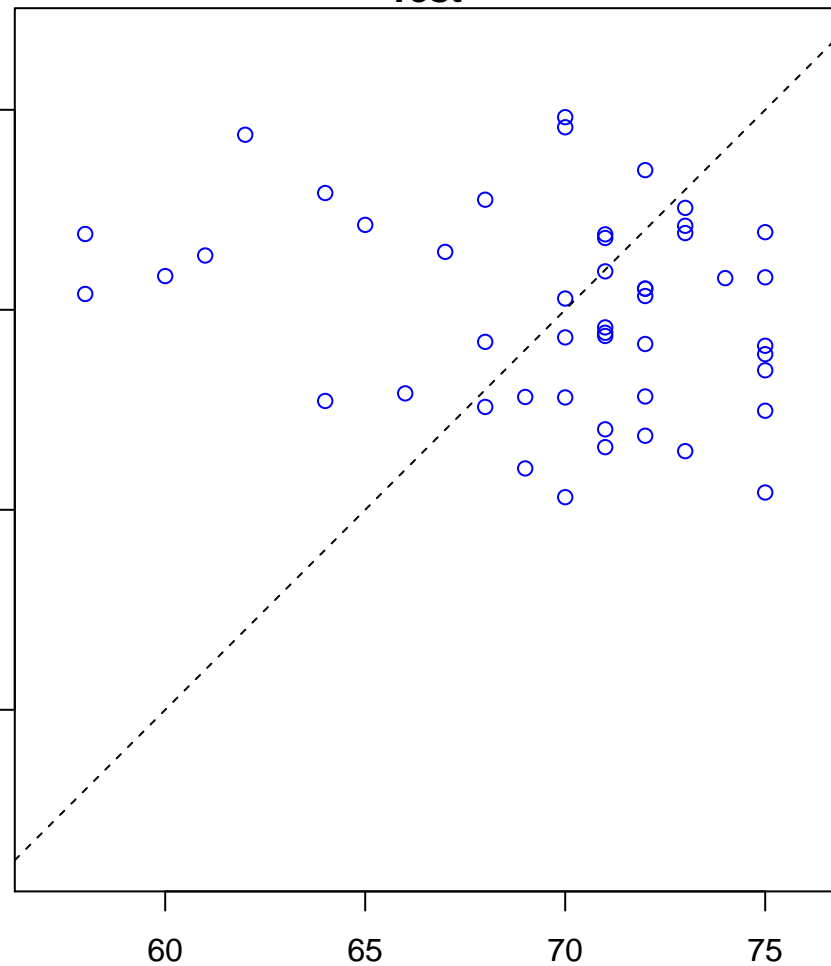


positive regulation of myoblast fusion (Score: 0.672456)

Control

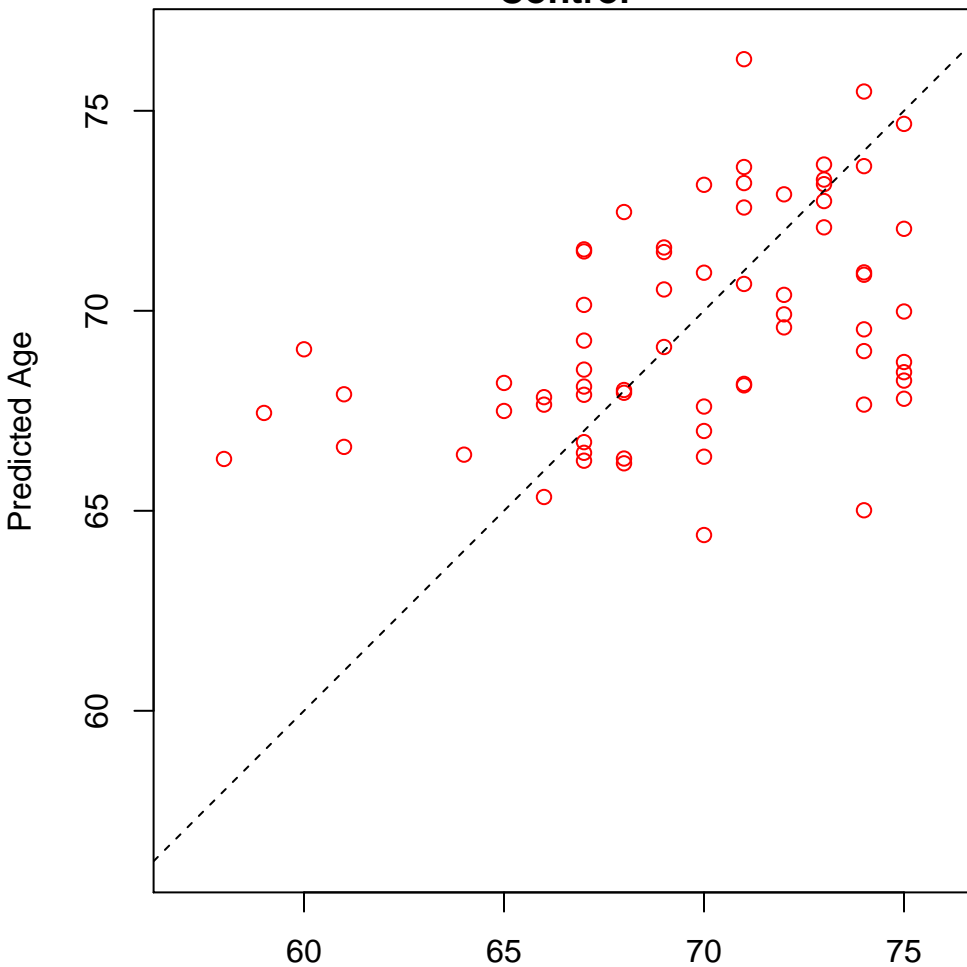


Test

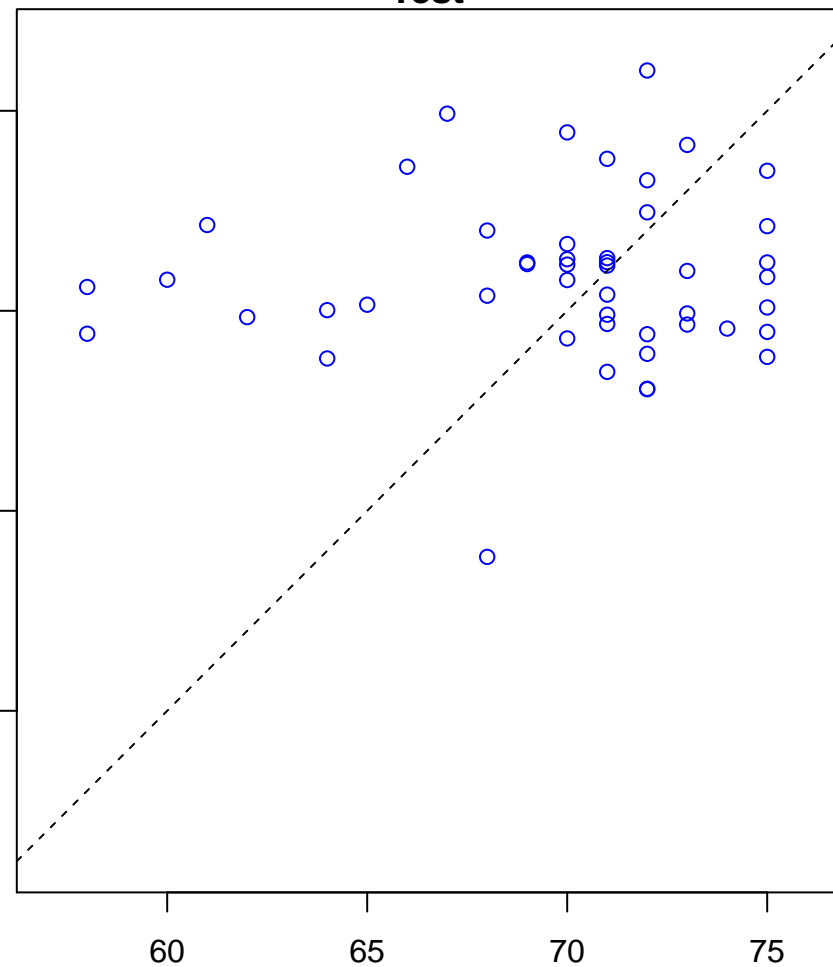


pyrimidine nucleotide metabolic process (Score: 0.672227)

Control

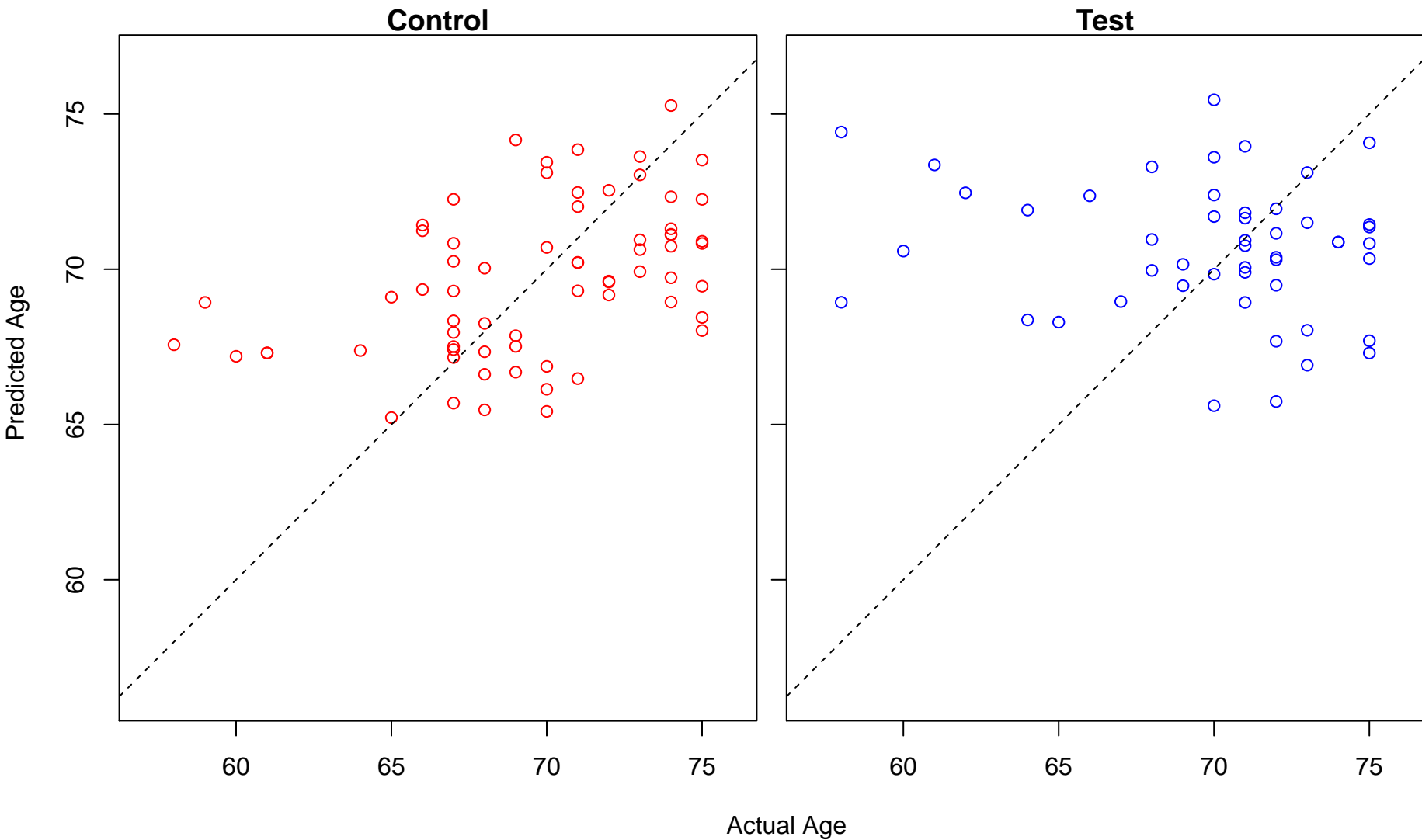


Test

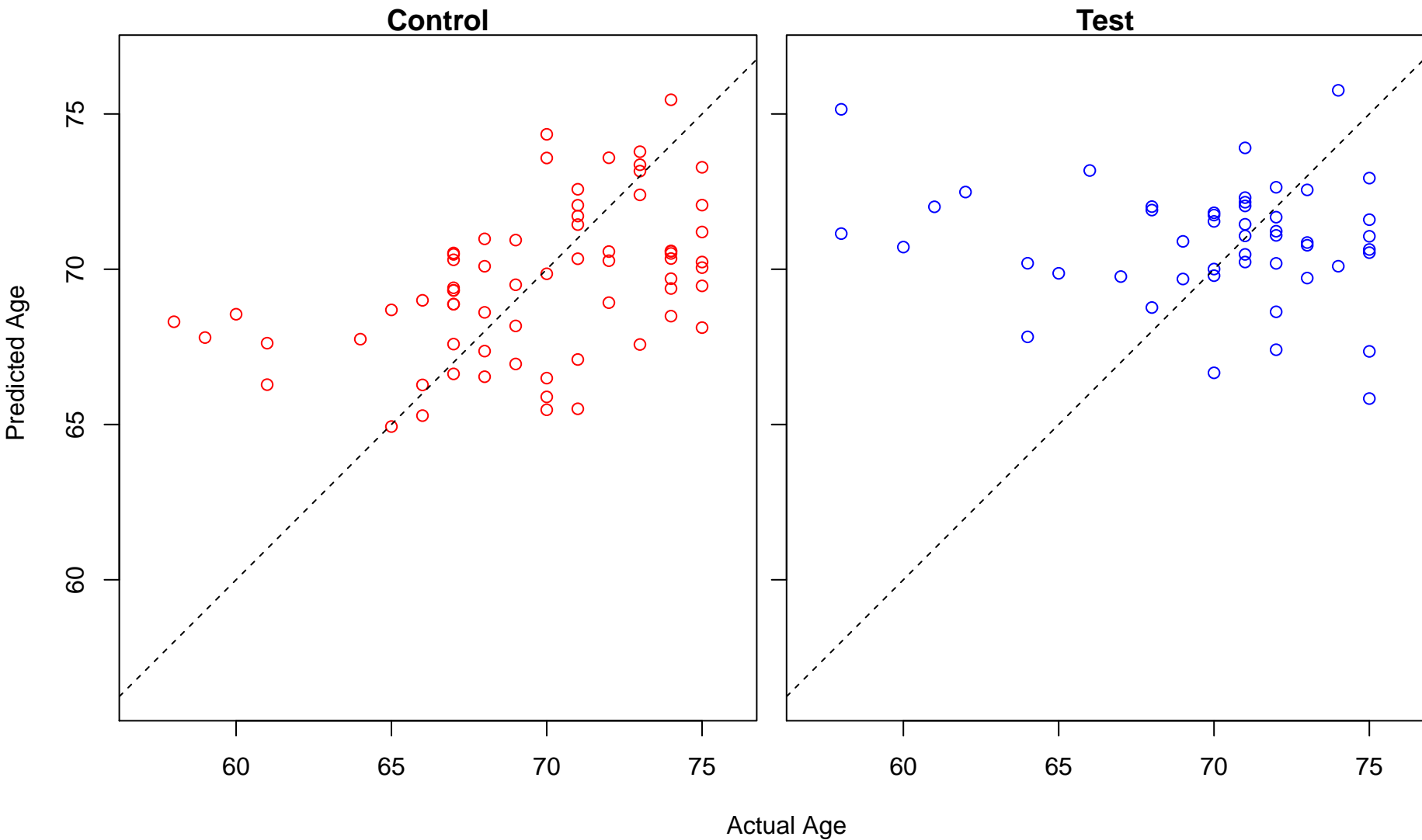


Actual Age

bile acid and bile salt transport (Score: 0.671967)

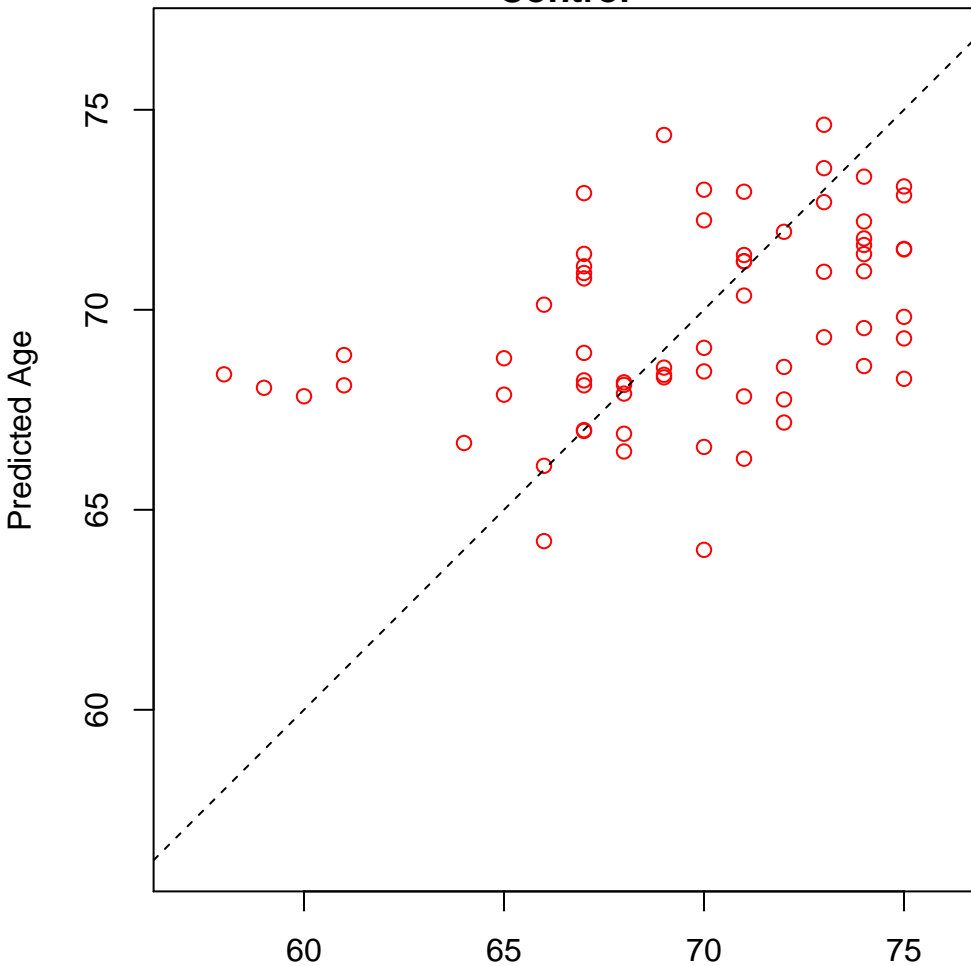


endodermal cell differentiation (Score: 0.671813)

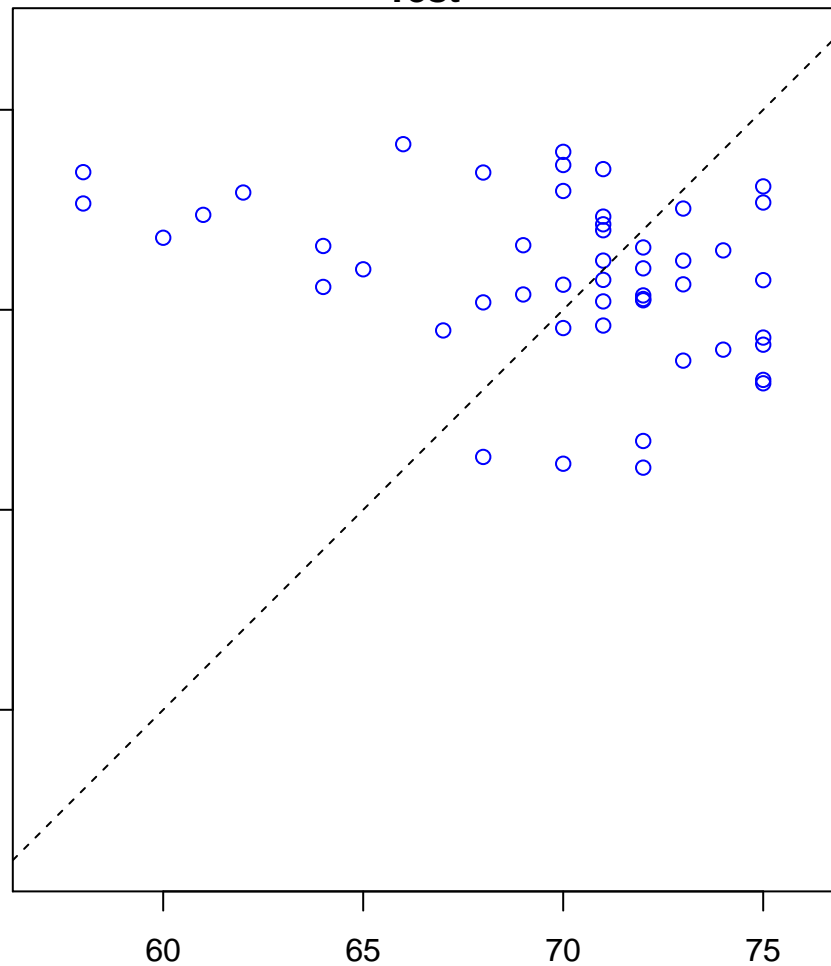


positive regulation of insulin secretion (Score: 0.671568)

Control

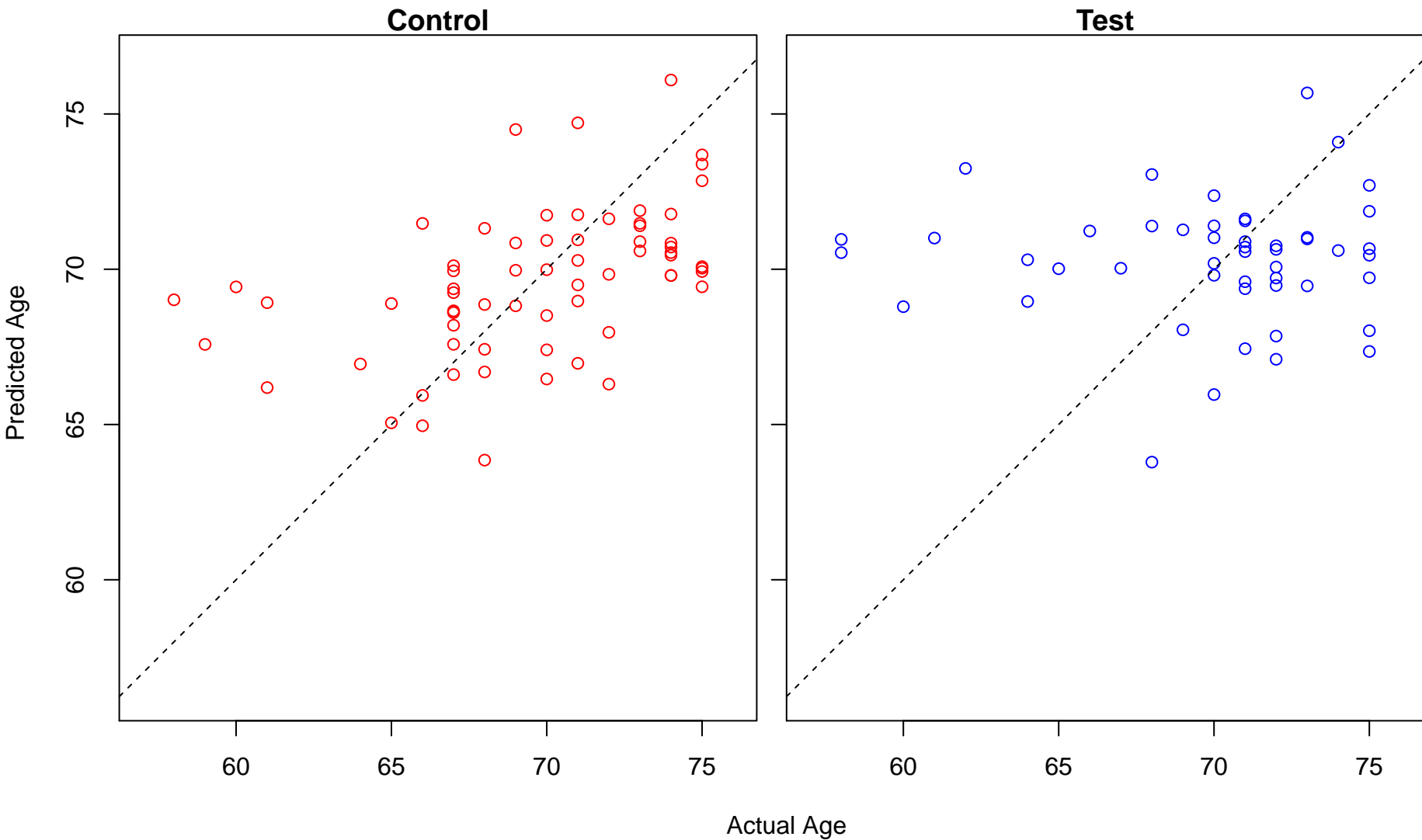


Test

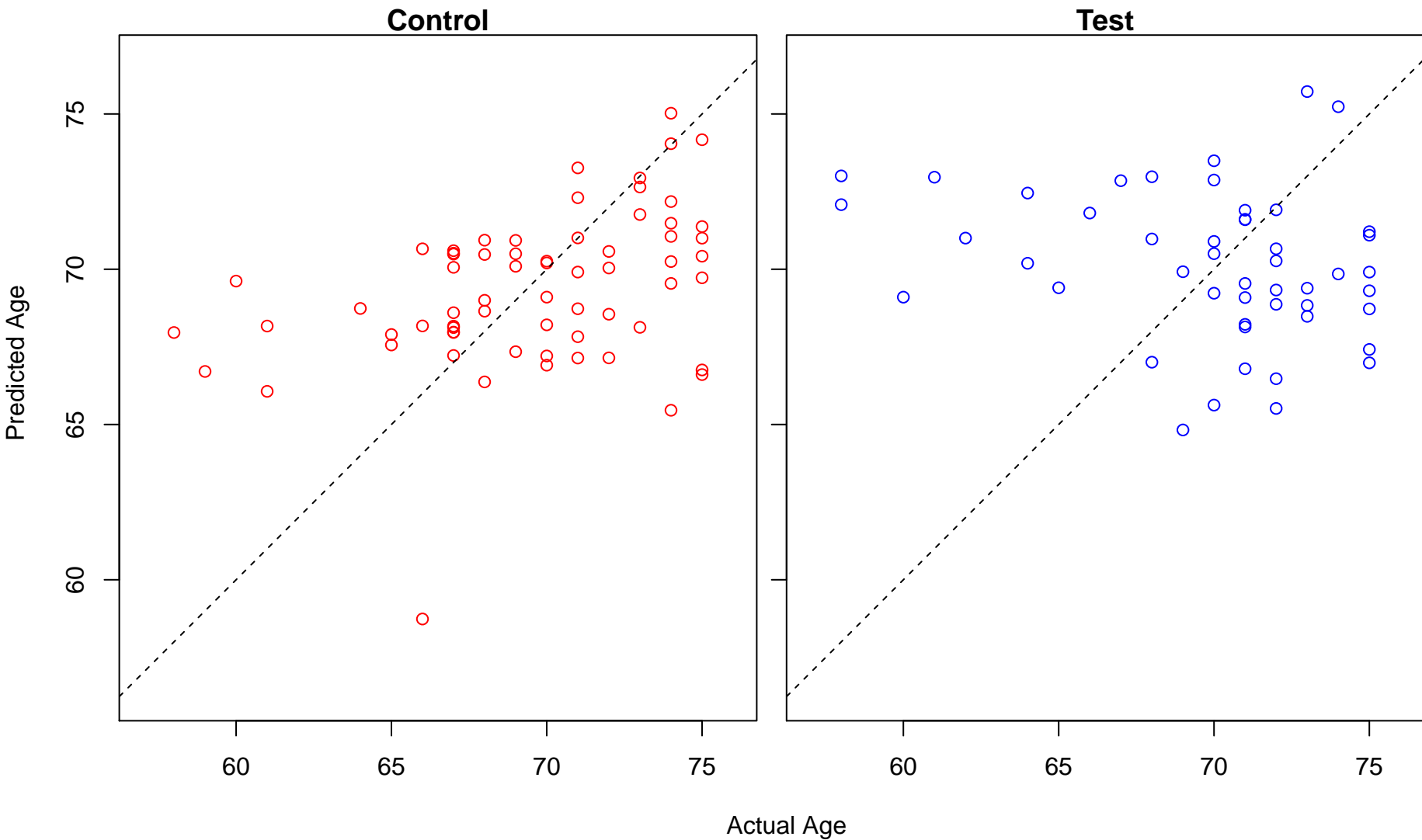


Actual Age

negative regulation of platelet-derived growth factor receptor signaling pathway (Score: 0.671501)

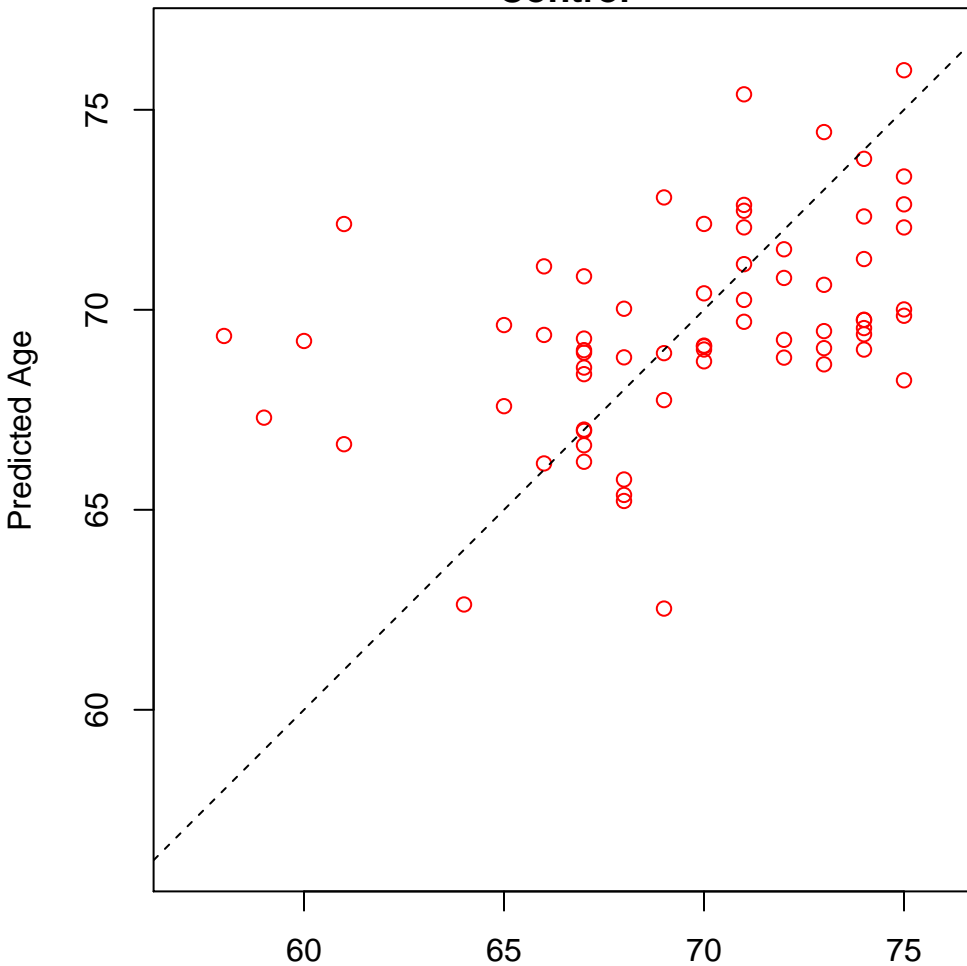


regulation of ruffle assembly (Score: 0.671448)

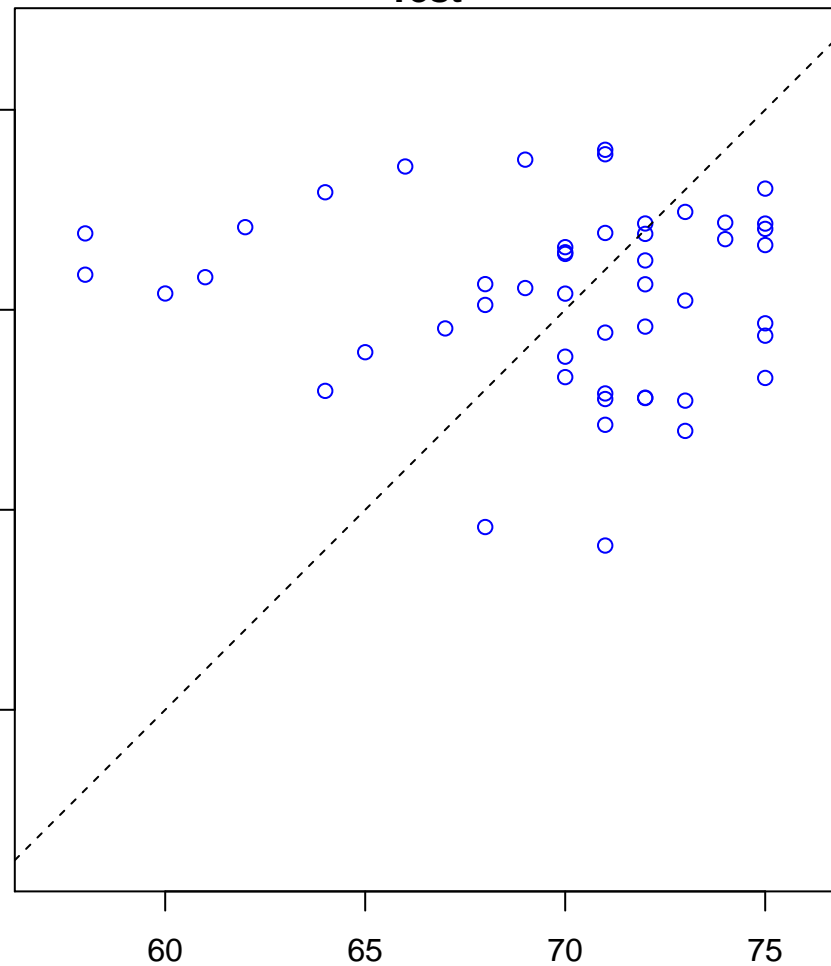


sympathetic nervous system development (Score: 0.671096)

Control

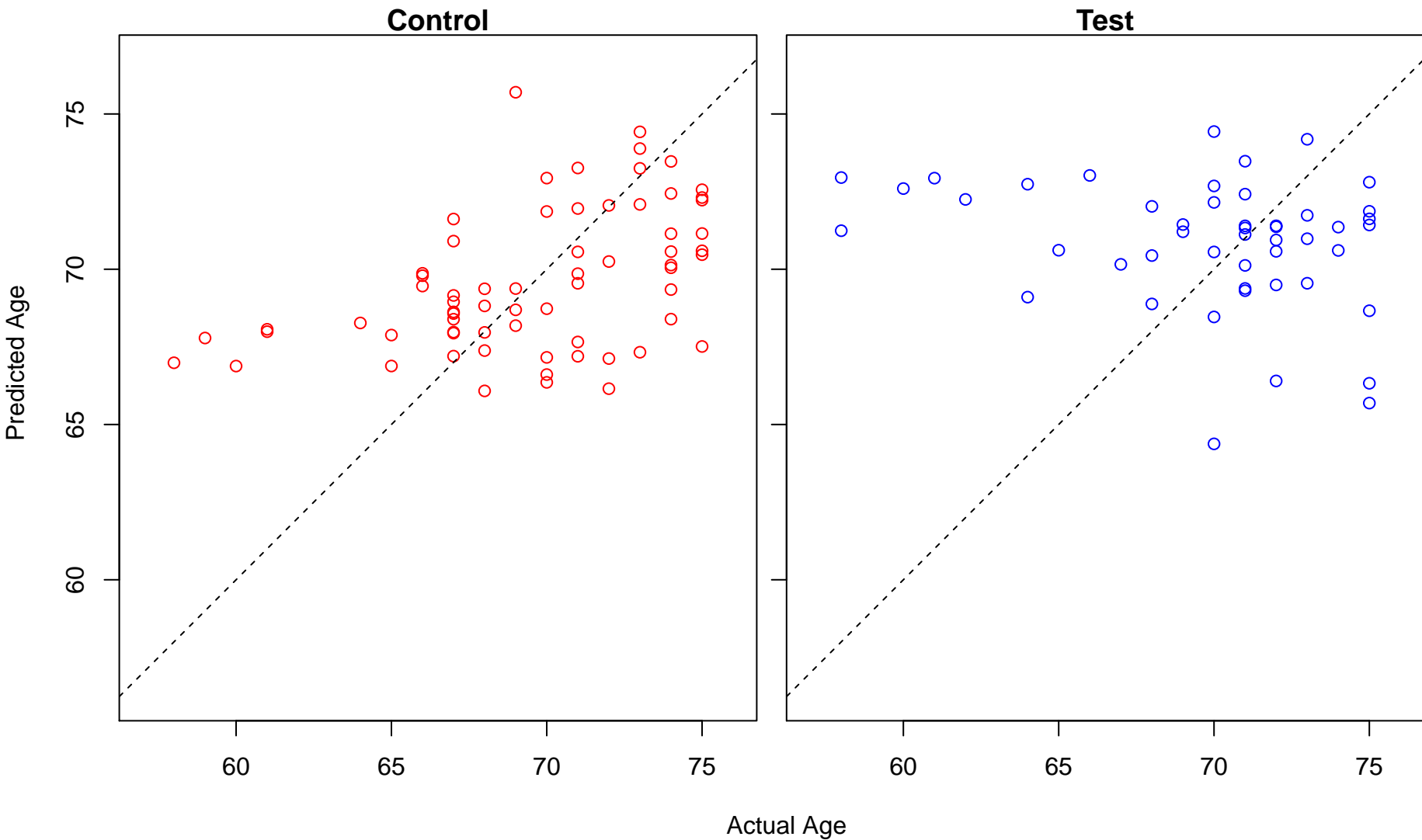


Test

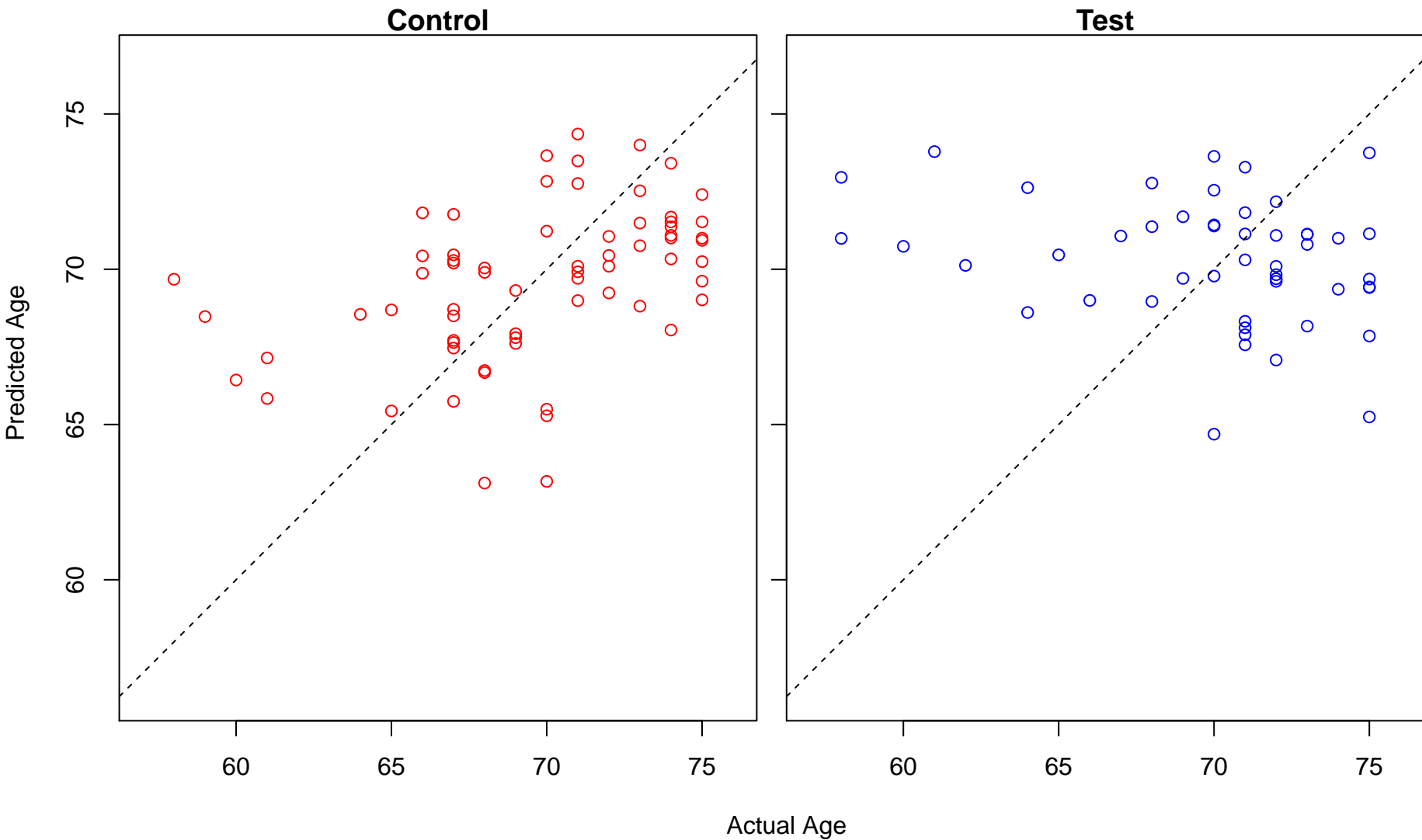


Actual Age

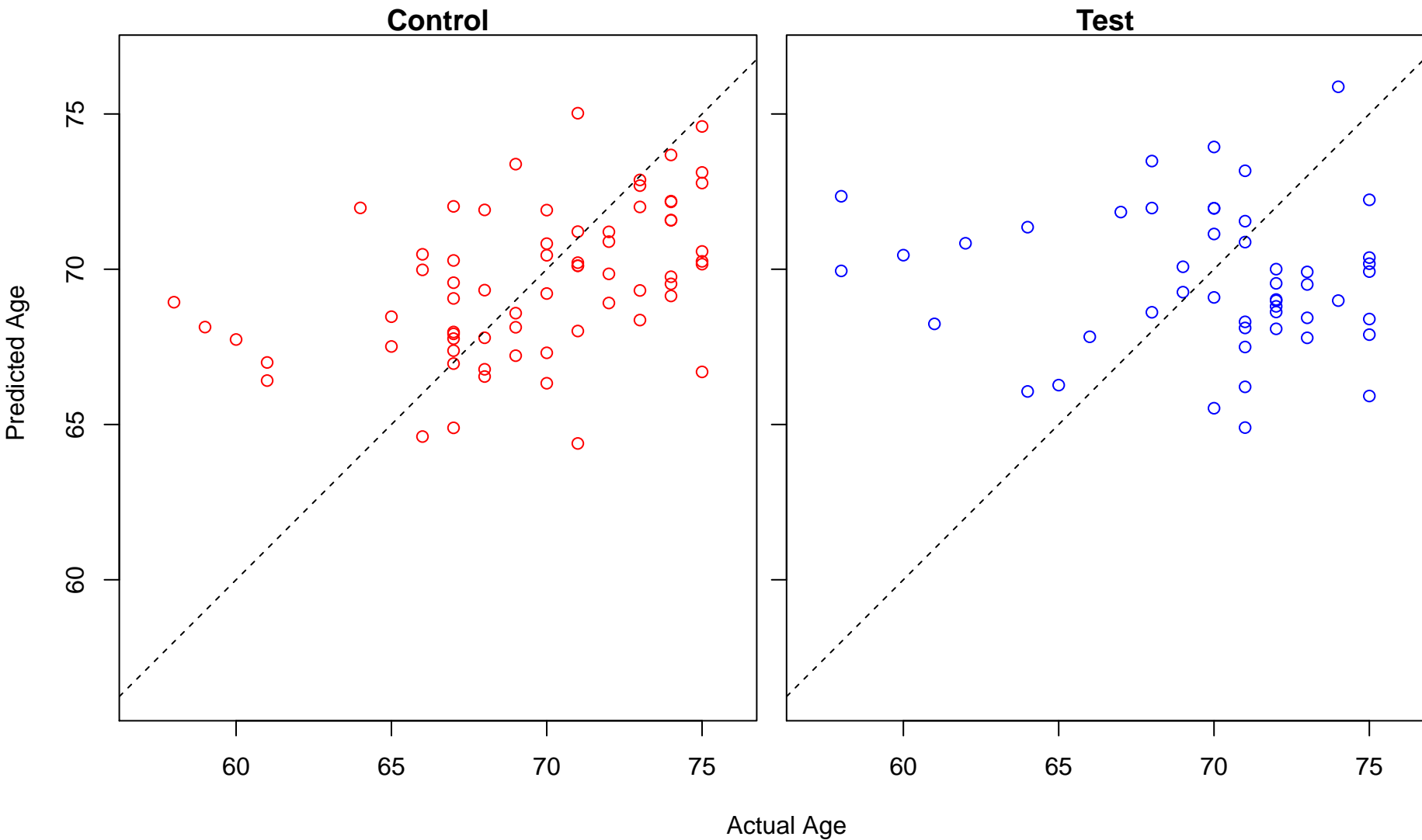
cytoplasmic sequestering of protein (Score: 0.670855)



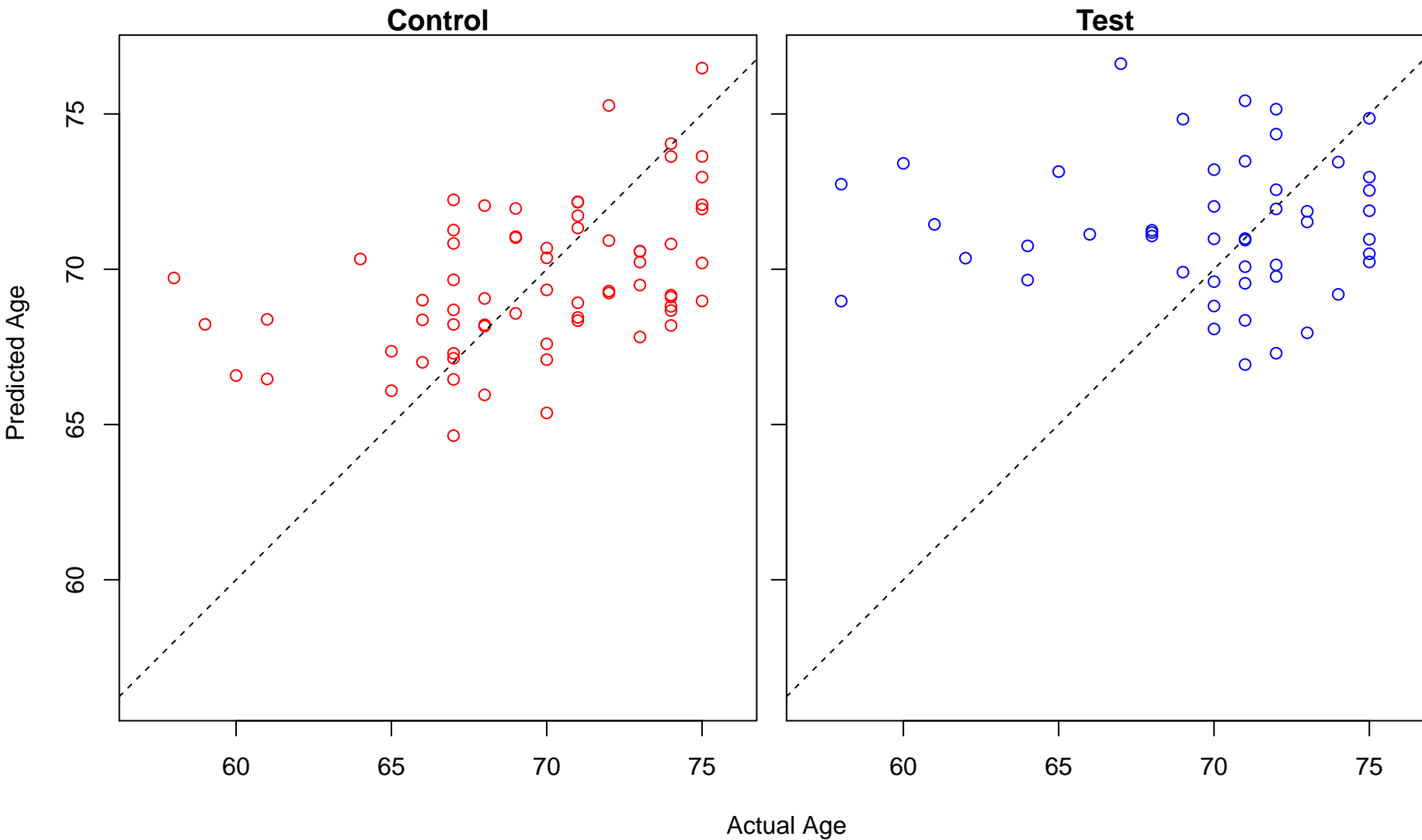
myeloid dendritic cell activation (Score: 0.670800)



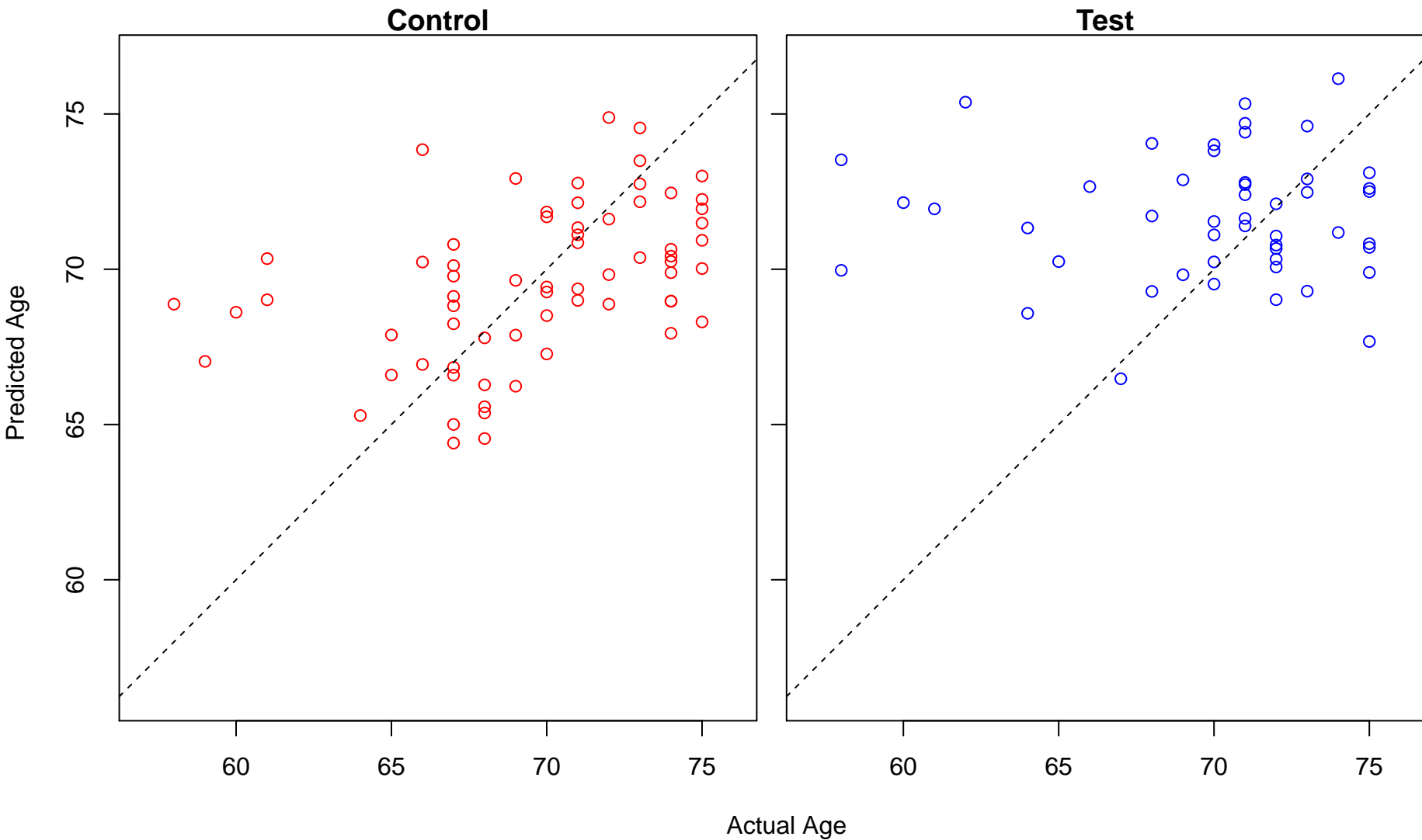
ER overload response (Score: 0.670547)



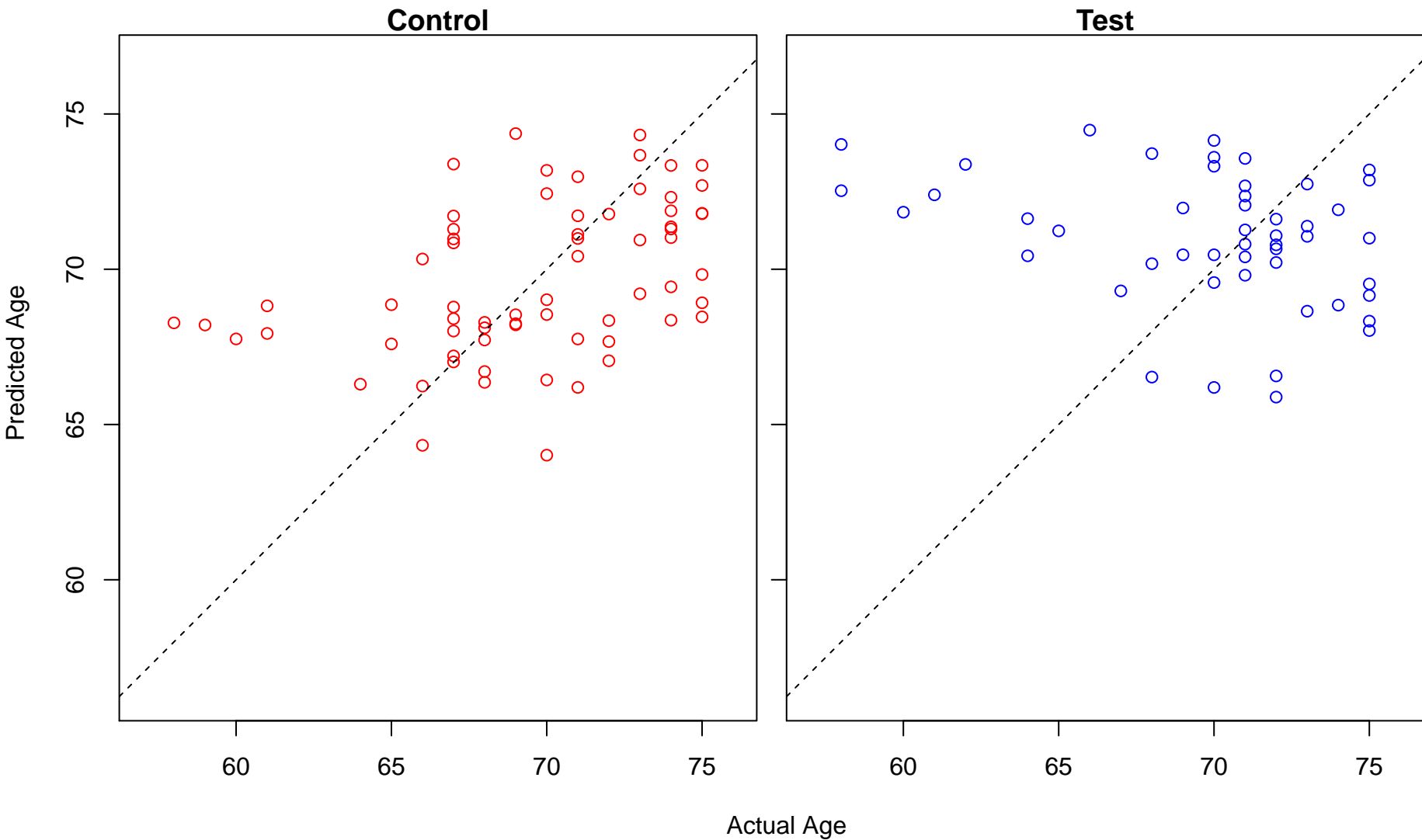
oligosaccharide biosynthetic process (Score: 0.669071)



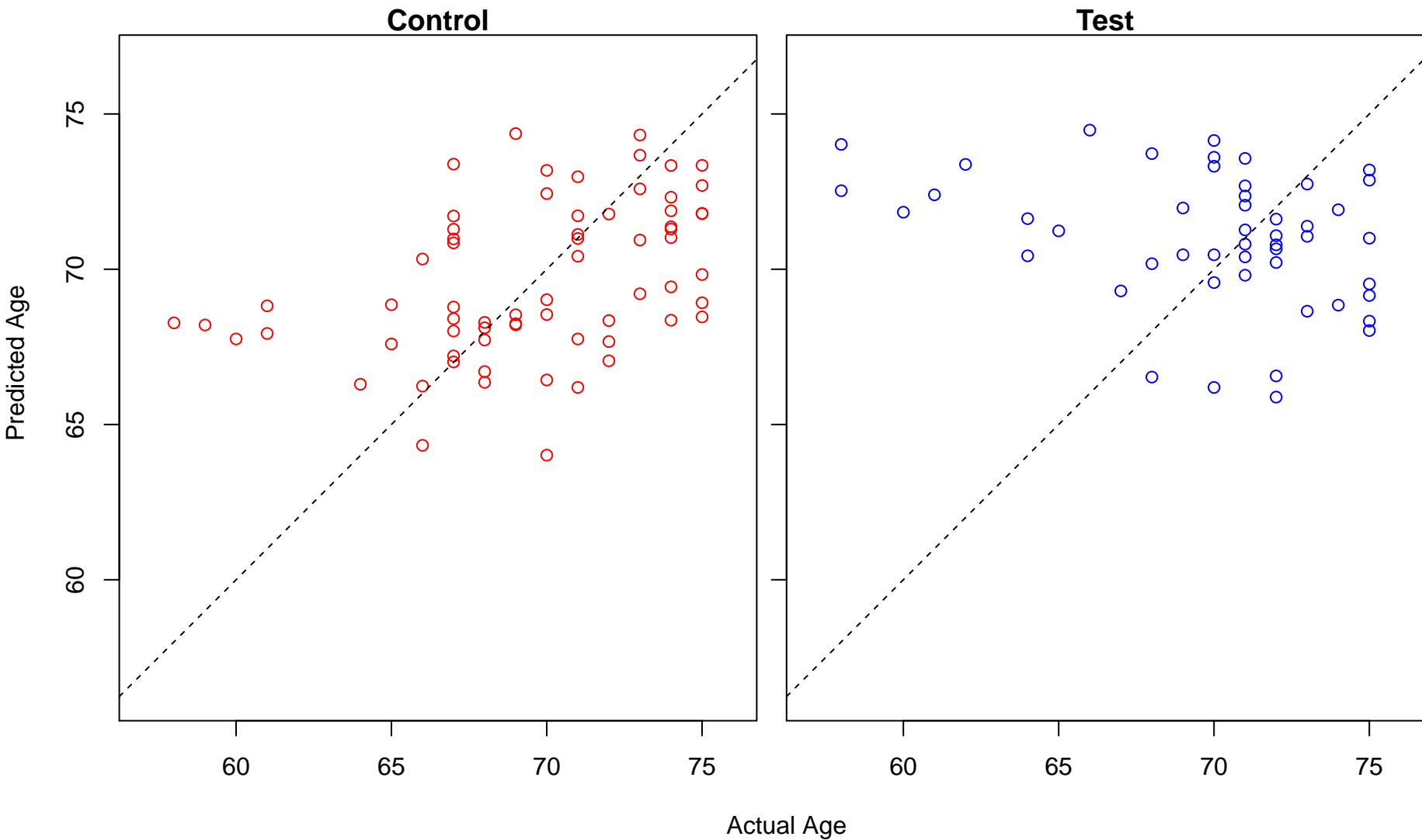
regulation of p38MAPK cascade (Score: 0.668962)



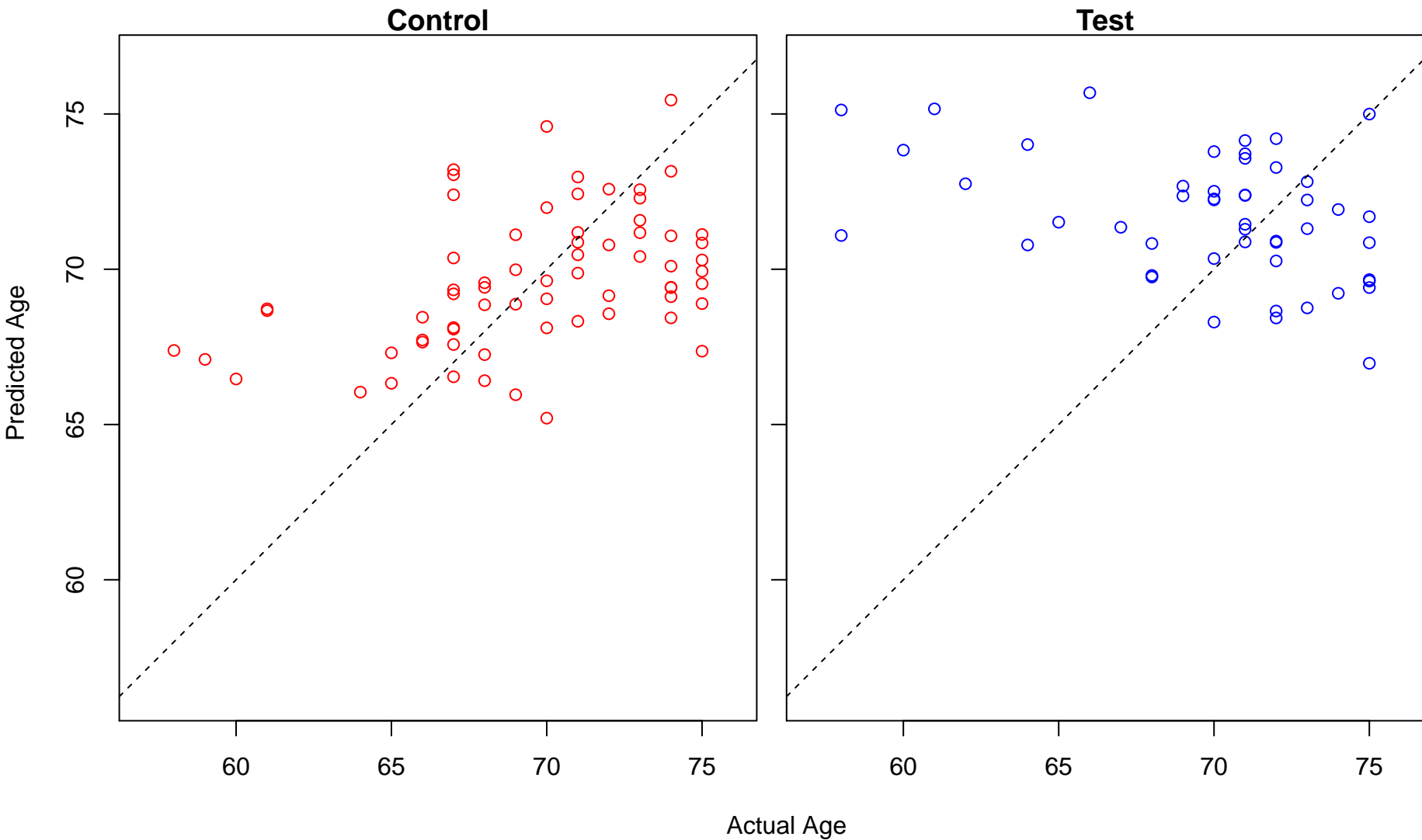
positive regulation of peptide secretion (Score: 0.668750)



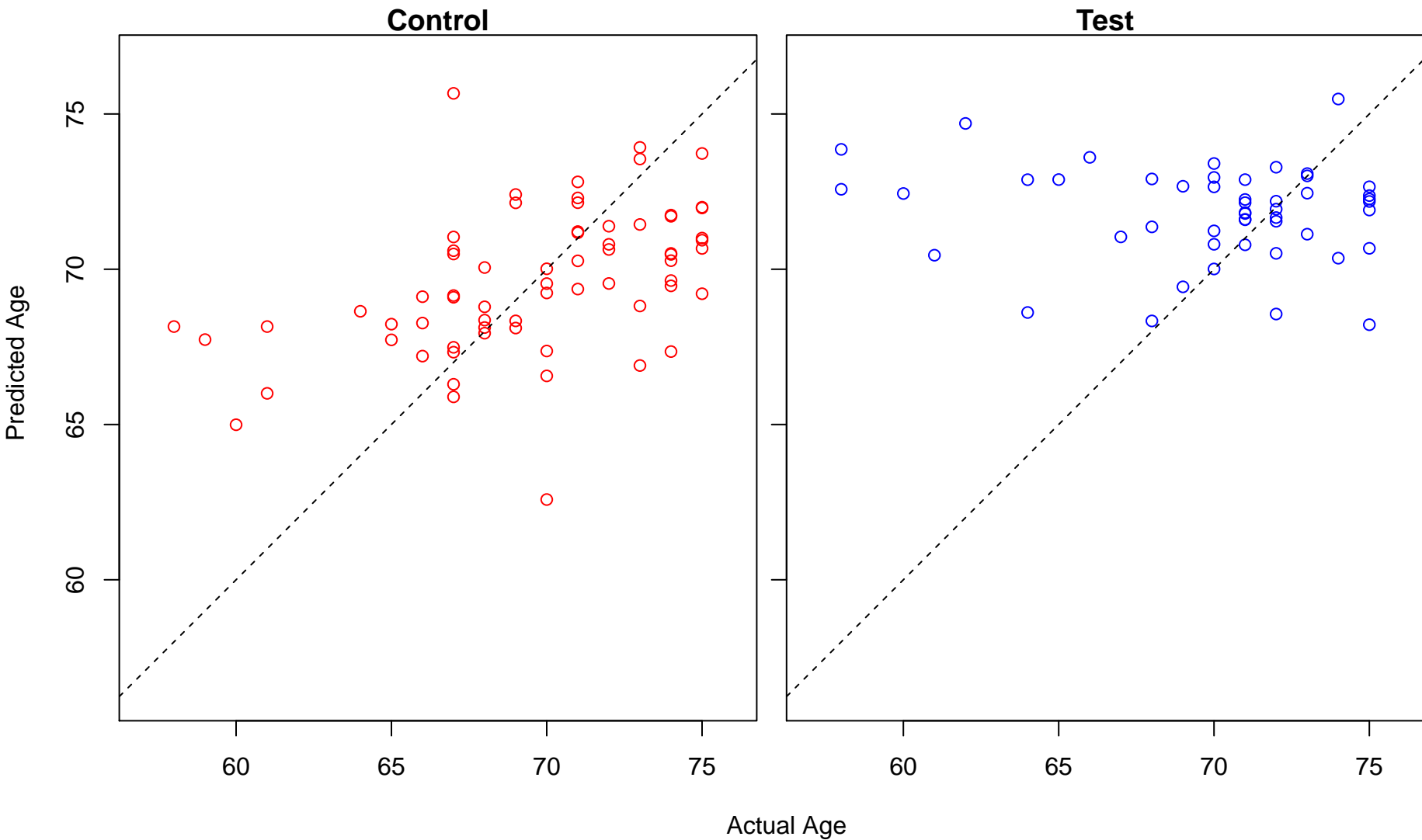
positive regulation of peptide hormone secretion (Score: 0.668750)



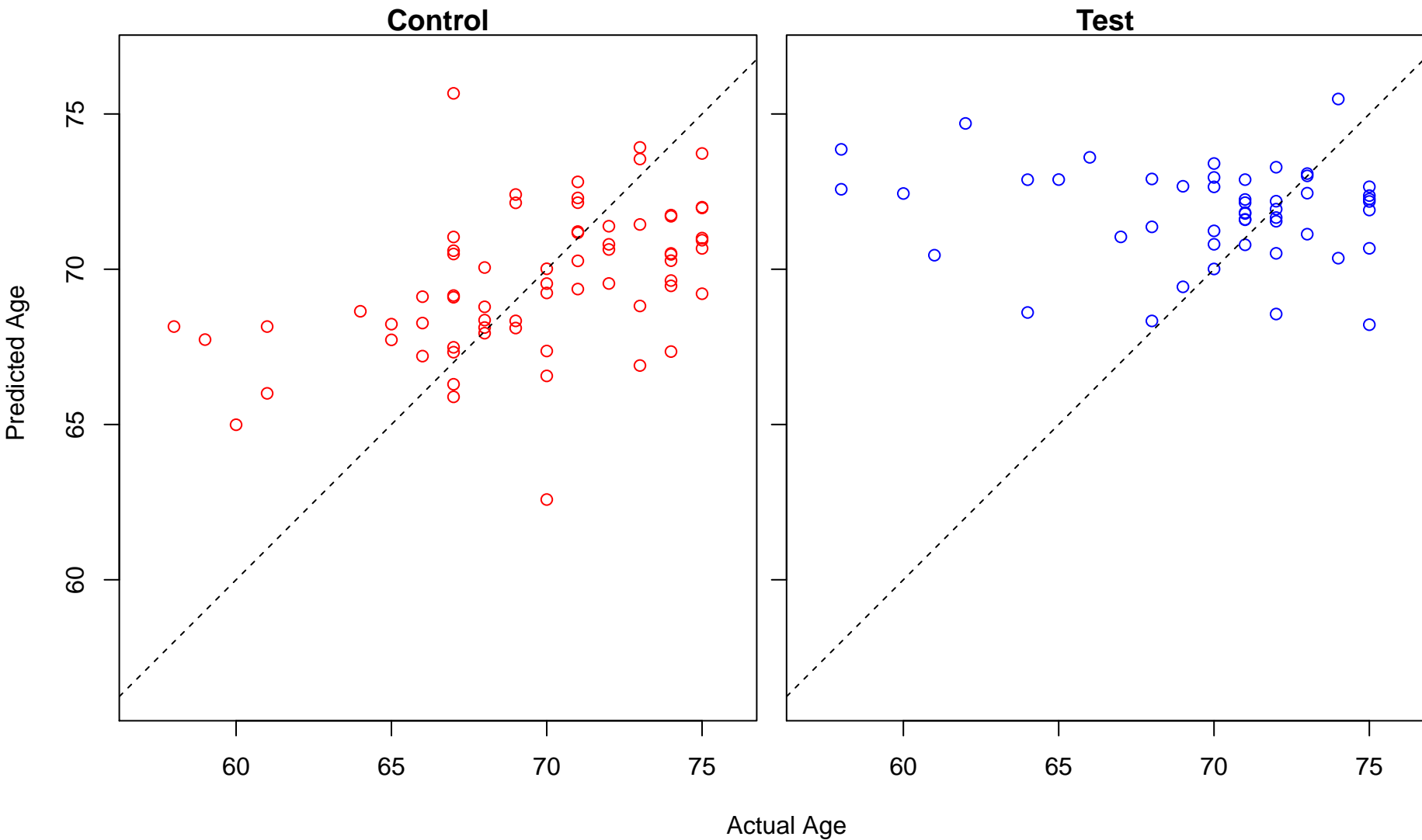
response to acidic pH (Score: 0.668741)



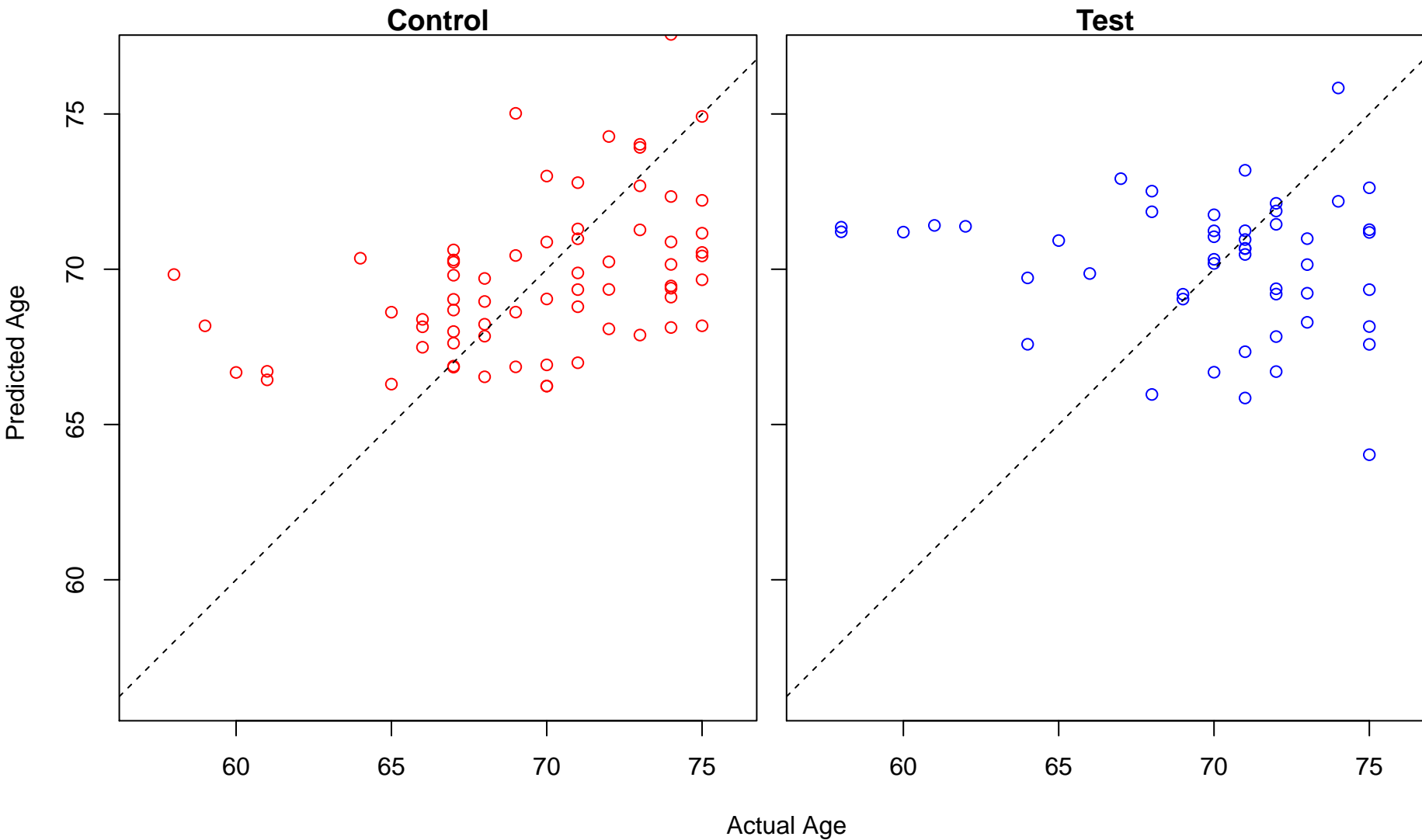
hyperosmotic response (Score: 0.668170)



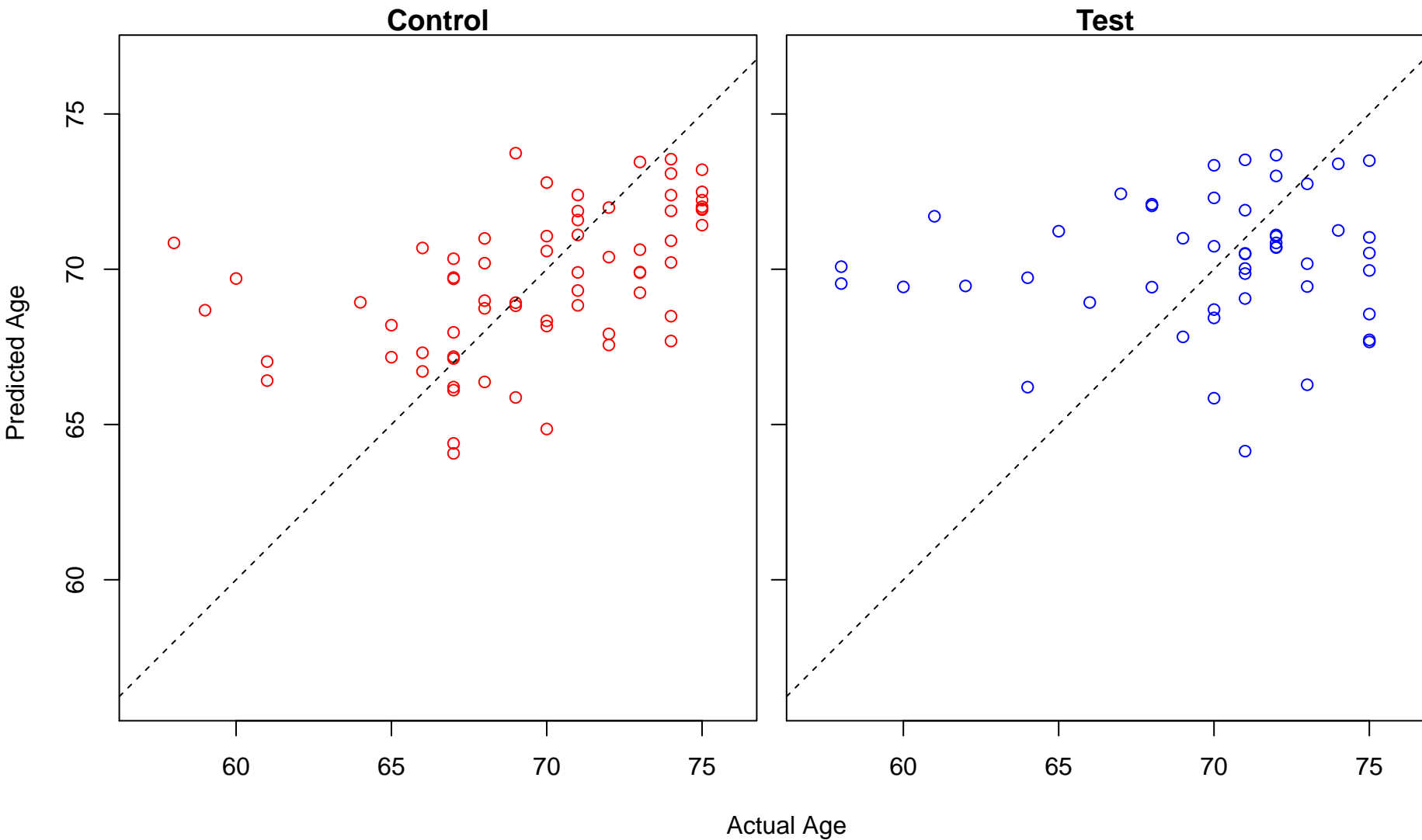
cellular hyperosmotic response (Score: 0.668170)



regulation of autophagosome maturation (Score: 0.668002)

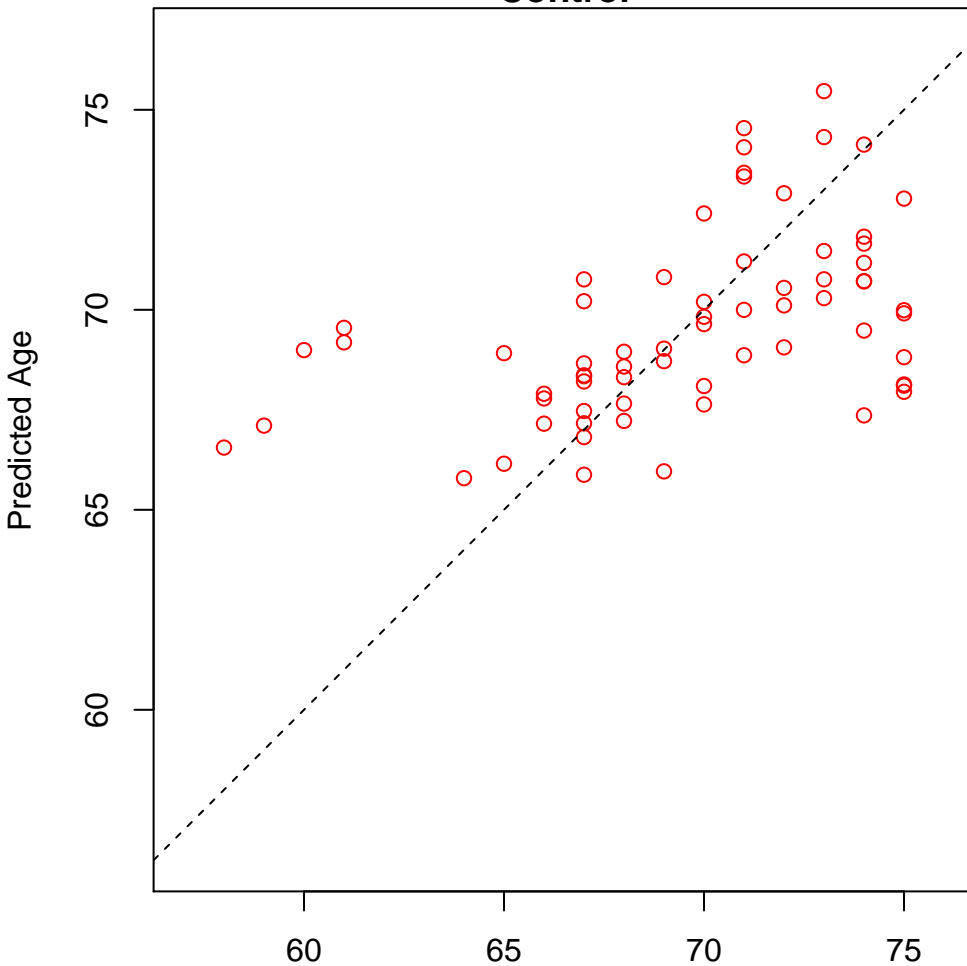


cofactor catabolic process (Score: 0.667036)

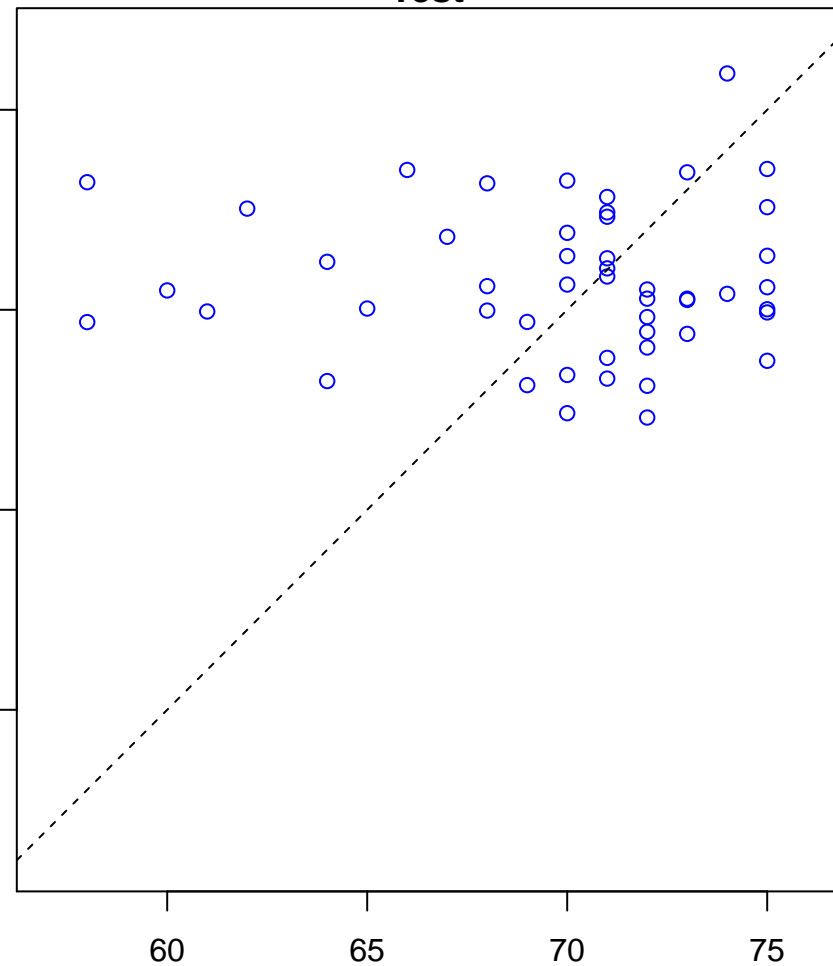


regulation of collagen metabolic process (Score: 0.666509)

Control

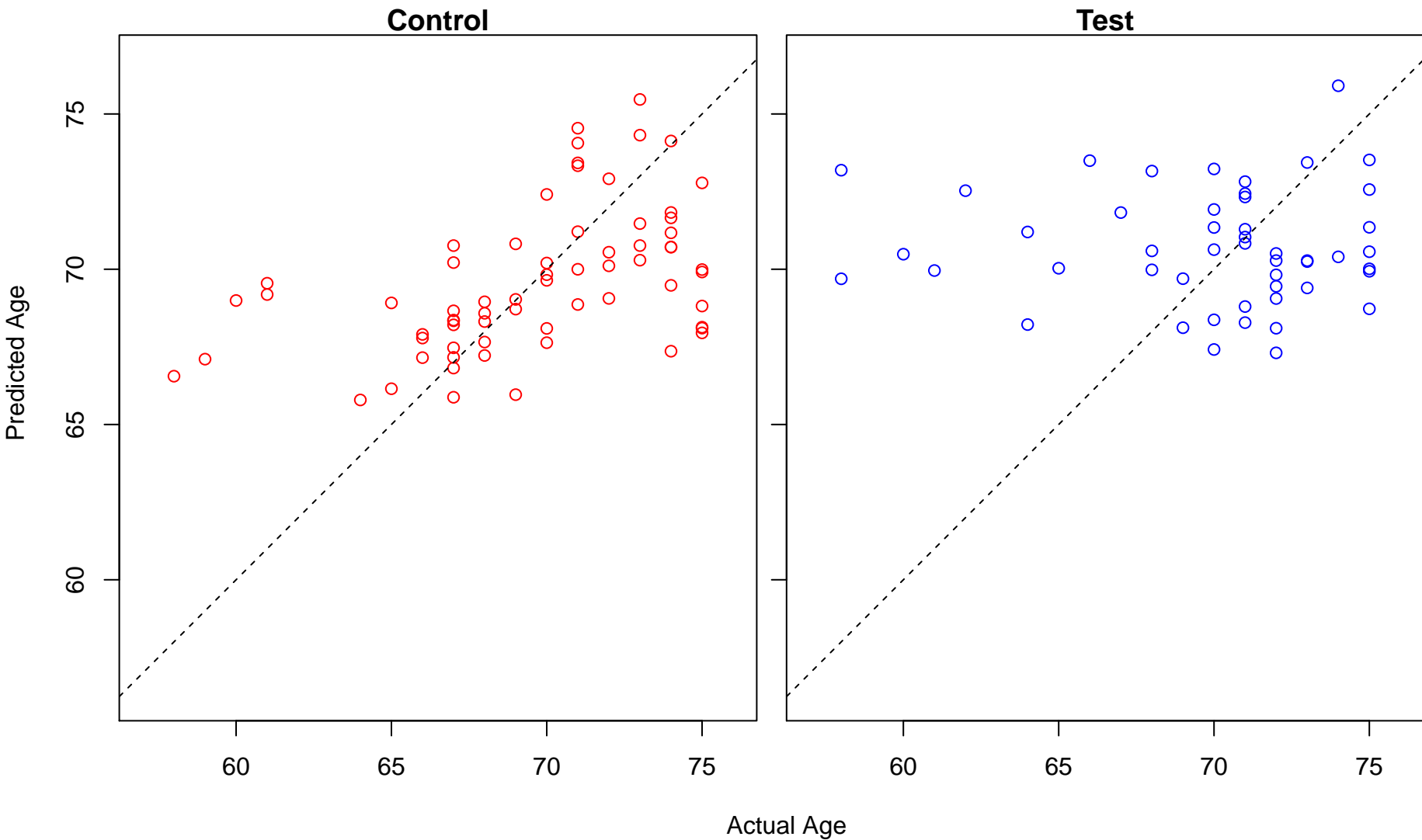


Test



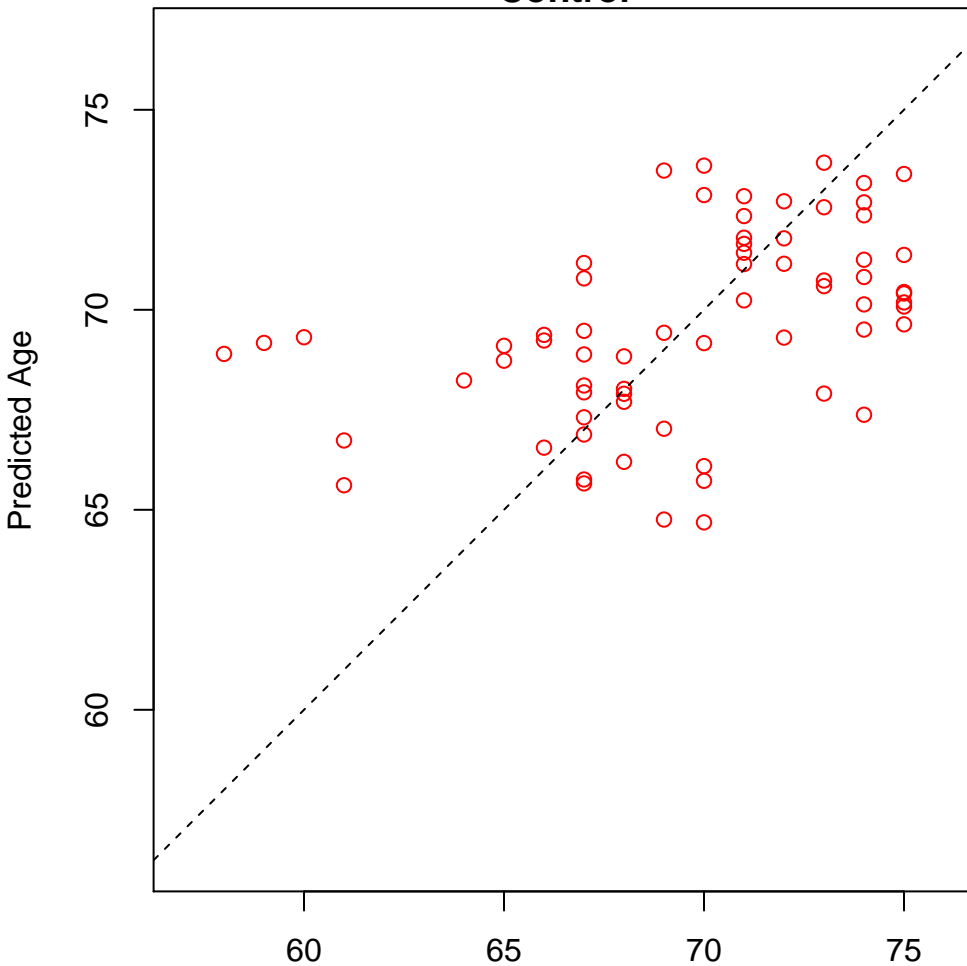
Actual Age

regulation of multicellular organismal metabolic process (Score: 0.666509)

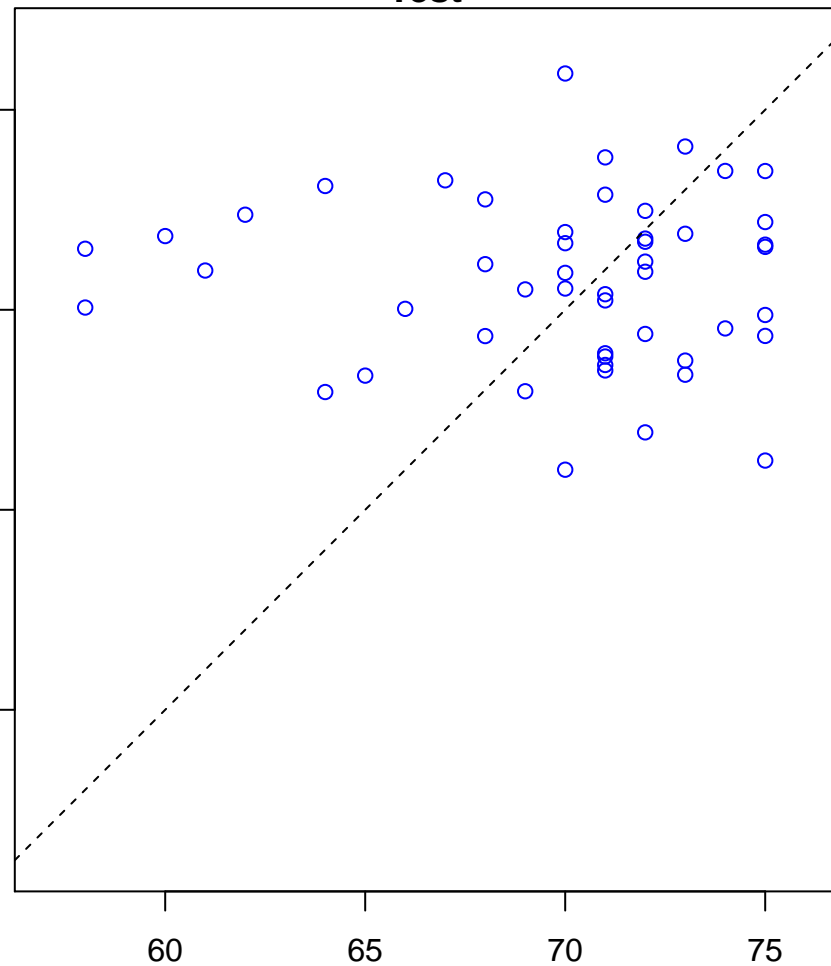


regulation of cardiac muscle hypertrophy (Score: 0.666349)

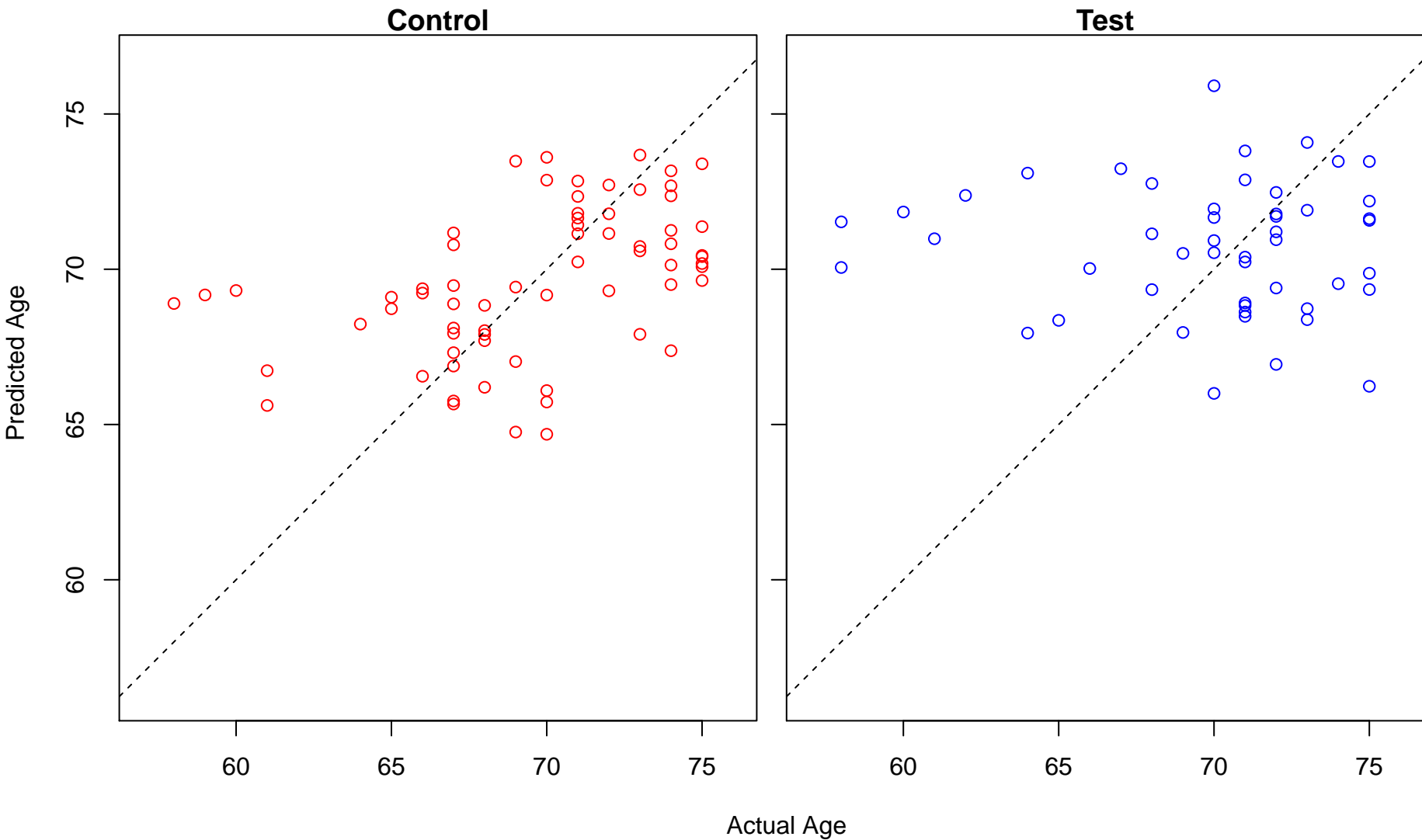
Control



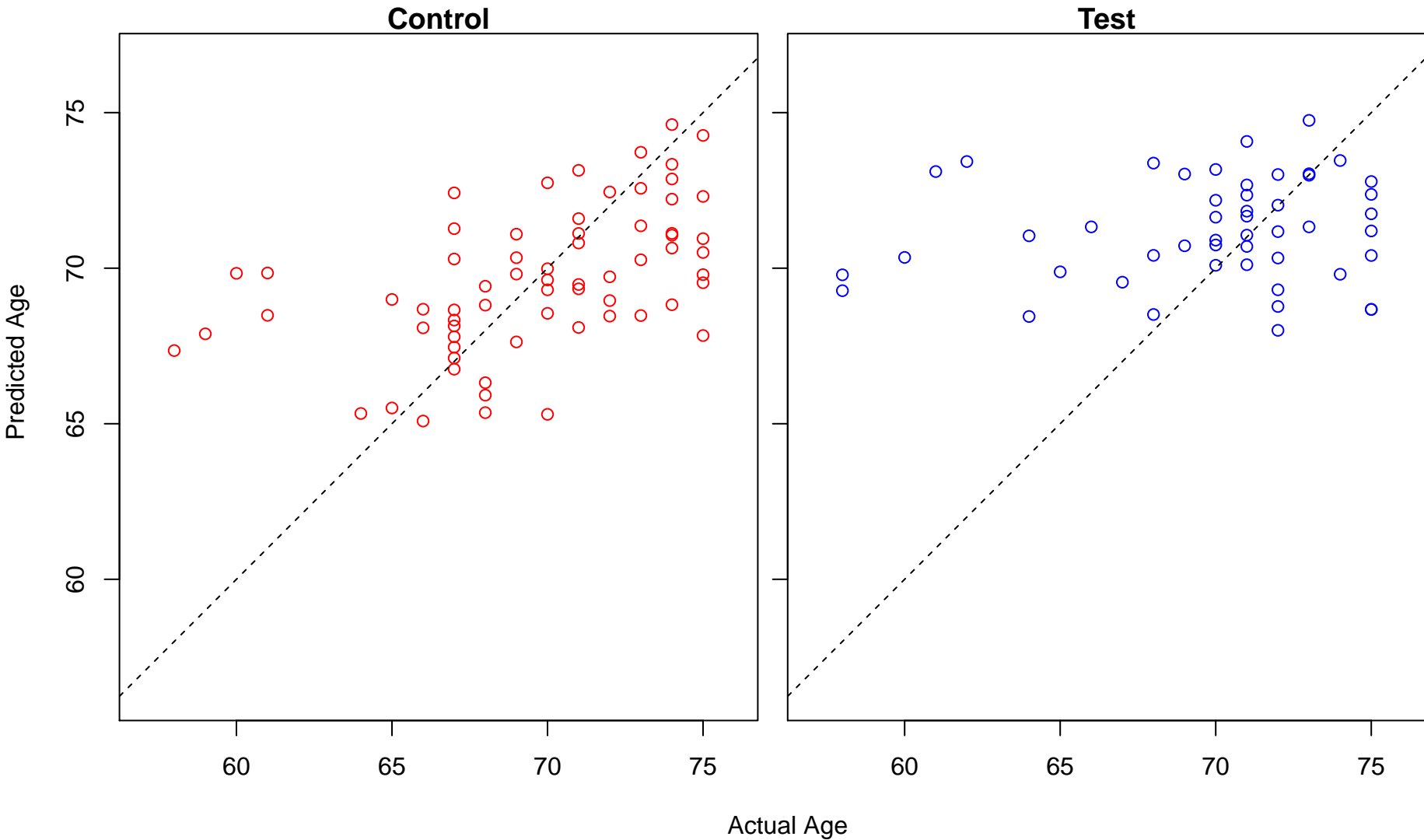
Test



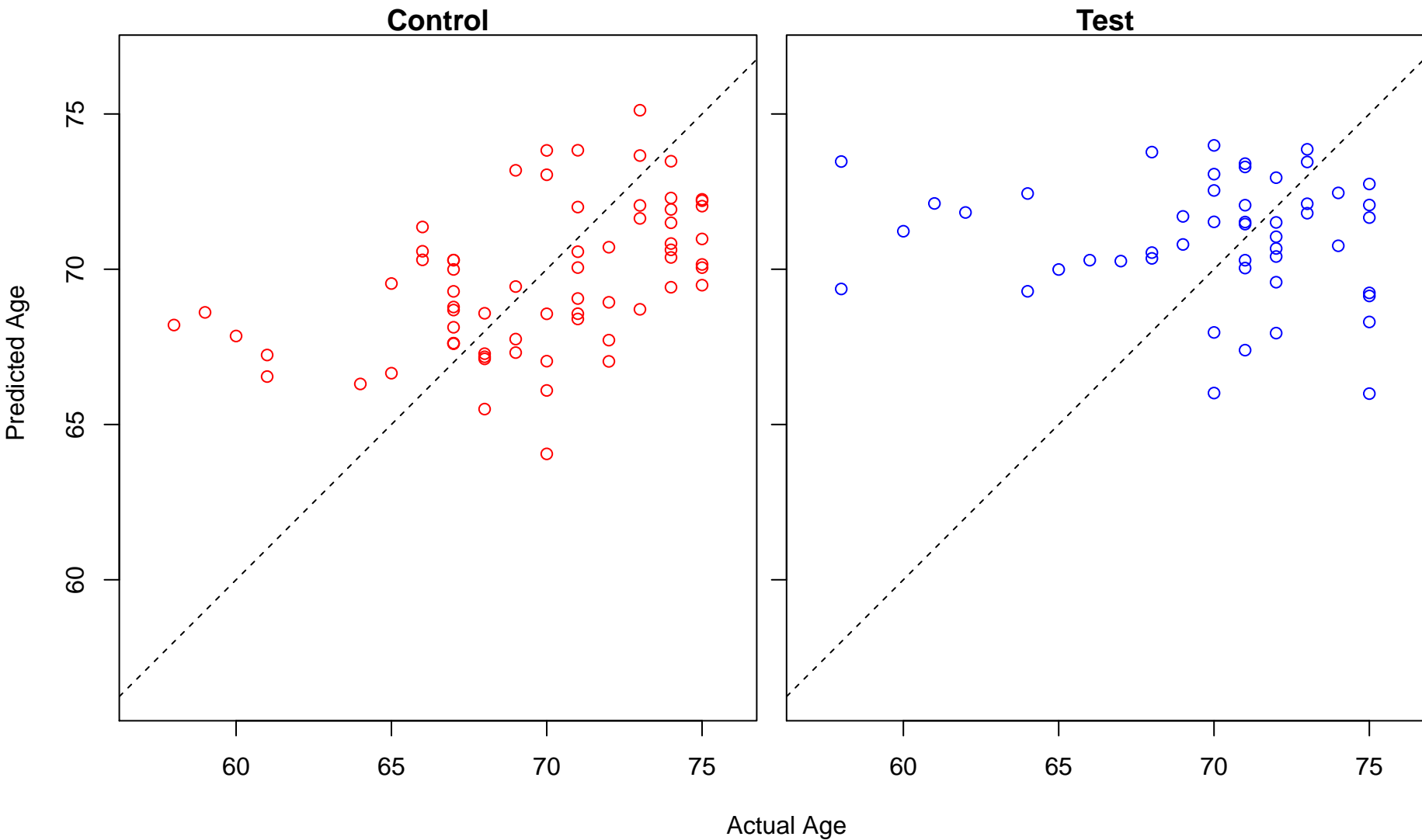
regulation of muscle hypertrophy (Score: 0.666349)



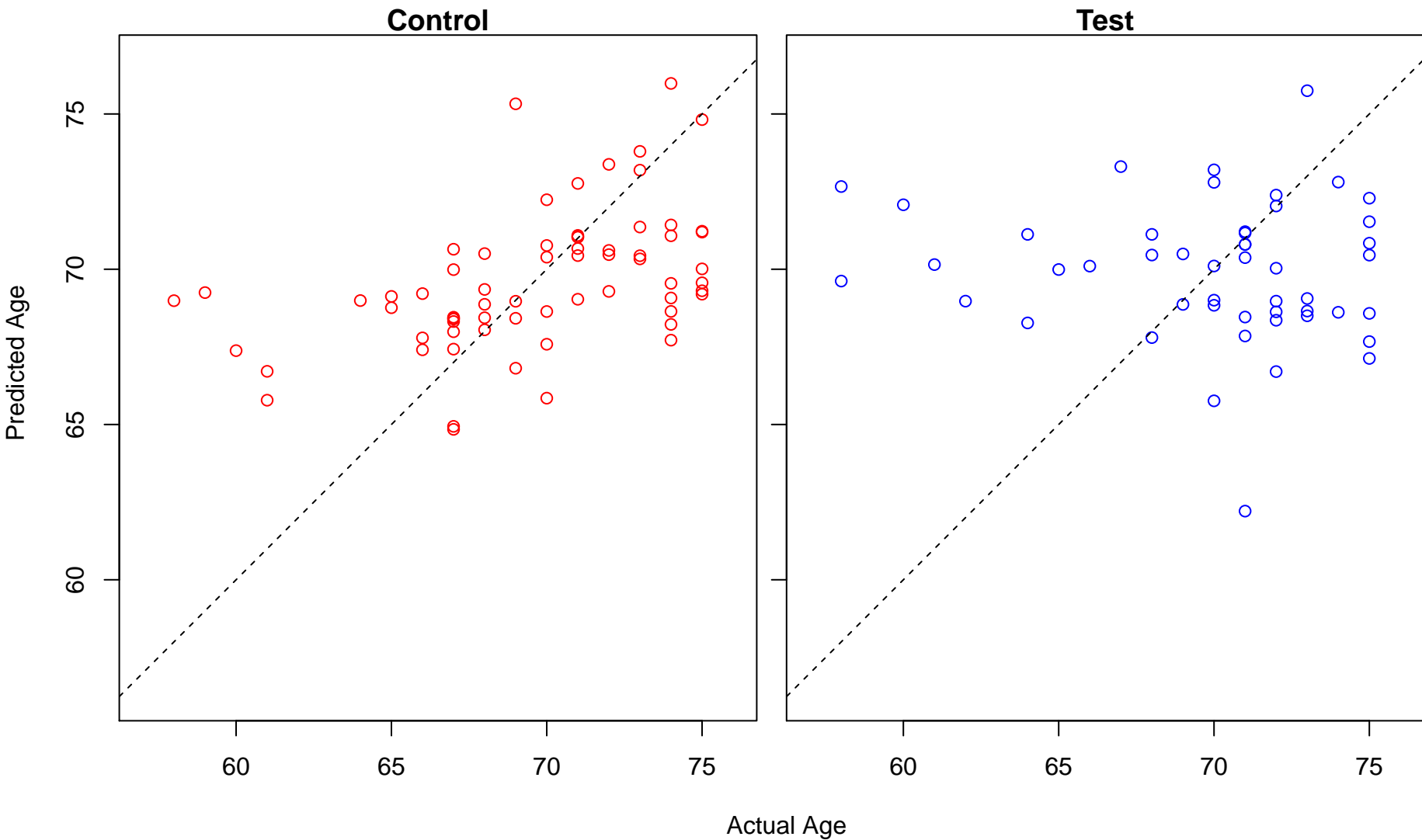
apolipoprotein A-I-mediated signaling pathway (Score: 0.666259)



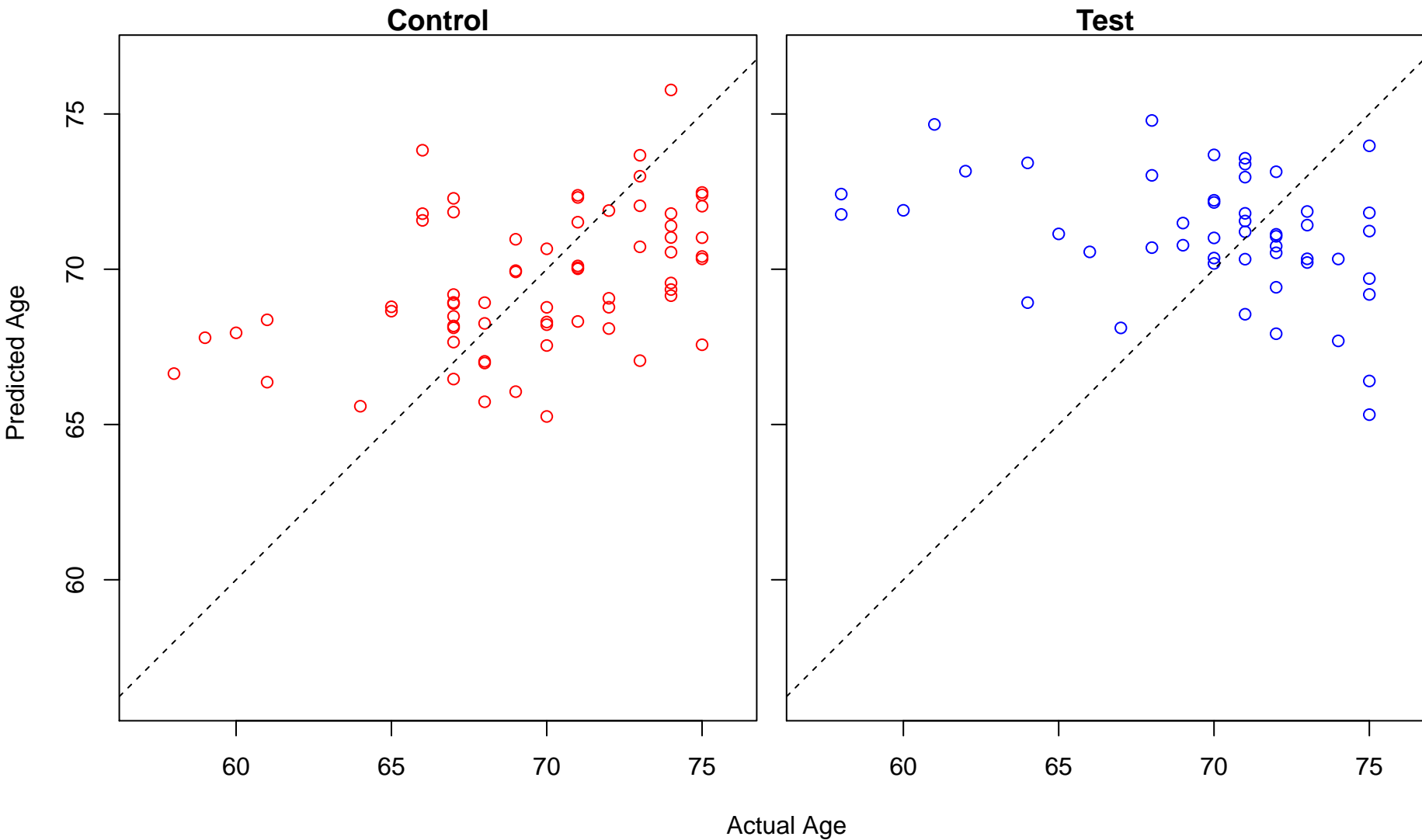
piRNA metabolic process (Score: 0.665697)



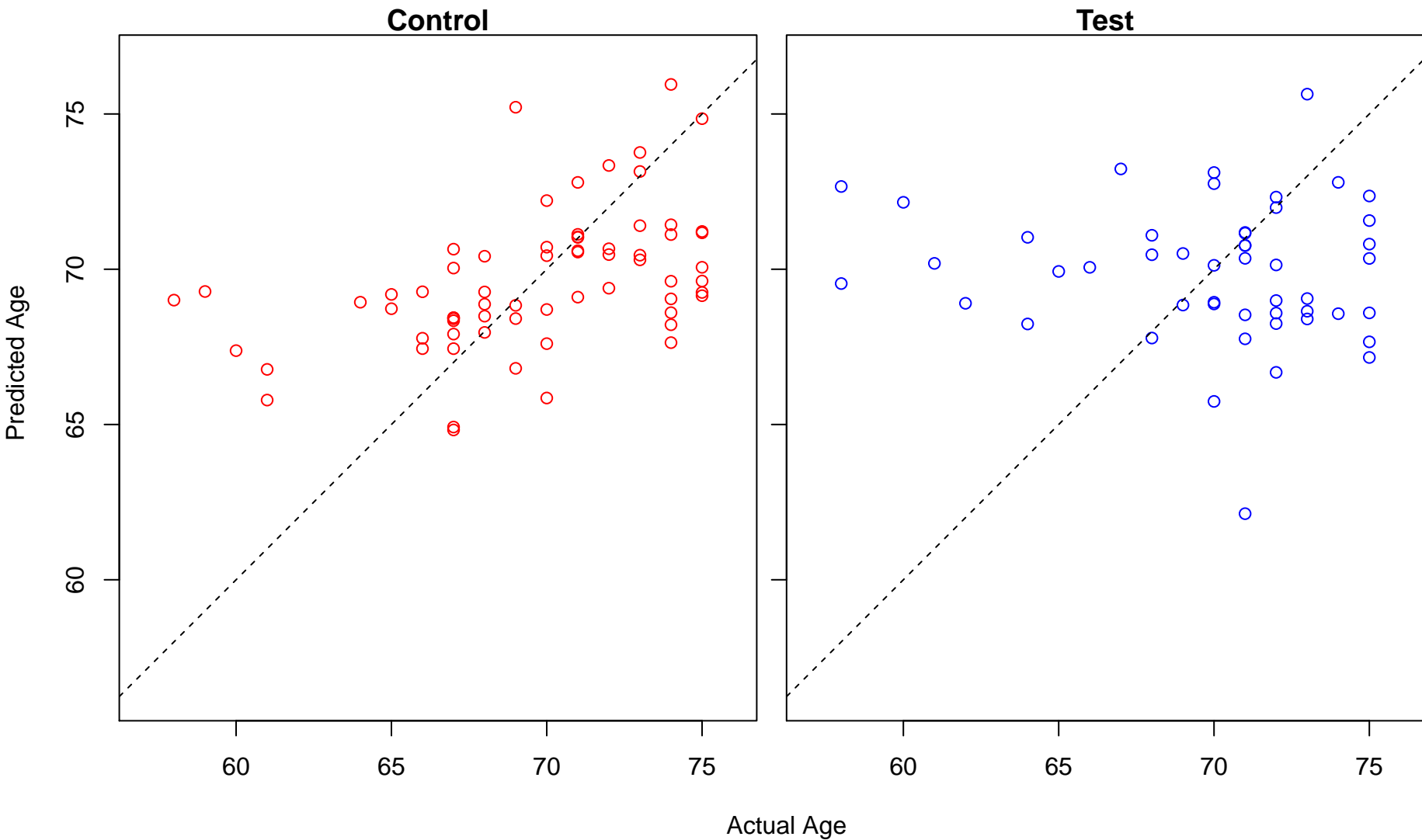
negative regulation of adherens junction organization (Score: 0.665631)



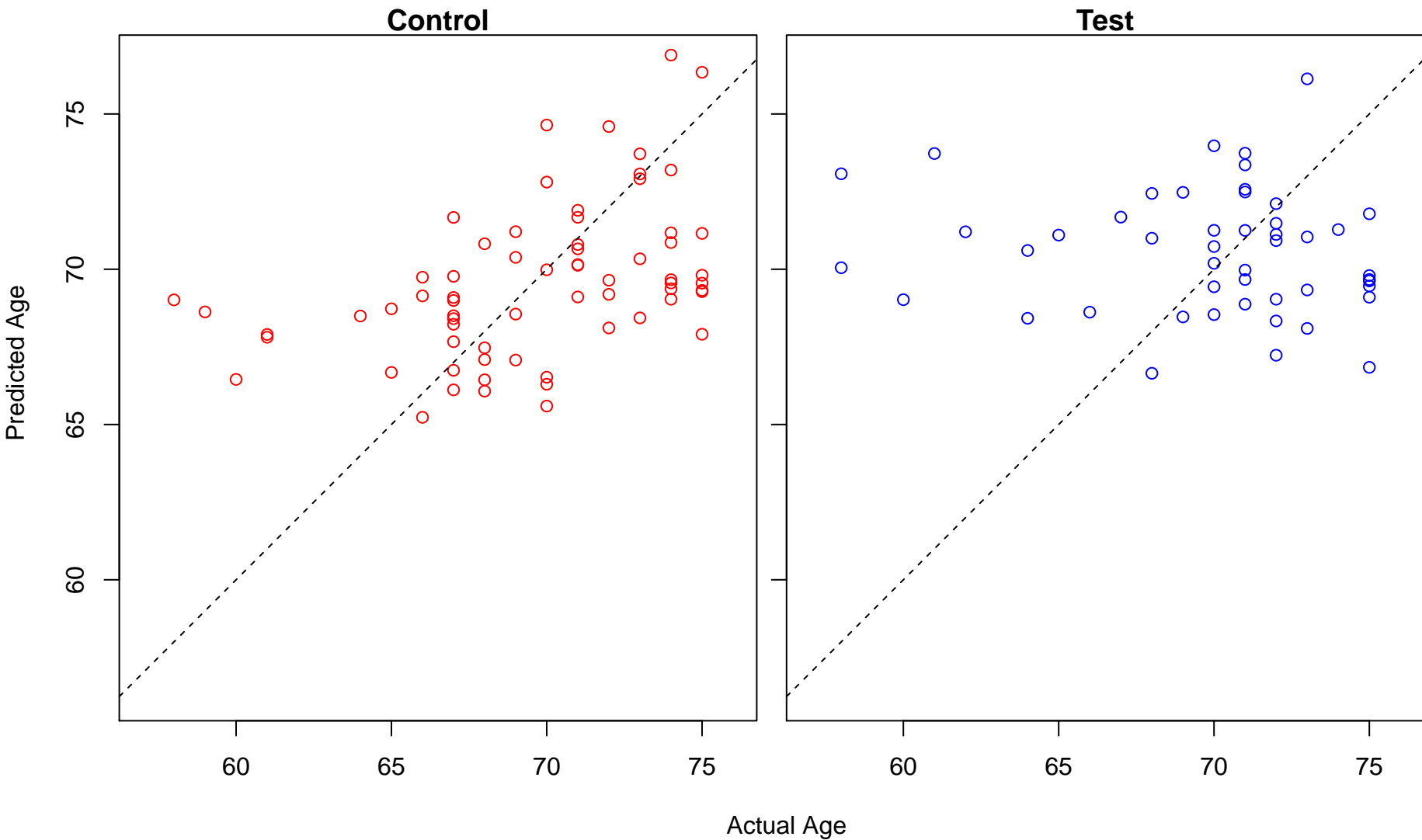
cellular lactam metabolic process (Score: 0.665619)



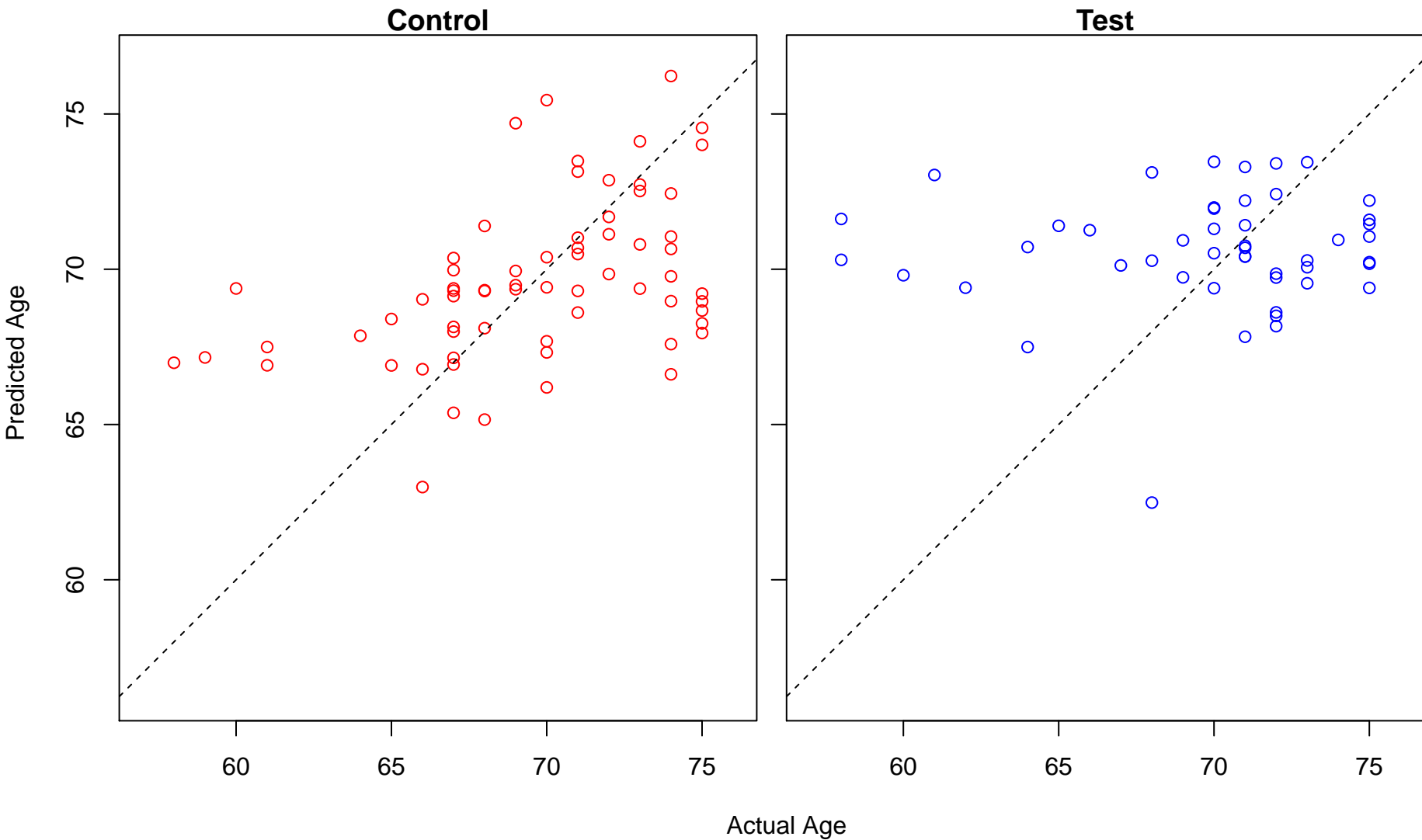
negative regulation of focal adhesion assembly (Score: 0.663964)



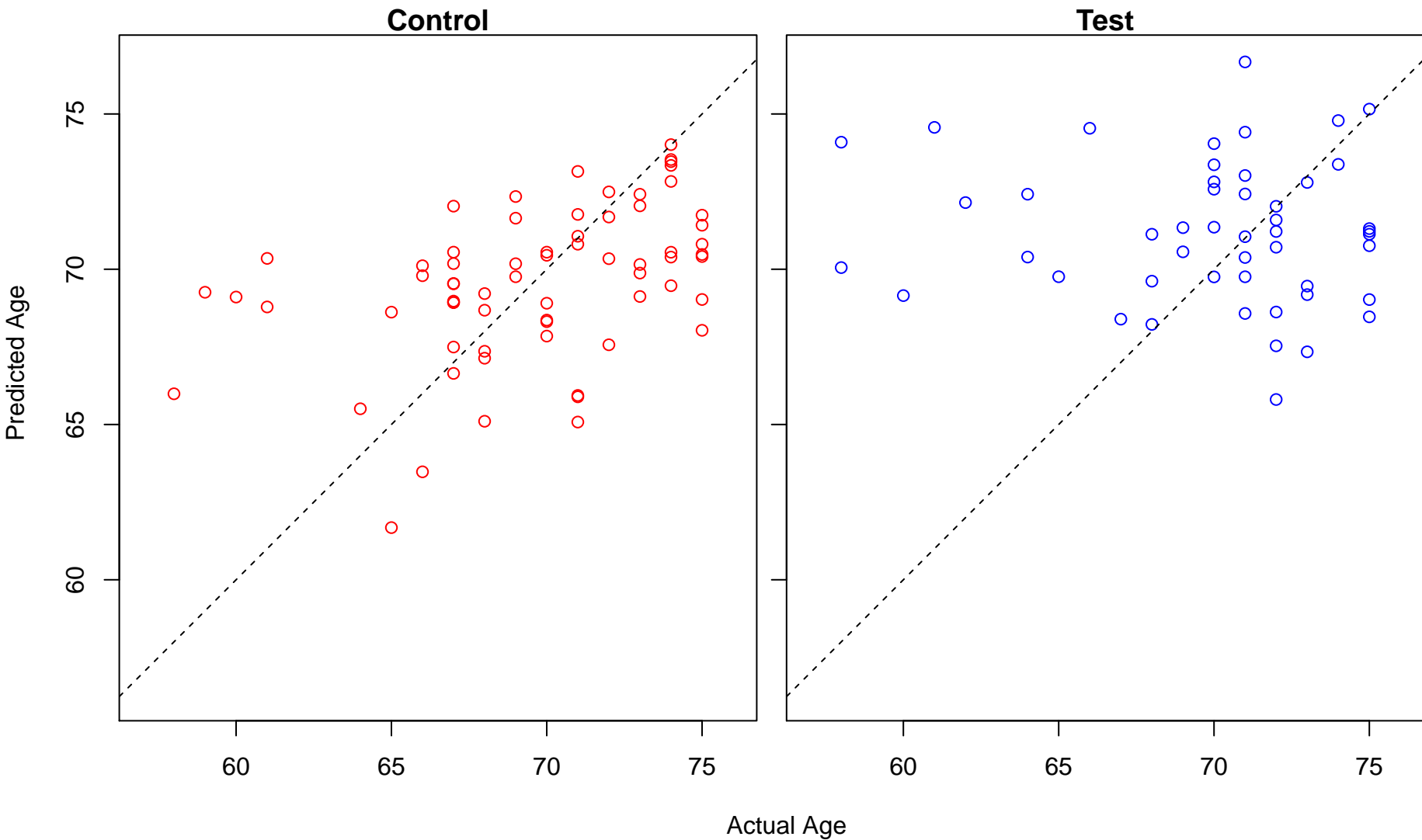
negative regulation of execution phase of apoptosis (Score: 0.663538)



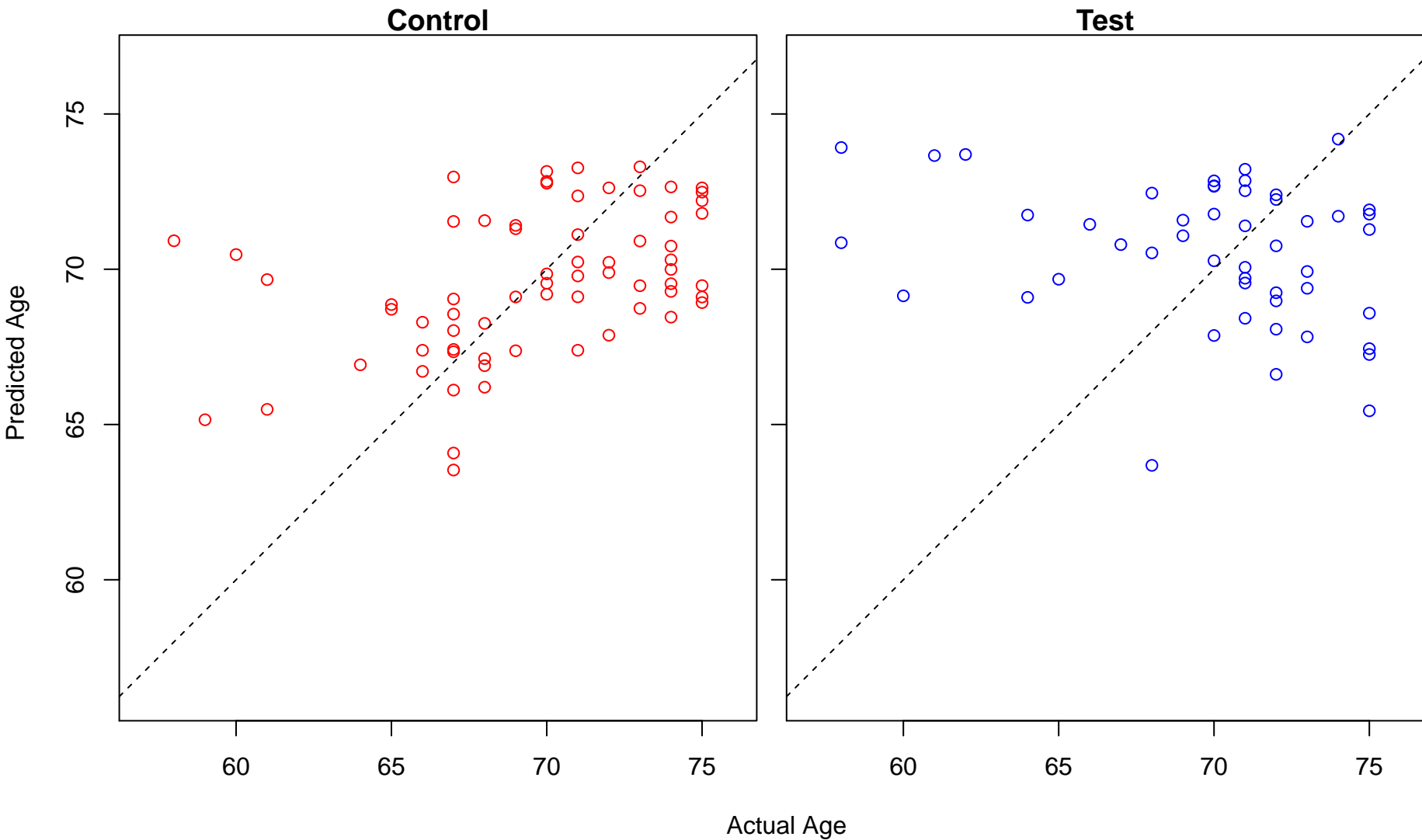
pyrimidine deoxyribonucleotide catabolic process (Score: 0.663468)



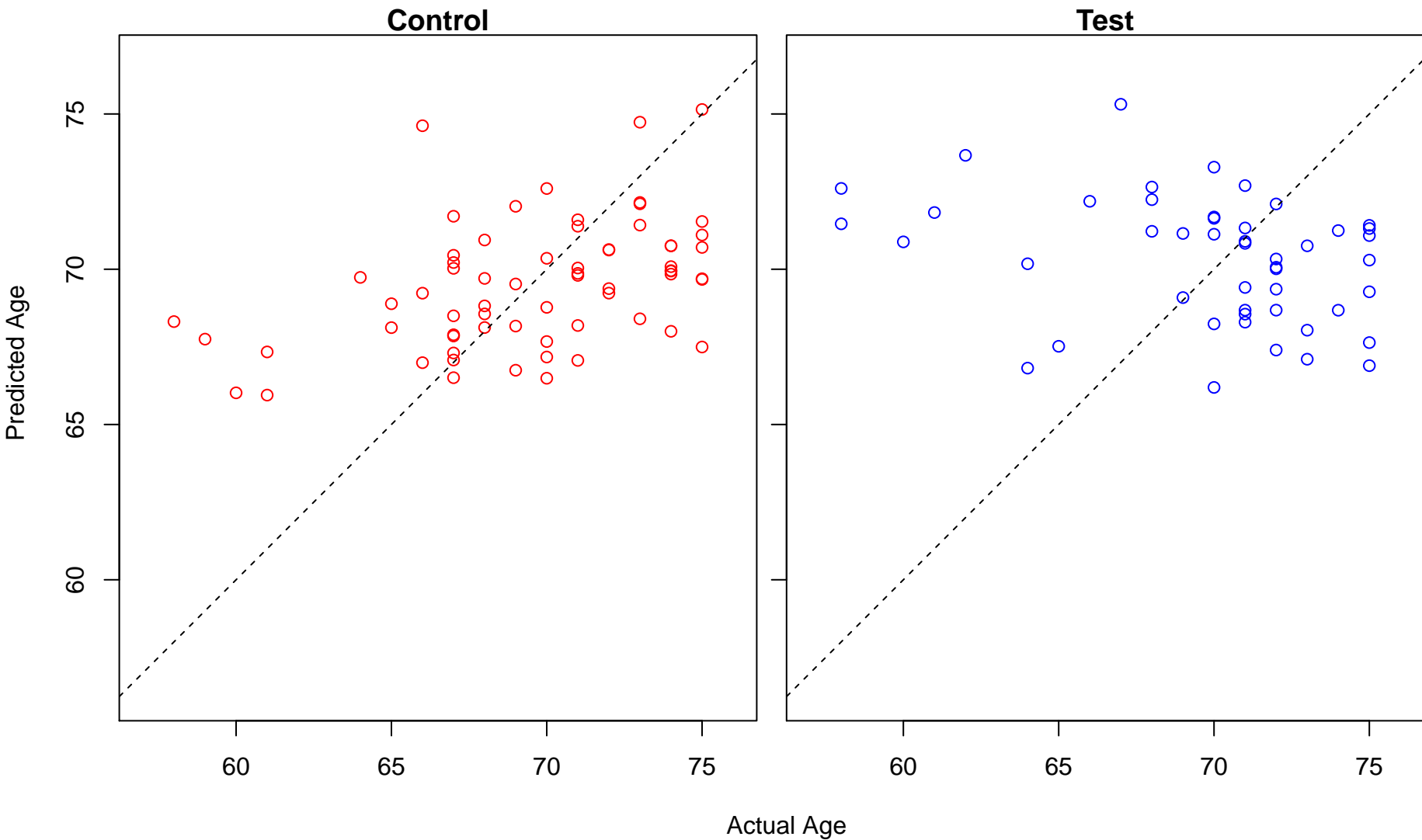
regulation of T-helper 2 cell cytokine production (Score: 0.663441)



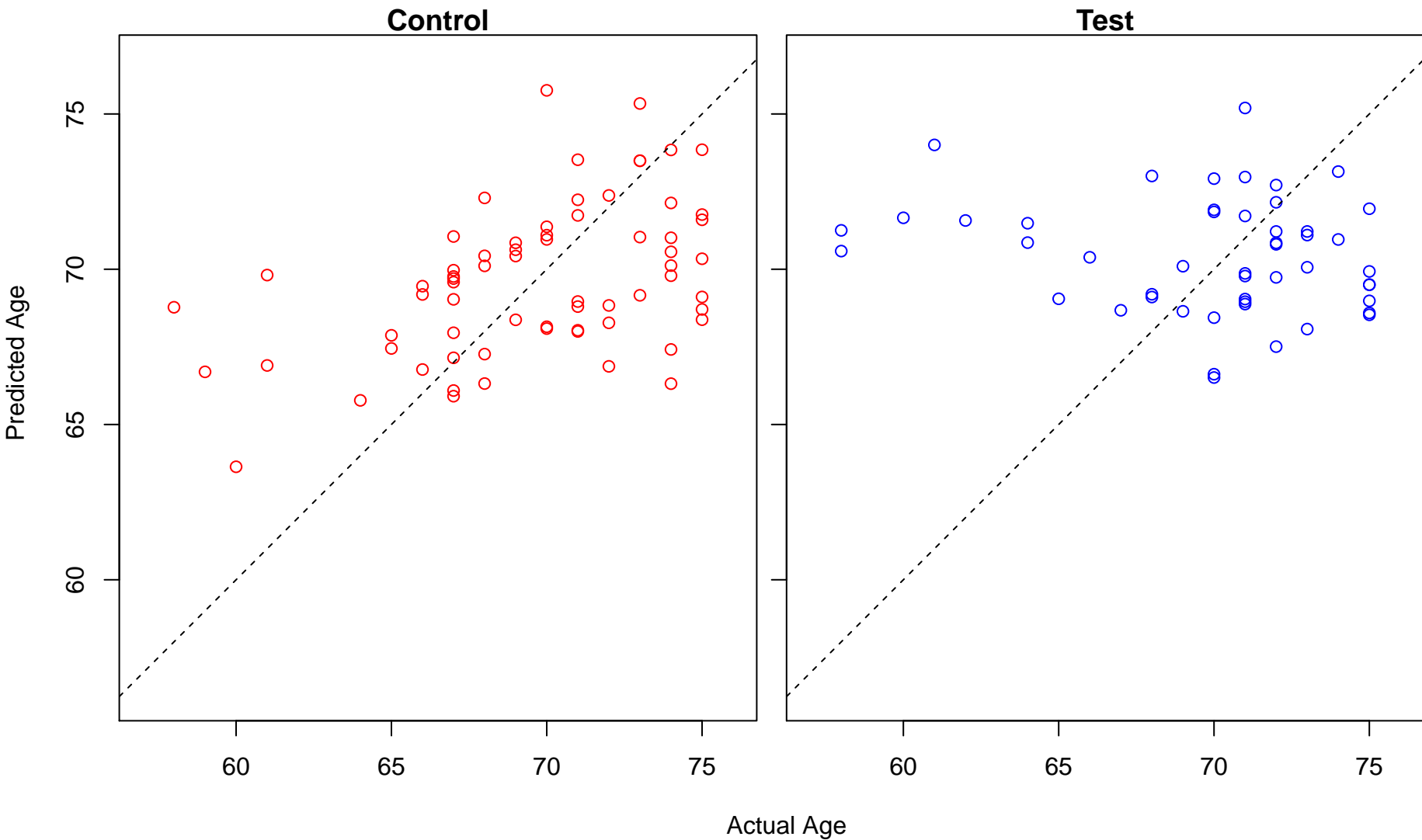
negative regulation of lymphocyte mediated immunity (Score: 0.662005)



regulation of cellular response to hypoxia (Score: 0.661815)

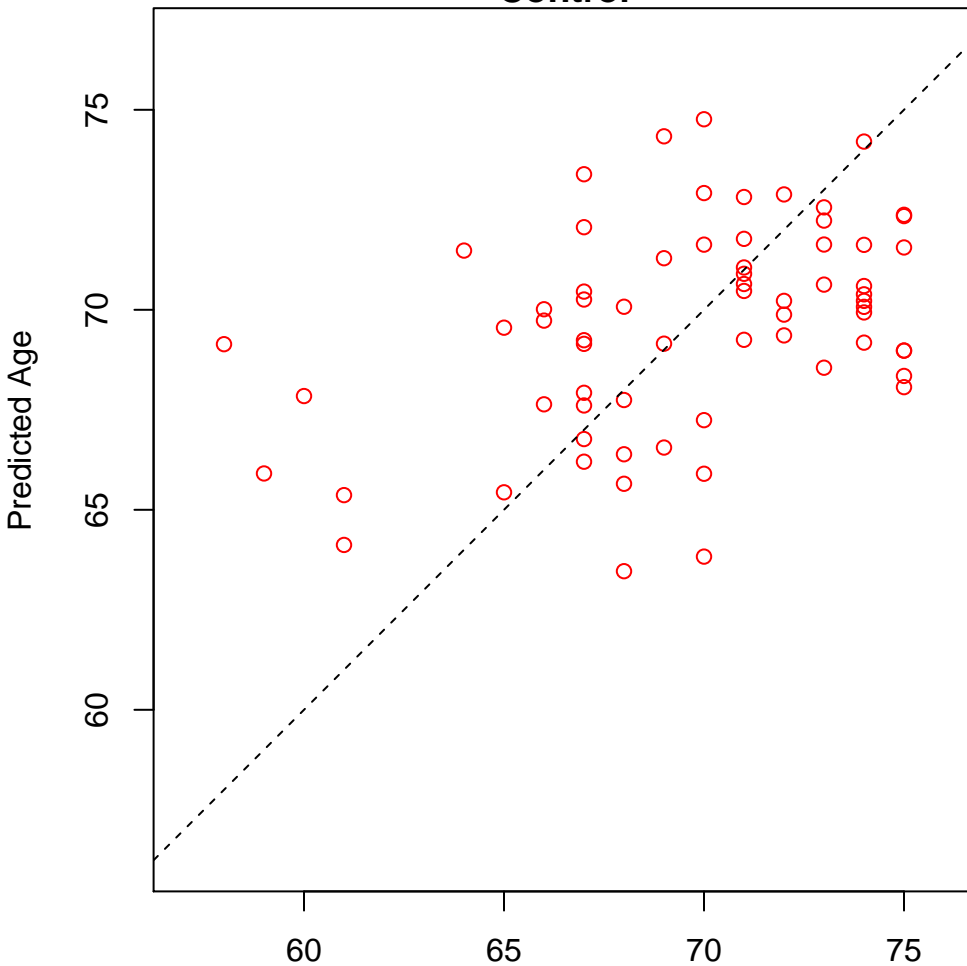


multicellular organismal iron ion homeostasis (Score: 0.660899)

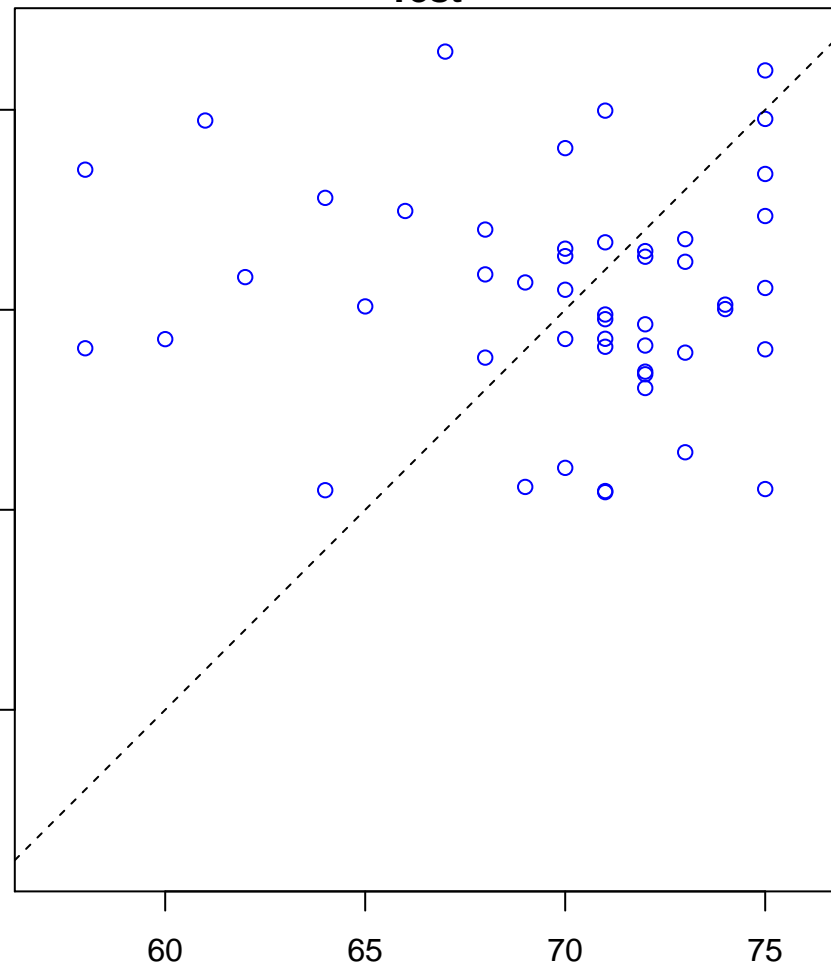


cranial skeletal system development (Score: 0.660818)

Control

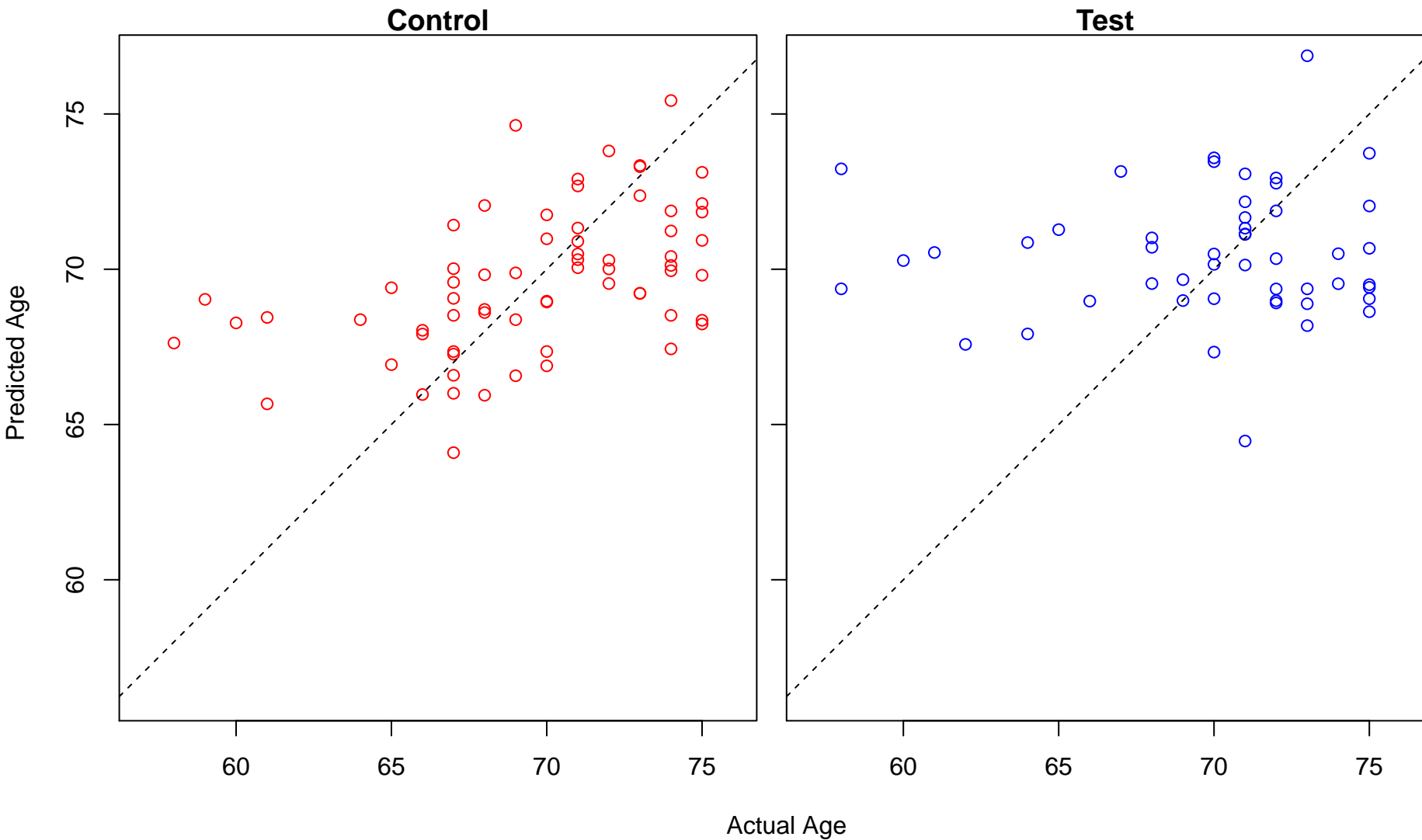


Test

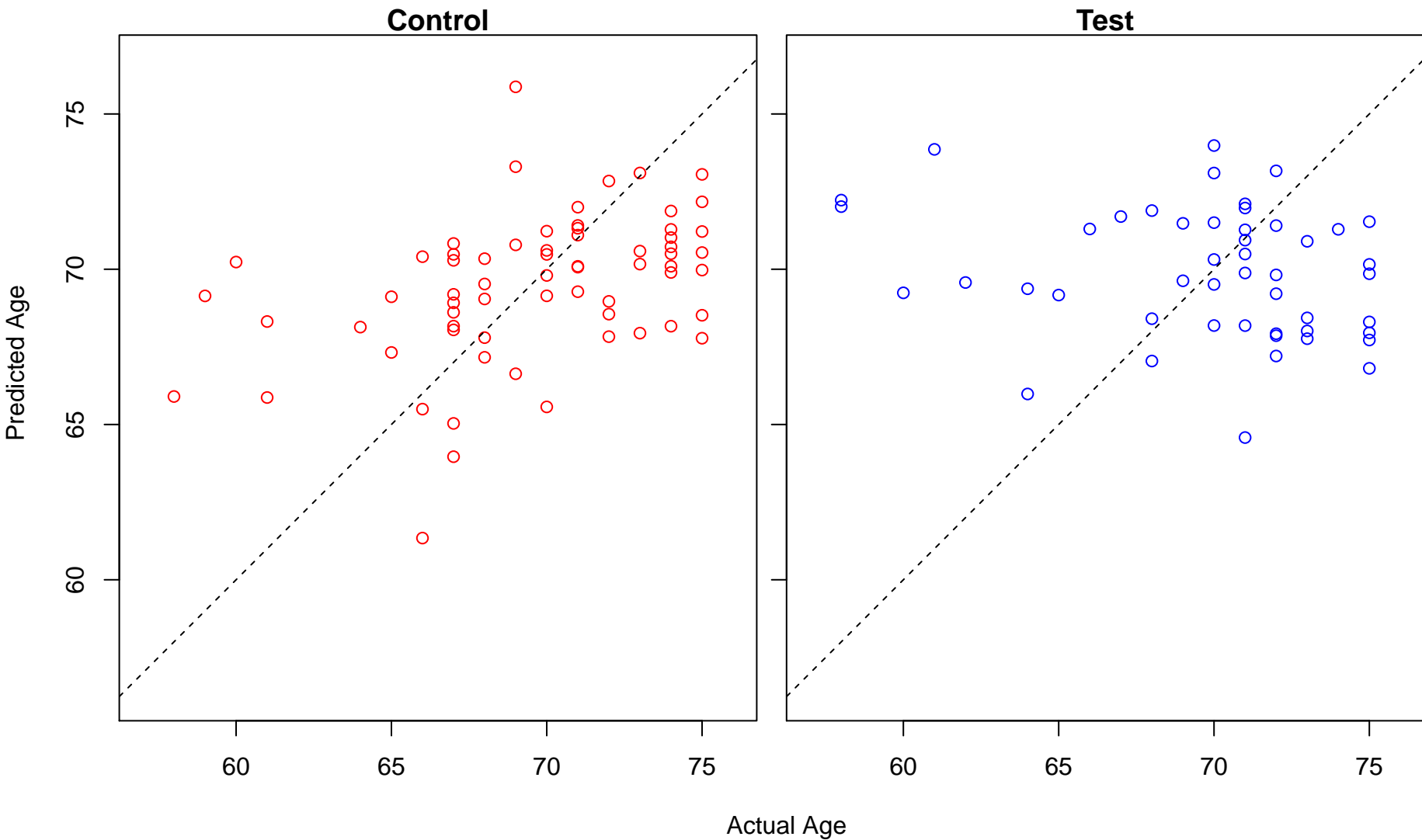


Actual Age

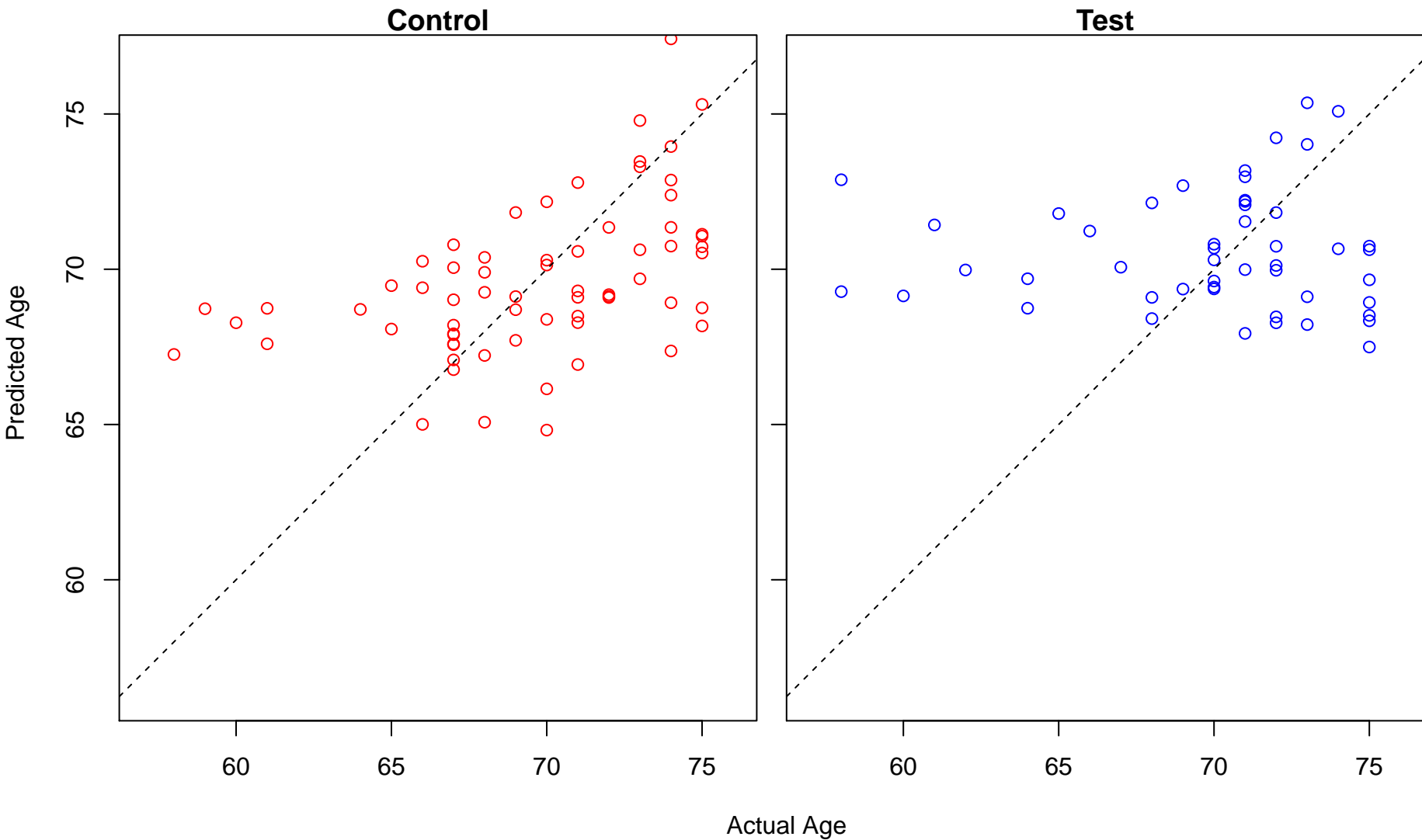
negative regulation of fat cell proliferation (Score: 0.660041)



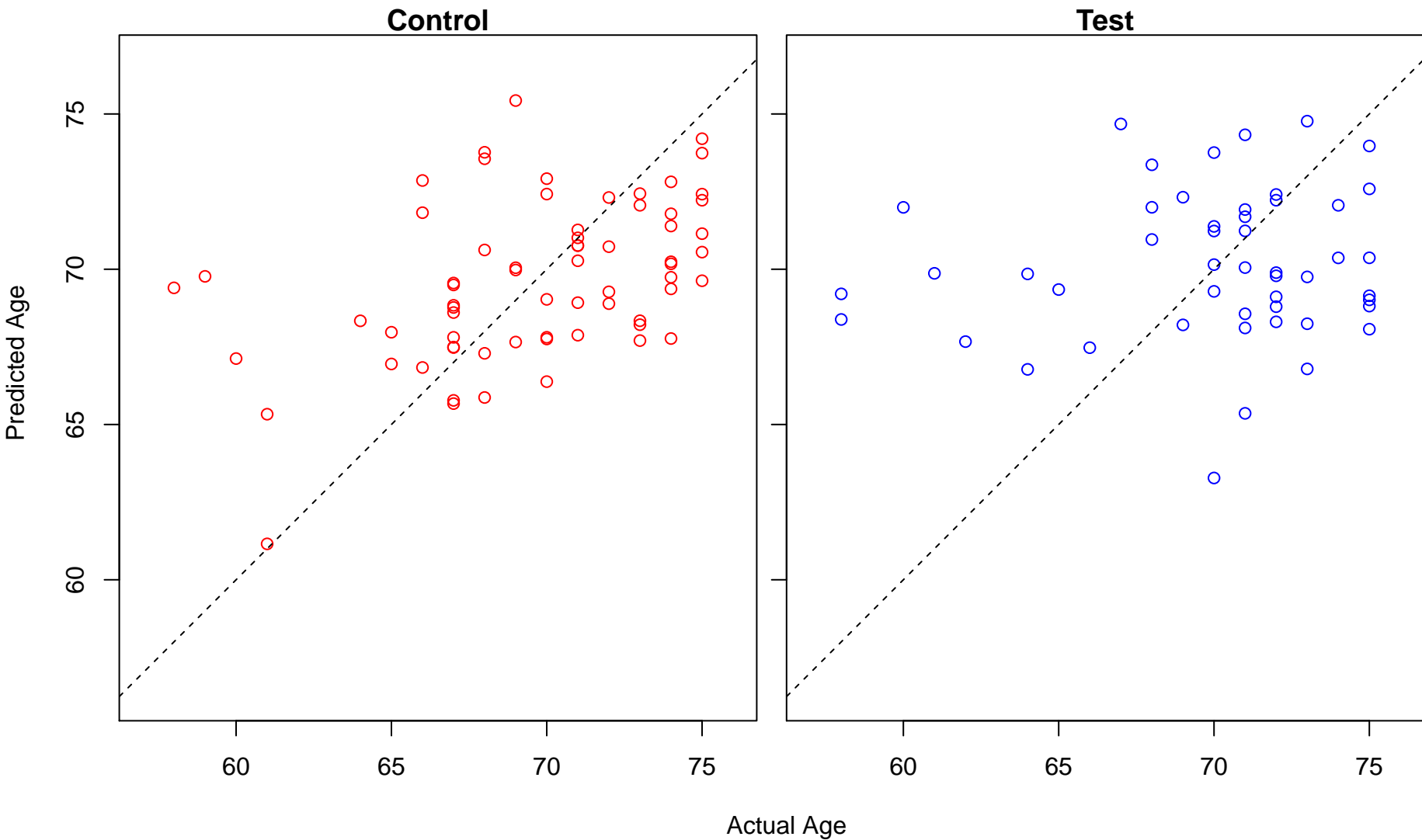
sperm-egg recognition (Score: 0.660030)



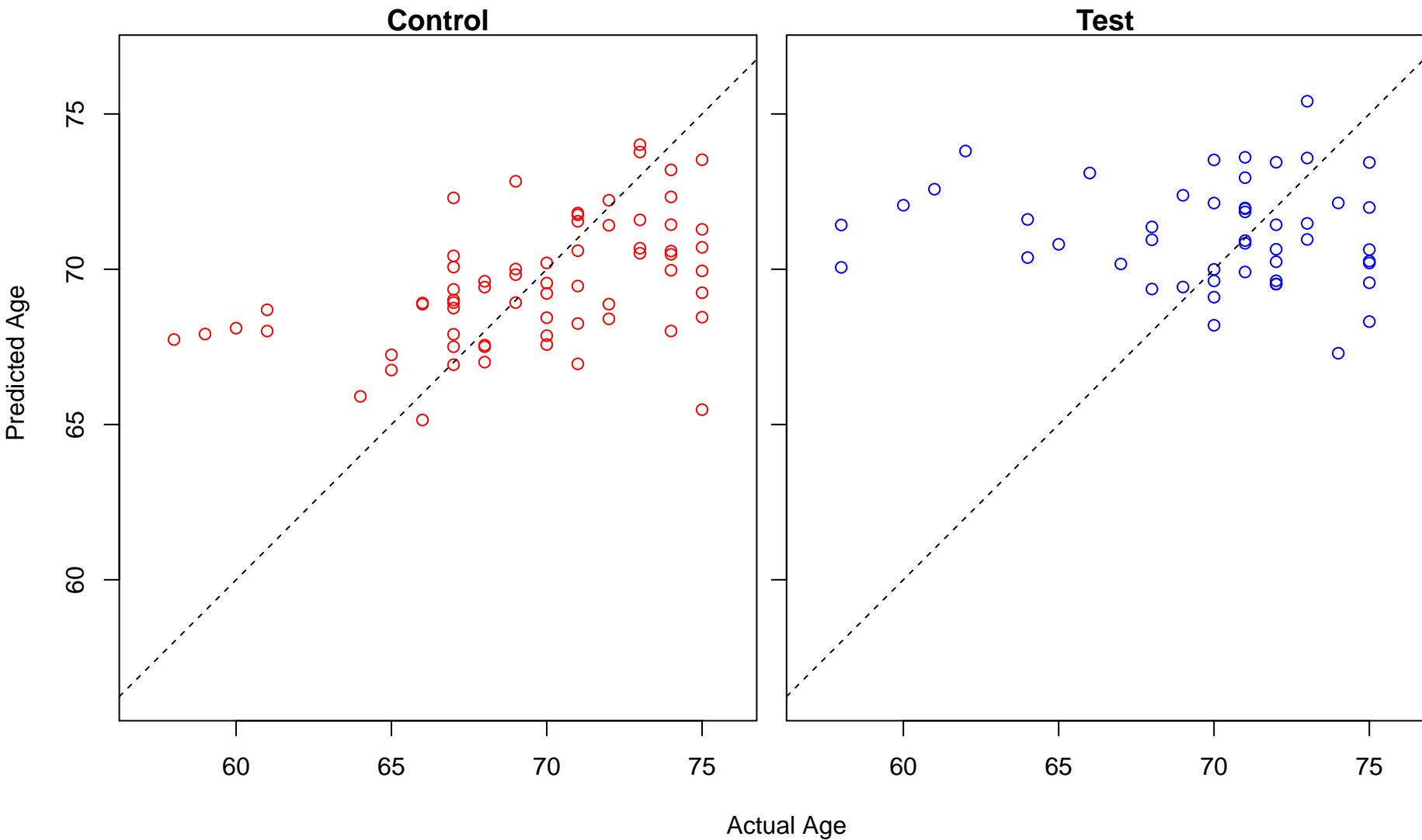
cardiac muscle hypertrophy (Score: 0.659494)



negative regulation of transcription regulatory region DNA binding (Score: 0.659203)

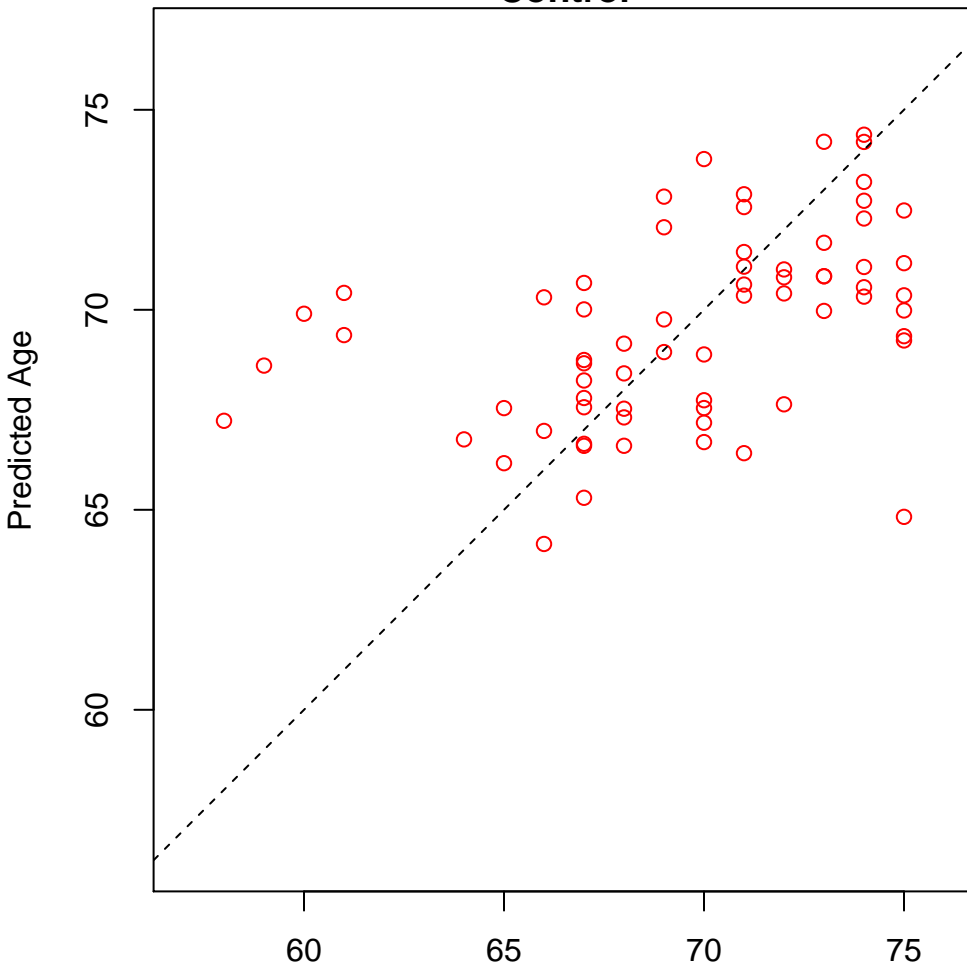


phospholipid scrambling (Score: 0.659190)

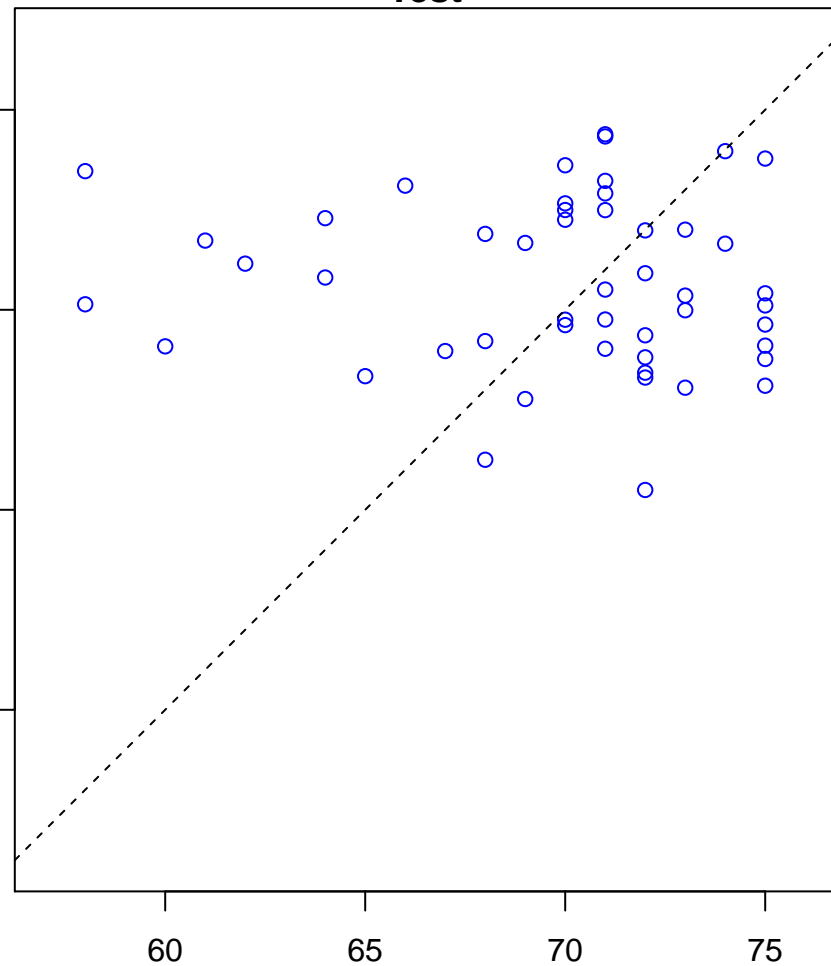


regulation of interleukin-5 production (Score: 0.659070)

Control

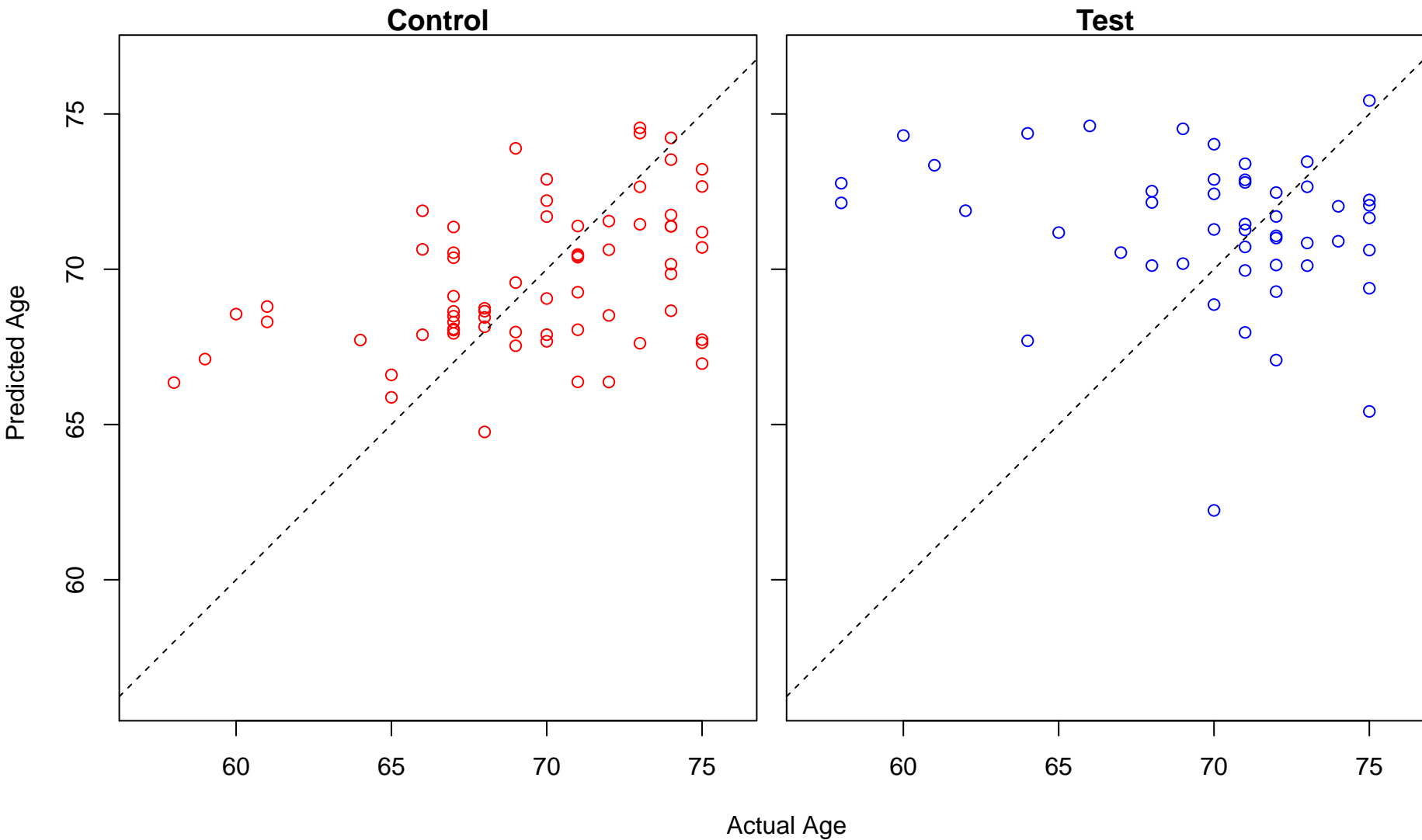


Test

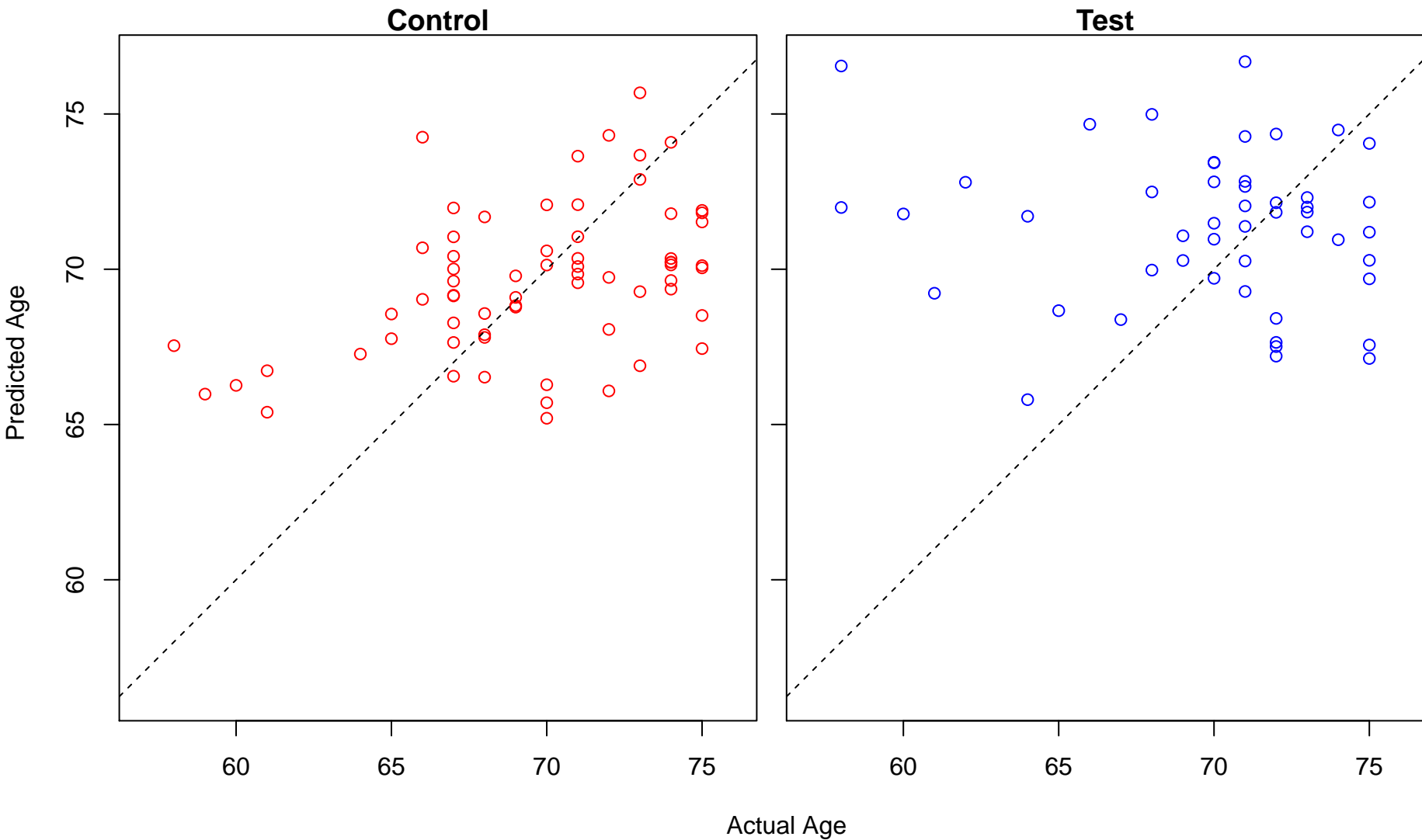


Actual Age

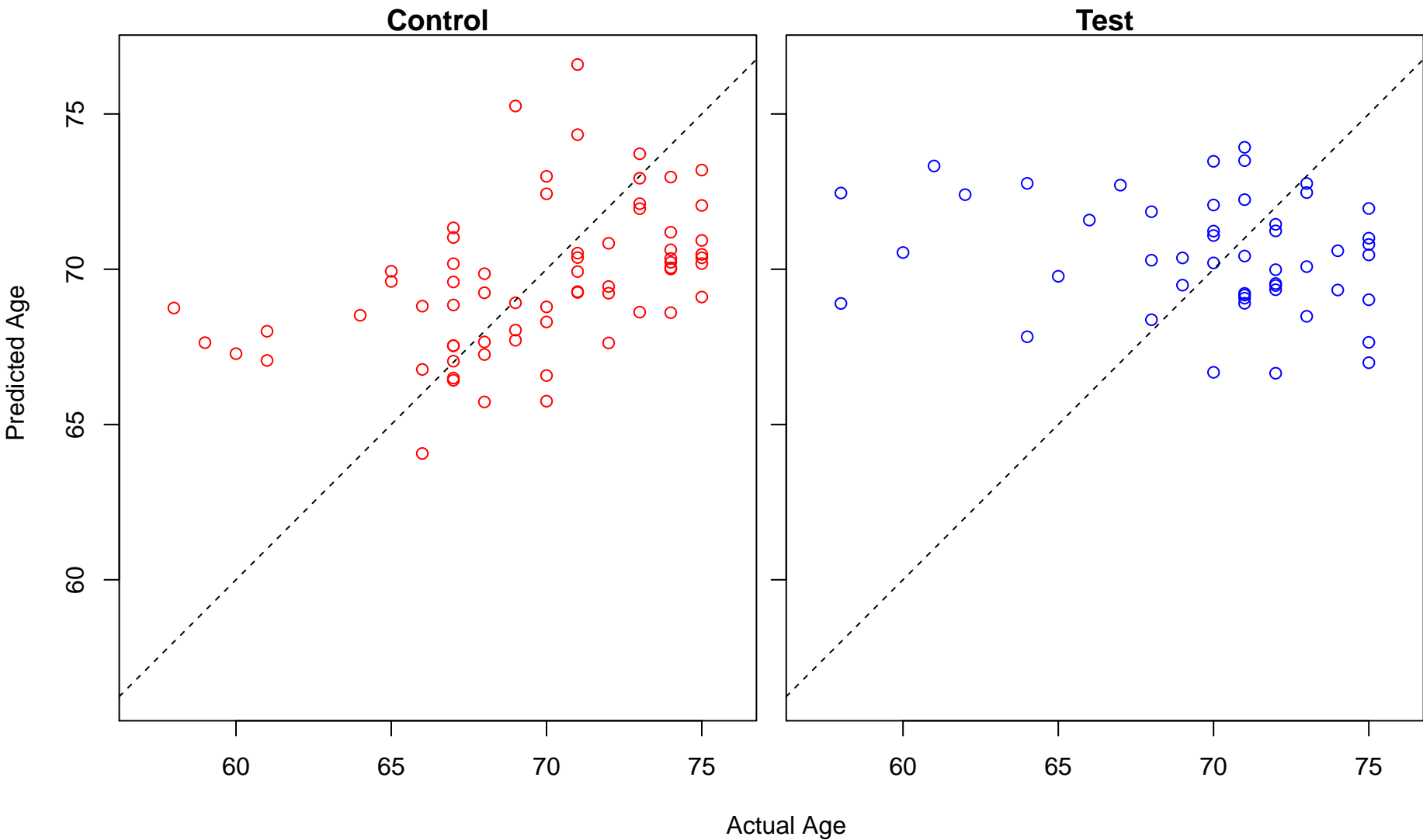
regulation of fatty acid beta-oxidation (Score: 0.659000)



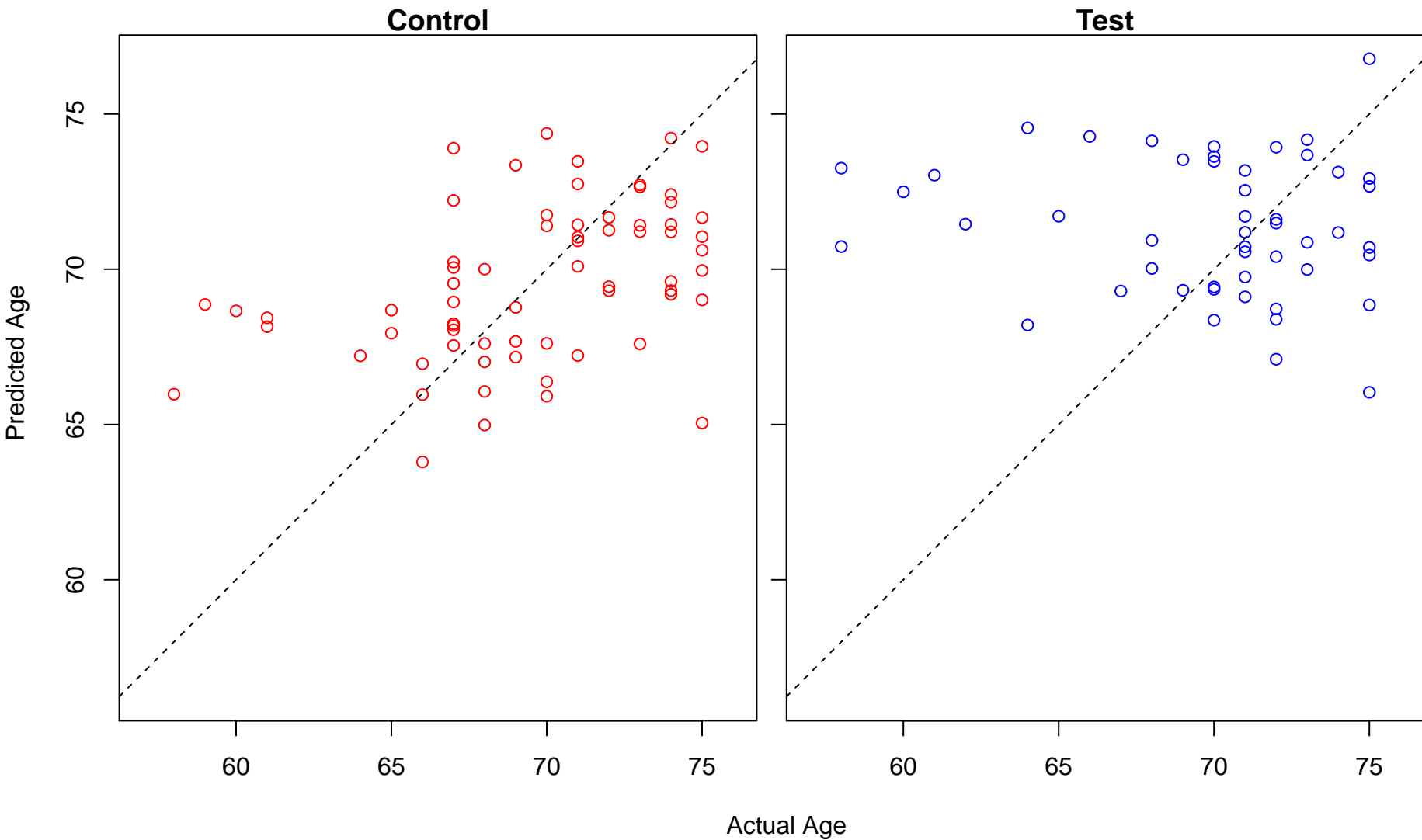
cell-substrate junction assembly (Score: 0.658641)



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

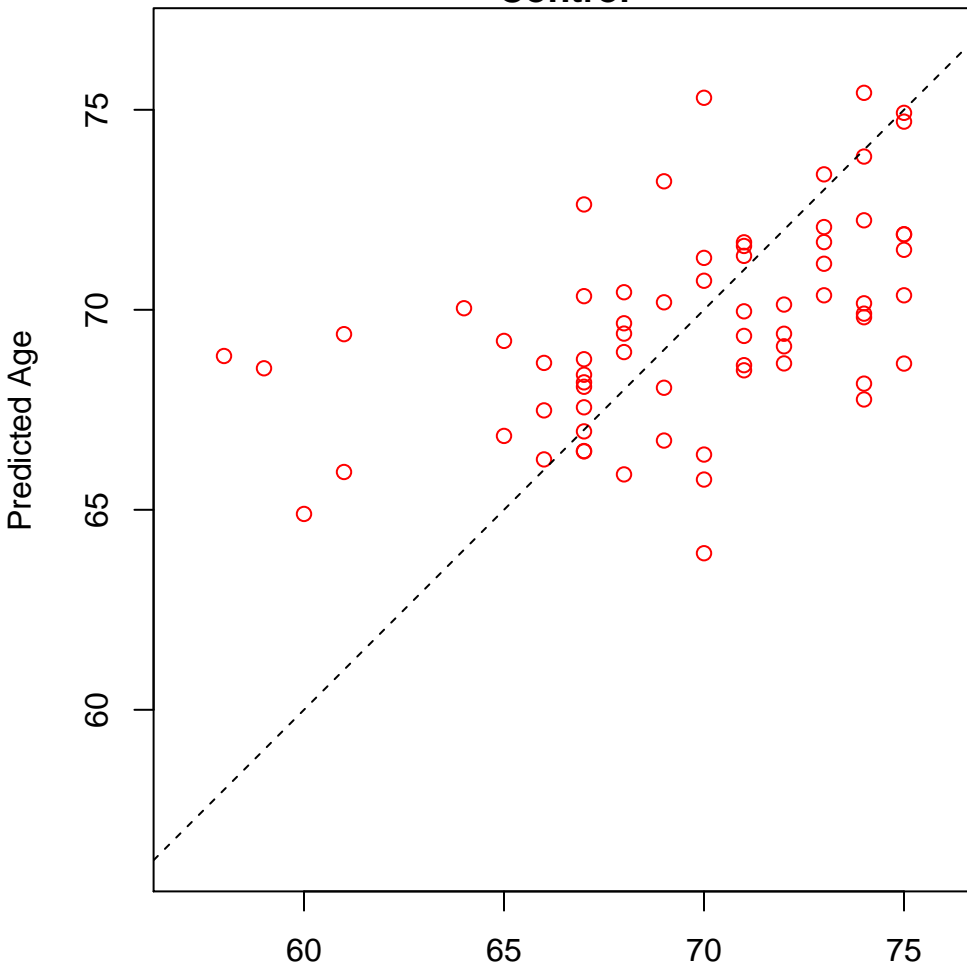


regulation of histone phosphorylation (Score: 0.658202)

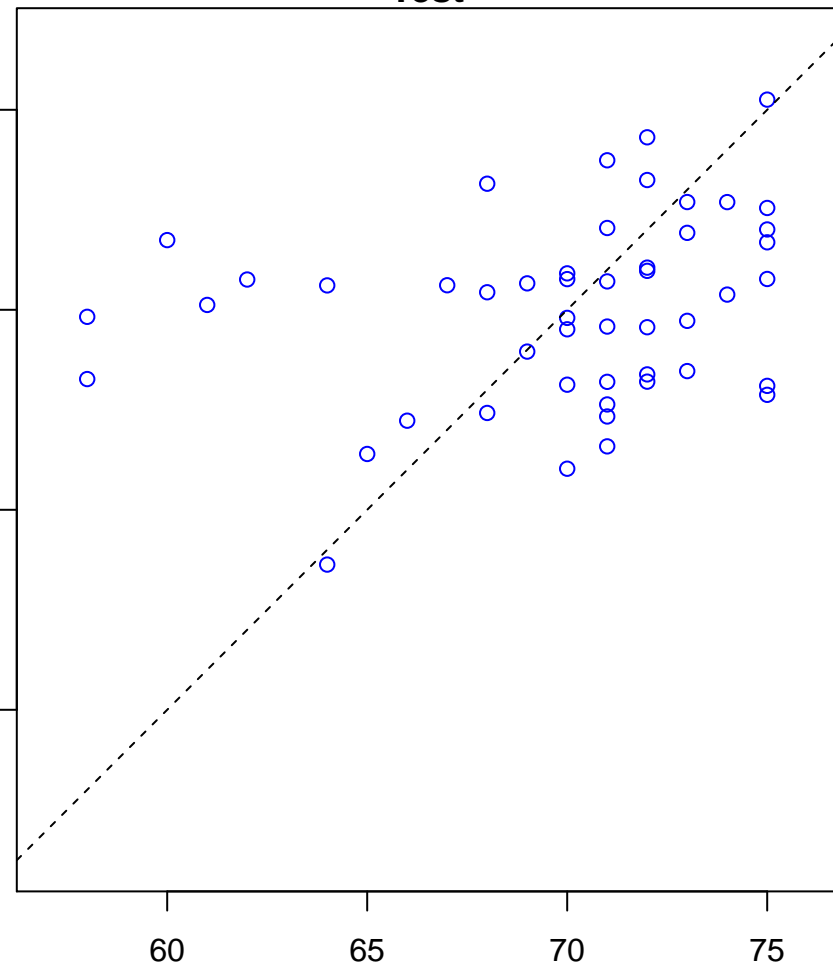


peptidyl-tyrosine autophosphorylation (Score: 0.657661)

Control

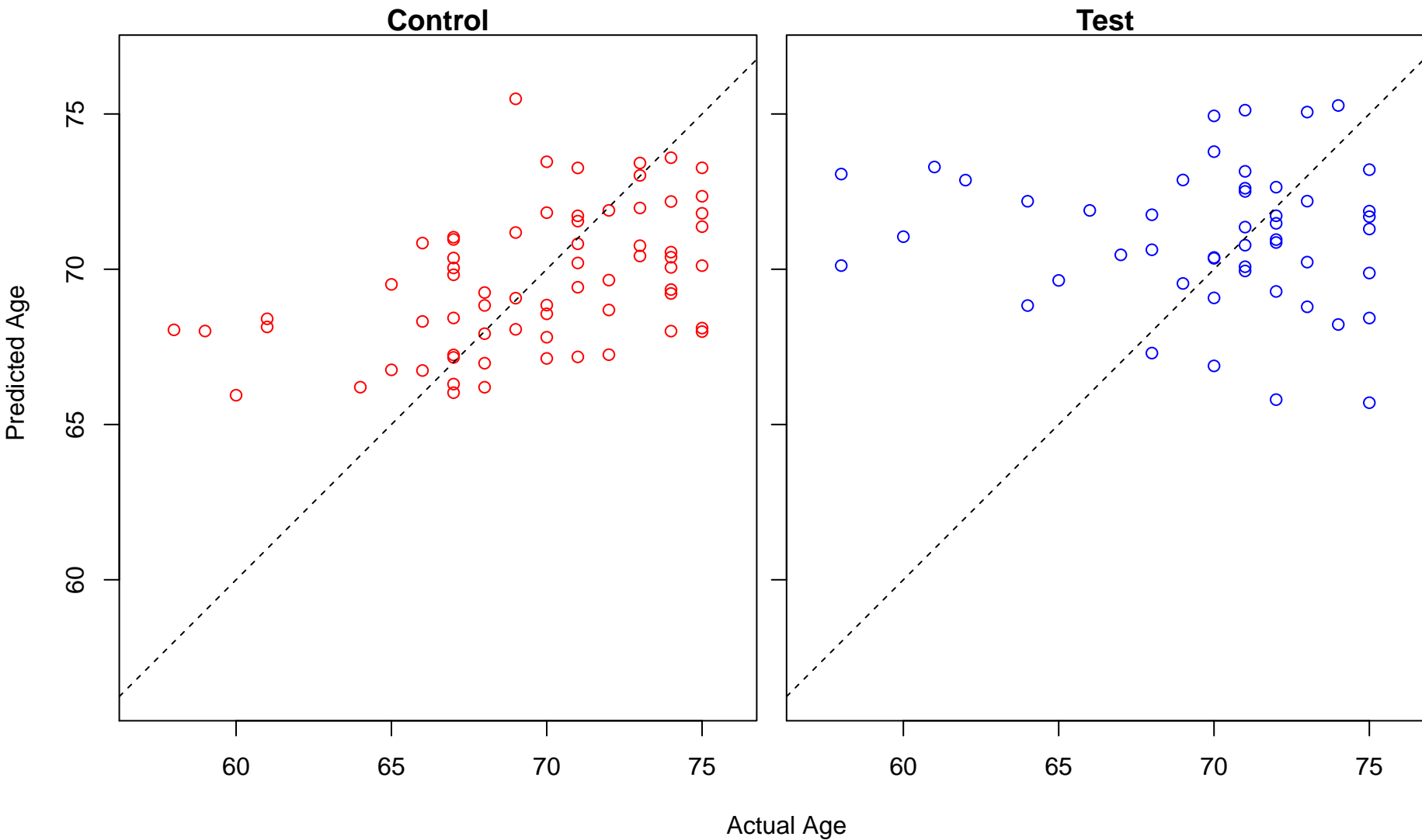


Test

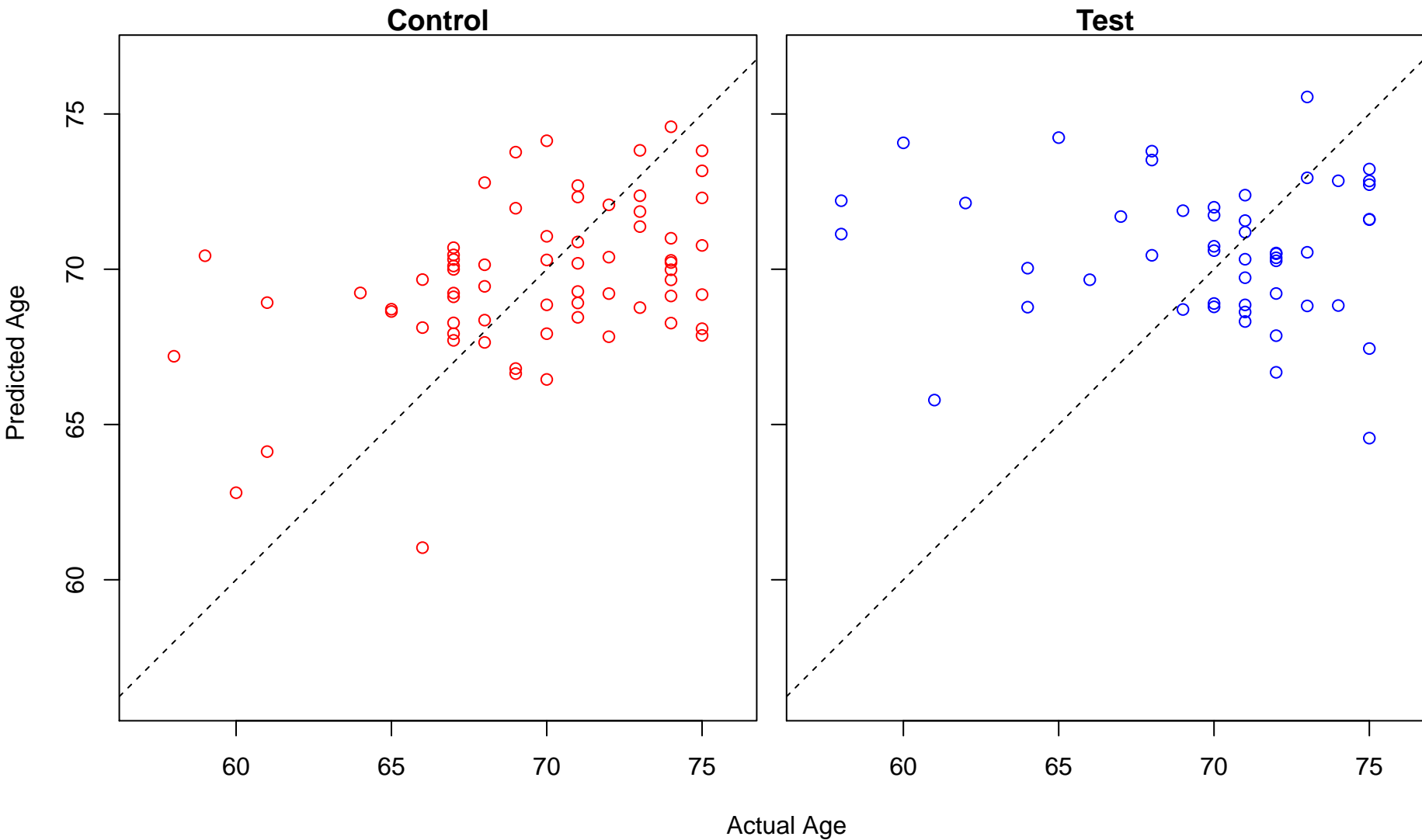


Actual Age

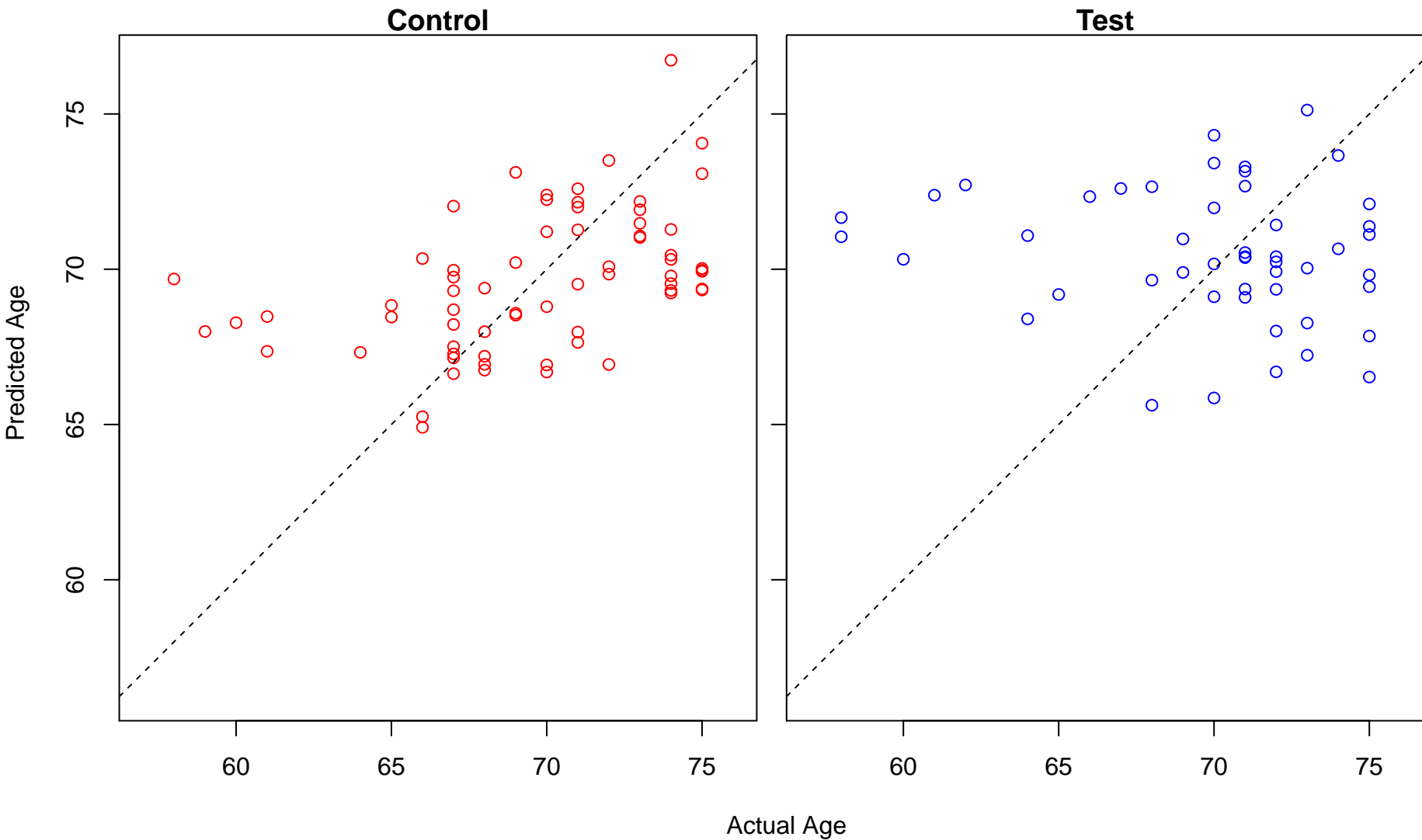
cargo loading into vesicle (Score: 0.657635)



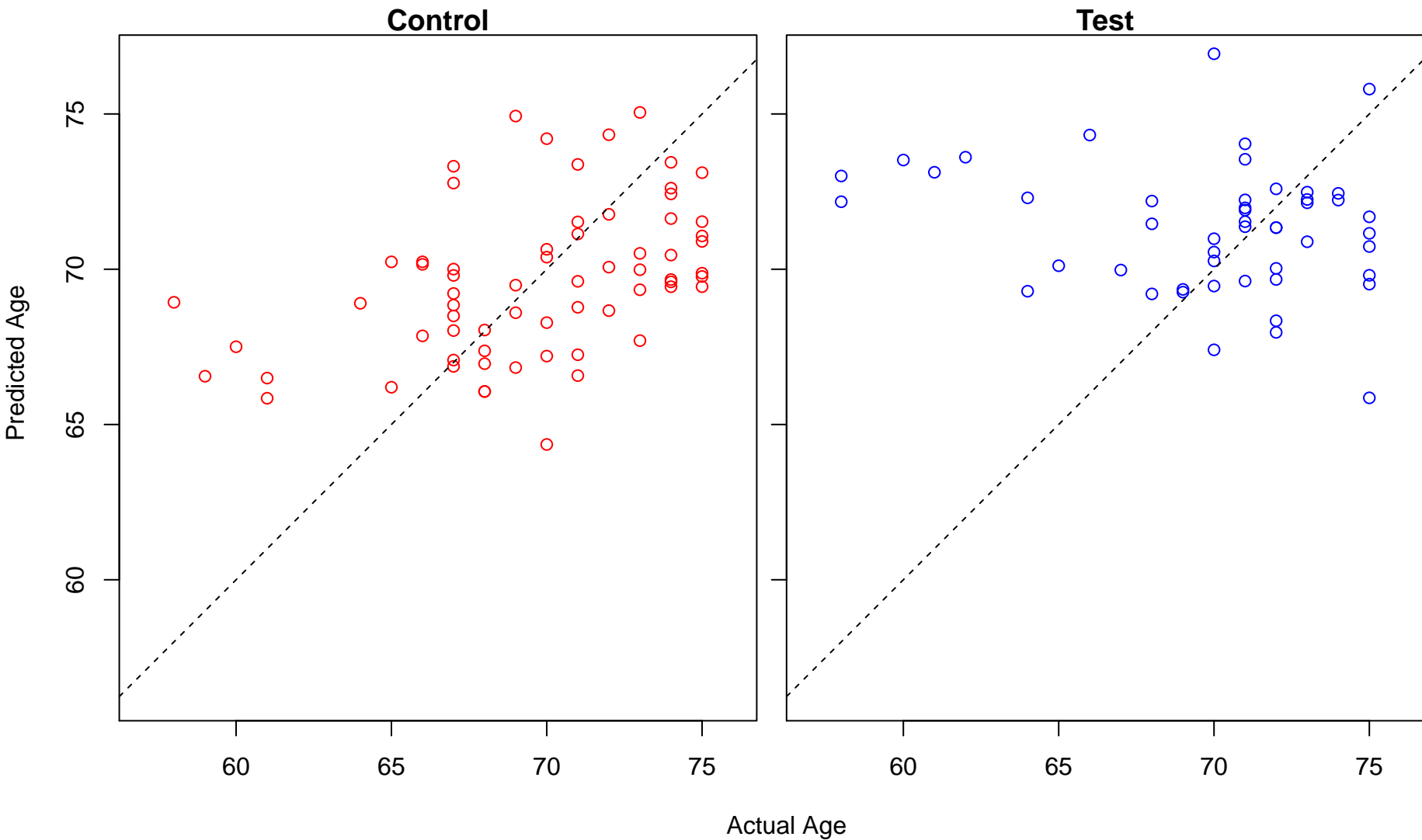
positive regulation of macrophage derived foam cell differentiation (Score: 0.656689)



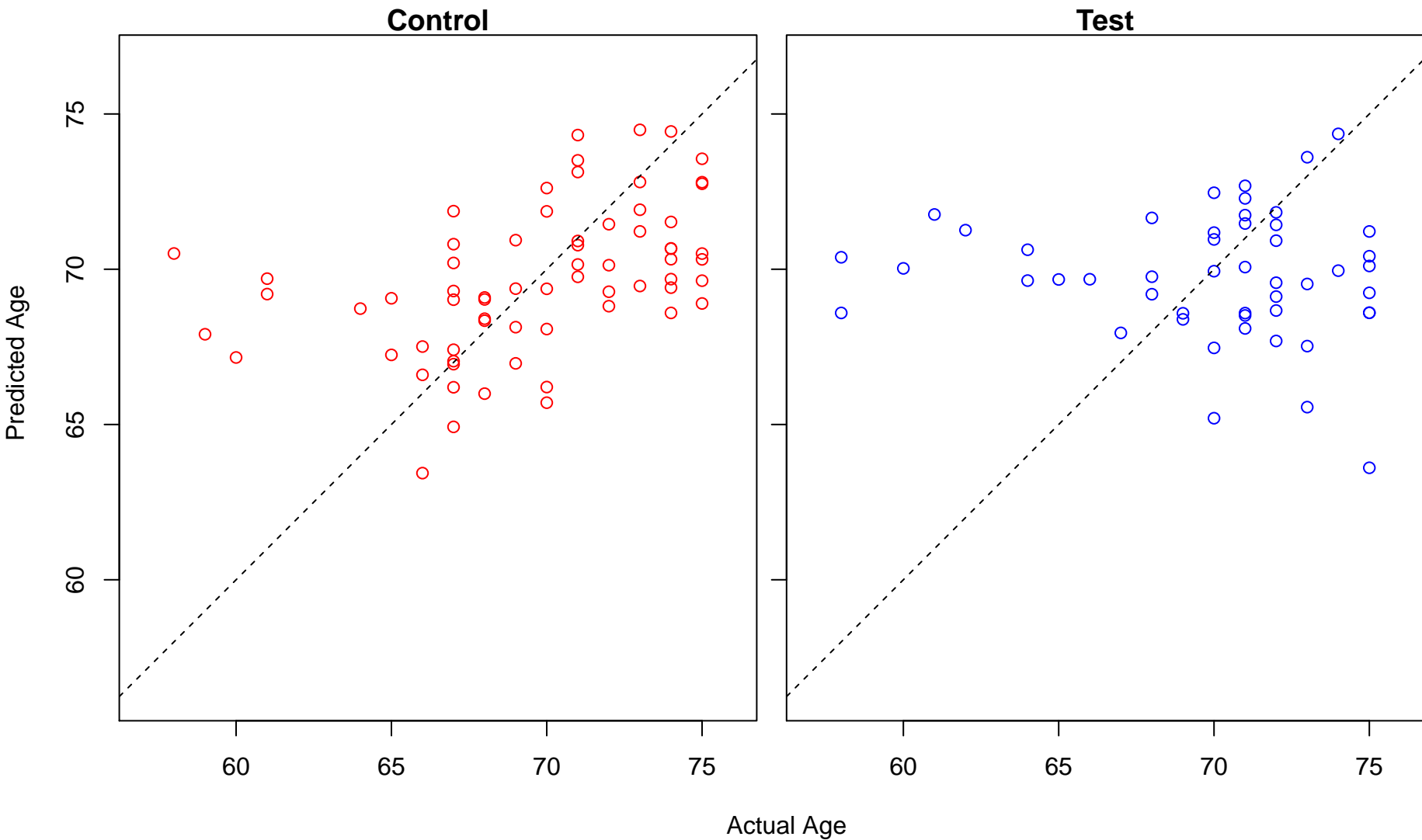
neuron death (Score: 0.656290)



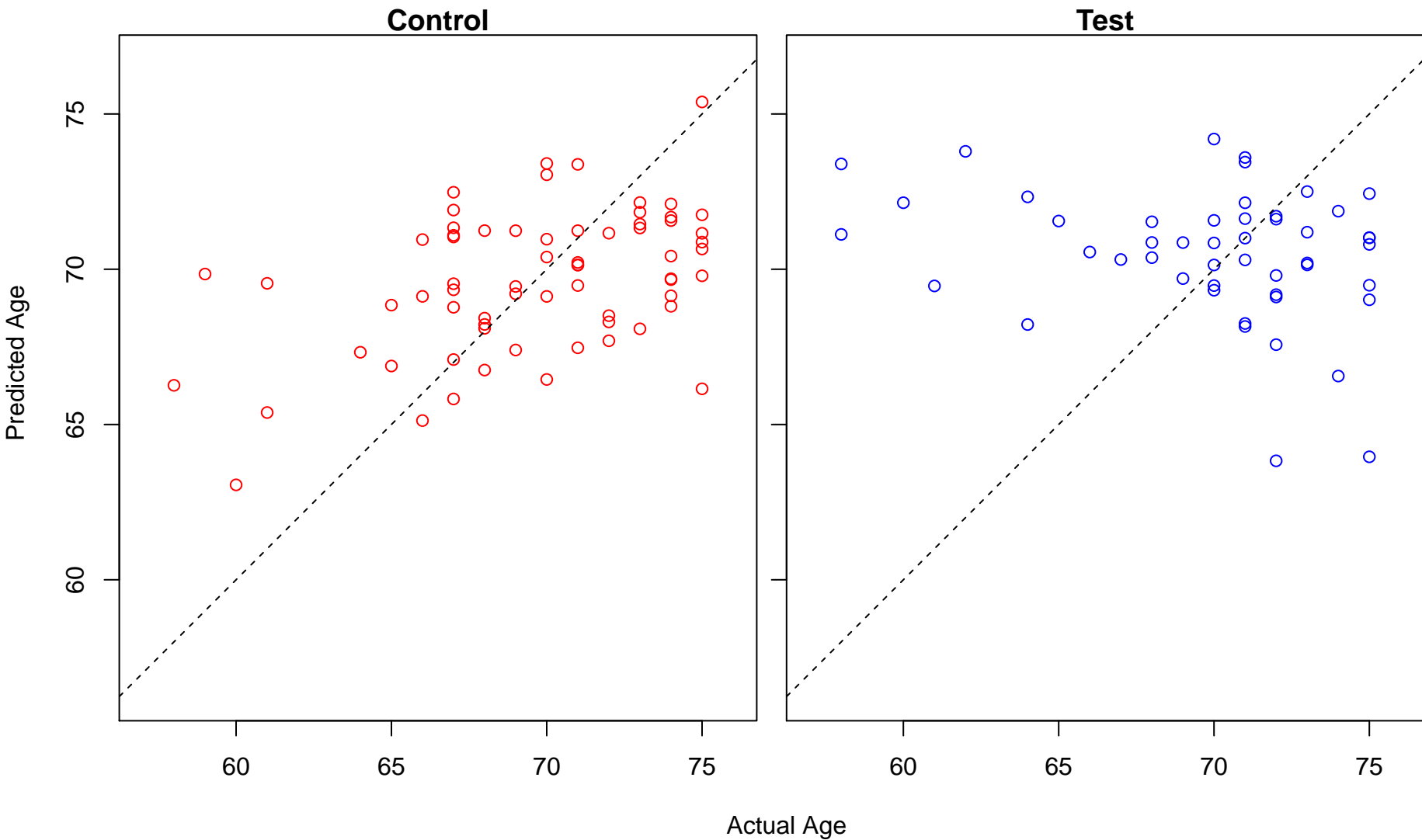
regulation of lysosomal lumen pH (Score: 0.655504)



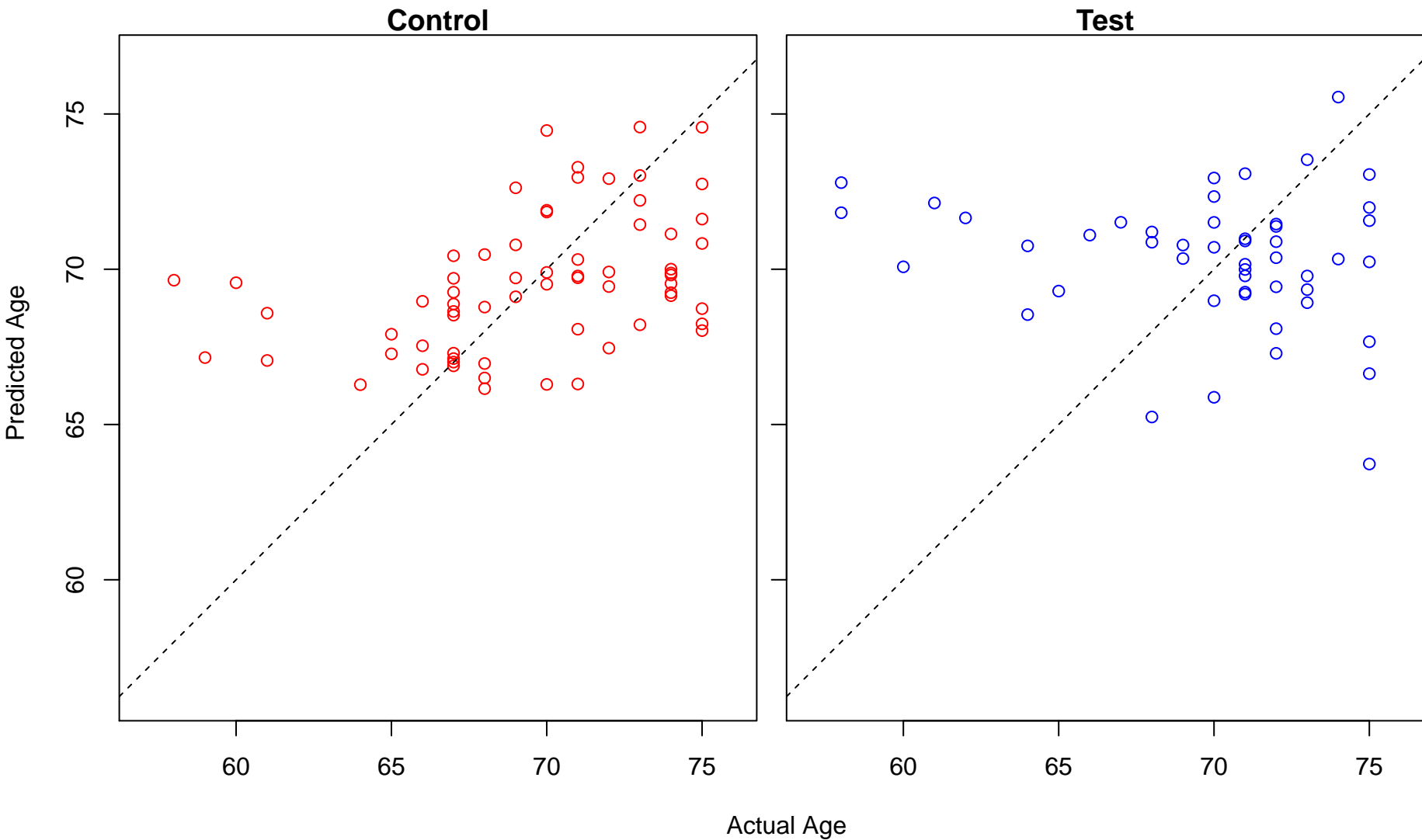
cobalamin metabolic process (Score: 0.654443)



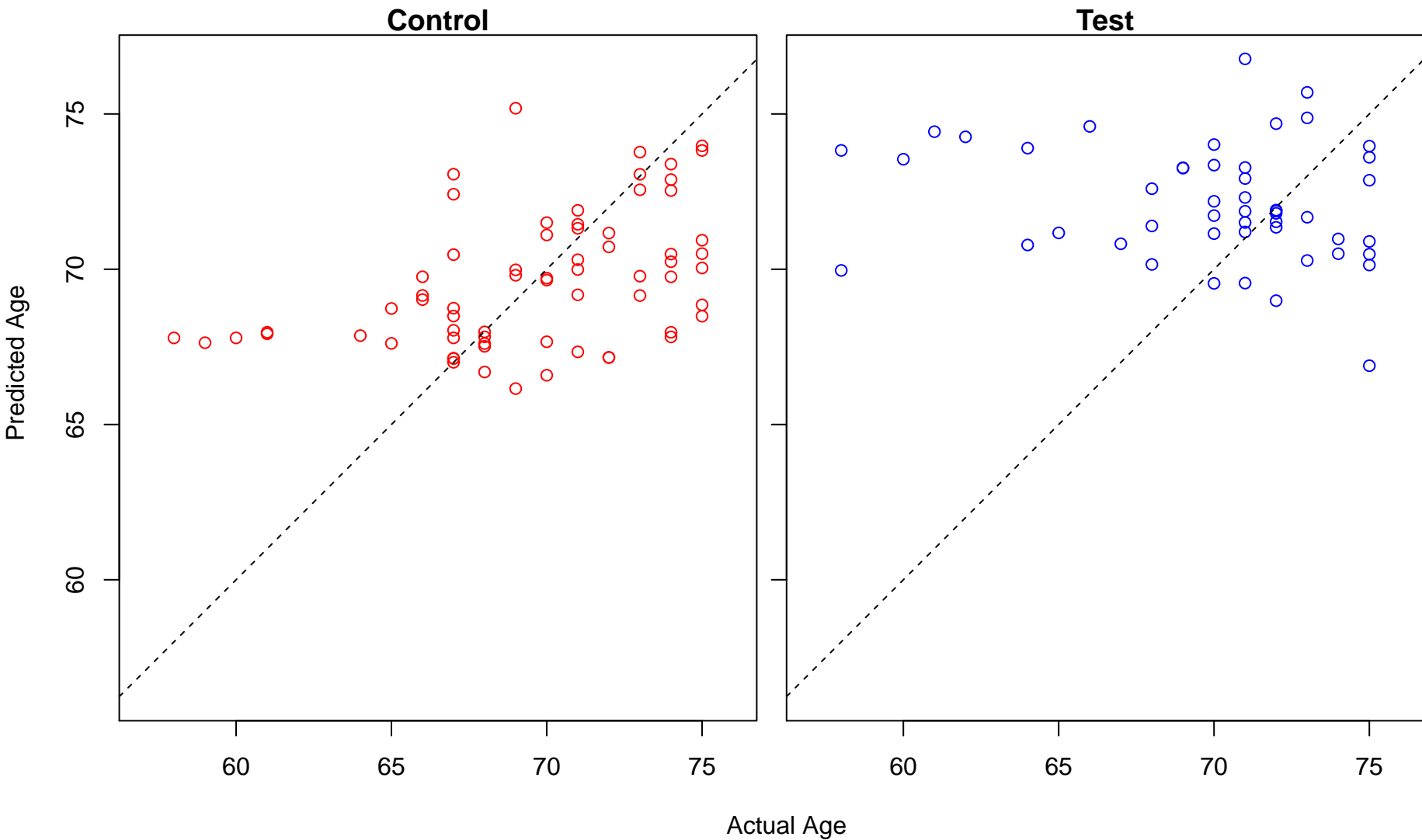
long-chain fatty acid import (Score: 0.653375)



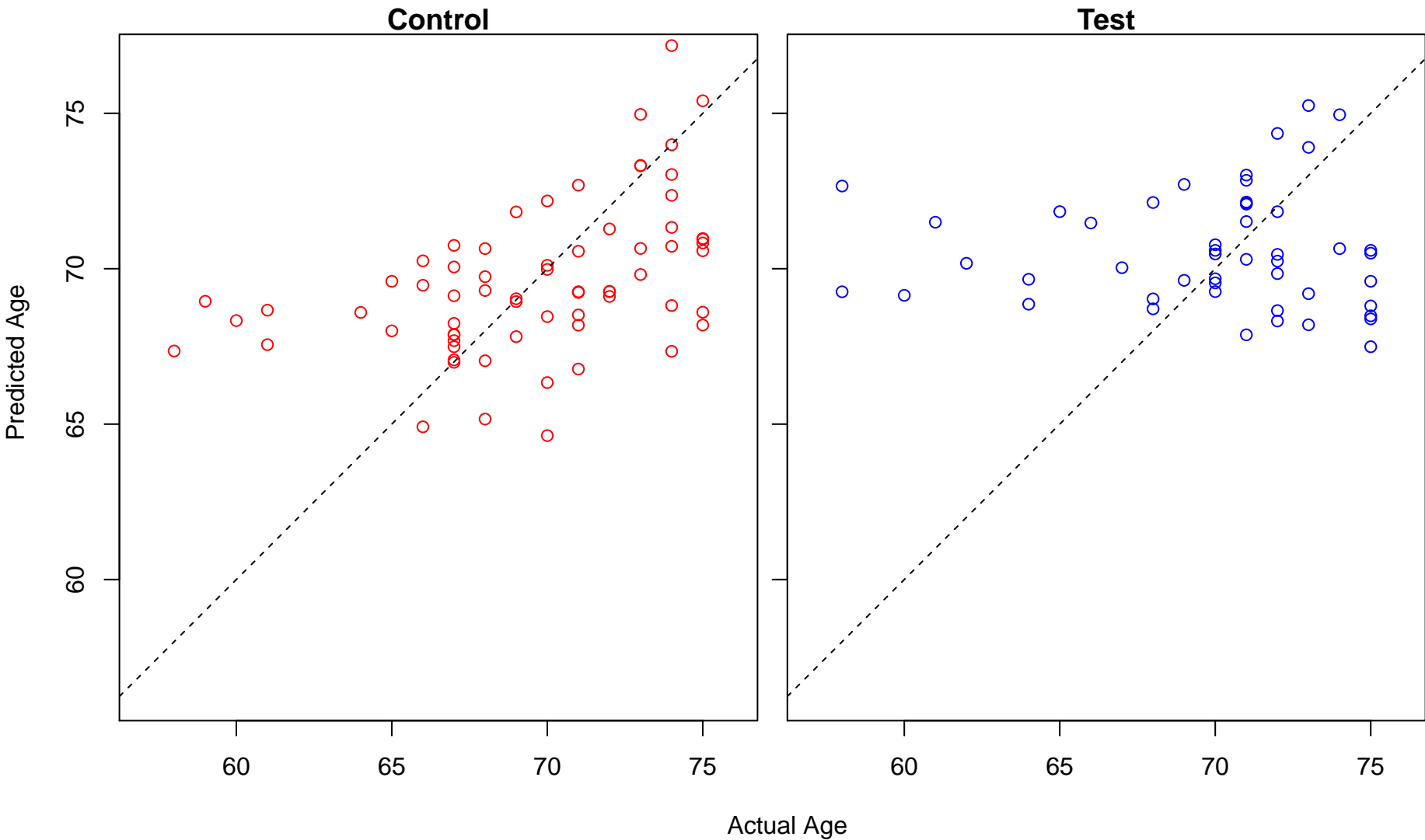
regulation of T cell mediated cytotoxicity (Score: 0.653161)



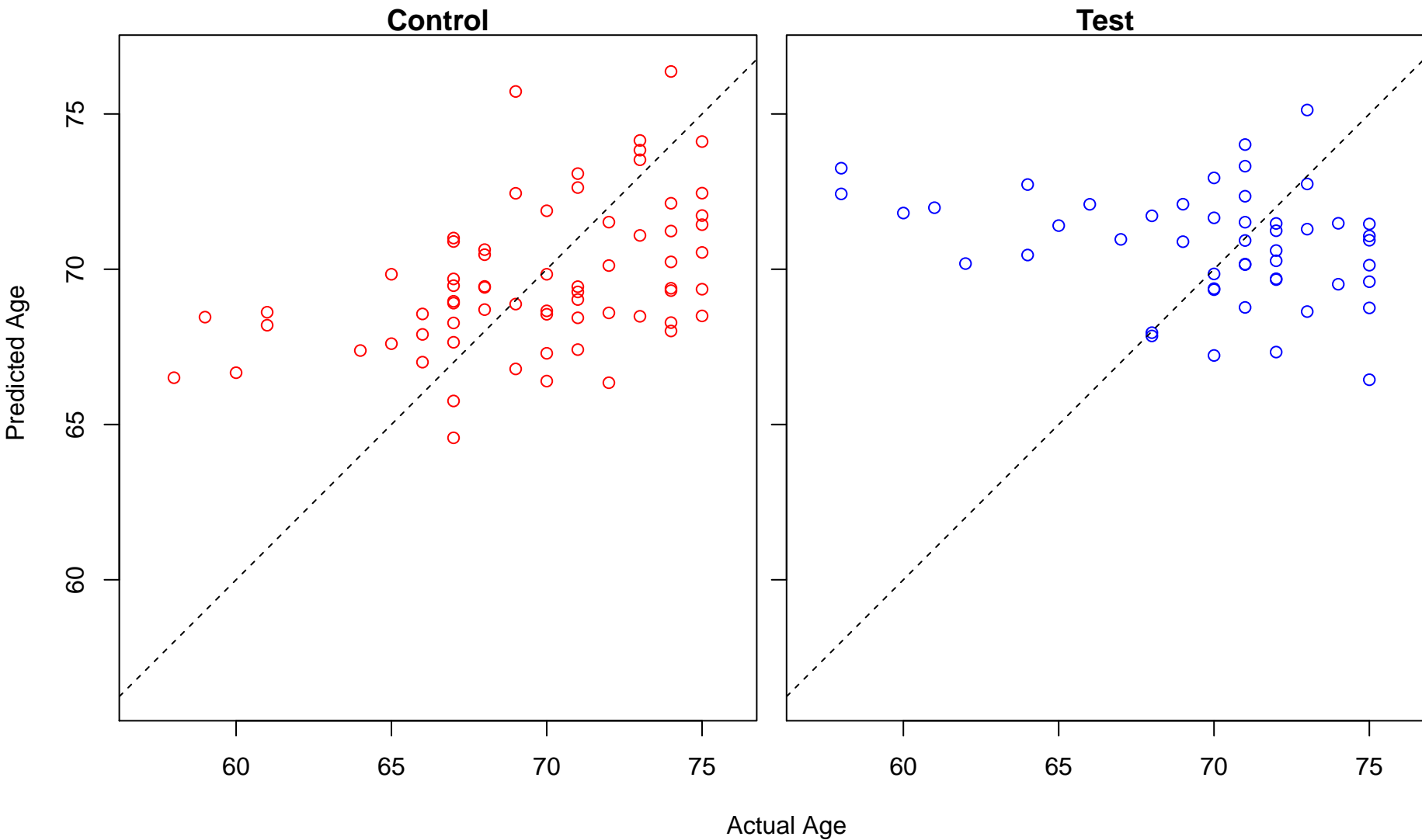
ear development (Score: 0.651804)



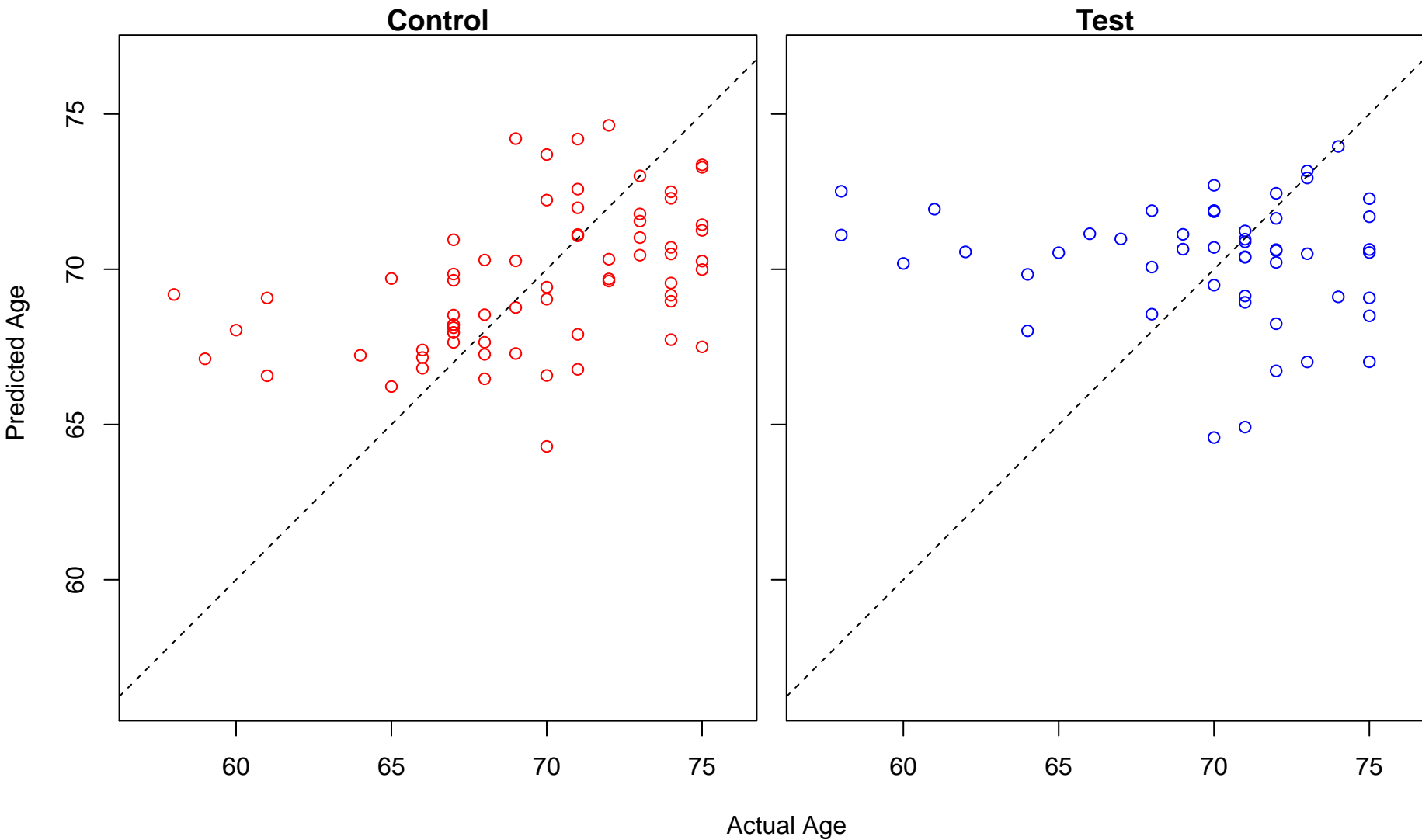
striated muscle hypertrophy (Score: 0.650327)



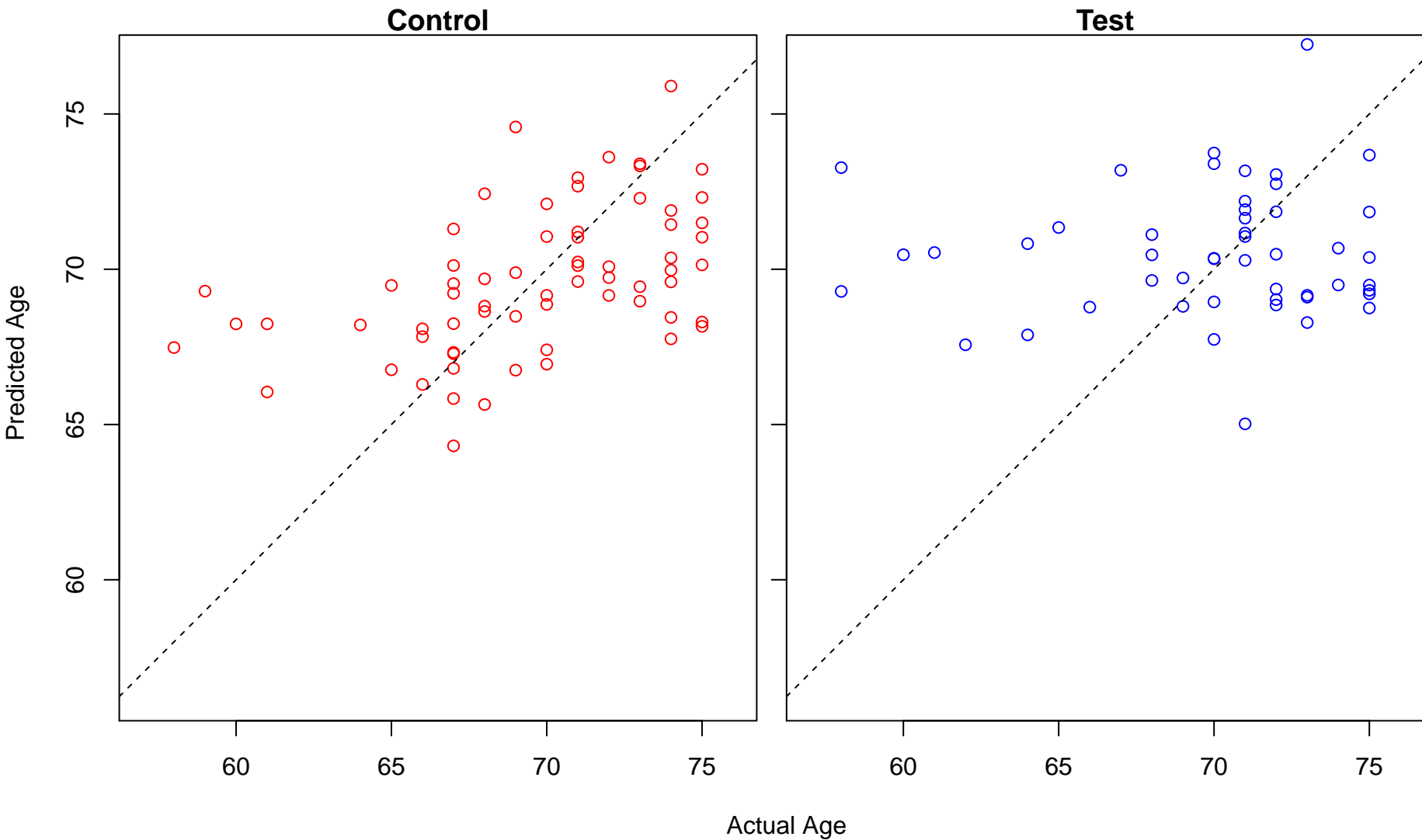
aspartate family amino acid catabolic process (Score: 0.650177)



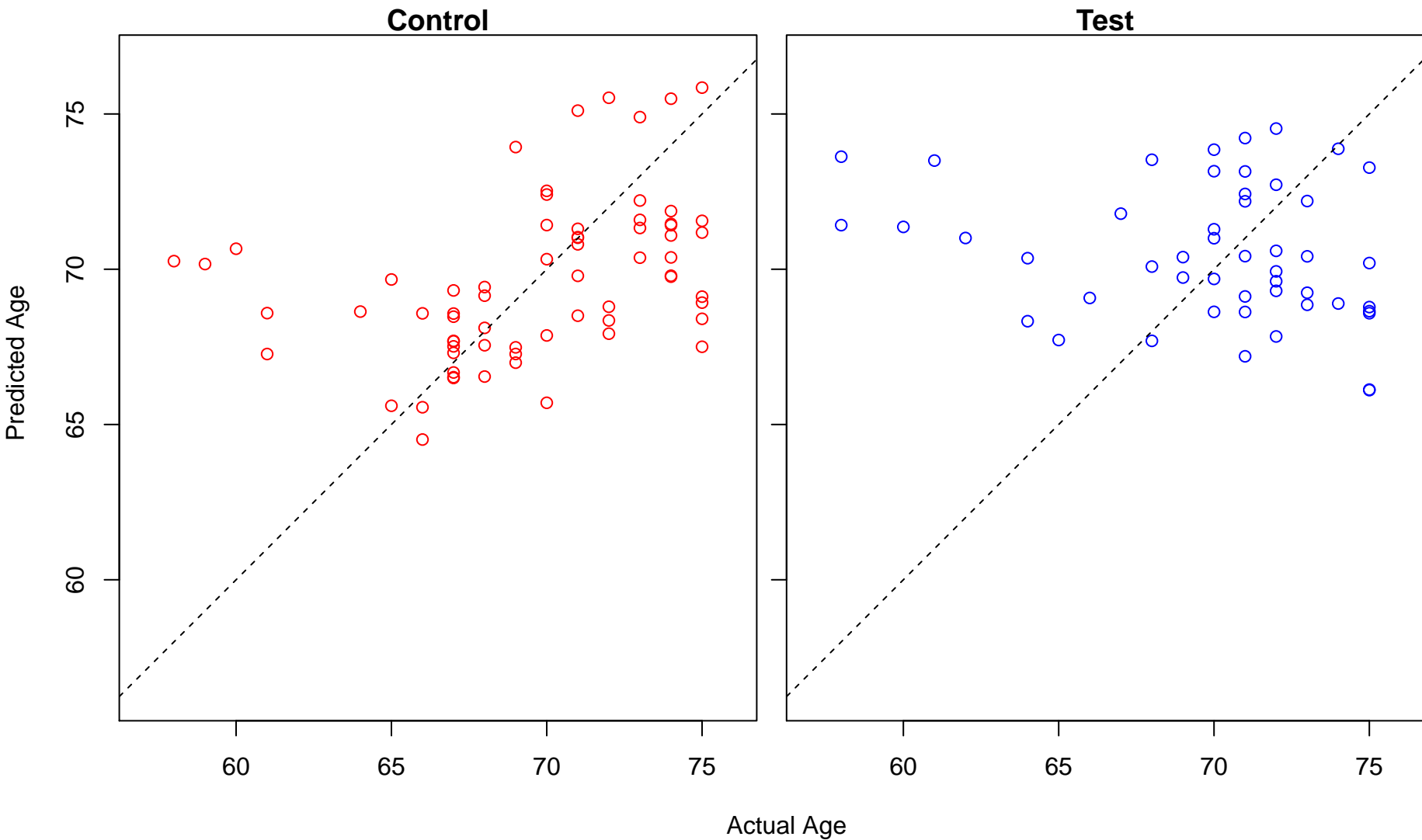
positive regulation of tyrosine phosphorylation of Stat3 protein (Score: 0.650139)



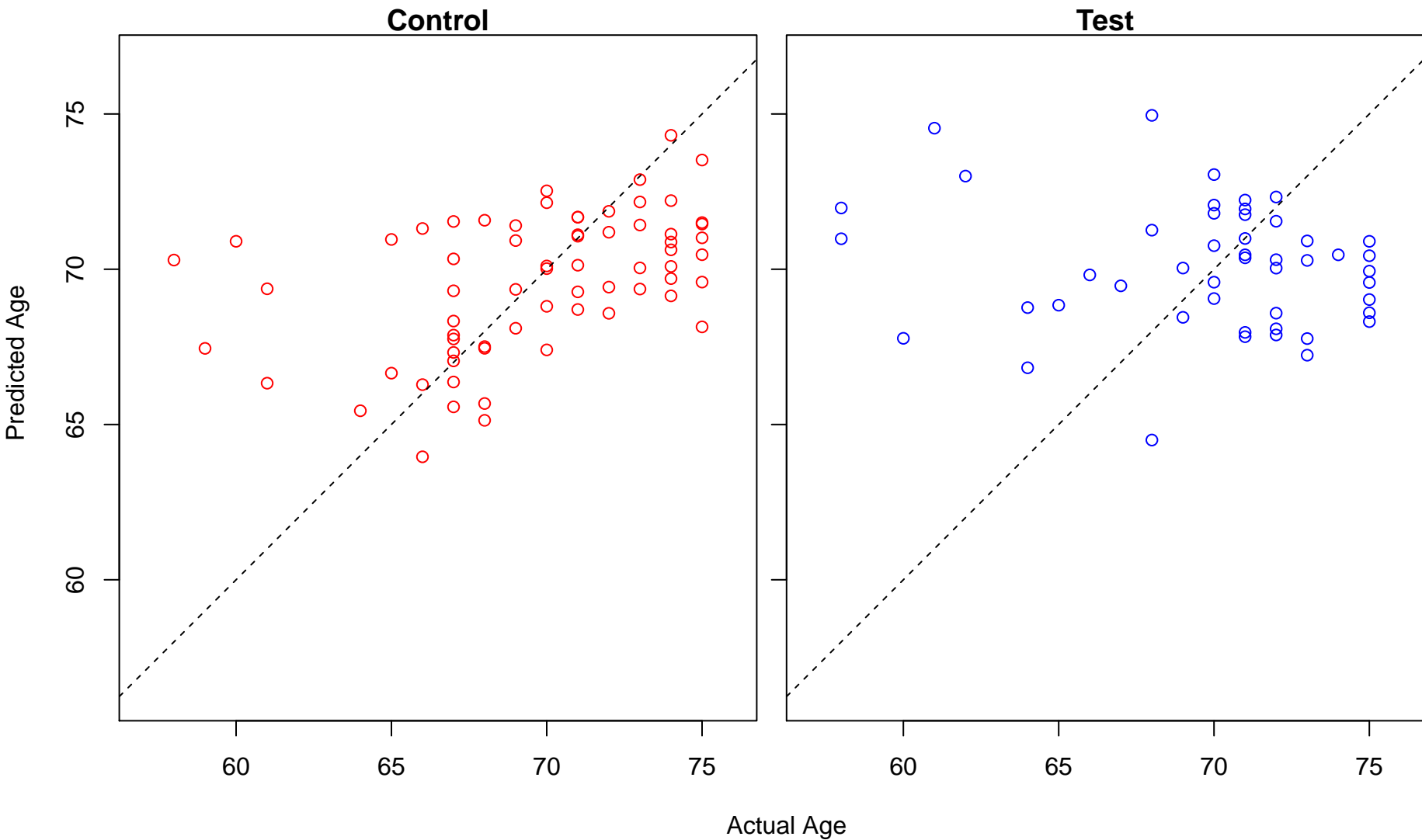
regulation of fat cell proliferation (Score: 0.649812)



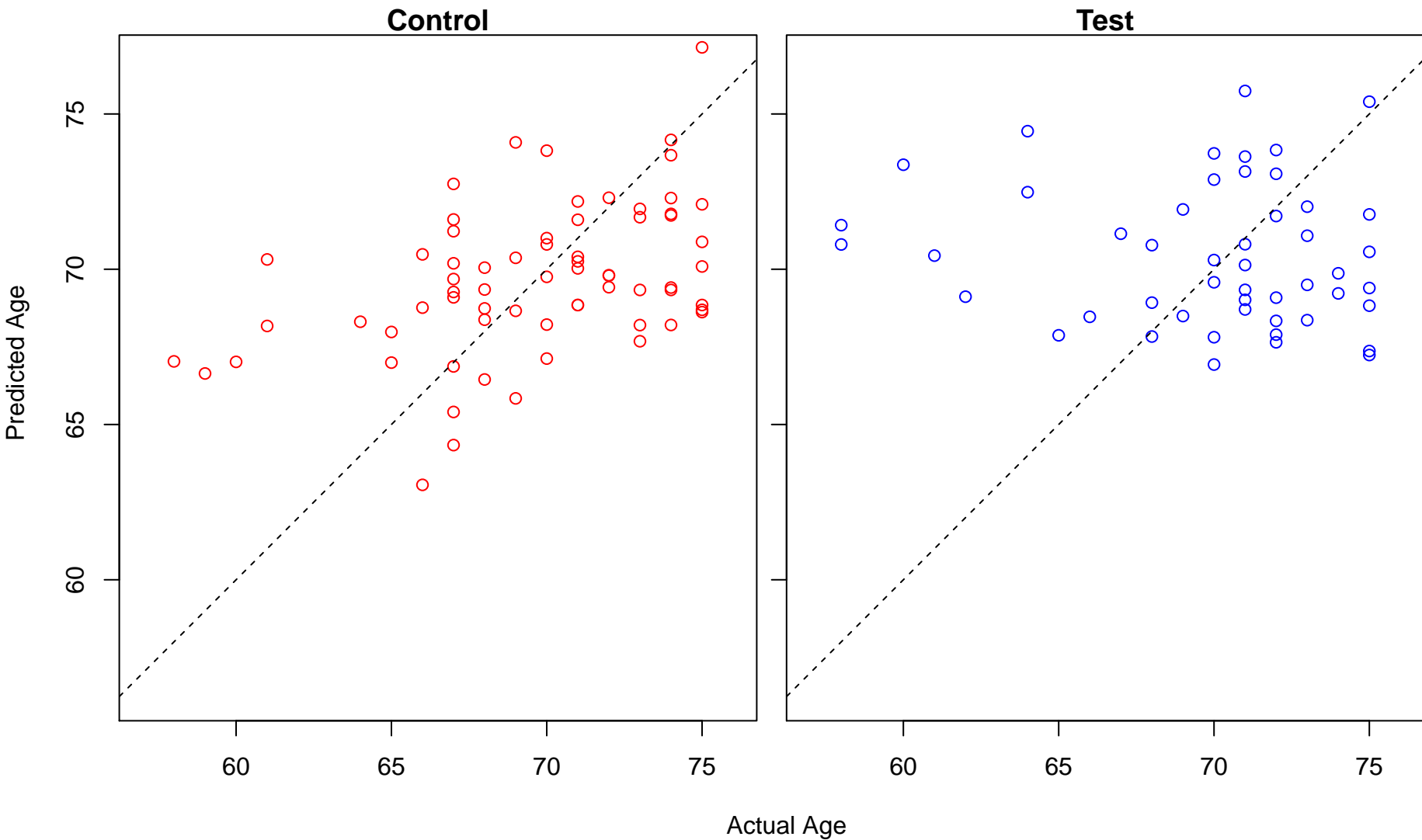
positive regulation of activated T cell proliferation (Score: 0.647398)



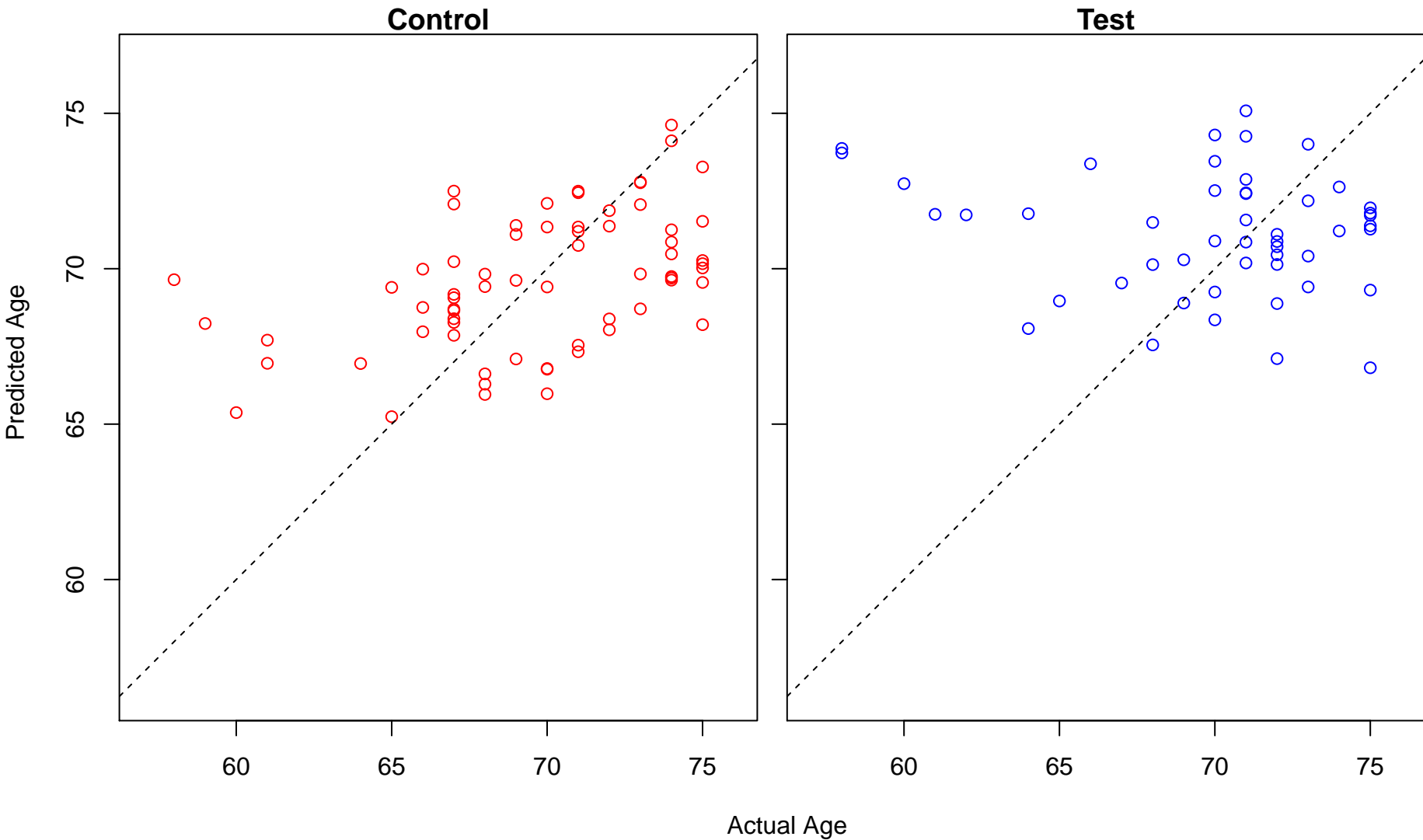
interferon-gamma production (Score: 0.647078)



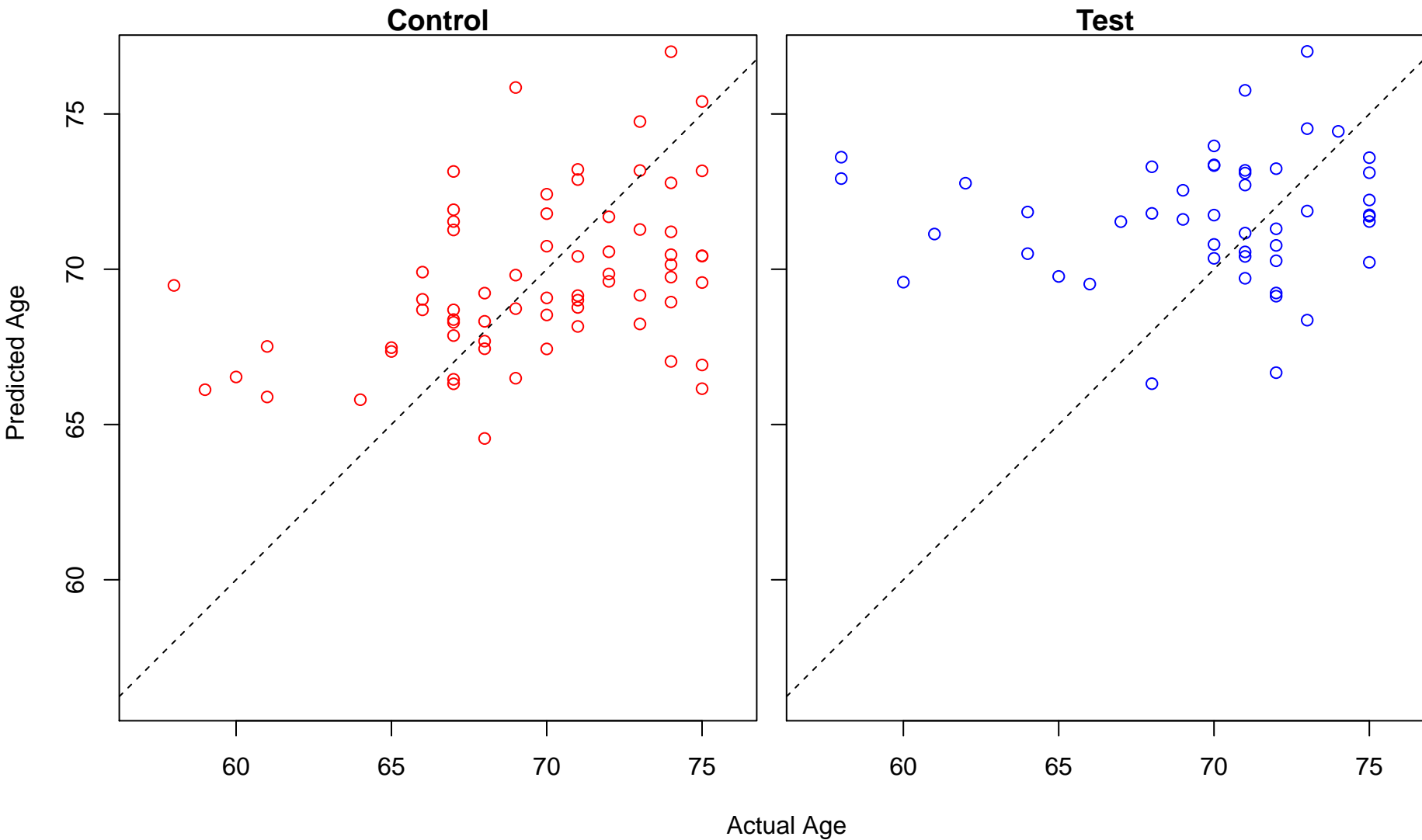
negative regulation of epidermal cell differentiation (Score: 0.646277)



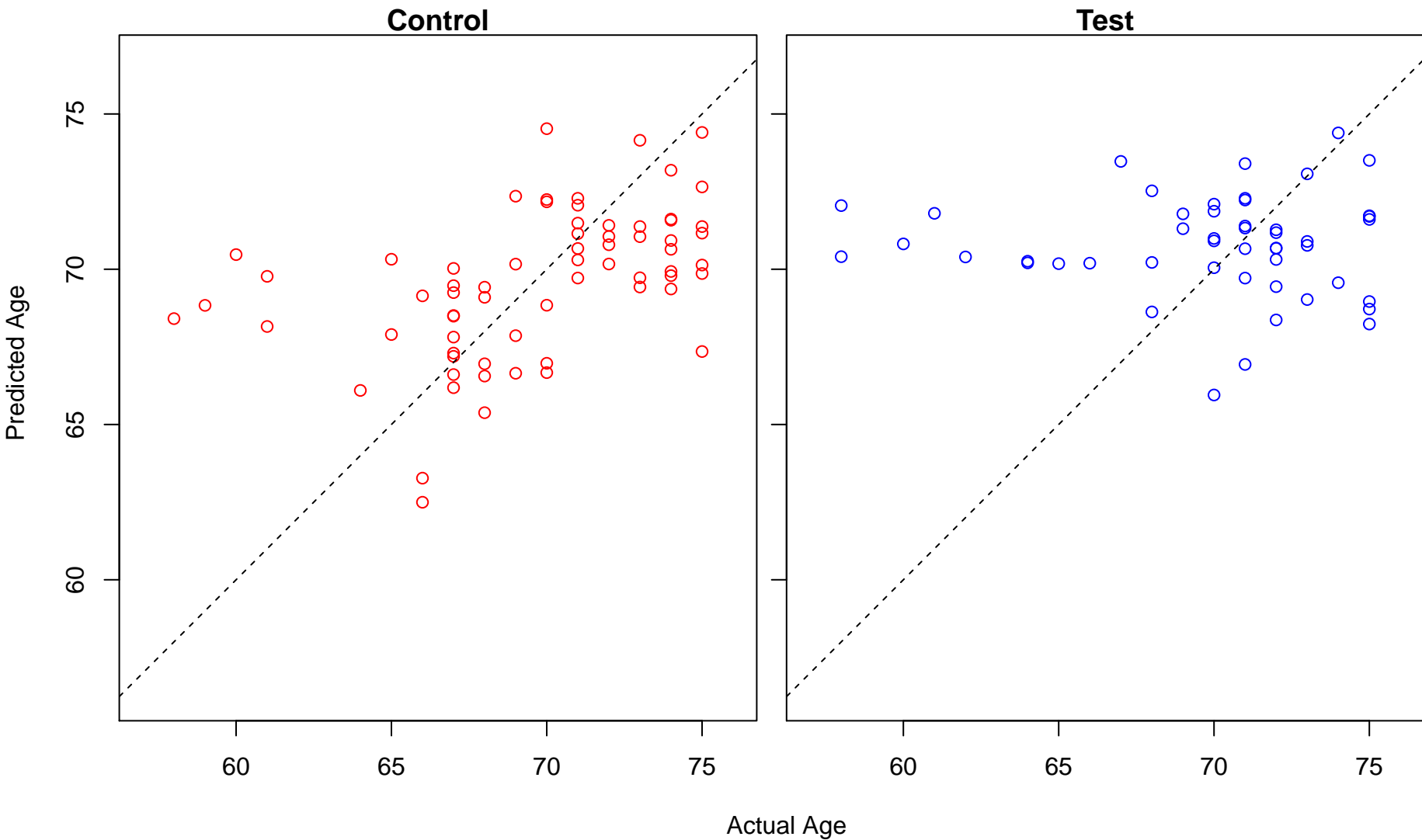
positive regulation of transcription from RNA polymerase III promoter (Score: 0.644815)



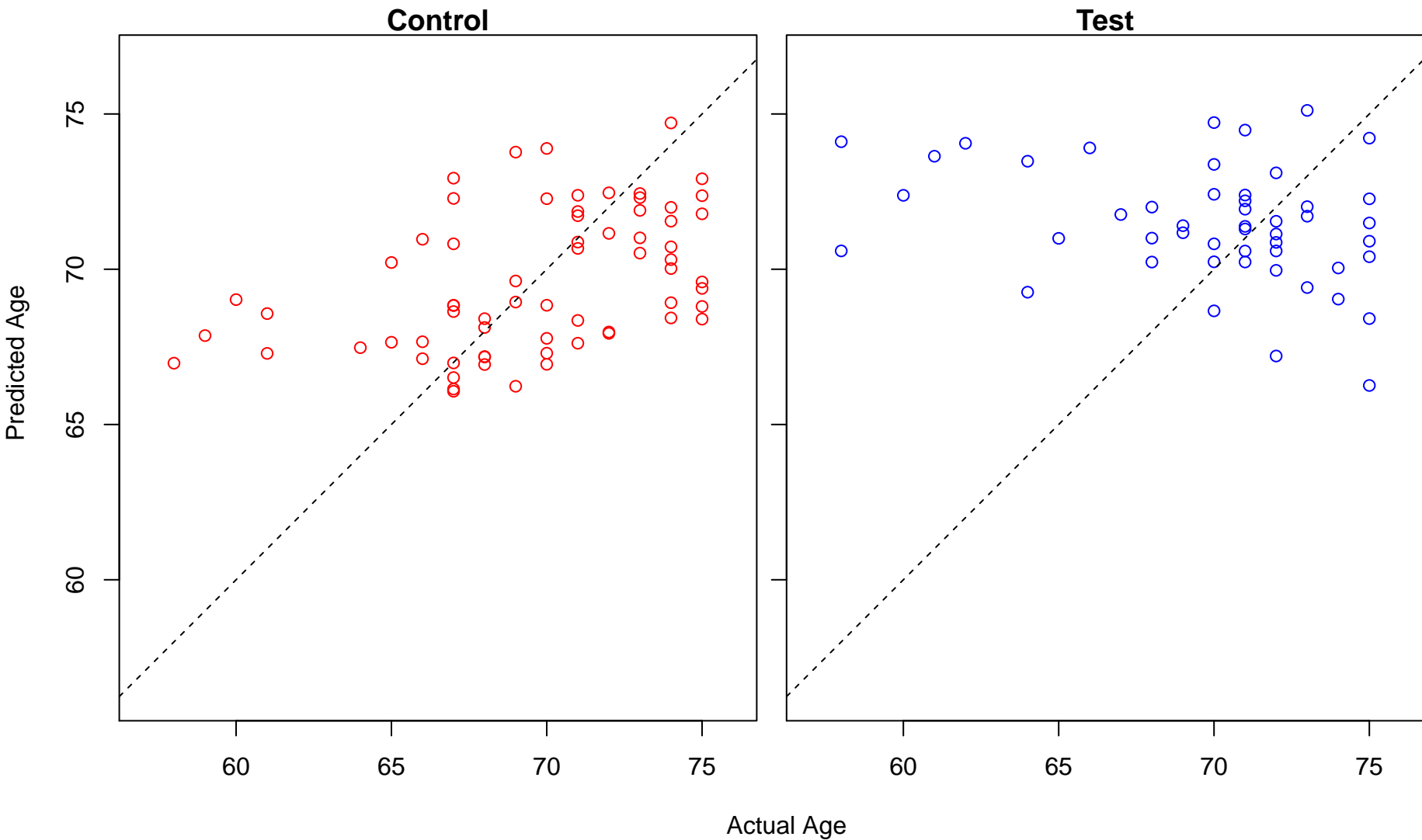
positive regulation of microtubule polymerization or depolymerization (Score: 0.644572)



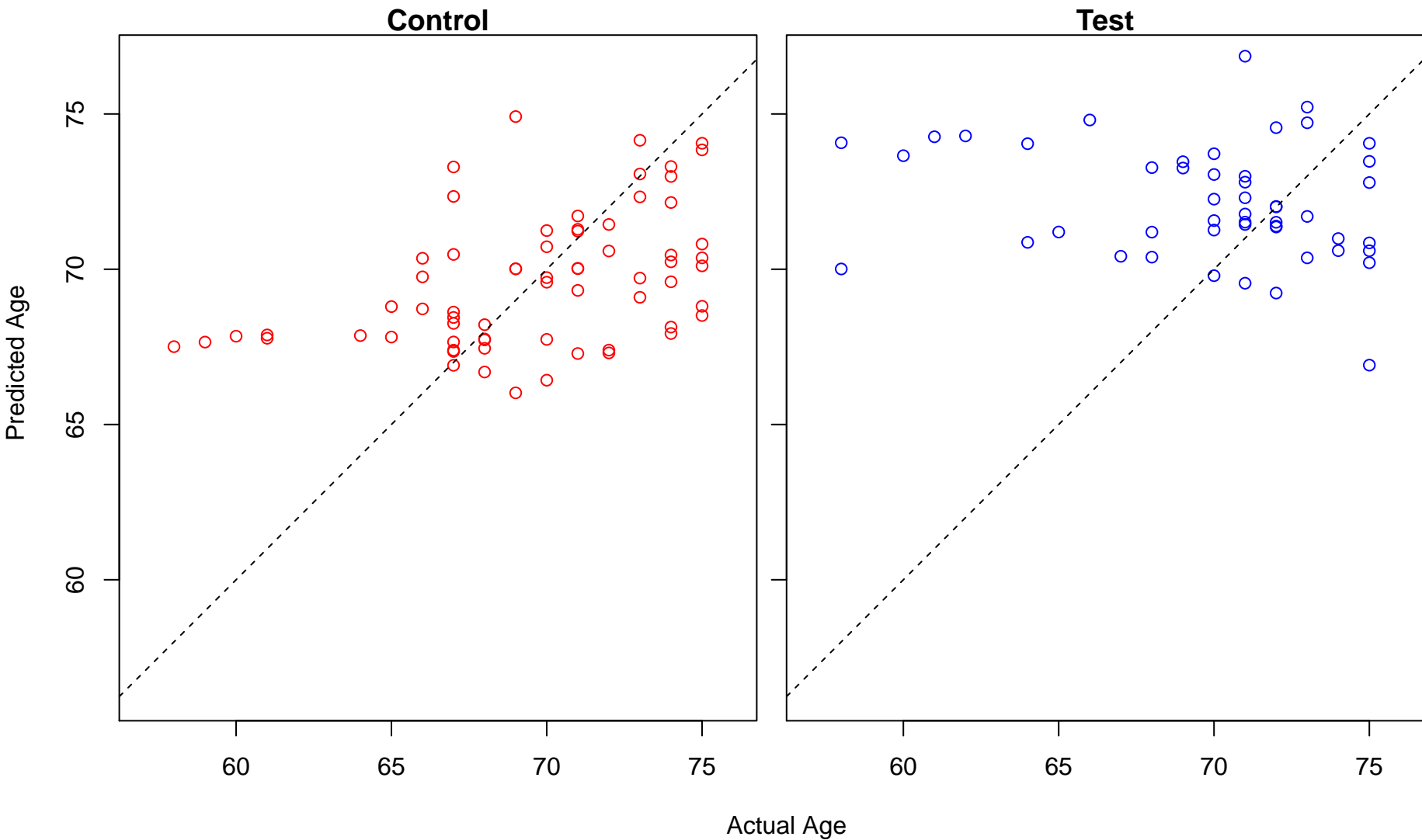
flavonoid metabolic process (Score: 0.644414)



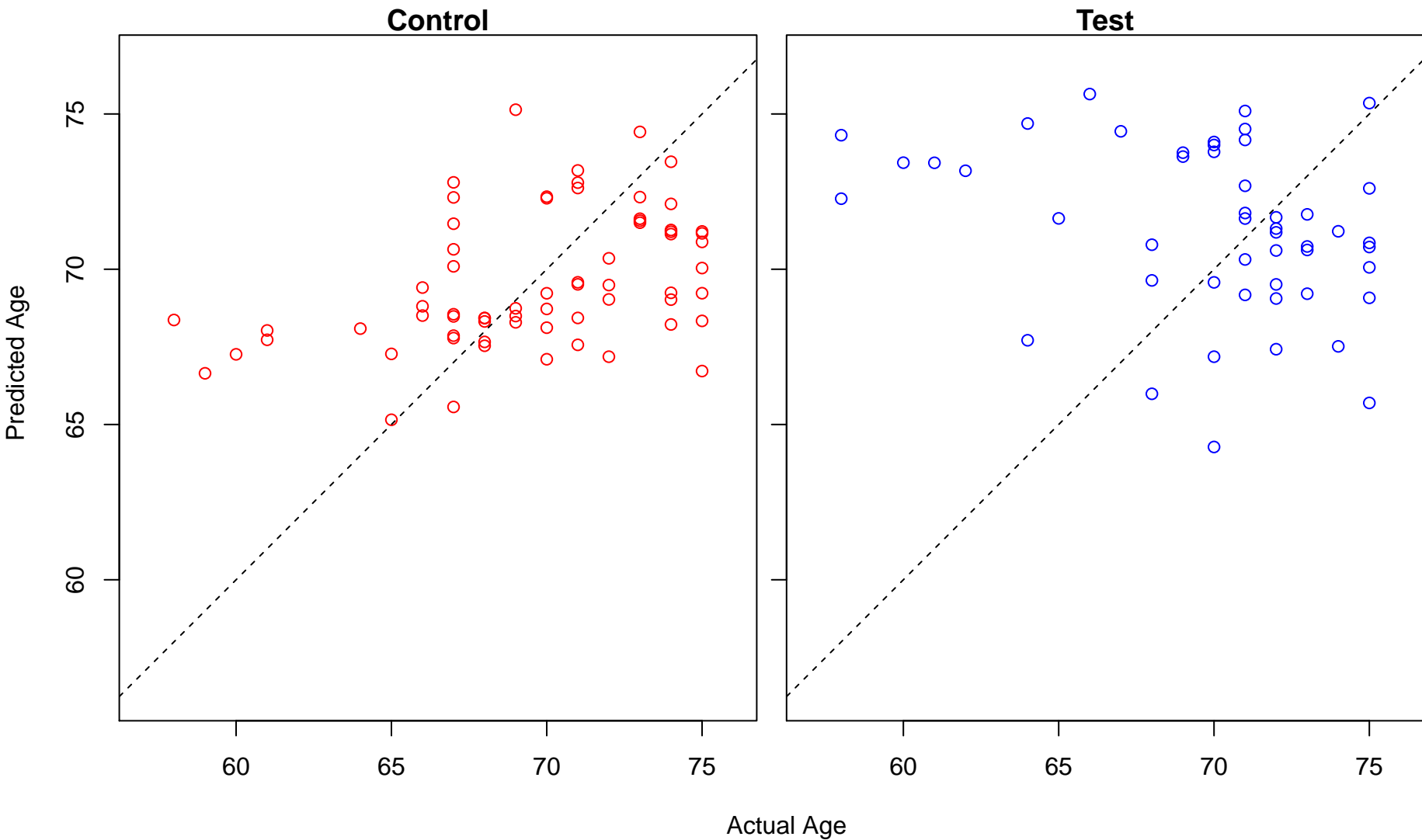
DNA replication checkpoint (Score: 0.644353)



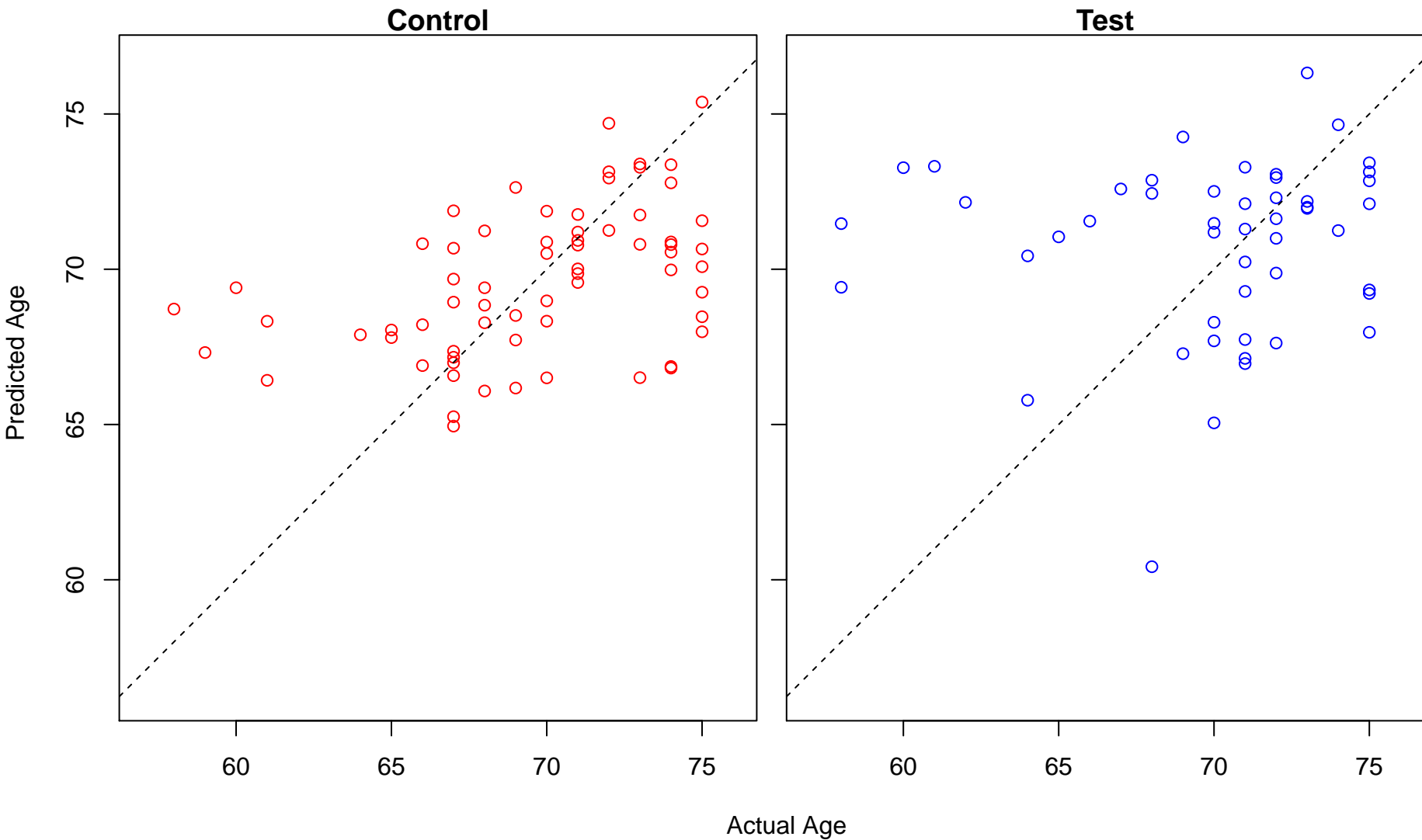
inner ear development (Score: 0.644109)



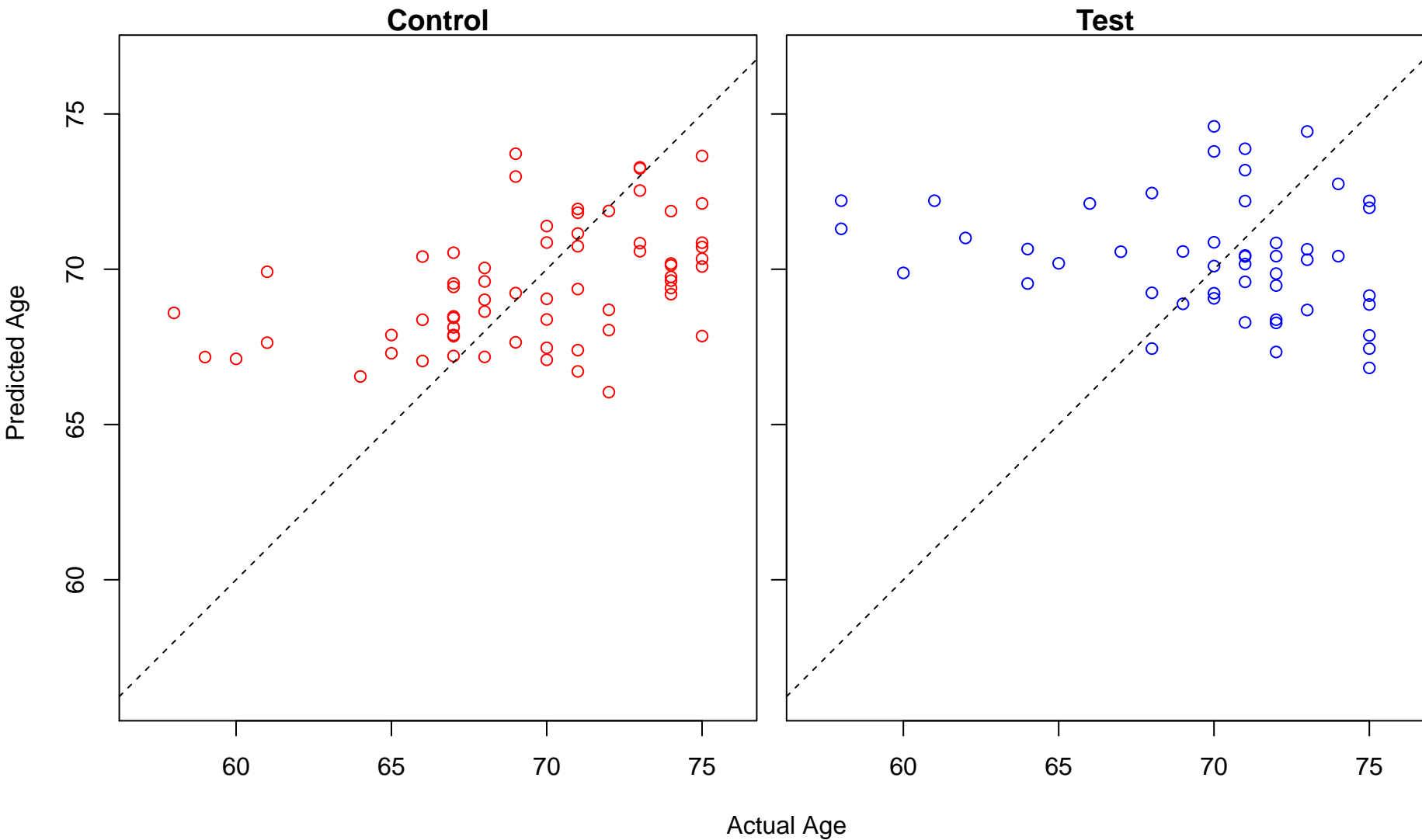
establishment of protein localization to chromosome (Score: 0.643450)



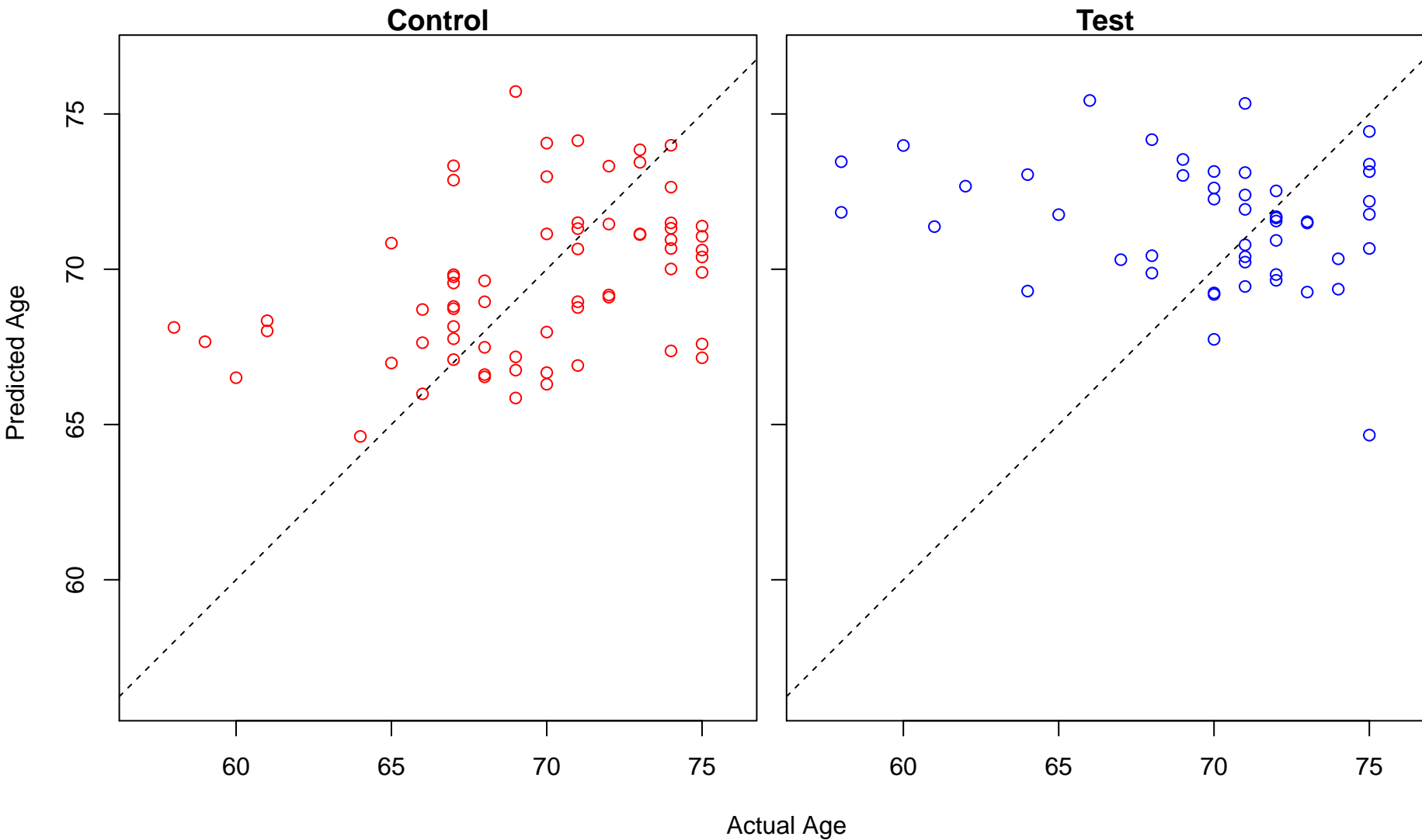
cerebellar cortex development (Score: 0.641924)



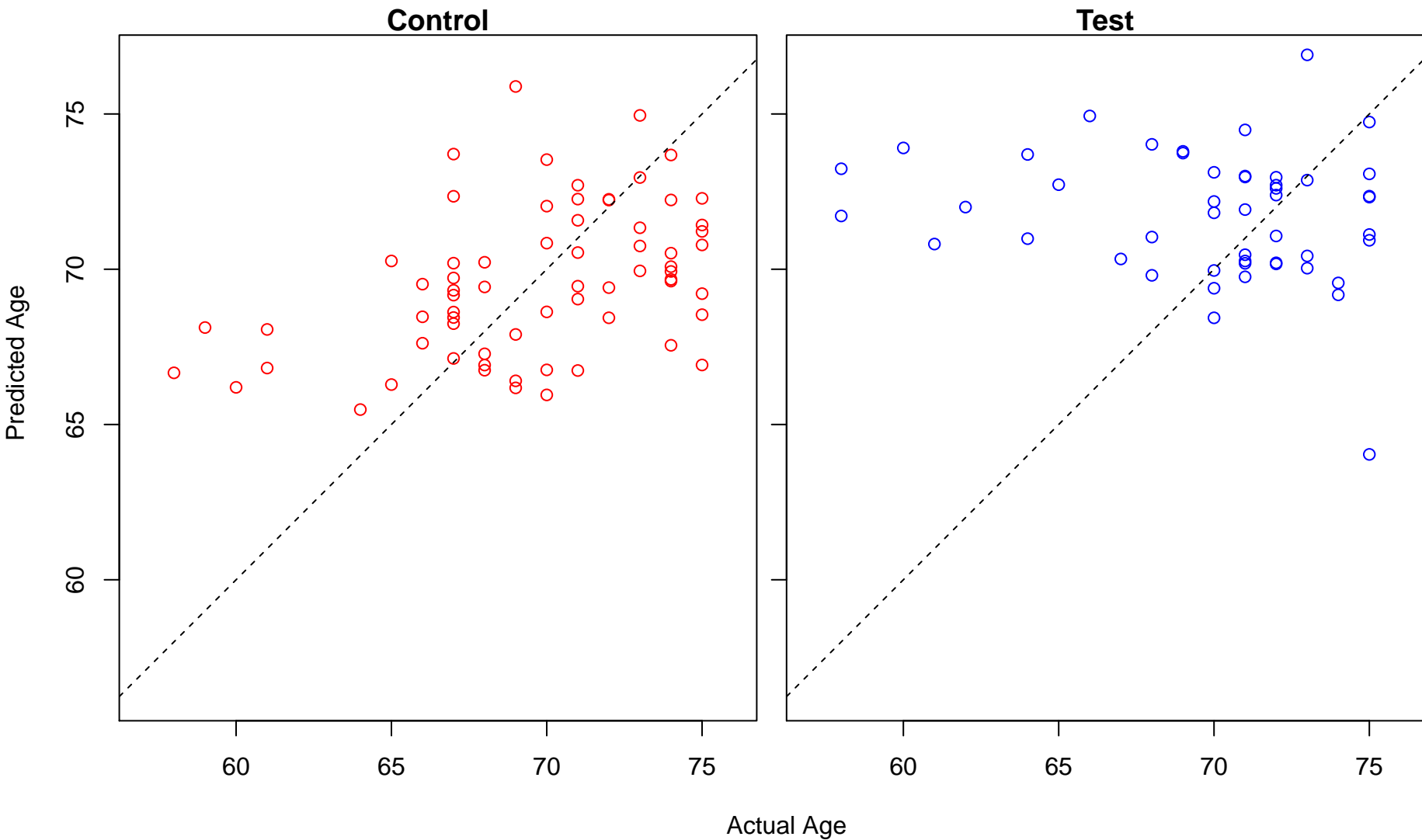
regulation of double-strand break repair via homologous recombination (Score: 0.641919)



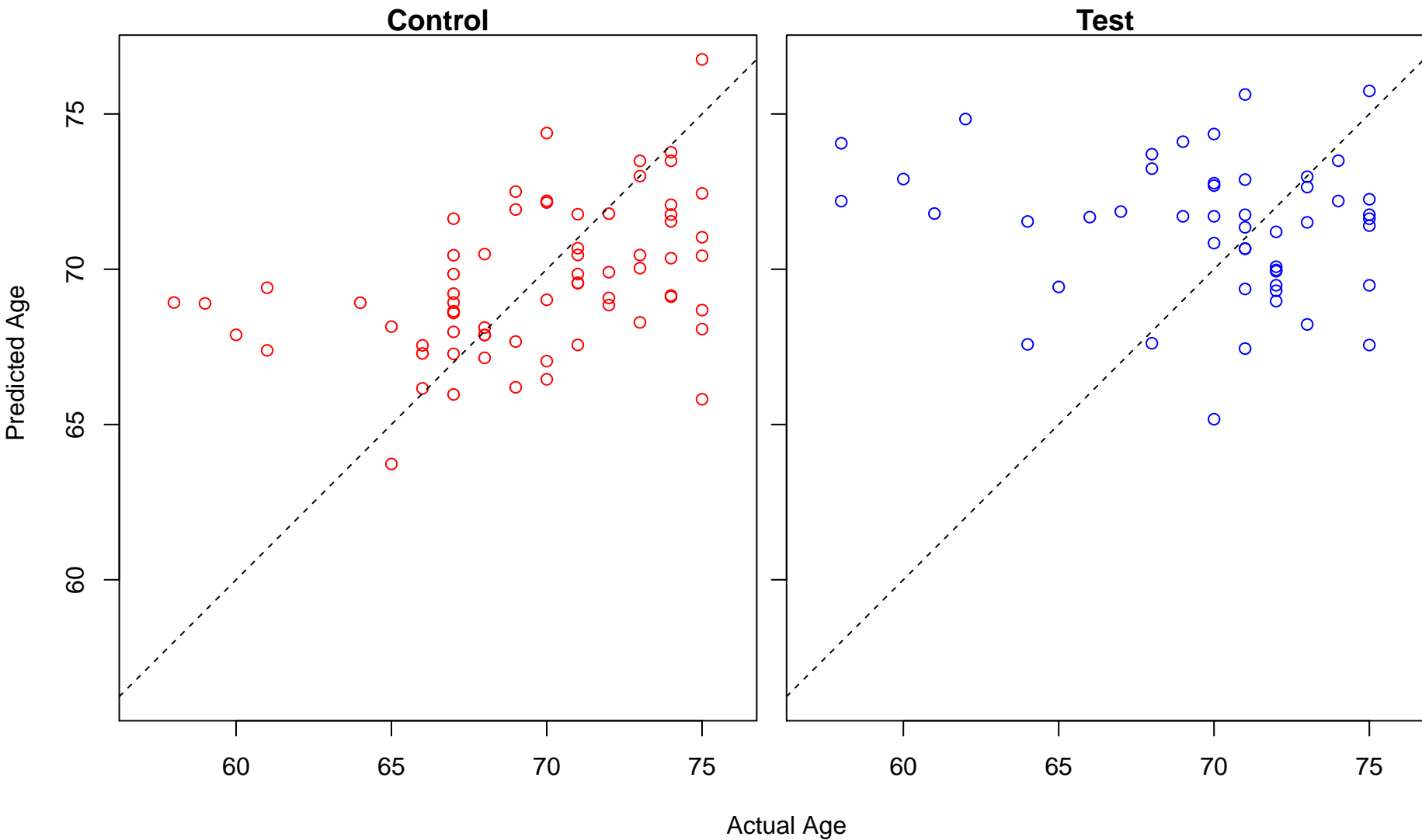
regulation of DNA-templated transcription, initiation (Score: 0.641580)



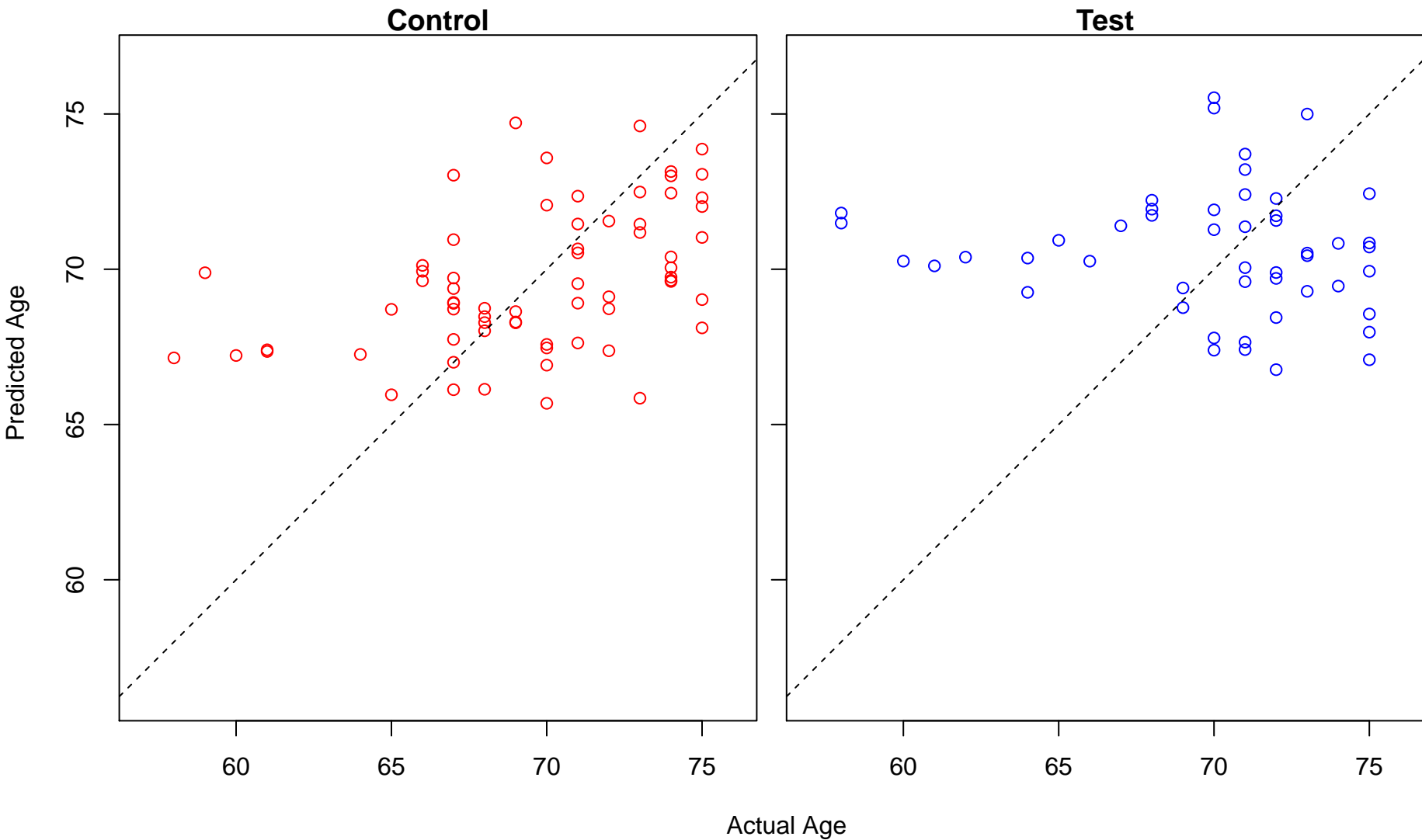
positive regulation of DNA-templated transcription, initiation (Score: 0.641250)



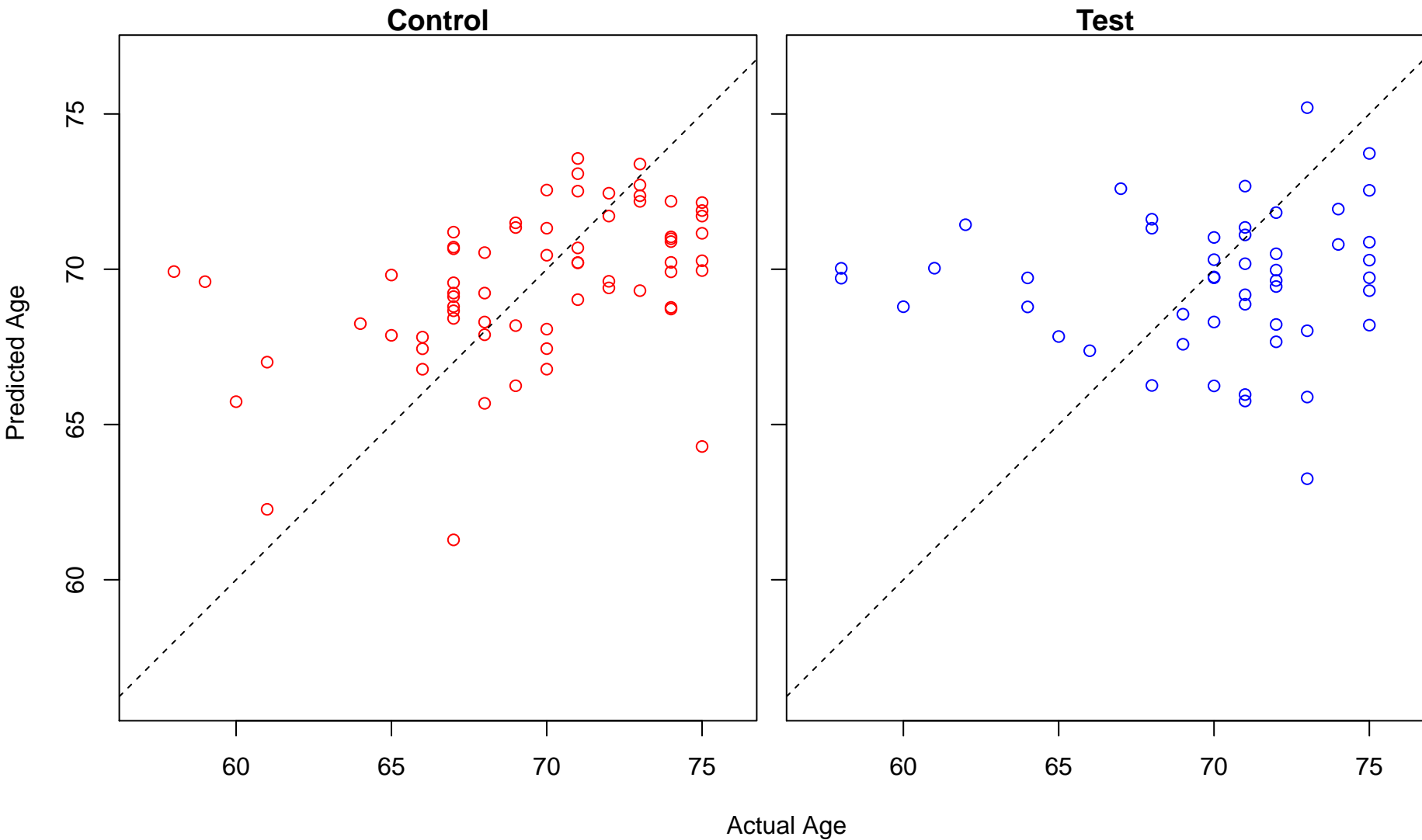
glutamate secretion (Score: 0.640950)



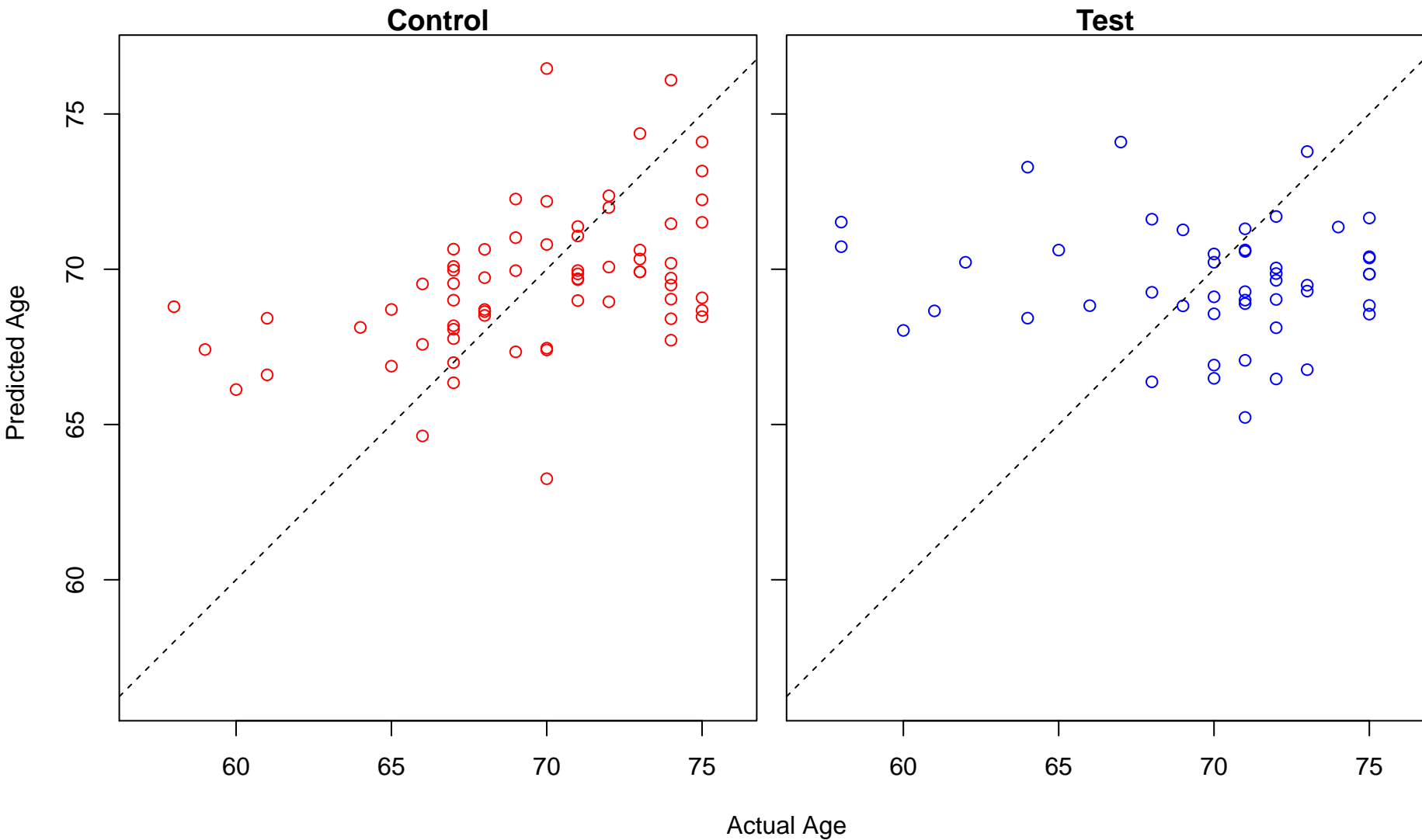
detection of stimulus involved in sensory perception (Score: 0.640243)



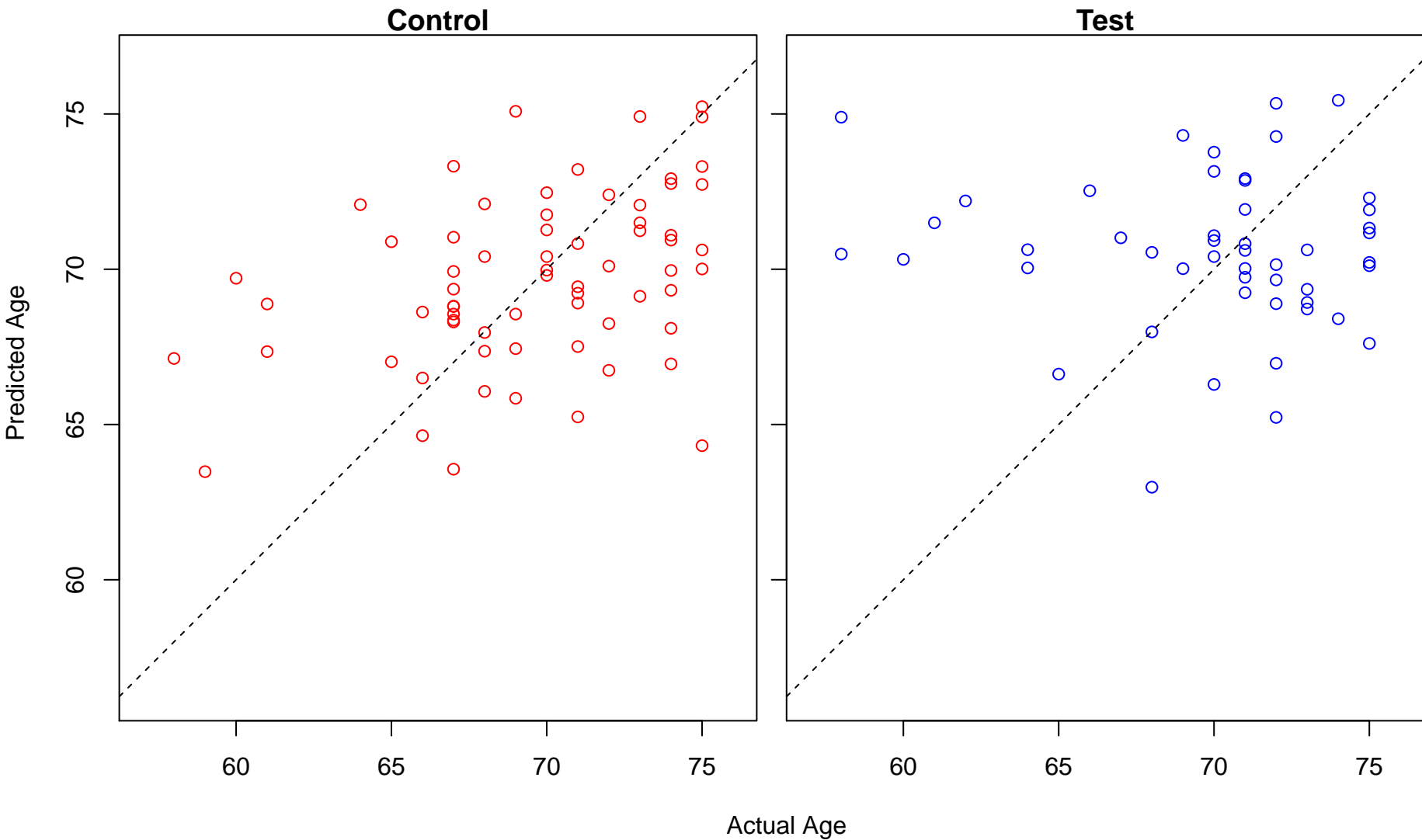
regulation of attachment of spindle microtubules to kinetochore (Score: 0.639907)



aromatic amino acid transport (Score: 0.639484)

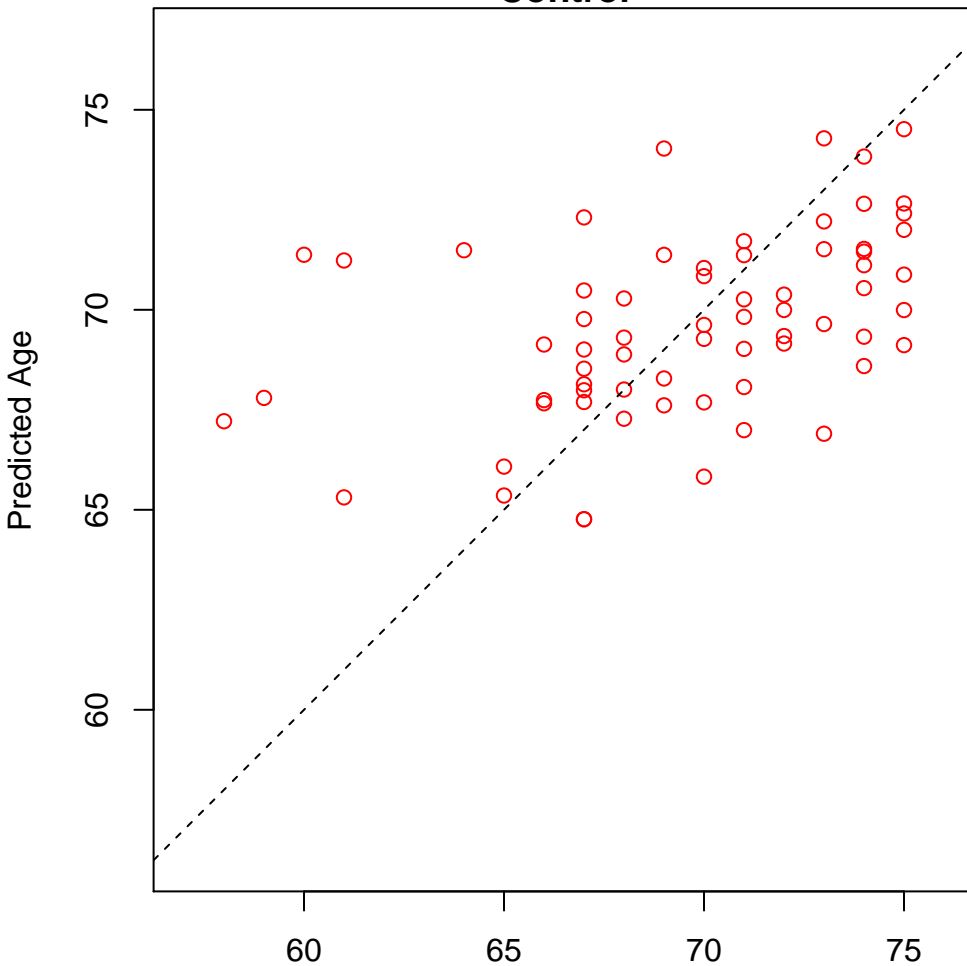


zinc II ion transport (Score: 0.639400)

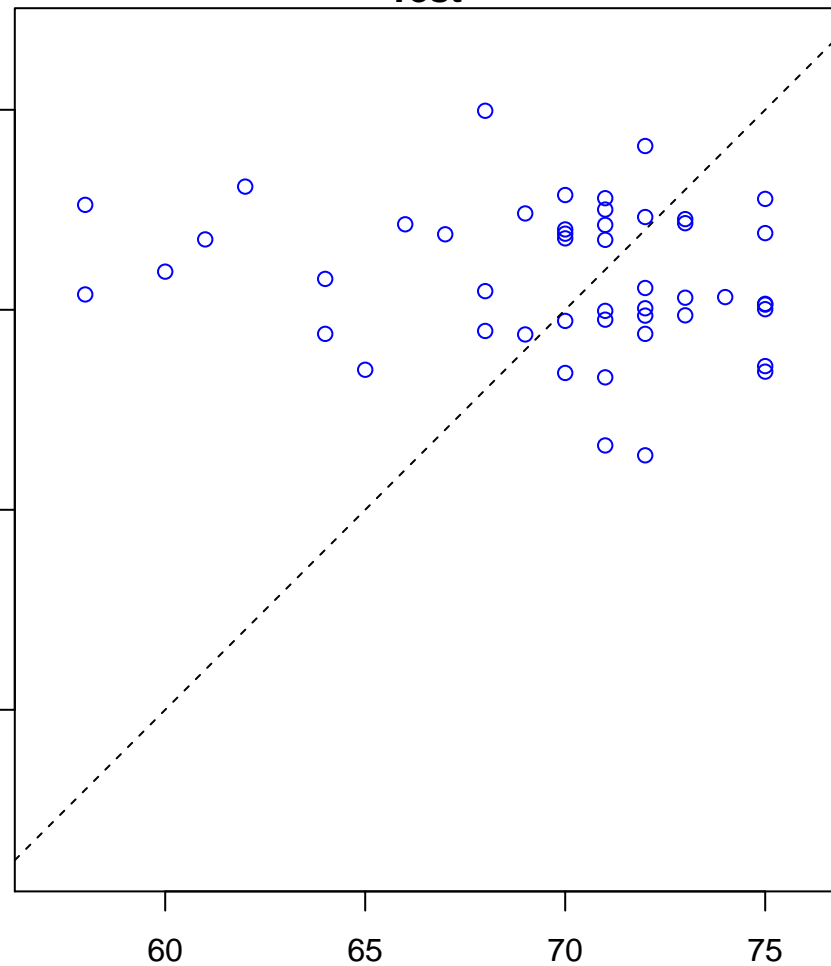


dicarboxylic acid biosynthetic process (Score: 0.639003)

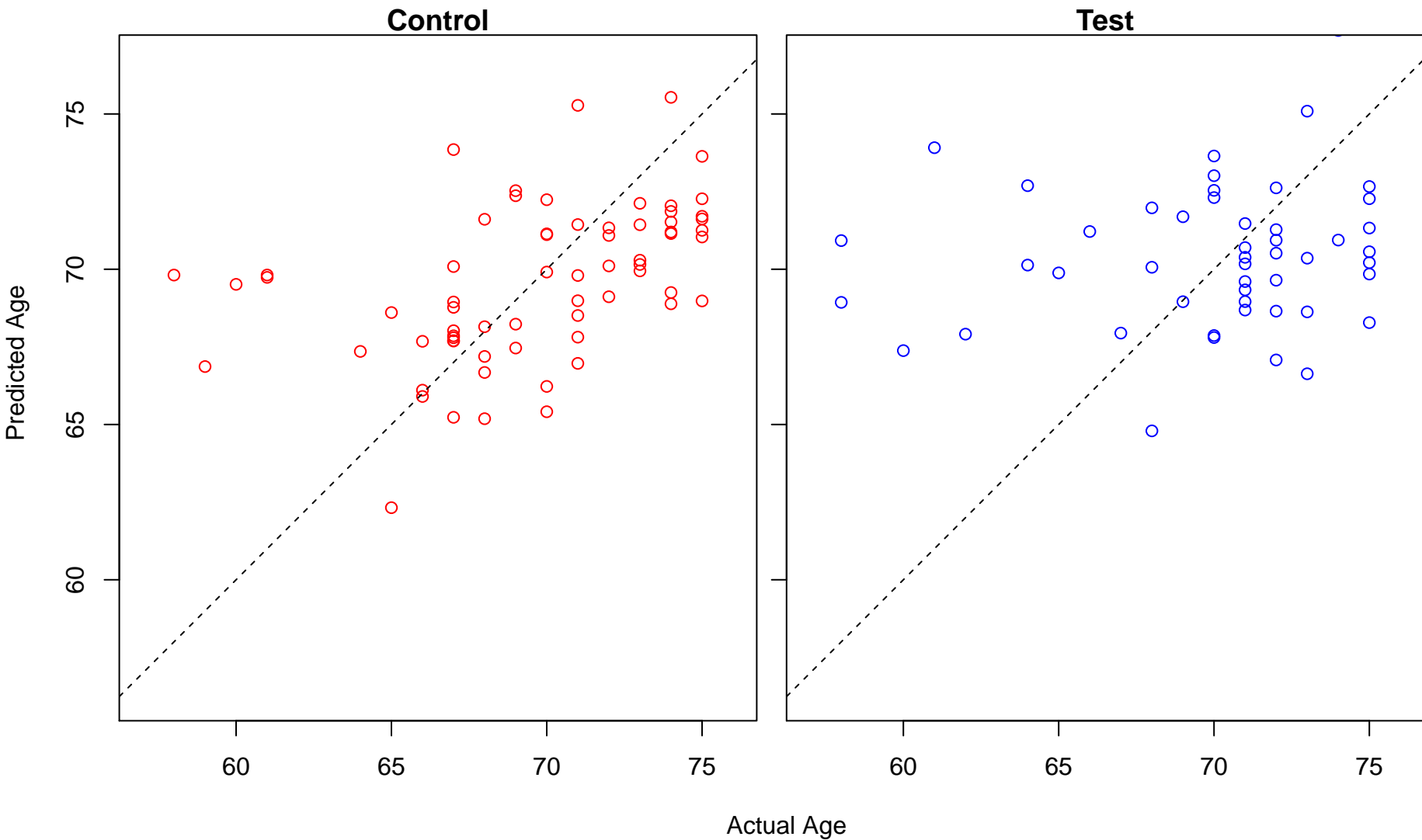
Control



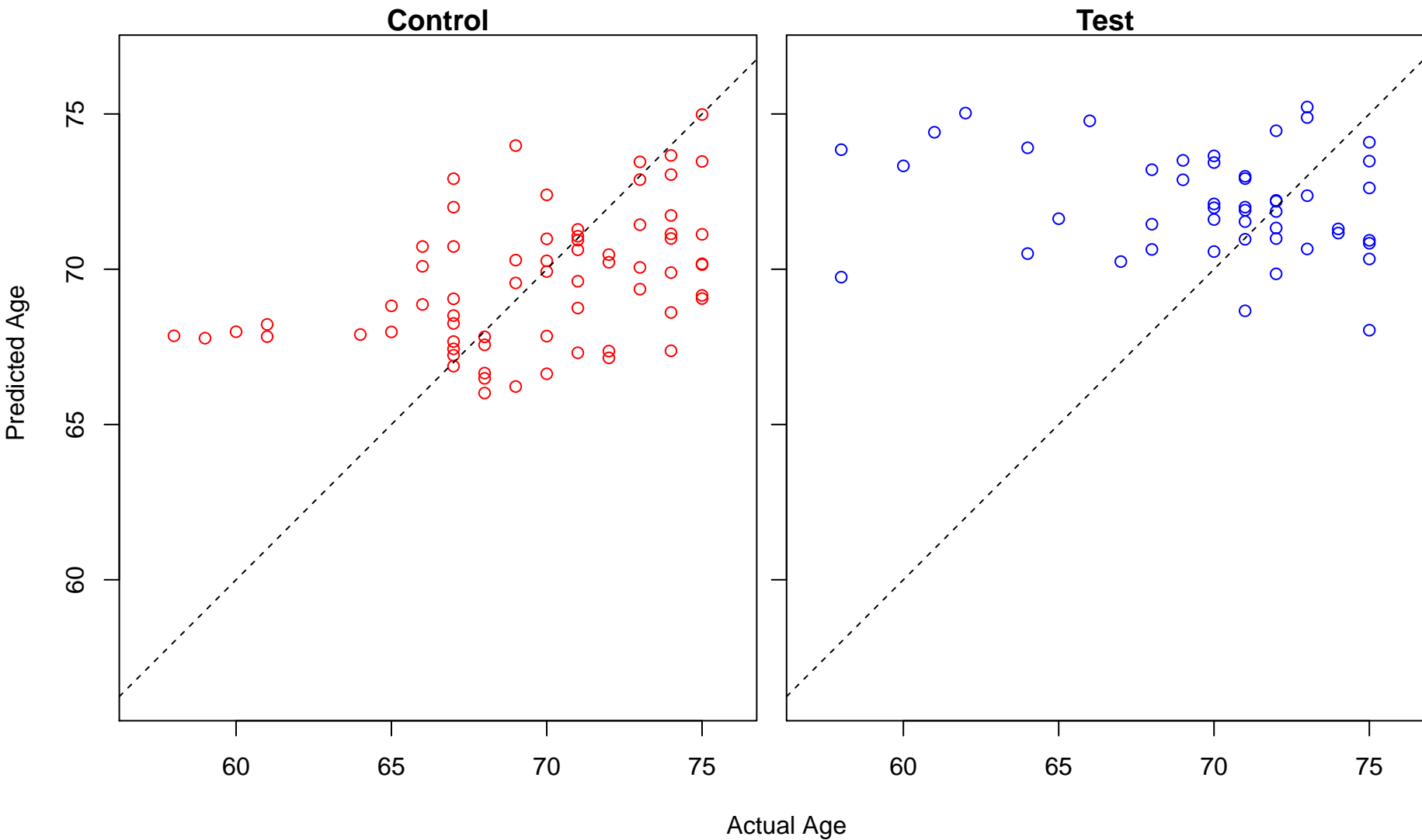
Test



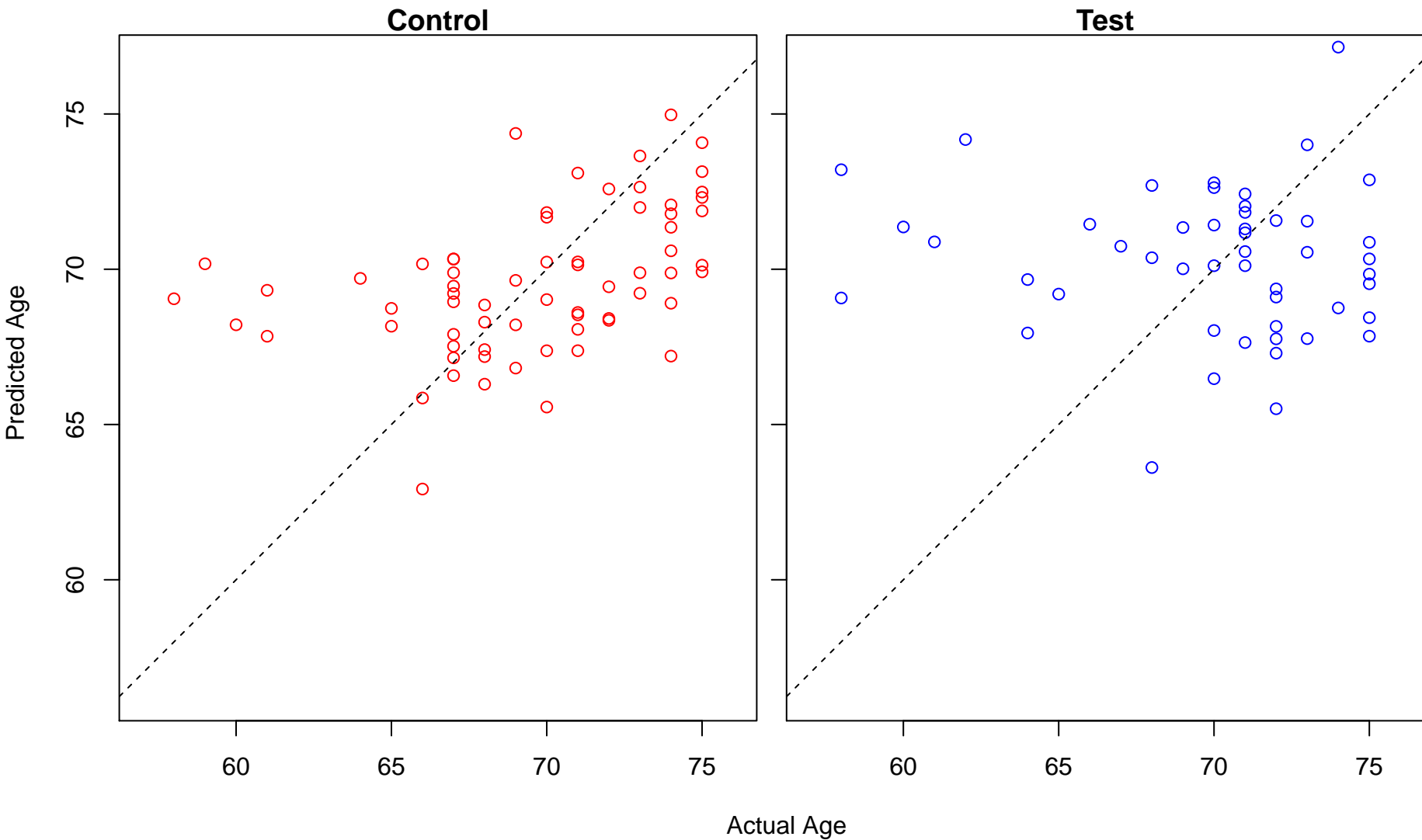
negative regulation of T cell receptor signaling pathway (Score: 0.638102)



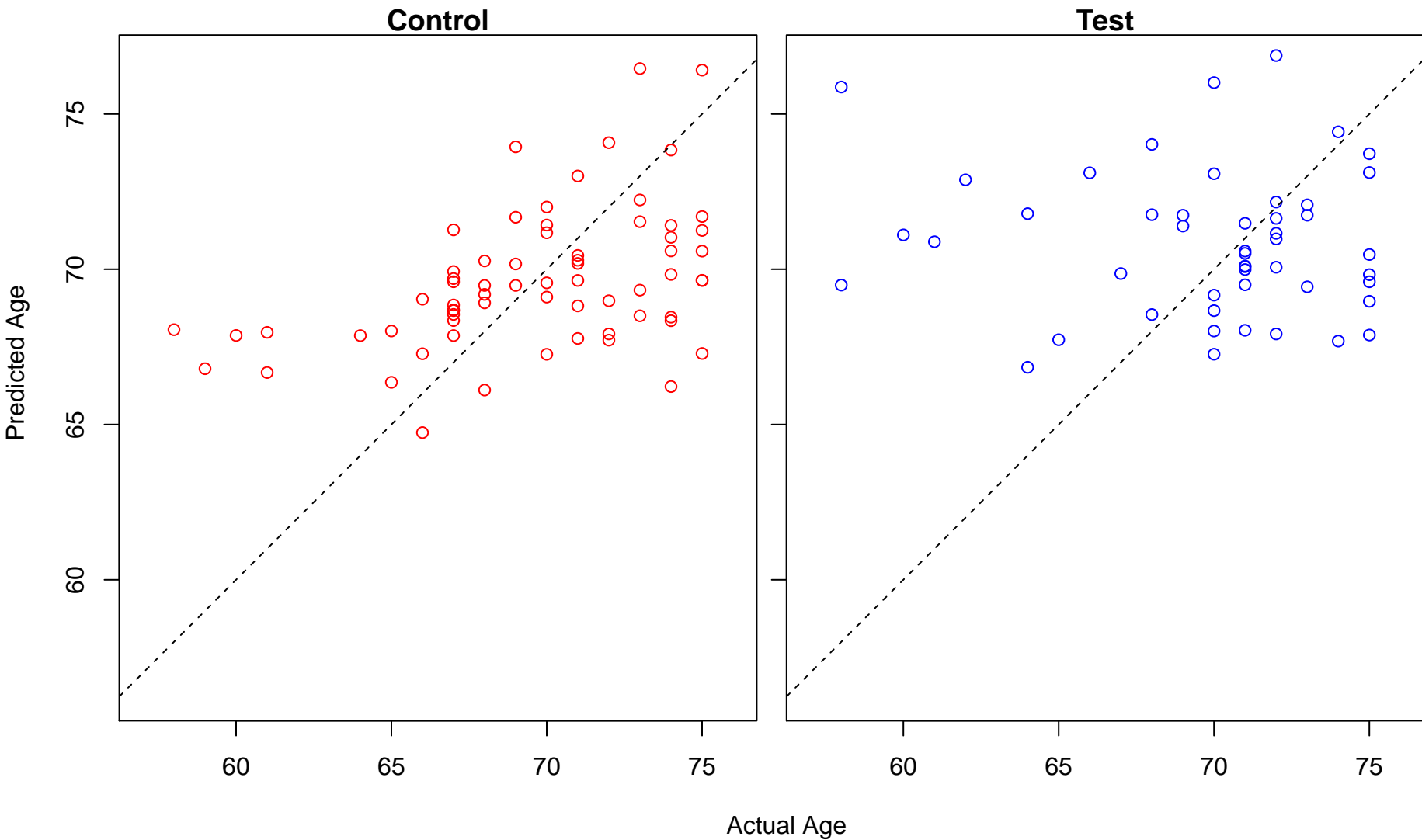
ear morphogenesis (Score: 0.637496)



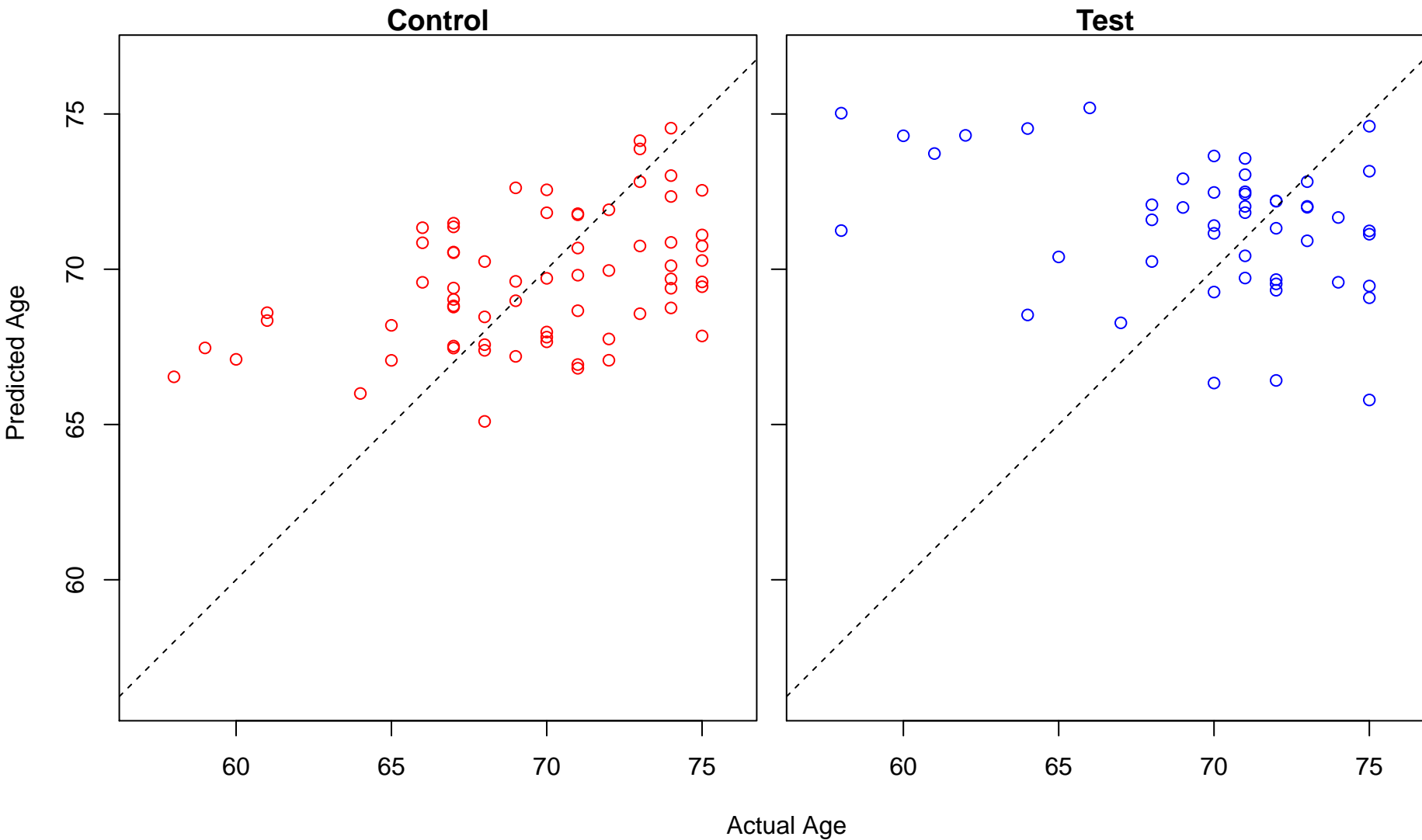
regulation of store-operated calcium channel activity (Score: 0.635840)



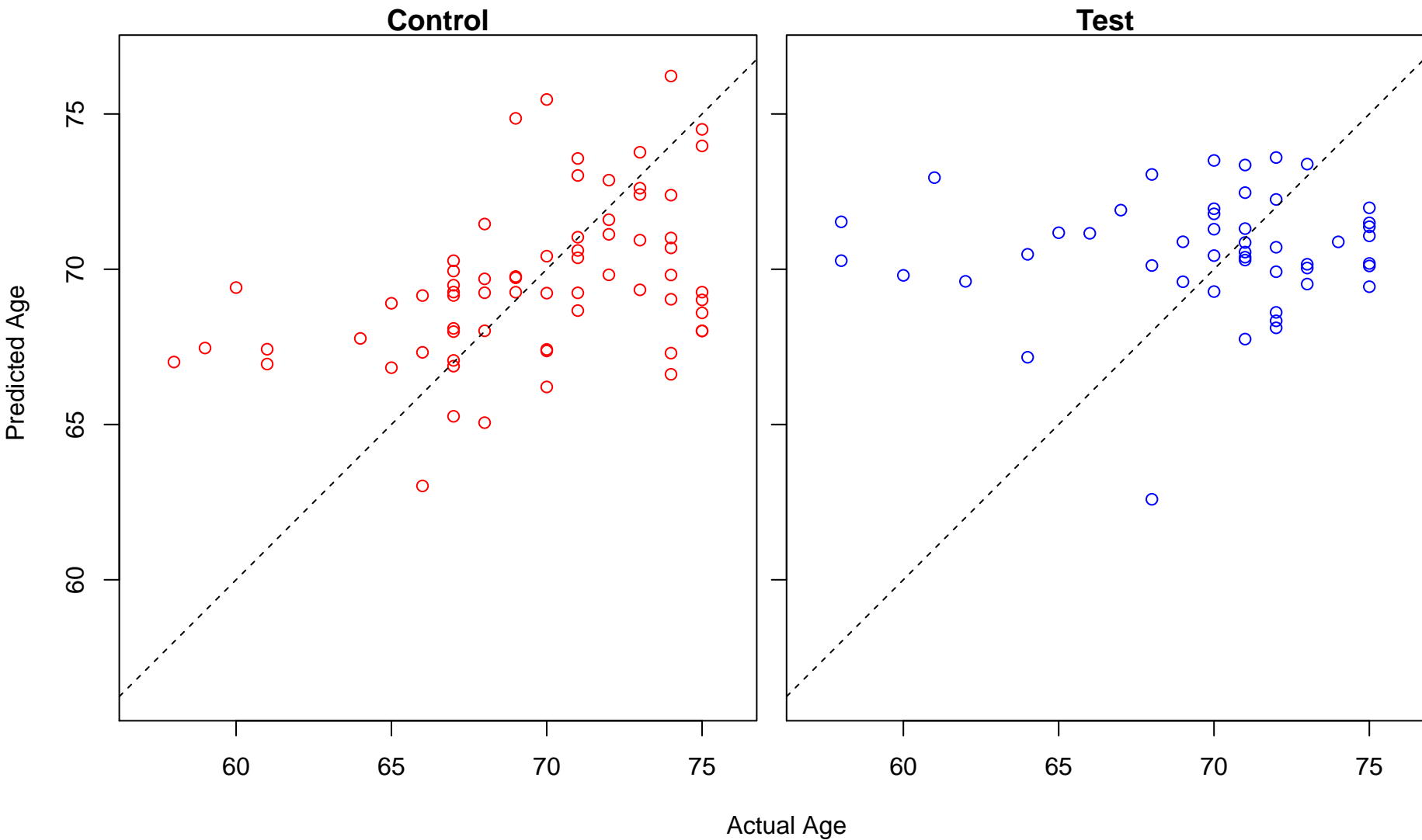
negative regulation of smoothened signaling pathway (Score: 0.635785)



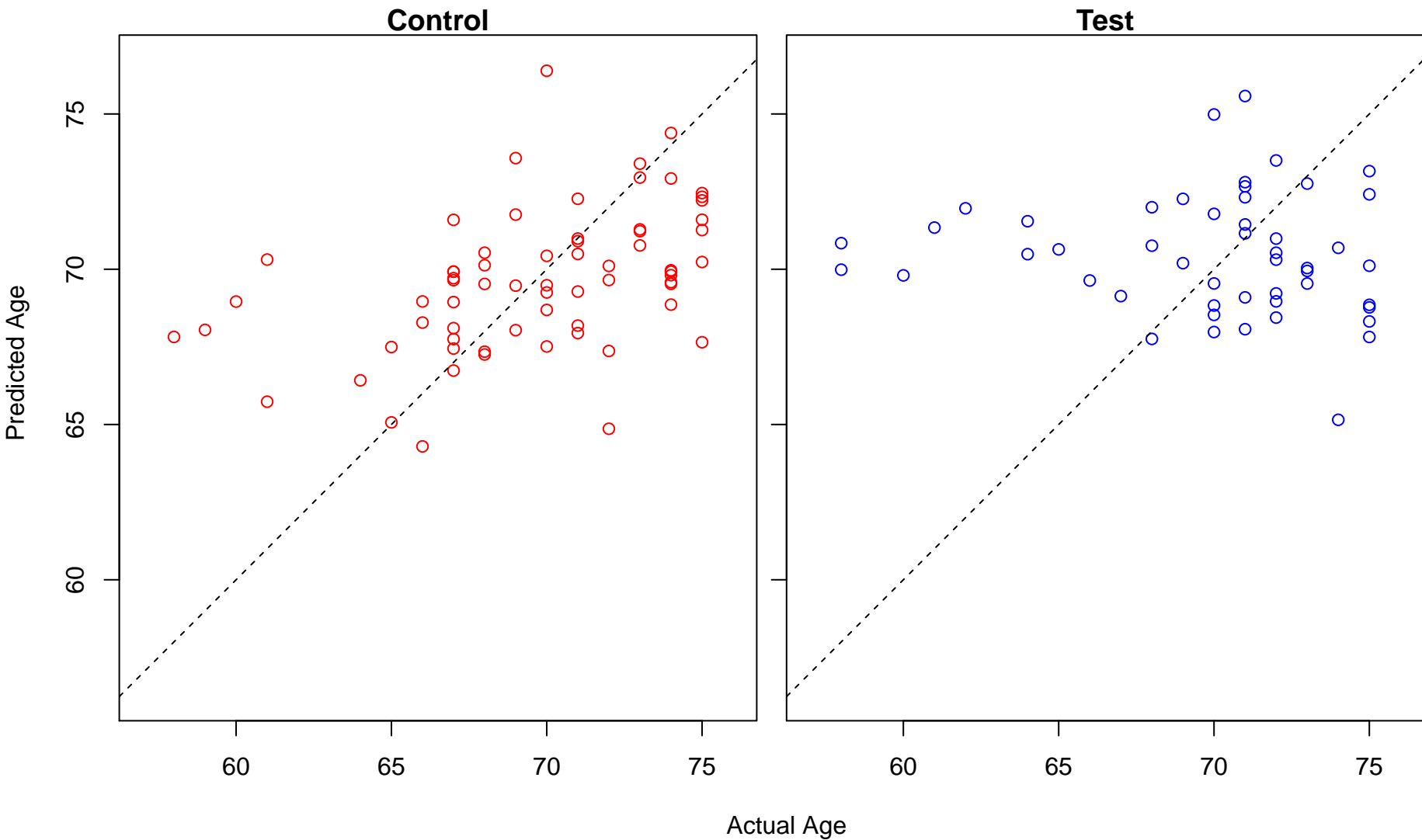
insulin-like growth factor receptor signaling pathway (Score: 0.635285)



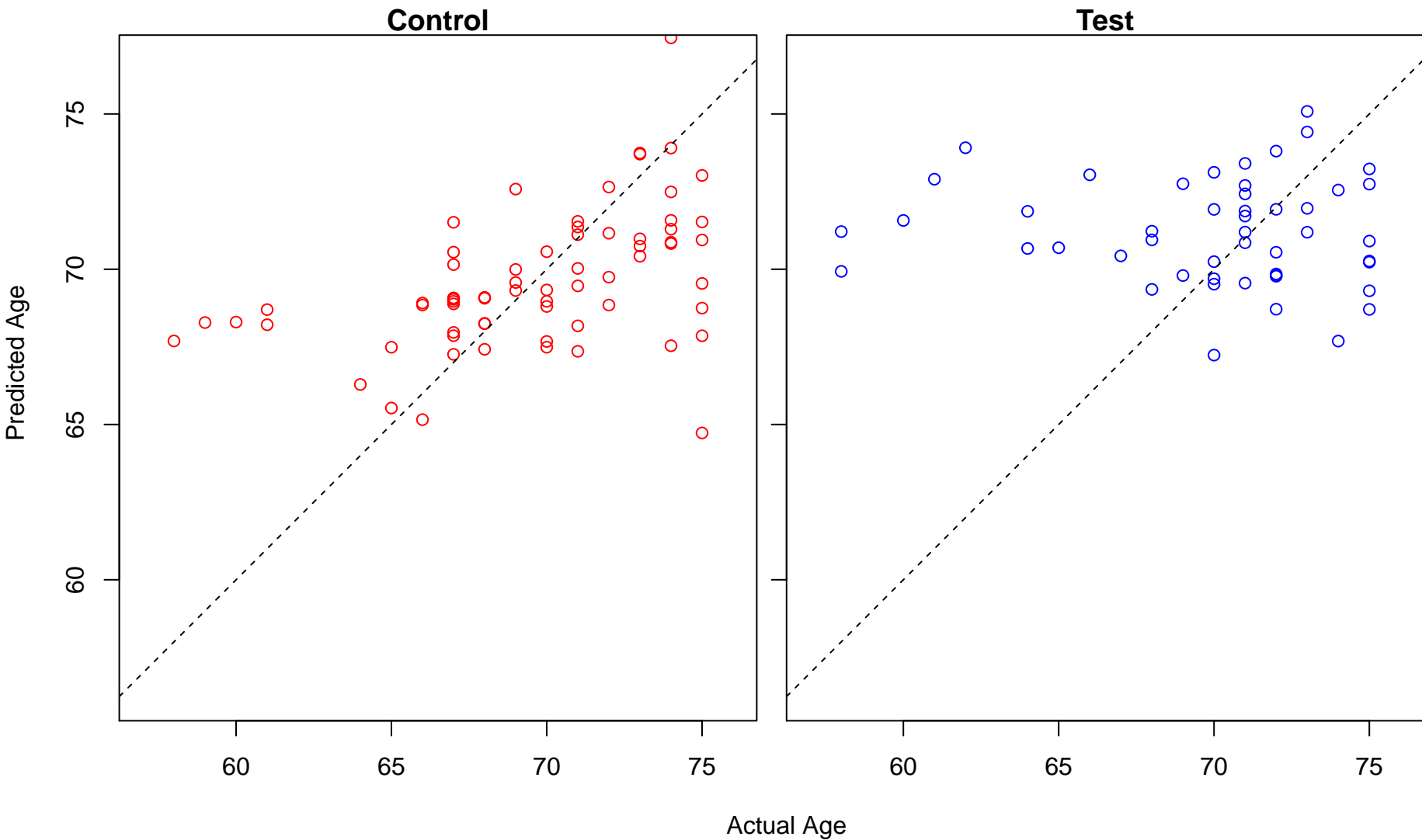
pyrimidine deoxyribonucleotide metabolic process (Score: 0.634864)



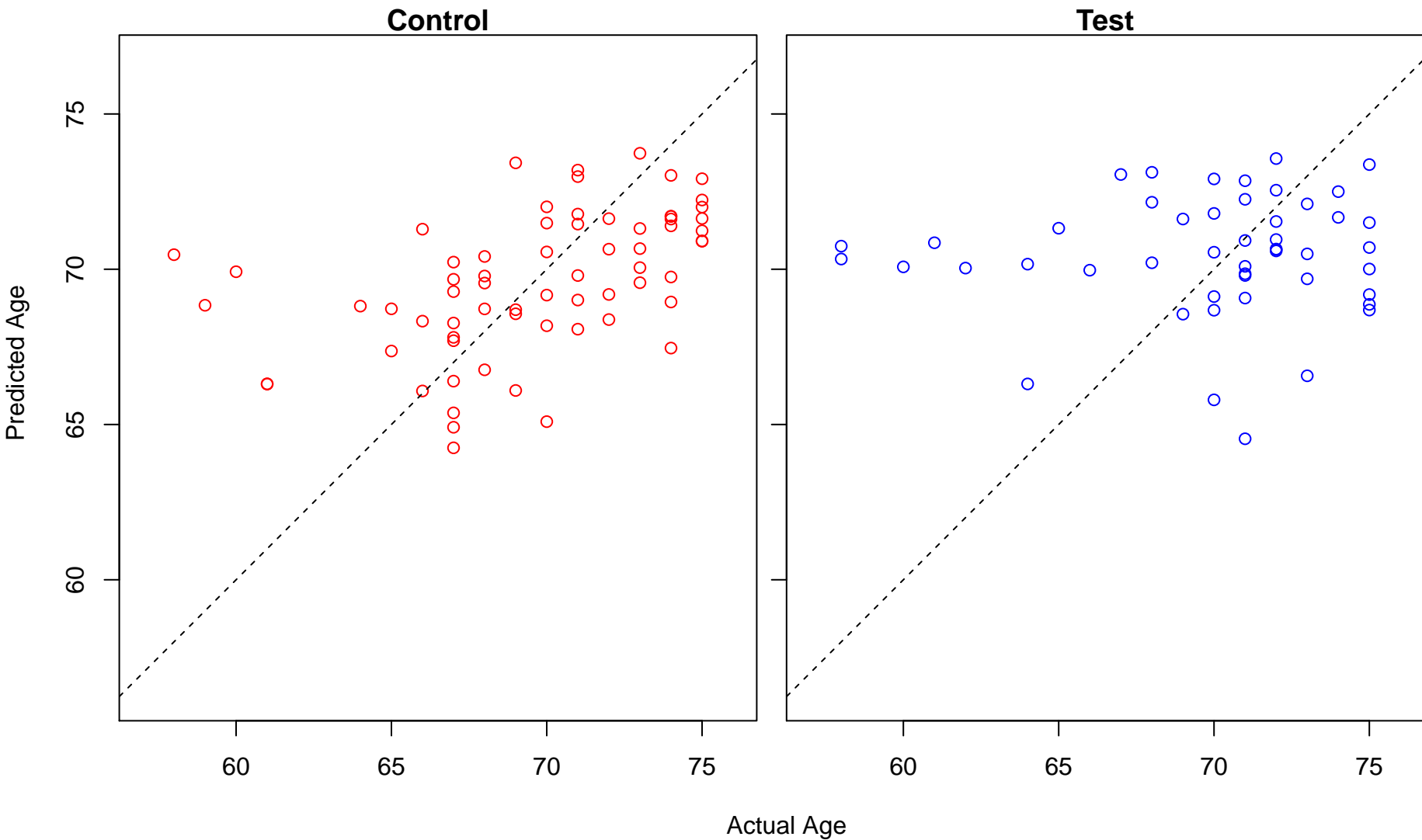
cardiolipin acyl-chain remodeling (Score: 0.634727)



positive regulation of apoptotic cell clearance (Score: 0.634557)

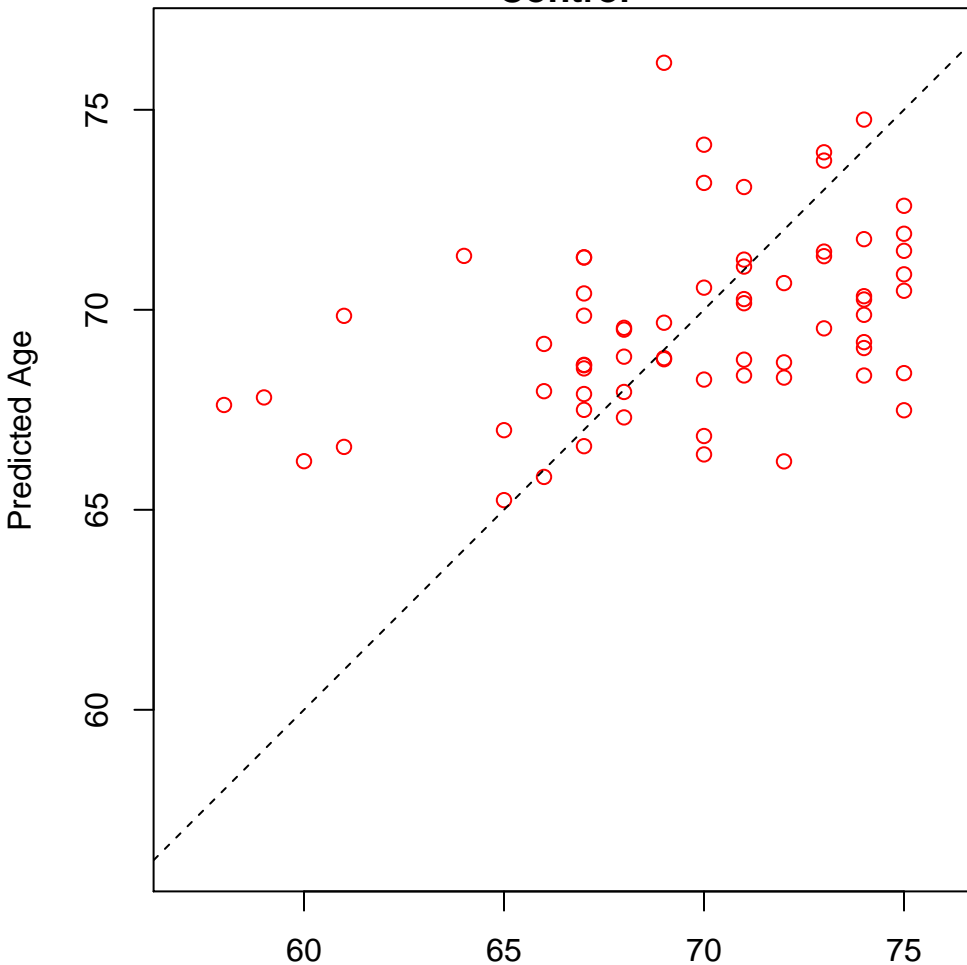


coenzyme catabolic process (Score: 0.634520)

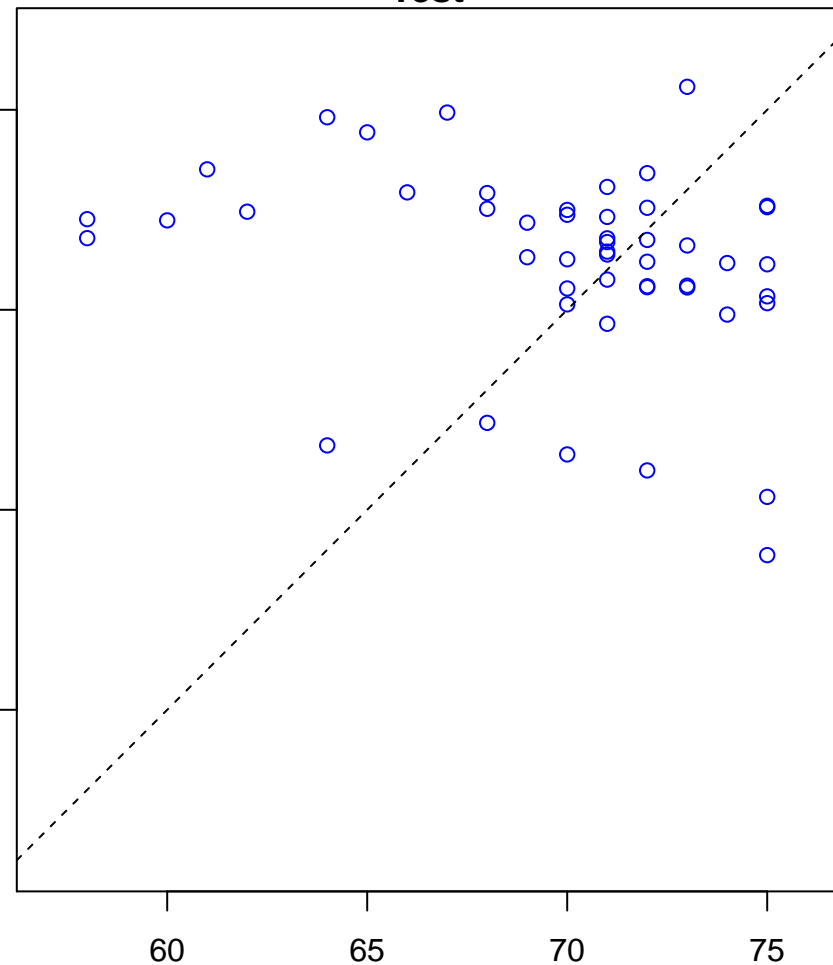


amino-acid betaine biosynthetic process (Score: 0.634233)

Control

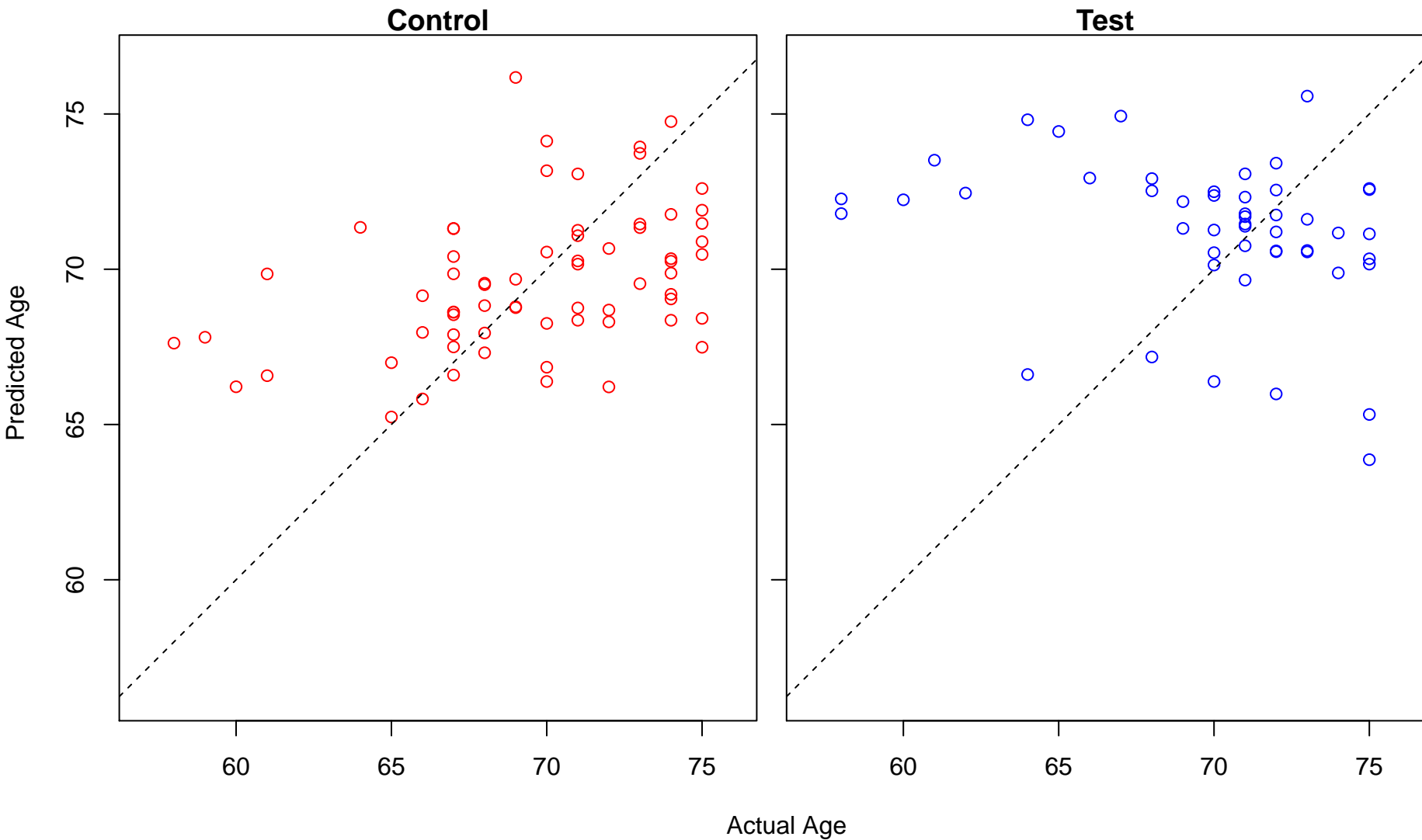


Test

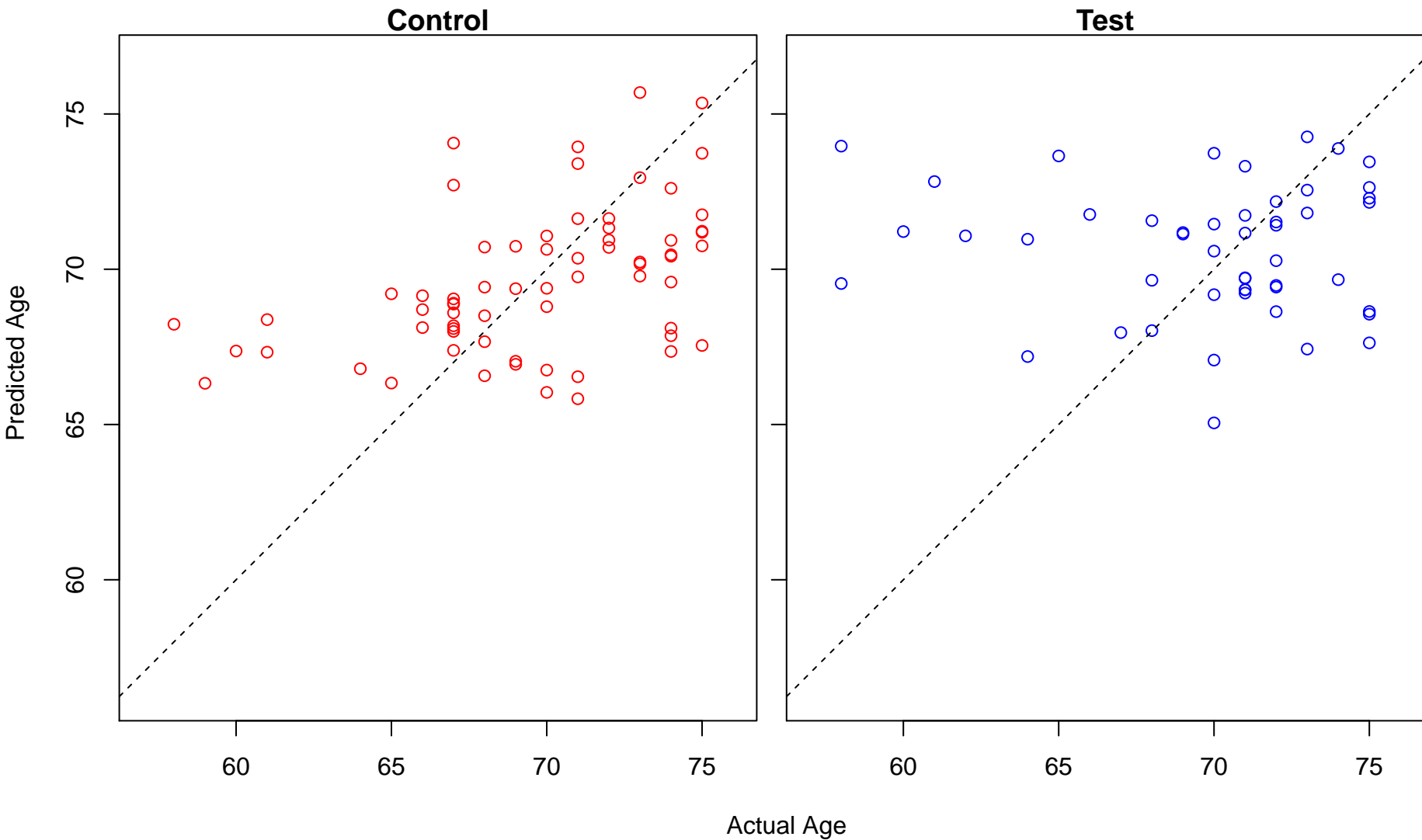


Actual Age

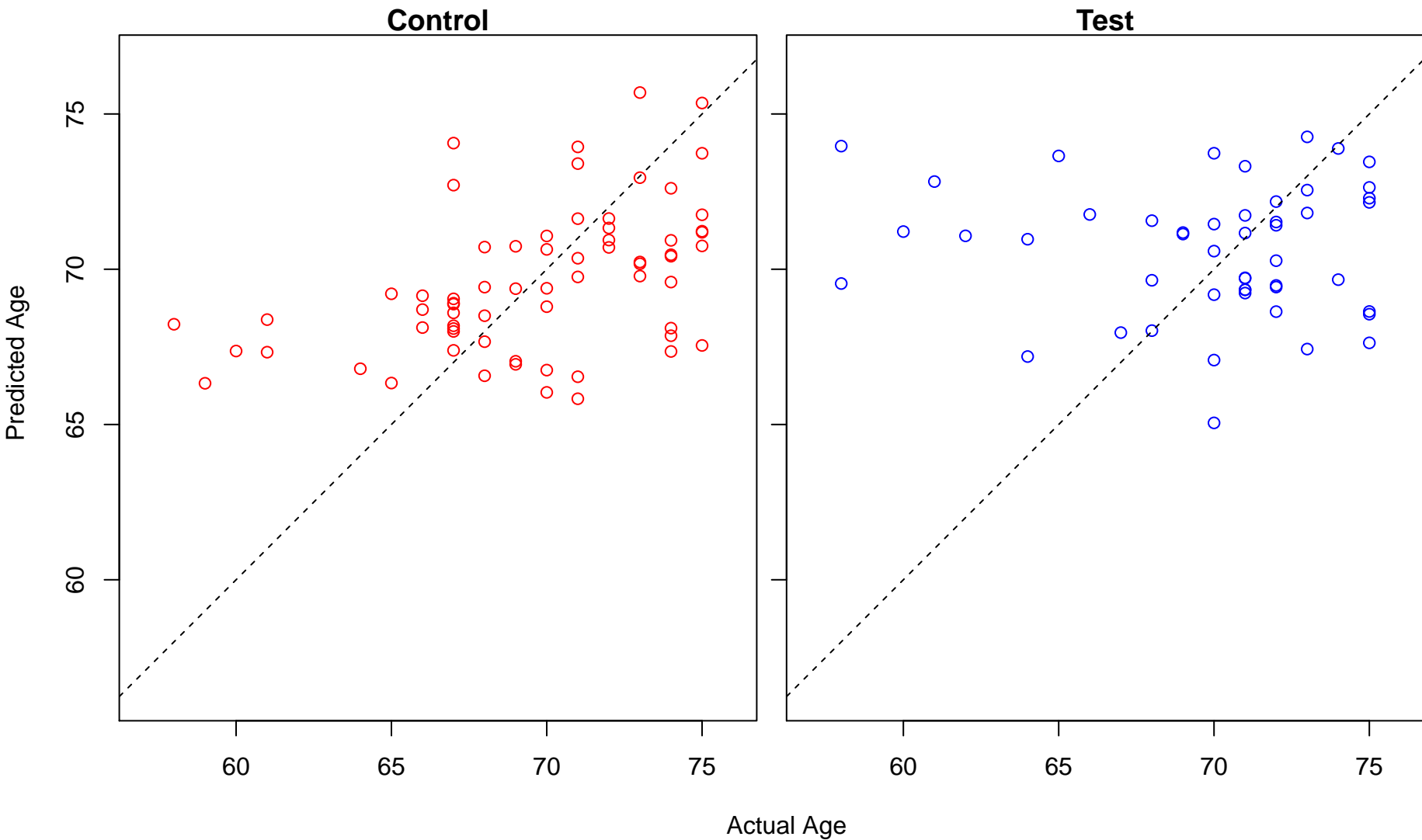
carnitine biosynthetic process (Score: 0.634233)



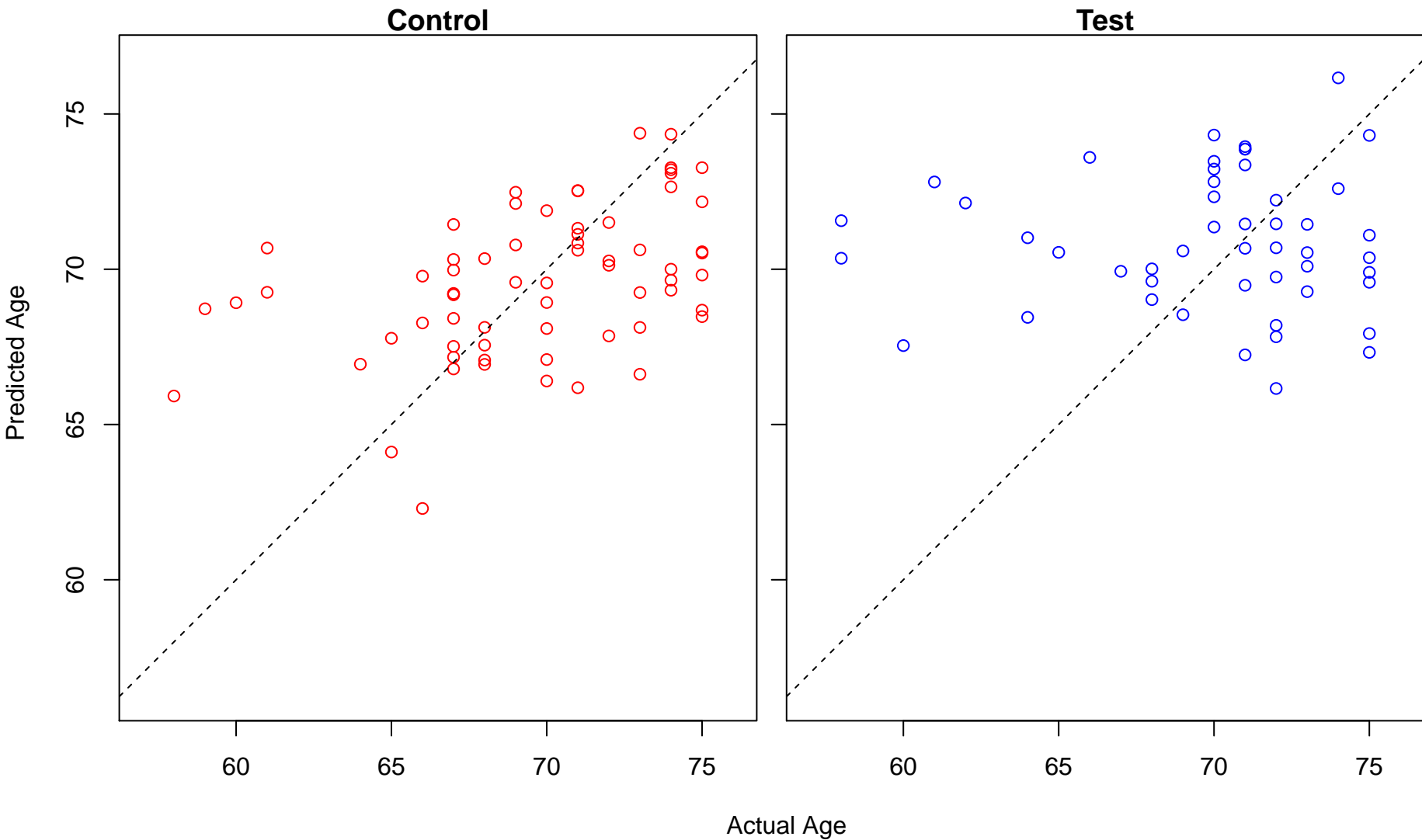
response to macrophage colony-stimulating factor (Score: 0.634221)



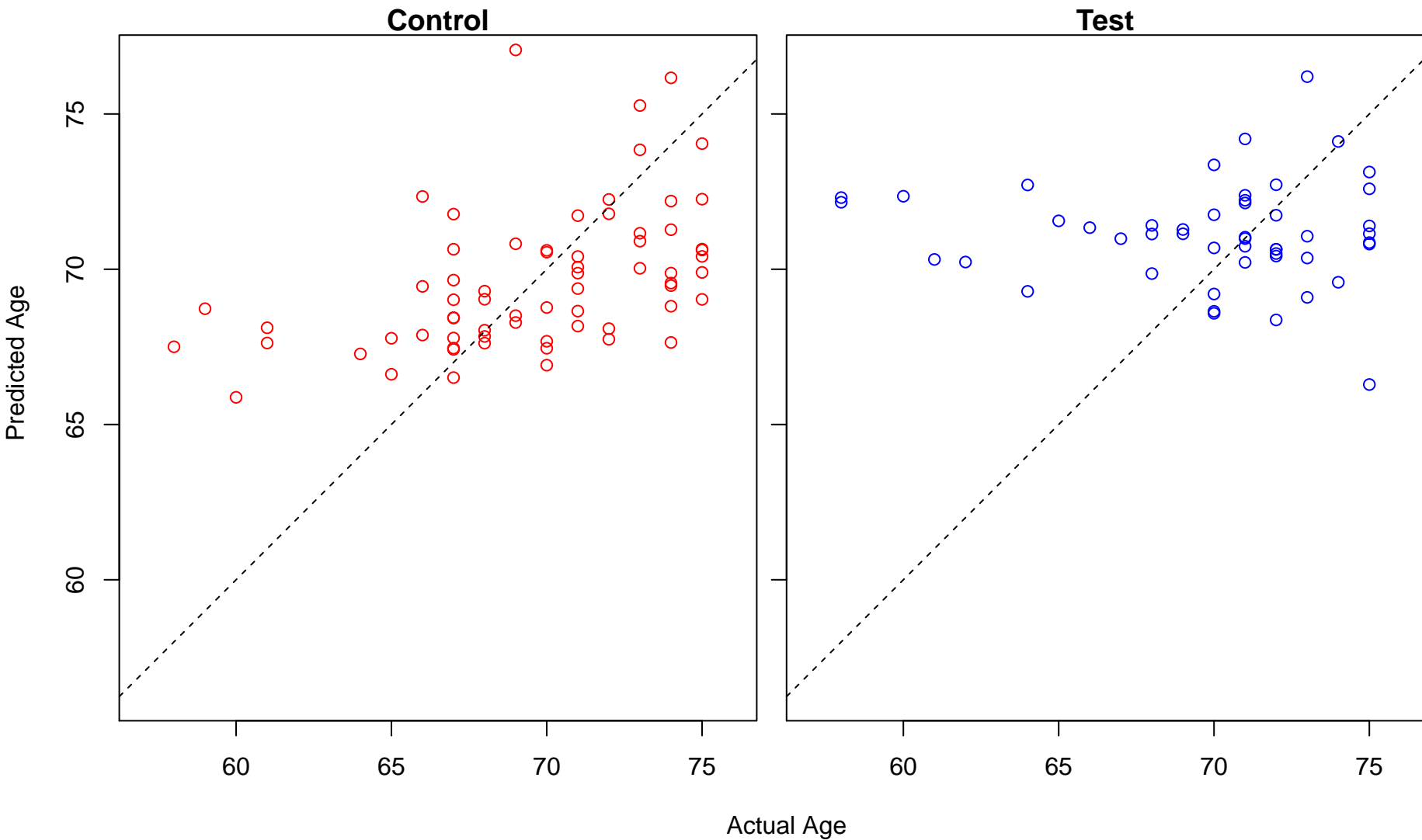
cellular response to macrophage colony-stimulating factor stimulus (Score: 0.634221)



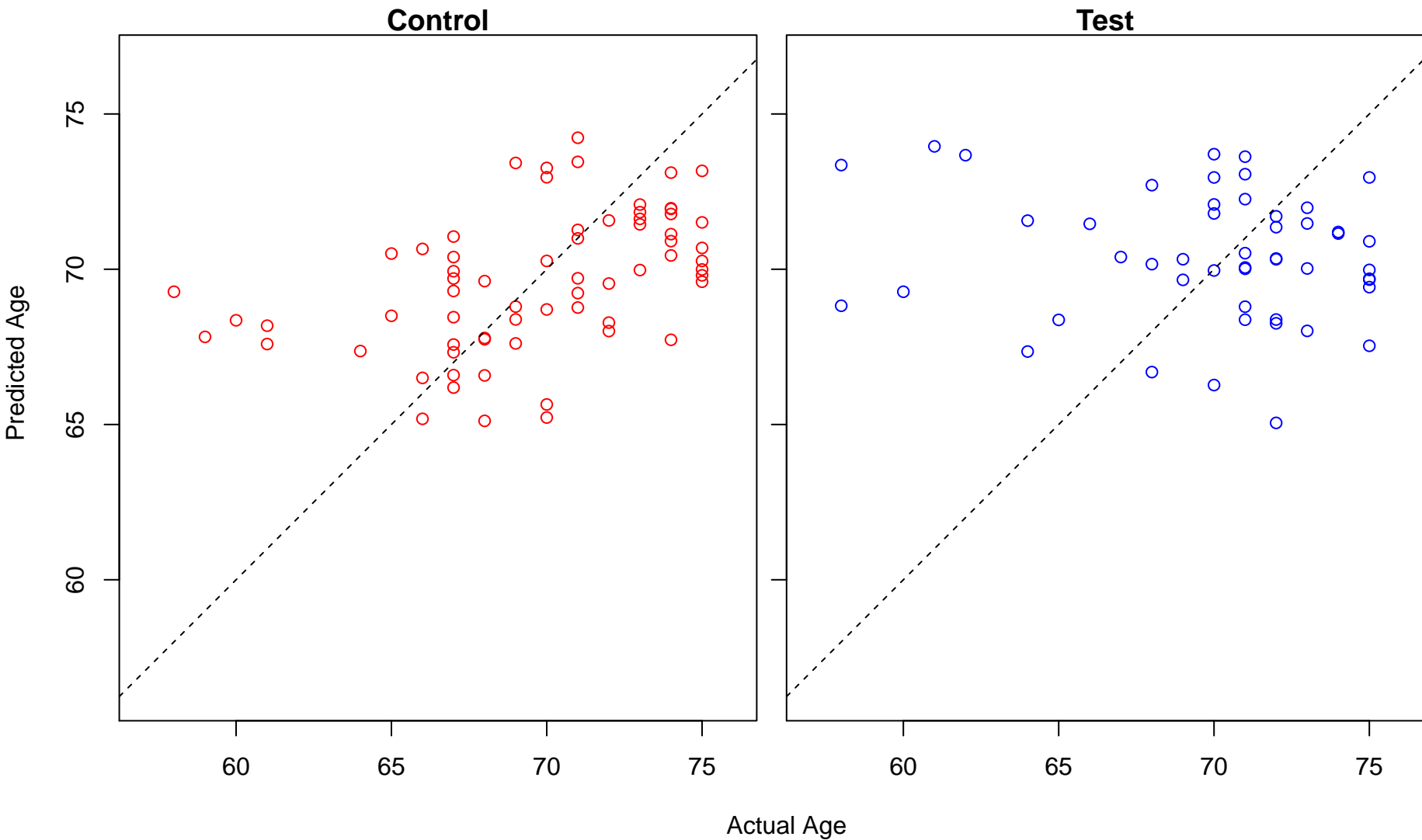
positive regulation of insulin receptor signaling pathway (Score: 0.634218)



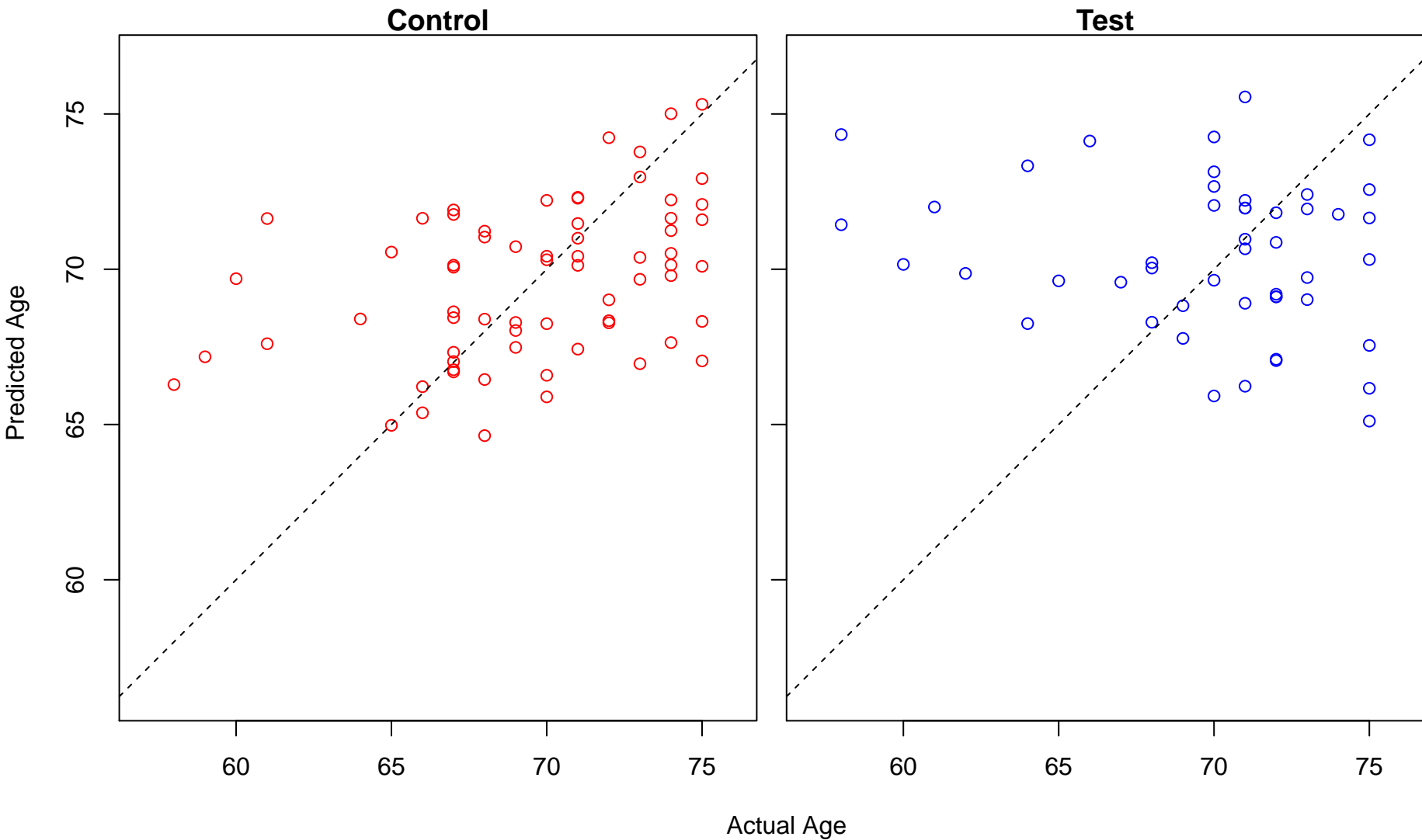
cellular glucuronidation (Score: 0.633927)



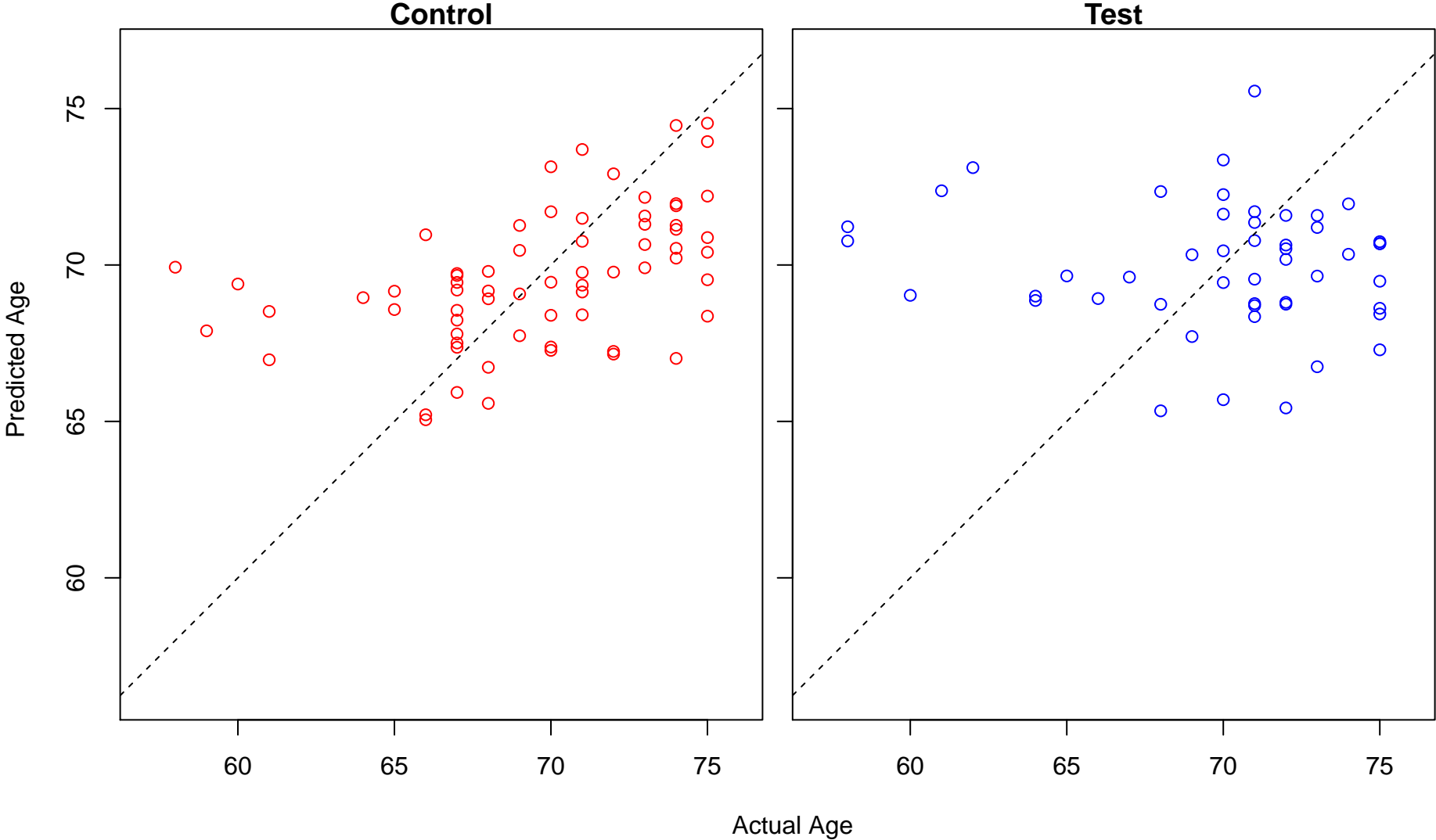
negative regulation of response to endoplasmic reticulum stress (Score: 0.633770)



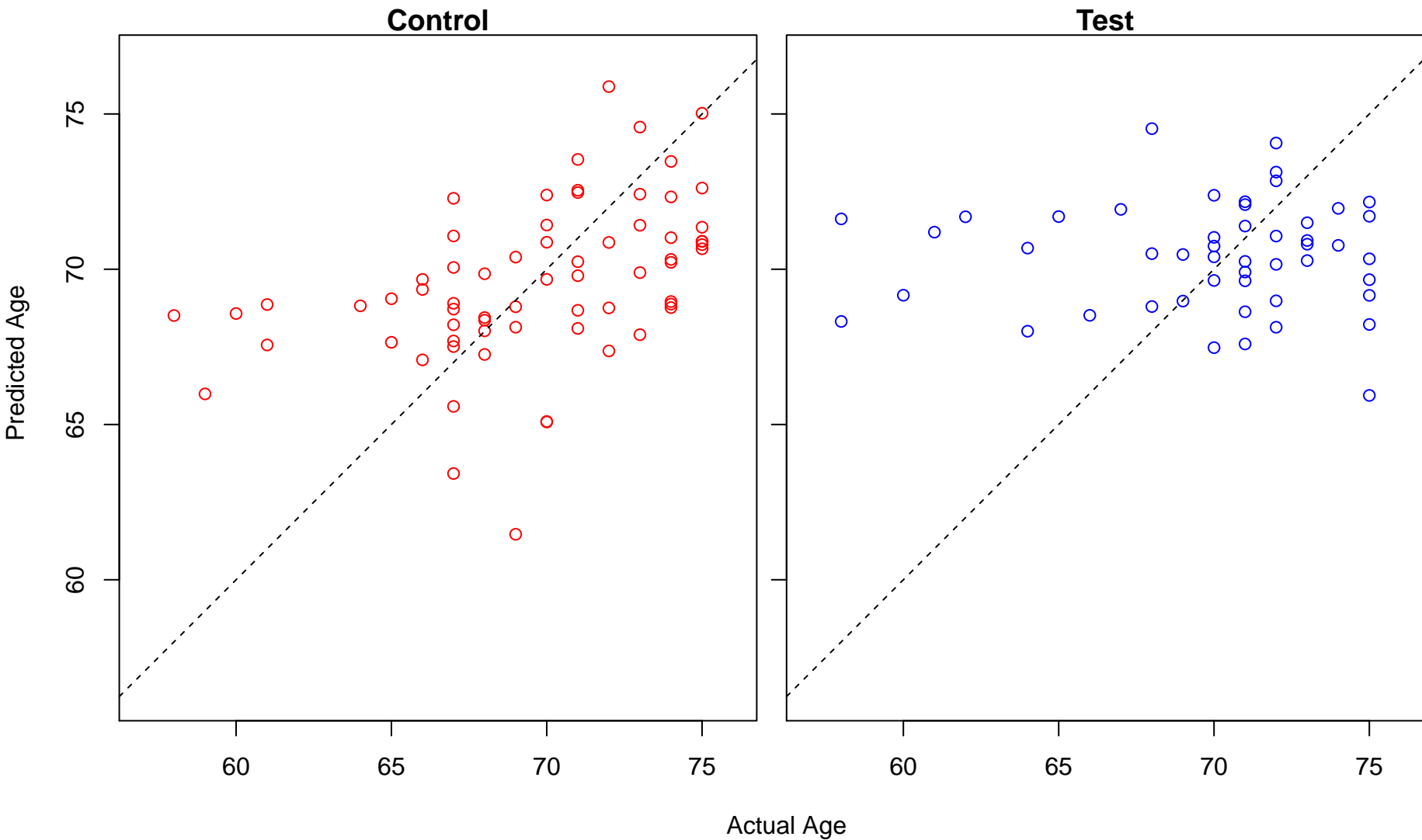
regulation of transcription by glucose (Score: 0.633734)



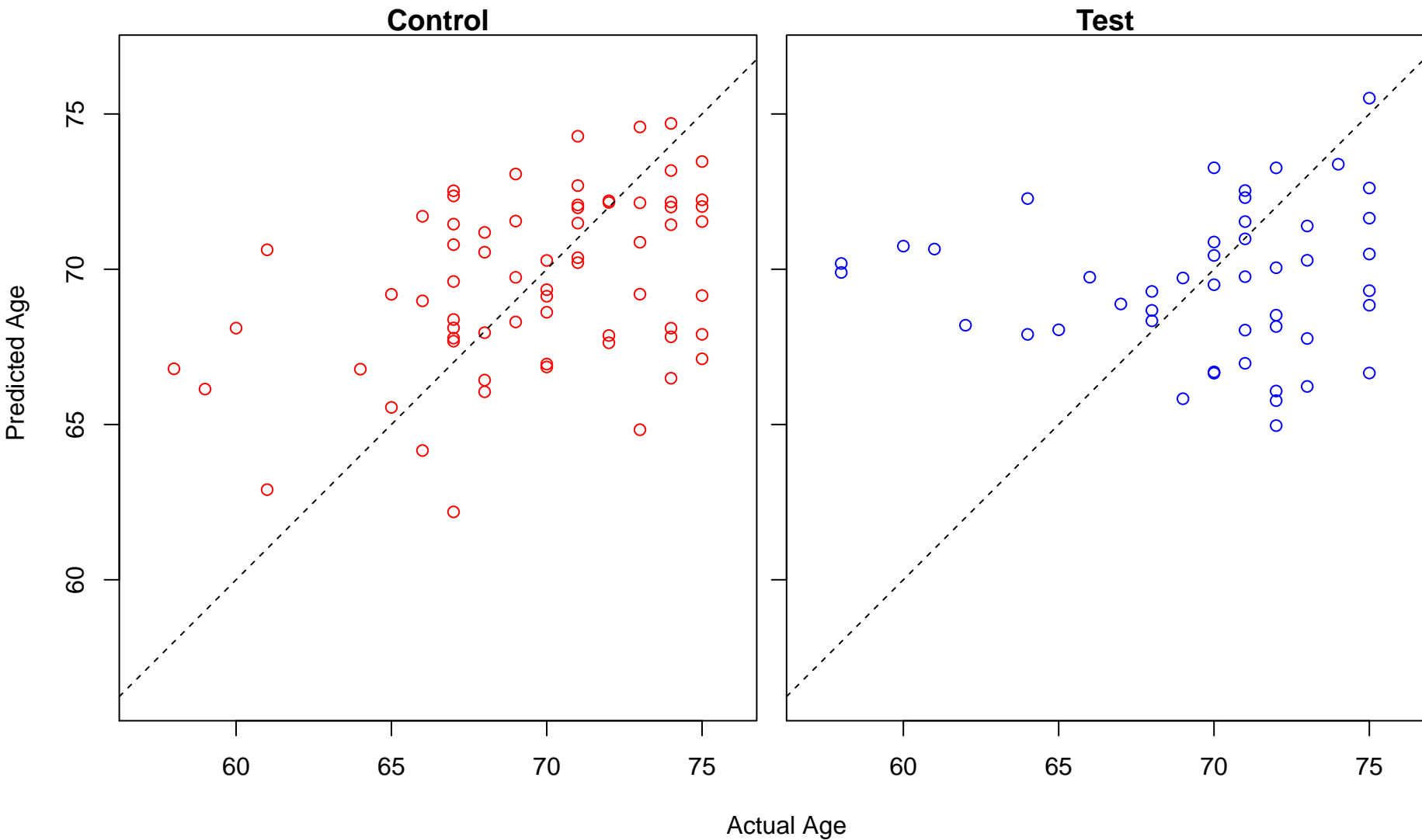
positive regulation of cell migration by vascular endothelial growth factor signaling pathway (Score: 0.6



activation of protein kinase B activity (Score: 0.632926)

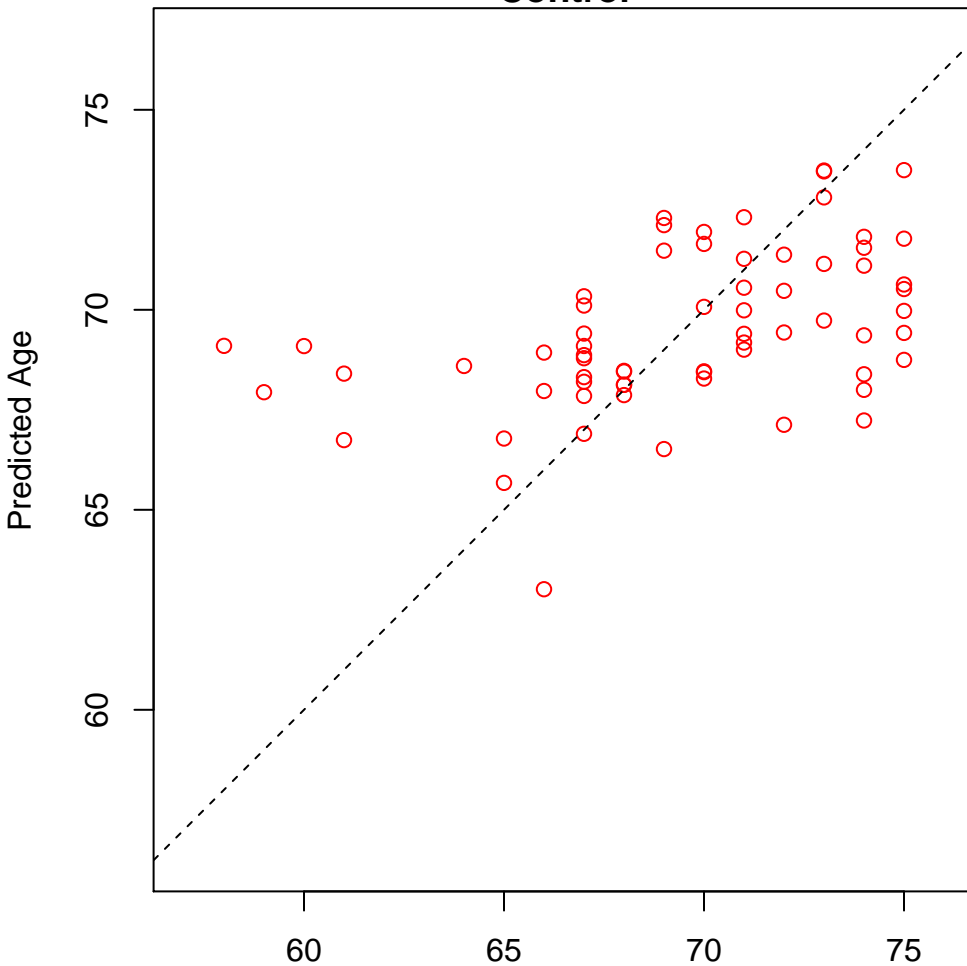


blood vessel remodeling (Score: 0.632829)

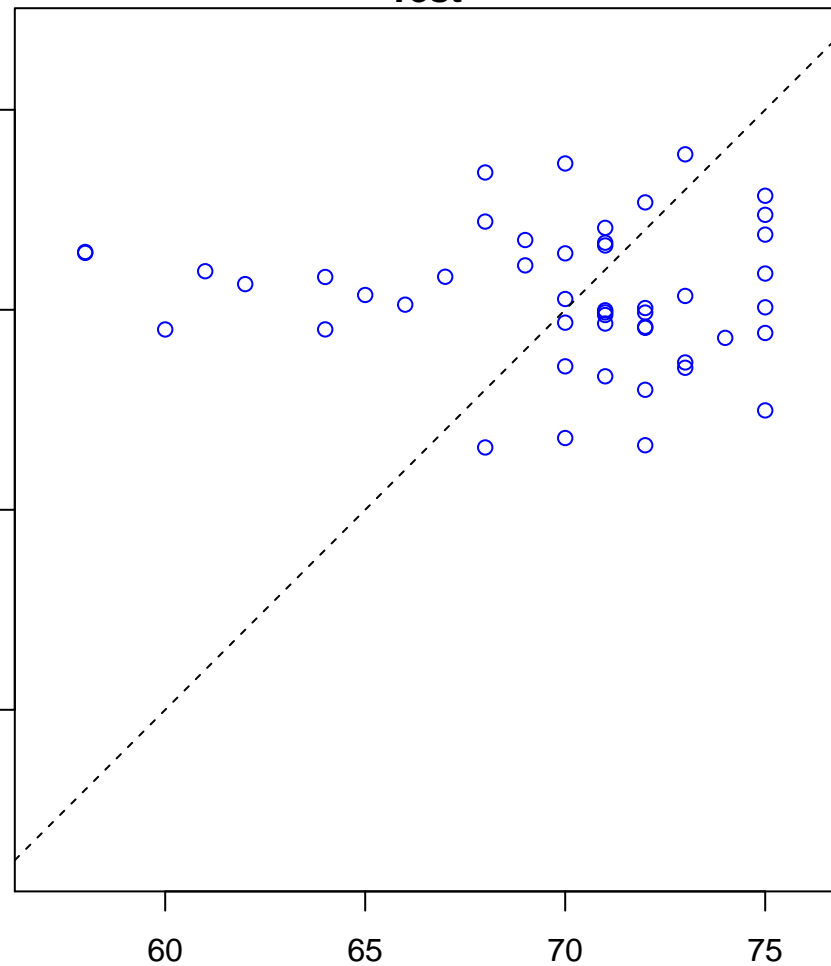


protein import into peroxisome matrix (Score: 0.632402)

Control

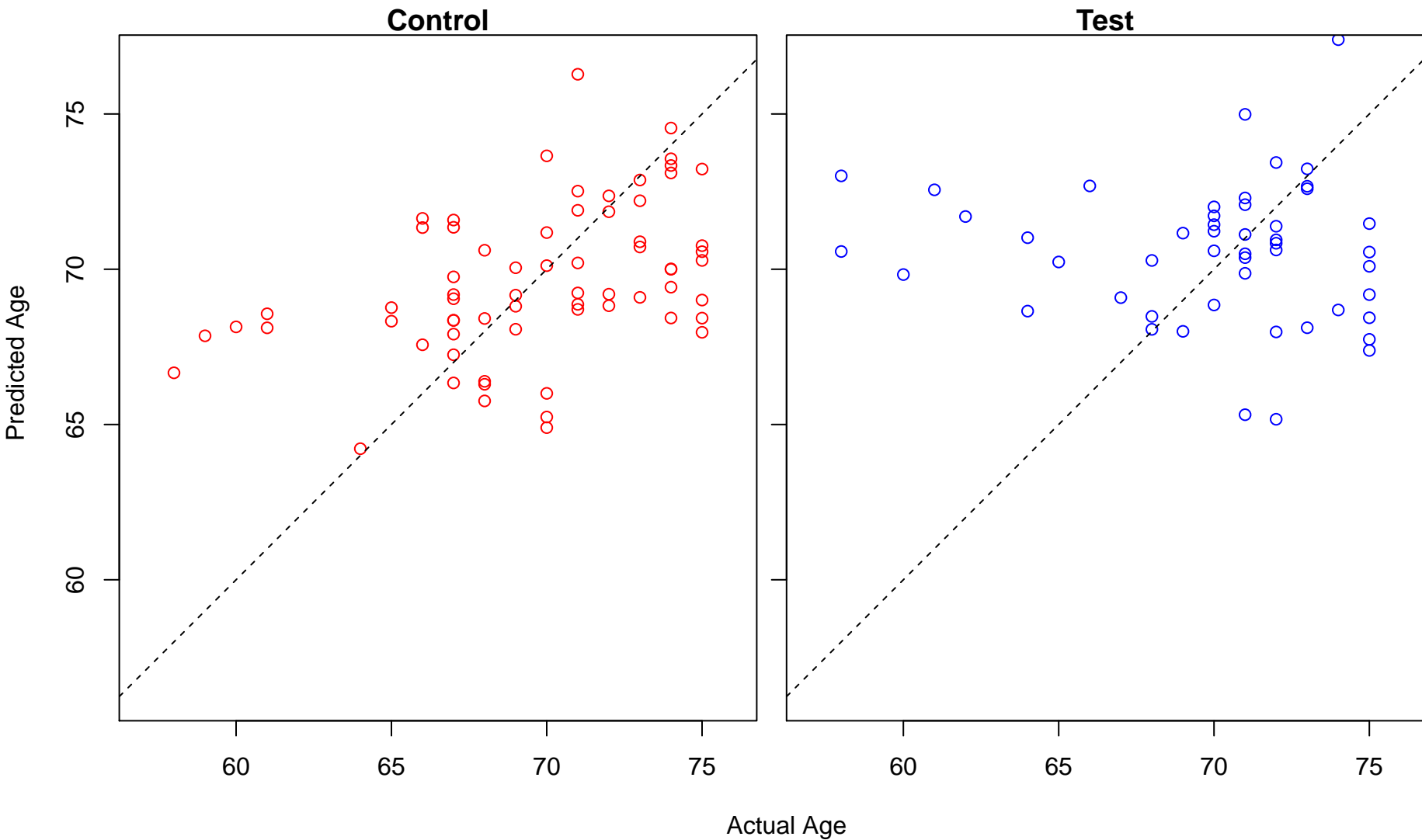


Test



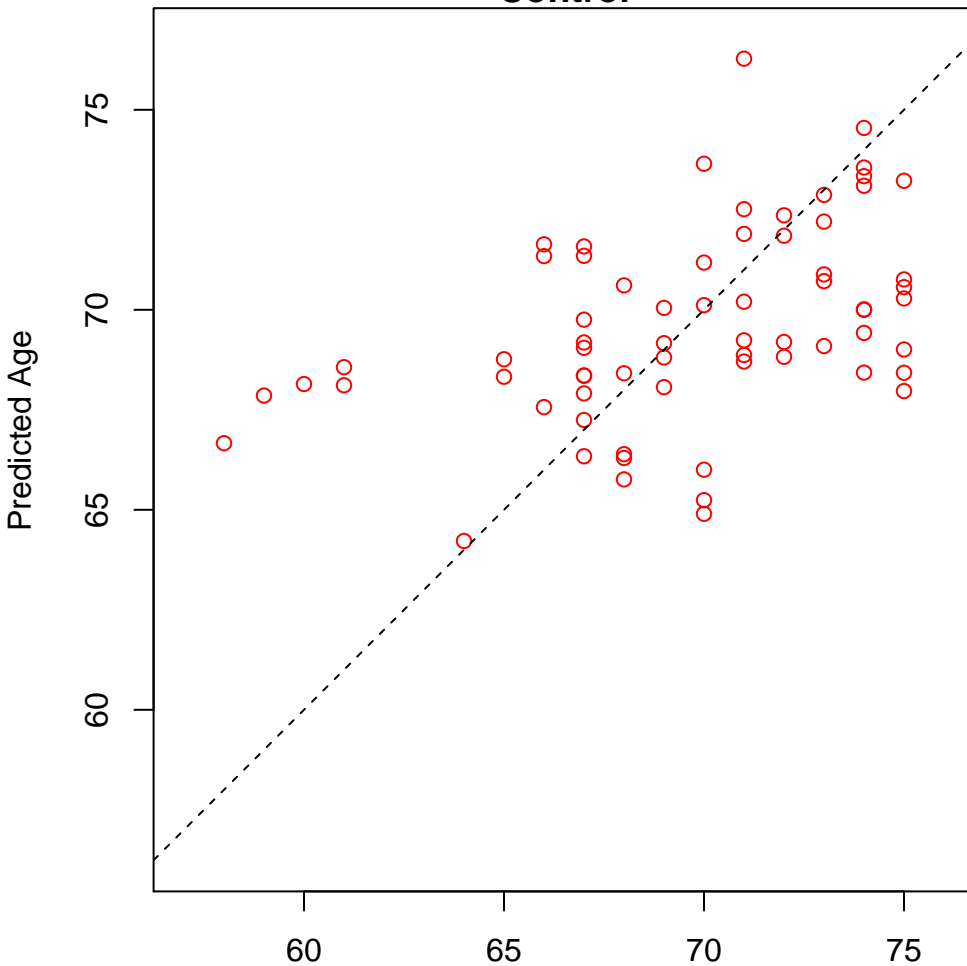
Actual Age

regulation of mitotic cell cycle spindle assembly checkpoint (Score: 0.632396)

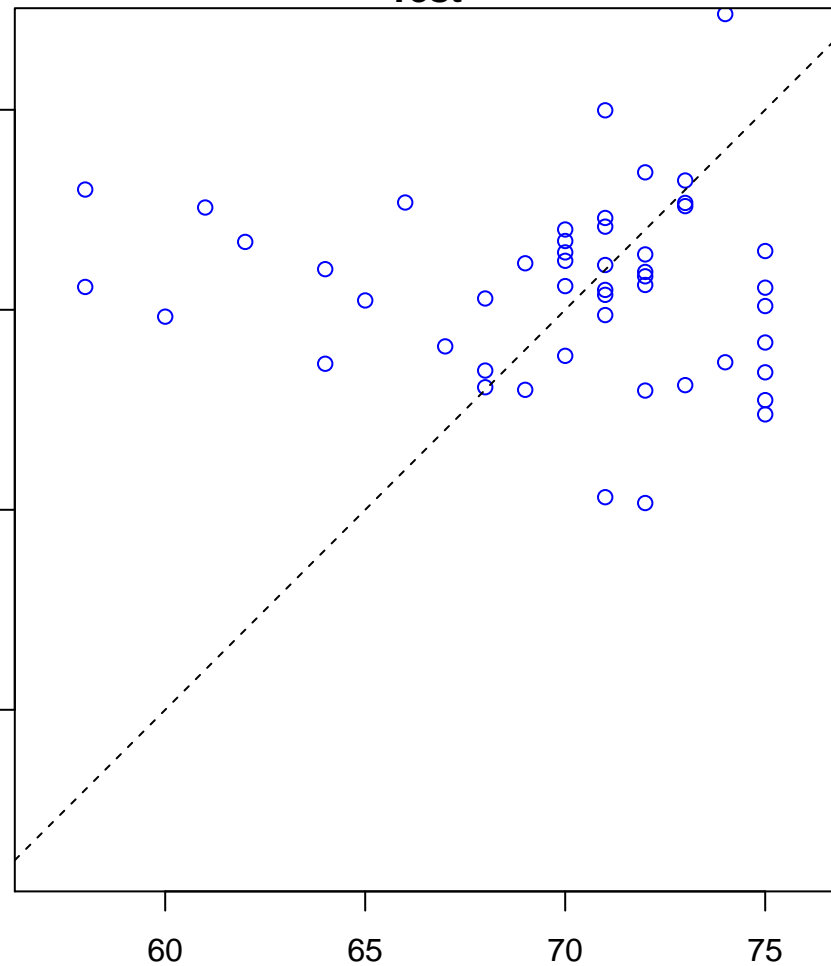


regulation of mitotic spindle checkpoint (Score: 0.632396)

Control

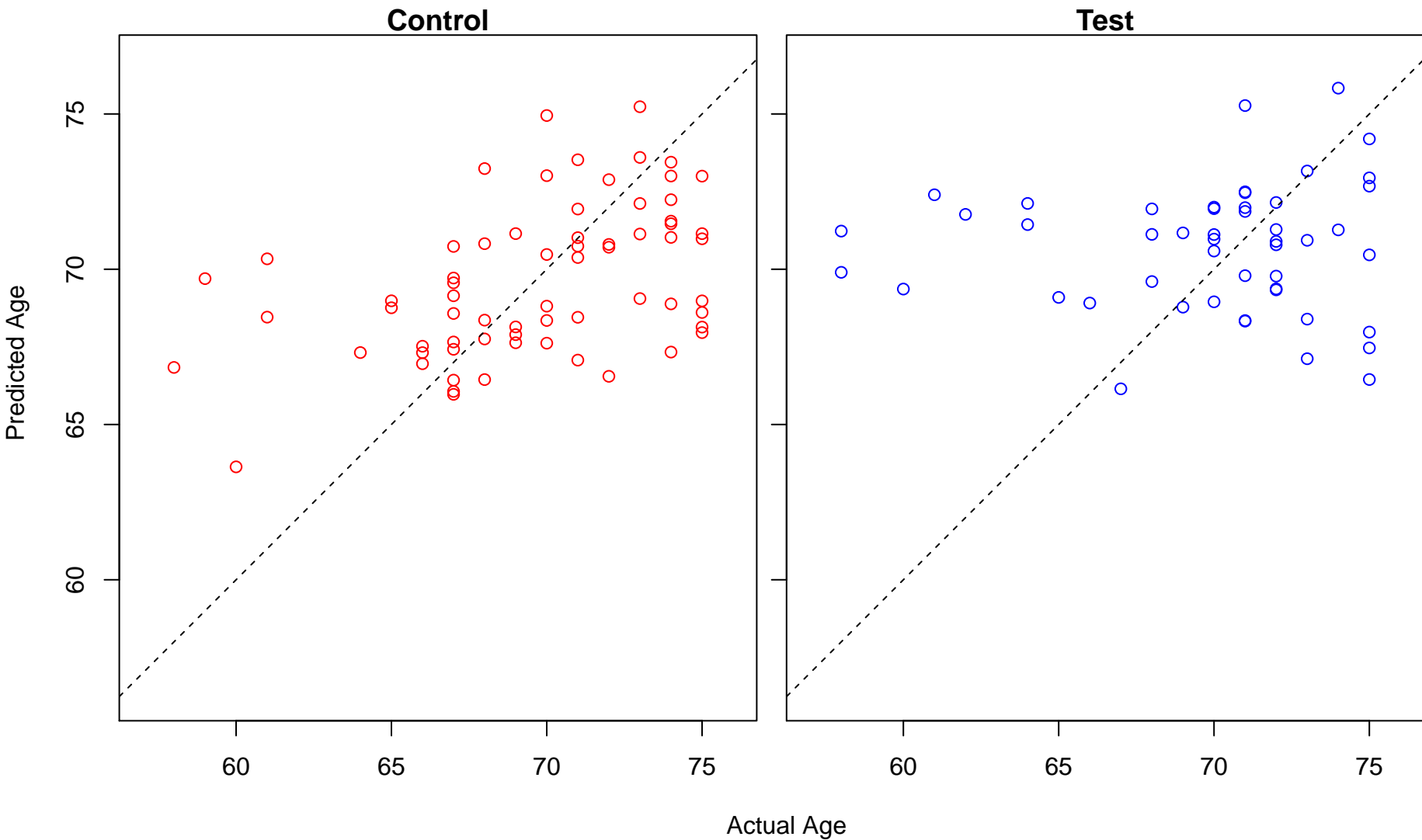


Test

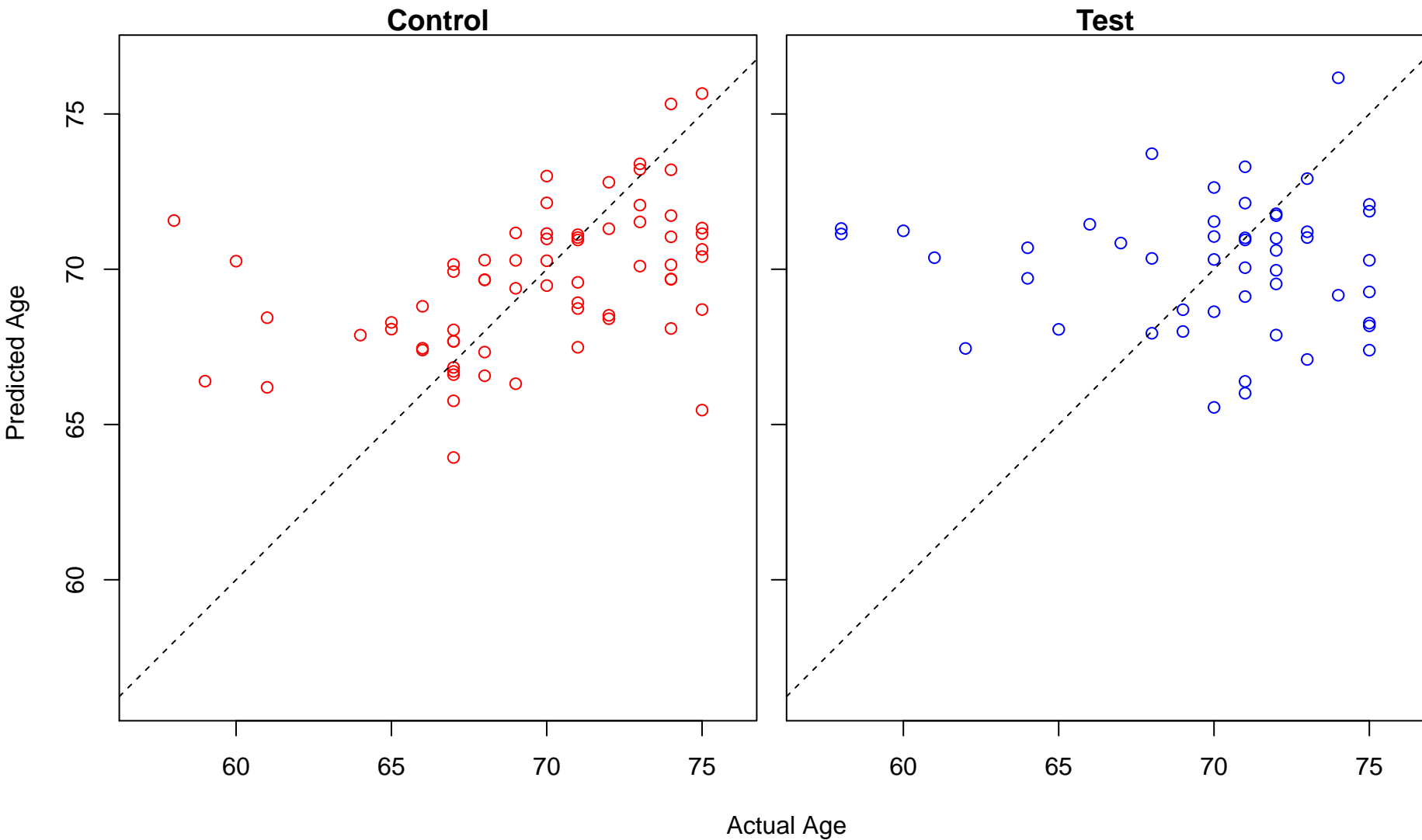


Actual Age

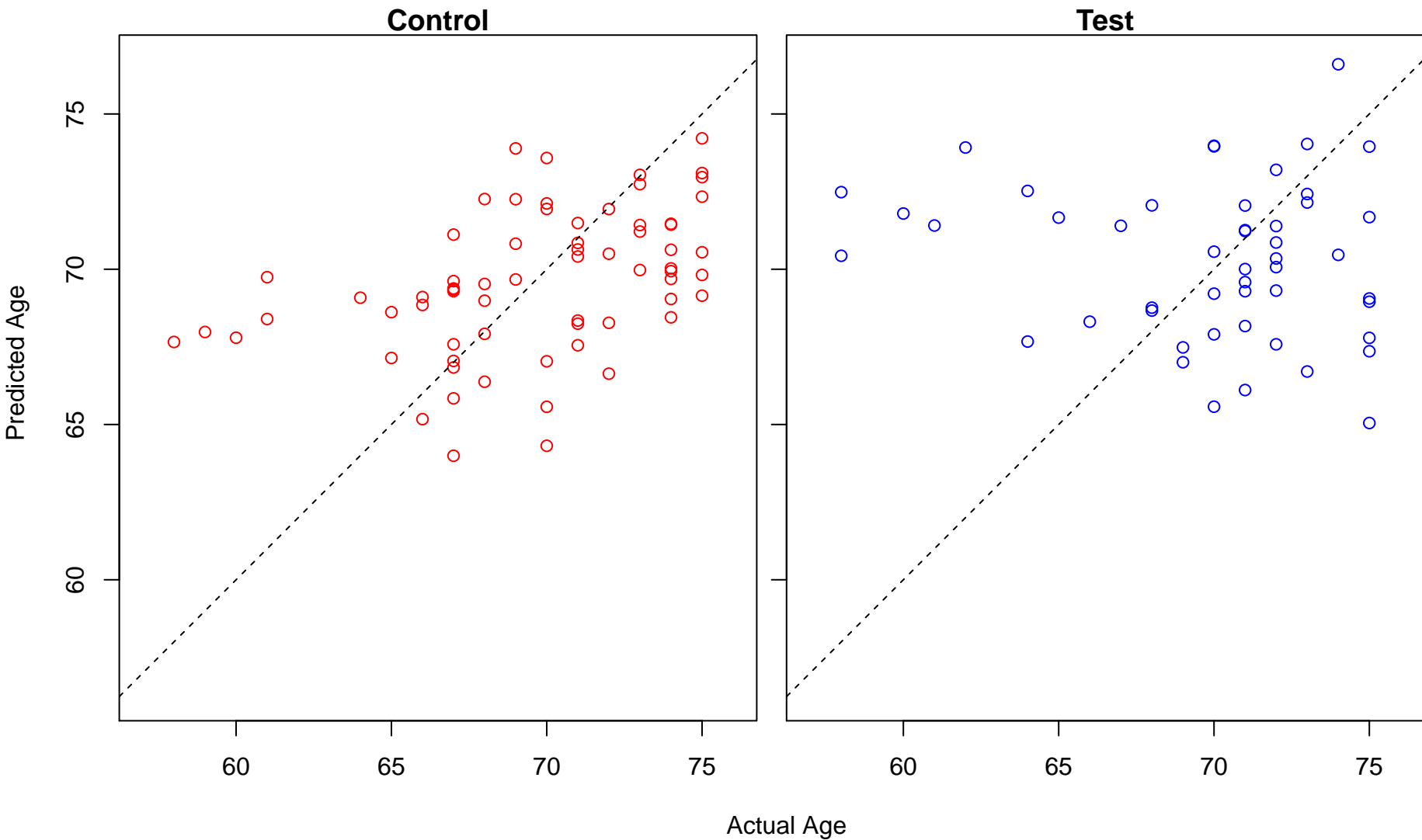
positive regulation of antigen processing and presentation (Score: 0.630786)



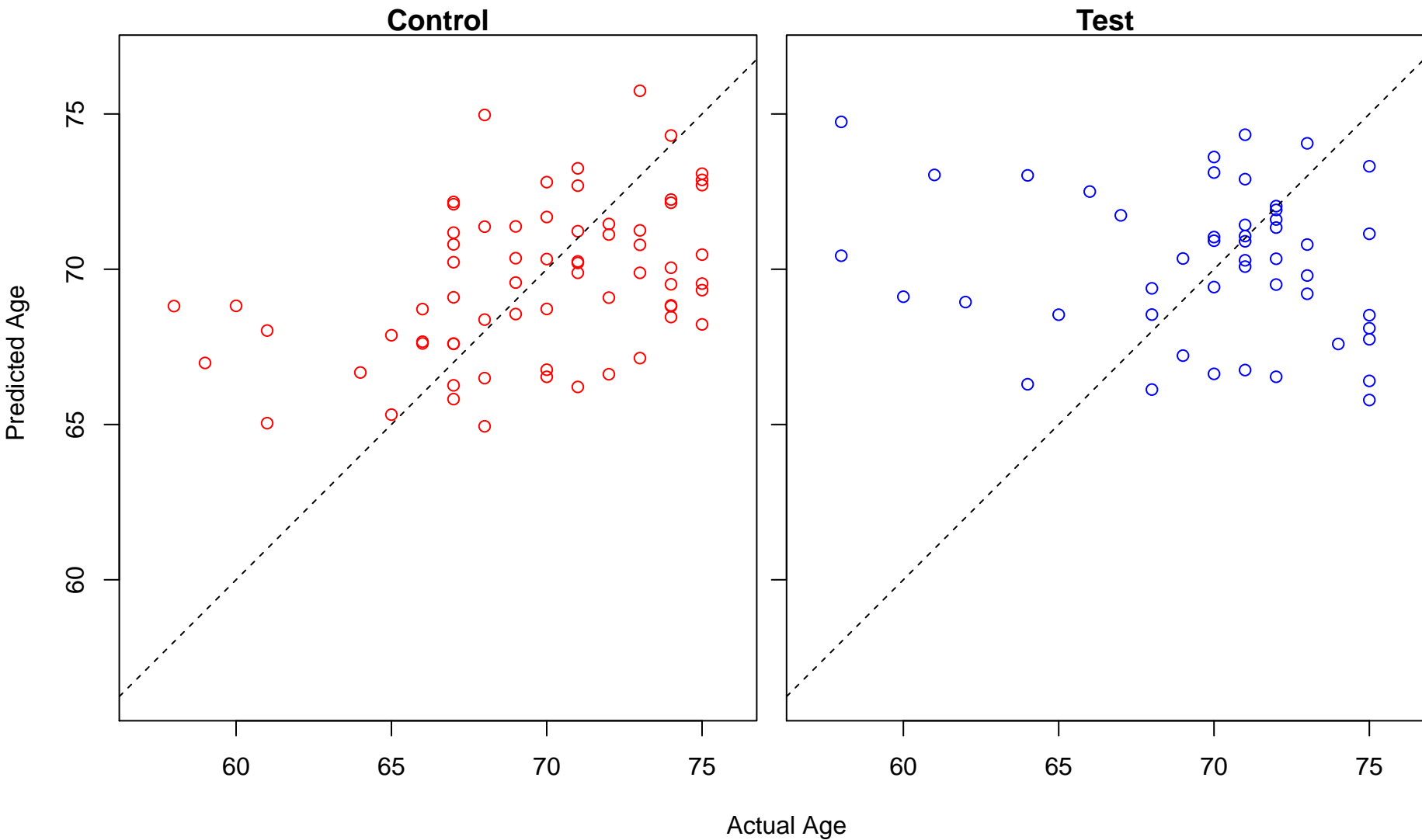
asymmetric protein localization (Score: 0.630246)



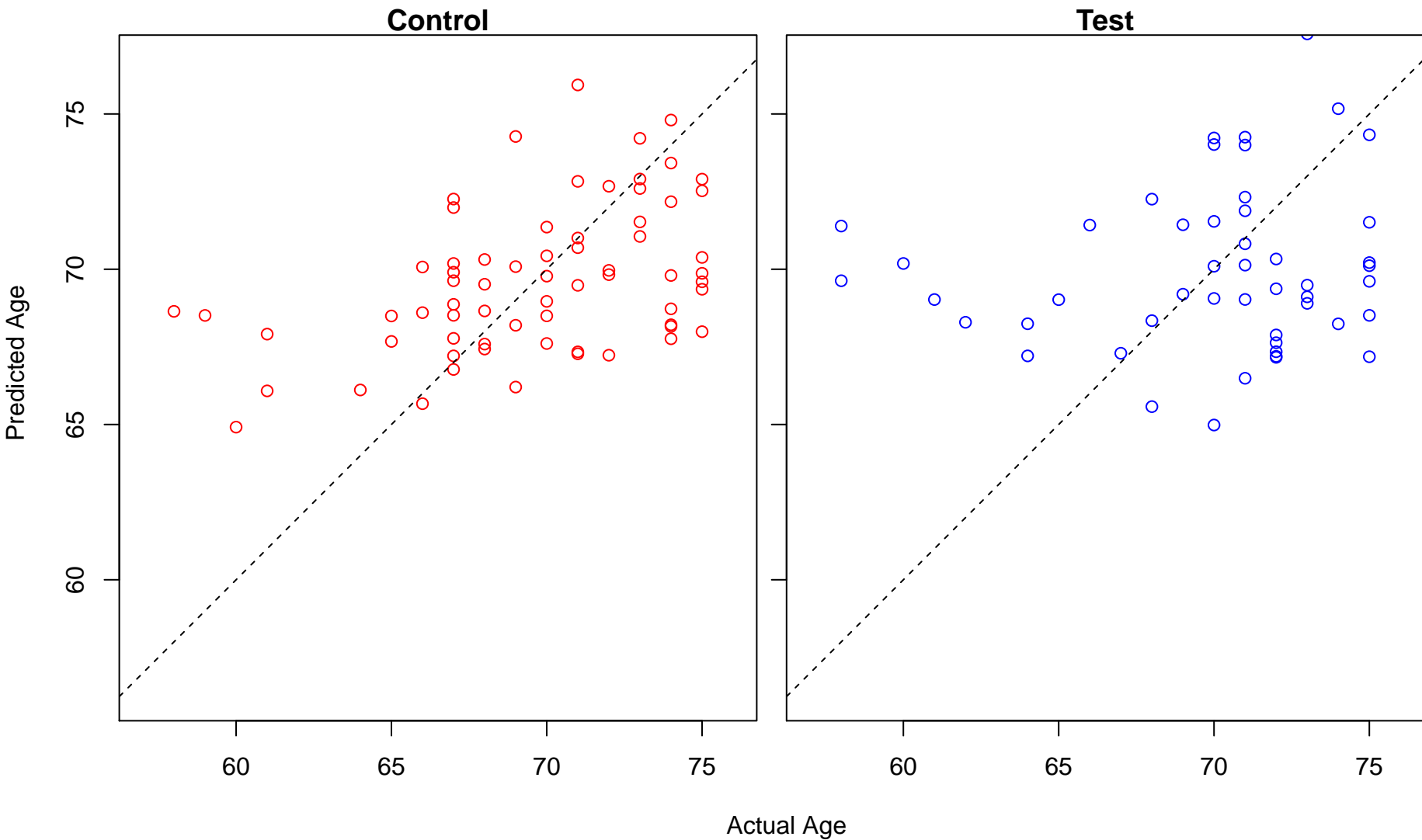
positive regulation of myotube differentiation (Score: 0.630213)



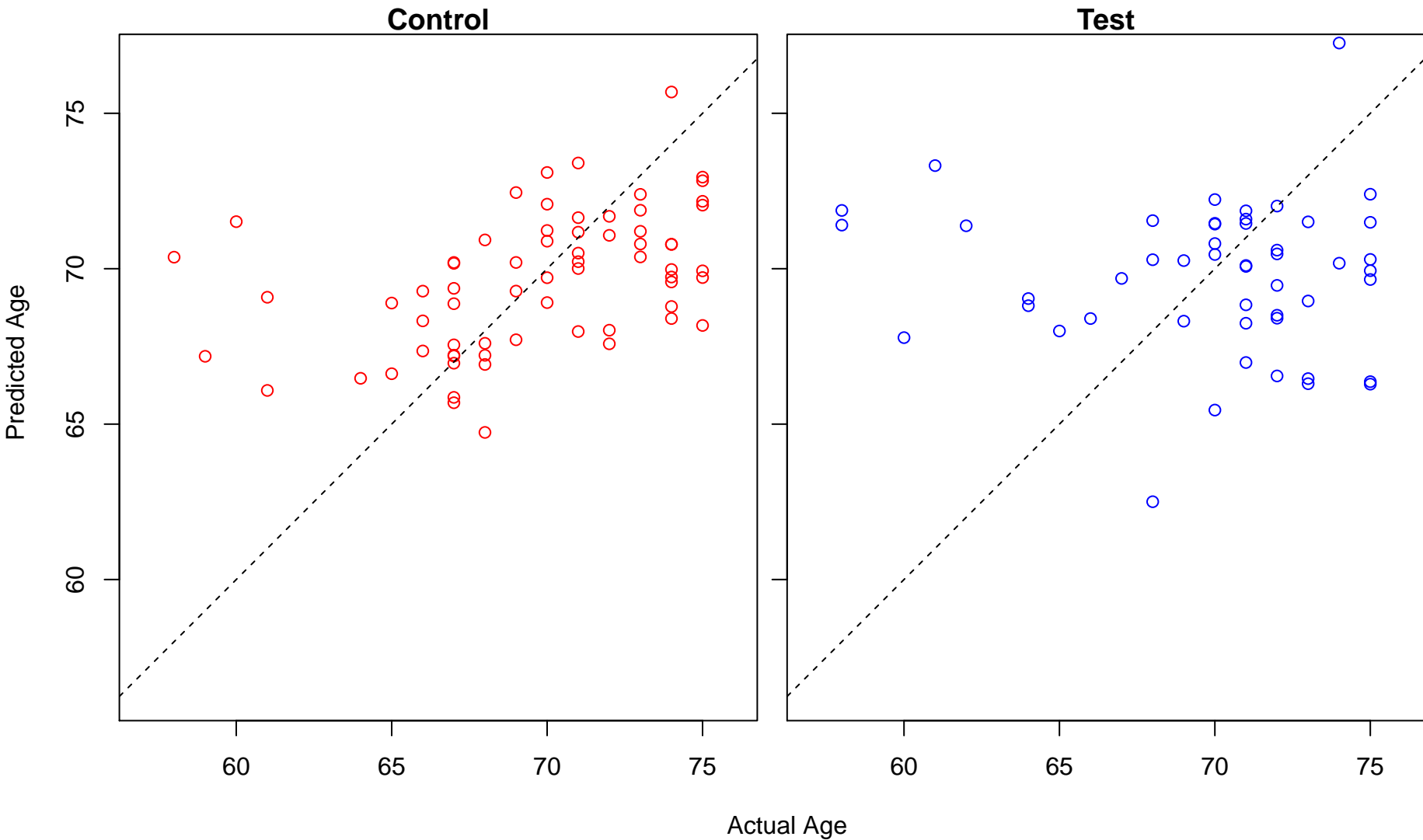
regulation of receptor biosynthetic process (Score: 0.630029)



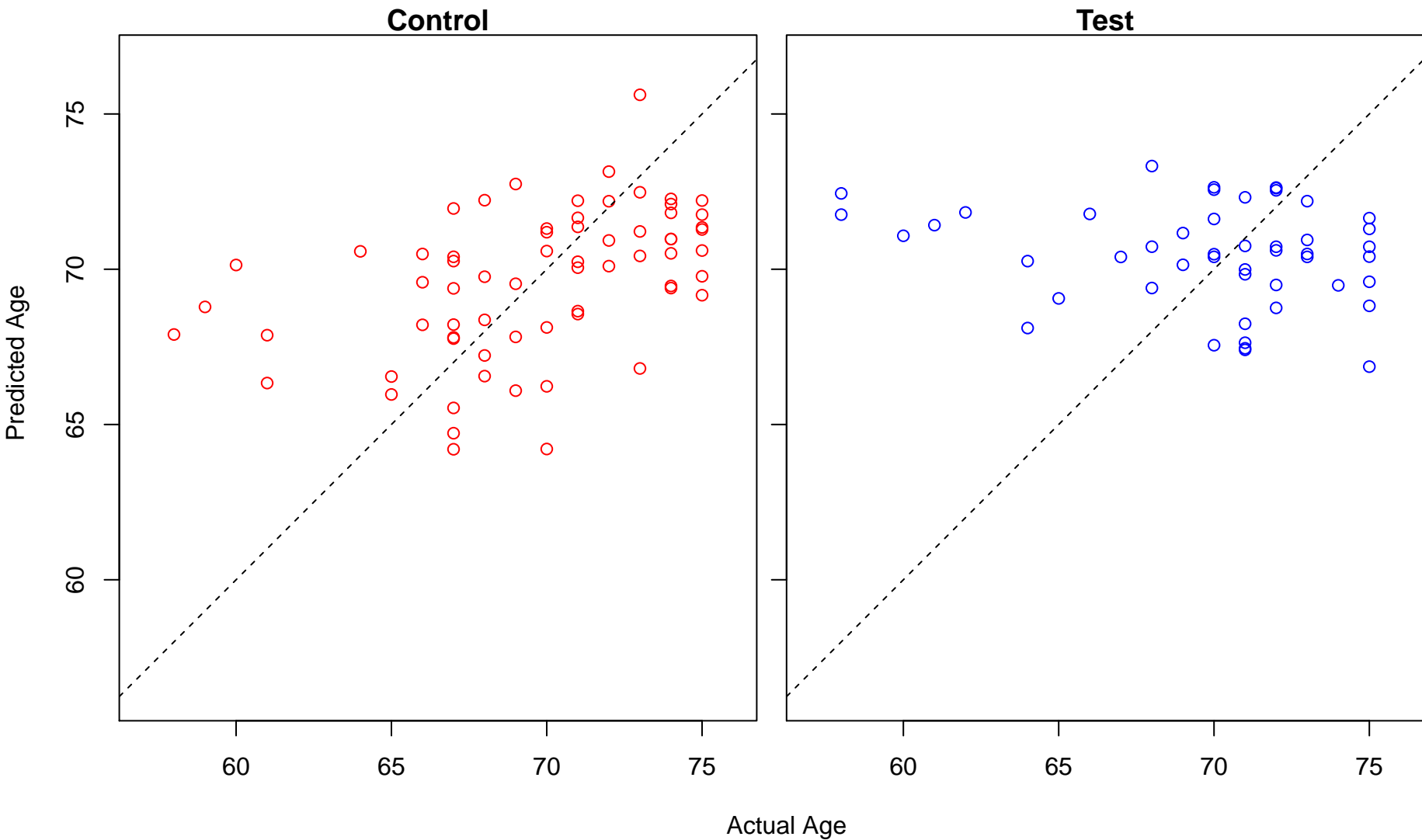
positive regulation of protein localization to cell surface (Score: 0.630019)



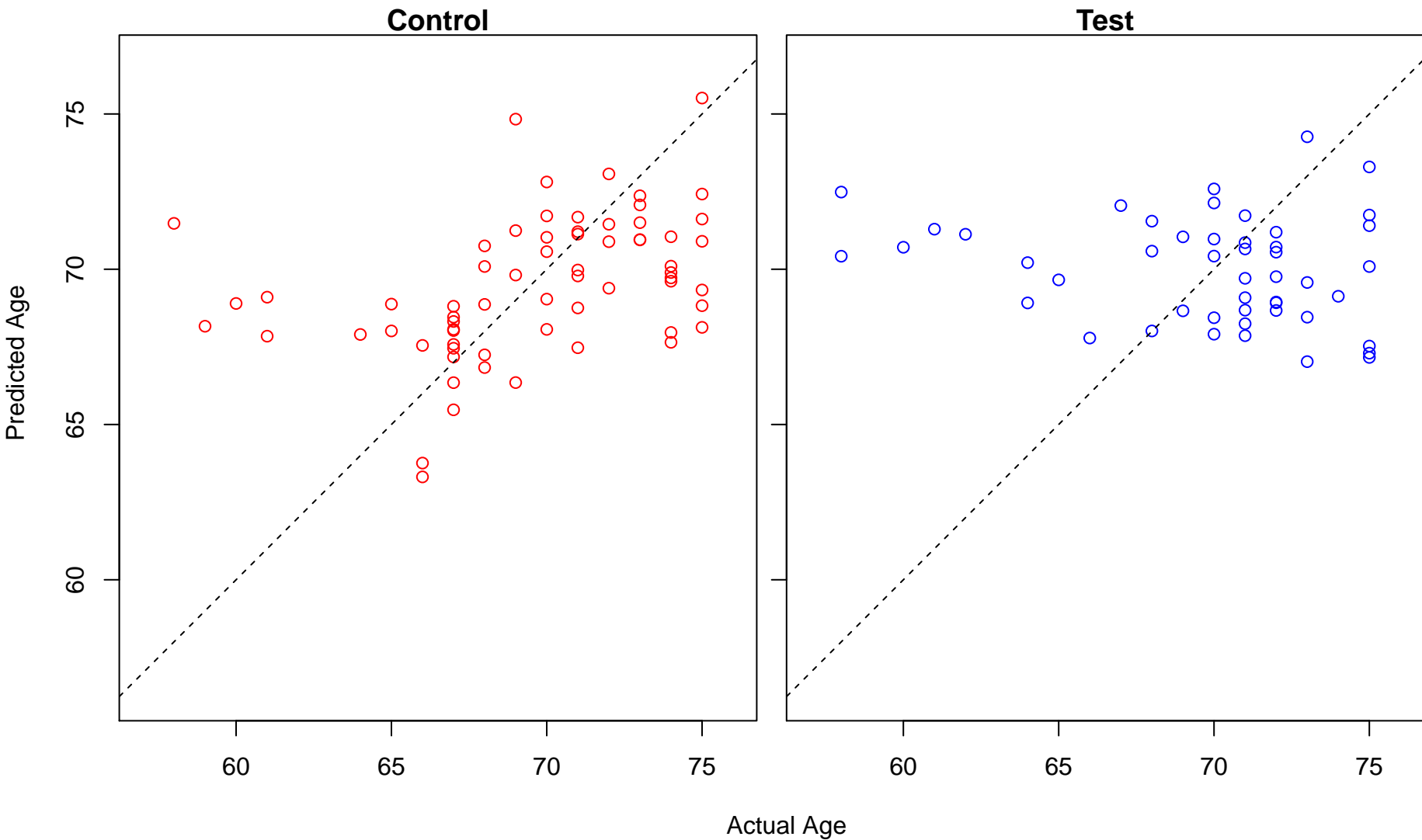
negative regulation of T cell mediated immunity (Score: 0.628815)



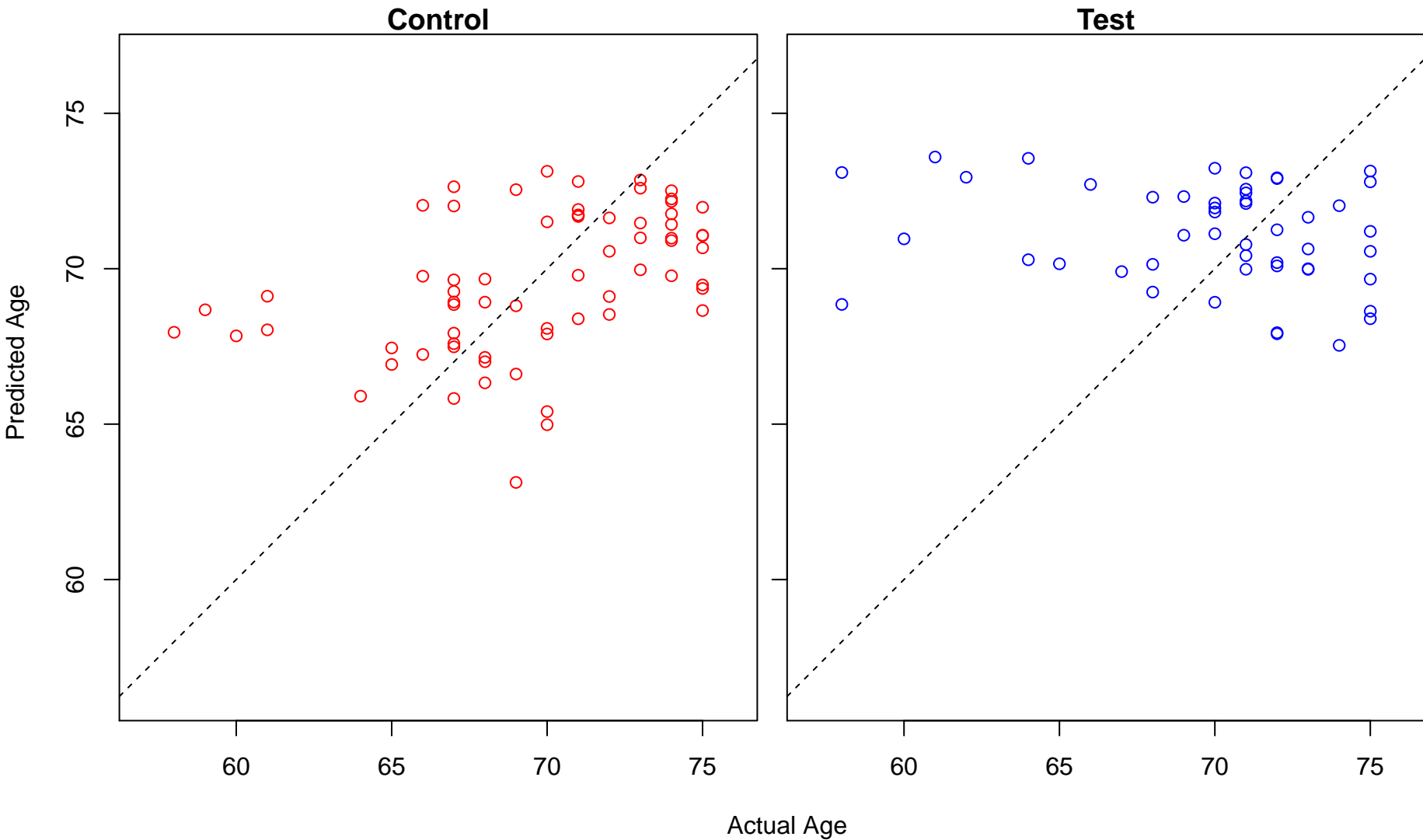
pyridine-containing compound biosynthetic process (Score: 0.628477)



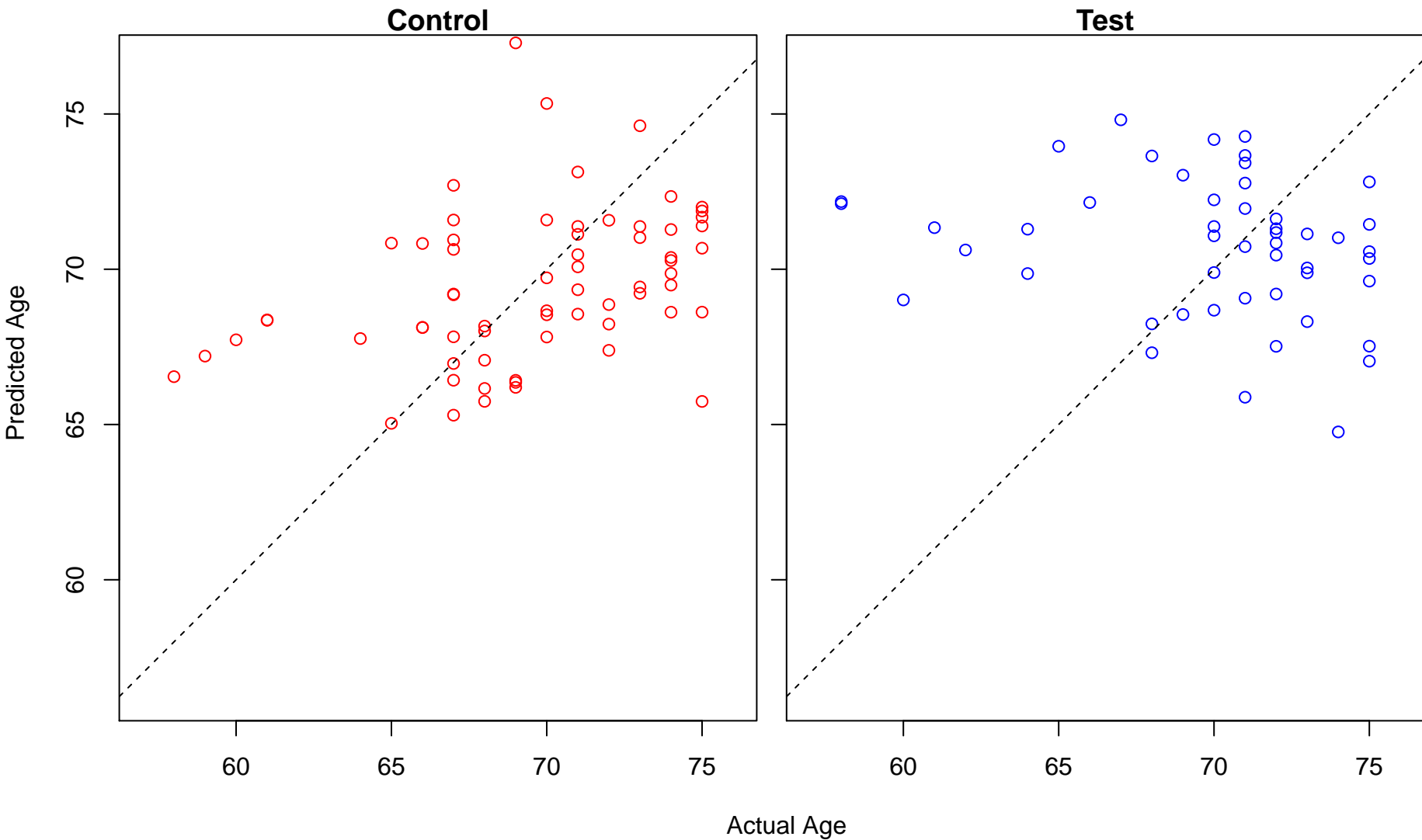
estrogen metabolic process (Score: 0.628175)



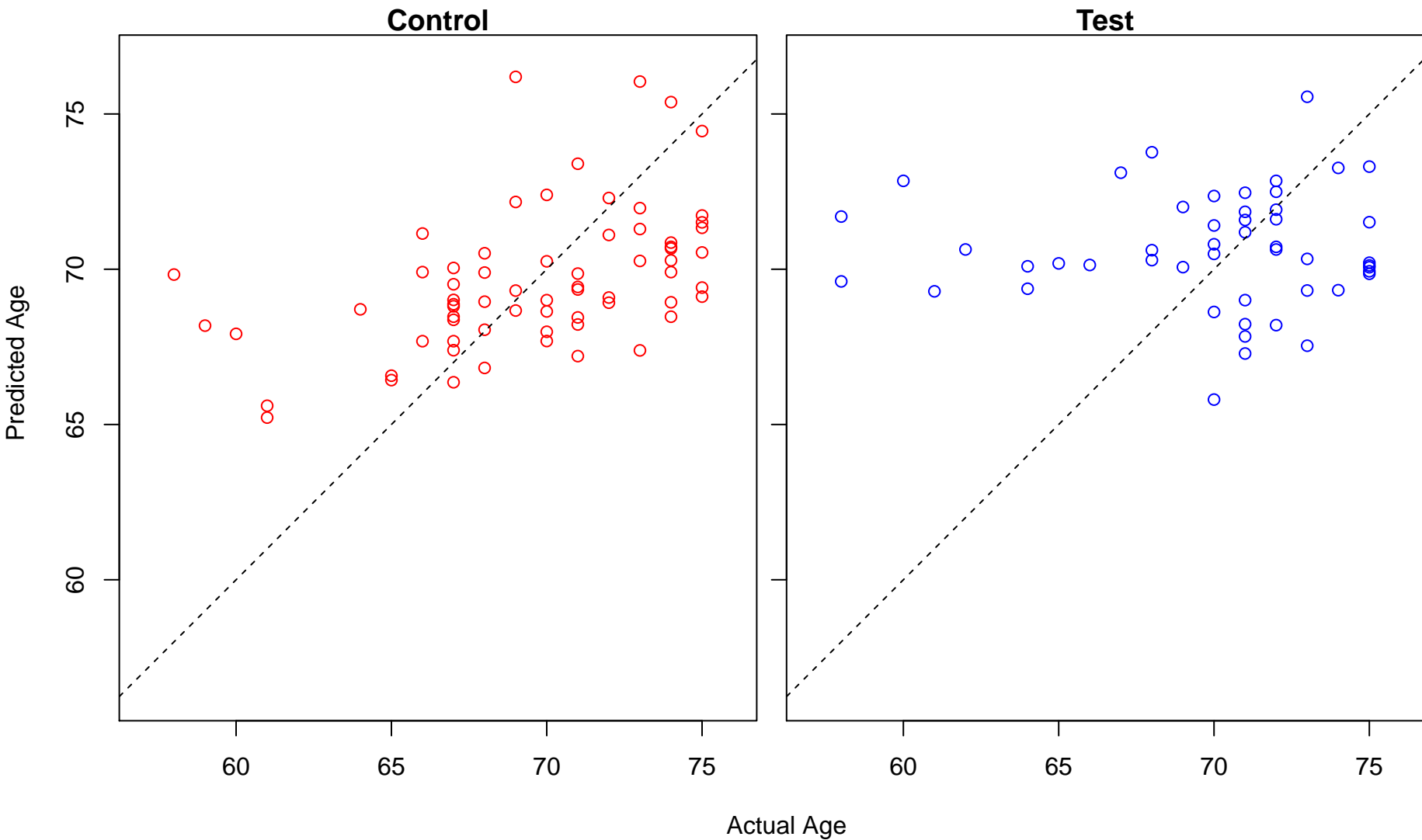
arachidonic acid metabolic process (Score: 0.627727)



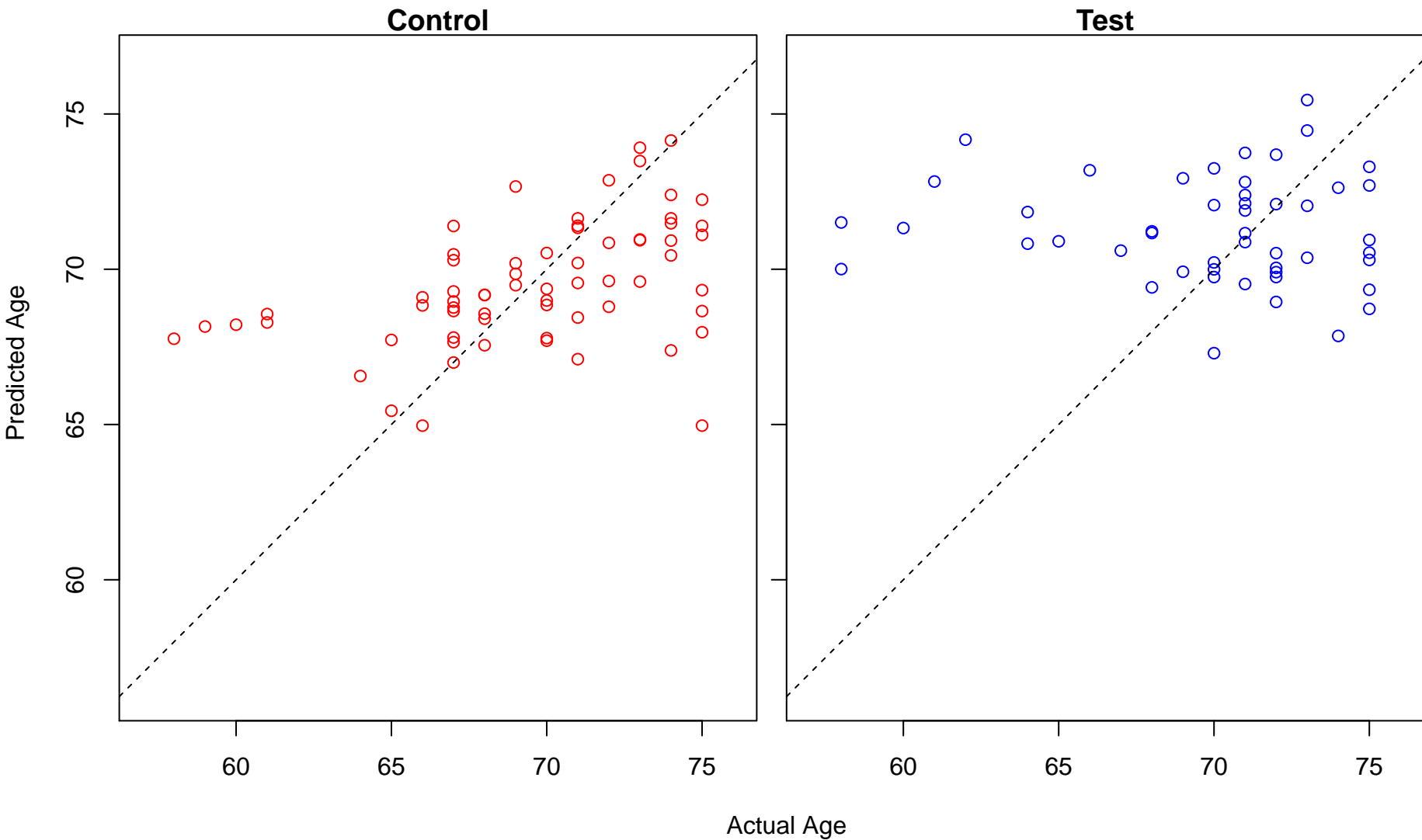
TOR signaling (Score: 0.626728)



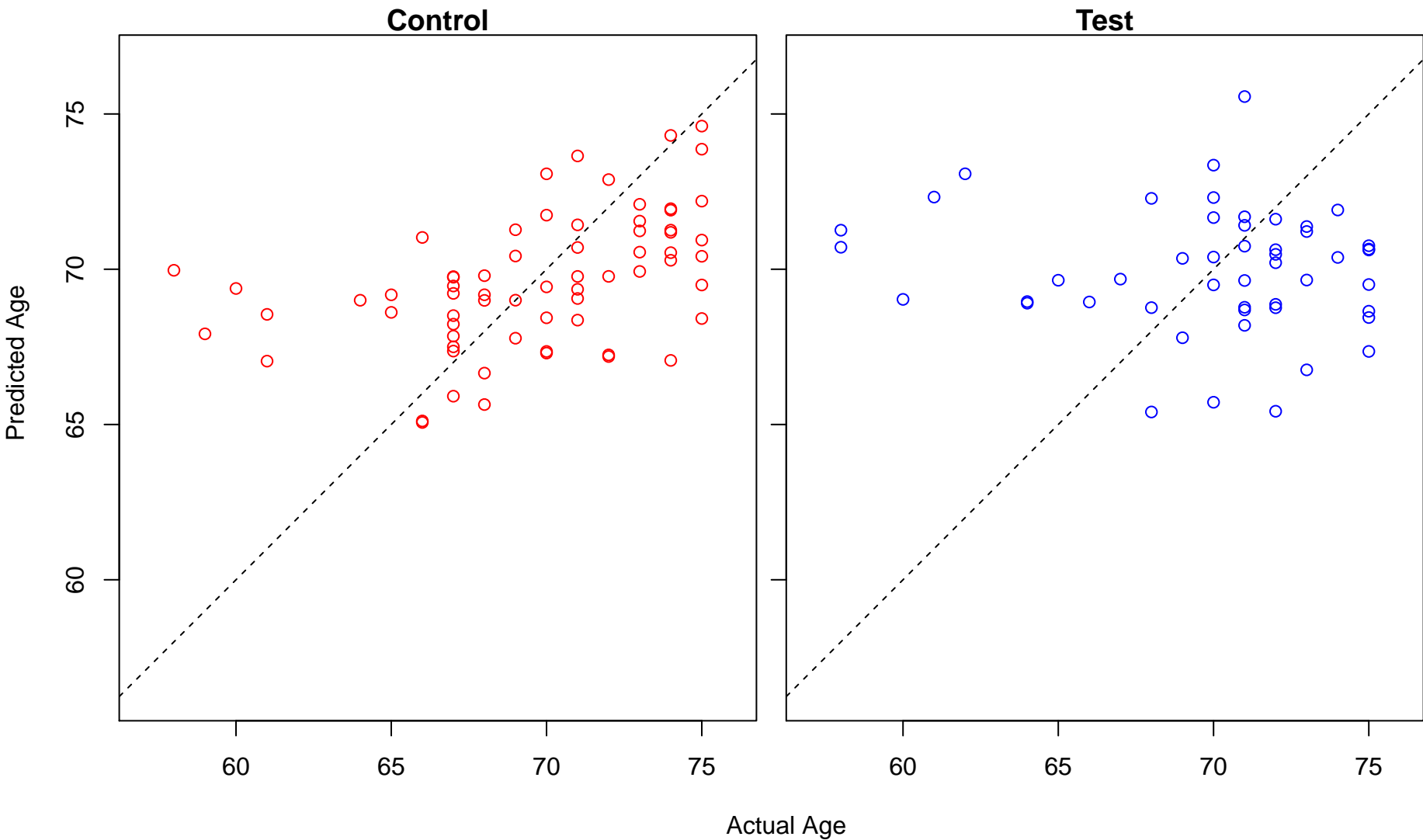
negative regulation of cytokinesis (Score: 0.626340)



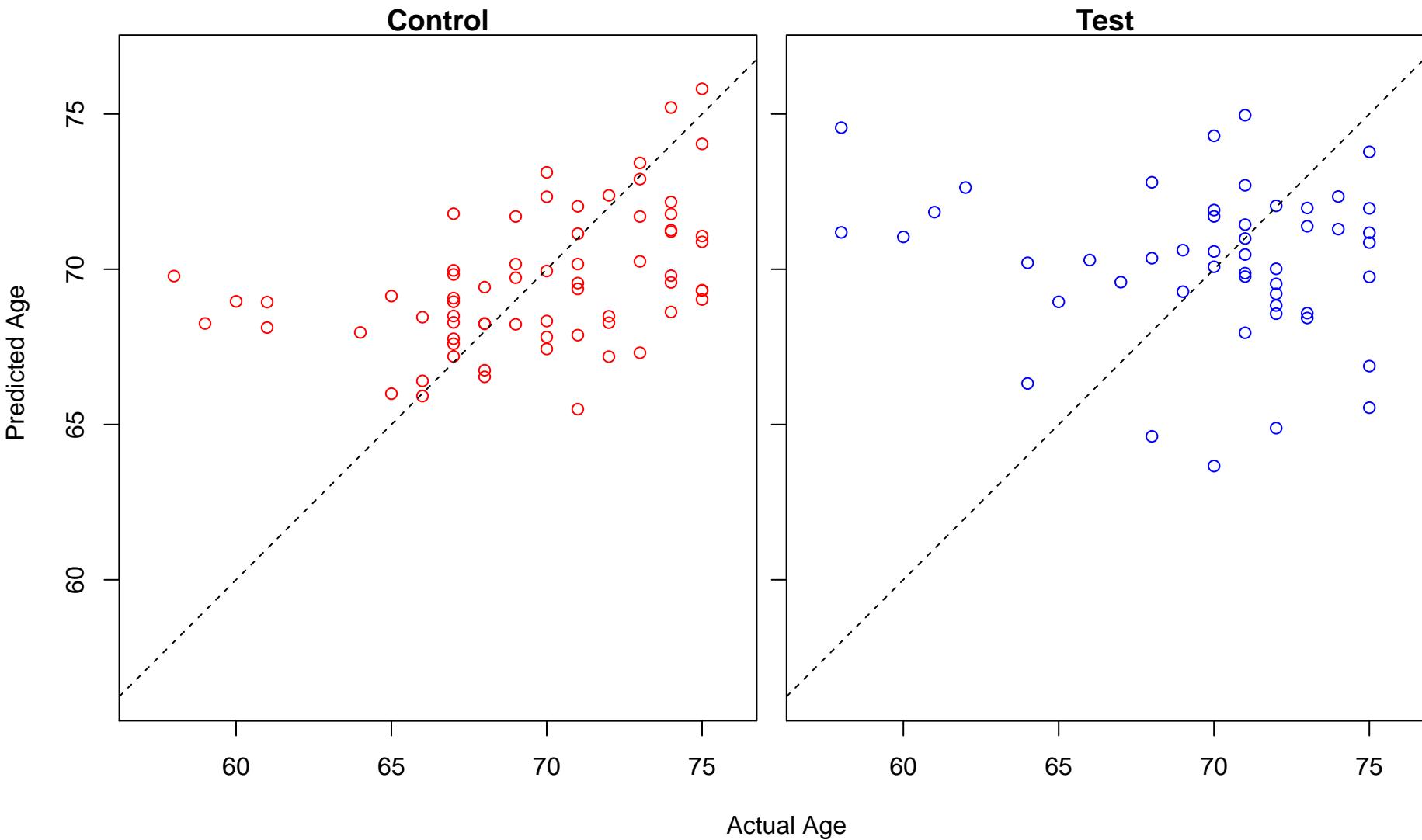
regulation of apoptotic cell clearance (Score: 0.625989)



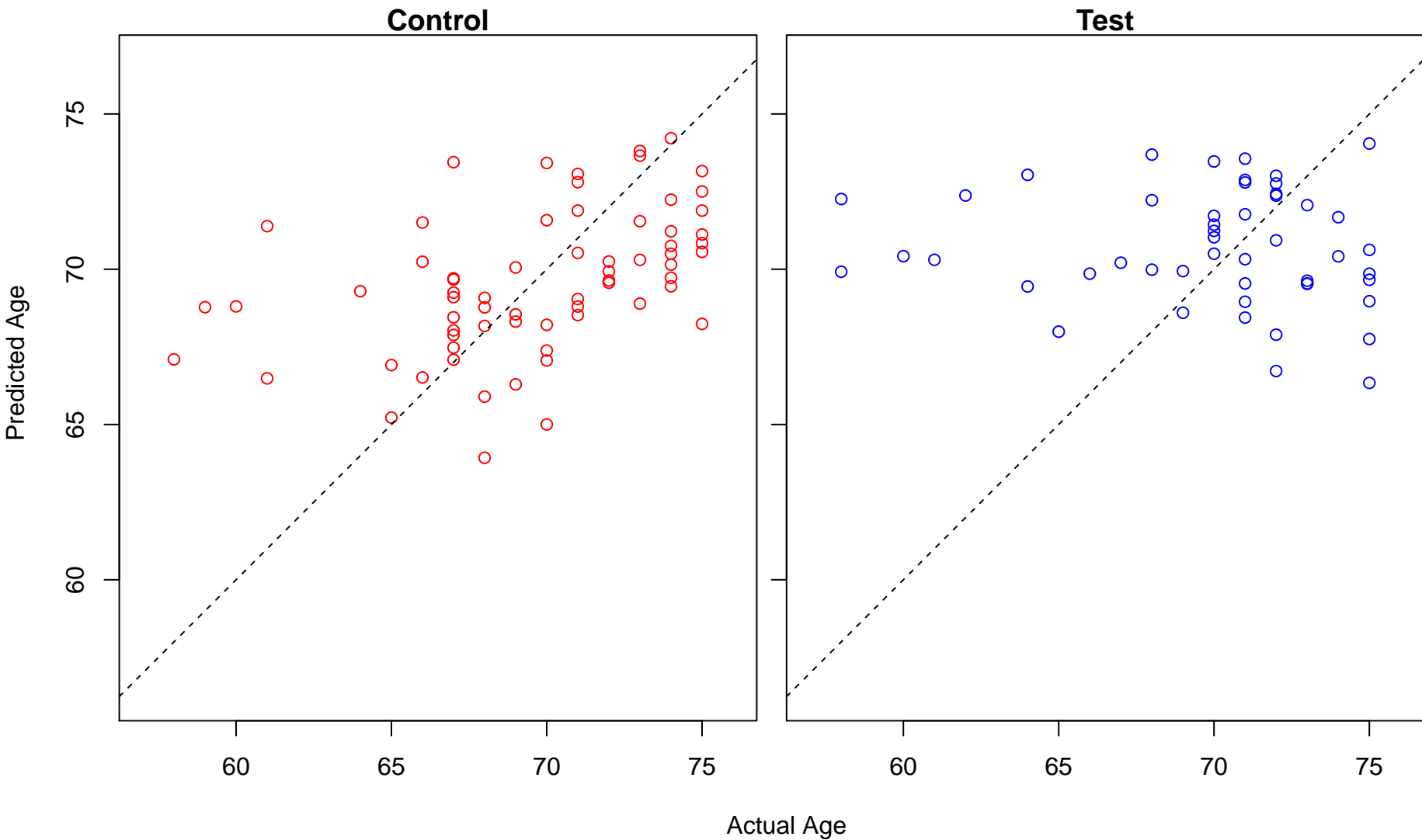
n of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling



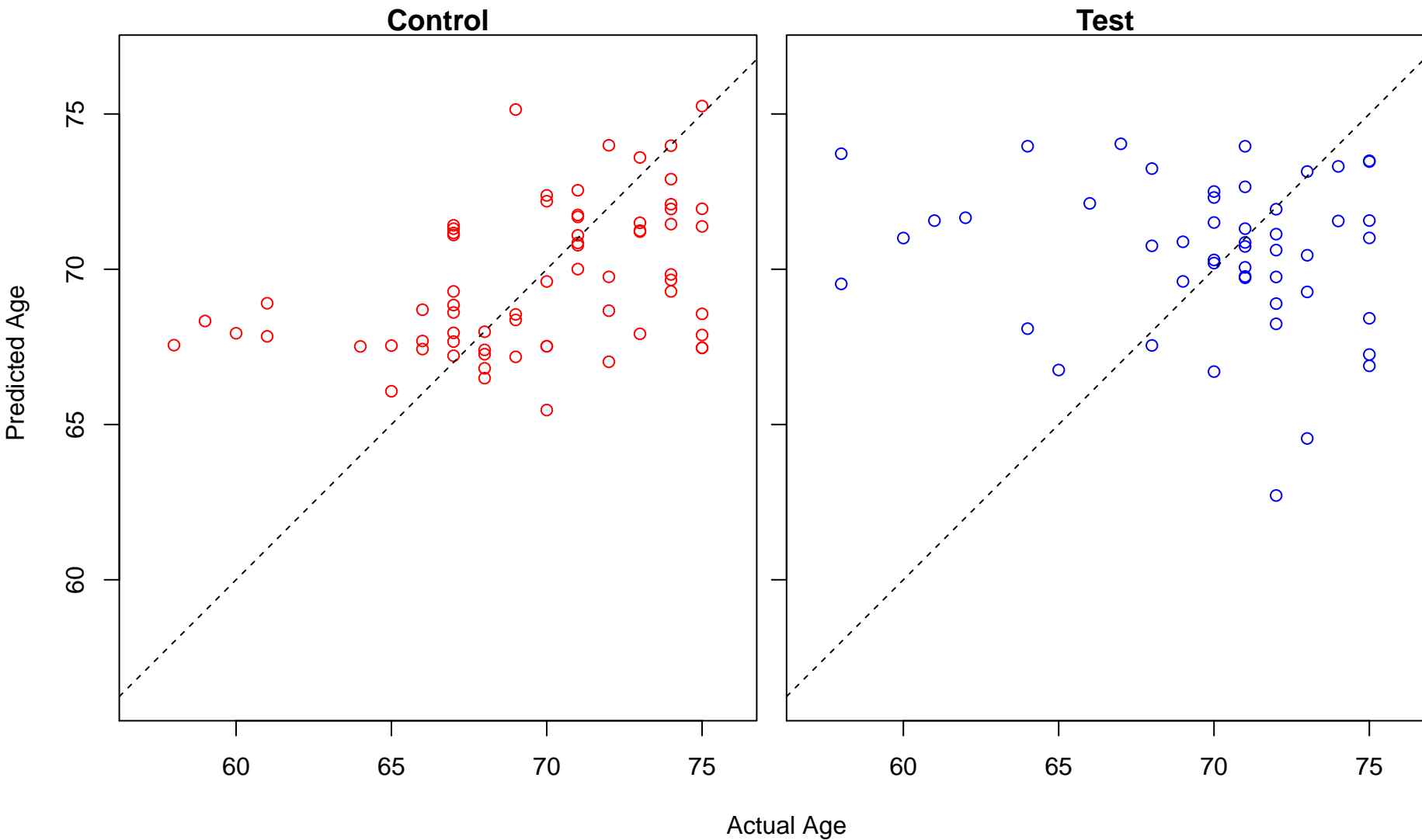
presynaptic process involved in synaptic transmission (Score: 0.625555)



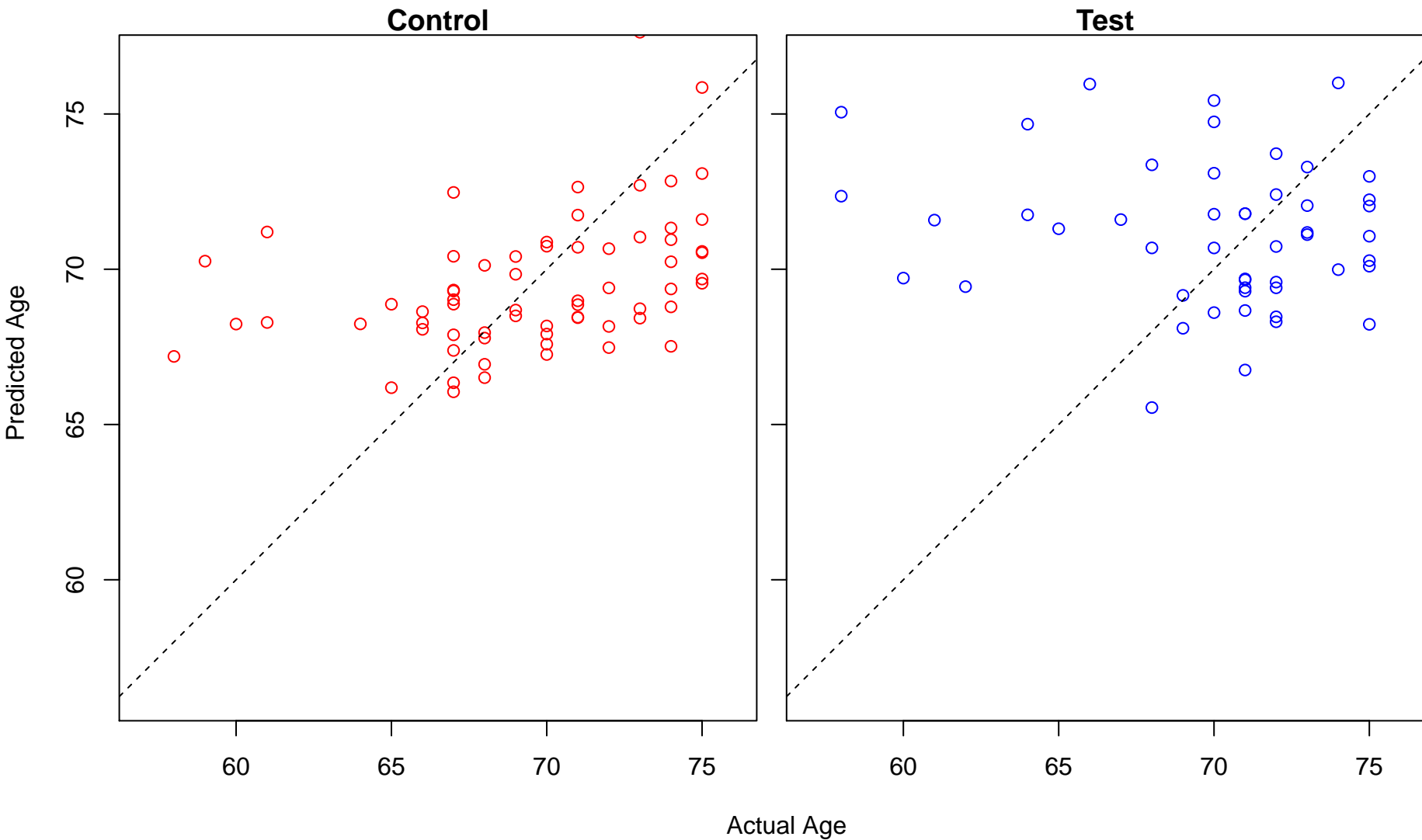
miRNA metabolic process (Score: 0.625020)



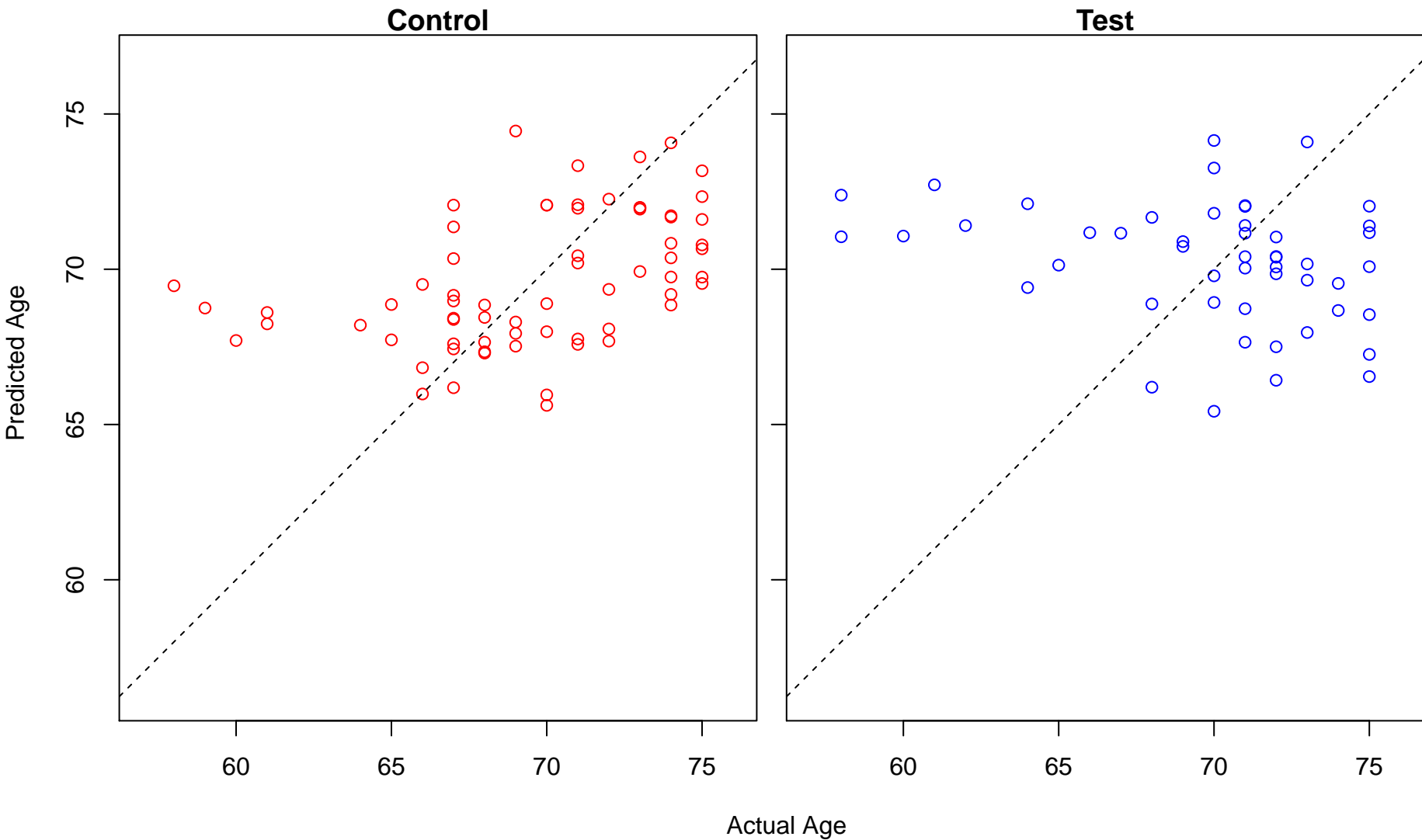
pyrimidine nucleotide–sugar transmembrane transport (Score: 0.624482)



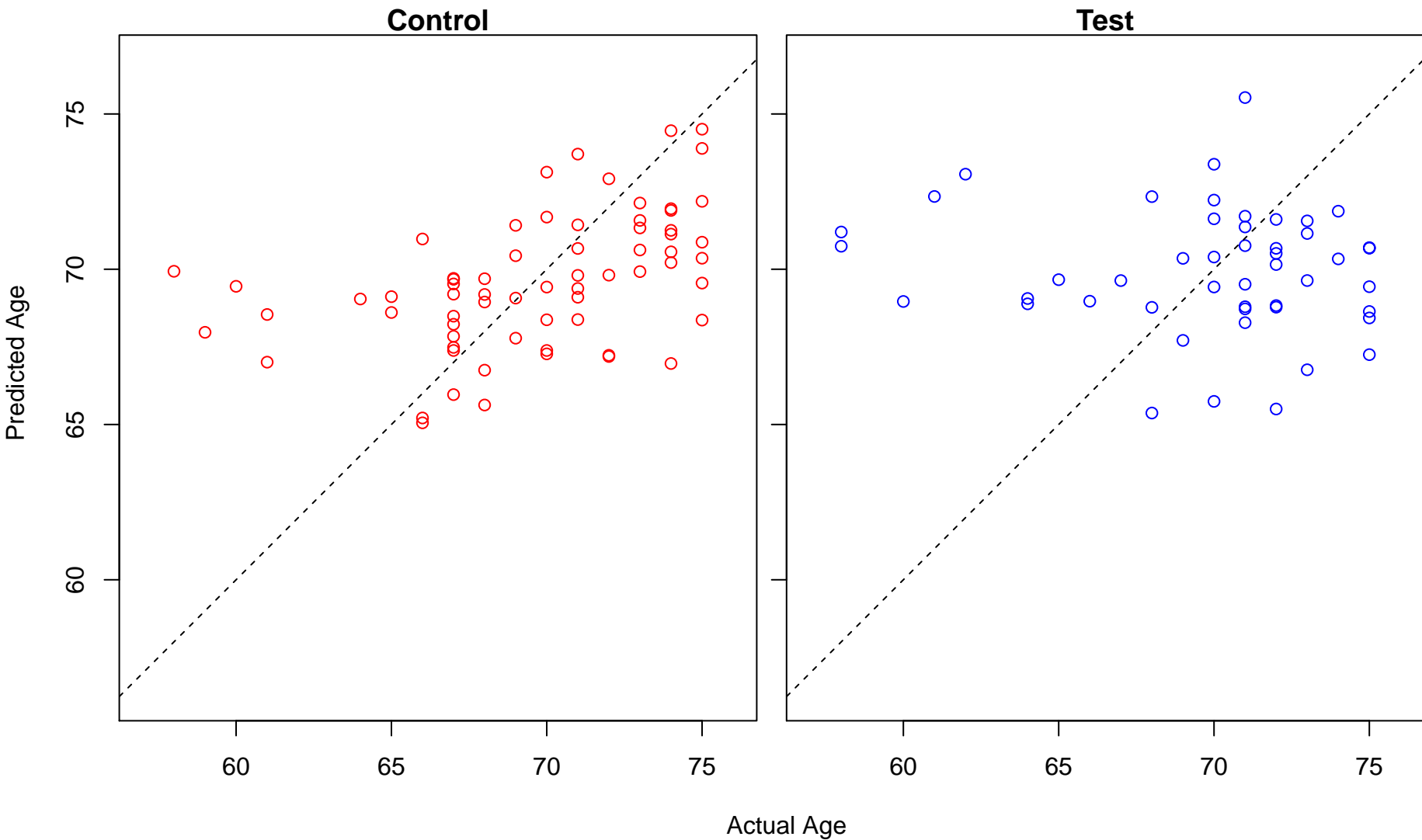
regulation of hydrogen peroxide metabolic process (Score: 0.624235)



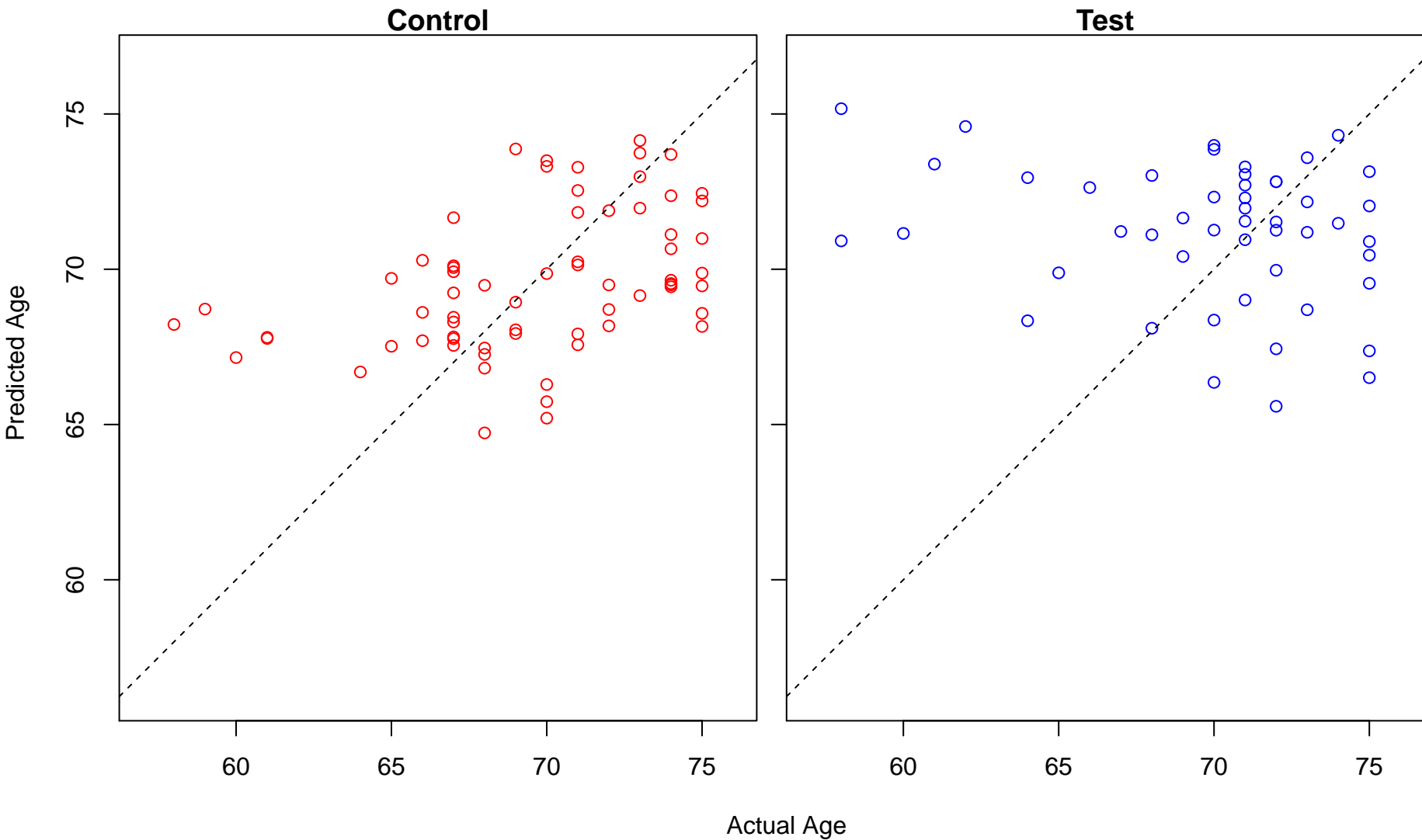
axon extension (Score: 0.624115)



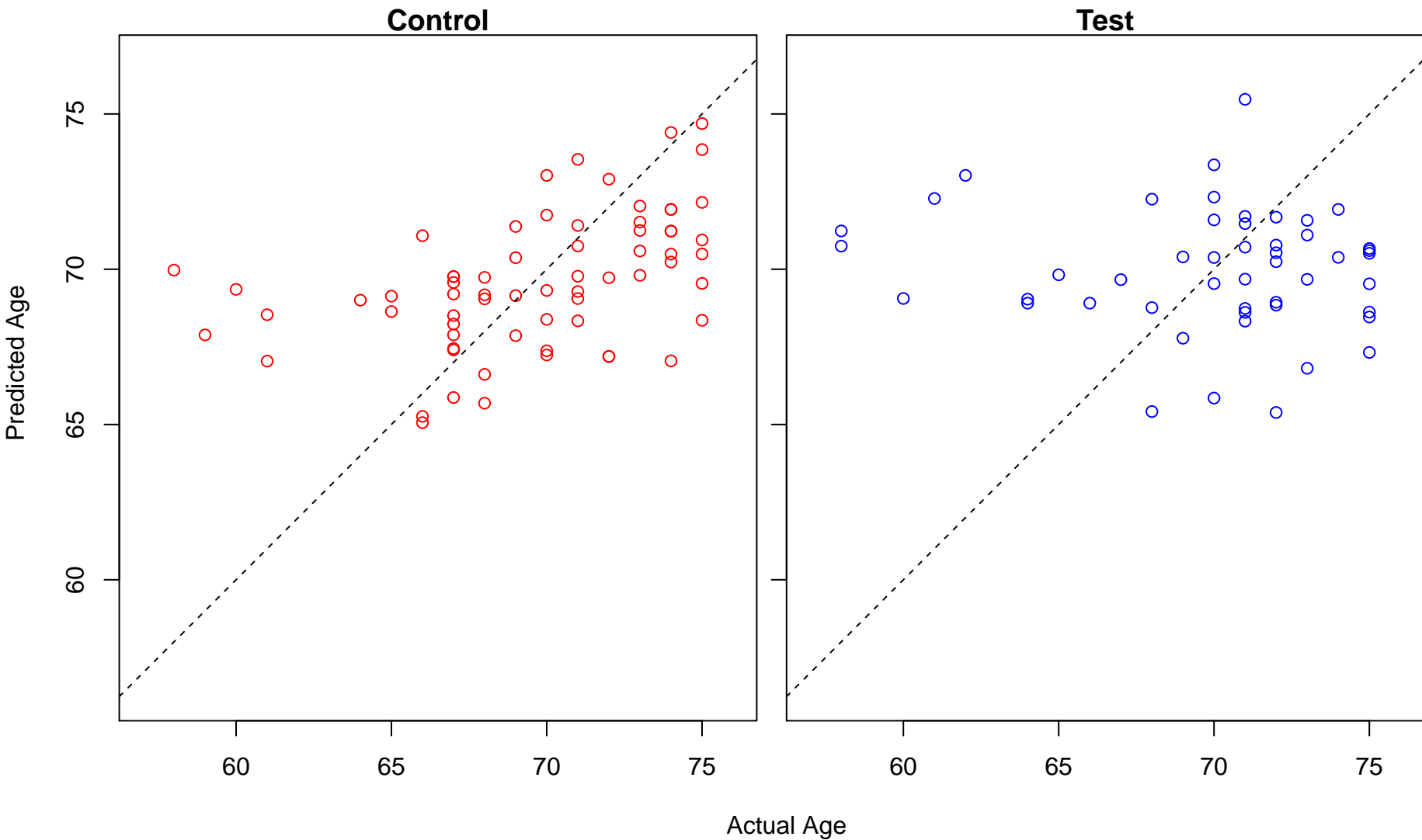
vascular endothelial growth factor signaling pathway (Score: 0.623763)



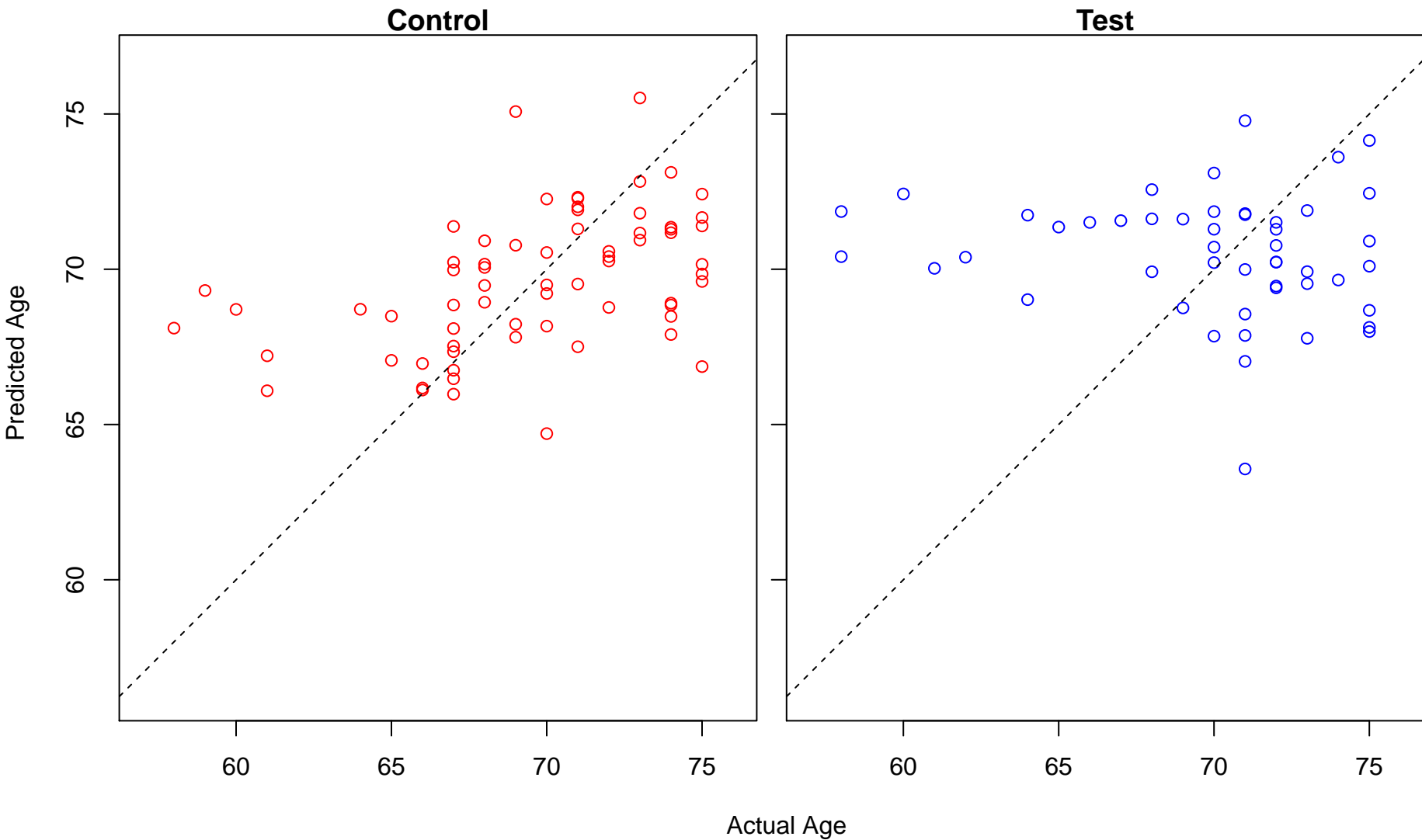
positive regulation of mRNA metabolic process (Score: 0.622554)



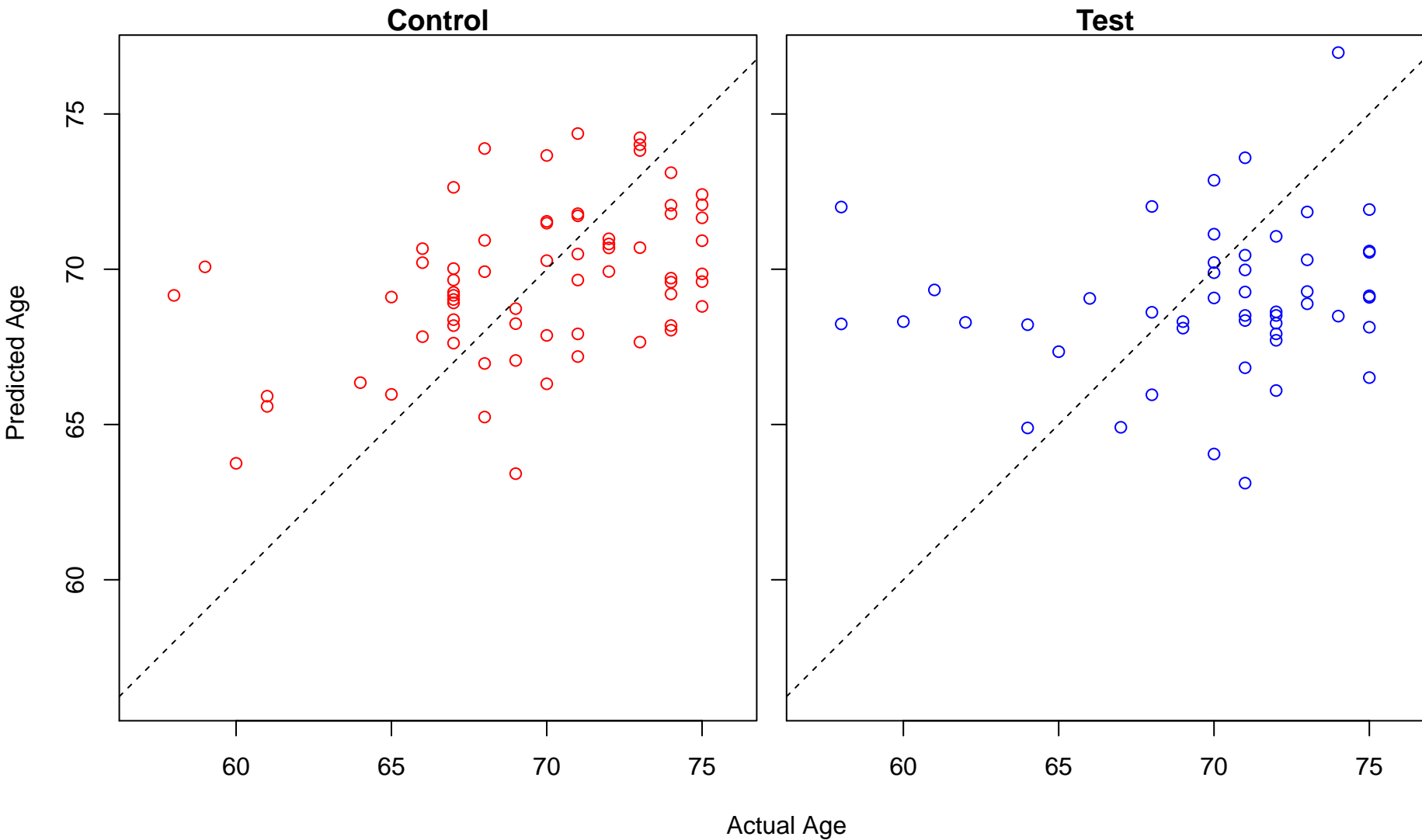
positive regulation of endothelial cell chemotaxis (Score: 0.621857)



positive regulation of fibroblast apoptotic process (Score: 0.621404)

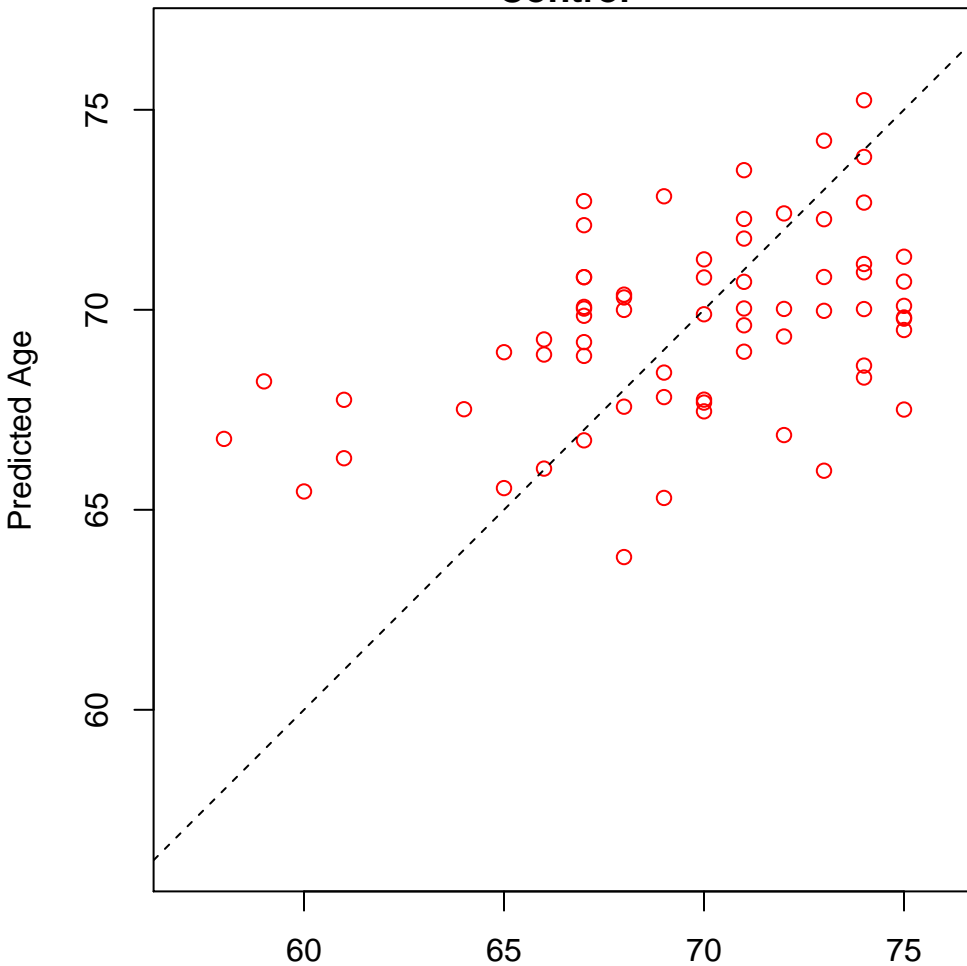


macropinocytosis (Score: 0.620872)

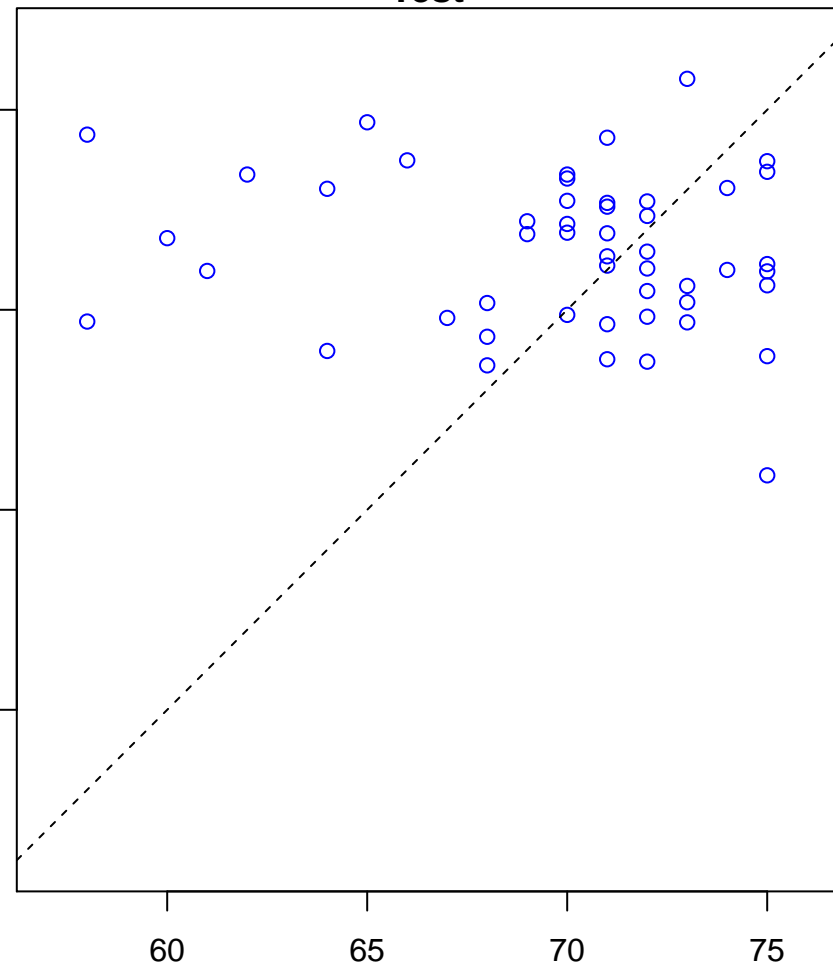


carbohydrate transmembrane transport (Score: 0.620680)

Control

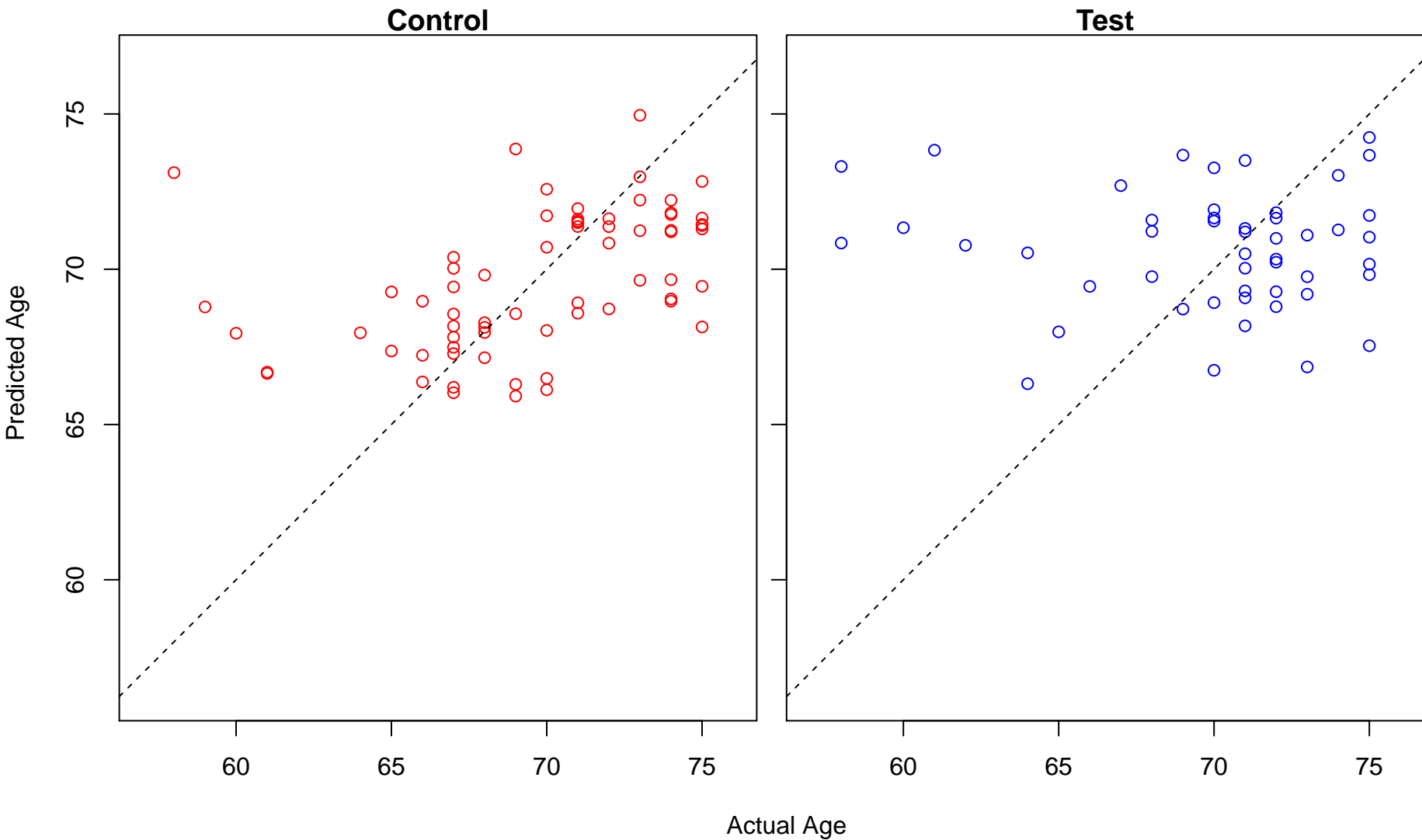


Test

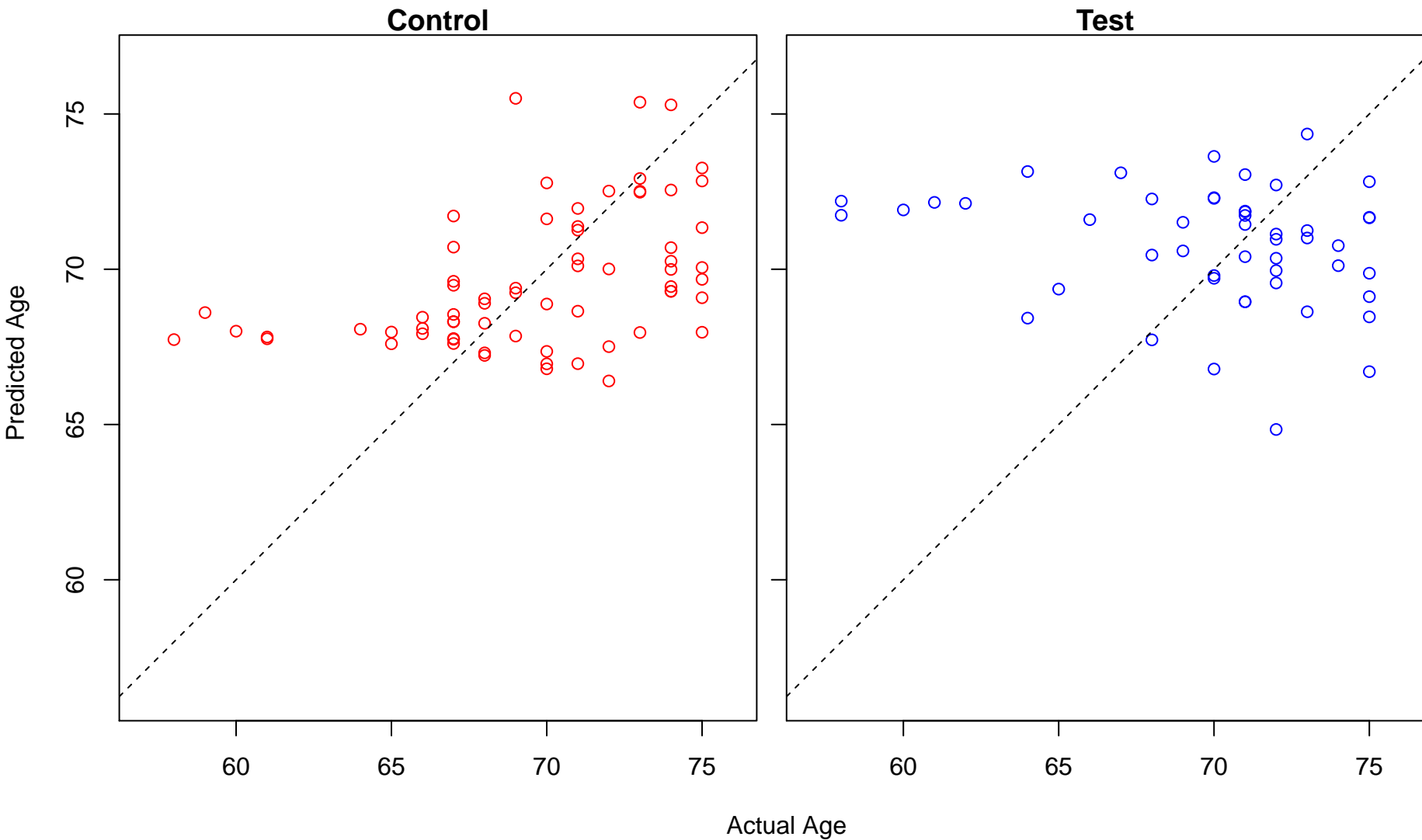


Actual Age

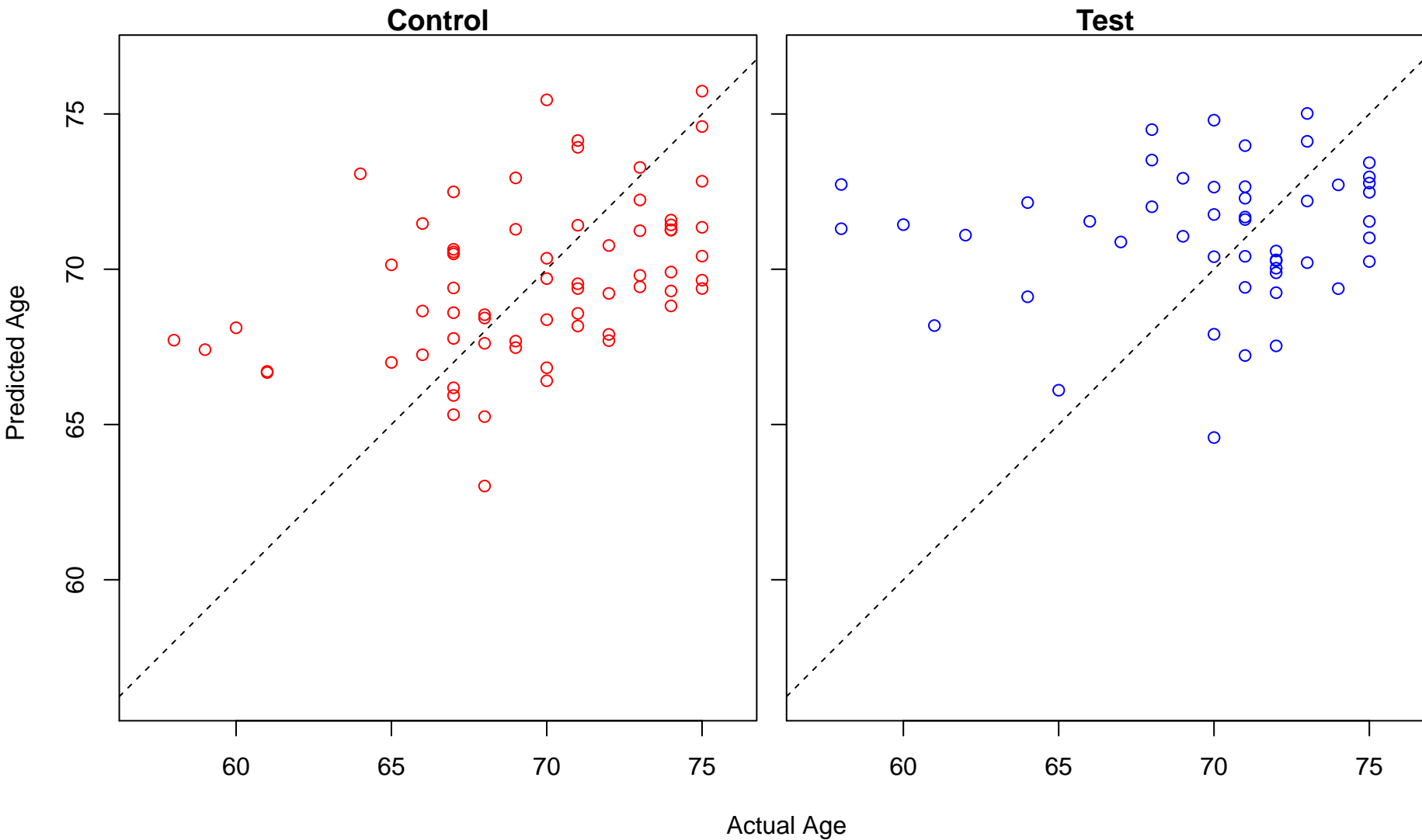
endothelial cell migration (Score: 0.620465)



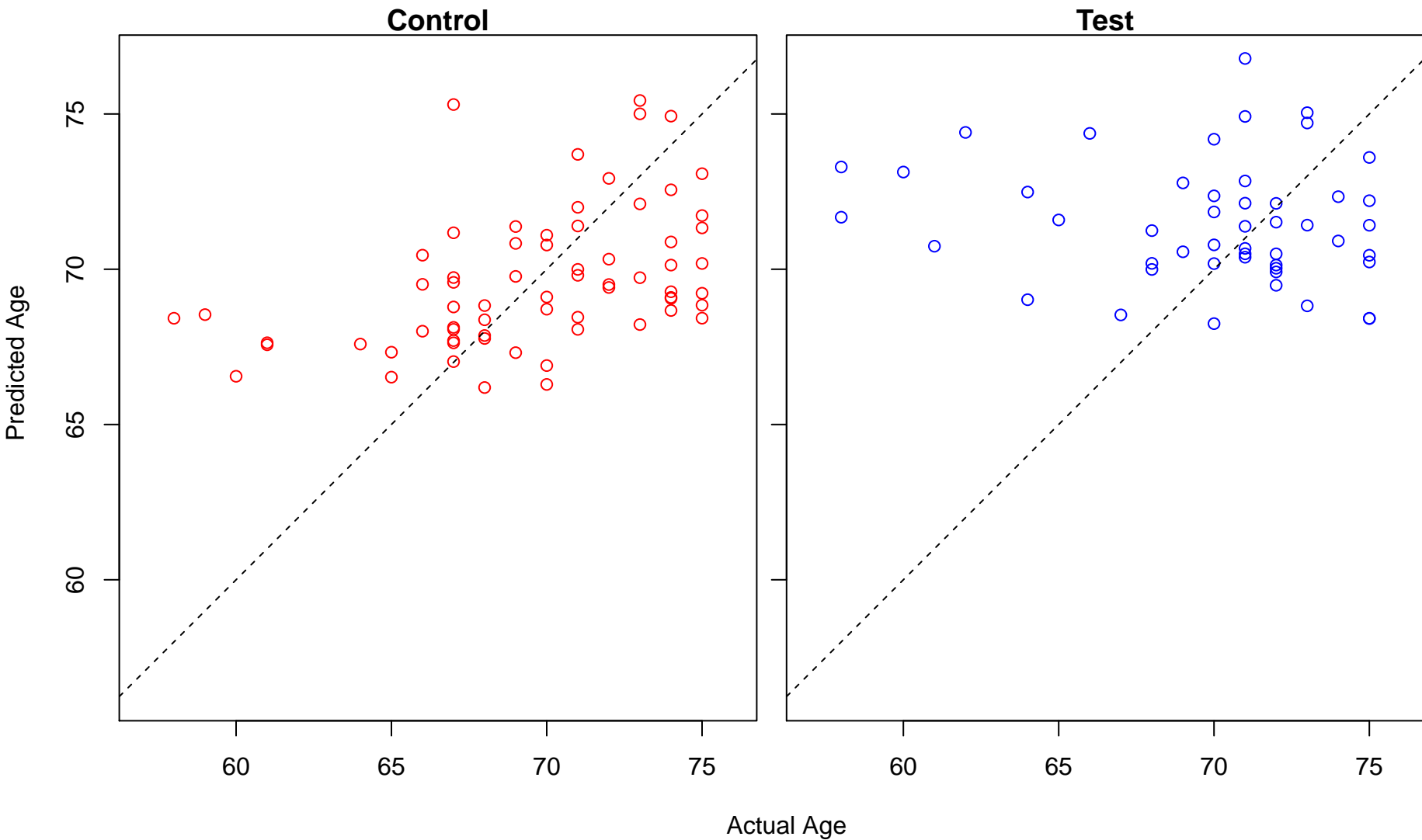
carbohydrate derivative transport (Score: 0.619741)



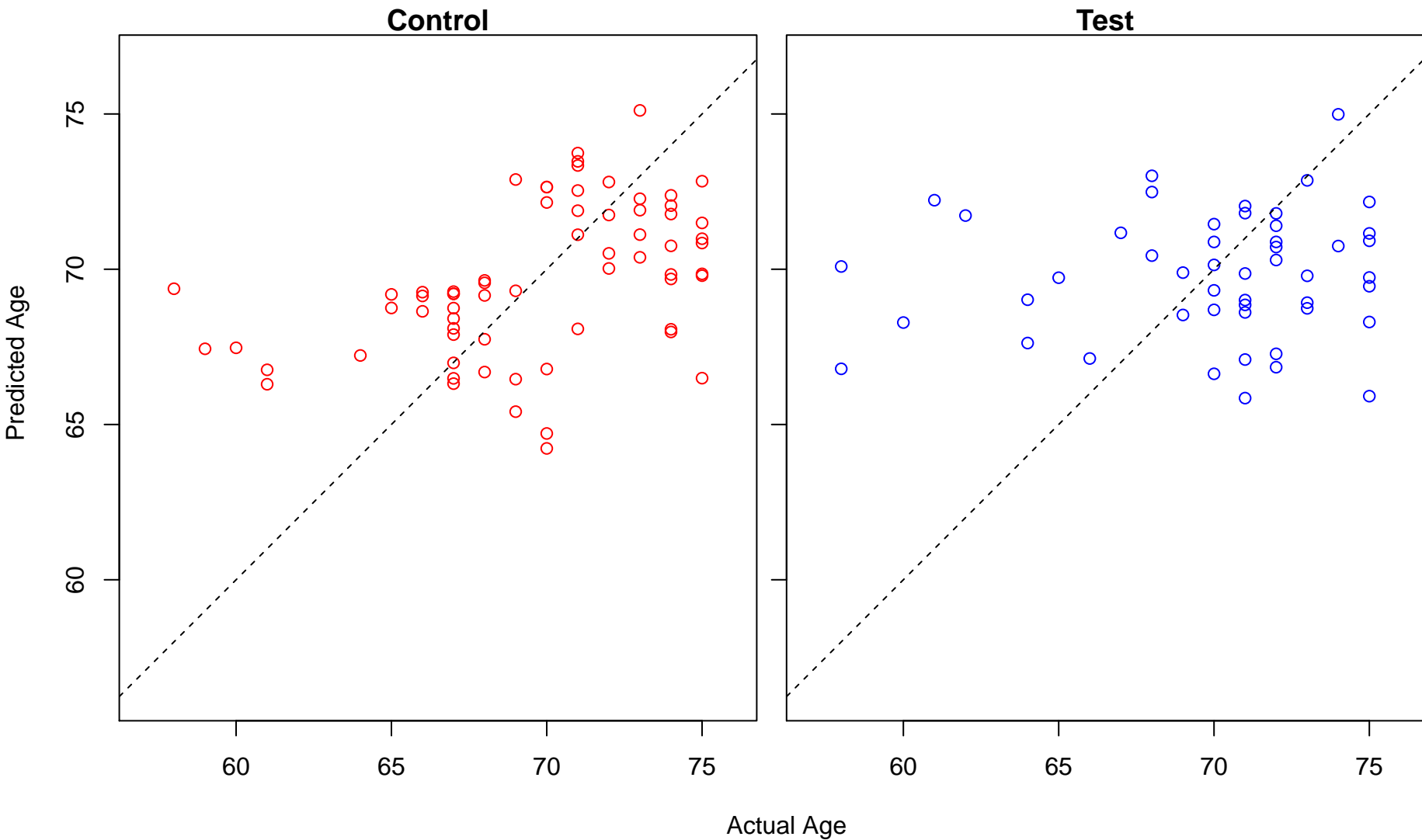
embryonic hemopoiesis (Score: 0.619037)



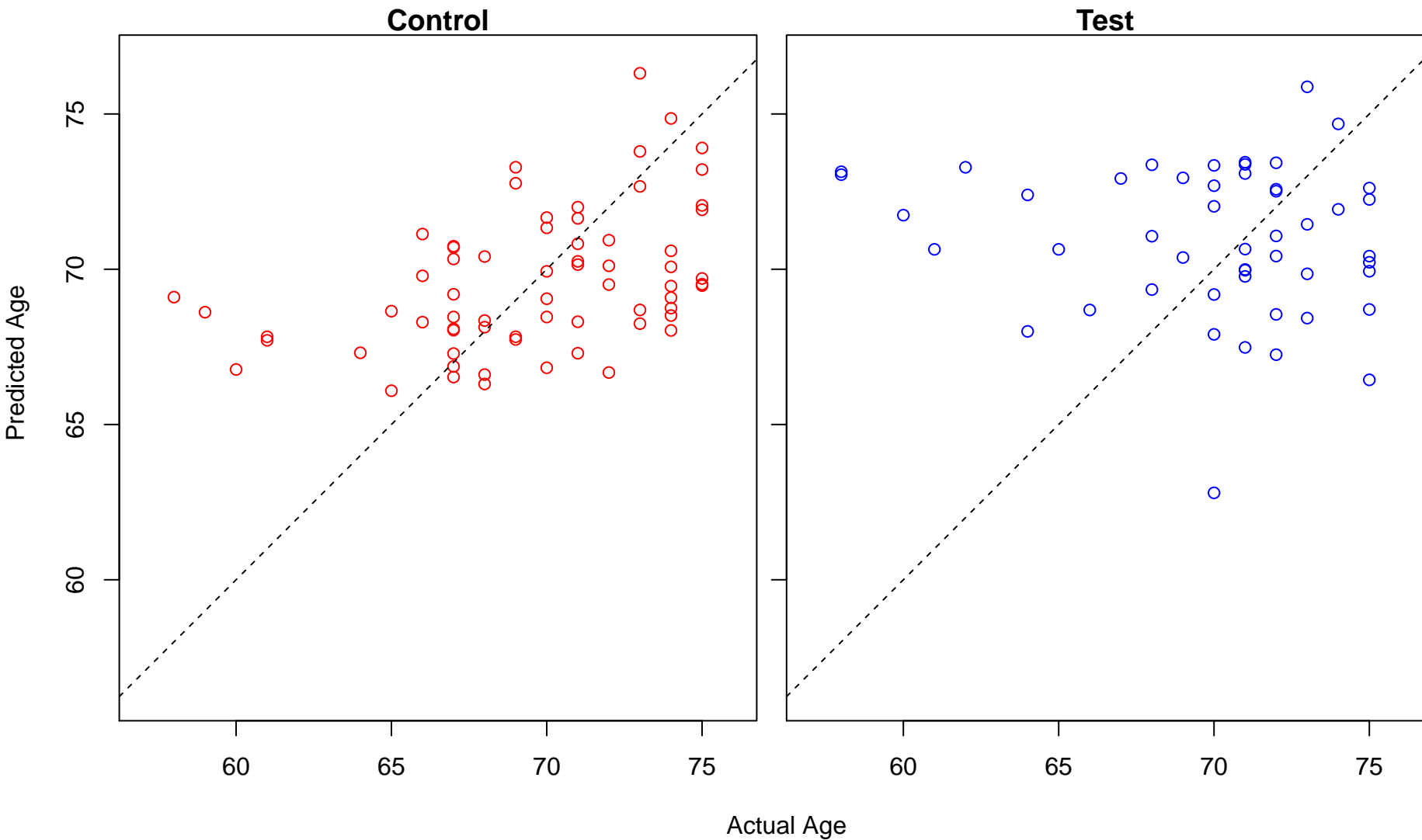
sulfur compound transport (Score: 0.618991)



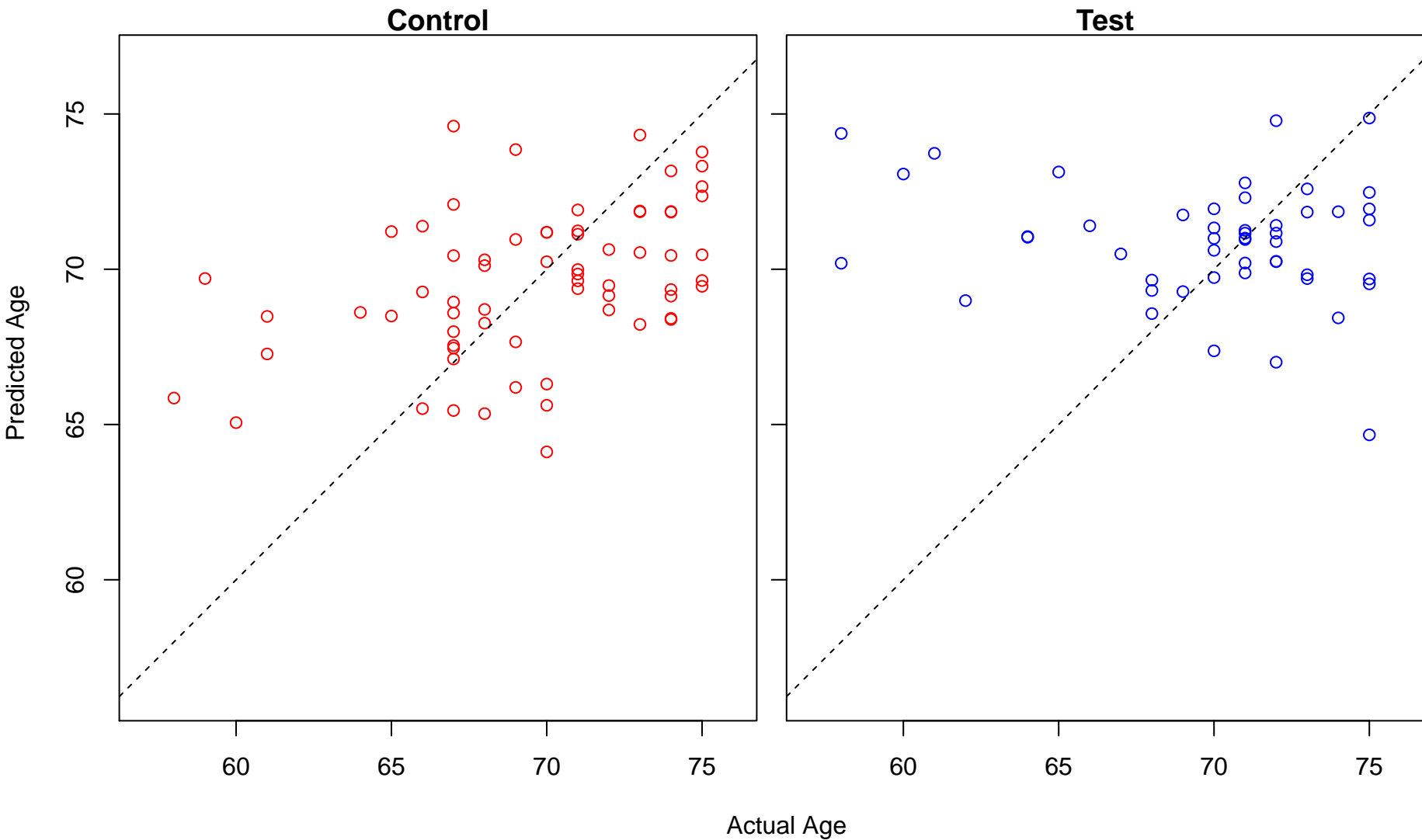
regulation of type B pancreatic cell development (Score: 0.618421)



cellular response to sterol (Score: 0.618137)

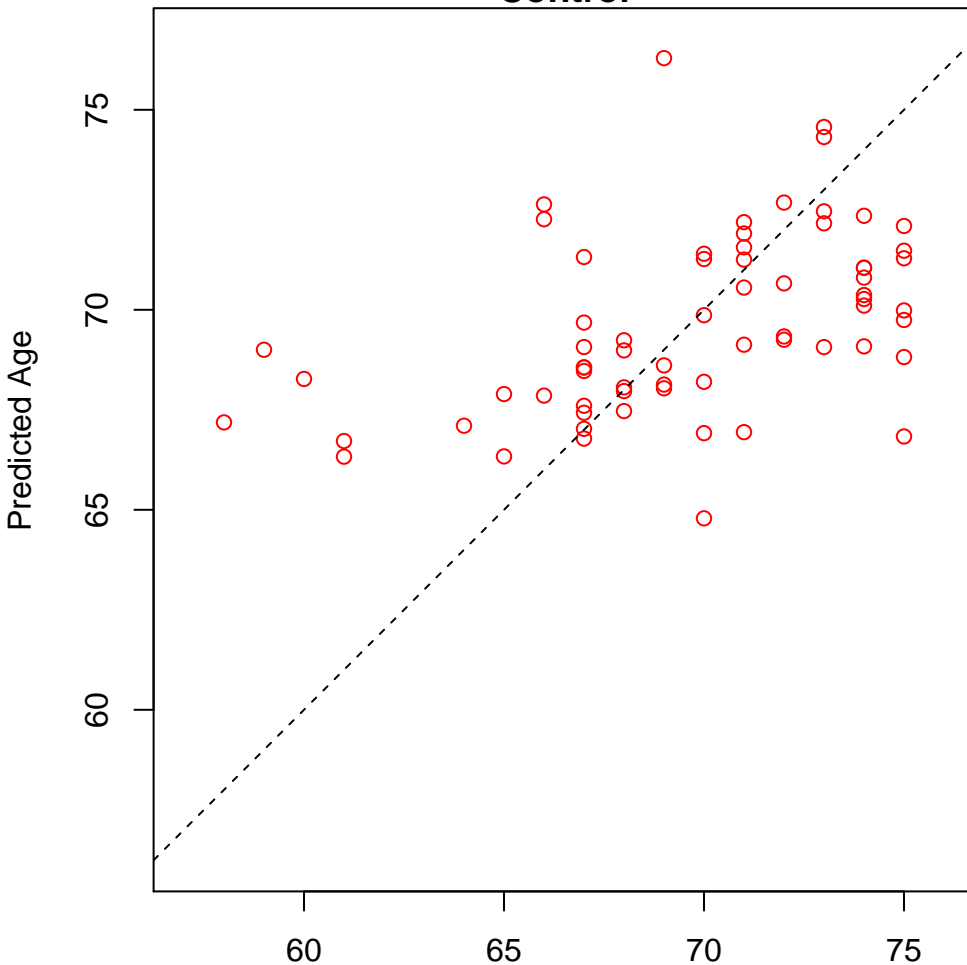


positive regulation of striated muscle contraction (Score: 0.617760)

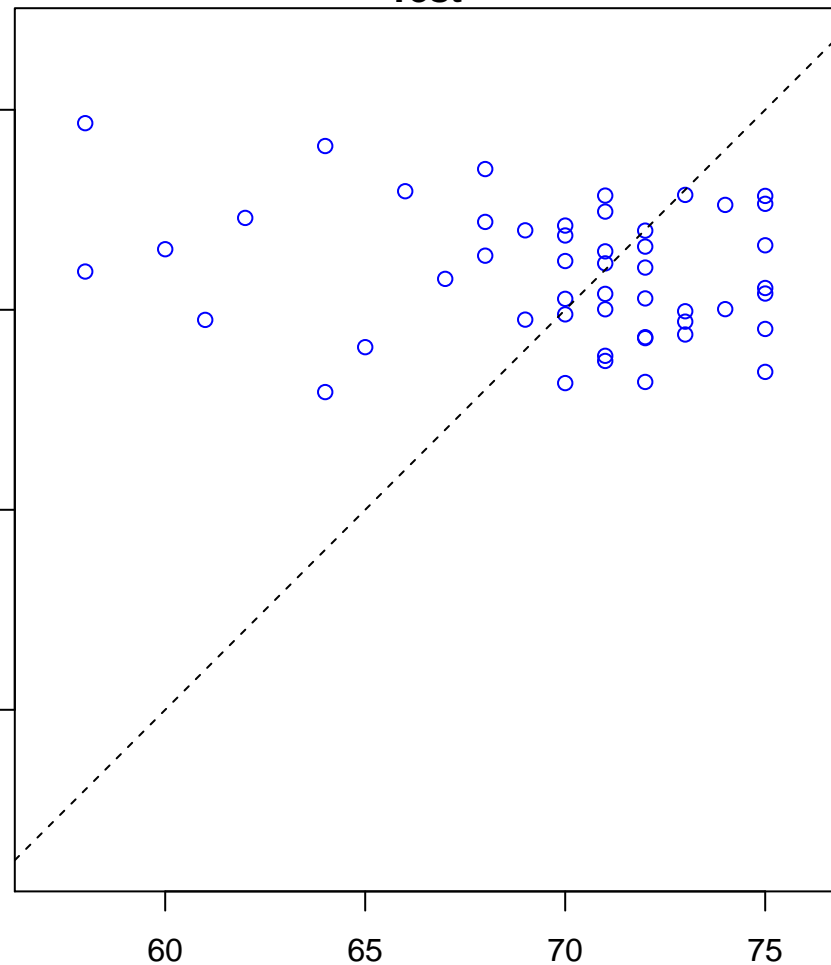


anterograde synaptic vesicle transport (Score: 0.617346)

Control



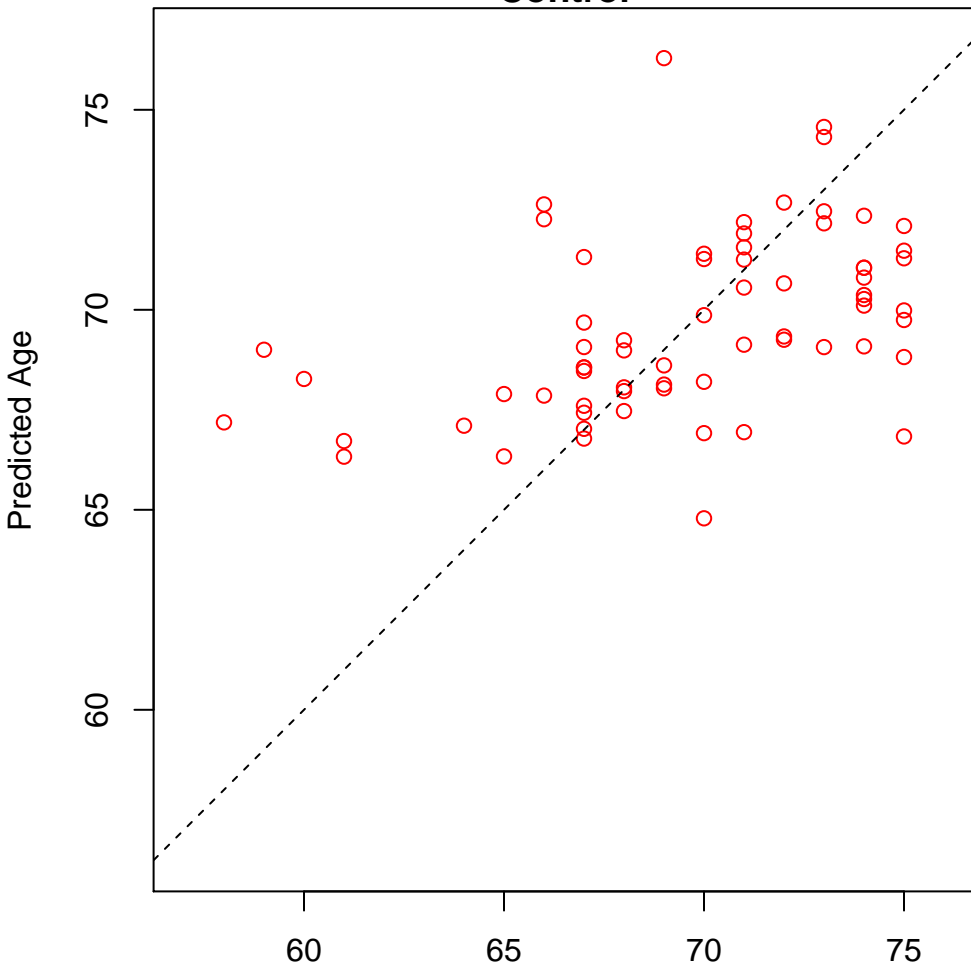
Test



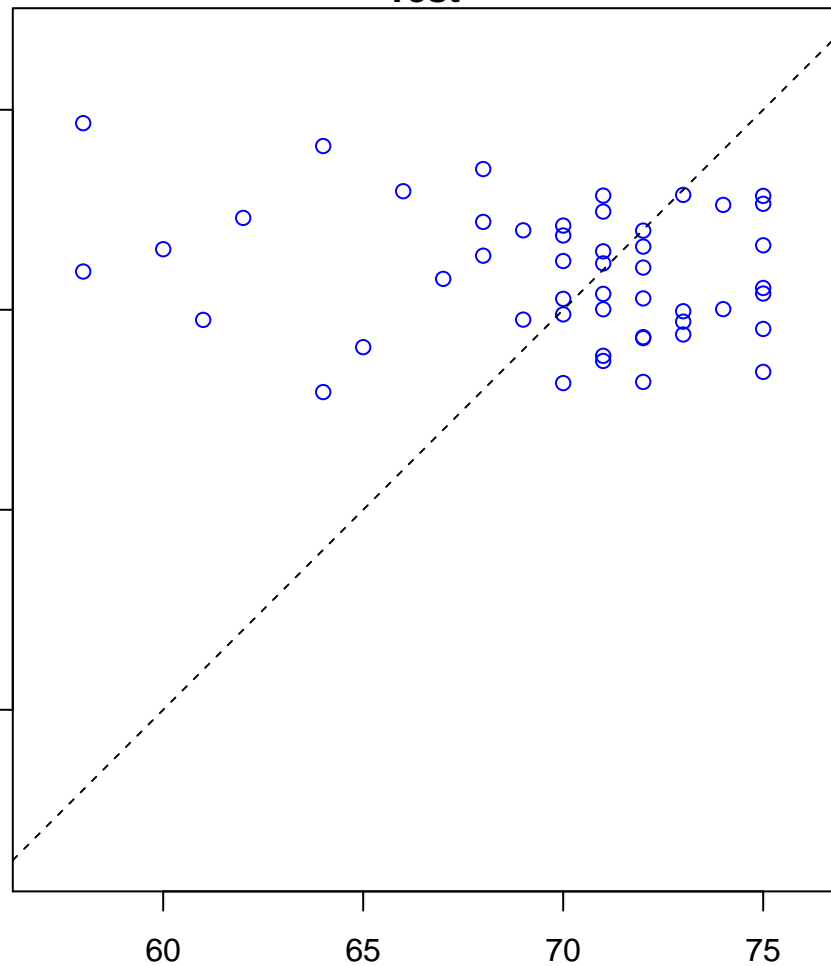
Actual Age

synaptic vesicle cytoskeletal transport (Score: 0.617346)

Control

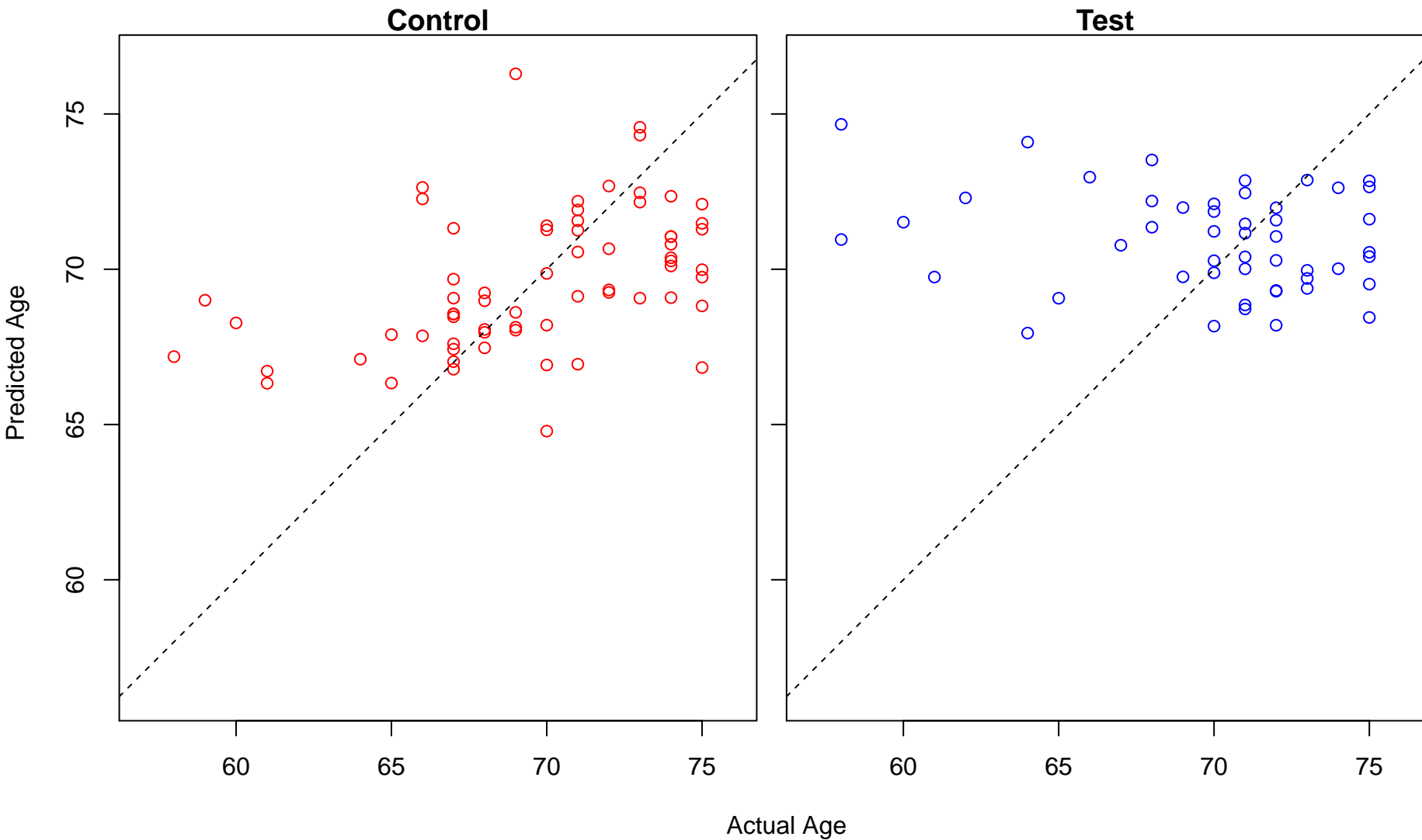


Test

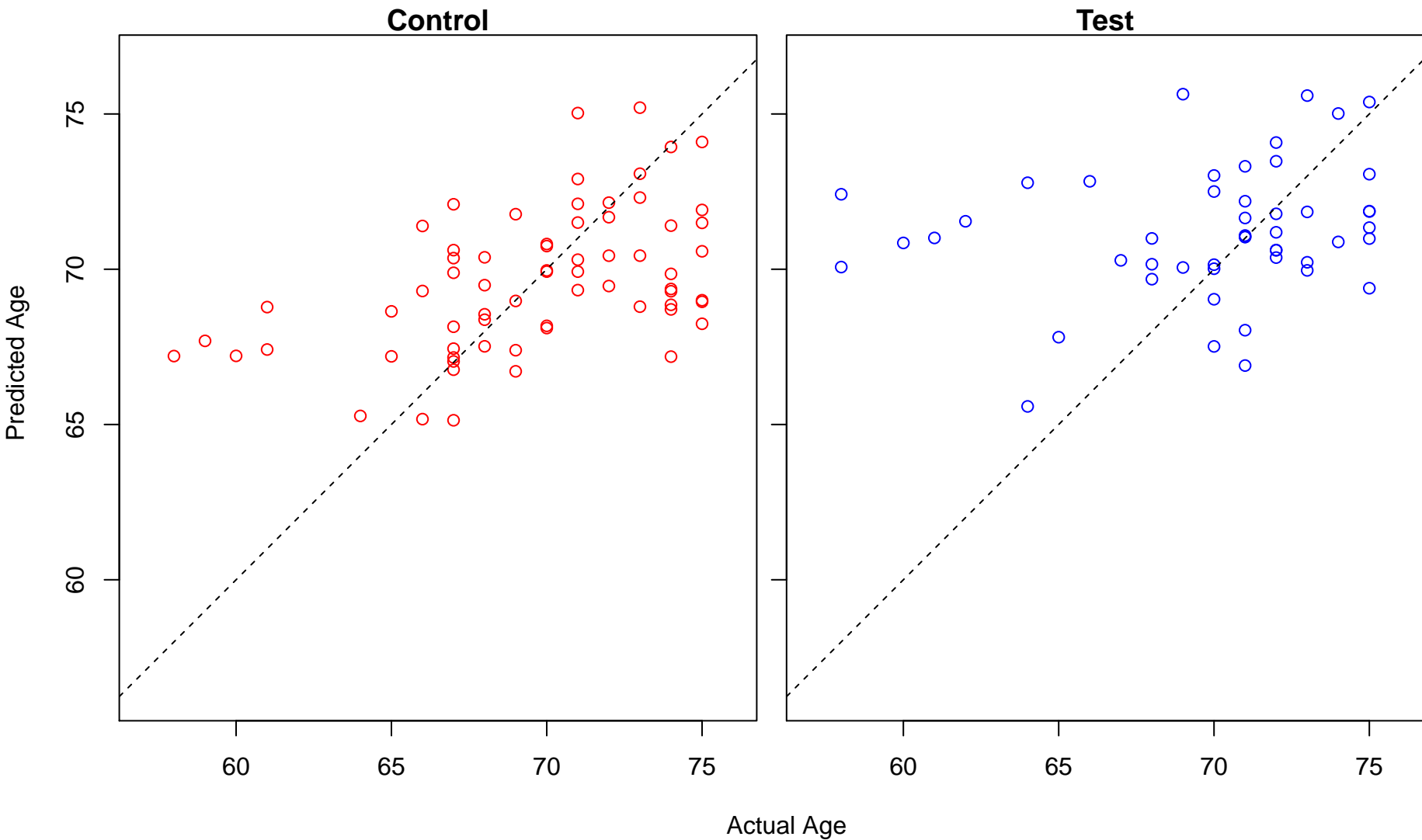


Actual Age

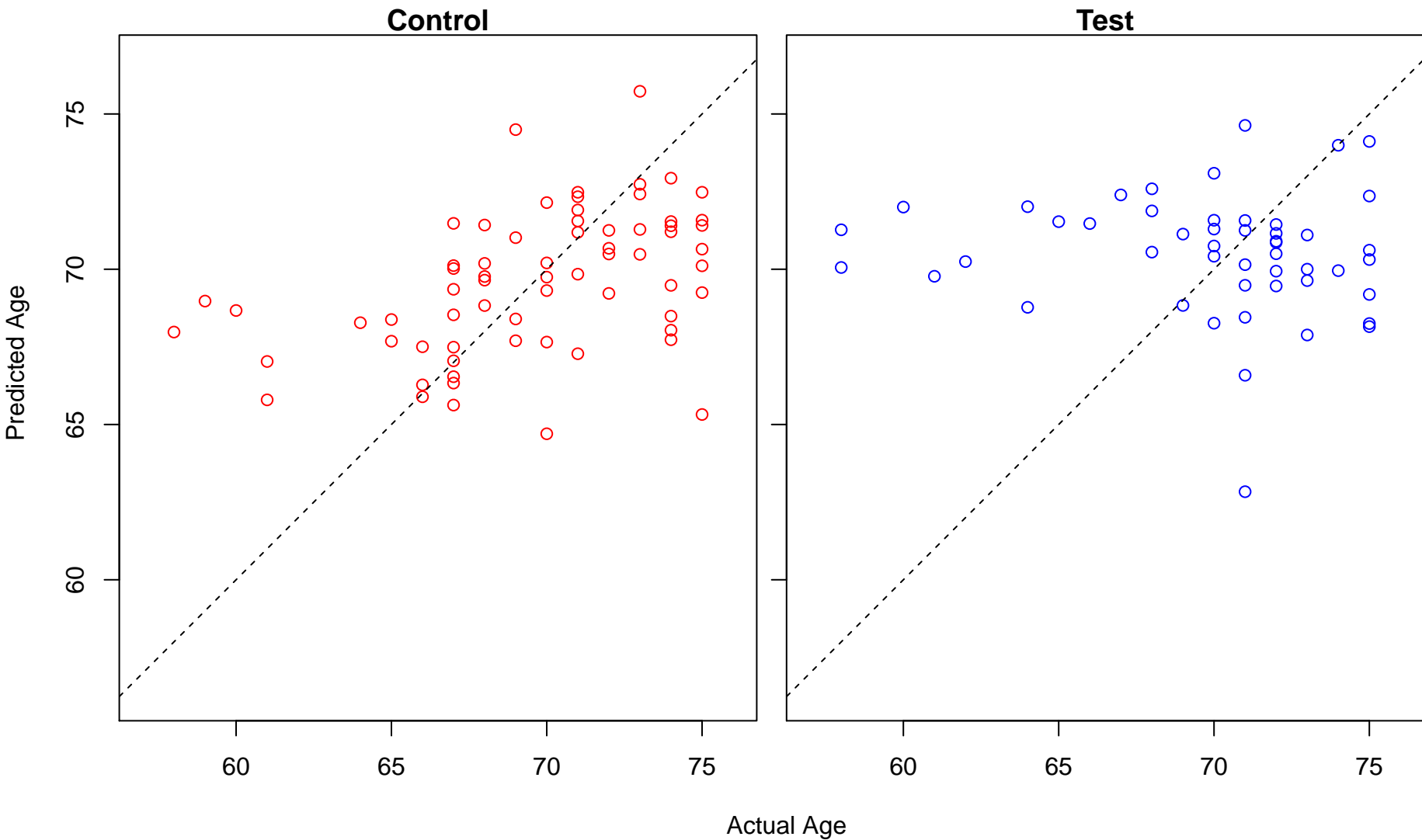
synaptic vesicle transport along microtubule (Score: 0.617346)



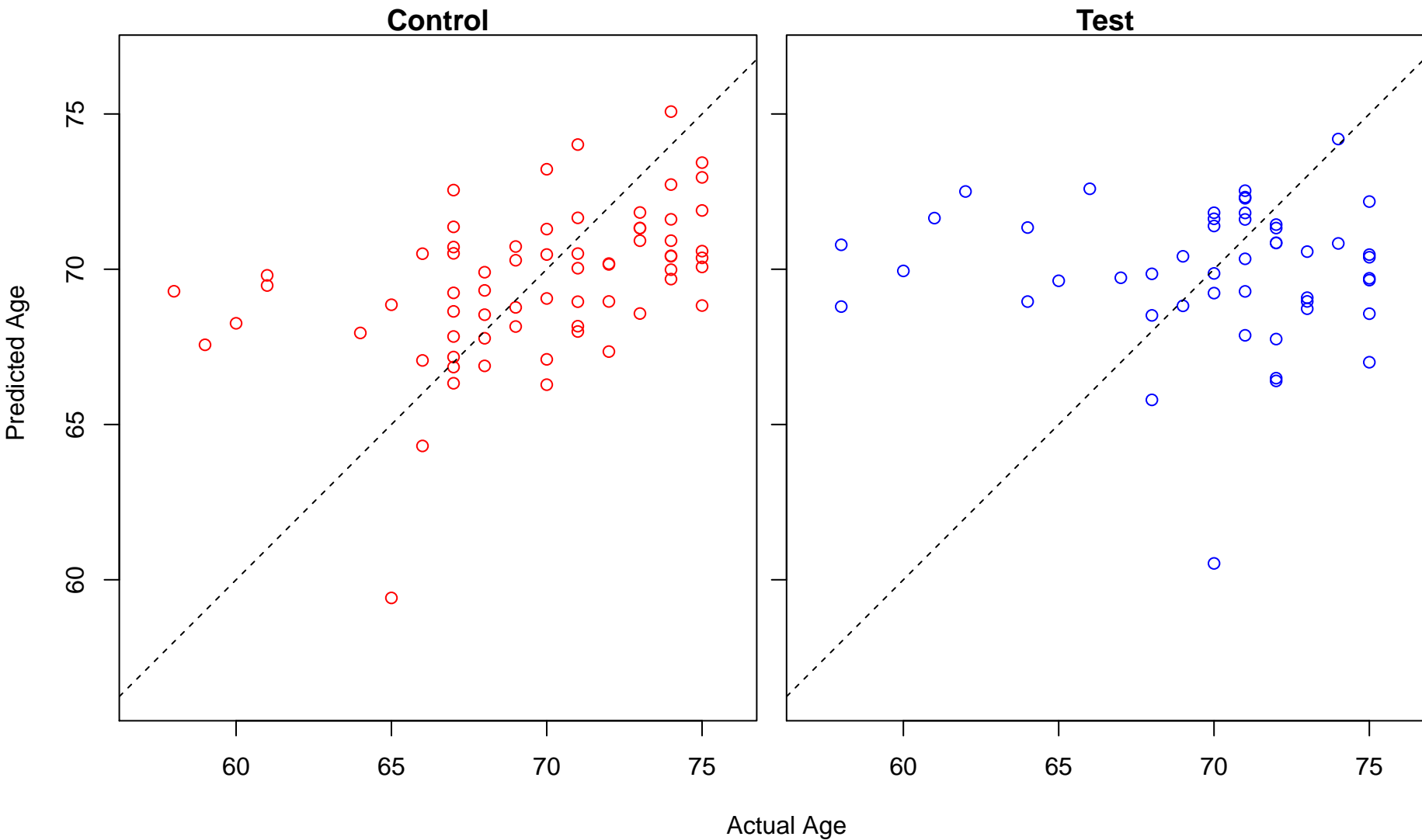
positive regulation of smoothened signaling pathway (Score: 0.616613)



regulation of fibroblast apoptotic process (Score: 0.616609)

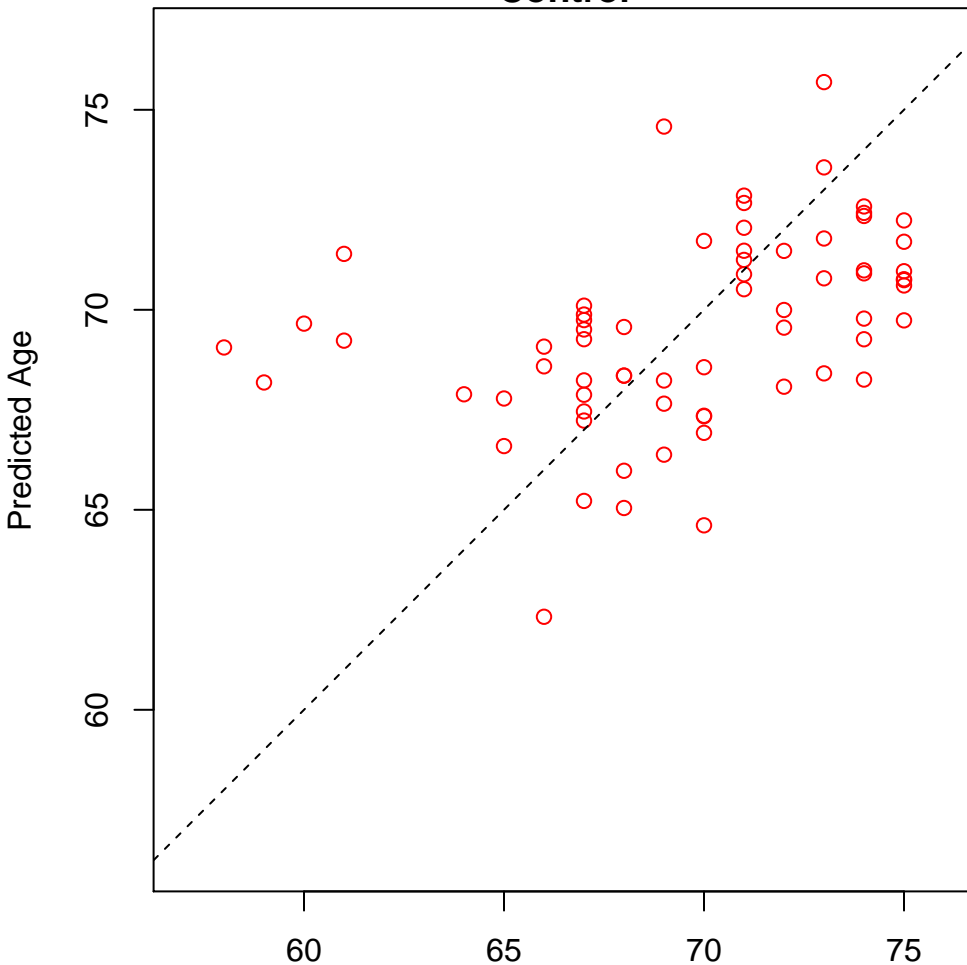


regulation of lymphocyte chemotaxis (Score: 0.616340)

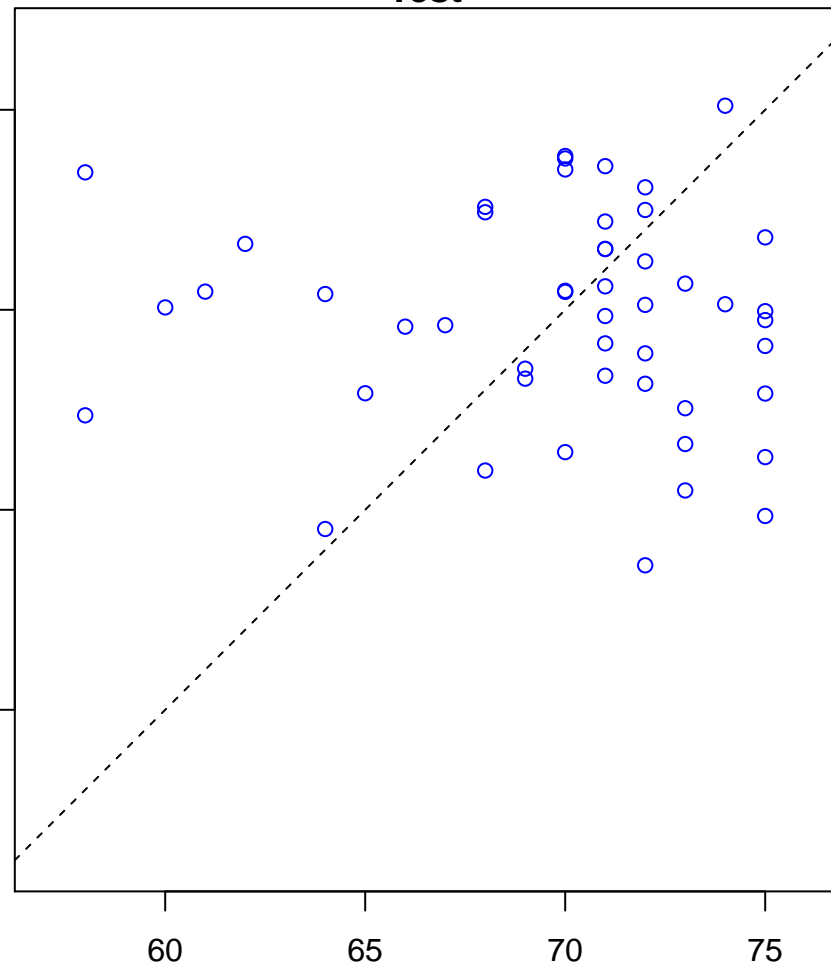


regulation of osteoblast proliferation (Score: 0.616316)

Control

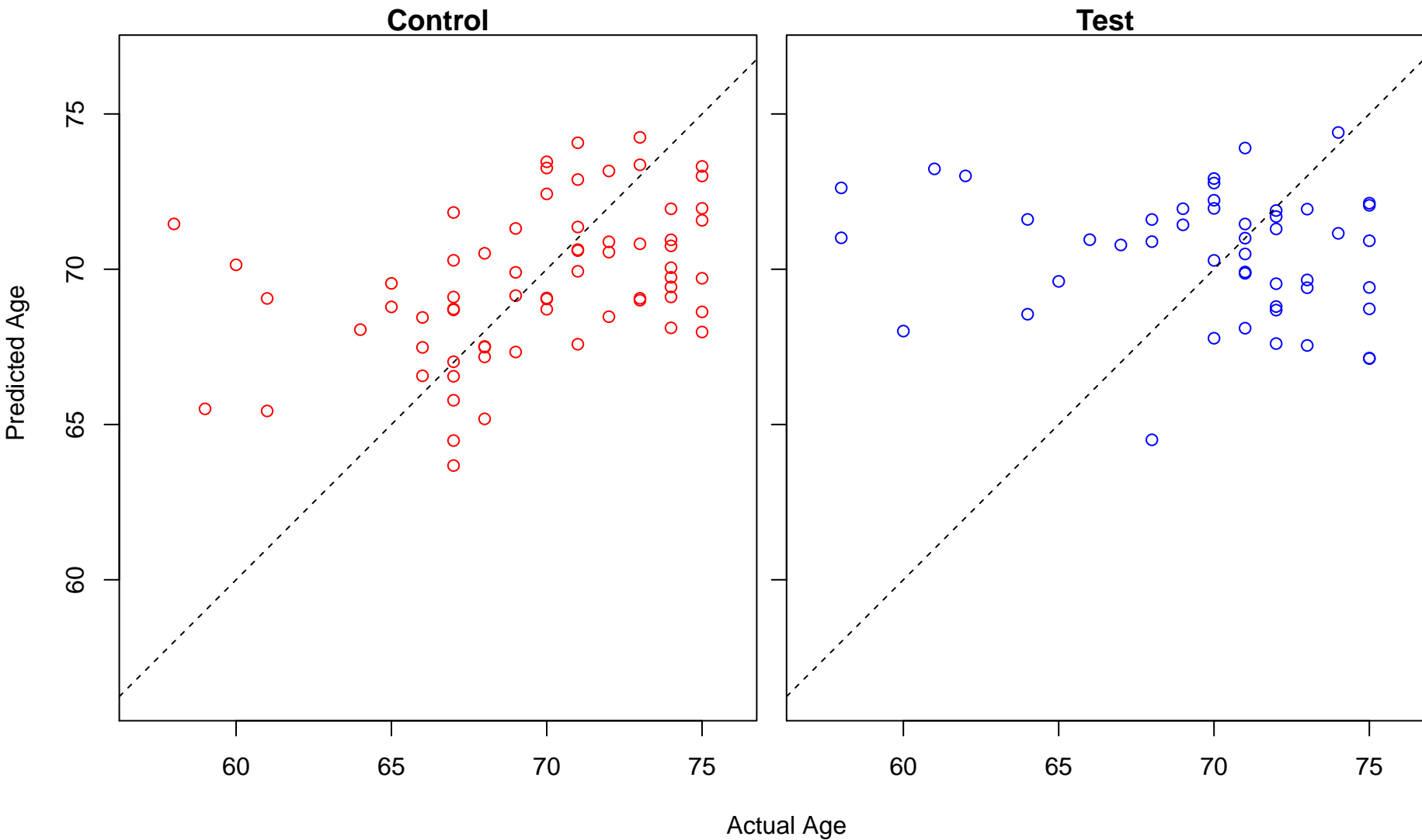


Test

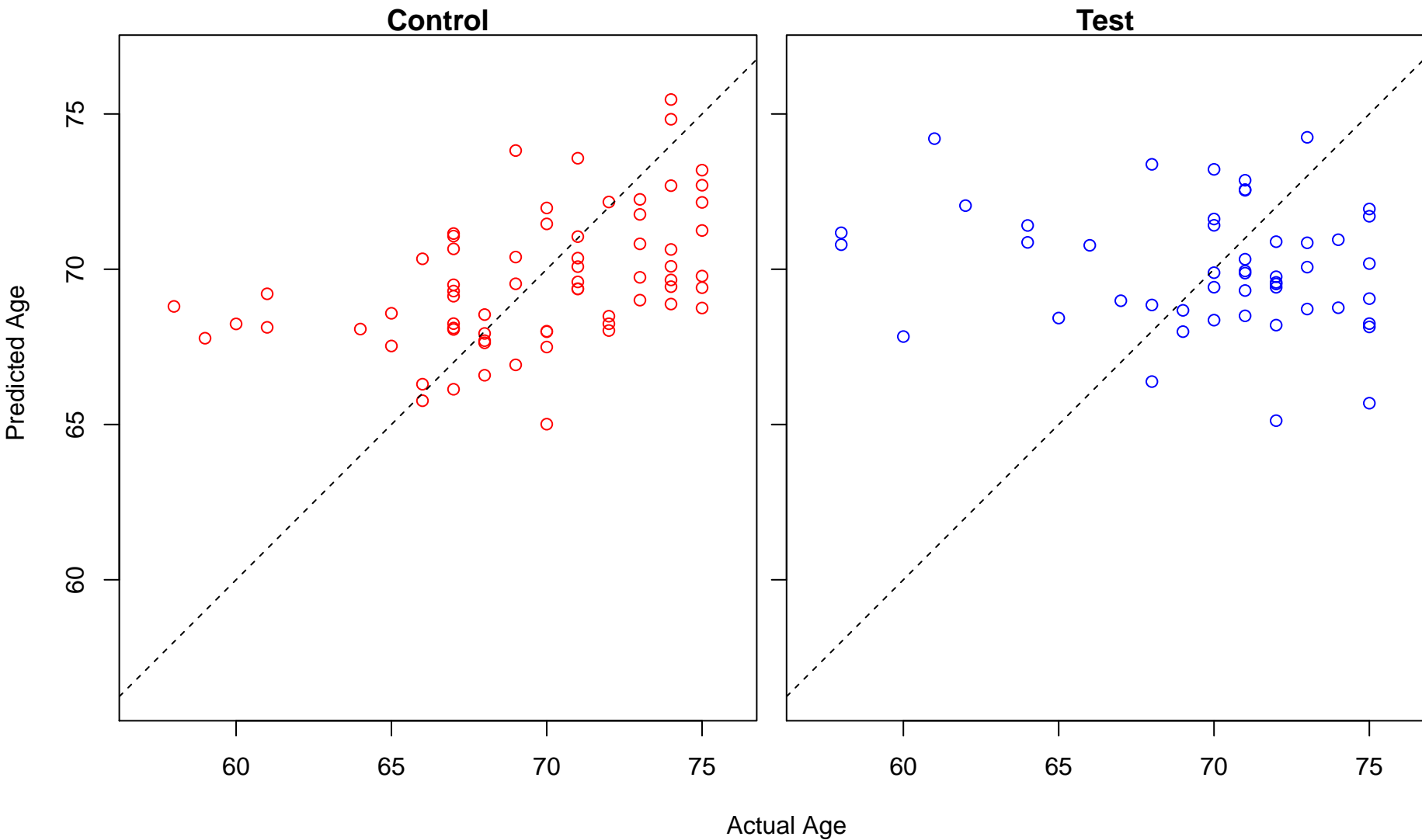


Actual Age

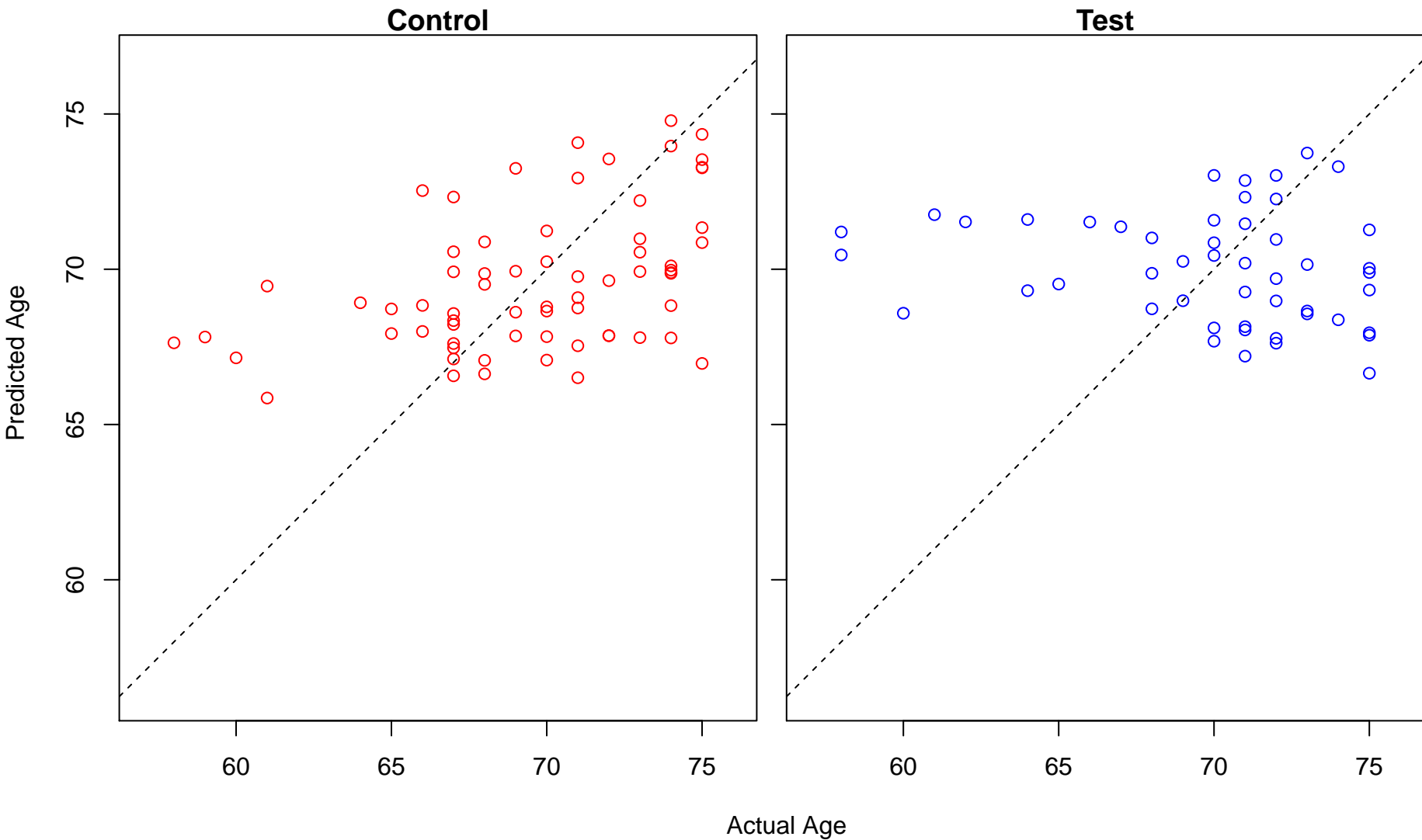
negative regulation of leukocyte mediated immunity (Score: 0.616059)



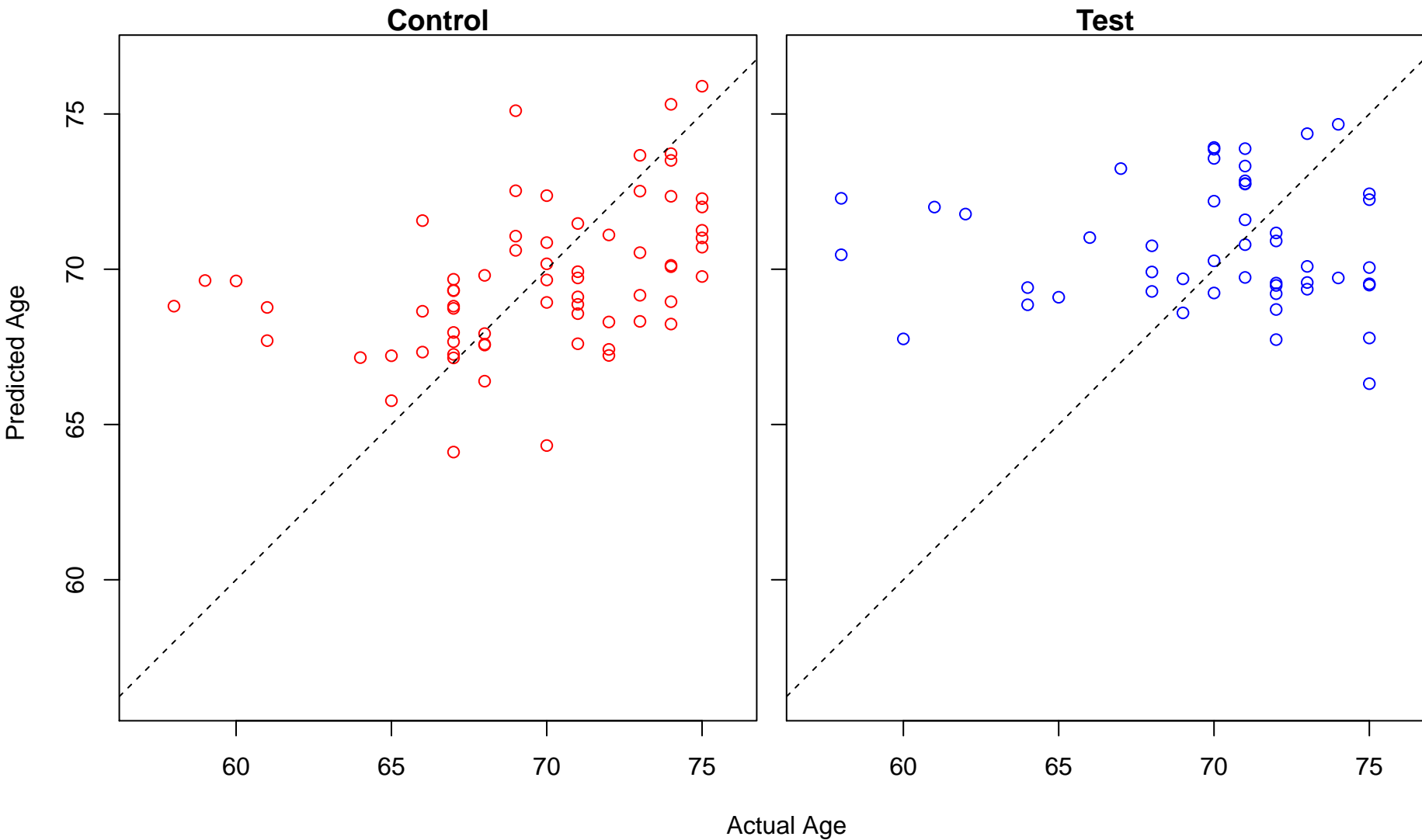
peptidyl-lysine monomethylation (Score: 0.616034)



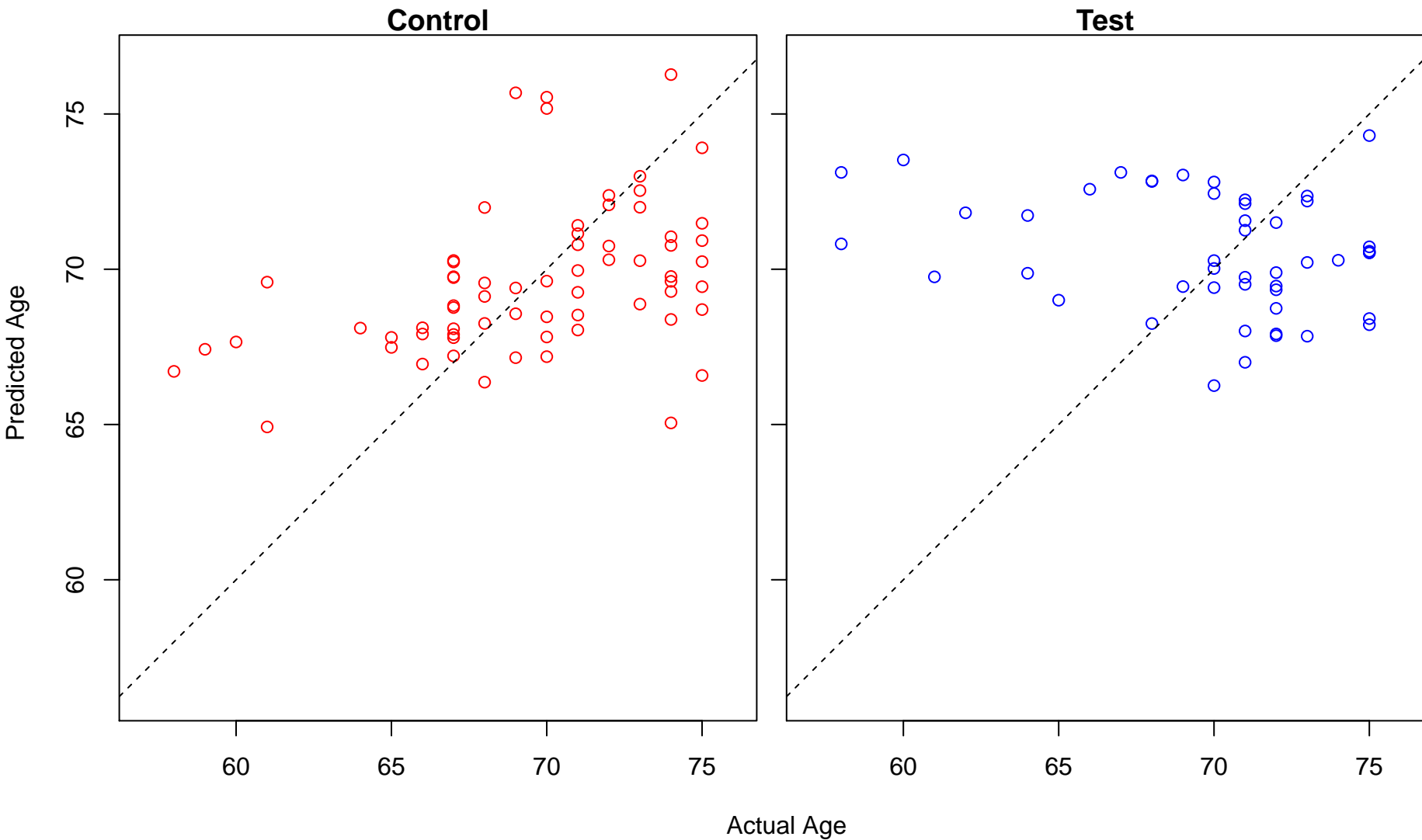
peptidyl-lysine deacetylation (Score: 0.615862)



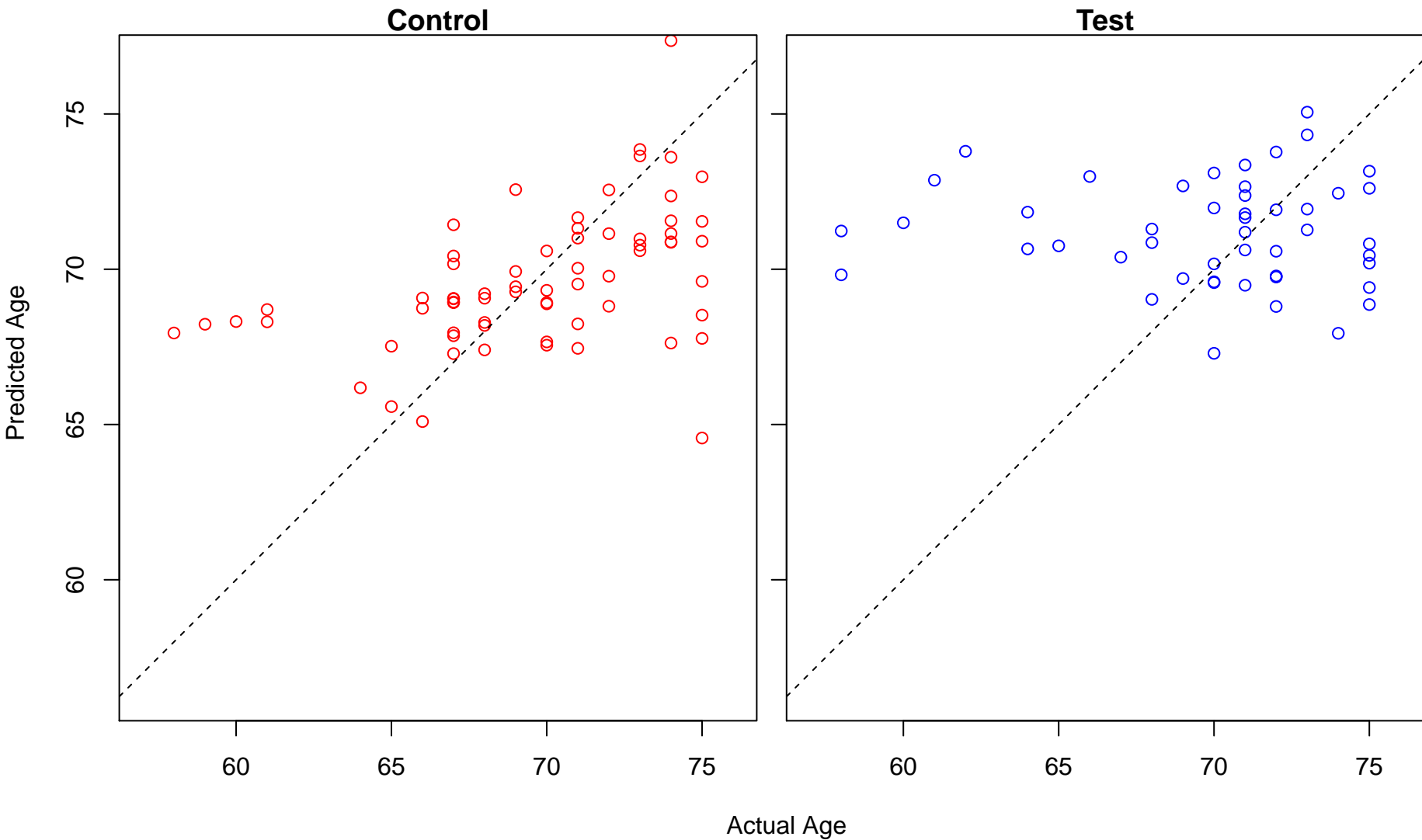
establishment of integrated proviral latency (Score: 0.615846)



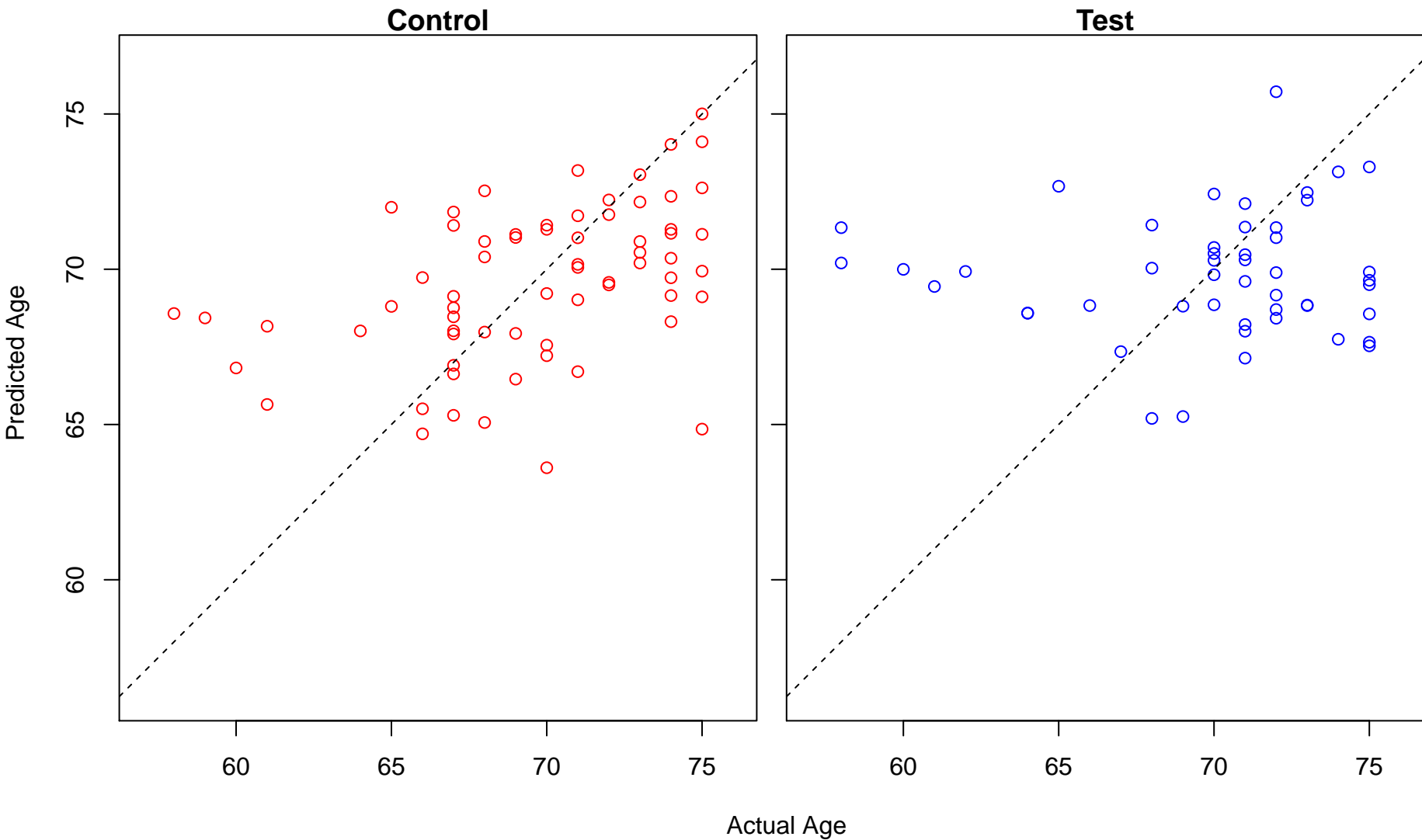
regulation of glucocorticoid receptor signaling pathway (Score: 0.615450)



regulation of amyloid precursor protein biosynthetic process (Score: 0.614396)

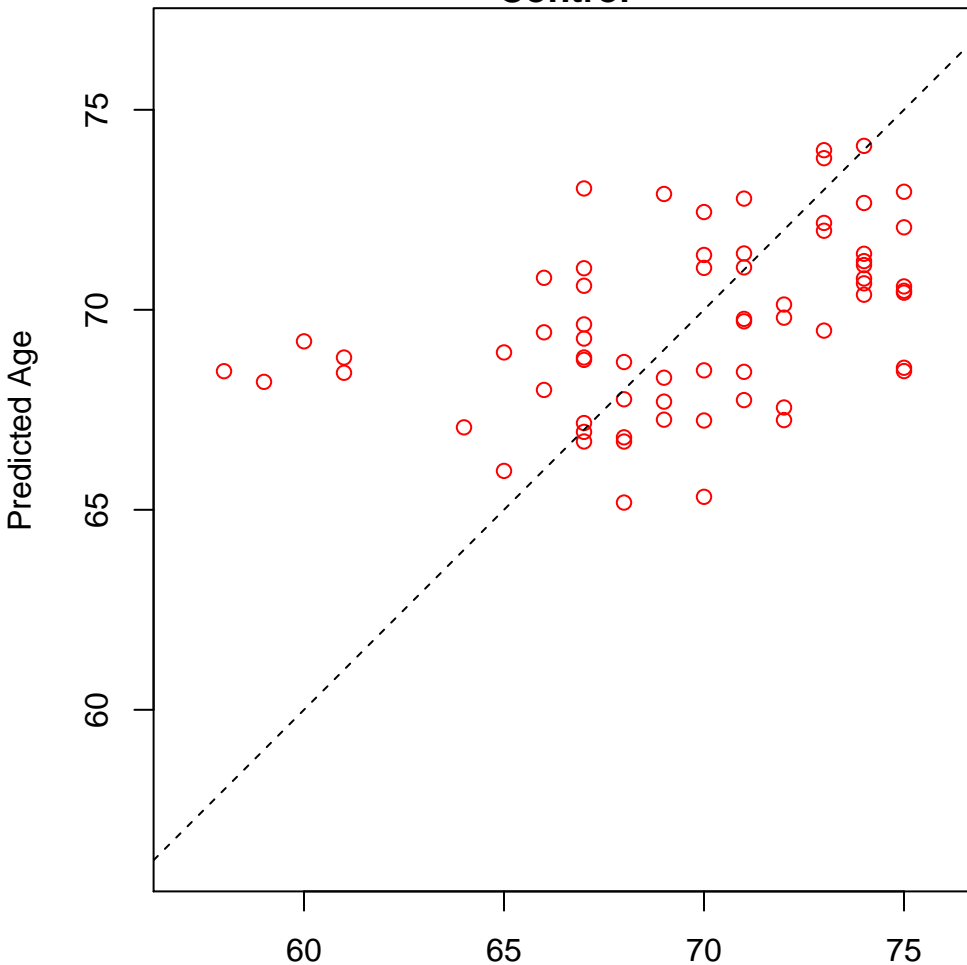


membrane repolarization (Score: 0.614333)

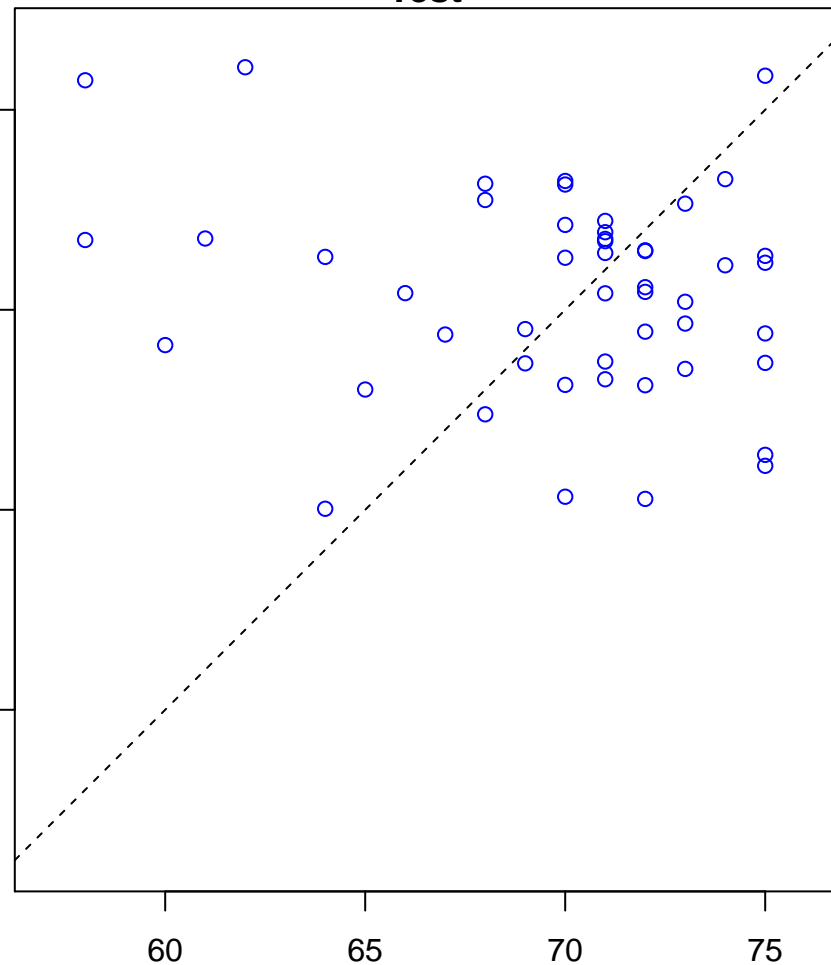


ossification involved in bone maturation (Score: 0.614160)

Control



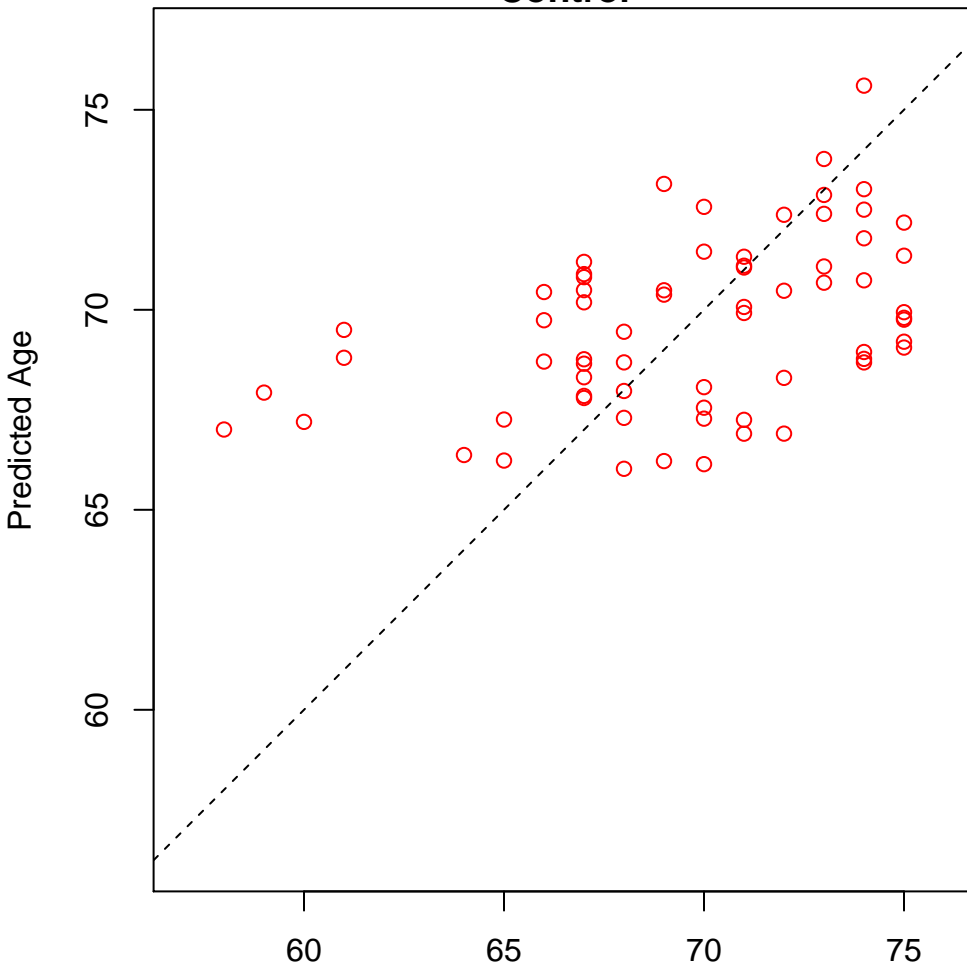
Test



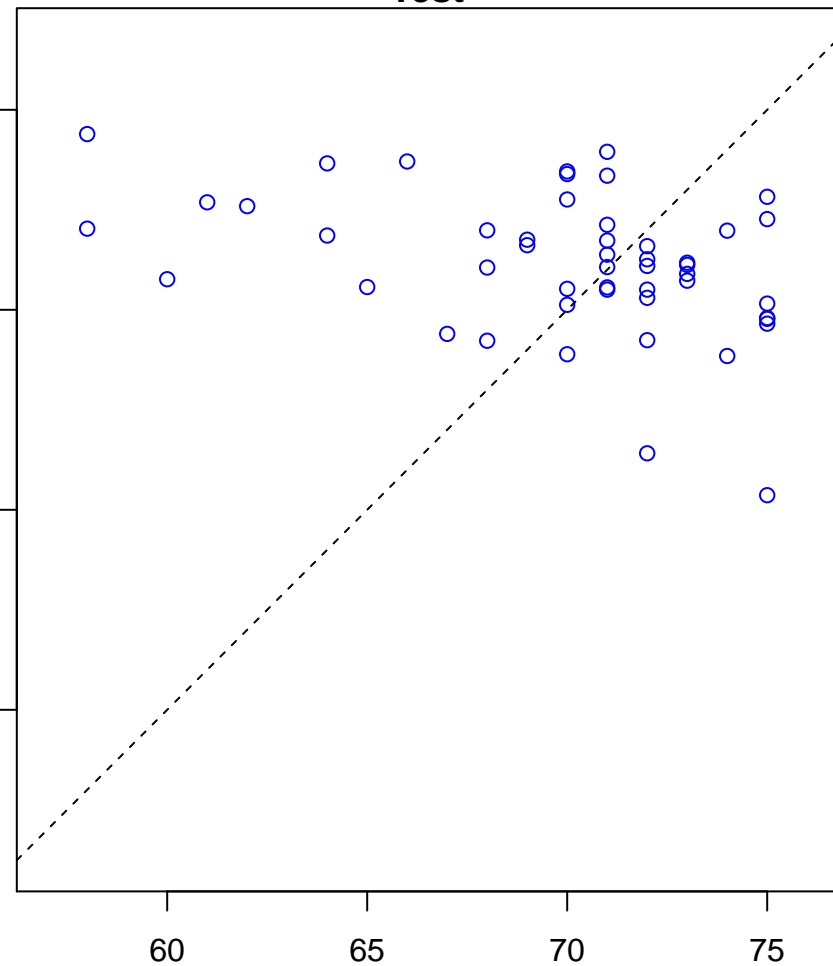
Actual Age

regulation of protein autophosphorylation (Score: 0.613927)

Control

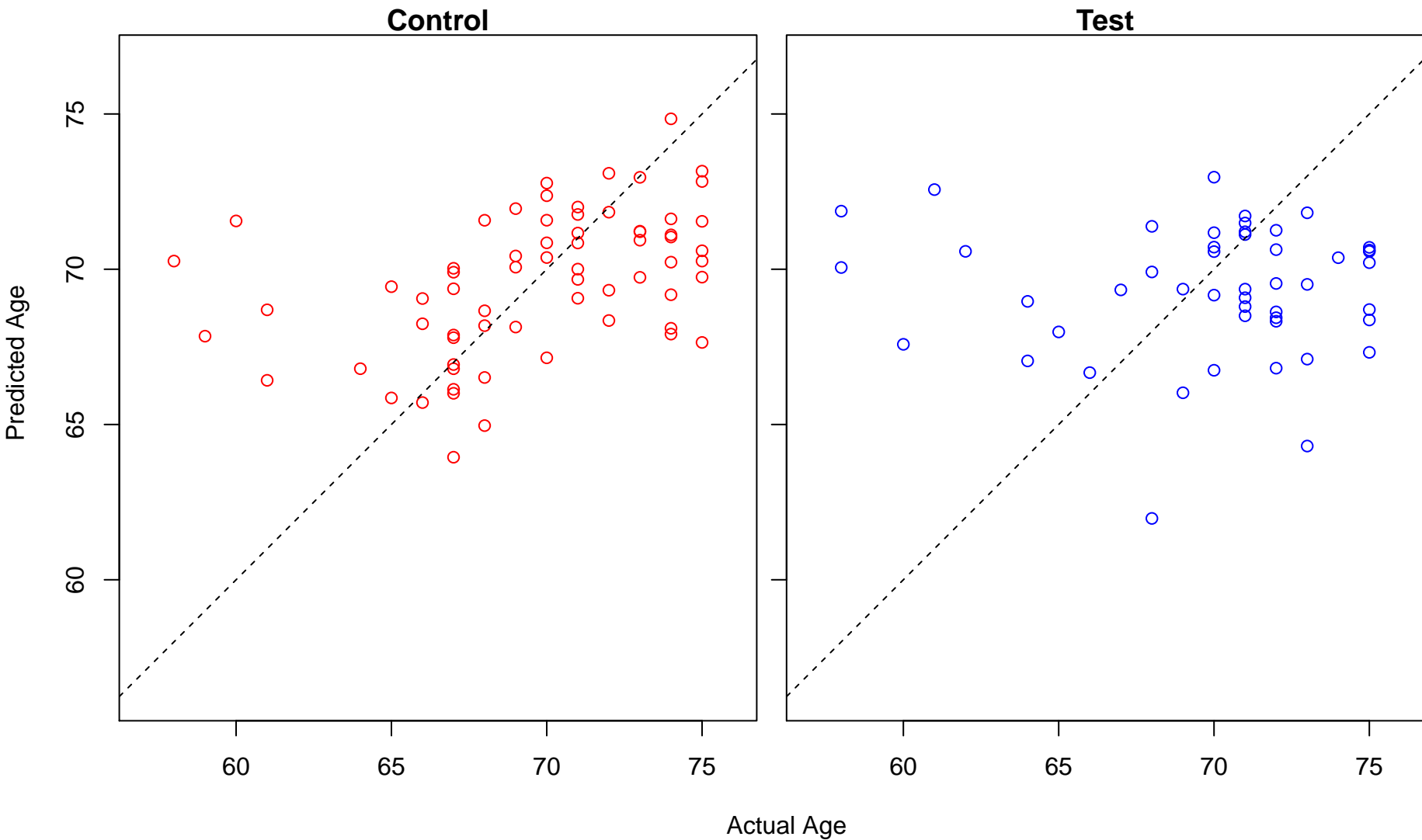


Test

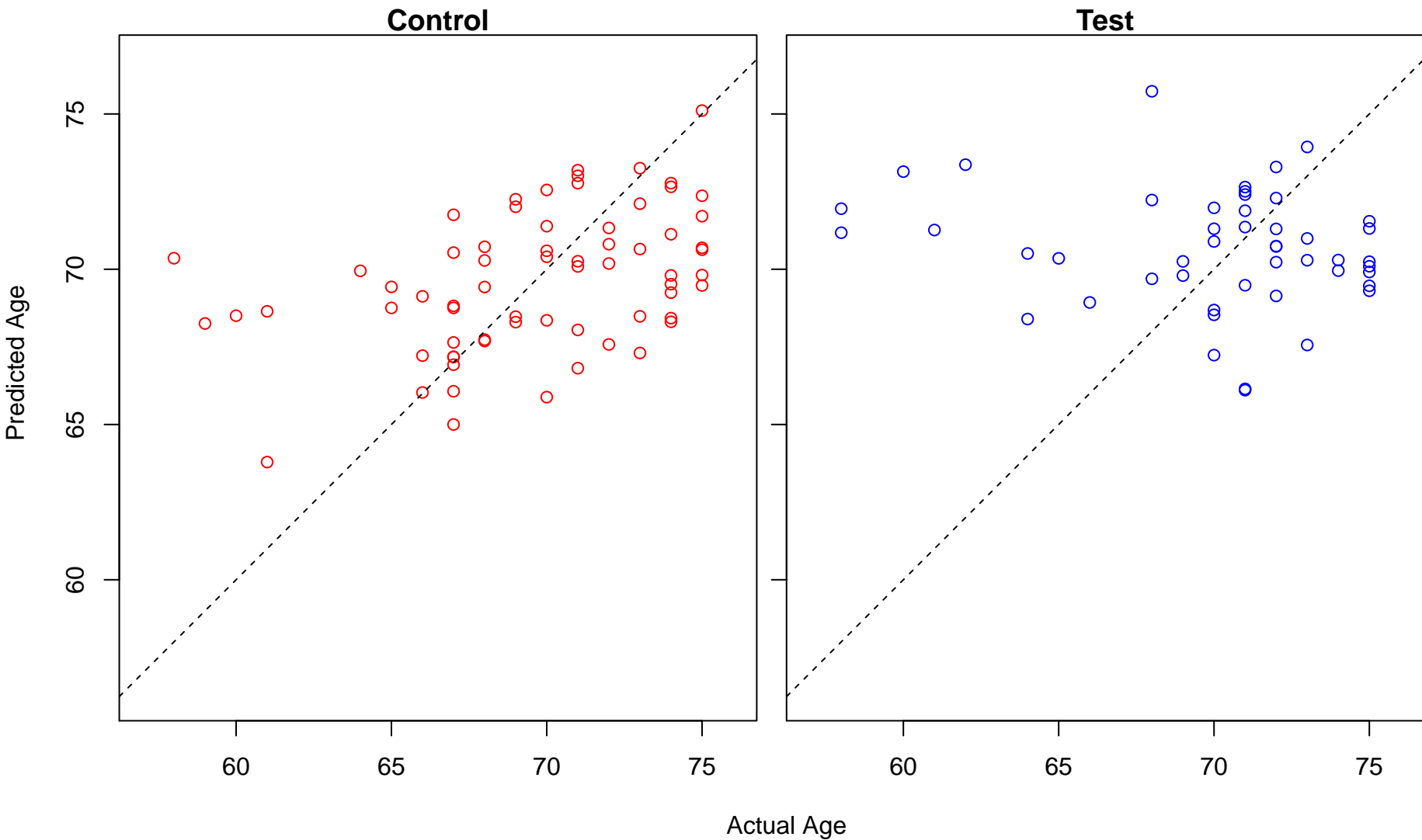


Actual Age

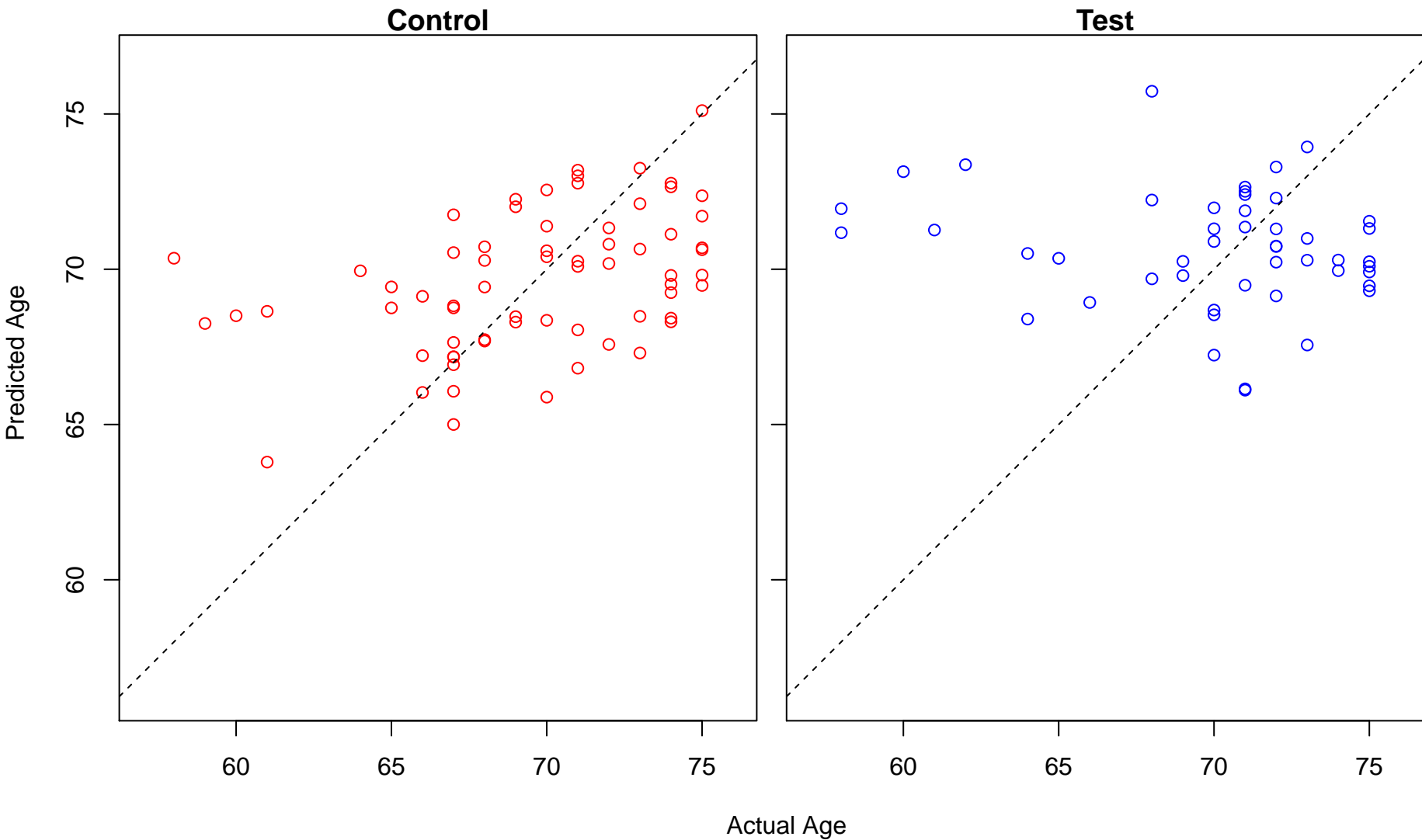
regulation of interleukin-12 secretion (Score: 0.613571)



cellular response to nitric oxide (Score: 0.613509)

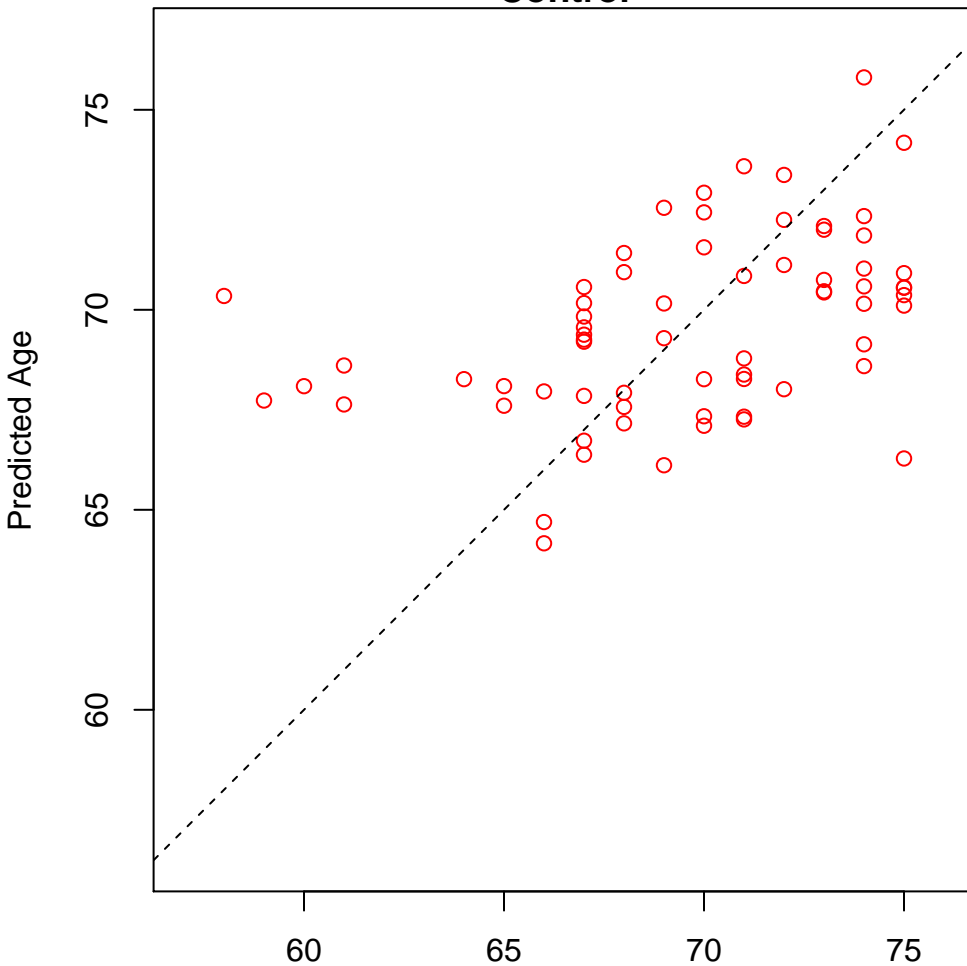


cellular response to reactive nitrogen species (Score: 0.613509)

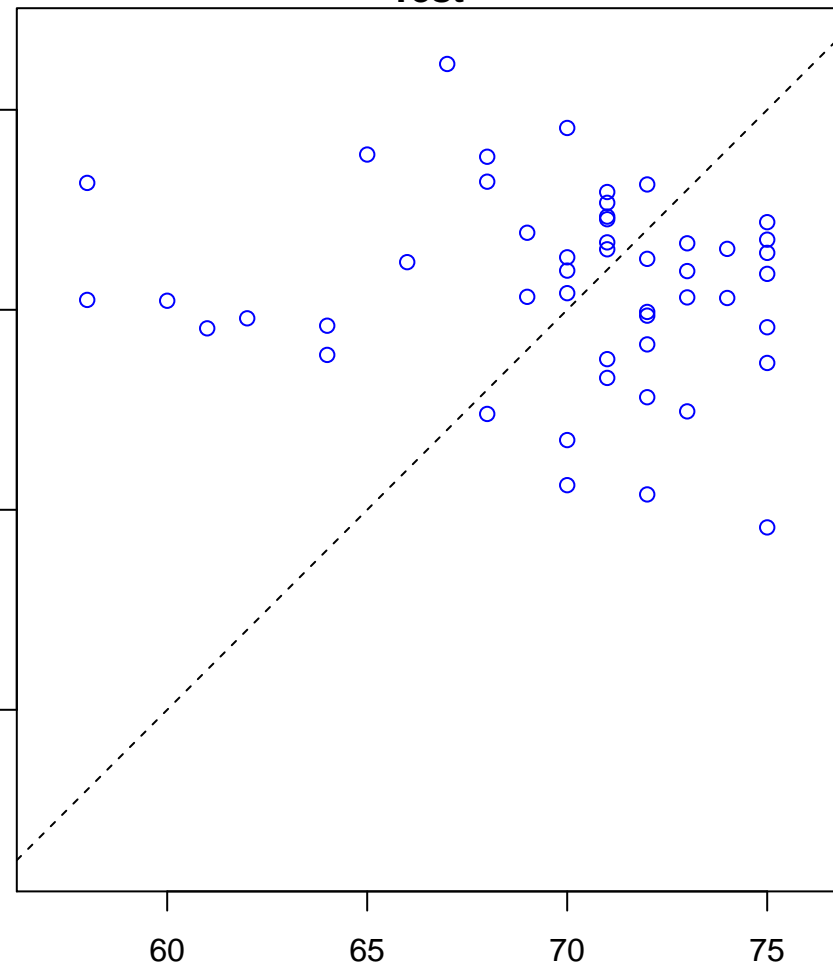


regulation of immunoglobulin secretion (Score: 0.613300)

Control

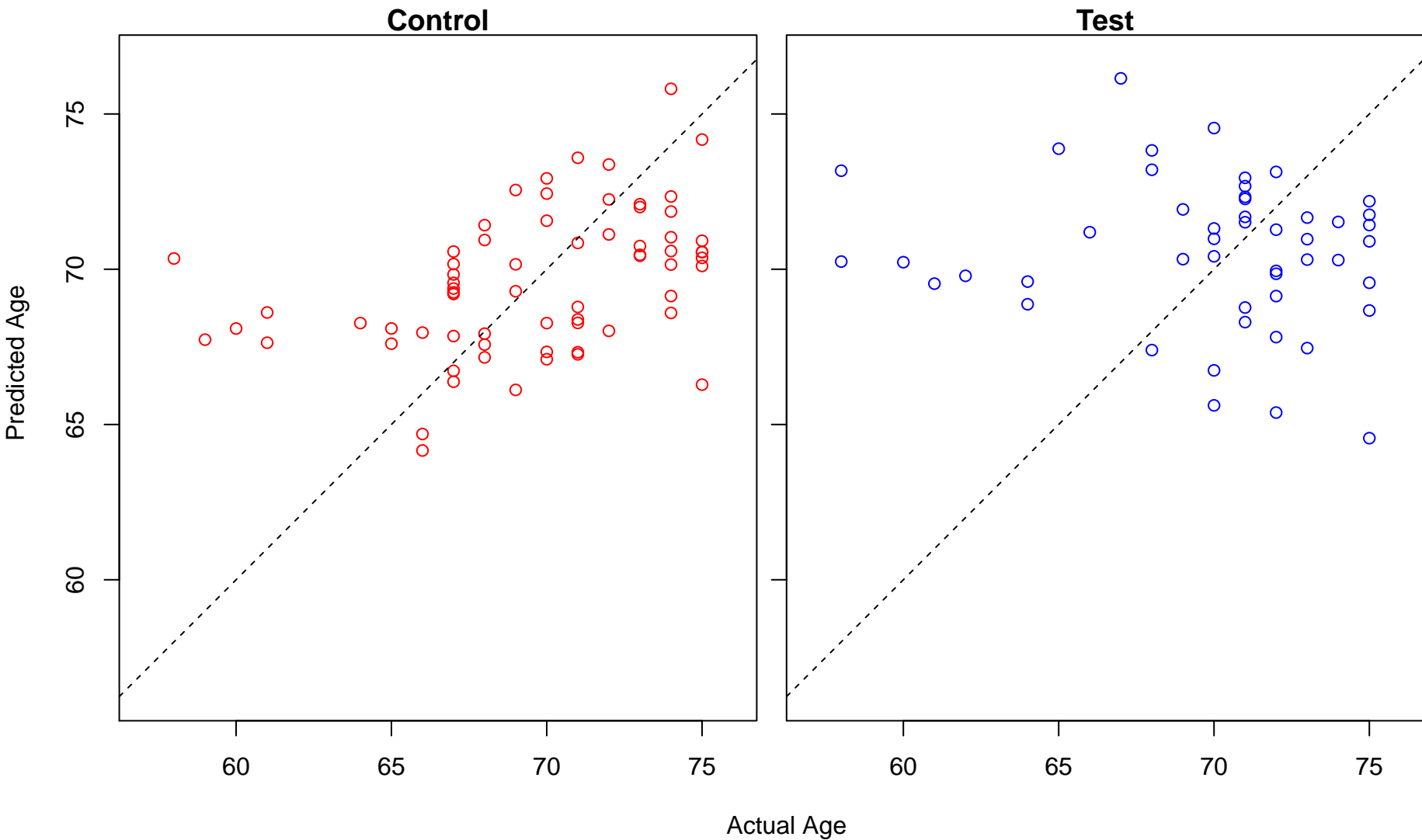


Test

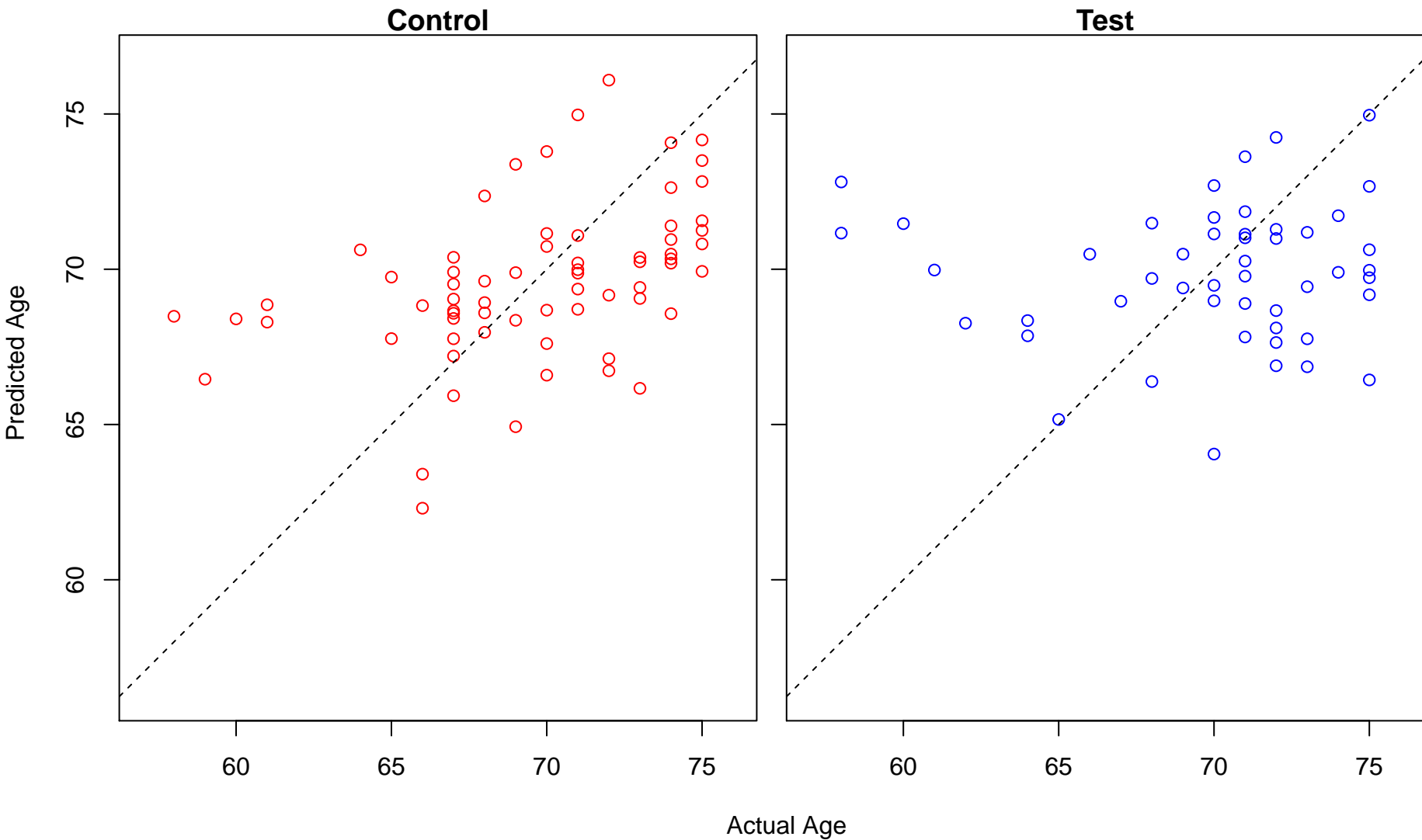


Actual Age

positive regulation of immunoglobulin secretion (Score: 0.613300)

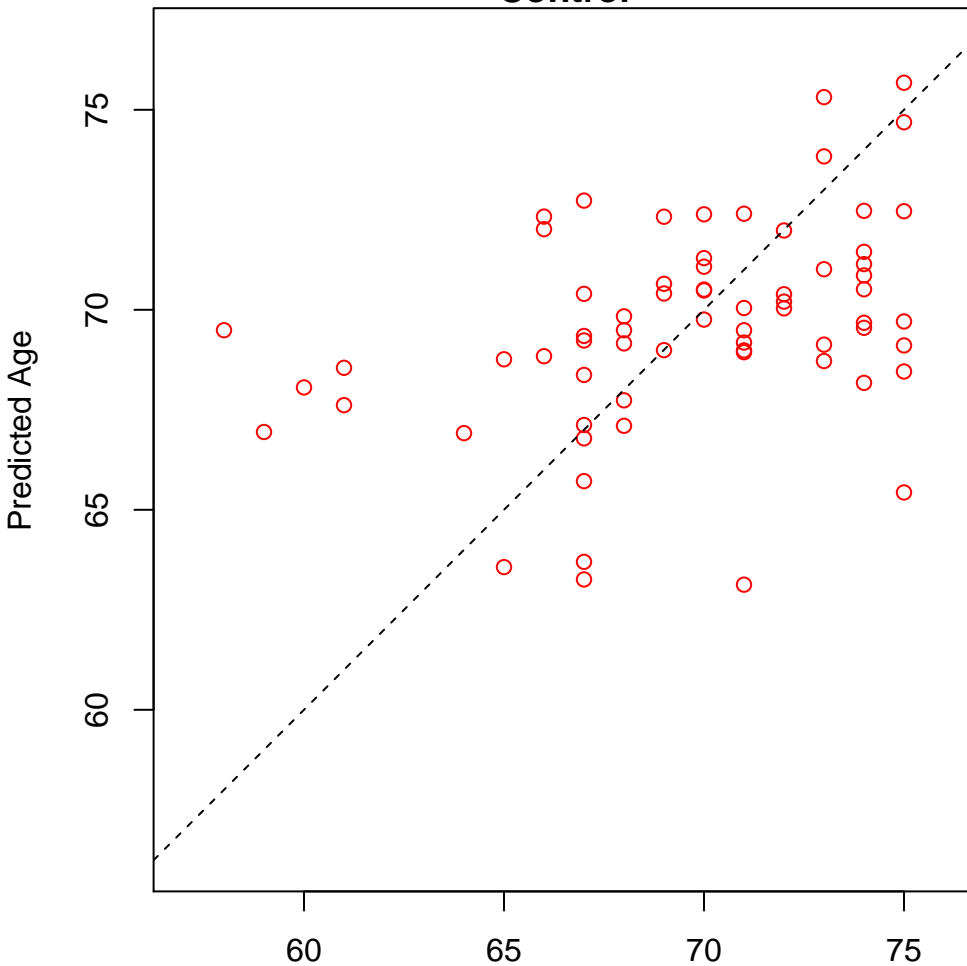


cytokine biosynthetic process (Score: 0.613083)

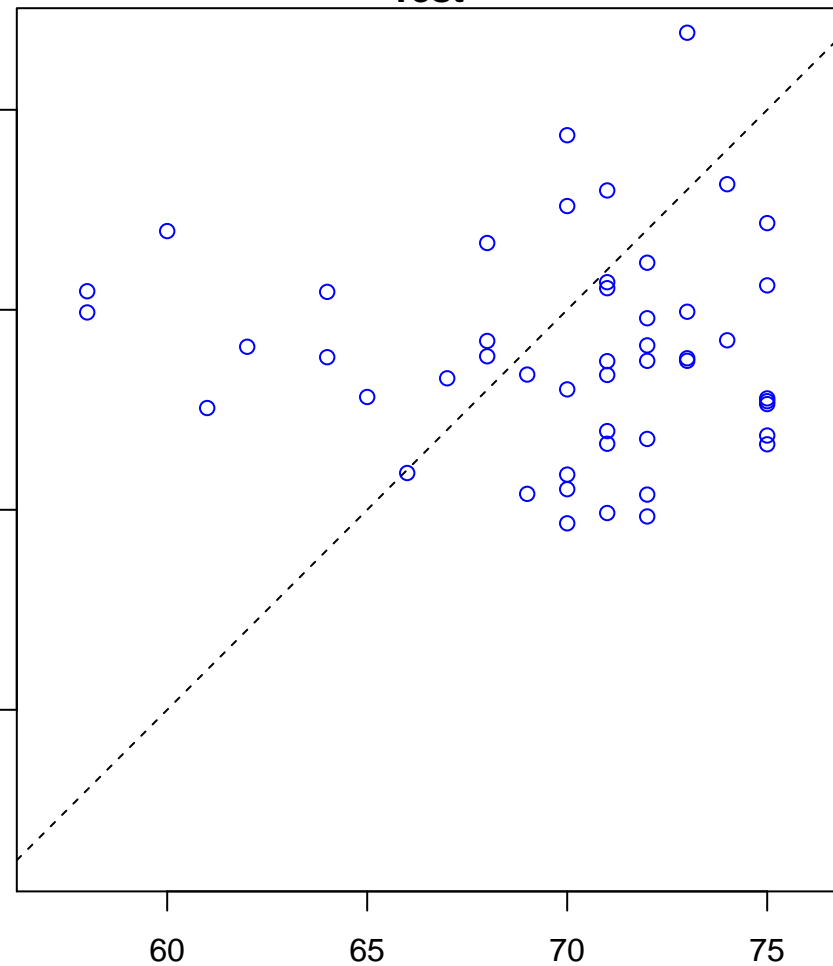


stress-induced premature senescence (Score: 0.612754)

Control

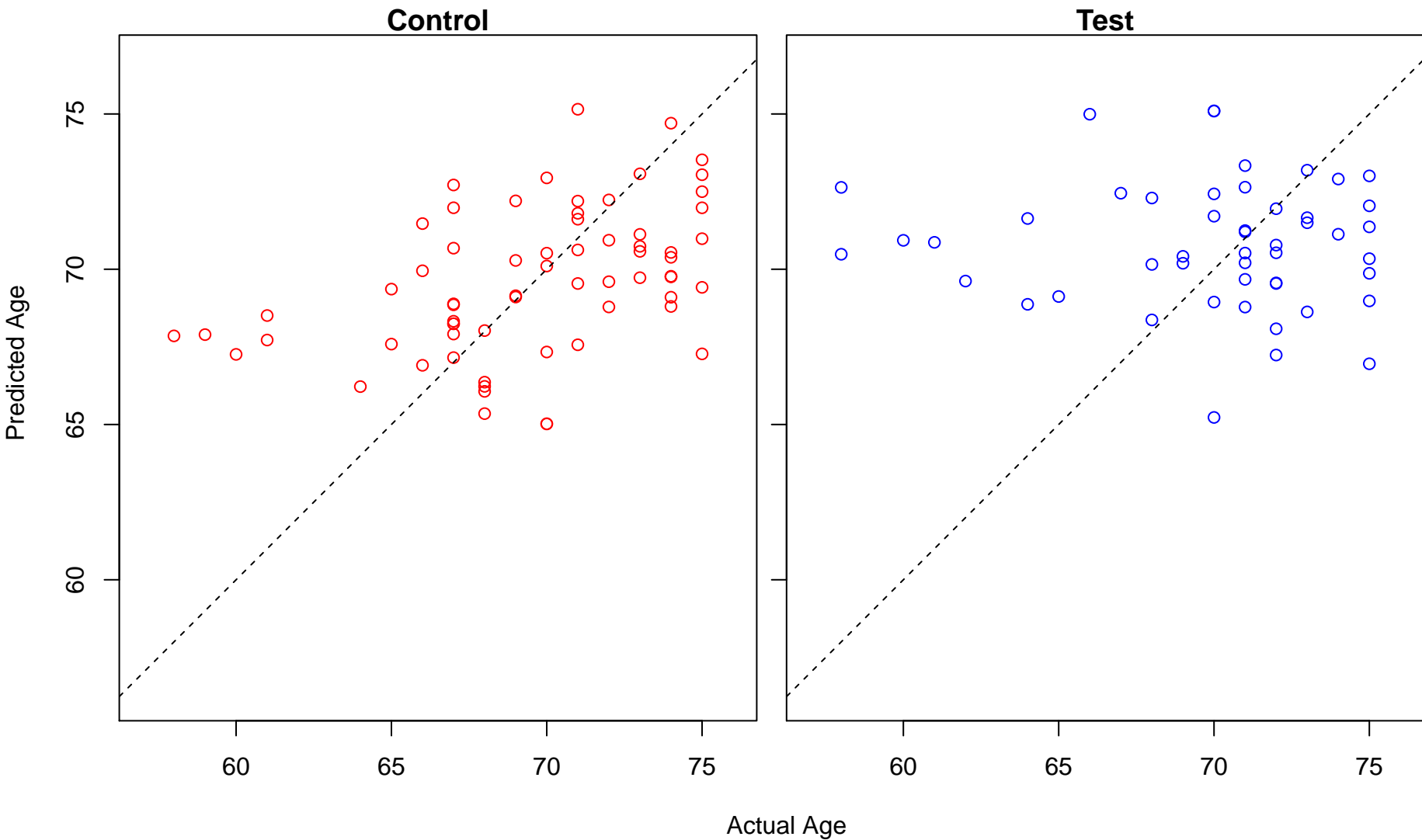


Test

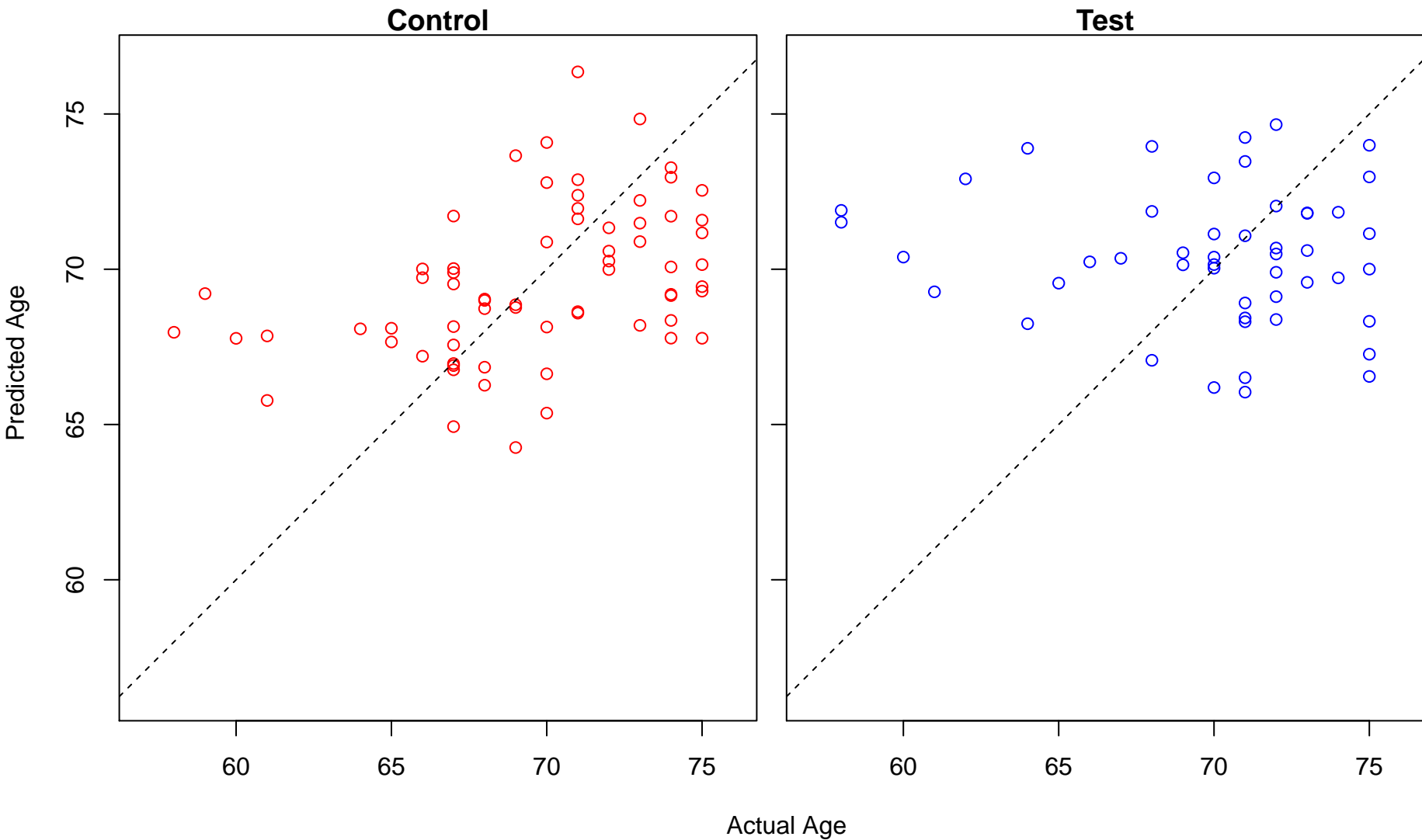


Actual Age

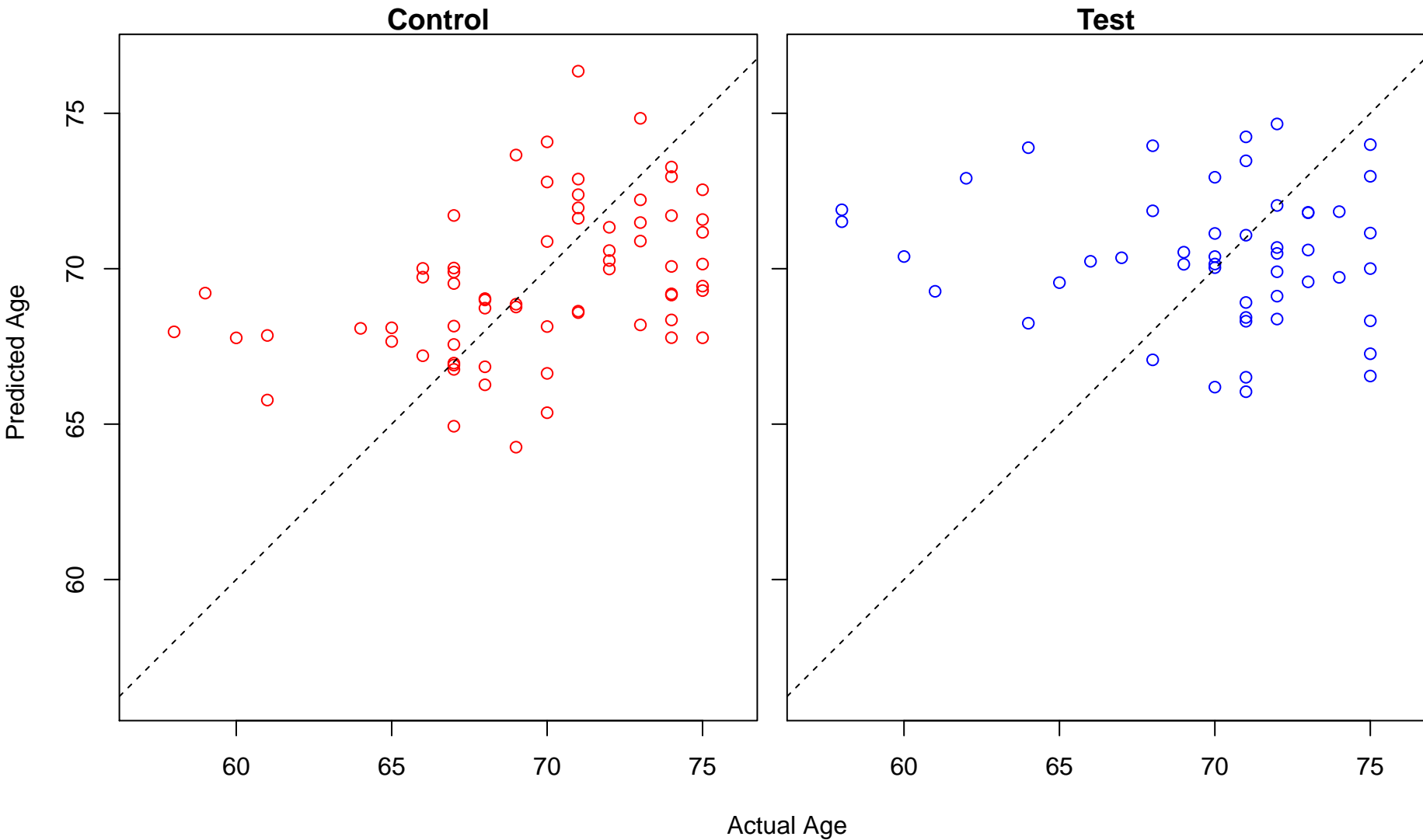
protein destabilization (Score: 0.612258)



dsRNA fragmentation (Score: 0.612237)

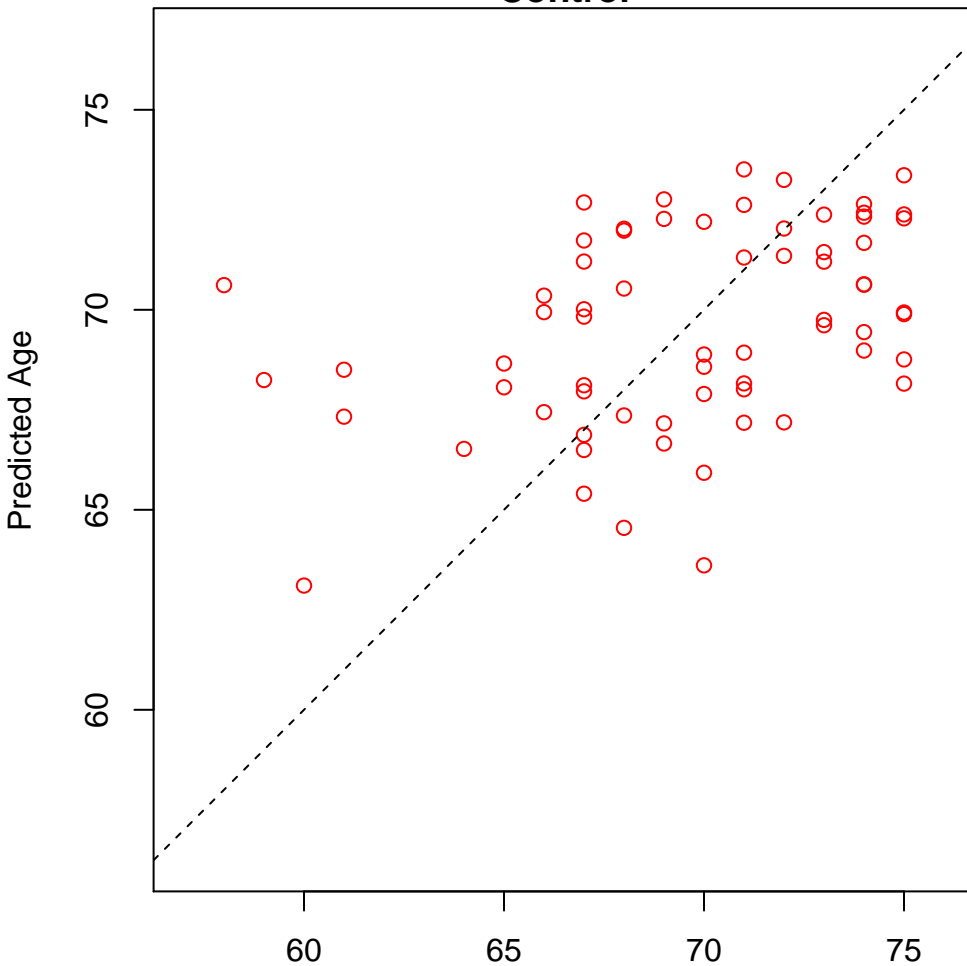


production of small RNA involved in gene silencing by RNA (Score: 0.612237)

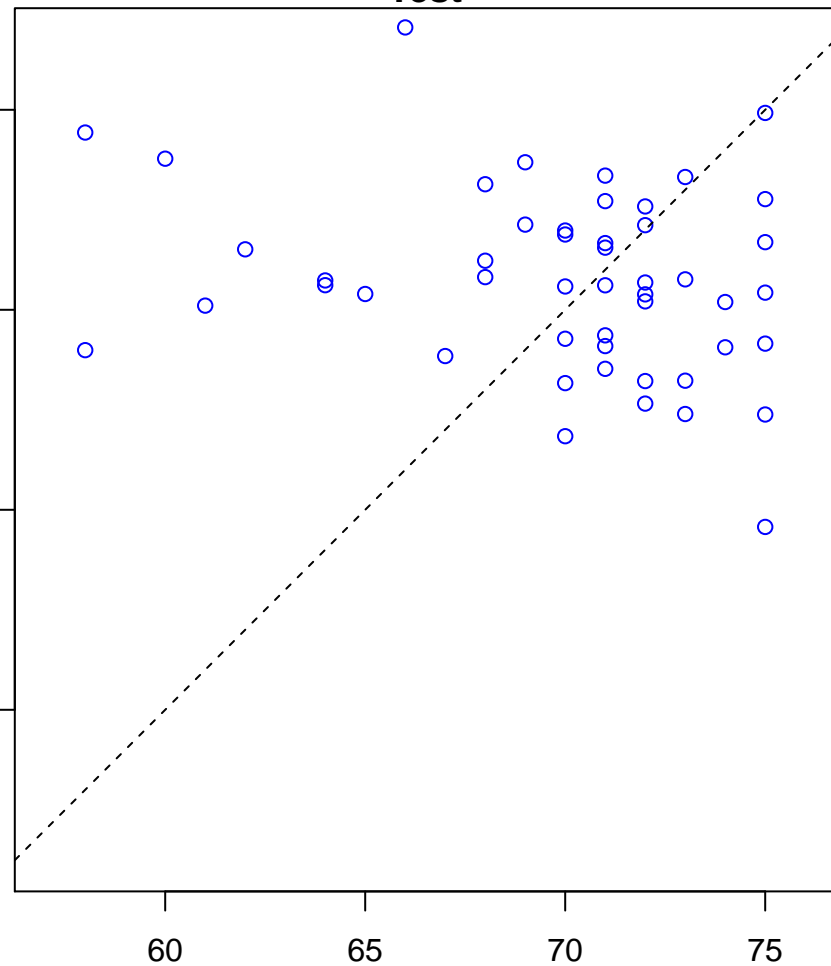


retinoic acid receptor signaling pathway (Score: 0.611504)

Control

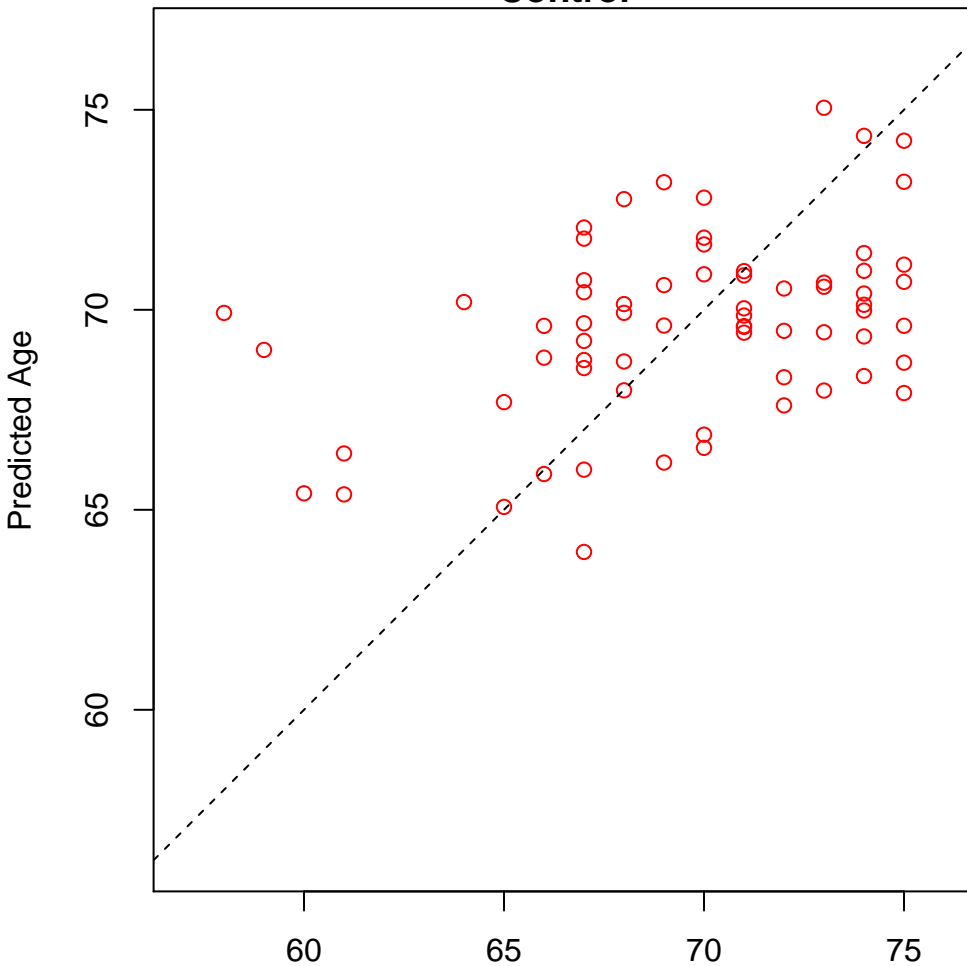


Test

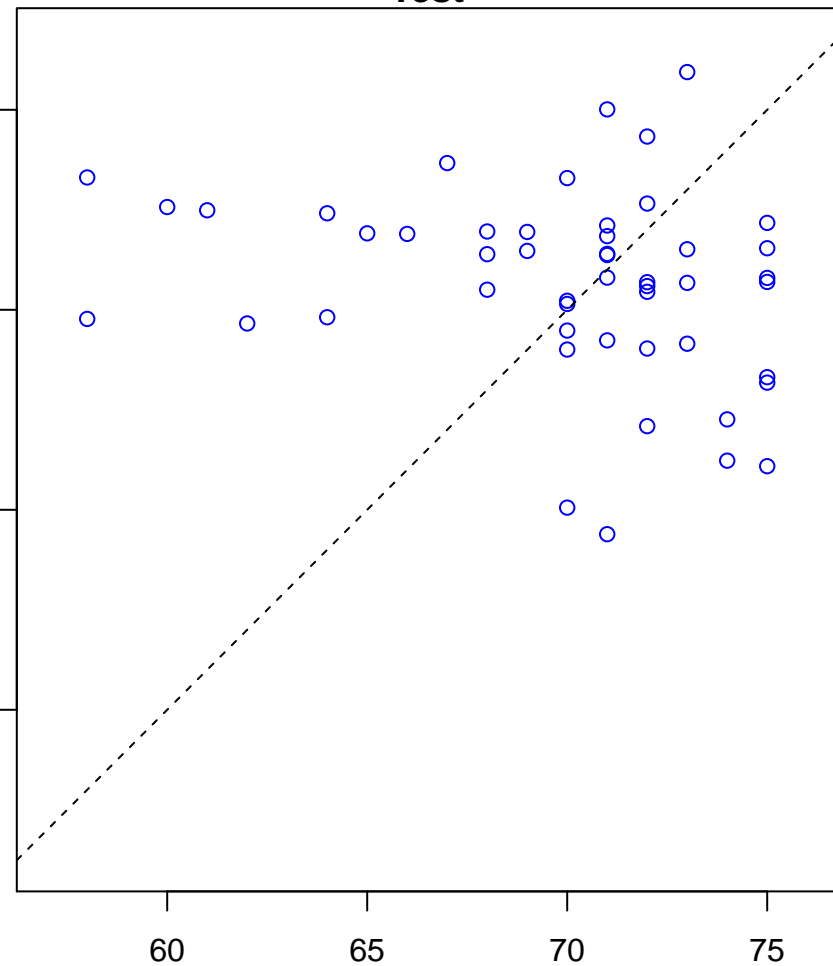


dopamine receptor signaling pathway (Score: 0.611286)

Control

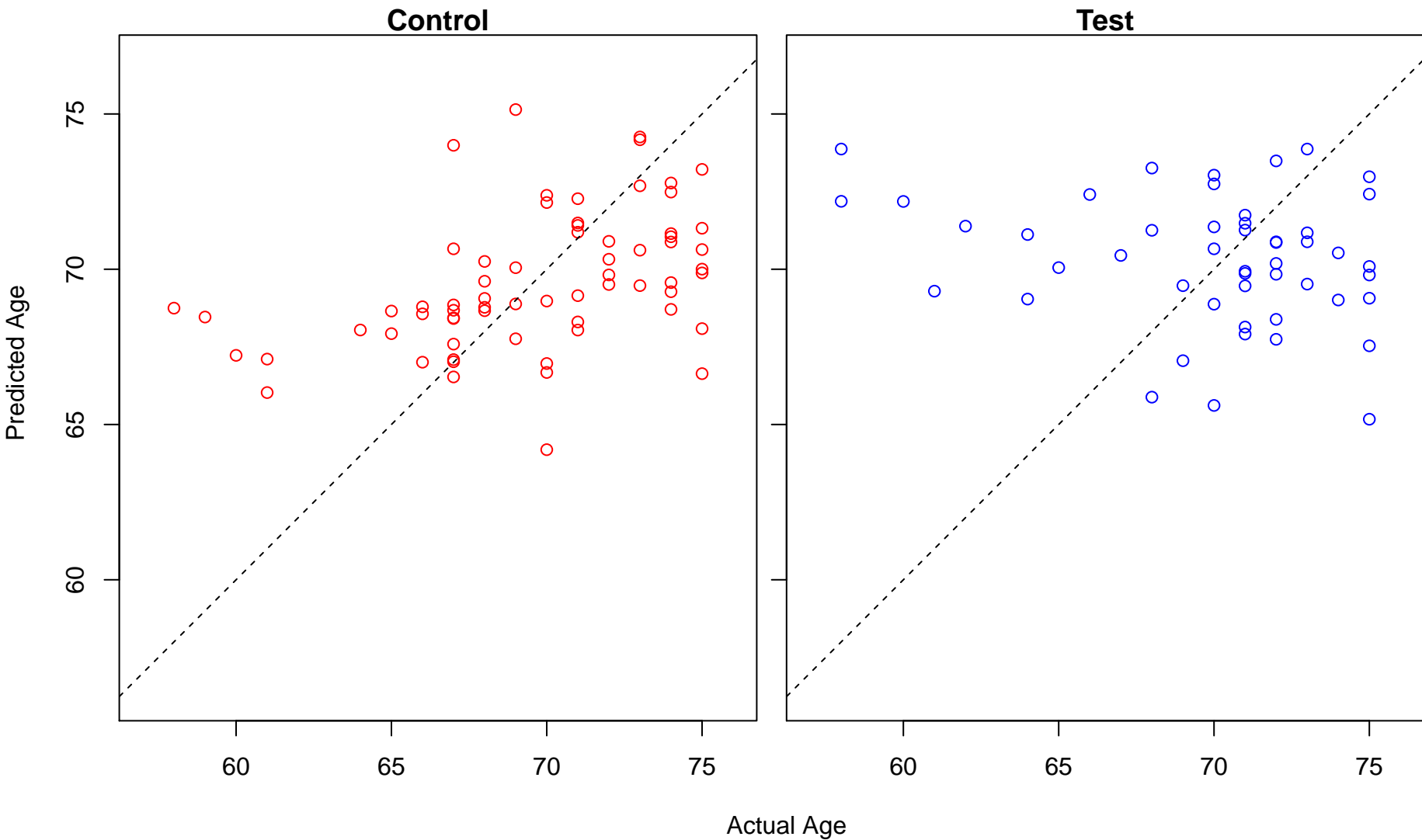


Test

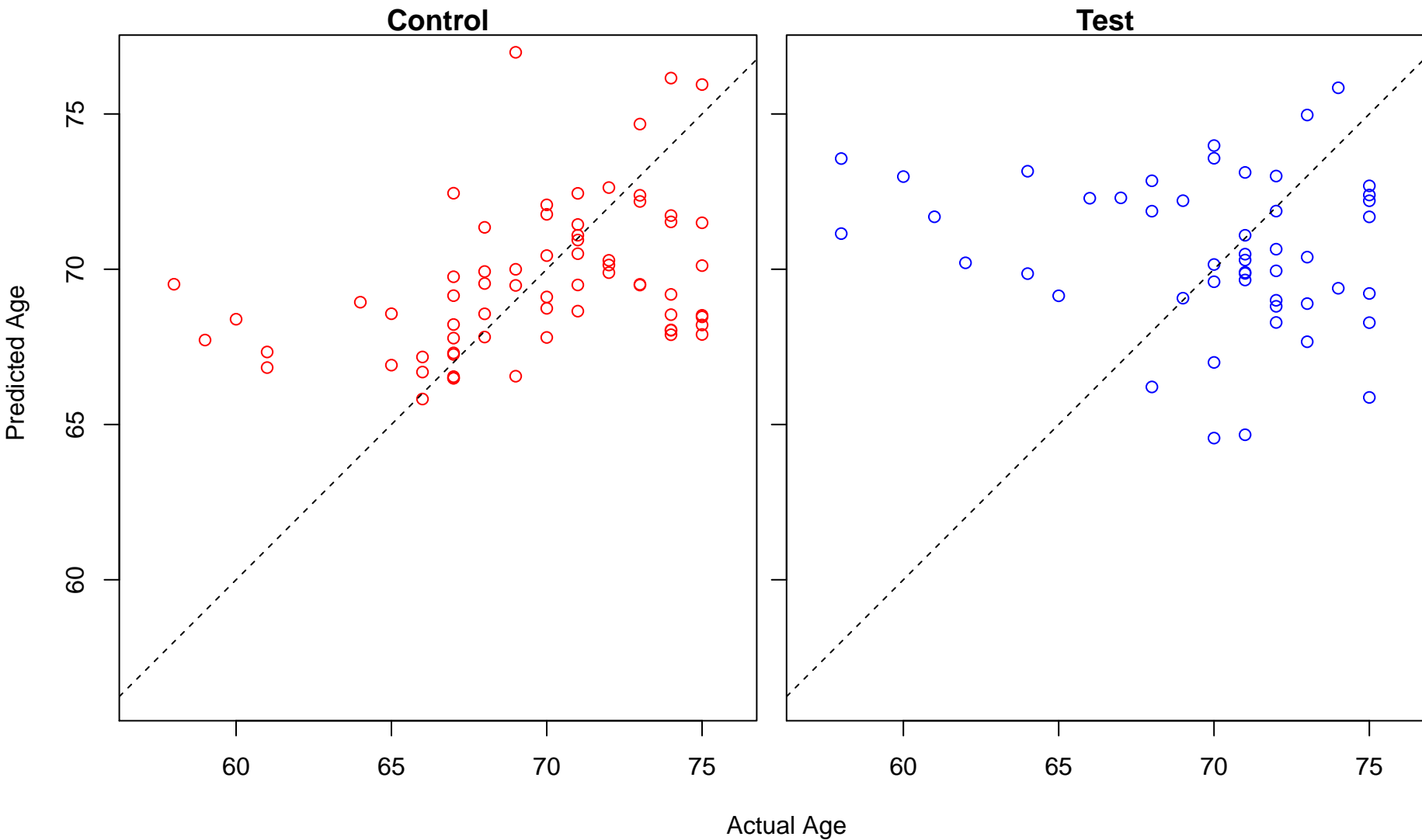


Actual Age

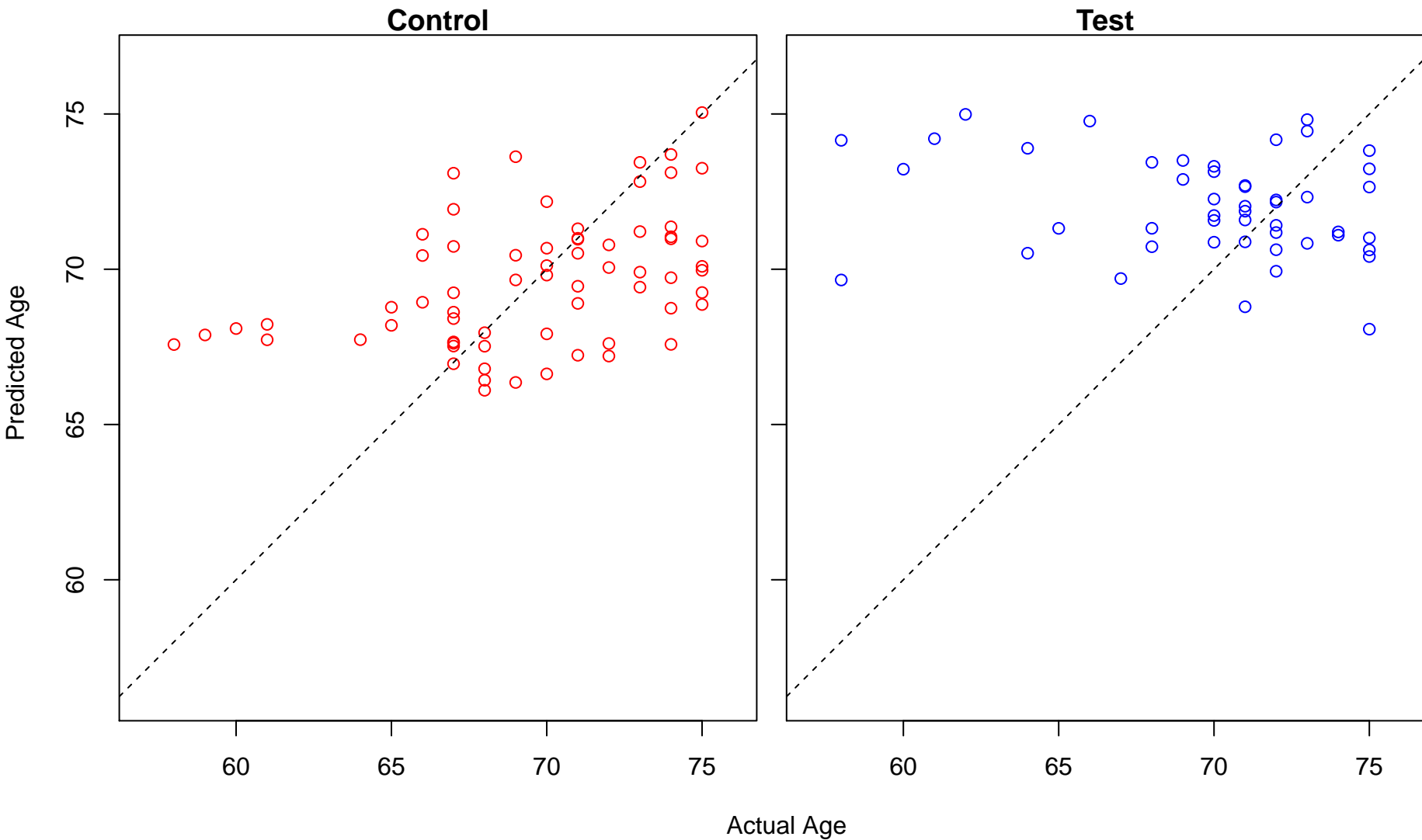
import across plasma membrane (Score: 0.610742)



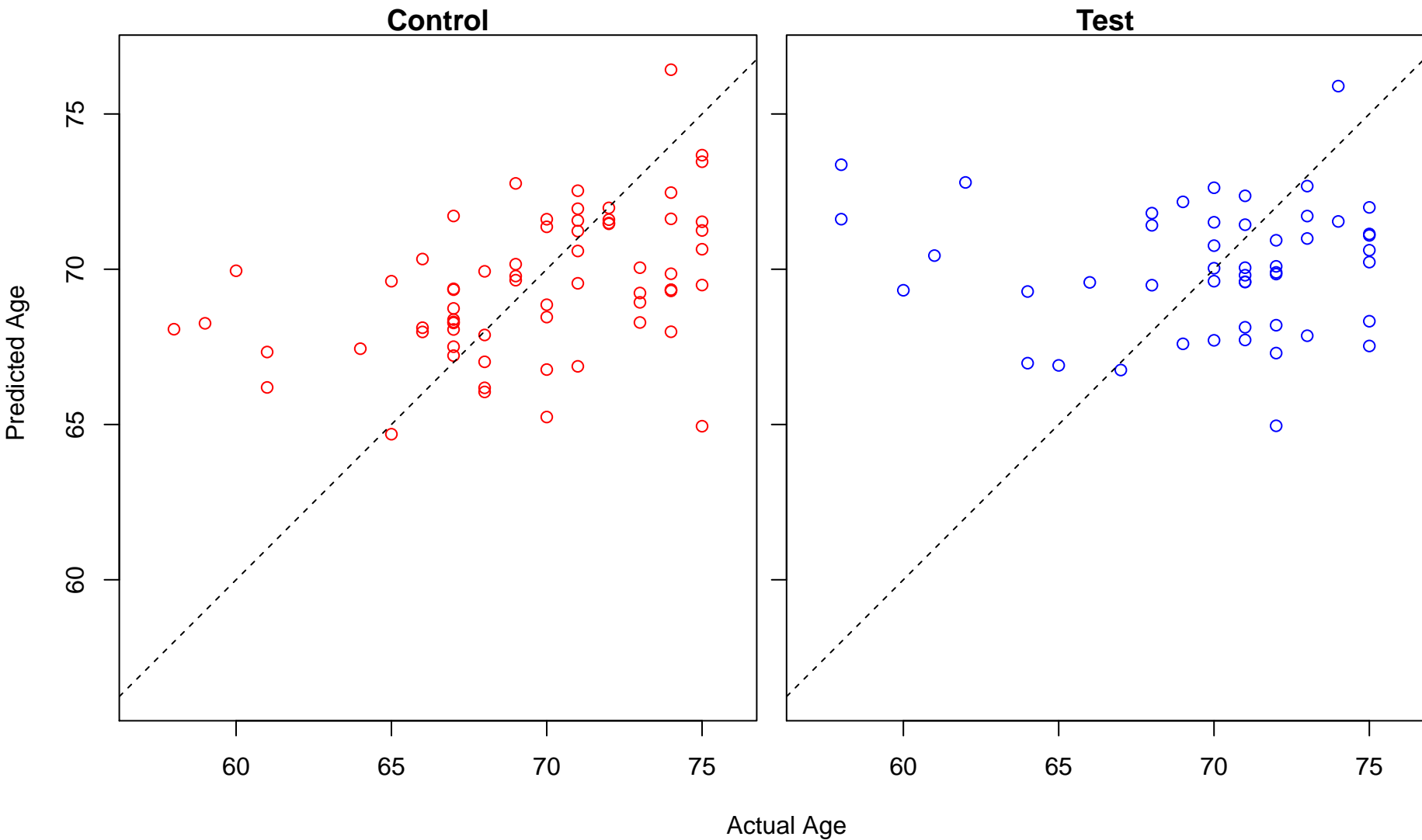
eye morphogenesis (Score: 0.609467)



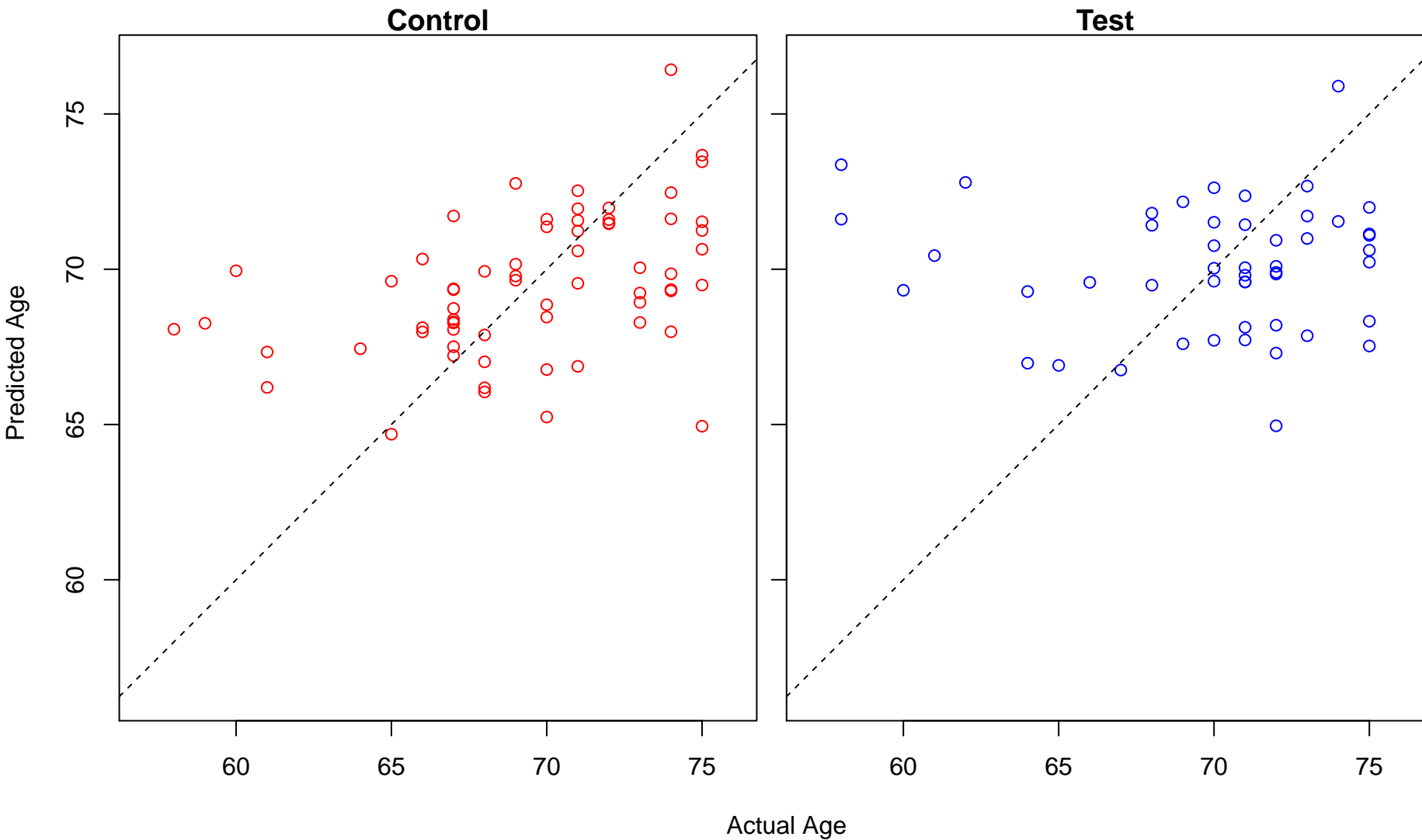
inner ear morphogenesis (Score: 0.609344)



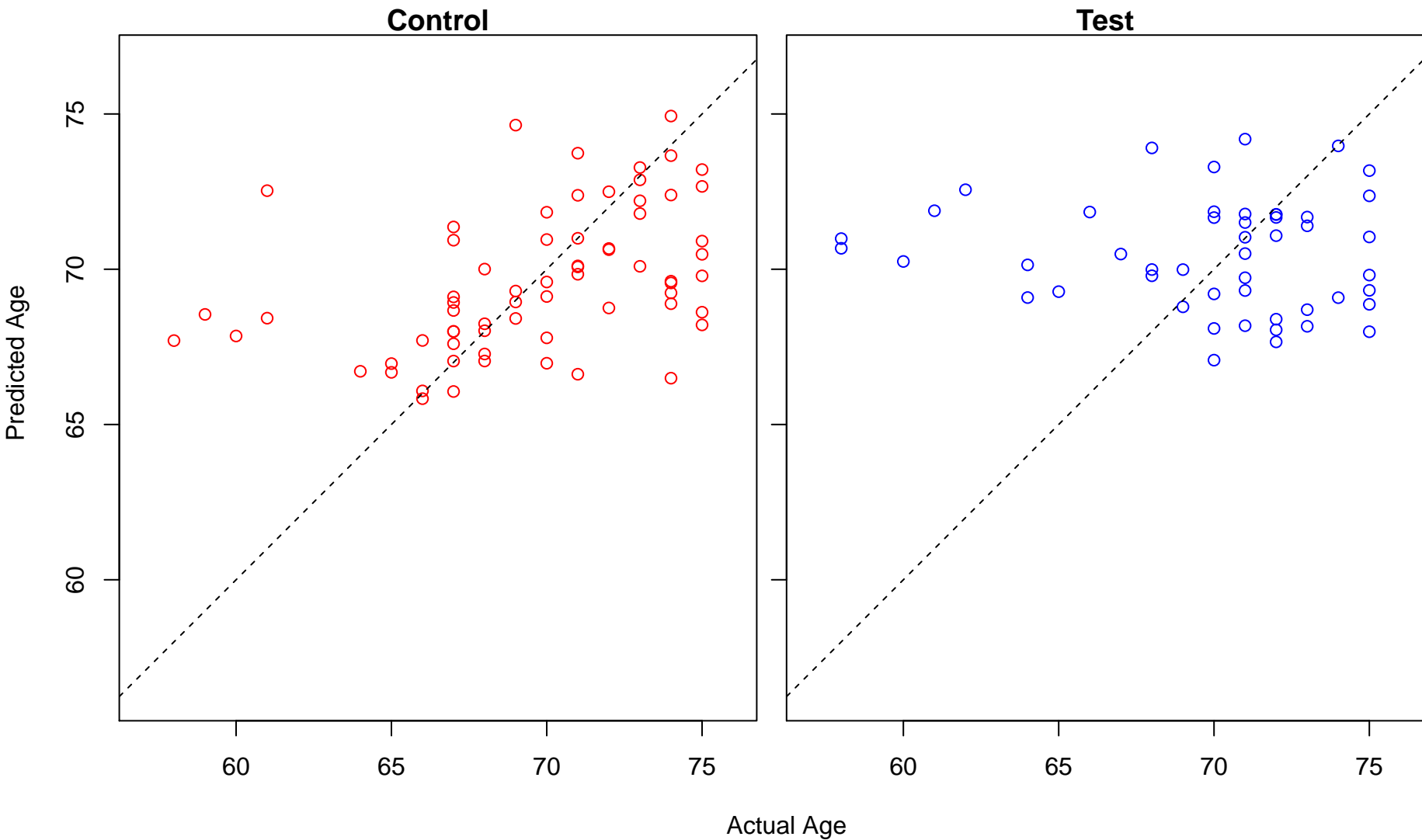
negative regulation of heterotypic cell-cell adhesion (Score: 0.607397)



regulation of cell-cell adhesion involved in gastrulation (Score: 0.607397)

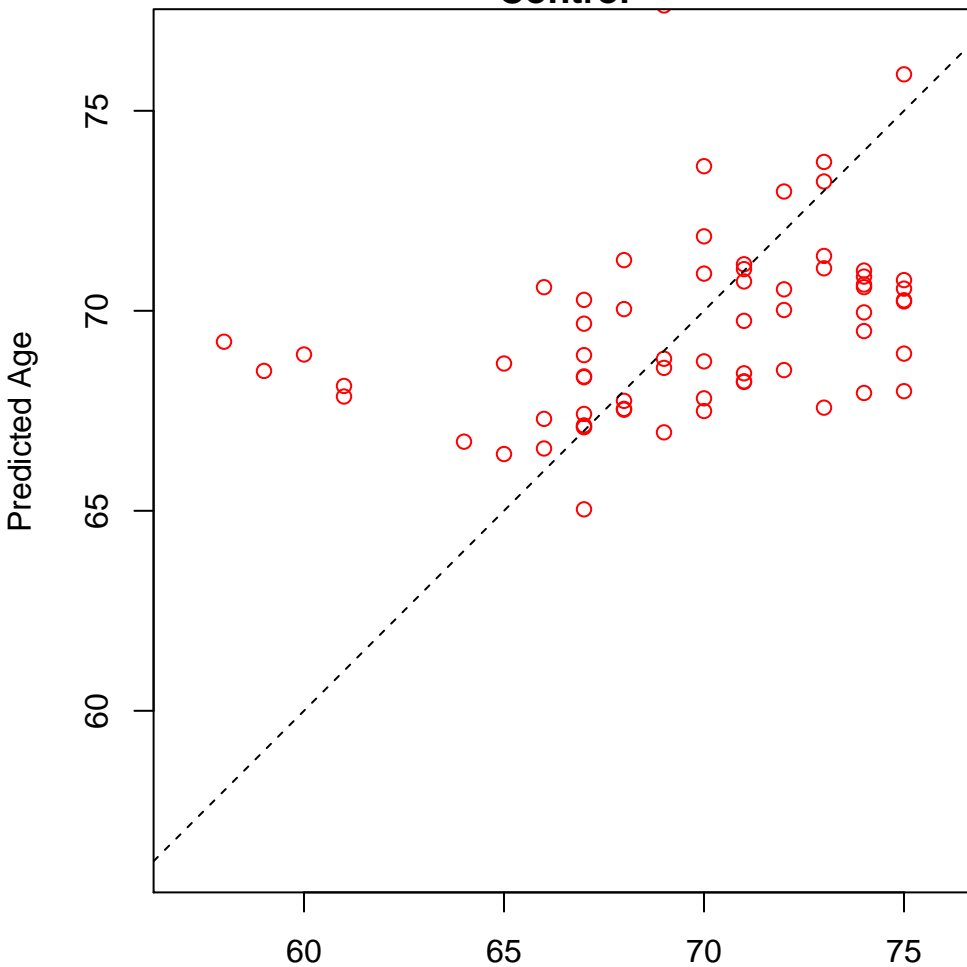


regulation of cytokine production involved in inflammatory response (Score: 0.607268)

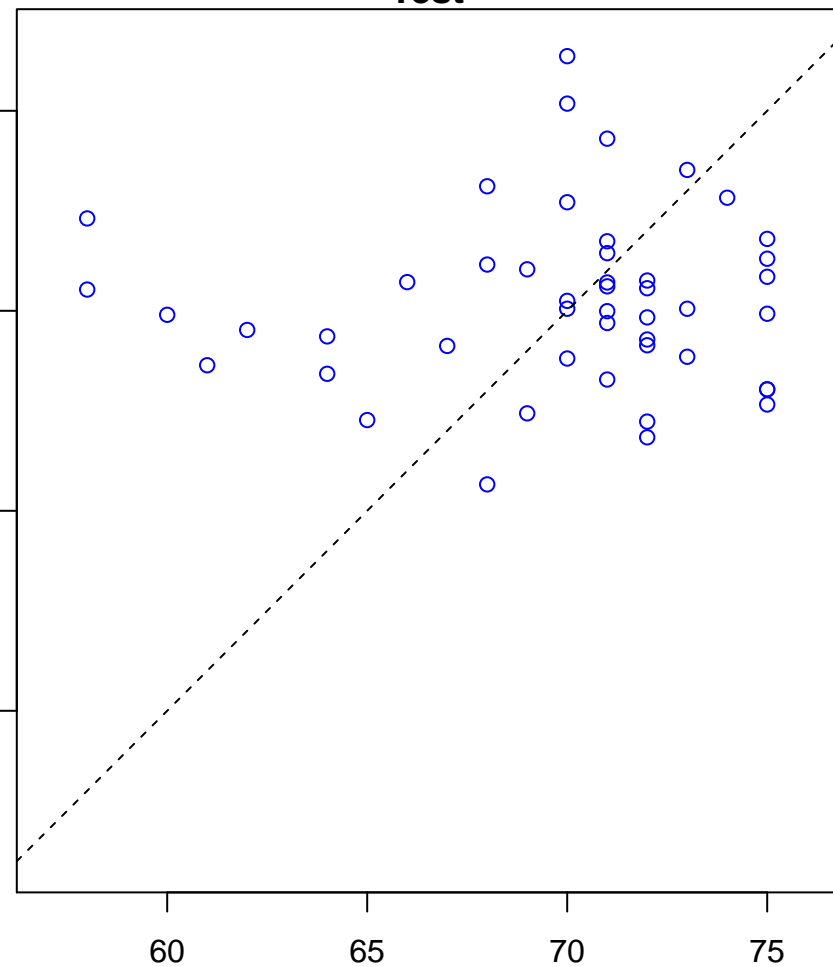


establishment of epithelial cell polarity (Score: 0.607034)

Control

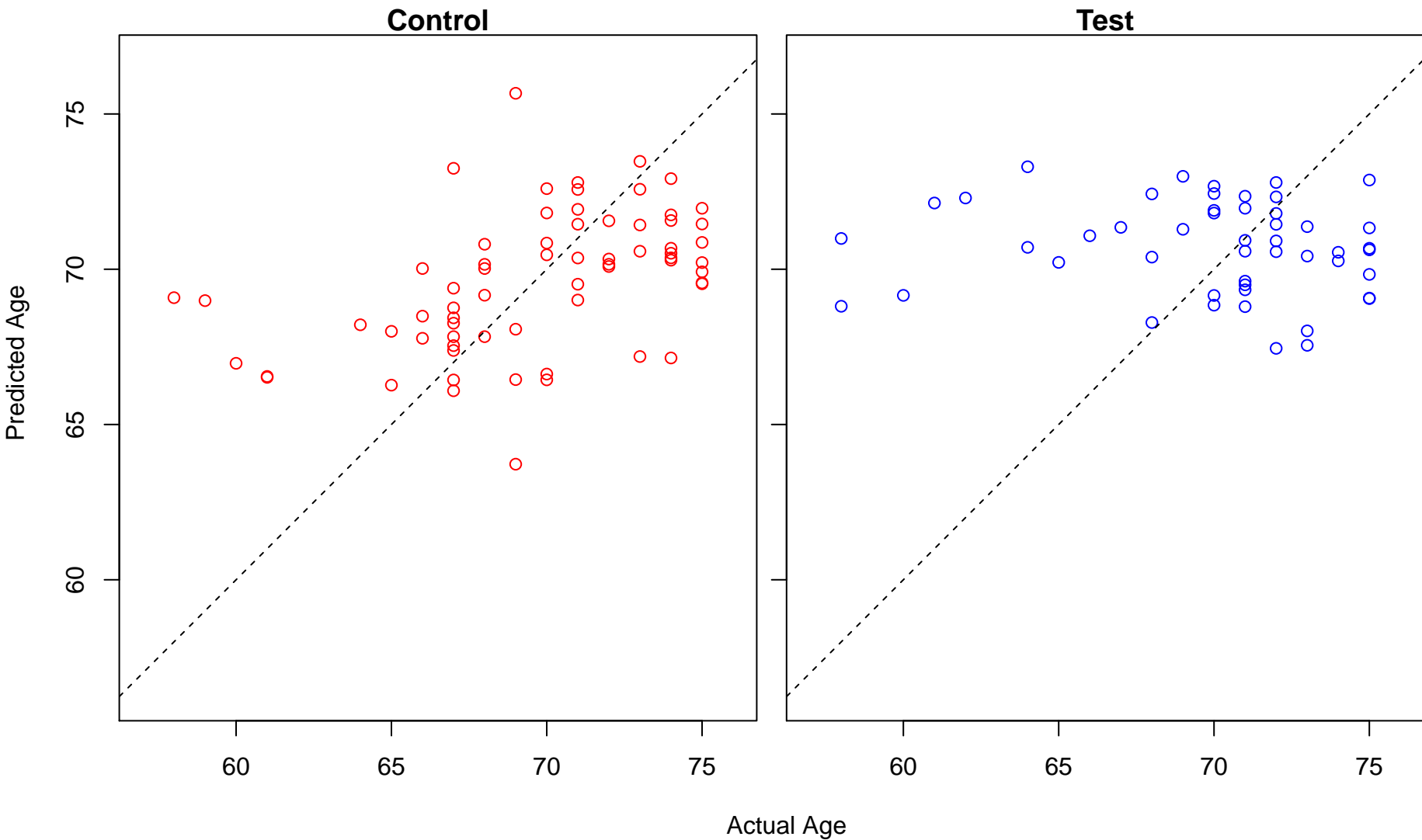


Test

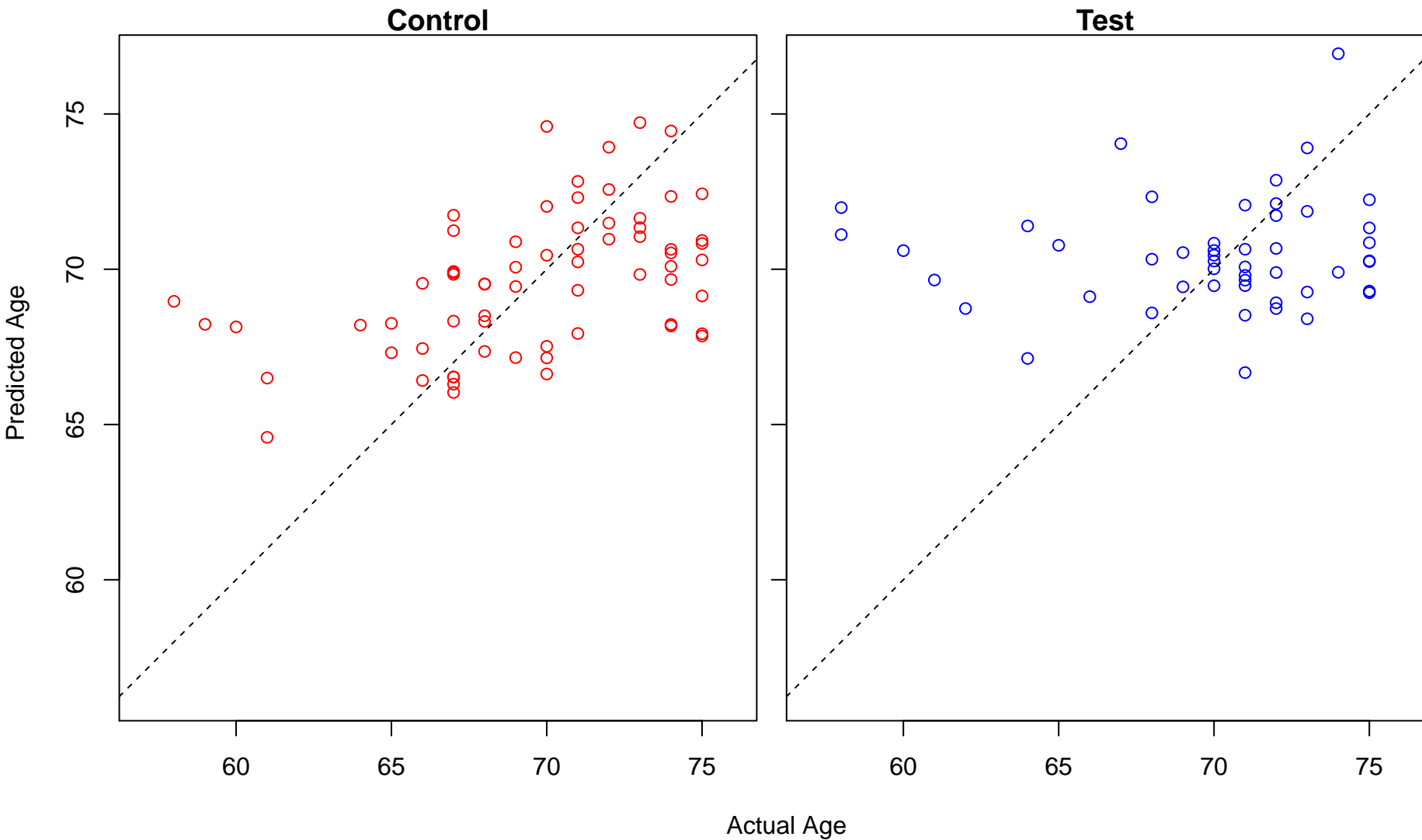


Actual Age

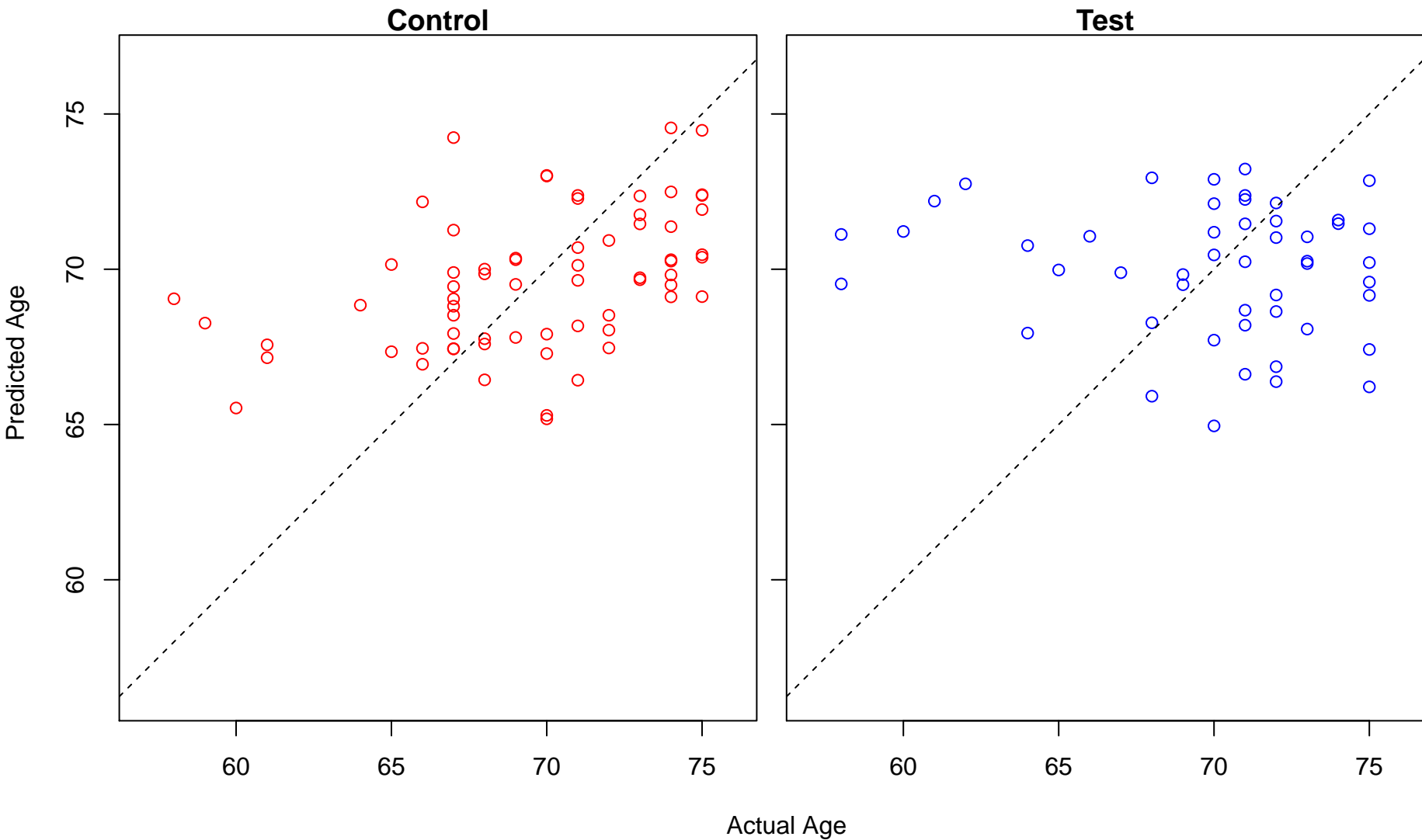
progesterone metabolic process (Score: 0.605942)



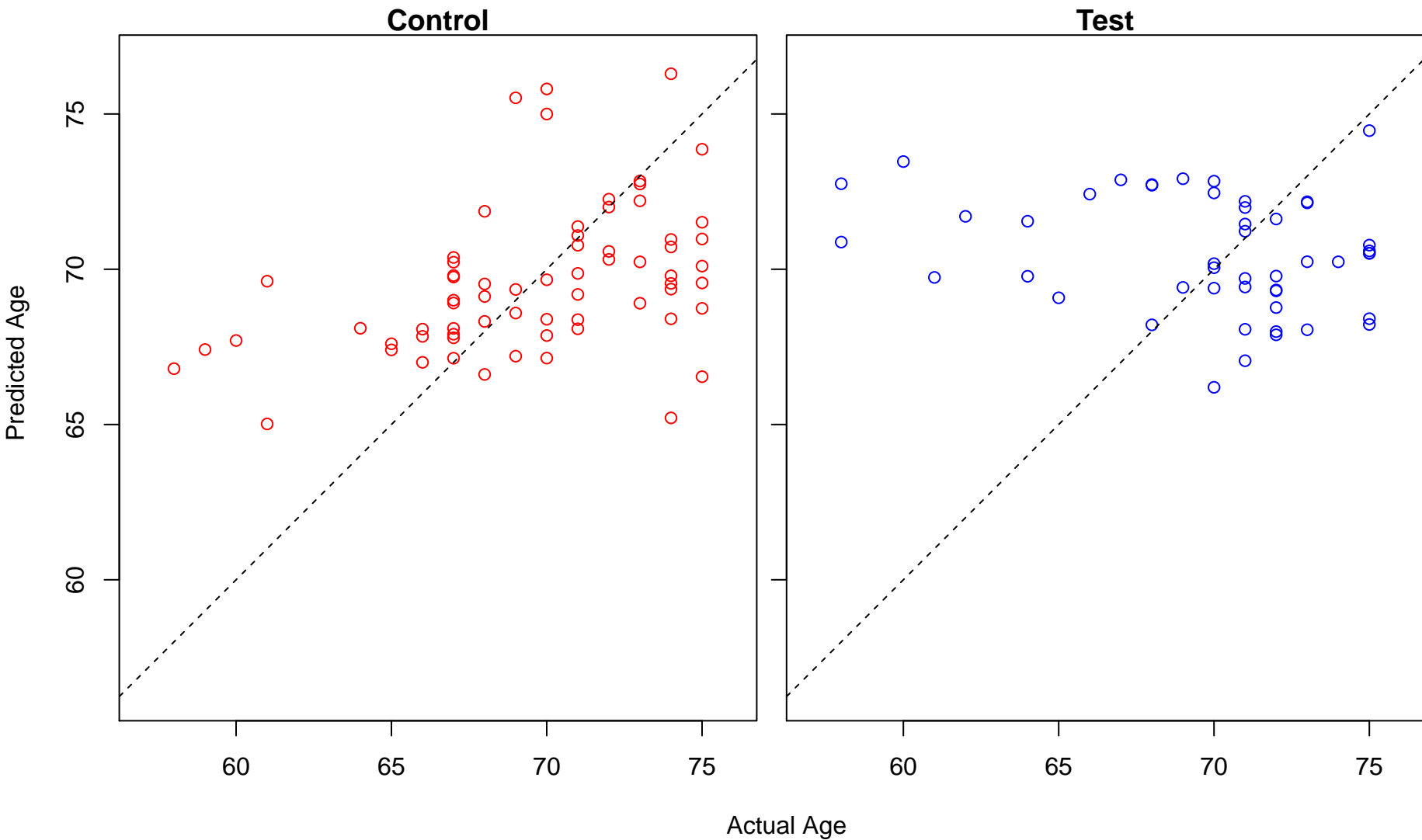
posttranslational protein targeting to membrane (Score: 0.605936)



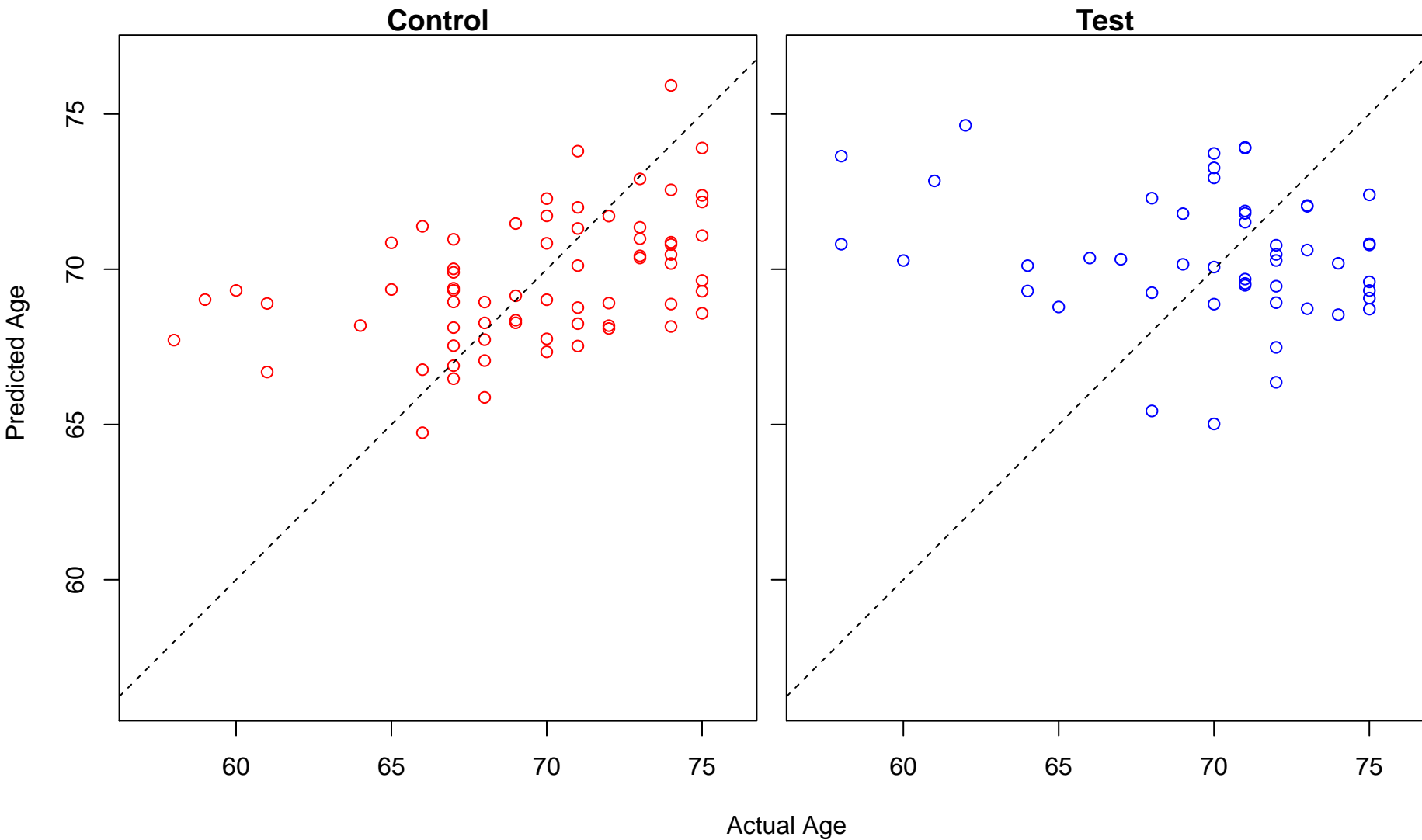
bone resorption (Score: 0.605615)



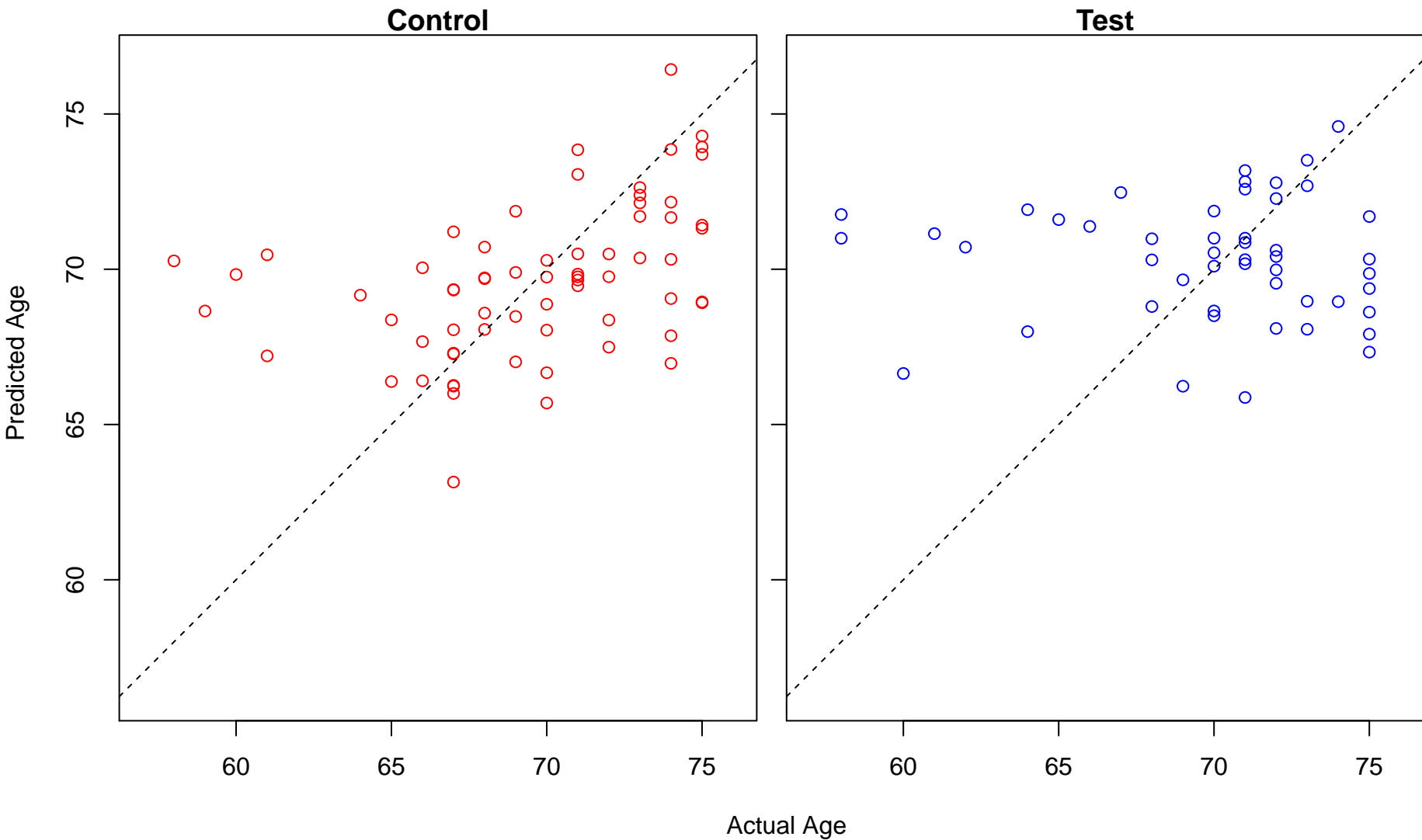
negative regulation of glucocorticoid receptor signaling pathway (Score: 0.605424)



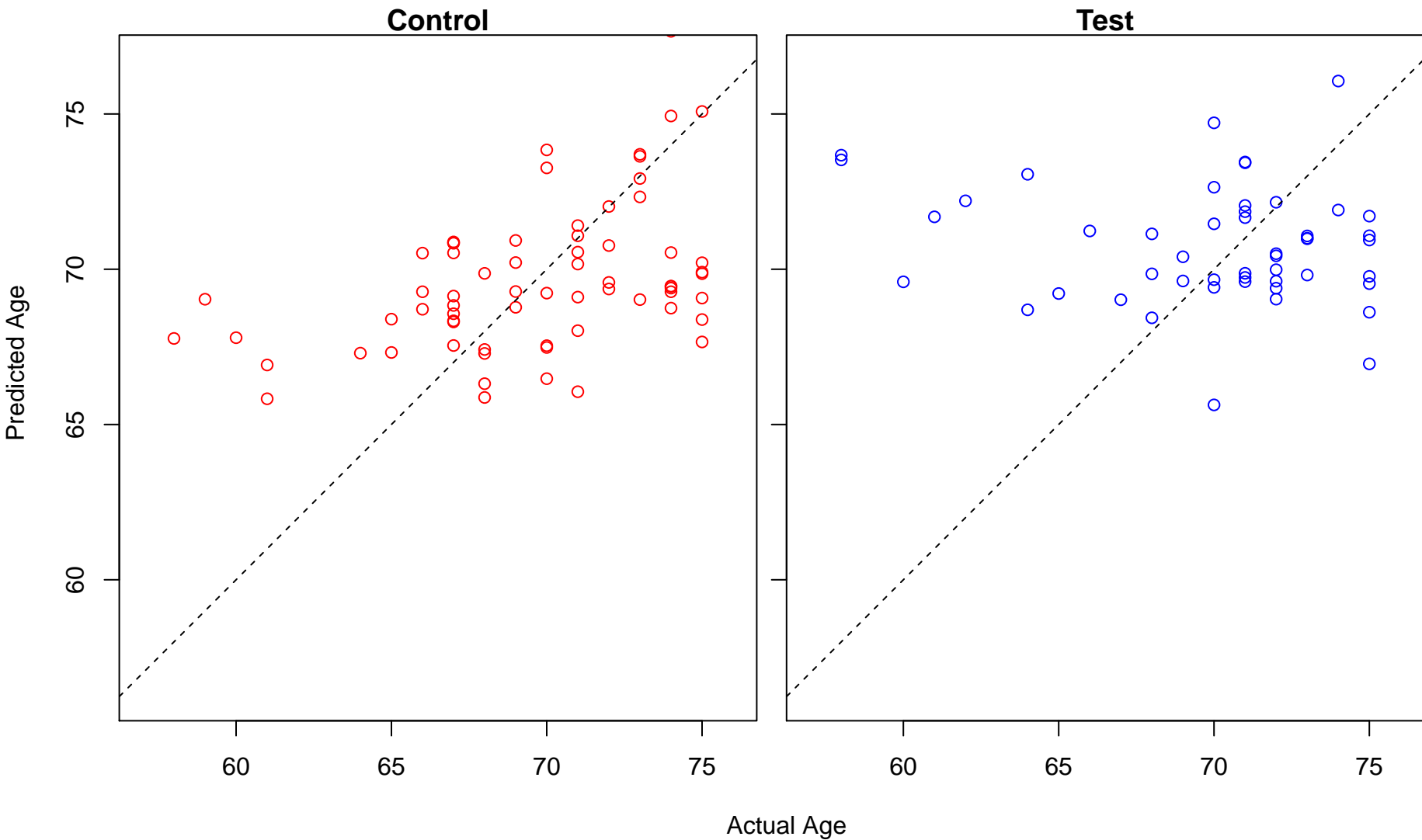
regulation of histone deacetylase activity (Score: 0.605309)



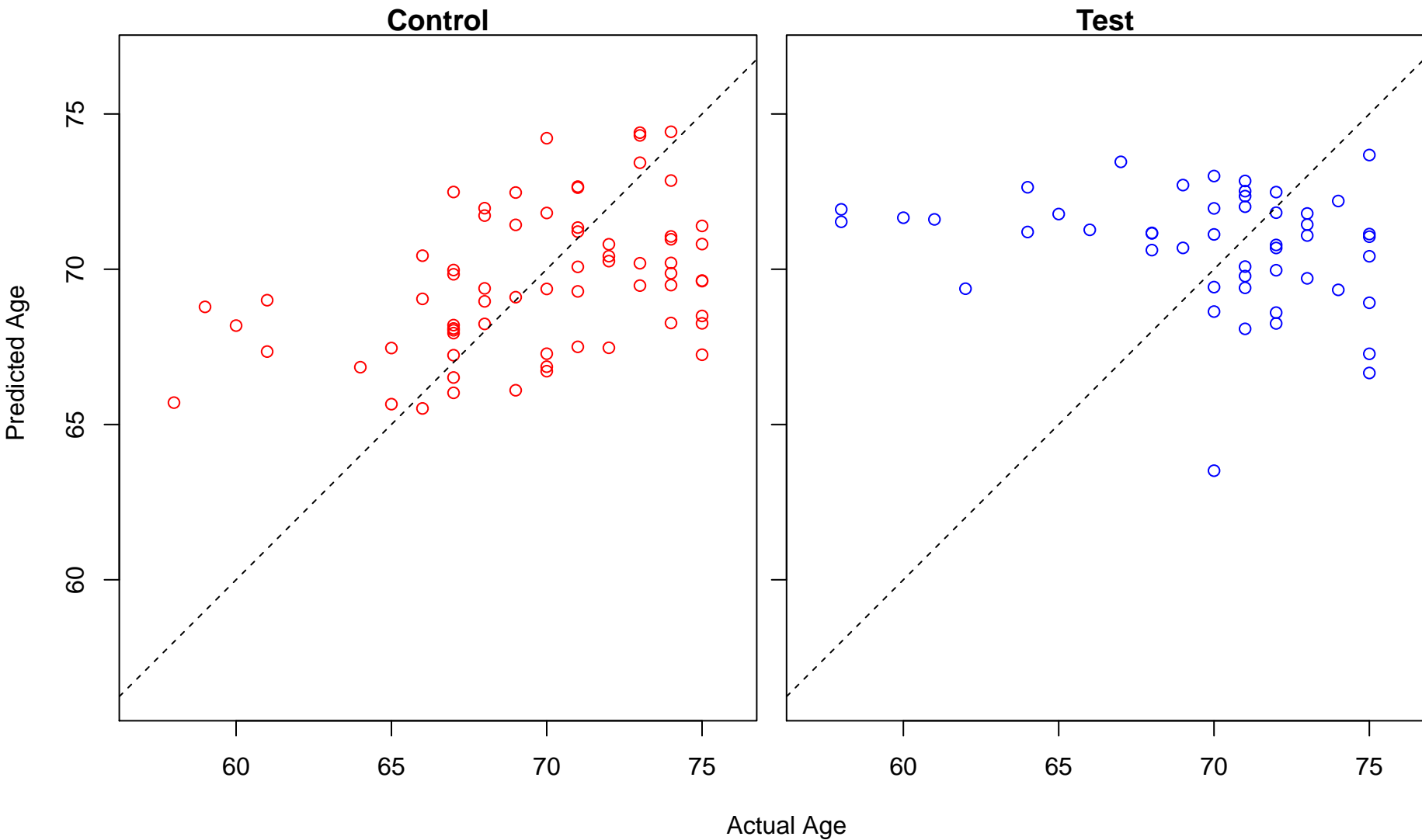
positive regulation of Rho protein signal transduction (Score: 0.605168)



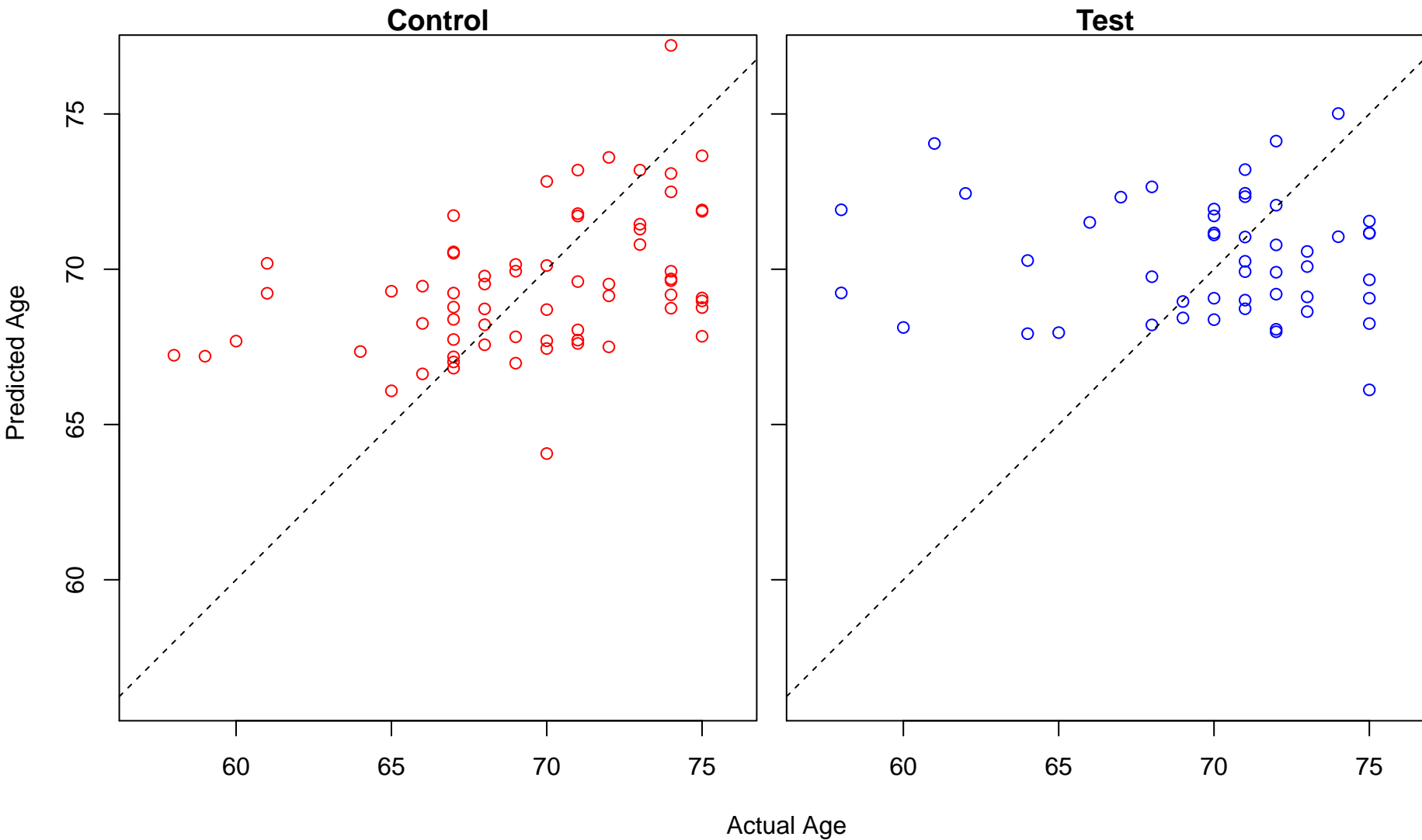
negative regulation of protein autophosphorylation (Score: 0.604145)



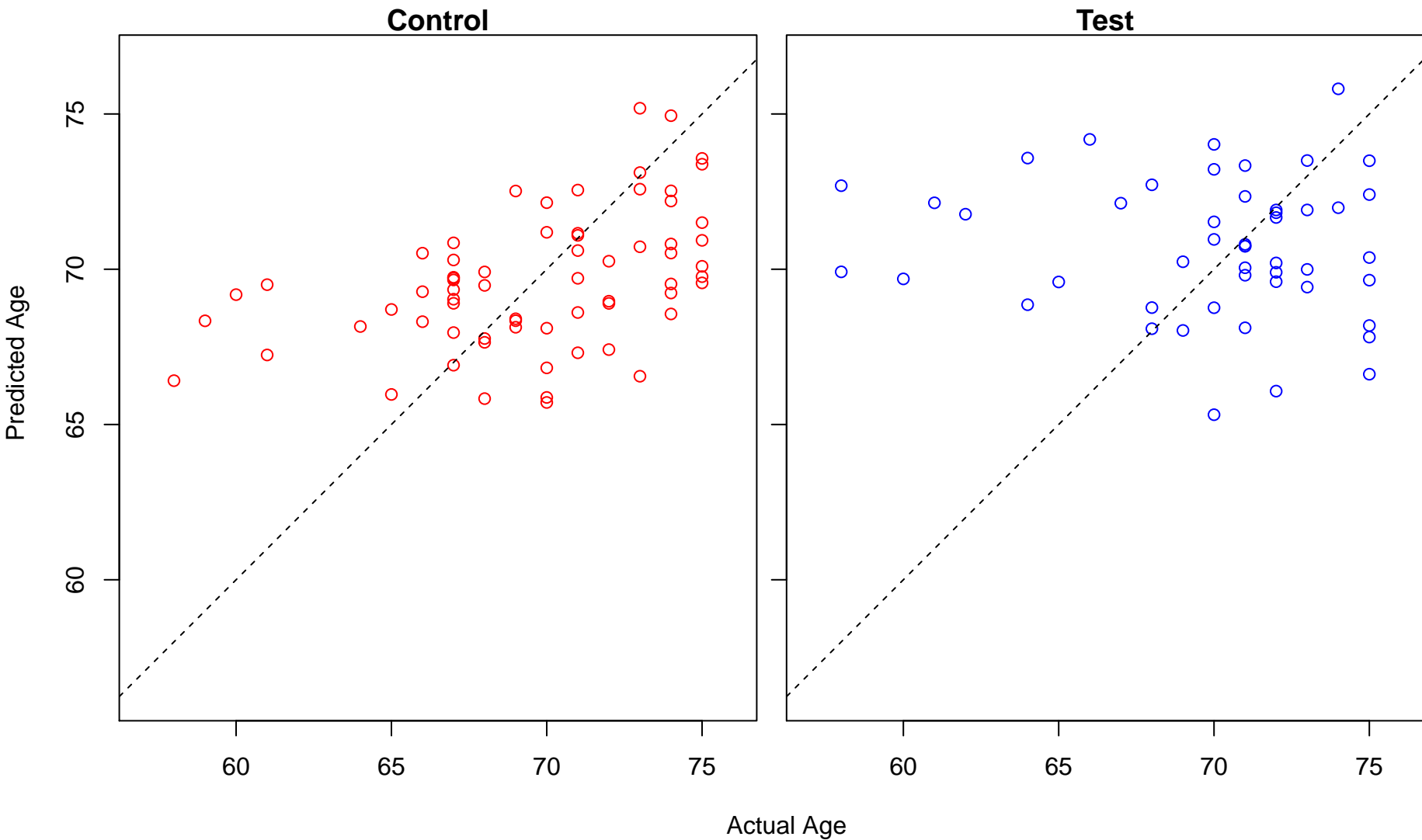
tyrosine phosphorylation of STAT protein (Score: 0.604028)



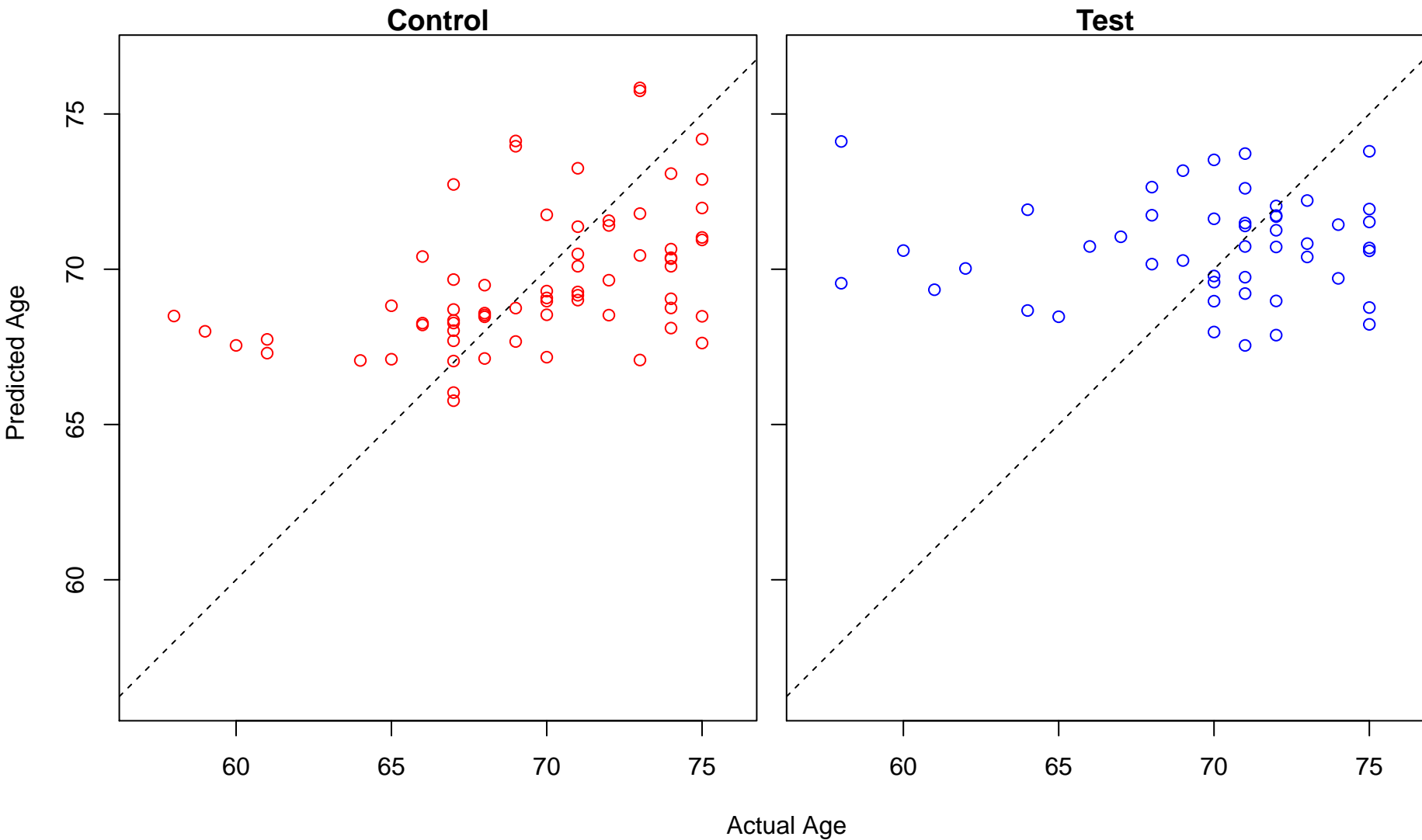
renal system process involved in regulation of systemic arterial blood pressure (Score: 0.603861)



positive regulation of extracellular matrix disassembly (Score: 0.603717)

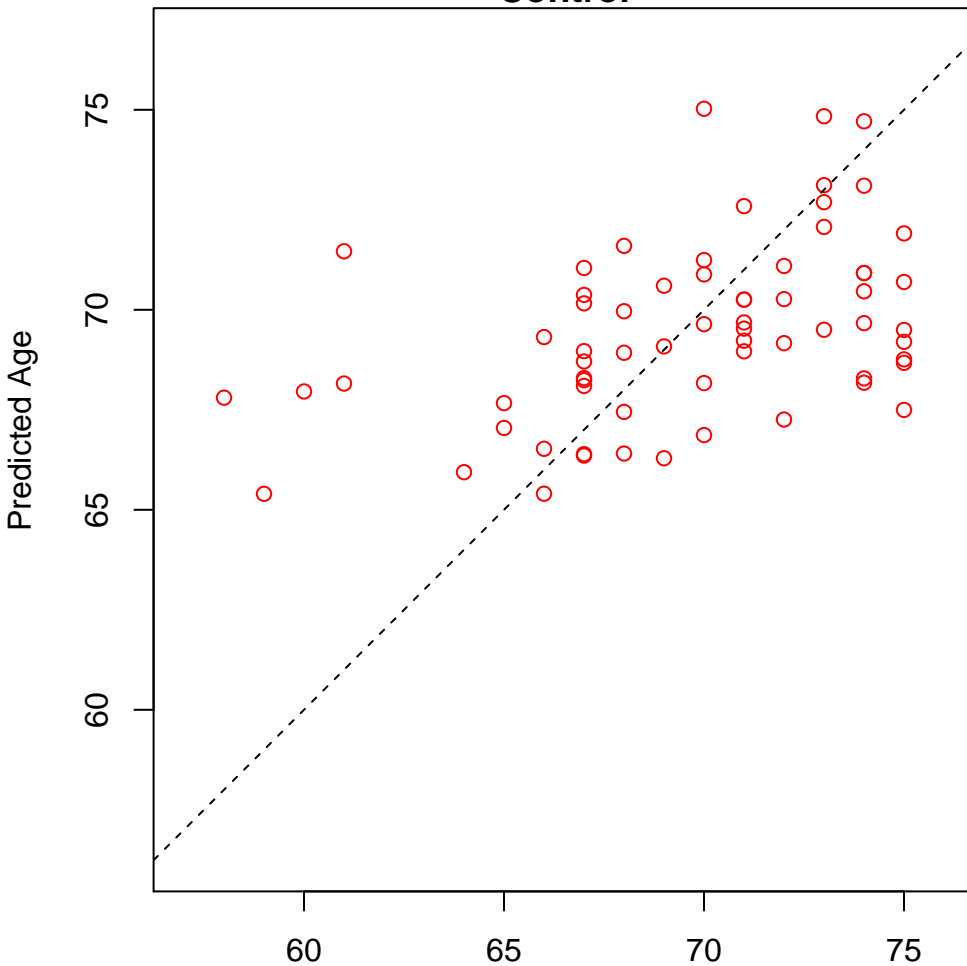


nephric duct development (Score: 0.603217)

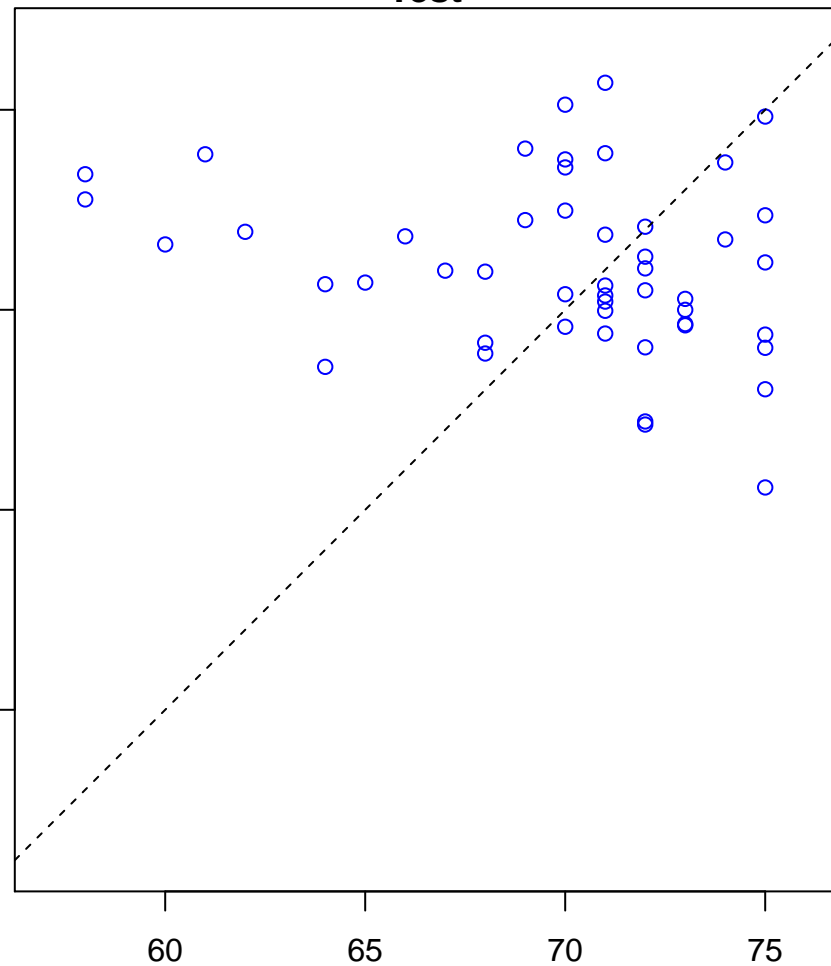


regulation of humoral immune response (Score: 0.603089)

Control

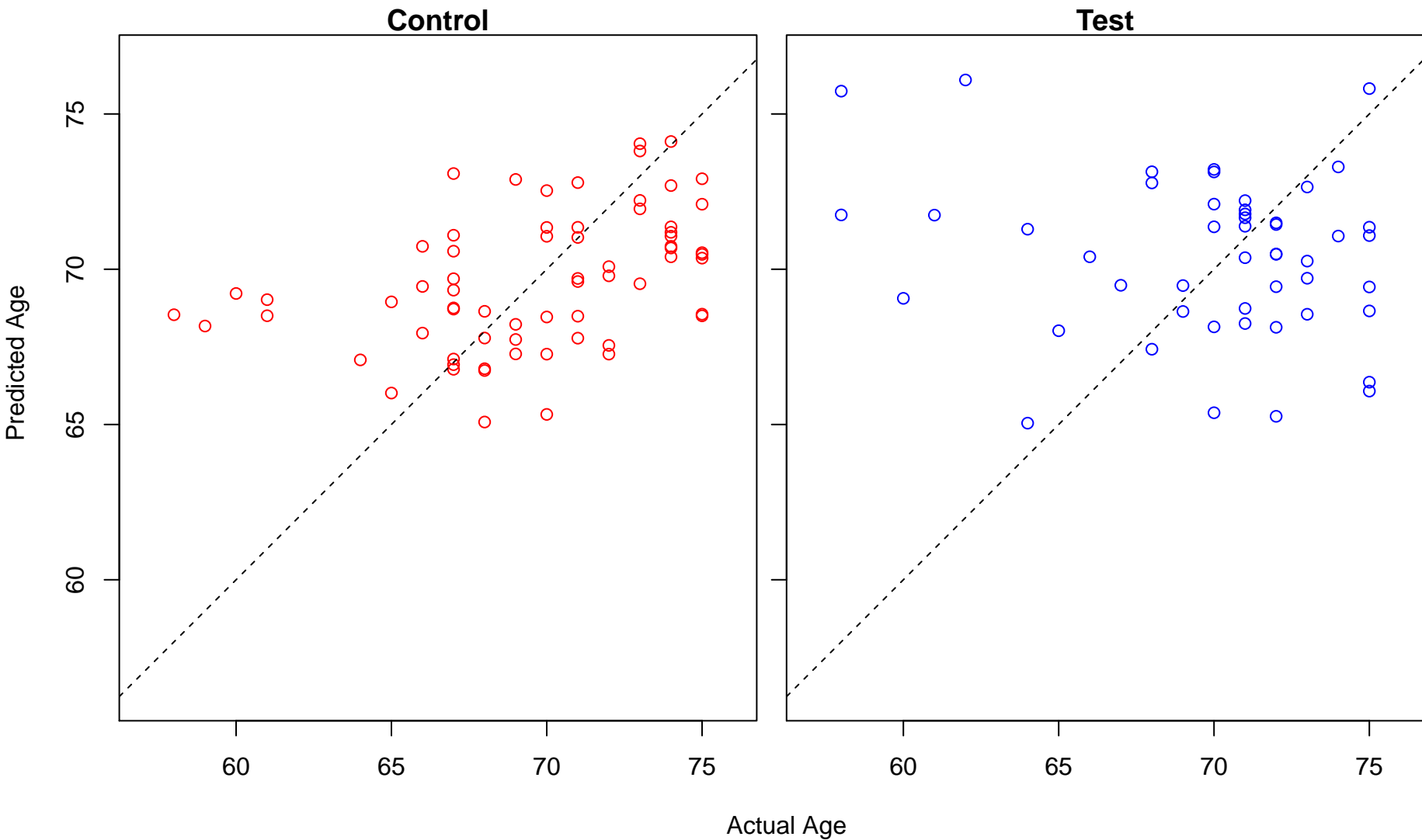


Test

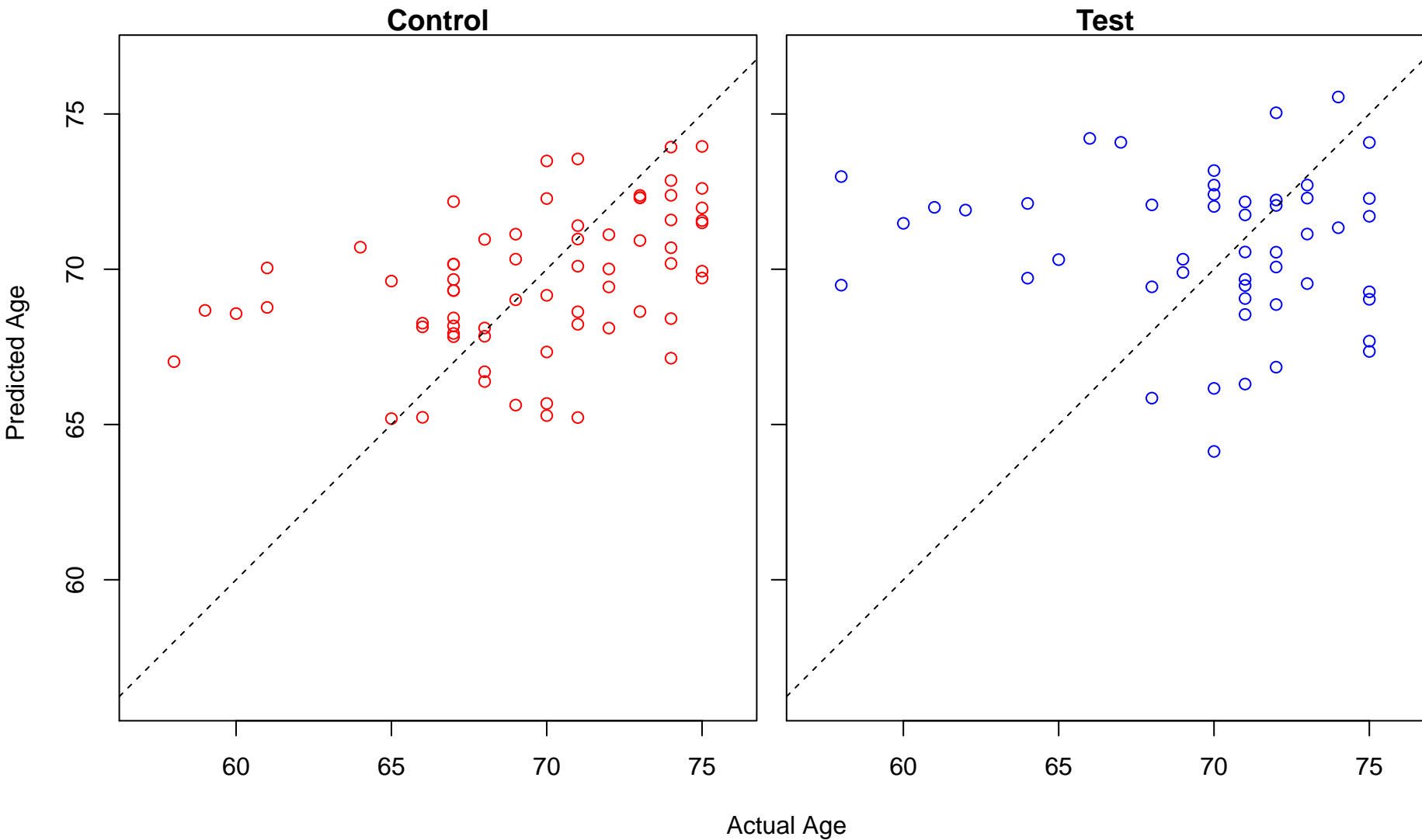


Actual Age

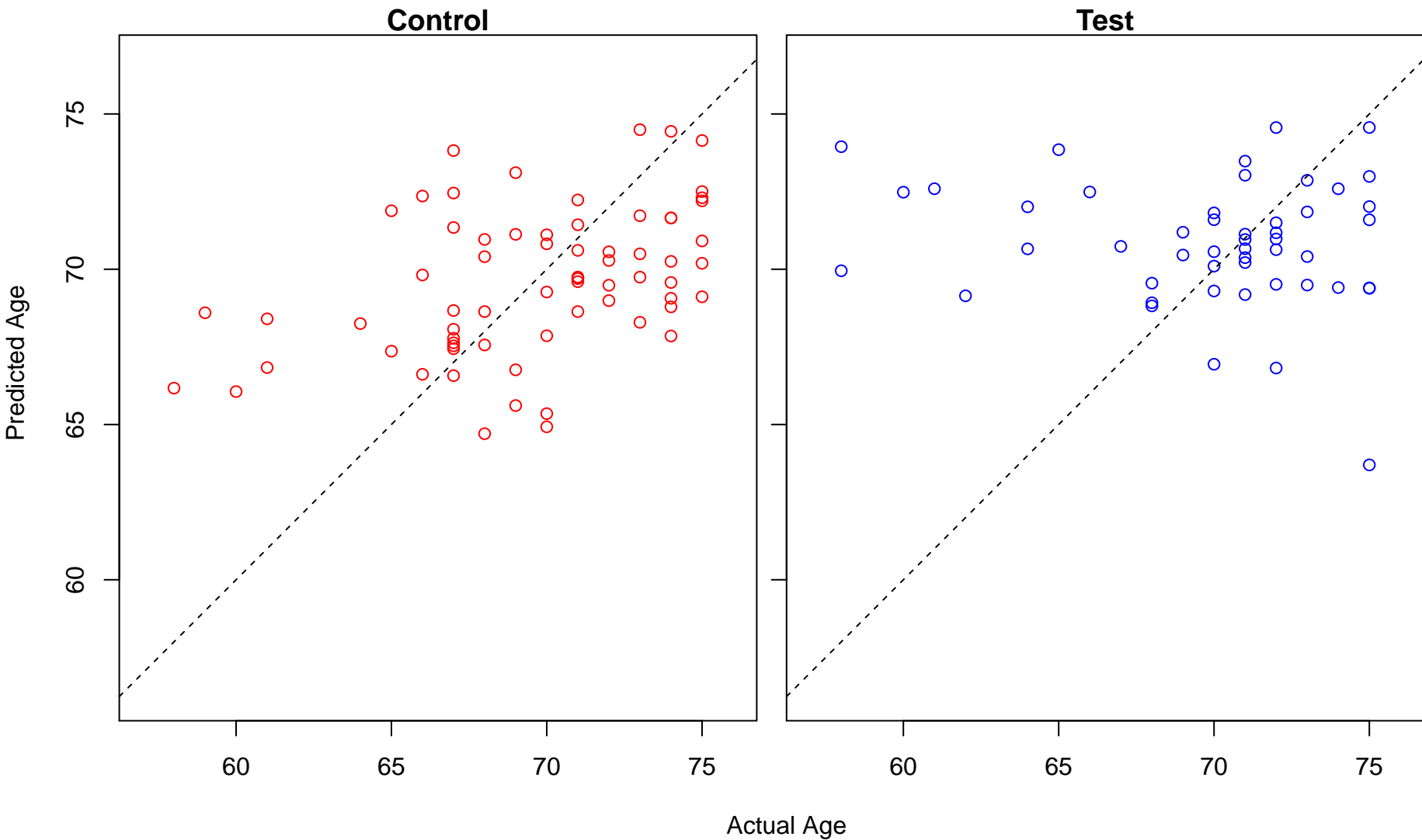
bone maturation (Score: 0.603053)



establishment of apical/basal cell polarity (Score: 0.603020)

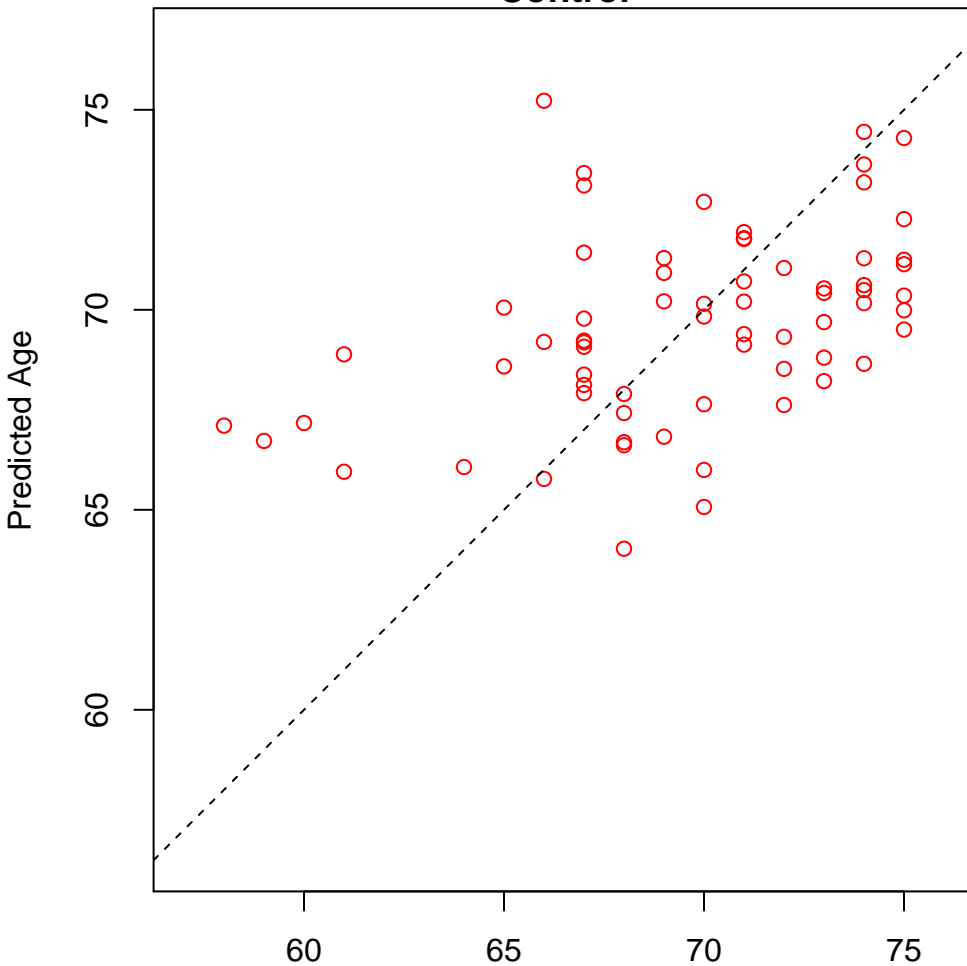


positive regulation of cardiac muscle contraction (Score: 0.602600)

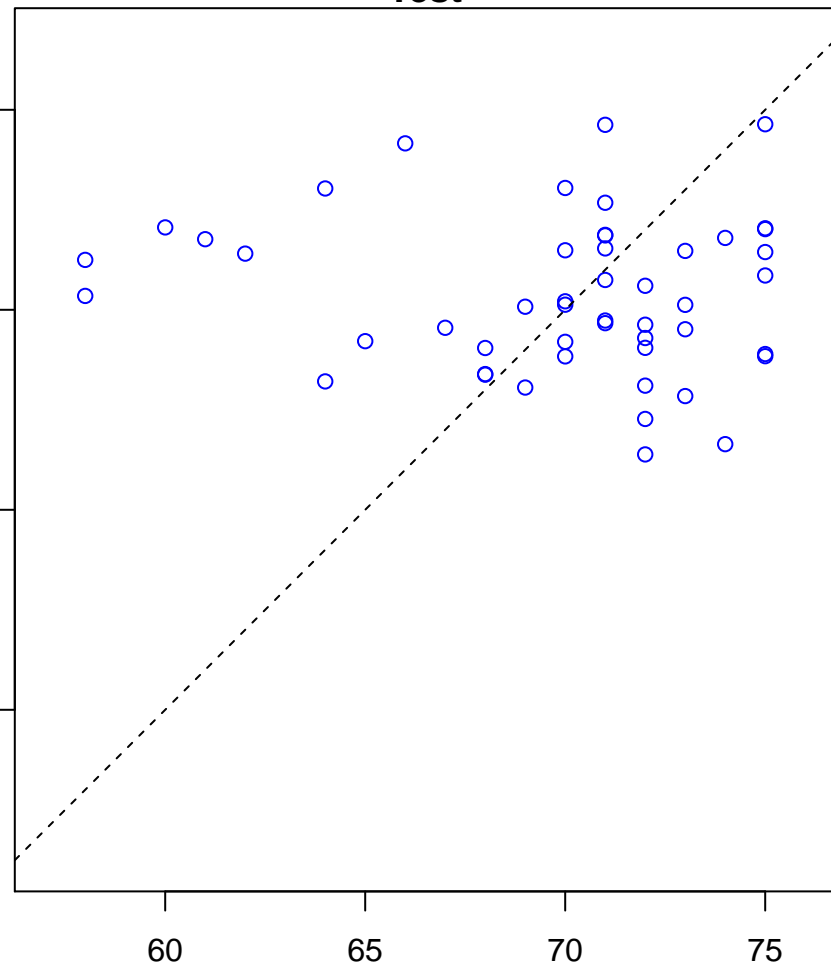


epithelial cell apoptotic process (Score: 0.602463)

Control

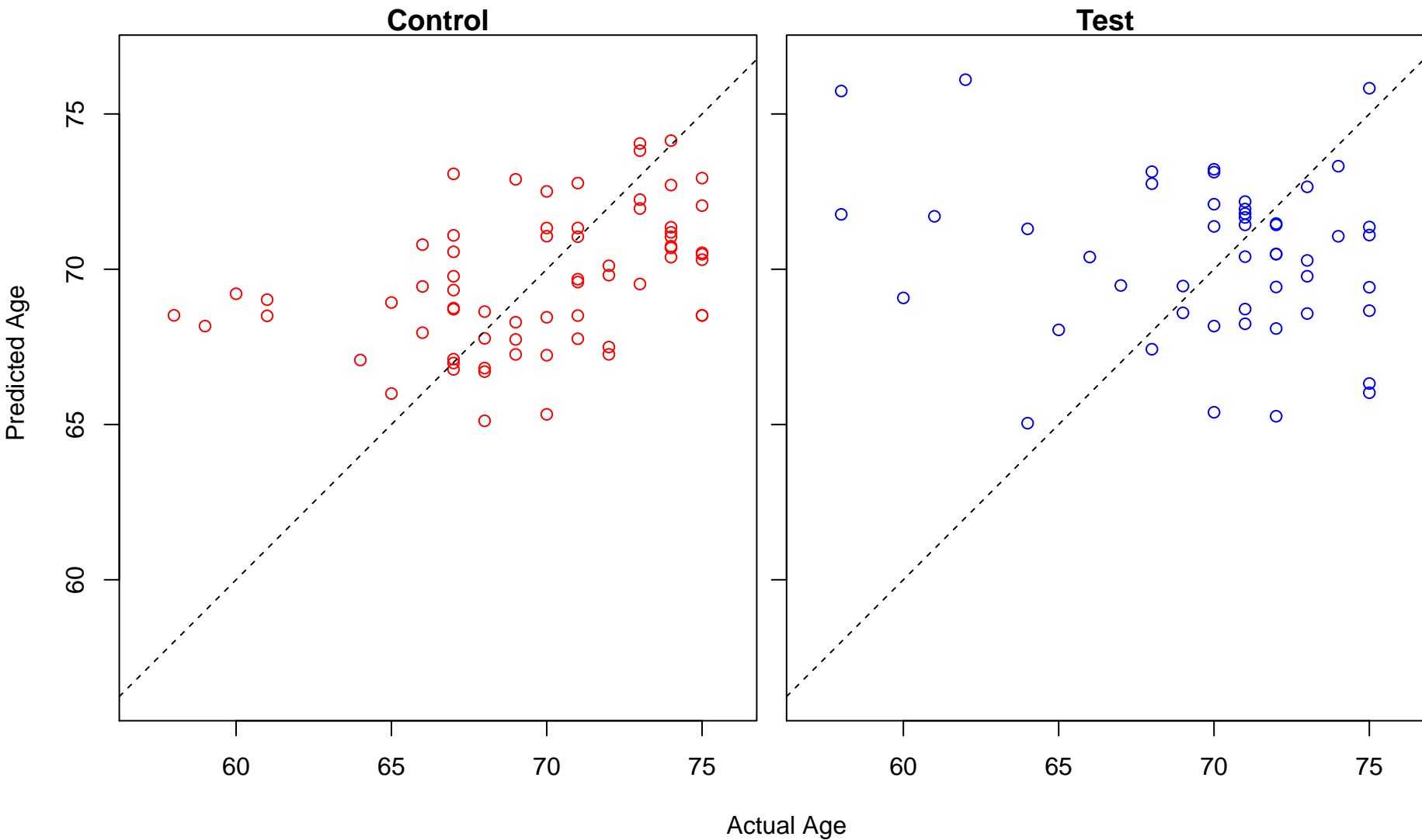


Test

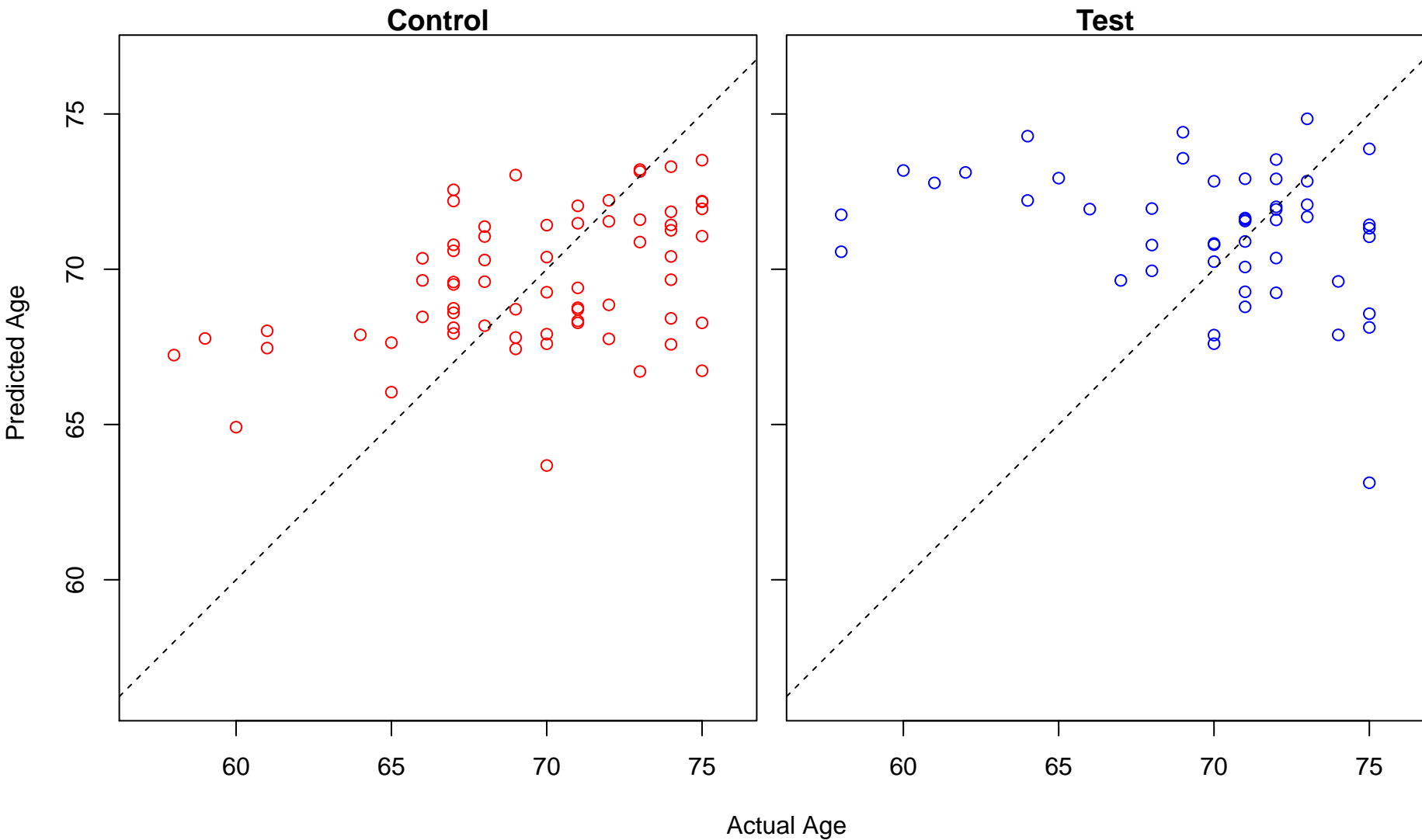


Actual Age

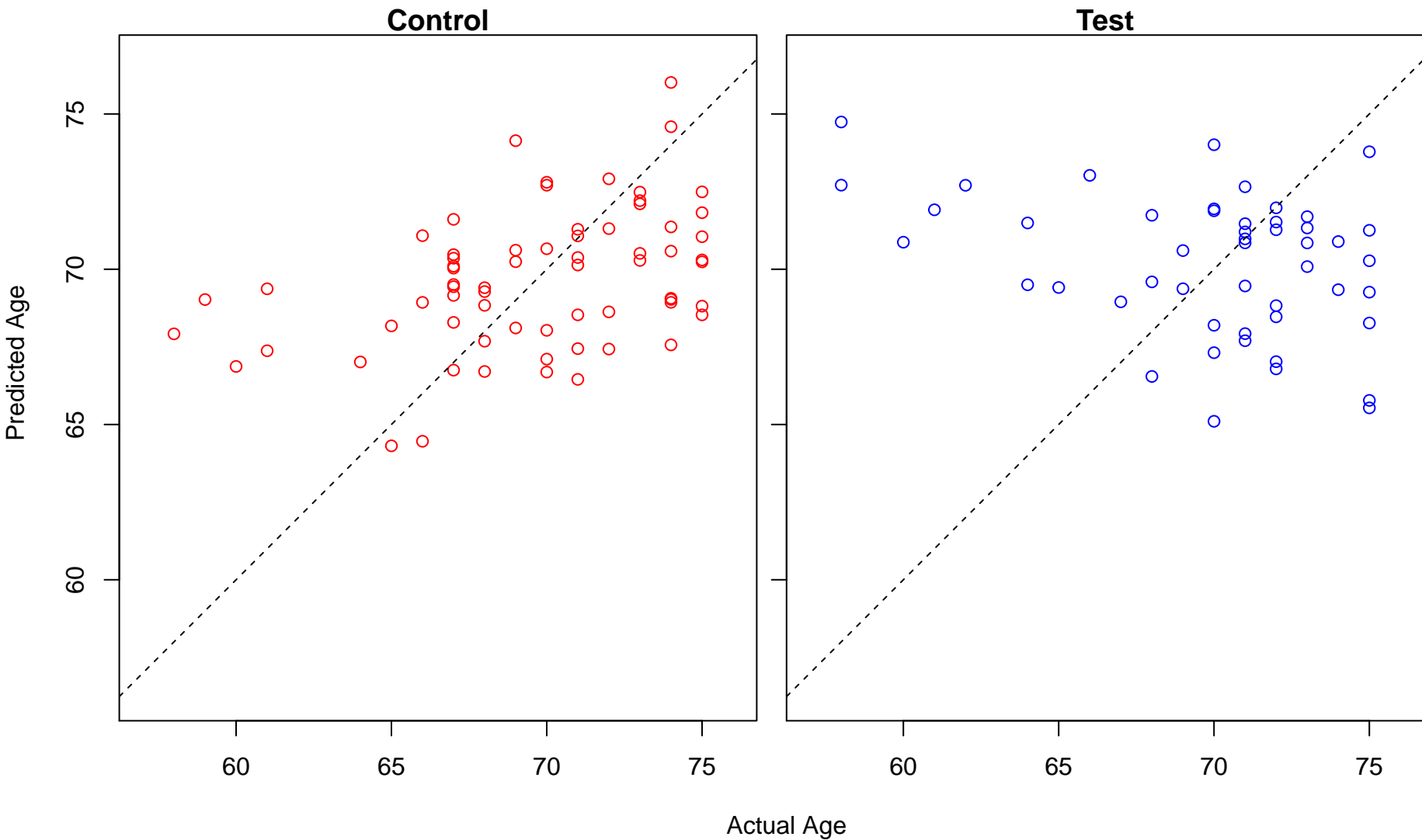
organ maturation (Score: 0.602077)



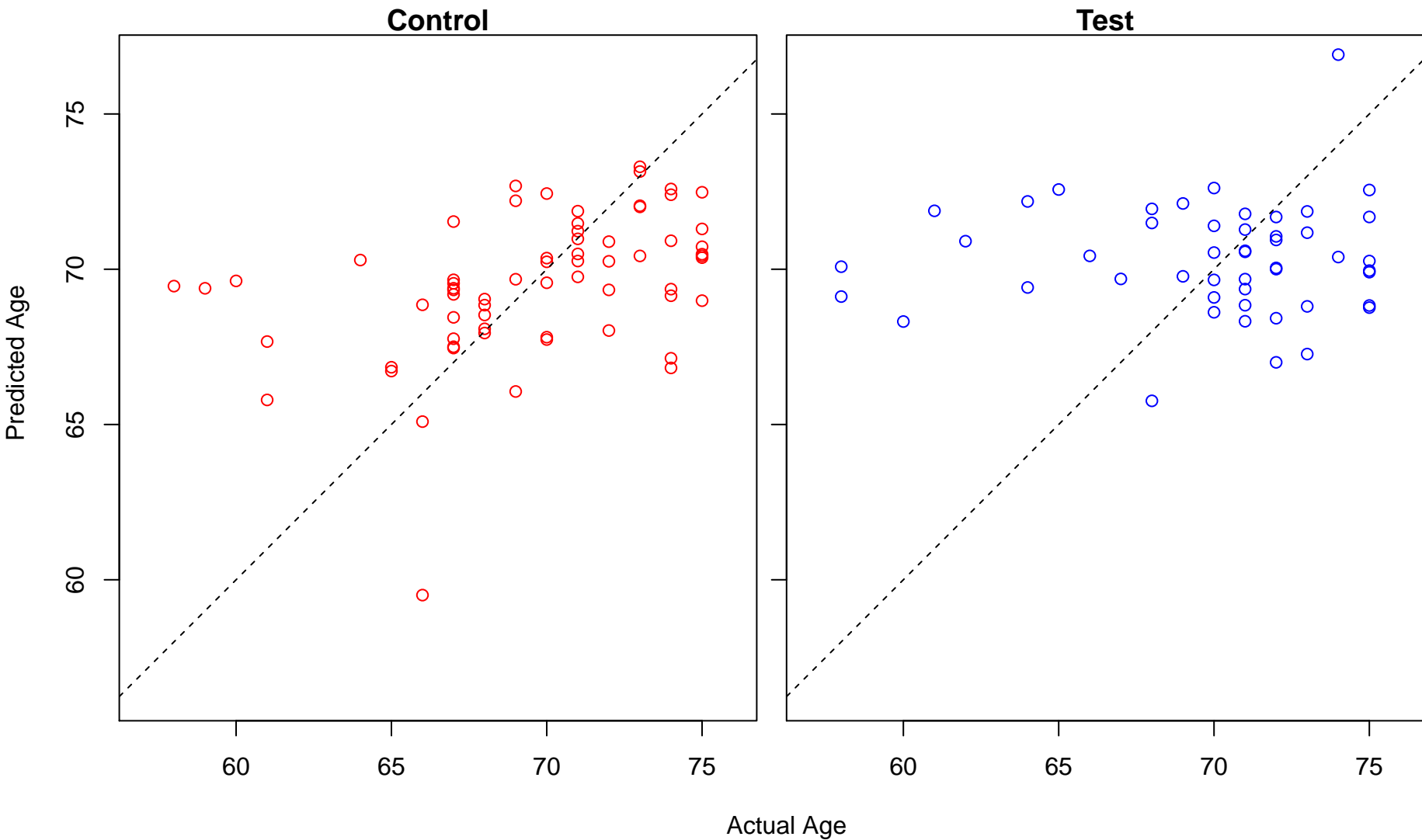
regulation of smooth muscle cell differentiation (Score: 0.601722)



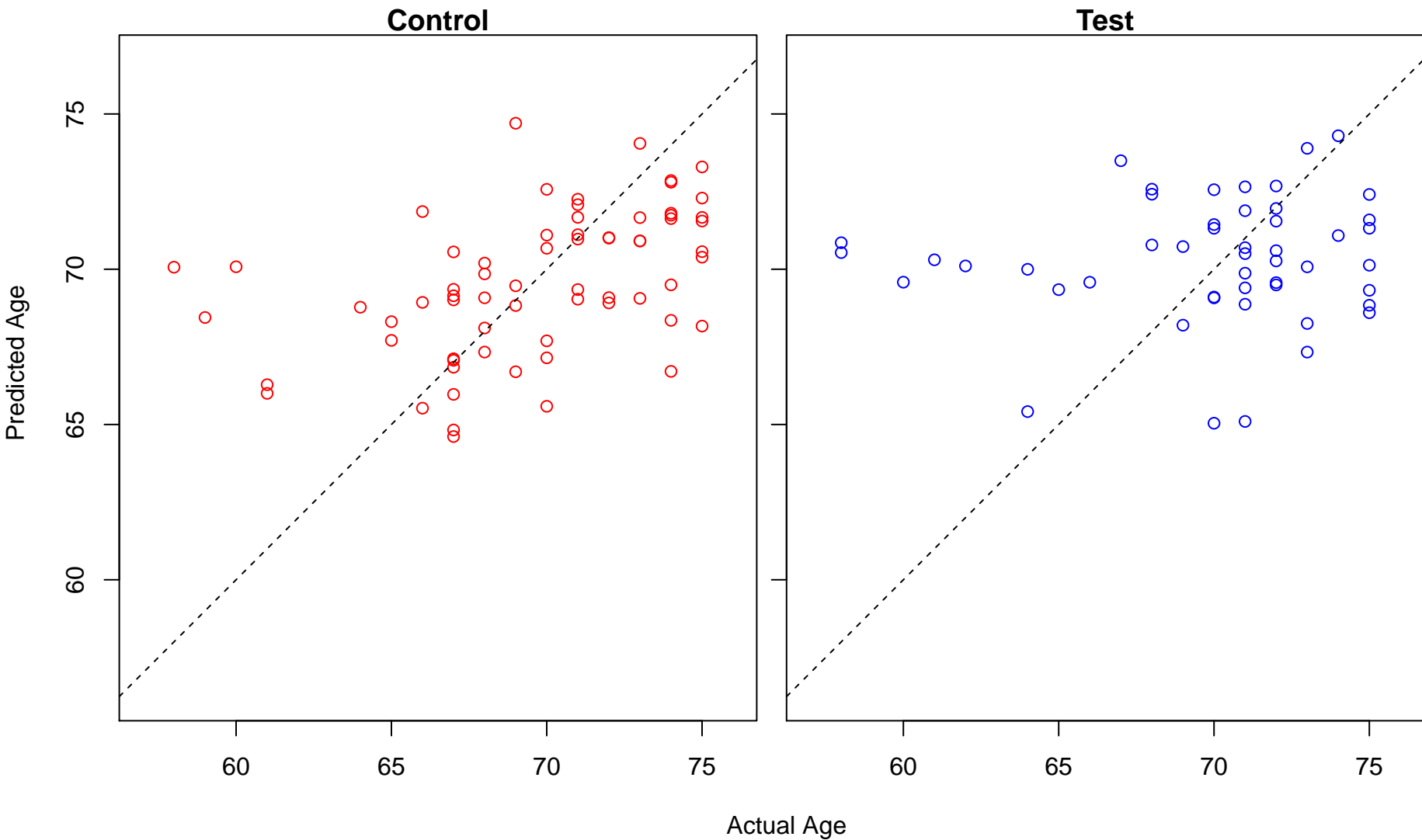
regulation of retrograde protein transport, ER to cytosol (Score: 0.600609)



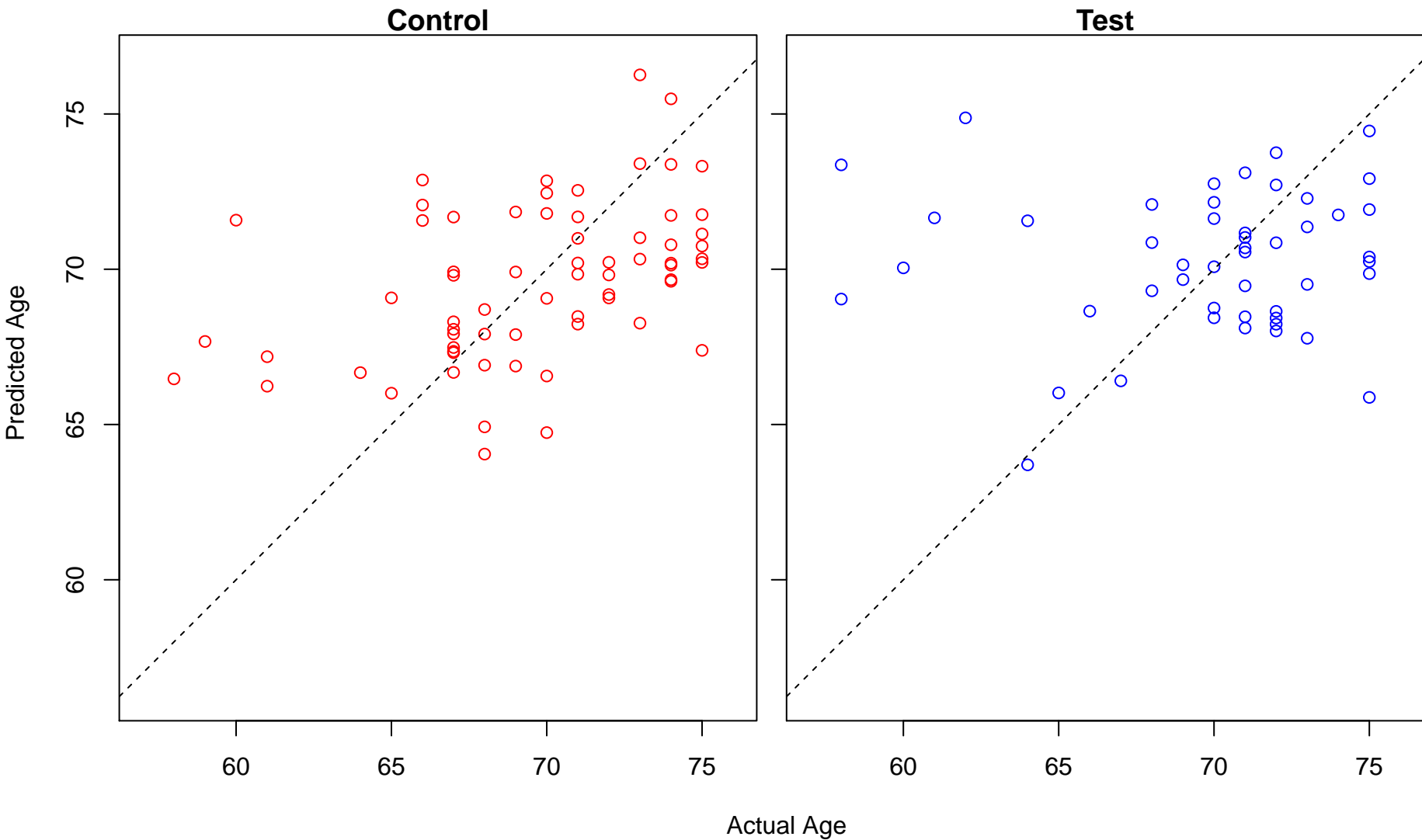
protein to membrane docking (Score: 0.600399)



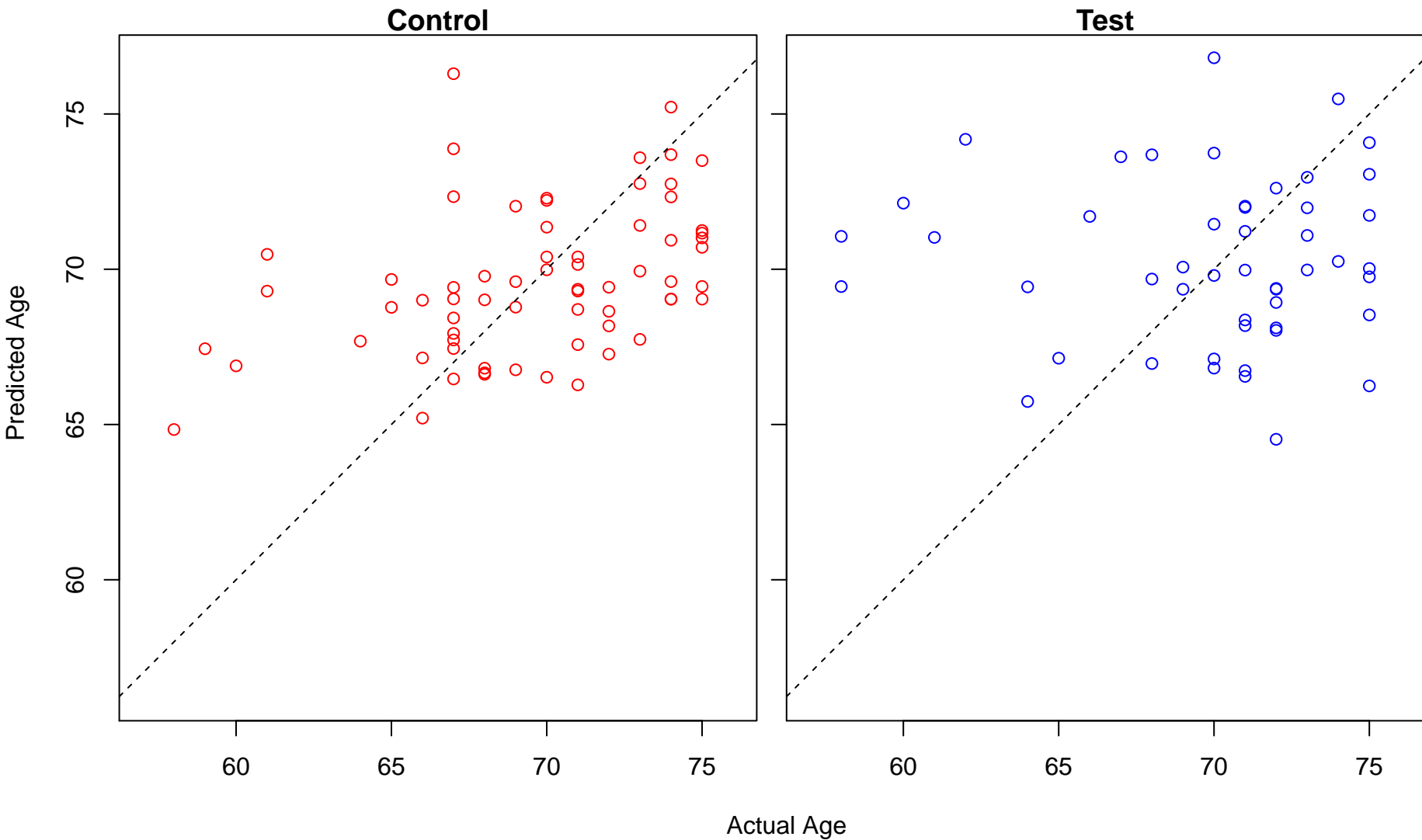
glutamate metabolic process (Score: 0.600144)



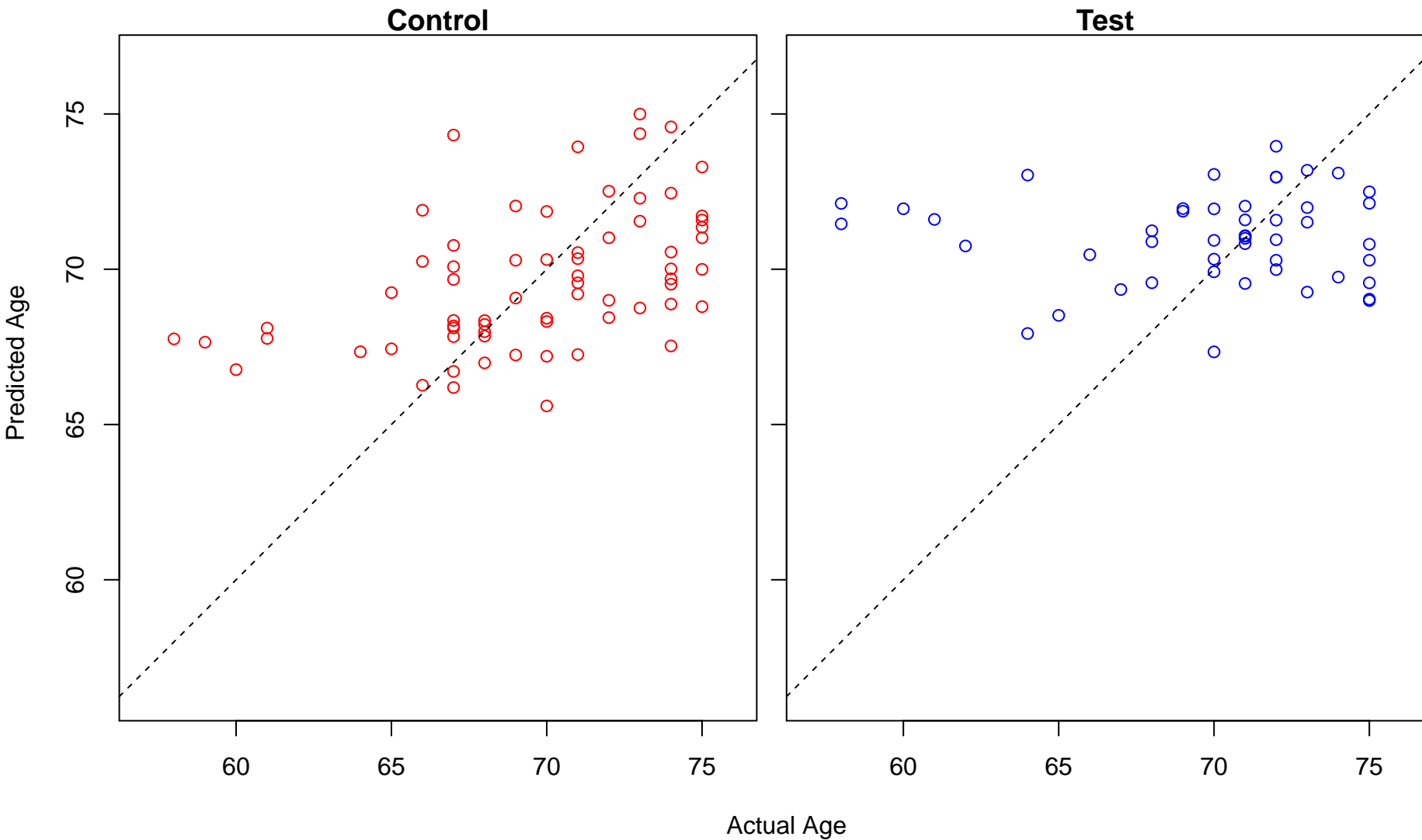
regulation of collateral sprouting (Score: 0.599237)



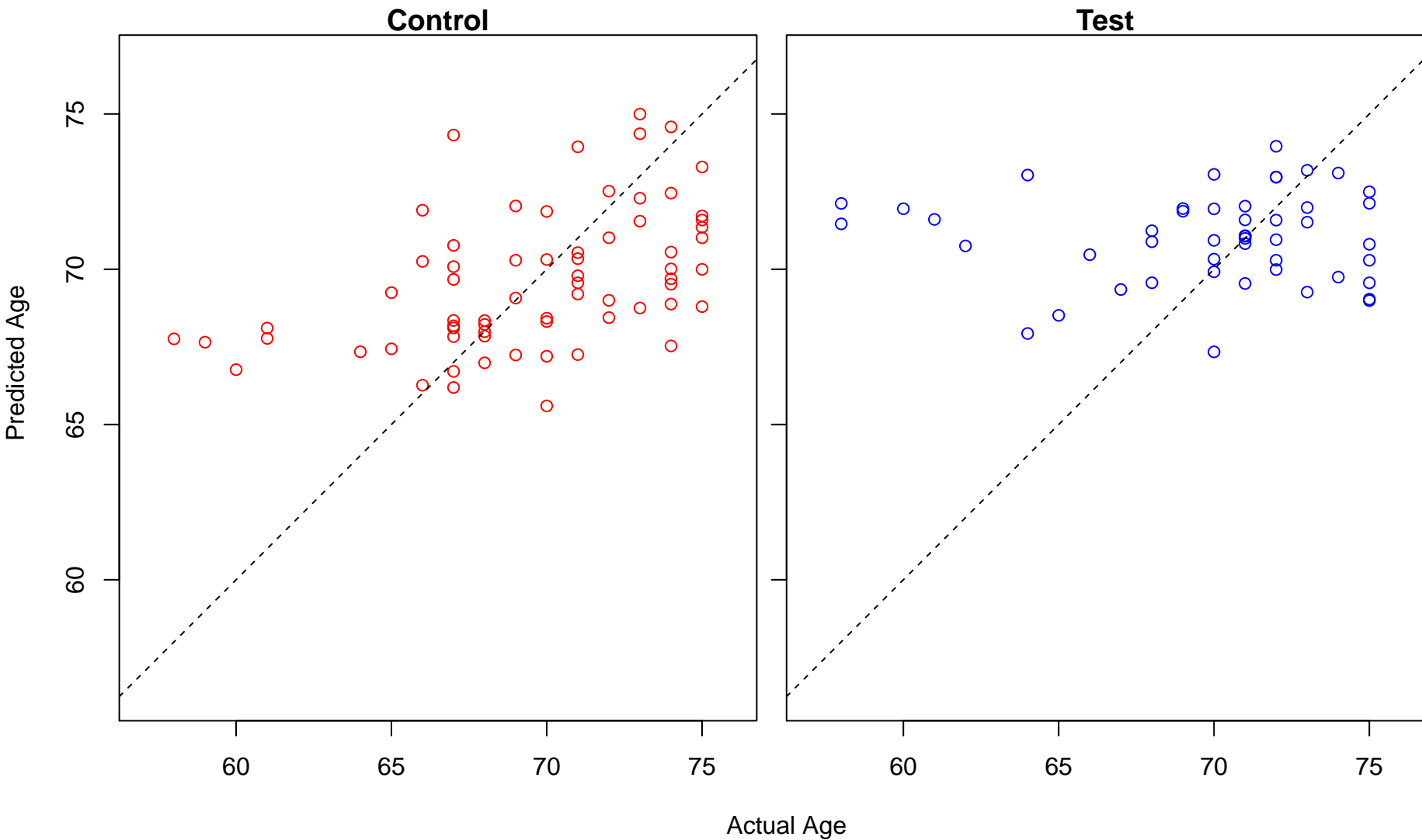
high-density lipoprotein particle remodeling (Score: 0.598787)



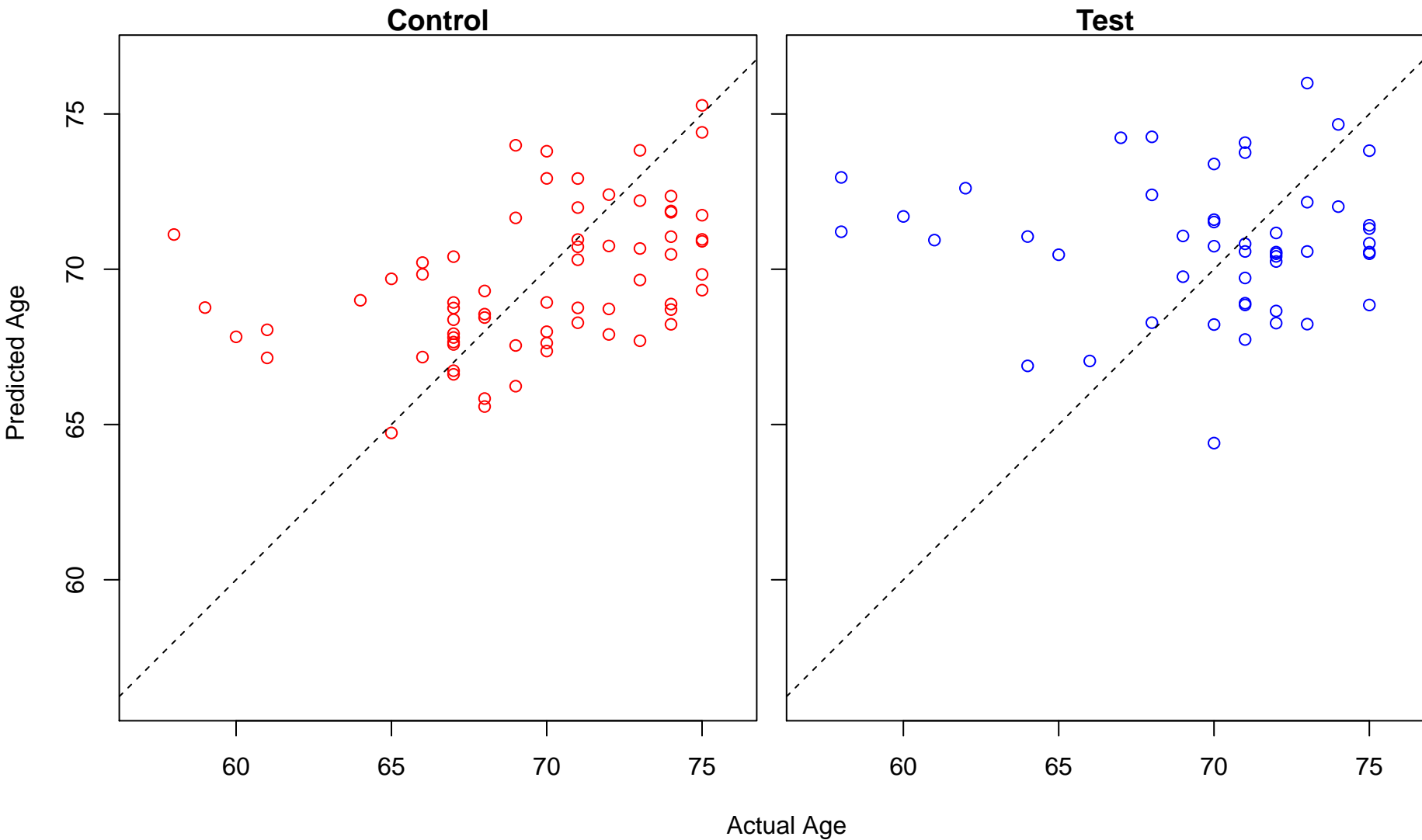
endochondral ossification (Score: 0.598201)



replacement ossification (Score: 0.598201)

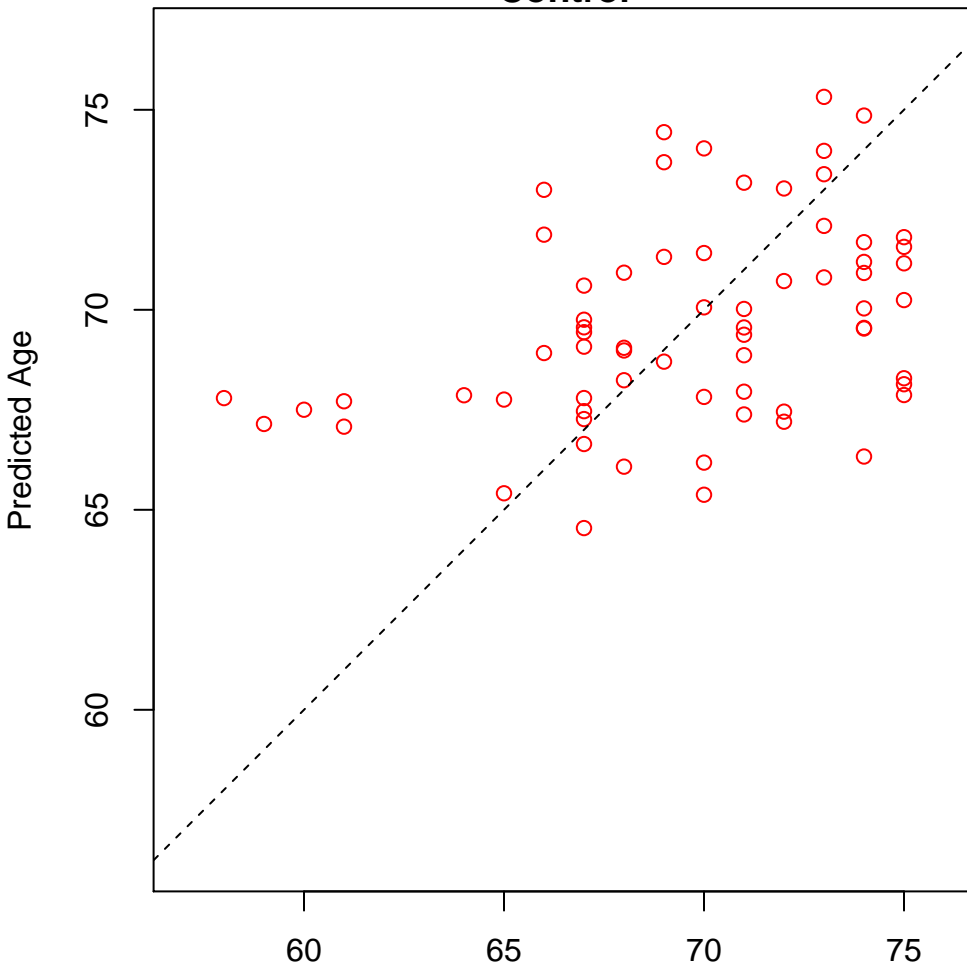


response to cholesterol (Score: 0.596834)

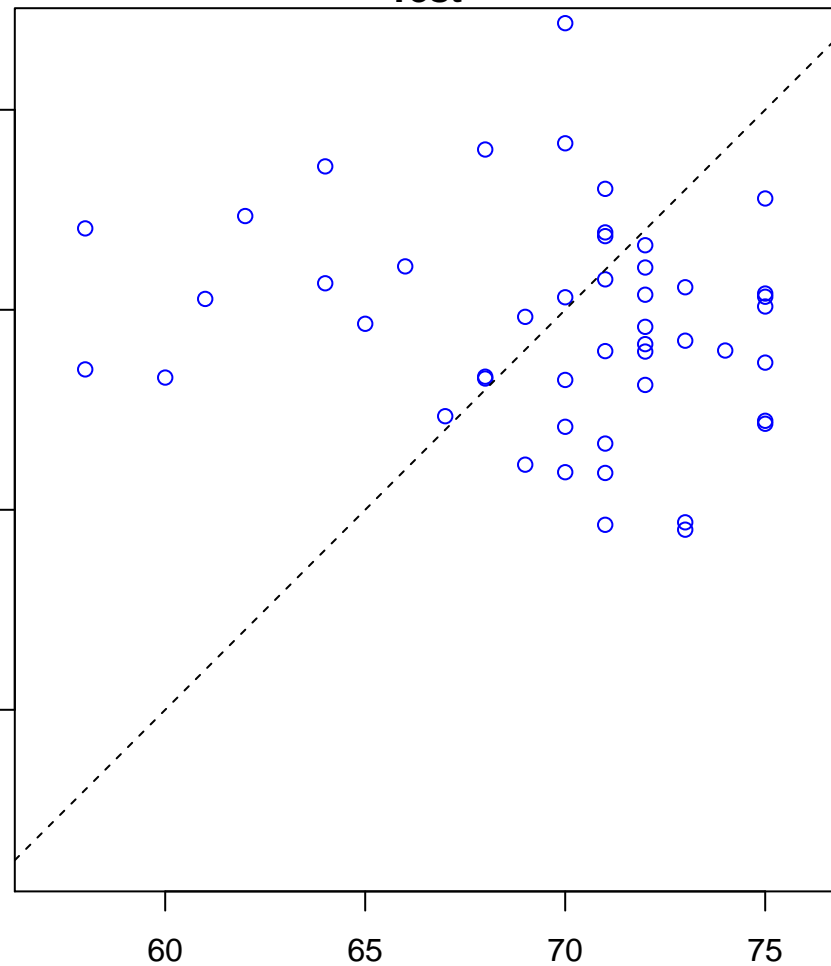


embryonic forelimb morphogenesis (Score: 0.596826)

Control

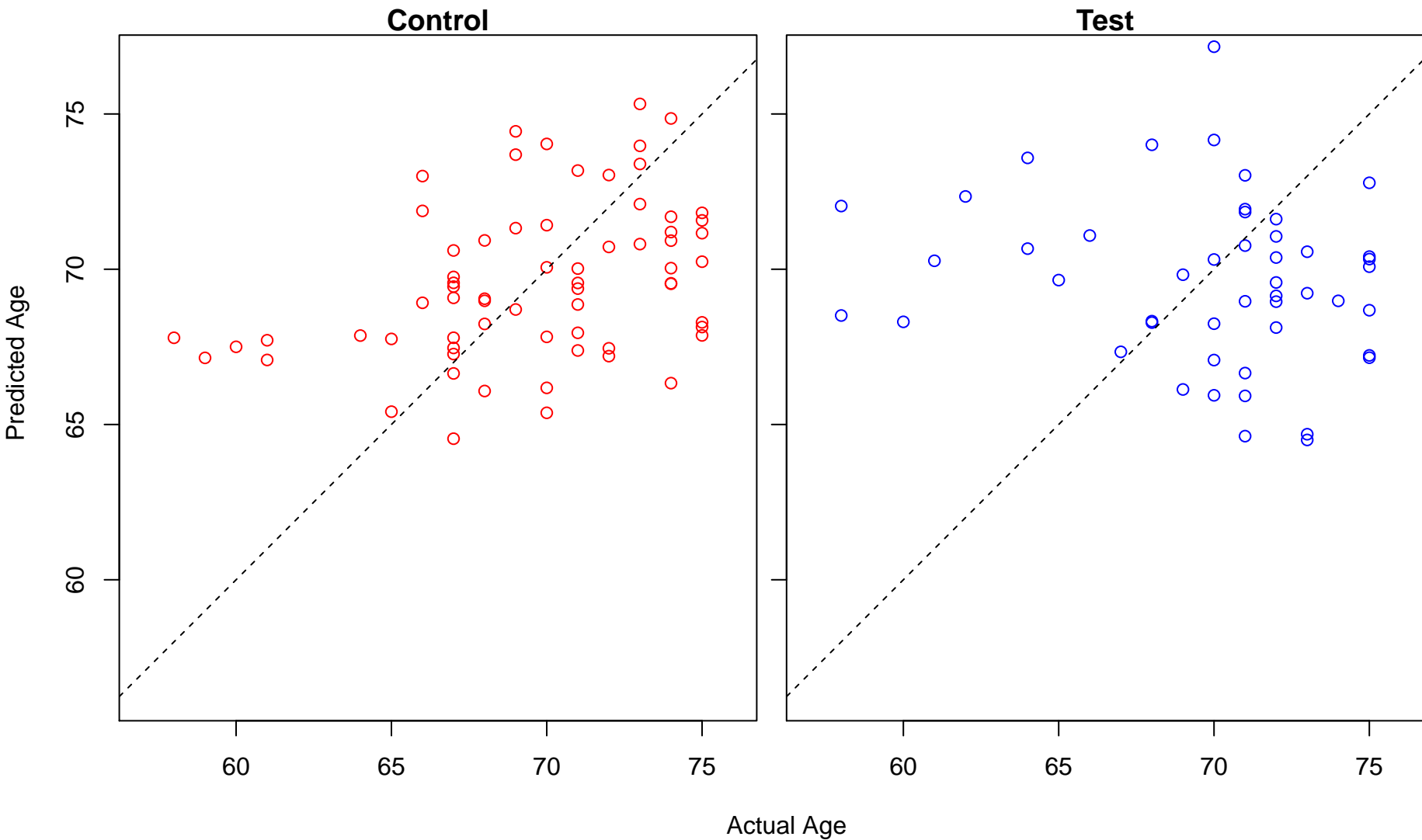


Test

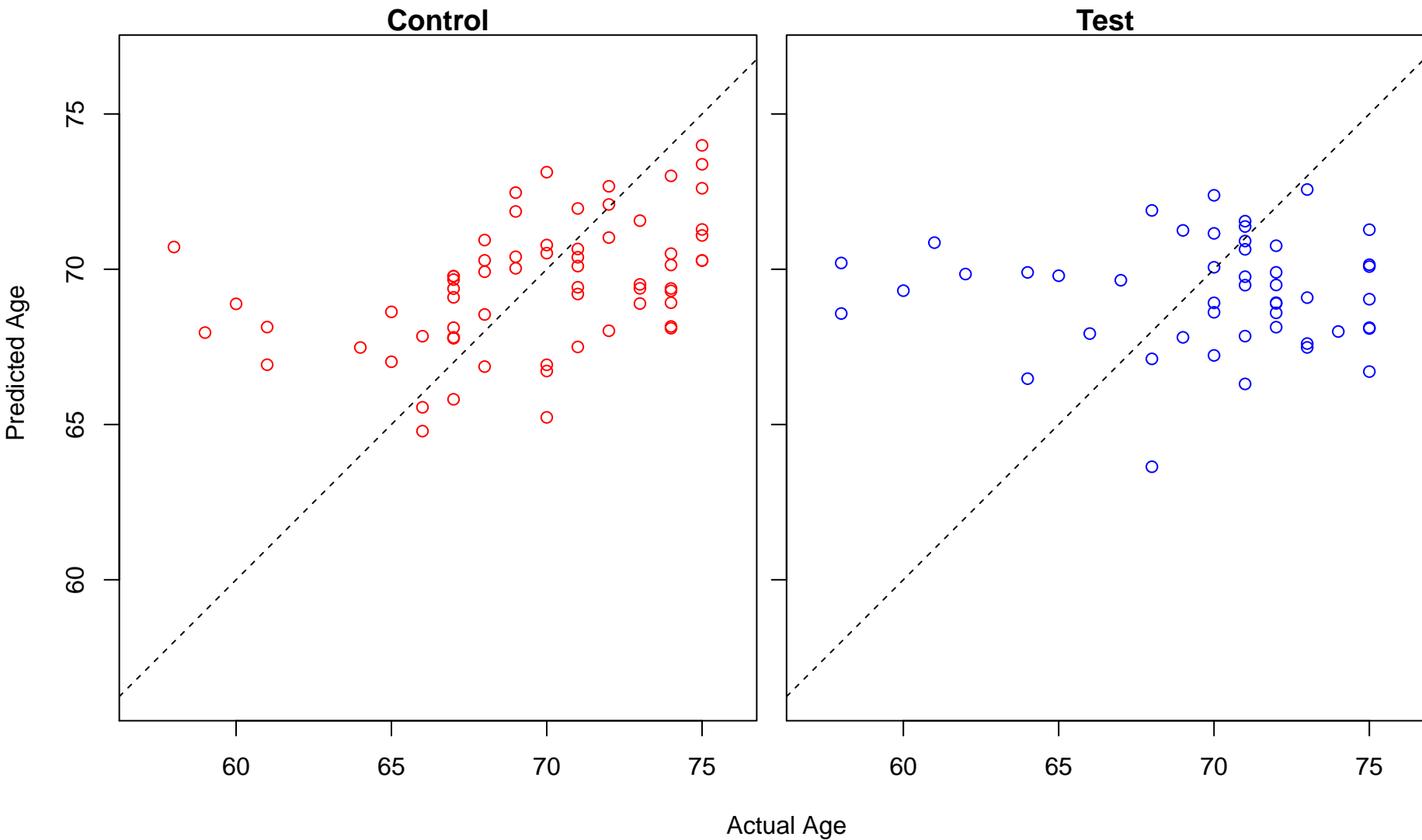


Actual Age

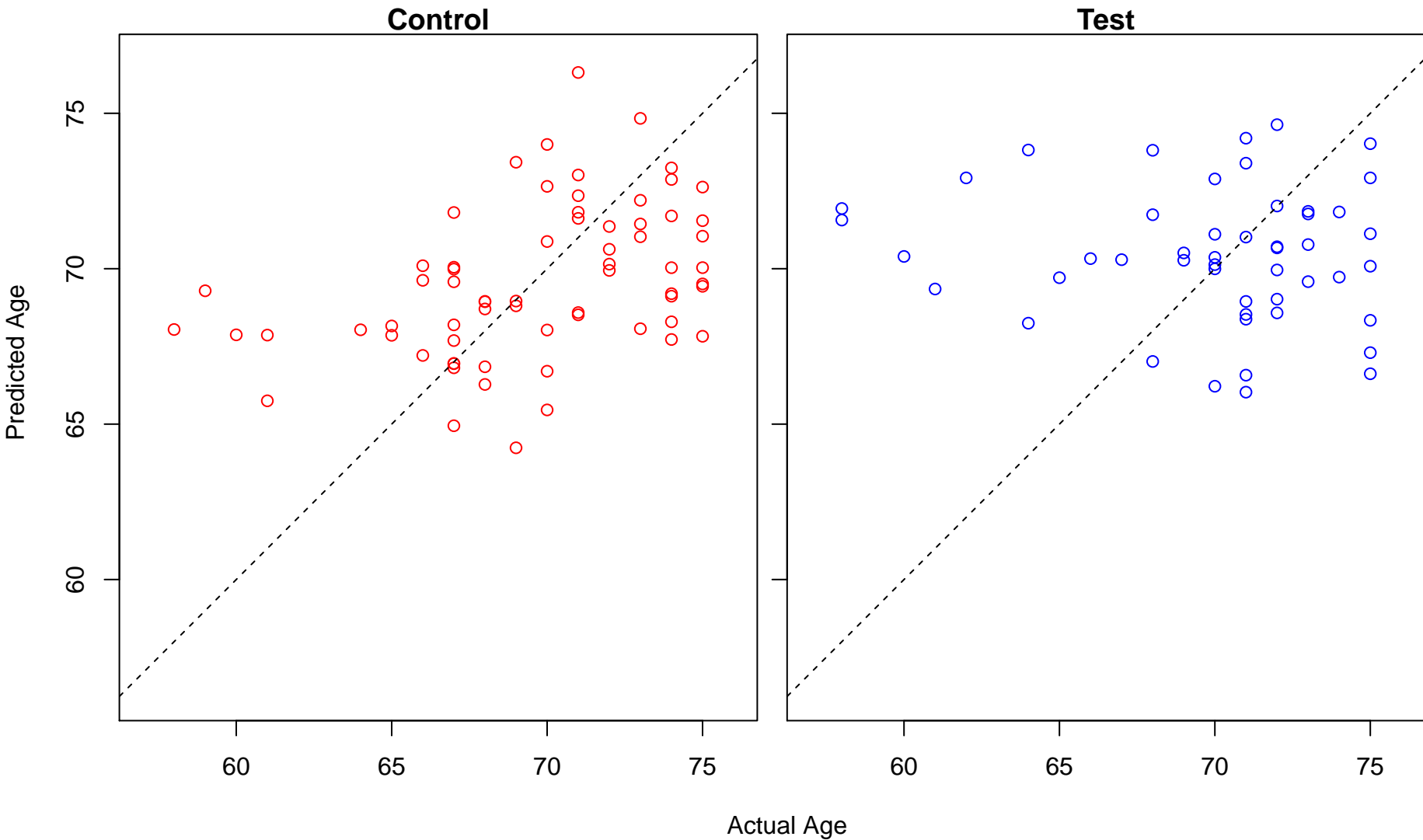
forelimb morphogenesis (Score: 0.596826)



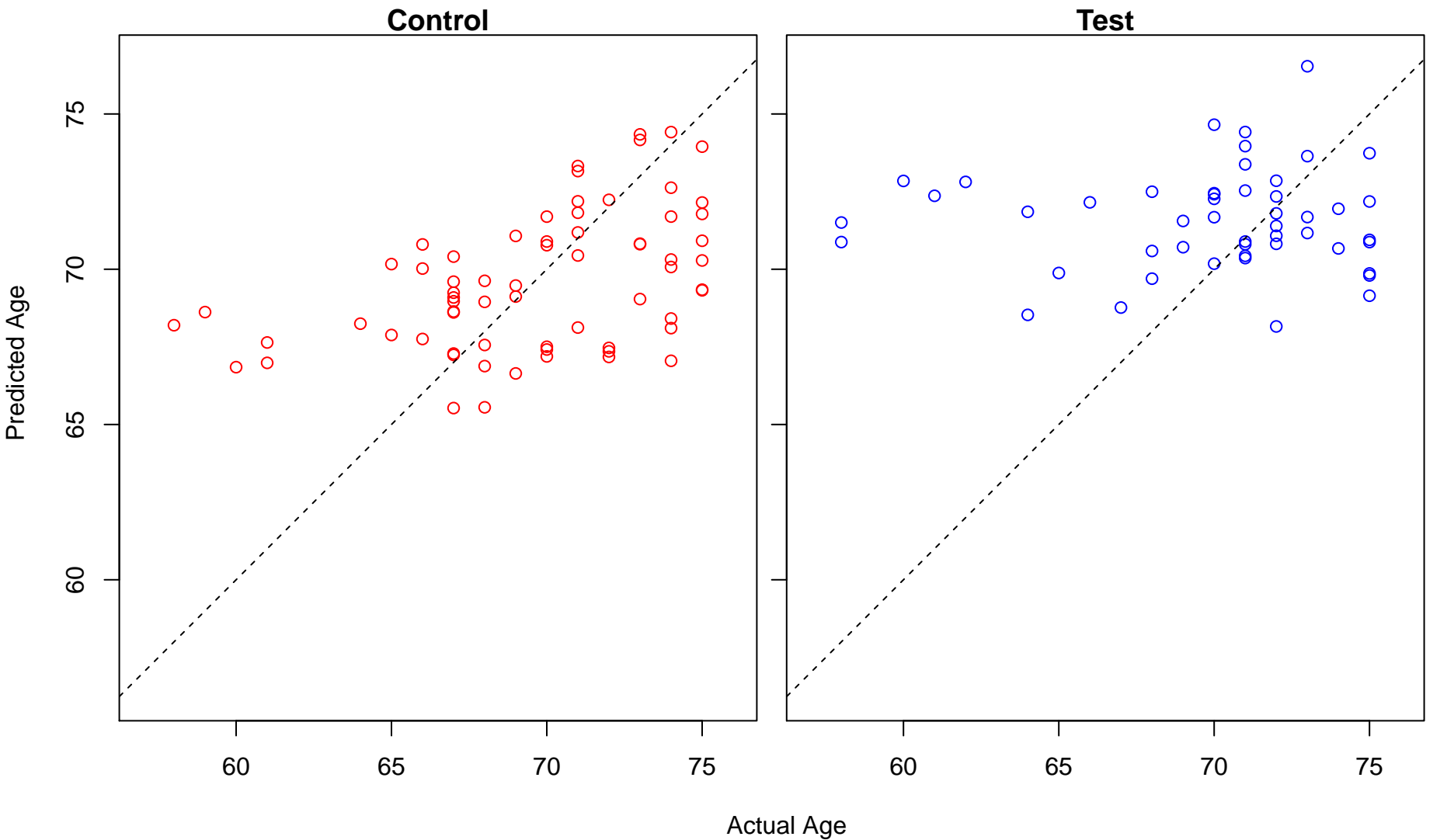
fructose 1,6-bisphosphate metabolic process (Score: 0.596695)



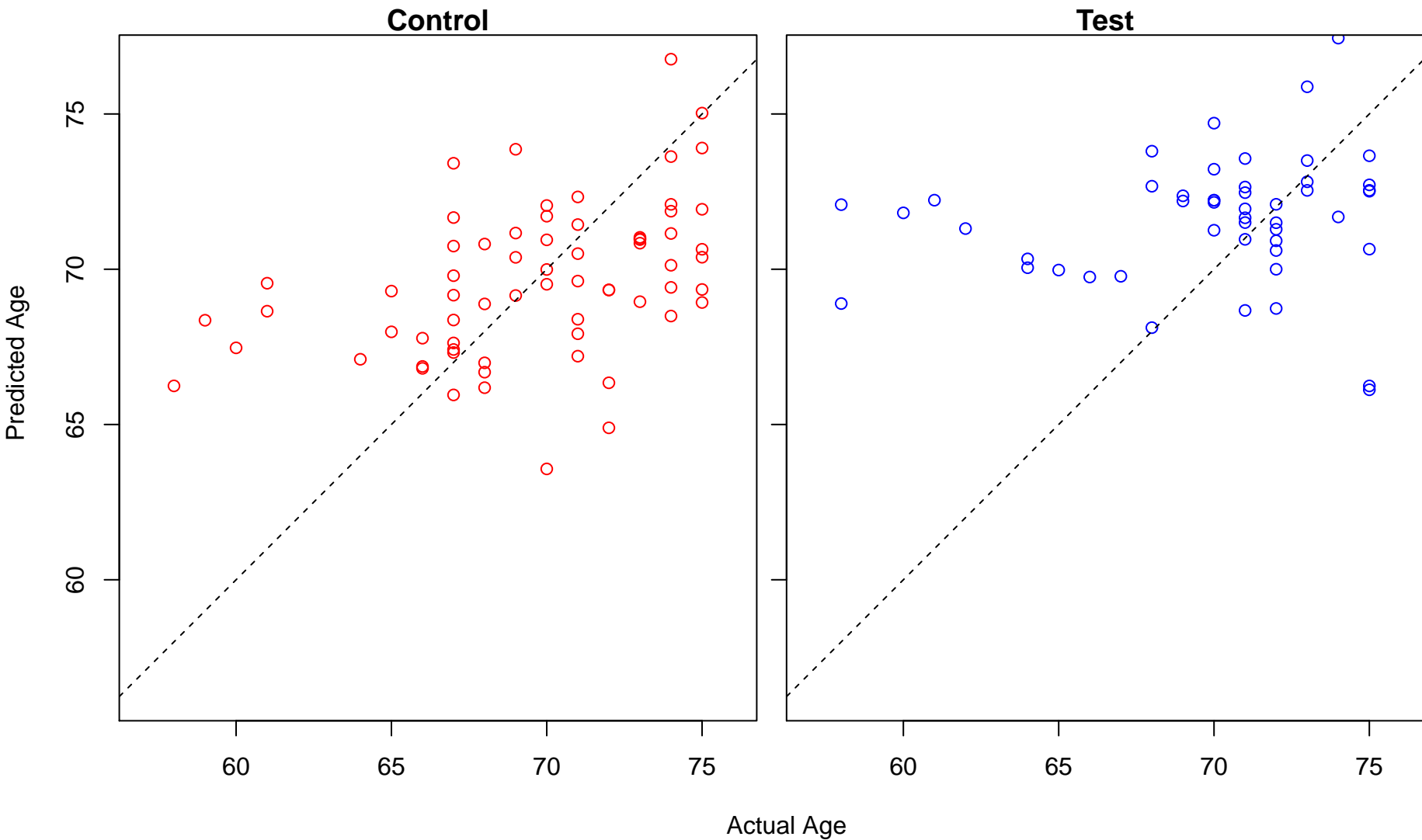
production of miRNAs involved in gene silencing by miRNA (Score: 0.596615)



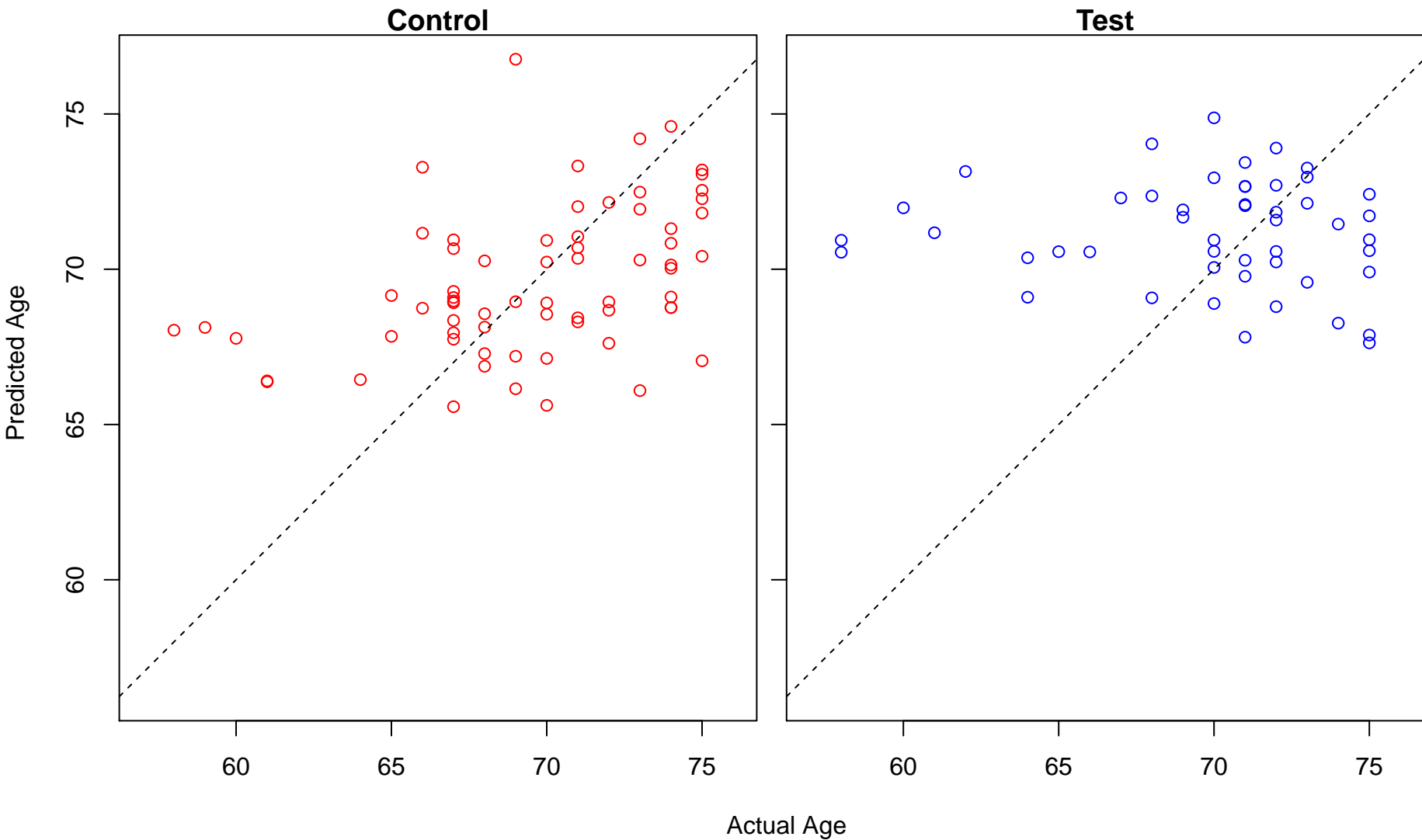
Regulatory regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score)



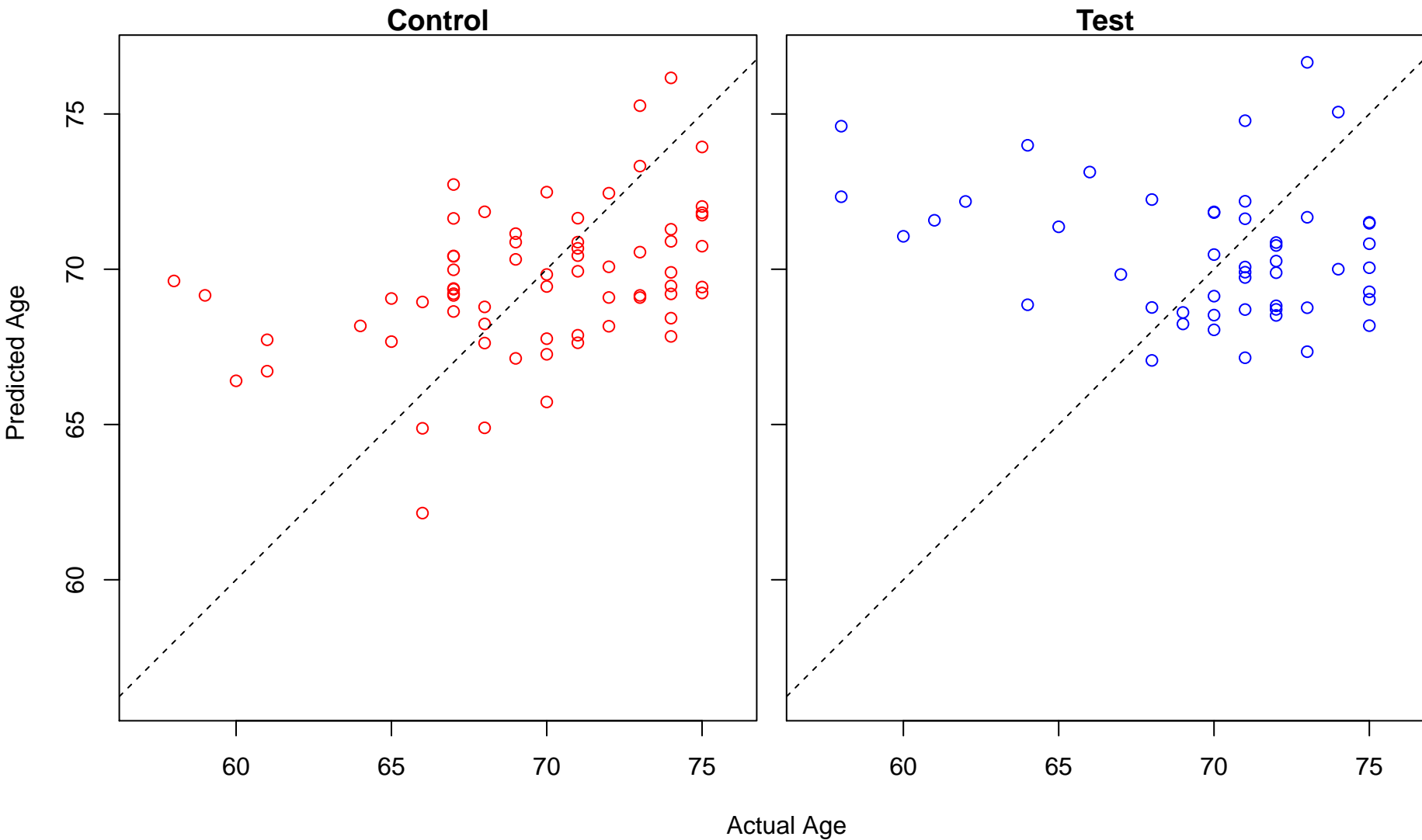
regulation of cholesterol storage (Score: 0.596466)



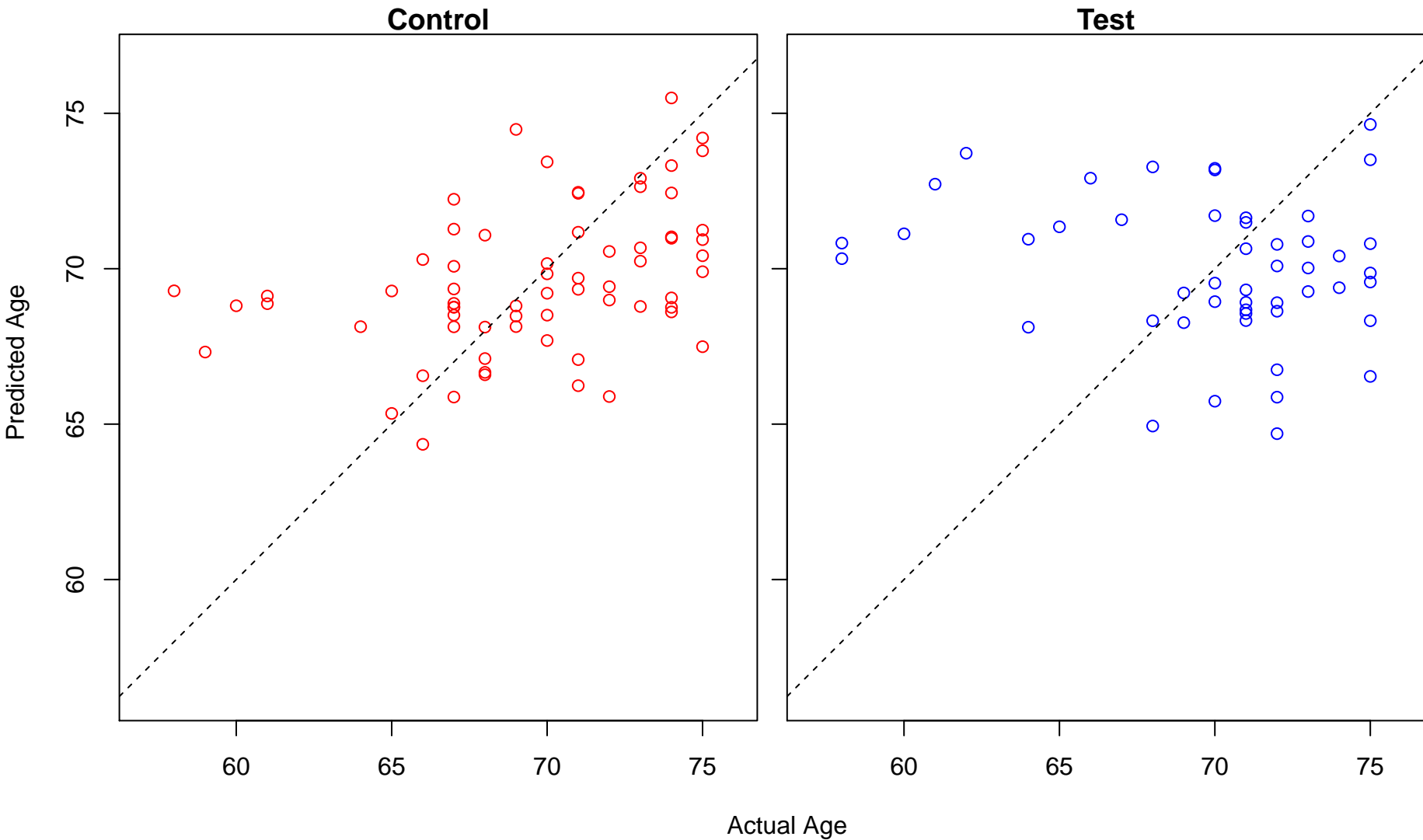
protein localization to endosome (Score: 0.596224)



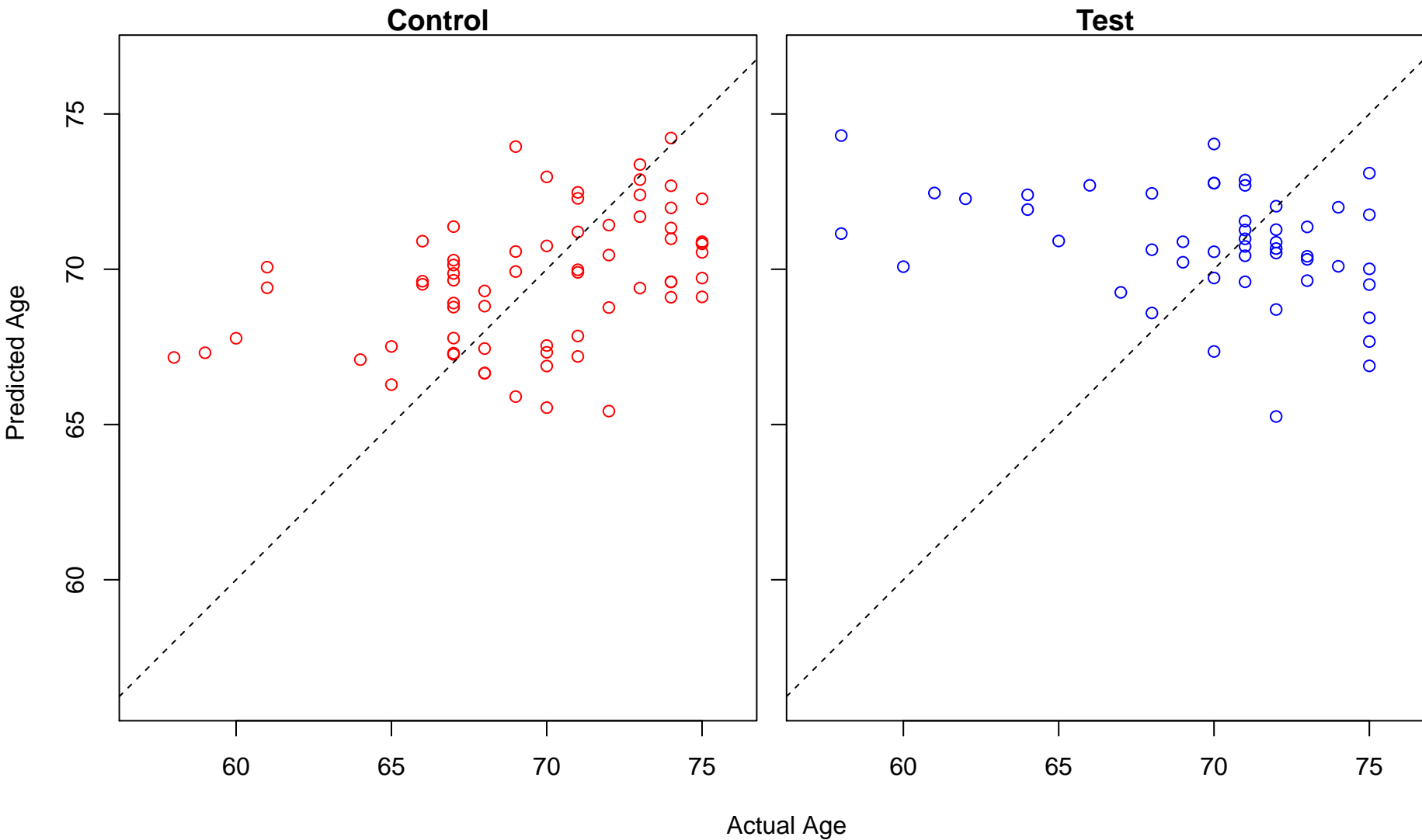
regulation of histone ubiquitination (Score: 0.595885)



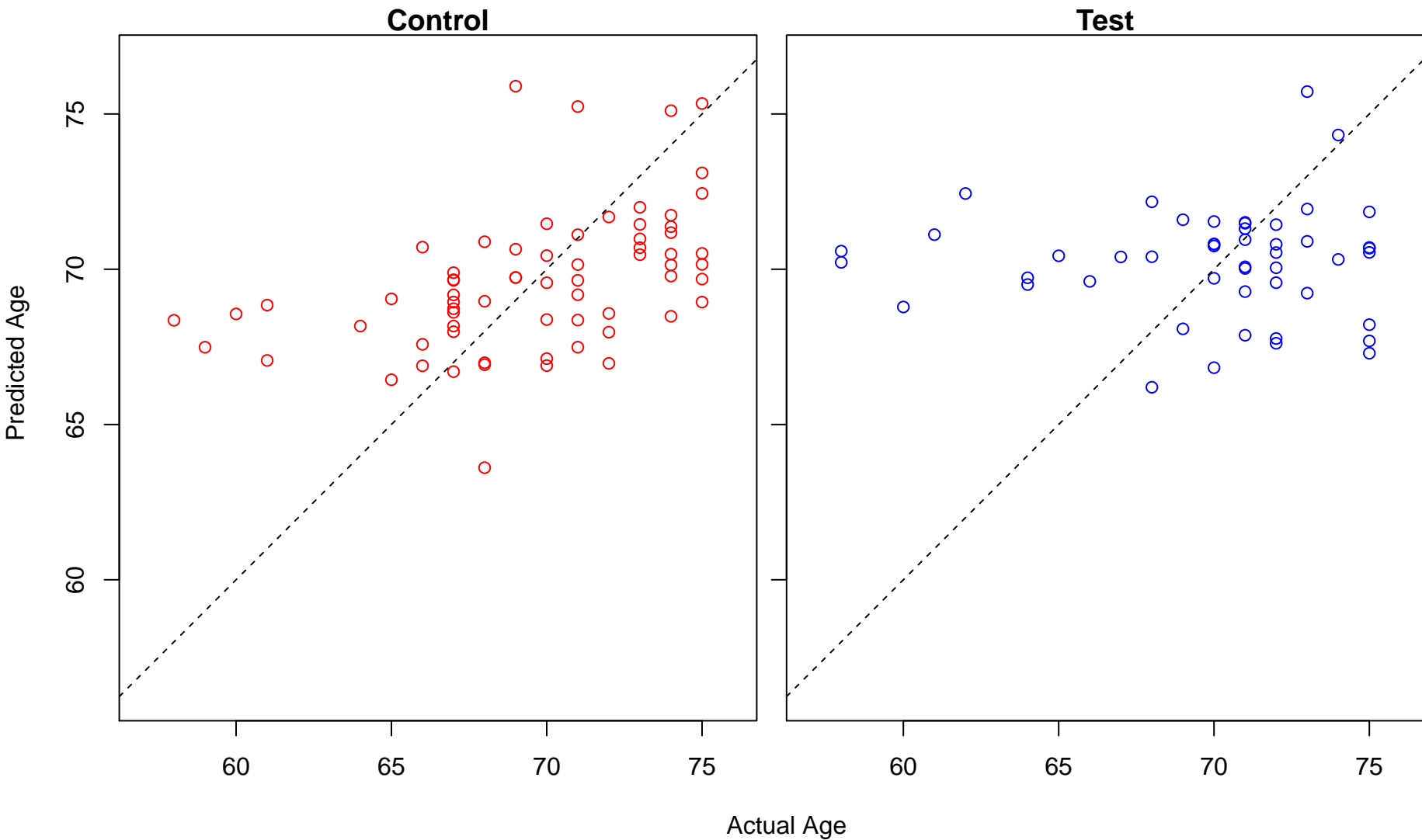
positive regulation of alcohol biosynthetic process (Score: 0.595801)



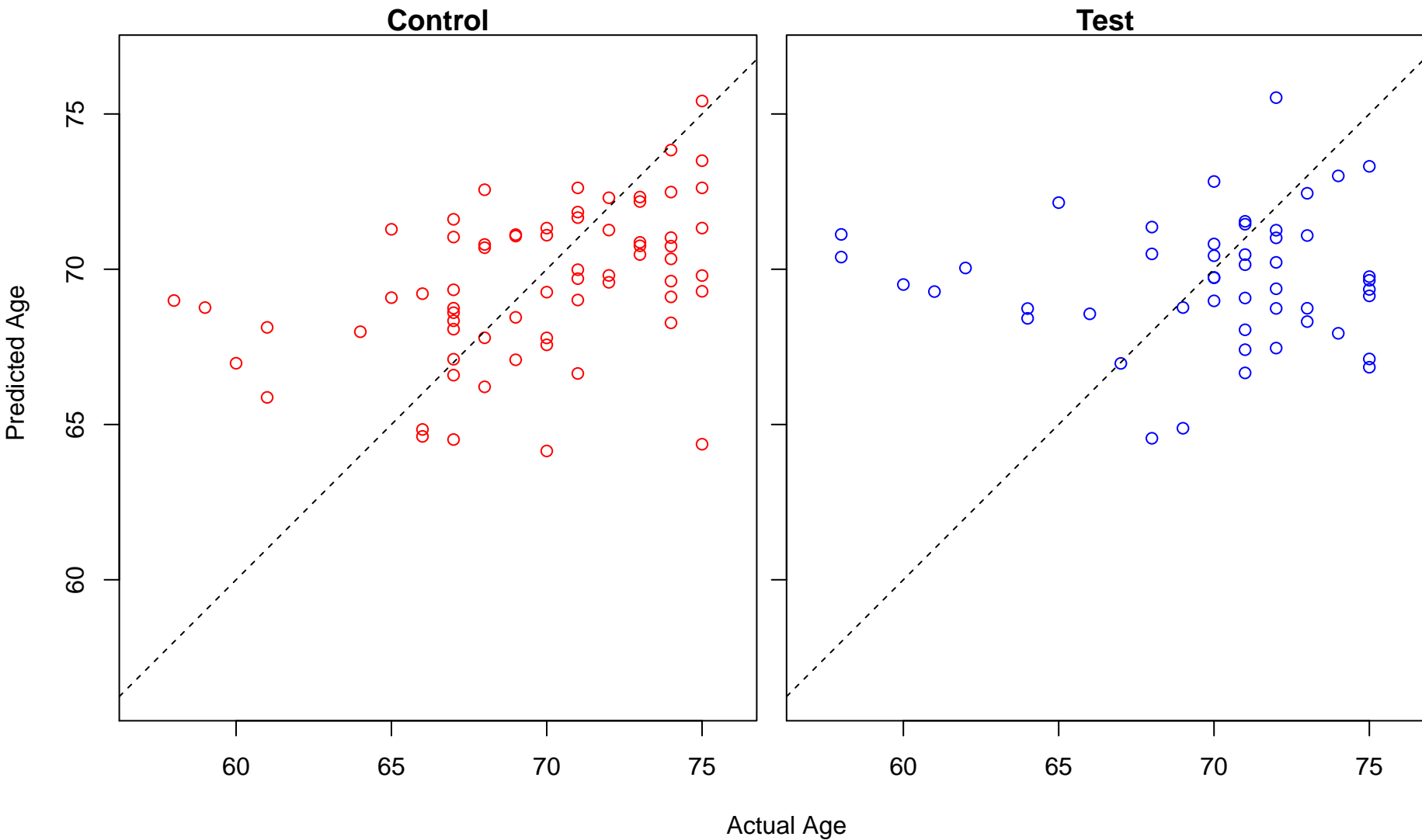
positive regulation of protein autophosphorylation (Score: 0.595031)



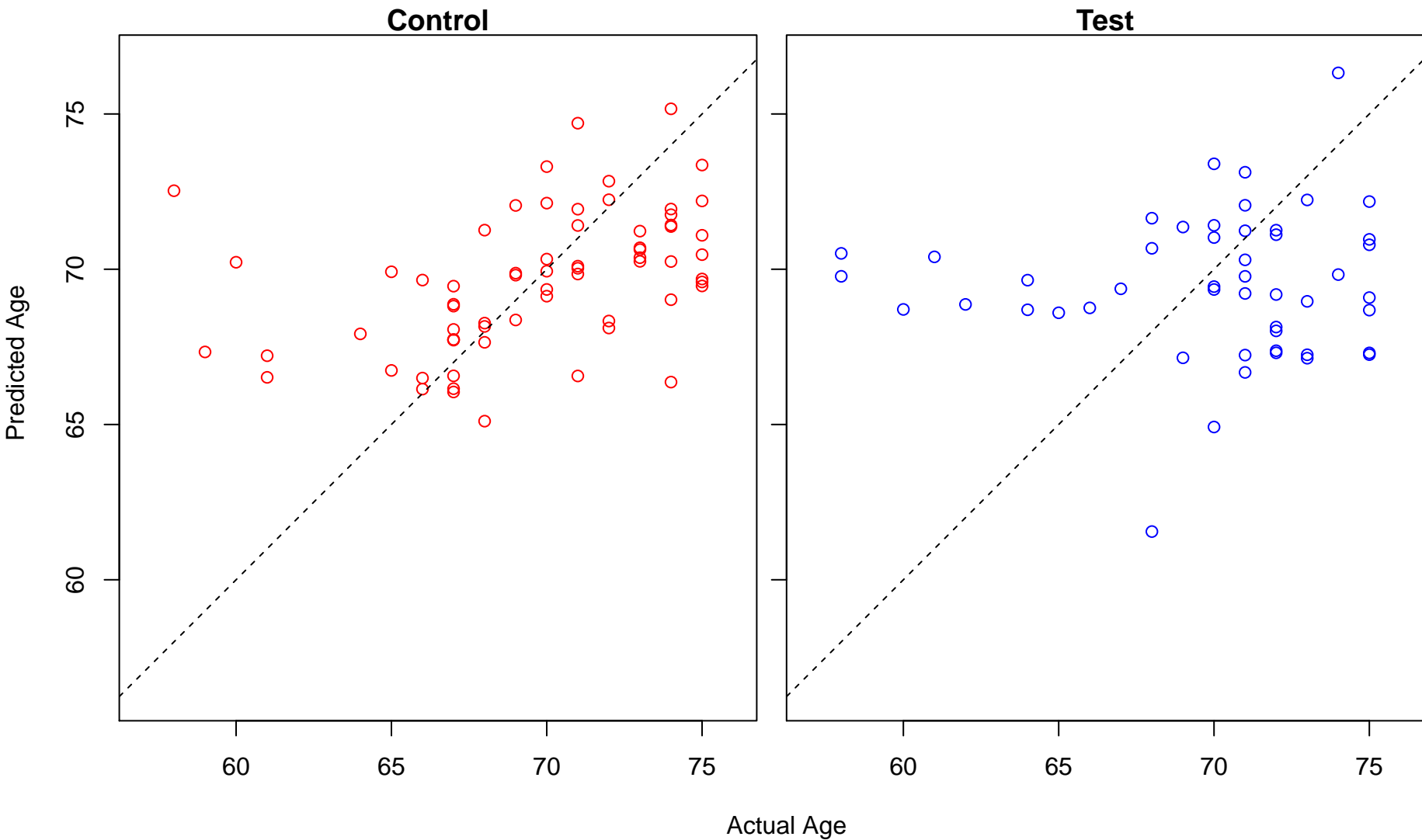
negative regulation of tyrosine phosphorylation of STAT protein (Score: 0.594877)



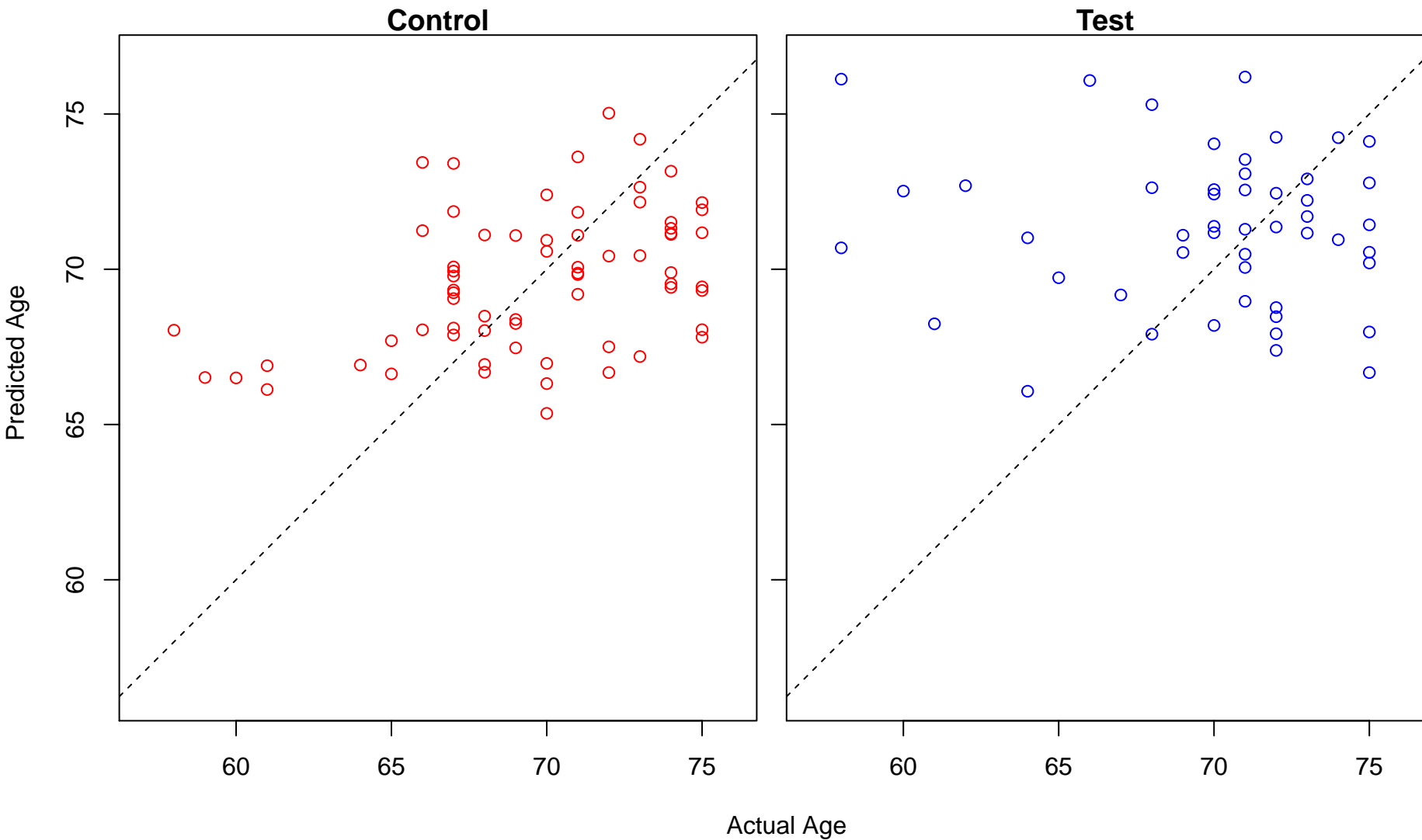
potassium ion homeostasis (Score: 0.594725)



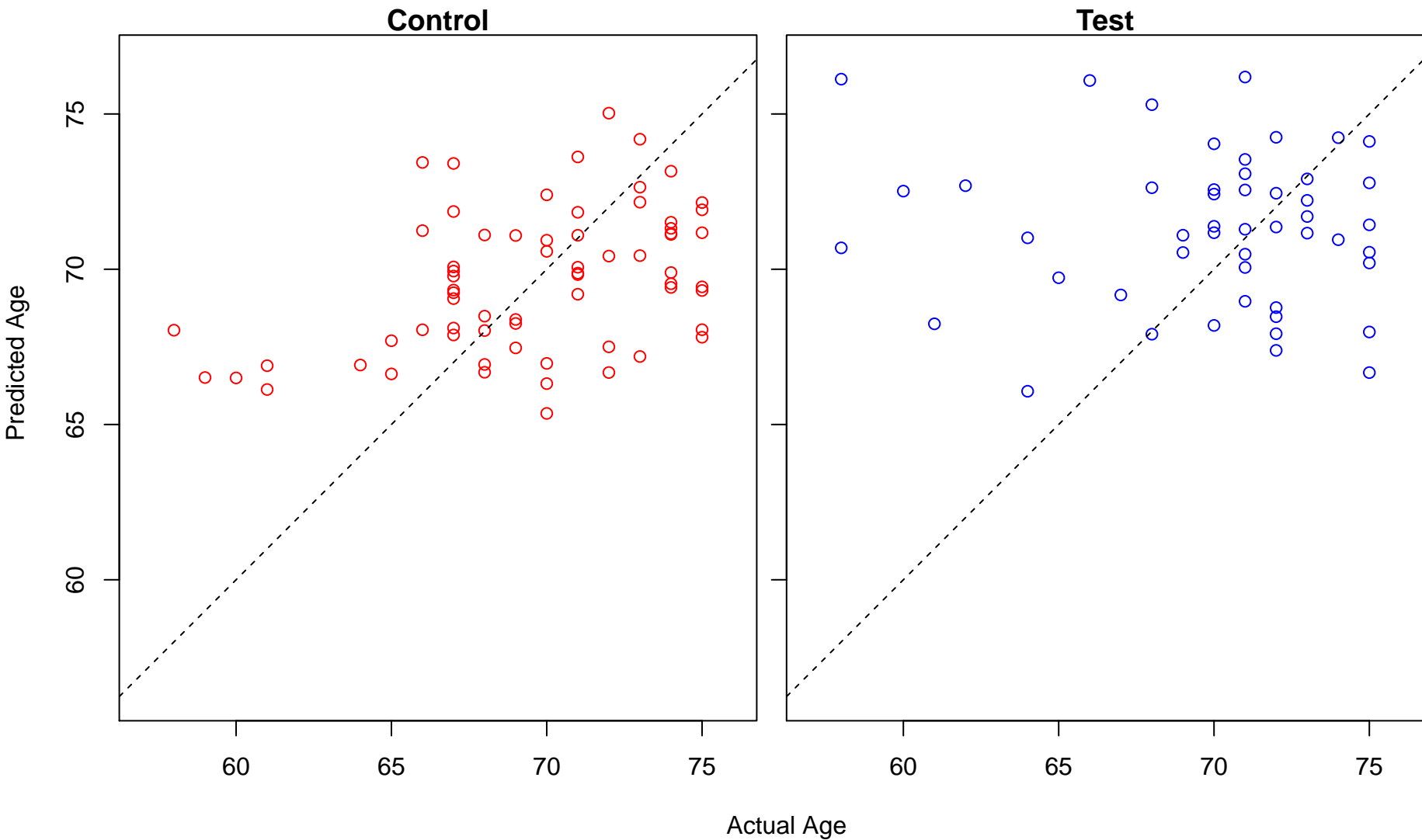
regulation of cytokine secretion involved in immune response (Score: 0.593896)



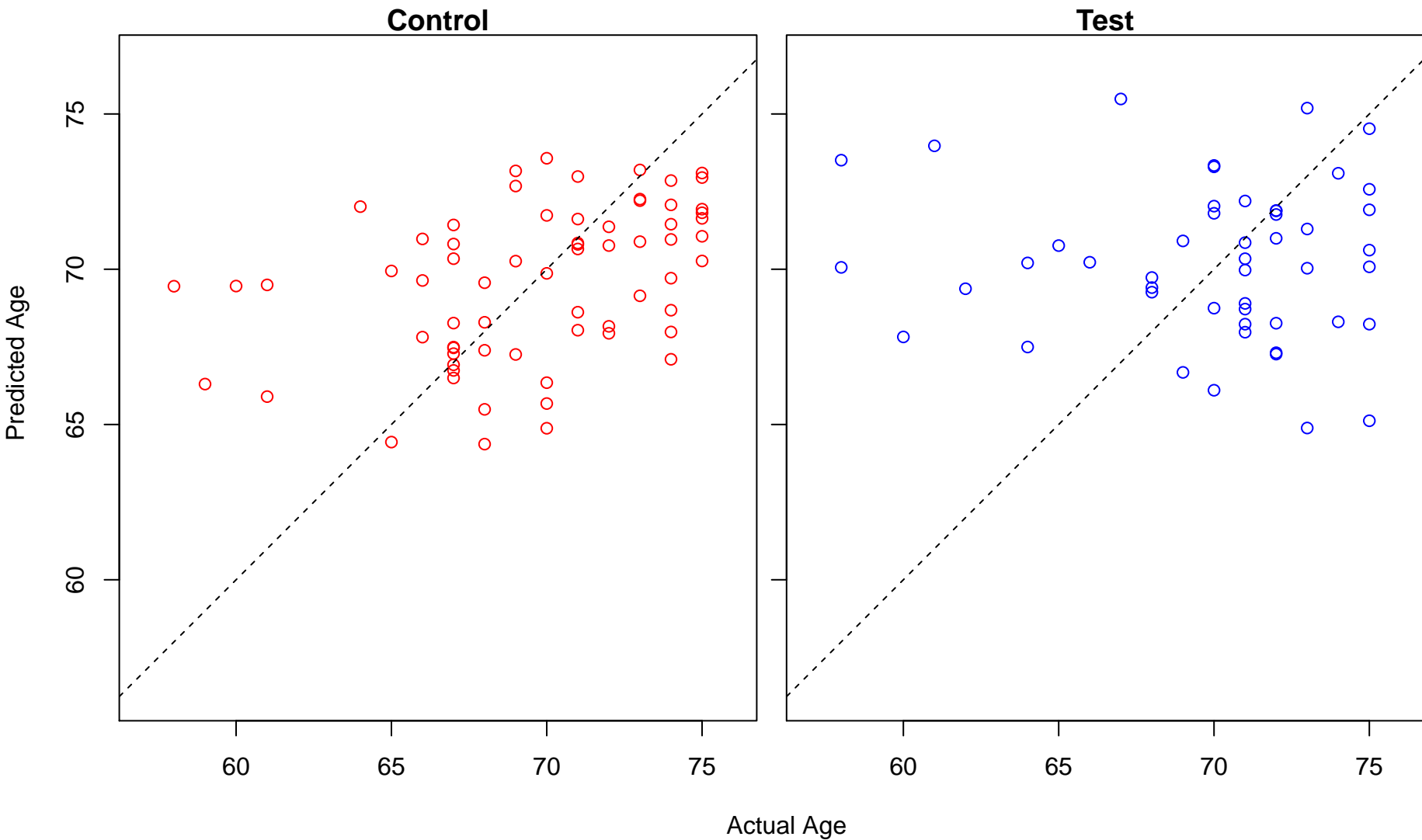
cell-substrate adherens junction assembly (Score: 0.593613)



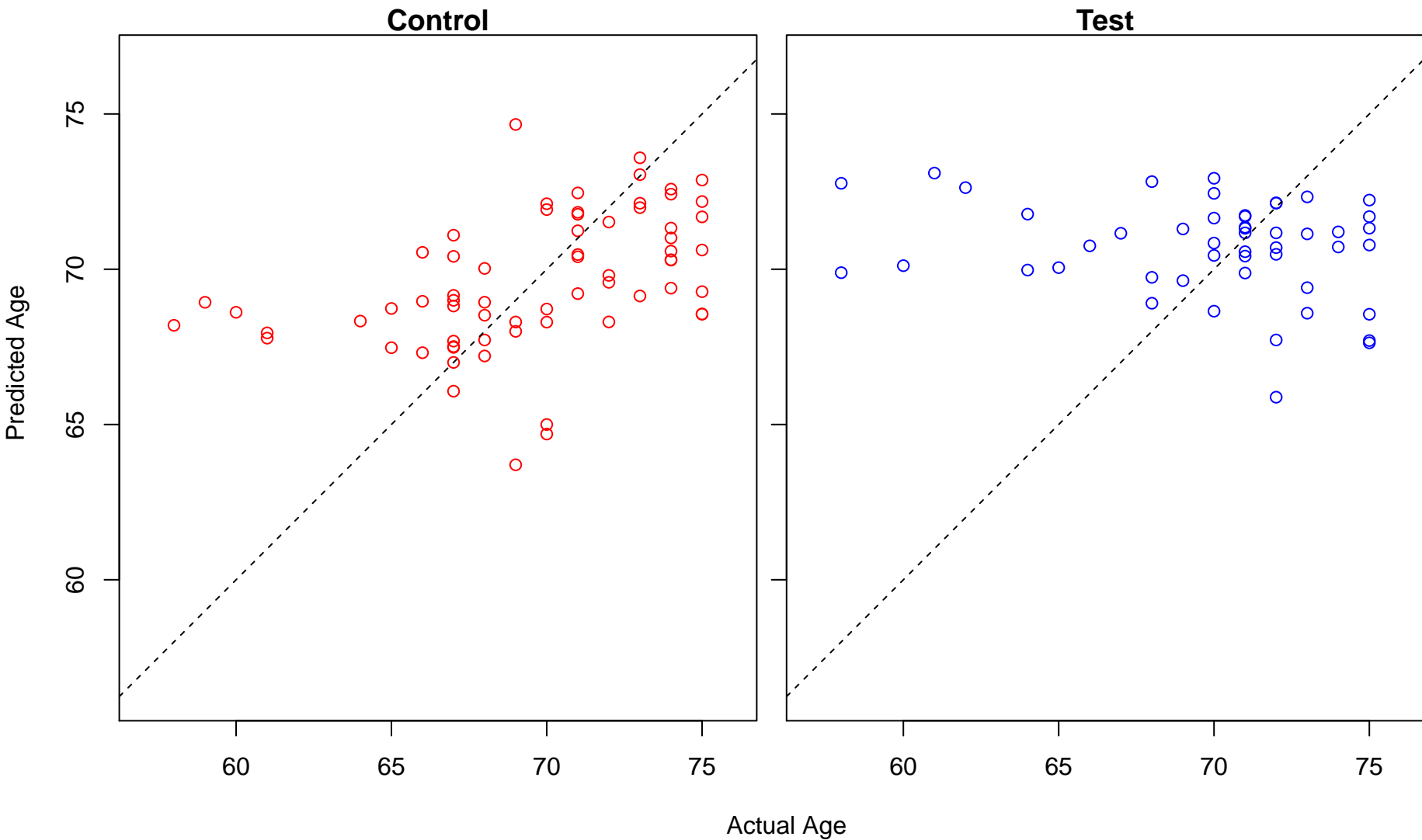
focal adhesion assembly (Score: 0.593613)



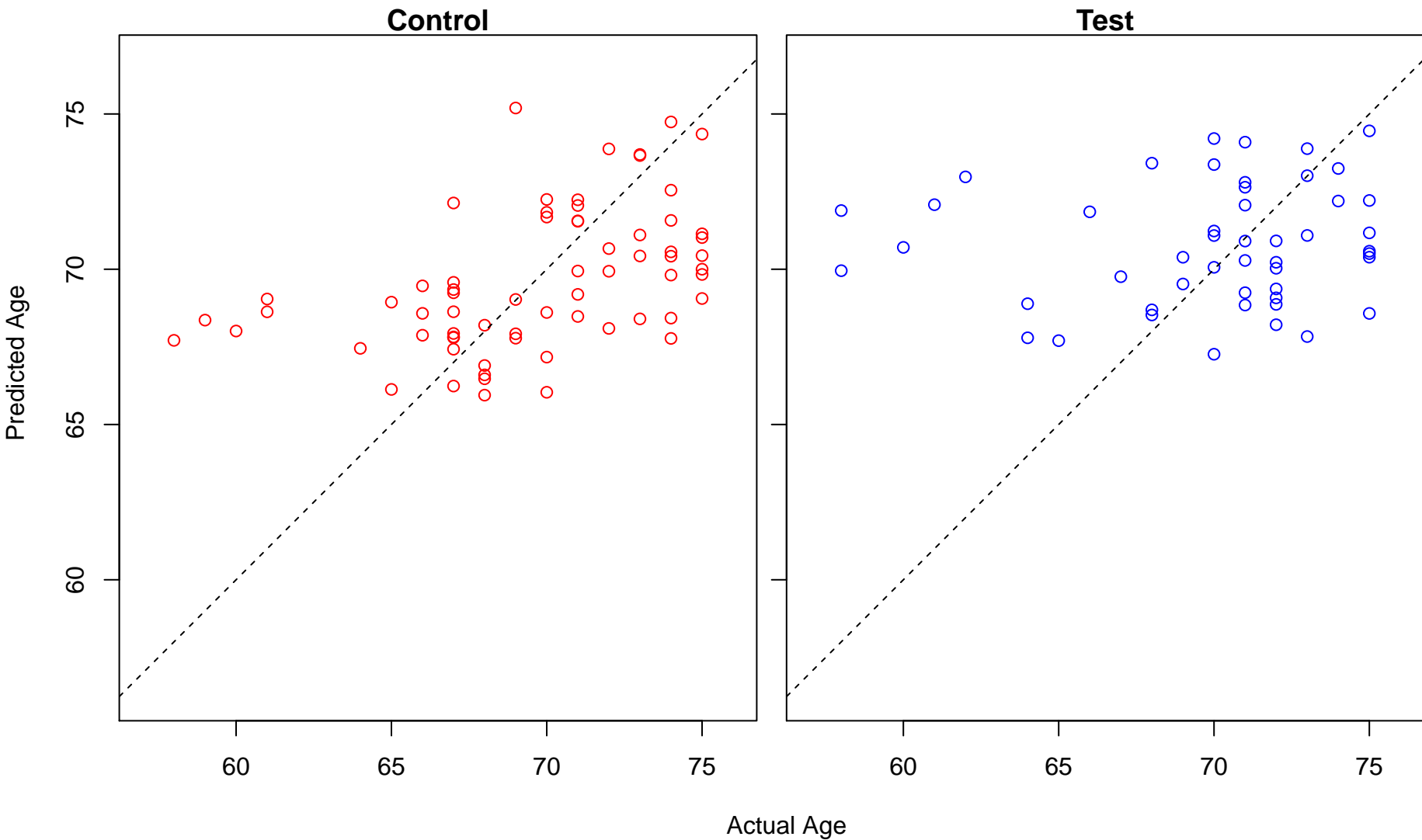
embryonic skeletal system morphogenesis (Score: 0.593581)



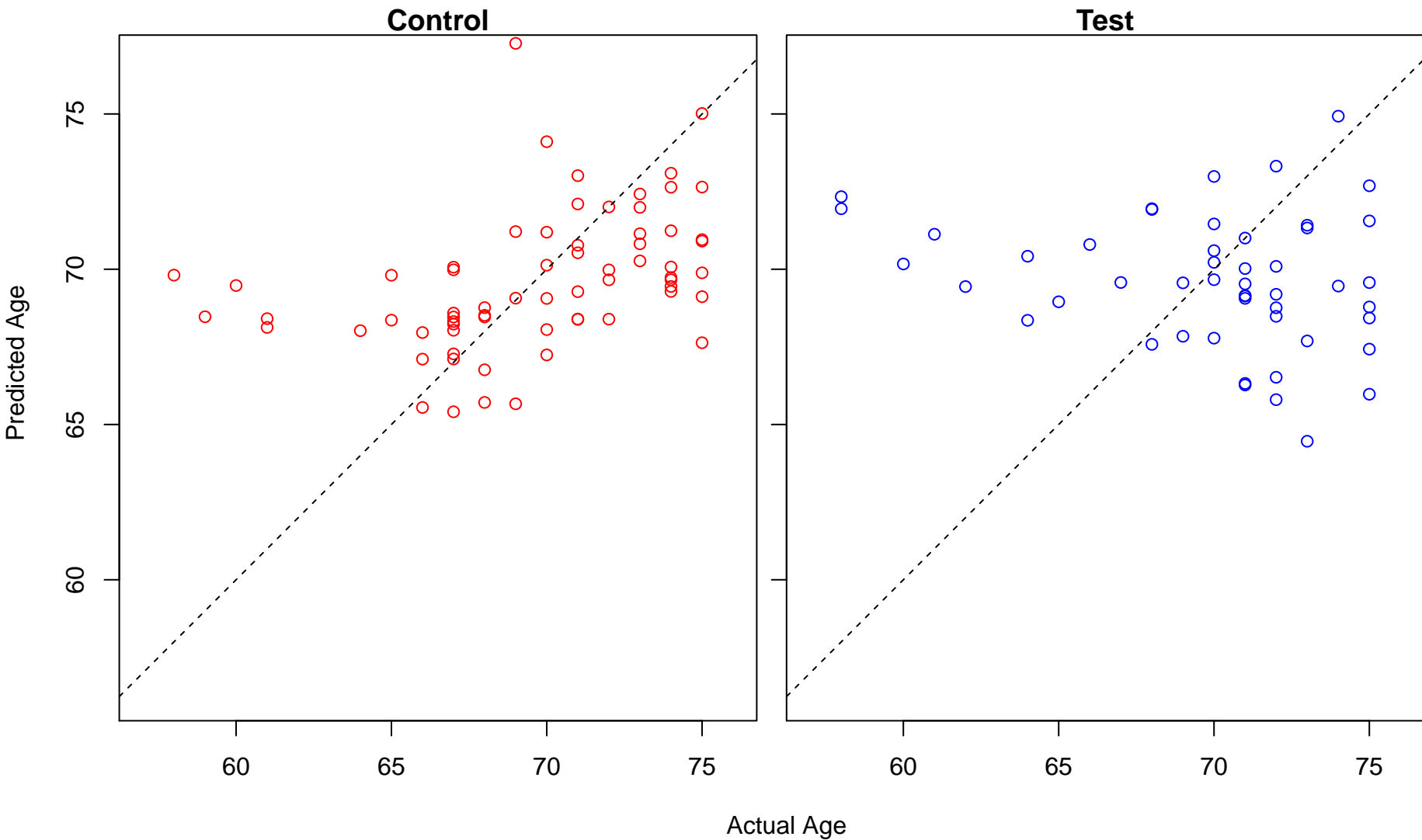
quinone metabolic process (Score: 0.592974)



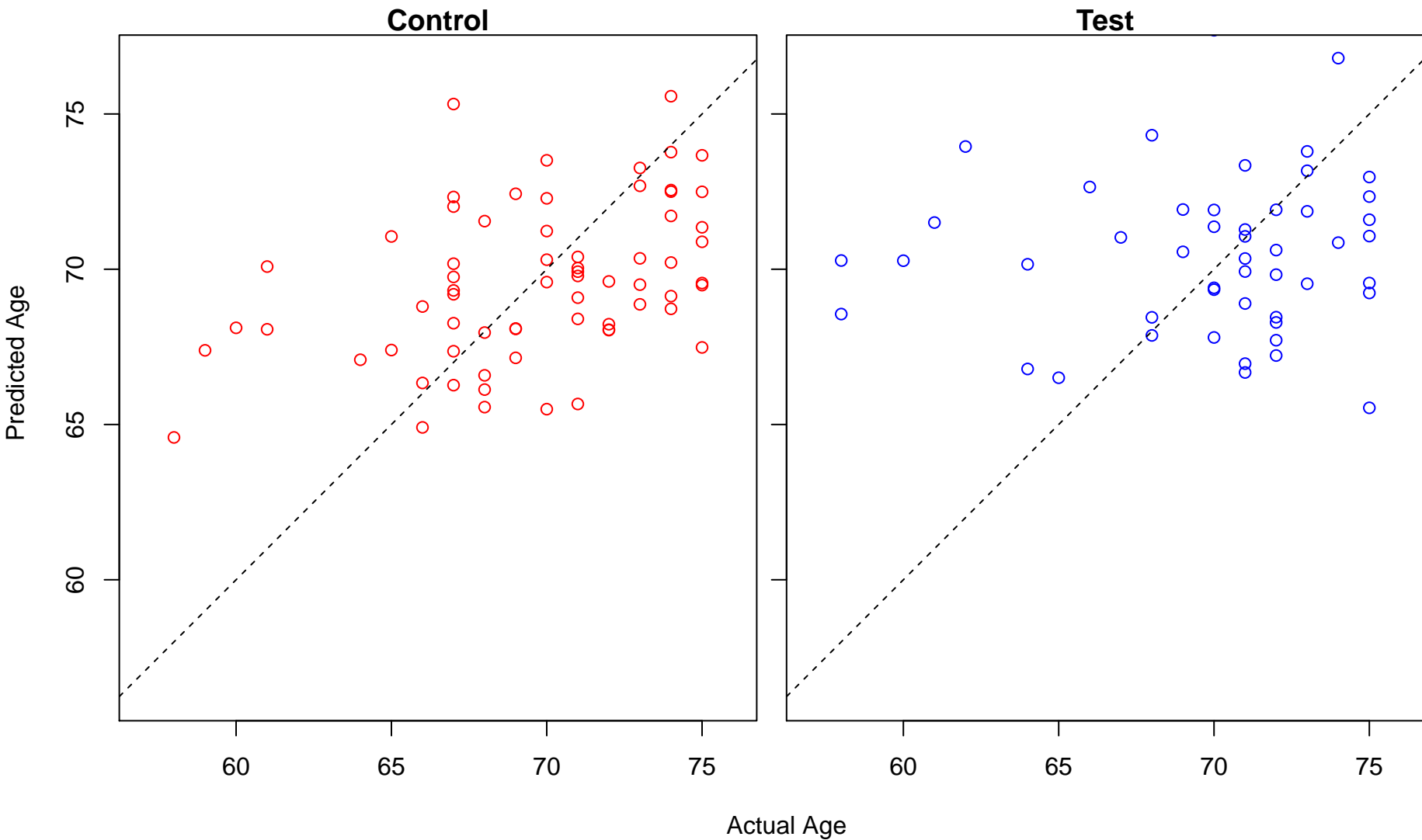
negative regulation of striated muscle contraction (Score: 0.592068)



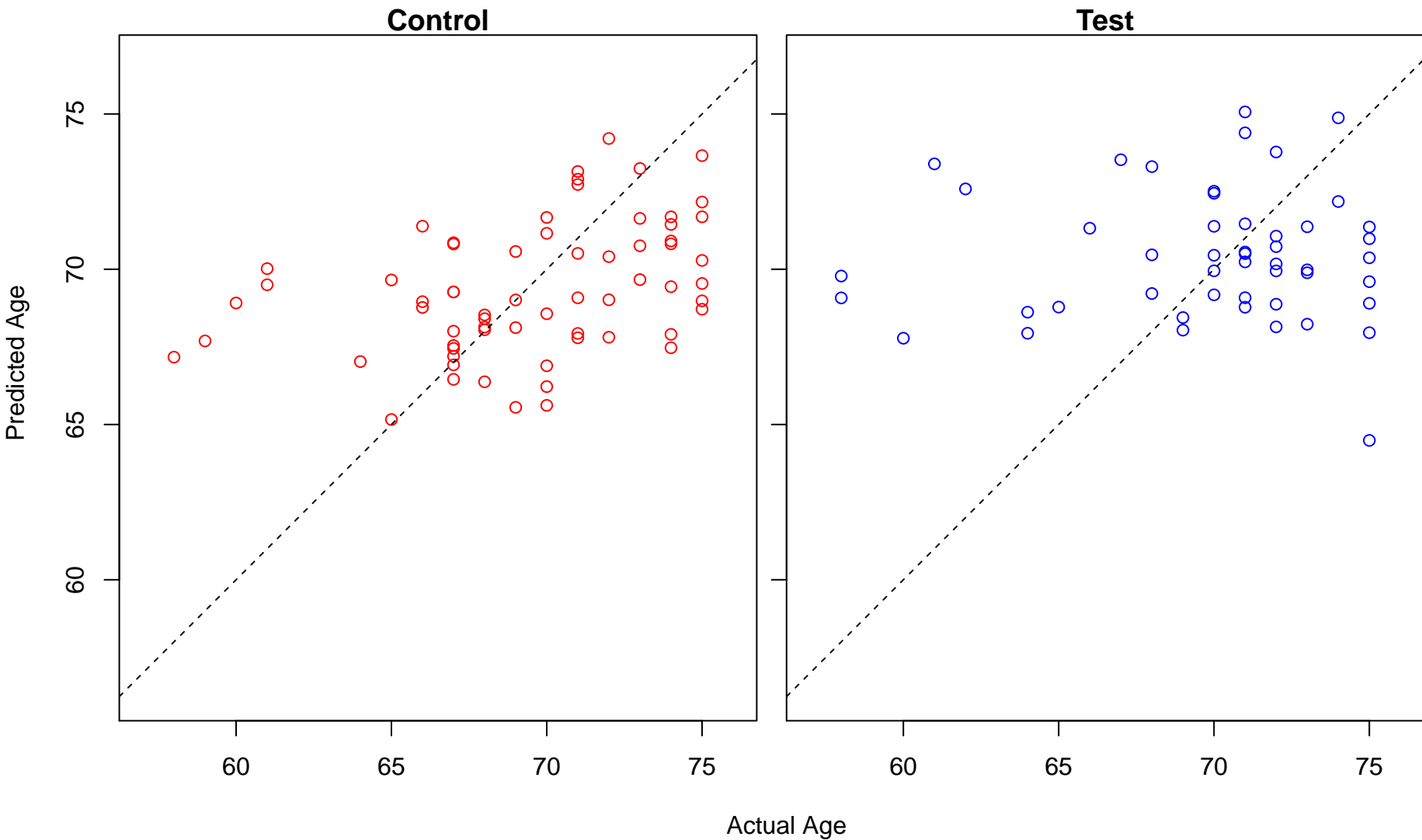
T-helper 1 type immune response (Score: 0.591375)



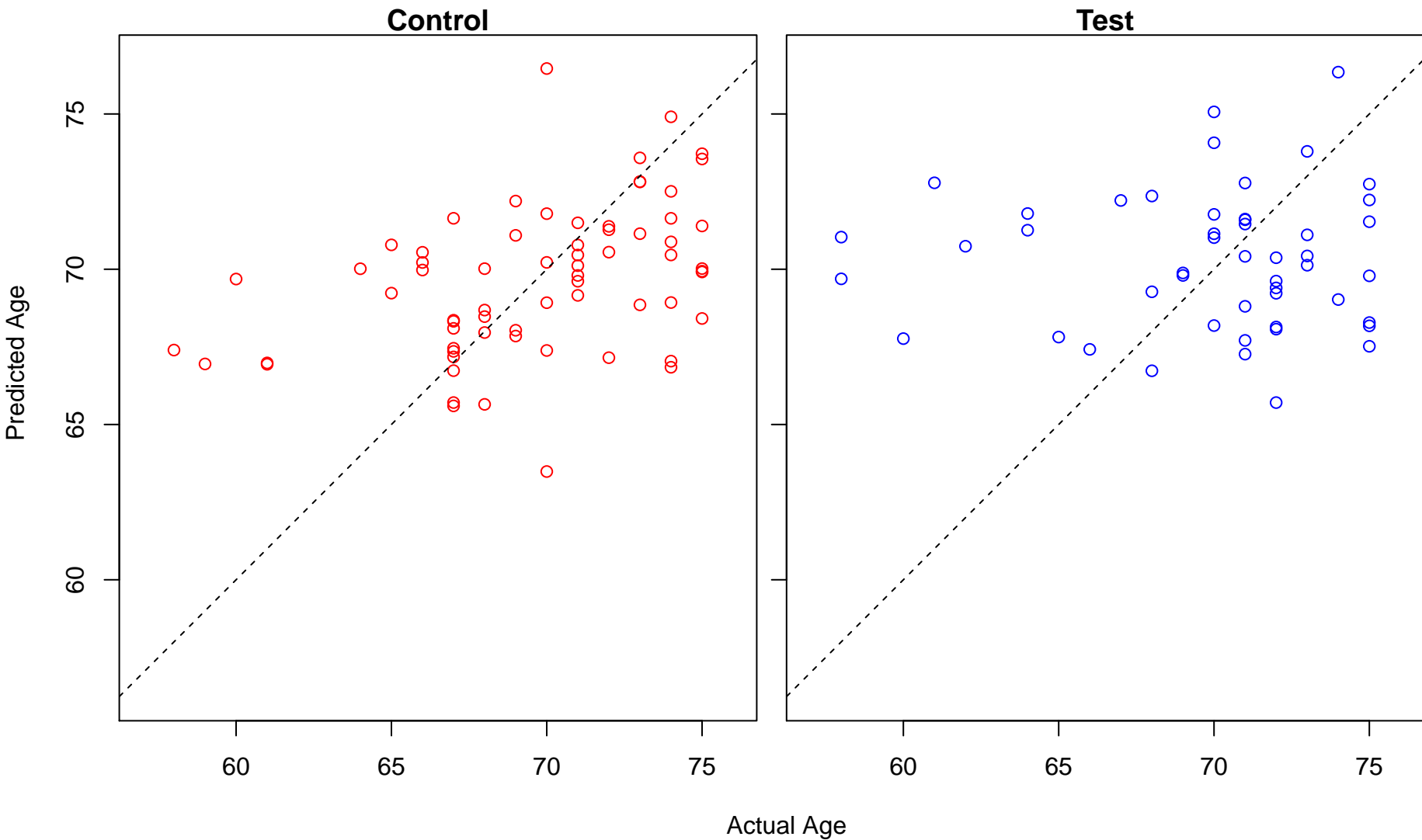
reverse cholesterol transport (Score: 0.590920)



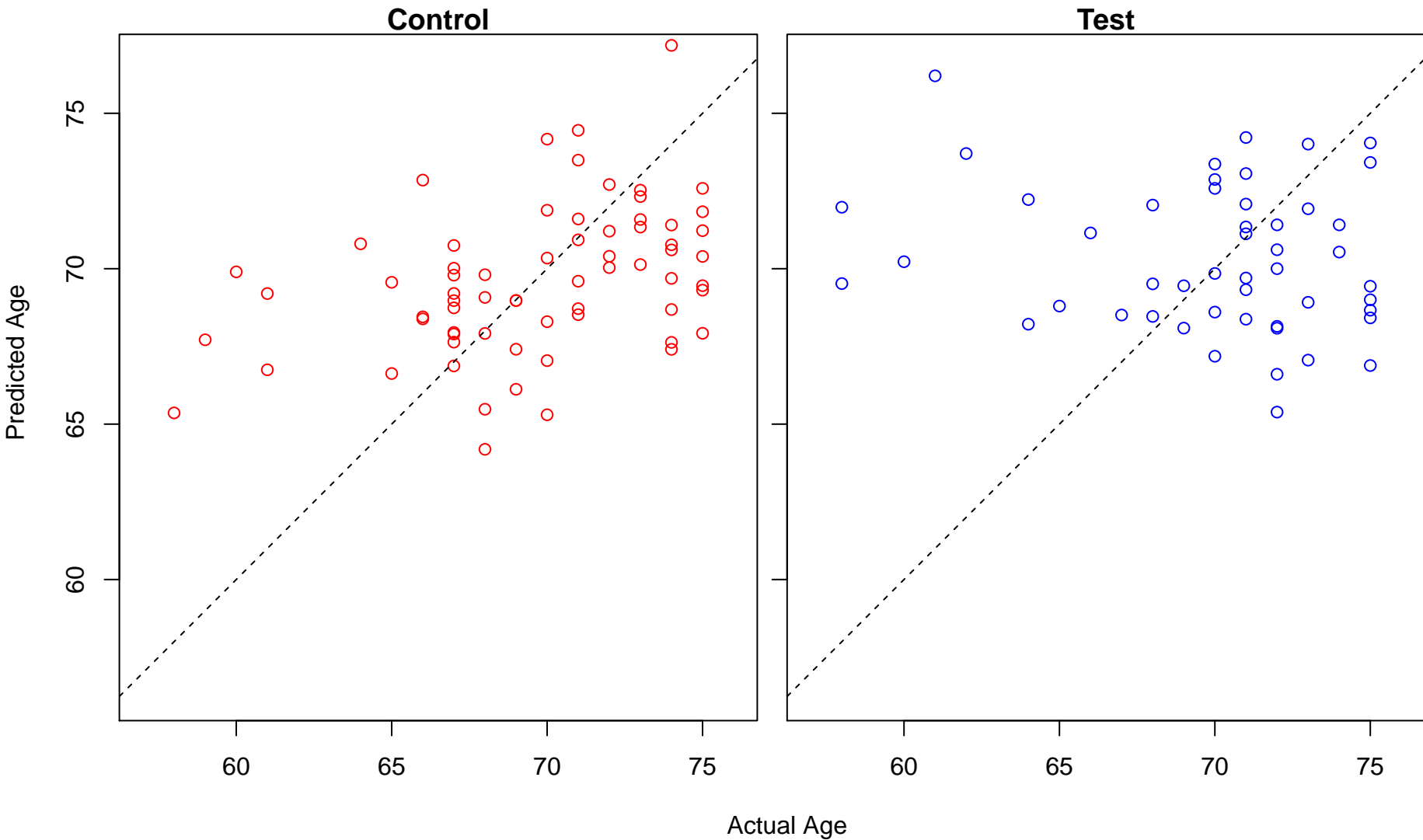
renal system process involved in regulation of blood volume (Score: 0.590574)



acrosome reaction (Score: 0.590172)

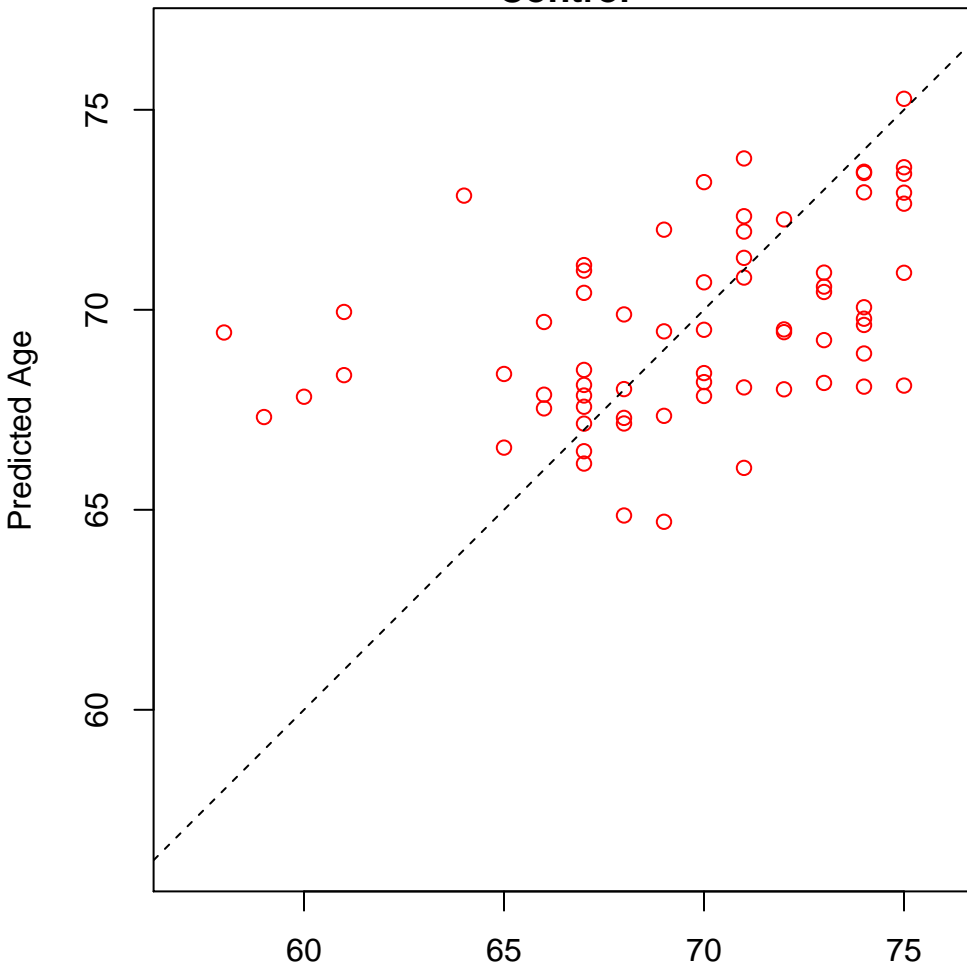


establishment of endothelial intestinal barrier (Score: 0.589422)

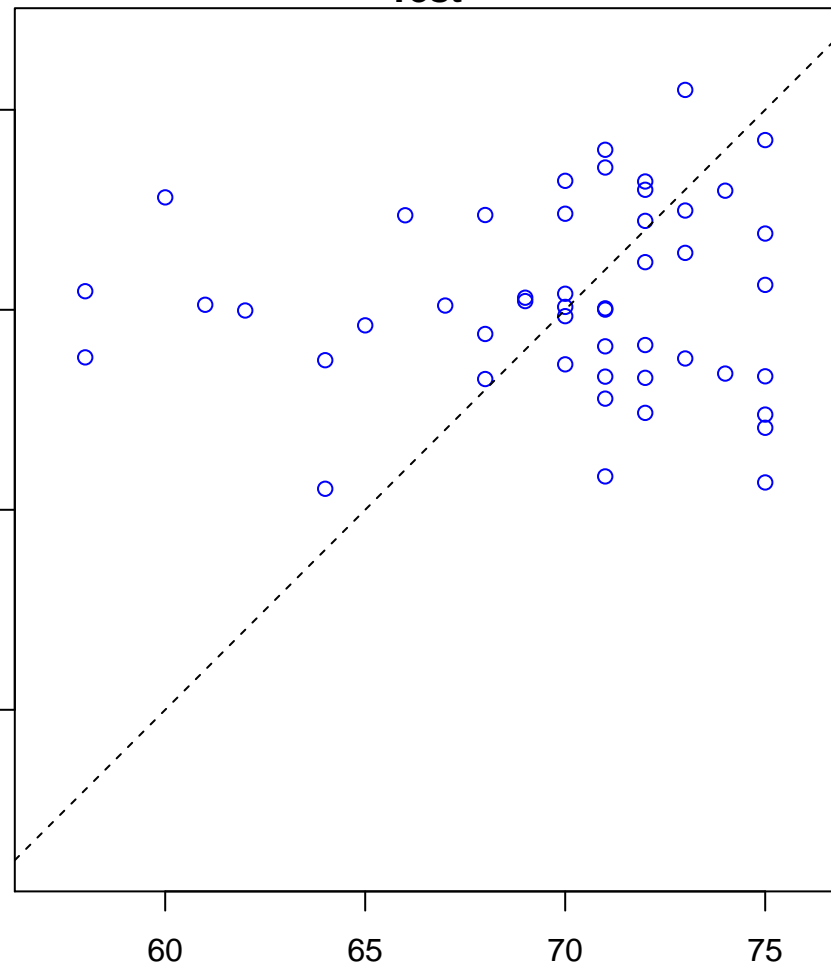


protein folding in endoplasmic reticulum (Score: 0.589407)

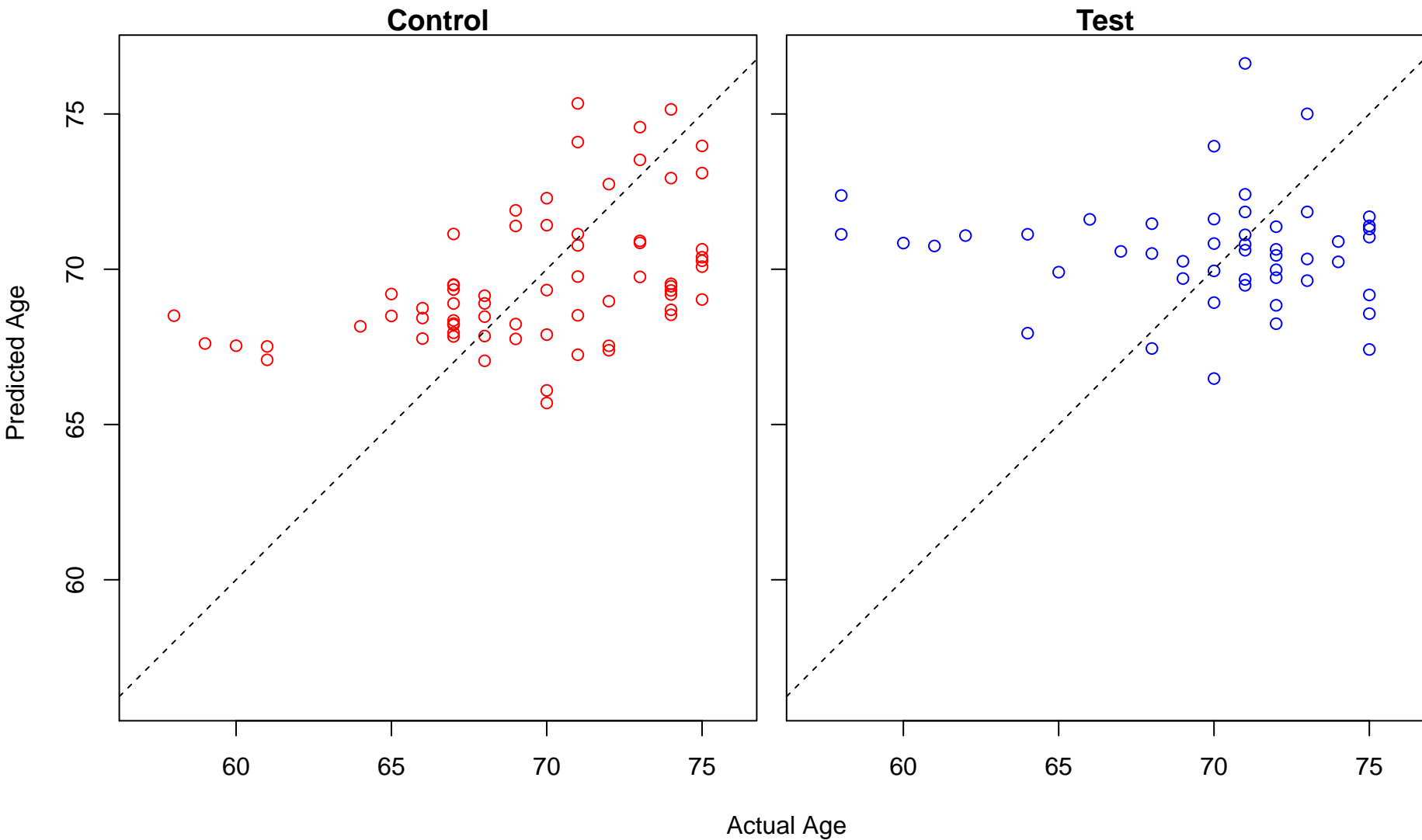
Control



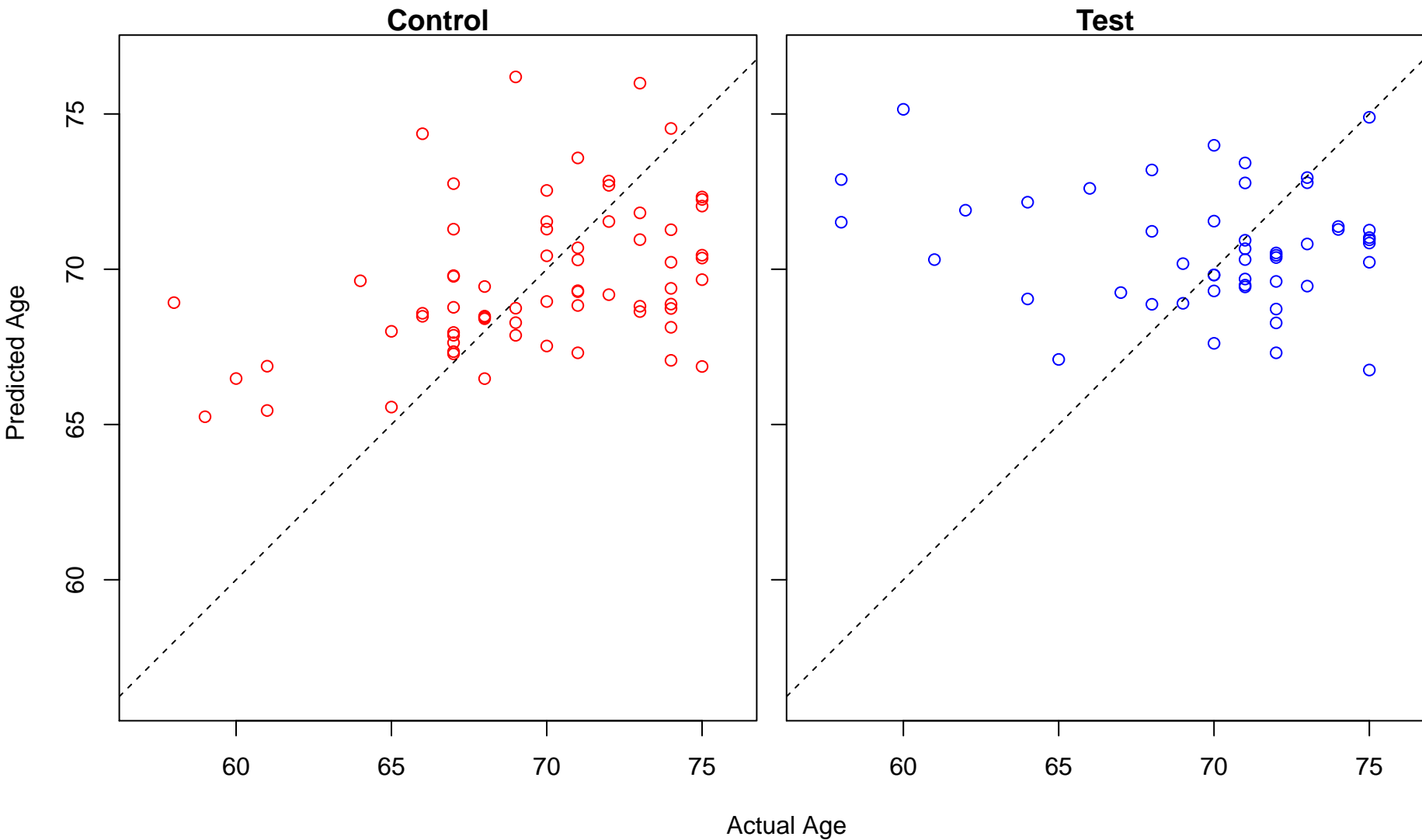
Test



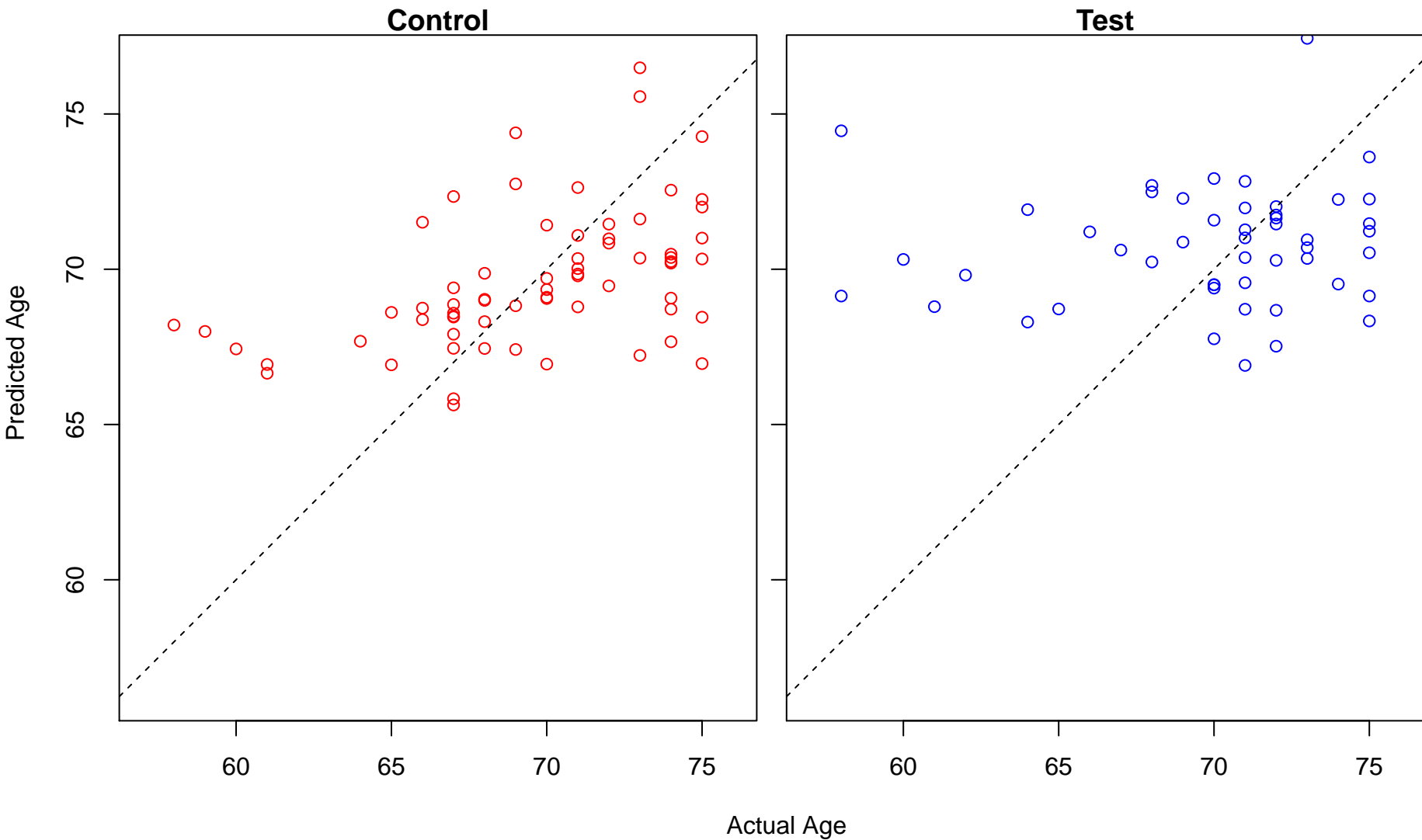
regulation of chromatin assembly or disassembly (Score: 0.588840)



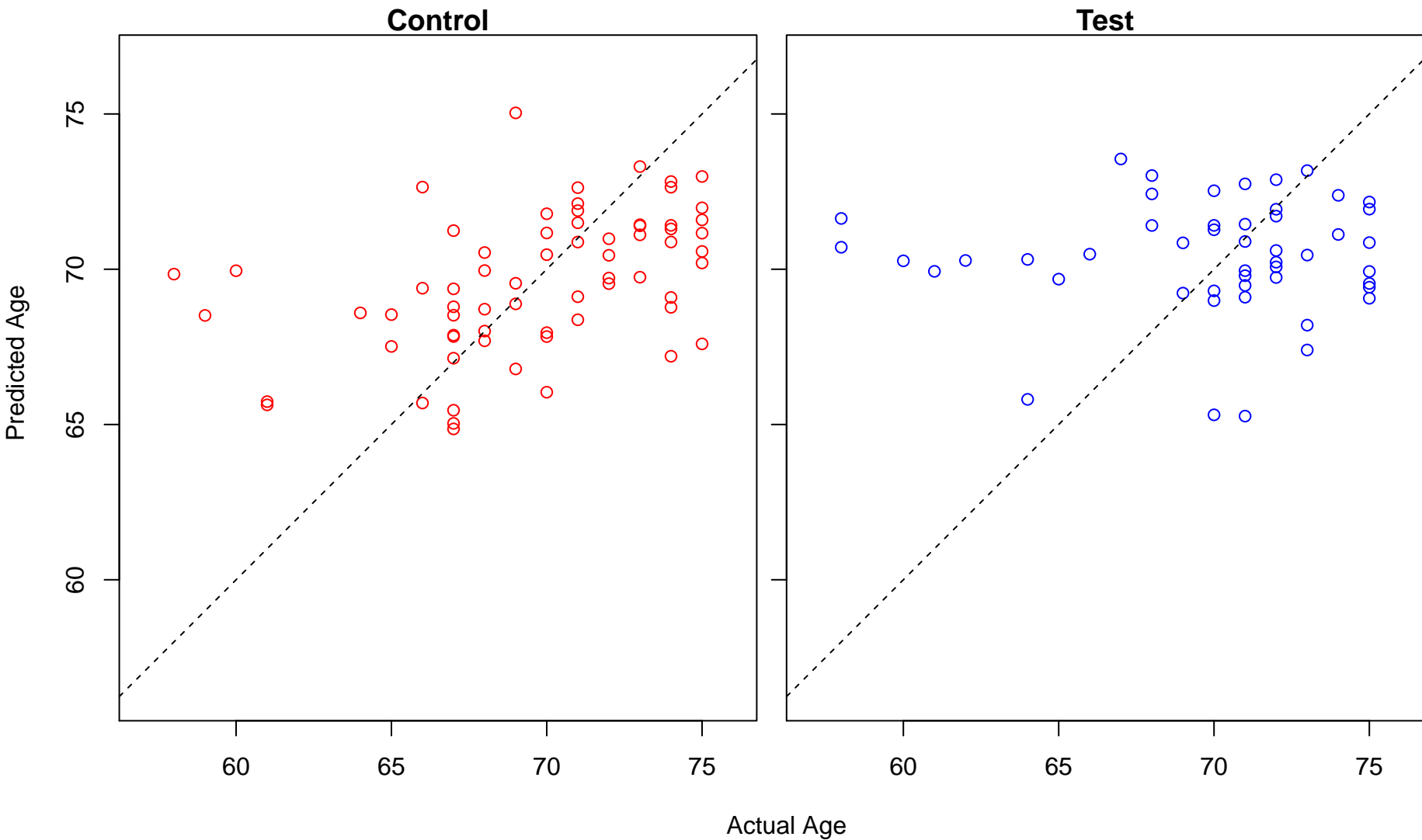
sphingomyelin metabolic process (Score: 0.588773)



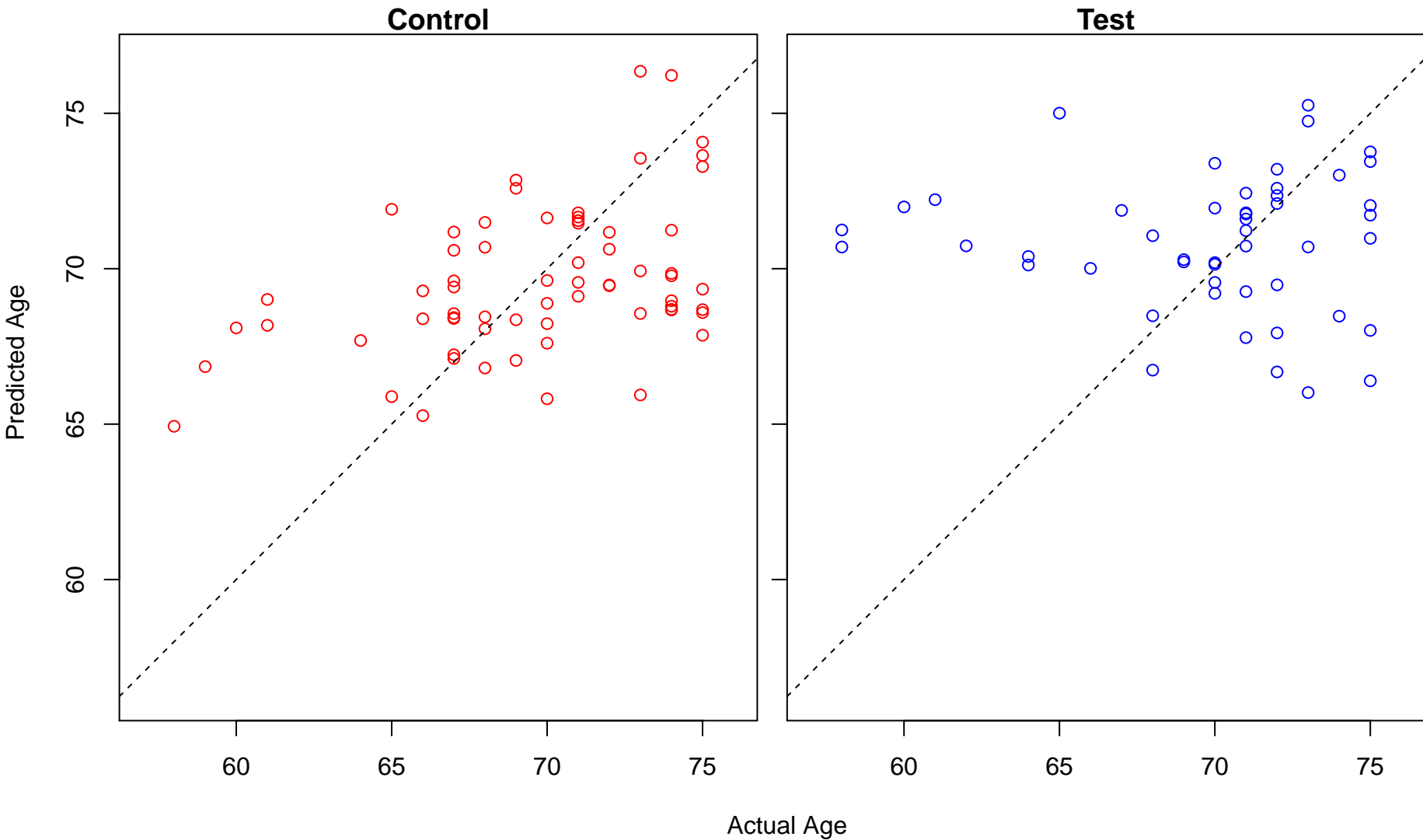
collecting duct development (Score: 0.588346)



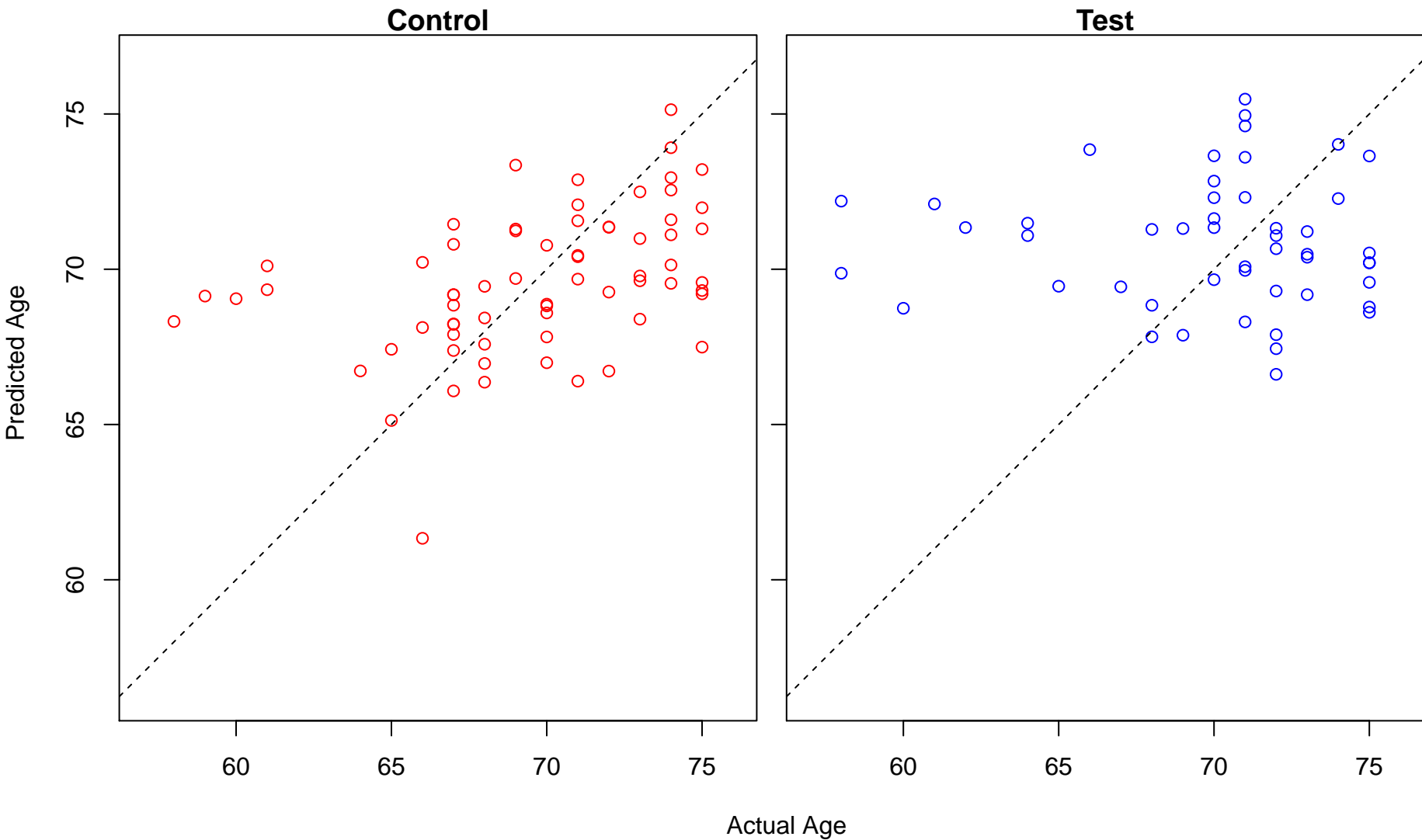
dicarboxylic acid catabolic process (Score: 0.587986)



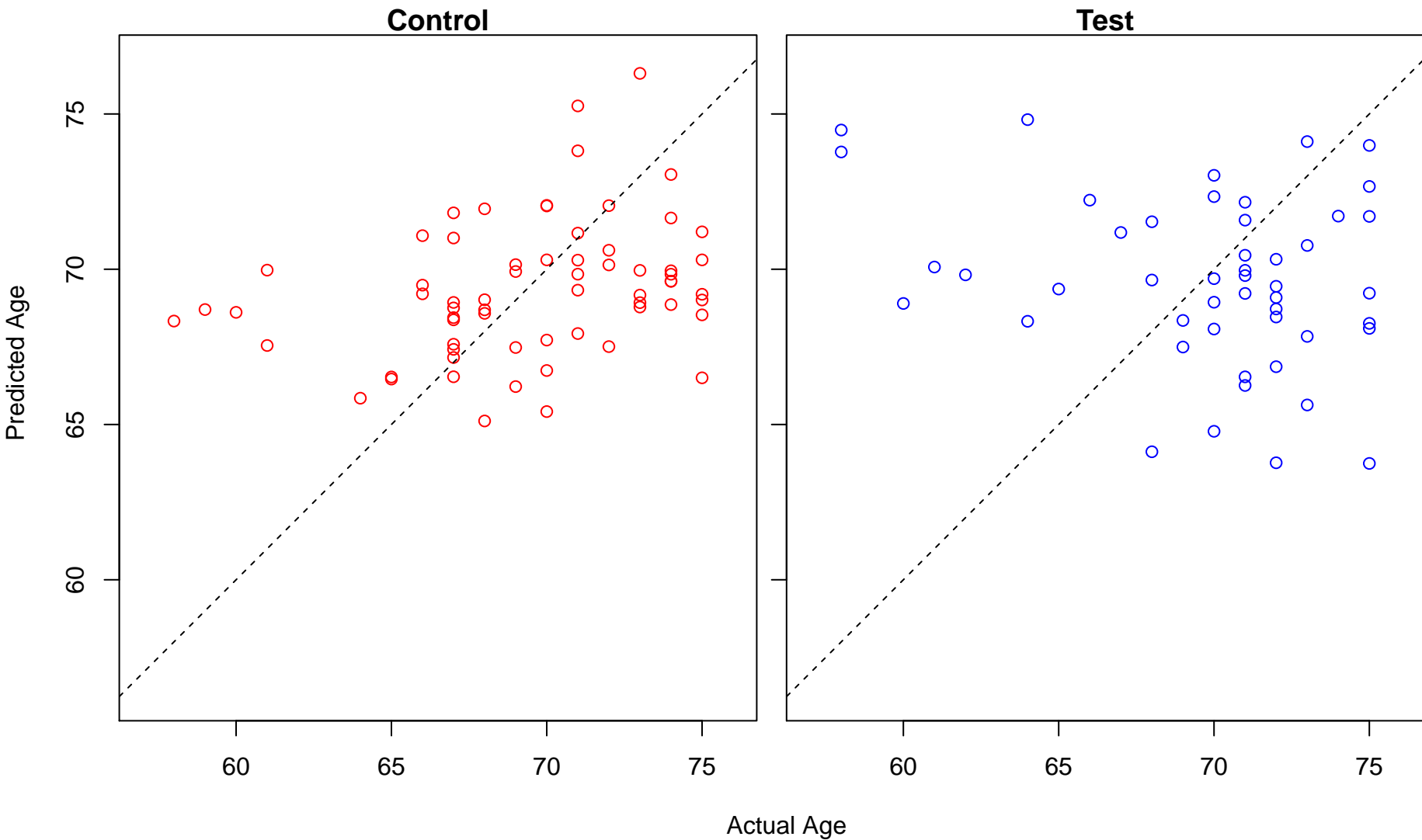
negative regulation of potassium ion transmembrane transport (Score: 0.587920)



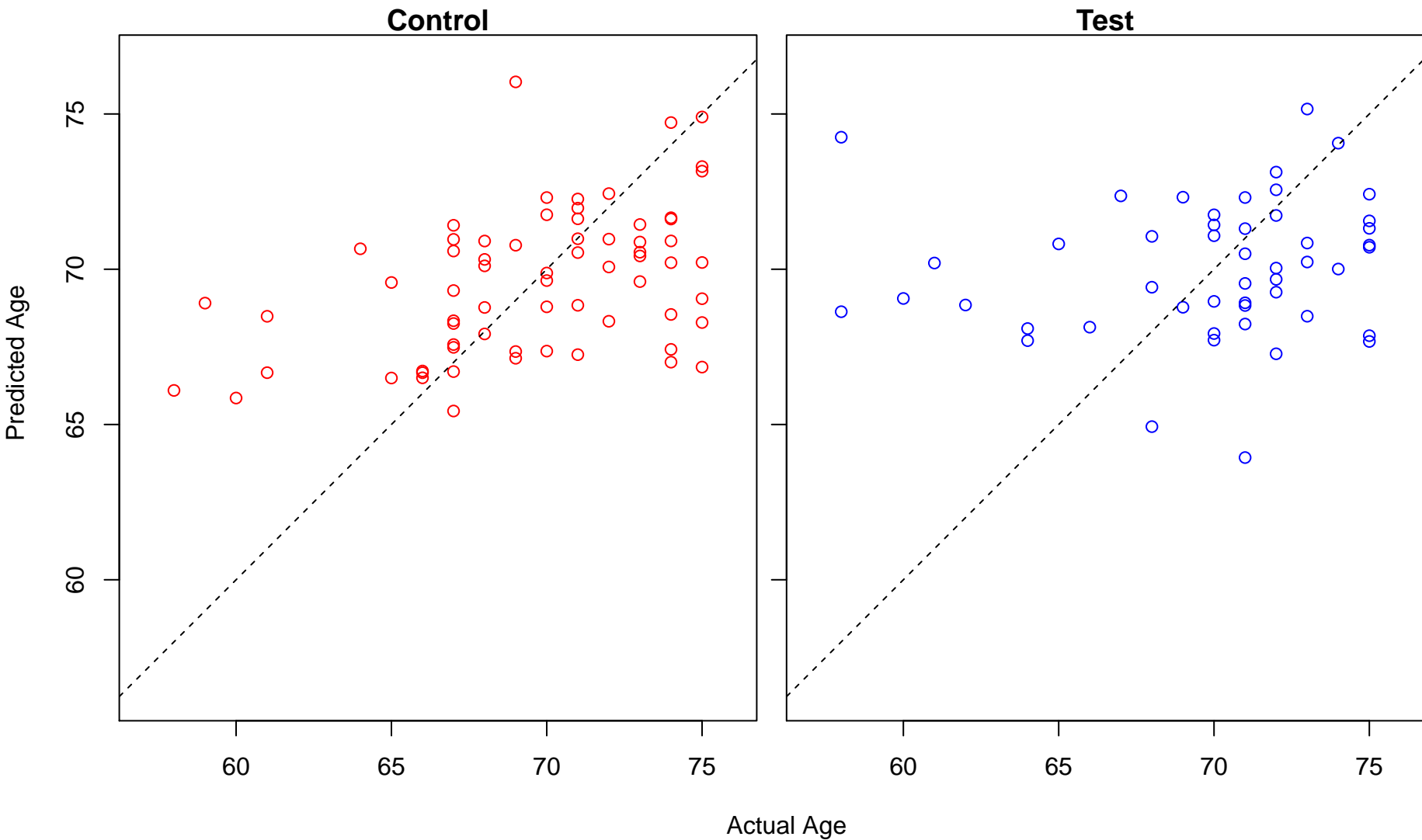
positive regulation of interleukin-5 production (Score: 0.587797)



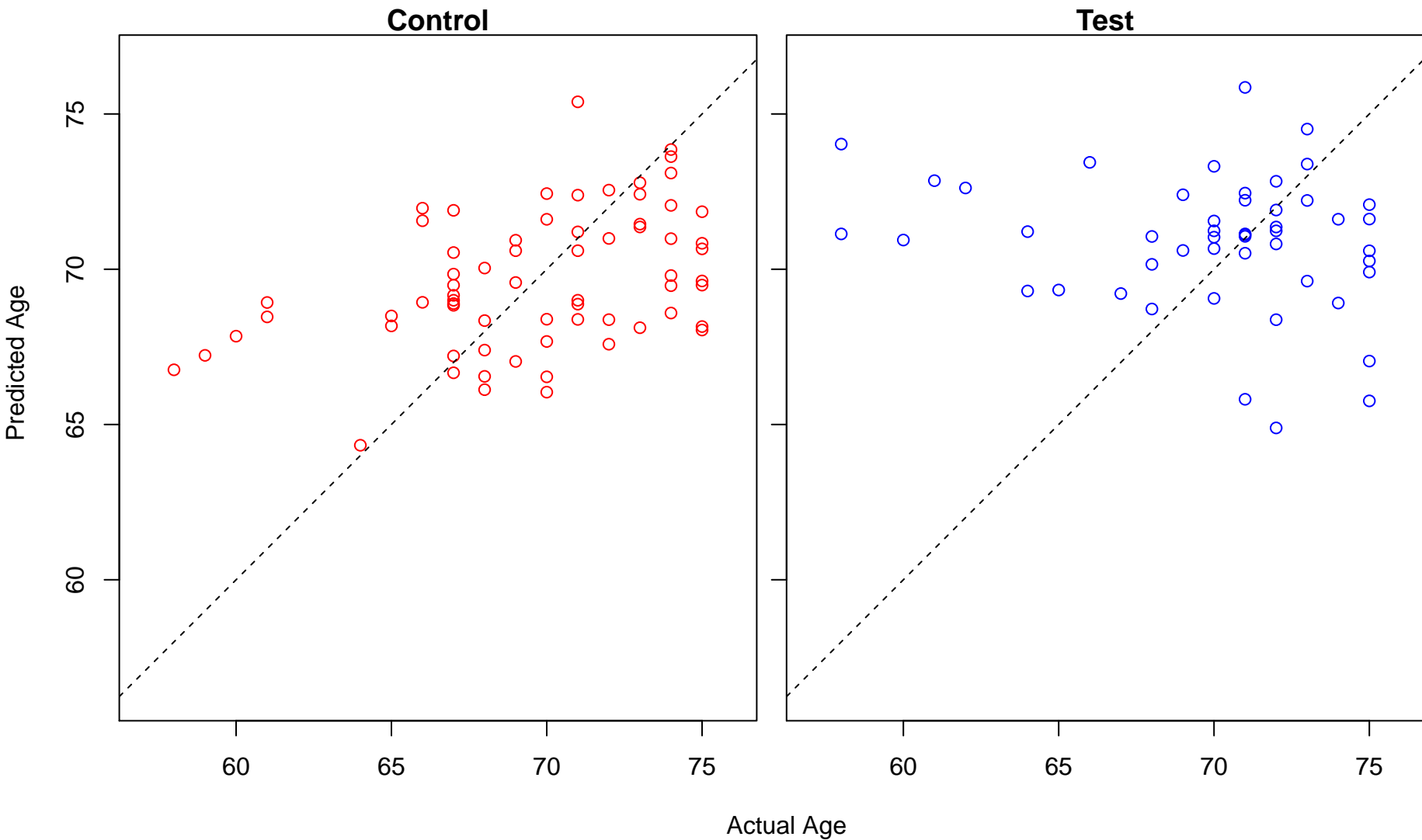
regulation of Golgi organization (Score: 0.587793)



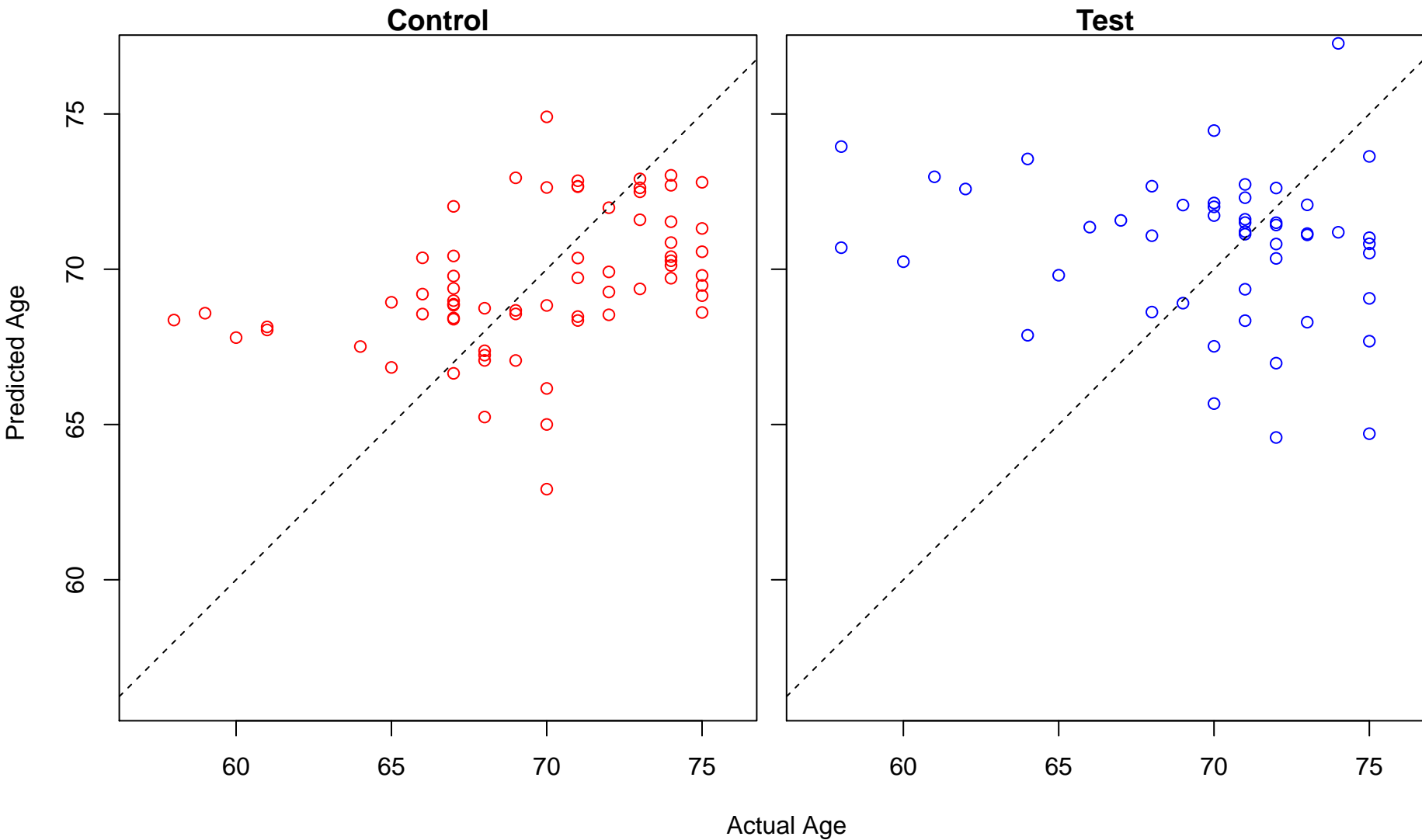
flavin-containing compound metabolic process (Score: 0.587659)



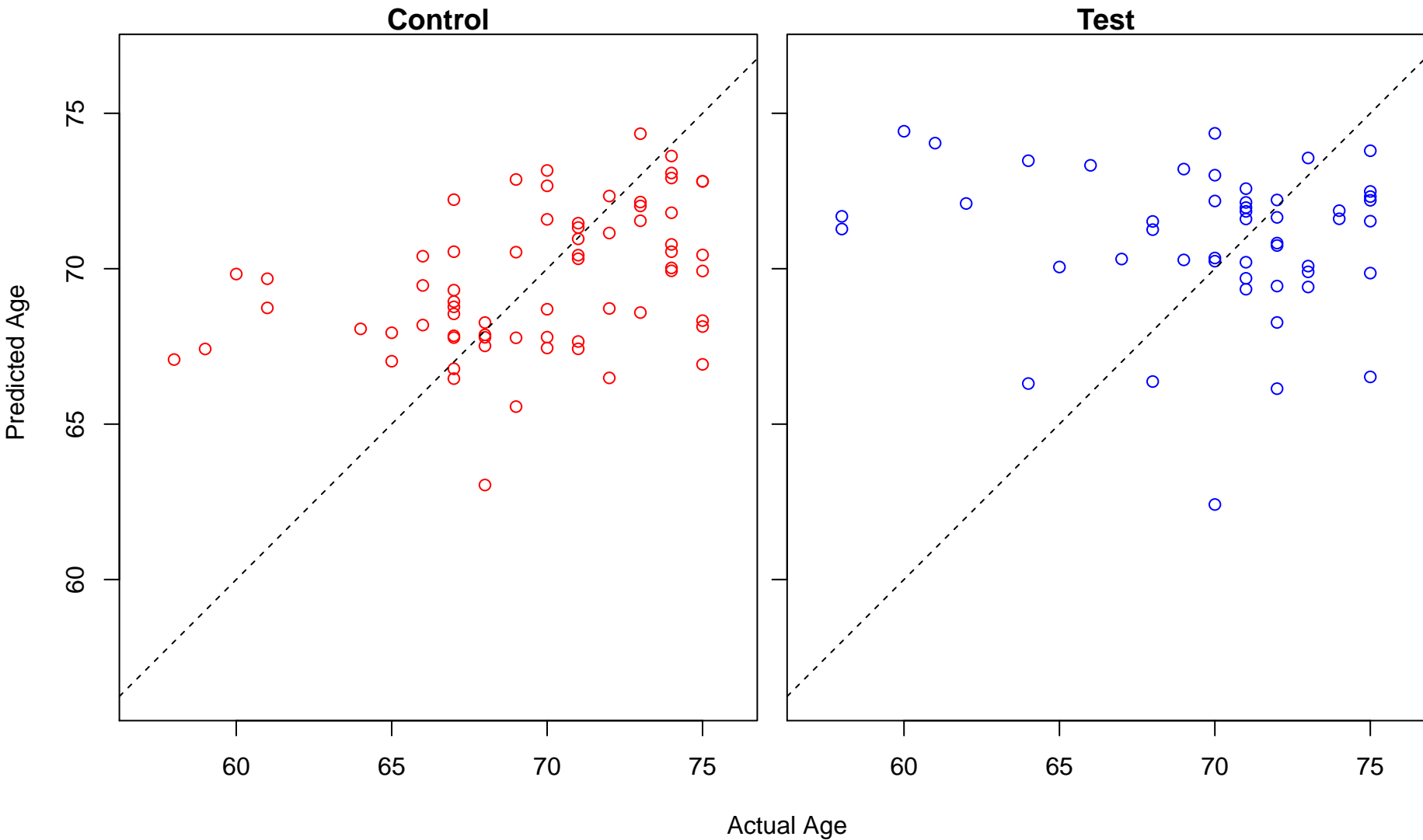
positive regulation of mitotic cell cycle spindle assembly checkpoint (Score: 0.586110)



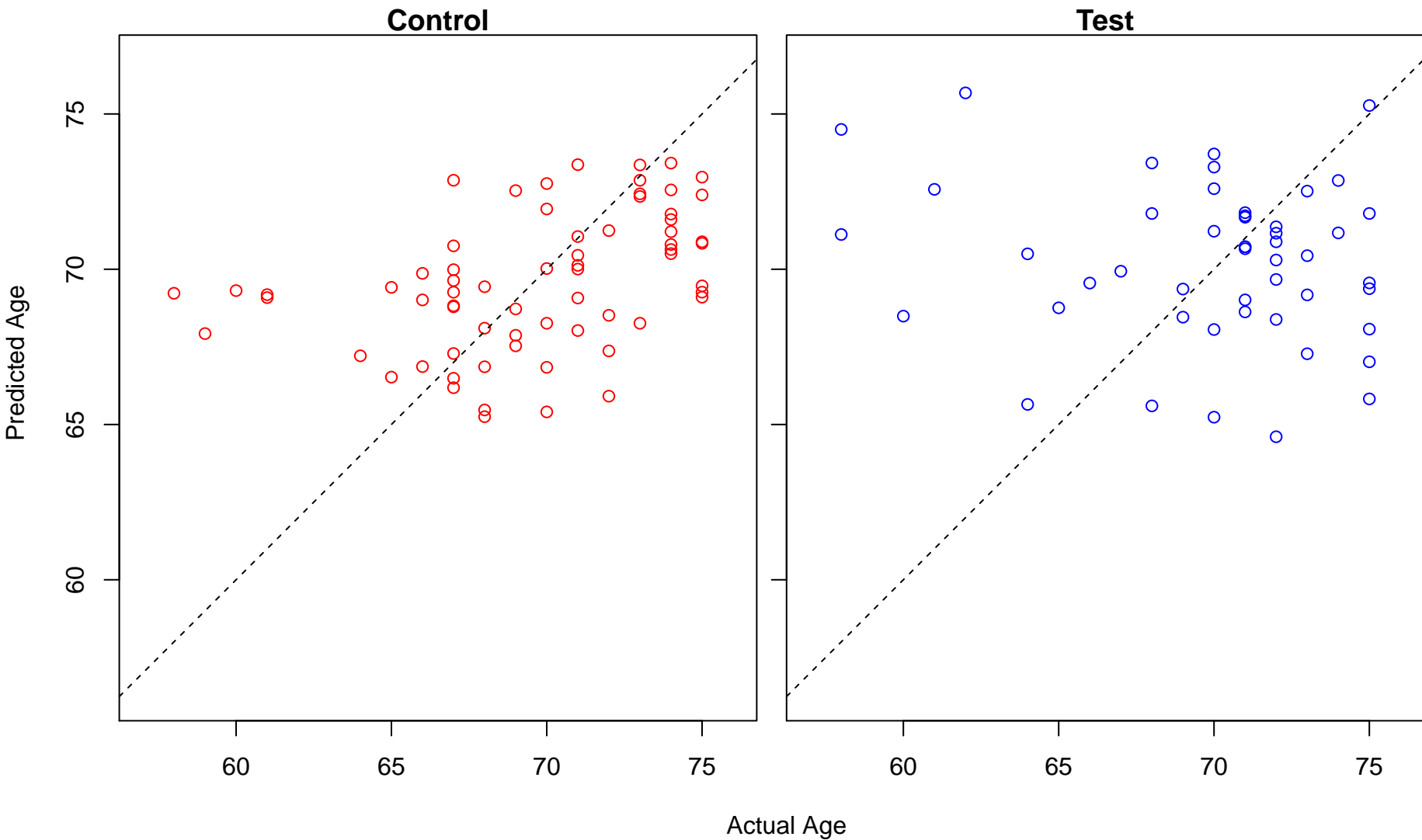
positive regulation of mRNA 3'-end processing (Score: 0.585886)



negative regulation of lipid transport (Score: 0.584926)

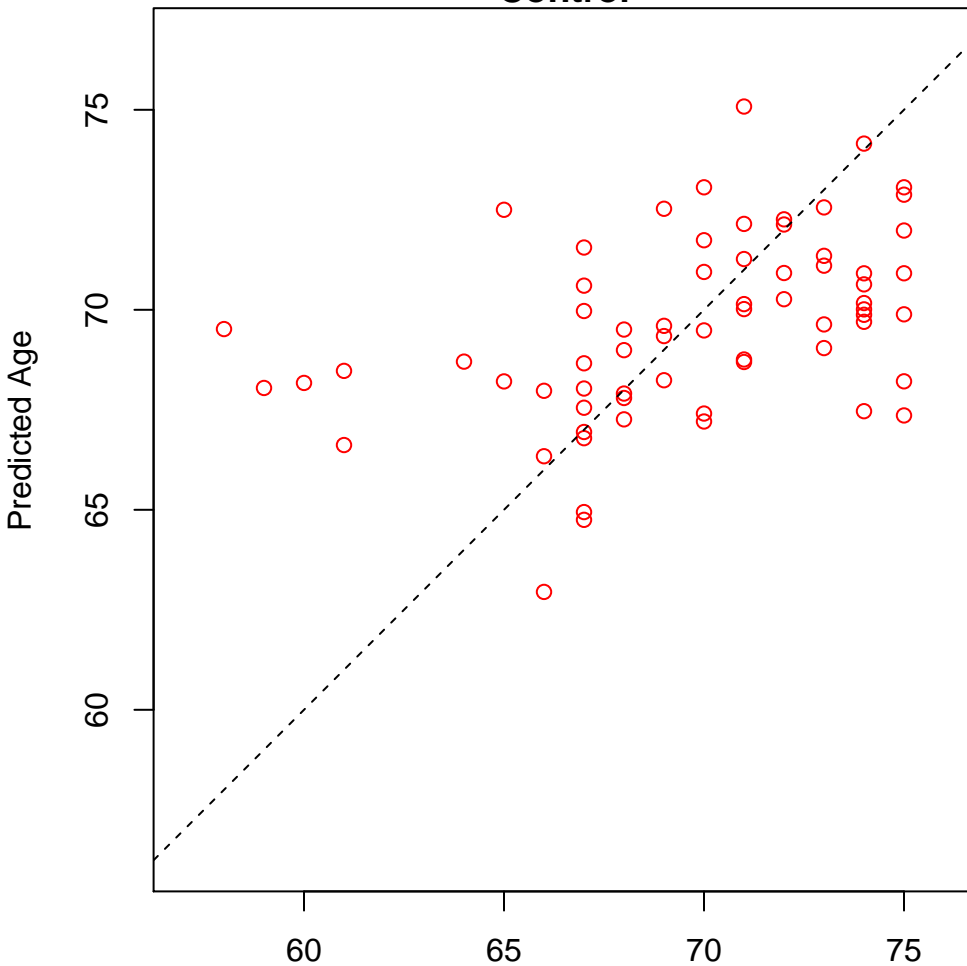


anatomical structure maturation (Score: 0.584105)

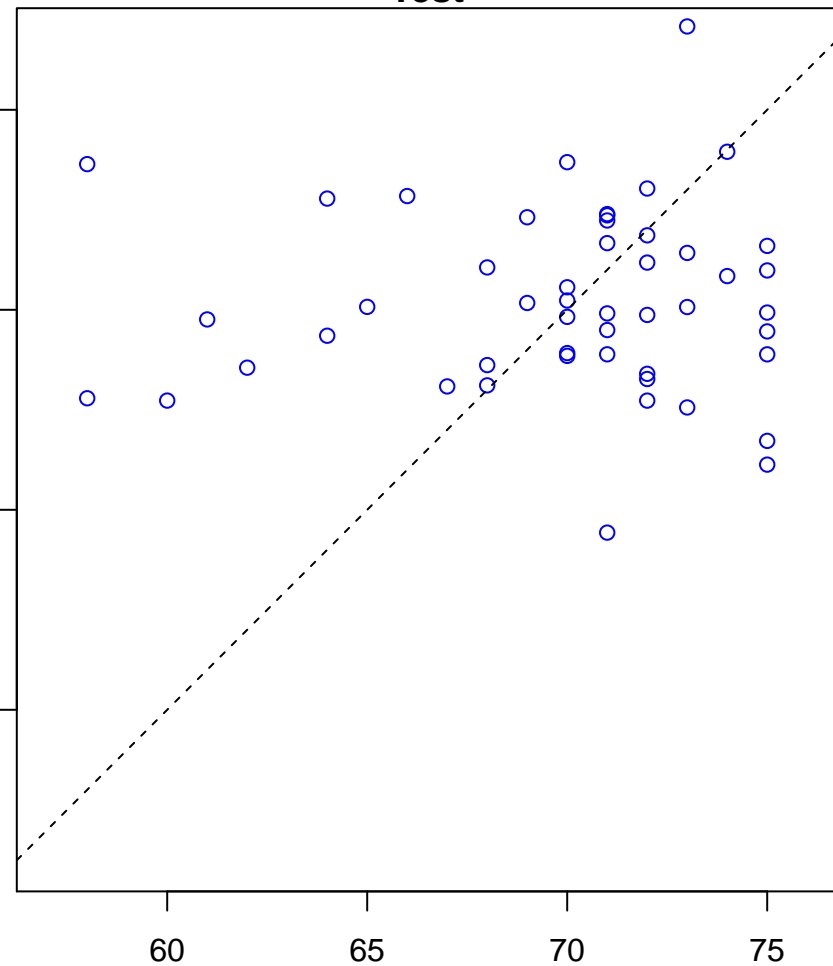


cellular response to amino acid stimulus (Score: 0.583663)

Control

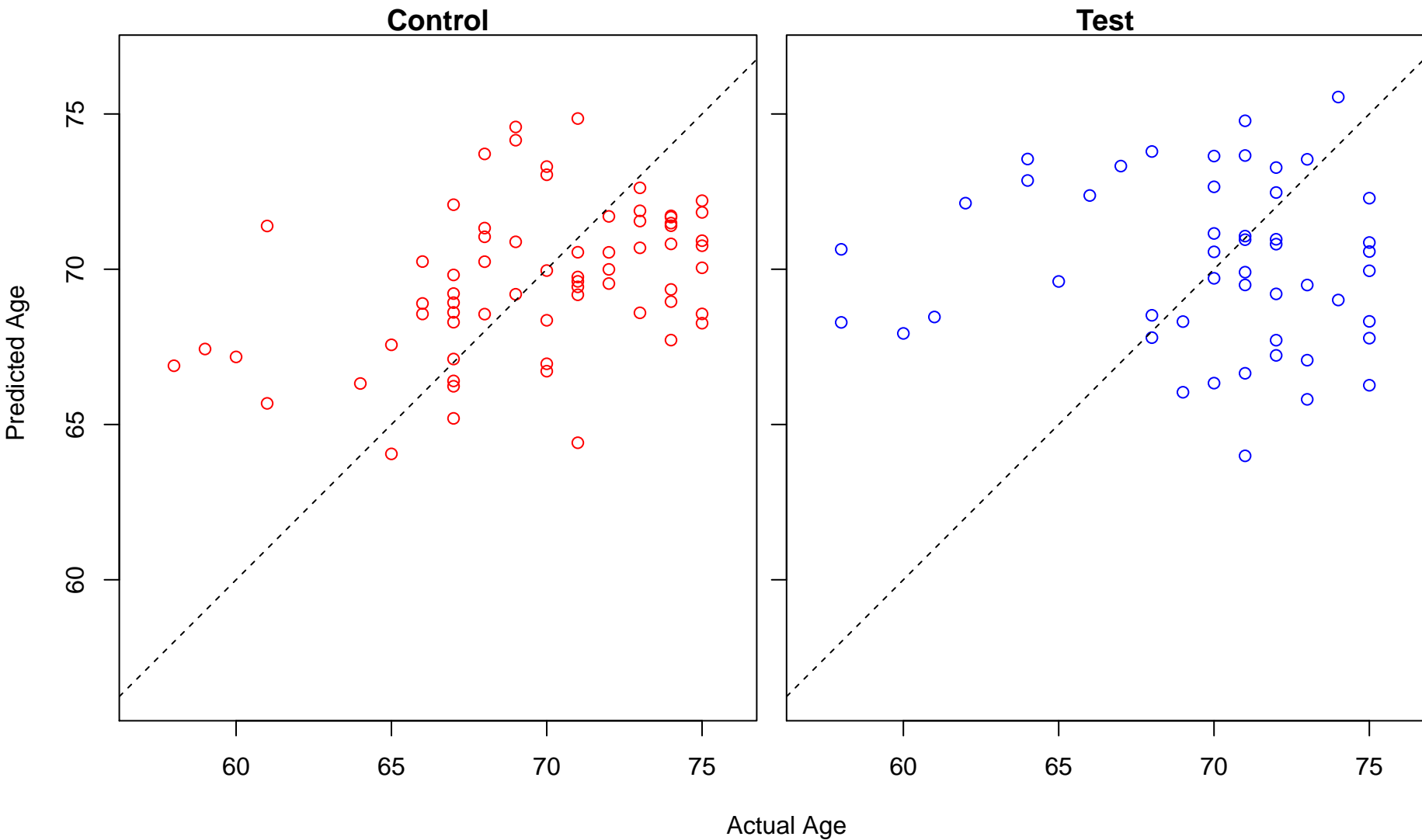


Test

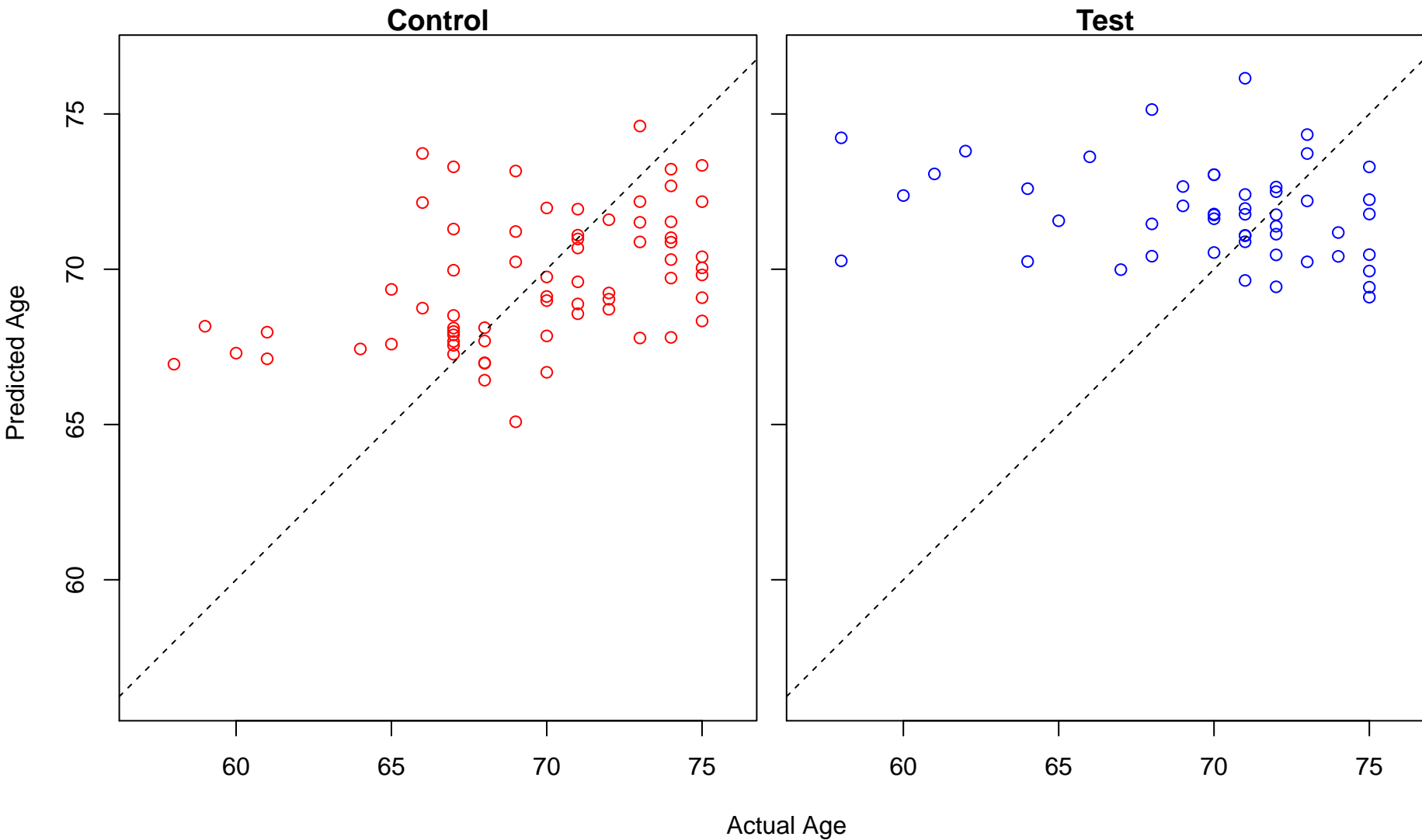


Actual Age

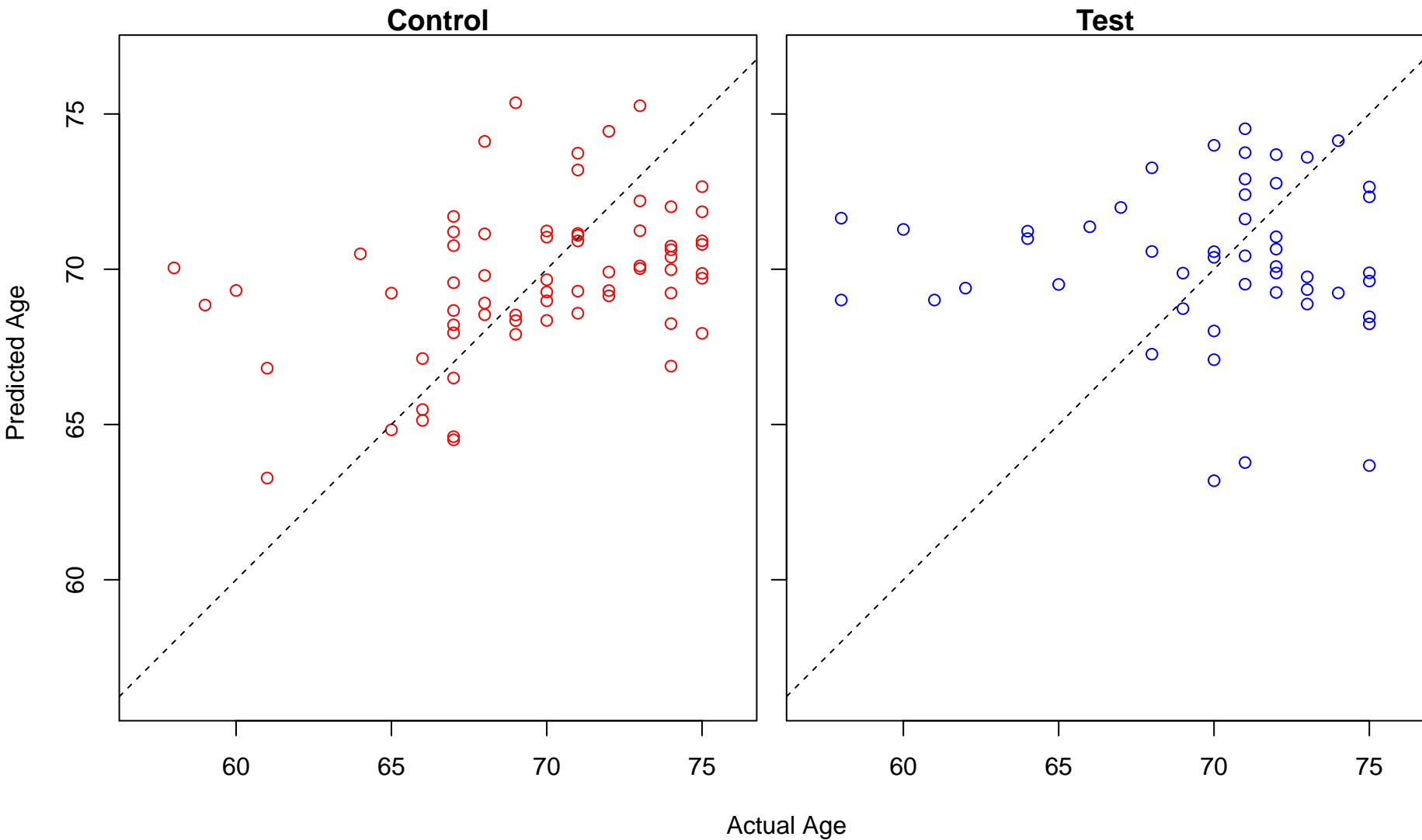
lens fiber cell differentiation (Score: 0.583200)



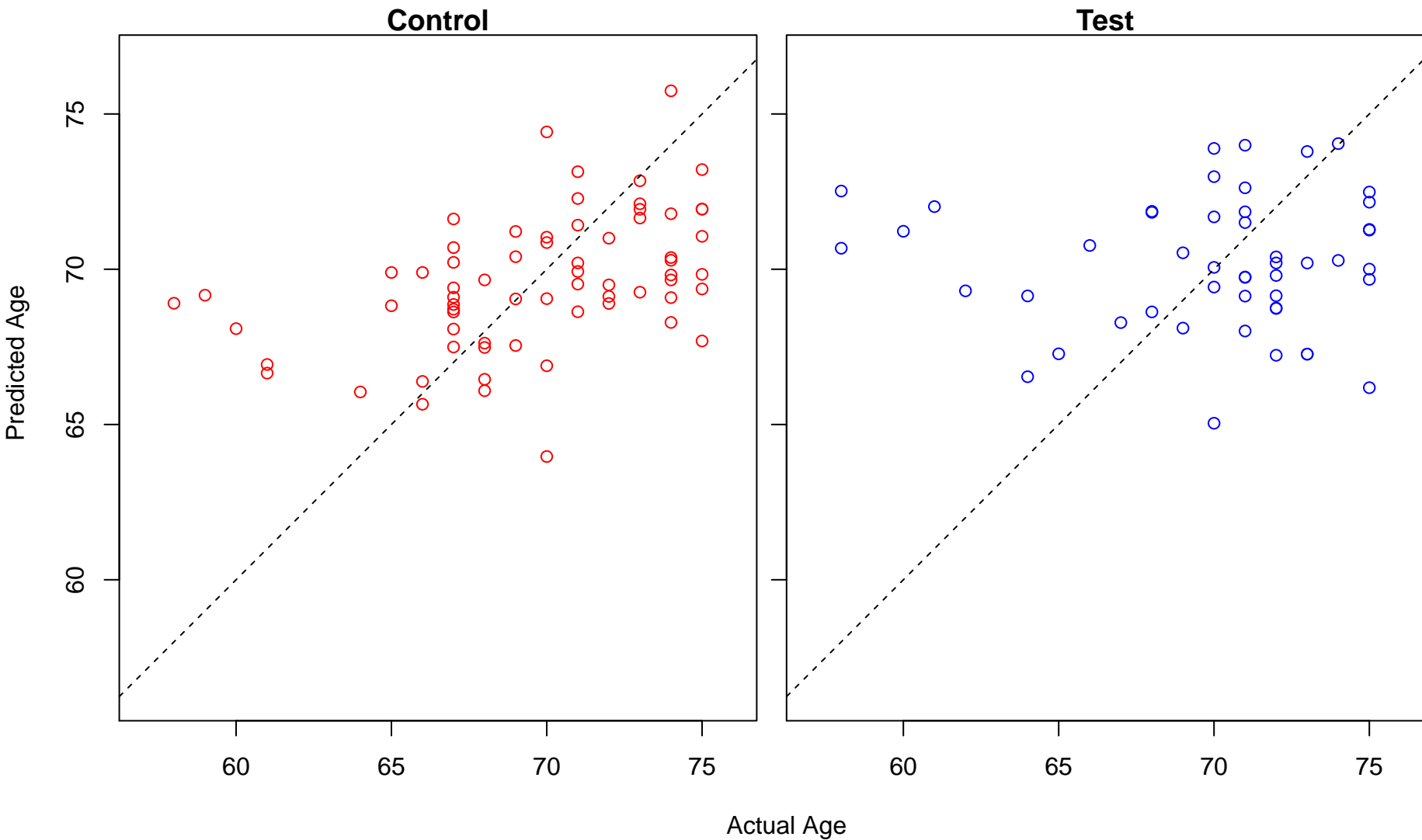
negative regulation of alcohol biosynthetic process (Score: 0.583188)



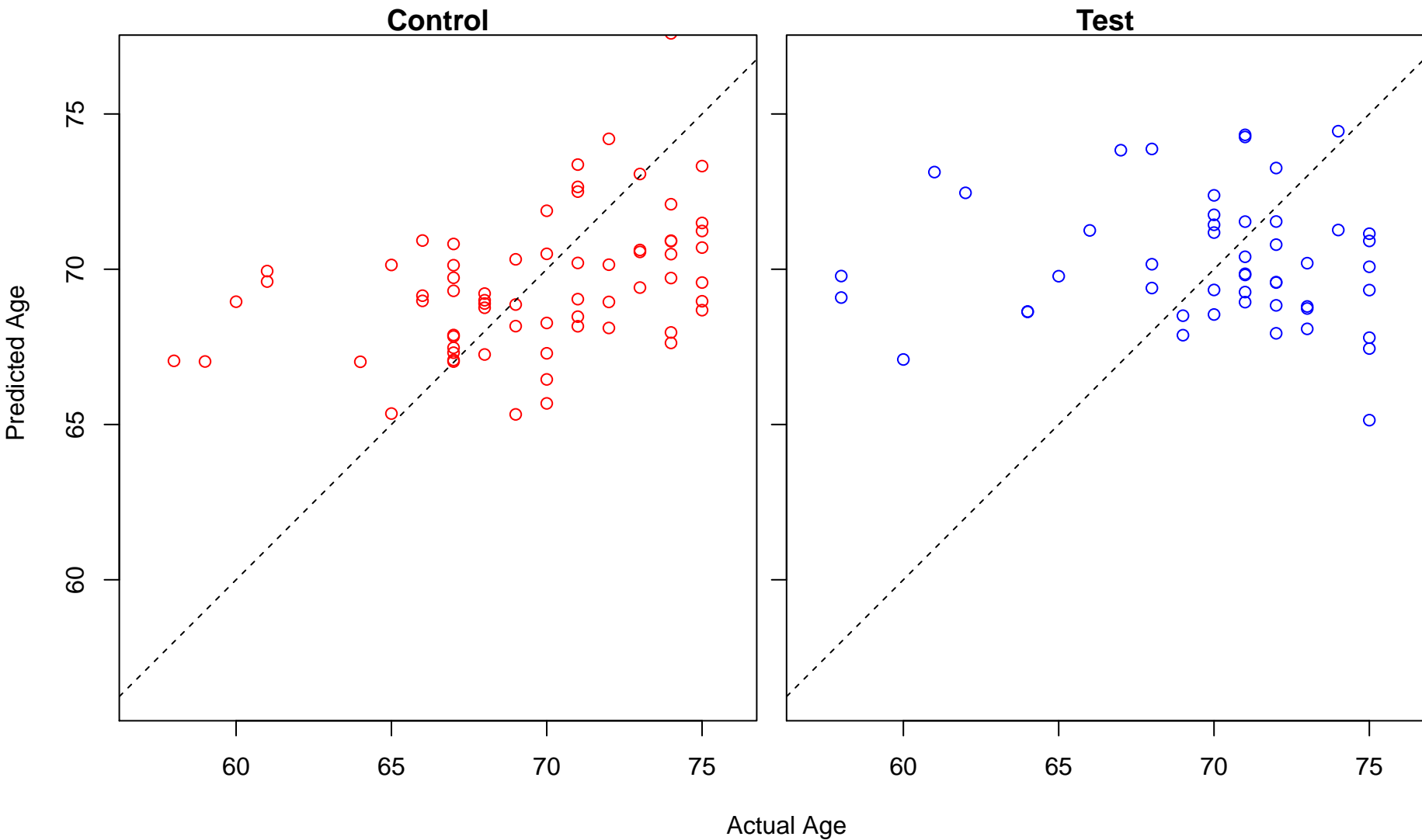
maintenance of protein location in nucleus (Score: 0.583154)



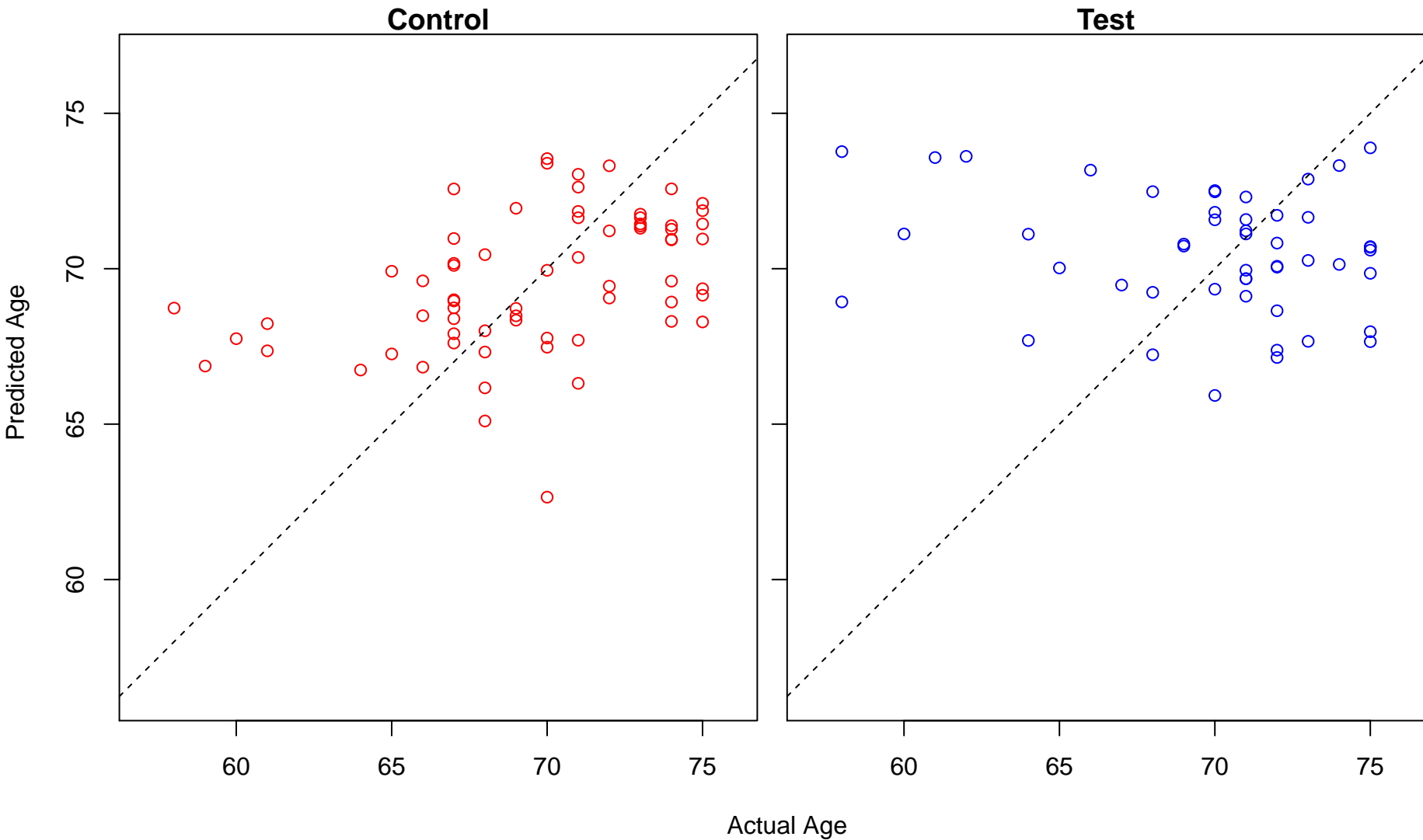
angiotensin-activated signaling pathway (Score: 0.580298)



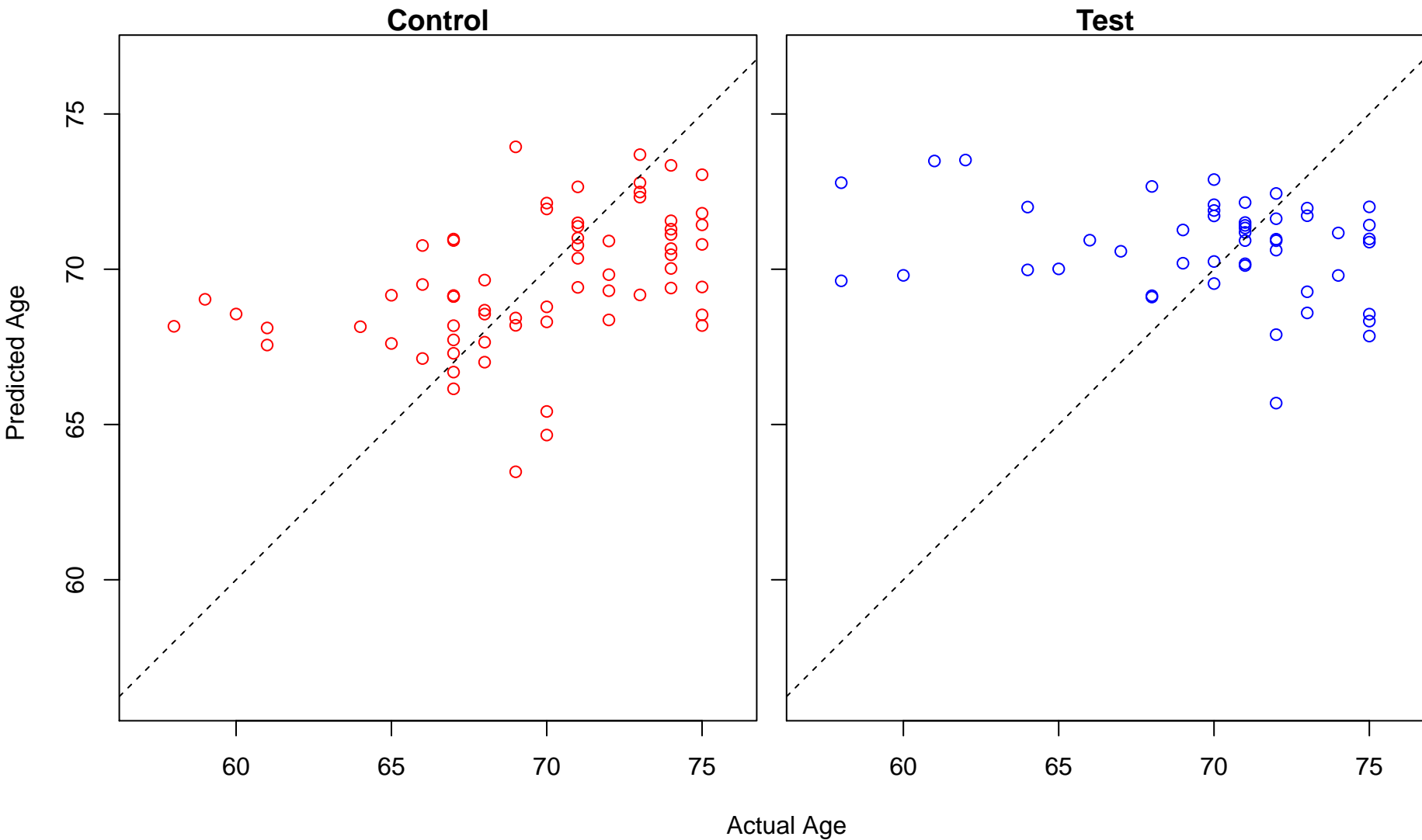
regulation of glomerular filtration (Score: 0.579985)



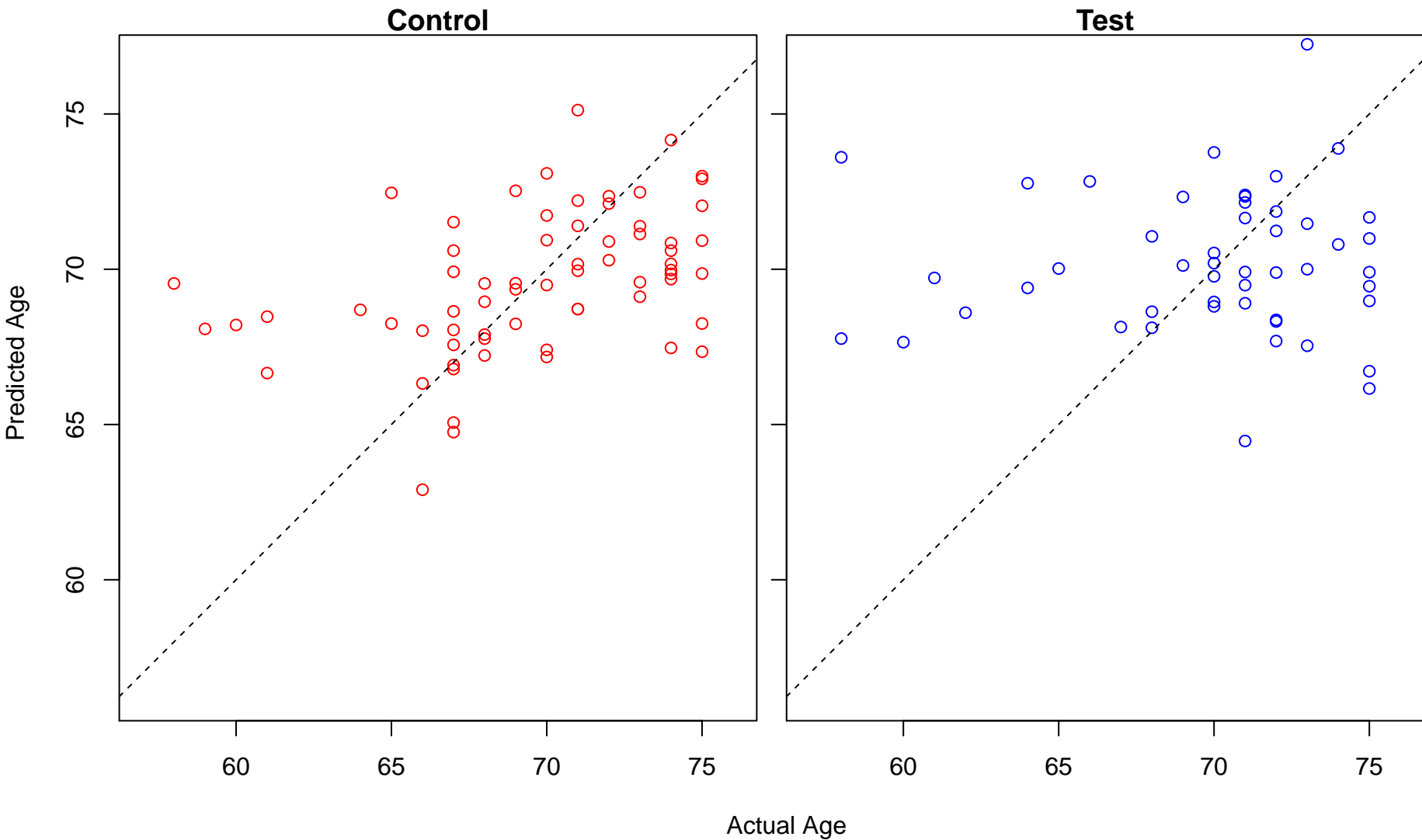
regulation of actin cytoskeleton reorganization (Score: 0.579927)



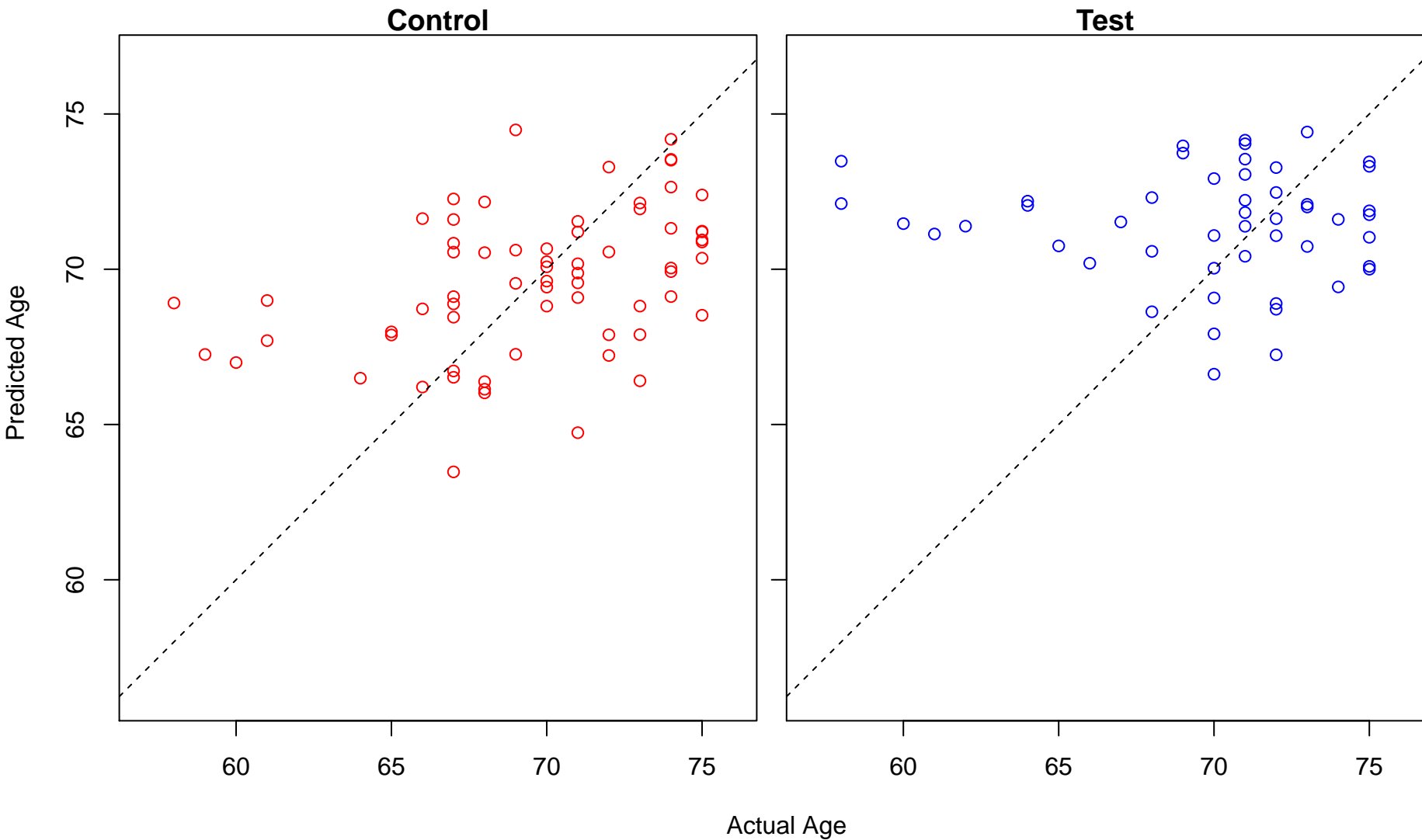
ketone biosynthetic process (Score: 0.579924)



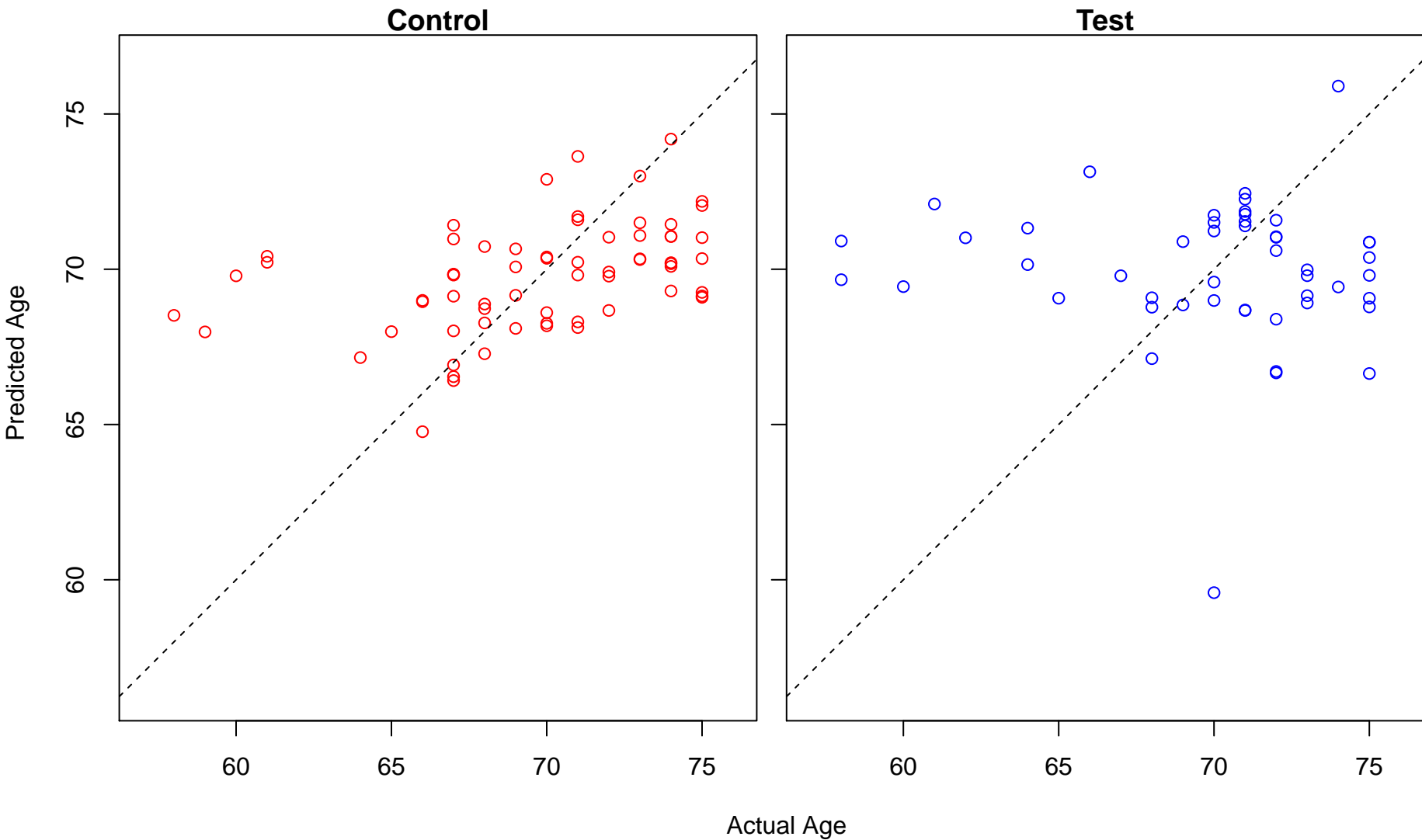
response to amino acid (Score: 0.579655)



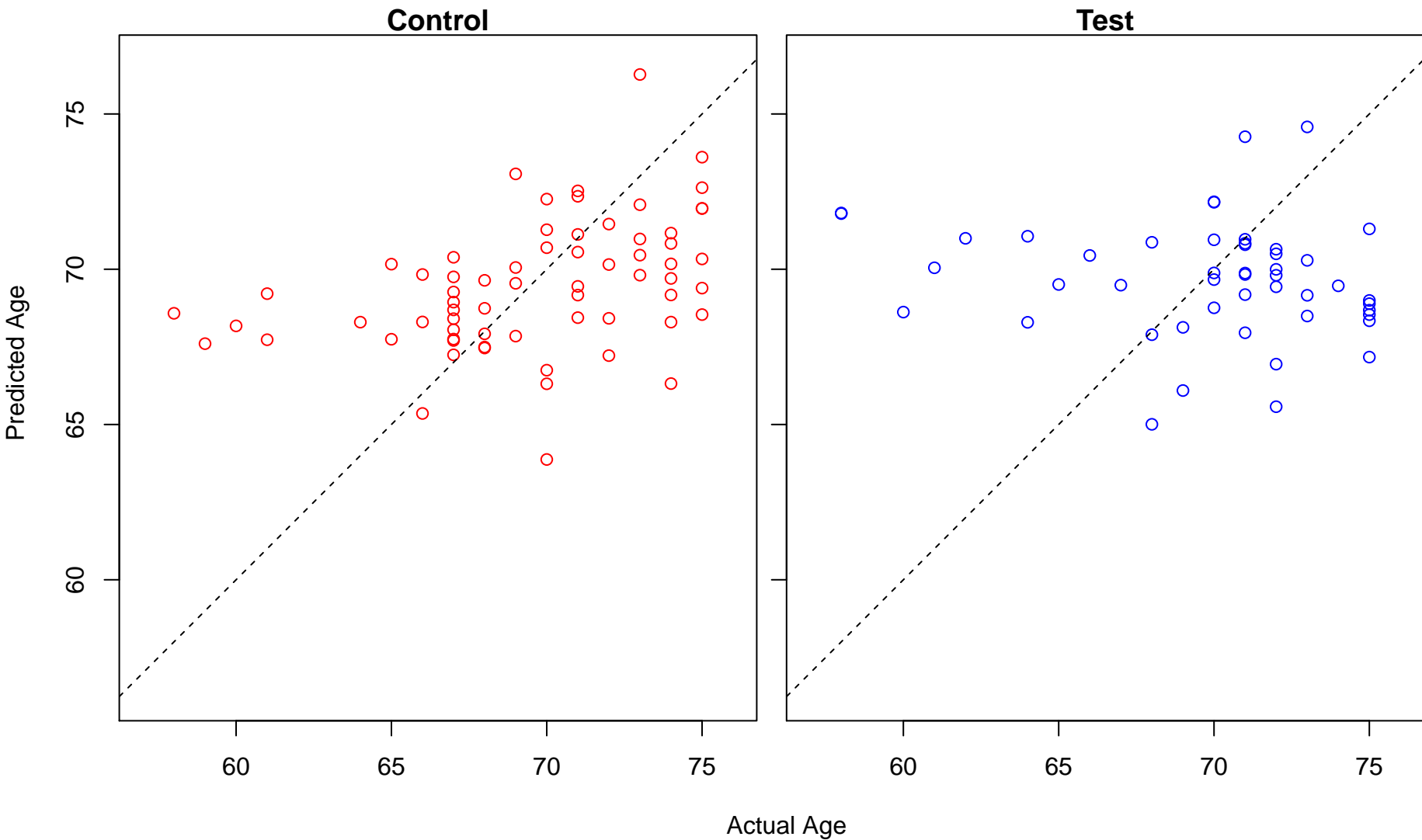
regulation of systemic arterial blood pressure by hormone (Score: 0.577634)



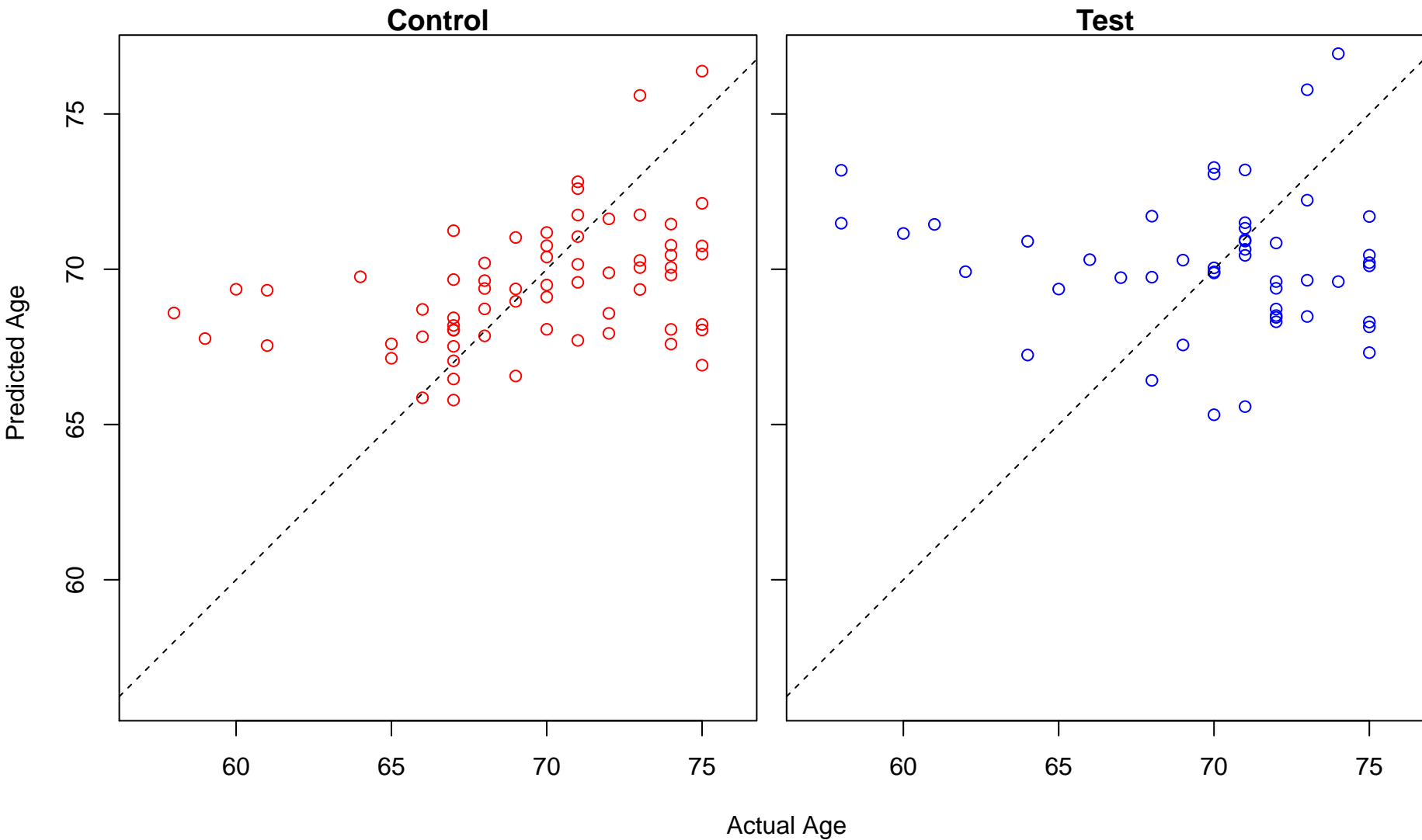
regulation of T cell chemotaxis (Score: 0.577577)



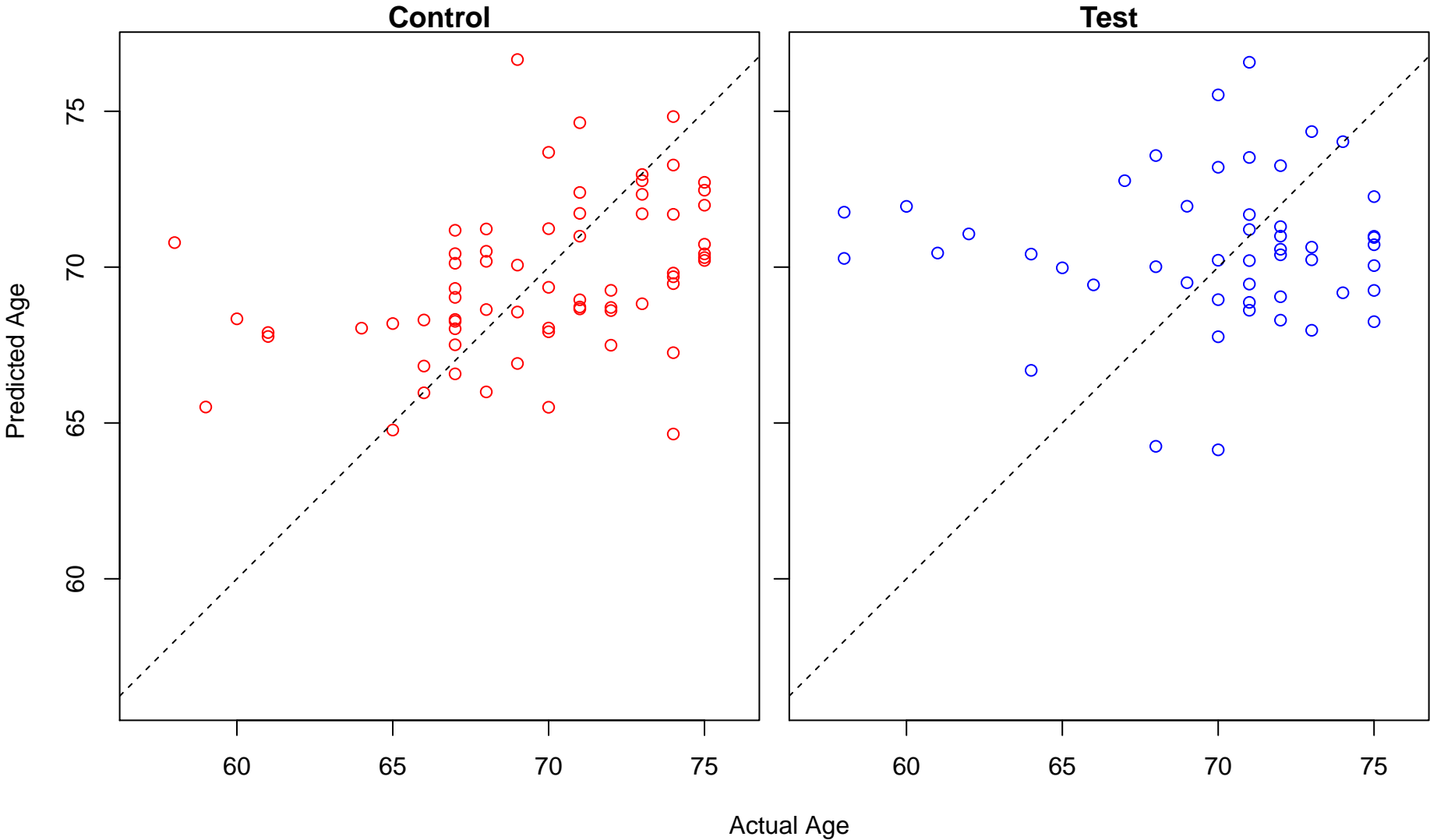
negative regulation of double-strand break repair (Score: 0.577171)



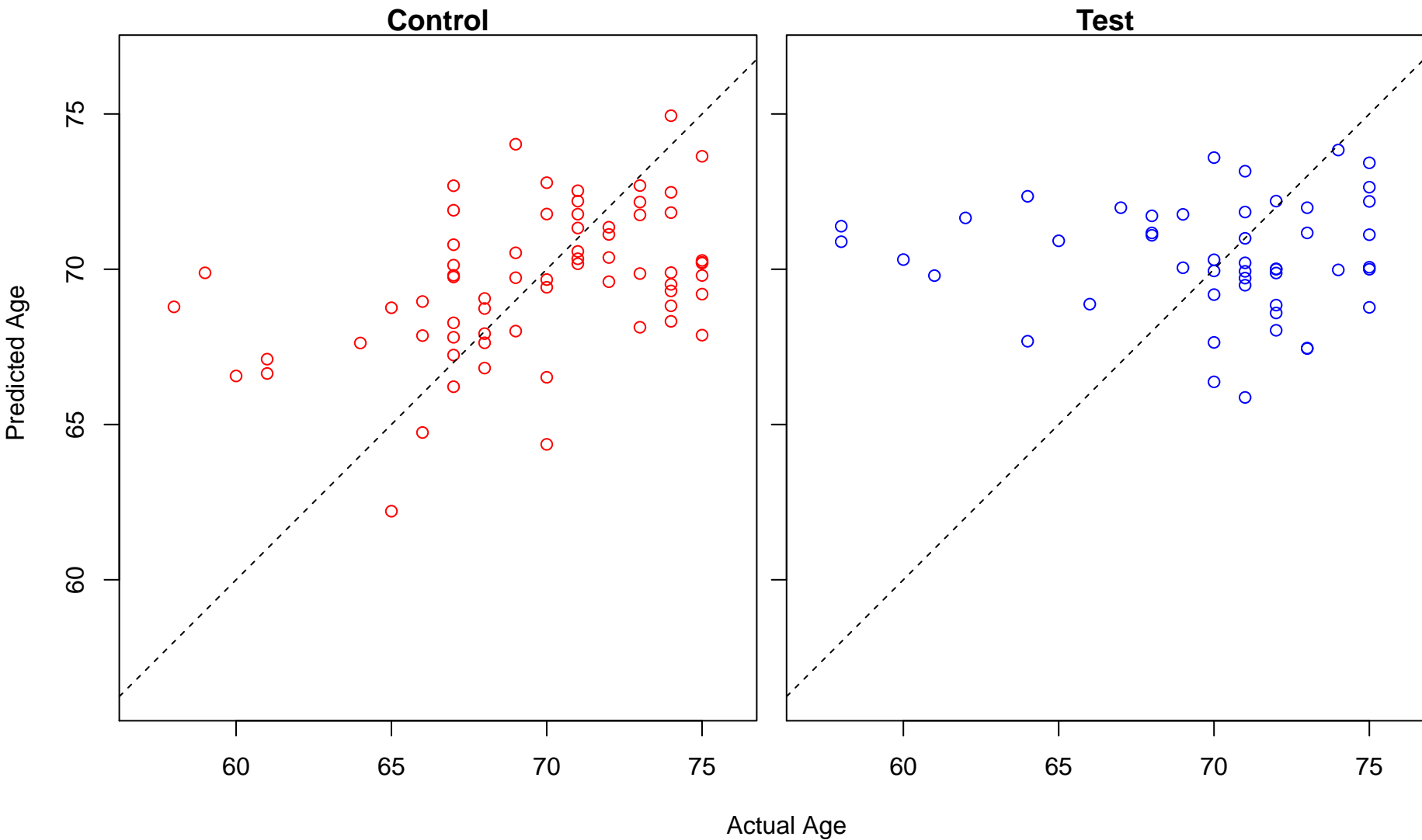
cellular response to amino acid starvation (Score: 0.576636)



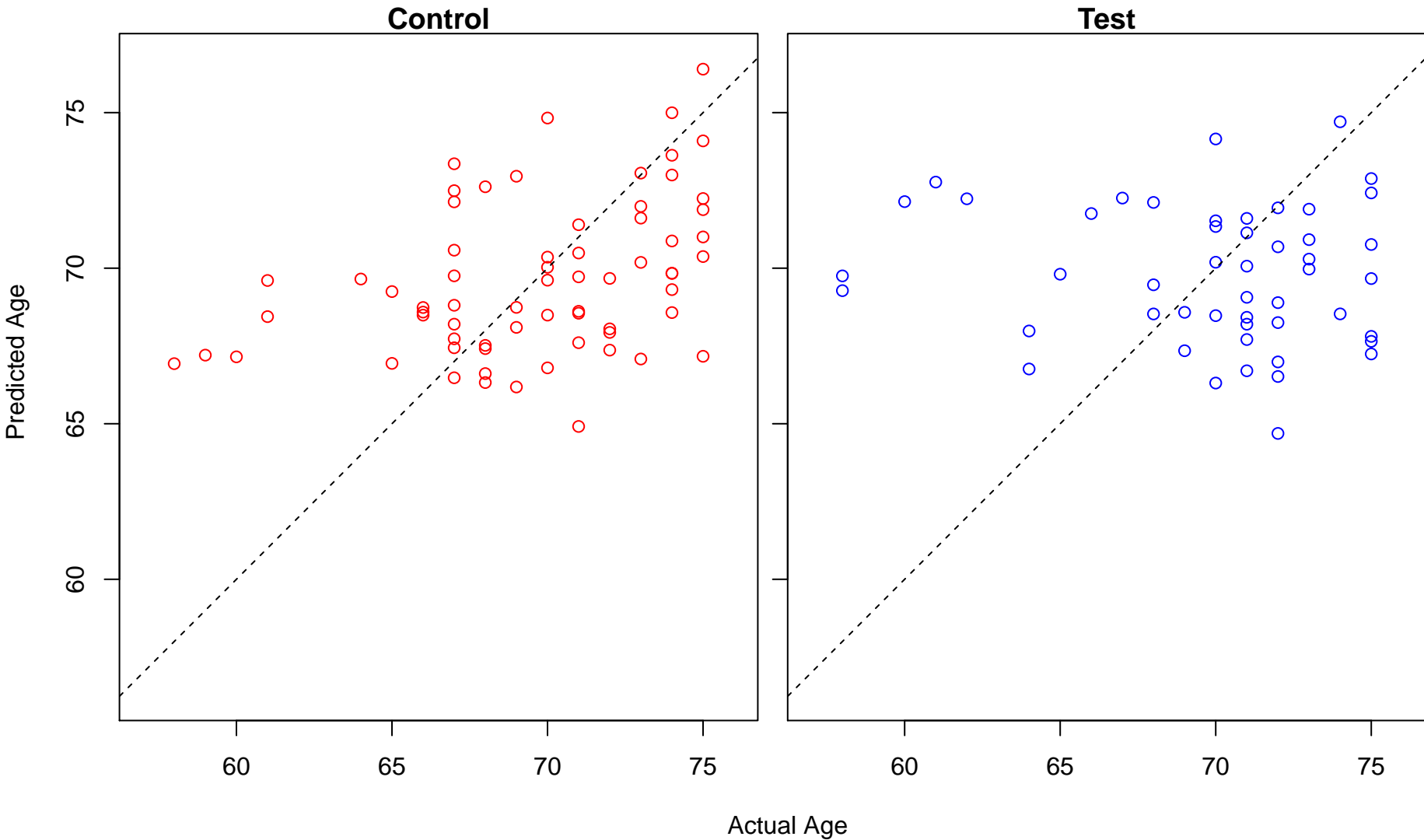
ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway (Score: 0.57)



regulation of Golgi to plasma membrane protein transport (Score: 0.576091)

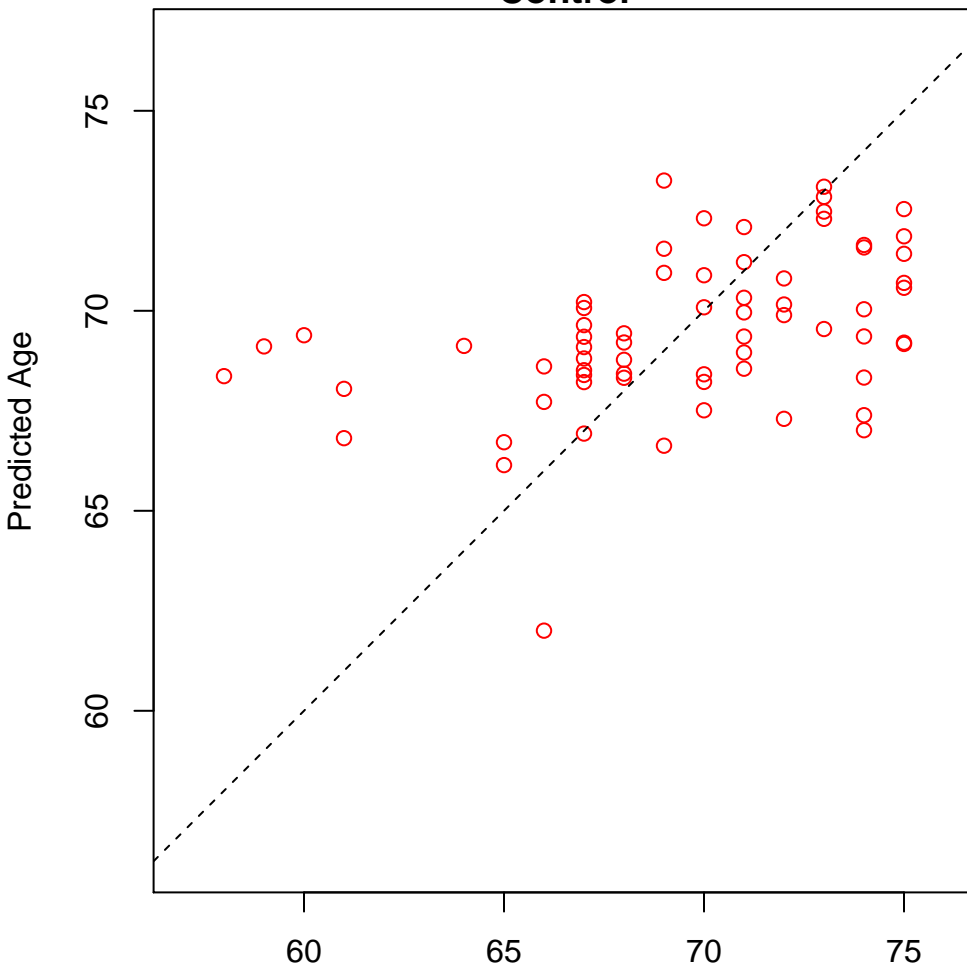


positive regulation of steroid biosynthetic process (Score: 0.576090)

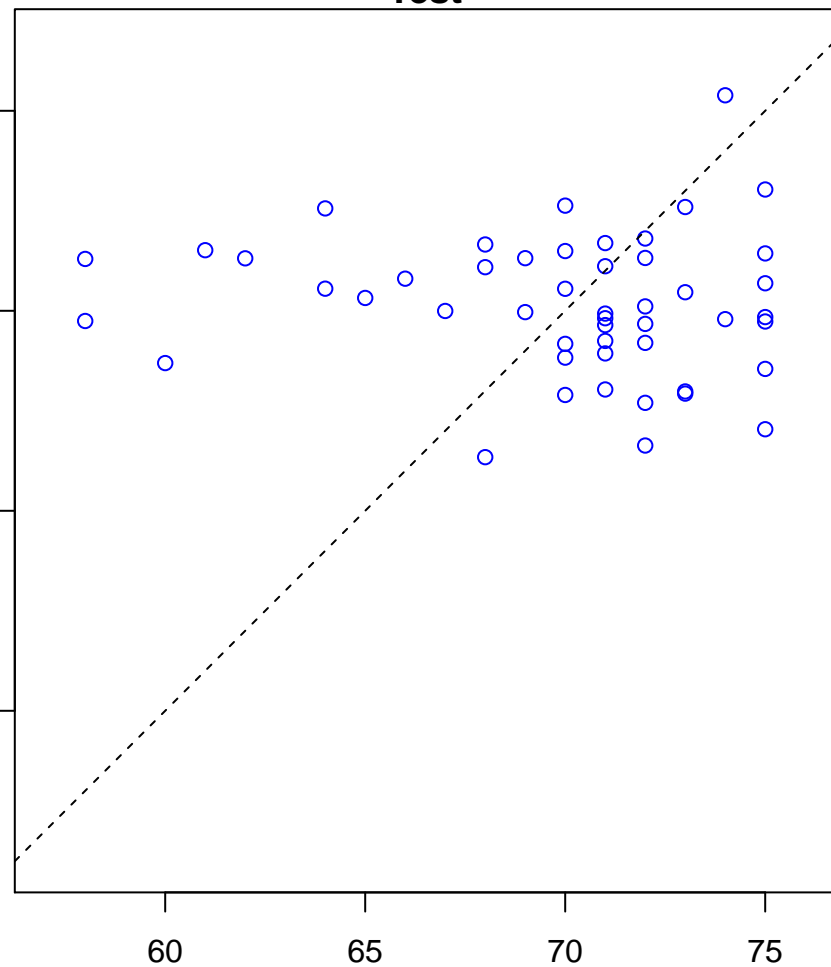


peroxisomal membrane transport (Score: 0.575672)

Control



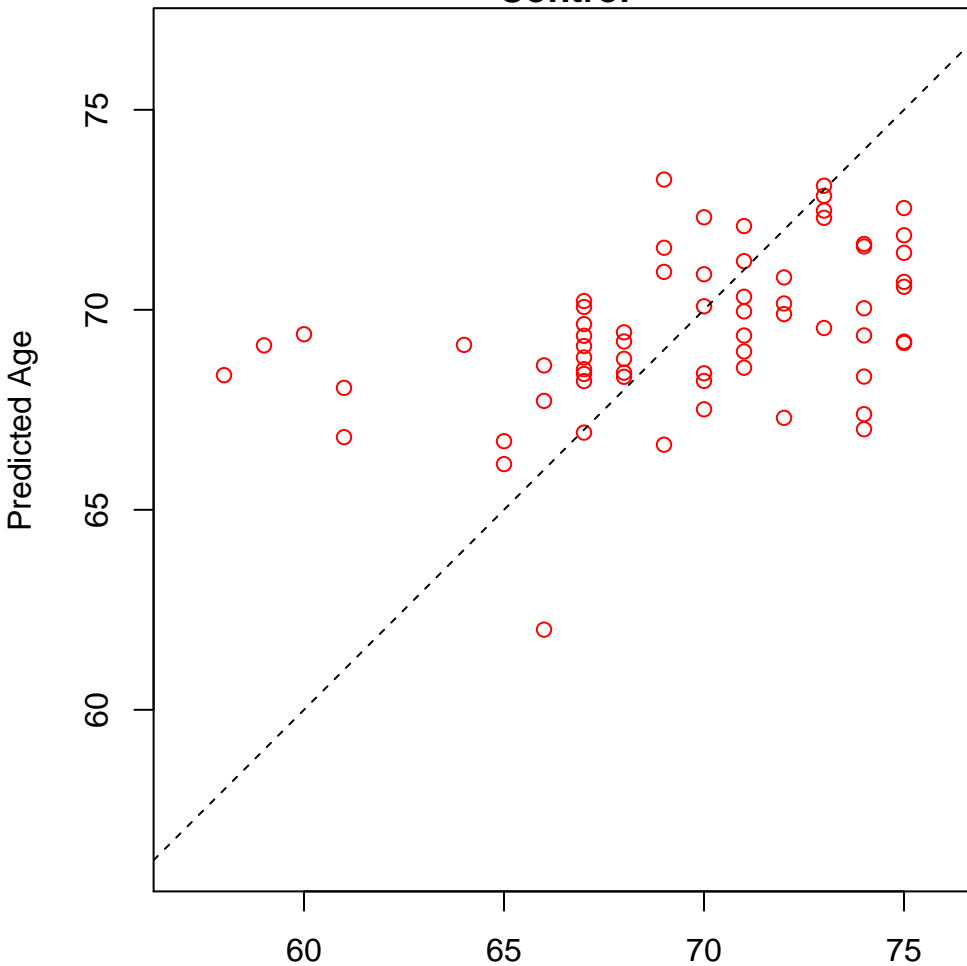
Test



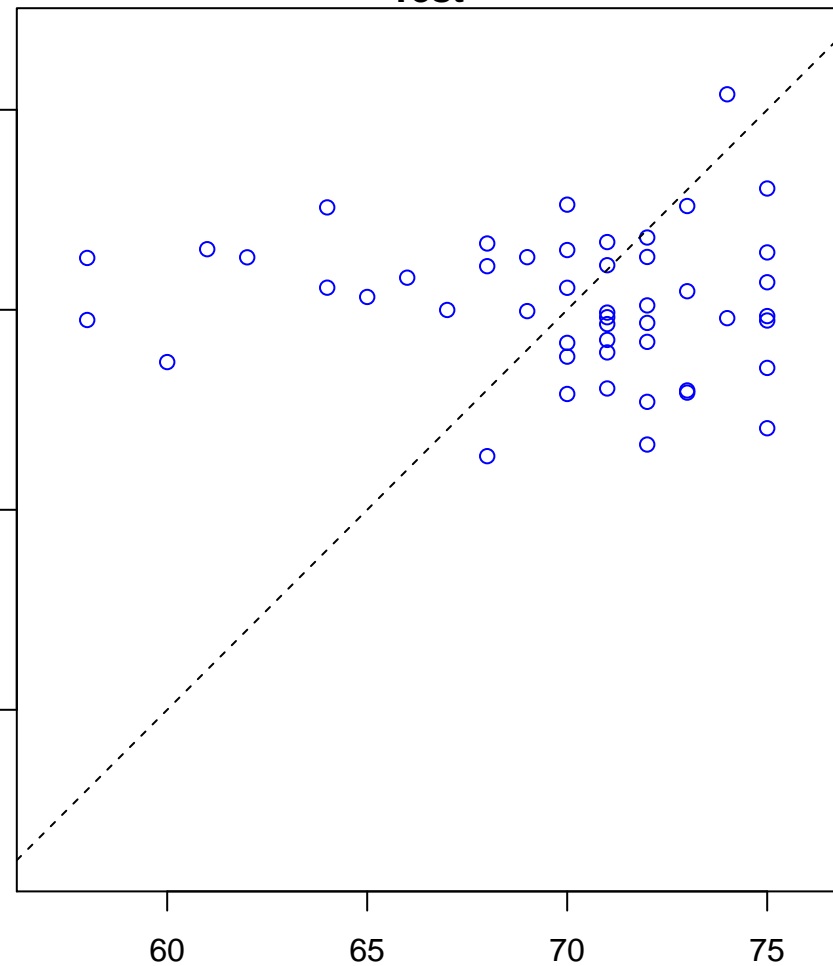
Actual Age

protein import into peroxisome membrane (Score: 0.575672)

Control

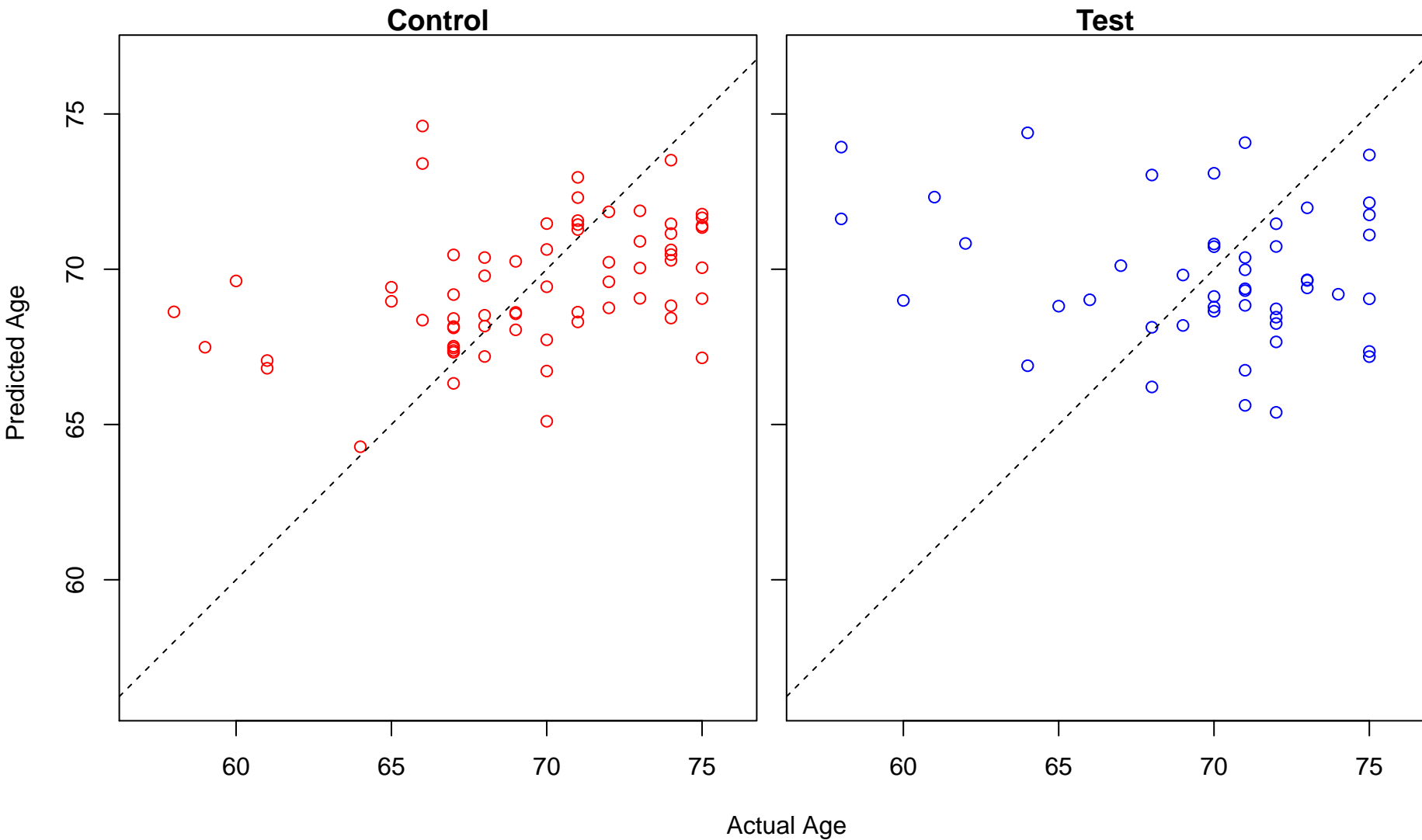


Test

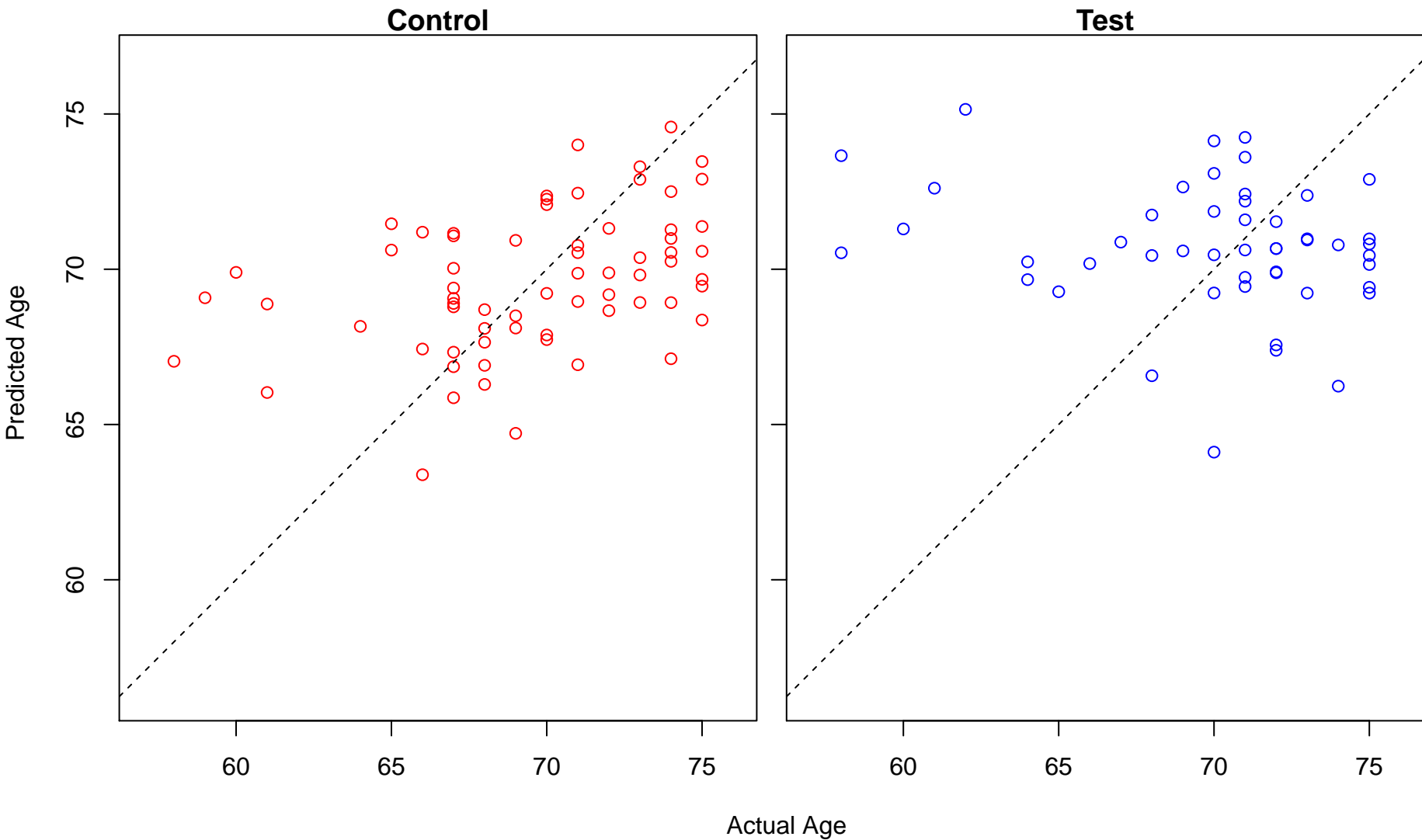


Actual Age

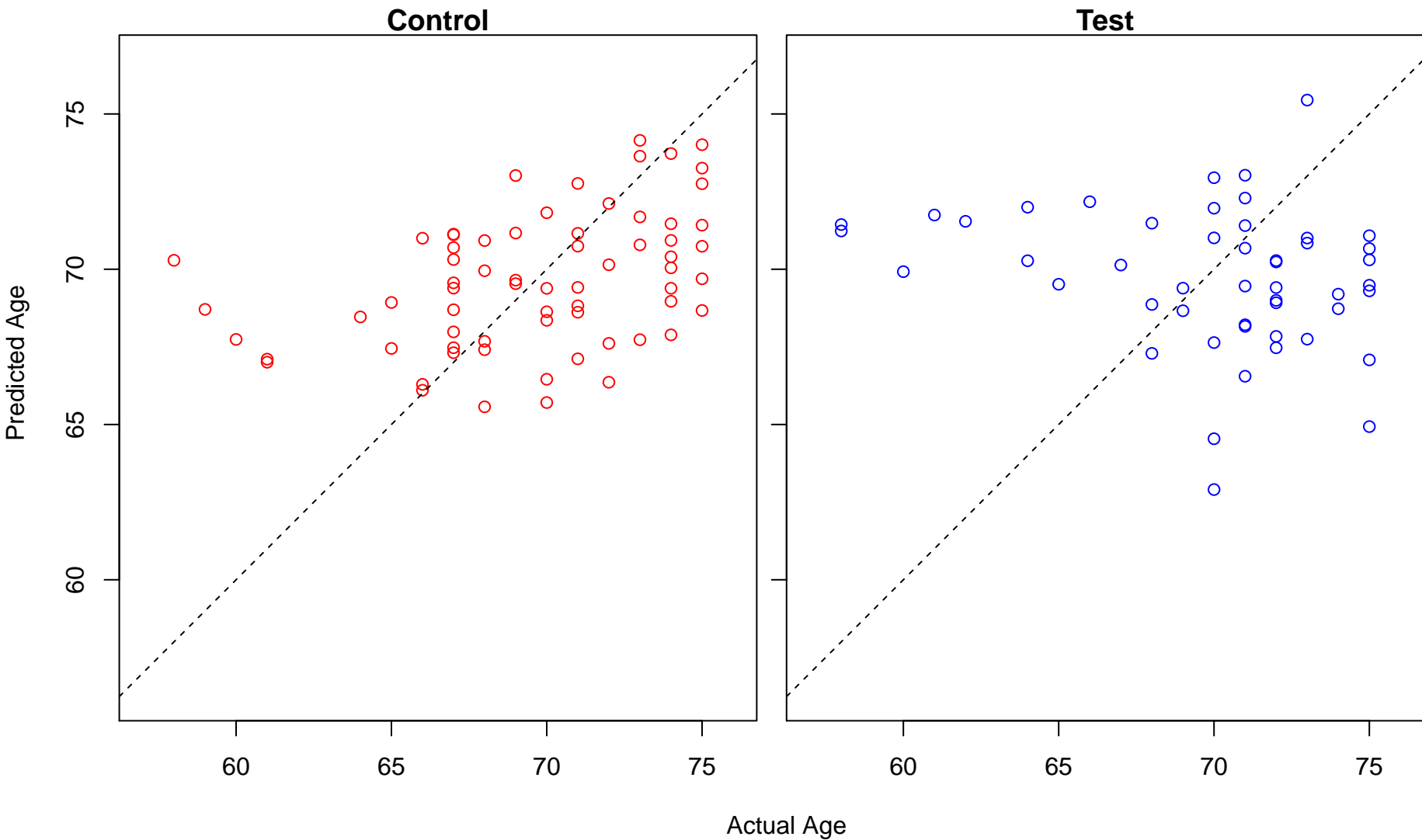
caveolin-mediated endocytosis (Score: 0.575550)



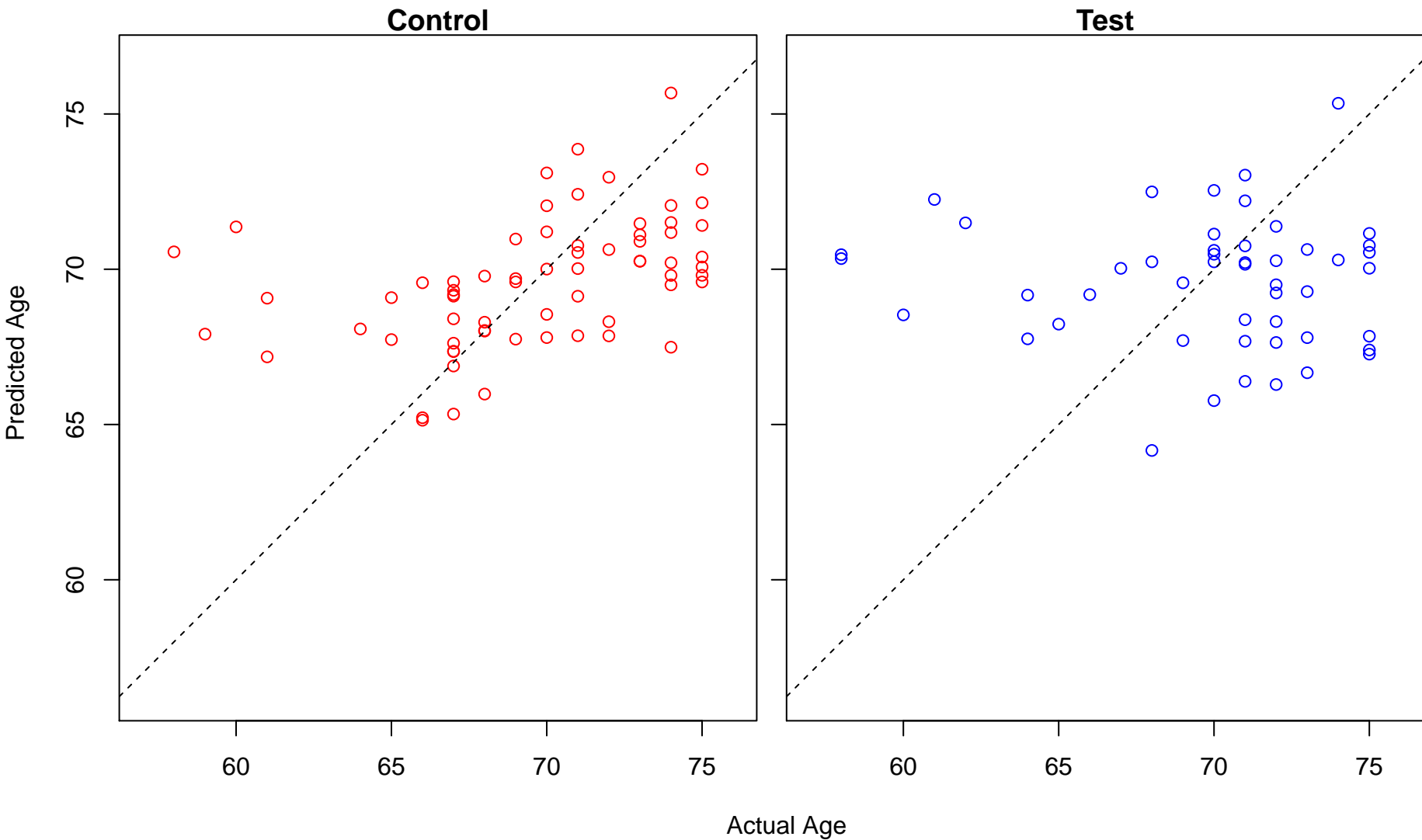
positive regulation of deacetylase activity (Score: 0.575482)



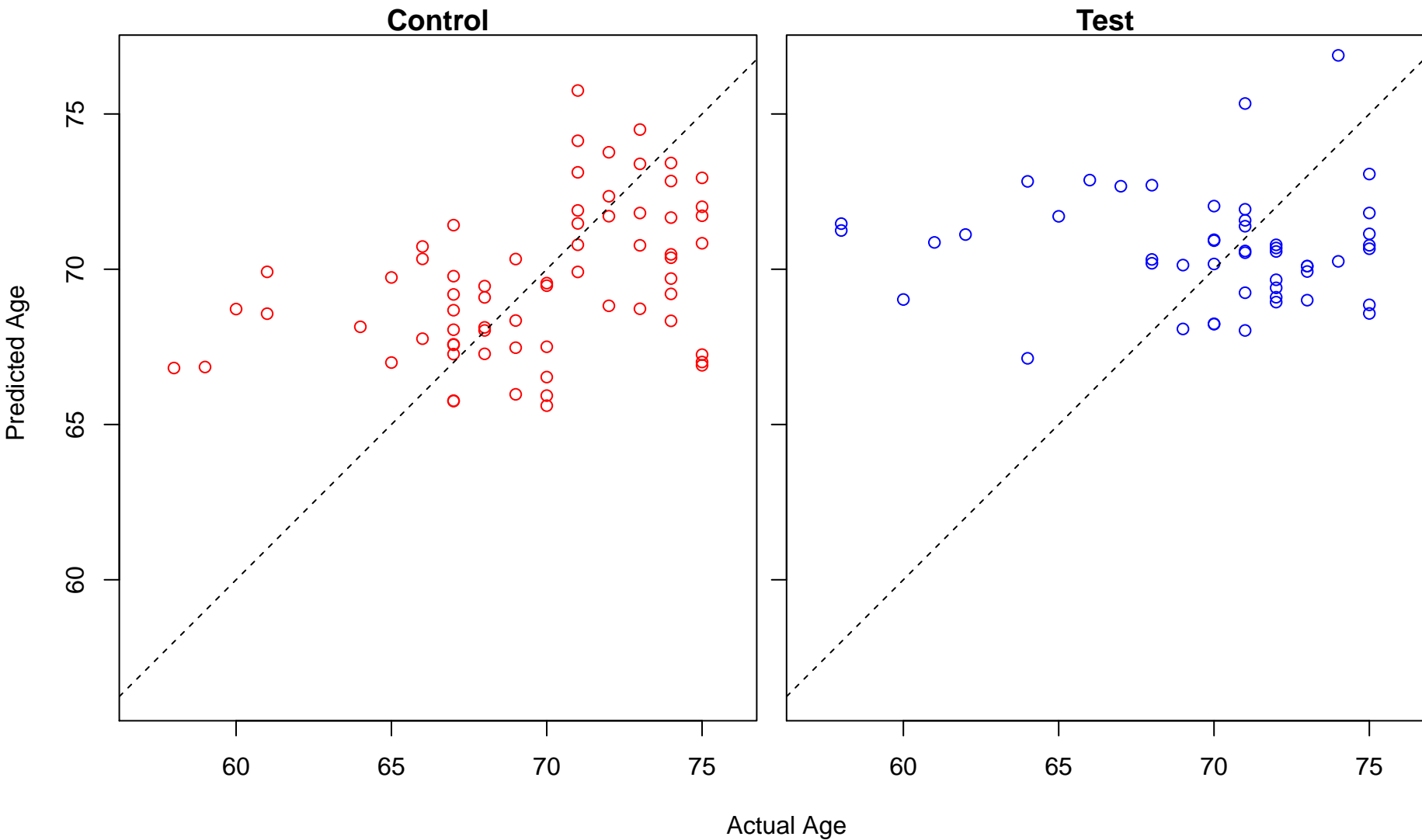
negative regulation of mRNA 3'-end processing (Score: 0.573425)



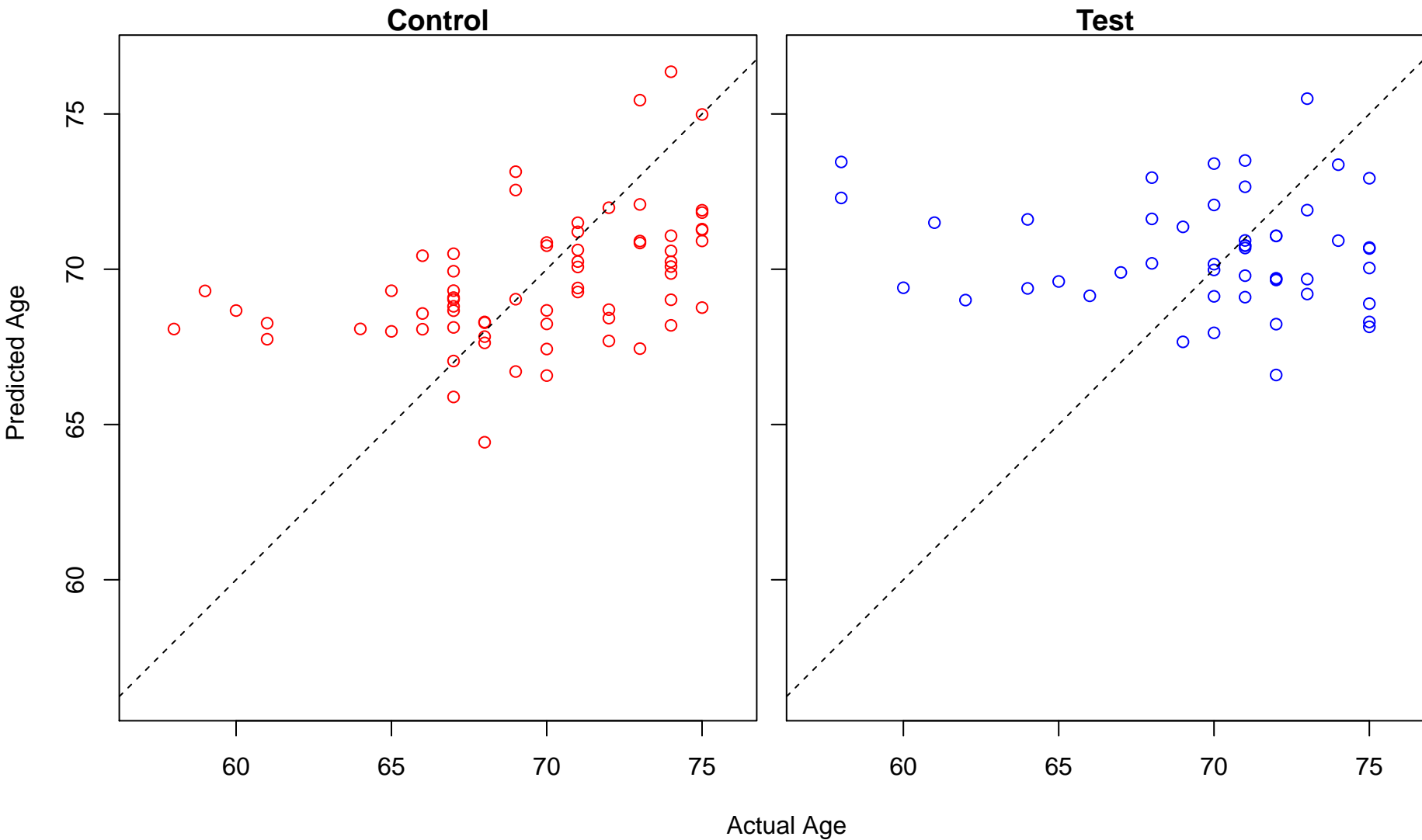
negative regulation of cytokine production involved in immune response (Score: 0.573162)



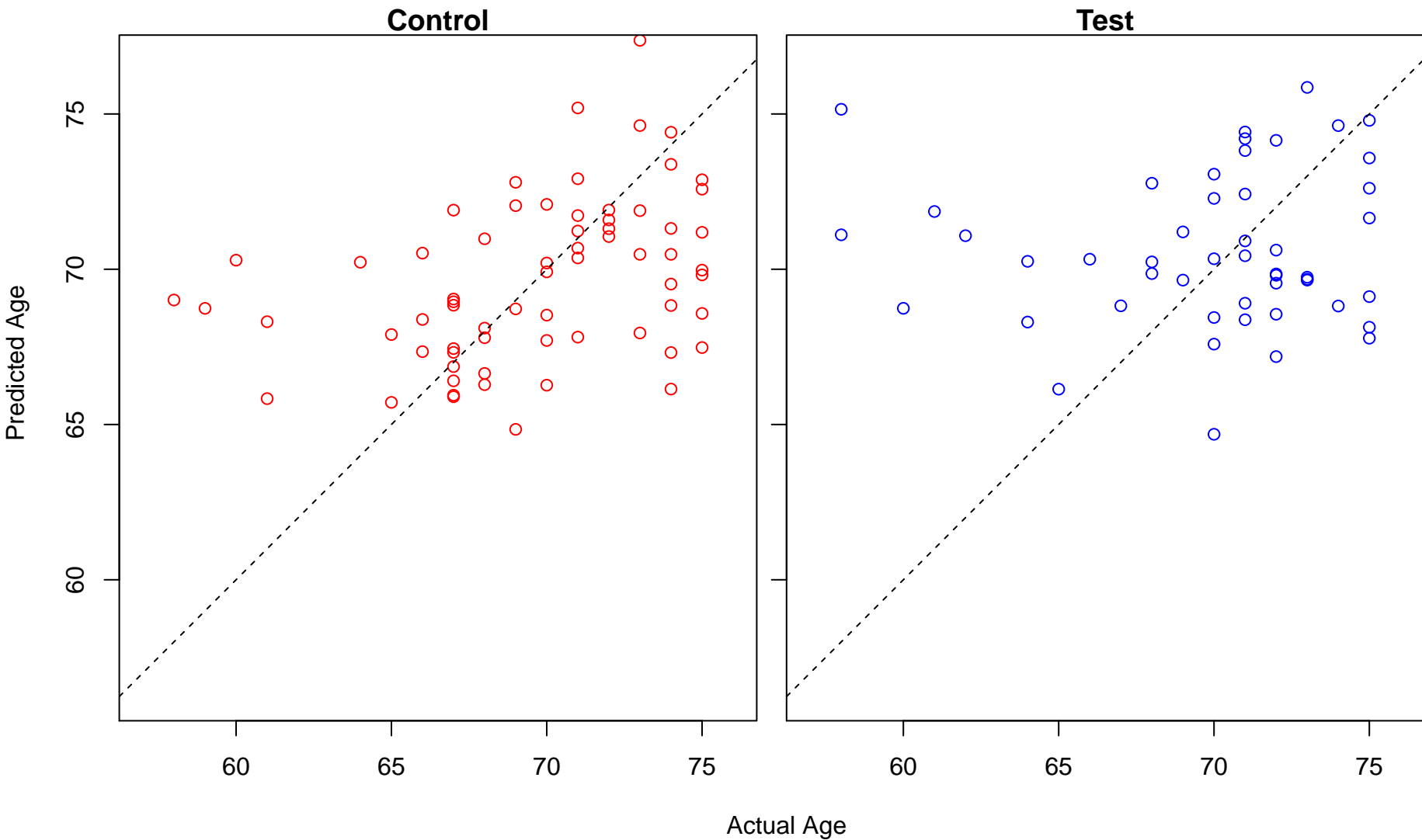
regulation of collagen biosynthetic process (Score: 0.573161)



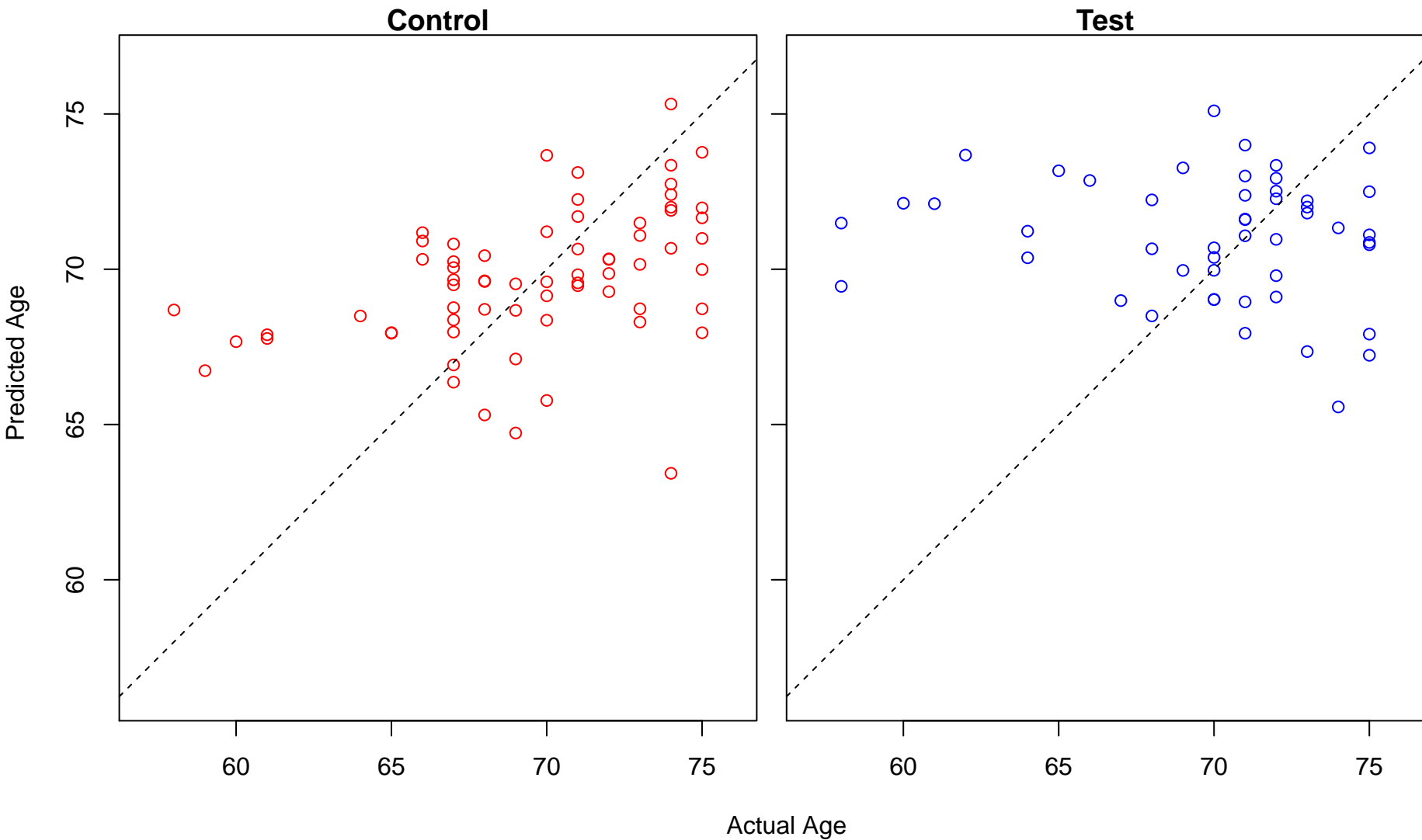
positive regulation of protein homodimerization activity (Score: 0.572892)



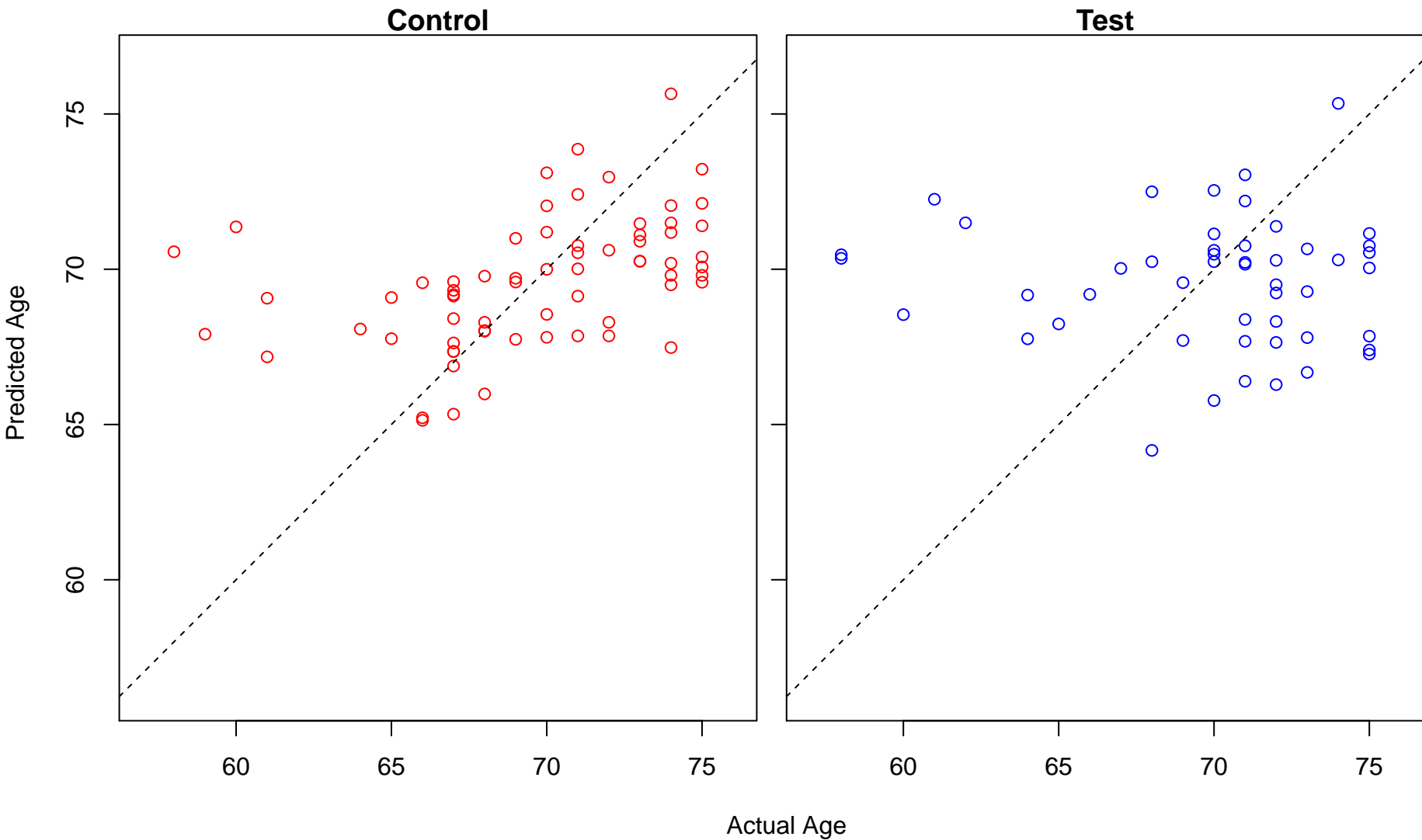
embryonic placenta development (Score: 0.572631)



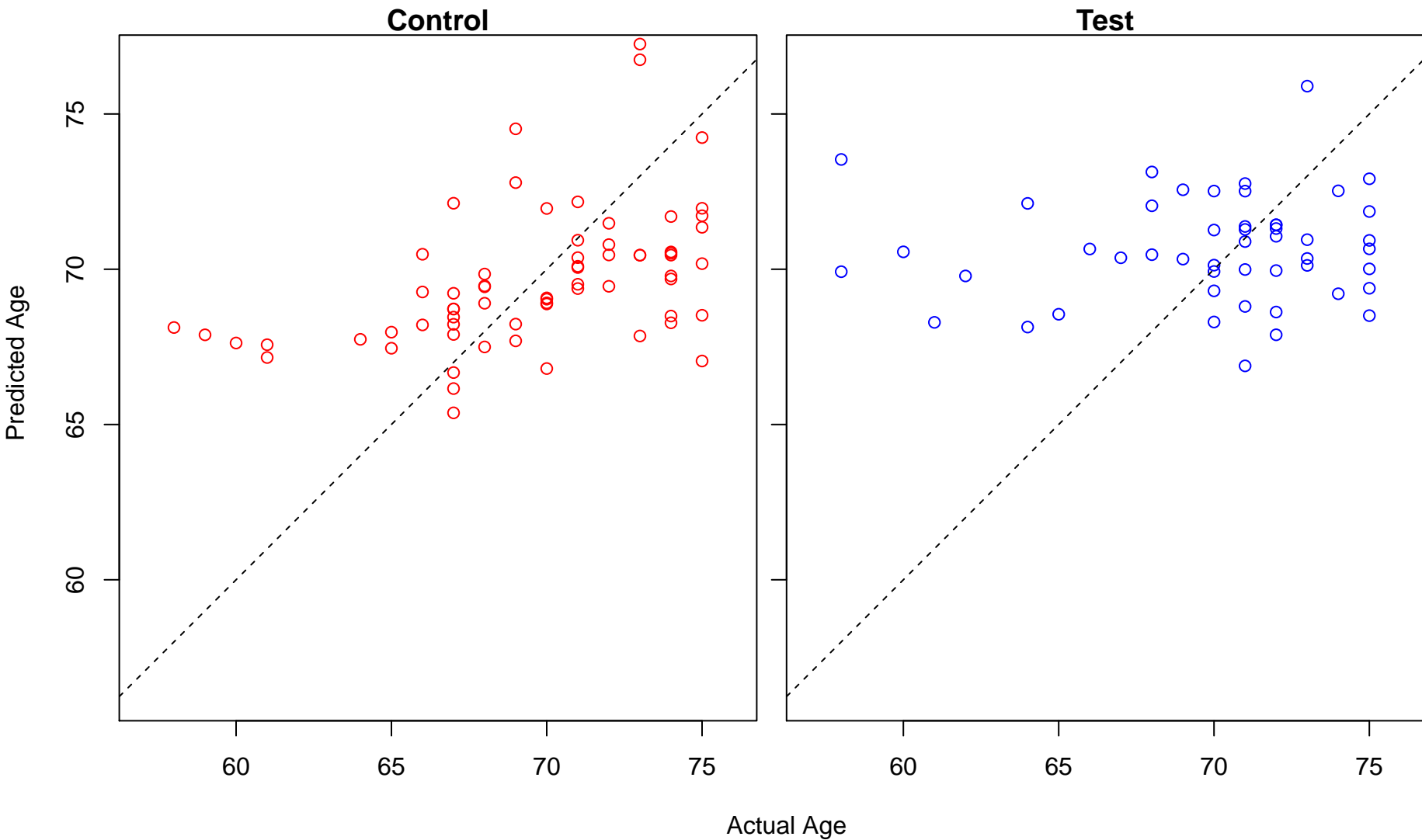
positive regulation of granulocyte differentiation (Score: 0.572323)



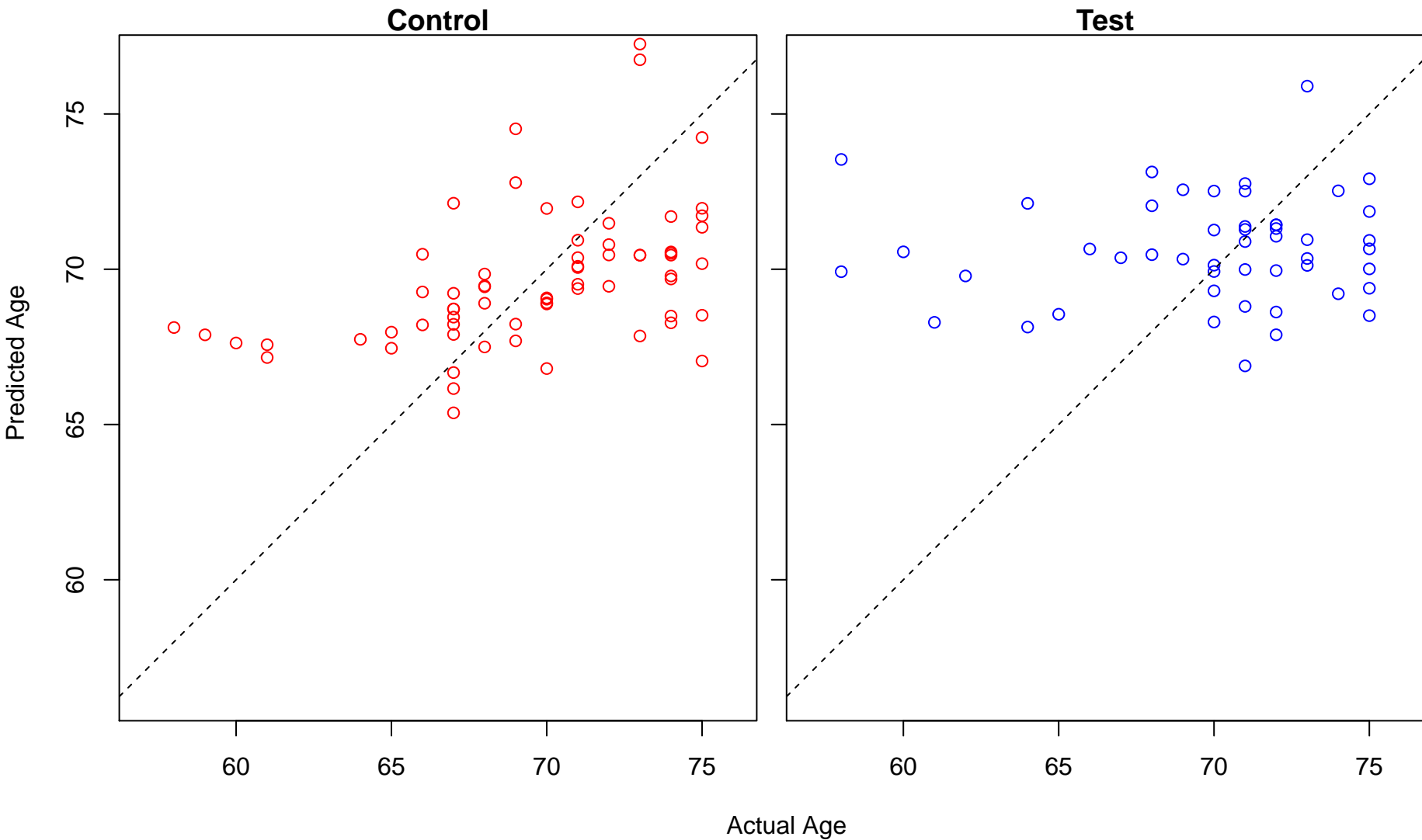
negative regulation of production of molecular mediator of immune response (Score: 0.571191)



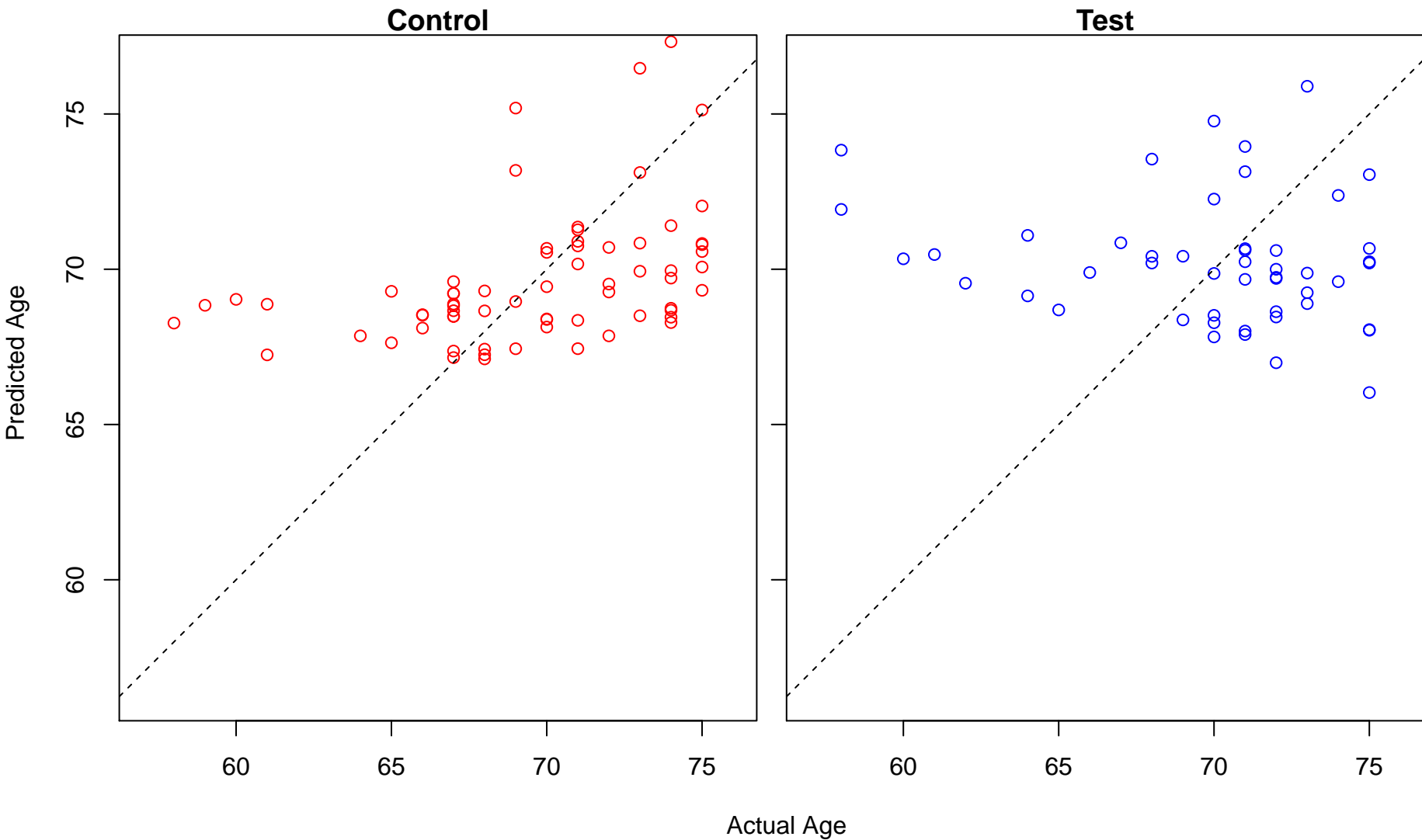
metanephric tubule morphogenesis (Score: 0.571085)



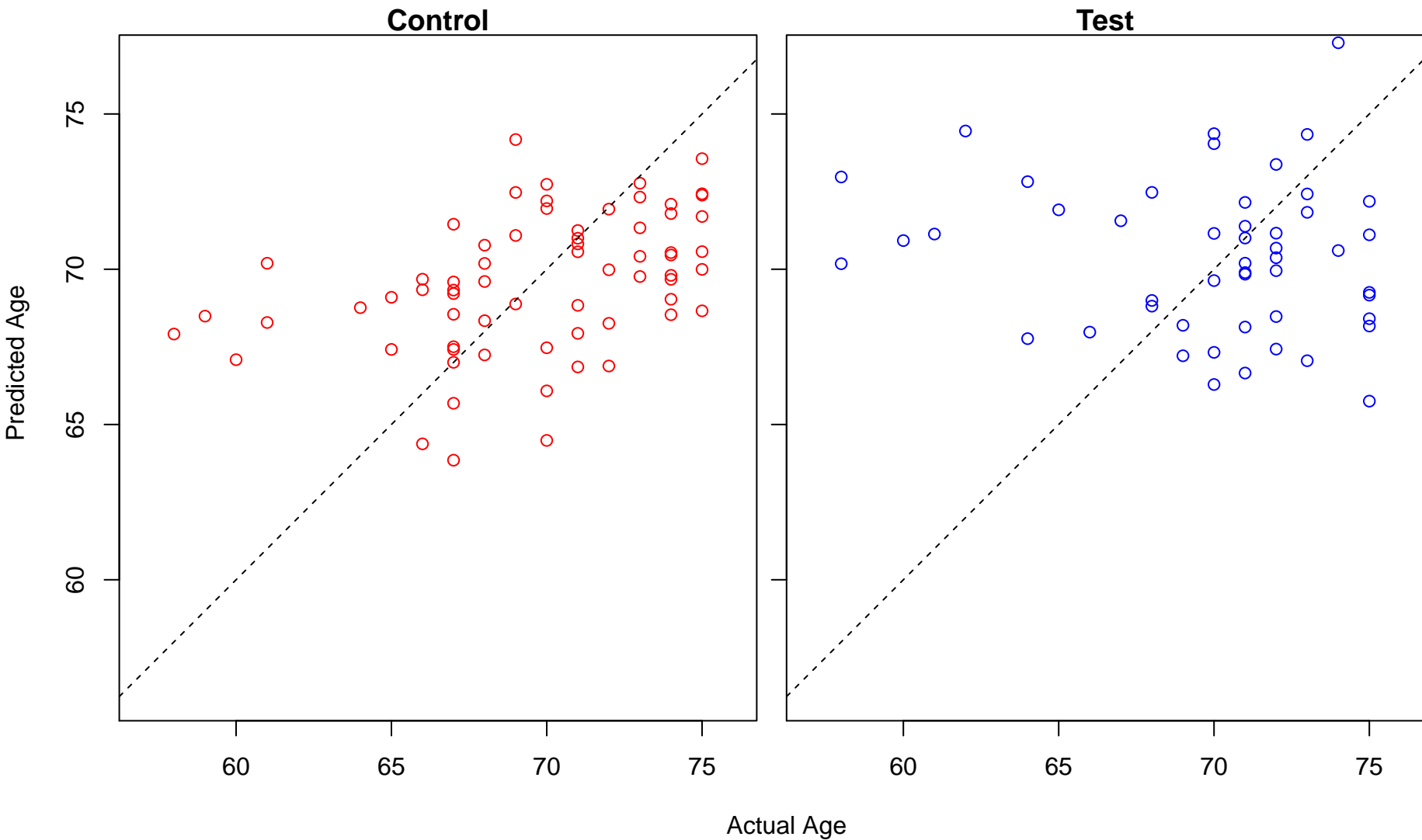
metanephric nephron tubule morphogenesis (Score: 0.571085)



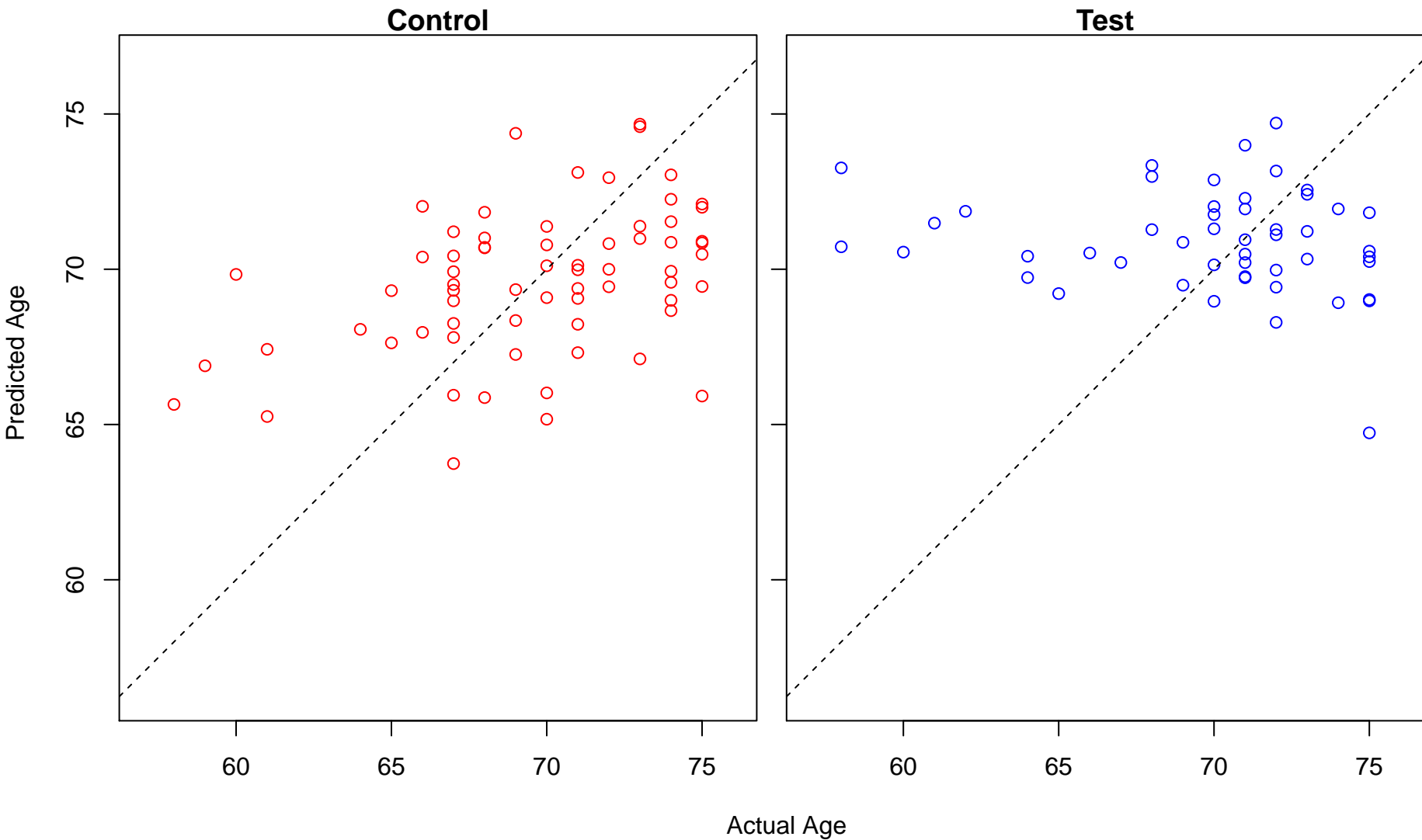
negative regulation of telomere maintenance via telomerase (Score: 0.571050)



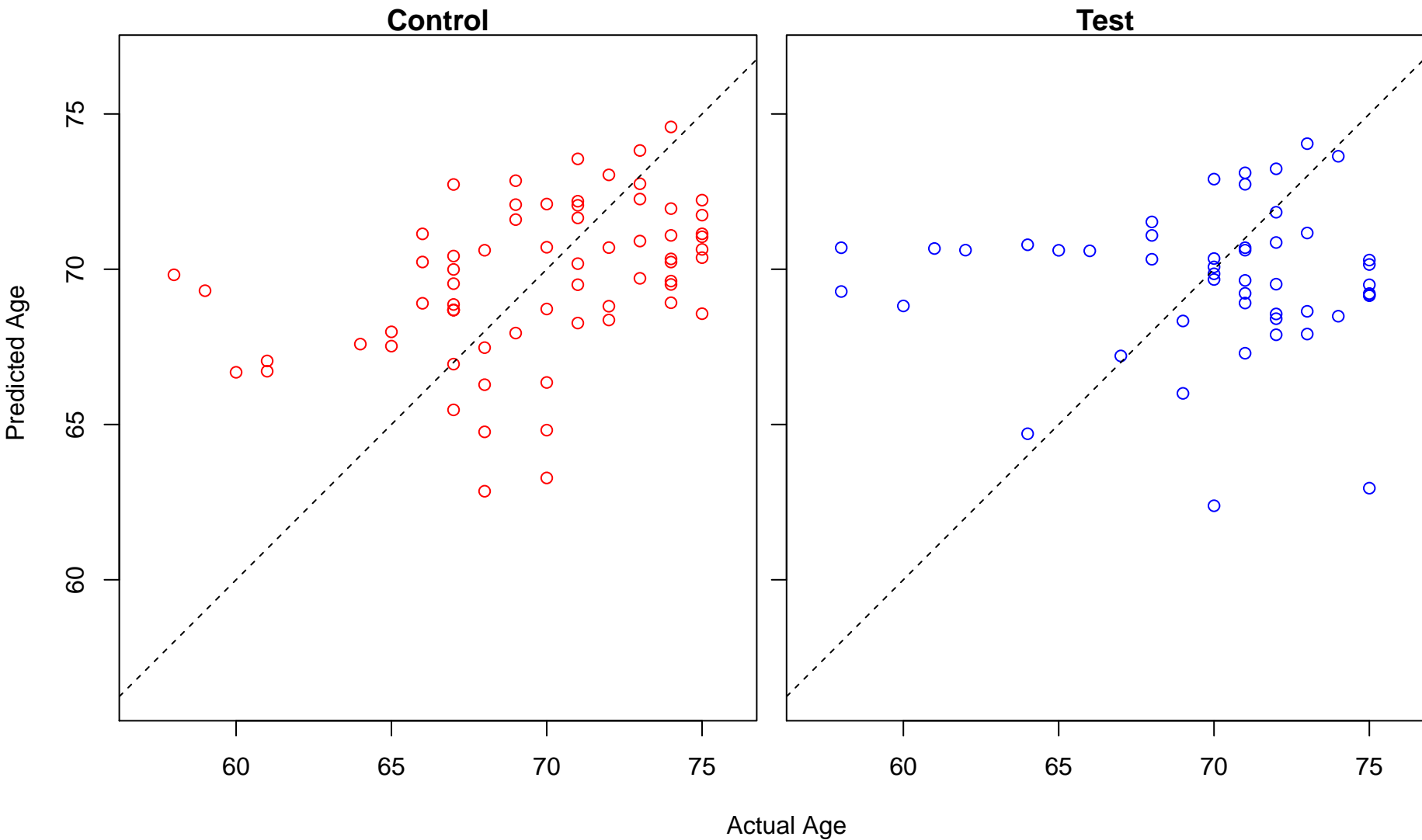
positive regulation of syncytium formation by plasma membrane fusion (Score: 0.570507)



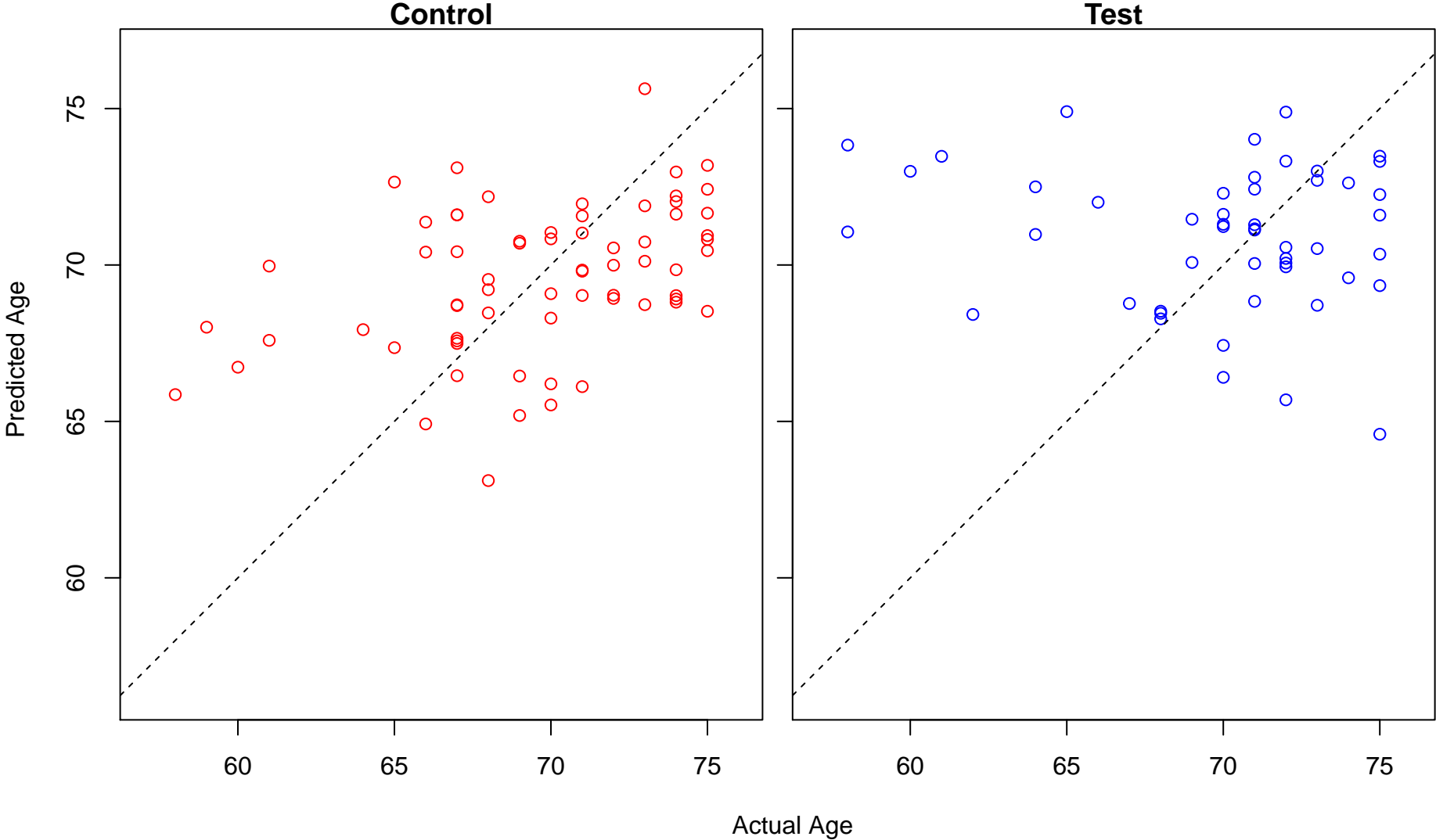
response to vitamin (Score: 0.570410)



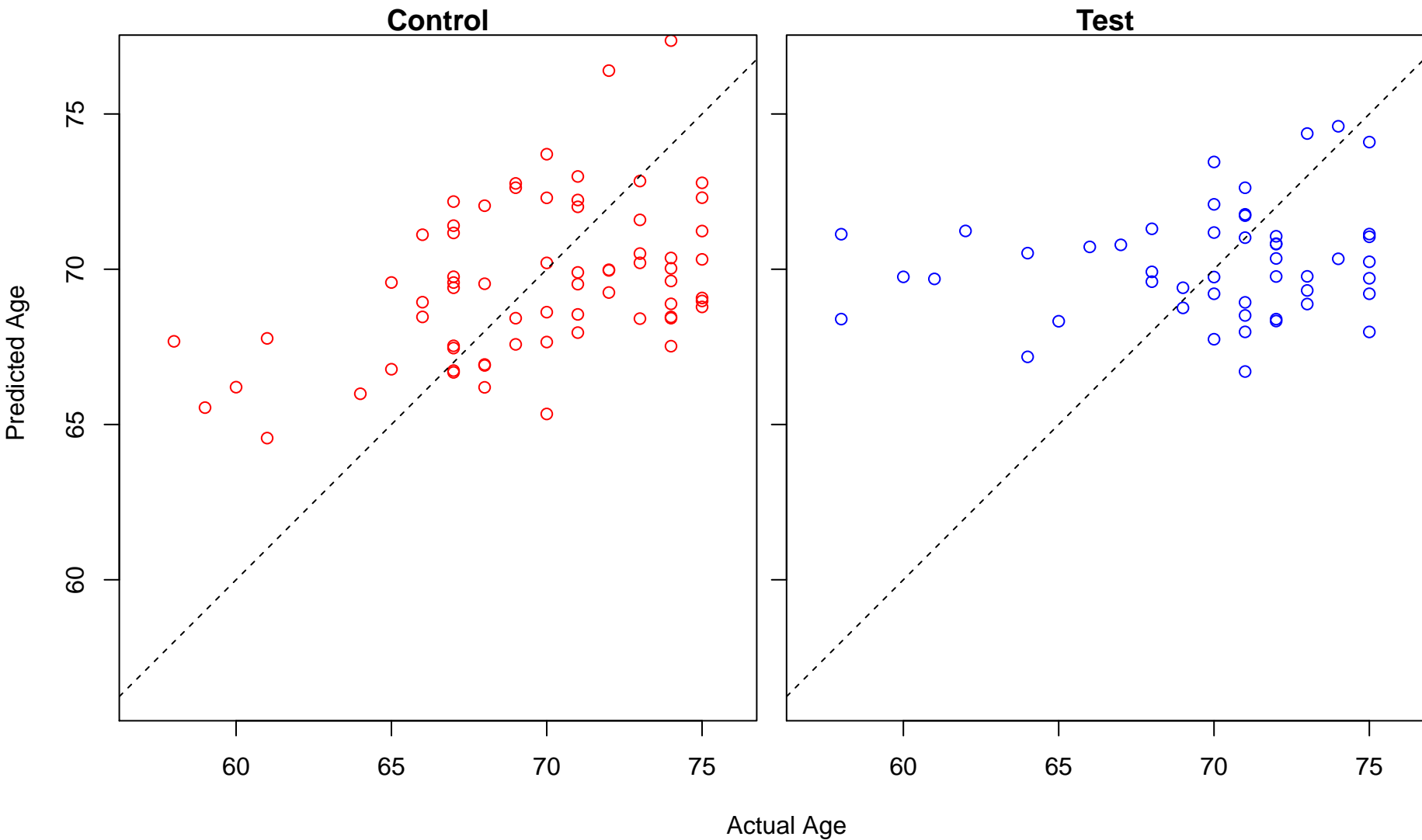
negative regulation of intracellular estrogen receptor signaling pathway (Score: 0.569202)



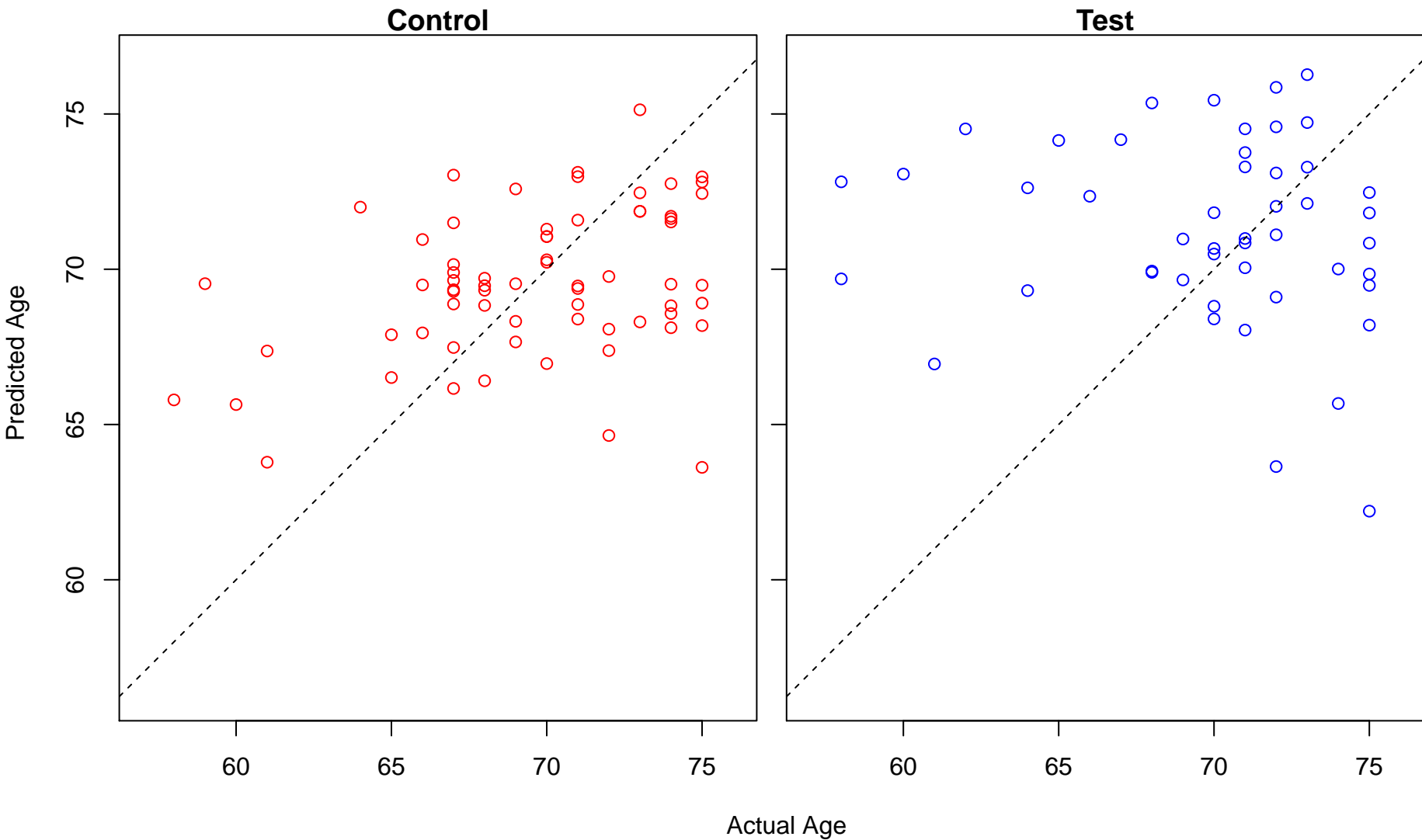
regulation of atrial cardiac muscle cell membrane repolarization (Score: 0.569035)



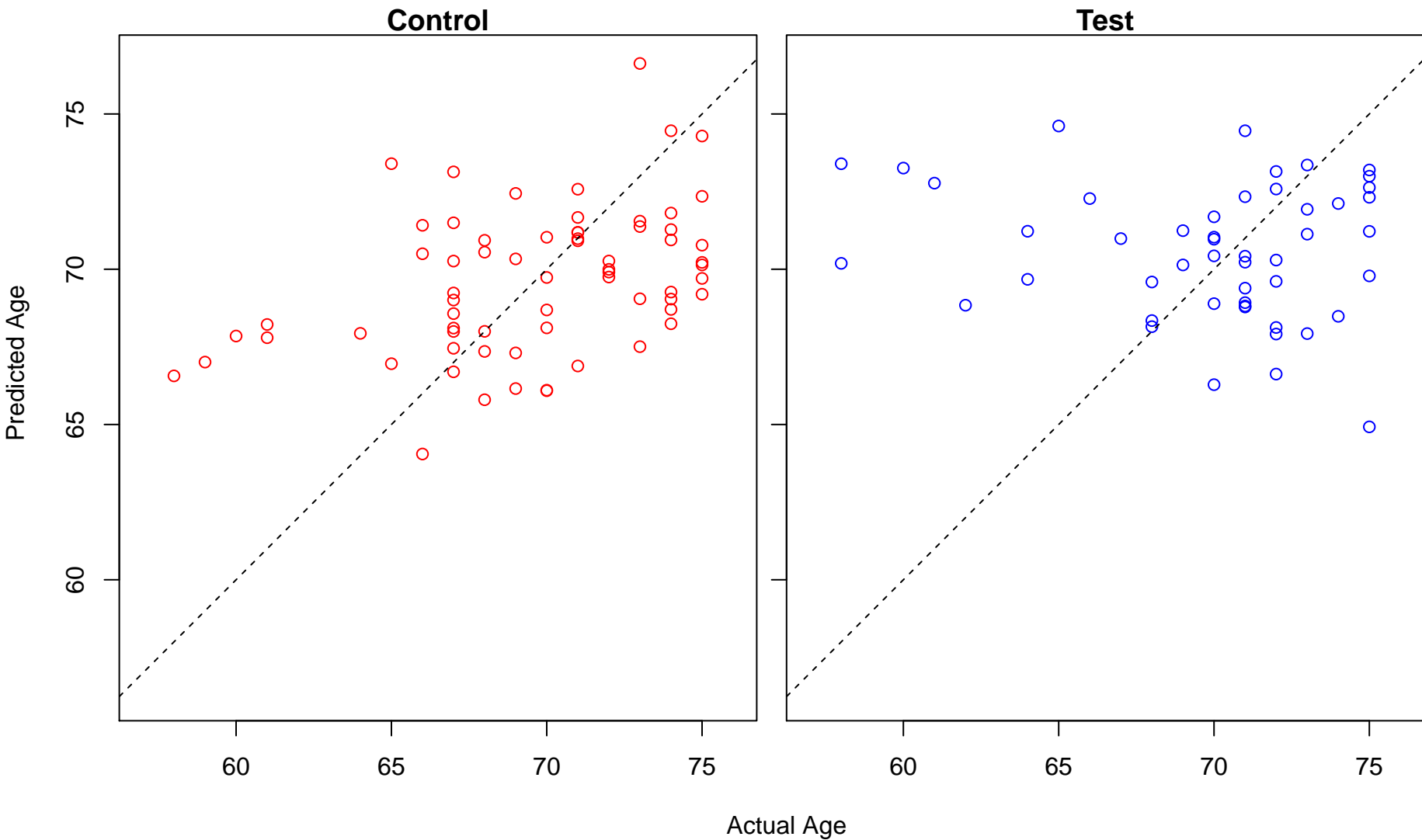
negative regulation of epithelial cell apoptotic process (Score: 0.568334)



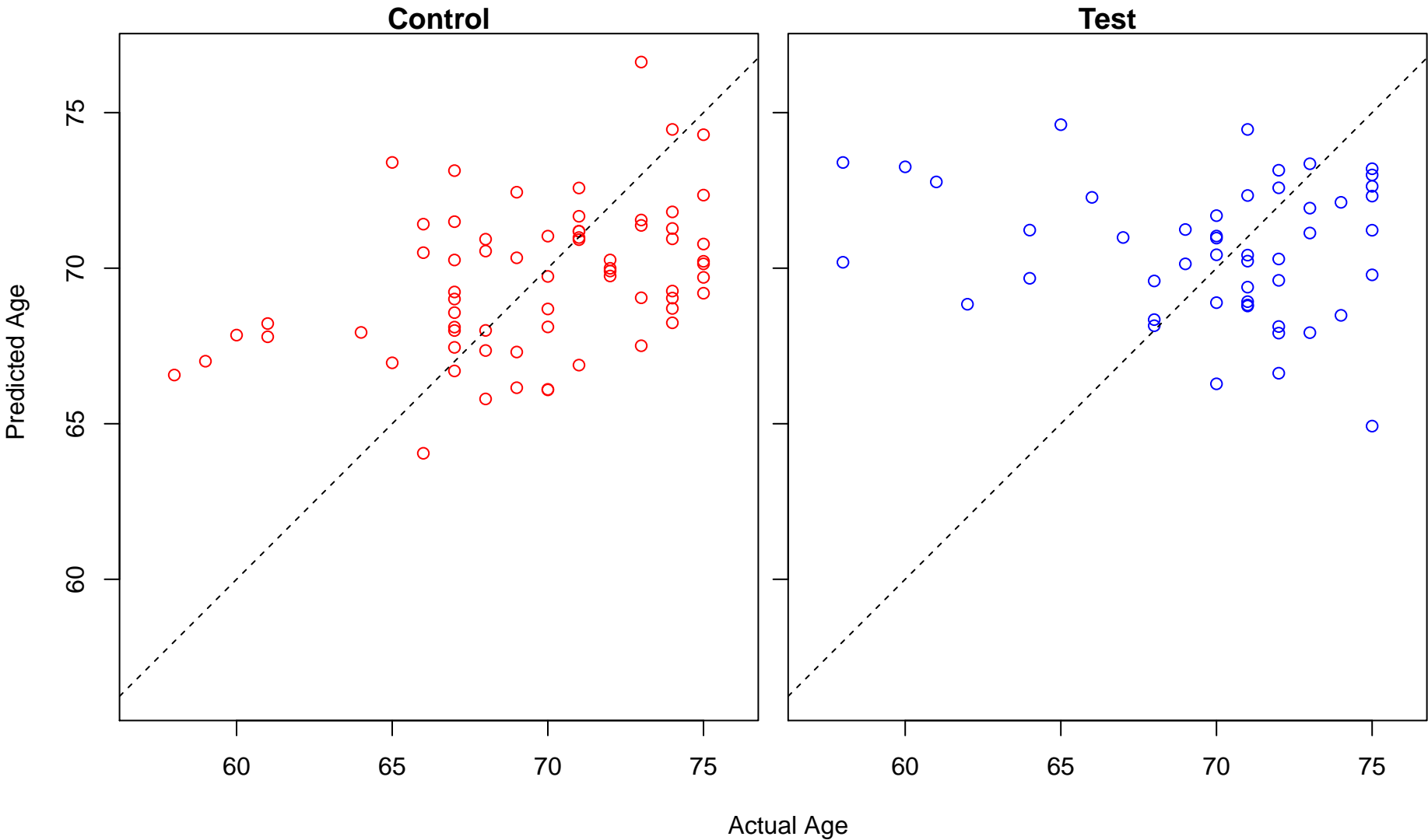
nitric oxide mediated signal transduction (Score: 0.567952)



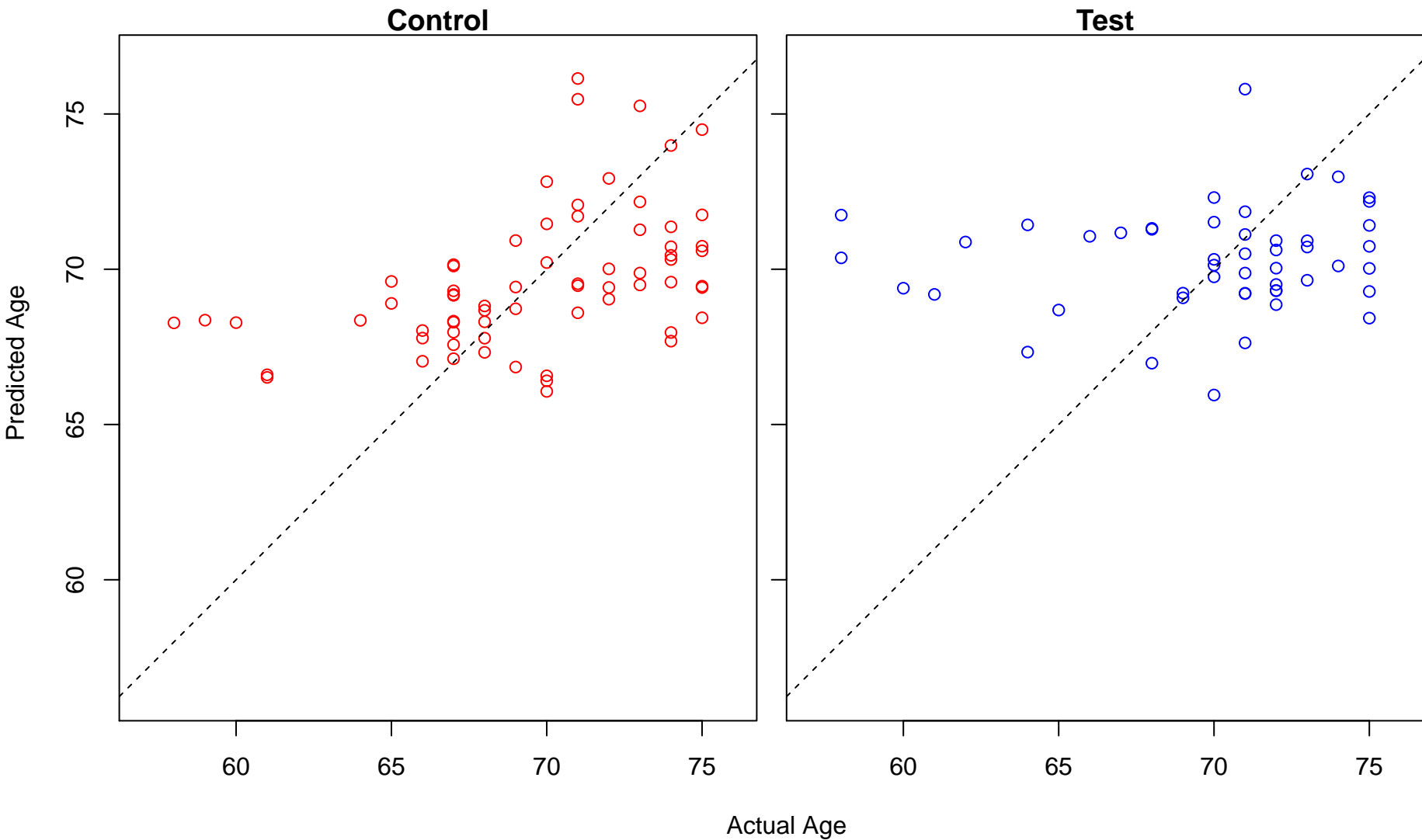
membrane repolarization during action potential (Score: 0.567910)



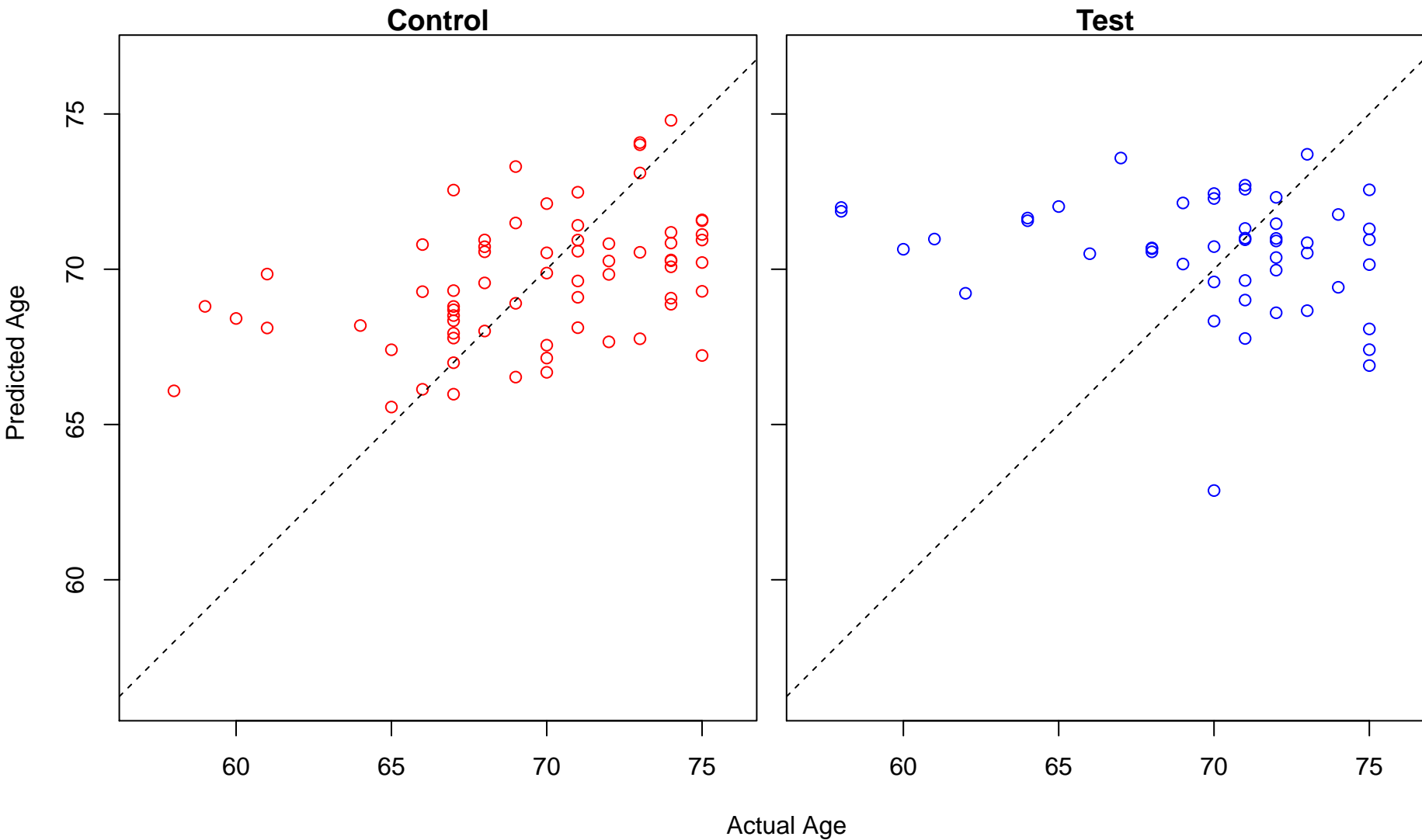
membrane repolarization during cardiac muscle cell action potential (Score: 0.567910)



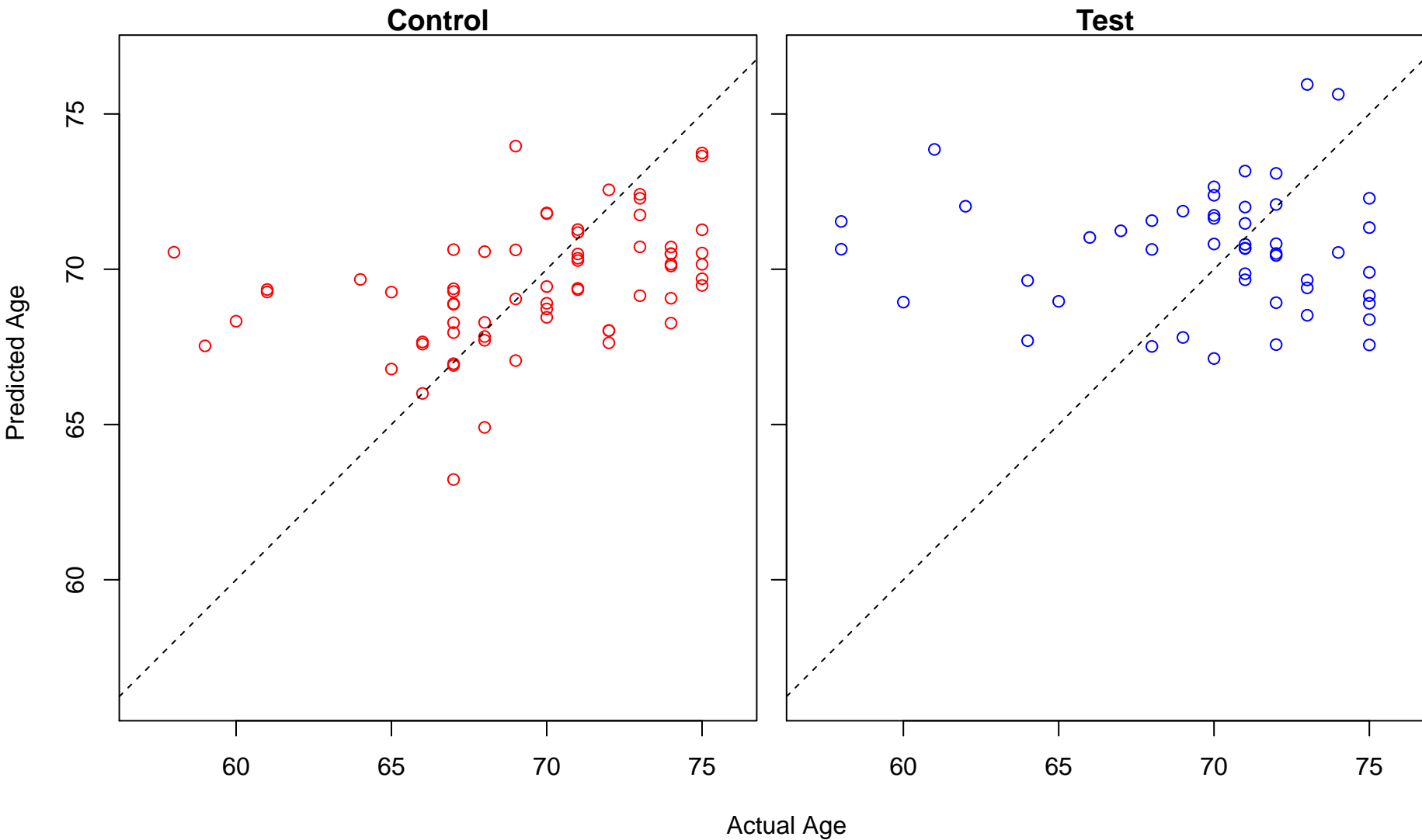
protein ADP-ribosylation (Score: 0.567699)



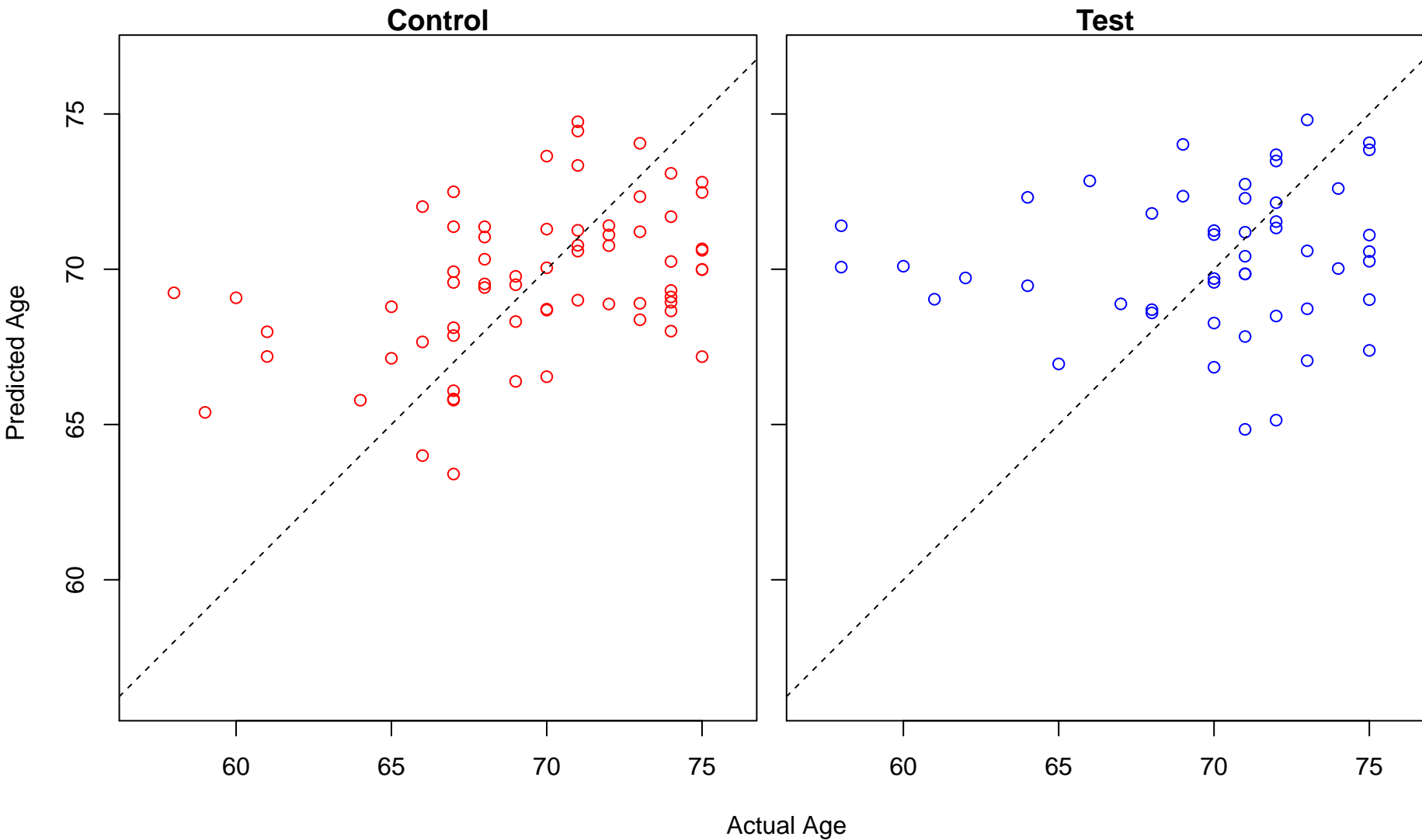
STAT protein import into nucleus (Score: 0.567238)



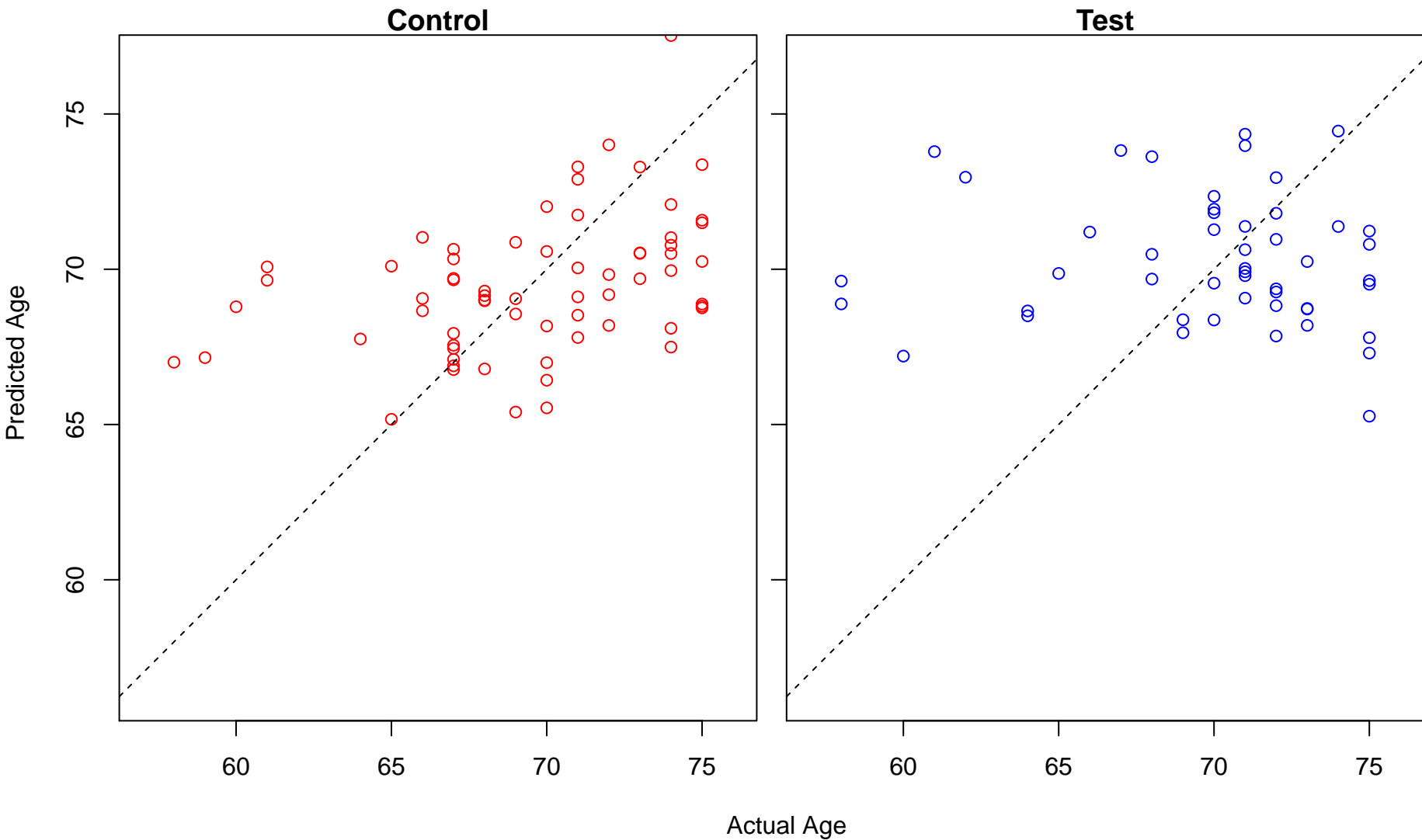
steroid catabolic process (Score: 0.565654)



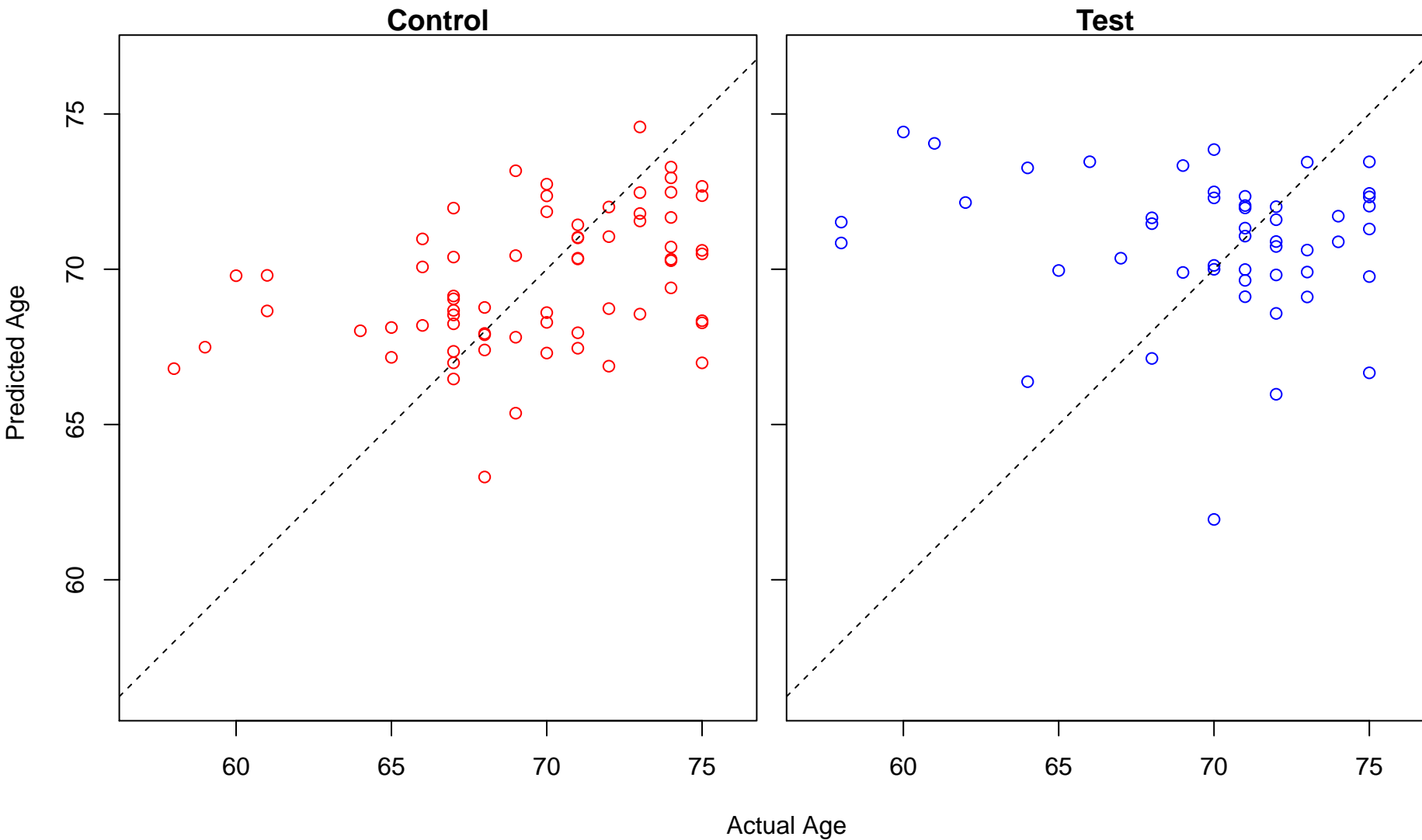
gamma-aminobutyric acid signaling pathway (Score: 0.565244)



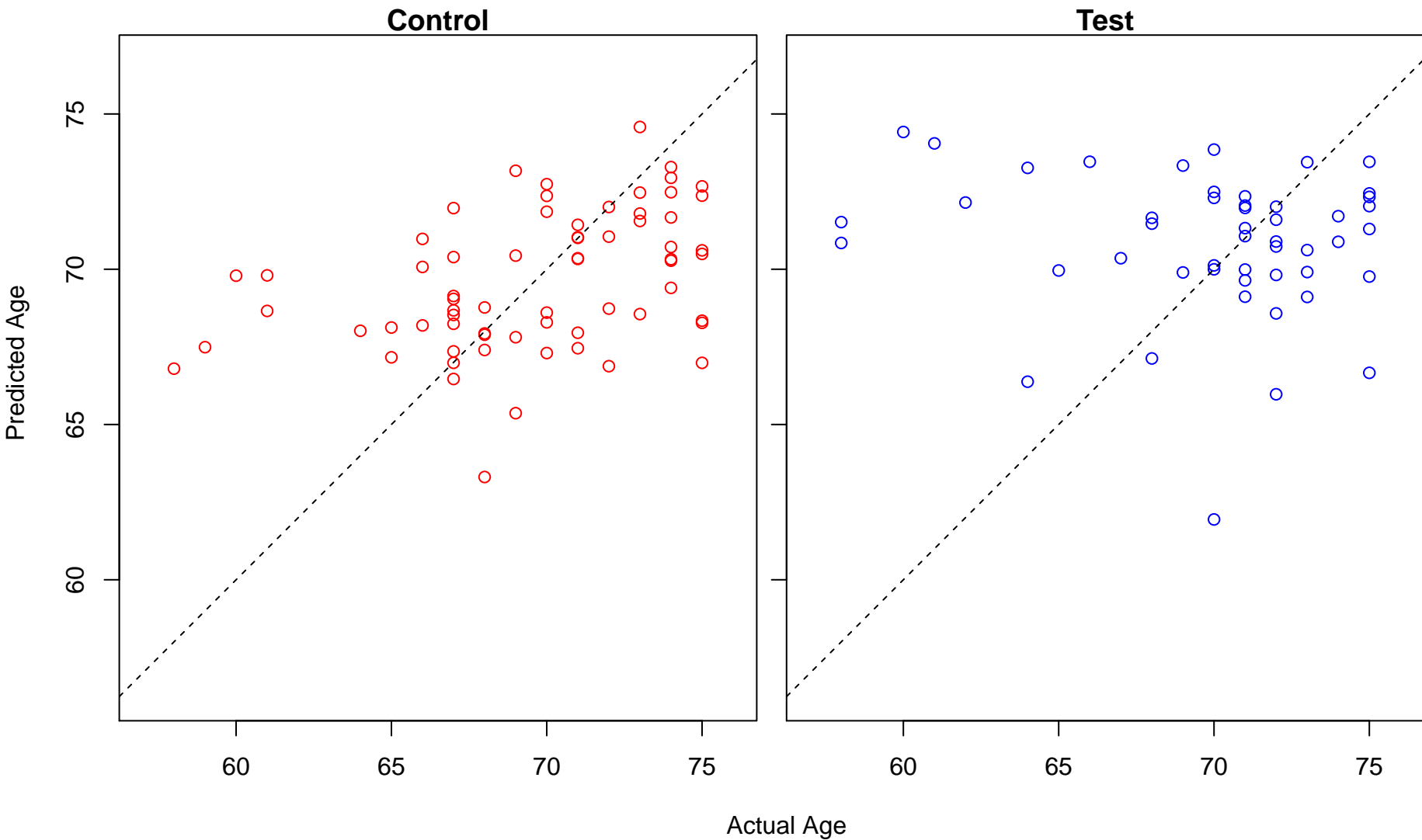
regulation of renal system process (Score: 0.565073)



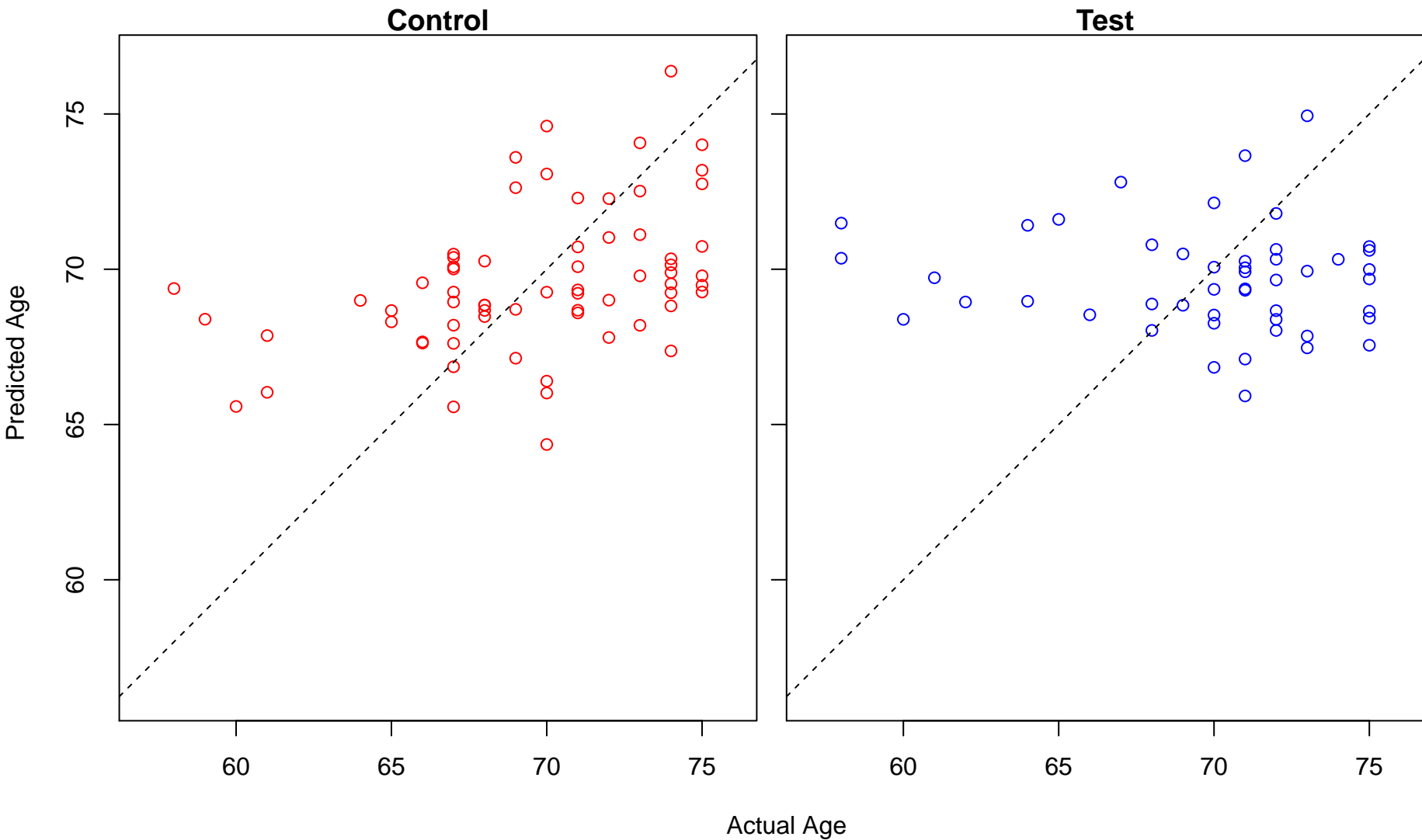
negative regulation of organic acid transport (Score: 0.564992)



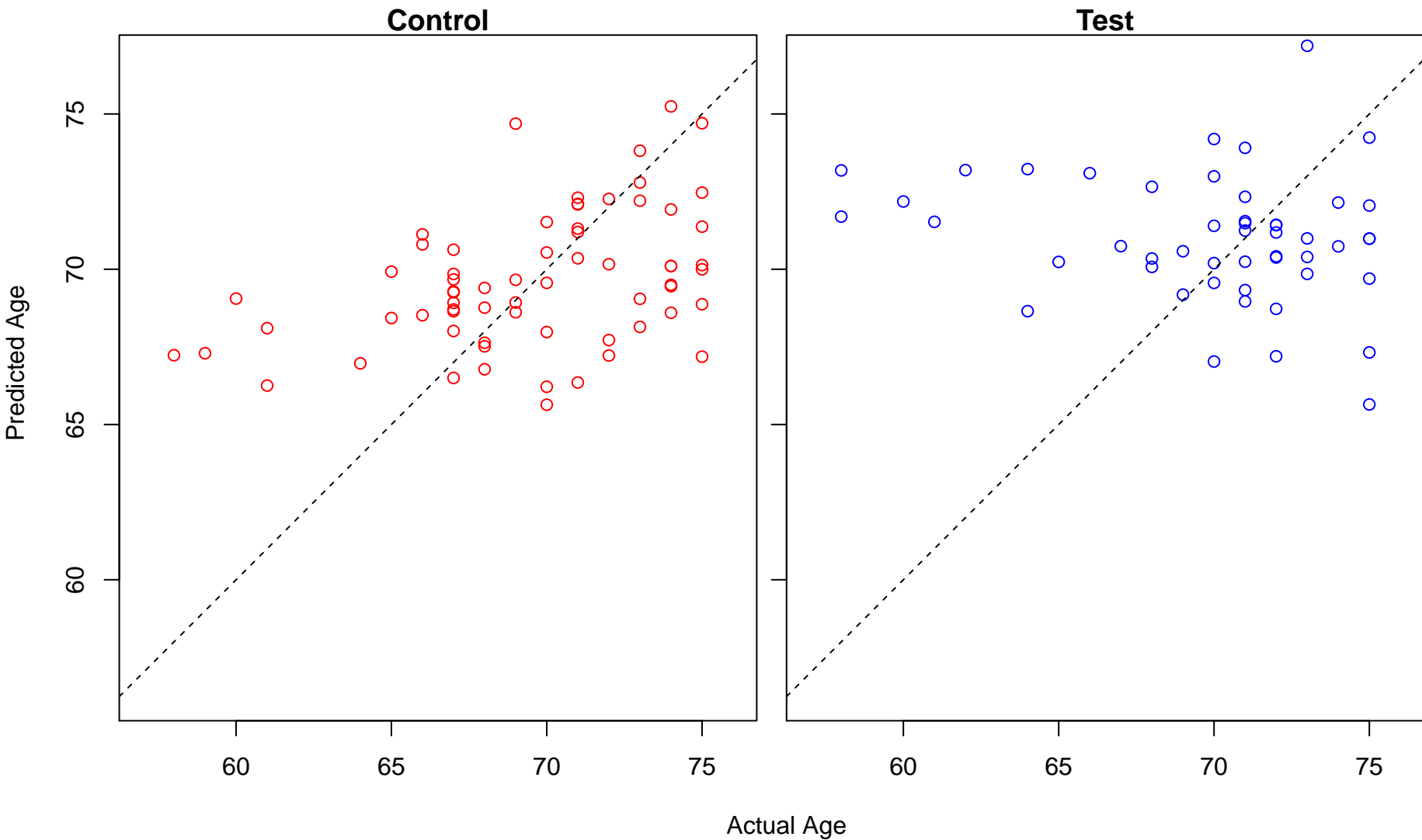
negative regulation of fatty acid transport (Score: 0.564992)



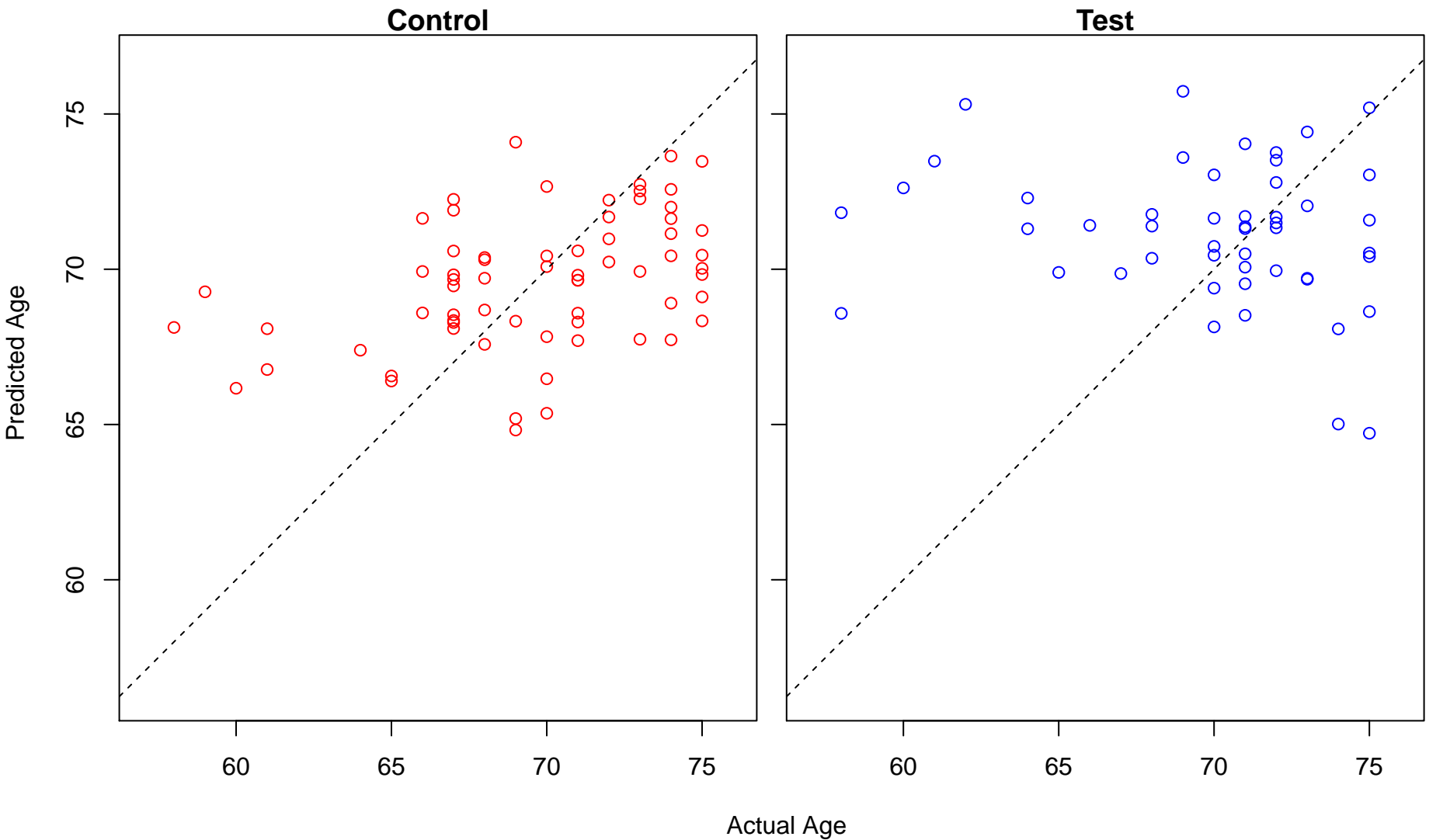
neutral amino acid transport (Score: 0.563981)



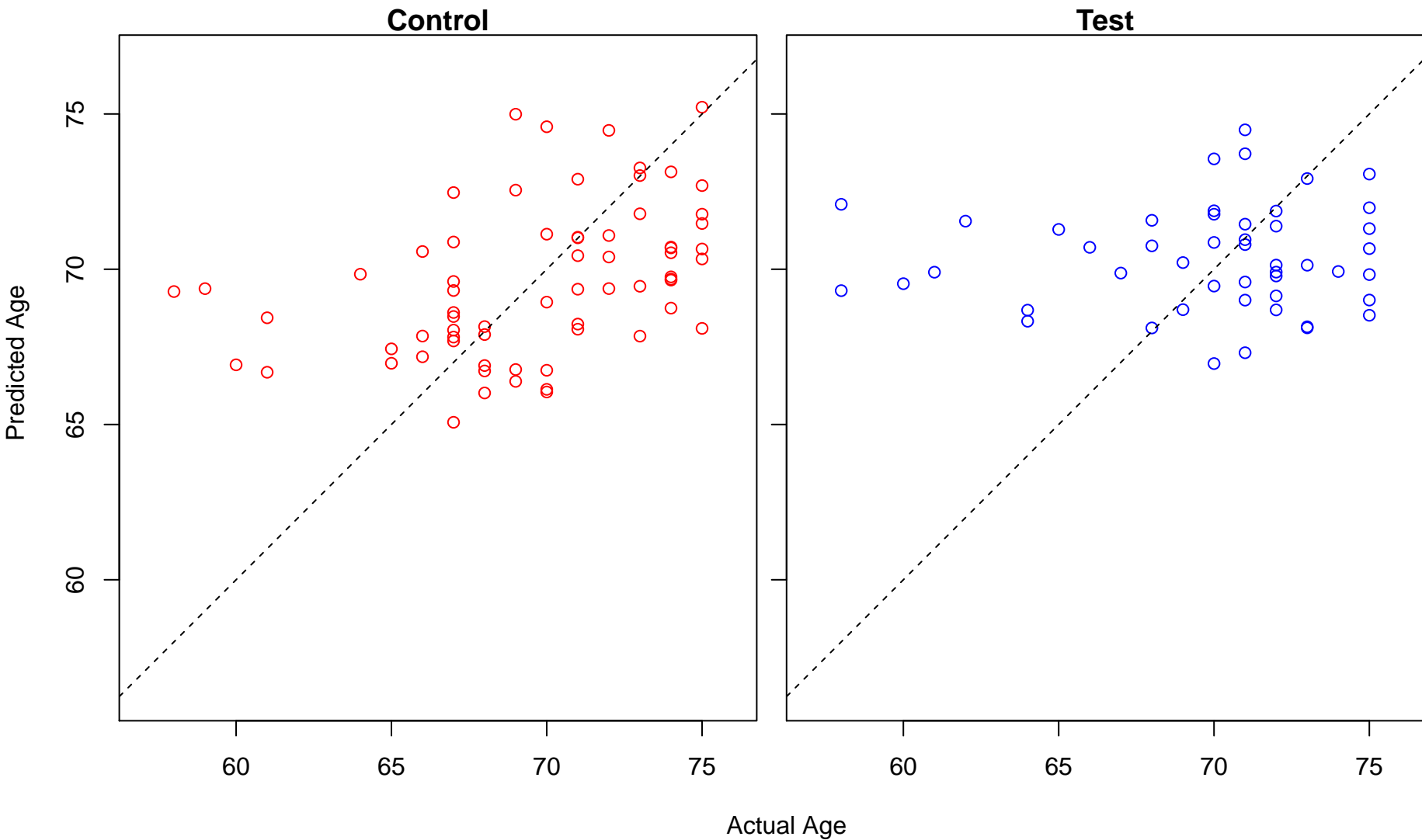
keratan sulfate catabolic process (Score: 0.563963)



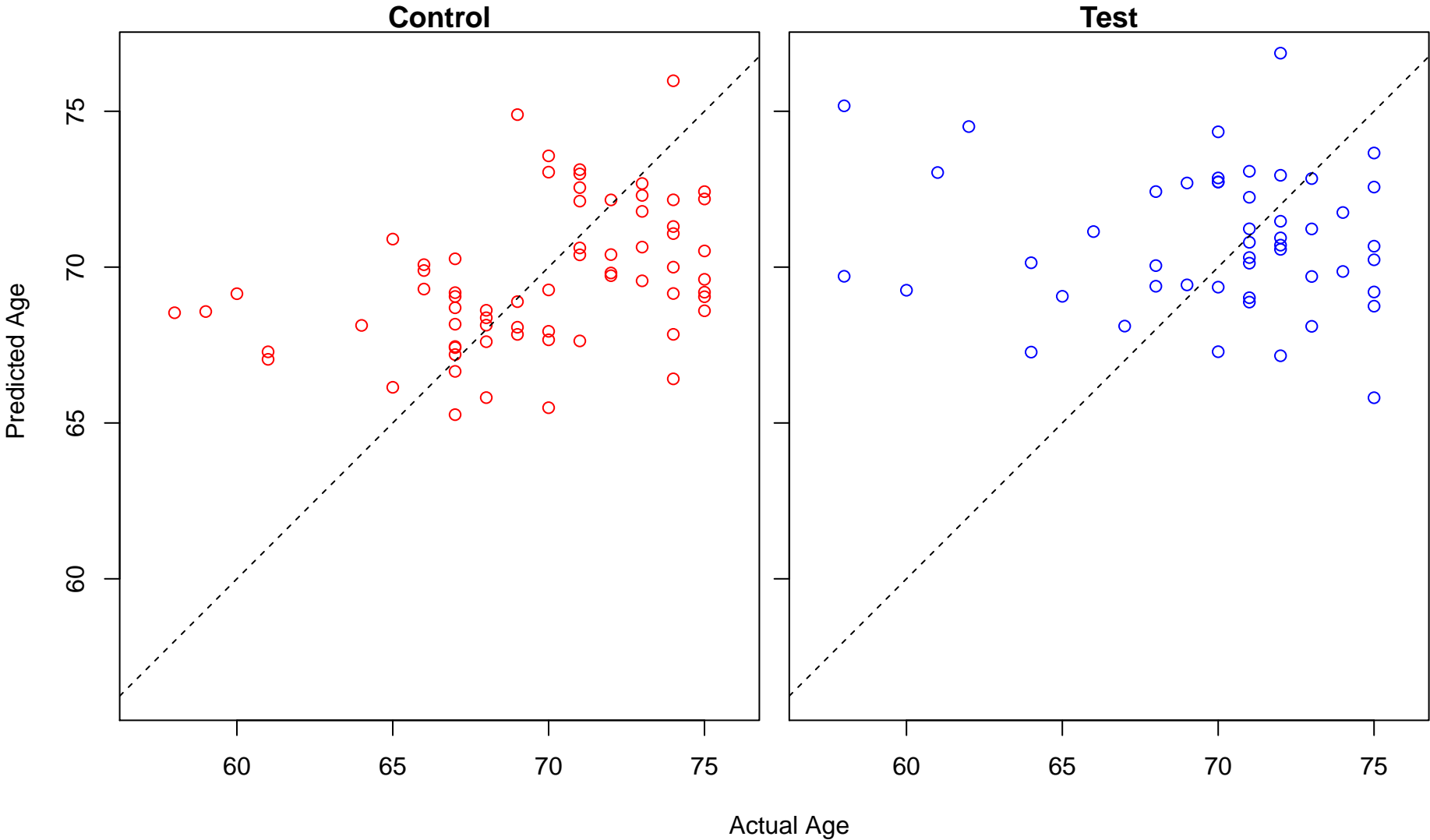
positive regulation of transcription from RNA polymerase II promoter involved in heart development (Score: 10)



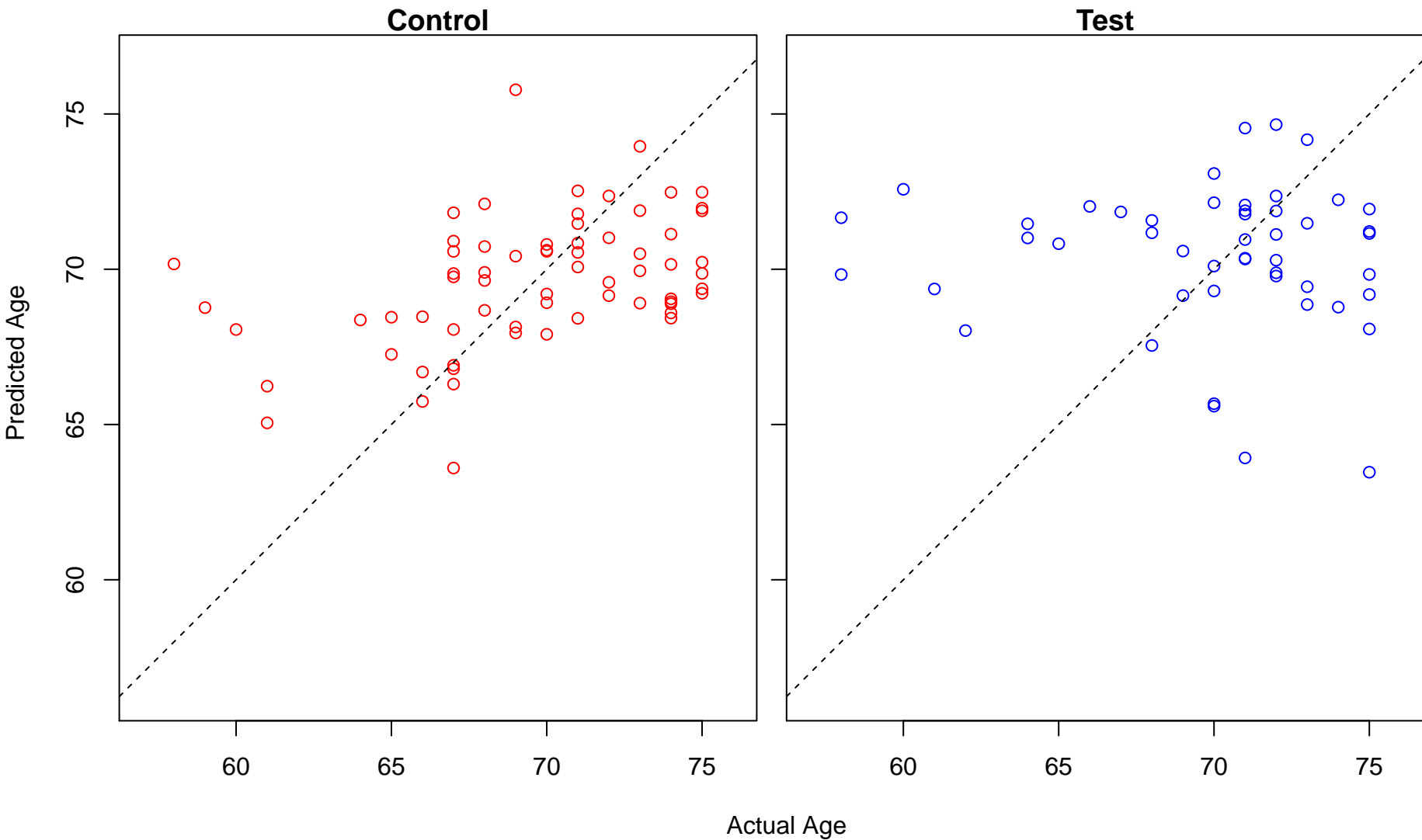
L-alpha-amino acid transmembrane transport (Score: 0.563455)



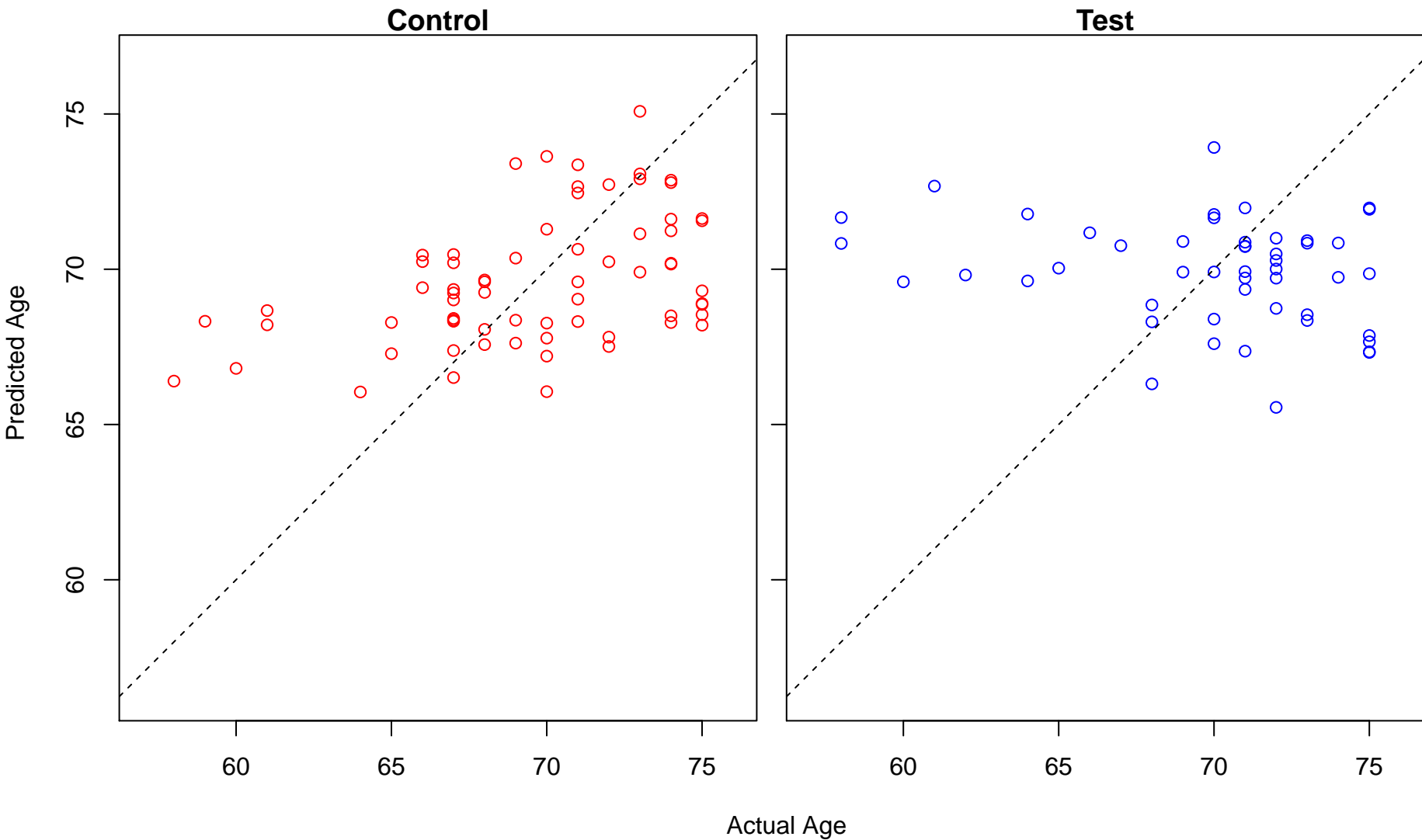
regulation of nucleotide-binding oligomerization domain containing signaling pathway (Score: 0.562)



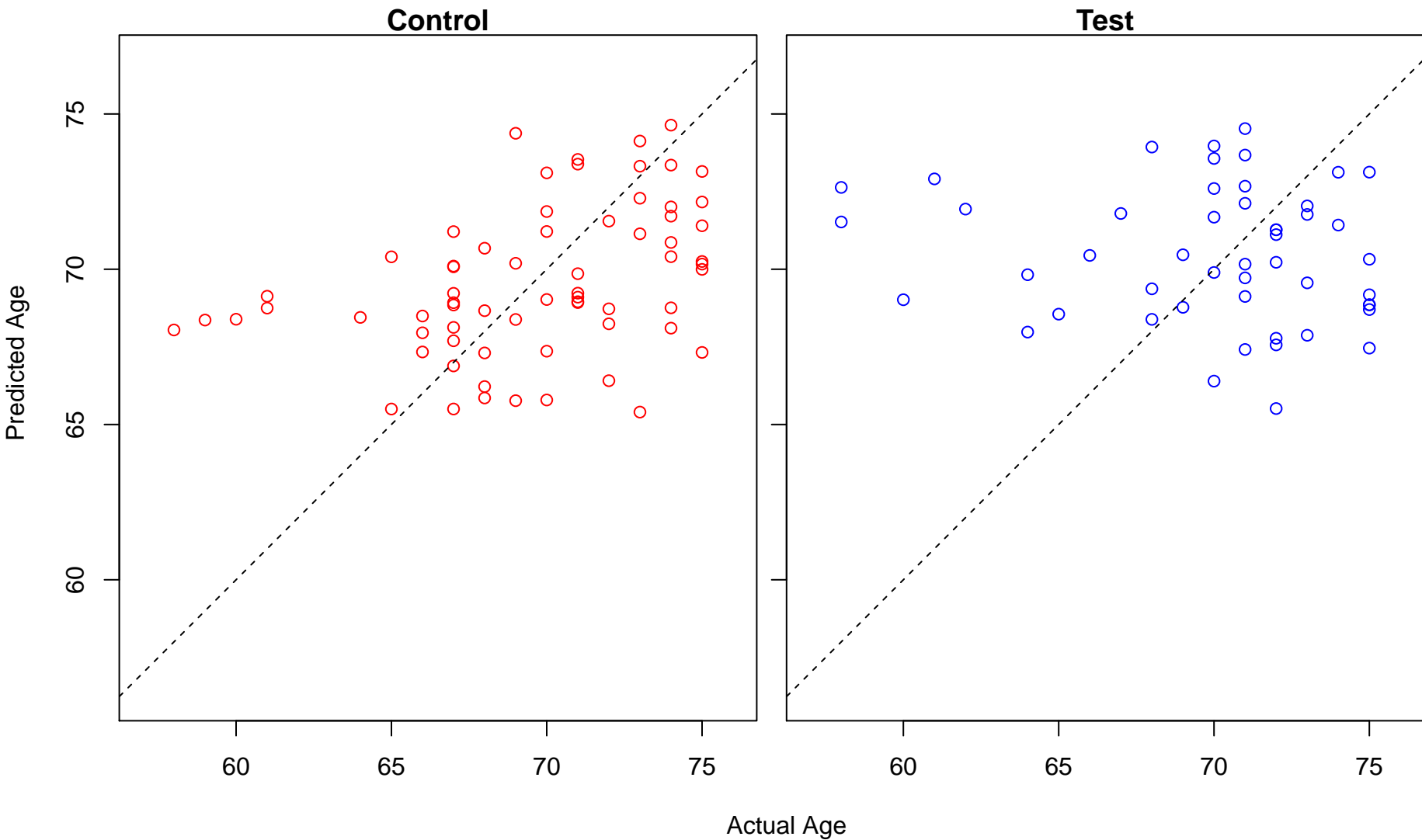
photoreceptor cell development (Score: 0.562900)



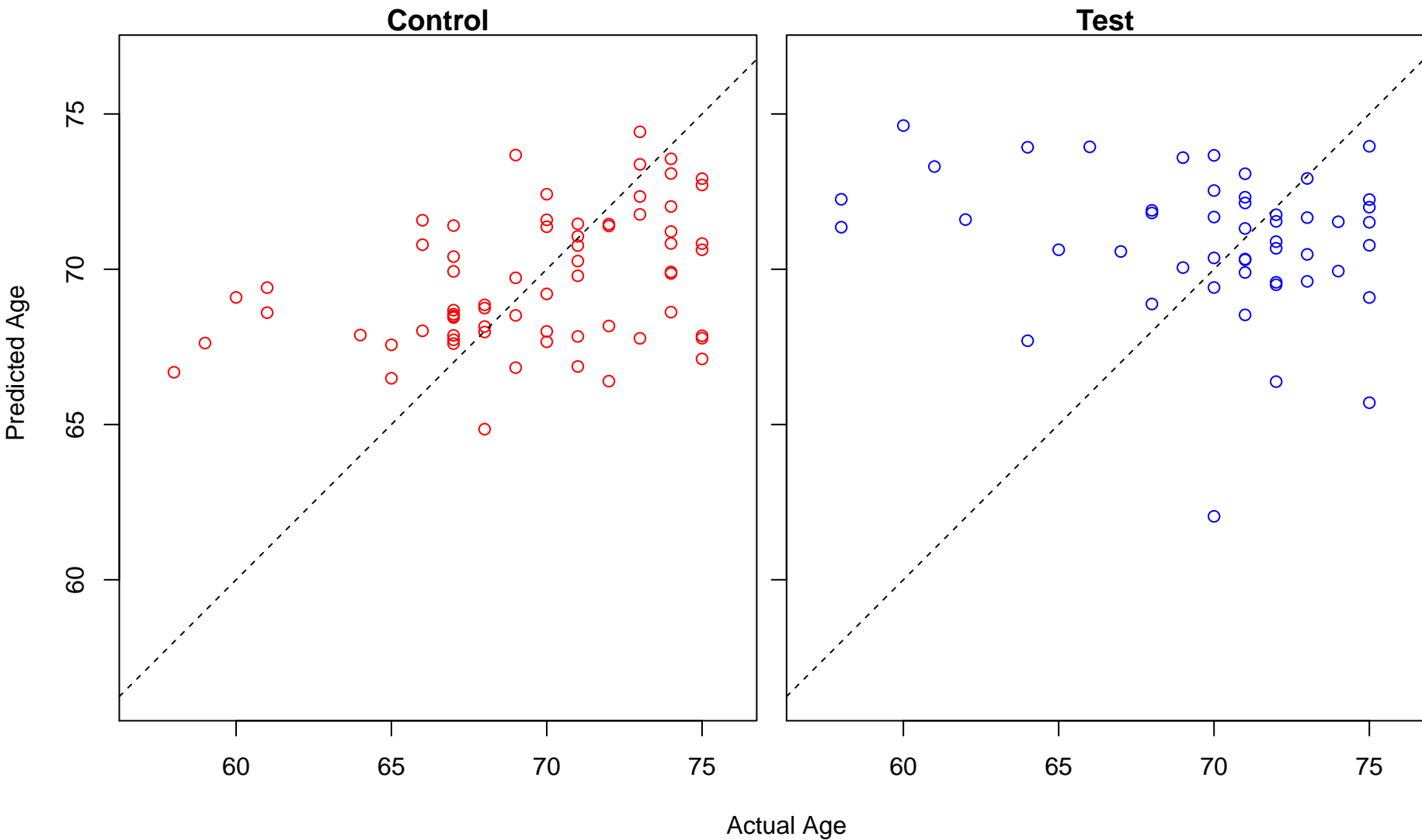
blastocyst formation (Score: 0.561919)



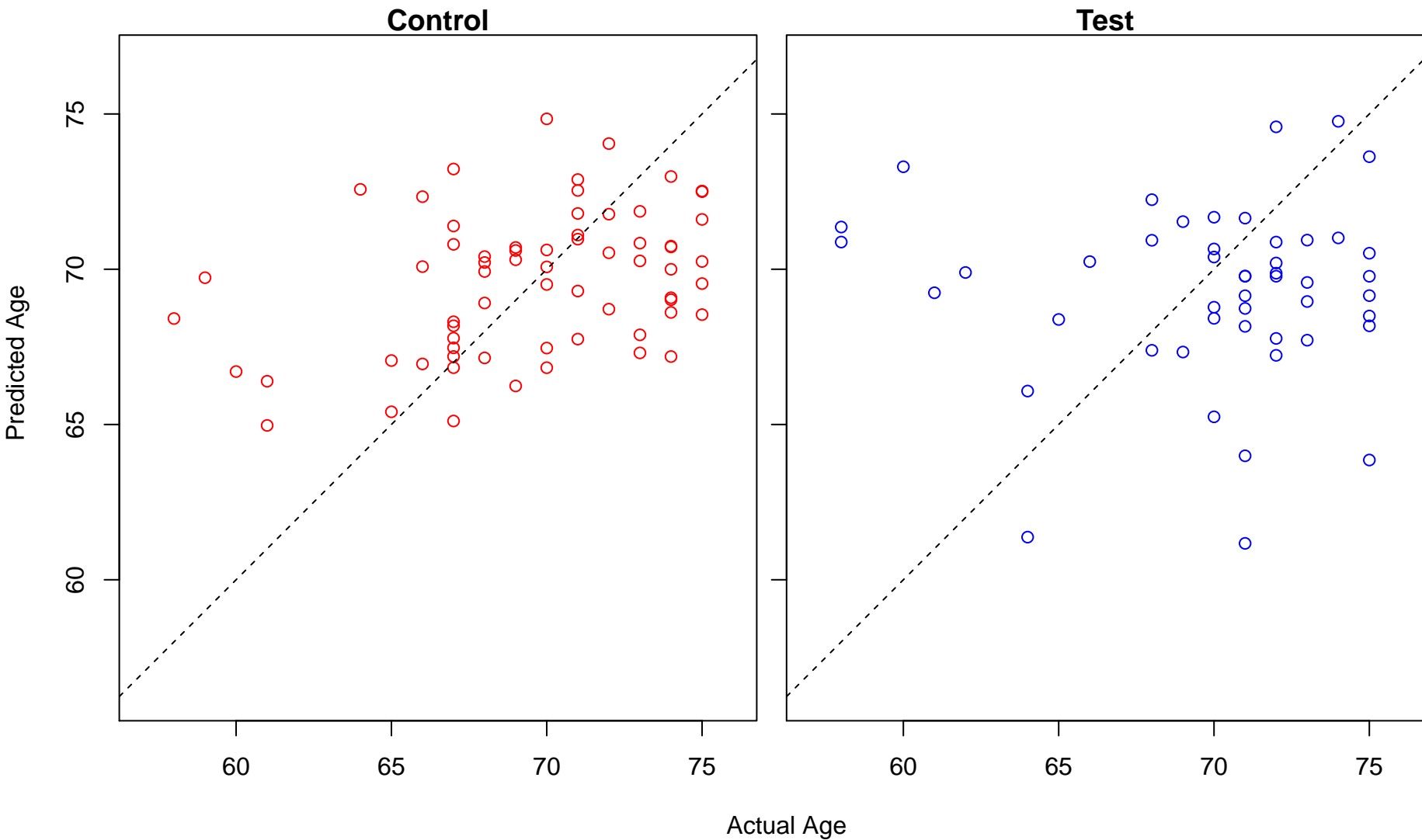
regulation of toll-like receptor 4 signaling pathway (Score: 0.561739)



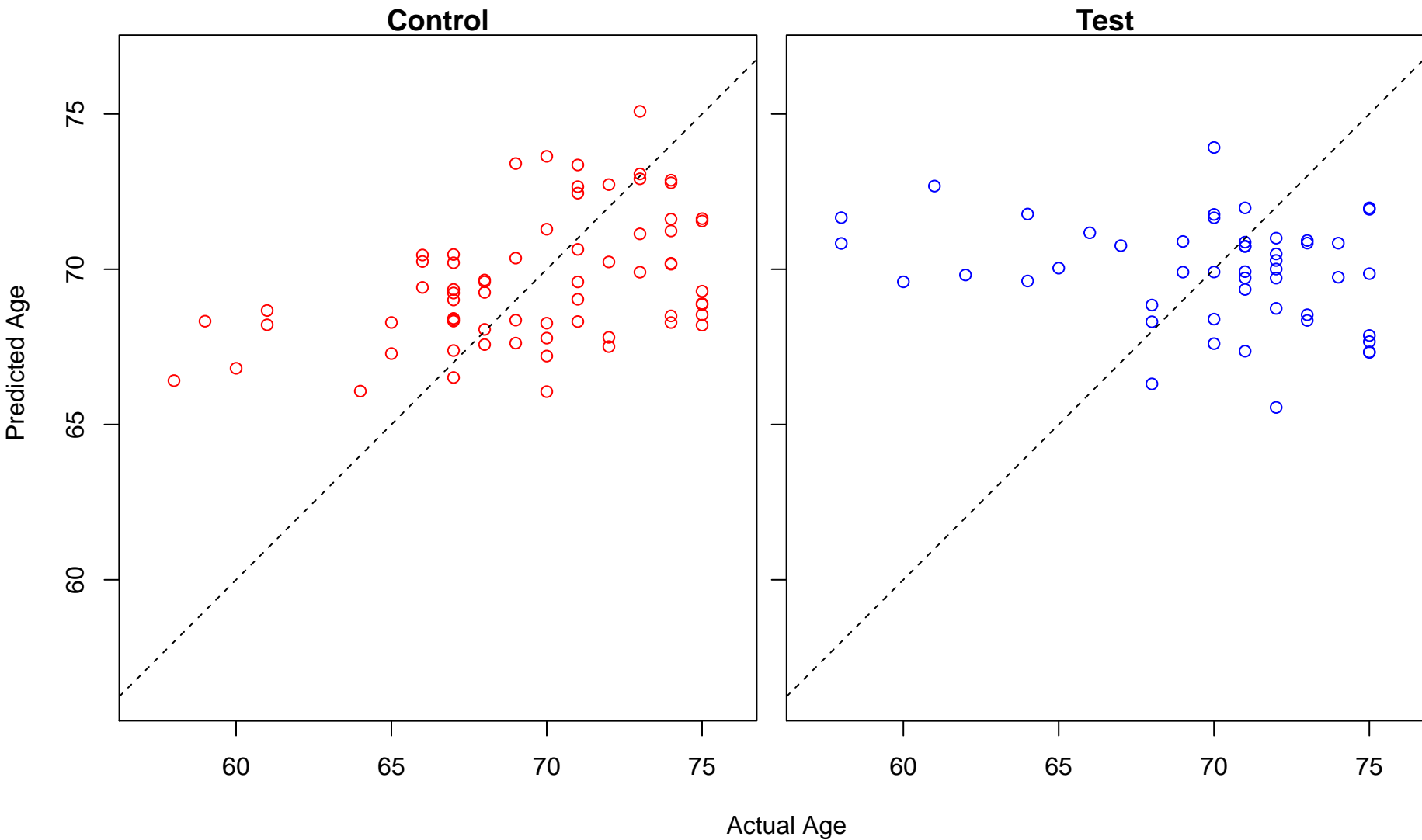
negative regulation of anion transmembrane transport (Score: 0.560811)



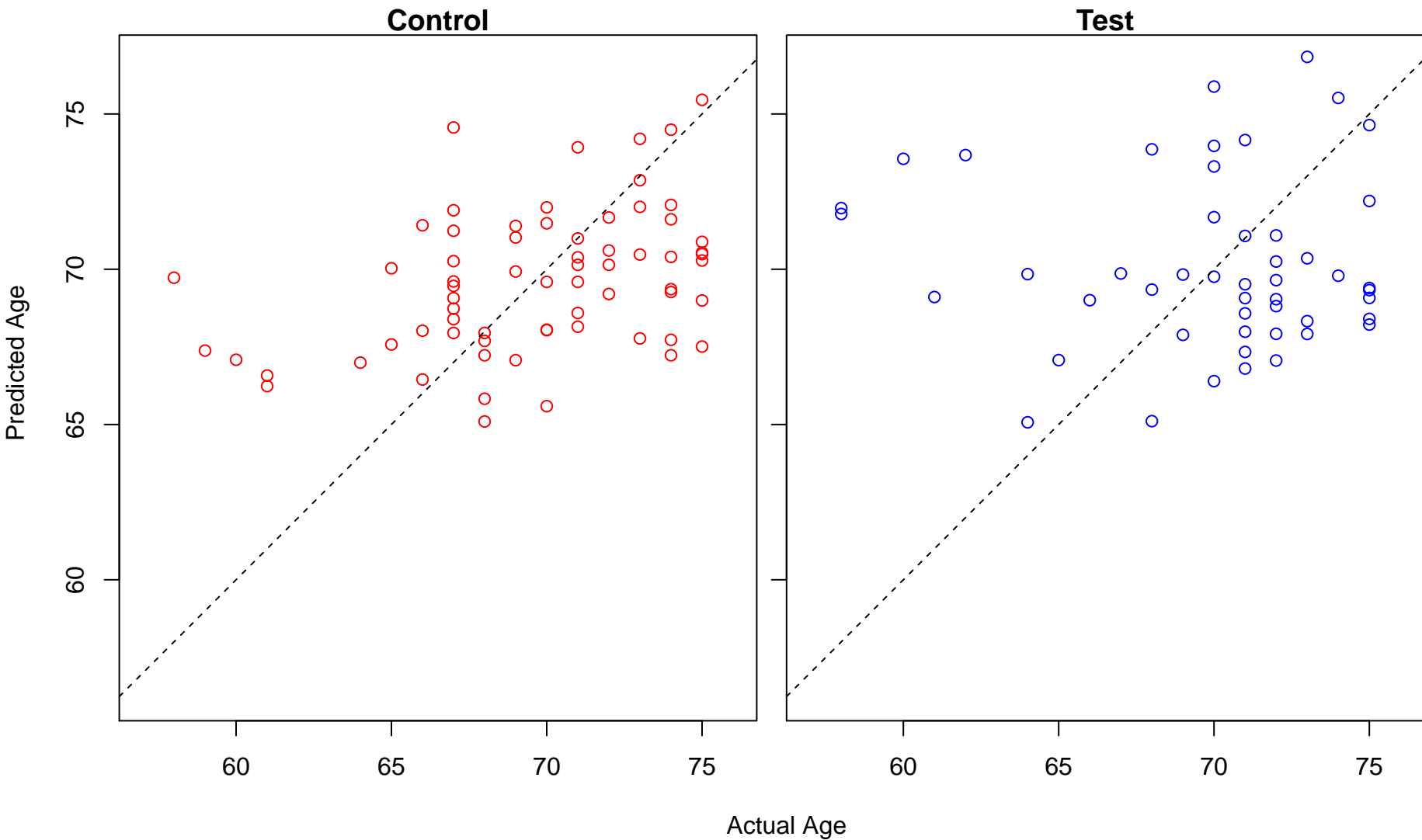
negative regulation of retinoic acid receptor signaling pathway (Score: 0.560601)



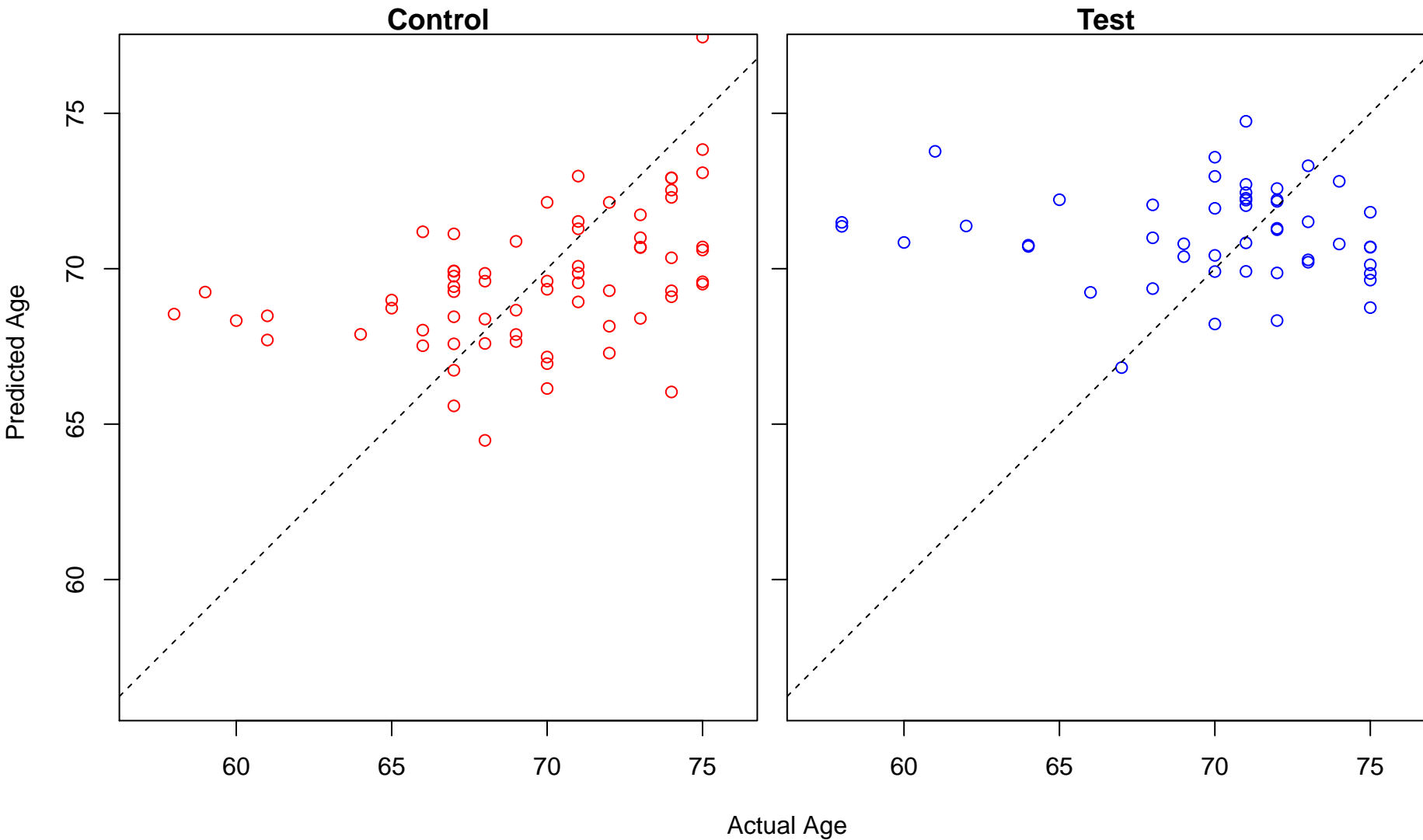
blastocyst development (Score: 0.559873)



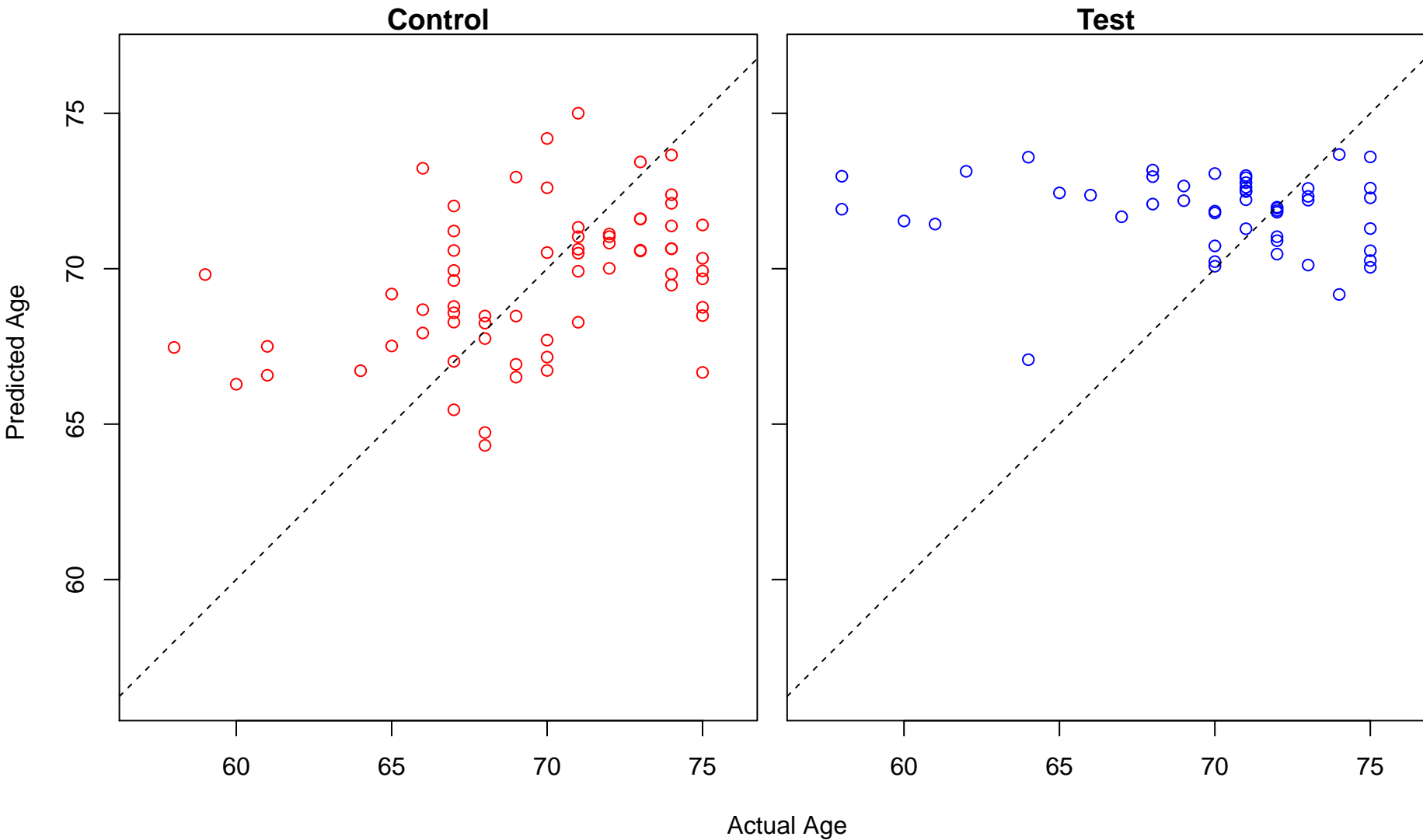
regulation of type B pancreatic cell apoptotic process (Score: 0.559365)



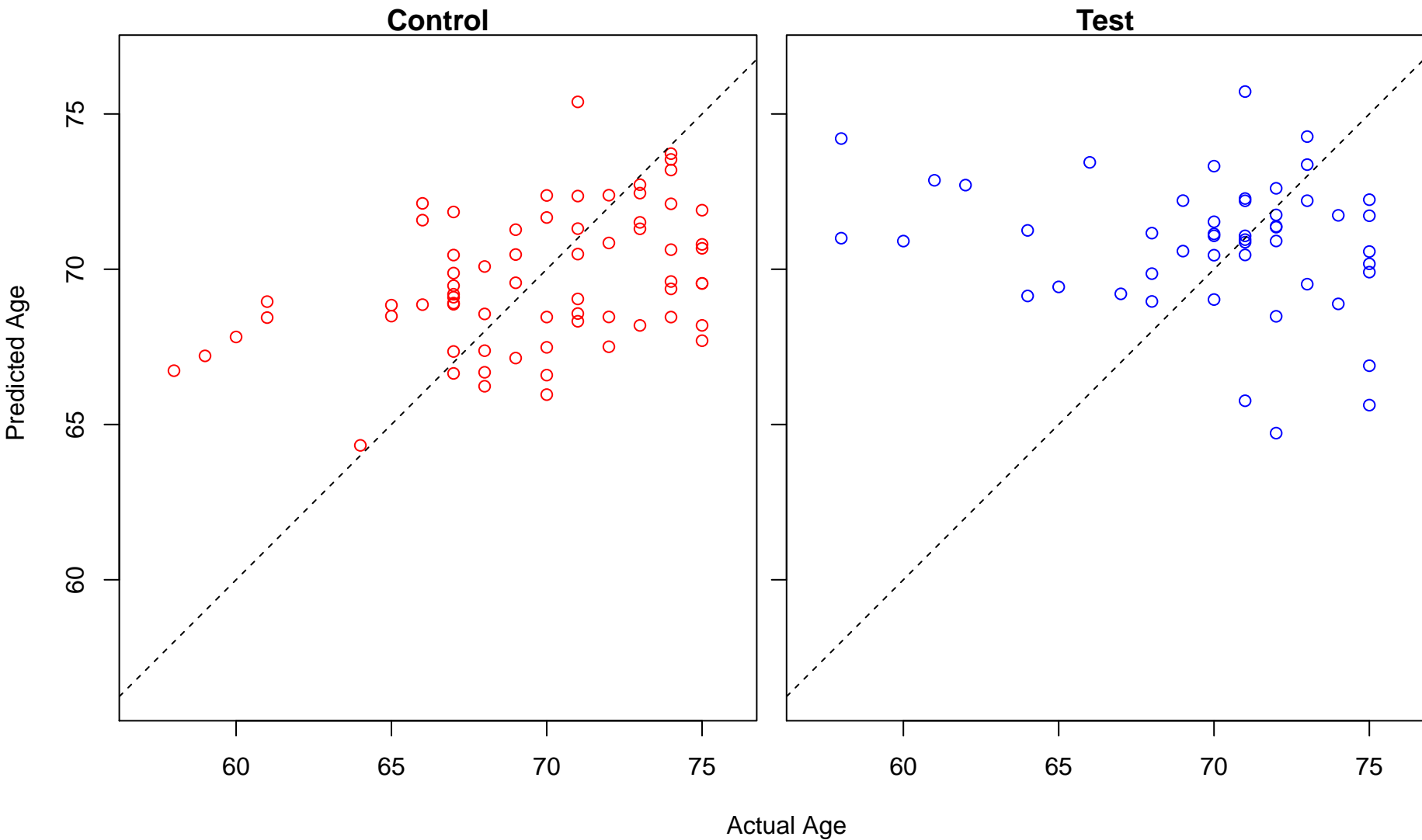
peptidyl-arginine methylation, to asymmetrical-dimethyl arginine (Score: 0.558770)



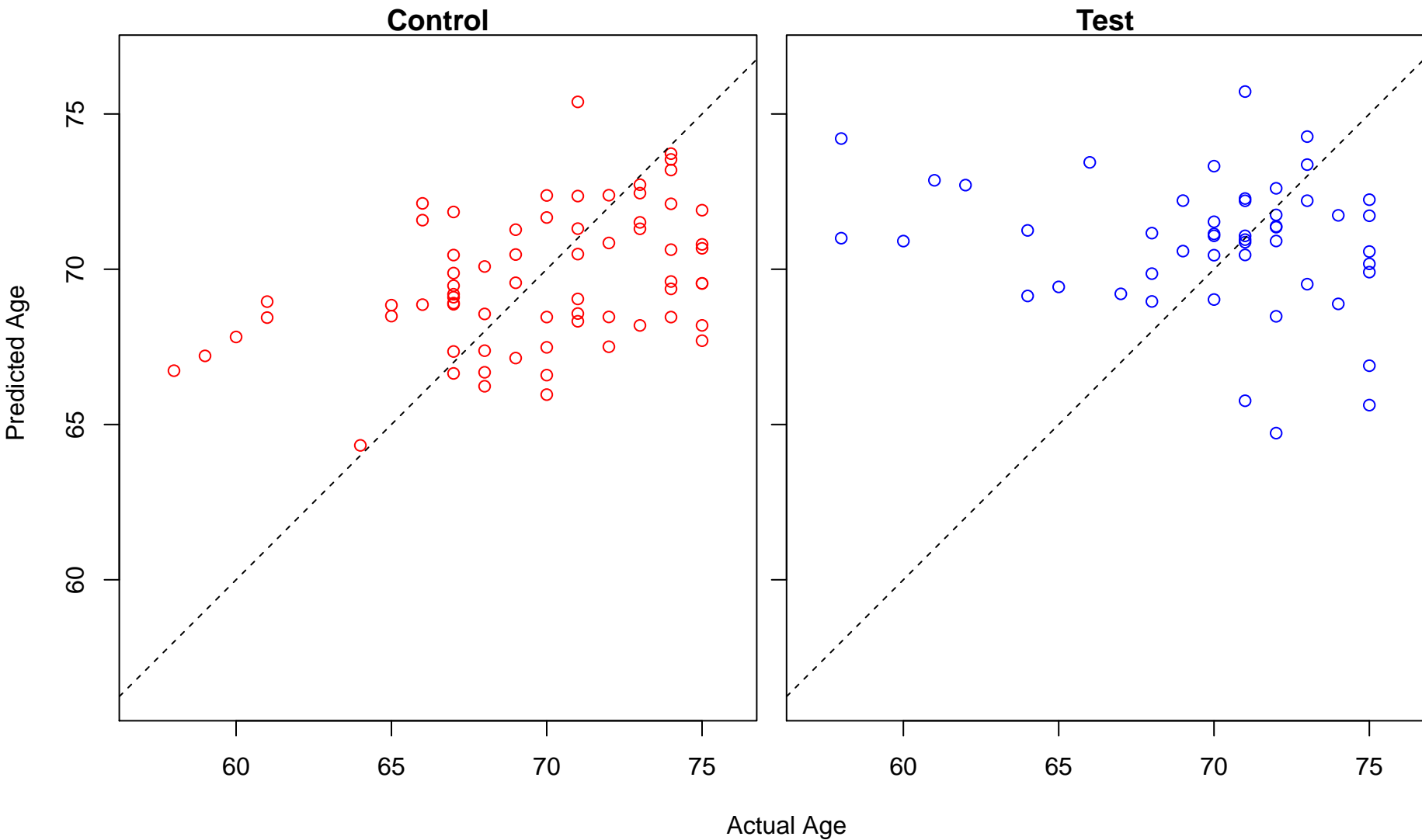
positive regulation of dendrite development (Score: 0.557595)



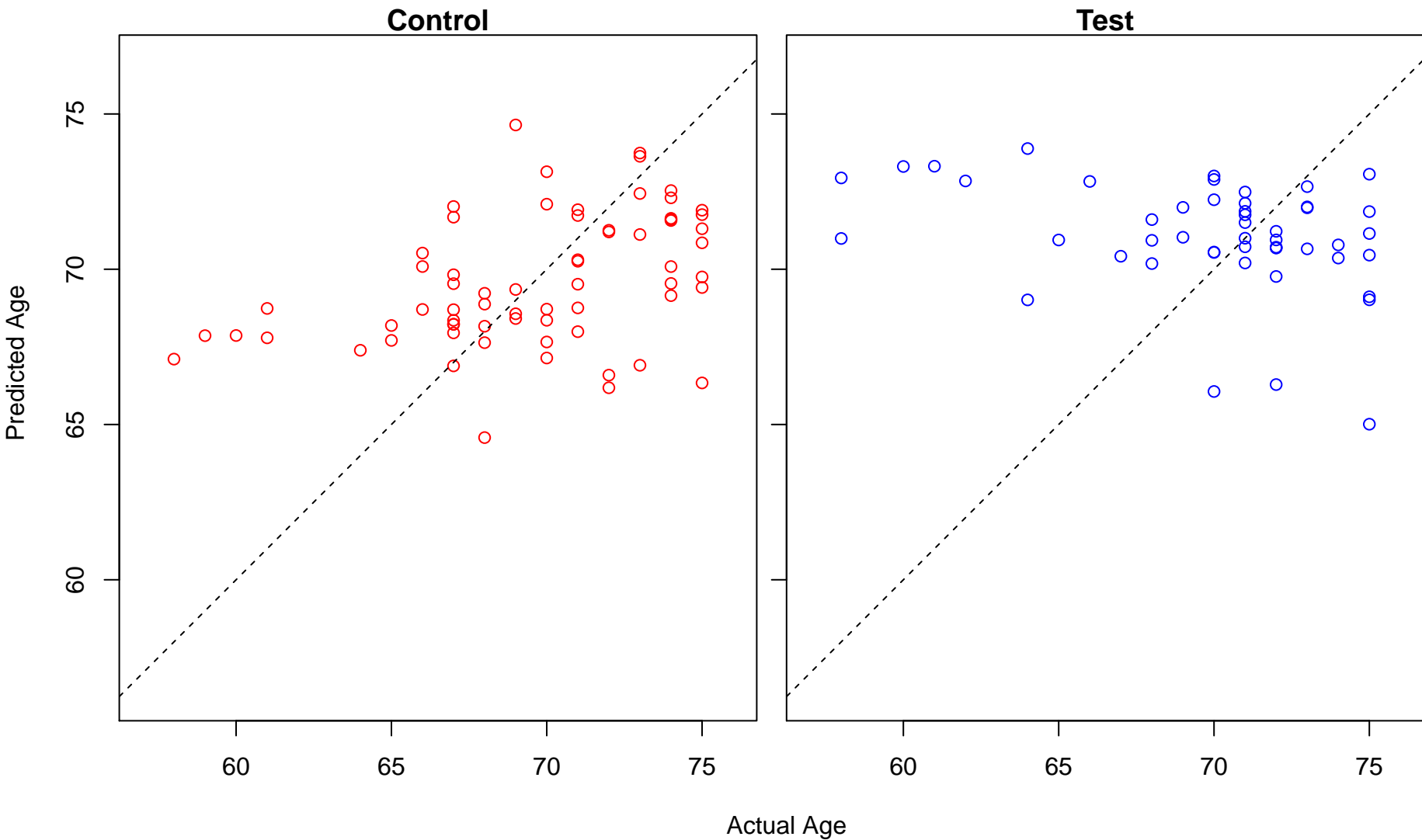
positive regulation of spindle checkpoint (Score: 0.557498)



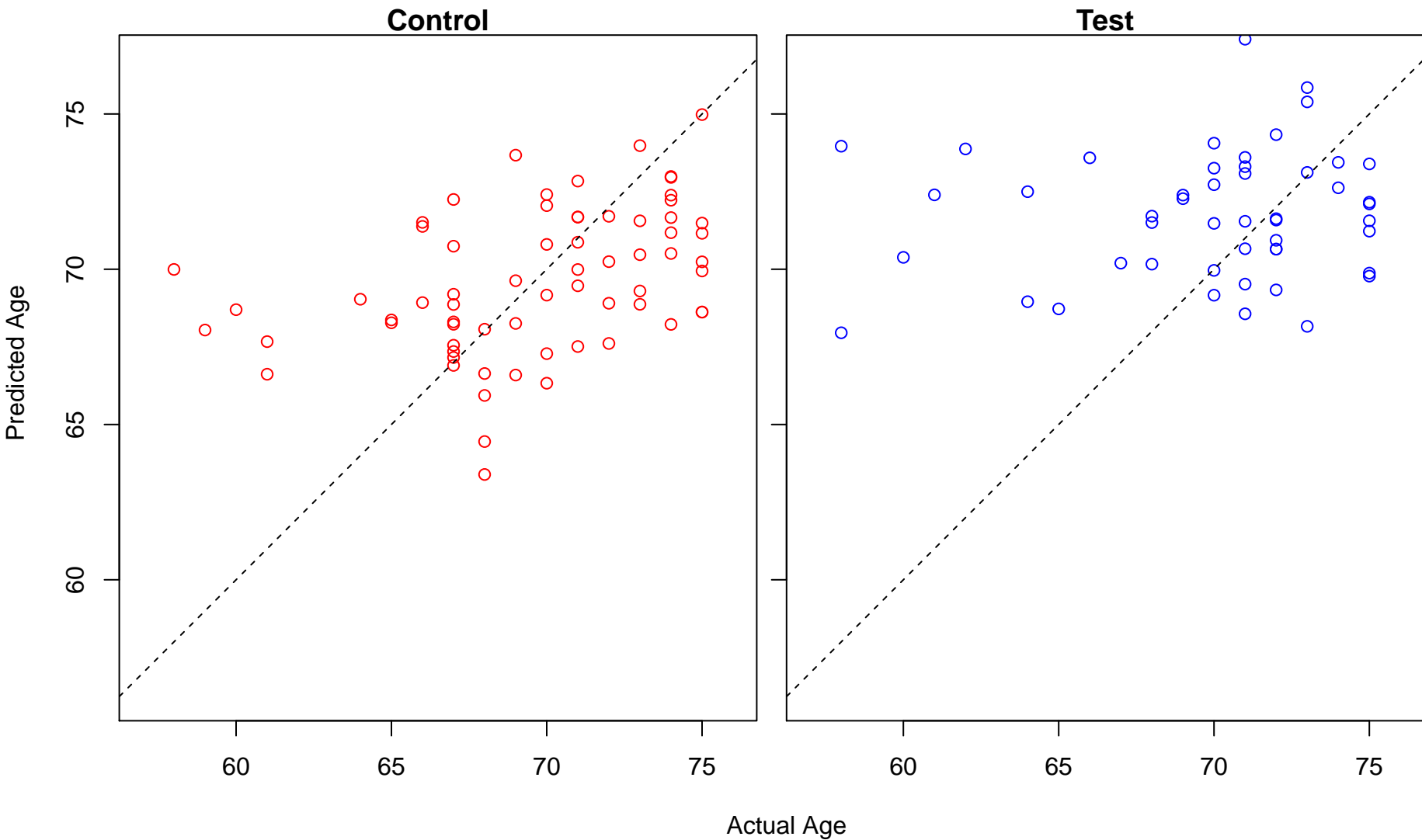
positive regulation of cell cycle checkpoint (Score: 0.557498)



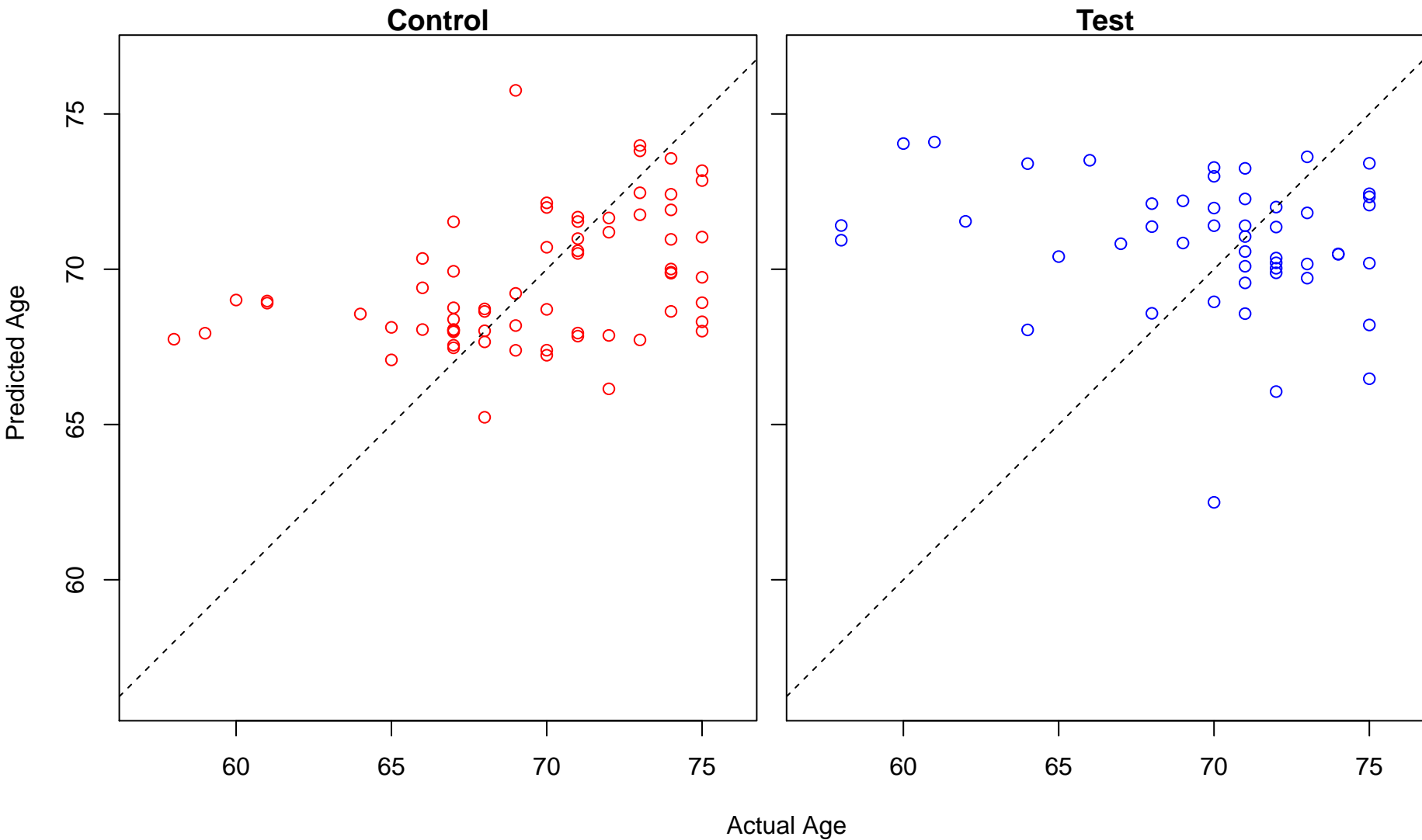
positive regulation of monooxygenase activity (Score: 0.557346)



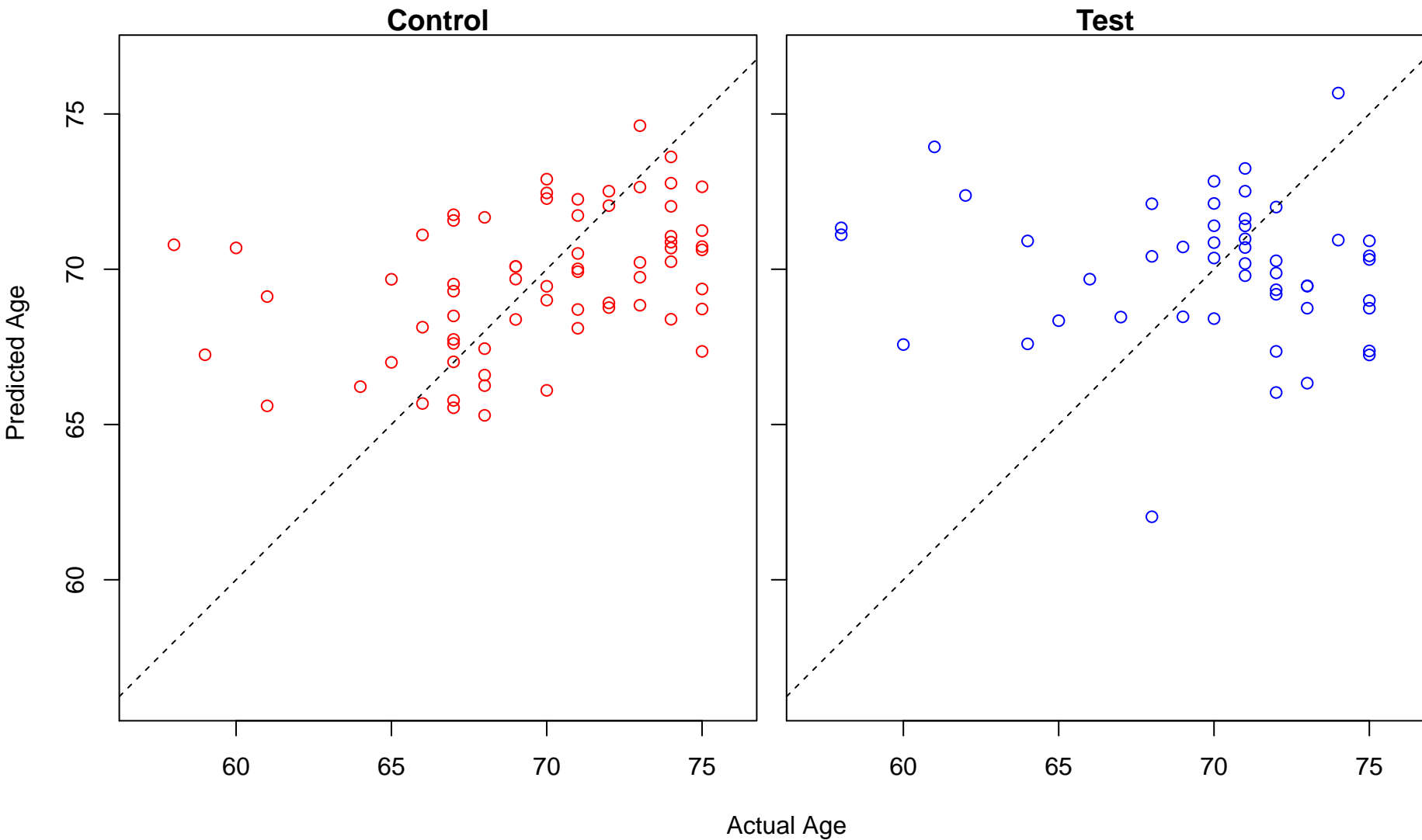
positive regulation of superoxide anion generation (Score: 0.557264)



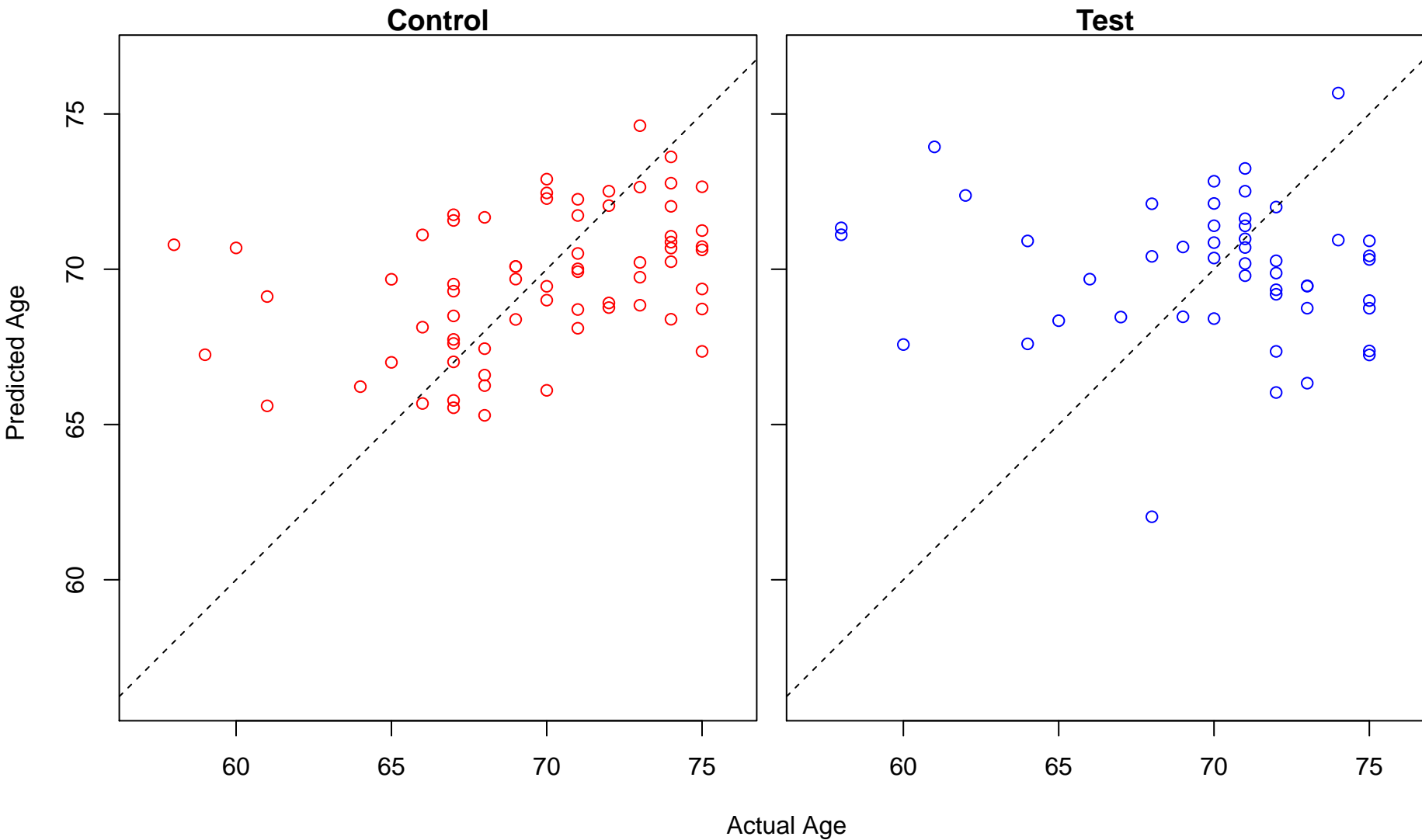
regulation of anion transmembrane transport (Score: 0.557242)



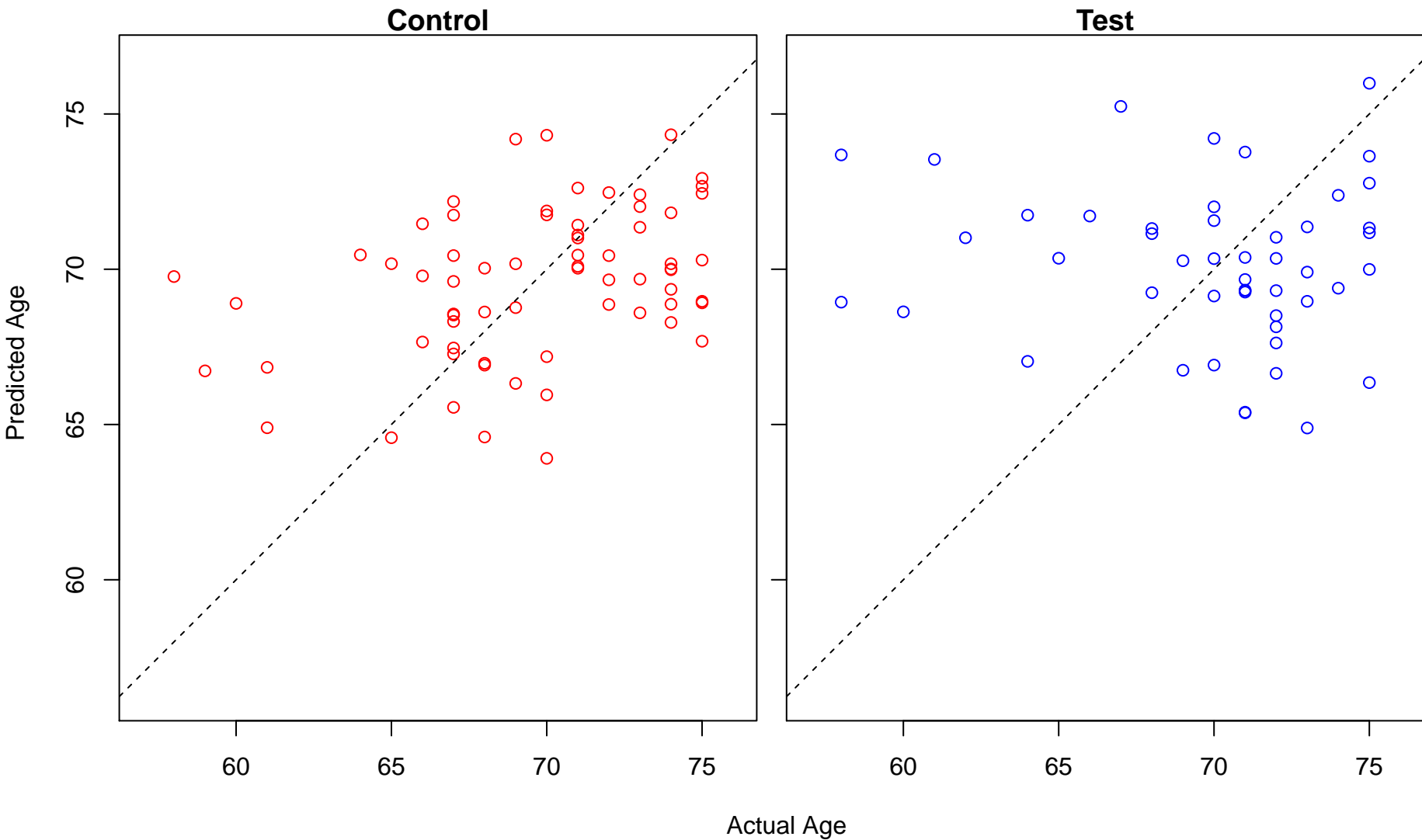
negative regulation of natural killer cell mediated immunity (Score: 0.556472)



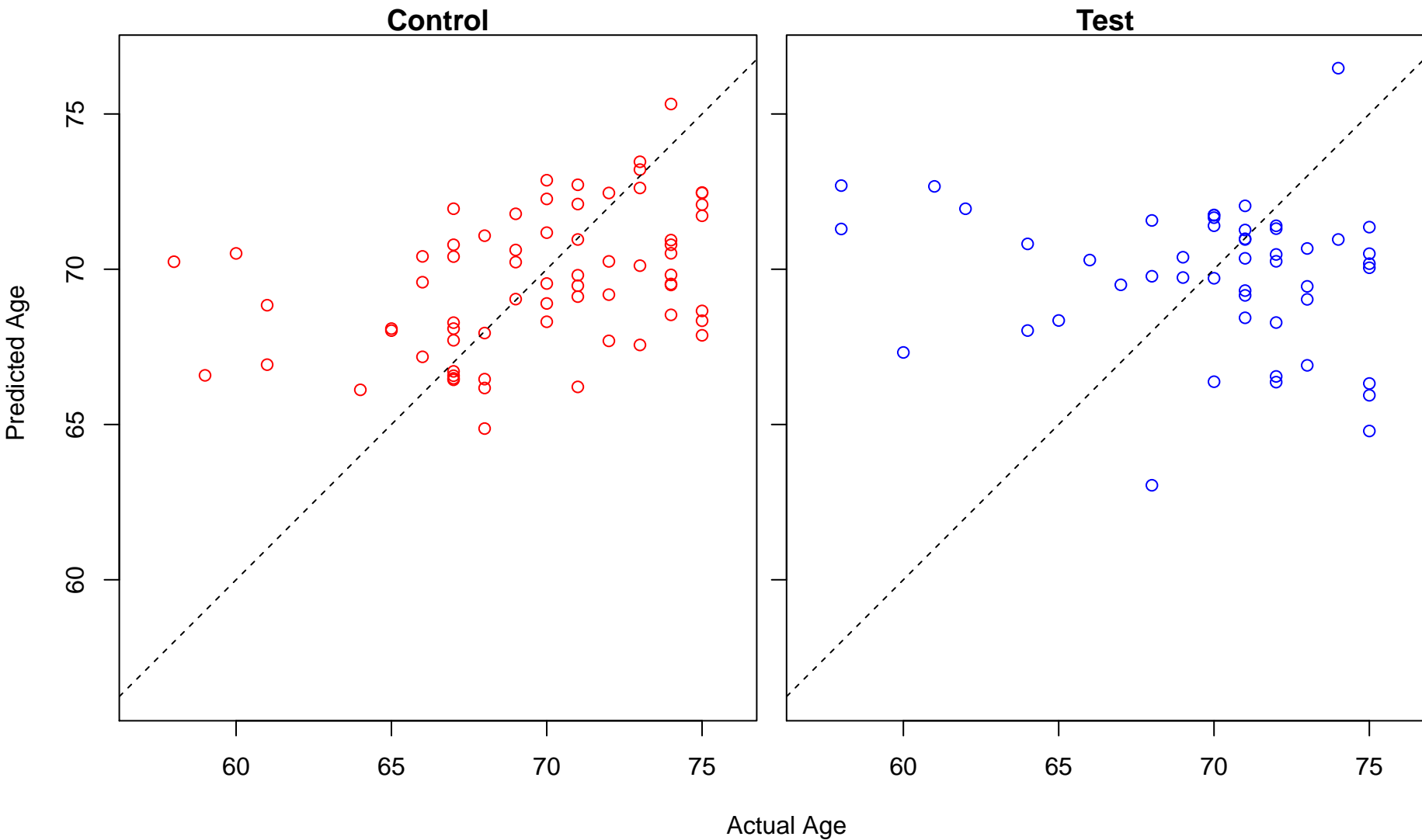
negative regulation of natural killer cell mediated cytotoxicity (Score: 0.556472)



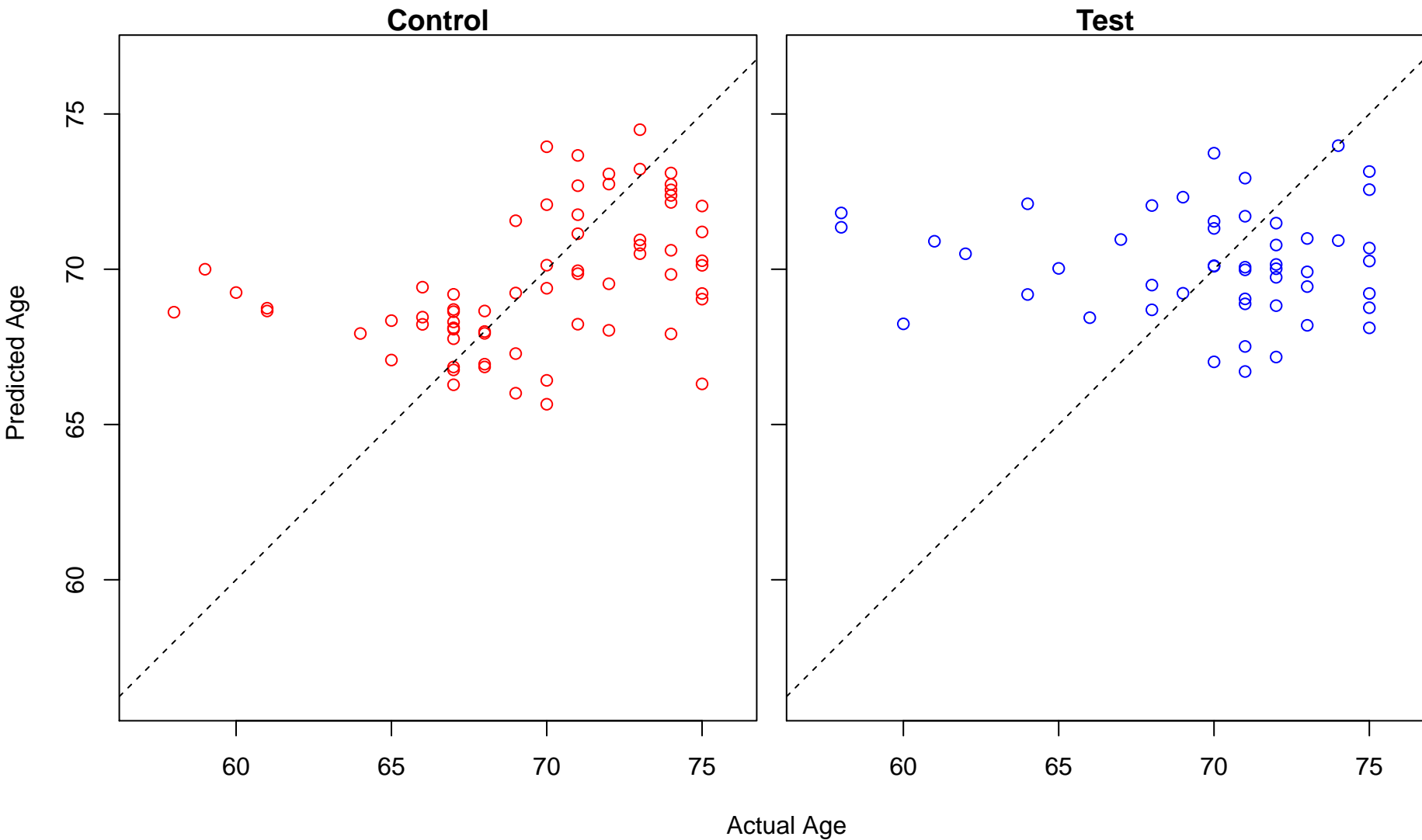
embryonic cranial skeleton morphogenesis (Score: 0.555723)



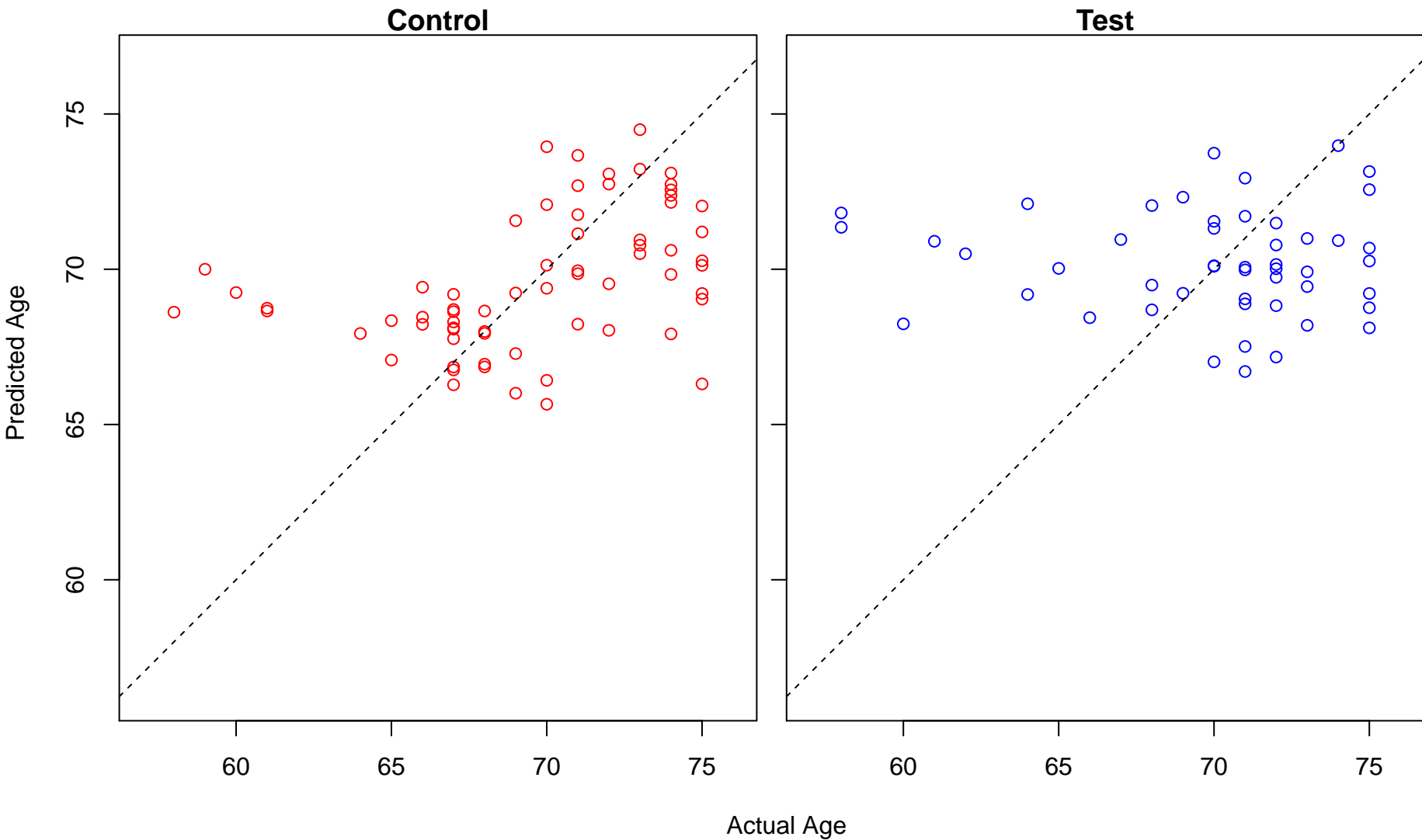
negative regulation of leukocyte mediated cytotoxicity (Score: 0.554821)



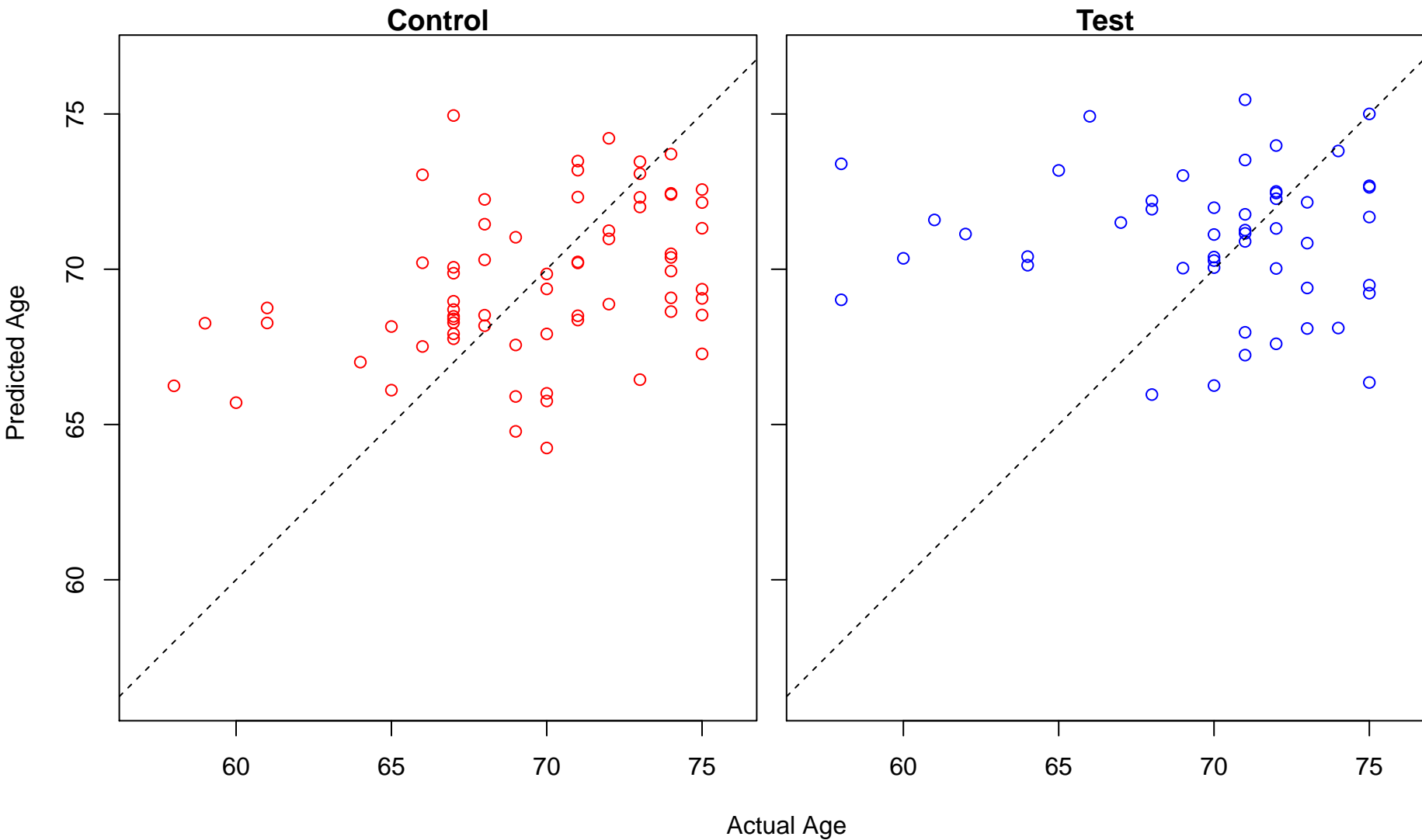
T cell lineage commitment (Score: 0.554323)



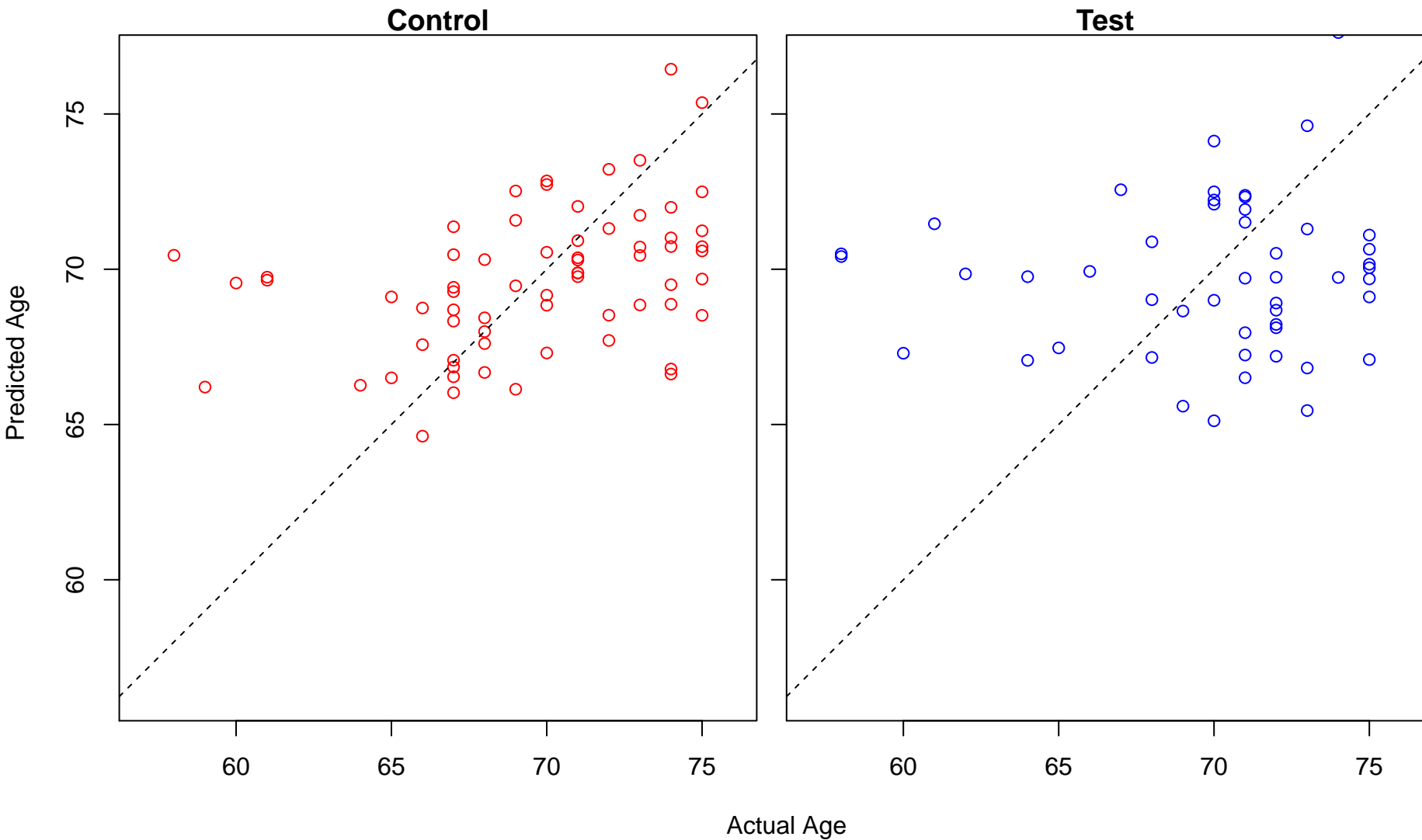
CD4-positive or CD8-positive, alpha-beta T cell lineage commitment (Score: 0.554323)



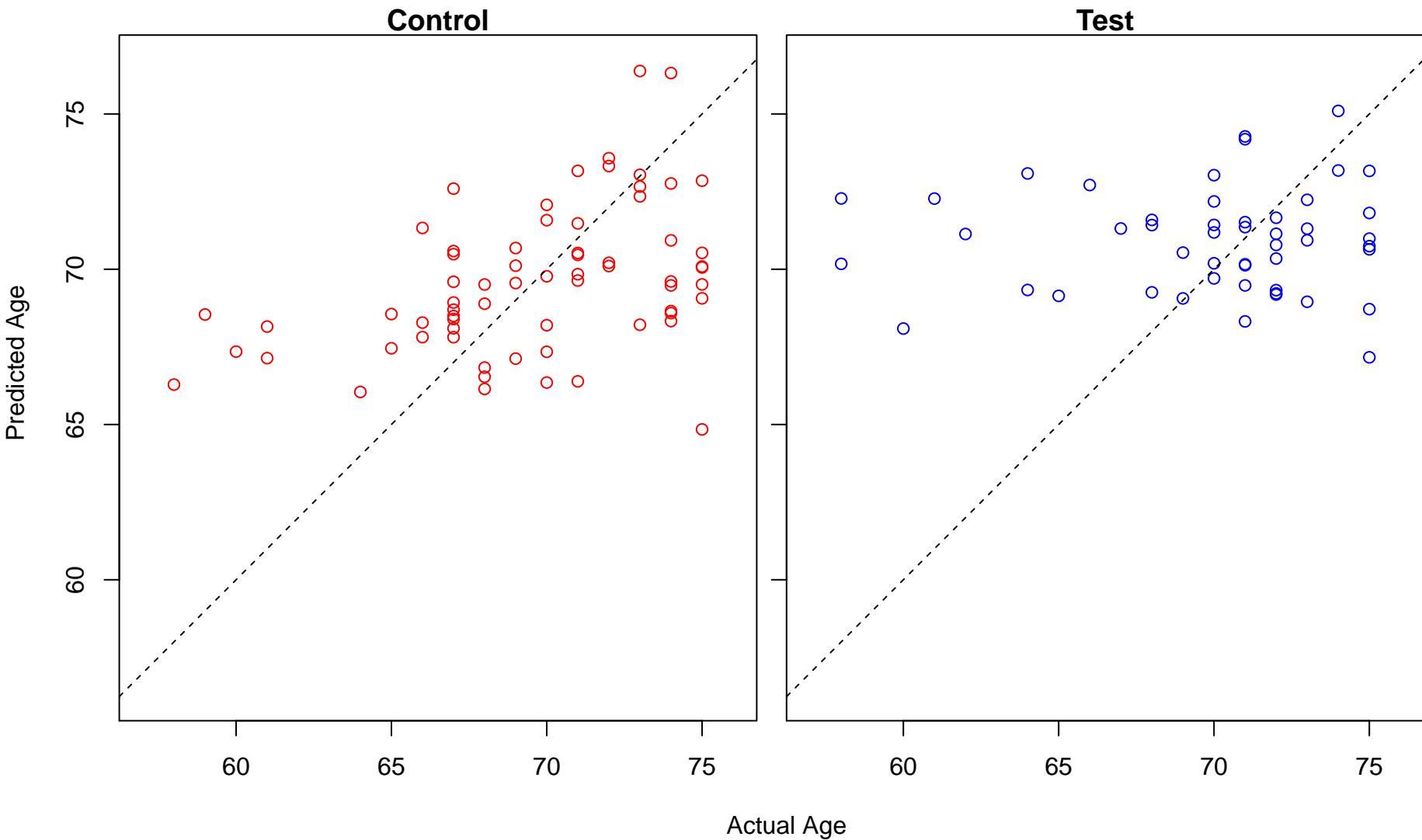
positive regulation of muscle contraction (Score: 0.554230)



hormone secretion (Score: 0.553539)

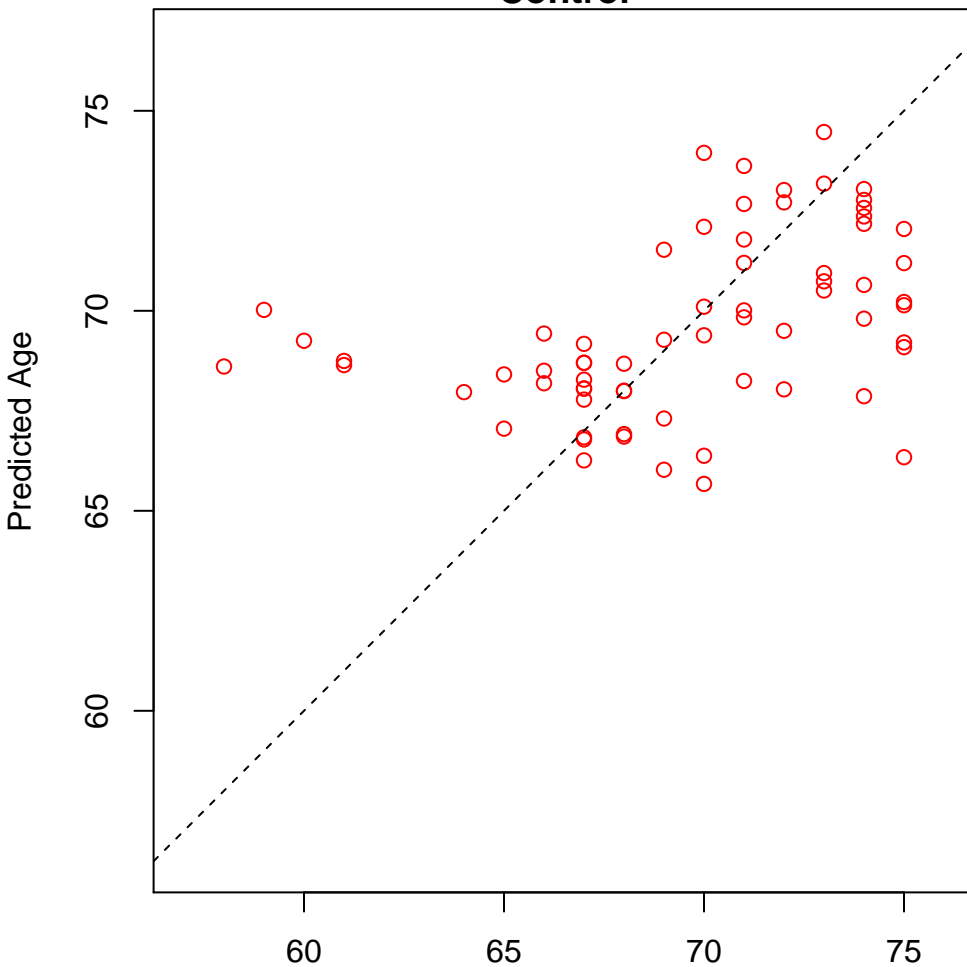


negative regulation of interleukin-1 secretion (Score: 0.553479)

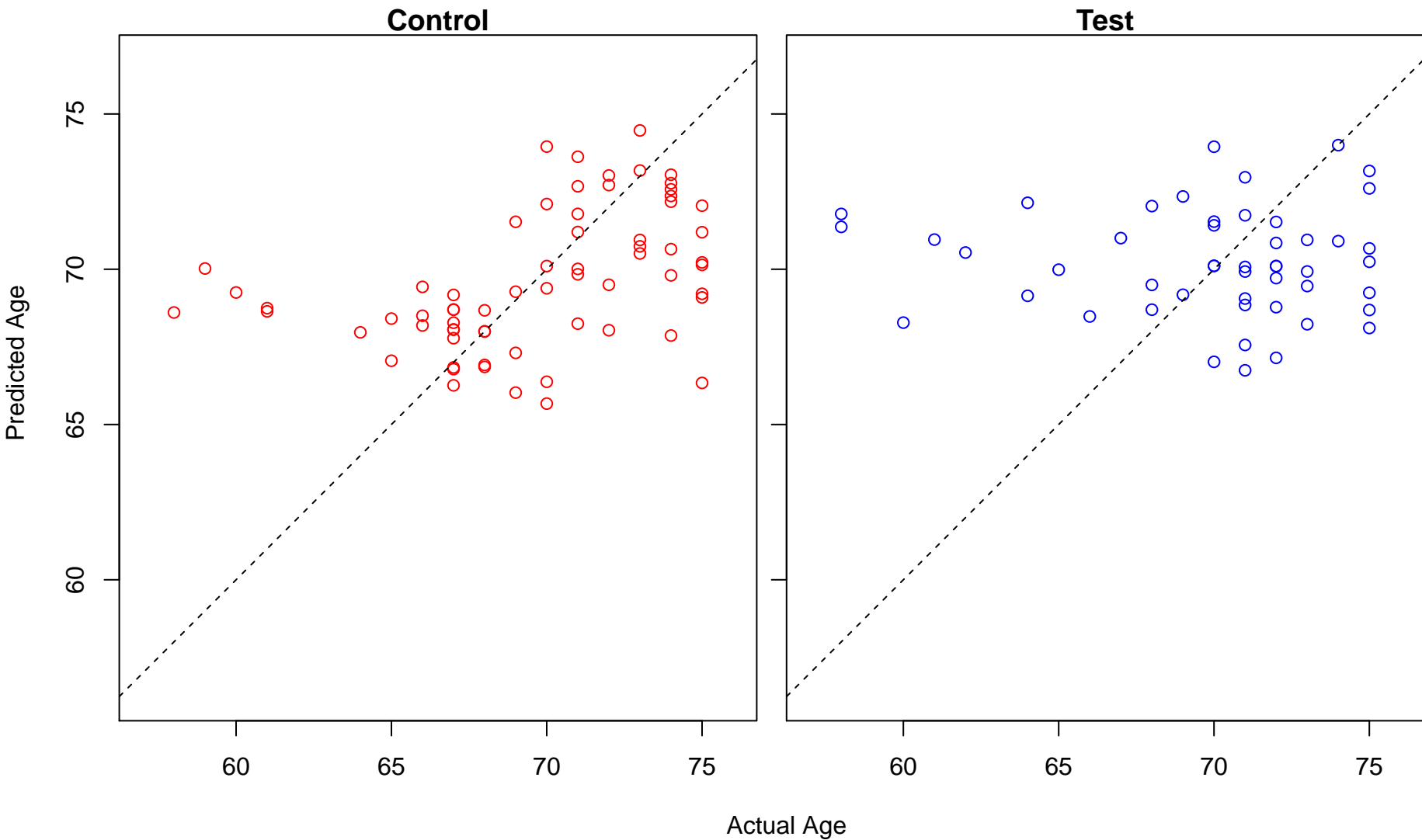


alpha-beta T cell lineage commitment (Score: 0.553410)

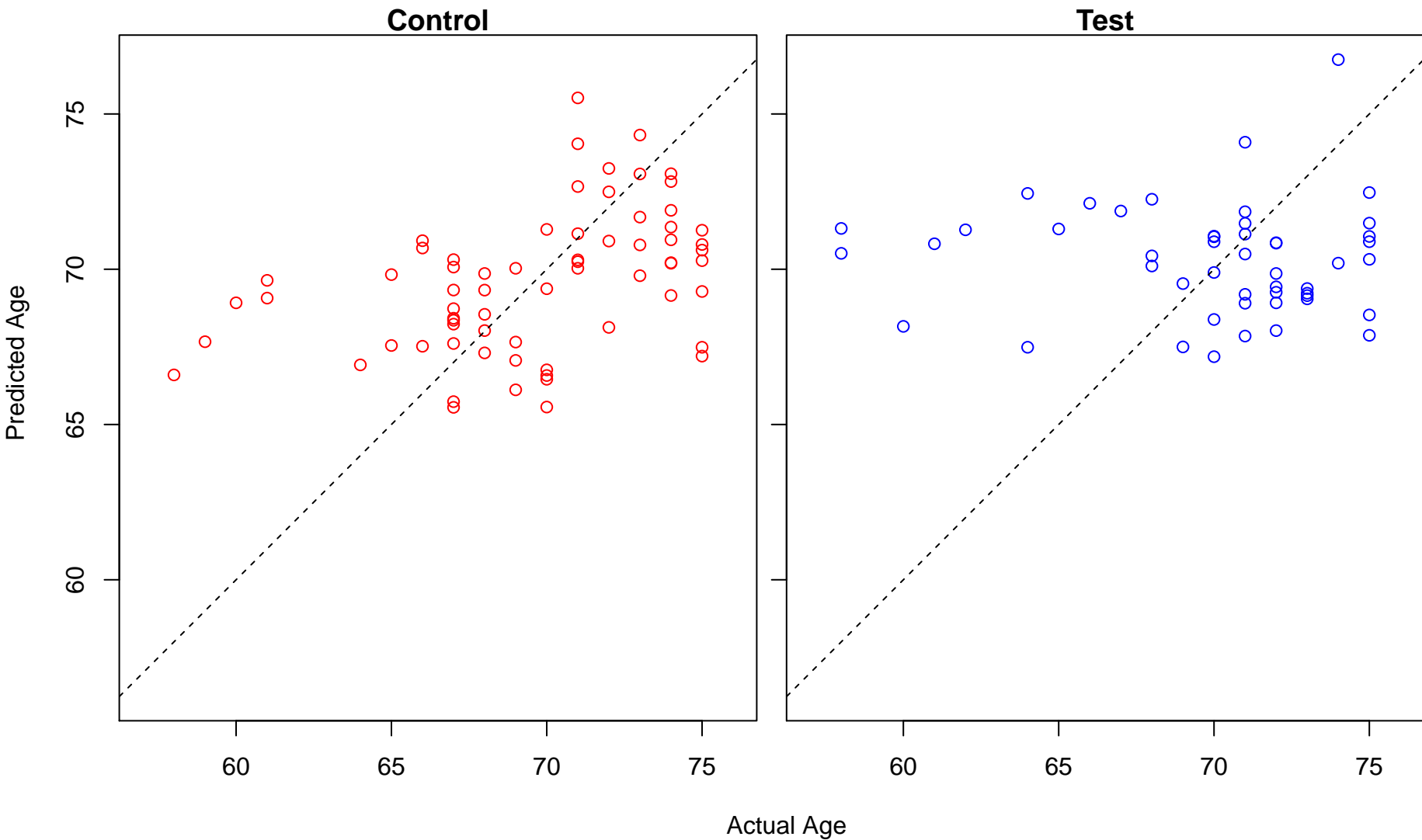
Control



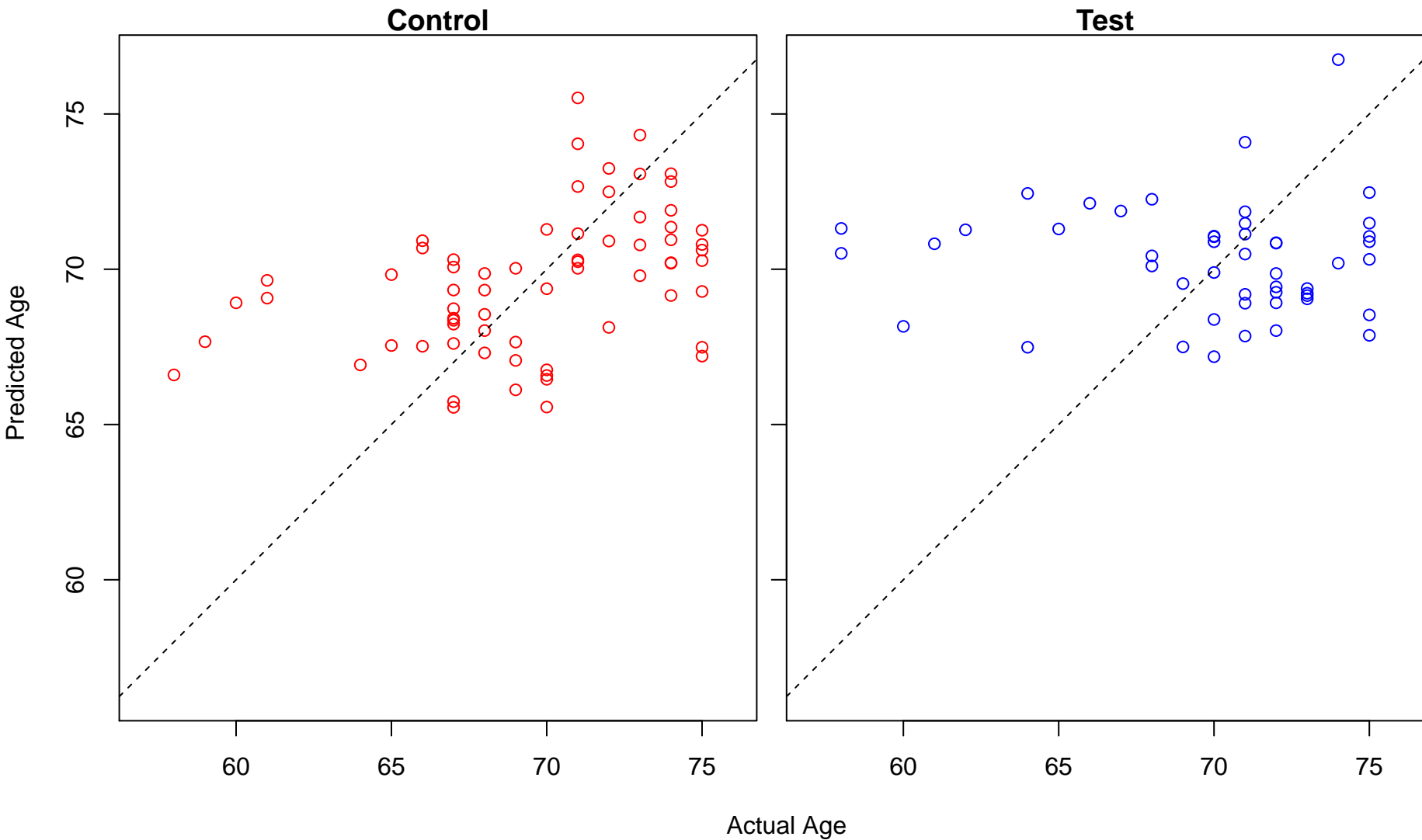
CD4-positive, alpha-beta T cell lineage commitment (Score: 0.553410)



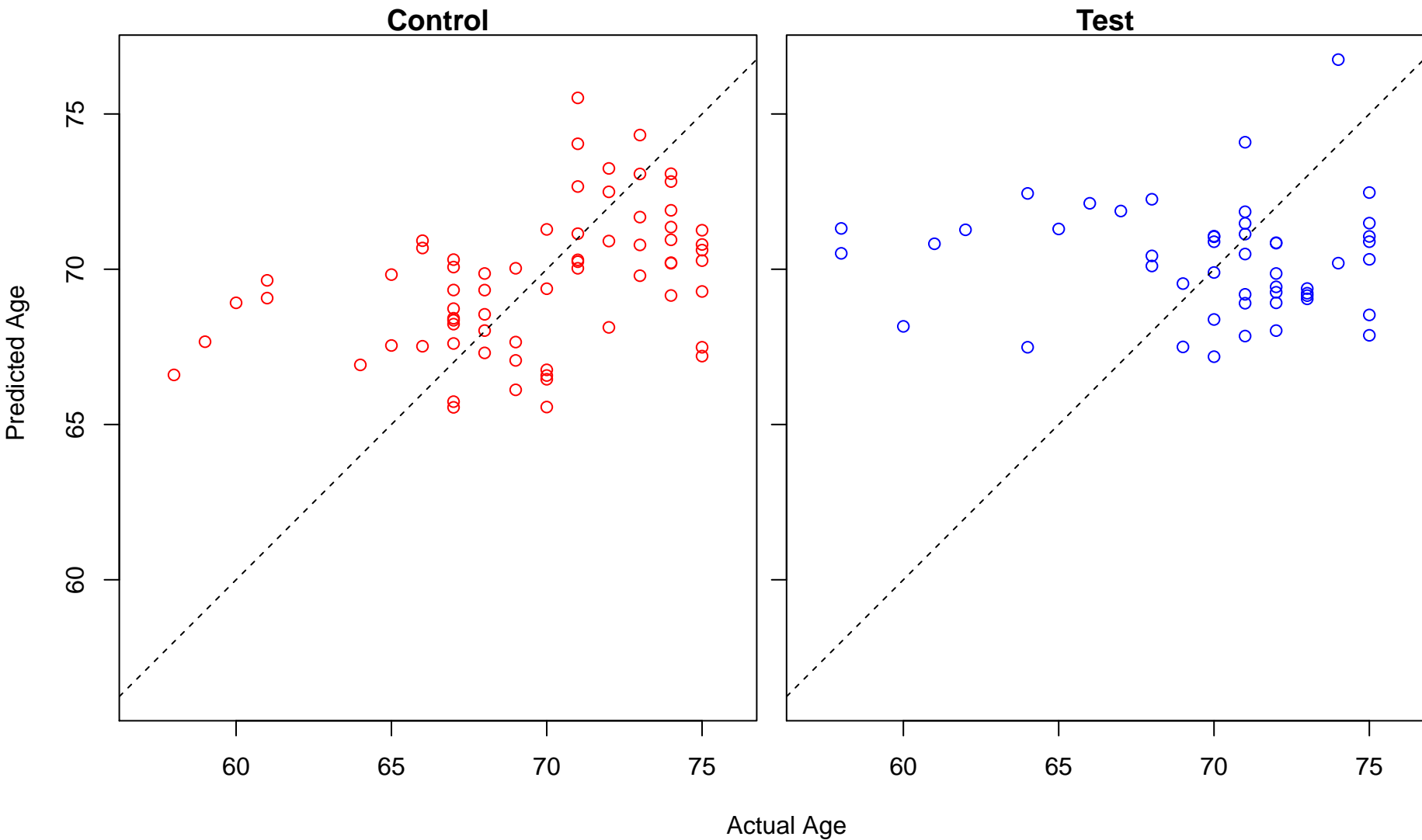
positive regulation of collagen metabolic process (Score: 0.553176)



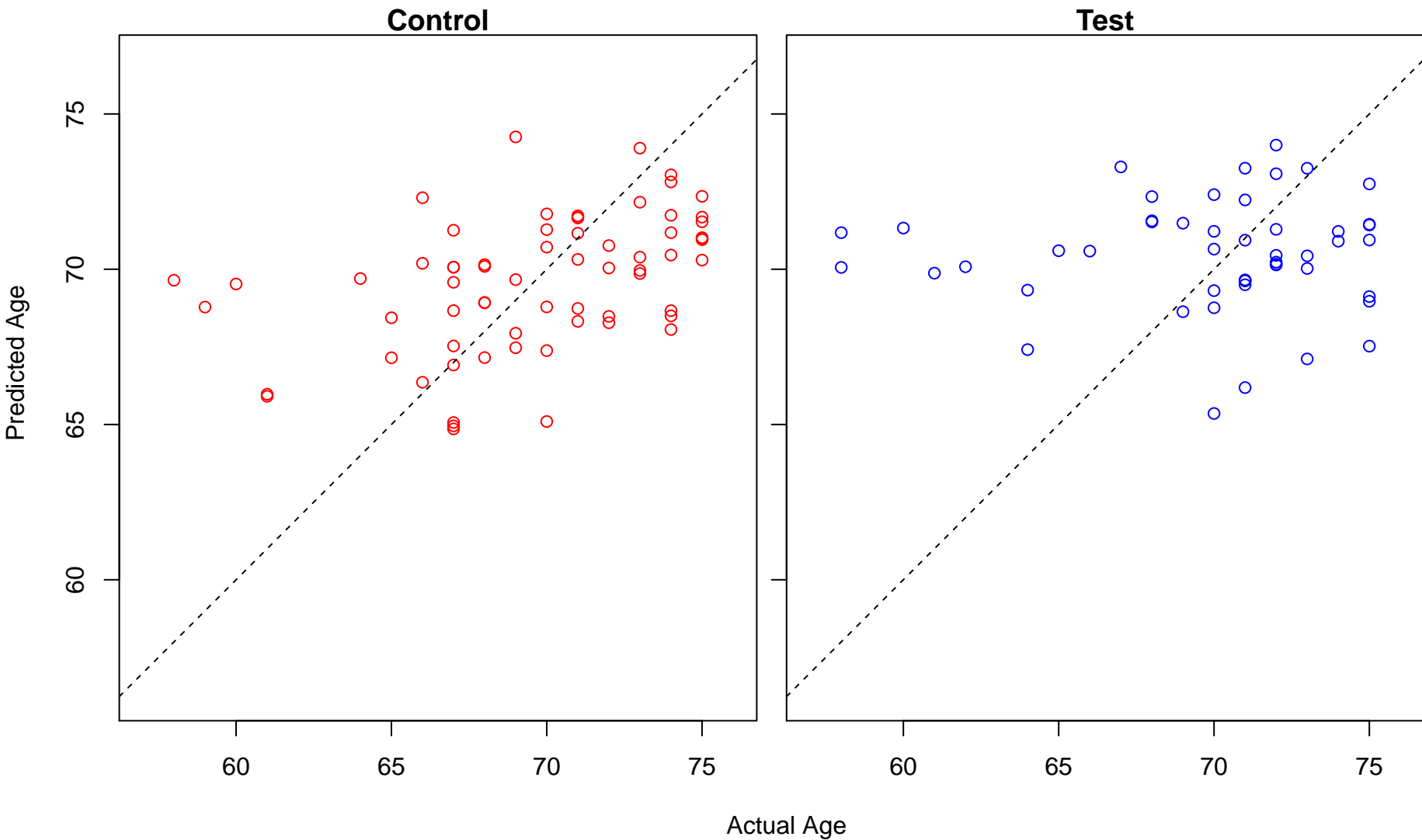
positive regulation of collagen biosynthetic process (Score: 0.553176)



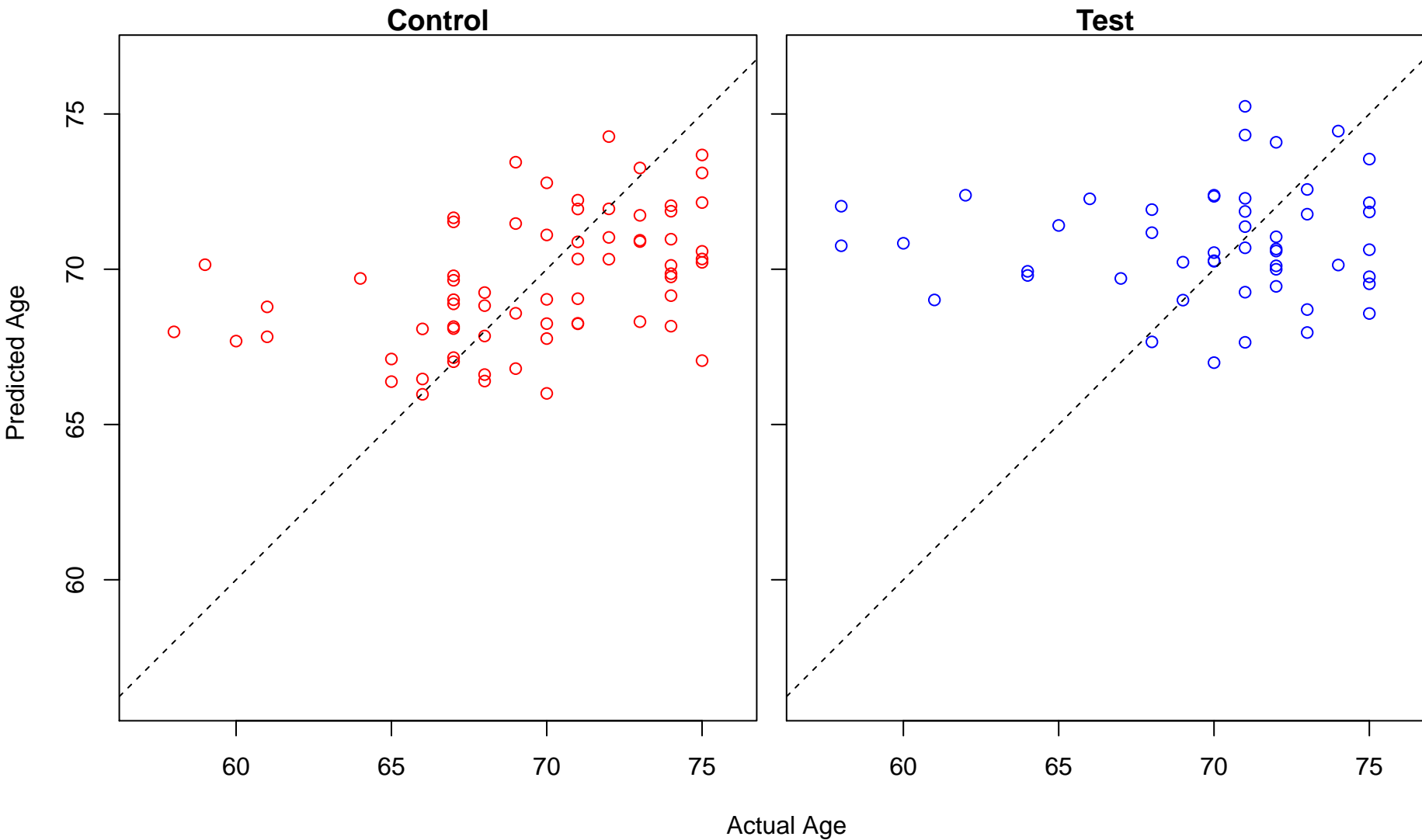
positive regulation of multicellular organismal metabolic process (Score: 0.553176)



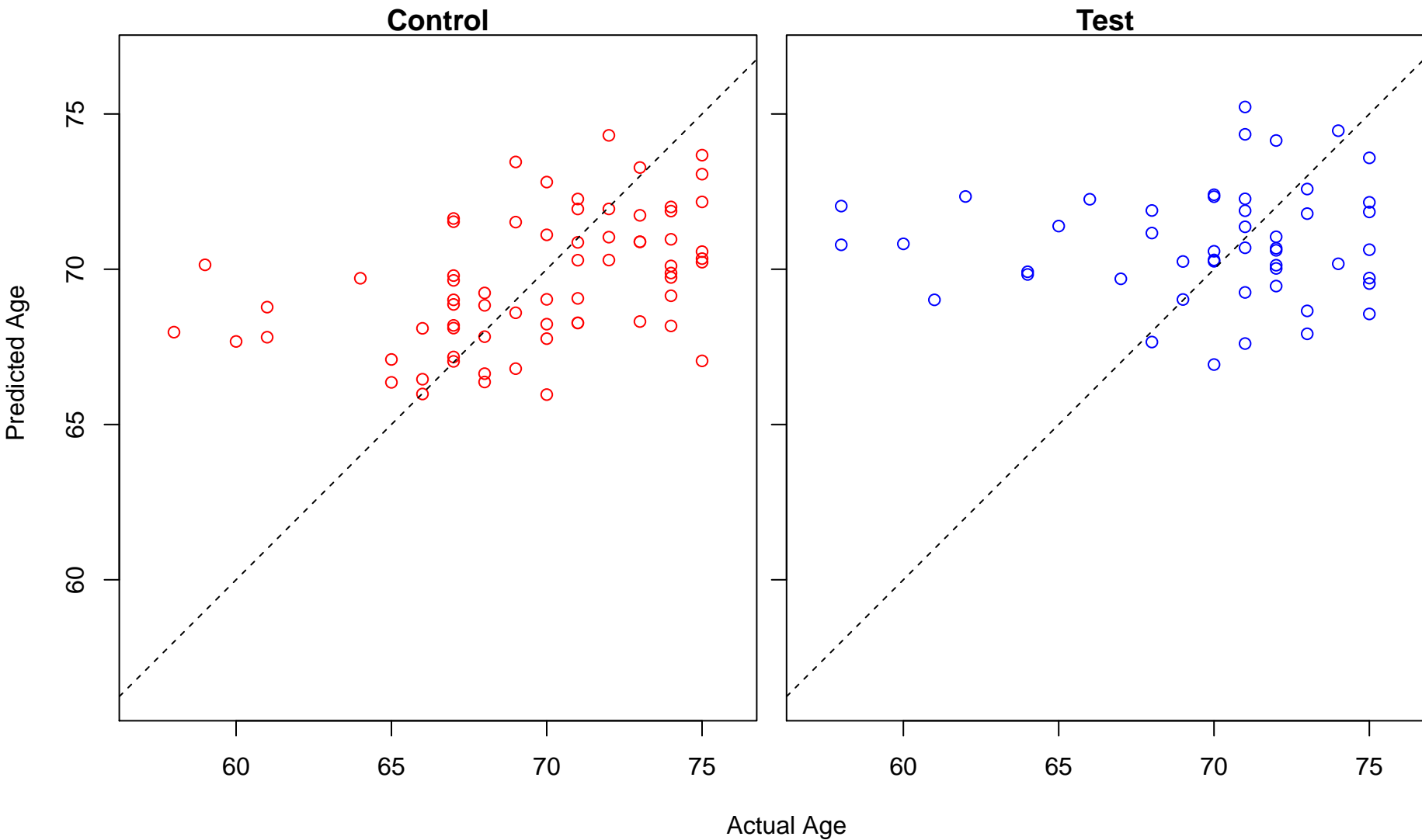
cellular modified amino acid catabolic process (Score: 0.553159)



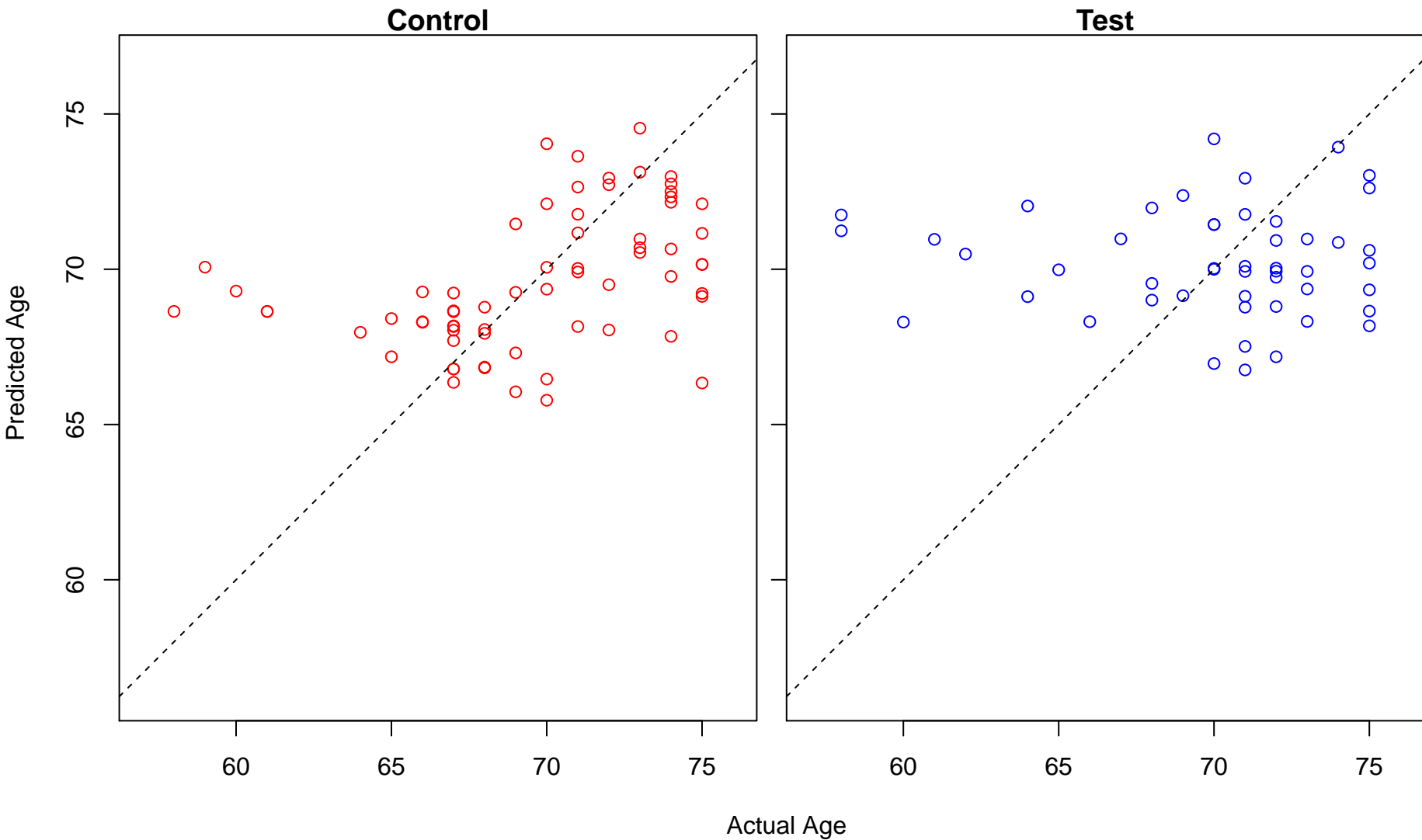
L-cystine transport (Score: 0.551663)



sulfur amino acid transport (Score: 0.551406)

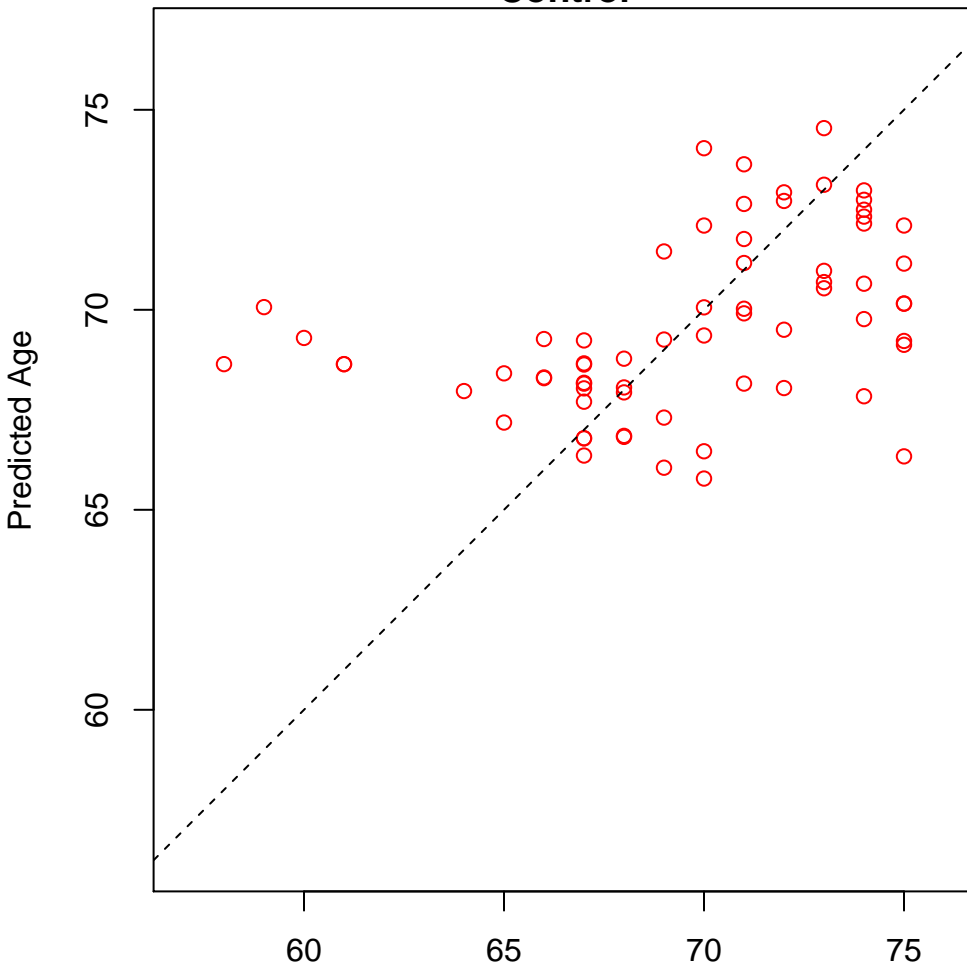


T-helper cell lineage commitment (Score: 0.551276)

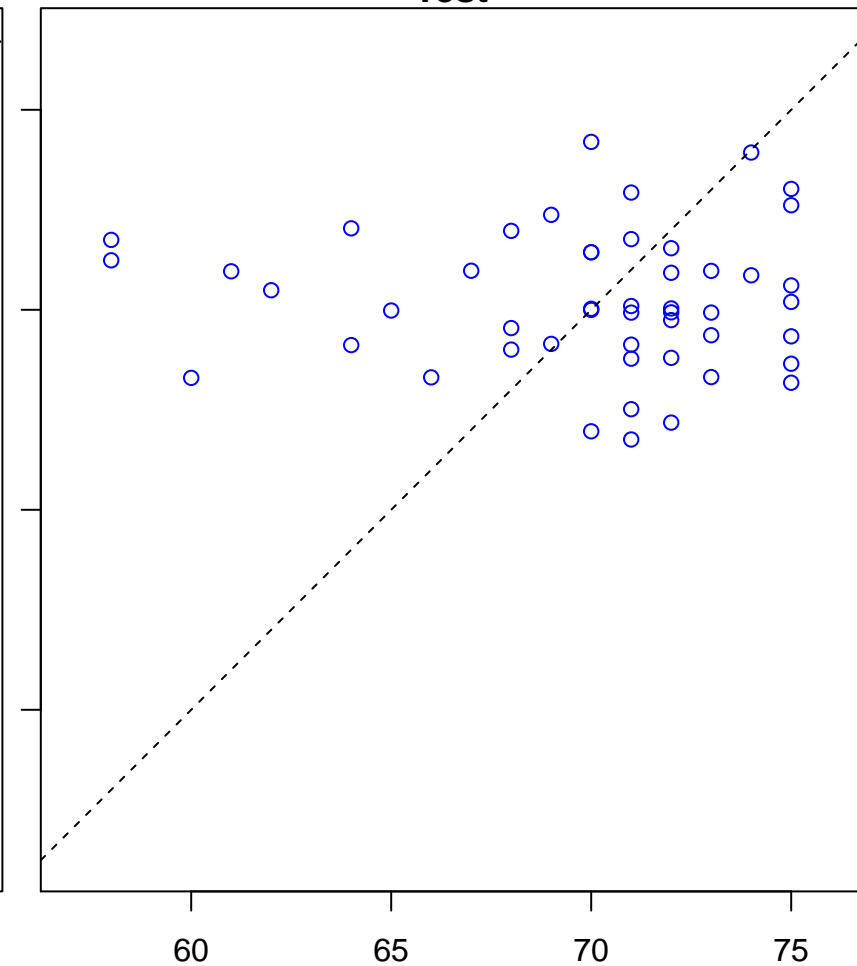


T-helper 17 cell lineage commitment (Score: 0.551276)

Control

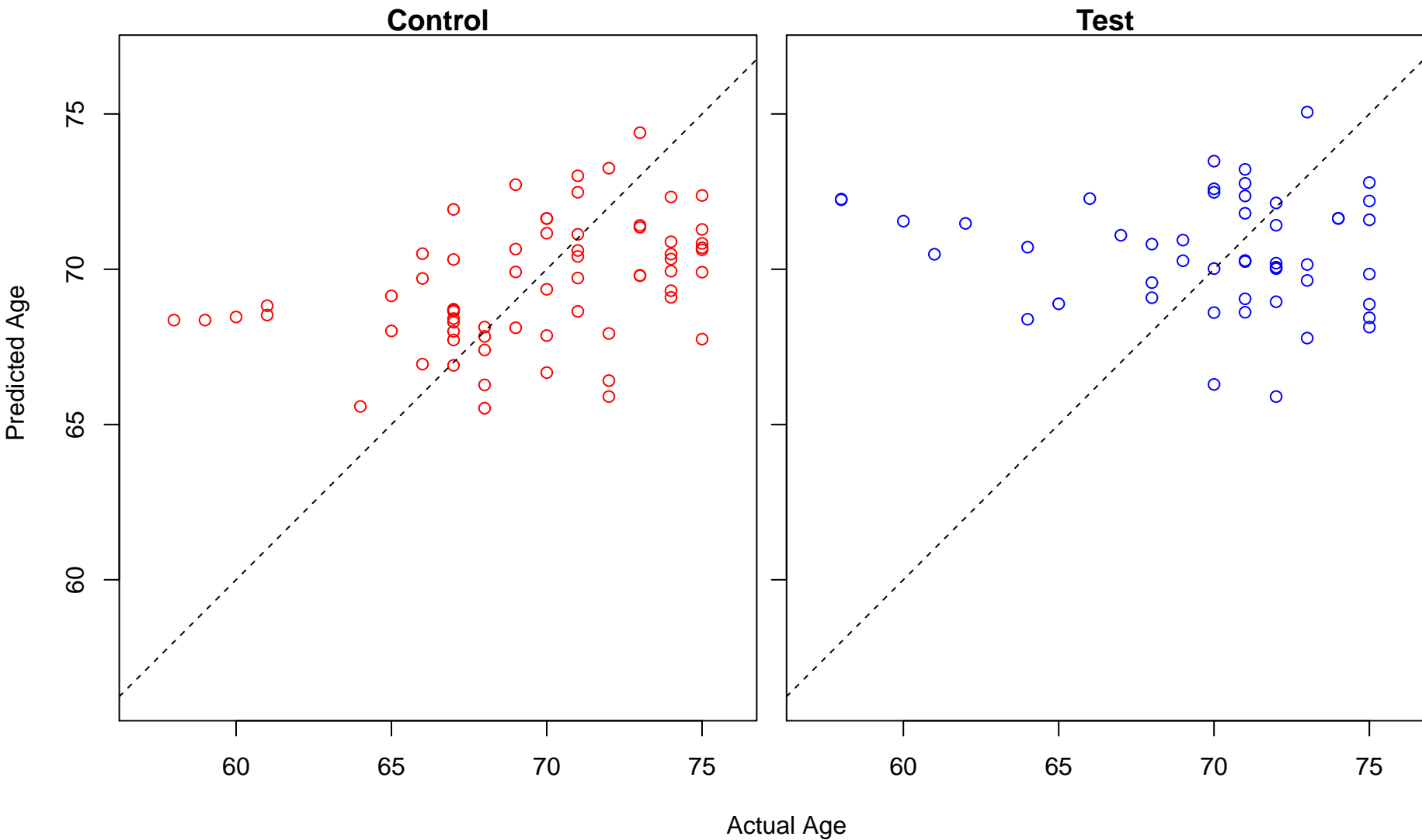


Test

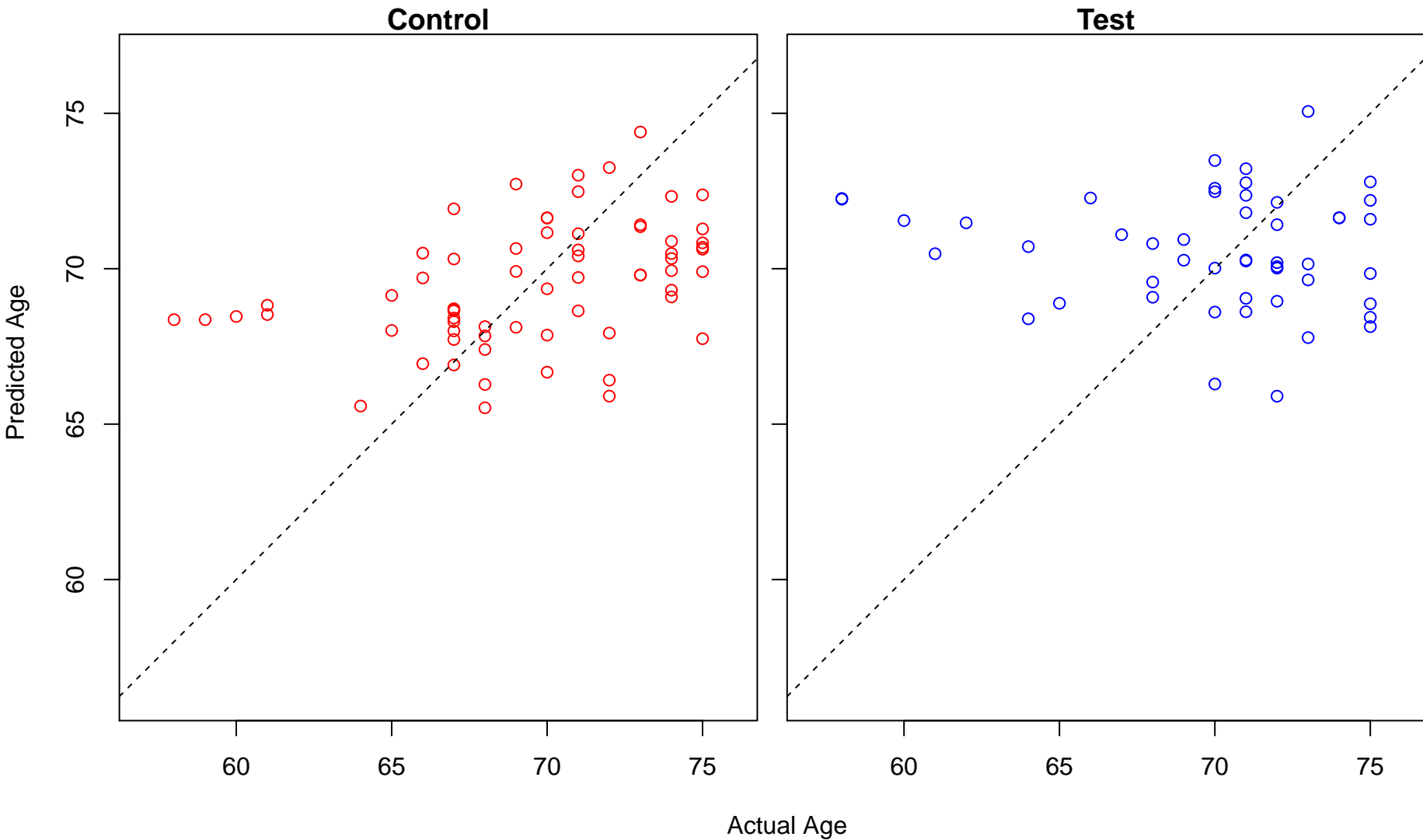


Actual Age

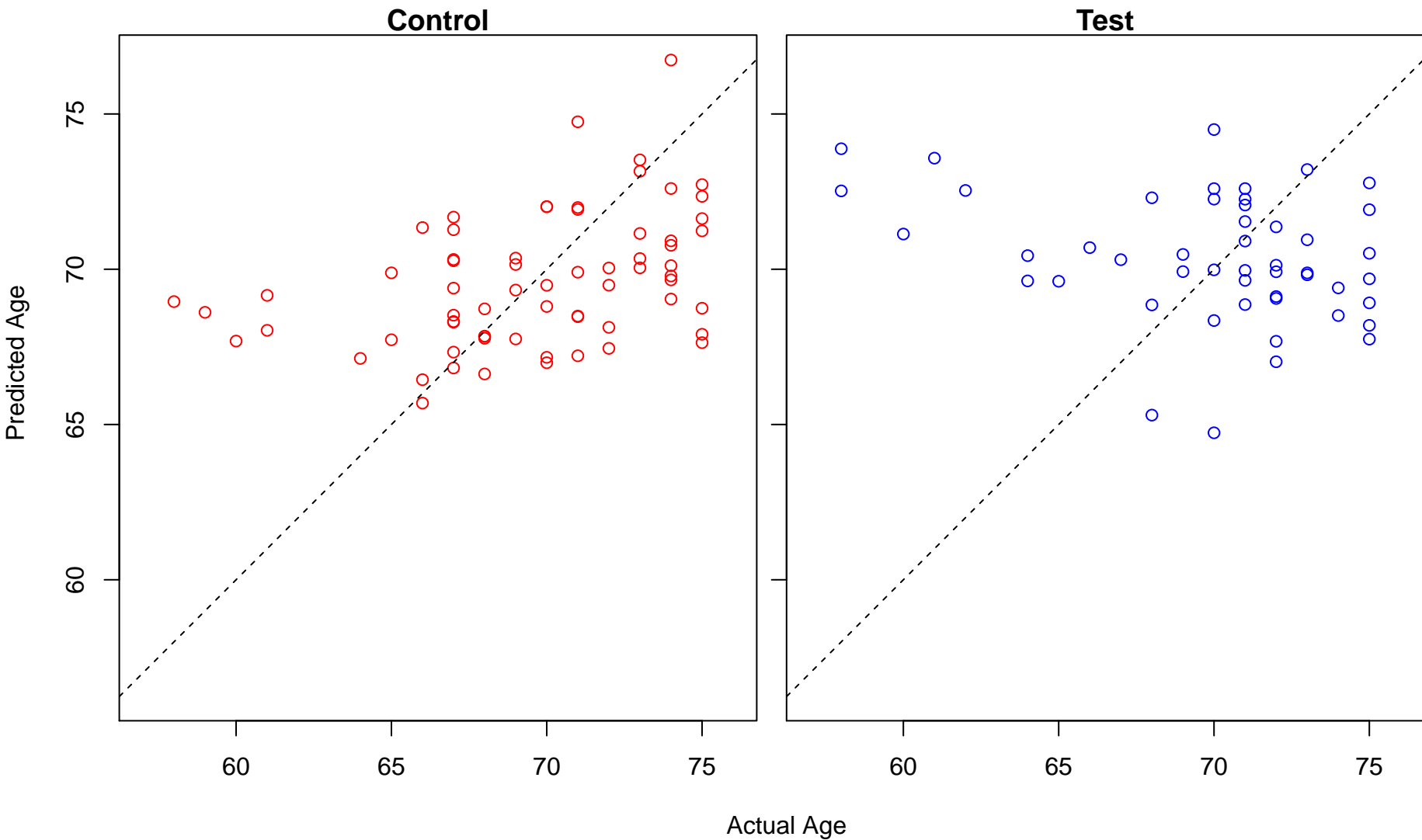
mesenchymal cell differentiation involved in kidney development (Score: 0.550546)



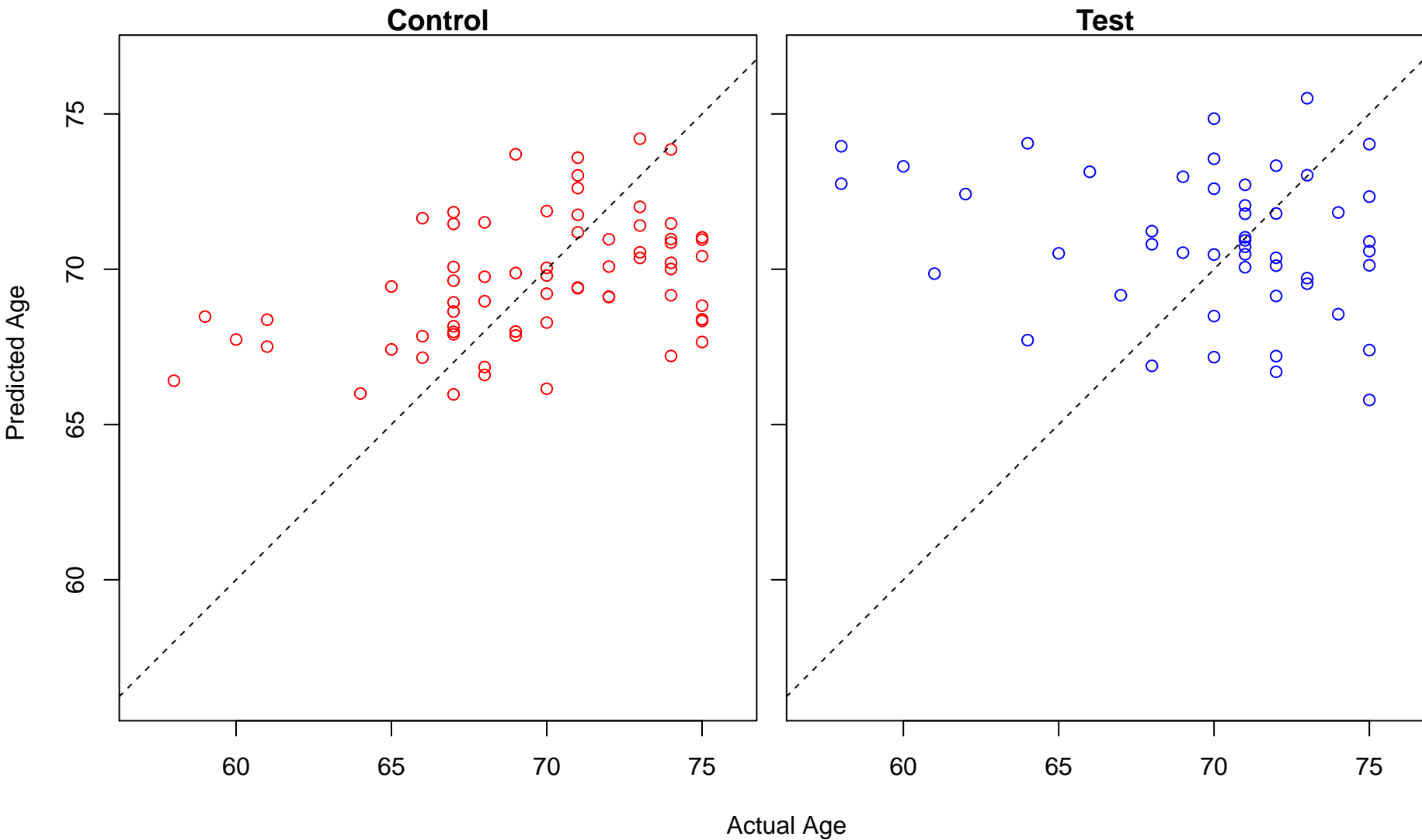
mesenchymal cell differentiation involved in renal system development (Score: 0.550546)



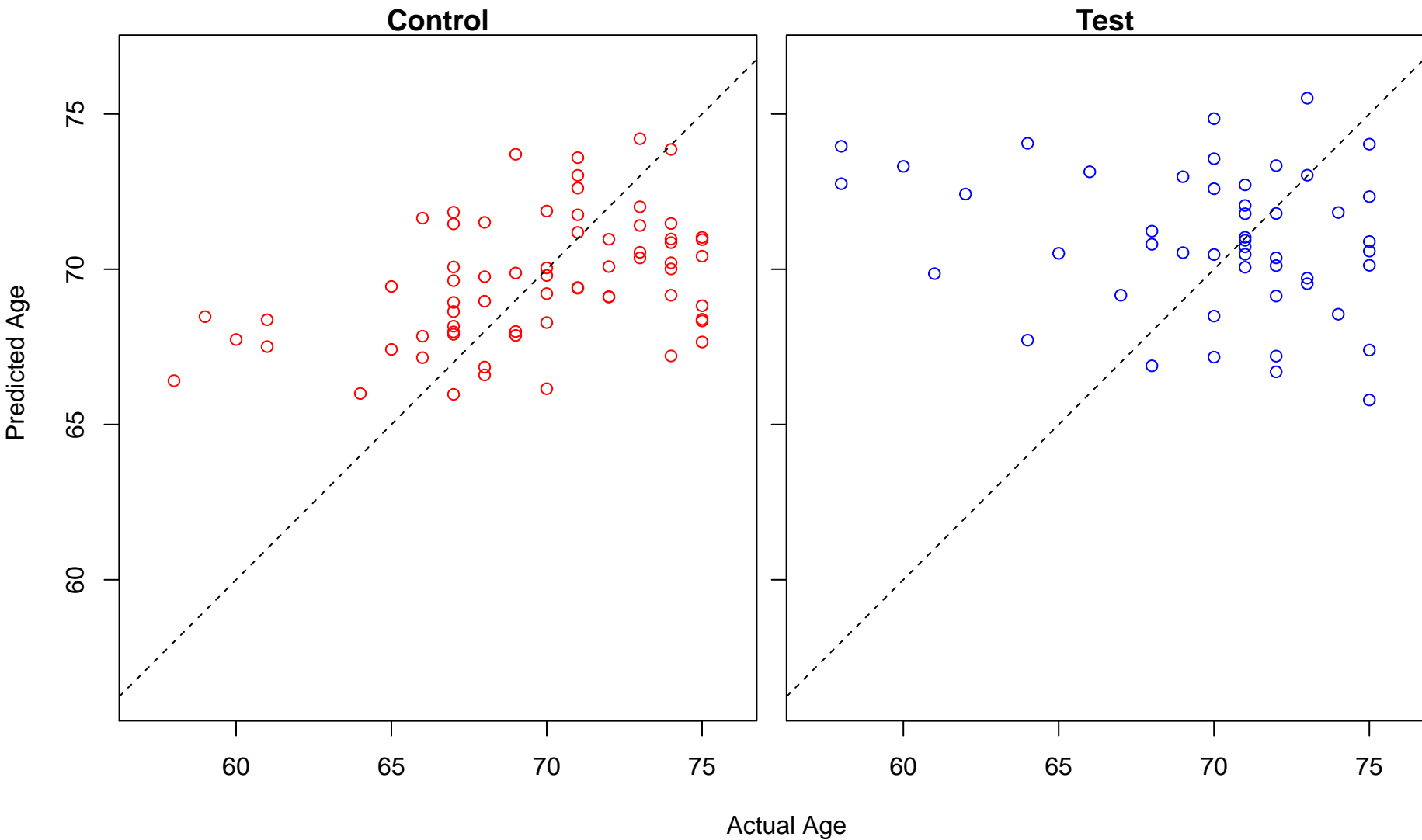
regulation of fibroblast growth factor receptor signaling pathway (Score: 0.550491)



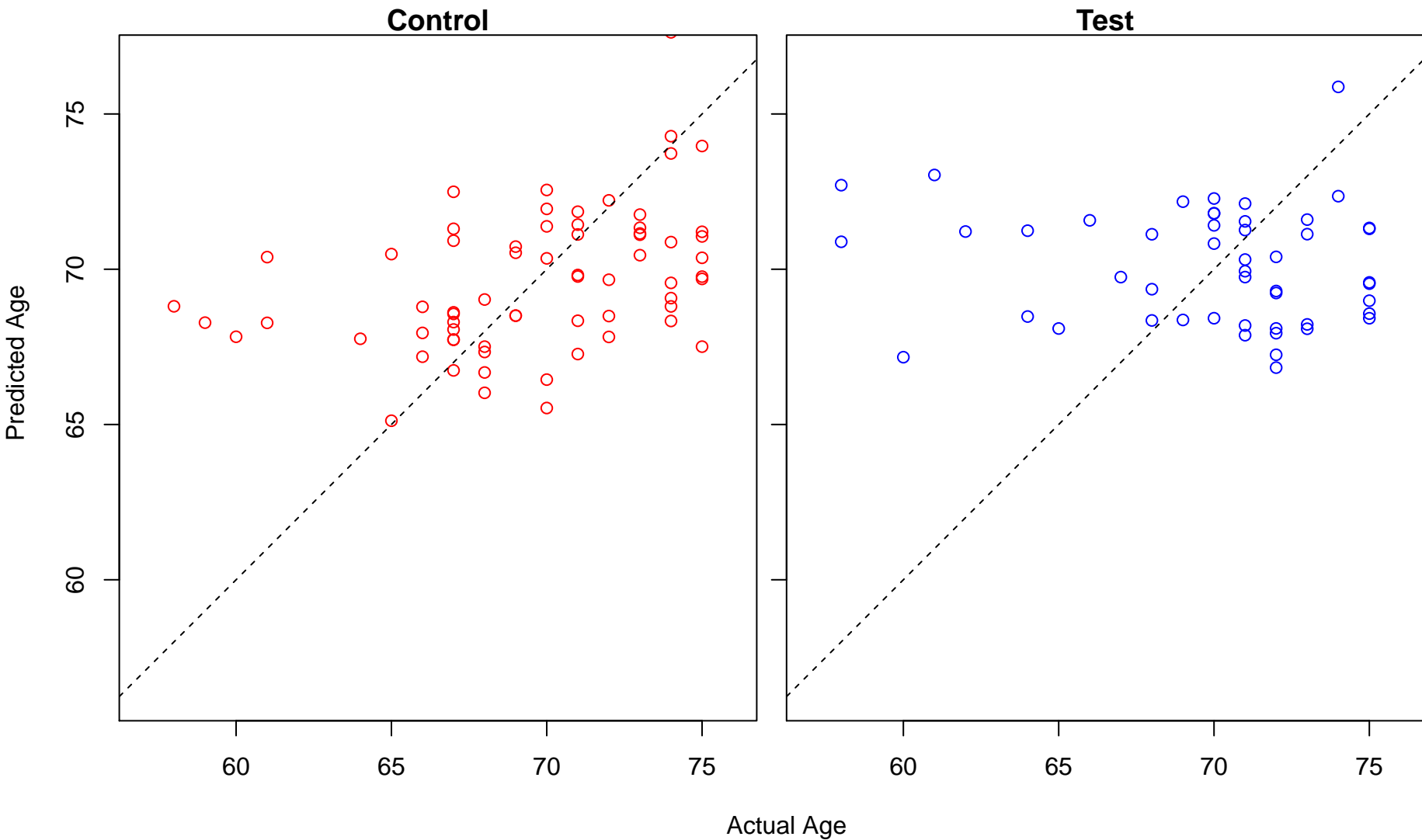
regulation of immature T cell proliferation (Score: 0.547896)



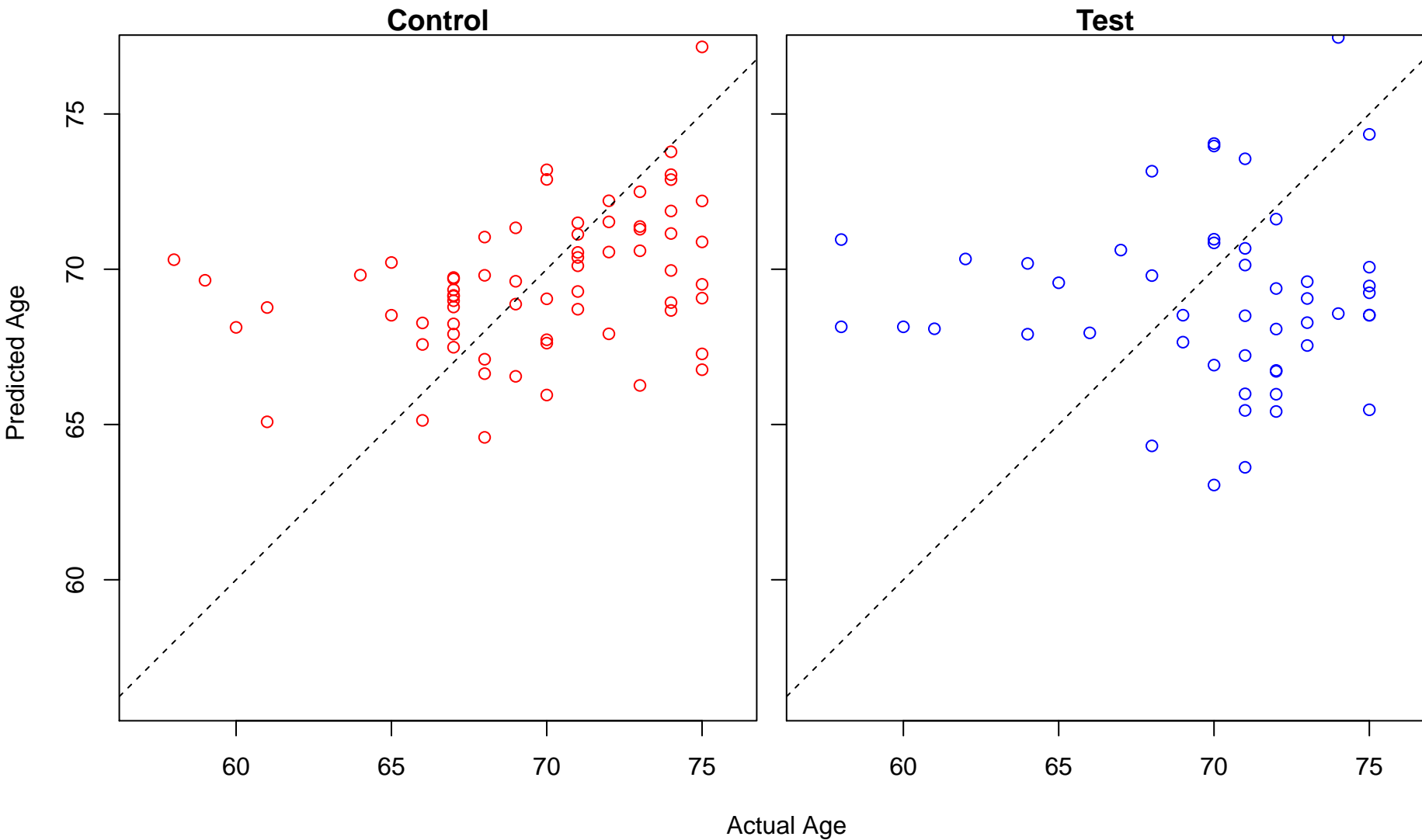
regulation of immature T cell proliferation in thymus (Score: 0.547896)



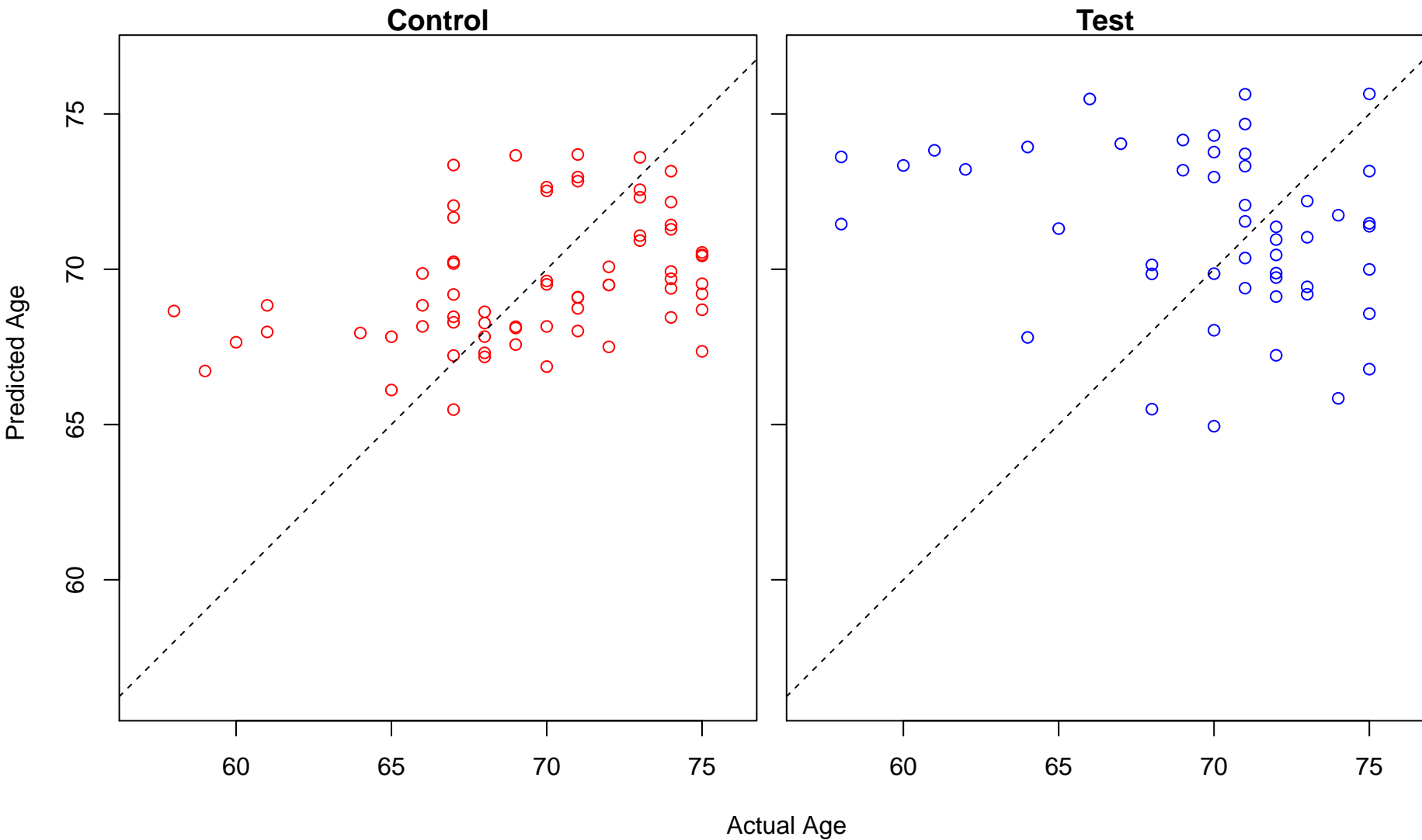
regulation of interleukin-6 biosynthetic process (Score: 0.547531)



negative regulation of androgen receptor signaling pathway (Score: 0.547188)

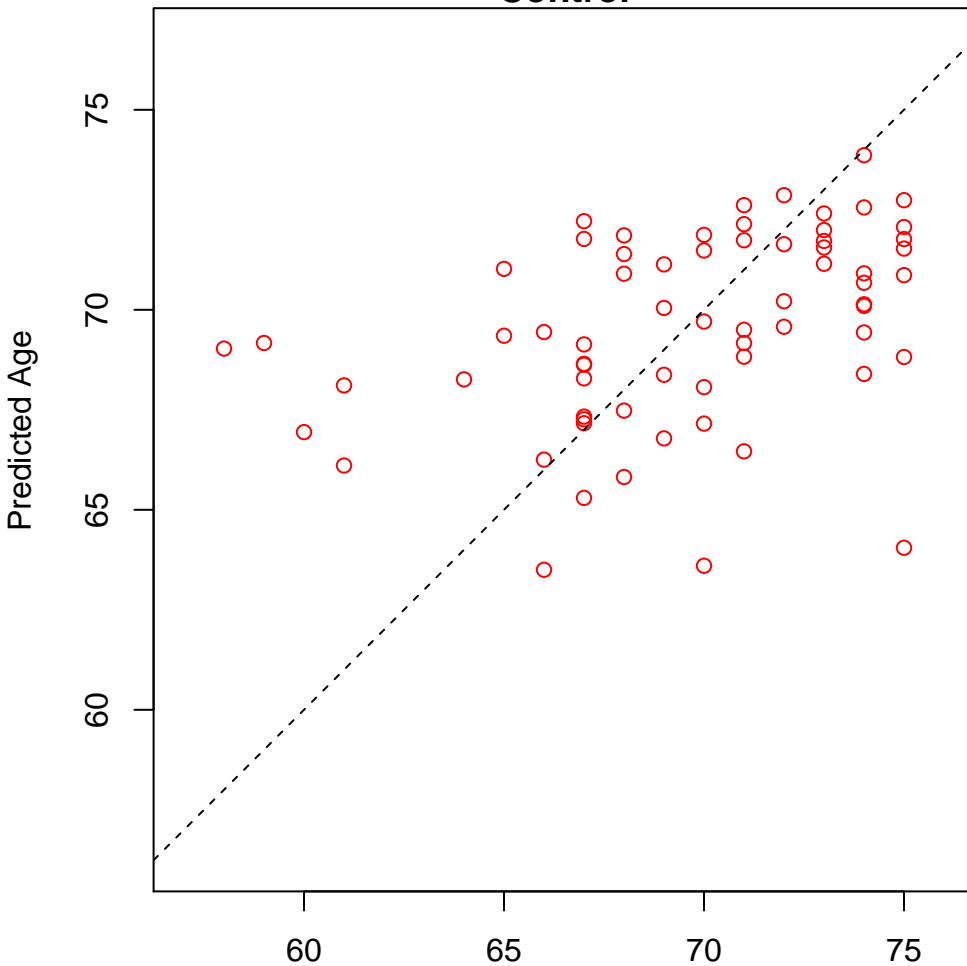


establishment of protein localization to chromatin (Score: 0.547175)

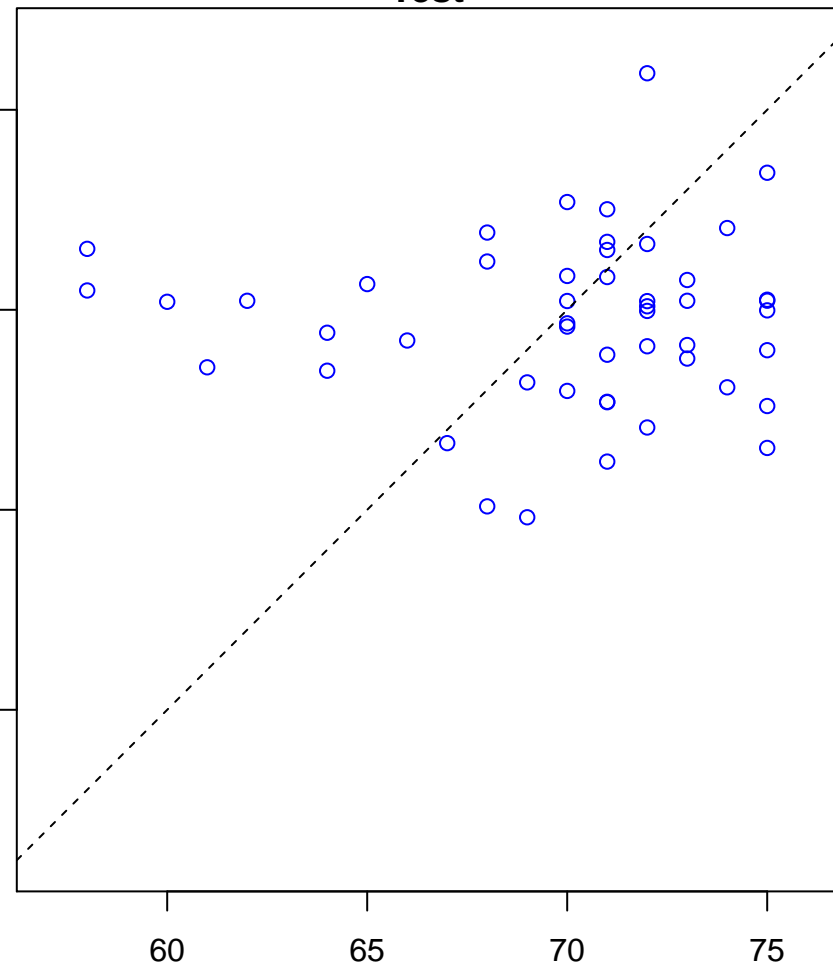


cellular potassium ion homeostasis (Score: 0.546907)

Control



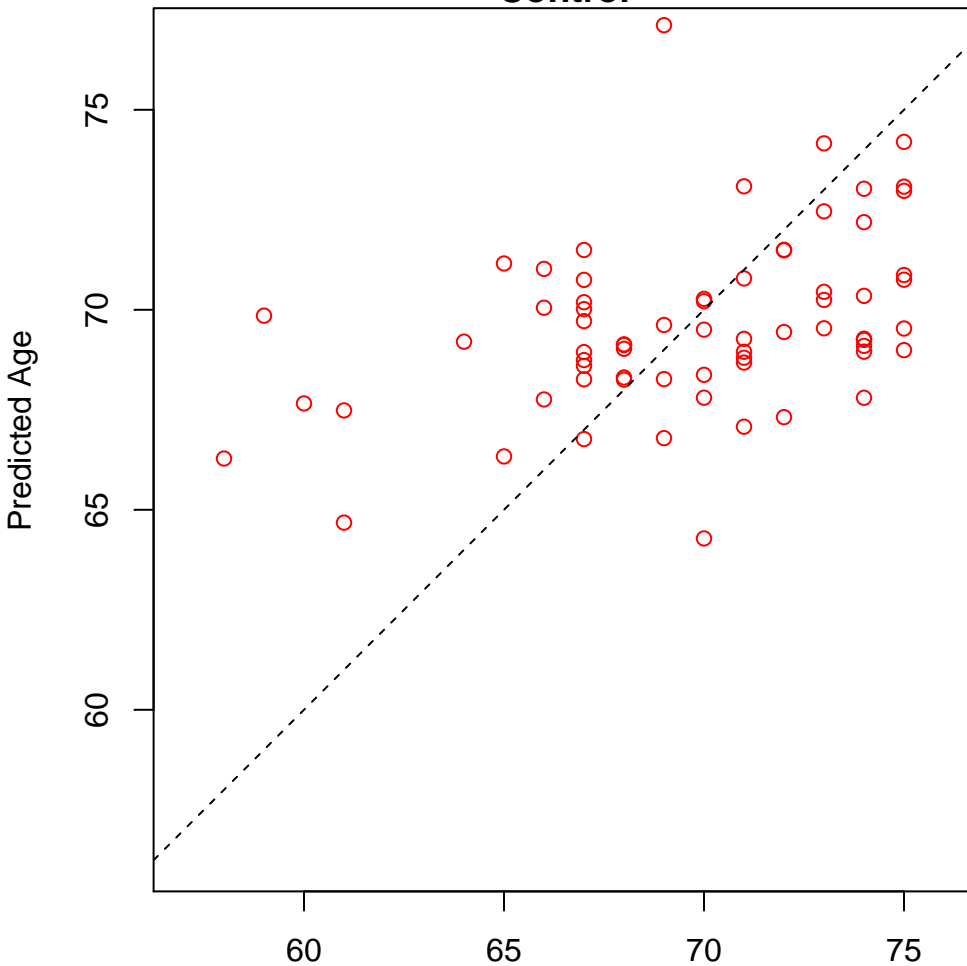
Test



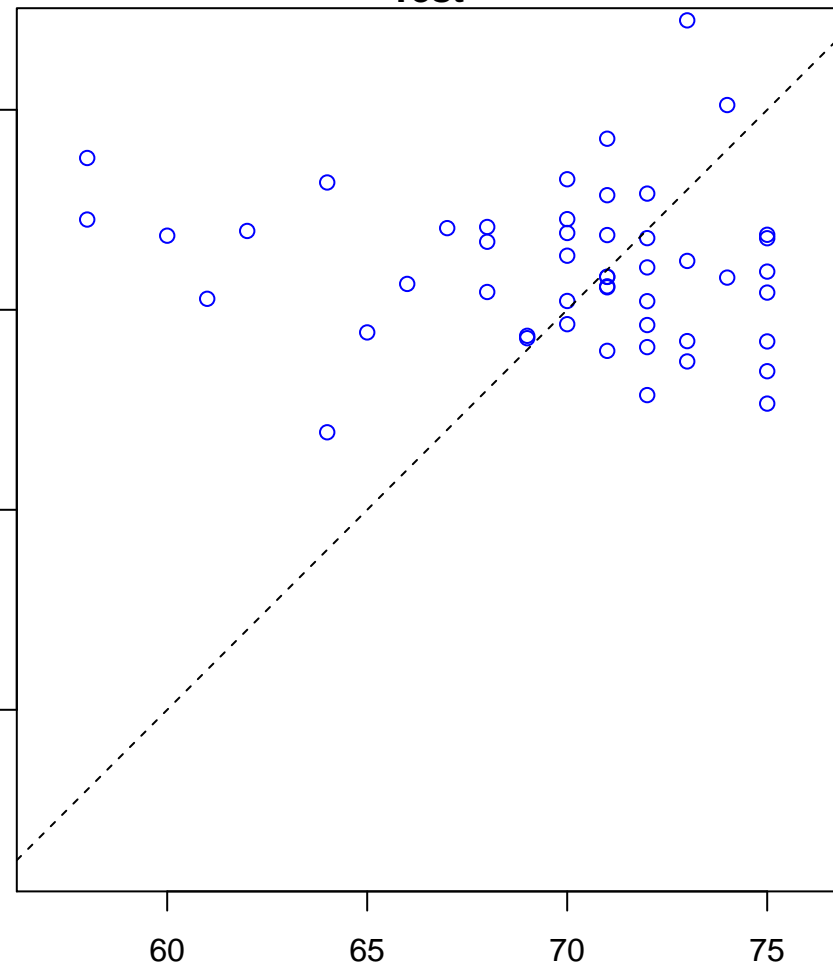
Actual Age

regulation of receptor catabolic process (Score: 0.546826)

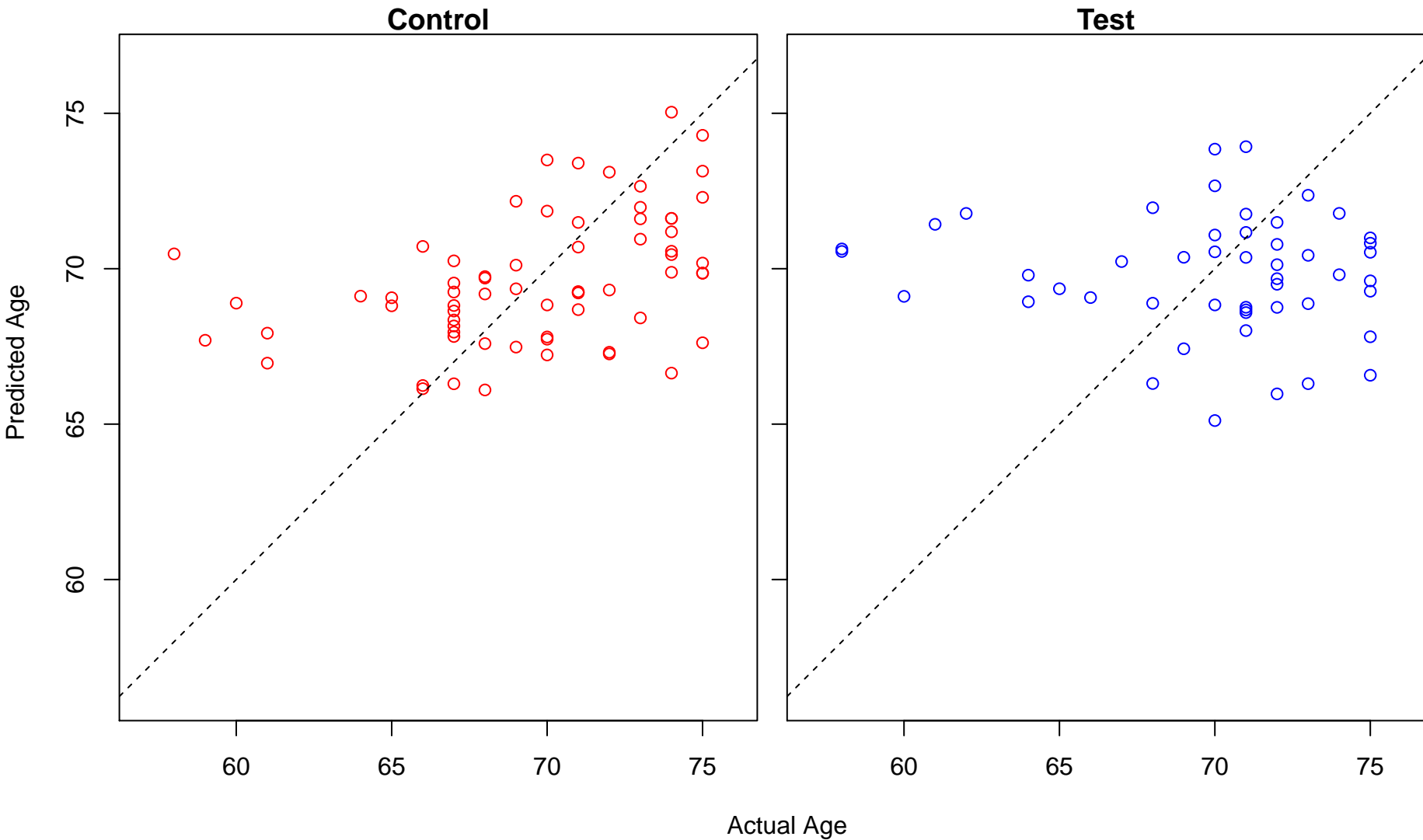
Control



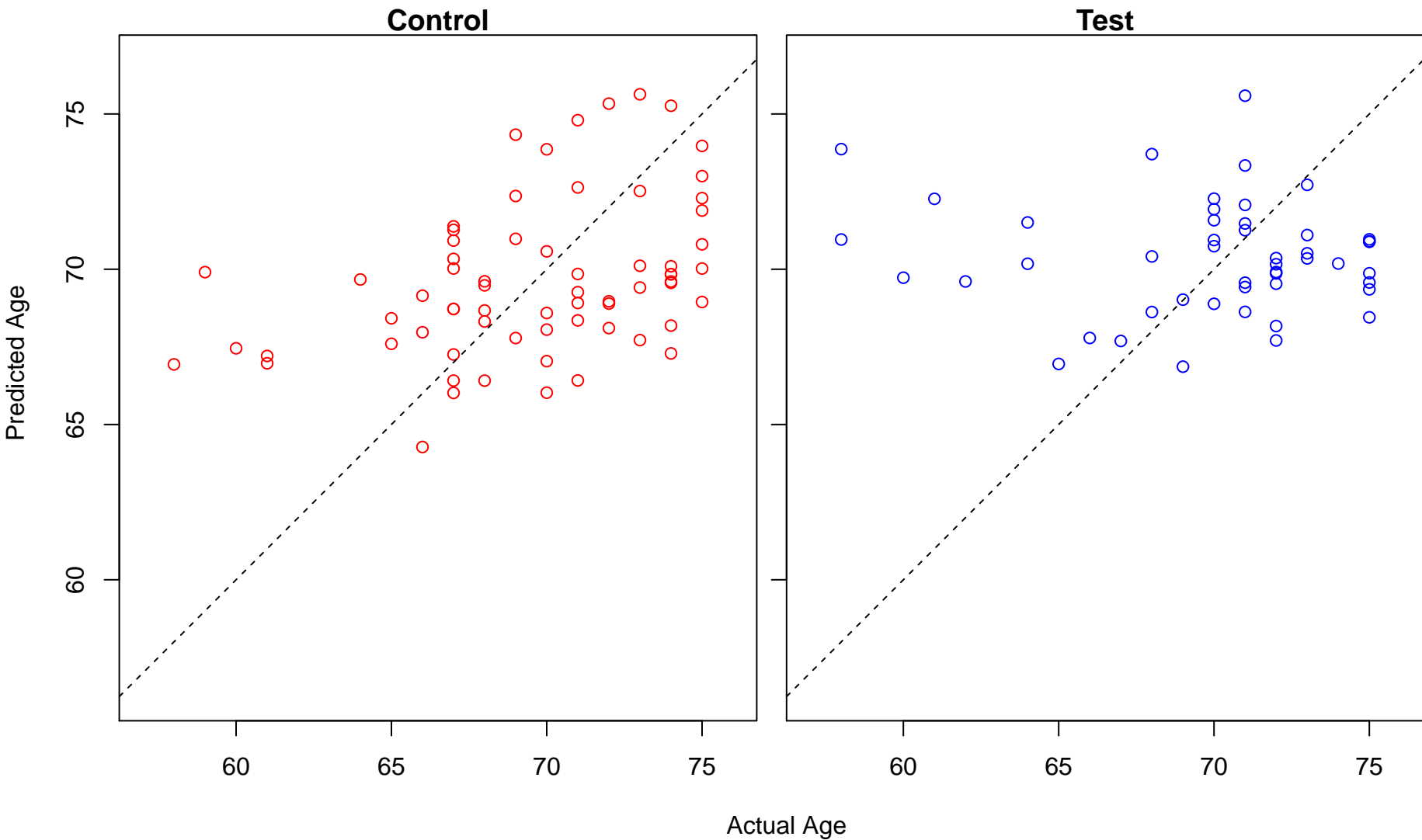
Test



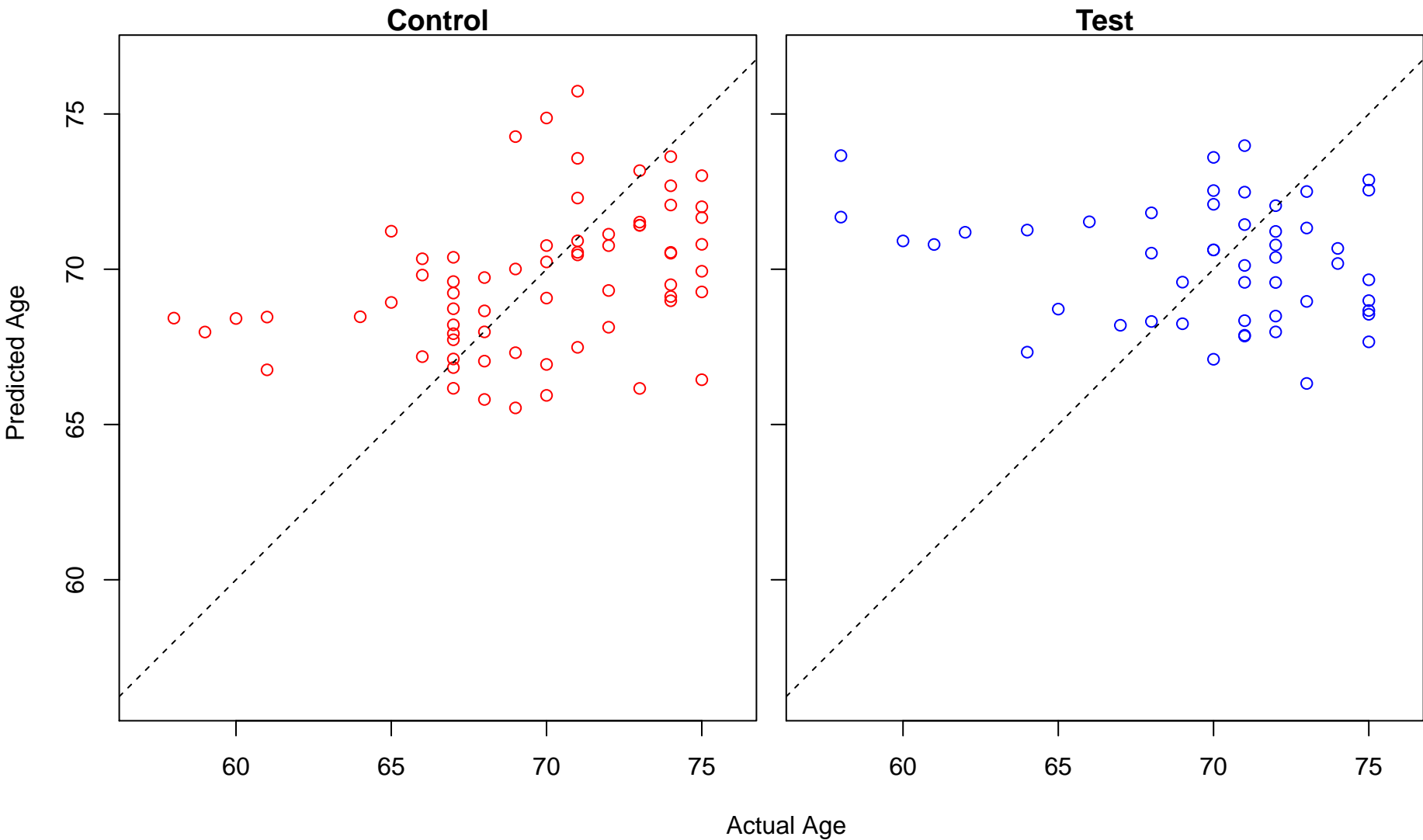
positive regulation of blood vessel endothelial cell migration (Score: 0.545927)



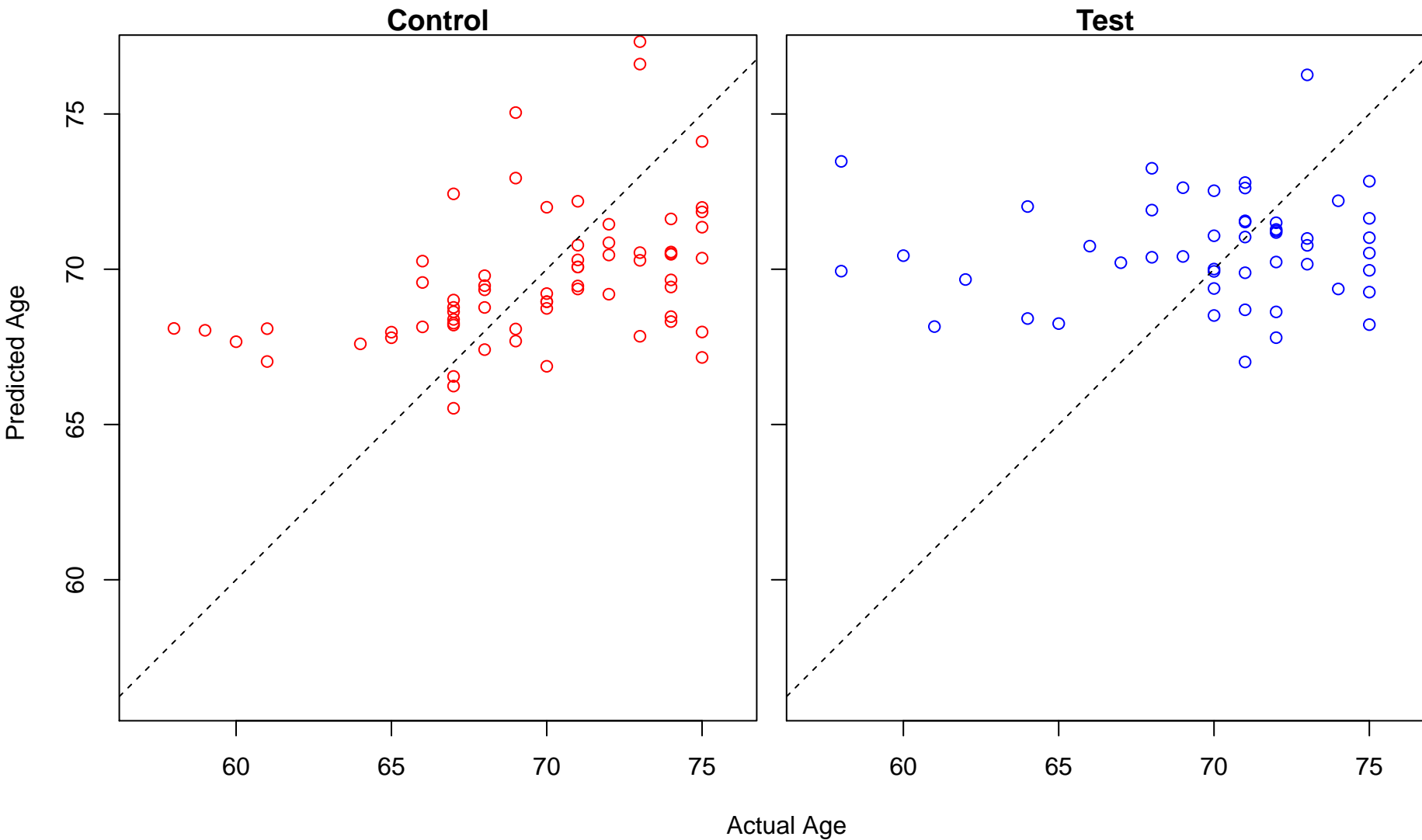
myeloid cell development (Score: 0.544216)



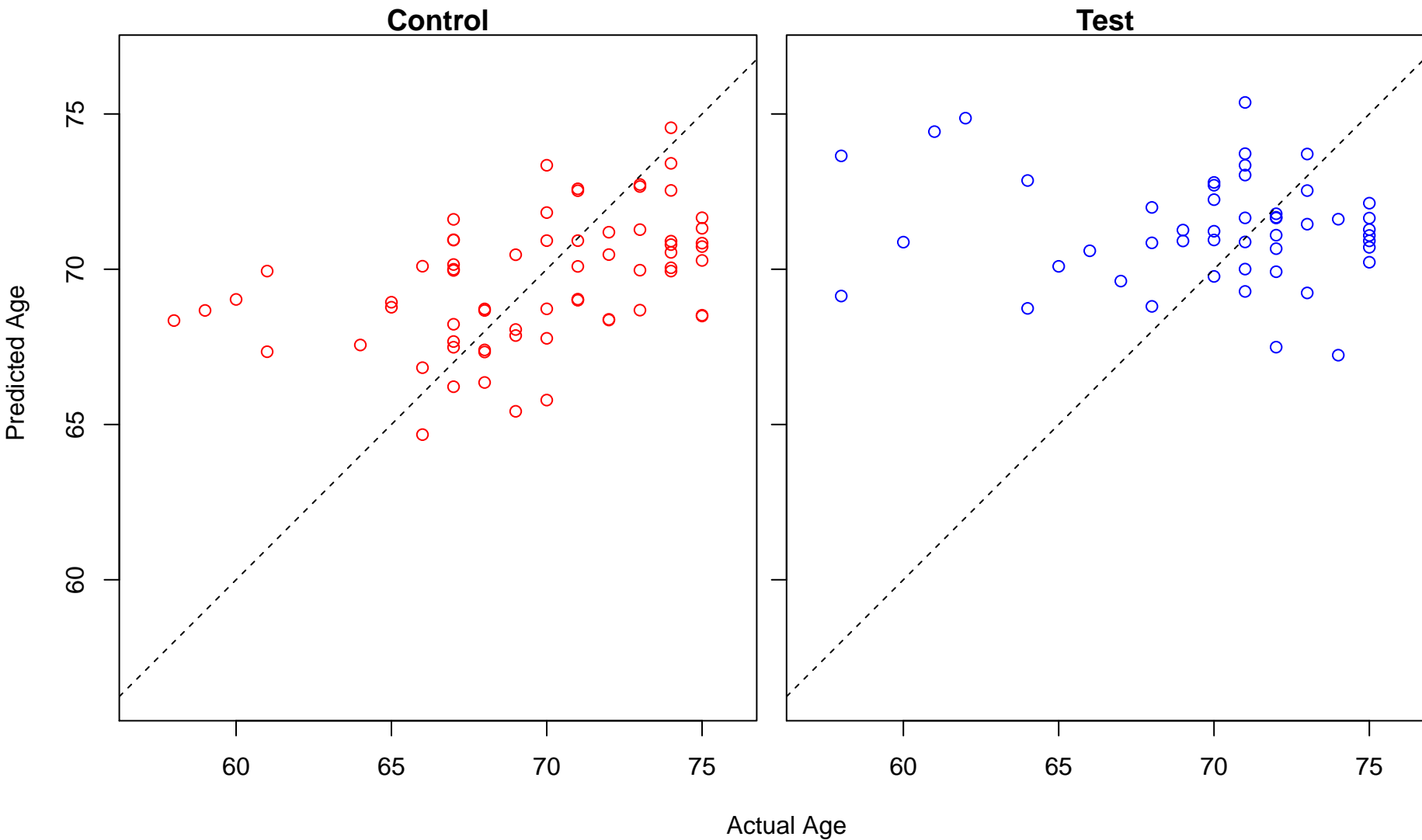
regulation of peroxisome proliferator activated receptor signaling pathway (Score: 0.543932)



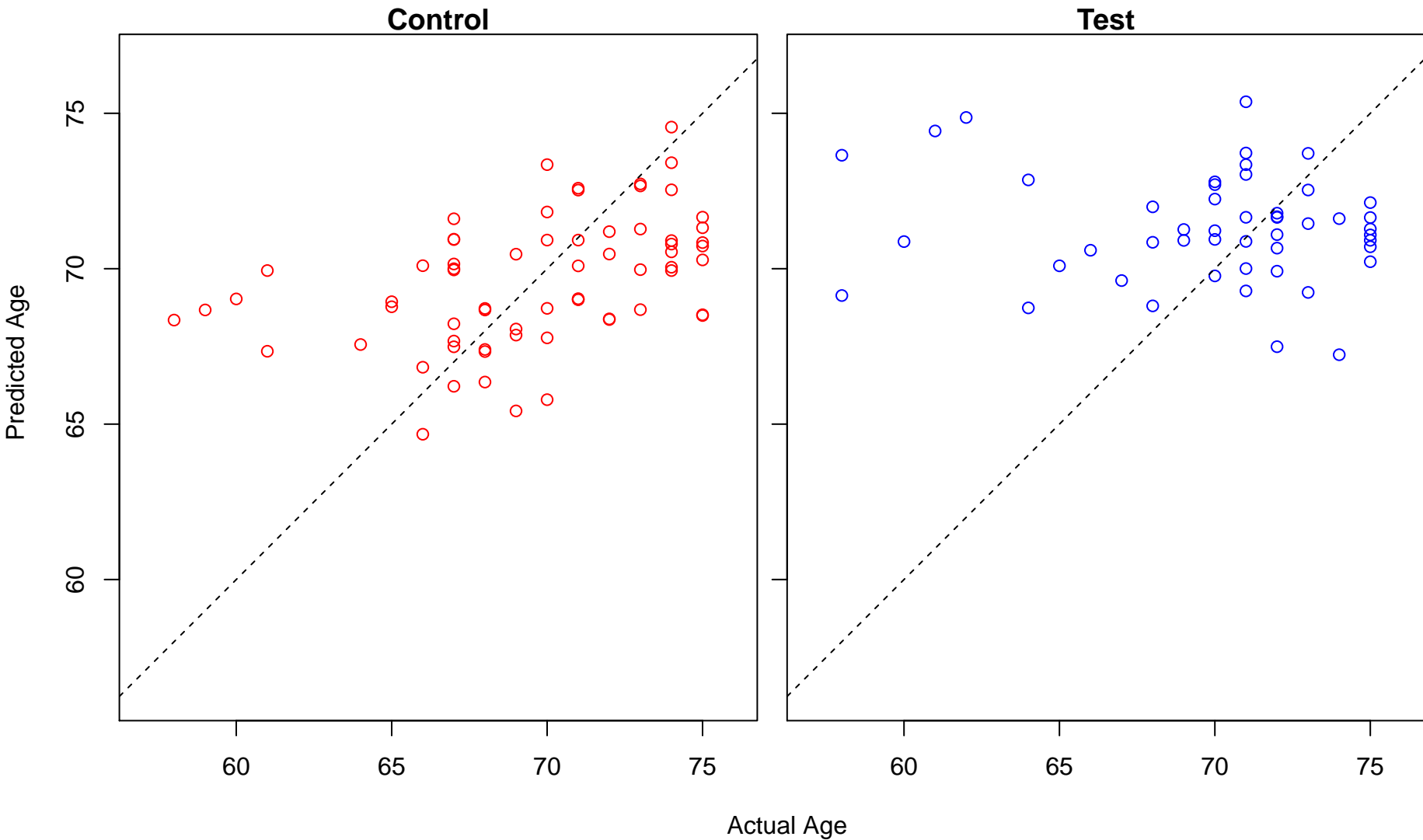
metanephric nephron morphogenesis (Score: 0.542968)



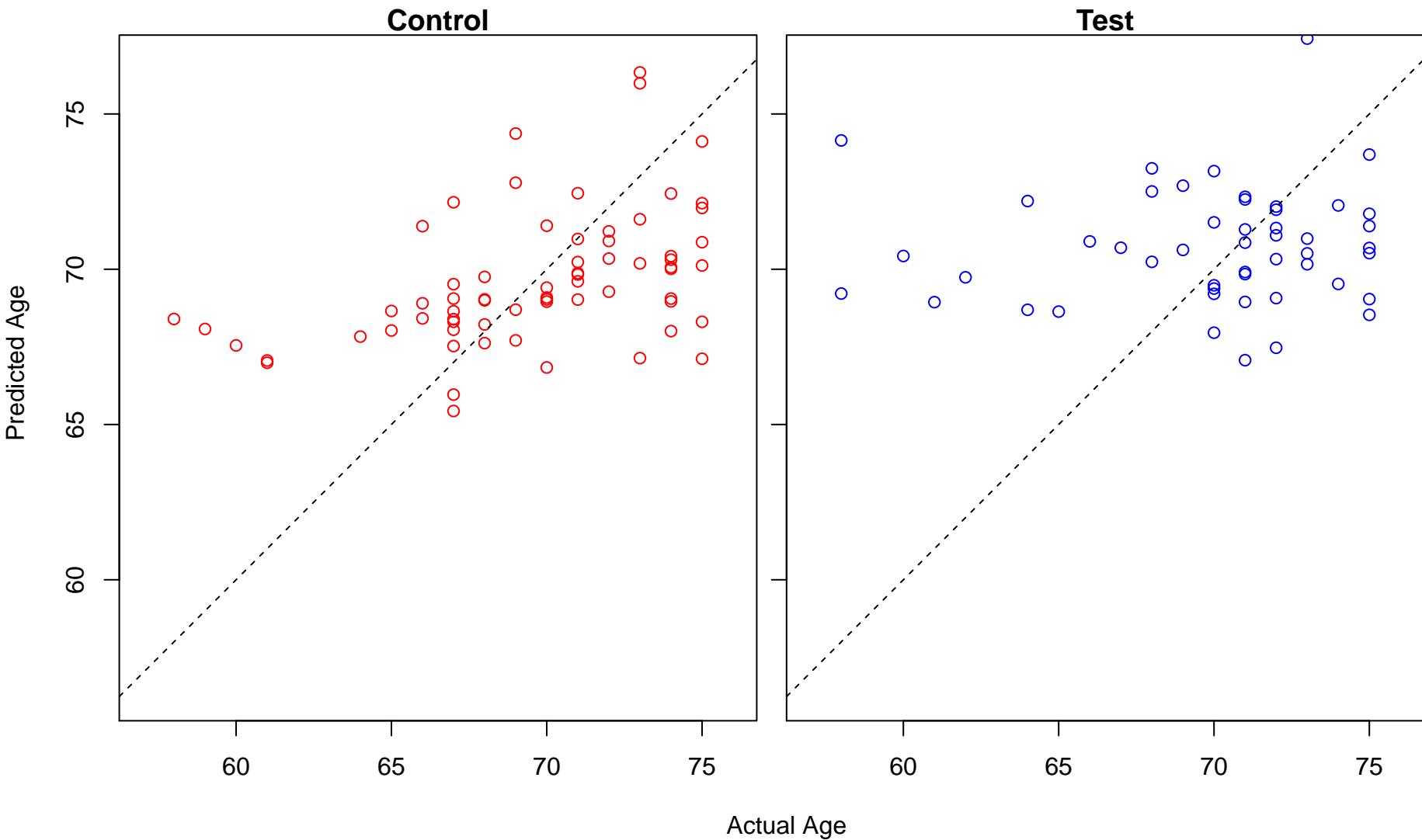
negative regulation of sodium ion transport (Score: 0.542936)



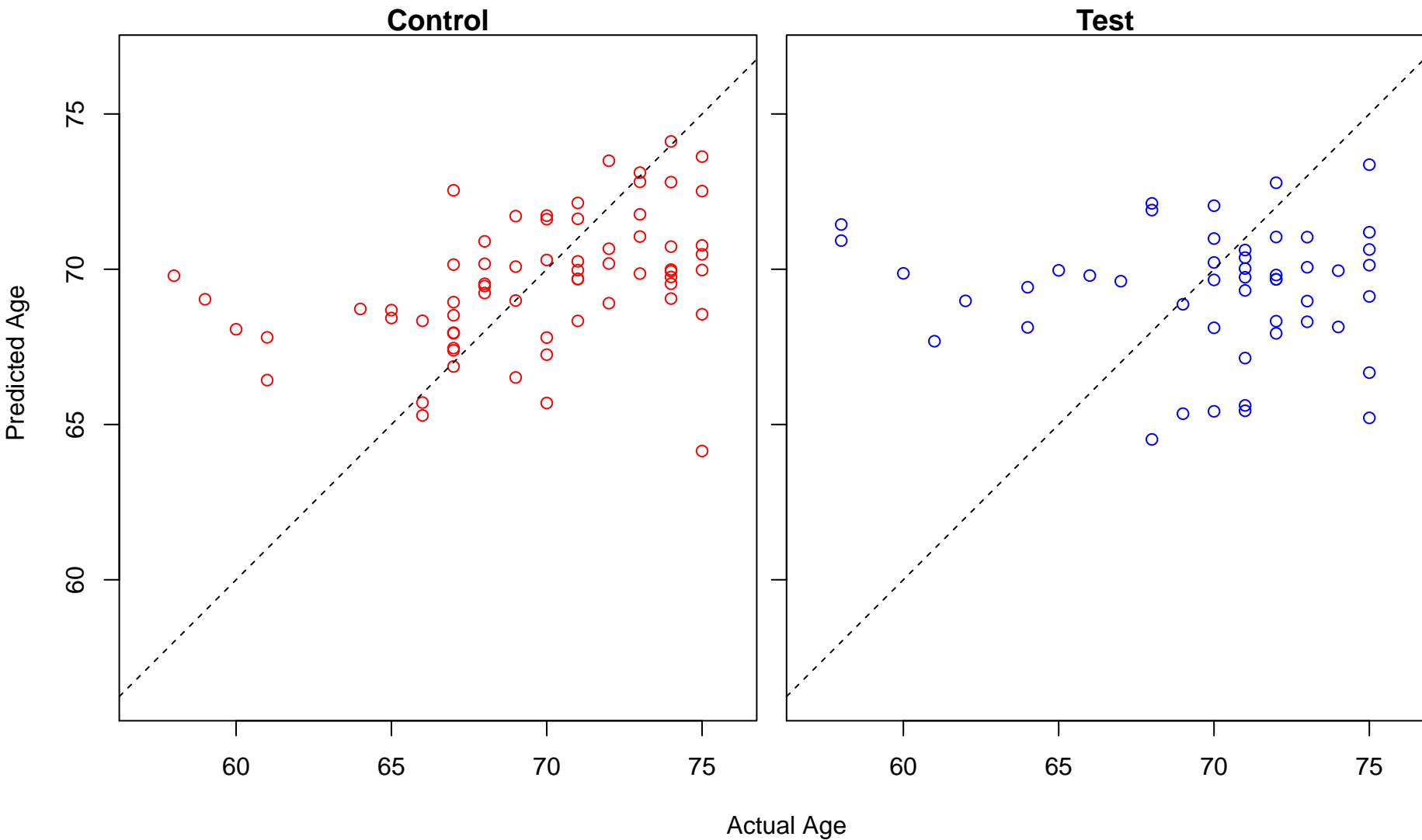
negative regulation of sodium ion transmembrane transport (Score: 0.542936)



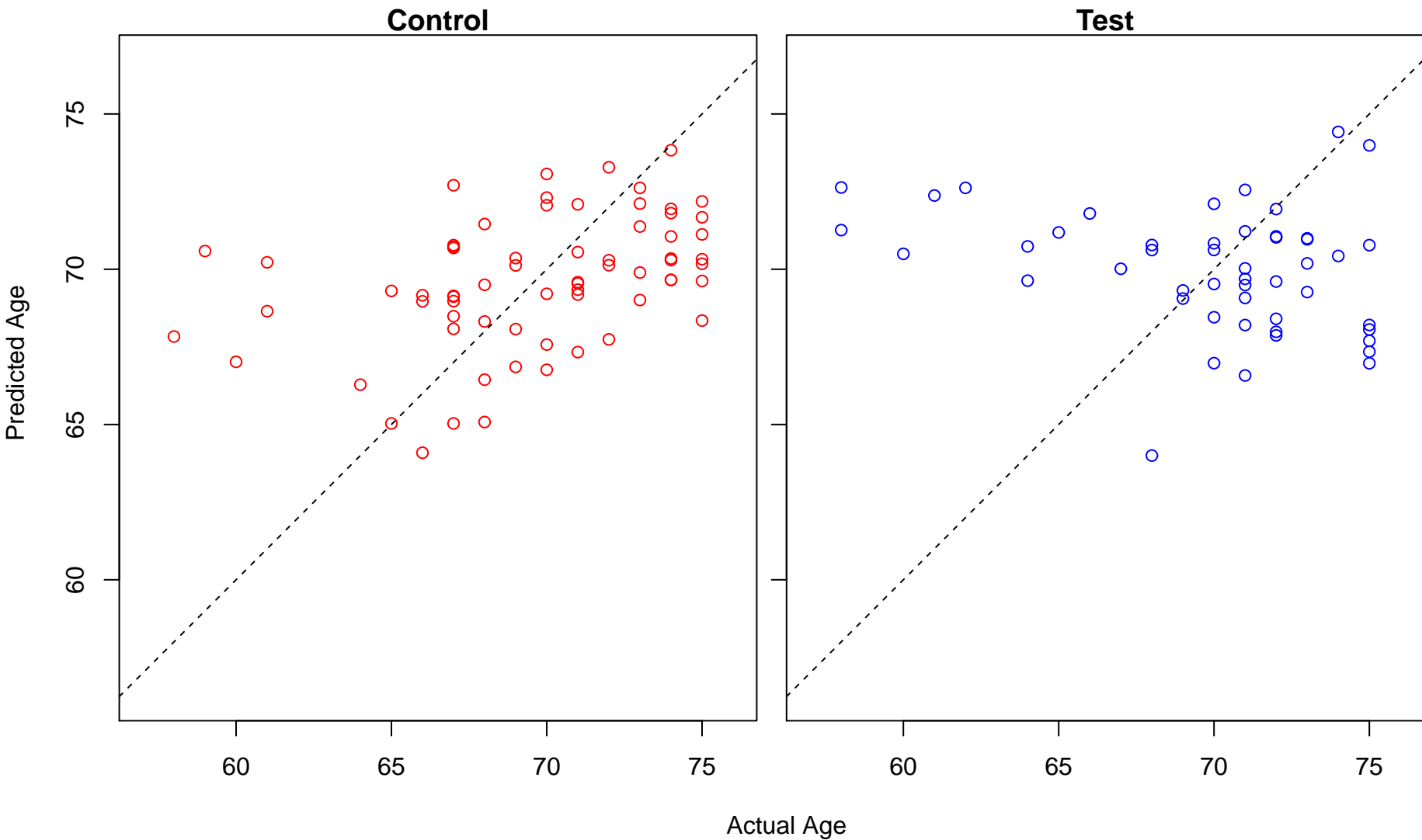
lung epithelium development (Score: 0.542911)



cell communication by electrical coupling (Score: 0.542650)

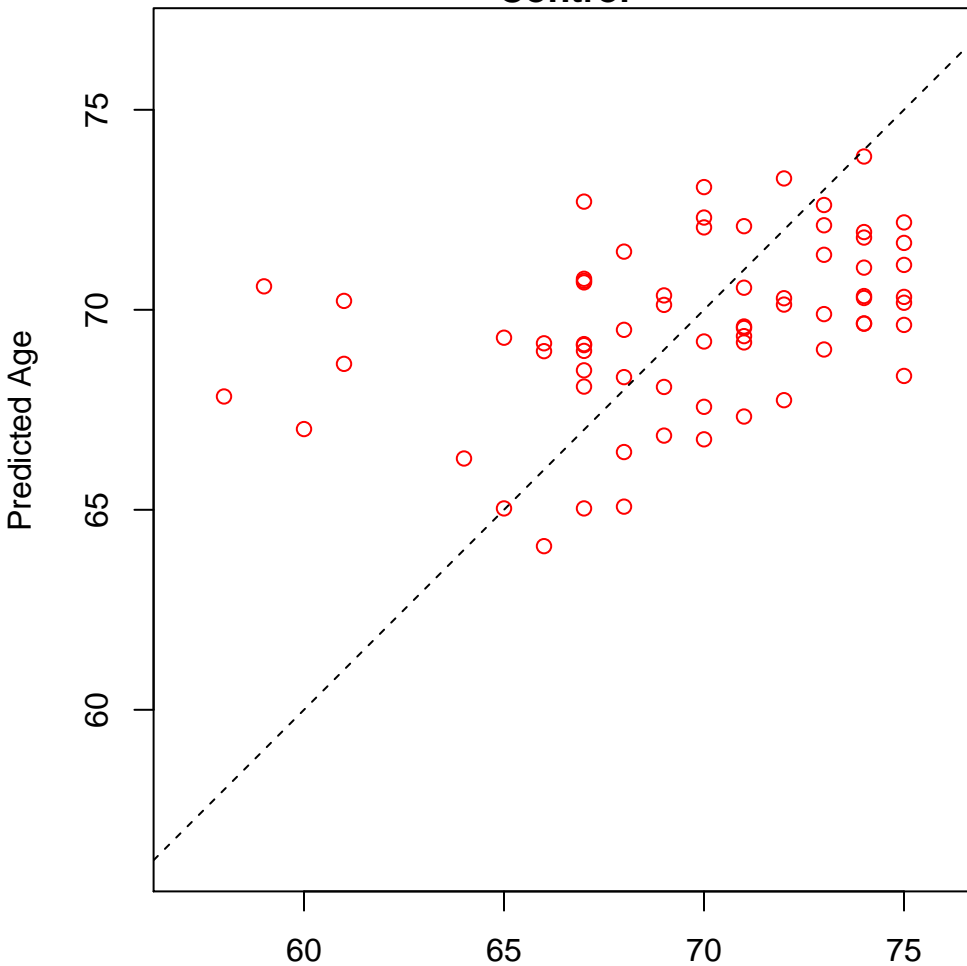


protein demannosylation (Score: 0.542594)

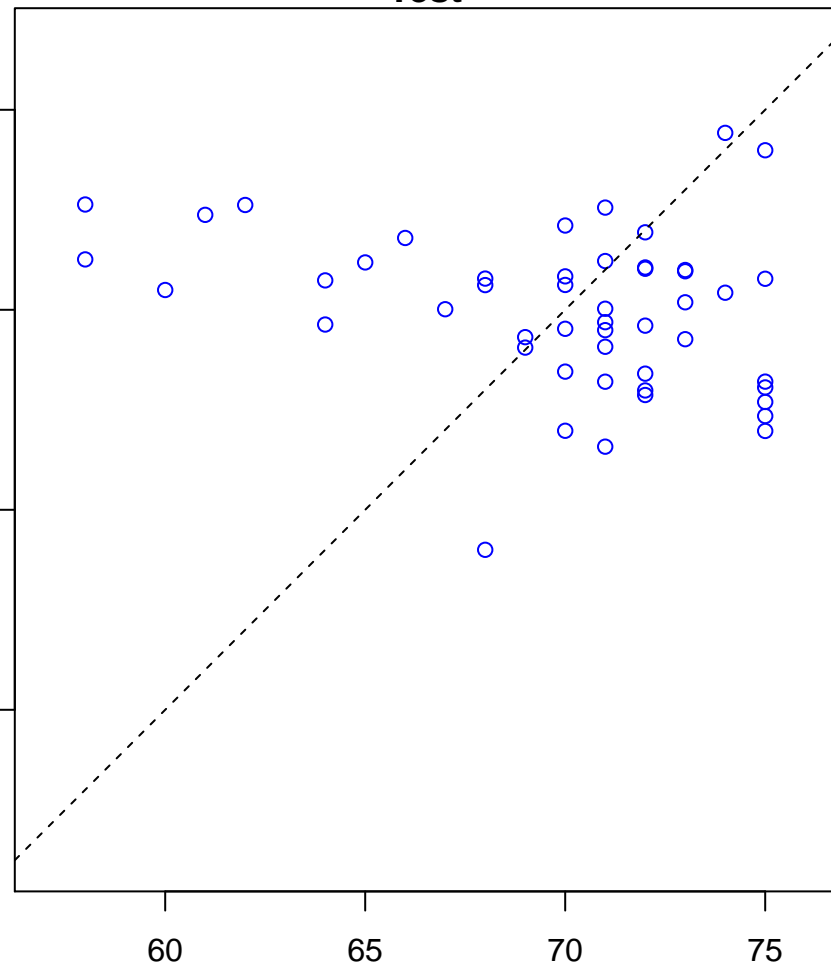


protein alpha-1,2-demannosylation (Score: 0.542594)

Control

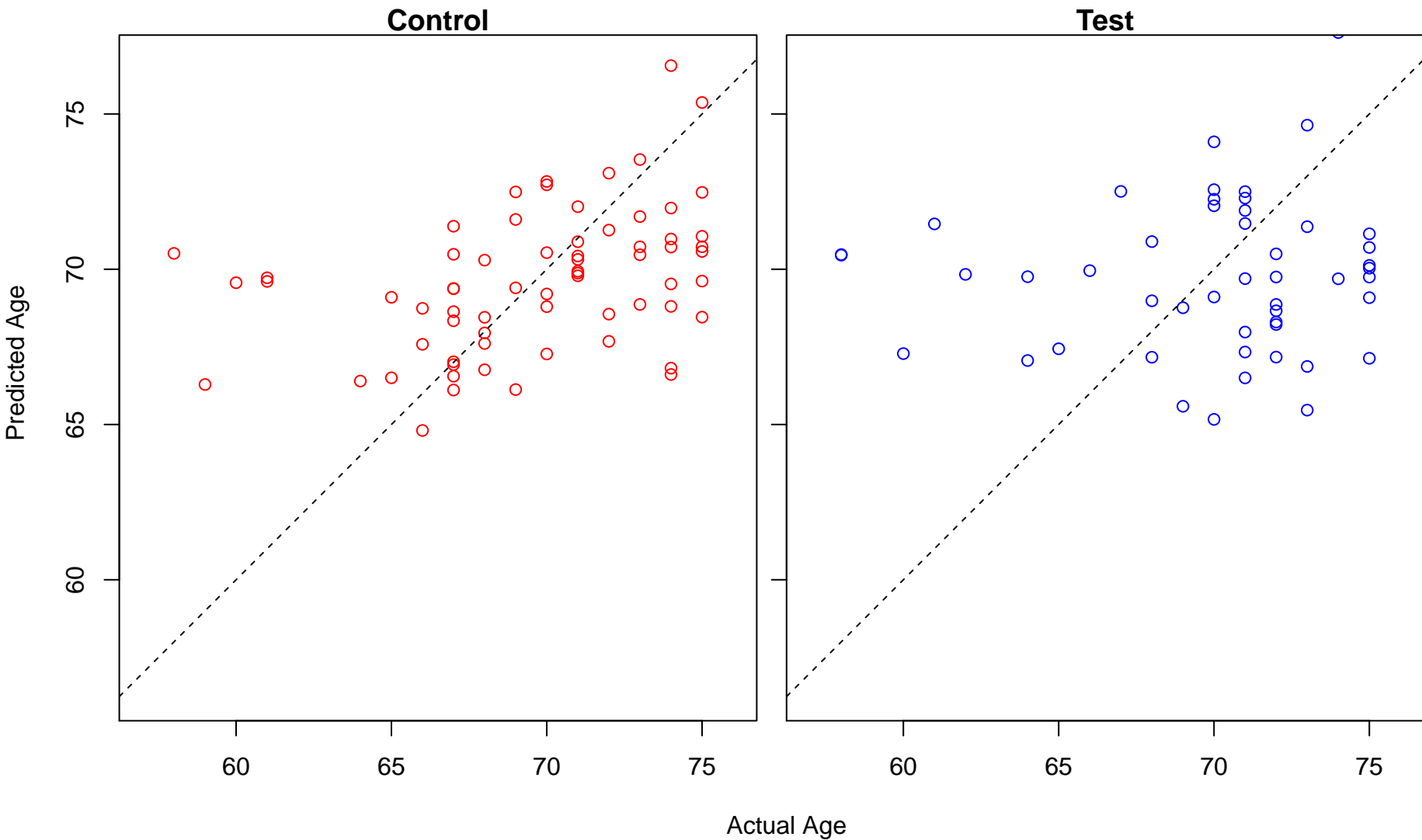


Test

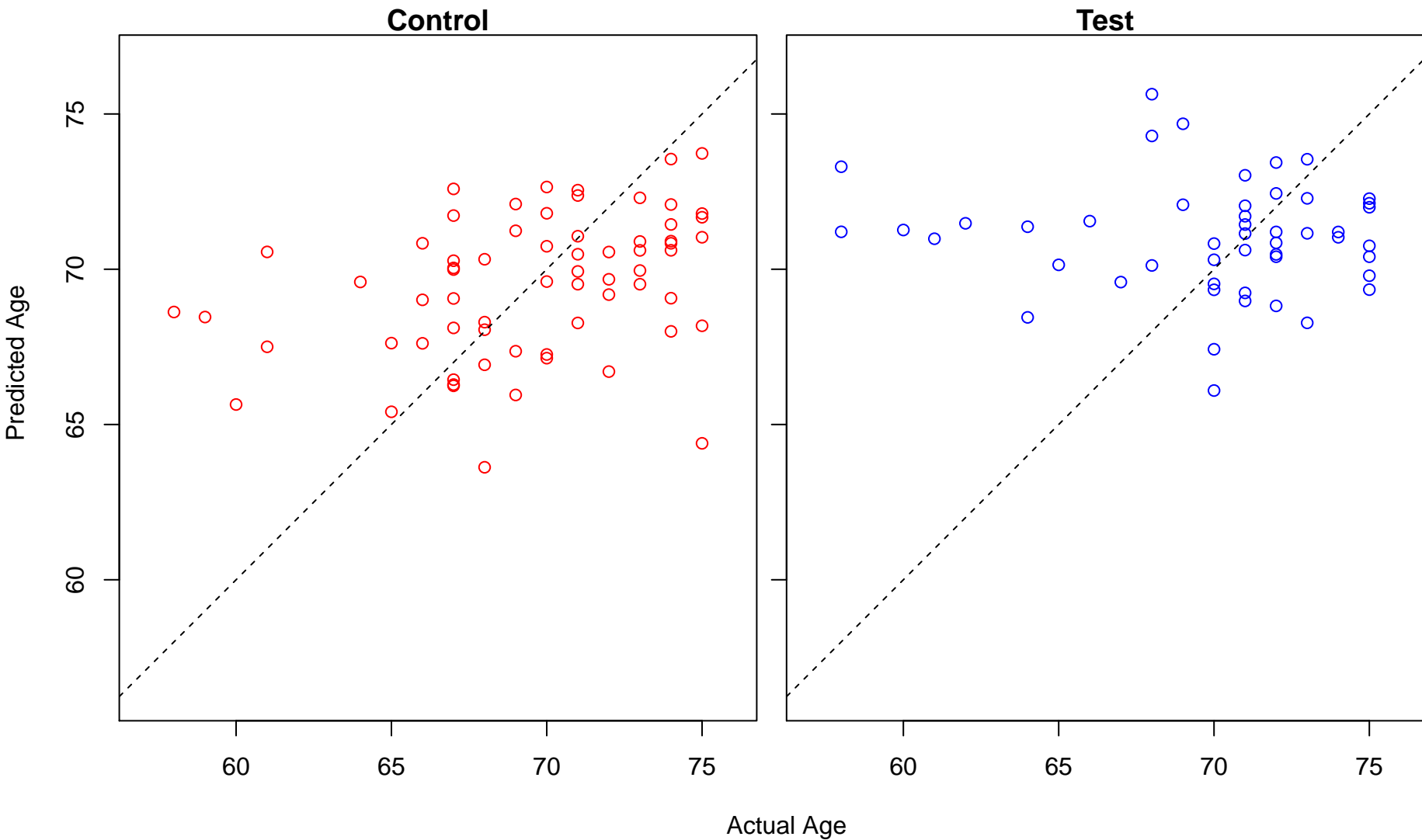


Actual Age

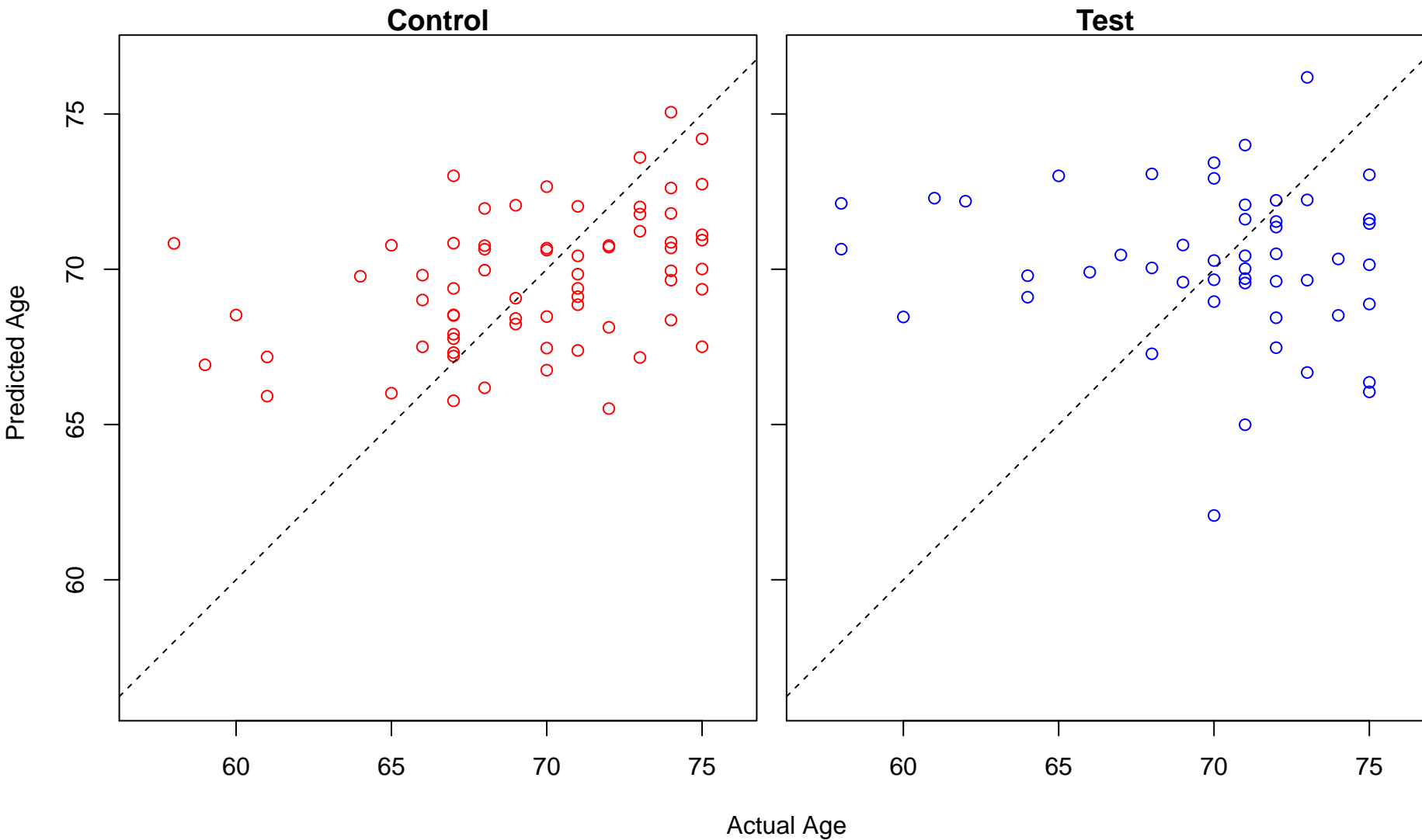
hormone transport (Score: 0.541247)



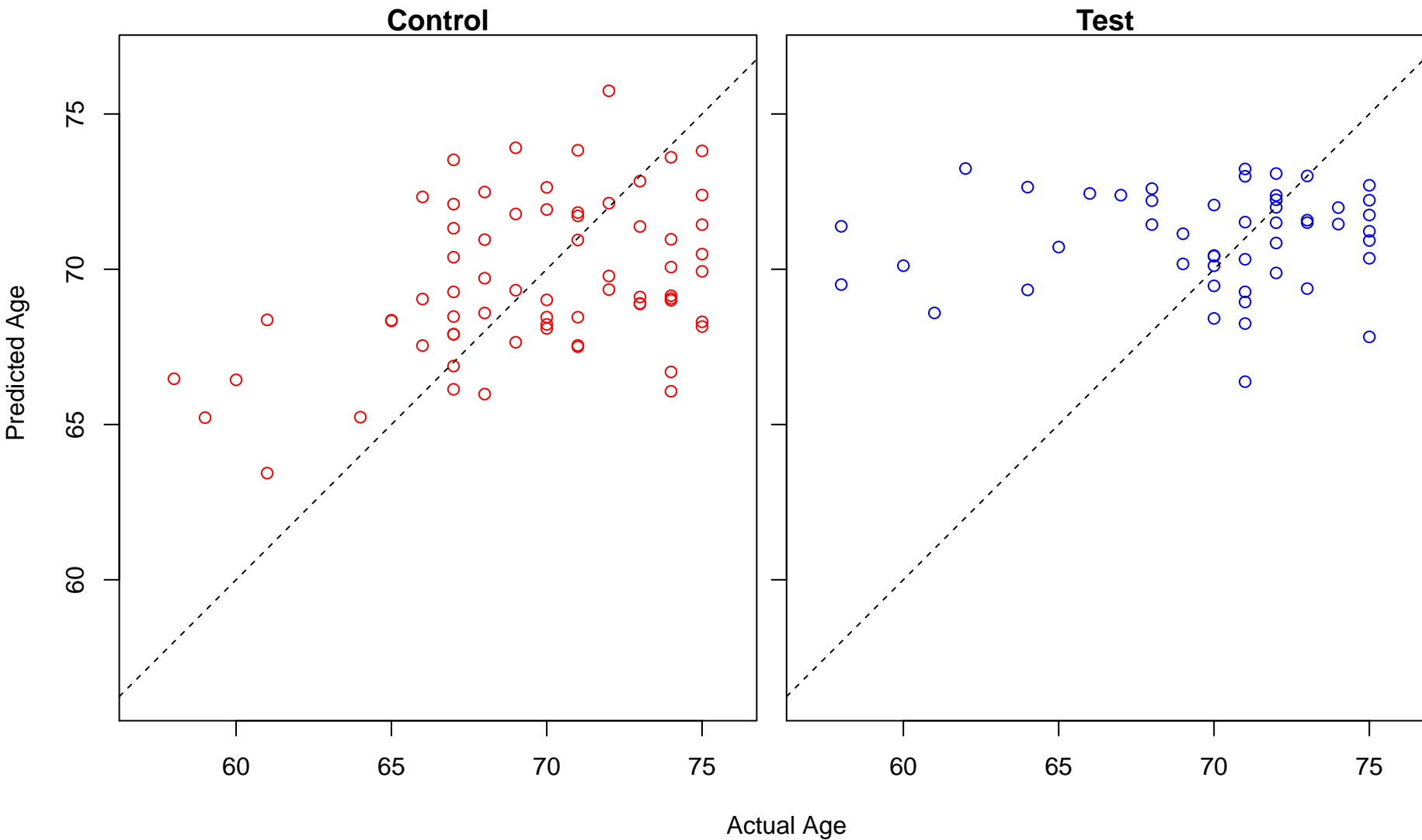
DNA damage induced protein phosphorylation (Score: 0.541171)



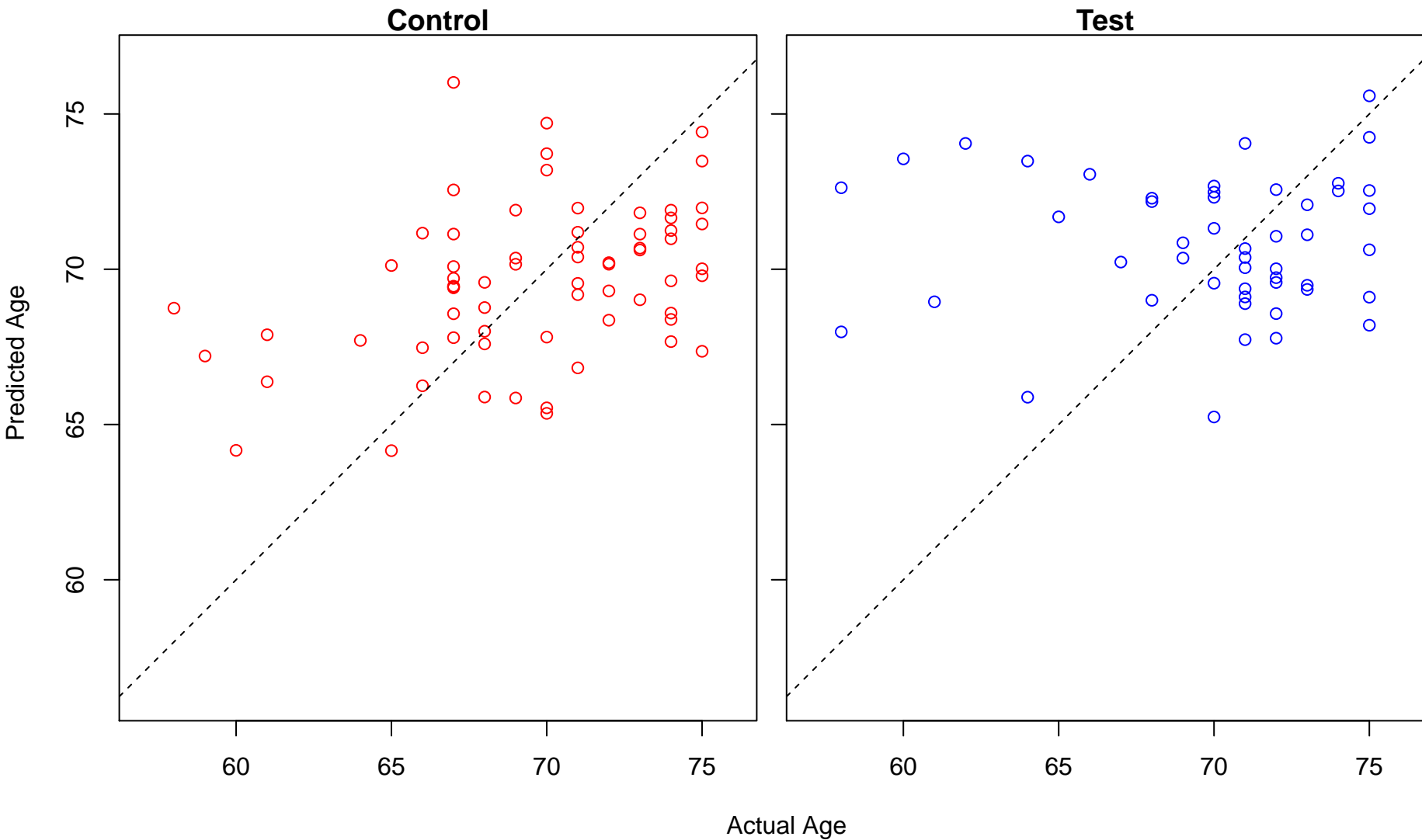
negative regulation of microtubule polymerization (Score: 0.540820)



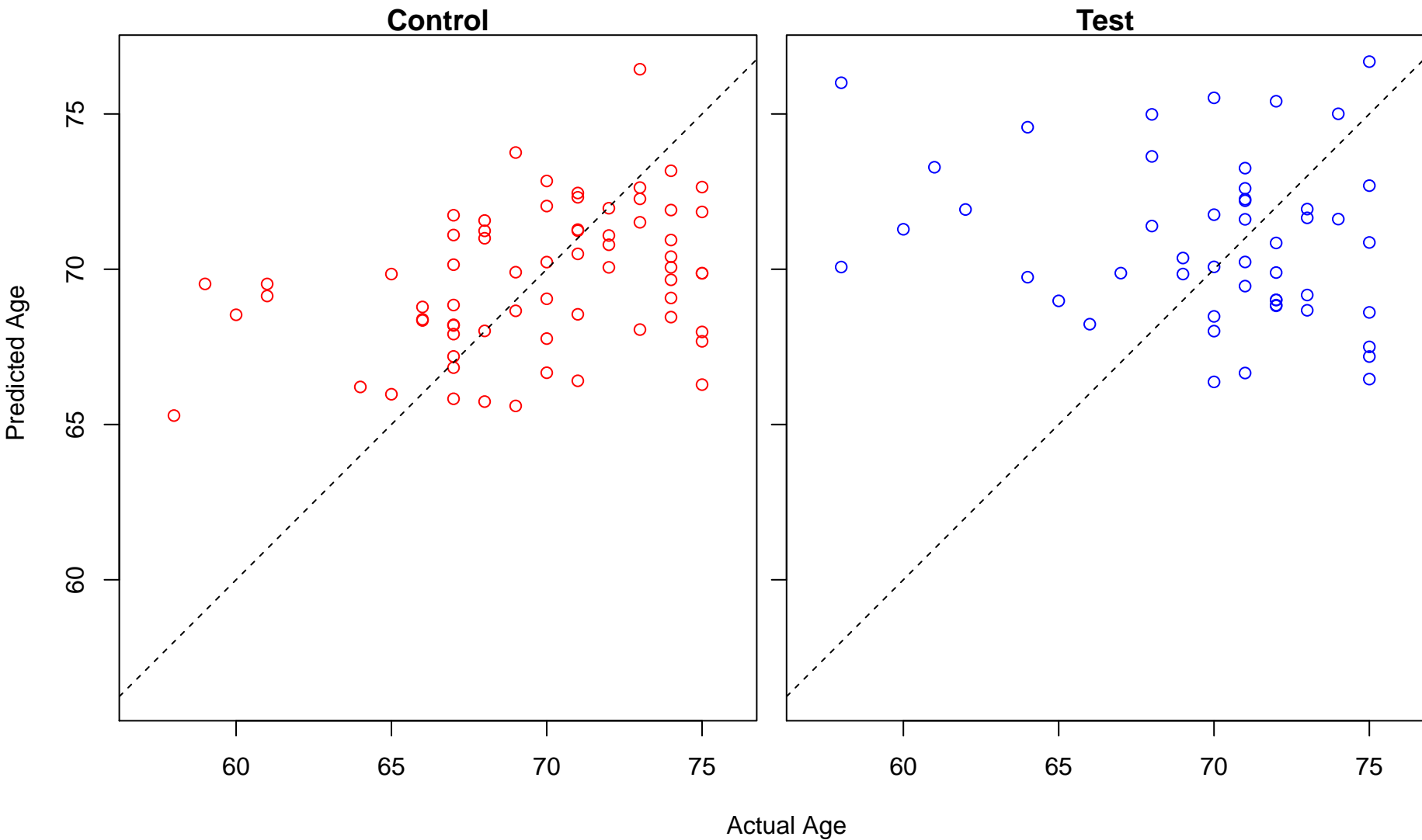
negative regulation of endothelial cell apoptotic process (Score: 0.540327)



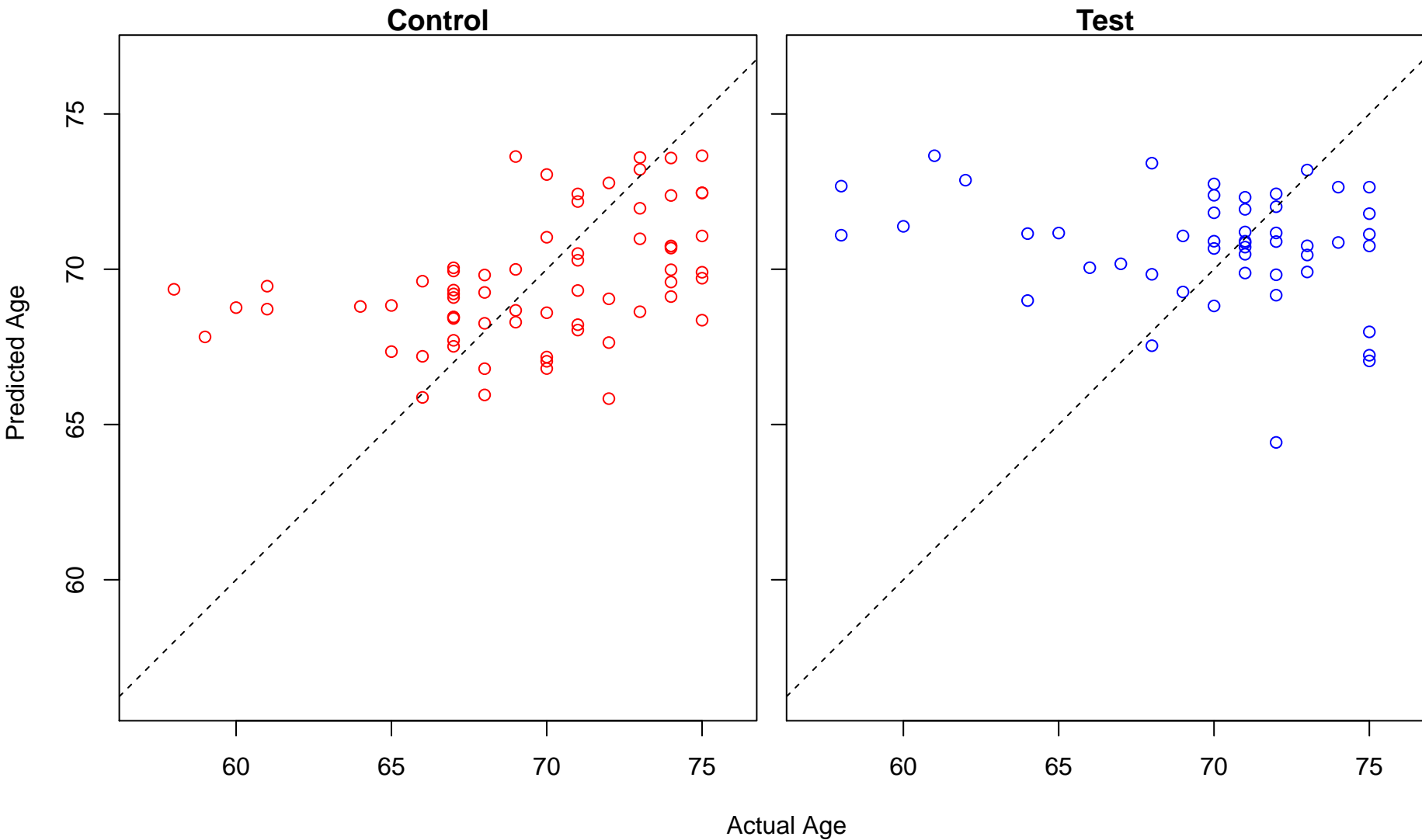
positive regulation of lipid kinase activity (Score: 0.540315)



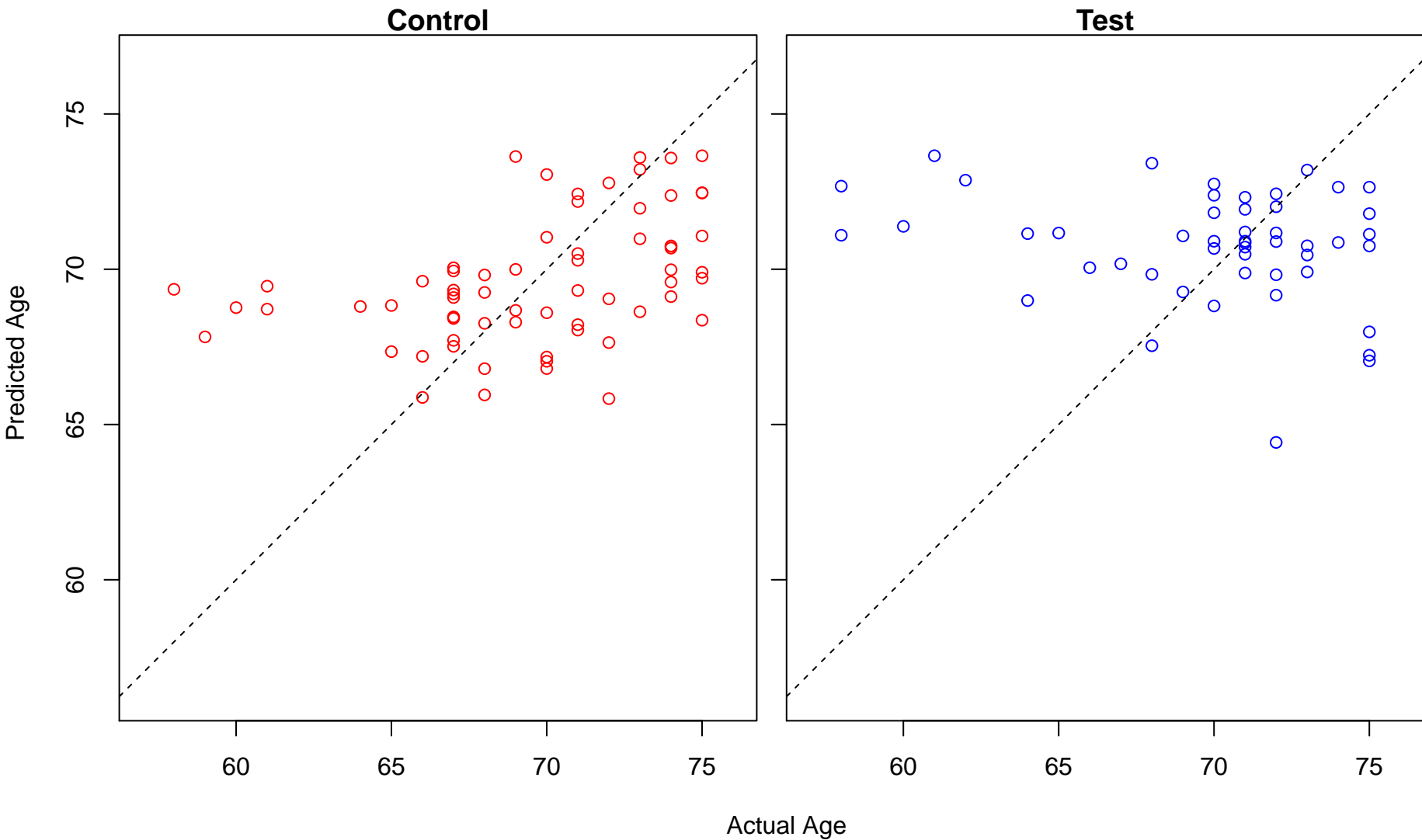
cytoskeletal anchoring at plasma membrane (Score: 0.539361)



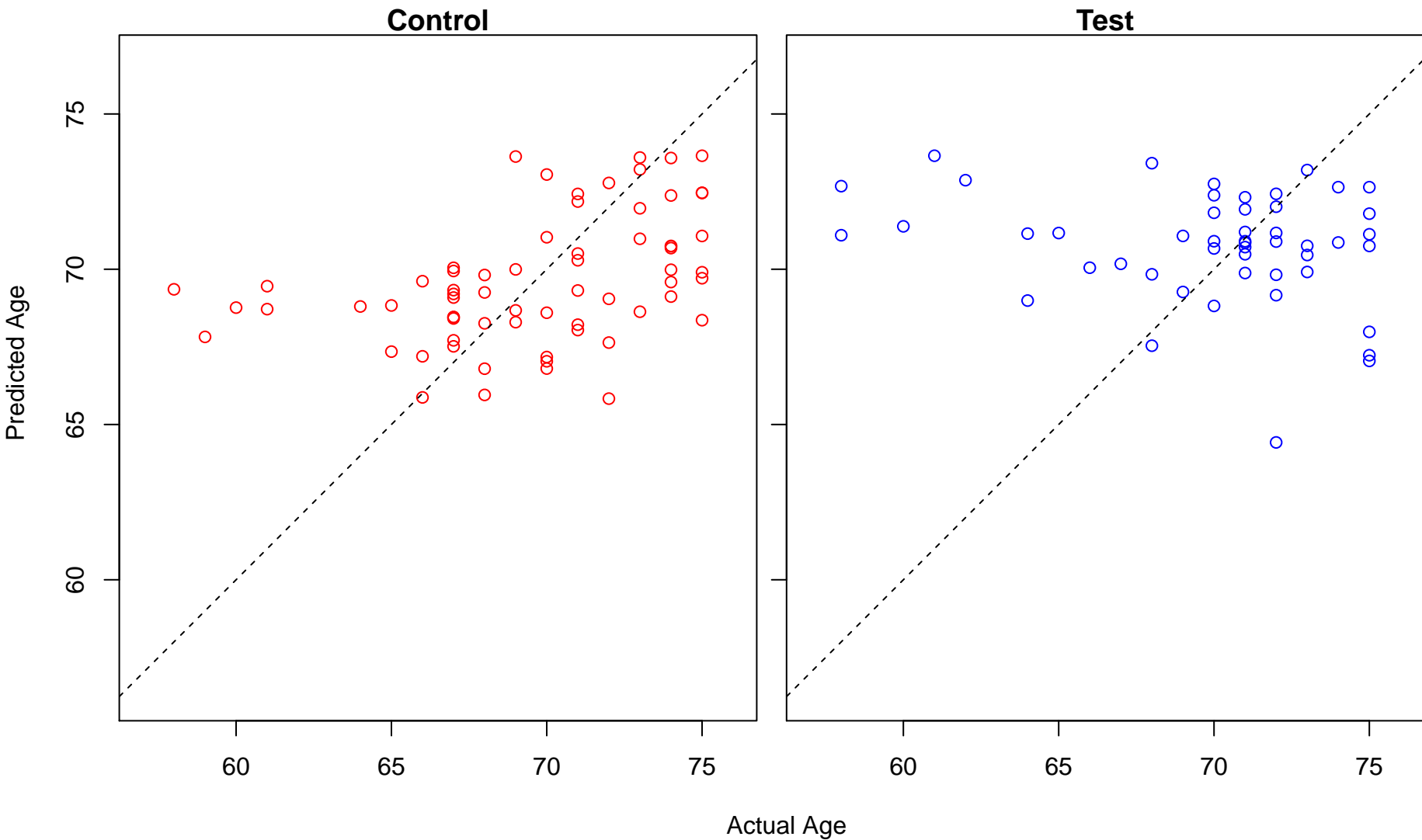
ubiquinone metabolic process (Score: 0.539342)



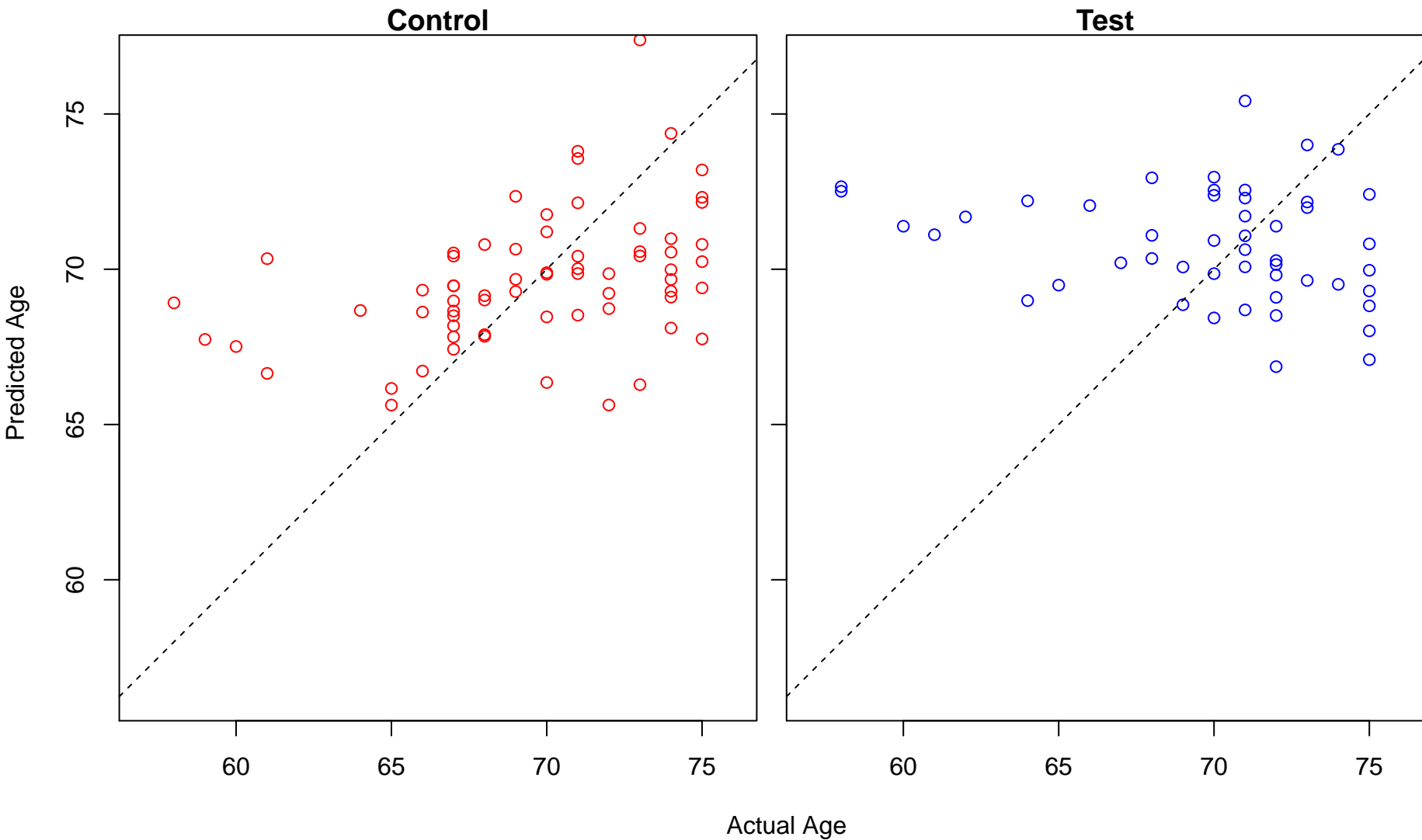
ubiquinone biosynthetic process (Score: 0.539342)



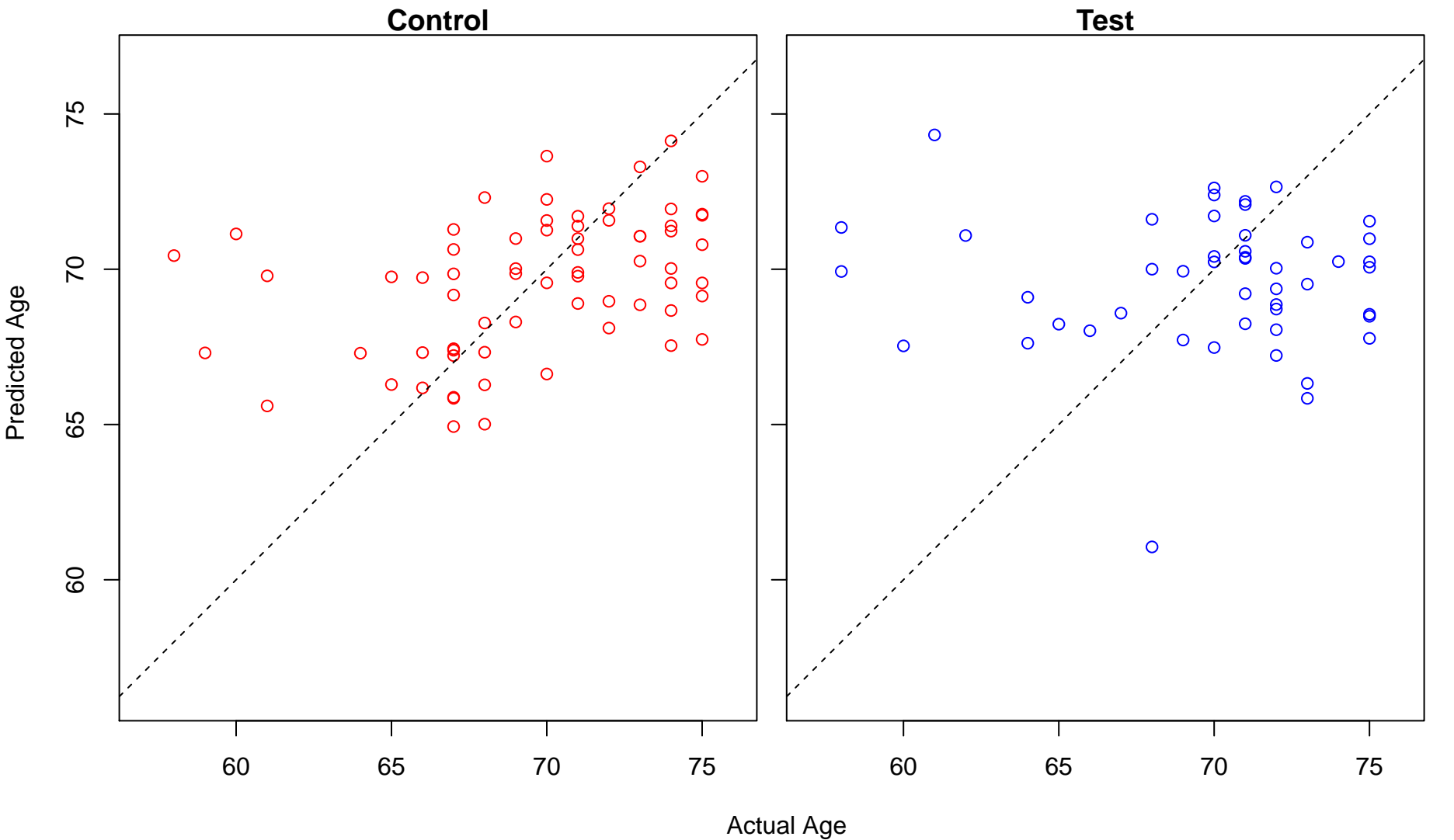
quinone biosynthetic process (Score: 0.539342)



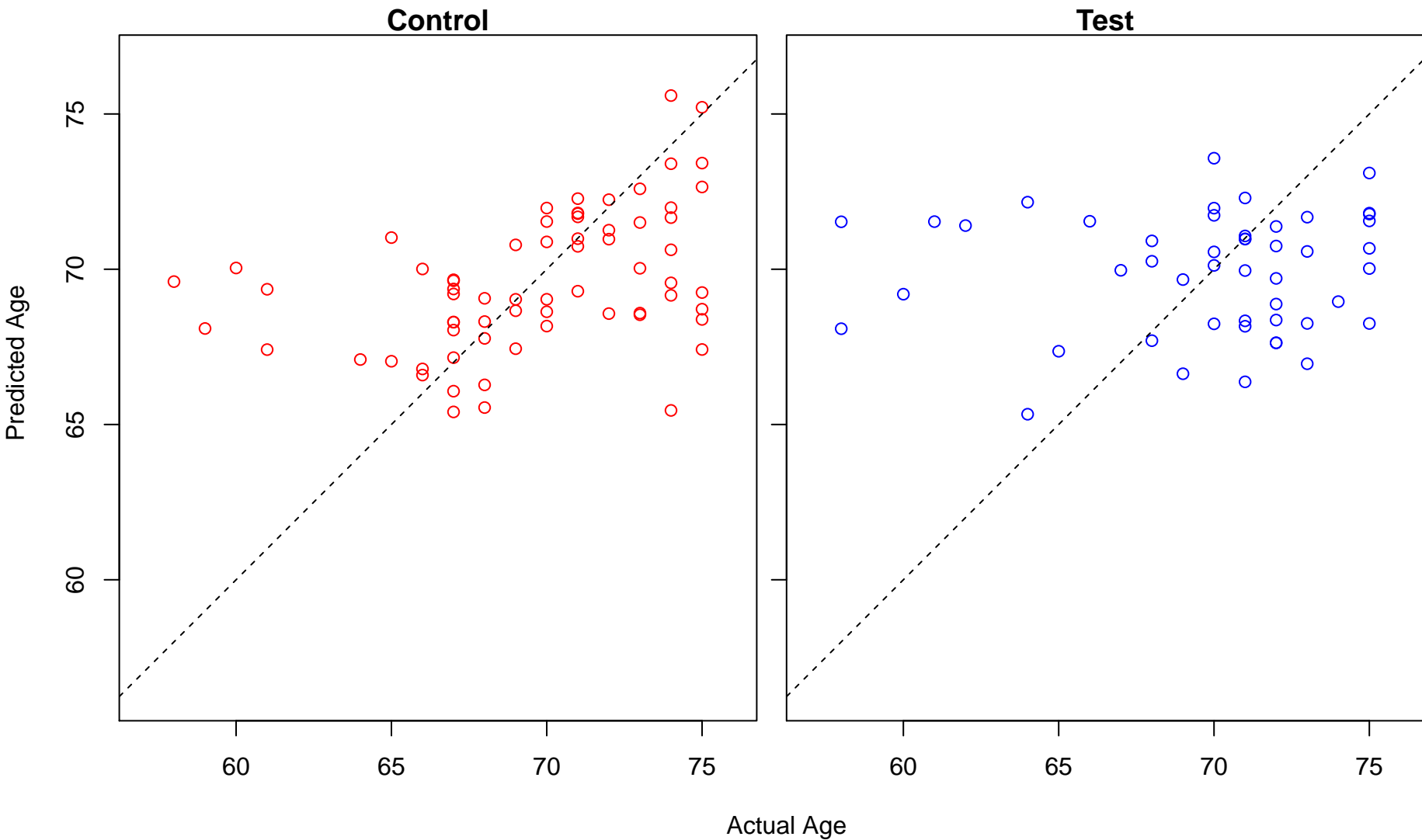
regulation of NLRP3 inflammasome complex assembly (Score: 0.538826)



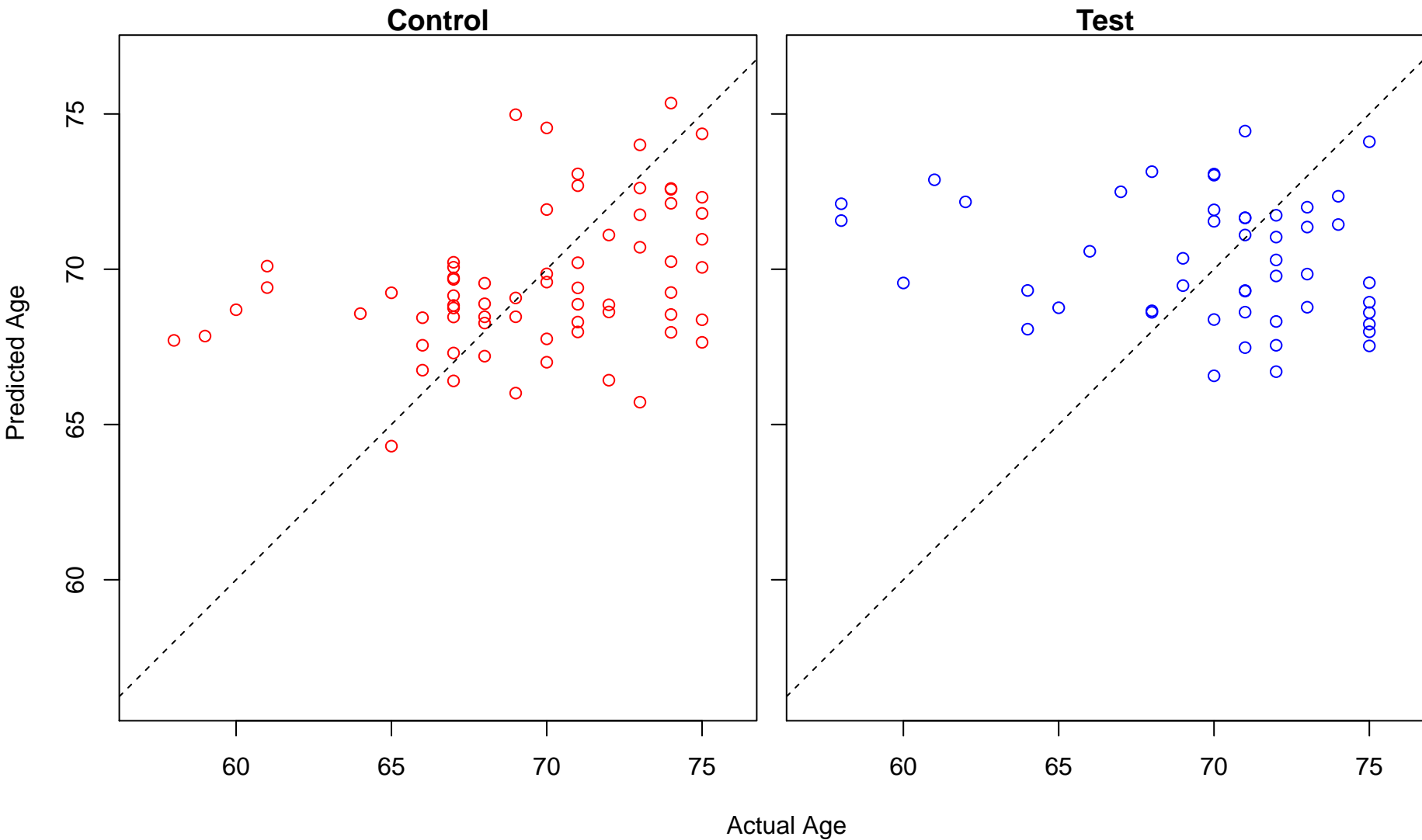
of T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting c



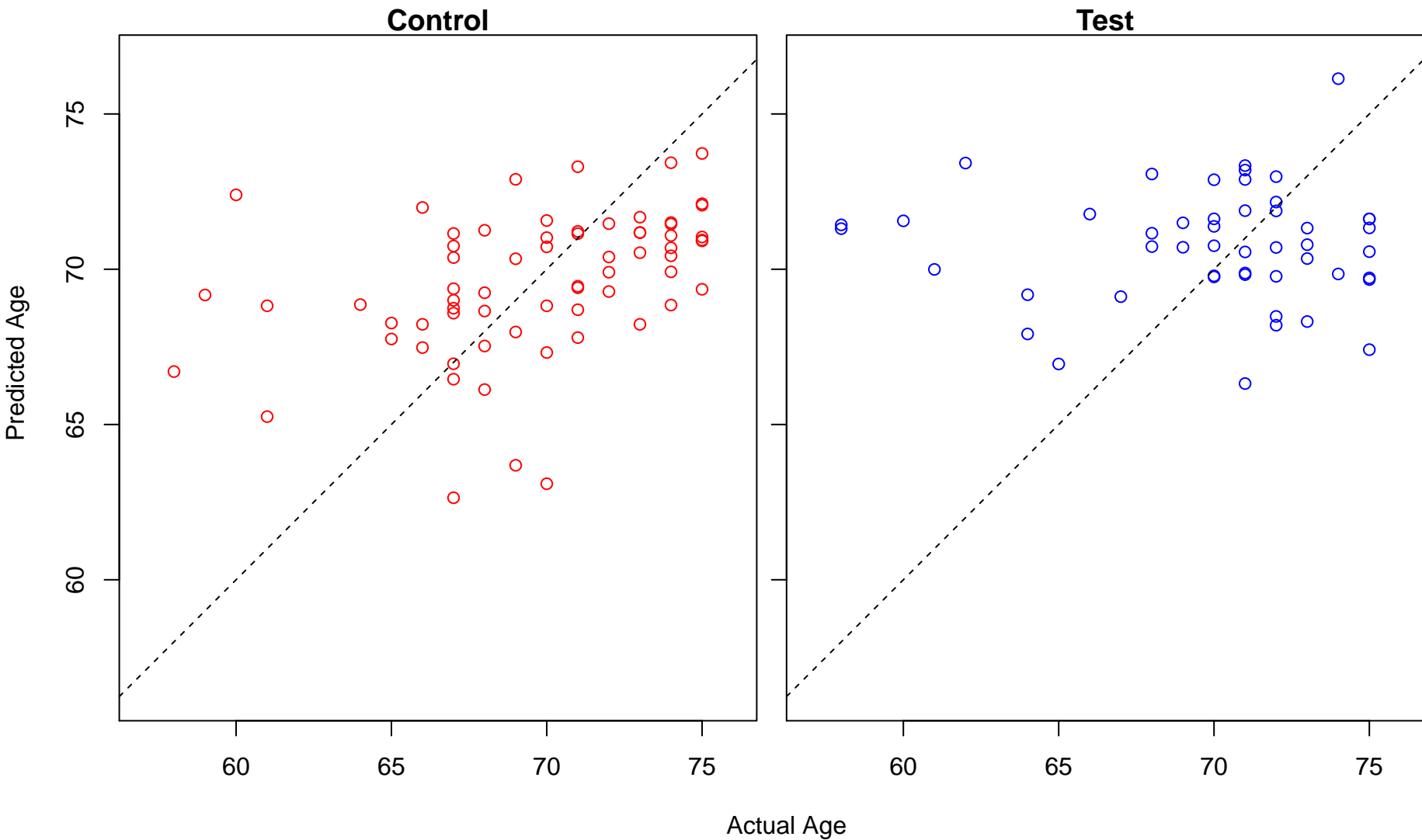
negative regulation of receptor-mediated endocytosis (Score: 0.538457)



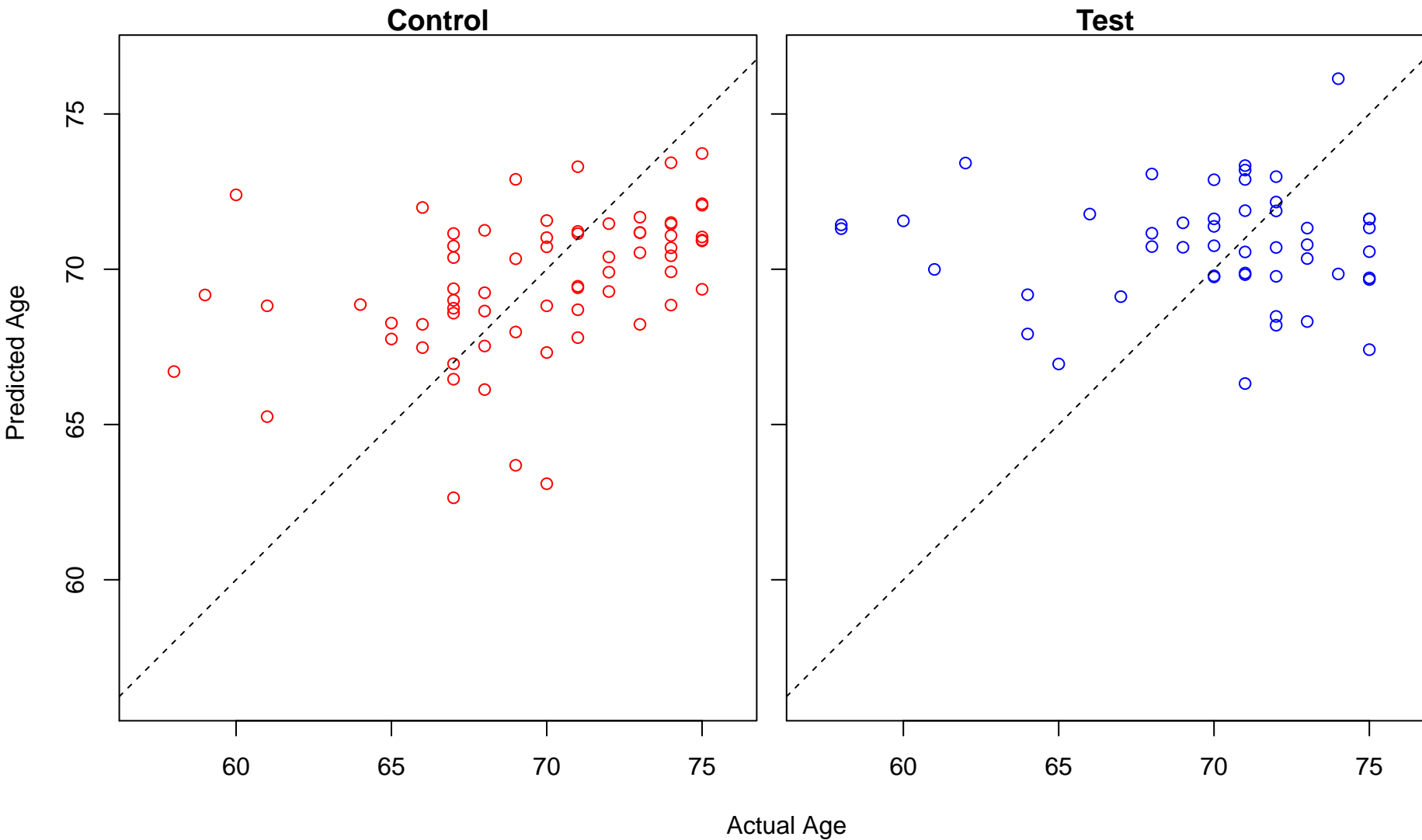
positive regulation of toll-like receptor 4 signaling pathway (Score: 0.537733)



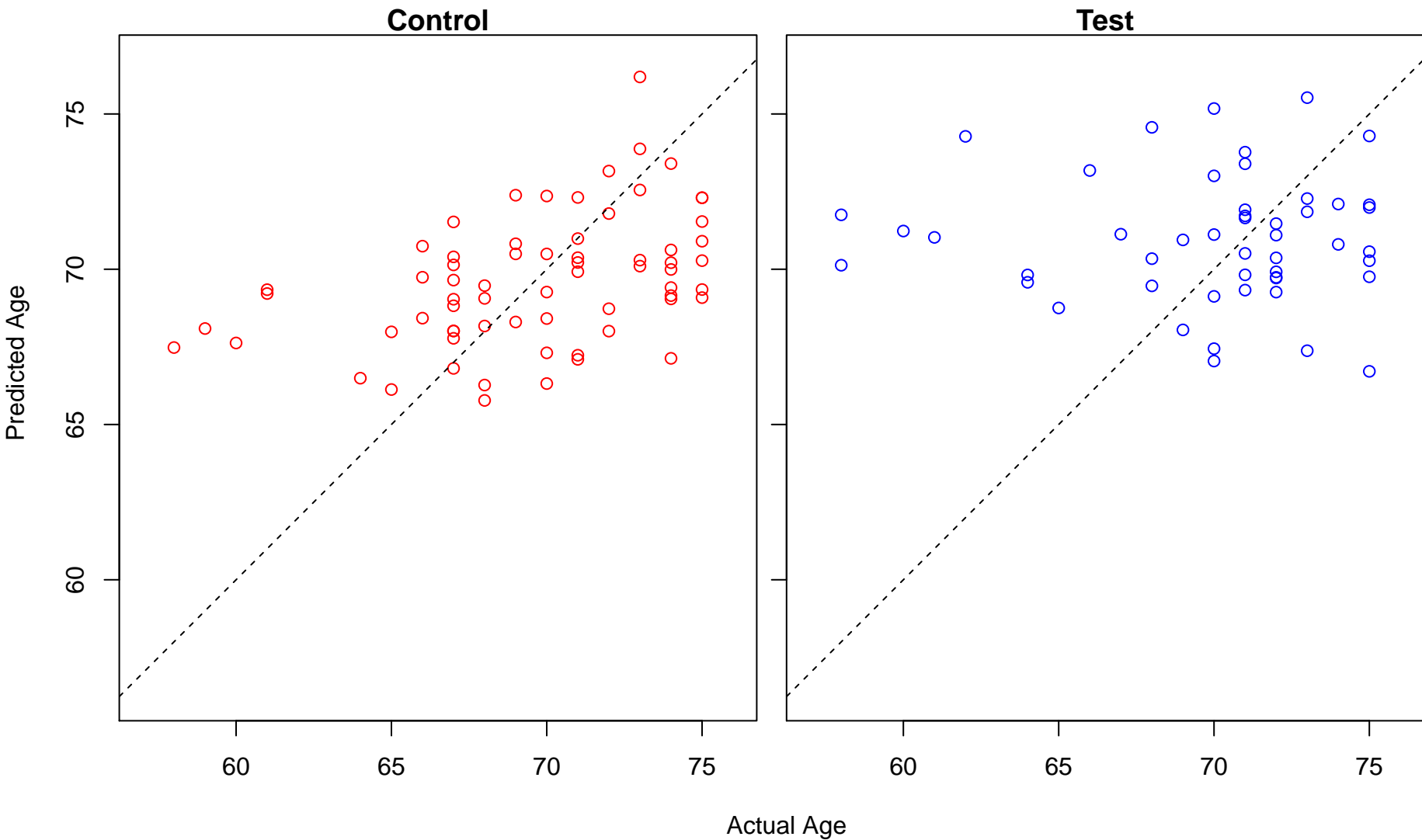
indole-containing compound catabolic process (Score: 0.537626)



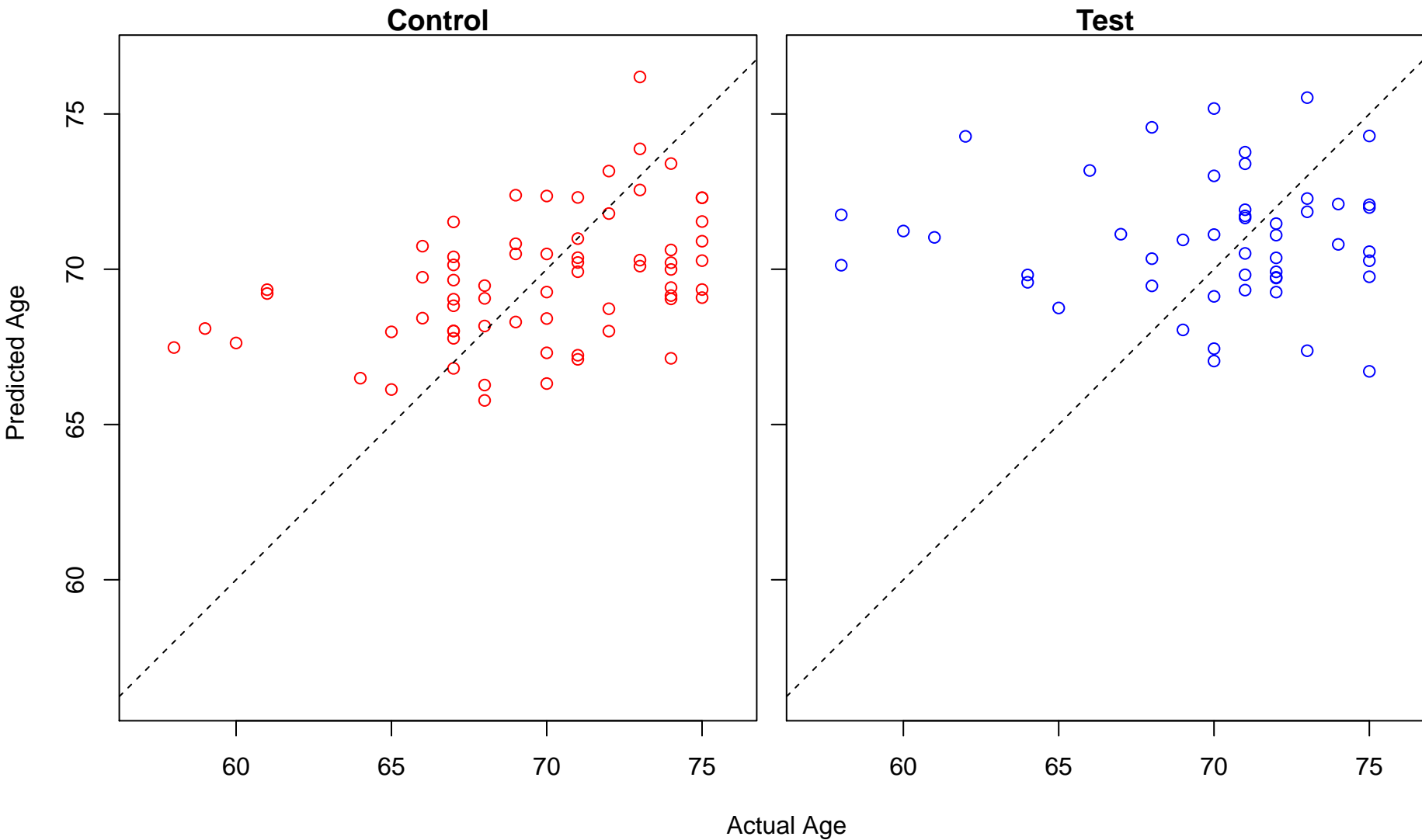
indolalkylamine catabolic process (Score: 0.537626)



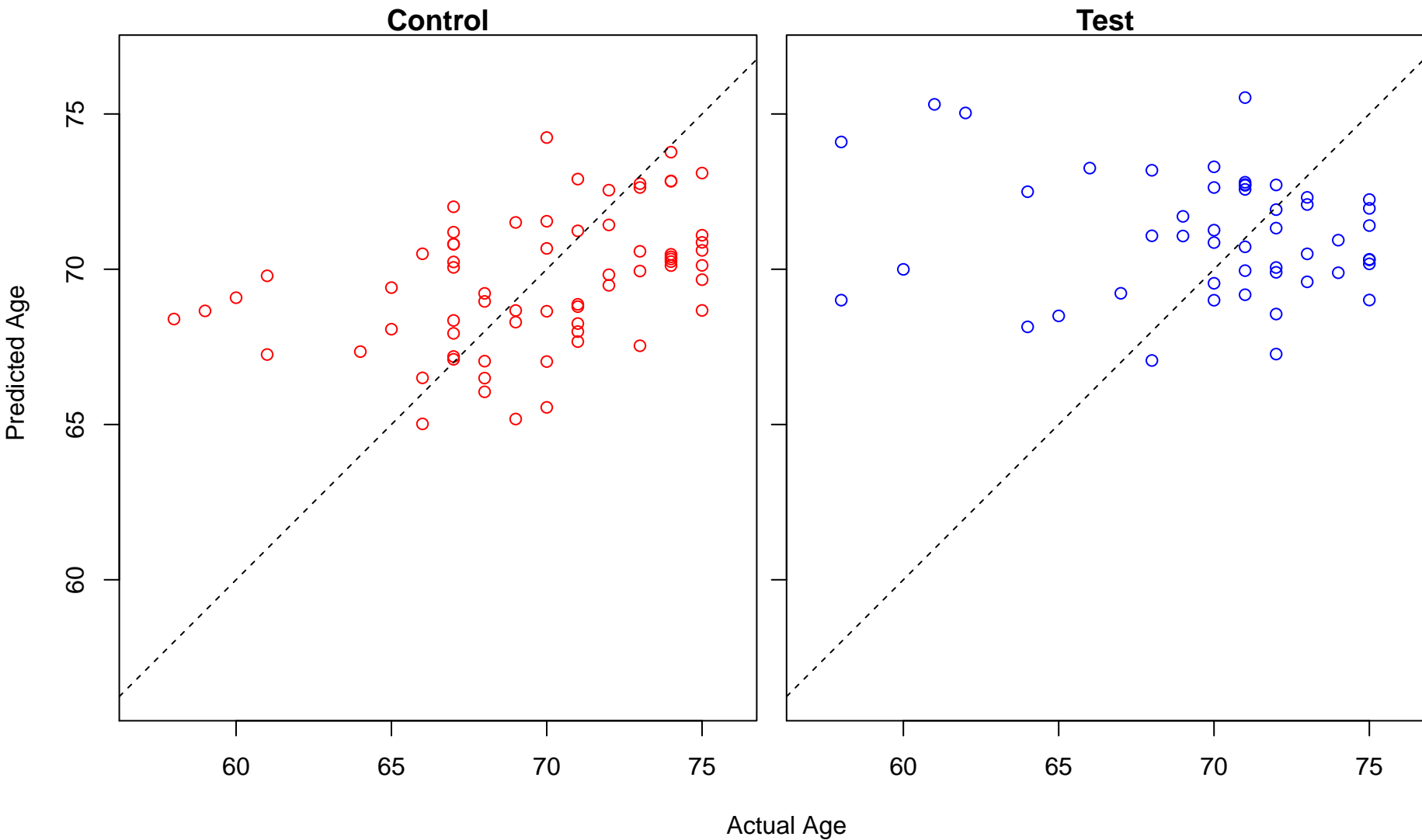
negative regulation of posttranscriptional gene silencing (Score: 0.535737)



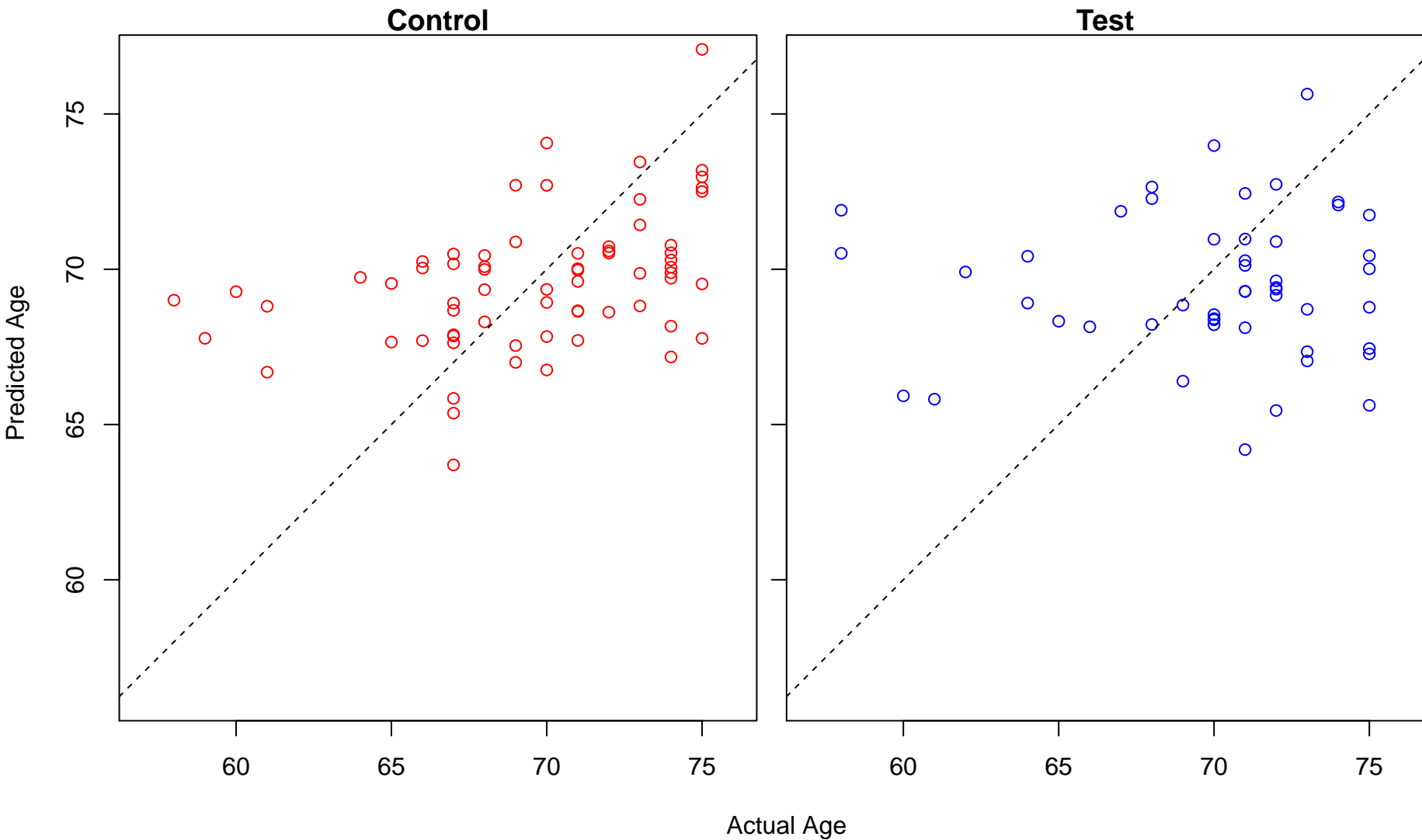
negative regulation of gene silencing by RNA (Score: 0.535737)



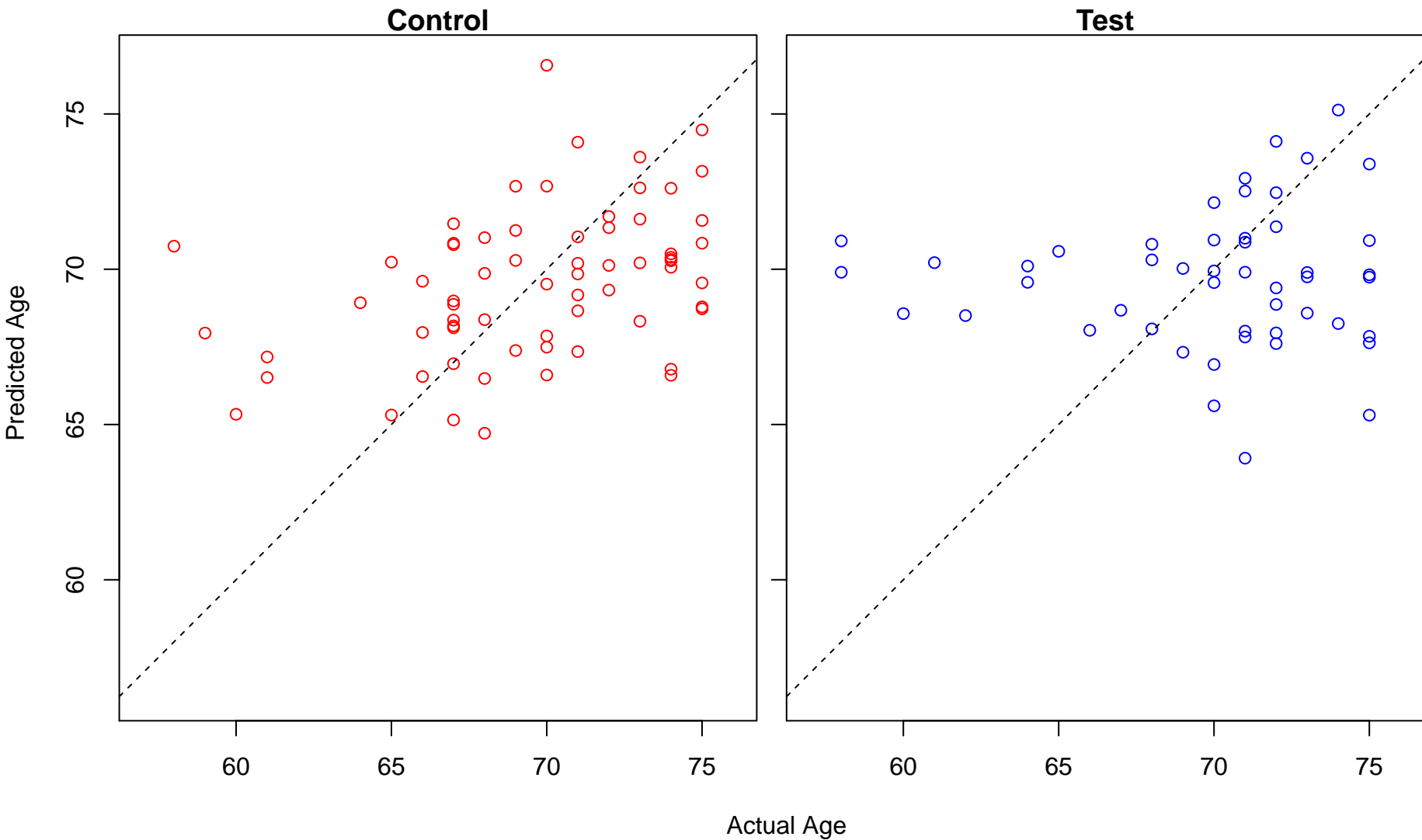
copper ion homeostasis (Score: 0.535266)



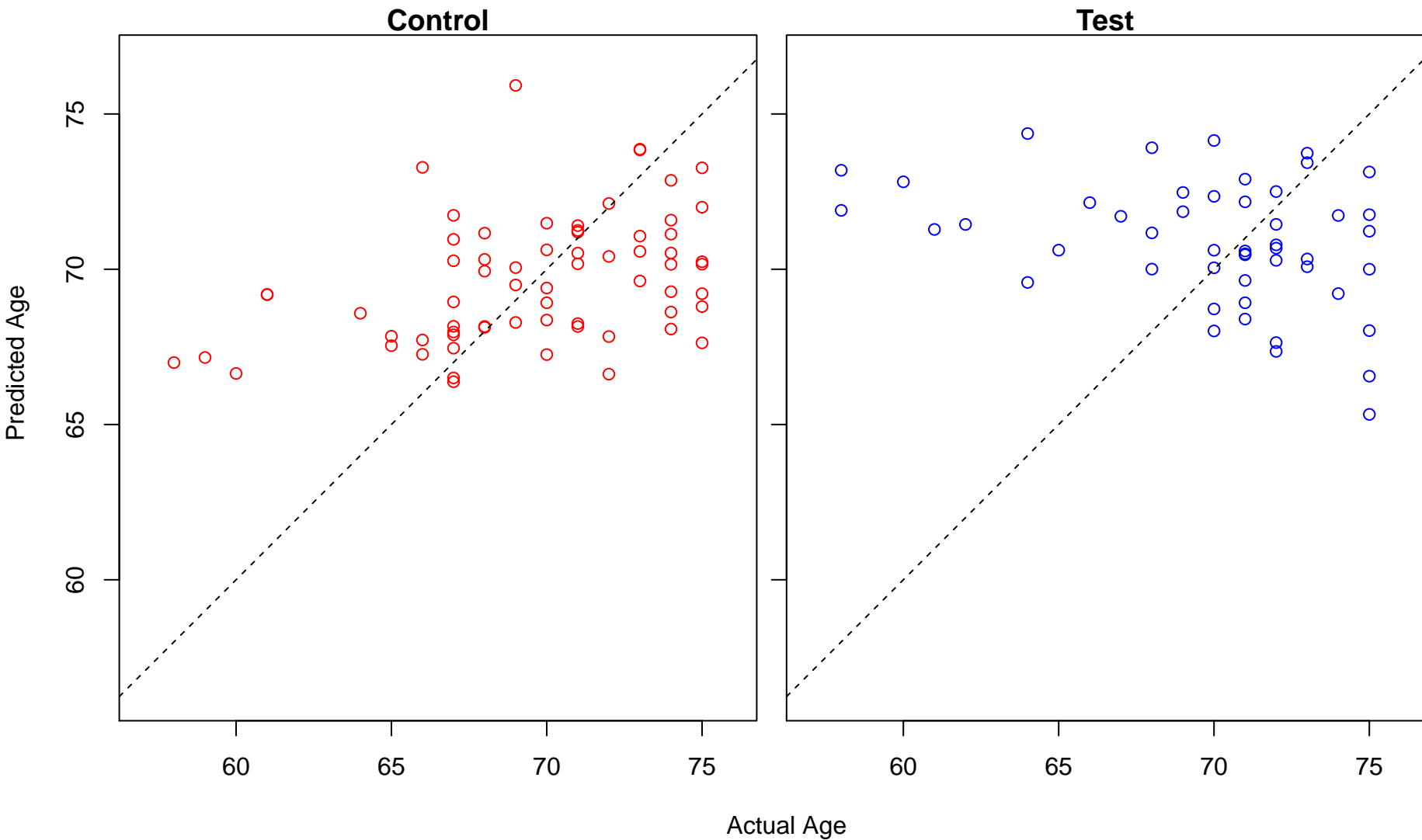
neuron cellular homeostasis (Score: 0.534356)



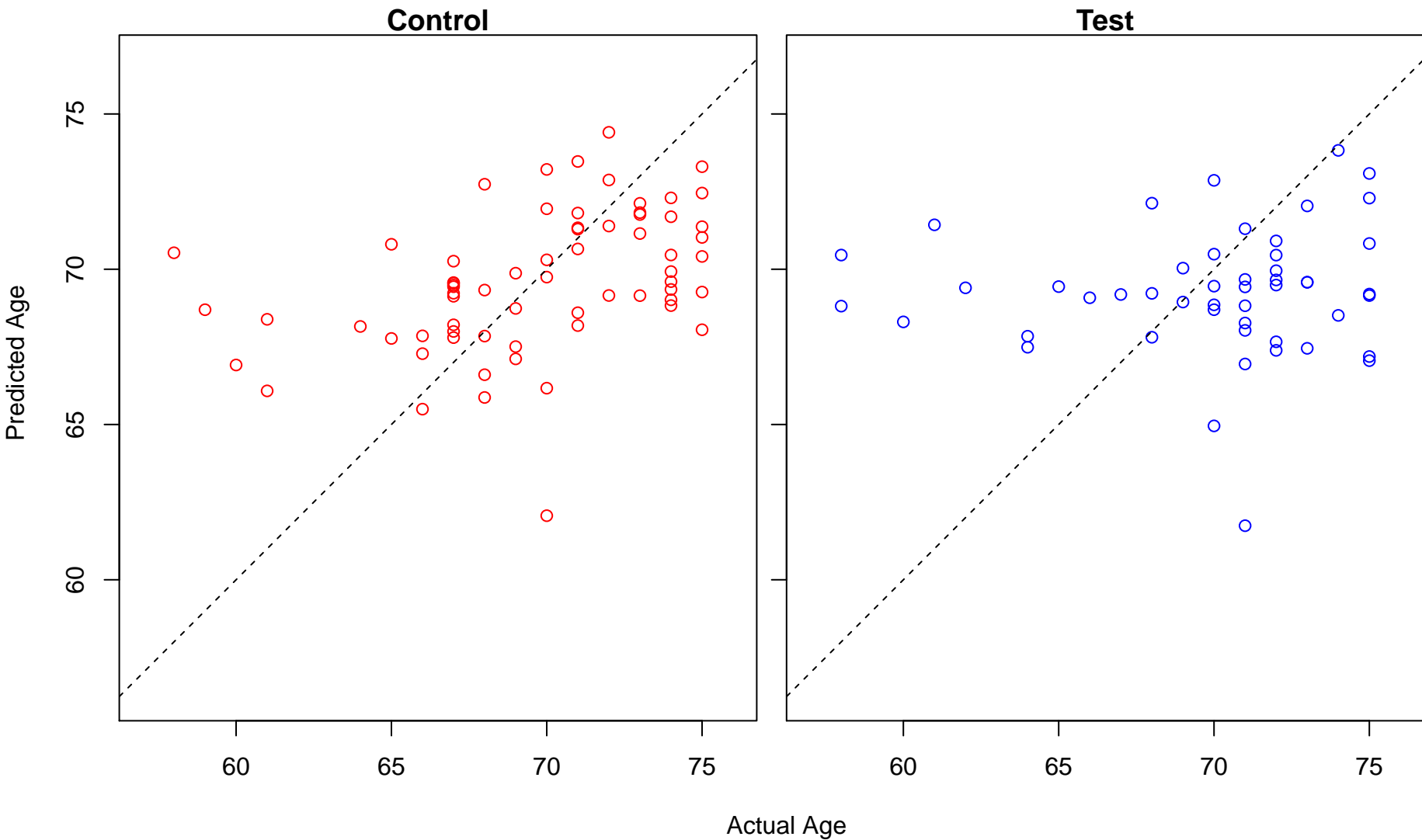
regulation of voltage-gated calcium channel activity (Score: 0.534282)



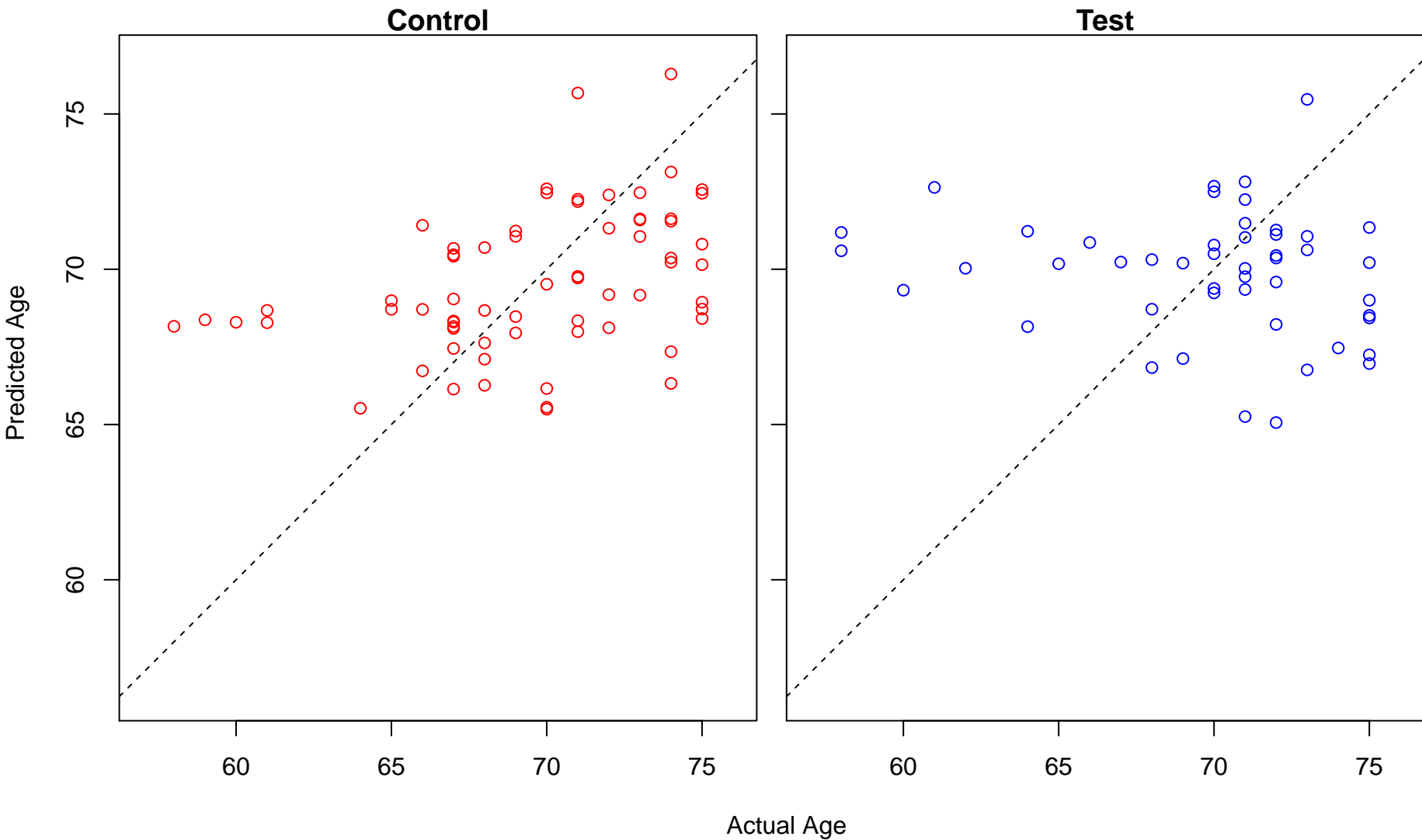
DNA strand renaturation (Score: 0.534151)



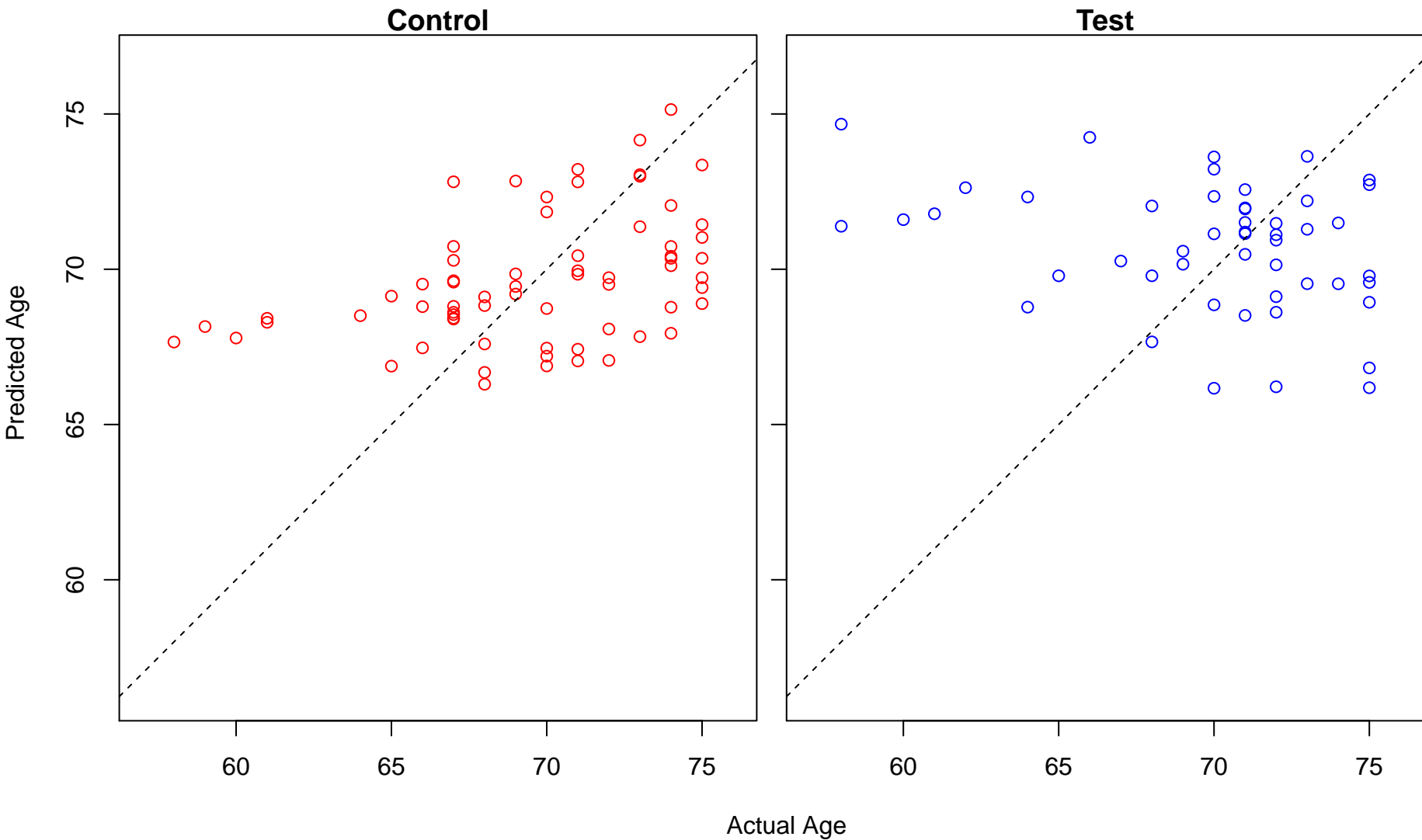
positive regulation of chemokine secretion (Score: 0.533669)



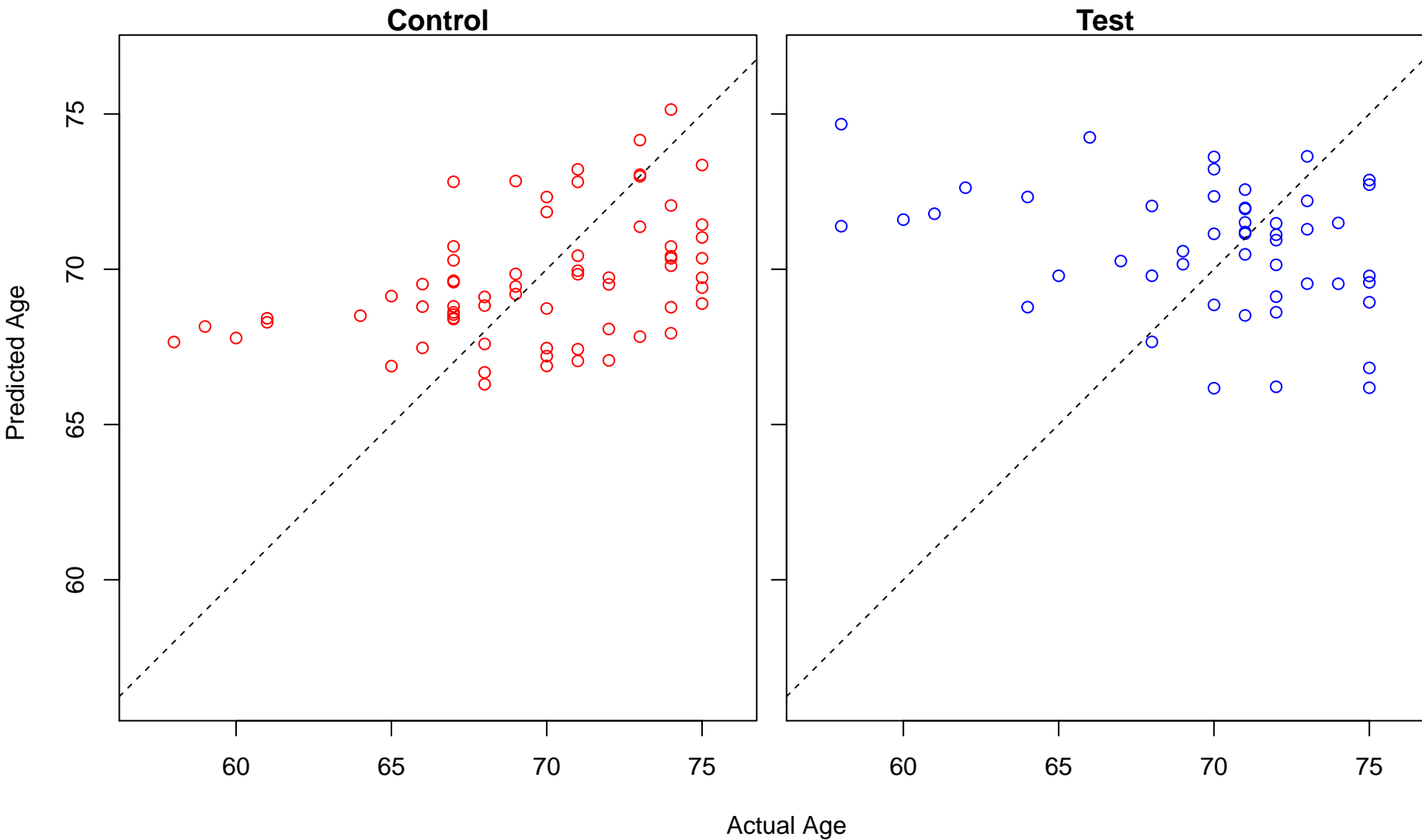
regulation of spindle checkpoint (Score: 0.532911)



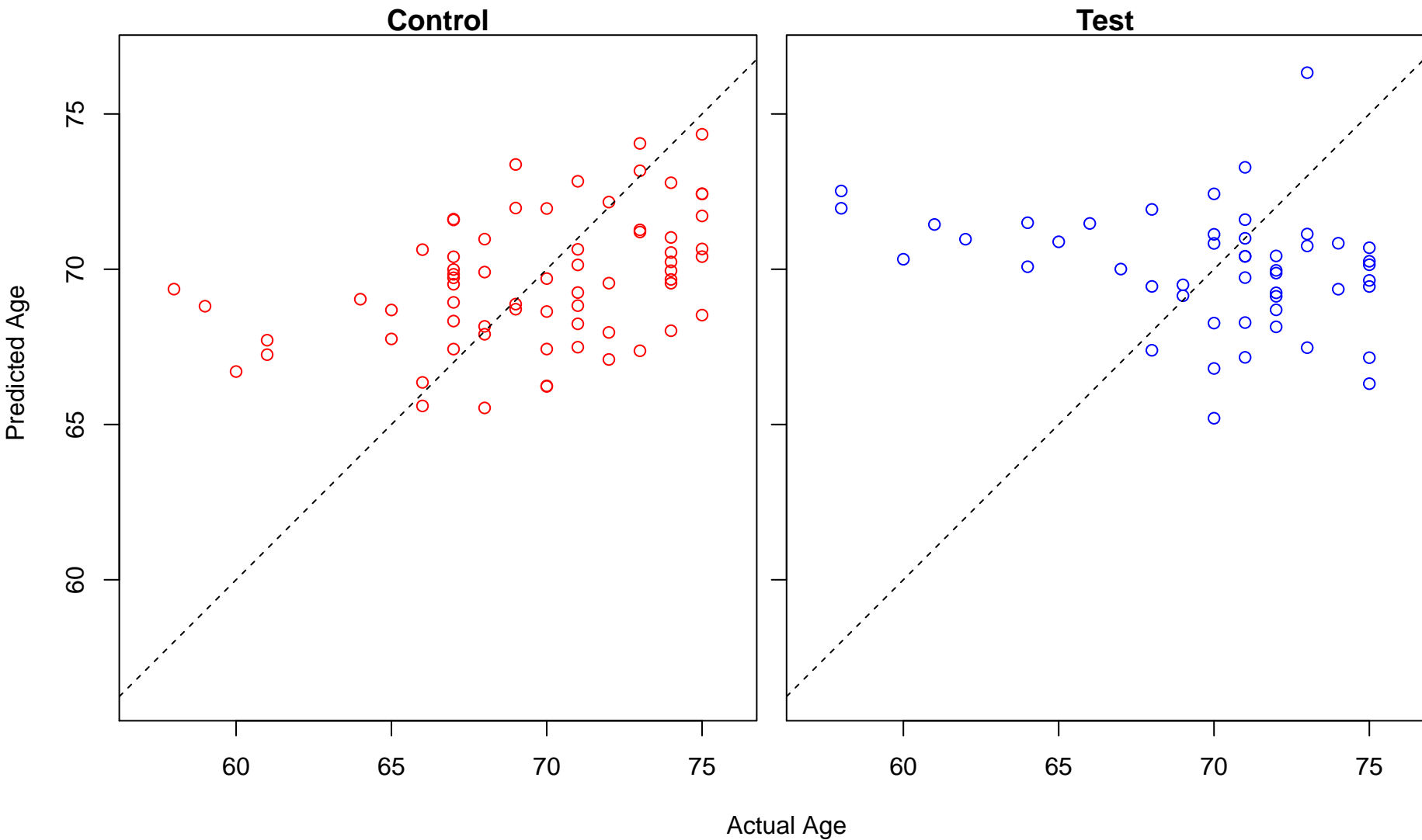
establishment or maintenance of apical/basal cell polarity (Score: 0.532244)



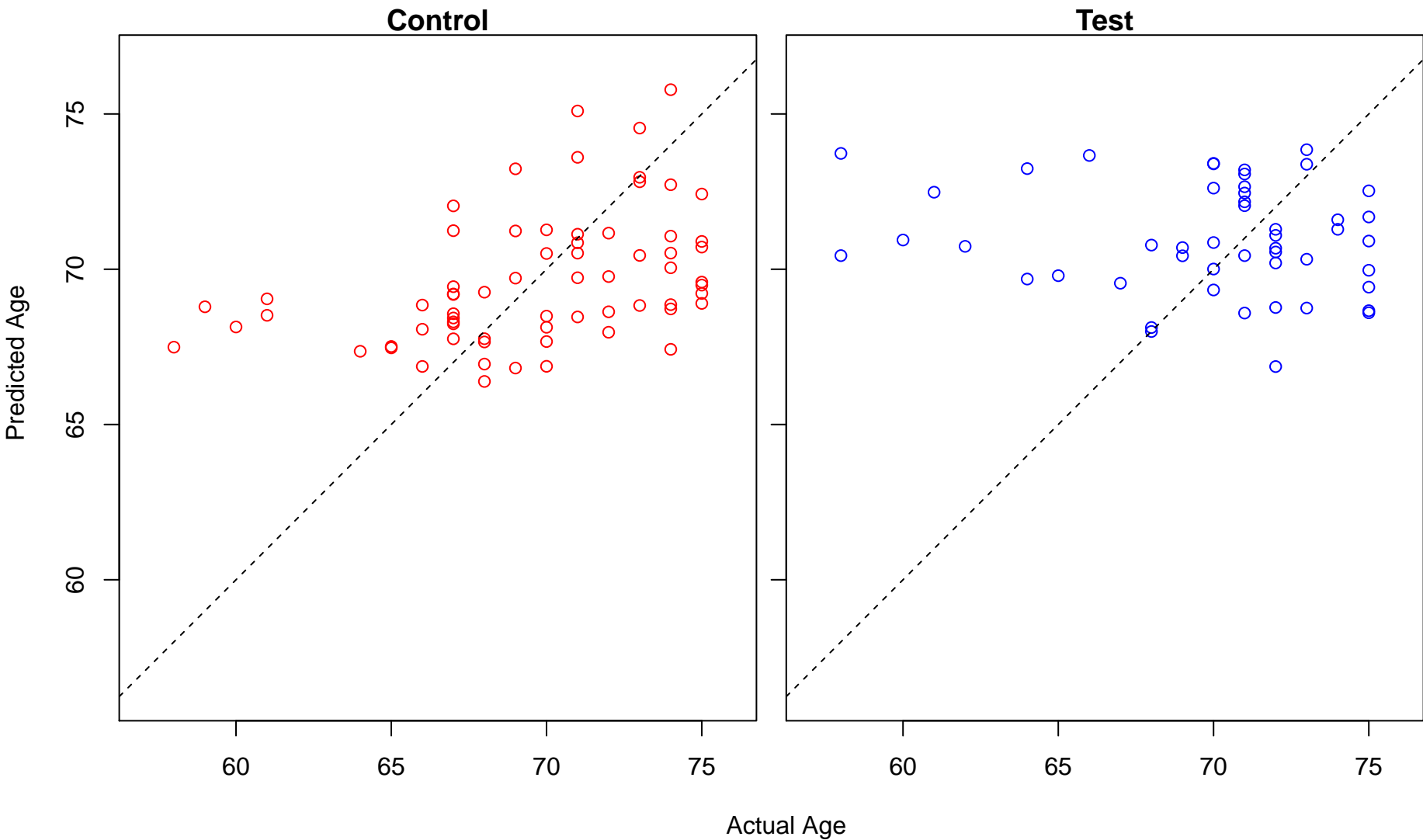
establishment or maintenance of bipolar cell polarity (Score: 0.532244)



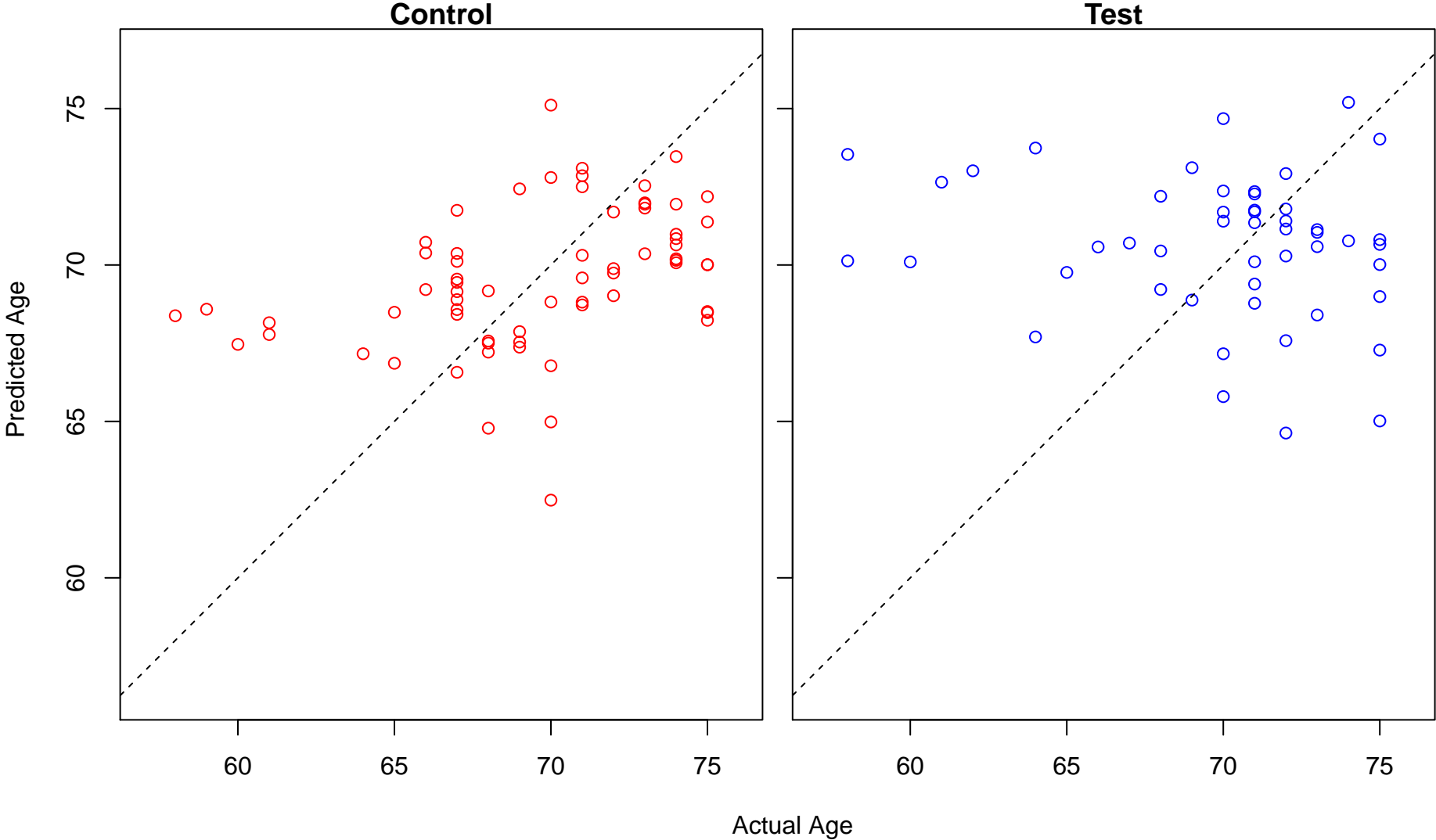
positive regulation of histone ubiquitination (Score: 0.531917)



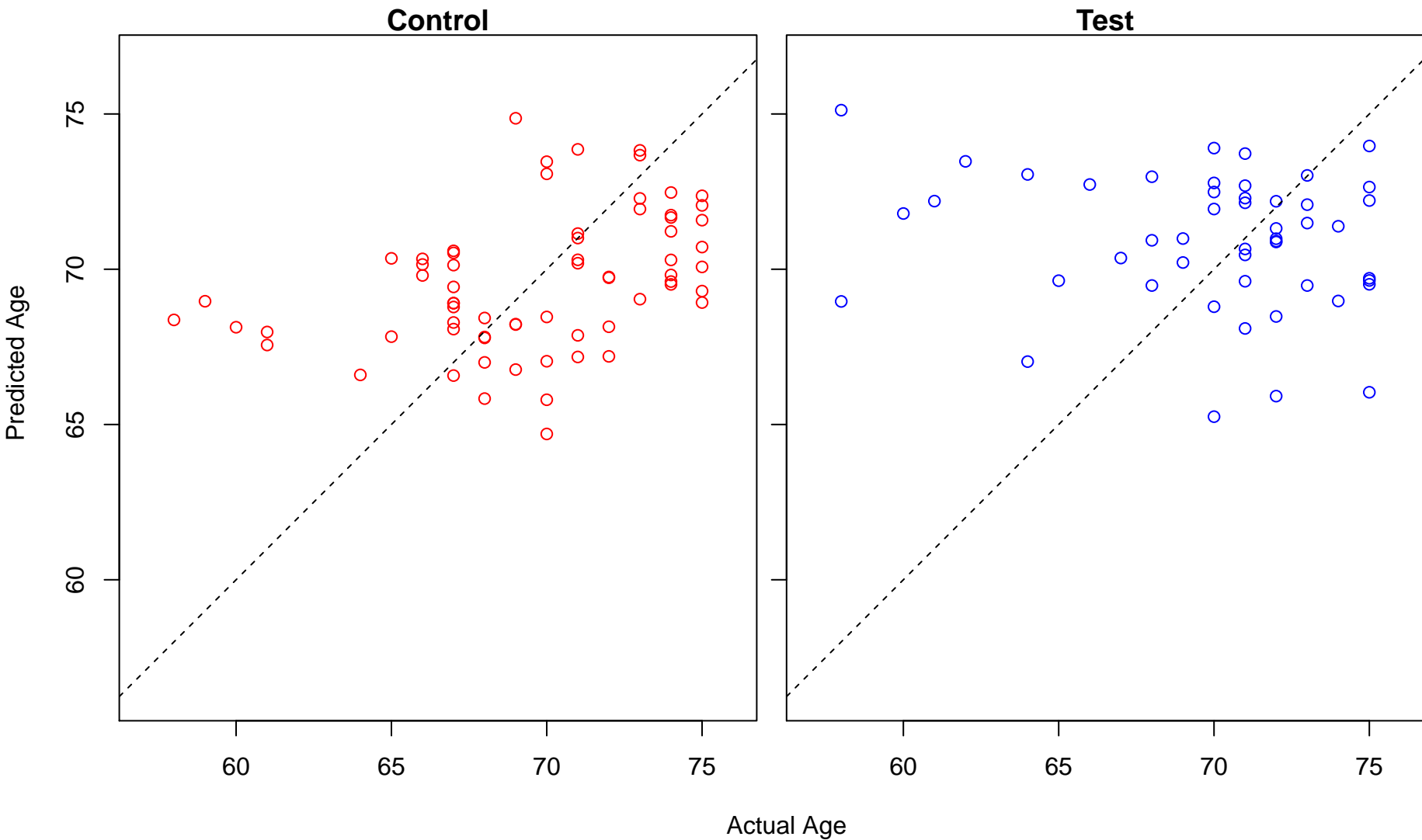
neuron migration (Score: 0.531605)



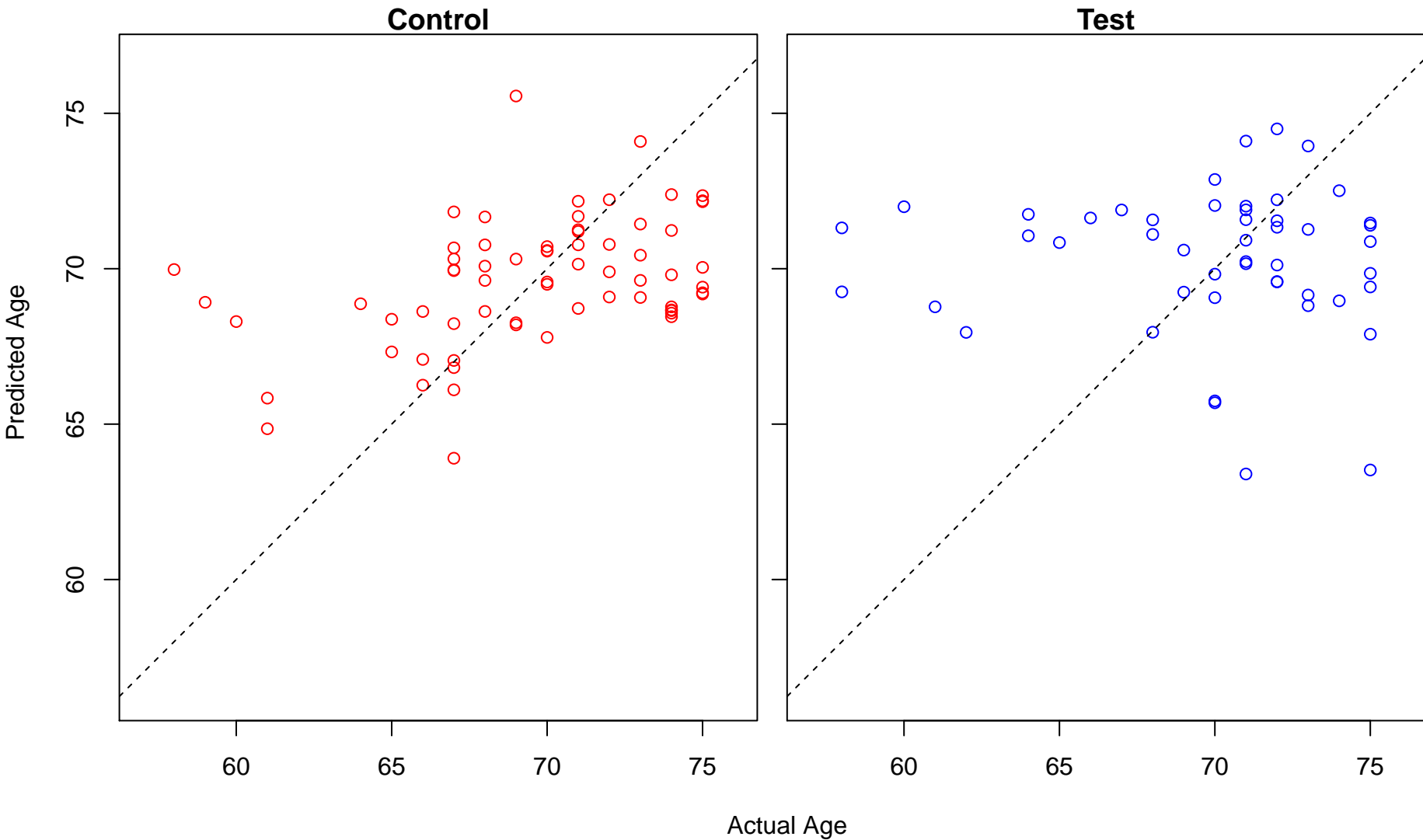
regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay (Score: 0.5



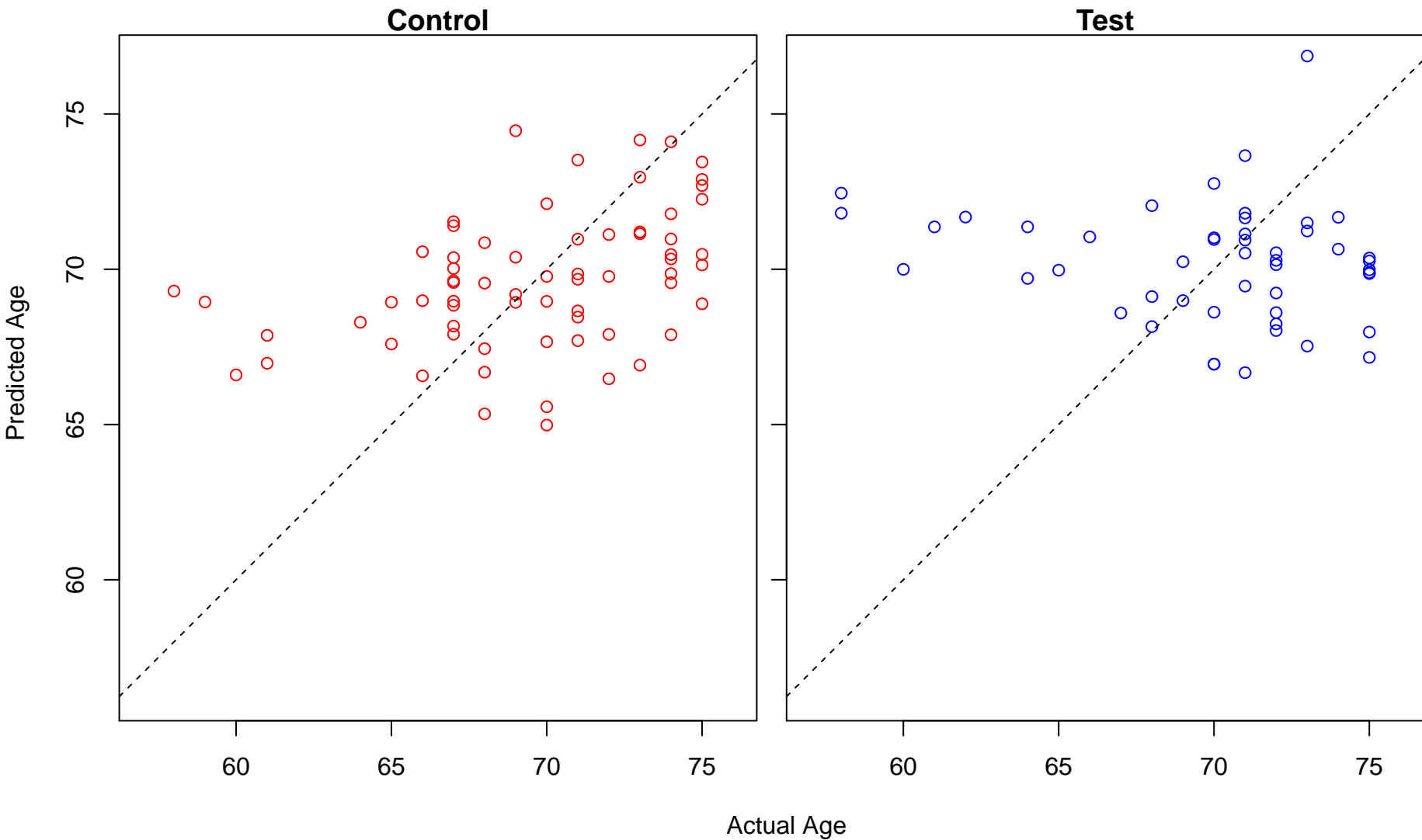
positive regulation of RNA splicing (Score: 0.530634)



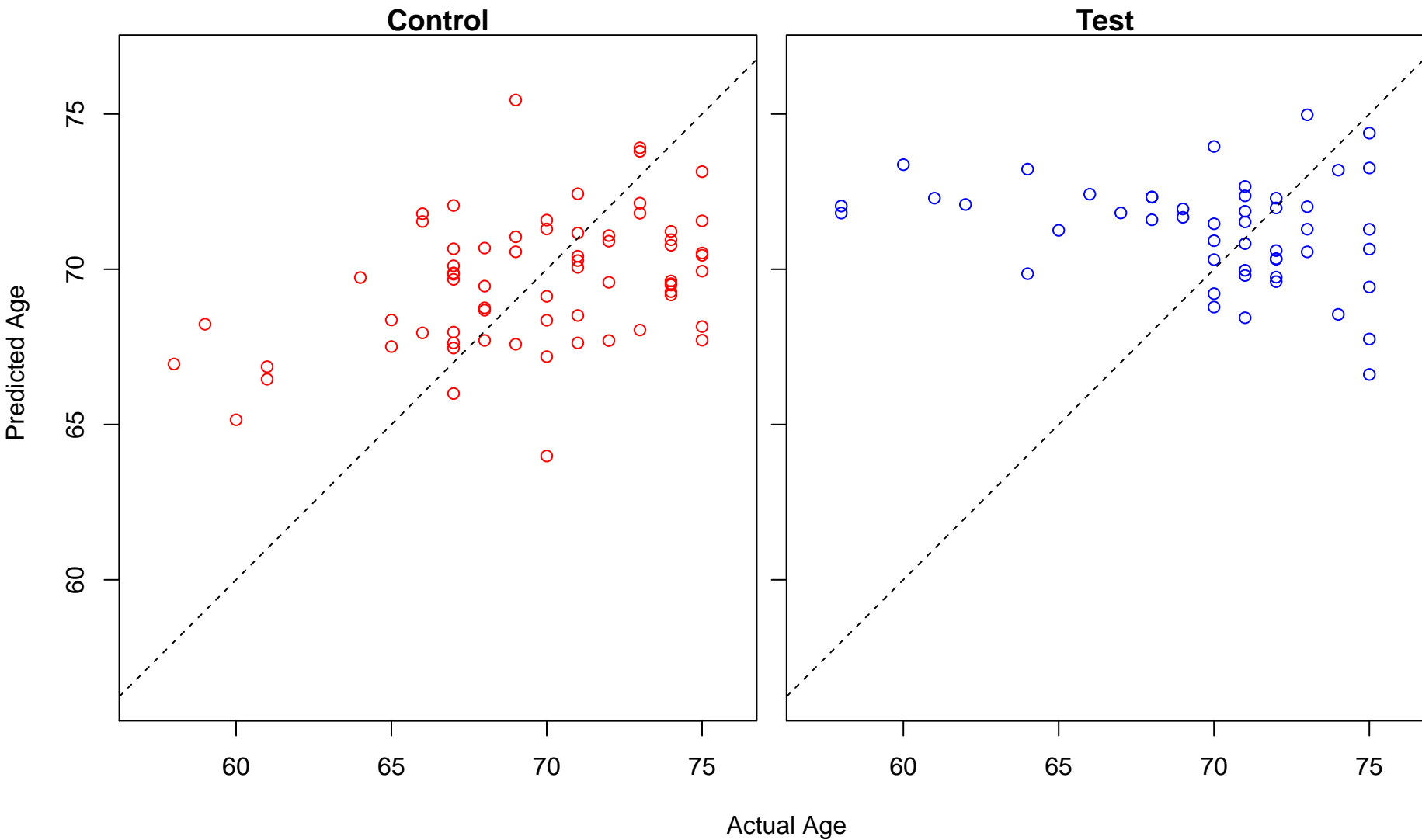
eye photoreceptor cell development (Score: 0.529403)



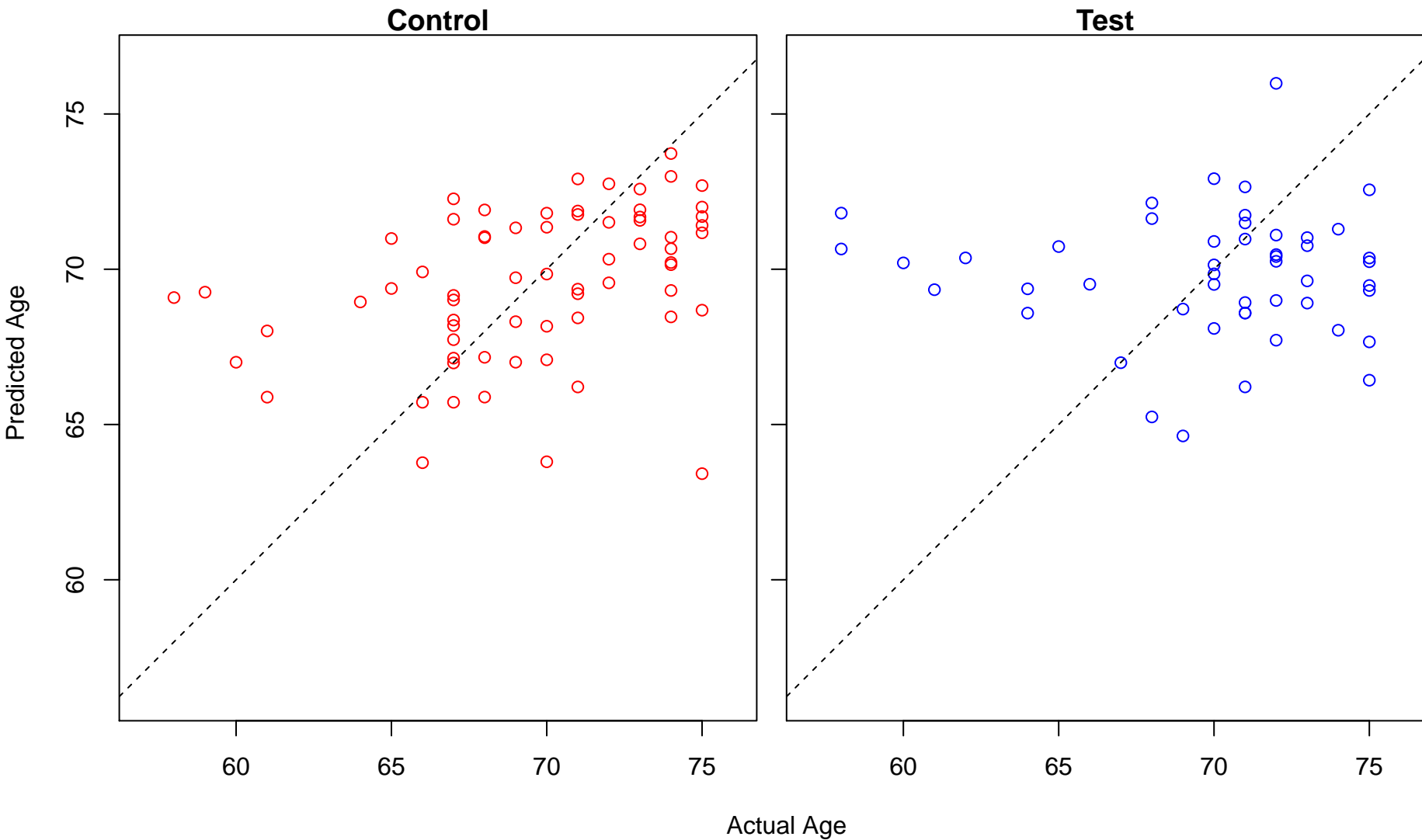
regulation of mRNA polyadenylation (Score: 0.528720)



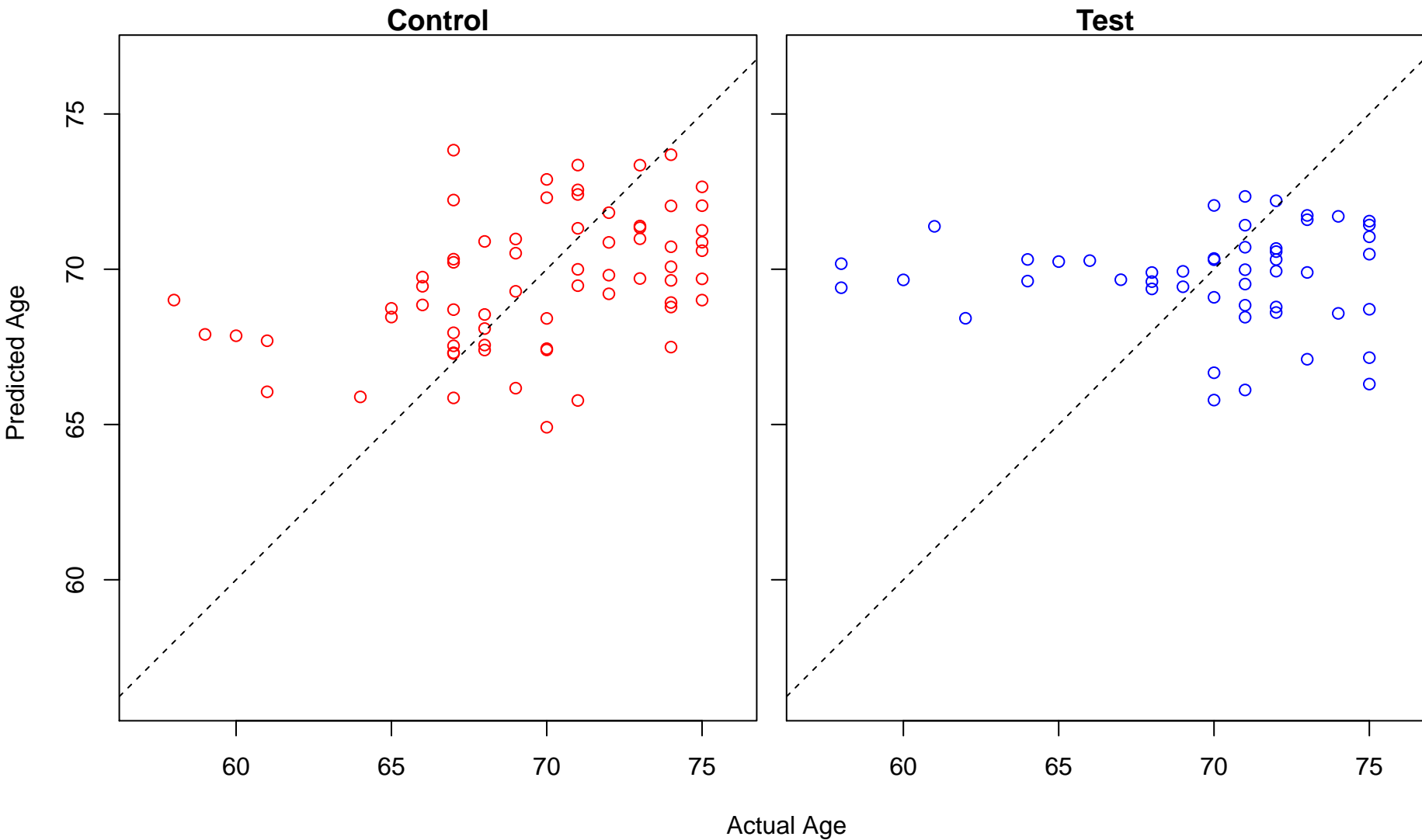
endocytic recycling (Score: 0.528409)



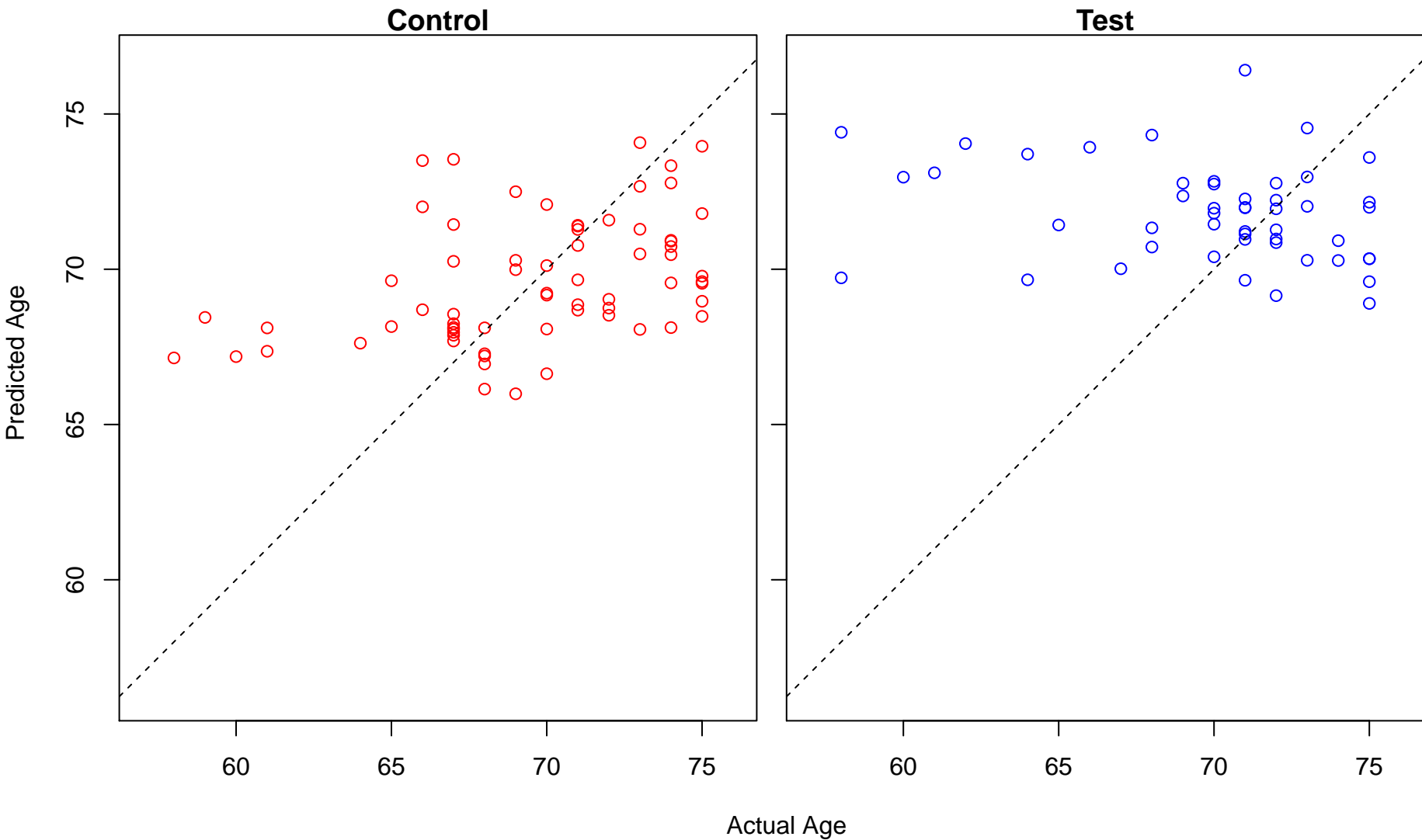
potassium ion import (Score: 0.528218)



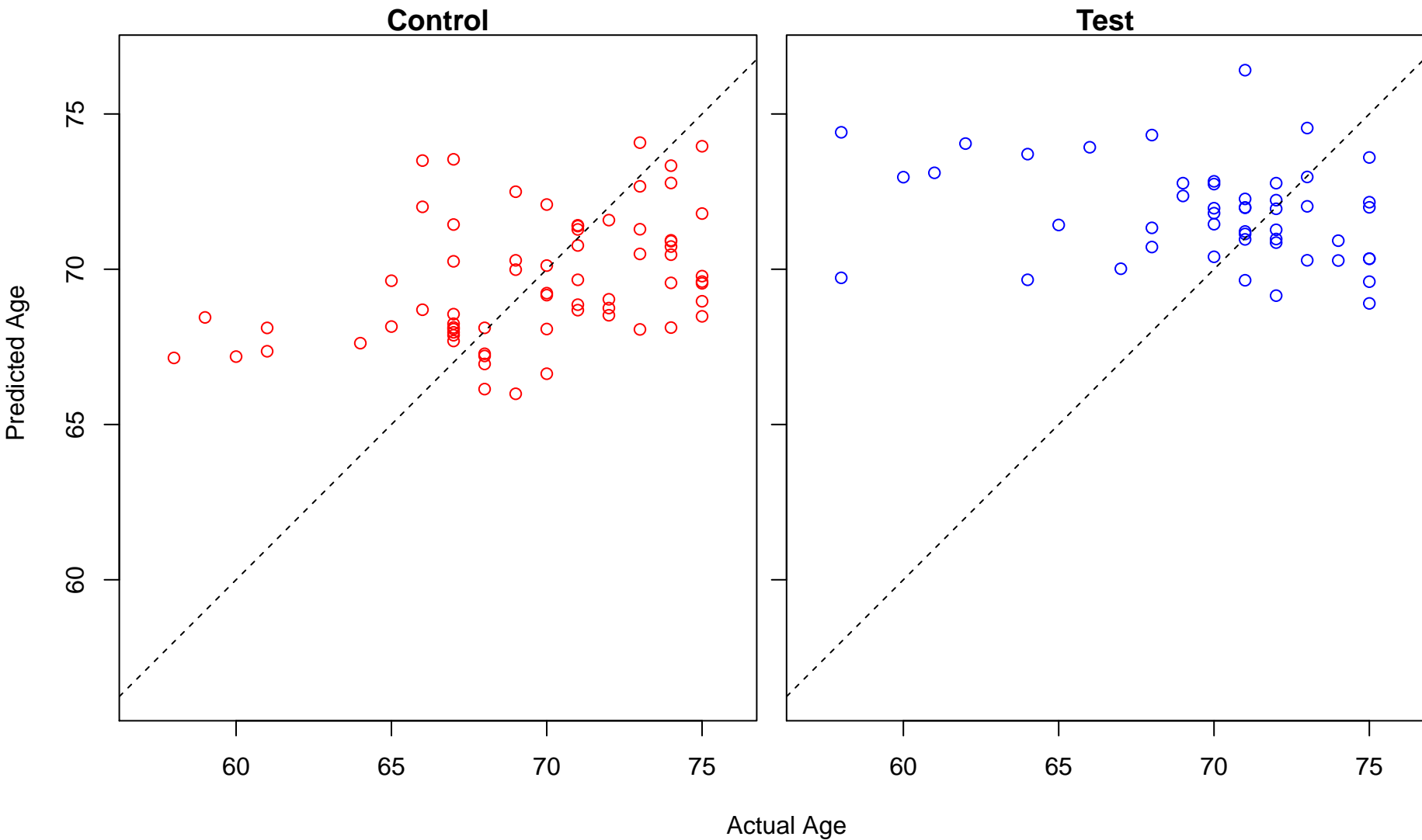
regulation of neuron migration (Score: 0.527110)



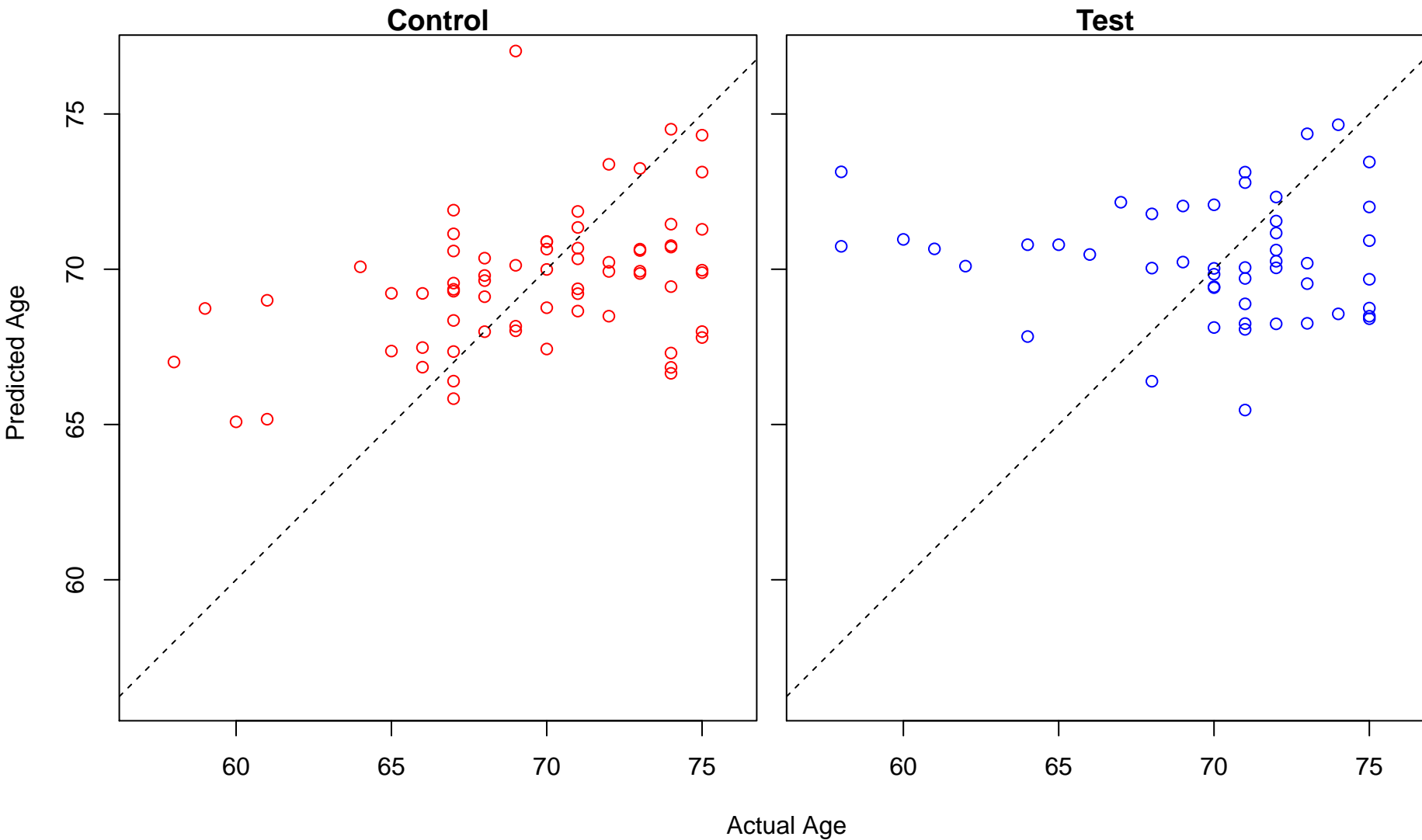
negative regulation of steroid biosynthetic process (Score: 0.527053)



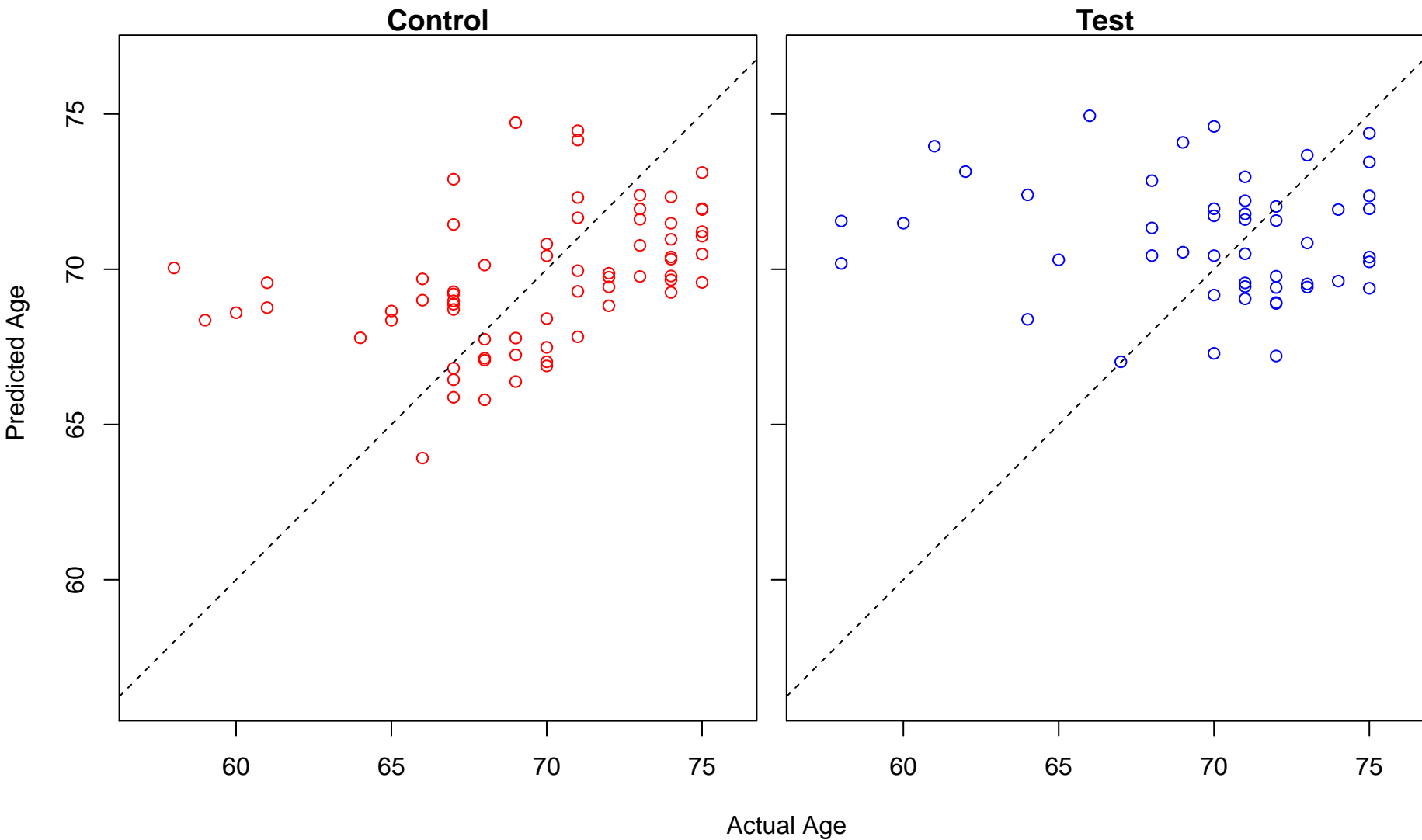
negative regulation of steroid metabolic process (Score: 0.527053)



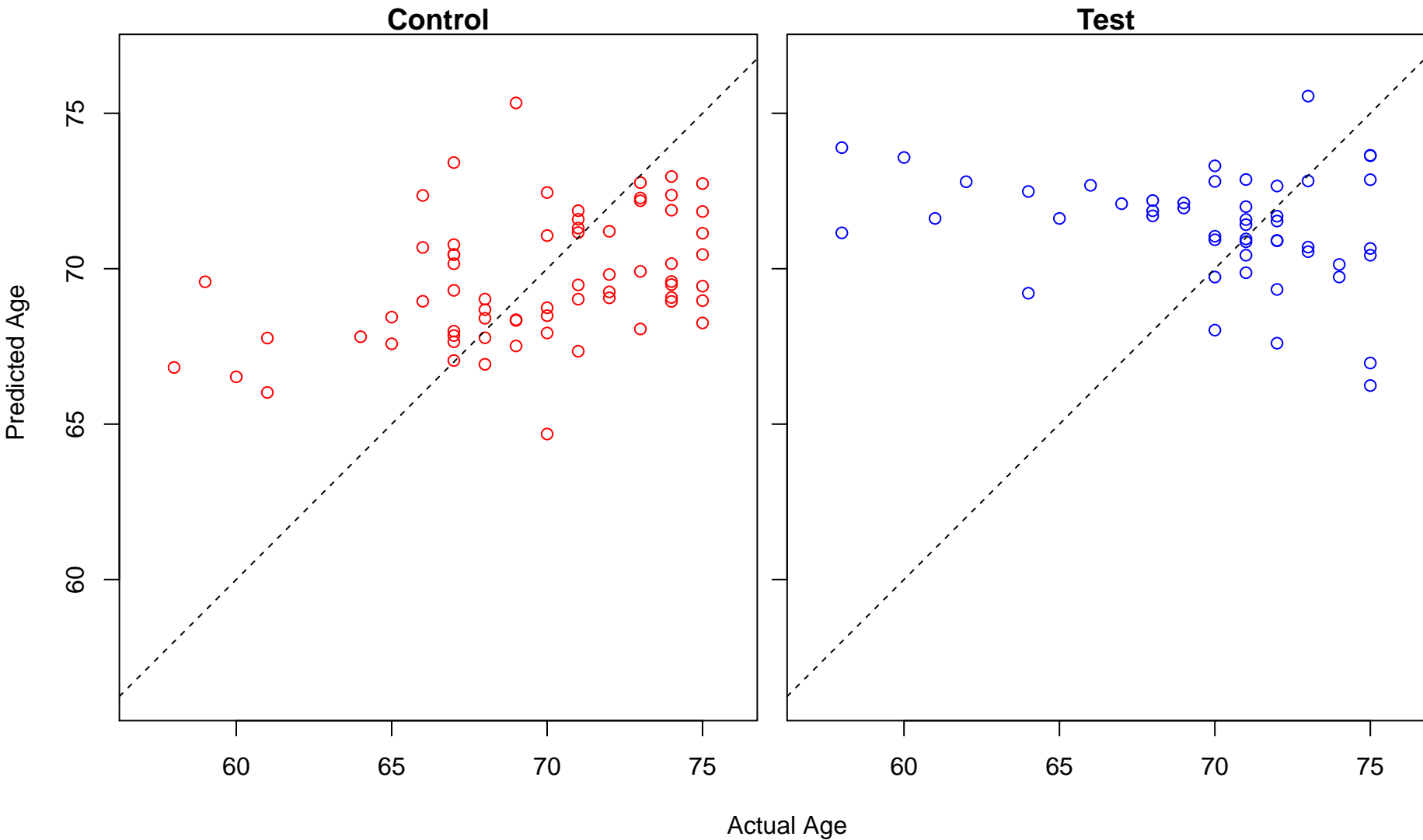
riboflavin metabolic process (Score: 0.526778)



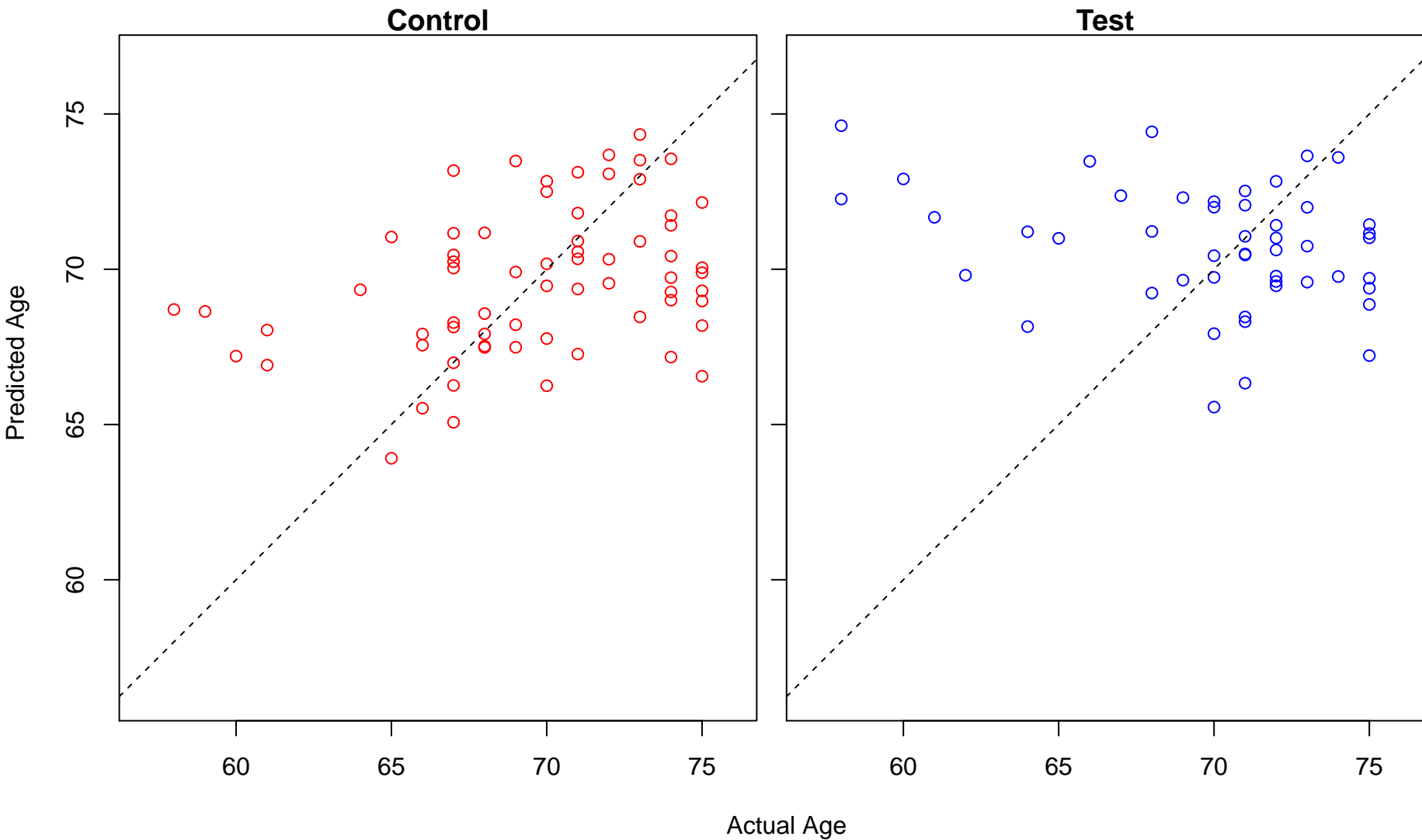
nucleobase transport (Score: 0.526694)



regulation of microtubule-based movement (Score: 0.526523)

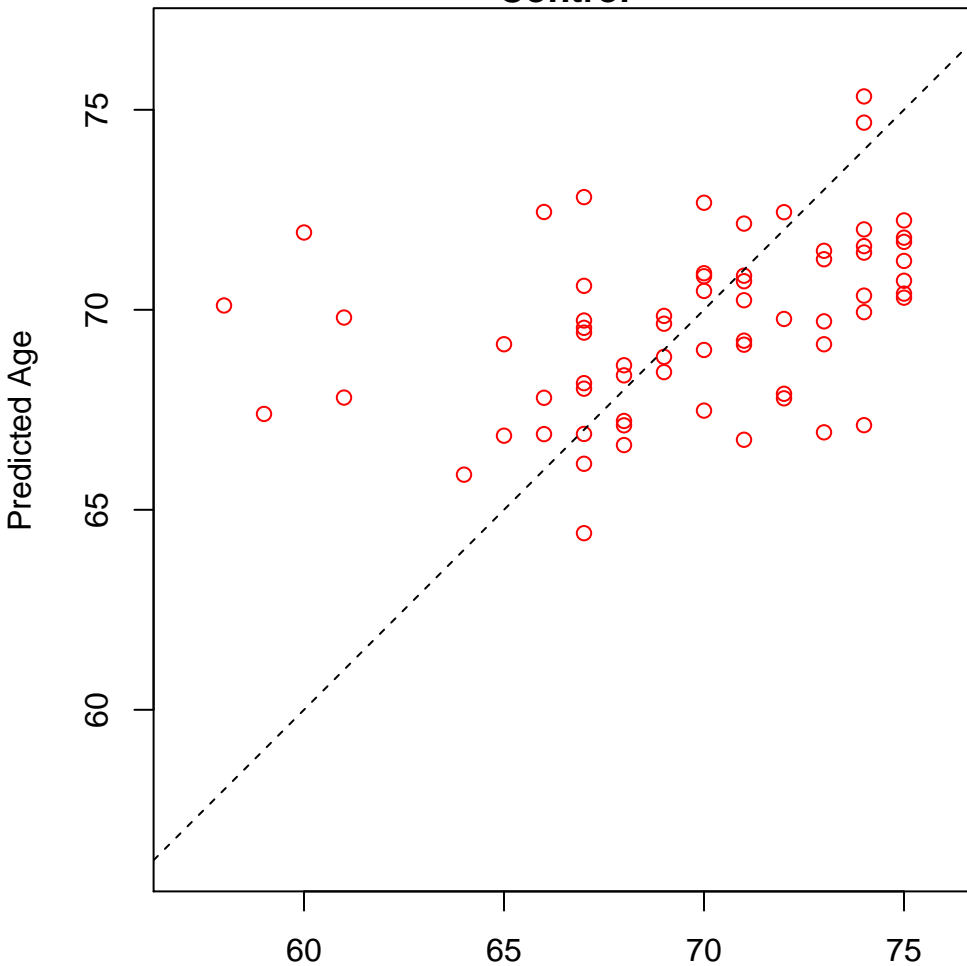


negative regulation of substrate adhesion-dependent cell spreading (Score: 0.525588)

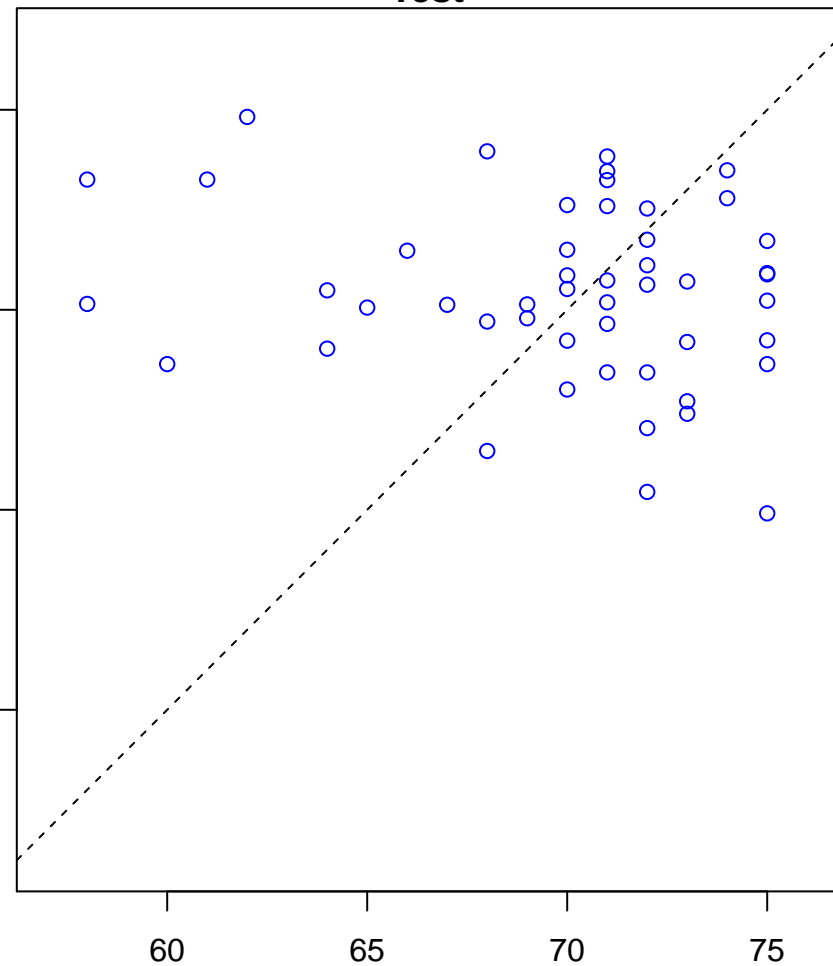


regulation of B cell apoptotic process (Score: 0.525543)

Control

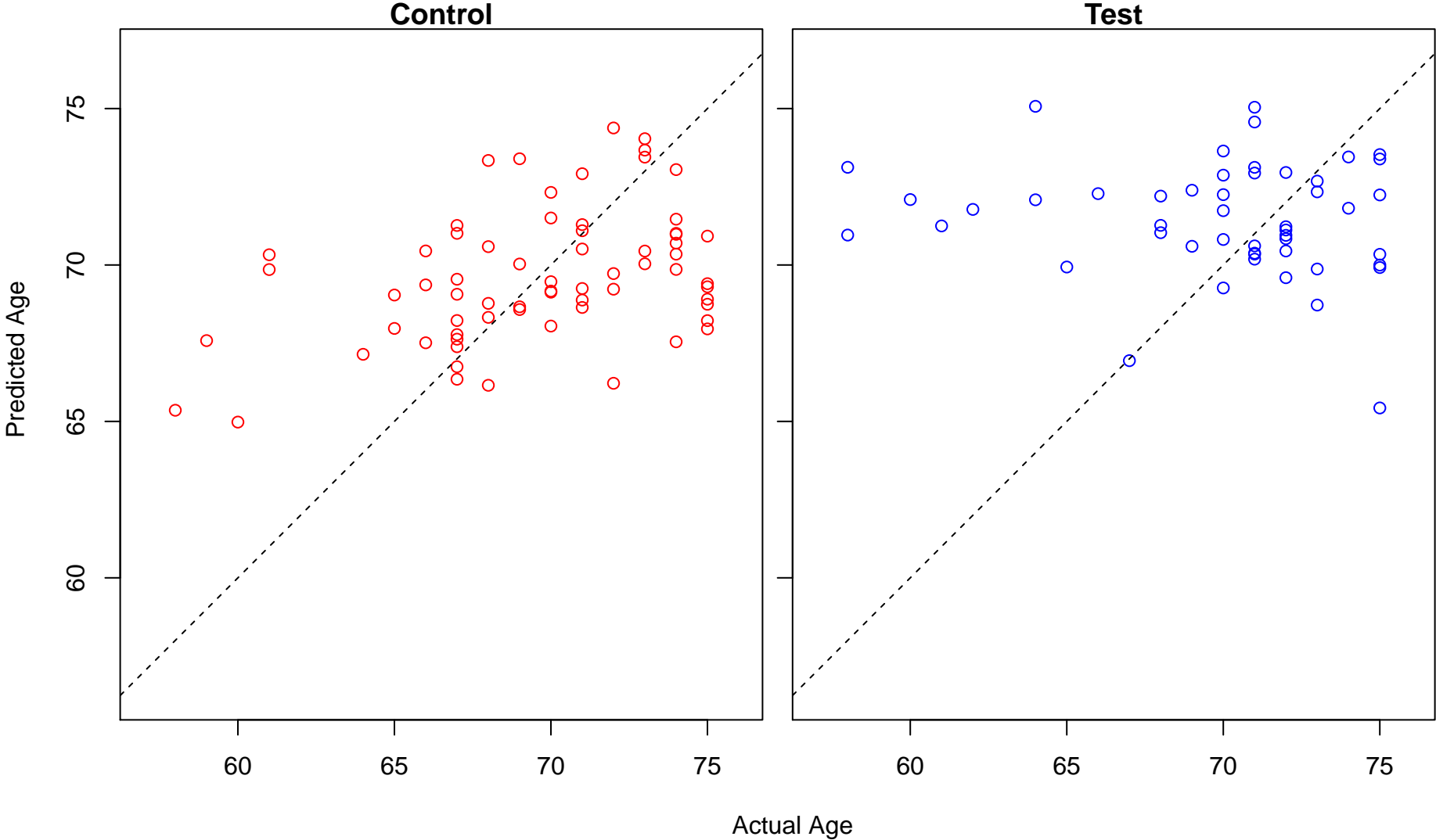


Test

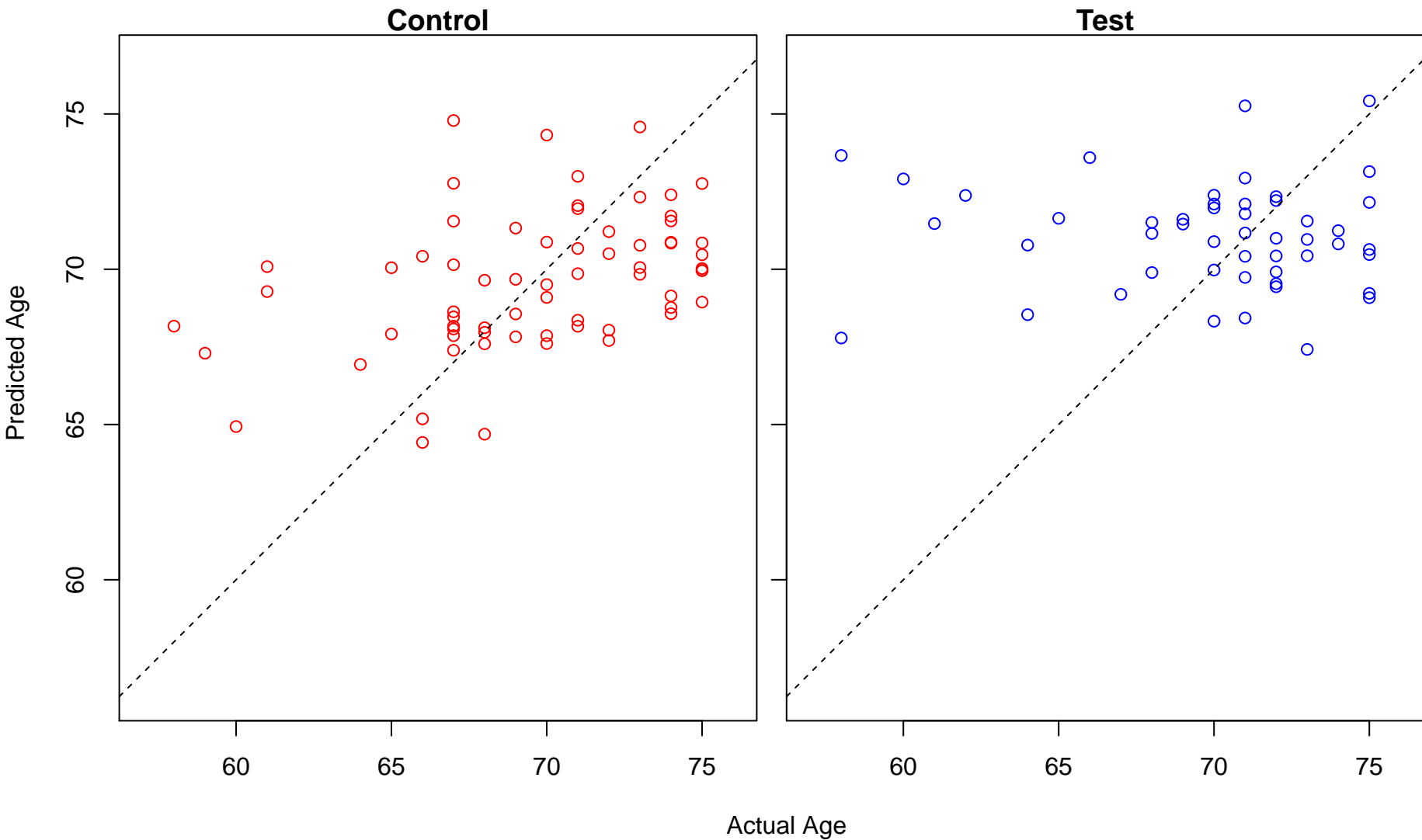


Actual Age

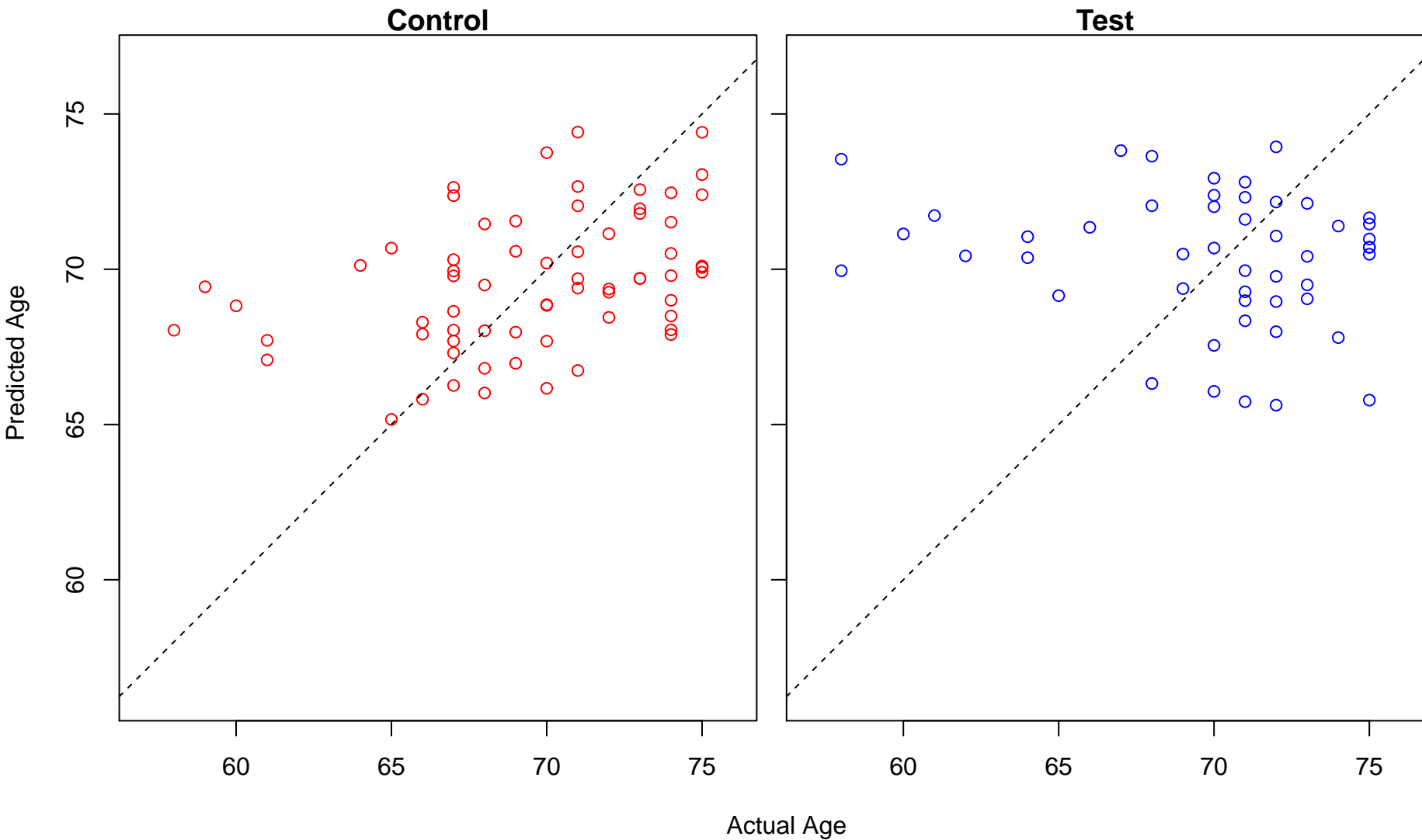
positive regulation of dendritic cell antigen processing and presentation (Score: 0.525334)



regulation of phosphatidylinositol 3-kinase activity (Score: 0.524213)

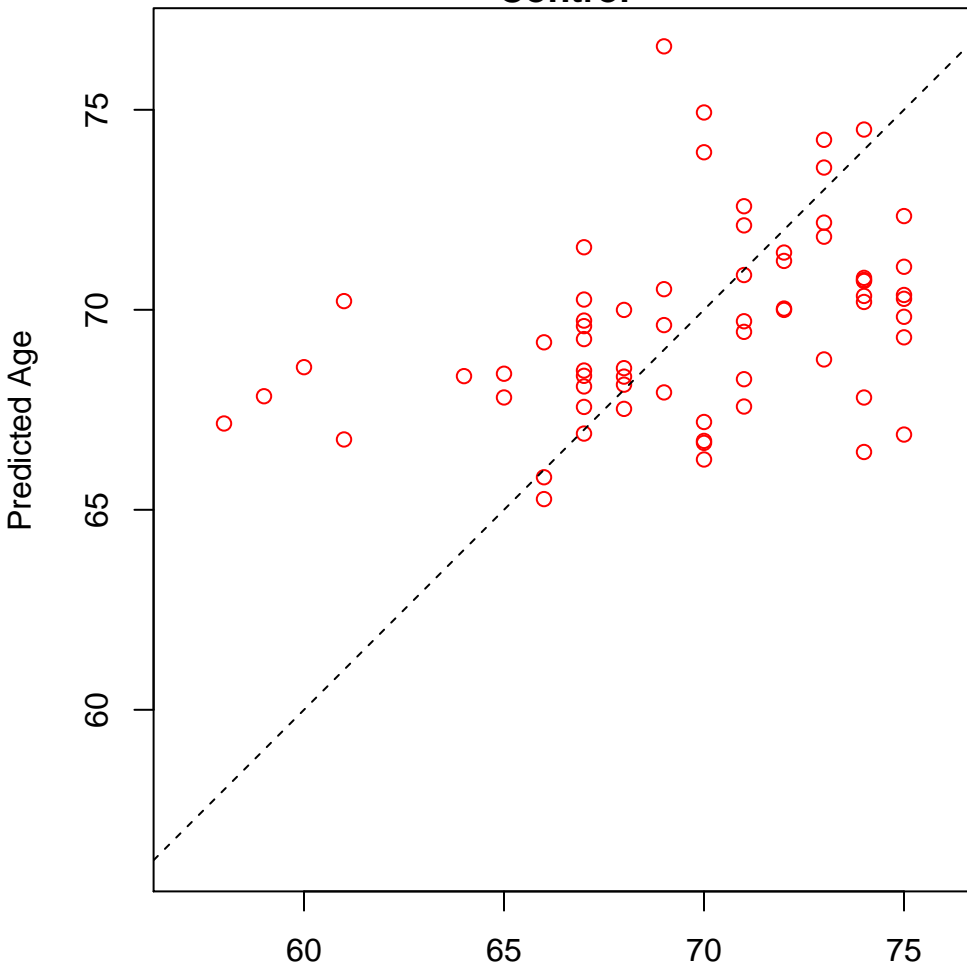


regulation of B cell differentiation (Score: 0.524197)

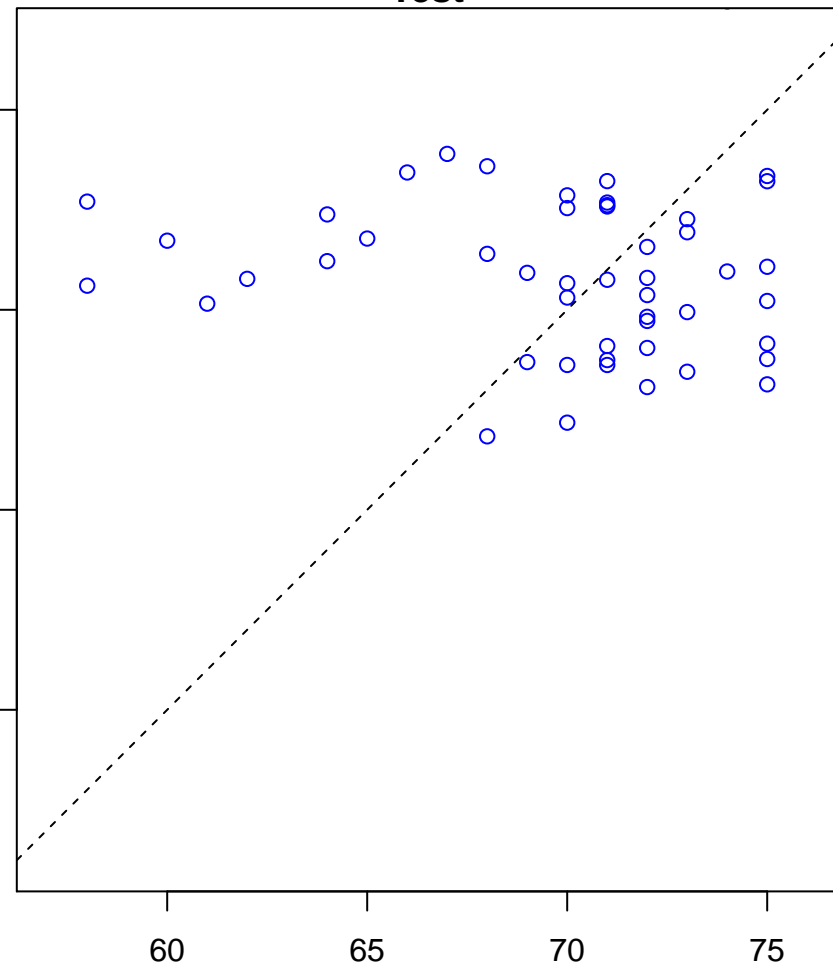


negative regulation of circadian rhythm (Score: 0.523015)

Control

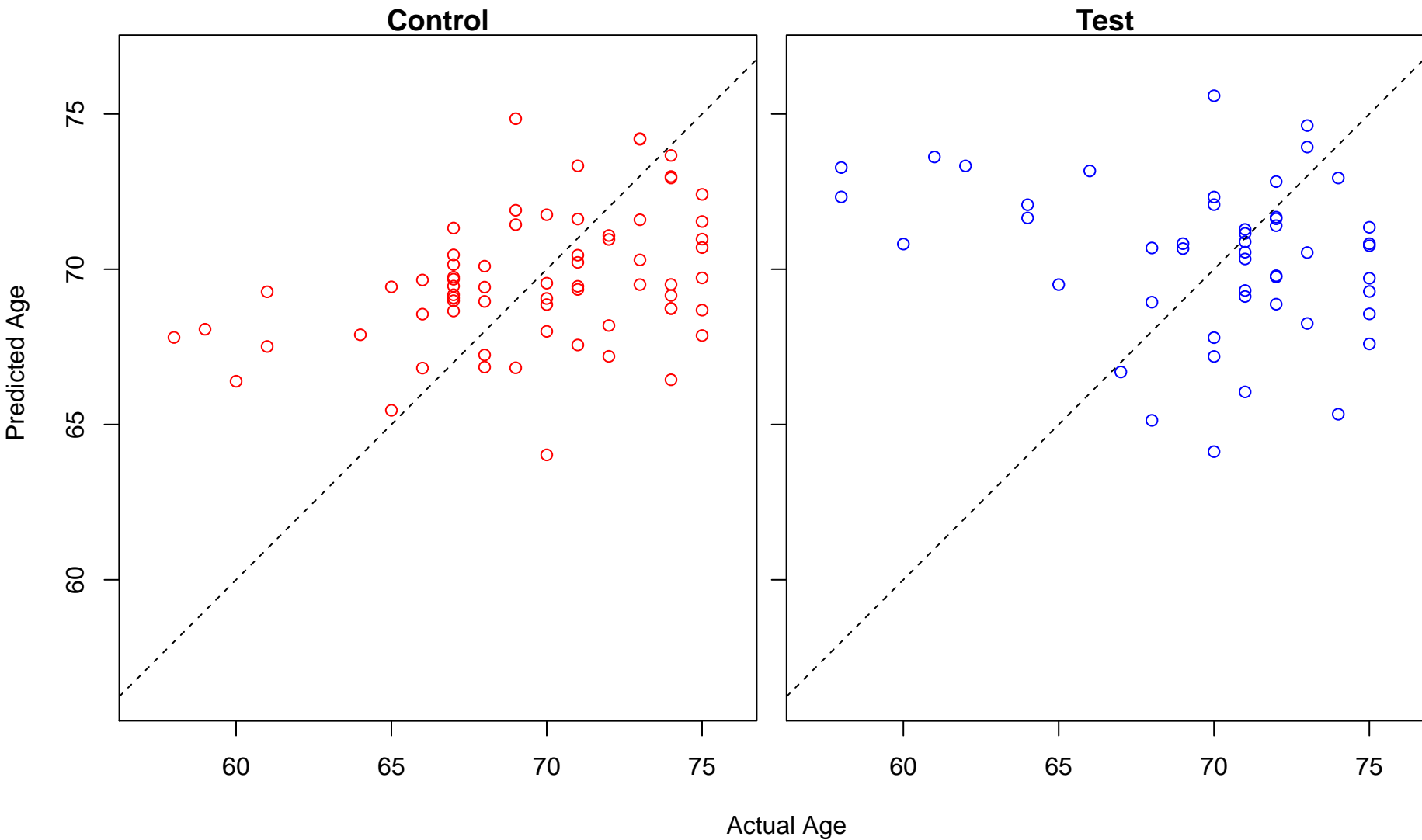


Test

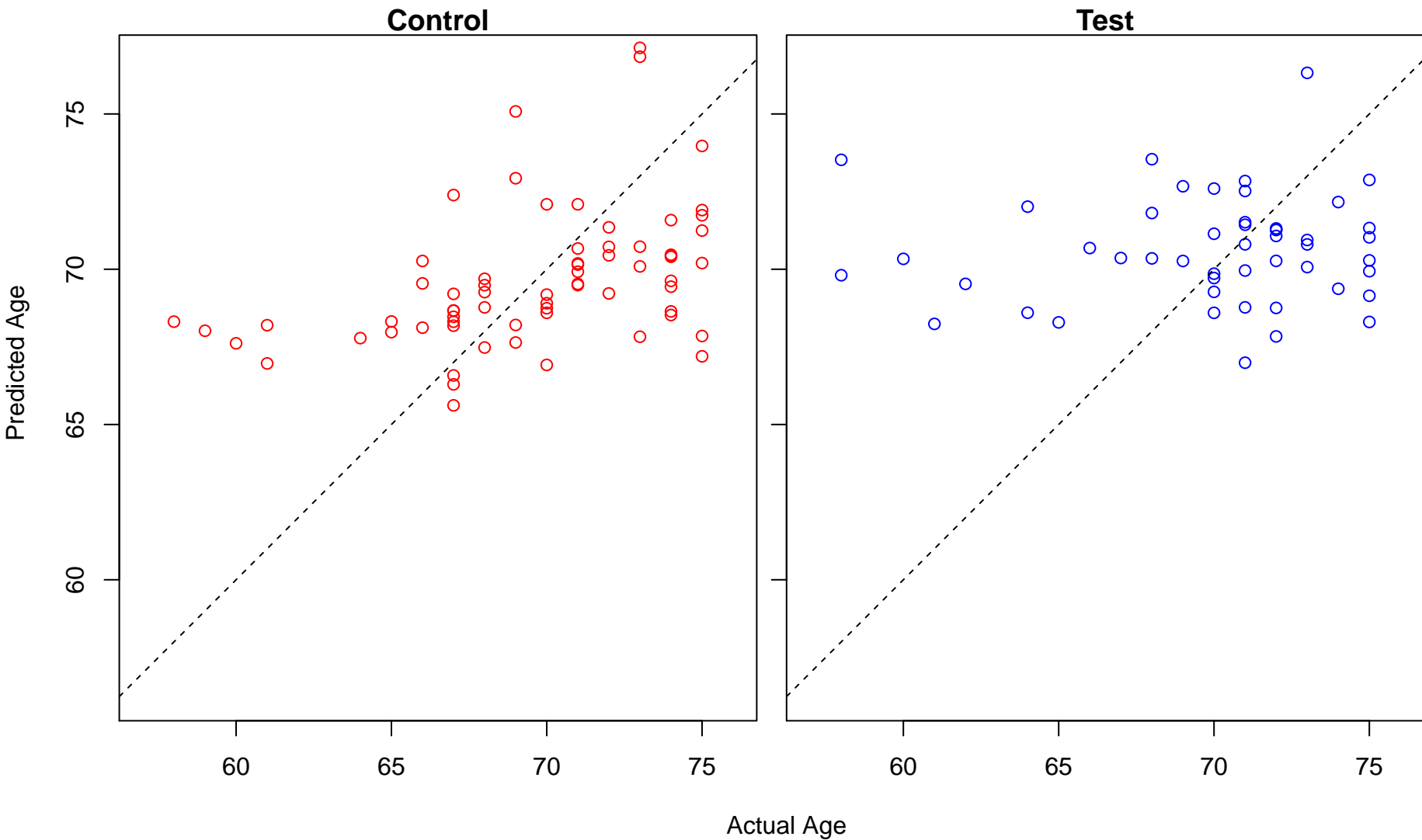


Actual Age

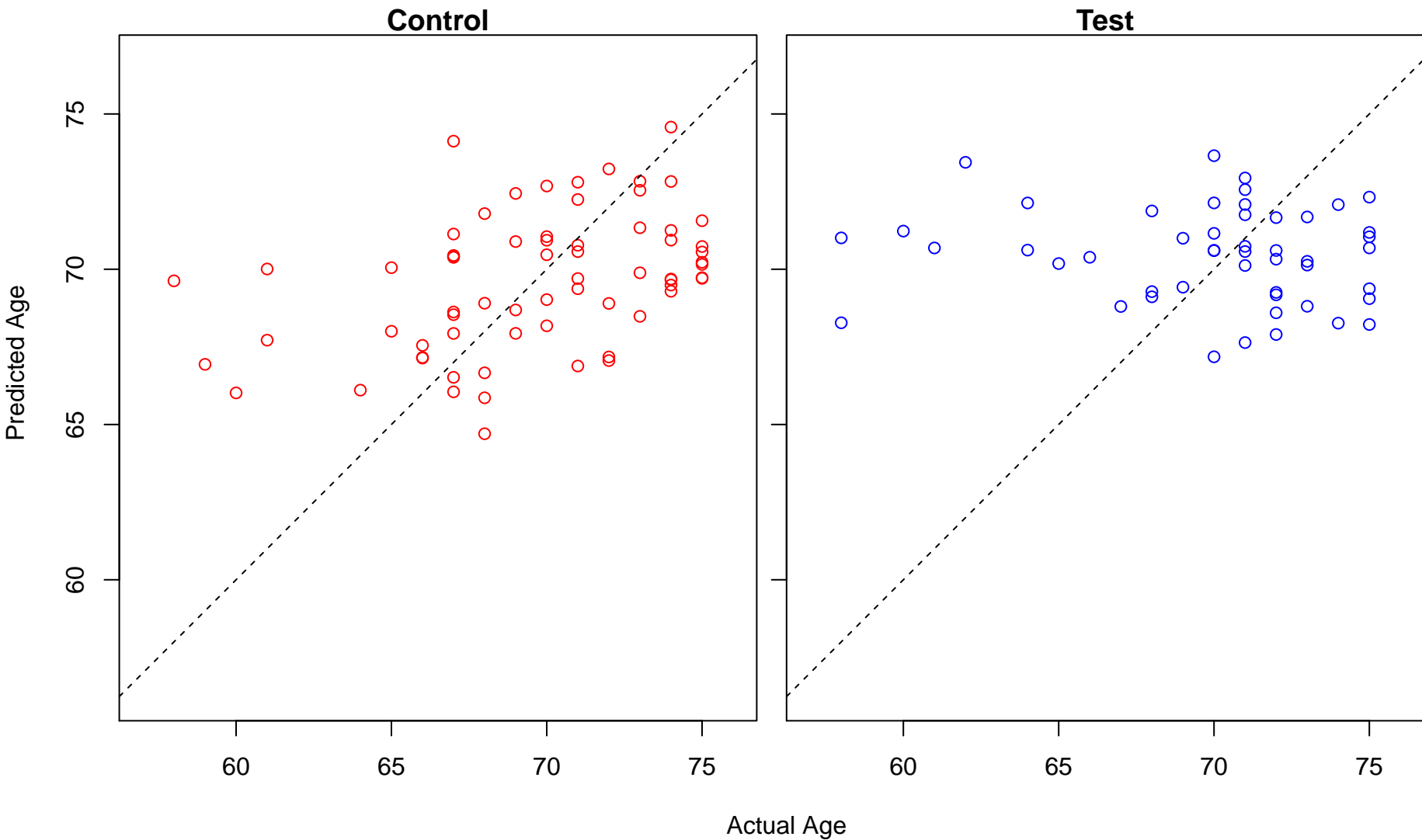
maintenance of protein localization in endoplasmic reticulum (Score: 0.522196)



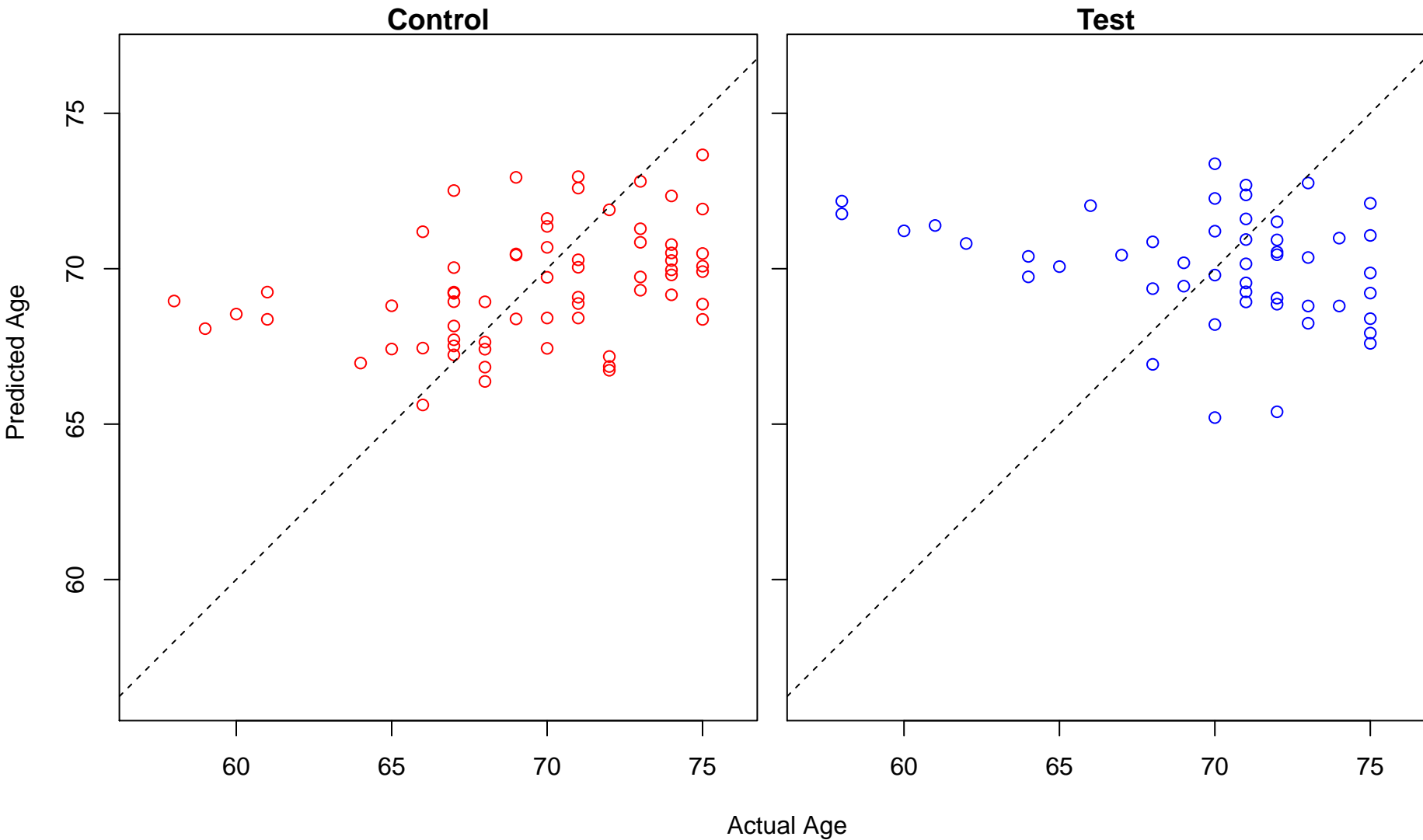
metanephros morphogenesis (Score: 0.521684)



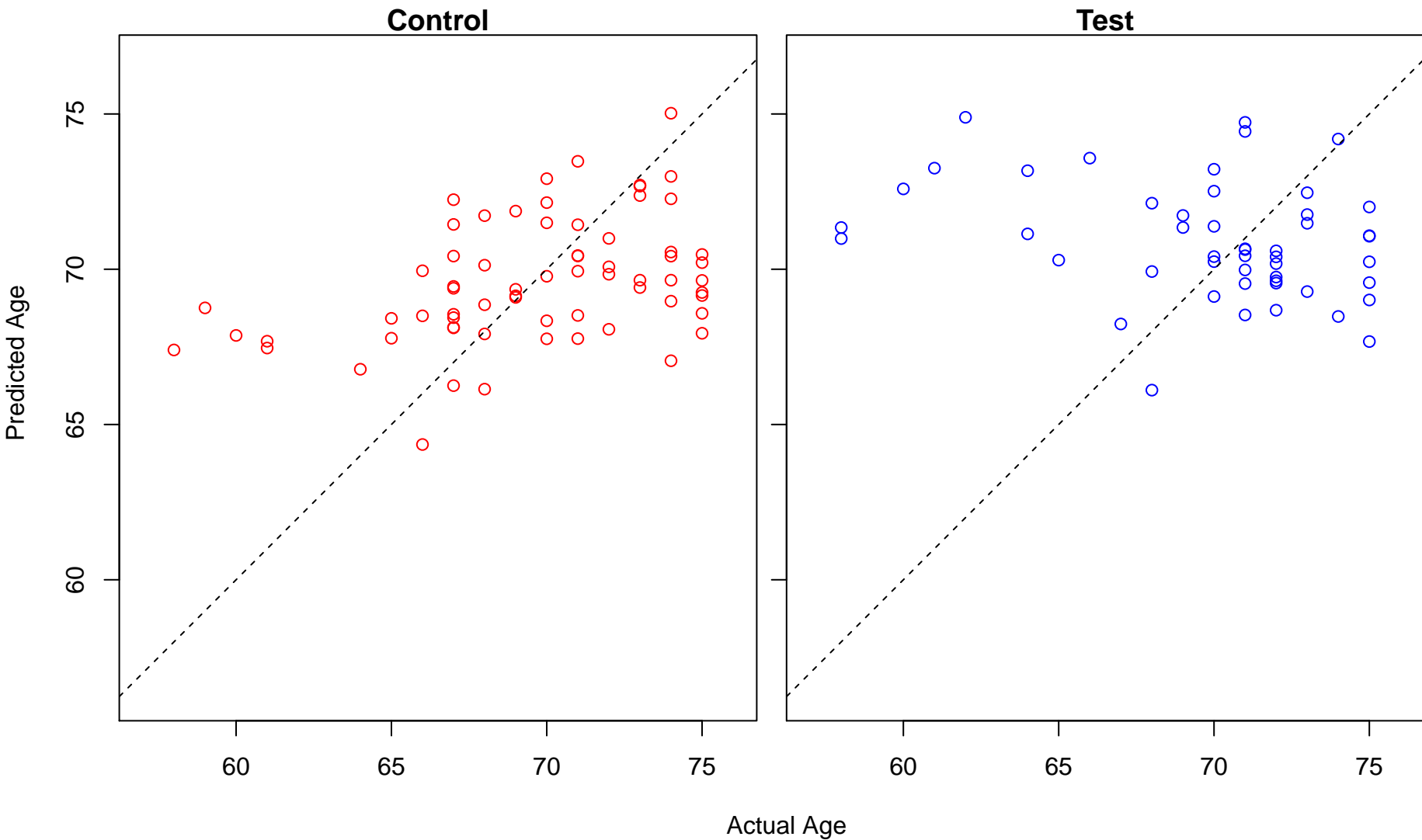
purinergic nucleotide receptor signaling pathway (Score: 0.519683)



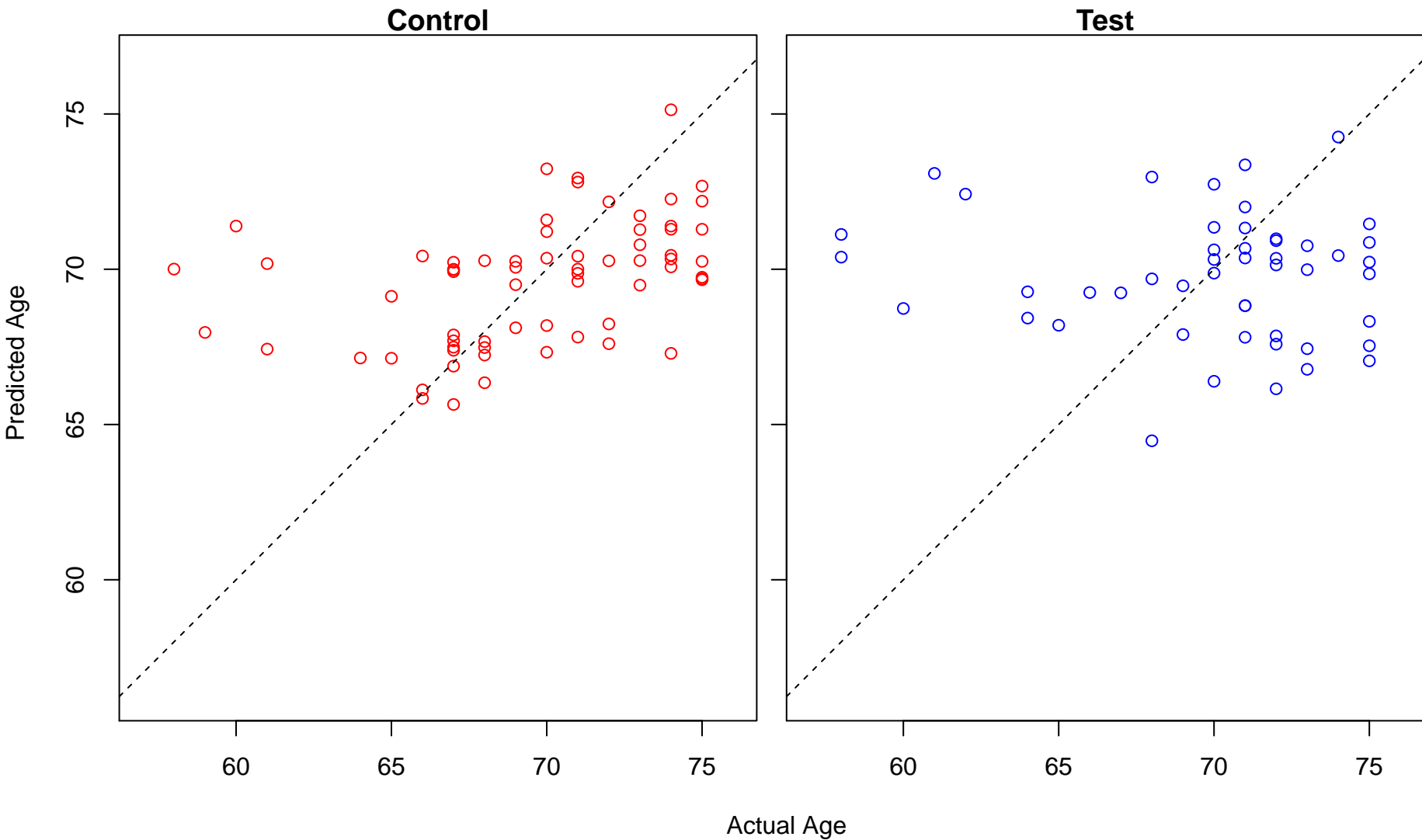
negative regulation of kidney development (Score: 0.519629)



interleukin-4-mediated signaling pathway (Score: 0.519171)

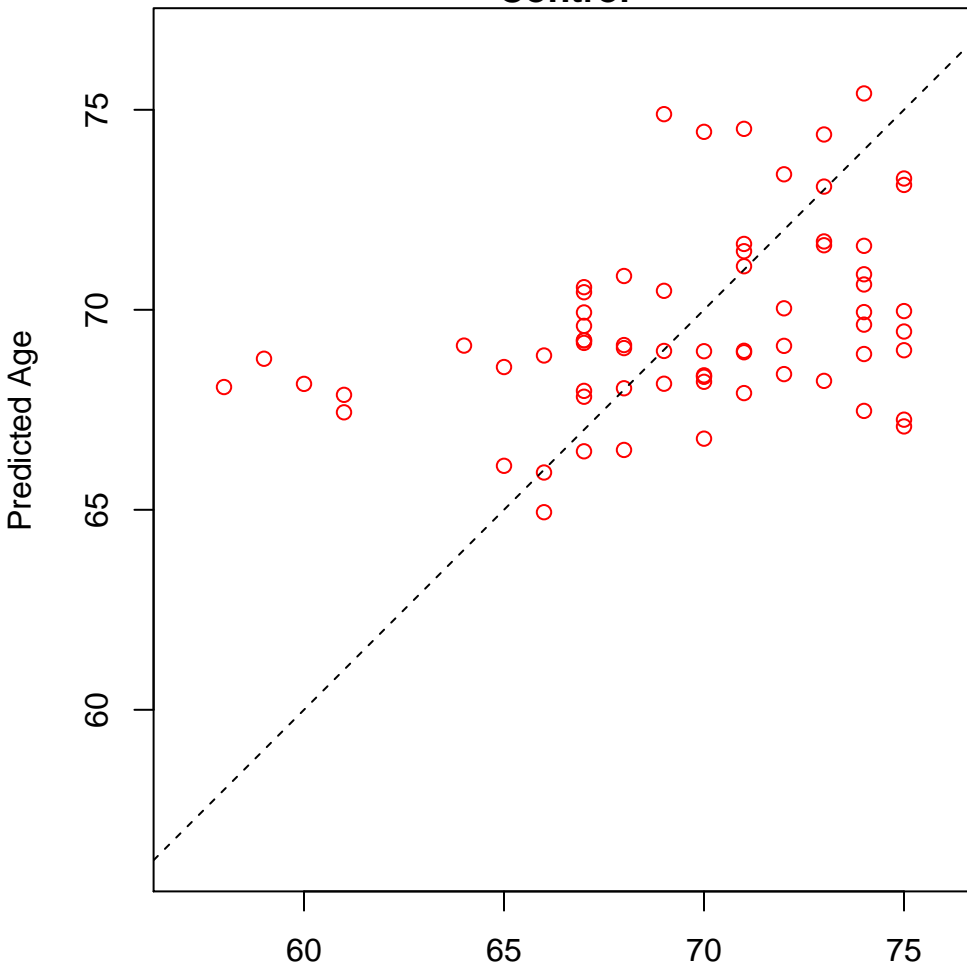


negative regulation of interleukin-12 production (Score: 0.518949)

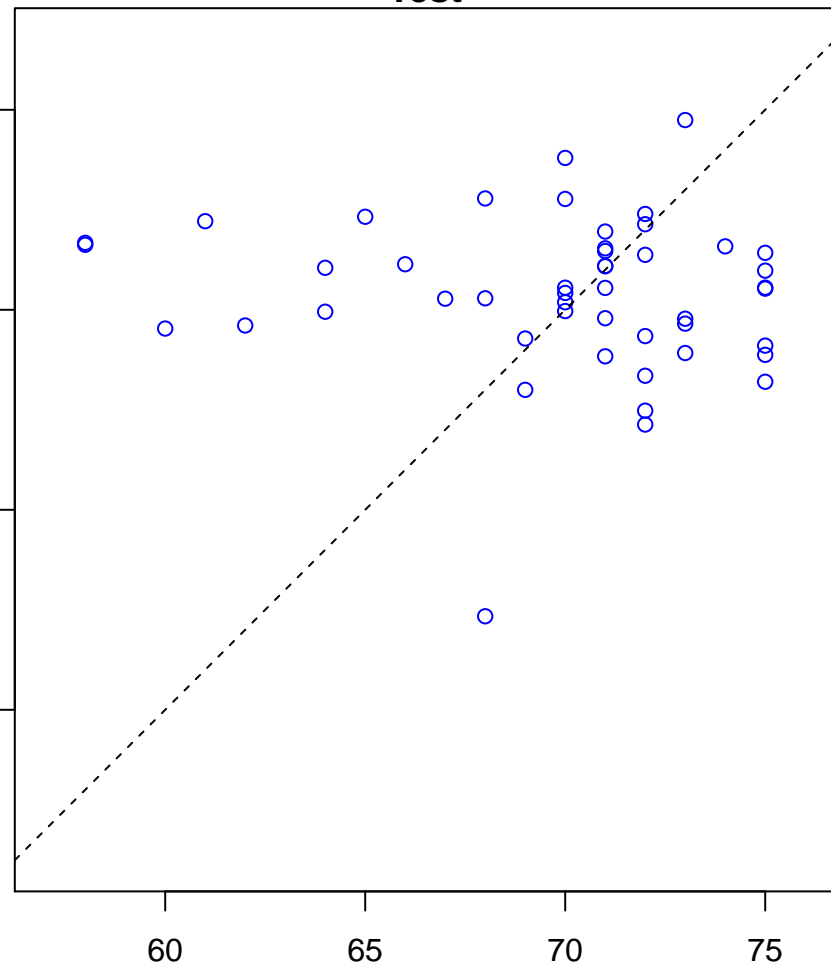


base-excision repair, AP site formation (Score: 0.518914)

Control

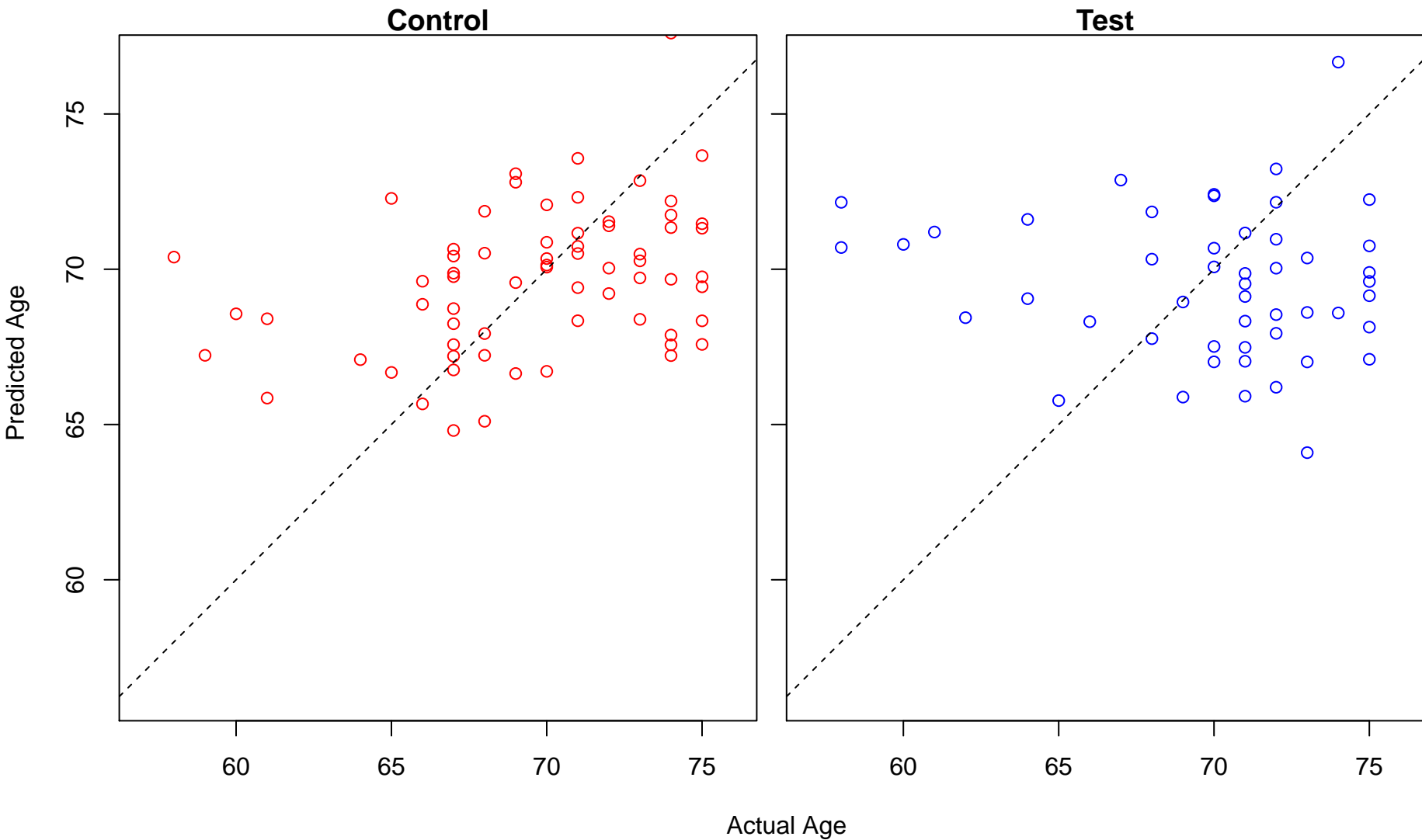


Test

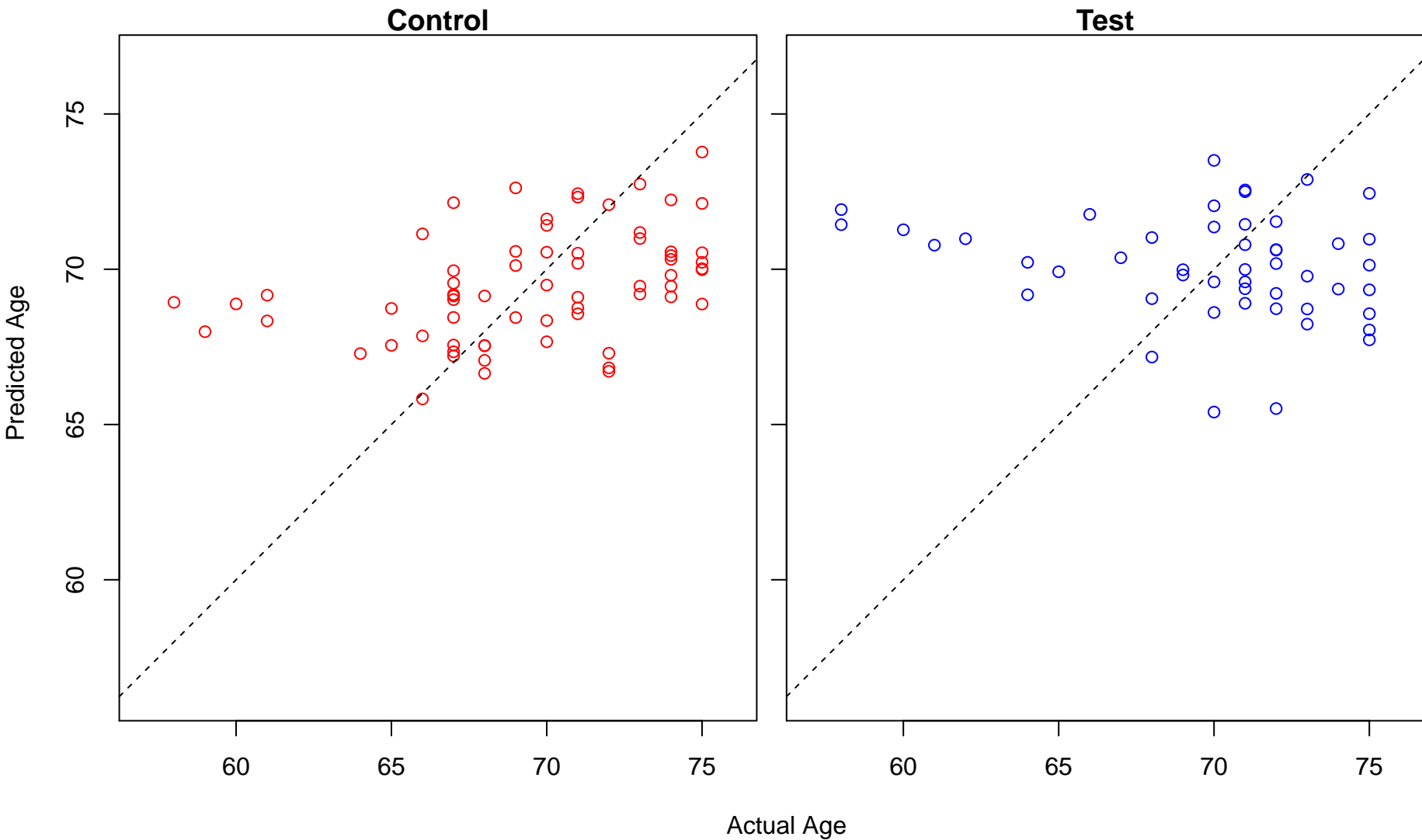


Actual Age

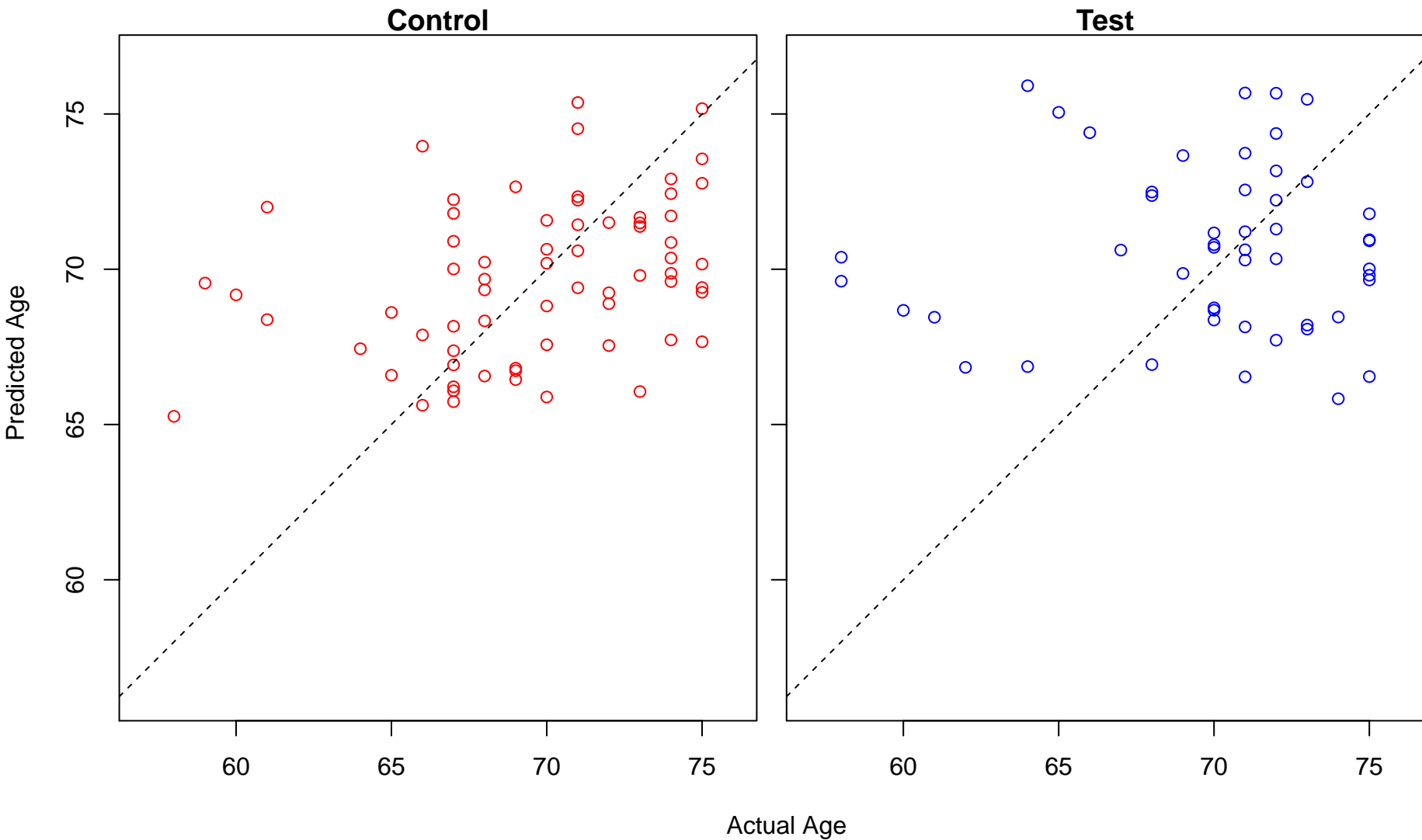
estrogen biosynthetic process (Score: 0.517905)



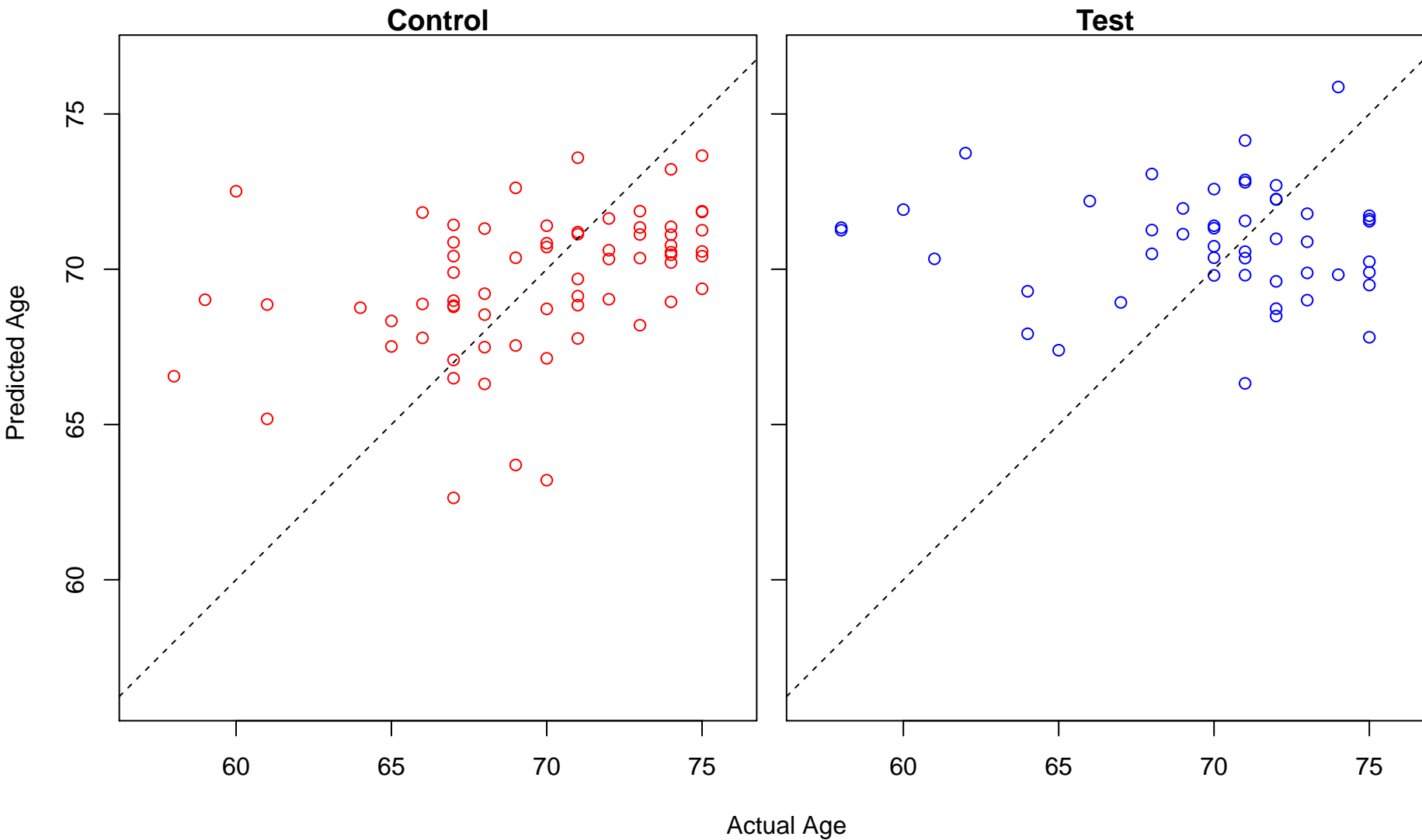
mesenchymal cell proliferation (Score: 0.517491)



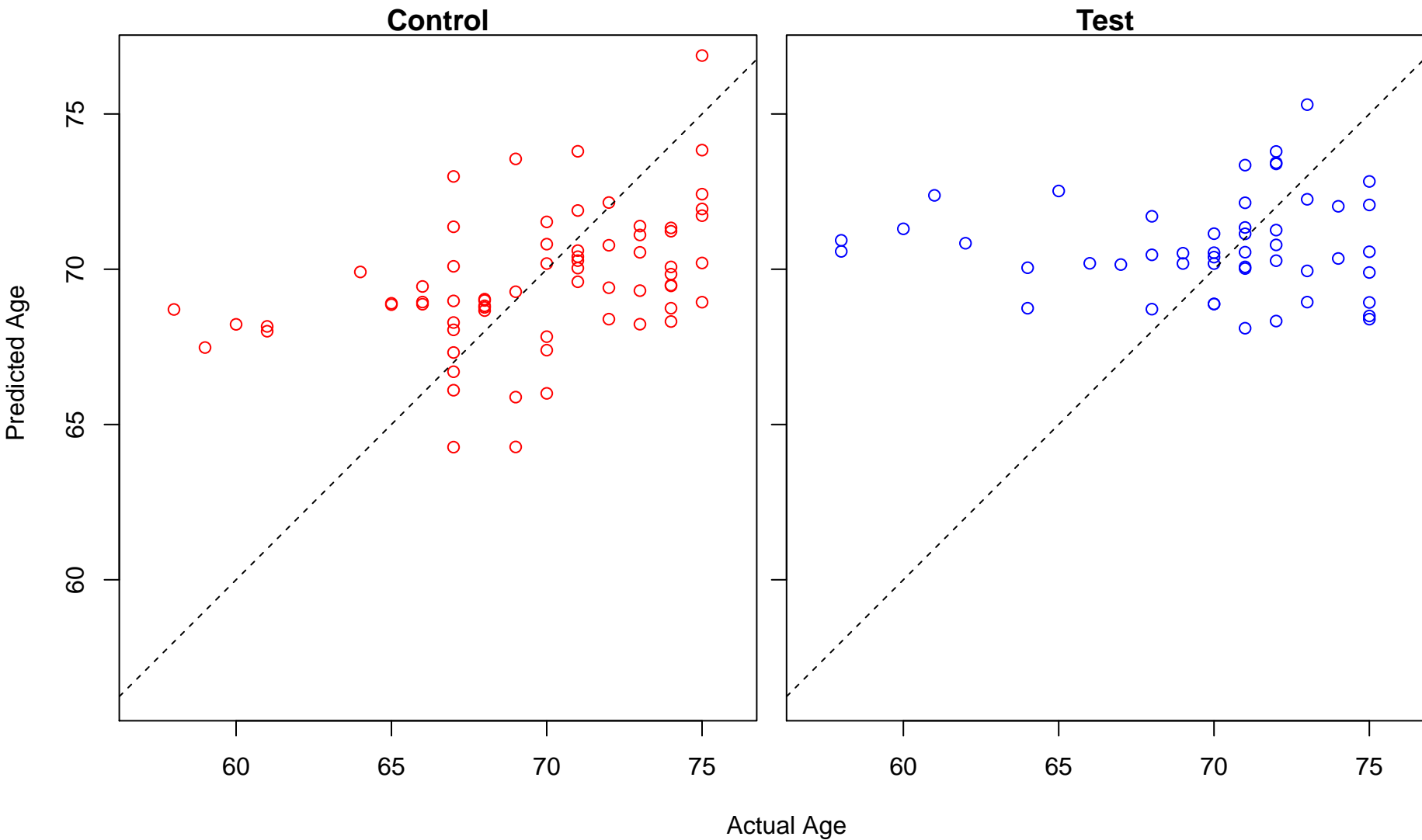
maintenance of organelle location (Score: 0.516877)



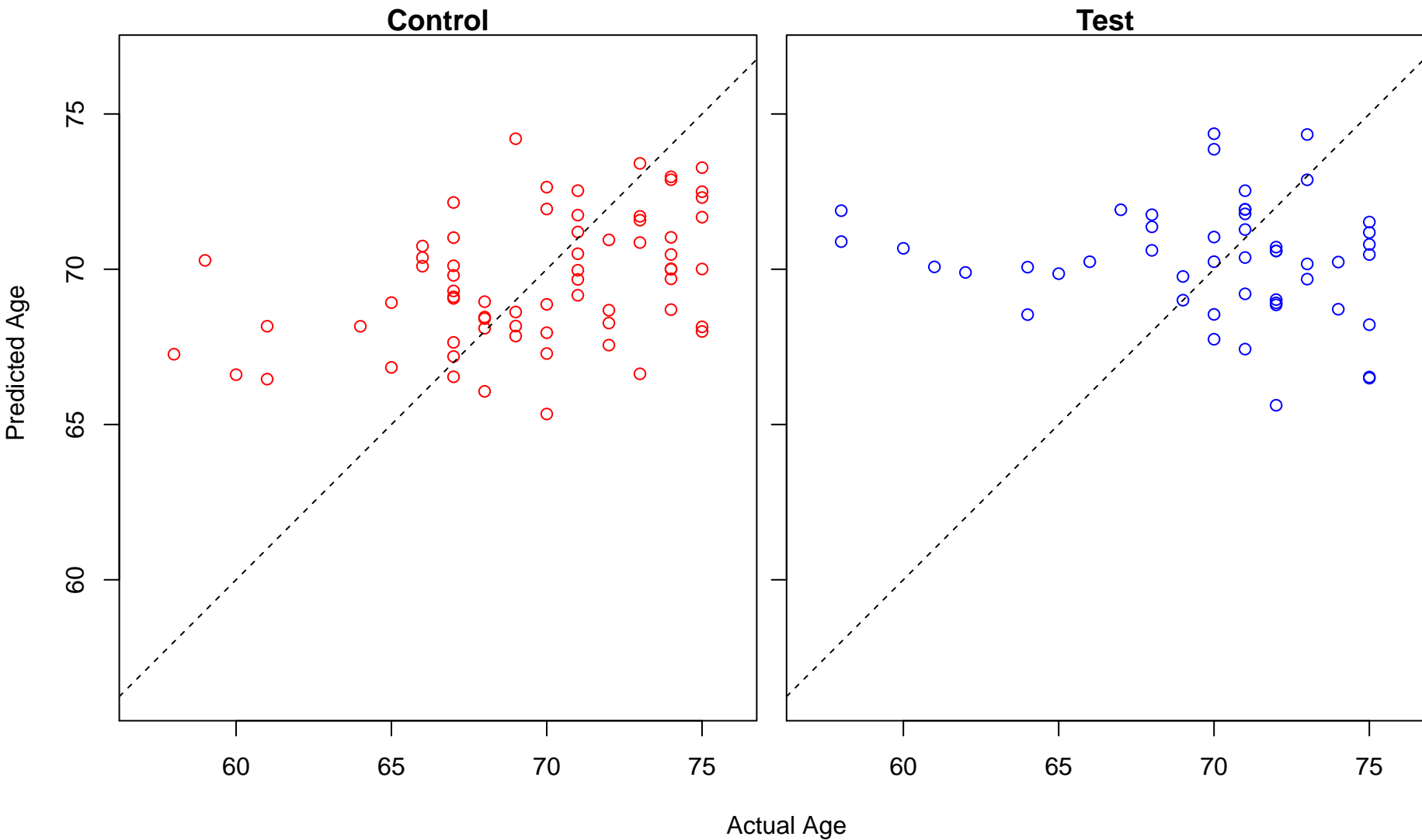
tryptophan metabolic process (Score: 0.516541)



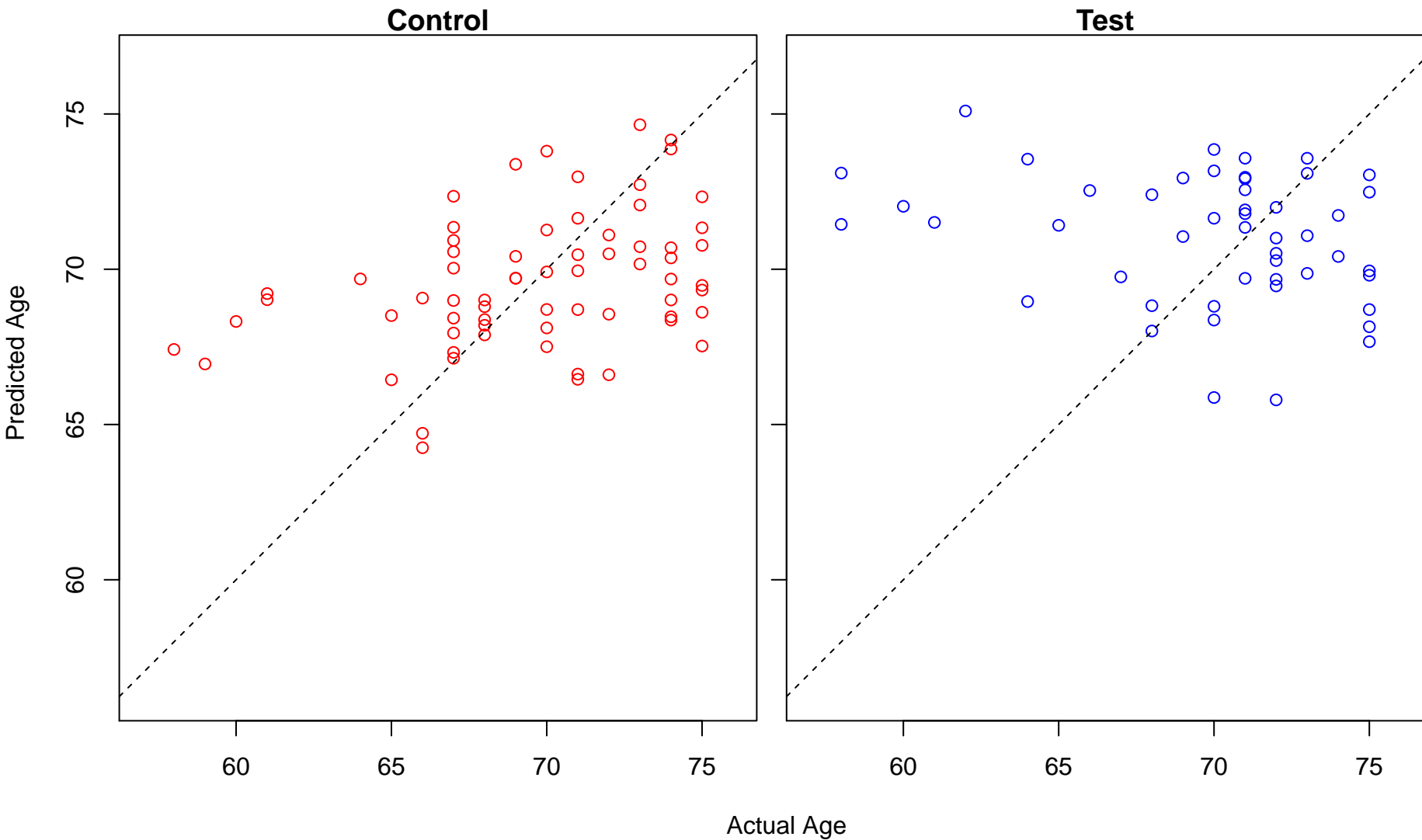
positive regulation of glucose import in response to insulin stimulus (Score: 0.516033)



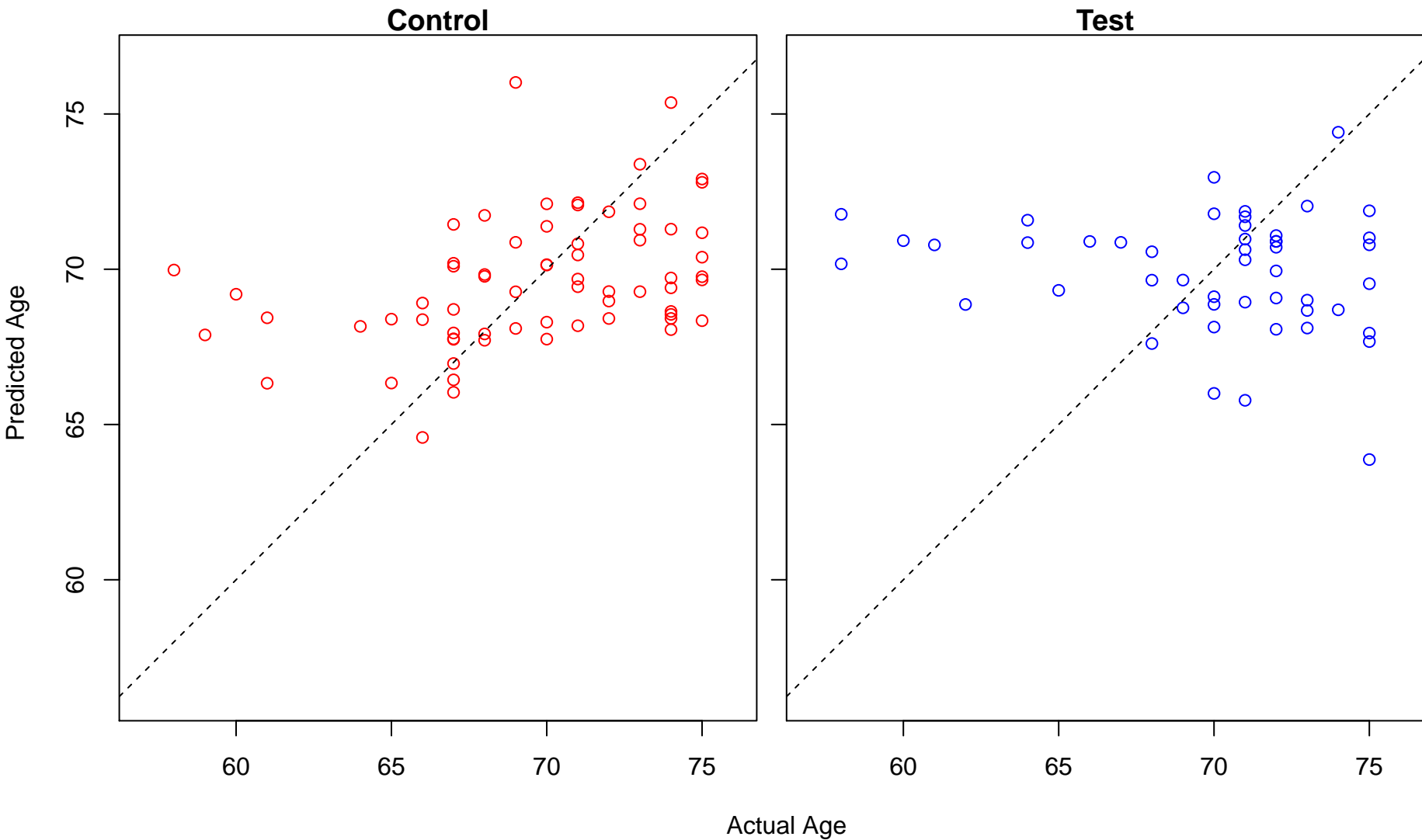
detection of mechanical stimulus involved in sensory perception (Score: 0.514293)



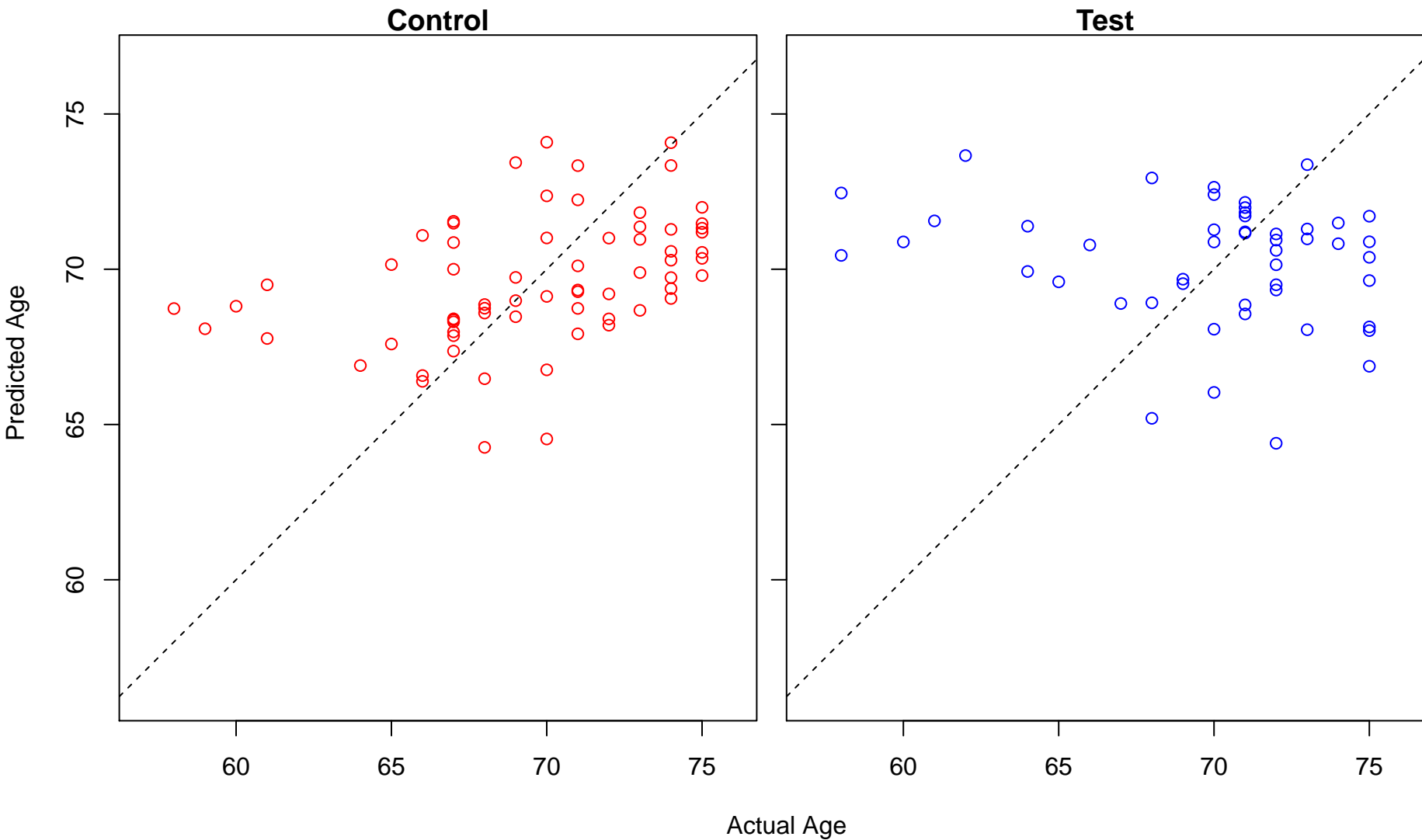
regulation of mitochondrial fission (Score: 0.514136)



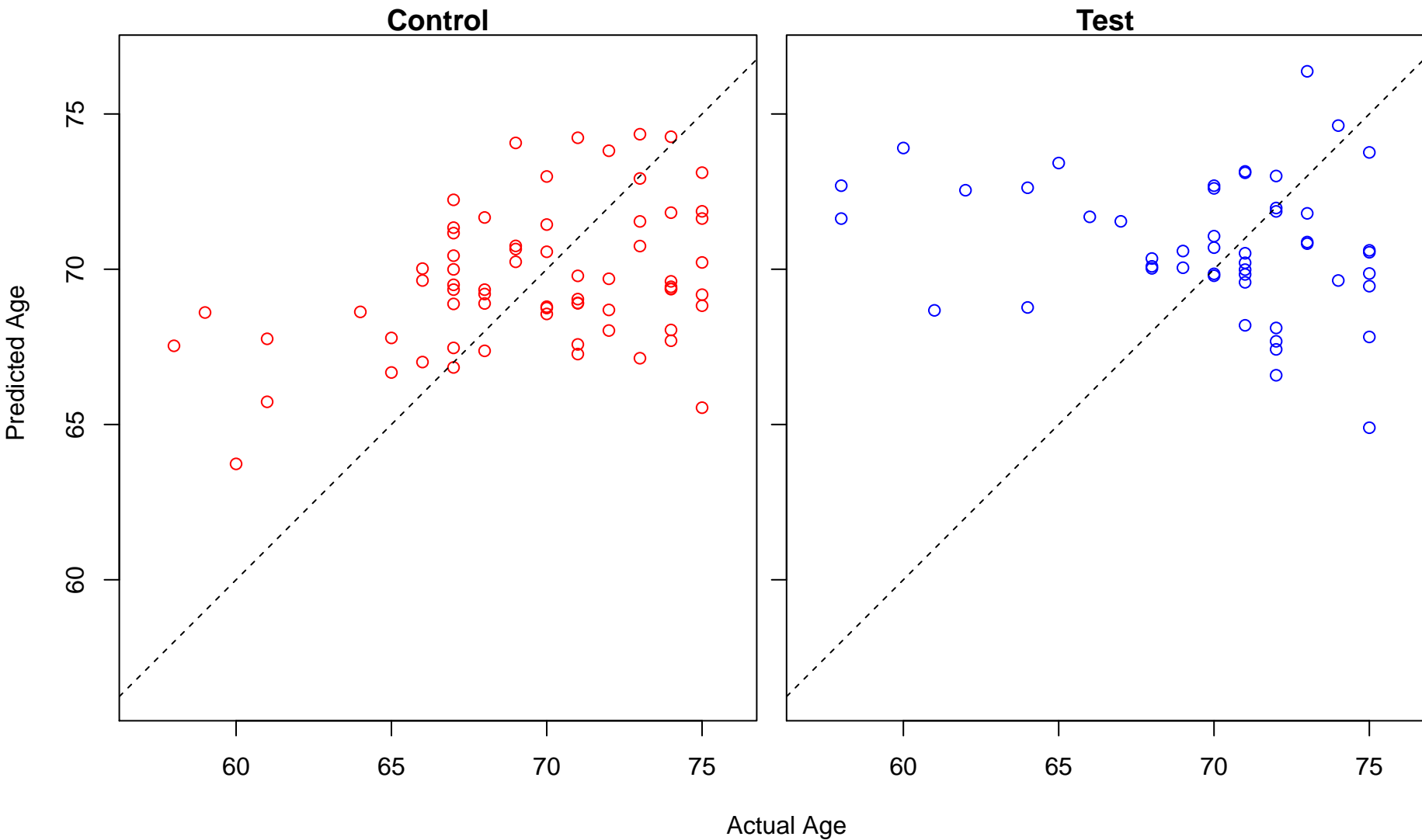
retina morphogenesis in camera-type eye (Score: 0.513916)



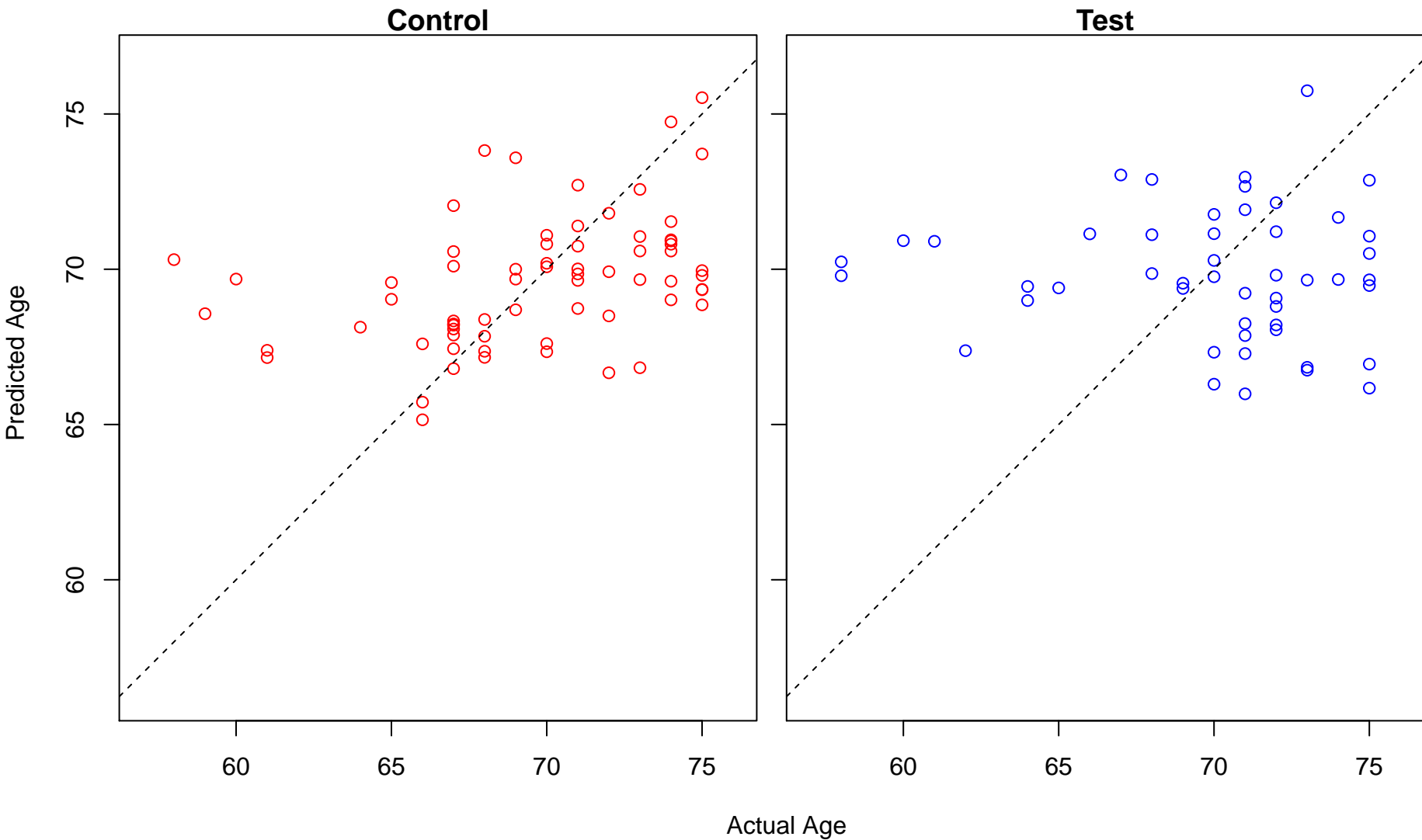
regulation of hematopoietic stem cell proliferation (Score: 0.513690)



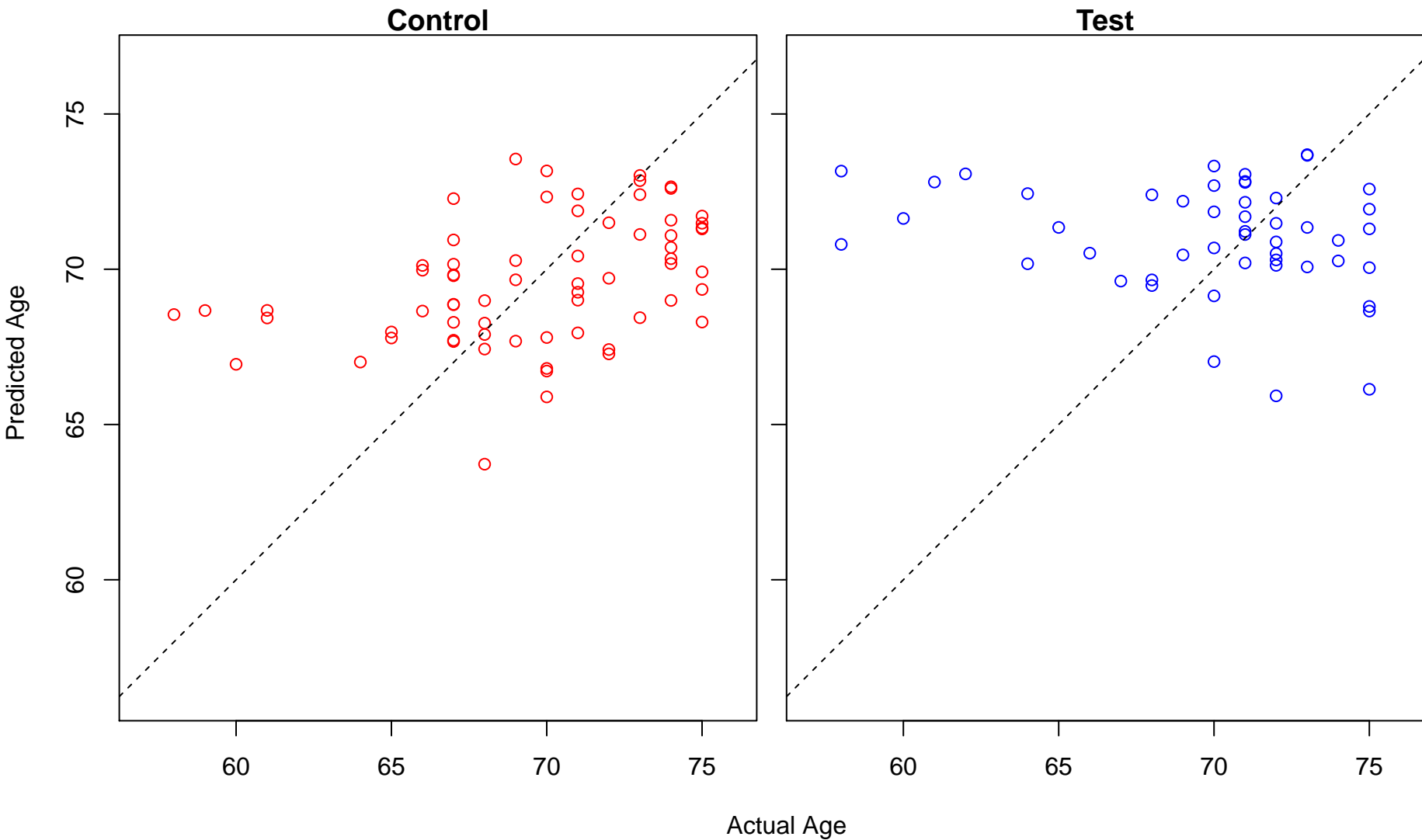
lipid storage (Score: 0.513363)



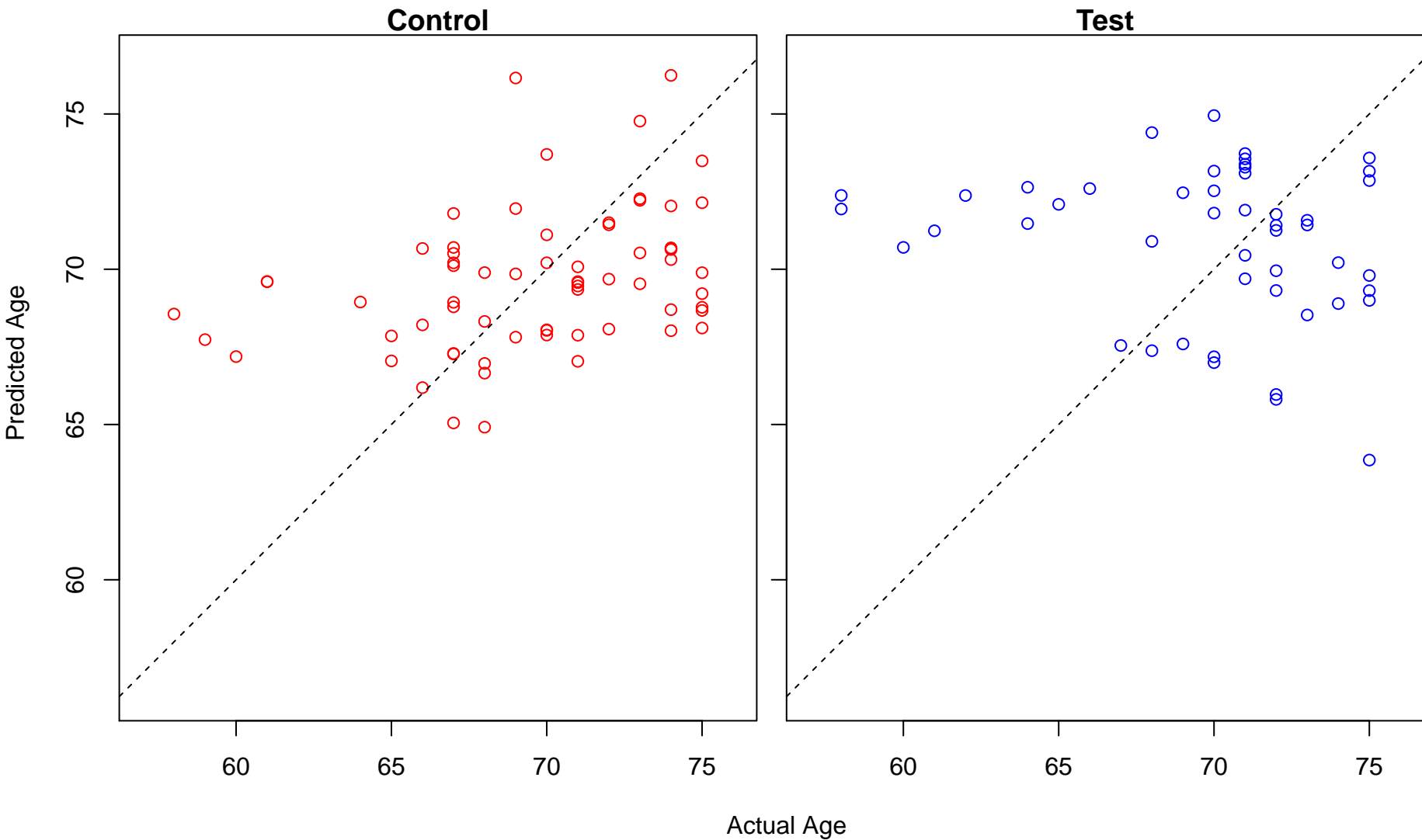
centrosome localization (Score: 0.512903)



positive regulation of cellular amine metabolic process (Score: 0.512468)

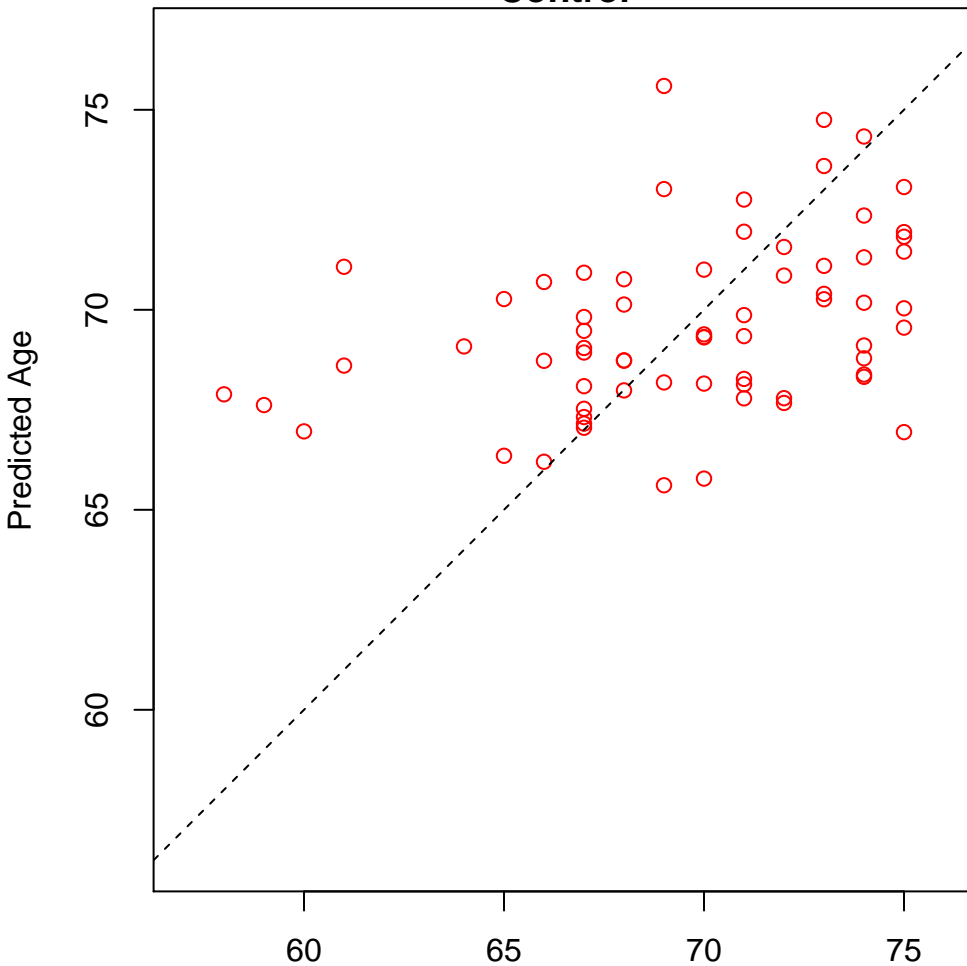


purine-containing compound salvage (Score: 0.512186)

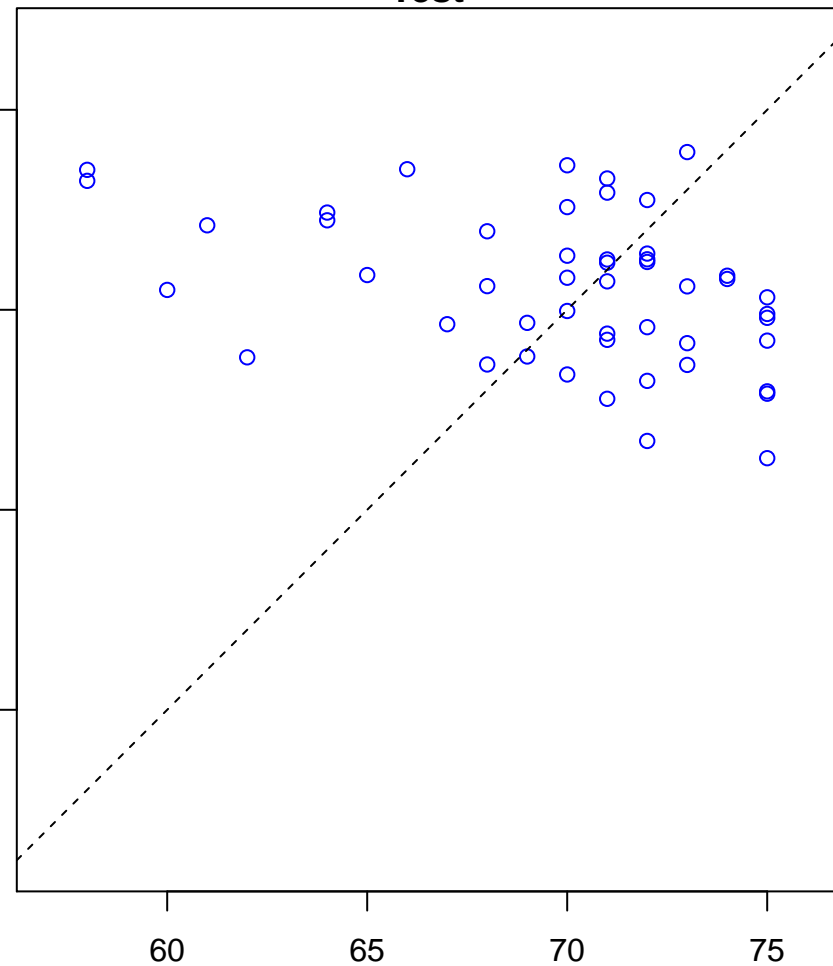


regulation of interleukin-23 production (Score: 0.512147)

Control

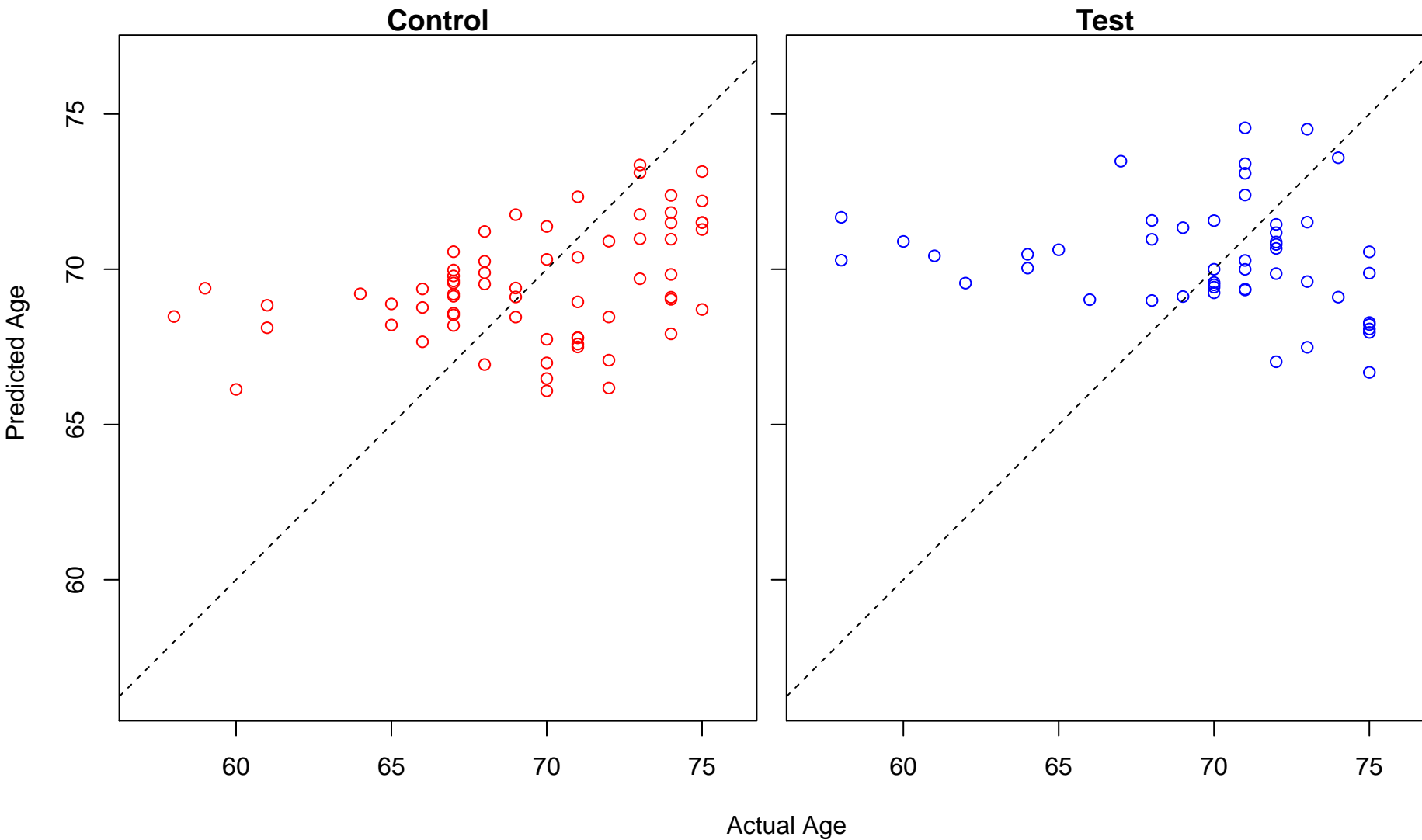


Test

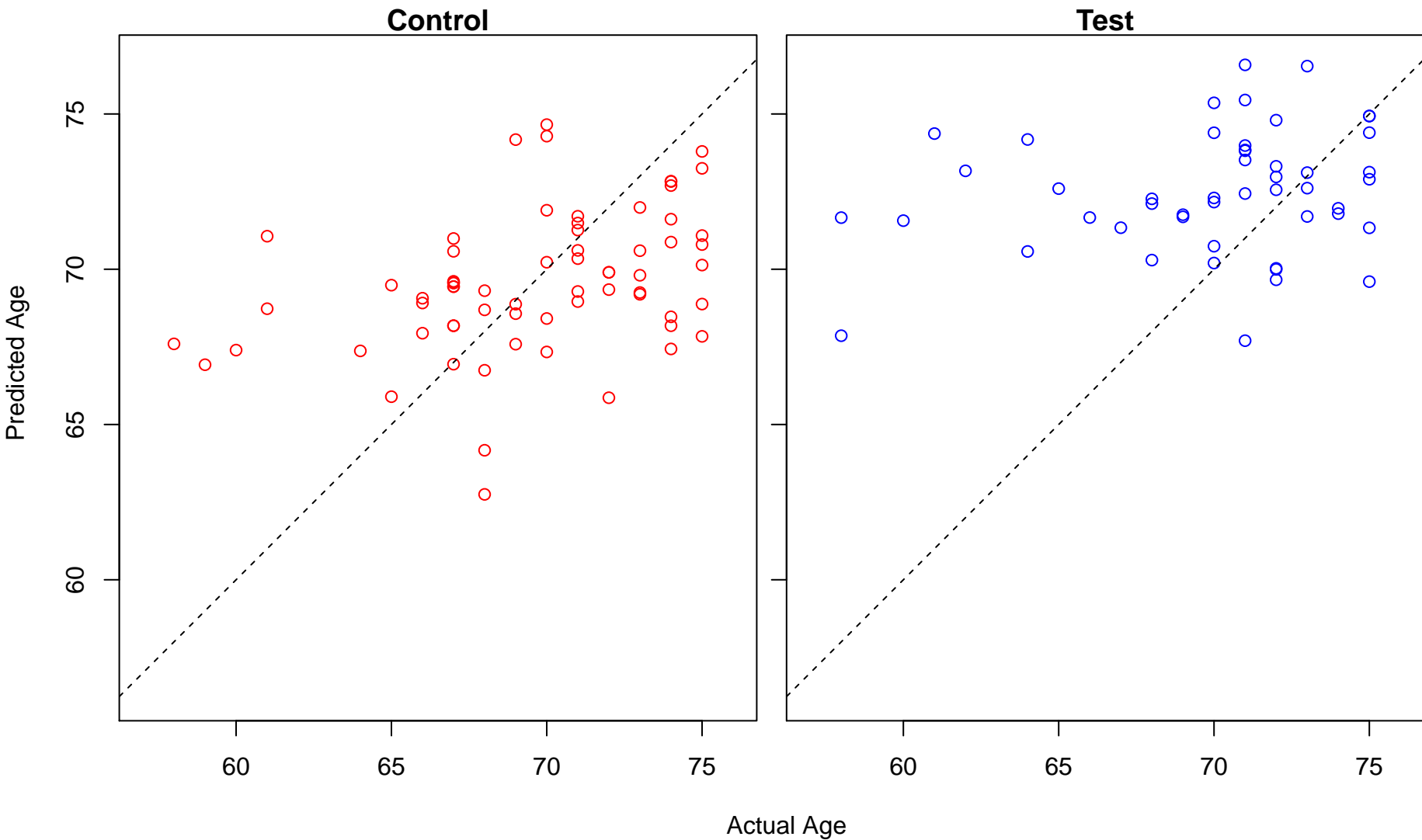


Actual Age

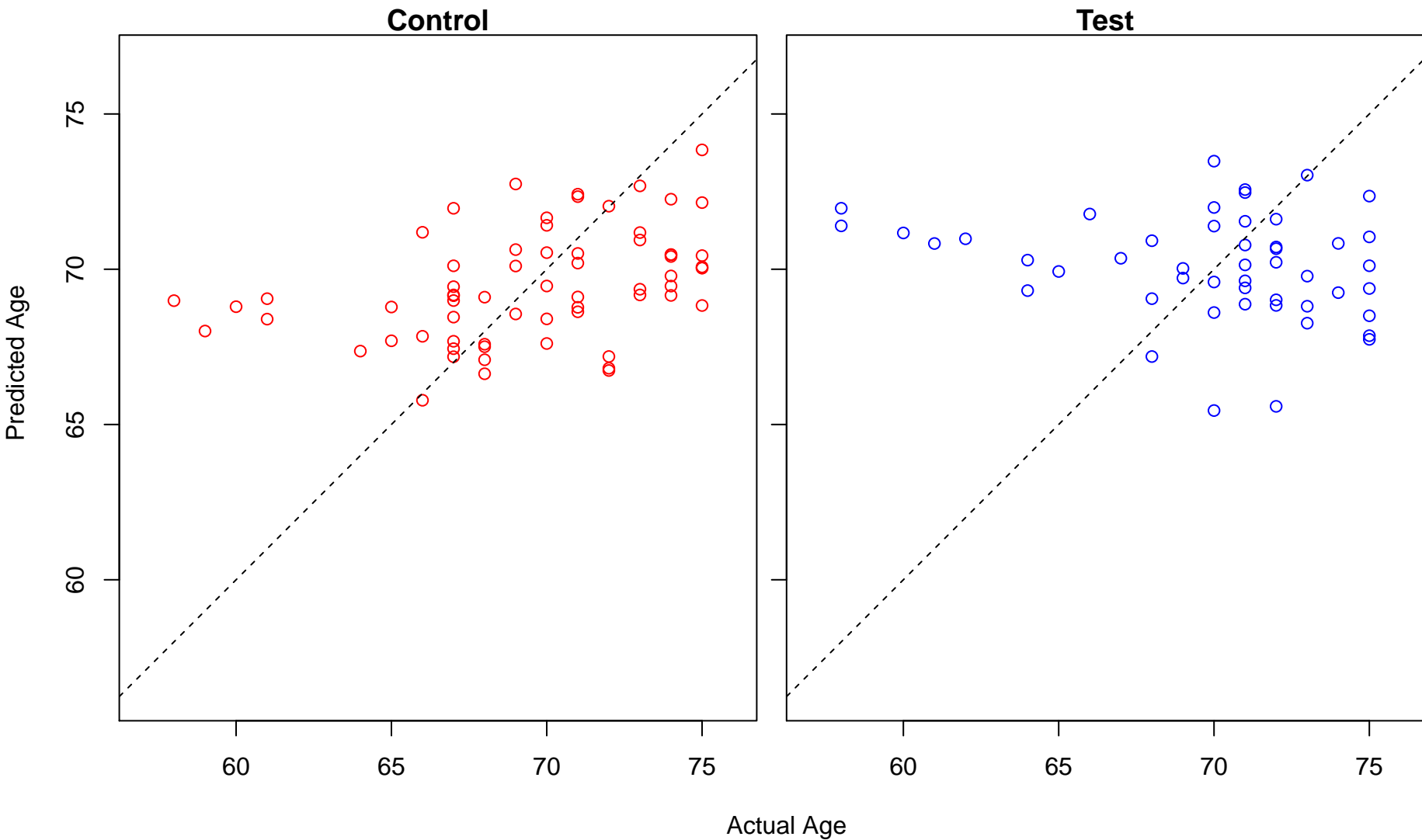
positive regulation of triglyceride catabolic process (Score: 0.512031)



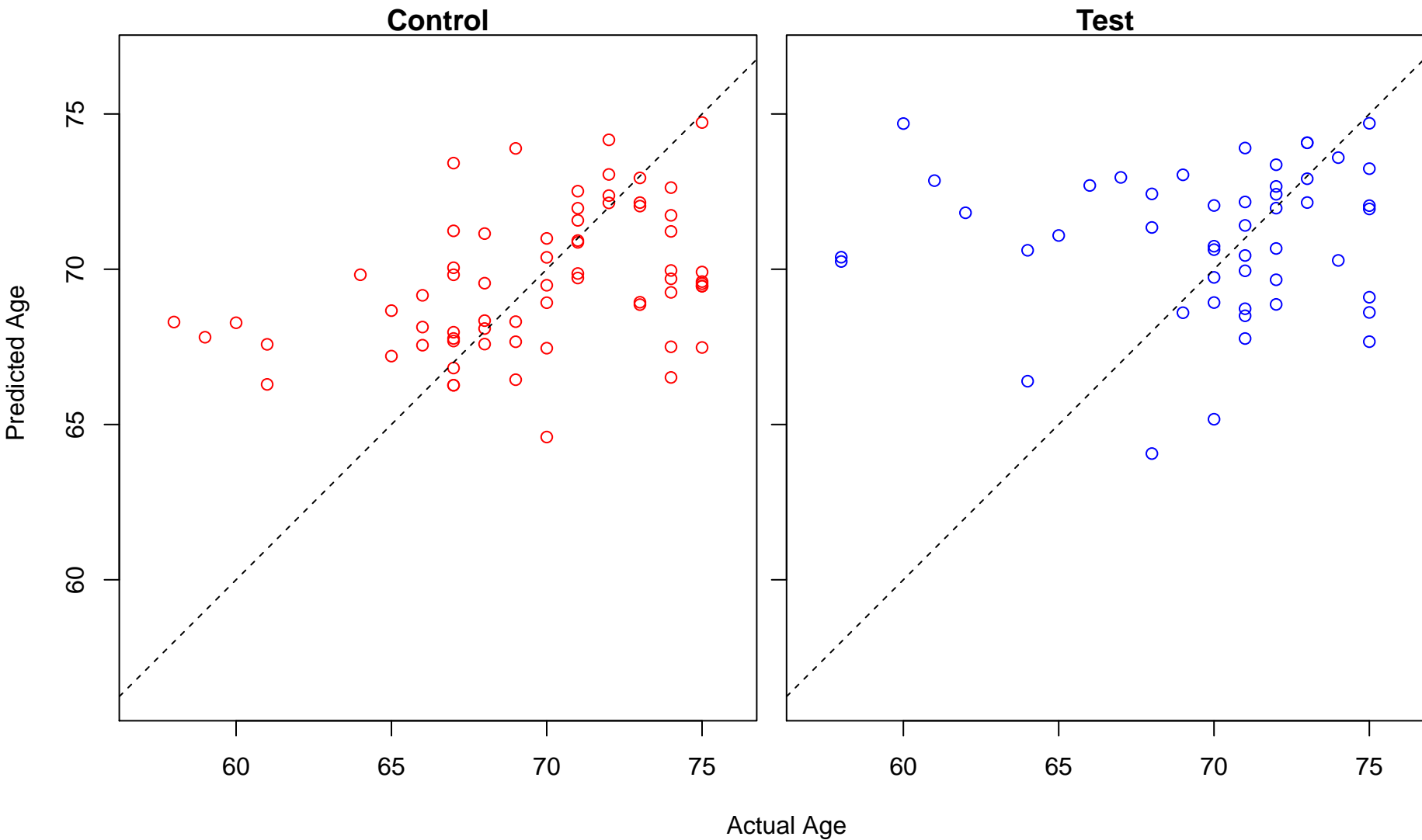
nucleobase-containing small molecule catabolic process (Score: 0.51829)



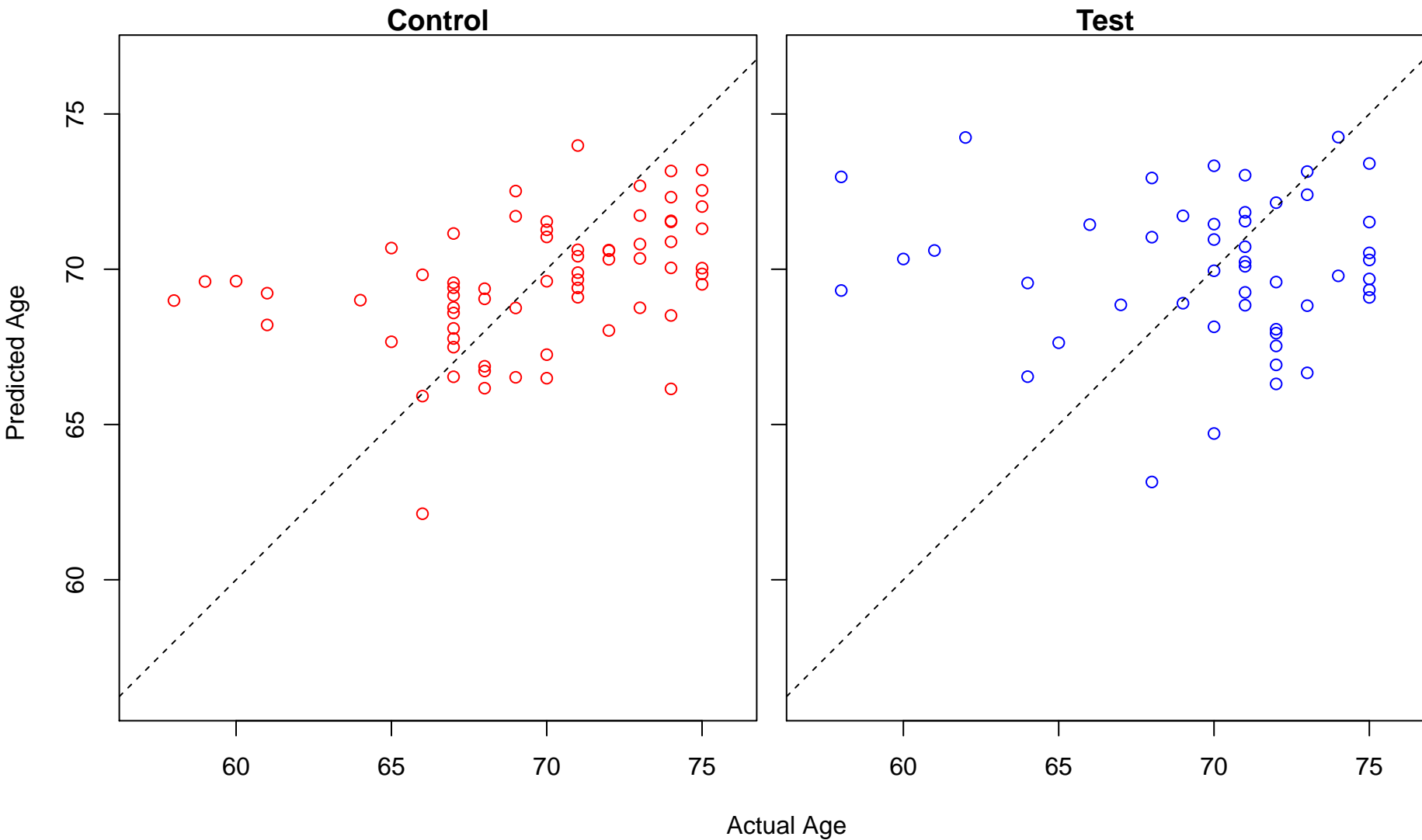
negative regulation of metanephros development (Score: 0.511808)



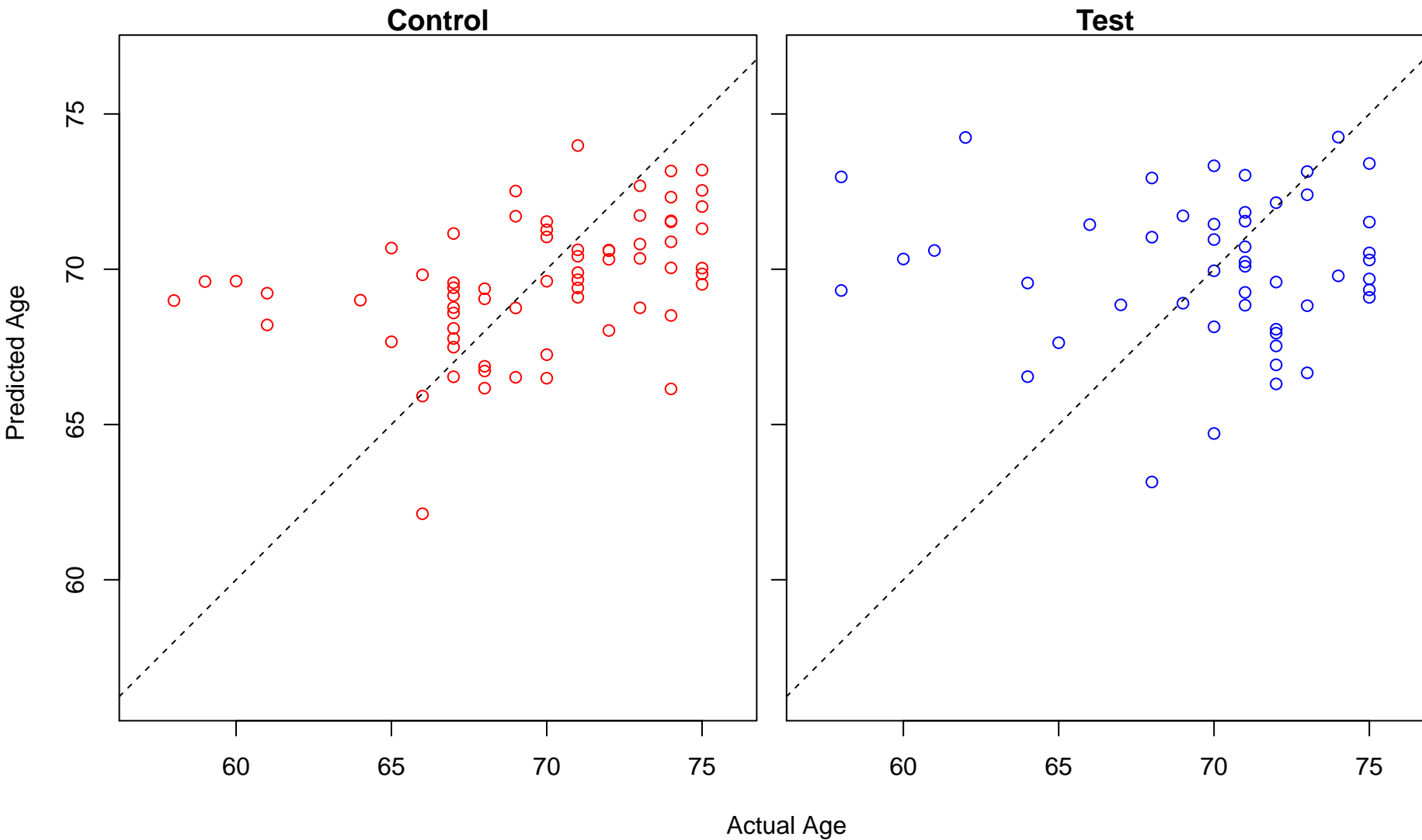
cerebellar cortex morphogenesis (Score: 0.511287)



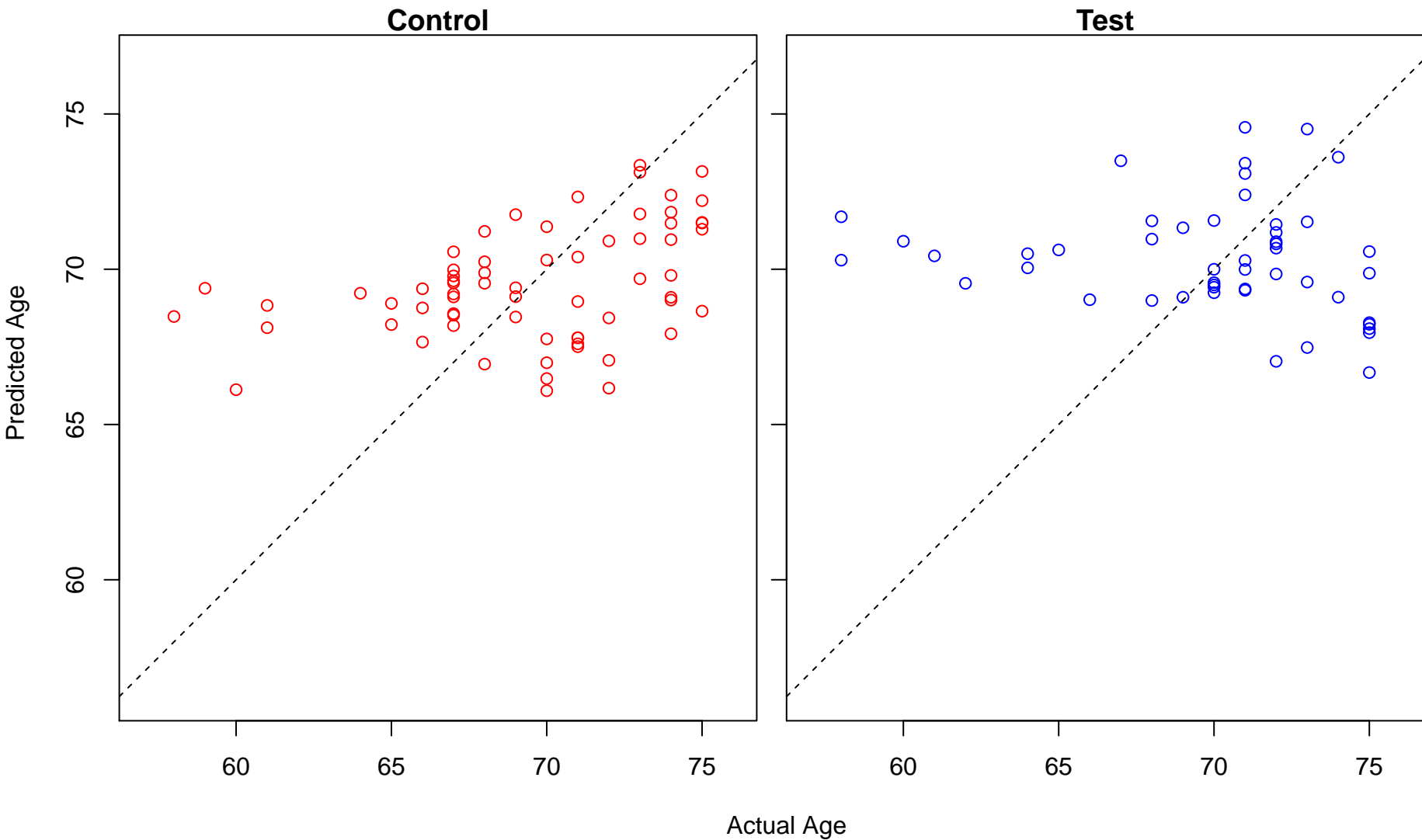
activation of store-operated calcium channel activity (Score: 0.511146)



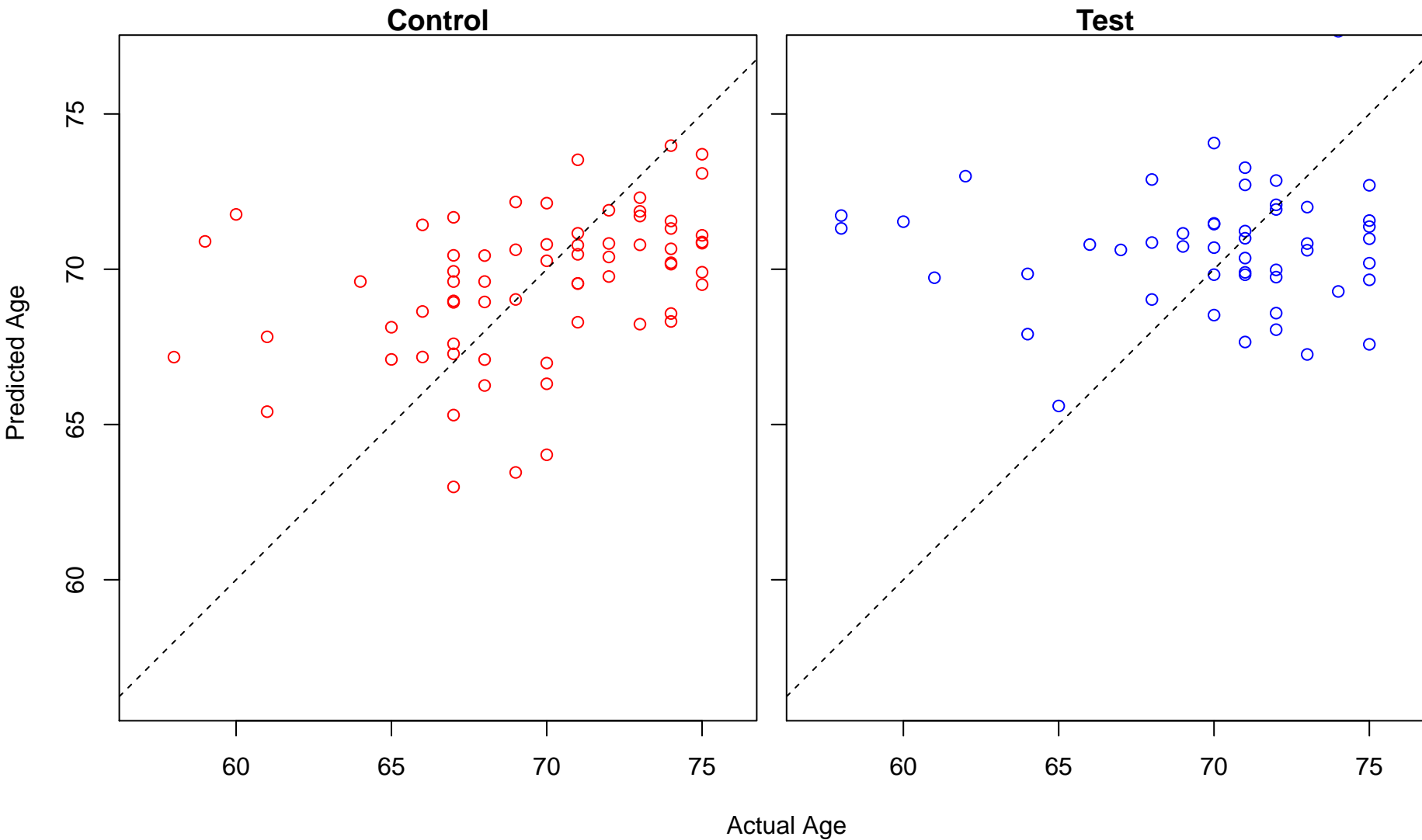
positive regulation of store-operated calcium channel activity (Score: 0.511146)



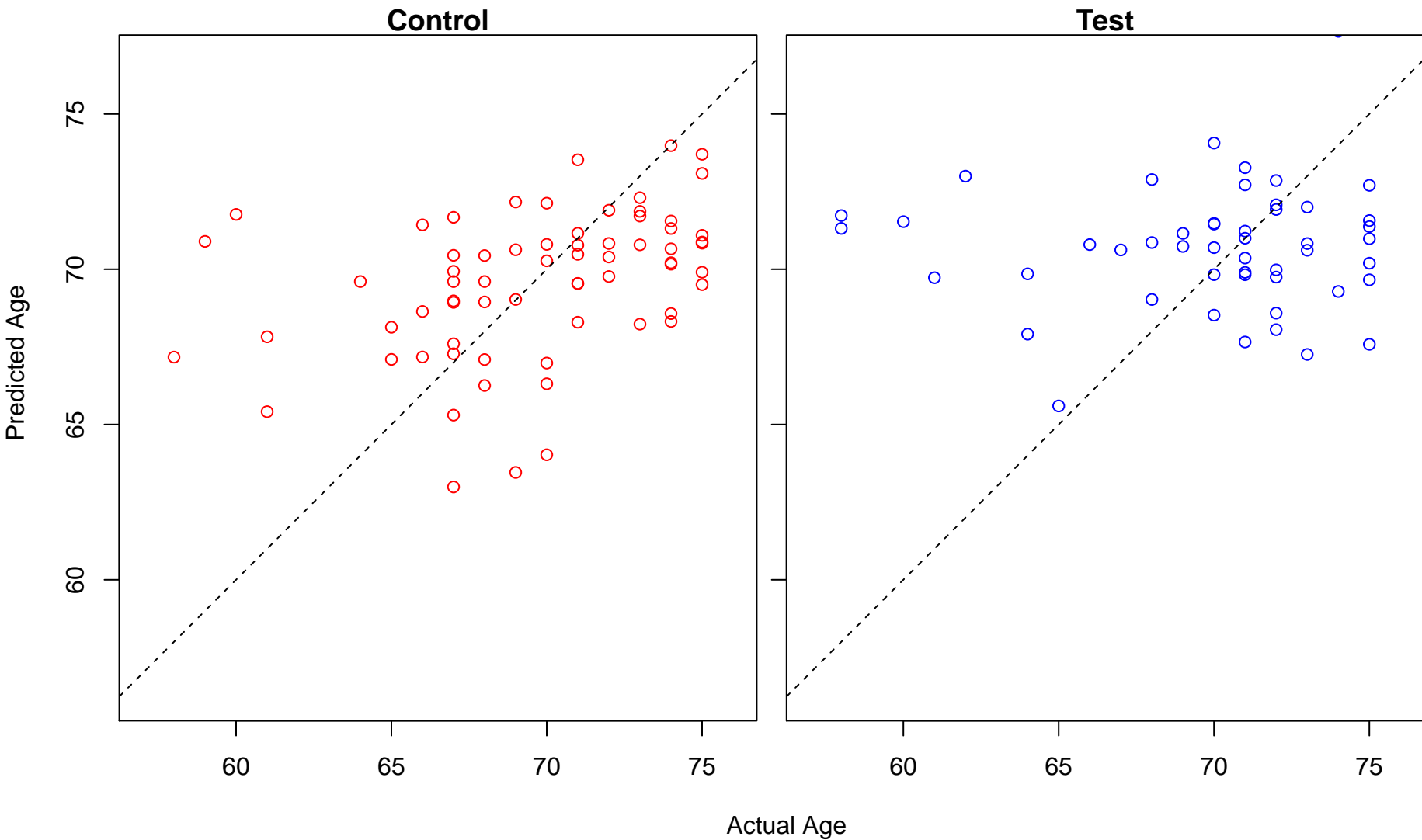
regulation of triglyceride catabolic process (Score: 0.511023)



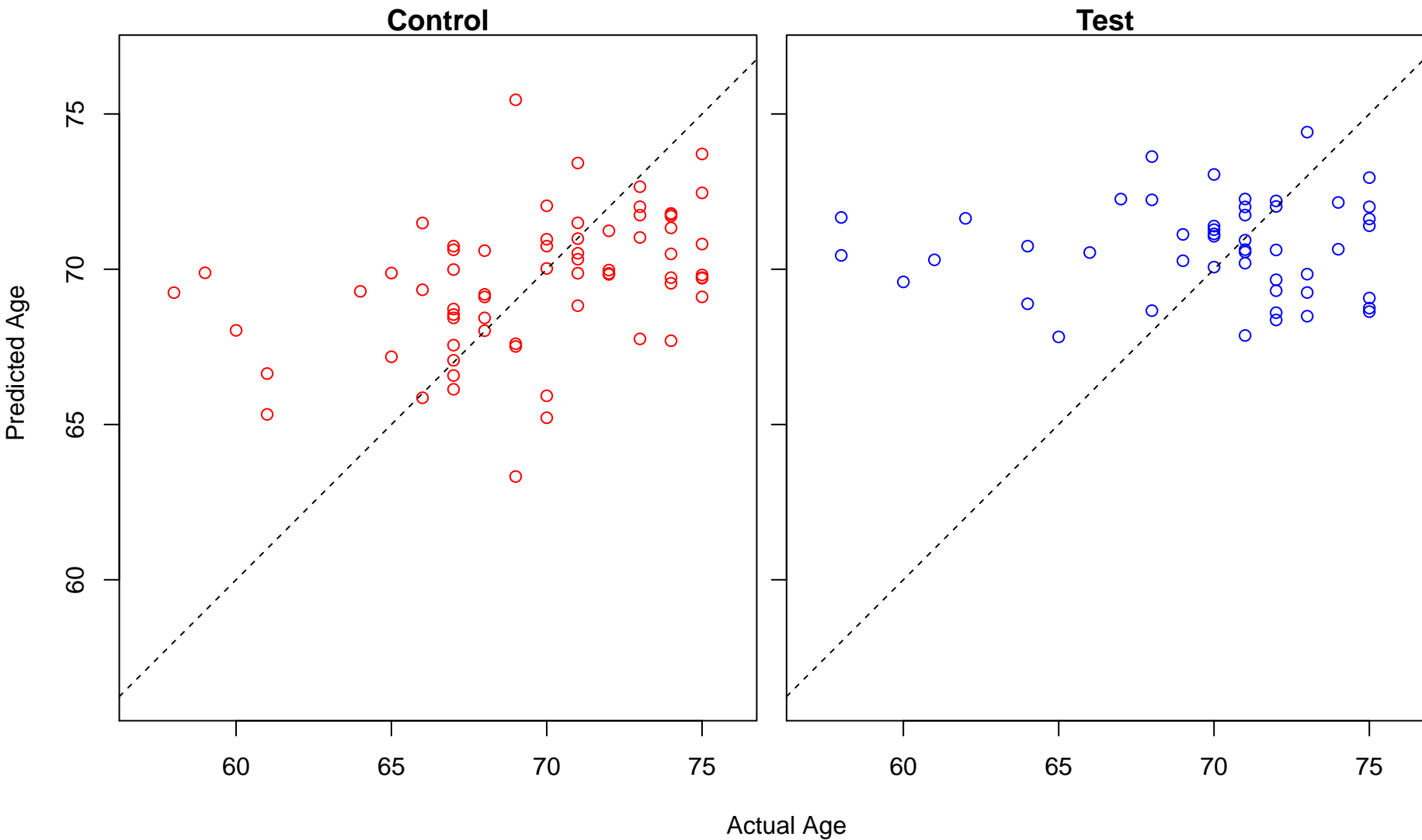
amine catabolic process (Score: 0.509810)



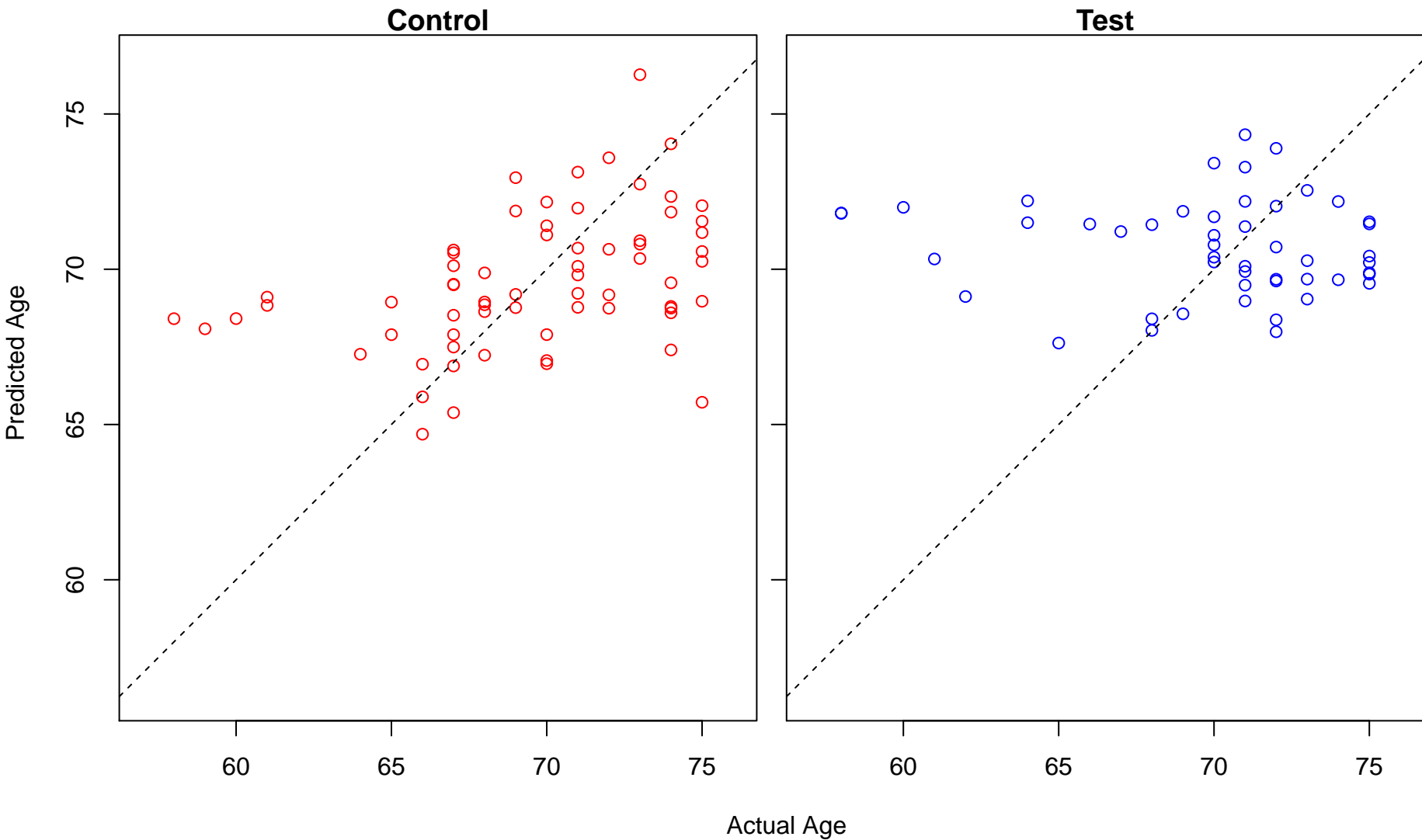
cellular biogenic amine catabolic process (Score: 0.509810)



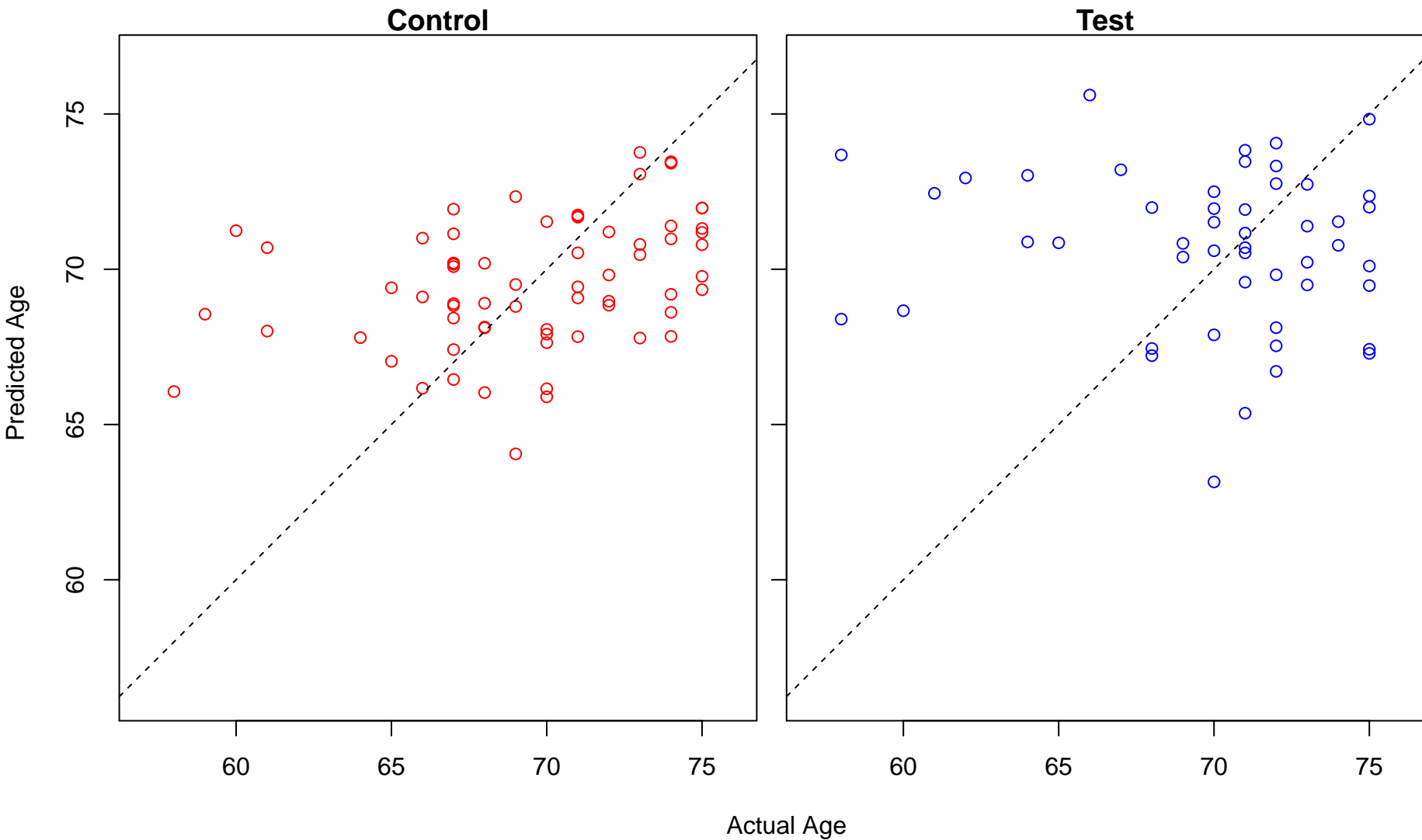
response to prostaglandin (Score: 0.509419)



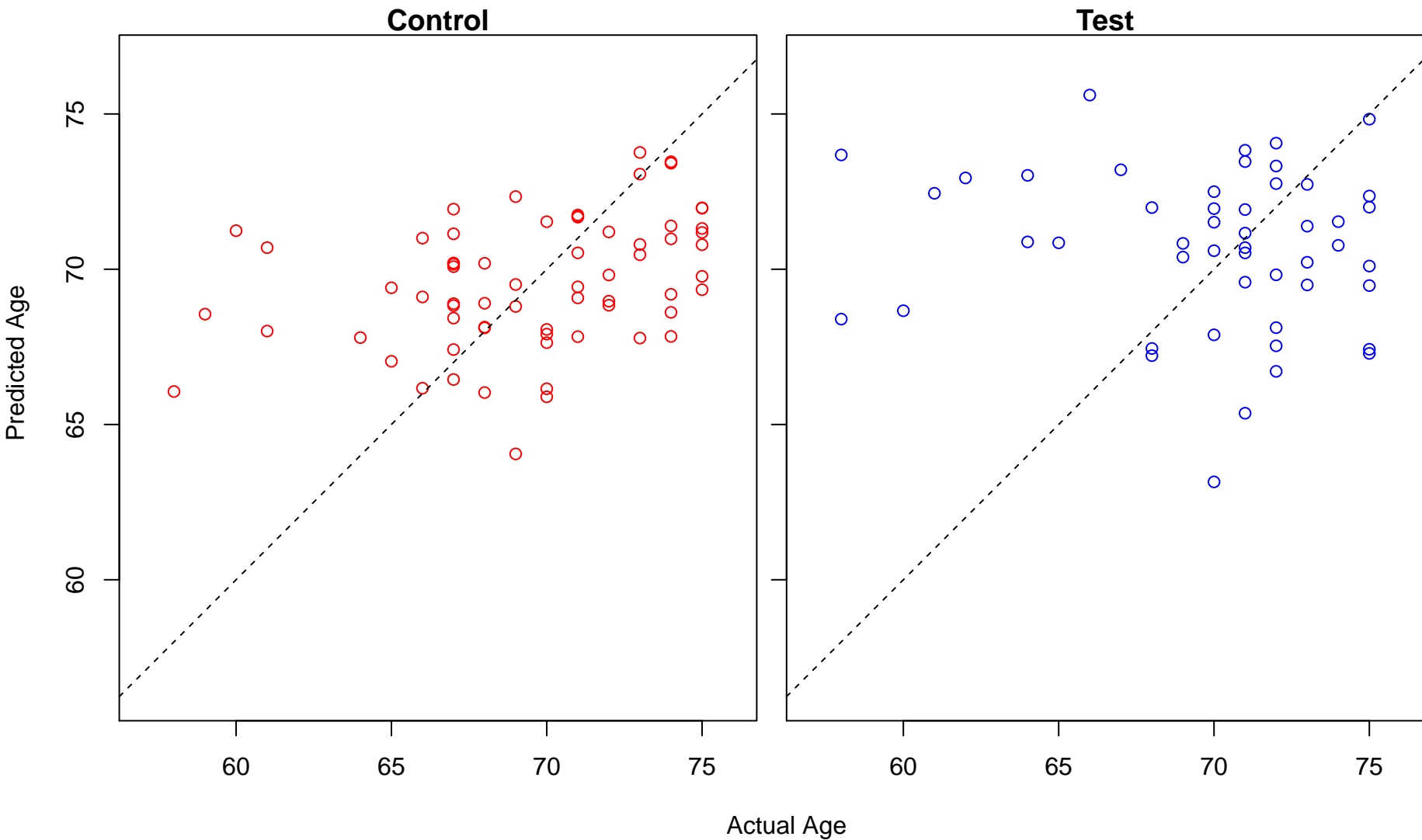
homocysteine metabolic process (Score: 0.509311)



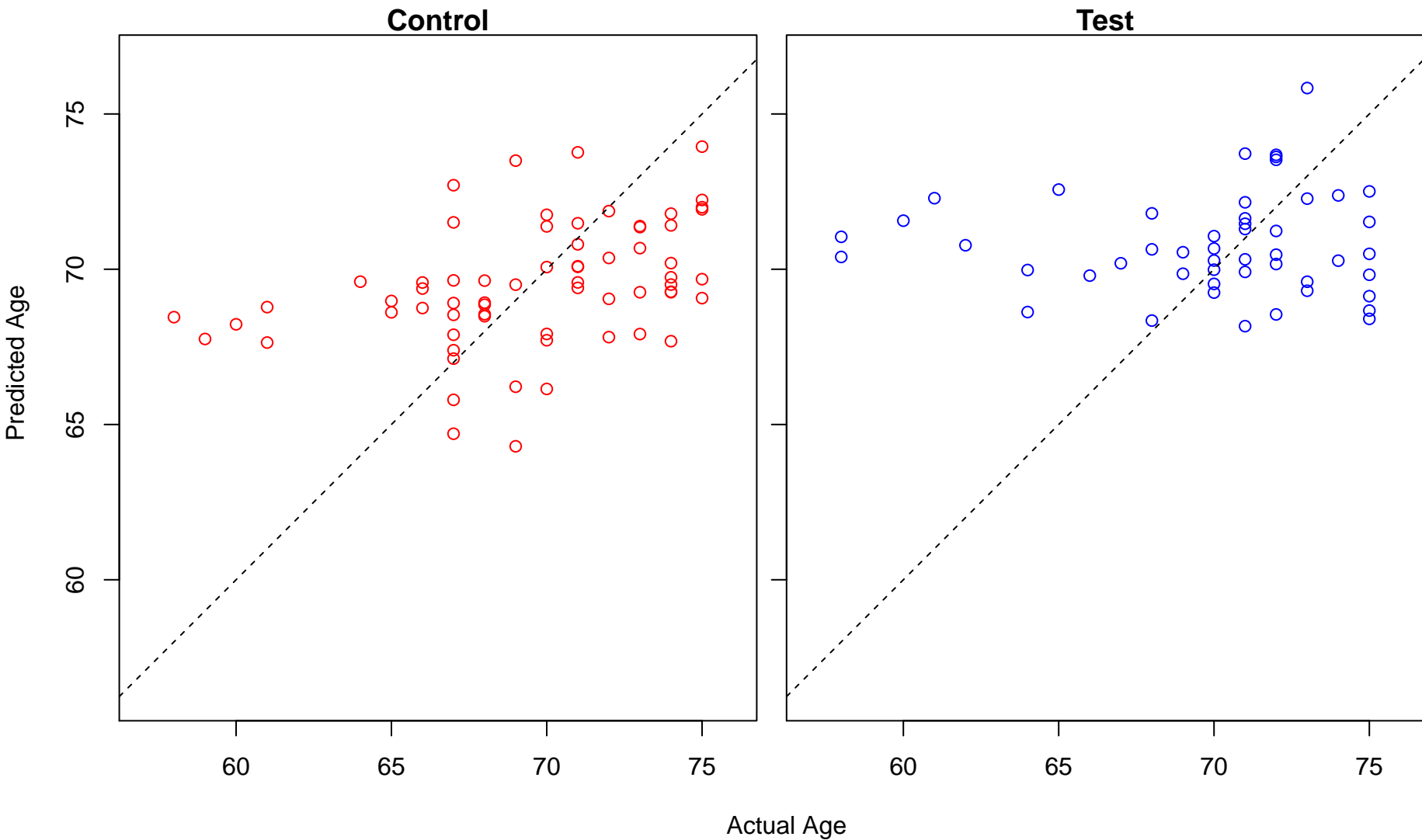
regulation of microvillus organization (Score: 0.509250)



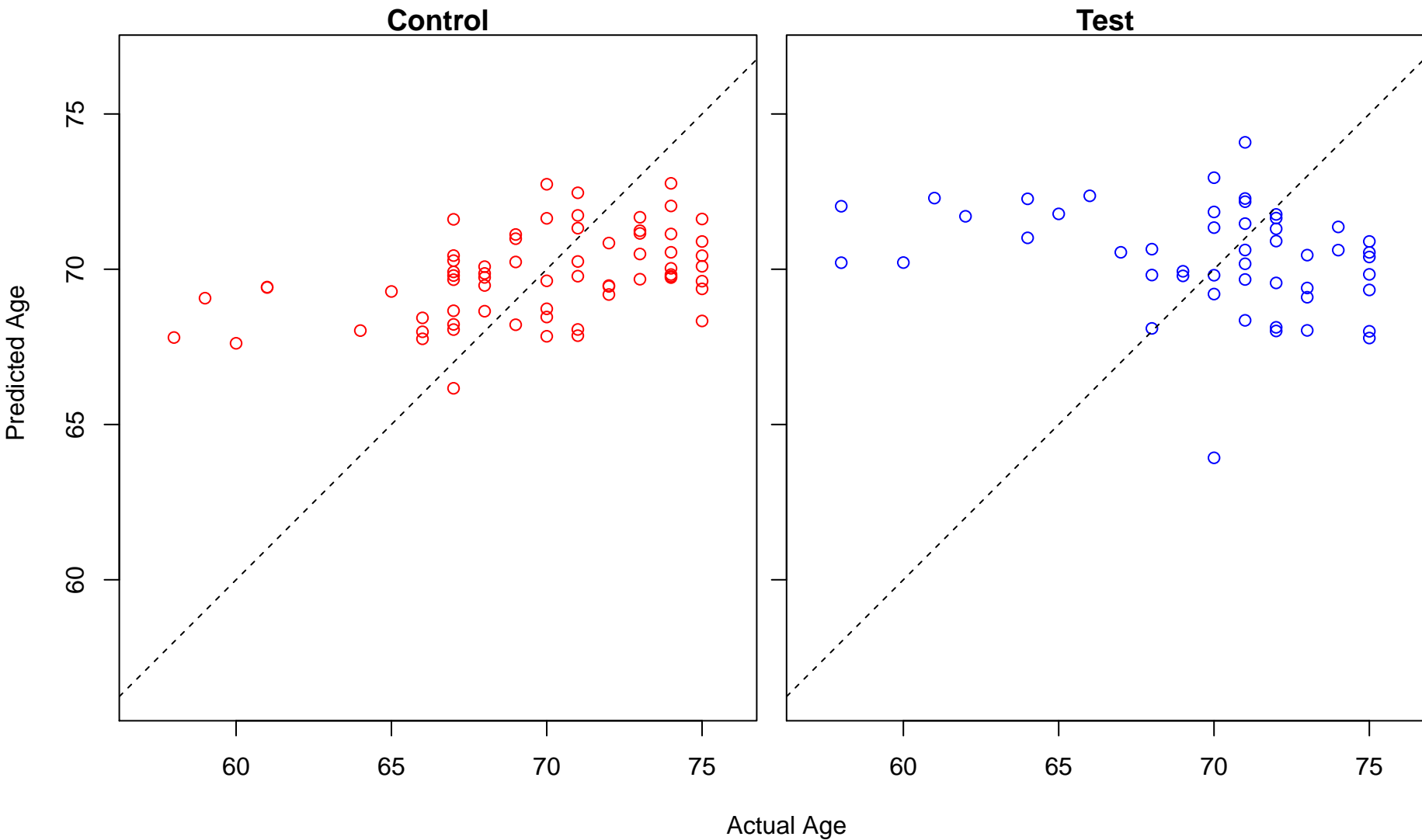
regulation of microvillus assembly (Score: 0.509250)



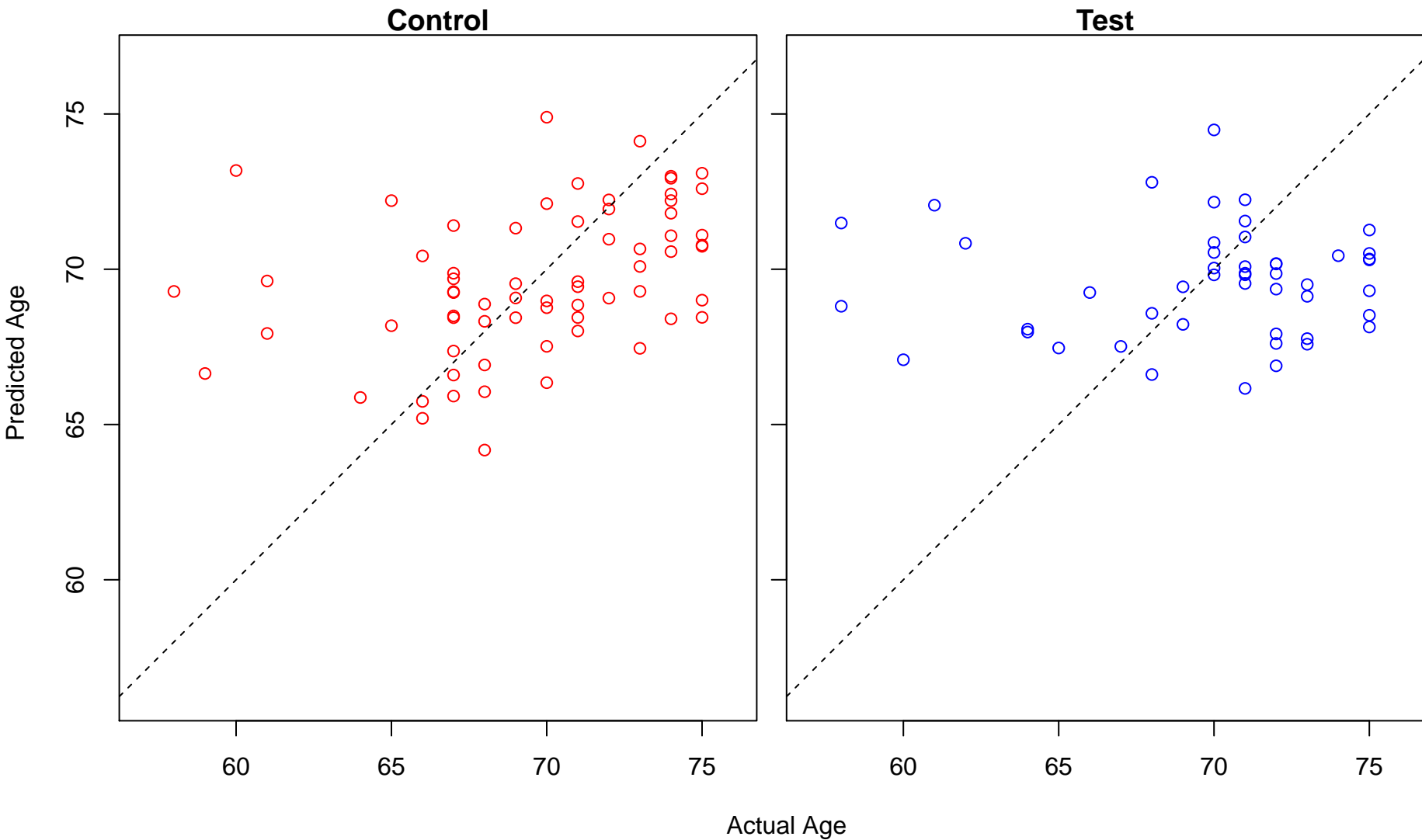
regulation of glucose import in response to insulin stimulus (Score: 0.508260)



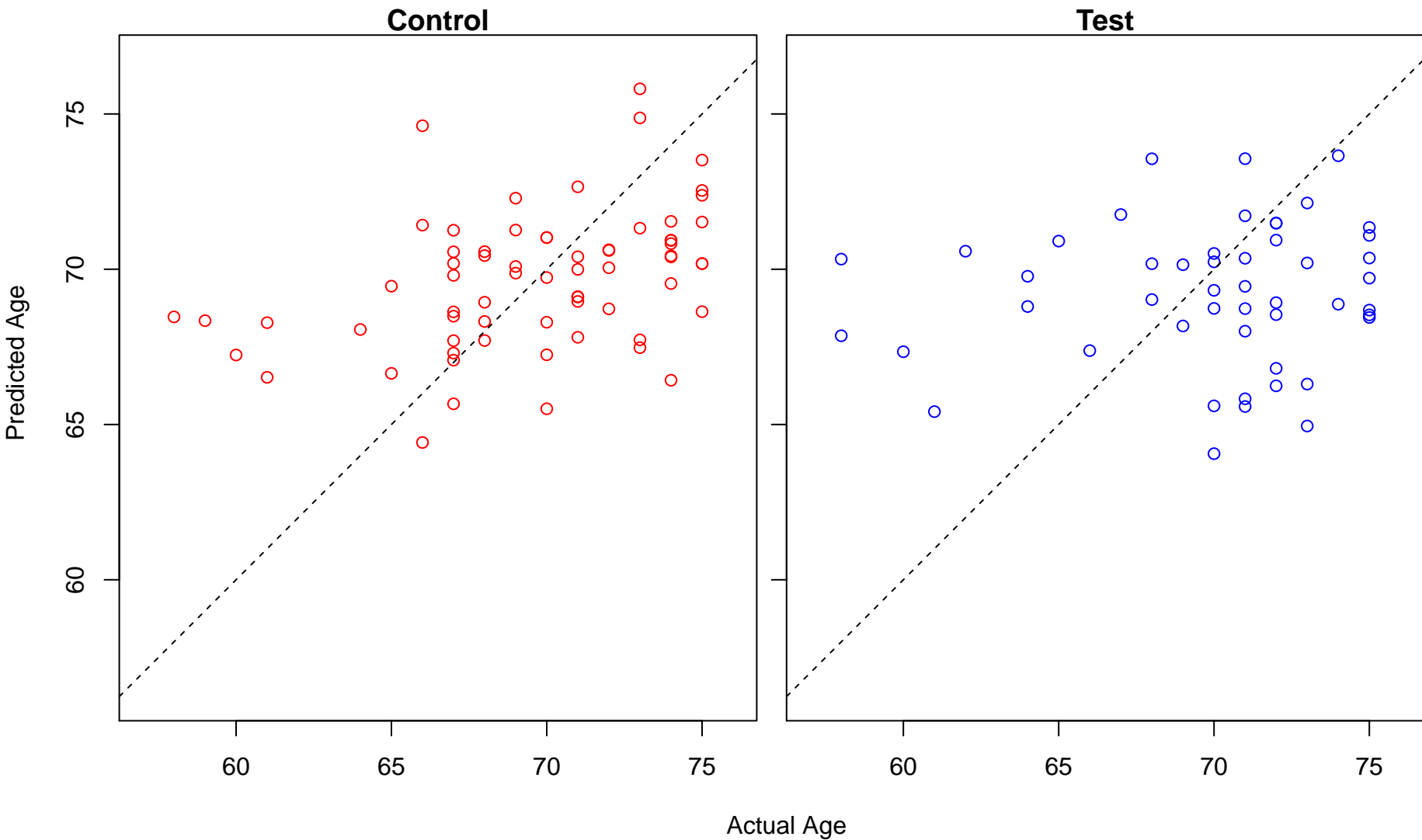
endothelial cell activation (Score: 0.508093)



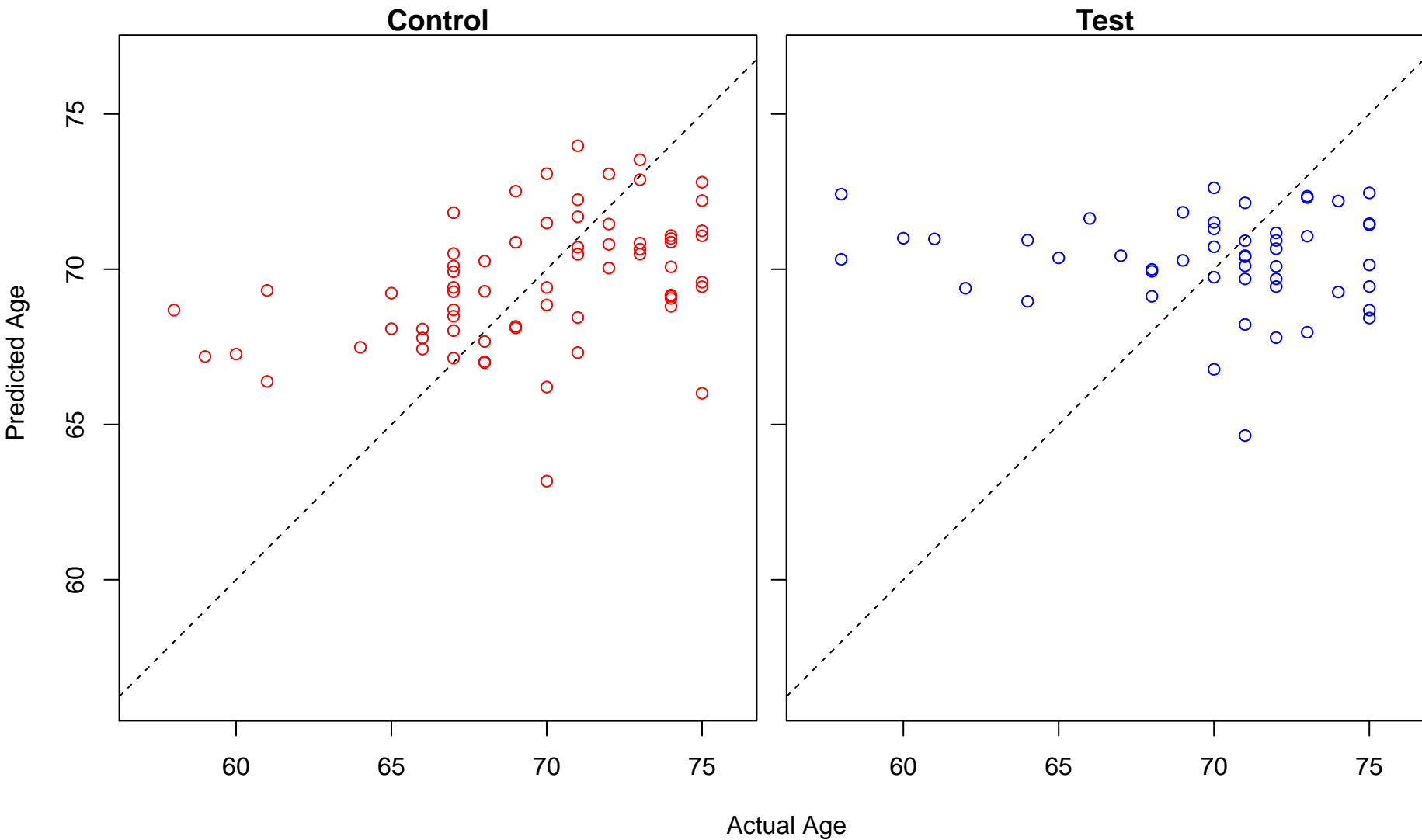
cellular response to zinc ion (Score: 0.508051)



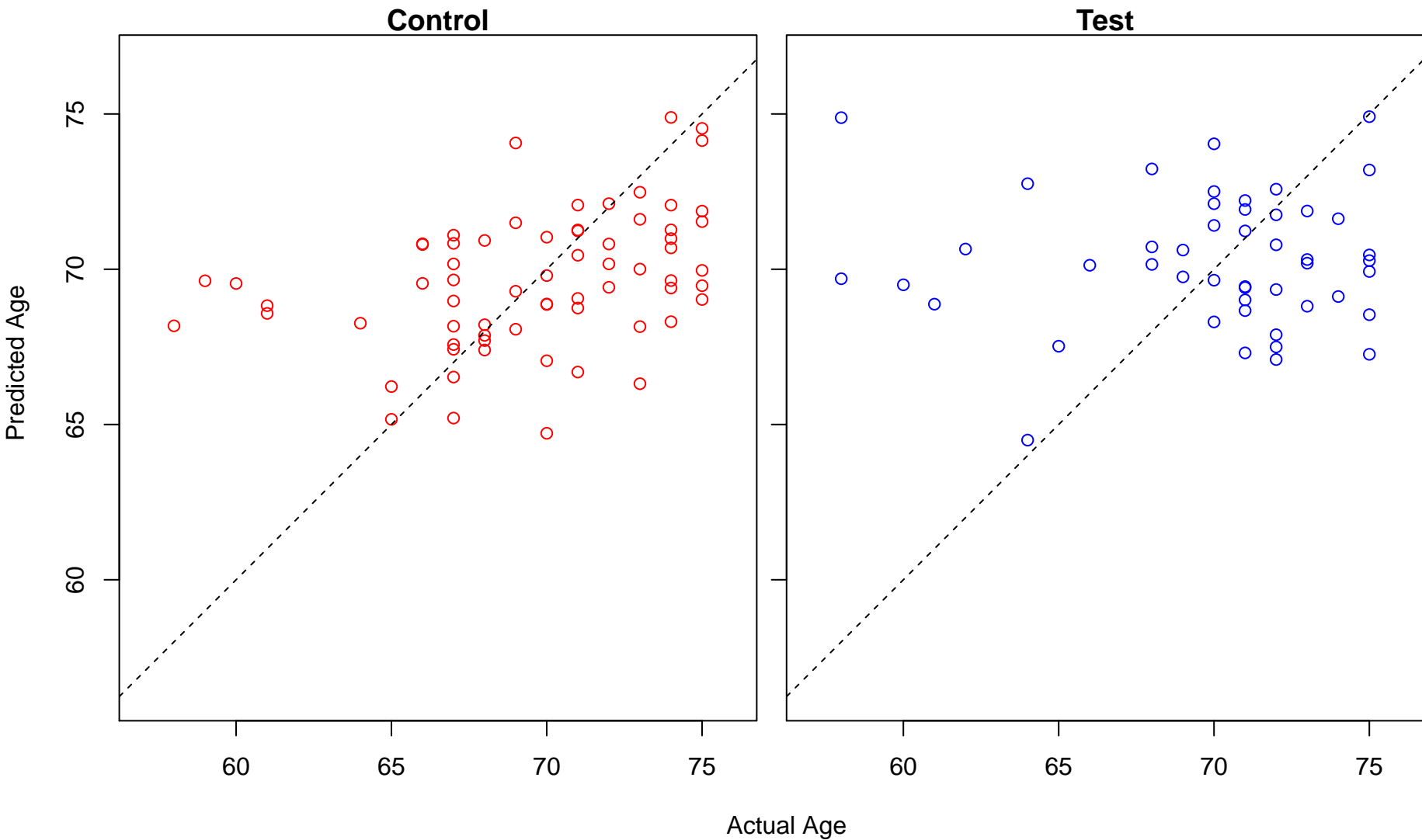
positive regulation of phospholipase A2 activity (Score: 0.507789)



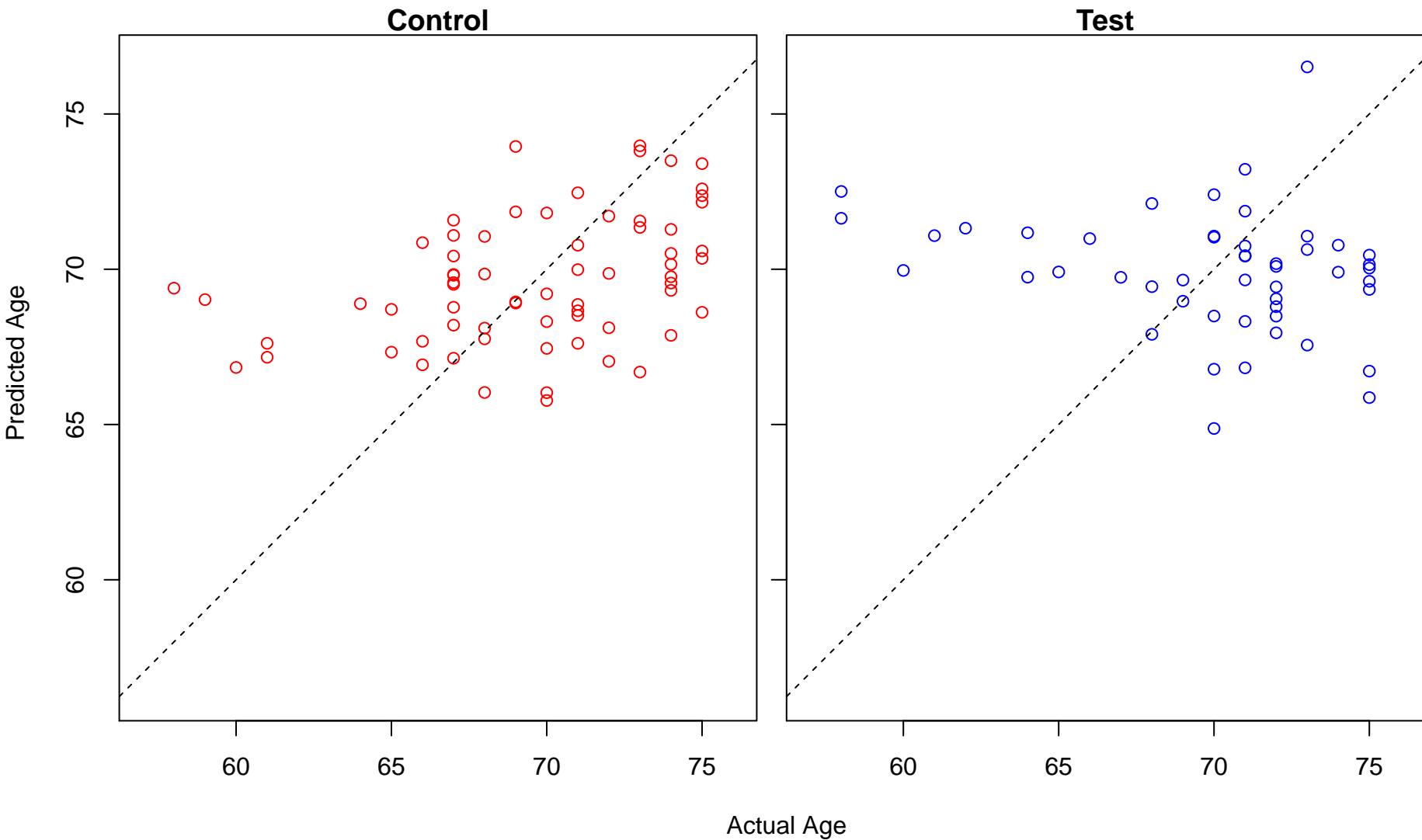
cellular component maintenance (Score: 0.507704)



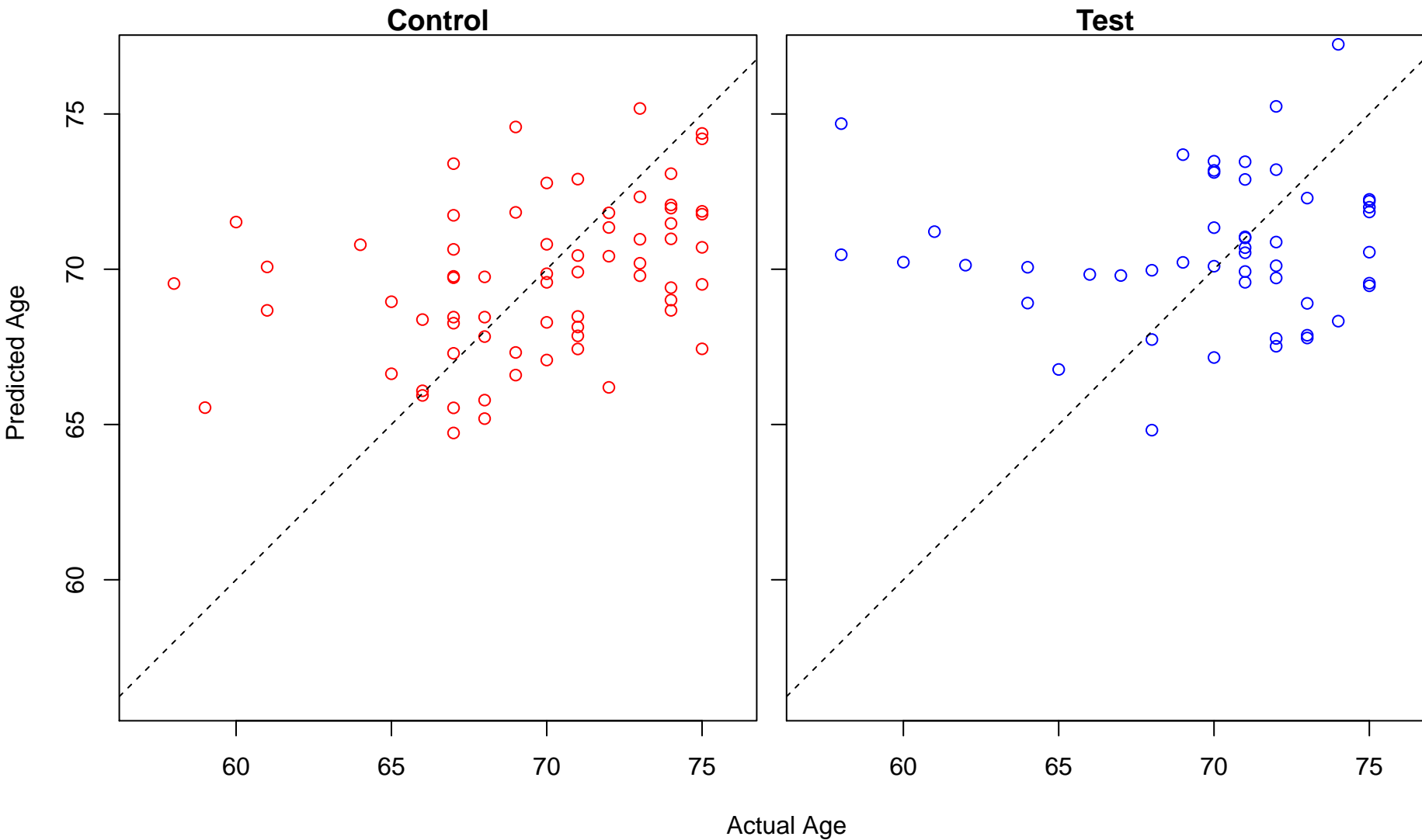
negative regulation of chromatin silencing (Score: 0.507458)



negative regulation of mRNA polyadenylation (Score: 0.506748)

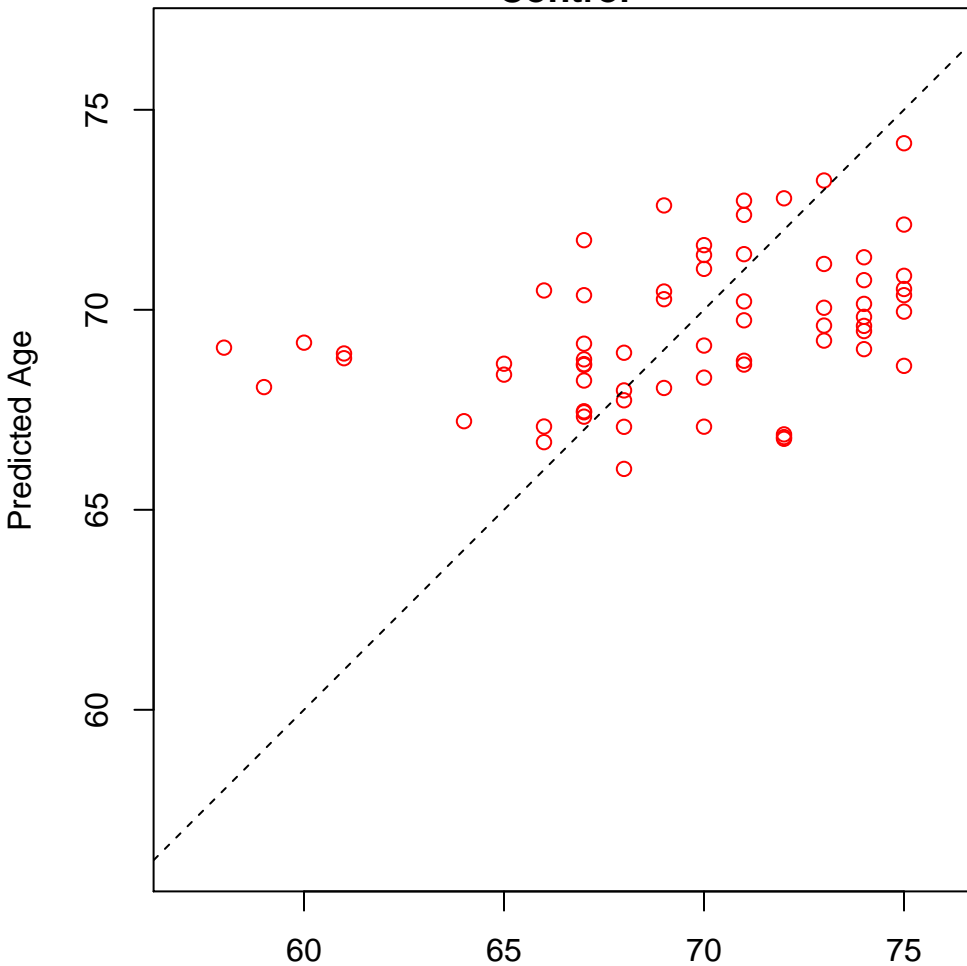


zinc II ion transmembrane transport (Score: 0.506110)

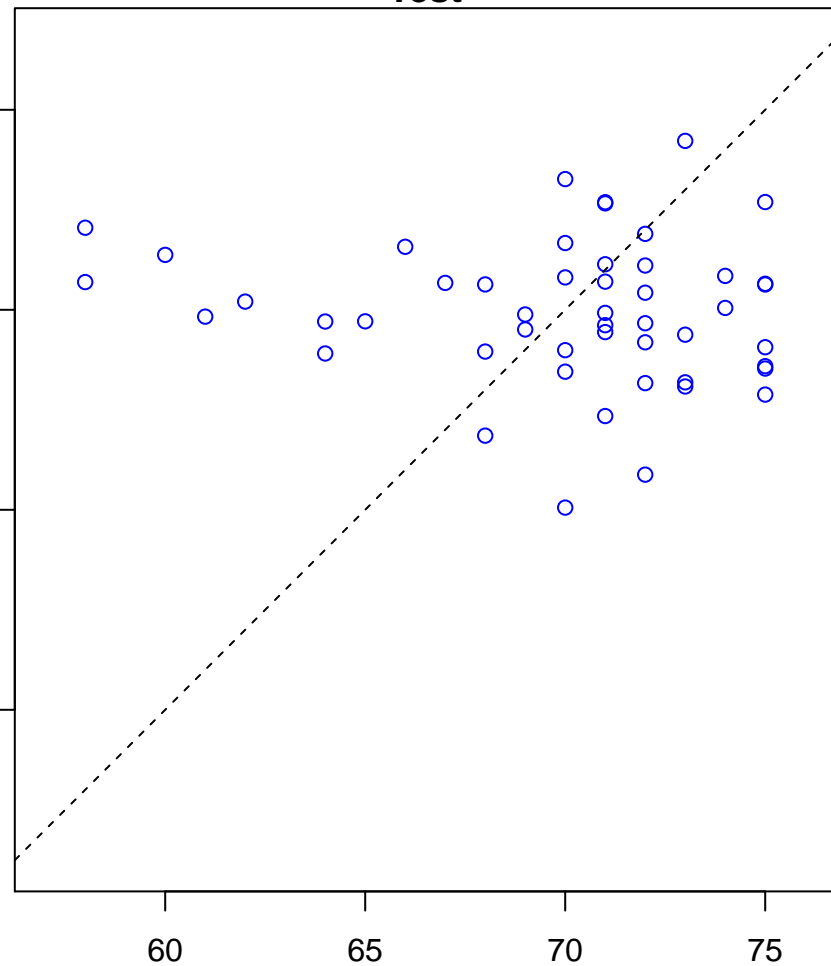


metanephric mesenchyme development (Score: 0.505952)

Control

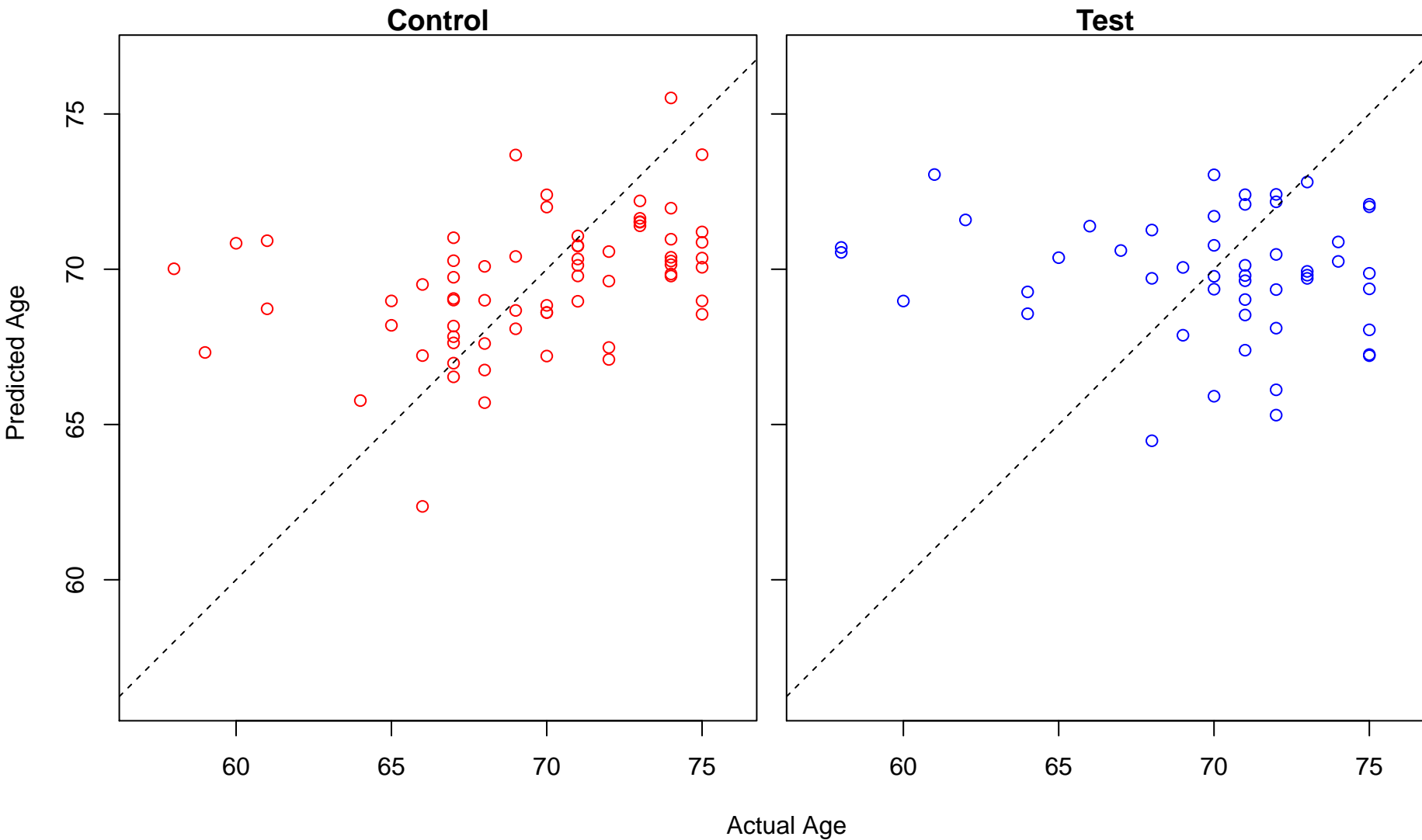


Test

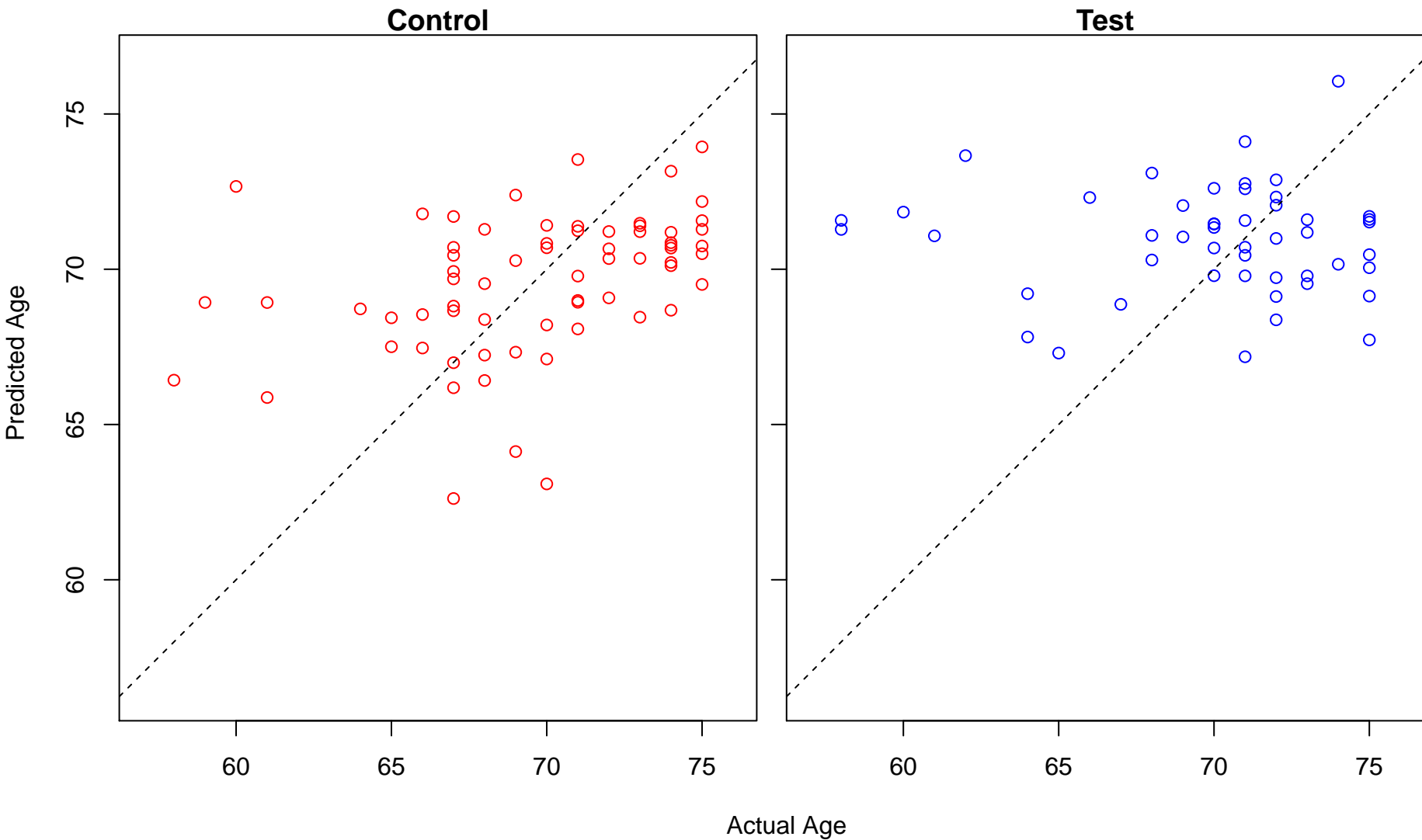


Actual Age

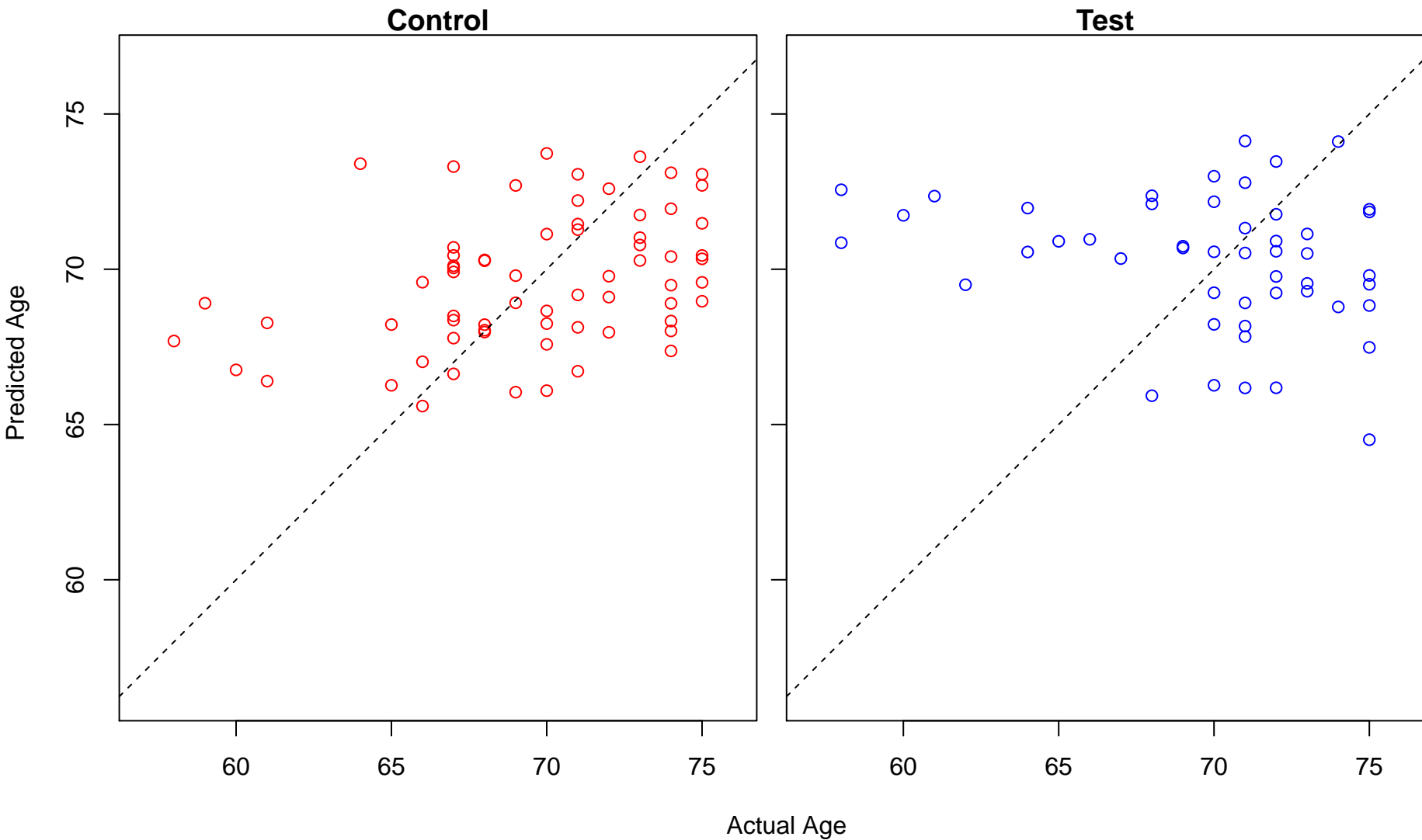
cardiac muscle cell action potential involved in contraction (Score: 0.505668)



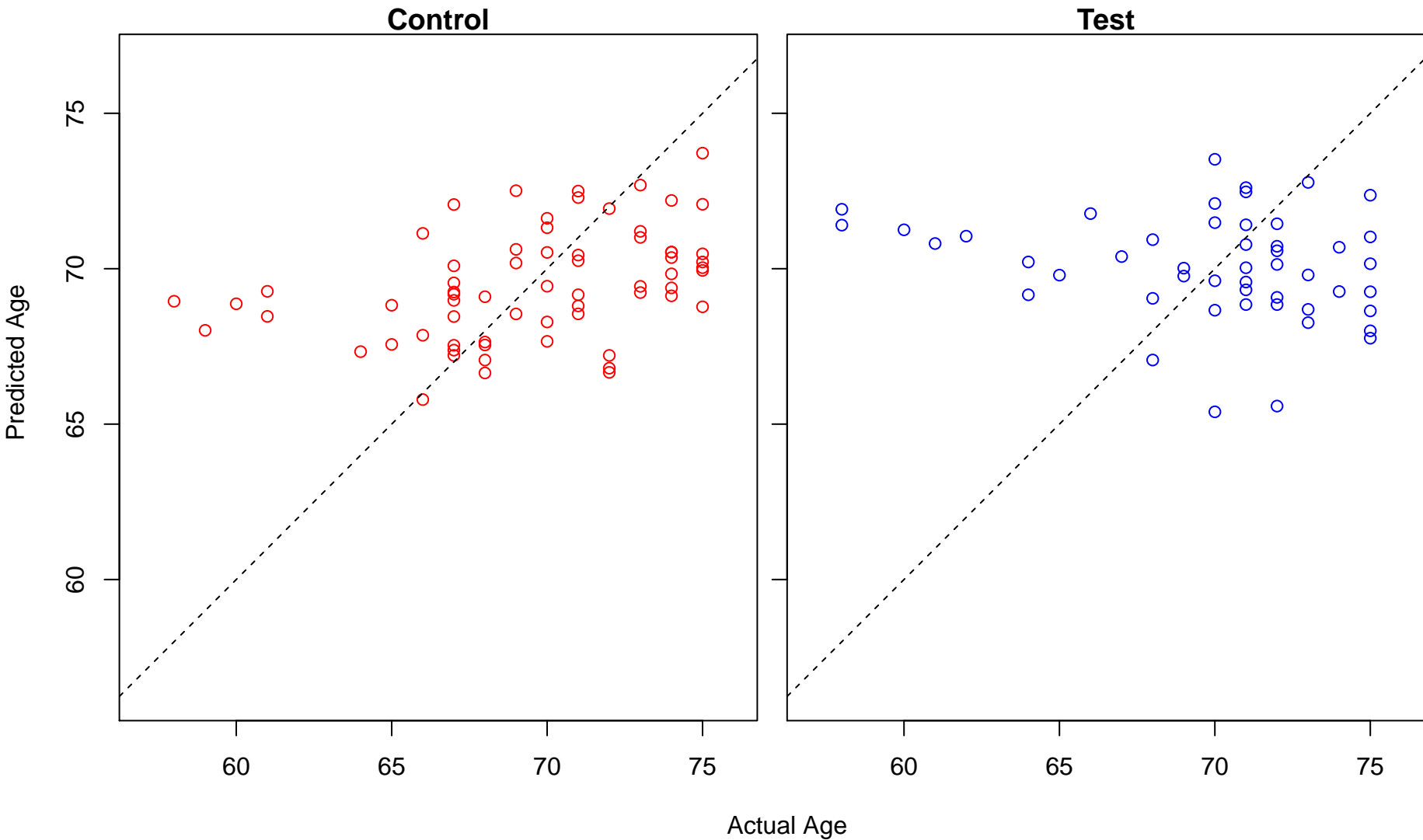
indole-containing compound metabolic process (Score: 0.505334)



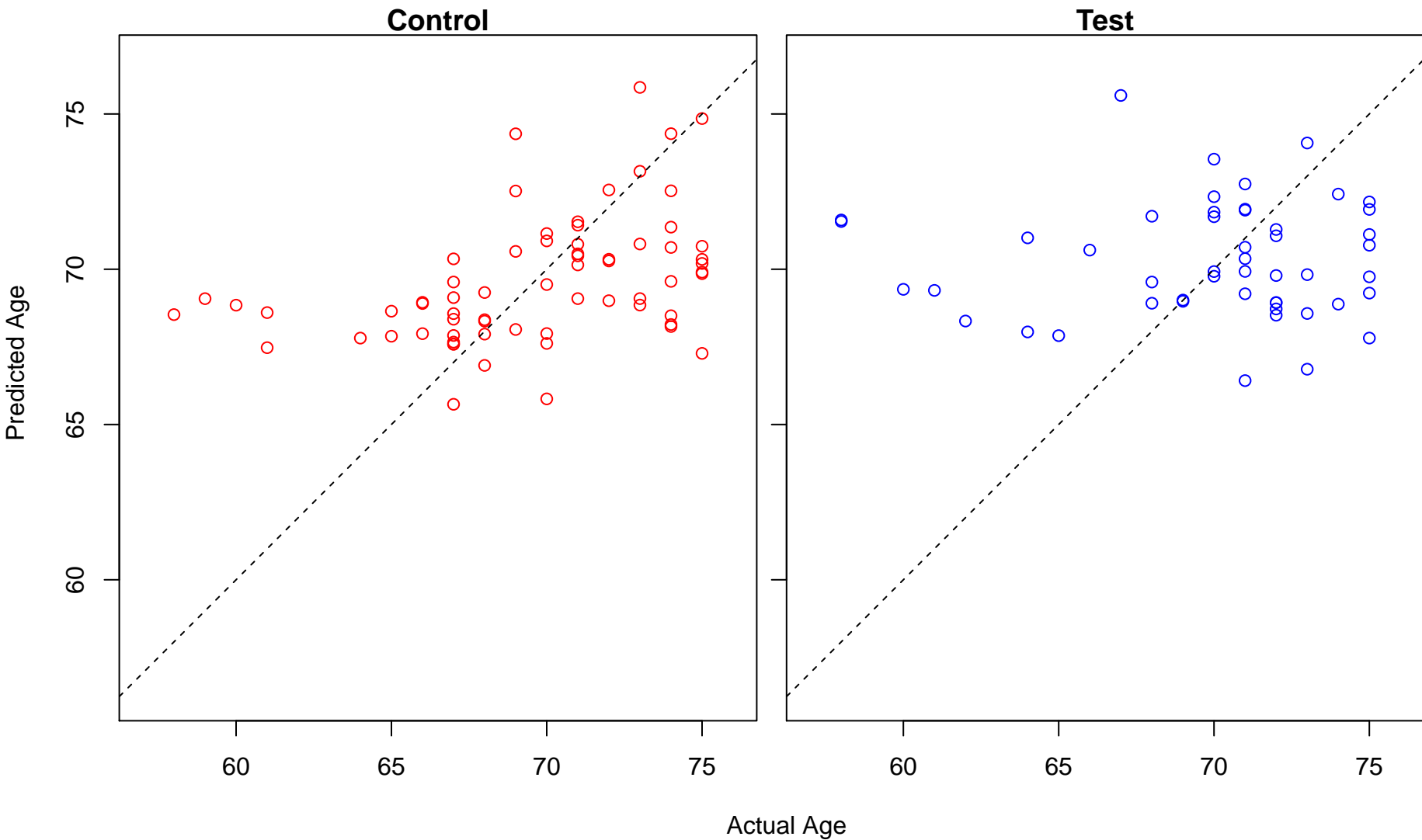
negative regulation of interleukin-17 production (Score: 0.504485)



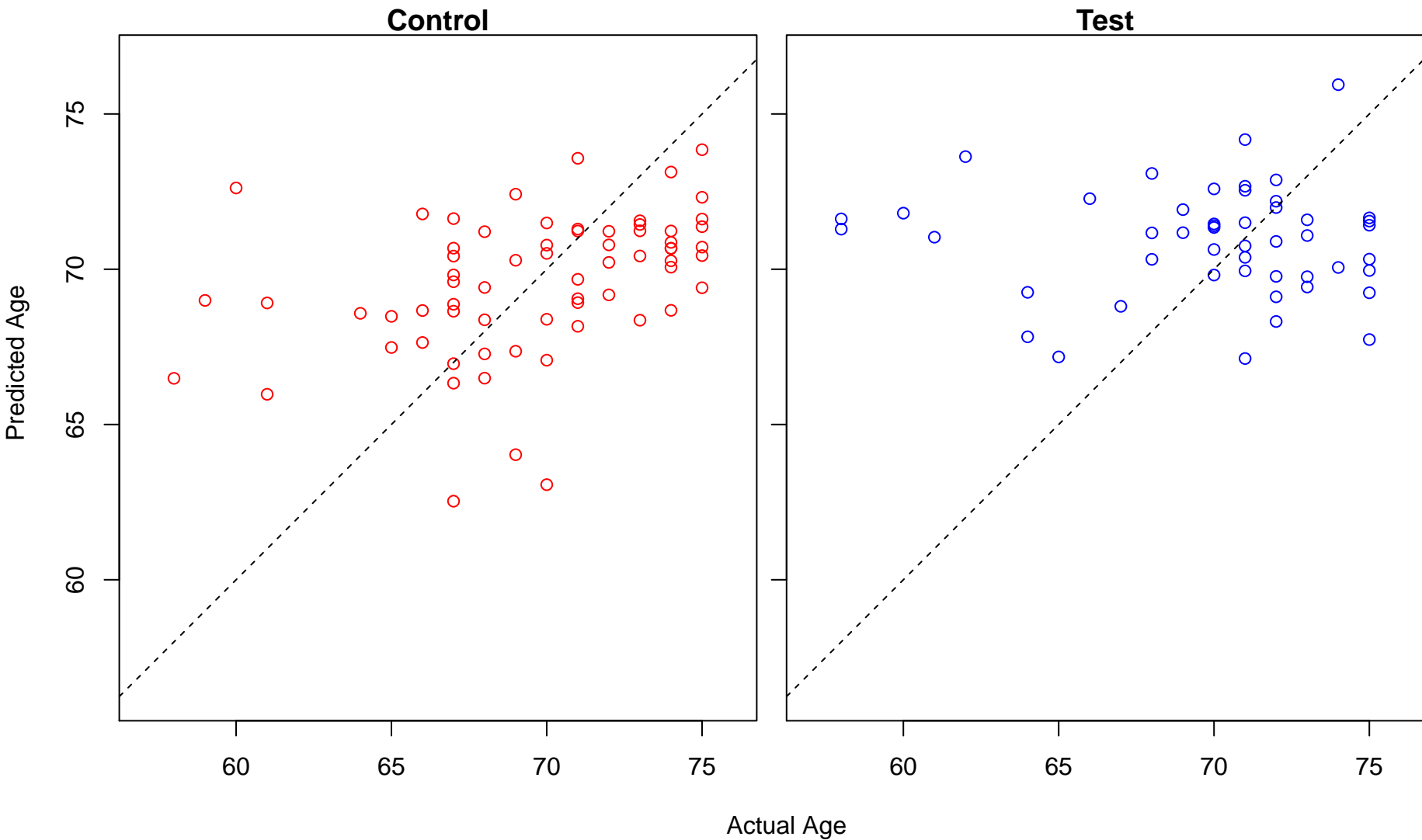
cell differentiation involved in metanephros development (Score: 0.504378)



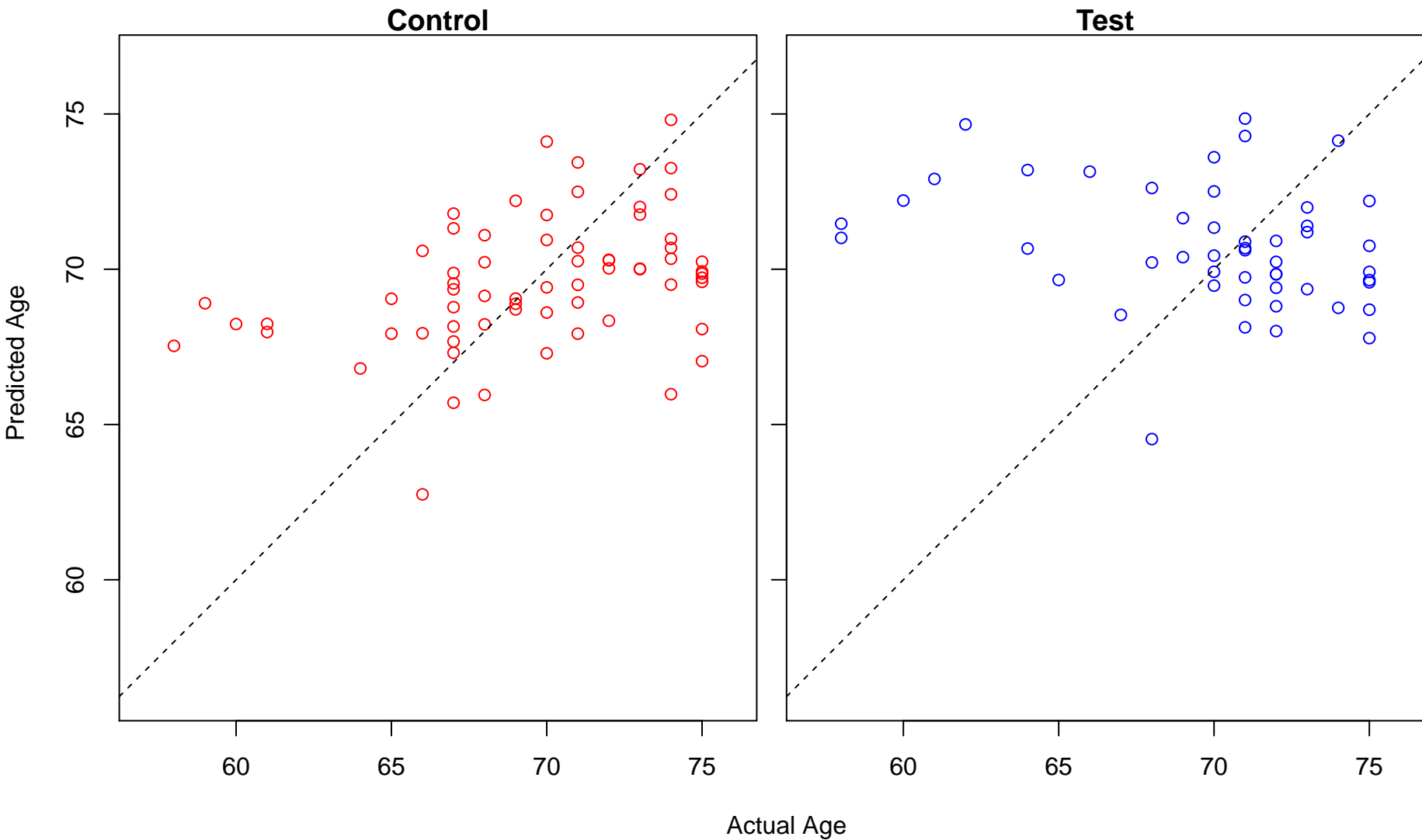
heterochromatin organization (Score: 0.504344)



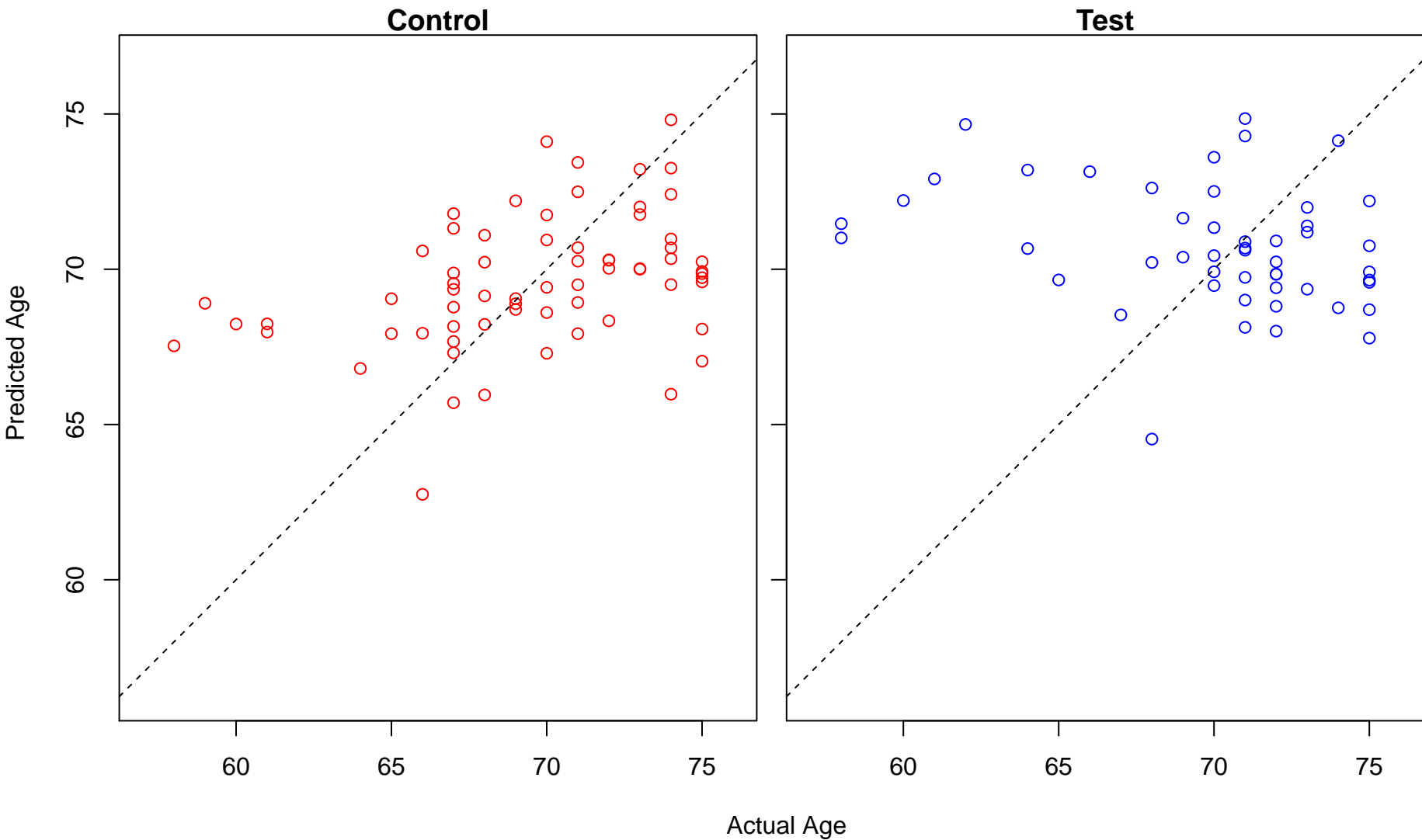
indolalkylamine metabolic process (Score: 0.504039)



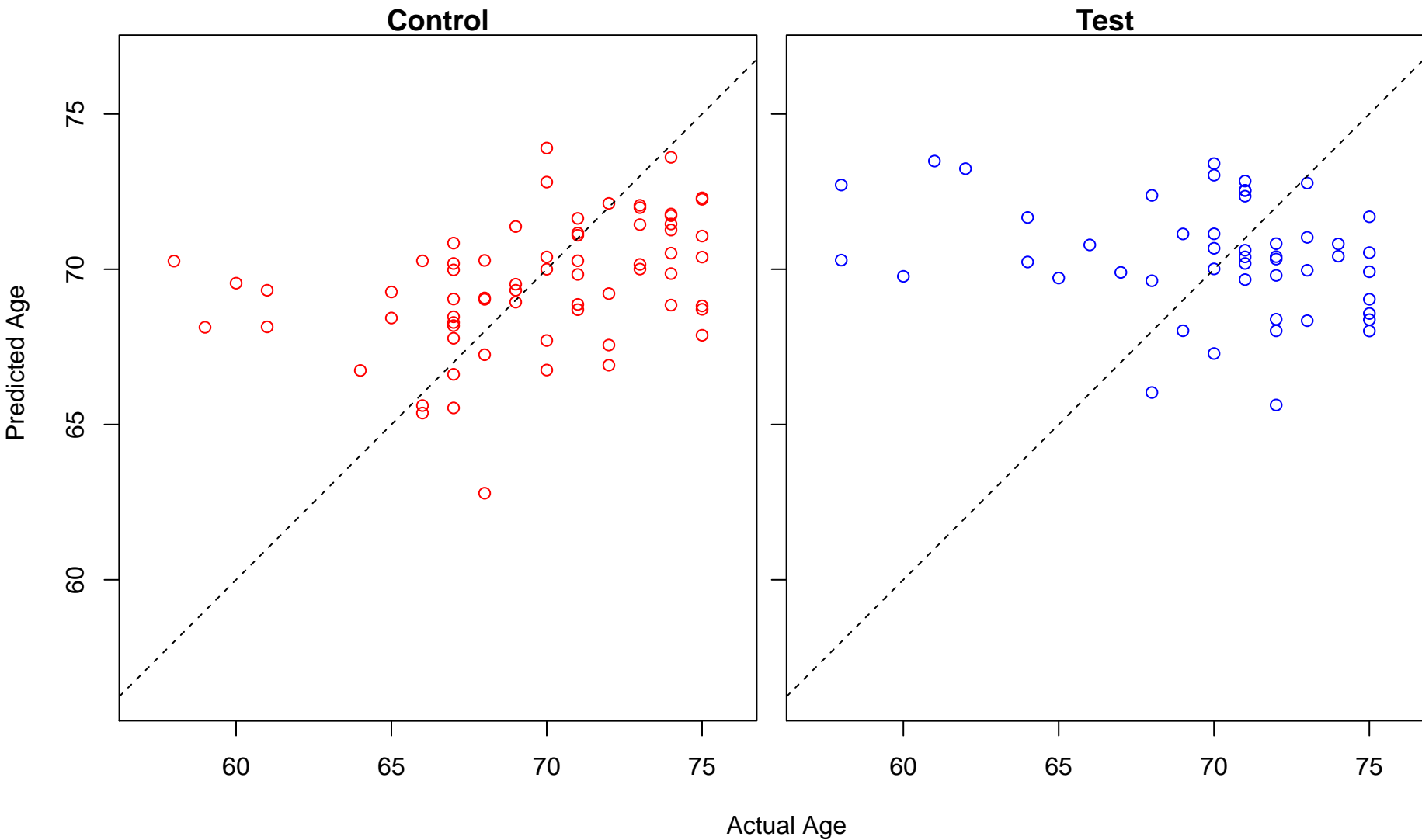
response to interleukin-4 (Score: 0.503969)



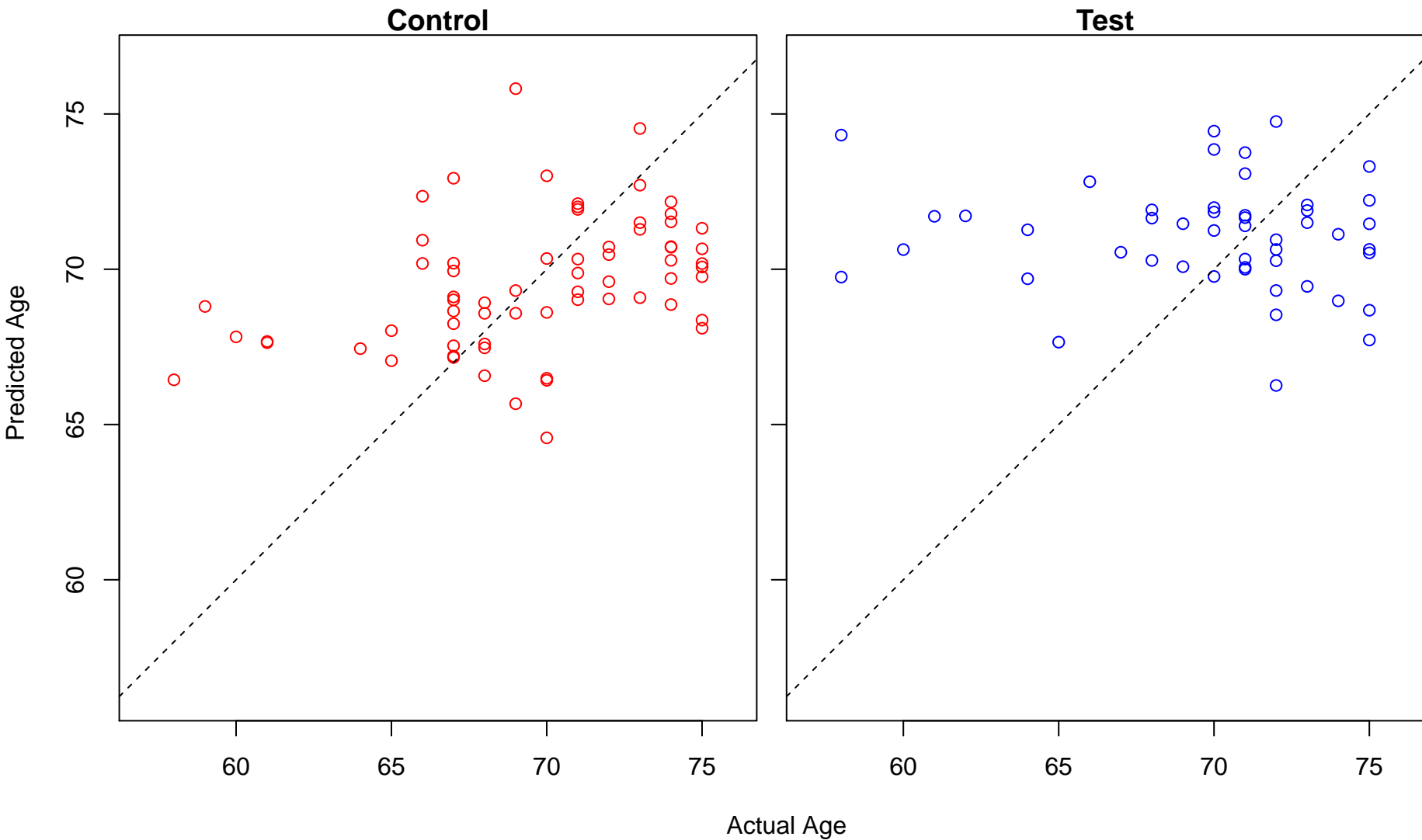
cellular response to interleukin-4 (Score: 0.503969)



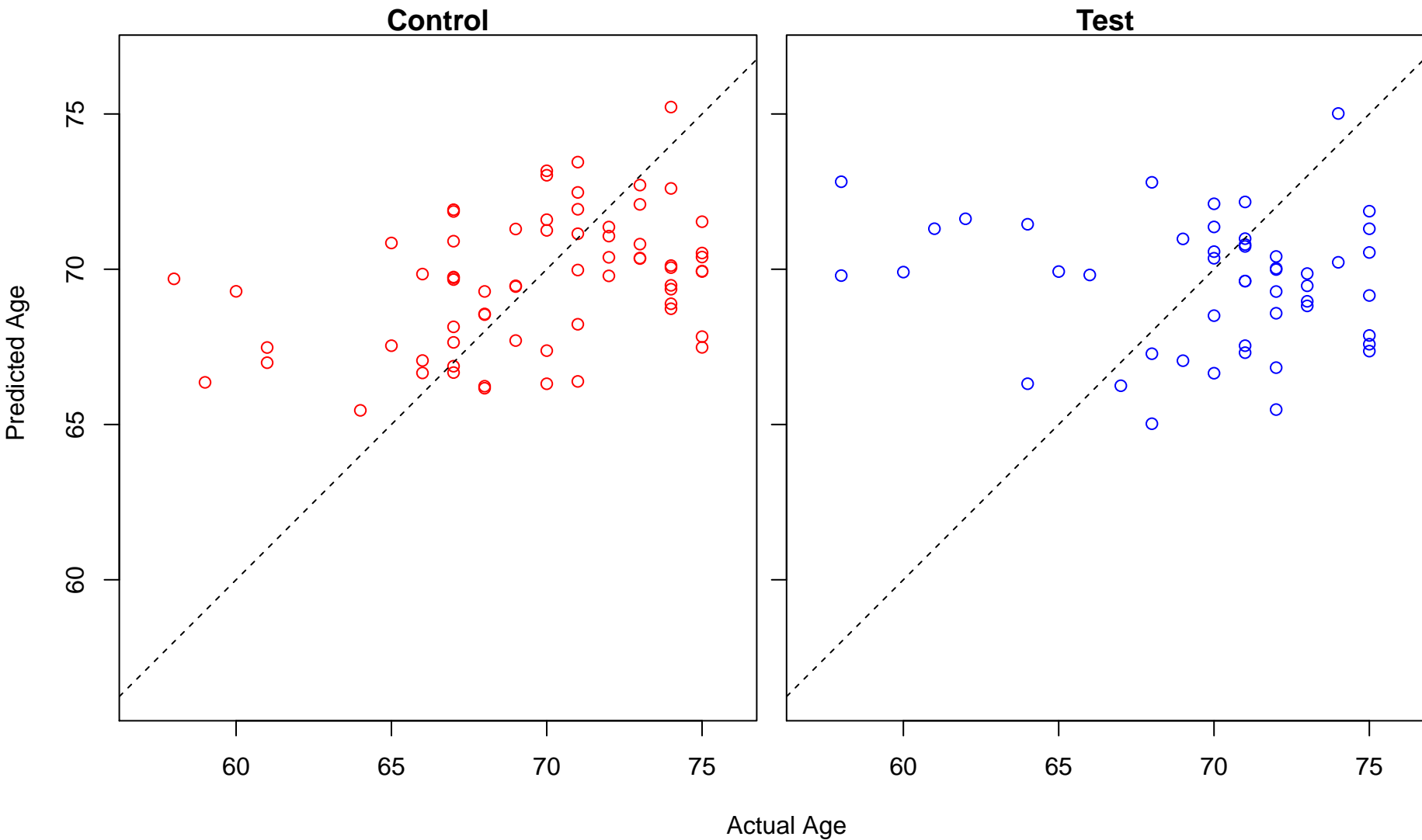
regulation of cellular respiration (Score: 0.503513)



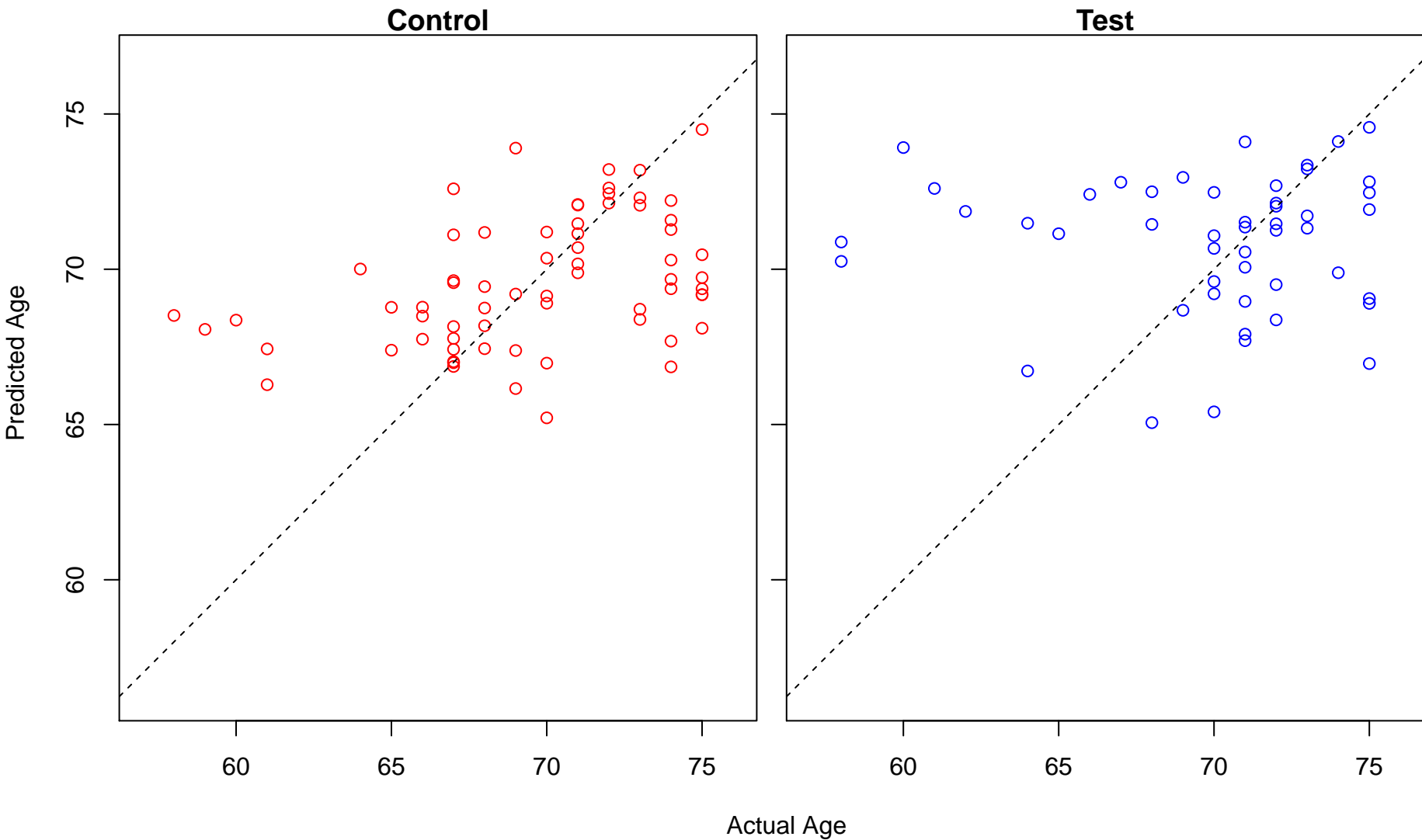
regulation of platelet activation (Score: 0.503368)



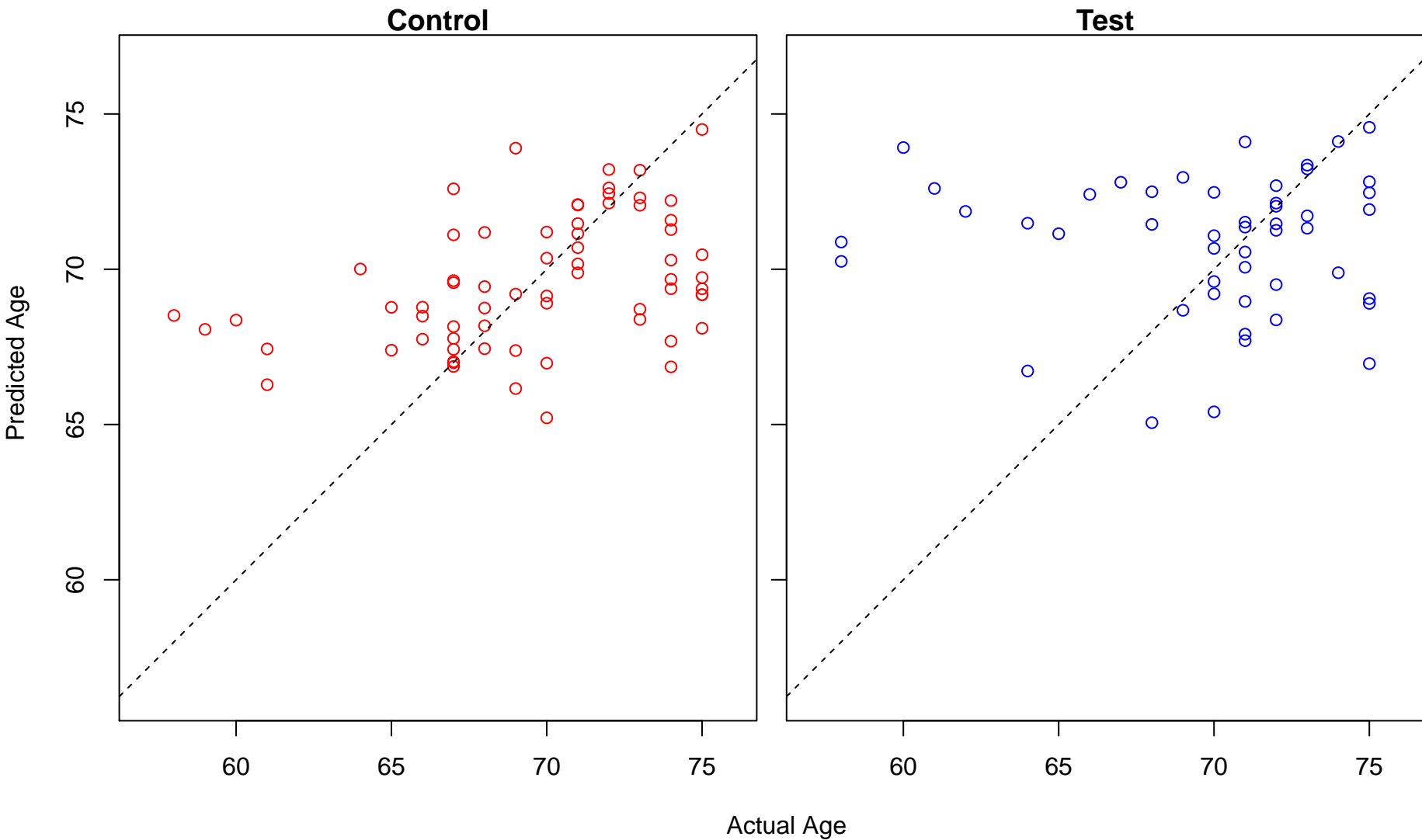
membrane tubulation (Score: 0.502654)



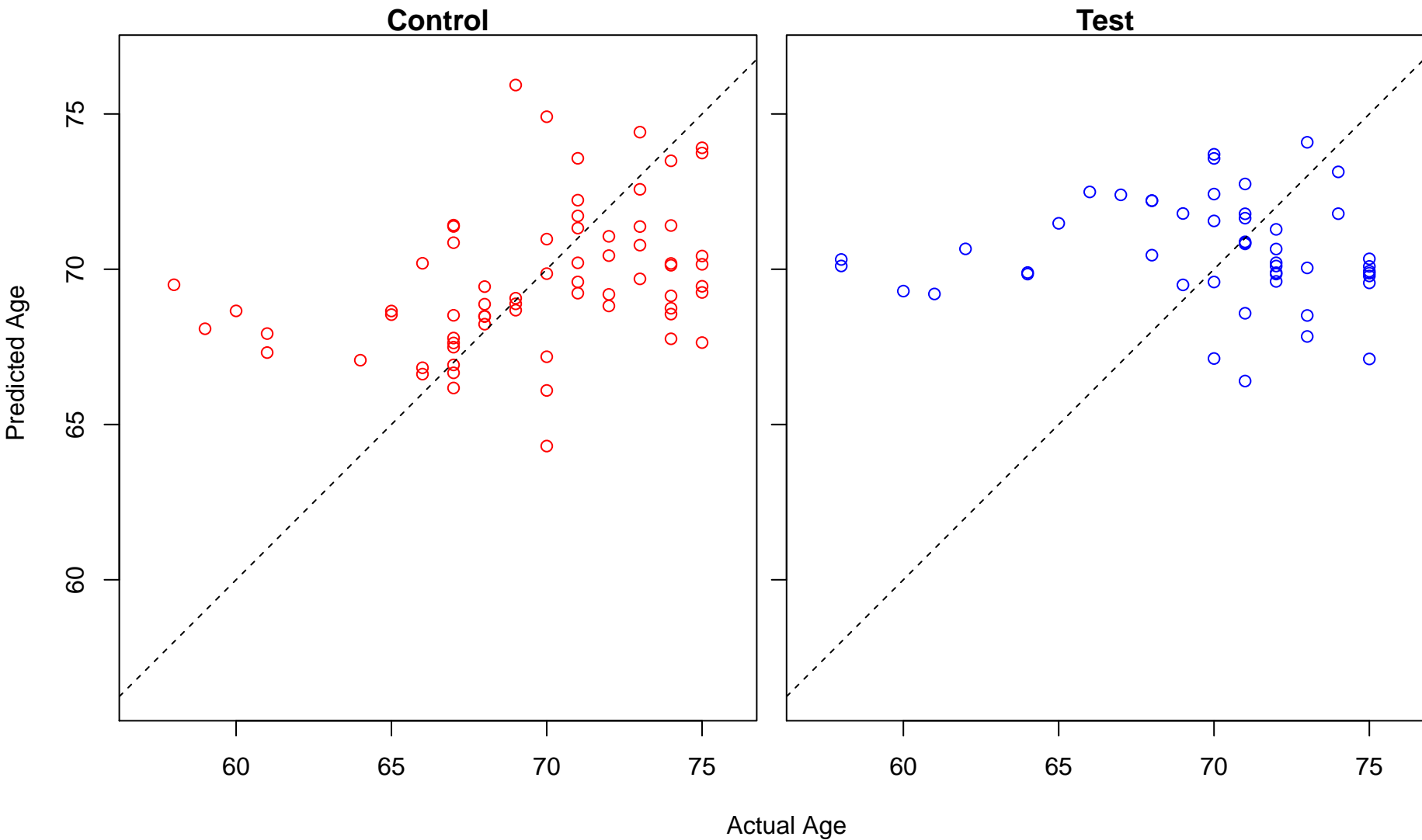
cerebellar Purkinje cell layer development (Score: 0.502056)



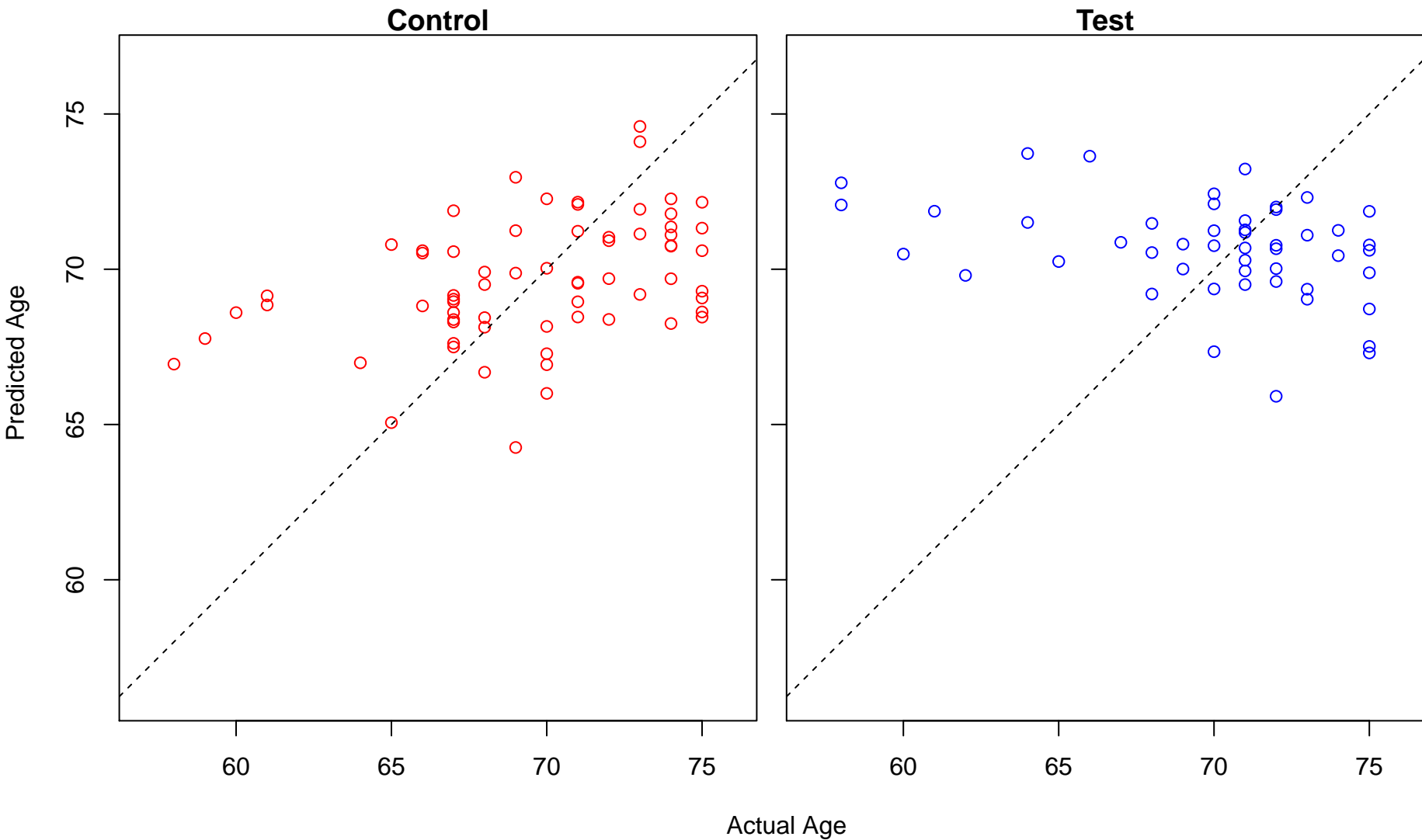
cerebellar Purkinje cell layer morphogenesis (Score: 0.502056)



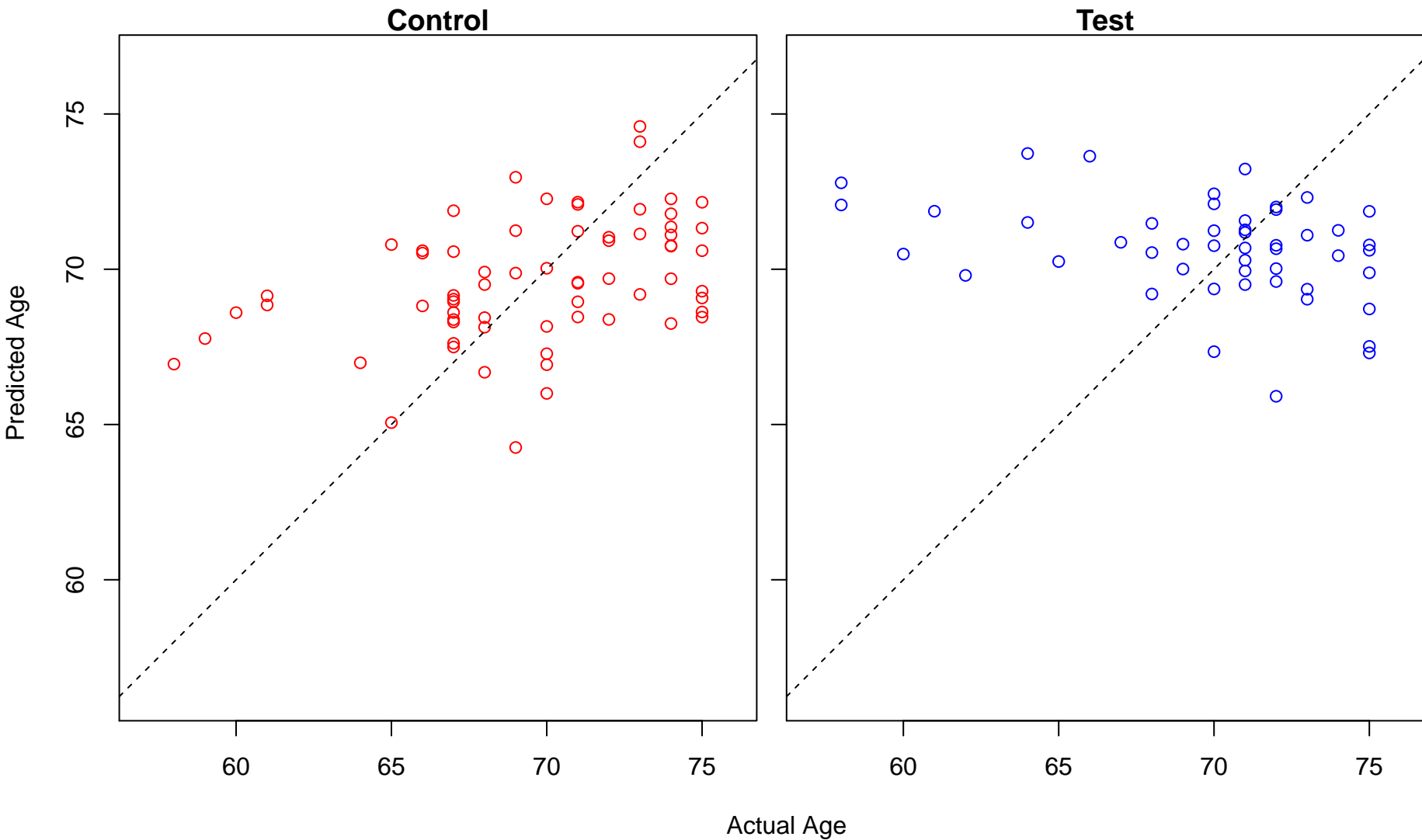
phagosome maturation (Score: 0.501584)



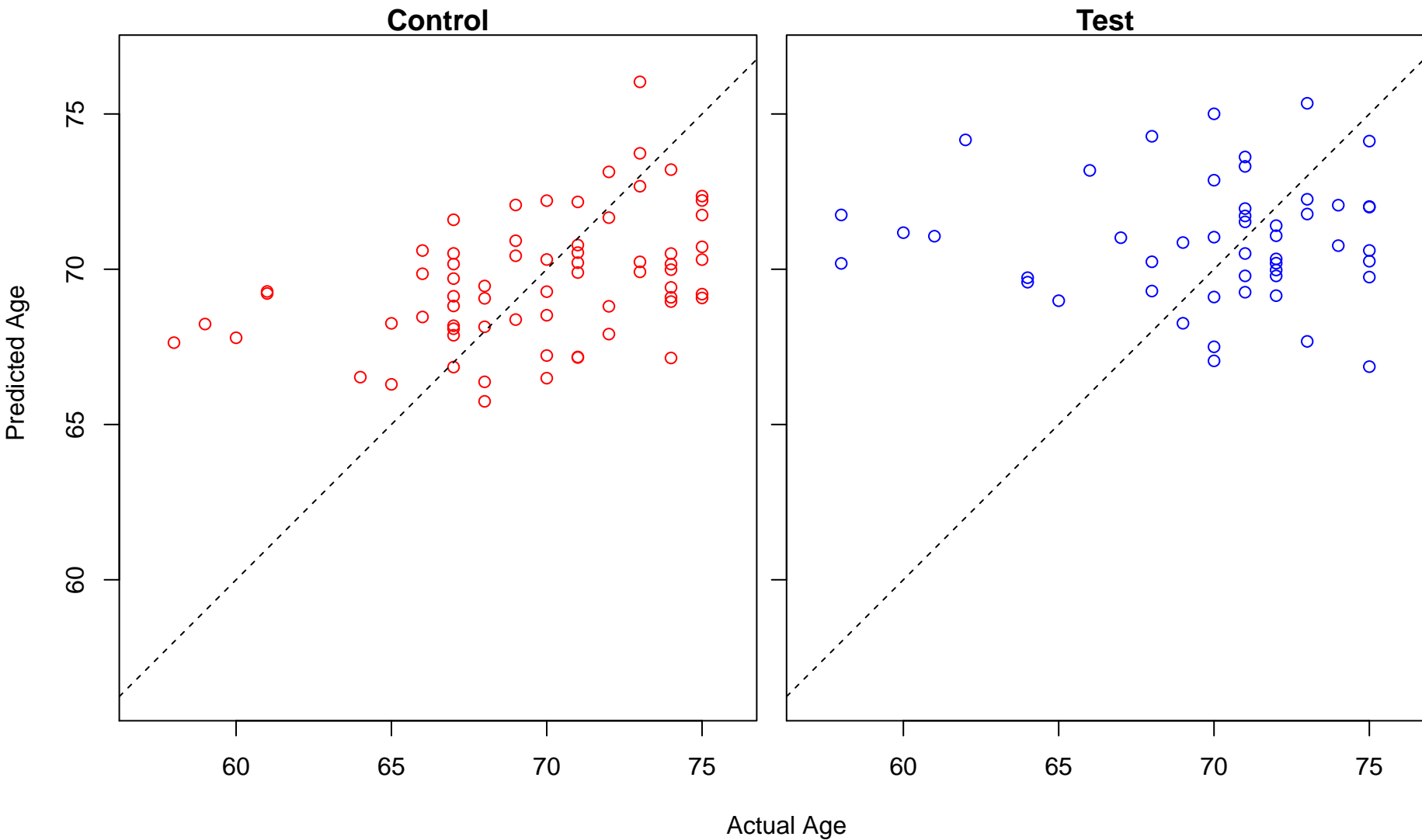
microvillus assembly (Score: 0.501382)



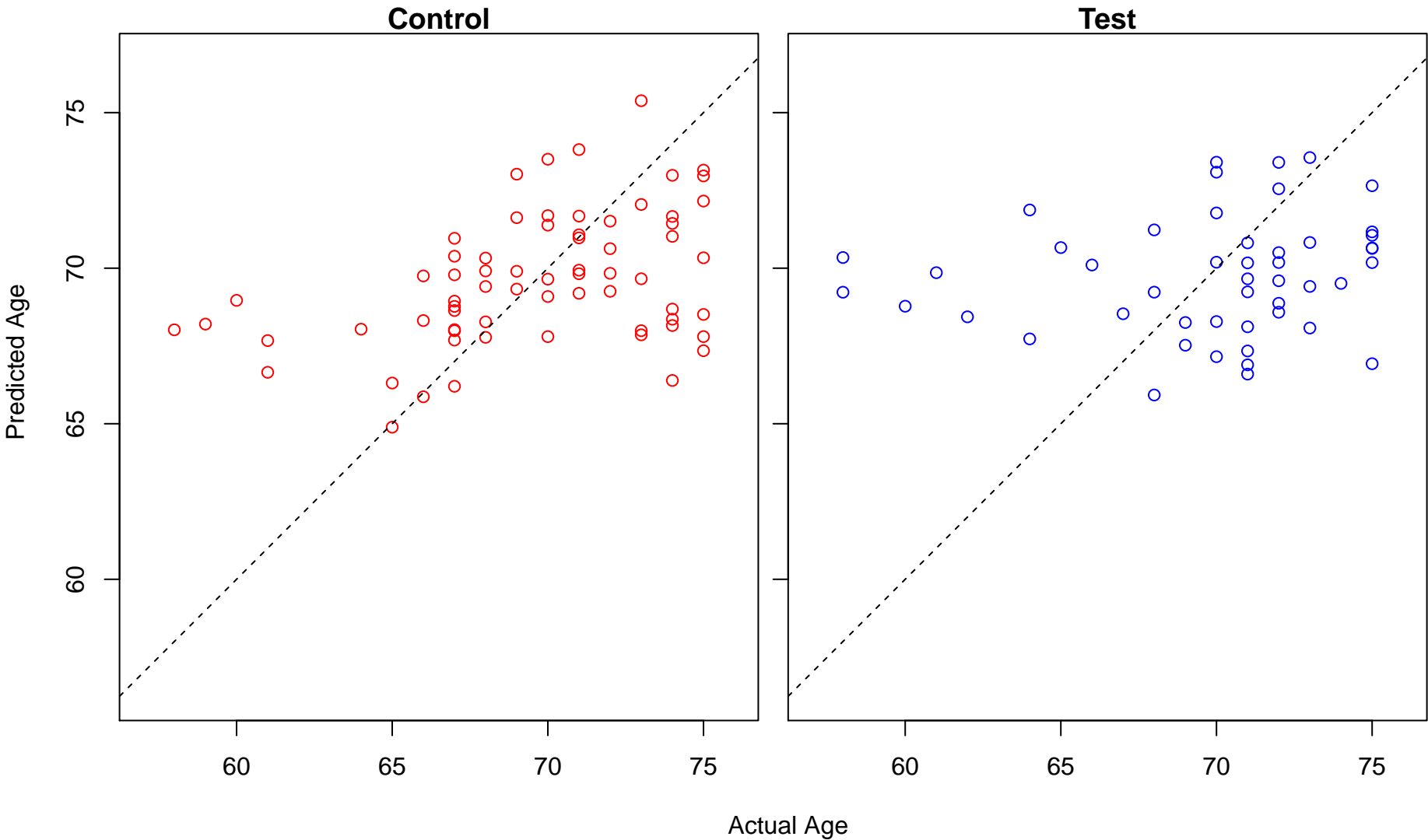
microvillus organization (Score: 0.501382)



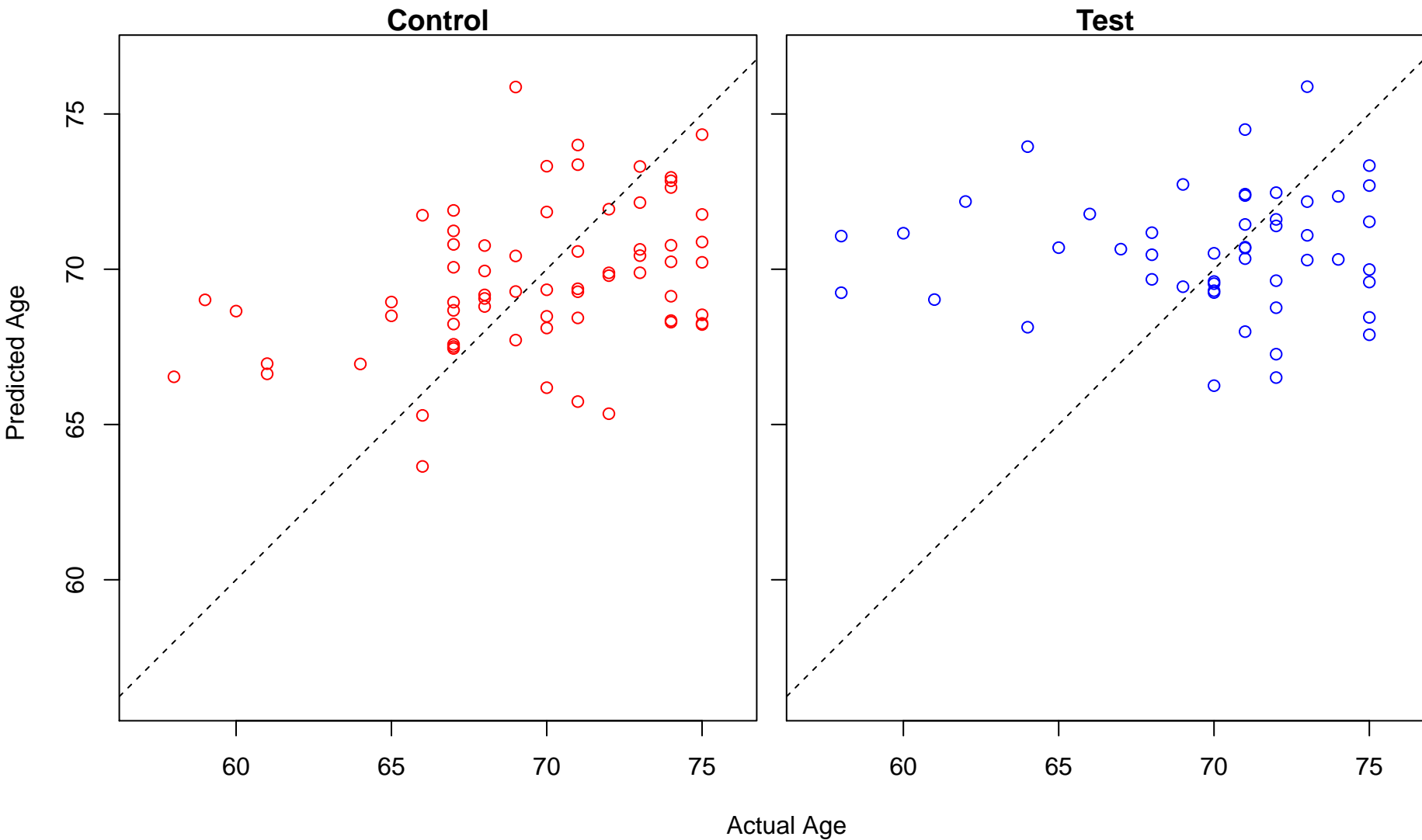
negative regulation of gene silencing by miRNA (Score: 0.500815)



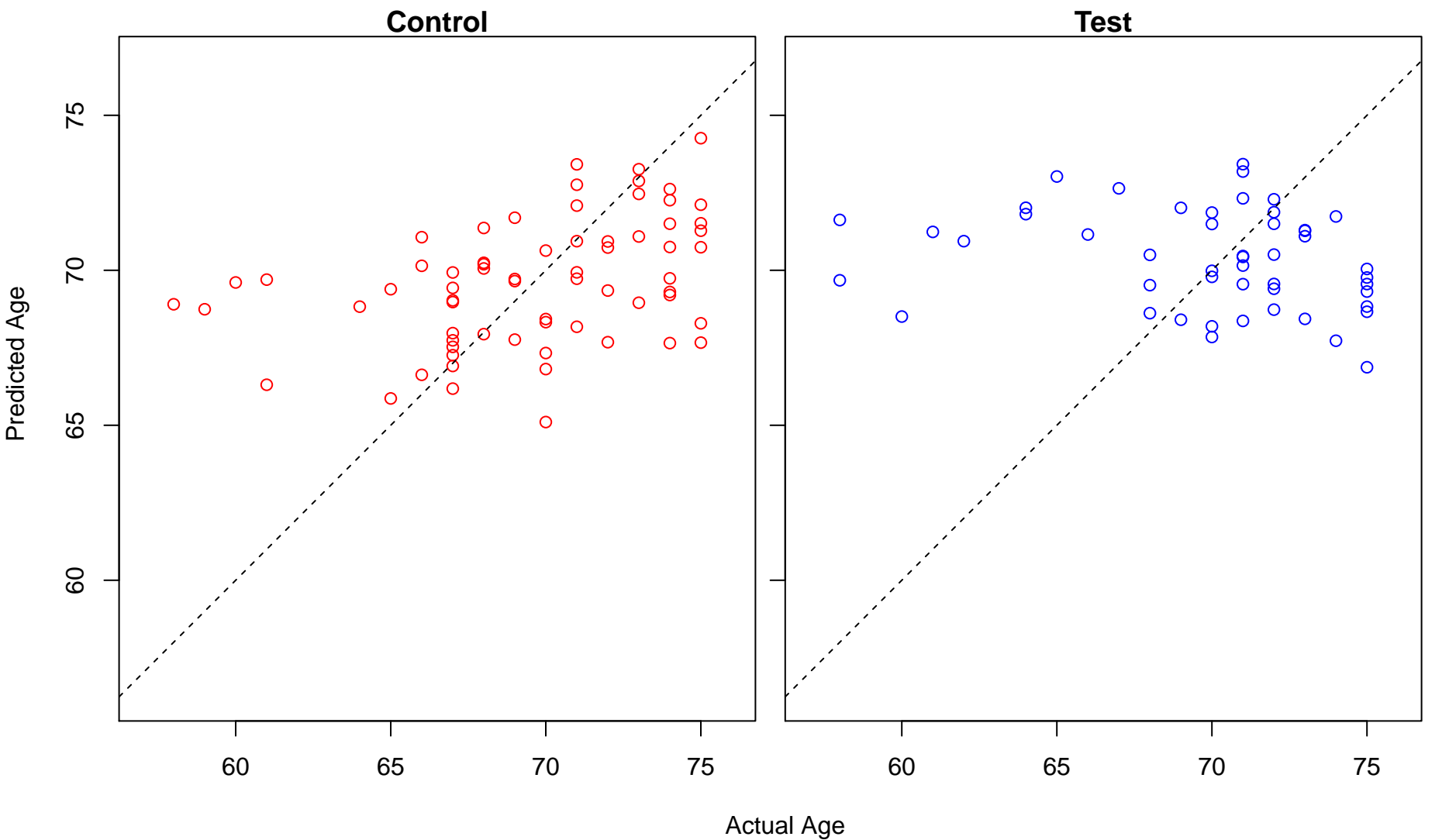
positive regulation of myeloid leukocyte cytokine production involved in immune response (Score: 0.50)



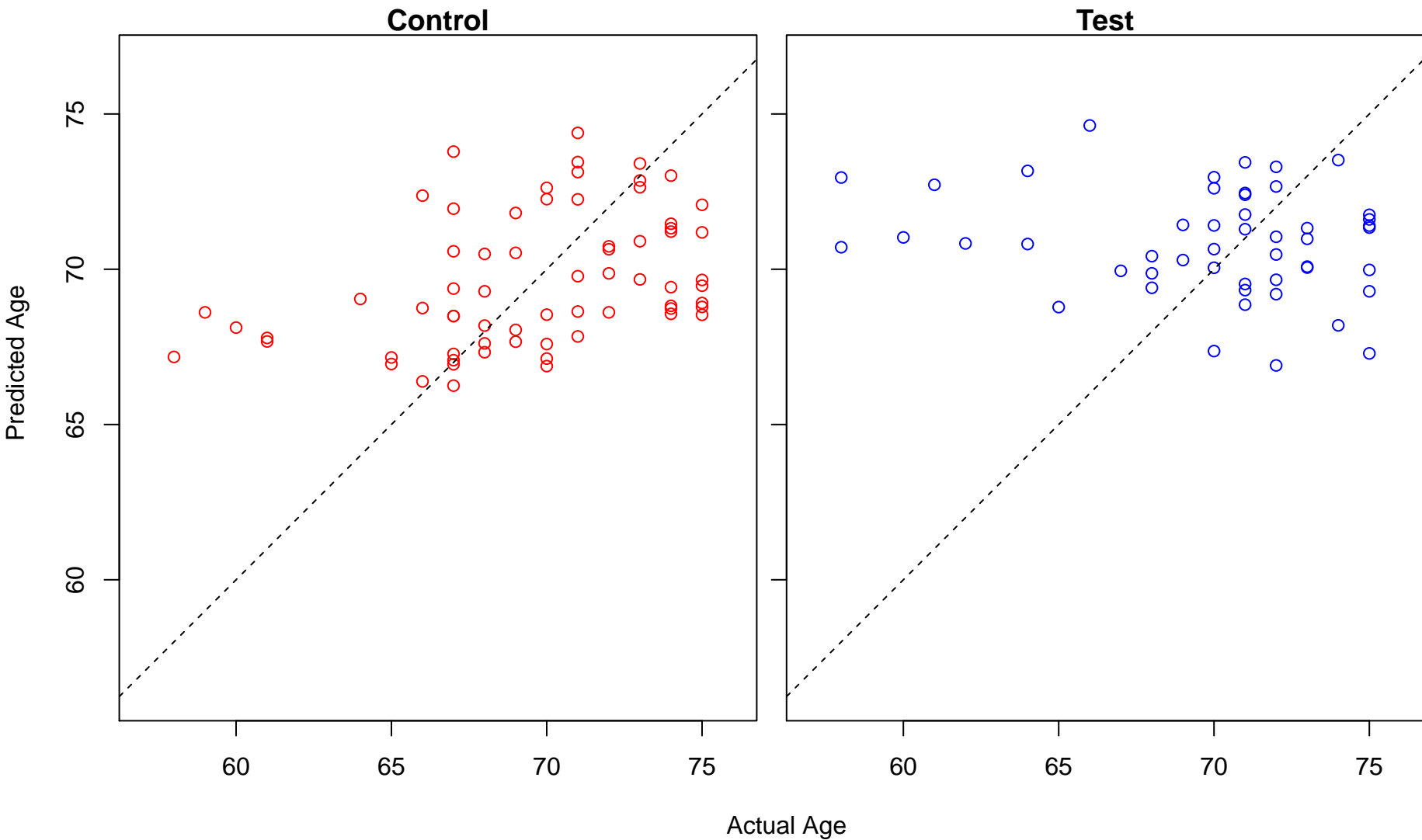
thymus development (Score: 0.500593)



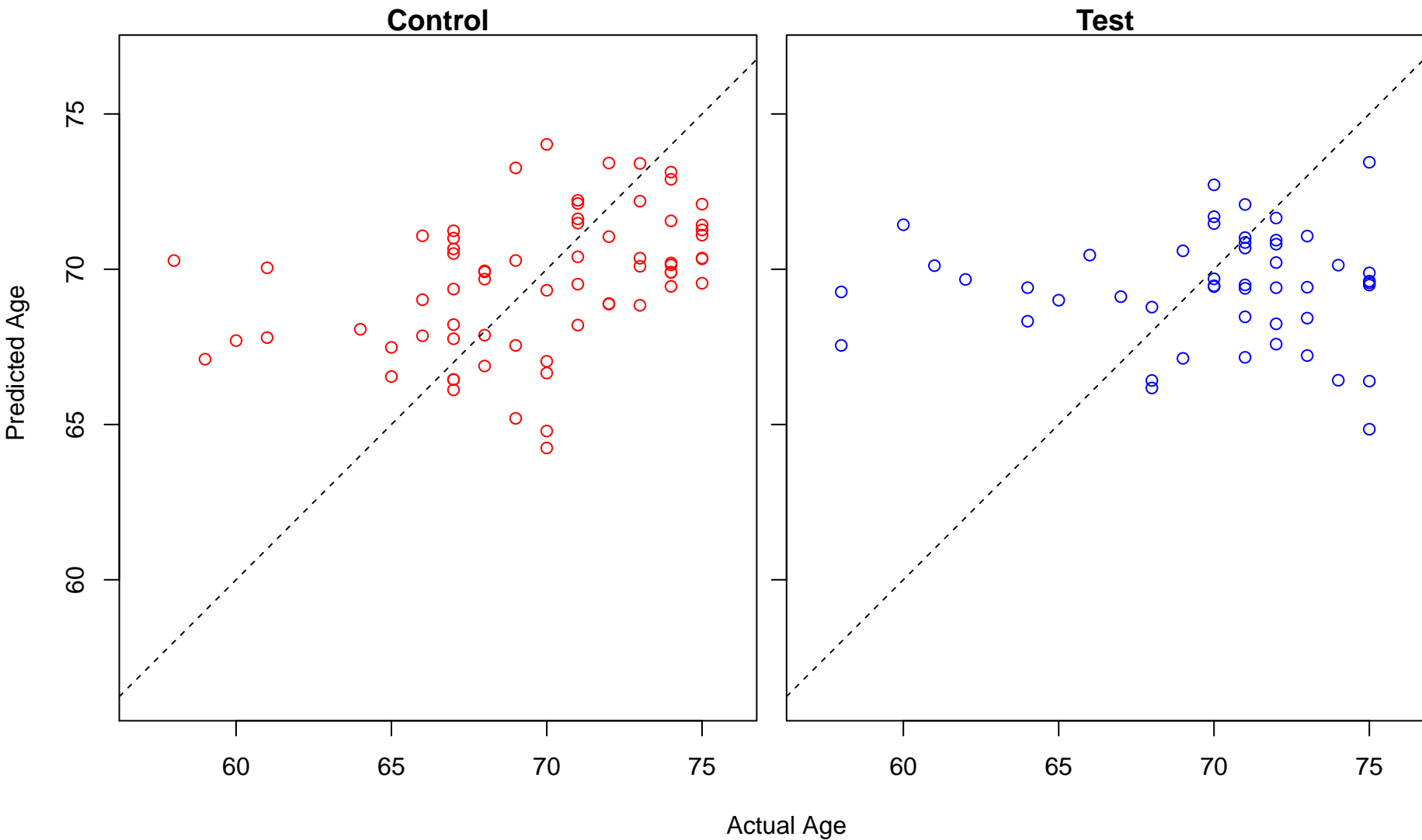
of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling



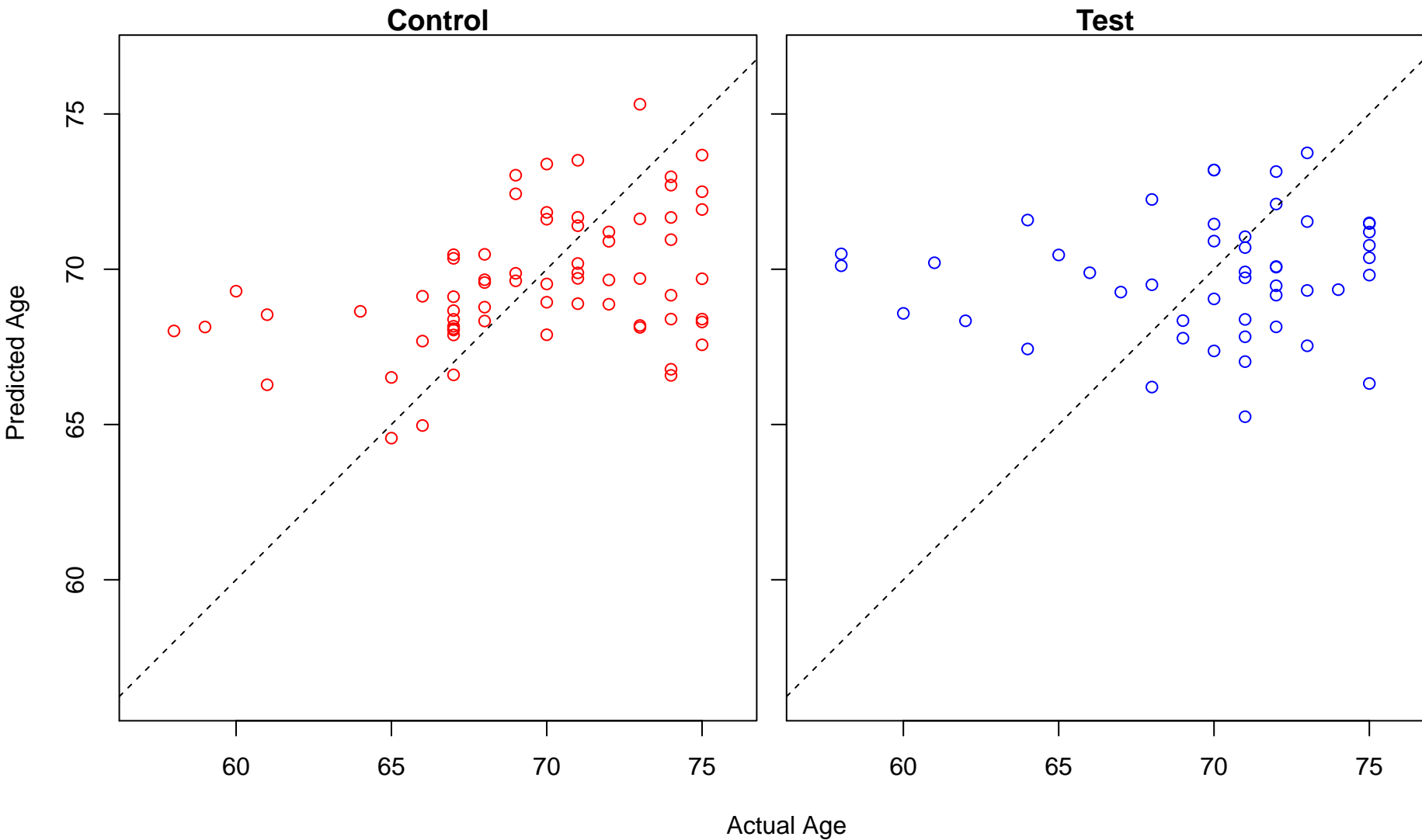
positive regulation of cell adhesion mediated by integrin (Score: 0.499125)



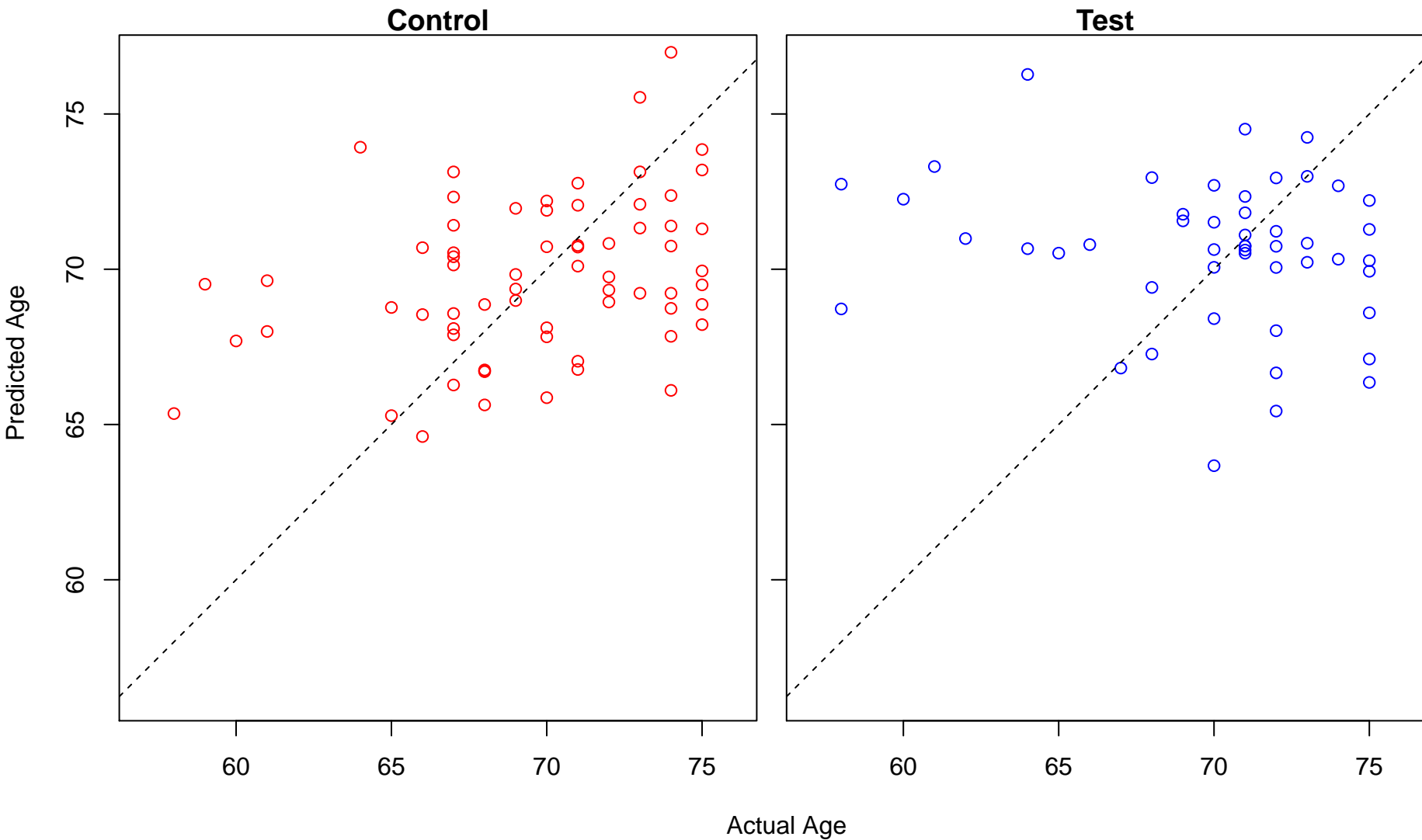
granulocyte differentiation (Score: 0.498936)



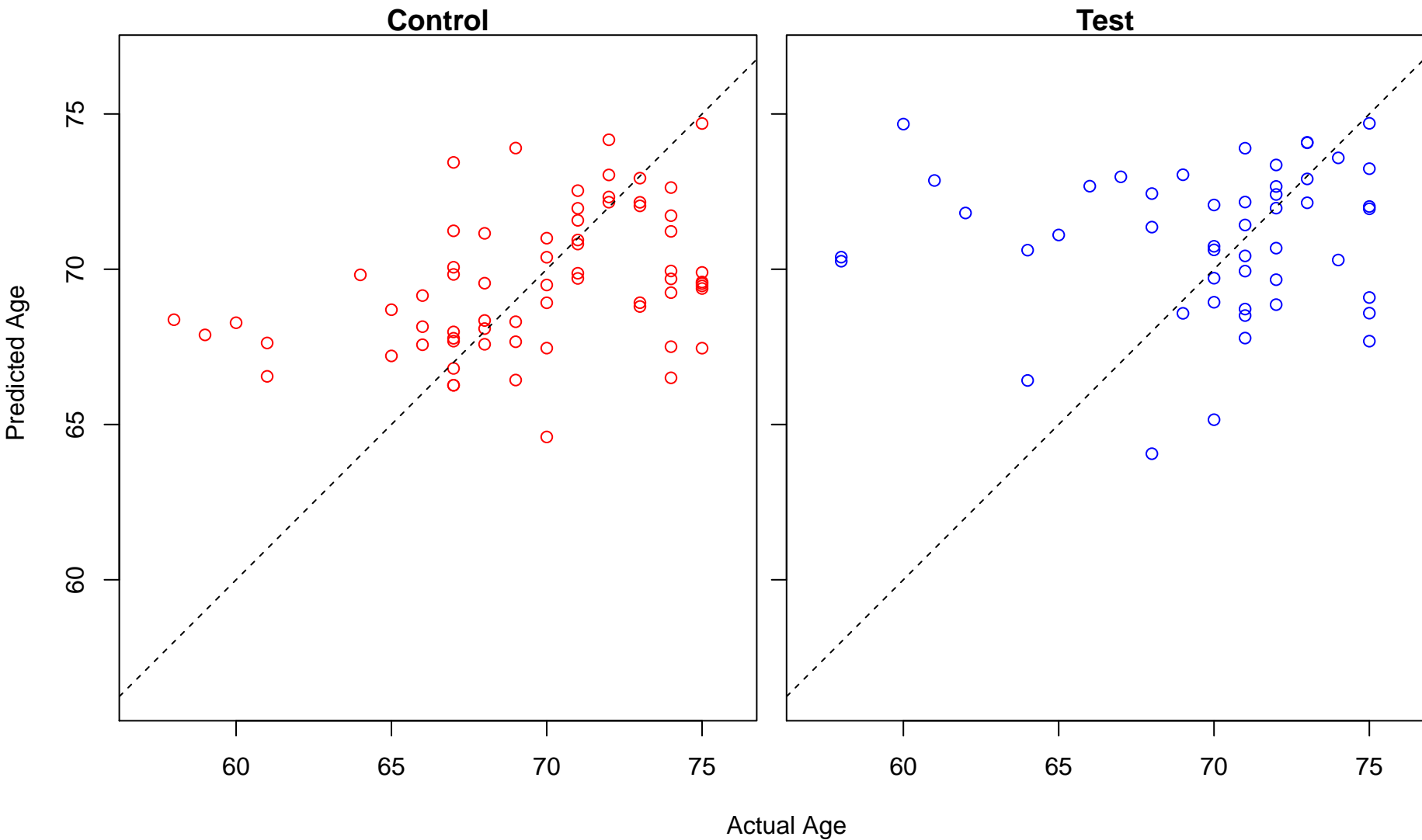
regulation of macrophage cytokine production (Score: 0.498134)



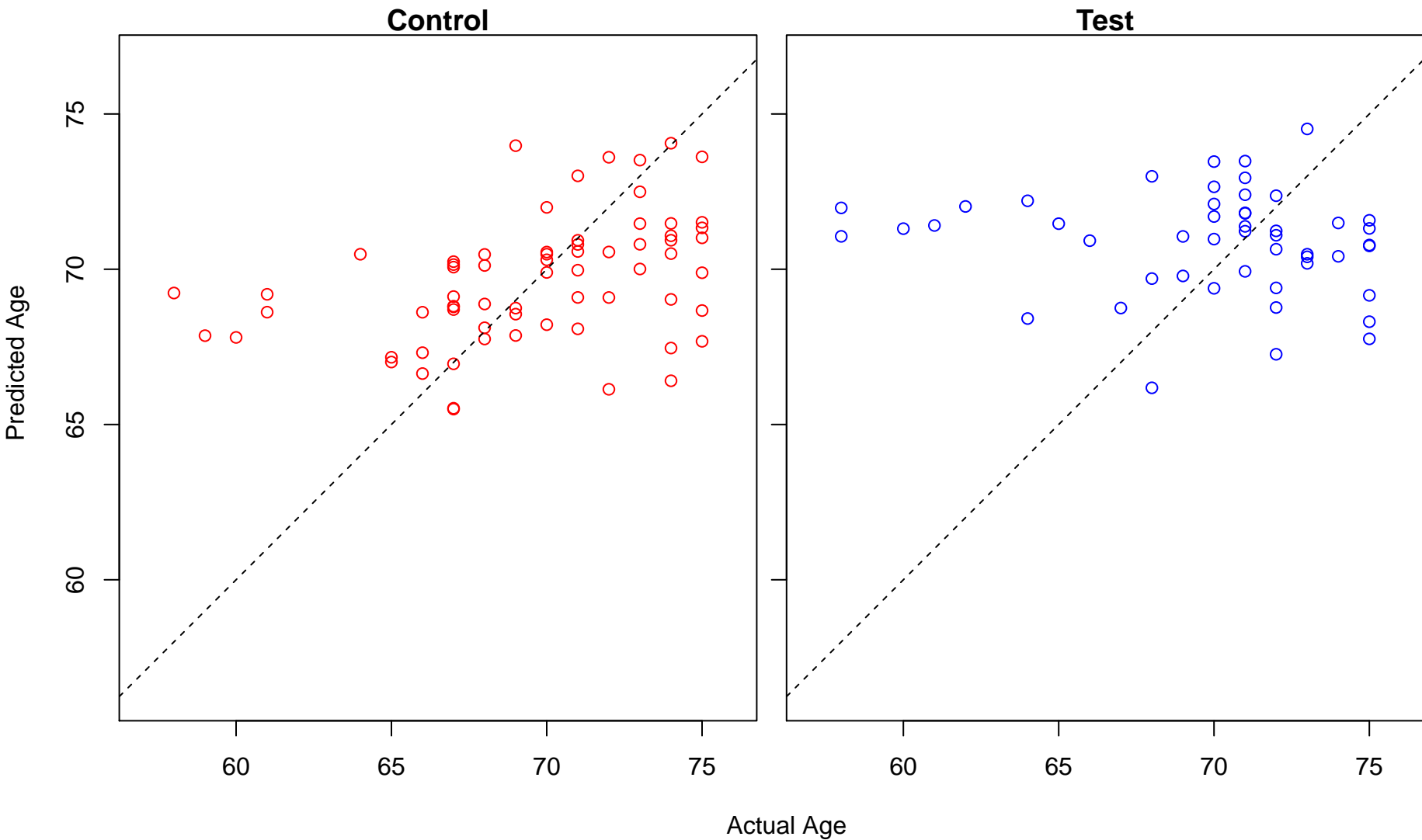
GMP metabolic process (Score: 0.497926)



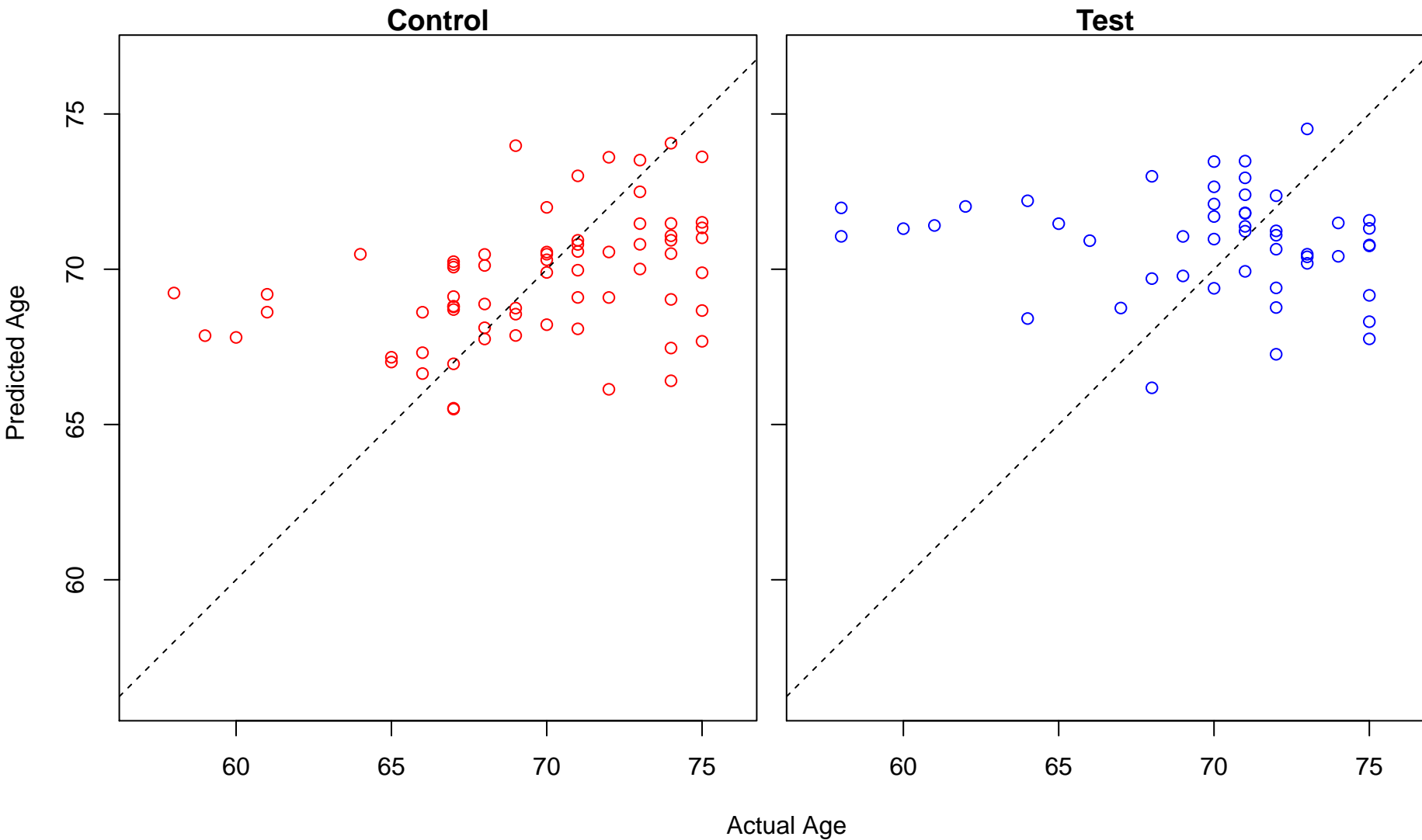
cerebellum morphogenesis (Score: 0.497279)



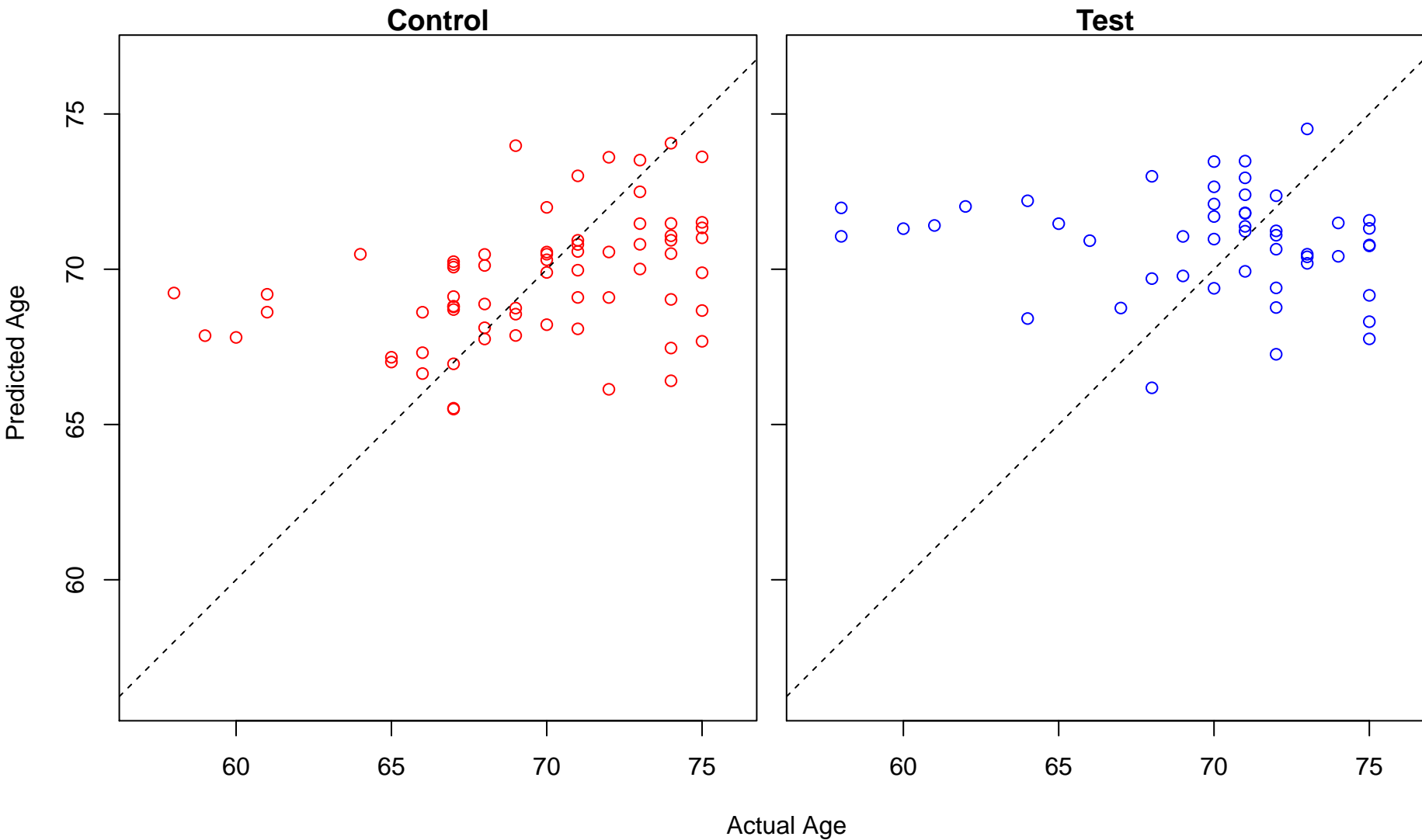
ether lipid biosynthetic process (Score: 0.497262)



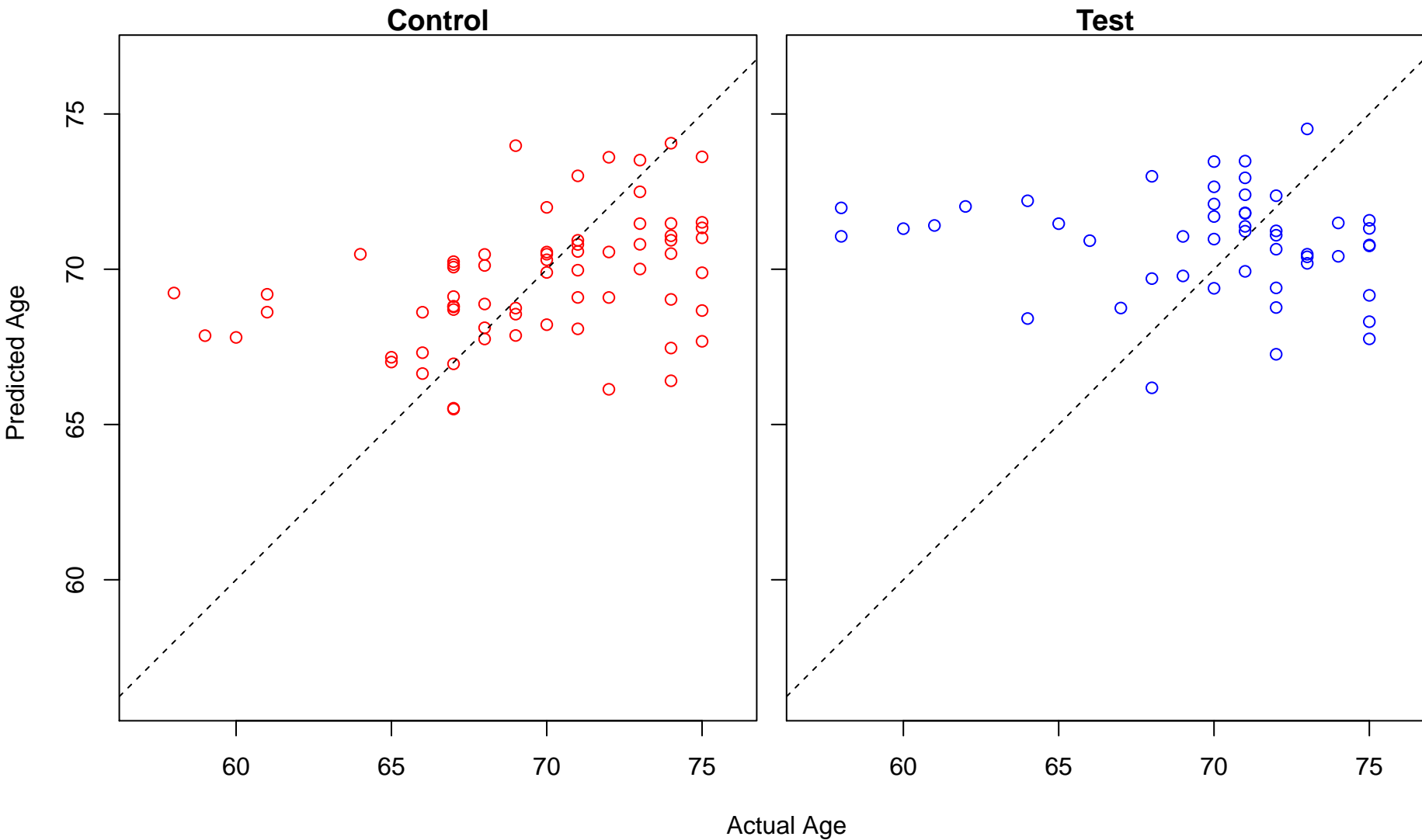
glycerol ether biosynthetic process (Score: 0.497262)



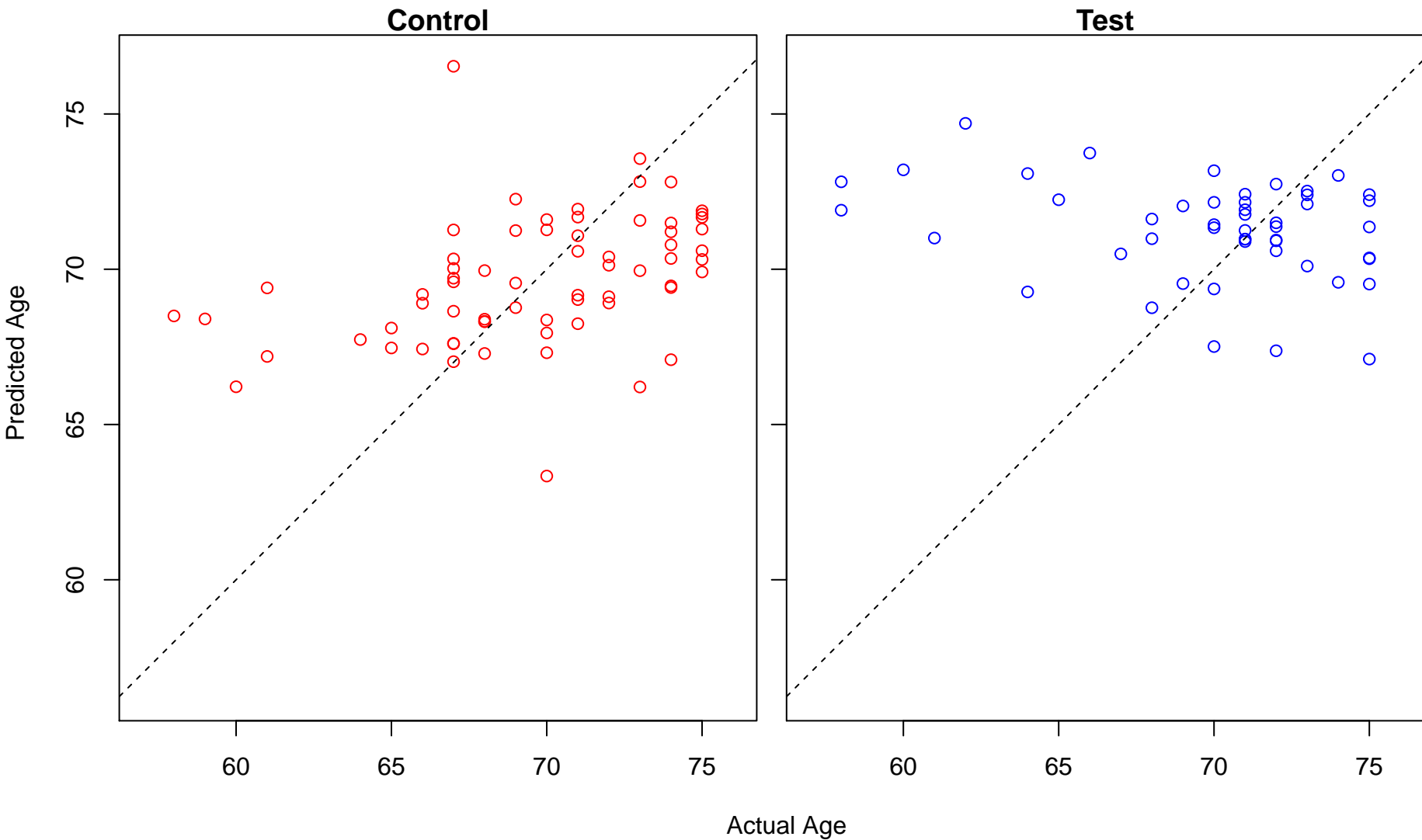
cellular lipid biosynthetic process (Score: 0.497262)



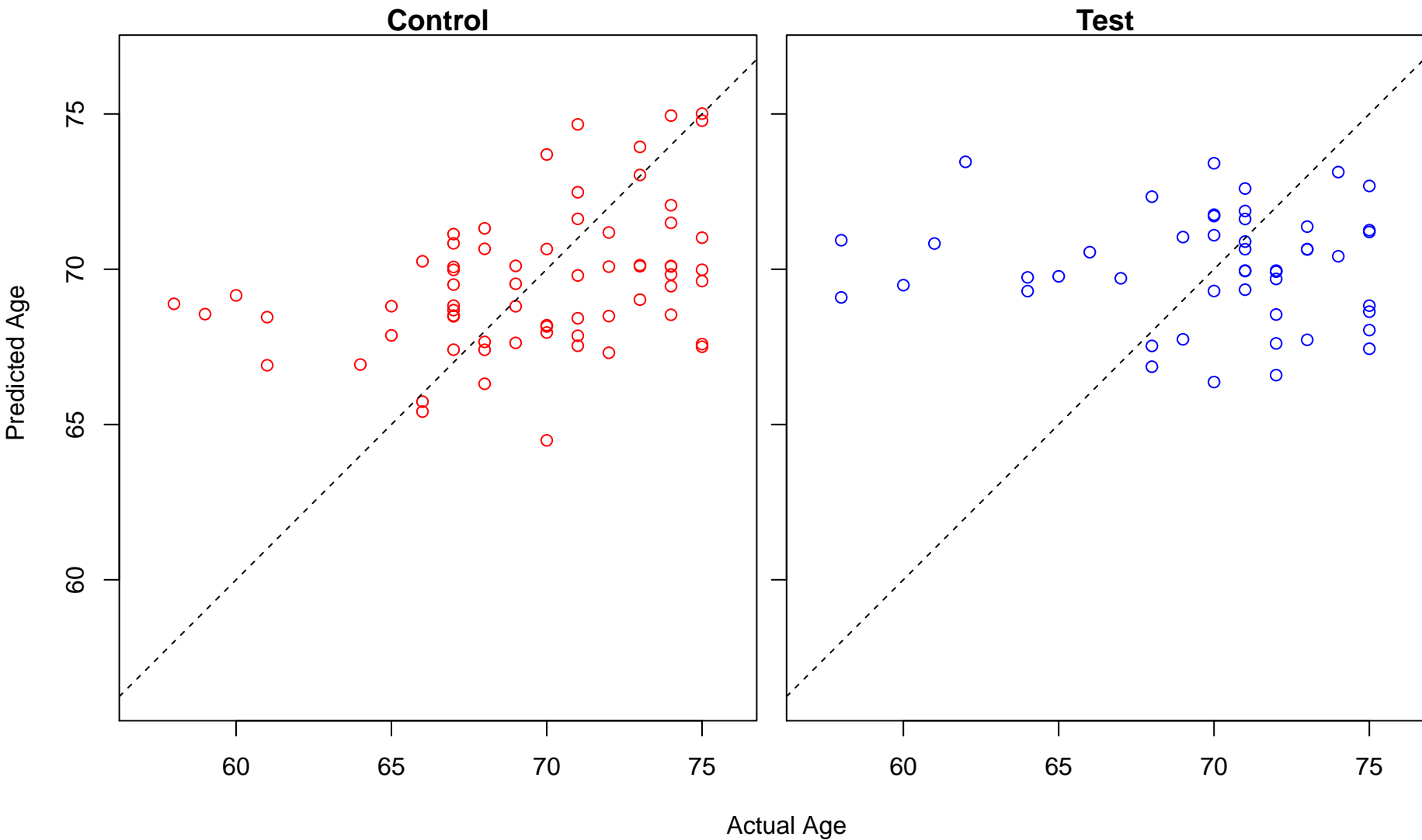
ether biosynthetic process (Score: 0.497262)



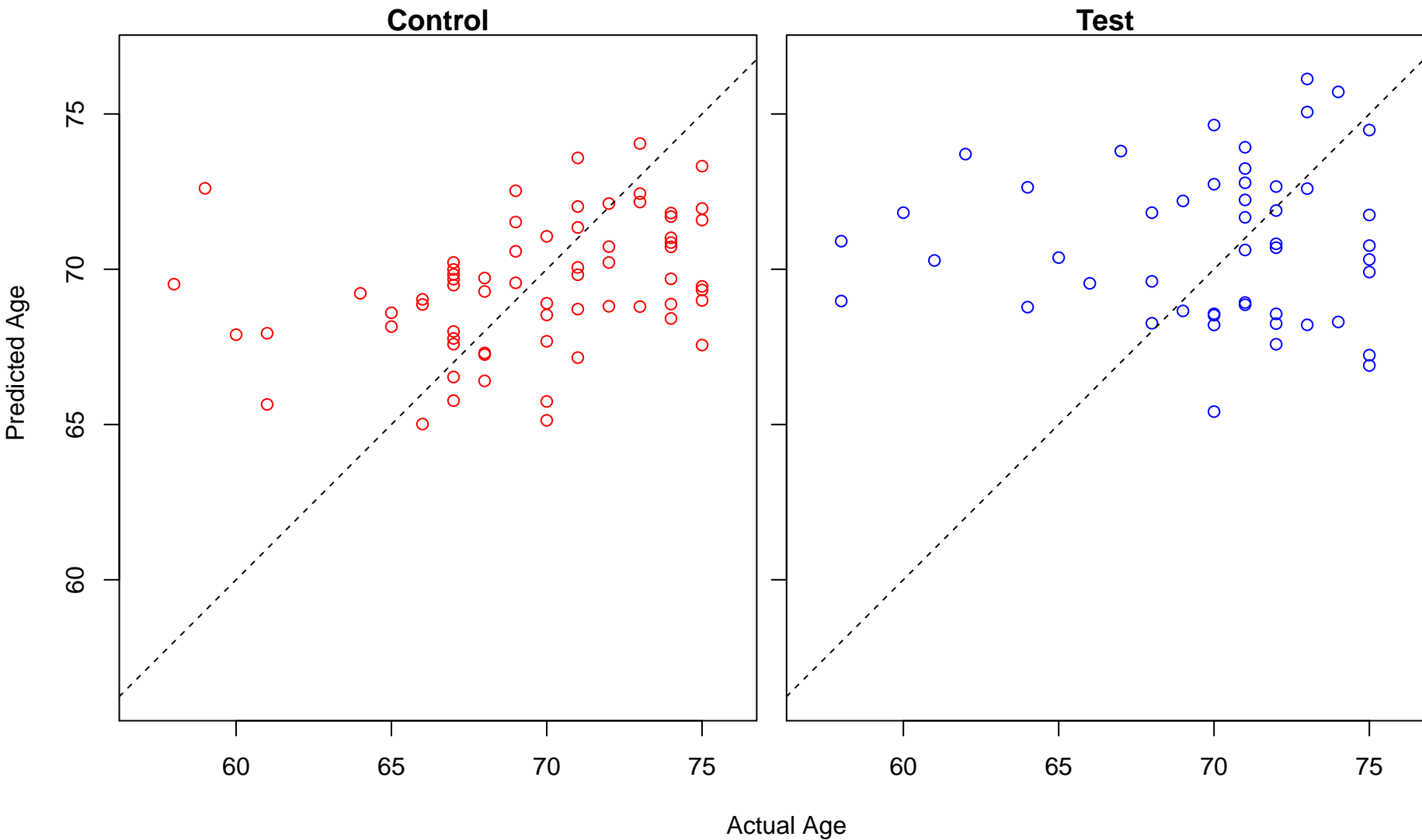
regulation of response to osmotic stress (Score: 0.496780)



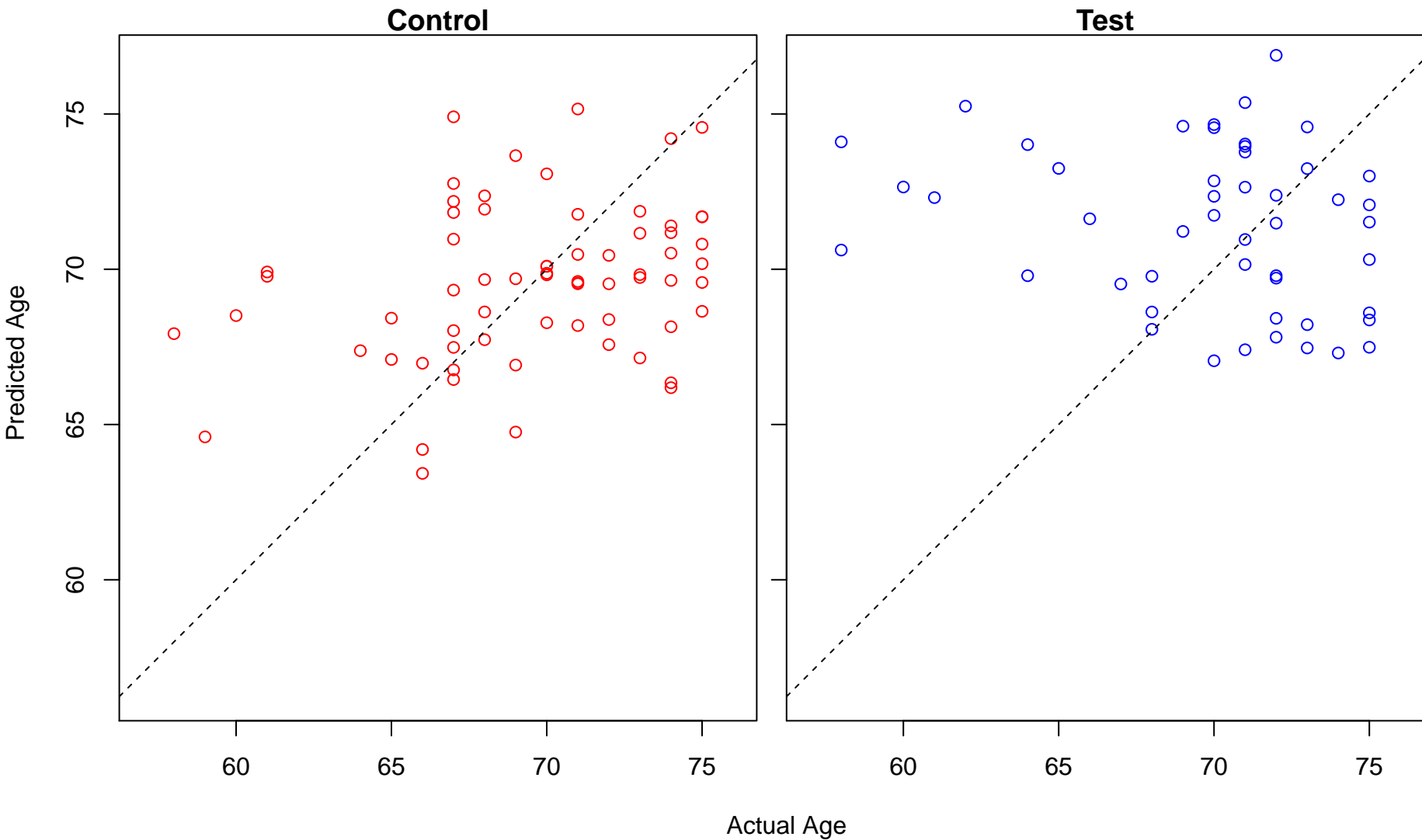
regulation of synaptic vesicle transport (Score: 0.496452)



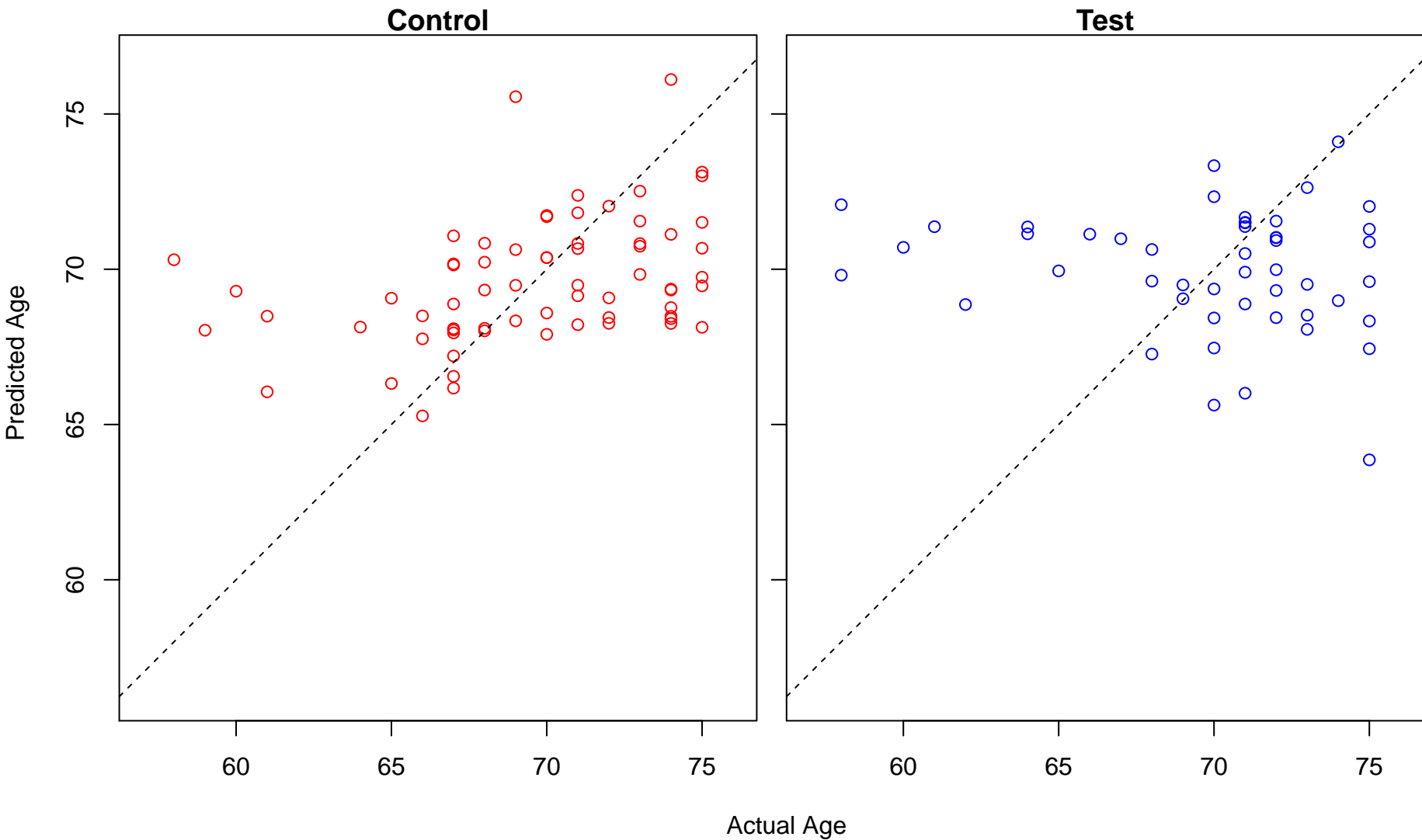
cytochrome complex assembly (Score: 0.495572)



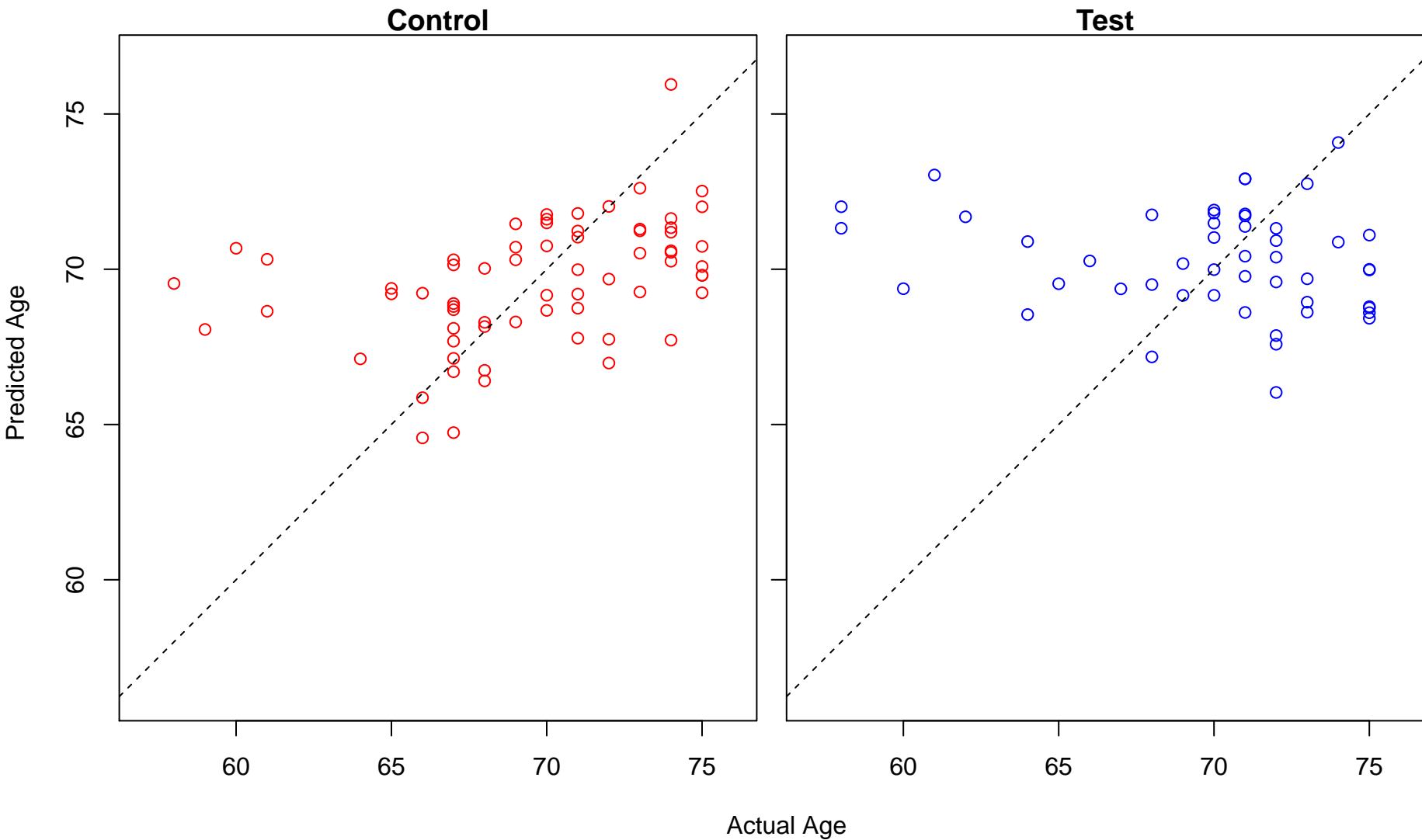
negative regulation of protein activation cascade (Score: 0.495444)



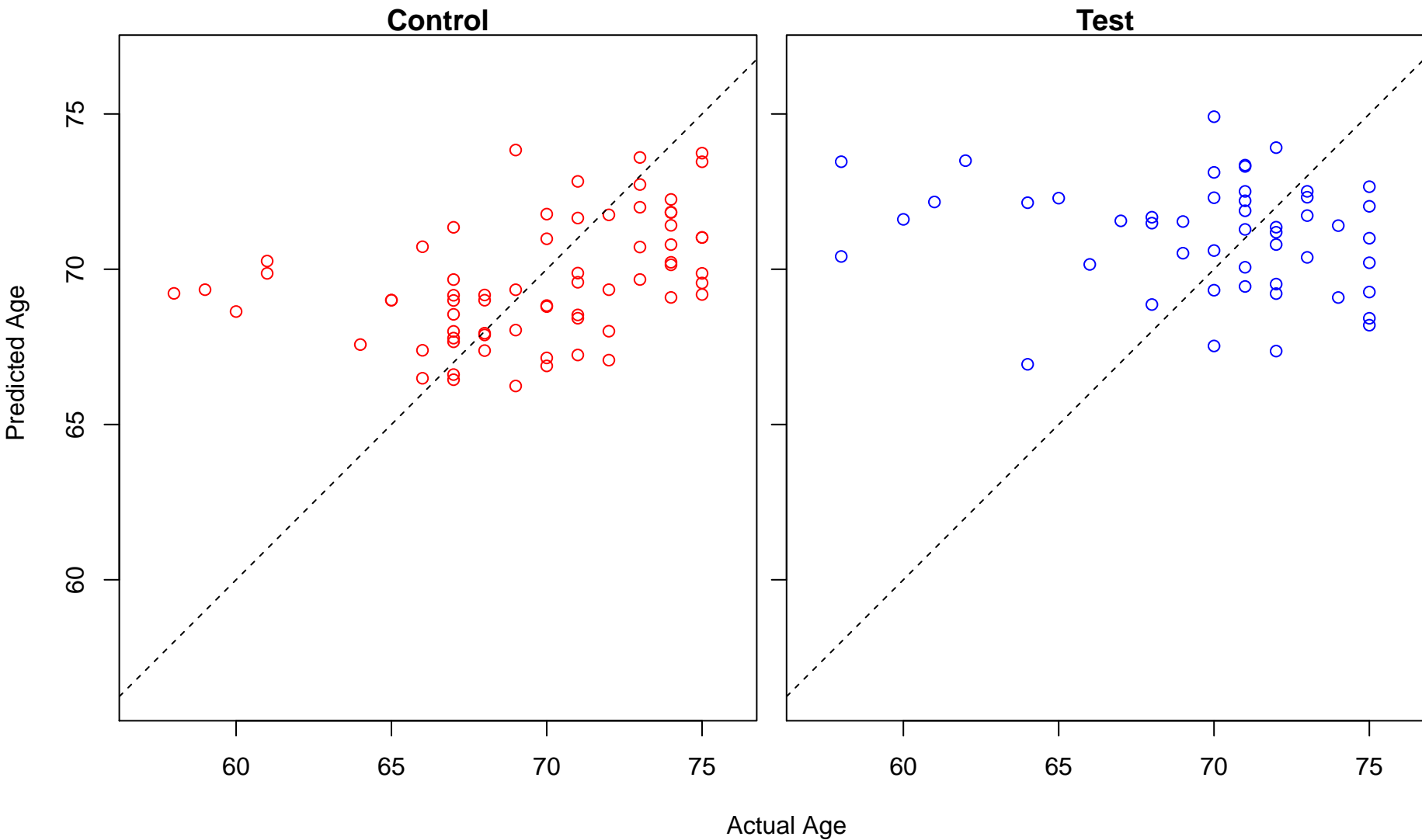
retina layer formation (Score: 0.495400)



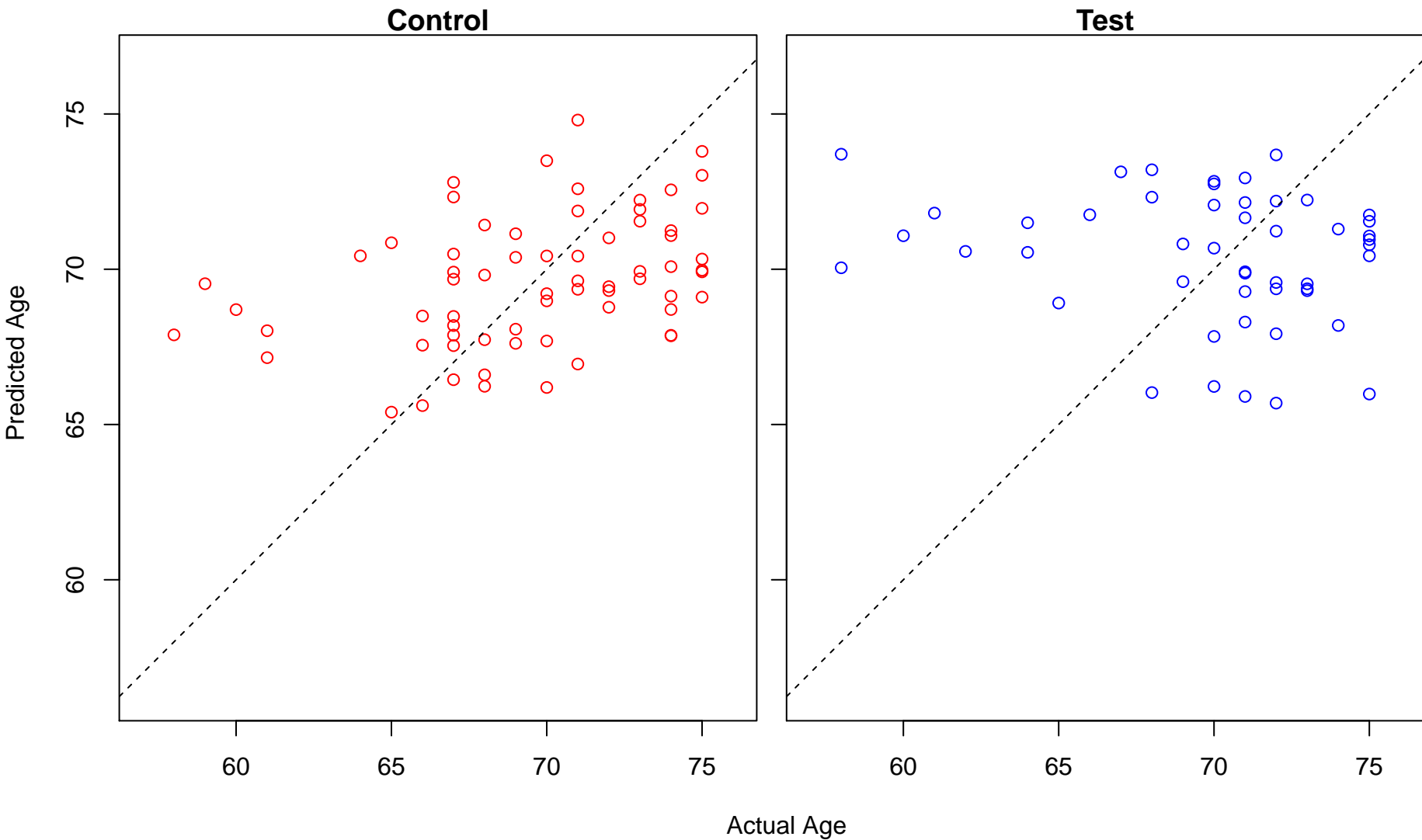
mitochondrion morphogenesis (Score: 0.494609)



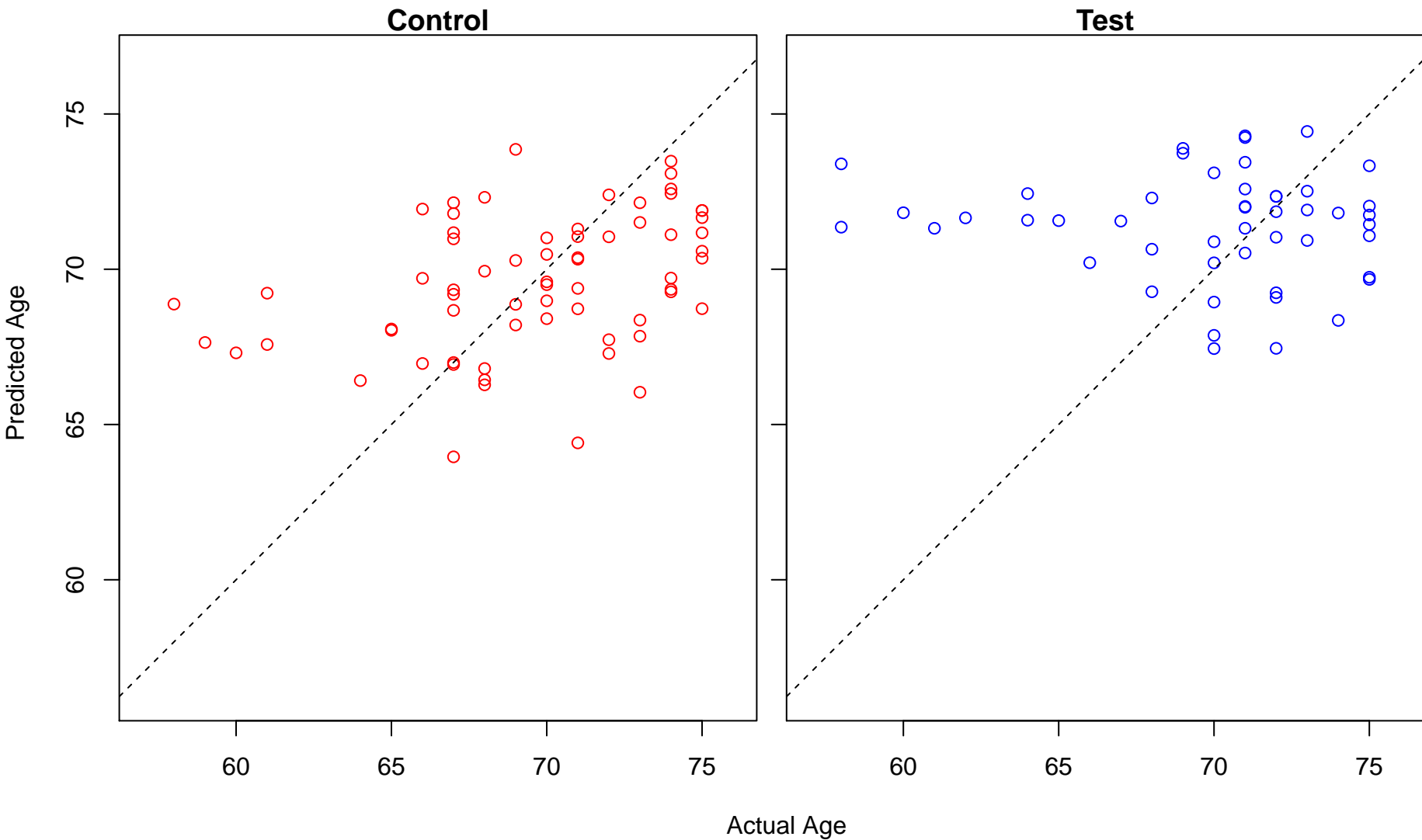
fatty acid alpha-oxidation (Score: 0.493797)



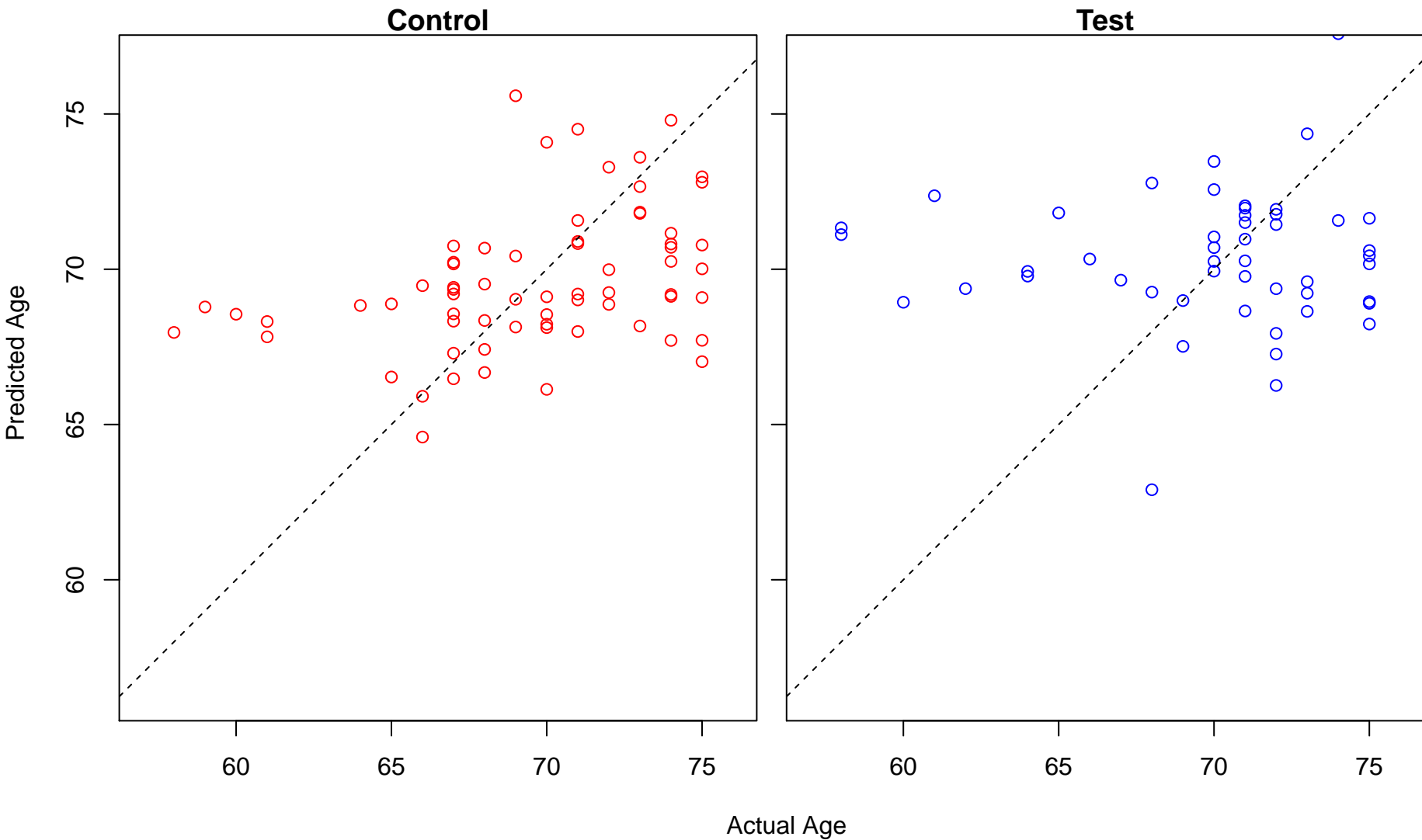
positive regulation of B cell differentiation (Score: 0.493361)



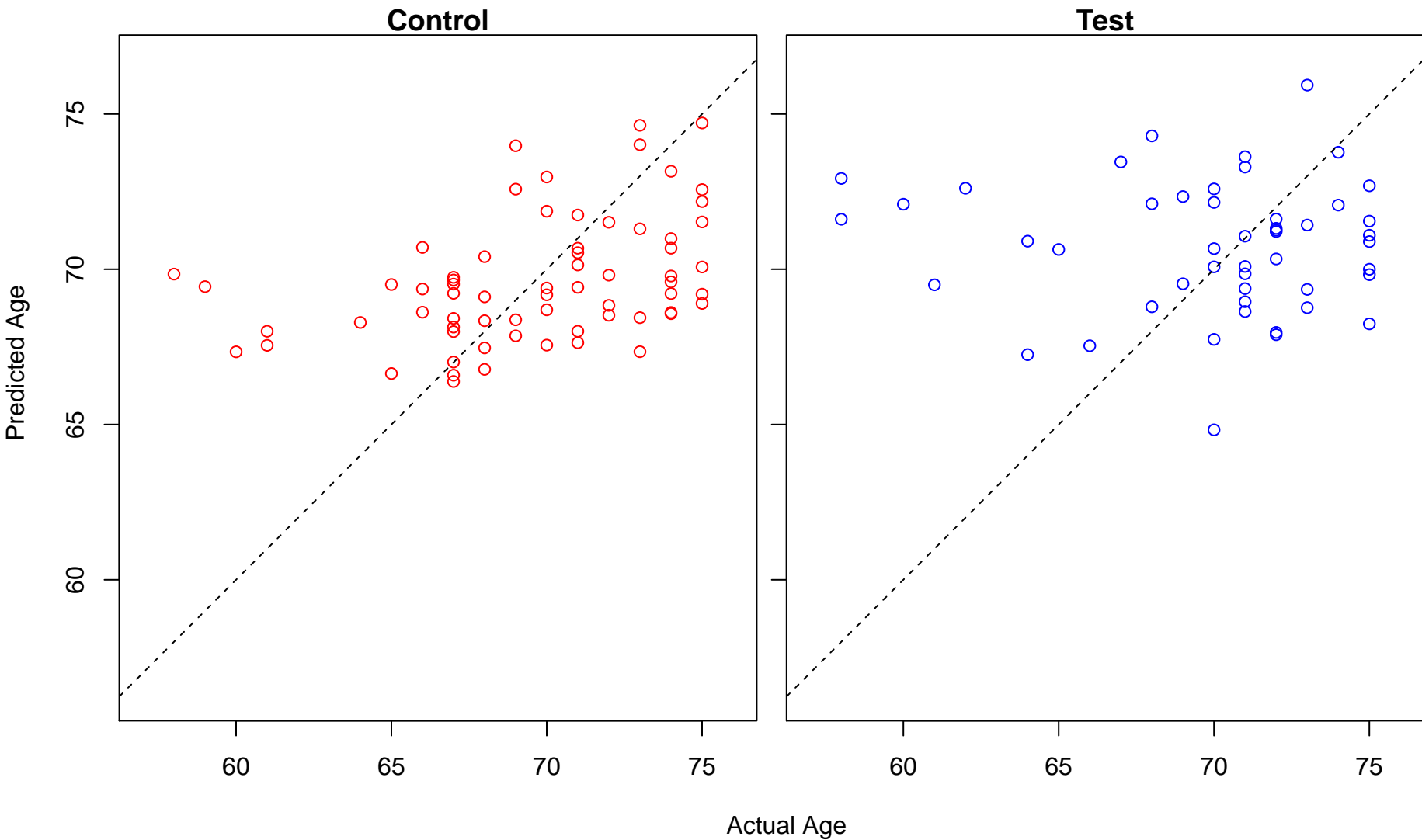
angiotensin maturation (Score: 0.491382)



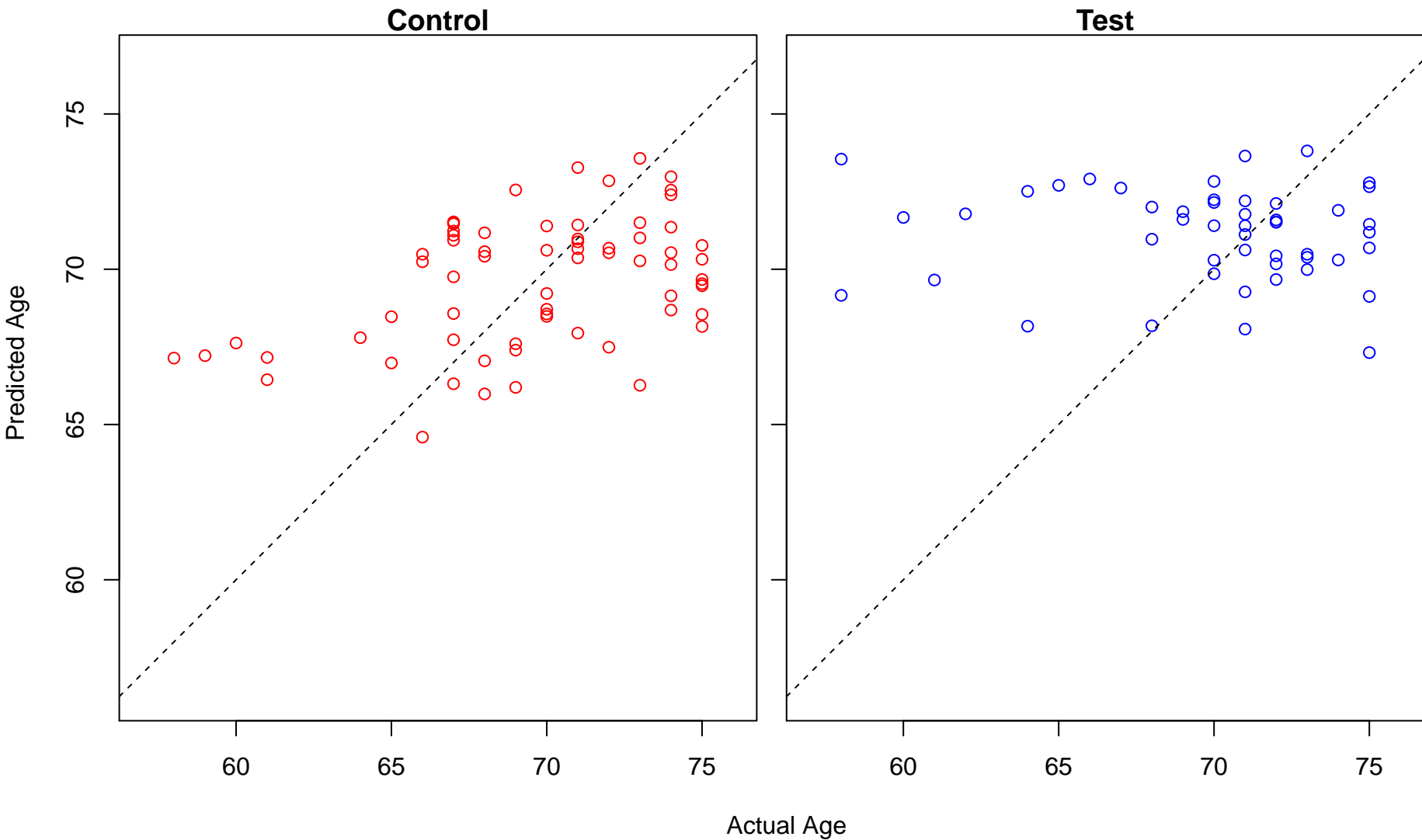
depyrimidination (Score: 0.491208)



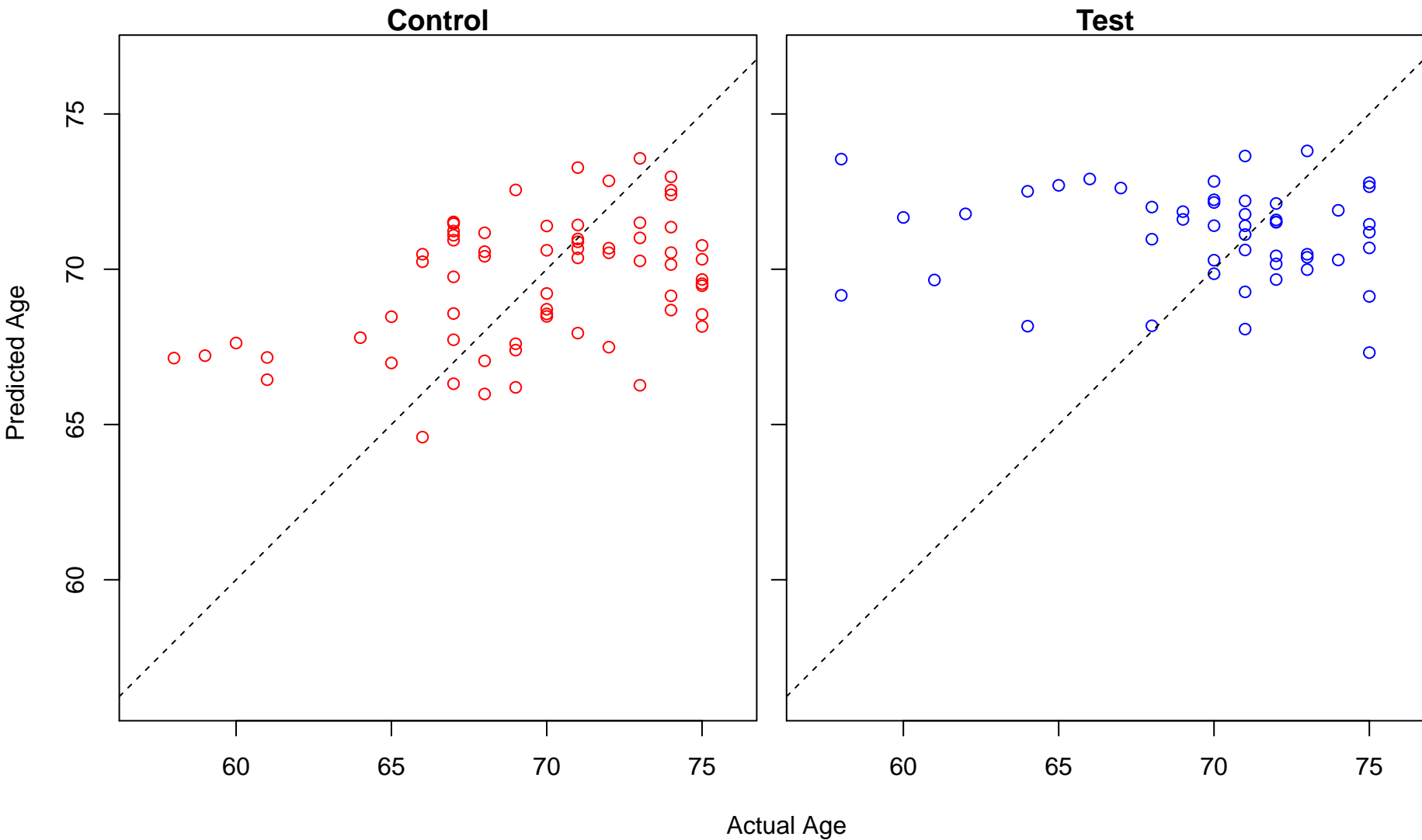
cellular response to cholesterol (Score: 0.490585)



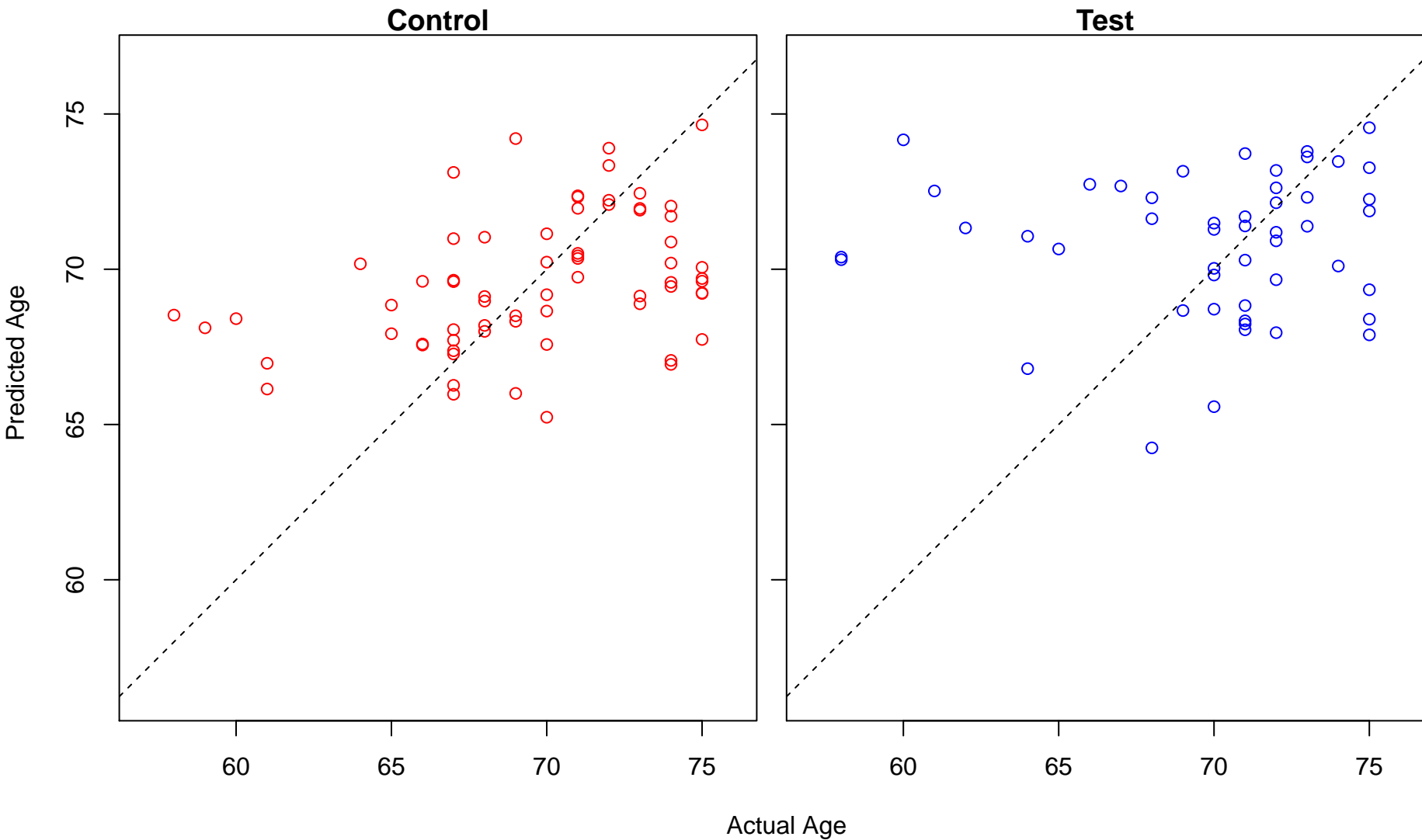
hexose transmembrane transport (Score: 0.489593)



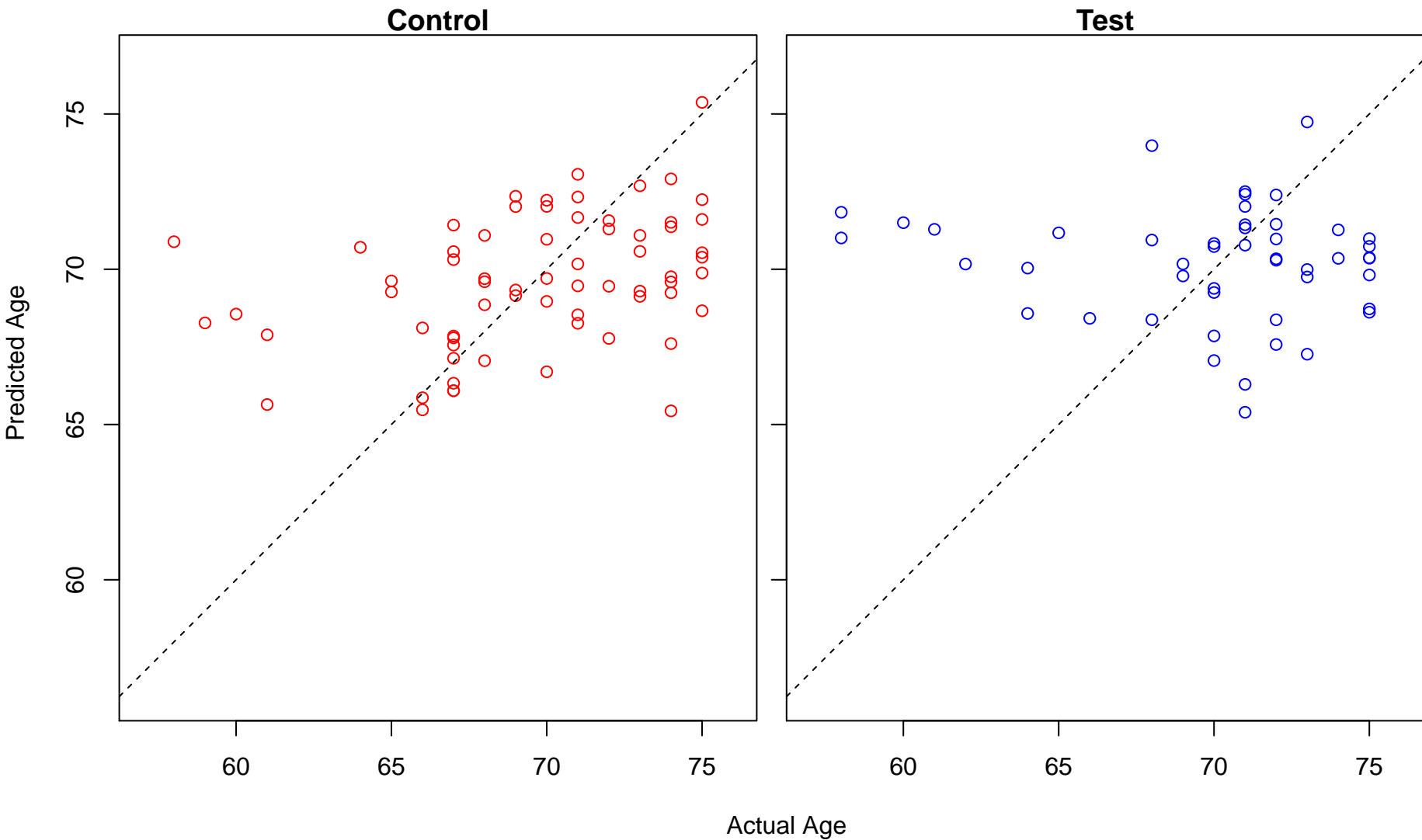
glucose transmembrane transport (Score: 0.489593)



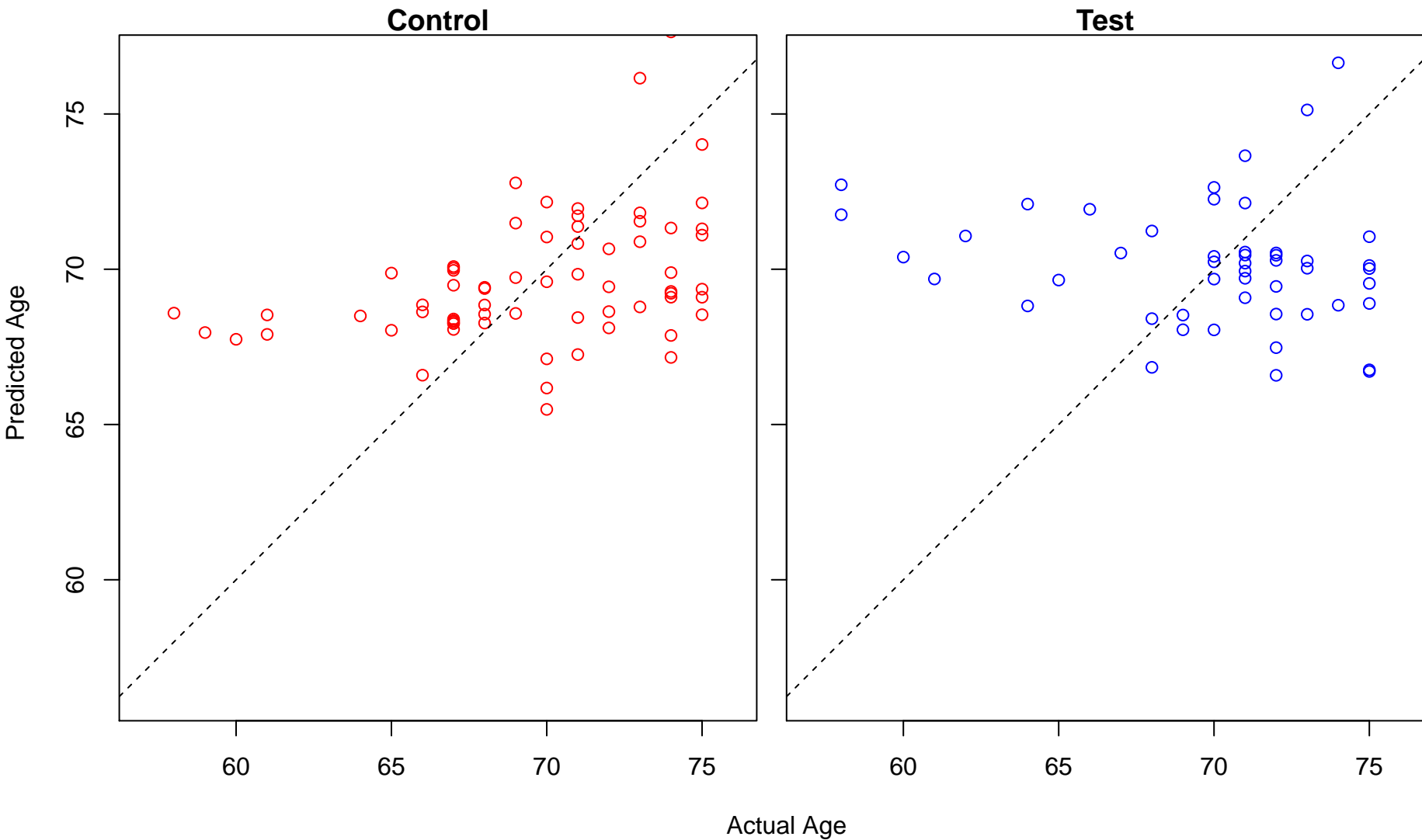
cerebellar cortex formation (Score: 0.489147)



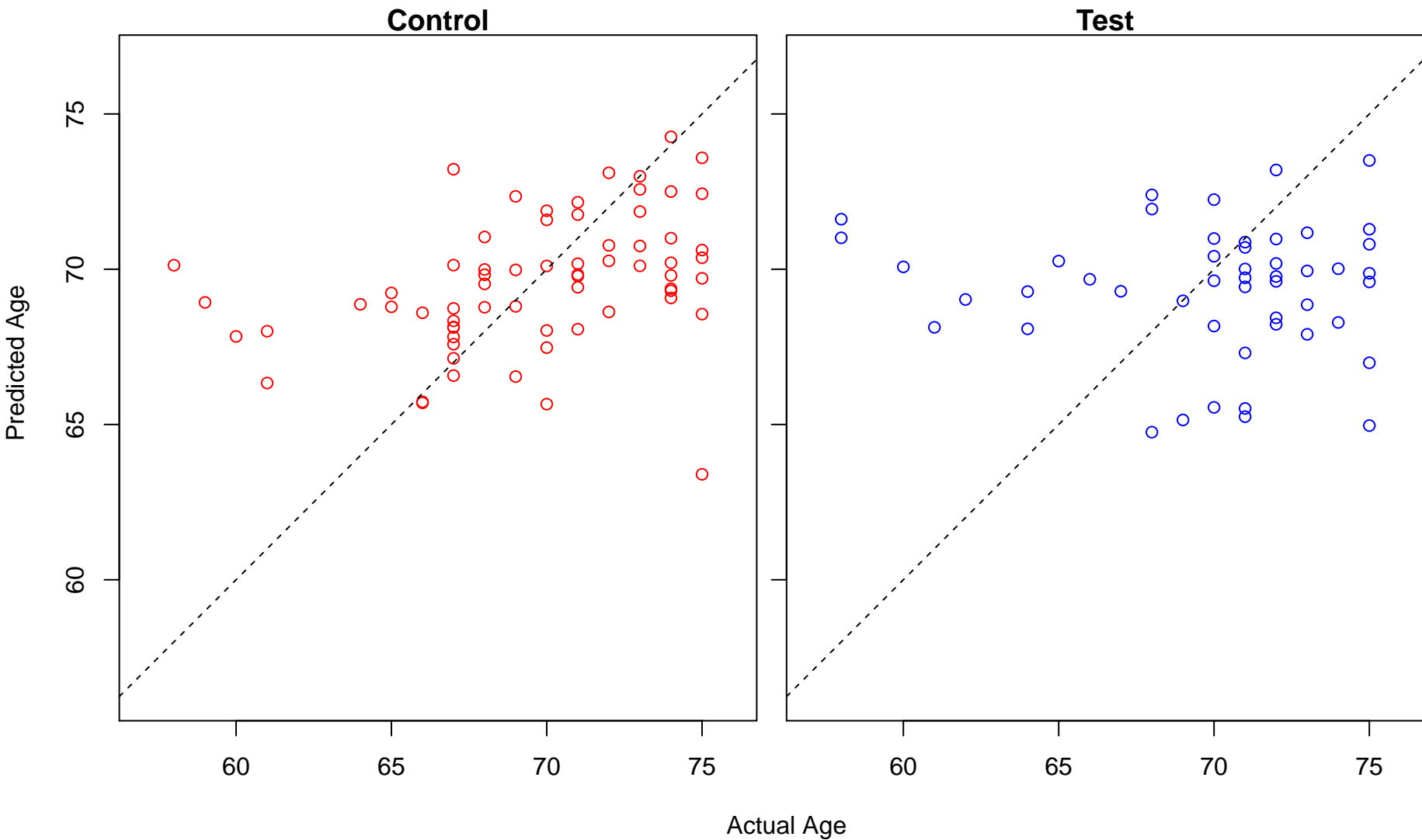
response to nitric oxide (Score: 0.489106)



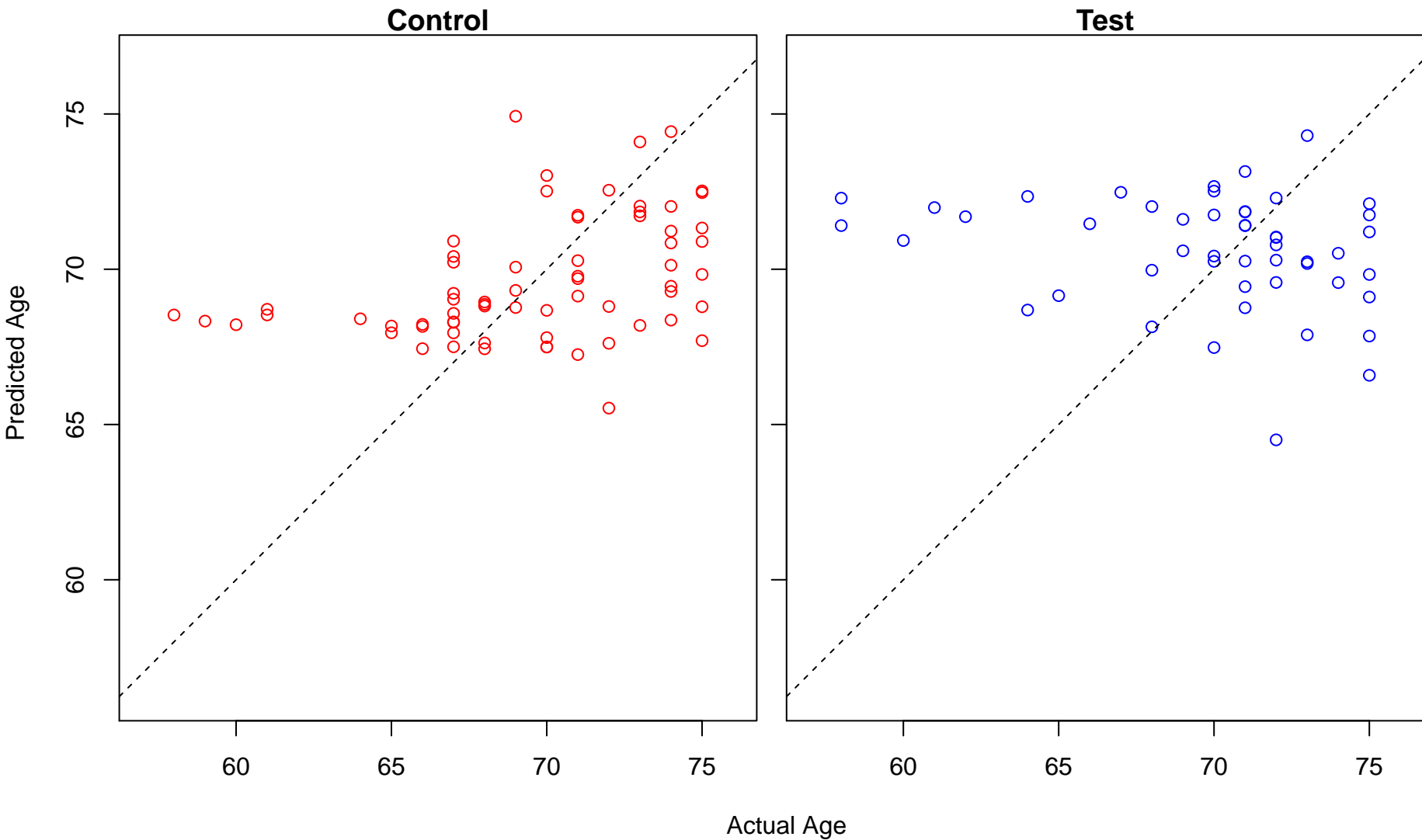
negative regulation of DNA repair (Score: 0.488402)



sodium ion export from cell (Score: 0.487105)

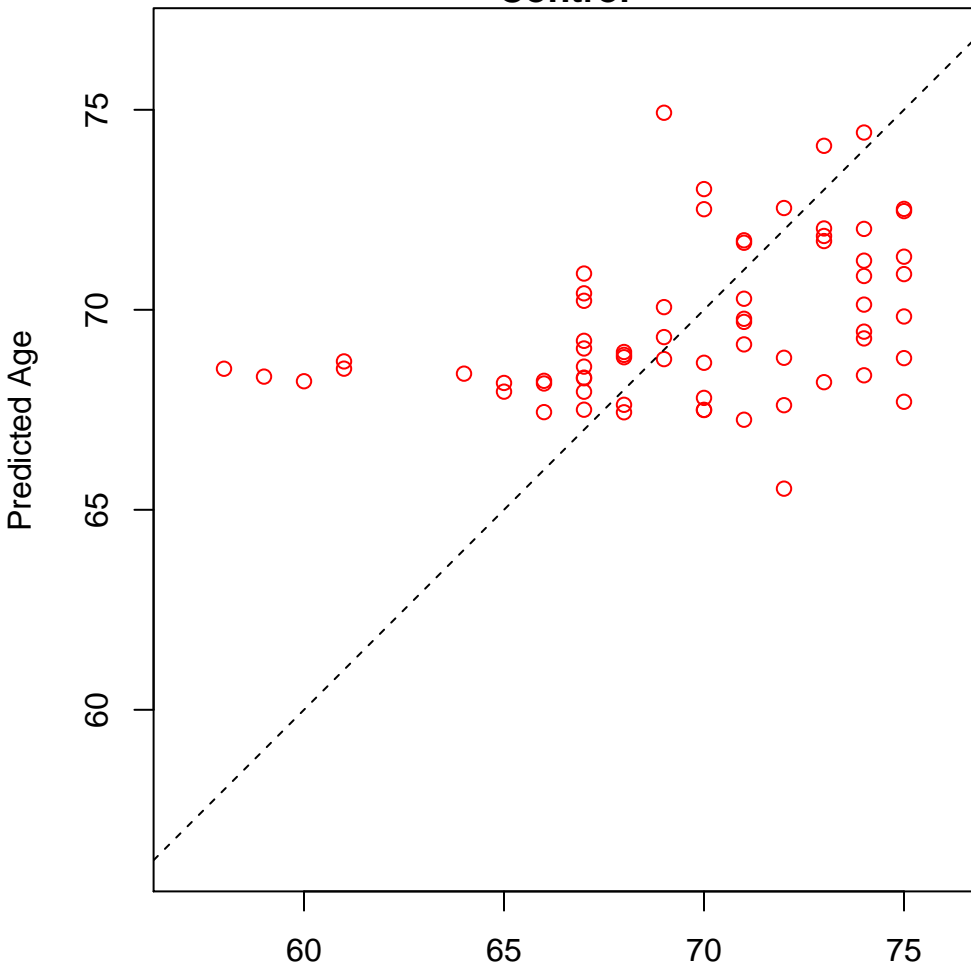


nucleotide-sugar transport (Score: 0.486824)

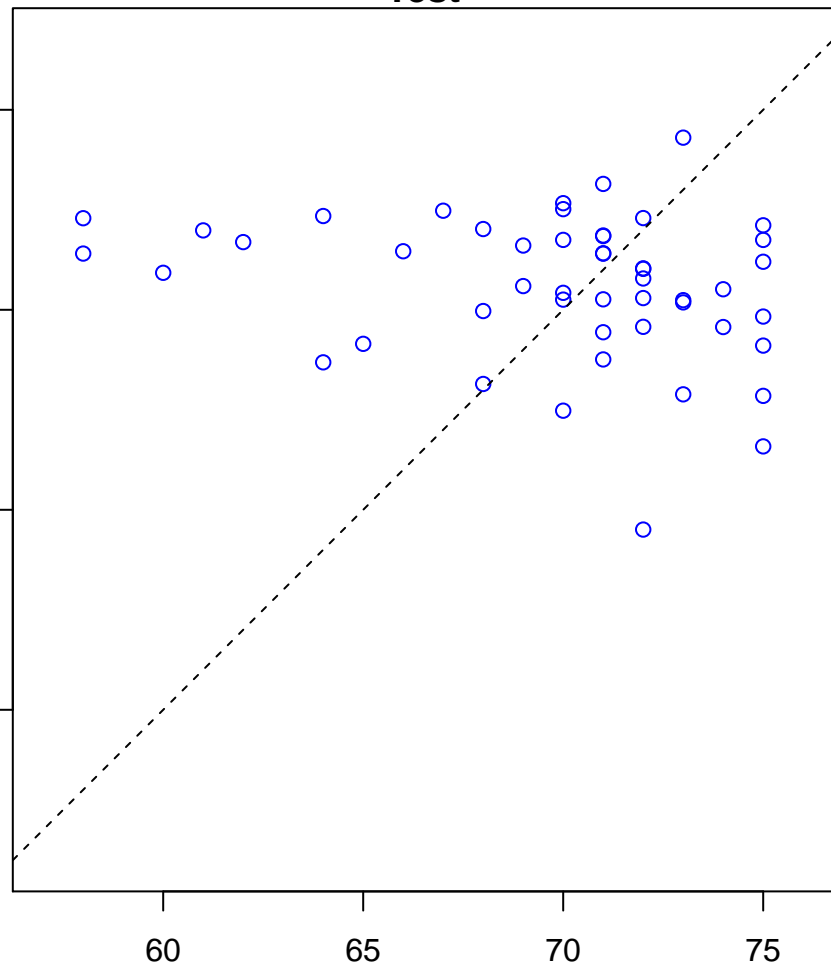


pyrimidine nucleotide–sugar transport (Score: 0.486824)

Control

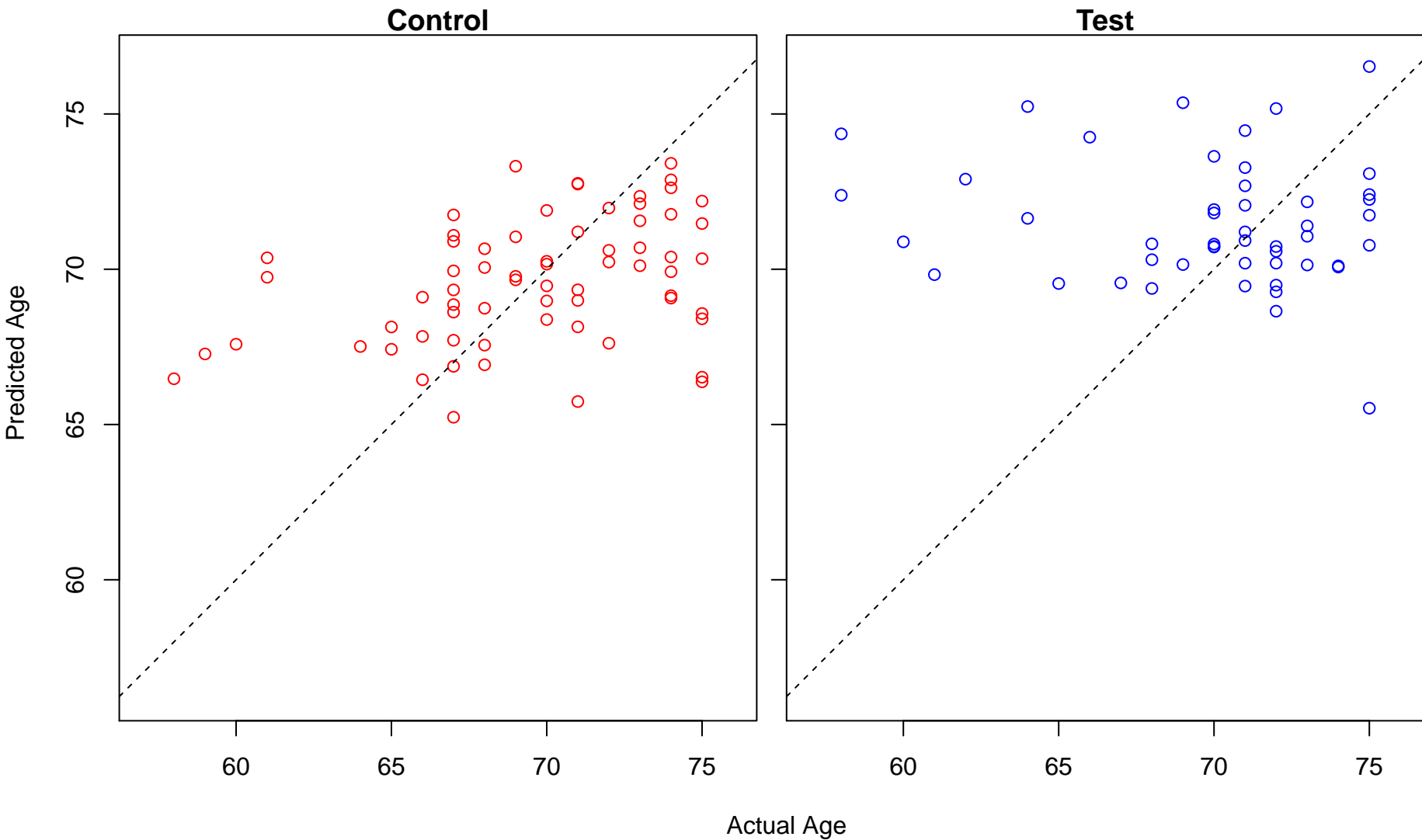


Test



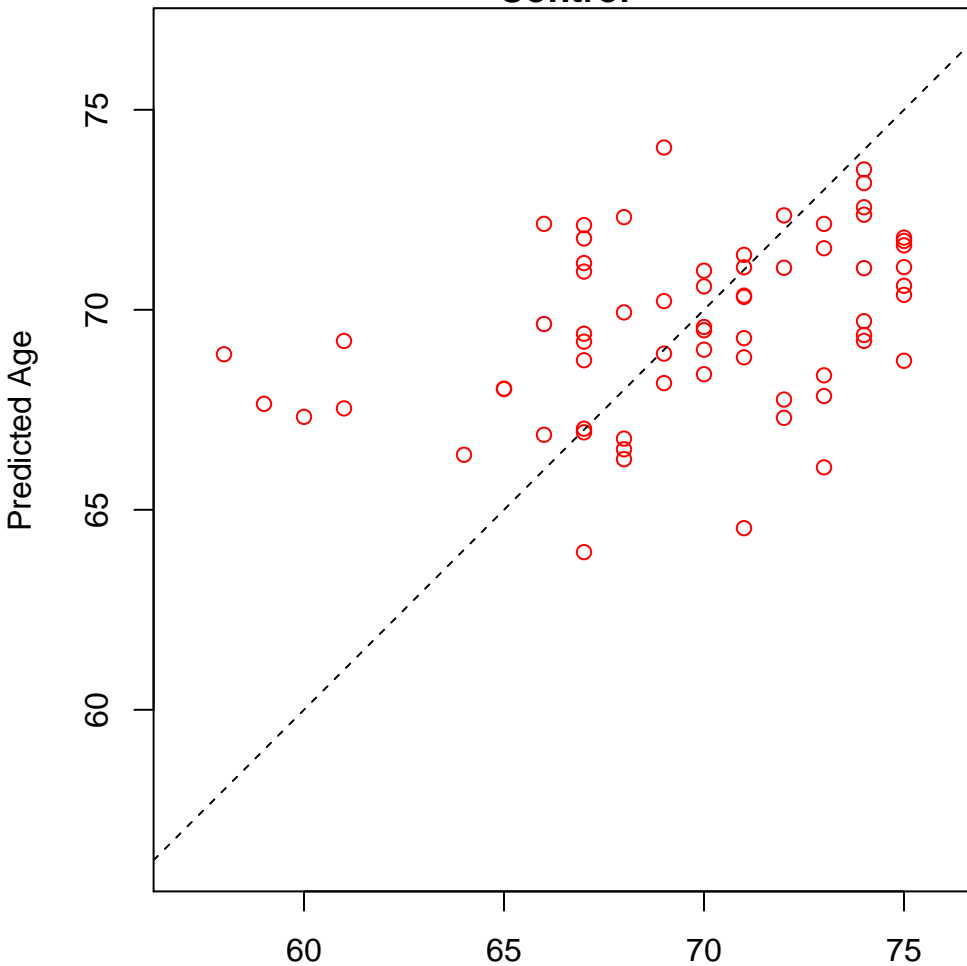
Actual Age

peptidyl-proline hydroxylation (Score: 0.485460)

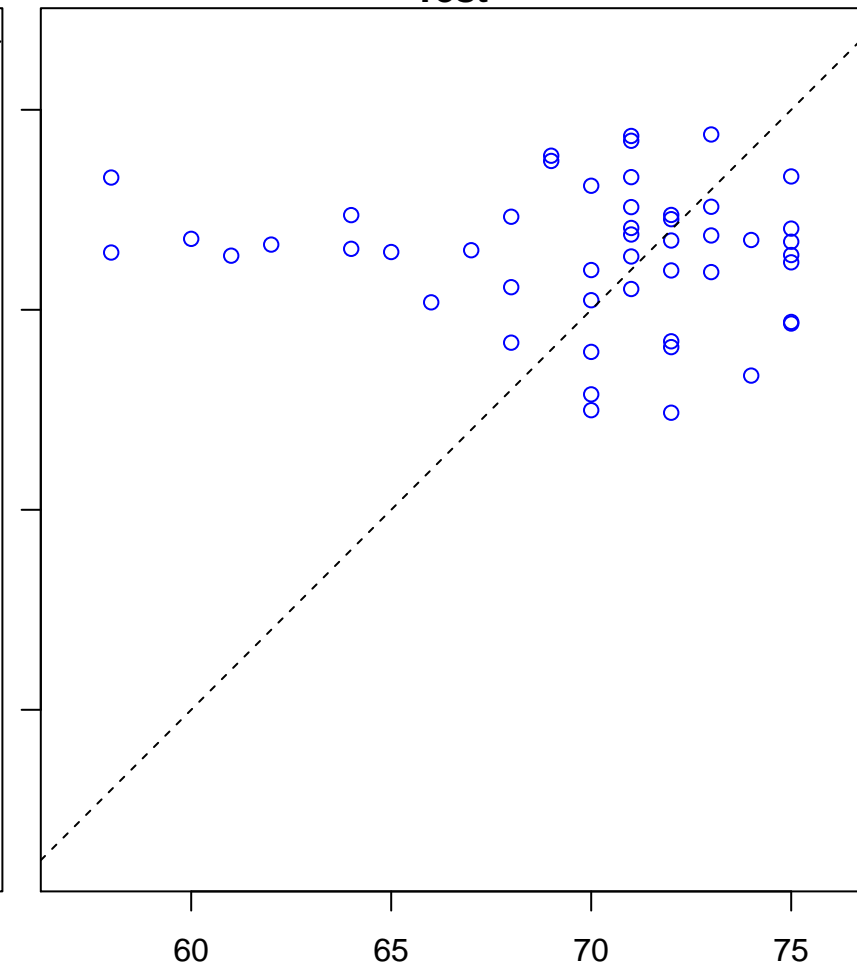


regulation of angiotensin levels in blood (Score: 0.485272)

Control

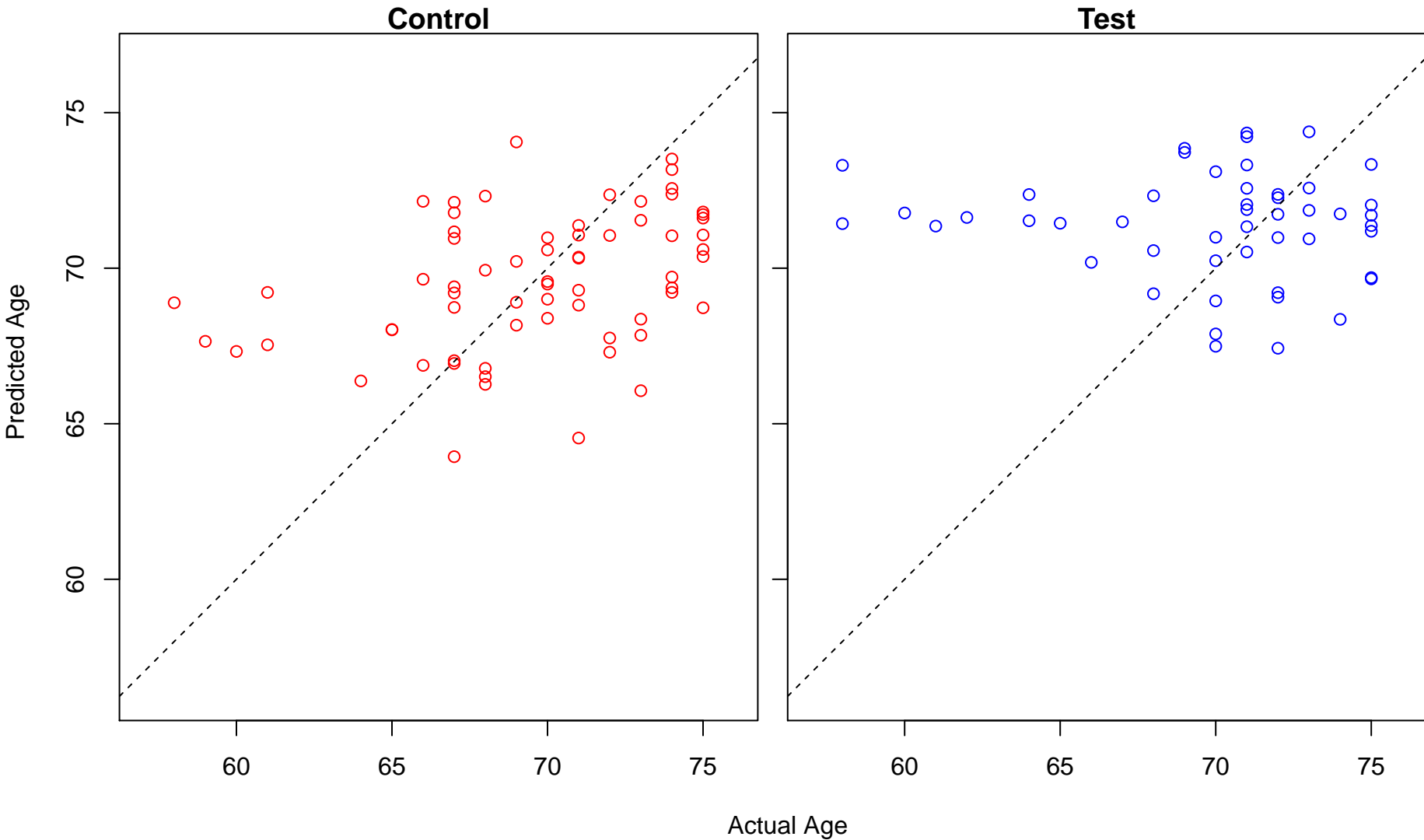


Test



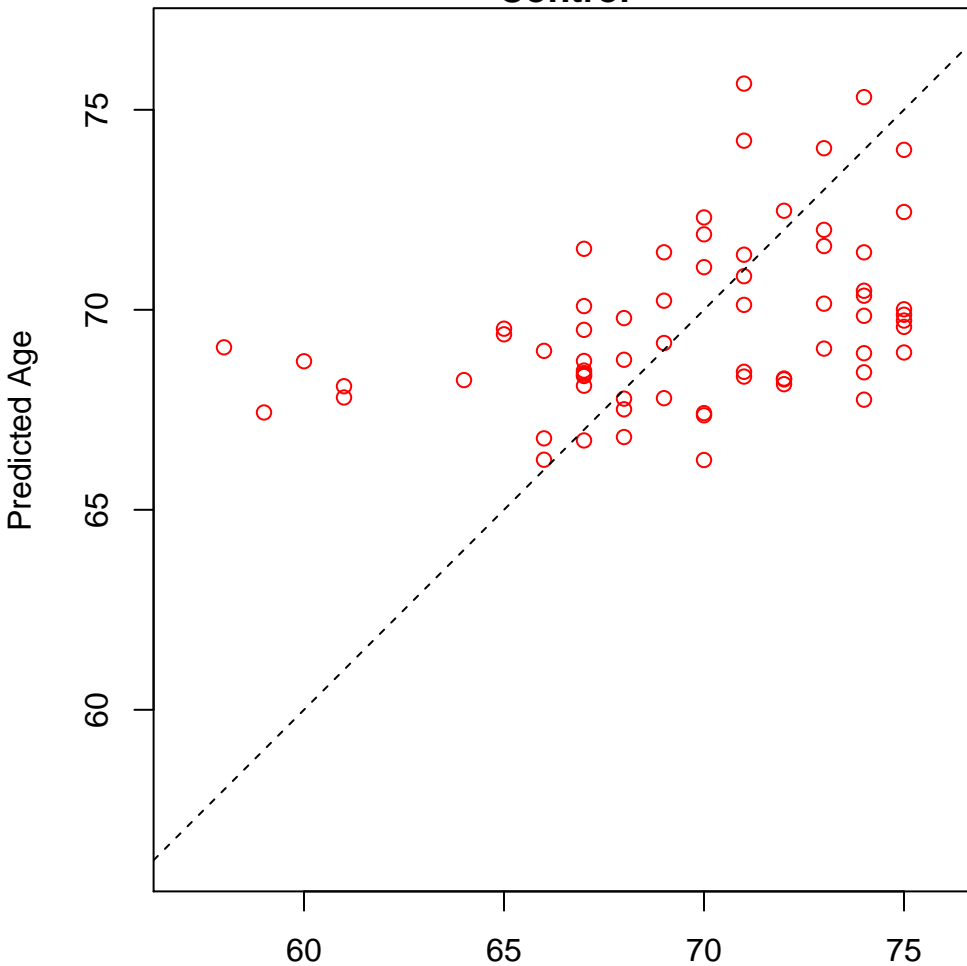
Actual Age

regulation of angiotensin metabolic process (Score: 0.485272)

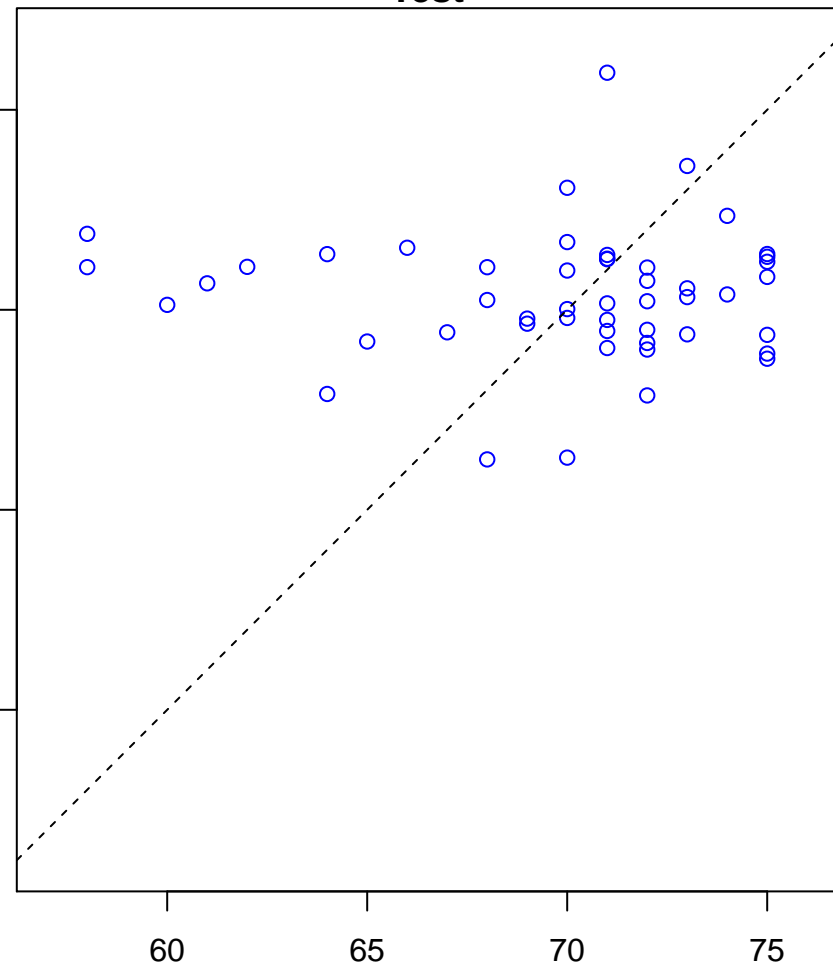


regulation of protein polyubiquitination (Score: 0.484811)

Control

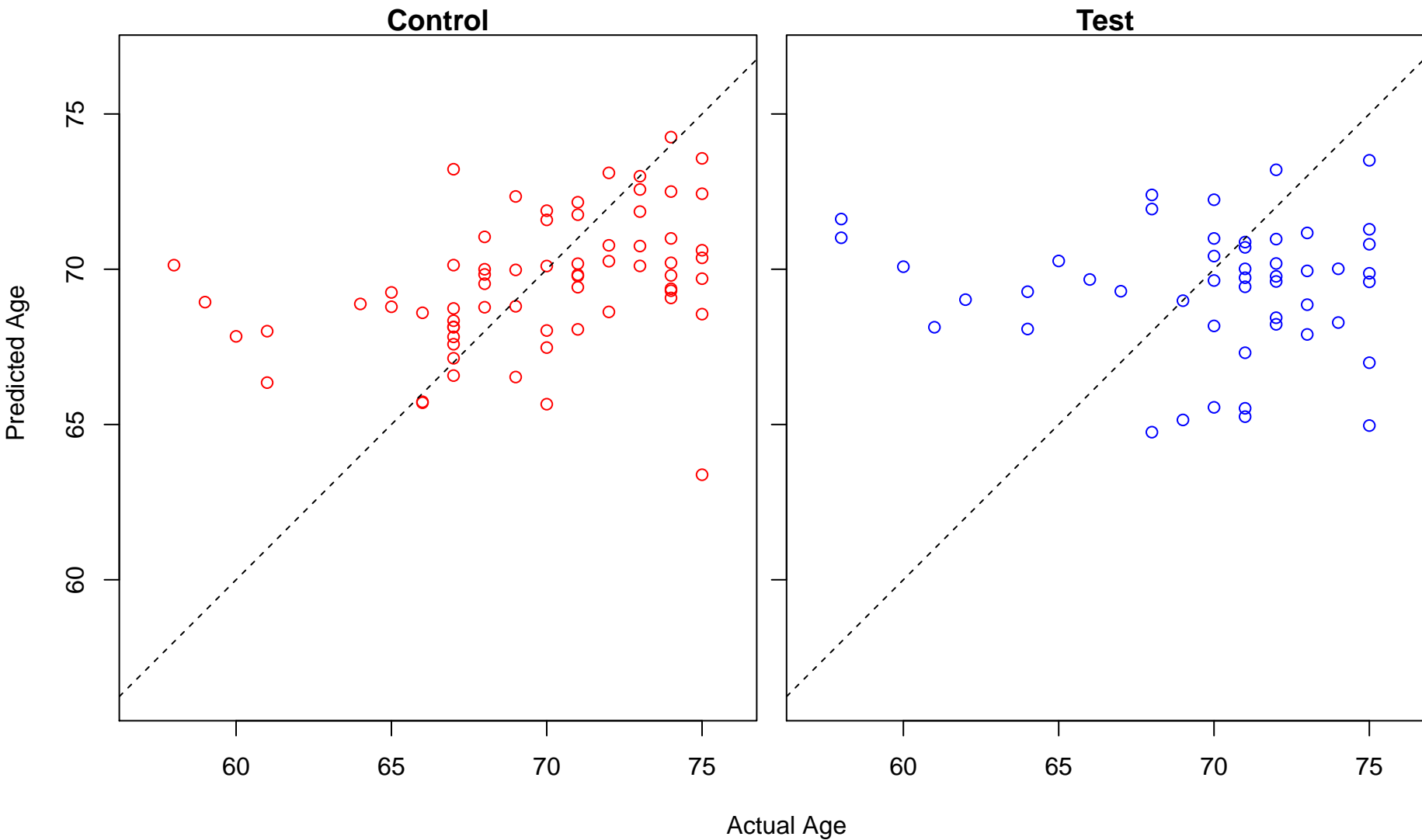


Test

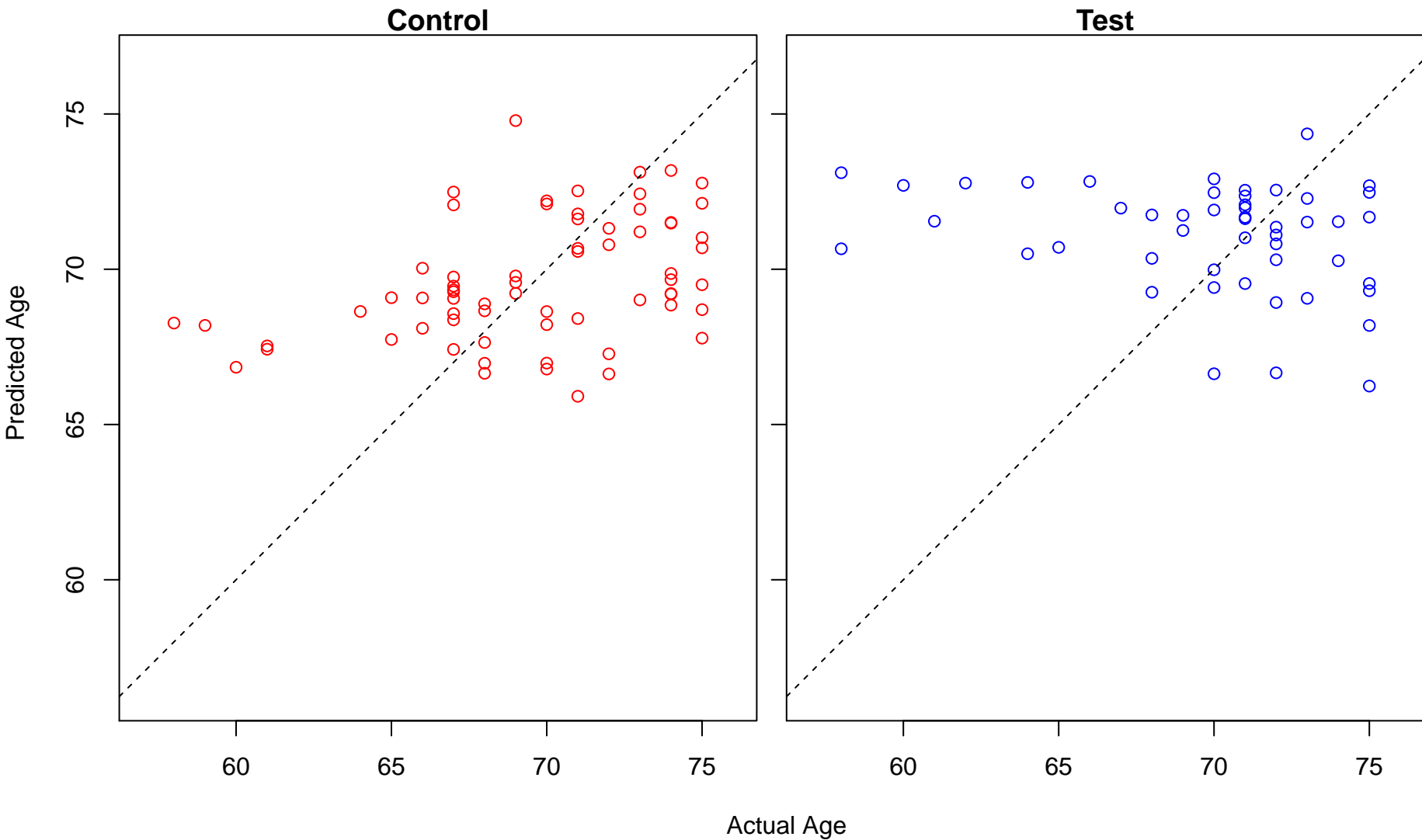


Actual Age

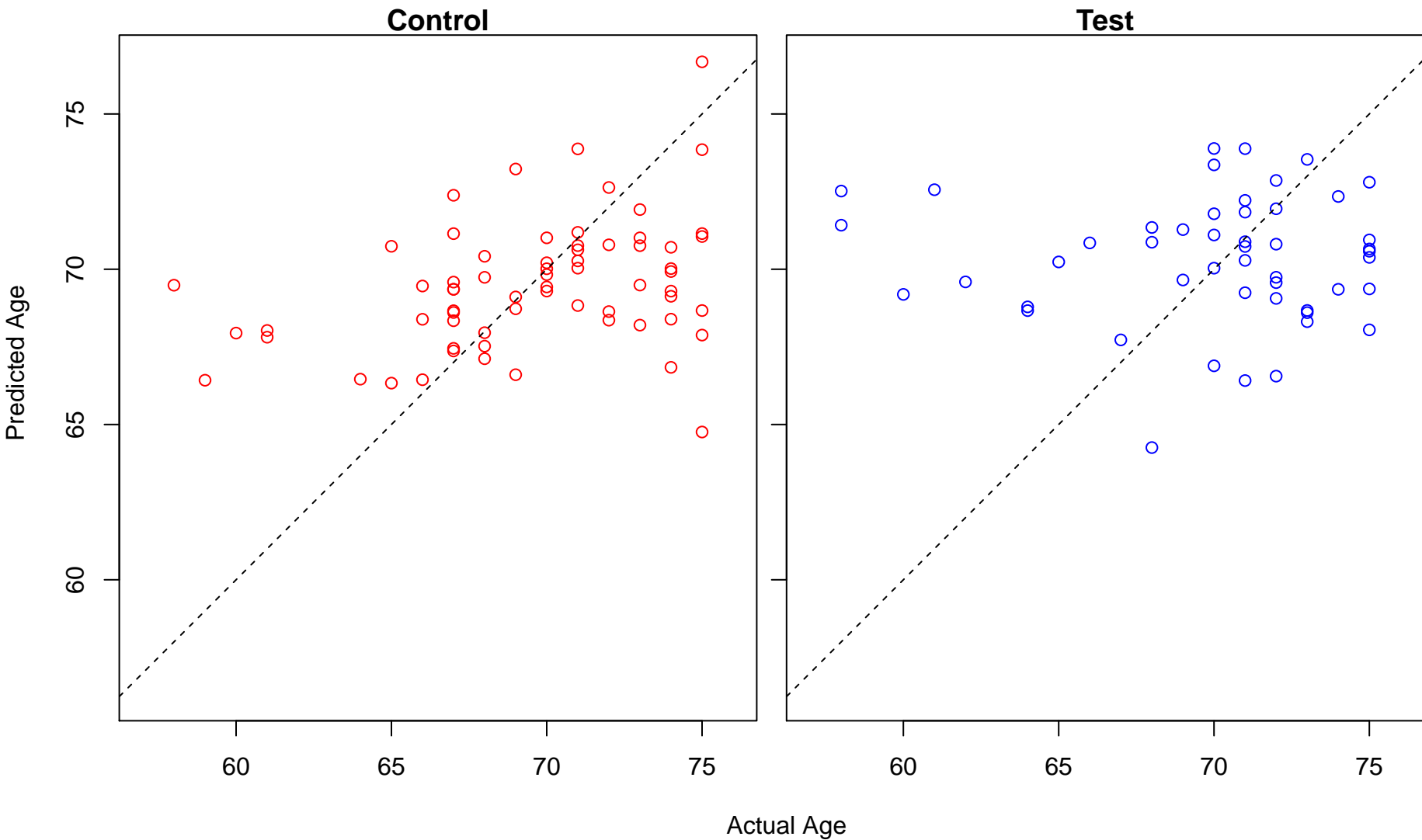
ATP hydrolysis coupled transmembrane transport (Score: 0.484618)



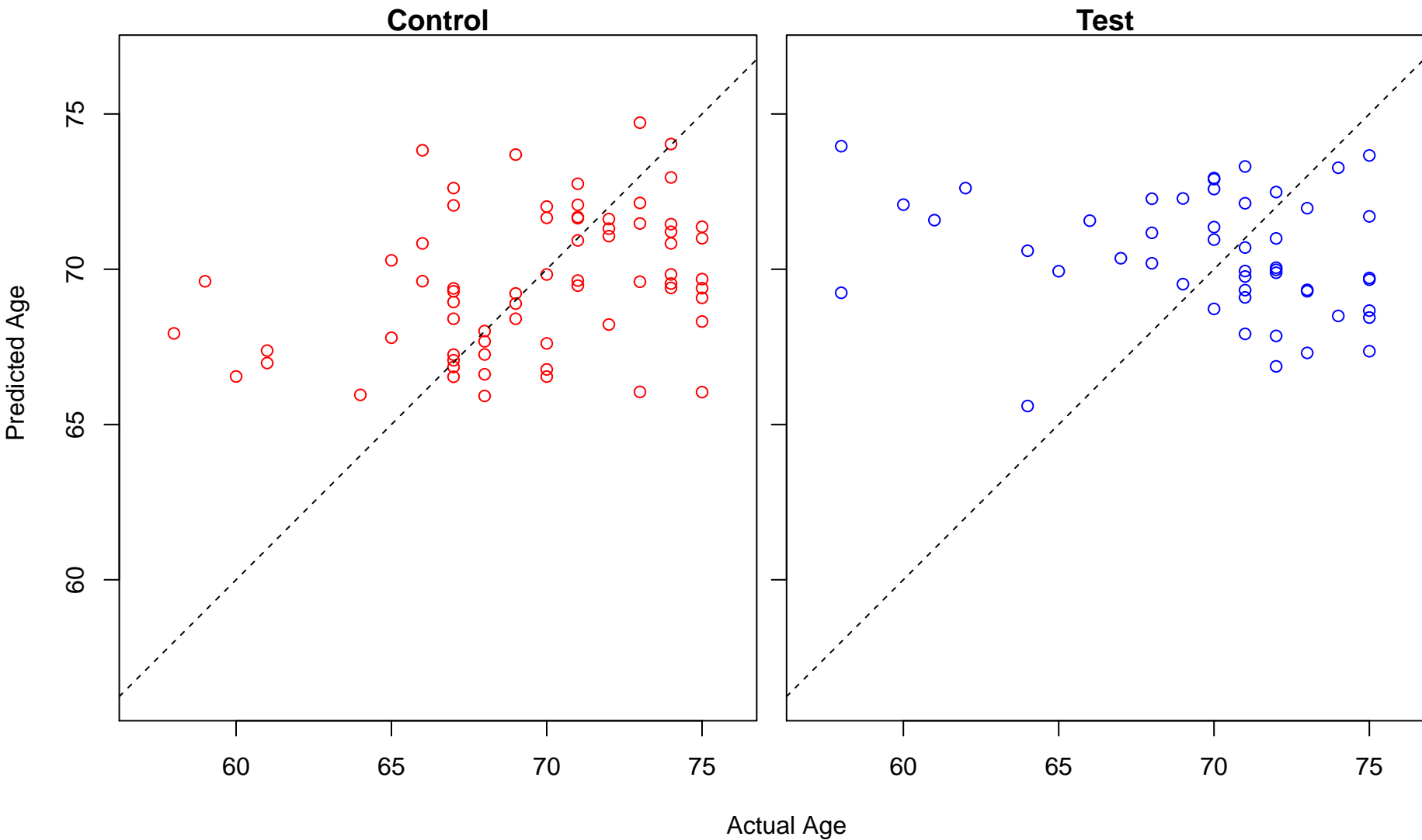
positive regulation of calcium-mediated signaling (Score: 0.484567)



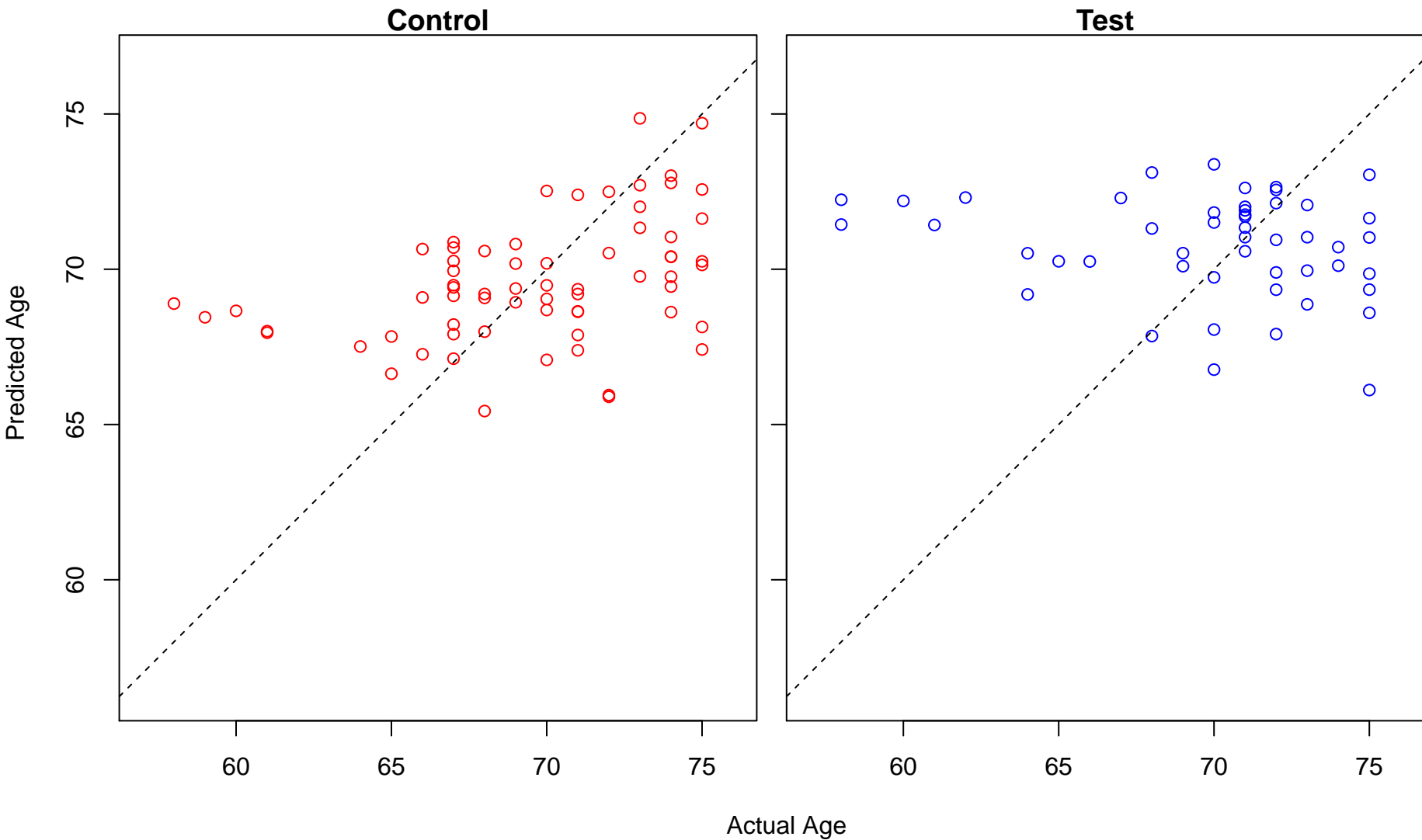
regulation of dopamine secretion (Score: 0.484364)



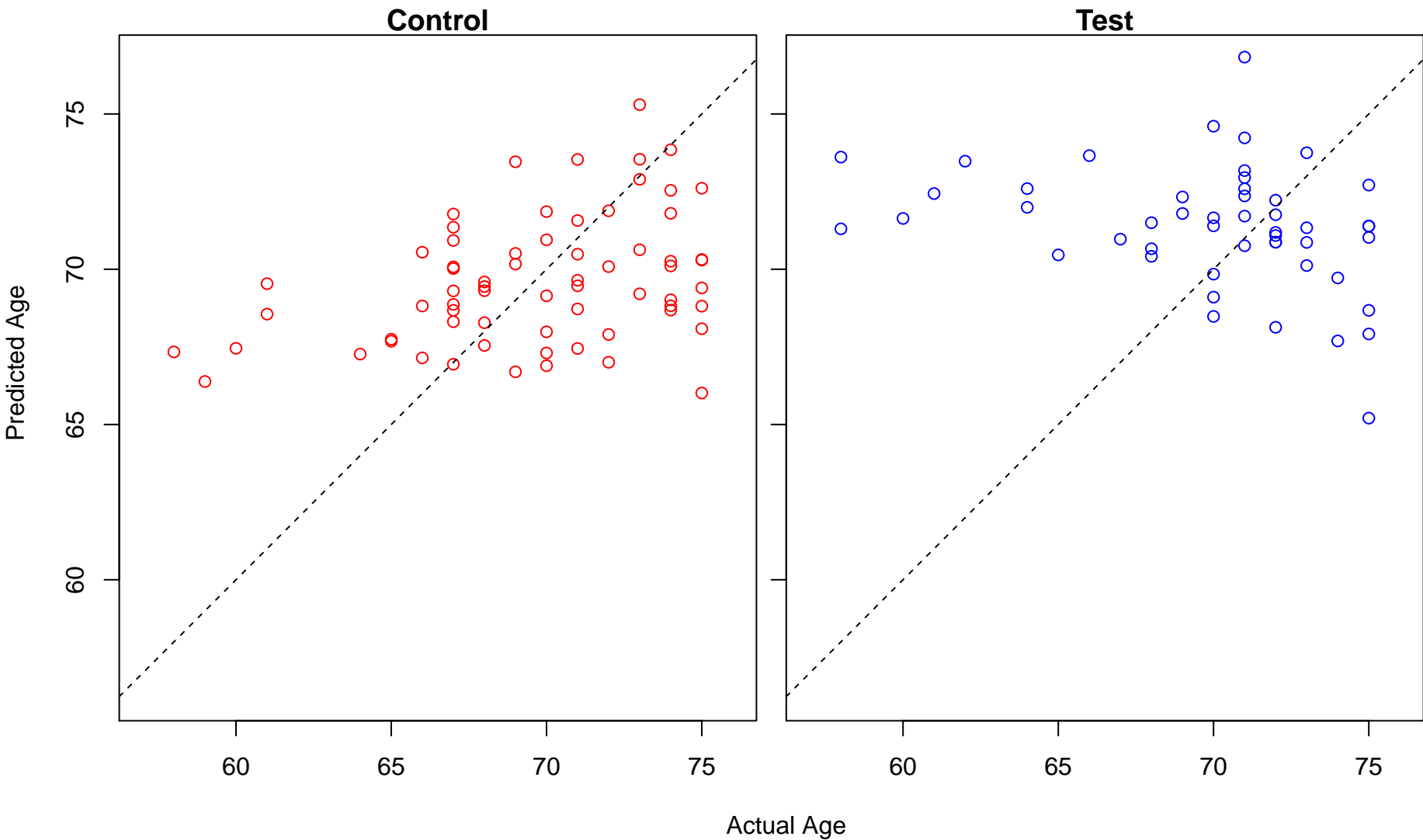
response to nicotine (Score: 0.484203)



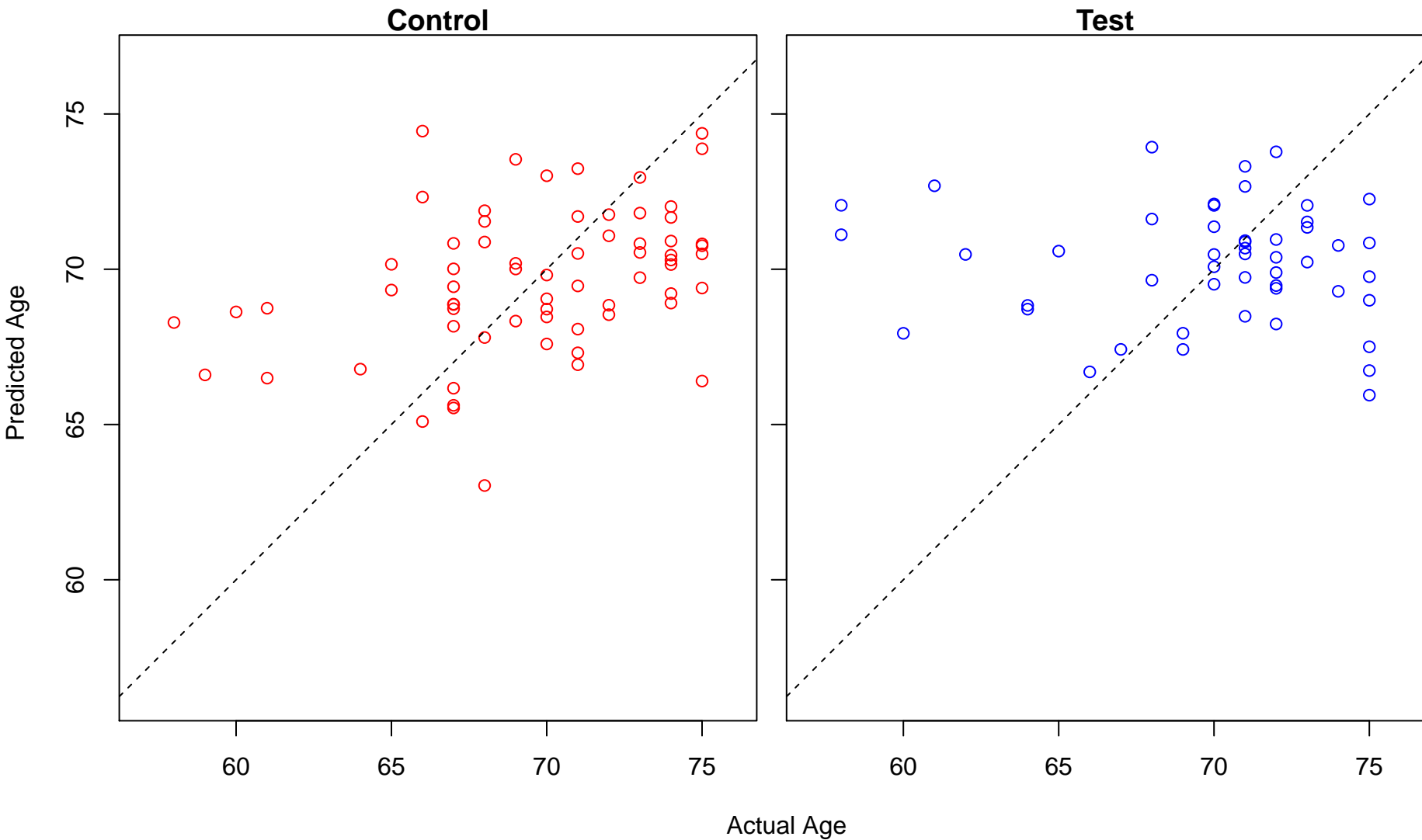
glycoside catabolic process (Score: 0.483637)



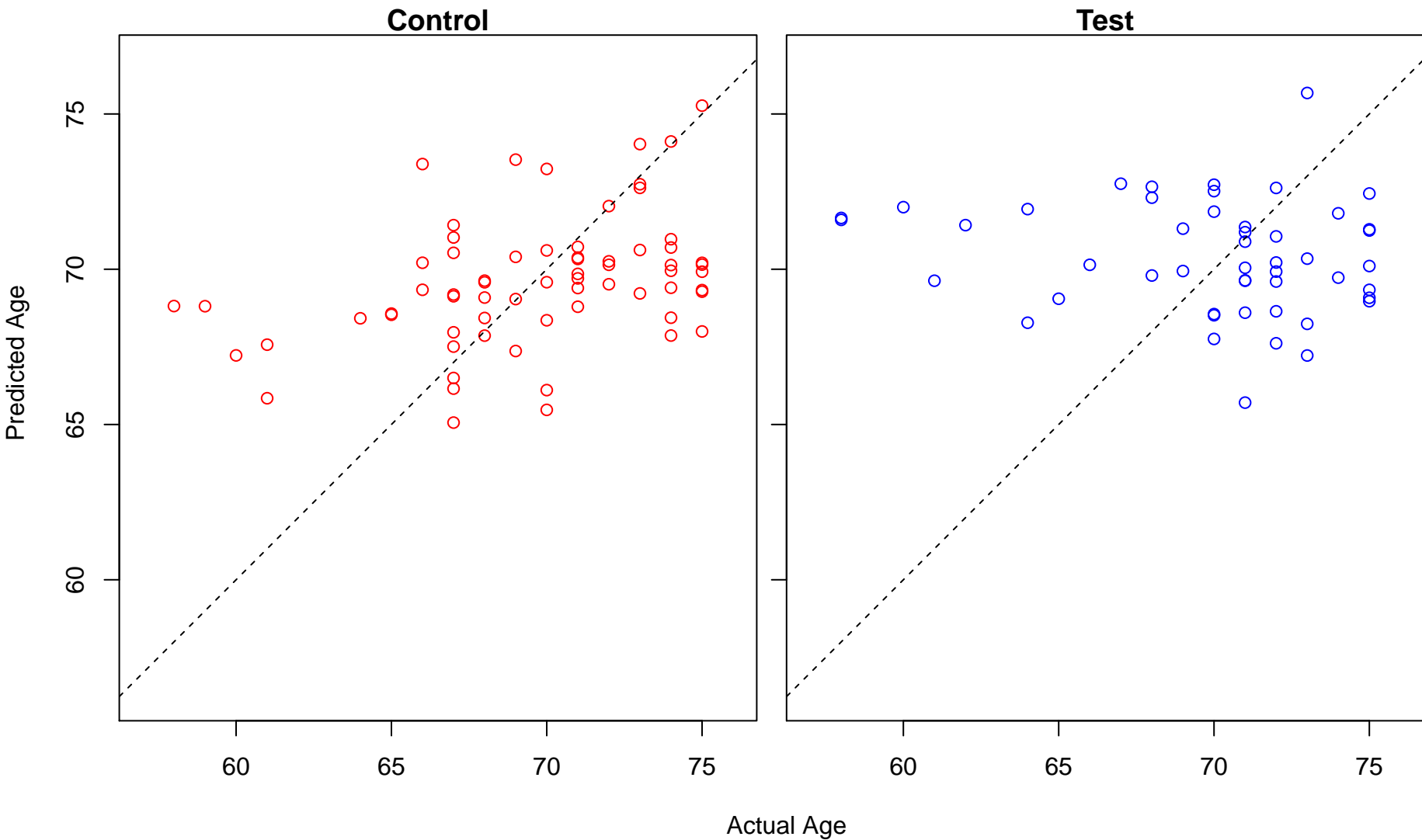
phospholipase C-activating G-protein coupled receptor signaling pathway (Score: 0.483287)



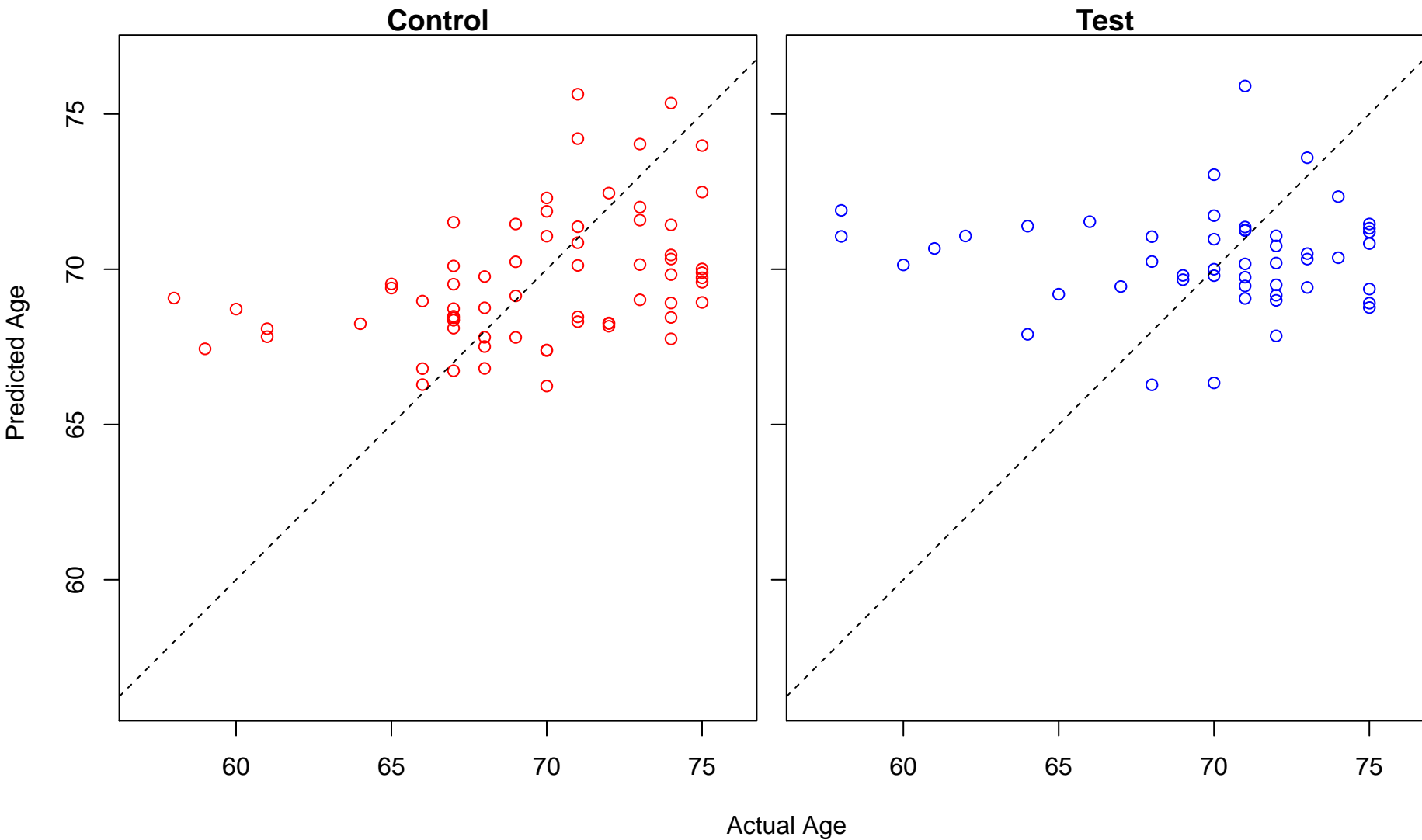
response to vitamin D (Score: 0.483242)



substrate adhesion-dependent cell spreading (Score: 0.482926)

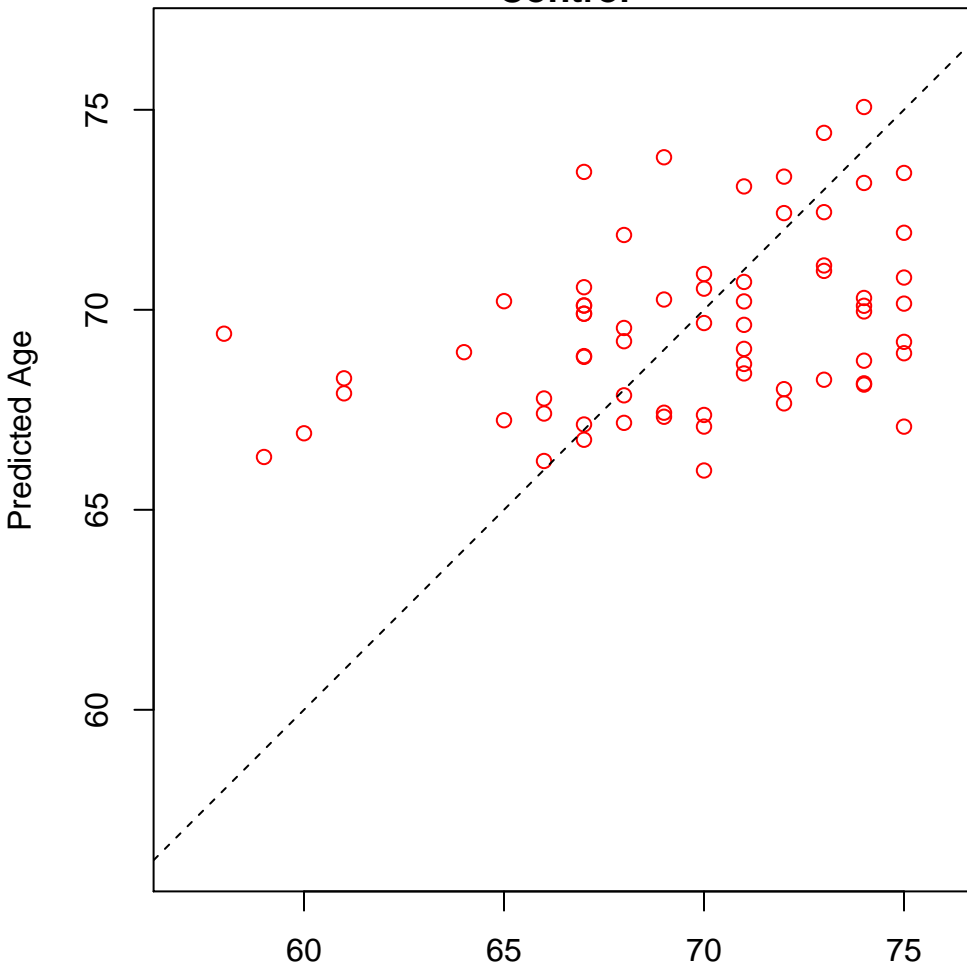


regulation of protein K63-linked ubiquitination (Score: 0.482819)

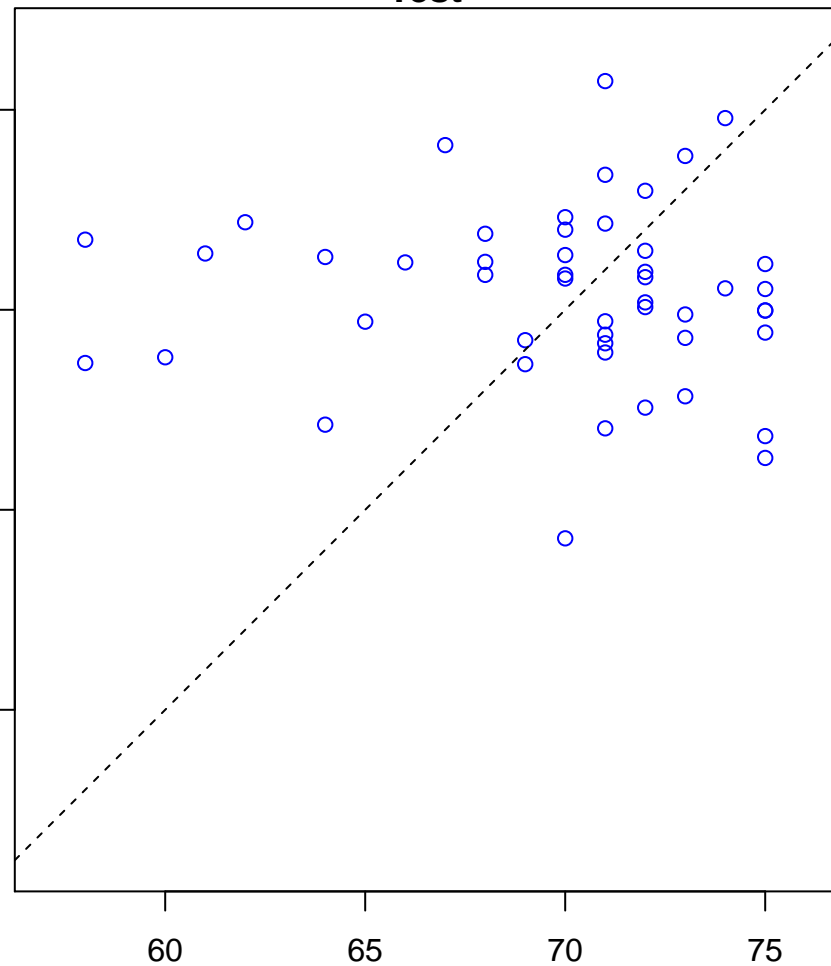


peptidyl-glutamic acid carboxylation (Score: 0.482100)

Control

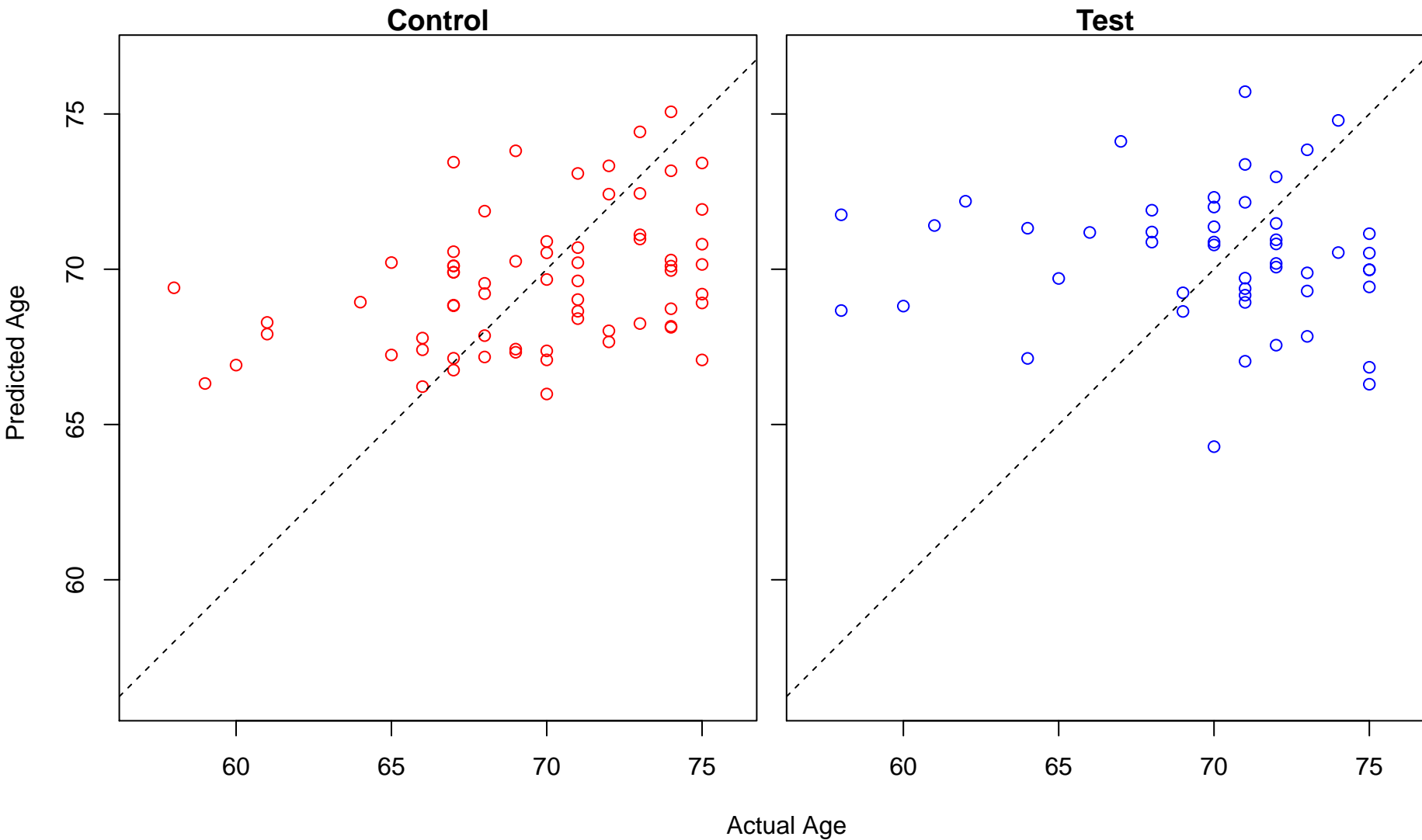


Test

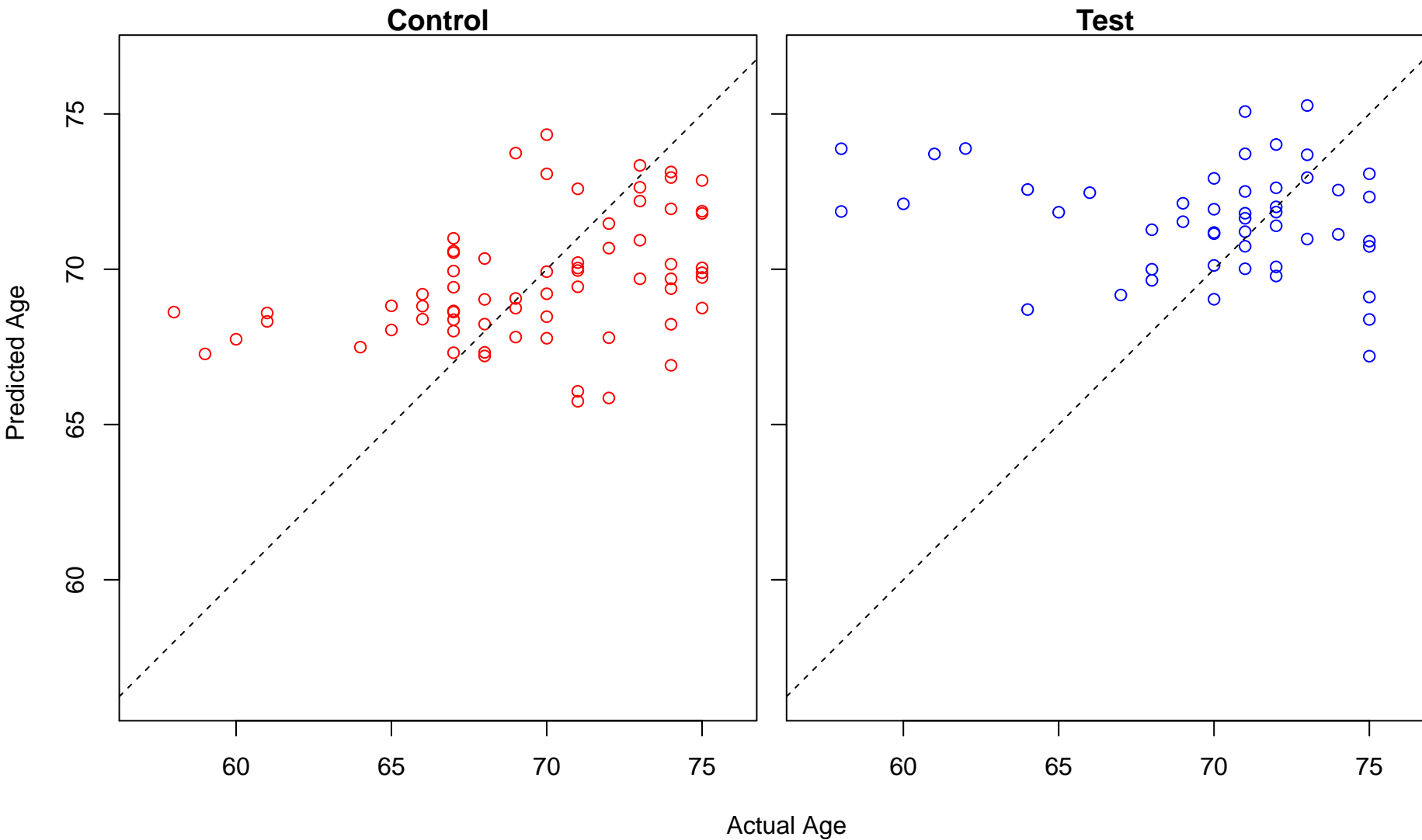


Actual Age

protein carboxylation (Score: 0.482100)

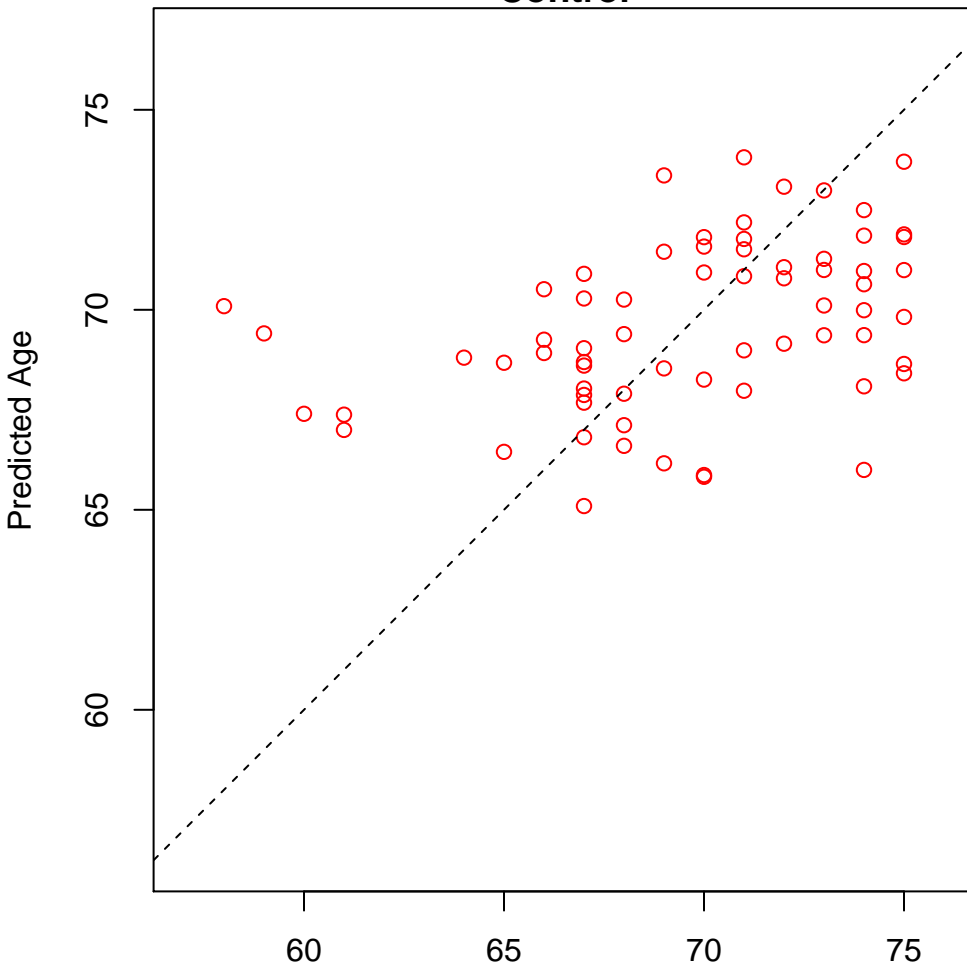


positive regulation of helicase activity (Score: 0.482065)

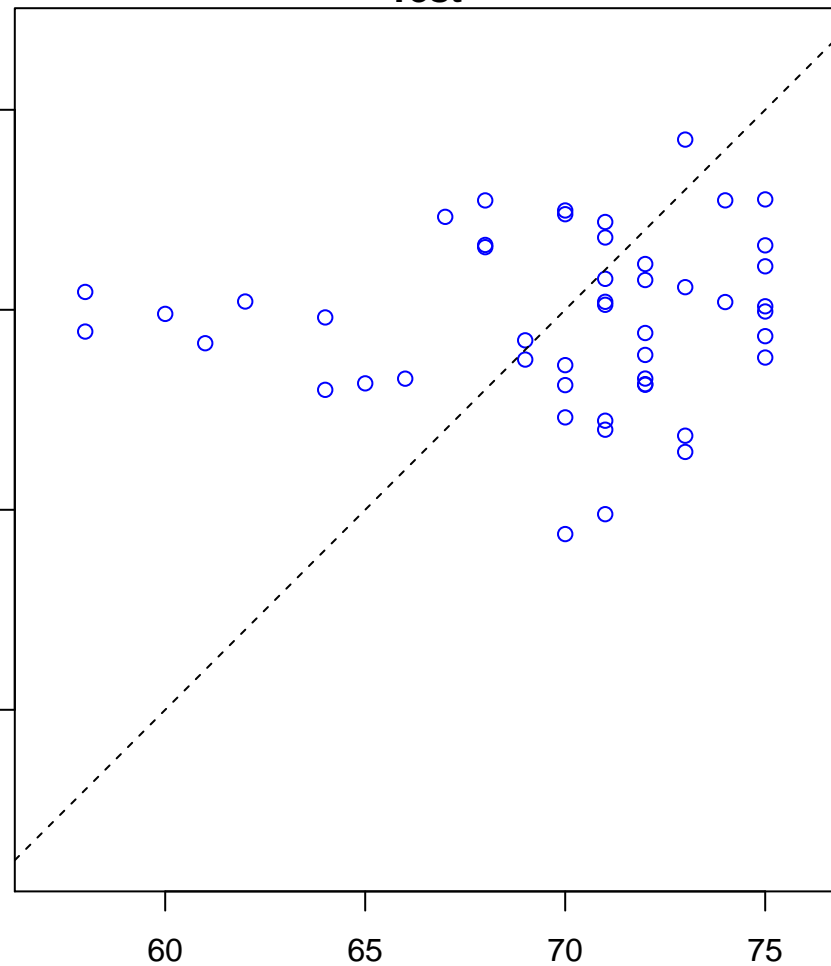


cellular response to gamma radiation (Score: 0.480934)

Control

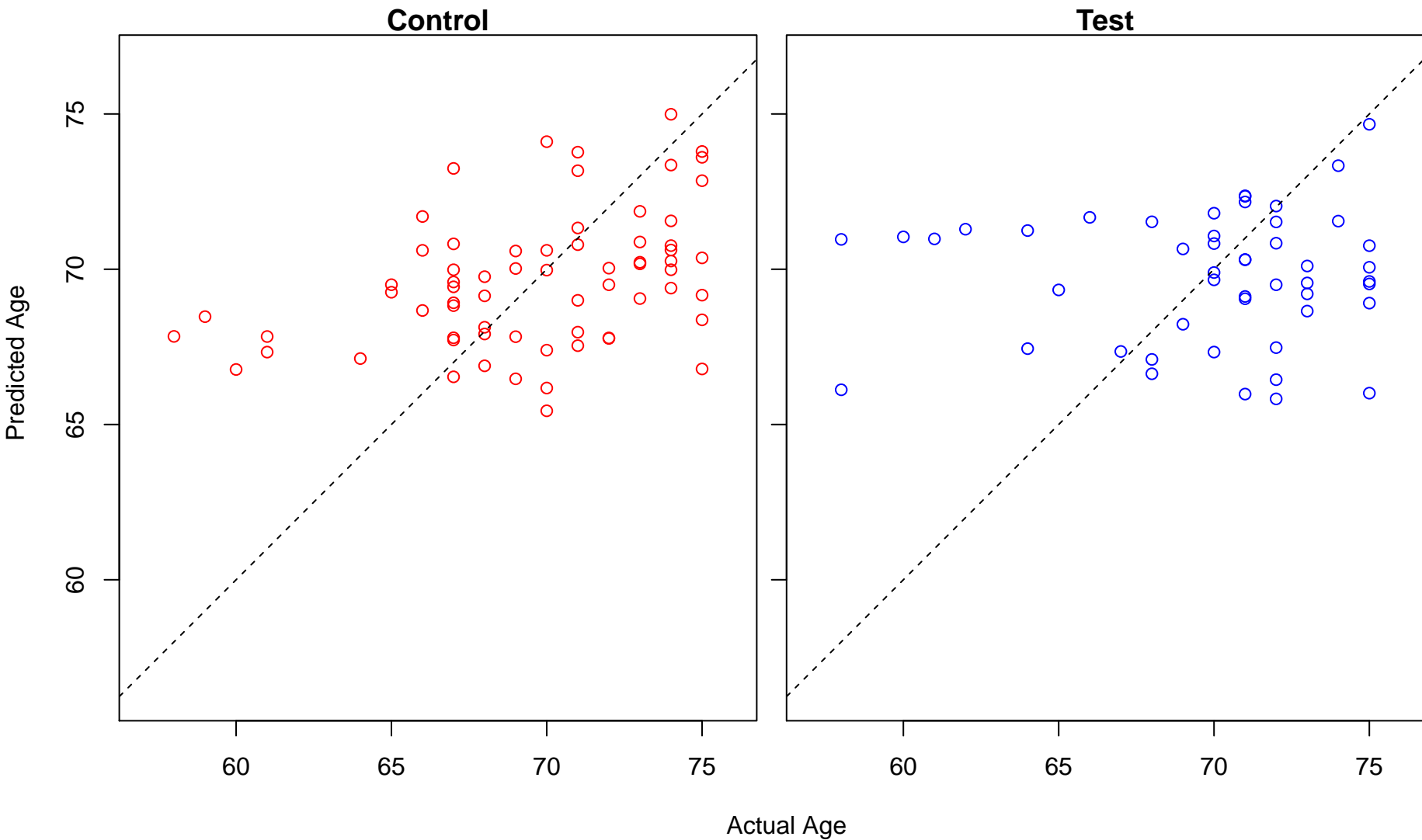


Test

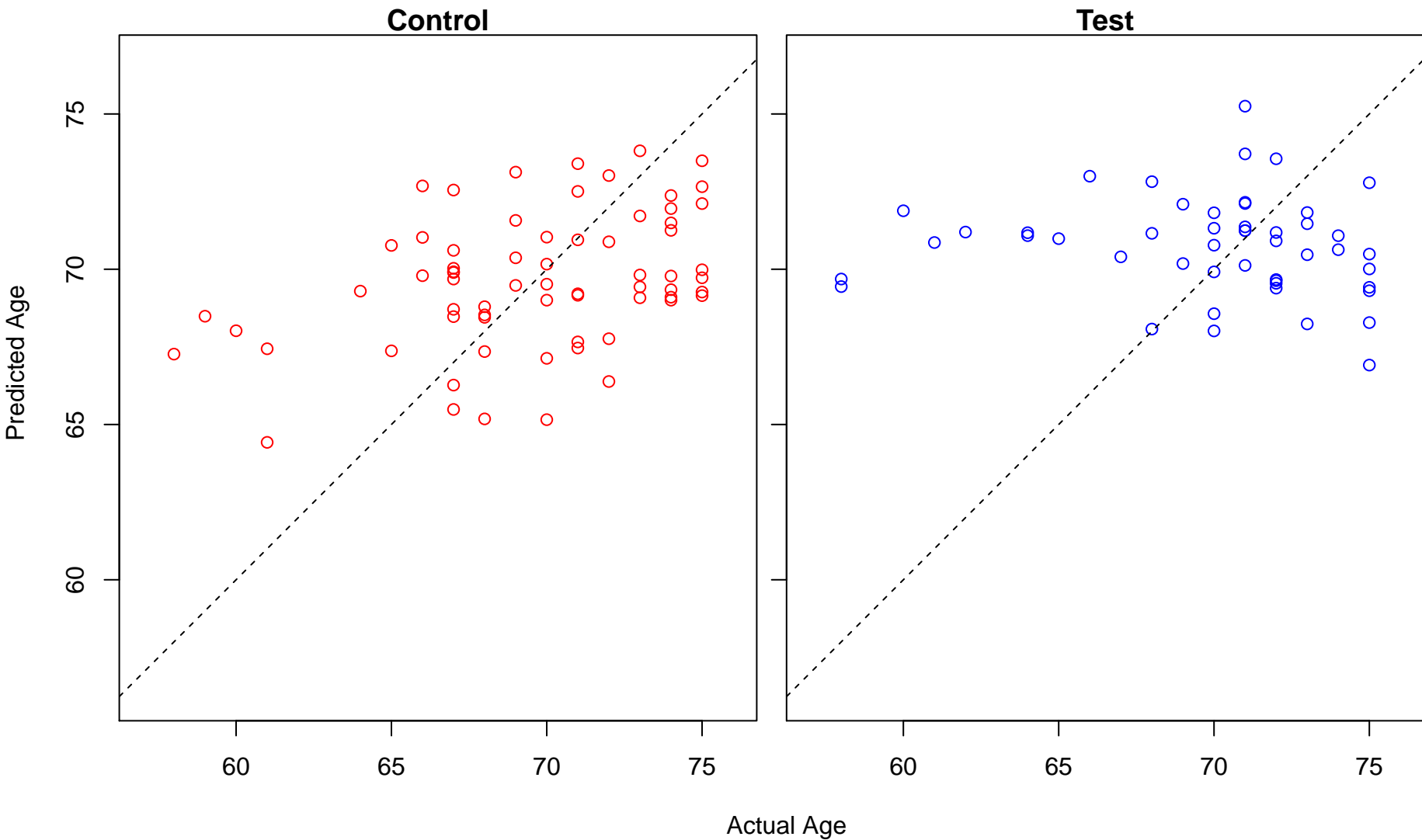


Actual Age

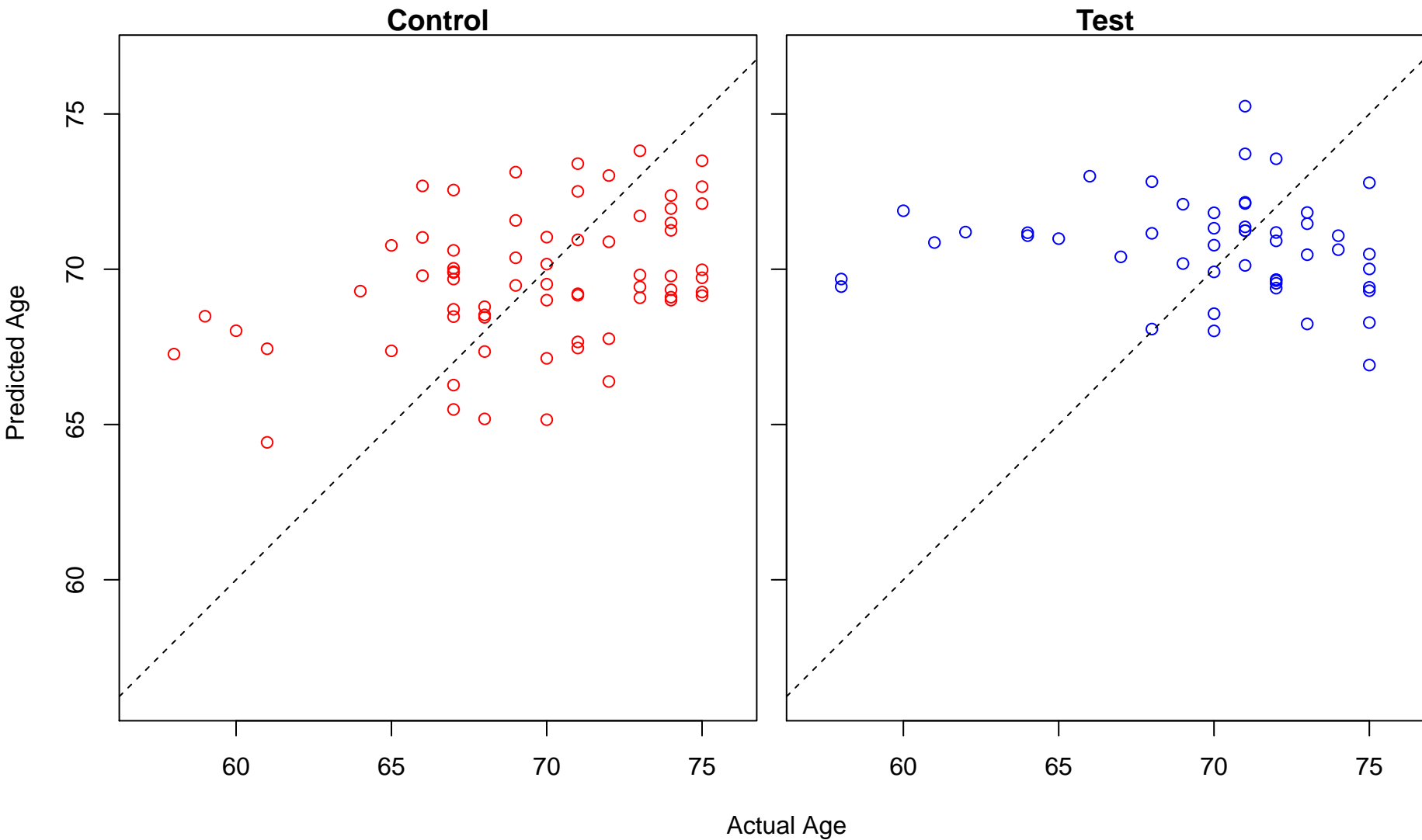
positive regulation of synaptic transmission, glutamatergic (Score: 0.480849)



molybdopterin cofactor biosynthetic process (Score: 0.480740)

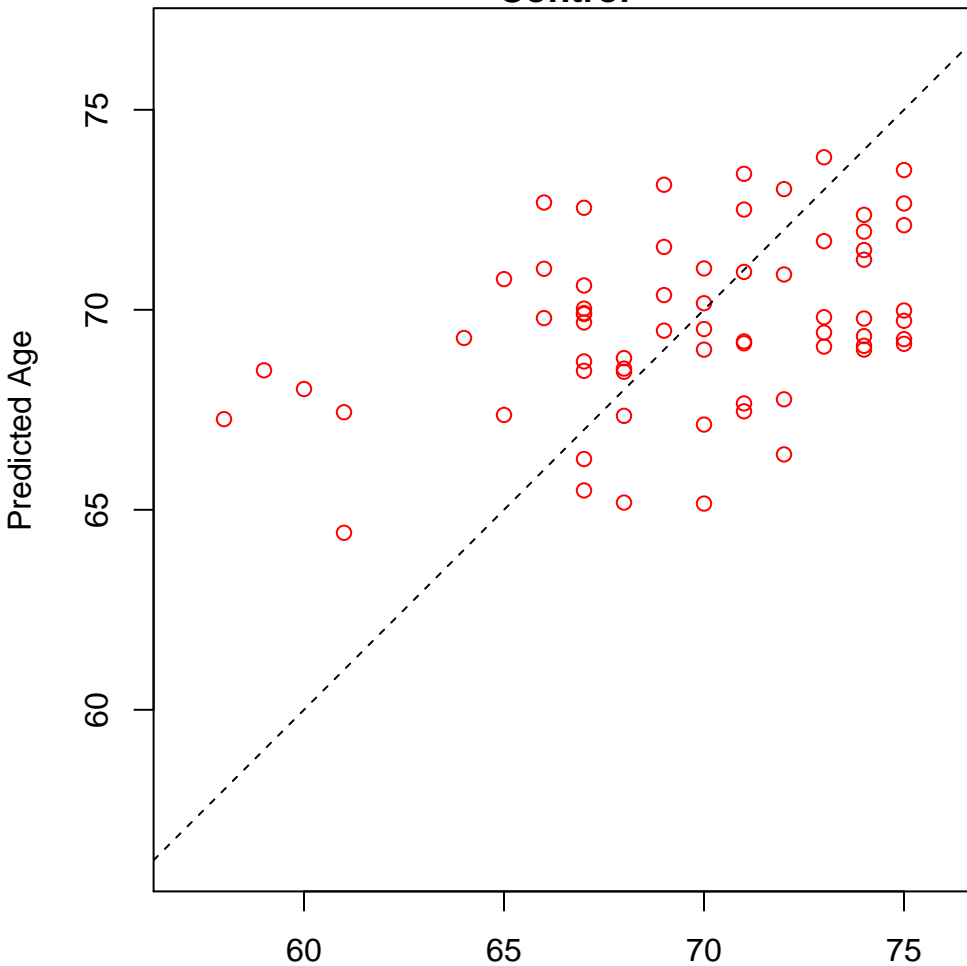


molybdopterin cofactor metabolic process (Score: 0.480740)

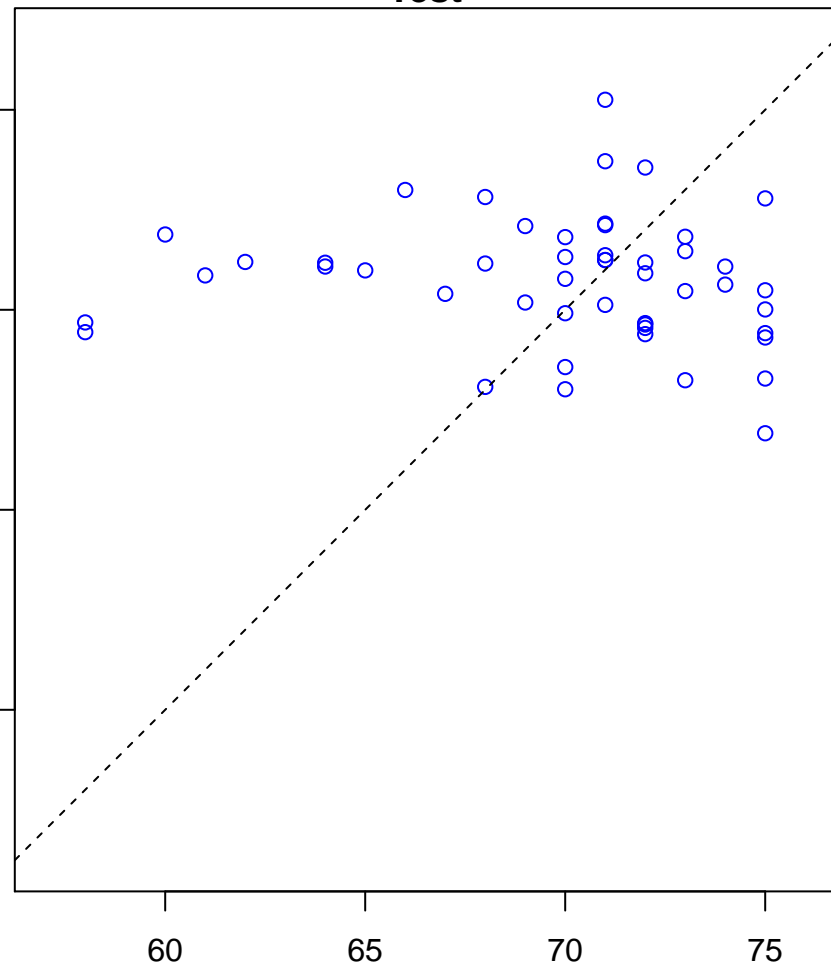


prosthetic group metabolic process (Score: 0.480740)

Control

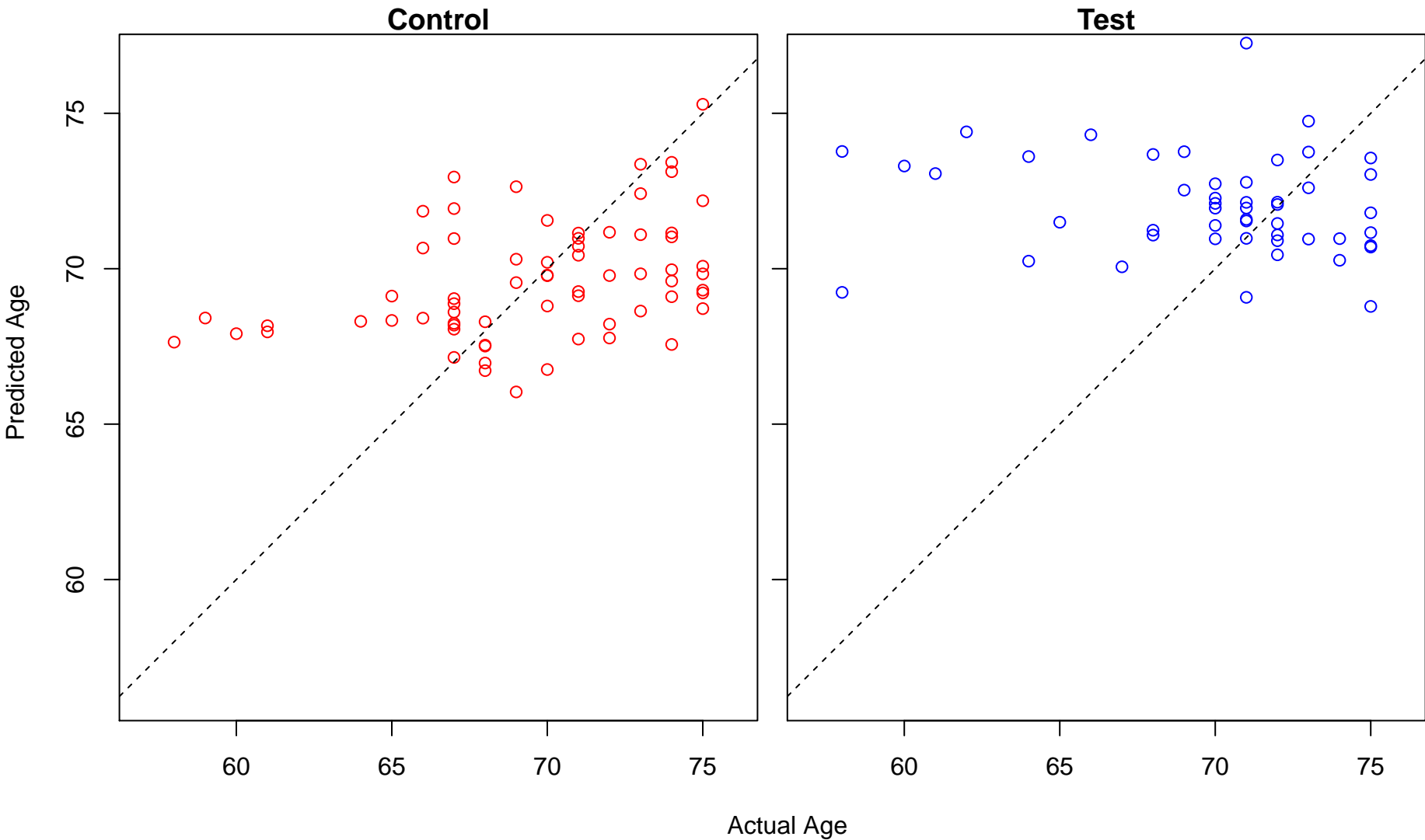


Test

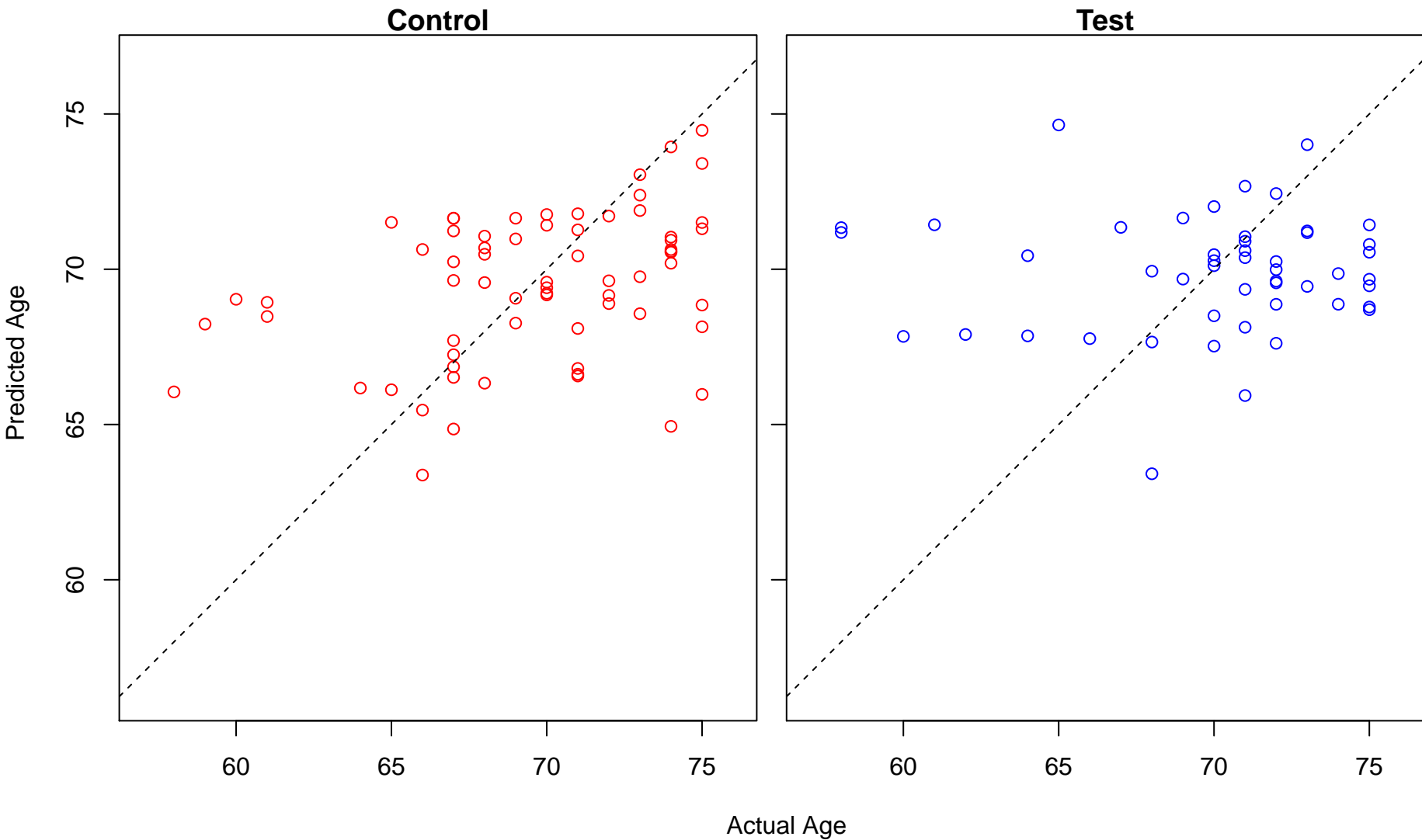


Actual Age

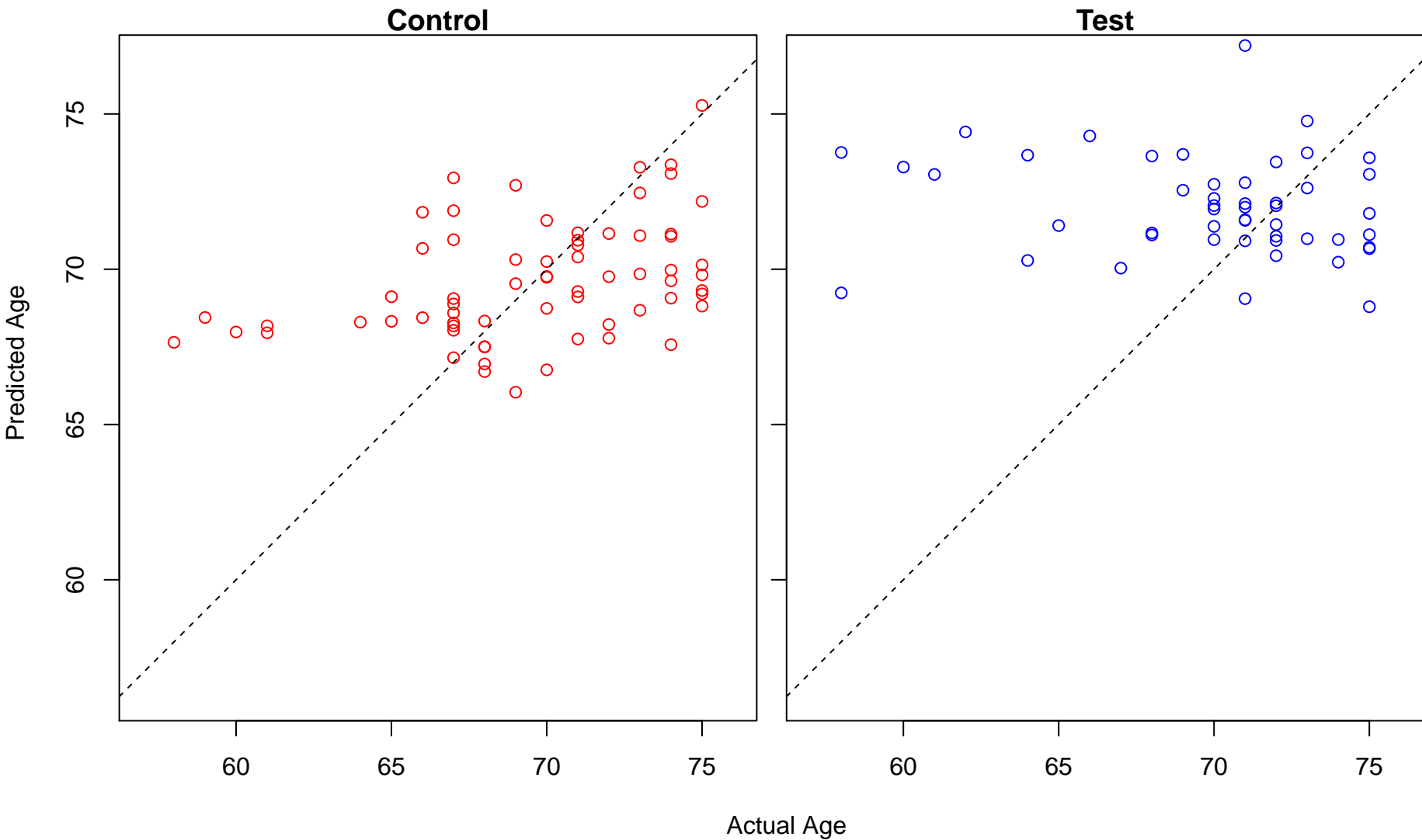
auditory receptor cell differentiation (Score: 0.479956)



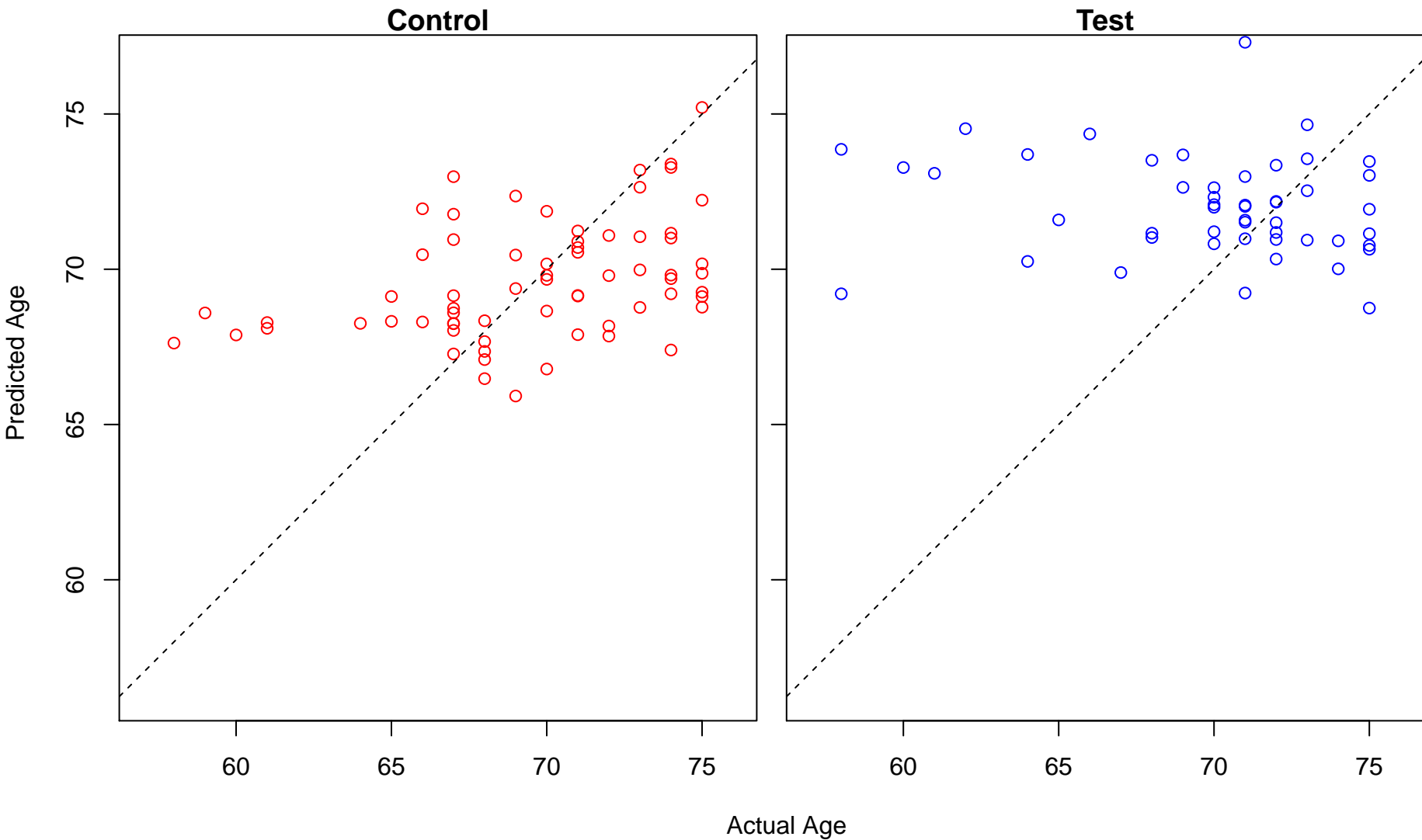
regulation of heart rate by cardiac conduction (Score: 0.479726)



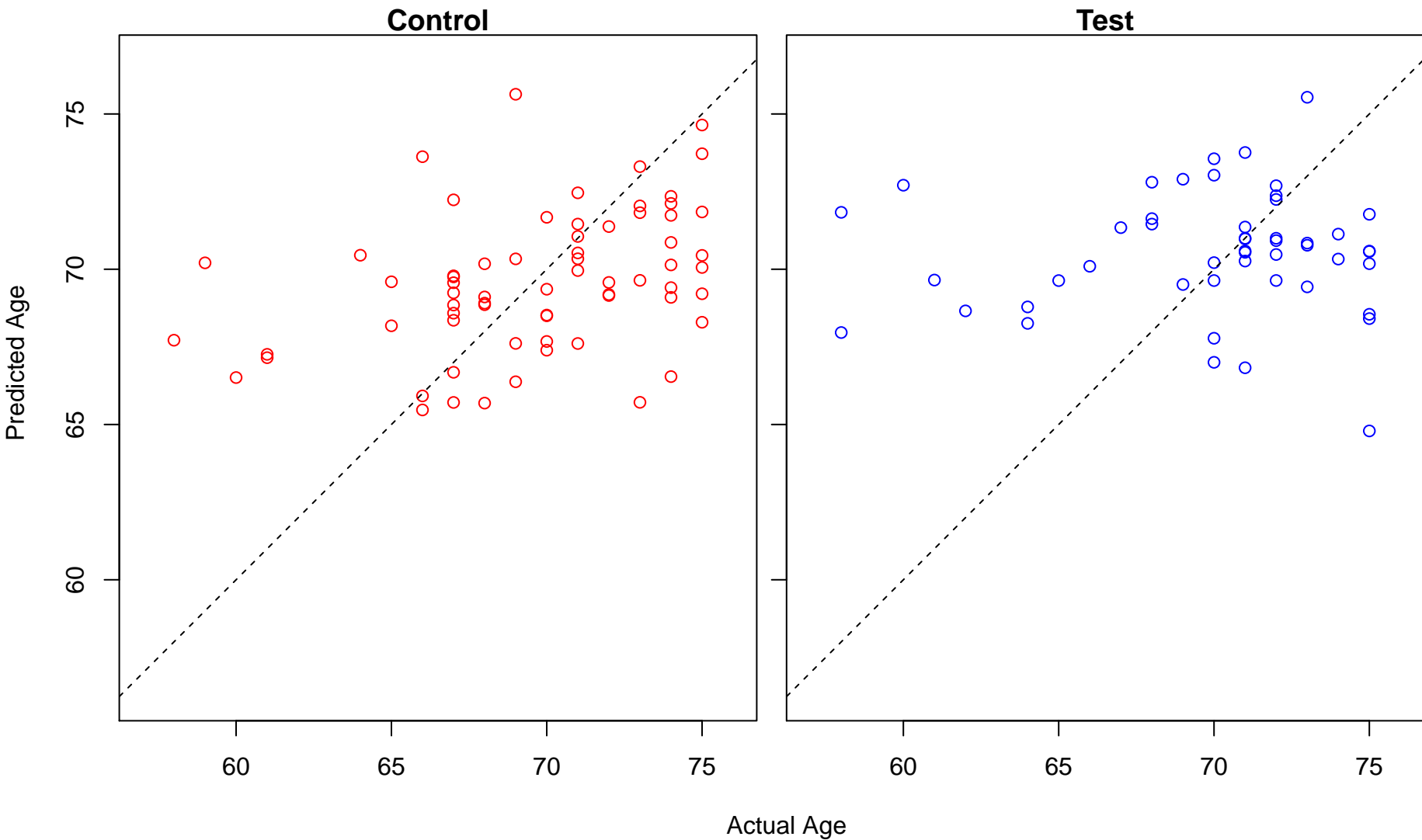
inner ear receptor cell development (Score: 0.478138)



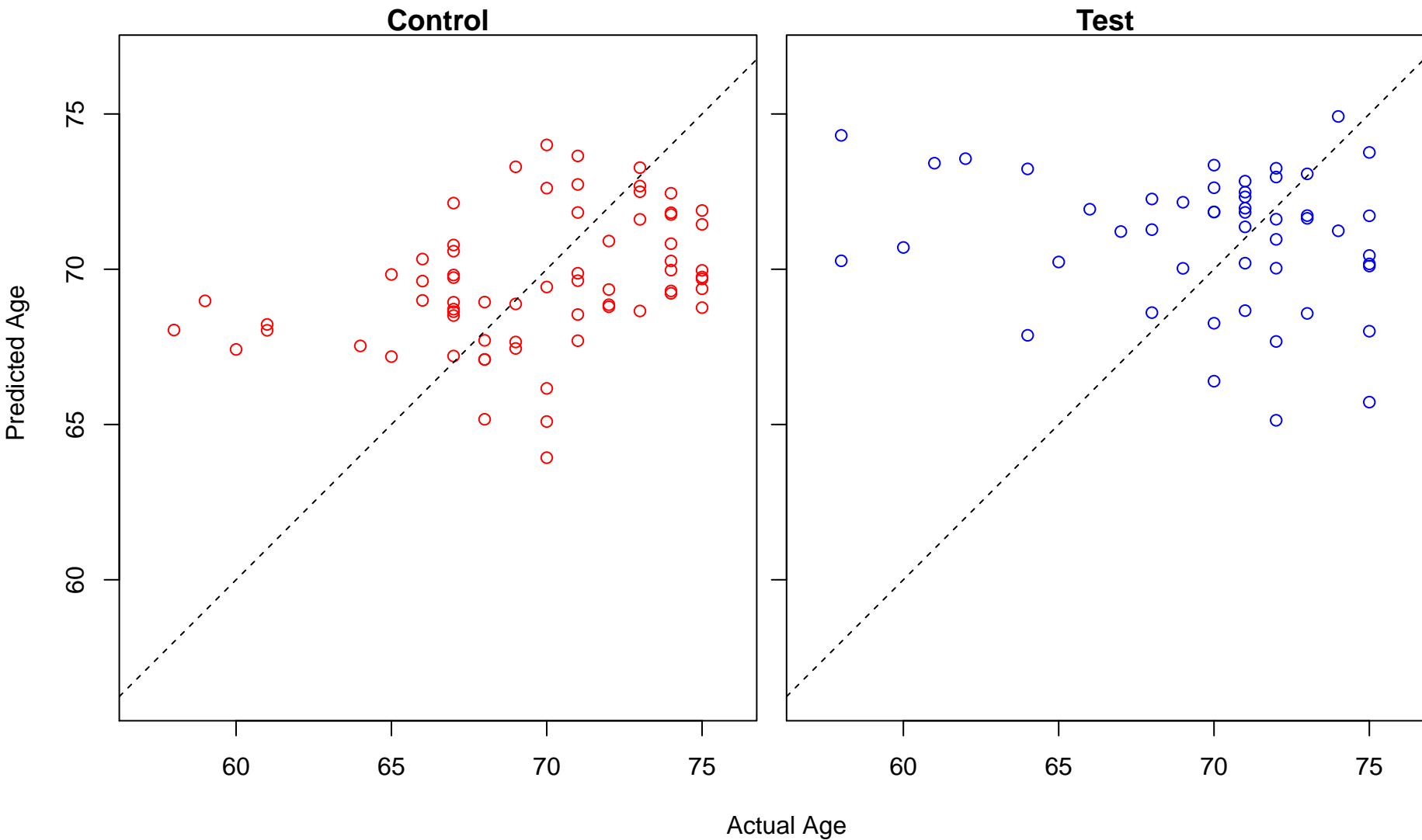
retrograde axonal transport (Score: 0.478025)



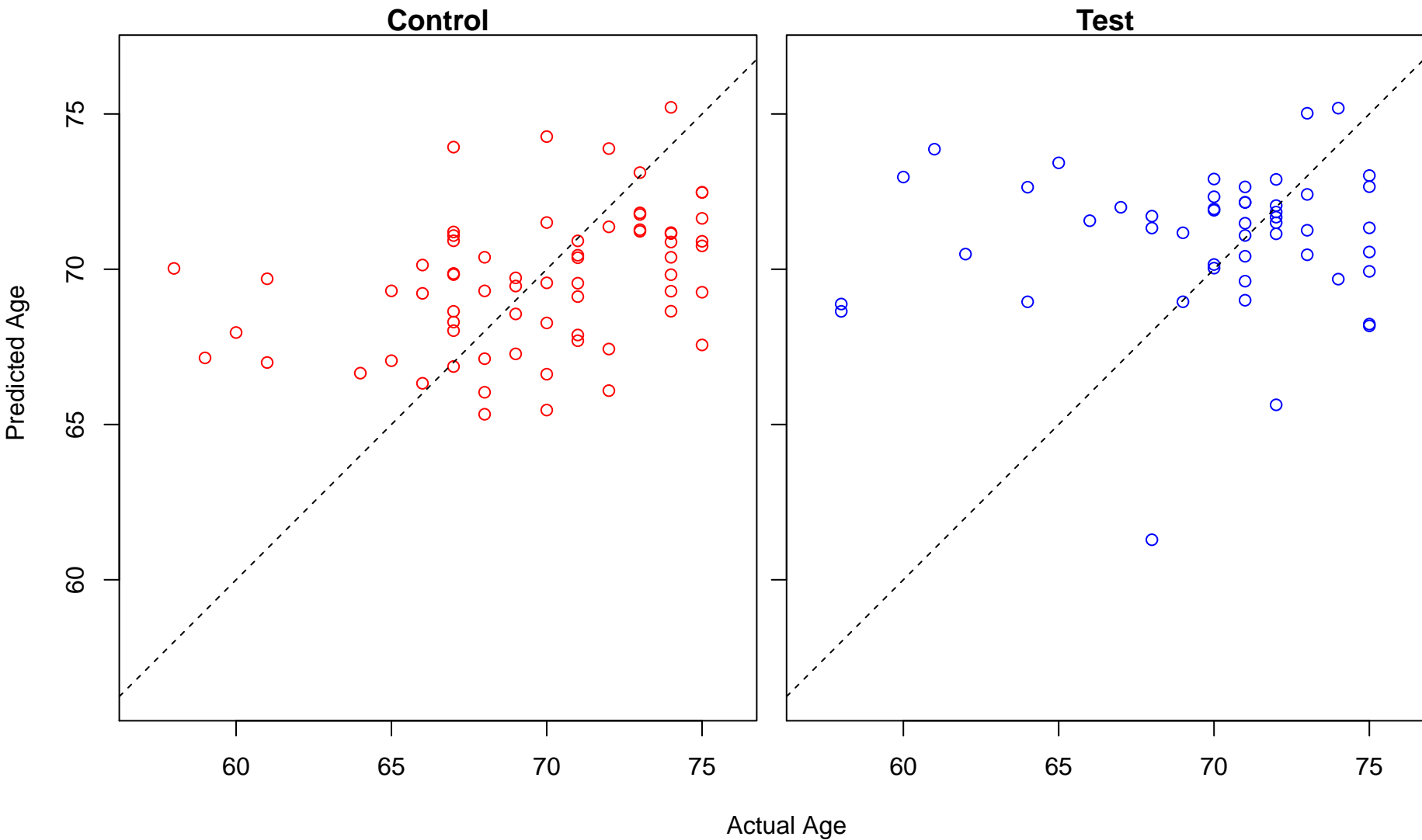
drug transport (Score: 0.477074)



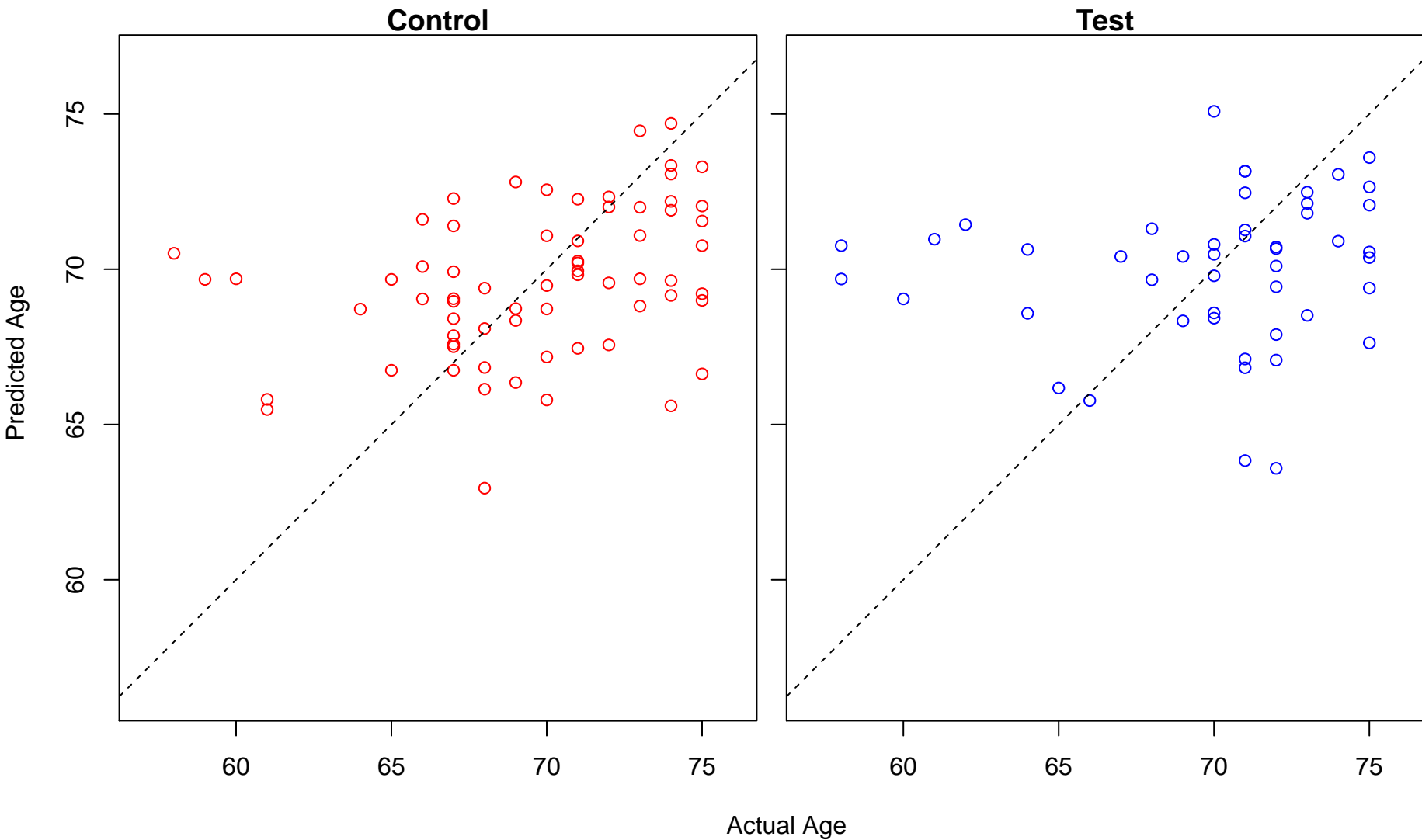
positive regulation of mRNA processing (Score: 0.476838)



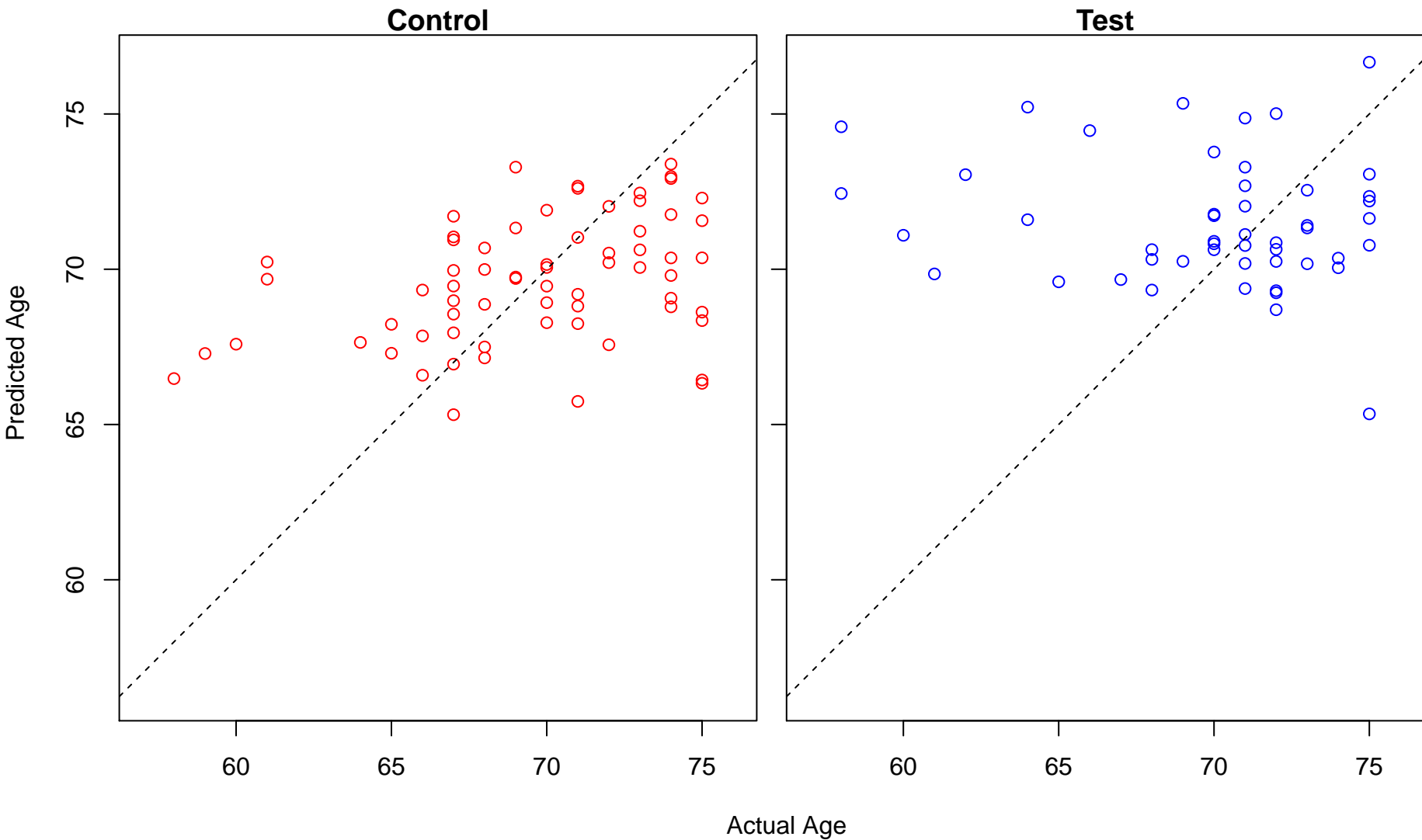
oxidative DNA demethylation (Score: 0.476631)



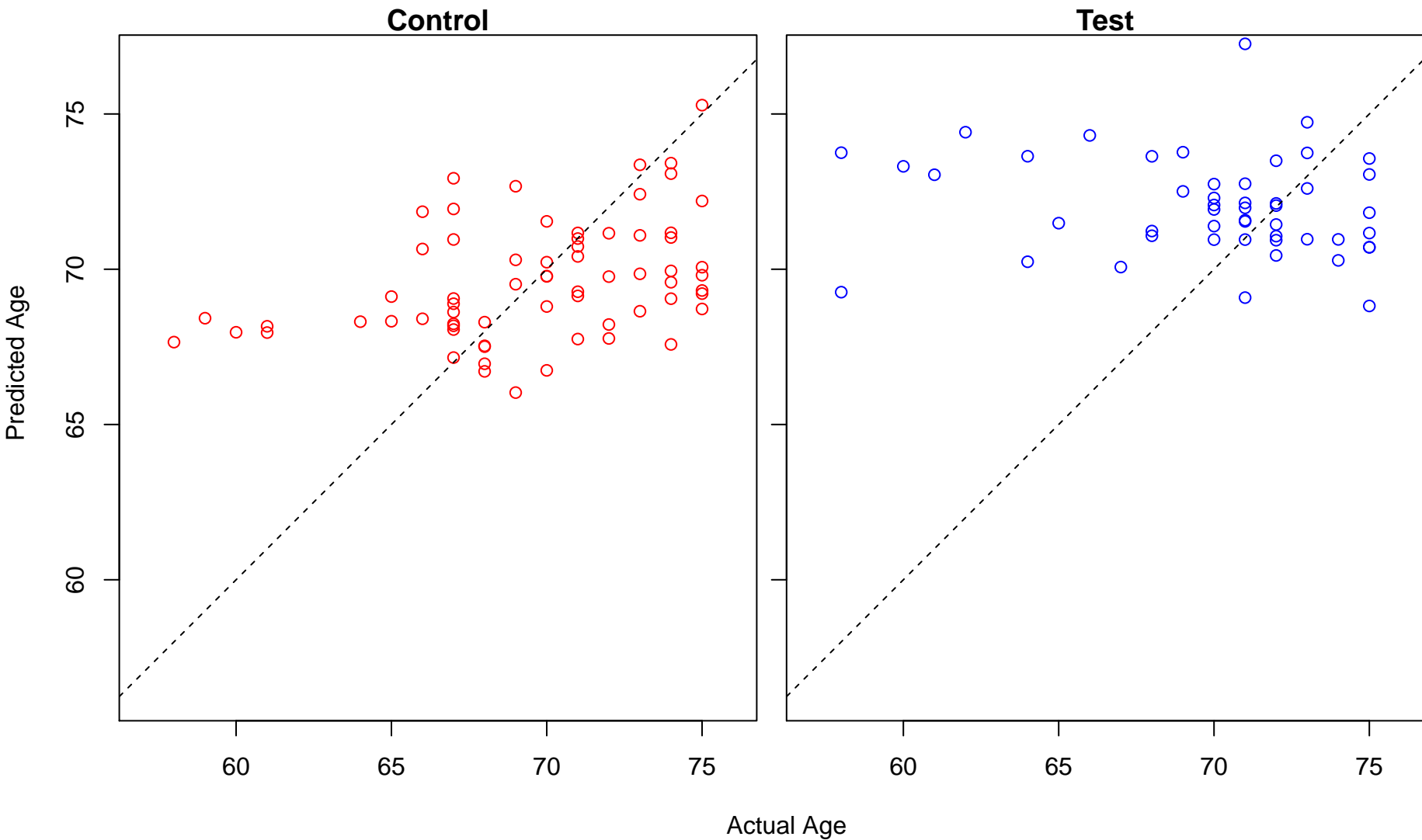
positive regulation of tolerance induction (Score: 0.476523)



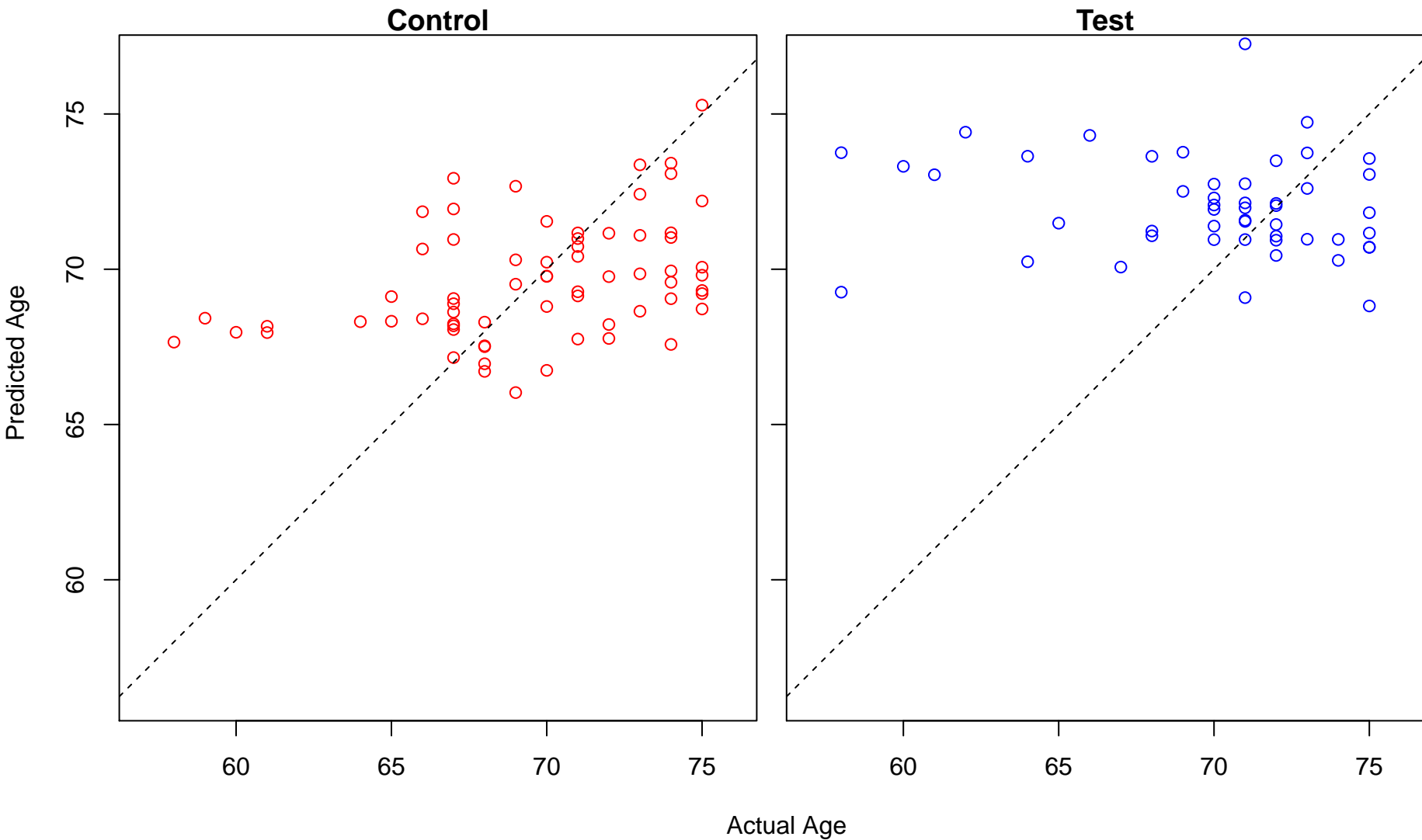
protein hydroxylation (Score: 0.476485)



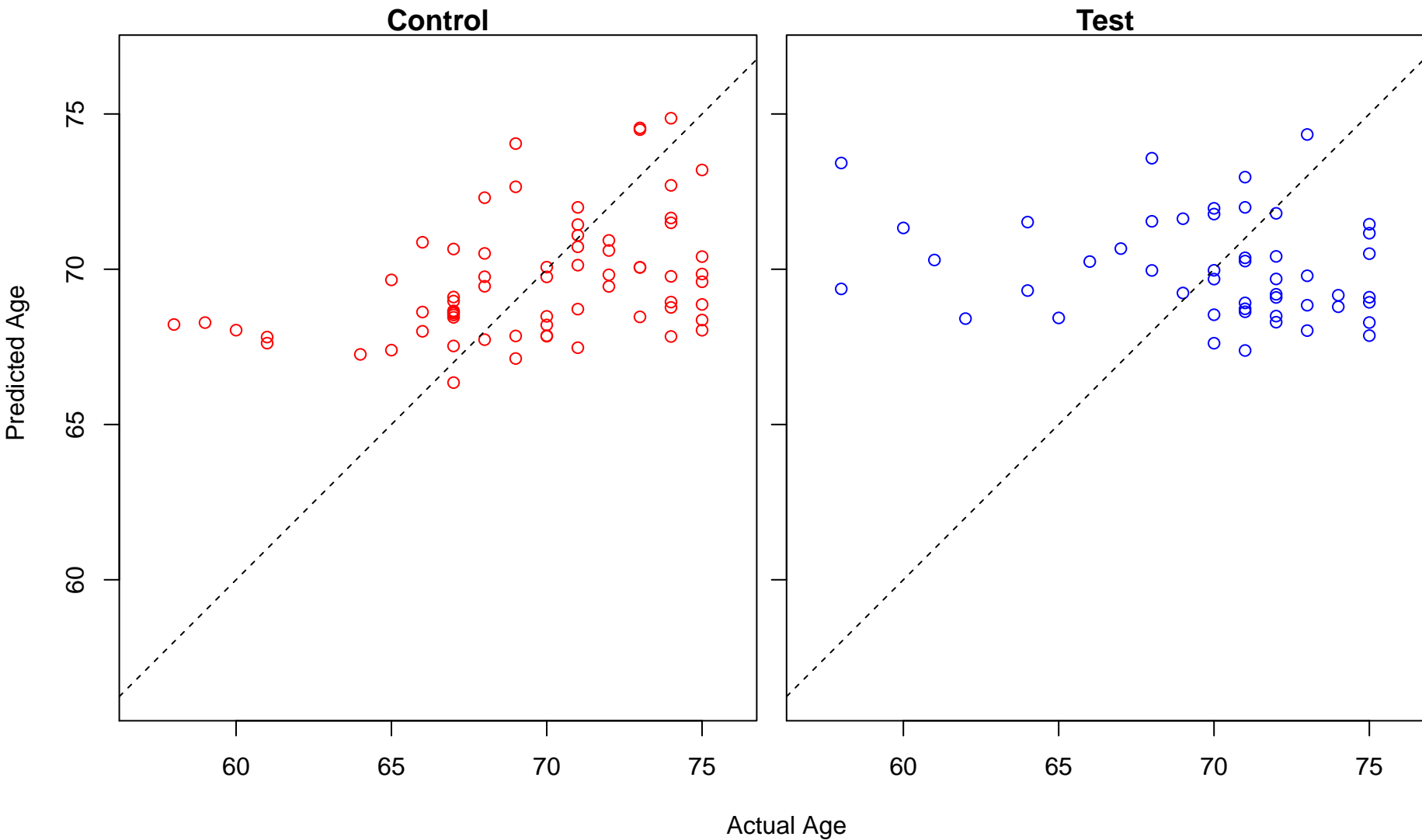
mechanoreceptor differentiation (Score: 0.476390)



inner ear receptor cell differentiation (Score: 0.476390)

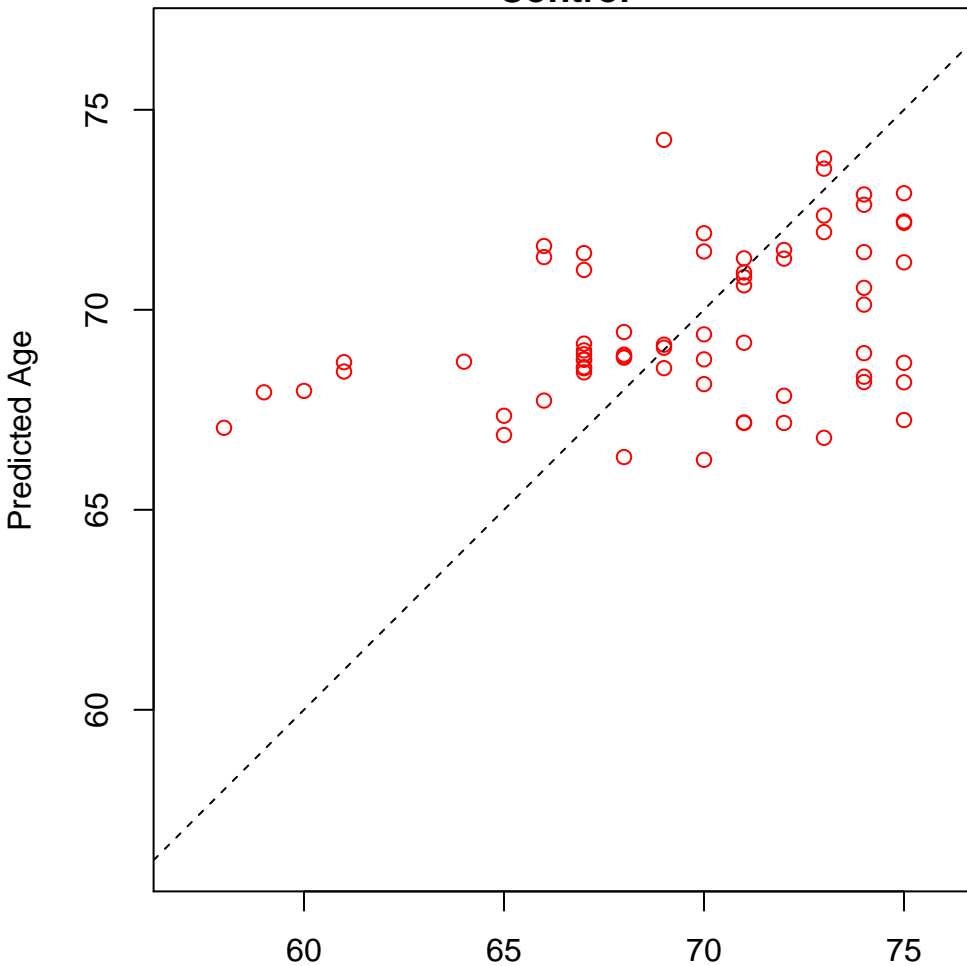


regulation of mesenchymal stem cell differentiation (Score: 0.475590)

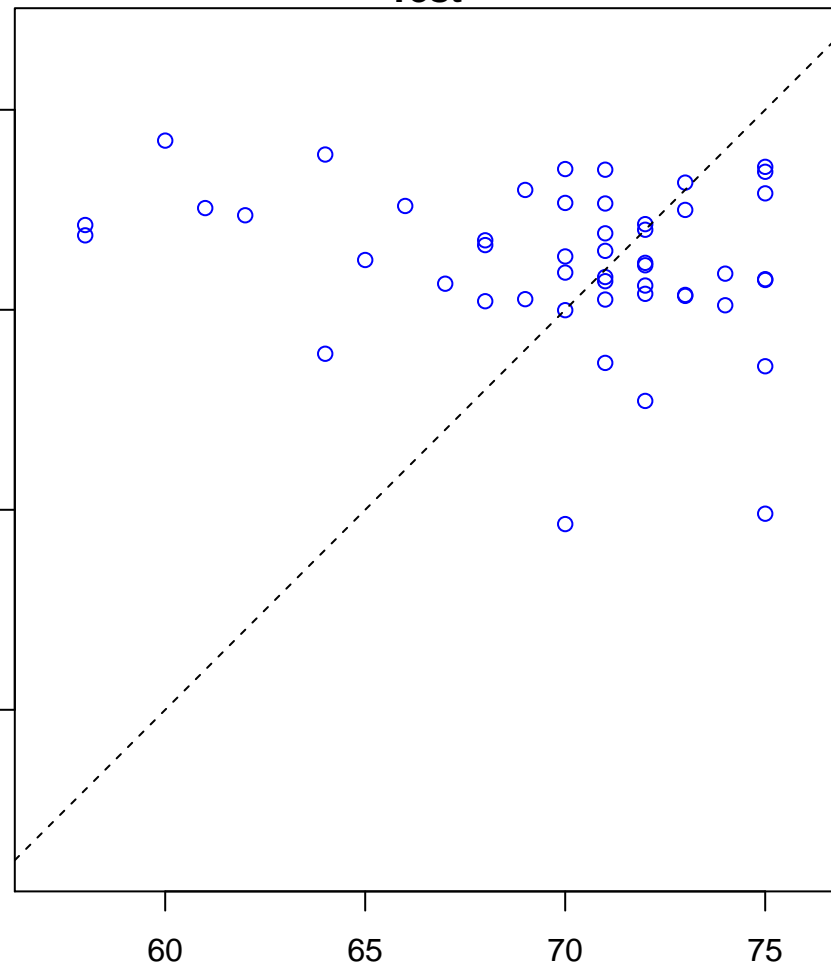


response to nerve growth factor (Score: 0.473617)

Control

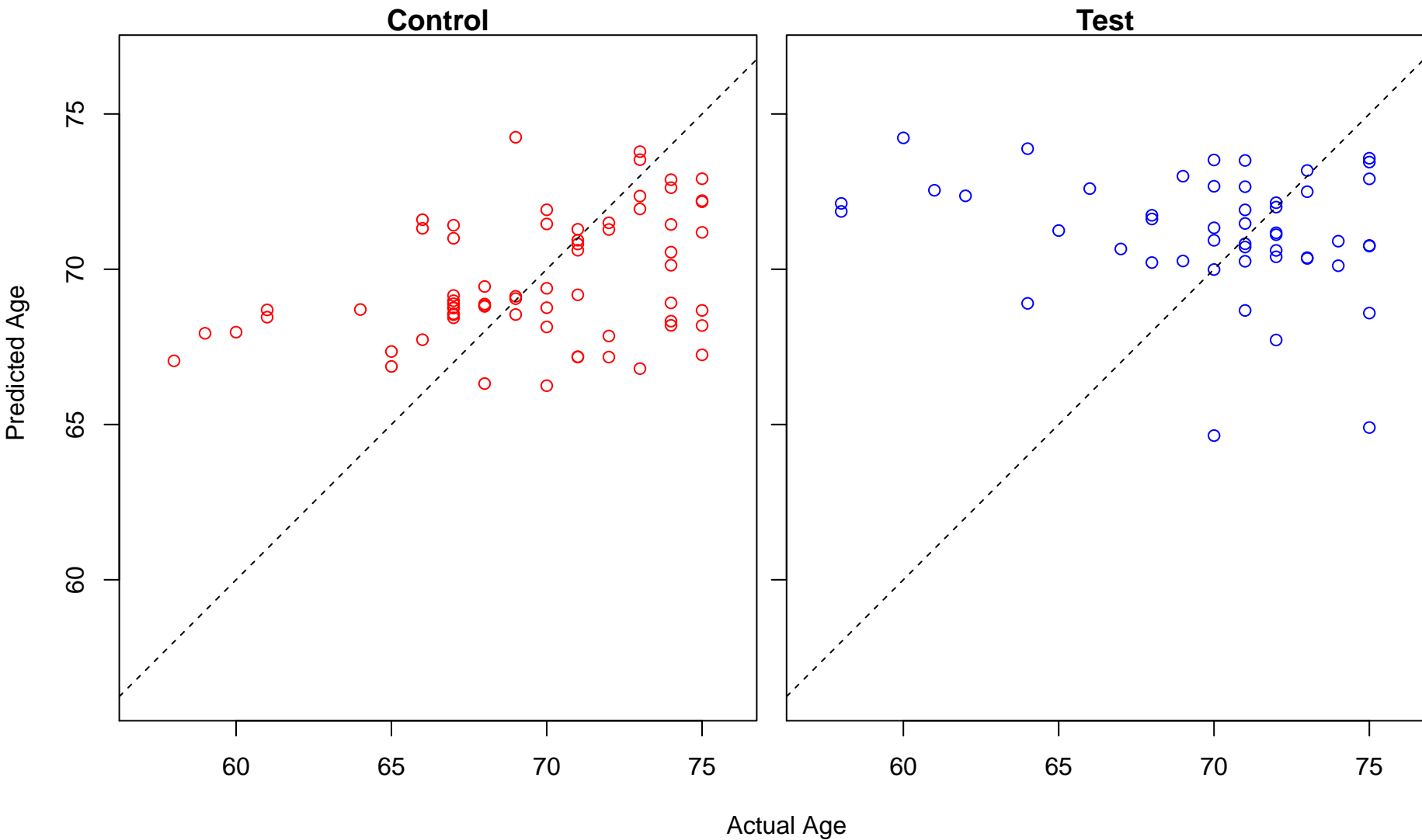


Test

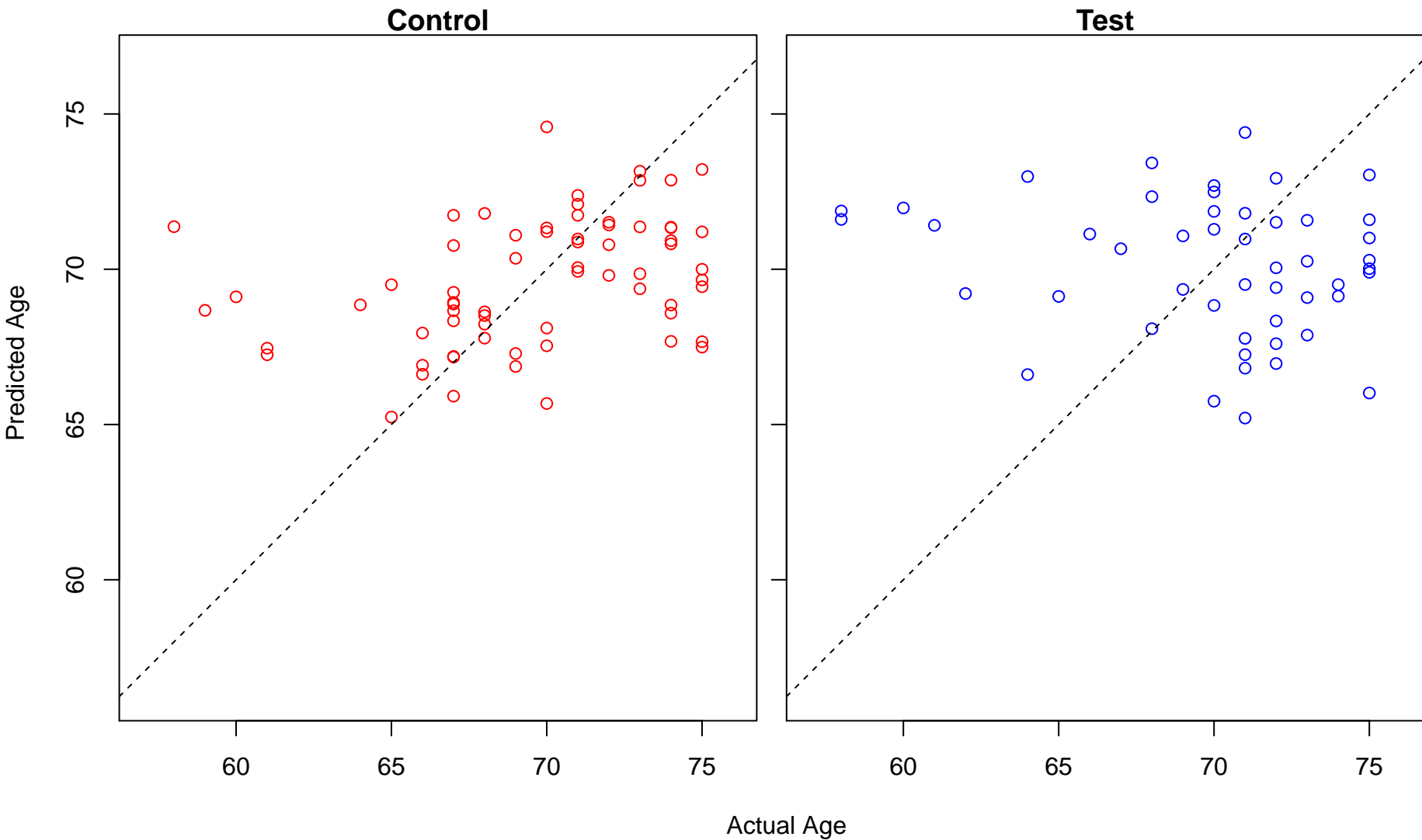


Actual Age

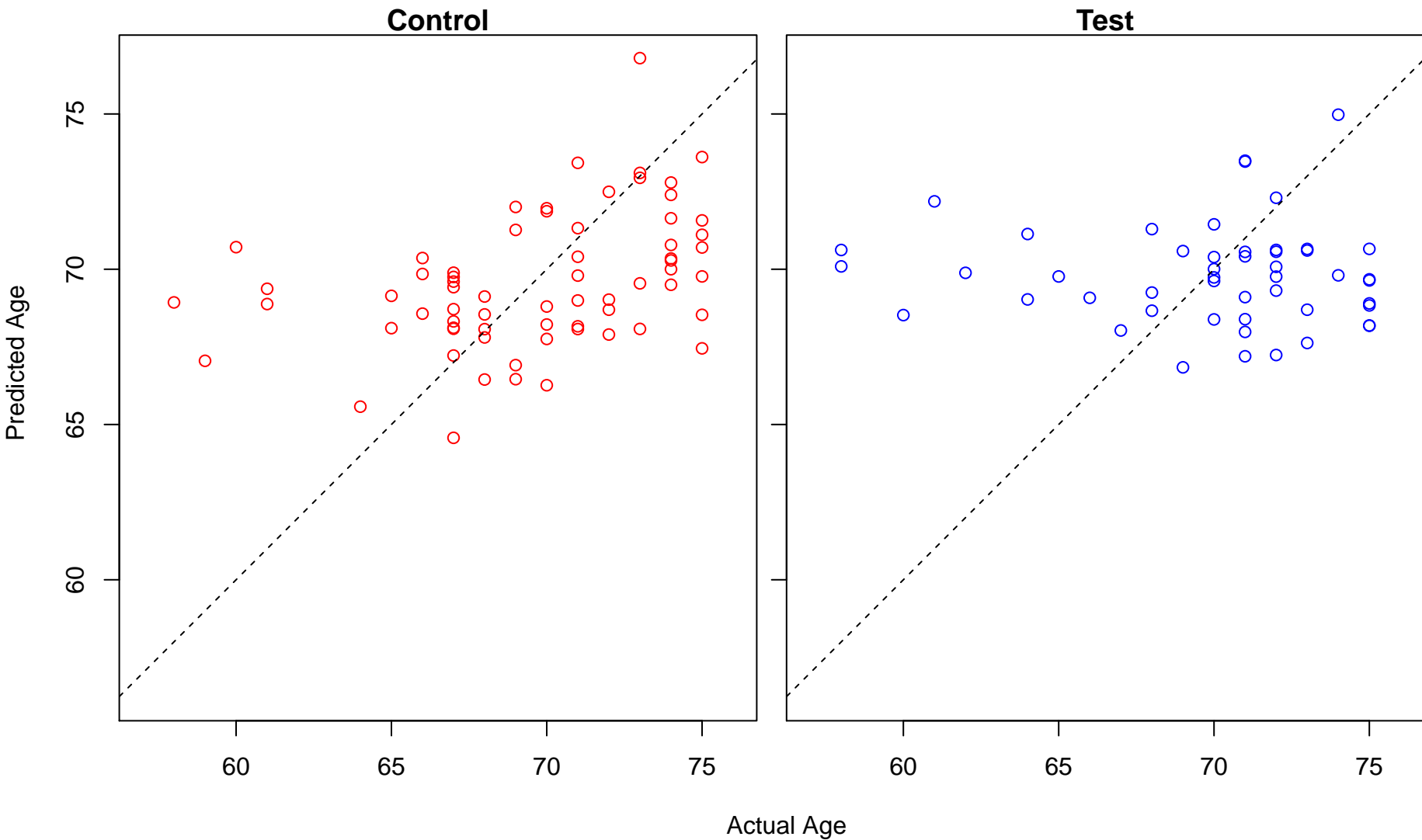
cellular response to nerve growth factor stimulus (Score: 0.473617)



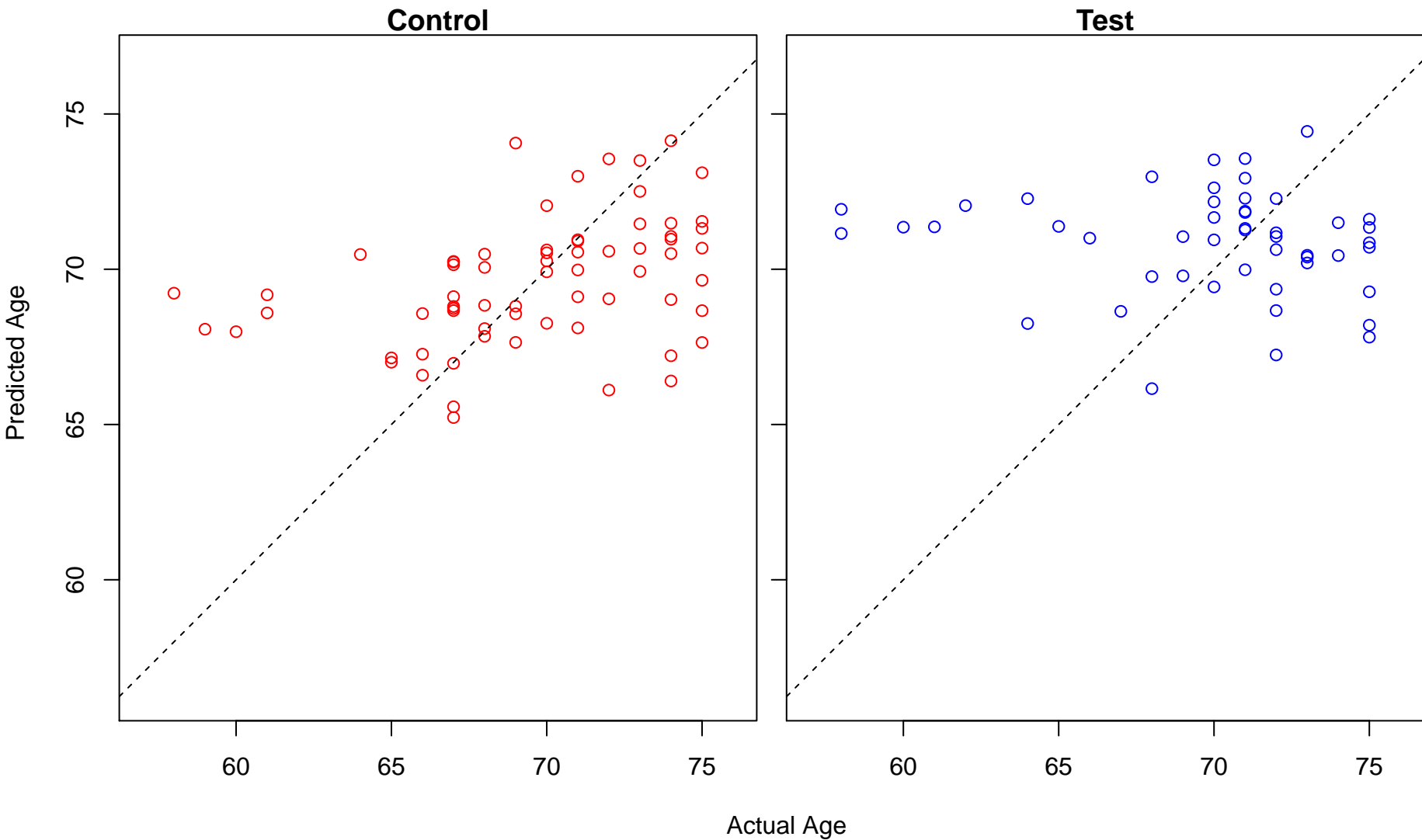
rRNA catabolic process (Score: 0.473444)



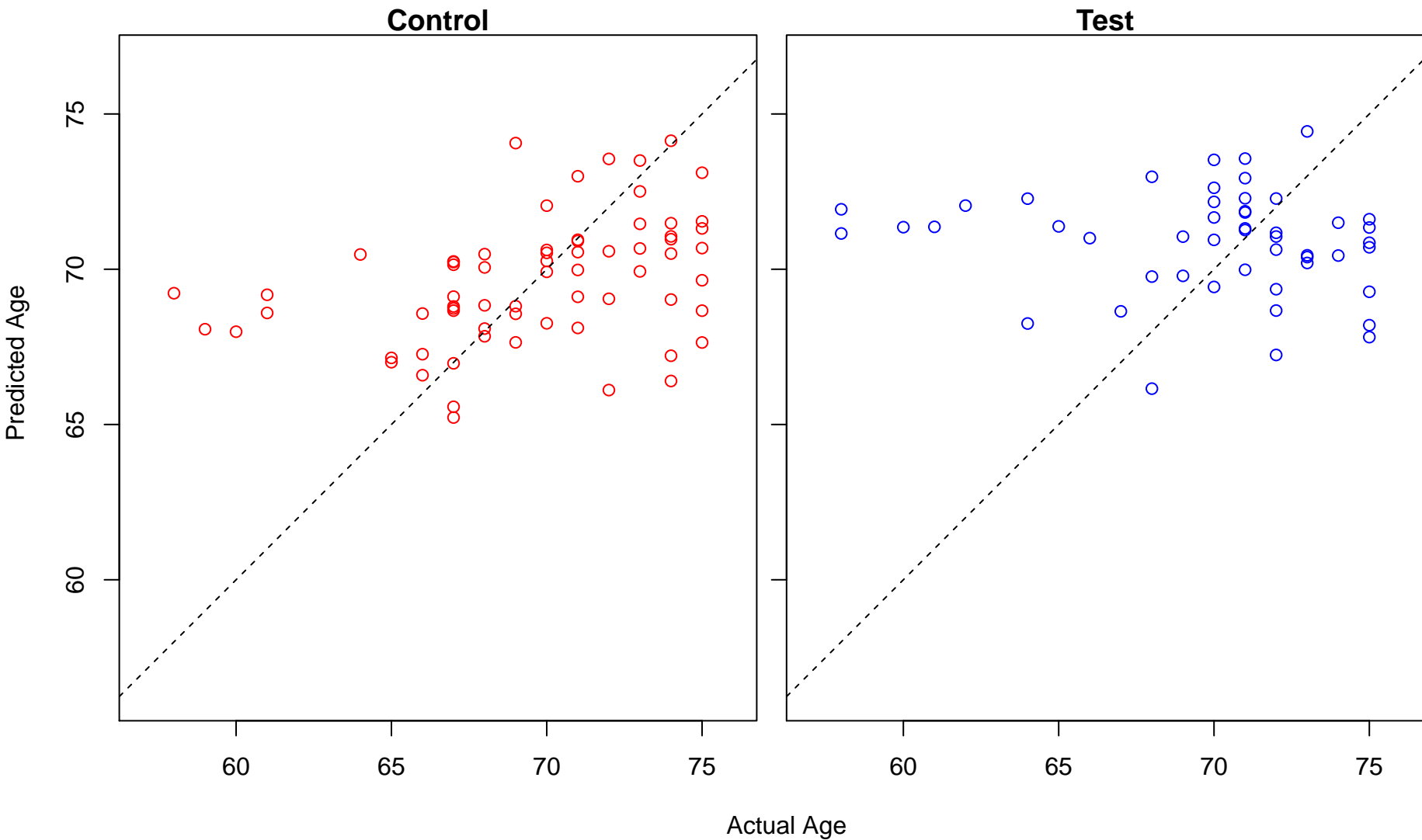
iron coordination entity transport (Score: 0.473248)



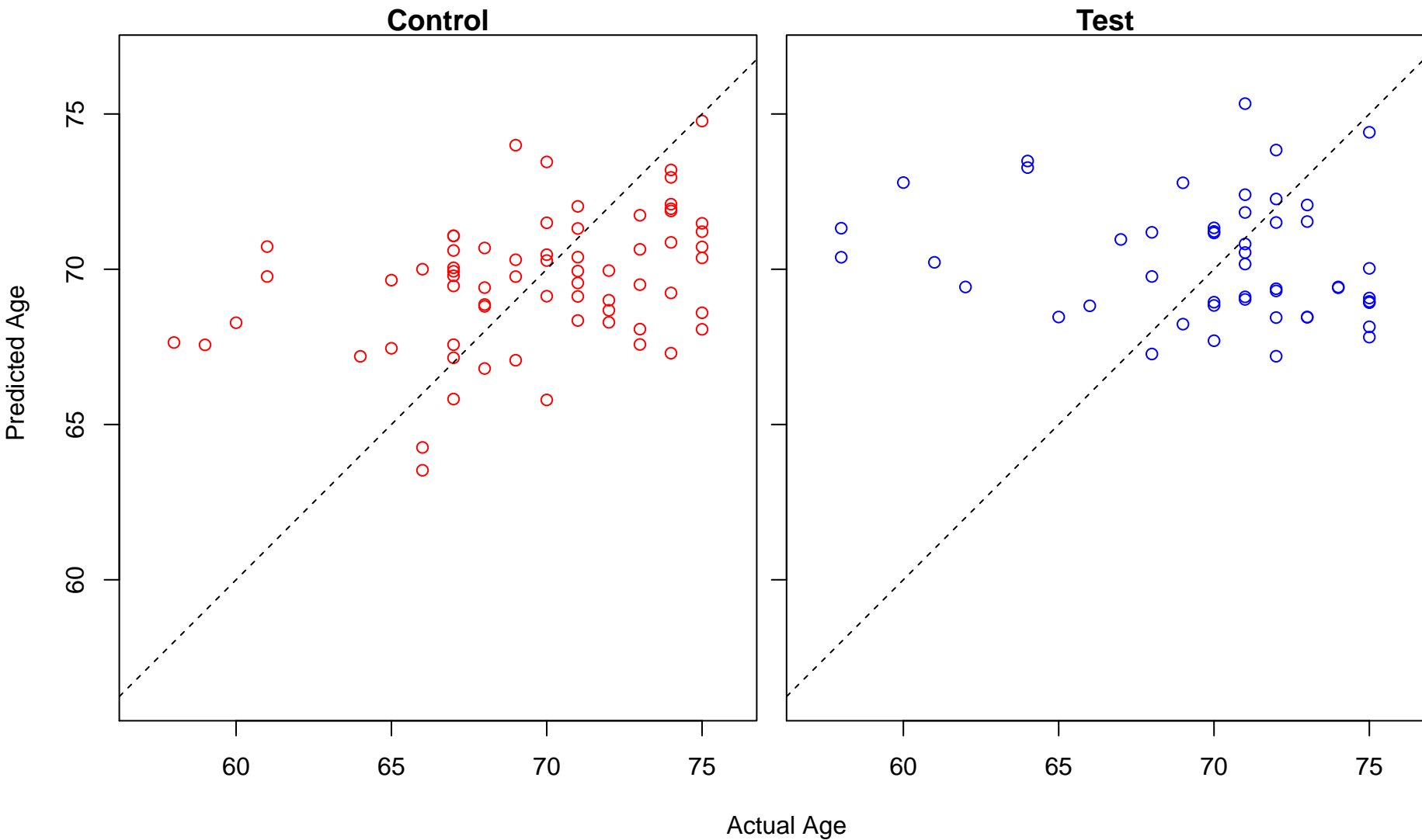
glycerol ether metabolic process (Score: 0.472717)



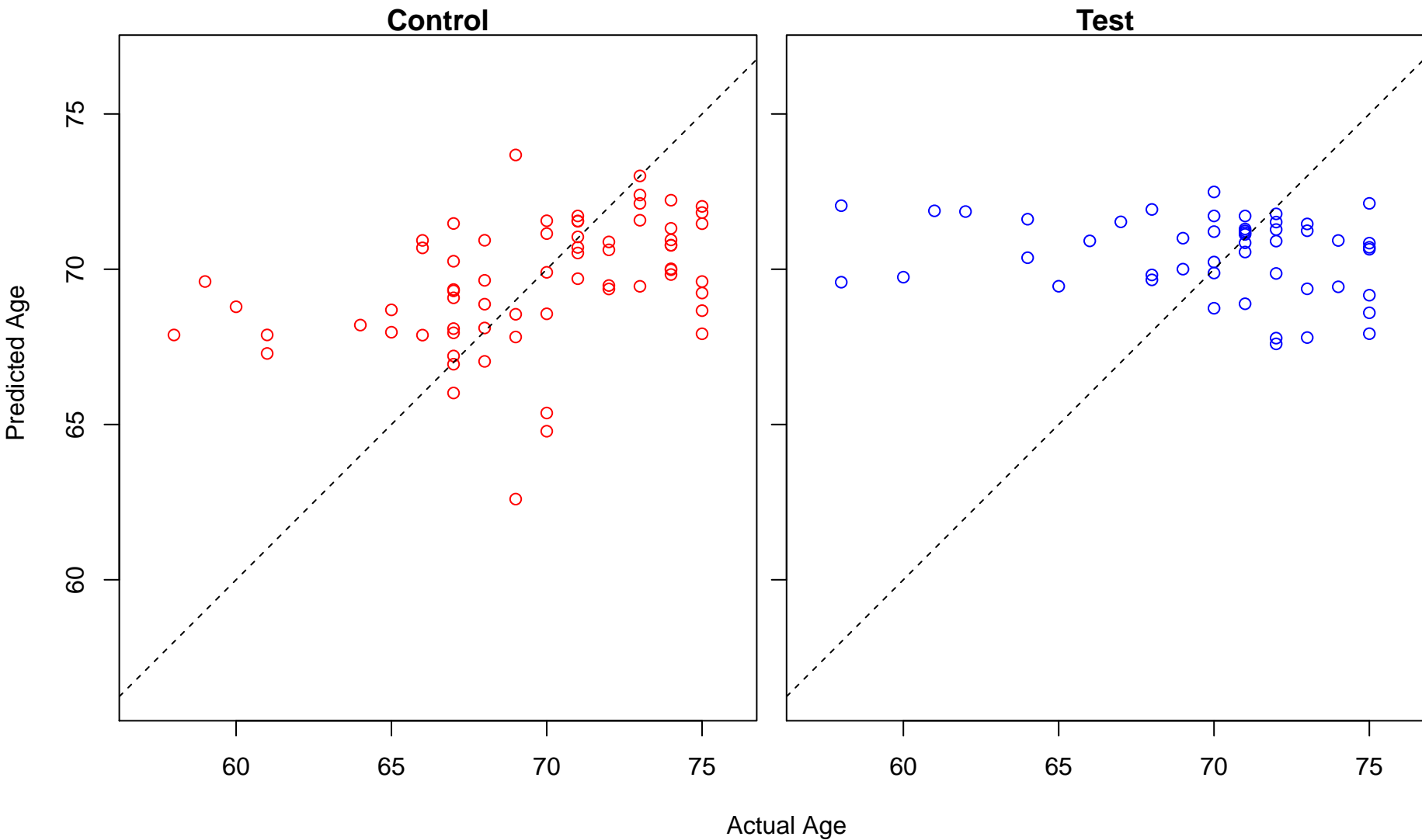
ether lipid metabolic process (Score: 0.472717)



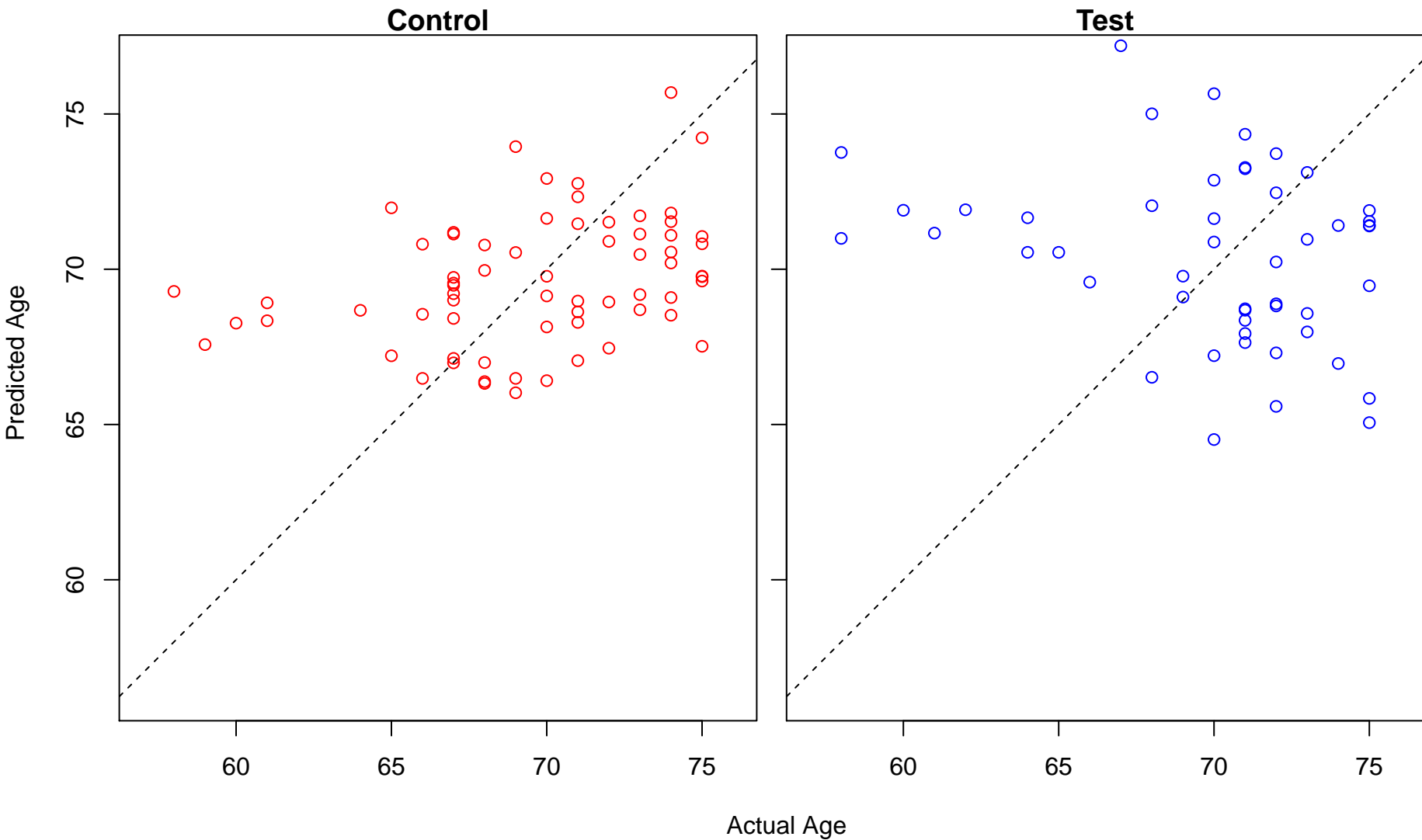
negative regulation of keratinocyte differentiation (Score: 0.472631)



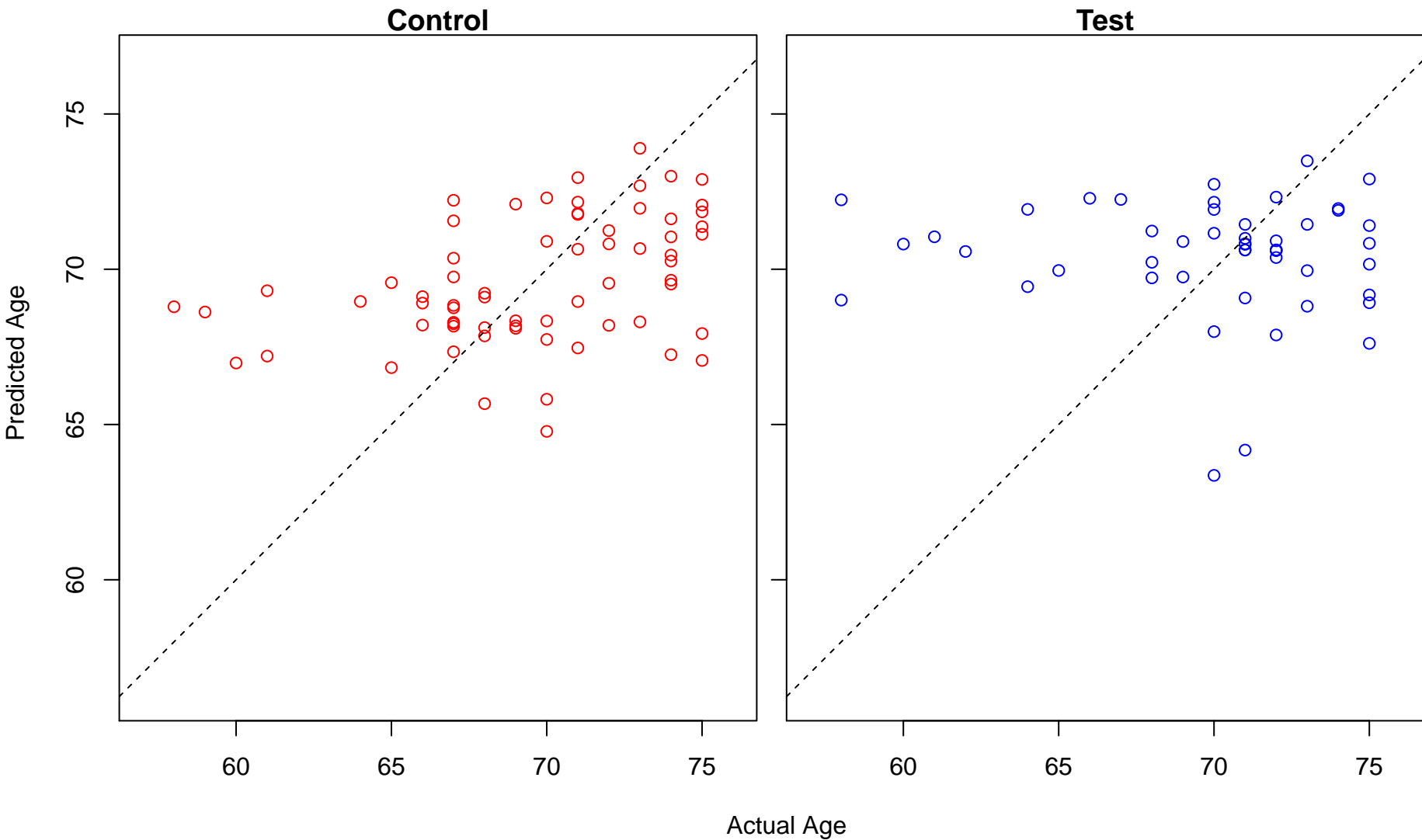
glycoside metabolic process (Score: 0.471921)



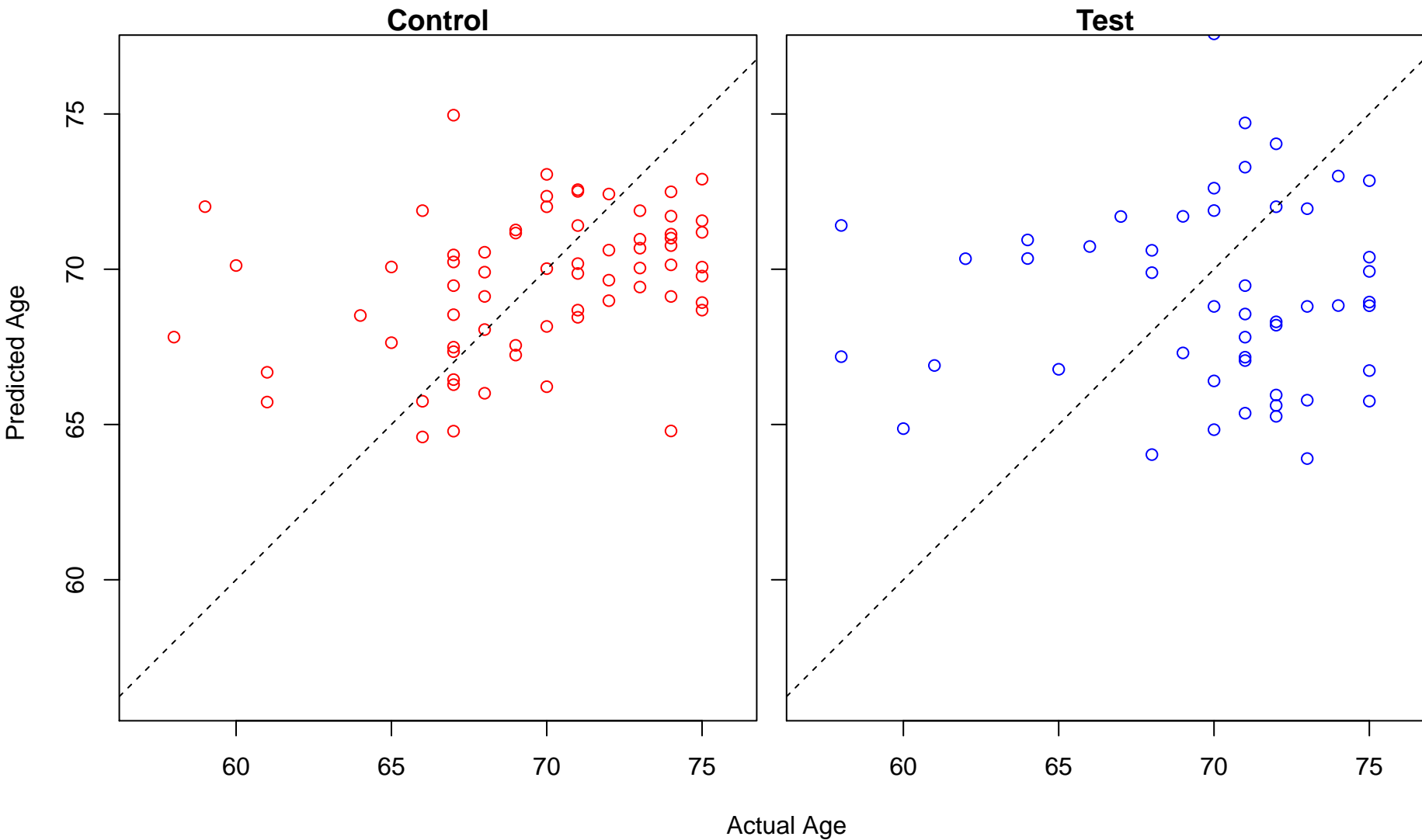
fatty acid homeostasis (Score: 0.471685)



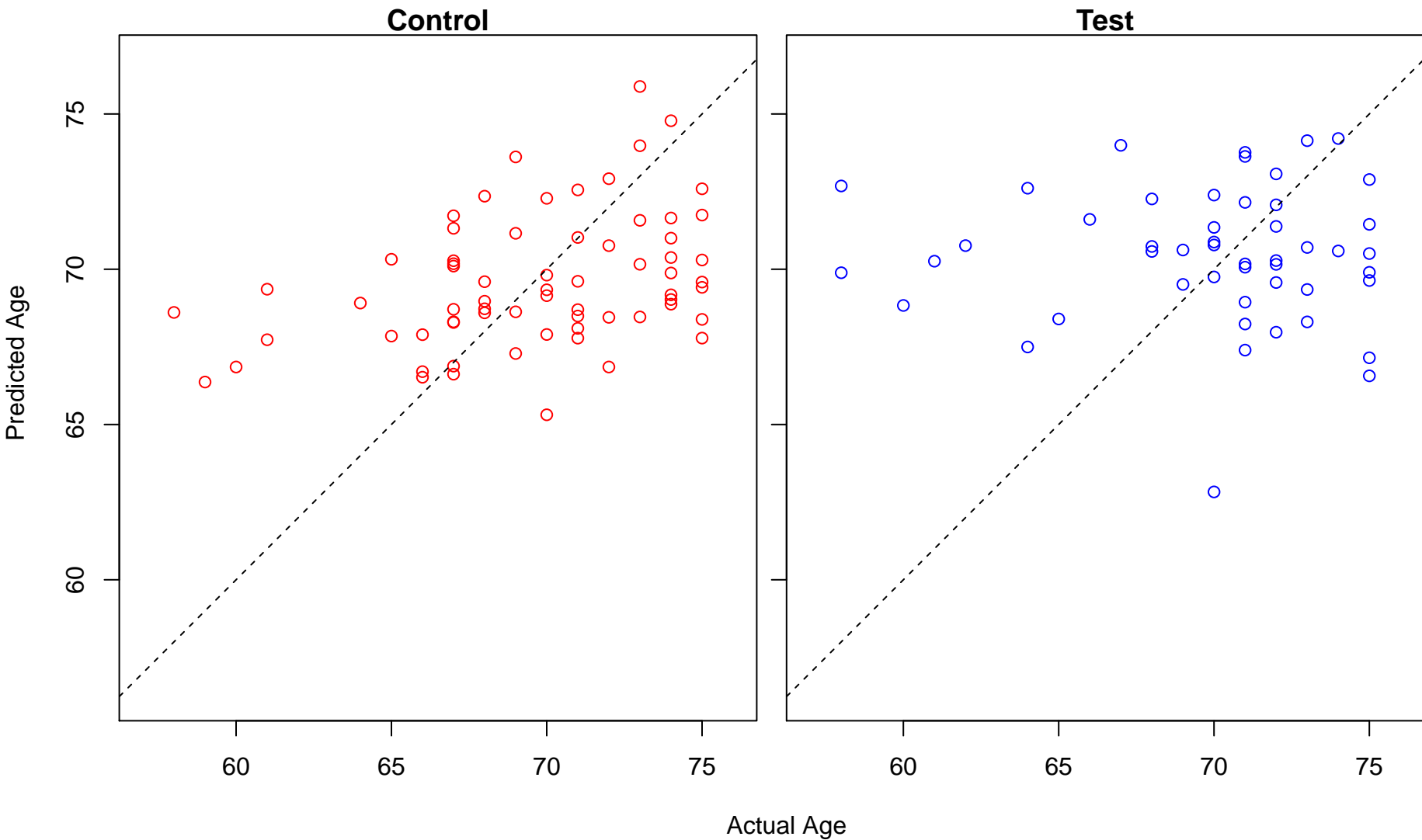
regulation of extracellular matrix disassembly (Score: 0.471354)



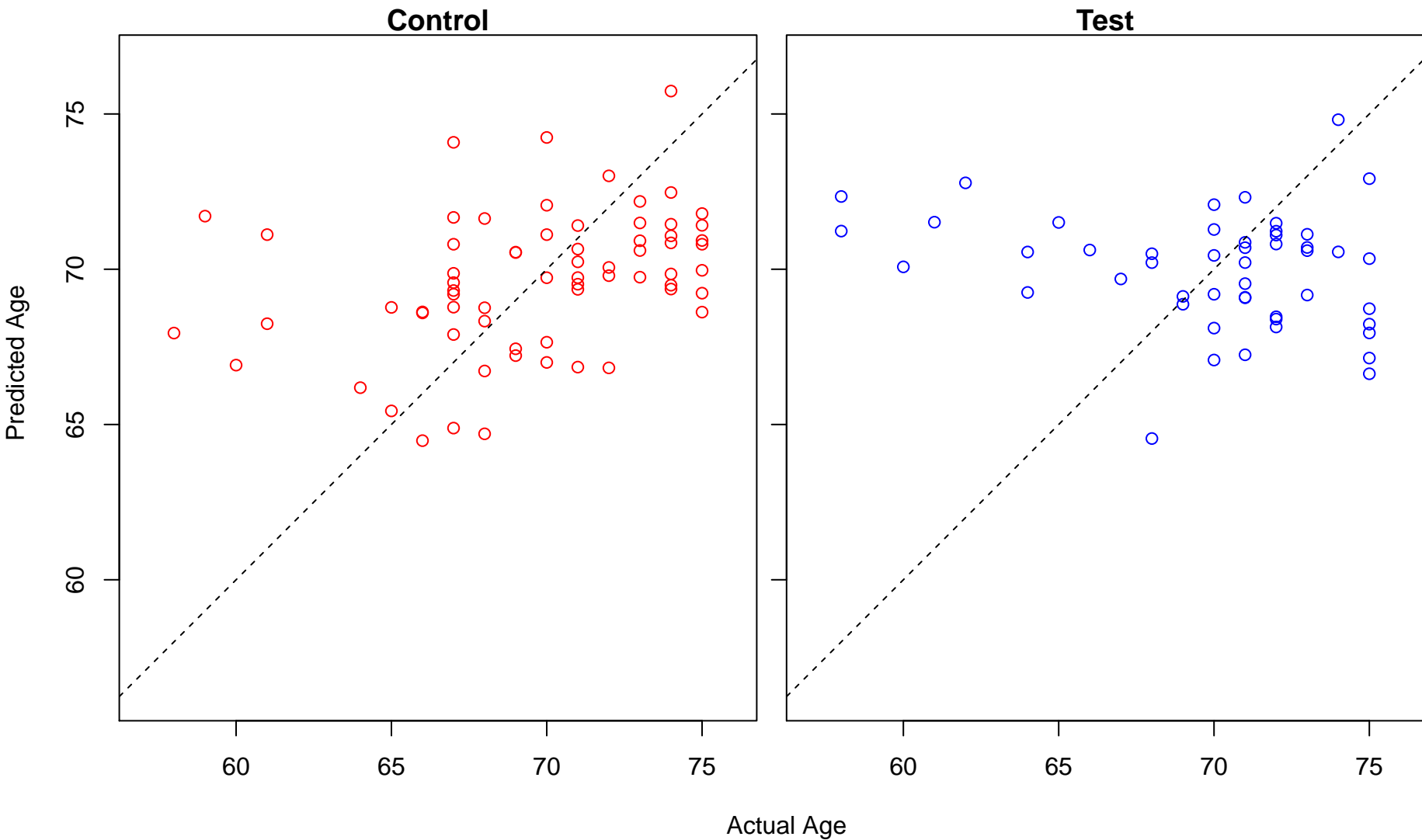
negative regulation of peptidyl–threonine phosphorylation (Score: 0.470649)



signal peptide processing (Score: 0.469969)

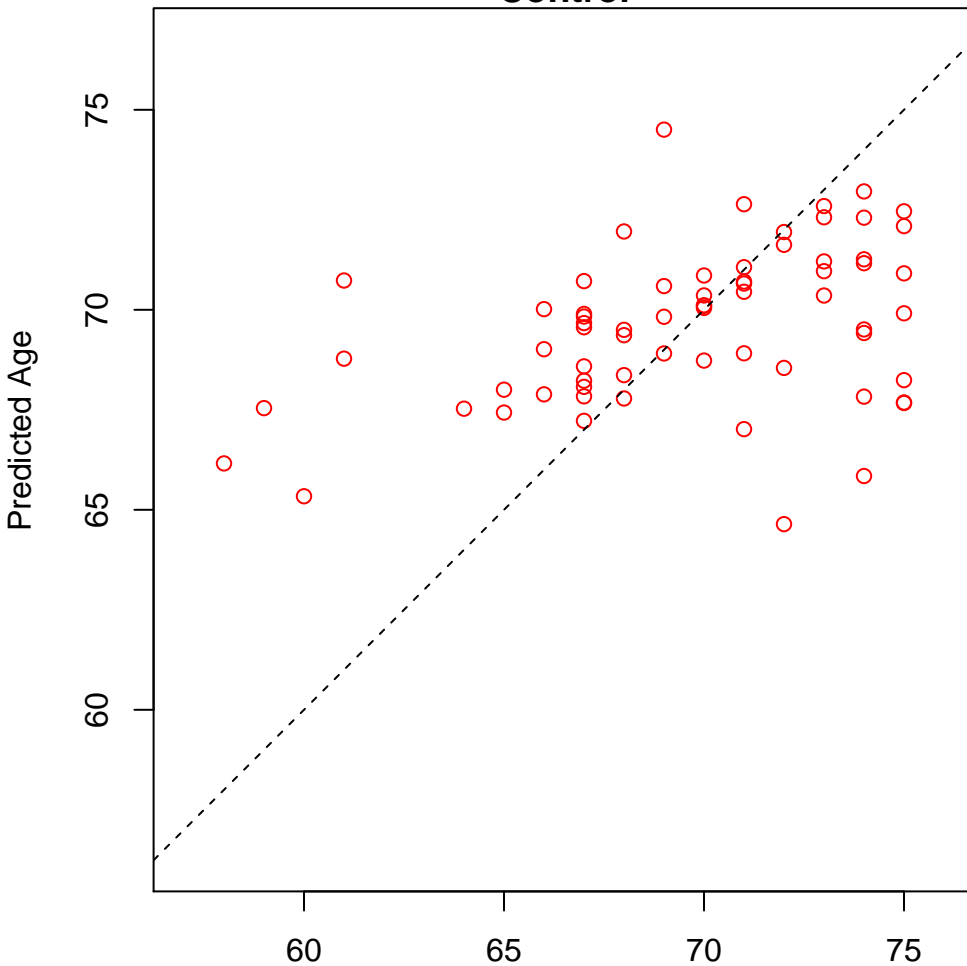


glycoprotein catabolic process (Score: 0.469803)

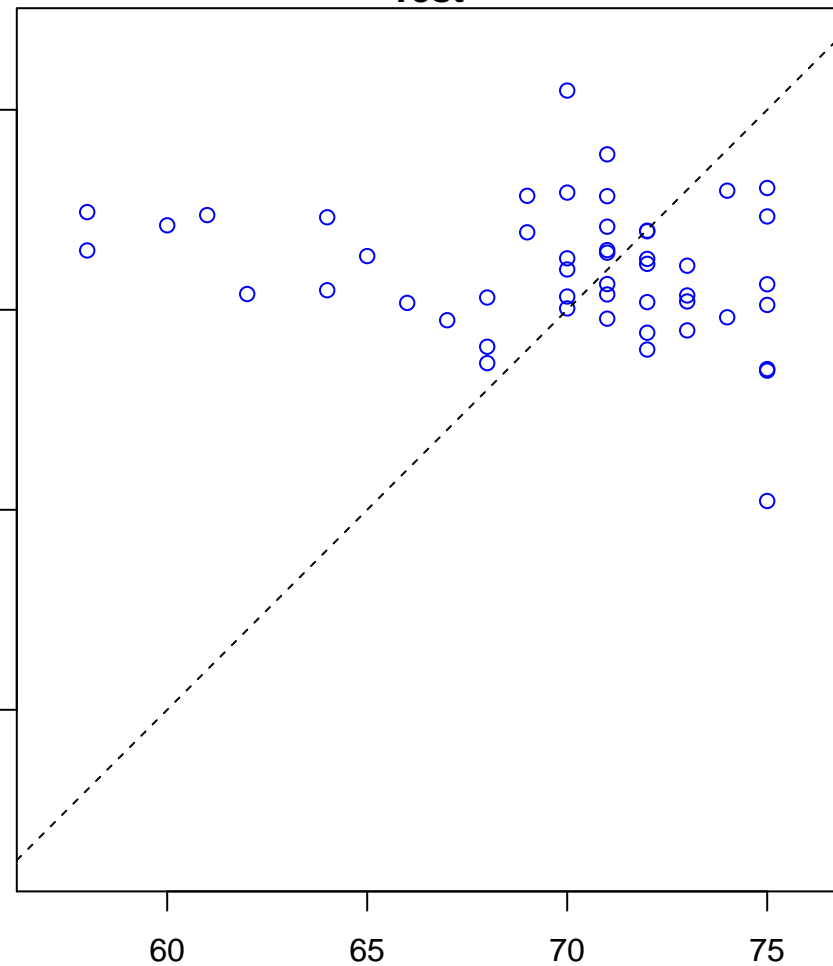


manganese ion transmembrane transport (Score: 0.468744)

Control

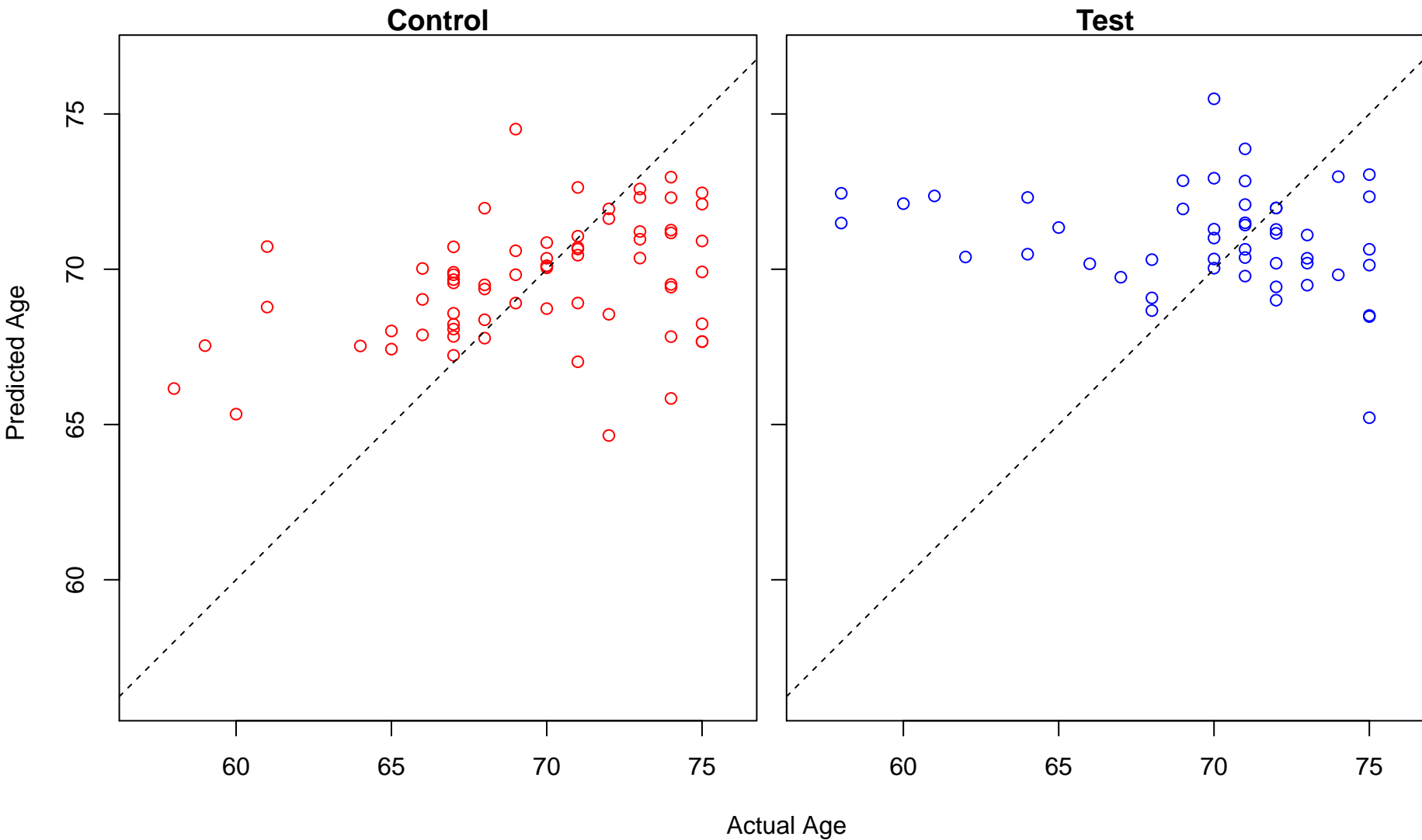


Test



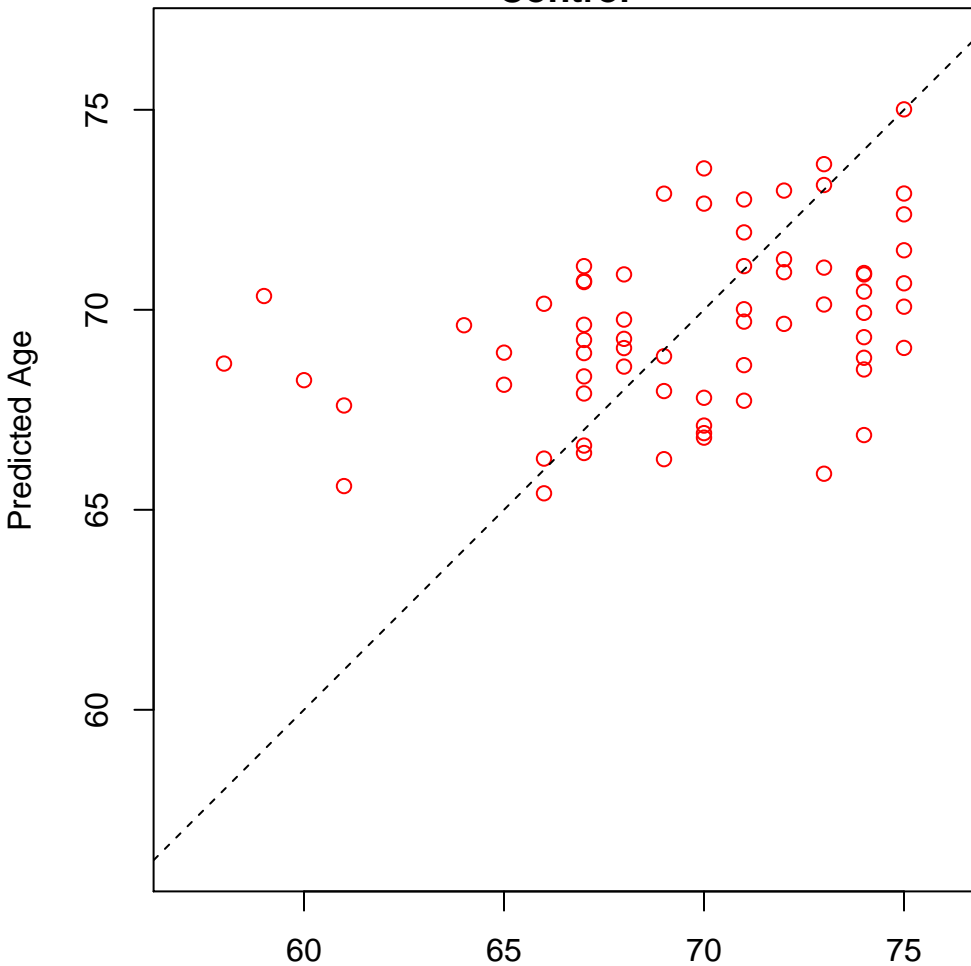
Actual Age

manganese ion transport (Score: 0.468738)

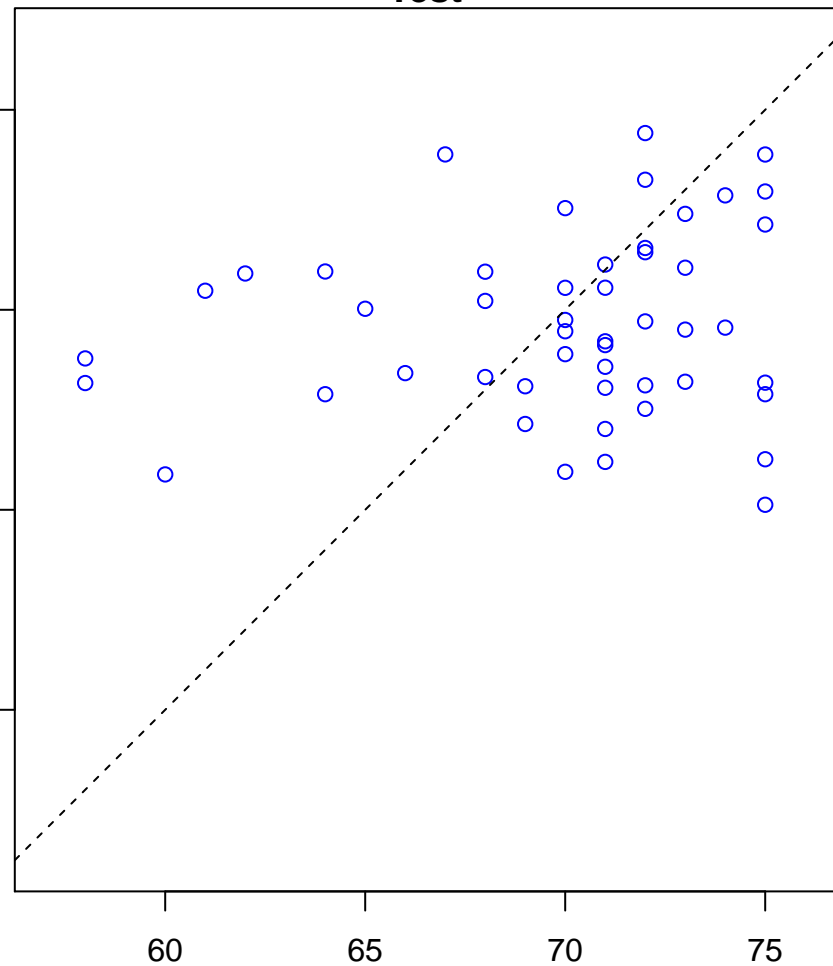


mitochondrial DNA metabolic process (Score: 0.468668)

Control

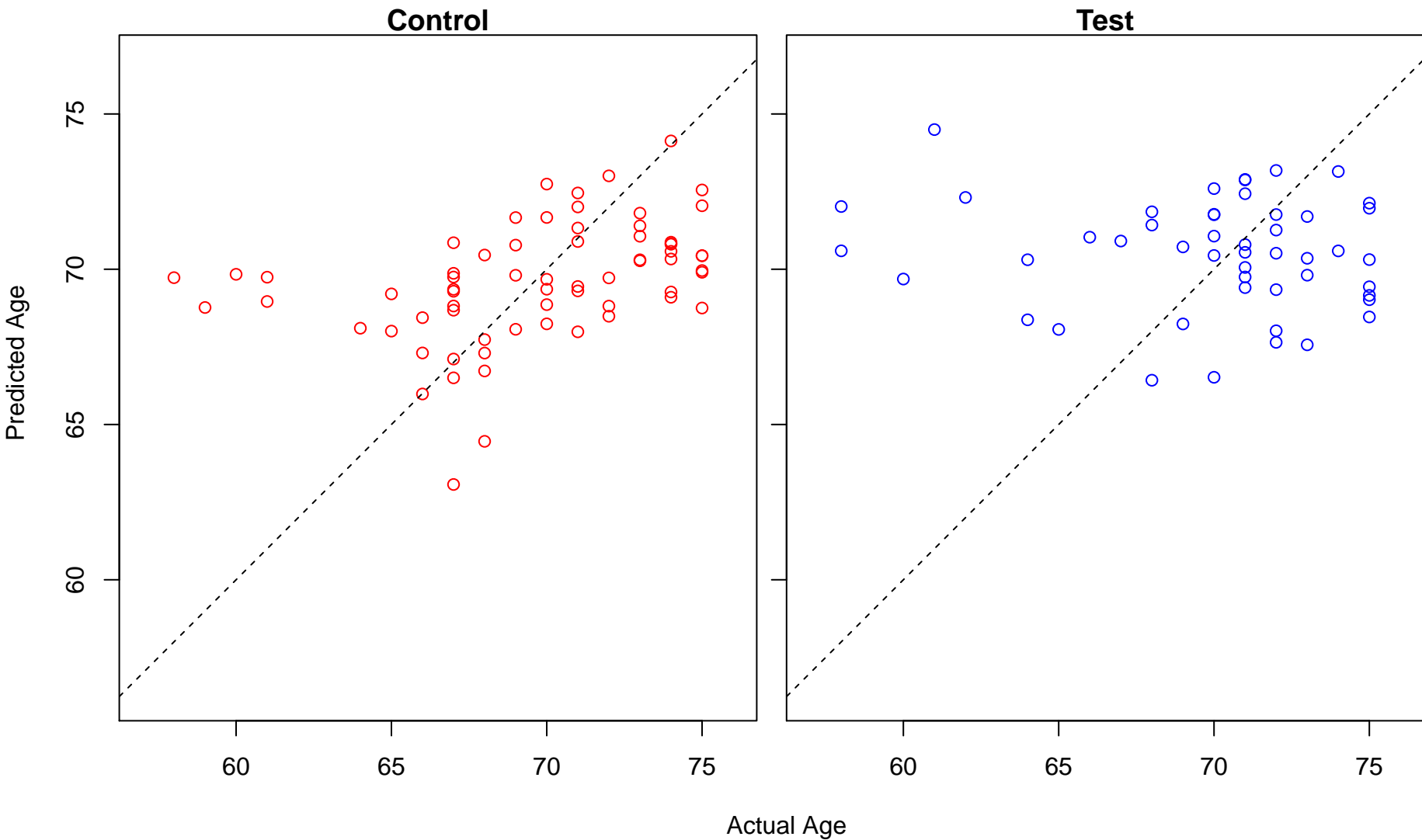


Test

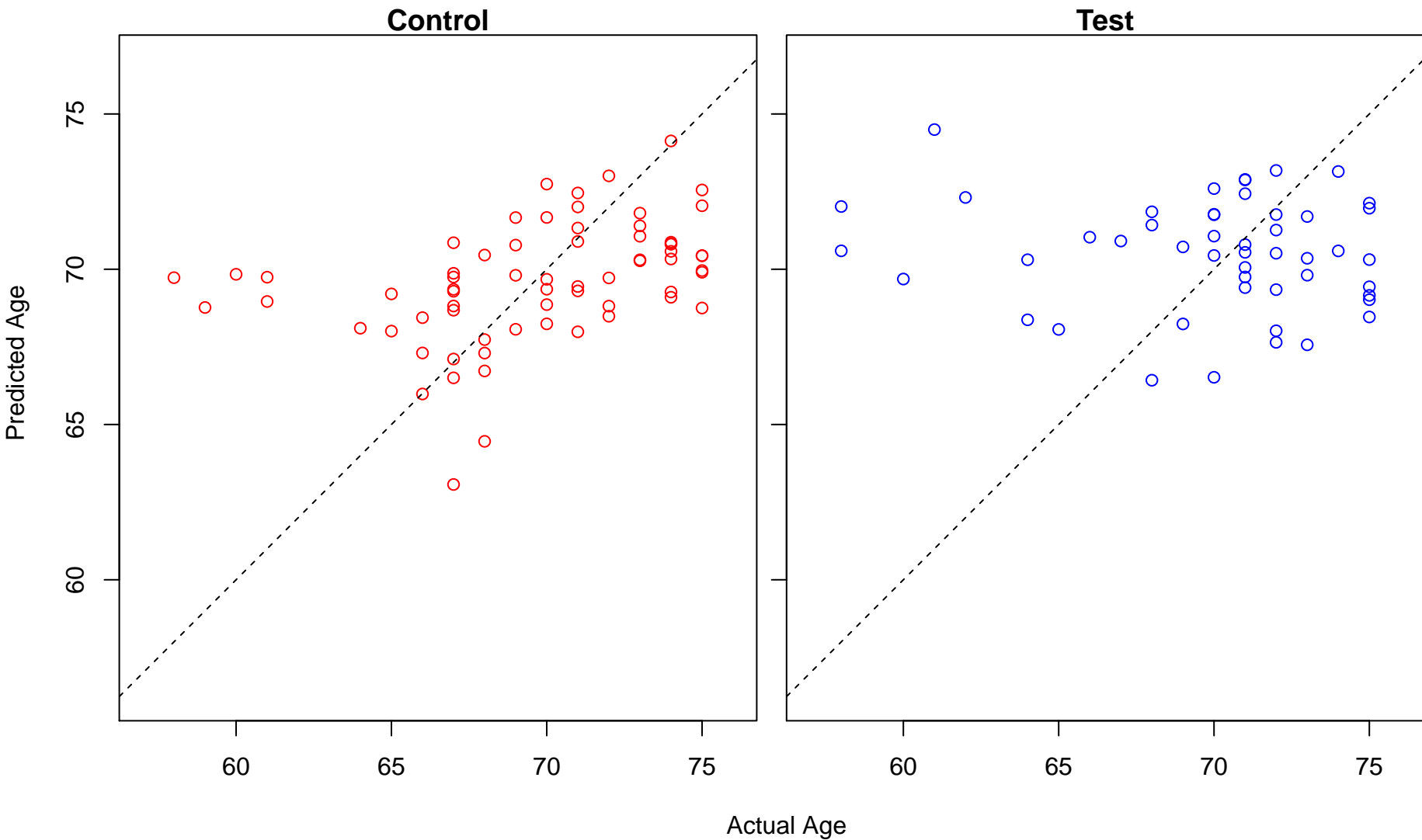


Actual Age

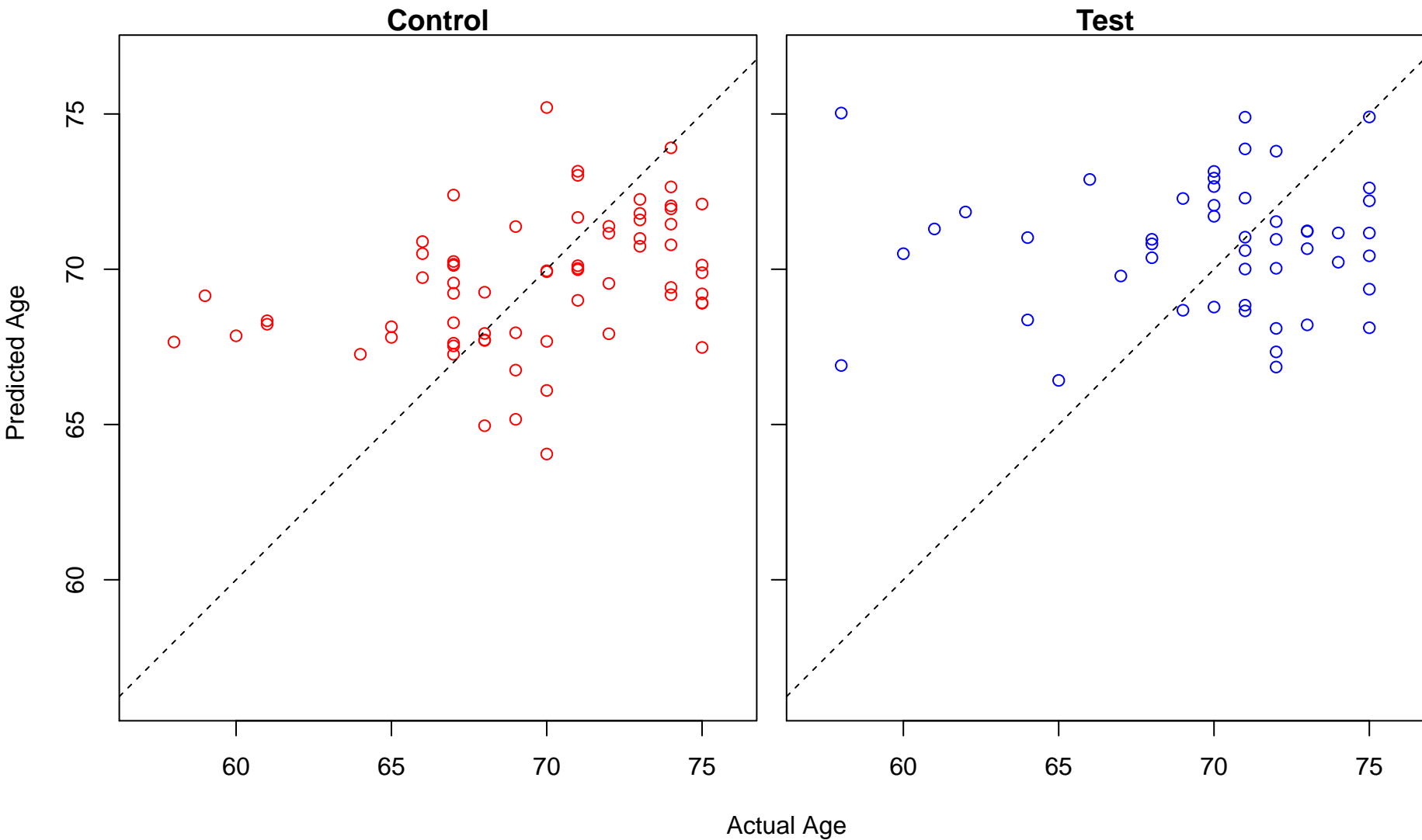
cholesterol catabolic process (Score: 0.468439)



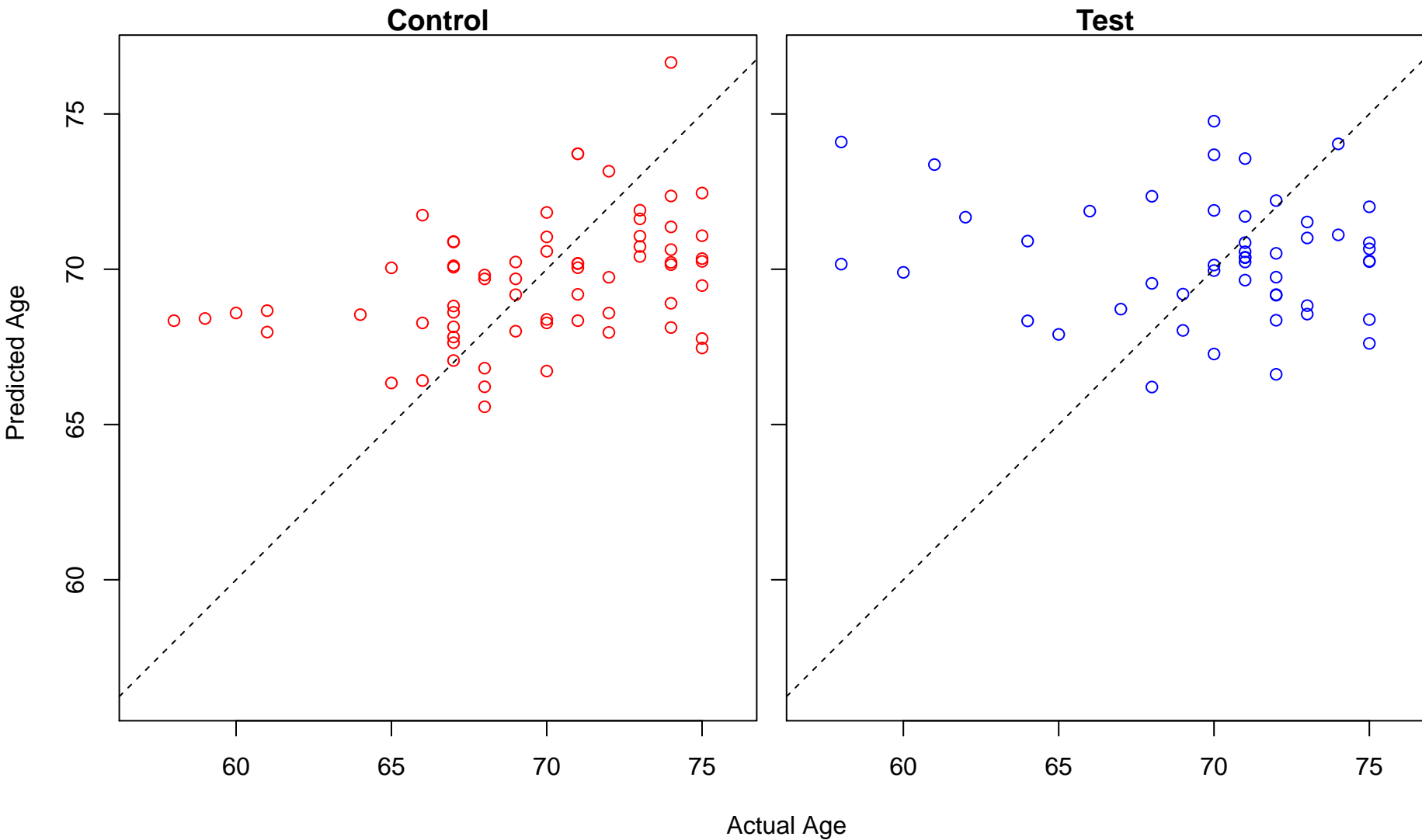
sterol catabolic process (Score: 0.468439)



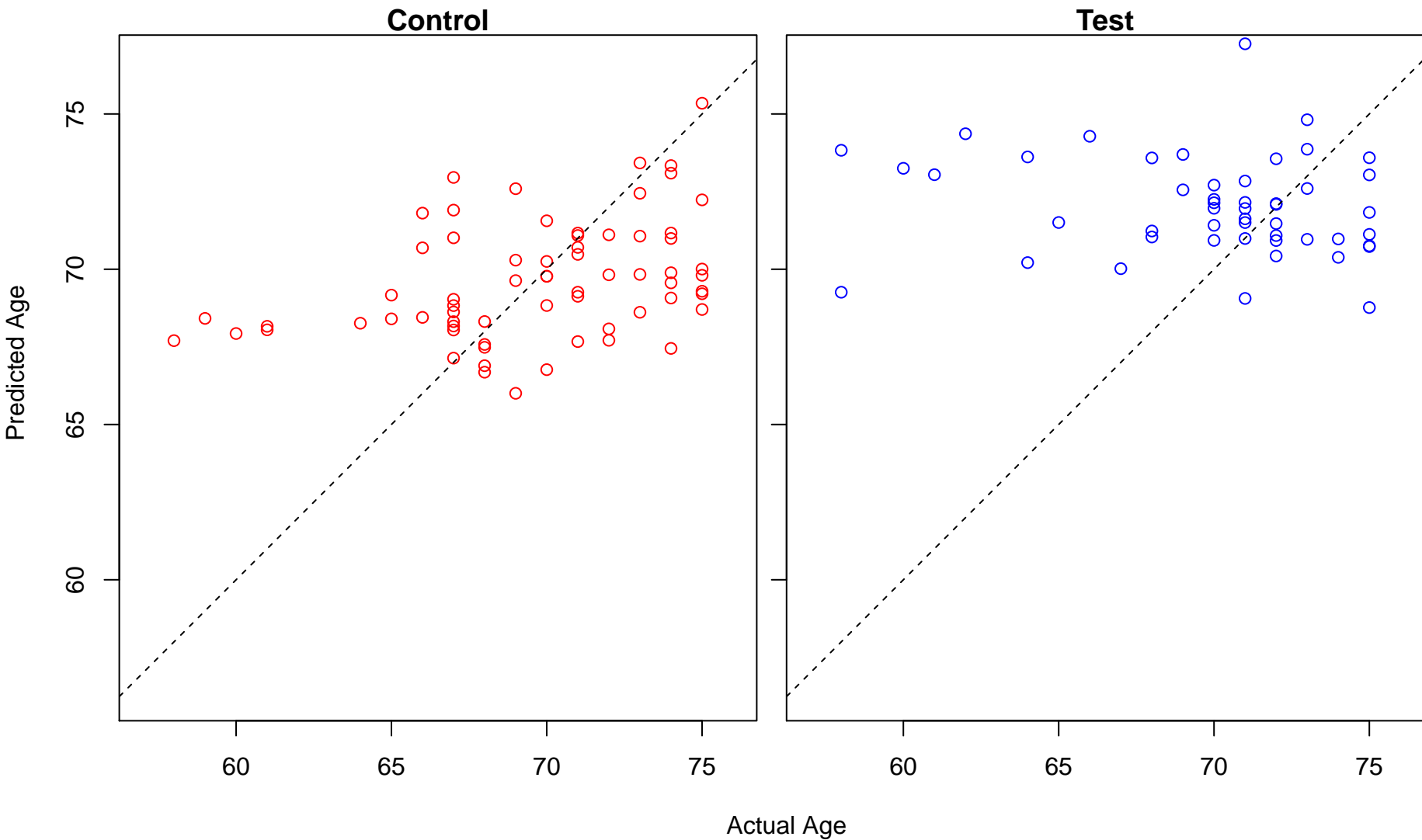
regulation of platelet aggregation (Score: 0.467973)



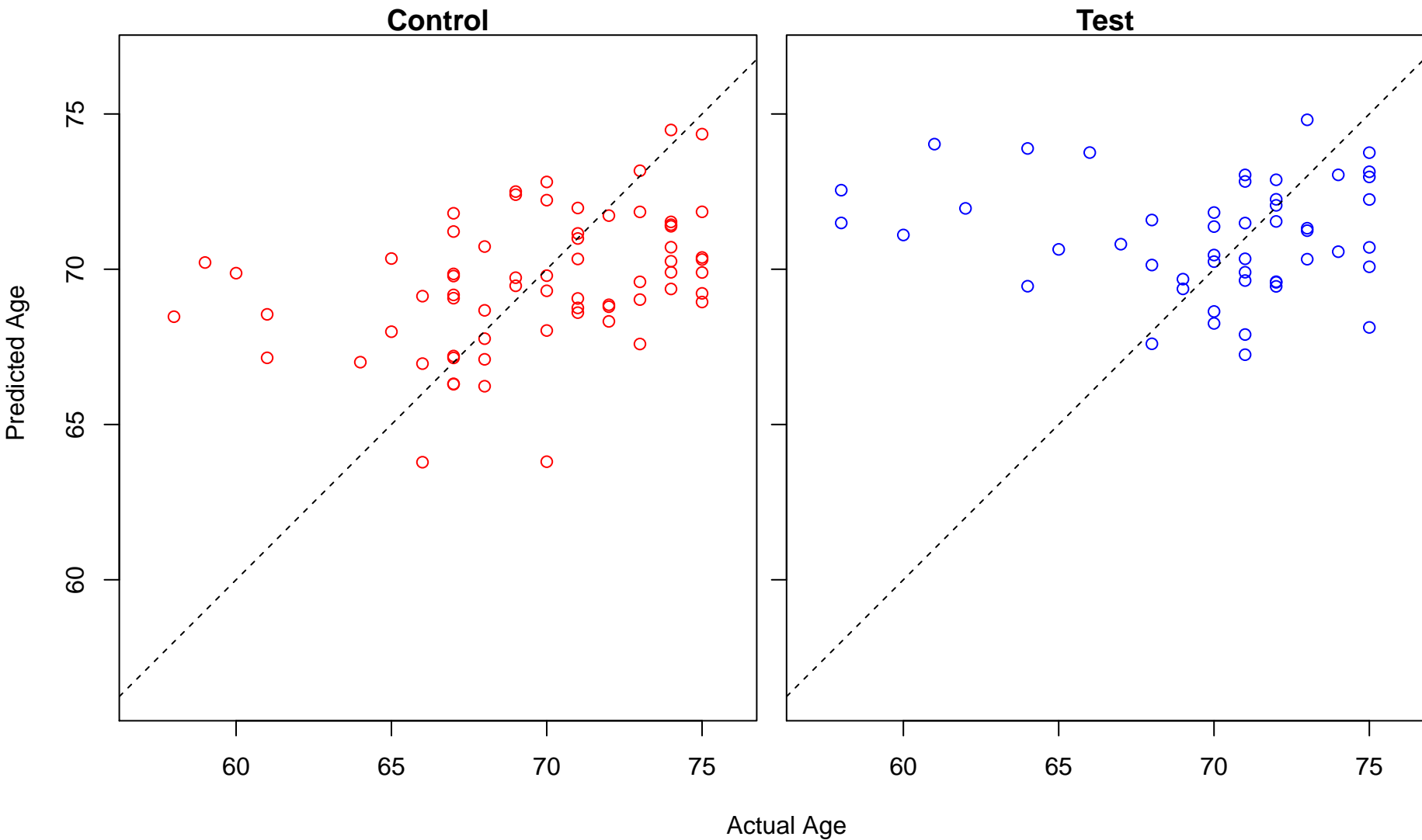
carbon catabolite regulation of transcription (Score: 0.467830)



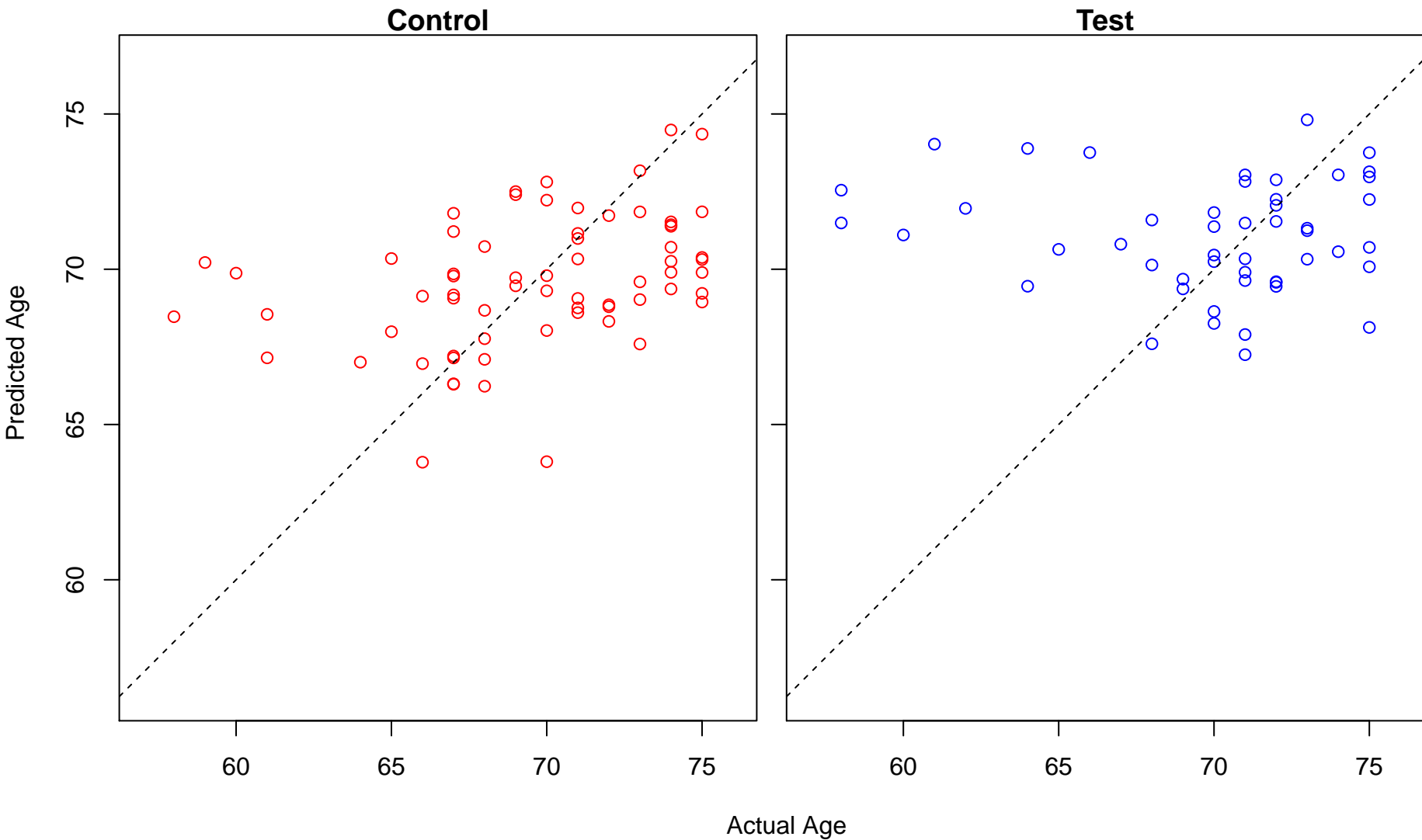
hair cell differentiation (Score: 0.467723)



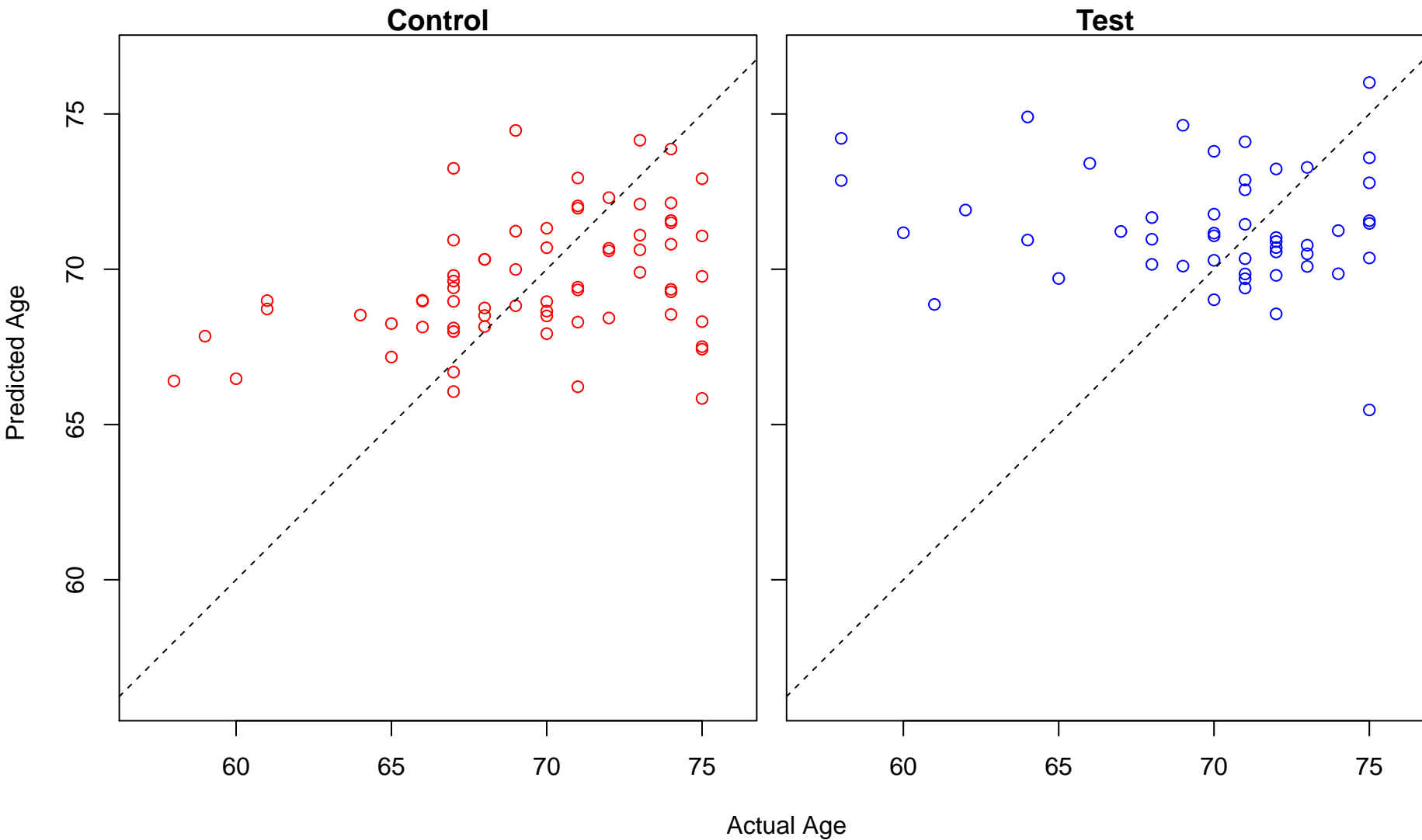
glutathione biosynthetic process (Score: 0.467258)



nonribosomal peptide biosynthetic process (Score: 0.467258)

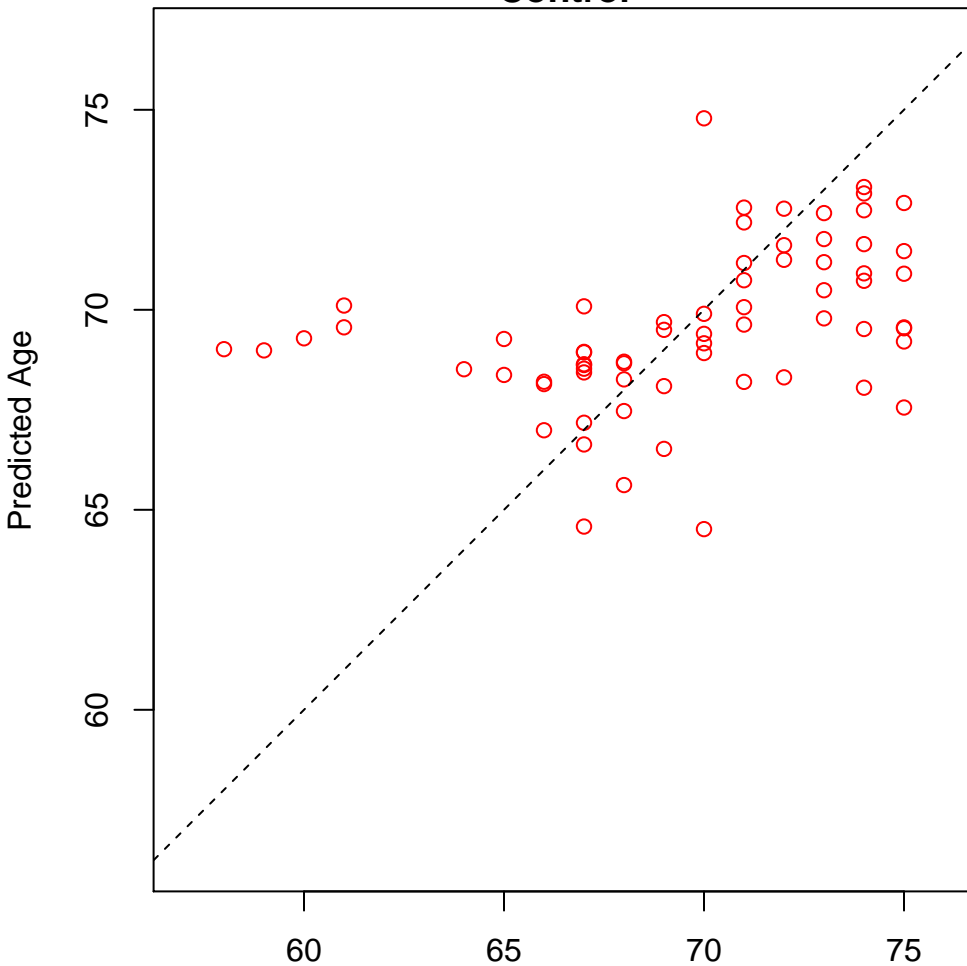


4-hydroxyproline metabolic process (Score: 0.466897)

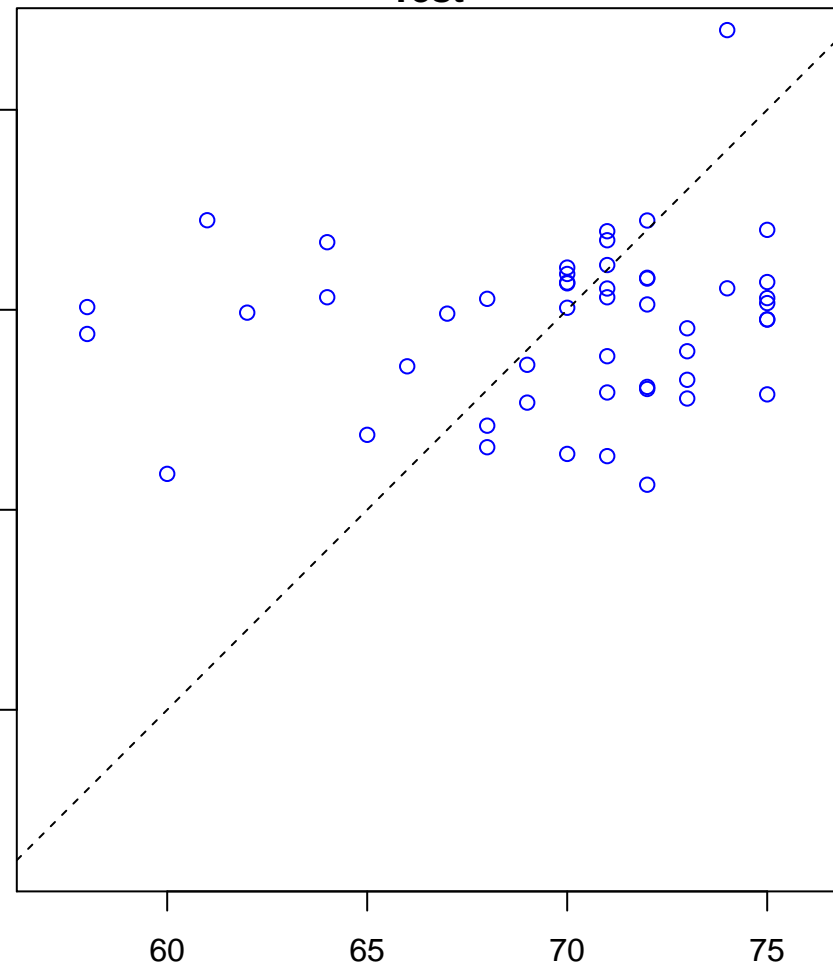


embryonic digestive tract development (Score: 0.466875)

Control

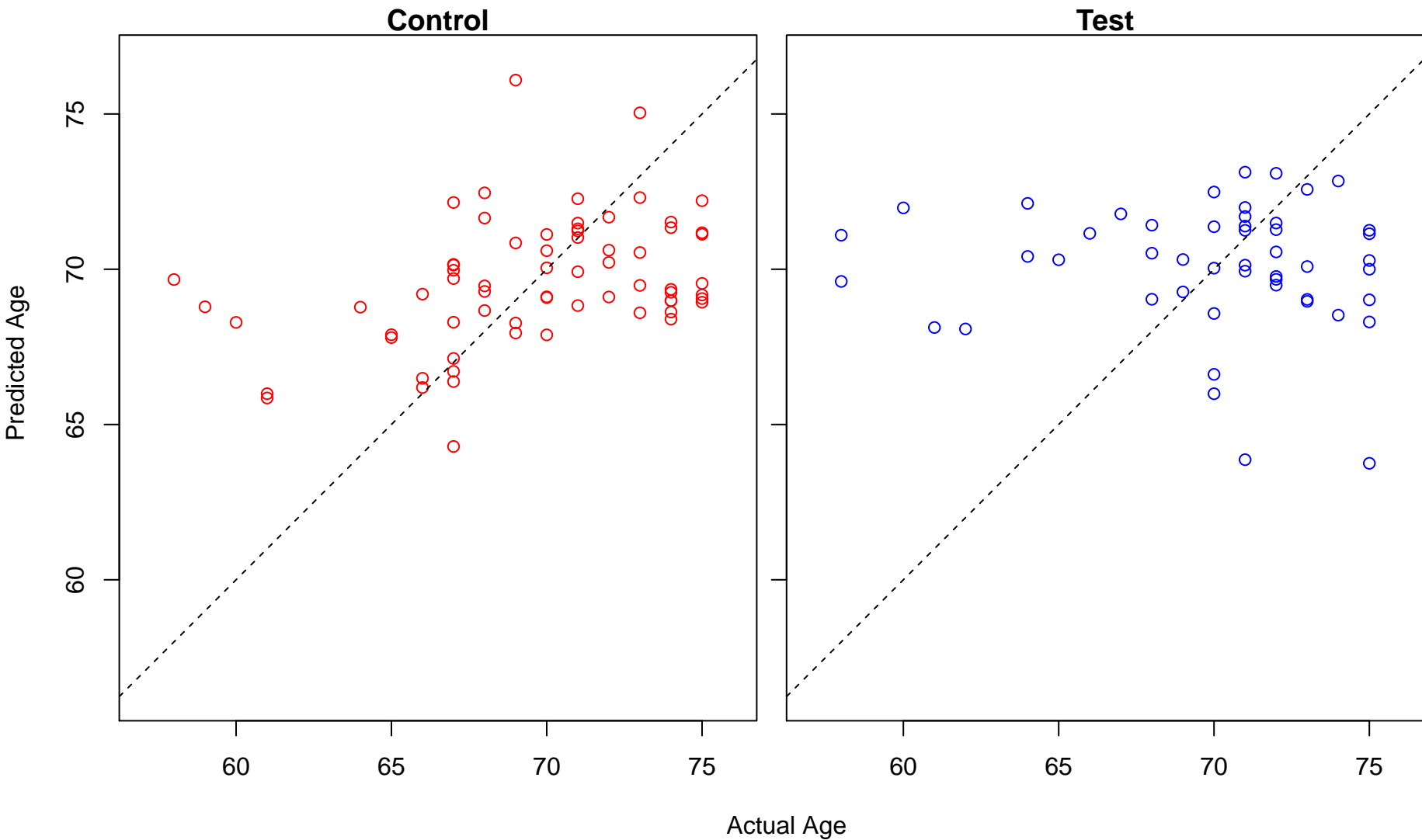


Test



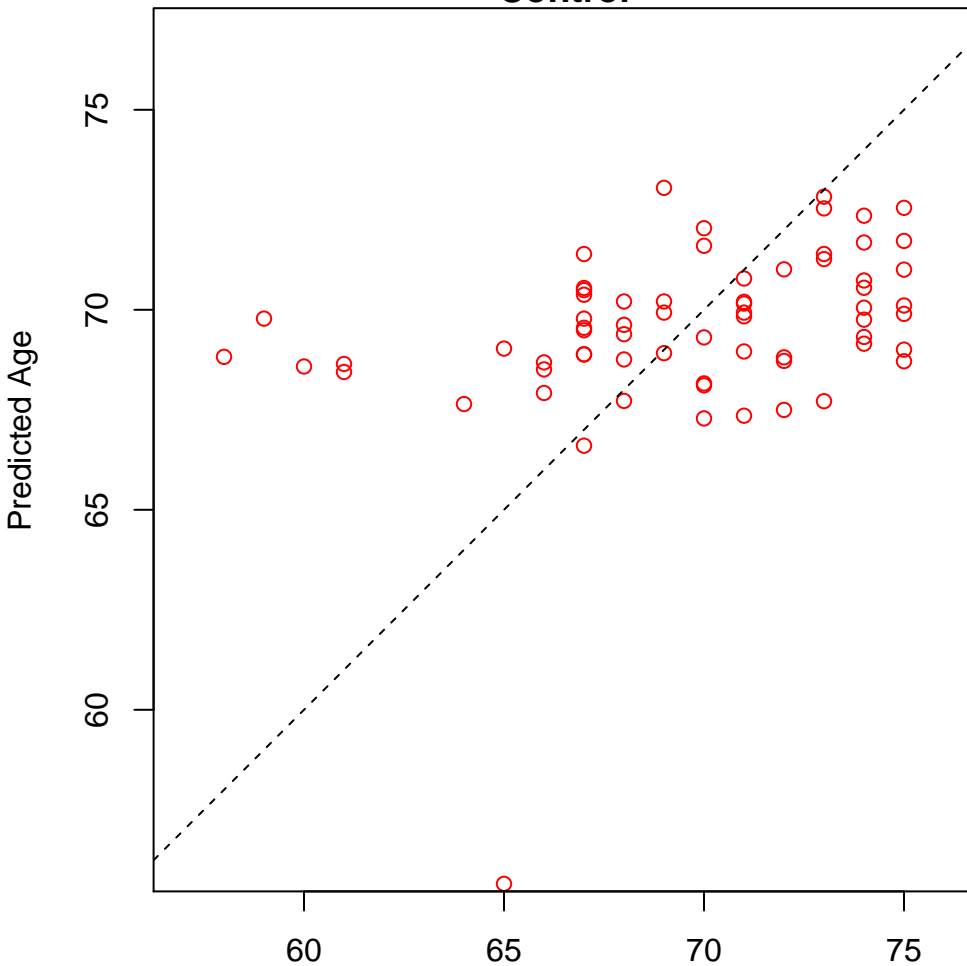
Actual Age

camera-type eye photoreceptor cell differentiation (Score: 0.465306)

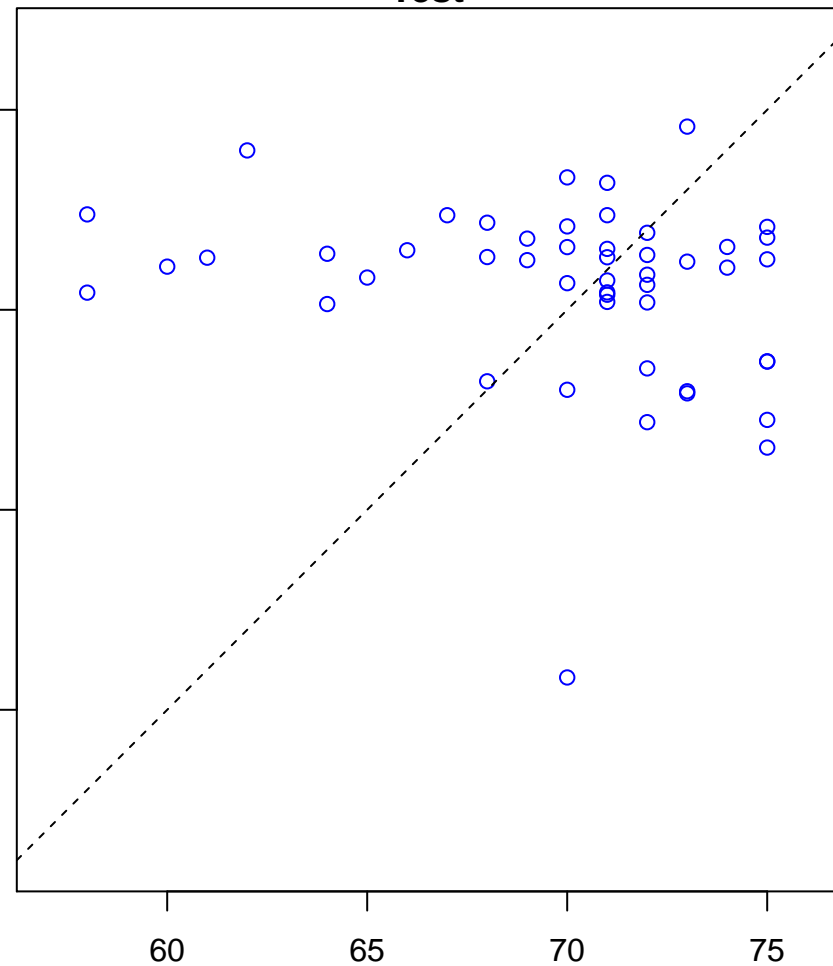


regulation of cAMP-mediated signaling (Score: 0.464505)

Control

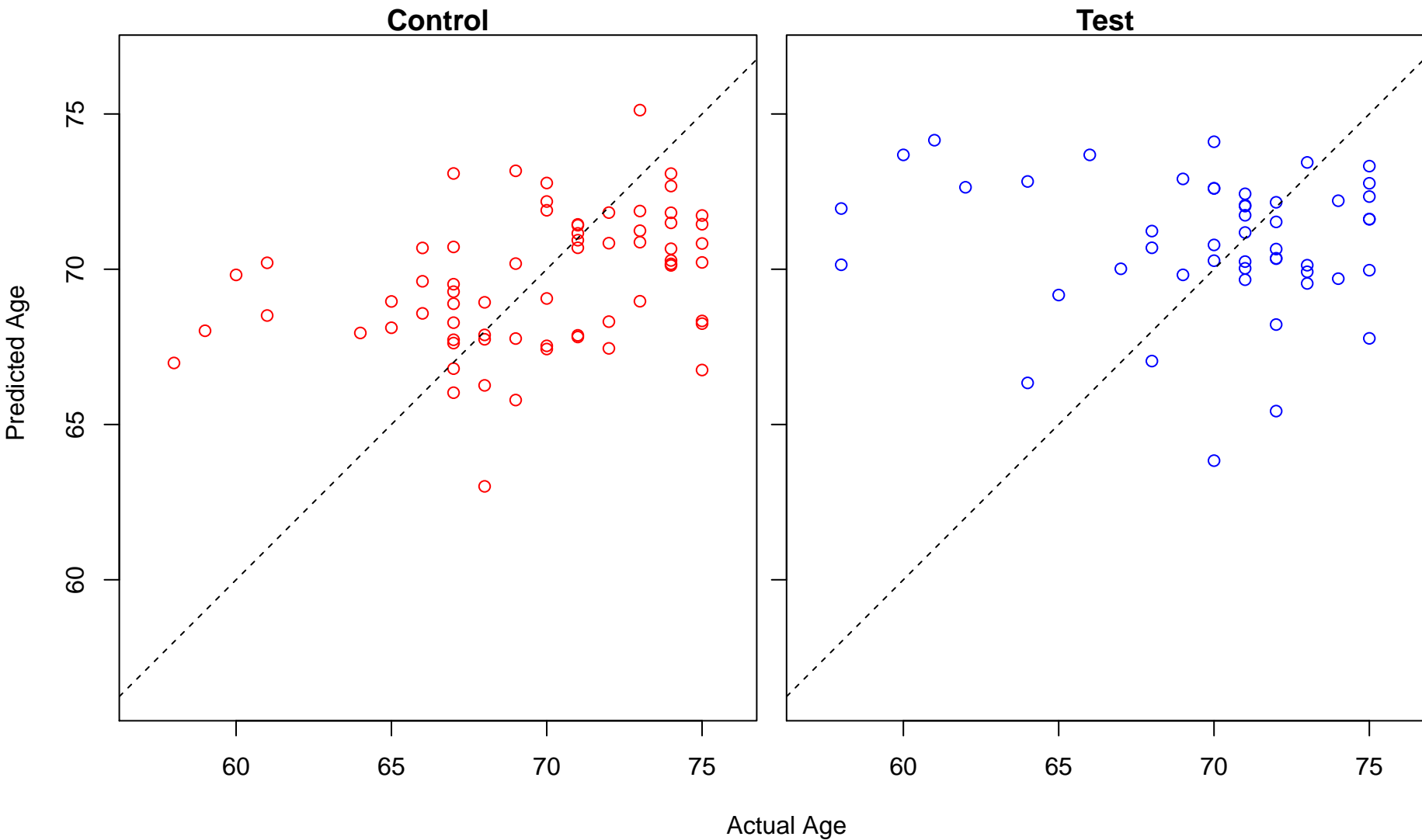


Test

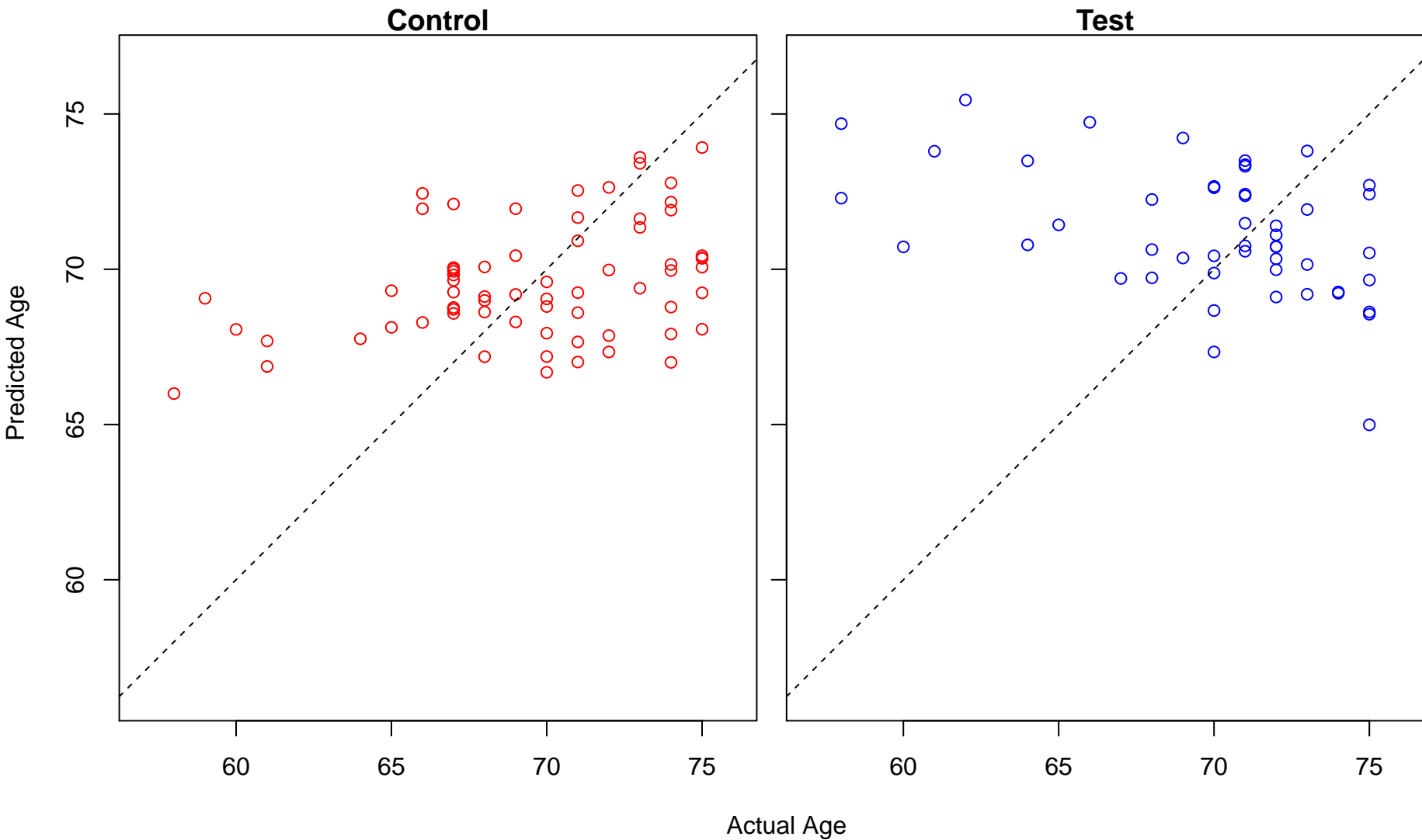


Actual Age

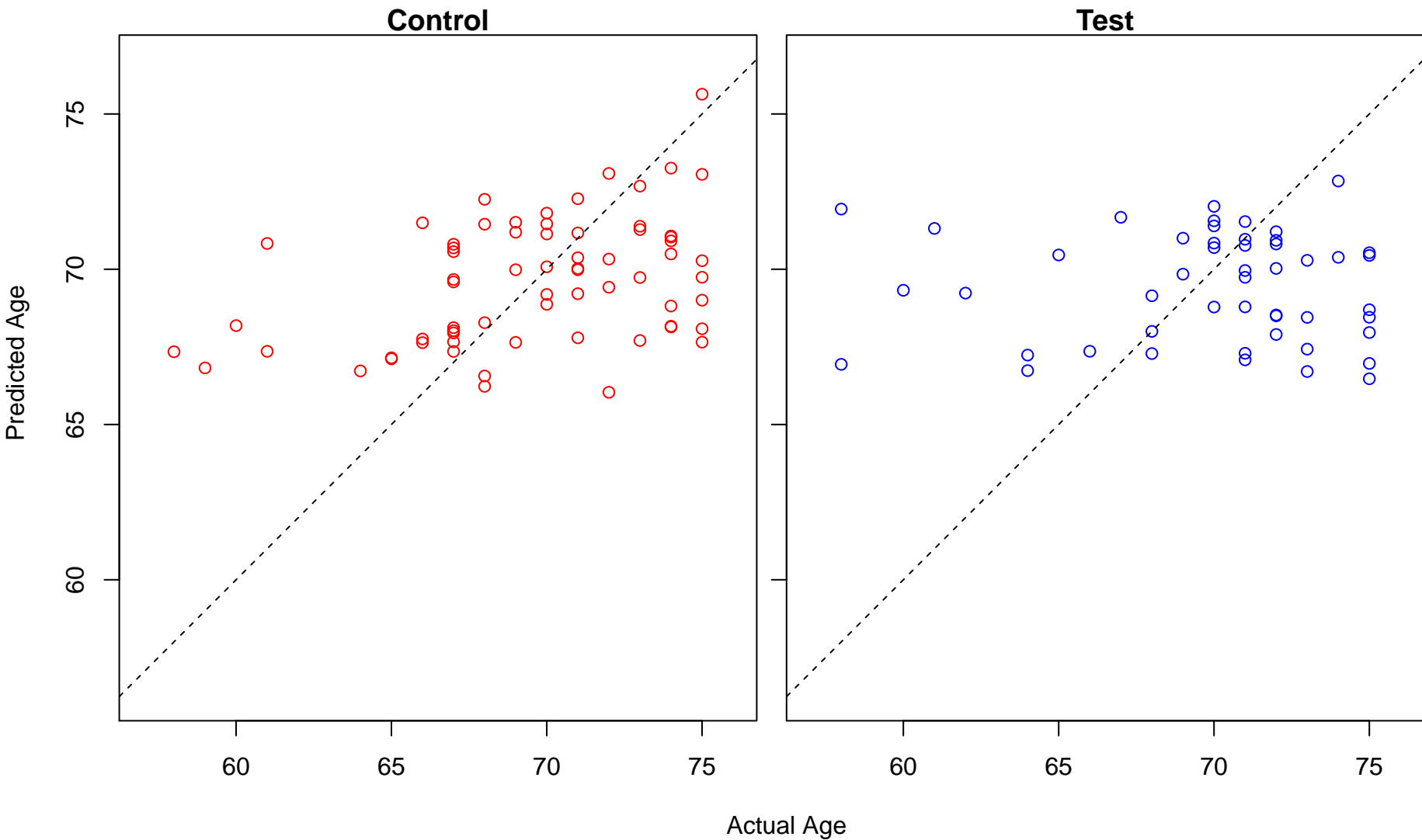
regulation of fatty acid transport (Score: 0.463082)



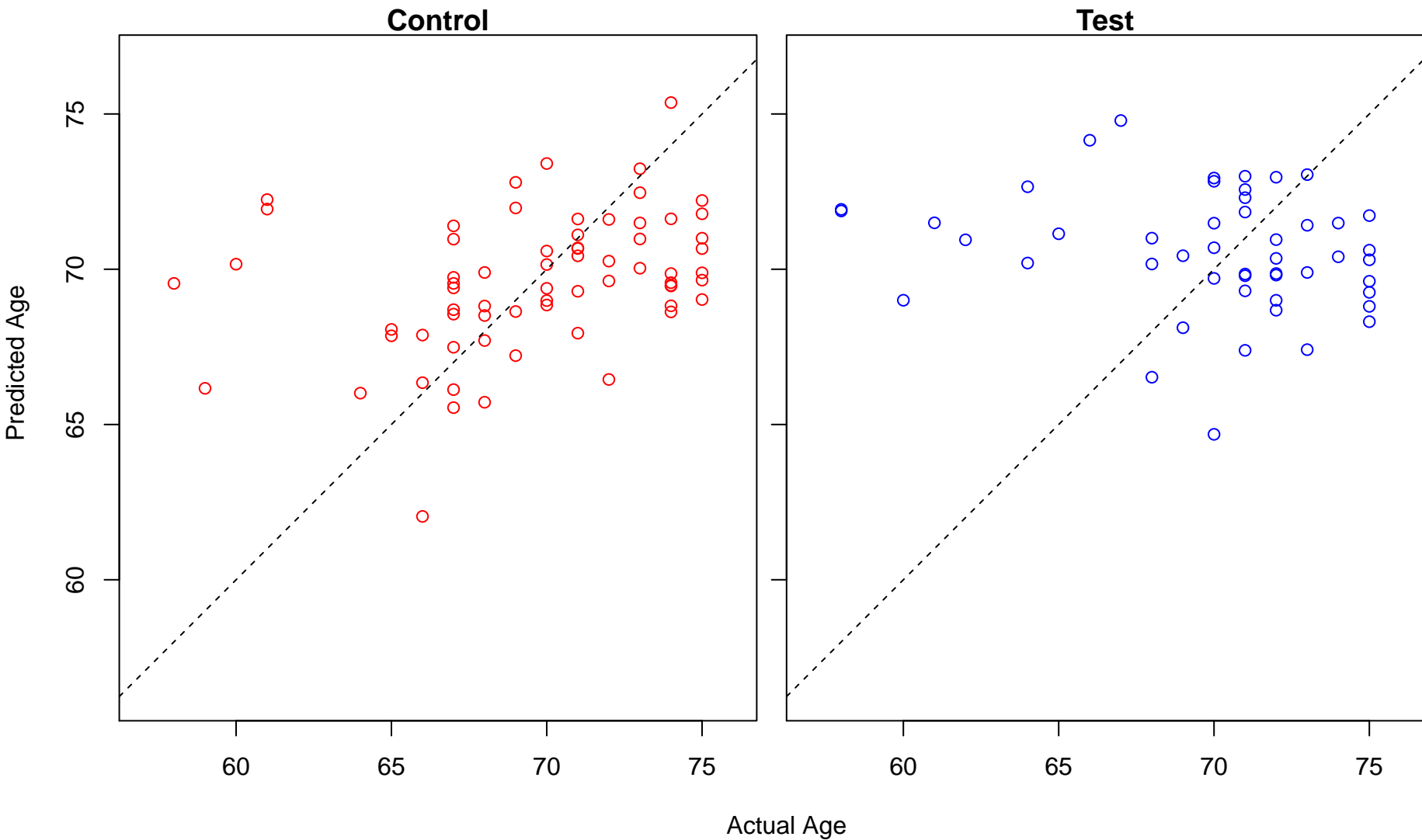
regulation of hippo signaling (Score: 0.462551)



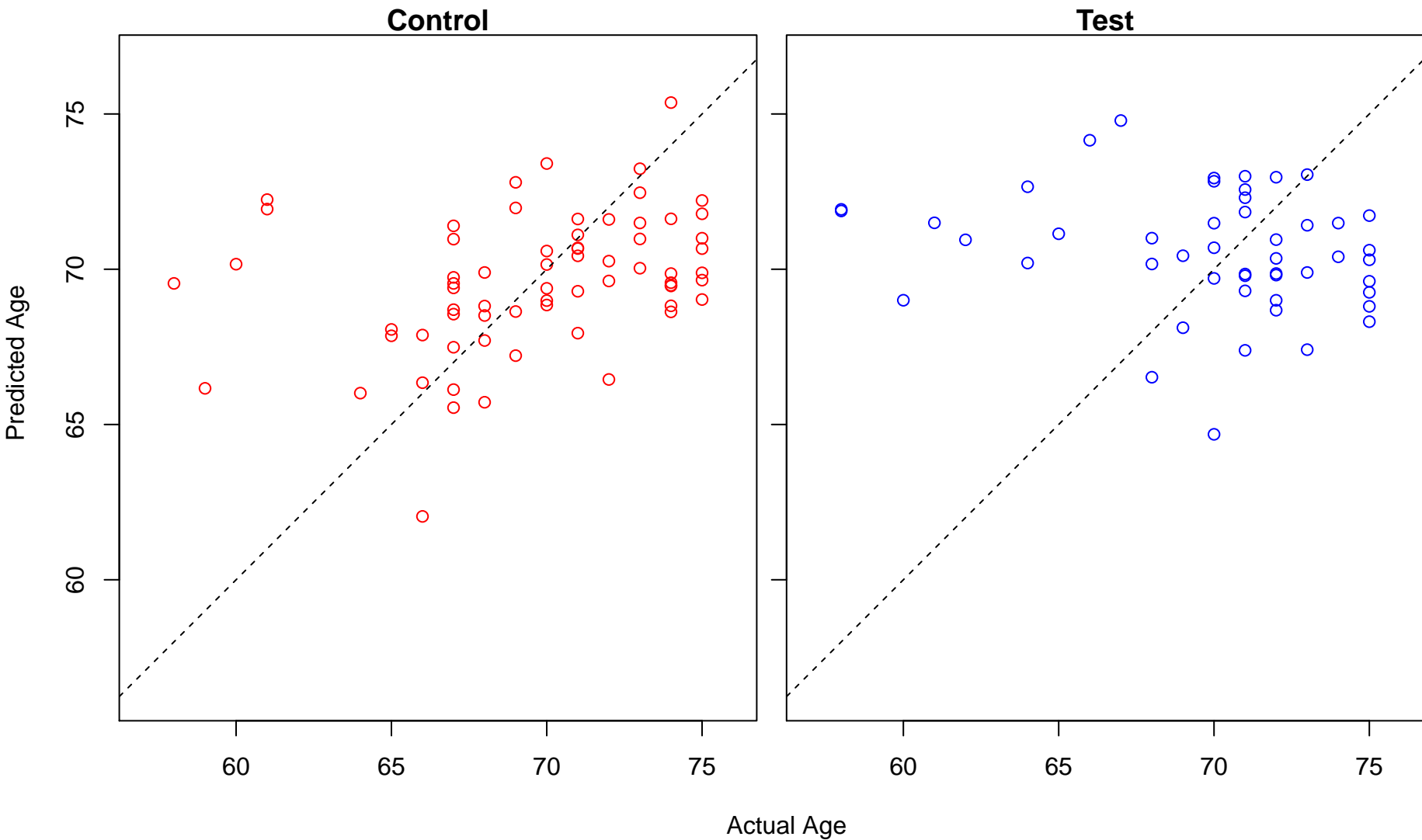
regulation of phosphatidylinositol biosynthetic process (Score: 0.461427)



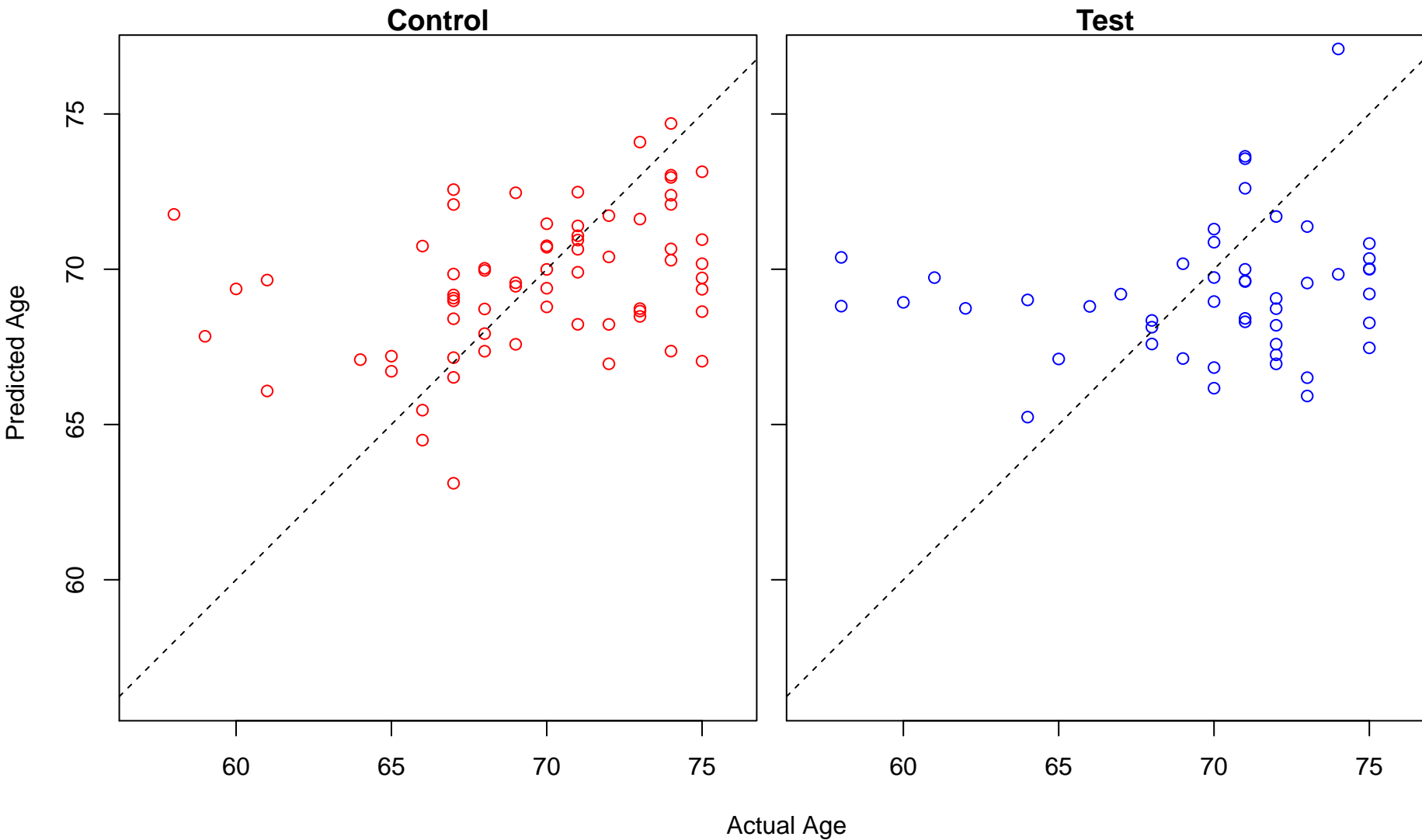
peptide secretion (Score: 0.459062)



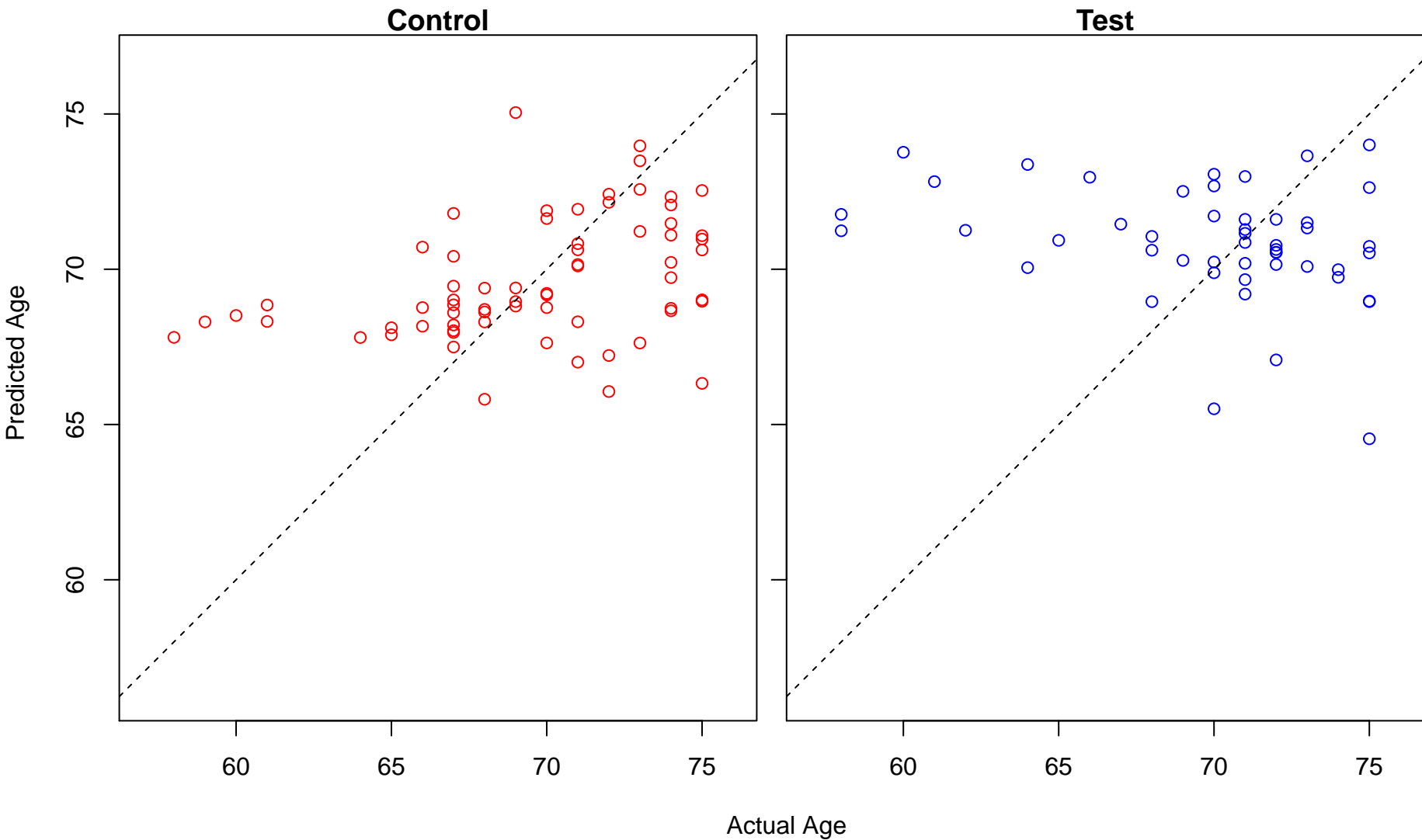
peptide hormone secretion (Score: 0.459062)



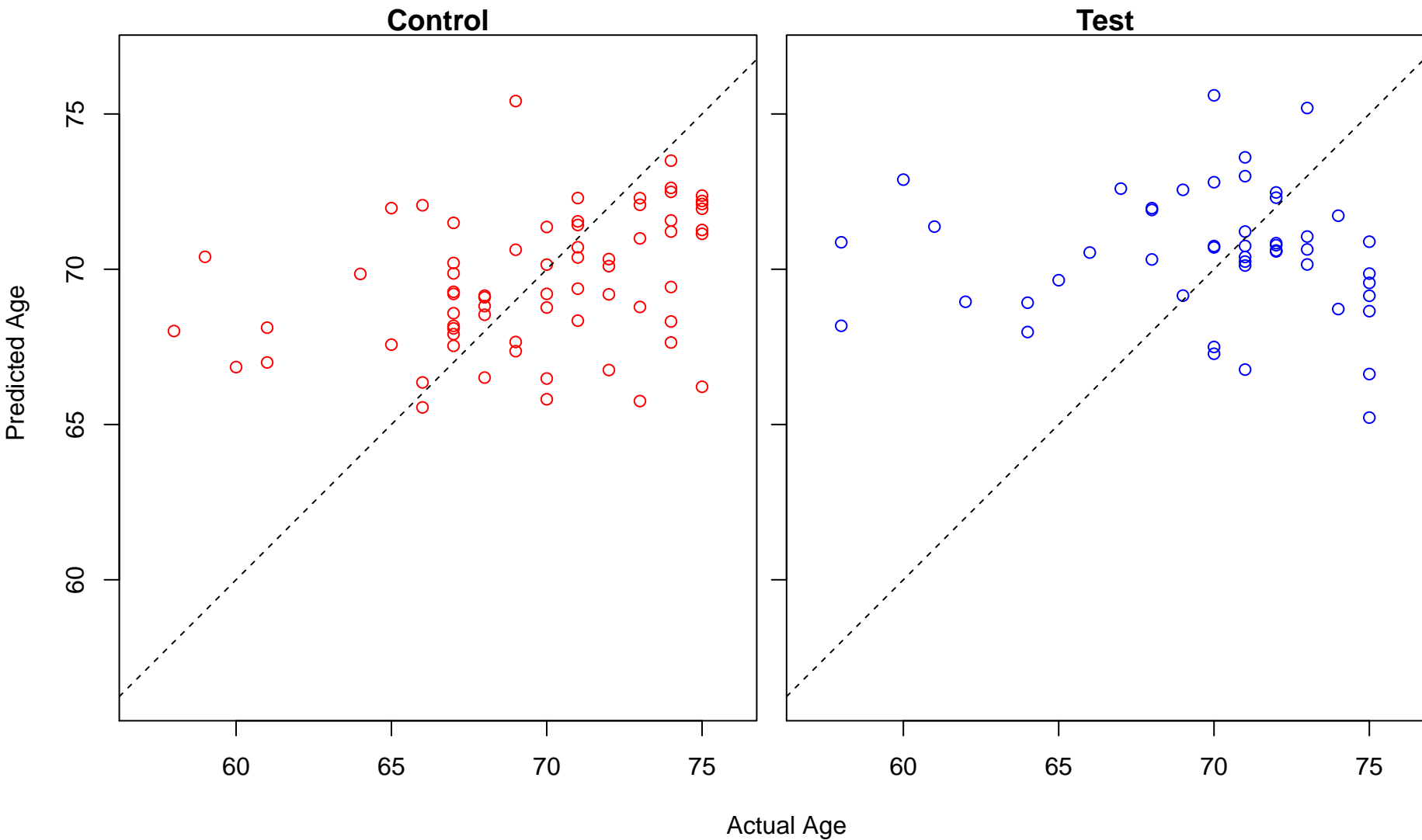
positive regulation of cell fate commitment (Score: 0.458567)



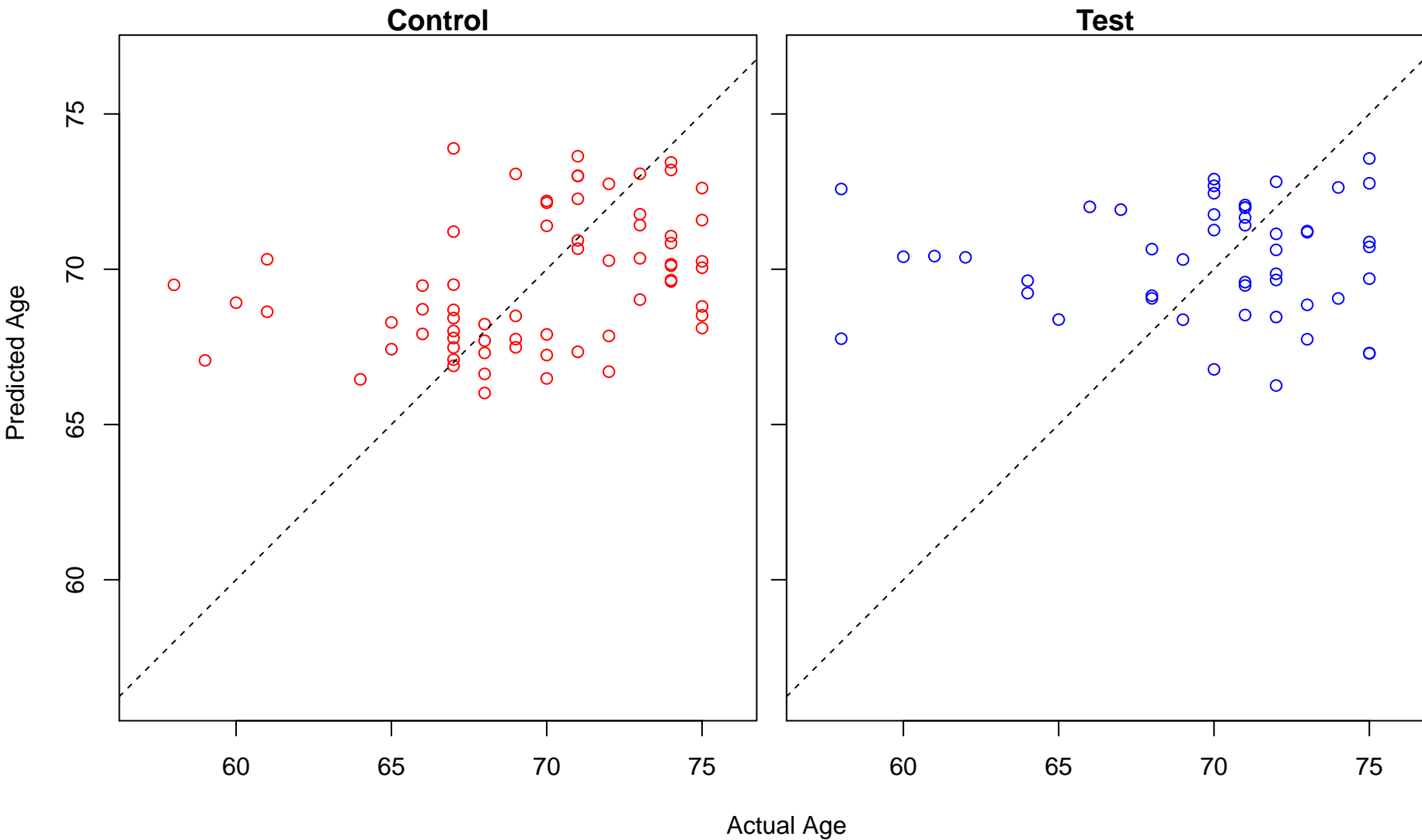
negative regulation of lipid catabolic process (Score: 0.457675)



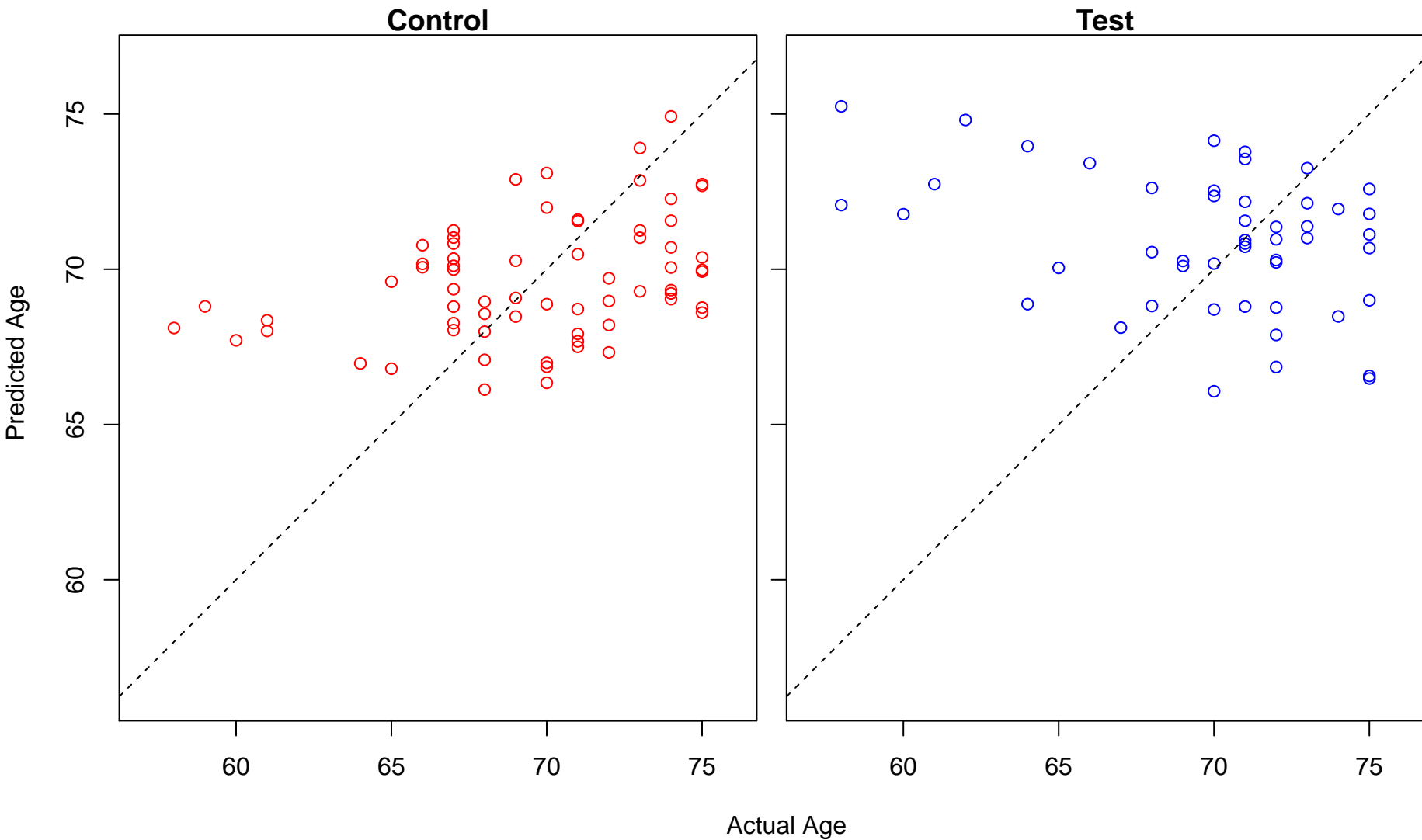
drug transmembrane transport (Score: 0.457653)



mesodermal cell differentiation (Score: 0.457259)

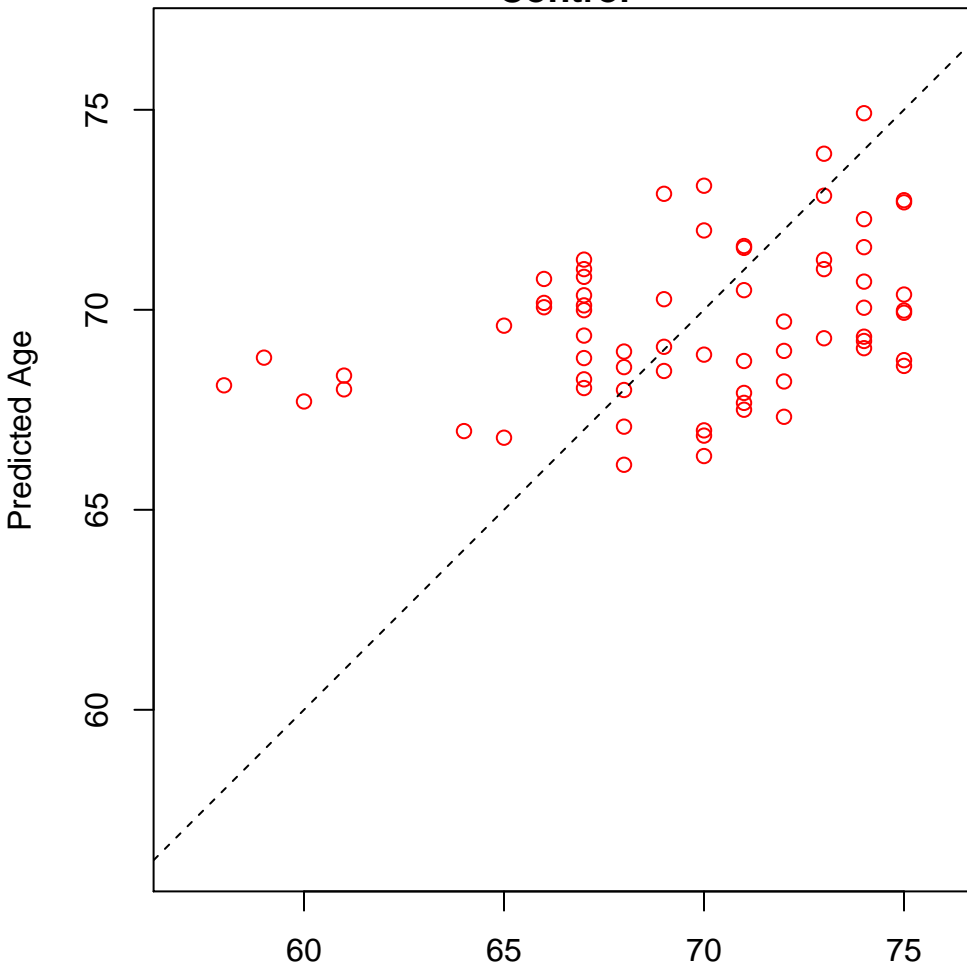


positive regulation of protein processing (Score: 0.456832)

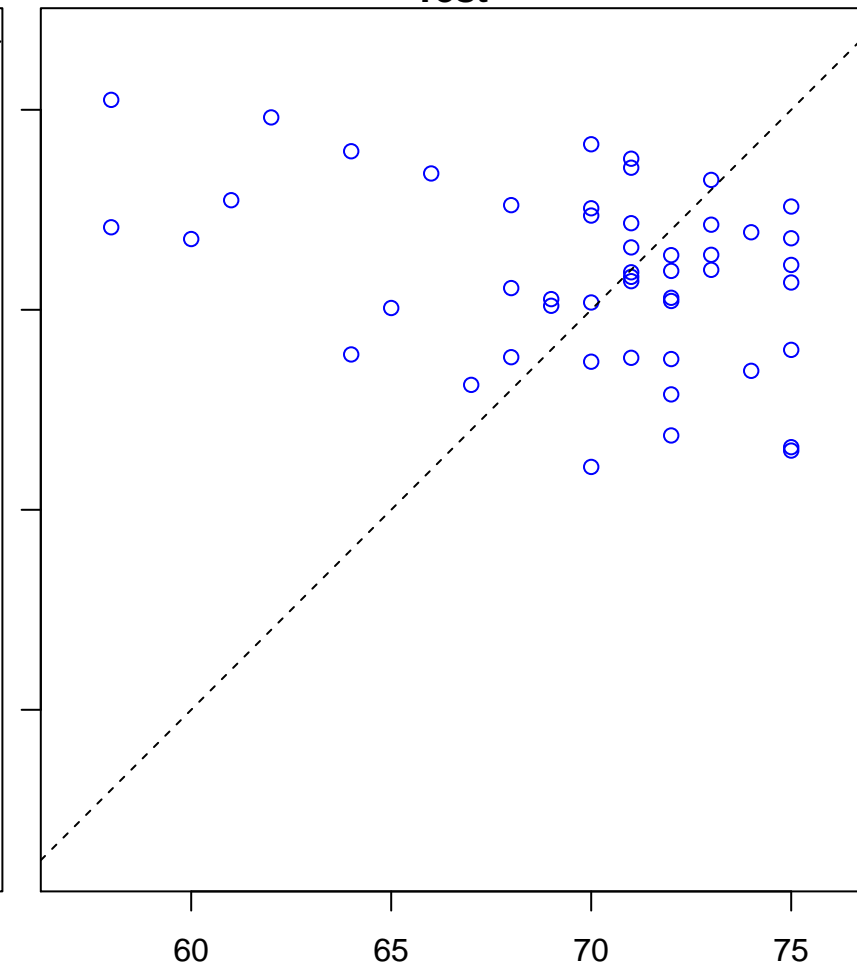


positive regulation of protein maturation (Score: 0.456047)

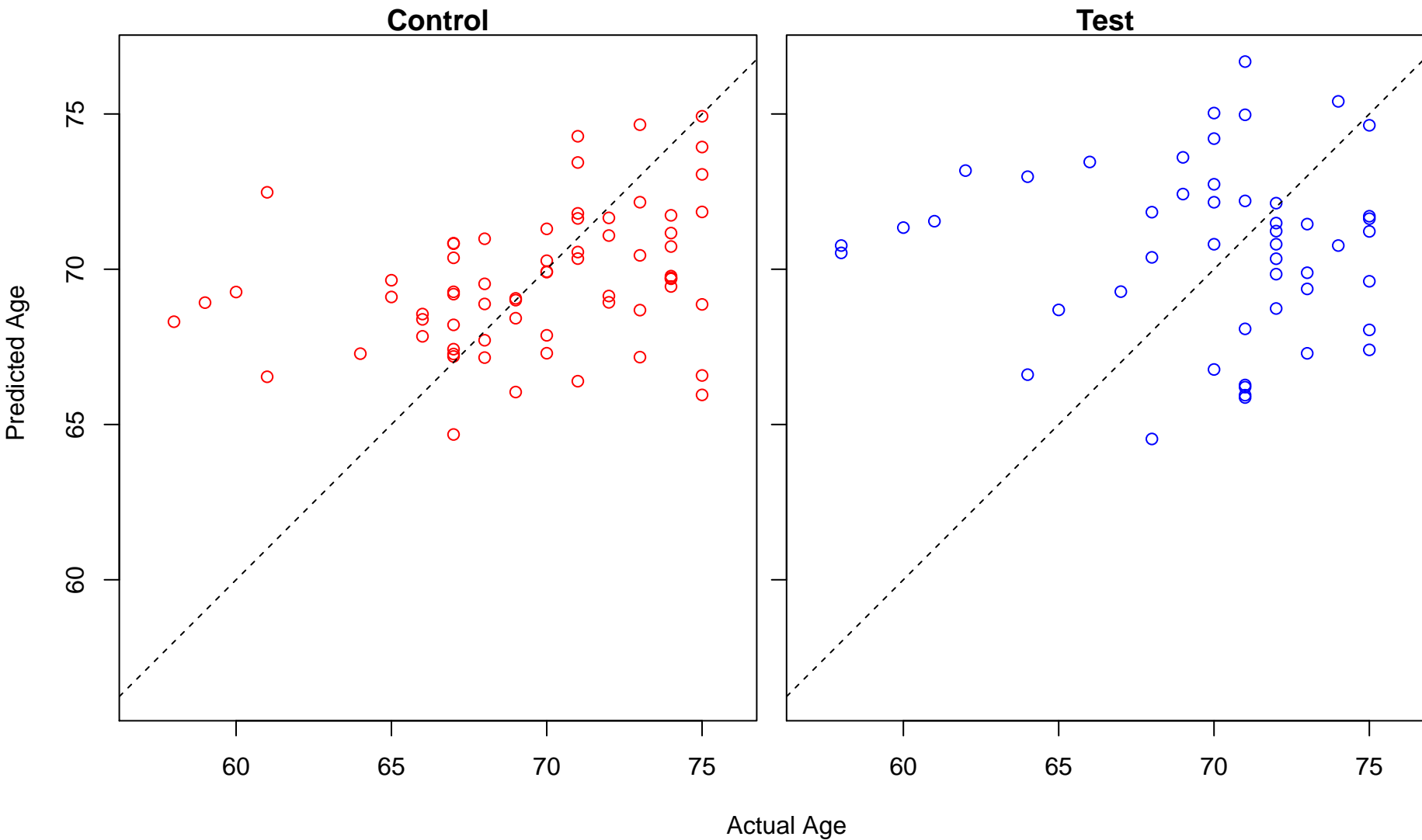
Control



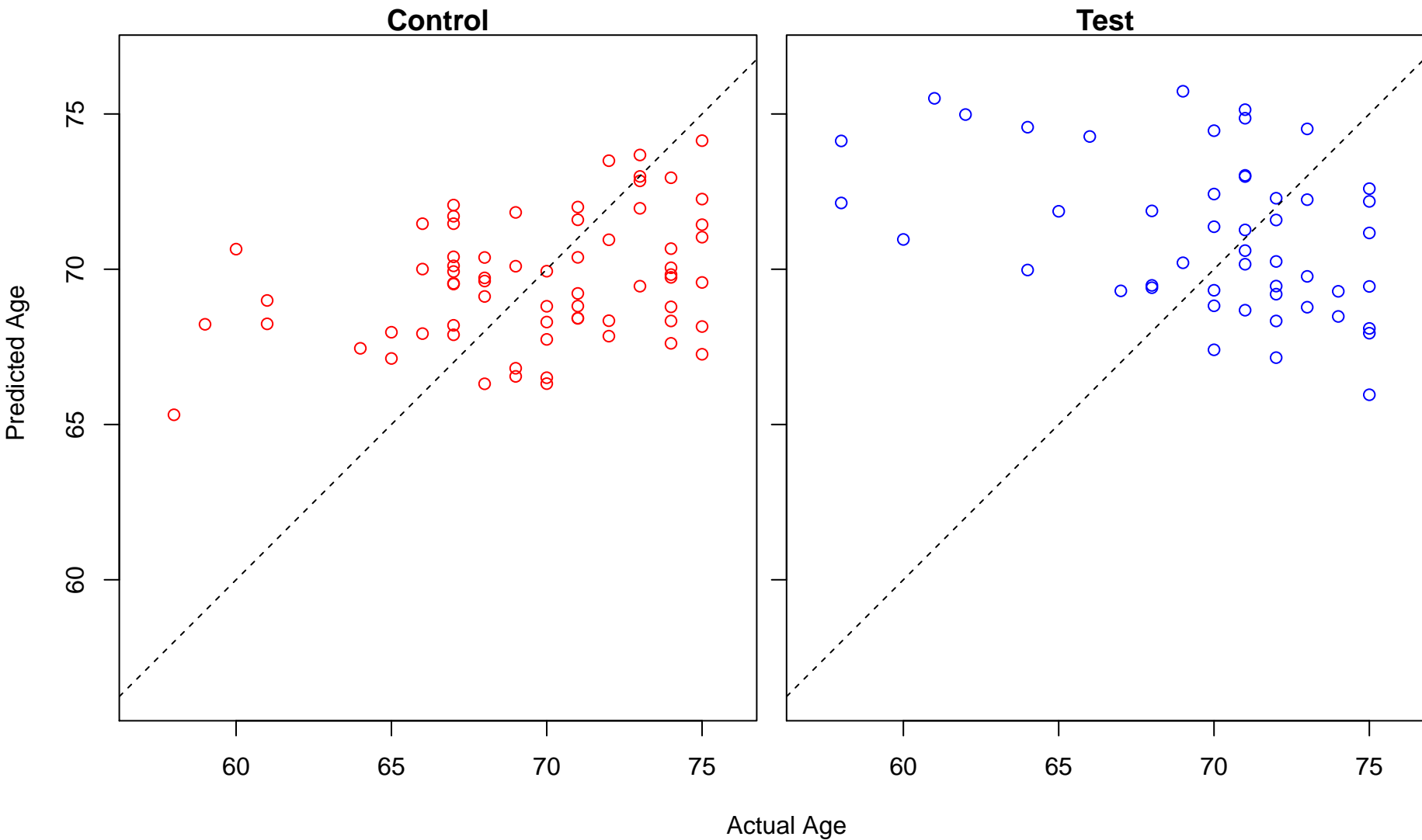
Test



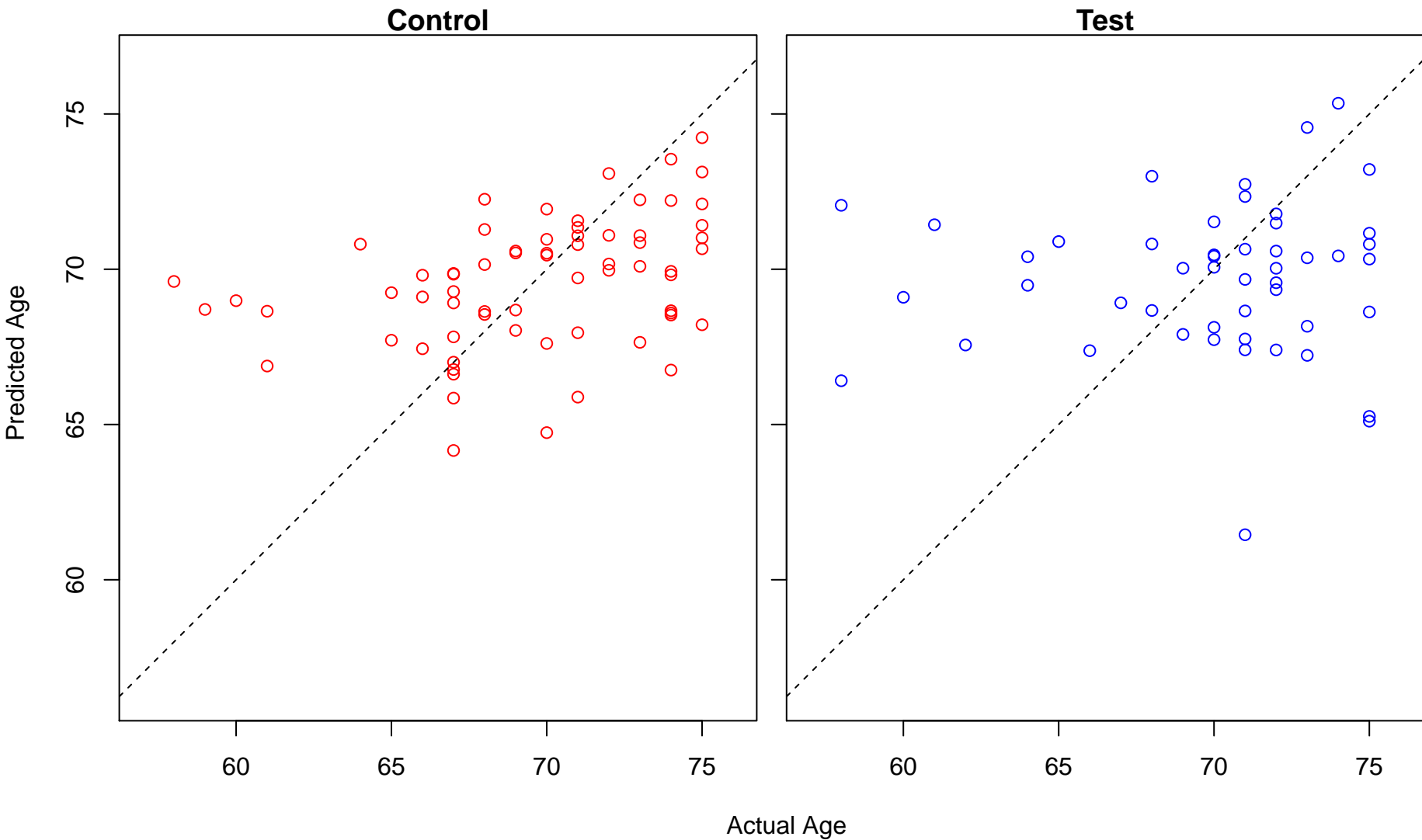
collagen fibril organization (Score: 0.455111)



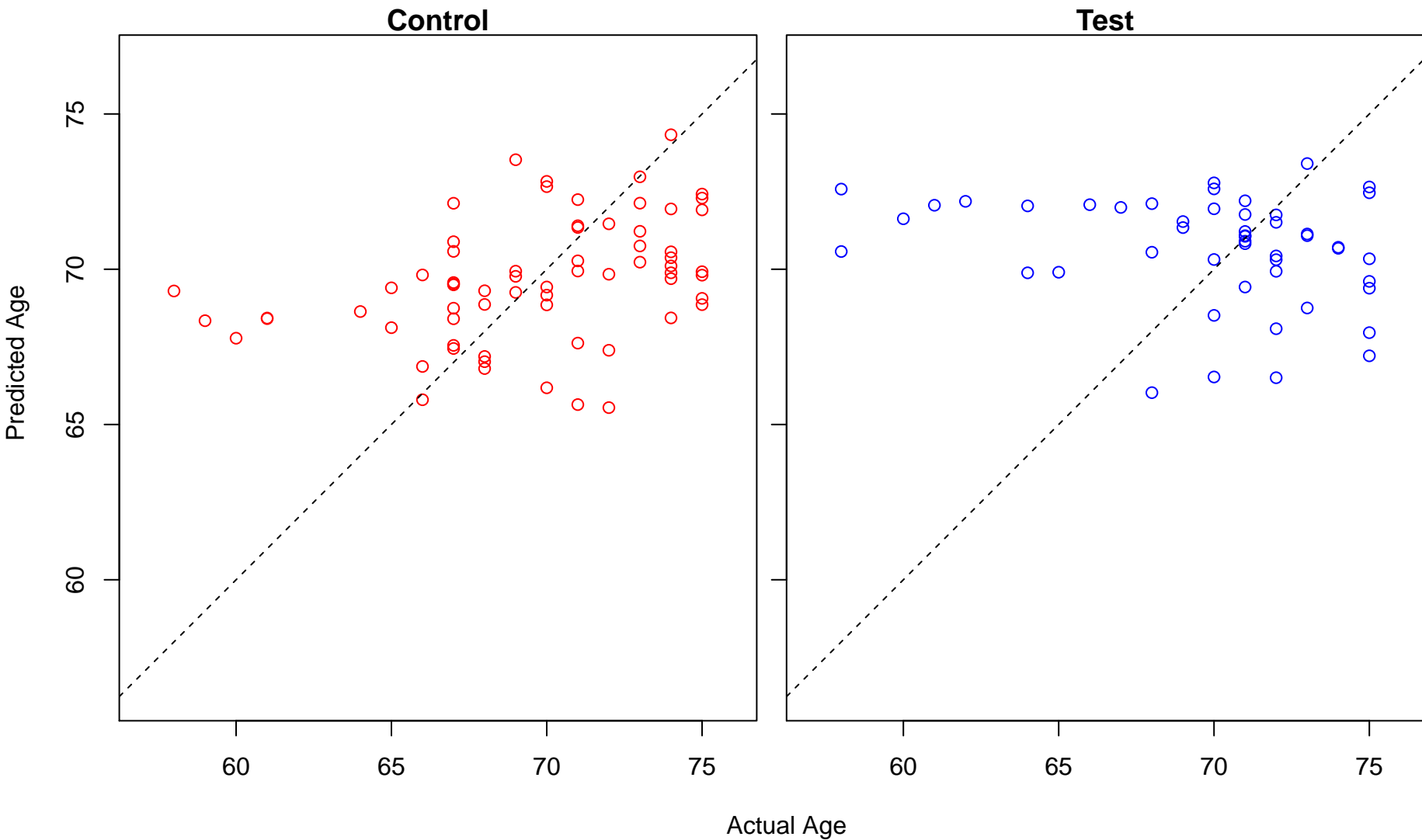
negative regulation of hippo signaling (Score: 0.453664)



SMAD protein complex assembly (Score: 0.453584)

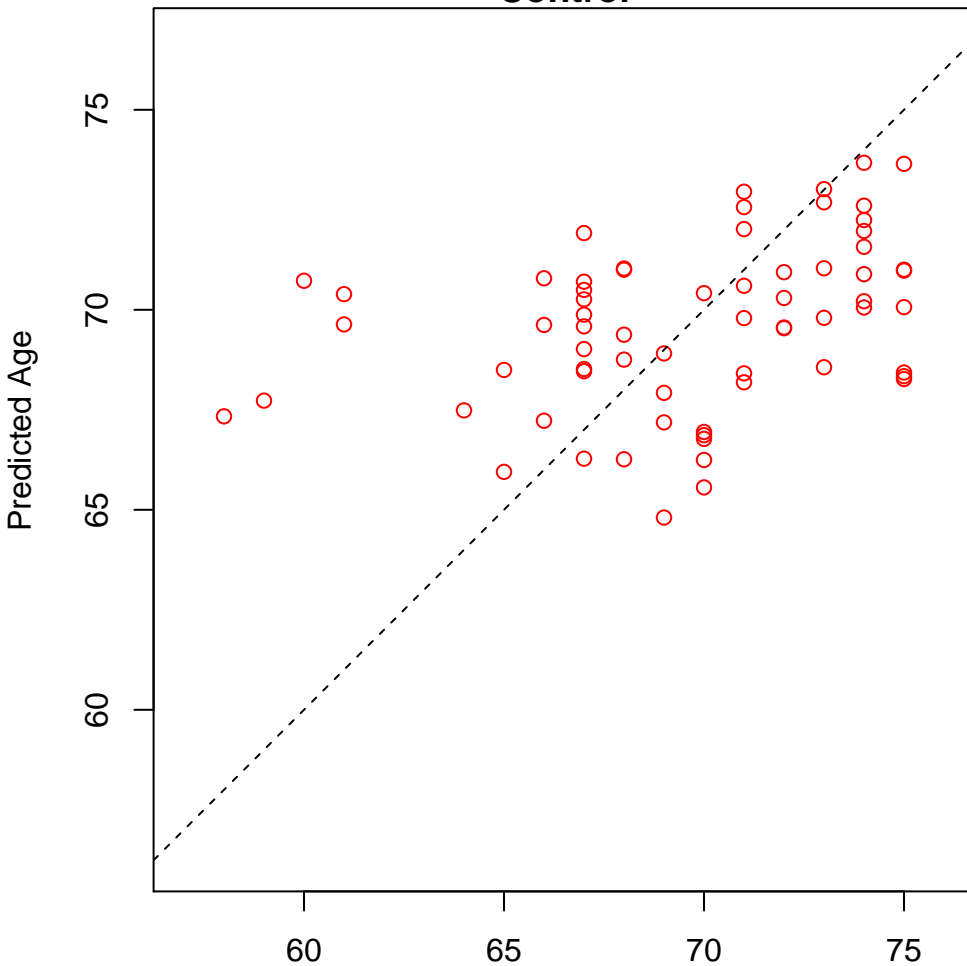


regulation of receptor recycling (Score: 0.453160)

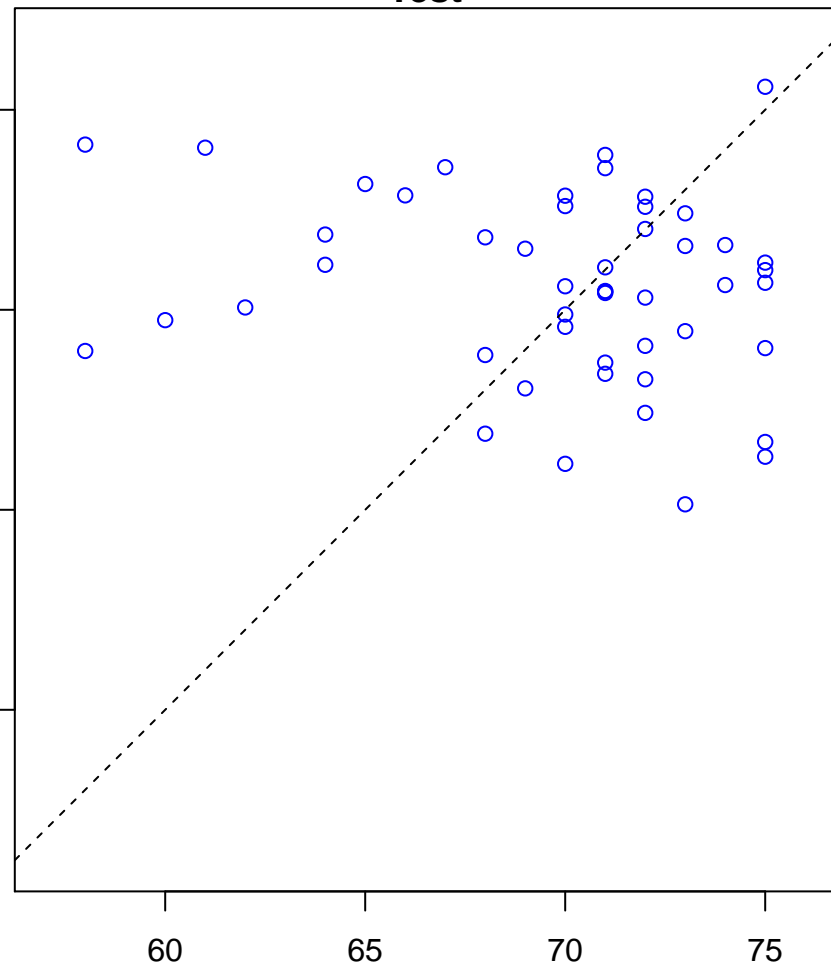


regulation of sensory perception of pain (Score: 0.452299)

Control

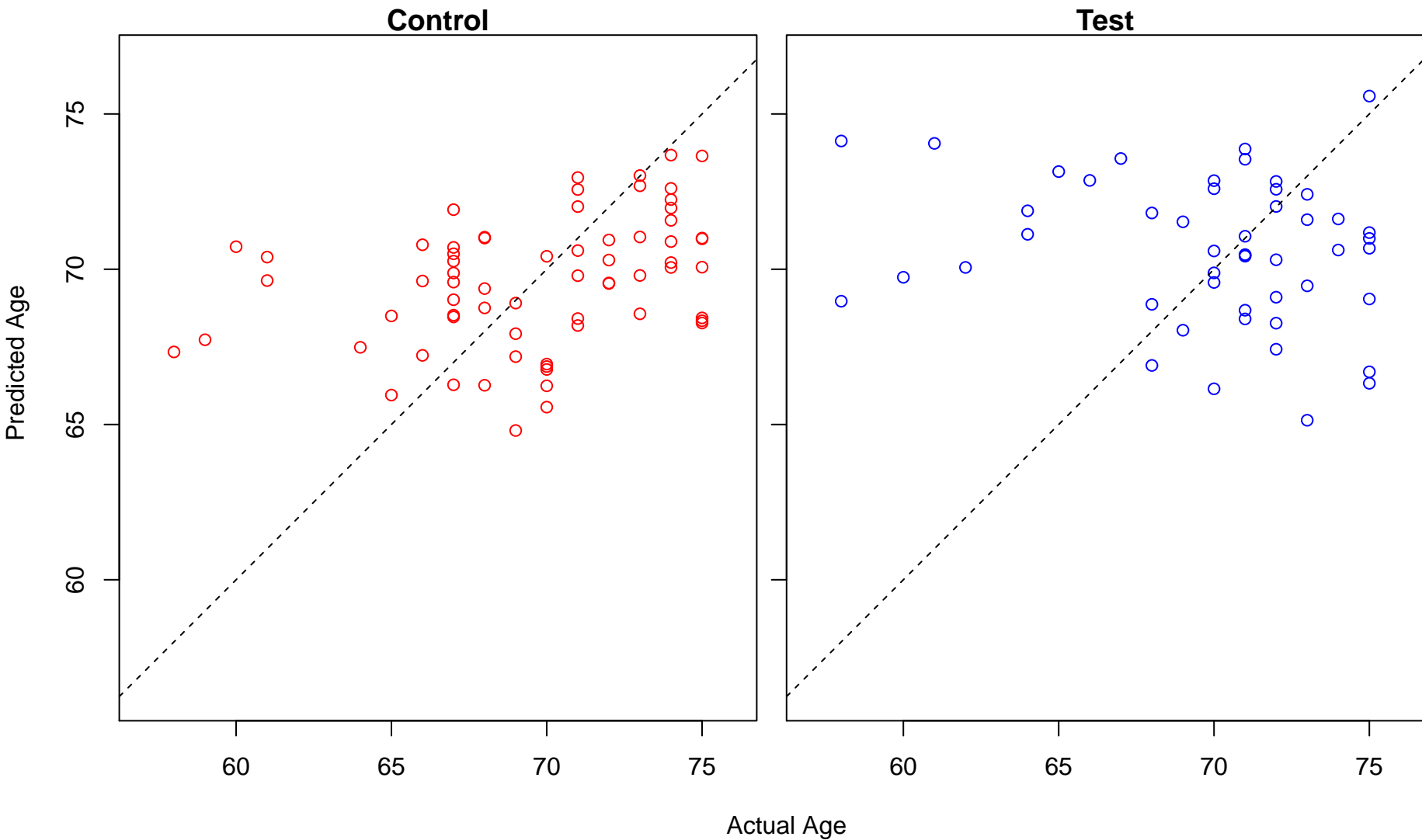


Test

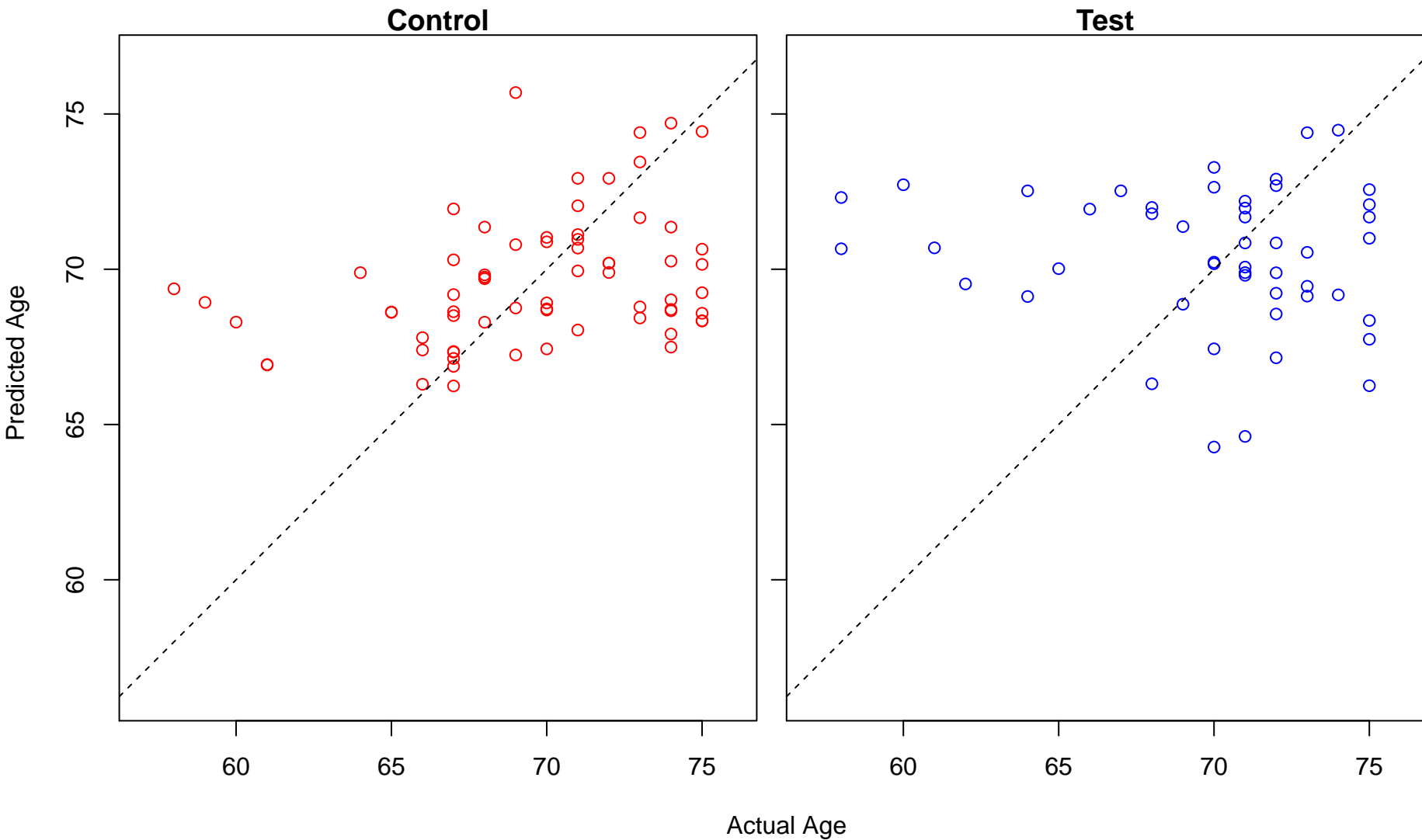


Actual Age

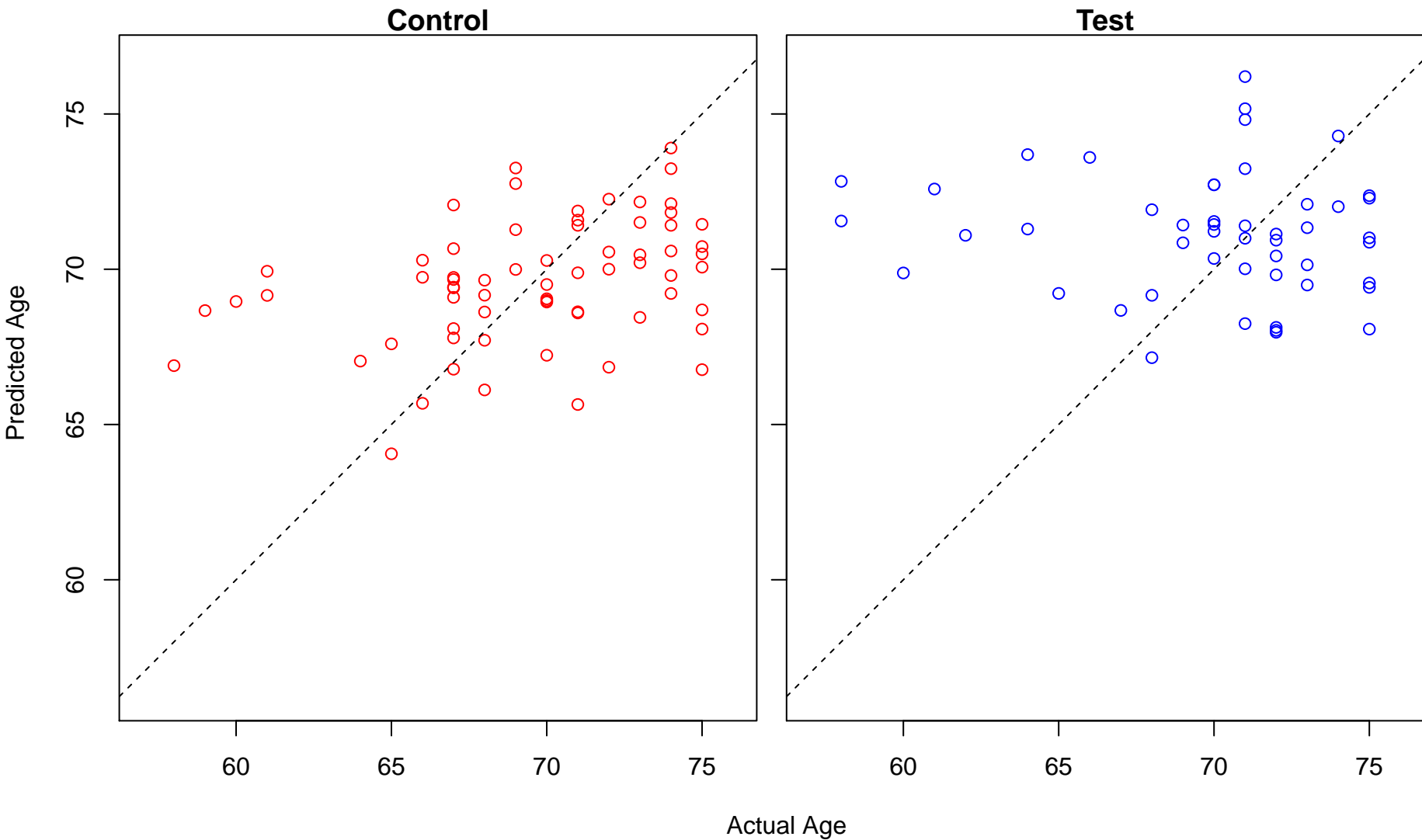
regulation of sensory perception (Score: 0.452299)



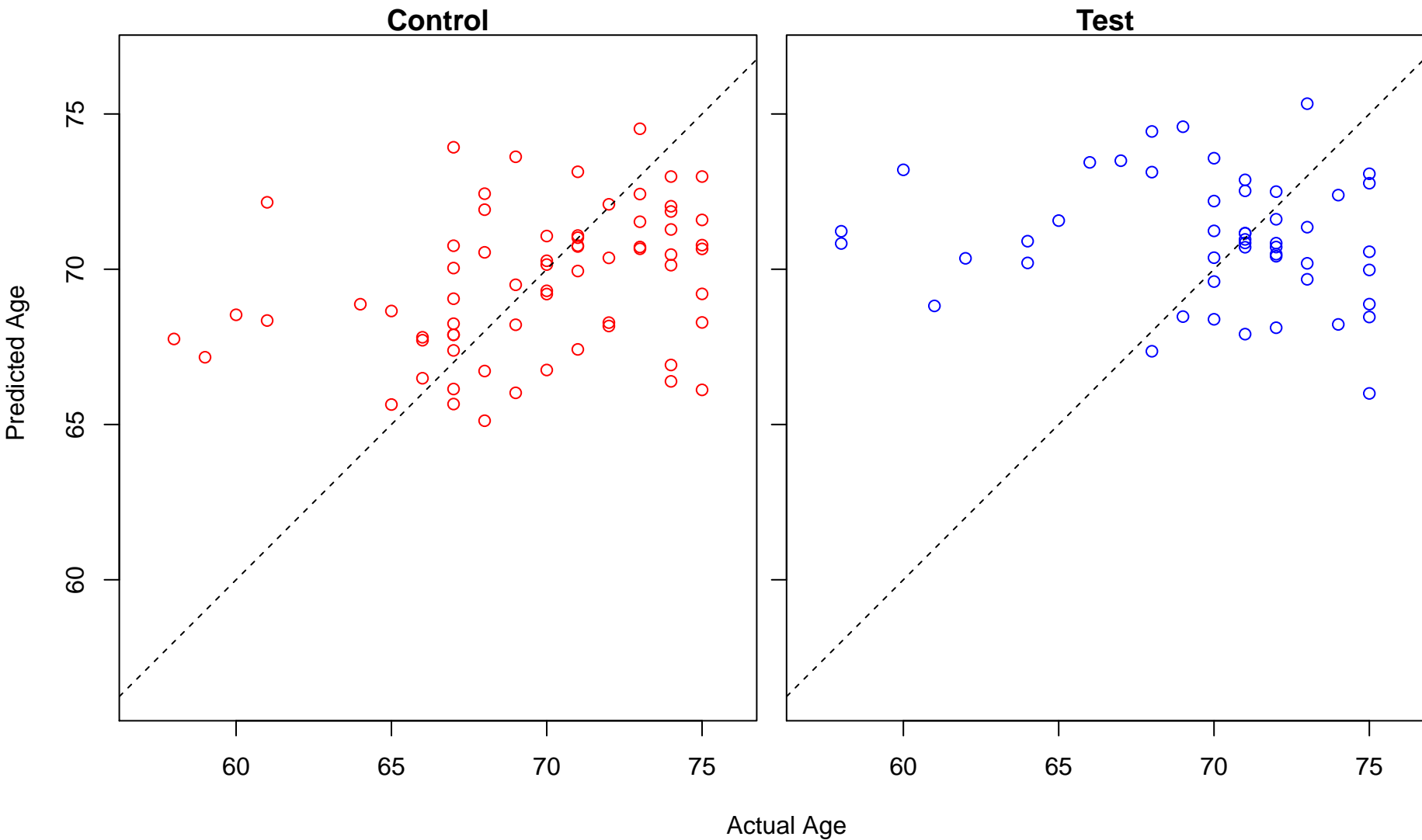
photoreceptor cell differentiation (Score: 0.450629)



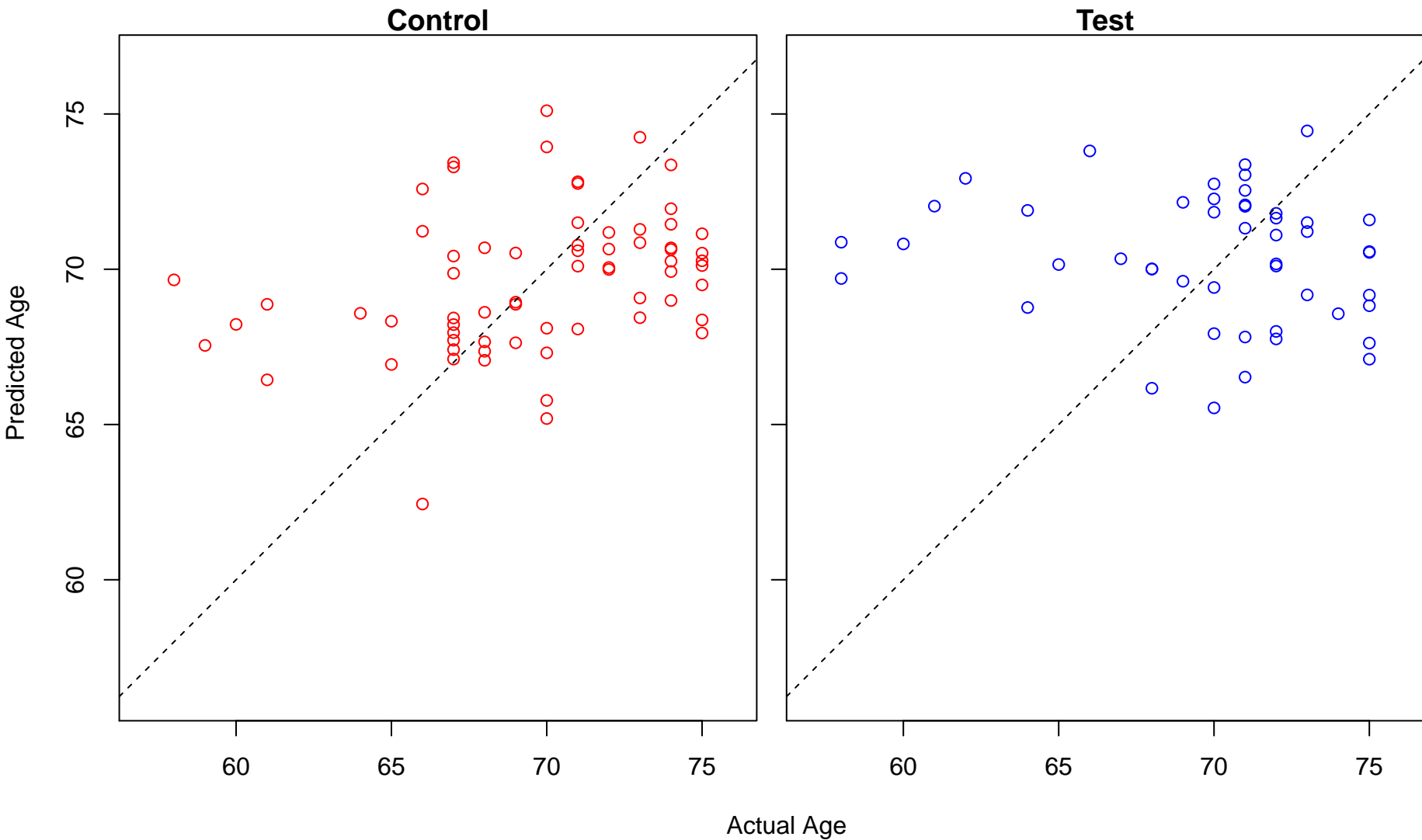
regulation of interleukin-13 secretion (Score: 0.450490)



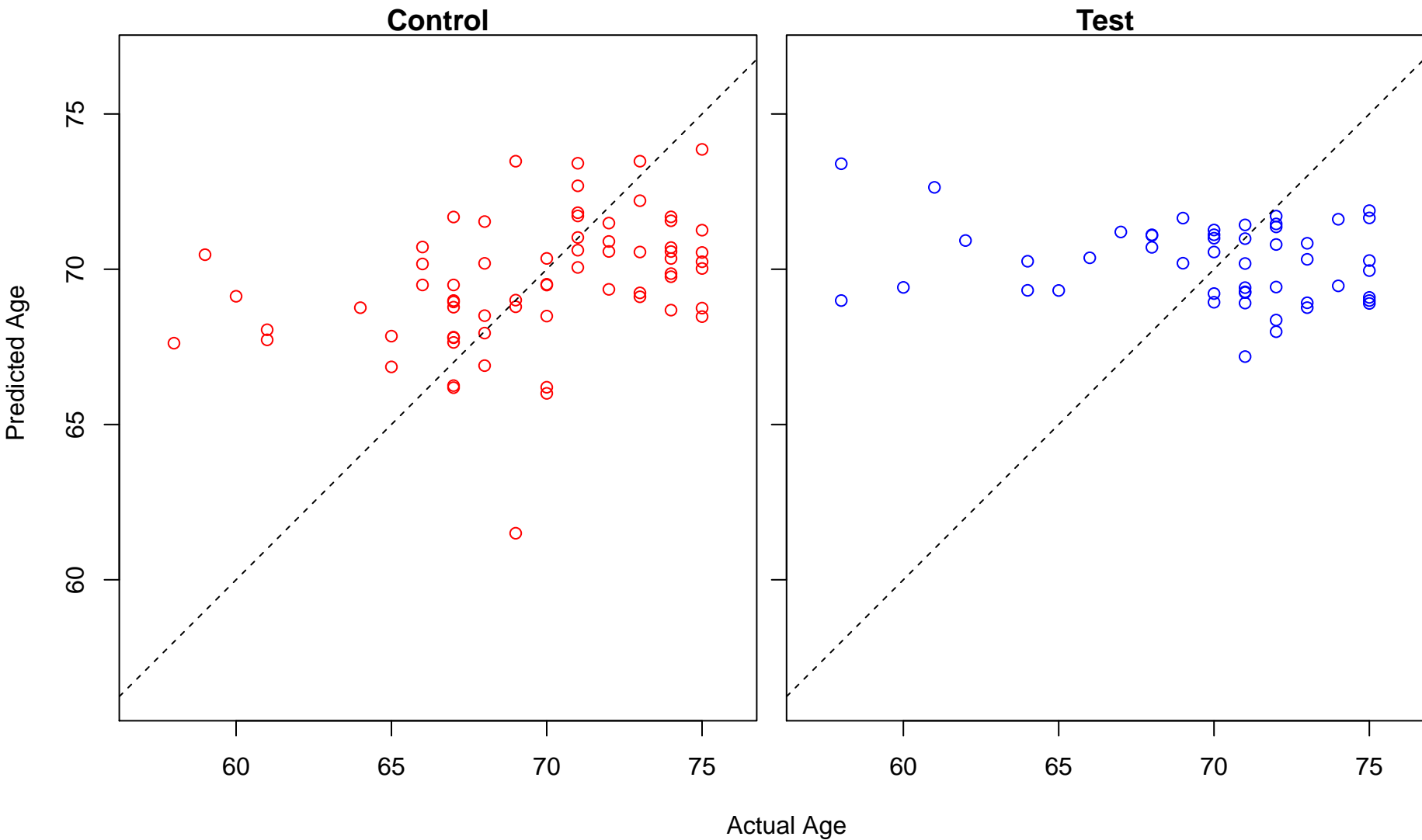
mitotic sister chromatid cohesion (Score: 0.449709)



regulation of cell-cell adhesion mediated by integrin (Score: 0.448685)

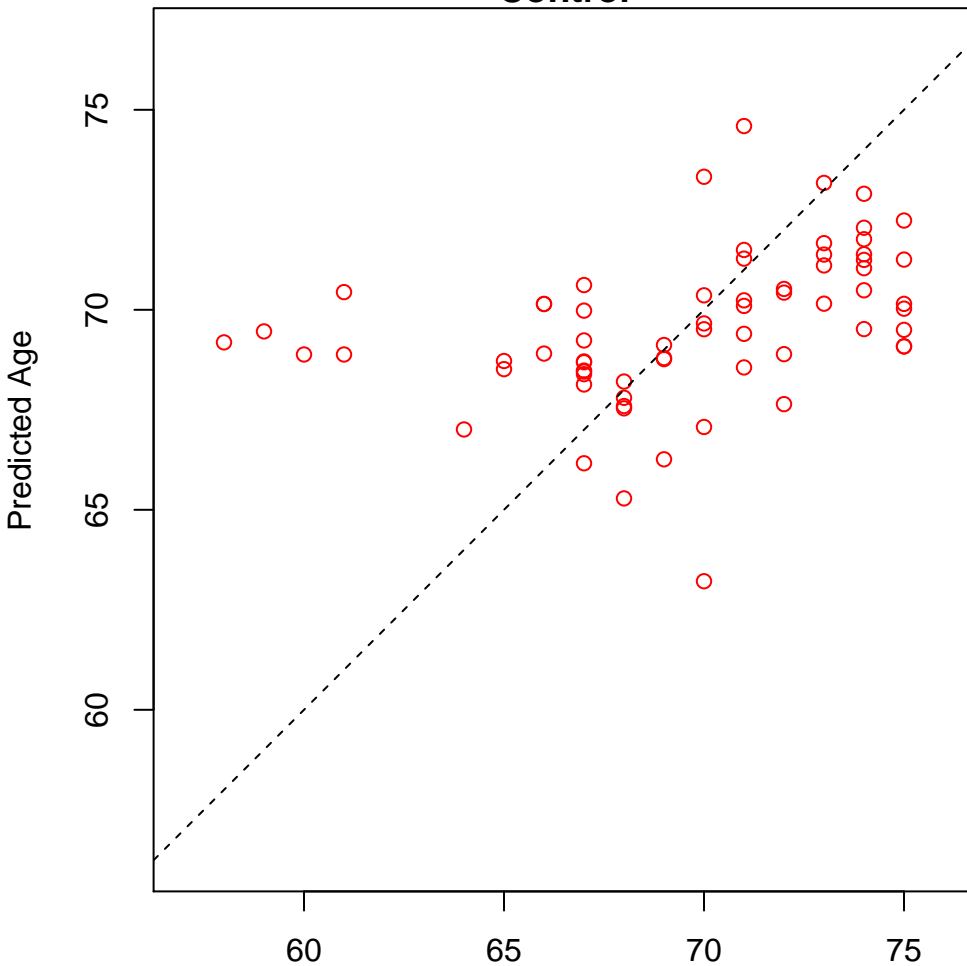


terpenoid catabolic process (Score: 0.448611)

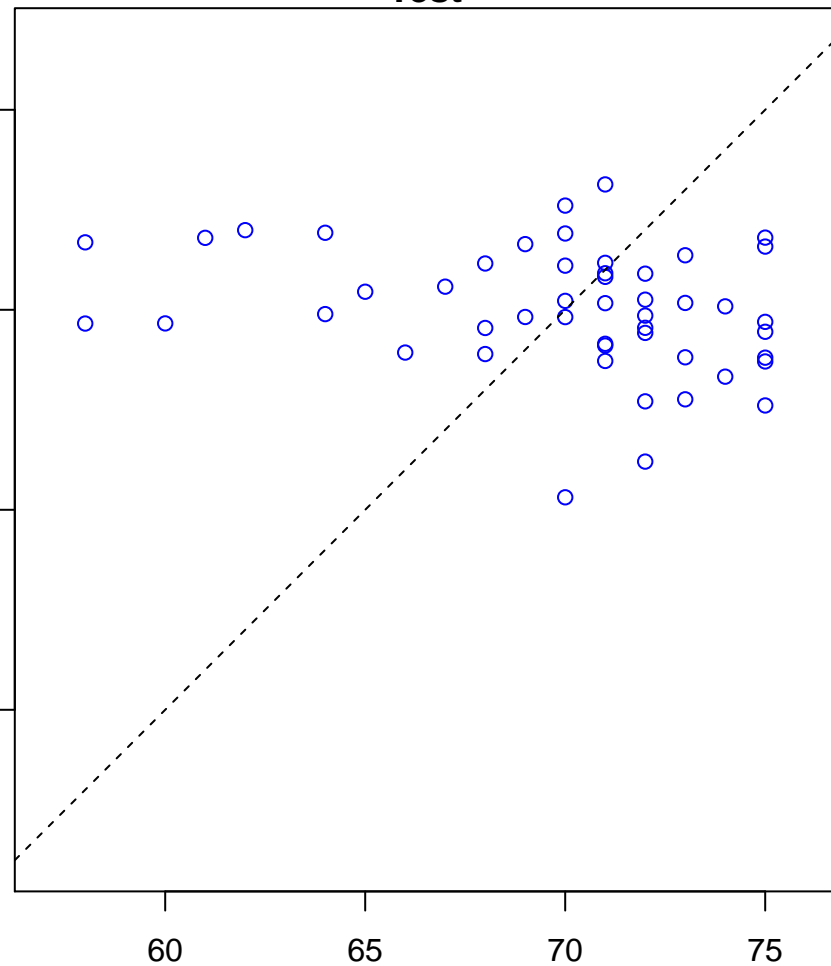


hematopoietic stem cell differentiation (Score: 0.448329)

Control

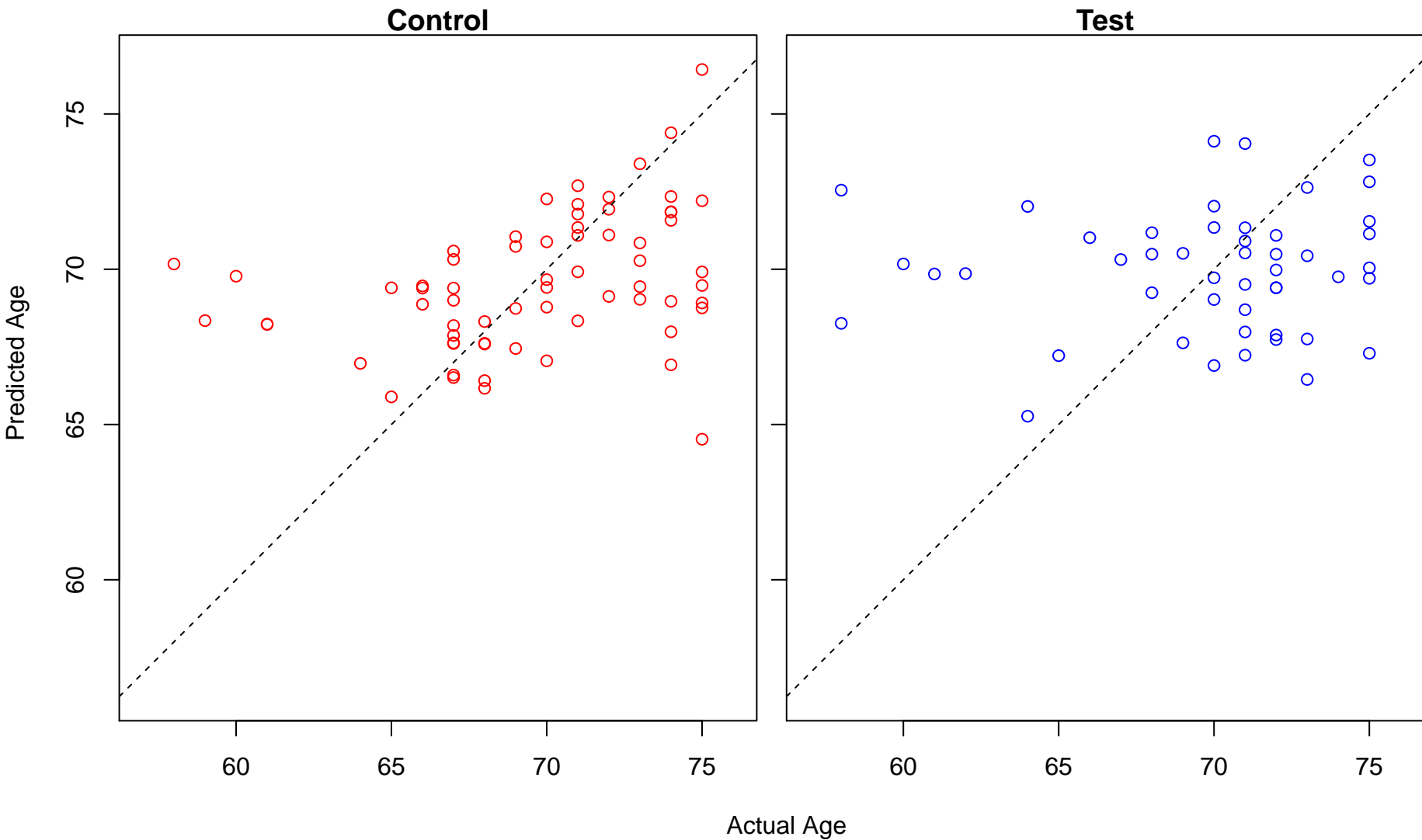


Test

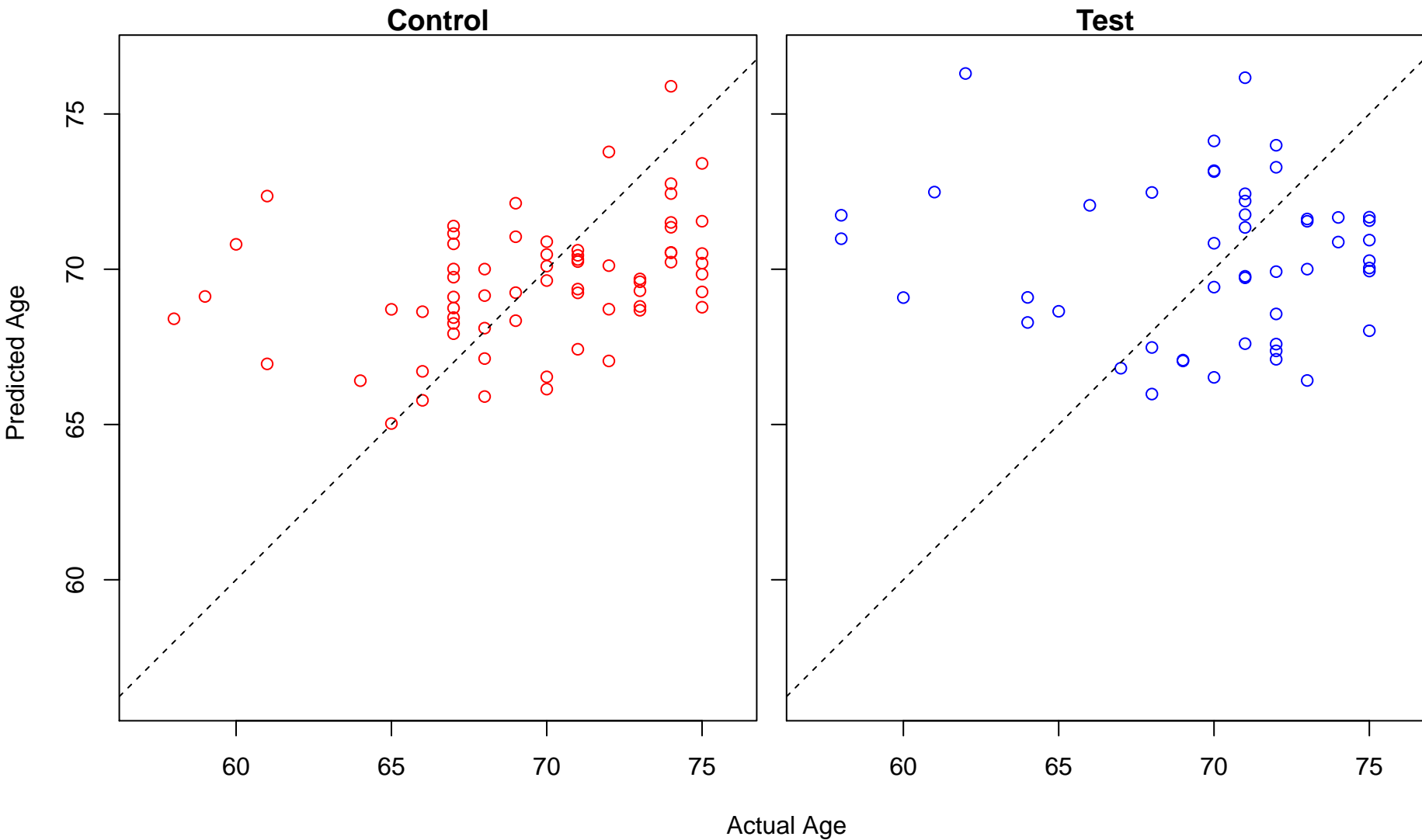


Actual Age

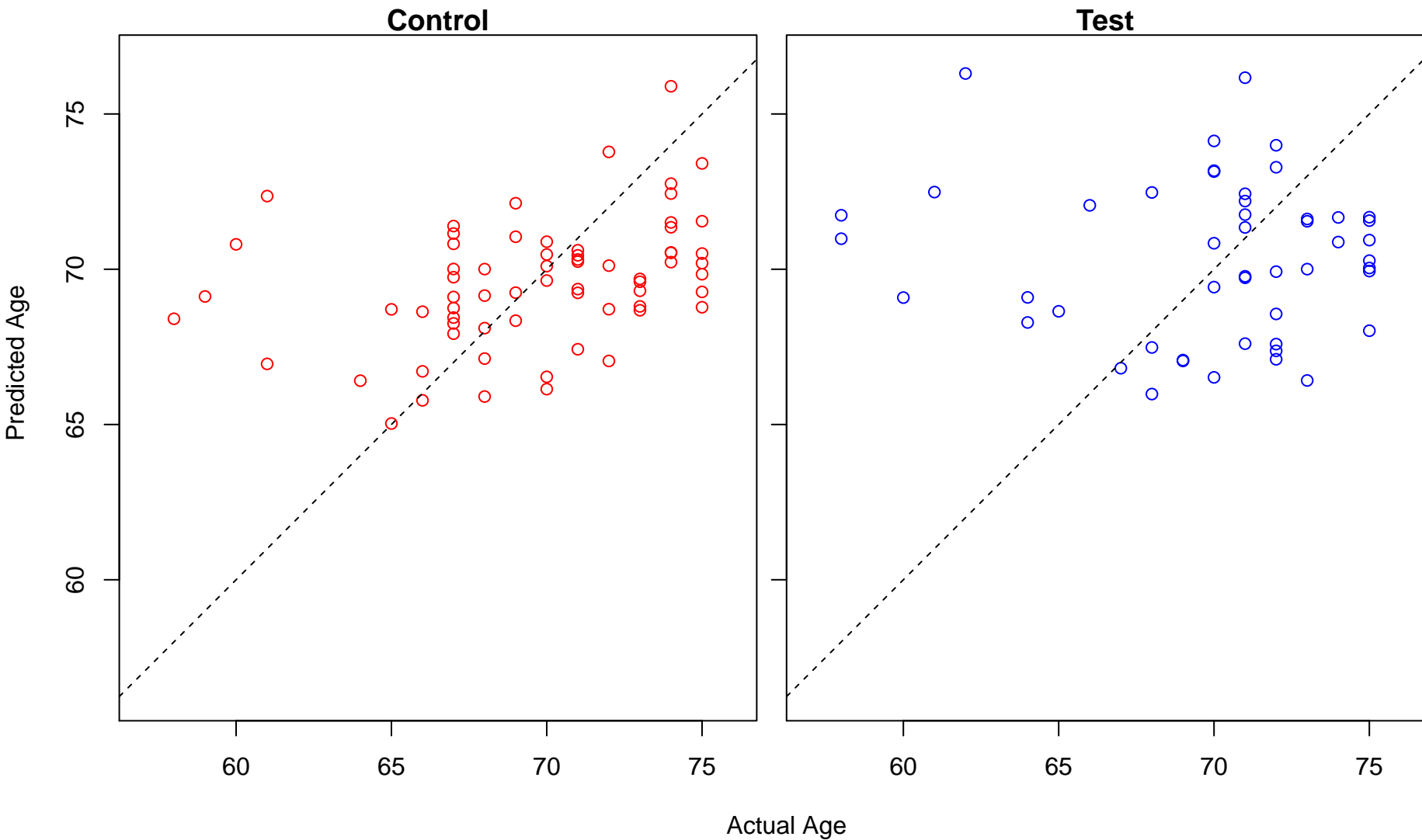
negative regulation of receptor internalization (Score: 0.448210)



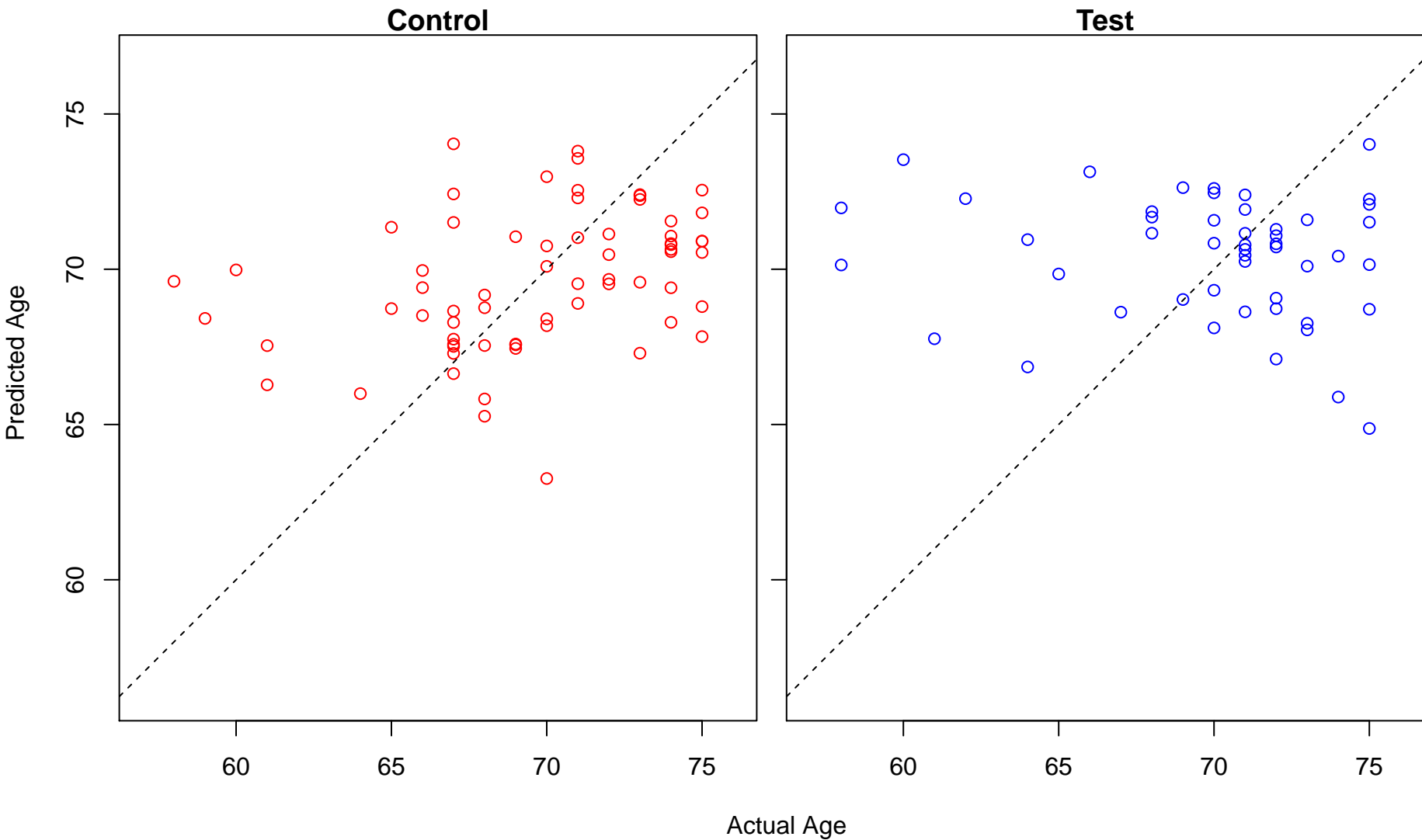
response to erythropoietin (Score: 0.447703)



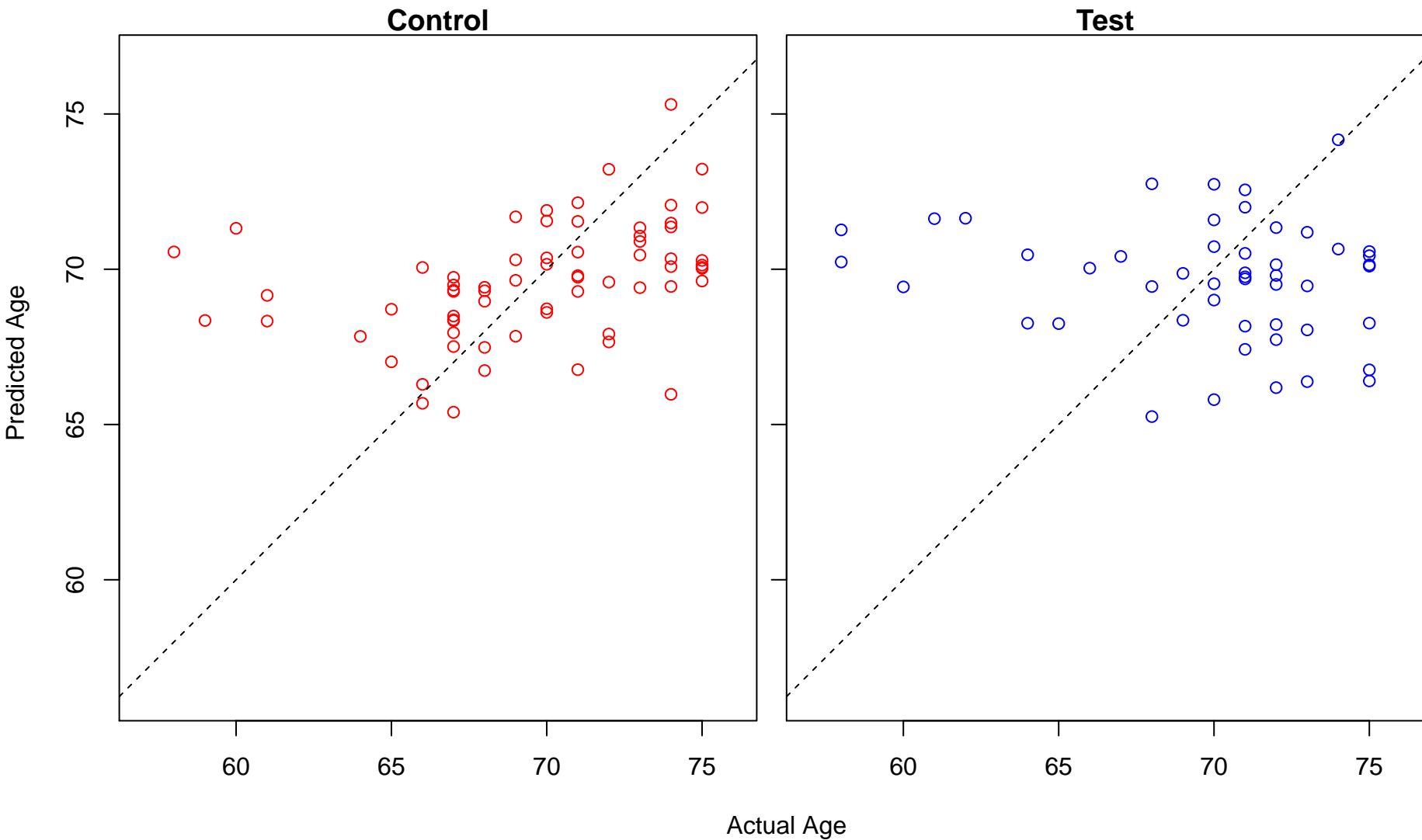
cellular response to erythropoietin (Score: 0.447703)



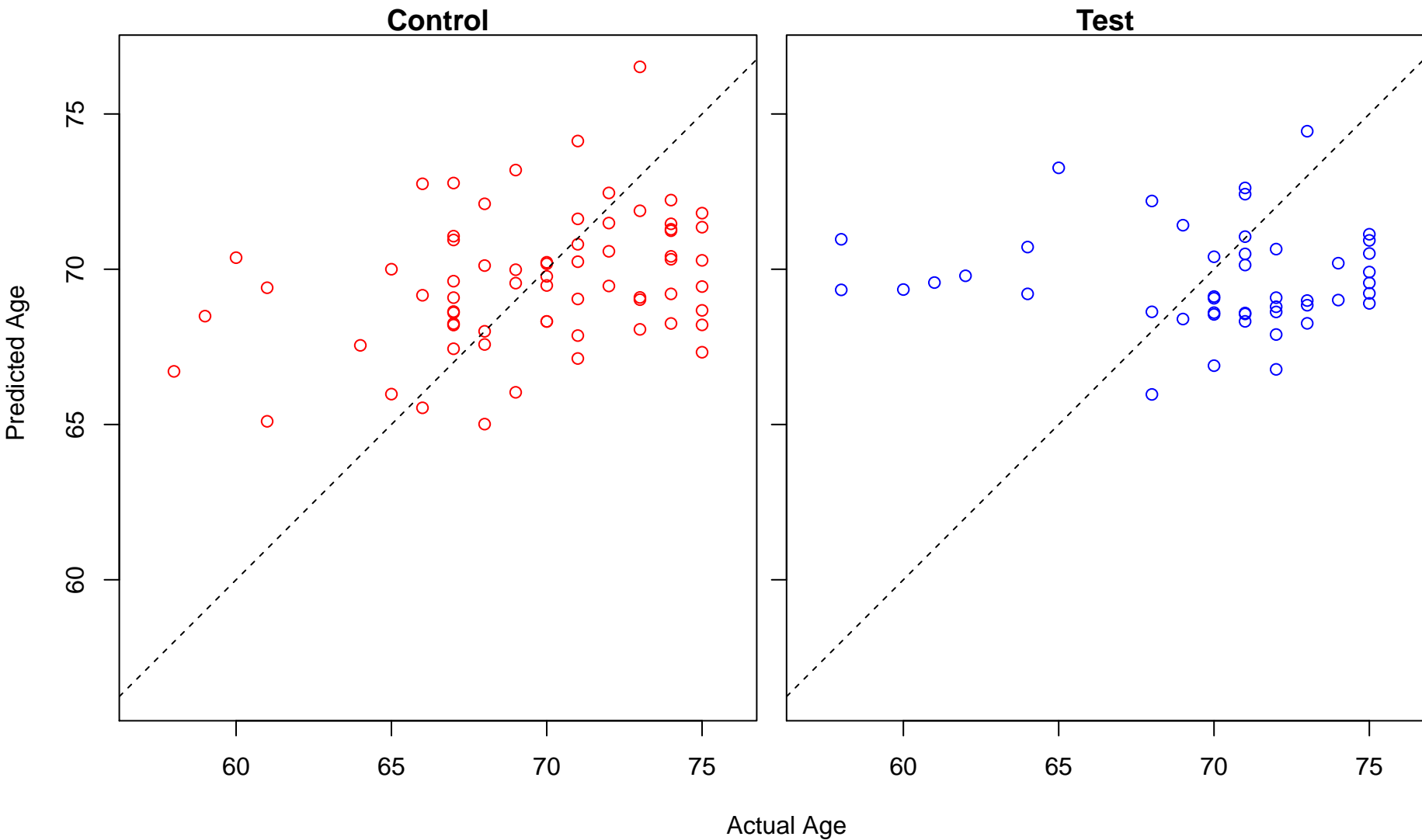
pore complex assembly (Score: 0.446957)



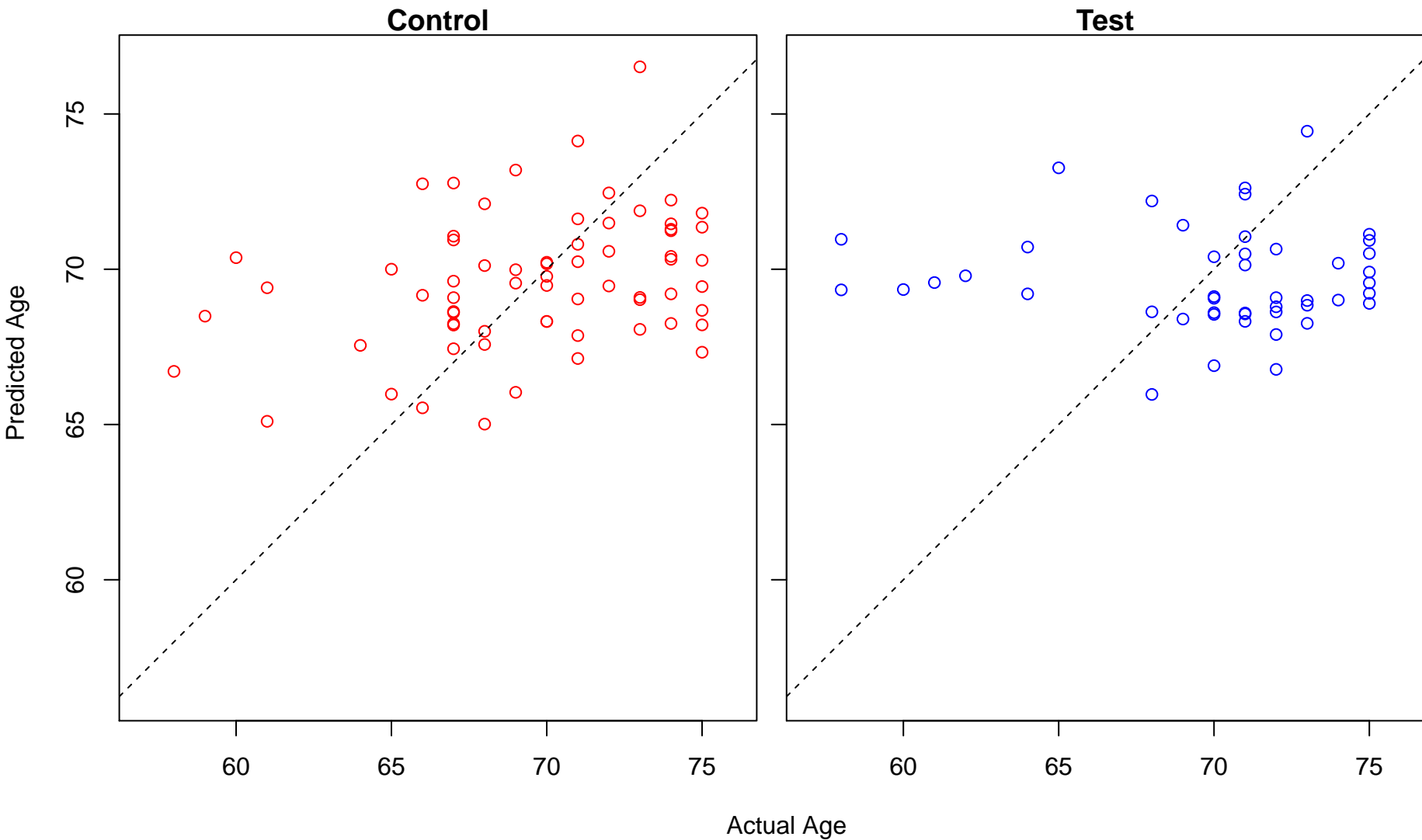
regulation of chemokine (C-C motif) ligand 5 production (Score: 0.446844)



spindle midzone assembly (Score: 0.446347)

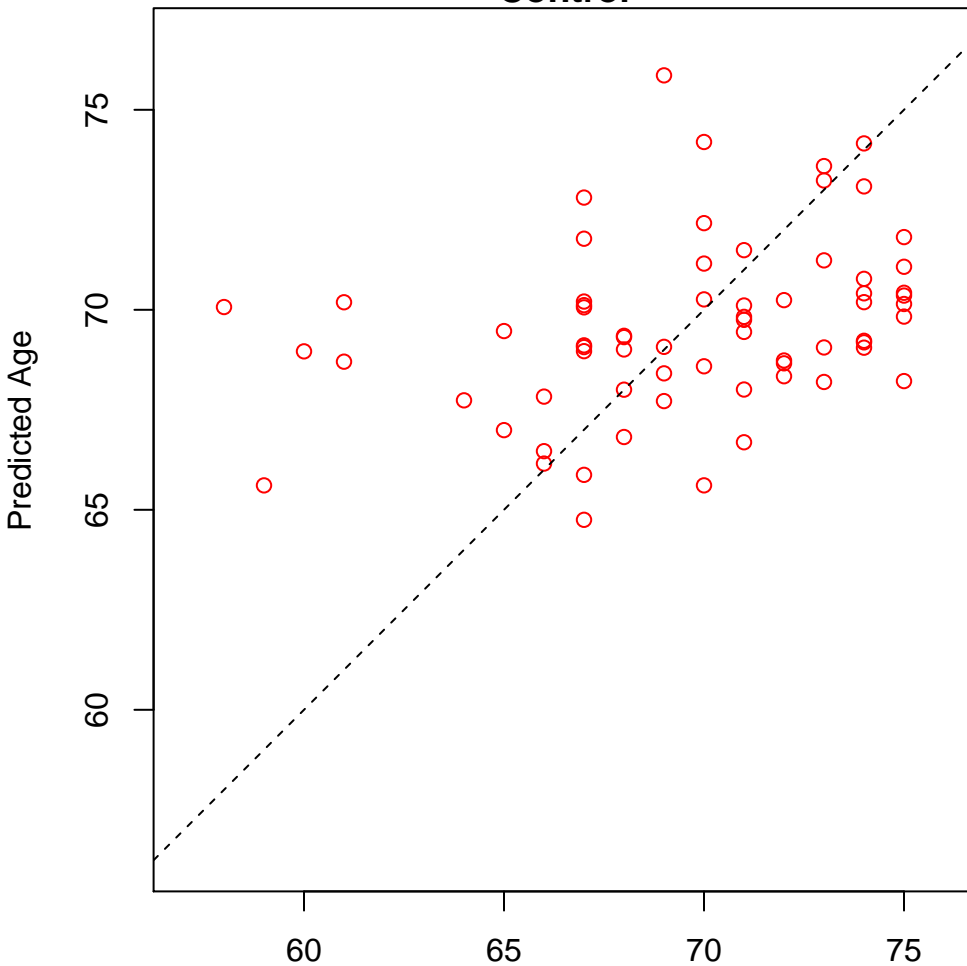


mitotic spindle midzone assembly (Score: 0.446347)

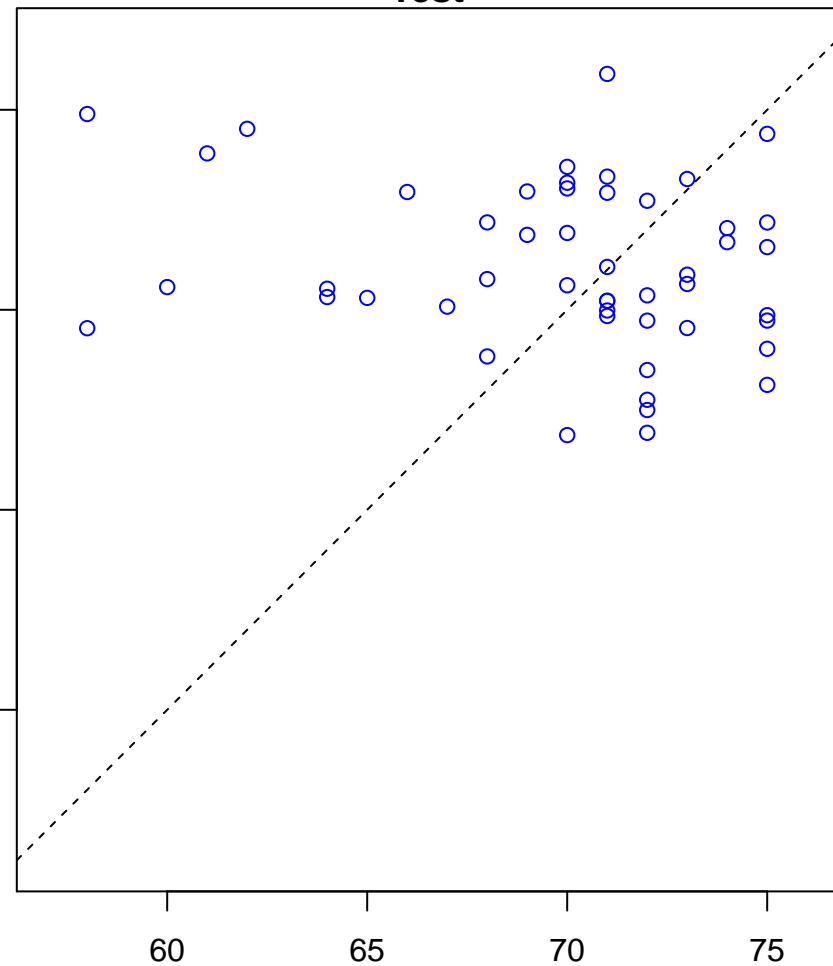


regulation of protein activation cascade (Score: 0.445338)

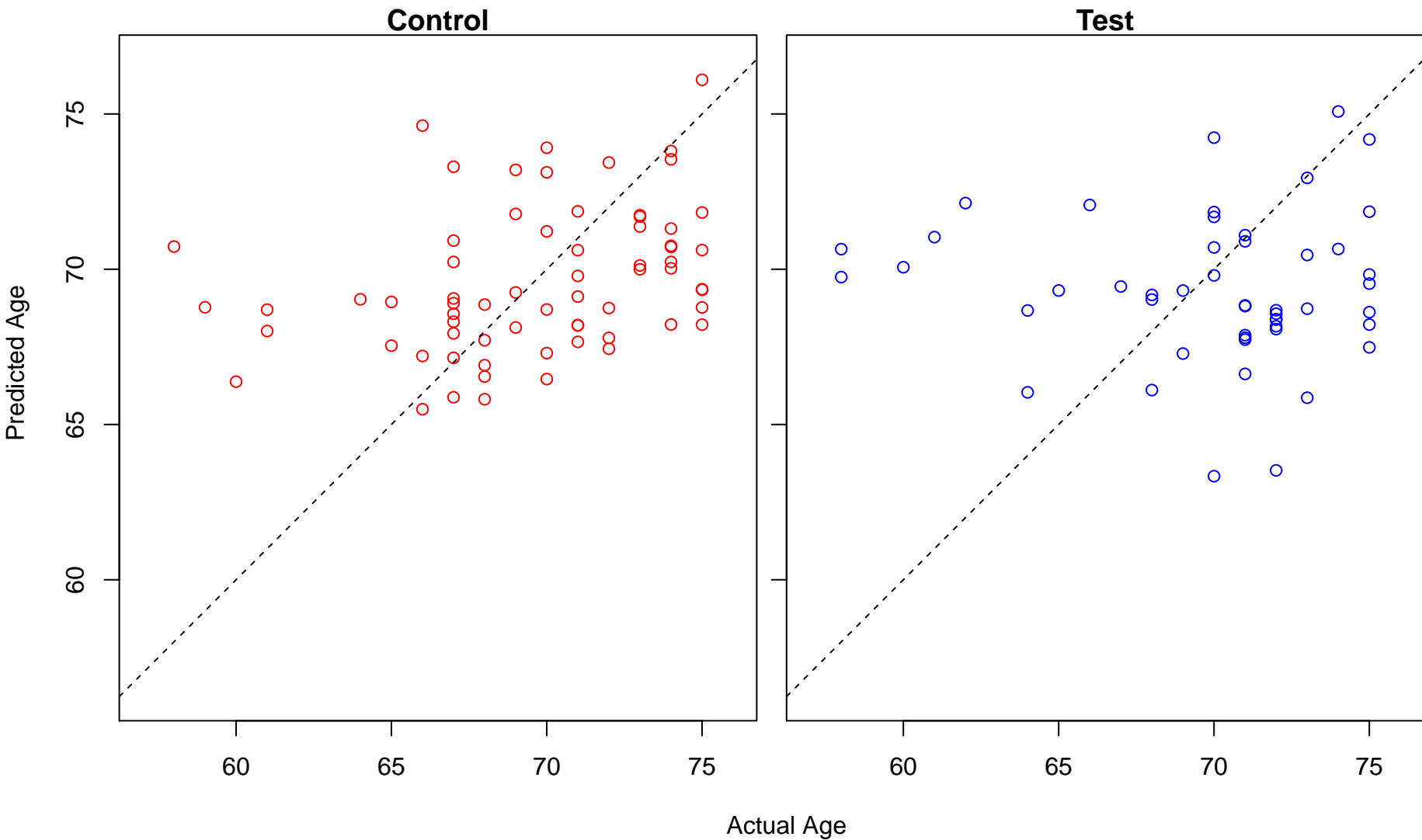
Control



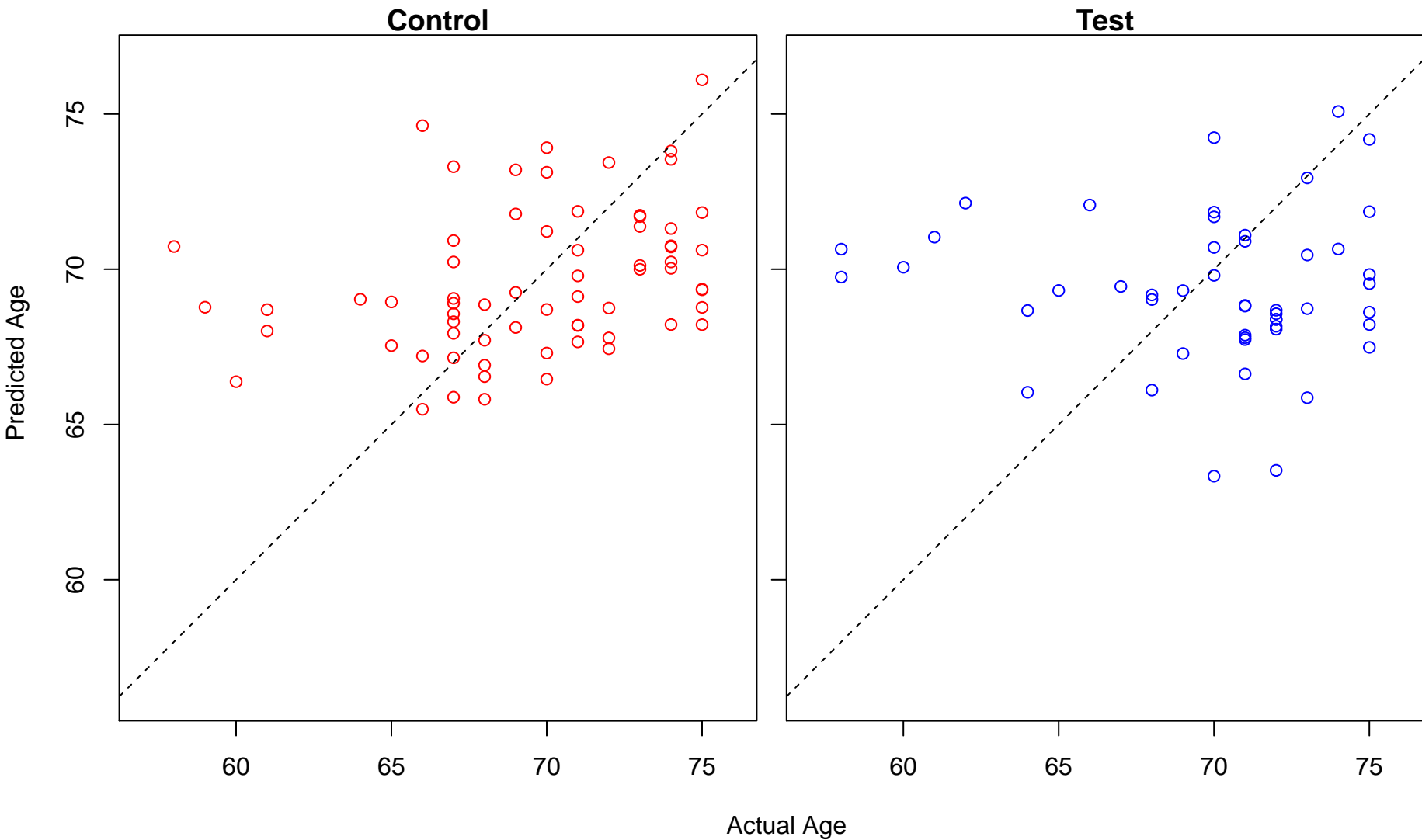
Test



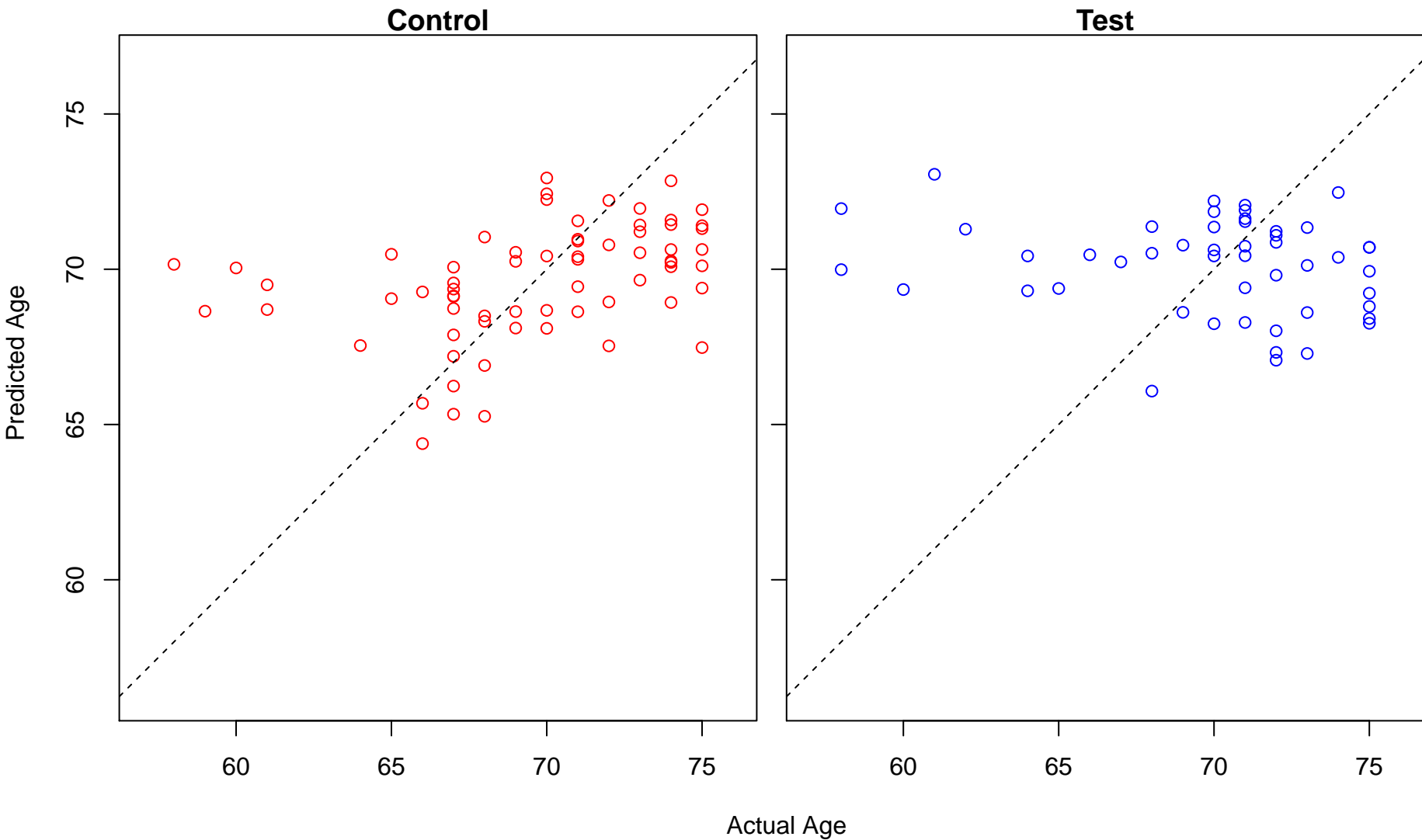
detection of bacterium (Score: 0.444984)



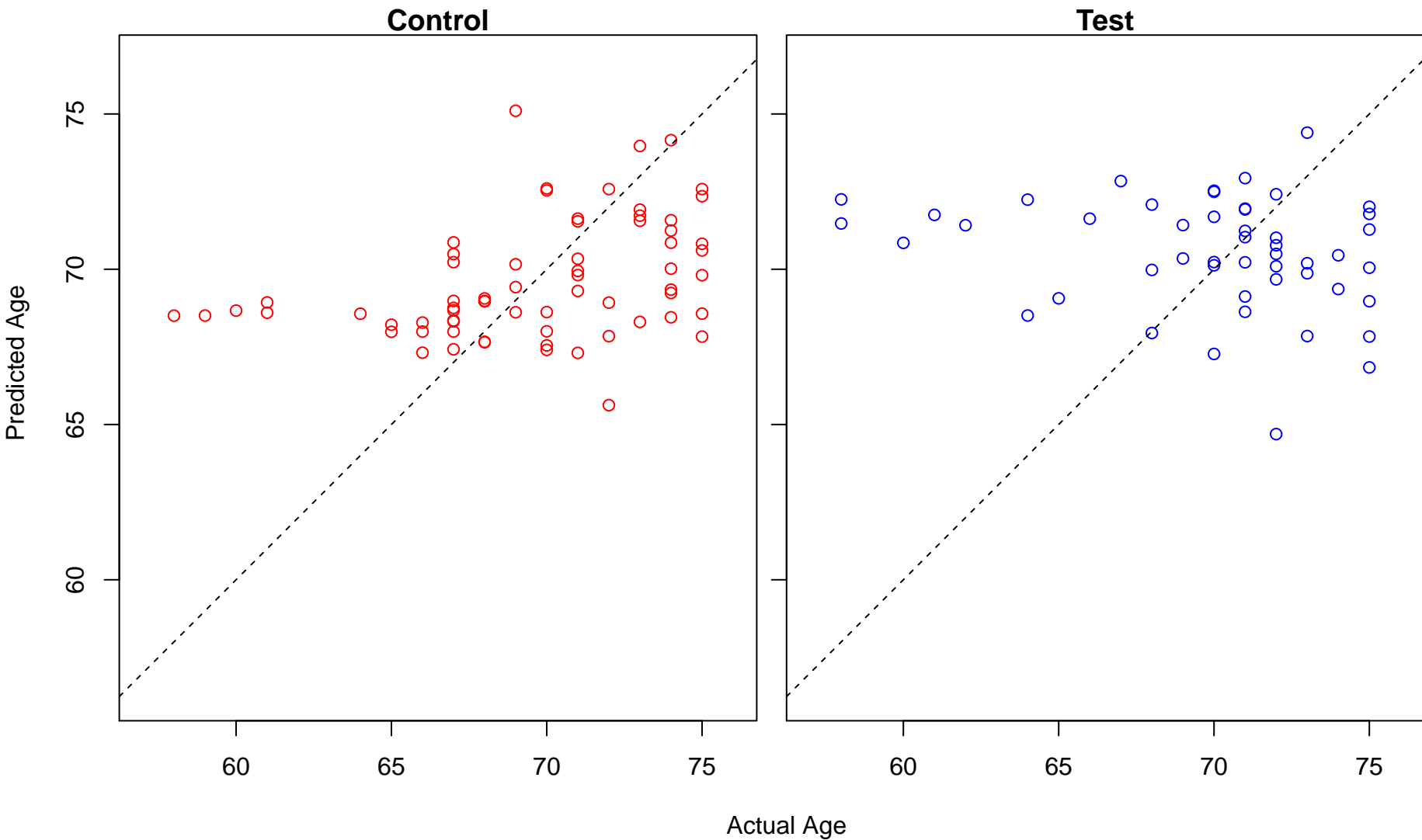
detection of other organism (Score: 0.444984)



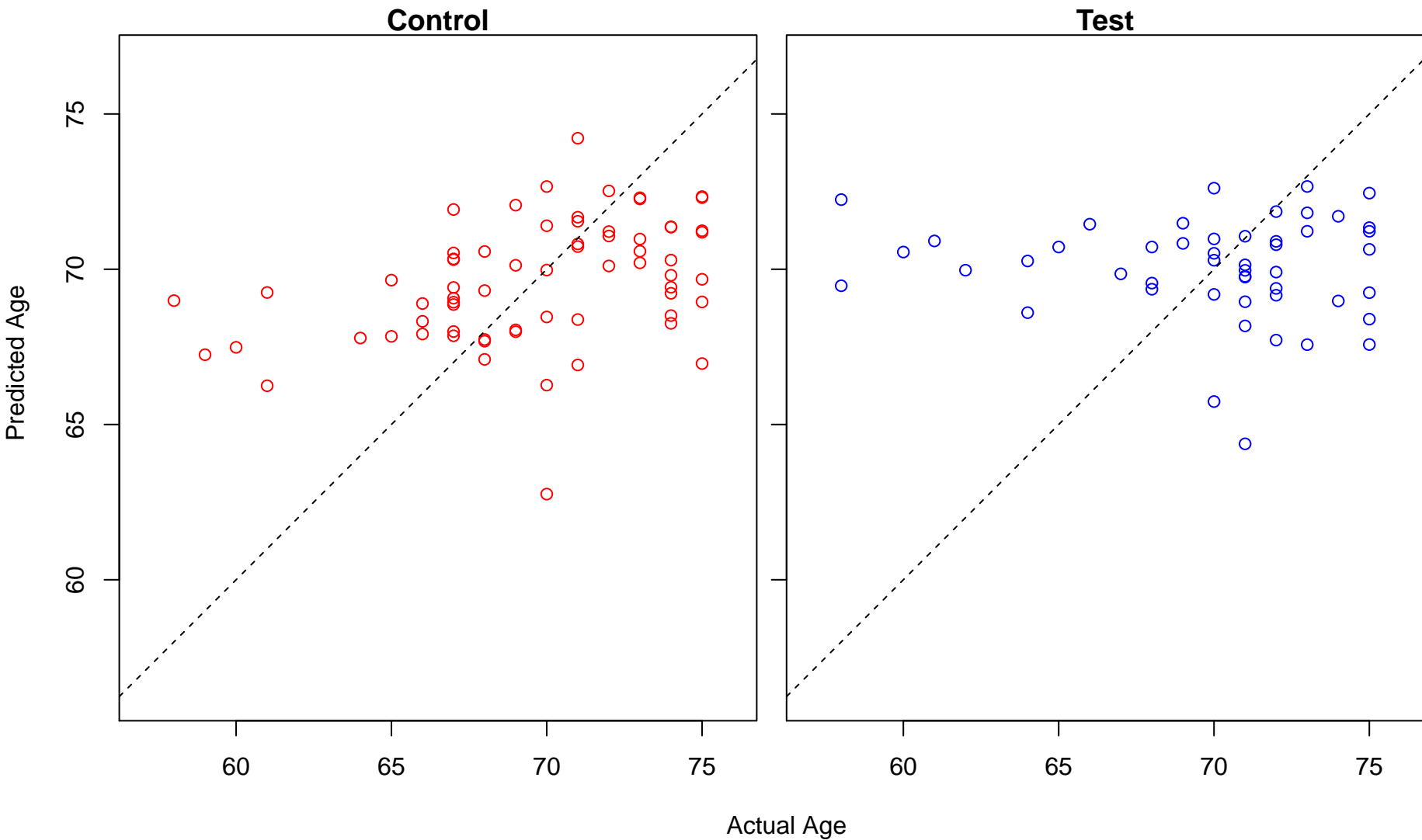
RNA 5'-end processing (Score: 0.444026)



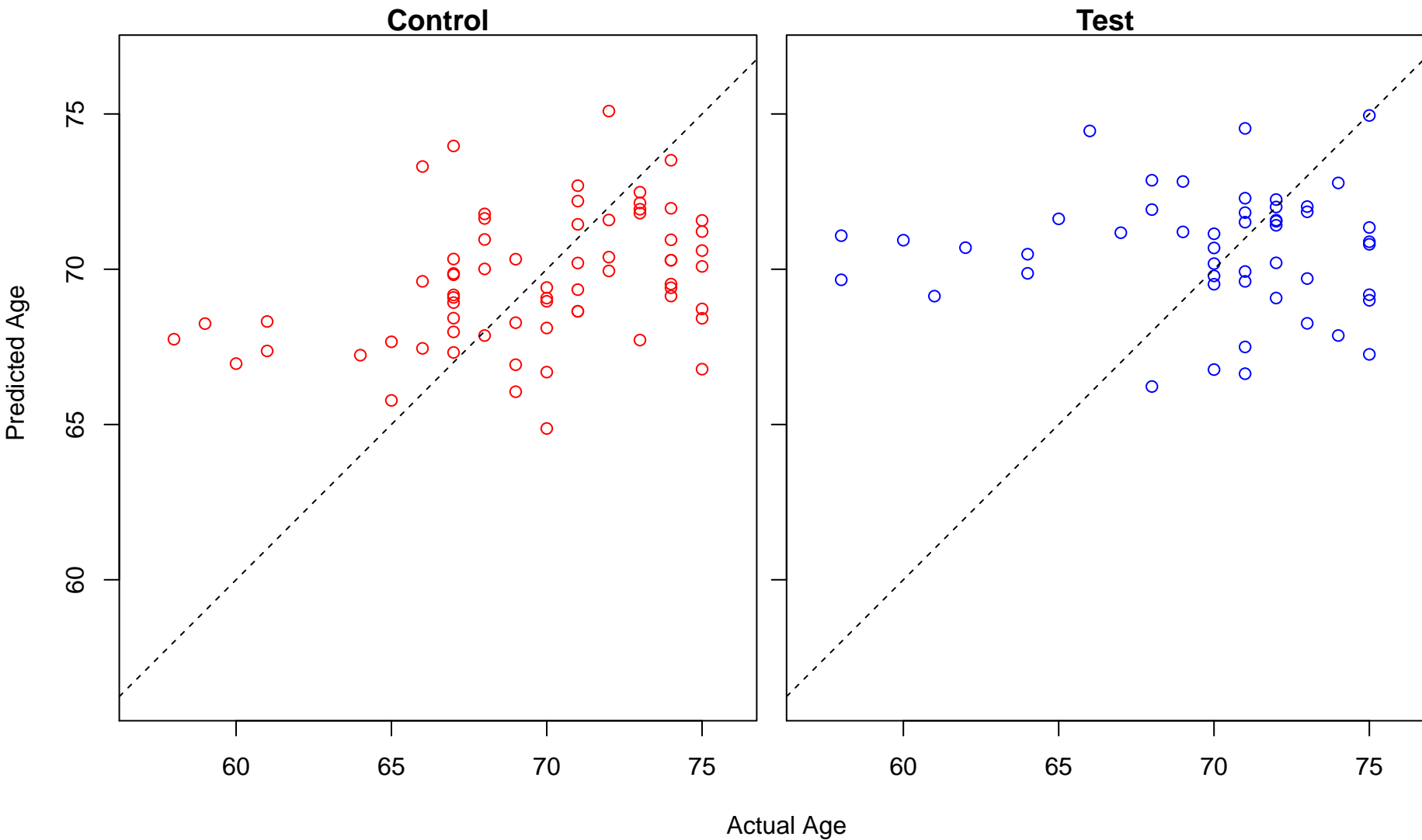
pyrimidine-containing compound transmembrane transport (Score: 0.443276)



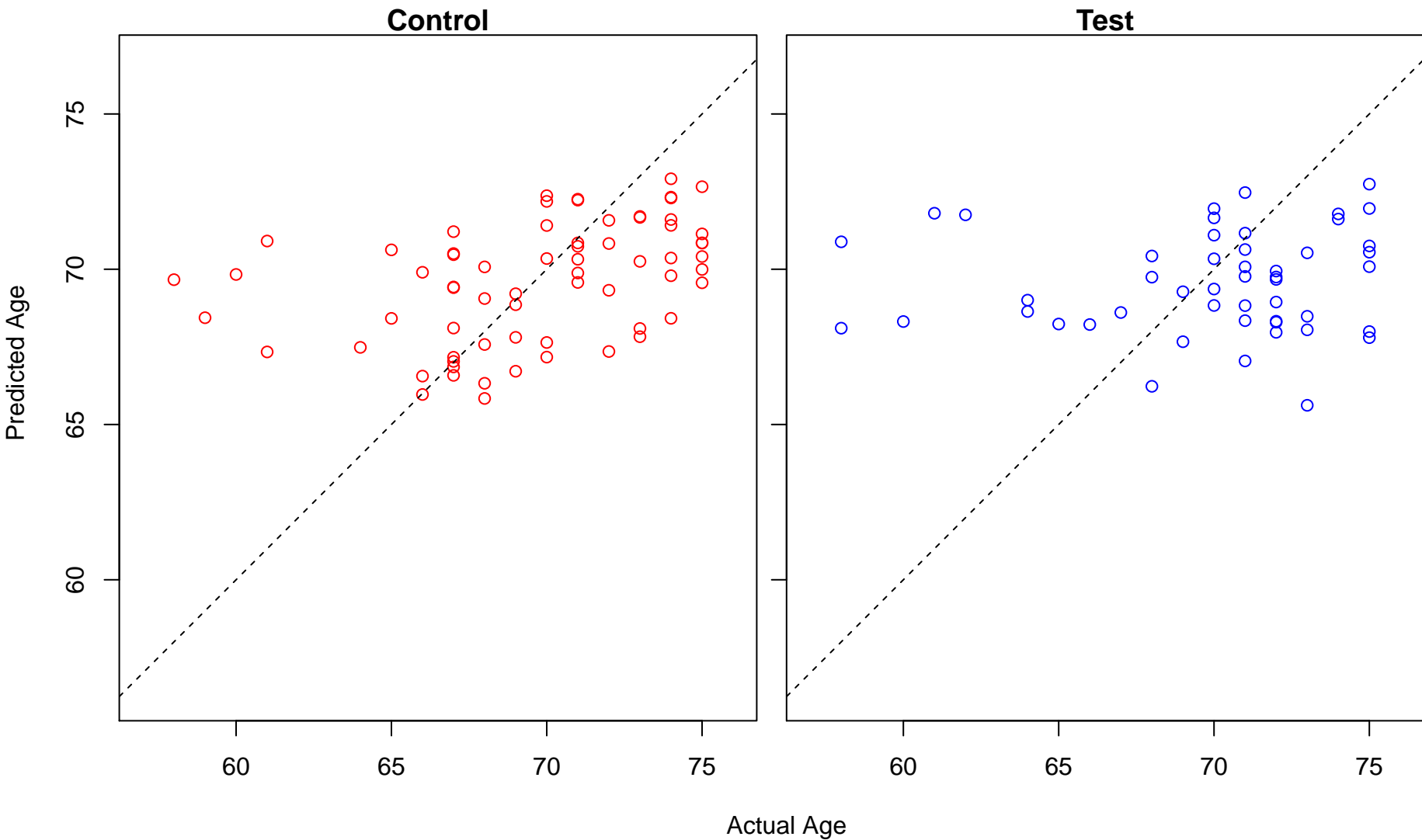
cell junction maintenance (Score: 0.442909)



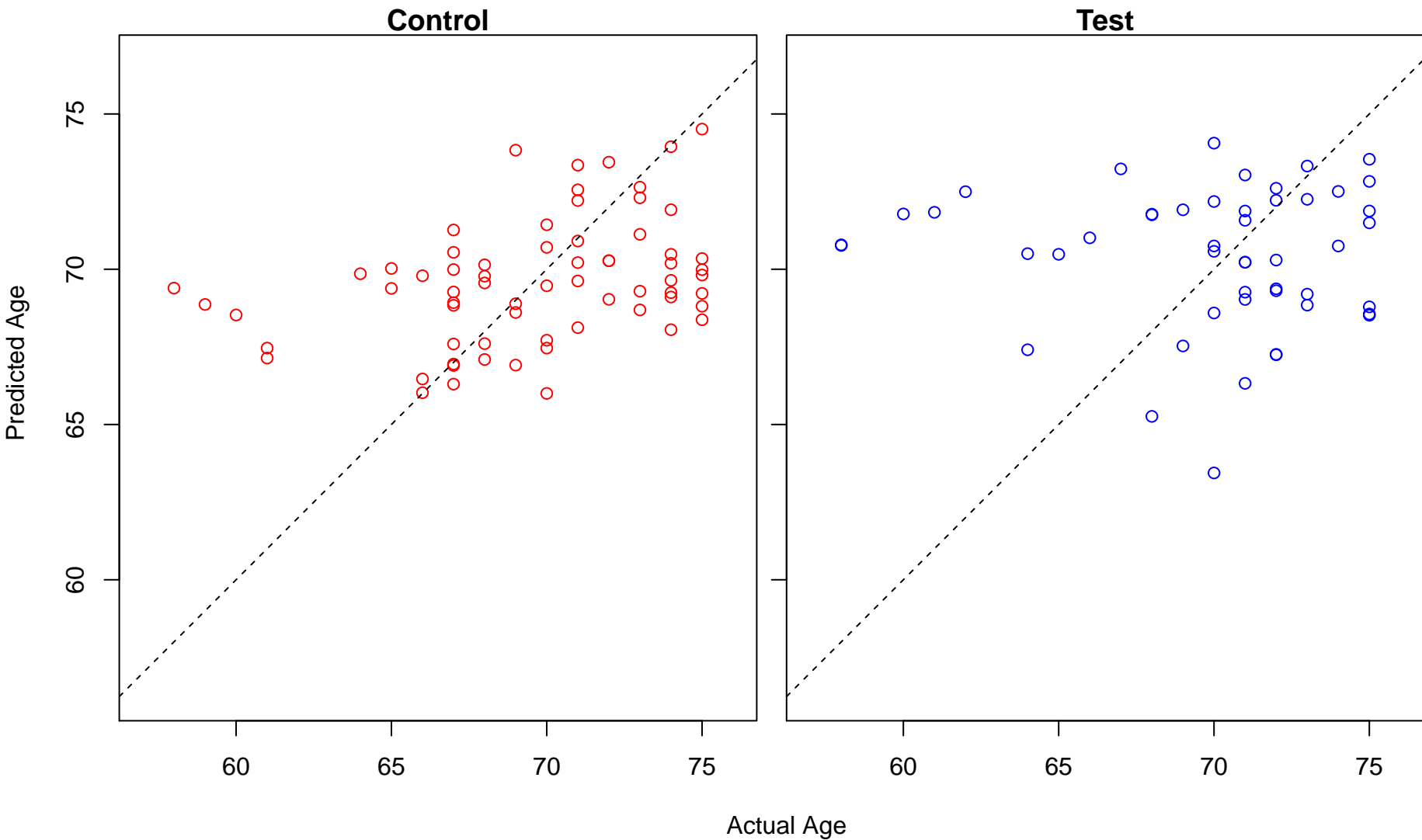
positive regulation of smooth muscle contraction (Score: 0.440828)



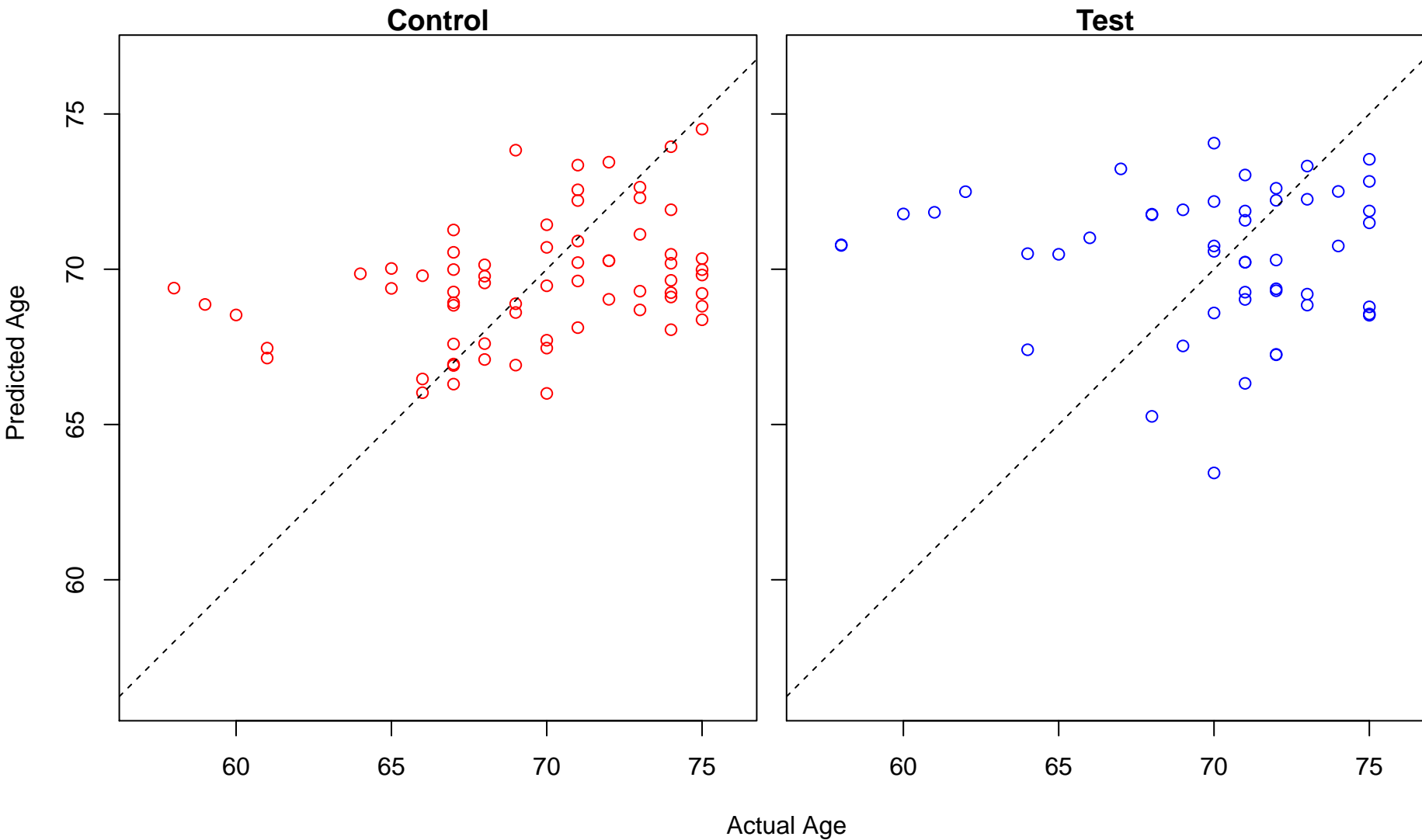
positive regulation of insulin-like growth factor receptor signaling pathway (Score: 0.440570)



olfactory bulb development (Score: 0.440147)

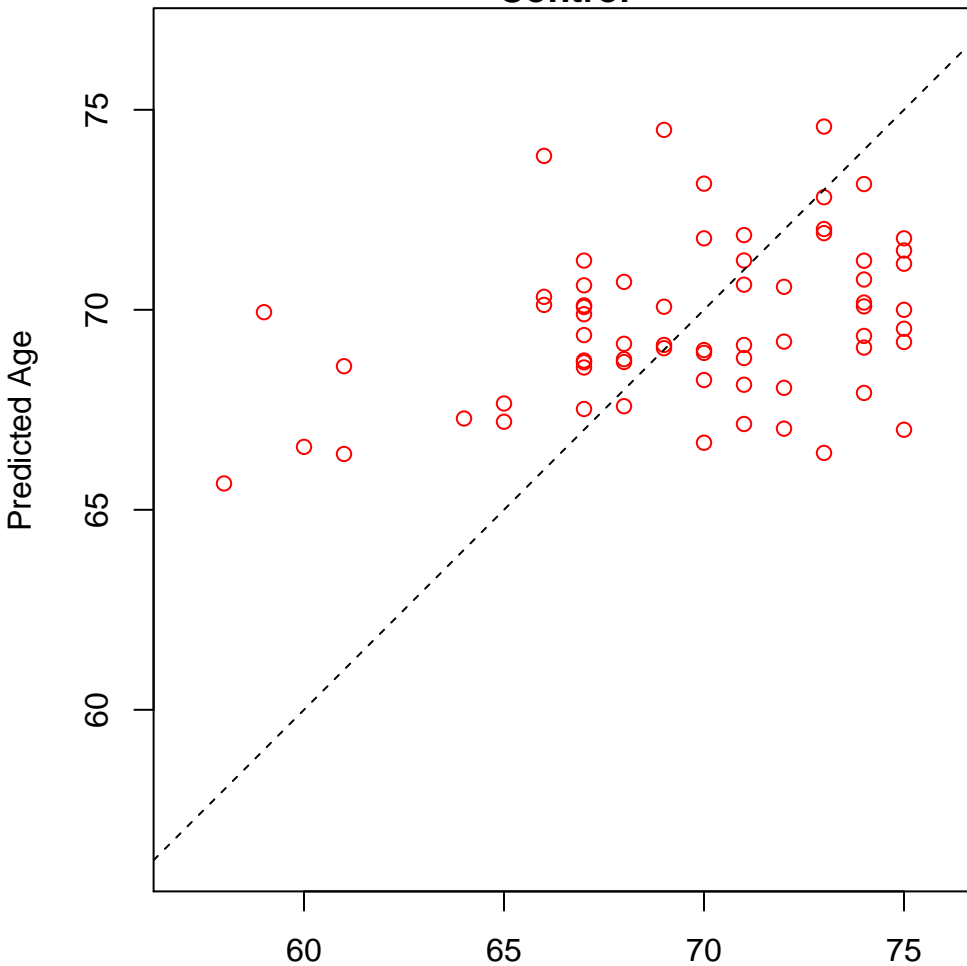


olfactory lobe development (Score: 0.440147)

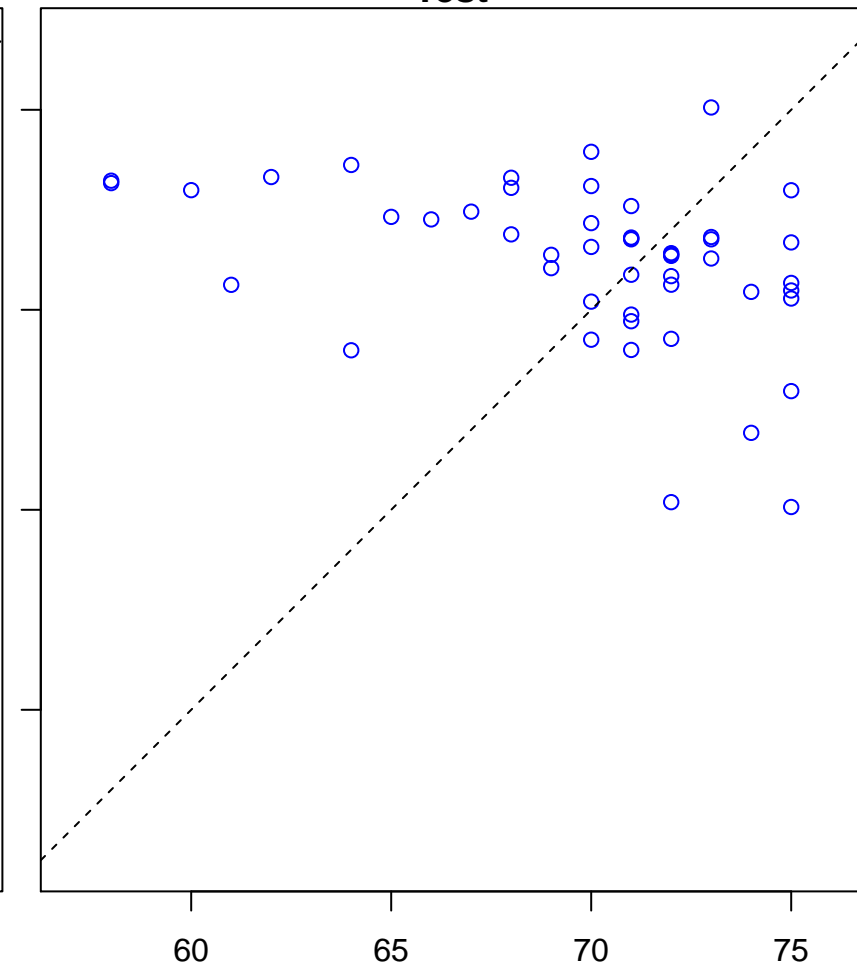


sensory perception of chemical stimulus (Score: 0.439823)

Control

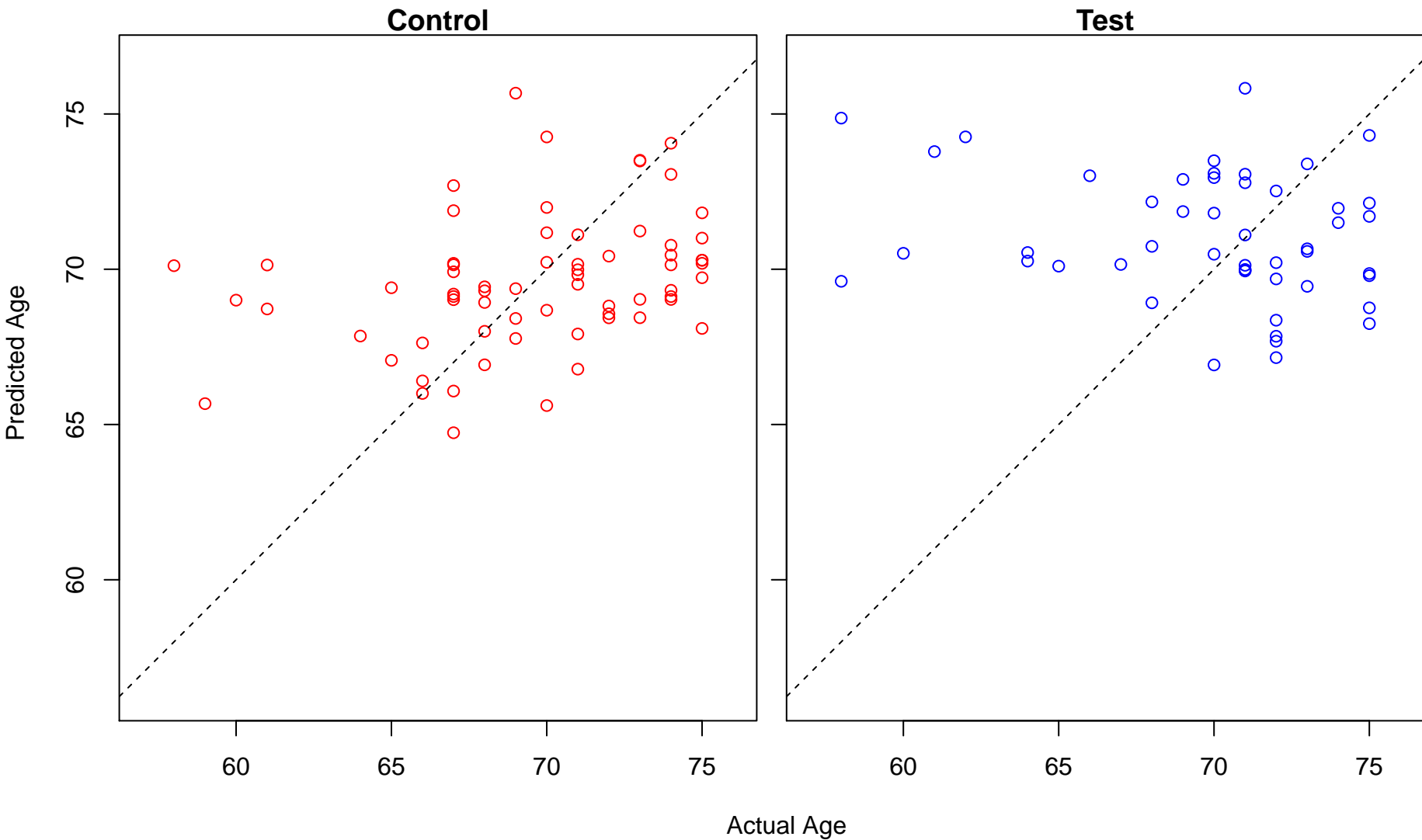


Test

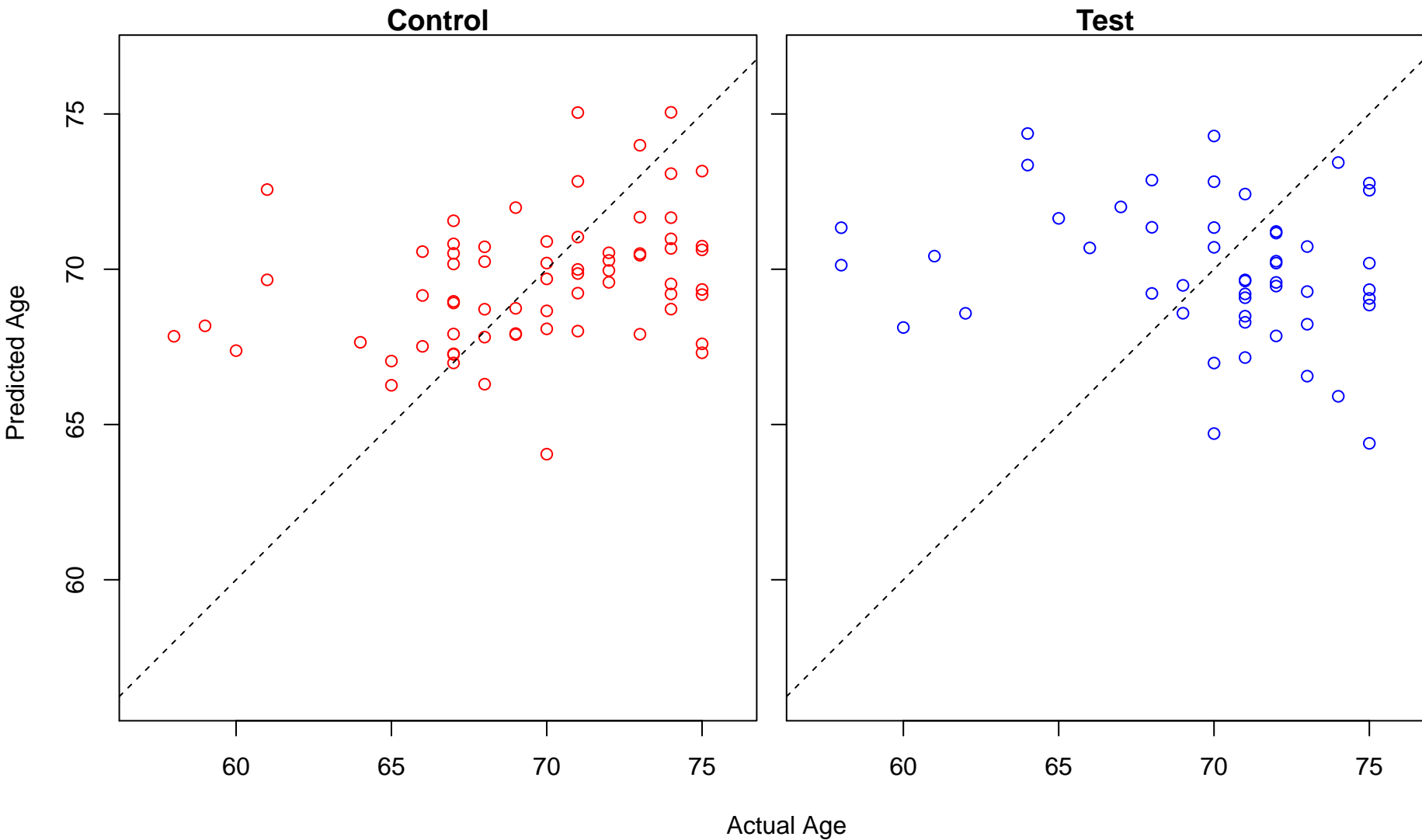


Actual Age

regulation of complement activation (Score: 0.438613)

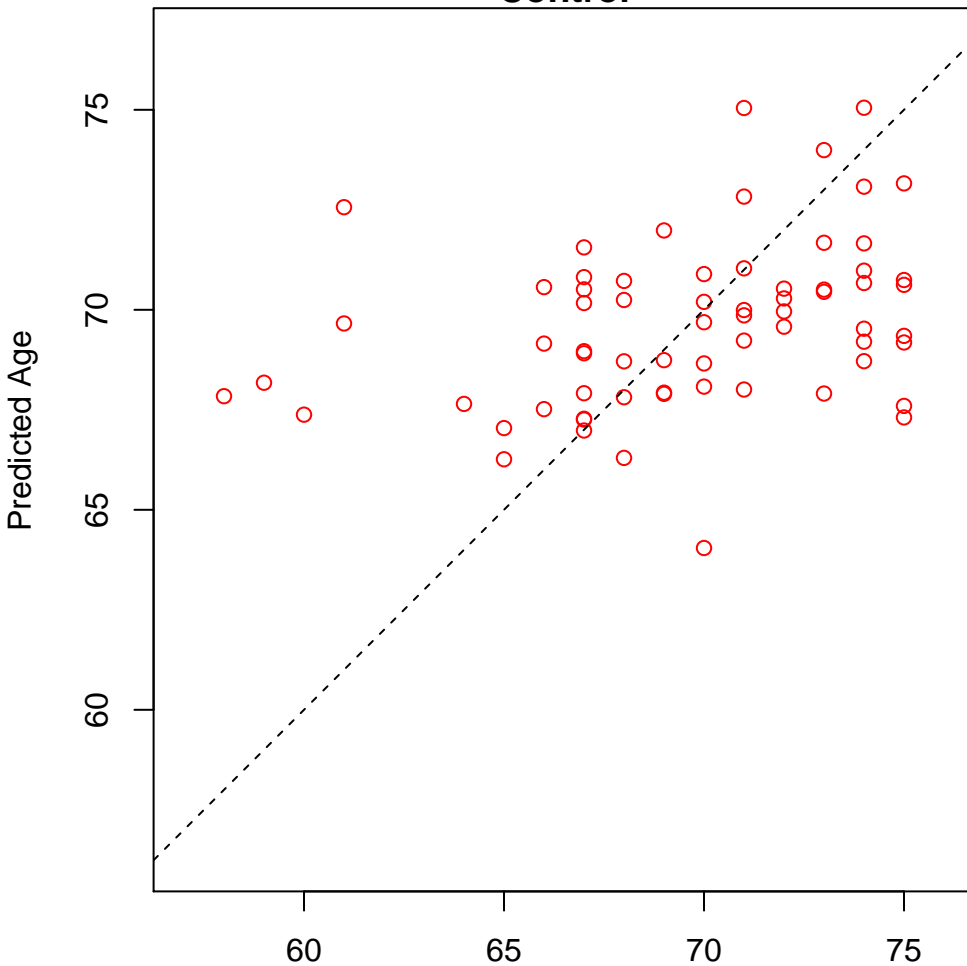


phosphate ion transport (Score: 0.435383)

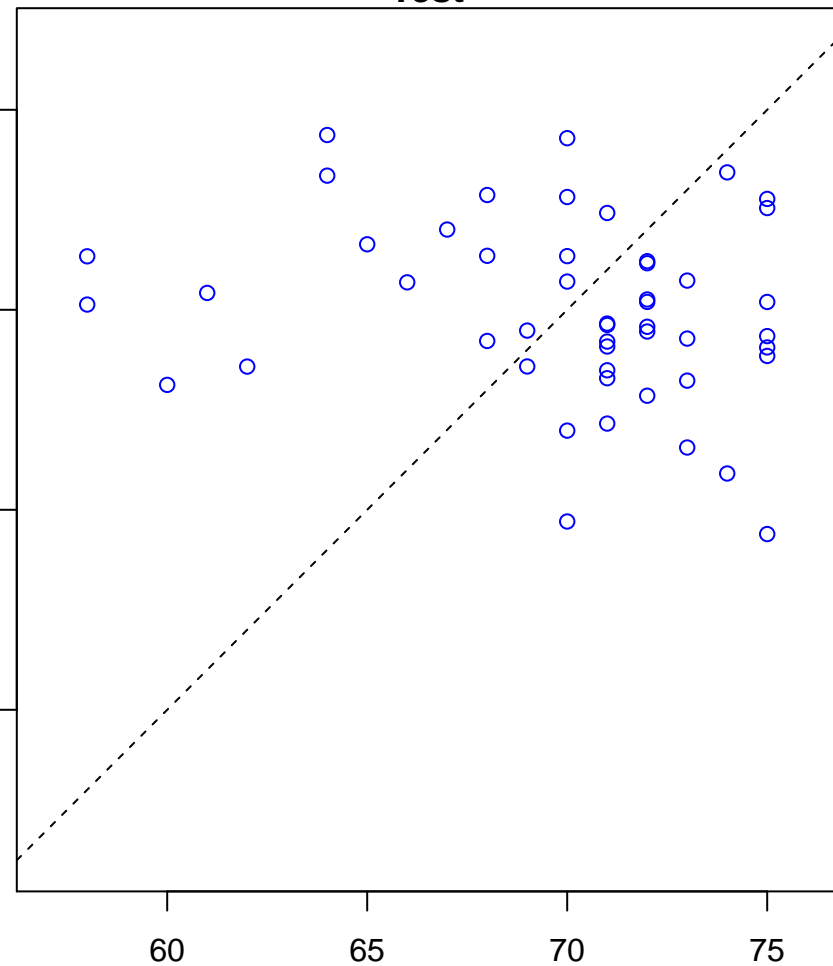


phosphate ion transmembrane transport (Score: 0.435383)

Control

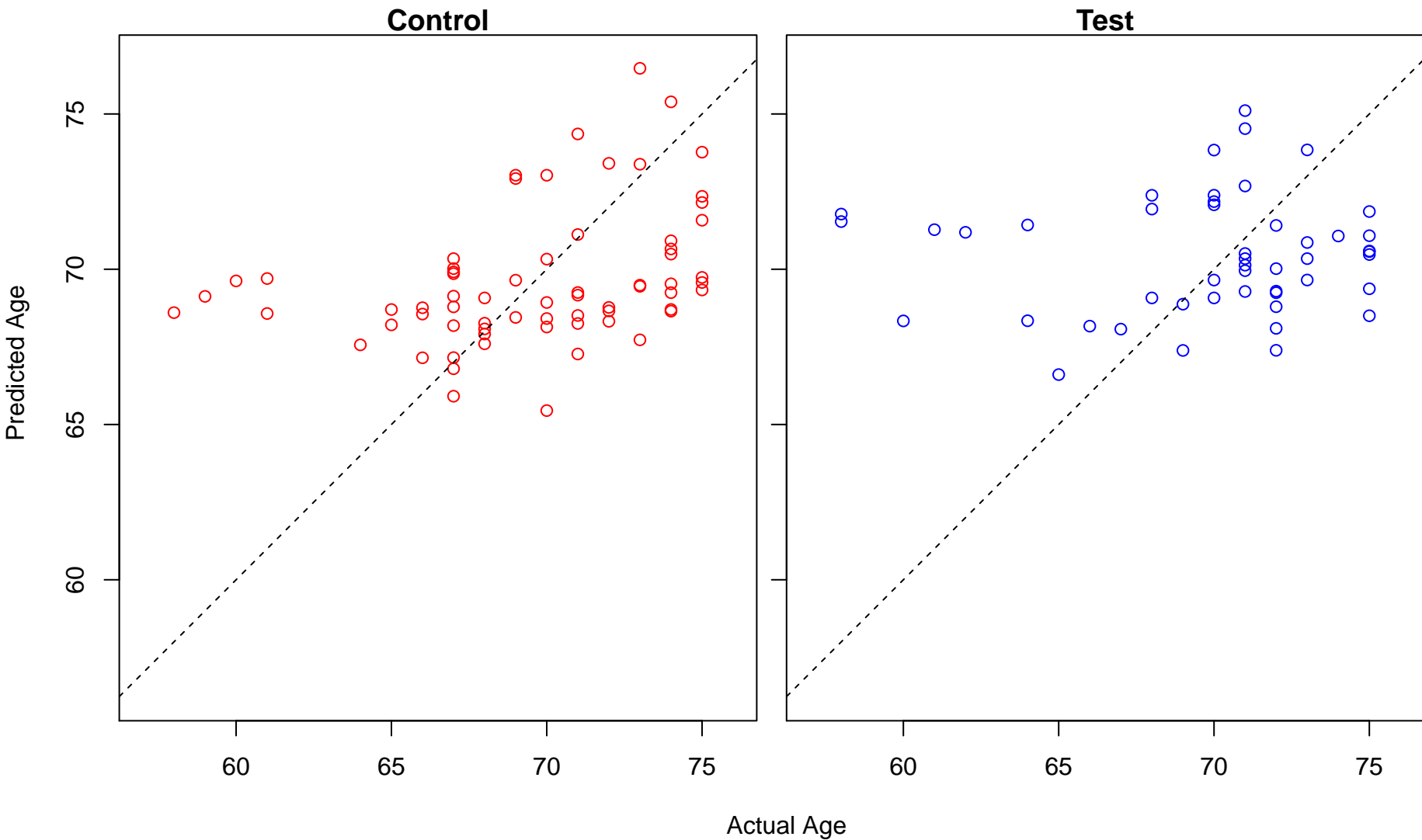


Test

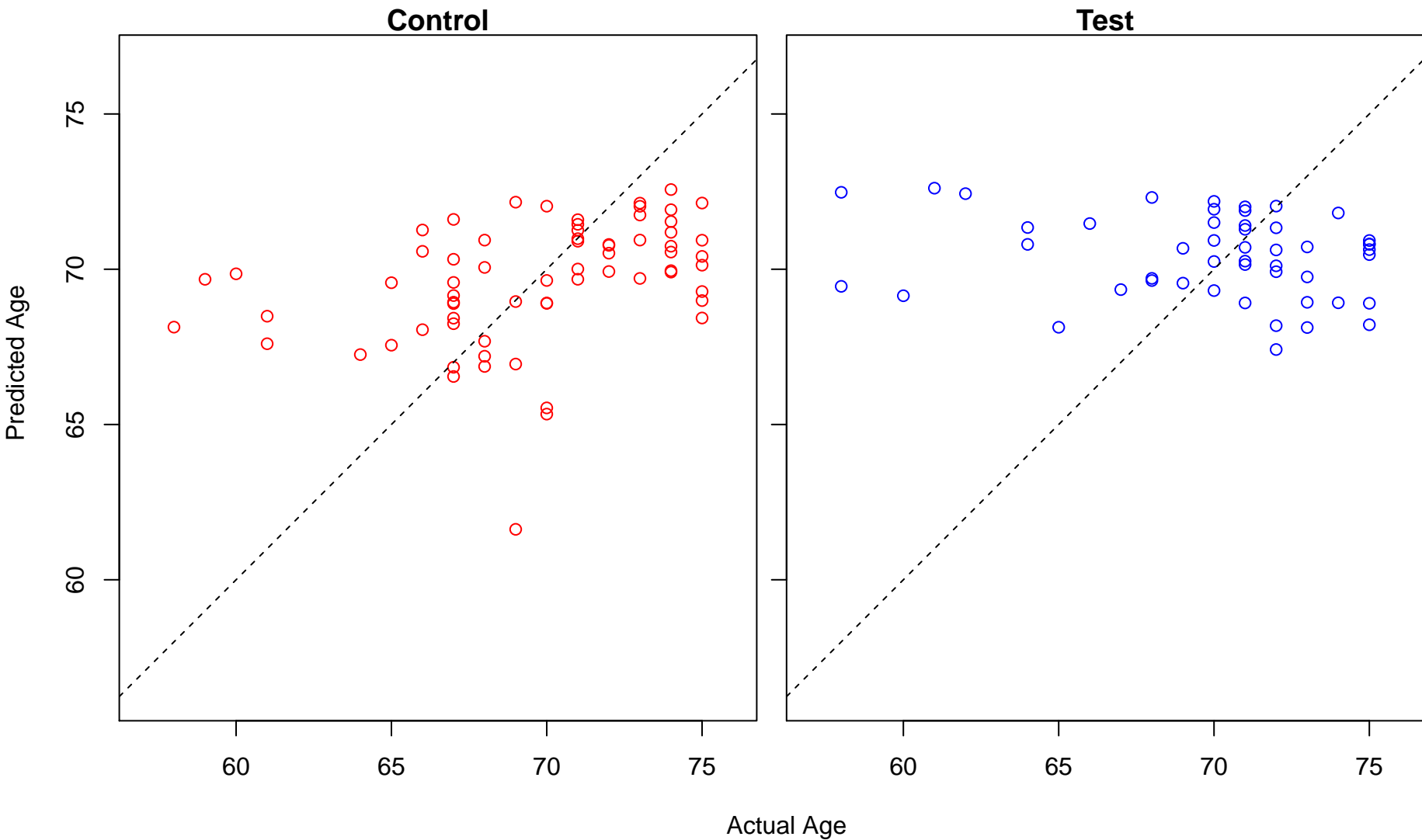


Actual Age

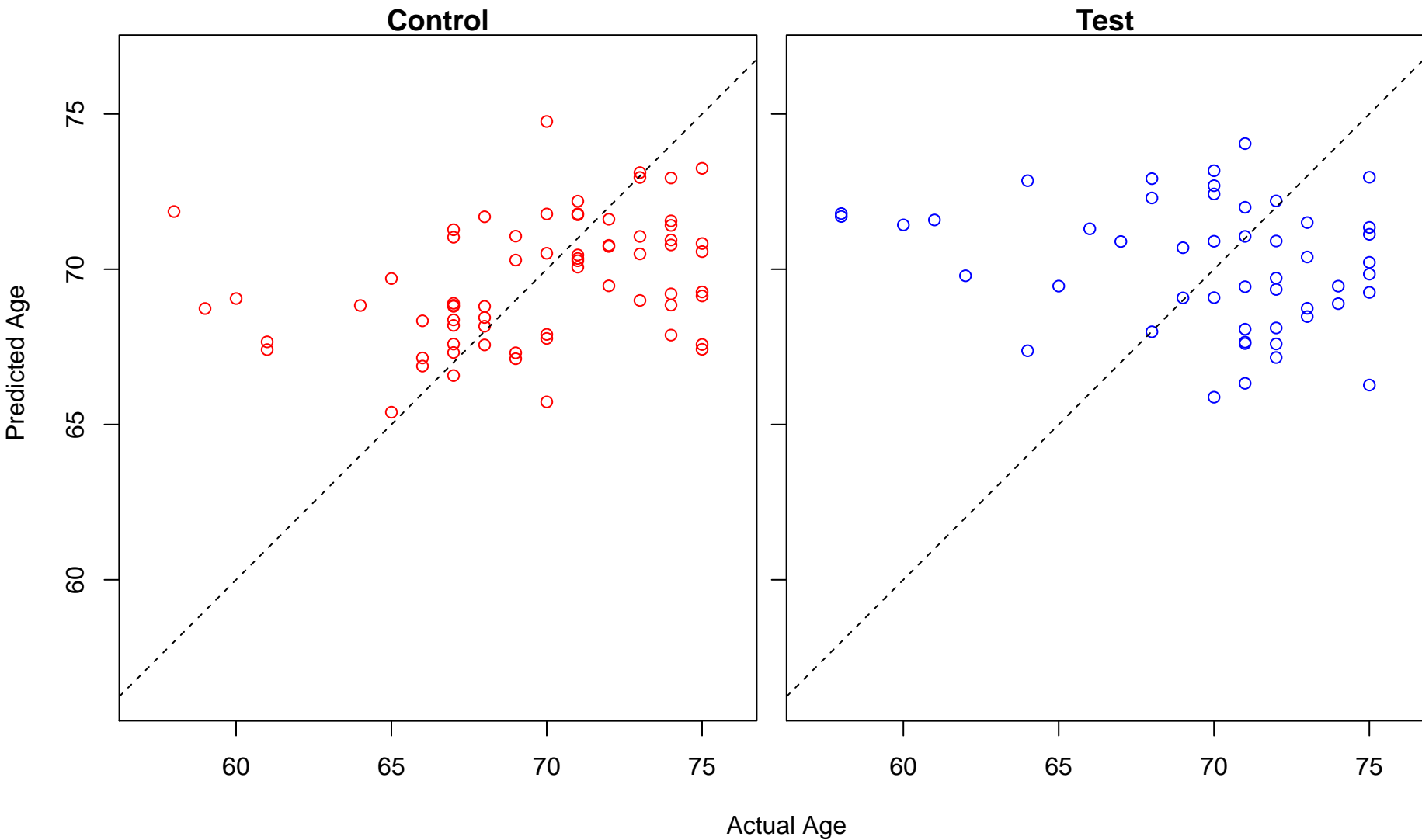
bone cell development (Score: 0.434120)



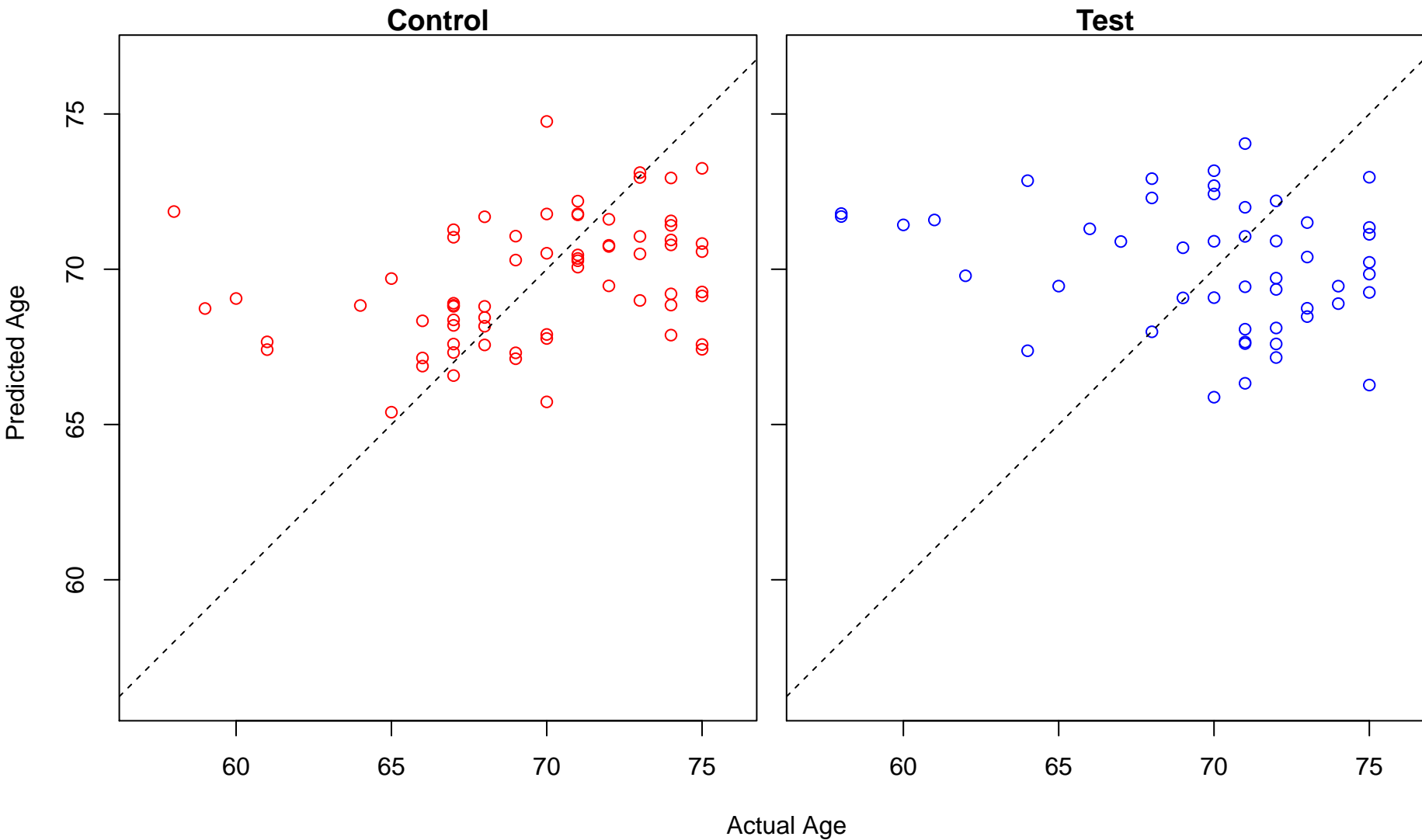
response to cadmium ion (Score: 0.433895)



nuclear RNA surveillance (Score: 0.433613)

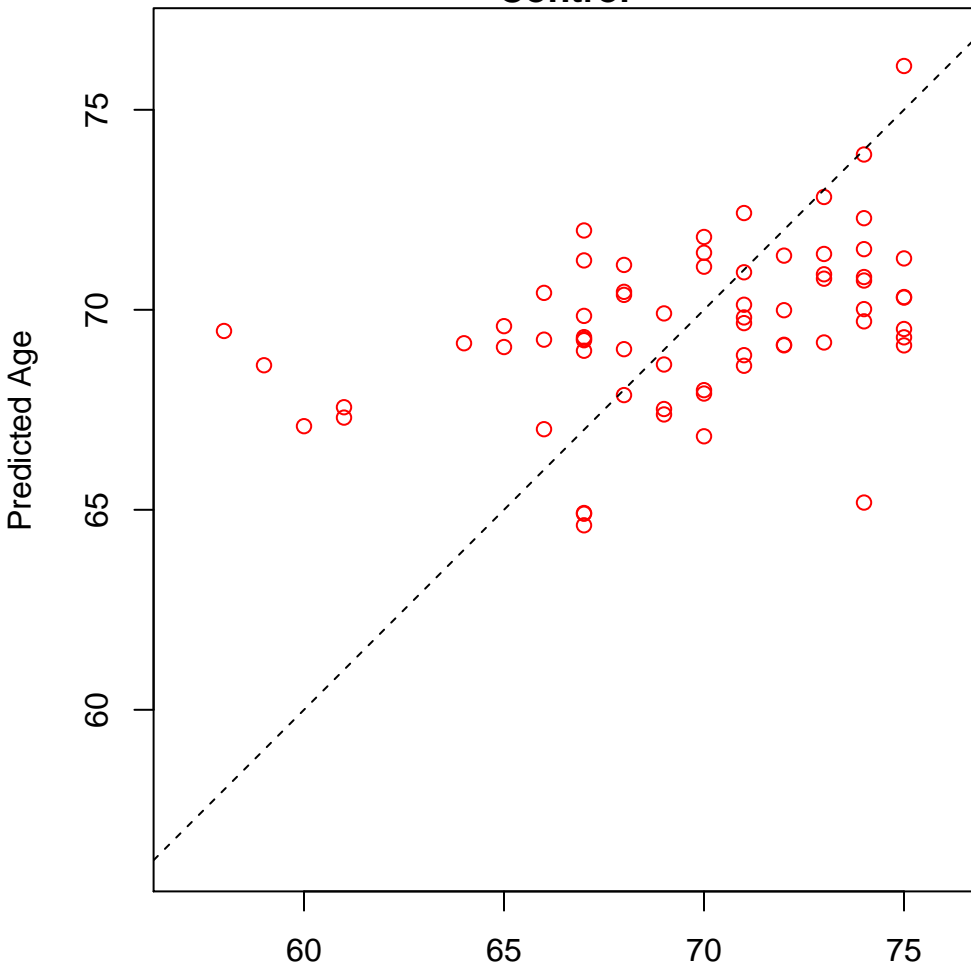


nuclear mRNA surveillance (Score: 0.433613)

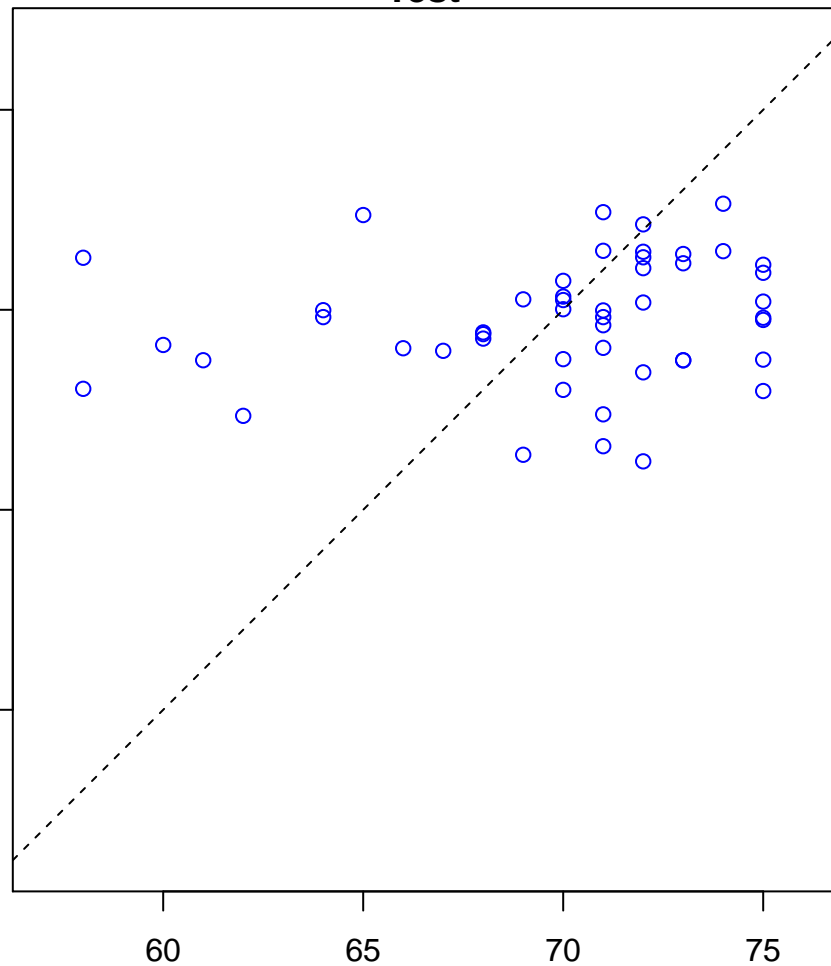


physiological muscle hypertrophy (Score: 0.433594)

Control



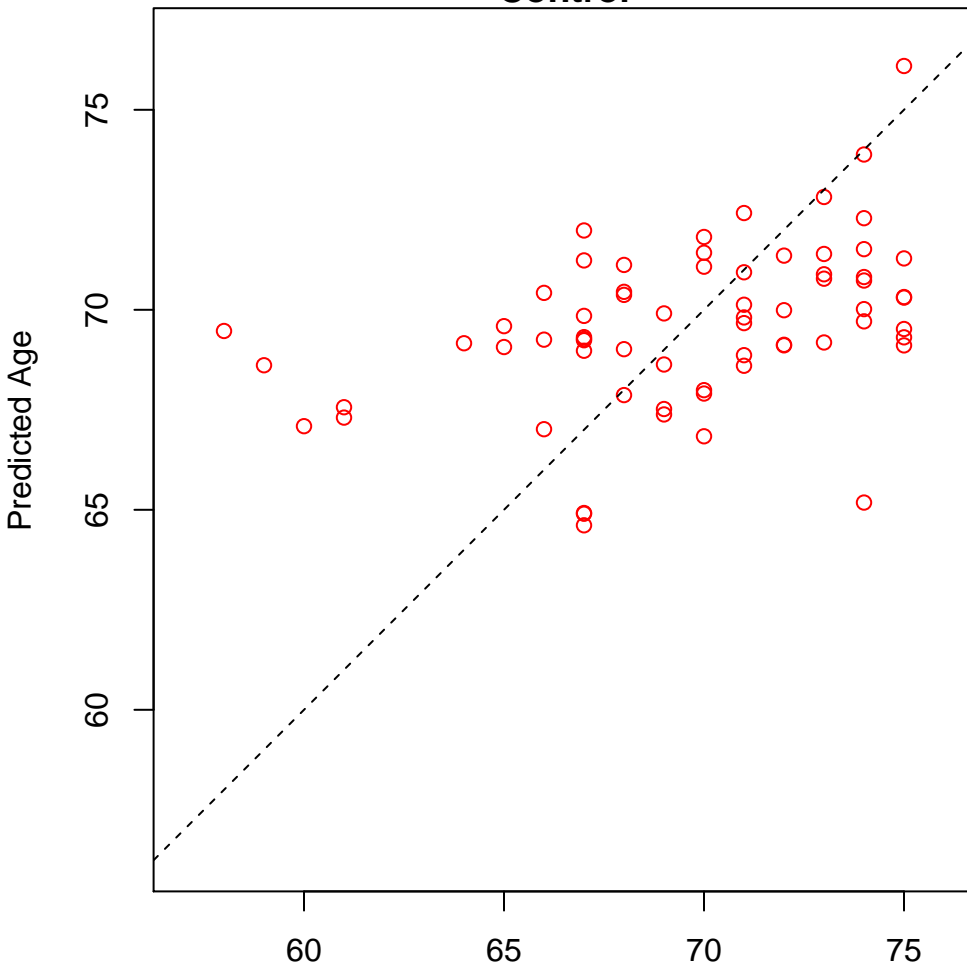
Test



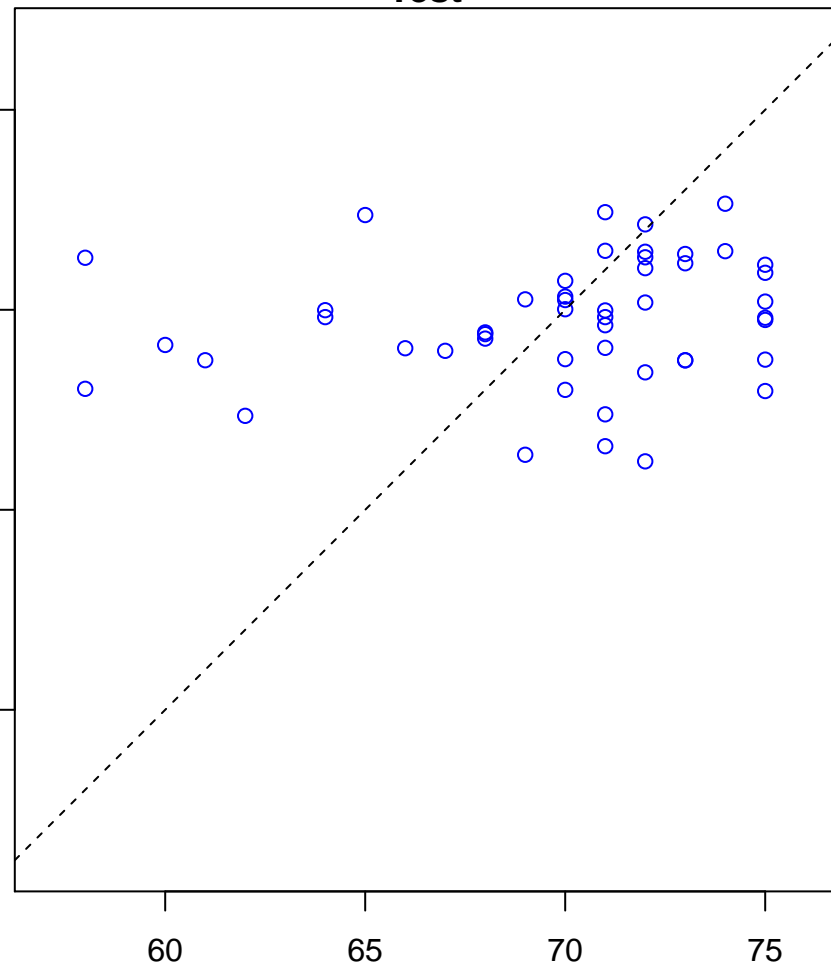
Actual Age

physiological cardiac muscle hypertrophy (Score: 0.433594)

Control

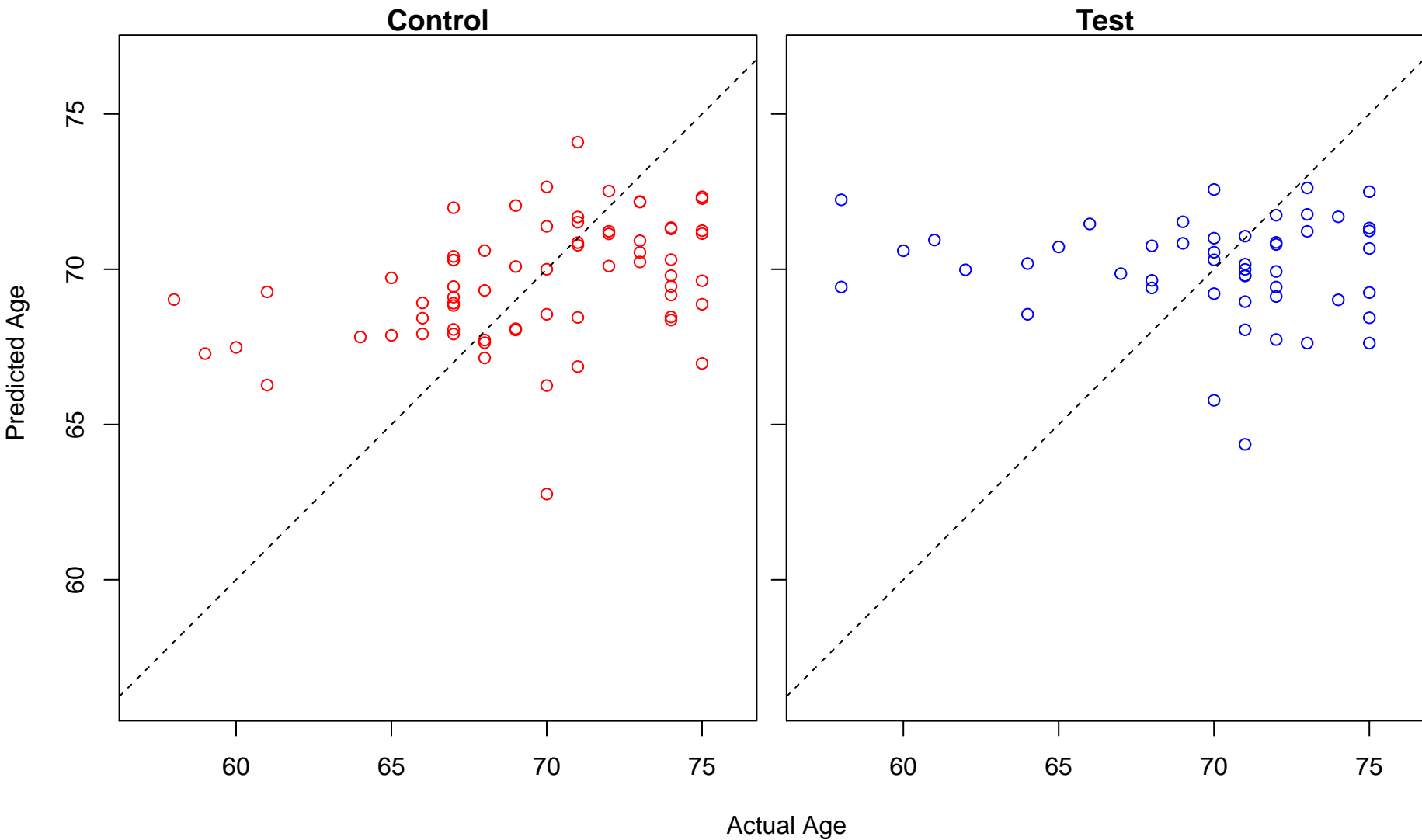


Test



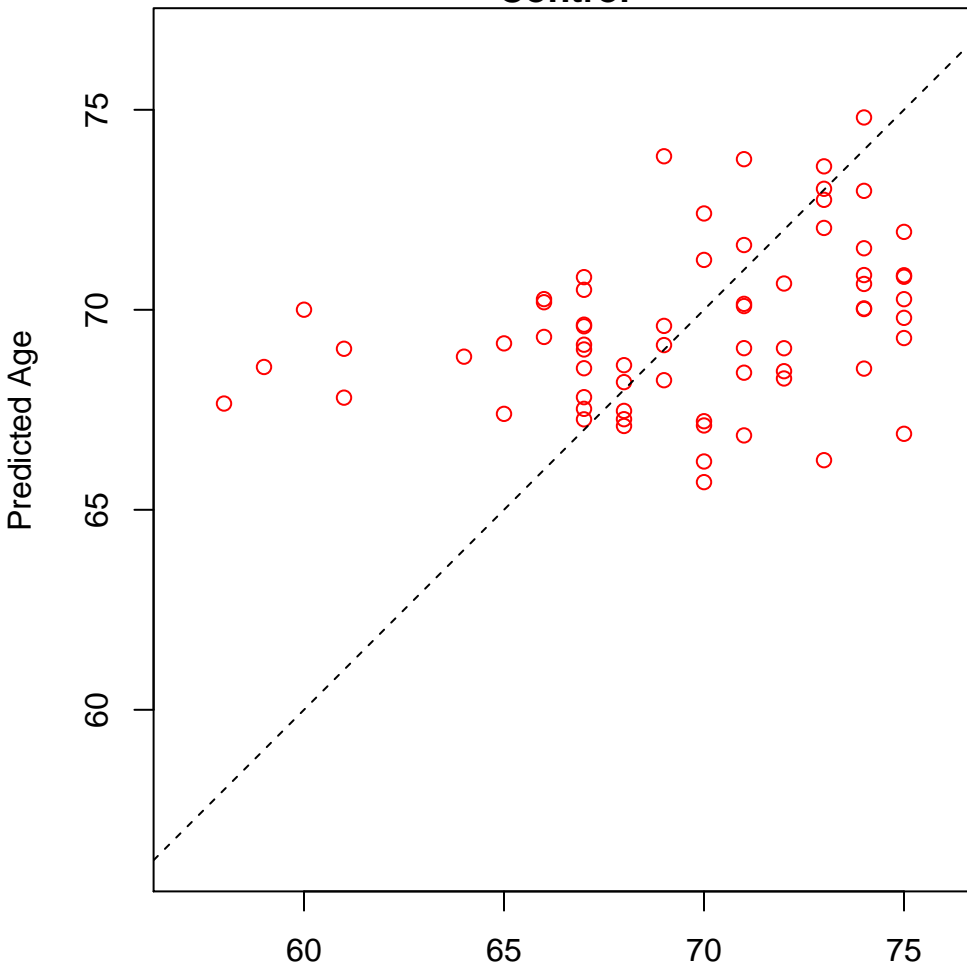
Actual Age

cell-cell junction maintenance (Score: 0.433384)

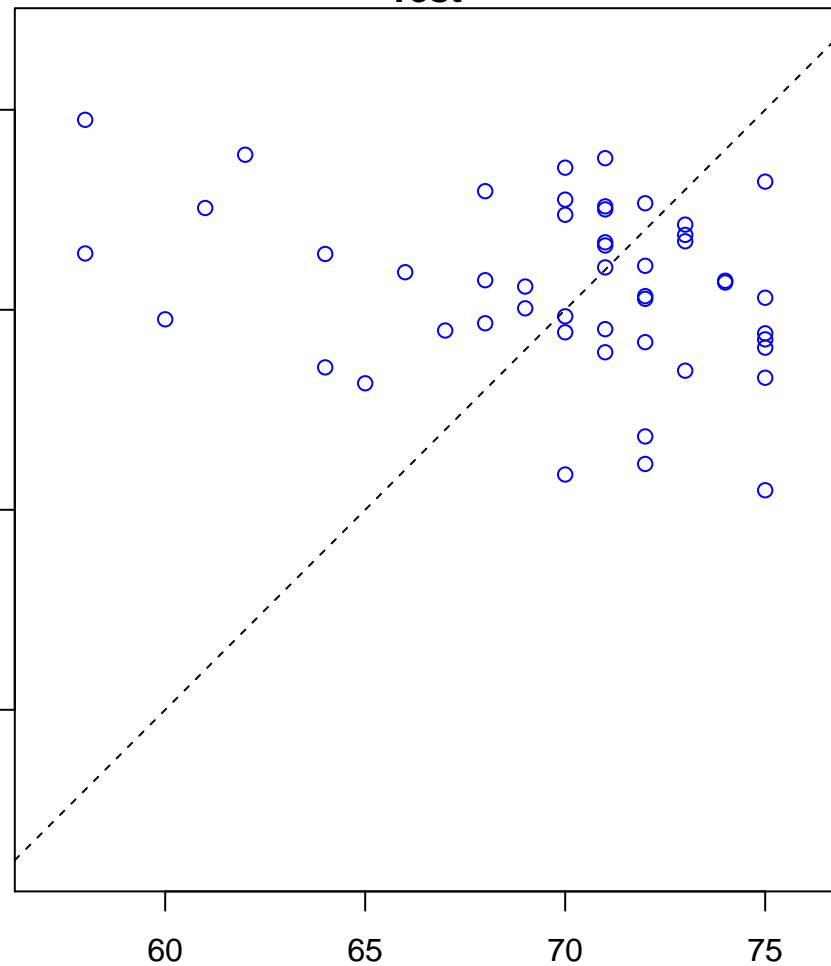


protein targeting to plasma membrane (Score: 0.431798)

Control



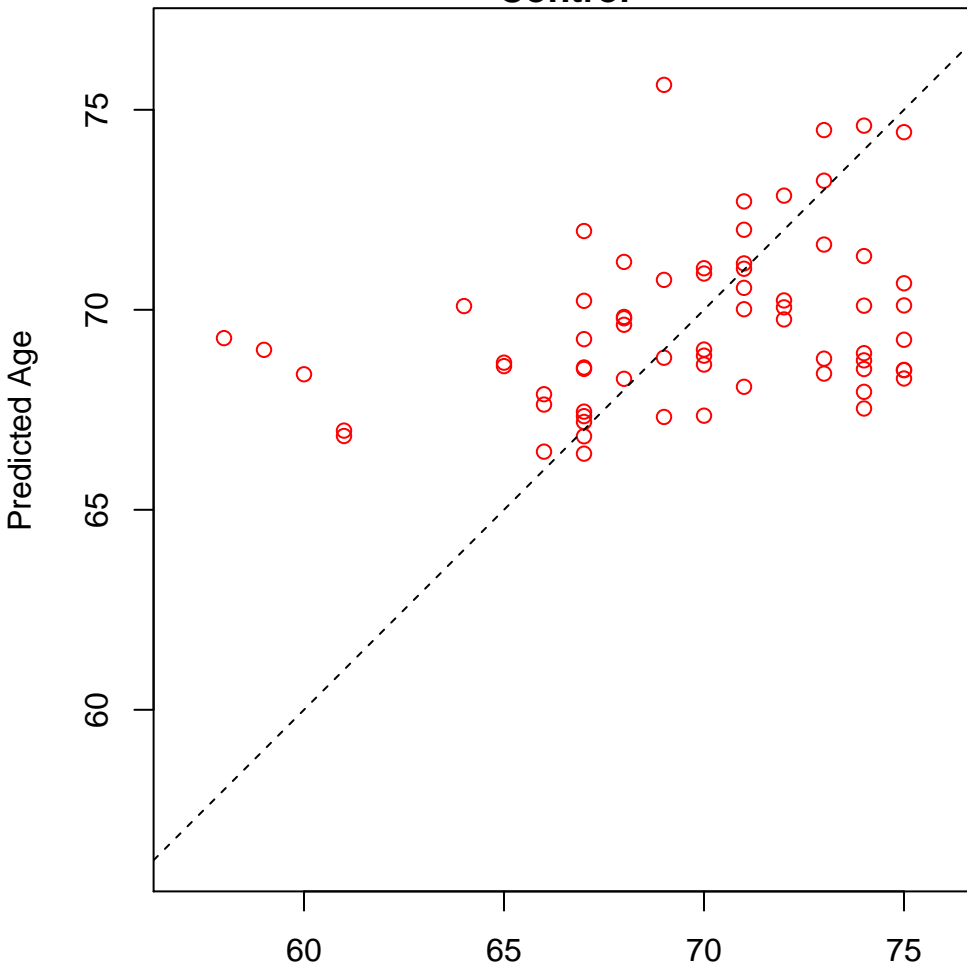
Test



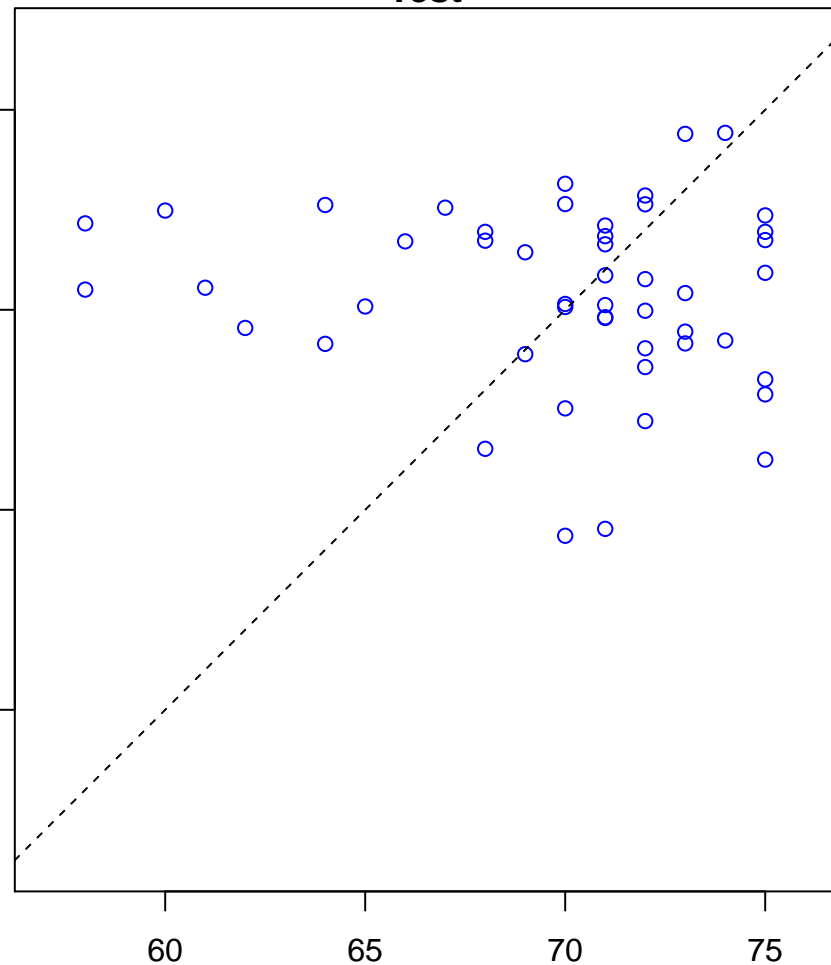
Actual Age

eye photoreceptor cell differentiation (Score: 0.430832)

Control

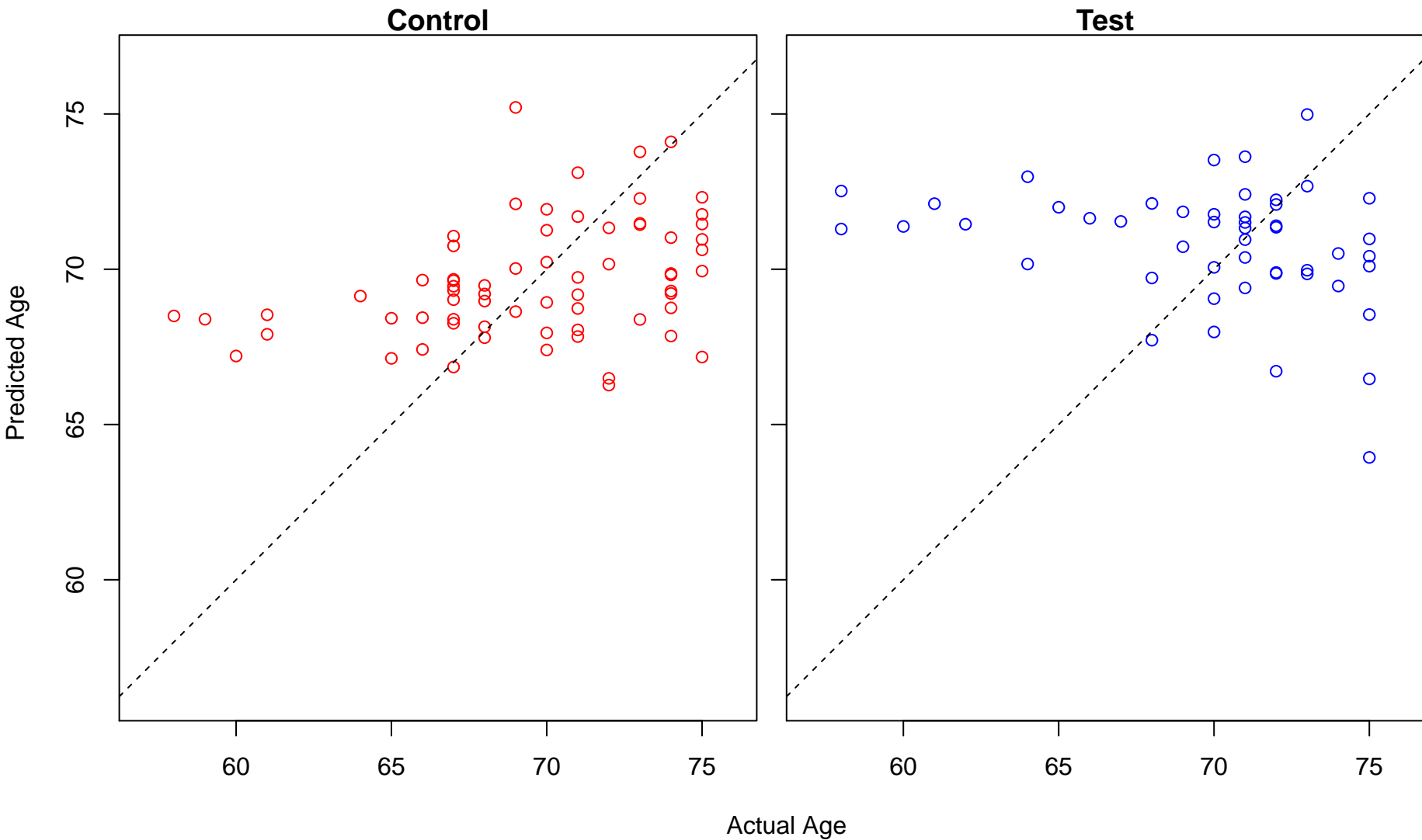


Test

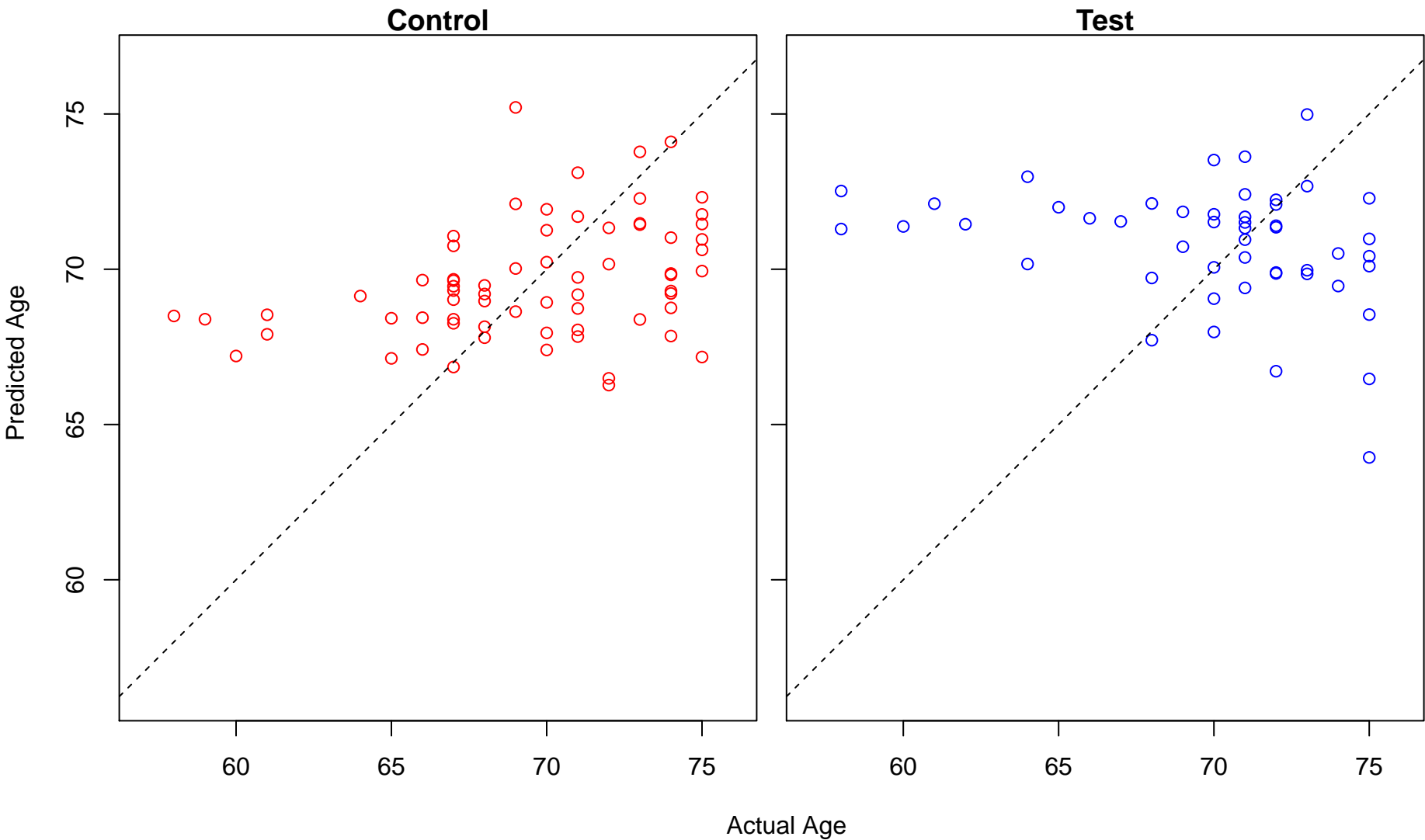


Actual Age

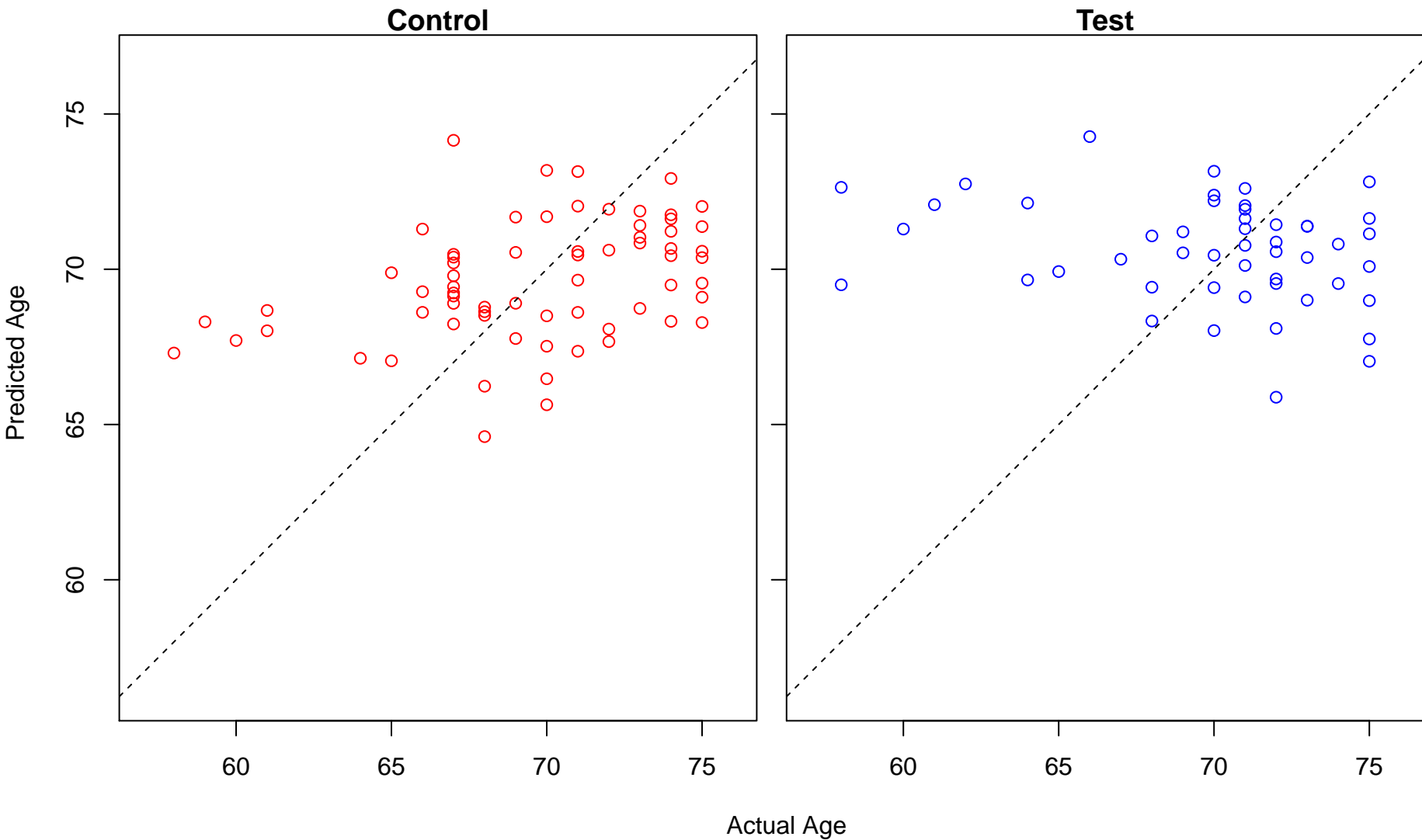
amino-acid betaine metabolic process (Score: 0.430464)



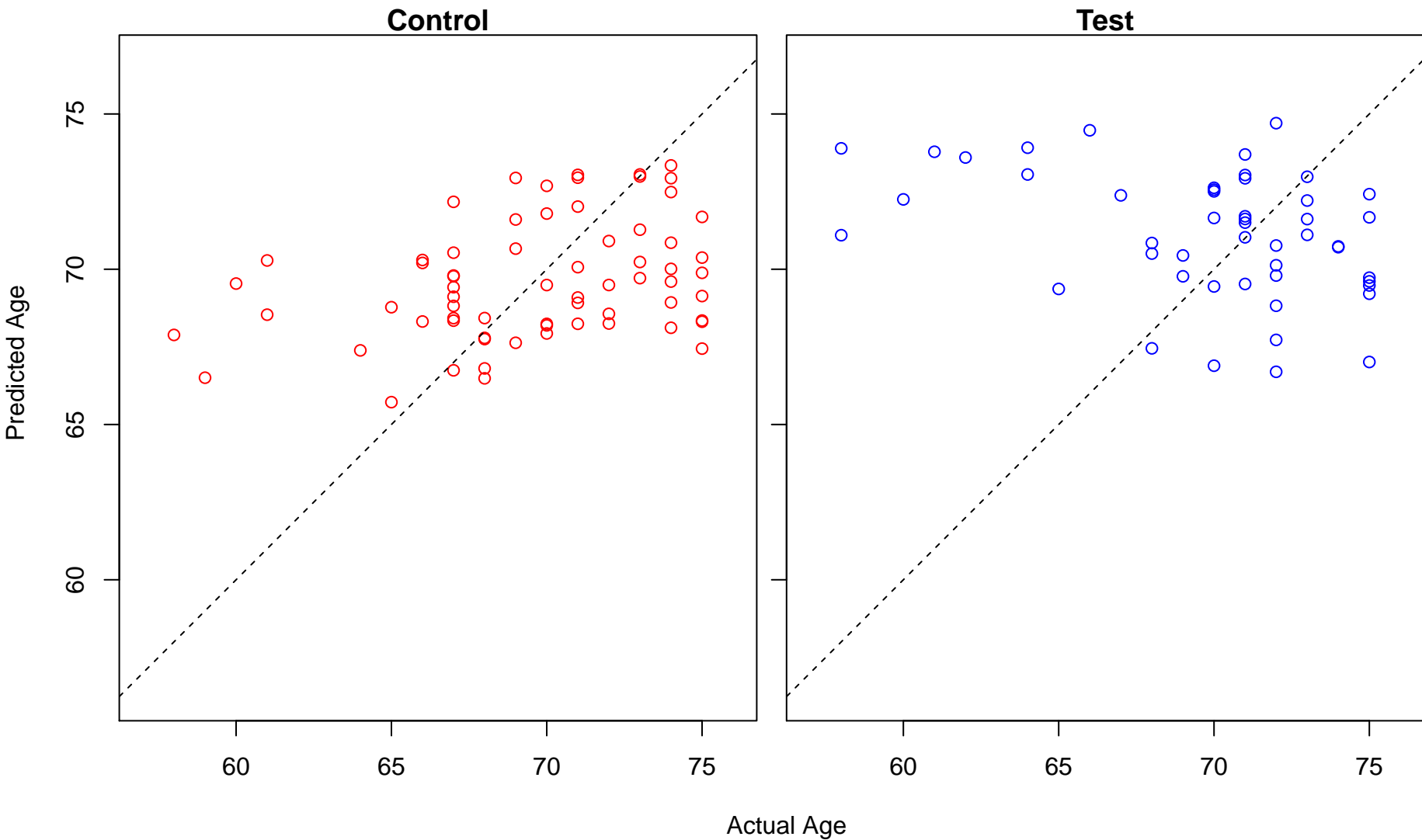
carnitine metabolic process (Score: 0.430464)



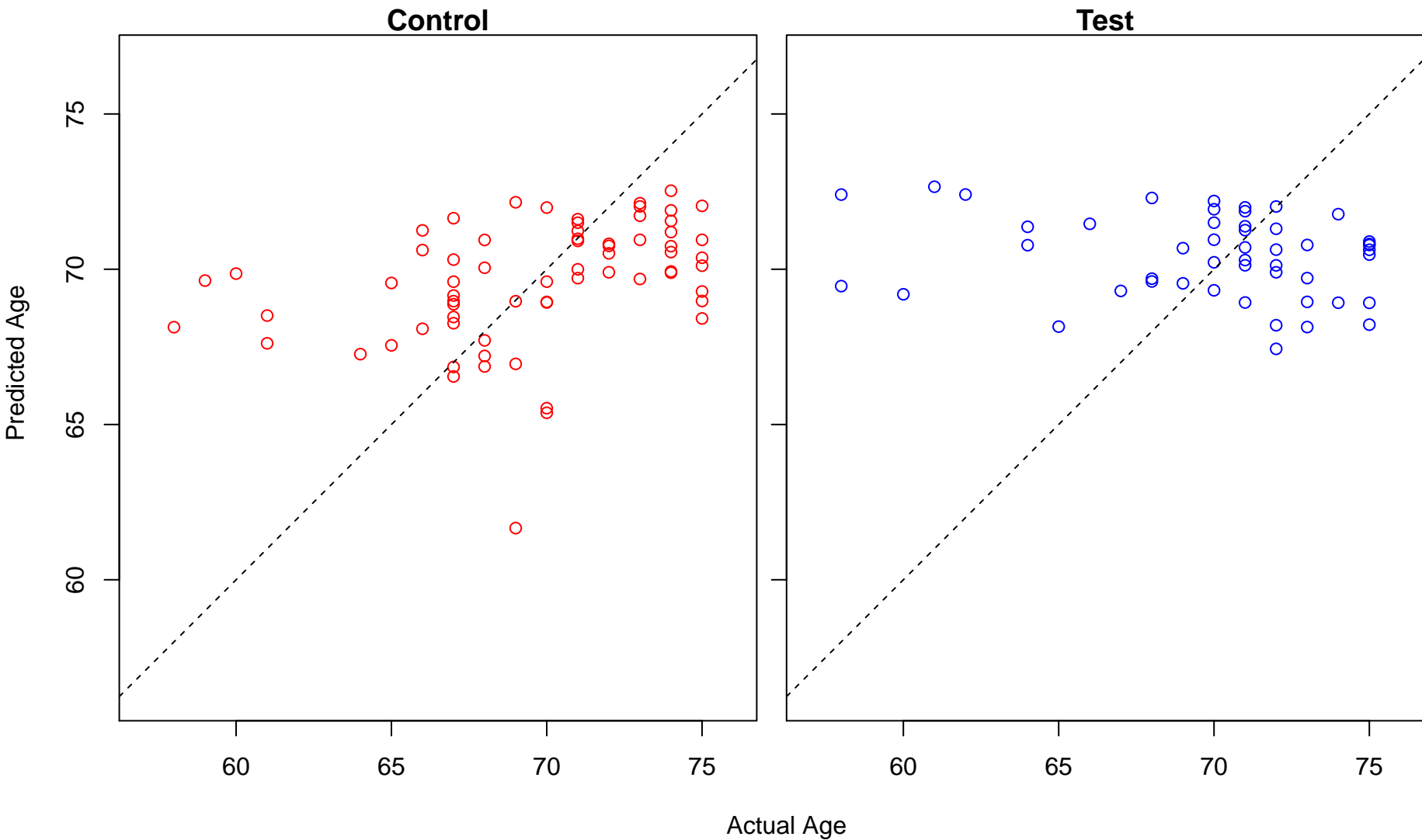
regulation of podosome assembly (Score: 0.430385)



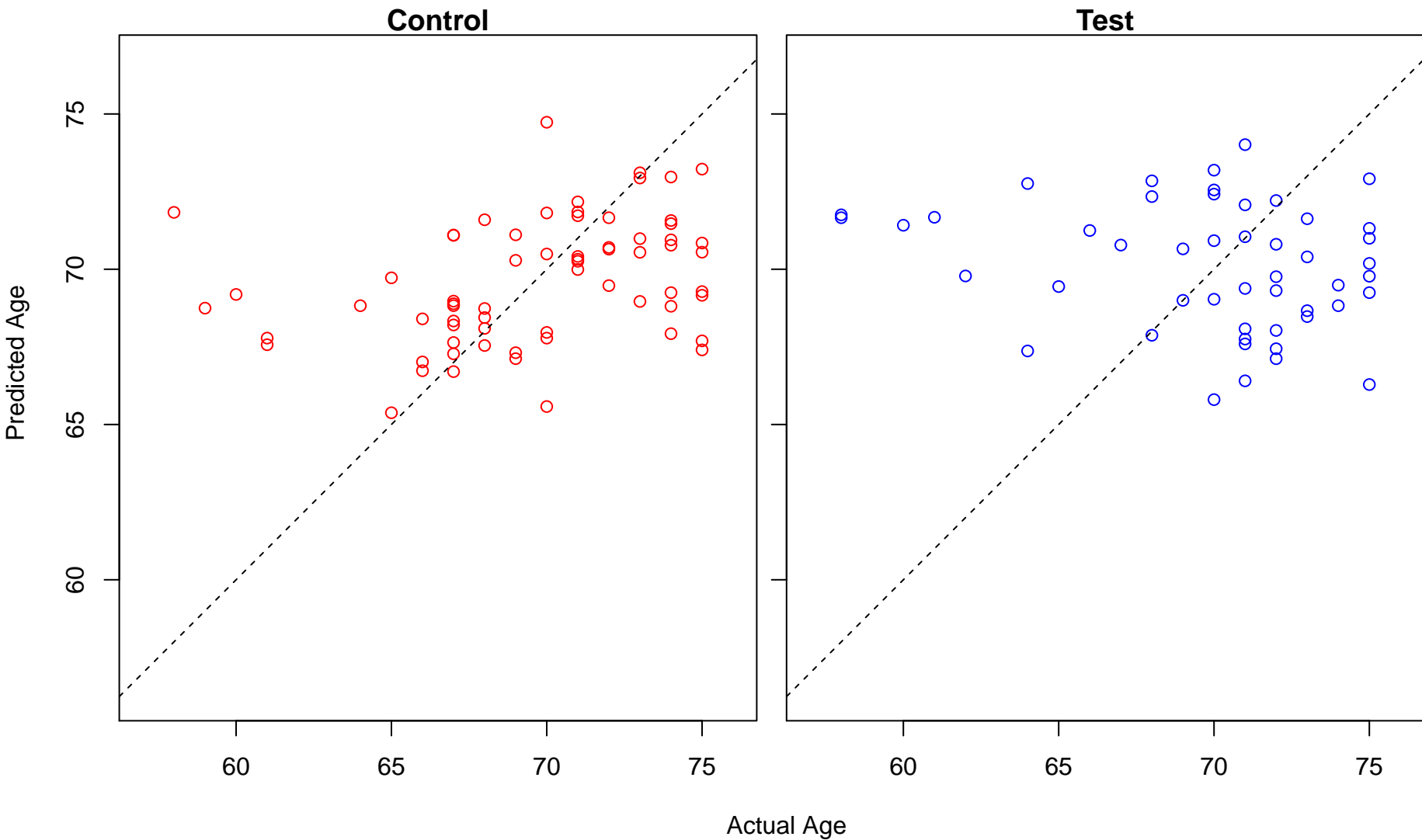
cellular response to acidic pH (Score: 0.429589)



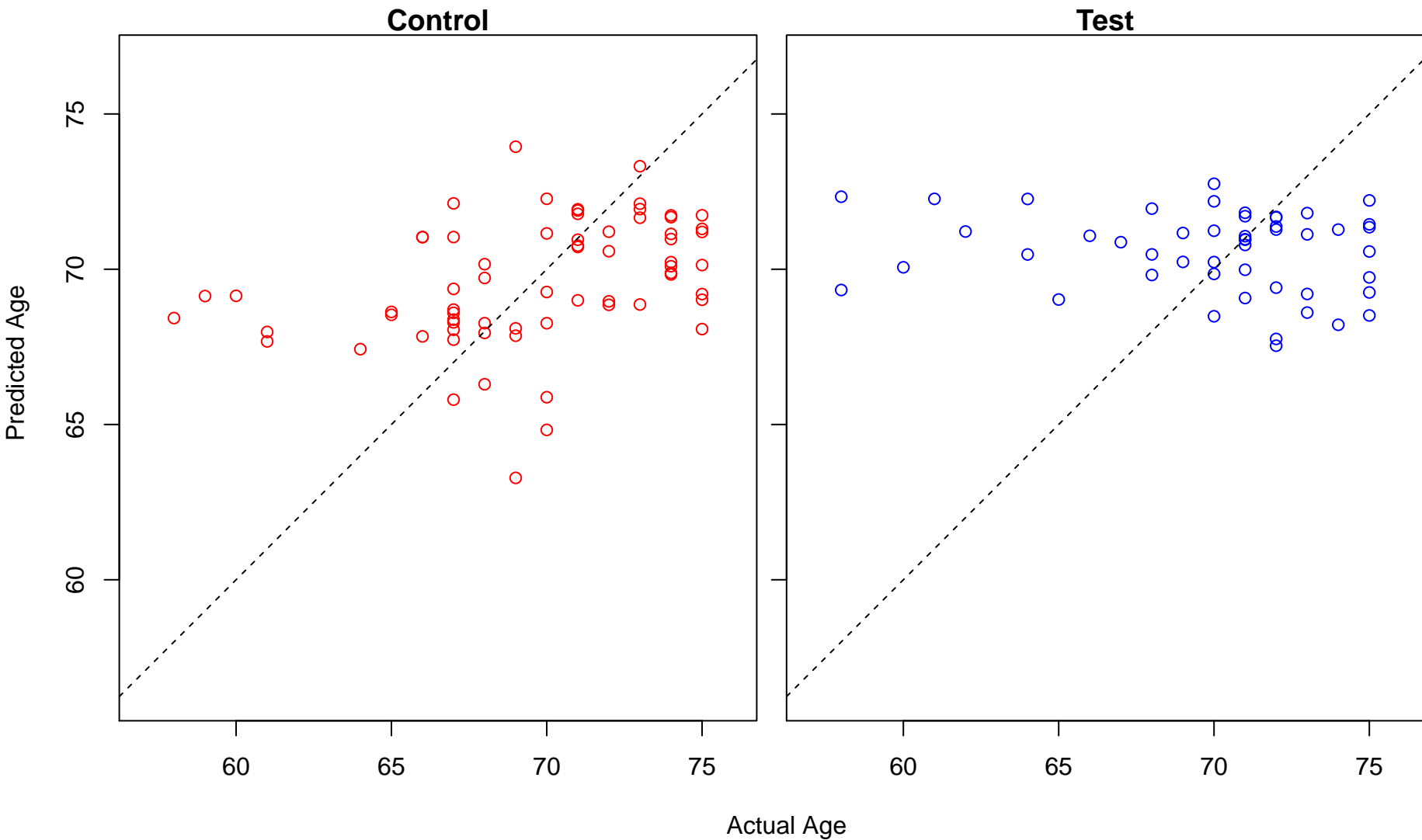
cellular response to cadmium ion (Score: 0.429521)



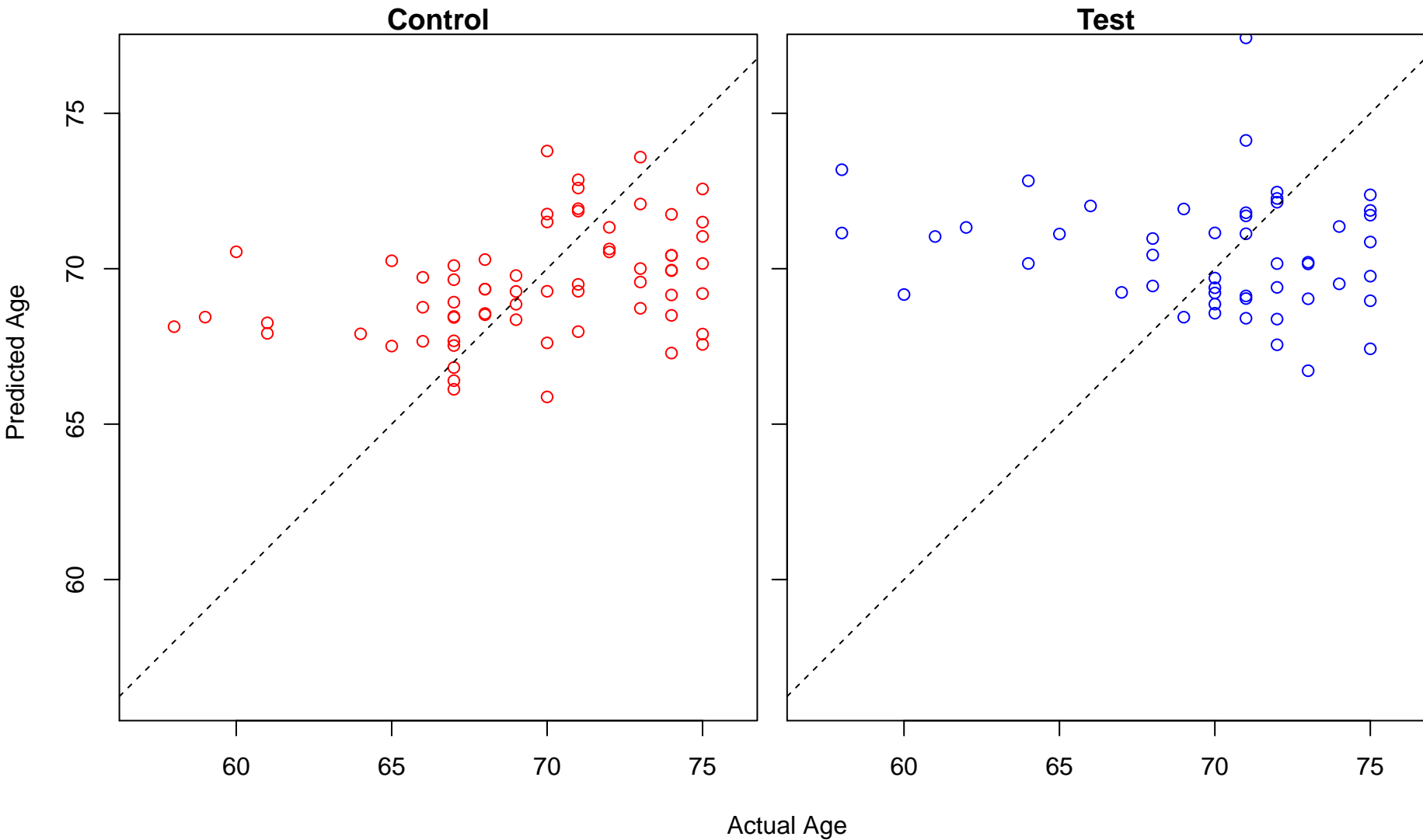
RNA surveillance (Score: 0.428241)



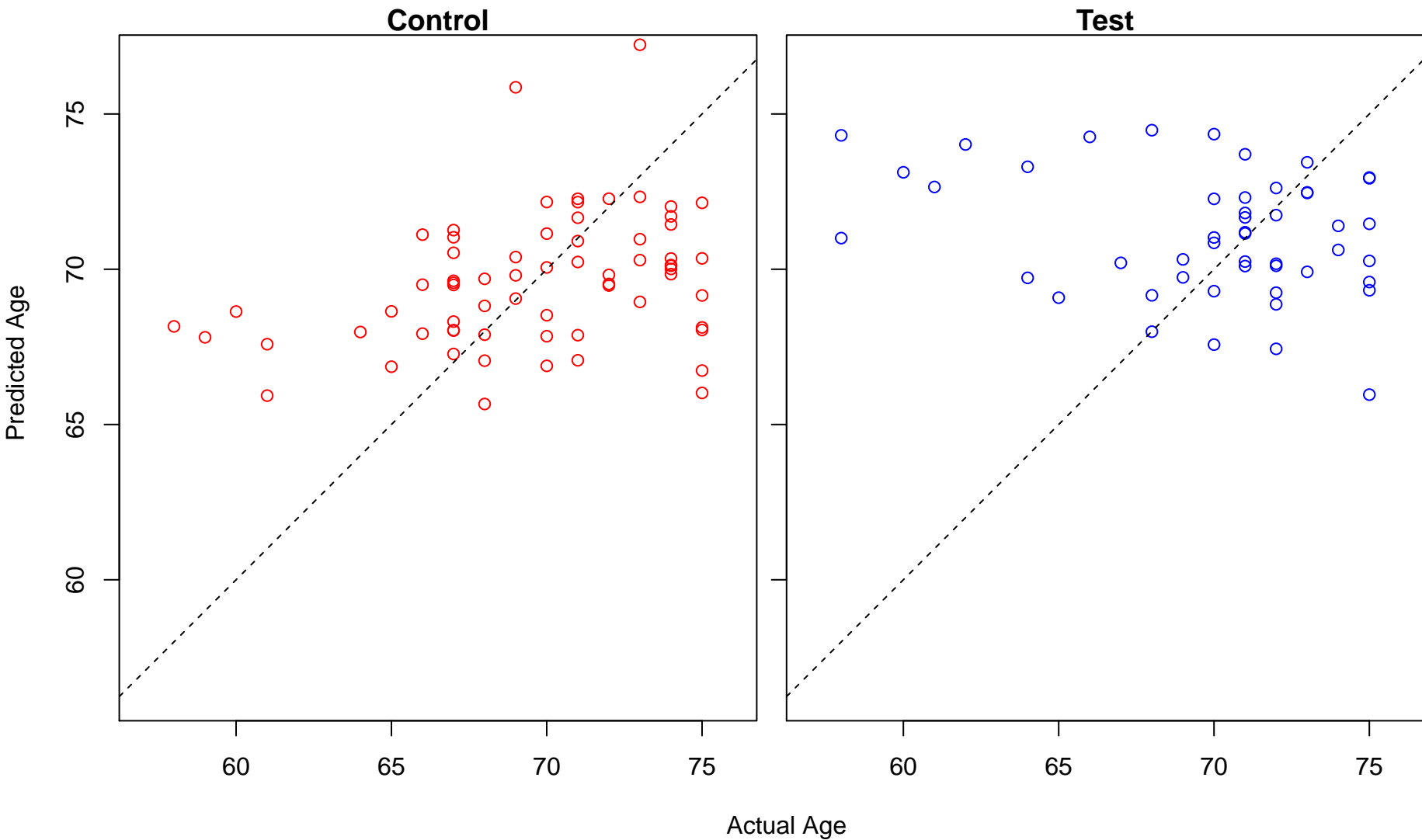
cyclooxygenase pathway (Score: 0.427647)



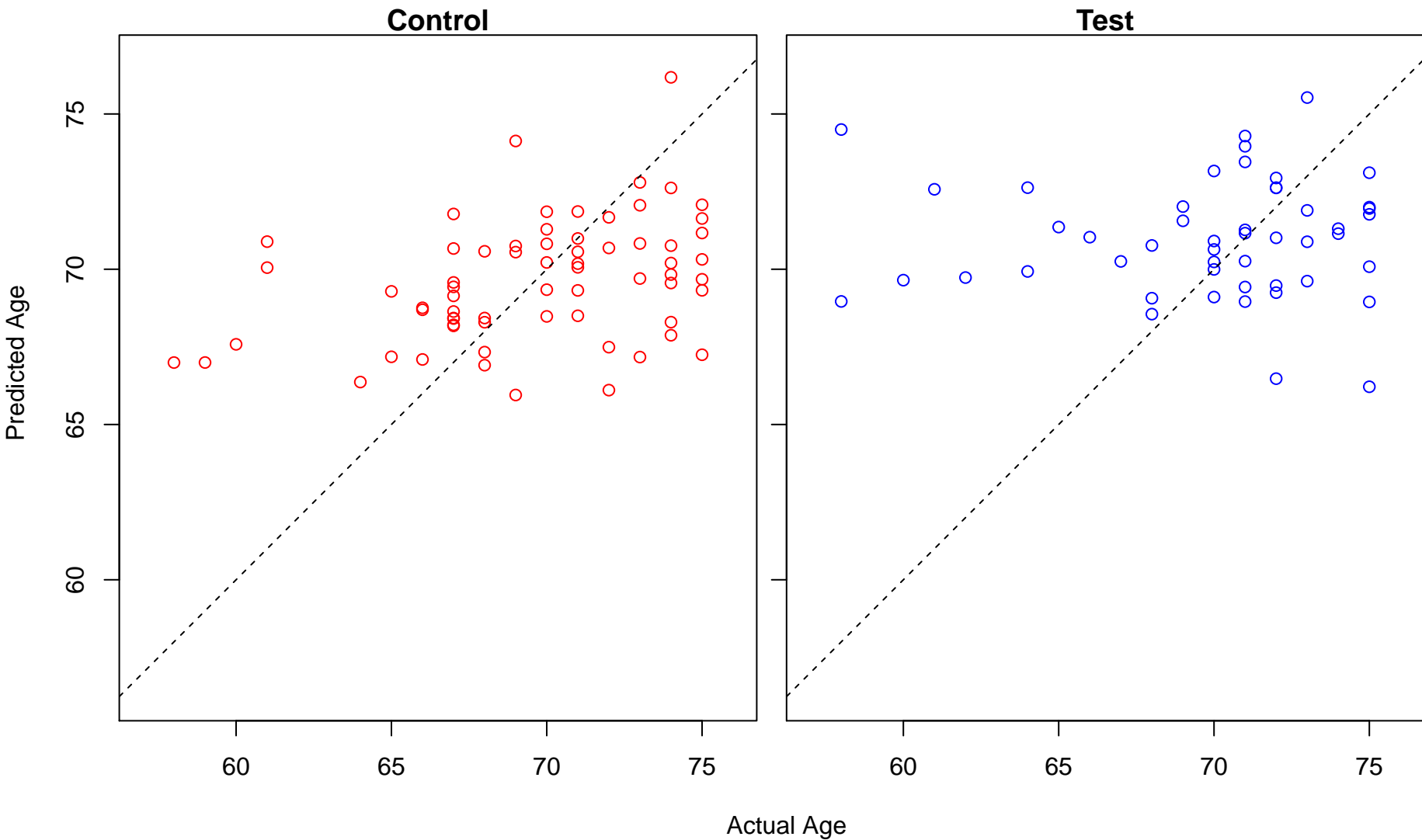
regulation of Wnt signaling pathway, planar cell polarity pathway (Score: 0.426406)



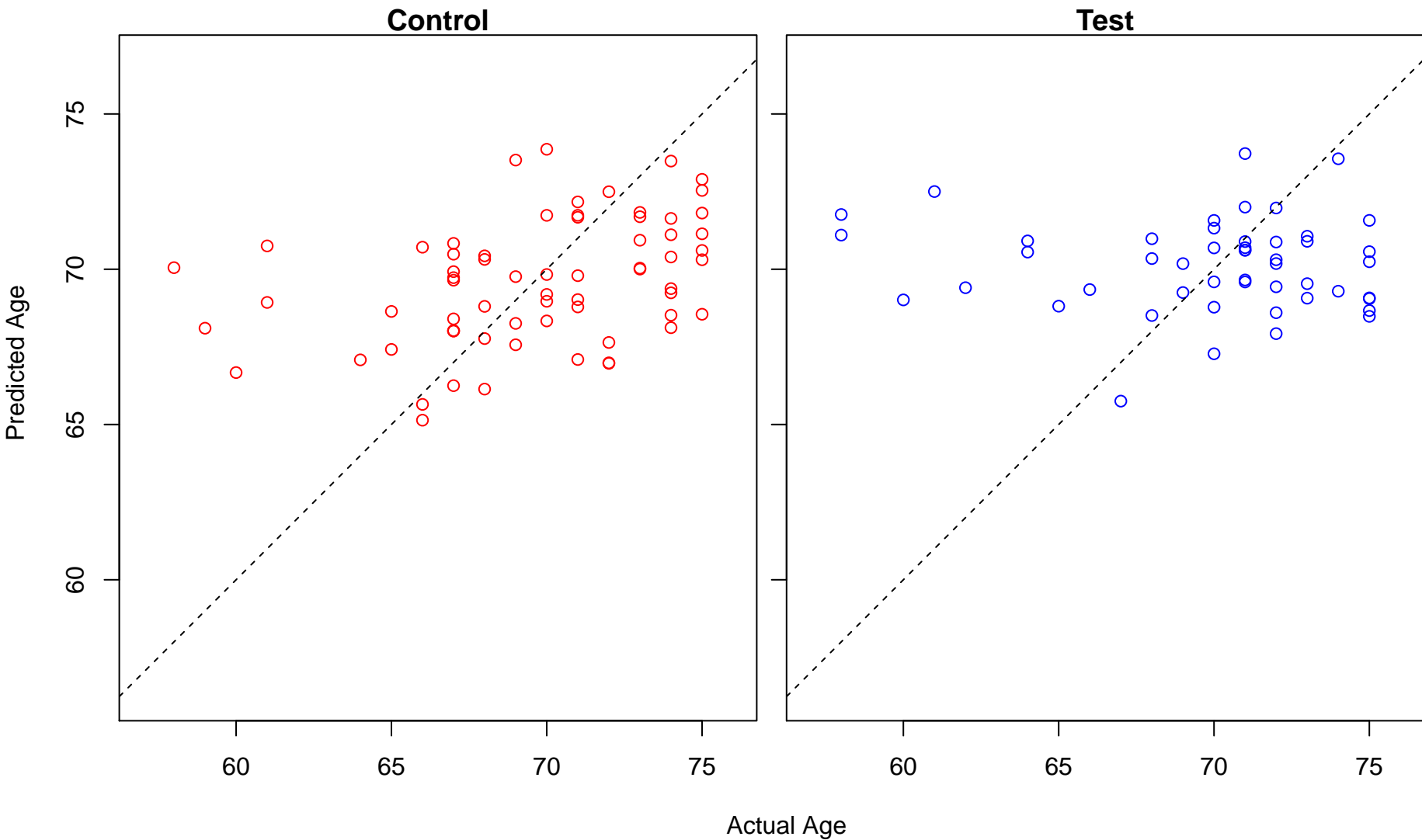
response to muscle stretch (Score: 0.425816)



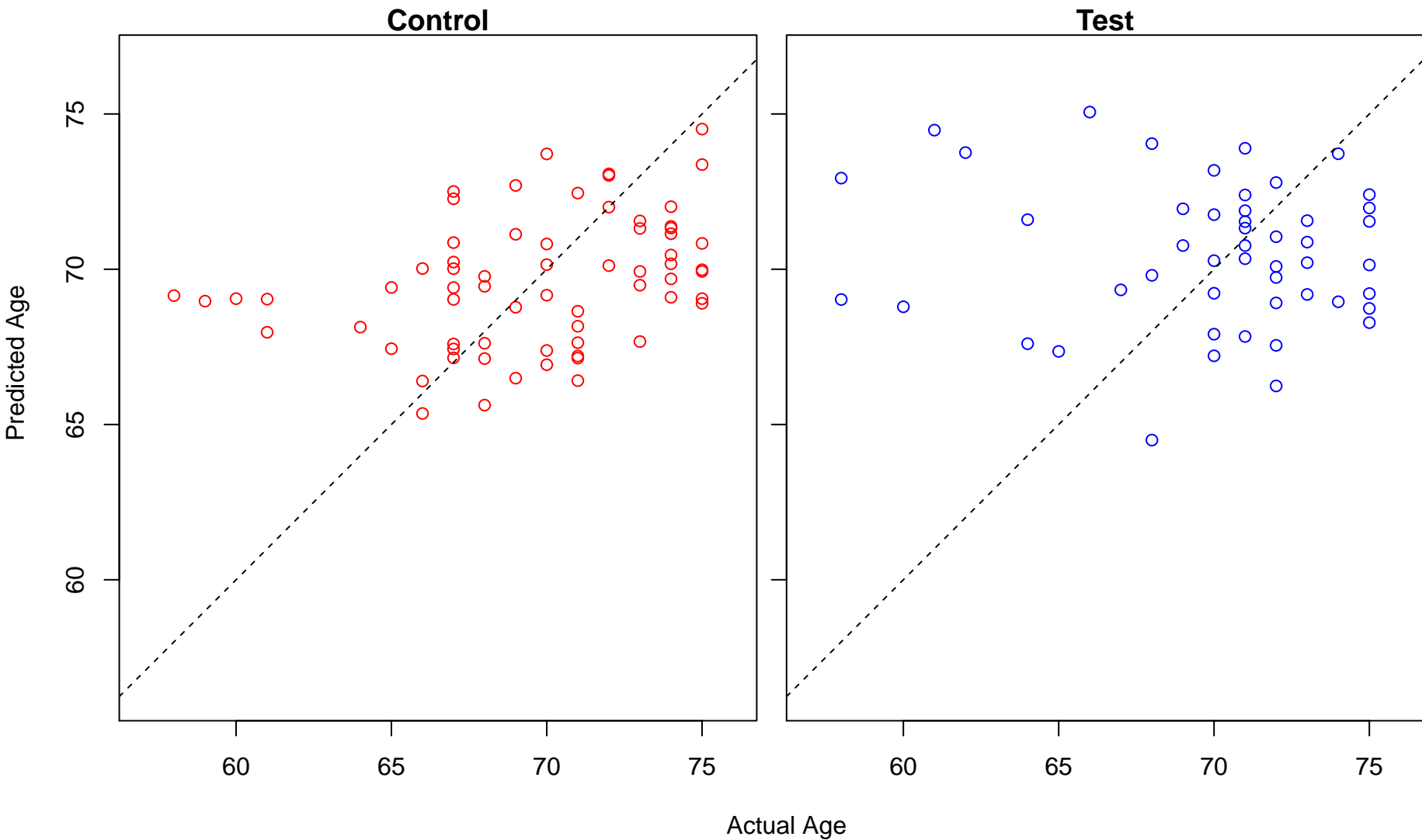
regulation of NK T cell activation (Score: 0.425401)



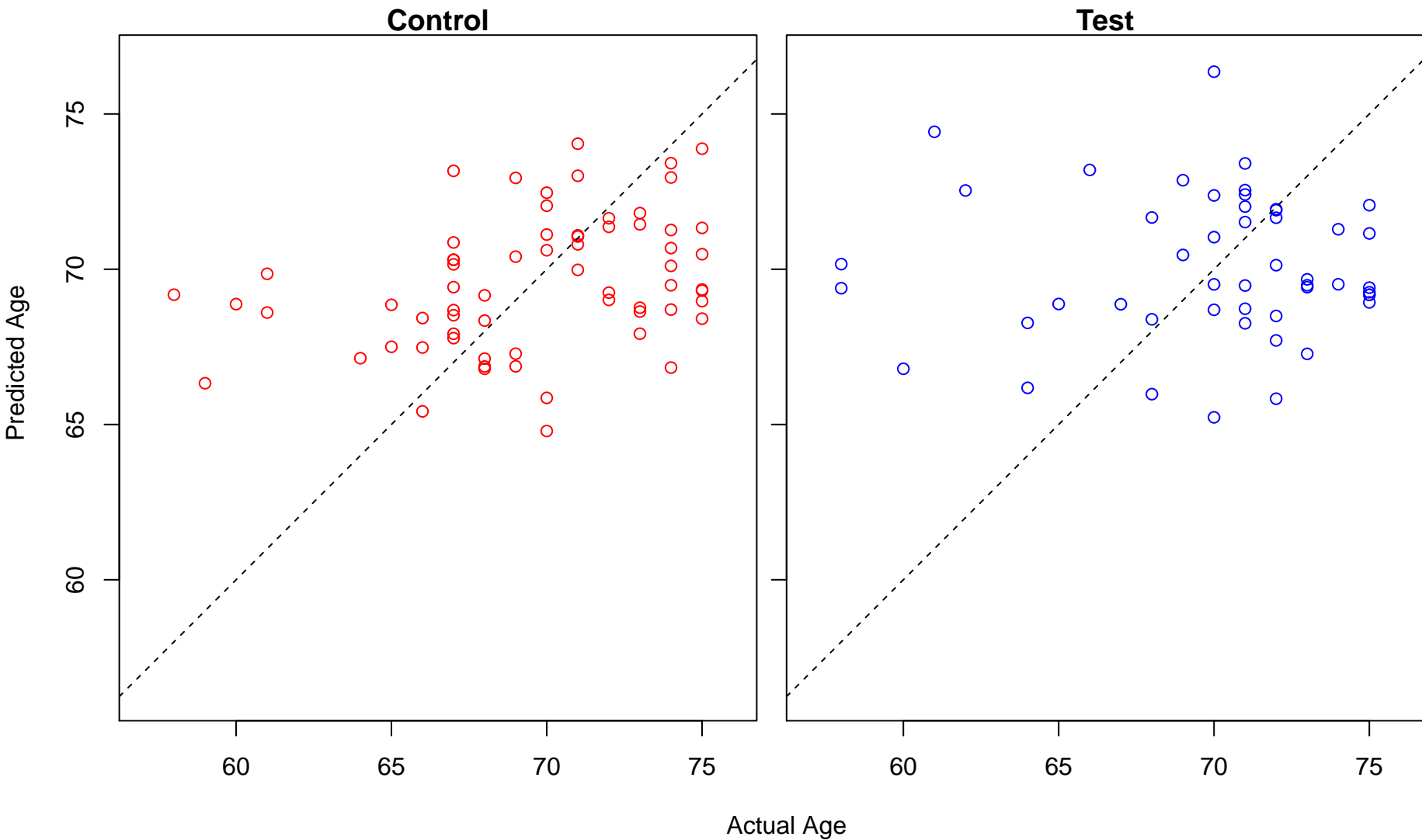
regulation of chromatin binding (Score: 0.424119)



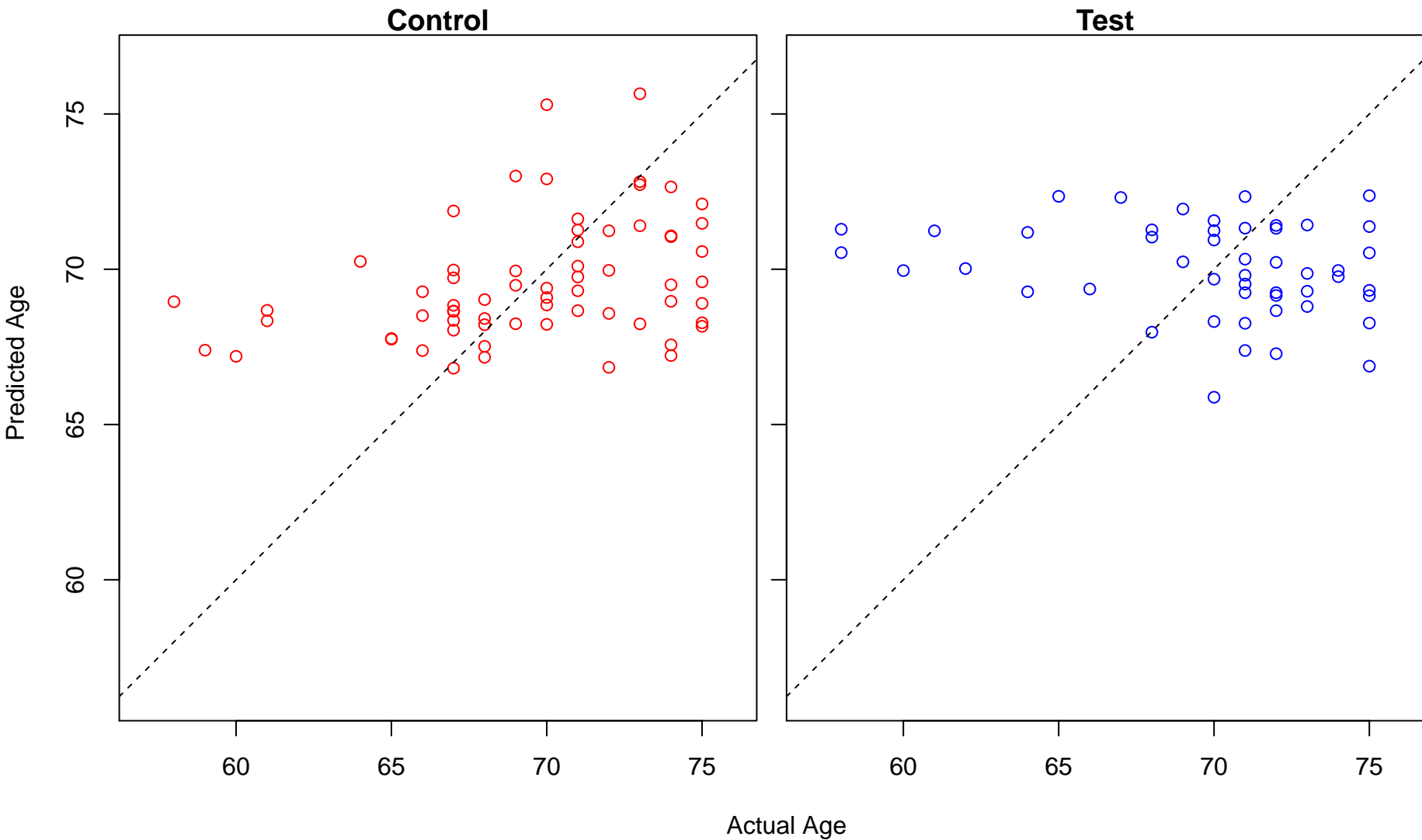
cellular copper ion homeostasis (Score: 0.423238)



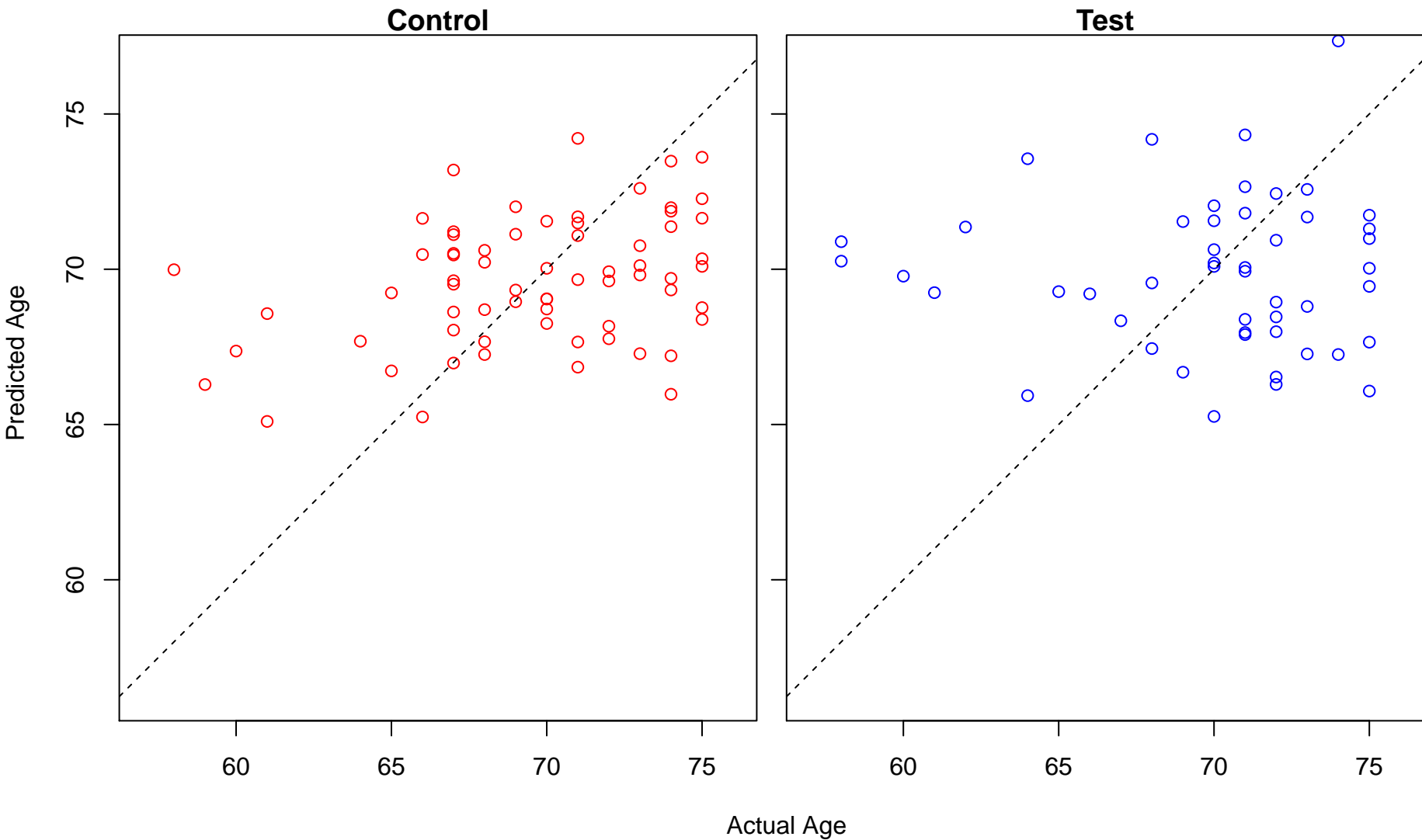
protein activation cascade (Score: 0.423160)



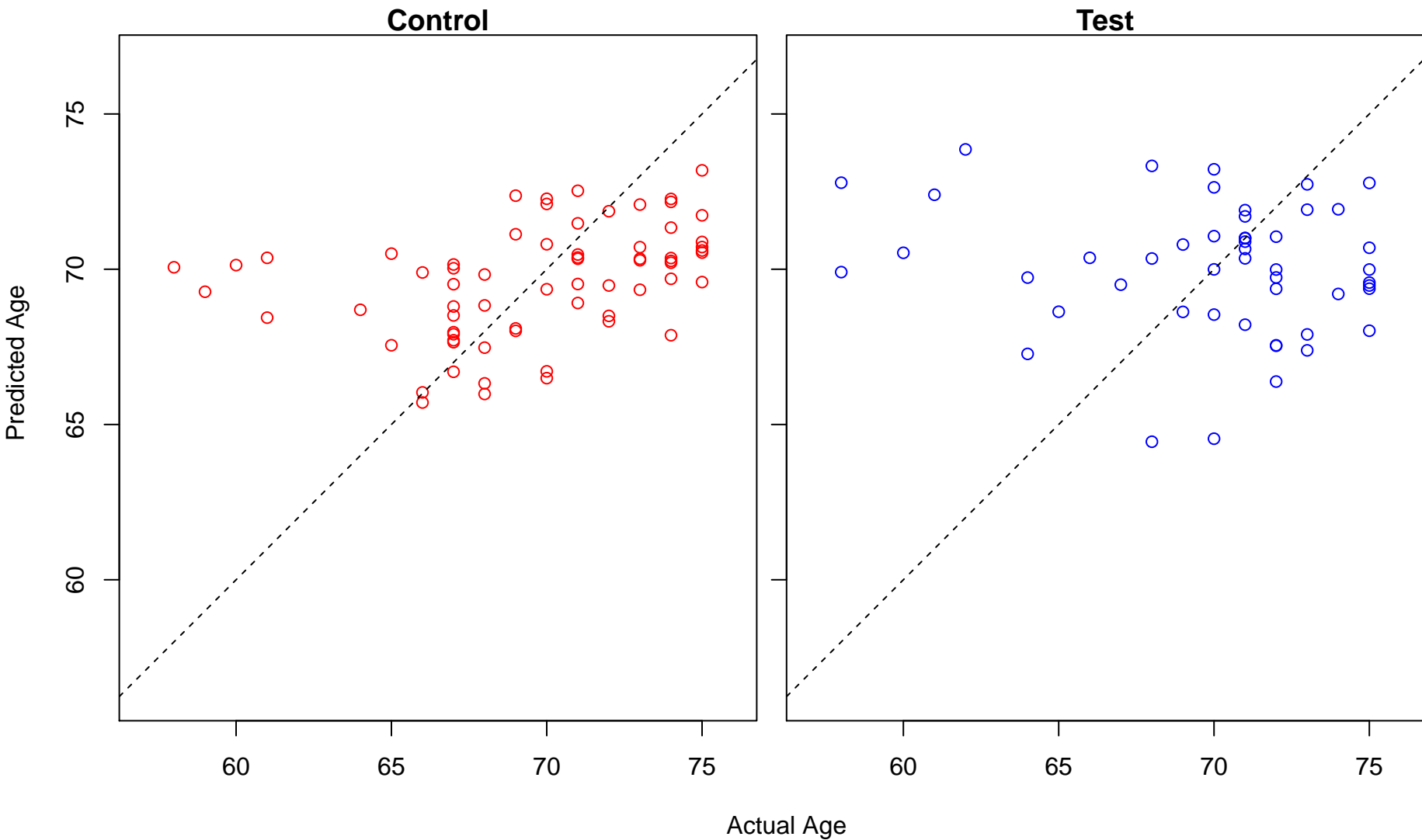
centriole-centriole cohesion (Score: 0.422045)



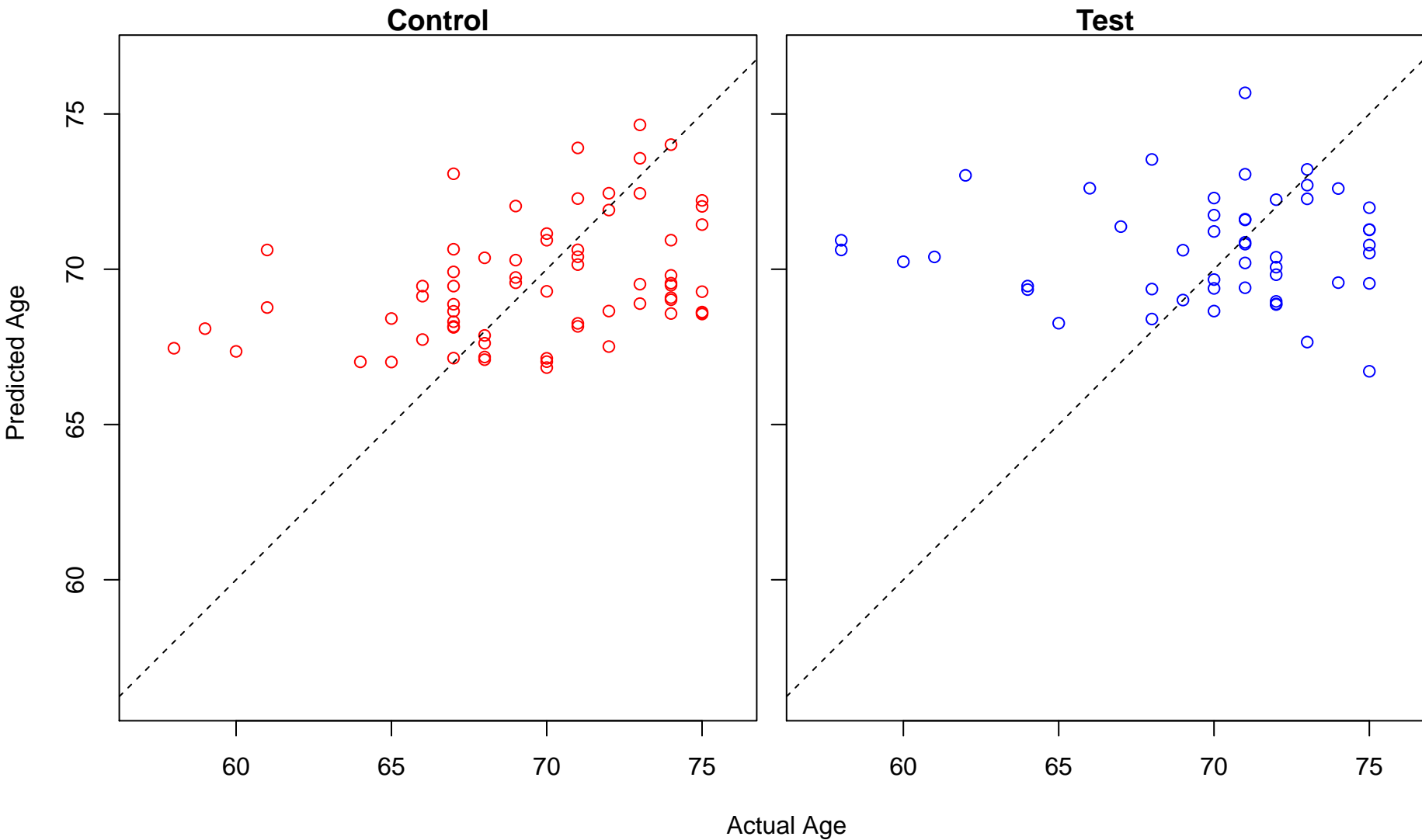
segment specification (Score: 0.420638)



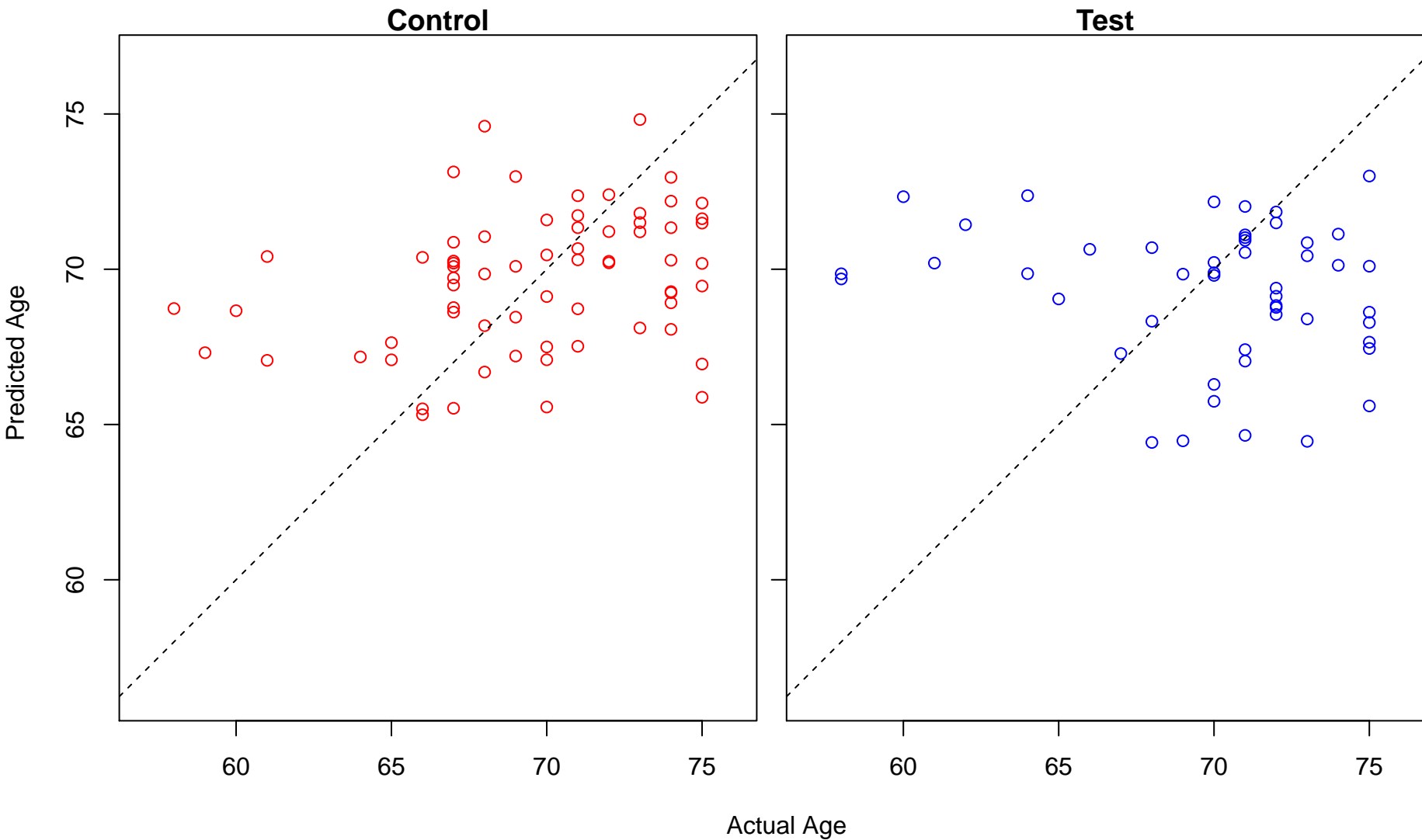
tooth mineralization (Score: 0.420454)



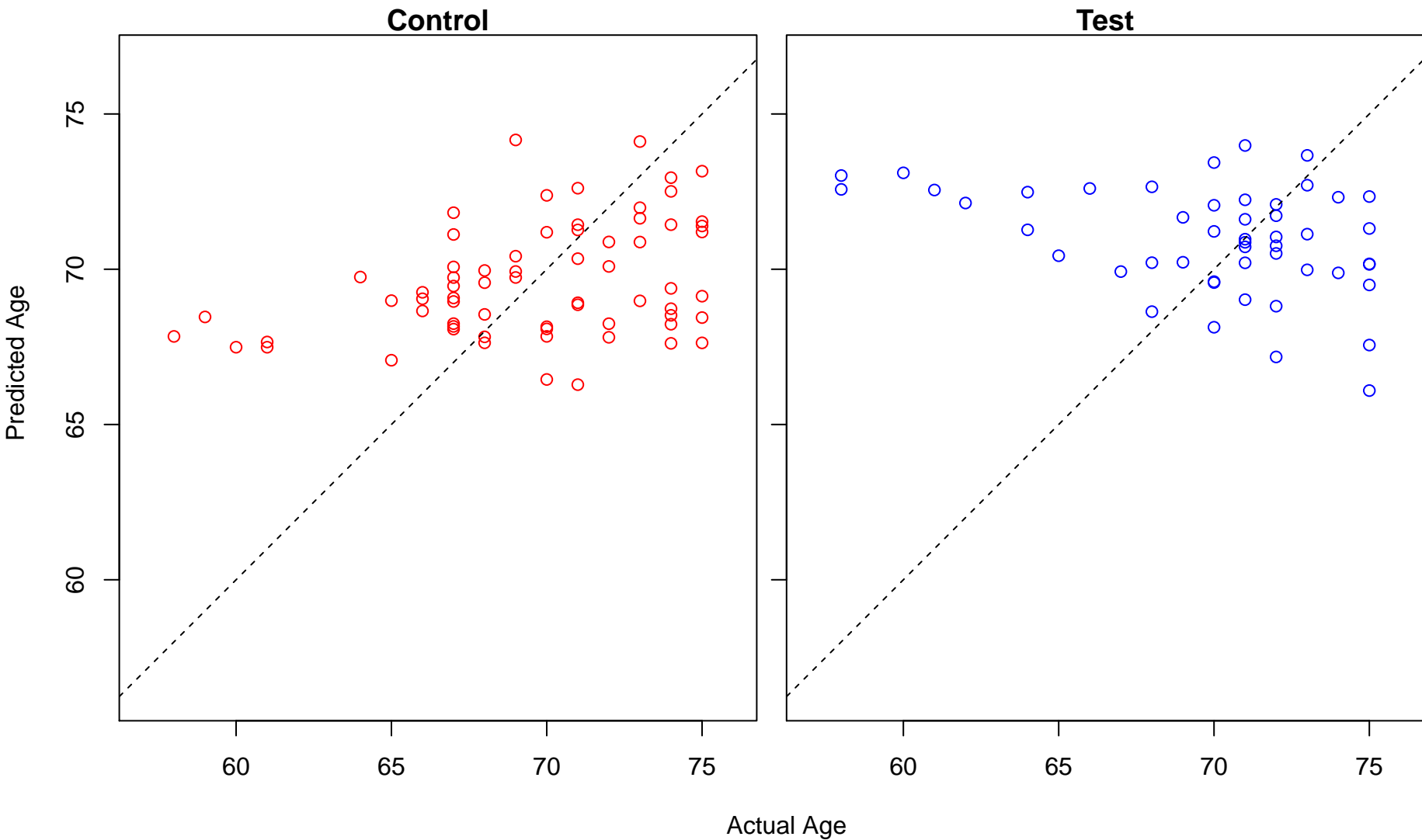
negative regulation of cytokine production involved in inflammatory response (Score: 0.418882)



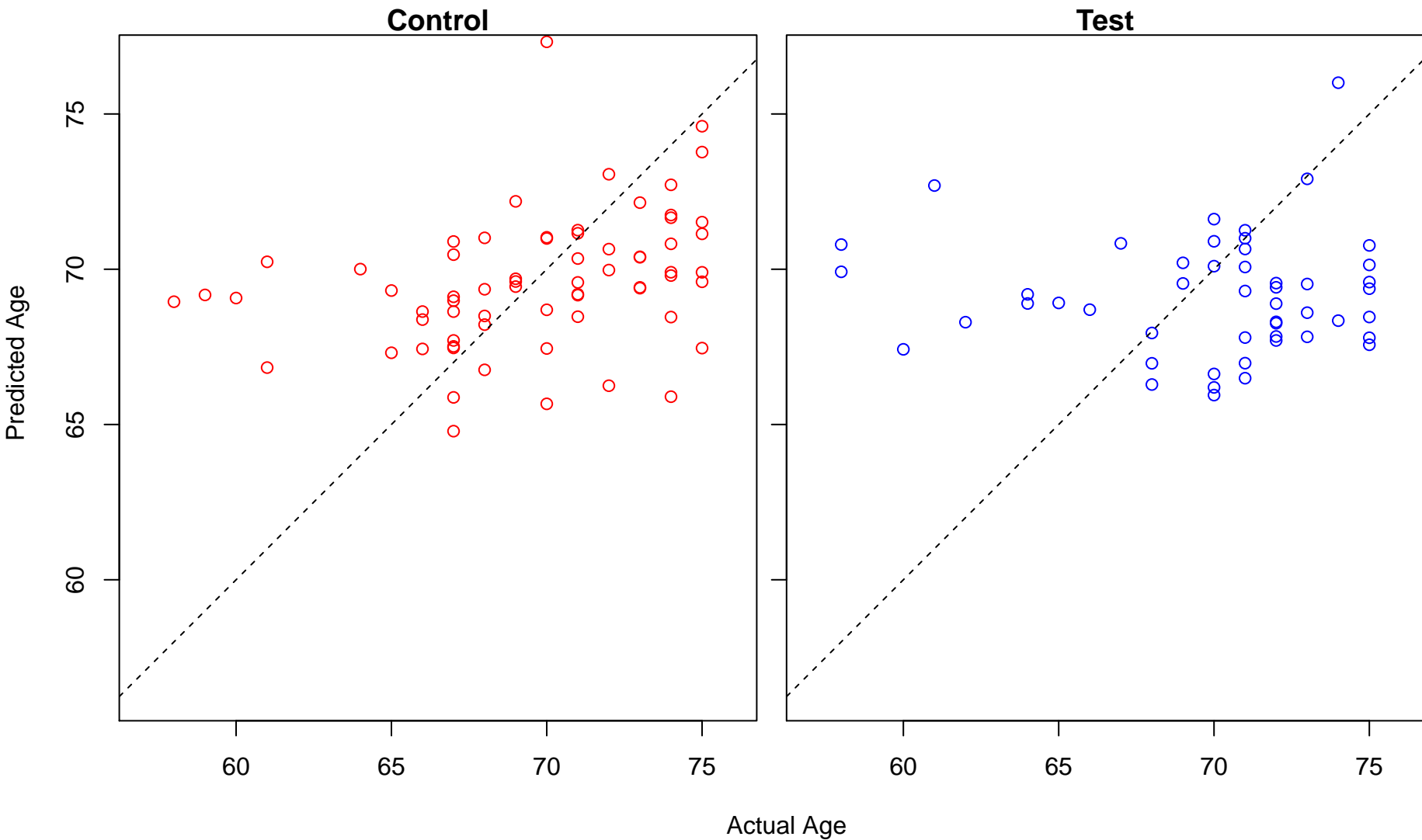
cell differentiation in spinal cord (Score: 0.417753)



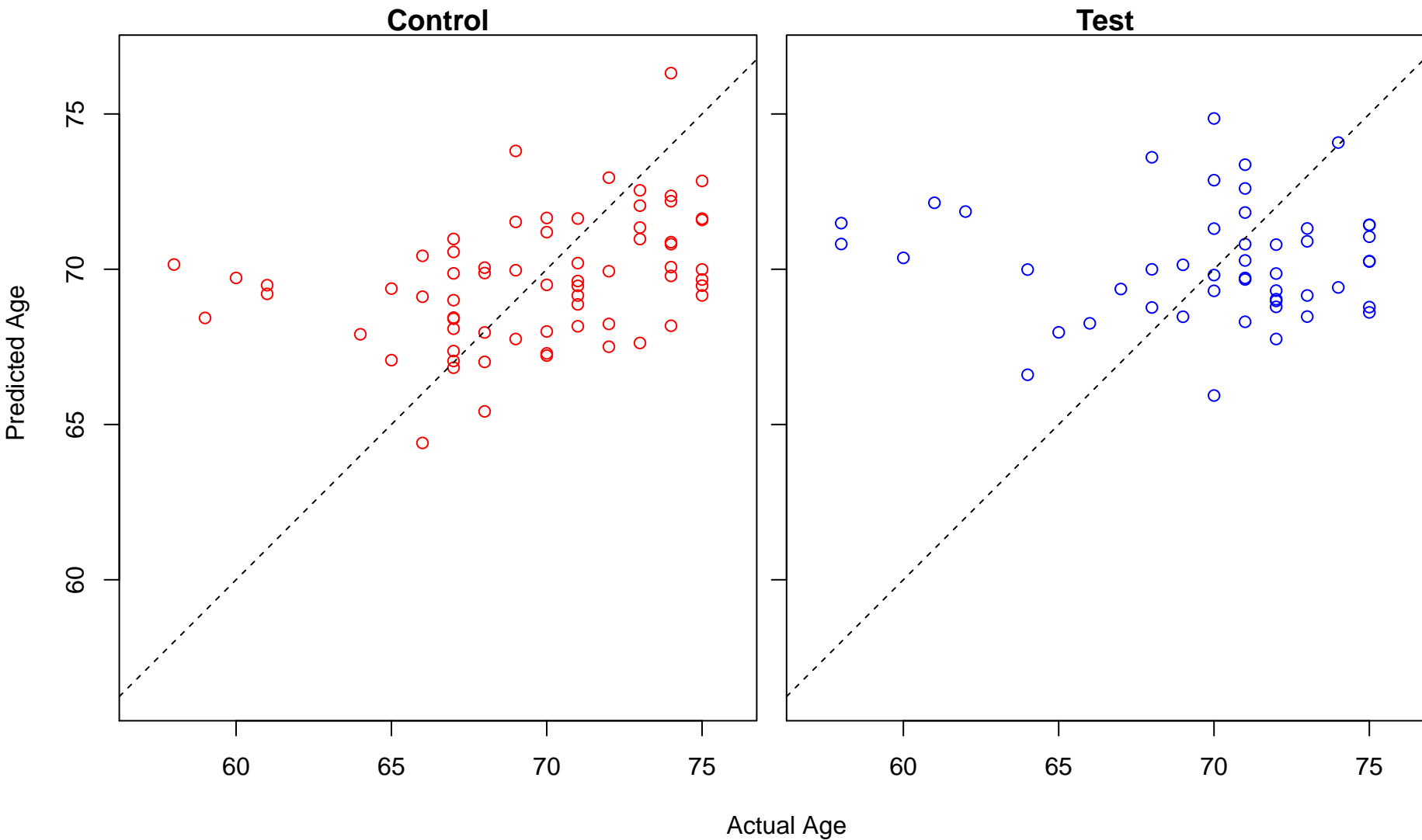
maintenance of cell polarity (Score: 0.417700)



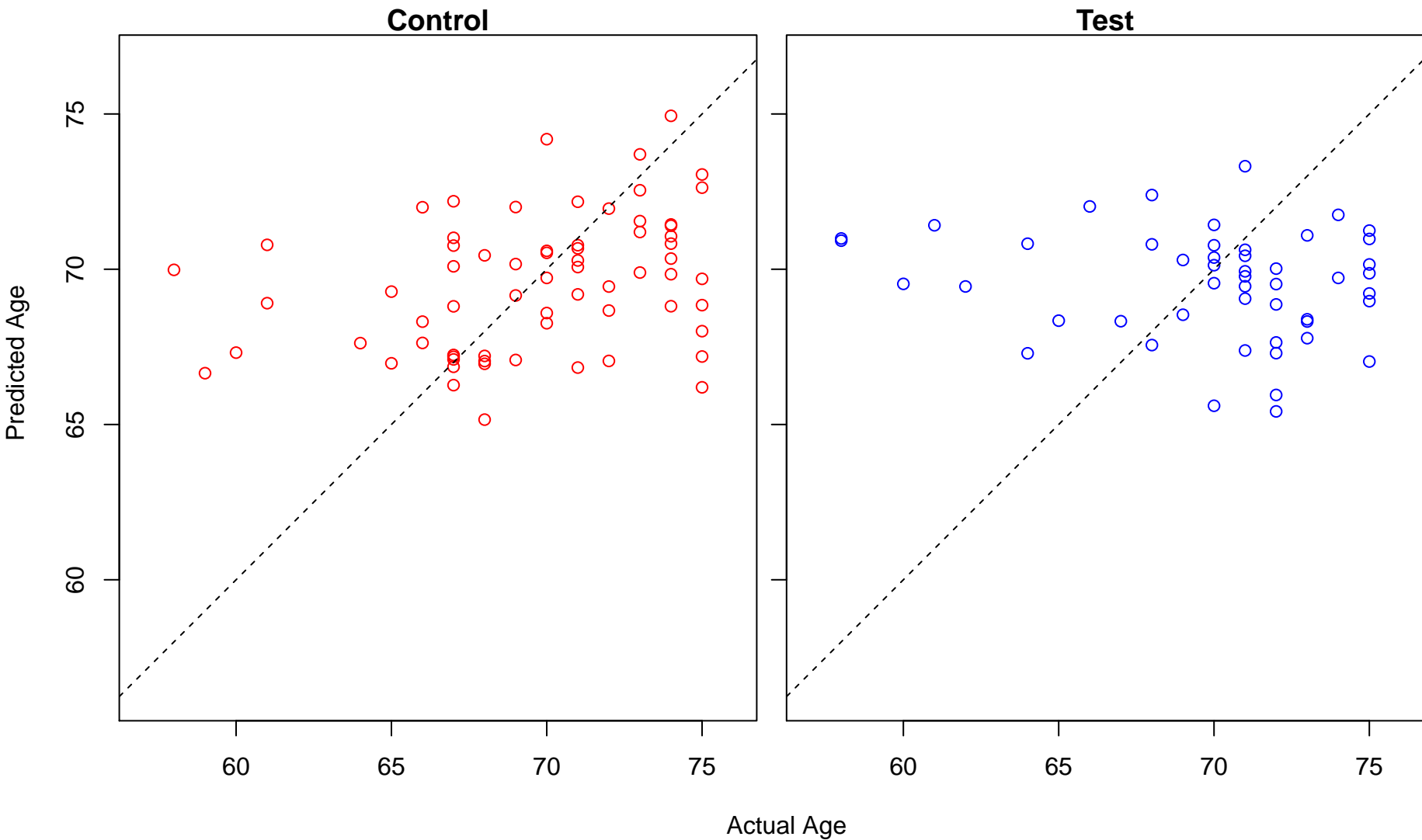
negative regulation of nucleotide catabolic process (Score: 0.417459)



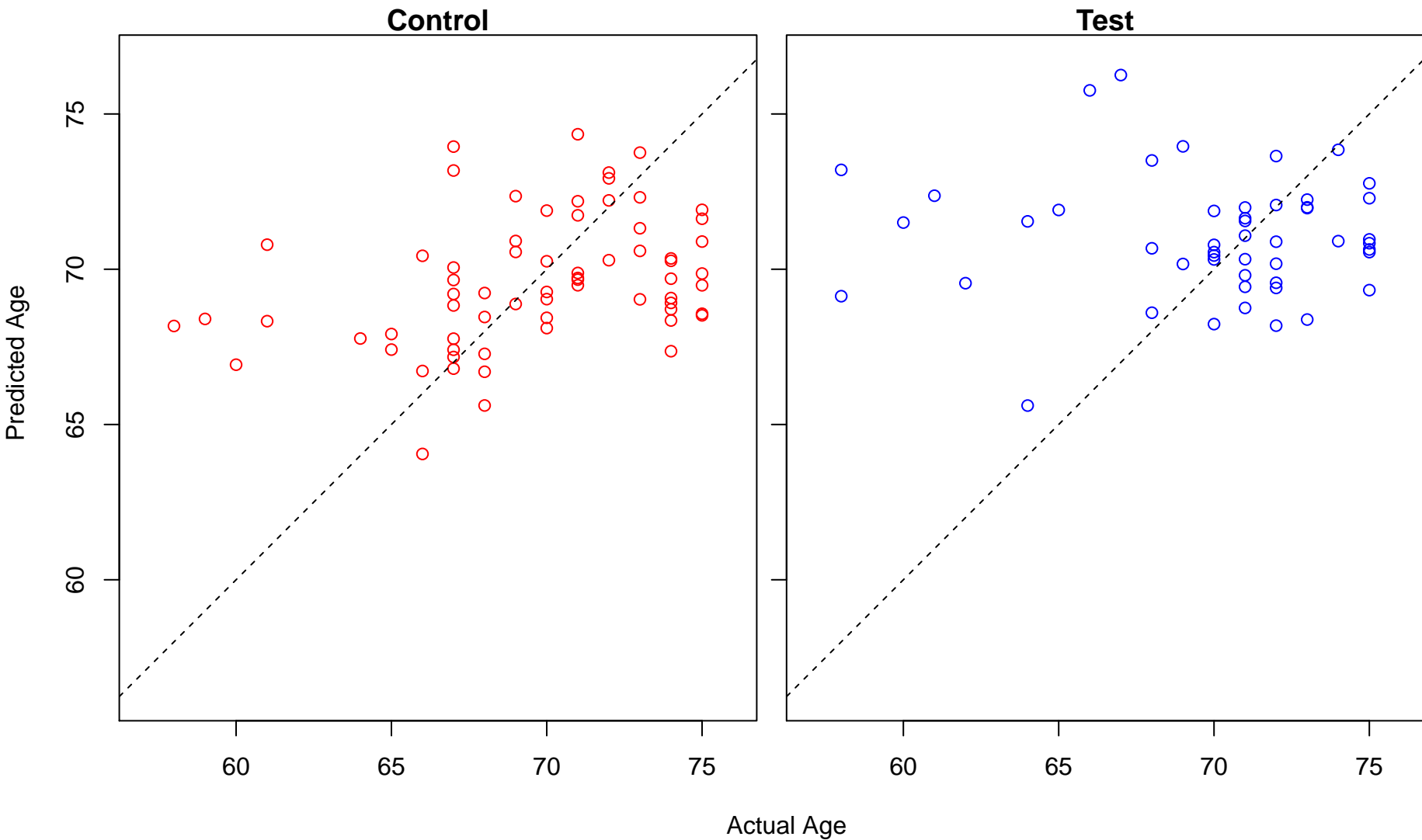
negative regulation of protein targeting to membrane (Score: 0.417195)



replicative senescence (Score: 0.416333)

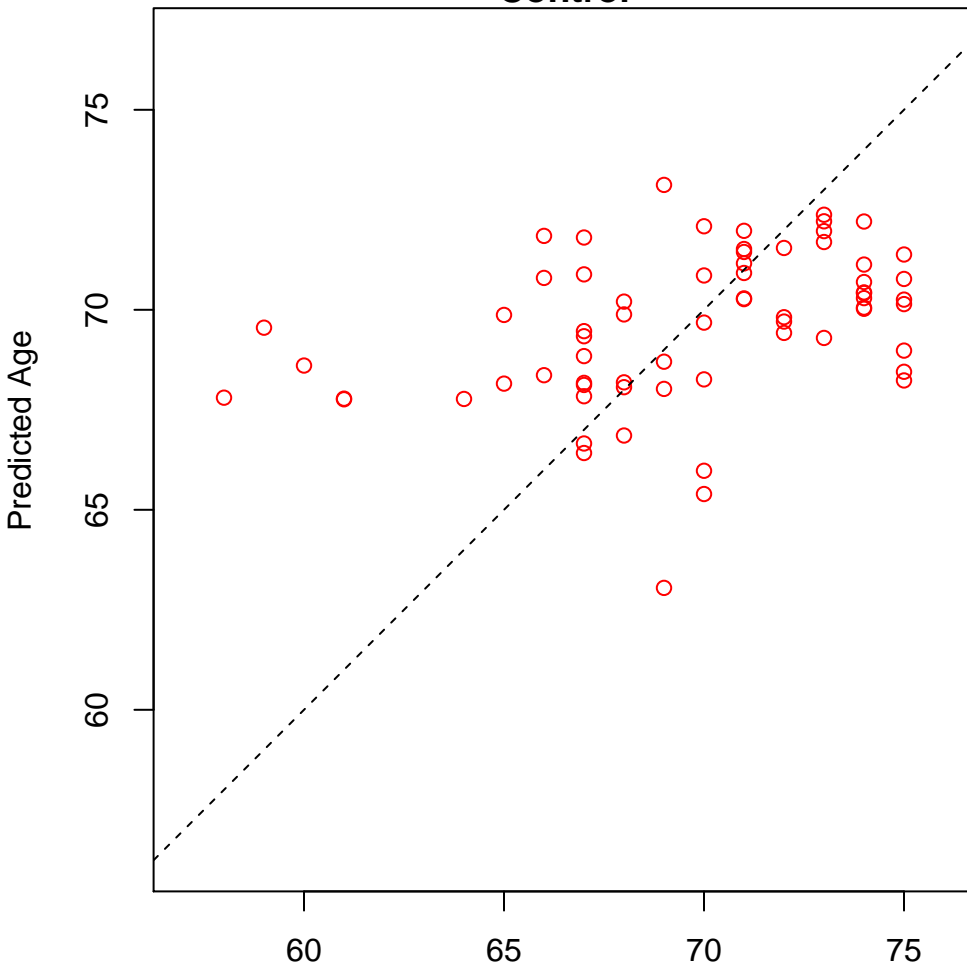


meiotic chromosome segregation (Score: 0.415756)

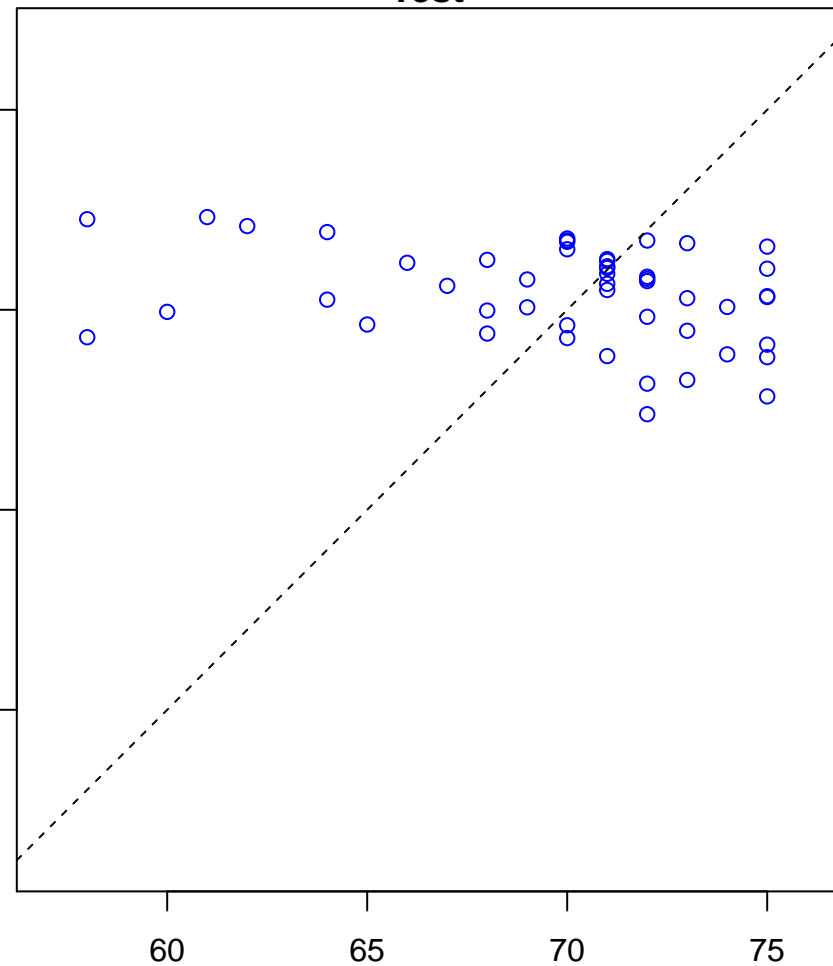


regulation of vitamin metabolic process (Score: 0.411955)

Control

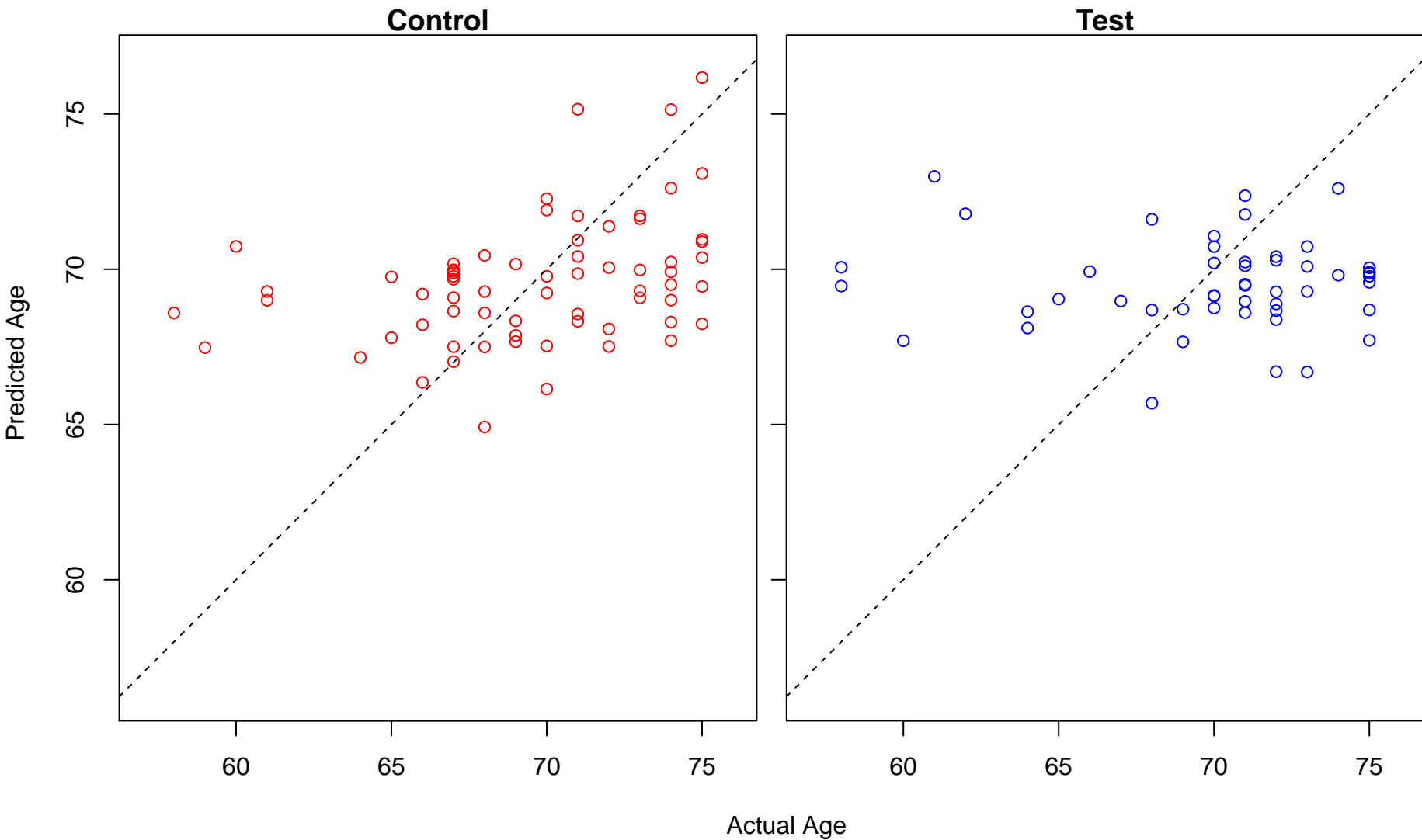


Test

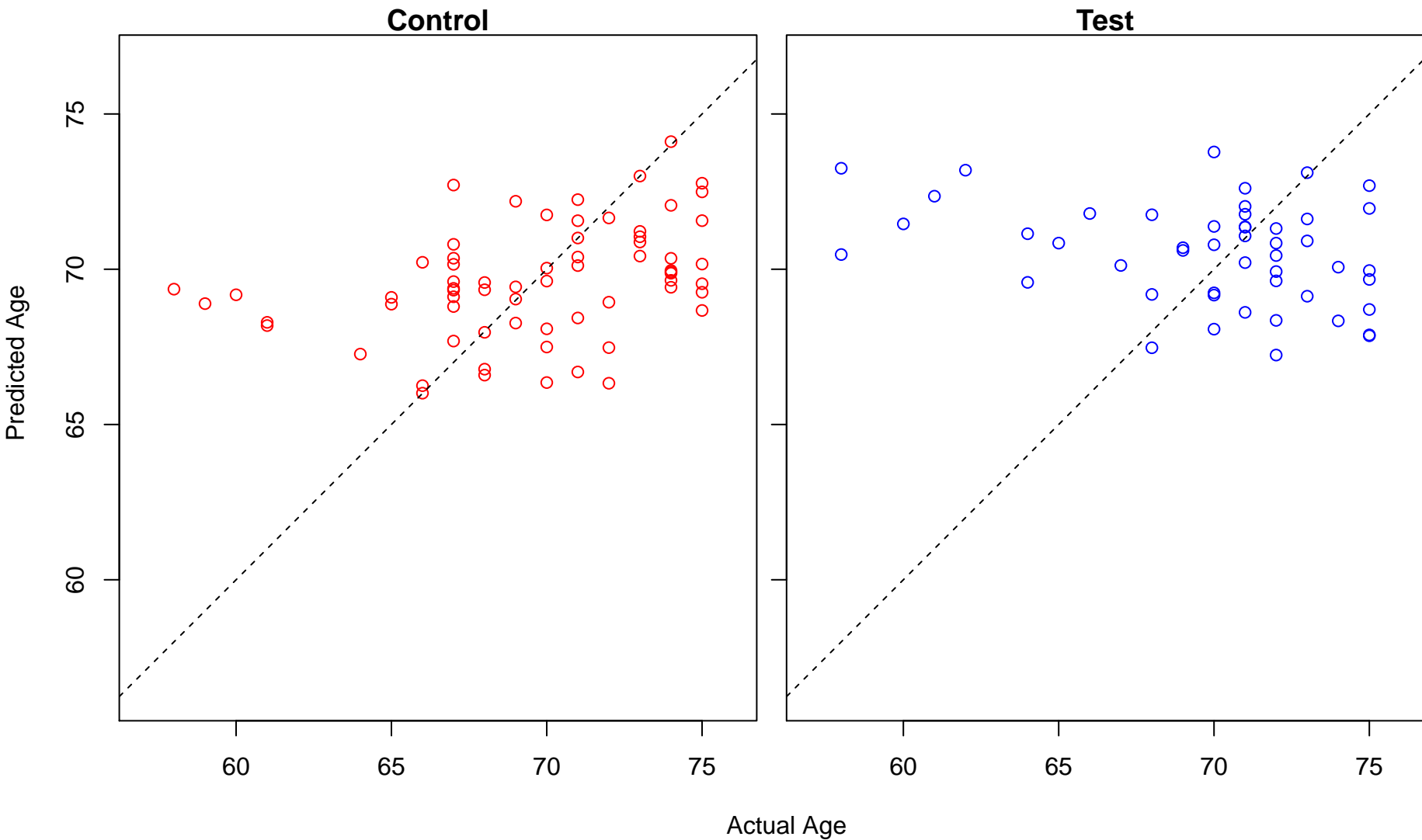


Actual Age

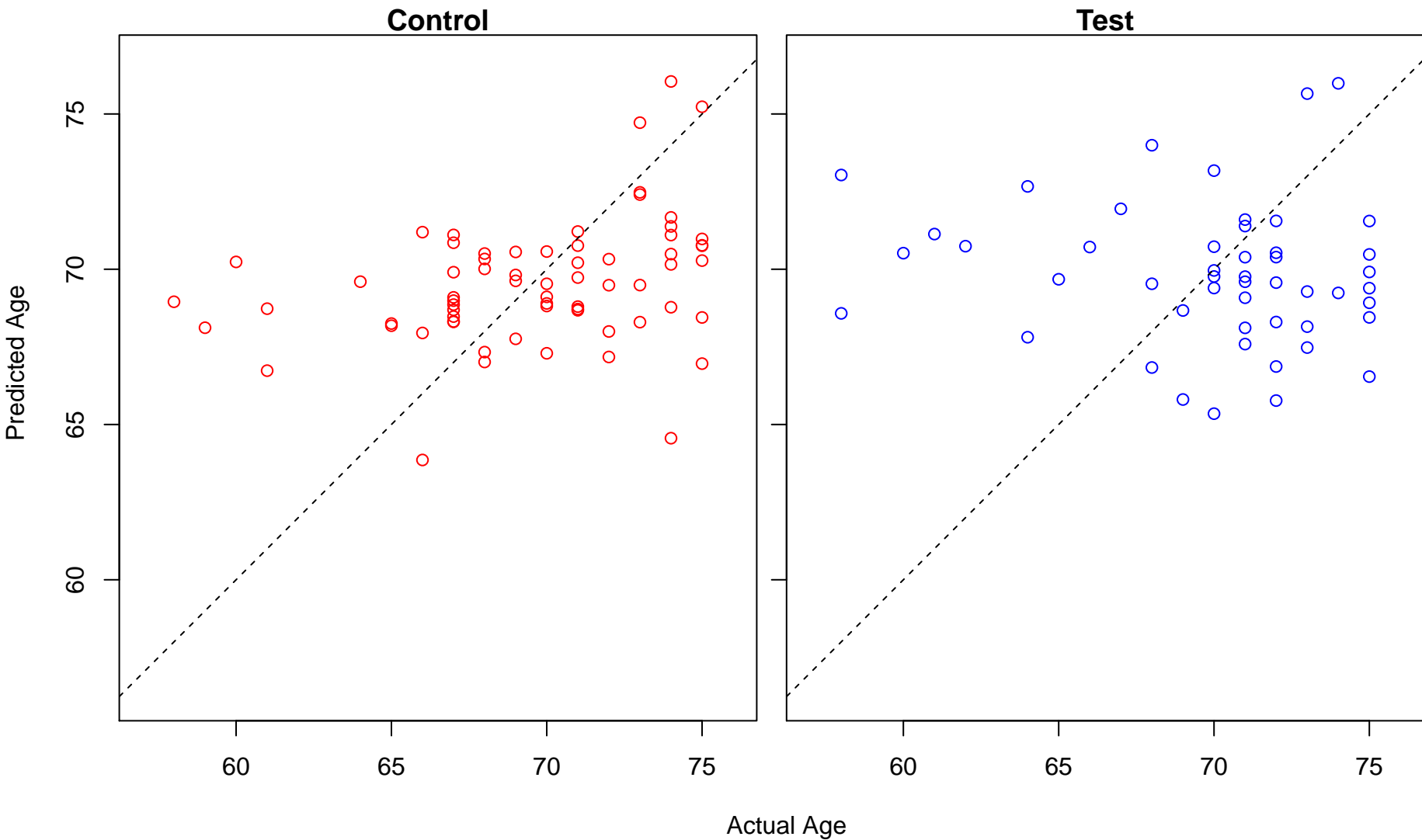
heme transport (Score: 0.411729)



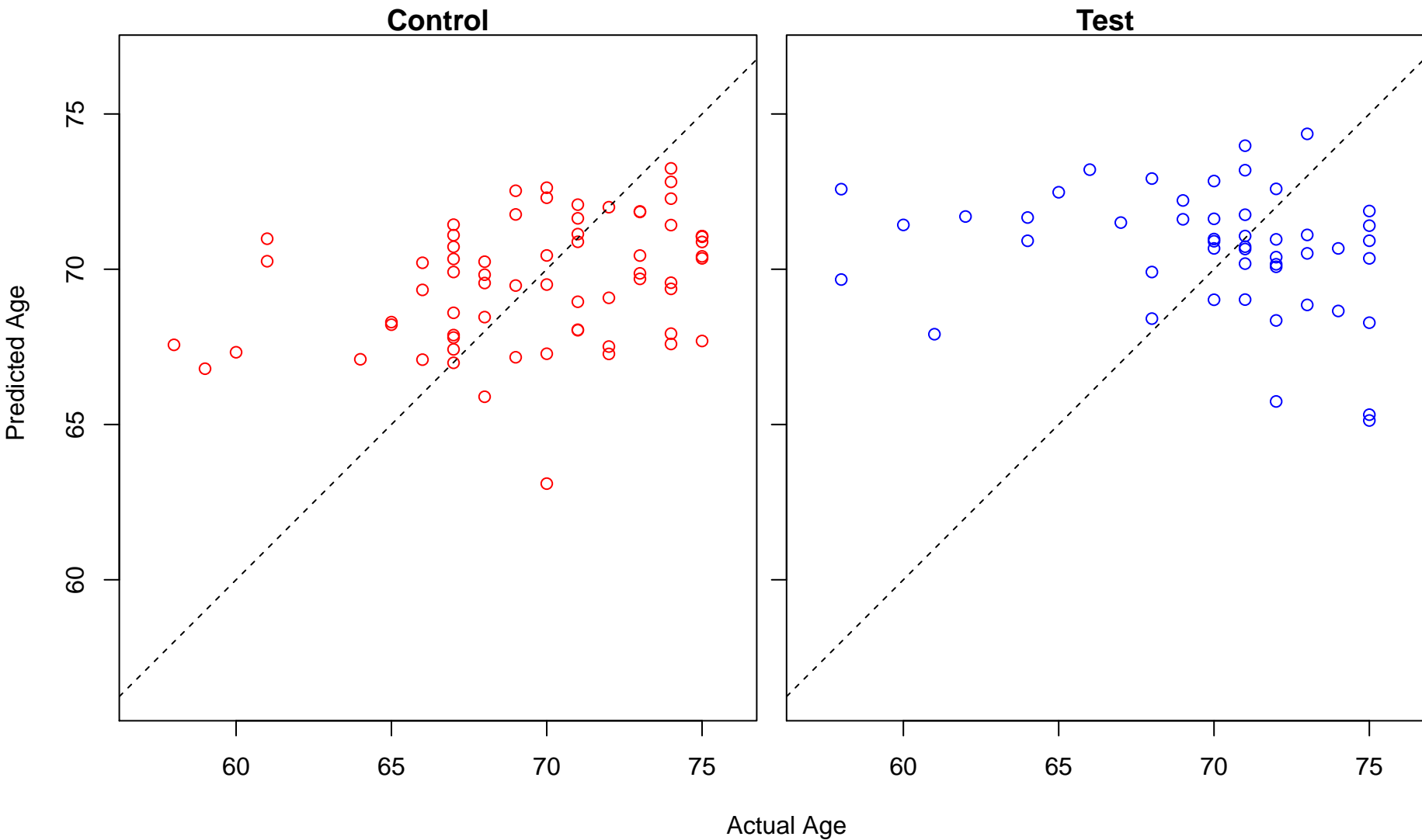
AMP metabolic process (Score: 0.411464)



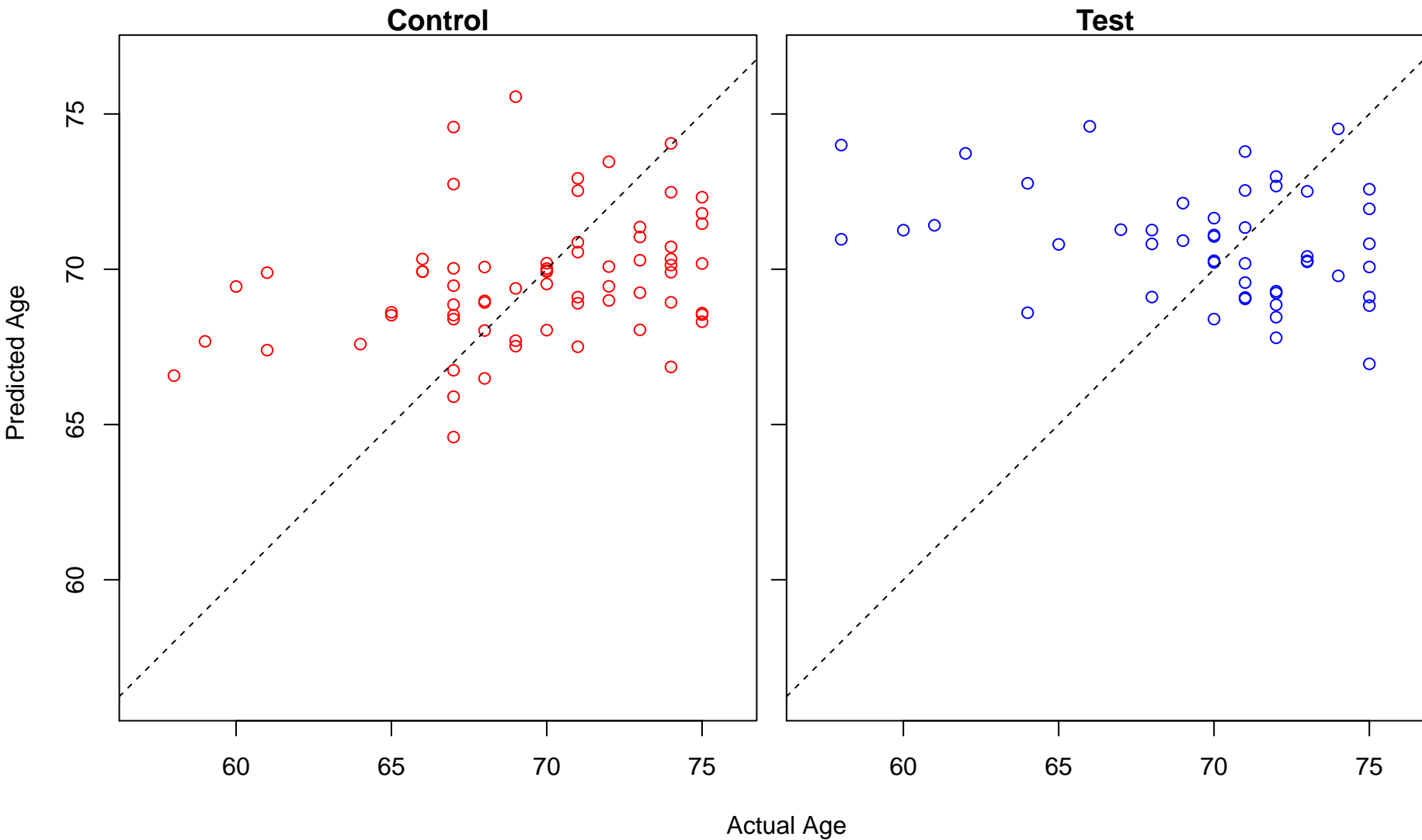
positive regulation of ruffle assembly (Score: 0.411308)



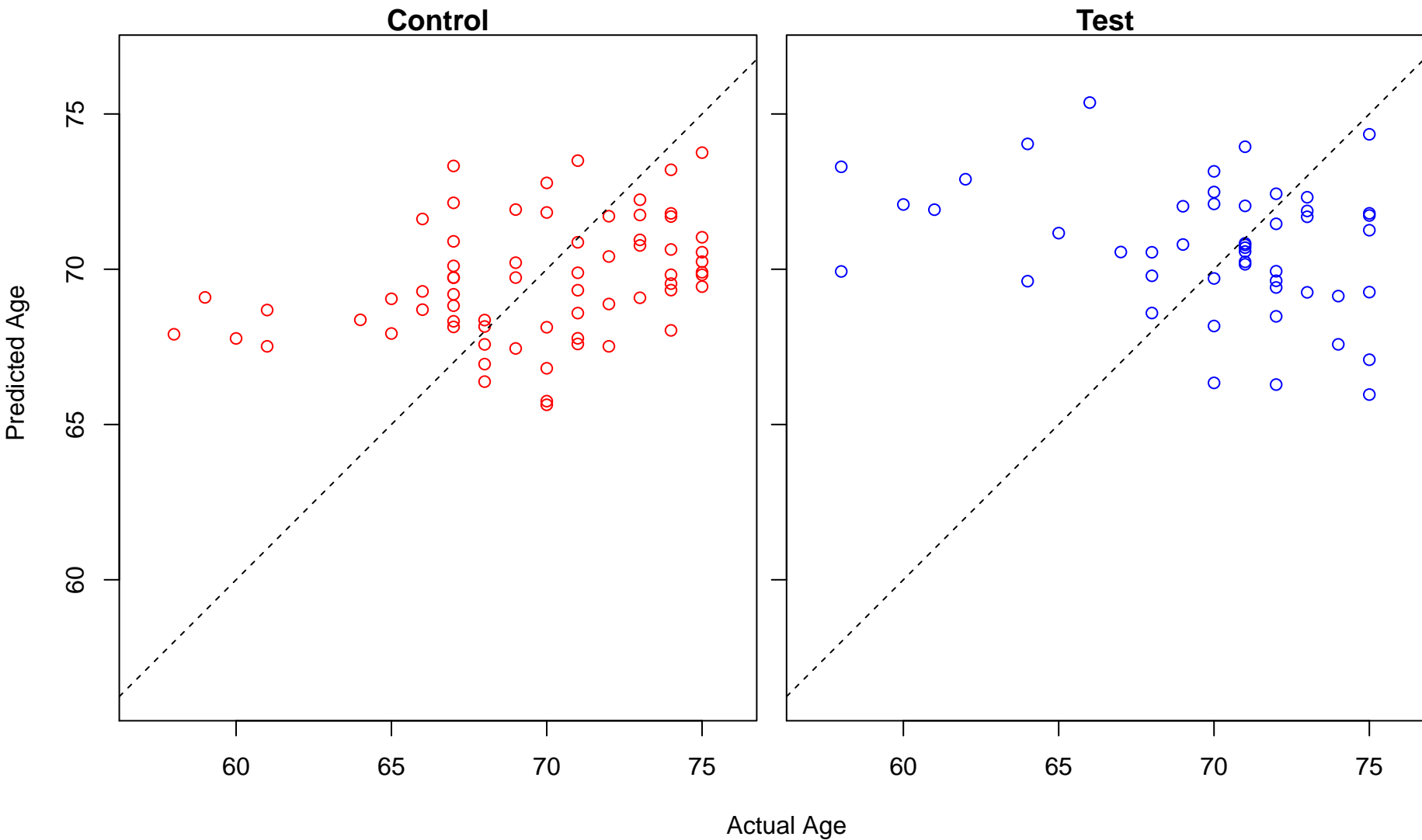
leukotriene signaling pathway (Score: 0.408125)



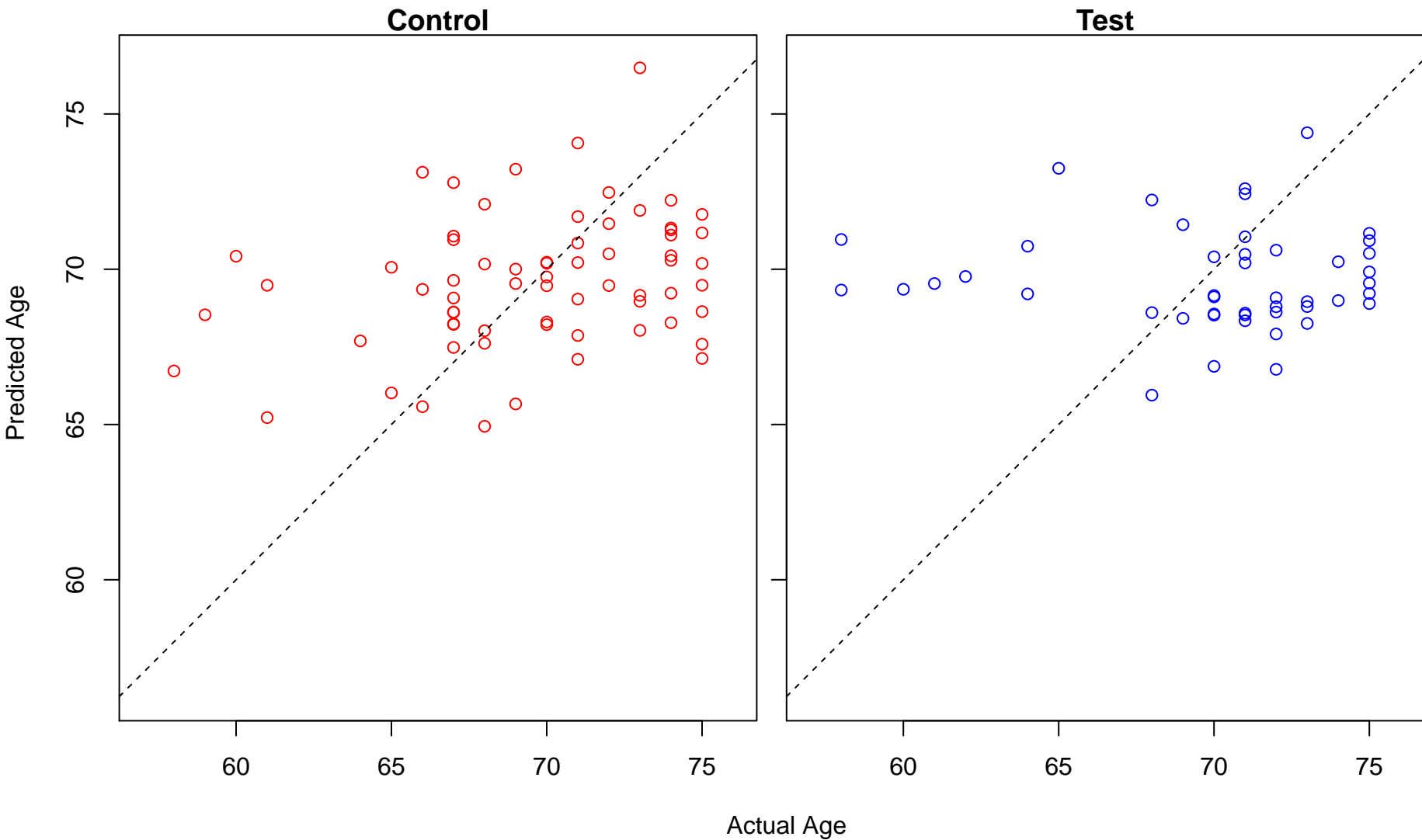
histone H4 deacetylation (Score: 0.408040)



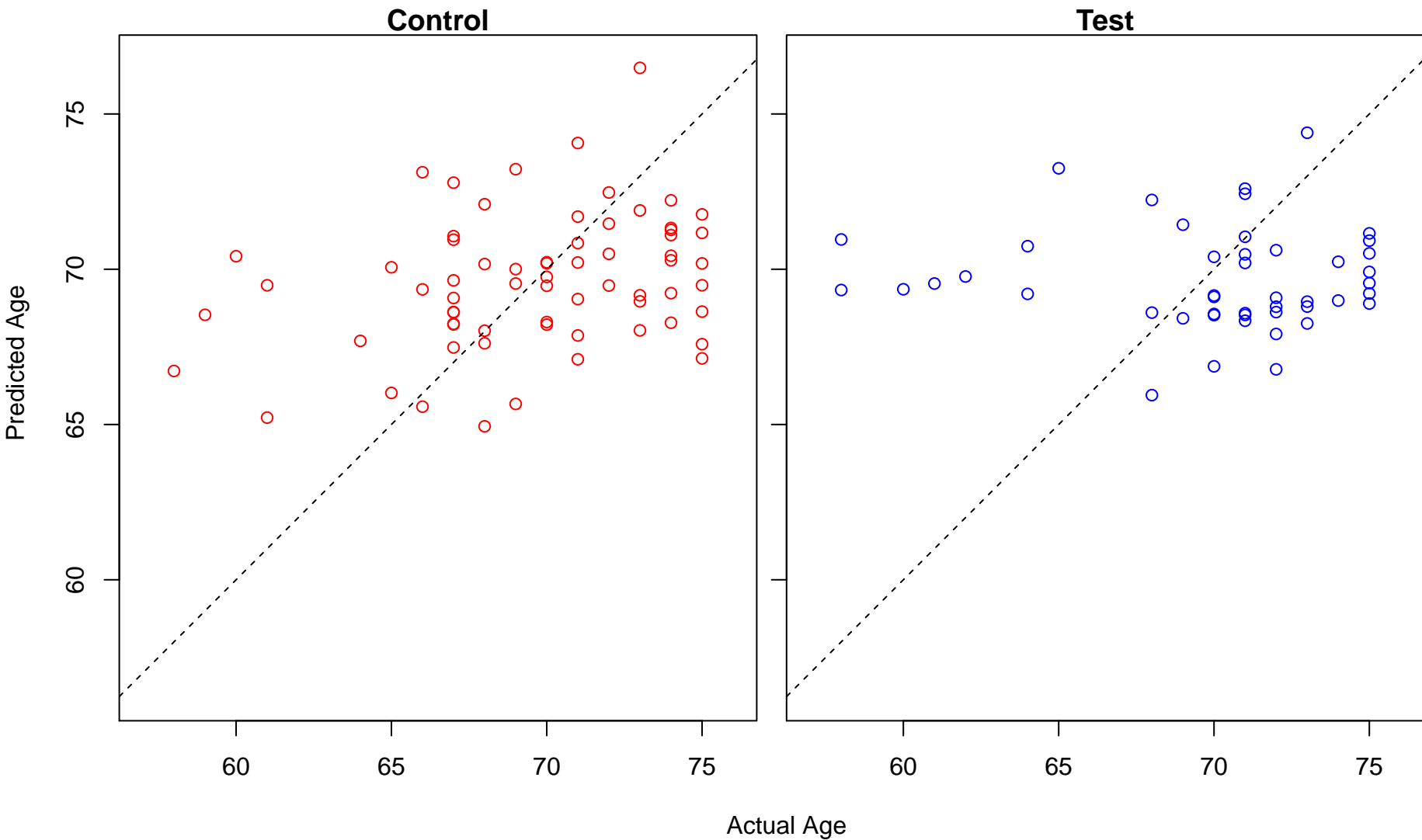
regulation of actin nucleation (Score: 0.407839)



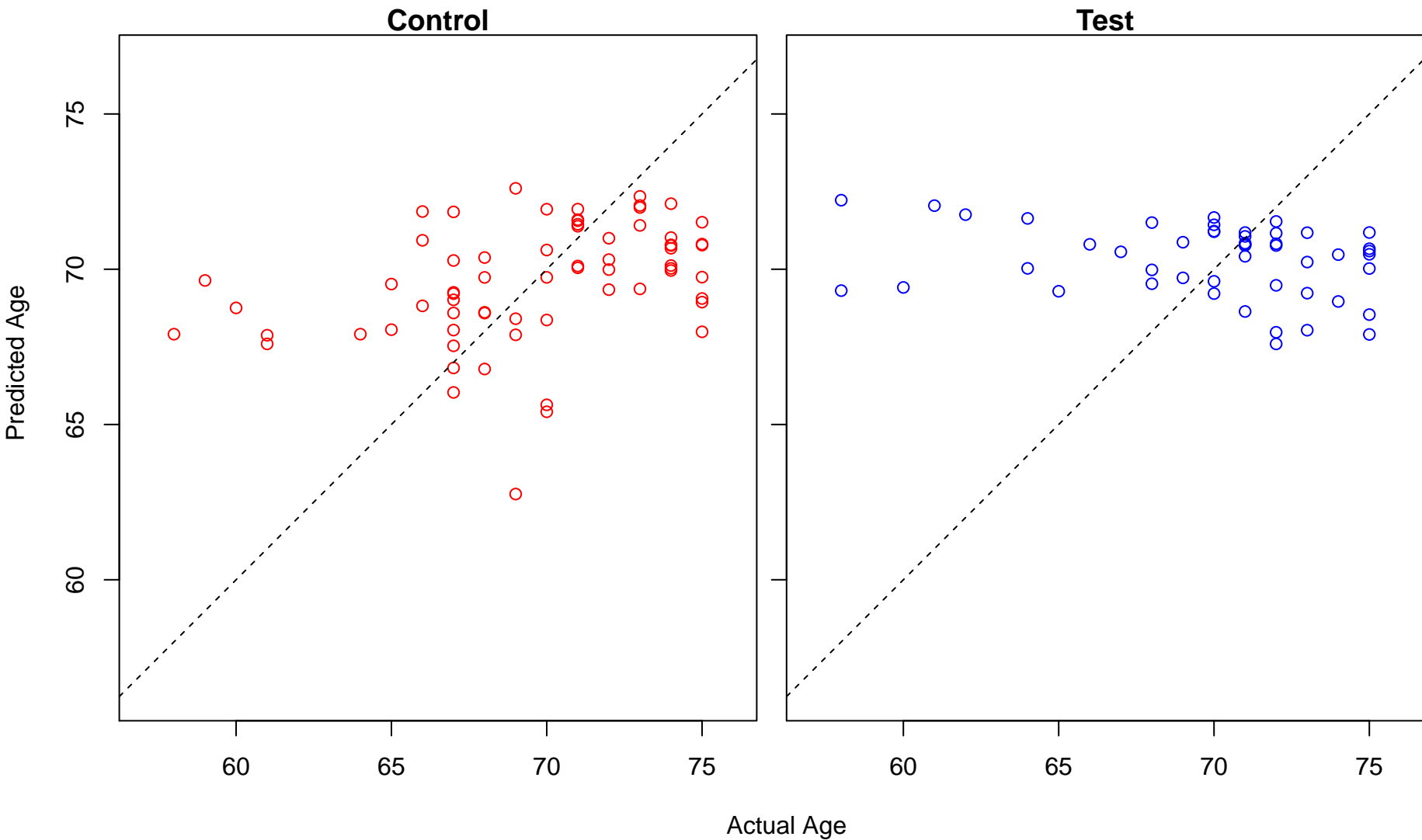
mitotic spindle elongation (Score: 0.407382)



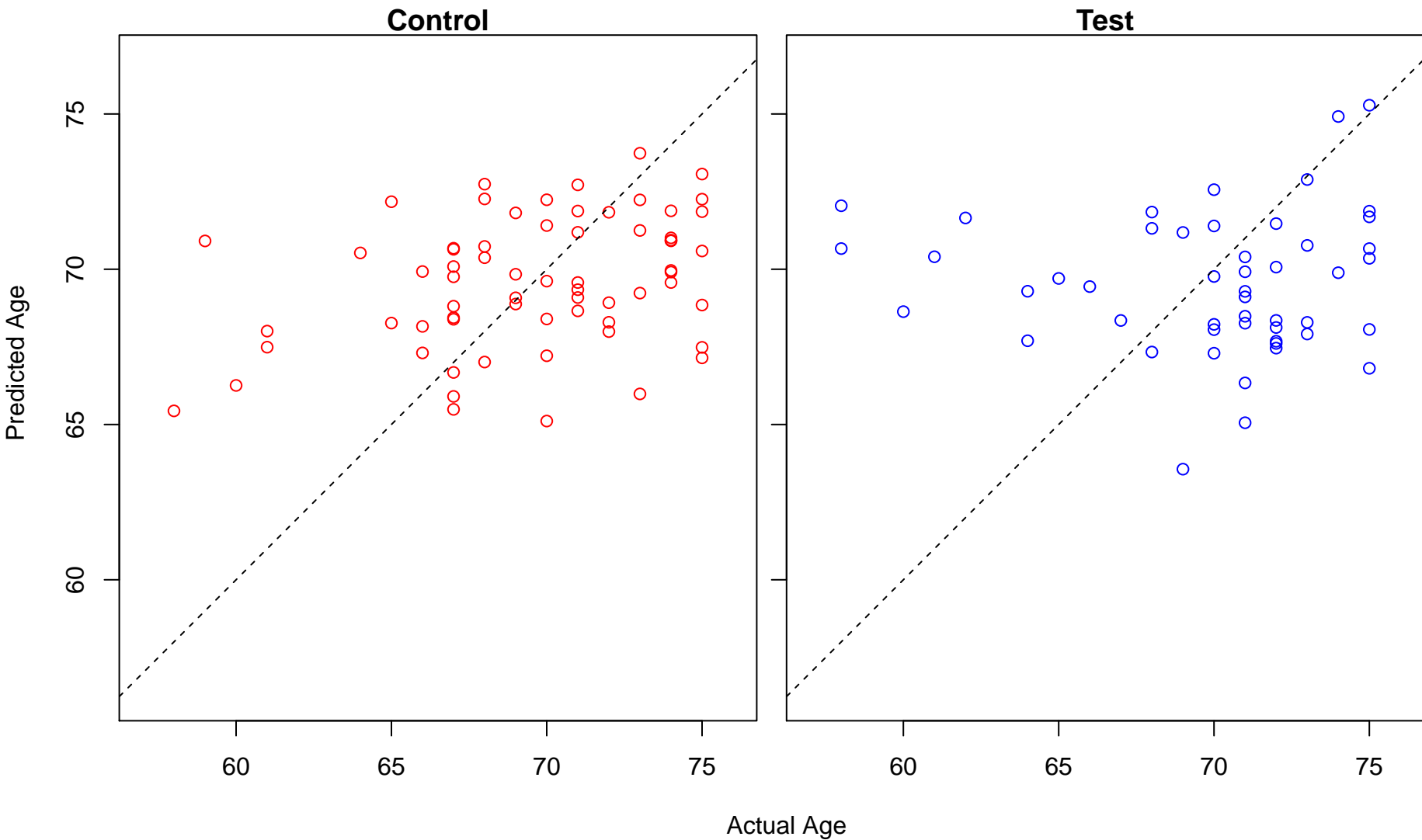
spindle elongation (Score: 0.407382)



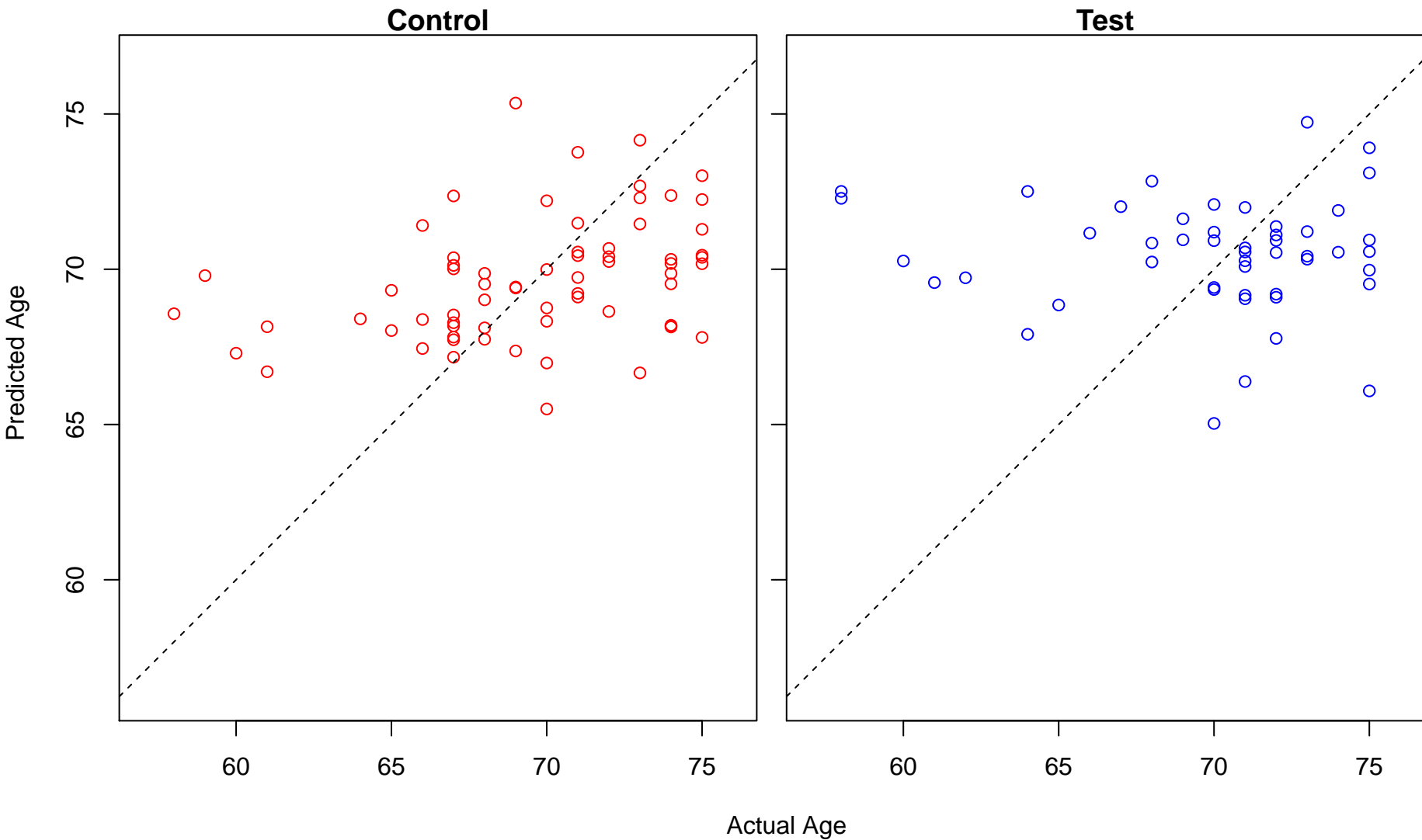
negative regulation of vitamin metabolic process (Score: 0.406964)



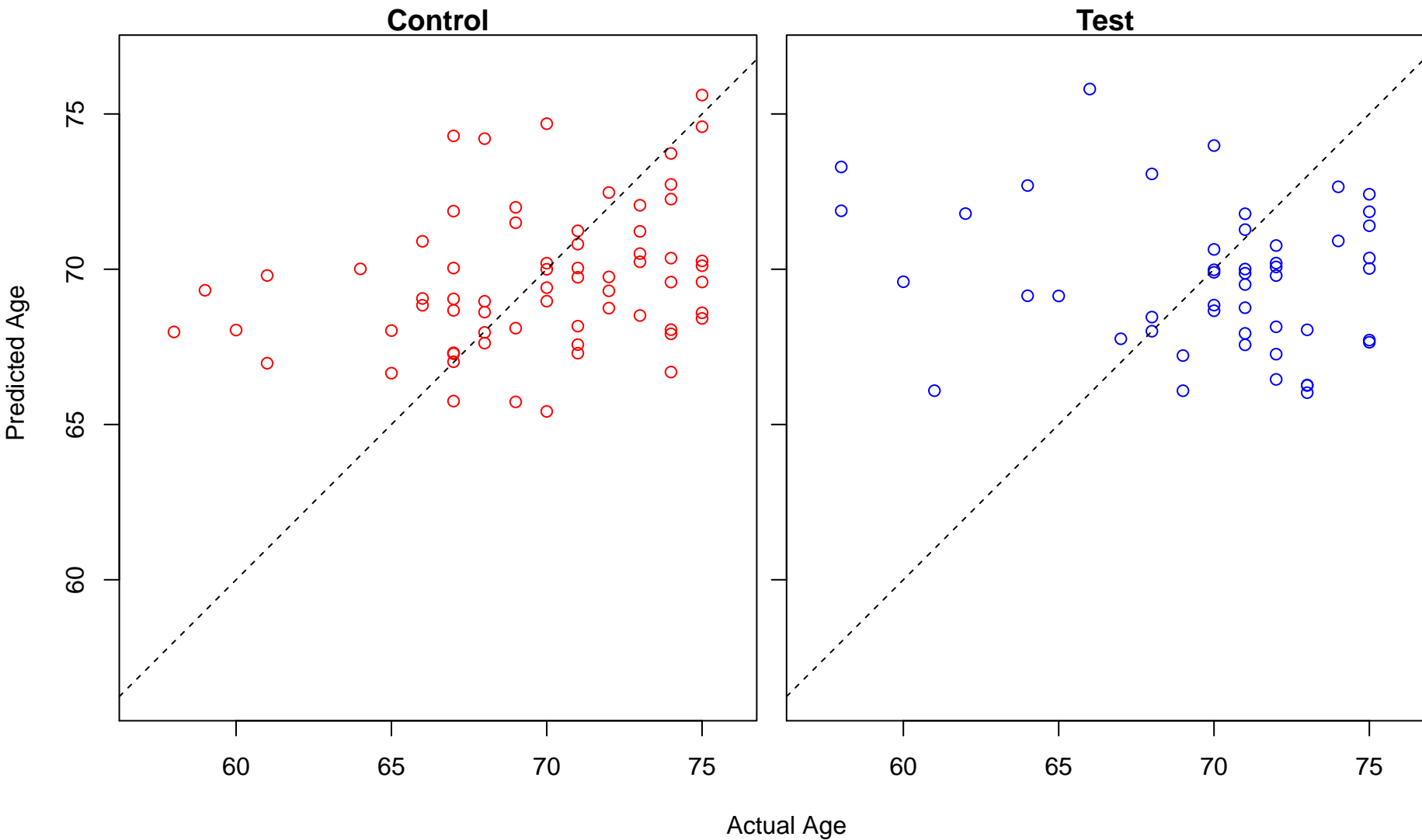
regulation of antigen processing and presentation of peptide antigen (Score: 0.406945)



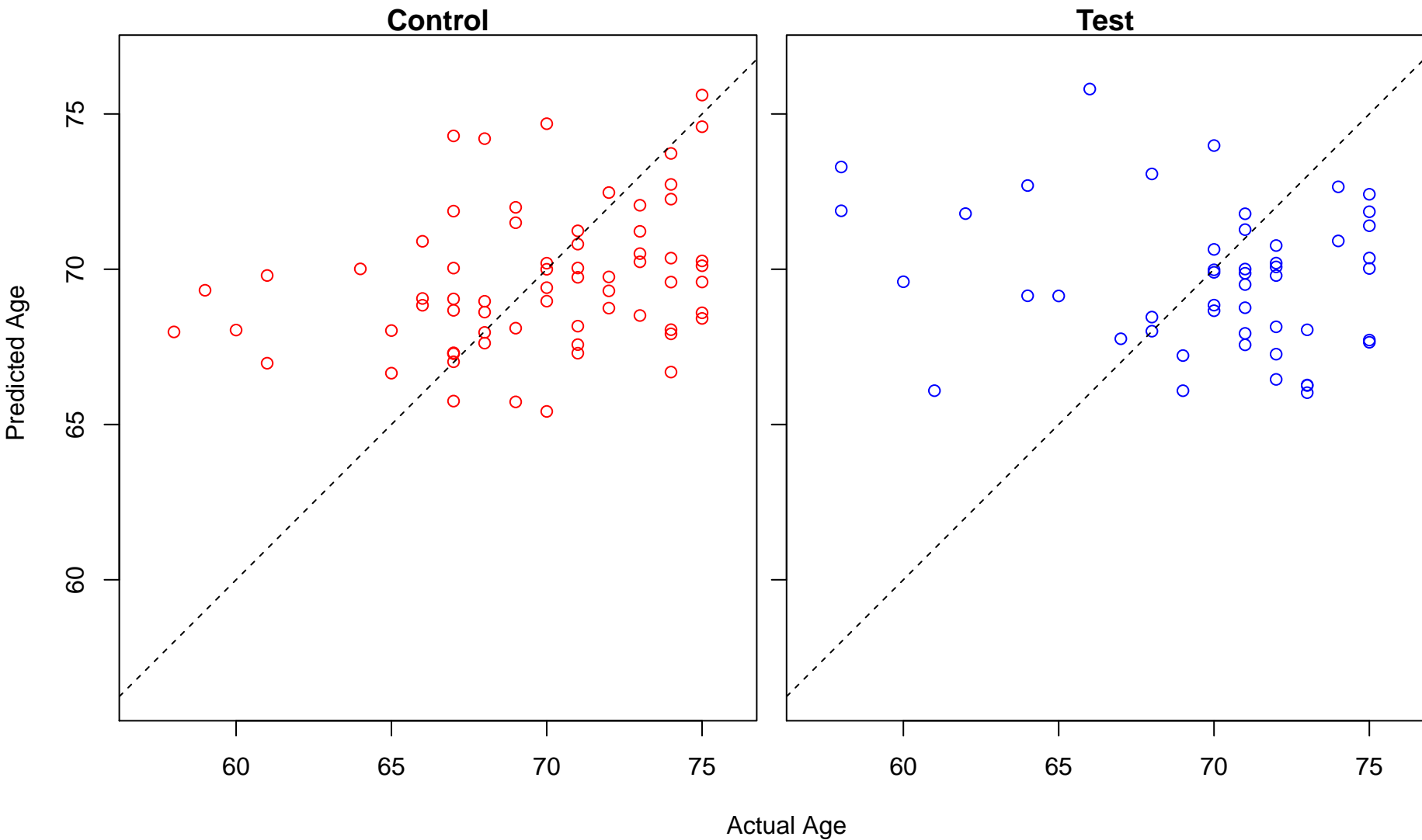
chromatin-mediated maintenance of transcription (Score: 0.406274)



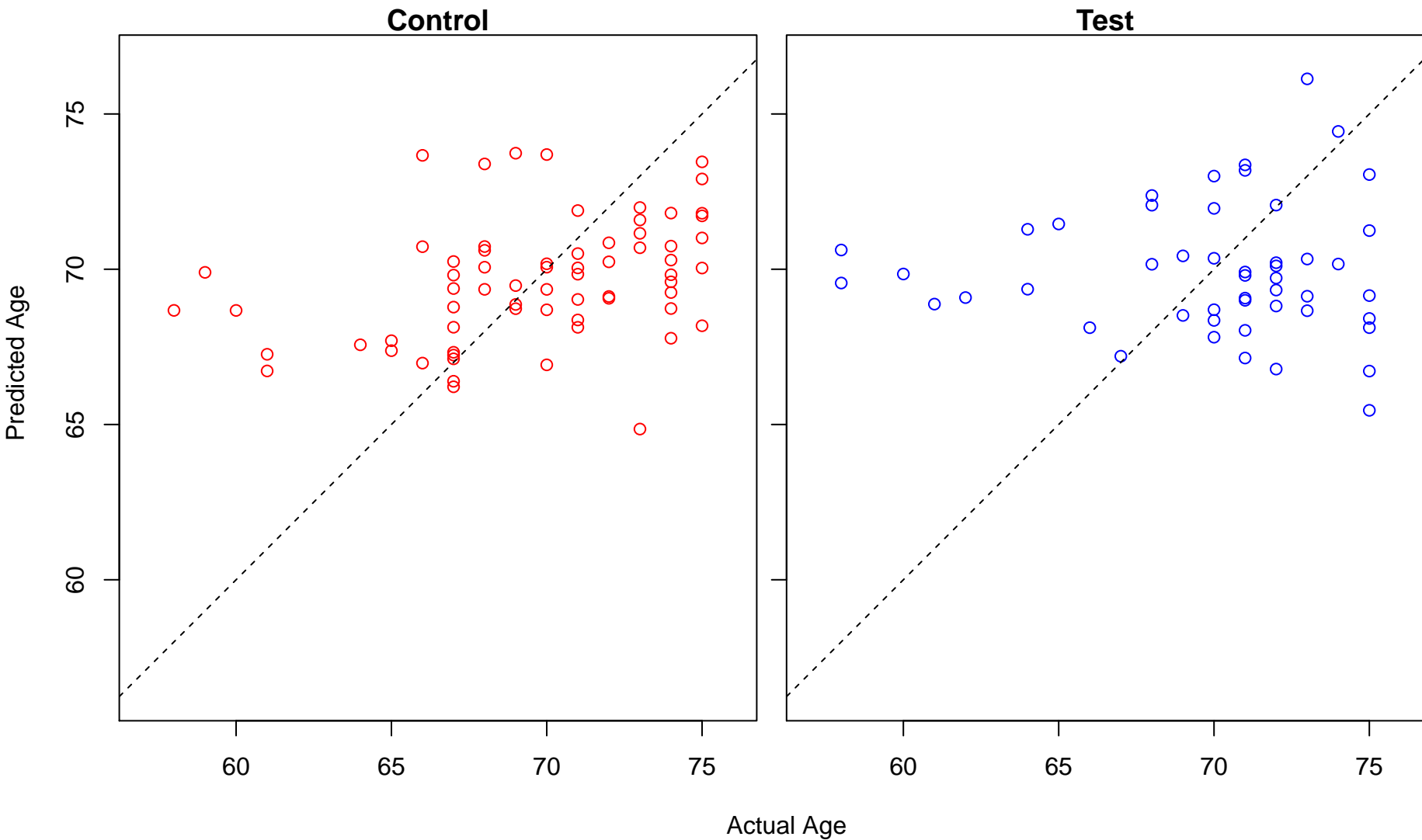
cartilage condensation (Score: 0.406125)



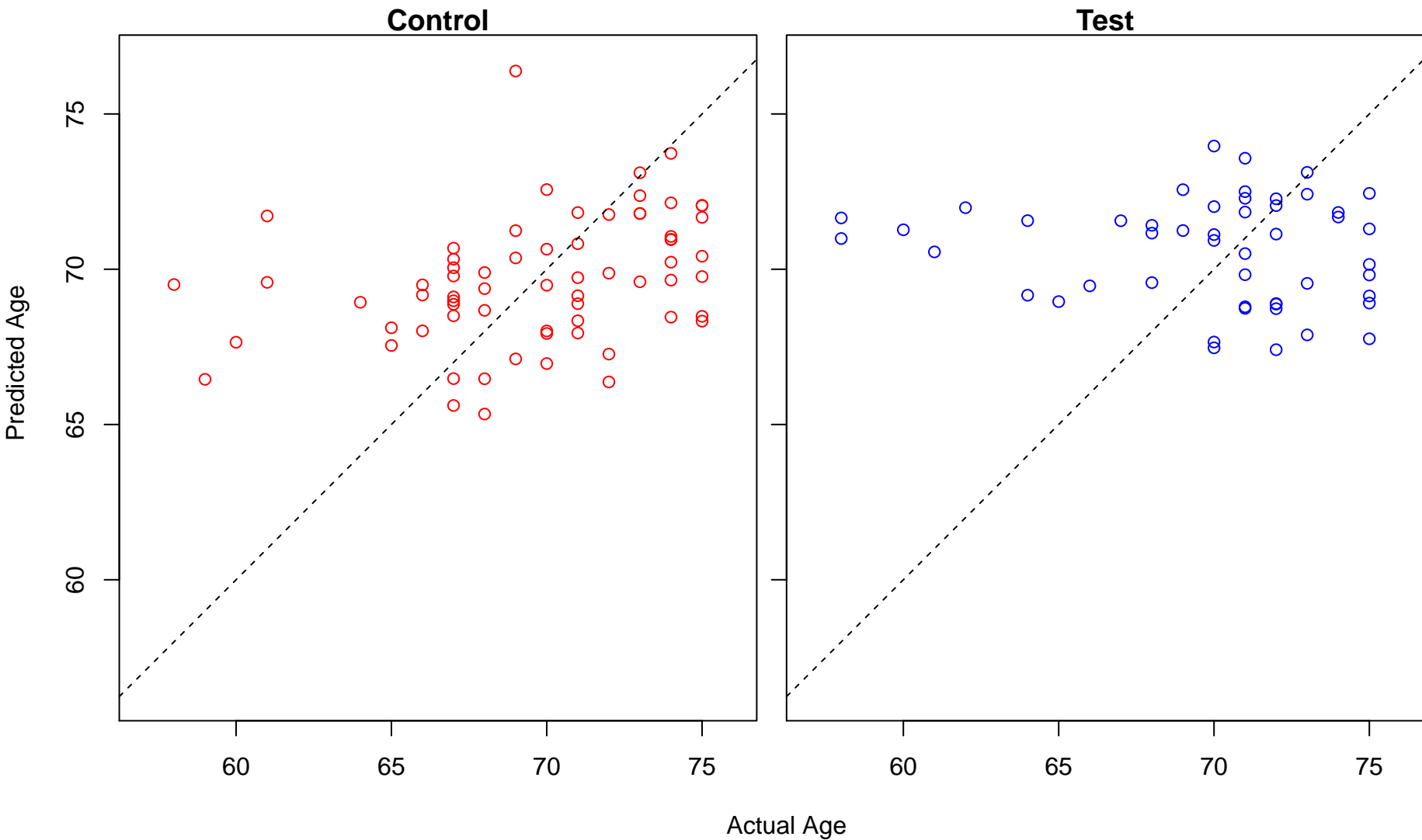
cell aggregation (Score: 0.406125)



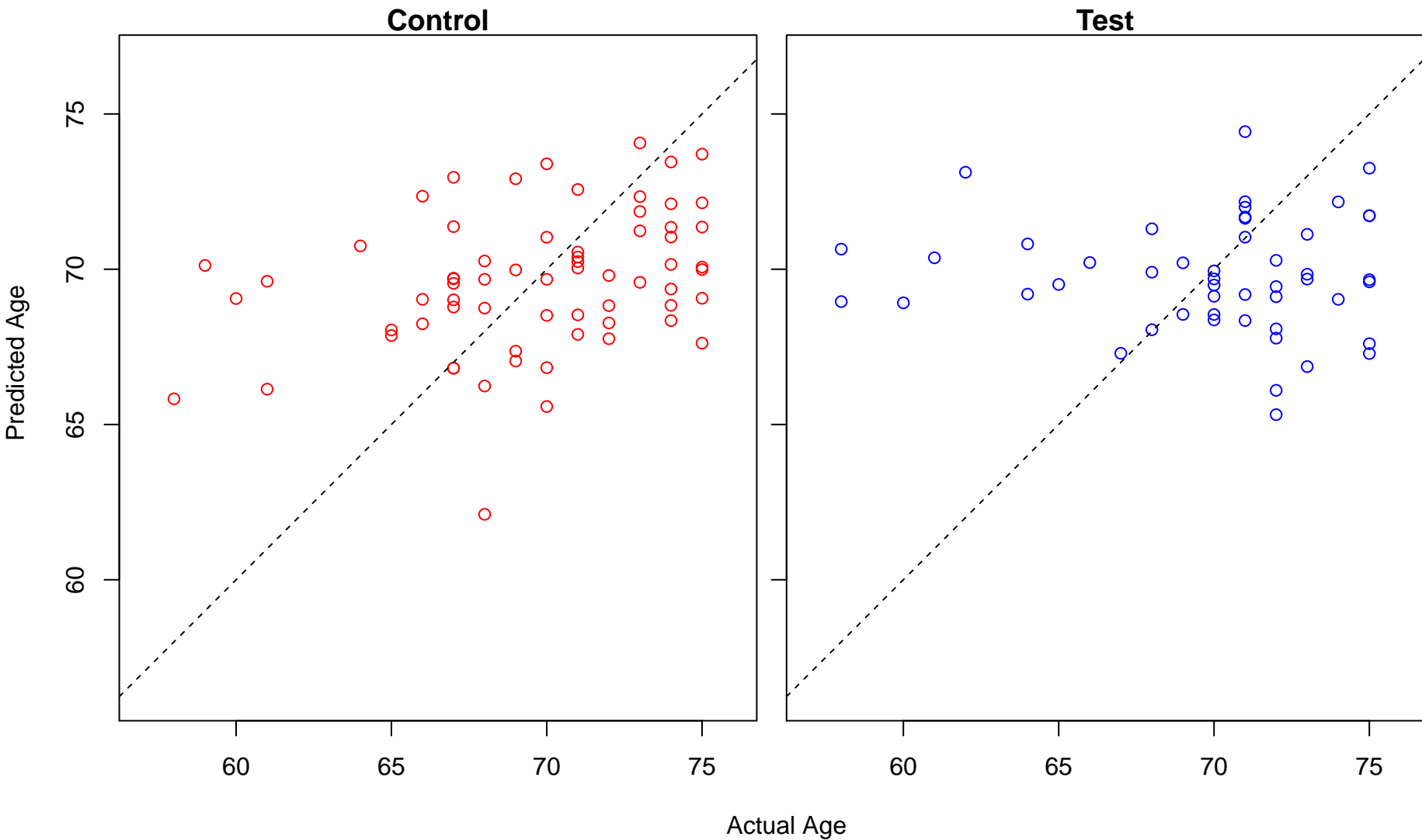
positive regulation of extracellular matrix assembly (Score: 0.405747)



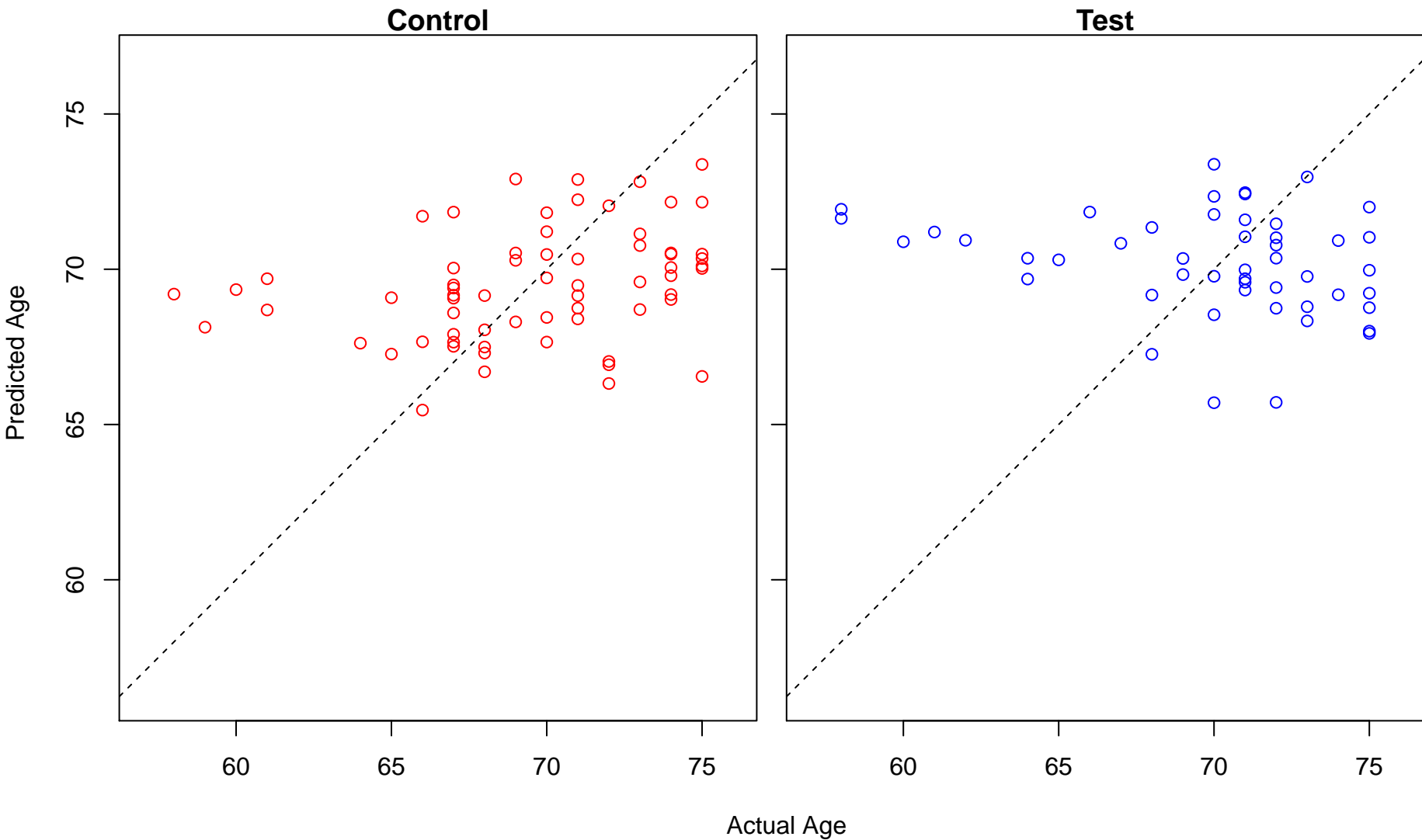
response to X-ray (Score: 0.405119)



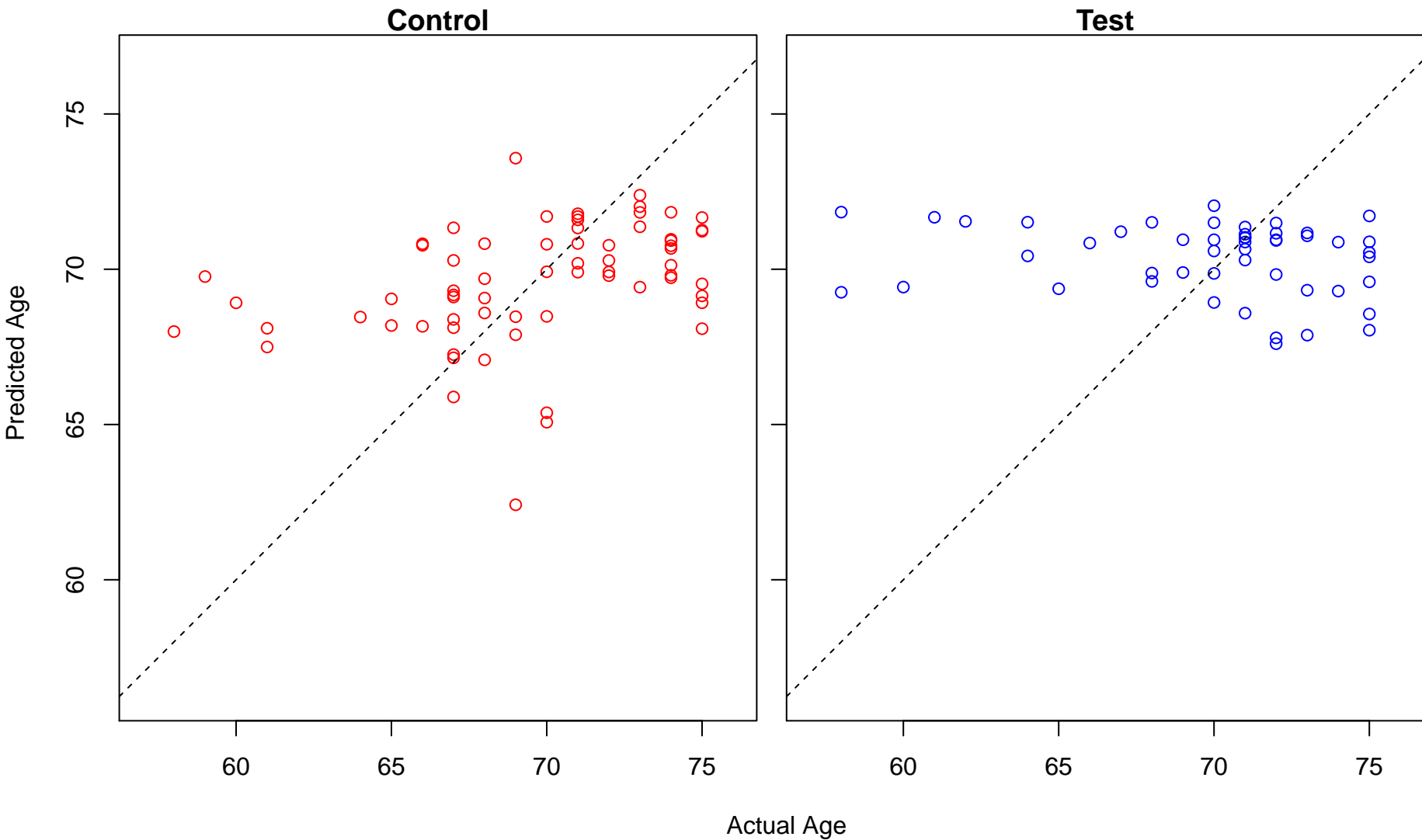
response to stimulus involved in regulation of muscle adaptation (Score: 0.404246)



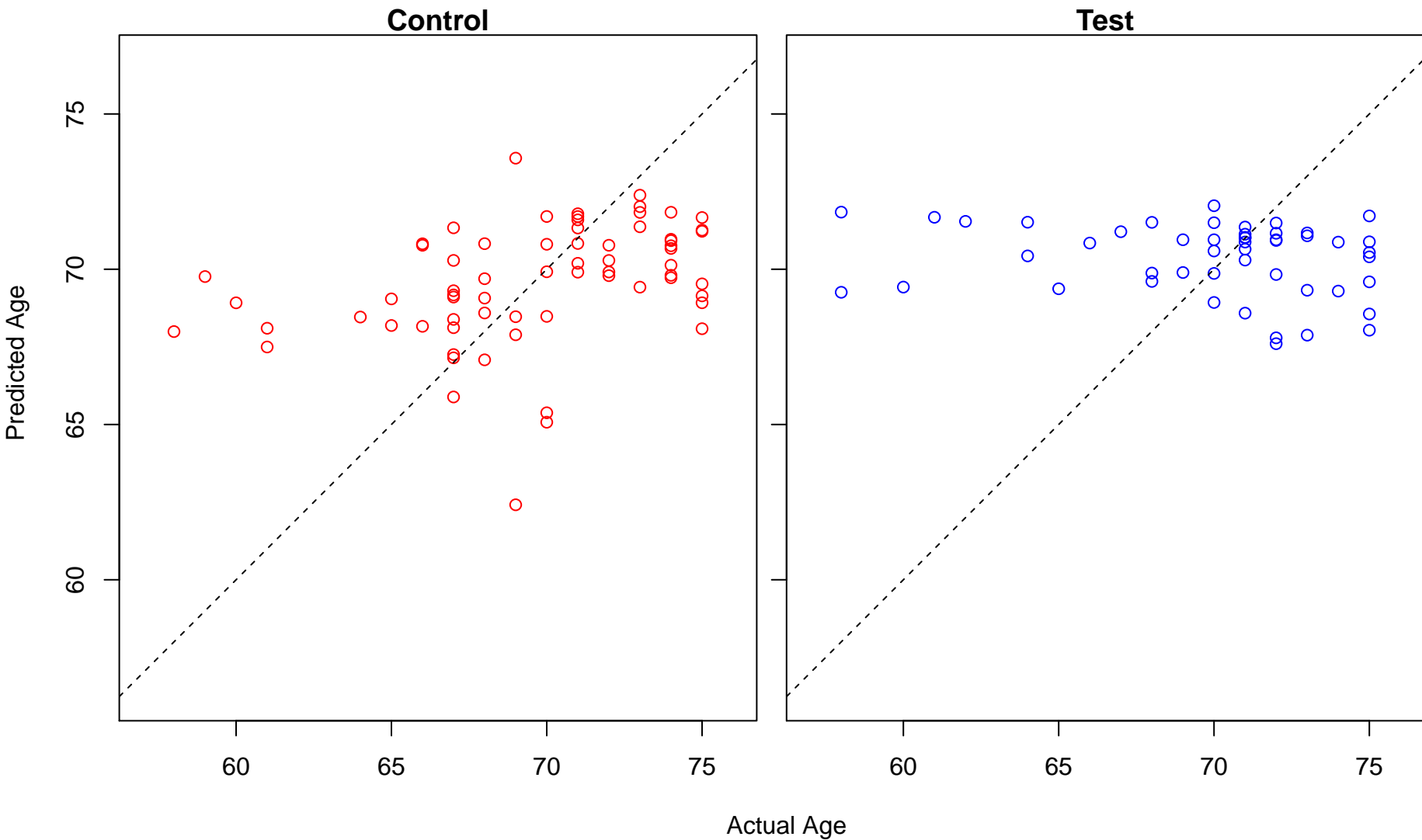
regulation of epithelial cell differentiation involved in kidney development (Score: 0.404171)



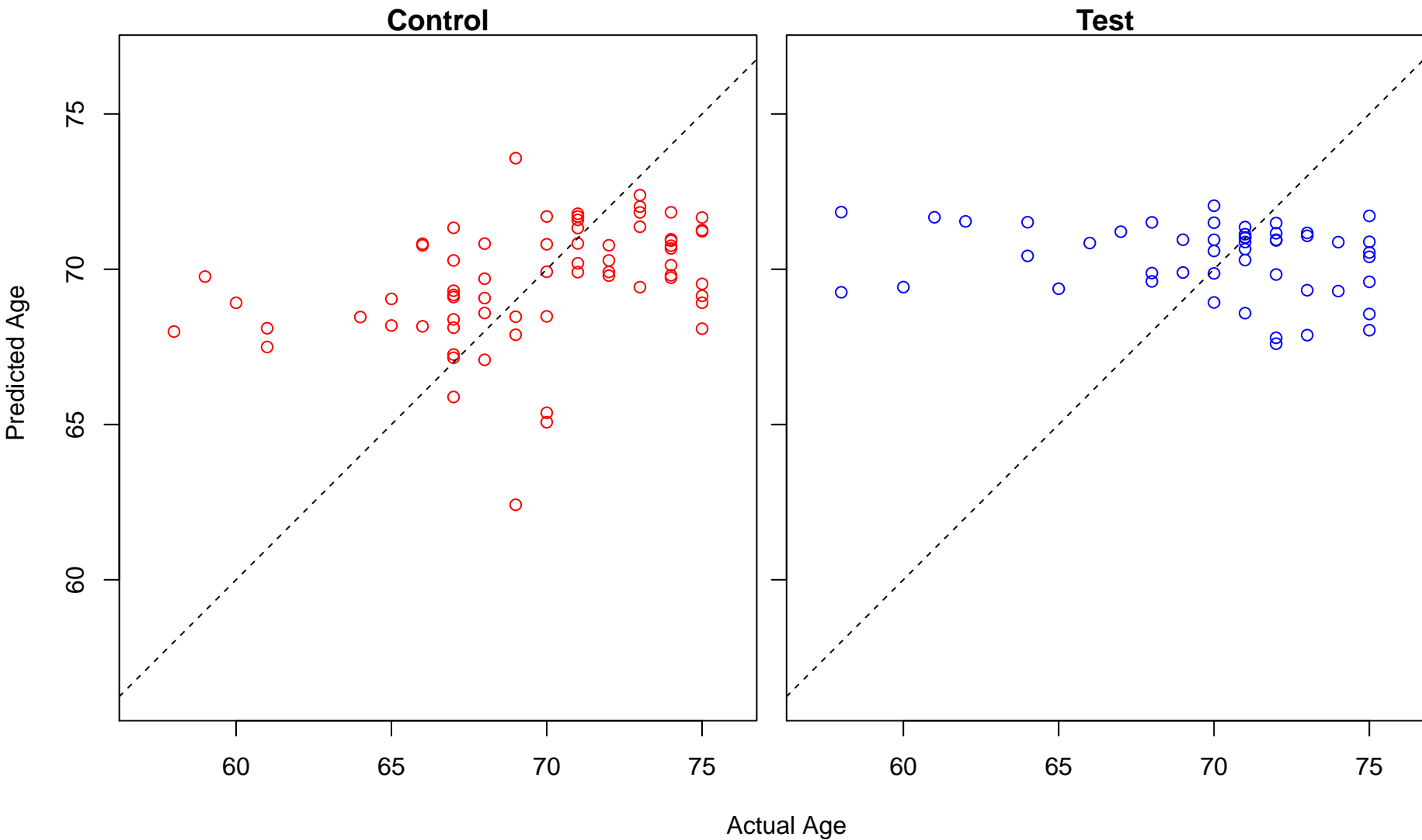
polyketide metabolic process (Score: 0.403406)



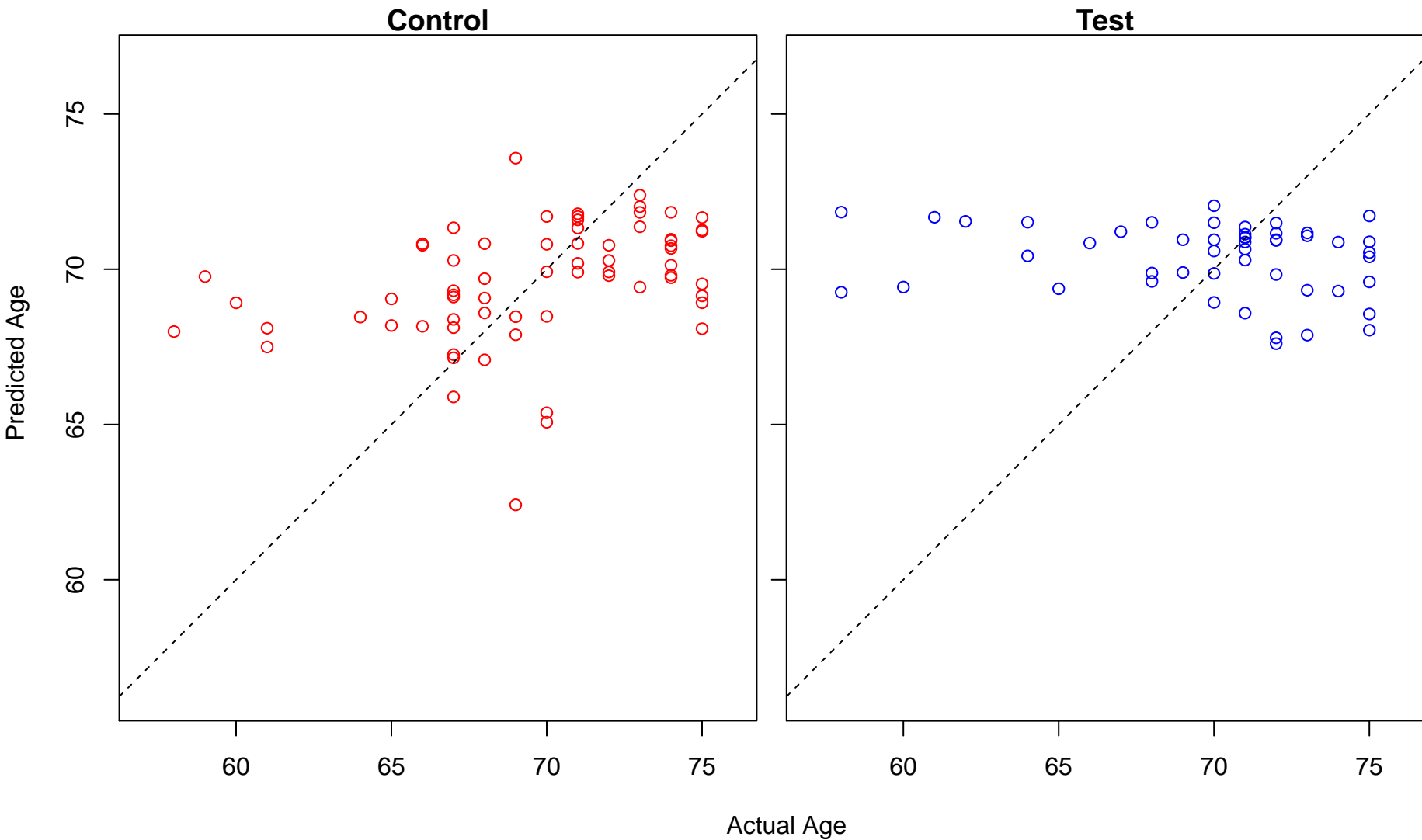
aminoglycoside antibiotic metabolic process (Score: 0.403406)



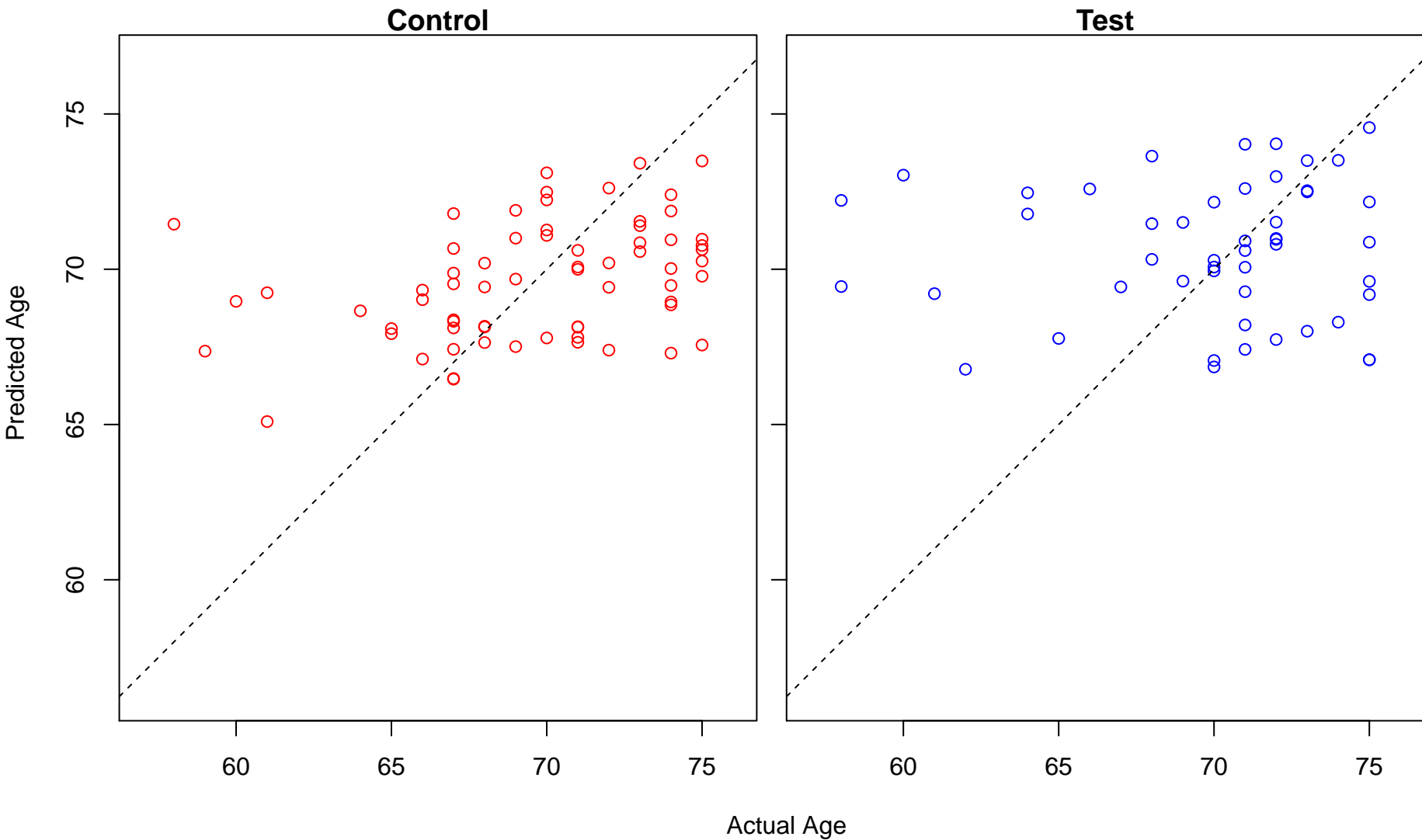
daunorubicin metabolic process (Score: 0.403406)



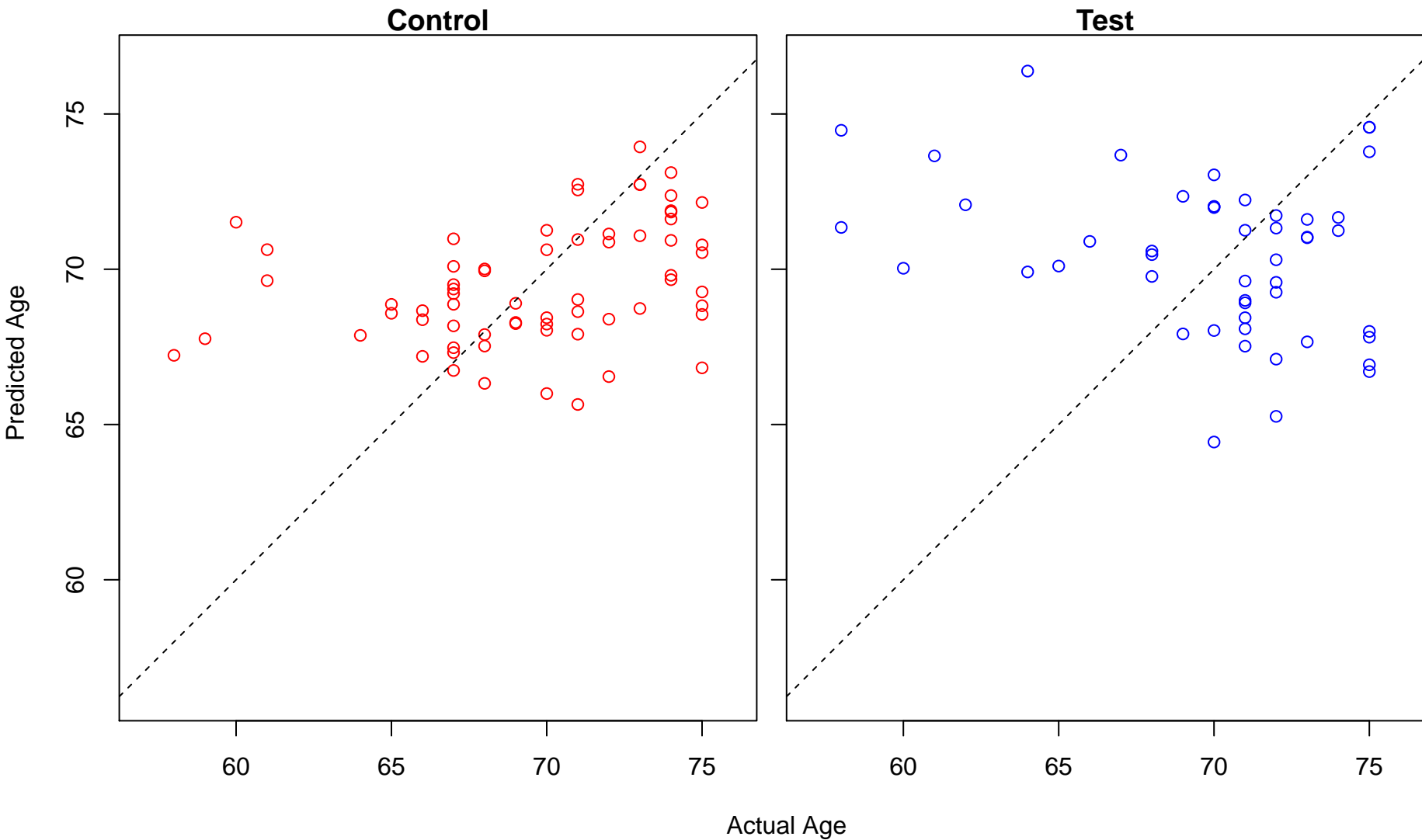
doxorubicin metabolic process (Score: 0.403406)



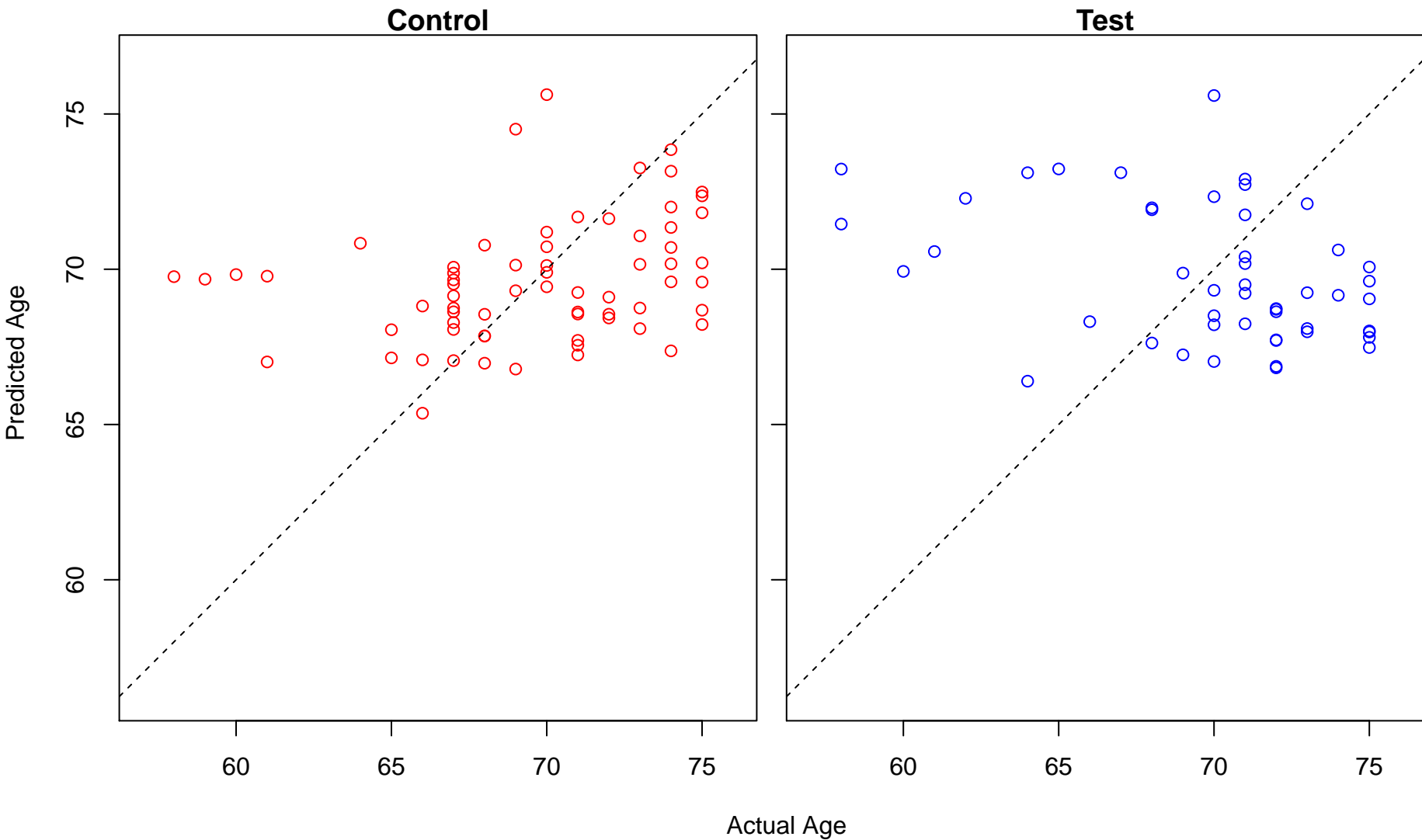
synaptic transmission, cholinergic (Score: 0.403253)



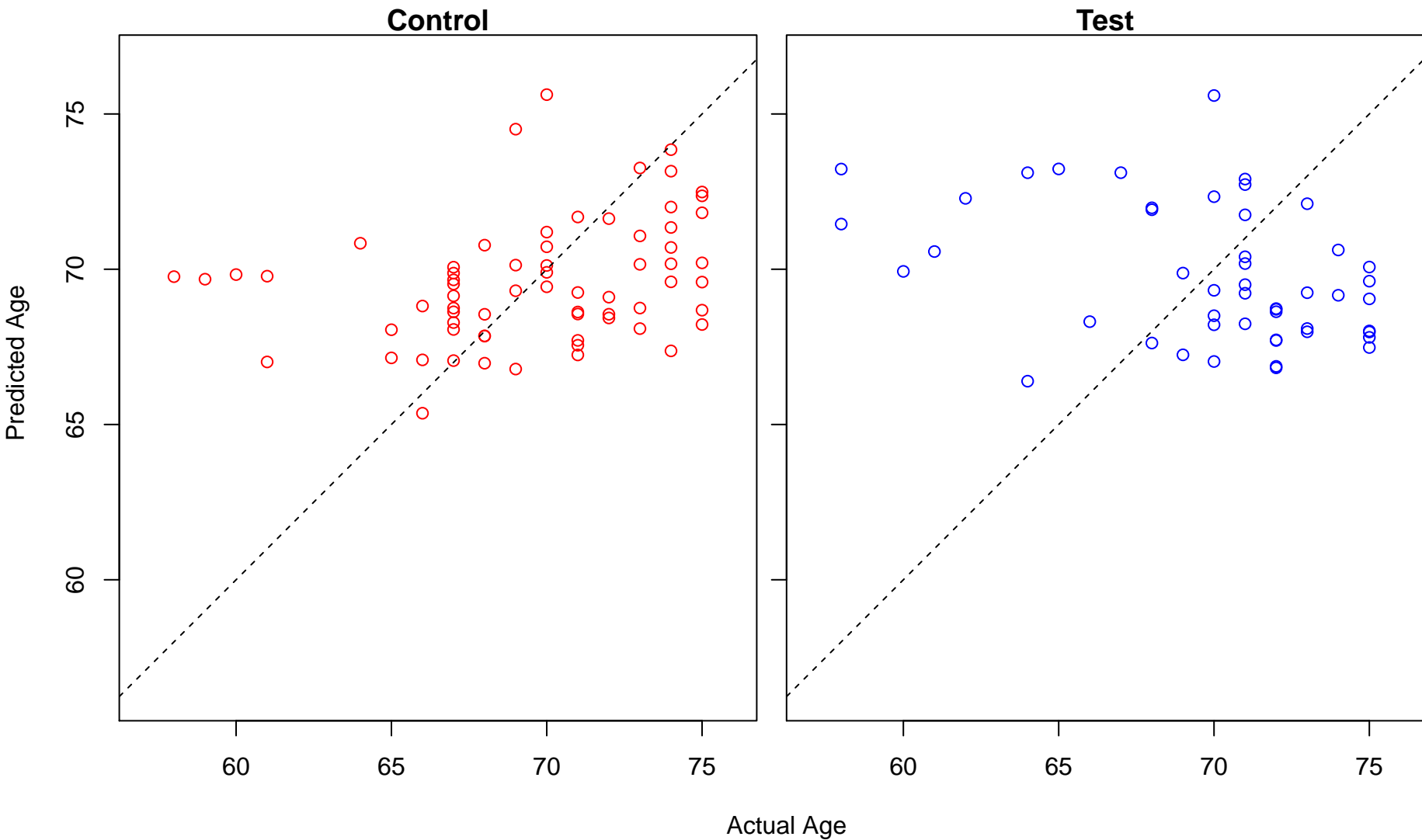
negative regulation of leukocyte migration (Score: 0.403080)



urea cycle (Score: 0.402842)

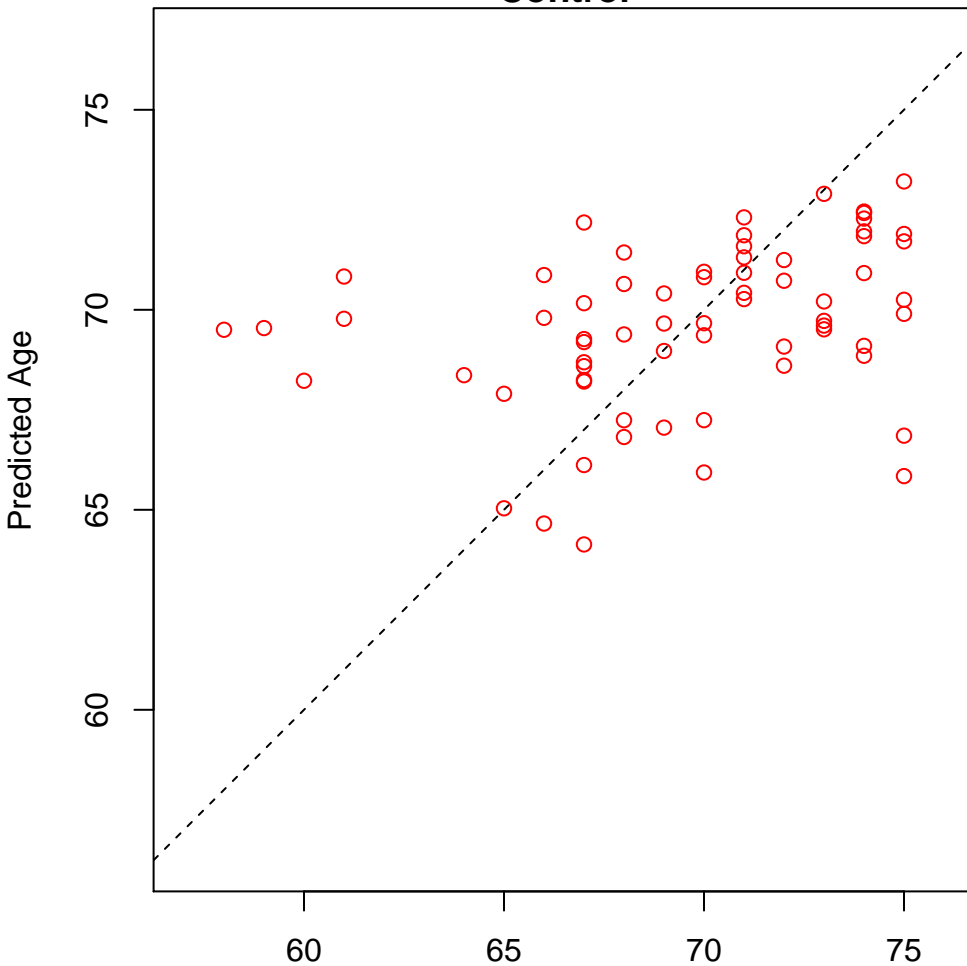


urea metabolic process (Score: 0.402842)

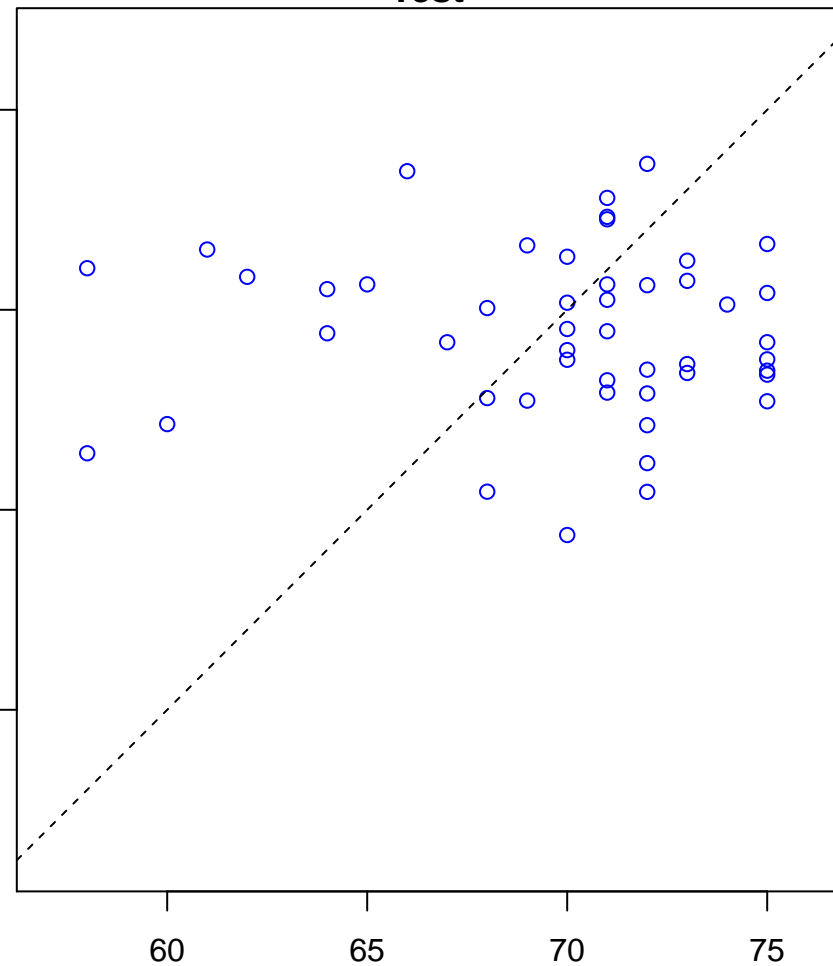


regulation of mononuclear cell migration (Score: 0.401937)

Control

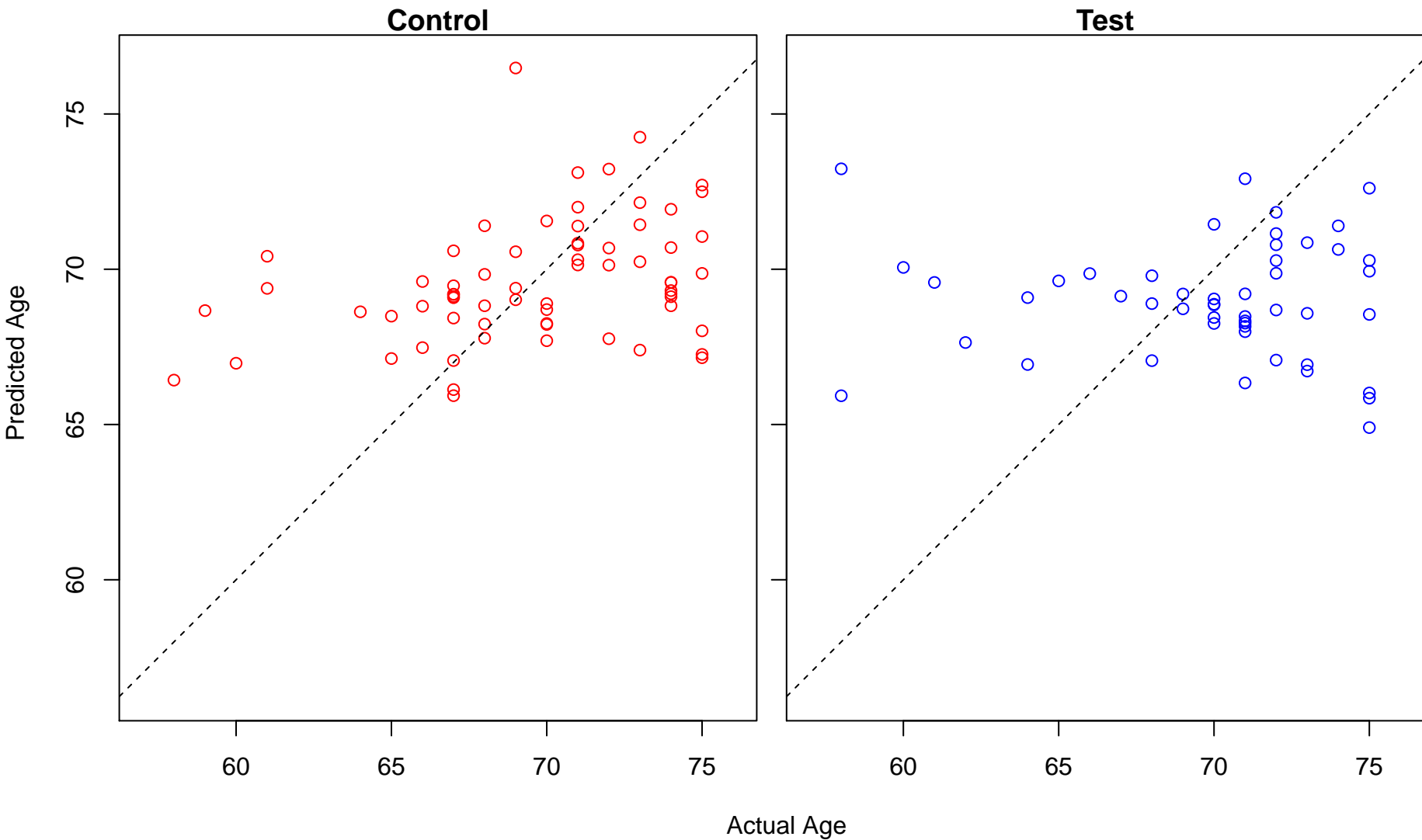


Test

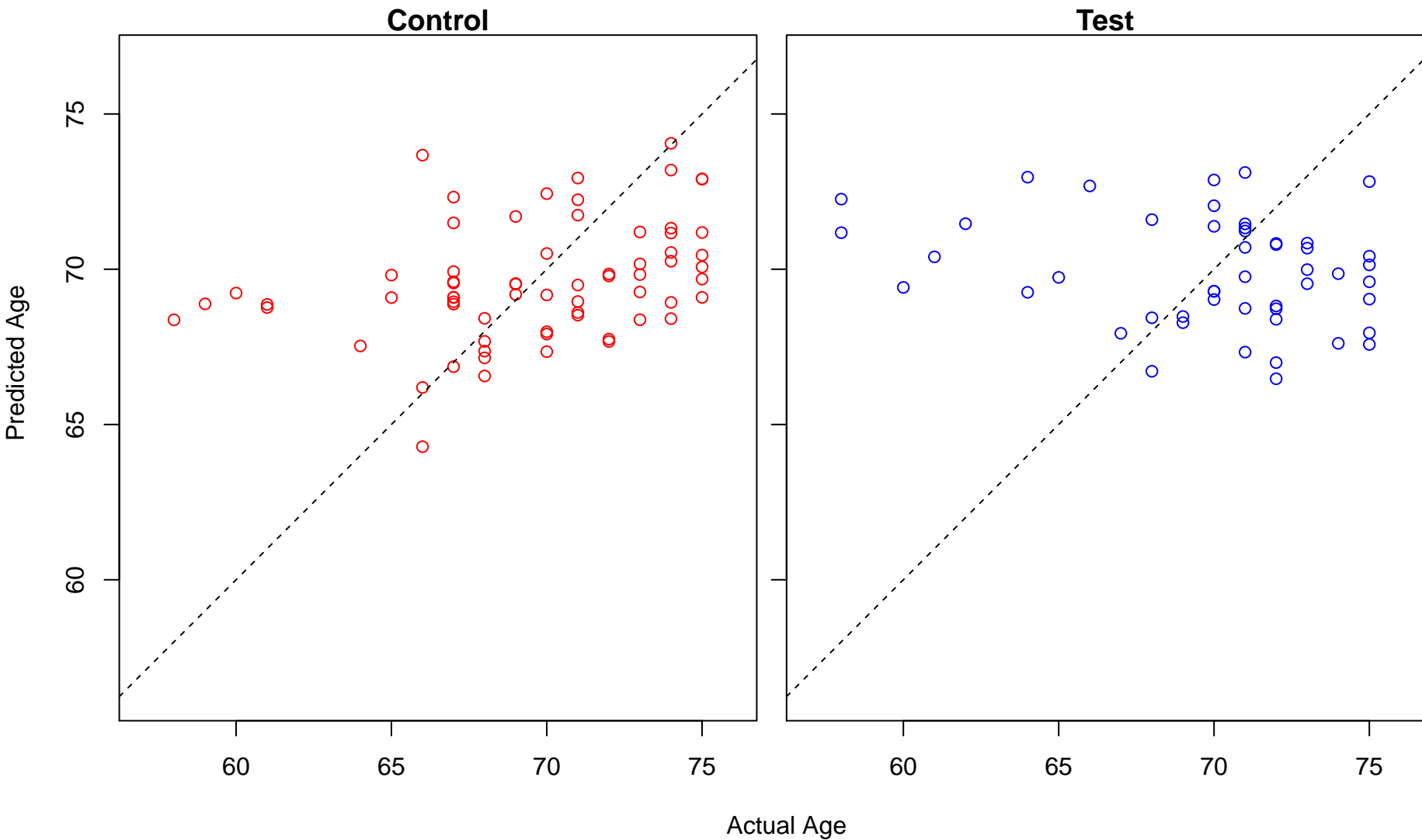


Actual Age

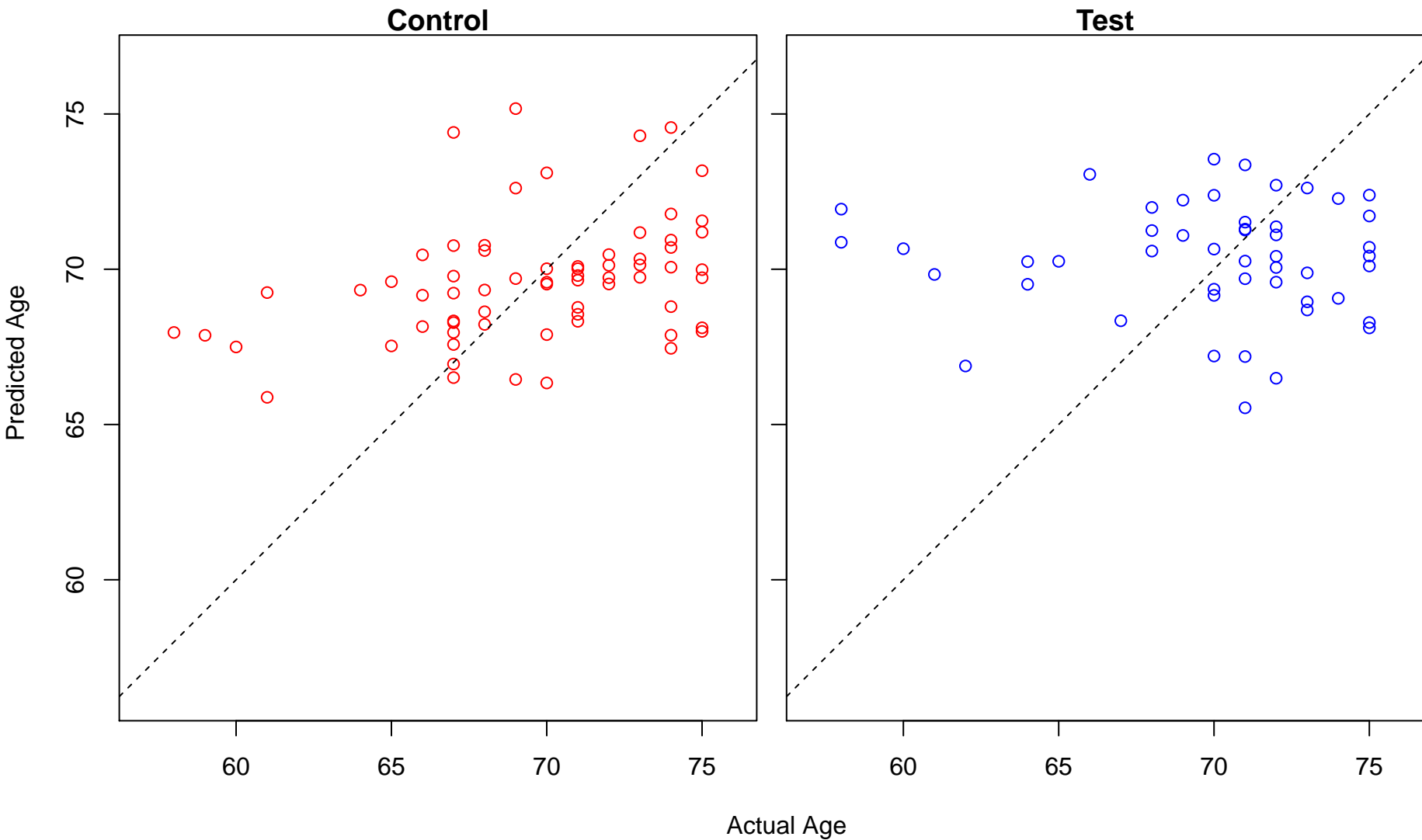
humoral immune response mediated by circulating immunoglobulin (Score: 0.400786)



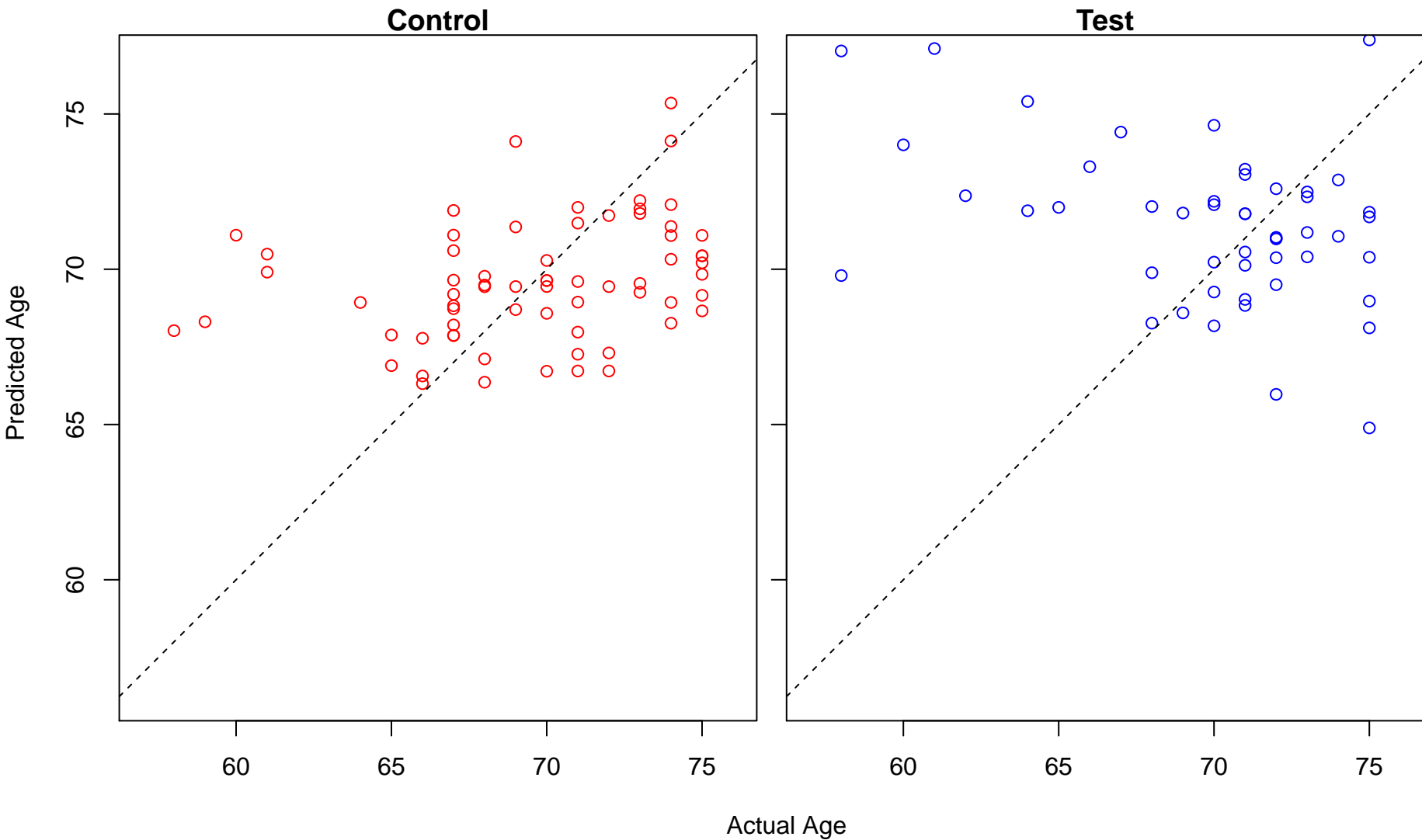
sequestering of actin monomers (Score: 0.400622)



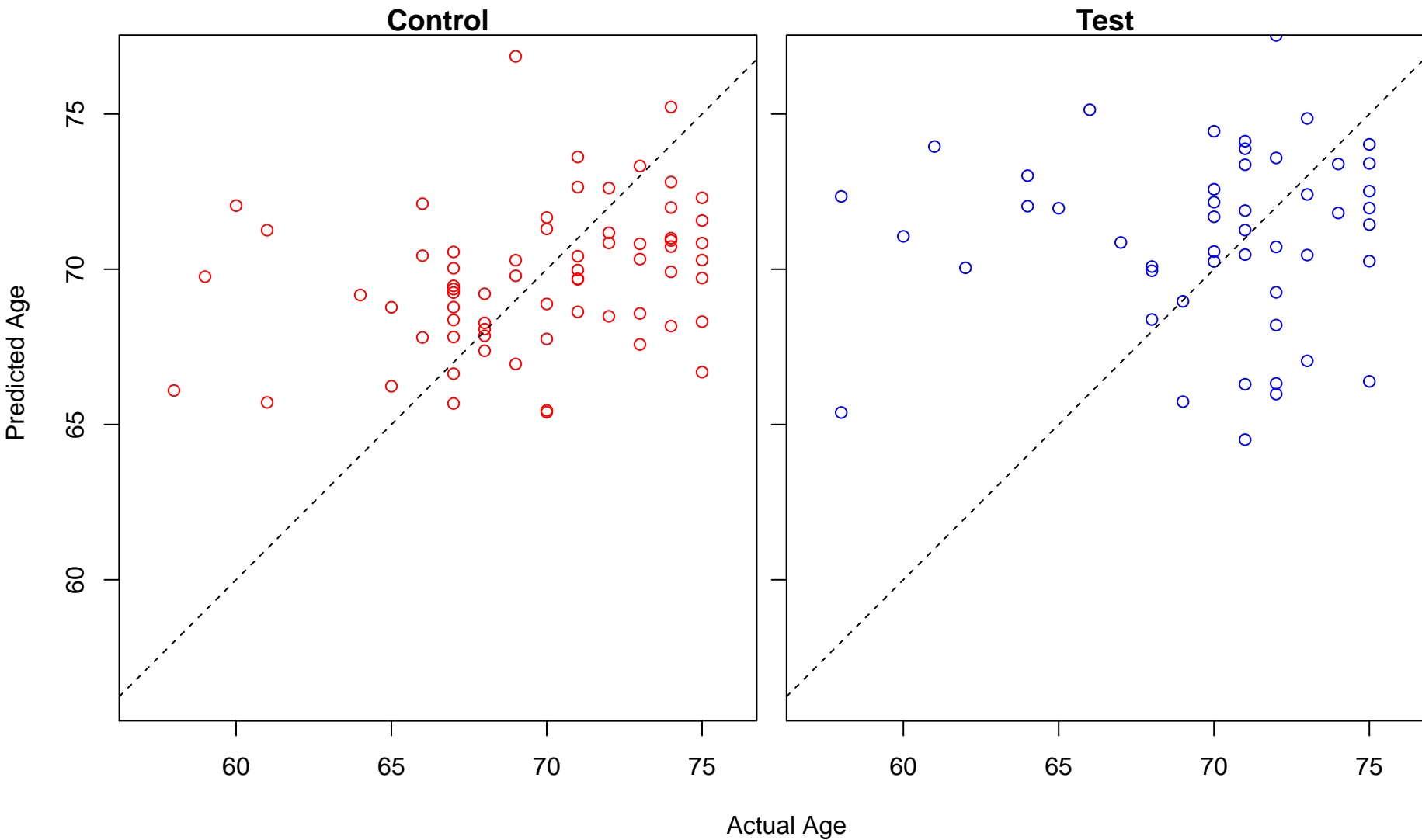
negative regulation of phospholipid metabolic process (Score: 0.400245)



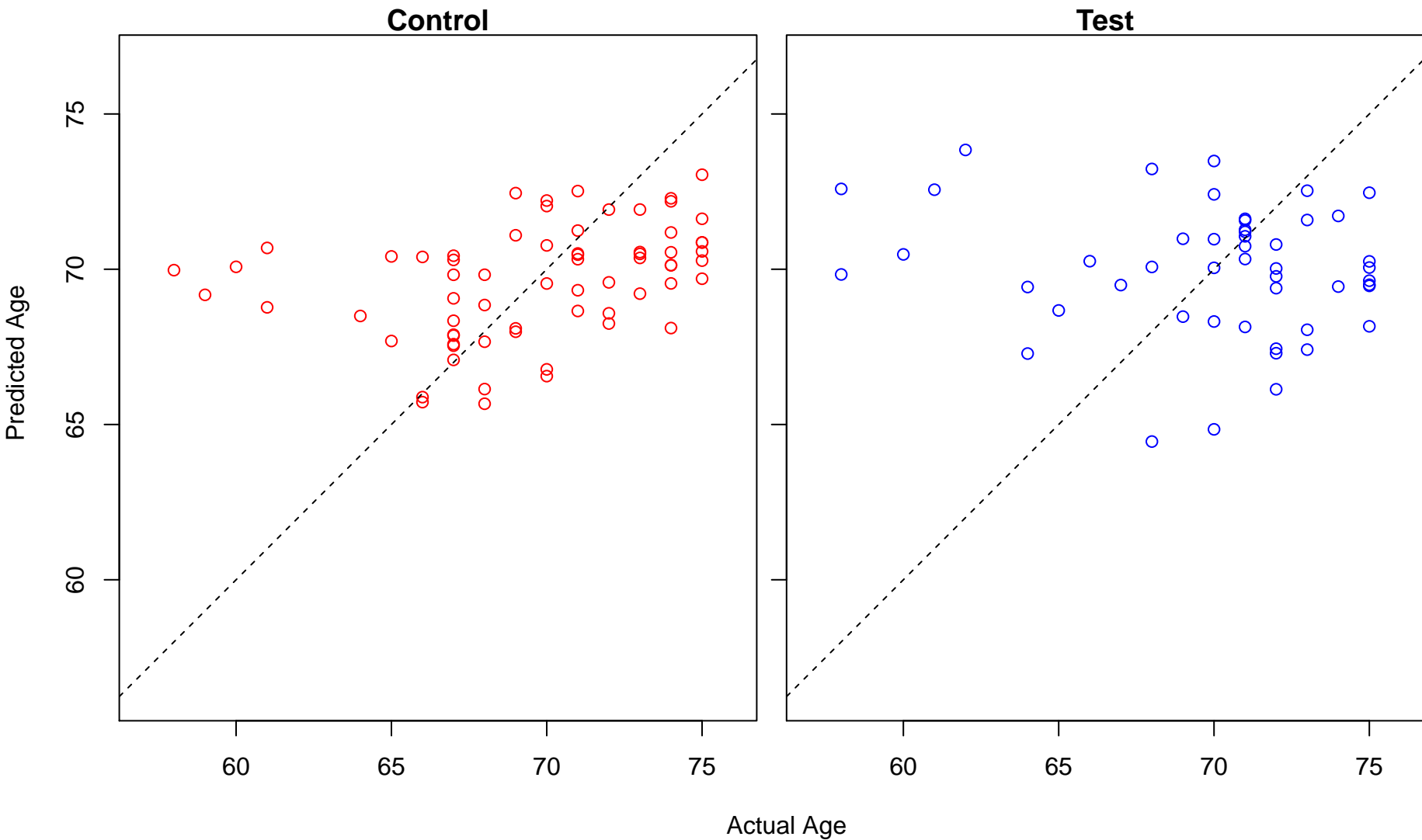
regulation of SMAD protein import into nucleus (Score: 0.399079)



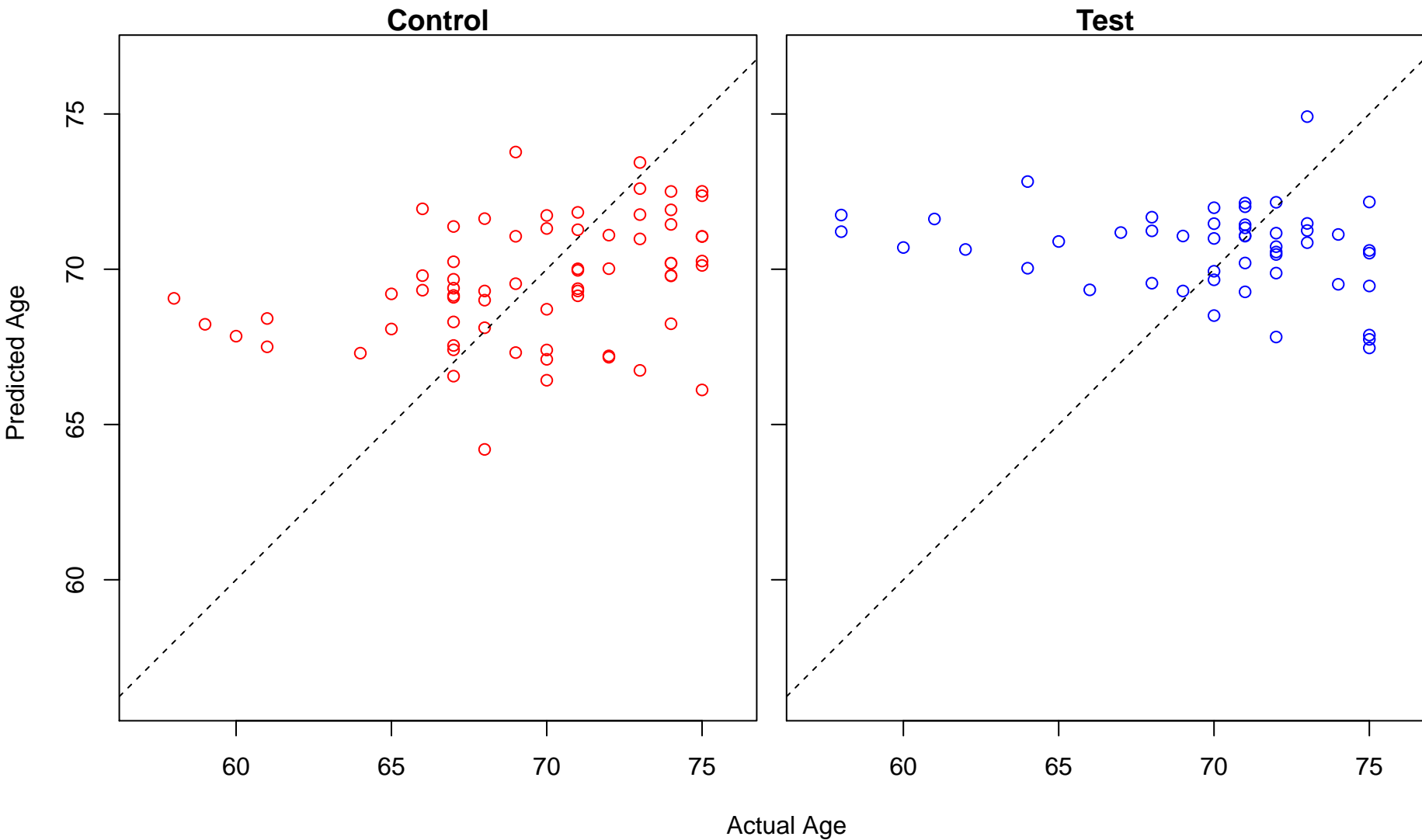
endothelial cell chemotaxis (Score: 0.398970)



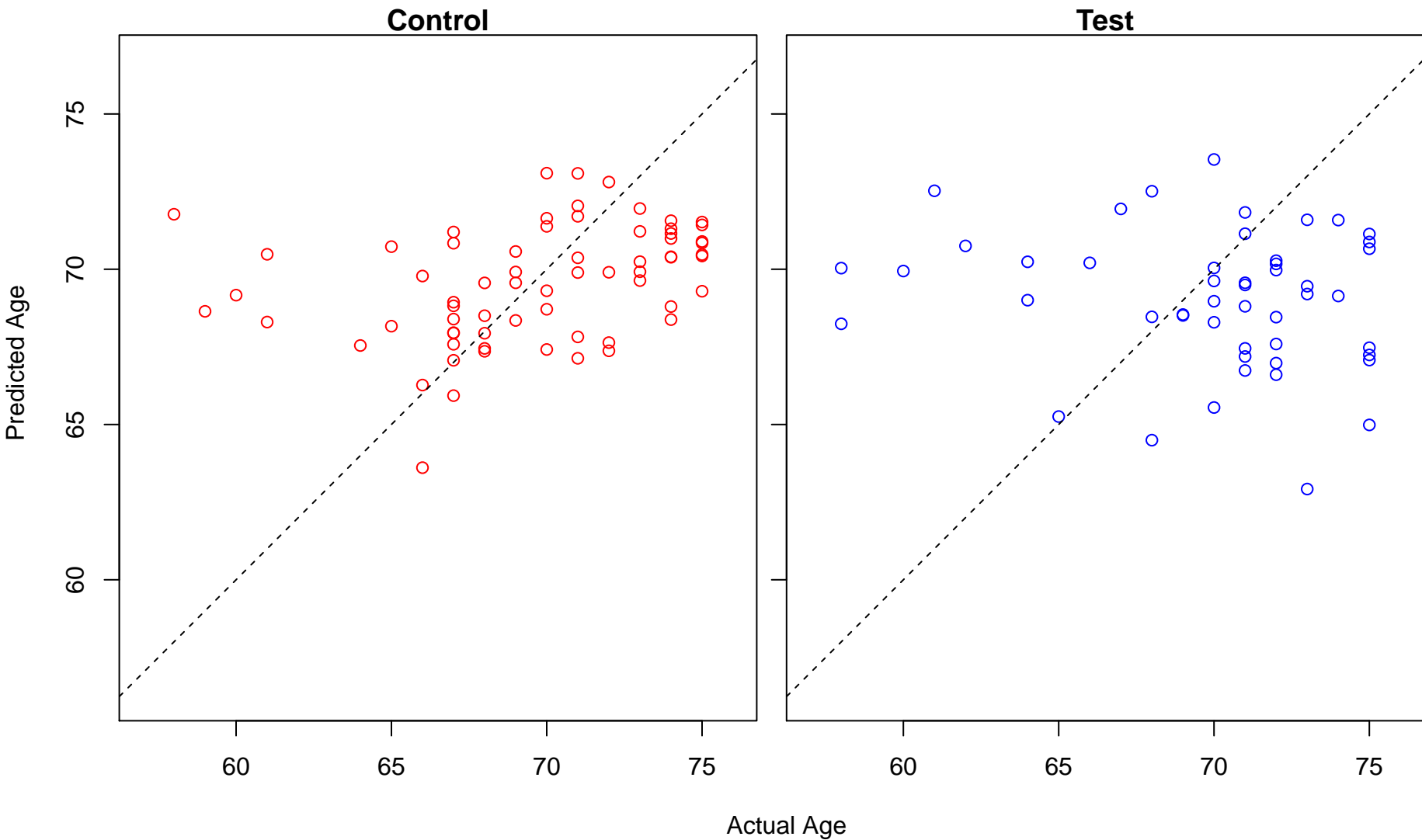
detection of calcium ion (Score: 0.398525)



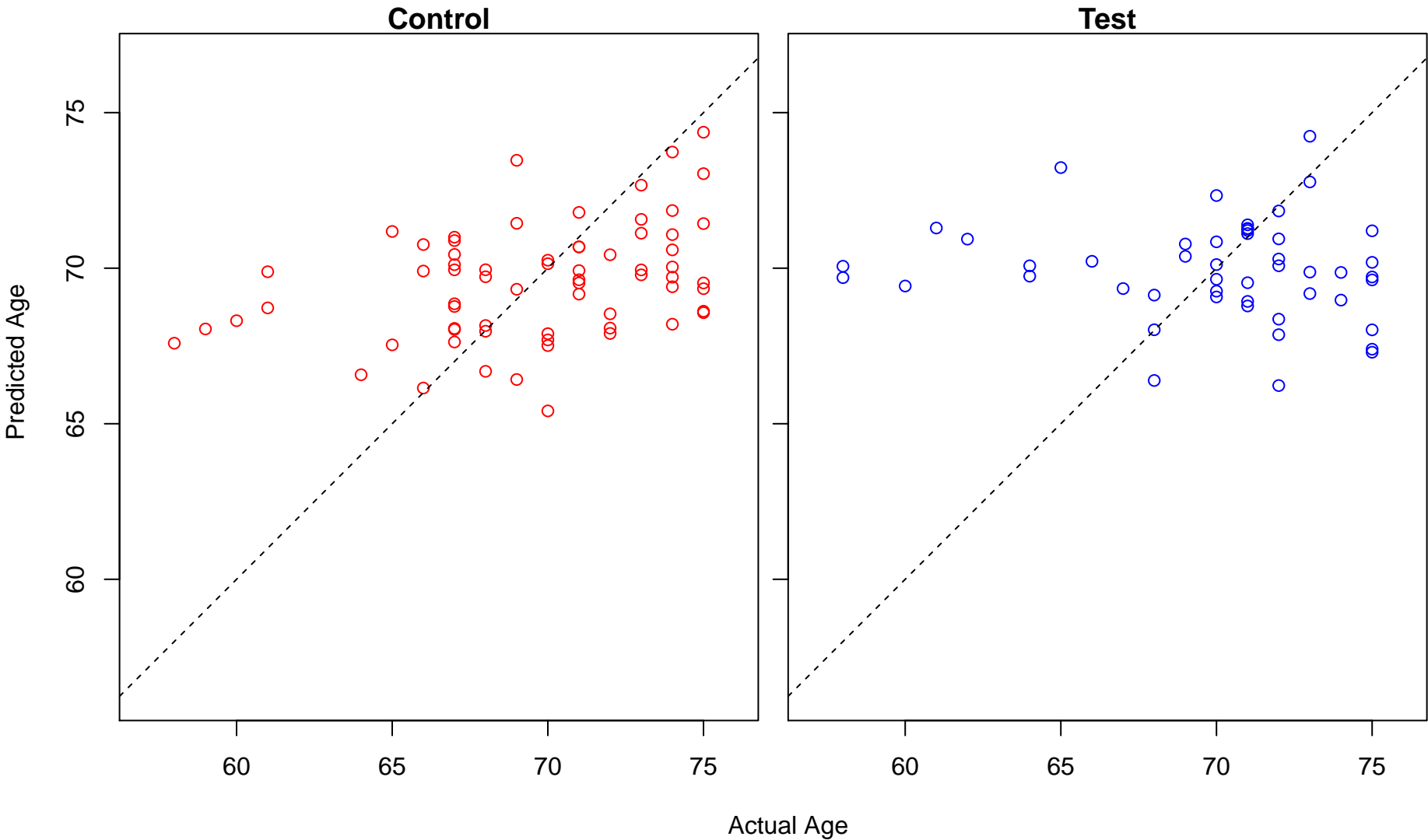
regulation of hydrogen peroxide-mediated programmed cell death (Score: 0.396774)



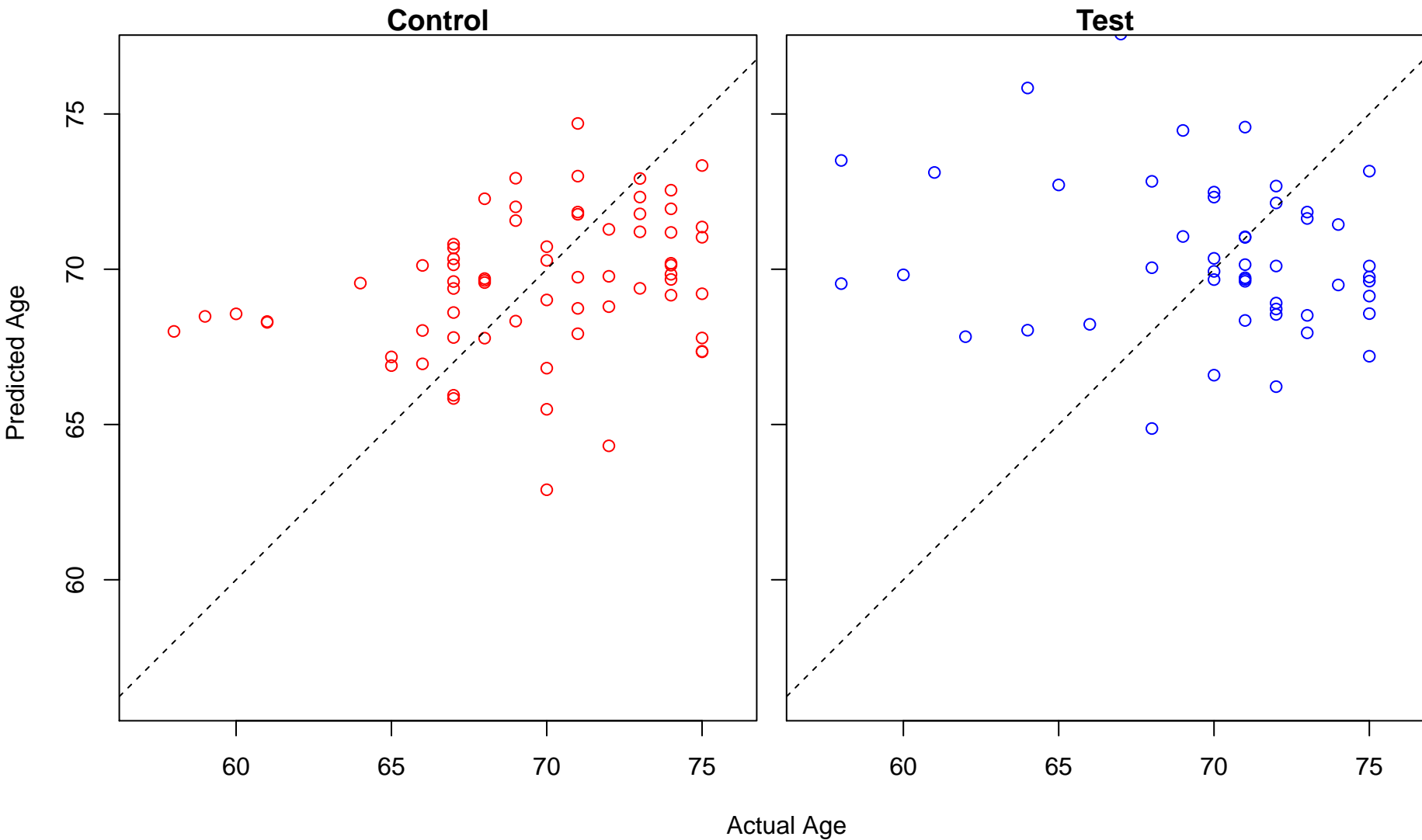
negative regulation of activin receptor signaling pathway (Score: 0.395226)



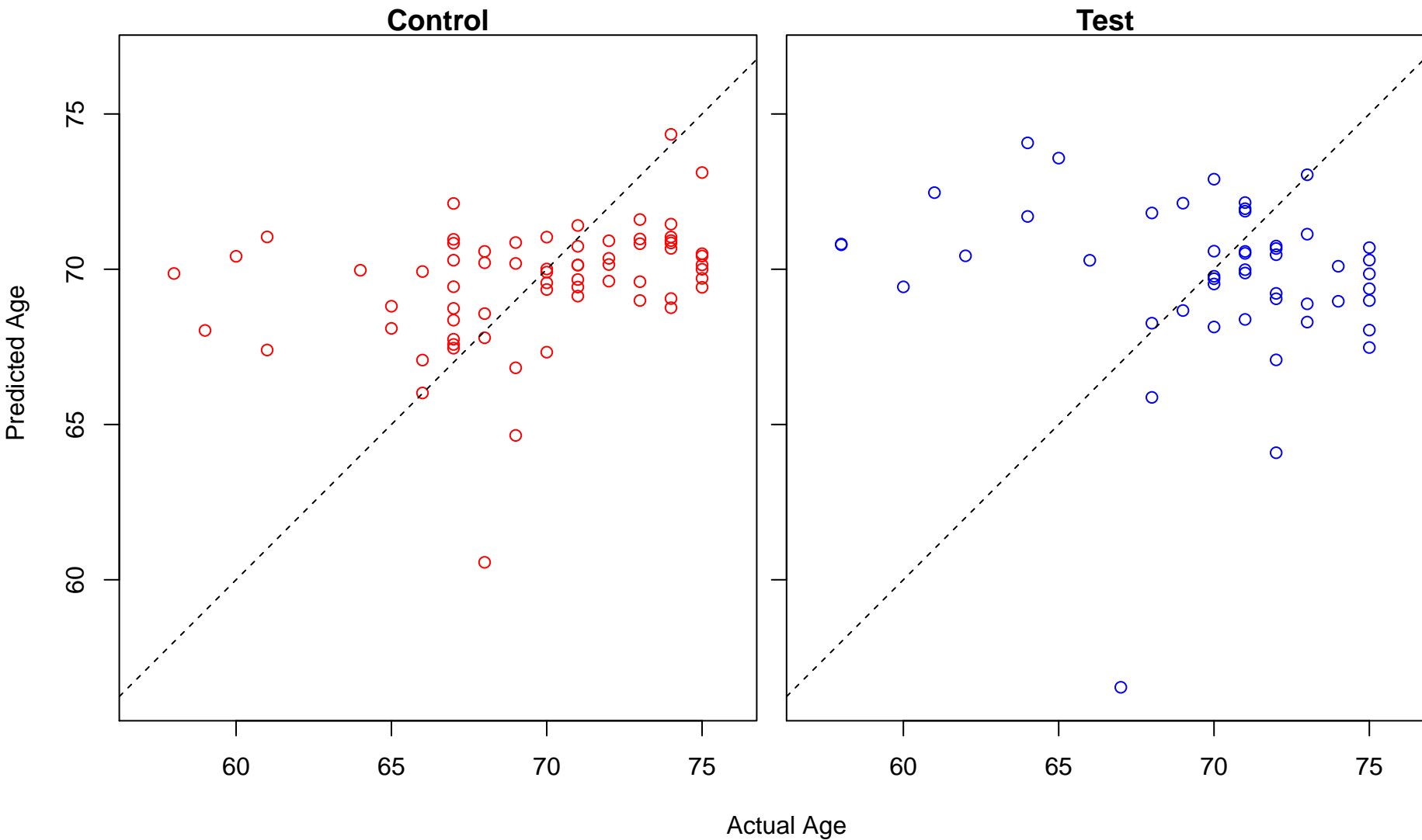
ventricular cardiac muscle cell action potential (Score: 0.394974)



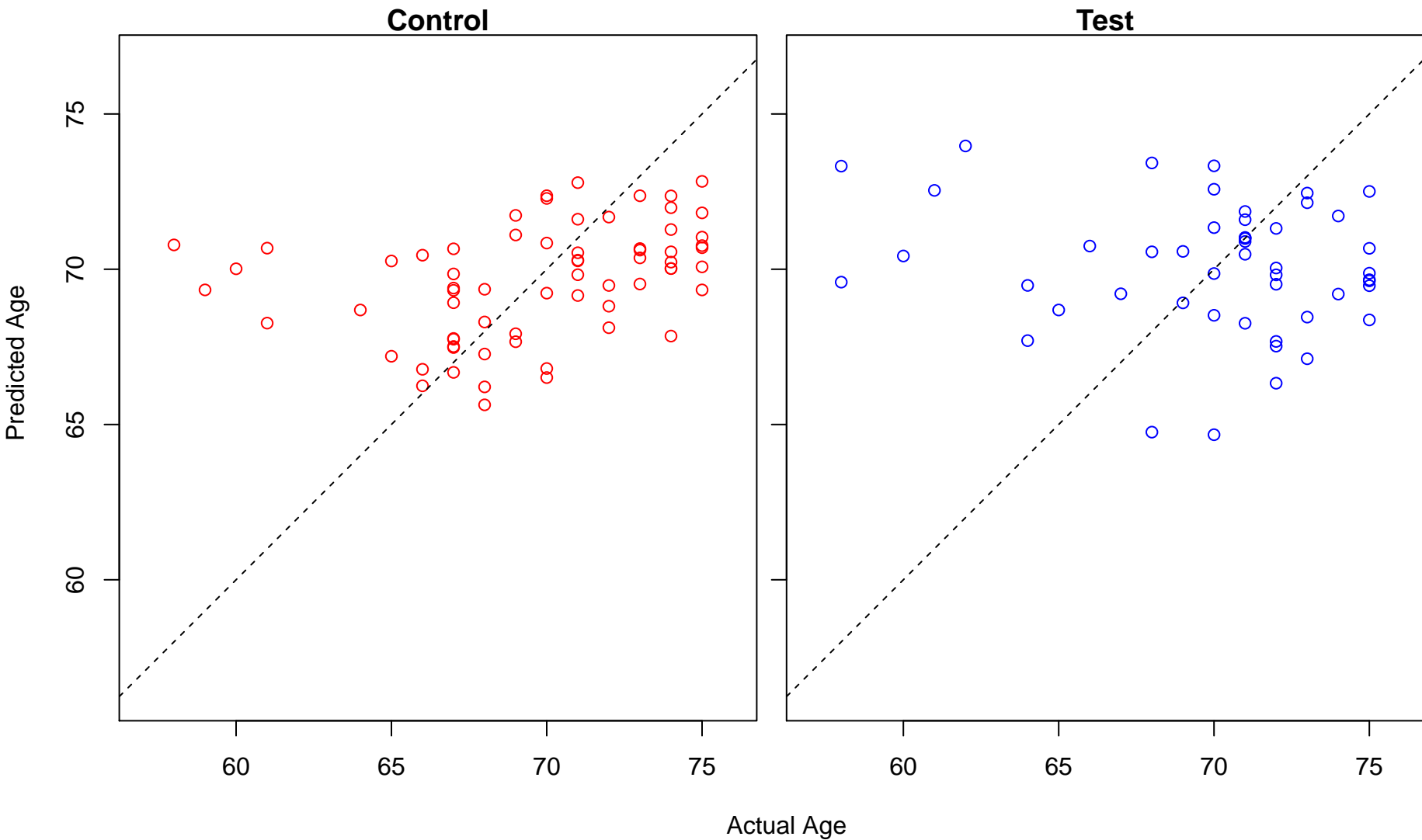
L-serine metabolic process (Score: 0.394314)



microtubule depolymerization (Score: 0.394079)

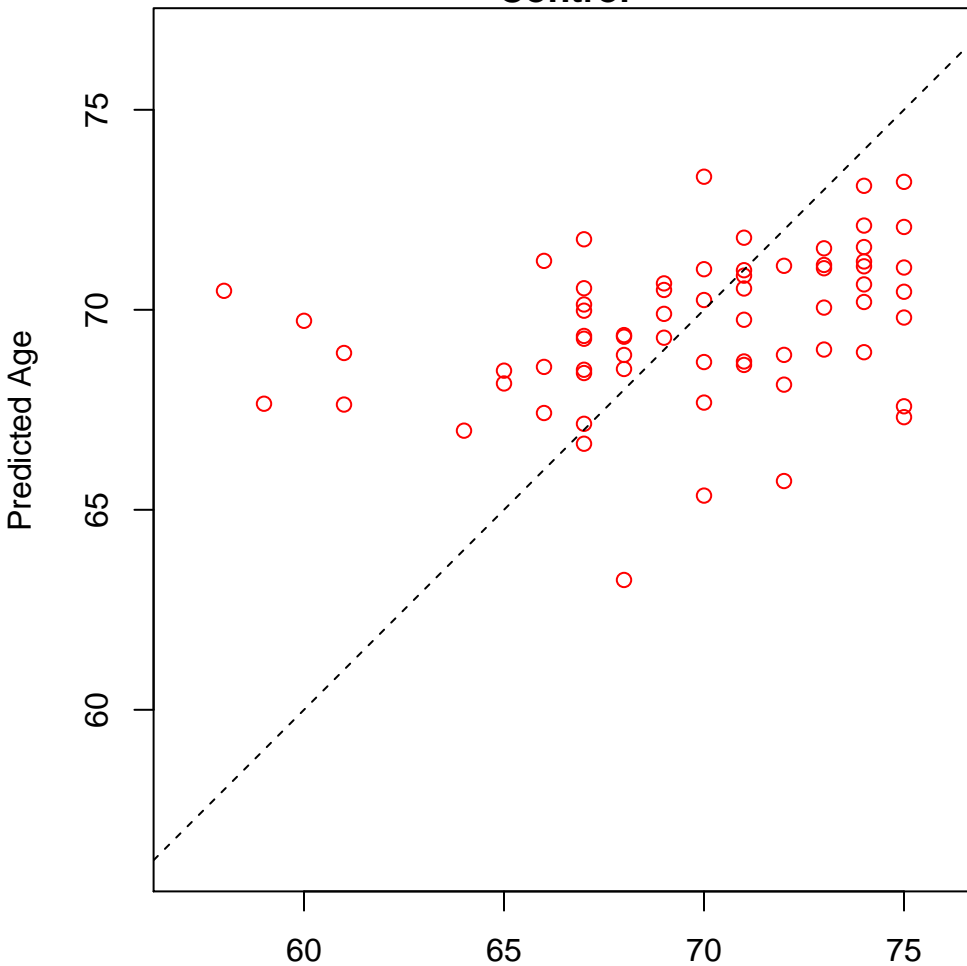


amelogenesis (Score: 0.393959)

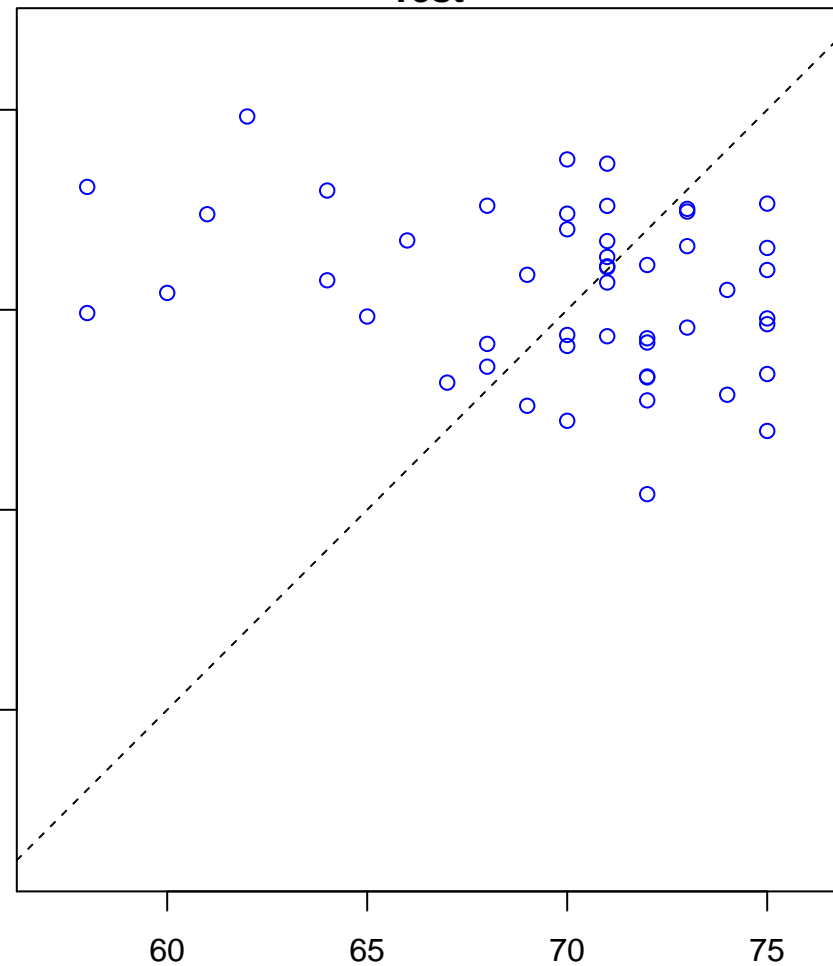


regulation of oxidative phosphorylation (Score: 0.392903)

Control

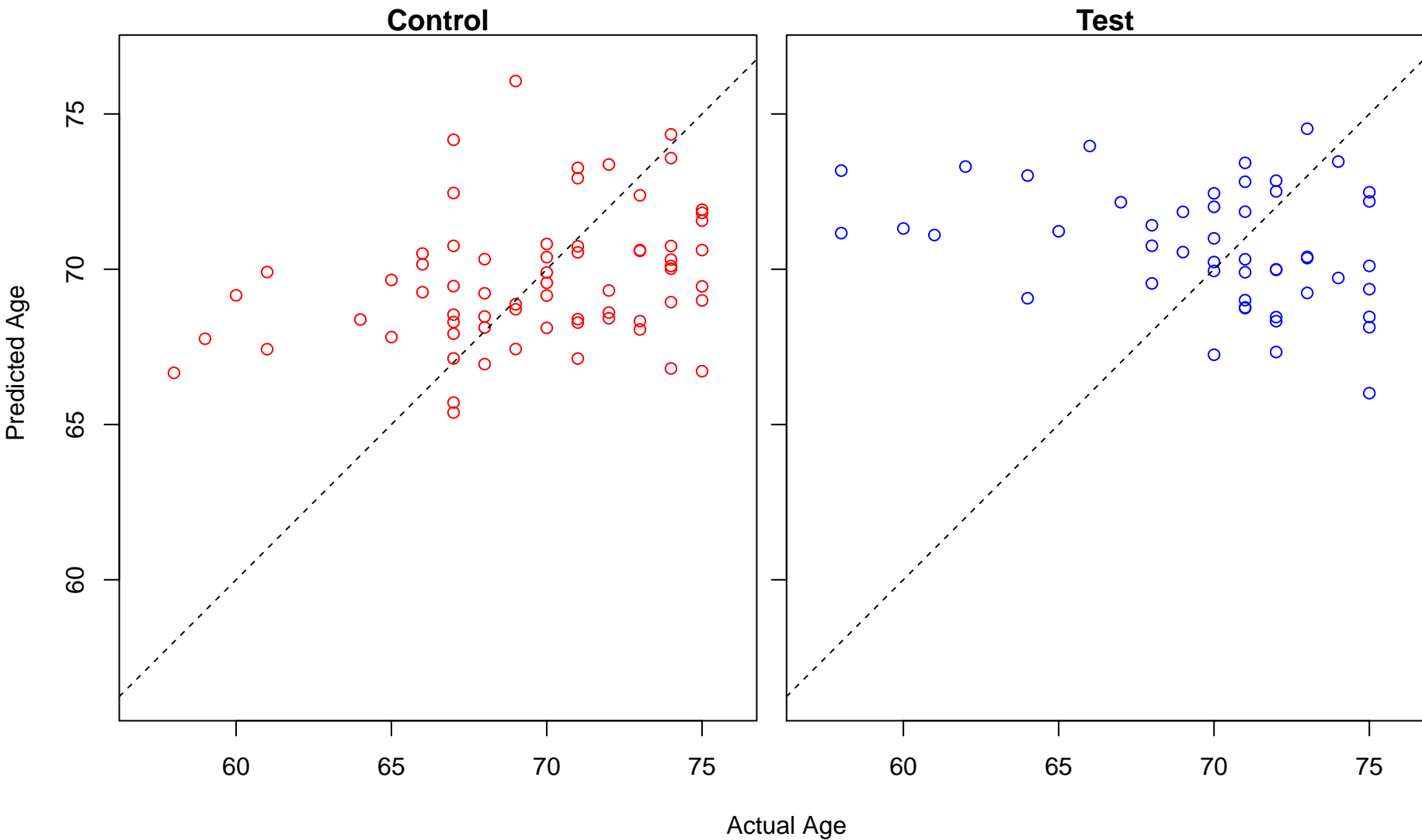


Test

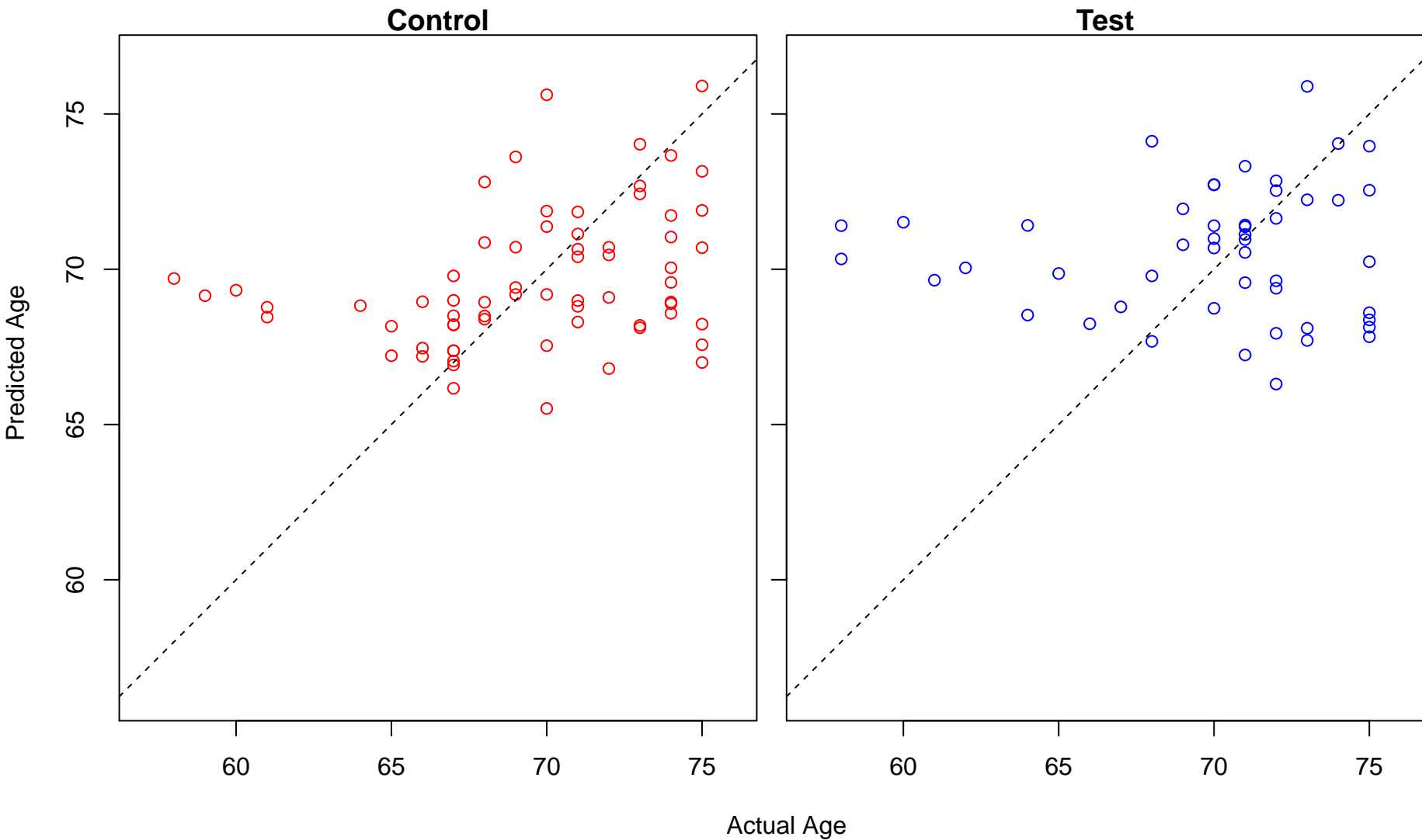


Actual Age

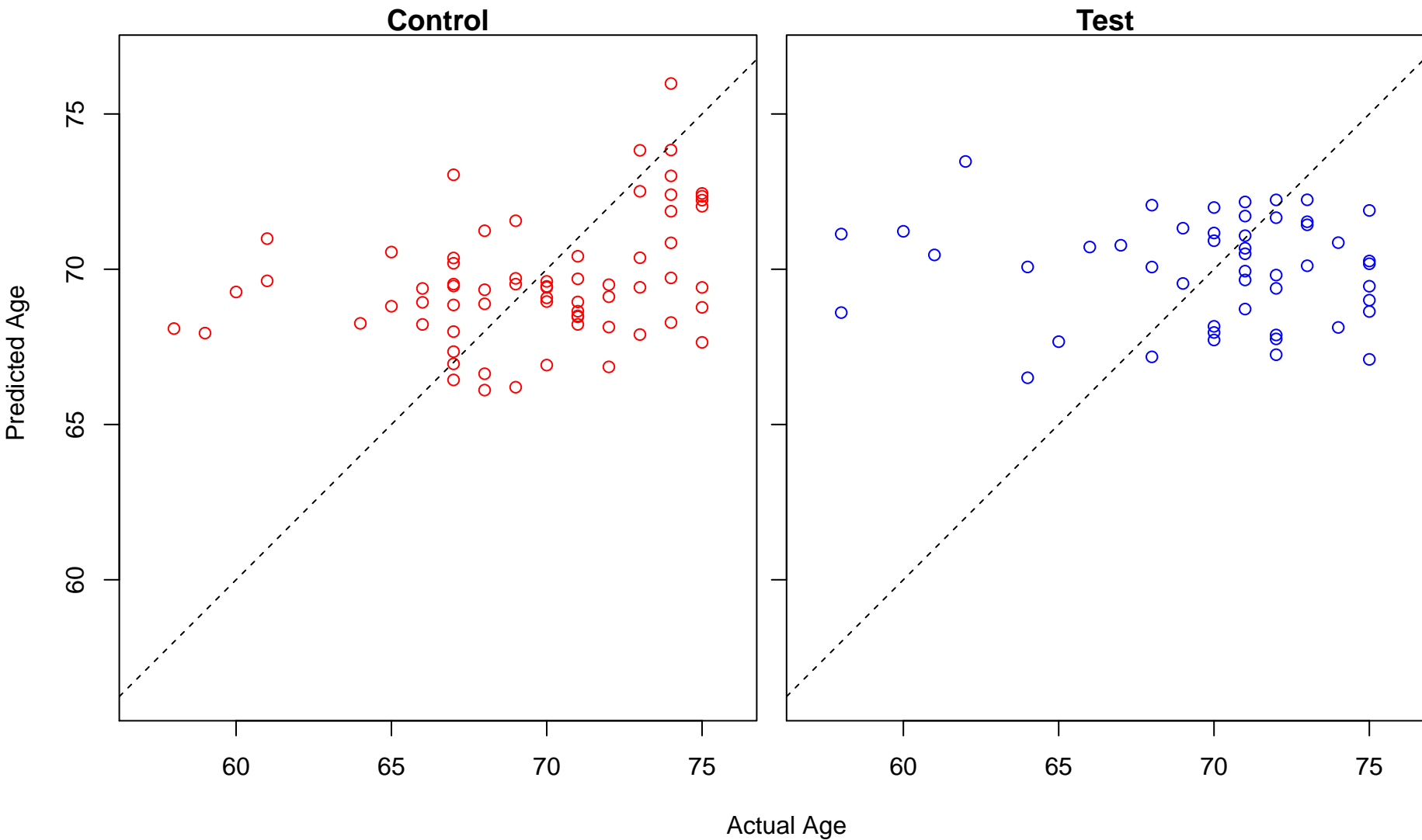
histone H3 deacetylation (Score: 0.392652)



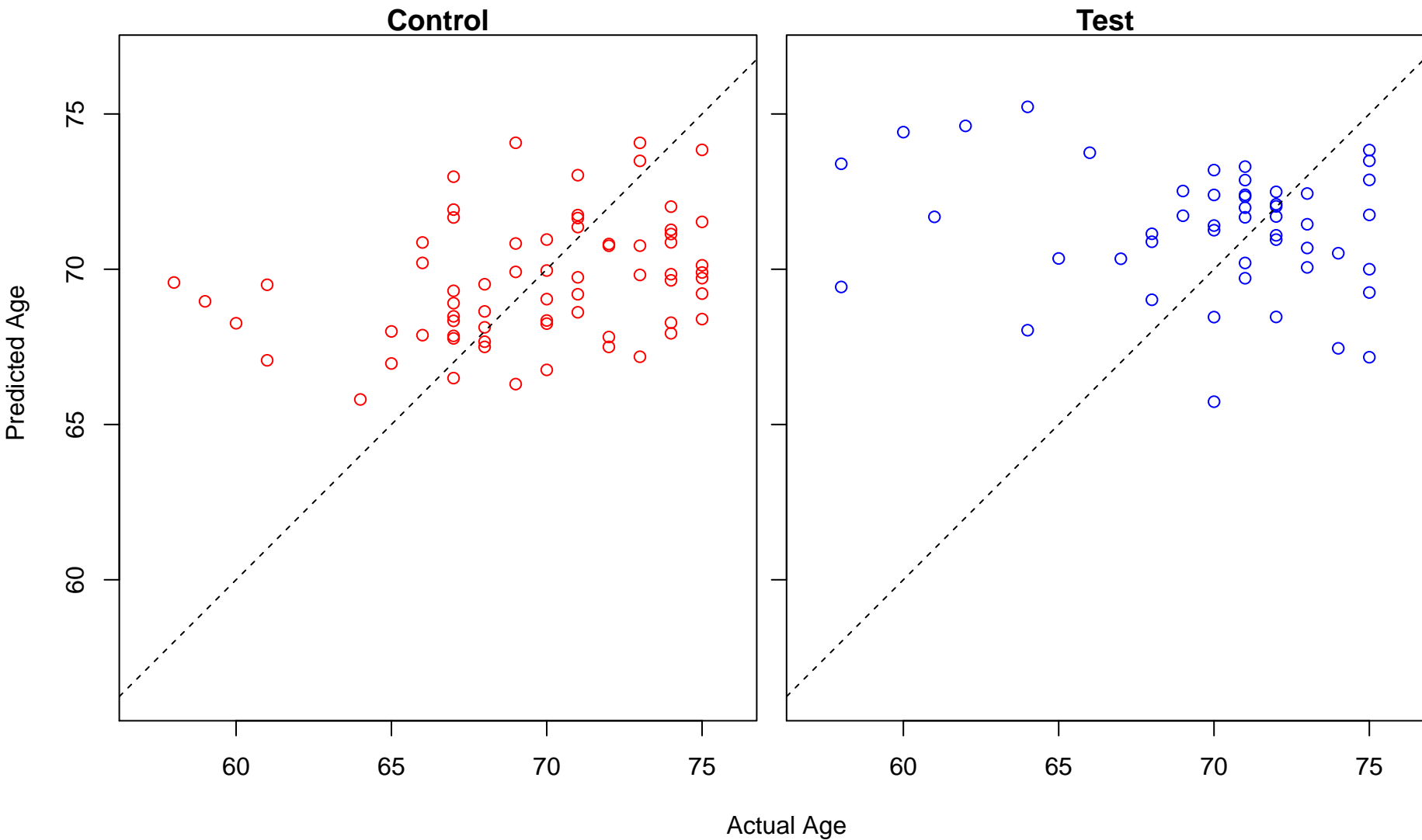
positive regulation of embryonic development (Score: 0.391679)



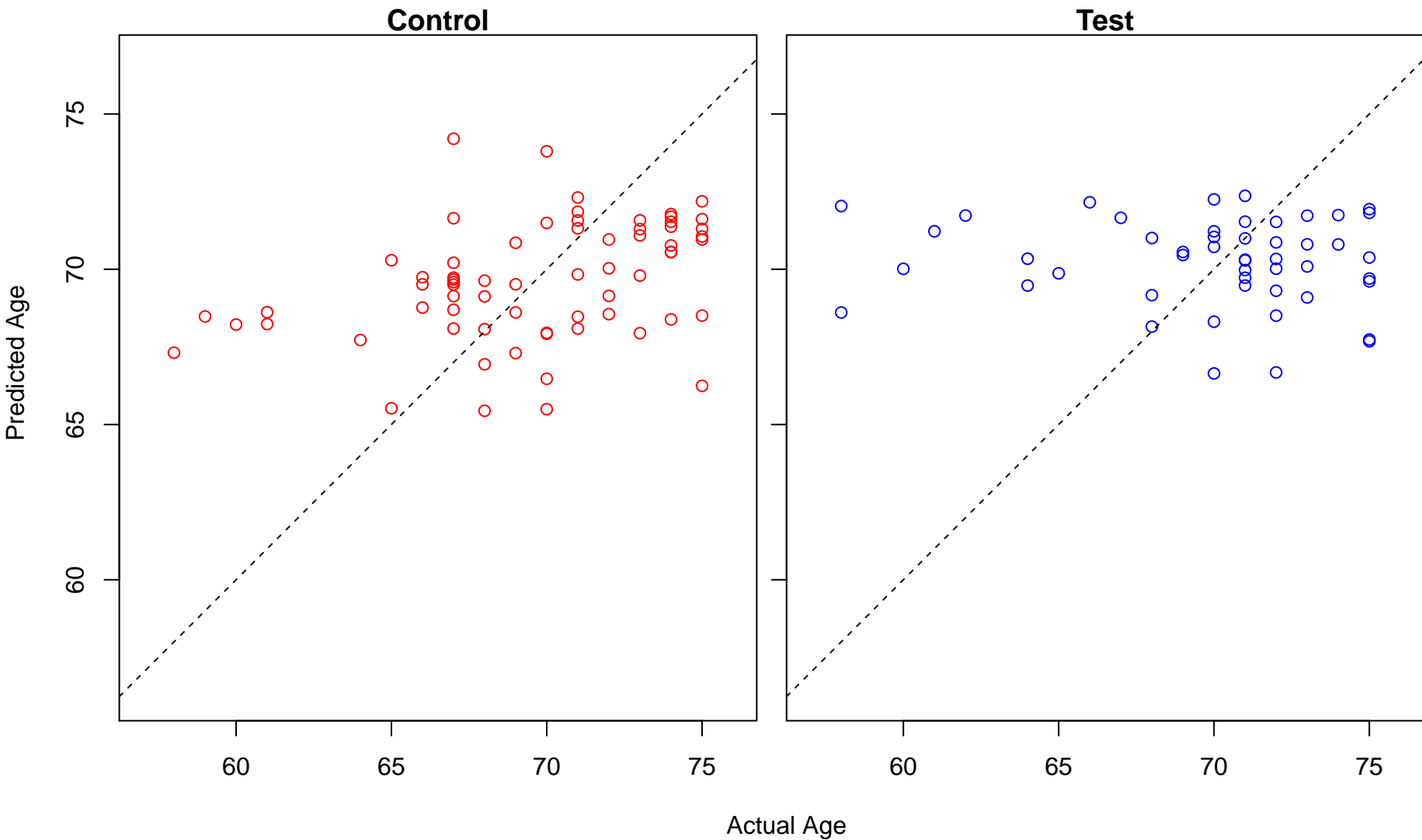
low-density lipoprotein particle remodeling (Score: 0.391620)



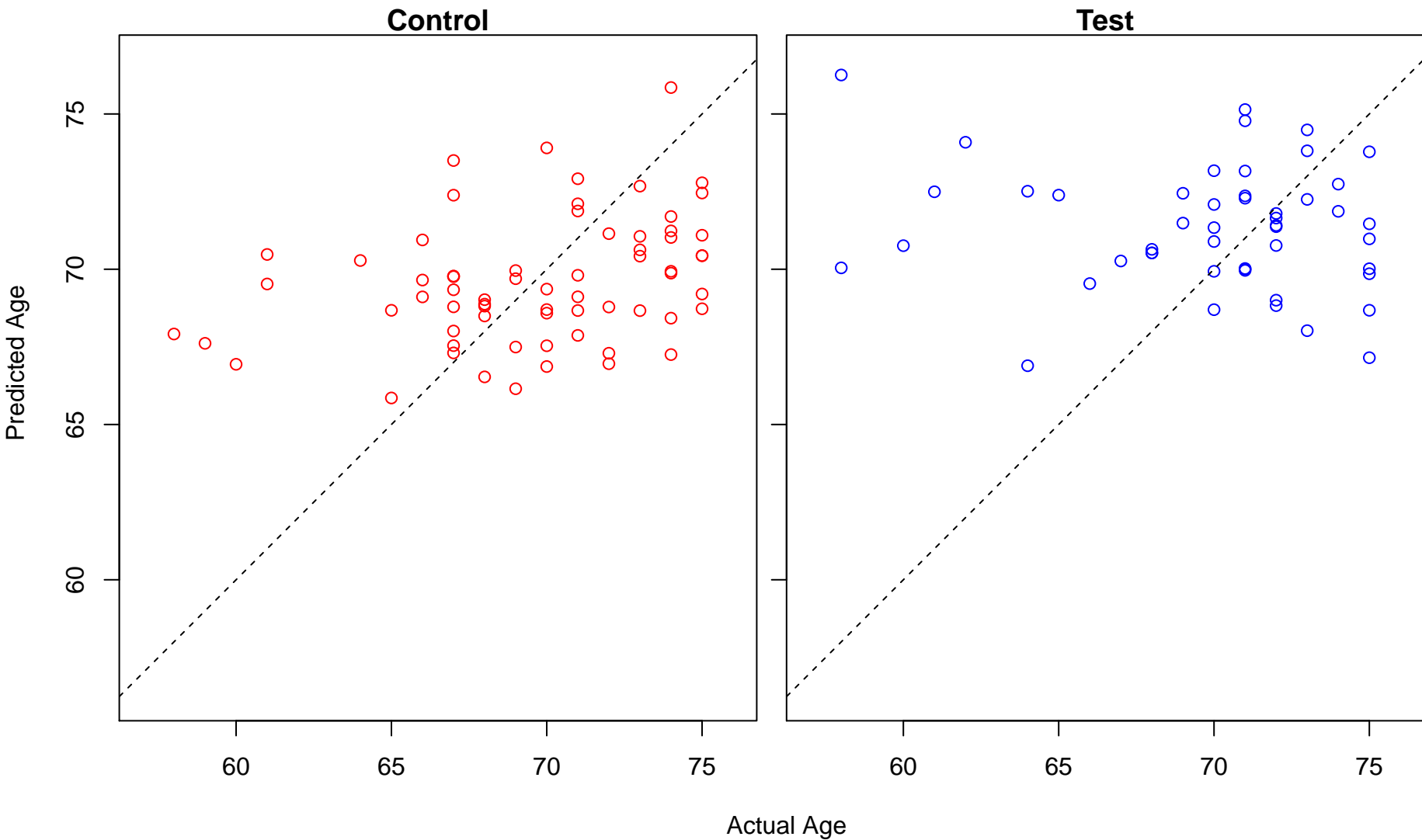
Wnt signaling pathway, planar cell polarity pathway (Score: 0.389180)



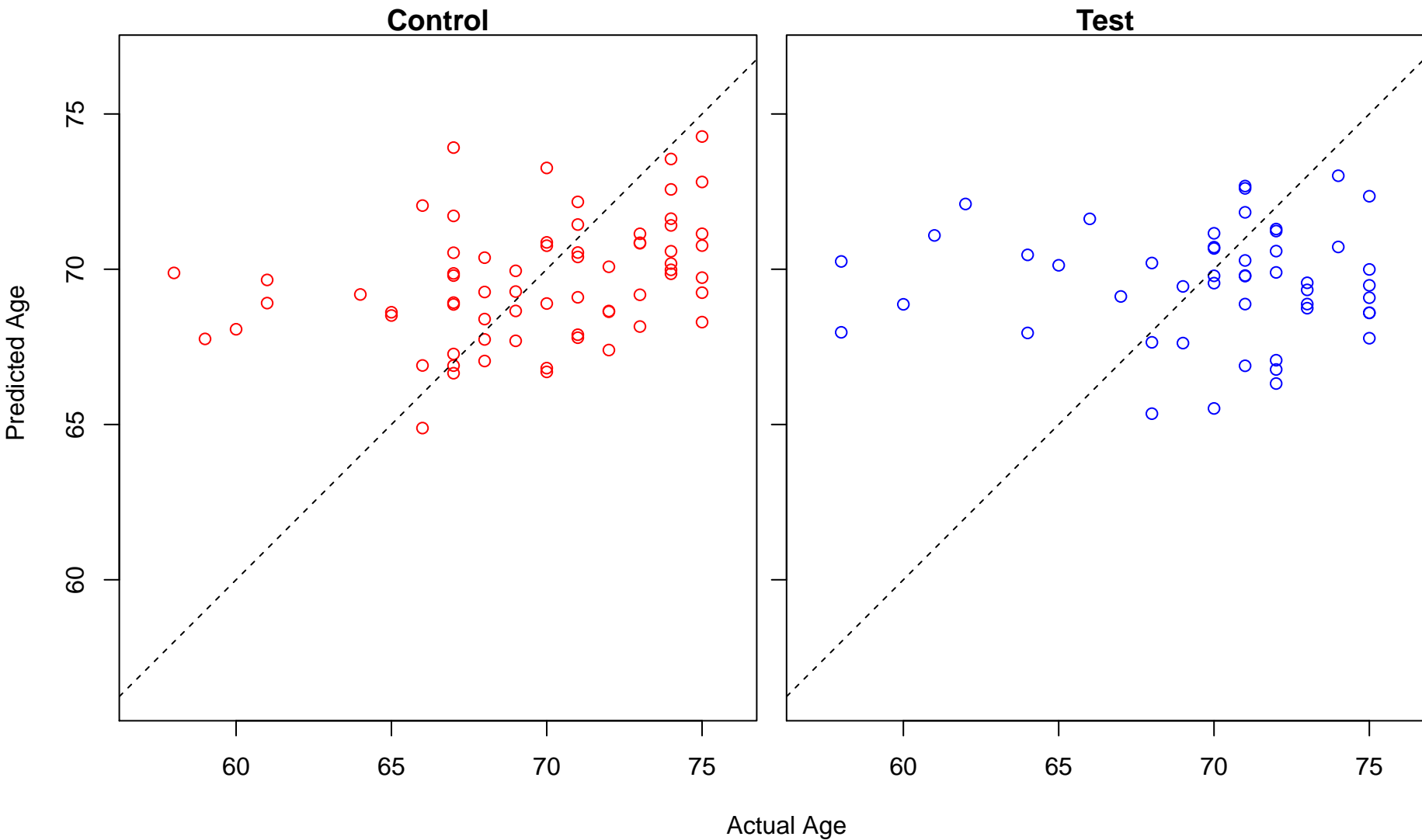
positive regulation of podosome assembly (Score: 0.388334)



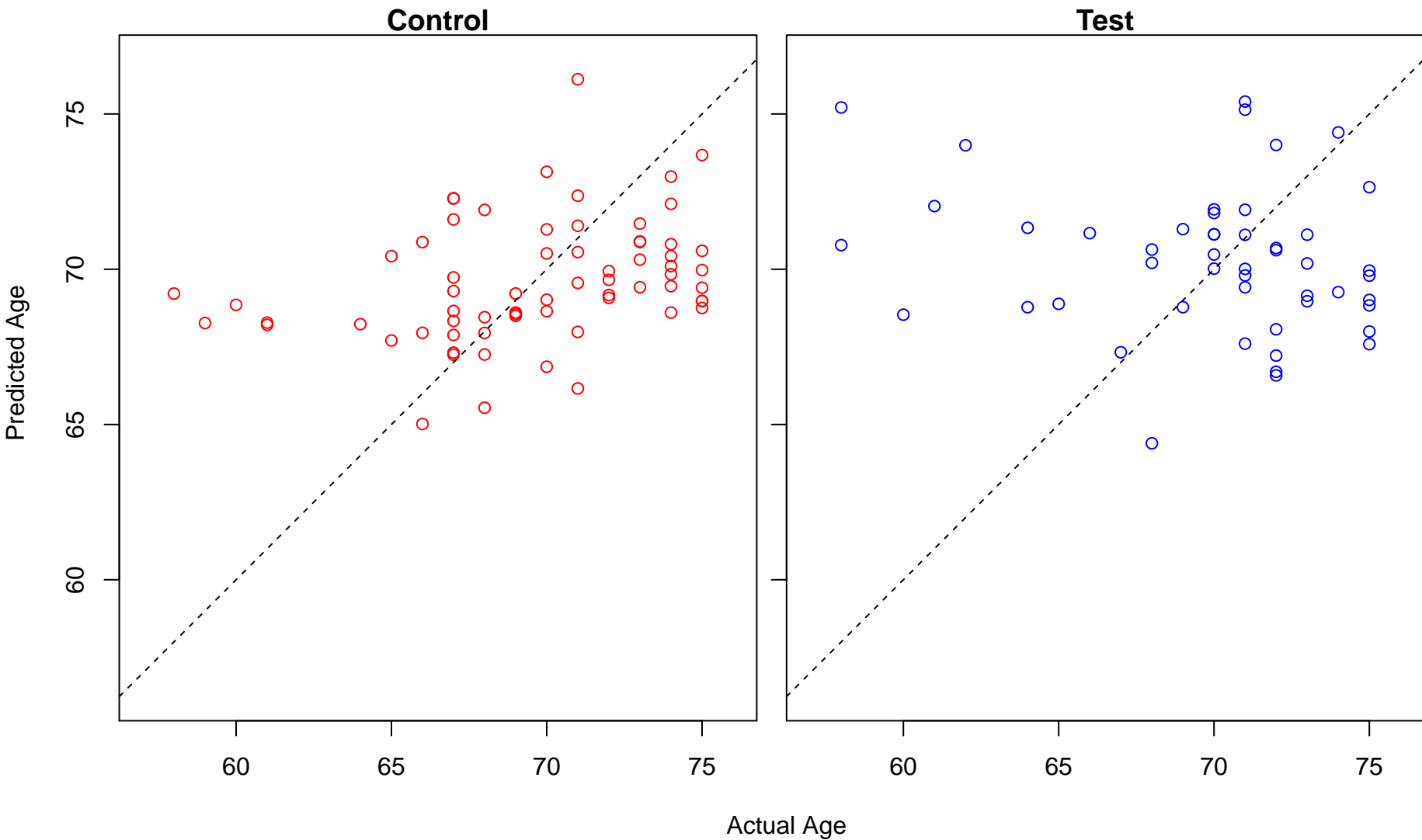
neuron maturation (Score: 0.387811)



regulation of macrophage chemotaxis (Score: 0.386254)

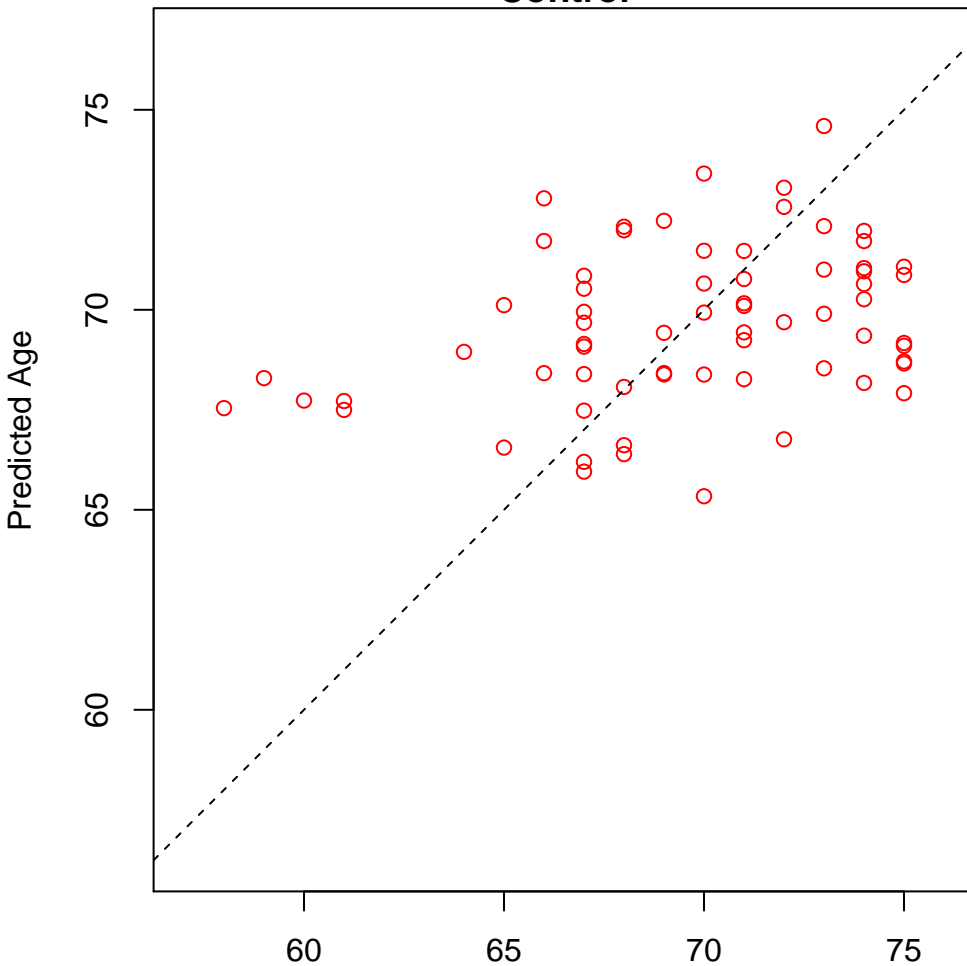


positive regulation of non-canoncal Wnt signaling pathway (Score: 0.386151)

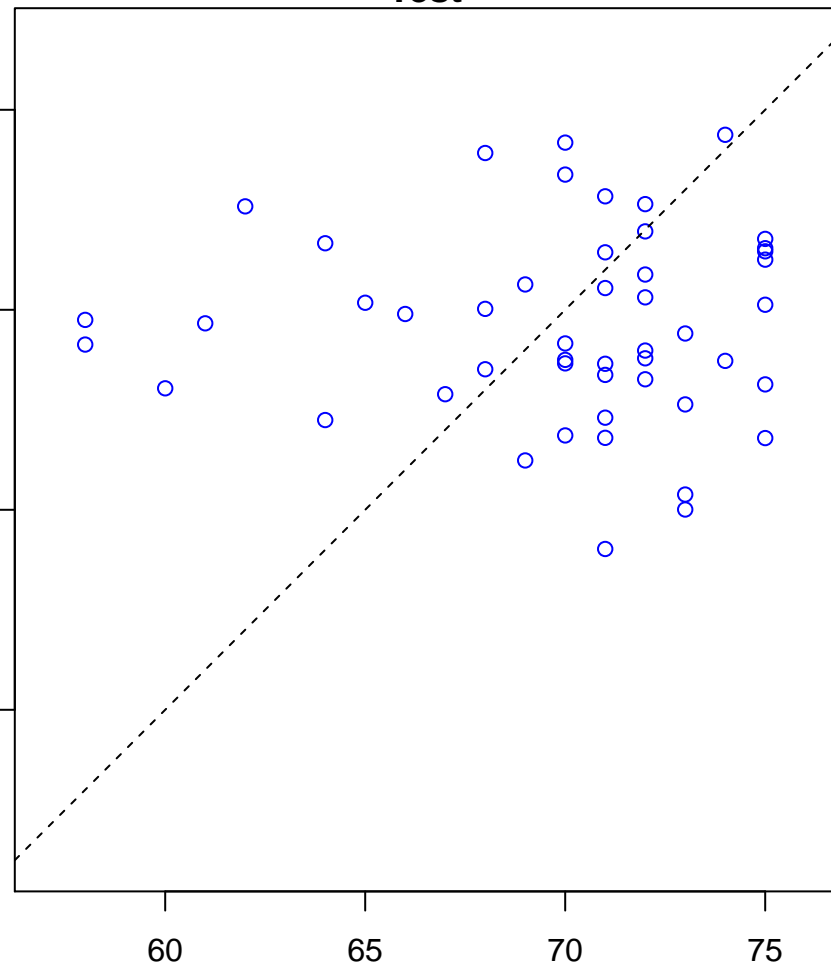


embryonic hindlimb morphogenesis (Score: 0.385516)

Control

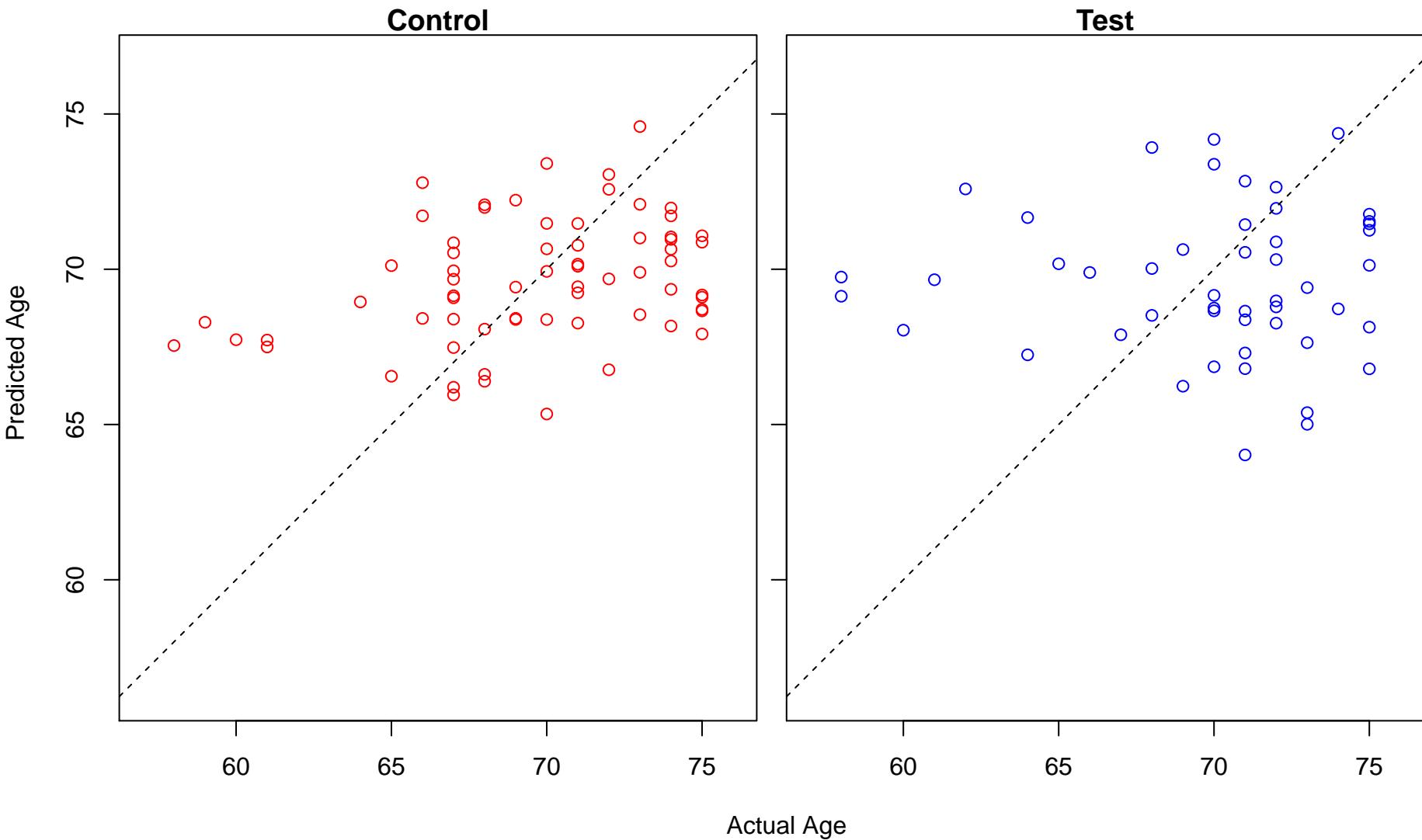


Test

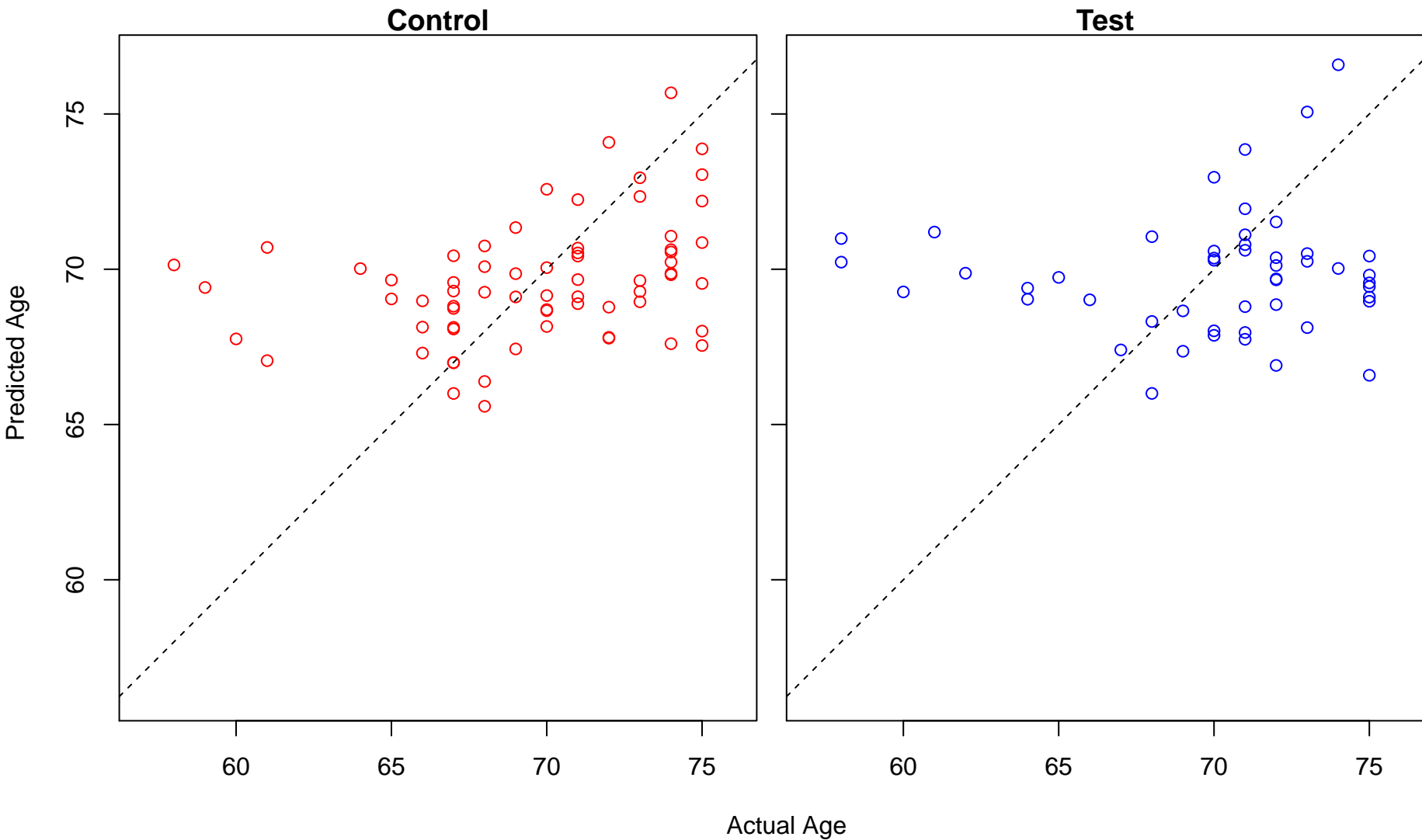


Actual Age

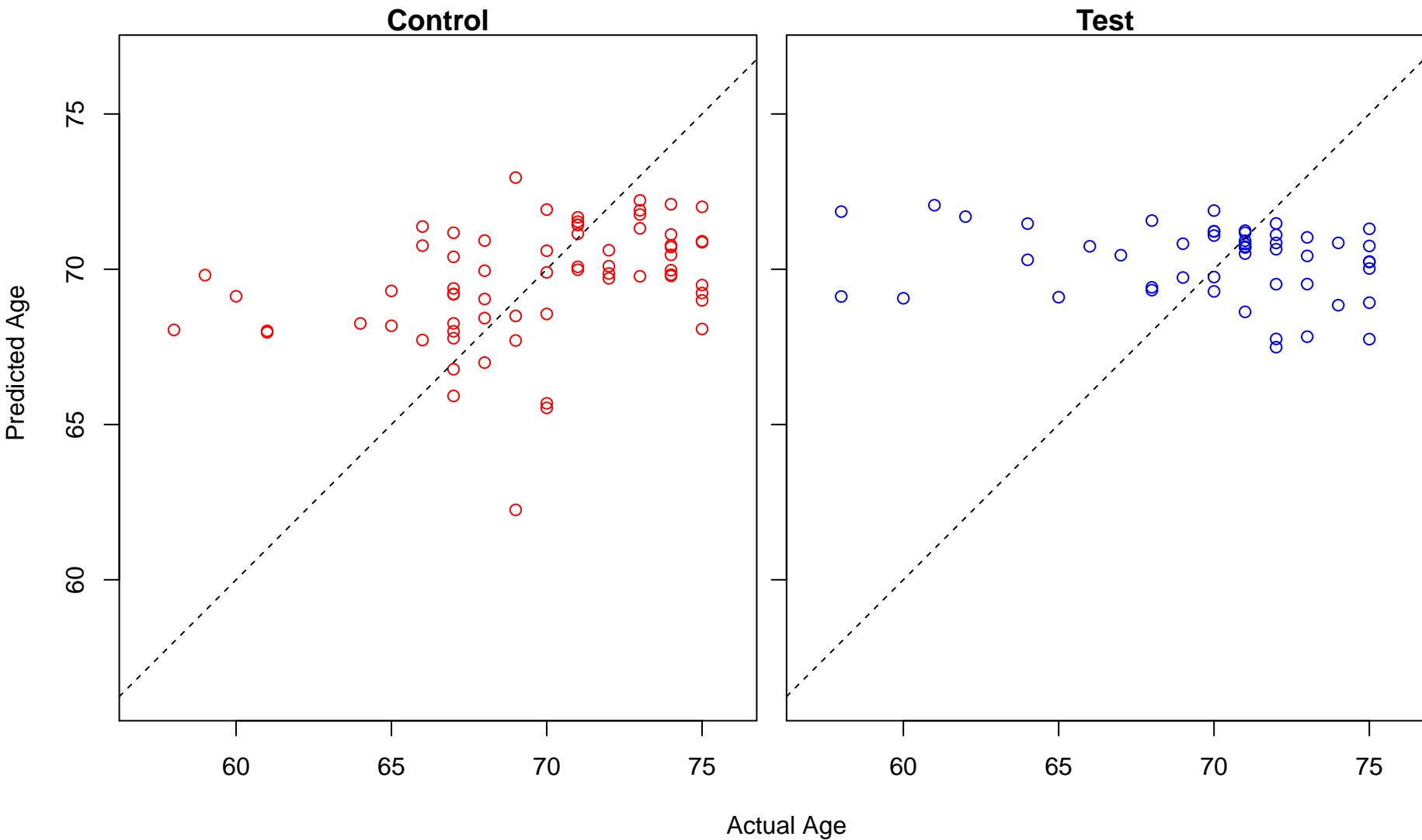
hindlimb morphogenesis (Score: 0.385516)



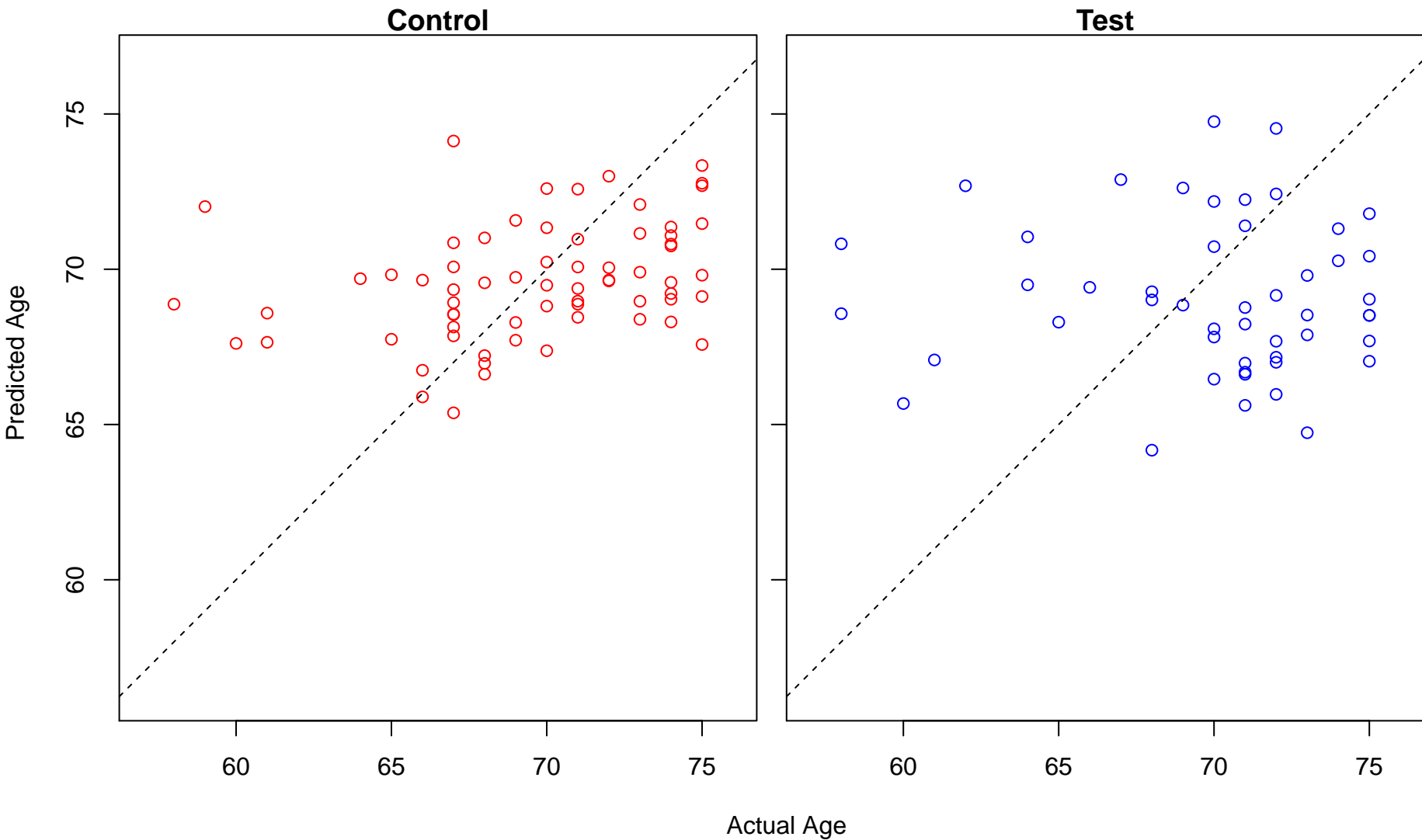
mRNA 3'-end processing by stem-loop binding and cleavage (Score: 0.384526)



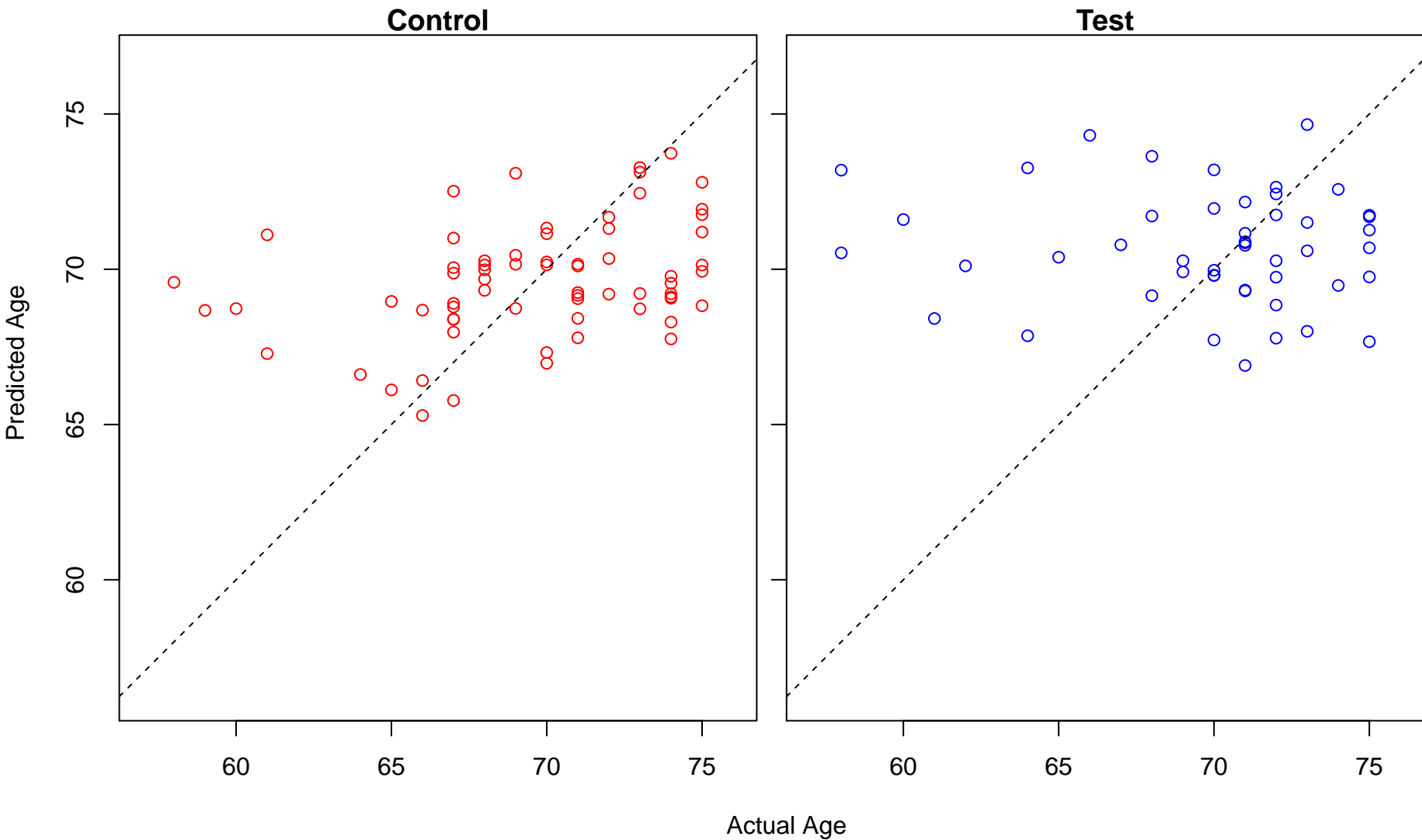
positive regulation of endothelial cell apoptotic process (Score: 0.383648)



regulation of oocyte development (Score: 0.382877)

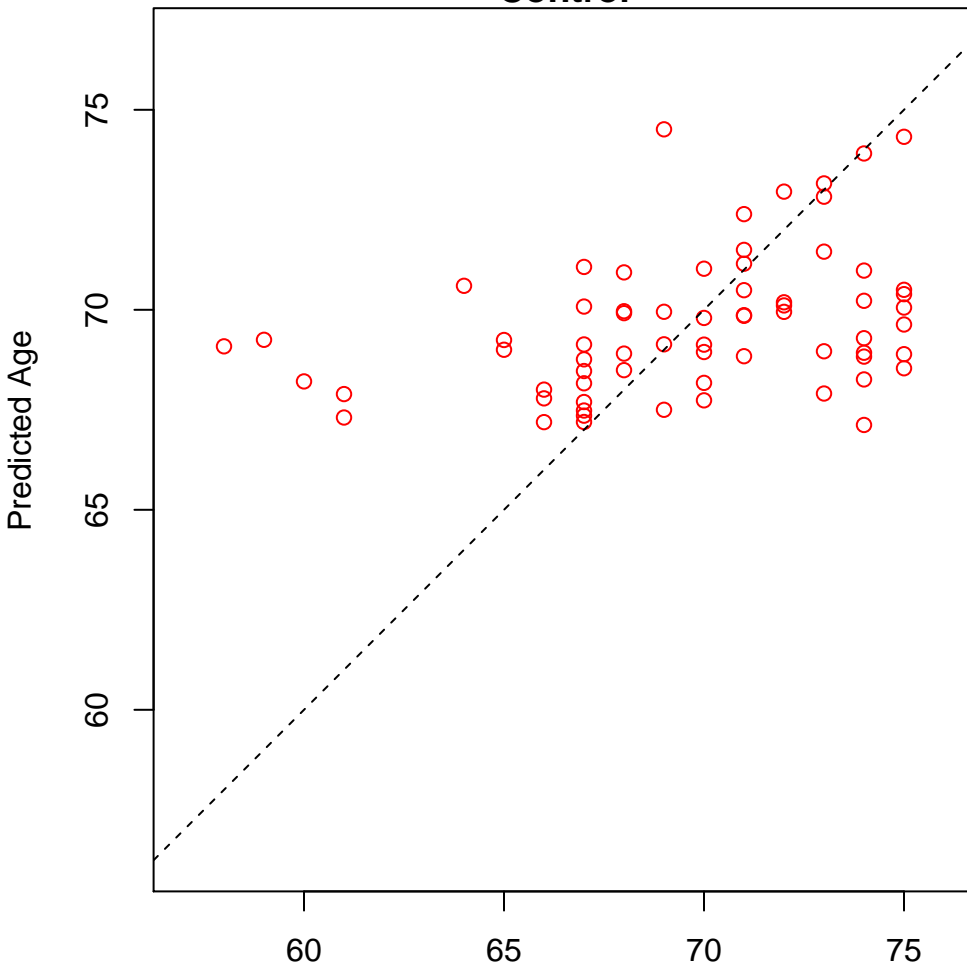


growth hormone secretion (Score: 0.382607)

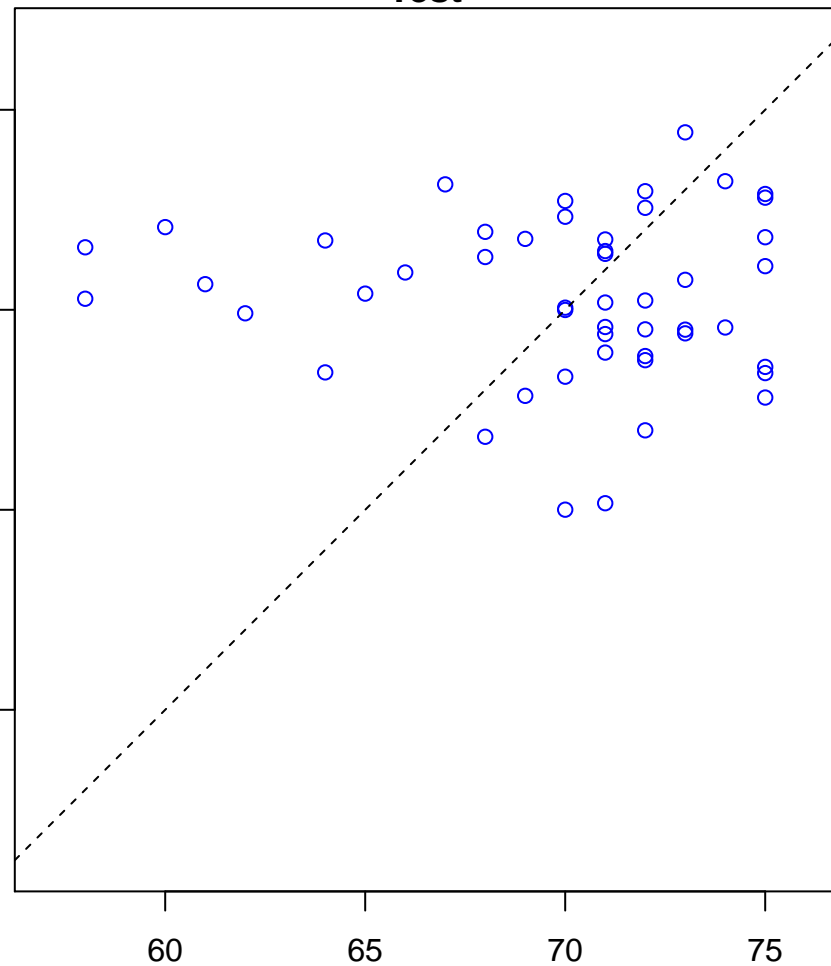


protein side chain deglutamylation (Score: 0.382296)

Control

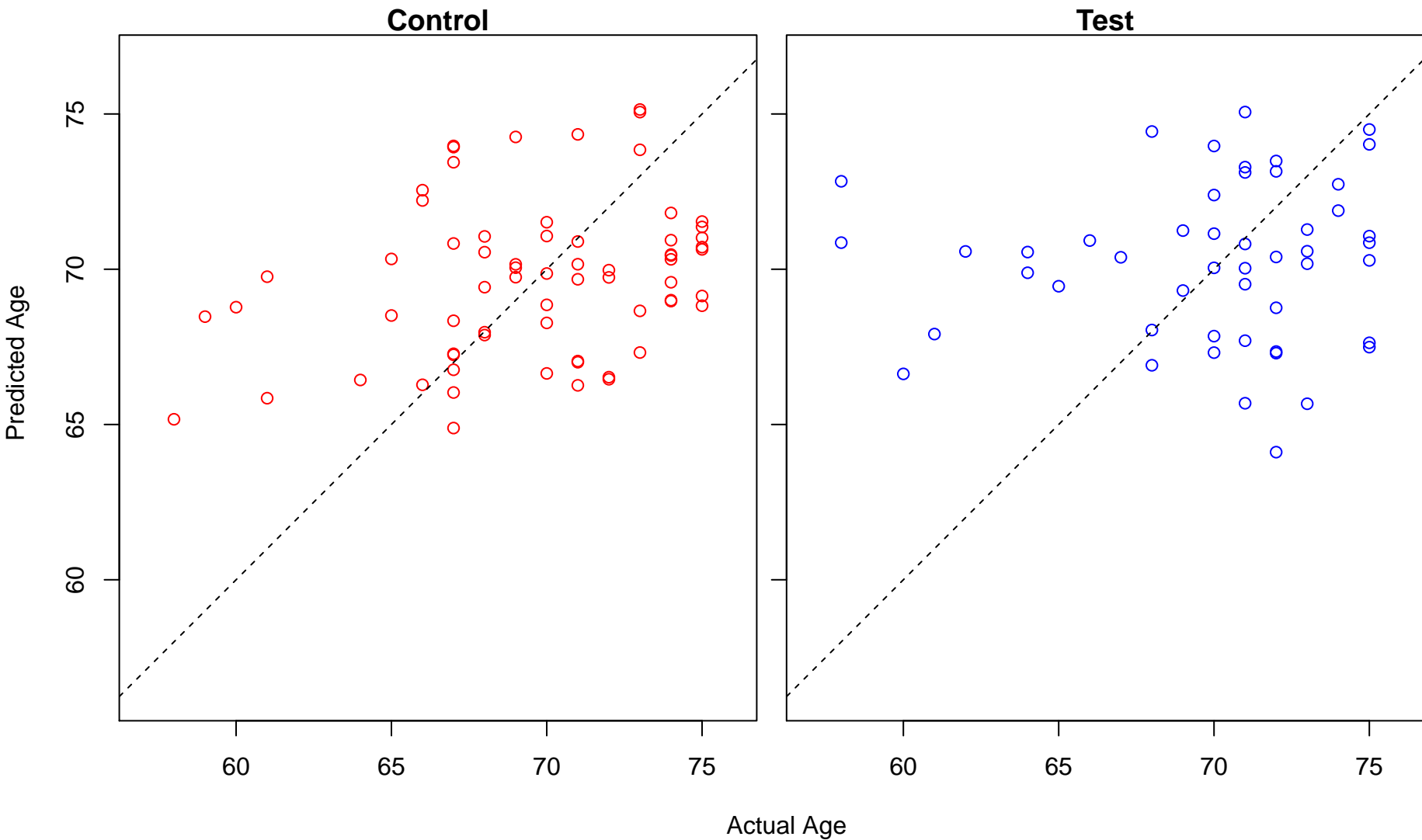


Test

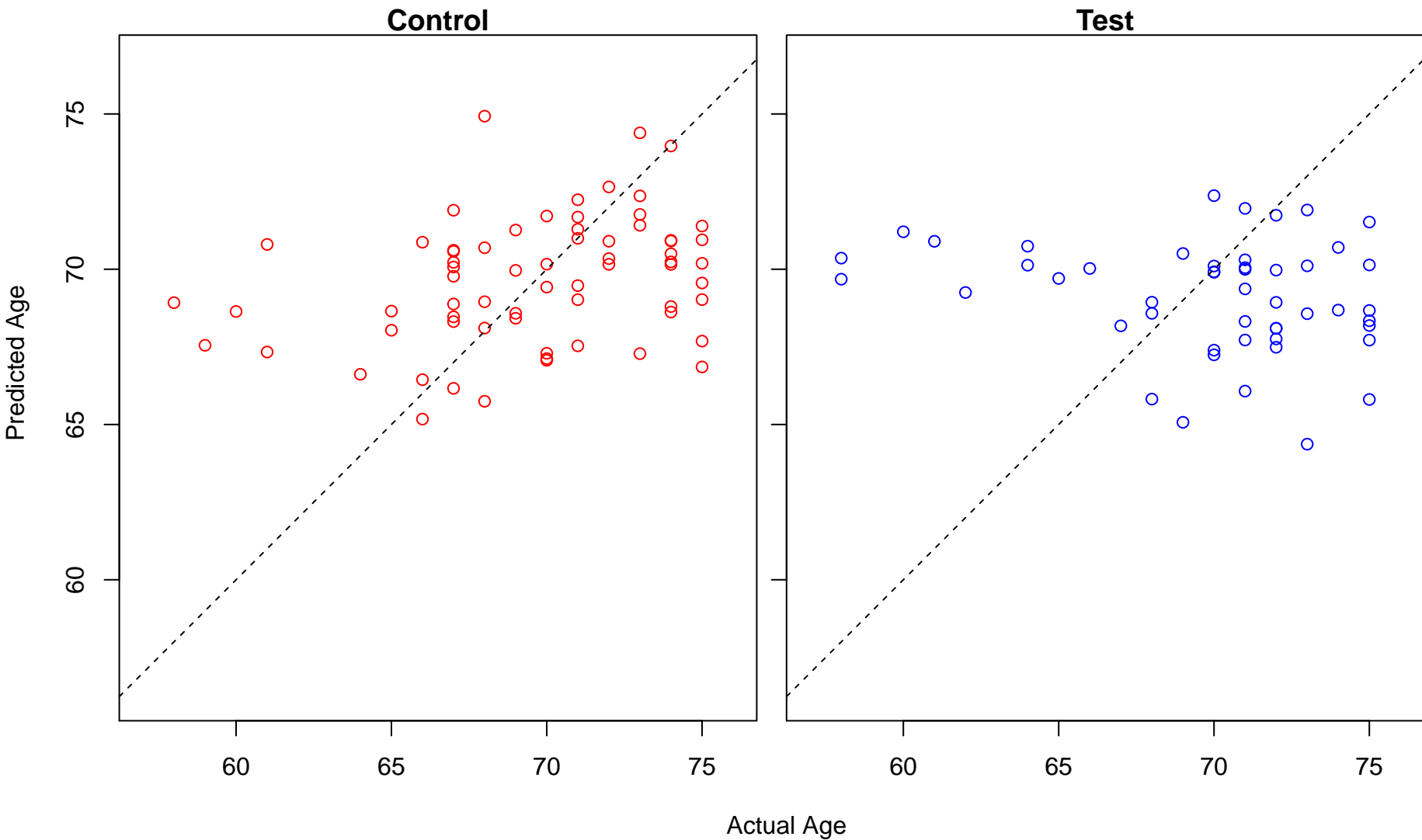


Actual Age

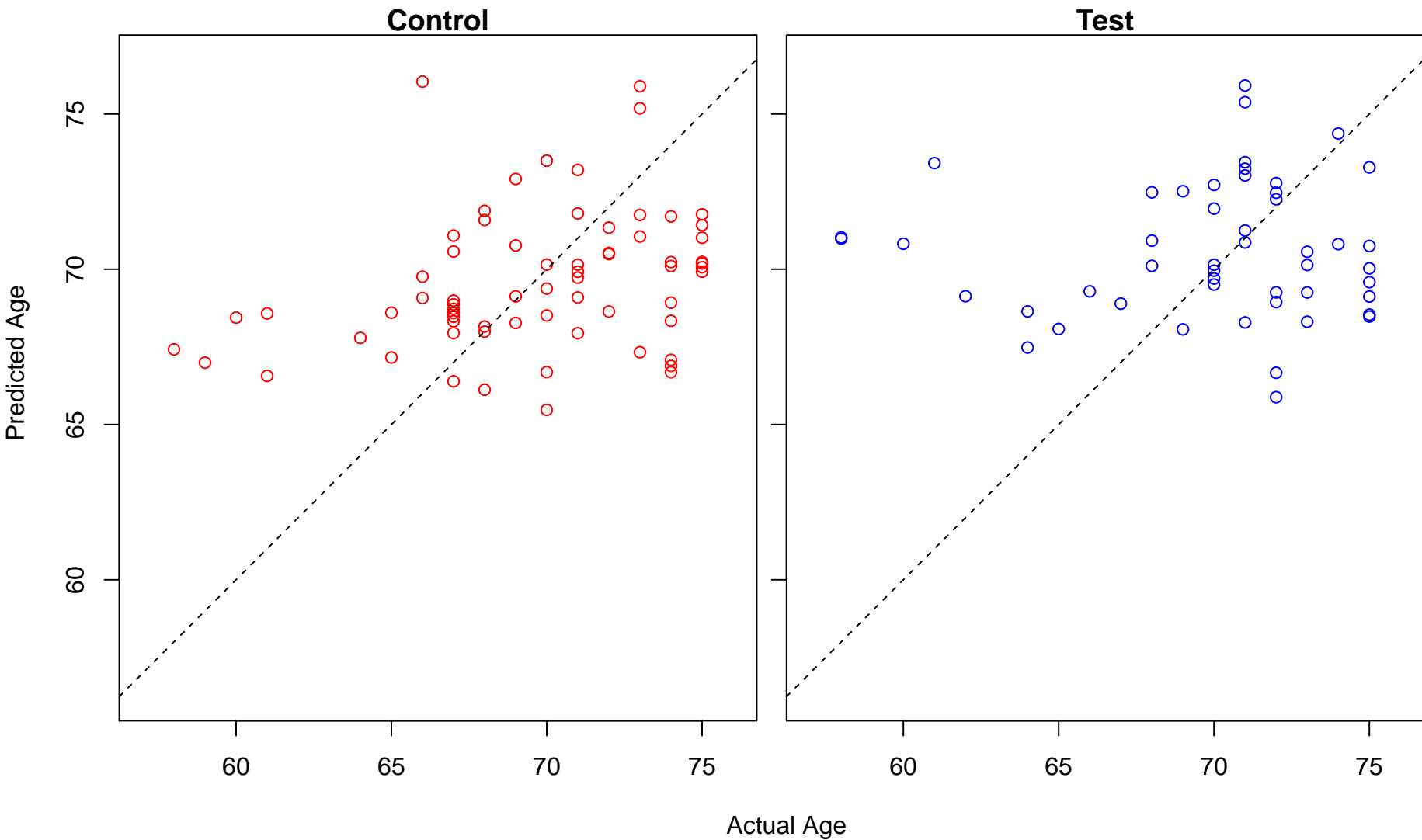
plasminogen activation (Score: 0.382117)



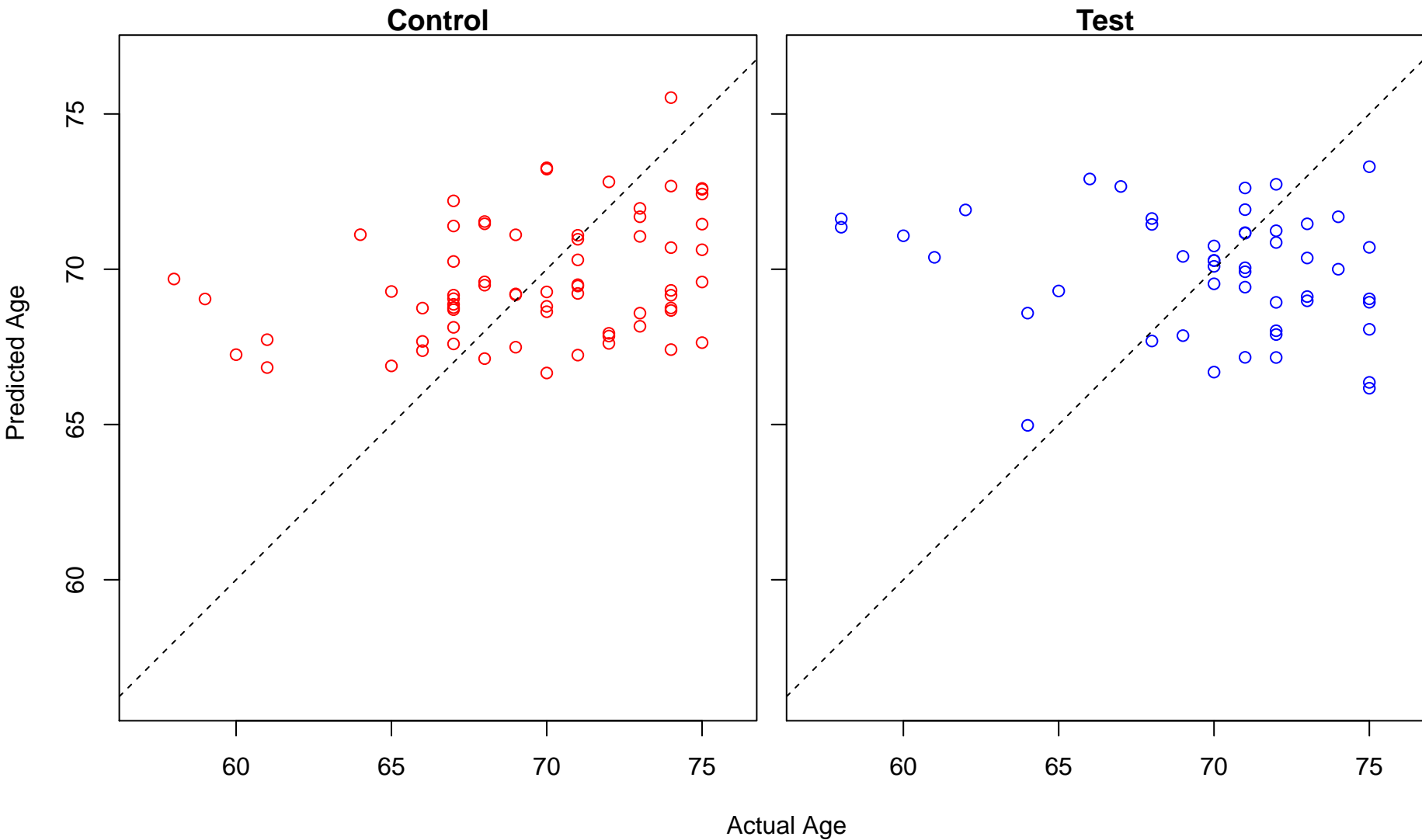
ventral spinal cord development (Score: 0.381038)



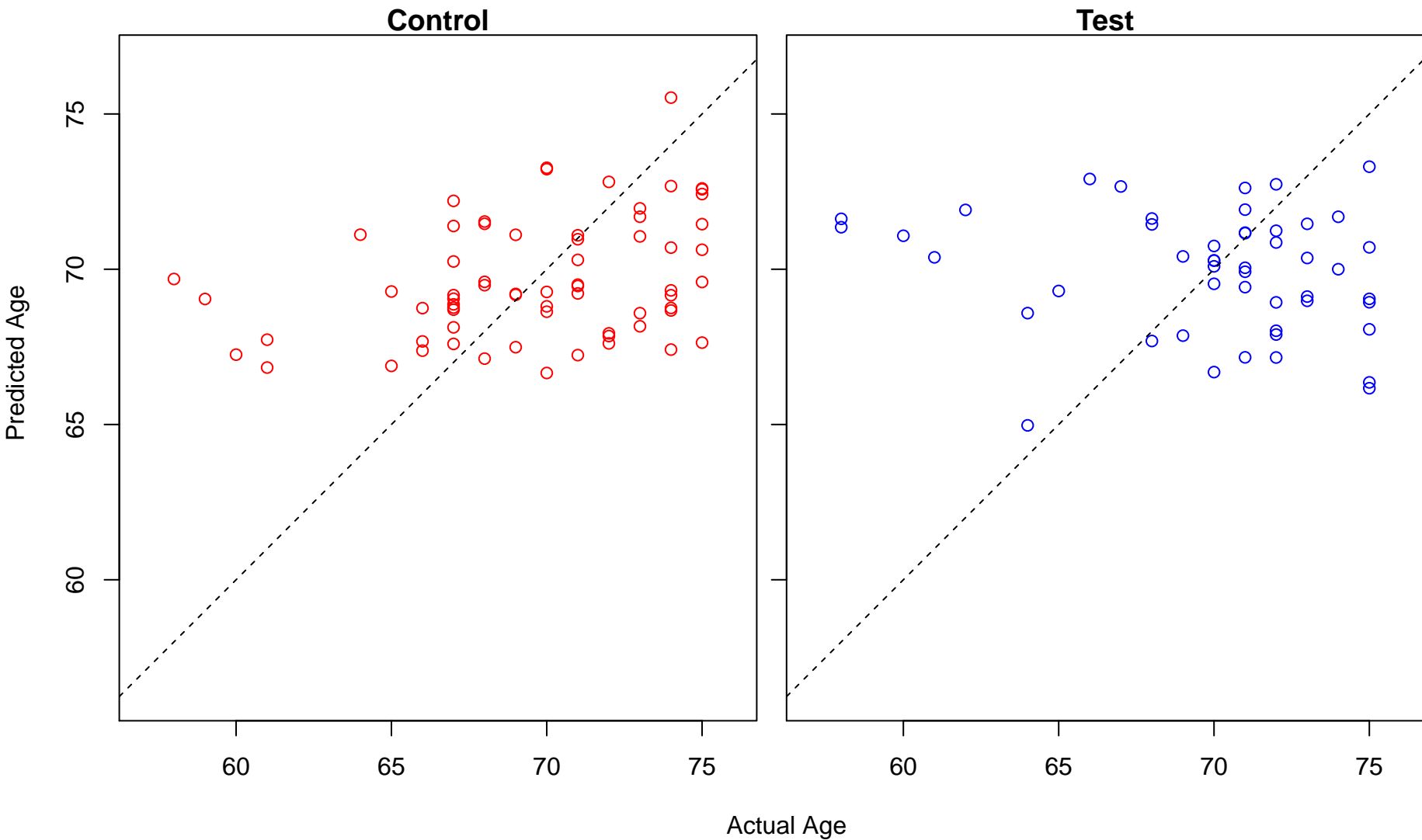
regulation of respiratory gaseous exchange (Score: 0.380011)



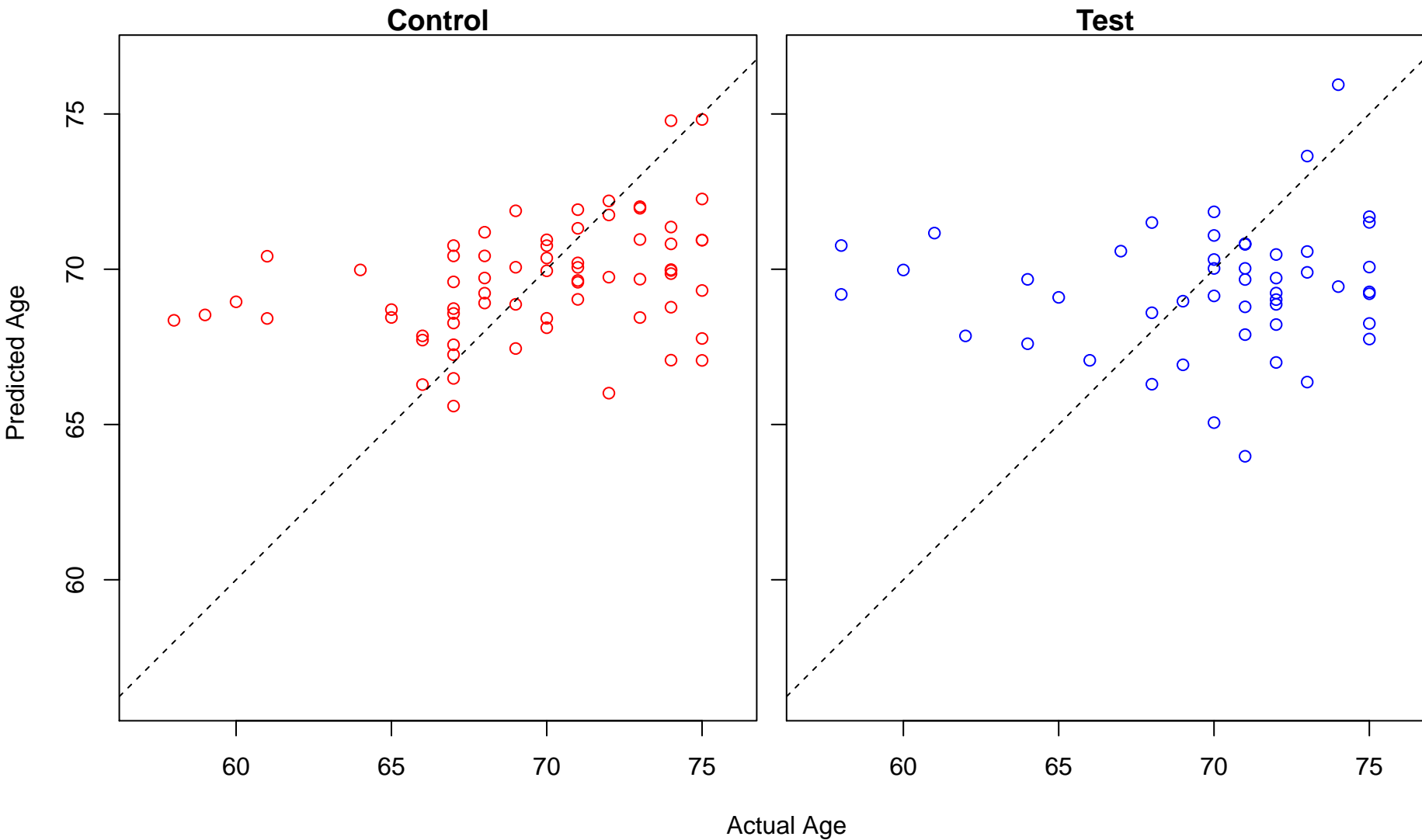
corticosteroid receptor signaling pathway (Score: 0.379822)



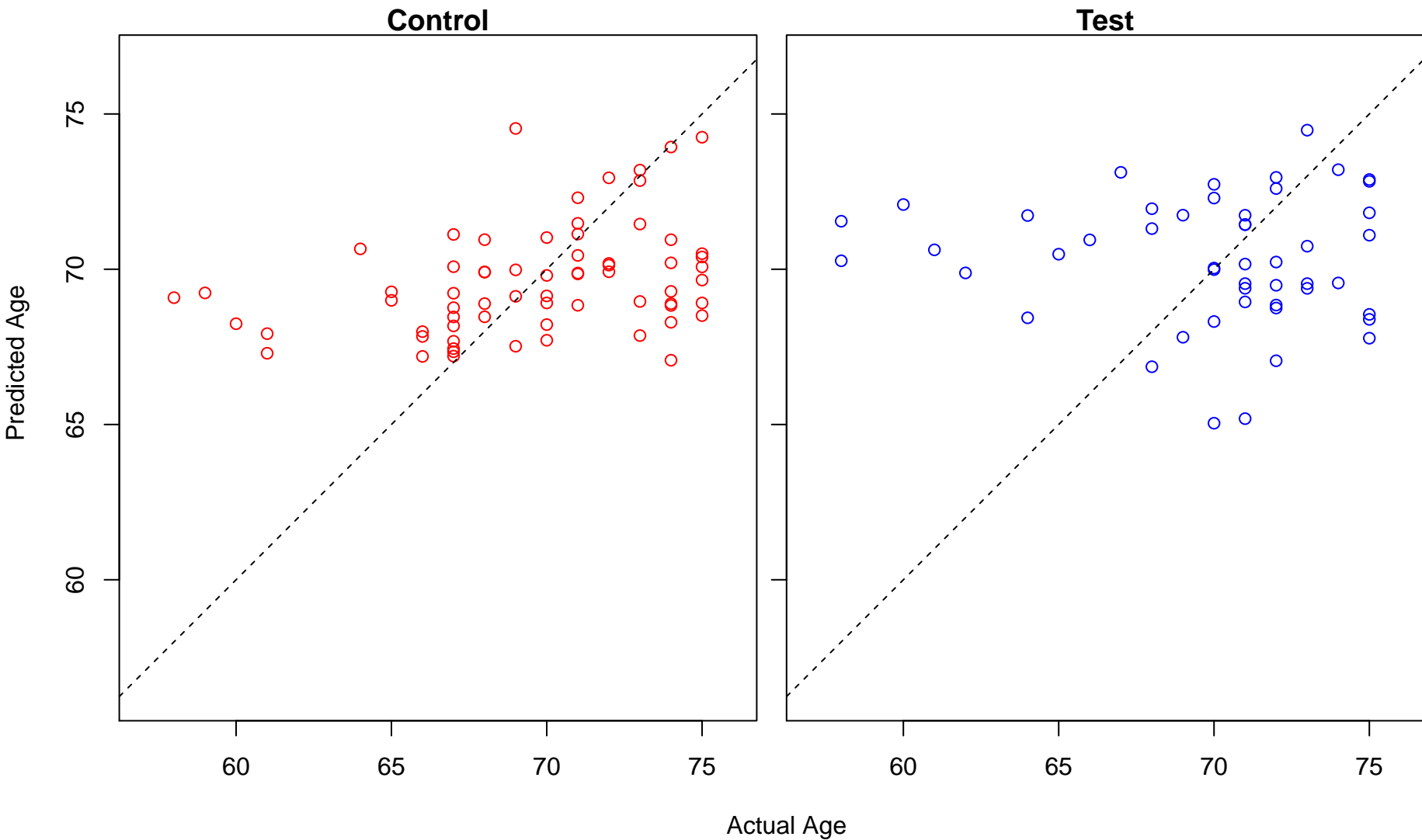
glucocorticoid receptor signaling pathway (Score: 0.379822)



receptor catabolic process (Score: 0.379155)

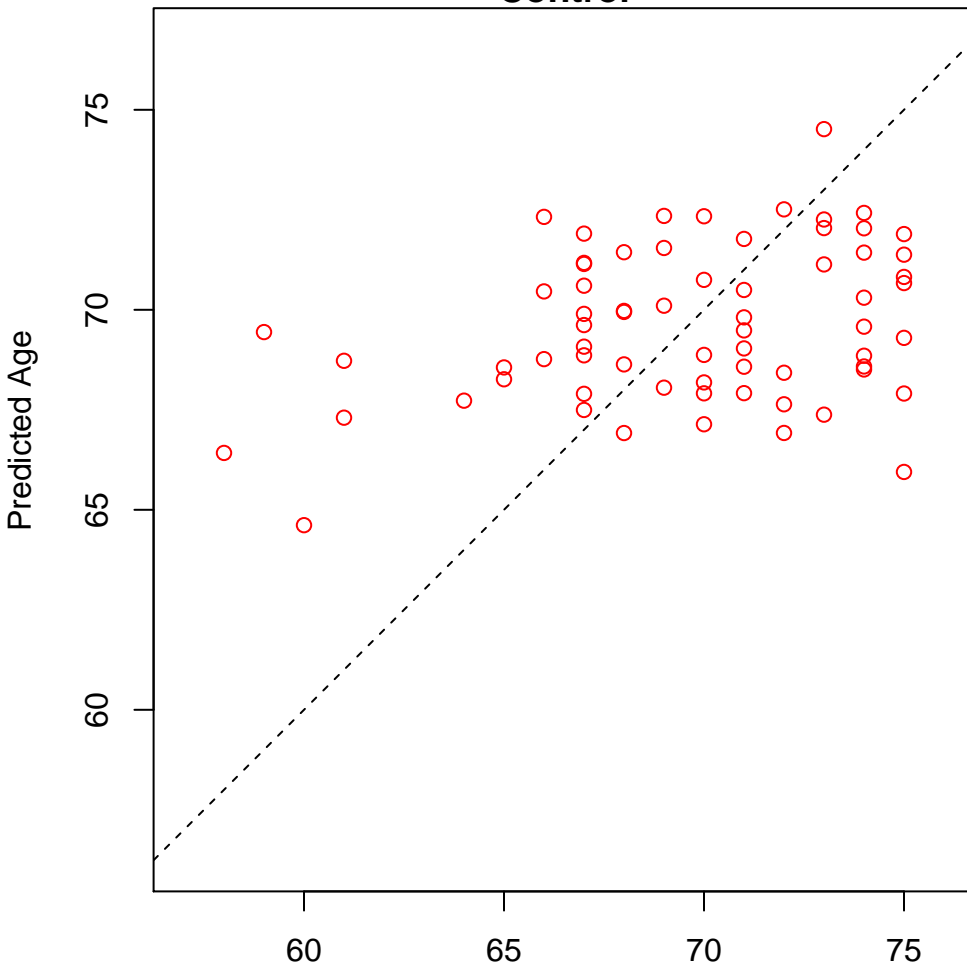


C-terminal protein deglutamylation (Score: 0.377768)

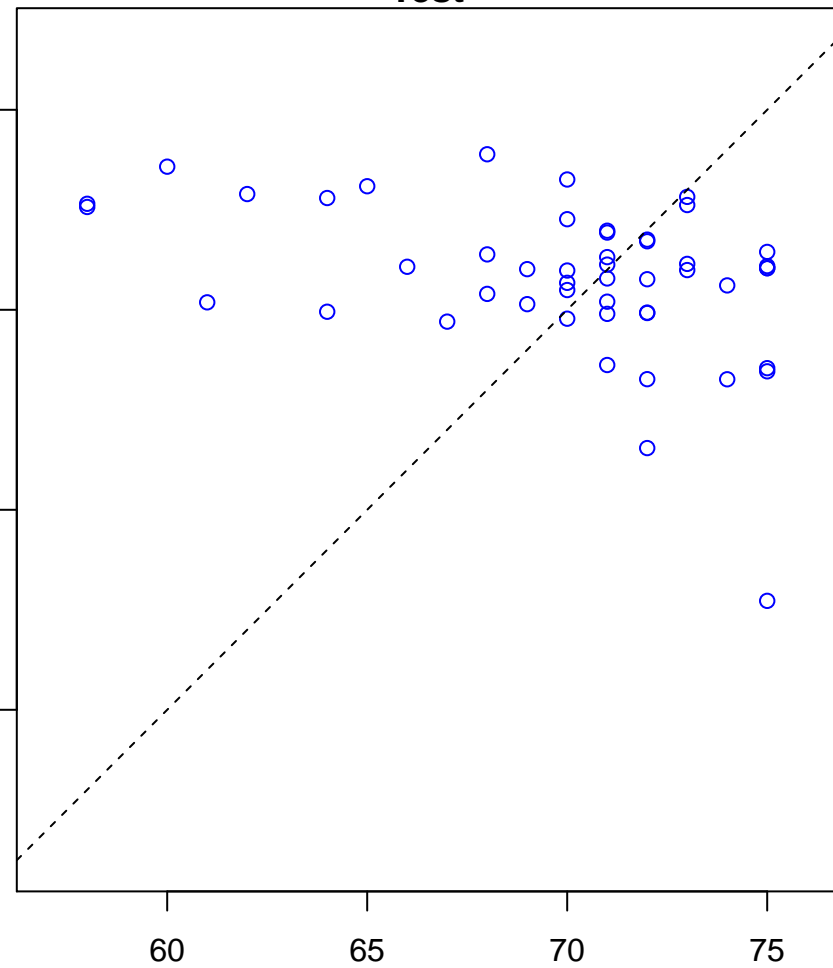


low-density lipoprotein particle clearance (Score: 0.377550)

Control

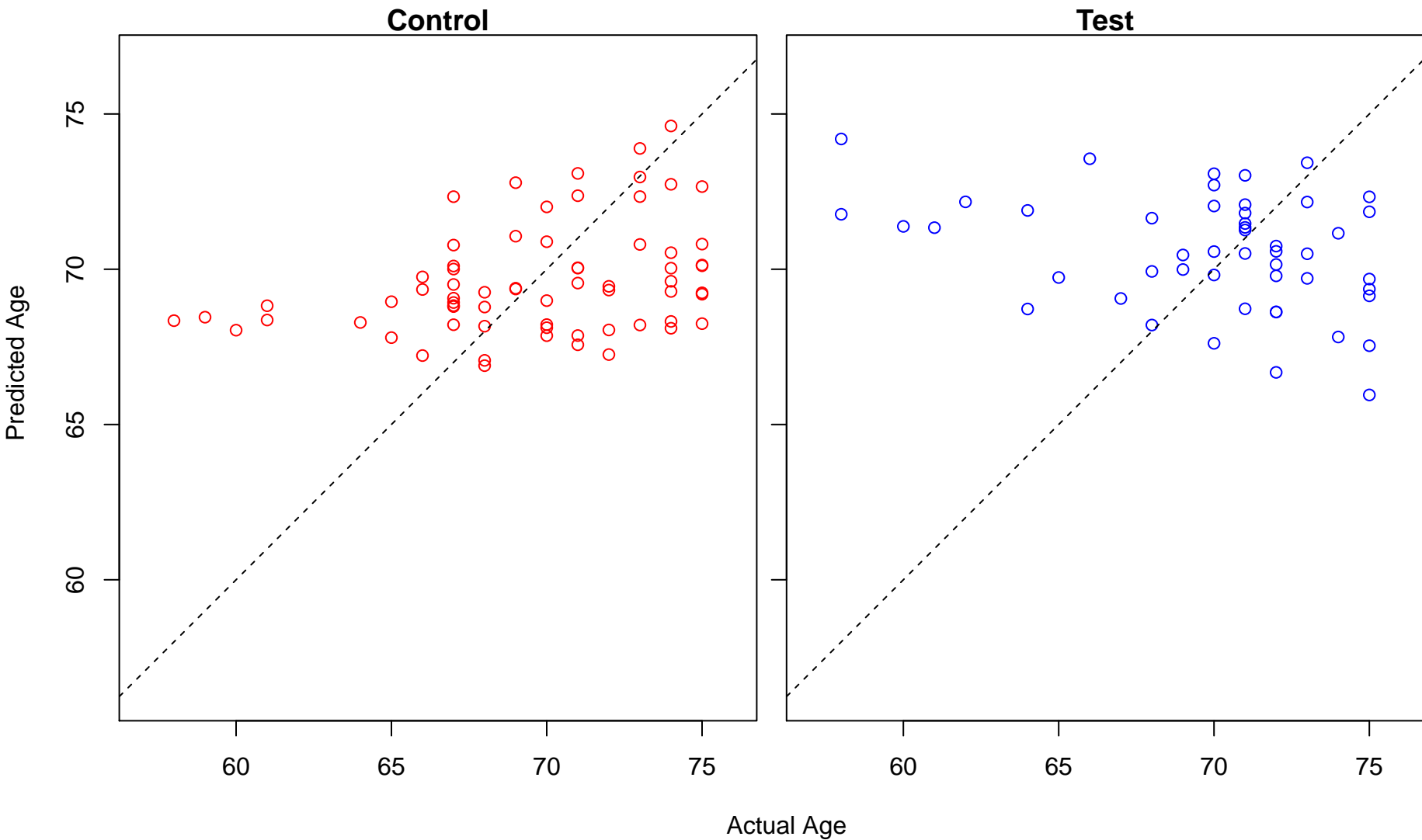


Test



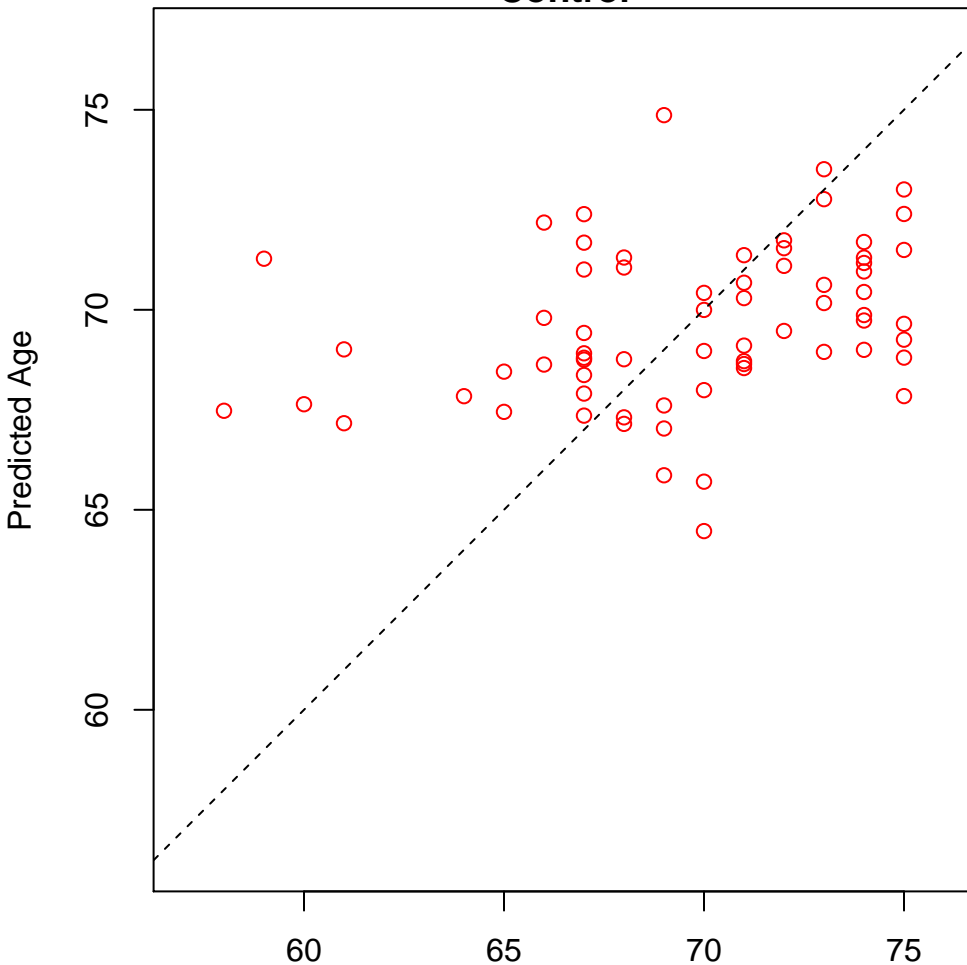
Actual Age

establishment or maintenance of epithelial cell apical/basal polarity (Score: 0.377078)

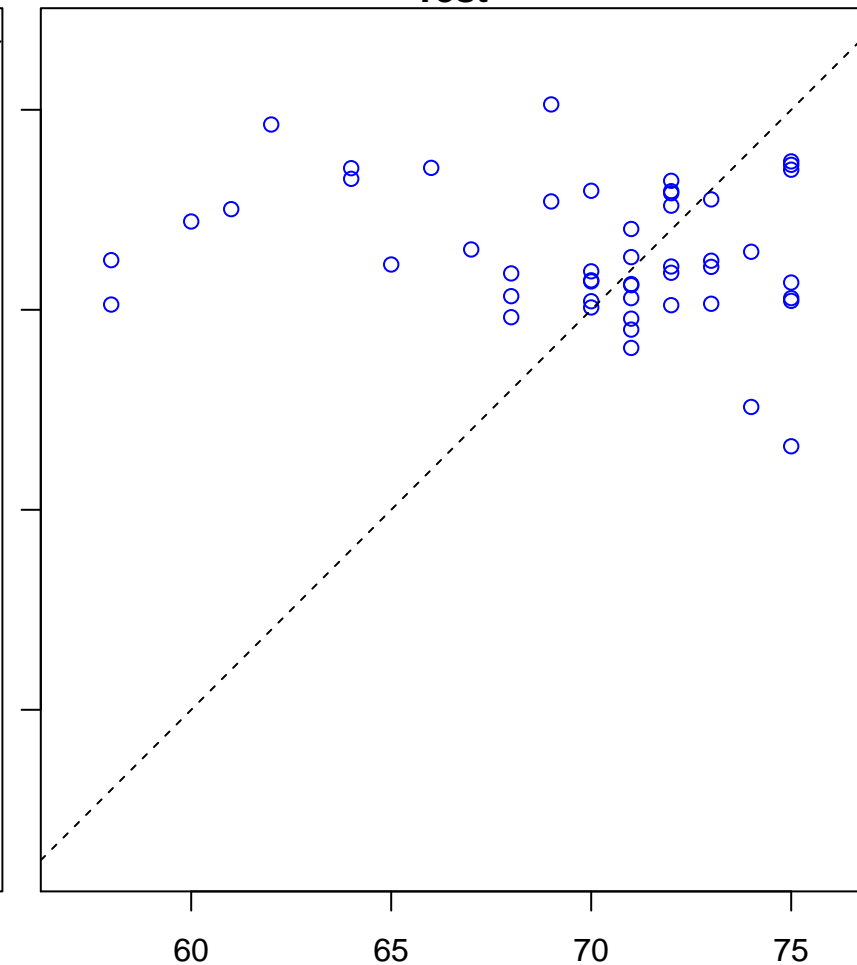


angiogenesis involved in wound healing (Score: 0.376049)

Control

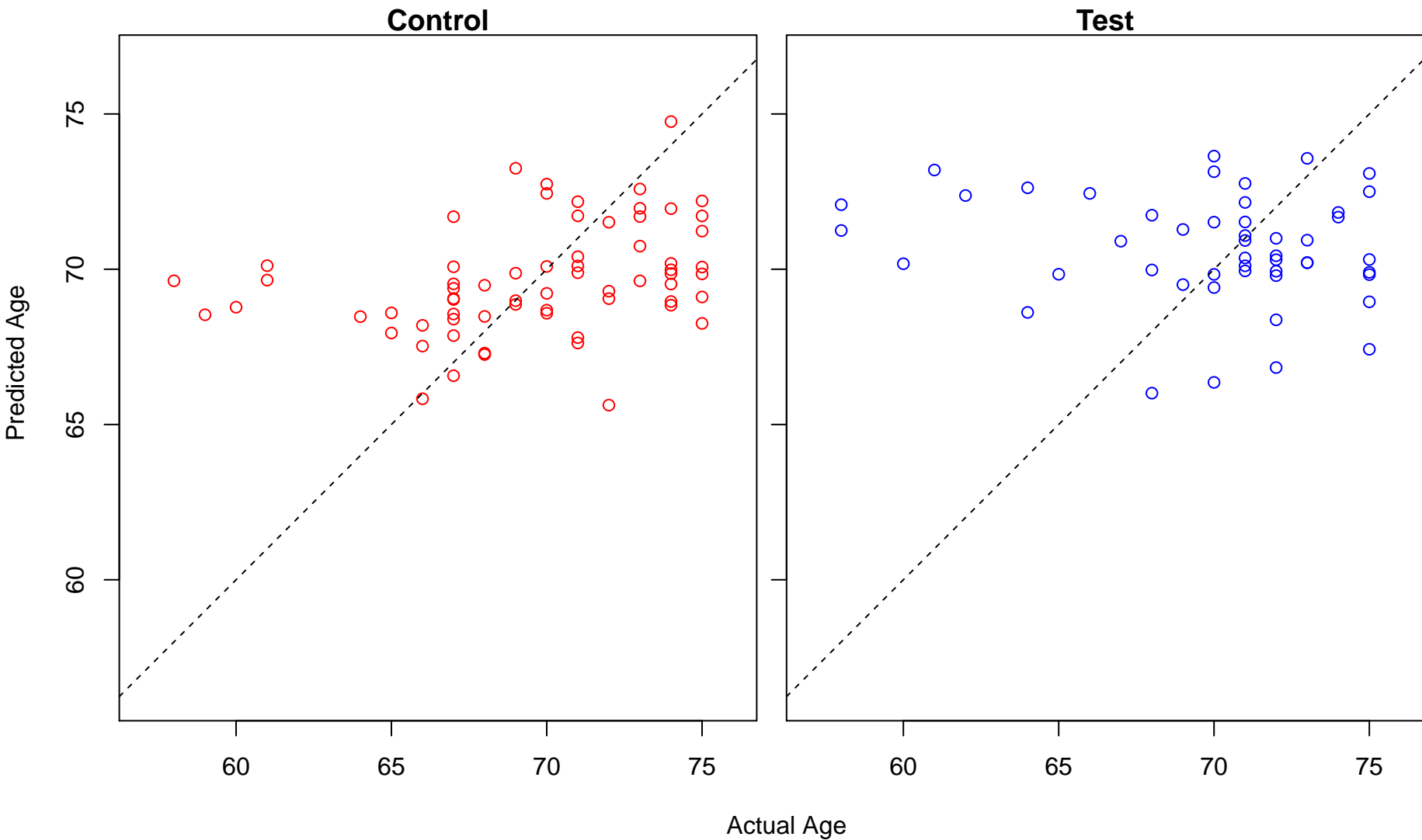


Test

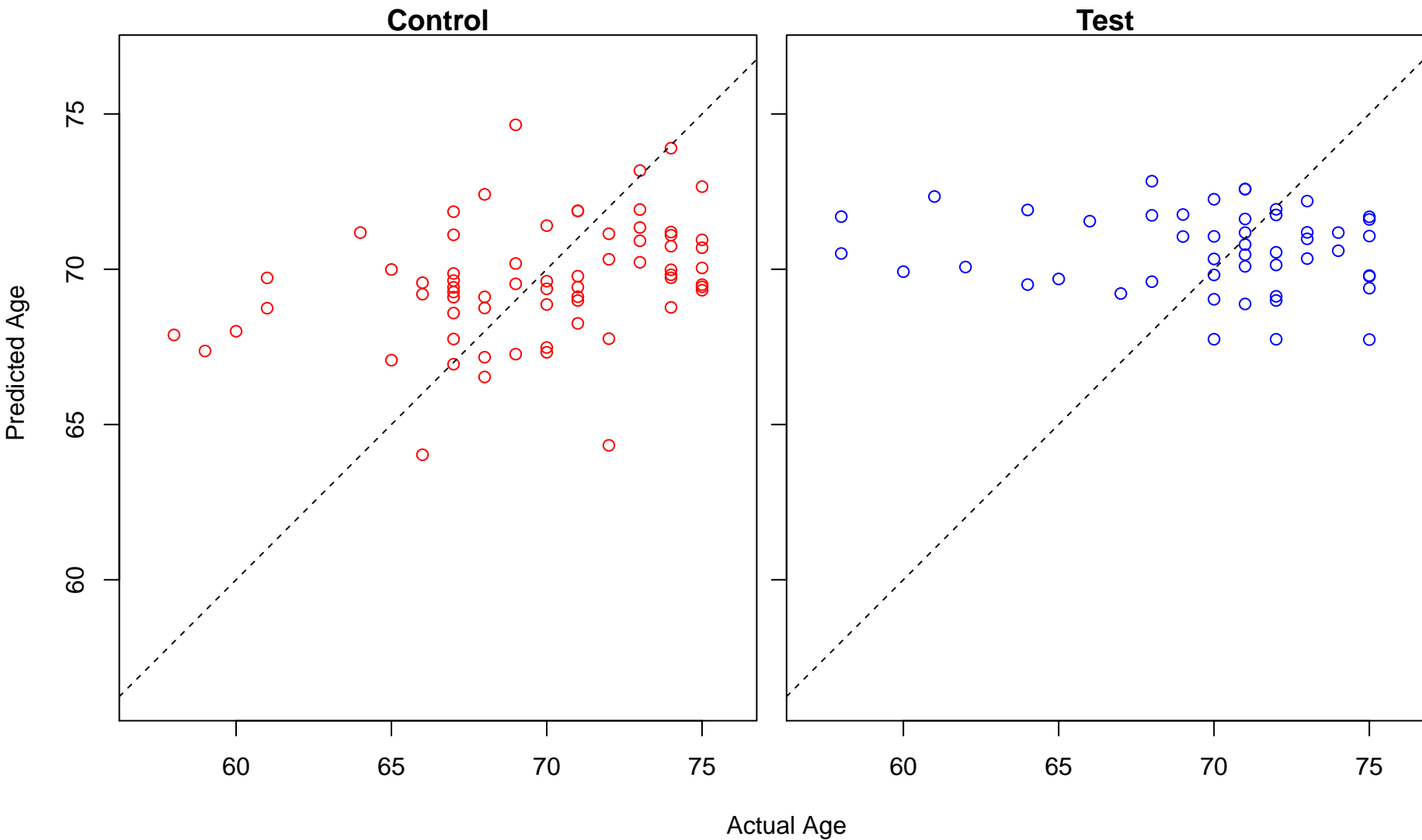


Actual Age

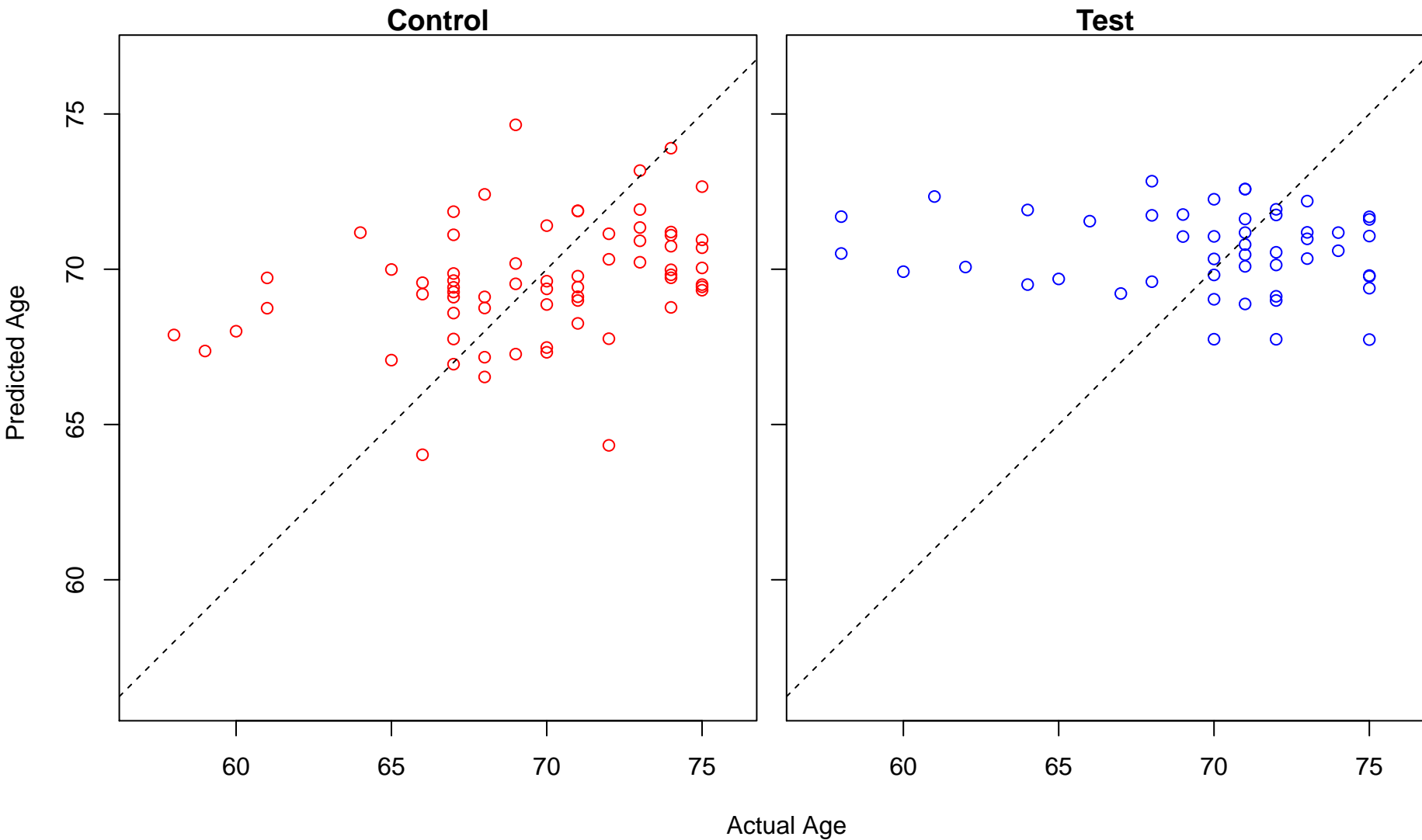
protein hexamerization (Score: 0.374831)



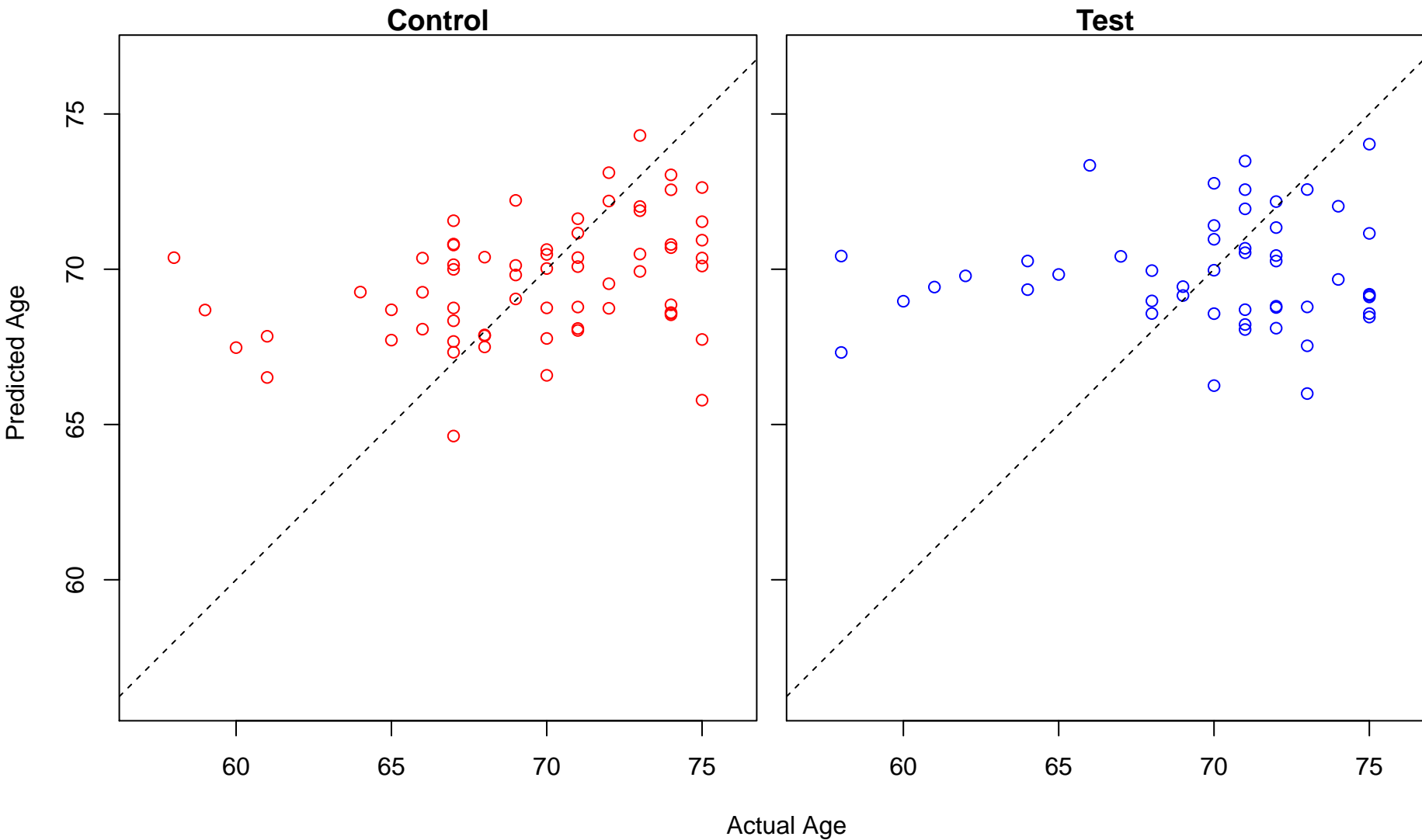
DNA double-strand break processing involved in repair via single-strand annealing (Score: 0.37450)



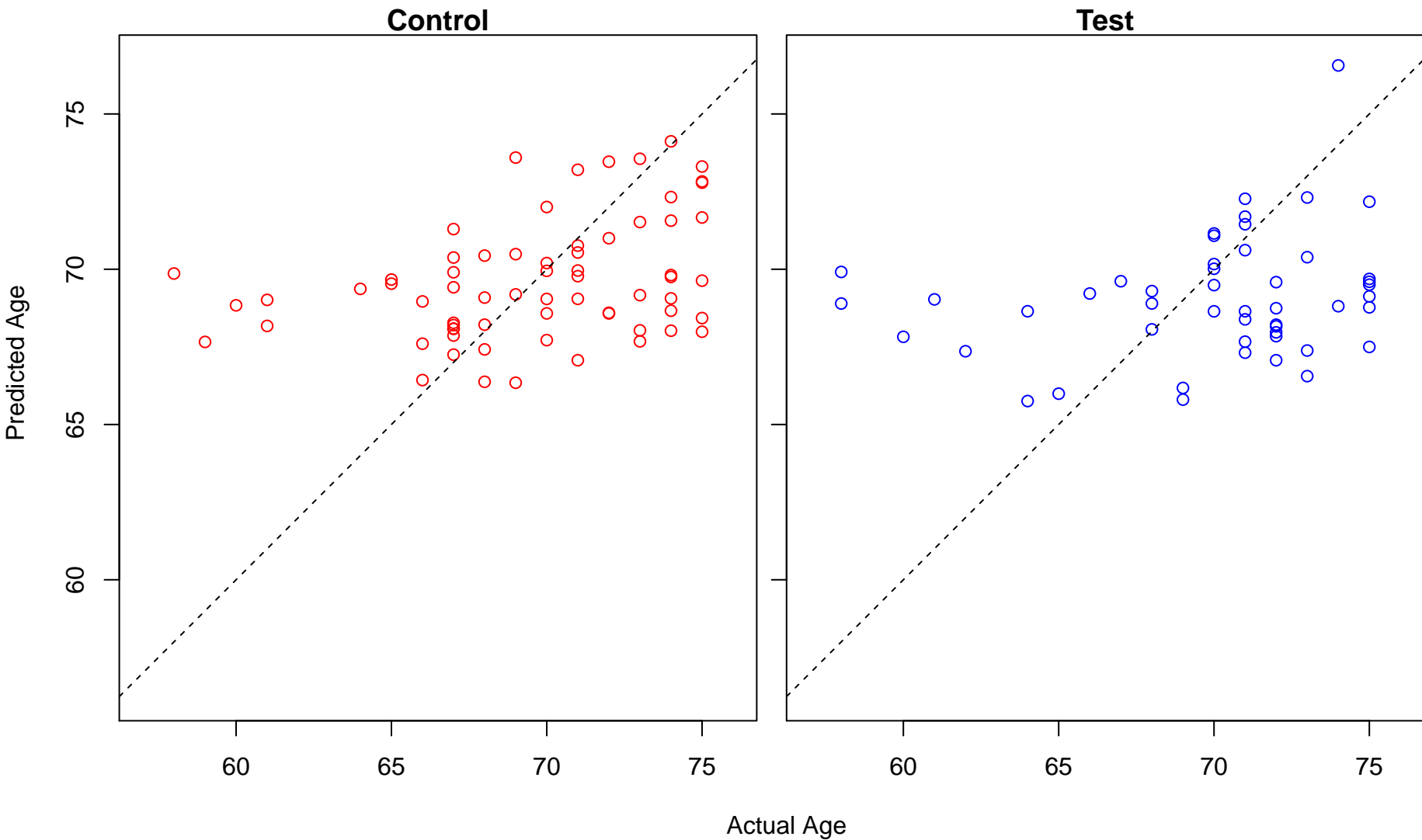
double-strand break repair via single-strand annealing (Score: 0.374507)



positive regulation of cGMP metabolic process (Score: 0.373264)

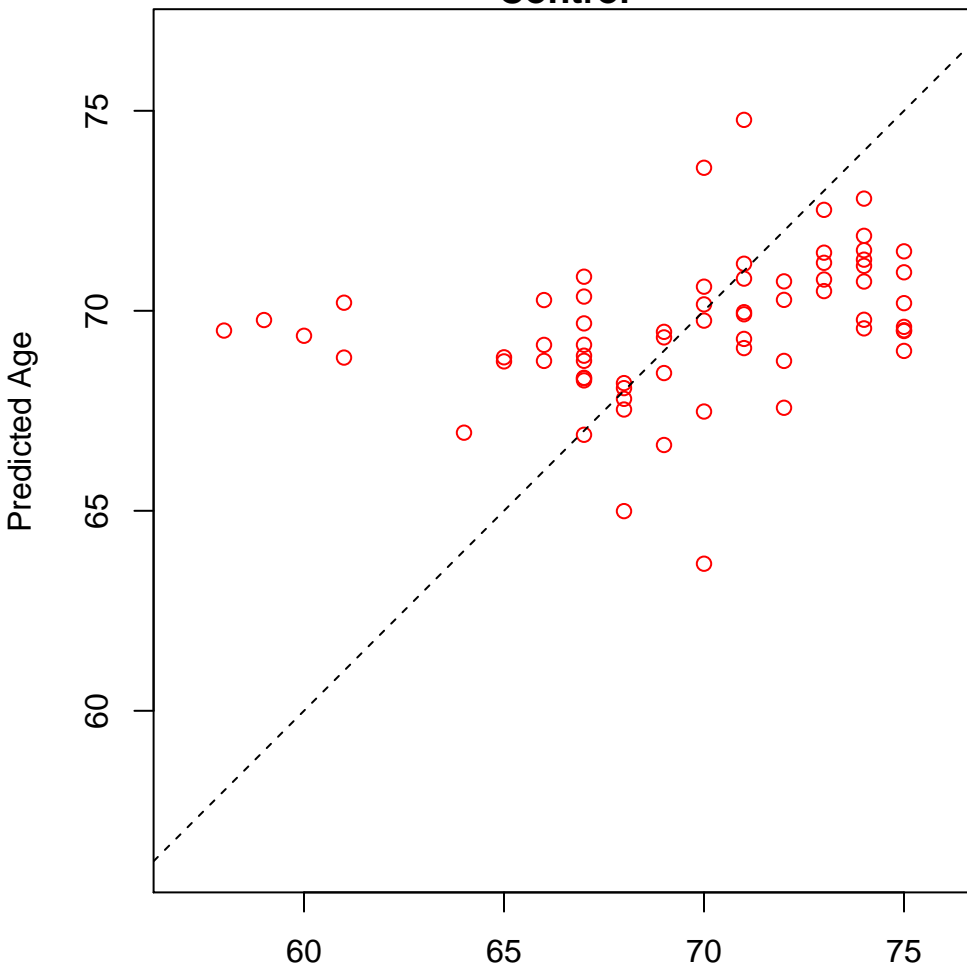


azole transport (Score: 0.373037)

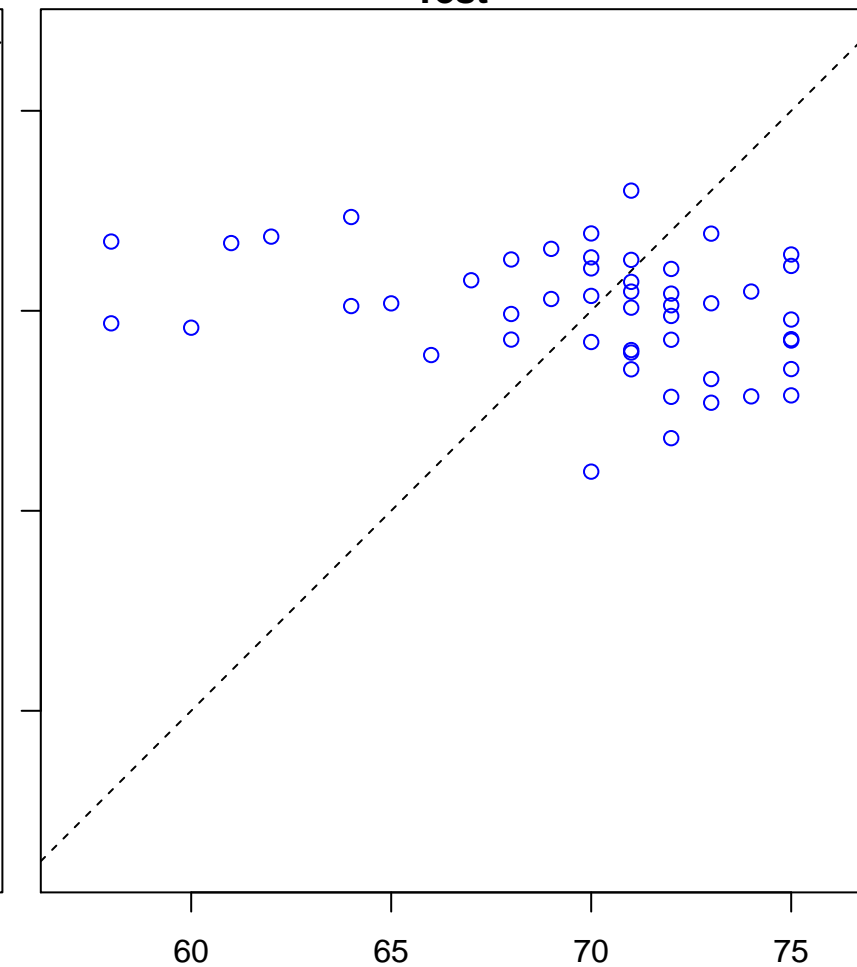


lymphoid progenitor cell differentiation (Score: 0.372424)

Control

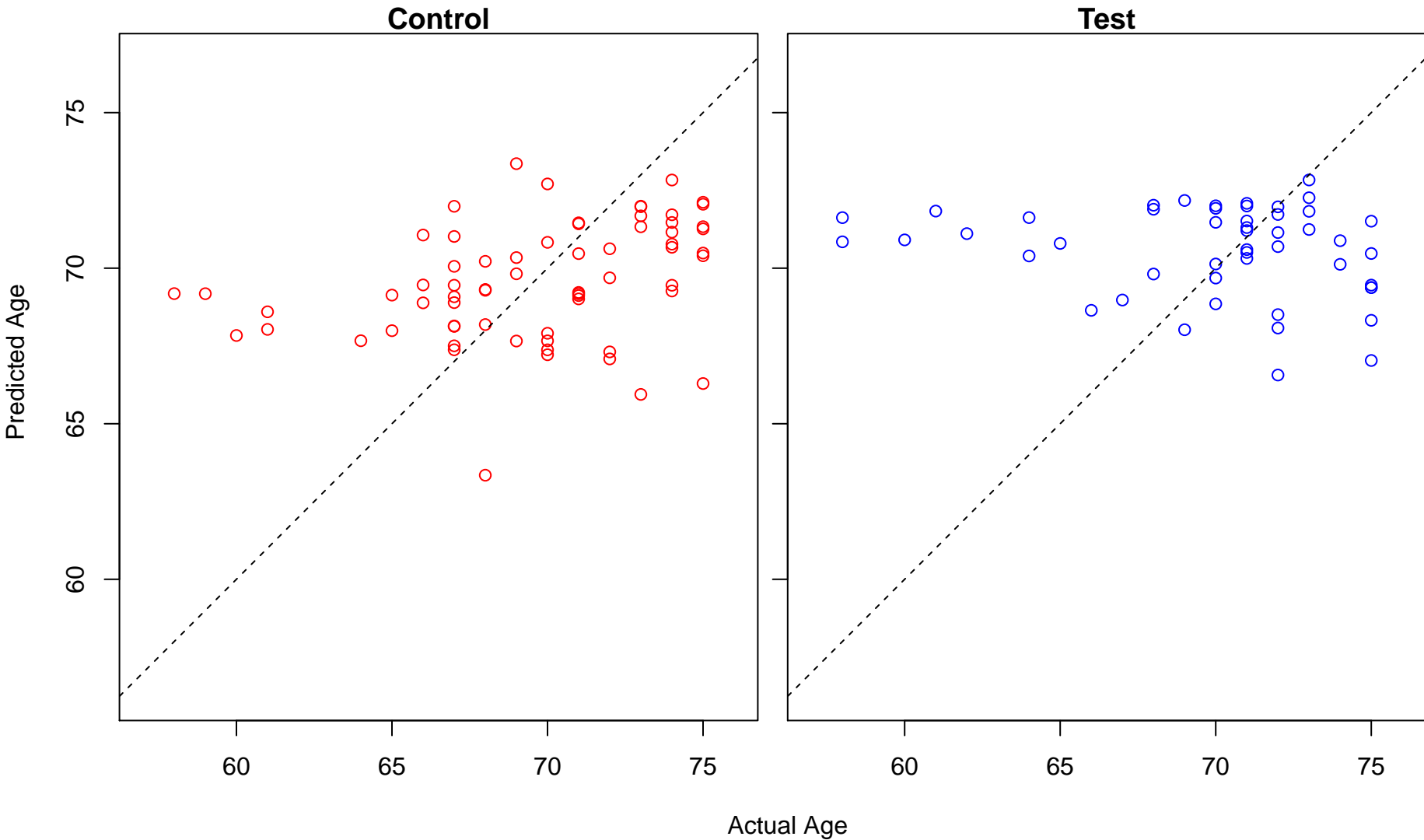


Test

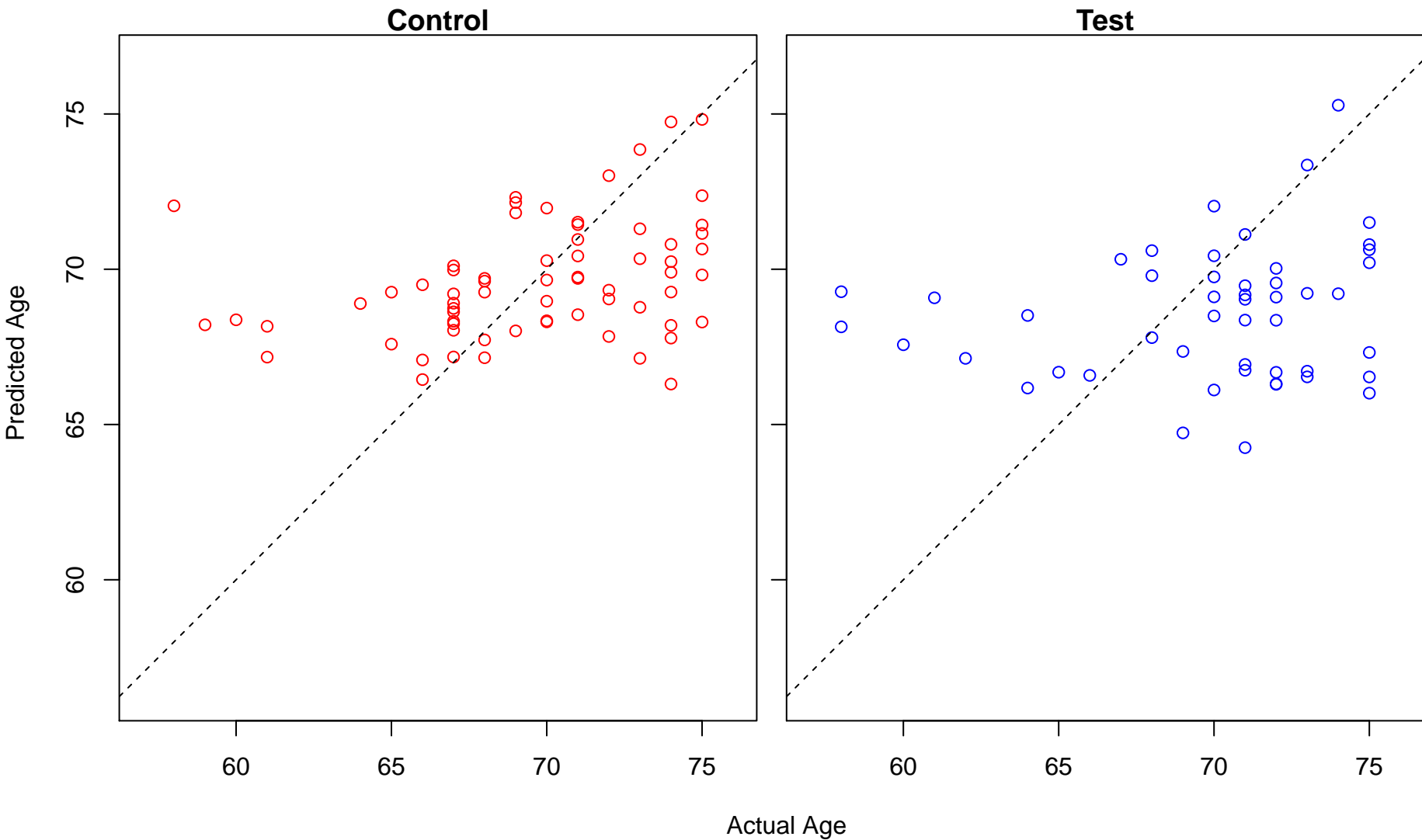


Actual Age

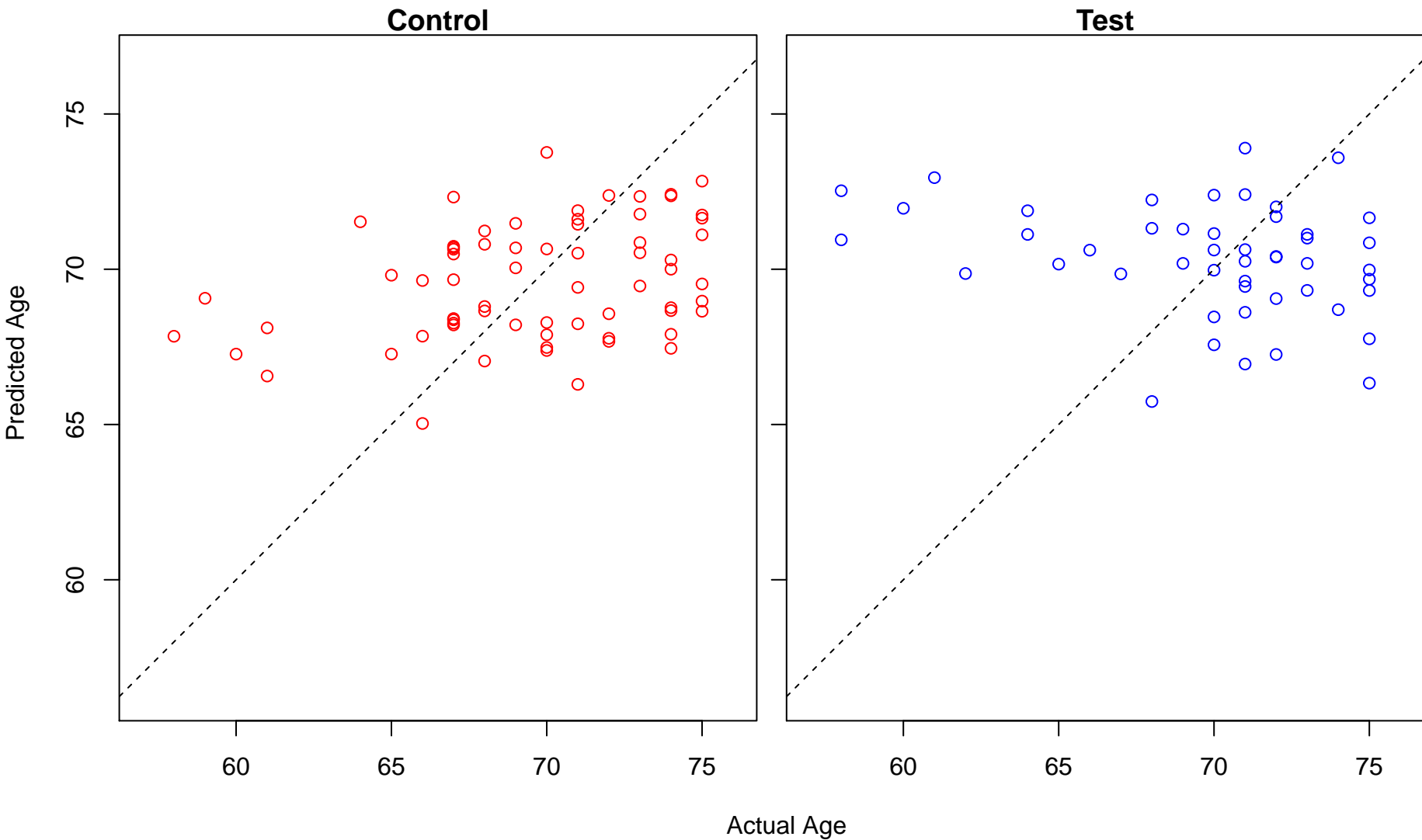
regulation of removal of superoxide radicals (Score: 0.371082)



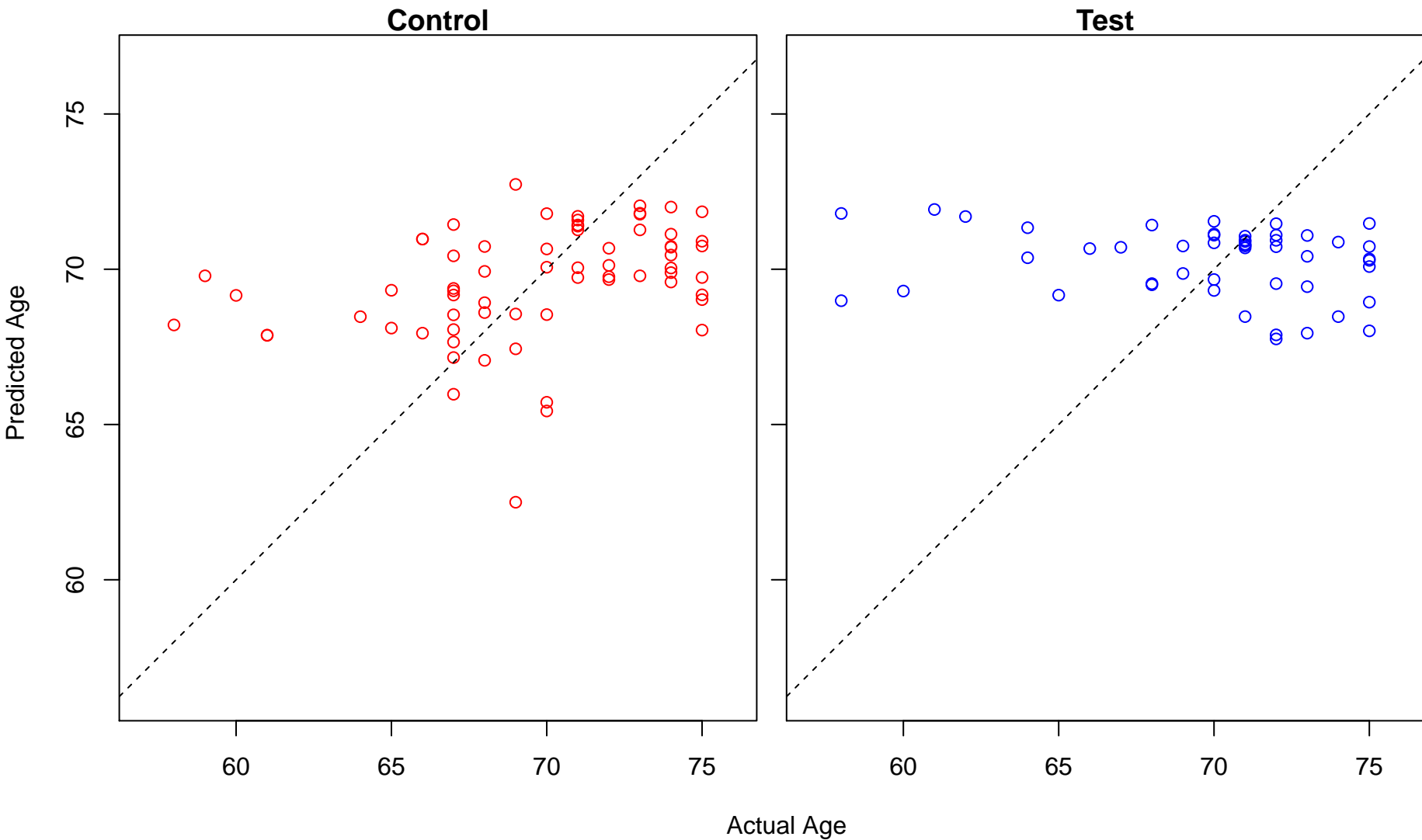
alkaloid metabolic process (Score: 0.368849)



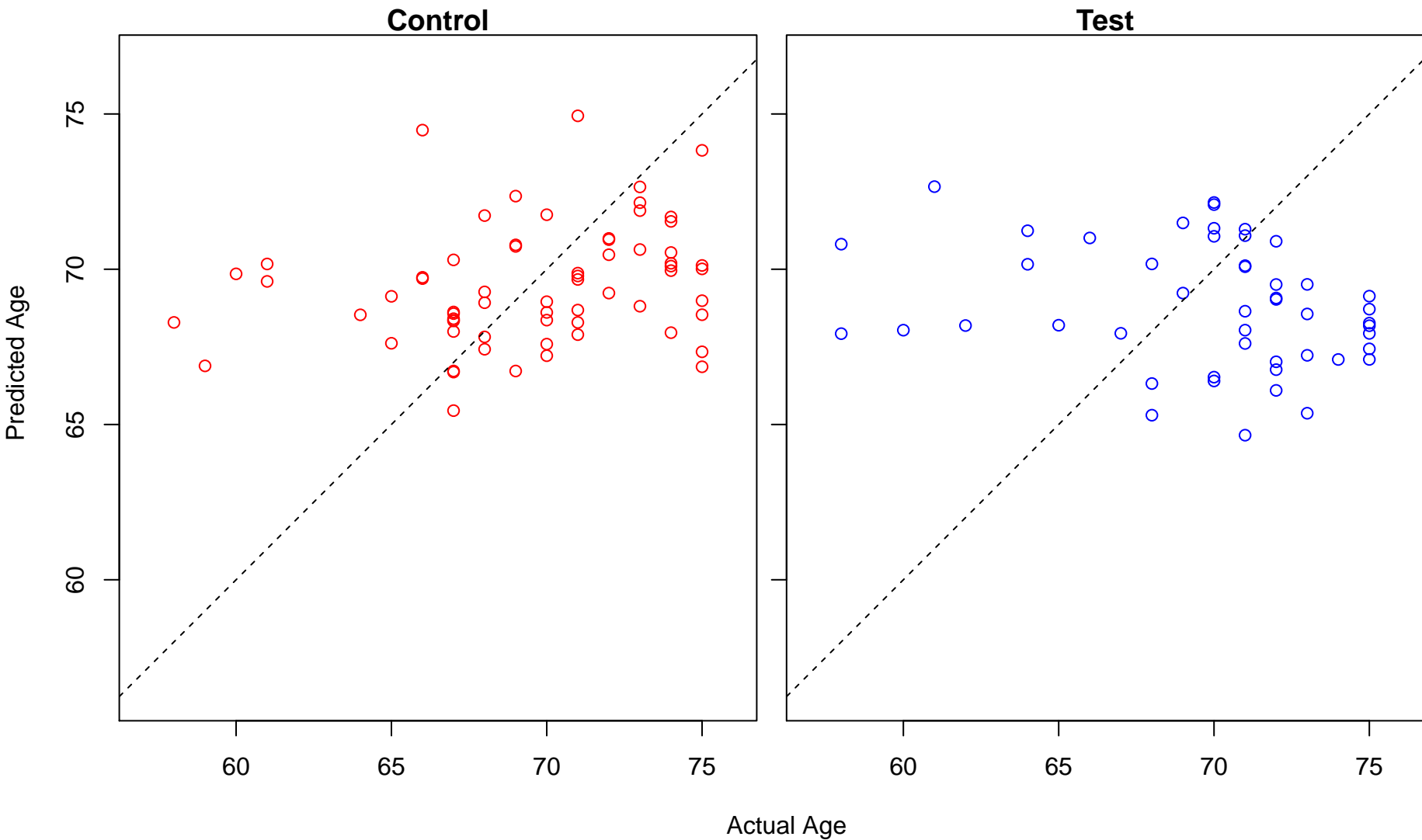
erythrocyte development (Score: 0.368634)



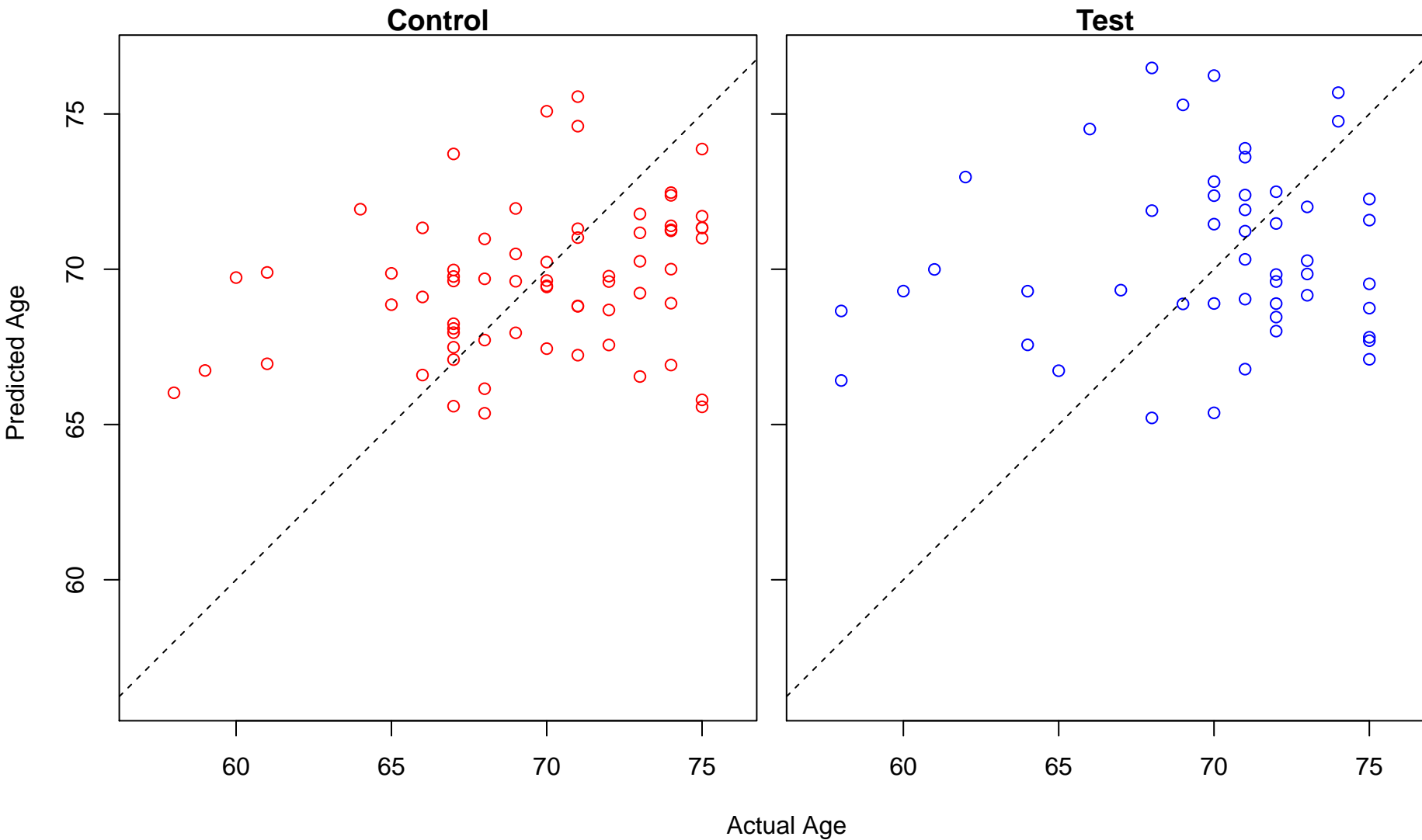
regulation of ketone biosynthetic process (Score: 0.368311)



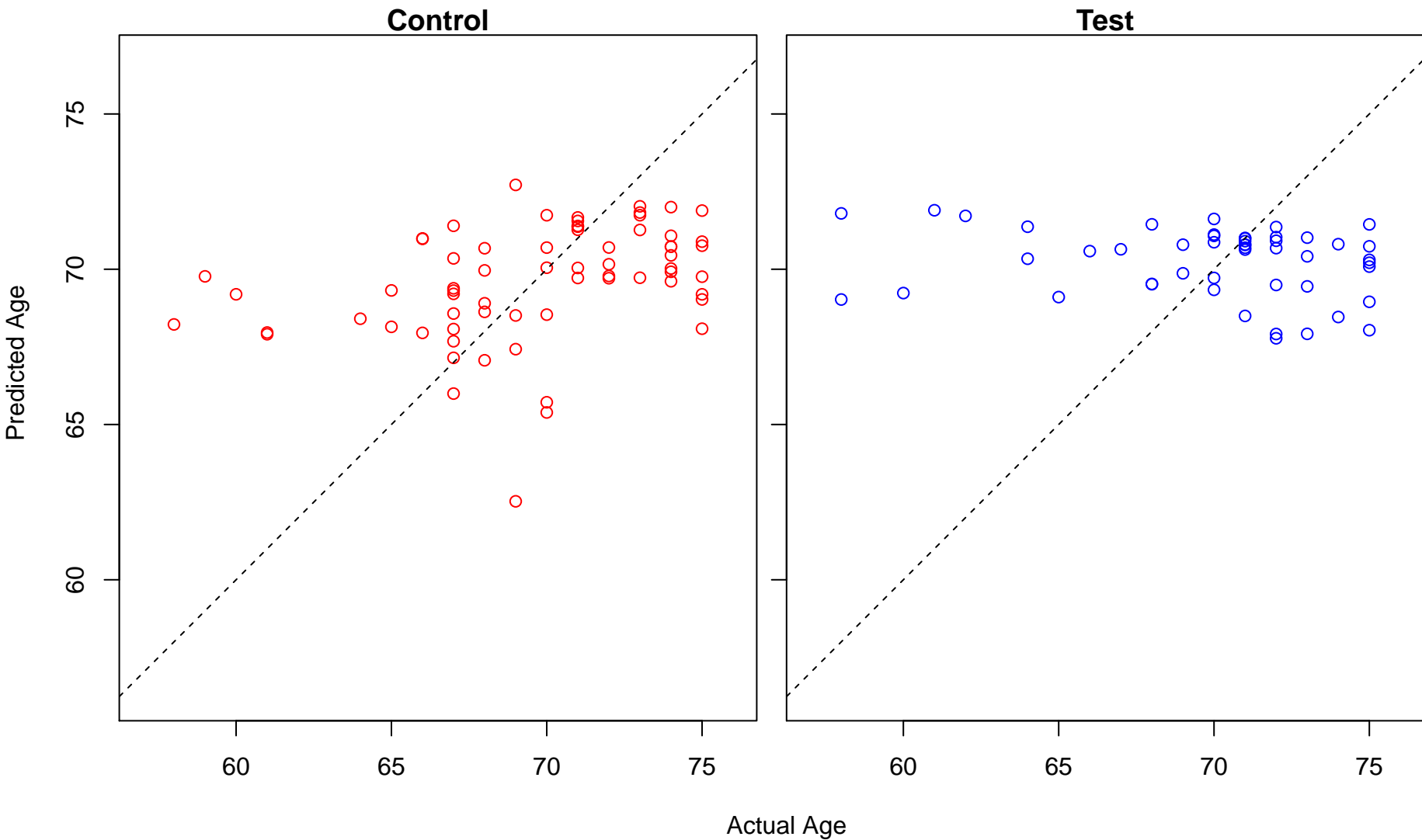
somite development (Score: 0.368093)



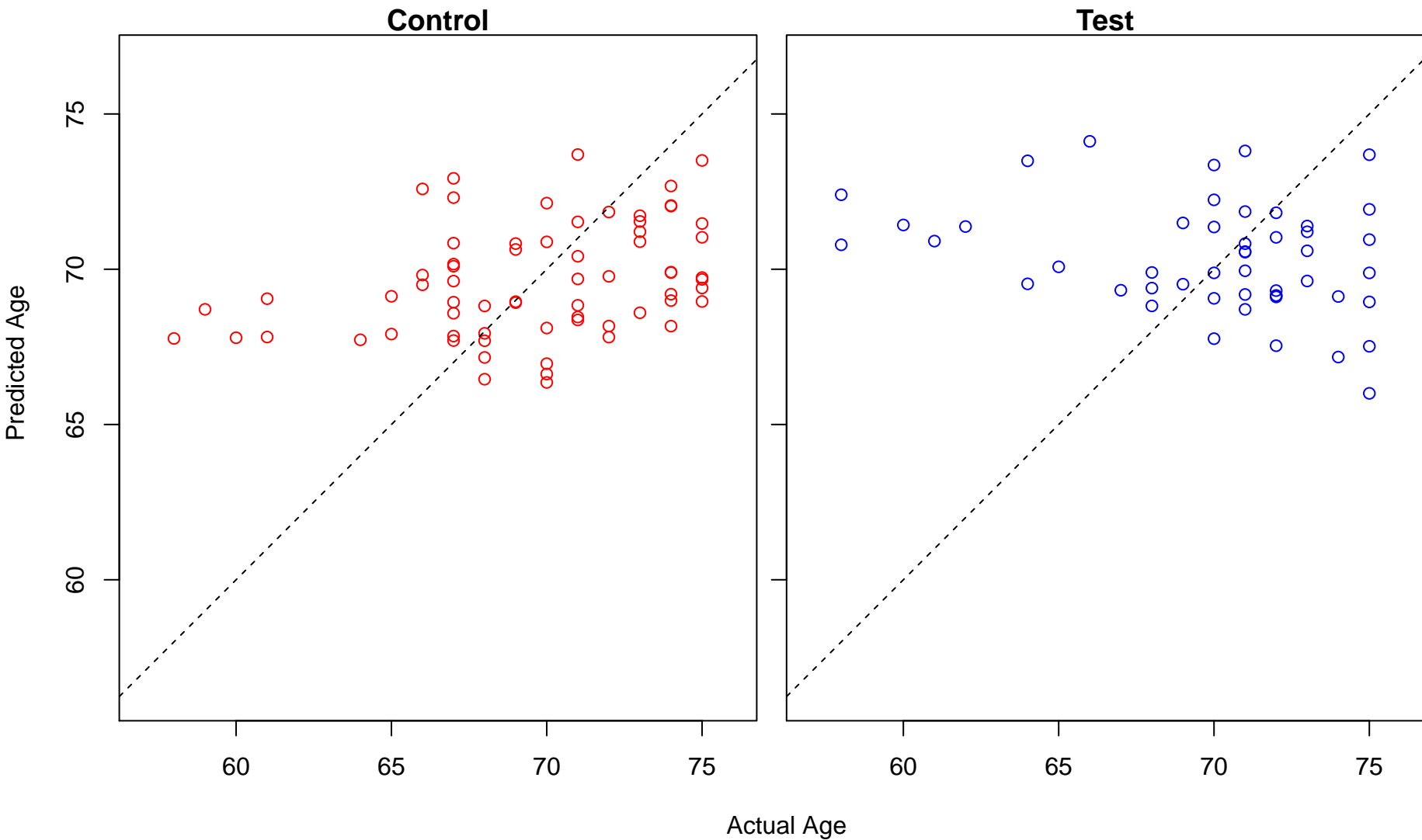
triglyceride-rich lipoprotein particle remodeling (Score: 0.367942)



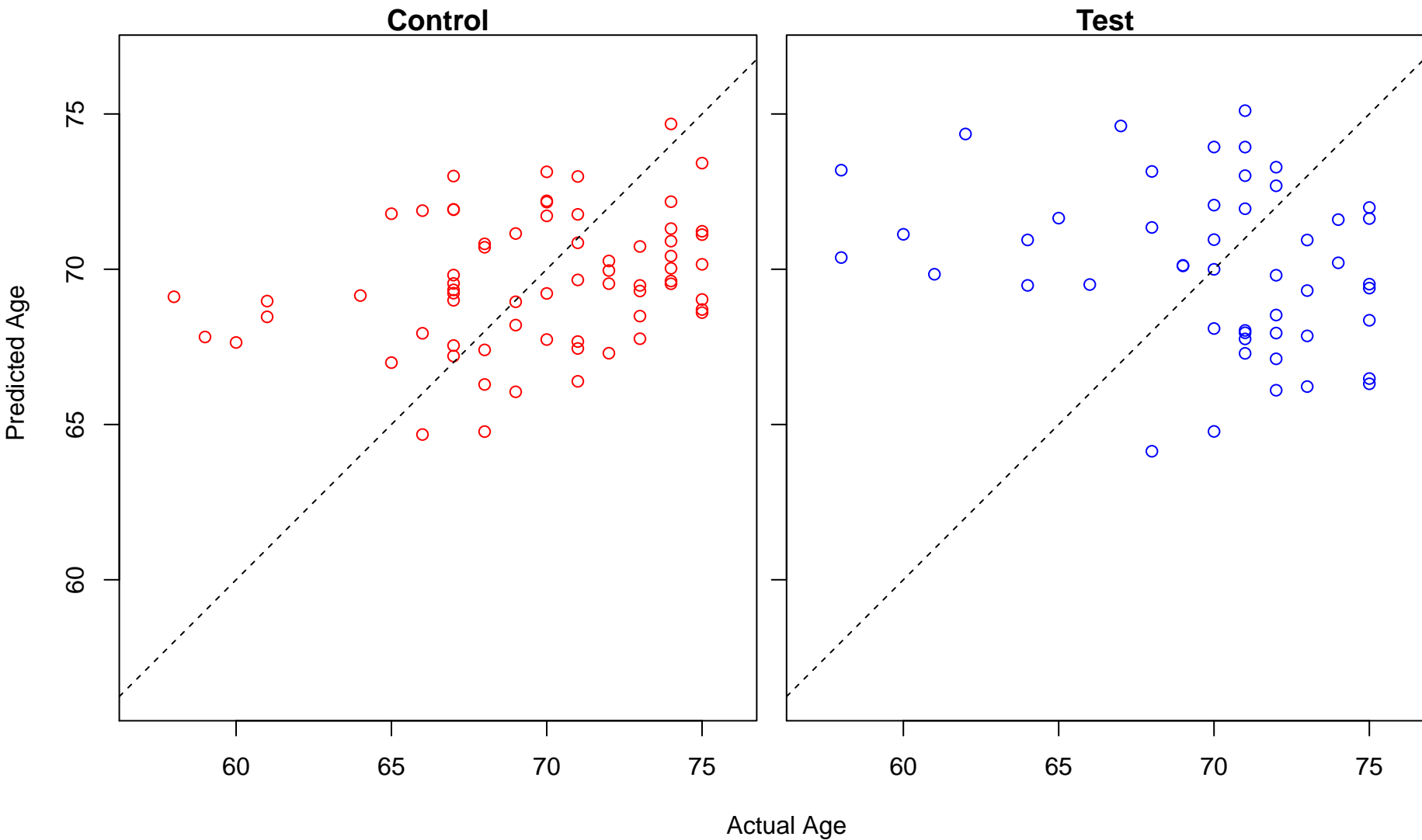
androgen biosynthetic process (Score: 0.366868)



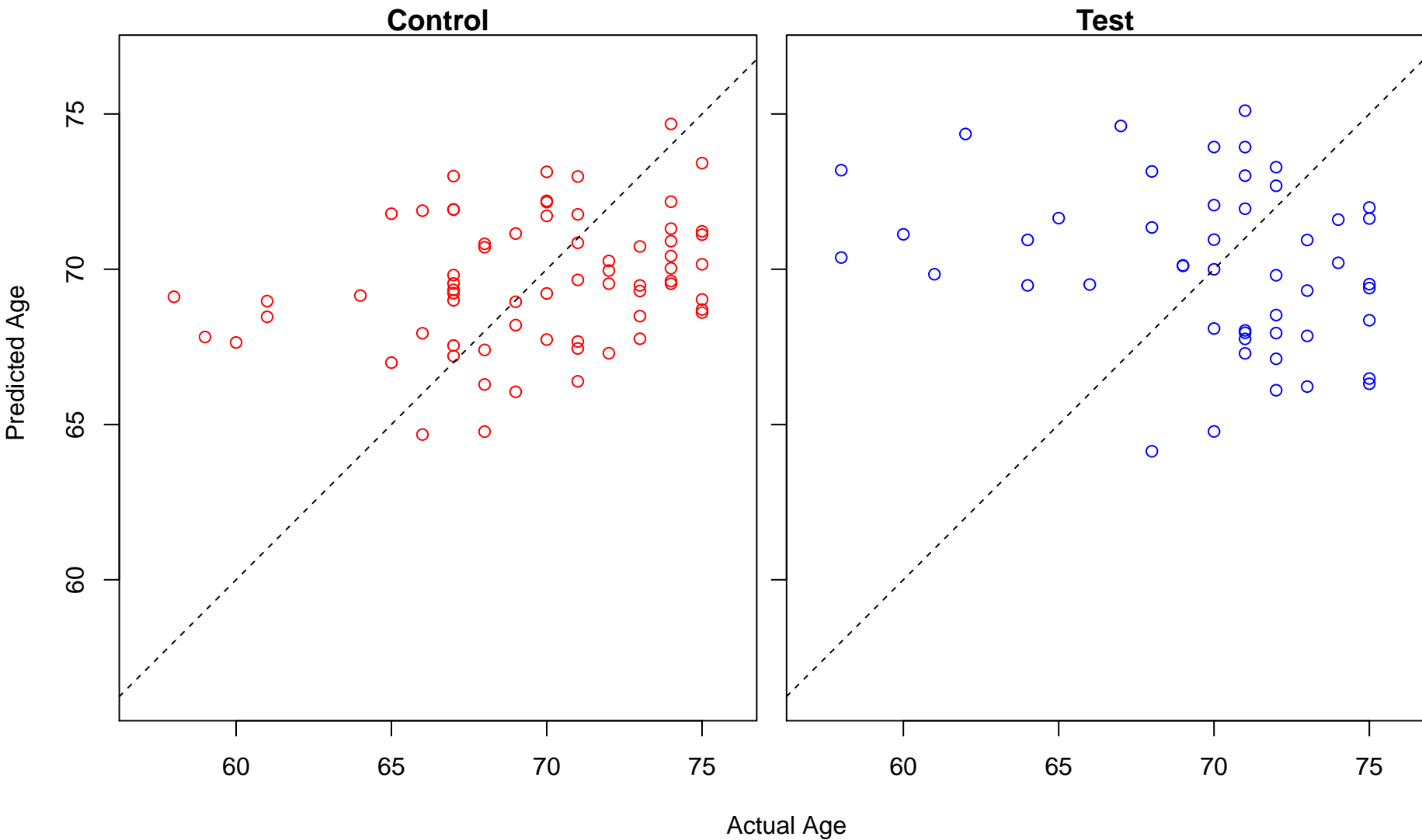
positive regulation of actin nucleation (Score: 0.366517)



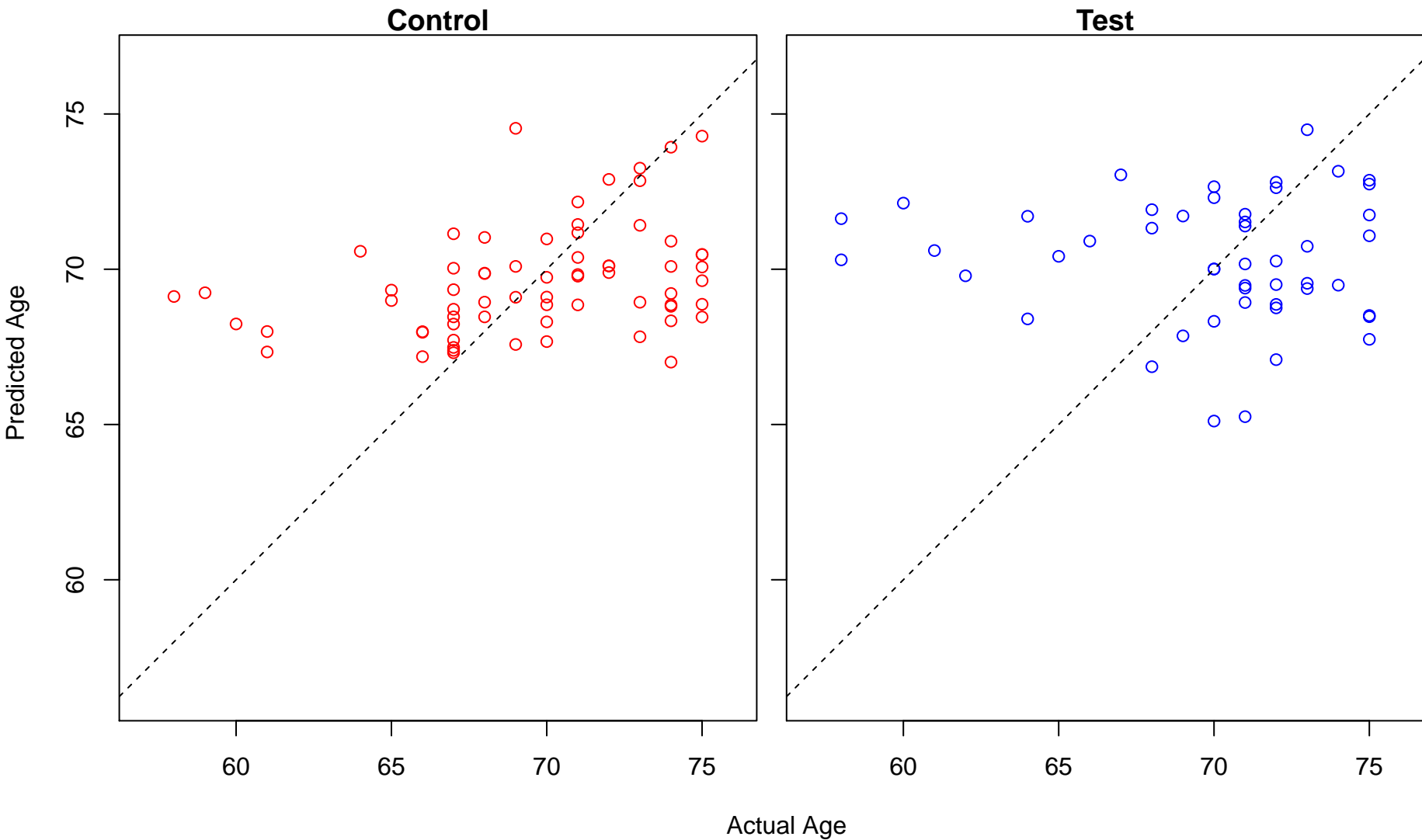
acylglycerol homeostasis (Score: 0.364804)



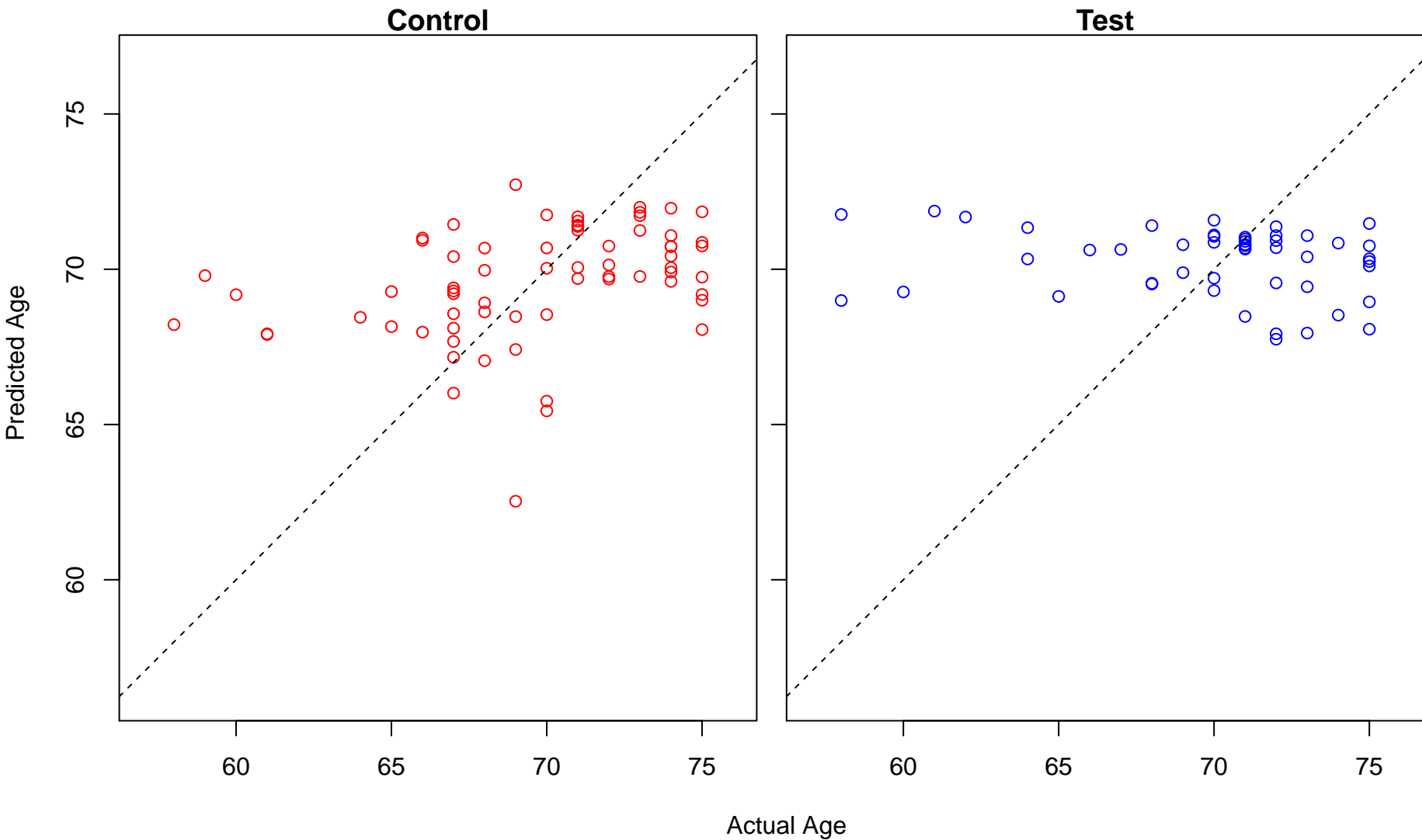
triglyceride homeostasis (Score: 0.364804)



protein deglutamylation (Score: 0.364463)

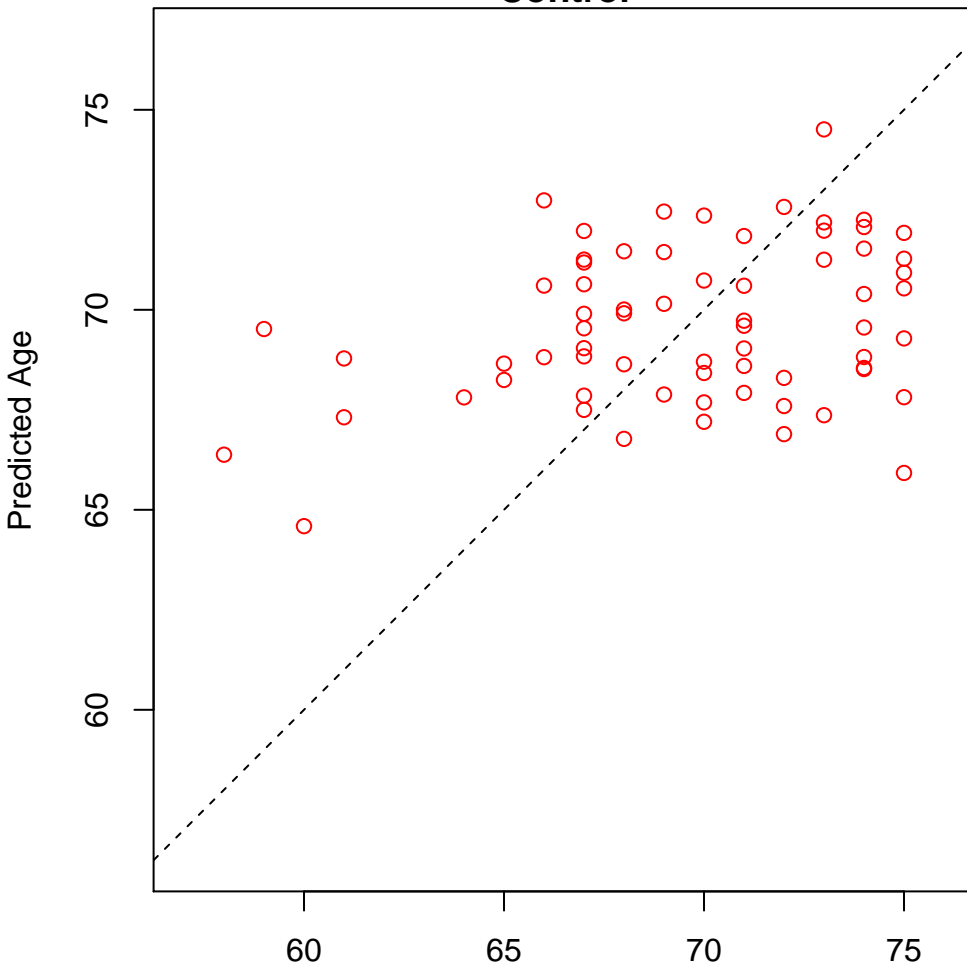


negative regulation of hormone metabolic process (Score: 0.363600)

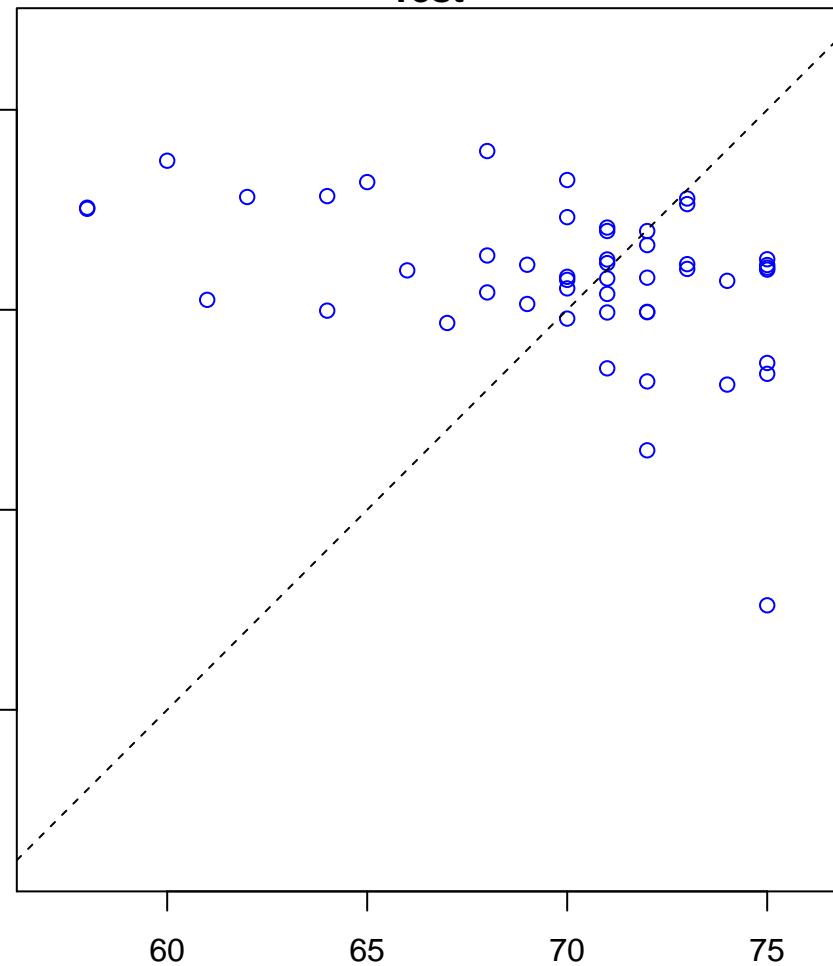


plasma lipoprotein particle clearance (Score: 0.363303)

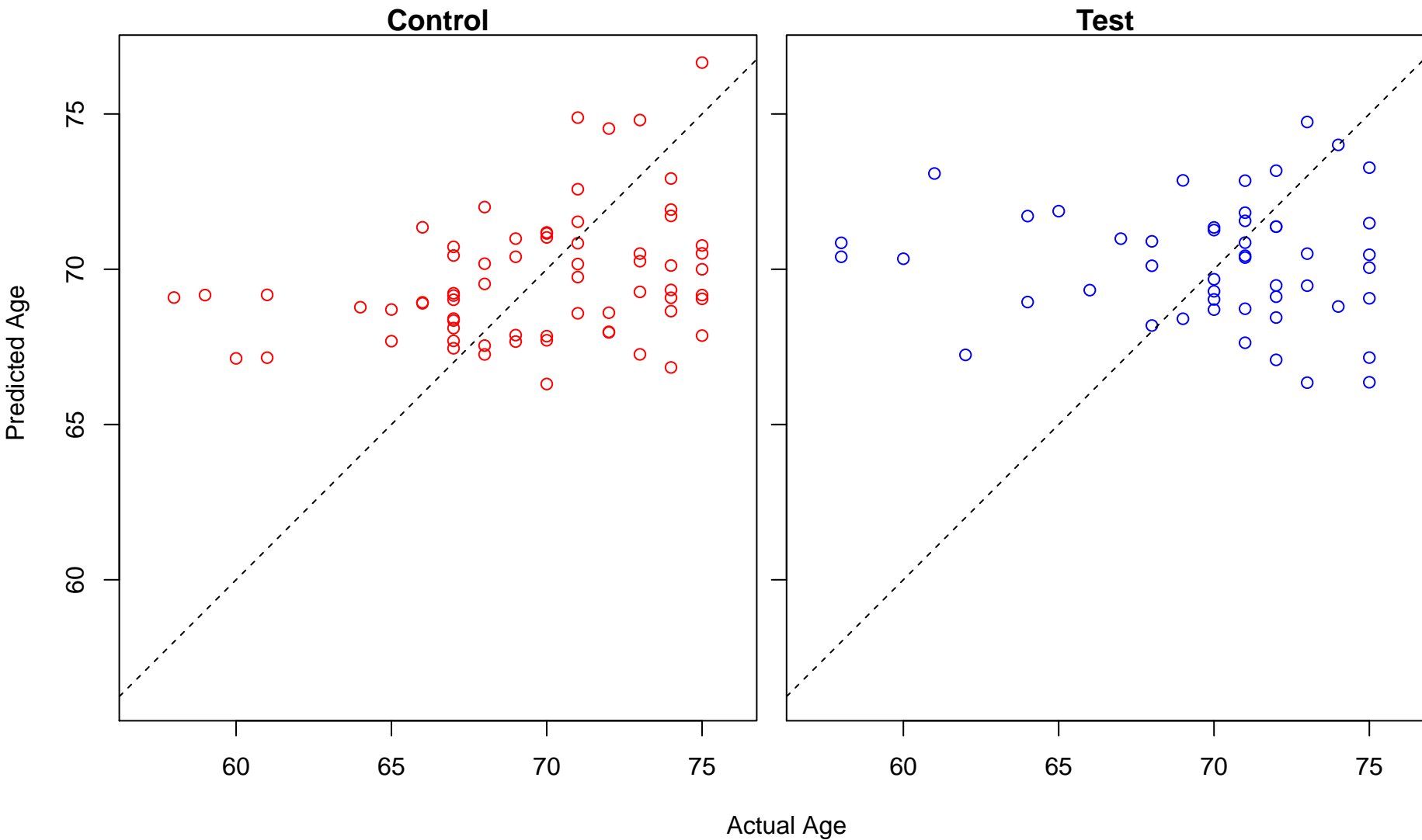
Control



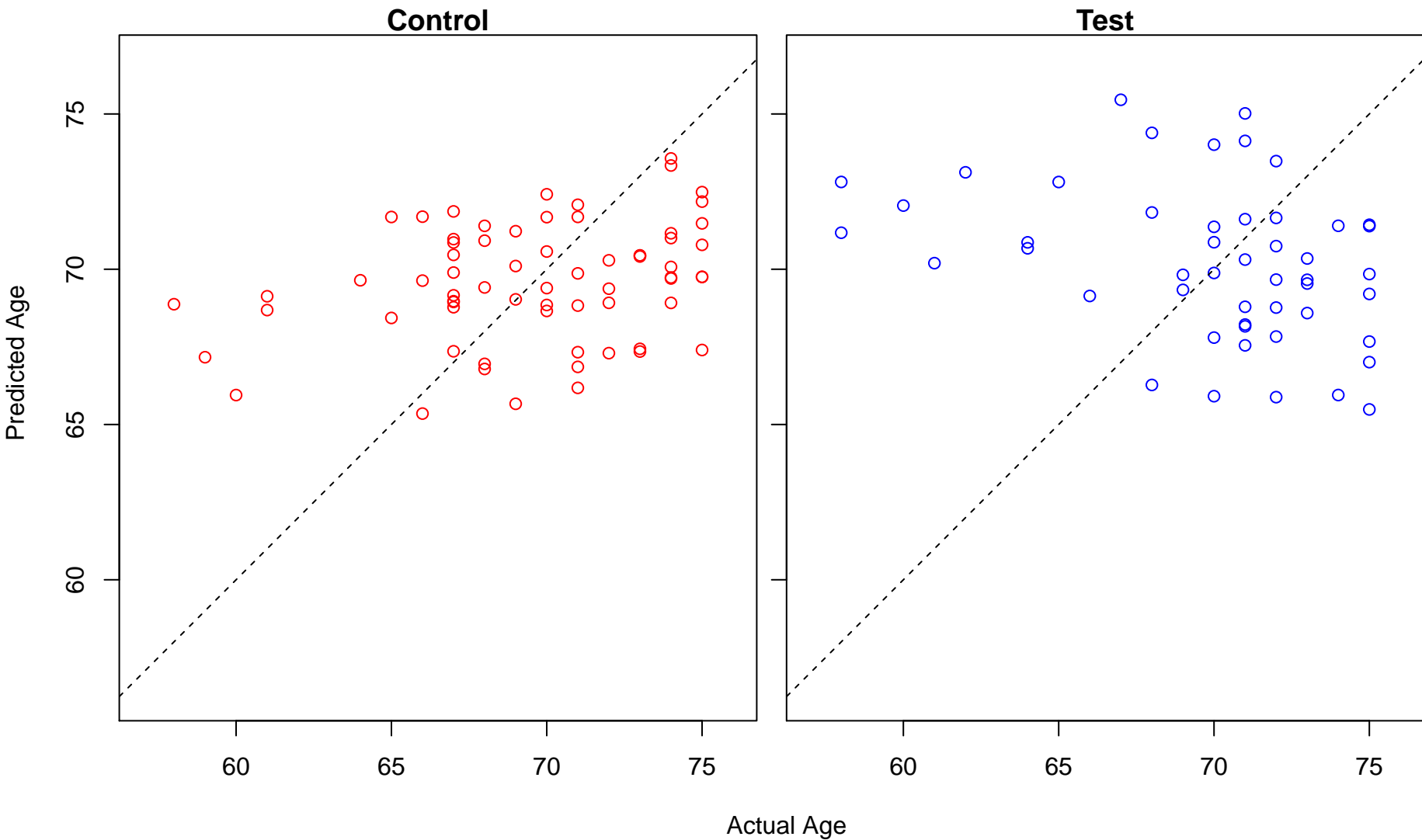
Test



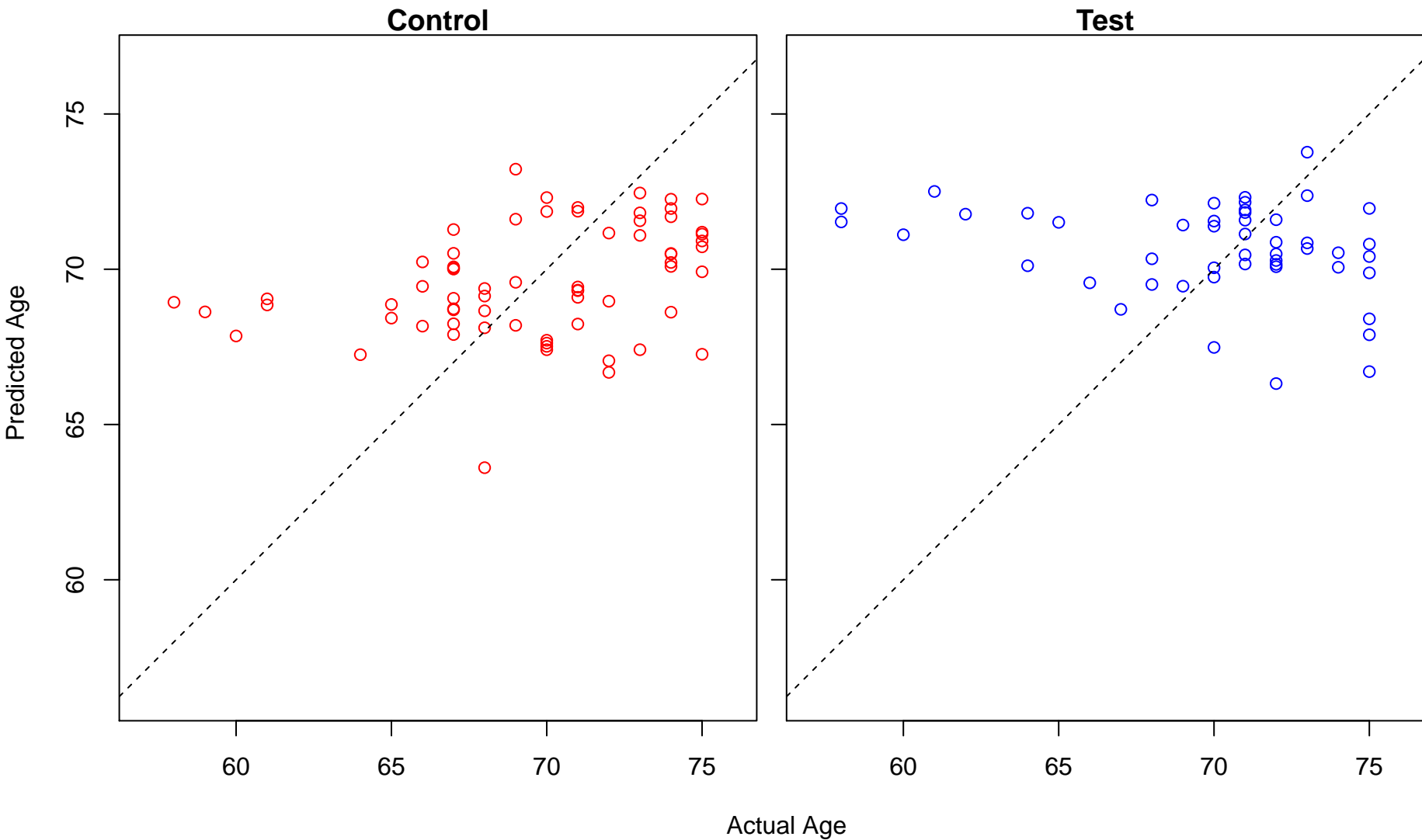
lipid particle organization (Score: 0.362699)



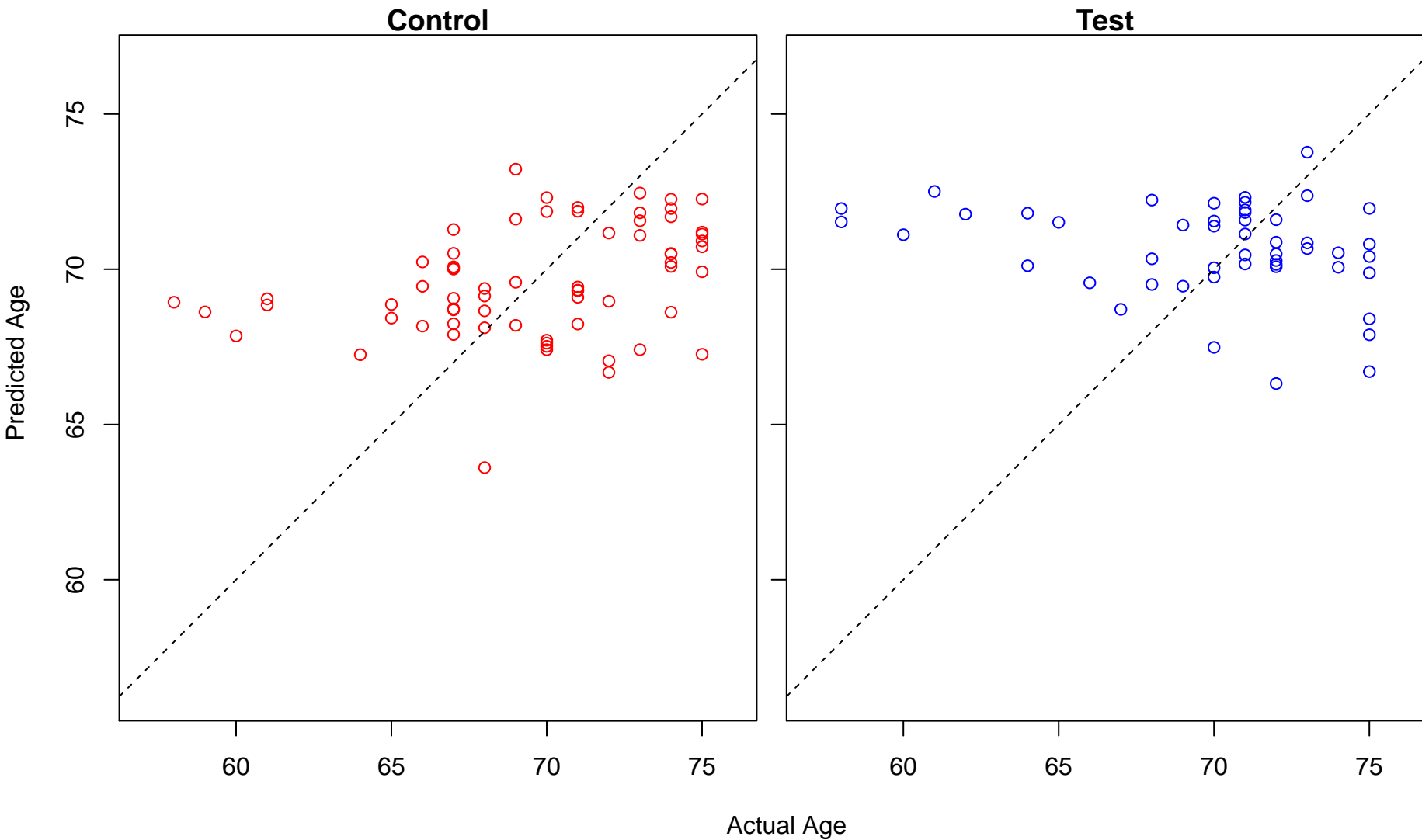
cellular triglyceride homeostasis (Score: 0.362443)



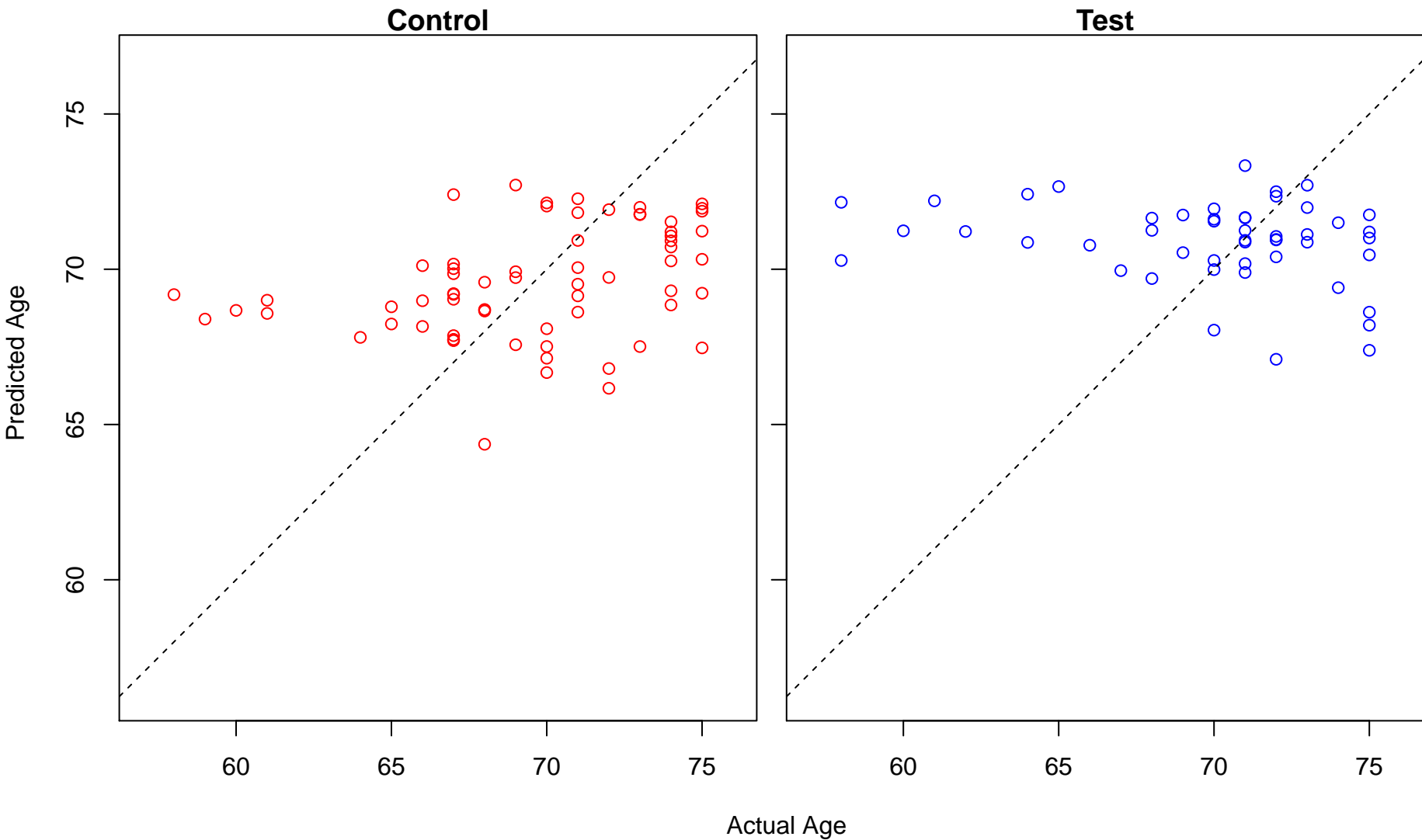
regulation of dopamine metabolic process (Score: 0.361814)



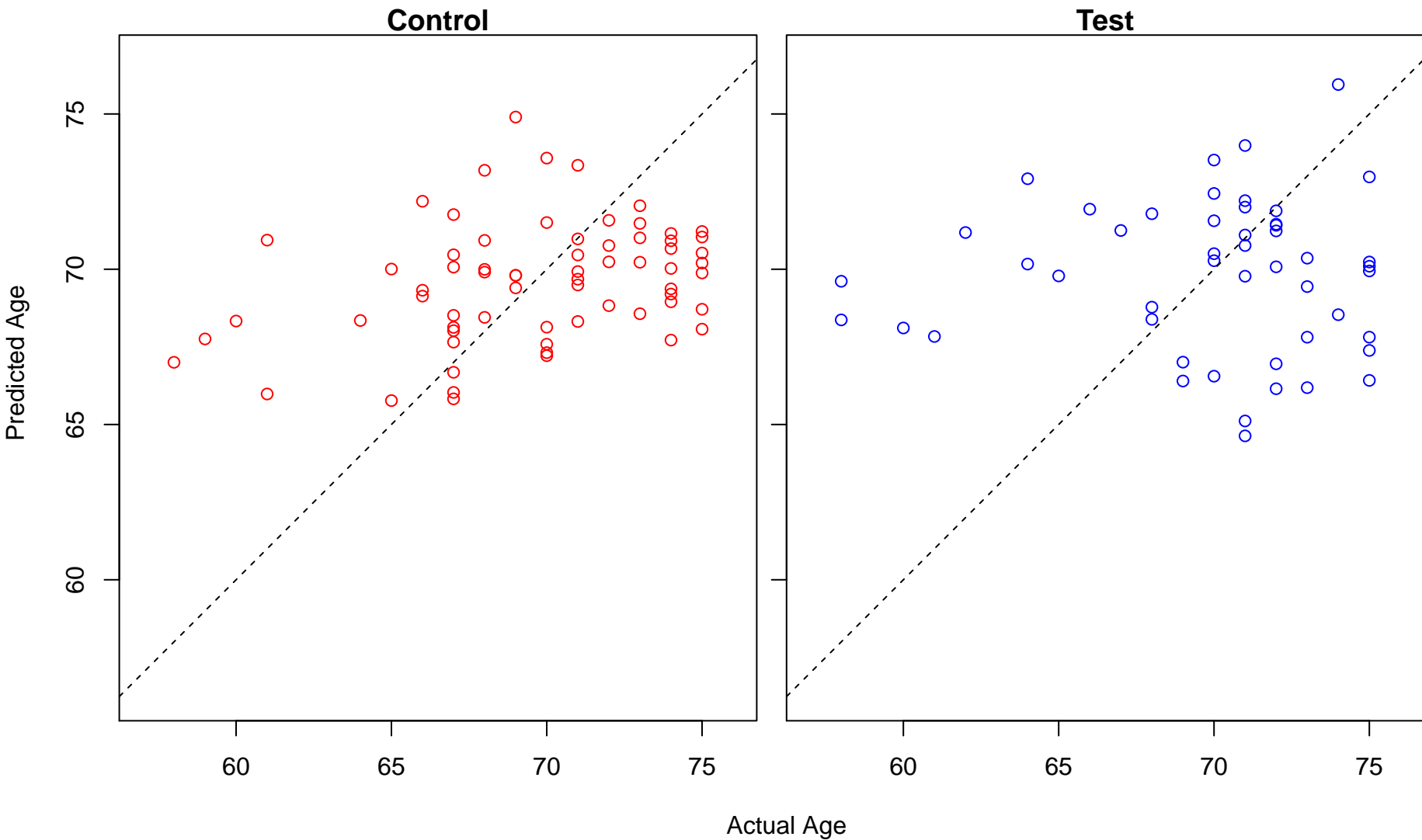
regulation of catecholamine metabolic process (Score: 0.361814)



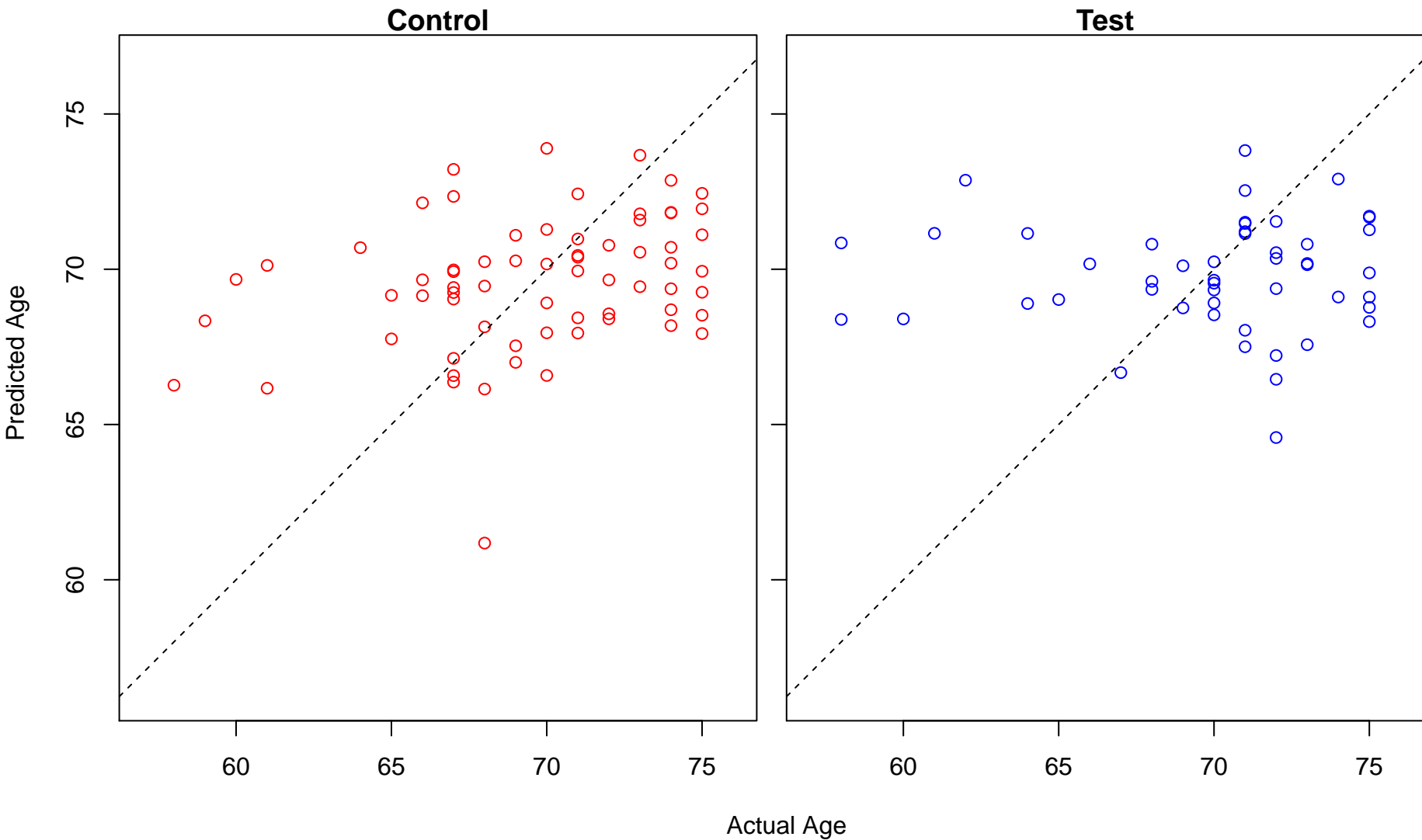
aldehyde catabolic process (Score: 0.361443)



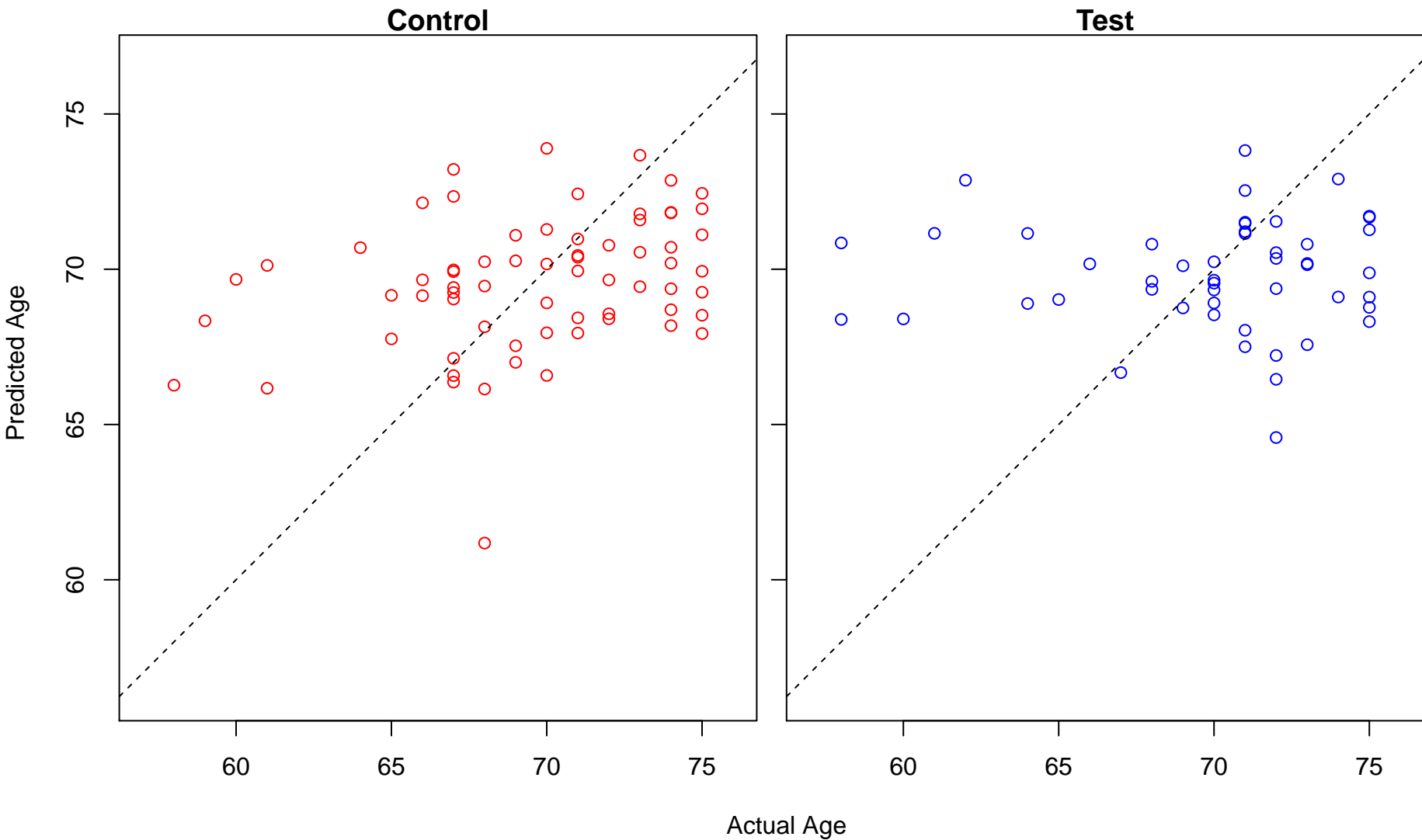
lens fiber cell development (Score: 0.360529)



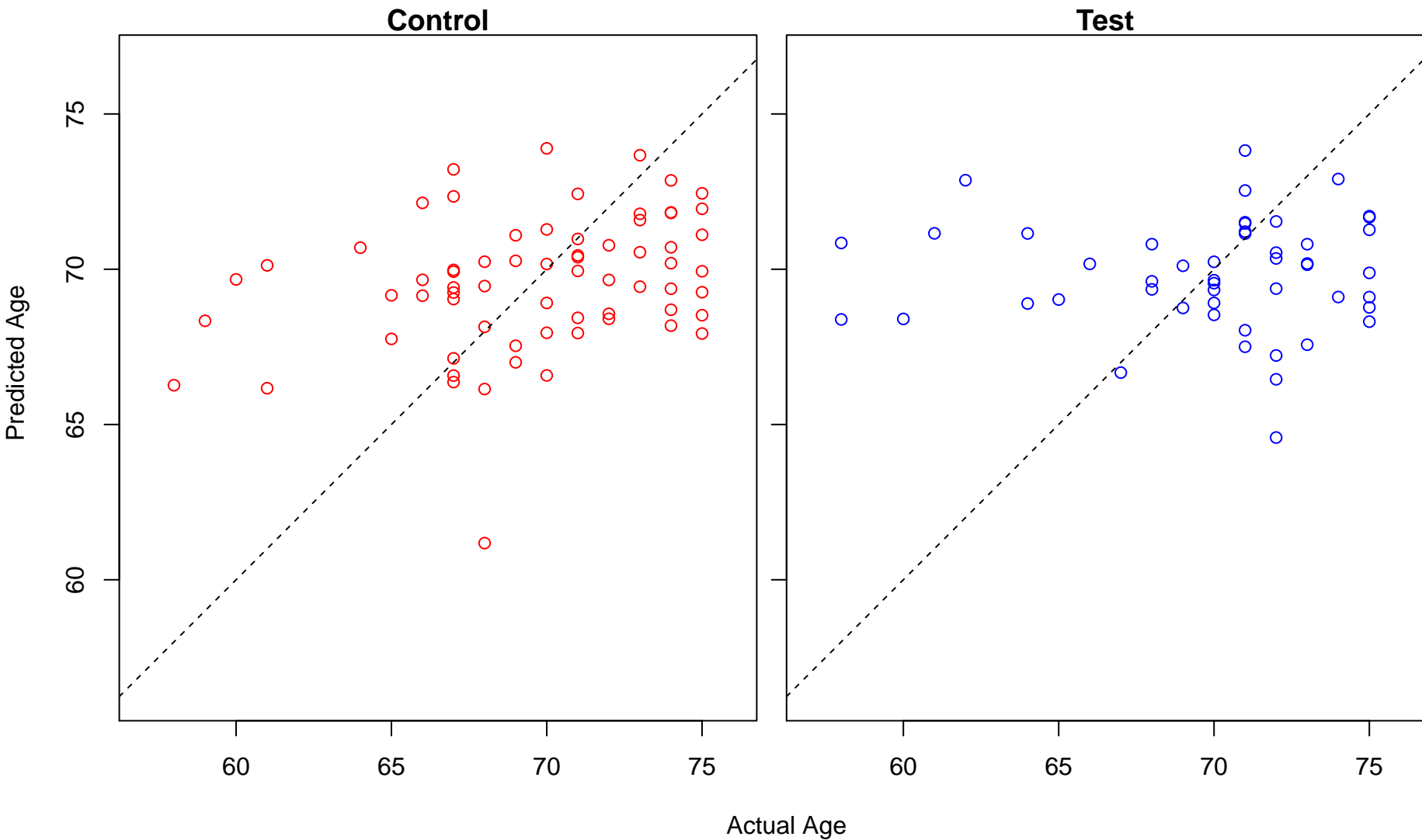
response to inactivity (Score: 0.360177)



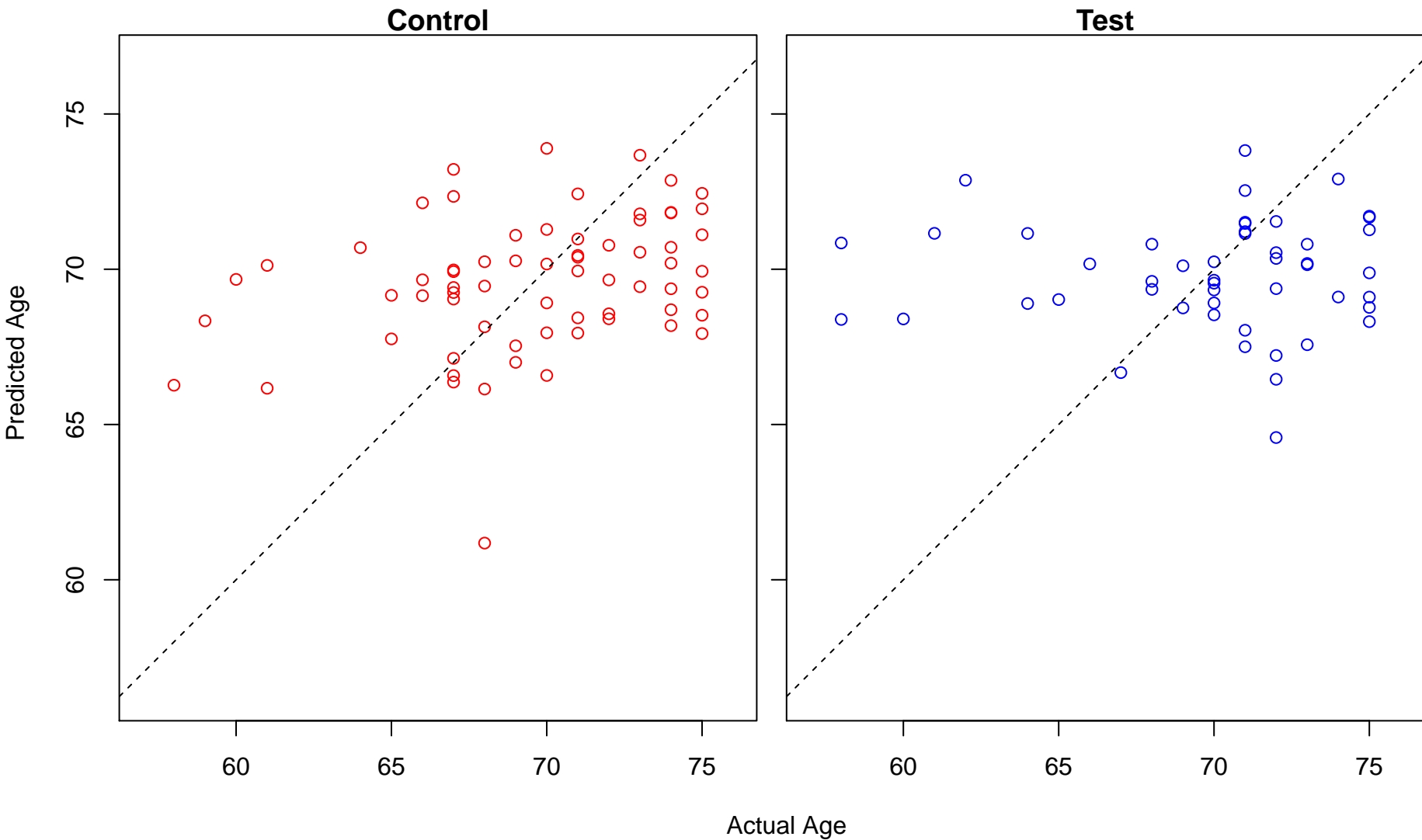
response to muscle inactivity (Score: 0.360177)



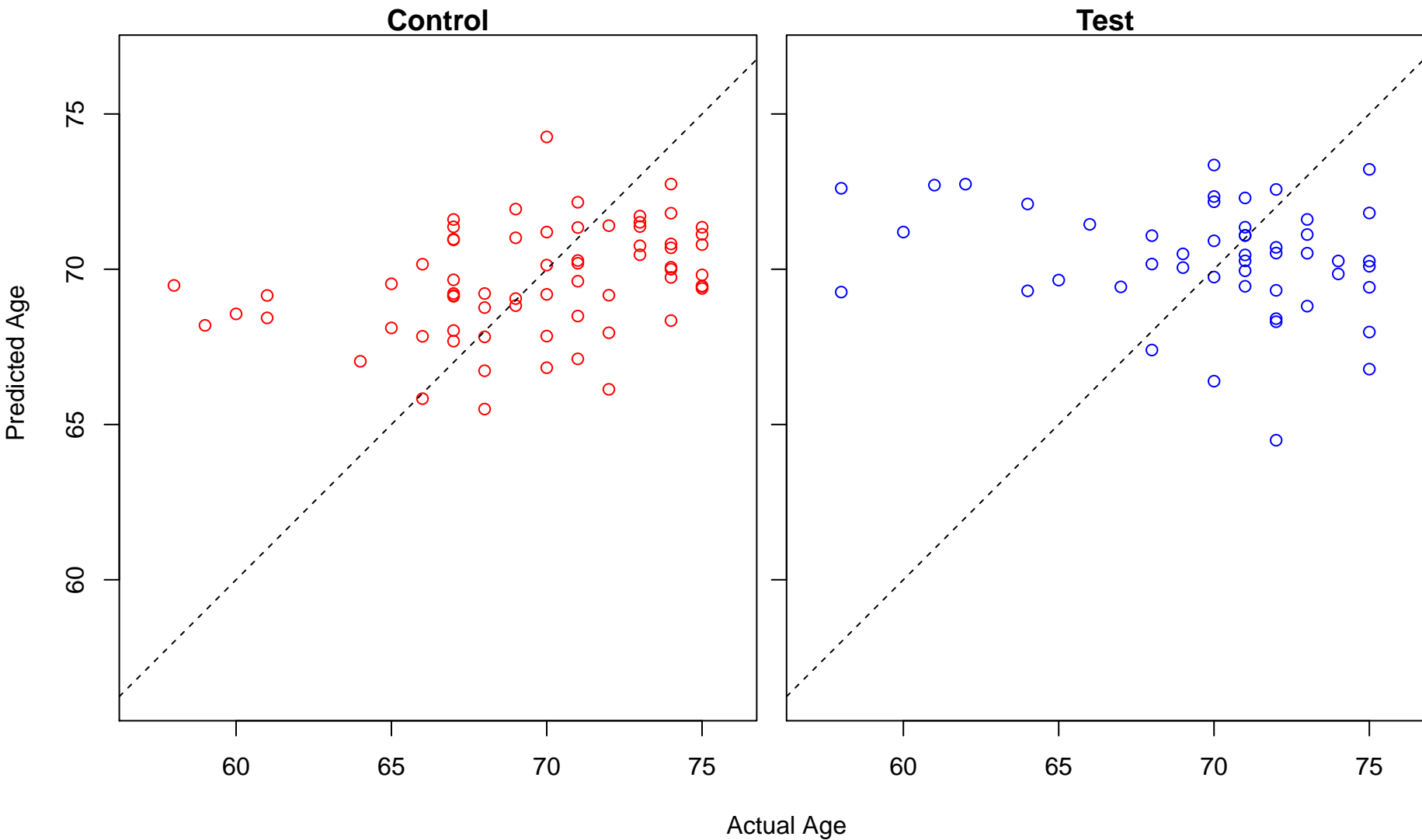
response to muscle inactivity involved in regulation of muscle adaptation (Score: 0.360177)



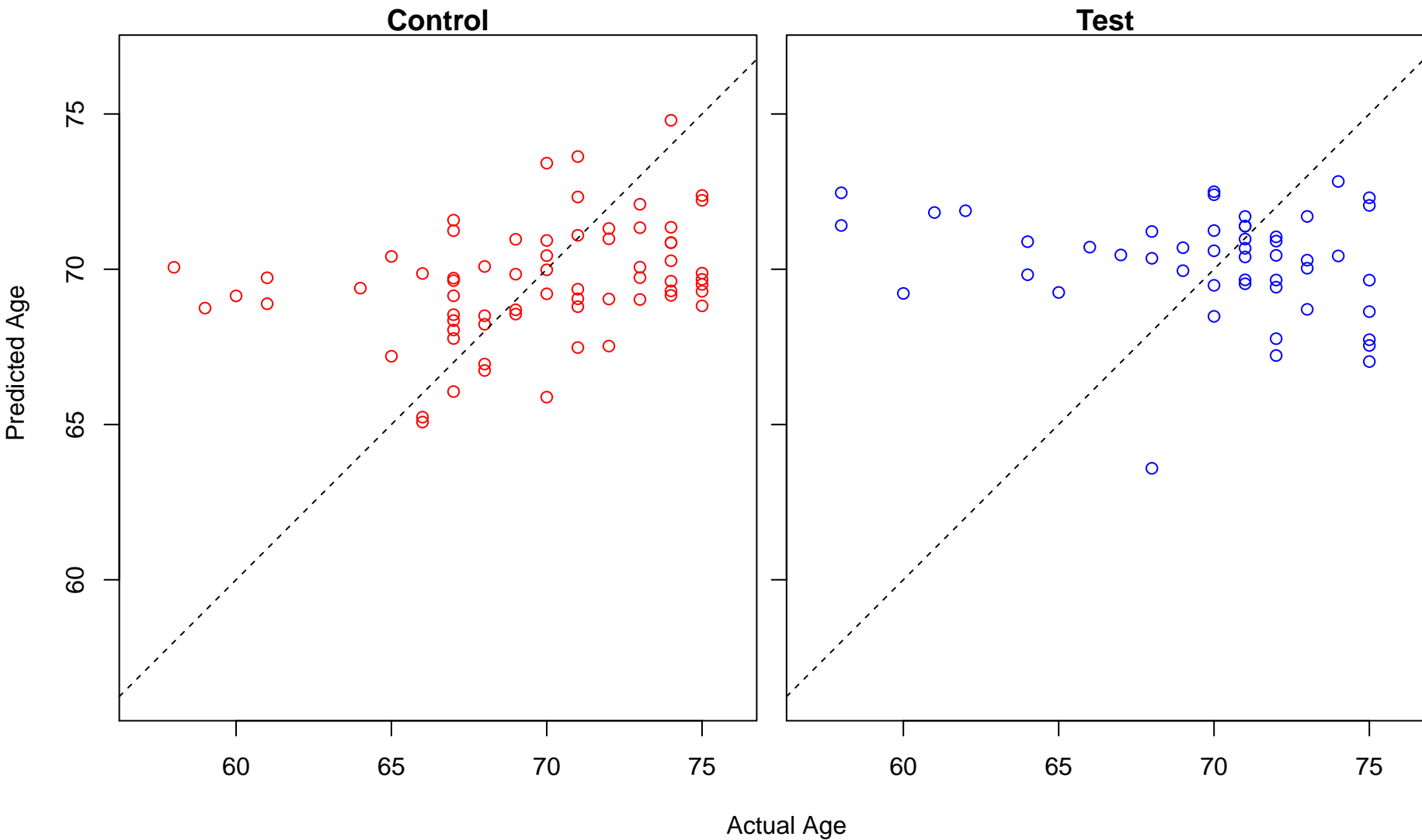
response to denervation involved in regulation of muscle adaptation (Score: 0.360177)



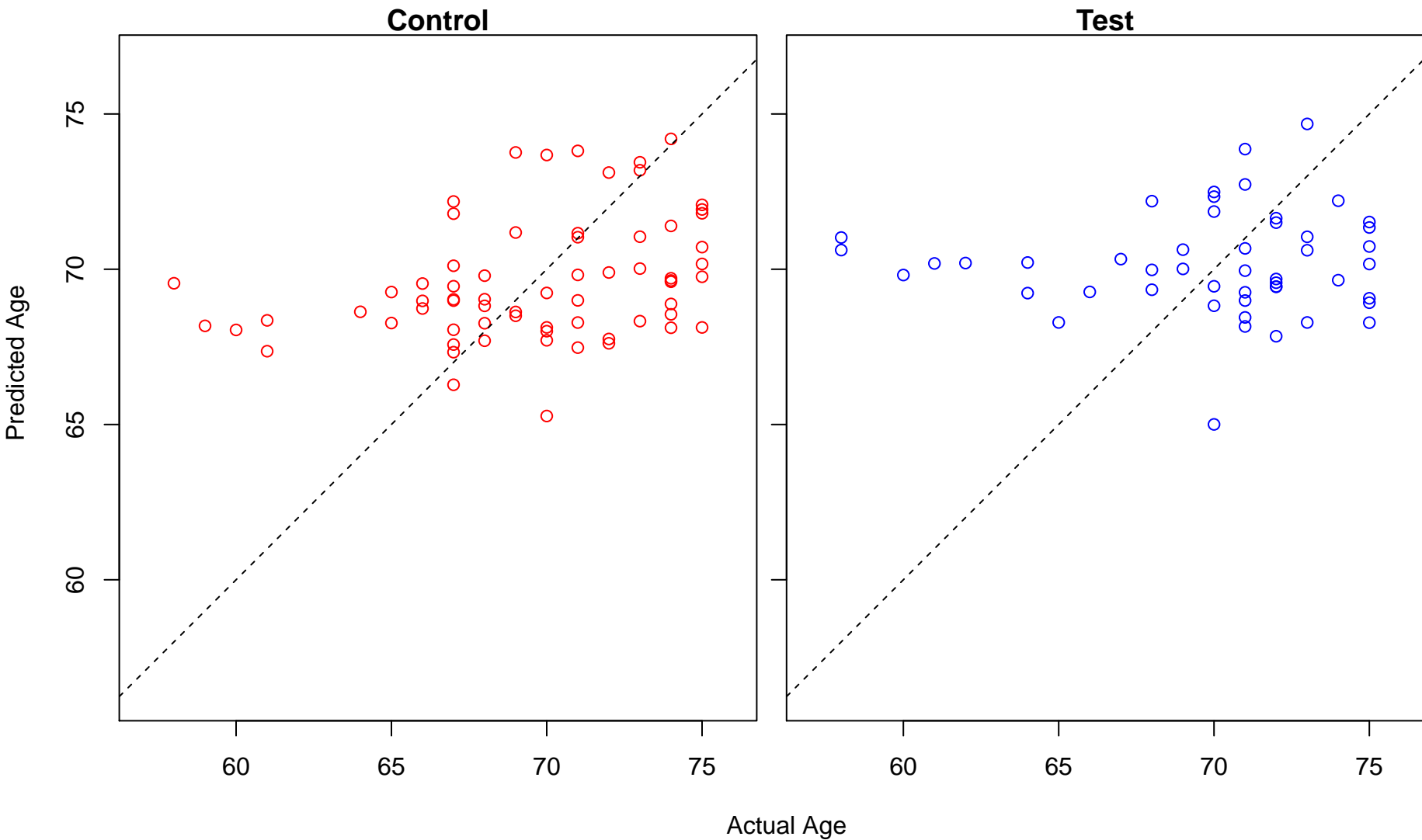
regulation of DNA methylation (Score: 0.359743)



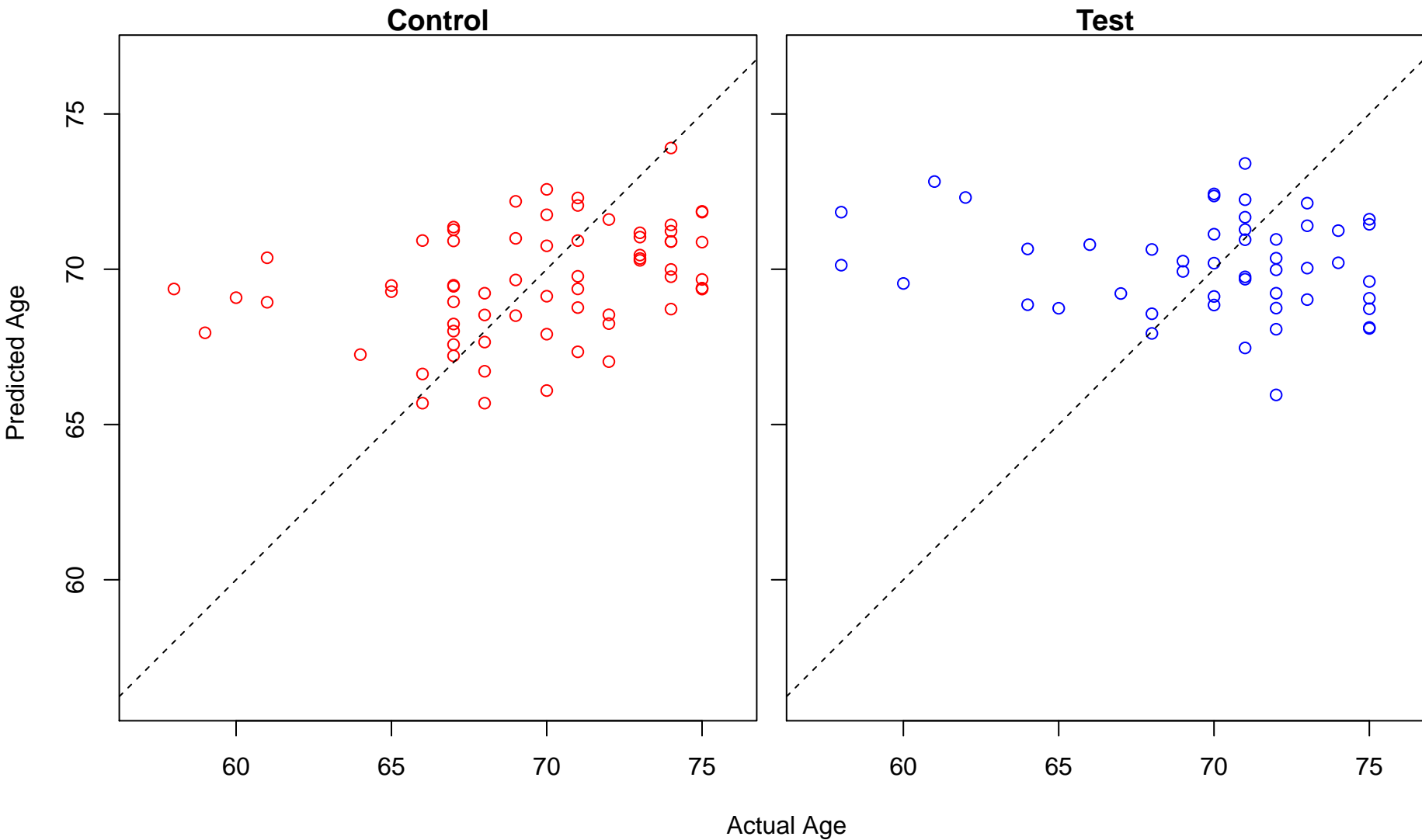
positive regulation of fatty acid biosynthetic process (Score: 0.359564)



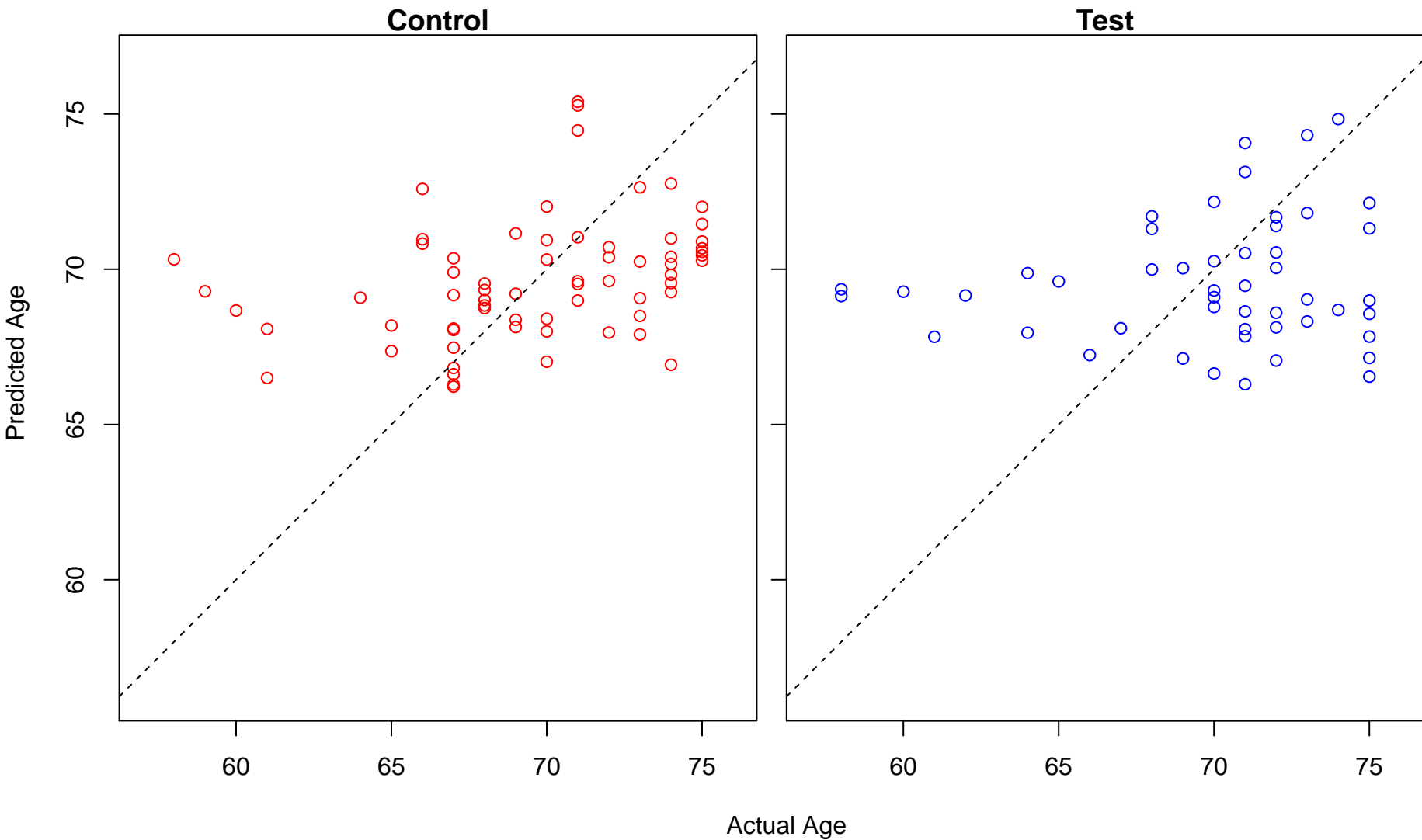
megakaryocyte differentiation (Score: 0.359510)



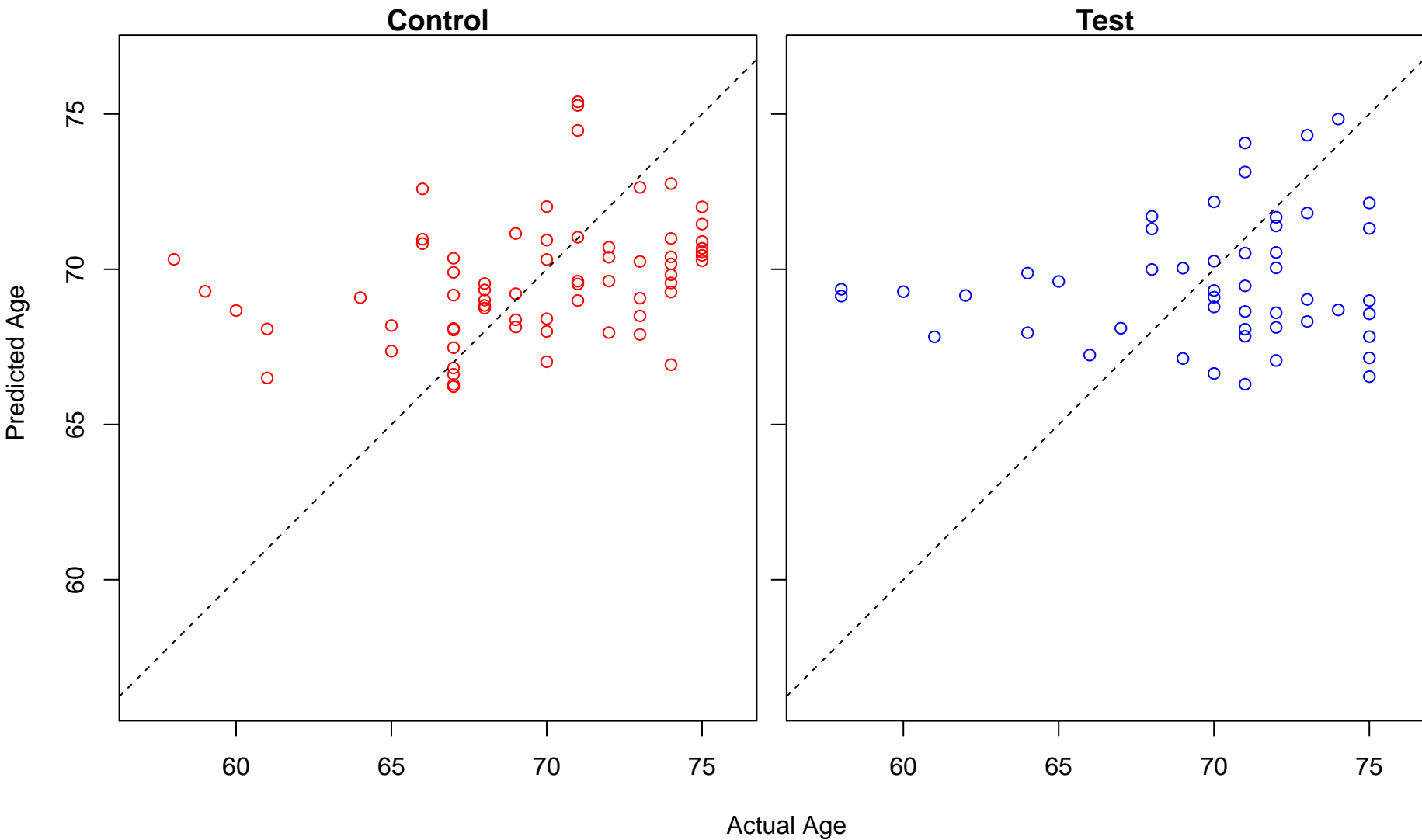
spleen development (Score: 0.357318)



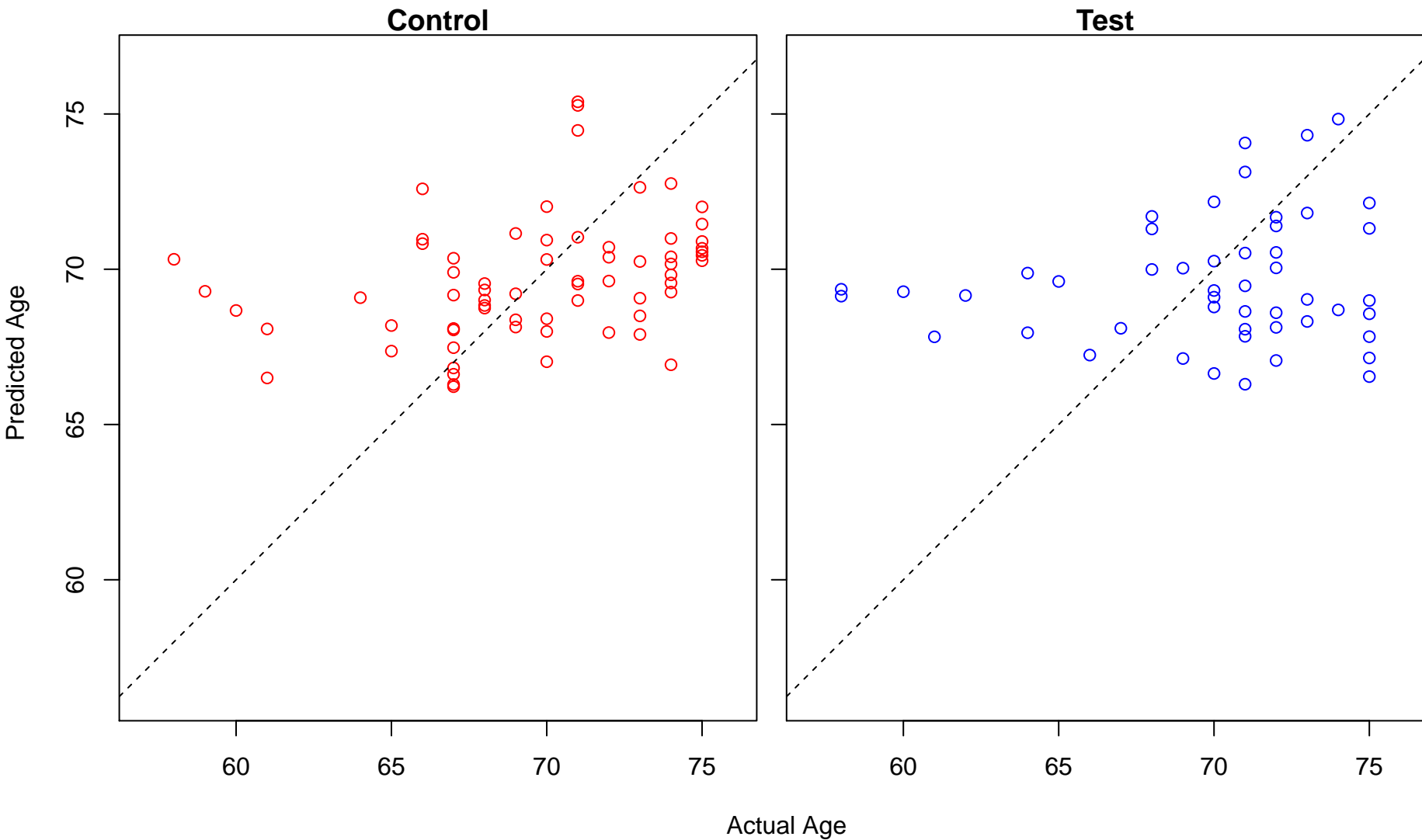
response to defenses of other organism involved in symbiotic interaction (Score: 0.356574)



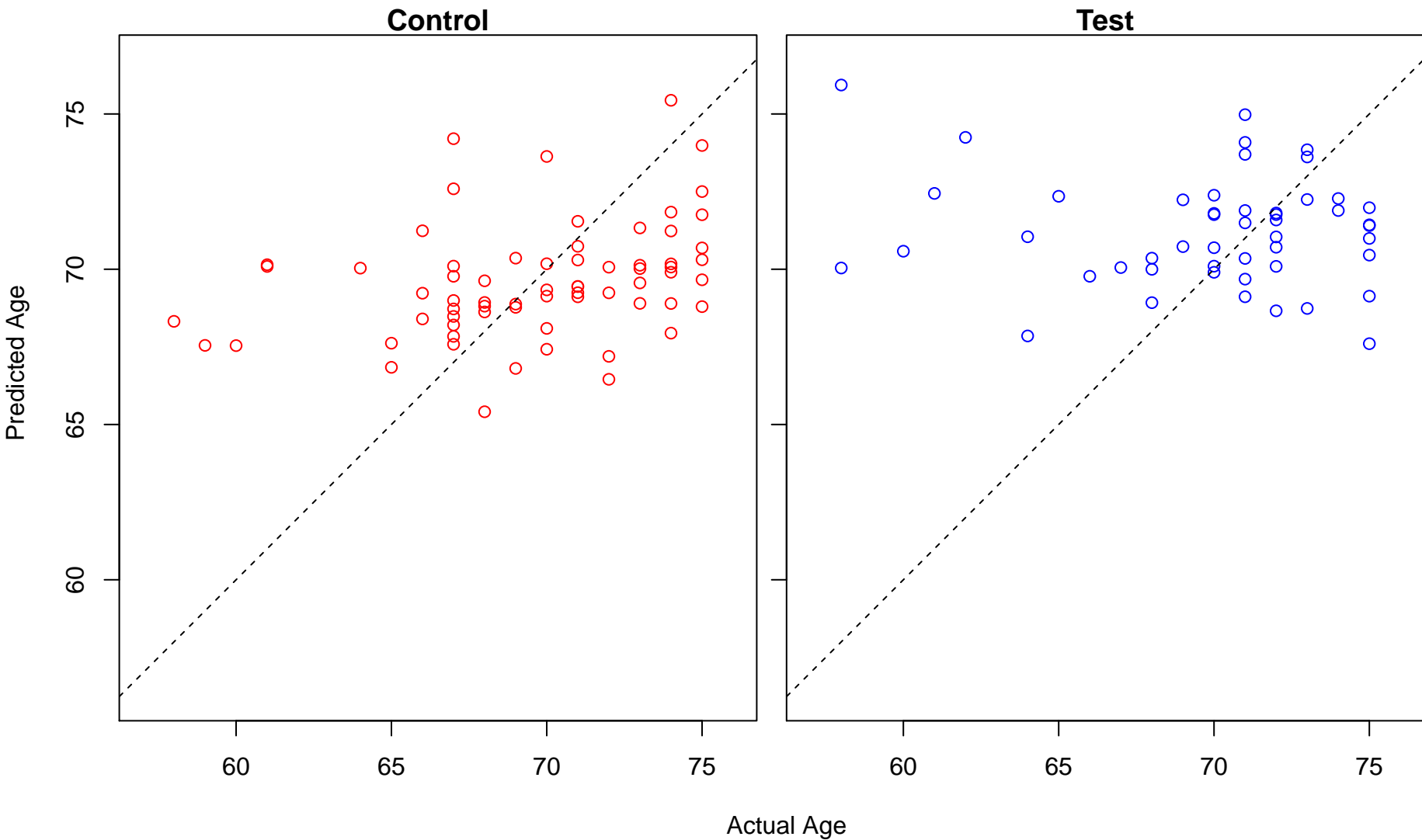
response to host defenses (Score: 0.356574)



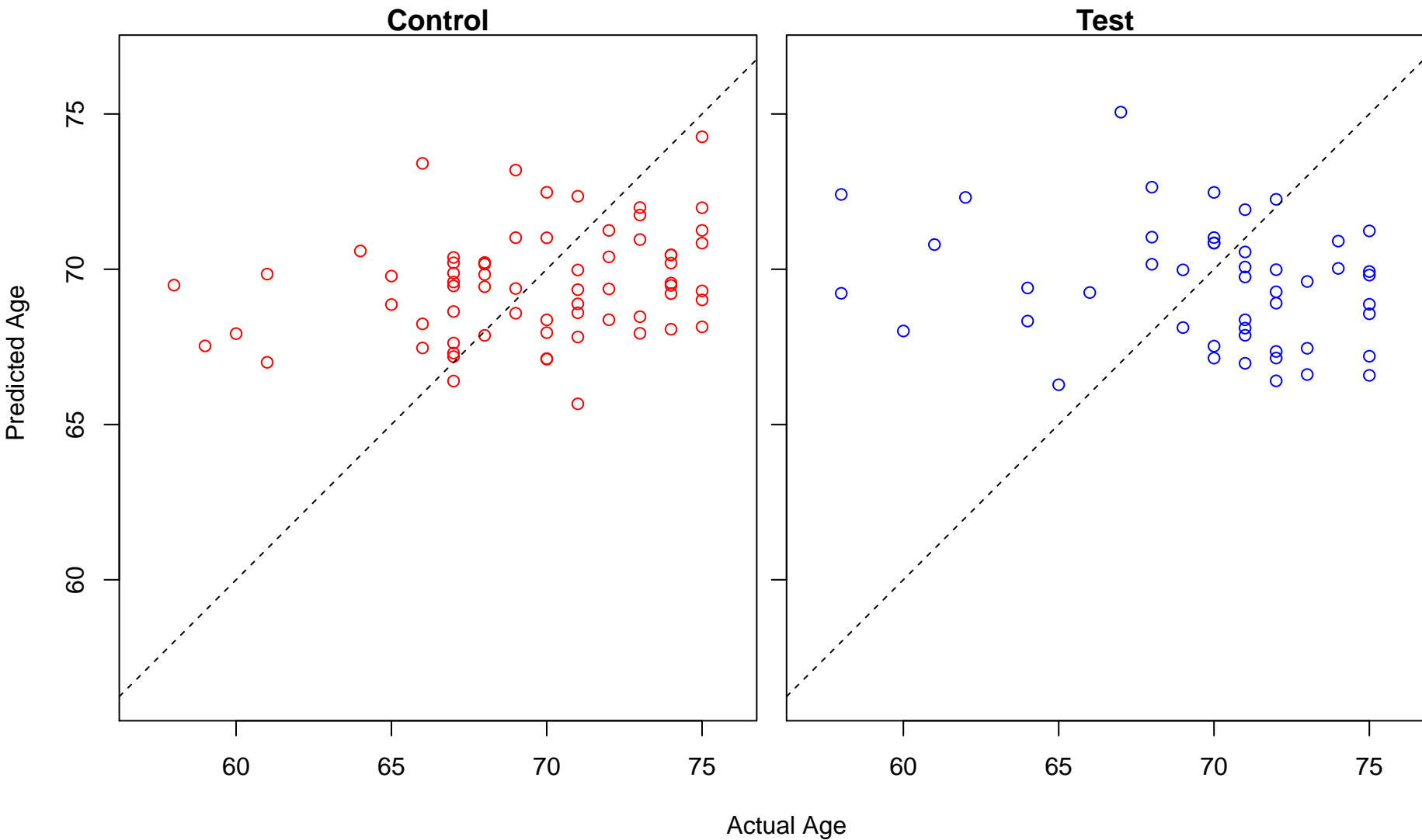
response to host (Score: 0.356574)



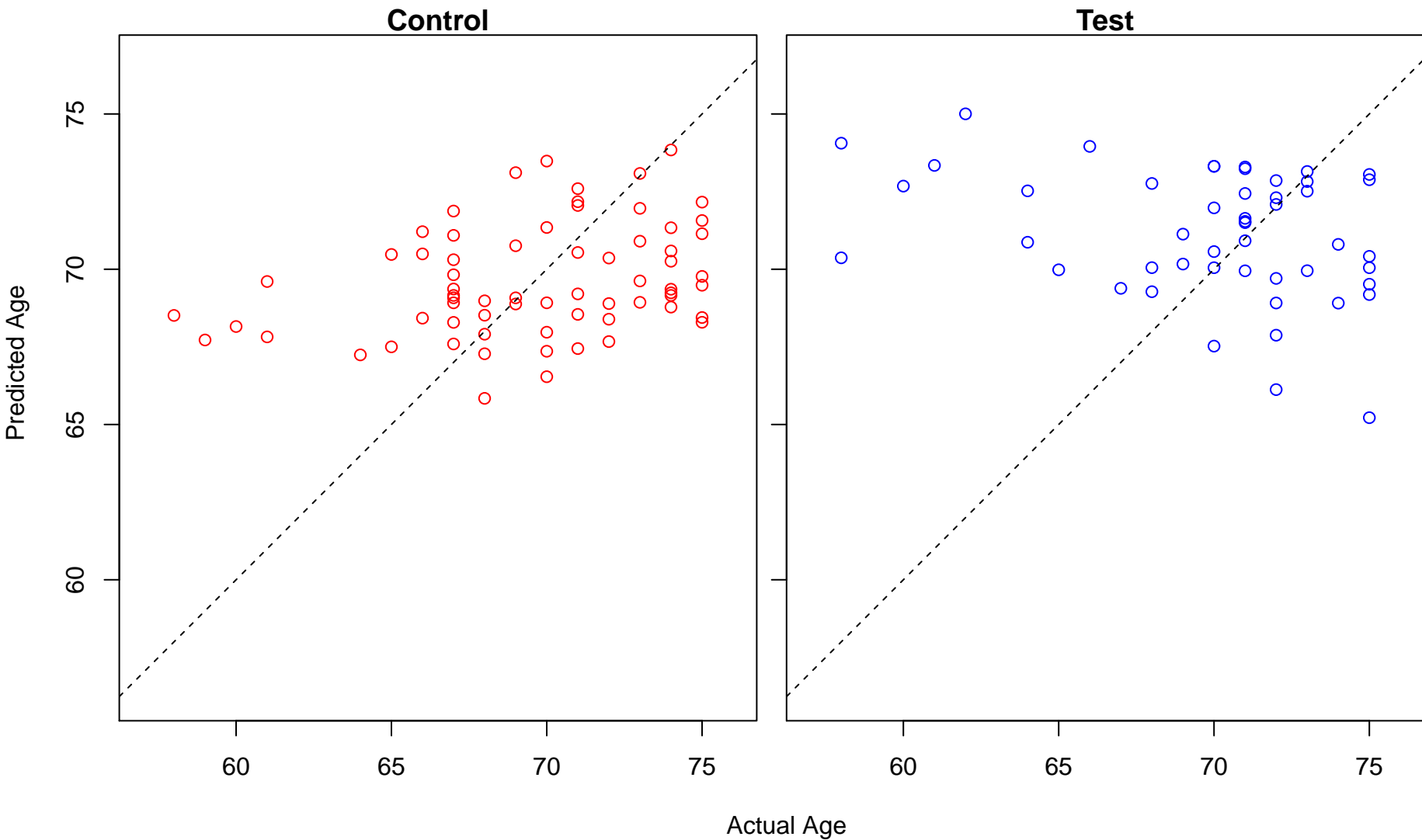
neuron remodeling (Score: 0.356347)



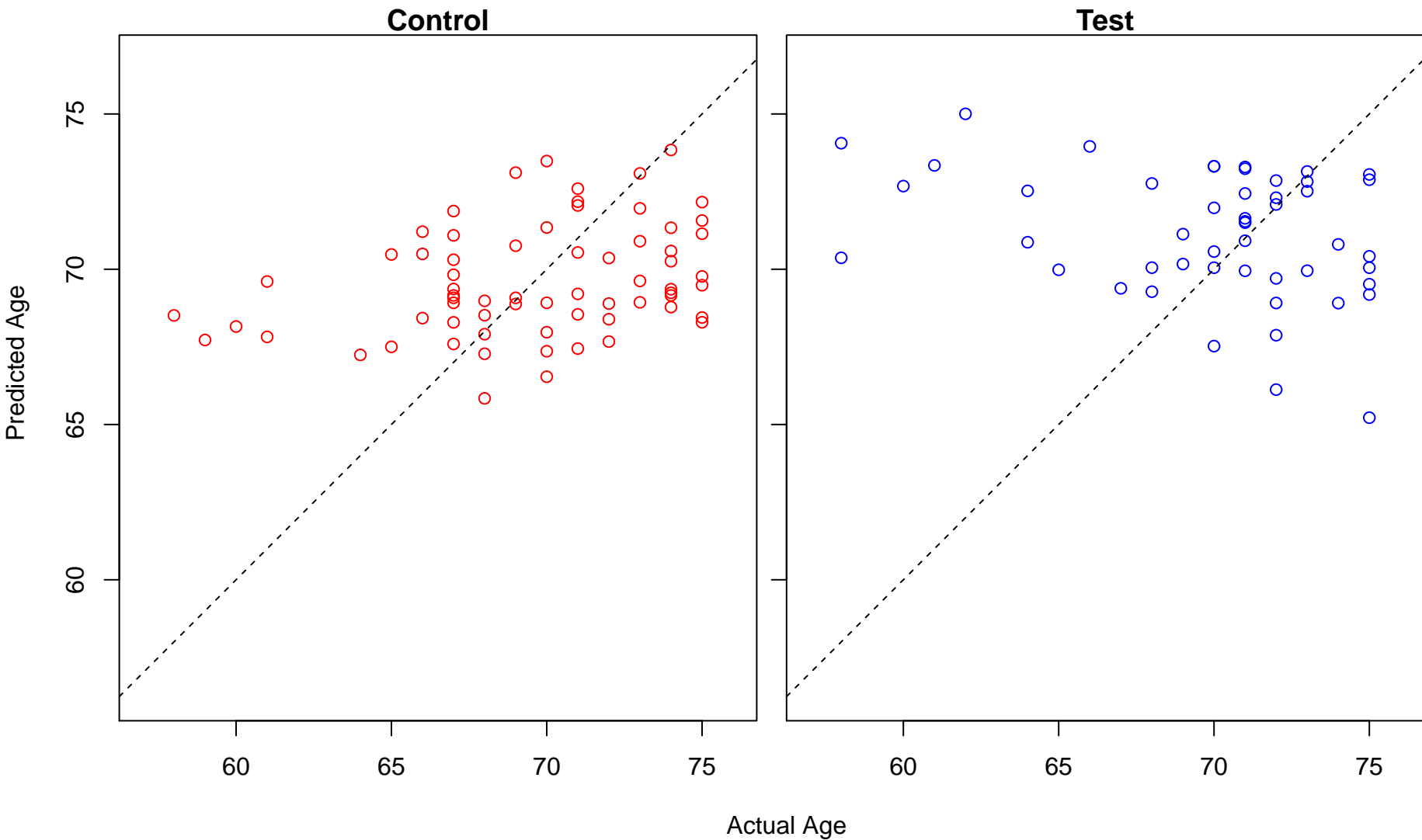
response to ischemia (Score: 0.355133)



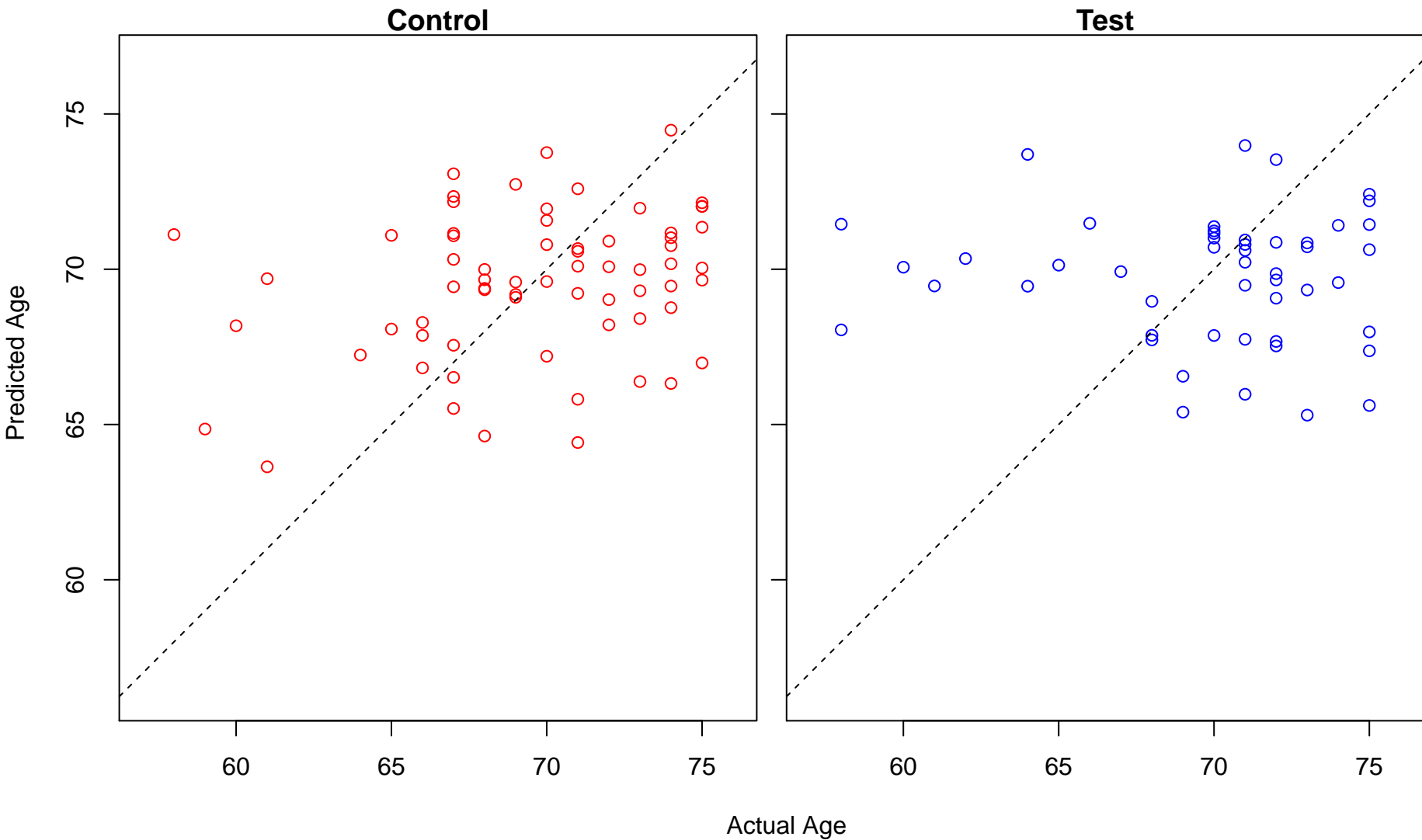
inorganic cation import into cell (Score: 0.354857)



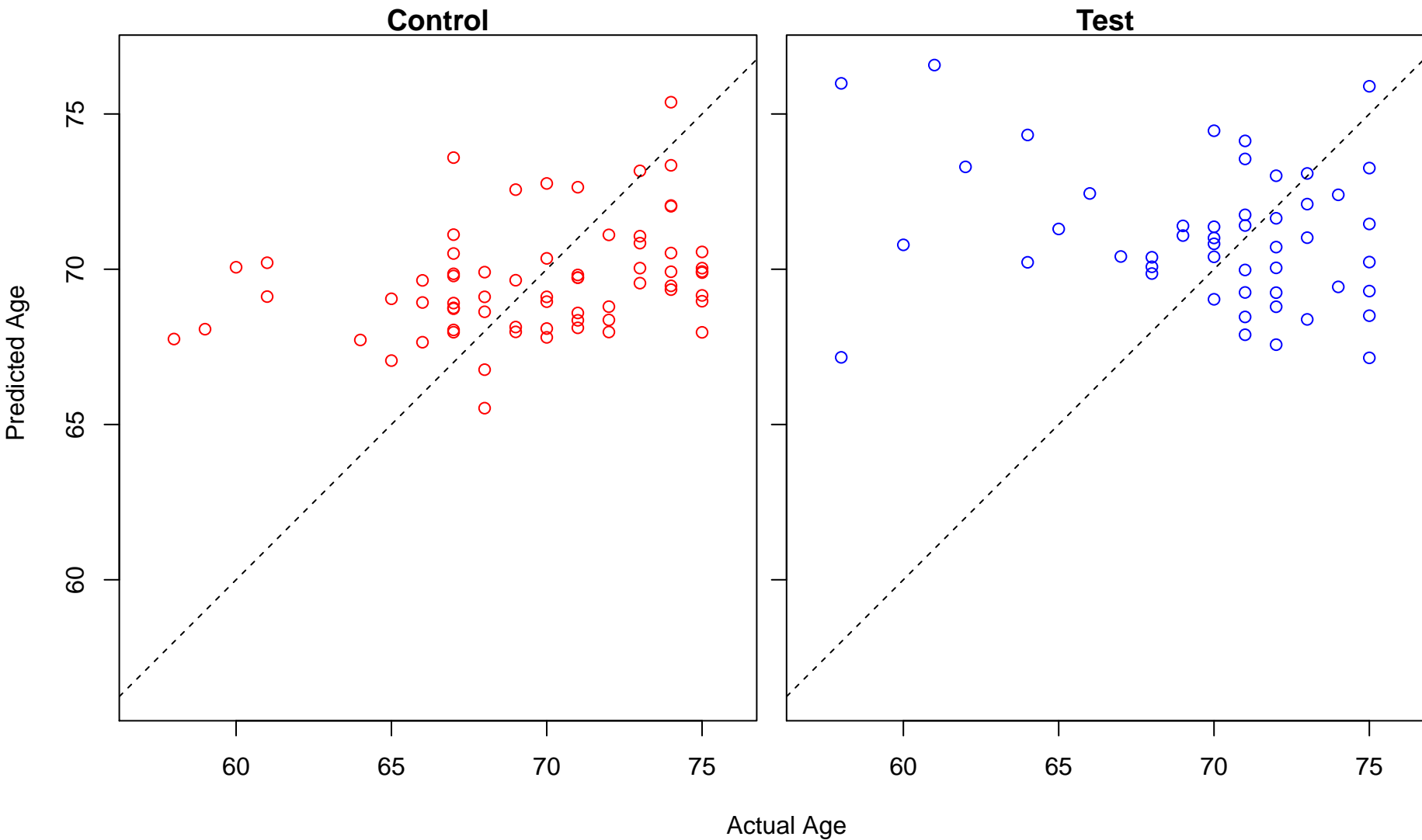
inorganic ion import into cell (Score: 0.354857)



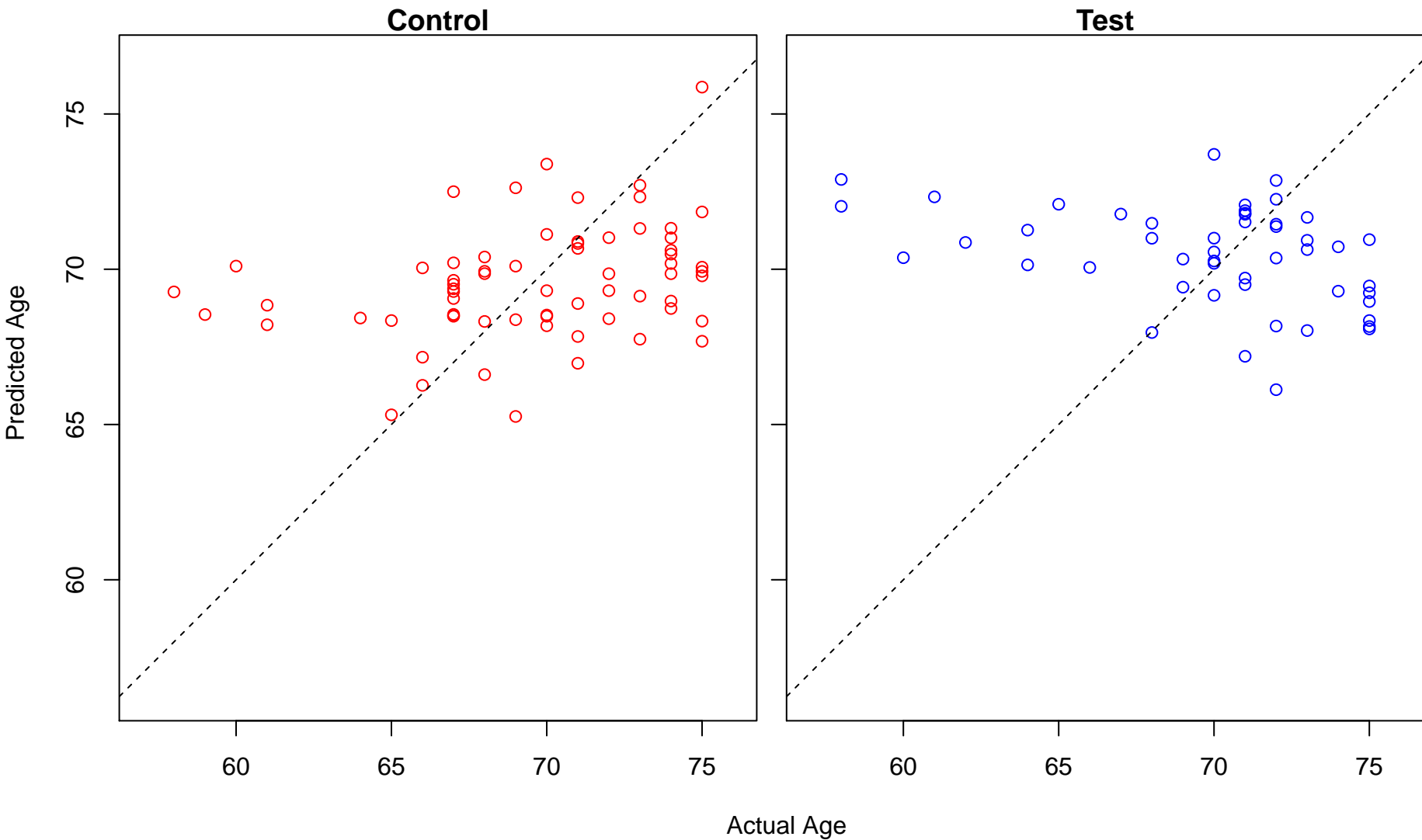
mesodermal cell fate commitment (Score: 0.354221)



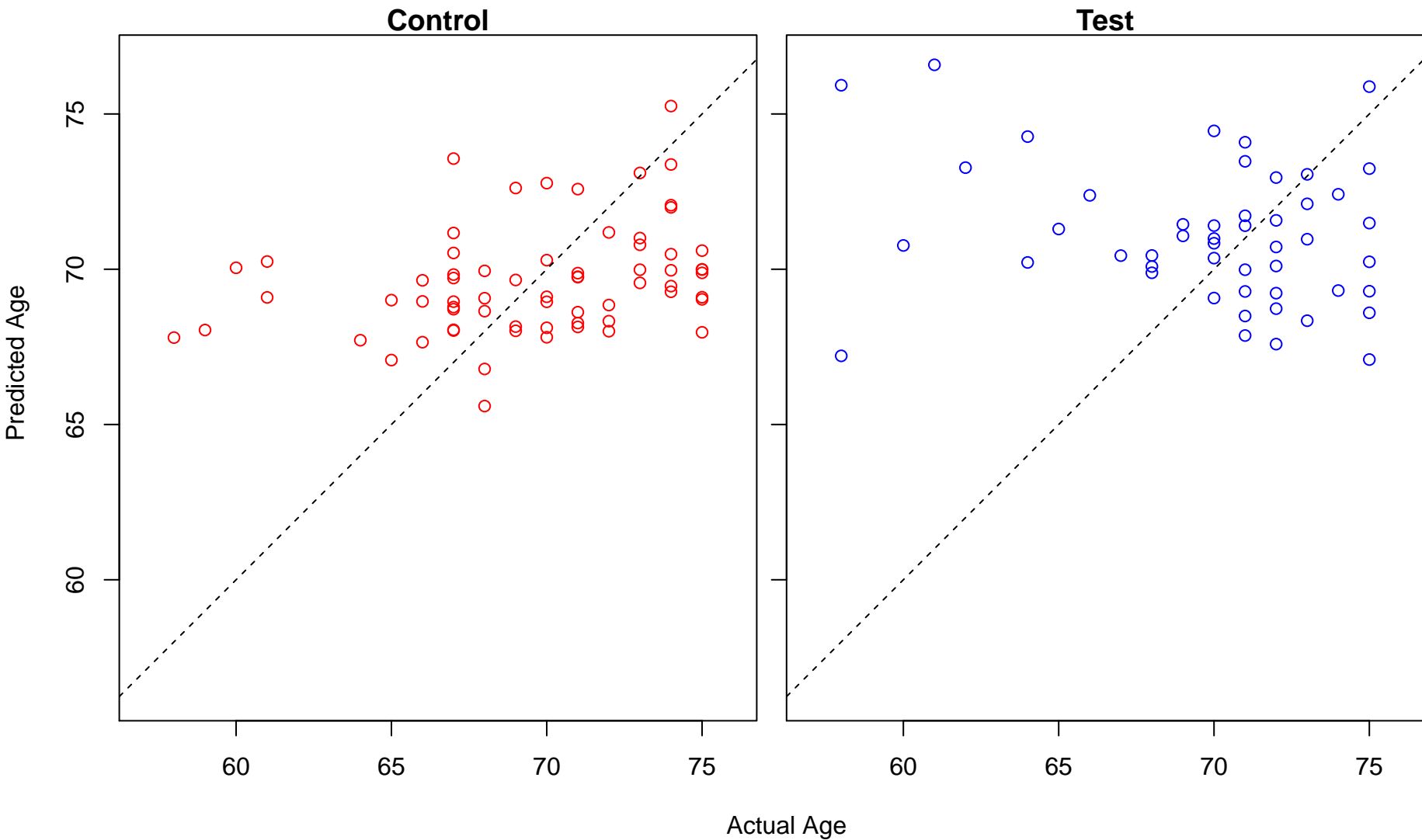
negative regulation of peptide hormone secretion (Score: 0.354206)



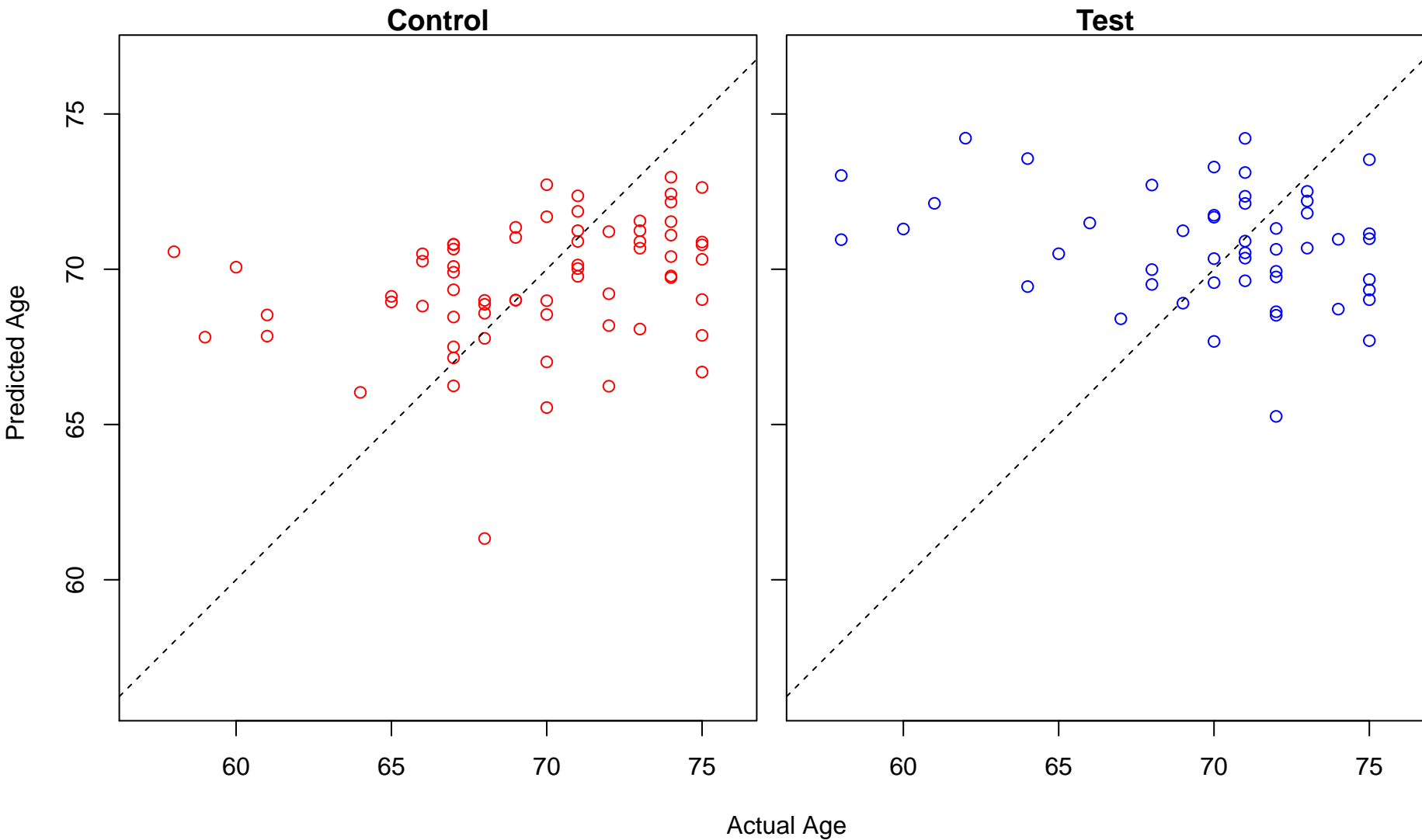
female meiotic division (Score: 0.352643)



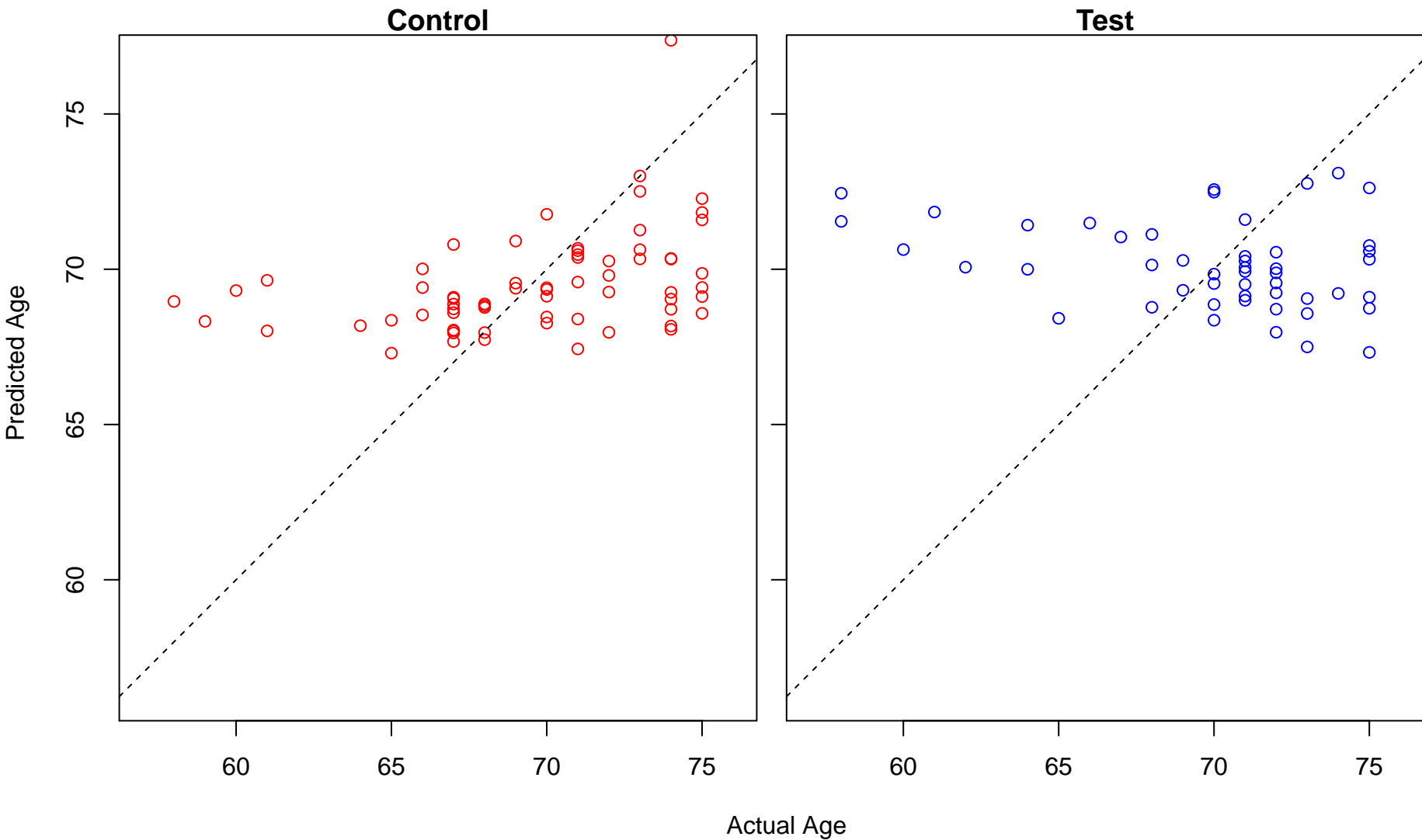
negative regulation of insulin secretion (Score: 0.350594)



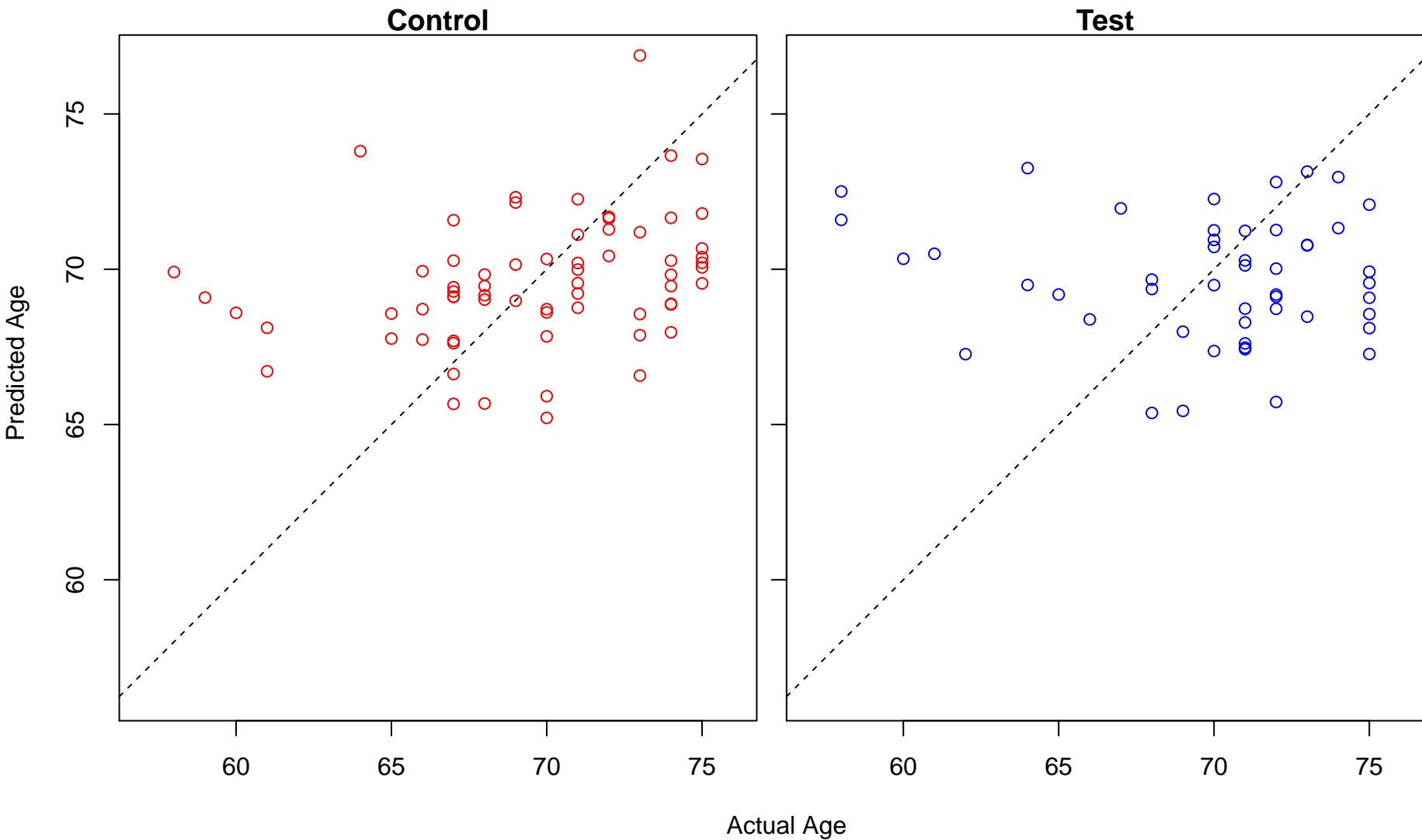
response to copper ion (Score: 0.349618)



cellular response to iron ion (Score: 0.349108)

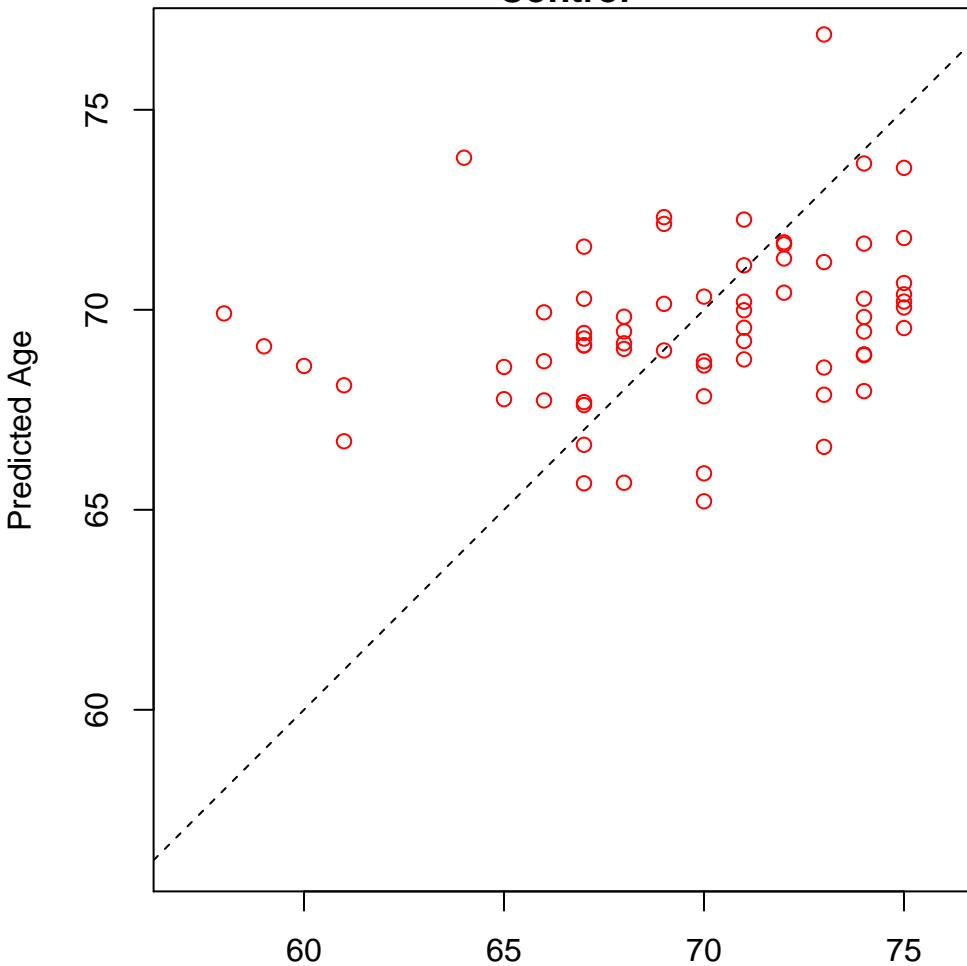


dolichyl diphosphate biosynthetic process (Score: 0.349089)

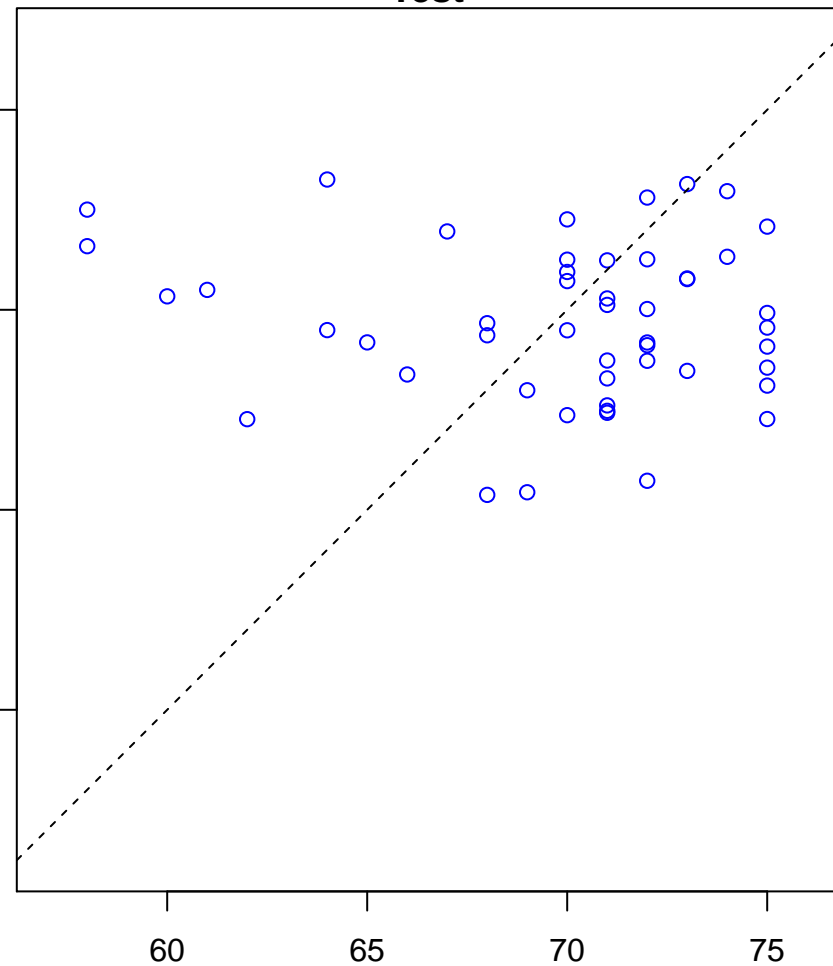


dolichyl diphosphate metabolic process (Score: 0.349089)

Control

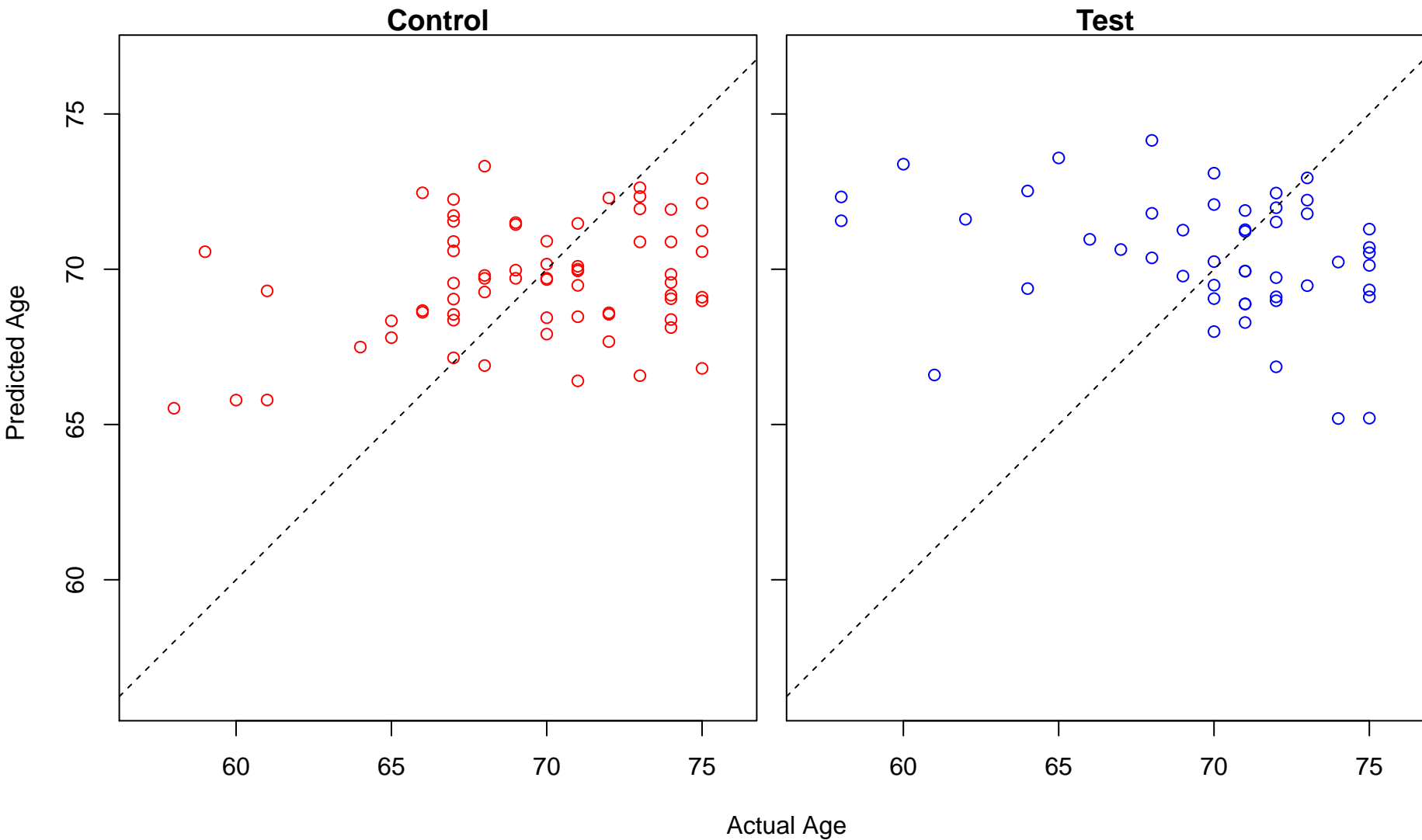


Test

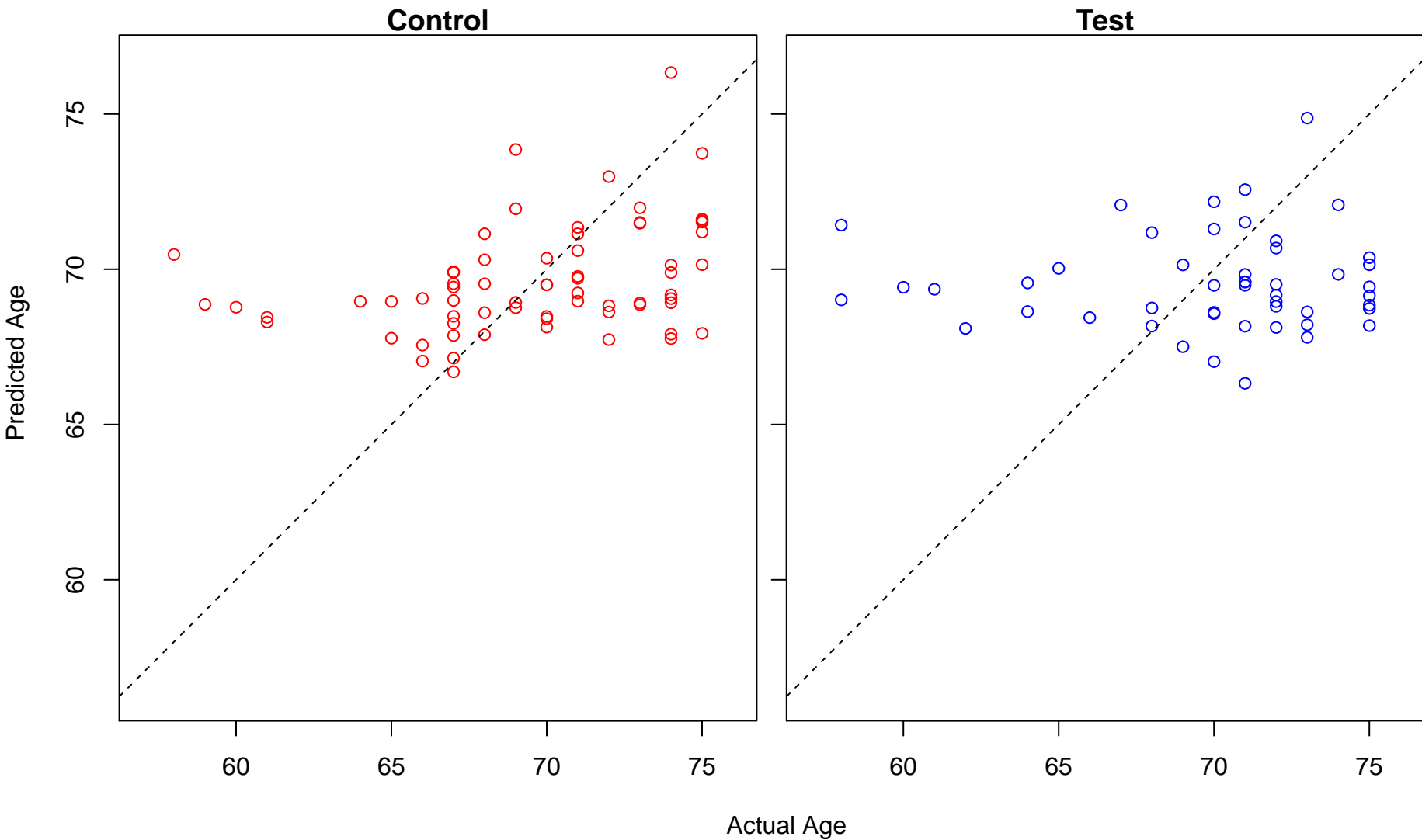


Actual Age

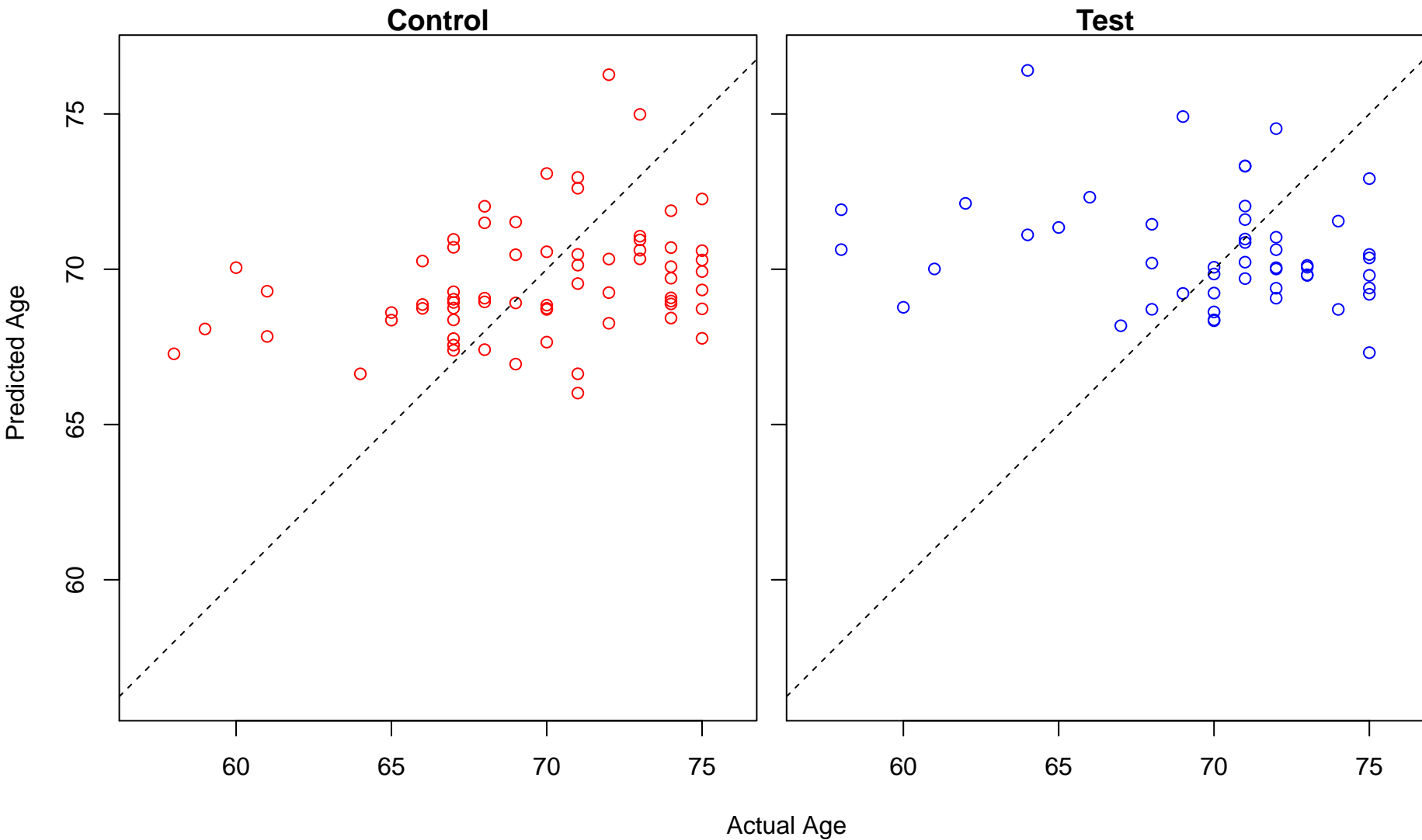
sensory perception of taste (Score: 0.348883)



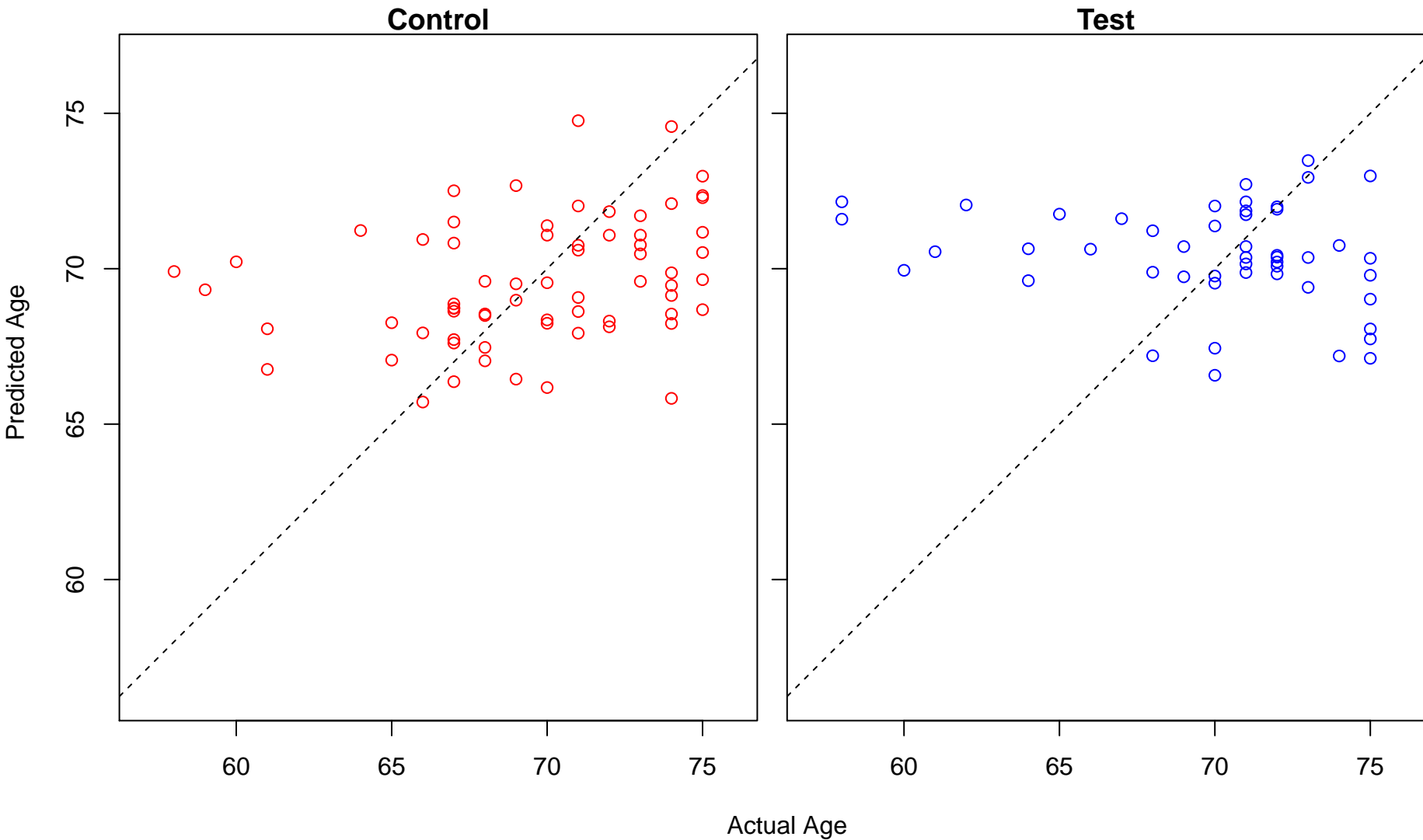
viral release from host cell (Score: 0.348656)



maintenance of organ identity (Score: 0.348326)

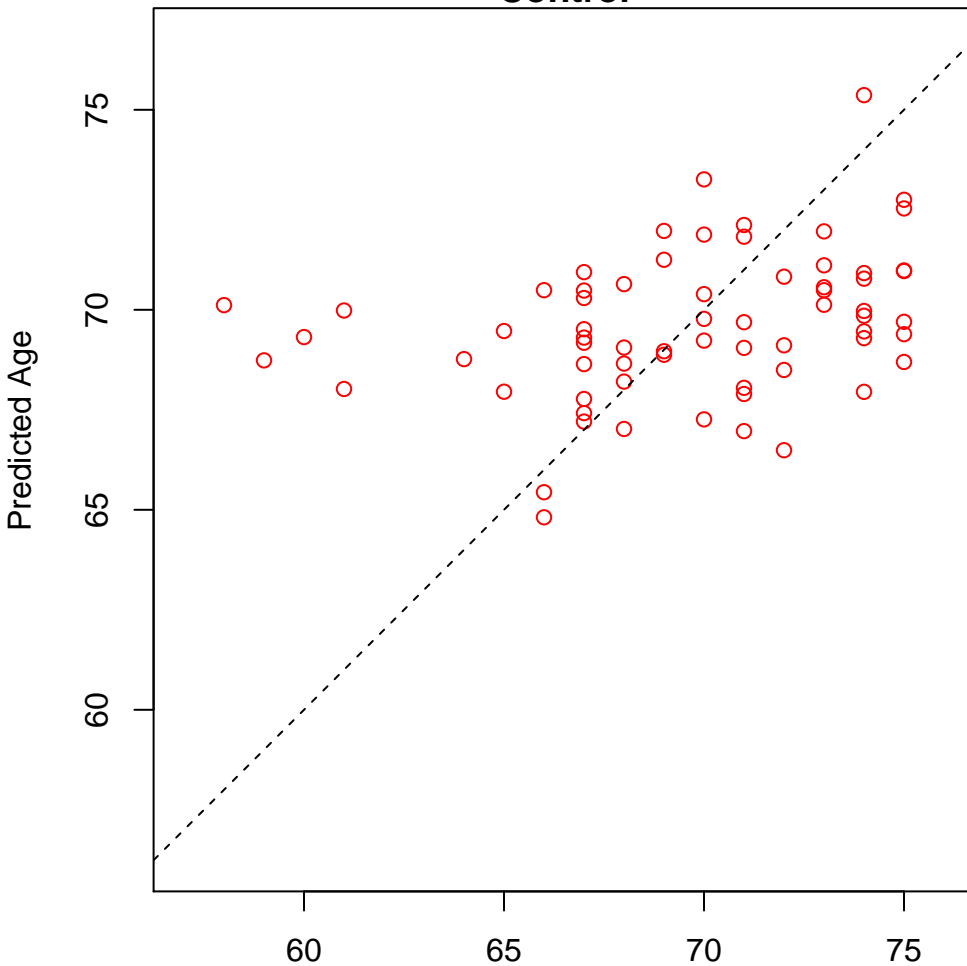


negative regulation of cAMP-dependent protein kinase activity (Score: 0.344858)

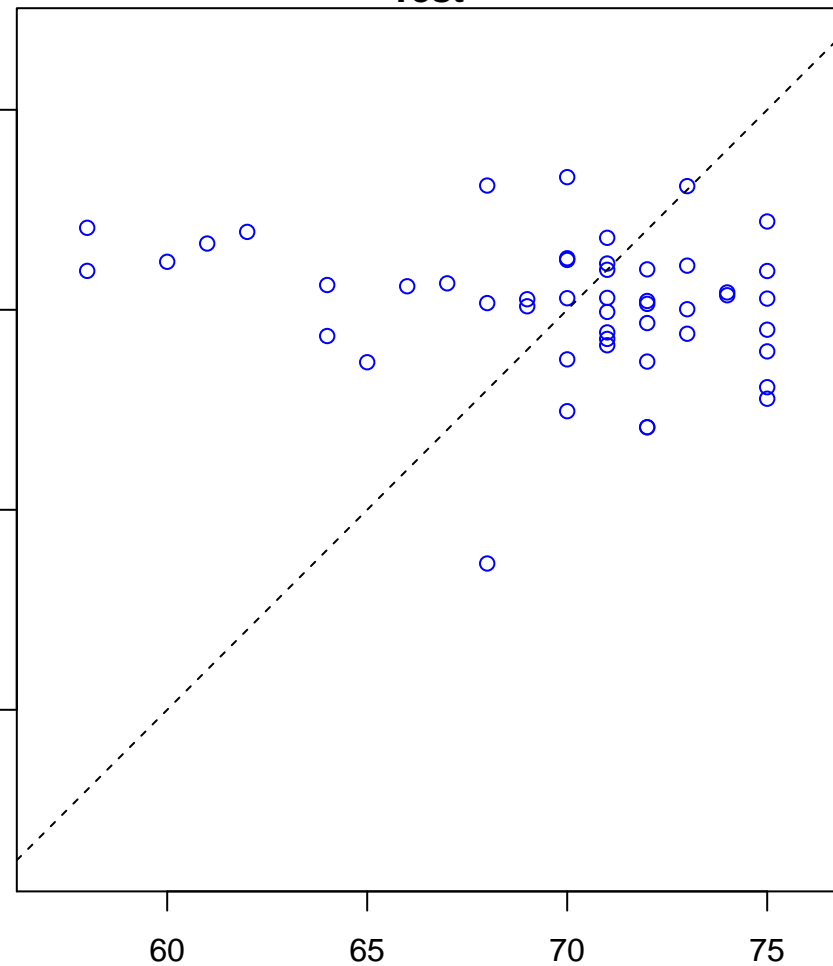


positive regulation of receptor recycling (Score: 0.343121)

Control

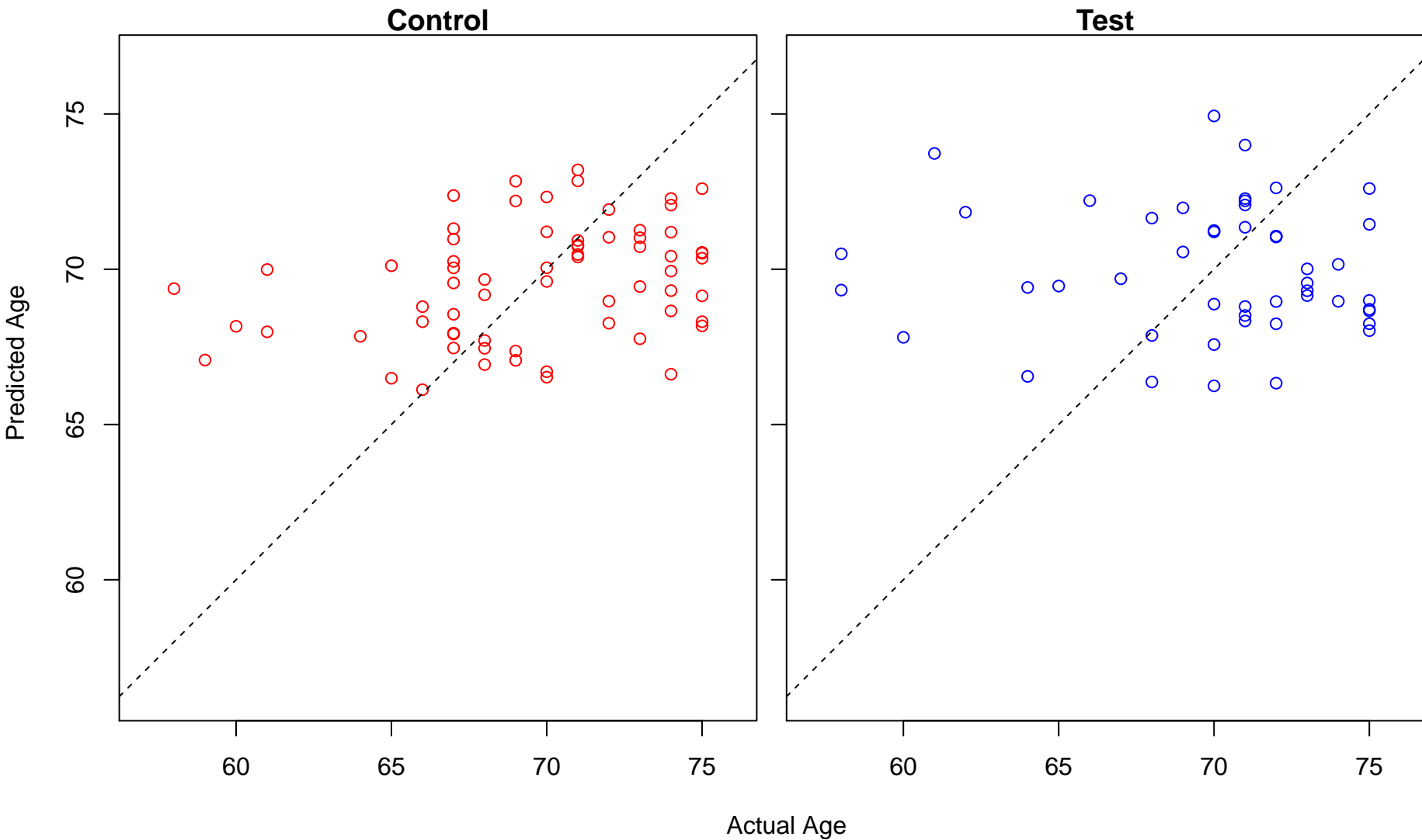


Test

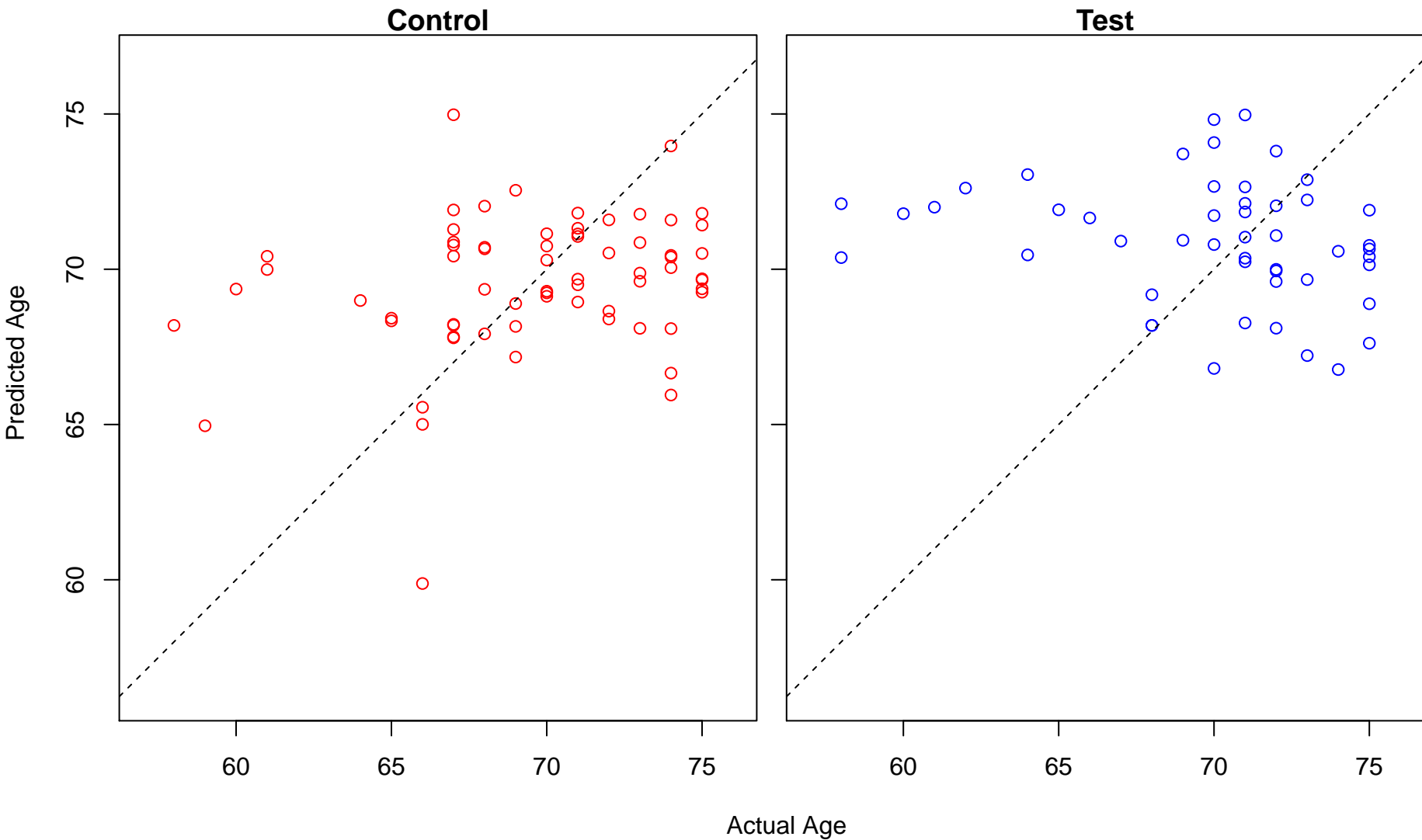


Actual Age

complement activation (Score: 0.342849)

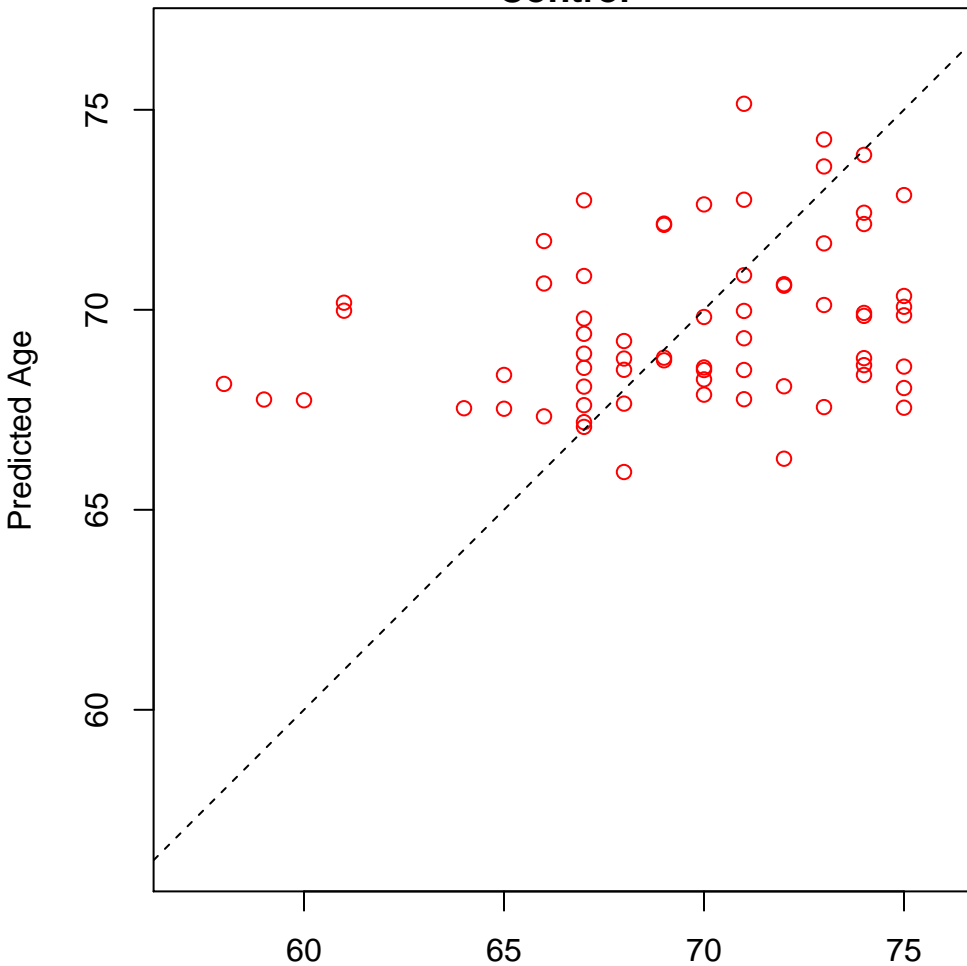


negative regulation of complement activation (Score: 0.342577)

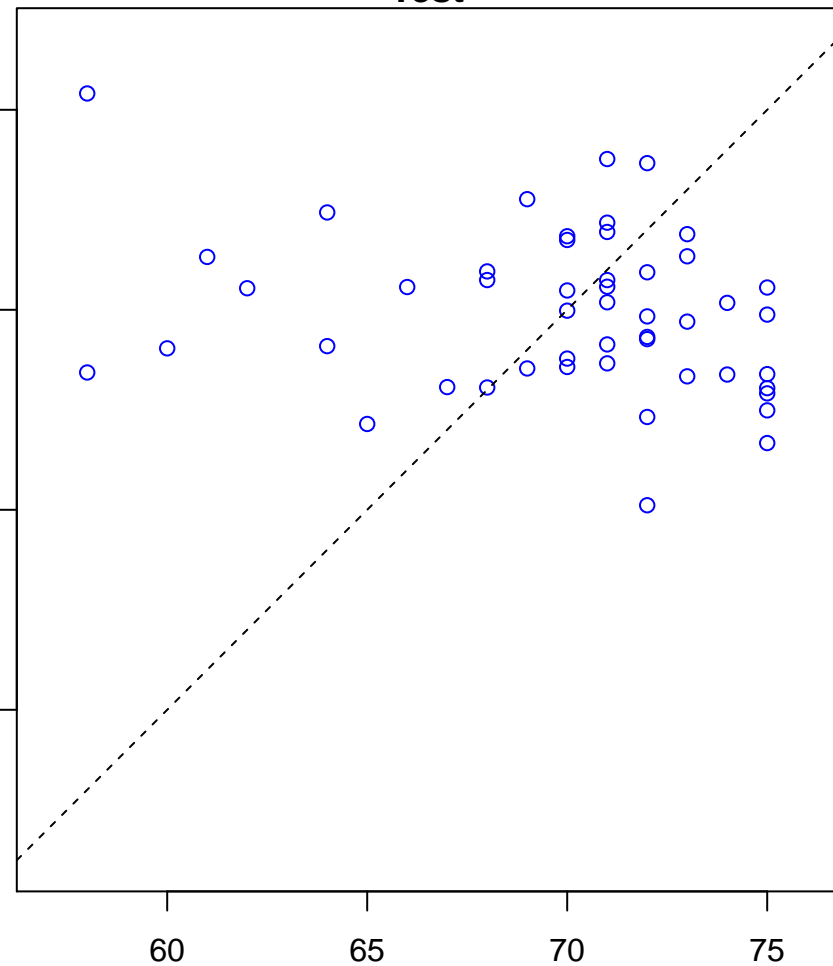


regulation of mesonephros development (Score: 0.342299)

Control



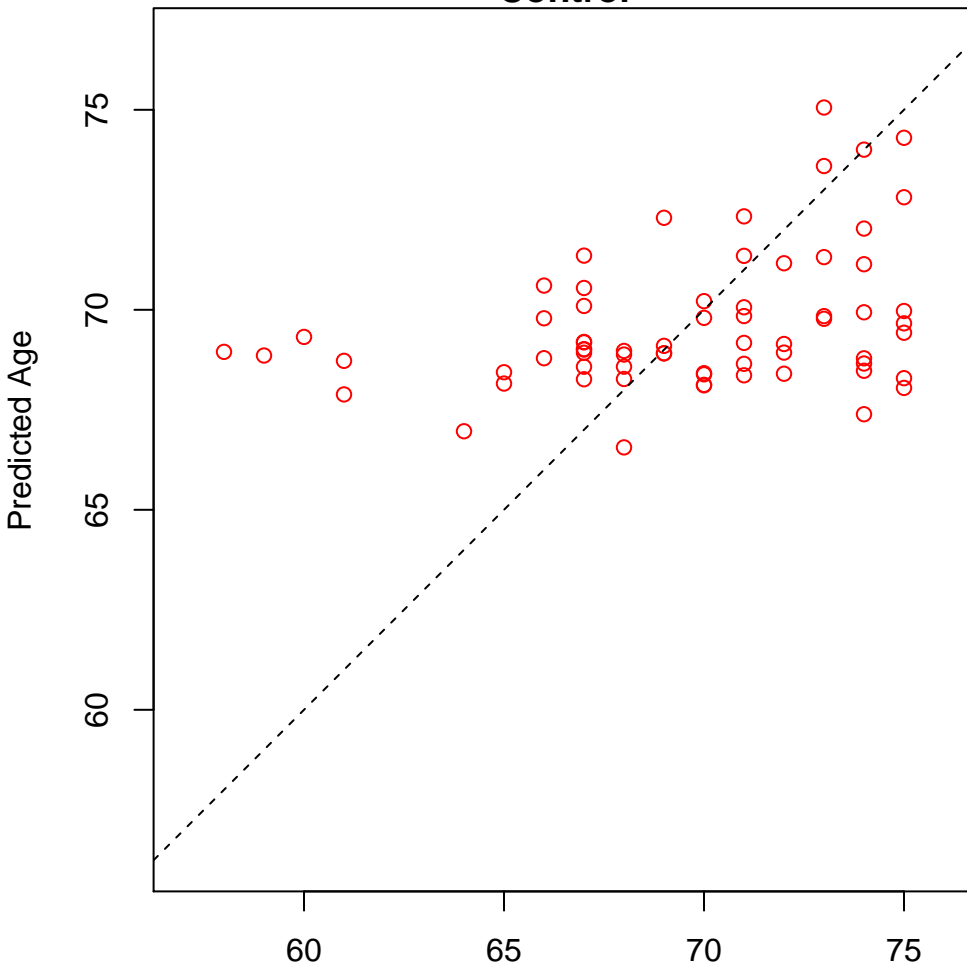
Test



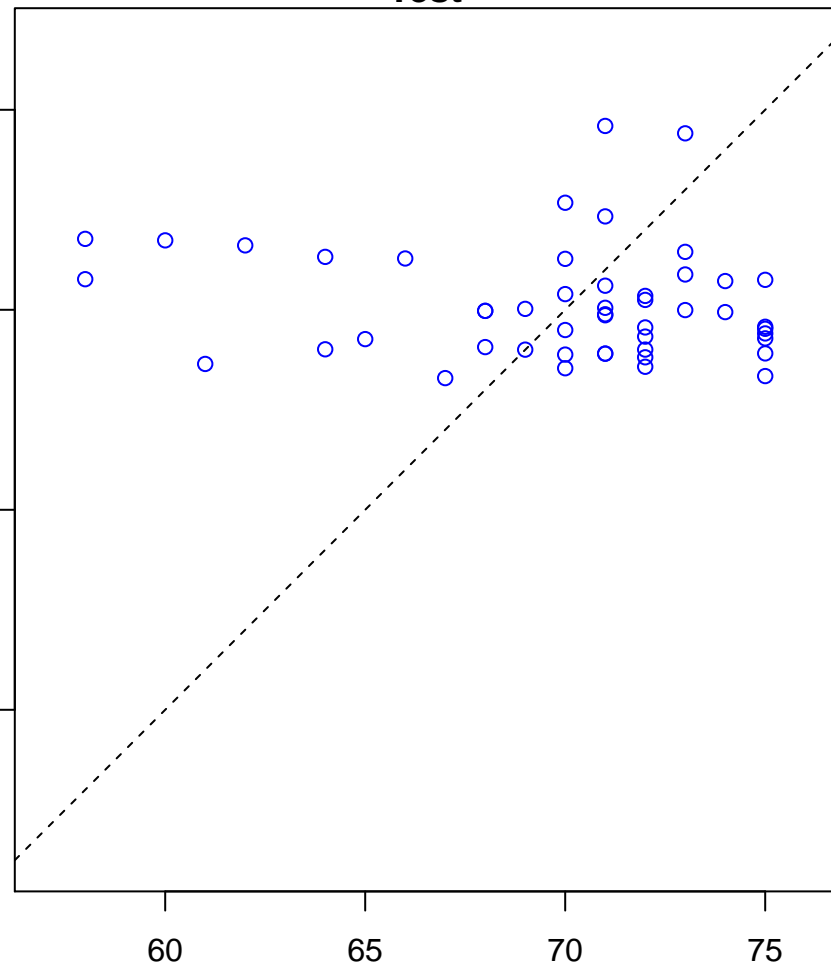
Actual Age

long-chain fatty acid catabolic process (Score: 0.341753)

Control

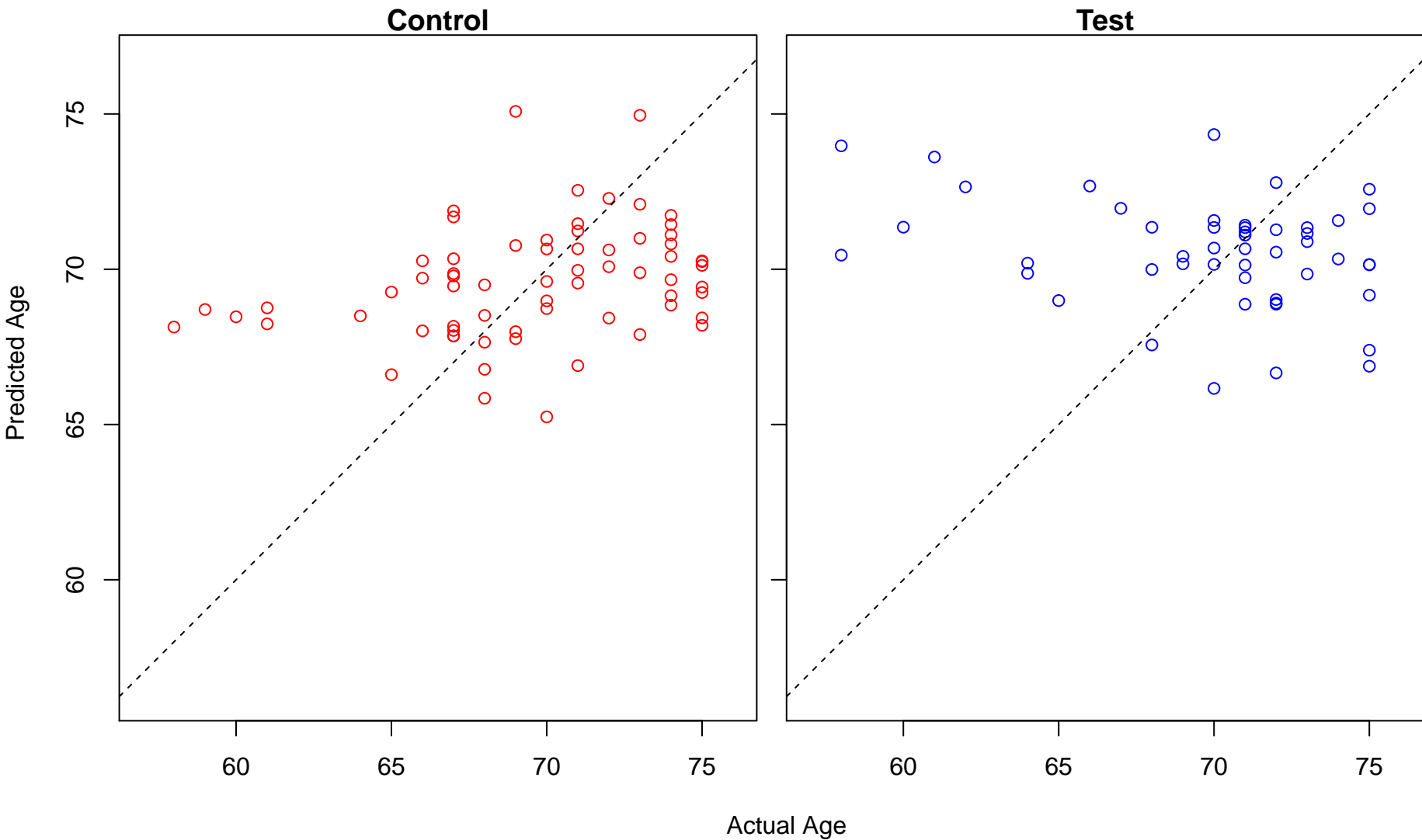


Test

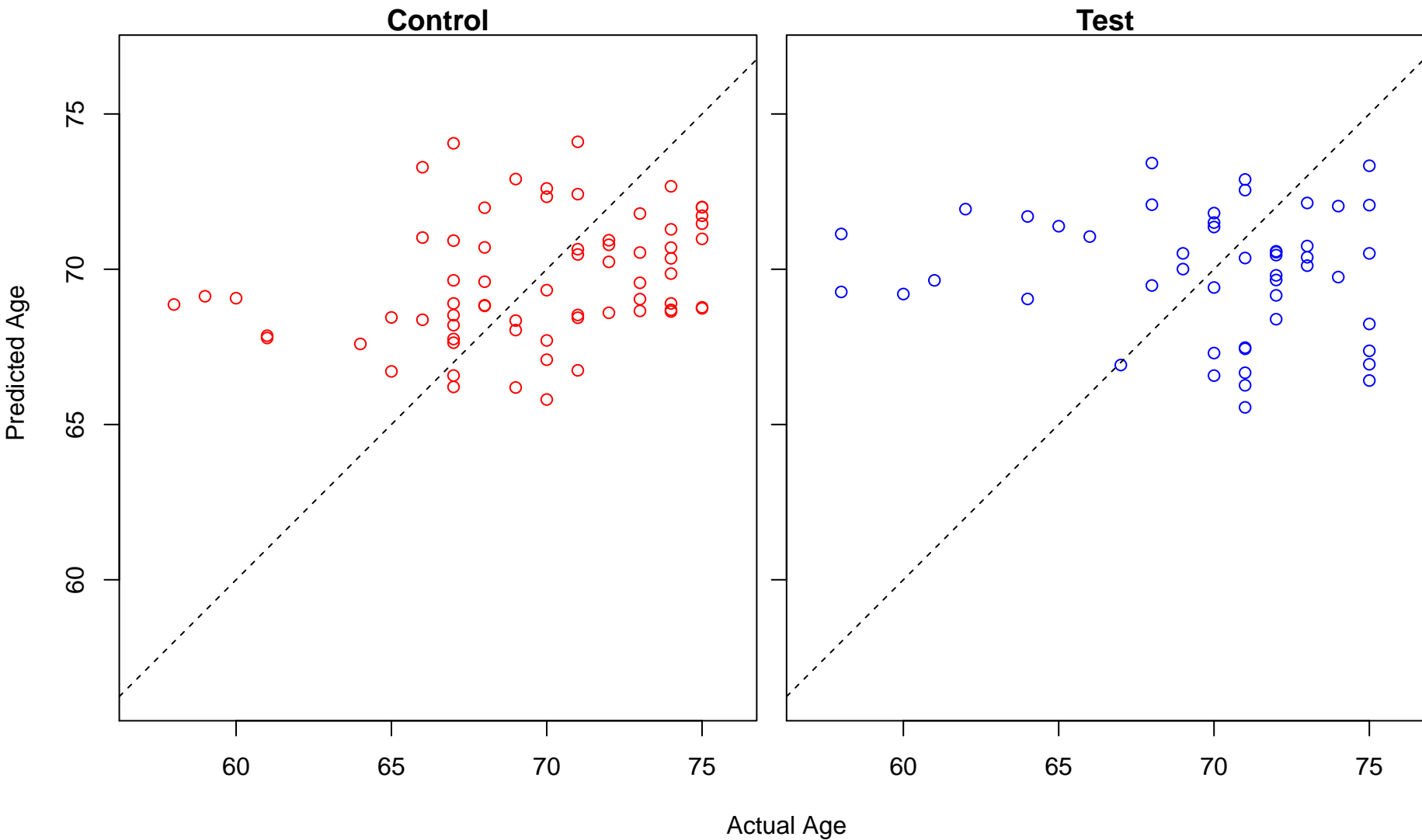


Actual Age

sphingolipid catabolic process (Score: 0.341511)

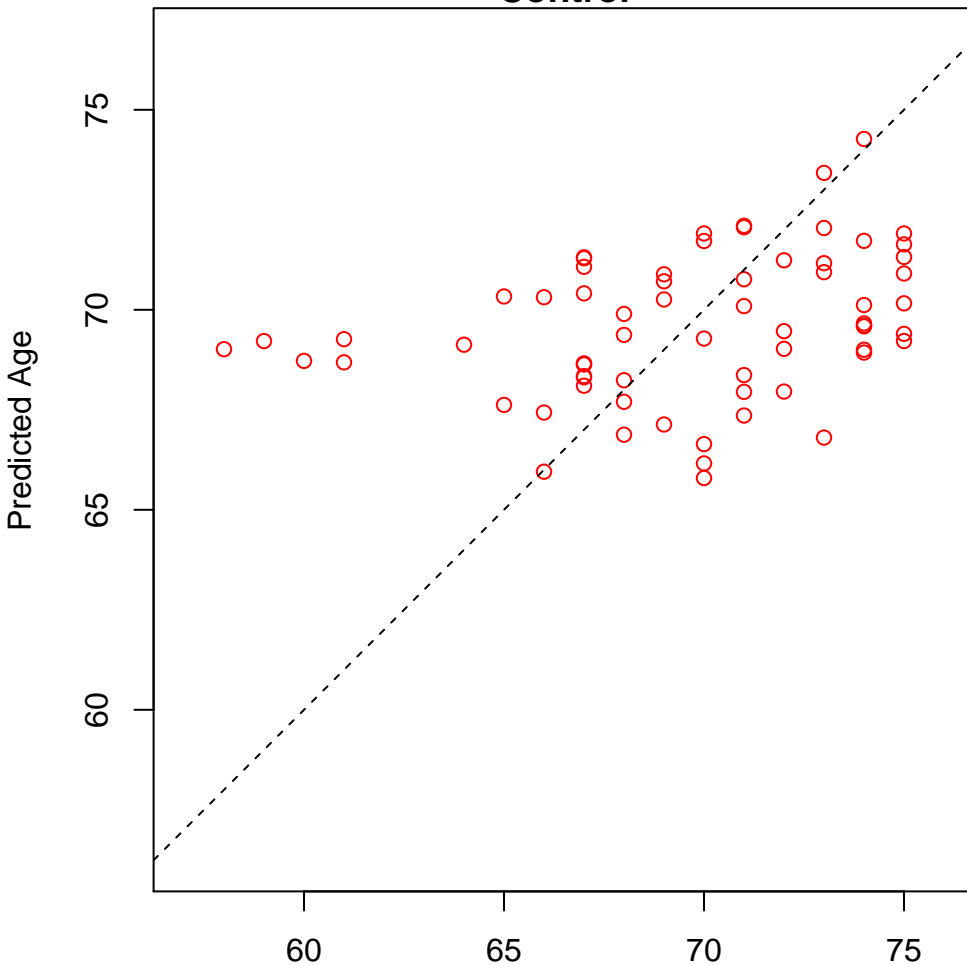


nodal signaling pathway (Score: 0.339958)

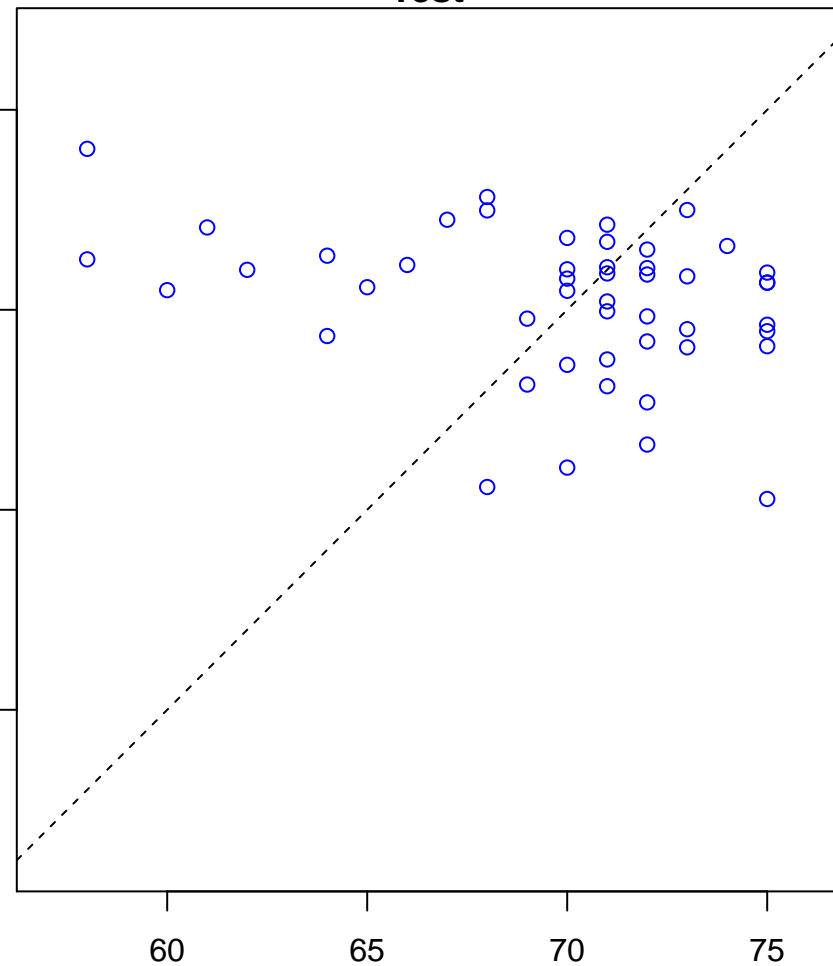


endodermal cell fate commitment (Score: 0.339565)

Control

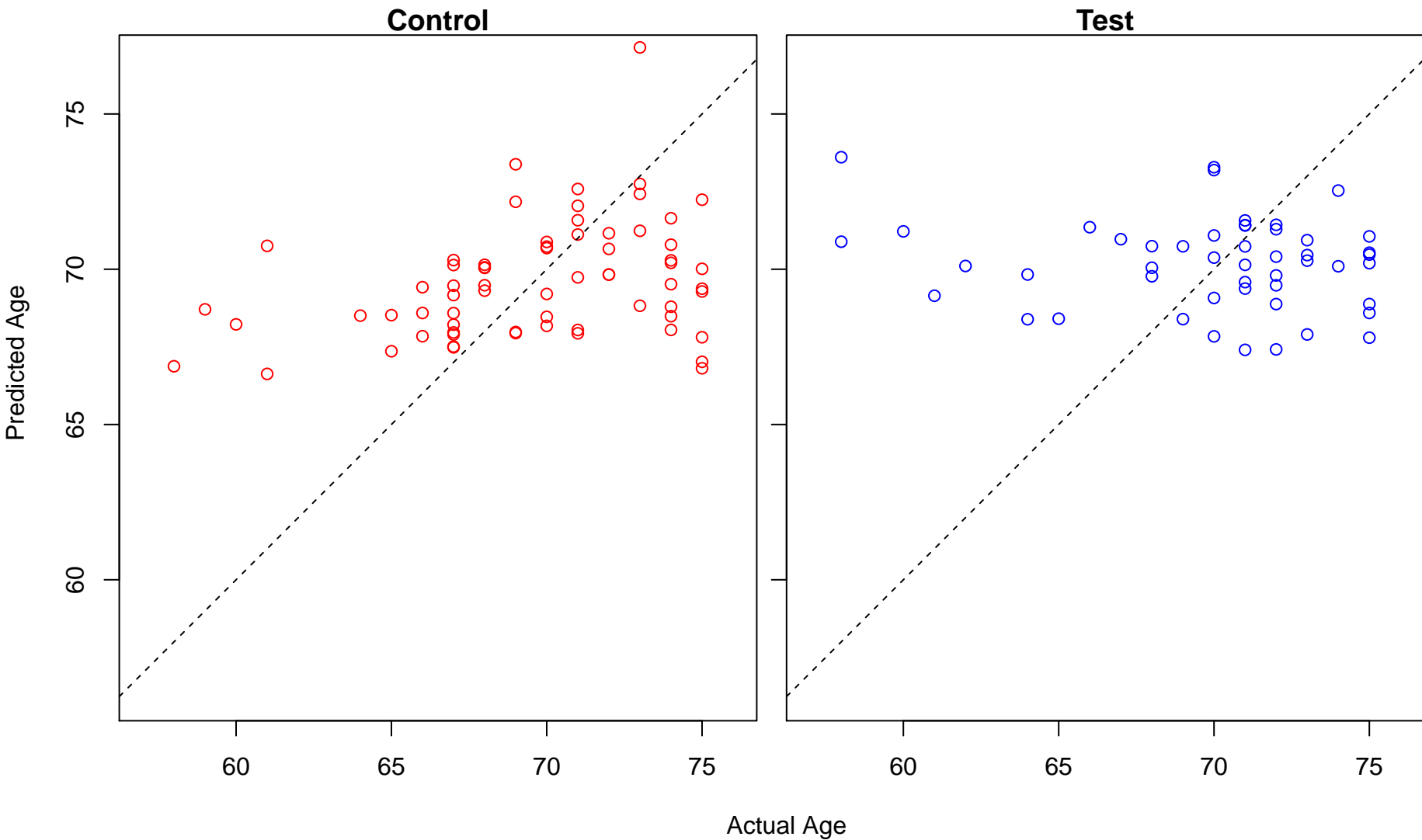


Test

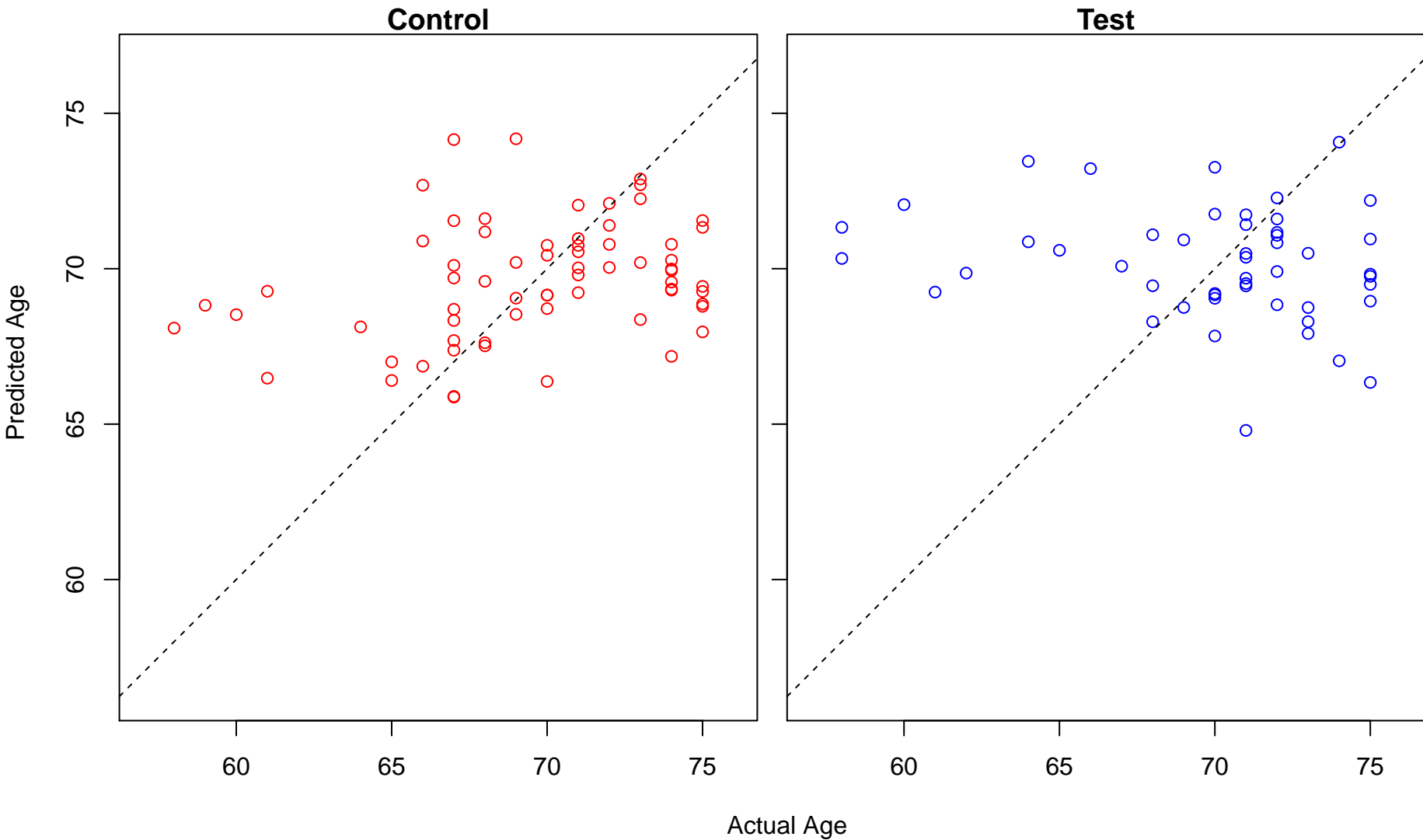


Actual Age

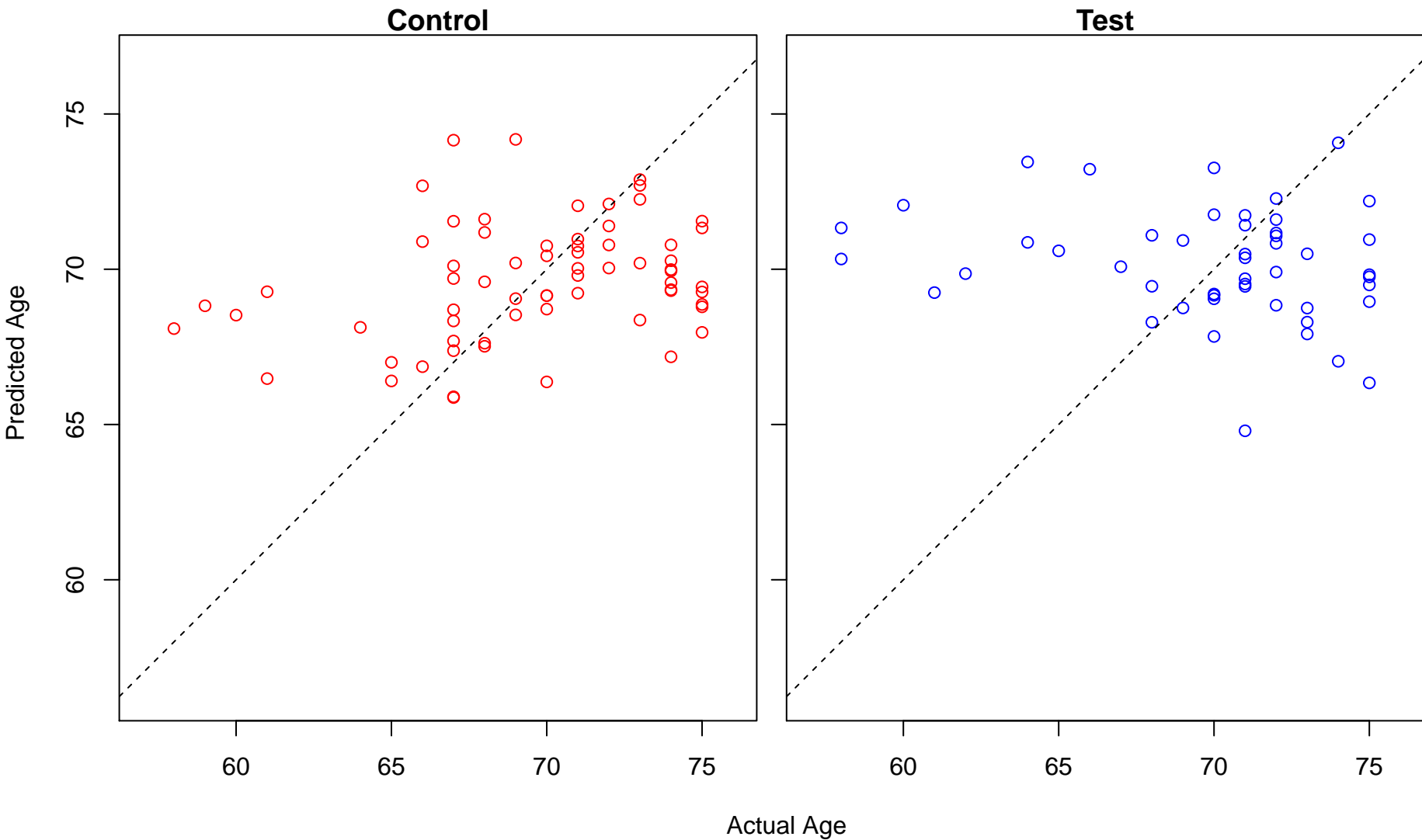
negative regulation of nitric-oxide synthase activity (Score: 0.339406)



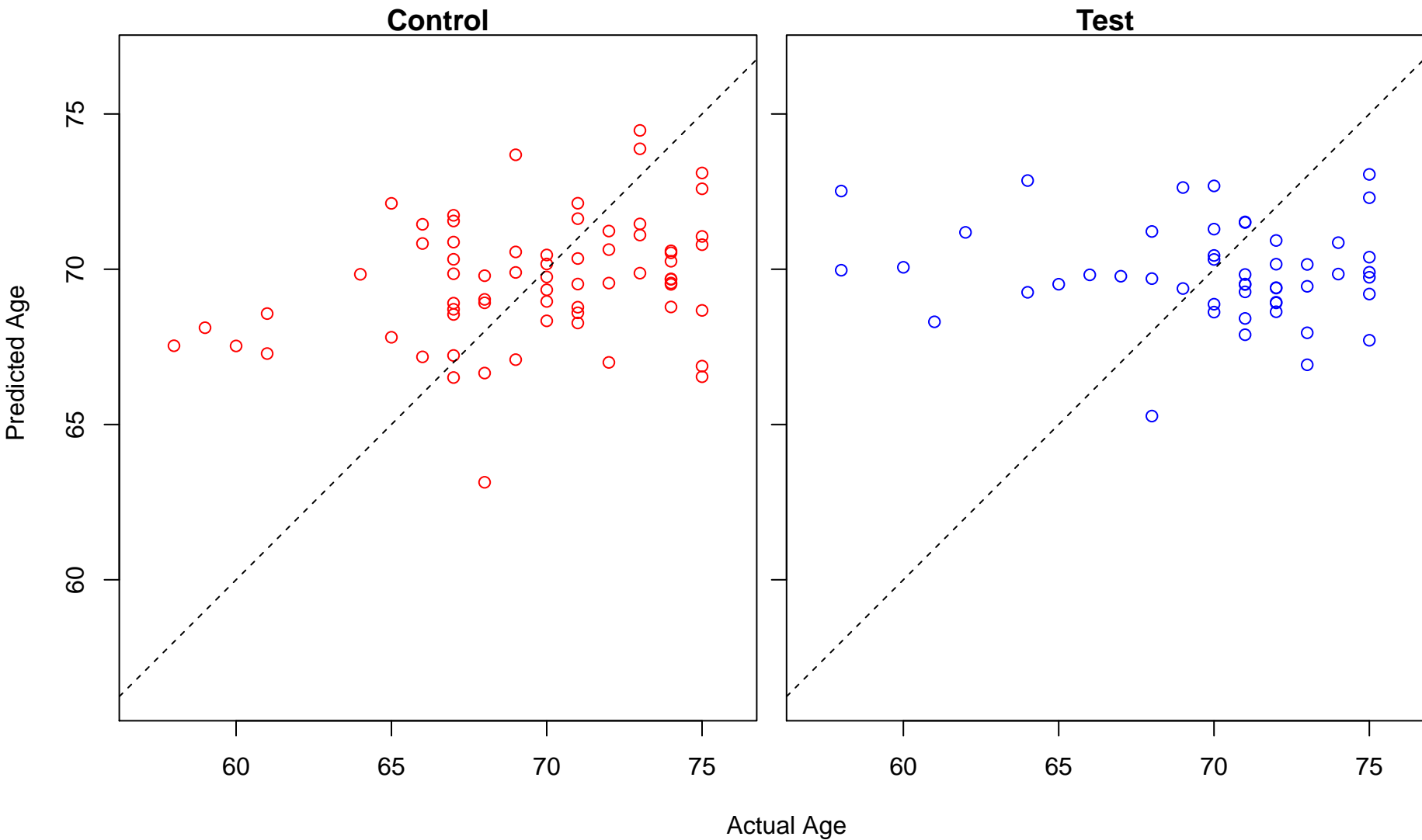
regulation of protein localization to synapse (Score: 0.338458)



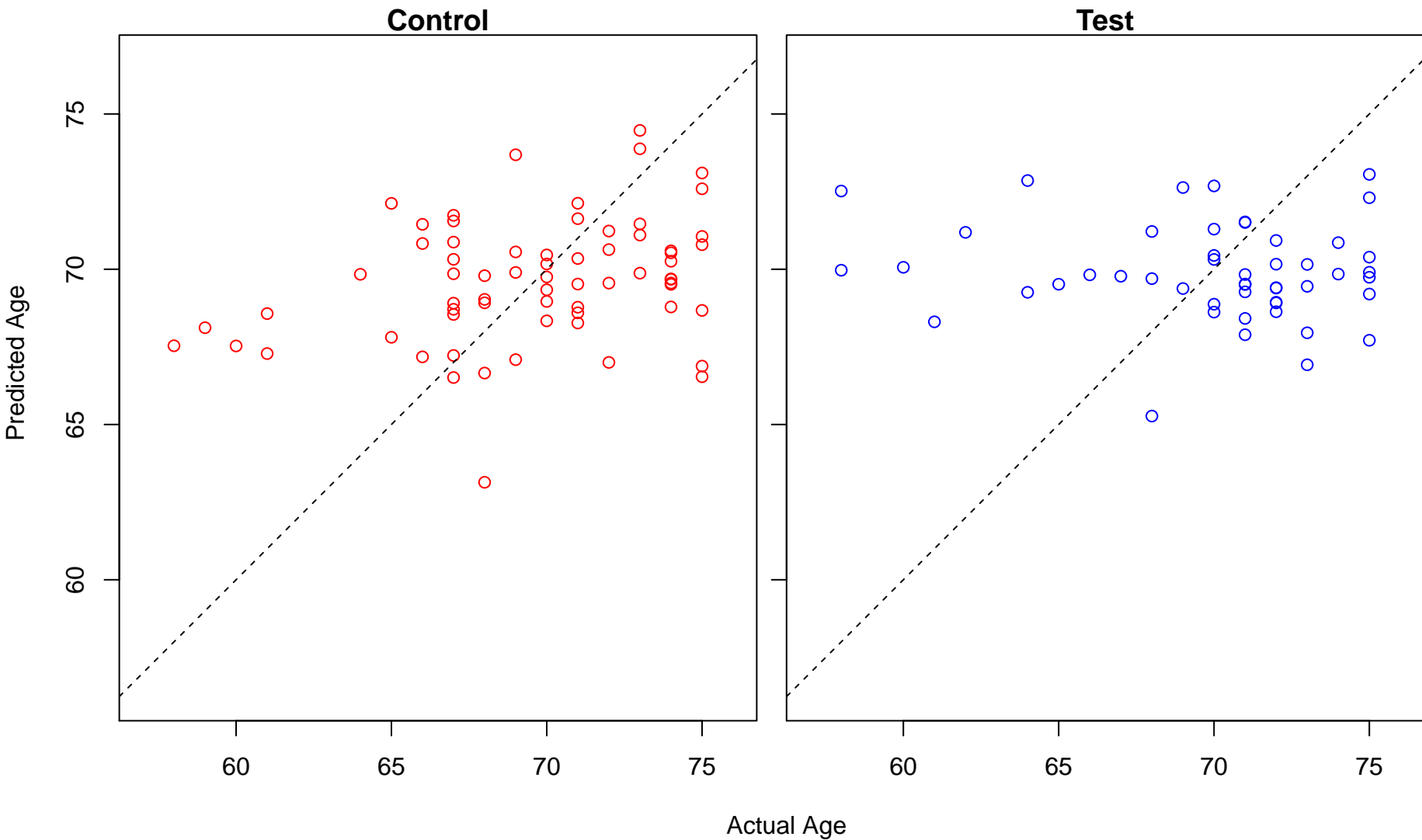
positive regulation of protein localization to synapse (Score: 0.338458)



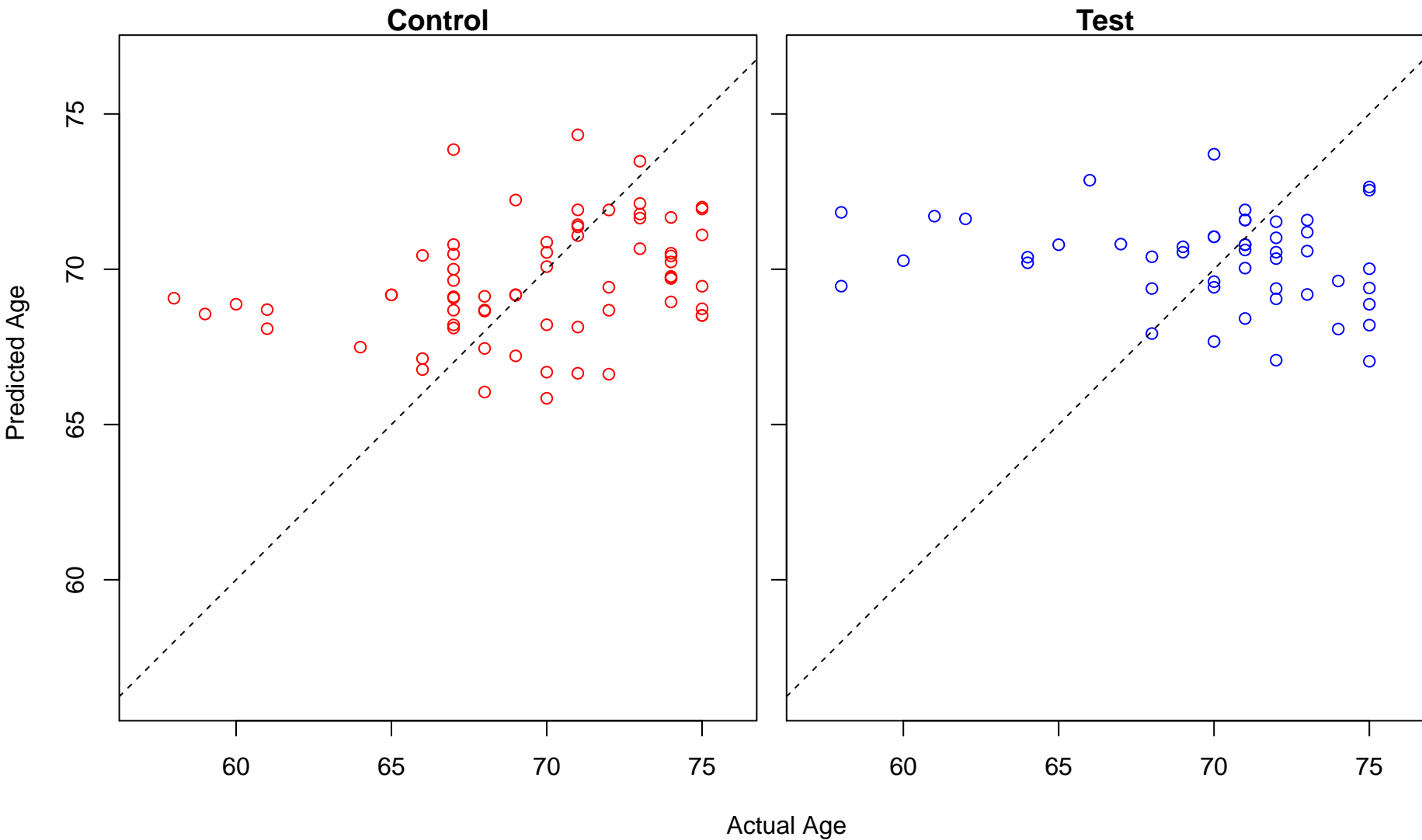
peripheral nervous system neuron differentiation (Score: 0.337304)



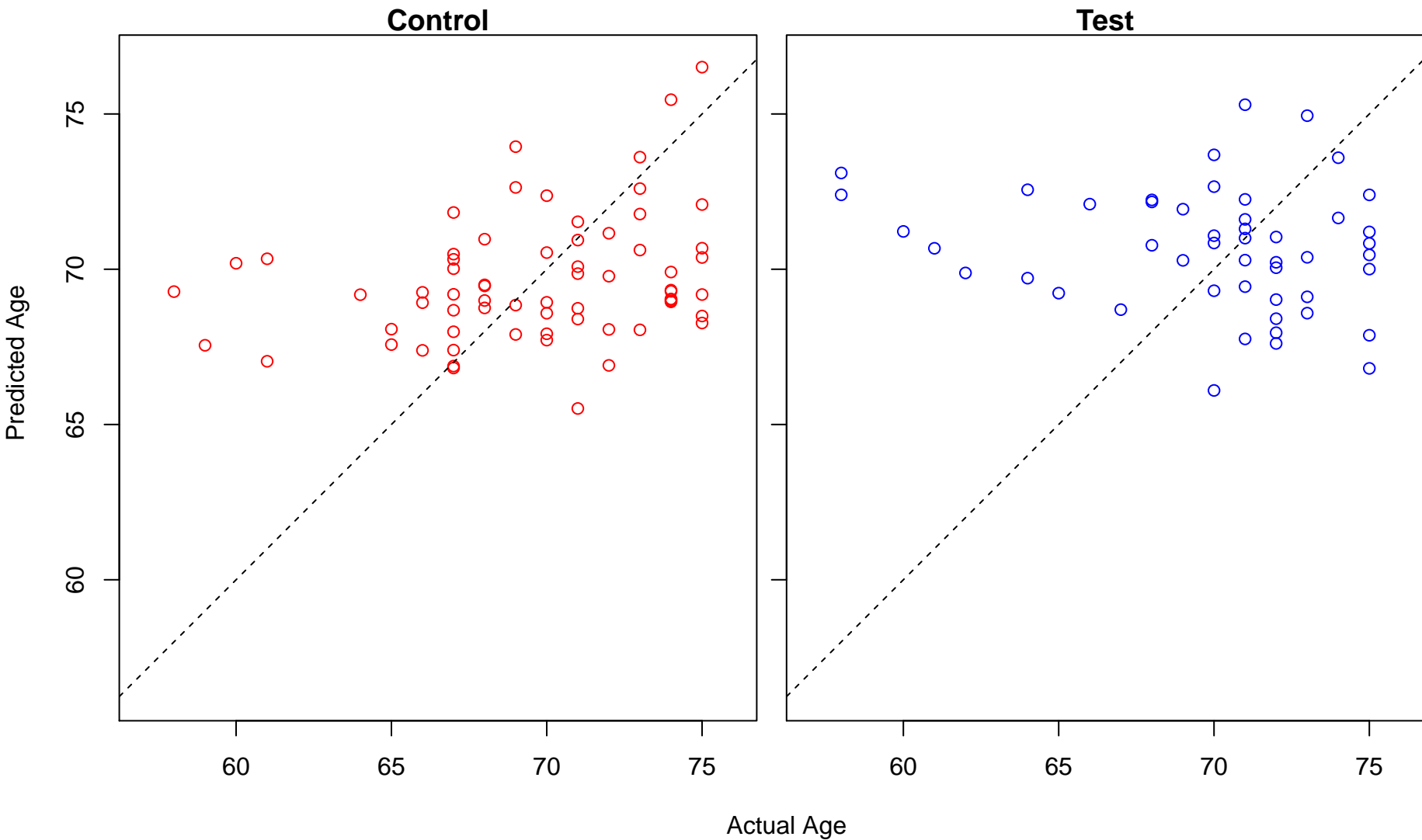
peripheral nervous system neuron development (Score: 0.337304)



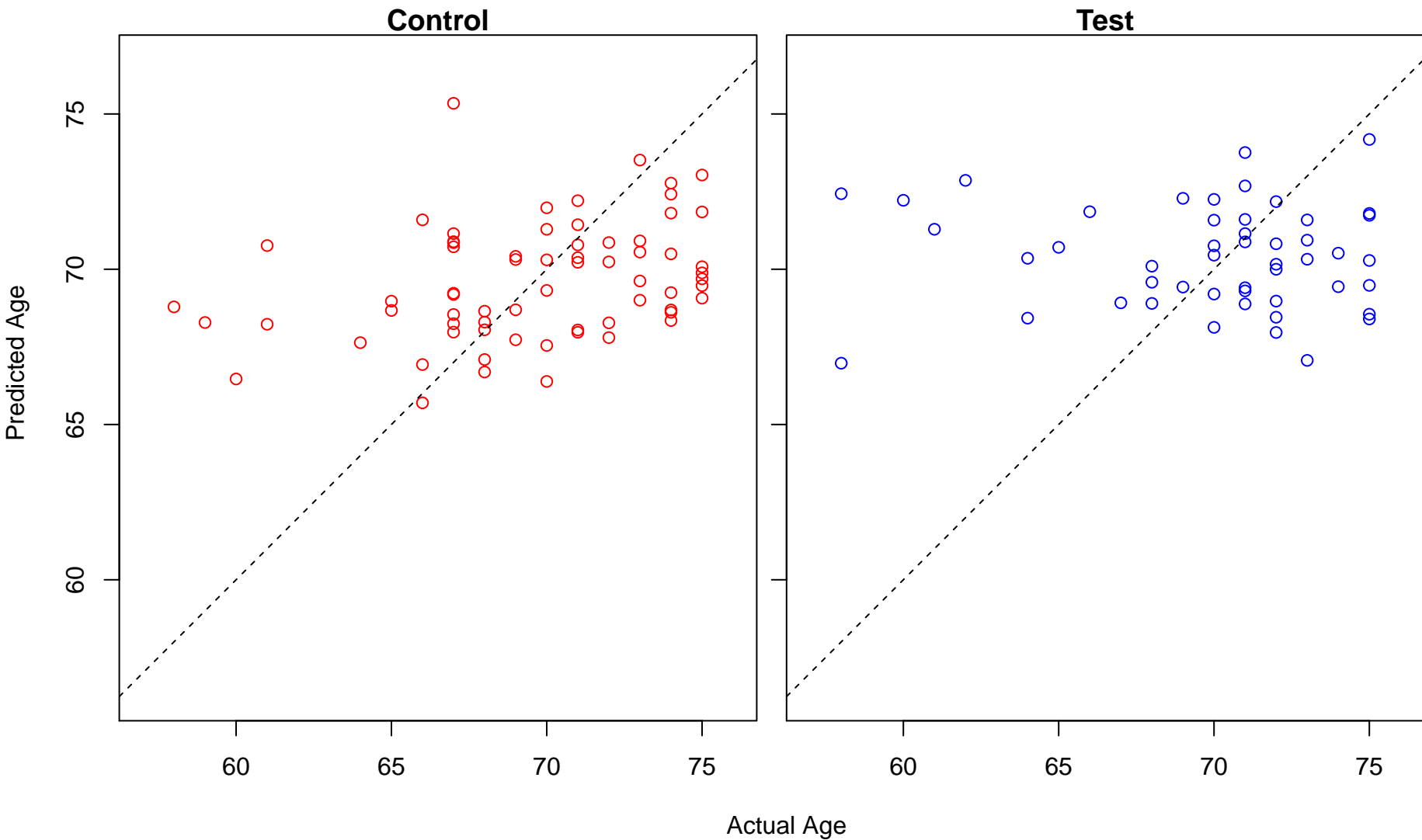
pyrimidine ribonucleotide metabolic process (Score: 0.336957)



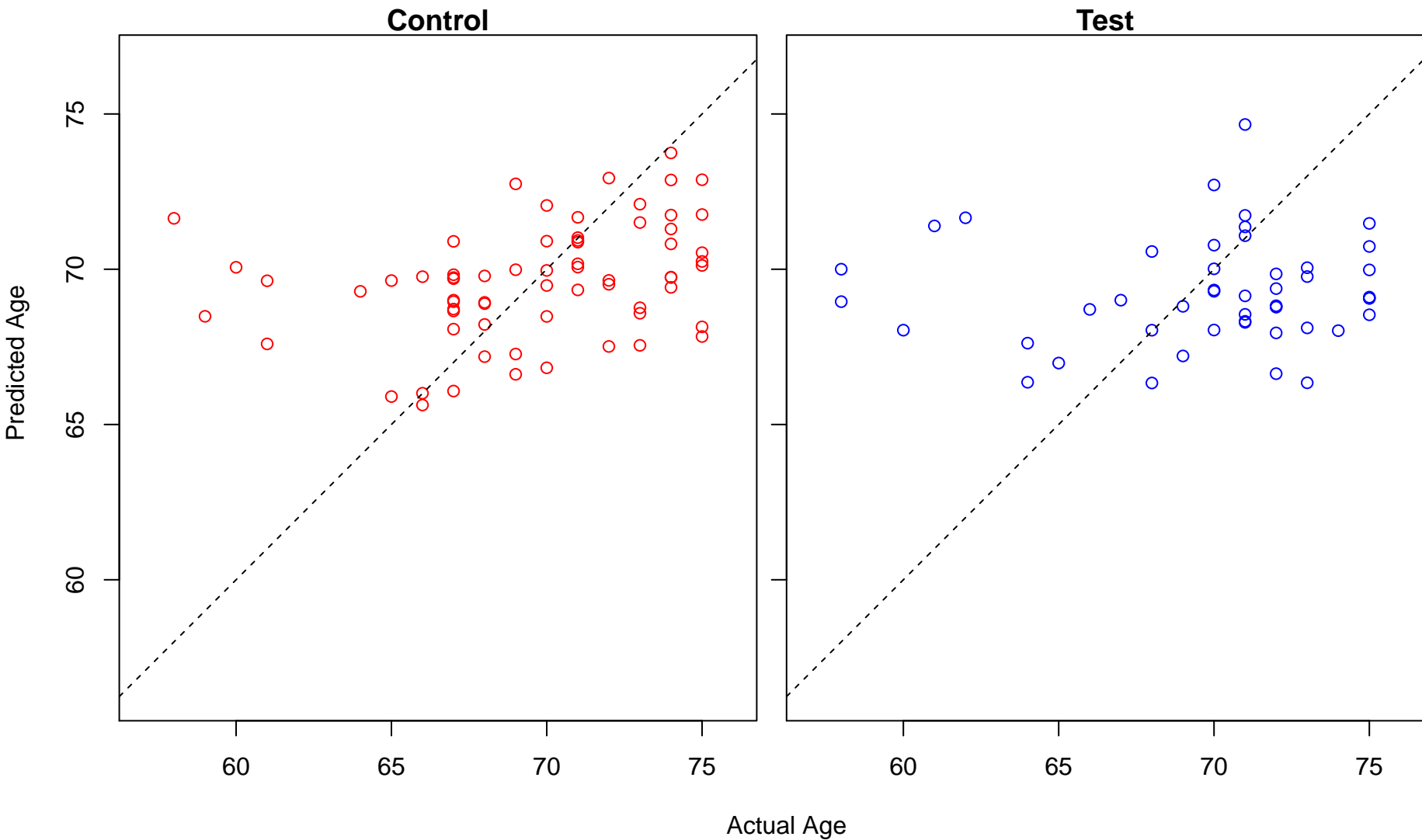
pentose-phosphate shunt (Score: 0.336839)



positive regulation of phosphatidylinositol 3-kinase activity (Score: 0.336246)

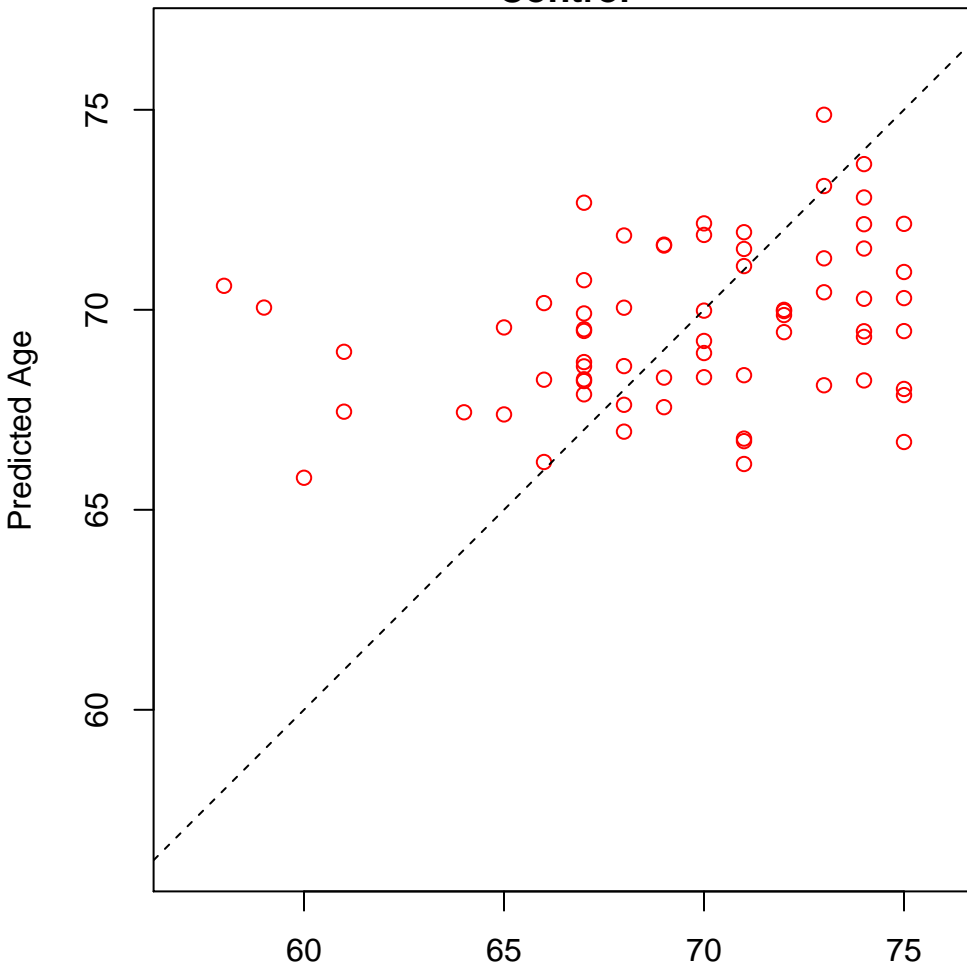


positive regulation of T-helper 17 type immune response (Score: 0.335372)

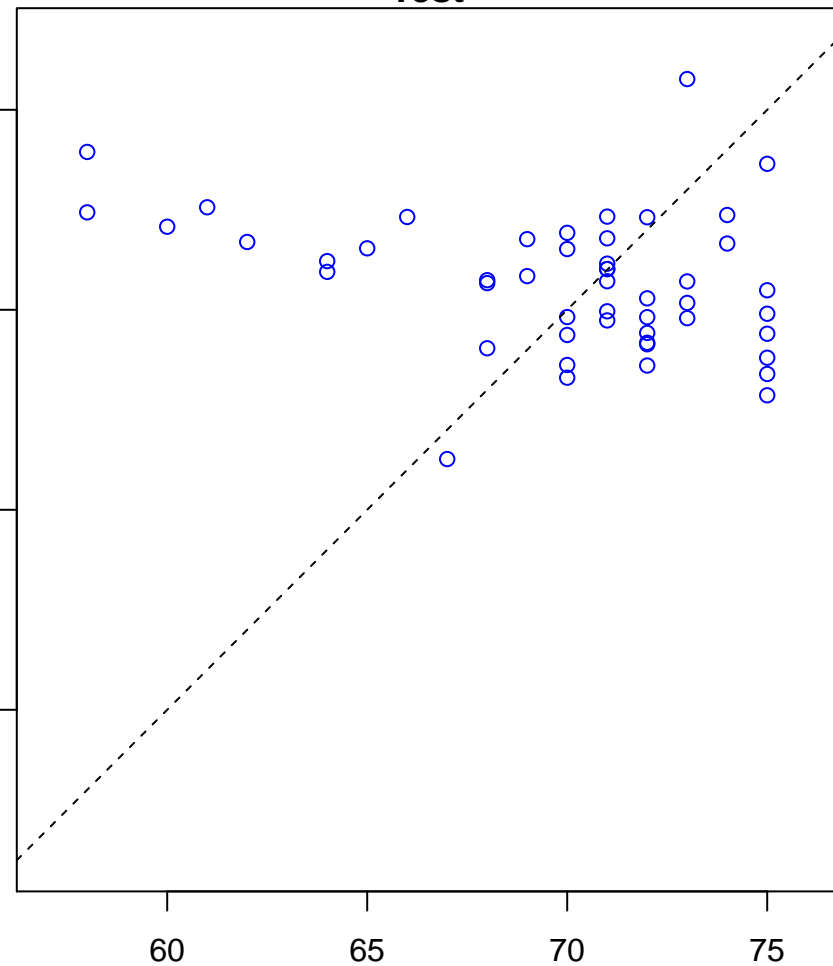


regulation of trophoblast cell migration (Score: 0.334612)

Control

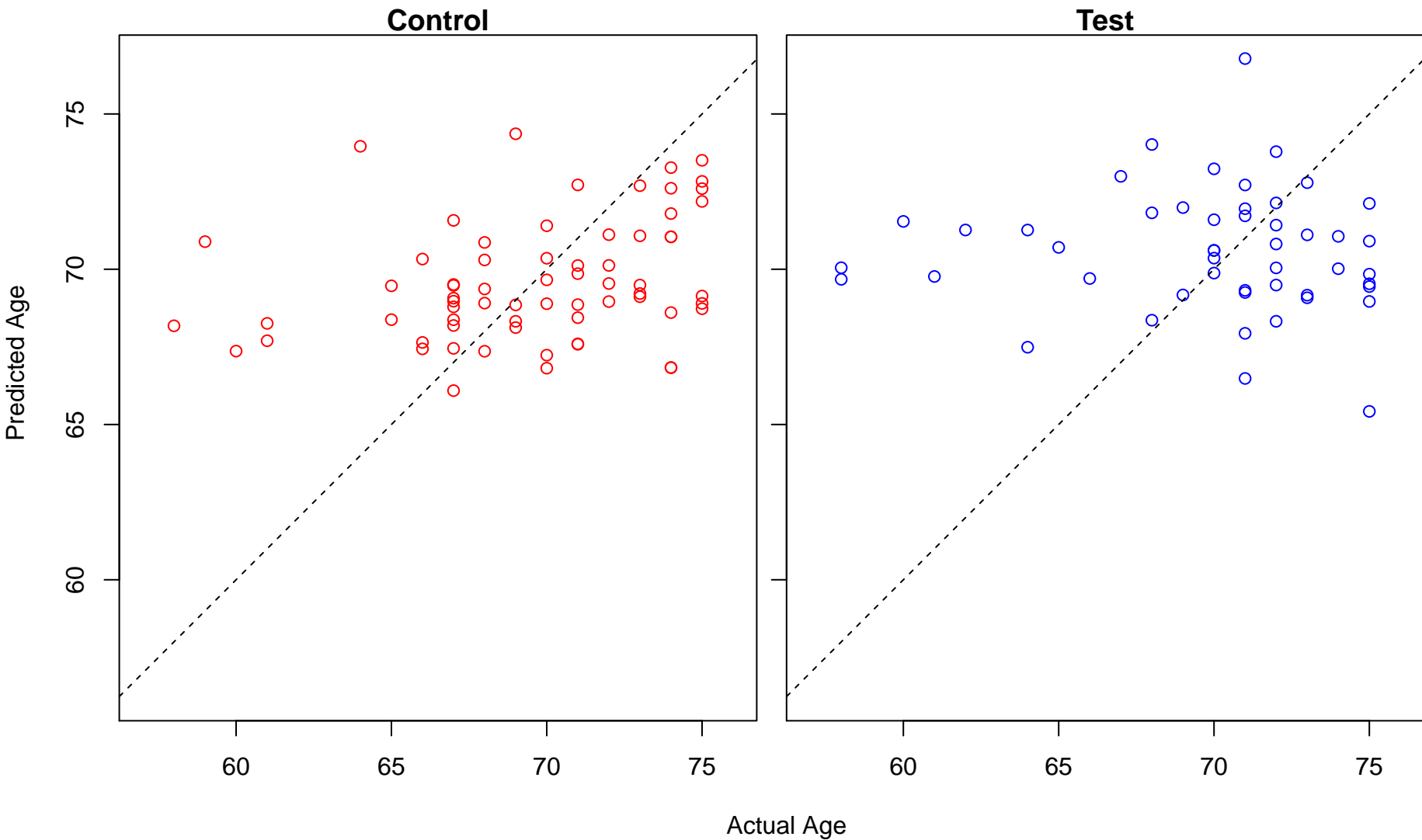


Test

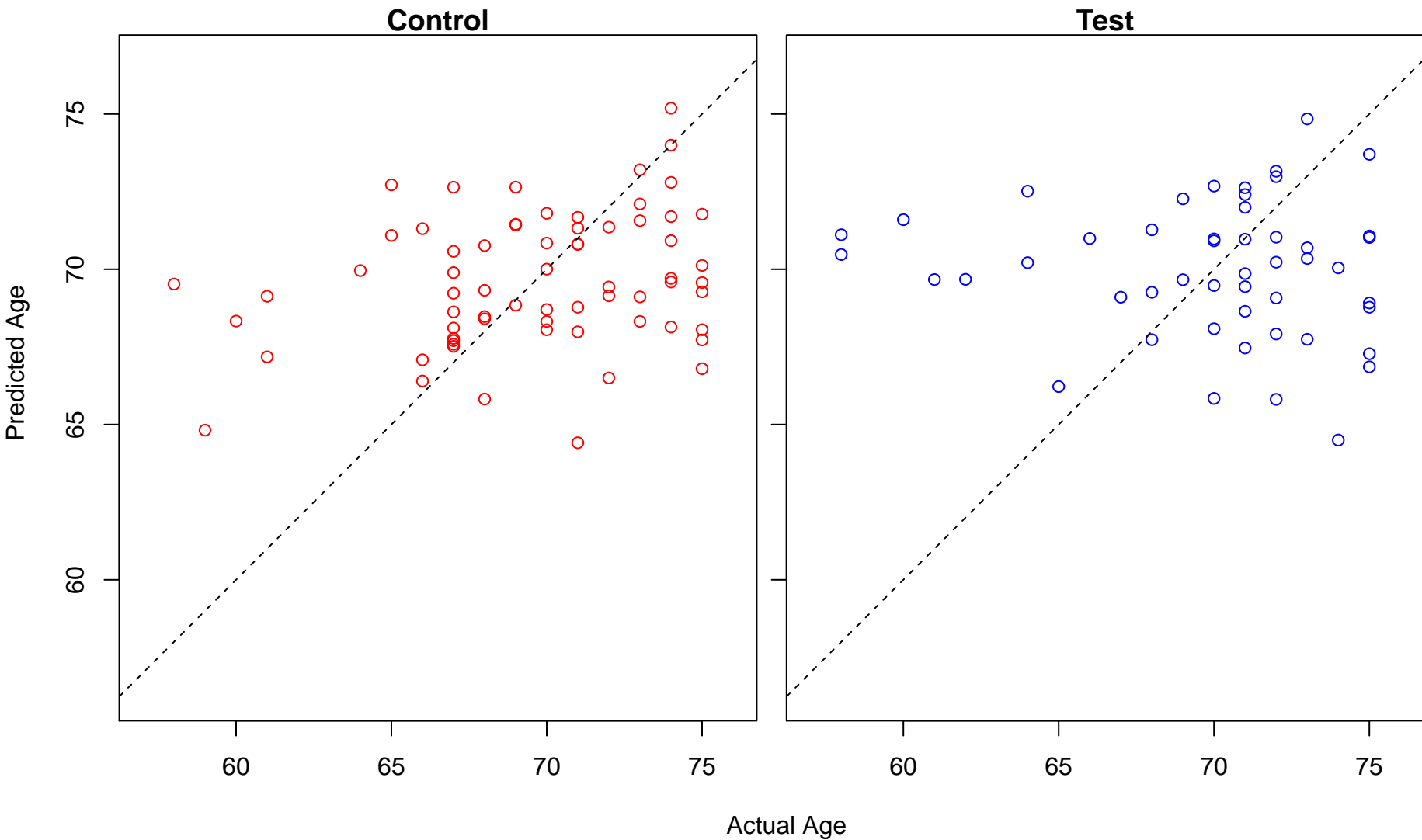


Actual Age

organic cation transport (Score: 0.333595)

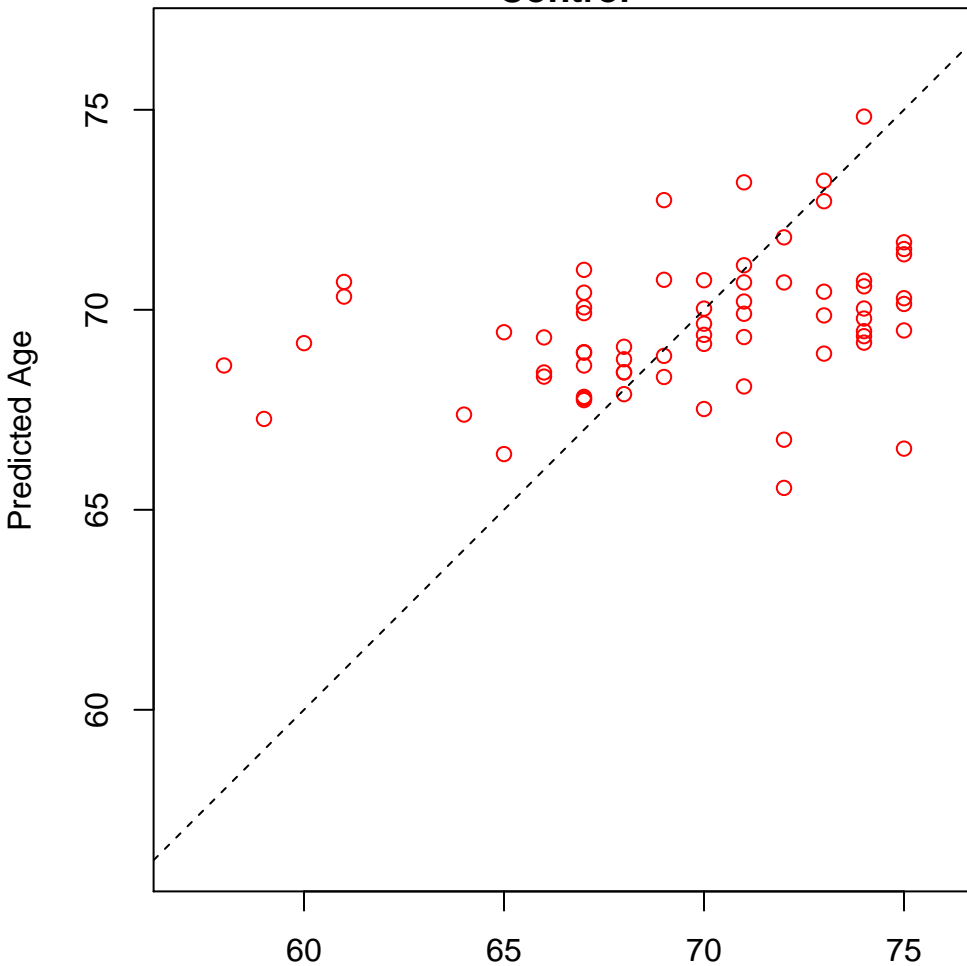


multicellular organismal aging (Score: 0.332235)

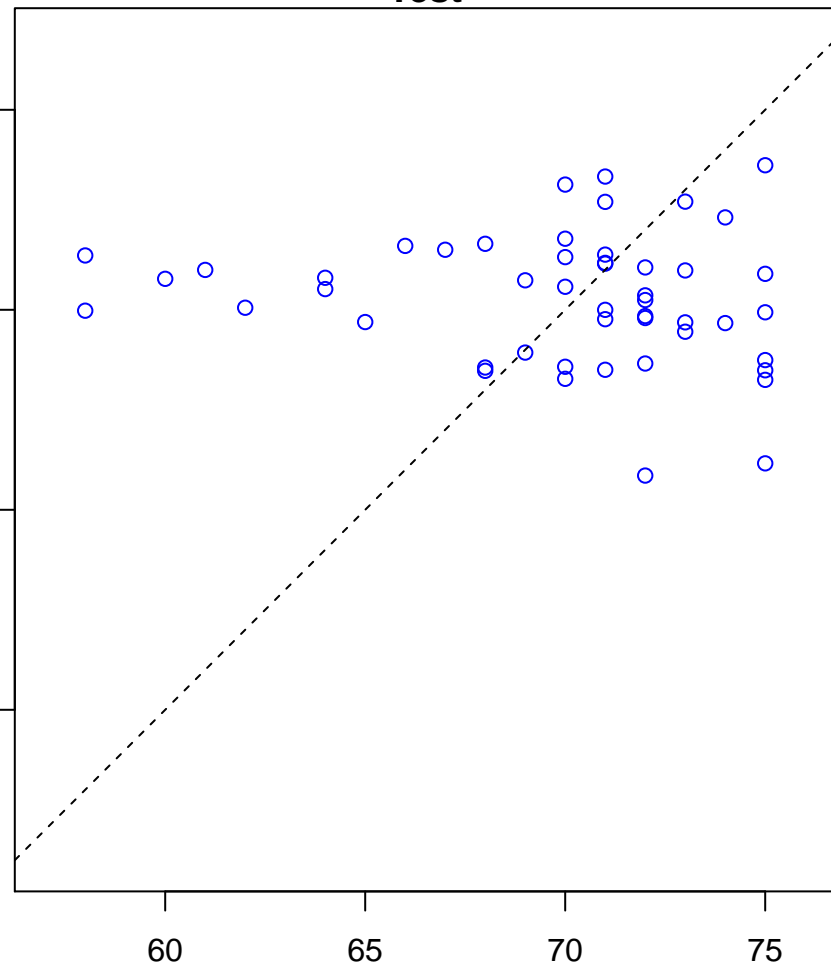


cell adhesion mediated by integrin (Score: 0.332033)

Control

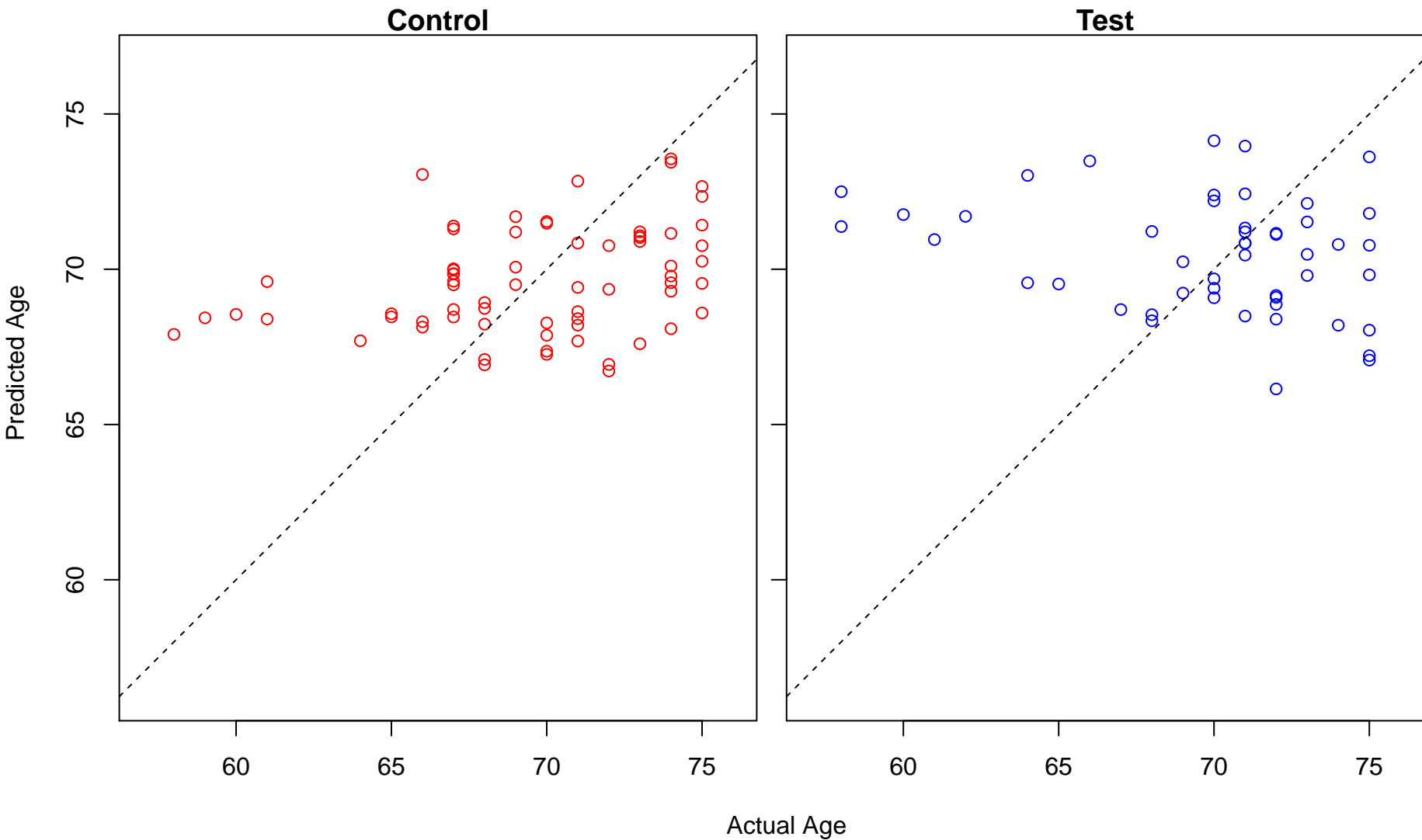


Test

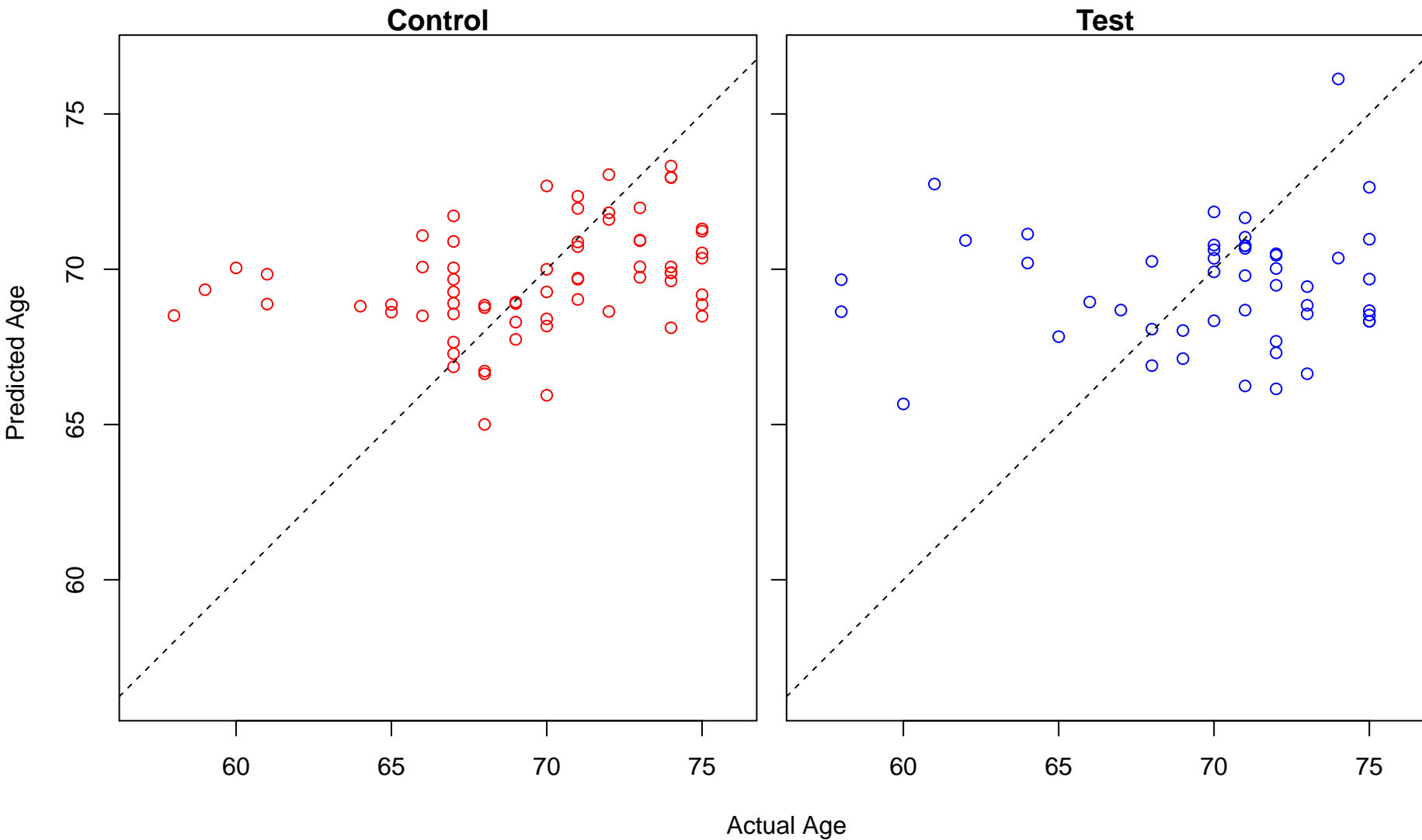


Actual Age

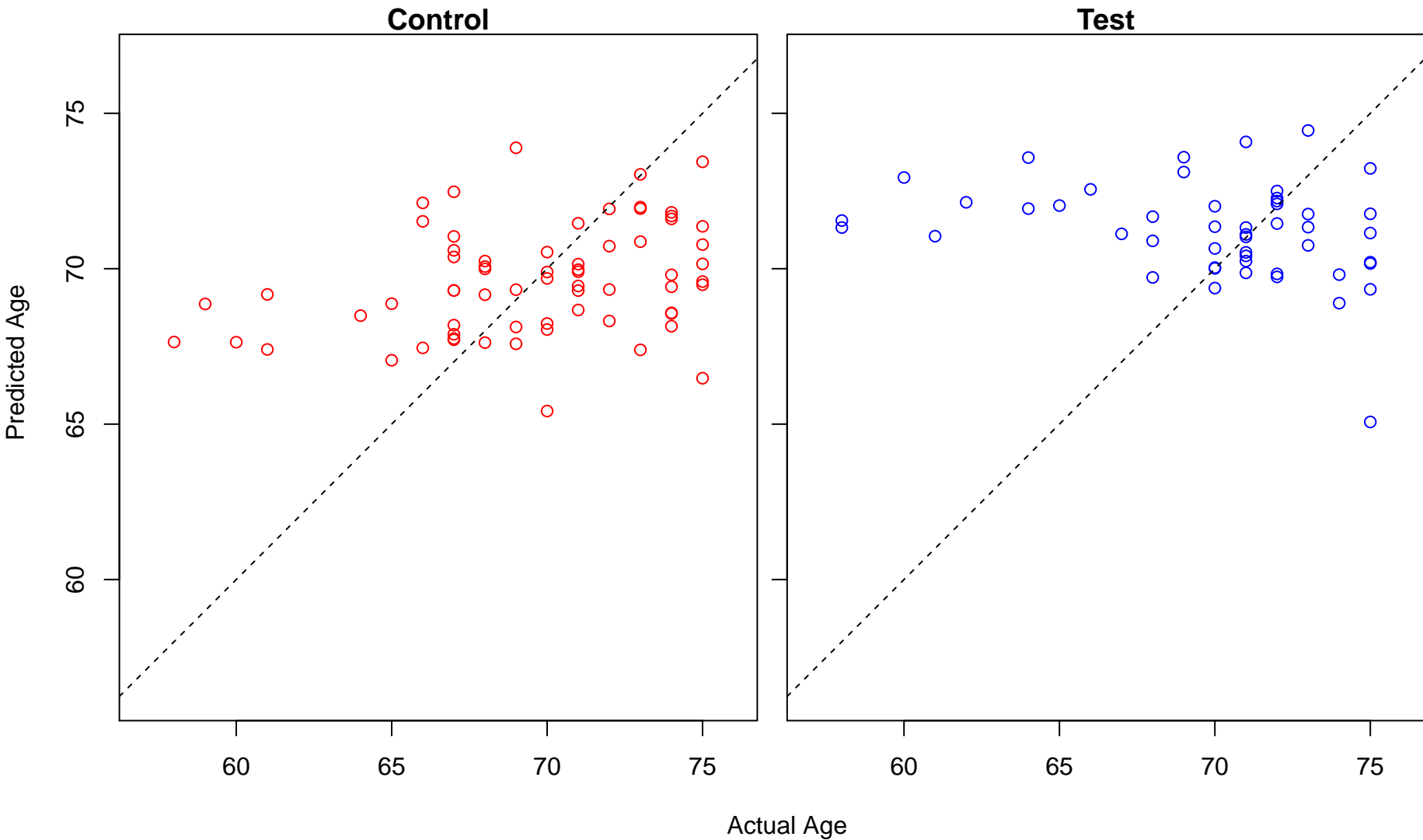
regulation of wound healing, spreading of epidermal cells (Score: 0.331510)



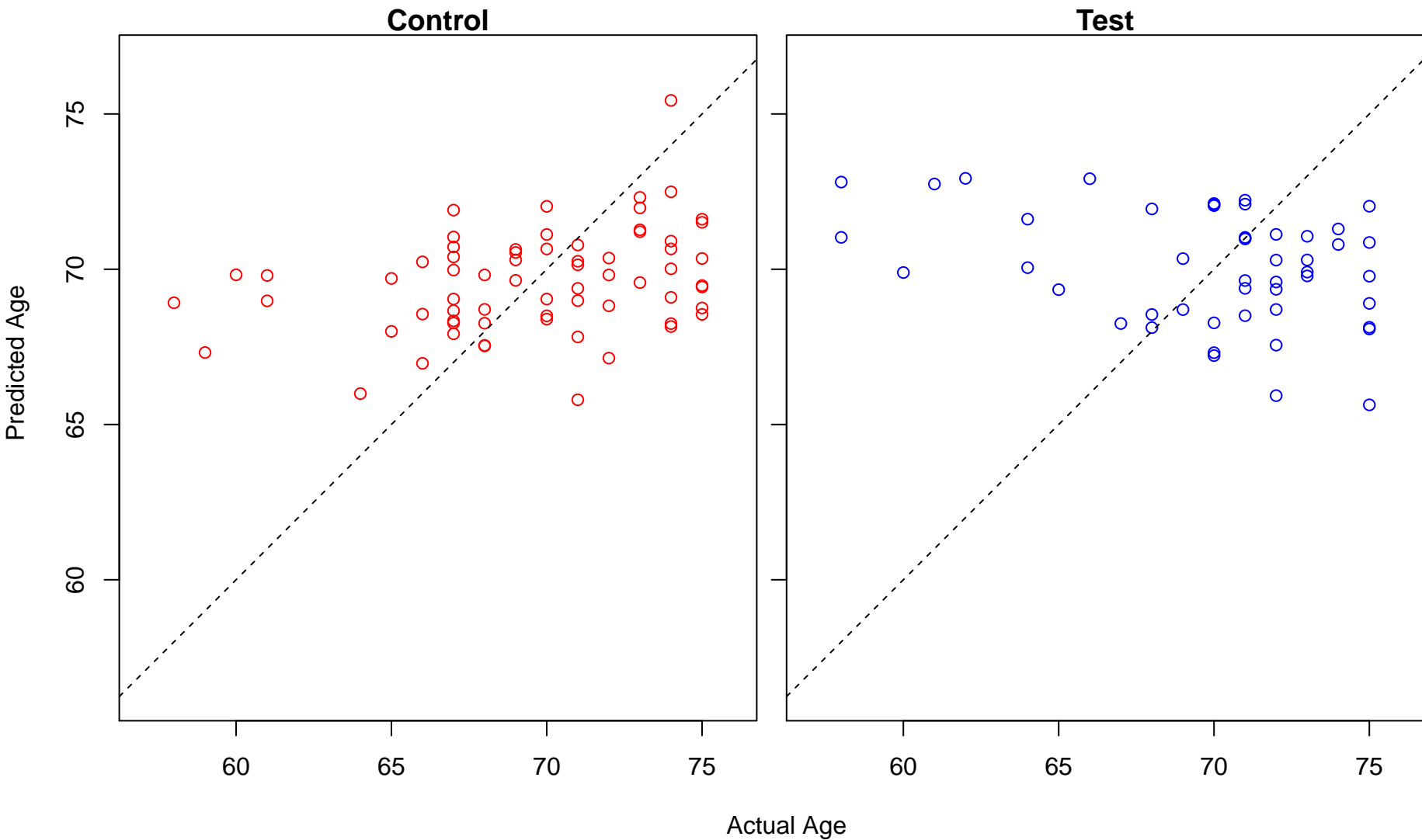
neuron fate commitment (Score: 0.330796)



regulation of transcription initiation from RNA polymerase II promoter (Score: 0.329646)

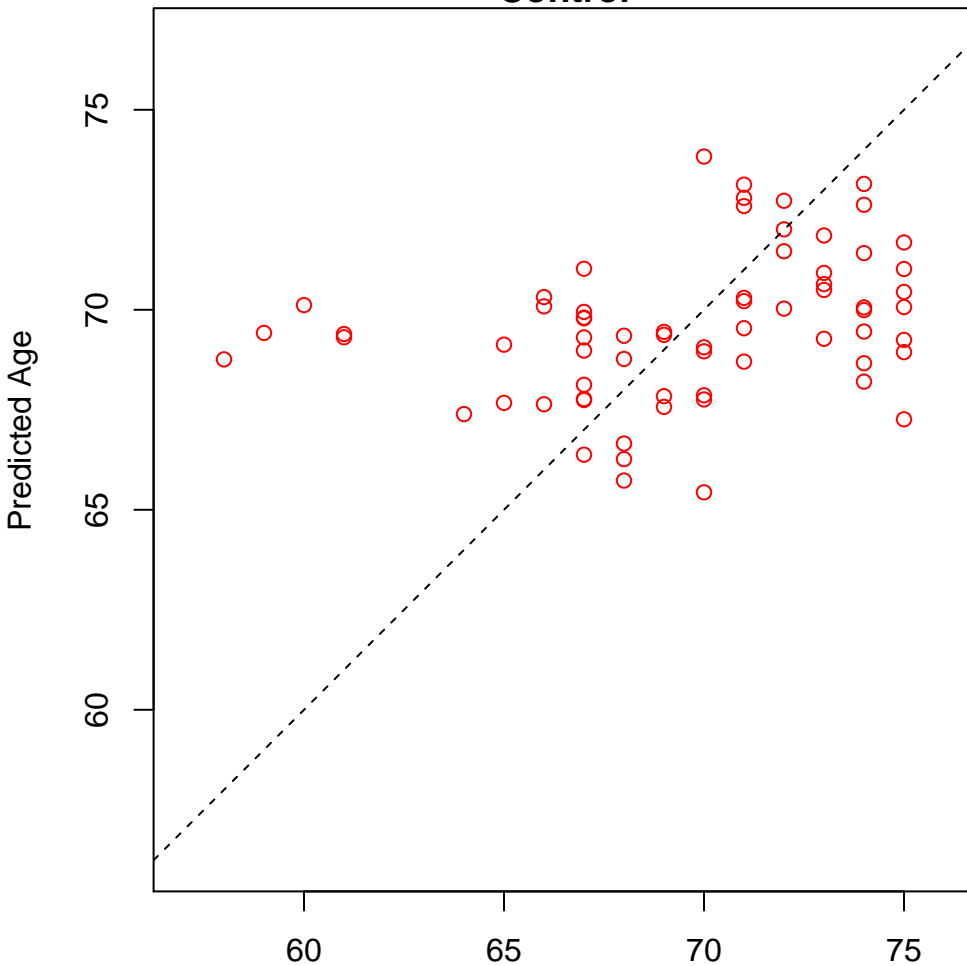


phosphatidylinositol acyl-chain remodeling (Score: 0.328516)

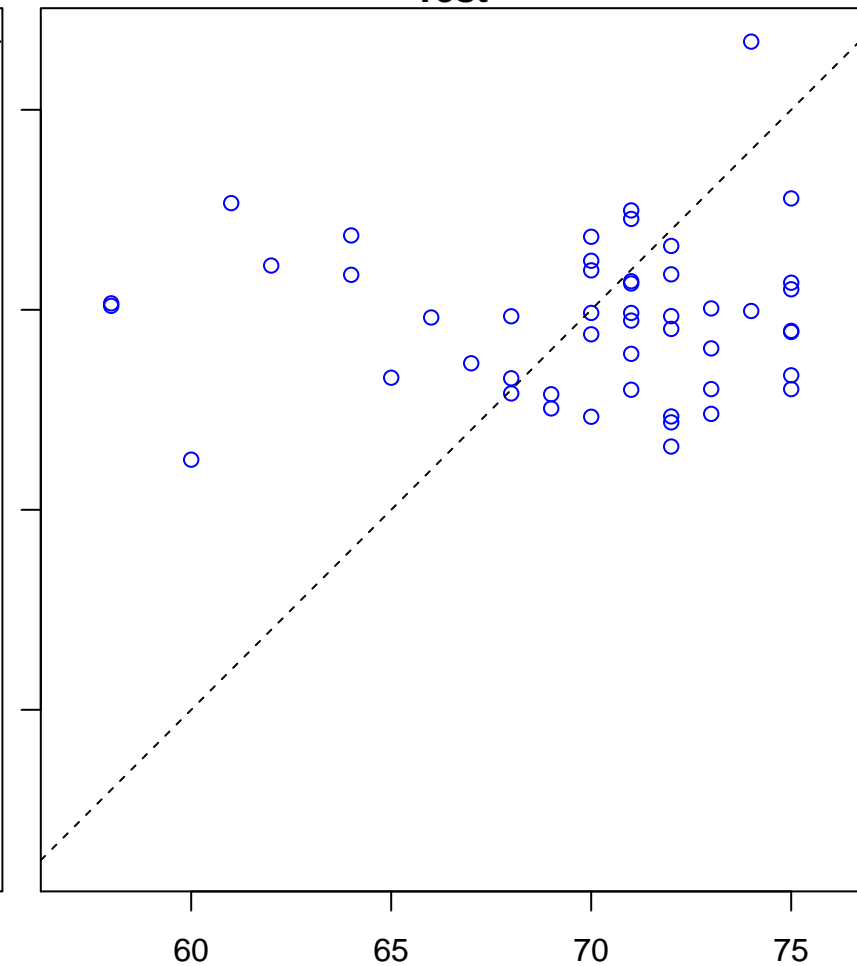


positive regulation of blood pressure (Score: 0.328078)

Control

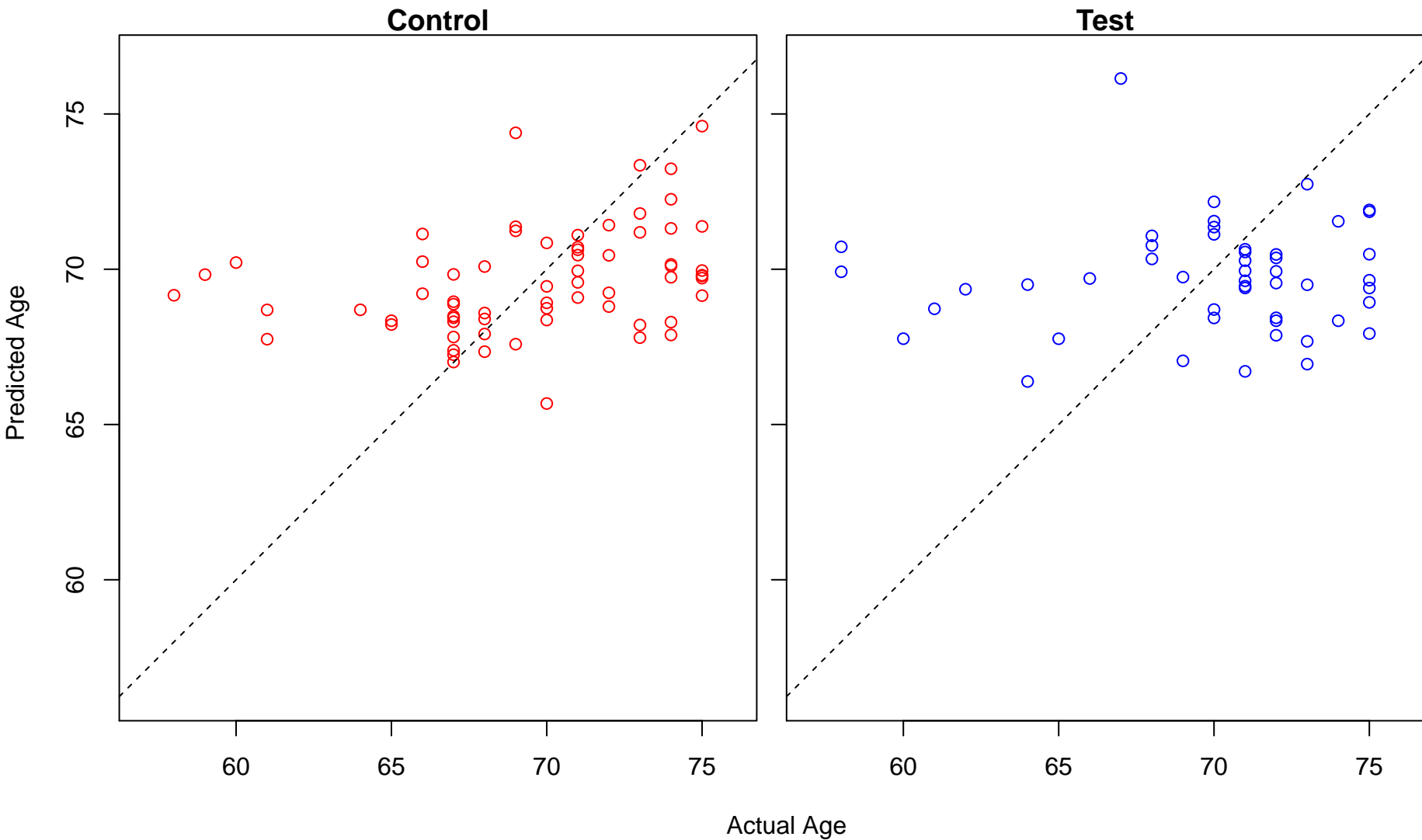


Test



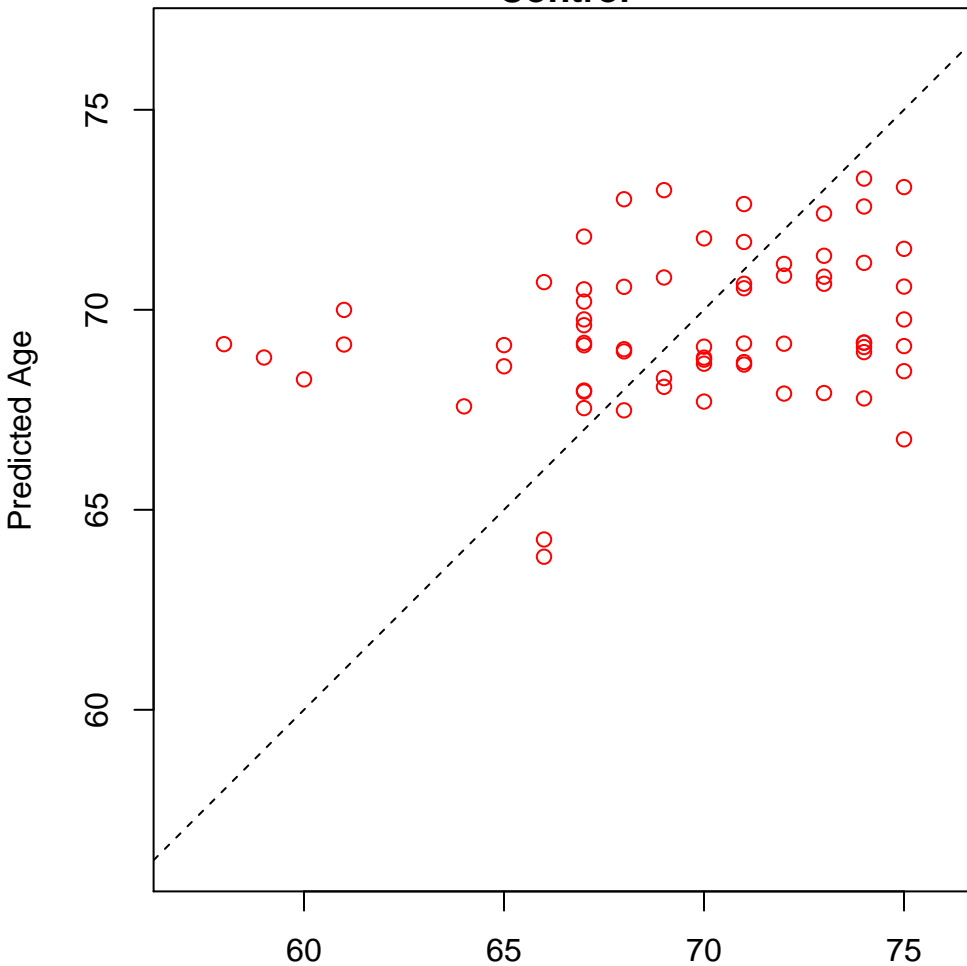
Actual Age

heterochromatin assembly (Score: 0.327594)

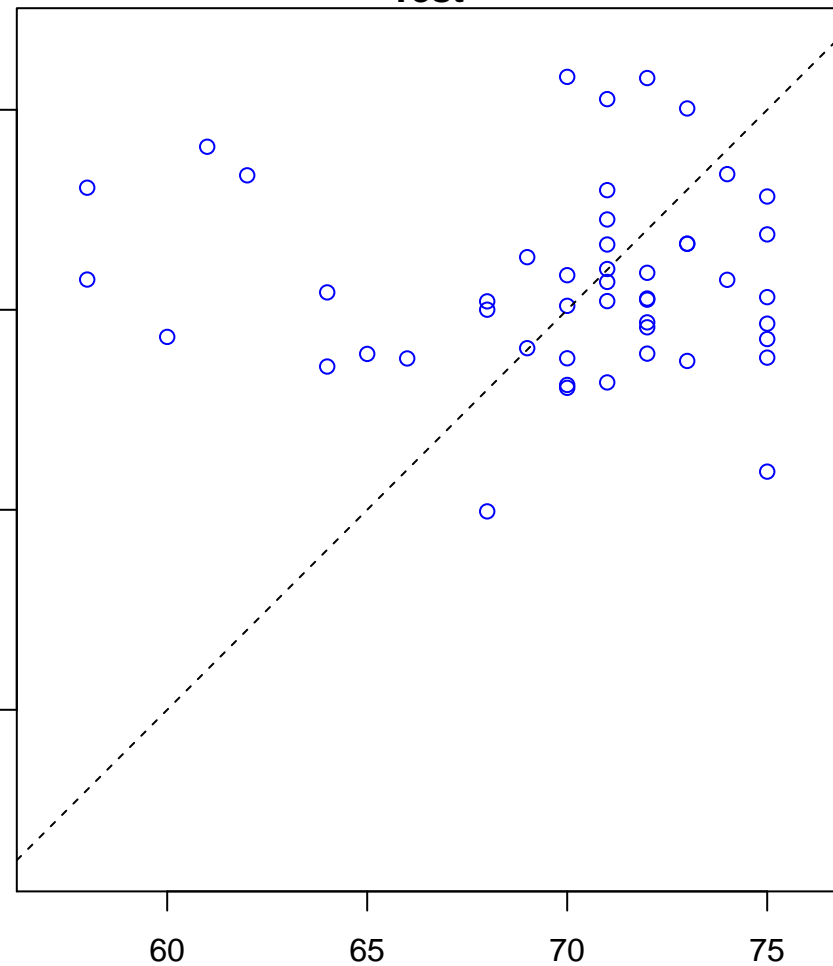


free ubiquitin chain polymerization (Score: 0.327516)

Control

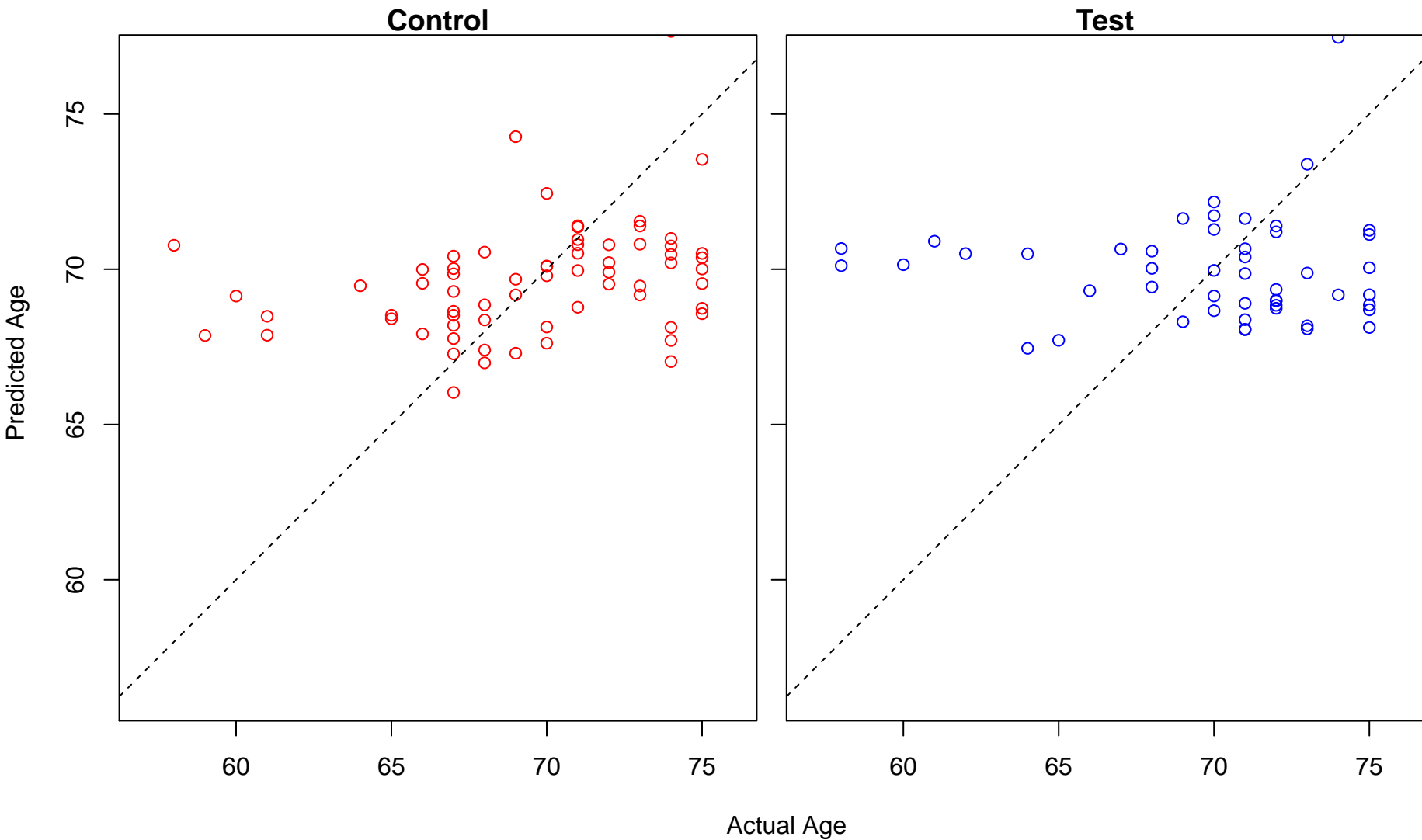


Test

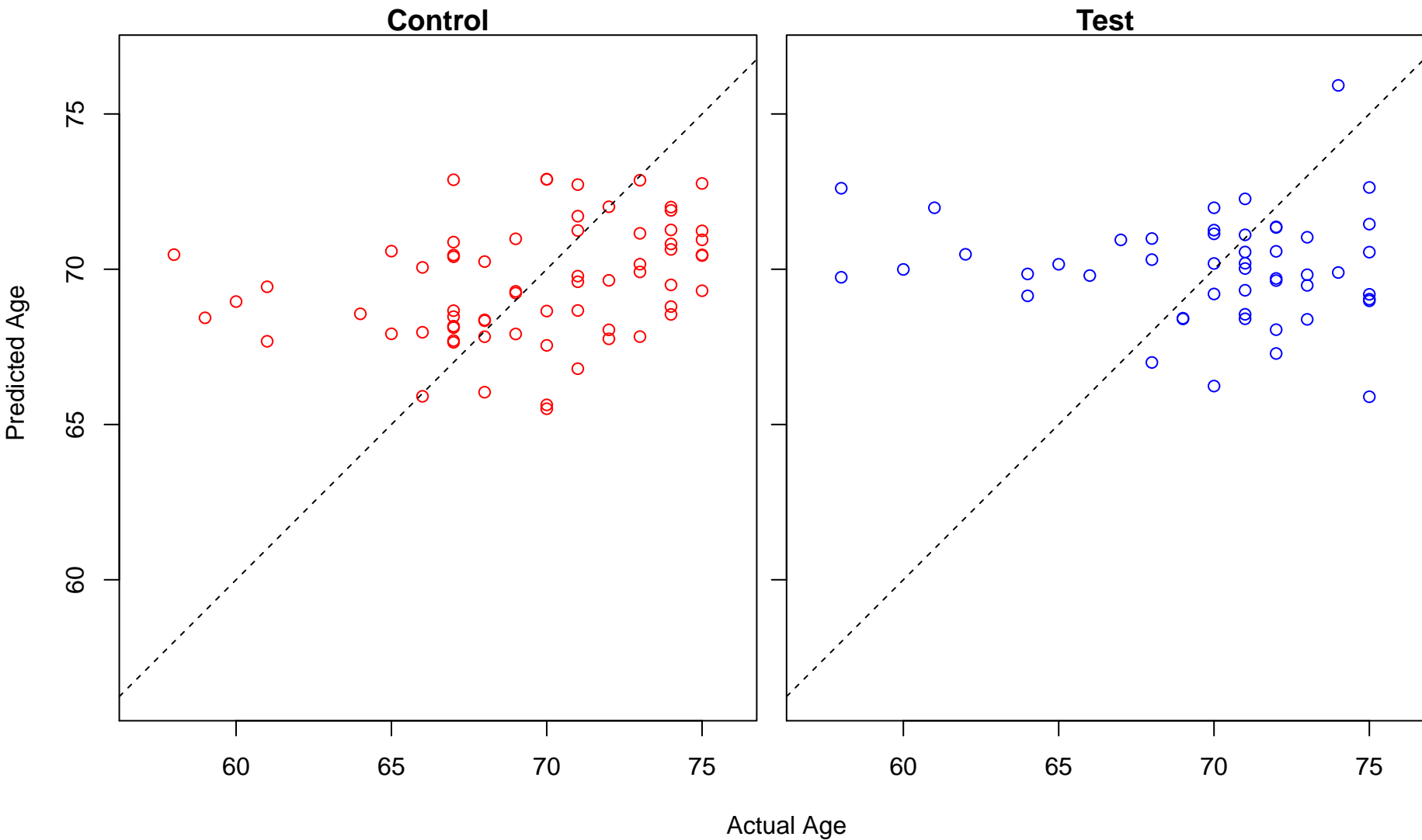


Actual Age

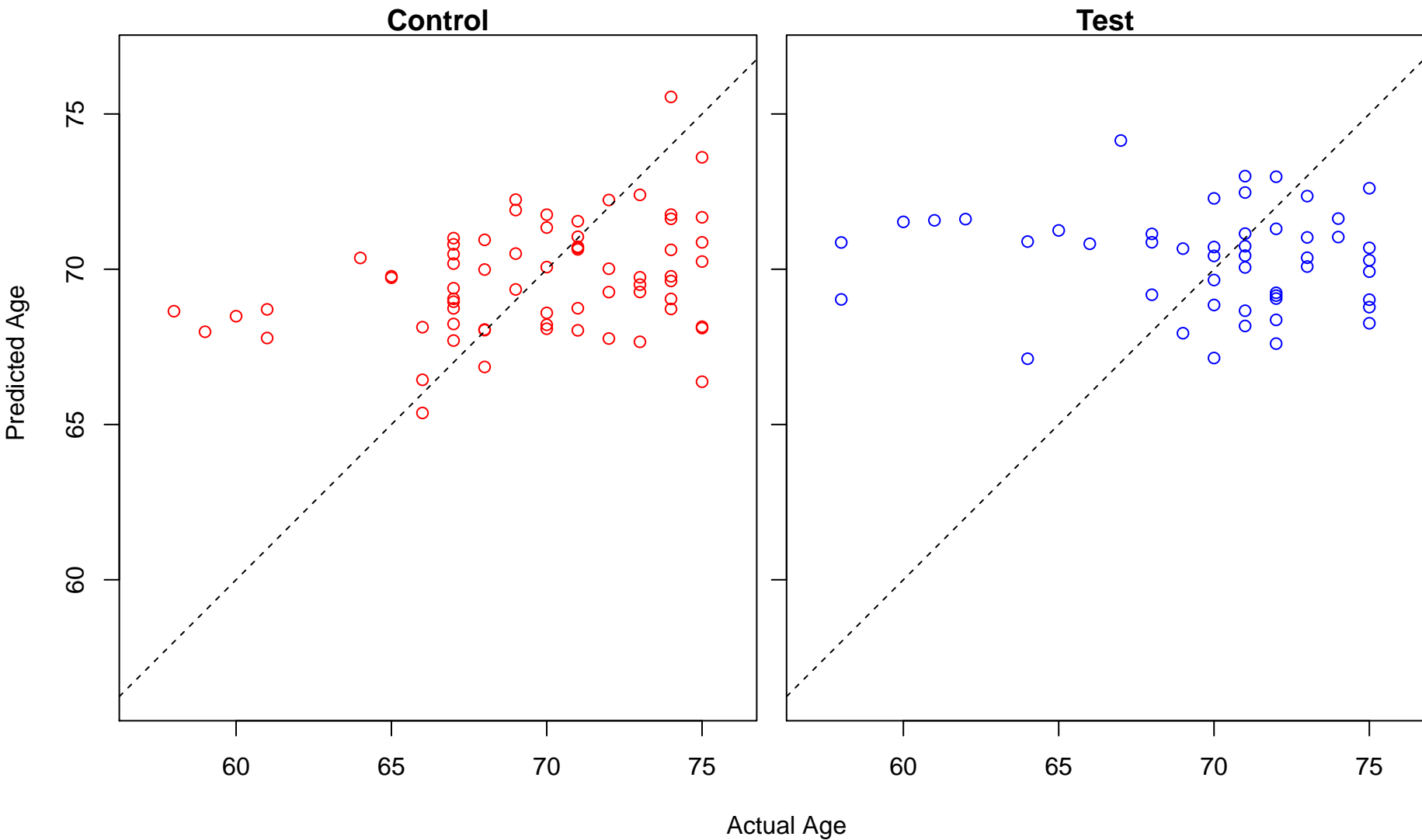
hormone catabolic process (Score: 0.327492)



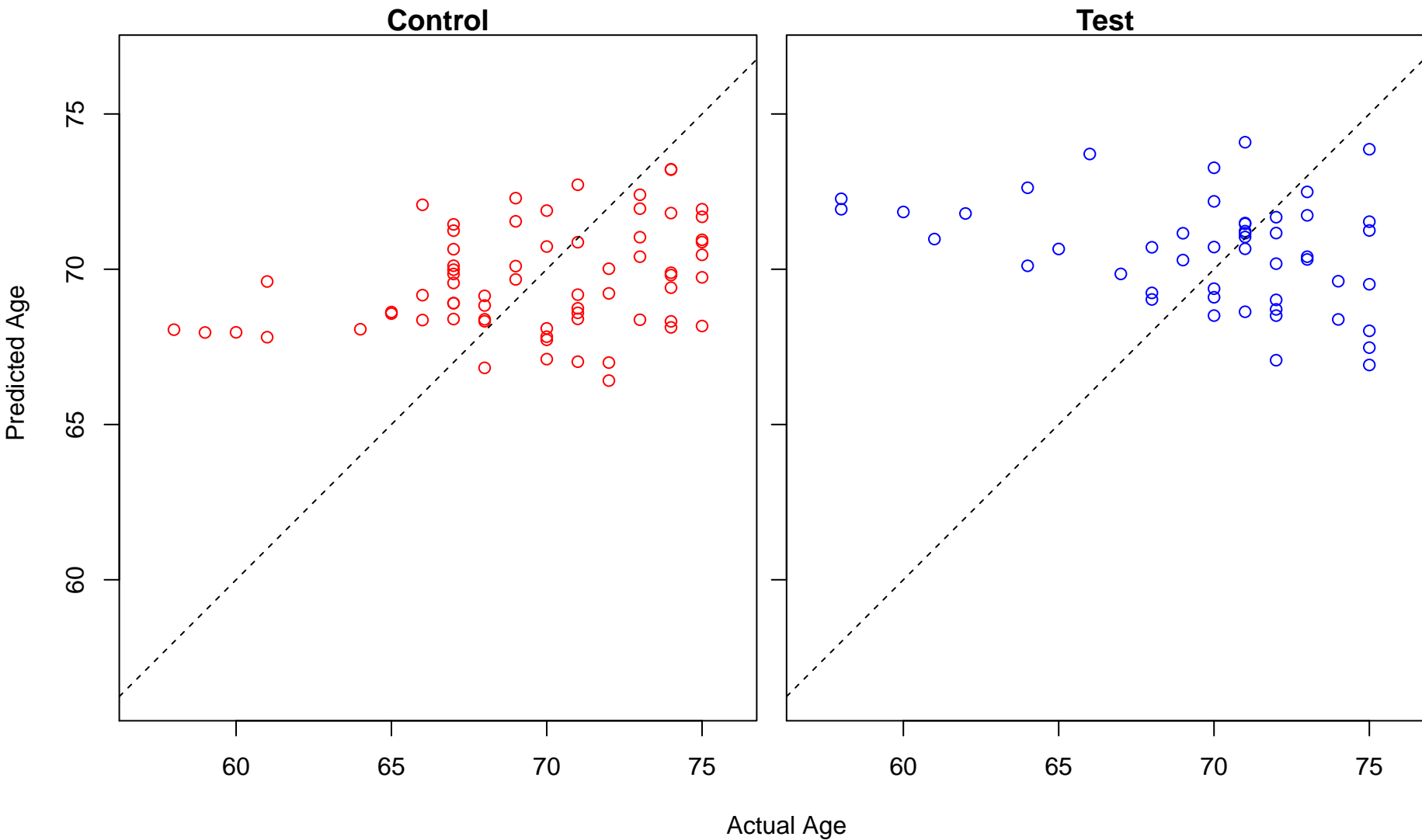
cell fate commitment involved in formation of primary germ layer (Score: 0.325328)



cytolysis (Score: 0.324677)

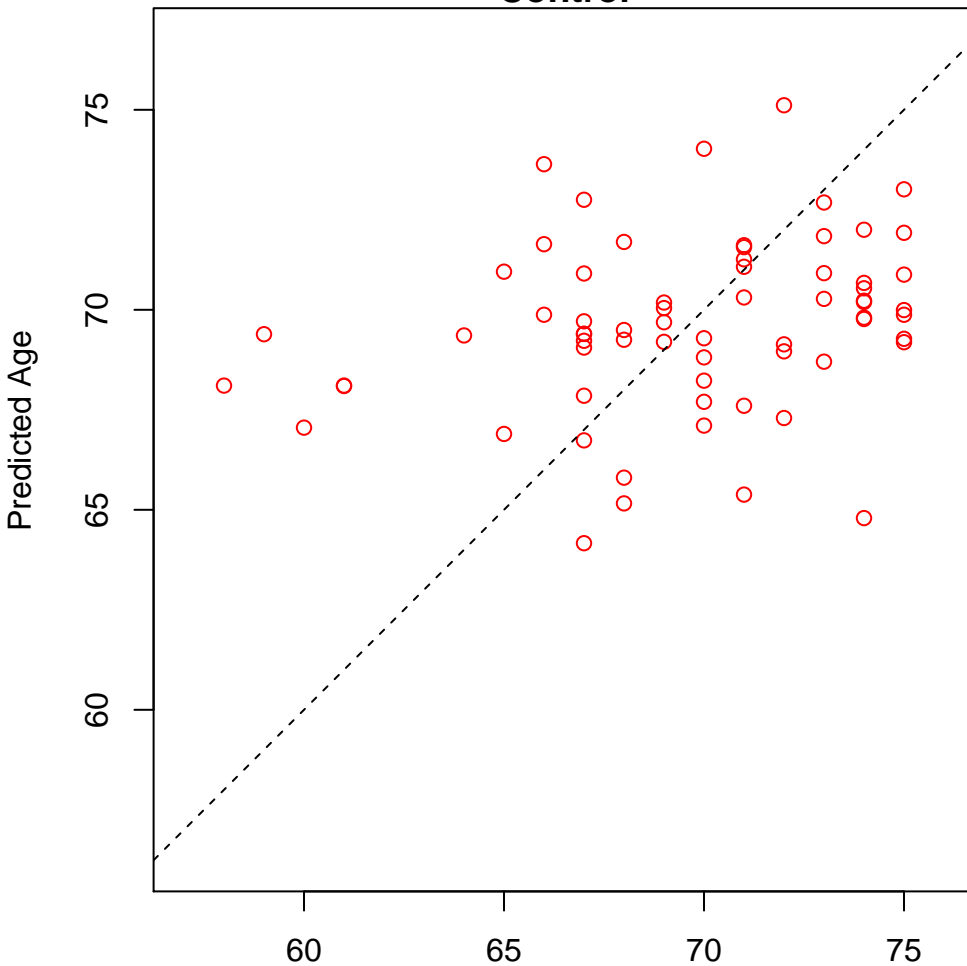


actin filament severing (Score: 0.323507)

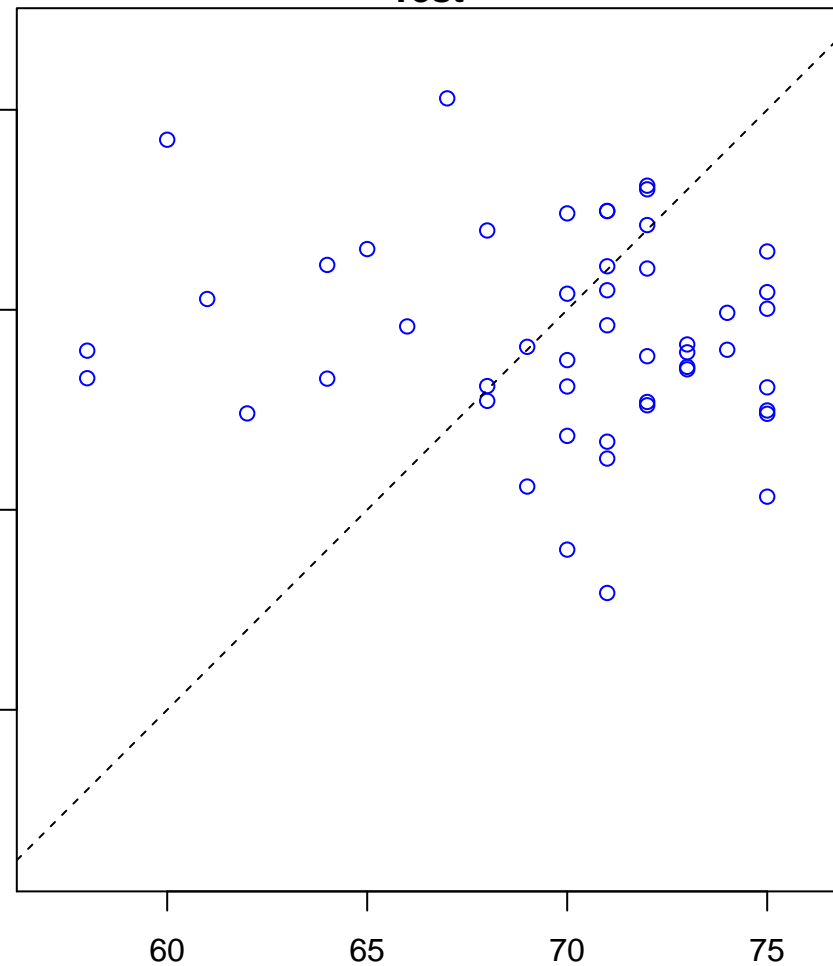


glandular epithelial cell differentiation (Score: 0.323264)

Control

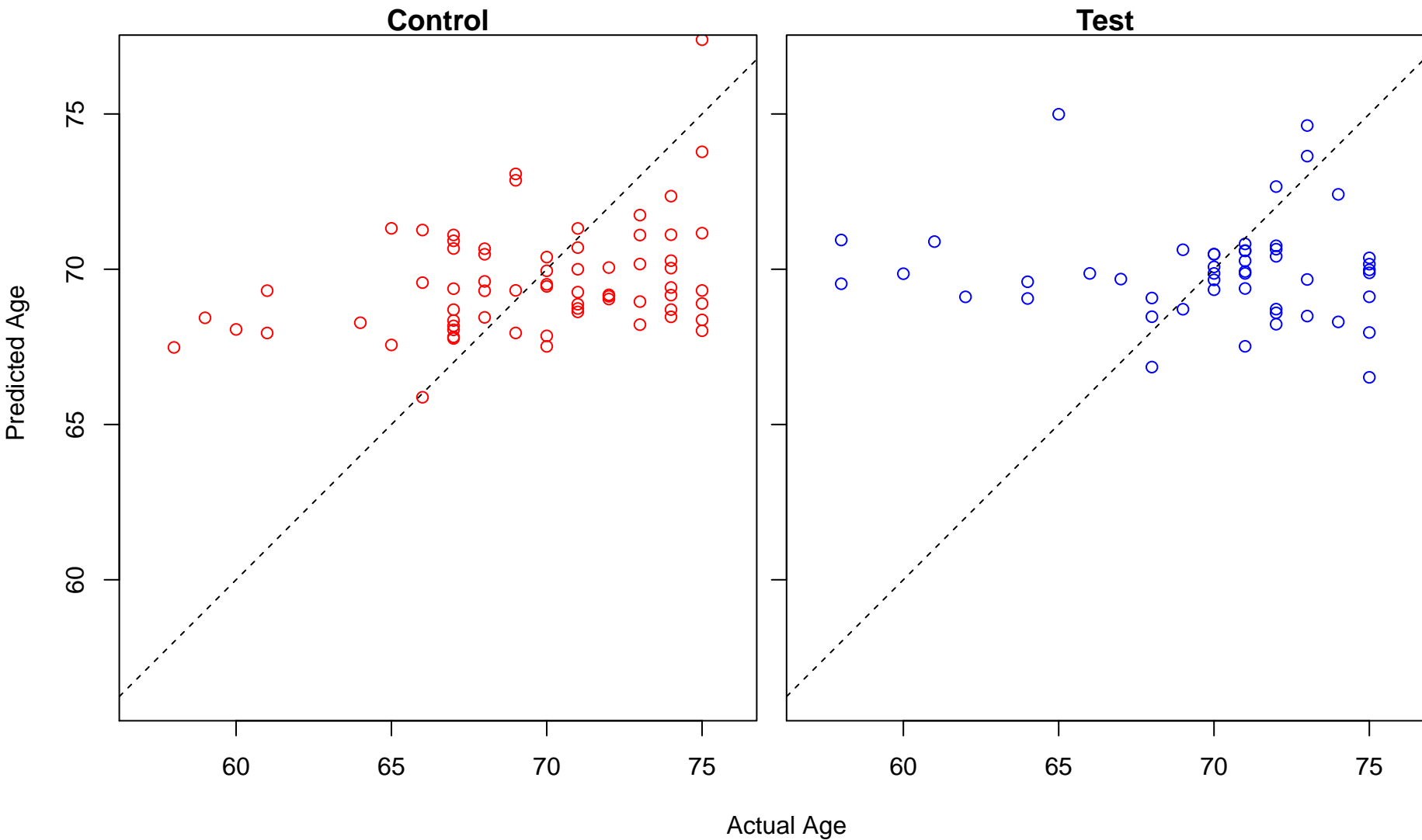


Test

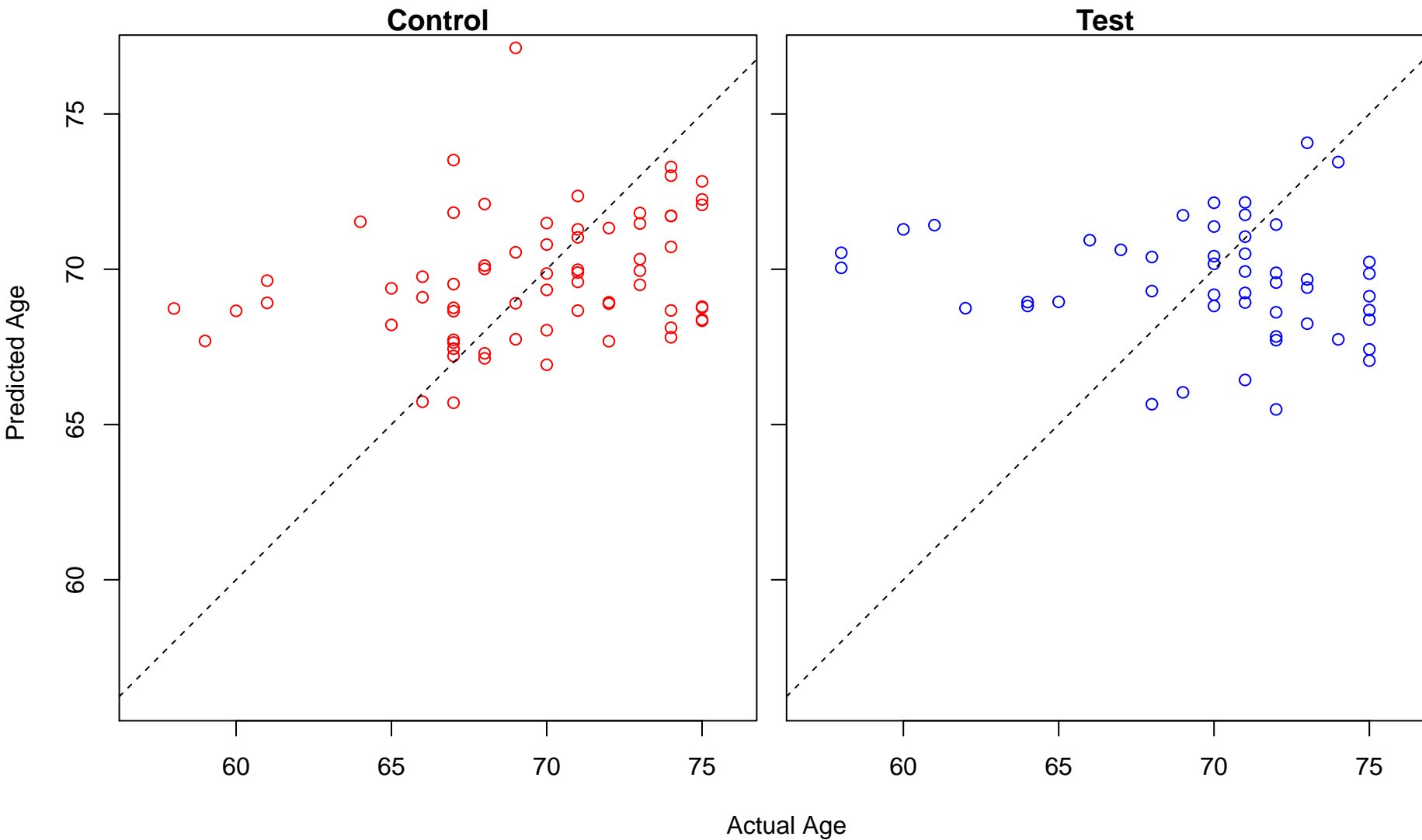


Actual Age

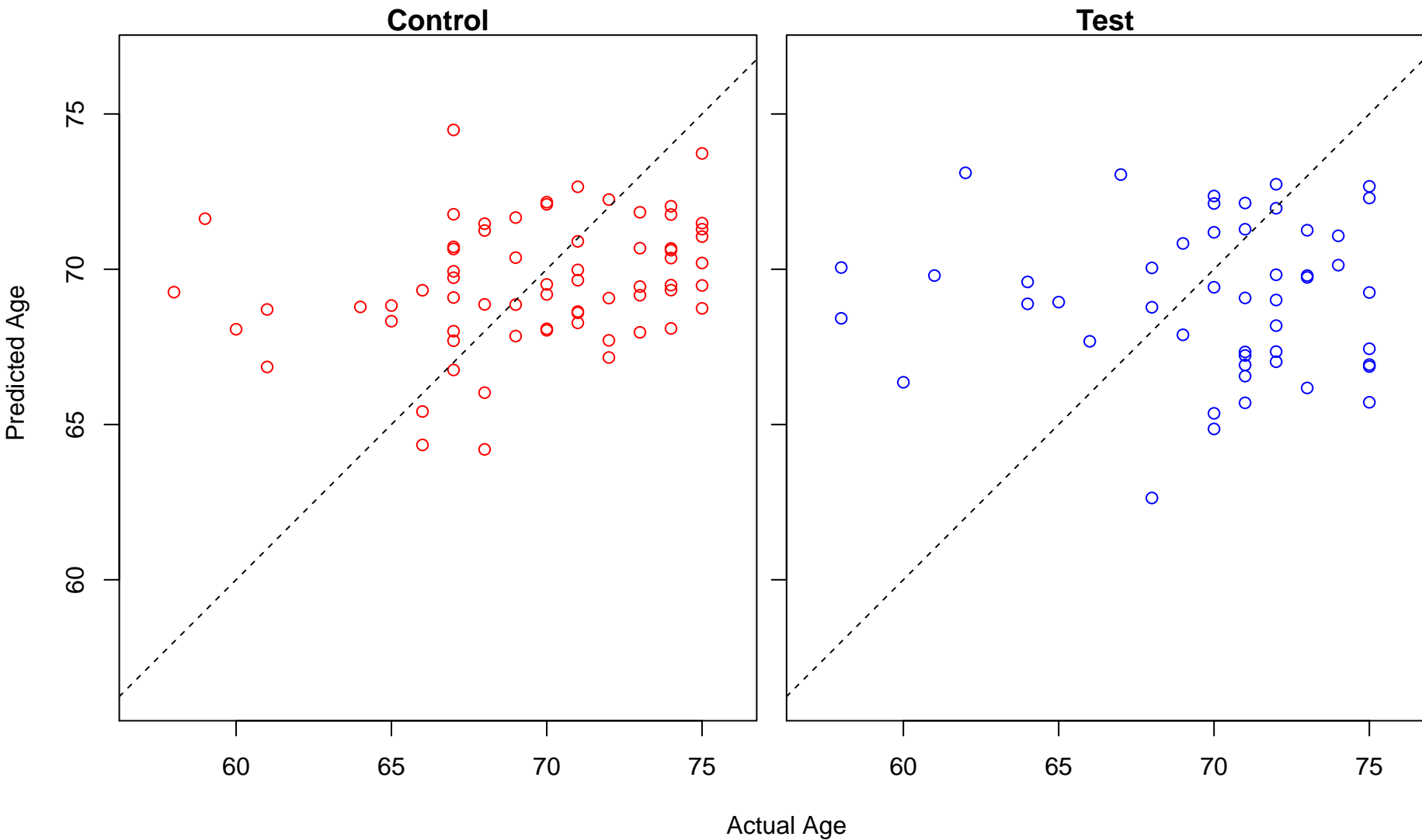
regulation of ventricular cardiac muscle cell membrane repolarization (Score: 0.322436)



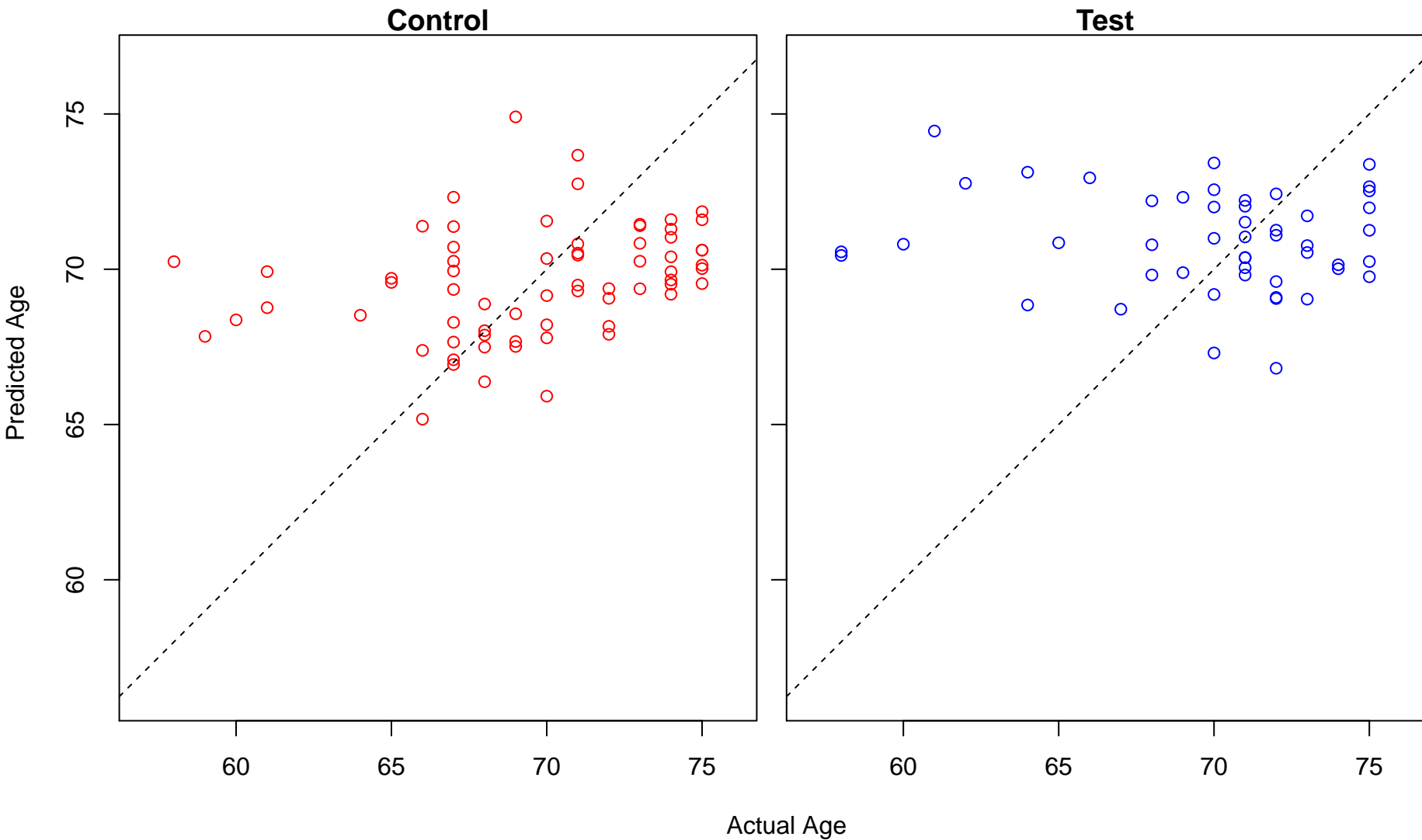
regulation of morphogenesis of a branching structure (Score: 0.321357)



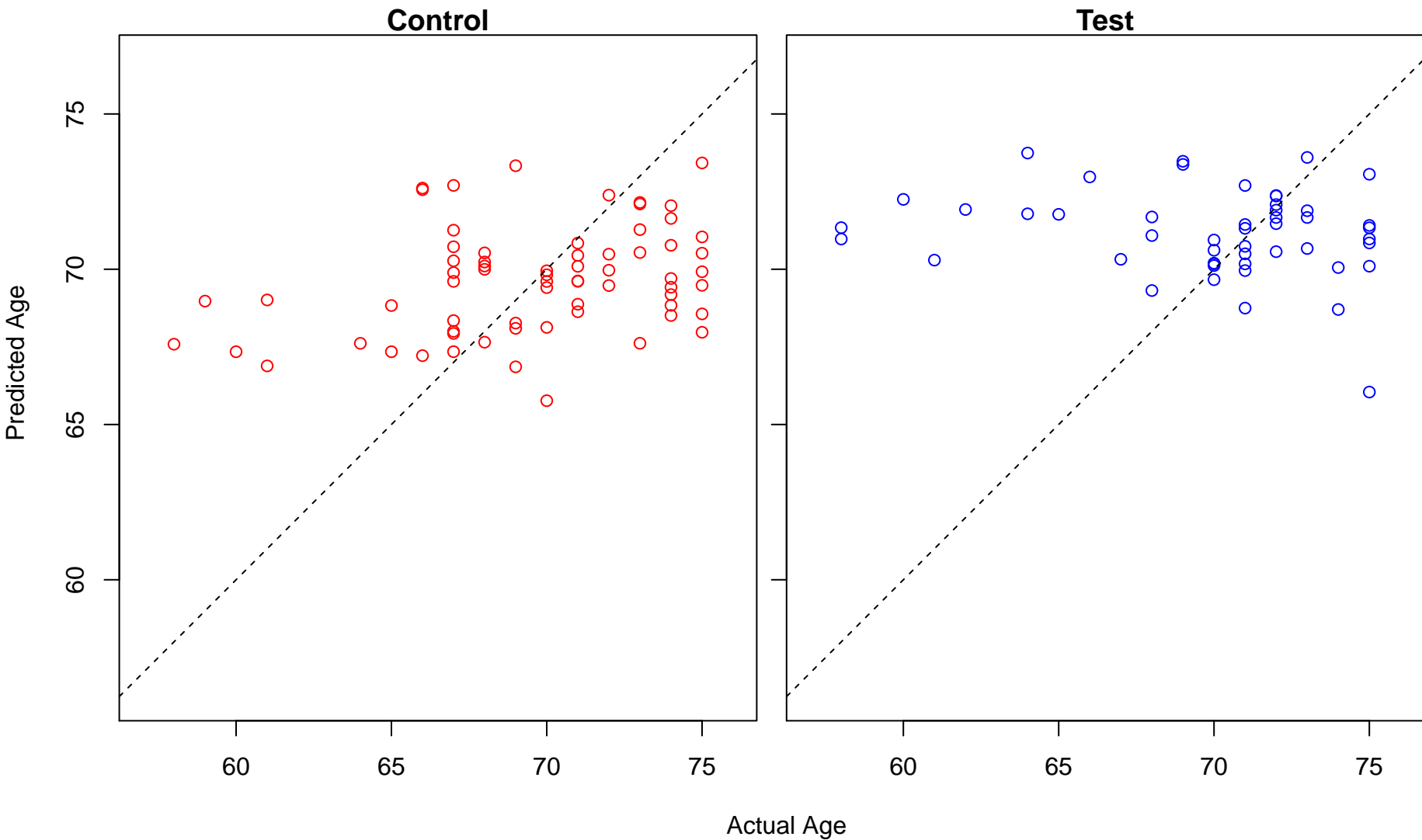
regulation of myelination (Score: 0.320912)



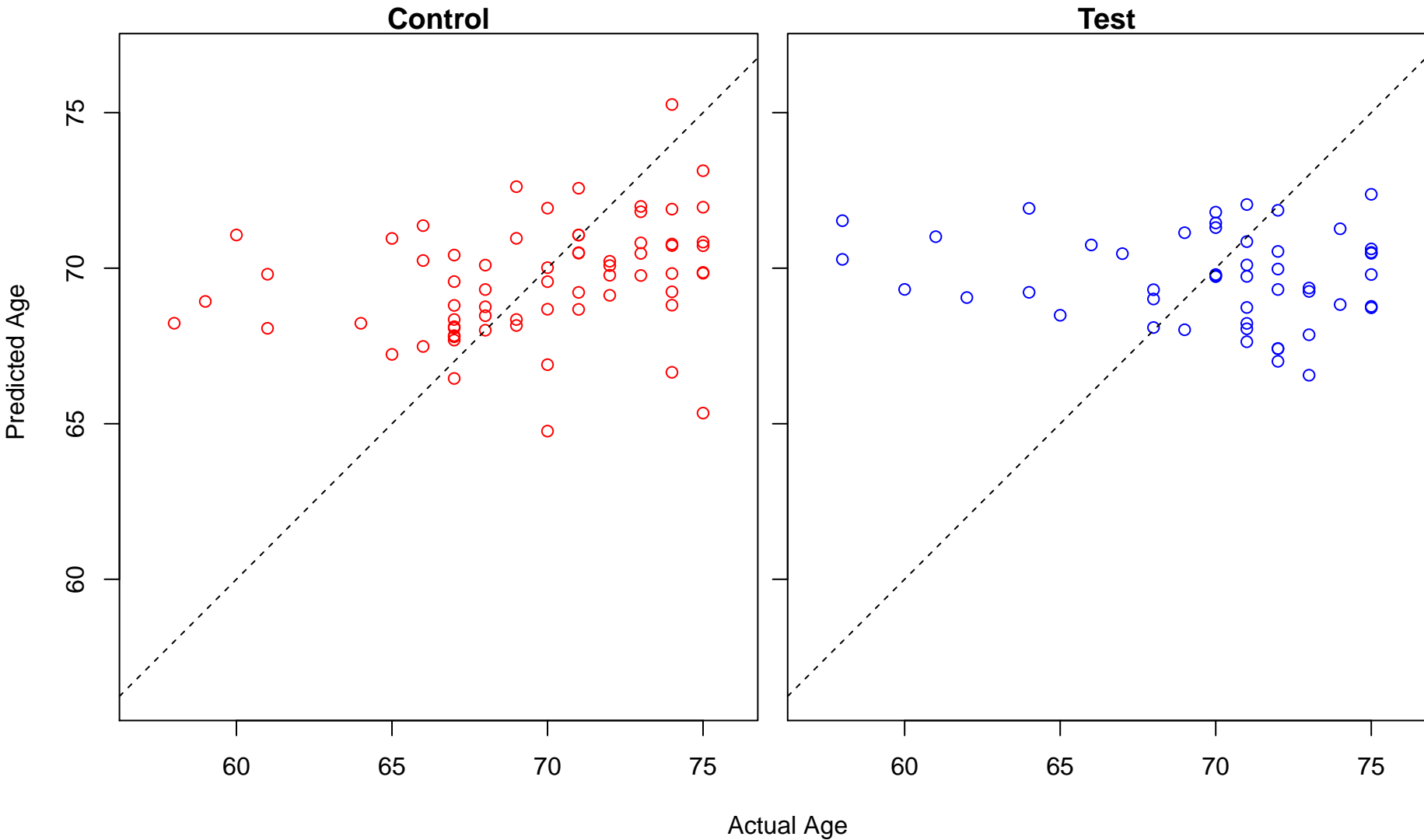
adenine transport (Score: 0.318738)



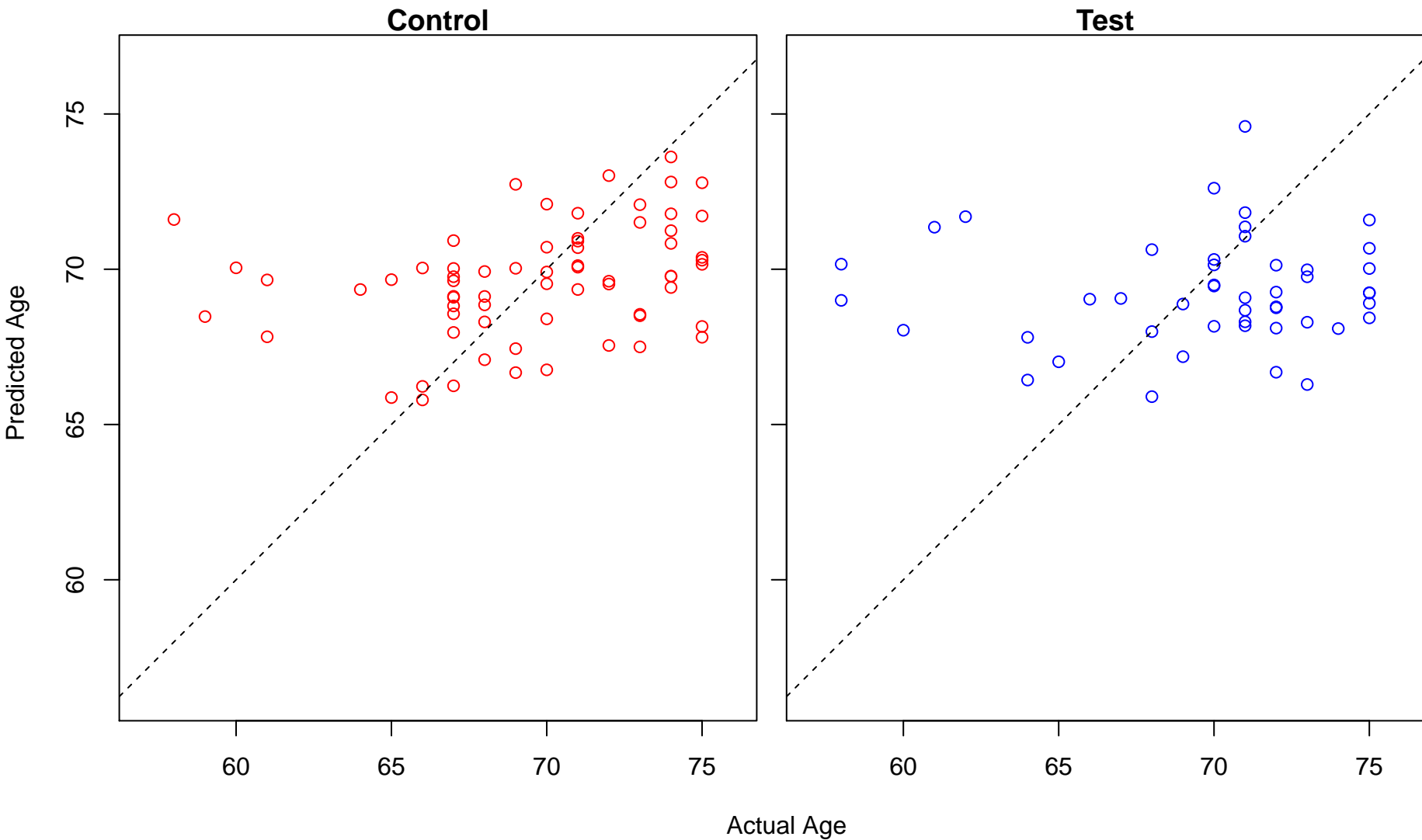
positive regulation of transcription initiation from RNA polymerase II promoter (Score: 0.318065)



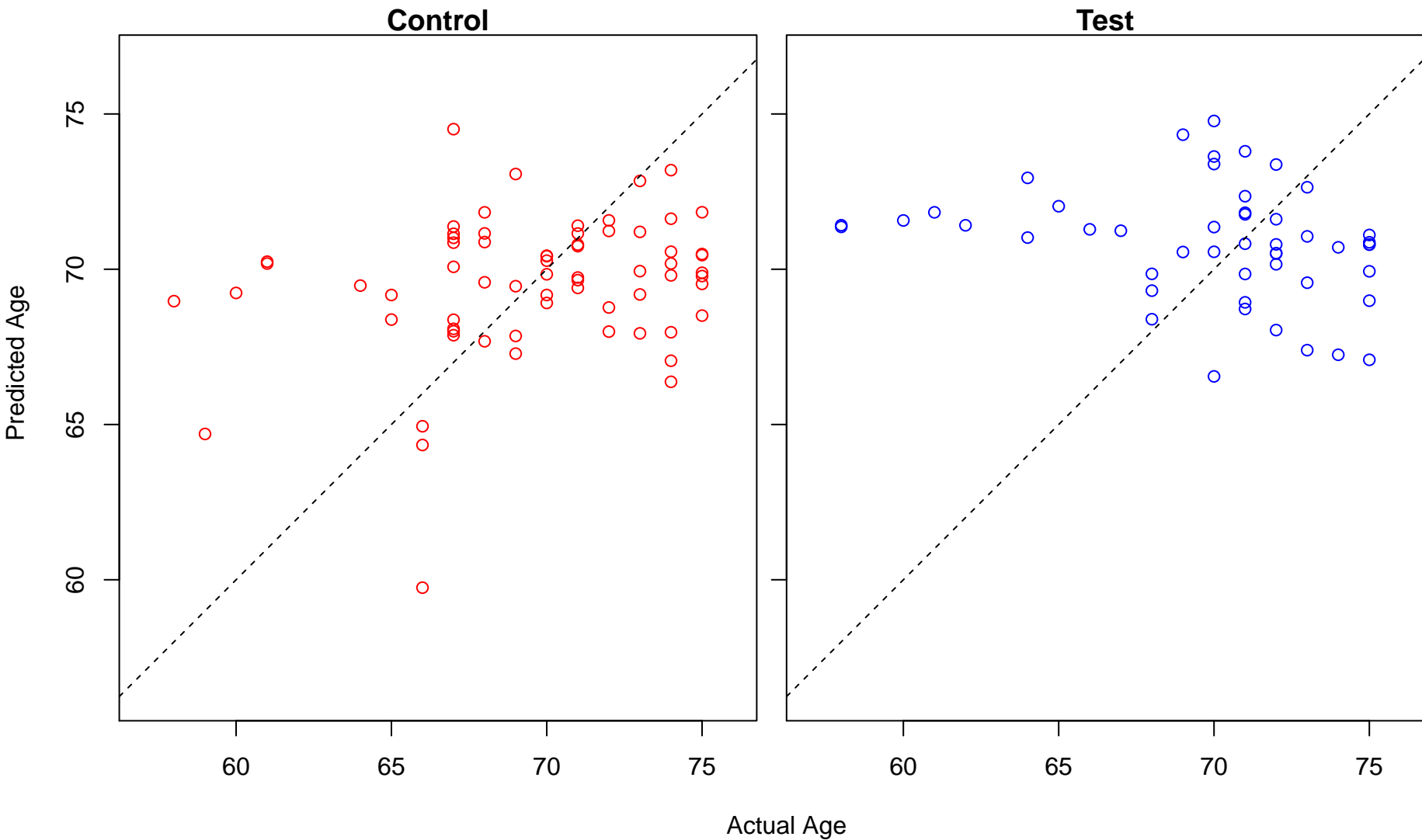
regulation of tooth mineralization (Score: 0.315929)



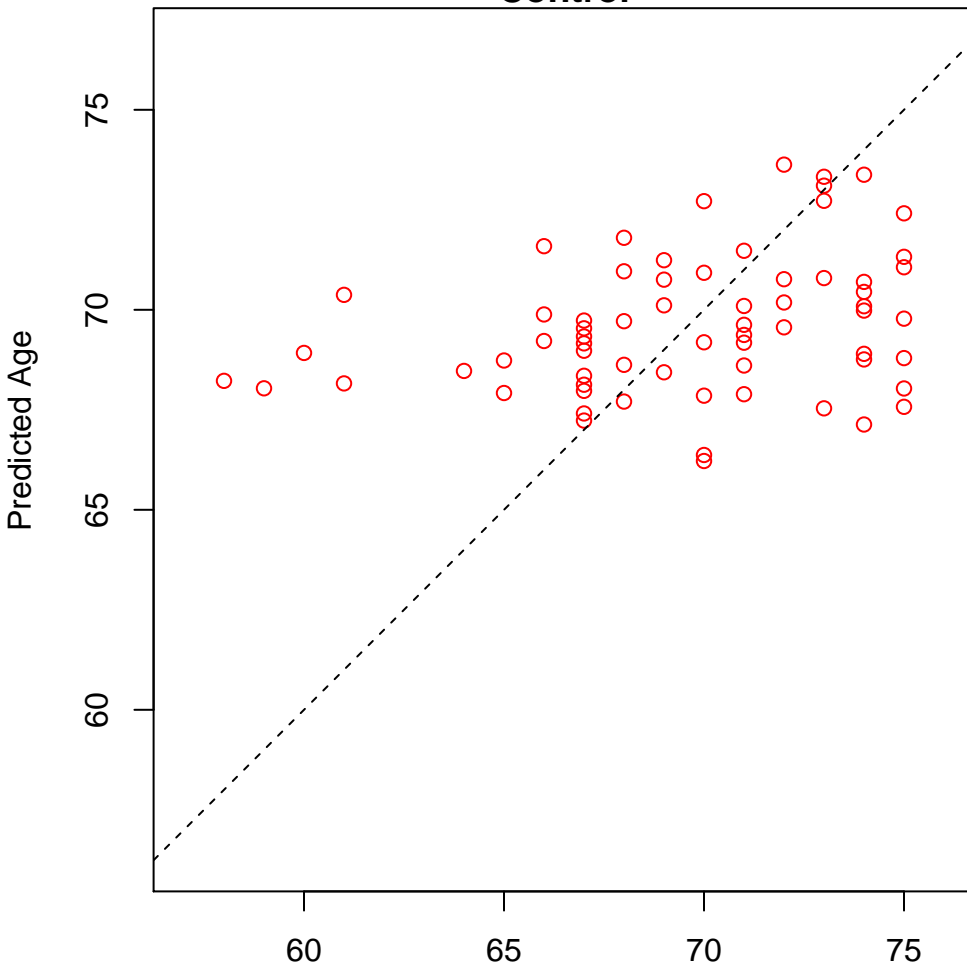
regulation of T-helper 17 type immune response (Score: 0.314296)



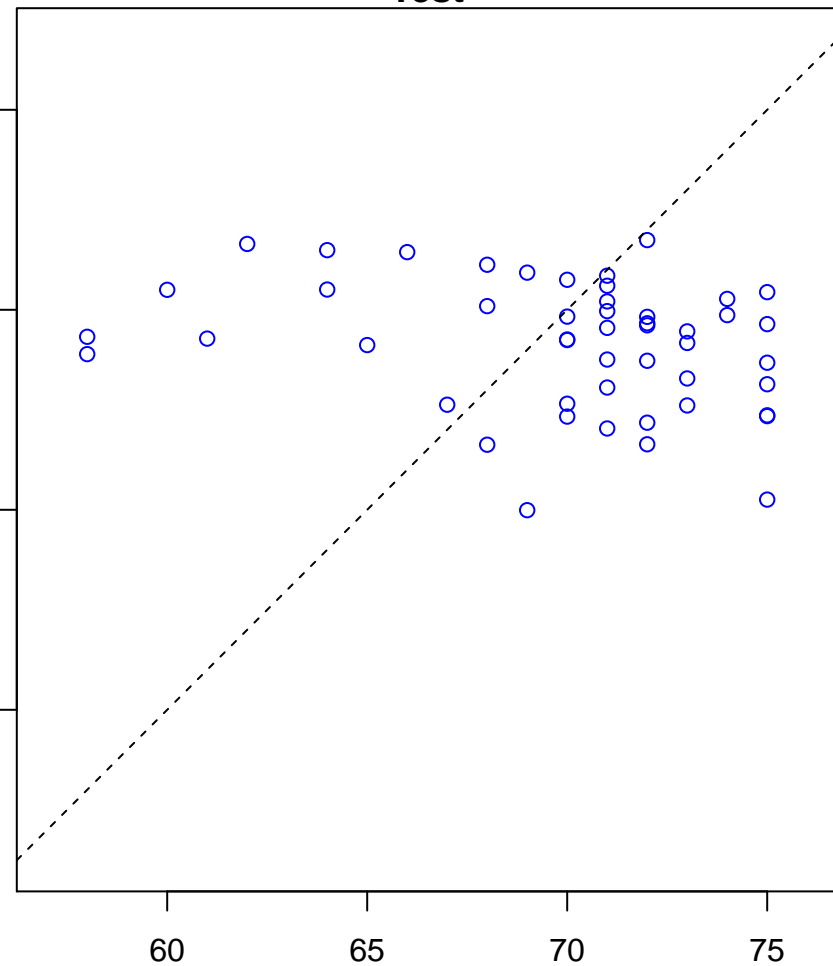
negative regulation of humoral immune response (Score: 0.313032)



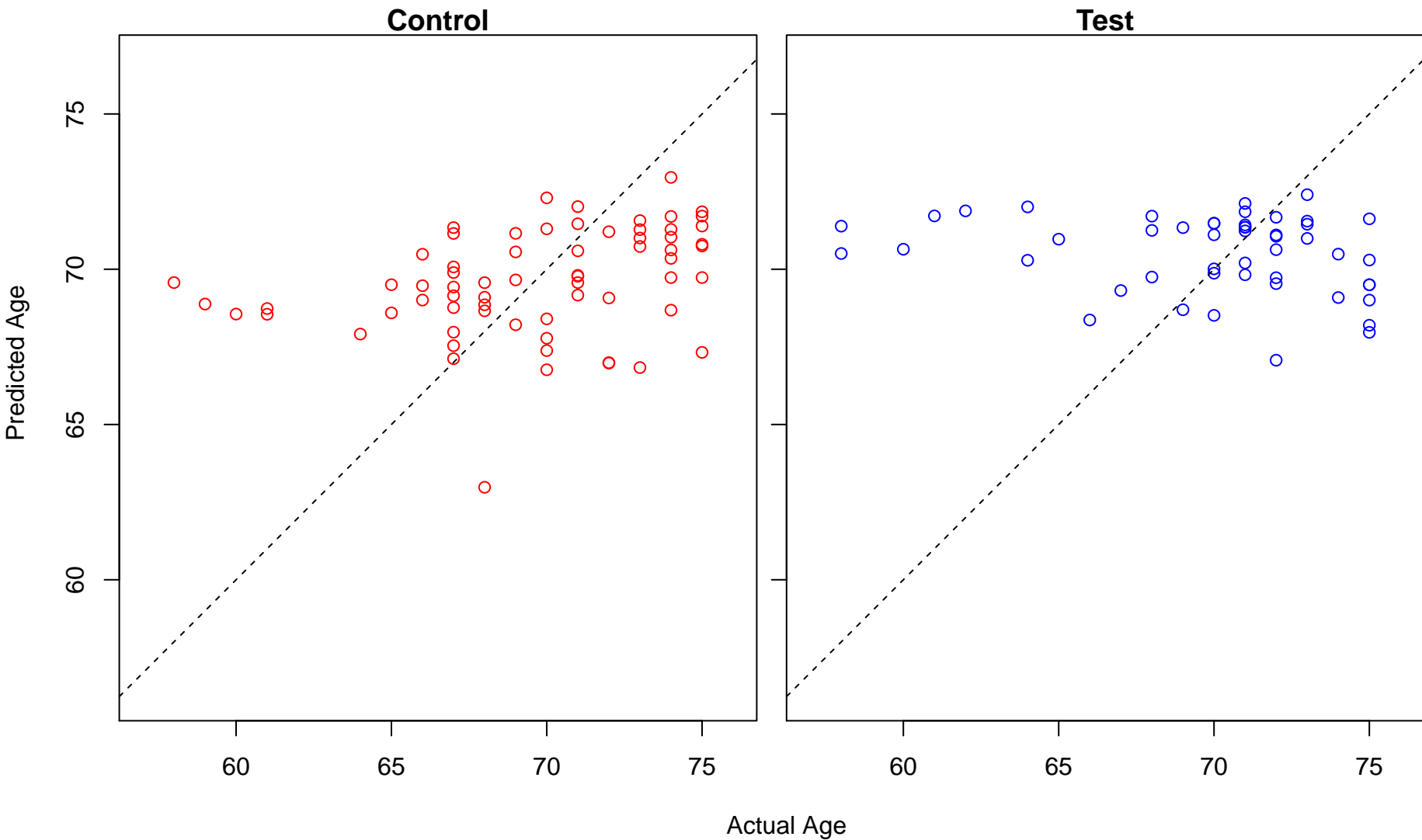
Control



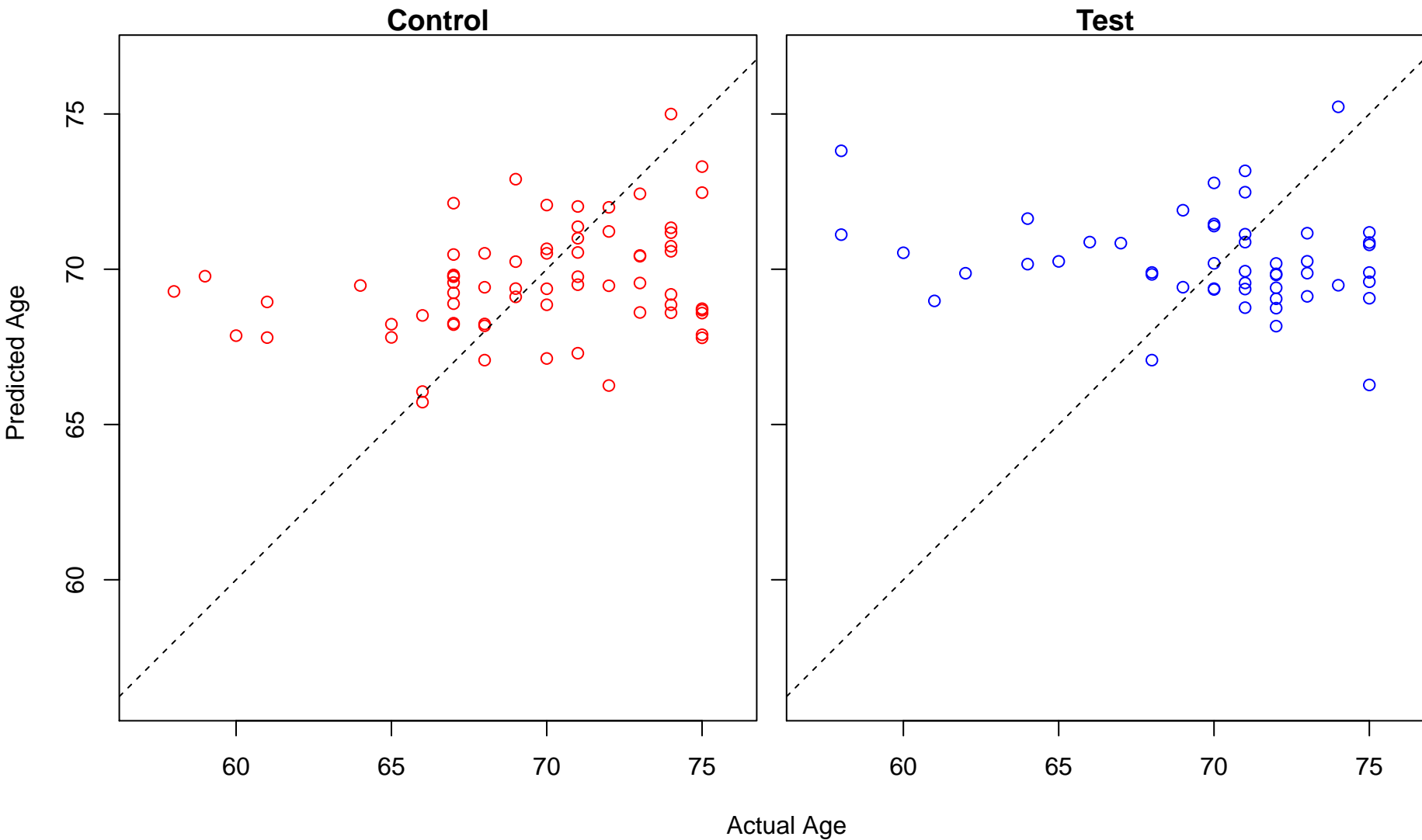
Test



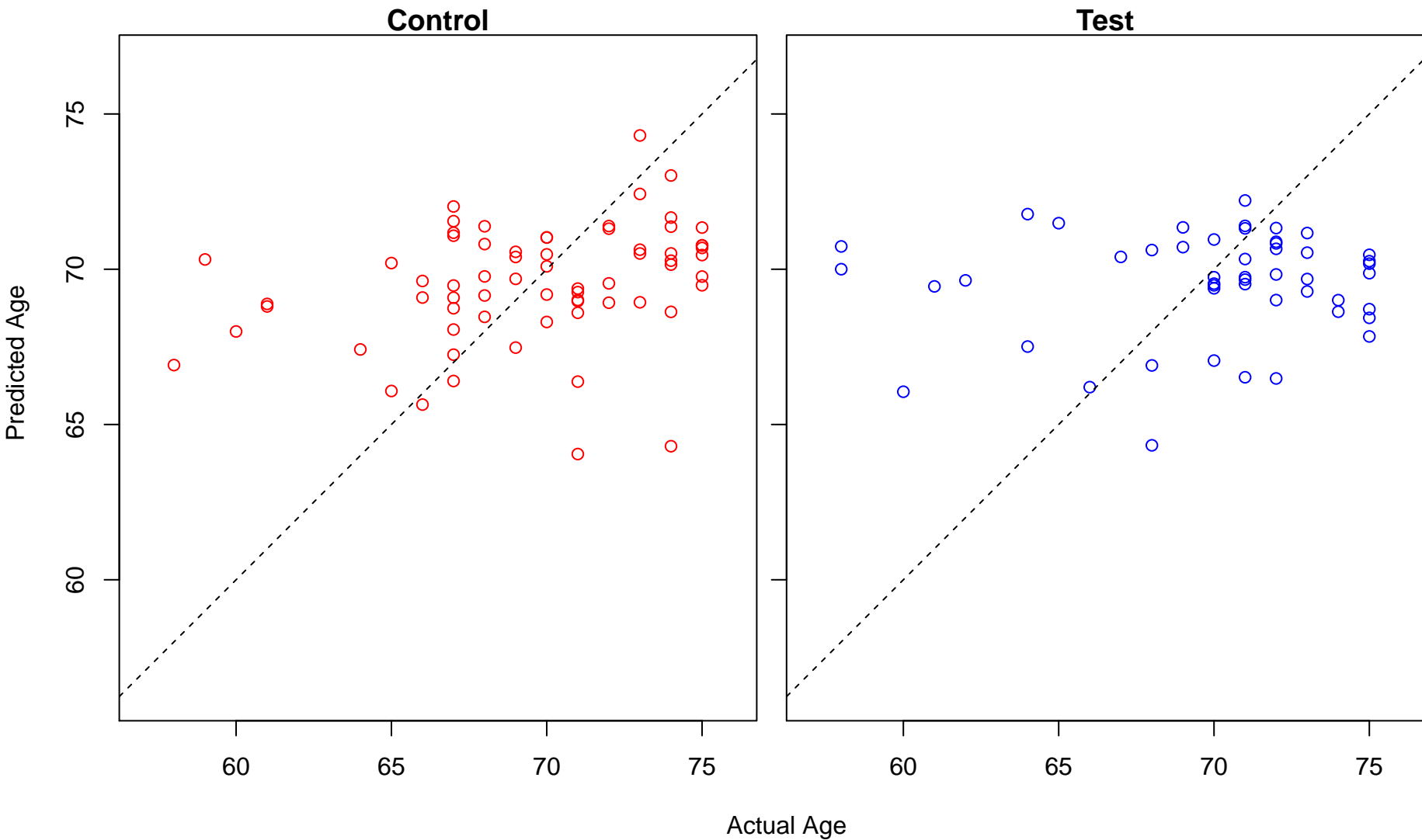
positive regulation of cellular amino acid metabolic process (Score: 0.312157)



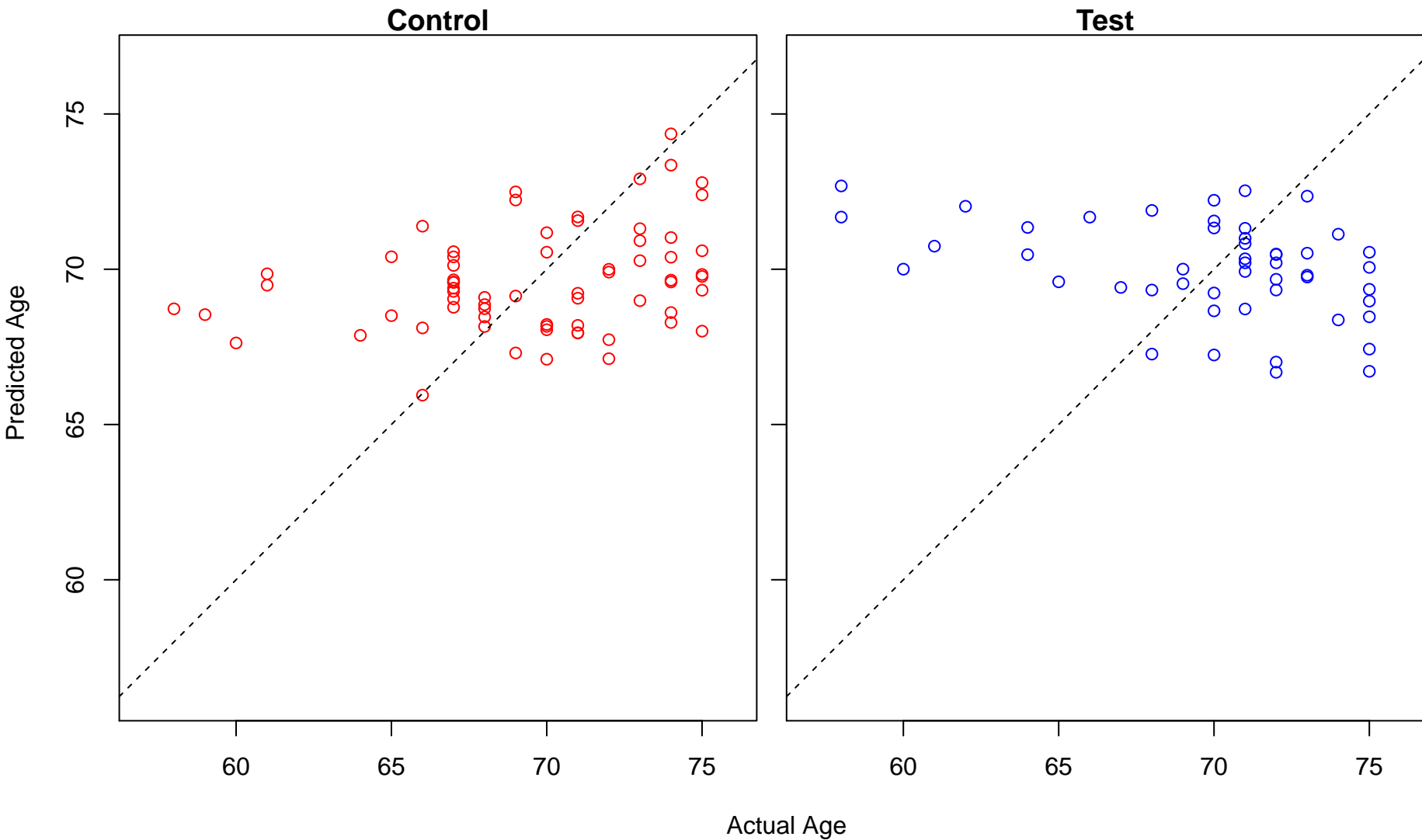
positive regulation of lipoprotein lipase activity (Score: 0.312137)



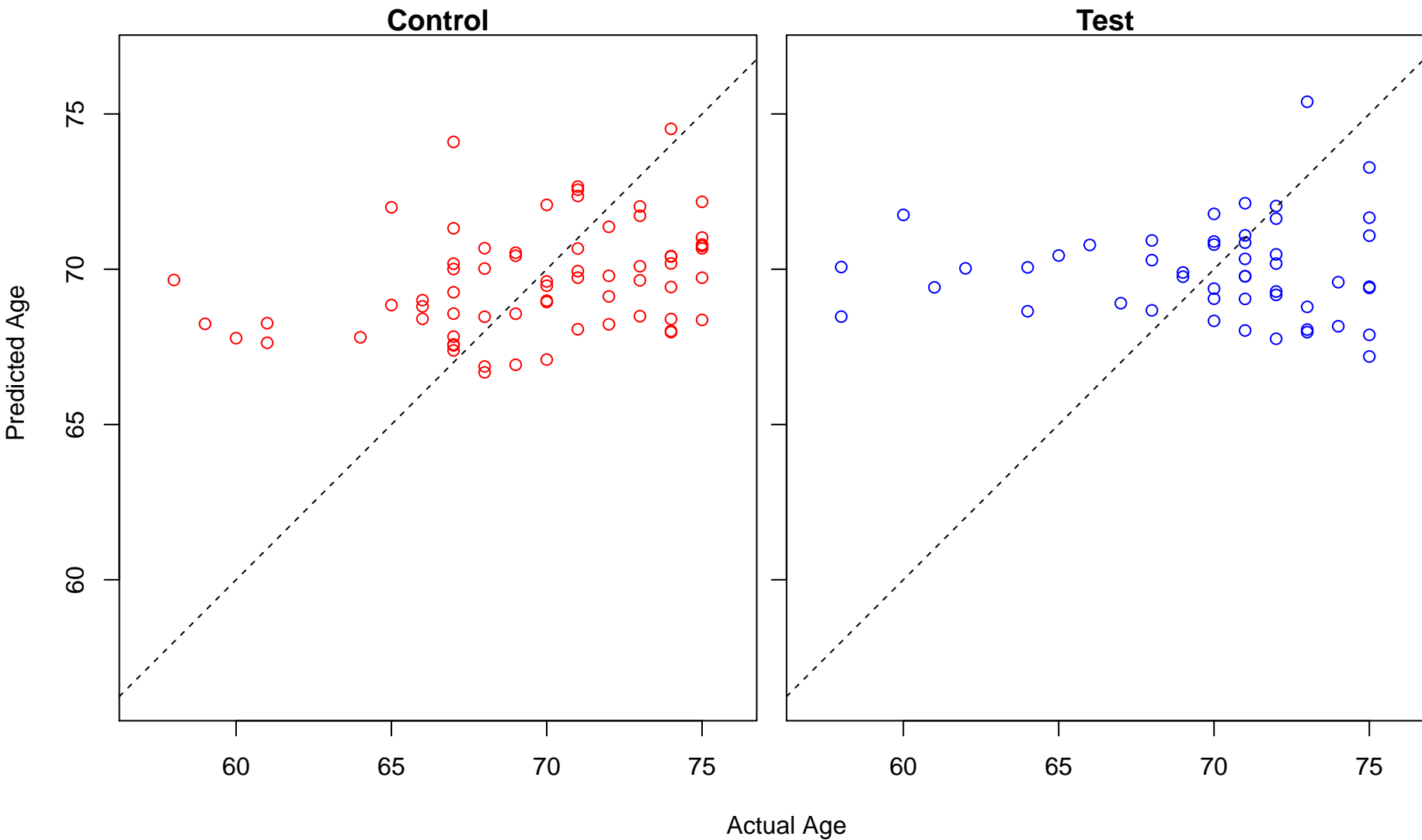
regulation of ventricular cardiac muscle cell action potential (Score: 0.311415)



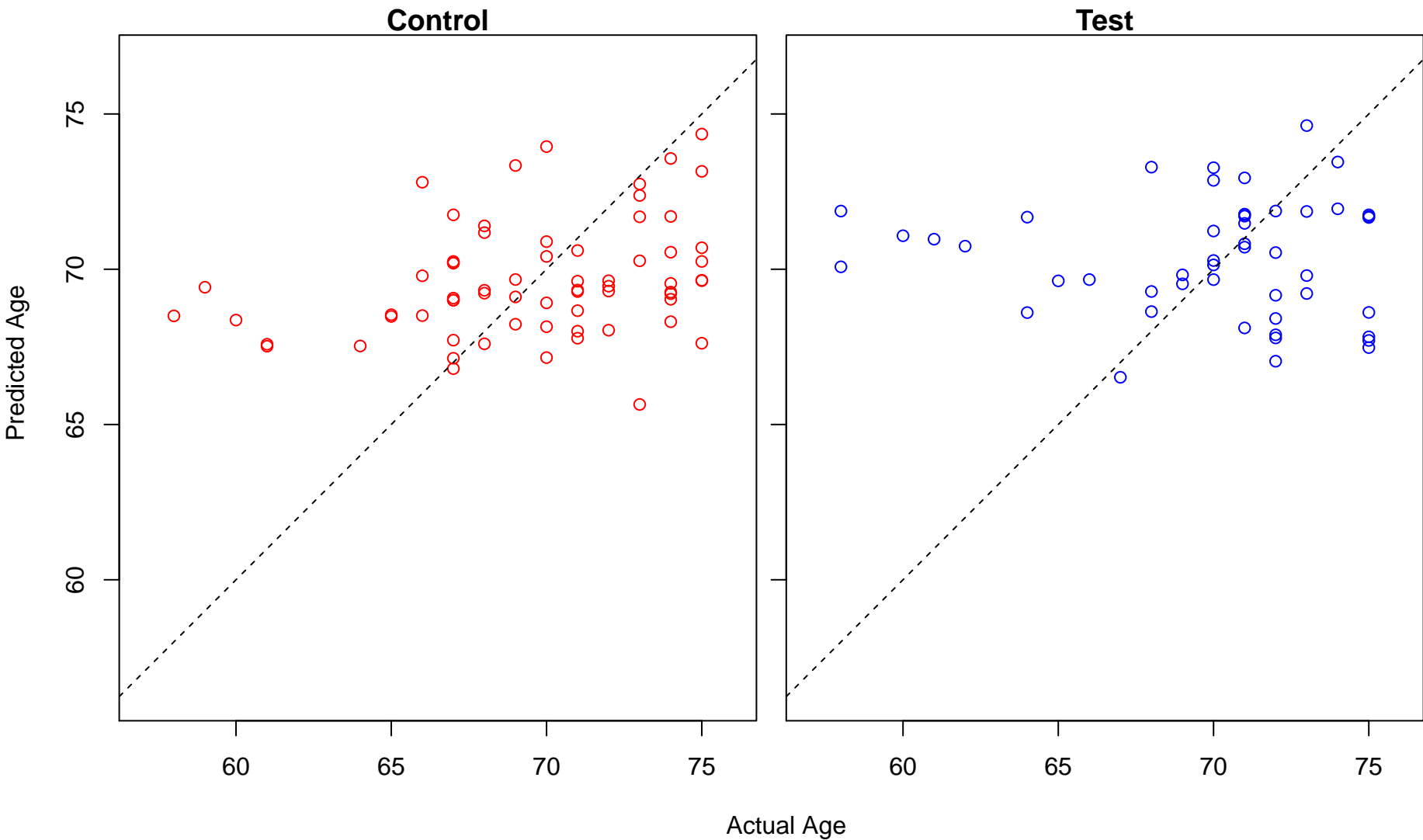
positive regulation of interleukin-23 production (Score: 0.310172)



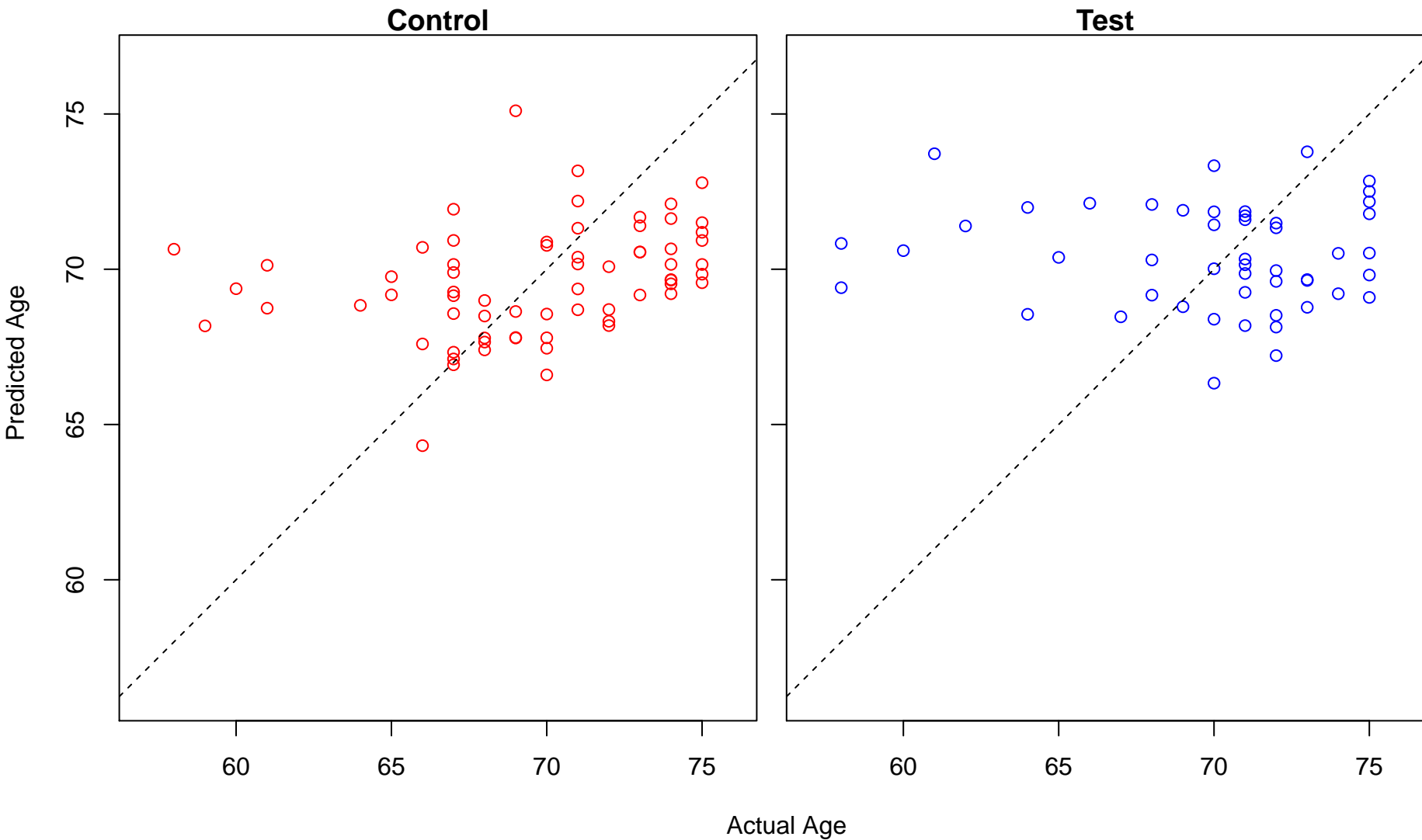
cell volume homeostasis (Score: 0.309825)



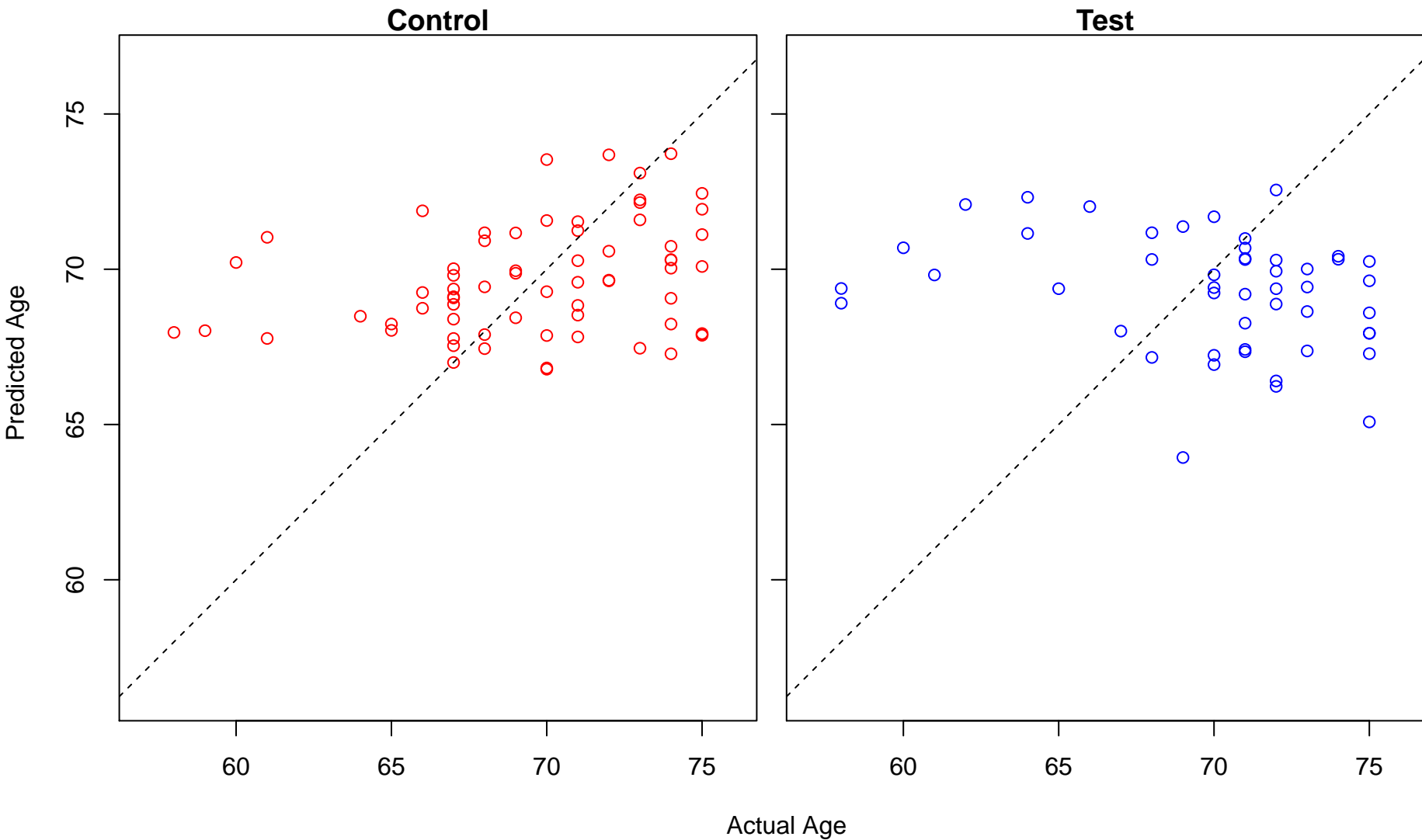
positive regulation of basement membrane assembly involved in embryonic body morphogenesis (Score: 0.0001)



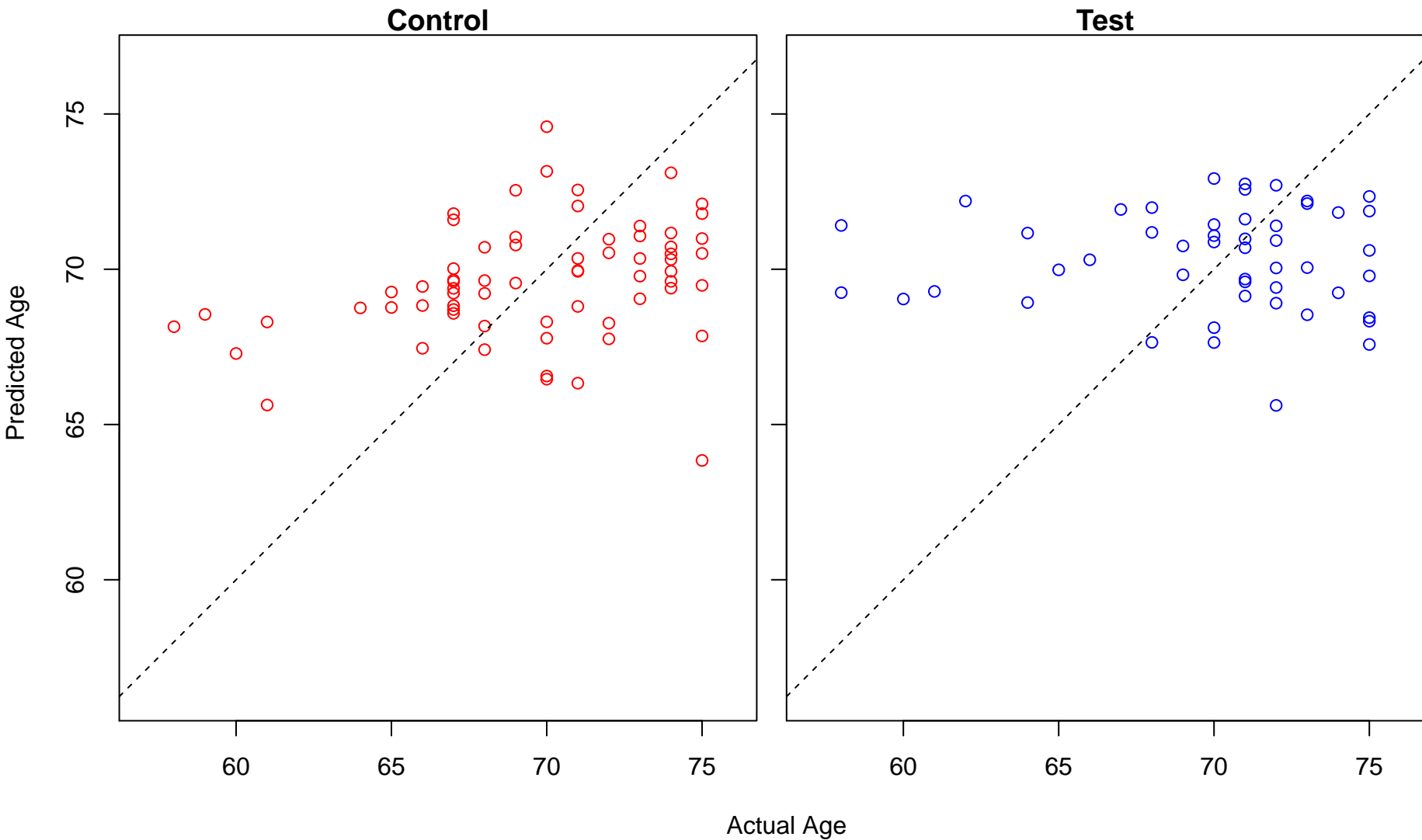
purine nucleobase transport (Score: 0.309490)



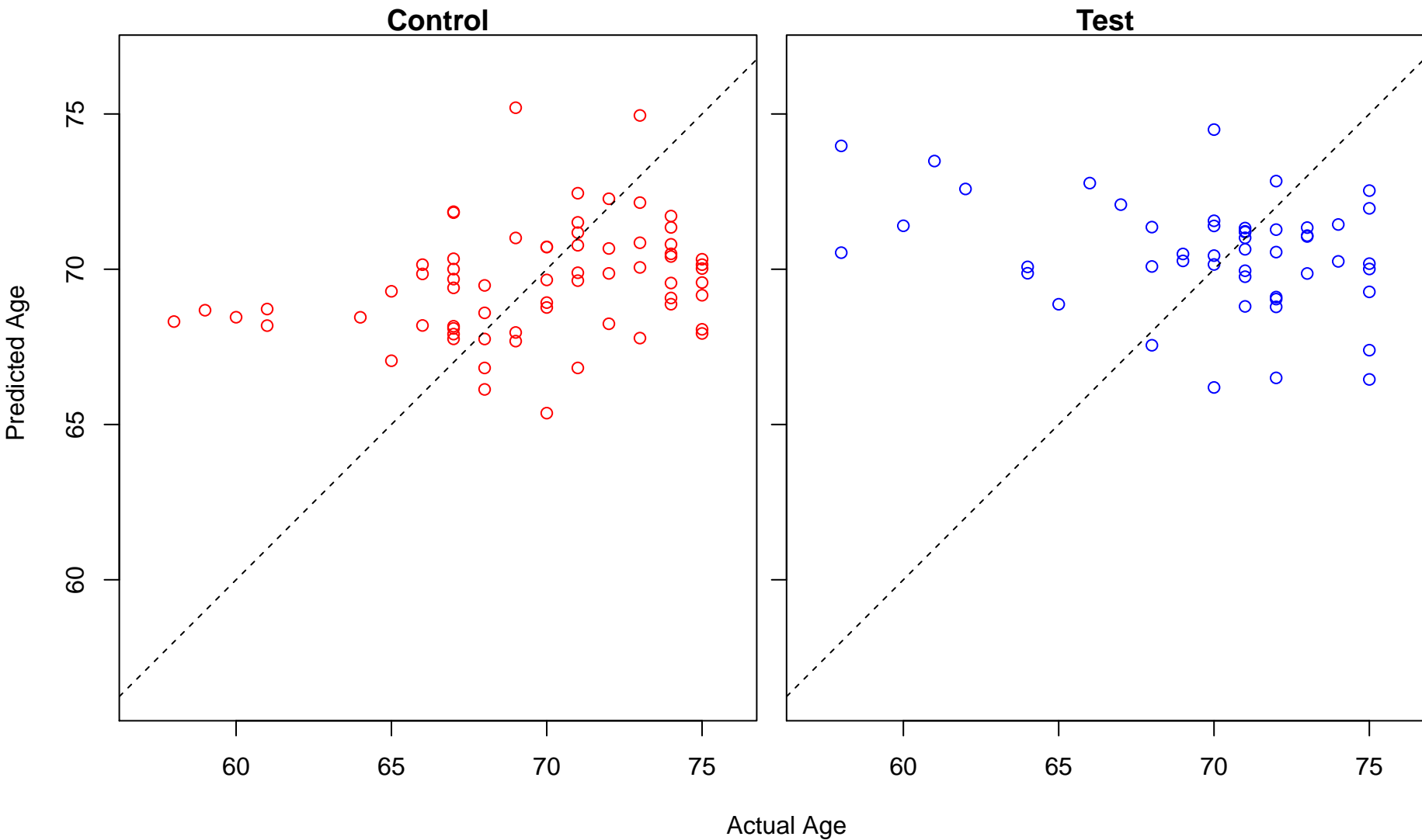
spinal cord patterning (Score: 0.309193)



protein kinase A signaling (Score: 0.308386)

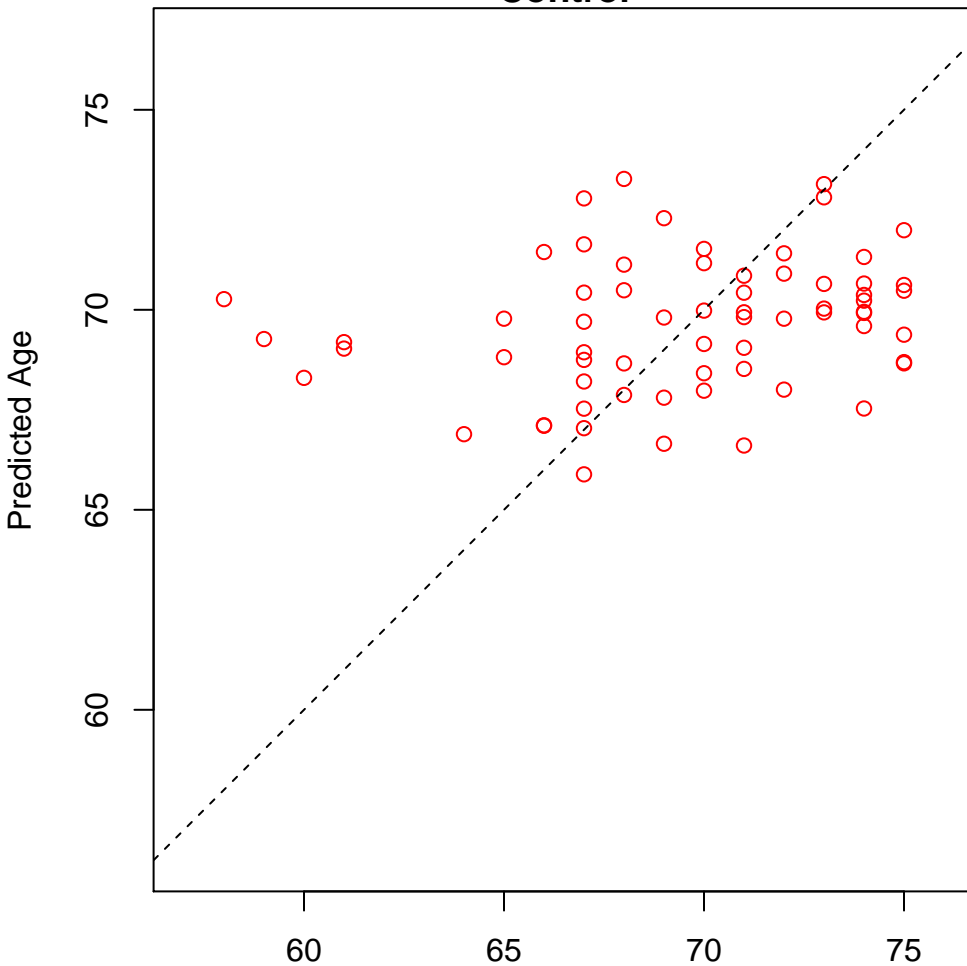


membrane lipid catabolic process (Score: 0.308301)

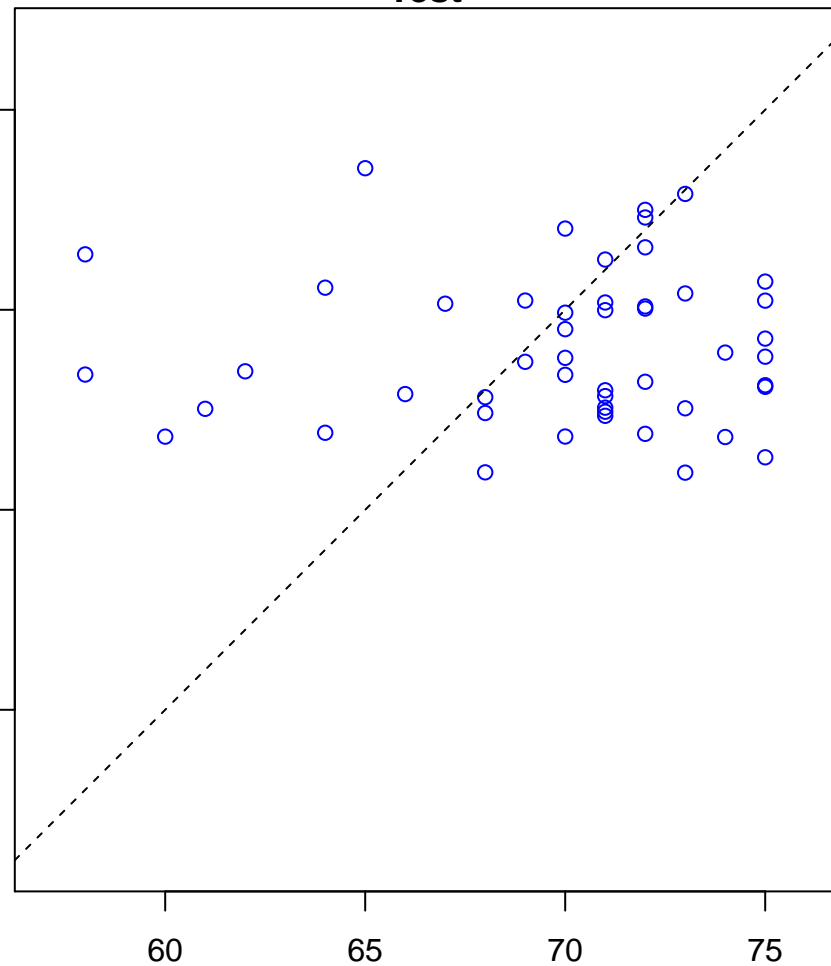


protein insertion into membrane (Score: 0.307931)

Control

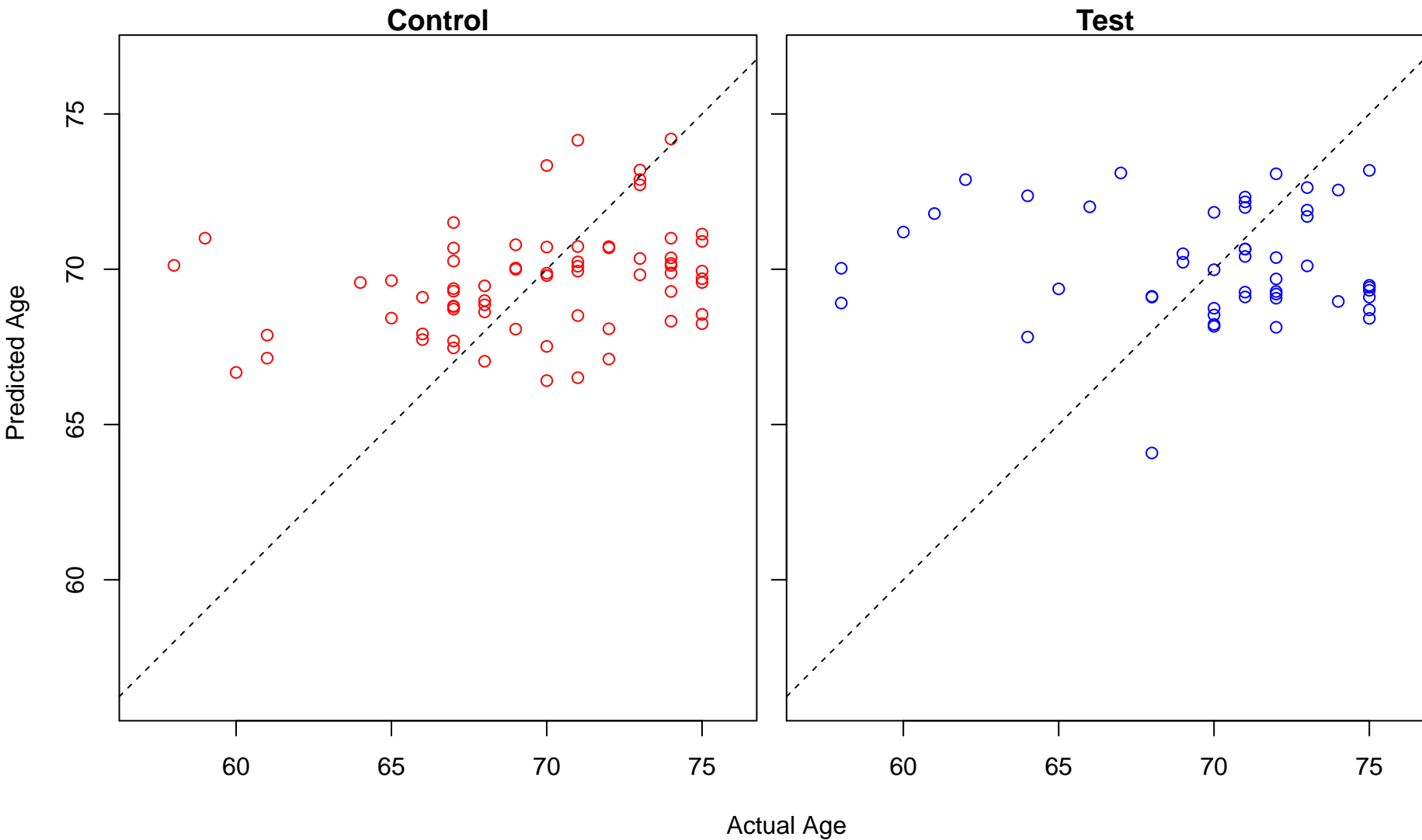


Test

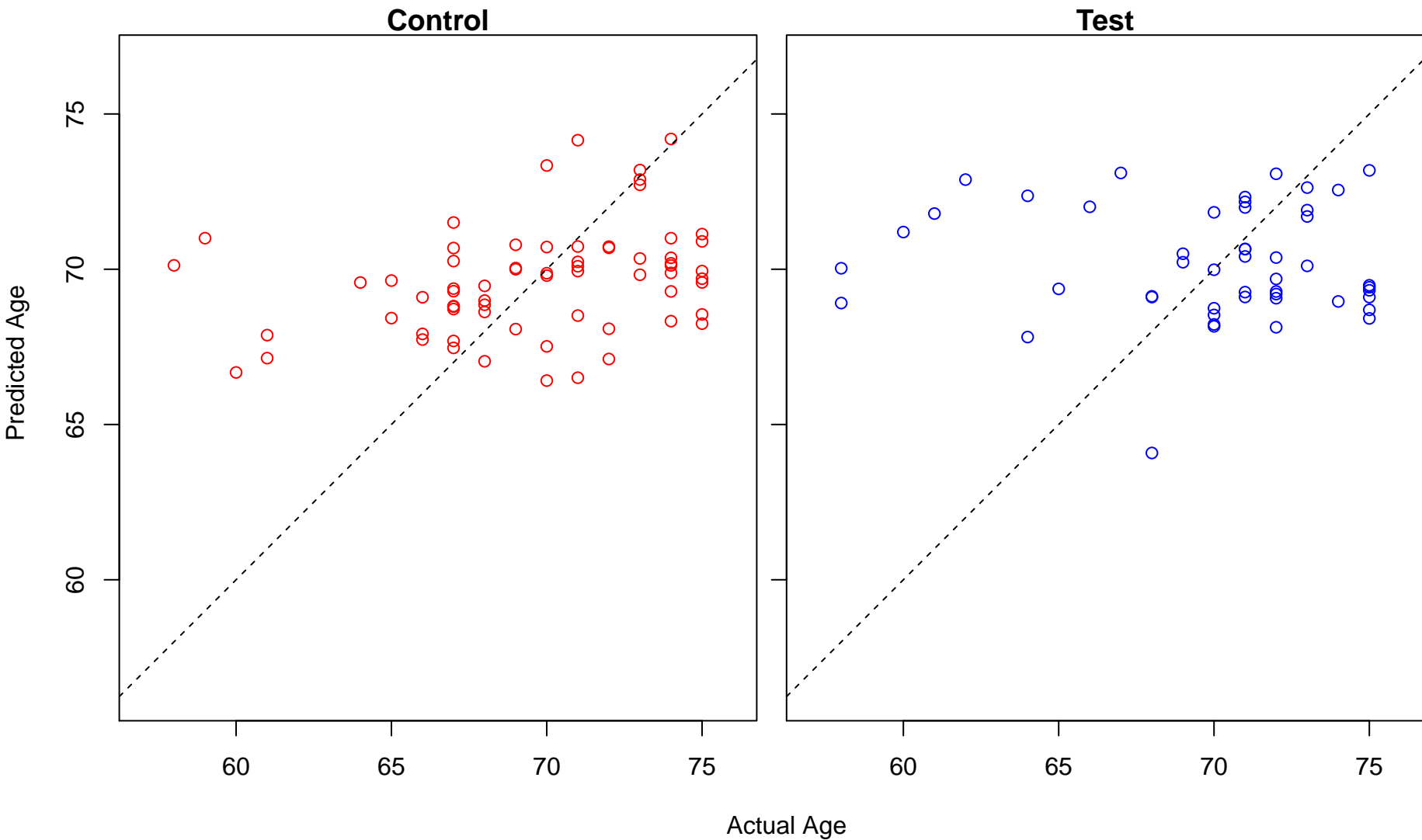


Actual Age

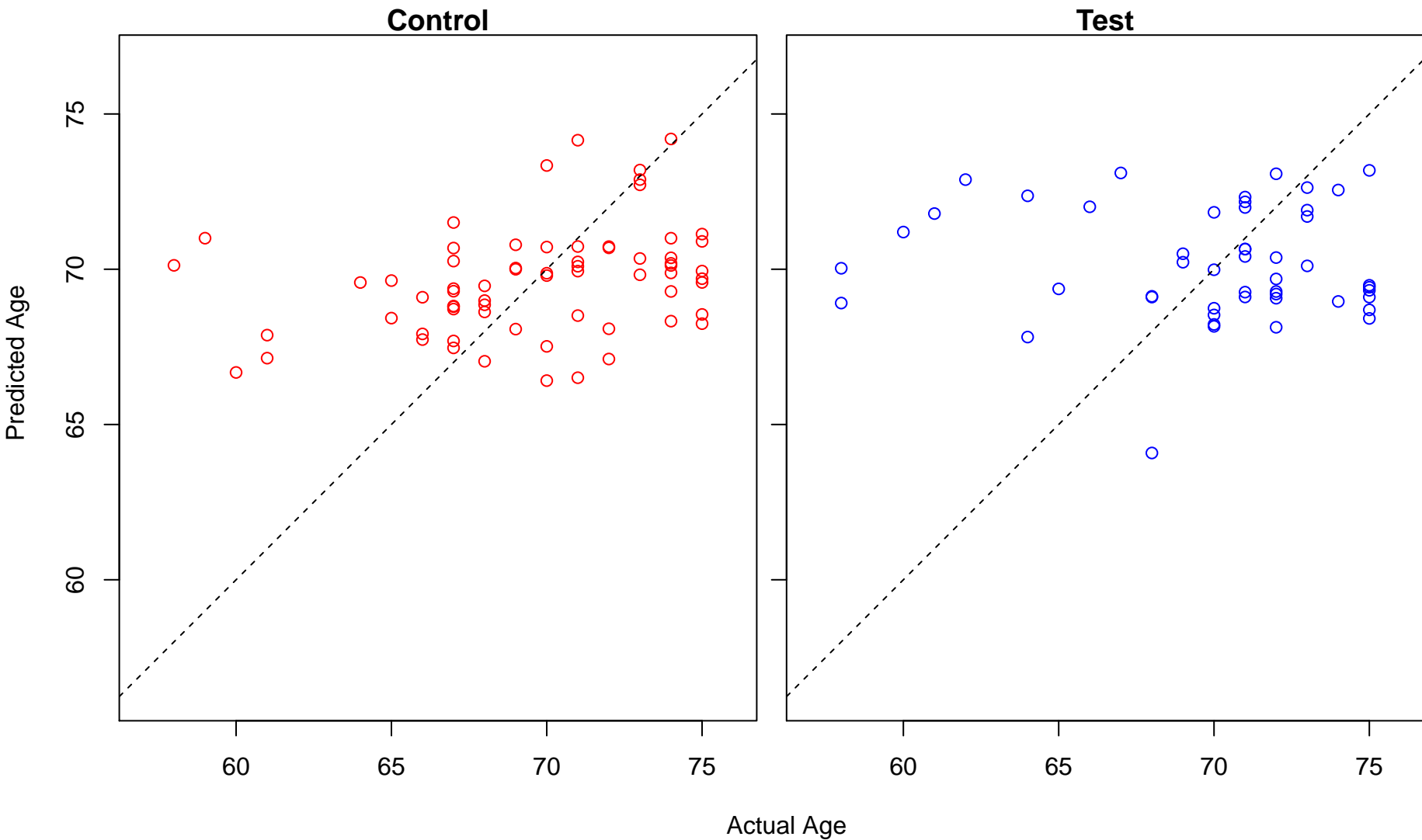
respiratory chain complex III assembly (Score: 0.306510)



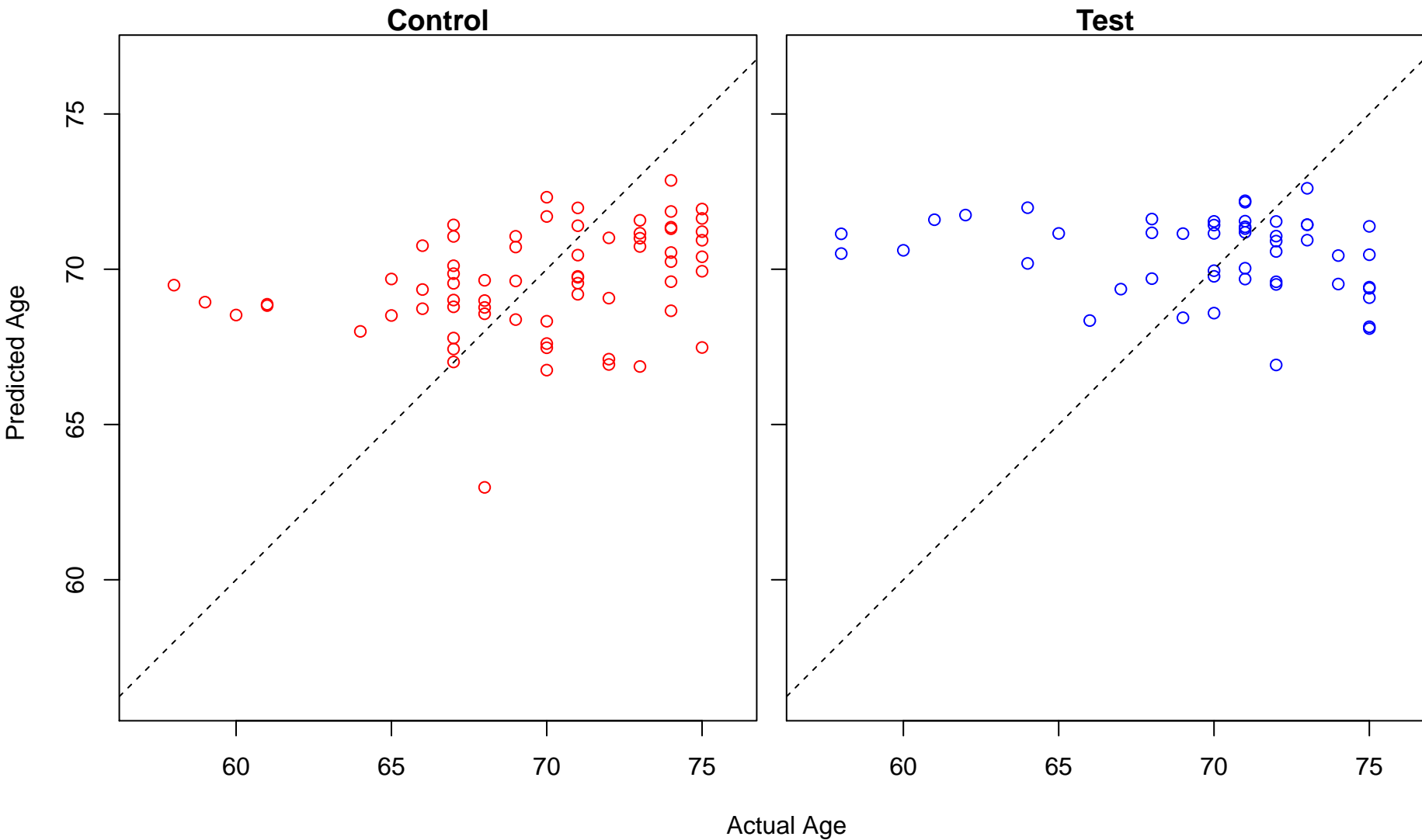
mitochondrial respiratory chain complex III assembly (Score: 0.306510)



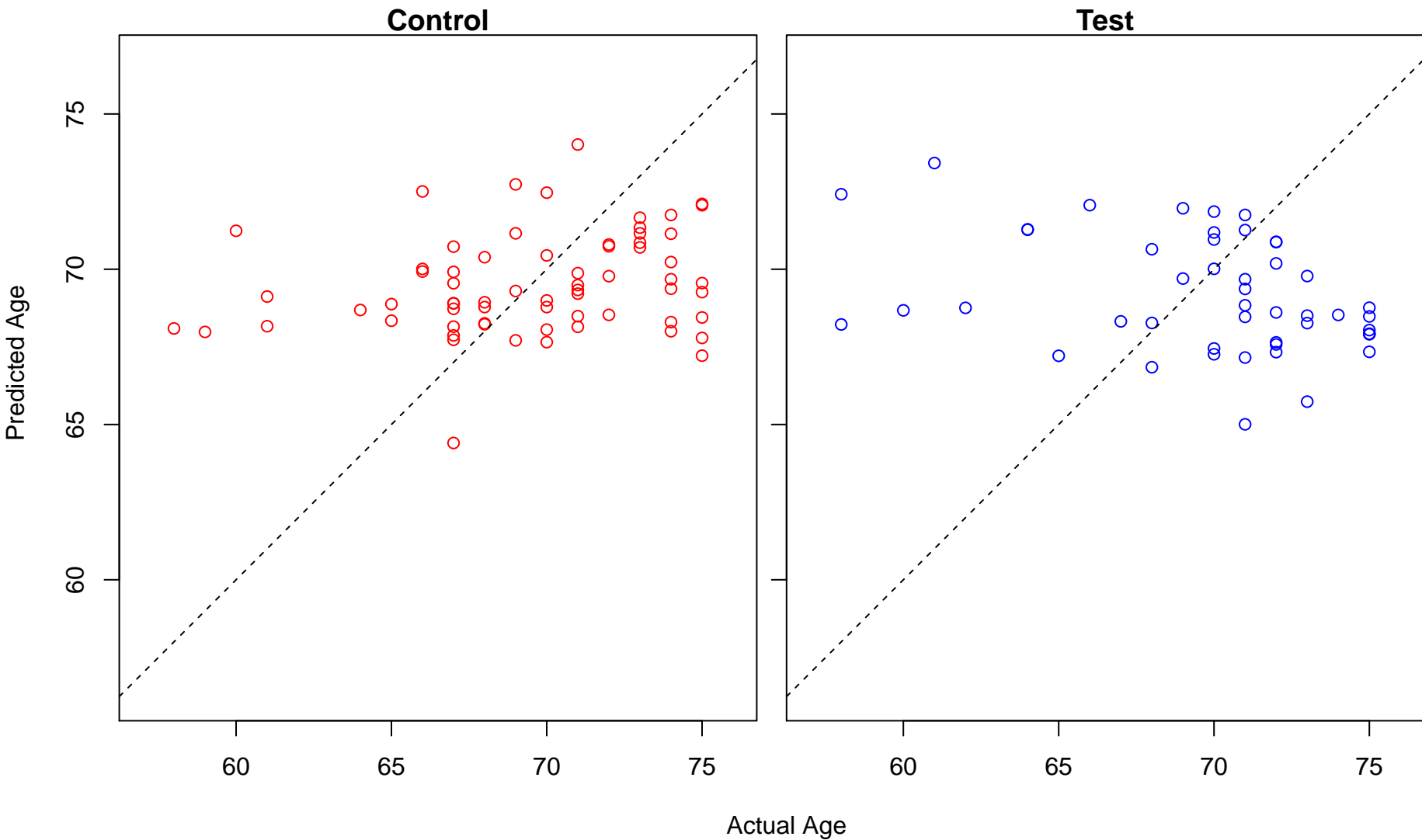
mitochondrial respiratory chain complex III biogenesis (Score: 0.306510)



positive regulation of transcription regulatory region DNA binding (Score: 0.304410)

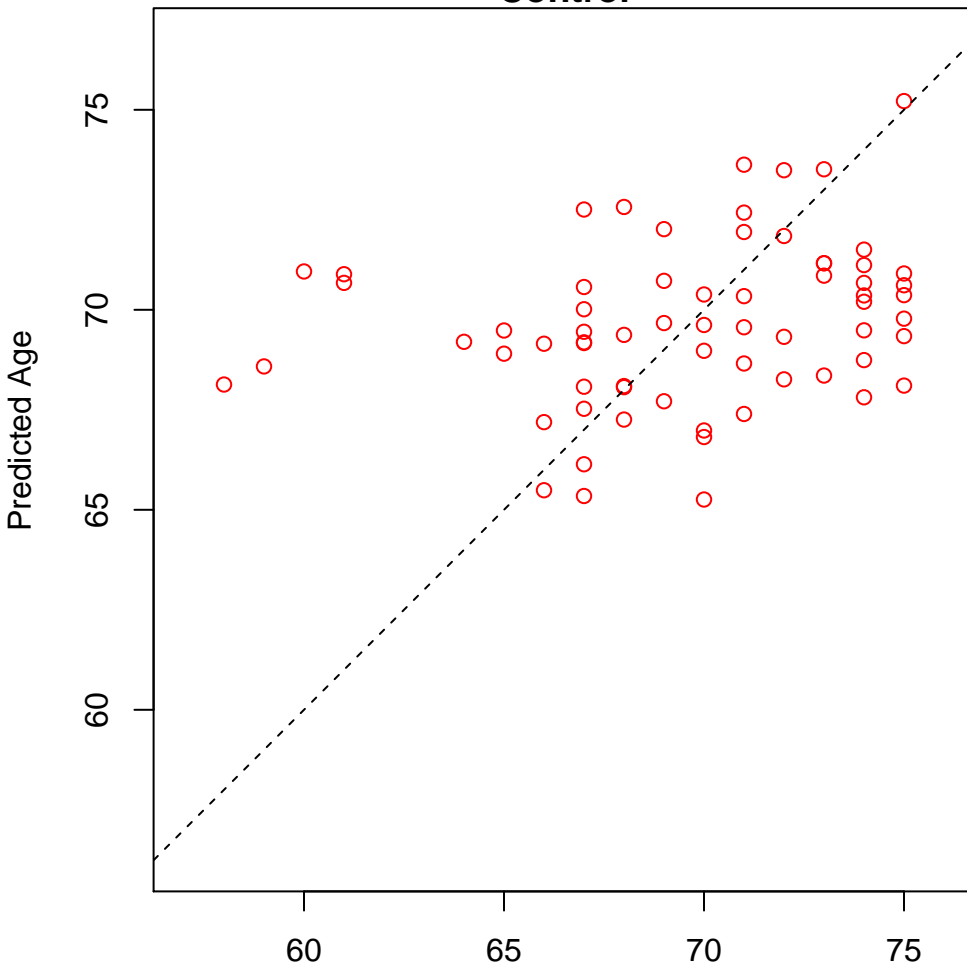


regulation of somitogenesis (Score: 0.303747)

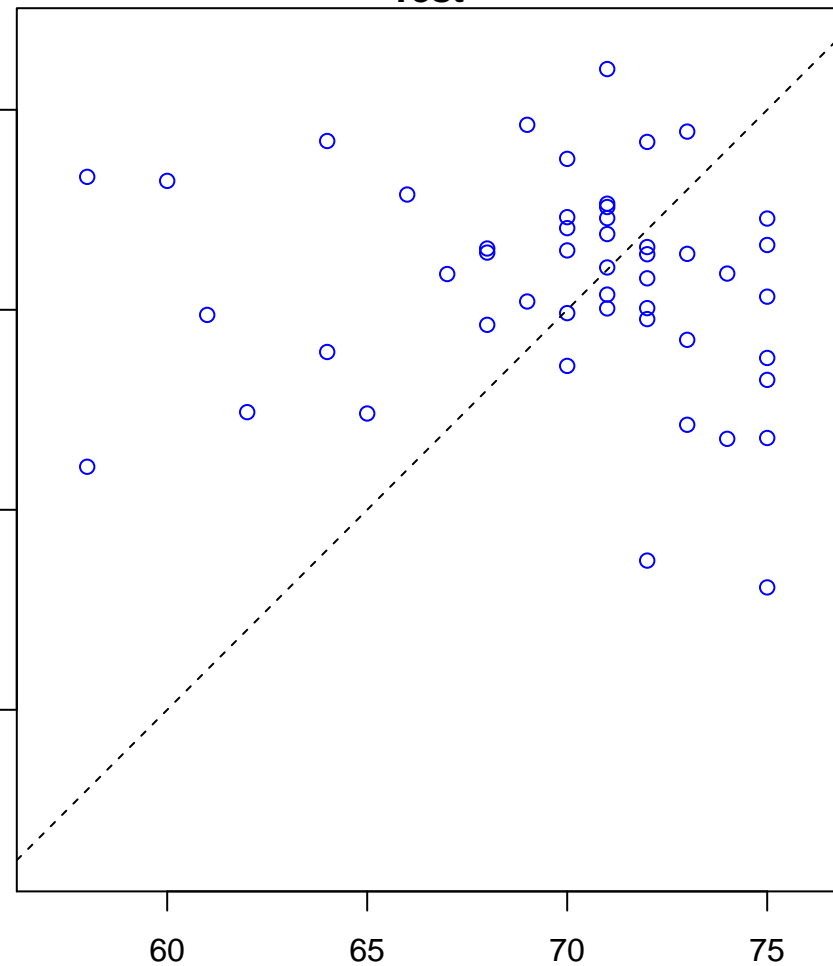


N-acetylglucosamine metabolic process (Score: 0.303615)

Control

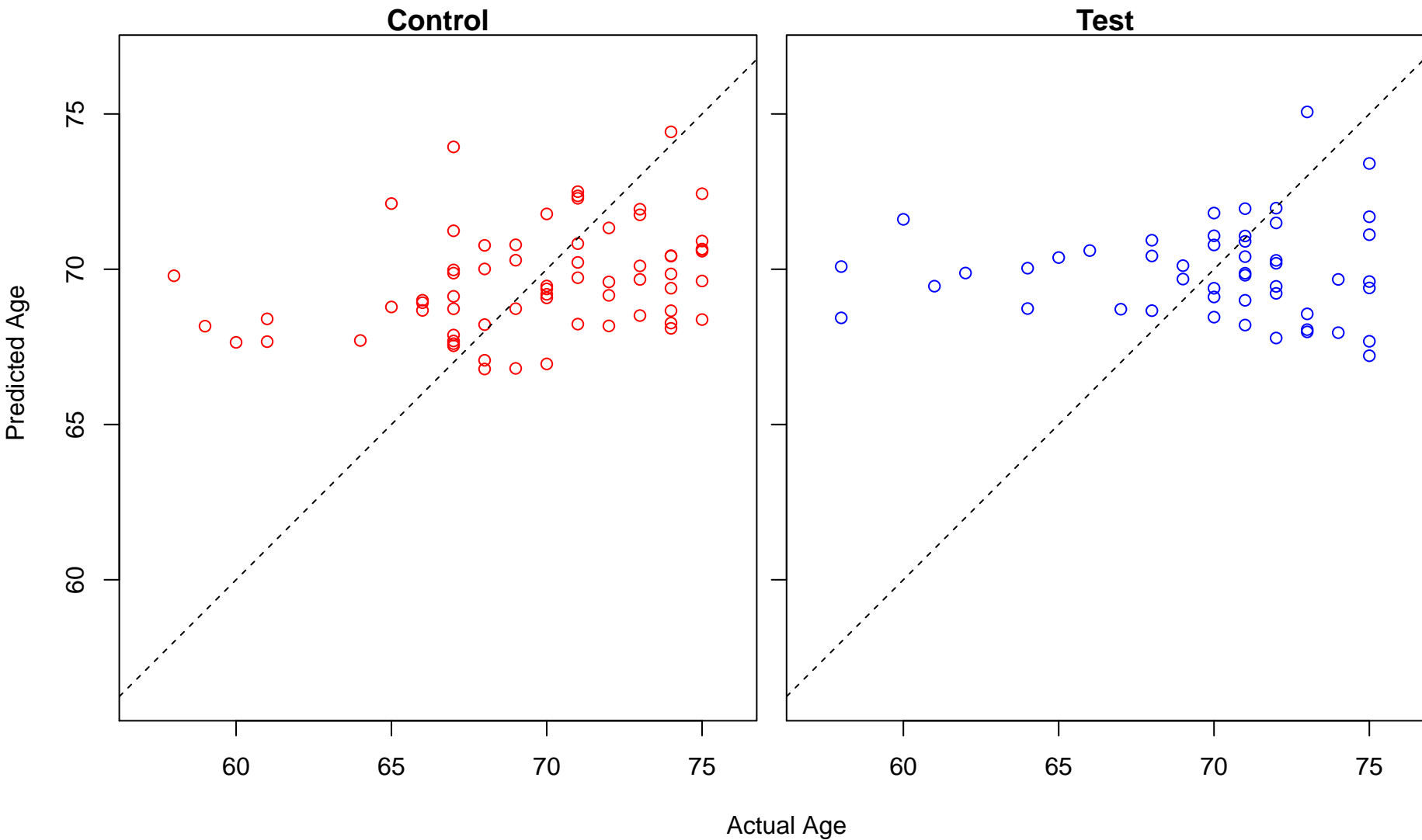


Test

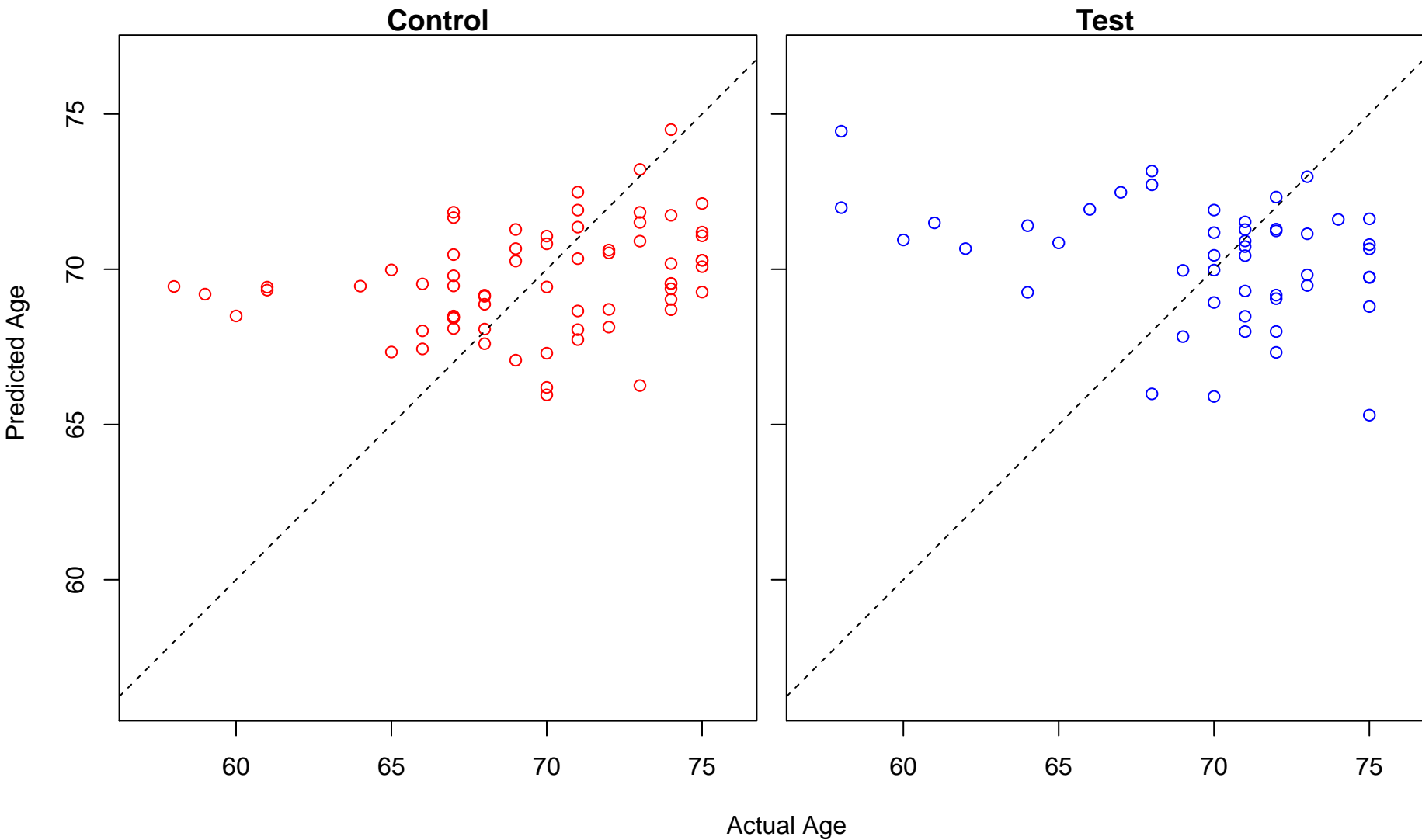


Actual Age

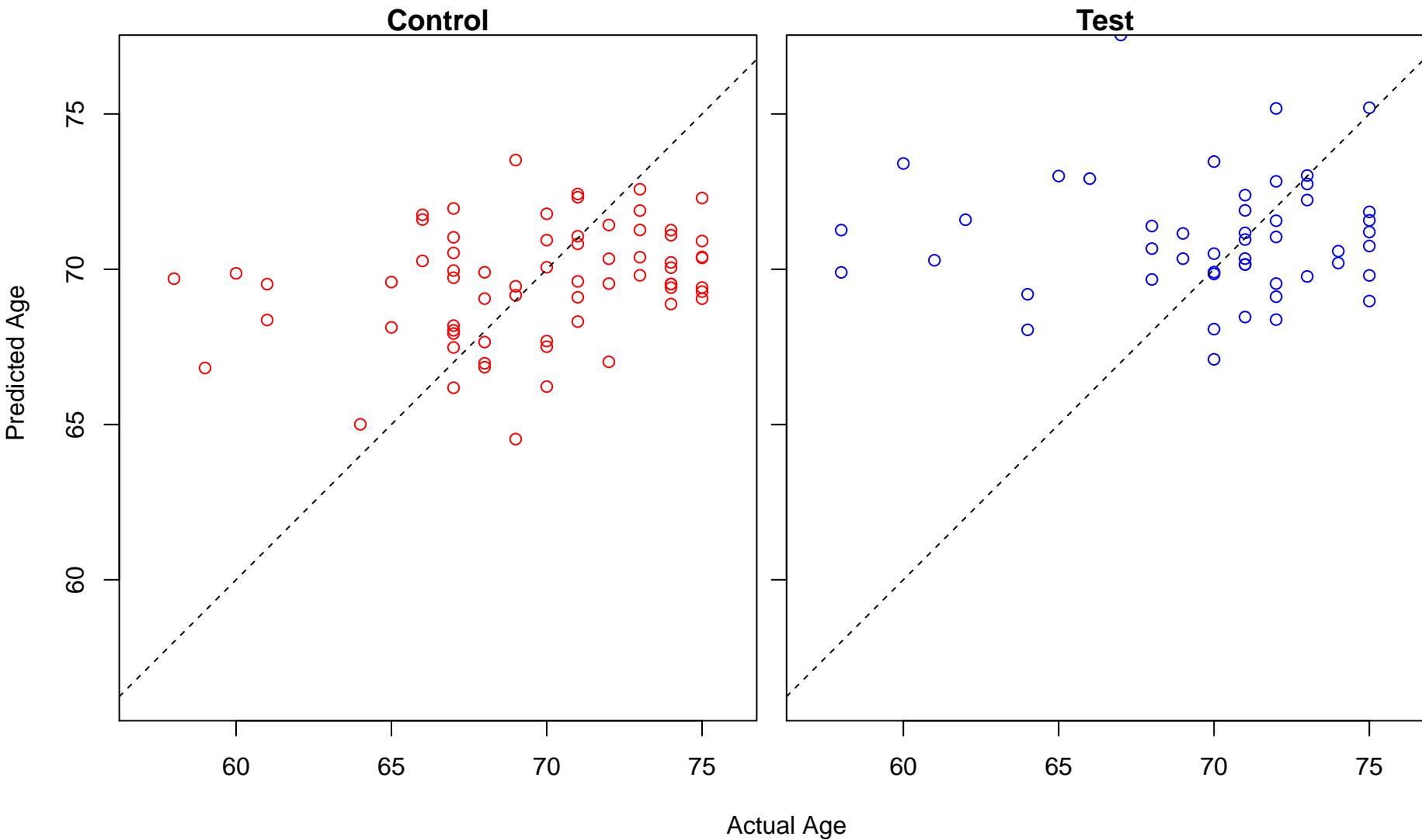
negative regulation of cell volume (Score: 0.303605)



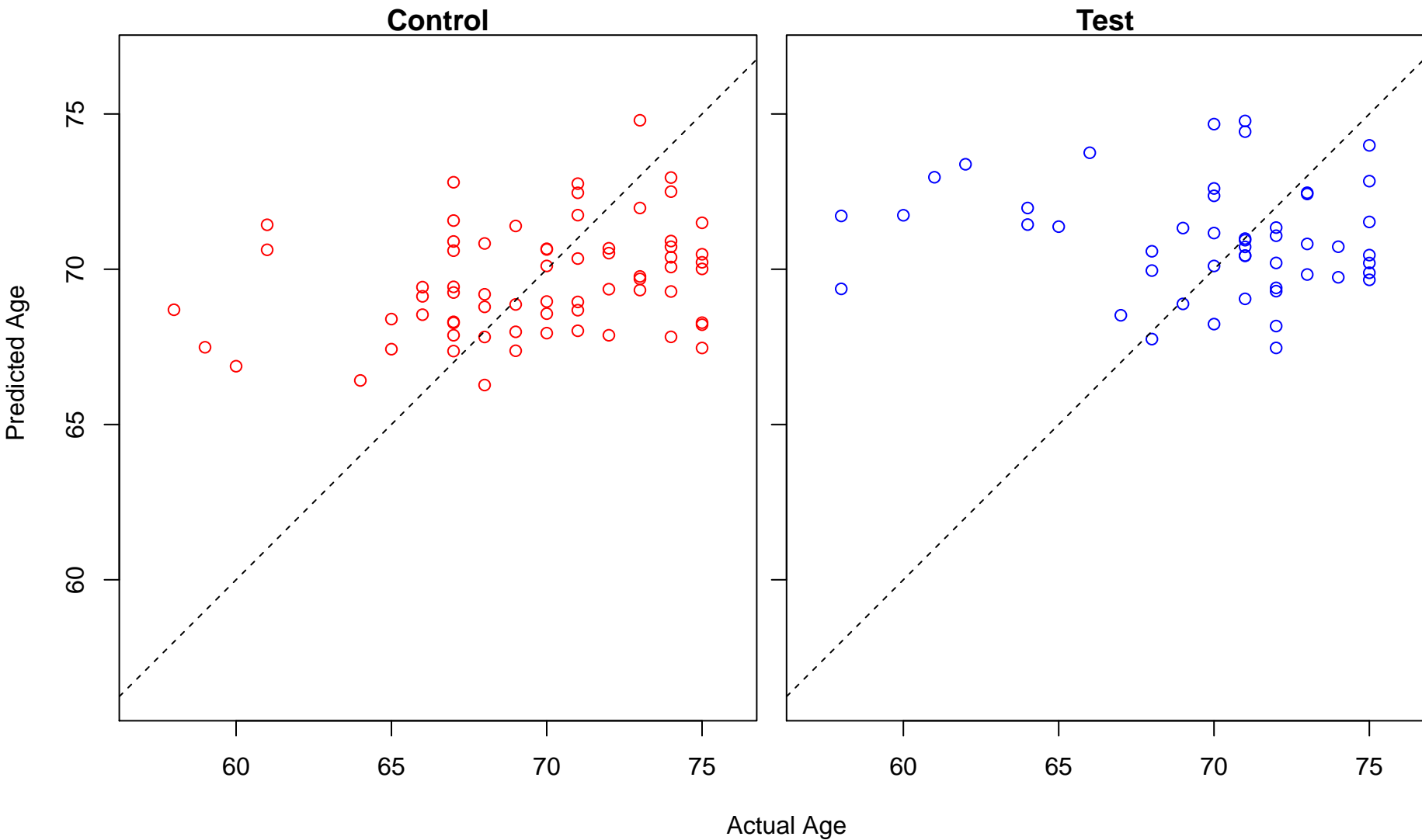
nucleosome positioning (Score: 0.302347)



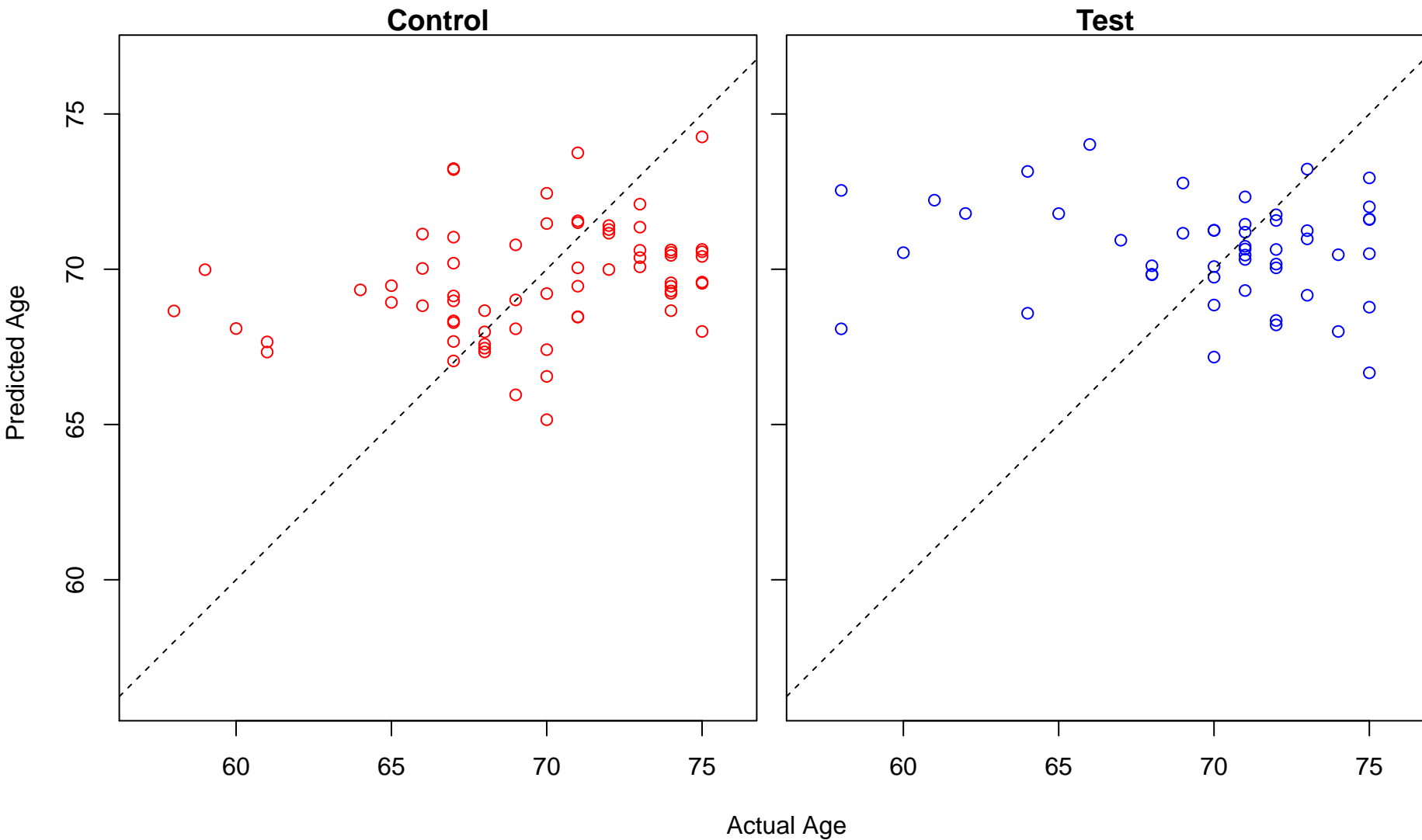
protein localization to chromosome, centromeric region (Score: 0.301915)



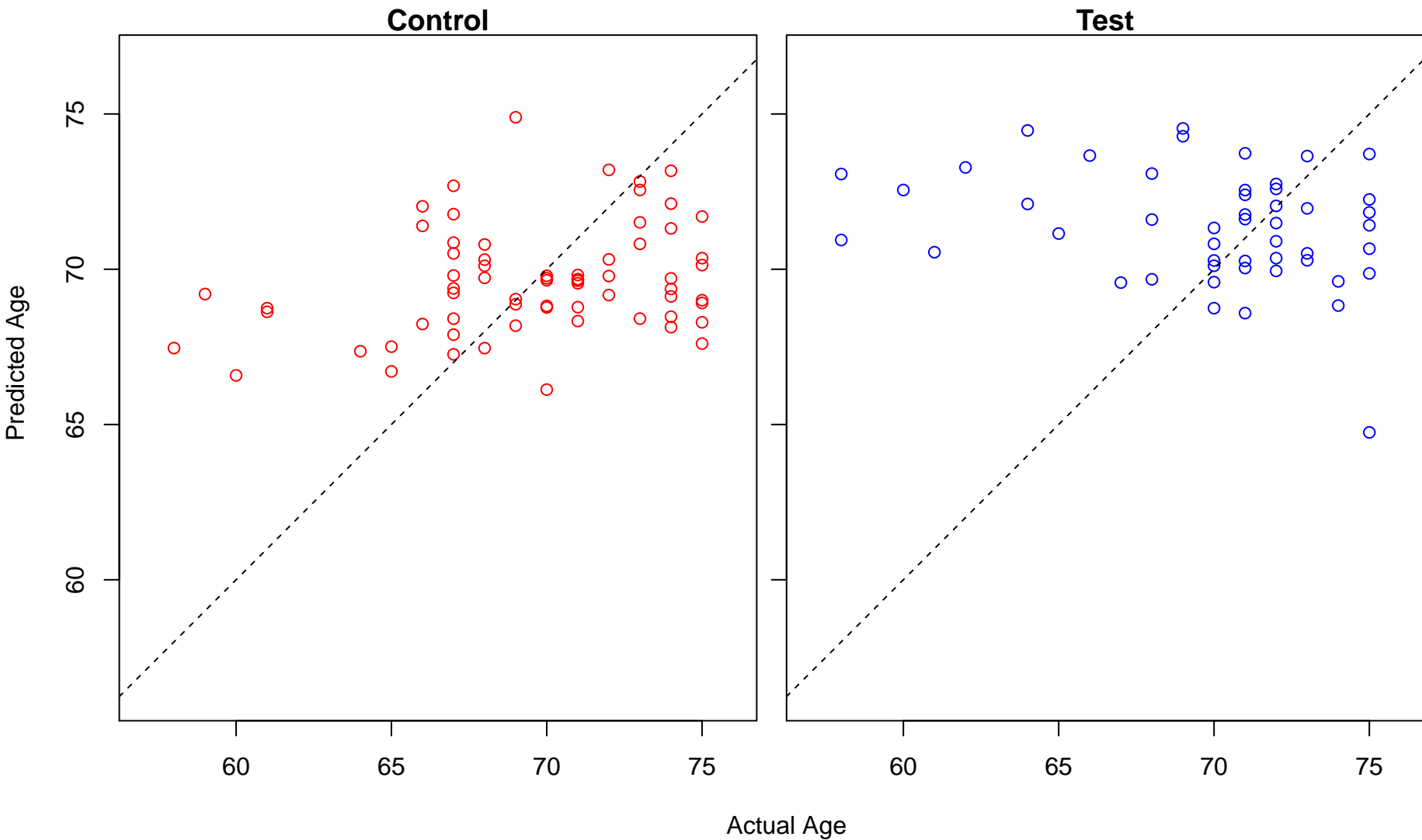
hyaluronan biosynthetic process (Score: 0.301551)



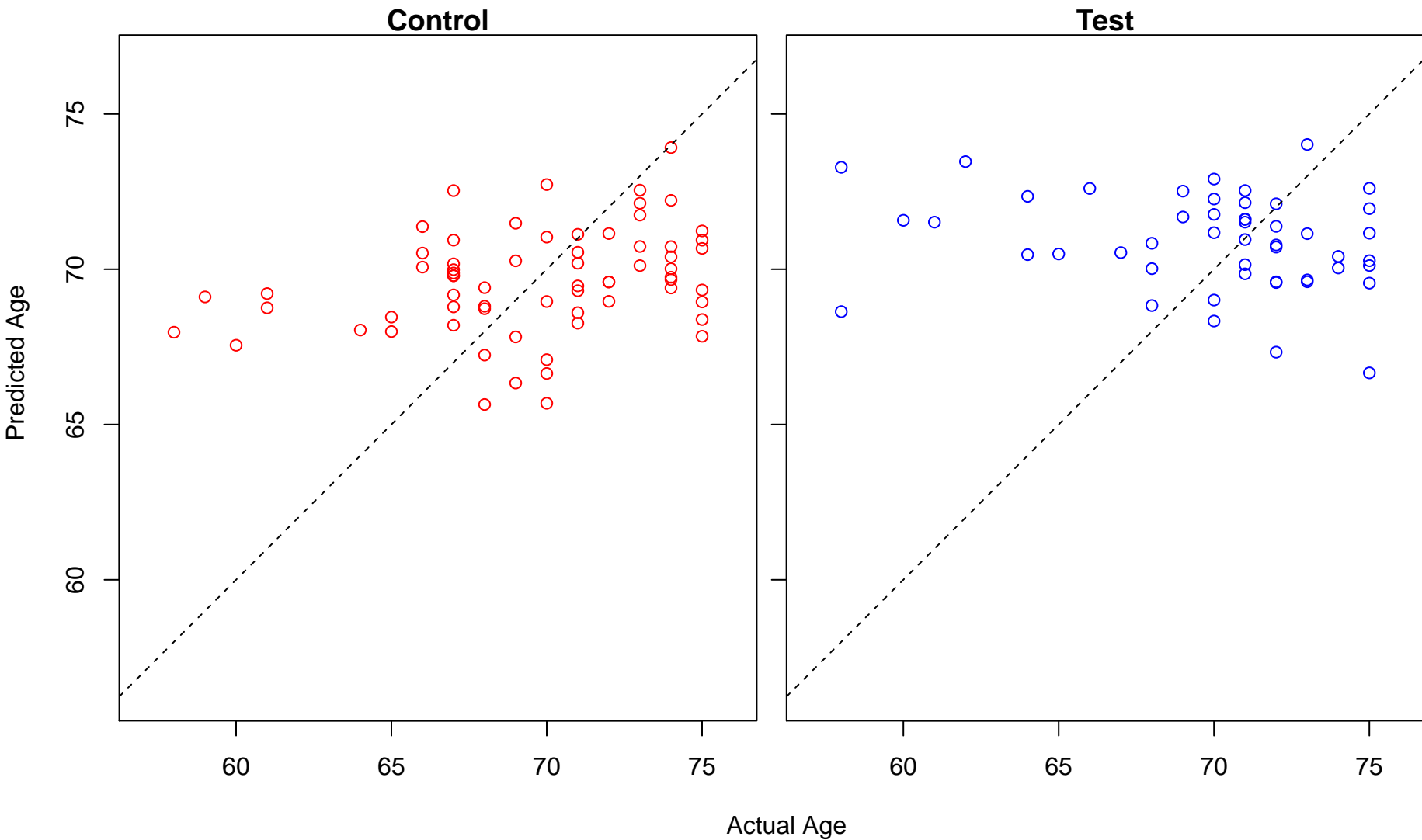
regulation of Arp2/3 complex-mediated actin nucleation (Score: 0.301449)



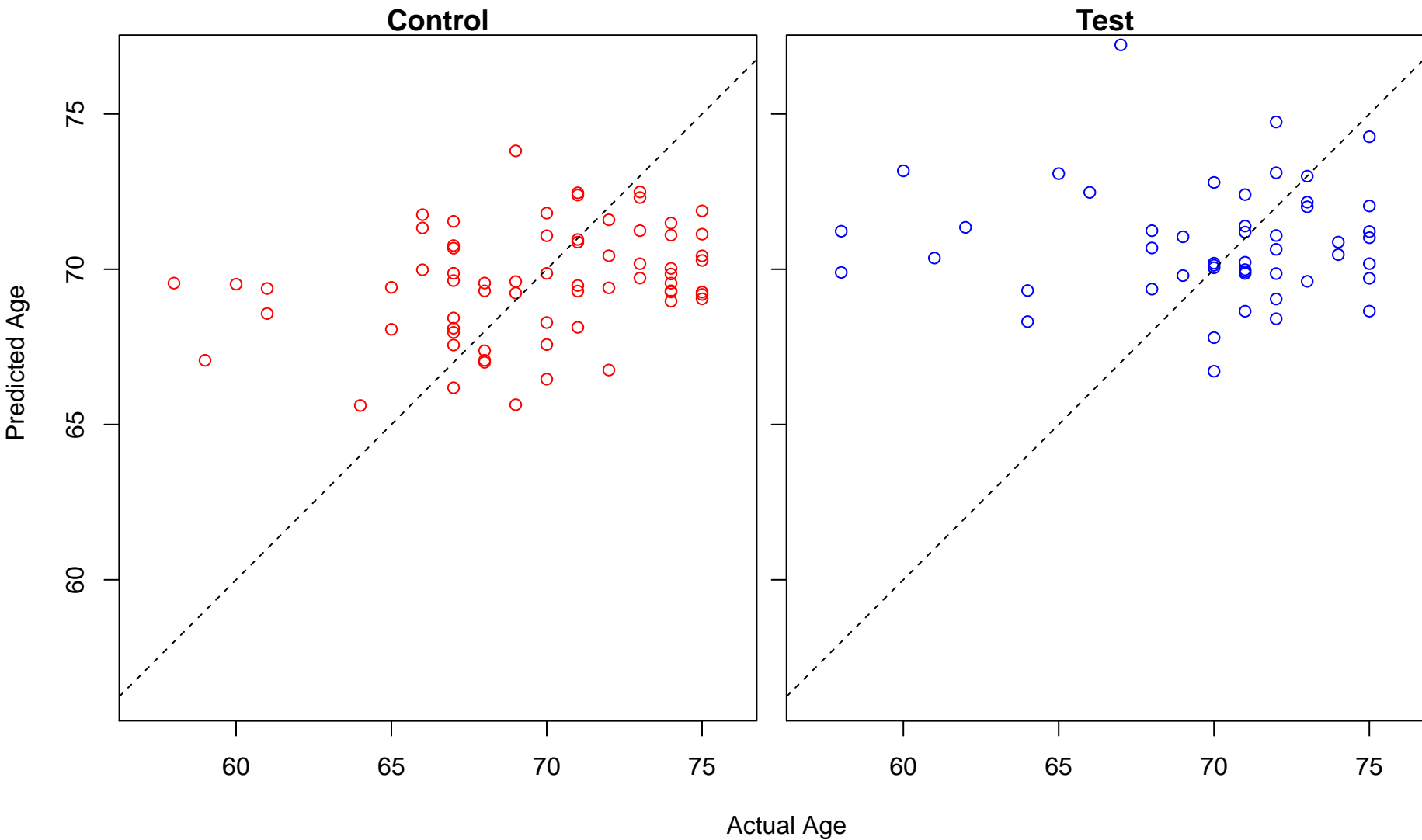
cell migration involved in sprouting angiogenesis (Score: 0.301173)



regulation of phospholipid catabolic process (Score: 0.298964)

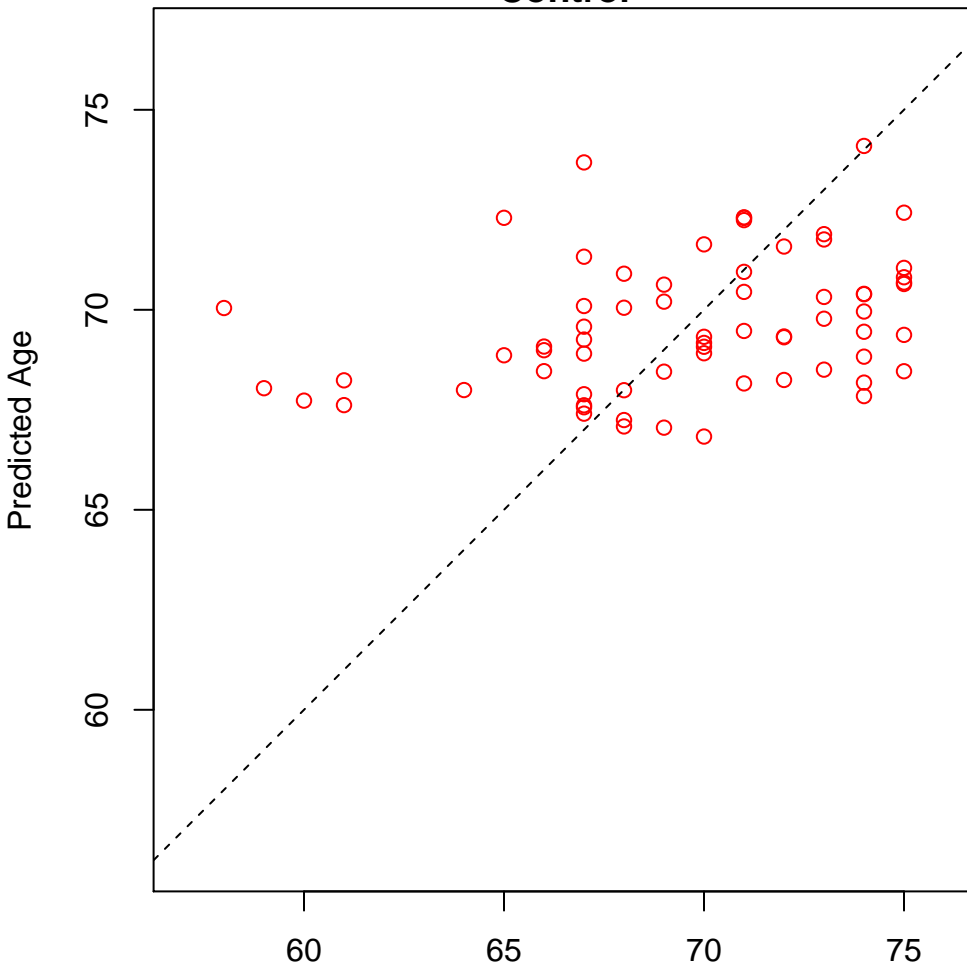


protein localization to kinetochore (Score: 0.298238)

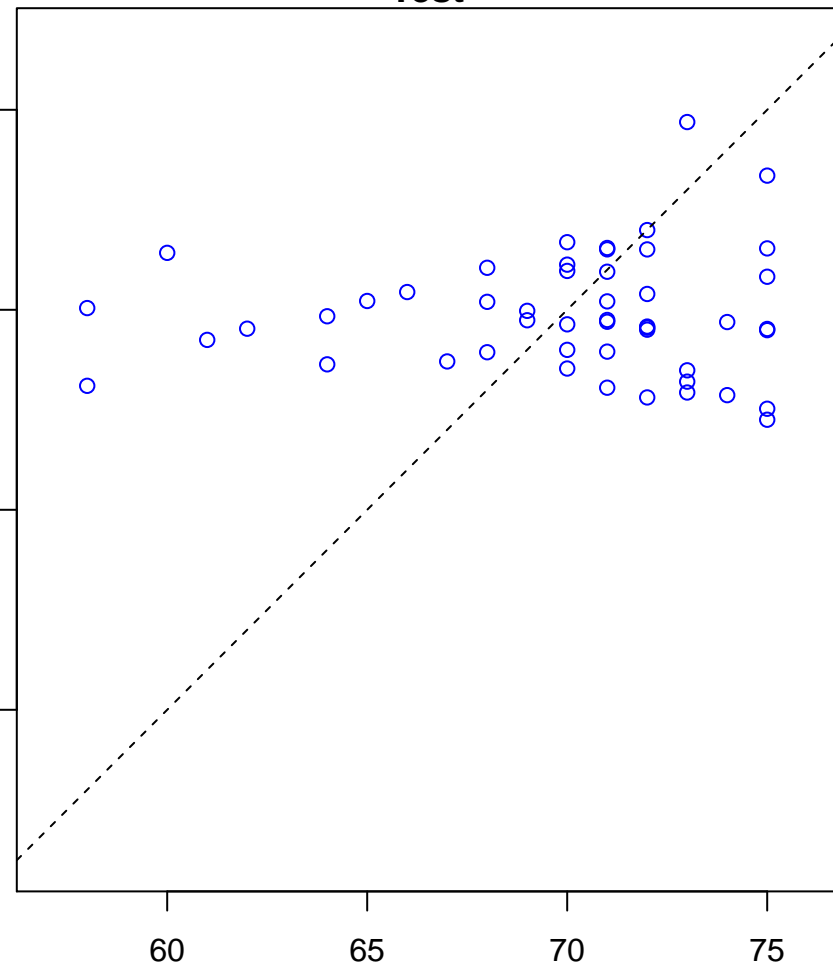


negative regulation of bone remodeling (Score: 0.296715)

Control

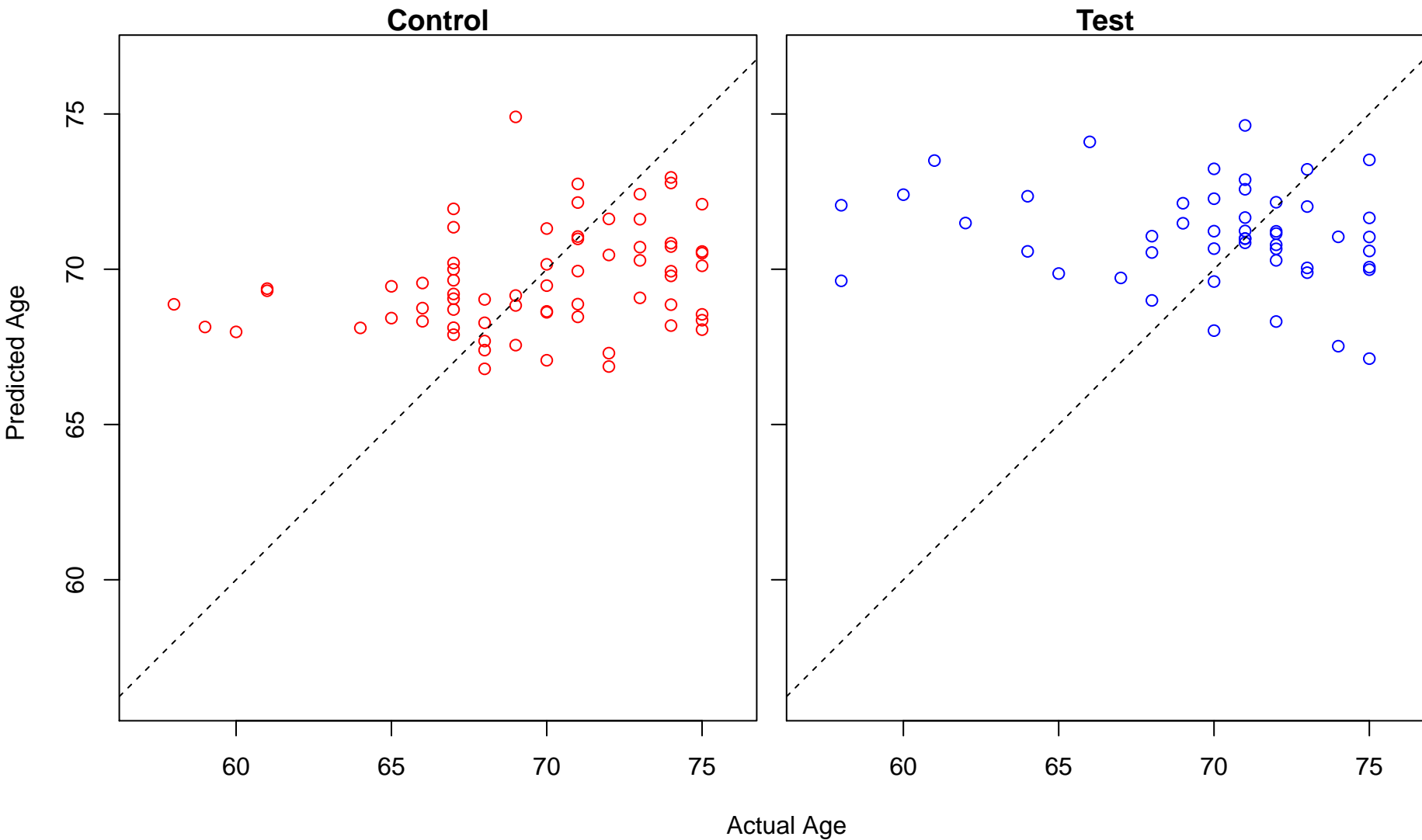


Test

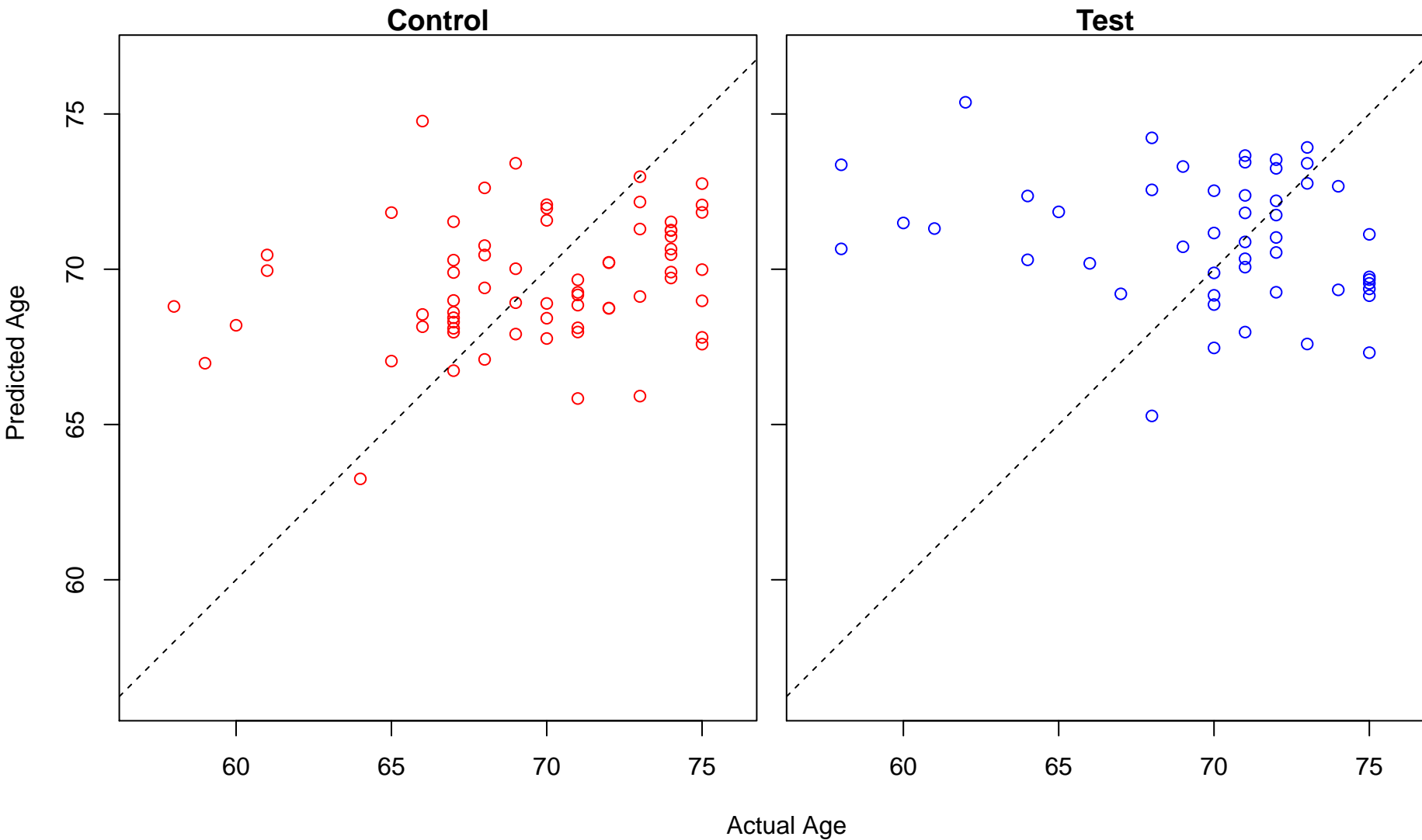


Actual Age

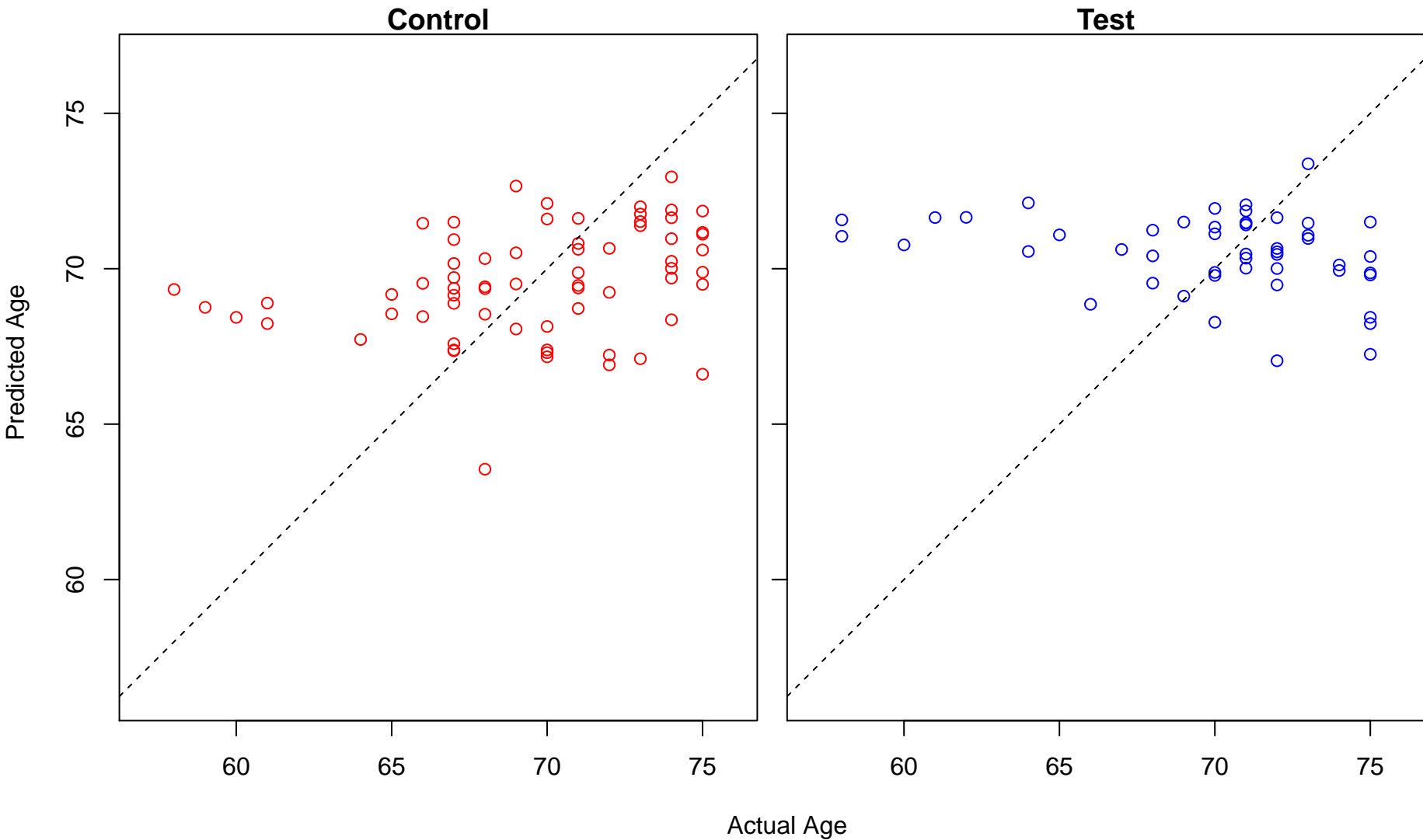
negative regulation of extracellular matrix organization (Score: 0.296183)



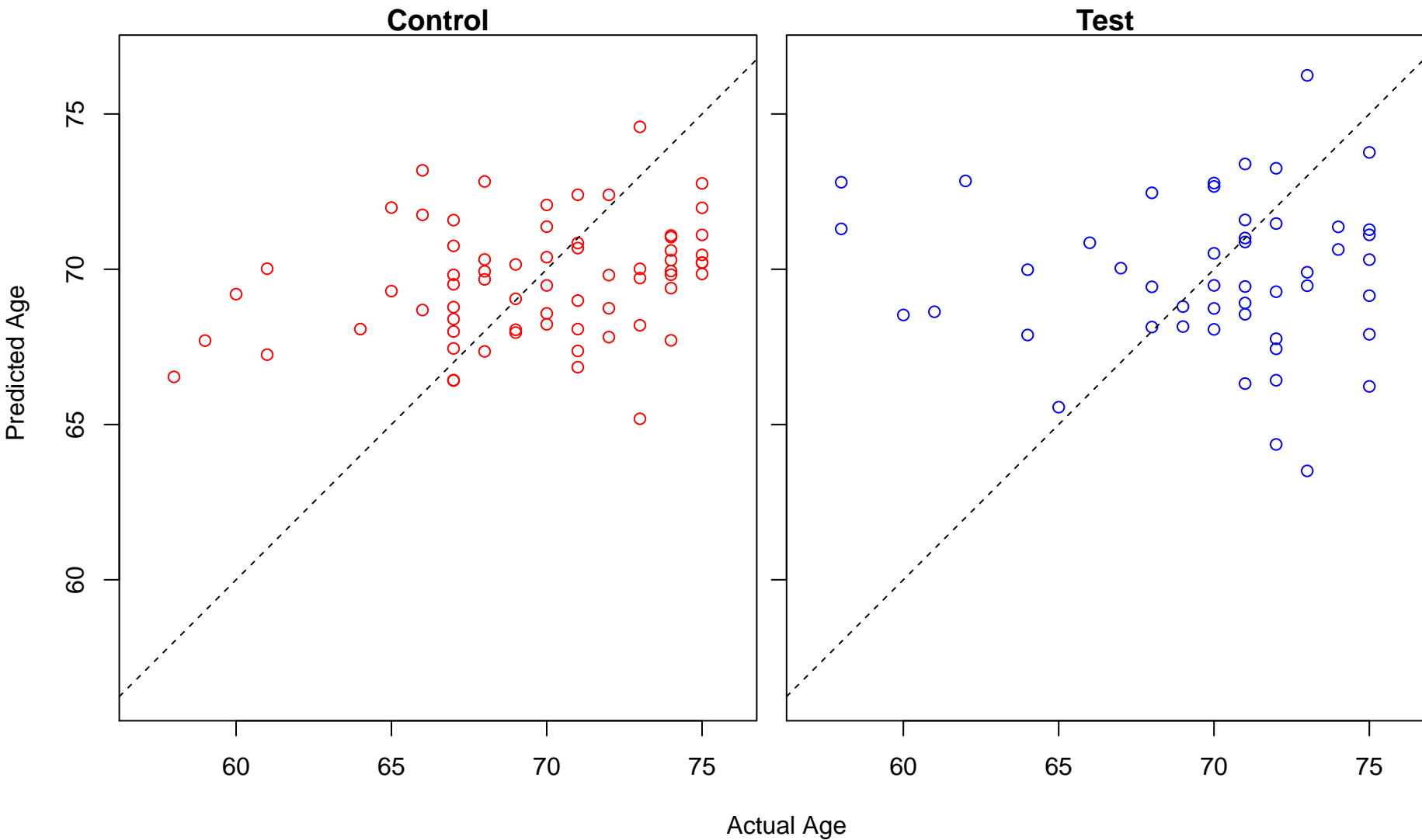
RNA interference (Score: 0.295105)



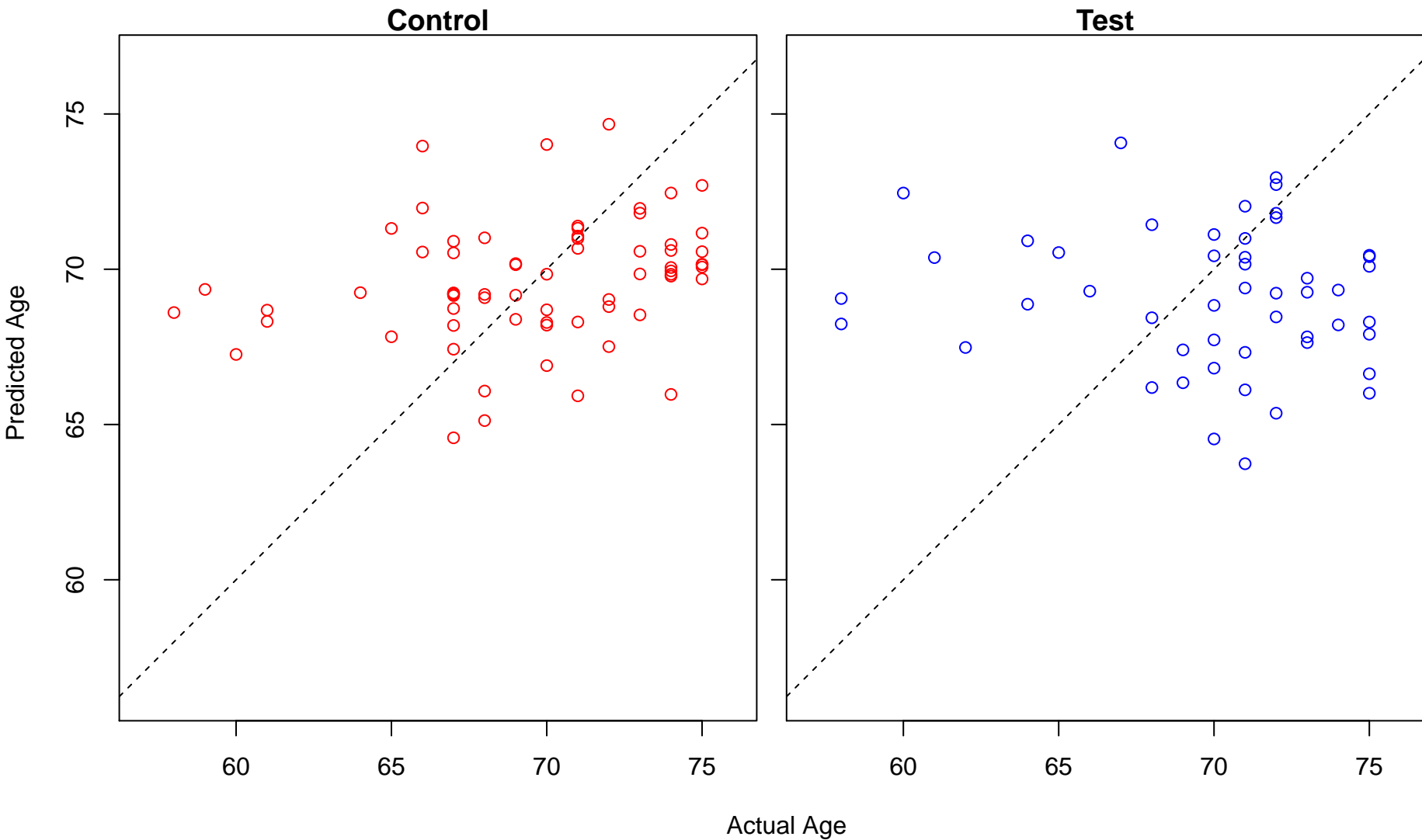
negative regulation of hydrogen peroxide-mediated programmed cell death (Score: 0.294923)



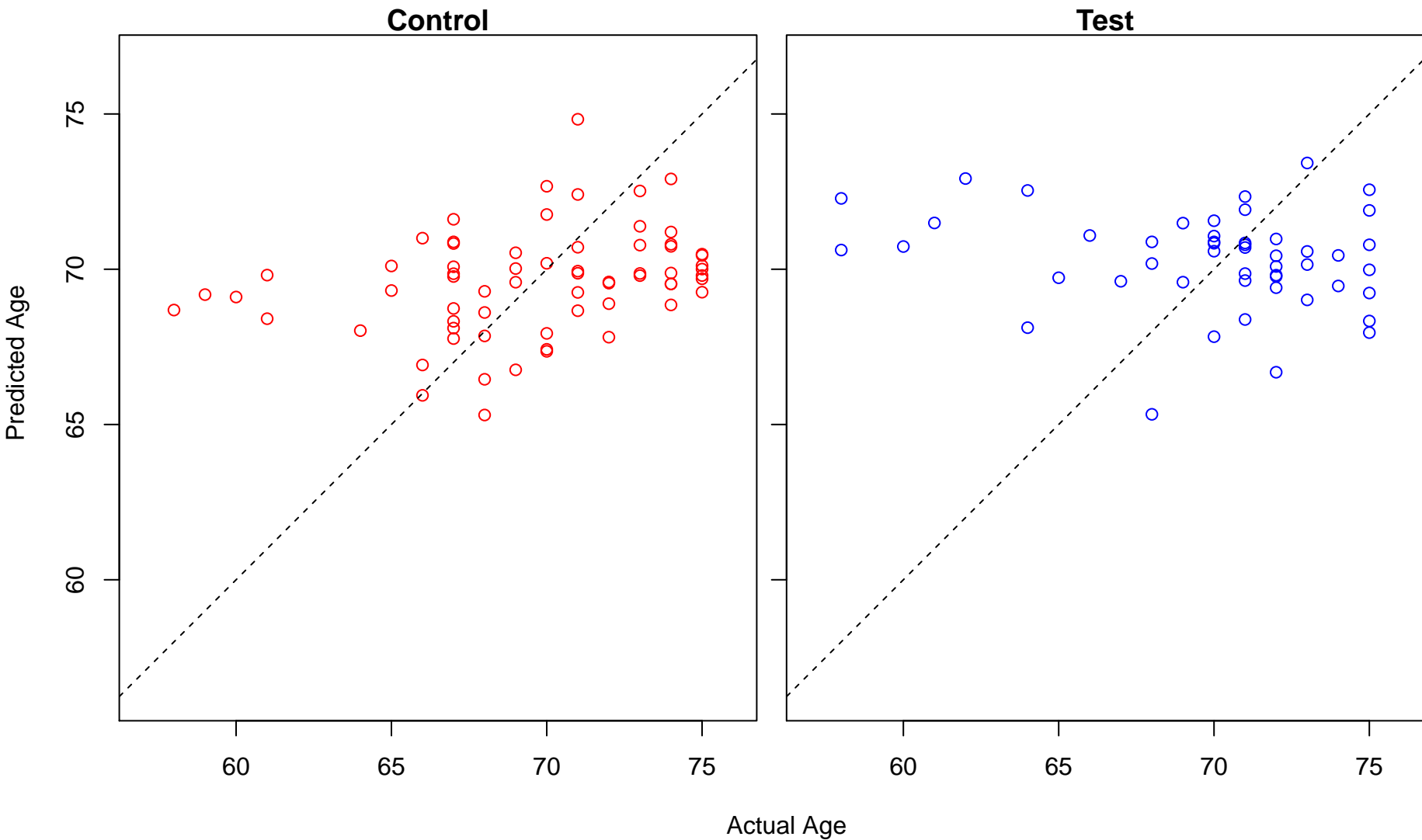
toxin metabolic process (Score: 0.293686)



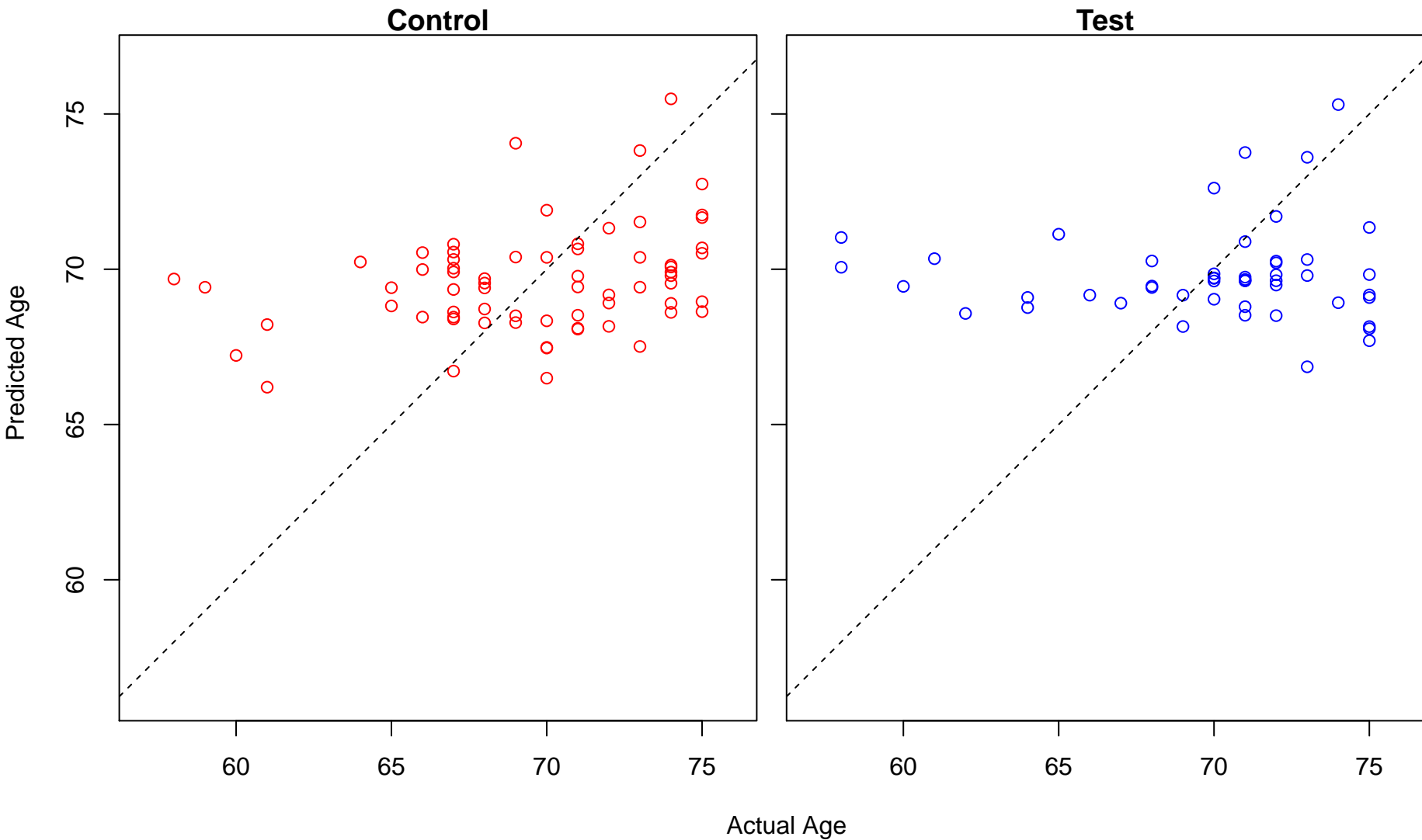
type B pancreatic cell differentiation (Score: 0.292865)



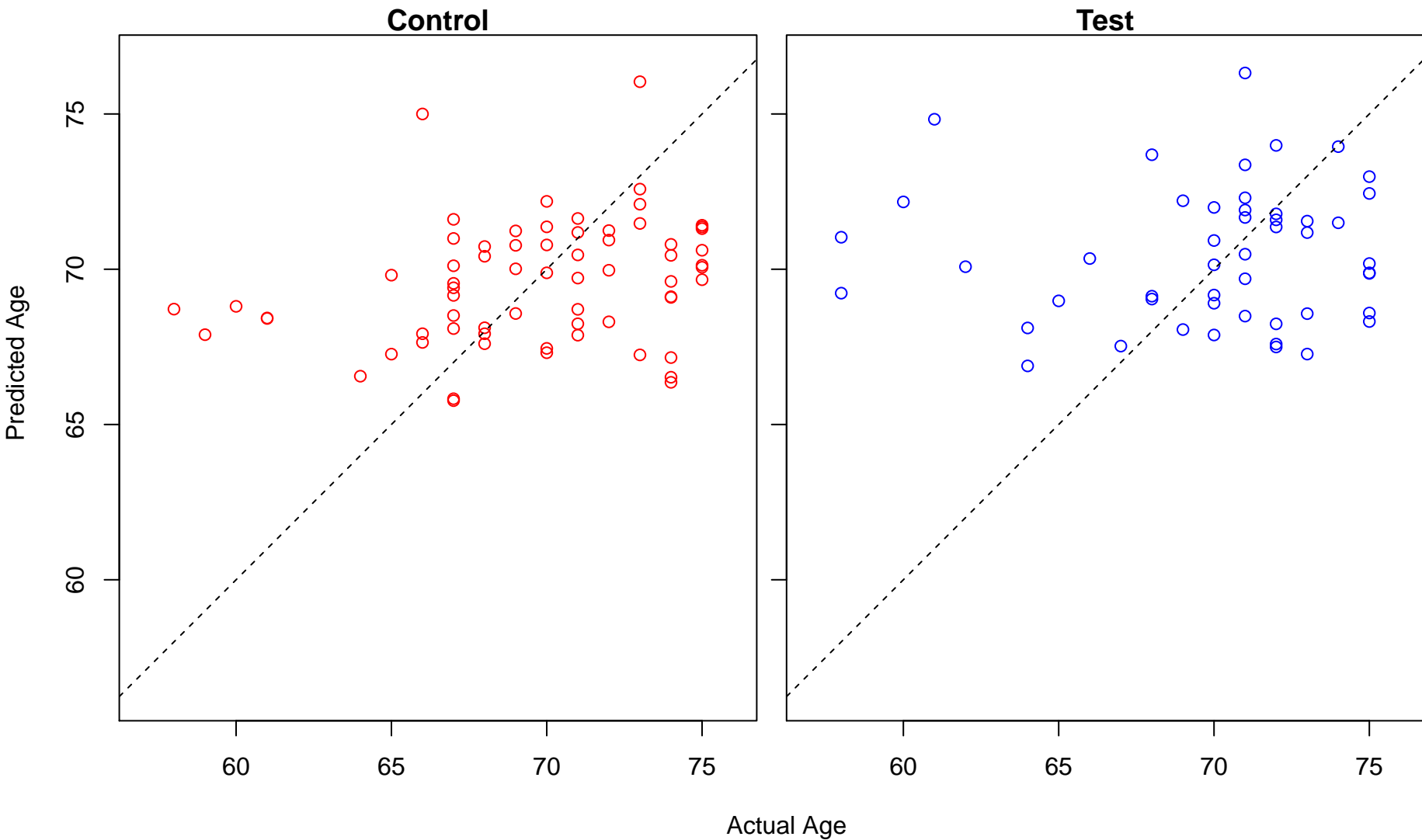
pre-miRNA processing (Score: 0.290511)



glutamine transport (Score: 0.290277)

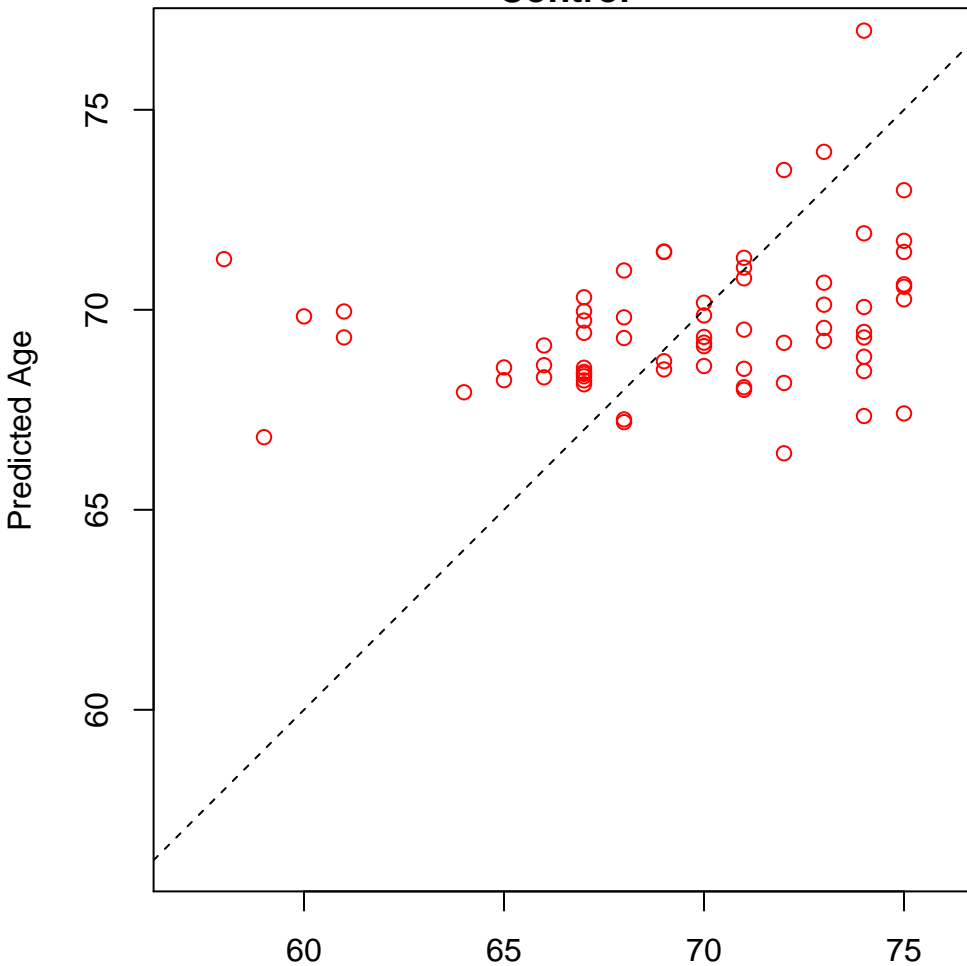


regulation of respiratory system process (Score: 0.290247)

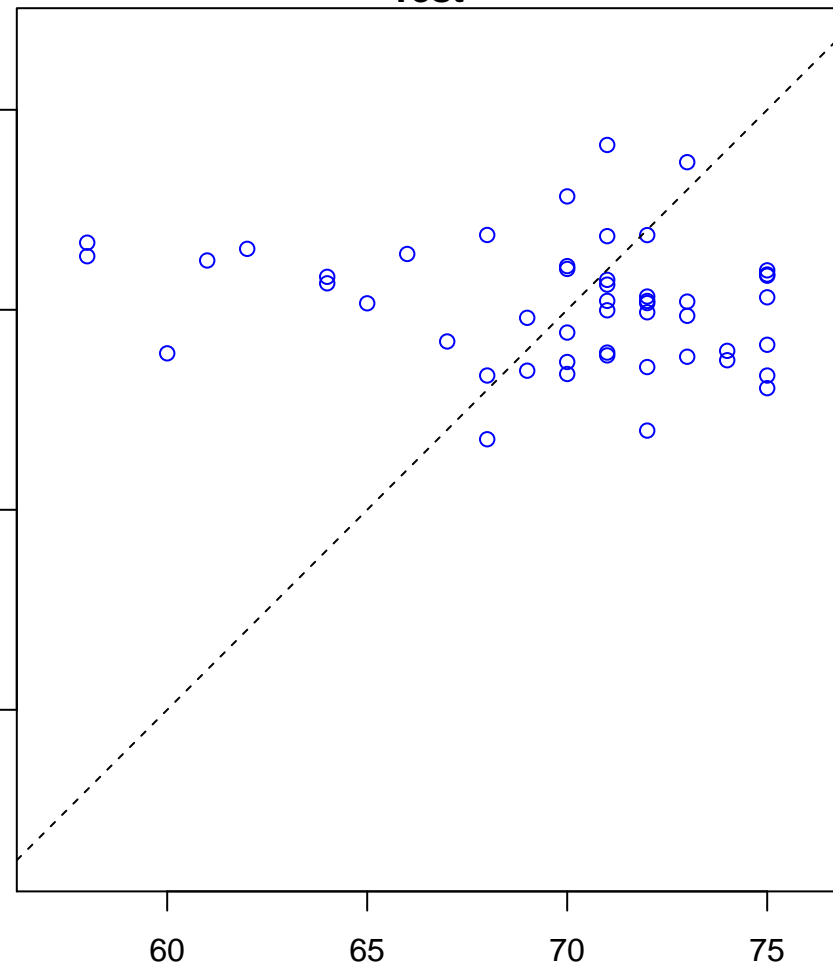


regulation of catecholamine secretion (Score: 0.287262)

Control

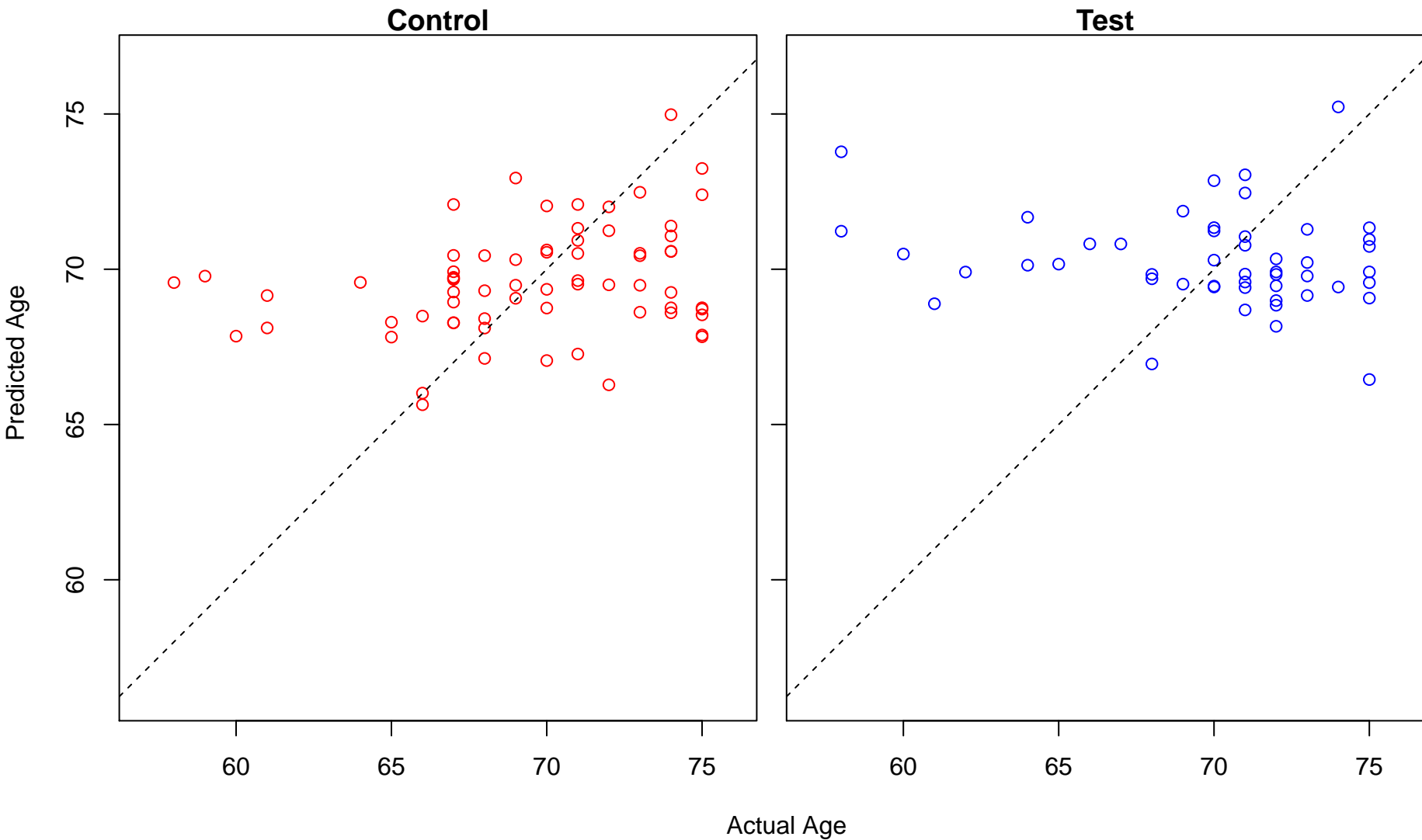


Test

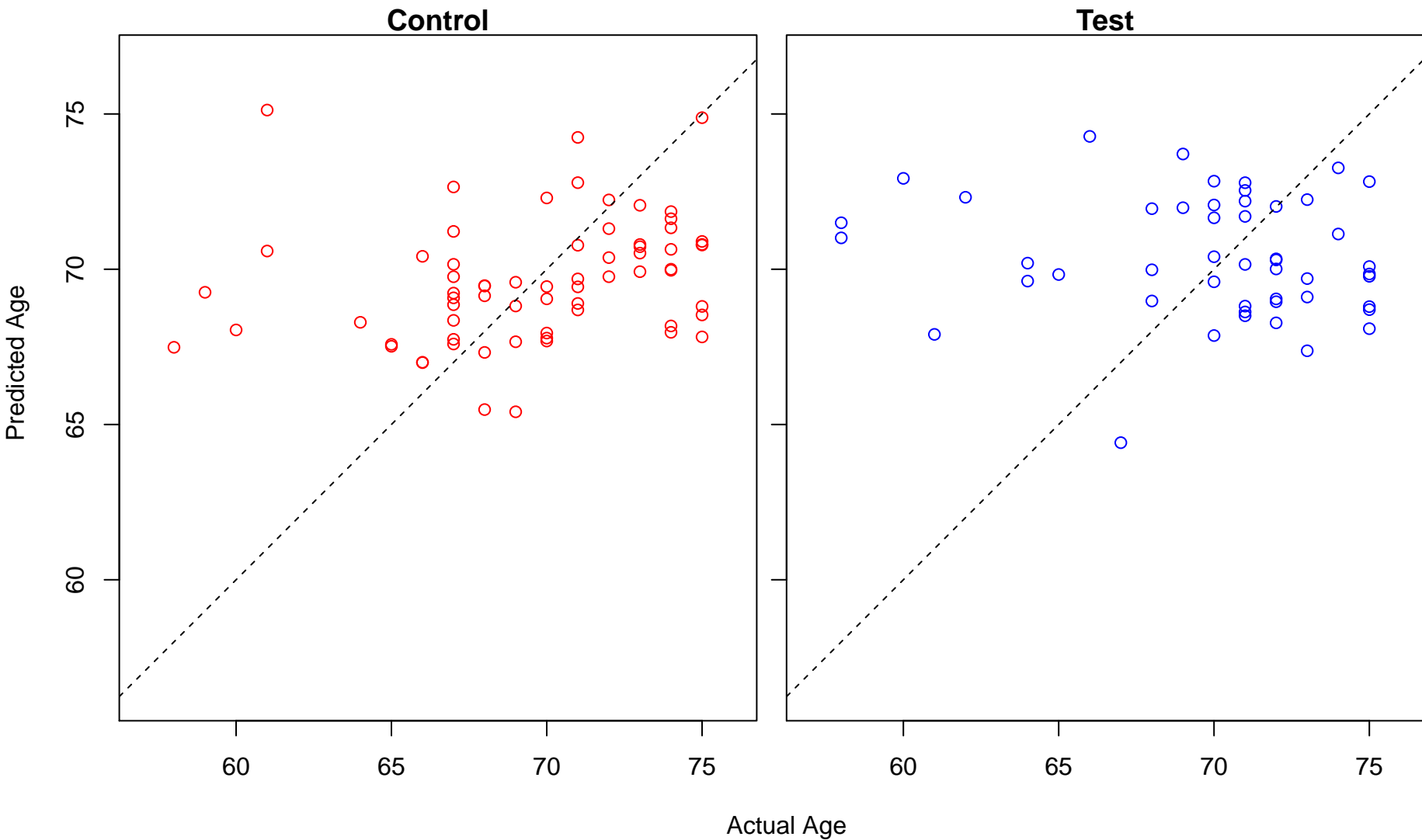


Actual Age

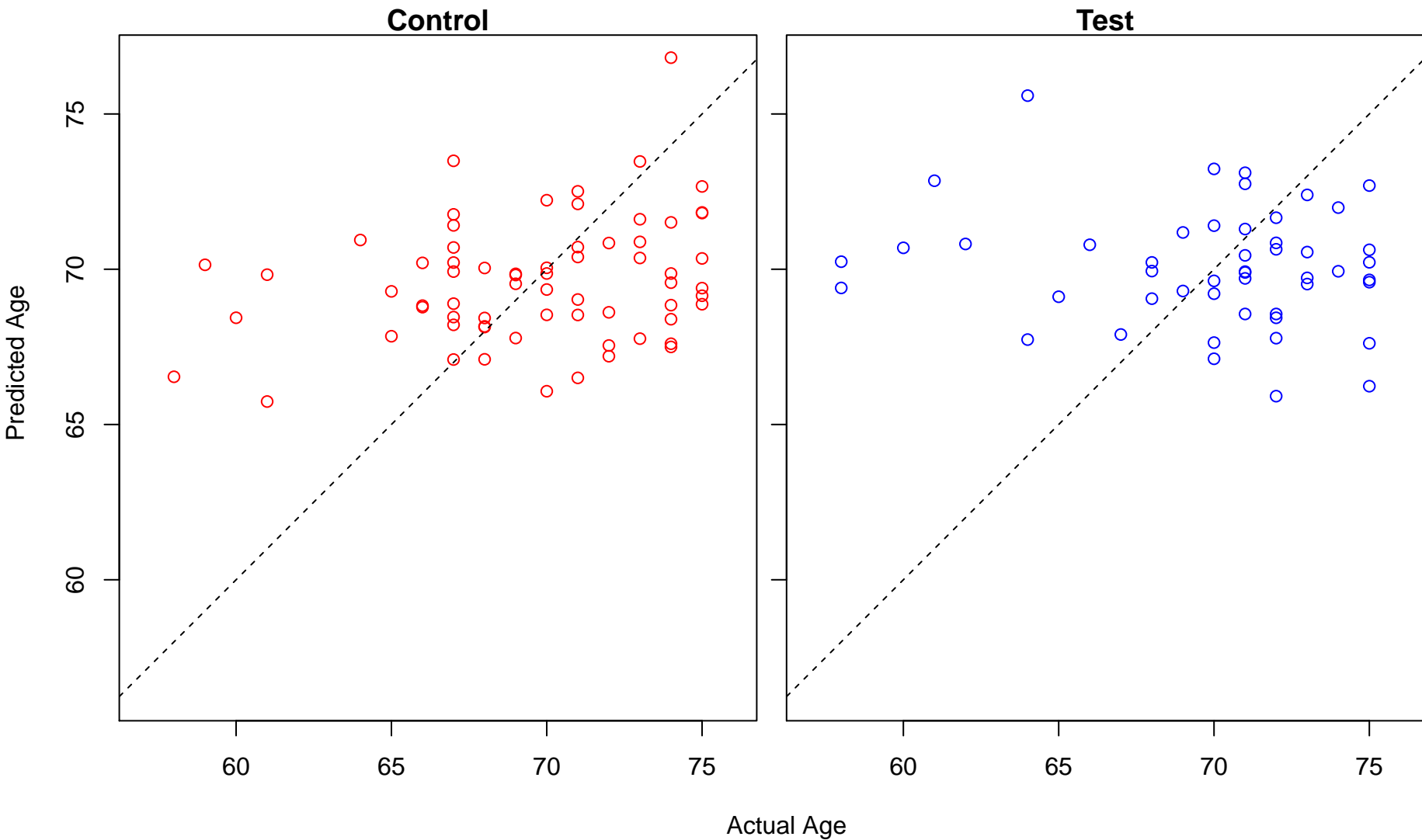
positive regulation of triglyceride lipase activity (Score: 0.286007)



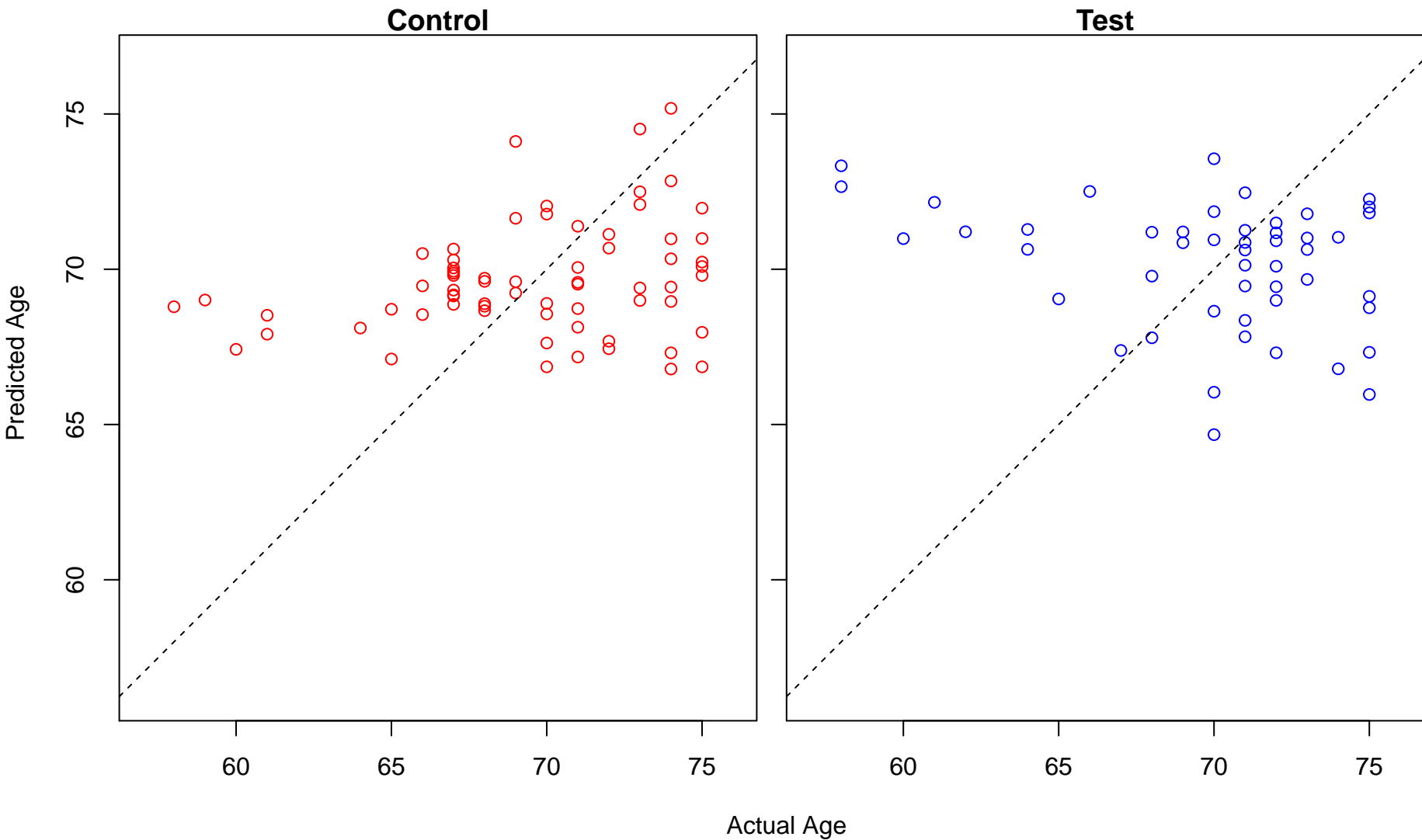
vitamin transmembrane transport (Score: 0.285076)



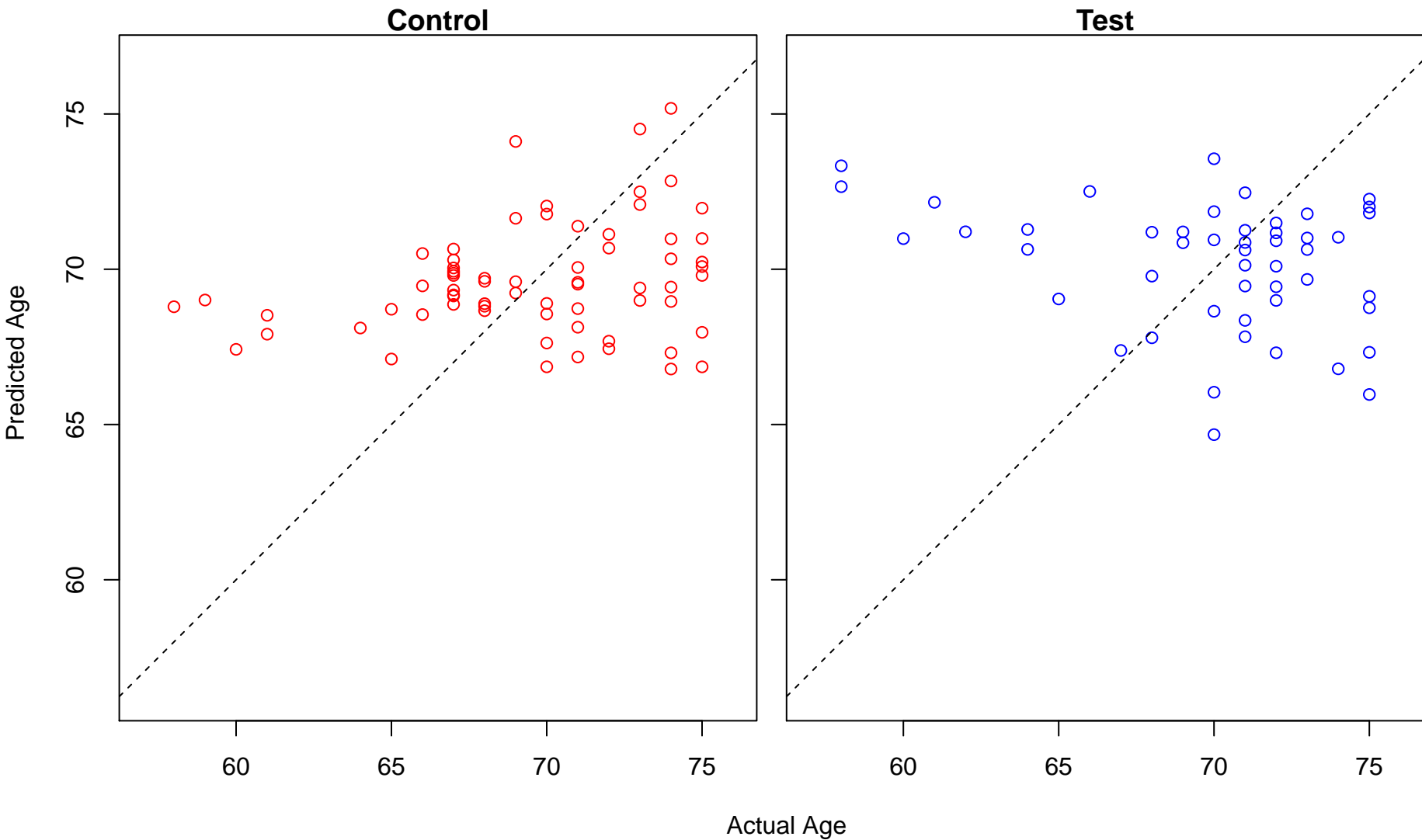
GDP metabolic process (Score: 0.283106)



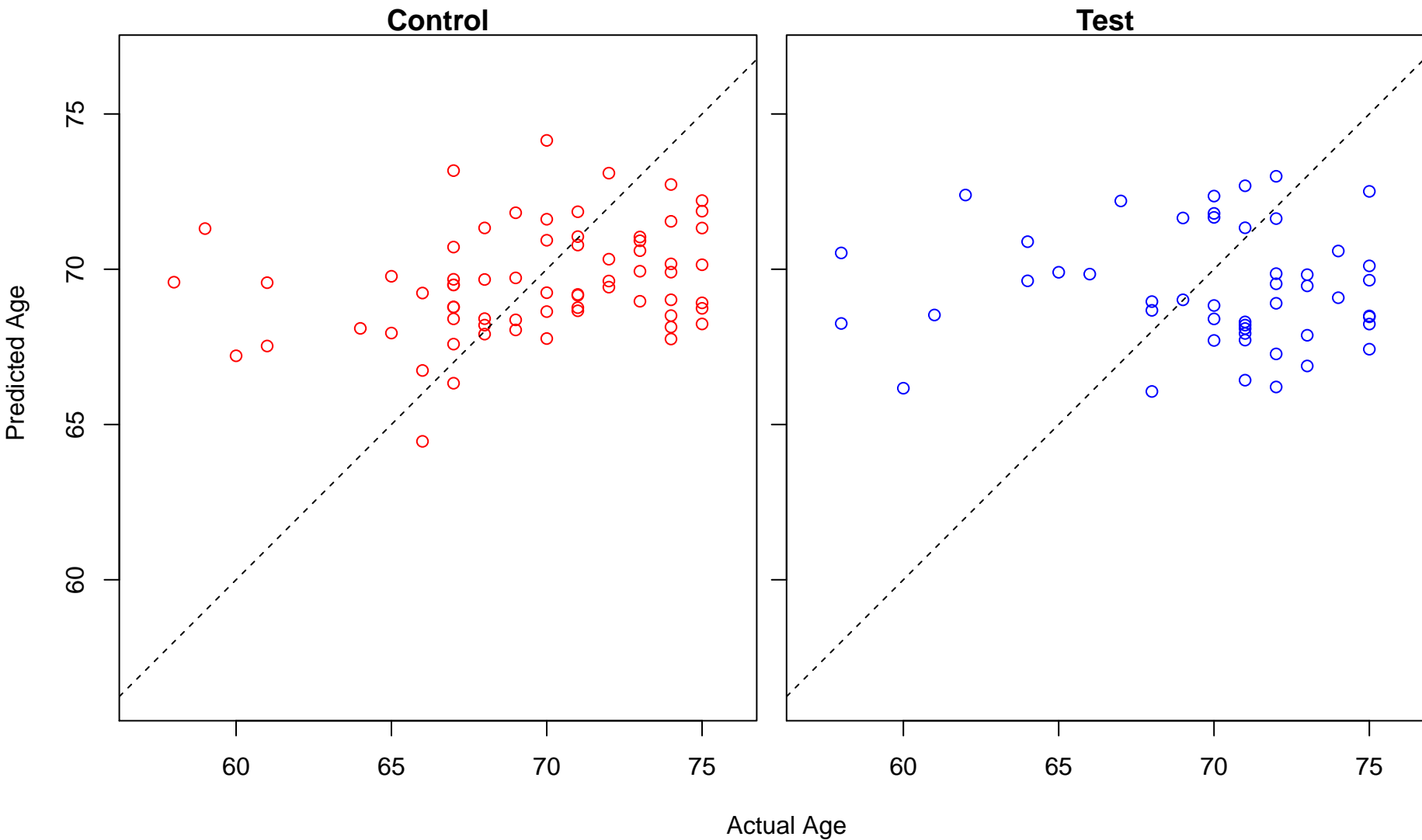
negative regulation of protein exit from endoplasmic reticulum (Score: 0.282071)



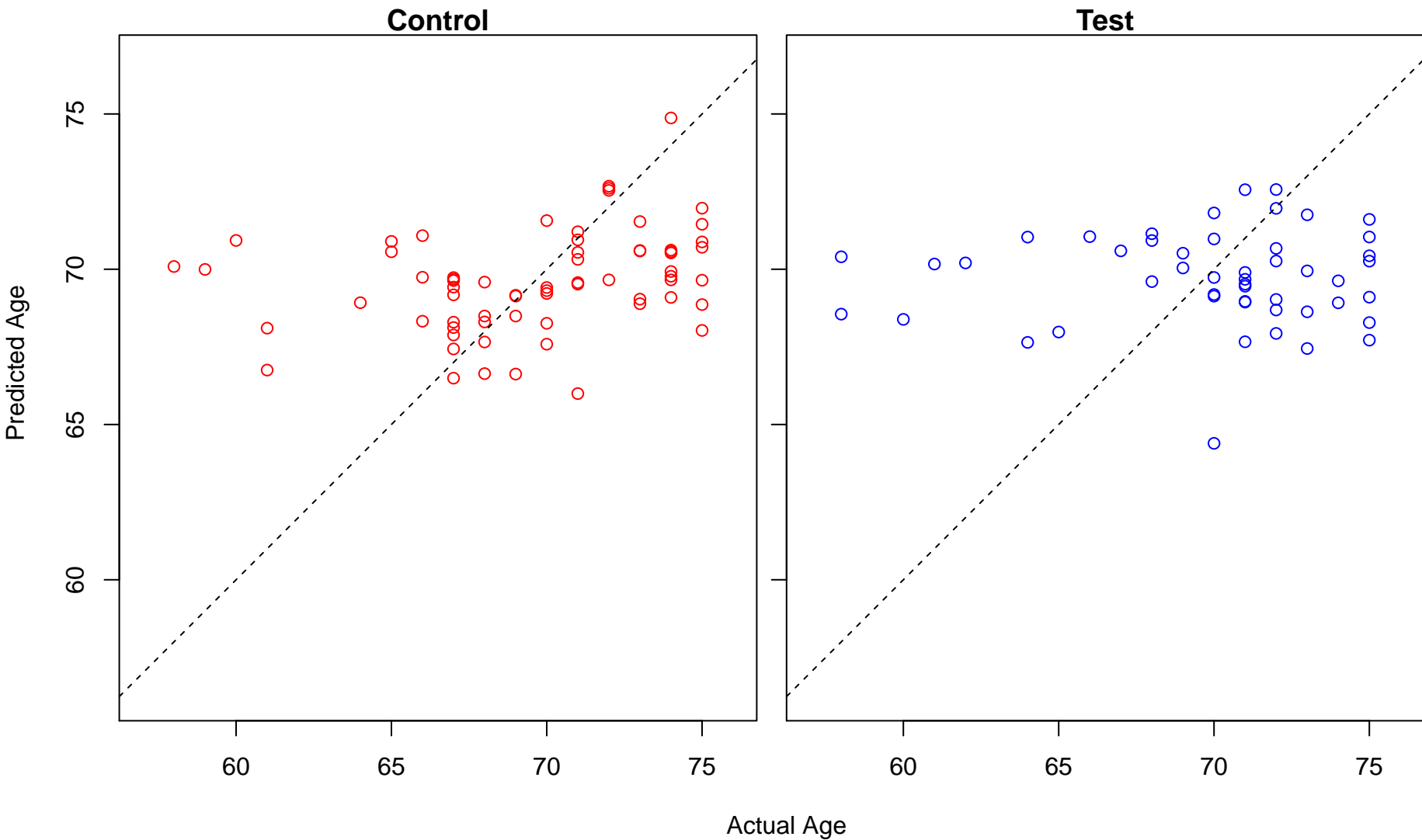
negative regulation of retrograde protein transport, ER to cytosol (Score: 0.282071)



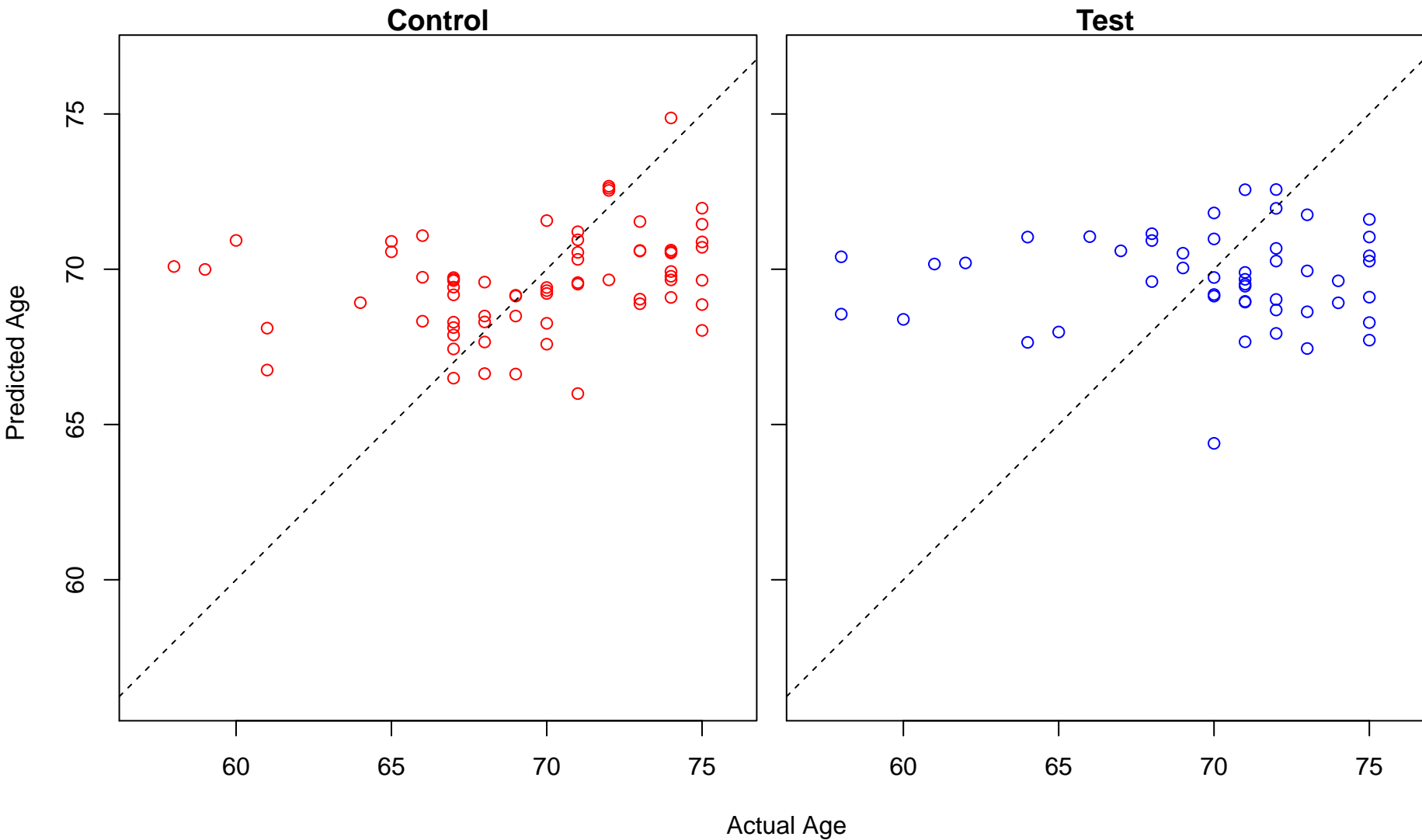
regulation of cell maturation (Score: 0.281073)



killing of cells of other organism (Score: 0.279932)

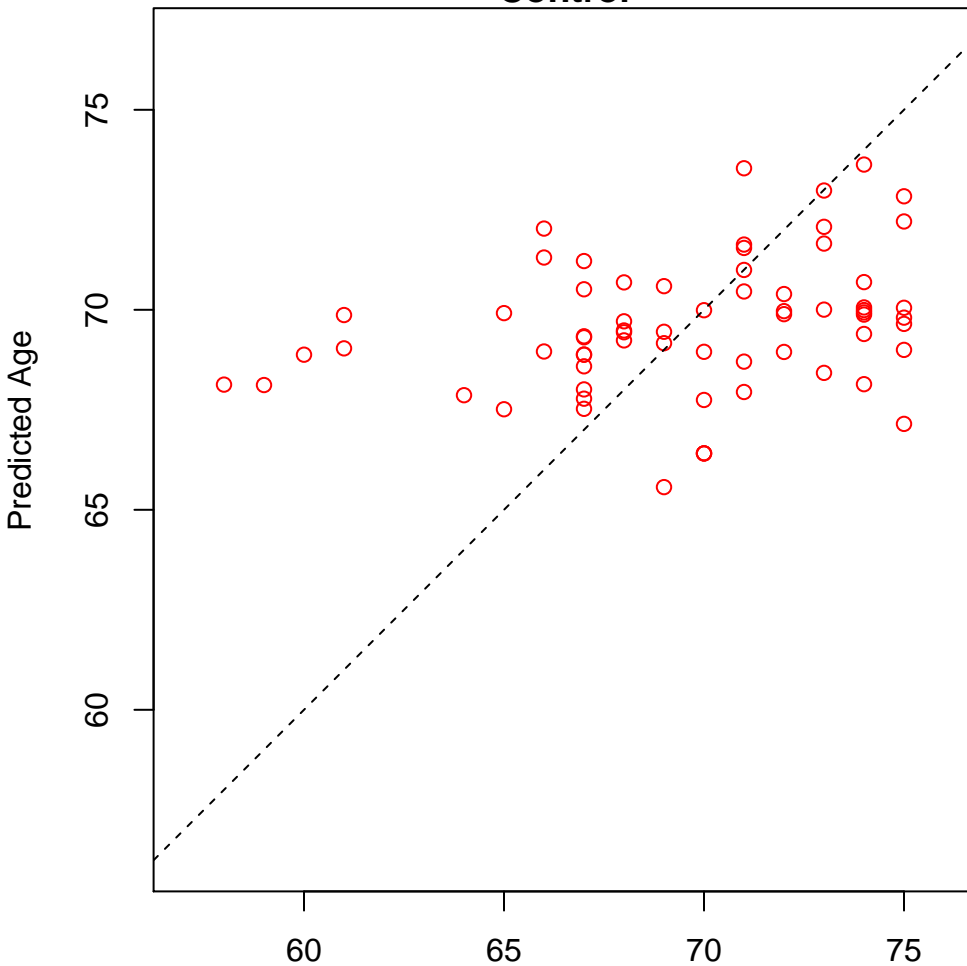


disruption of cells of other organism (Score: 0.279932)

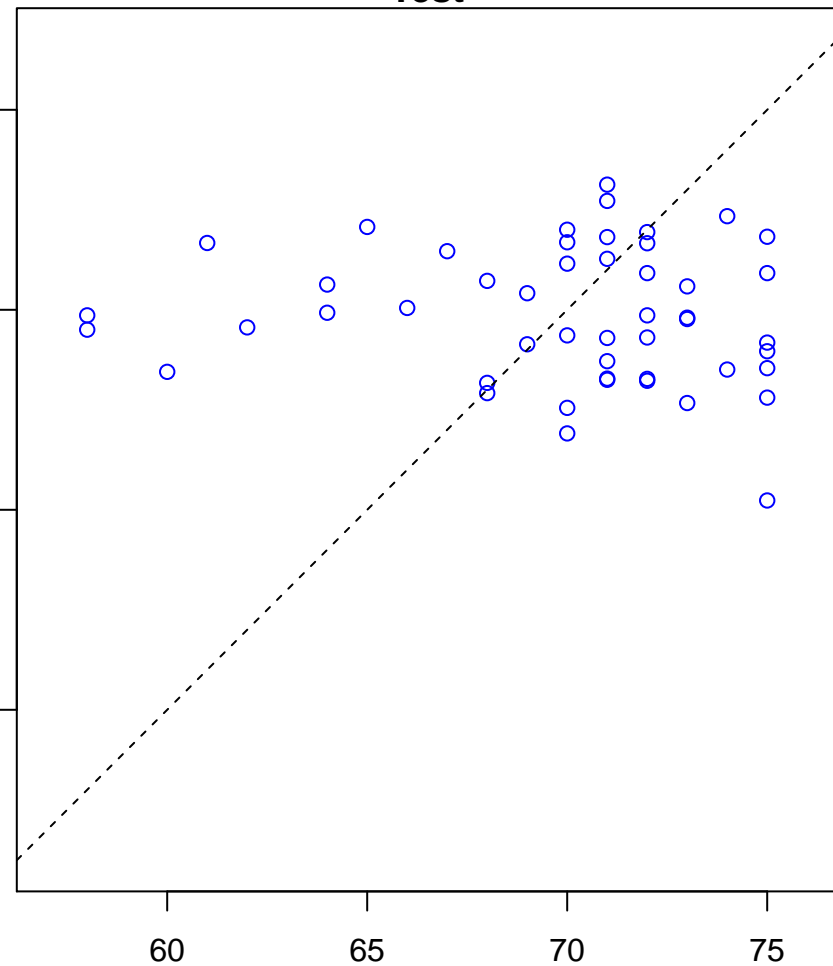


positive regulation of vasoconstriction (Score: 0.278743)

Control

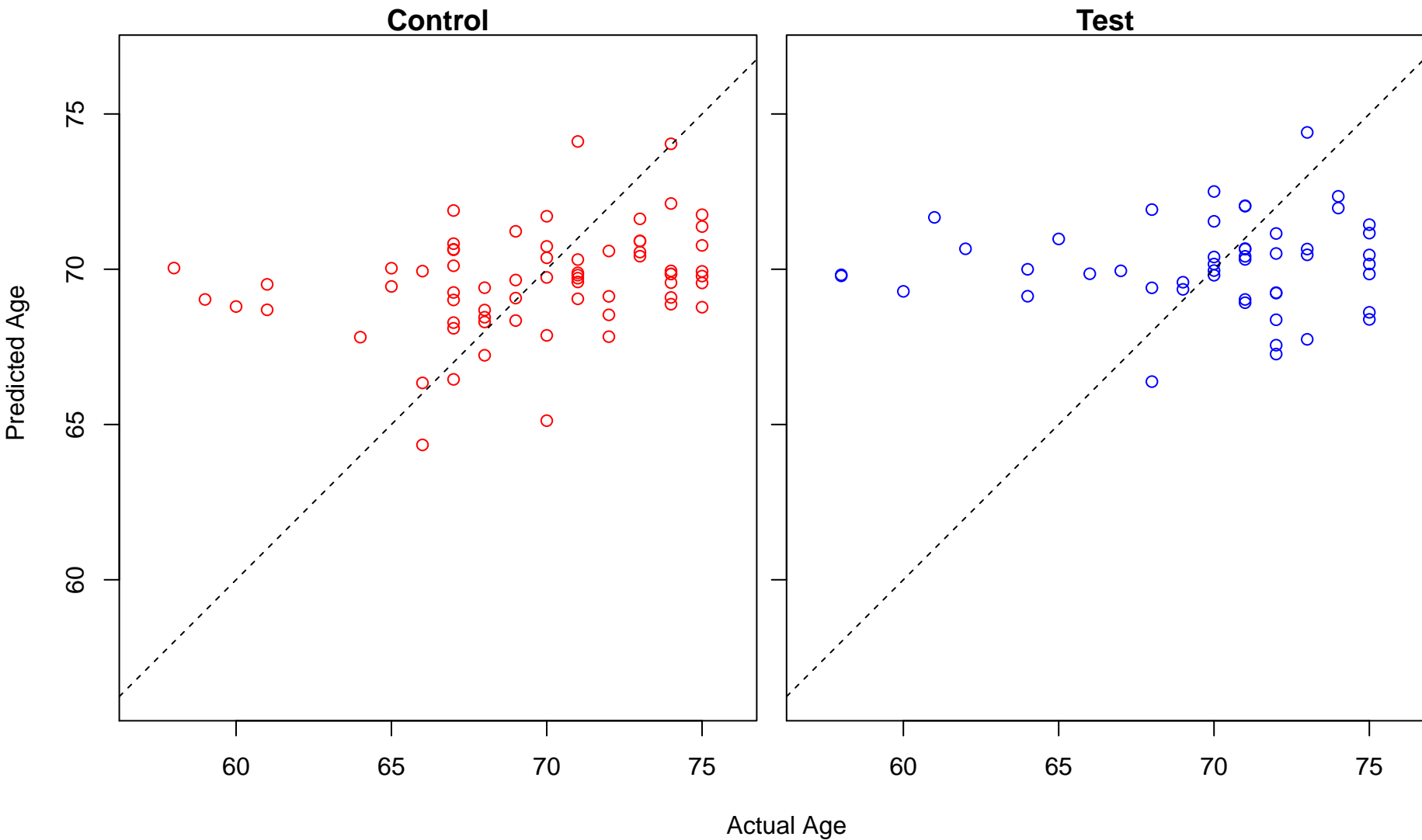


Test

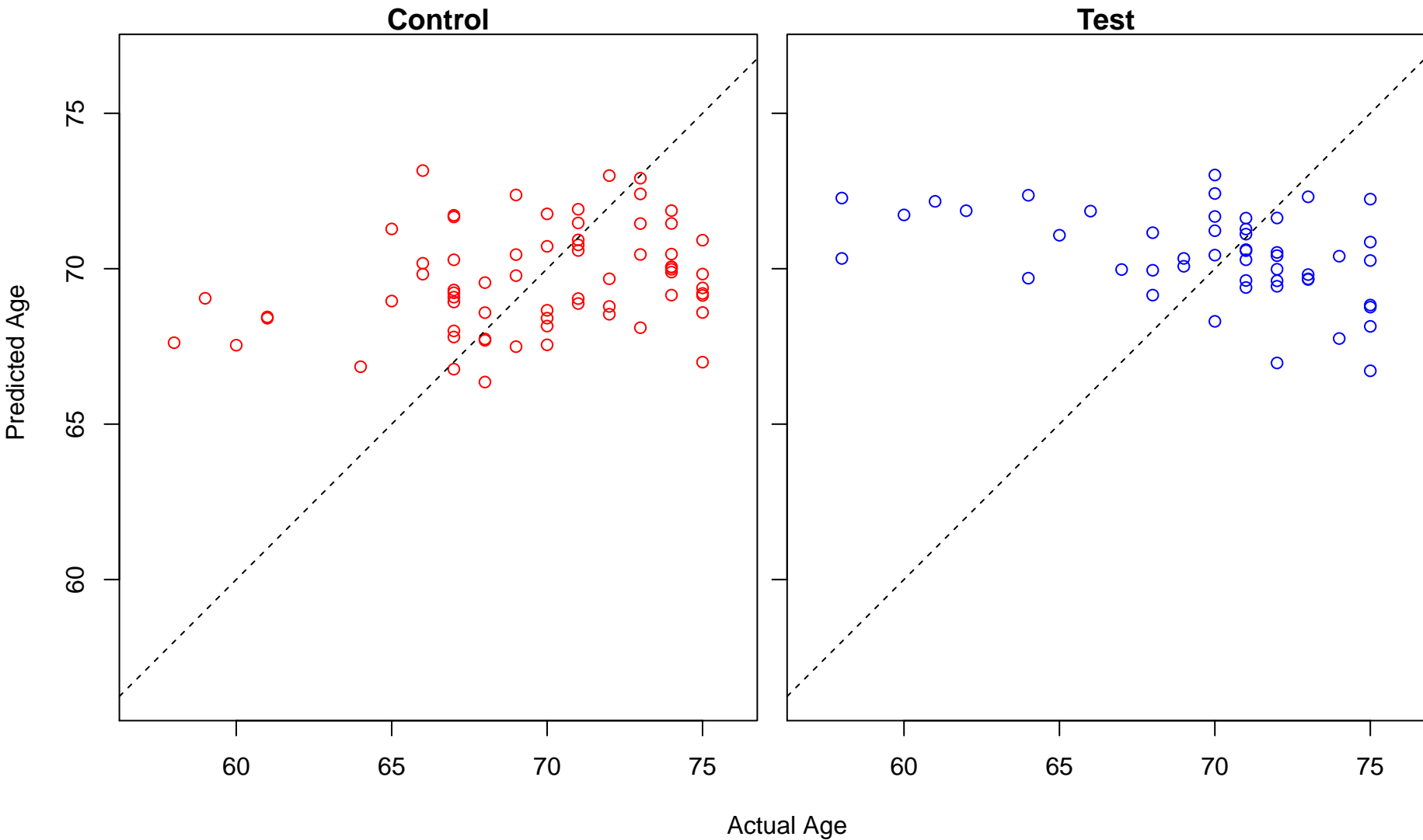


Actual Age

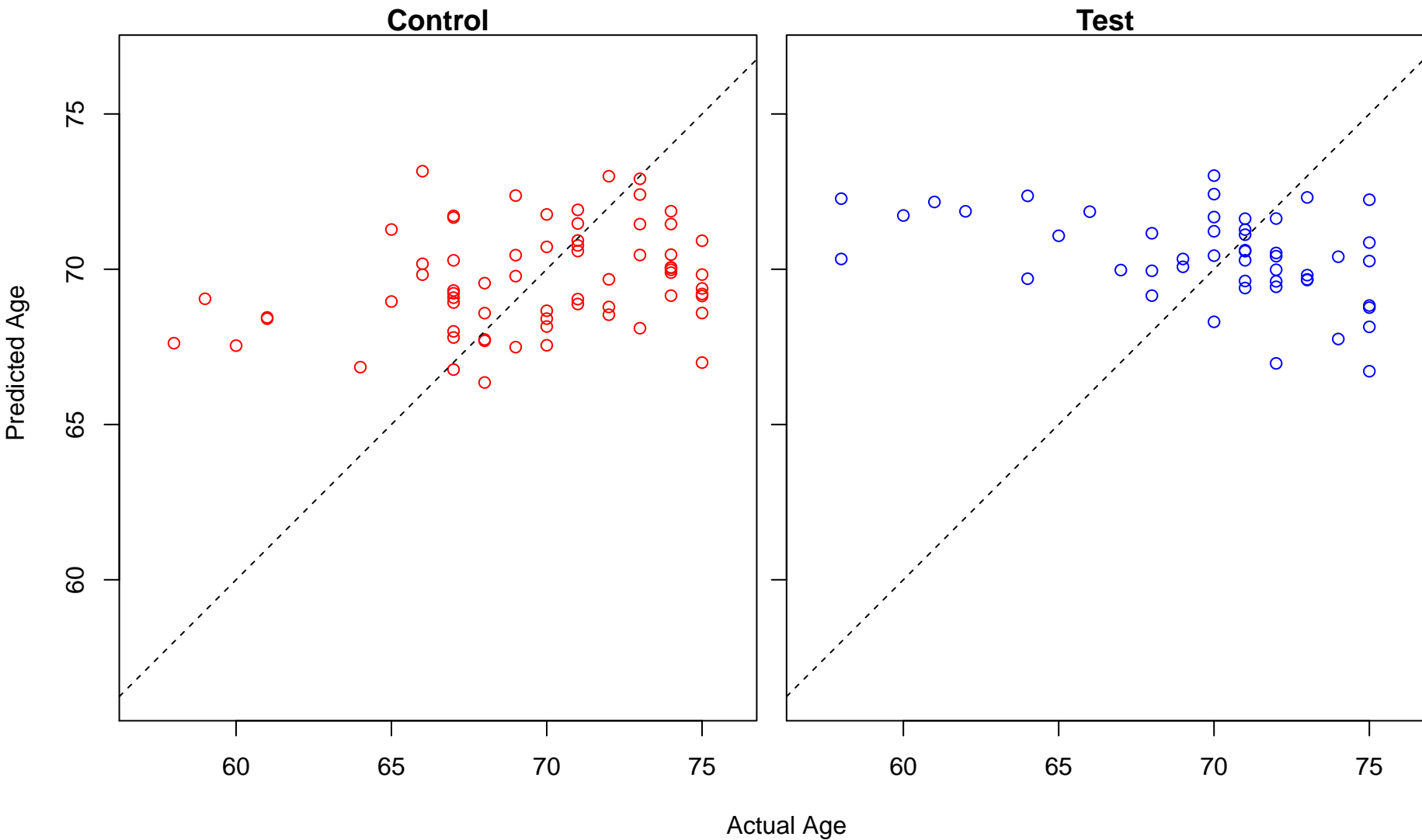
JUN phosphorylation (Score: 0.278576)



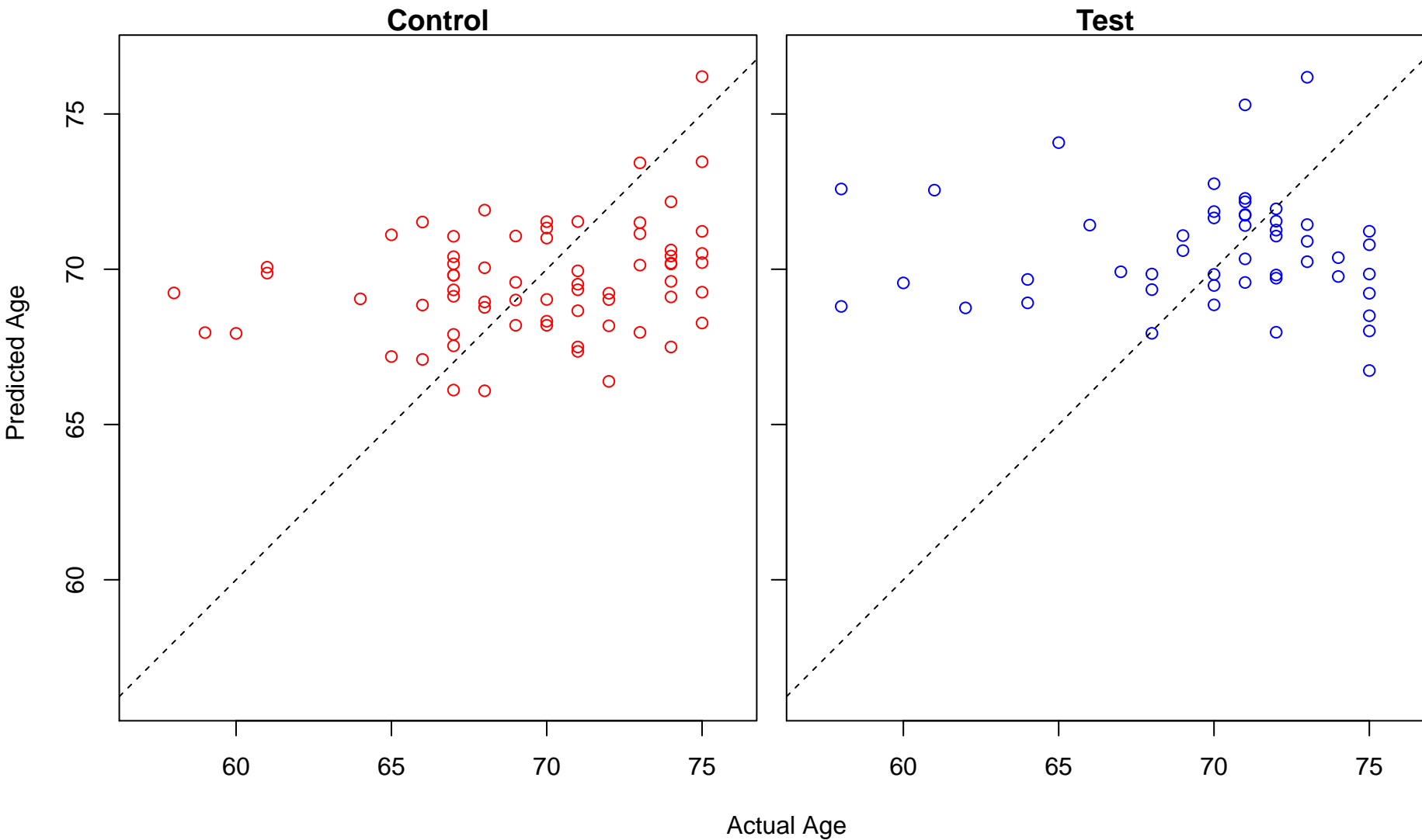
regulation of vitamin D biosynthetic process (Score: 0.278383)



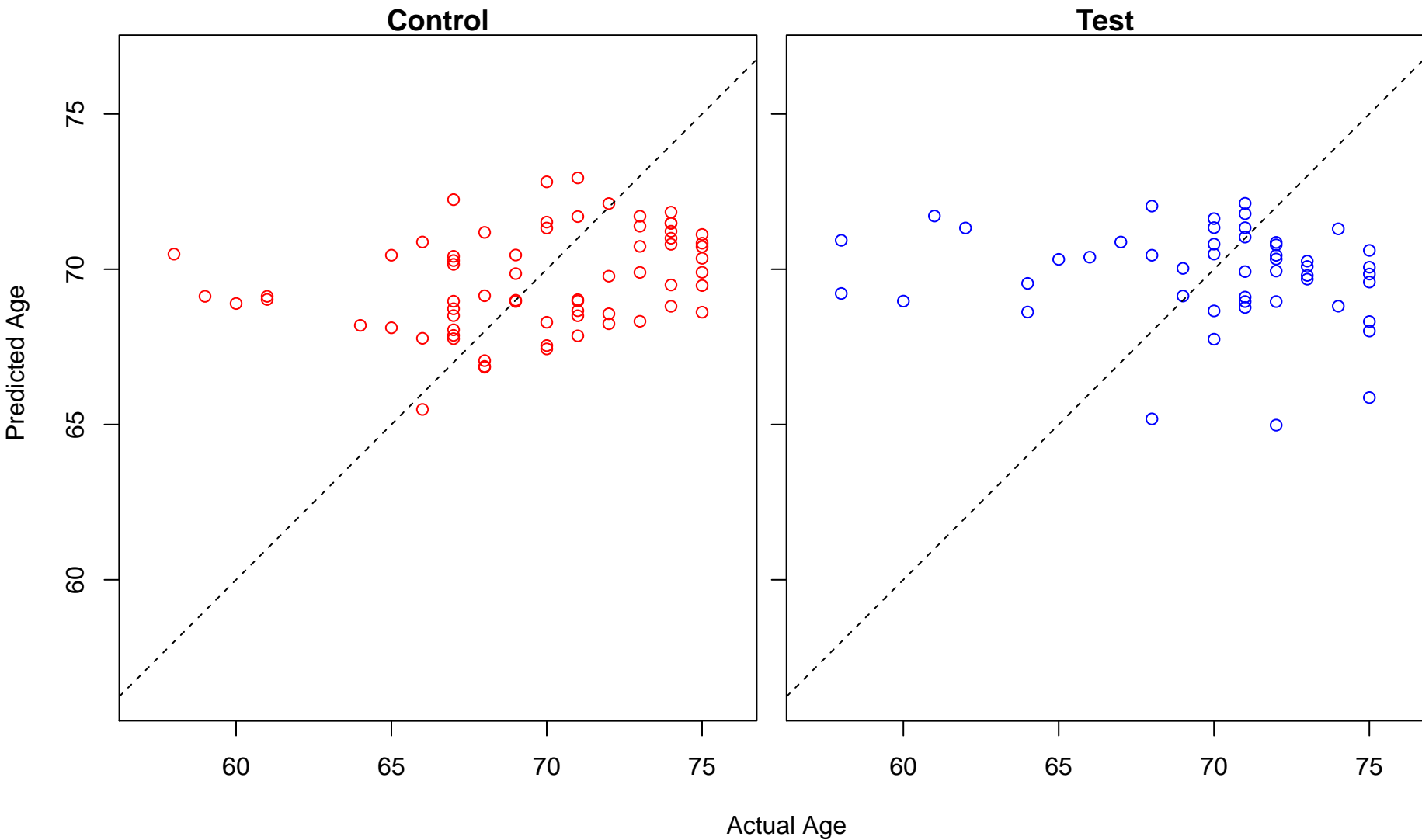
regulation of calcidiol 1-monooxygenase activity (Score: 0.278383)



glucocorticoid metabolic process (Score: 0.277814)

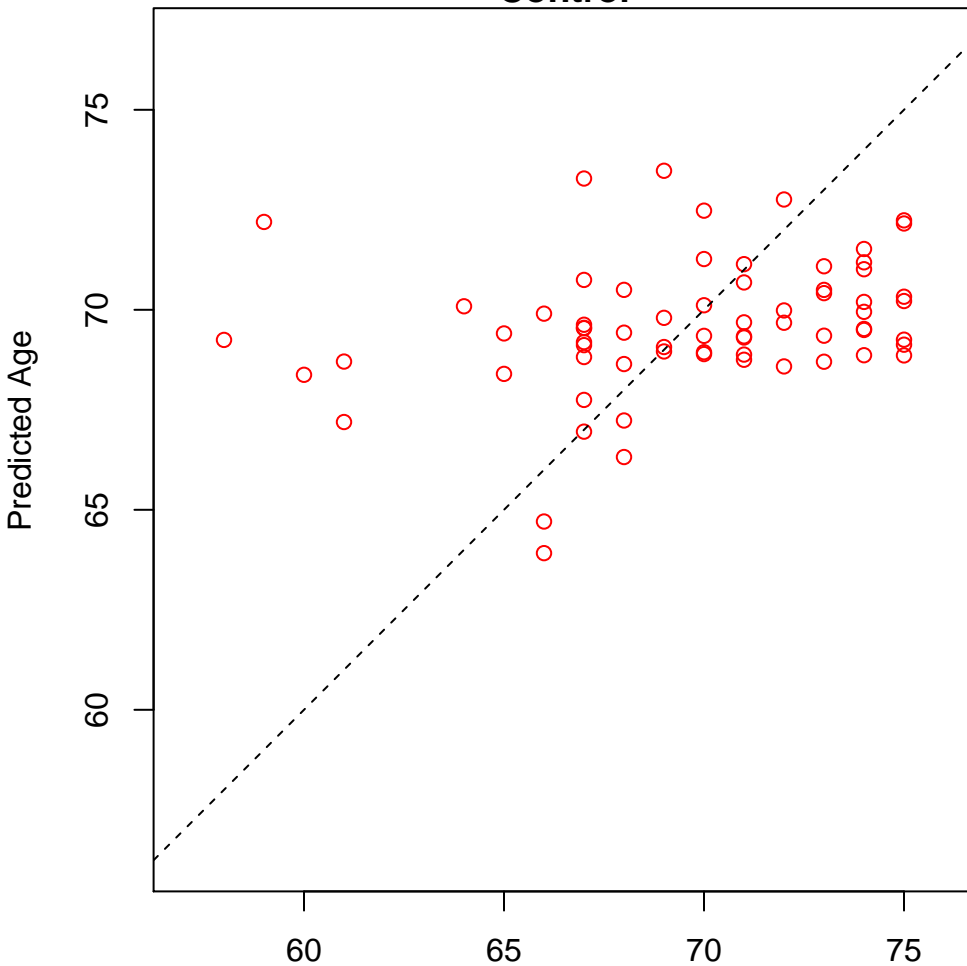


protection from natural killer cell mediated cytotoxicity (Score: 0.276826)

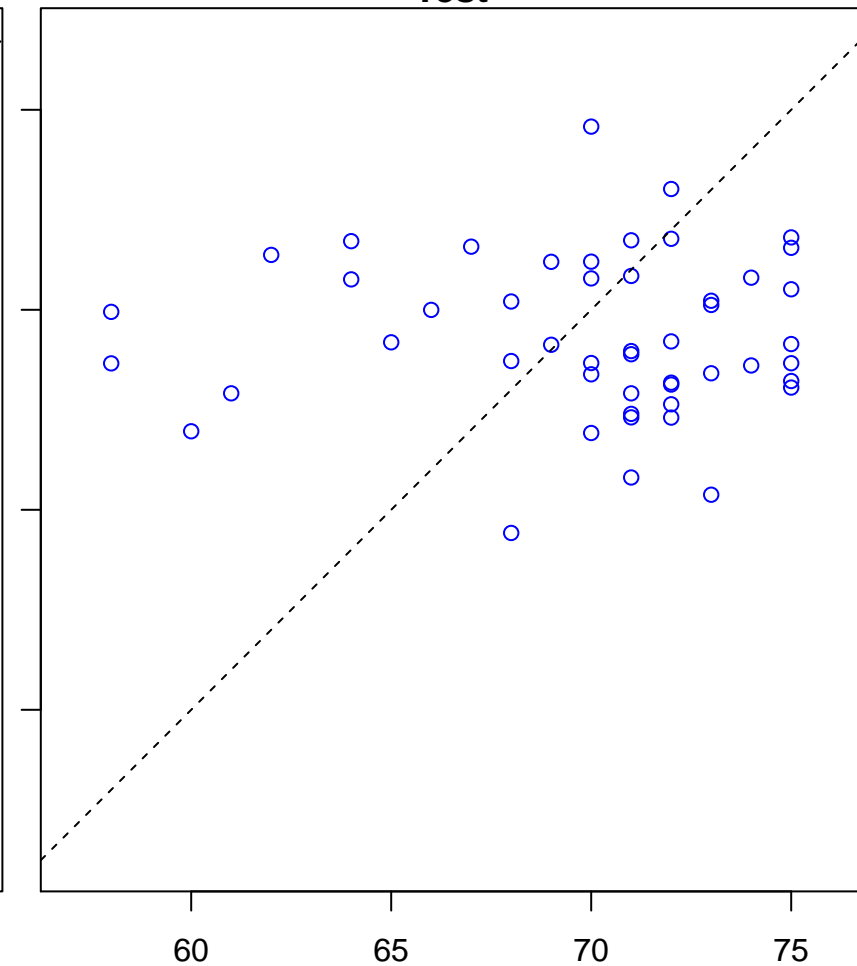


response to hepatocyte growth factor (Score: 0.276682)

Control

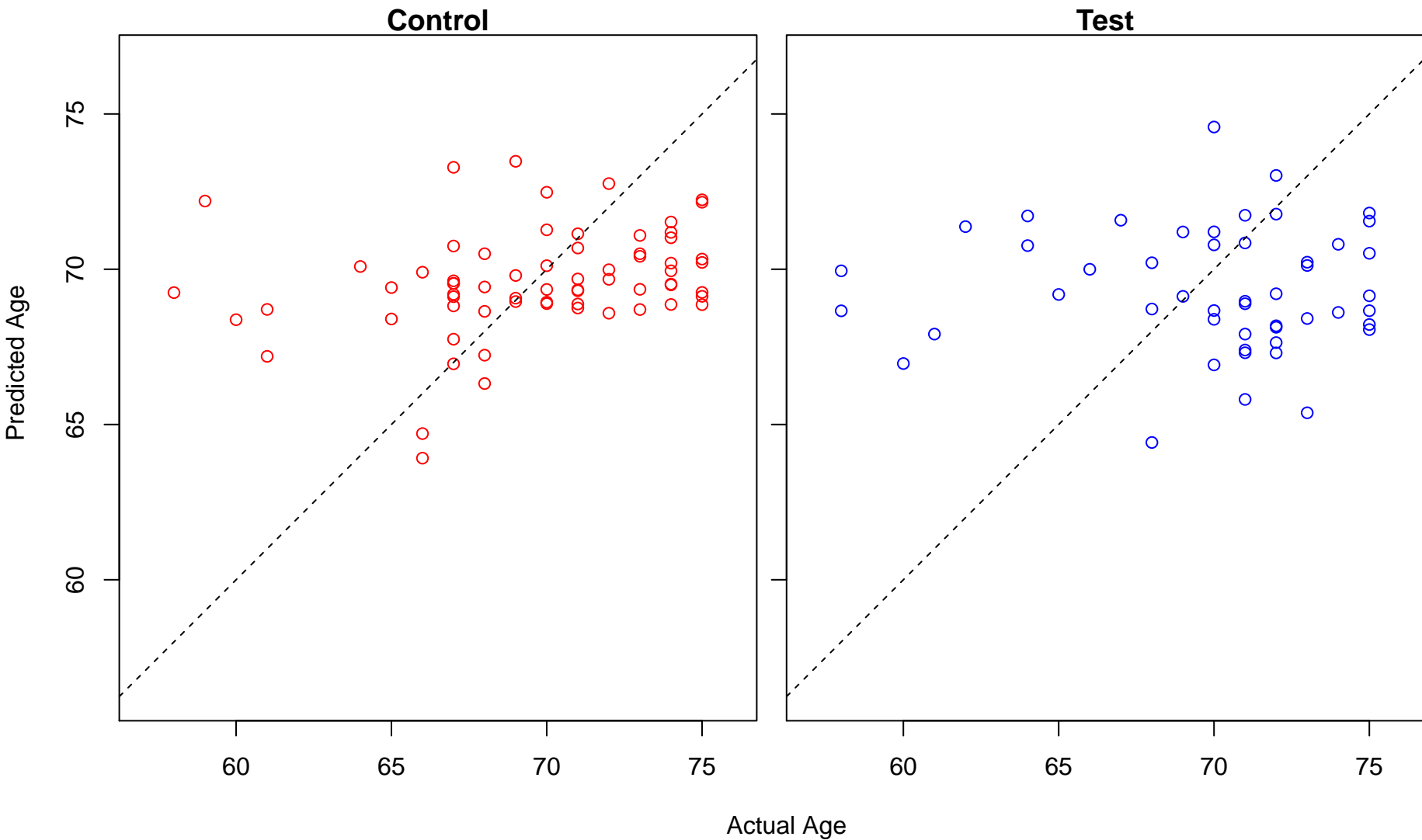


Test

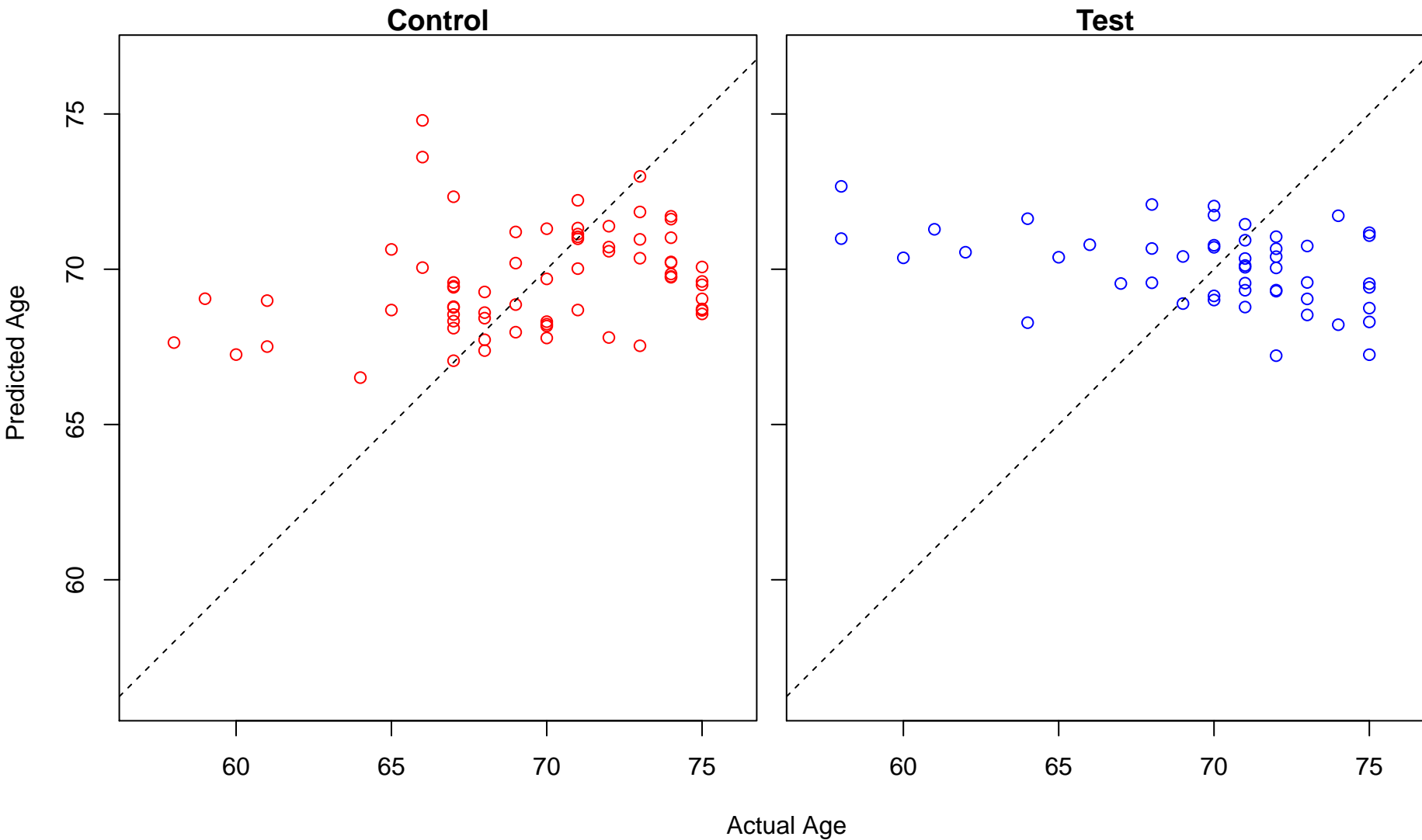


Actual Age

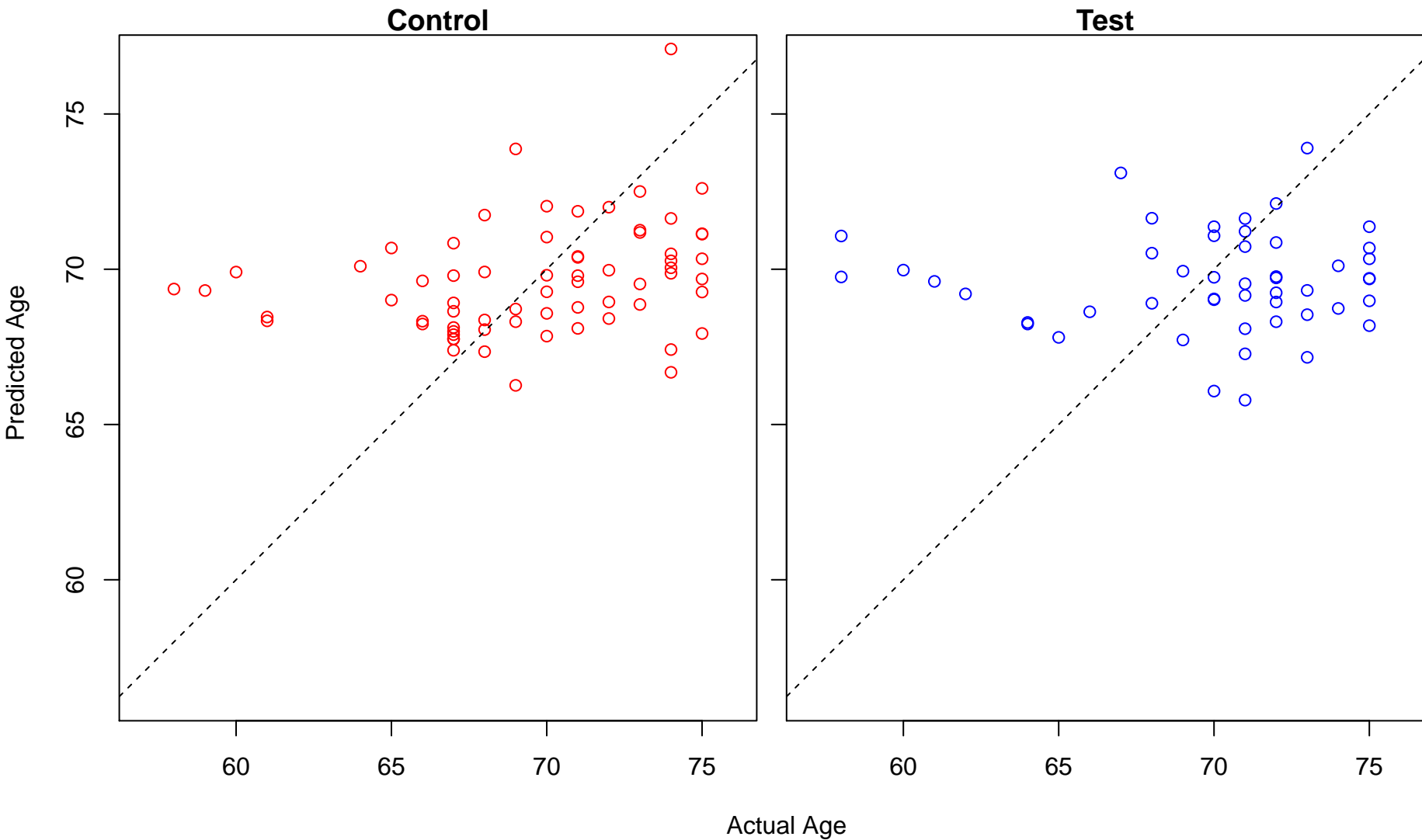
cellular response to hepatocyte growth factor stimulus (Score: 0.276682)



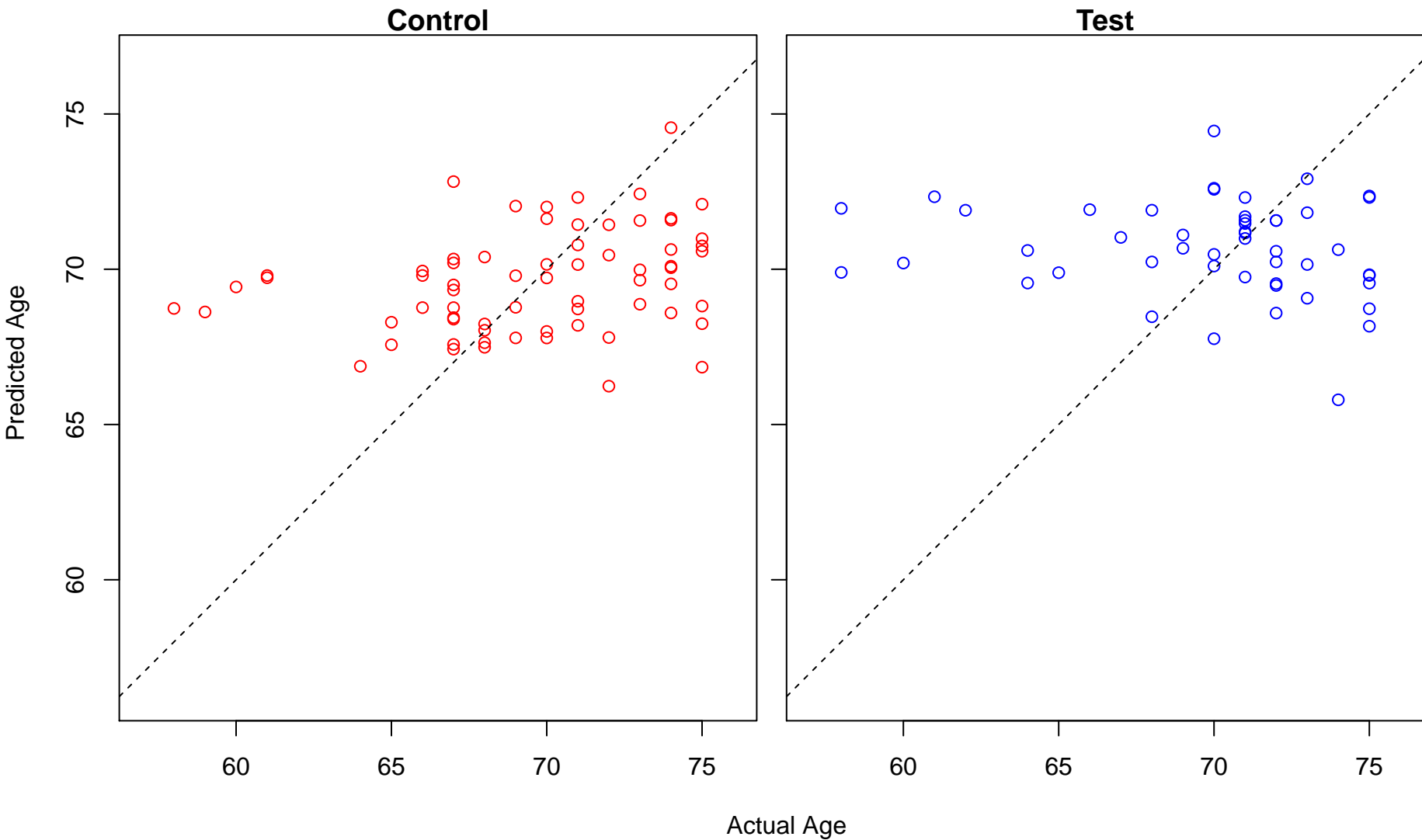
negative regulation of vitamin D biosynthetic process (Score: 0.275934)



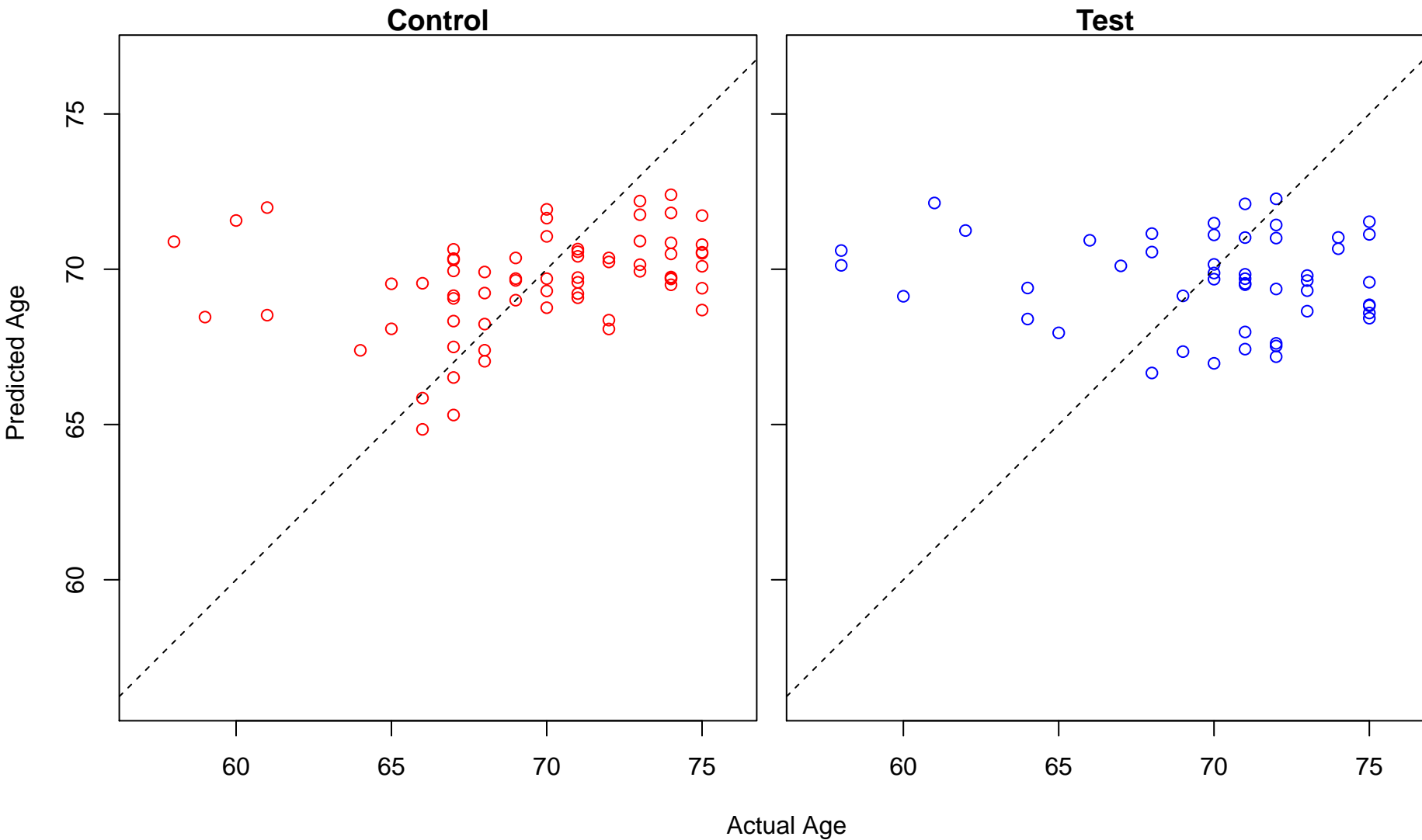
endoplasmic reticulum tubular network organization (Score: 0.275254)



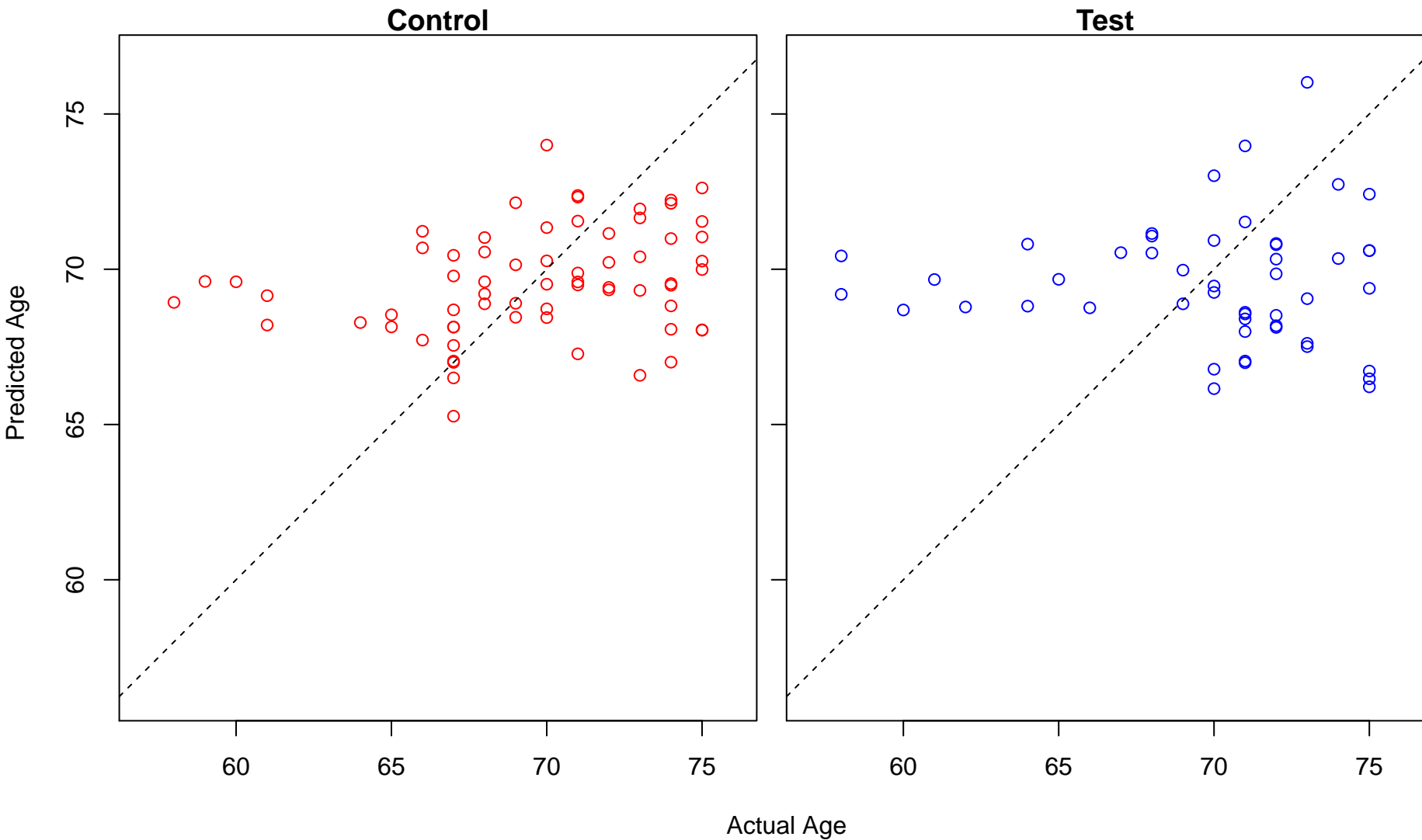
negative regulation of membrane potential (Score: 0.274586)



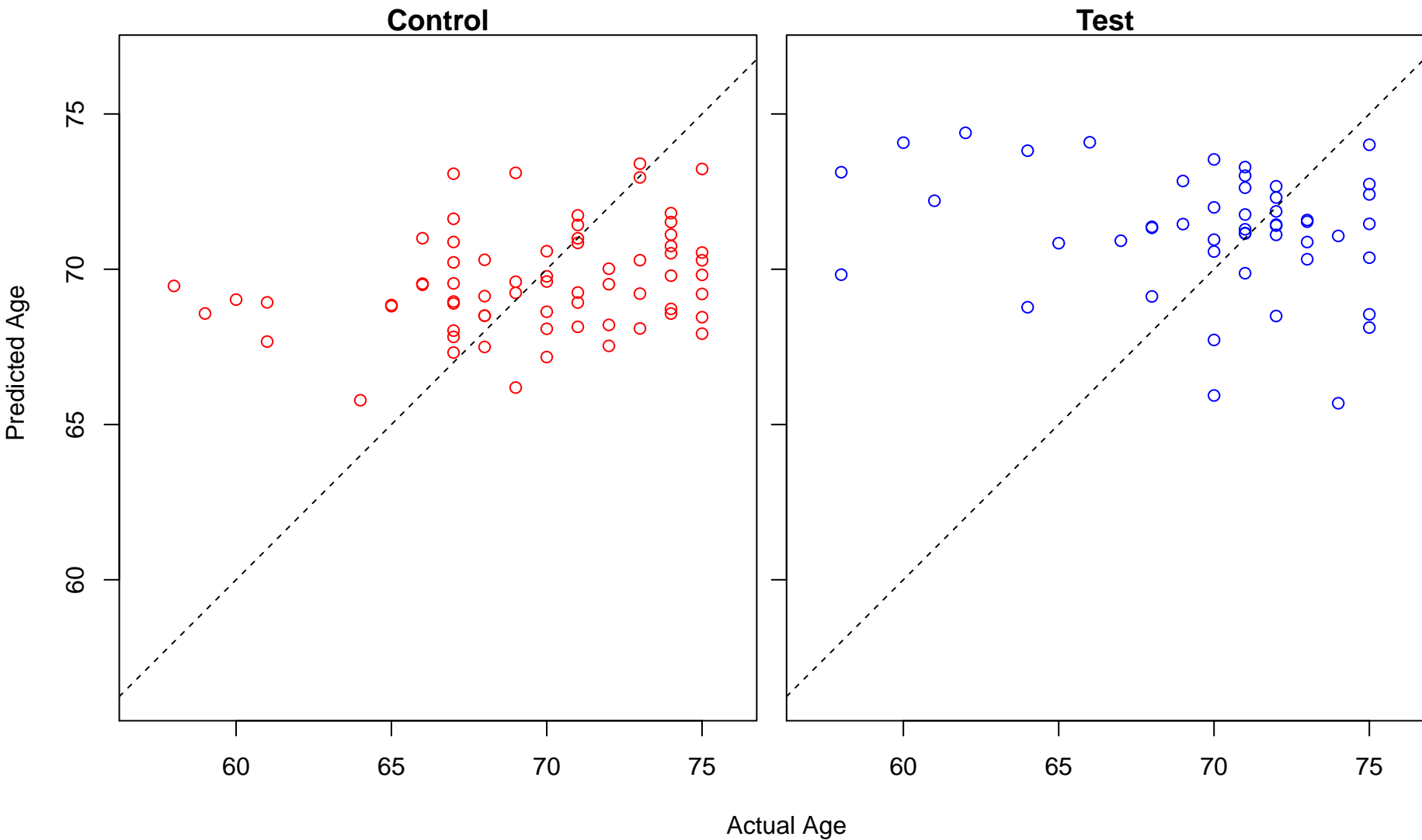
gap junction assembly (Score: 0.273877)



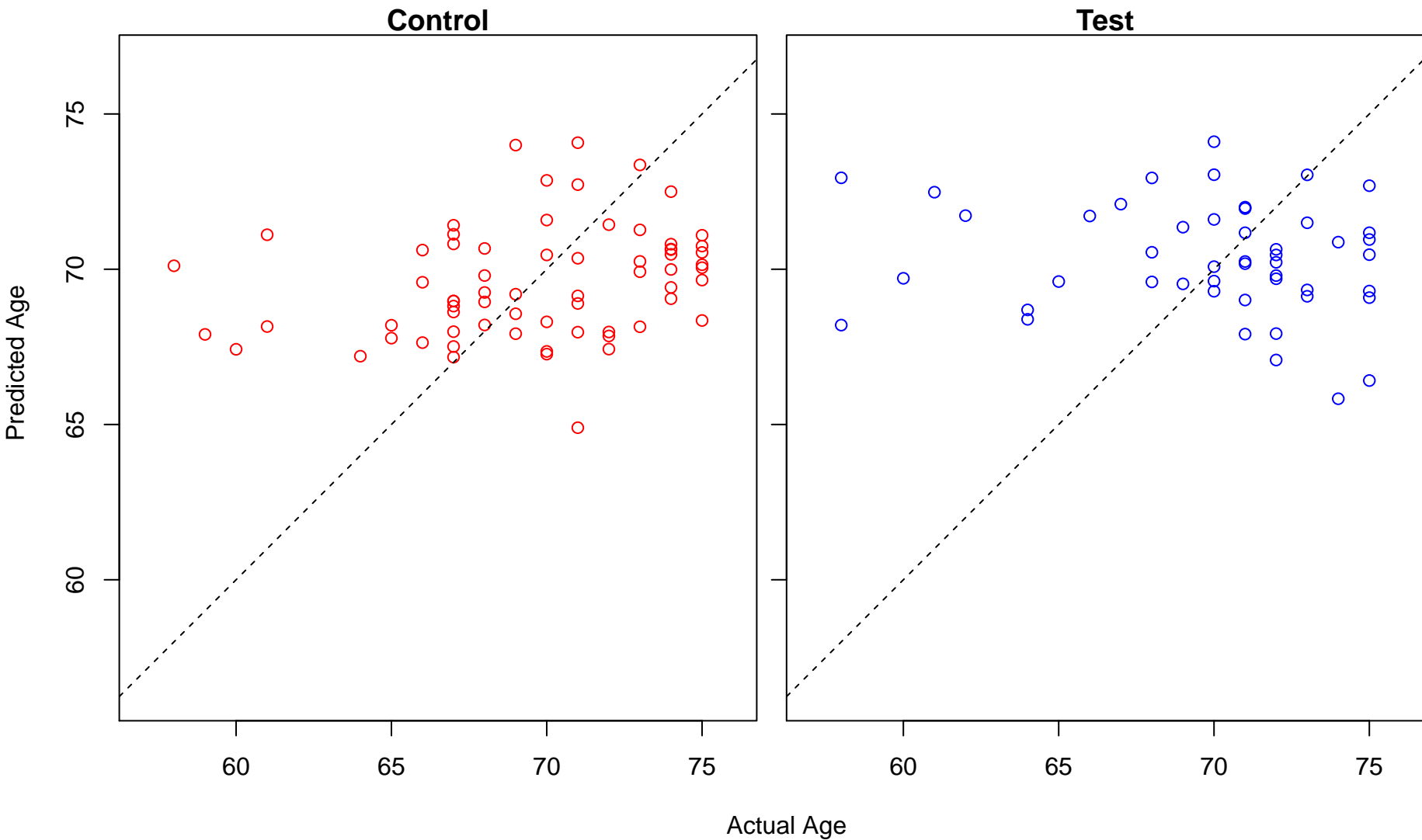
regulation of transforming growth factor beta2 production (Score: 0.273430)



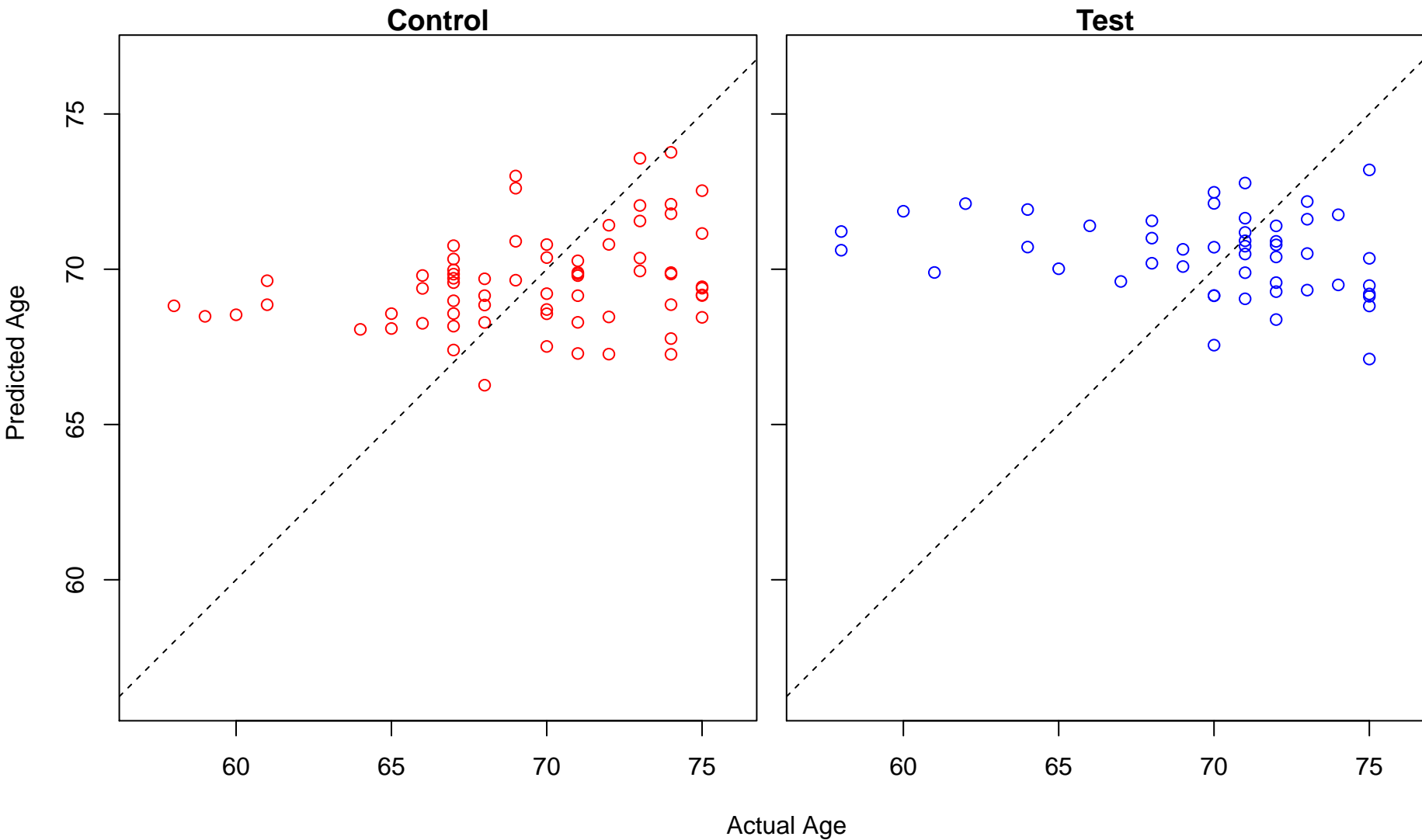
non-canonical Wnt signaling pathway via MAPK cascade (Score: 0.273114)



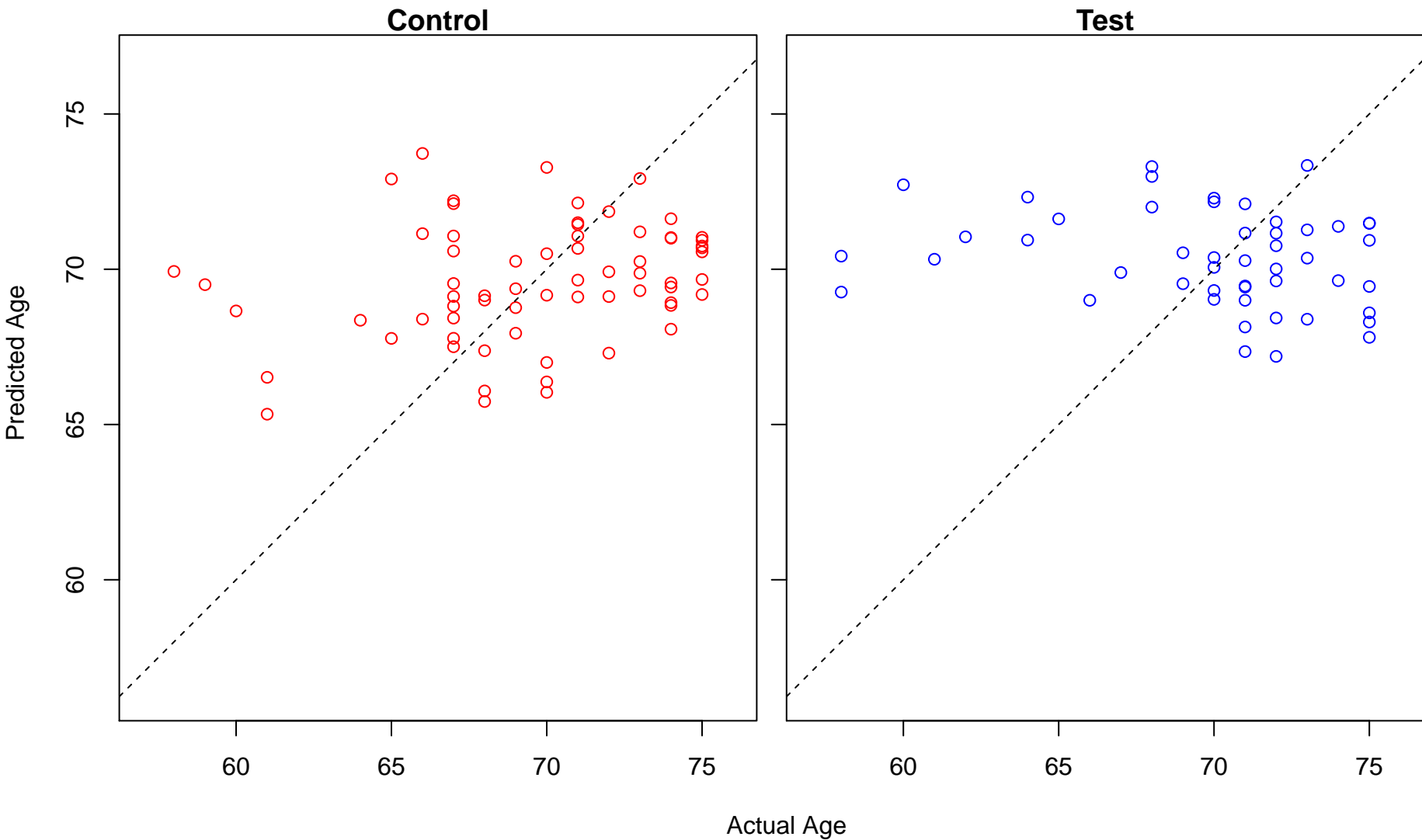
regulation of DNA damage checkpoint (Score: 0.268948)



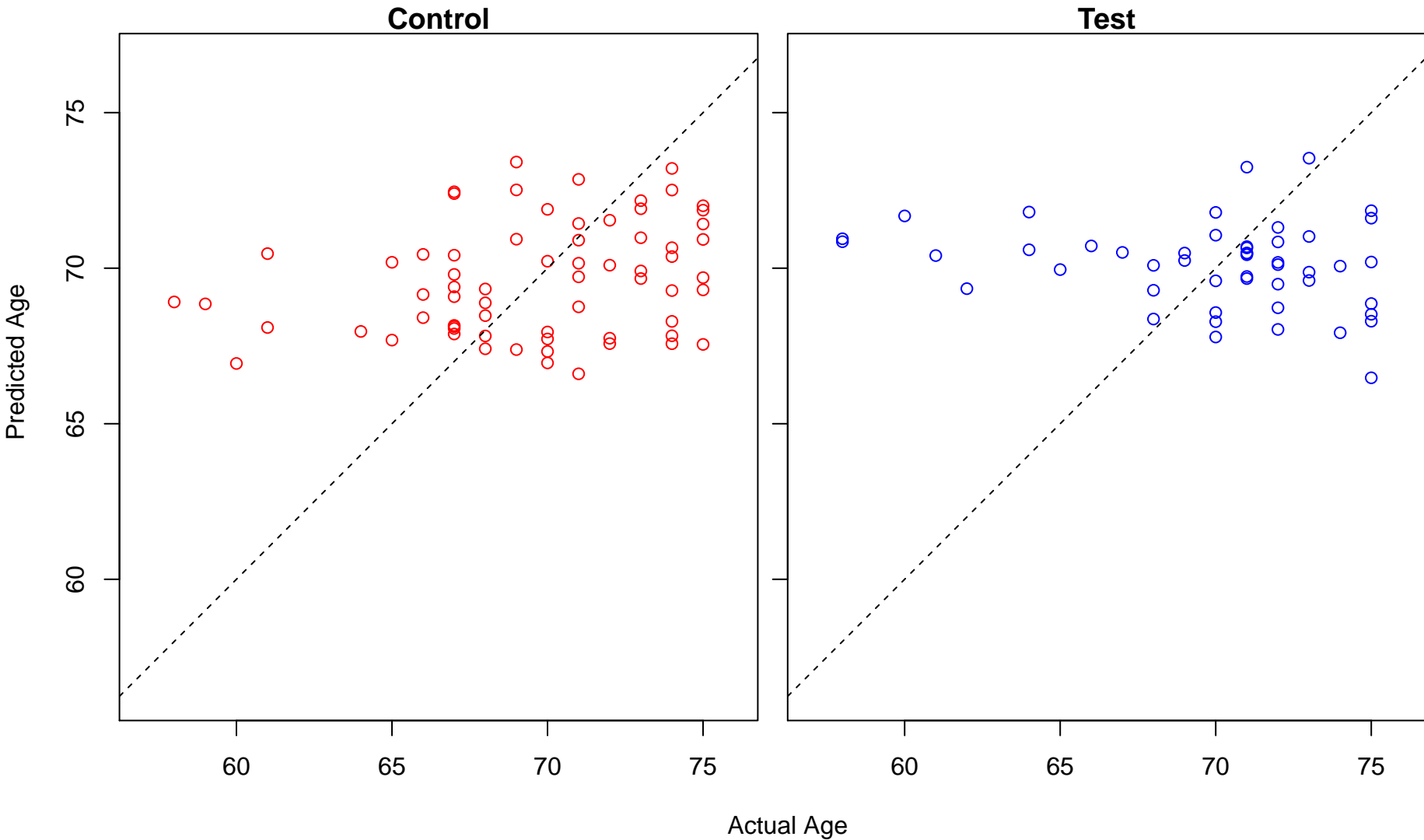
activation of JNKK activity (Score: 0.268945)



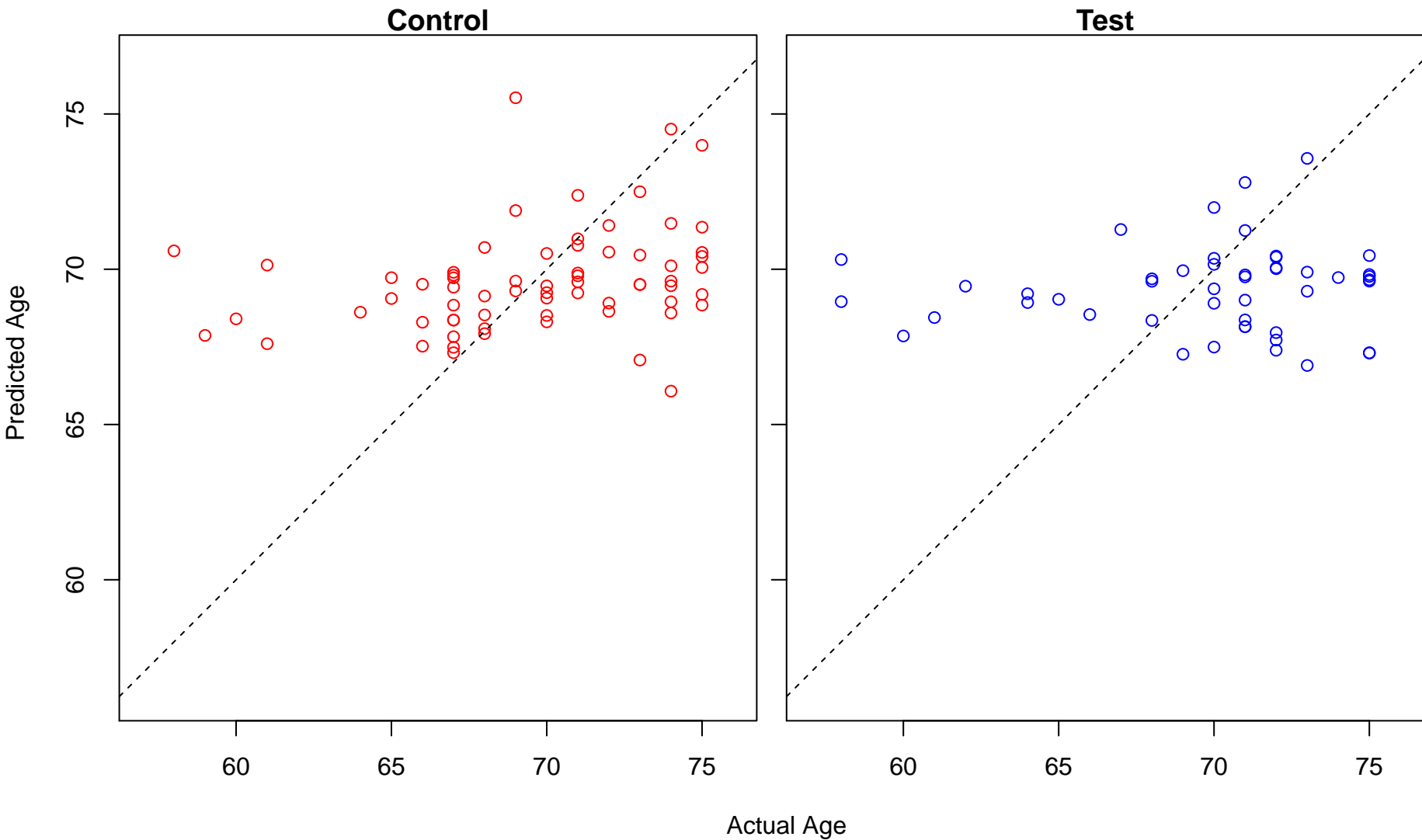
positive regulation of lamellipodium morphogenesis (Score: 0.268259)



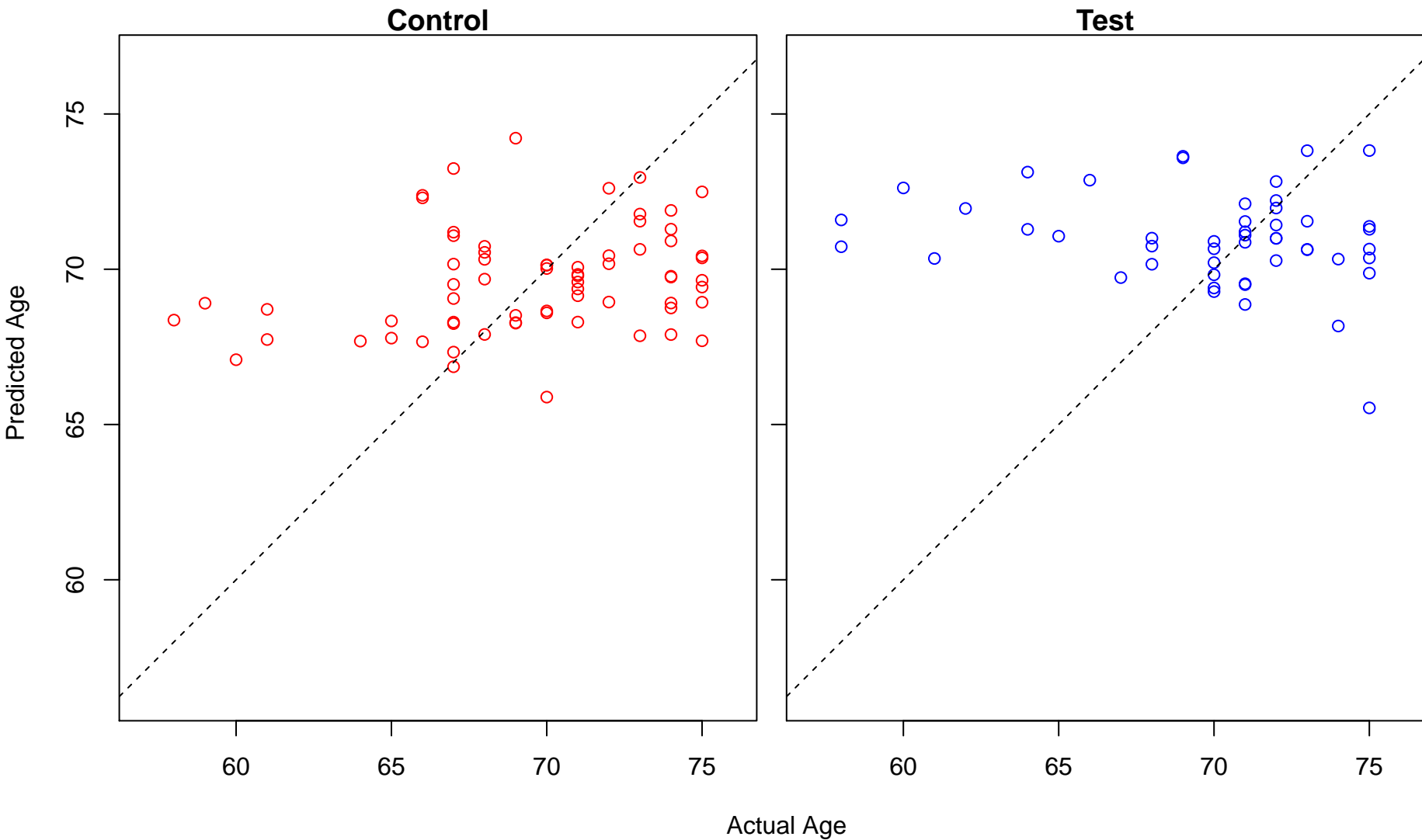
regulation of interleukin-2 biosynthetic process (Score: 0.267466)



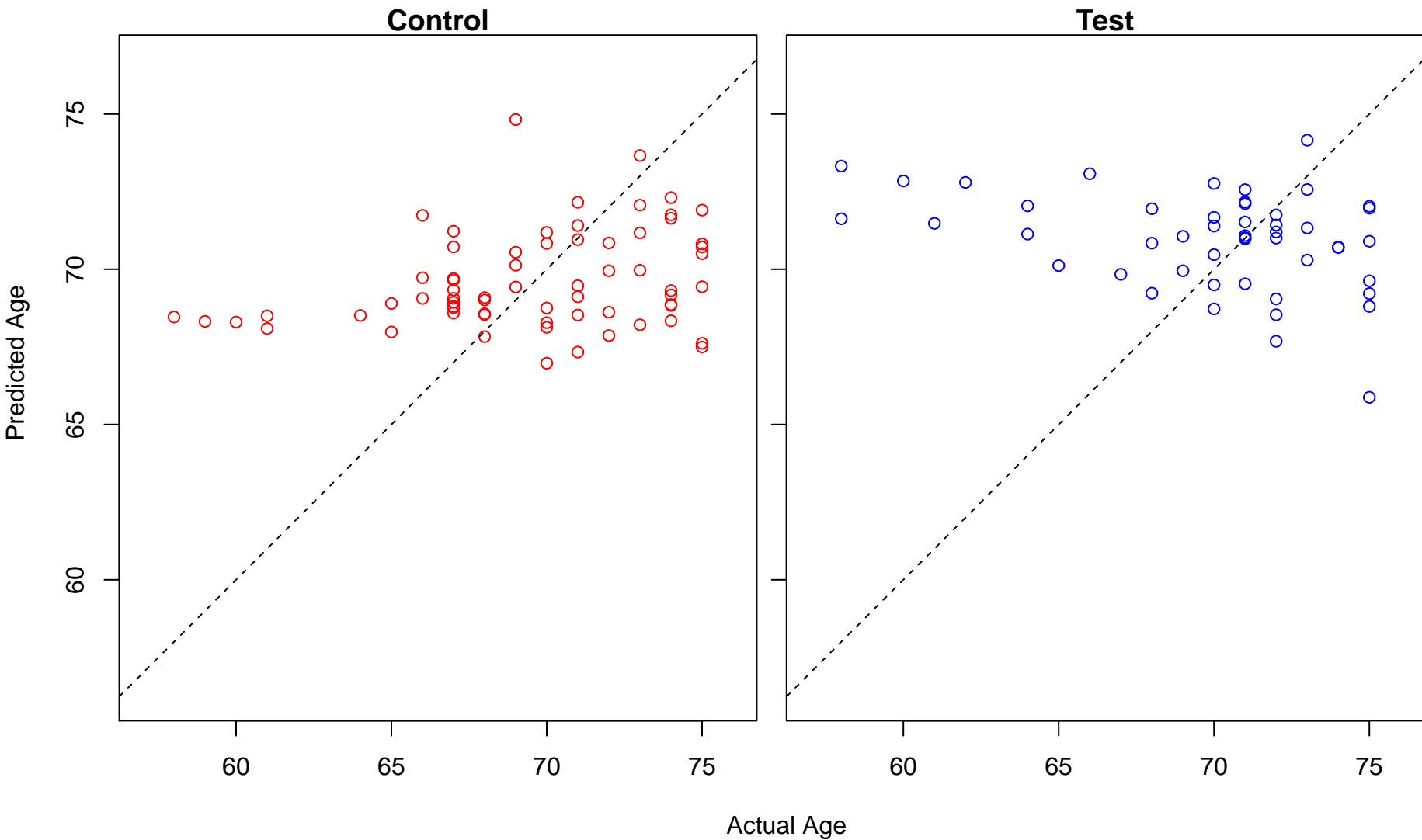
intermediate filament organization (Score: 0.266274)



negative regulation of pri-miRNA transcription from RNA polymerase II promoter (Score: 0.264026)

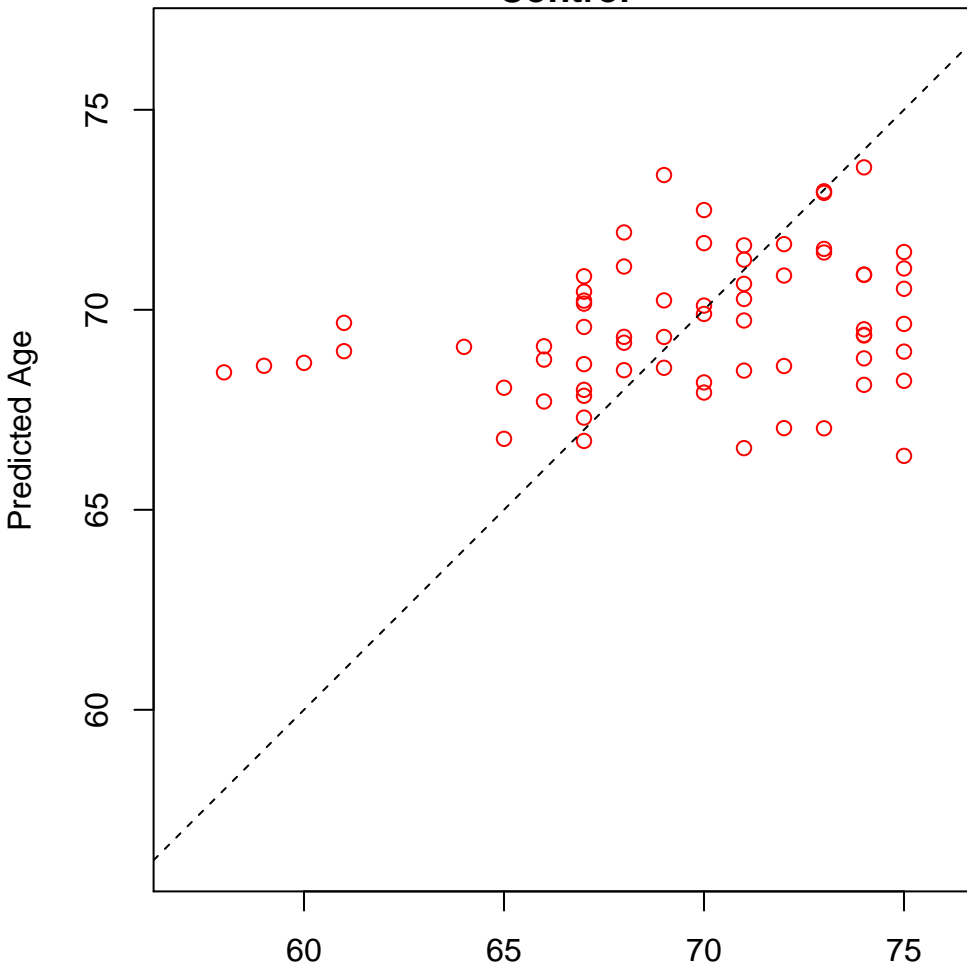


positive regulation of the force of heart contraction (Score: 0.262141)

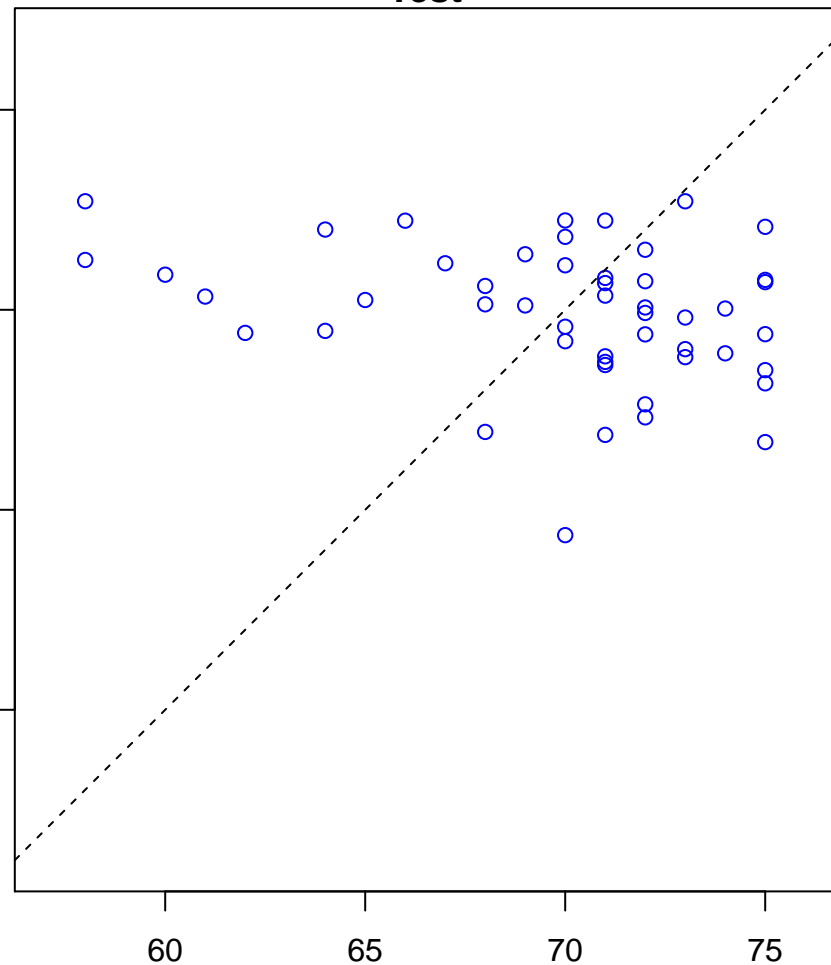


protein K11-linked deubiquitination (Score: 0.261827)

Control

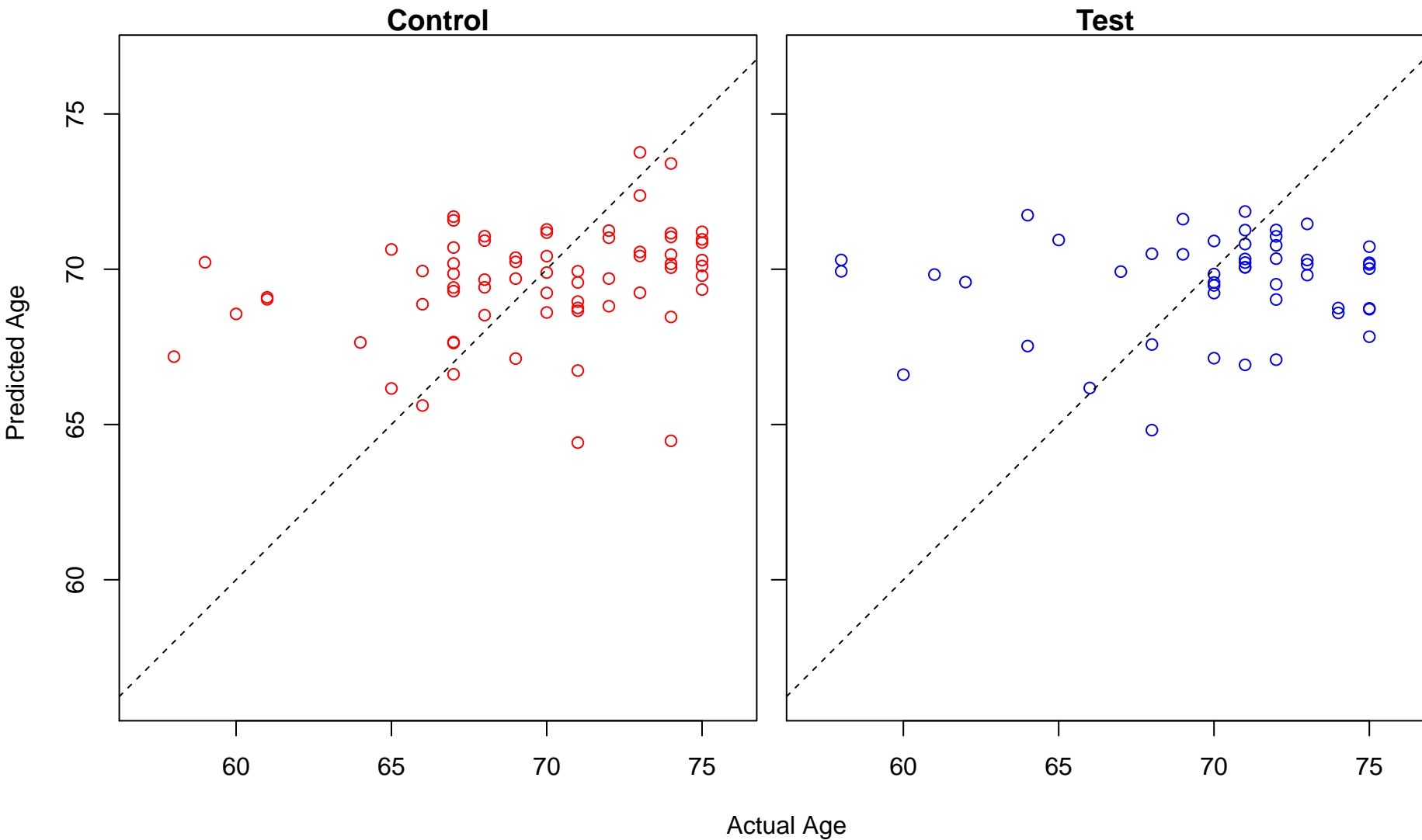


Test

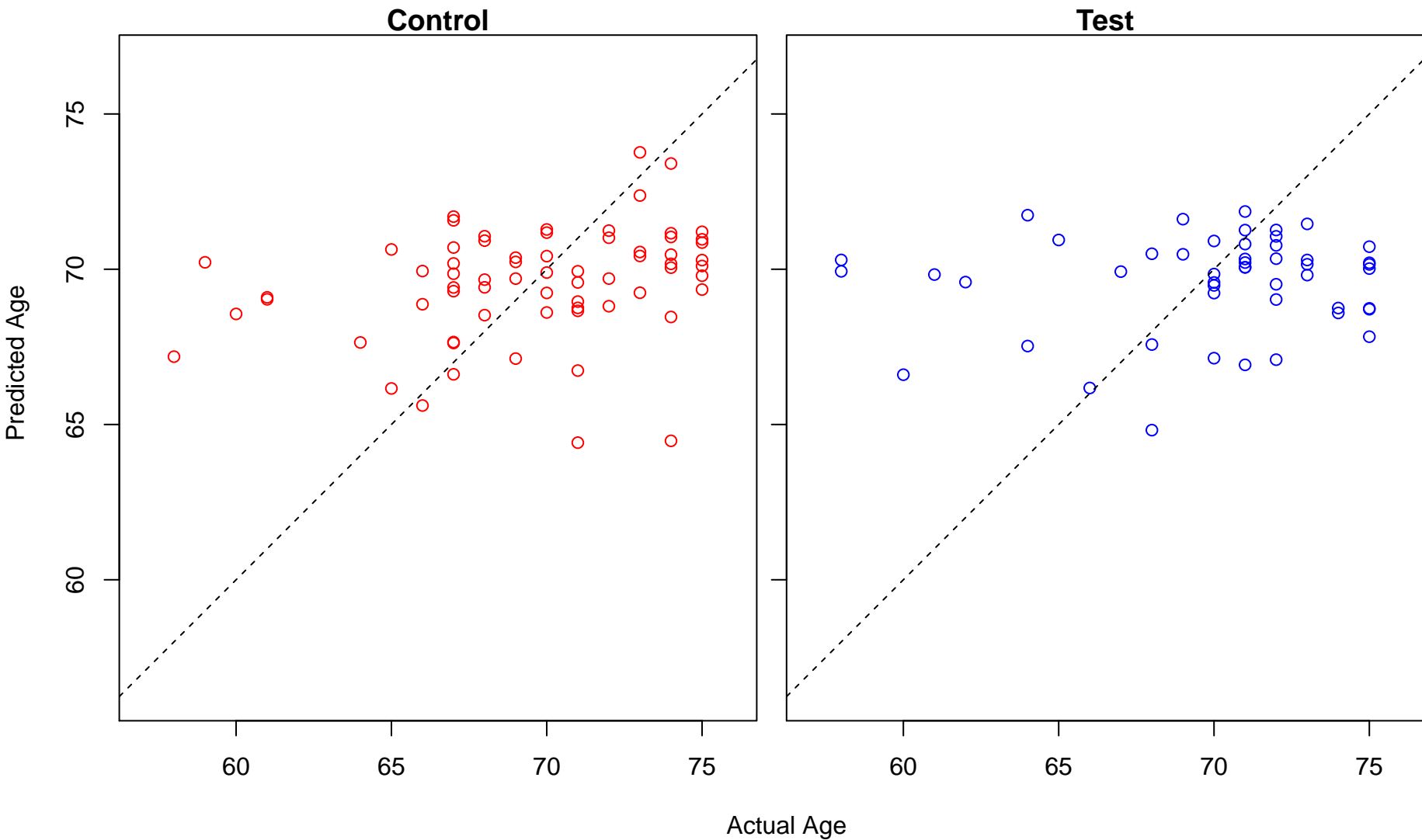


Actual Age

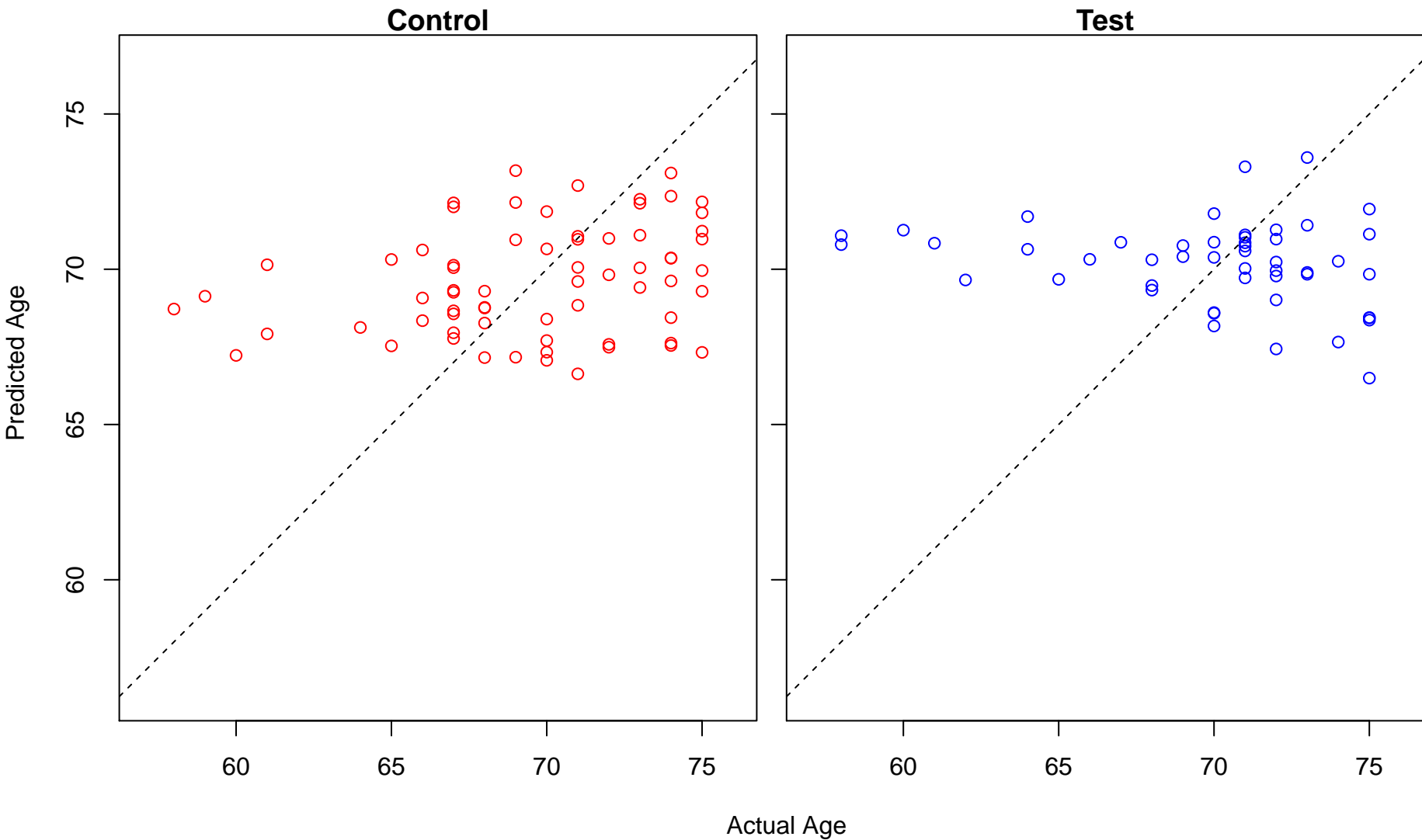
cardiac muscle cell–cardiac muscle cell adhesion (Score: 0.261773)



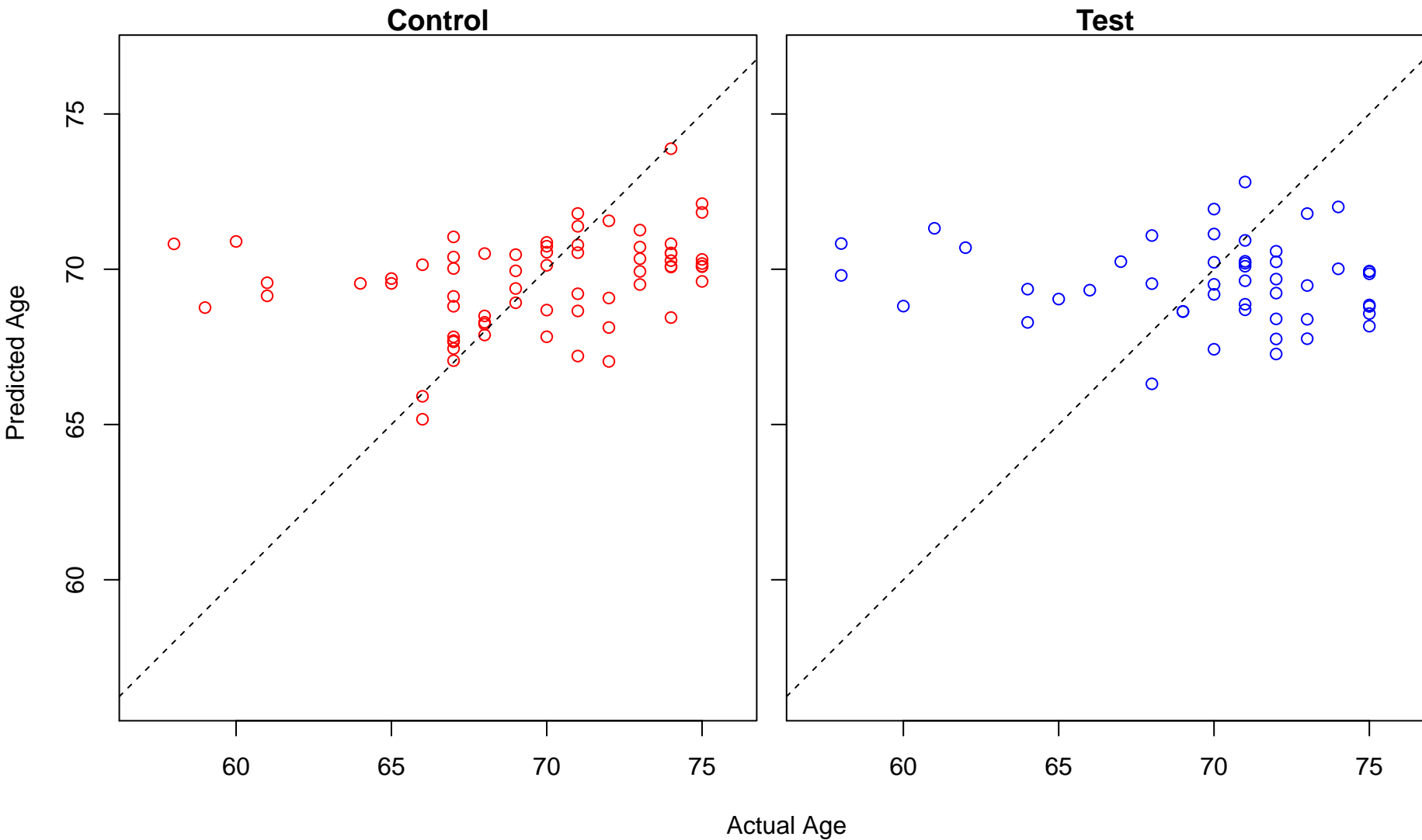
bundle of His cell–Purkinje myocyte adhesion involved in cell communication (Score: 0.261773)



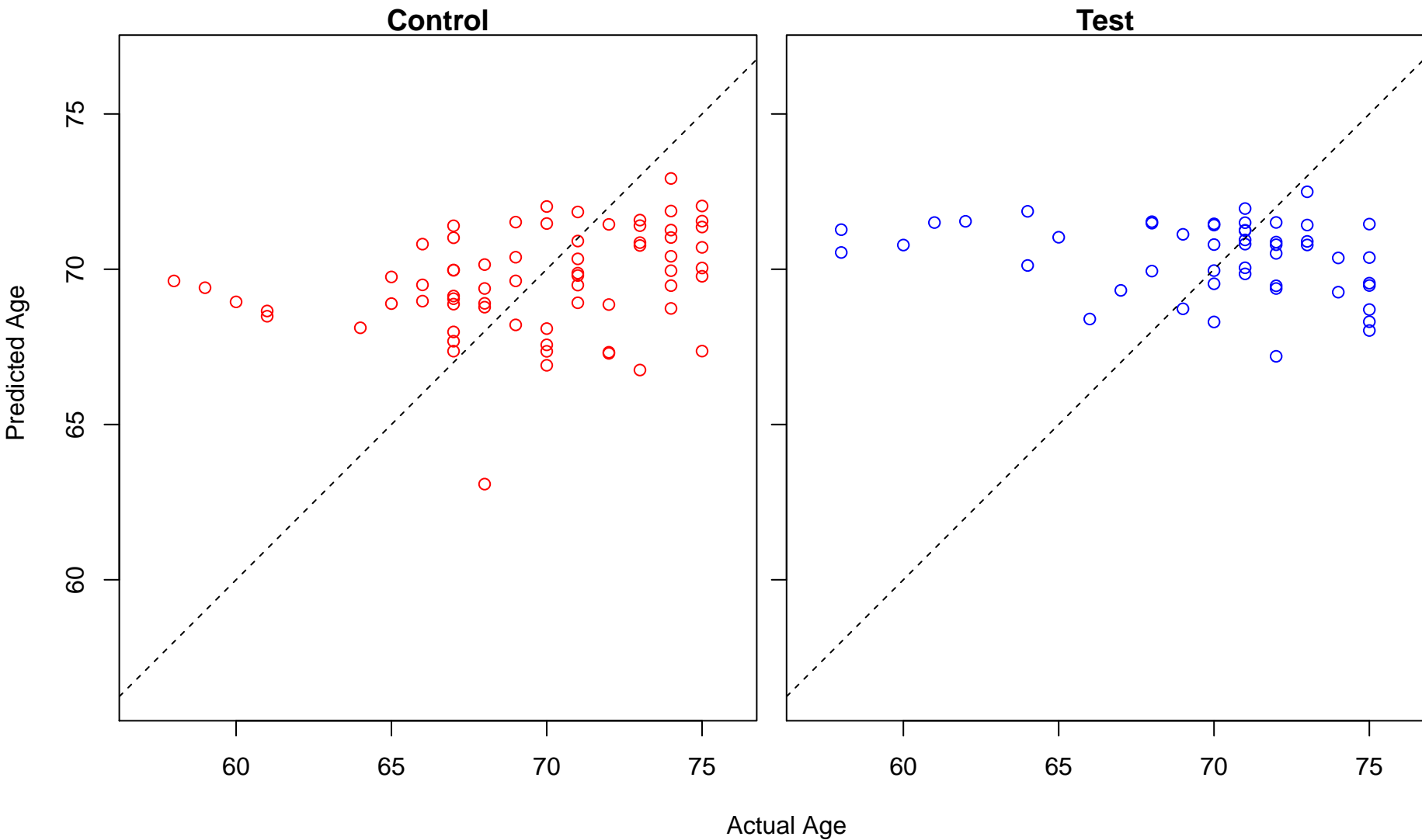
positive regulation of interleukin-2 biosynthetic process (Score: 0.261464)



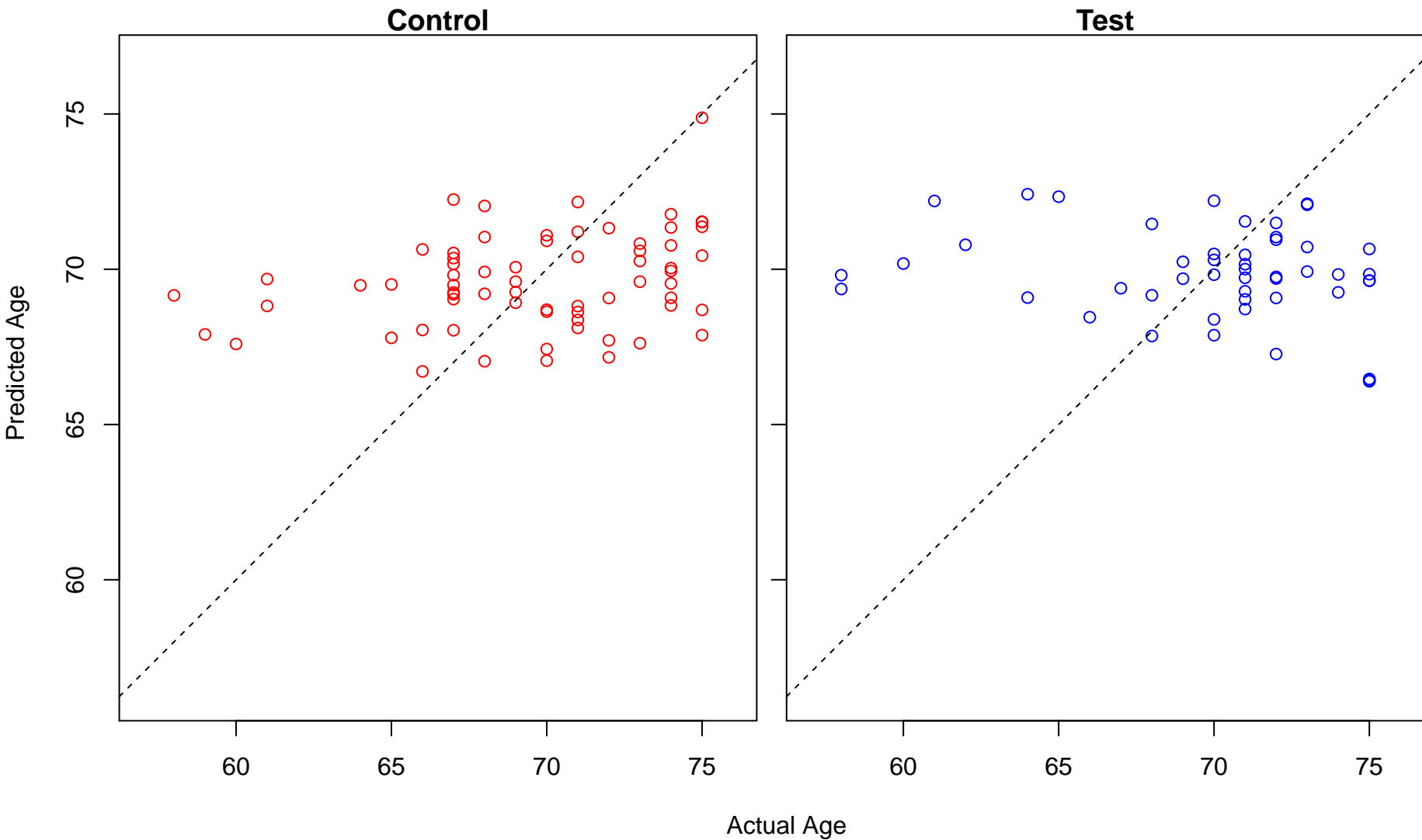
cellular response to cold (Score: 0.260936)



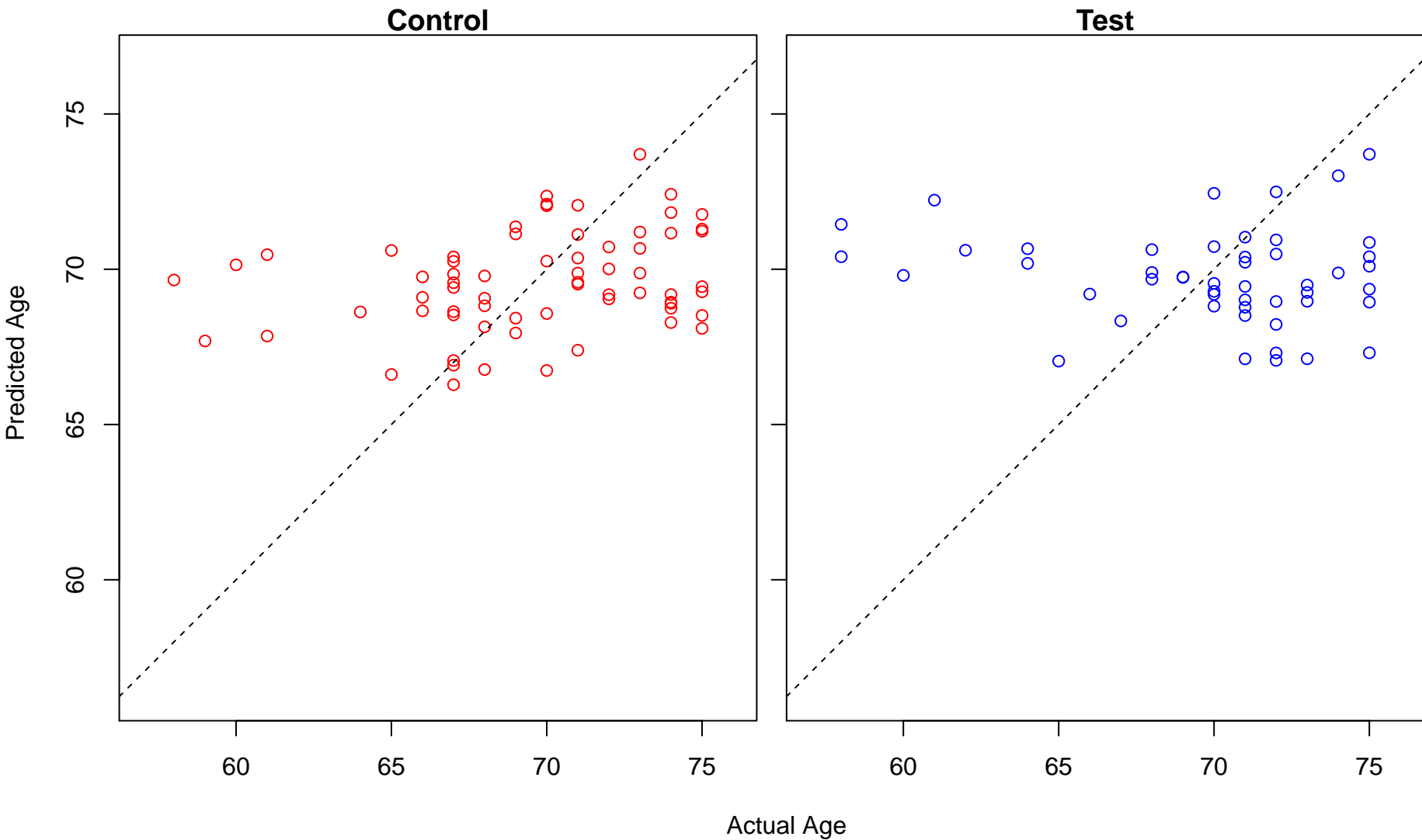
response to mercury ion (Score: 0.259074)



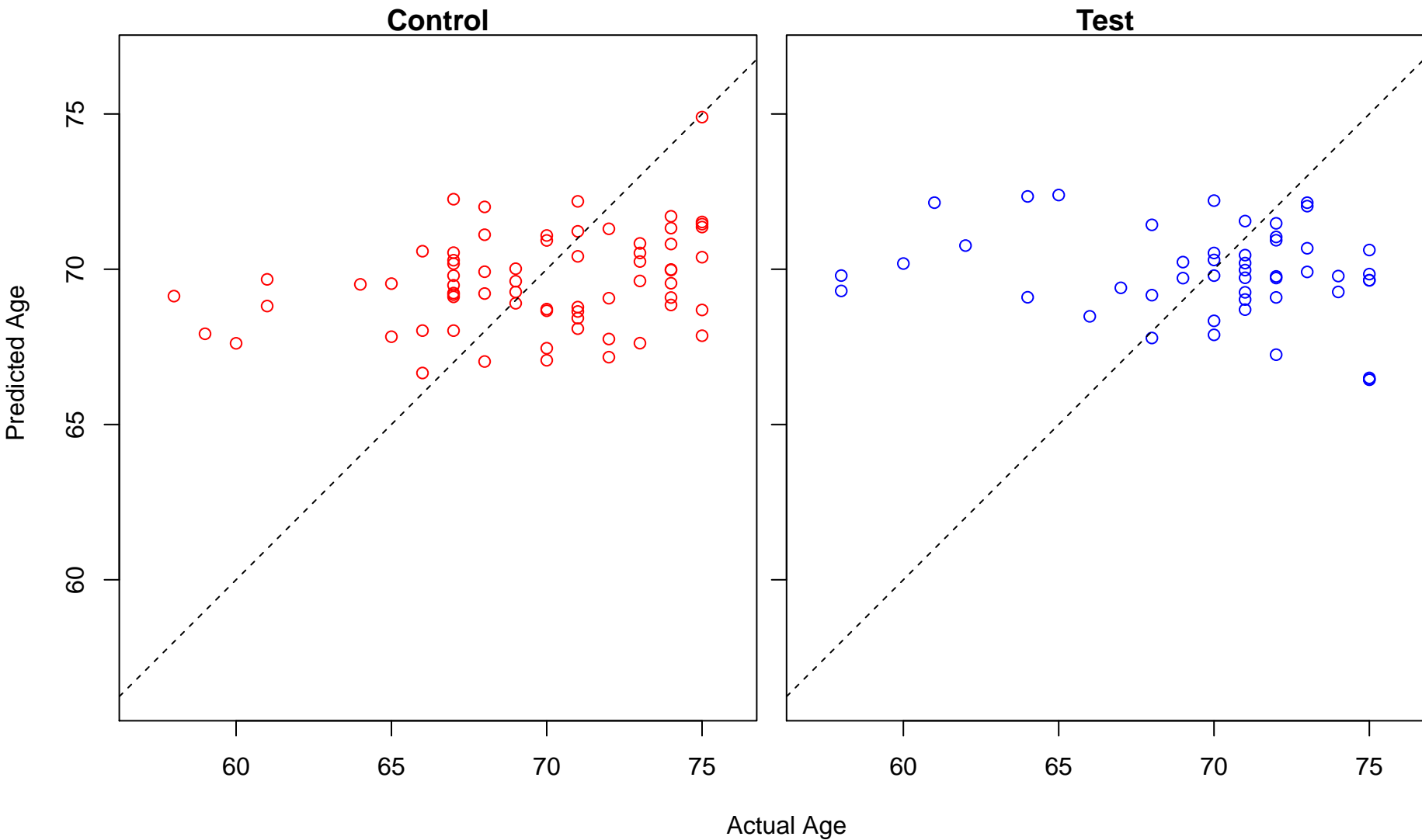
negative regulation of smooth muscle cell differentiation (Score: 0.258002)



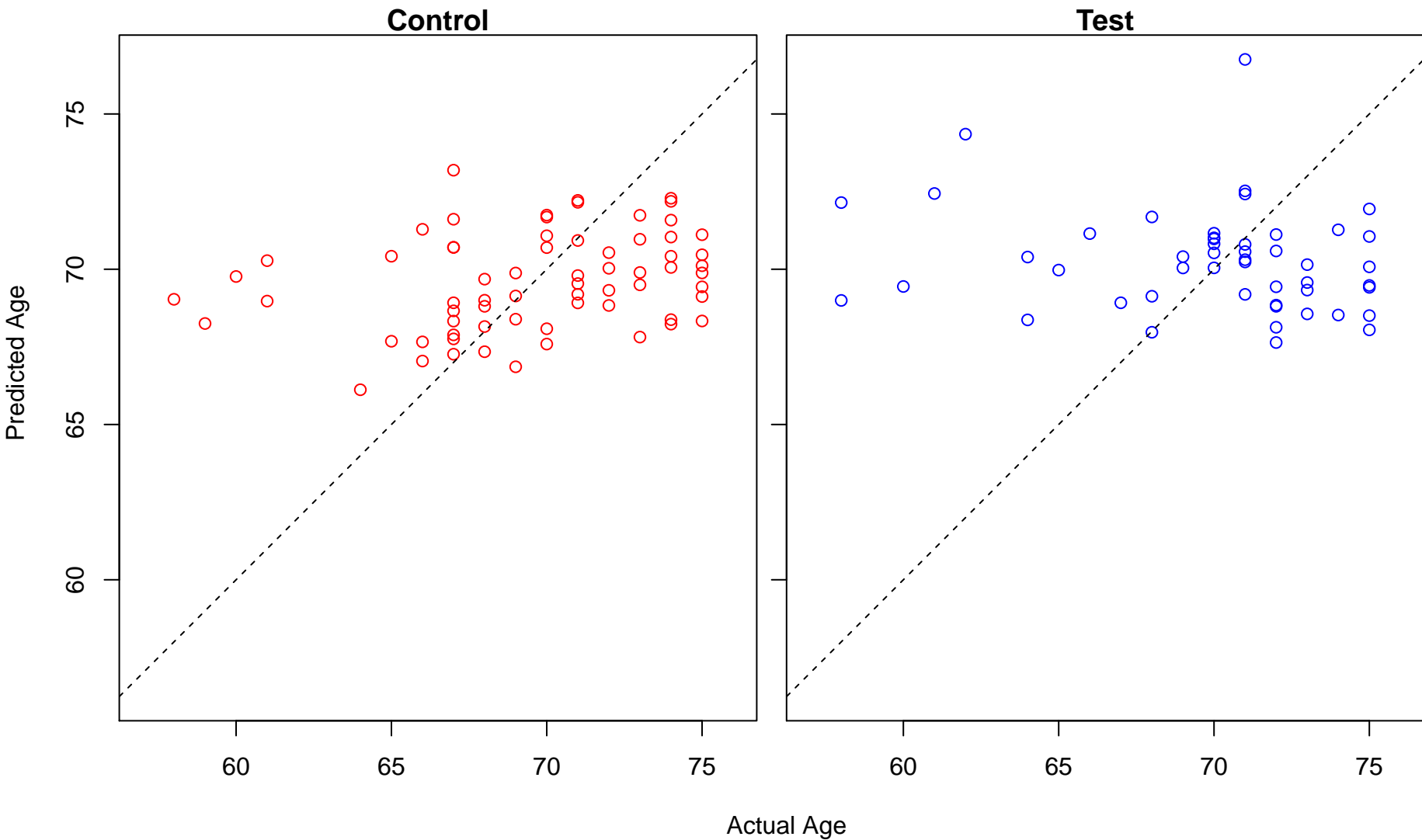
optic cup morphogenesis involved in camera-type eye development (Score: 0.257688)



regulation of G0 to G1 transition (Score: 0.255903)

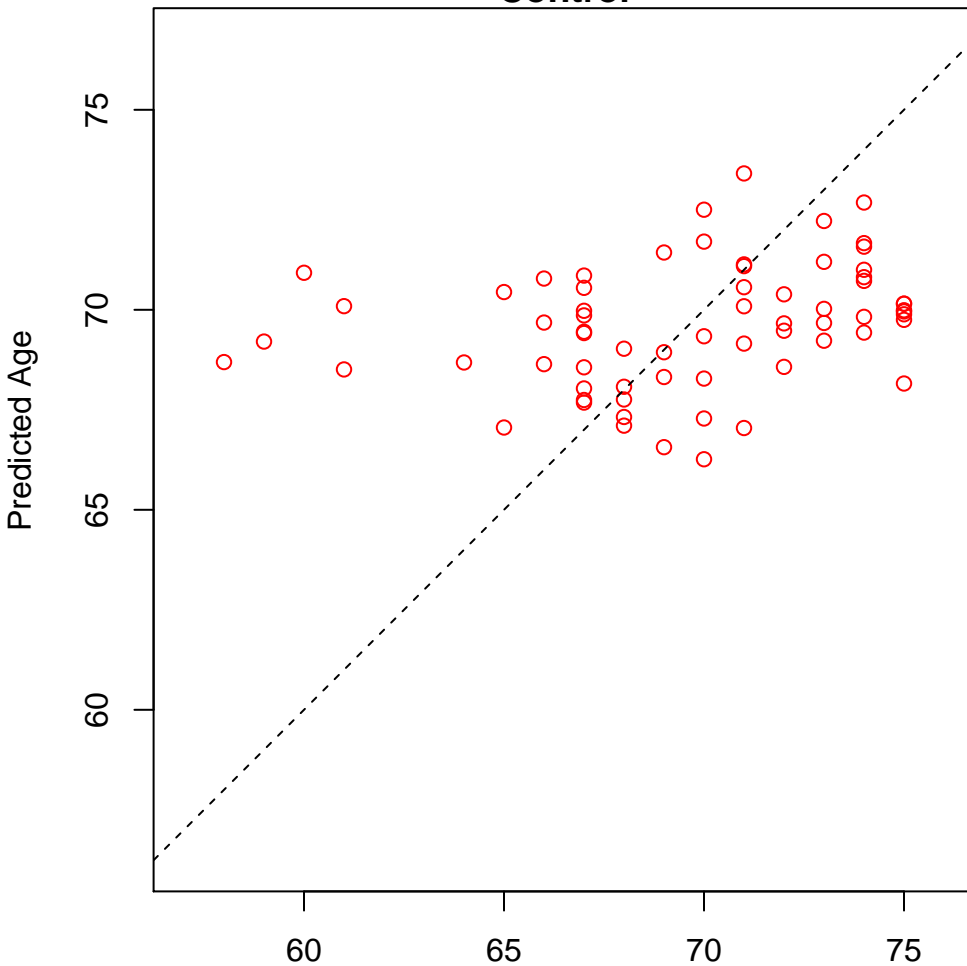


polysaccharide digestion (Score: 0.254742)

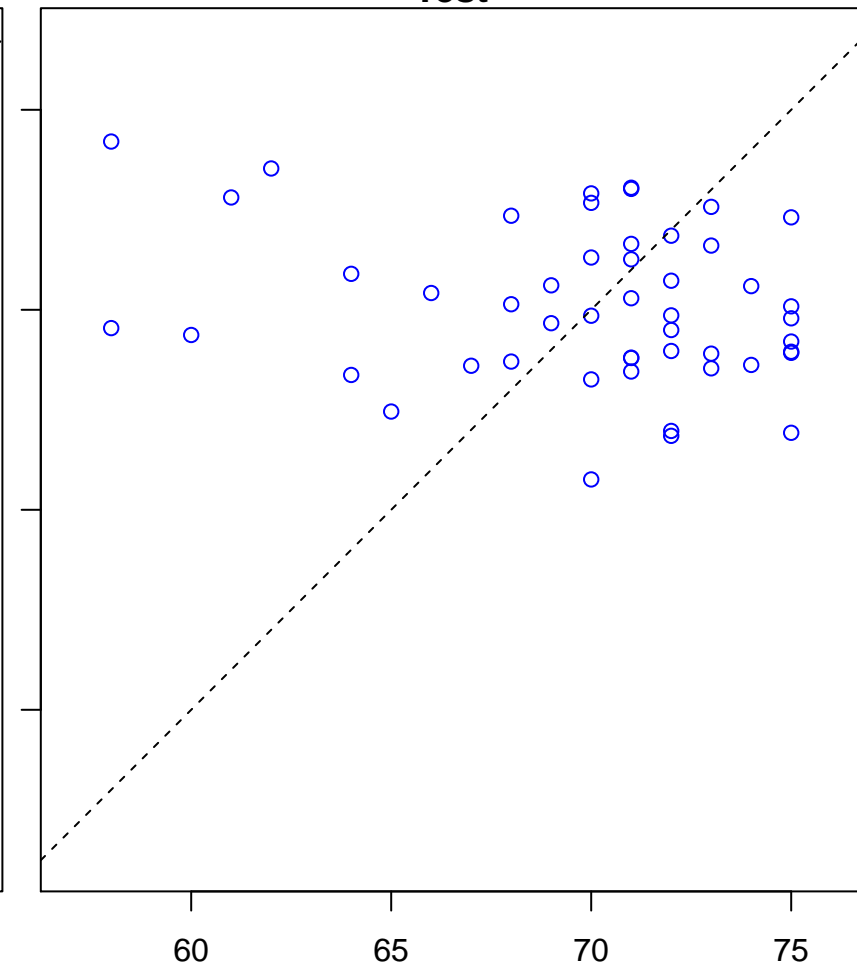


regulation of protein kinase C signaling (Score: 0.254327)

Control

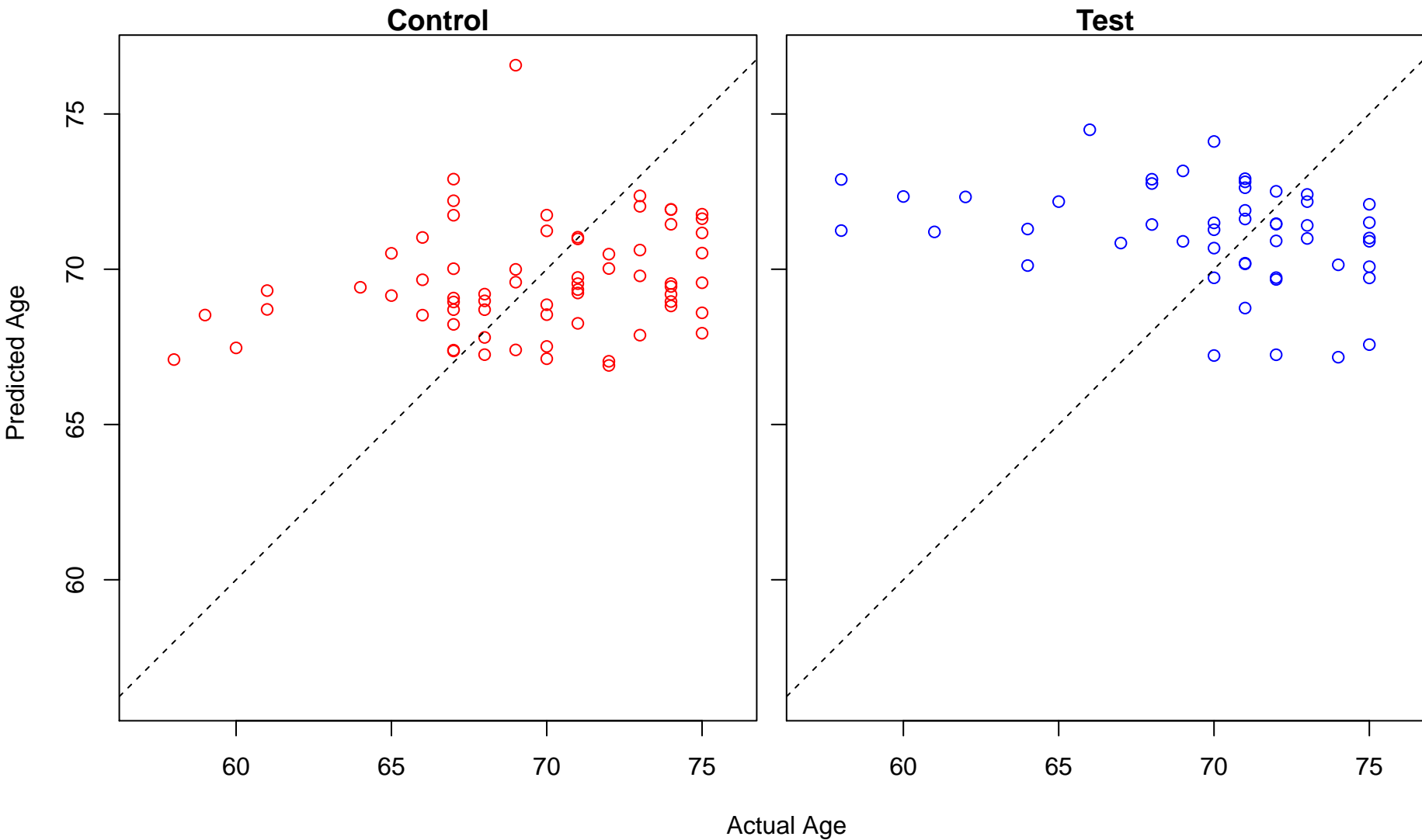


Test

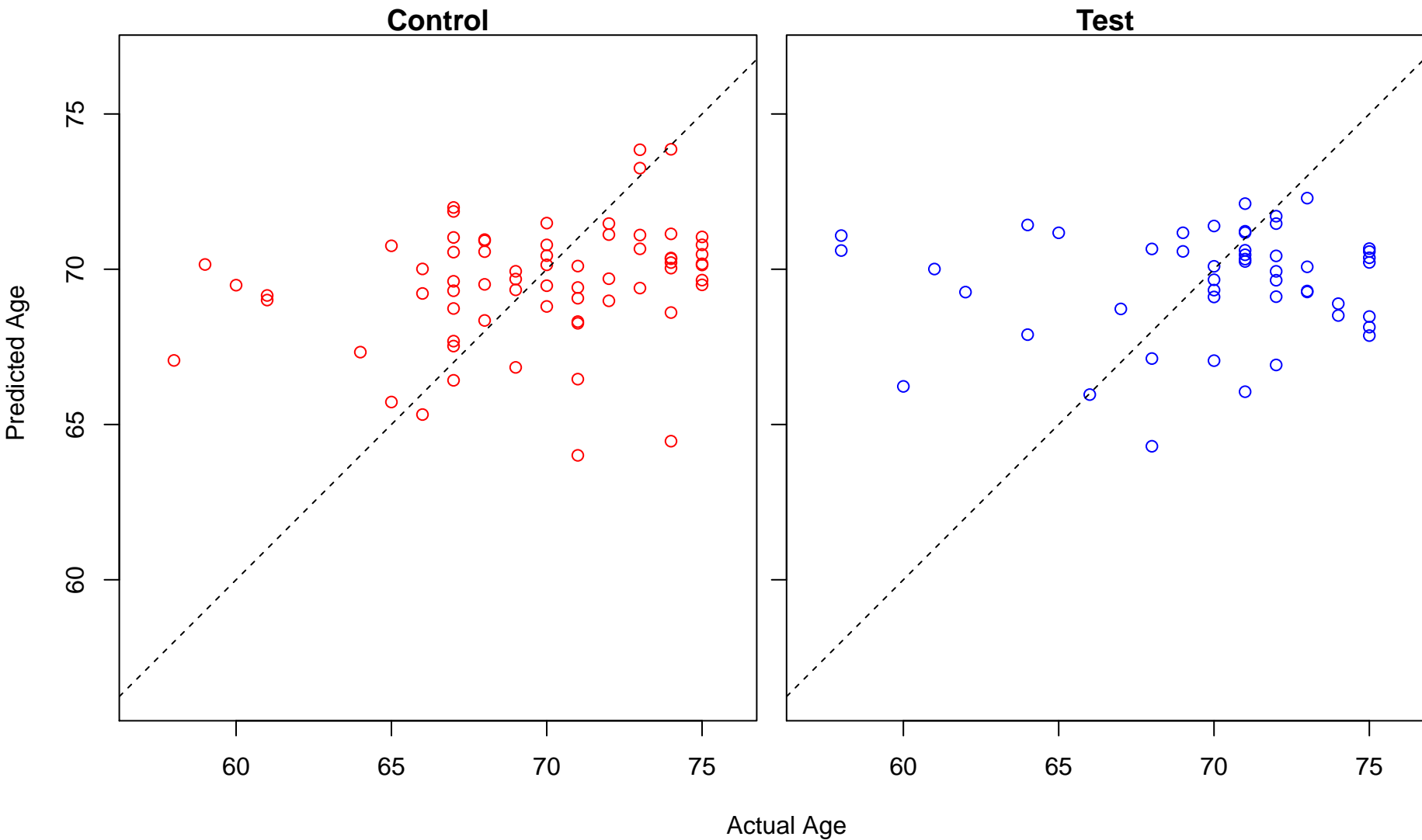


Actual Age

positive regulation of interferon-gamma biosynthetic process (Score: 0.252897)

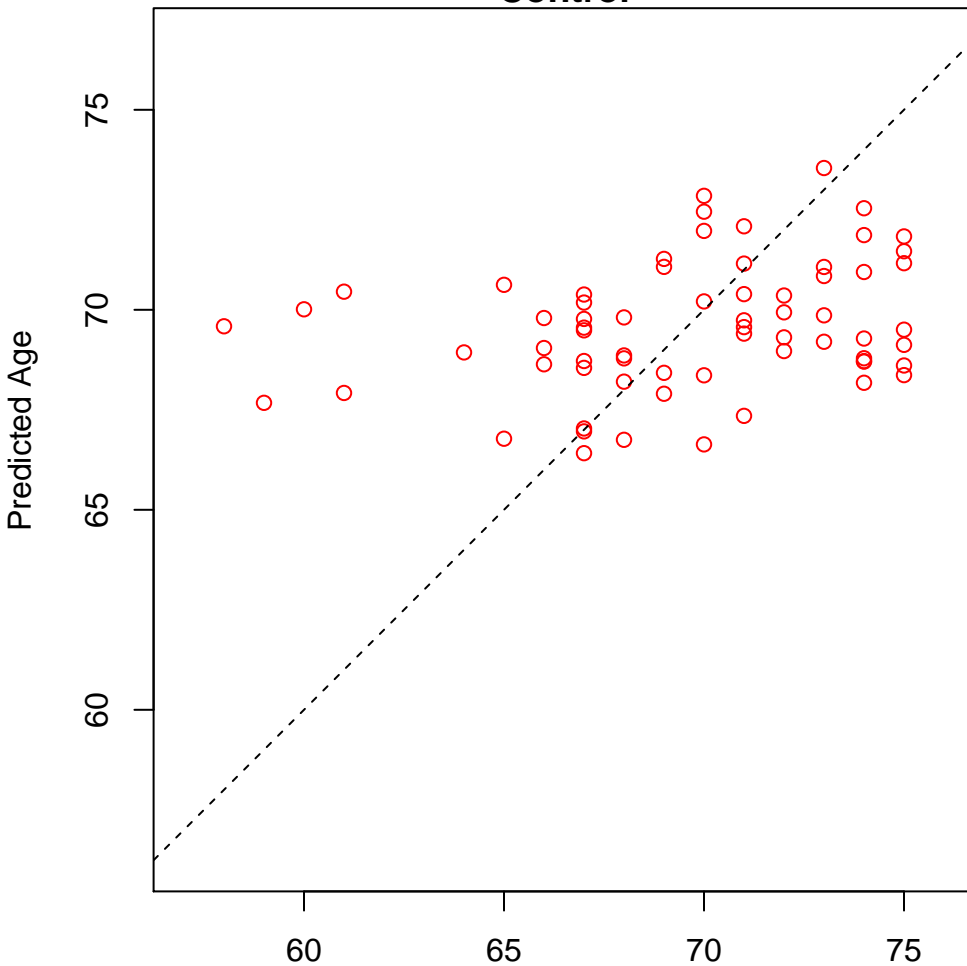


bundle of His cell to Purkinje myocyte communication (Score: 0.252347)

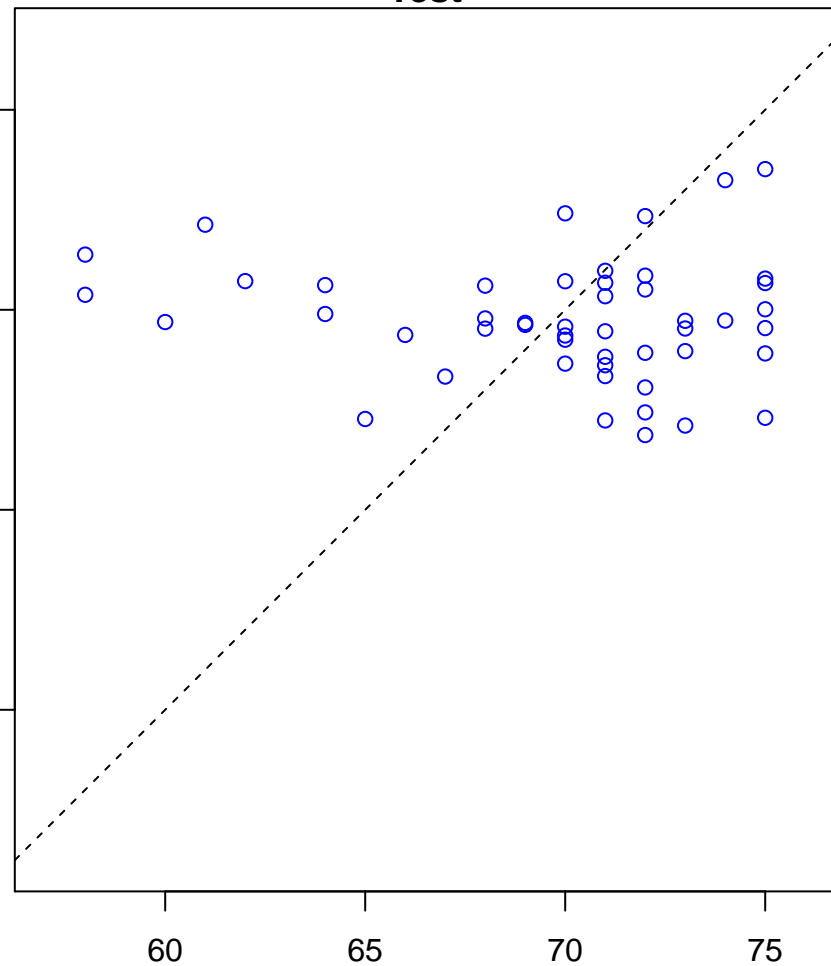


embryonic camera-type eye formation (Score: 0.251247)

Control

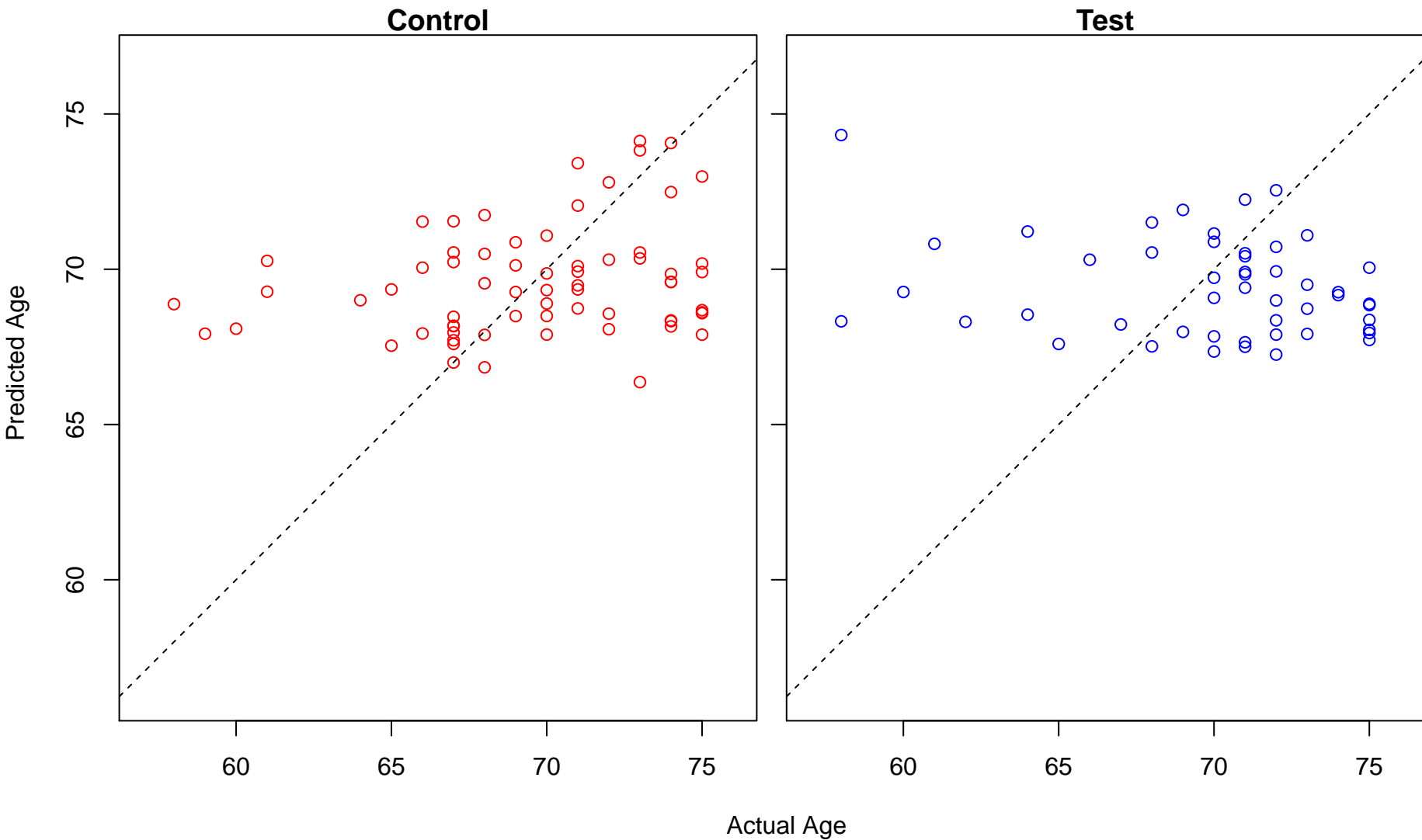


Test

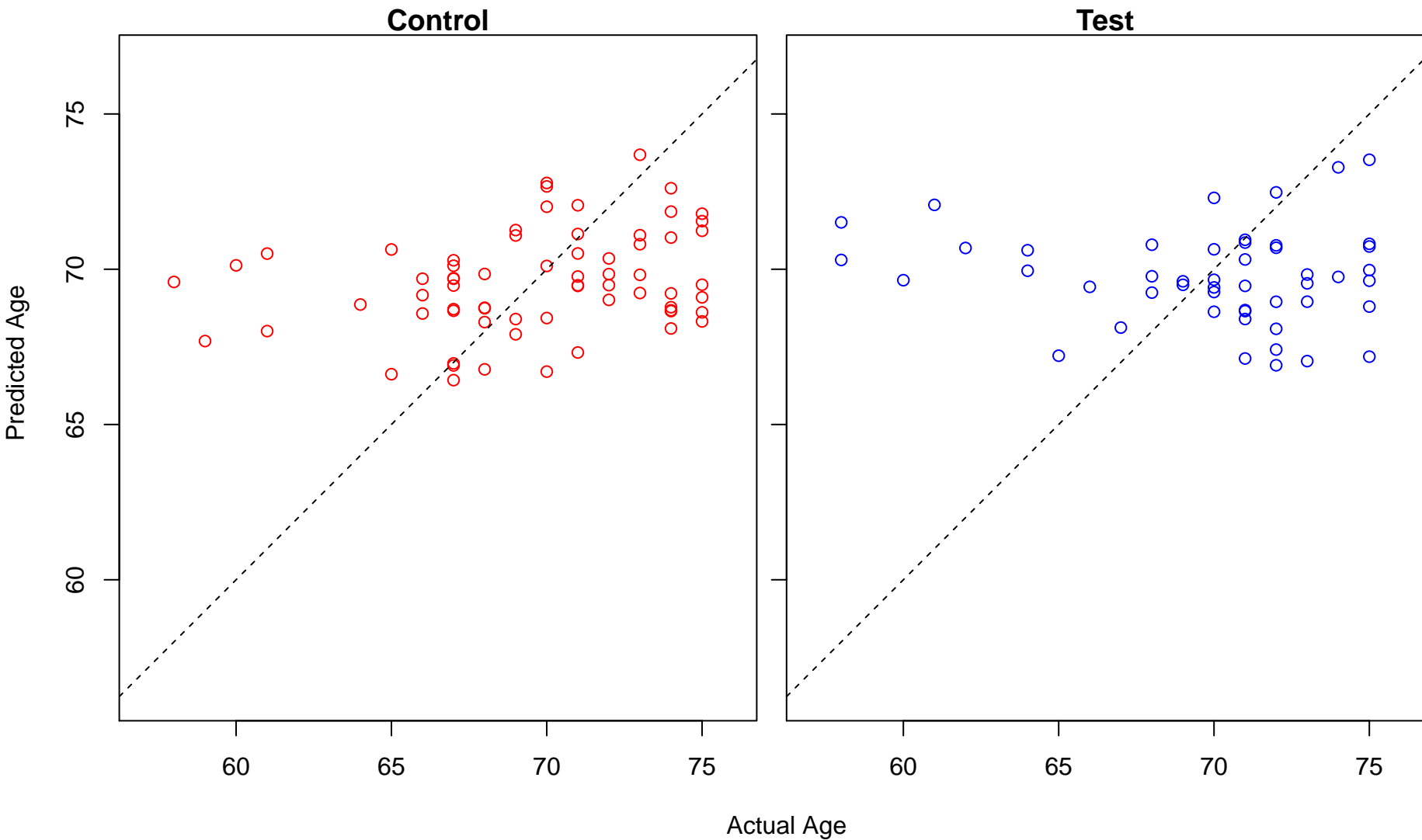


Actual Age

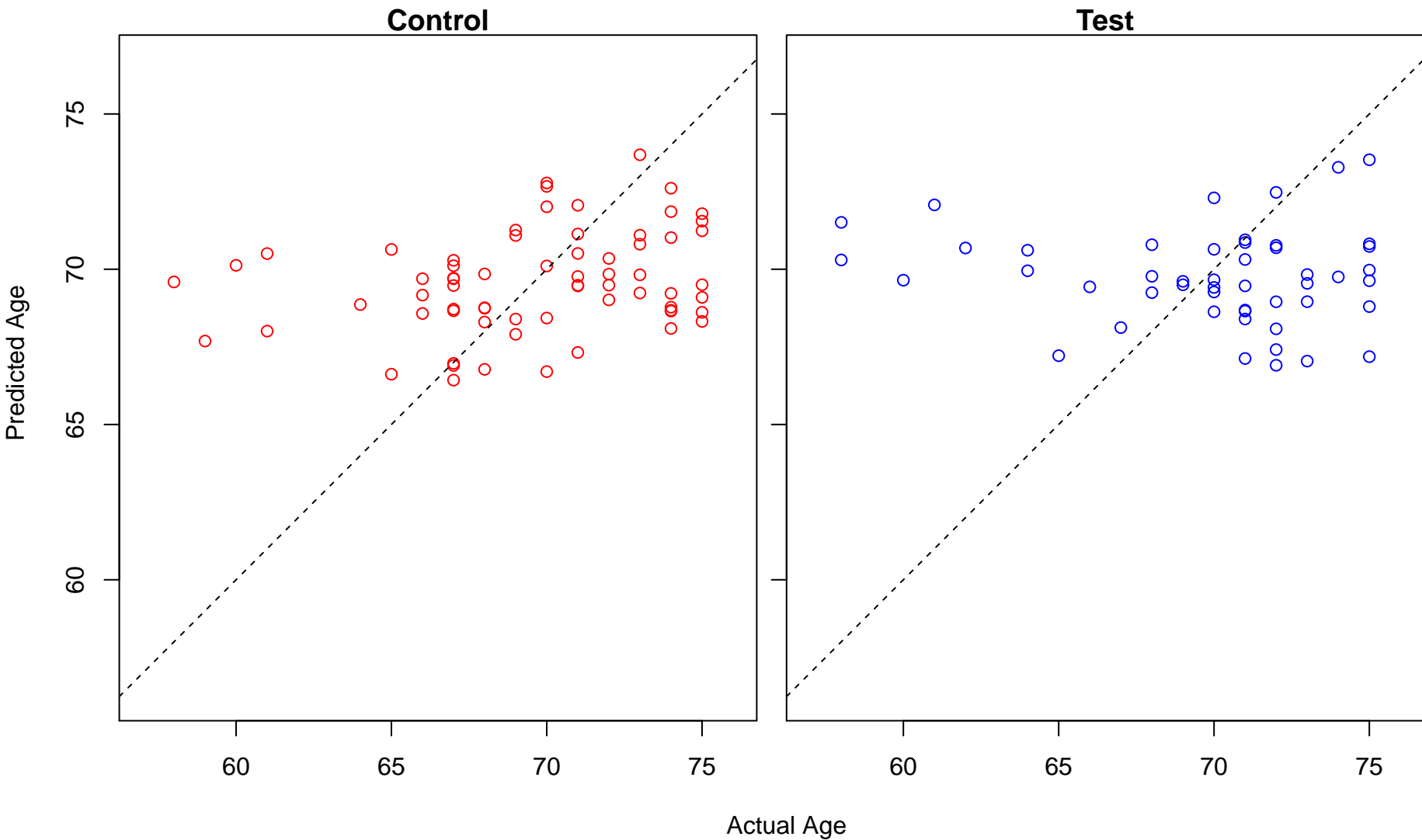
regulation of branching involved in ureteric bud morphogenesis (Score: 0.249955)



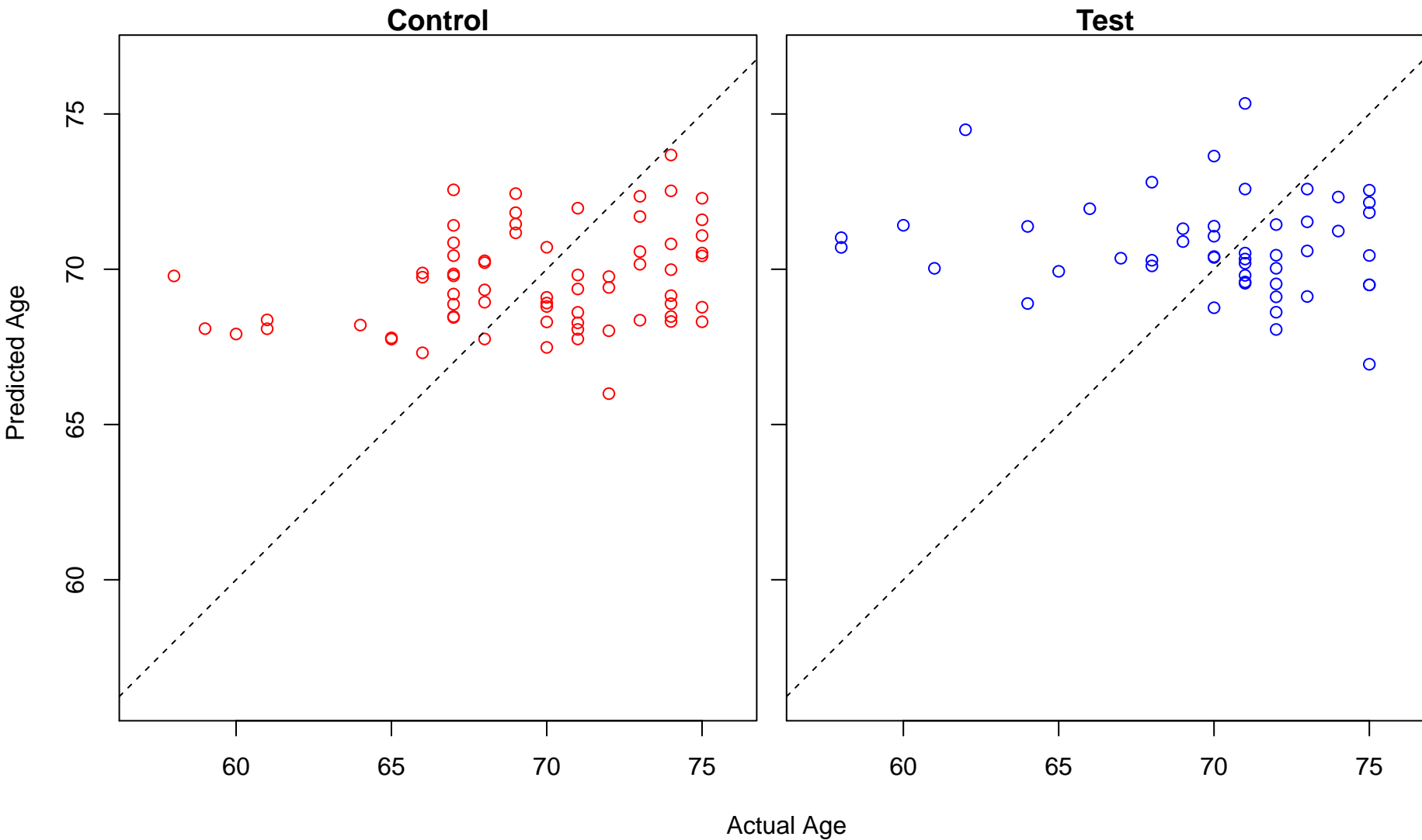
embryonic camera-type eye development (Score: 0.249121)



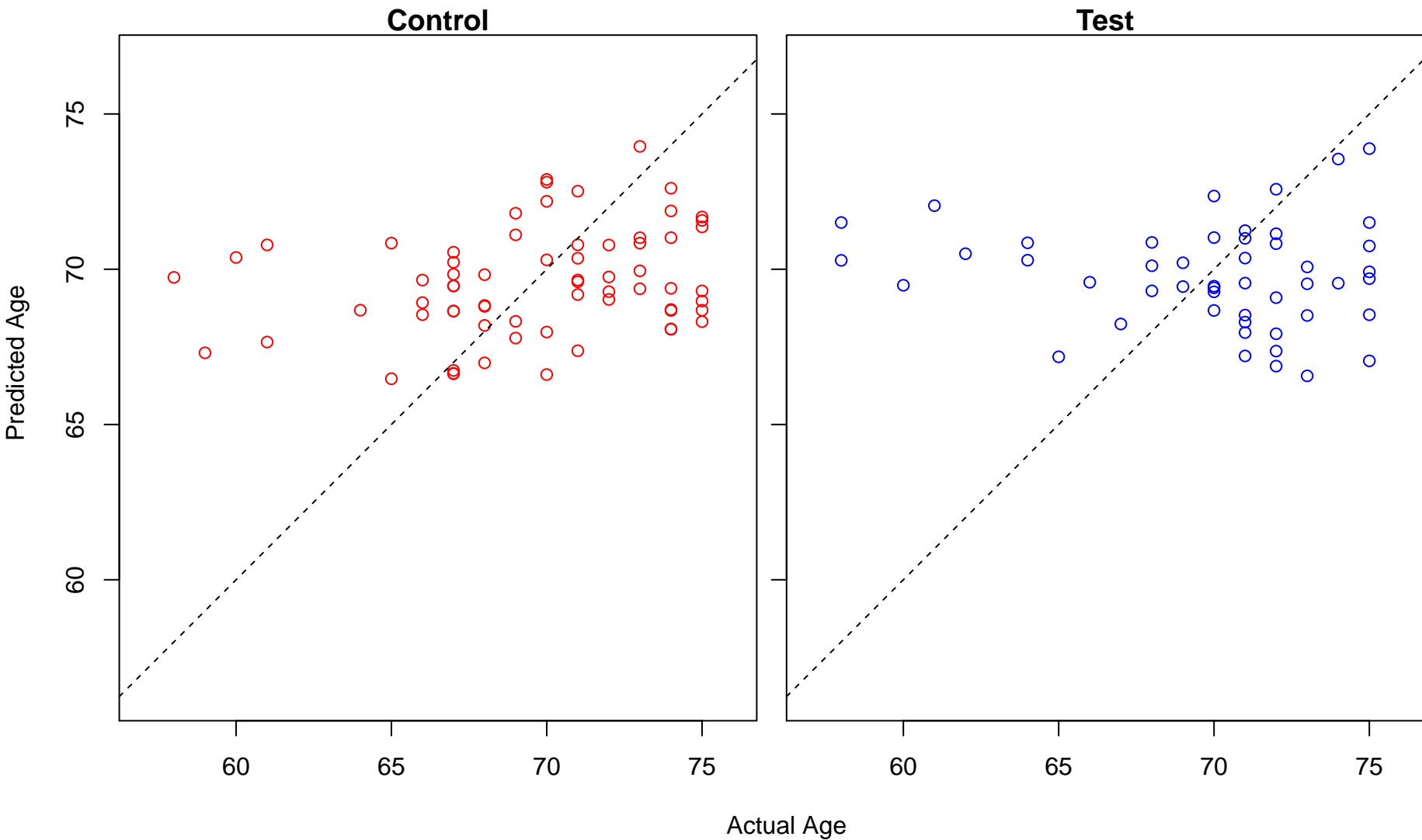
embryonic camera-type eye morphogenesis (Score: 0.249121)



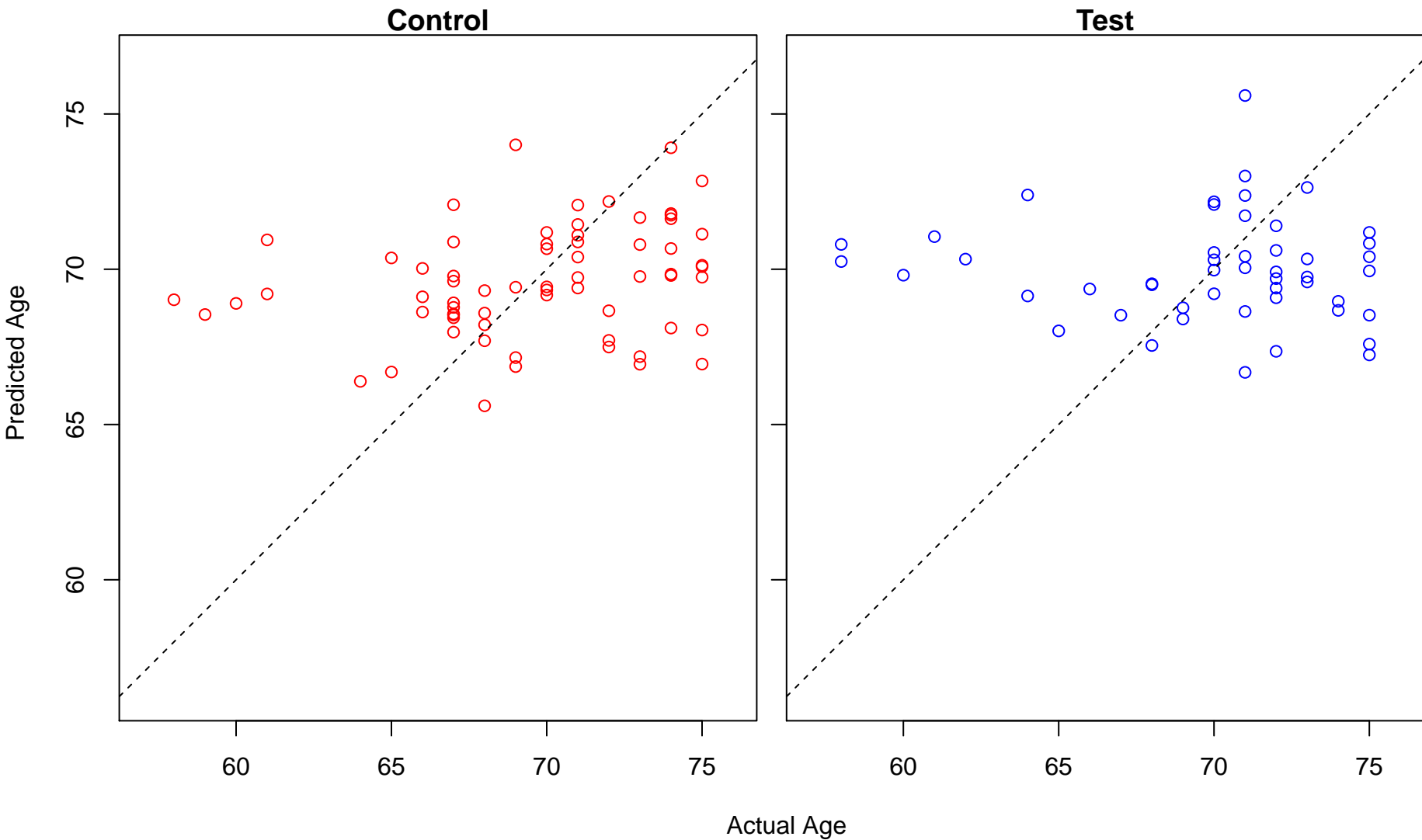
regulation of viral budding via host ESCRT complex (Score: 0.247975)



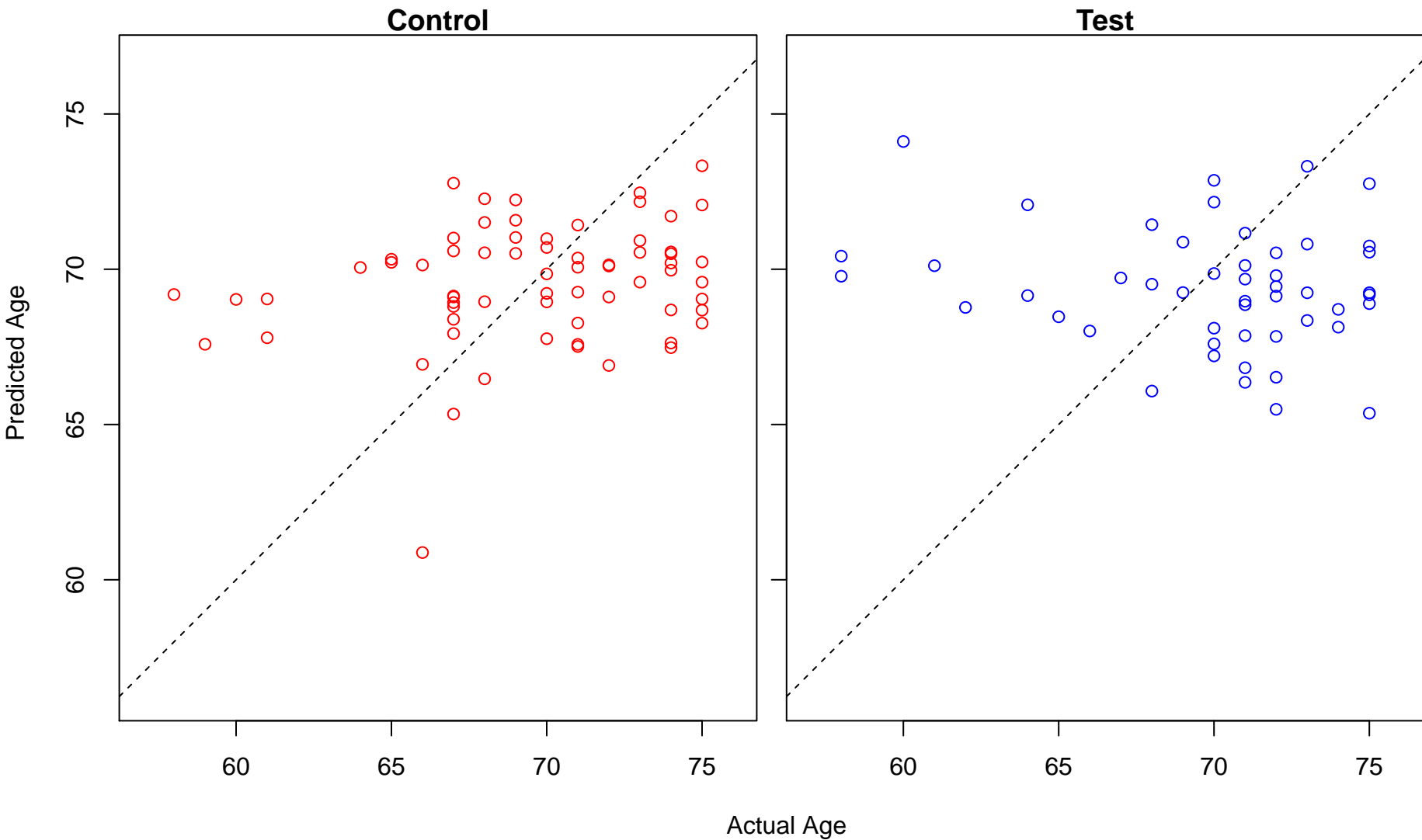
embryonic eye morphogenesis (Score: 0.247652)



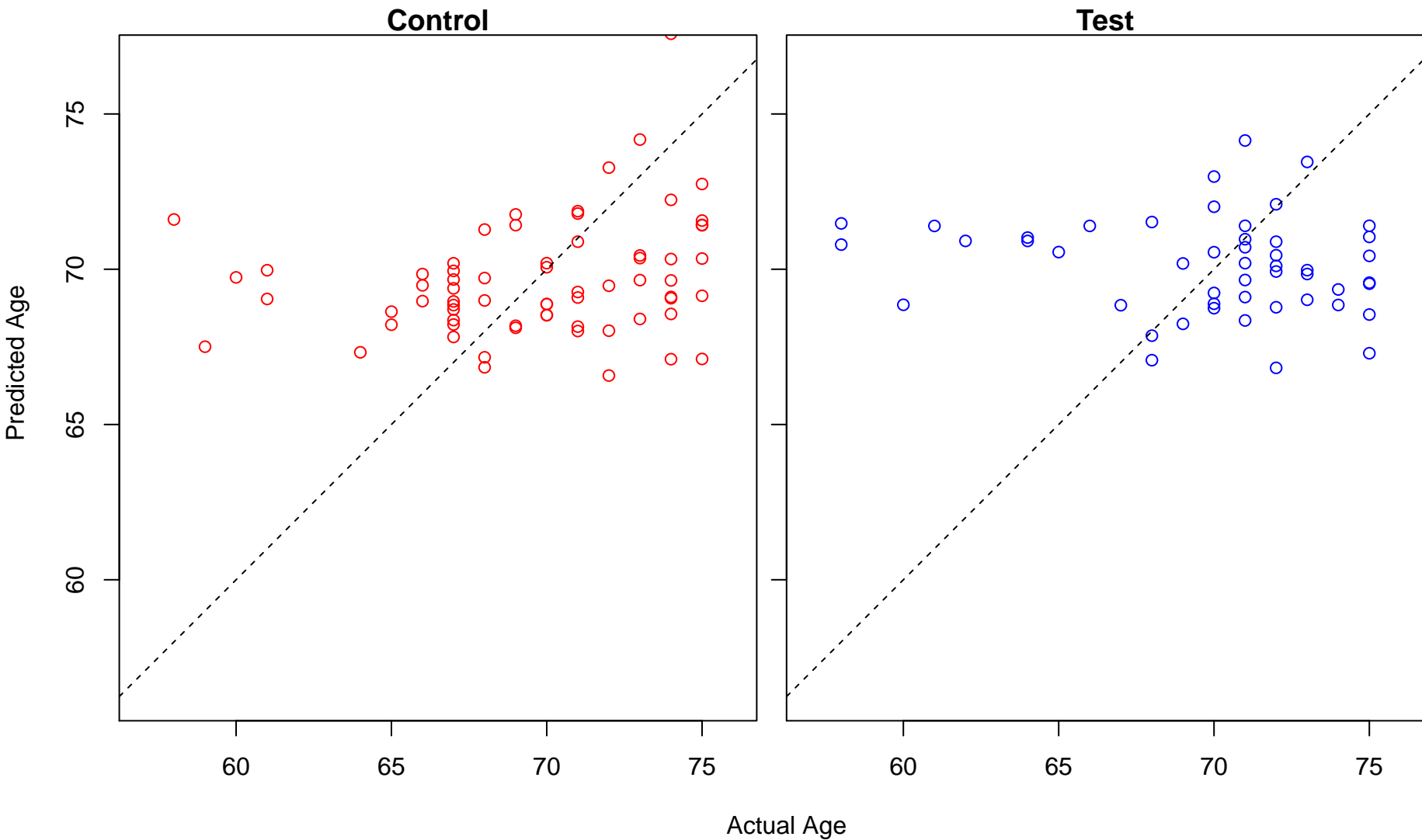
vasoconstriction (Score: 0.246261)



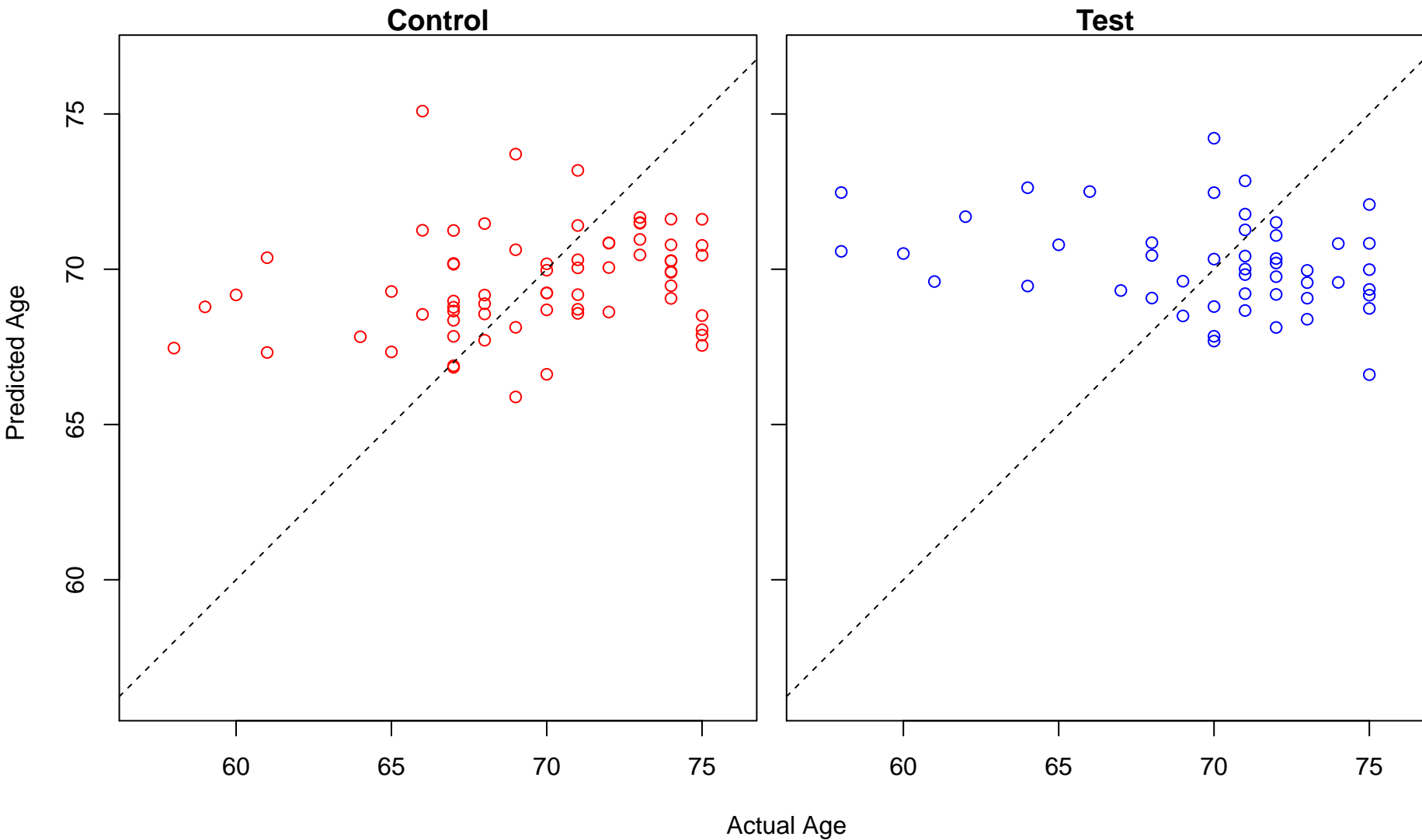
cellular response to histamine (Score: 0.245568)



regulation of amine transport (Score: 0.244133)

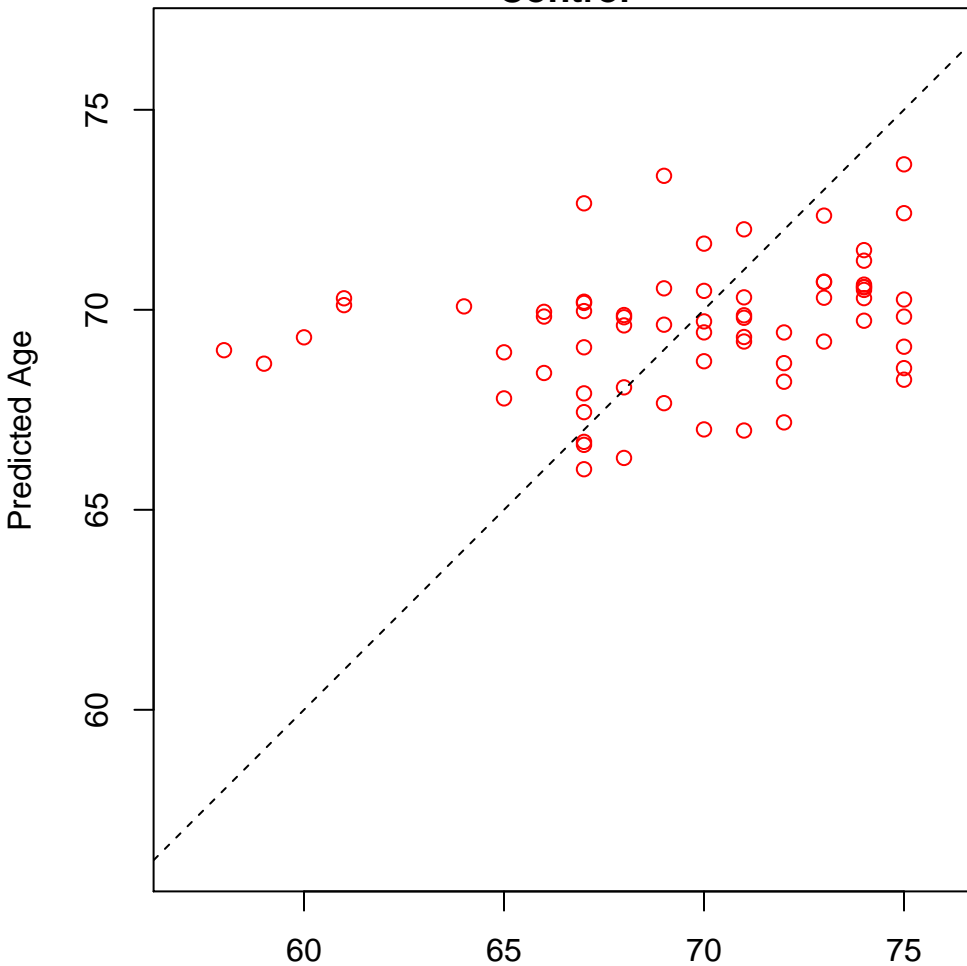


positive regulation of epithelial cell proliferation involved in wound healing (Score: 0.240551)

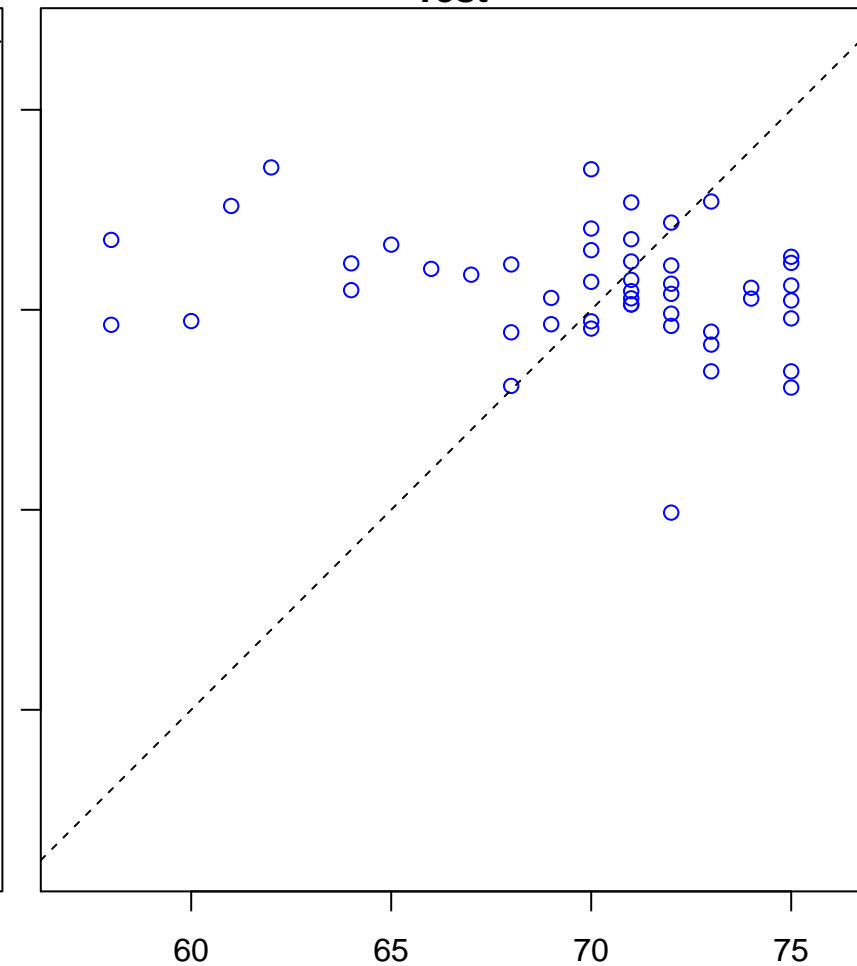


RNA secondary structure unwinding (Score: 0.237977)

Control

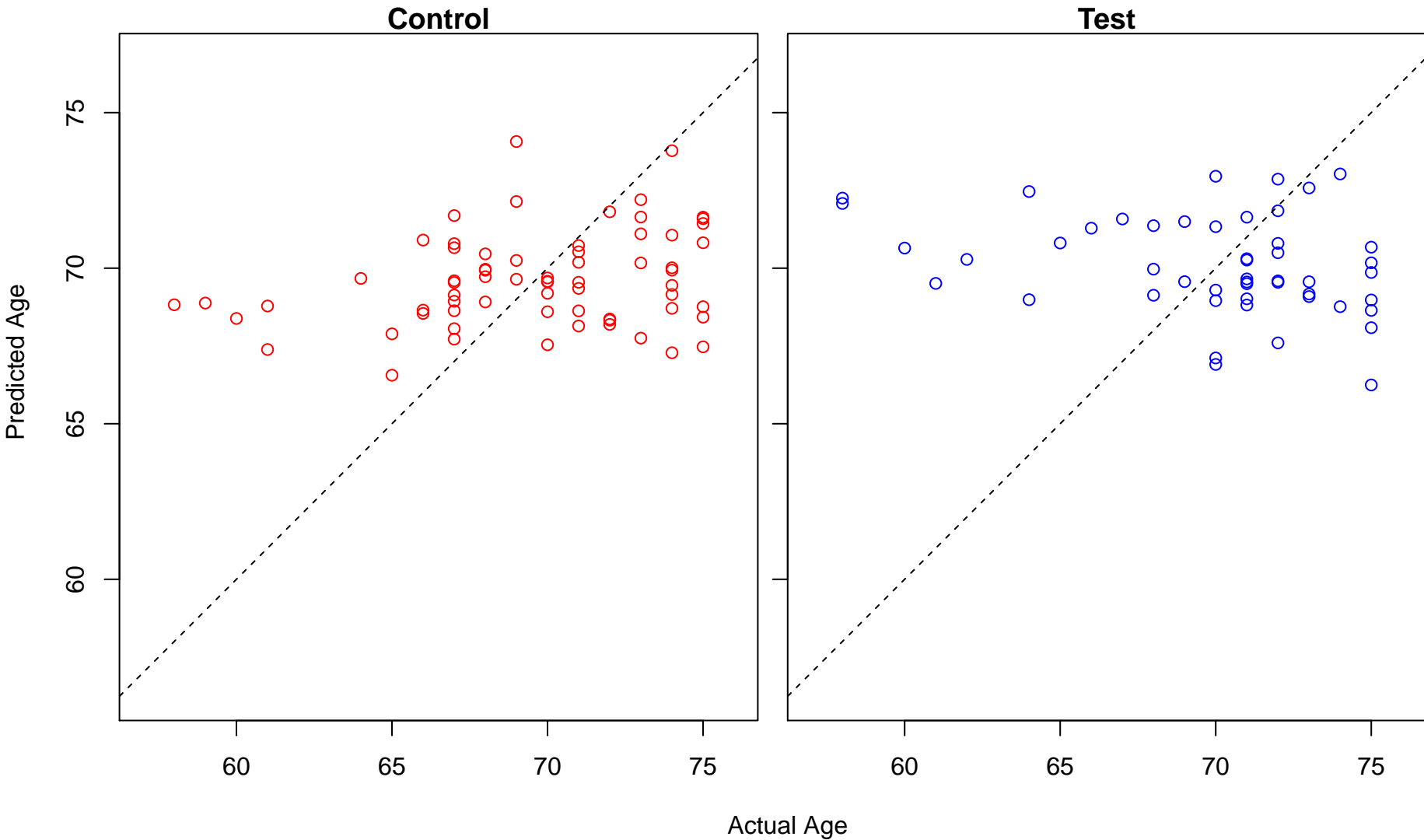


Test

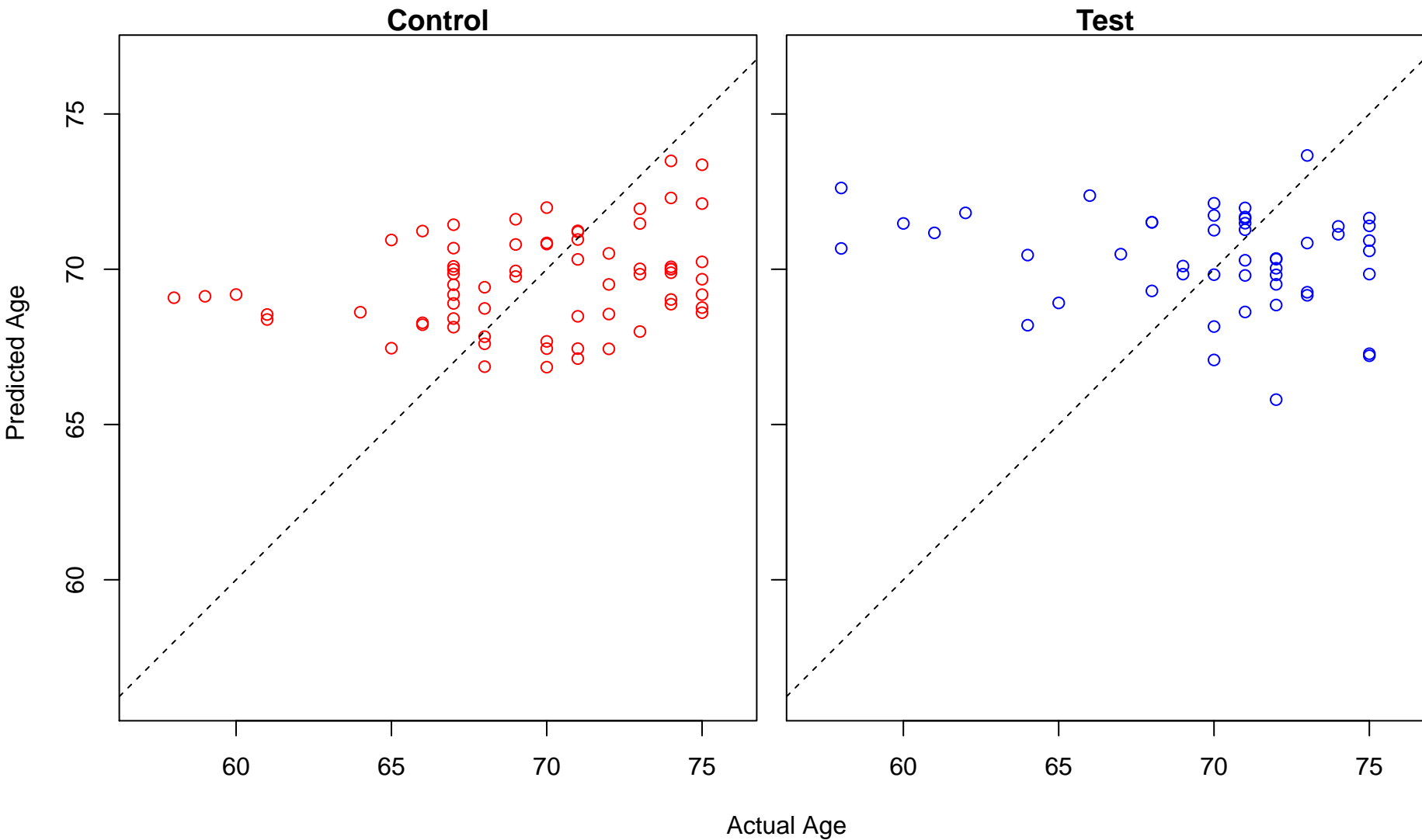


Actual Age

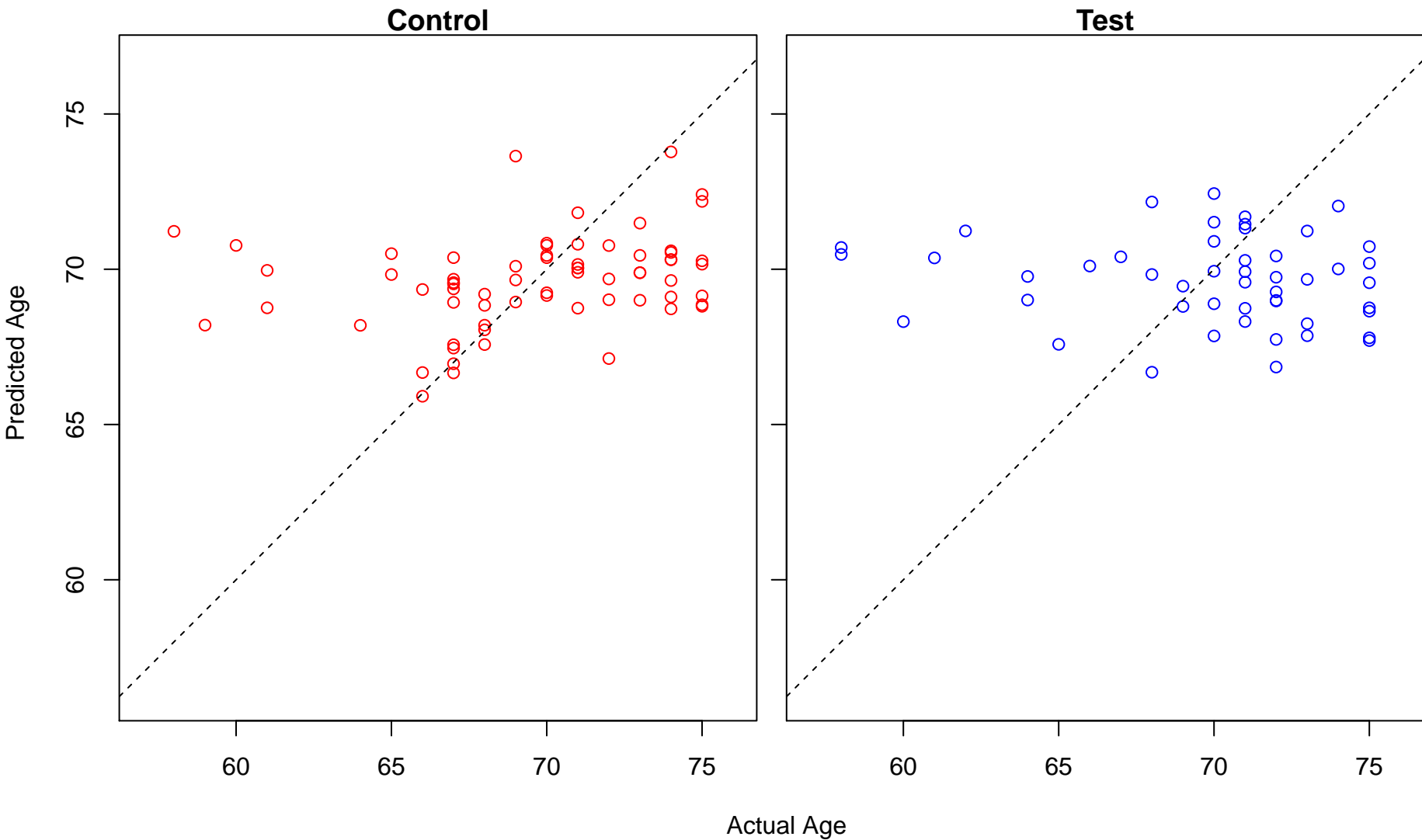
establishment of protein localization to telomere (Score: 0.237943)



actin filament-based transport (Score: 0.237602)

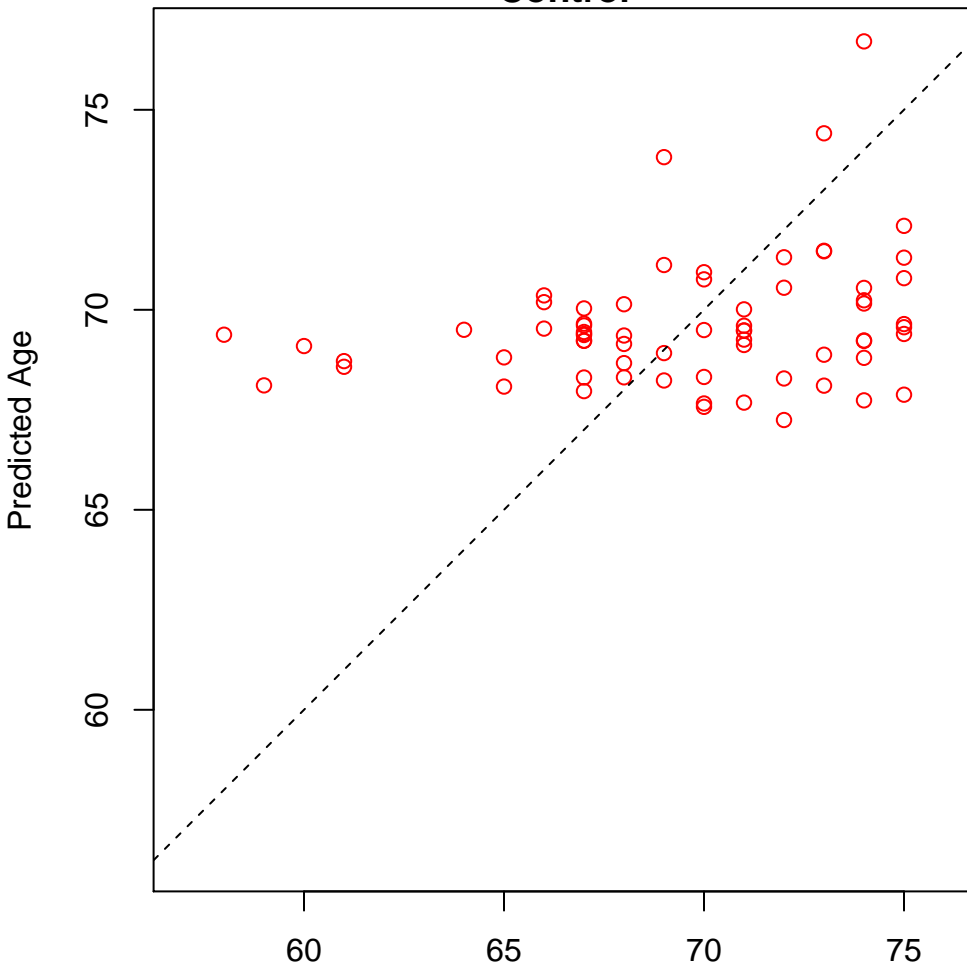


magnesium ion transmembrane transport (Score: 0.234826)

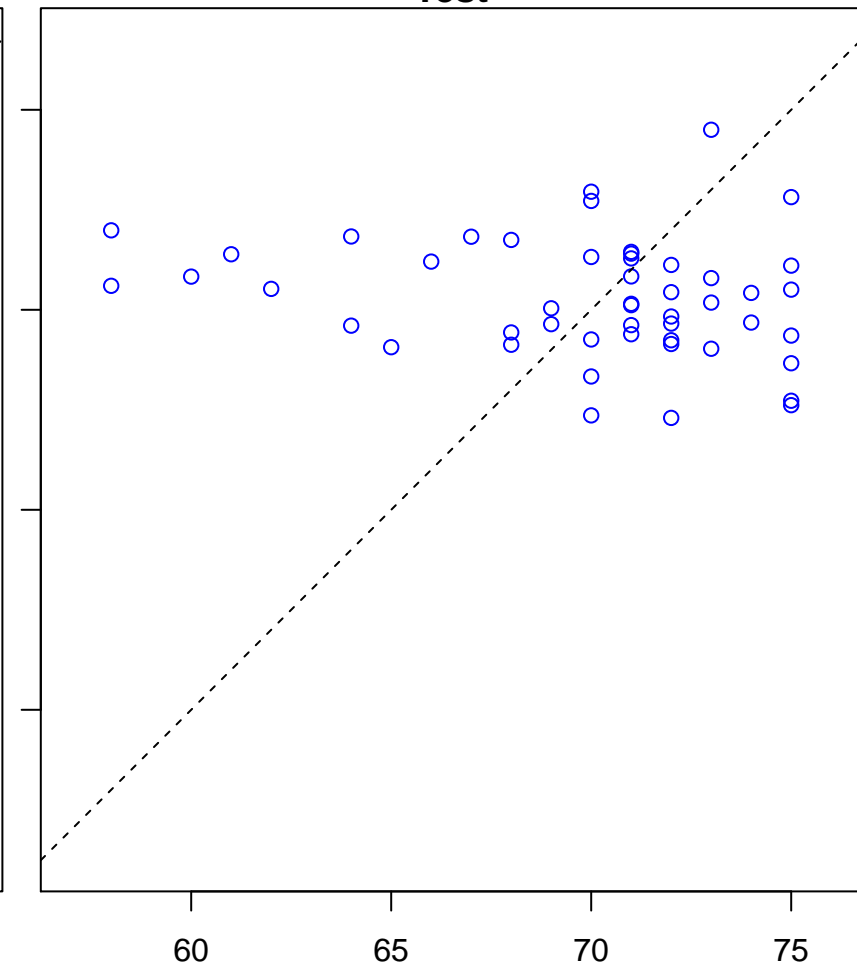


mitotic chromosome condensation (Score: 0.231227)

Control

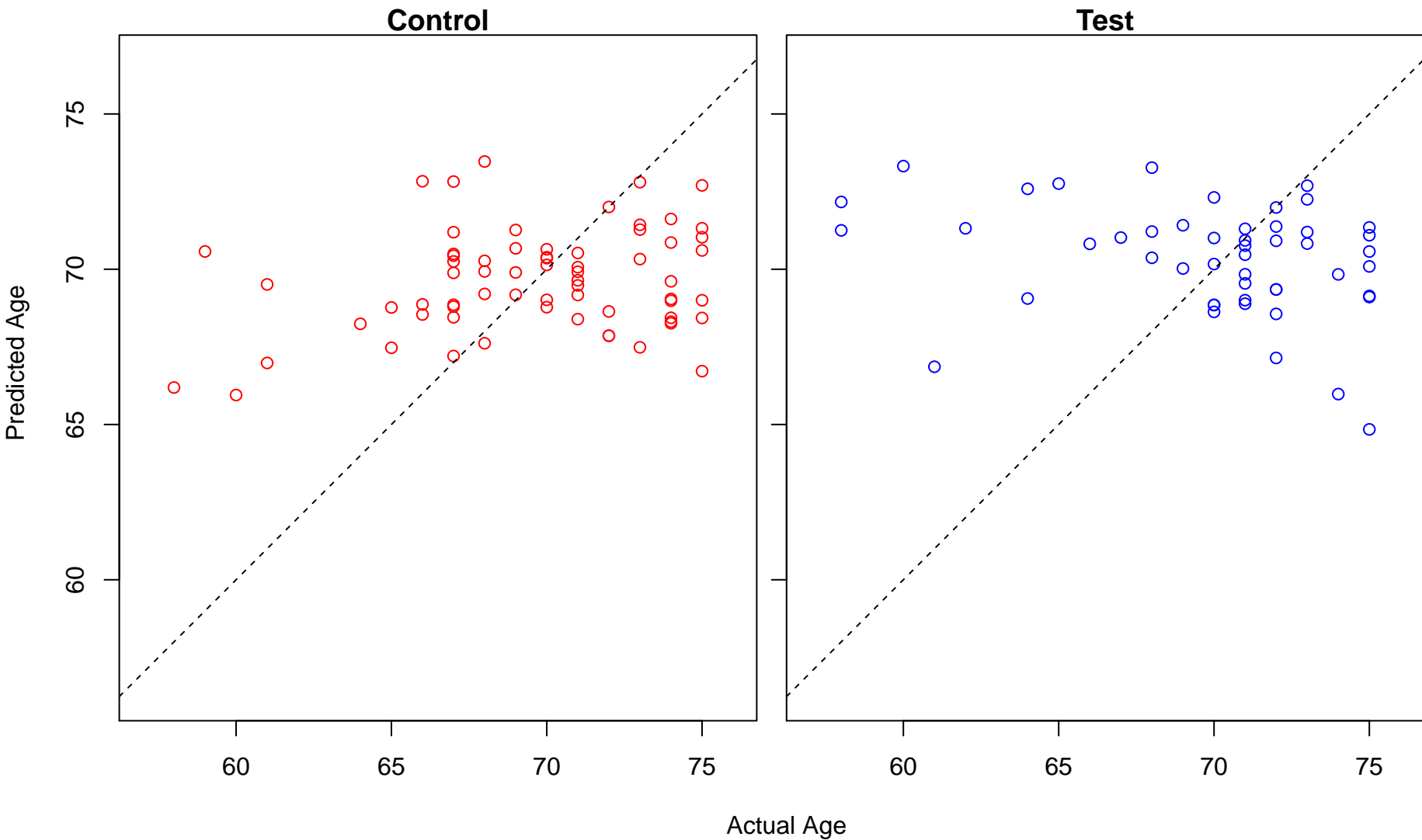


Test

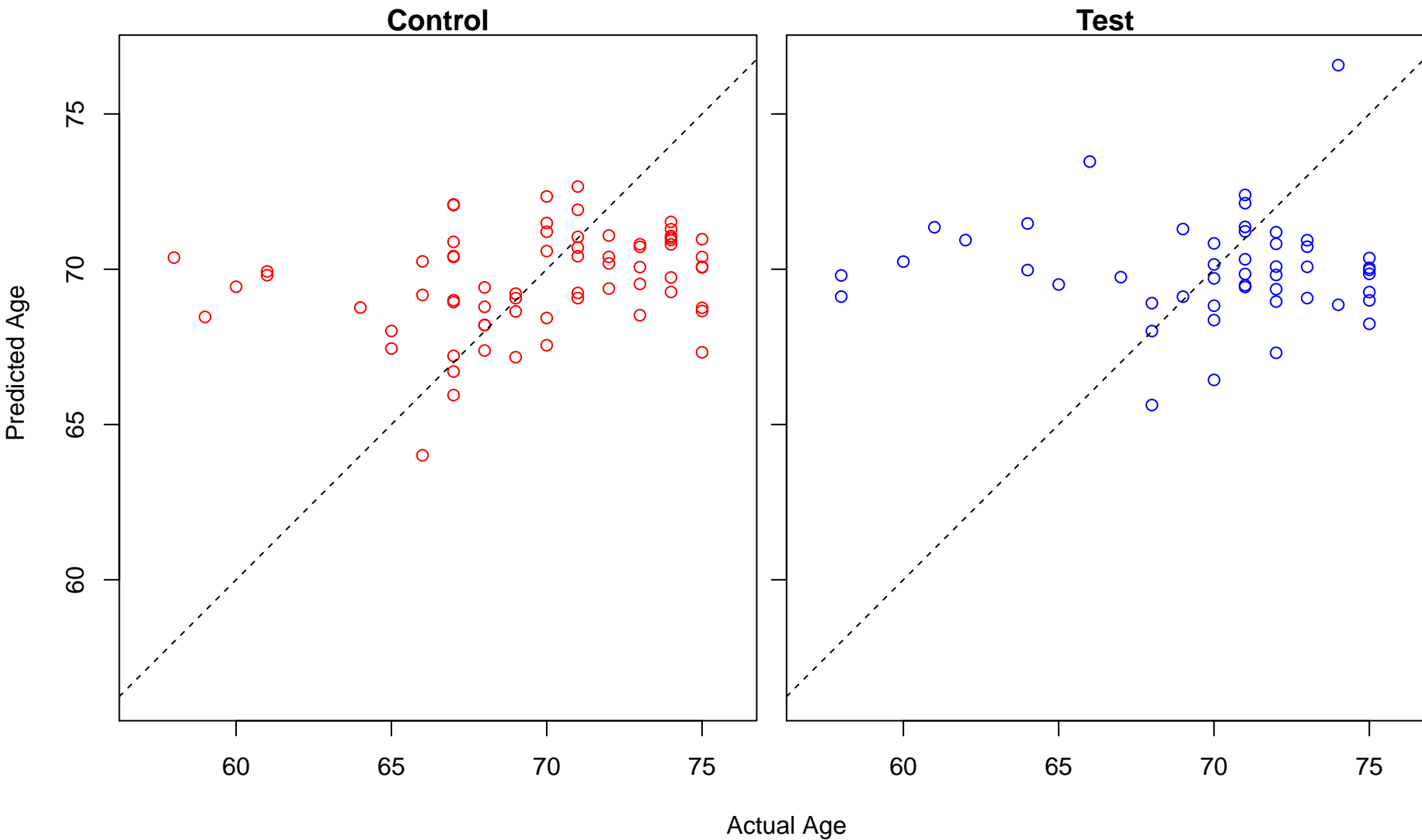


Actual Age

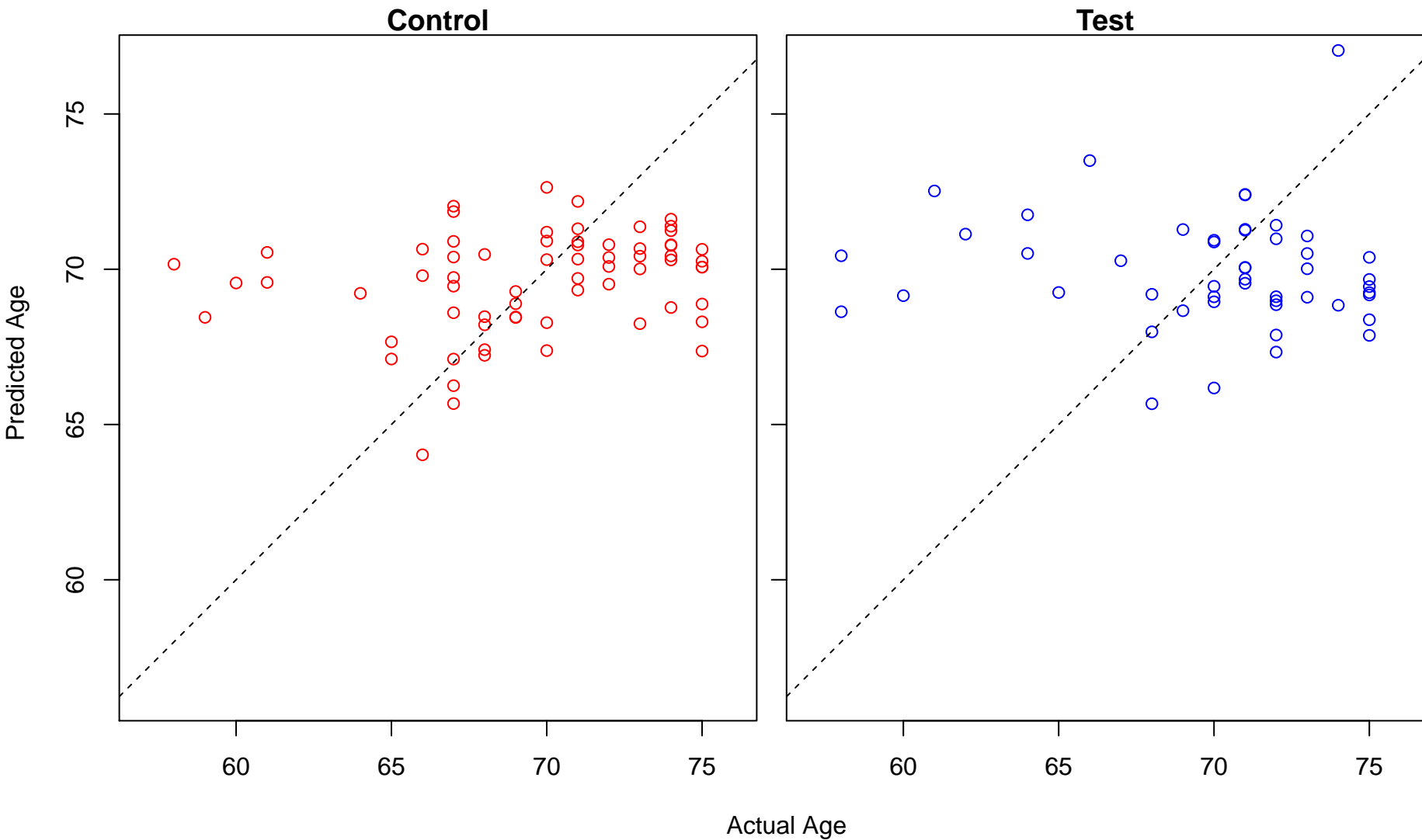
lipid digestion (Score: 0.230497)



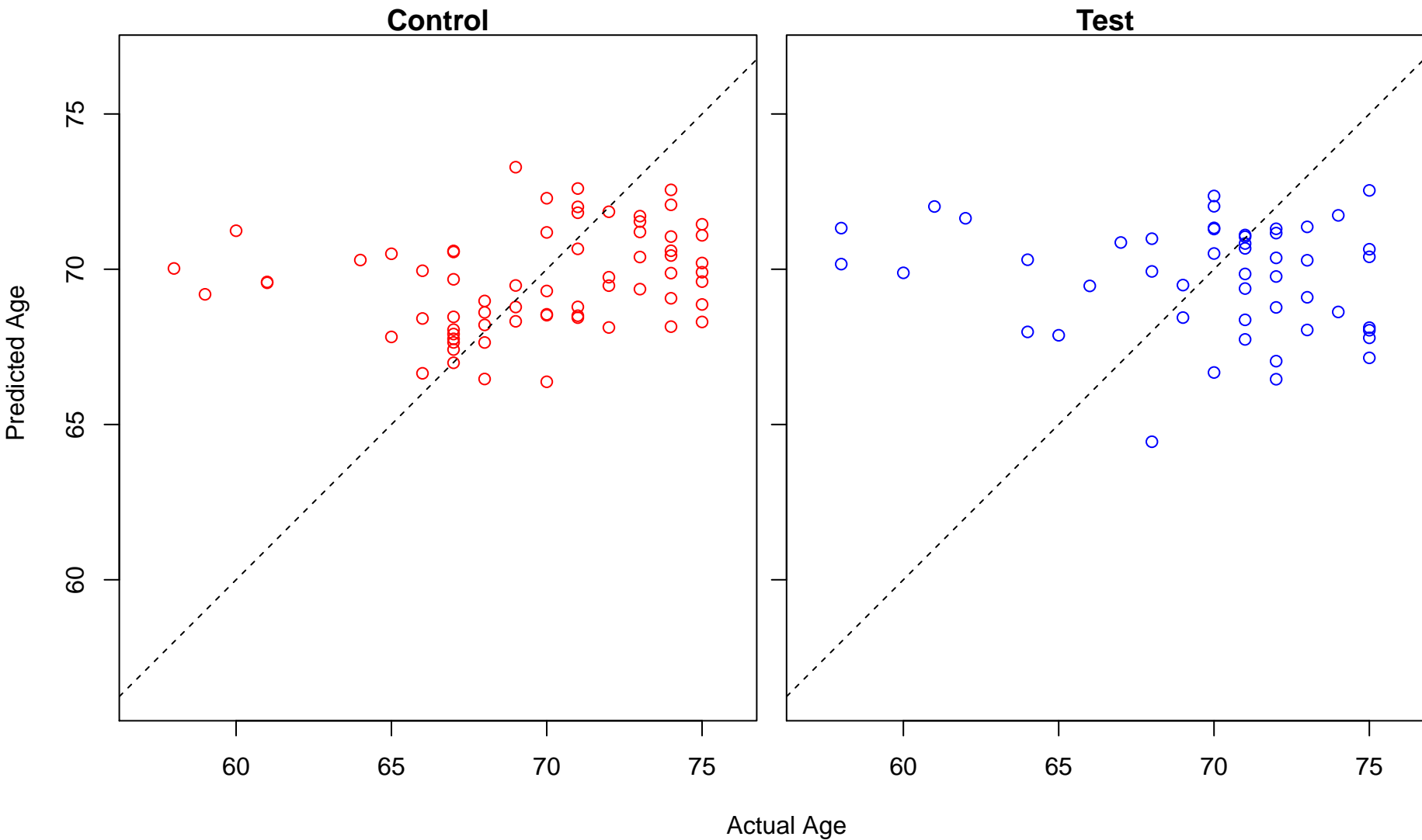
positive regulation of natural killer cell chemotaxis (Score: 0.229337)



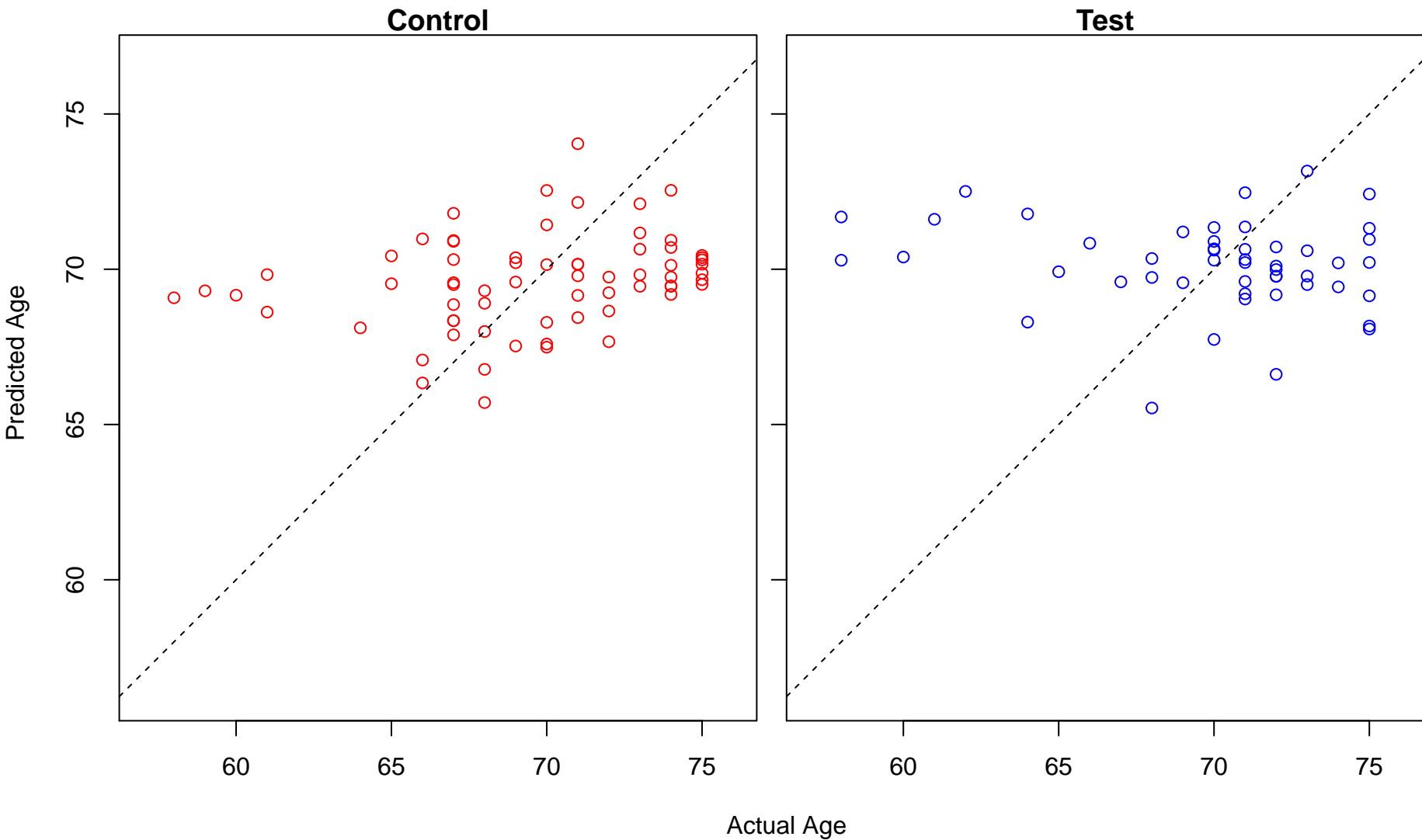
negative regulation of chemokine-mediated signaling pathway (Score: 0.227506)



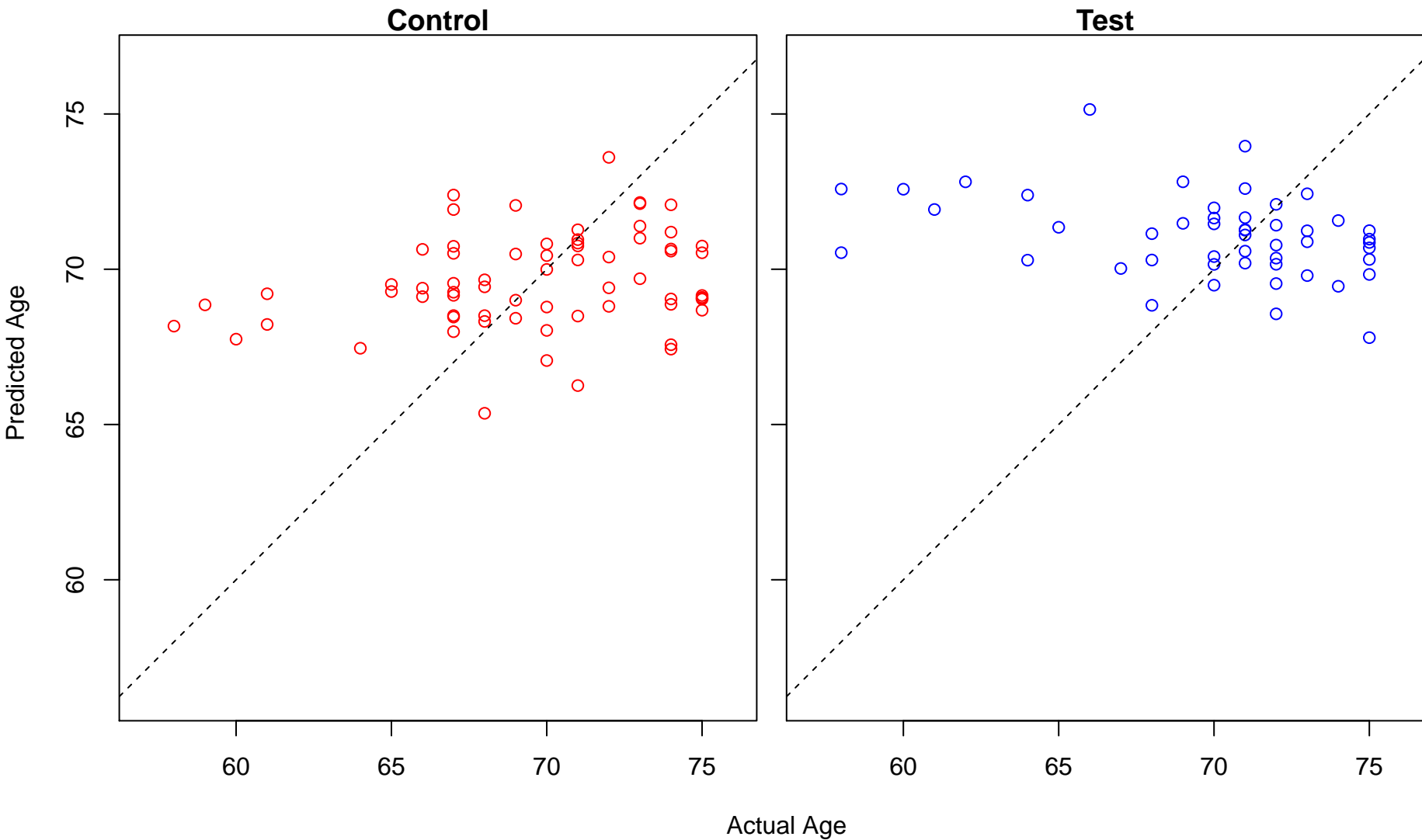
positive regulation of fatty acid metabolic process (Score: 0.226935)



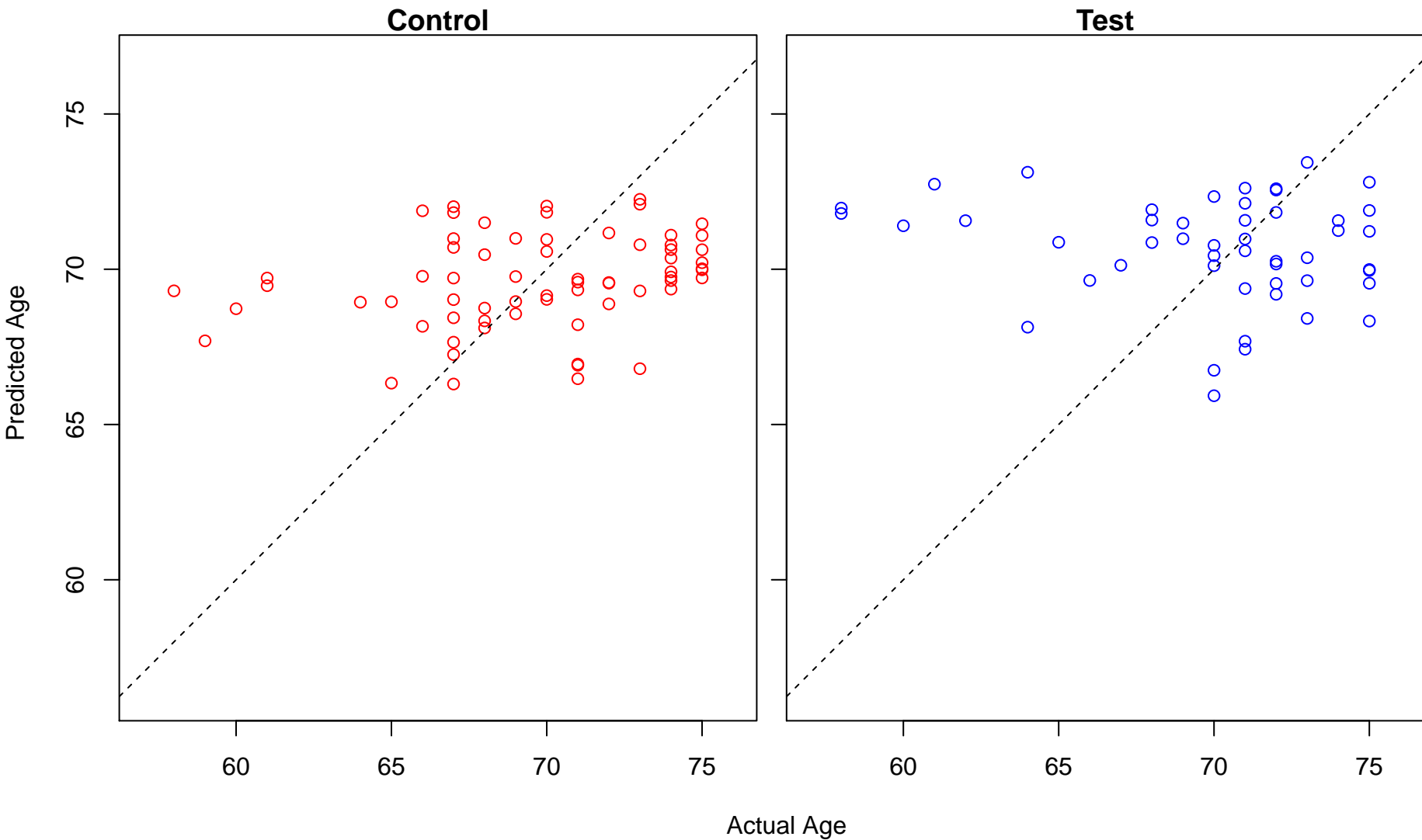
miRNA loading onto RISC involved in gene silencing by miRNA (Score: 0.226414)



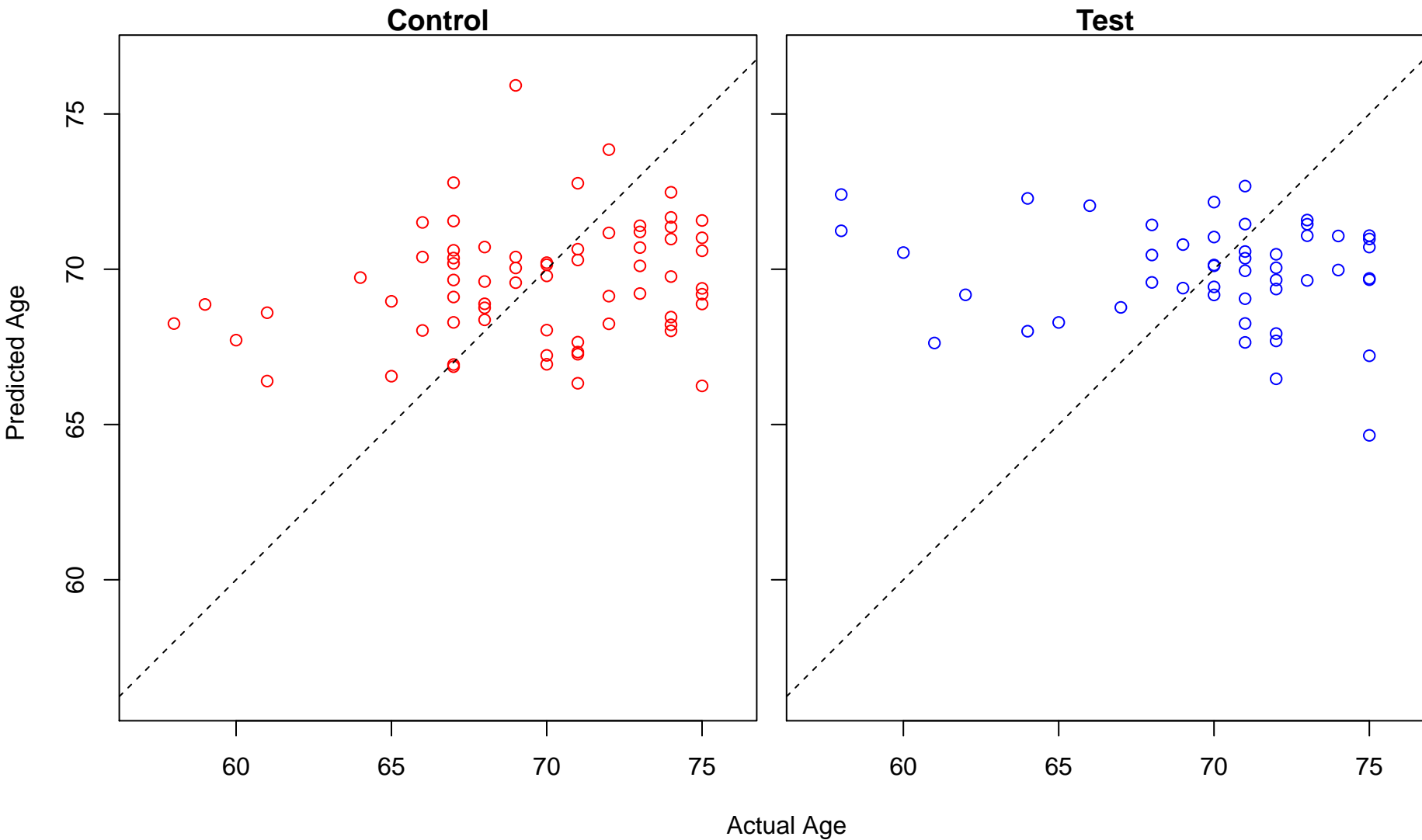
positive regulation of actin cytoskeleton reorganization (Score: 0.225707)



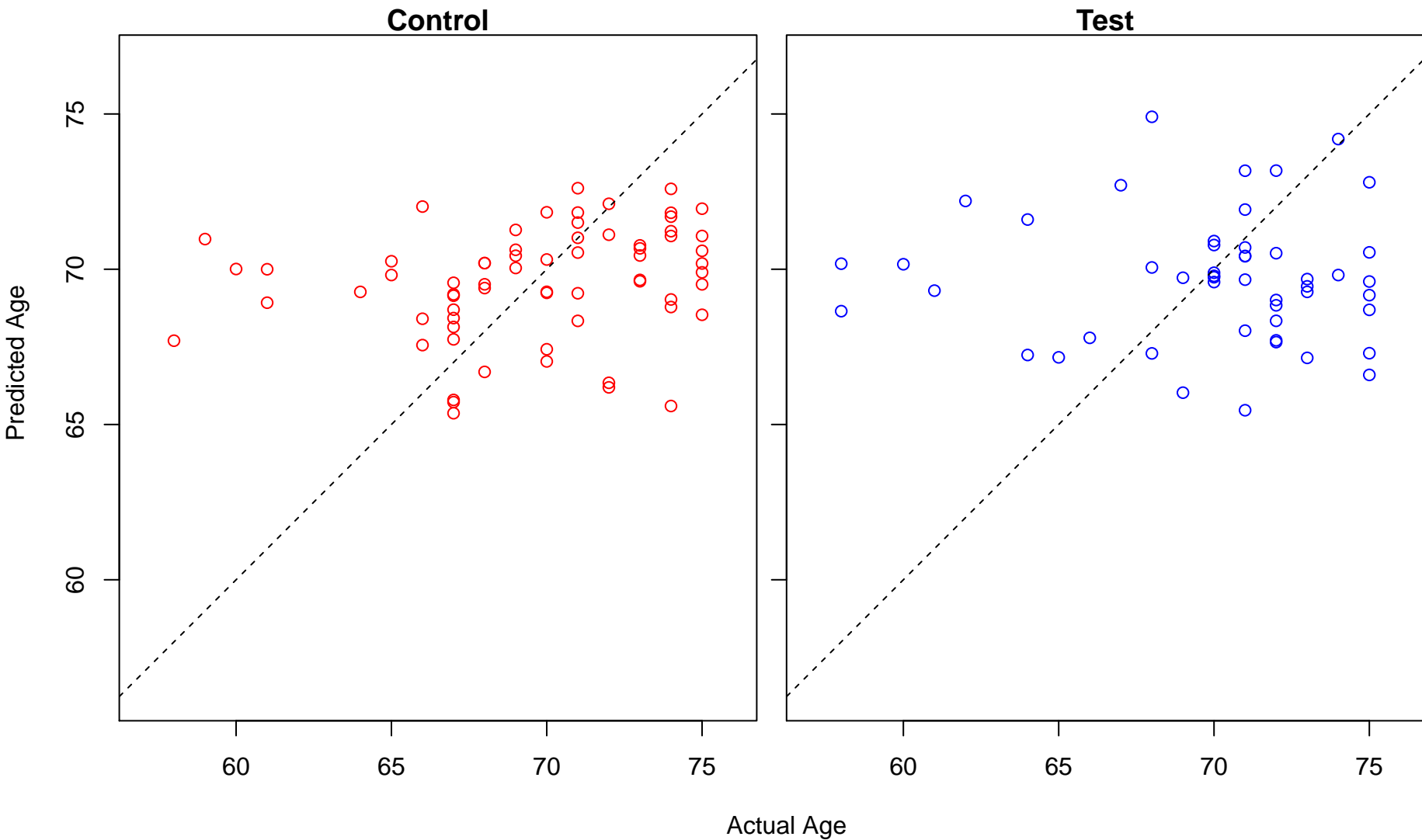
adult heart development (Score: 0.225092)



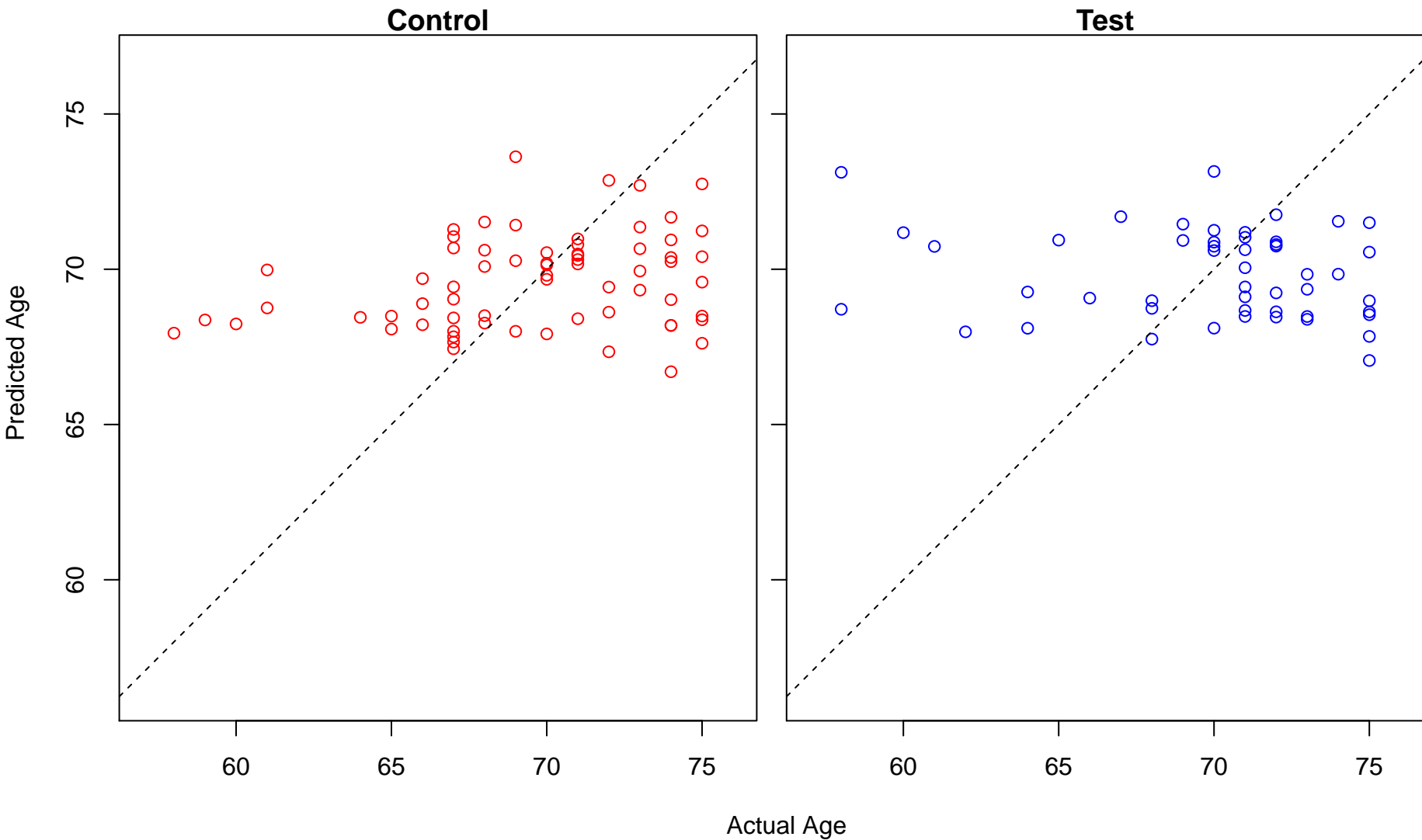
calcium-mediated signaling using intracellular calcium source (Score: 0.223726)



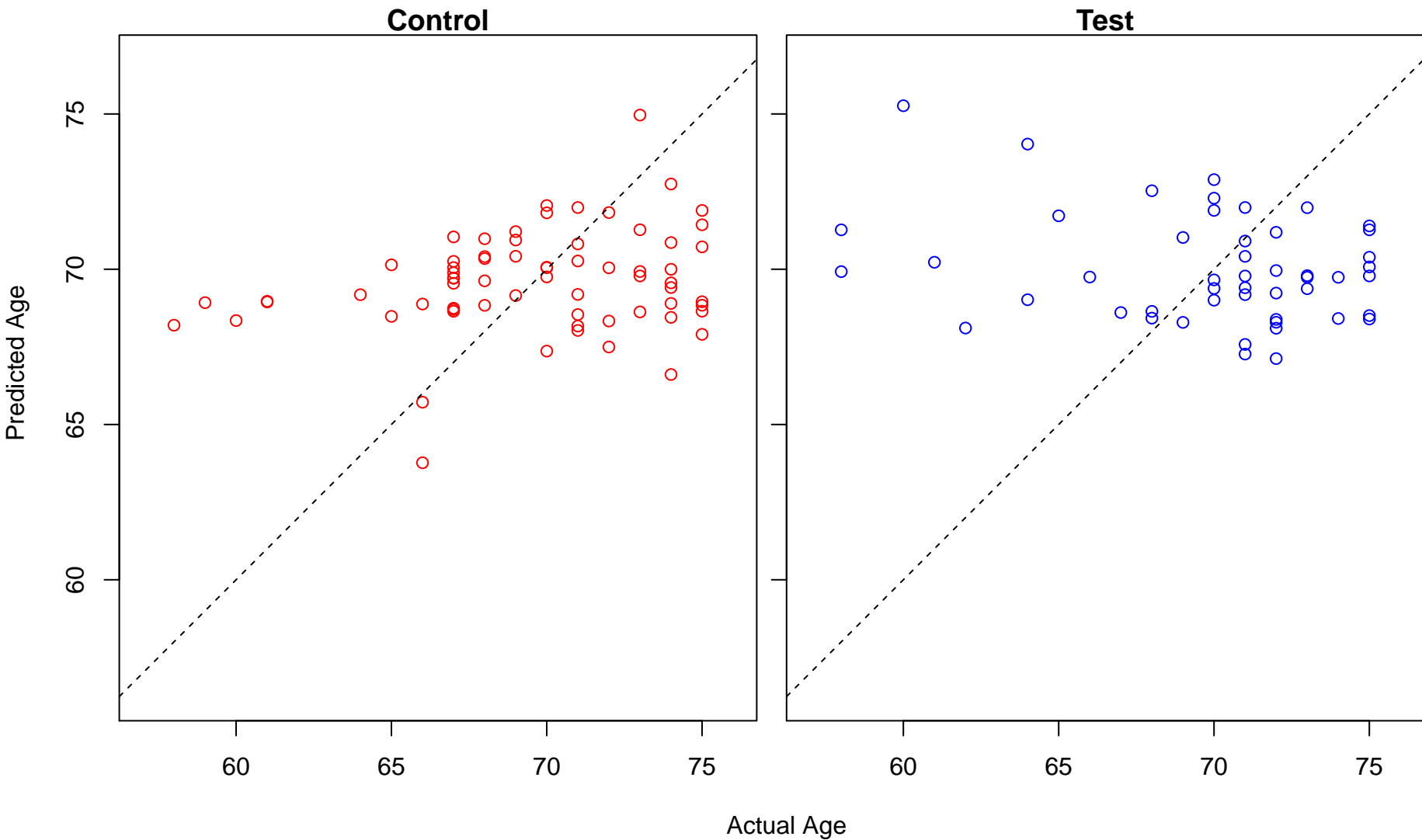
positive regulation of lipopolysaccharide-mediated signaling pathway (Score: 0.223594)



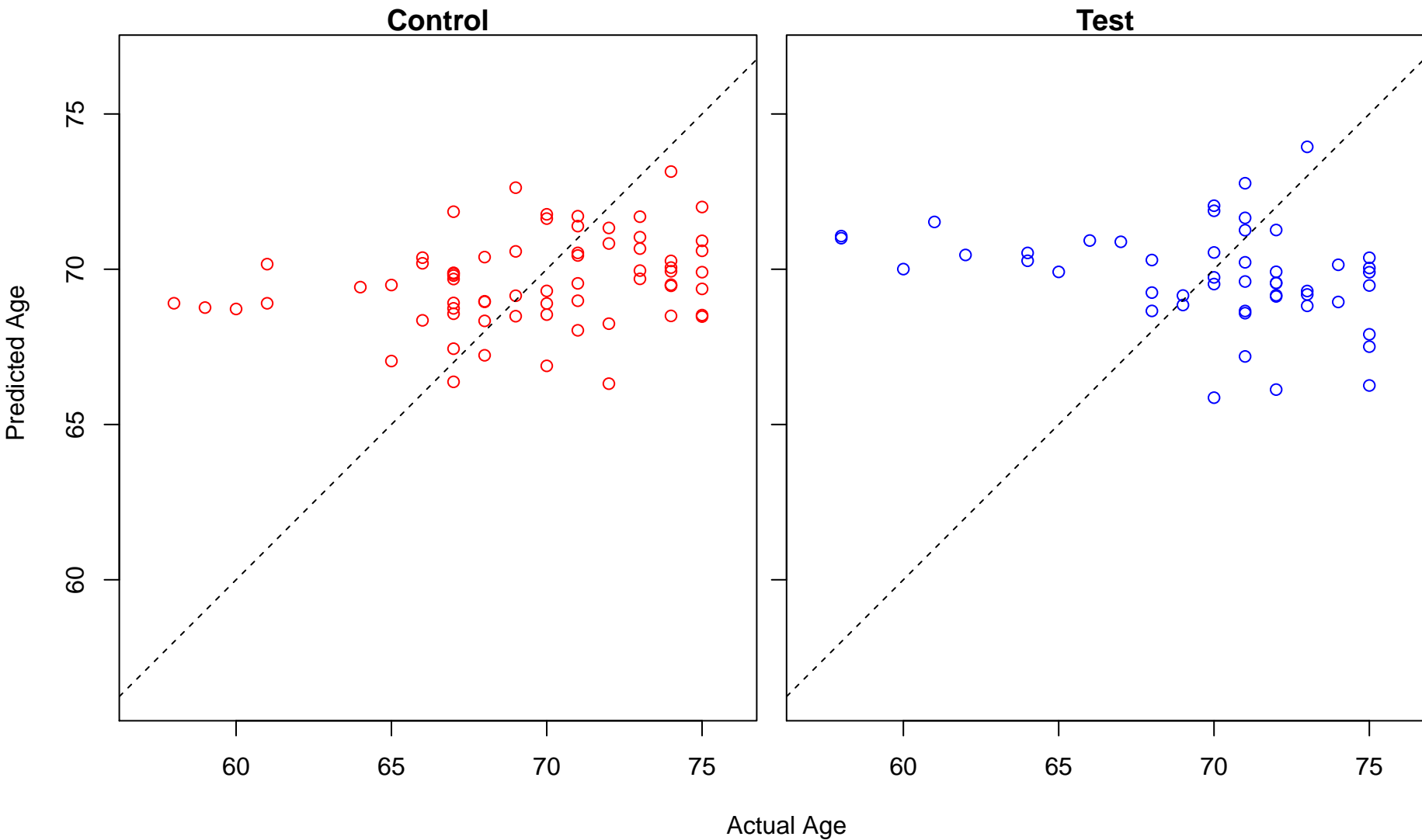
binding of sperm to zona pellucida (Score: 0.220948)



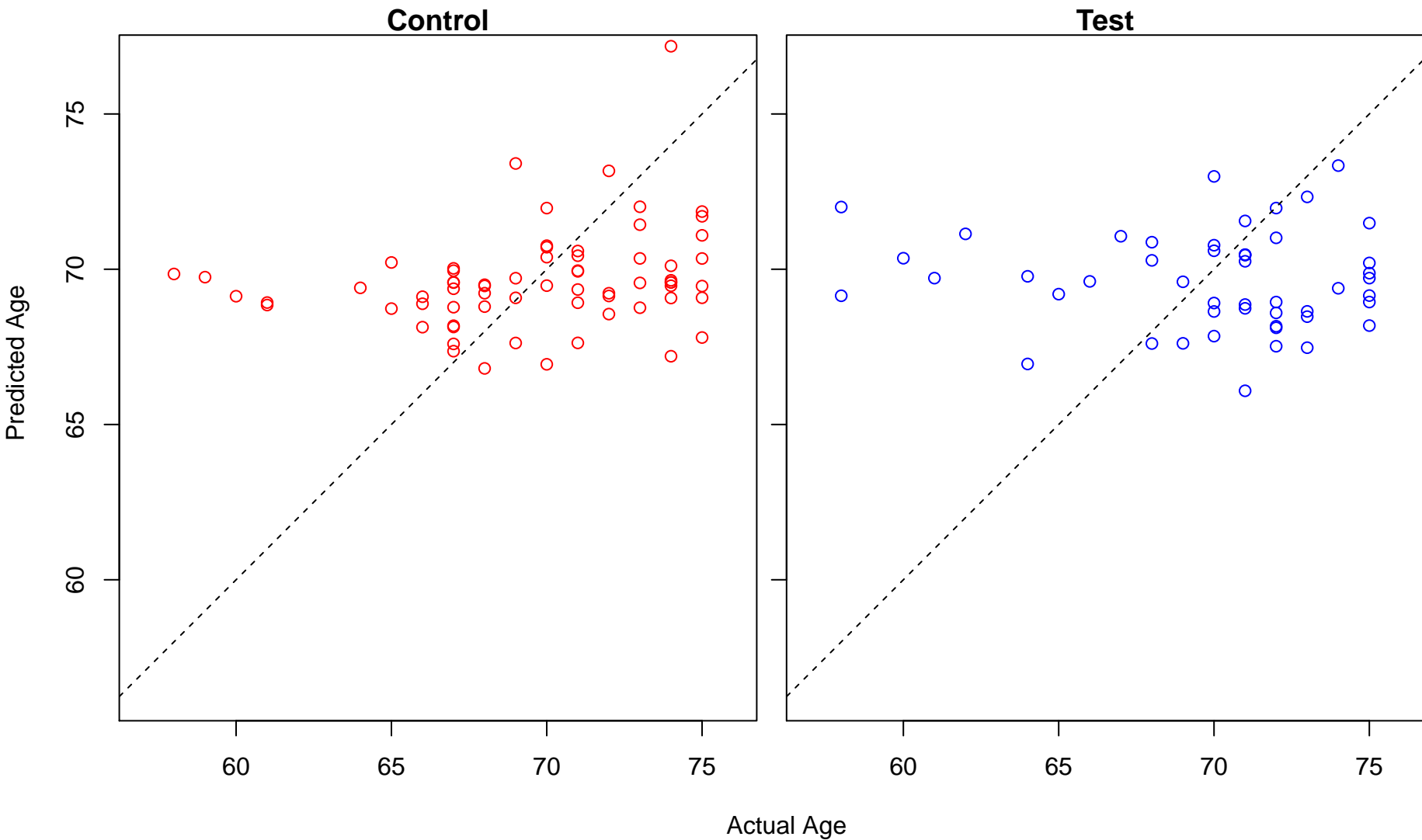
negative regulation of insulin-like growth factor receptor signaling pathway (Score: 0.220597)



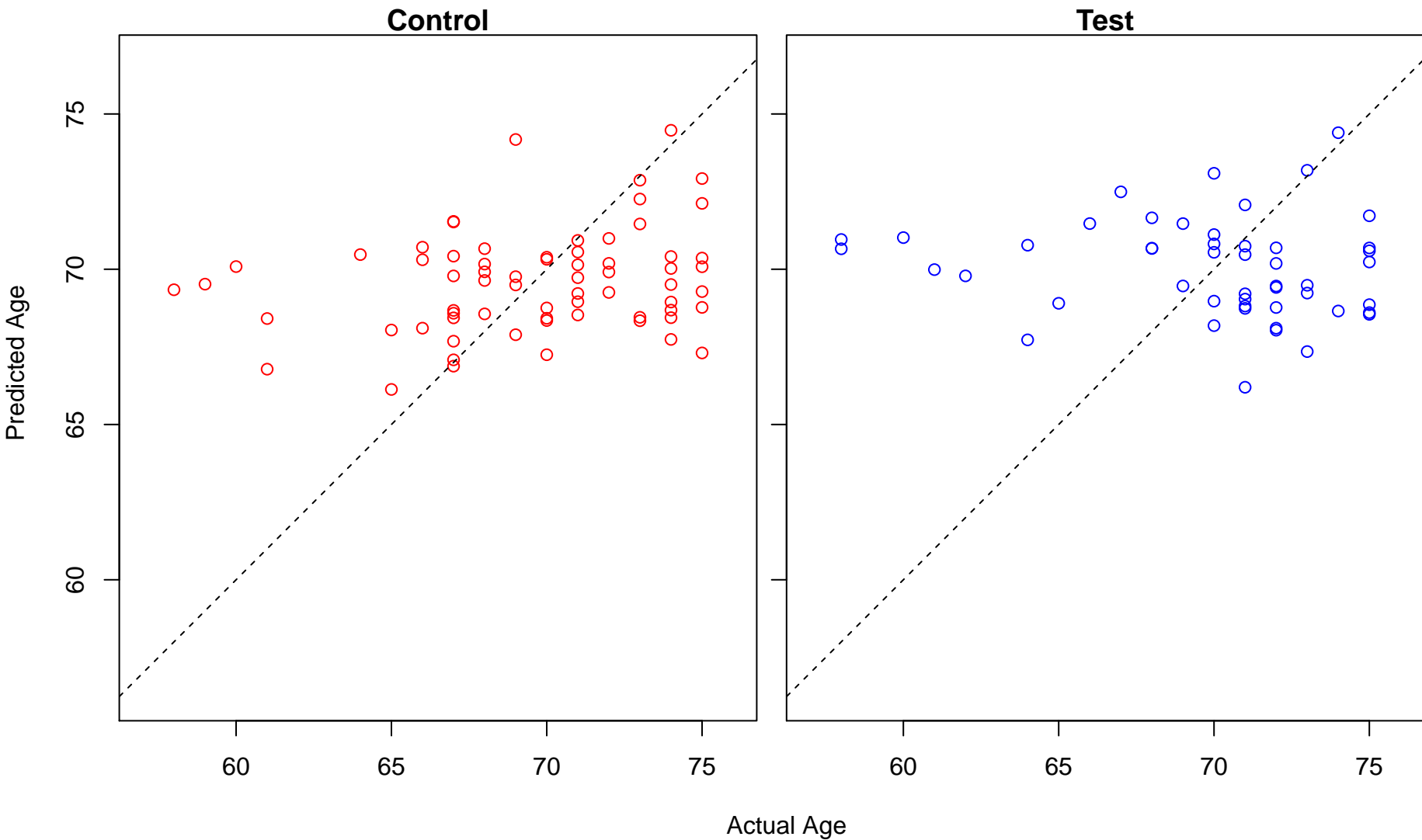
negative regulation of keratinocyte proliferation (Score: 0.219183)



interleukin-8 production (Score: 0.217398)

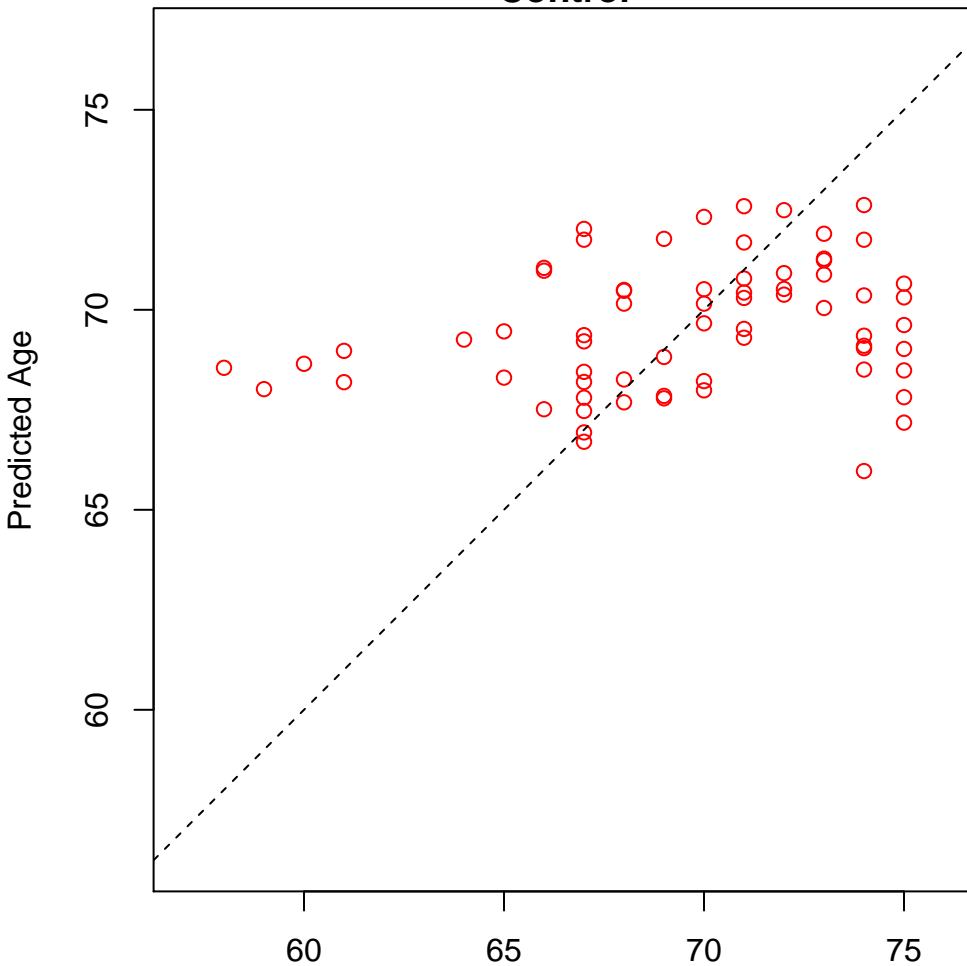


polyamine biosynthetic process (Score: 0.216296)

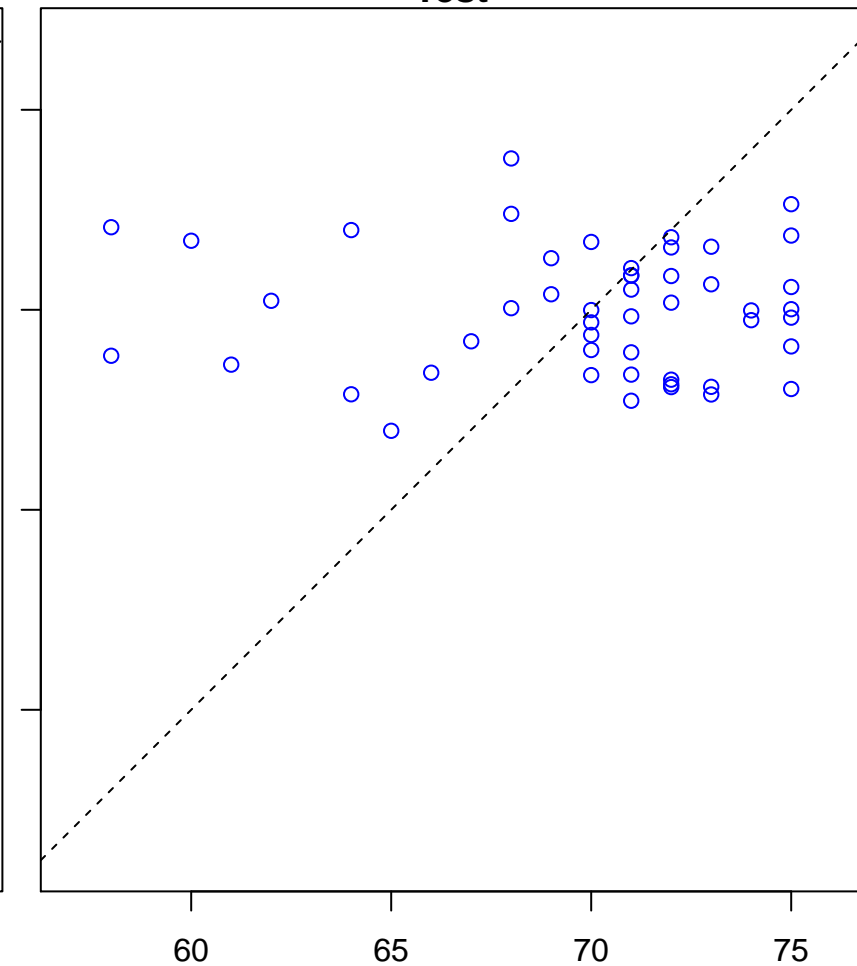


enteric nervous system development (Score: 0.216171)

Control

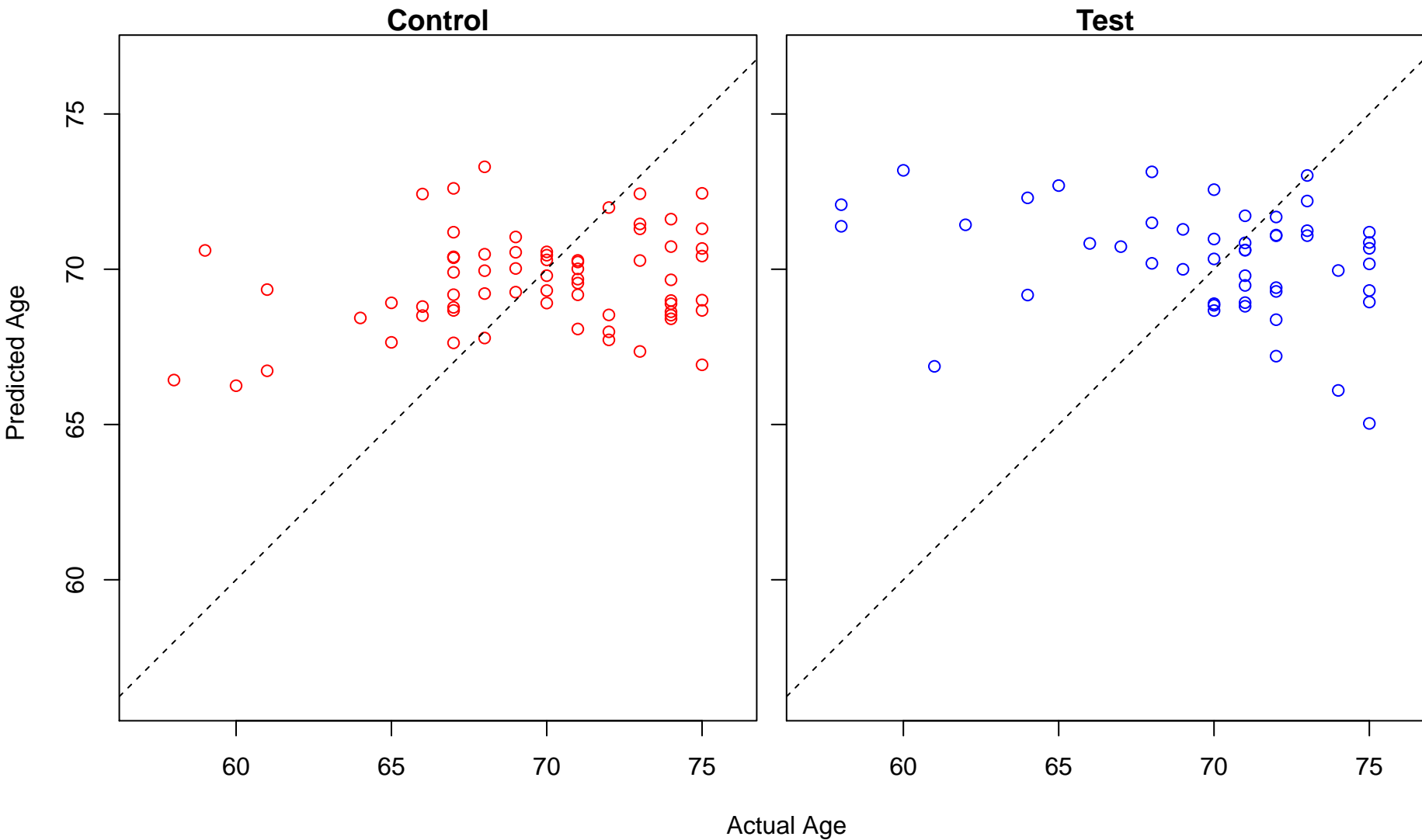


Test

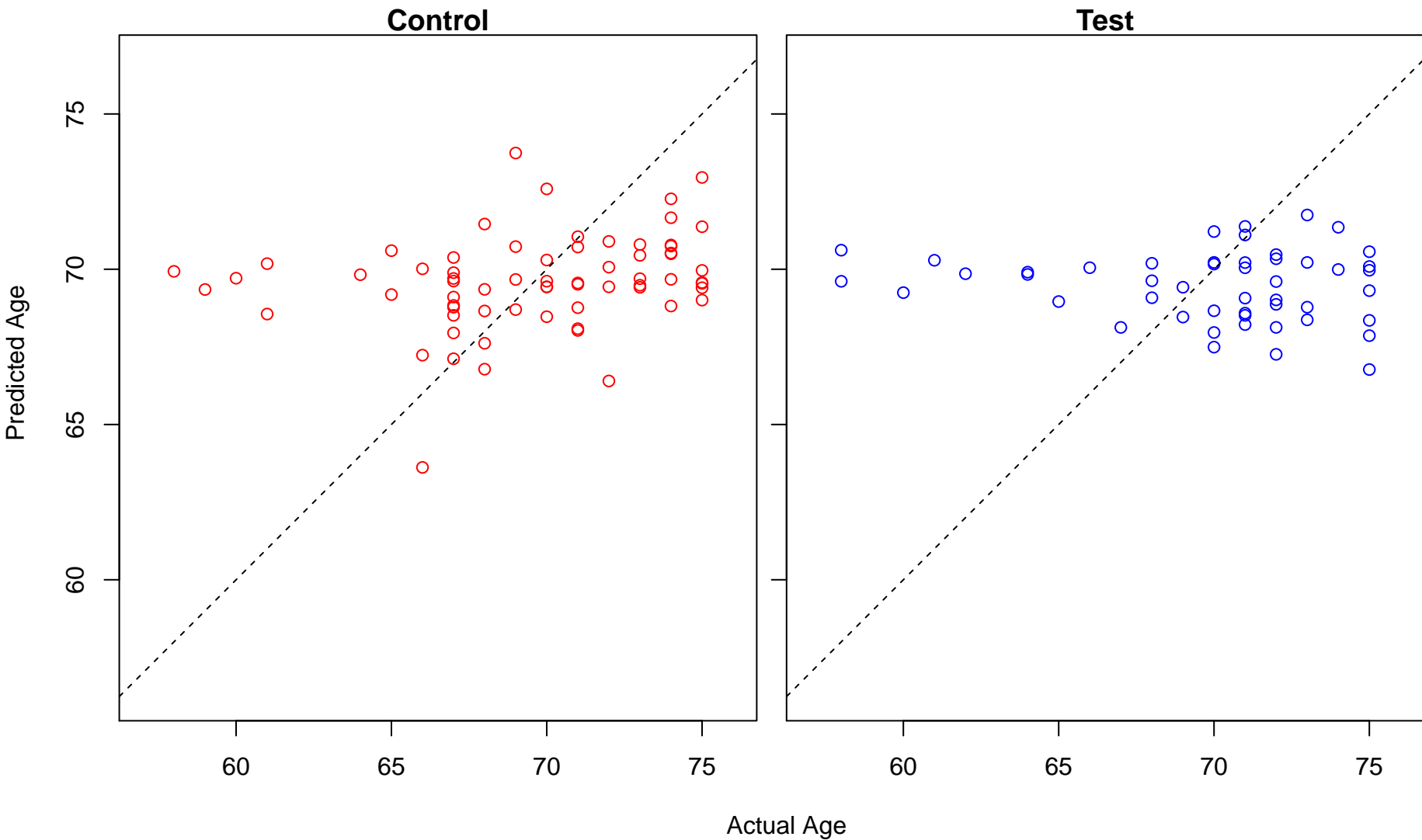


Actual Age

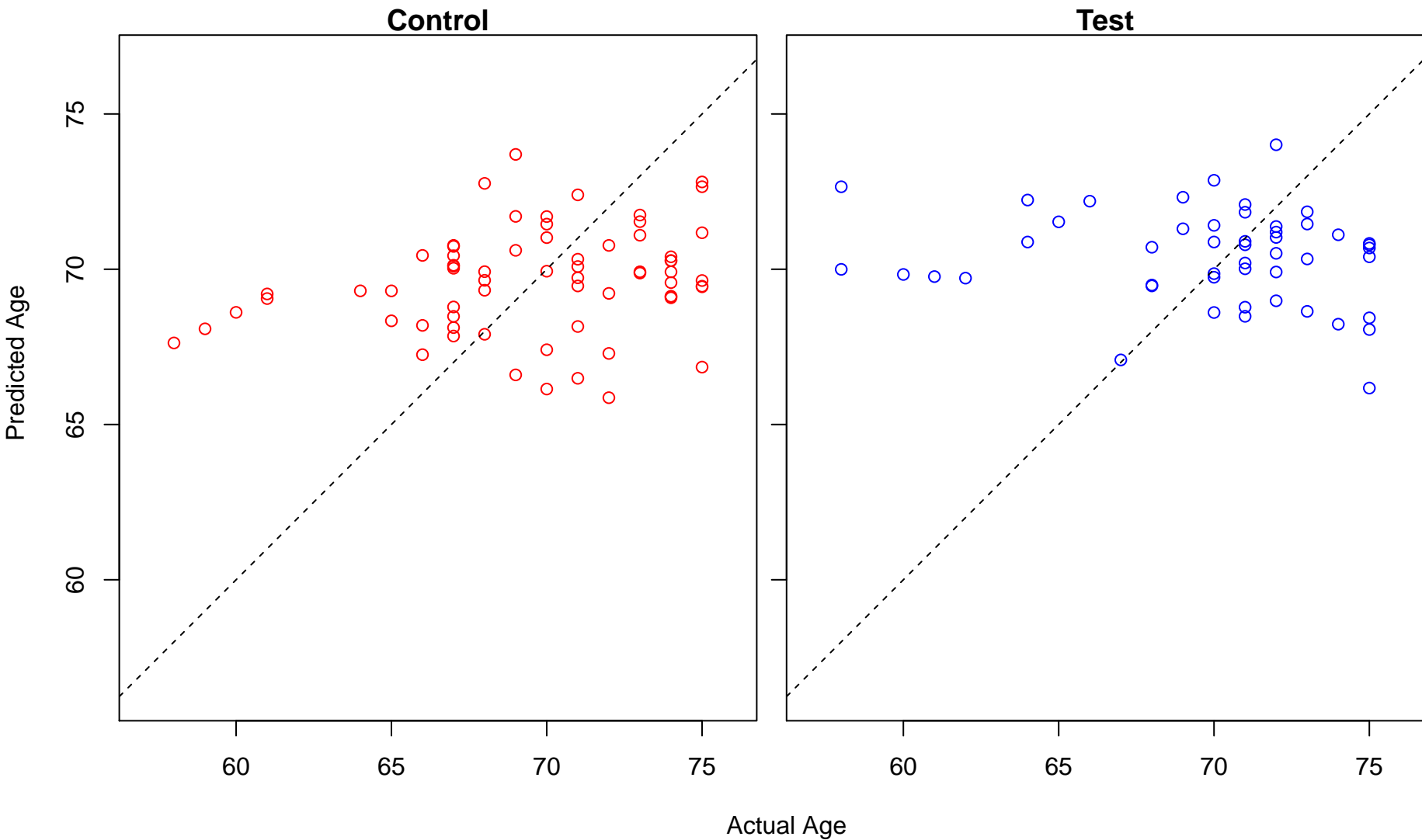
cGMP-mediated signaling (Score: 0.212704)



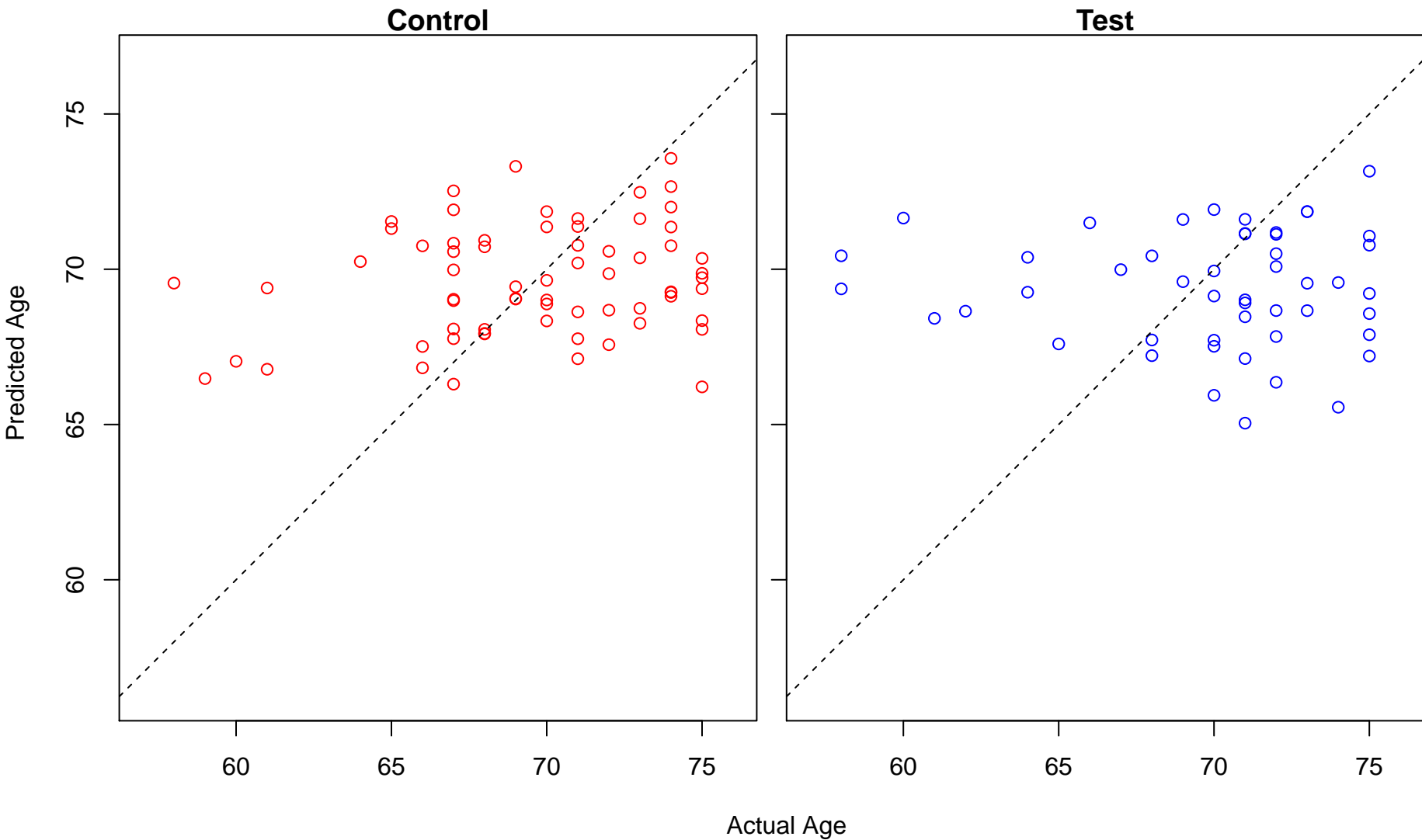
intra-S DNA damage checkpoint (Score: 0.208294)



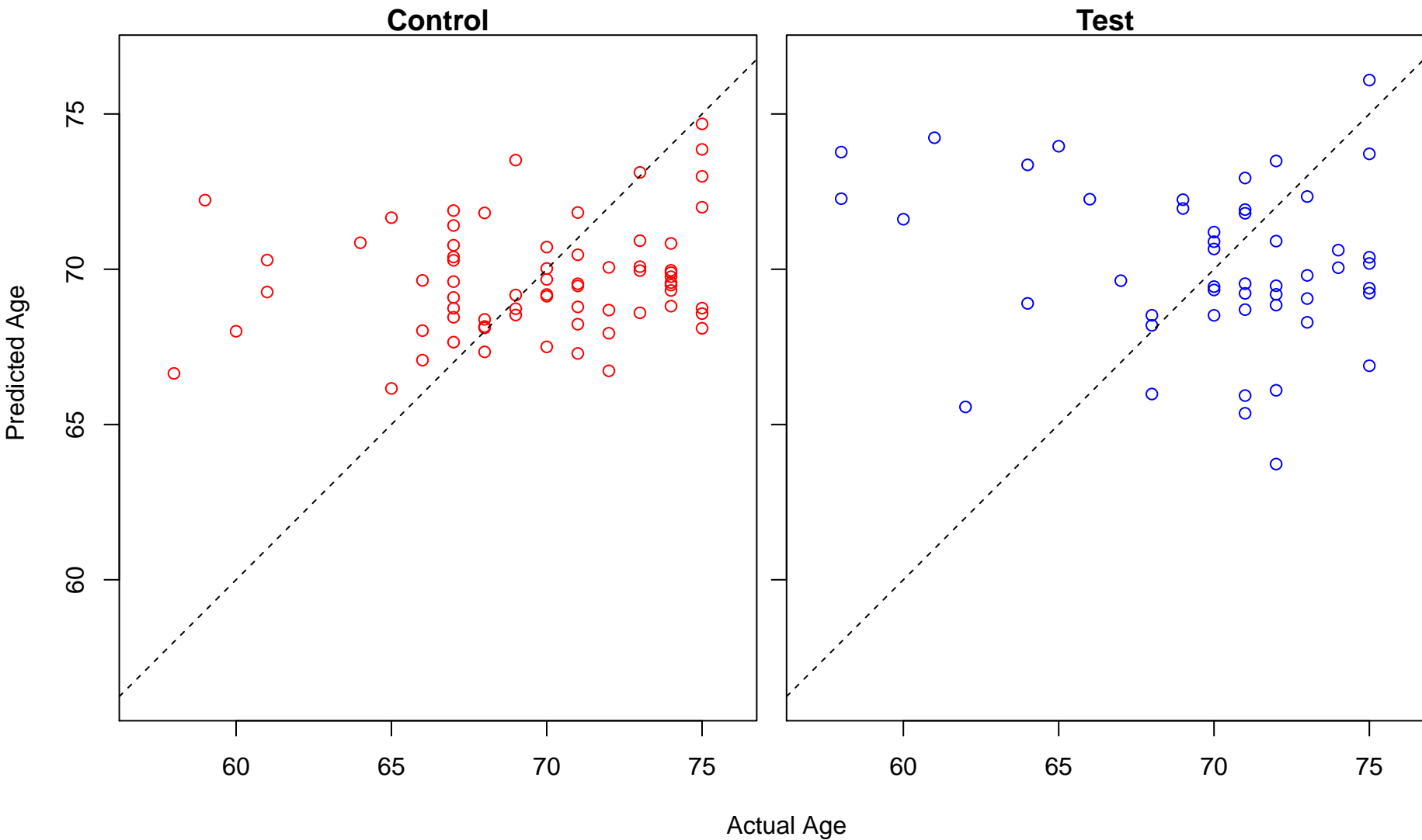
amino sugar biosynthetic process (Score: 0.207037)



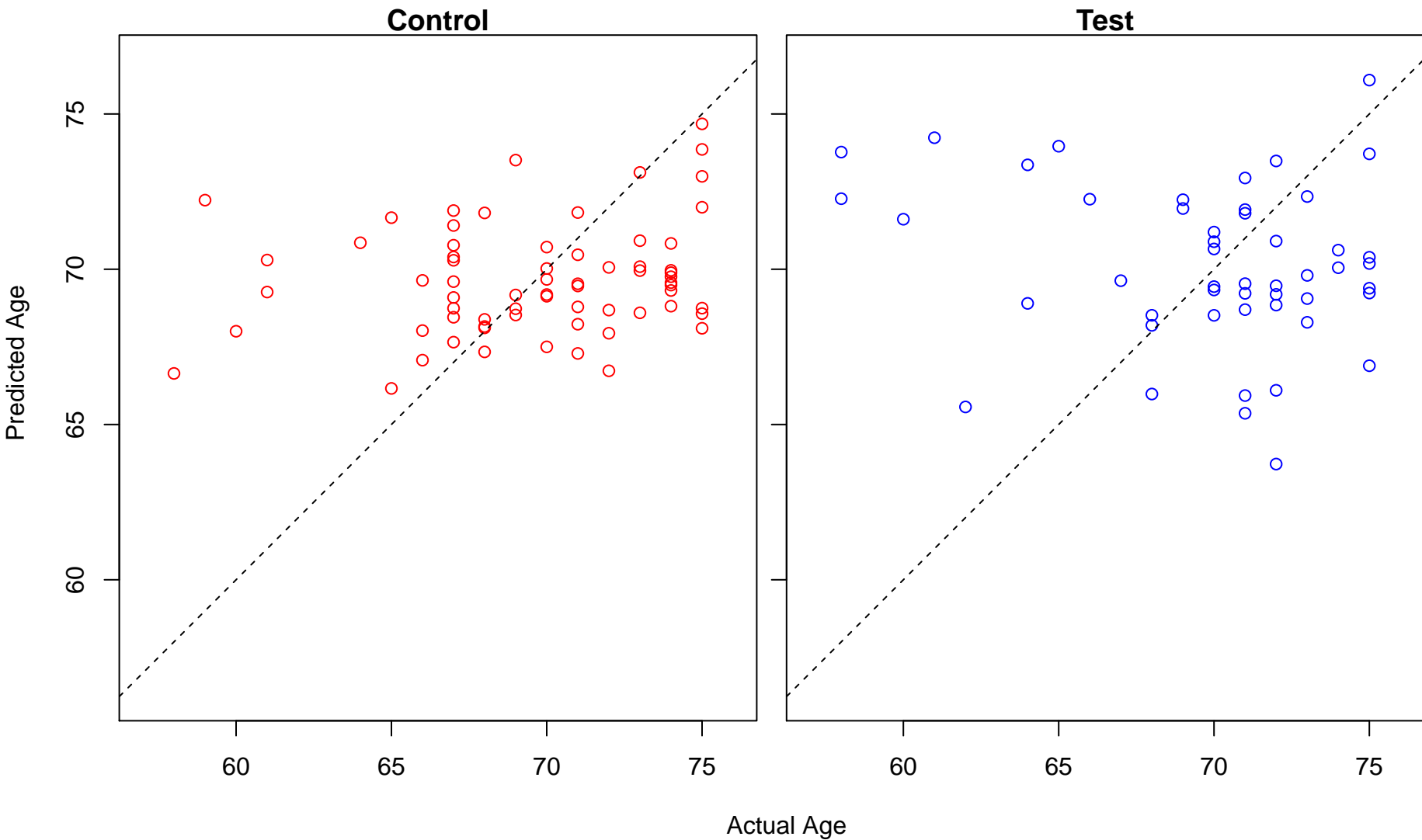
determination of adult lifespan (Score: 0.206631)



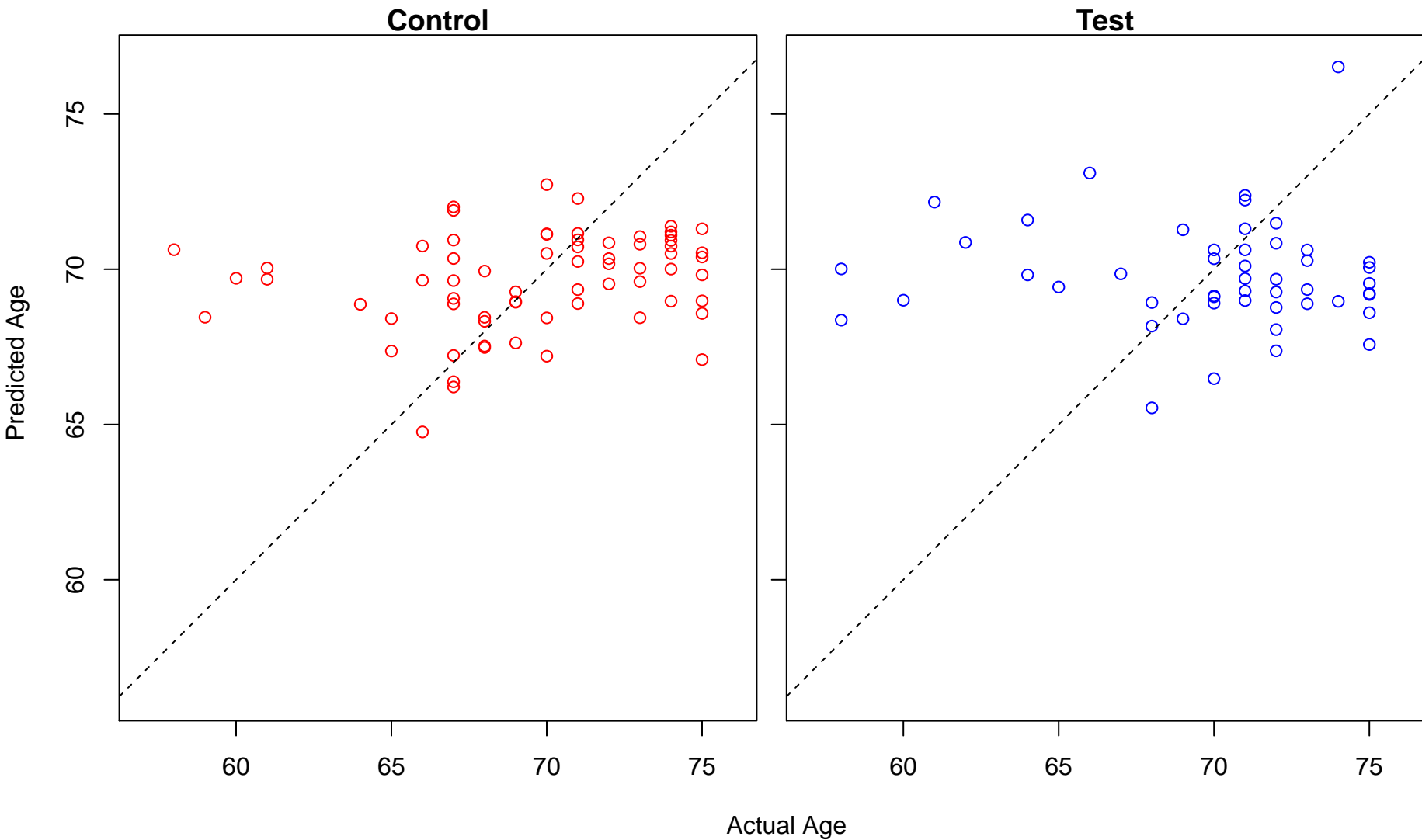
negative regulation of chondrocyte differentiation (Score: 0.205399)



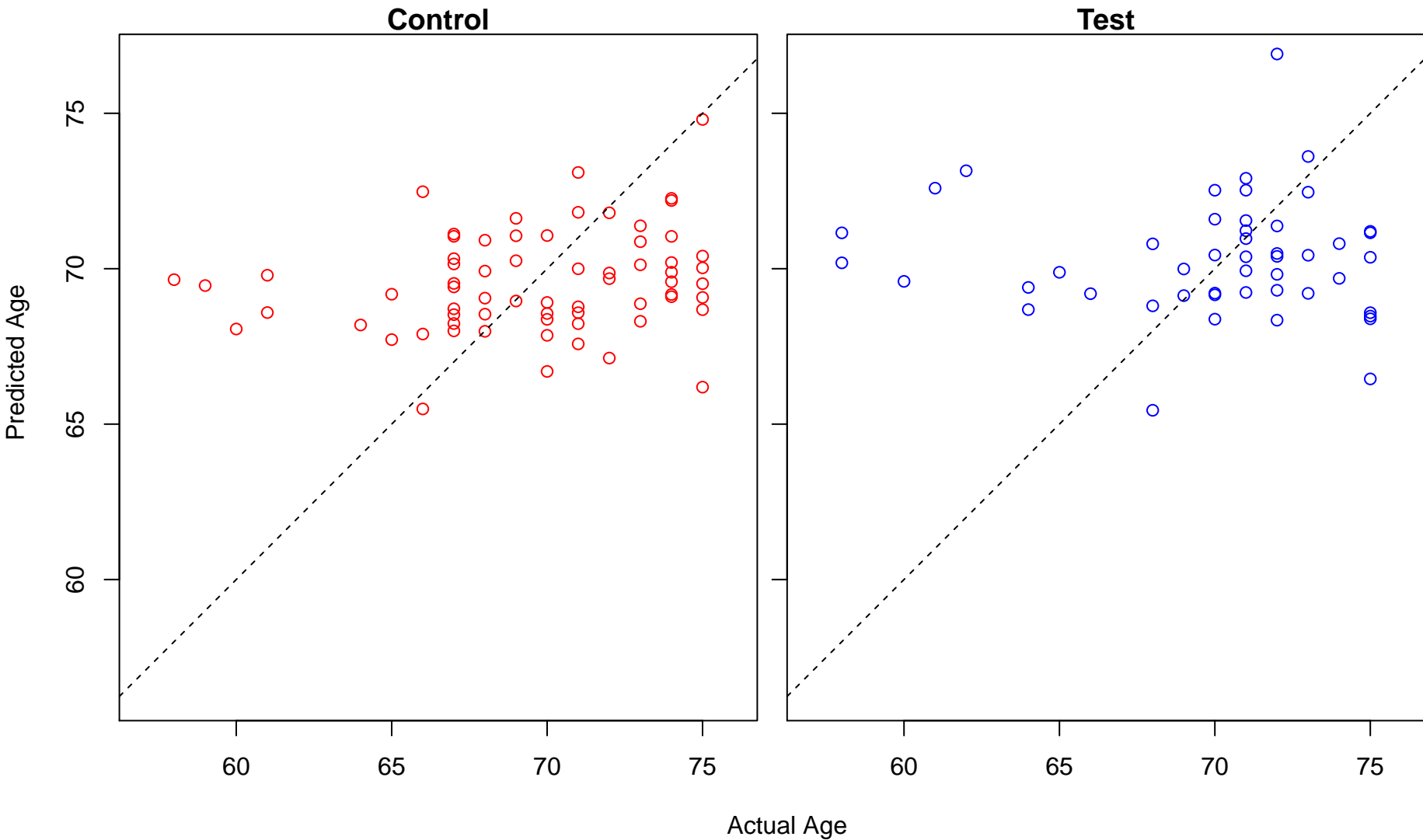
negative regulation of cartilage development (Score: 0.205399)



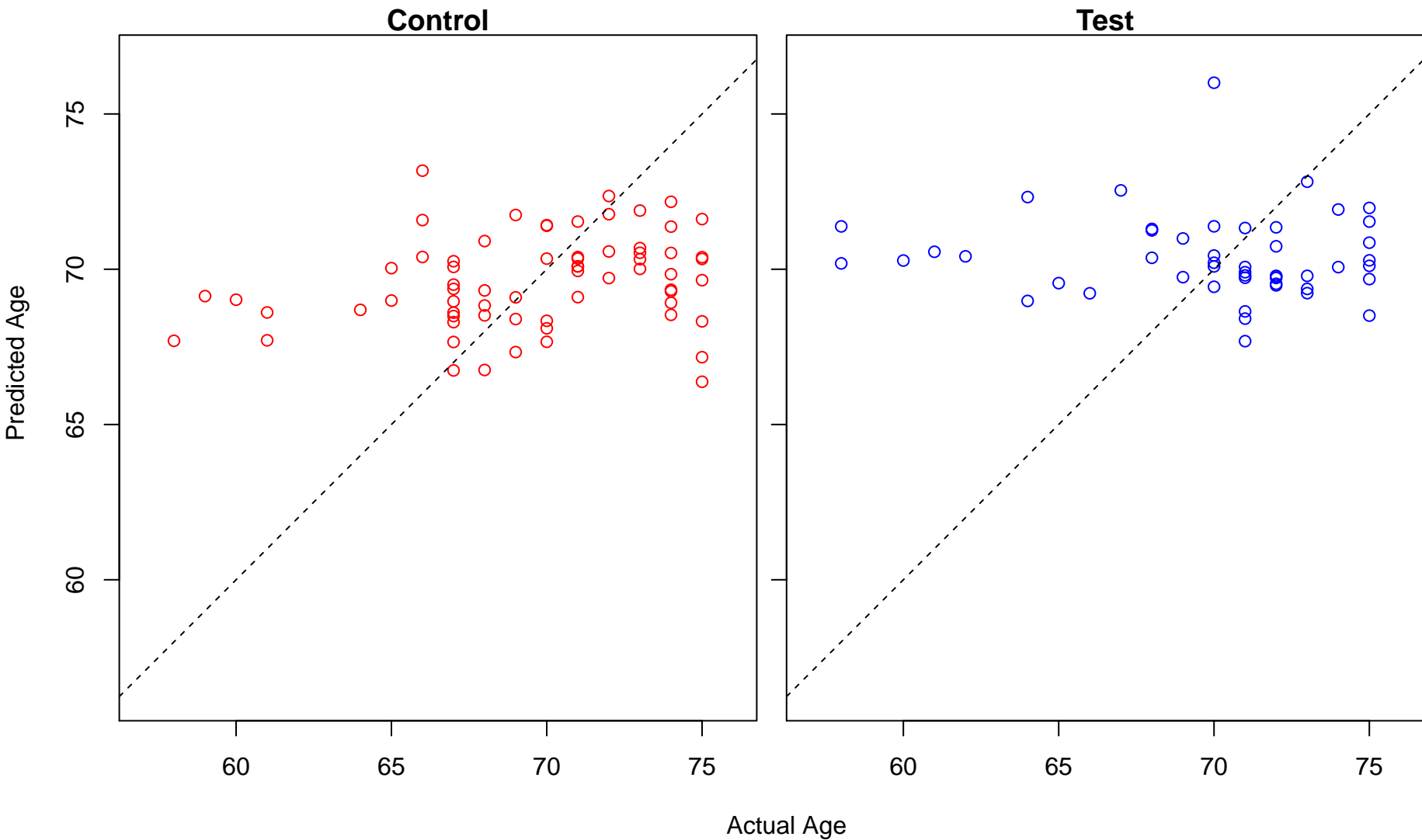
positive regulation of activation of JAK2 kinase activity (Score: 0.203428)



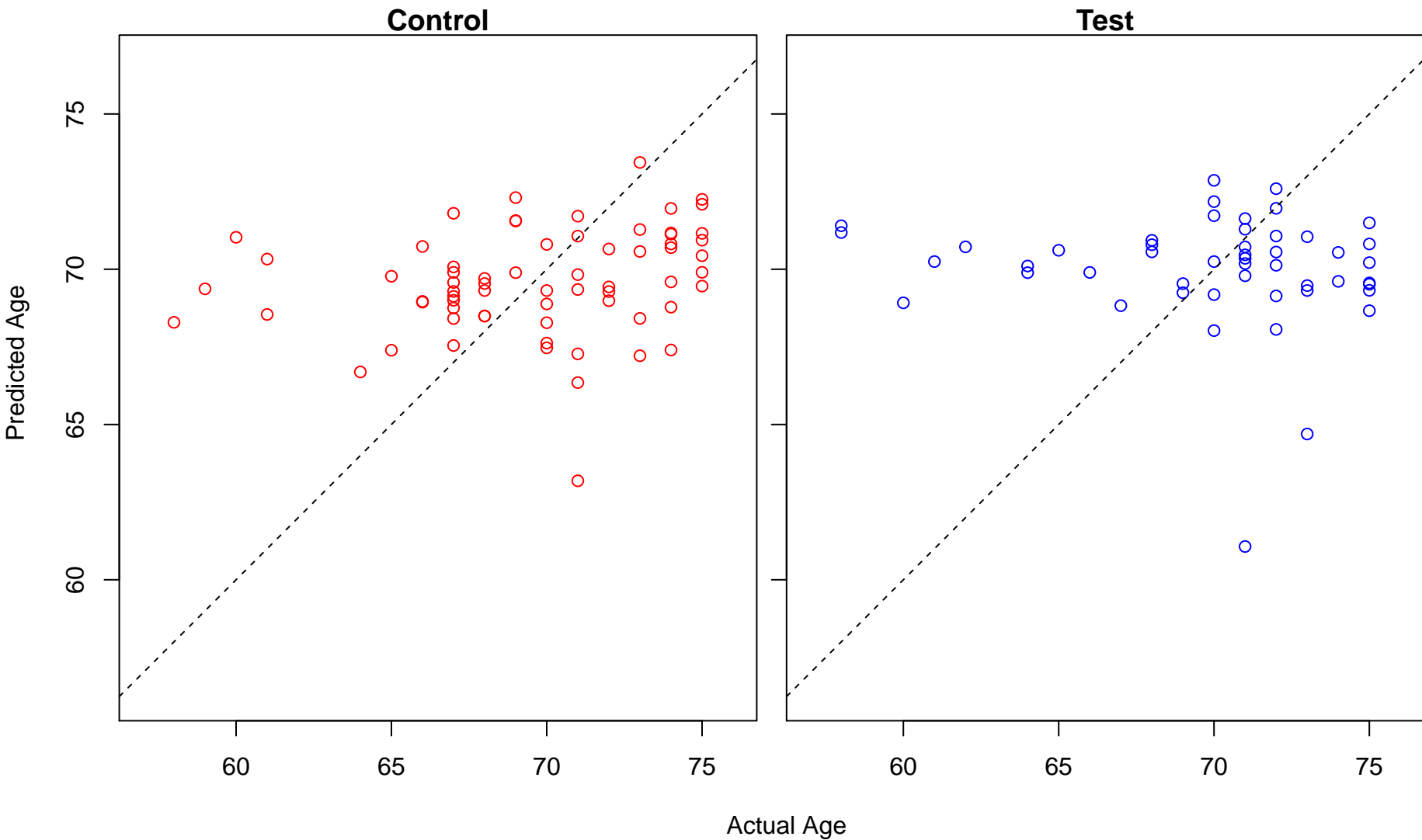
regulation of ubiquitin homeostasis (Score: 0.201700)



response to forskolin (Score: 0.198530)

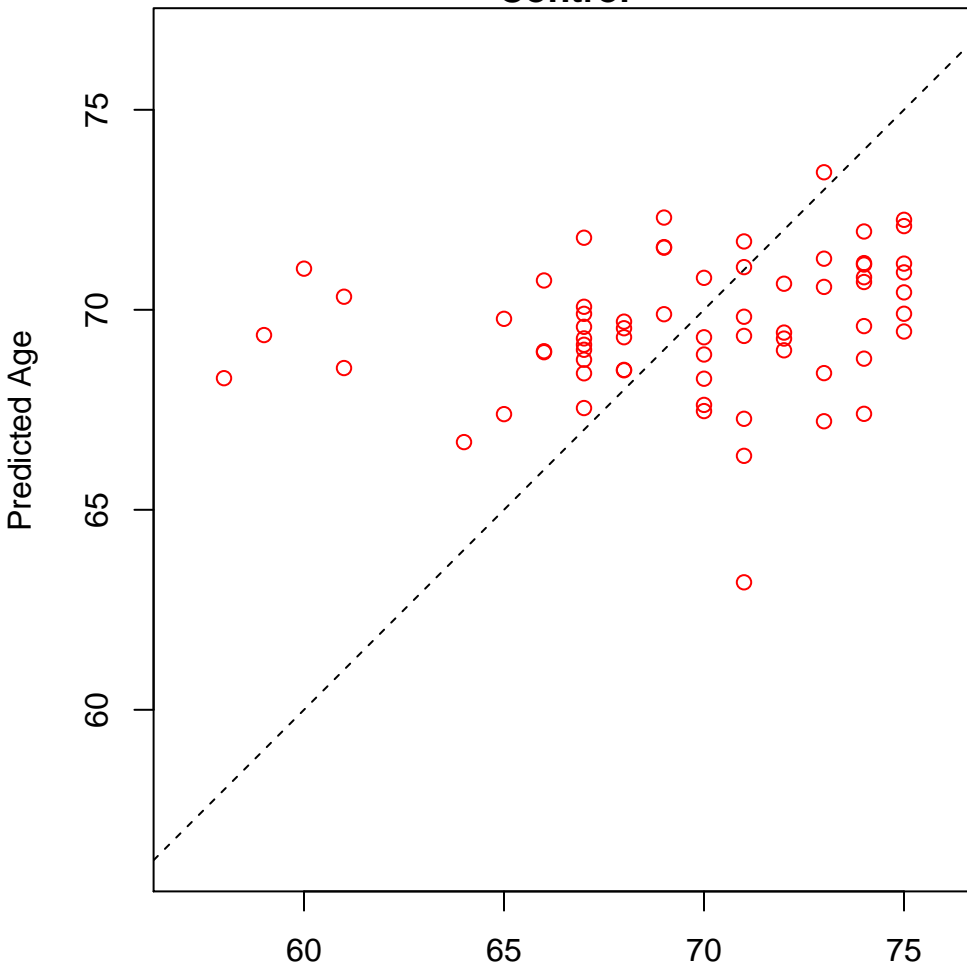


detection of chemical stimulus involved in sensory perception of bitter taste (Score: 0.197958)

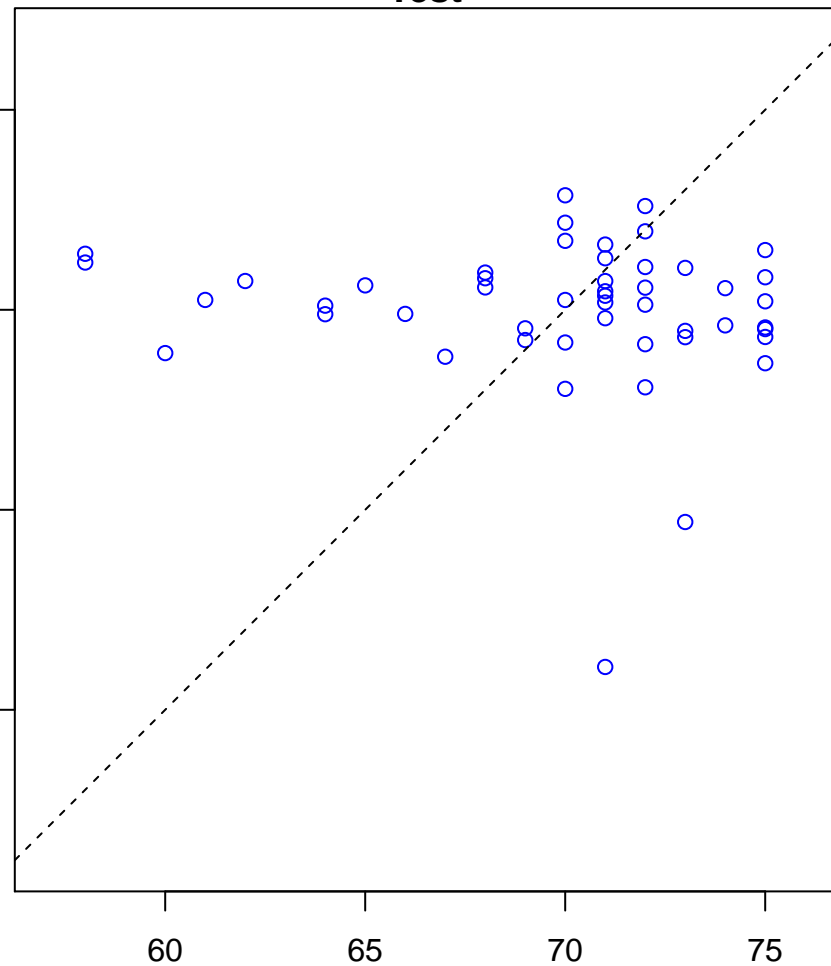


sensory perception of bitter taste (Score: 0.197958)

Control

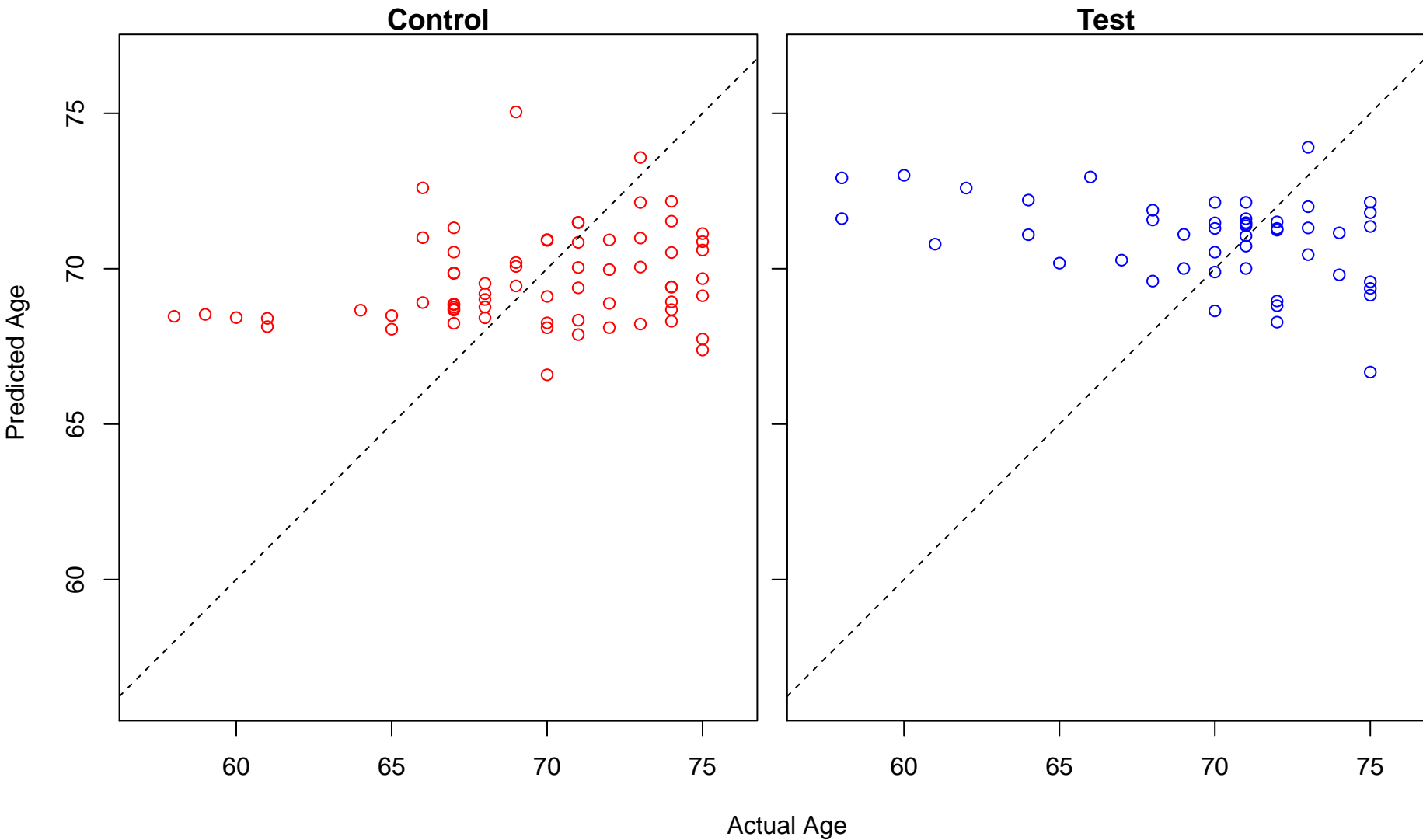


Test



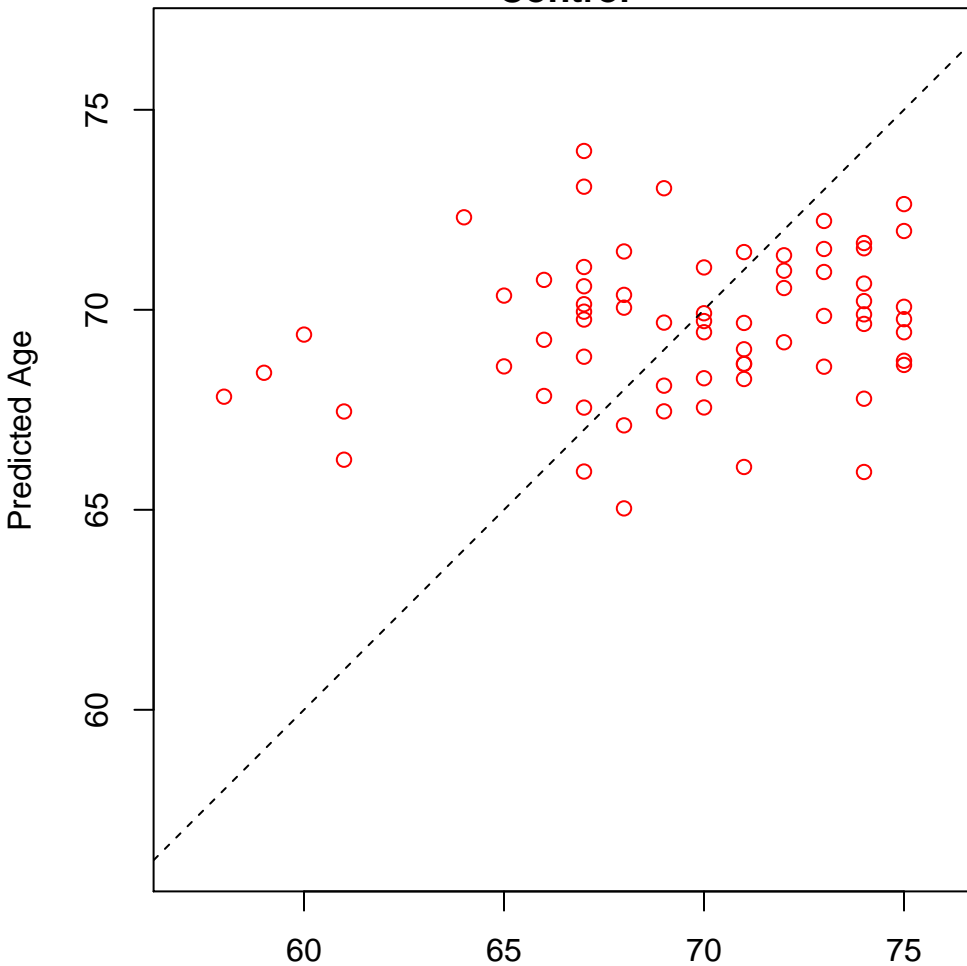
Actual Age

positive regulation of calcineurin–NFAT signaling cascade (Score: 0.197766)

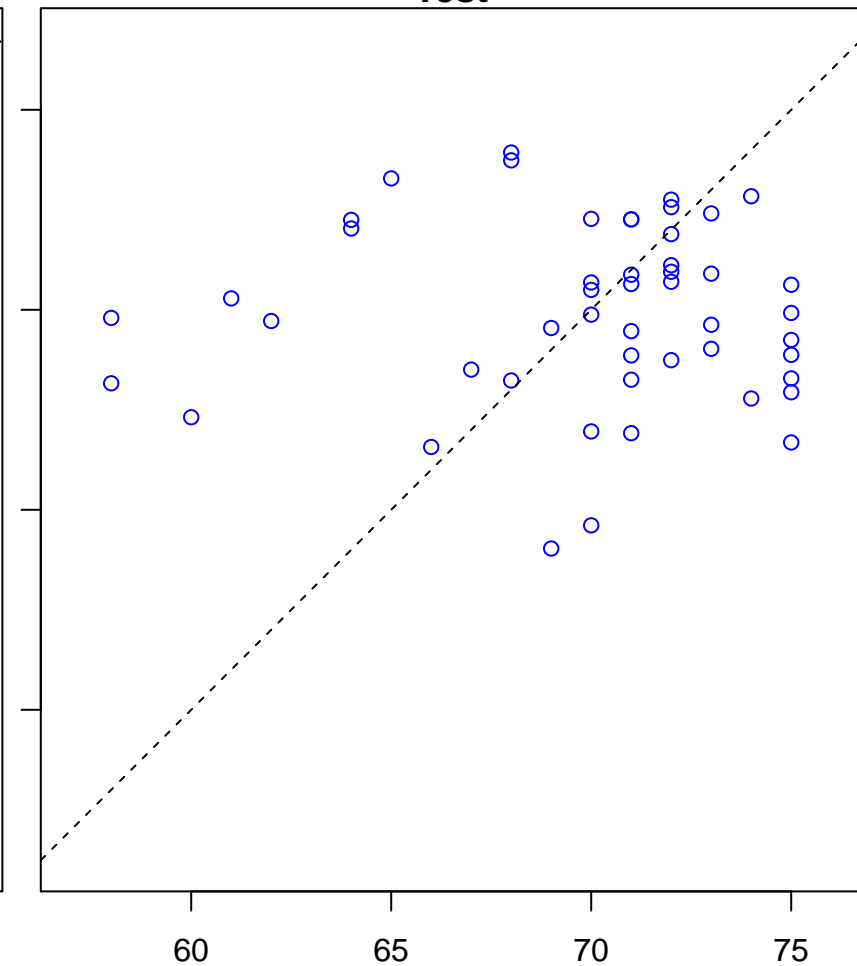


blood coagulation, extrinsic pathway (Score: 0.194607)

Control

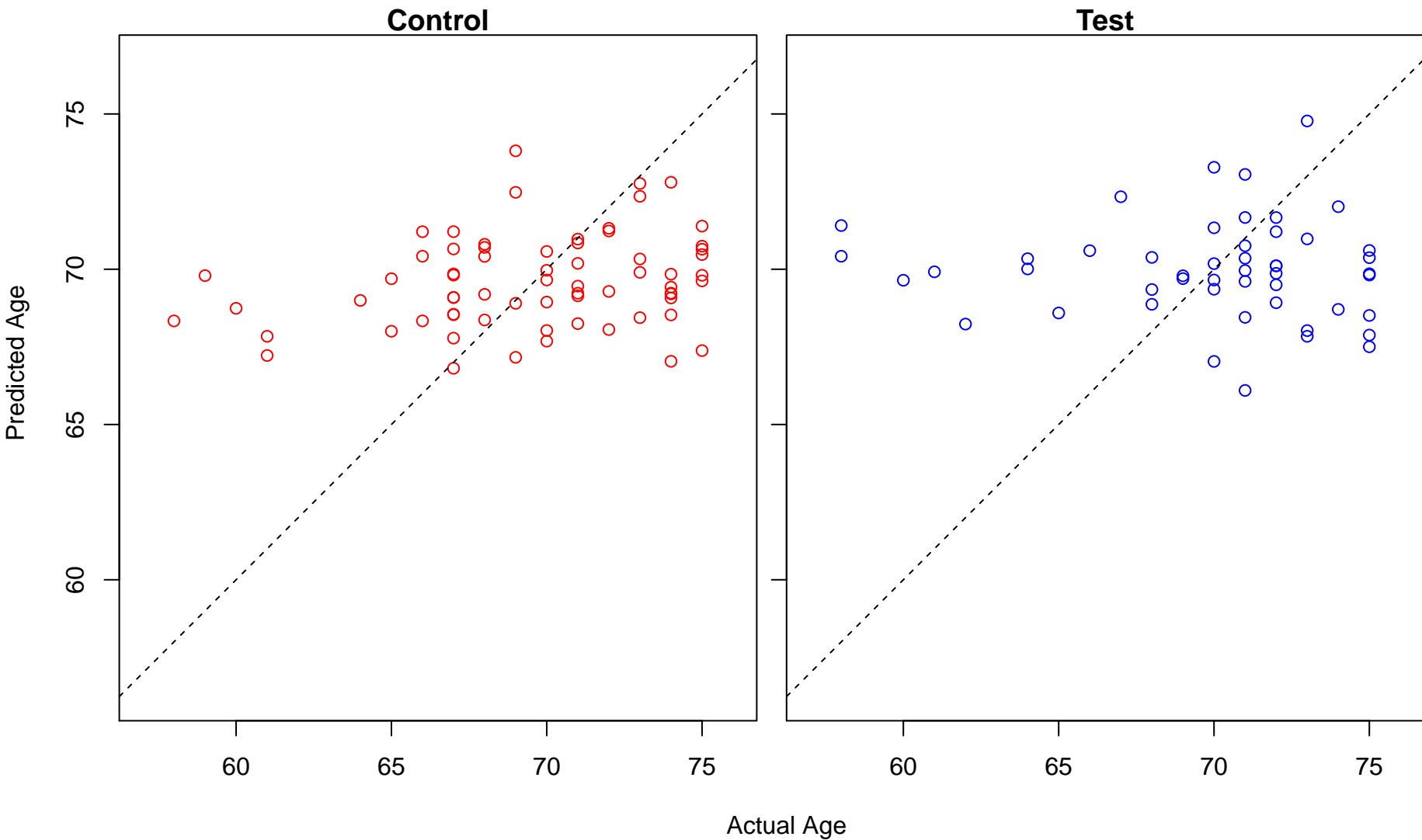


Test

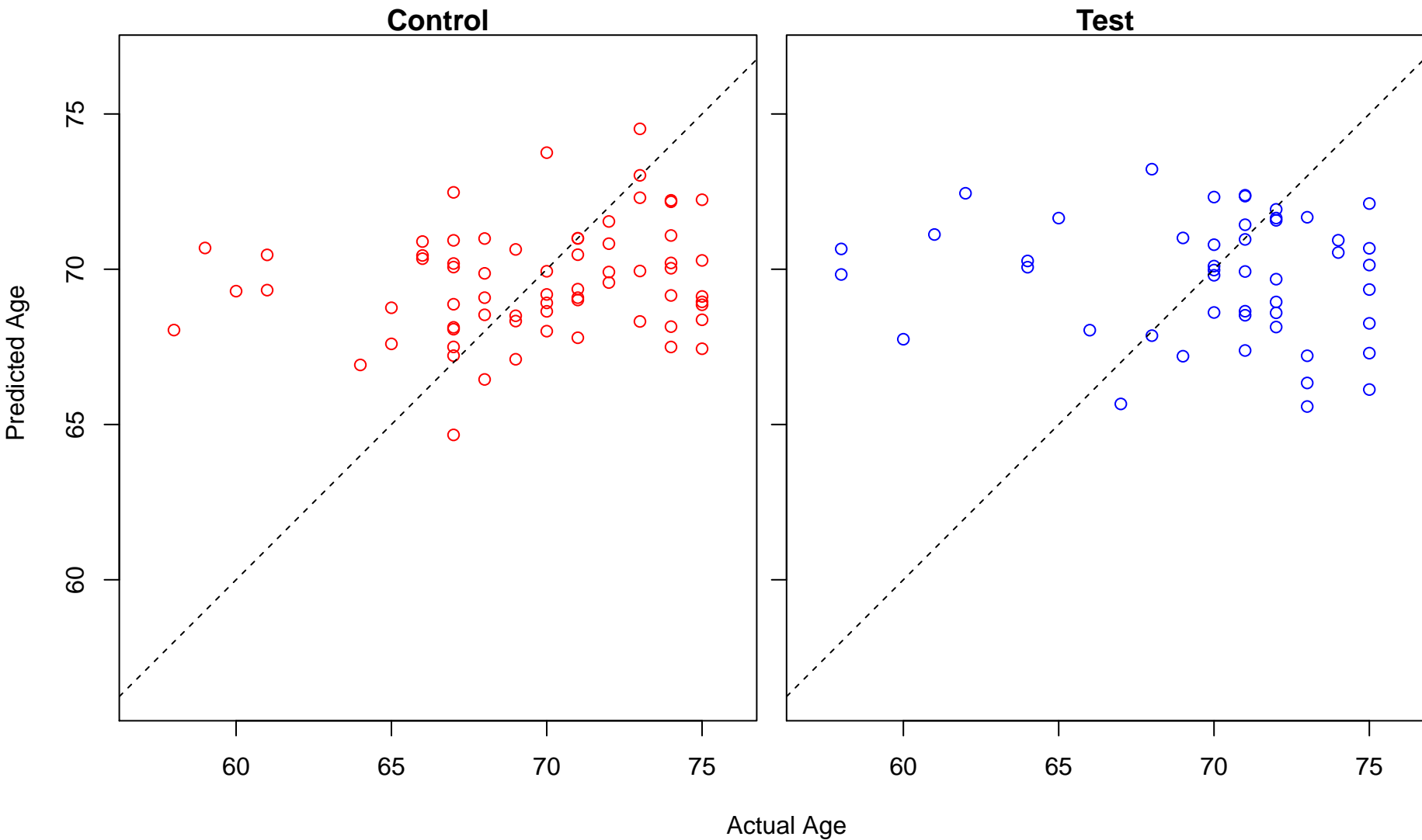


Actual Age

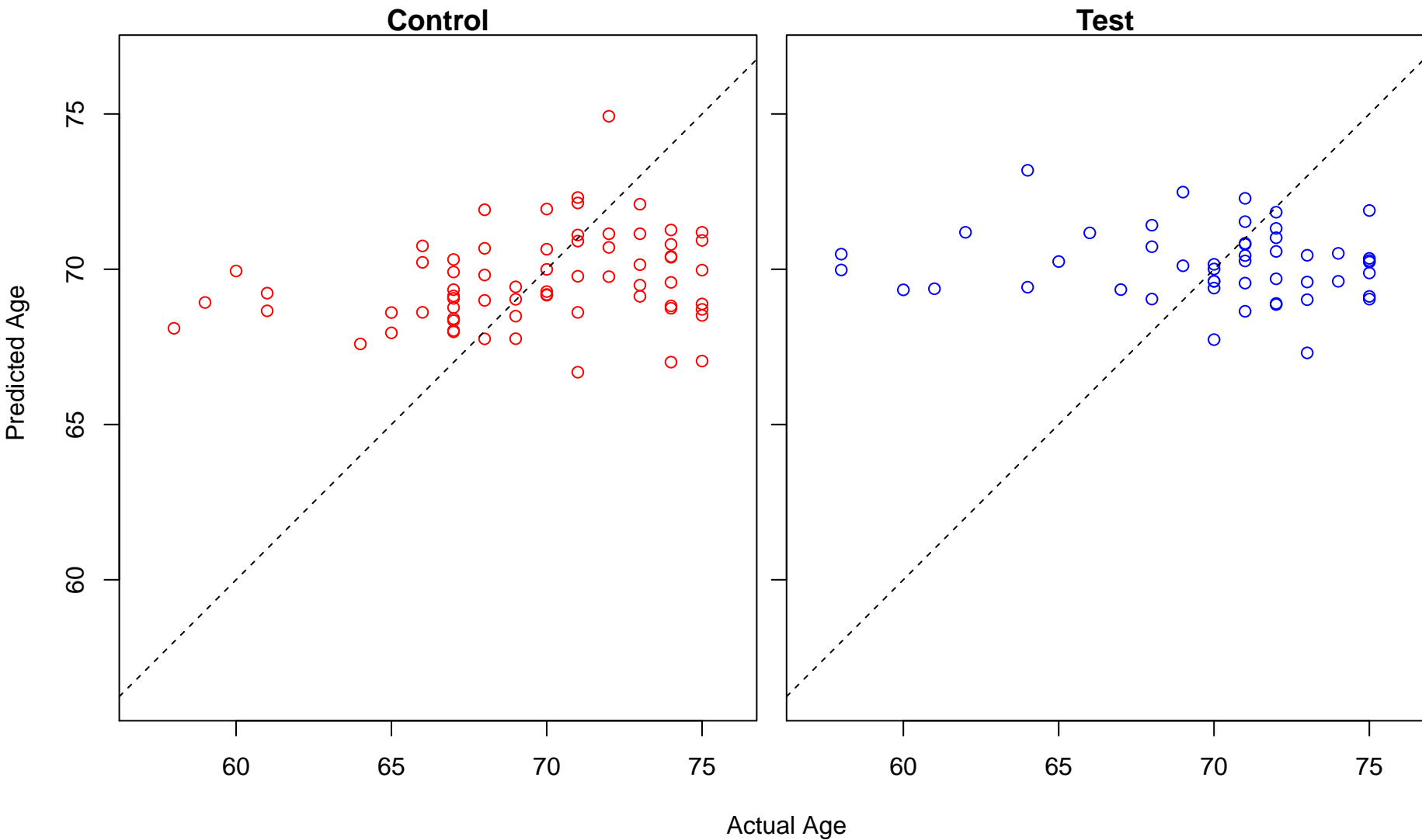
adenylate cyclase-activating dopamine receptor signaling pathway (Score: 0.194550)



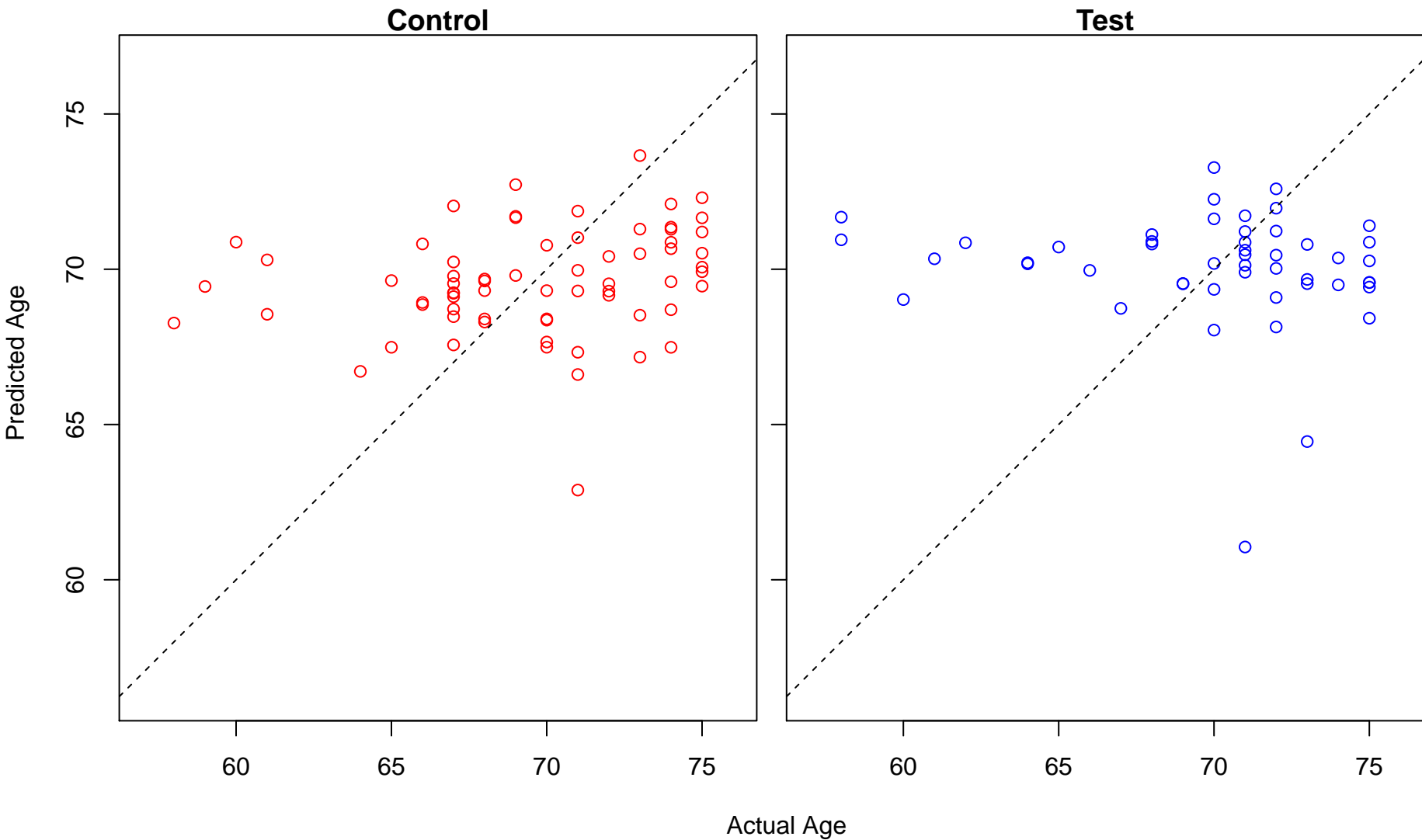
positive regulation of action potential (Score: 0.191578)



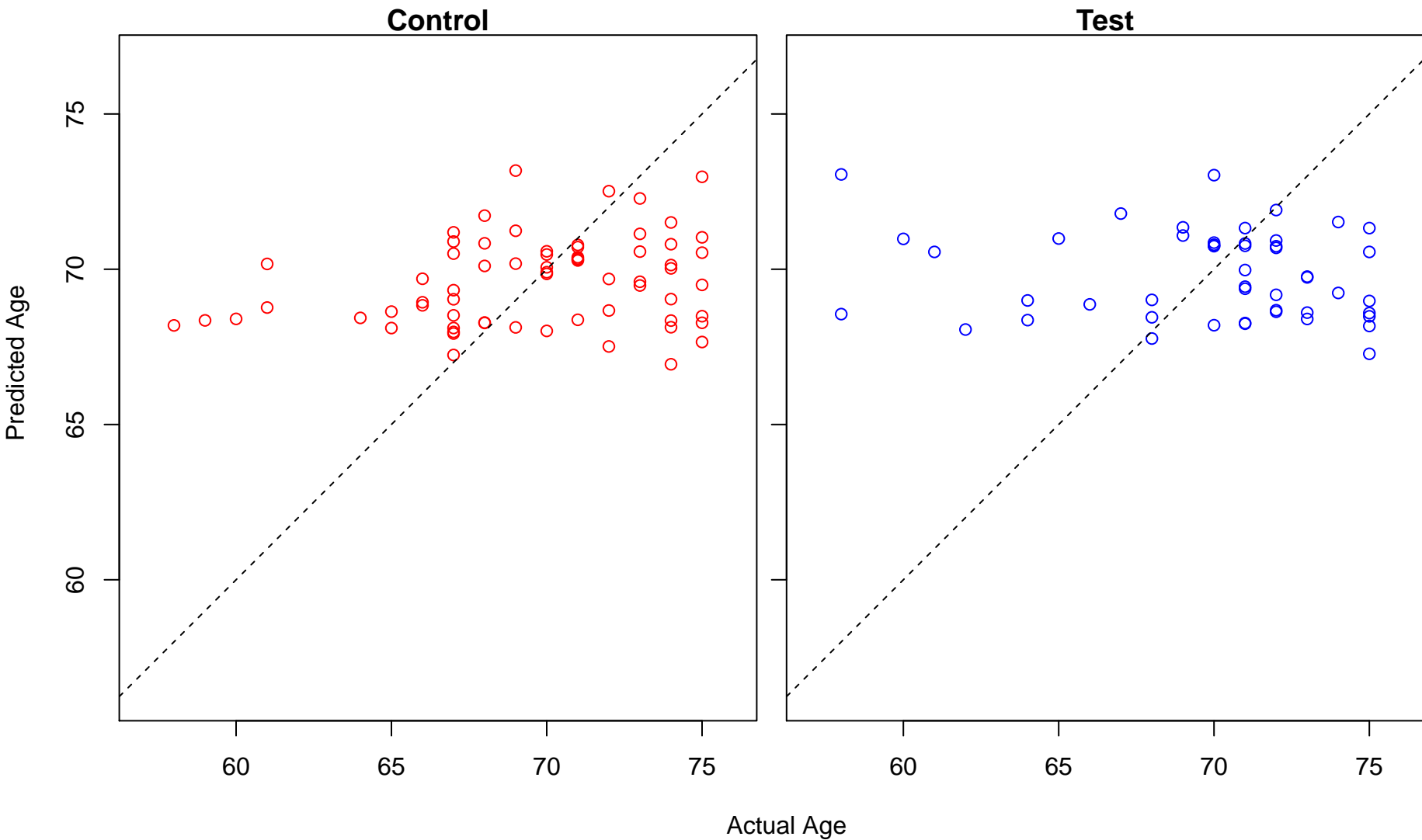
ureter development (Score: 0.191329)



detection of chemical stimulus involved in sensory perception of taste (Score: 0.191322)

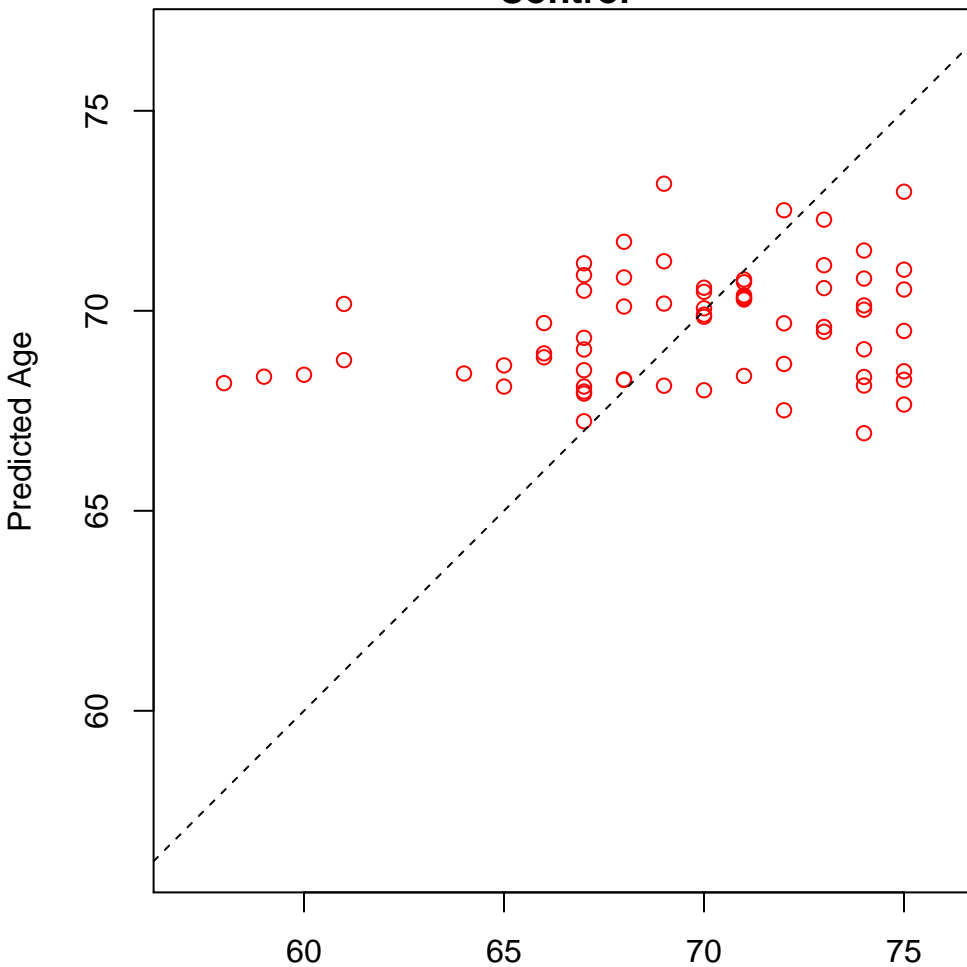


regulation of acrosome reaction (Score: 0.188816)

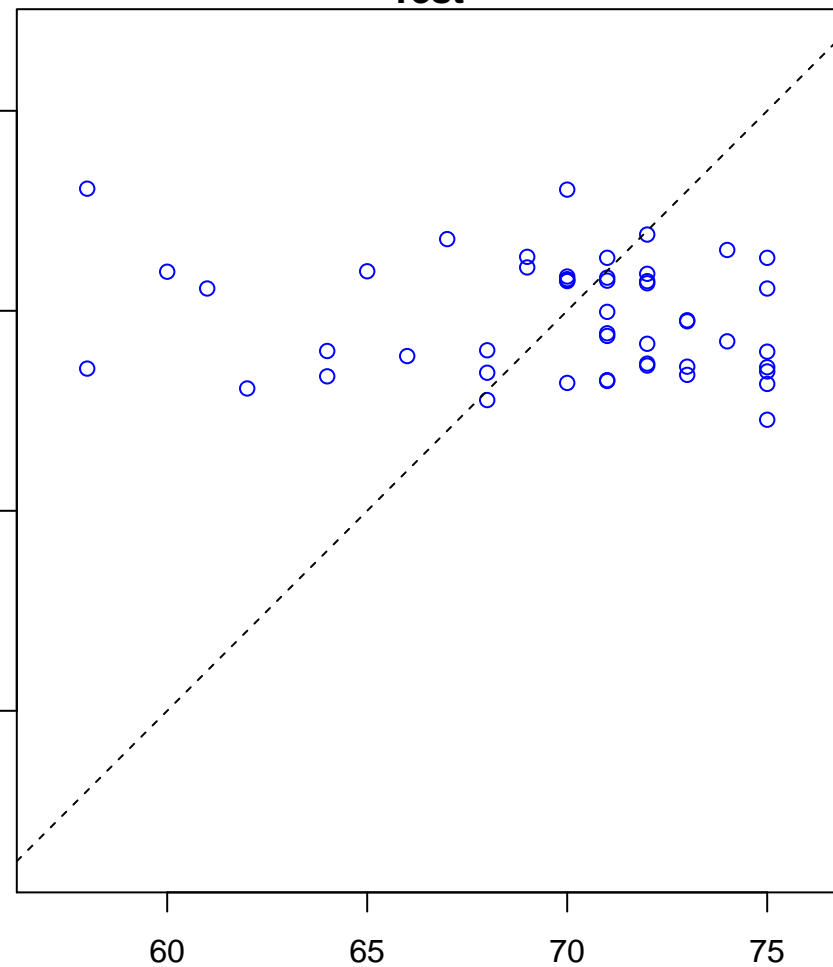


positive regulation of acrosome reaction (Score: 0.188816)

Control

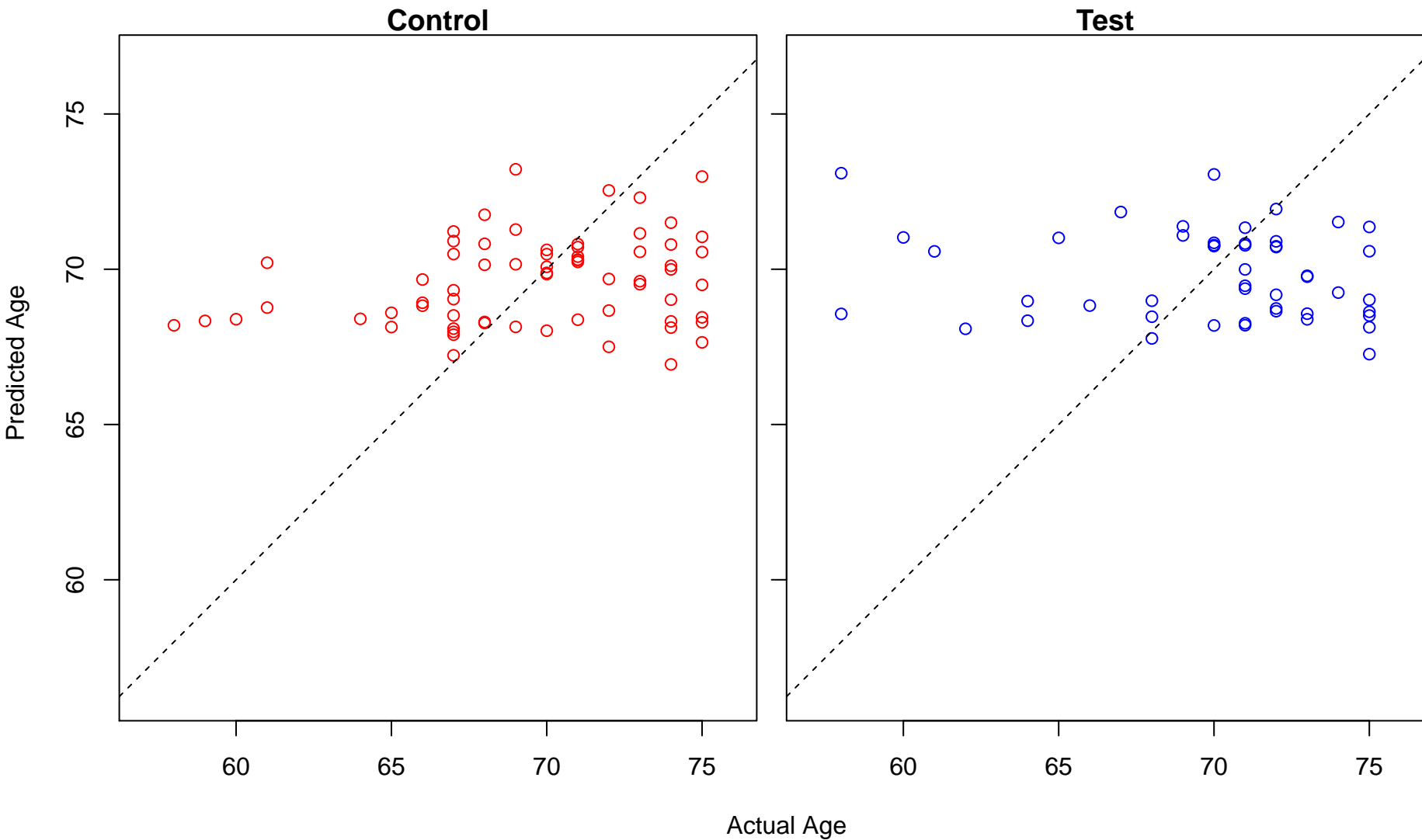


Test

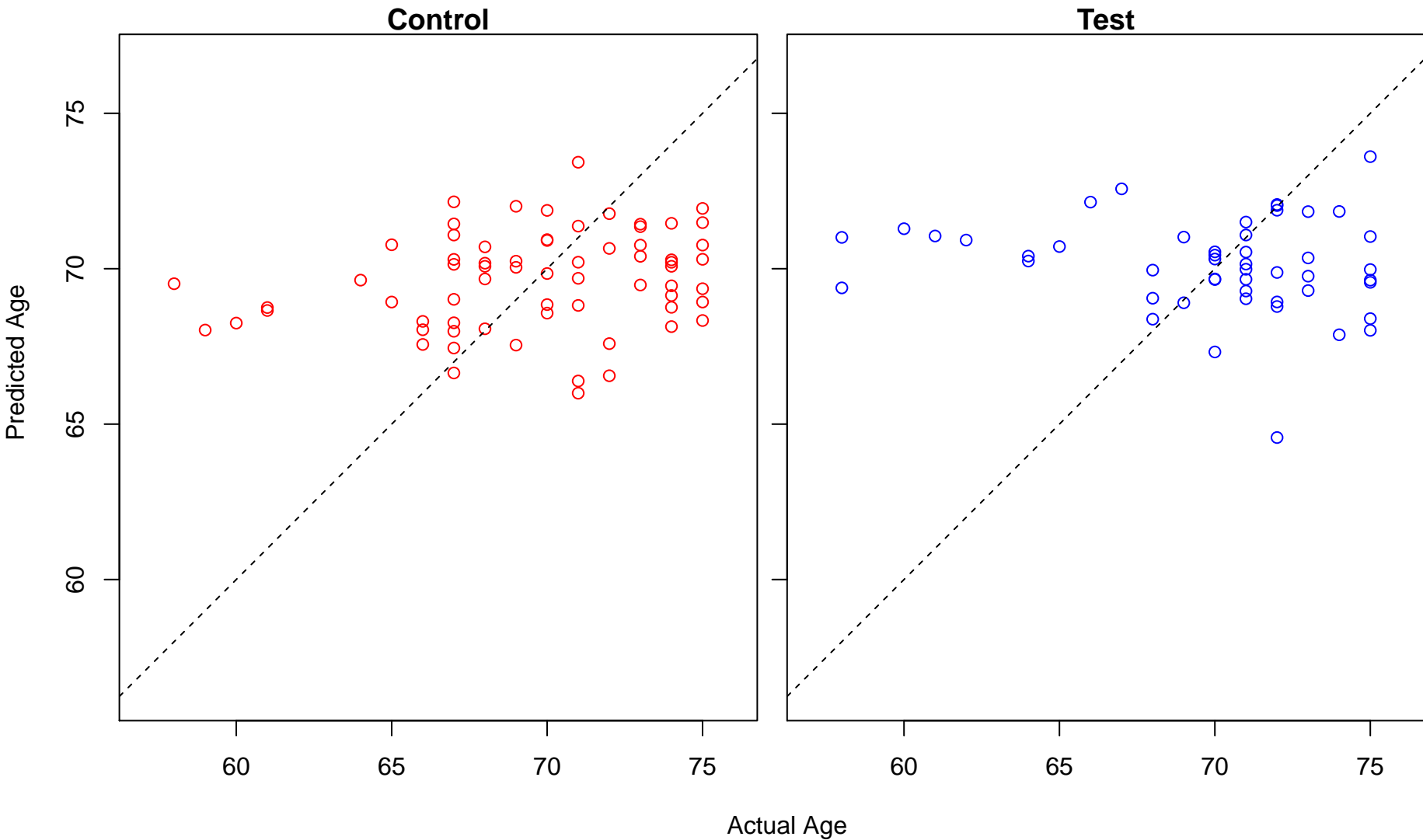


Actual Age

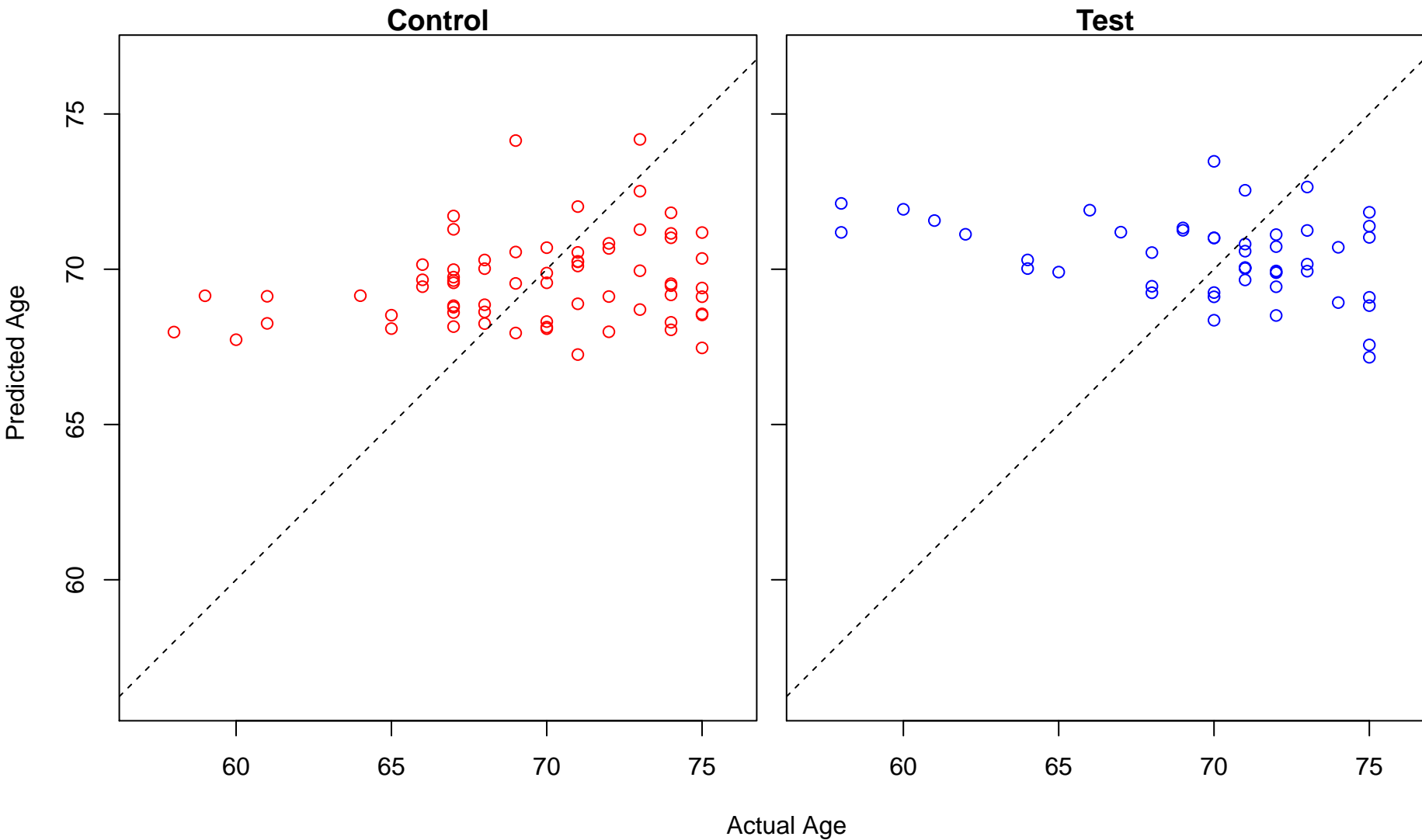
positive regulation of calcium ion-dependent exocytosis (Score: 0.188647)



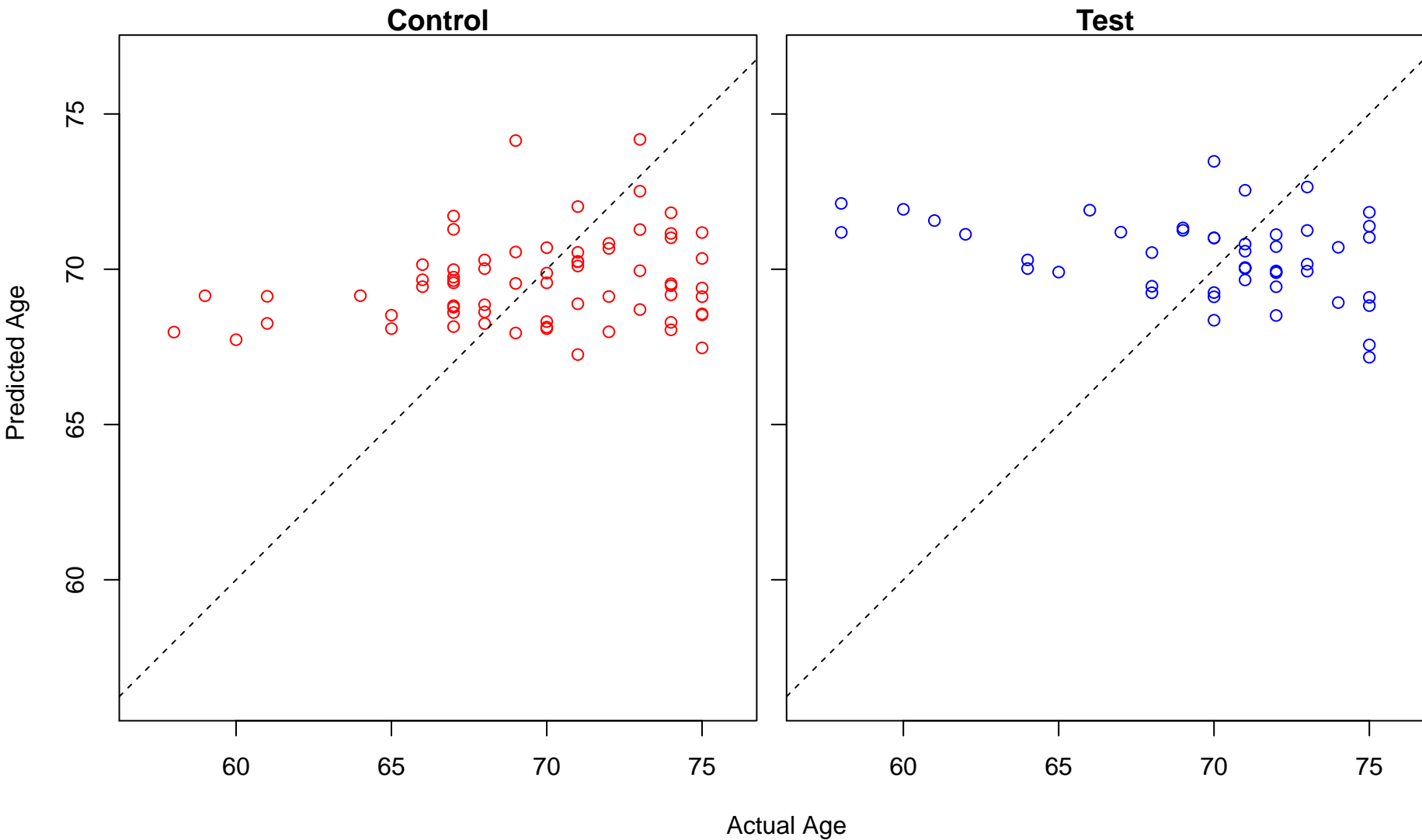
secondary metabolite biosynthetic process (Score: 0.188443)



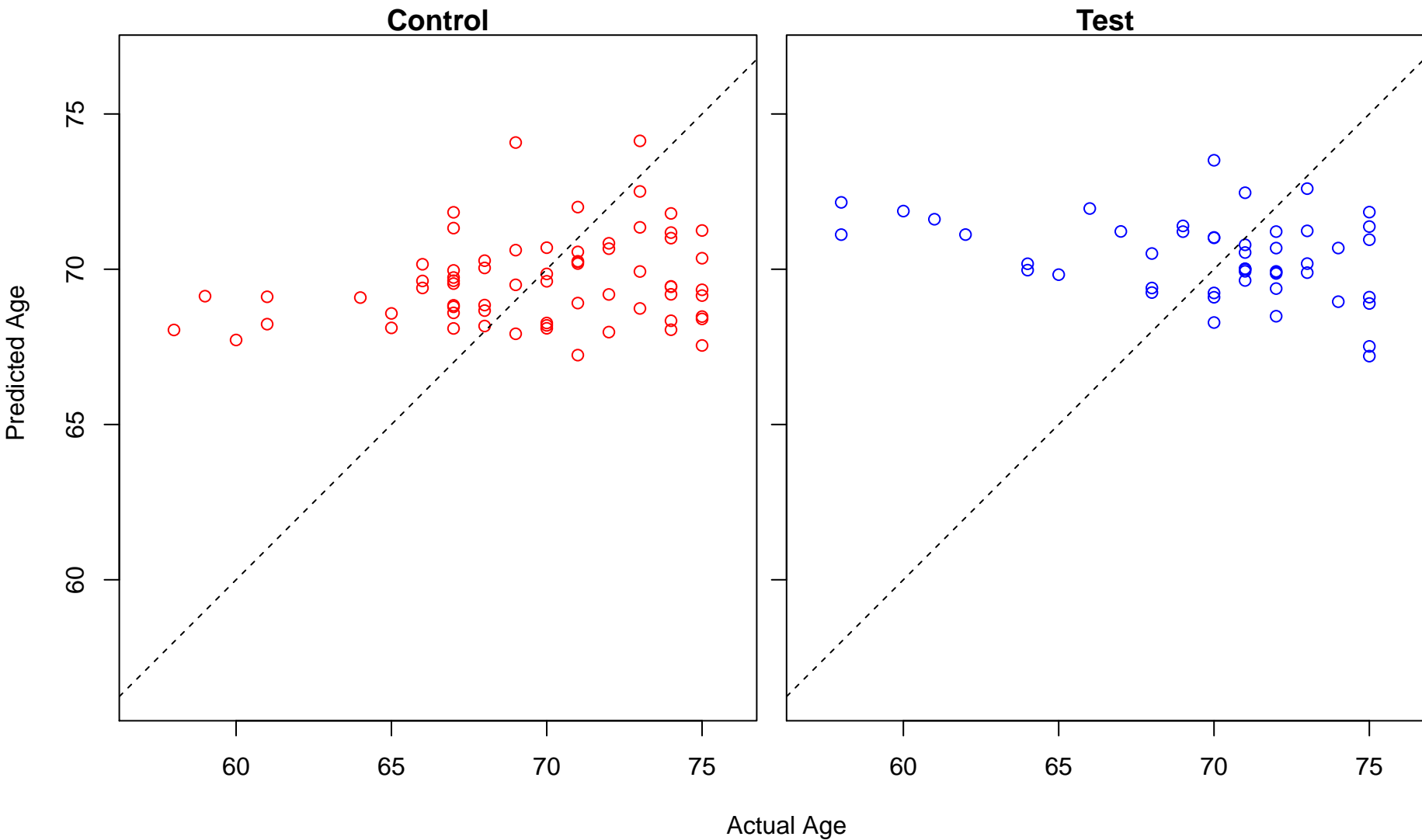
glycosphingolipid catabolic process (Score: 0.187259)



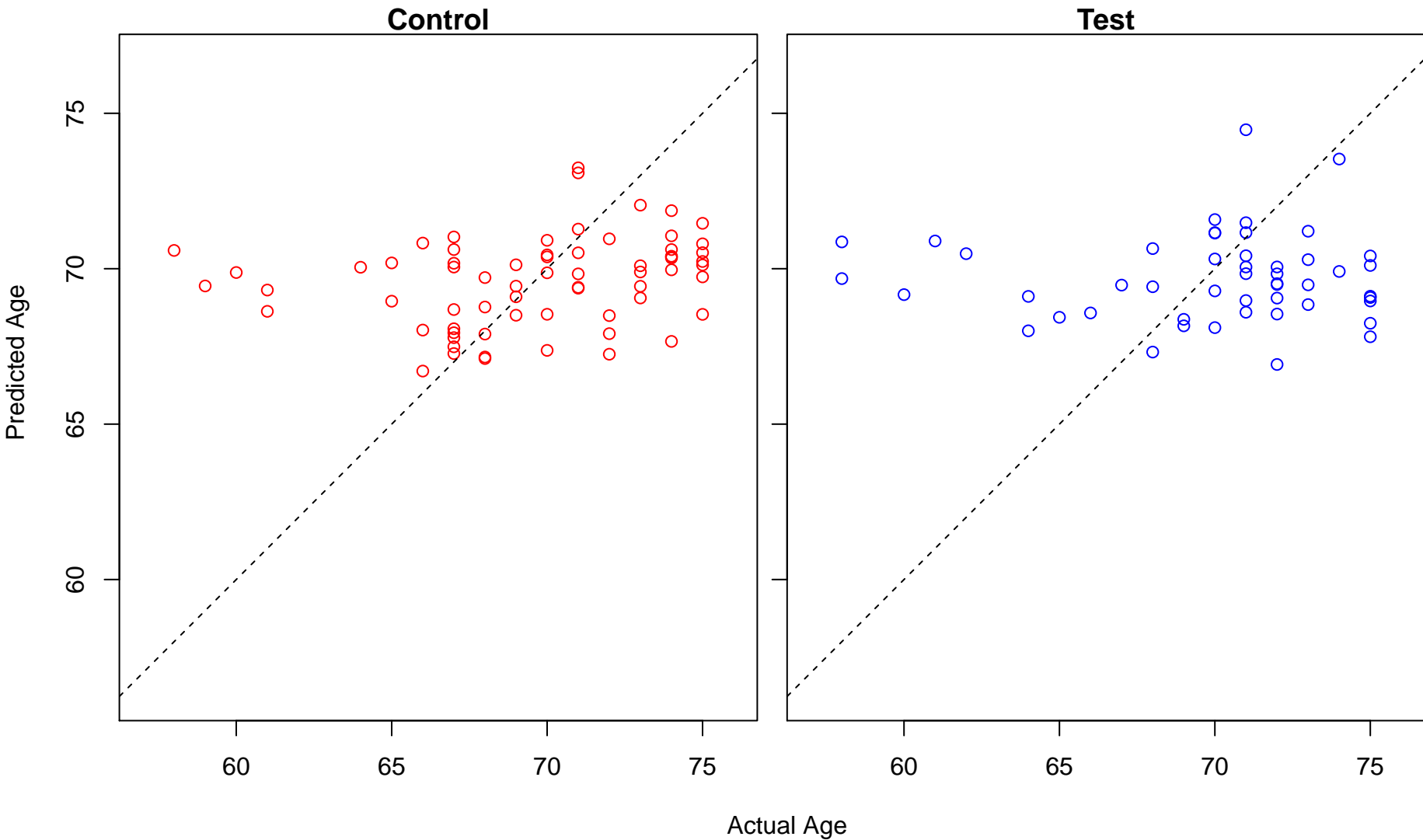
ceramide catabolic process (Score: 0.187259)



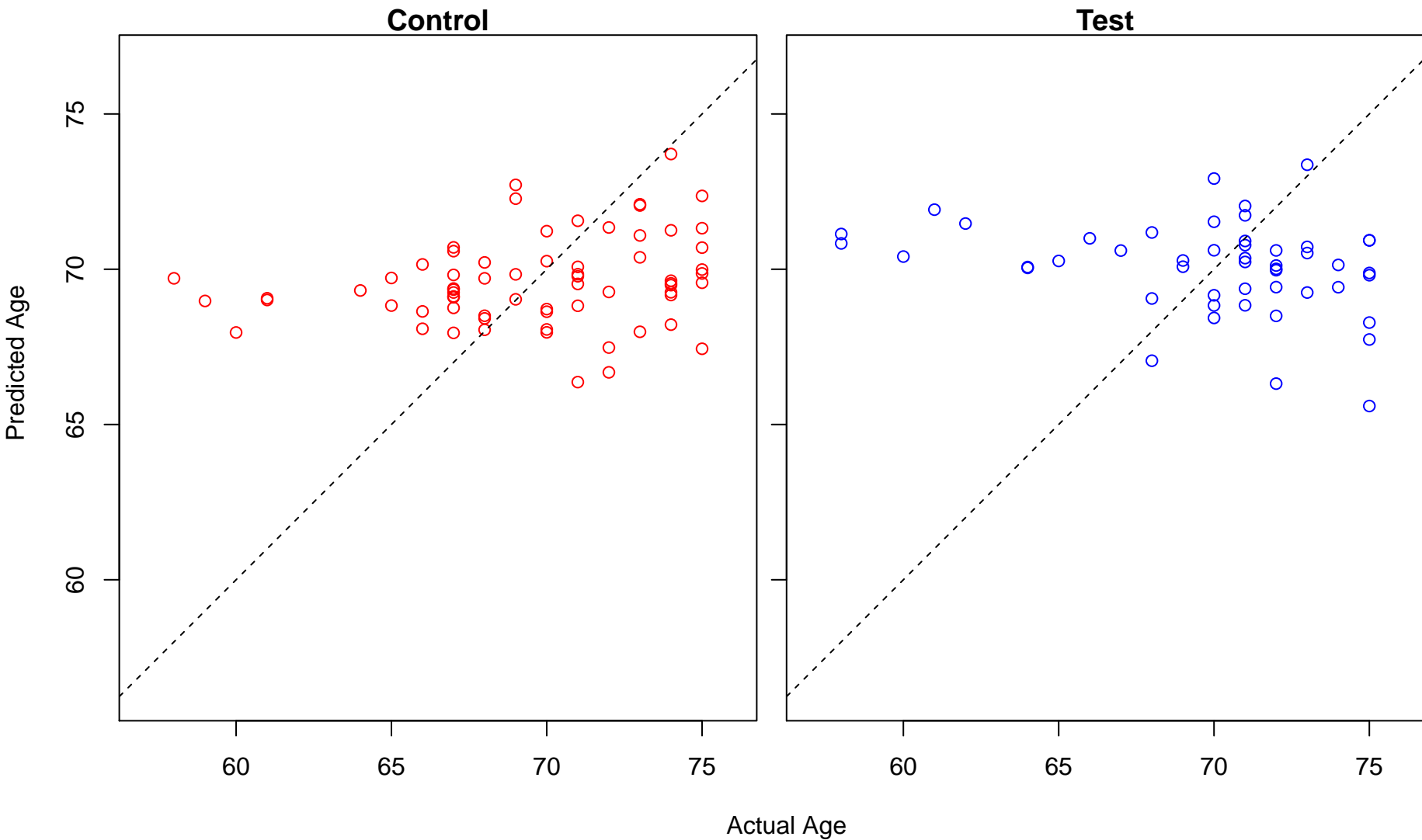
glycolipid catabolic process (Score: 0.186400)



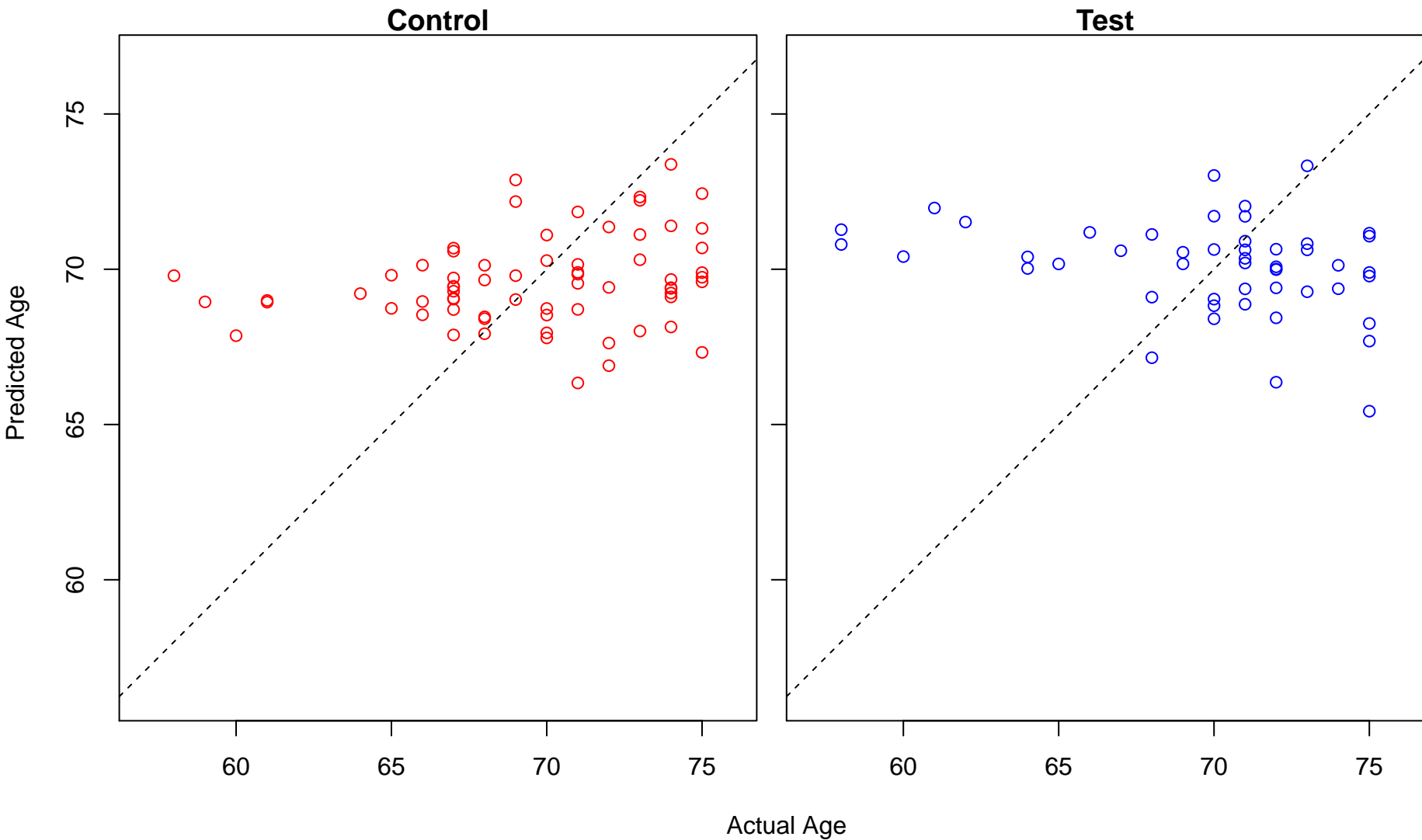
regulation of translational initiation by eIF2 alpha phosphorylation (Score: 0.185737)



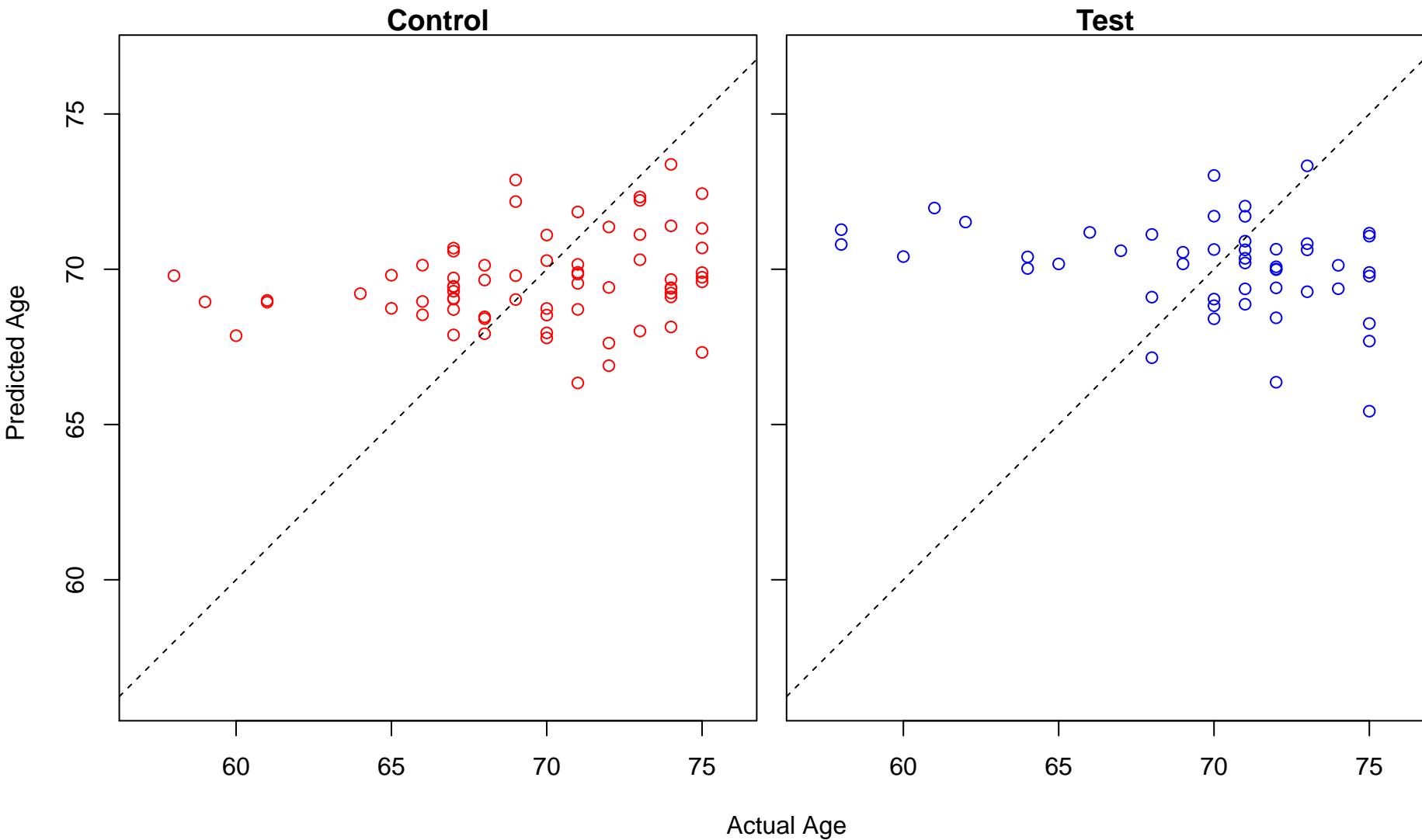
protein geranylgeranylation (Score: 0.185453)



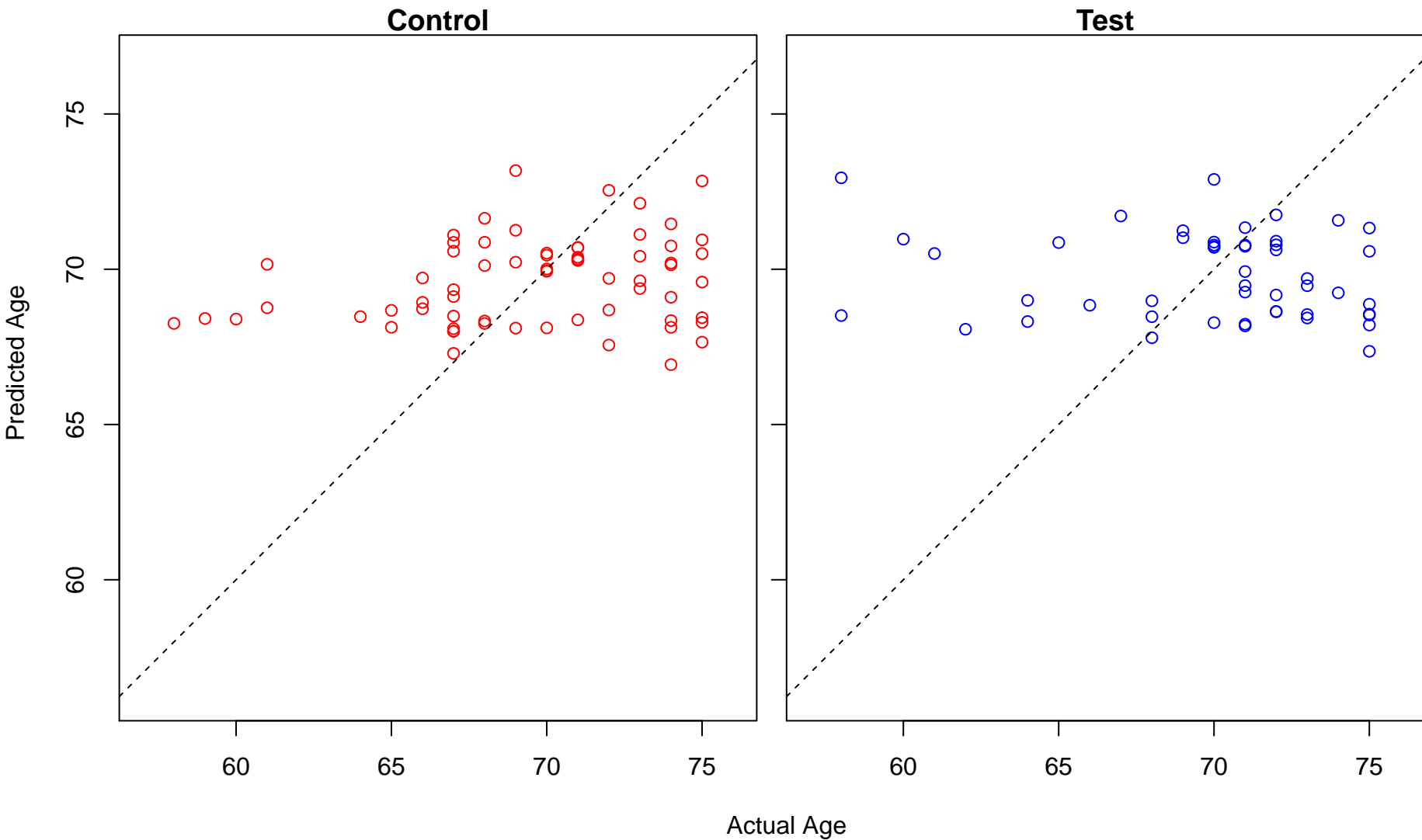
protein prenylation (Score: 0.184294)



prenylation (Score: 0.184294)

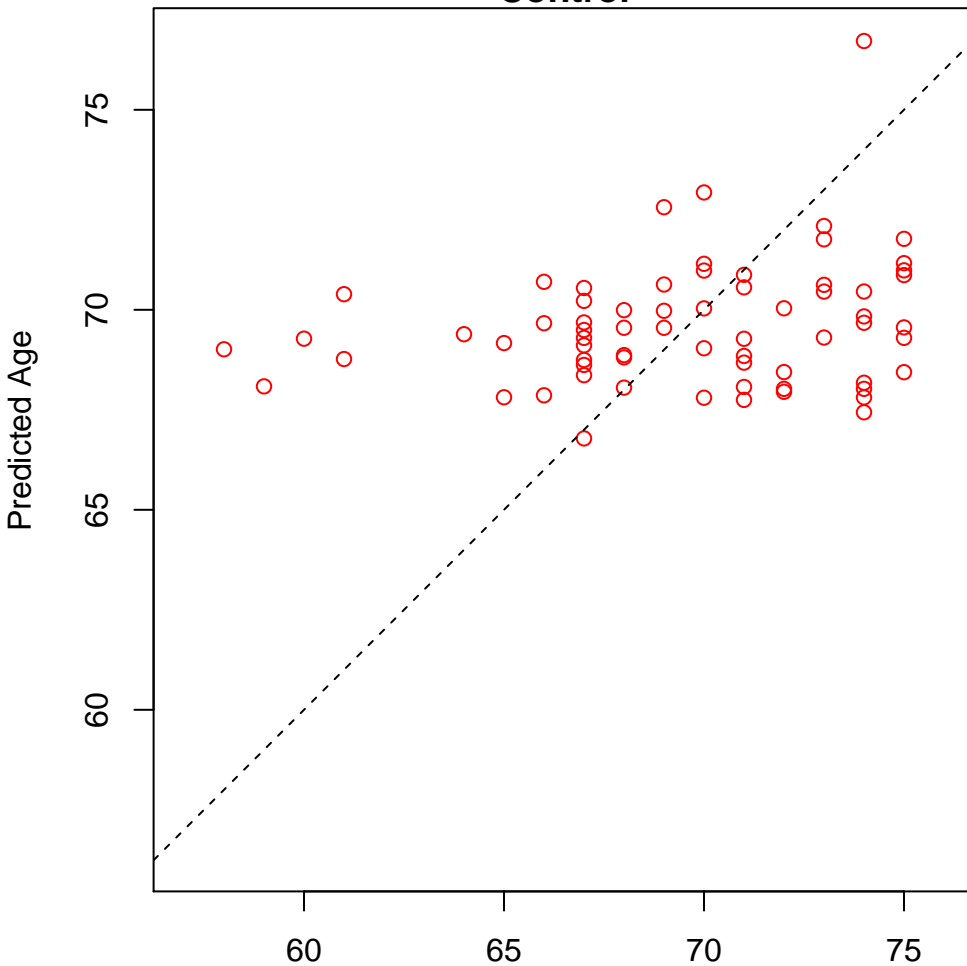


oocyte differentiation (Score: 0.180455)

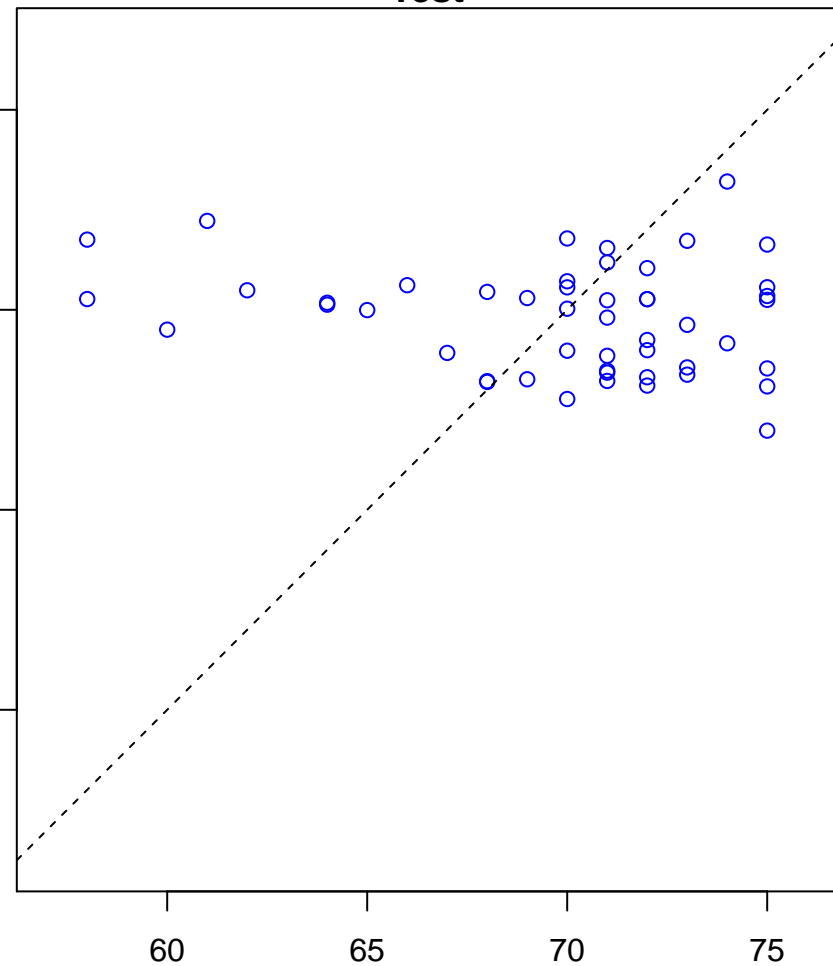


eyelid development in camera-type eye (Score: 0.178946)

Control

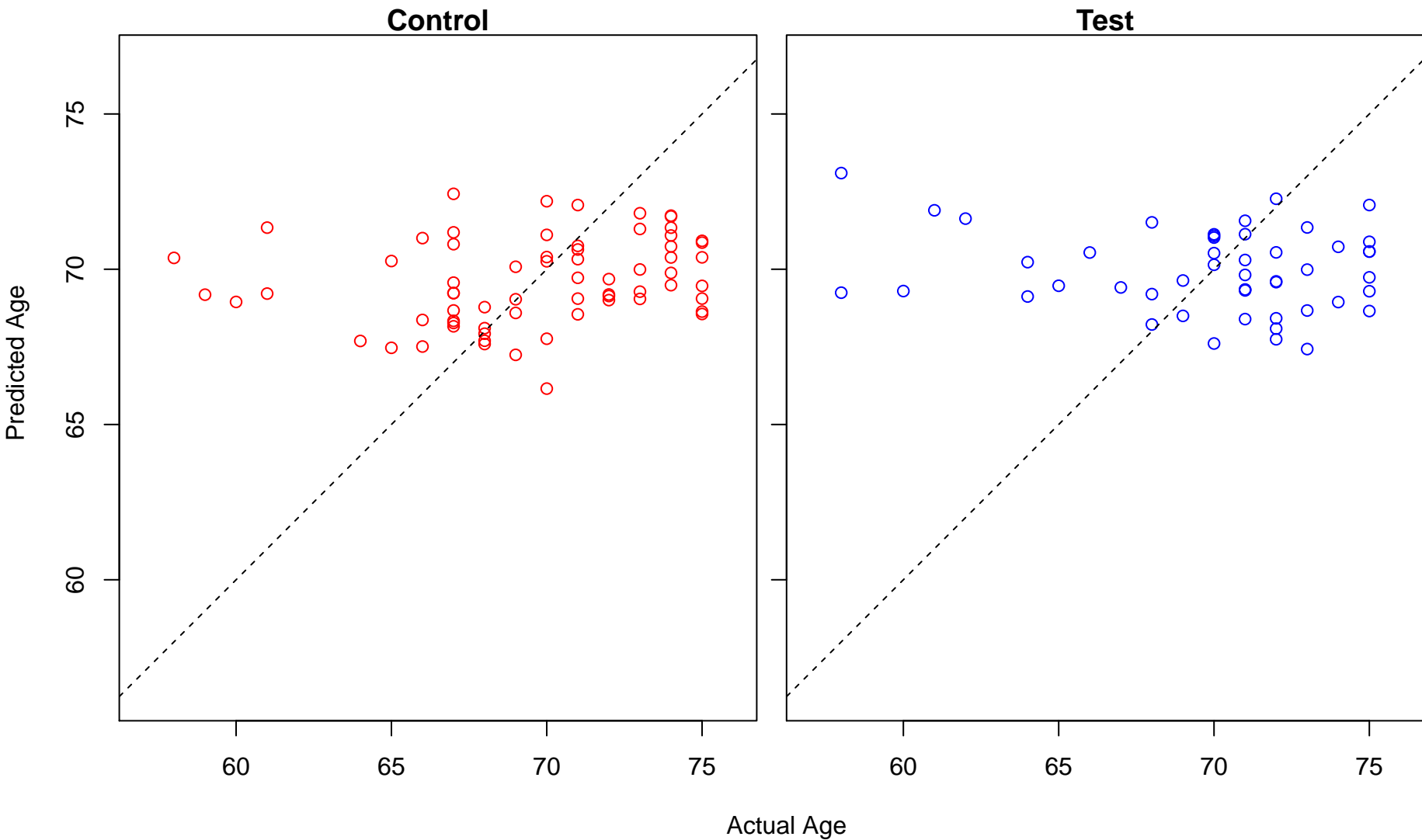


Test

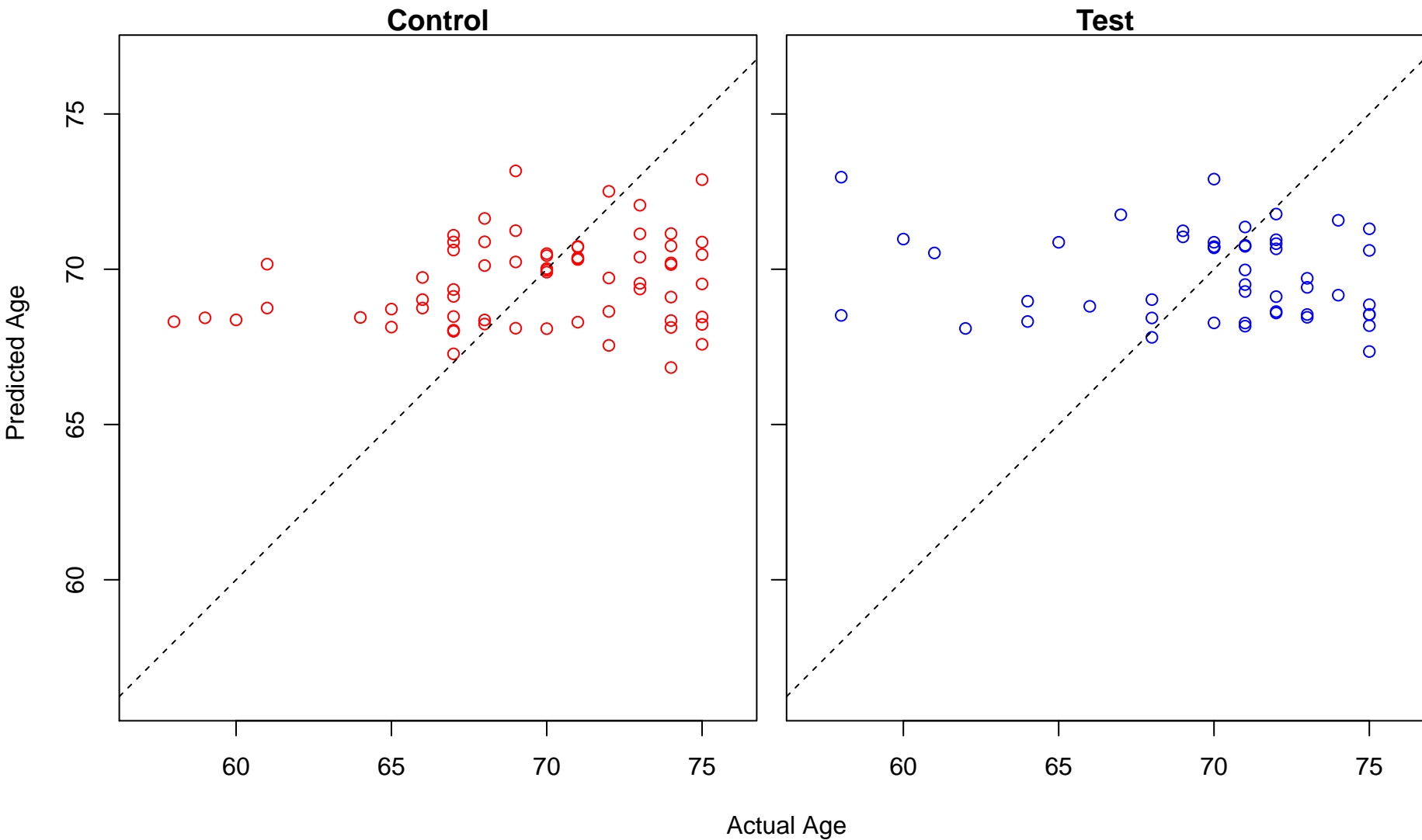


Actual Age

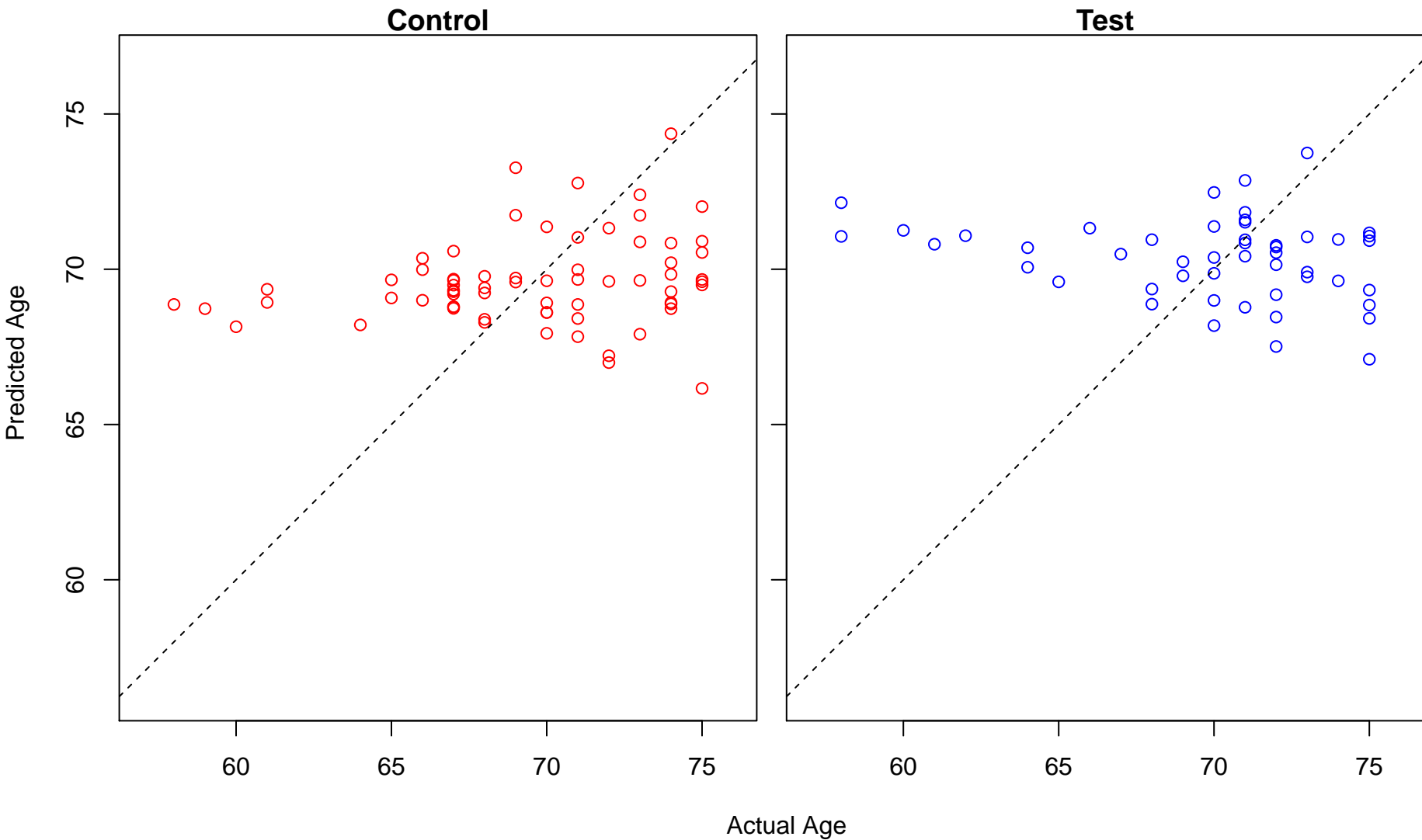
renal filtration (Score: 0.169992)



oogenesis (Score: 0.168370)

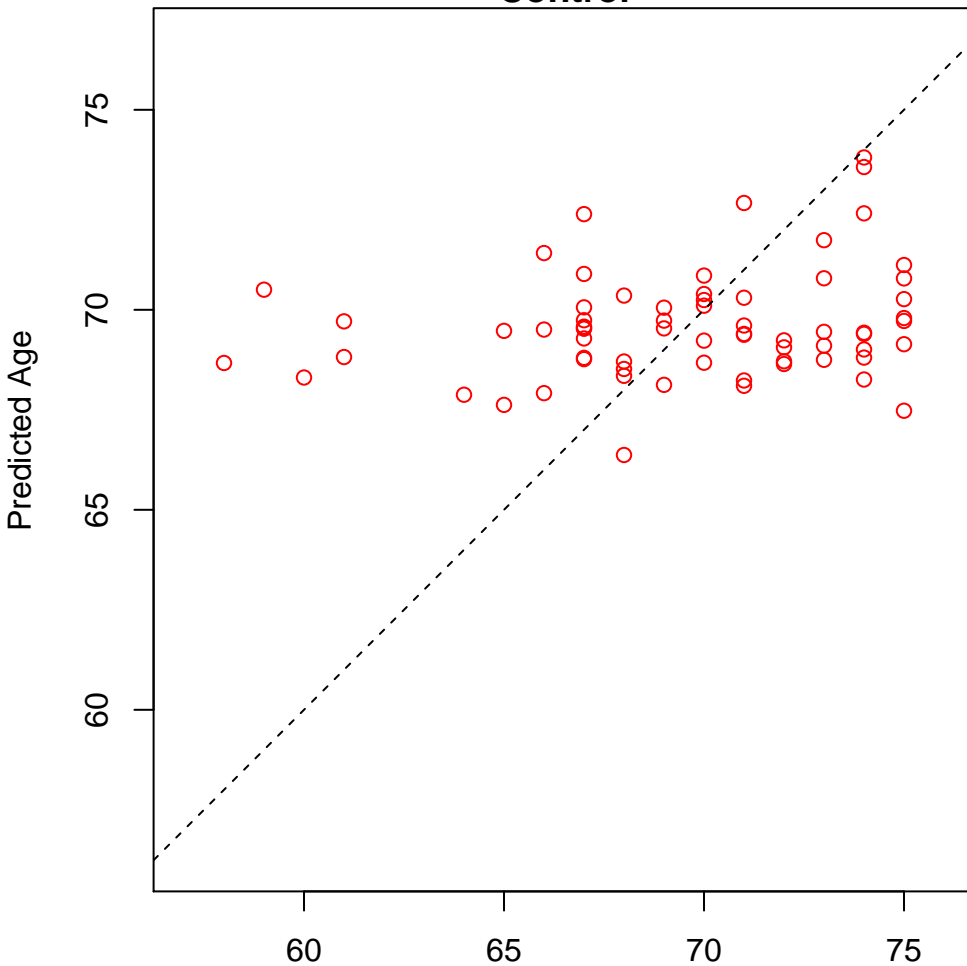


regulation of calcineurin–NFAT signaling cascade (Score: 0.166581)

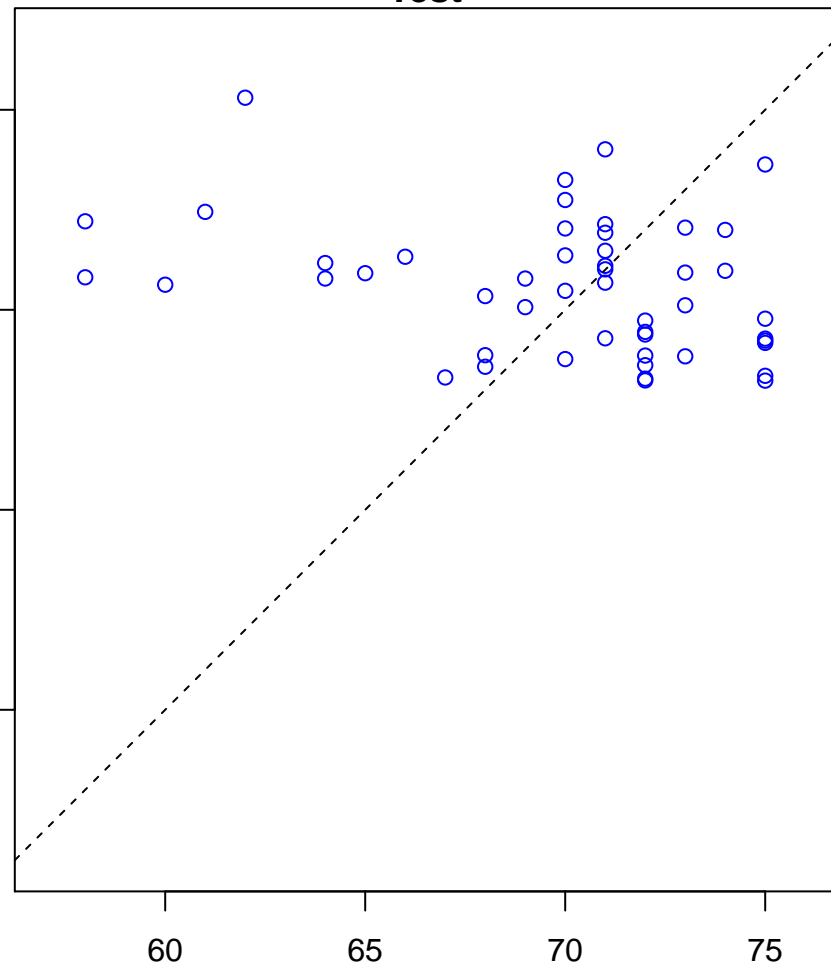


neuromuscular synaptic transmission (Score: 0.166370)

Control

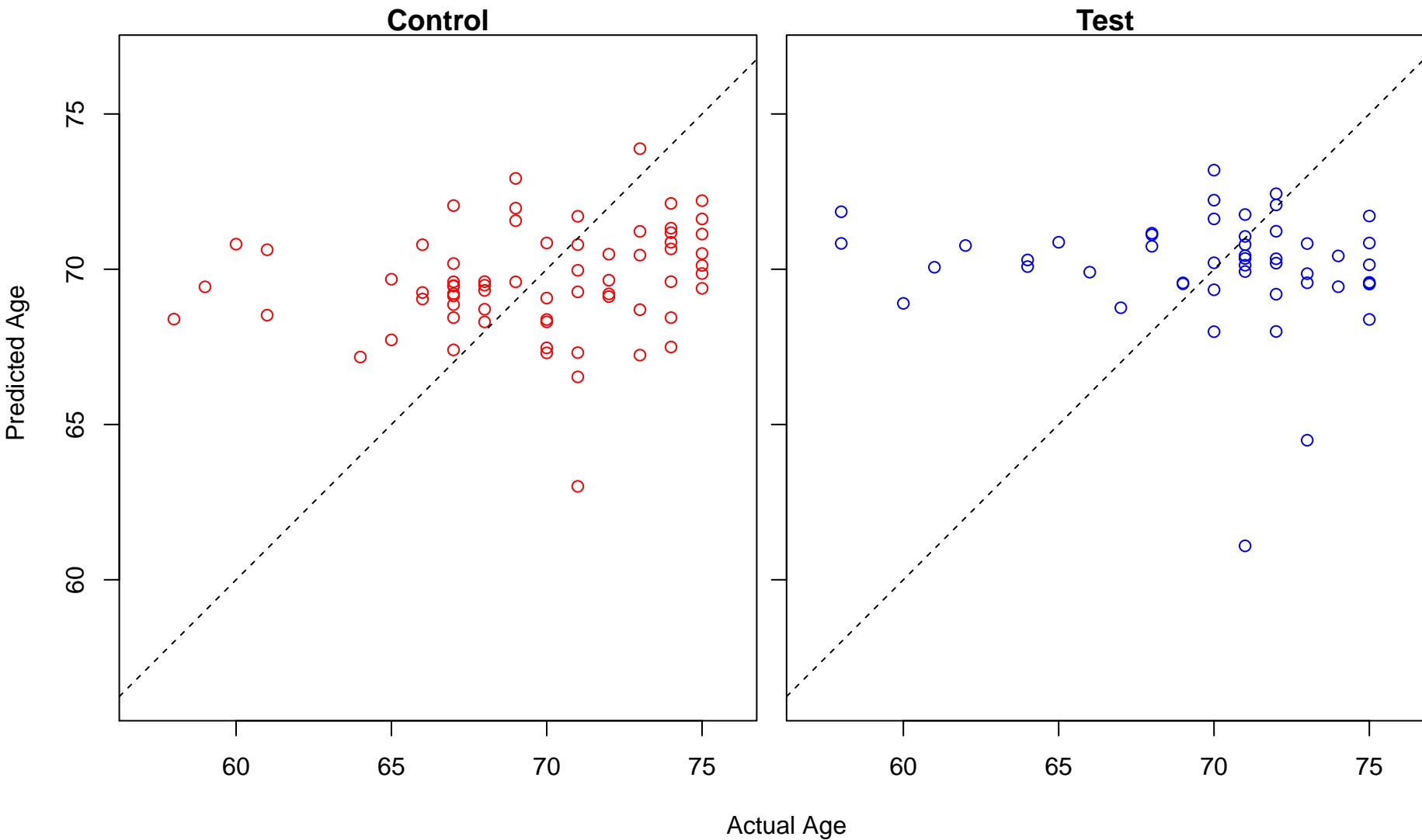


Test

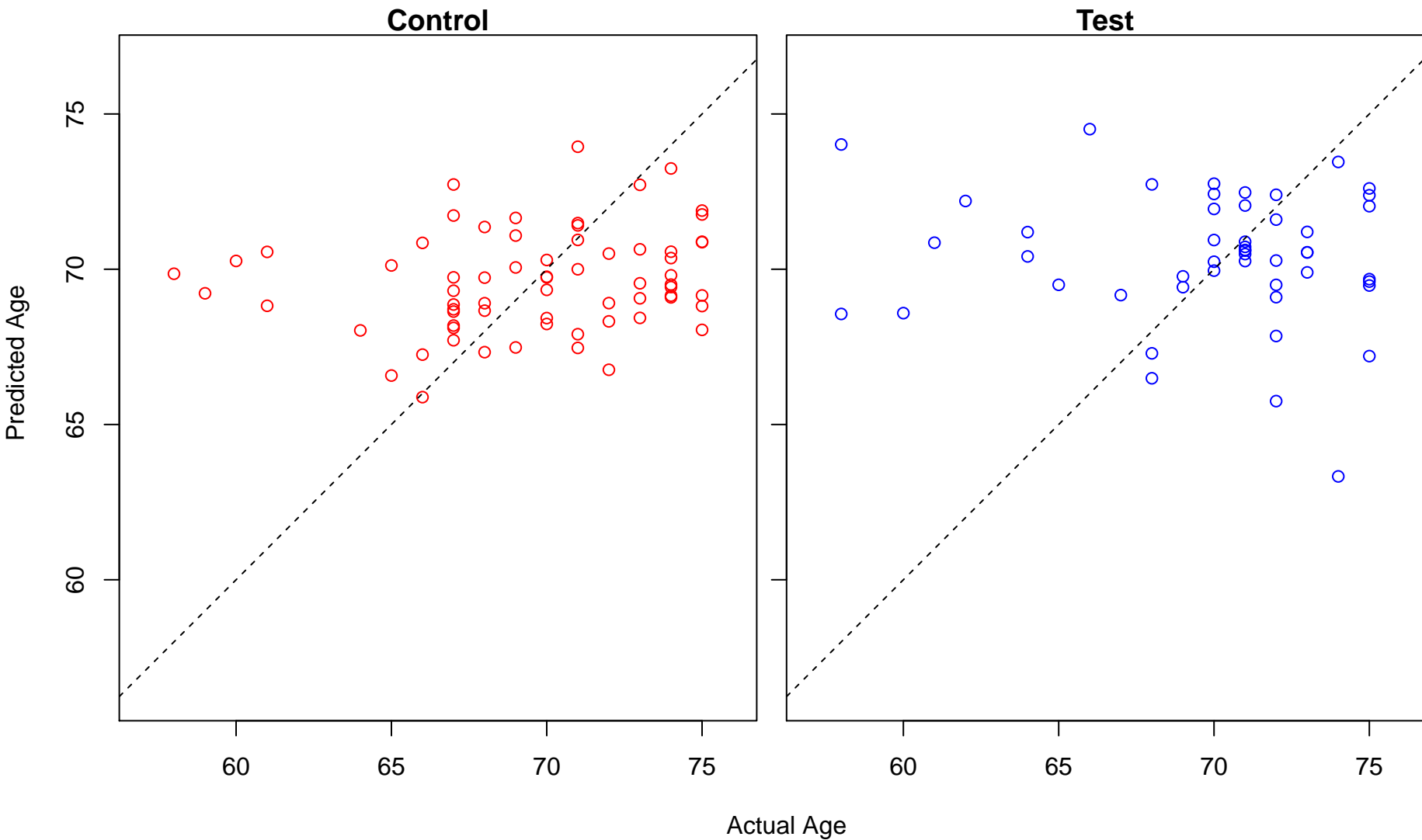


Actual Age

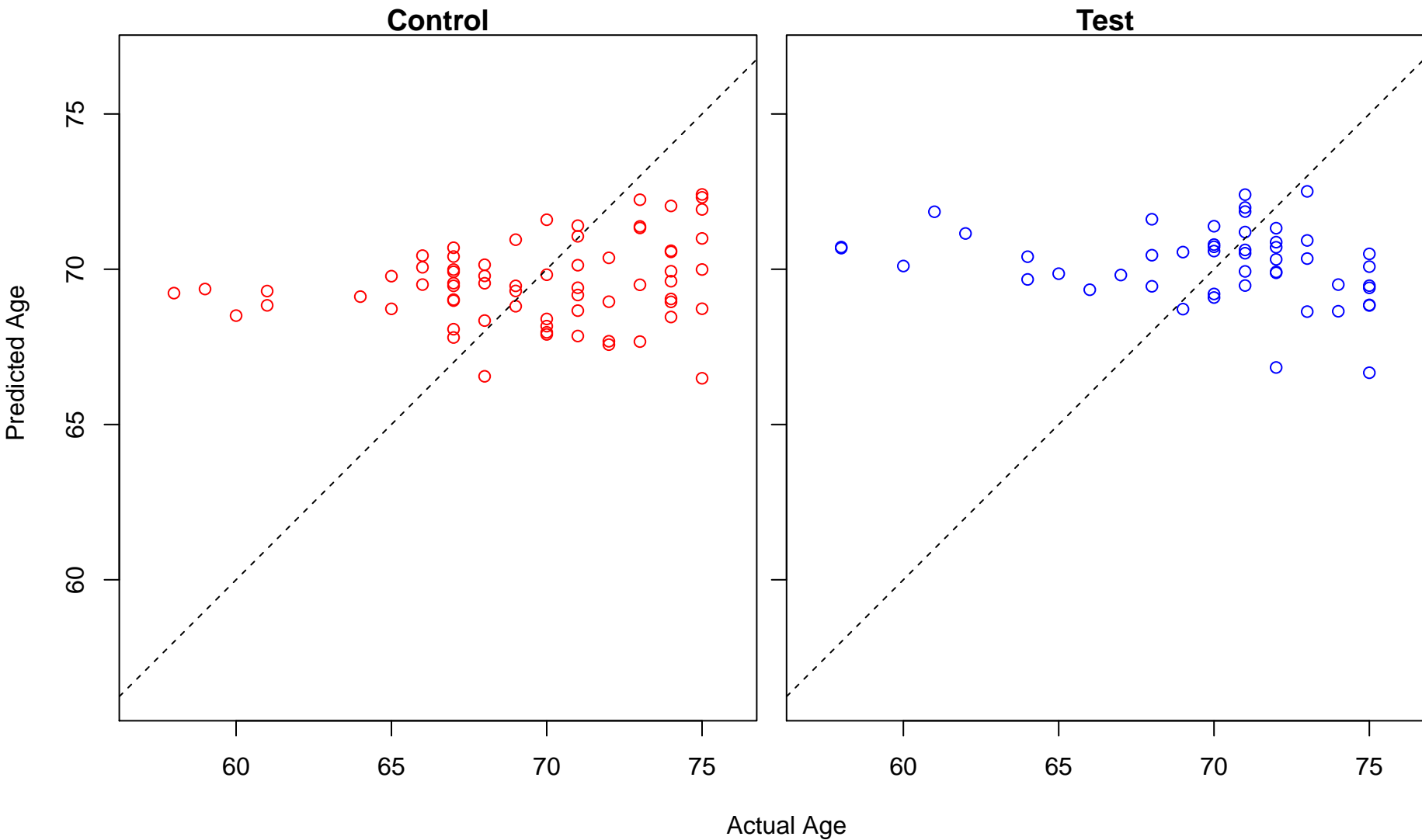
detection of chemical stimulus involved in sensory perception (Score: 0.160713)



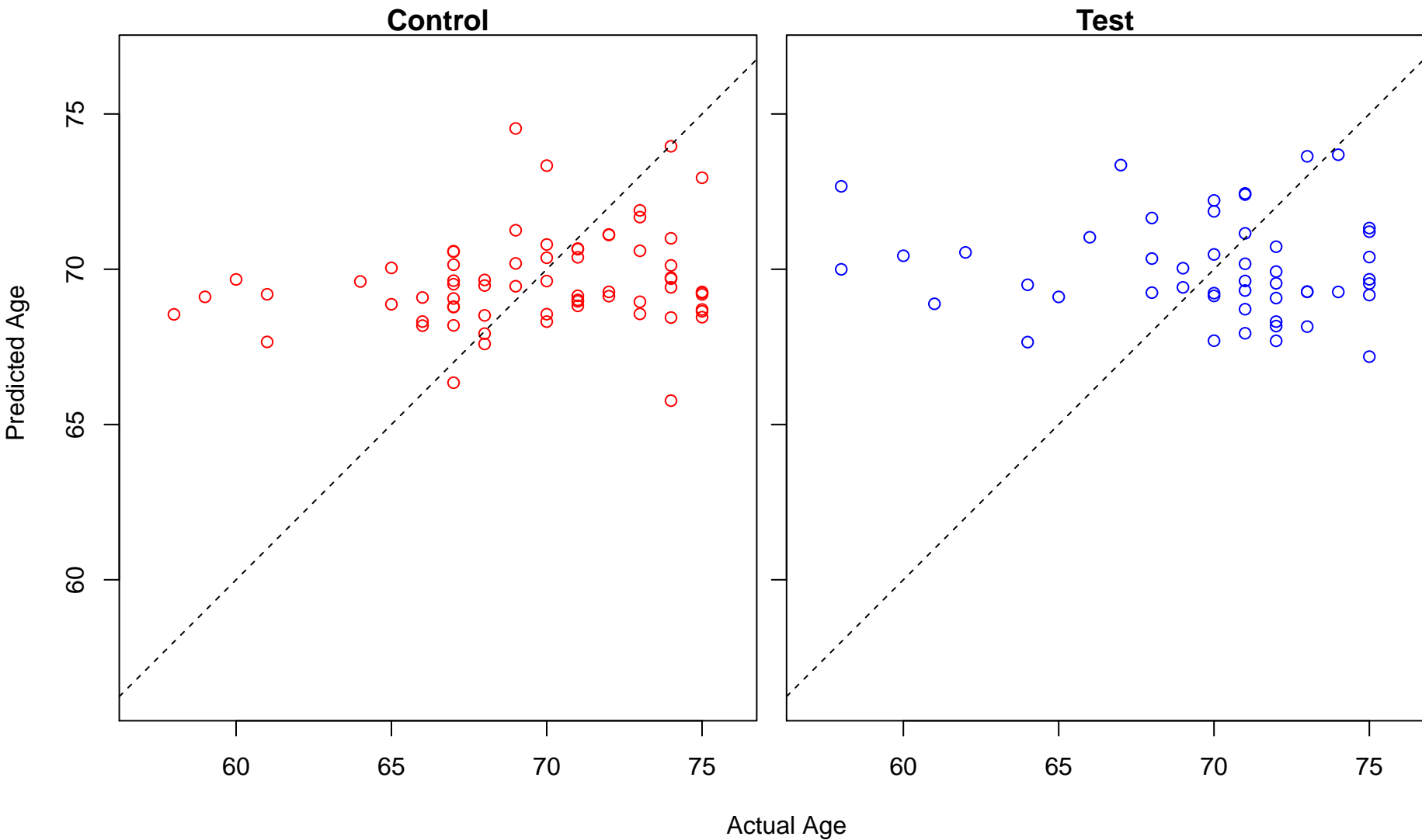
monoamine transport (Score: 0.158485)



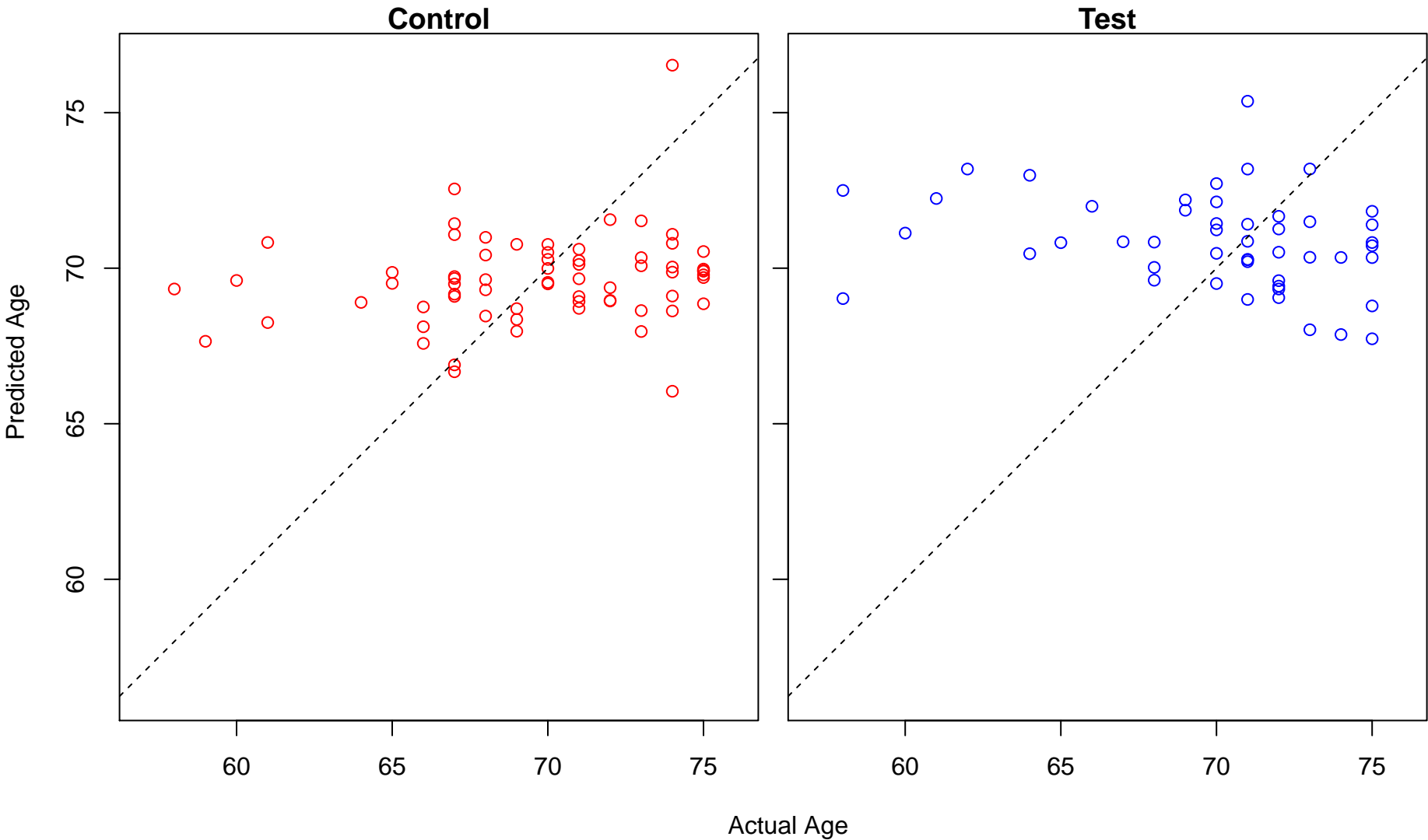
negative regulation of toll-like receptor 4 signaling pathway (Score: 0.158463)



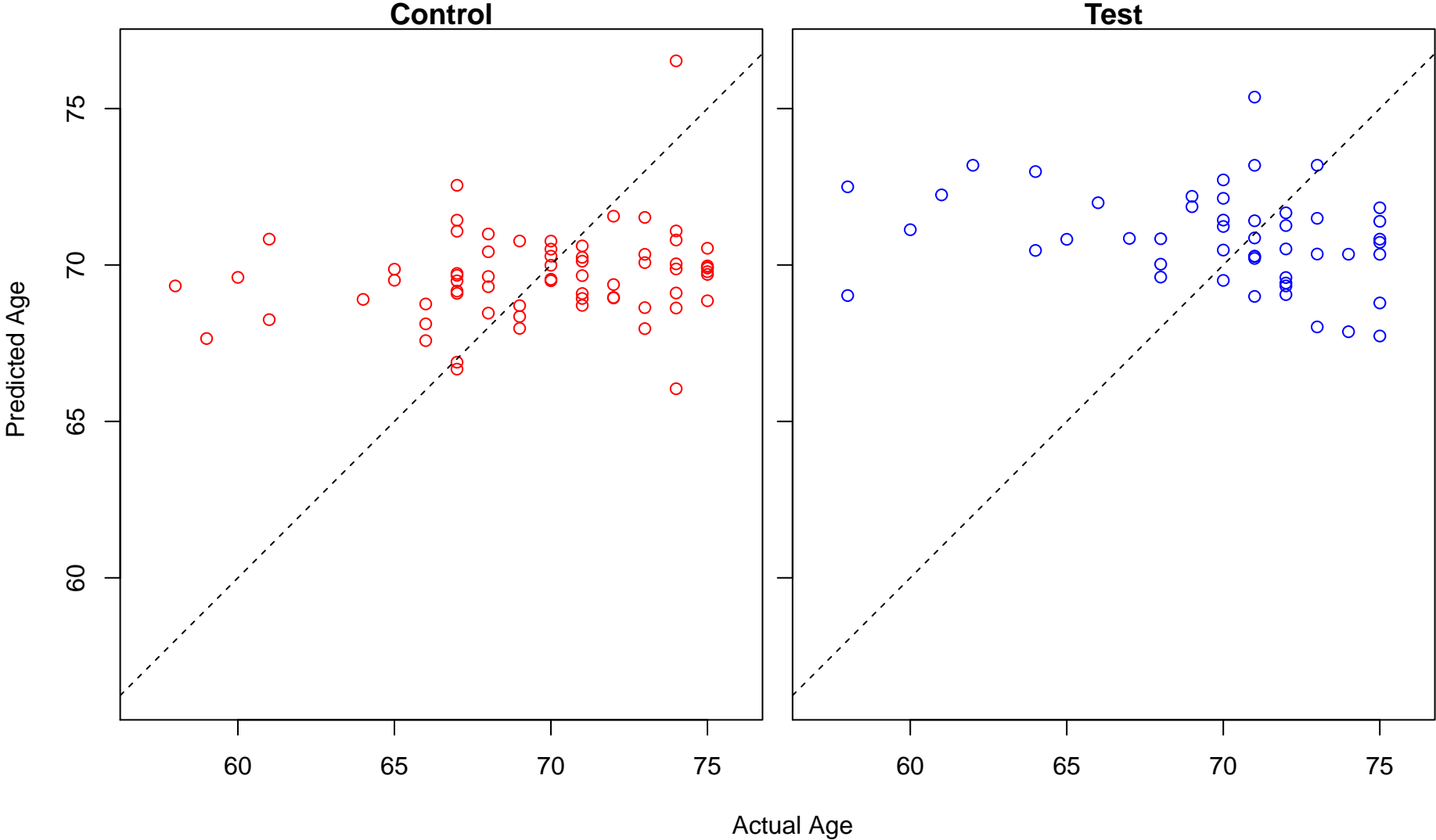
response to interleukin-2 (Score: 0.157748)



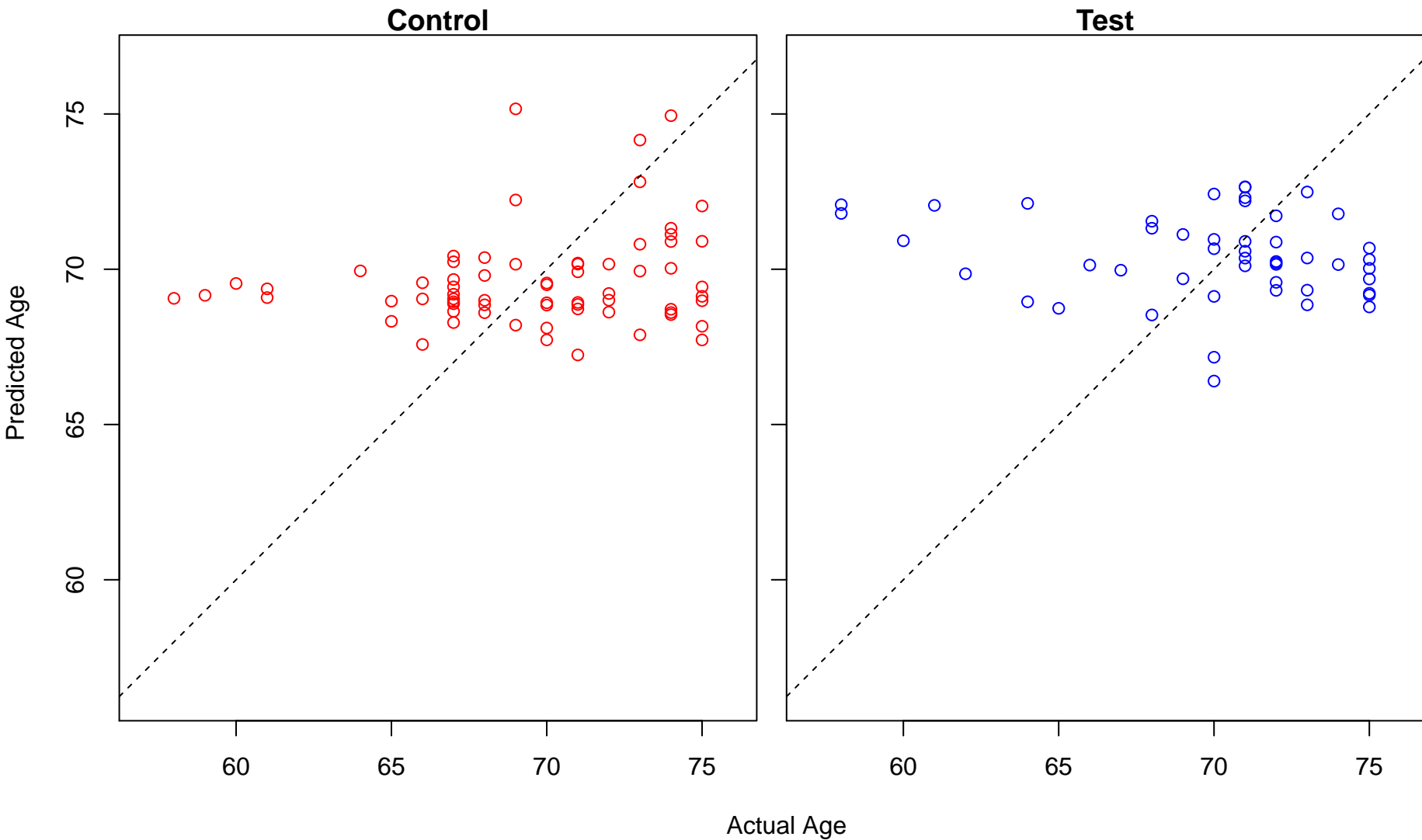
regulation of humoral immune response mediated by circulating immunoglobulin (Score: 0.150526)



negative regulation of humoral immune response mediated by circulating immunoglobulin (Score: 0.15)

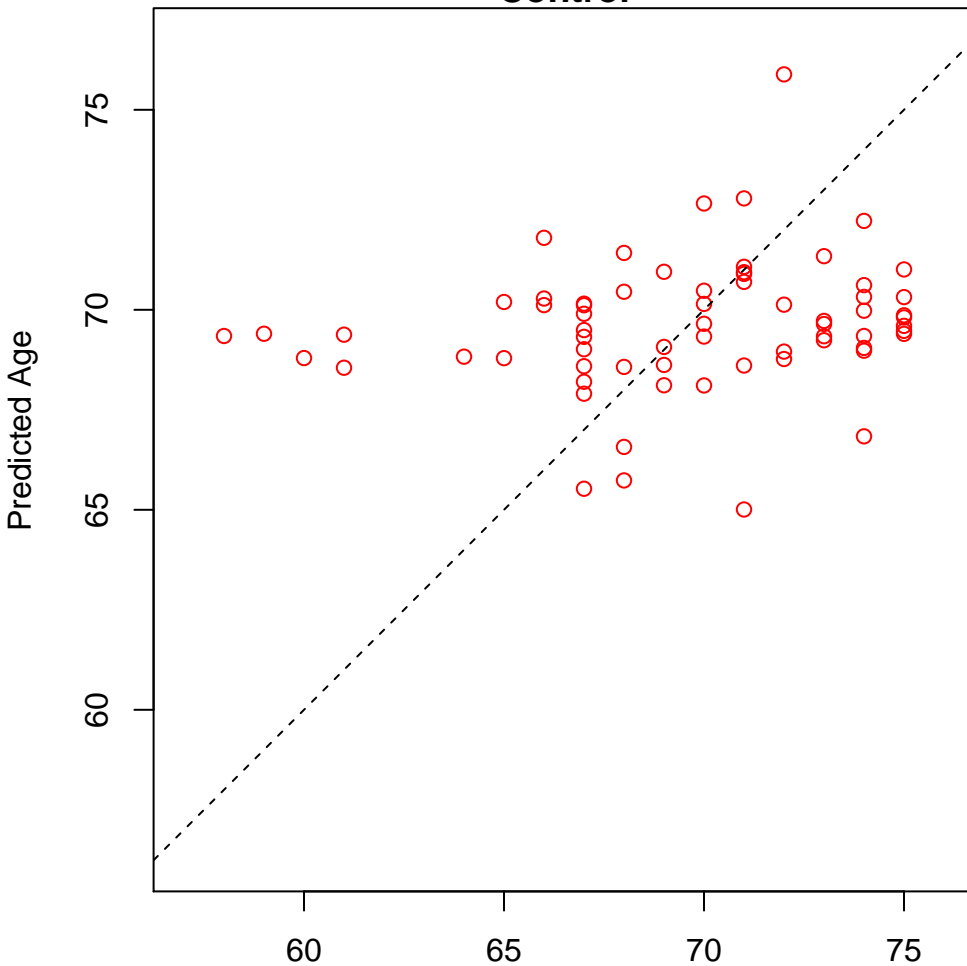


regulation of interleukin-2 secretion (Score: 0.149276)

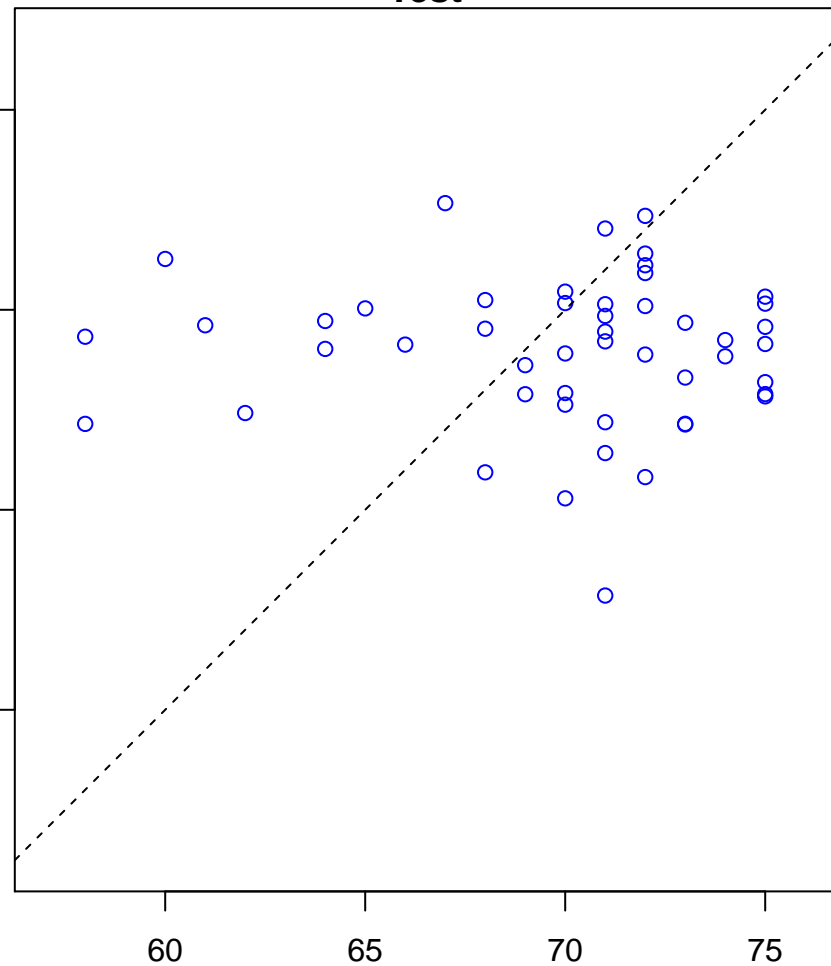


enteroendocrine cell differentiation (Score: 0.146590)

Control

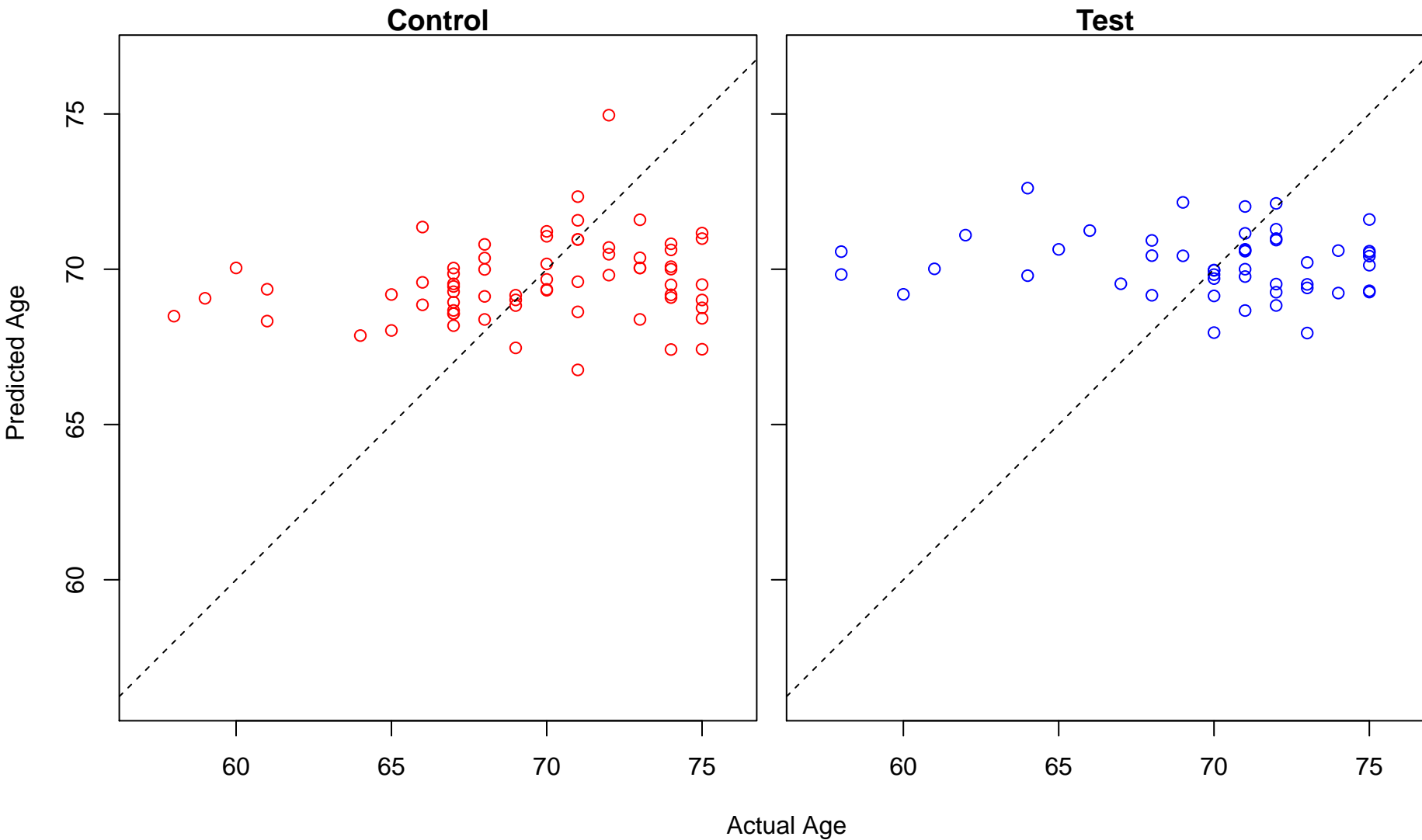


Test

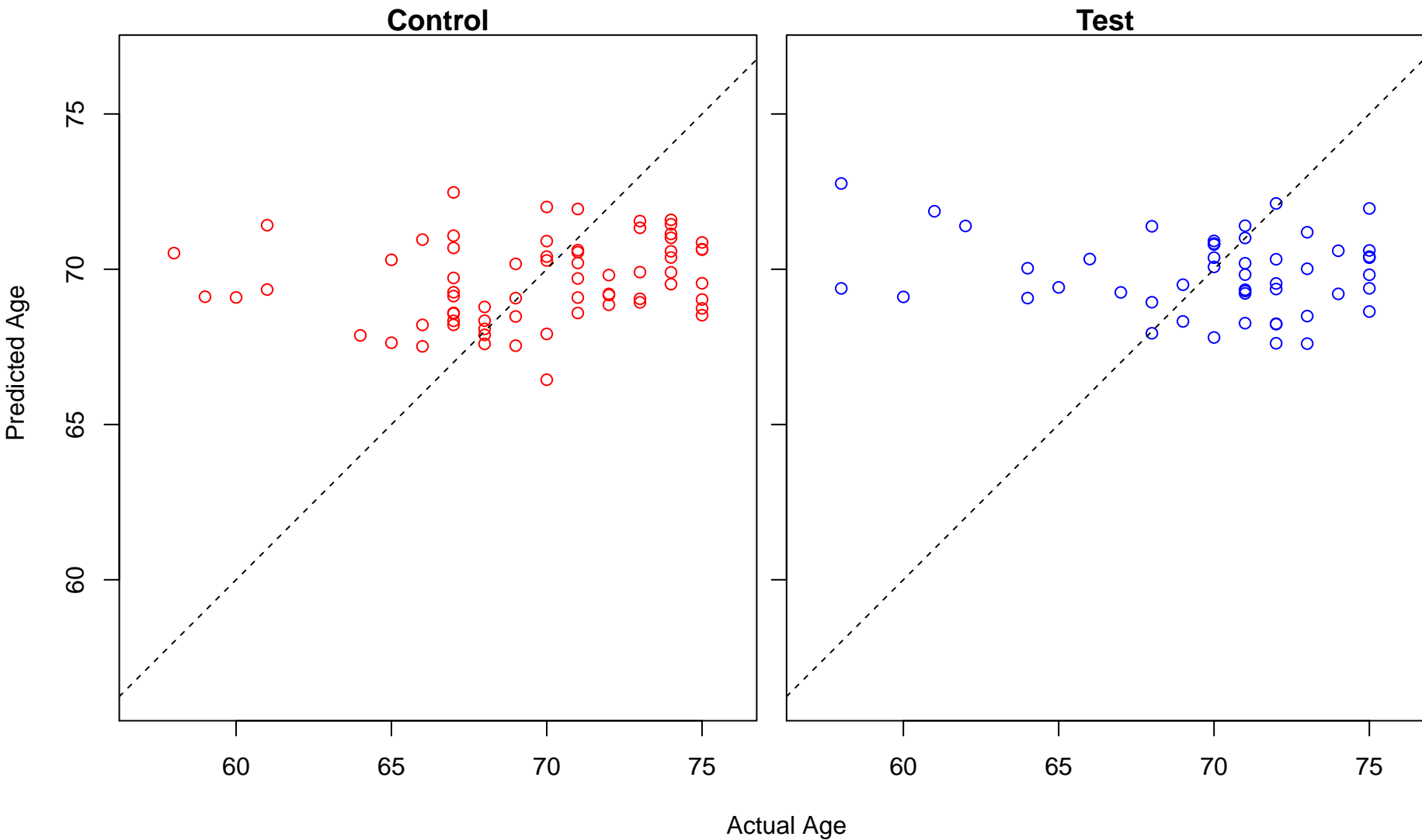


Actual Age

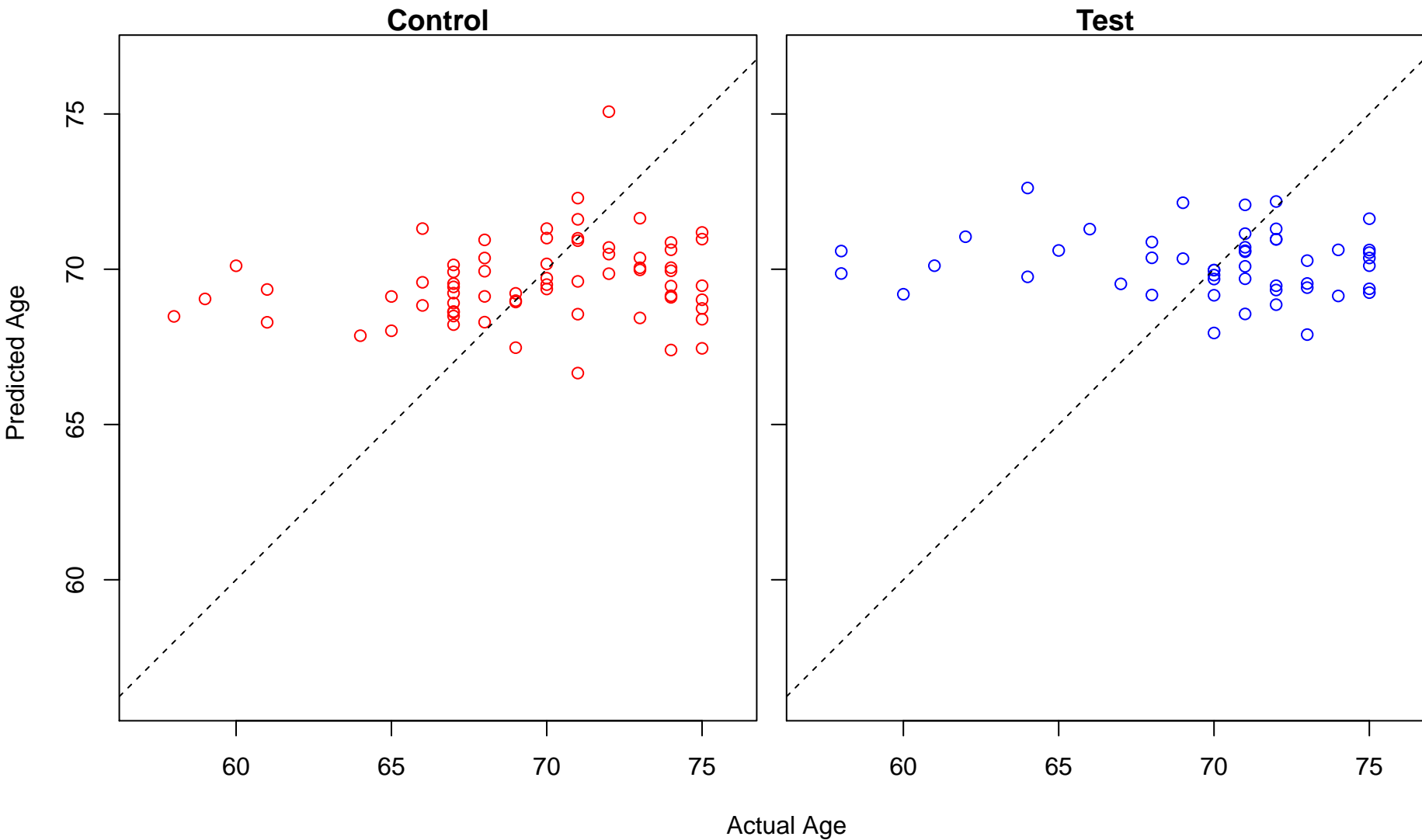
determination of pancreatic left/right asymmetry (Score: 0.140161)



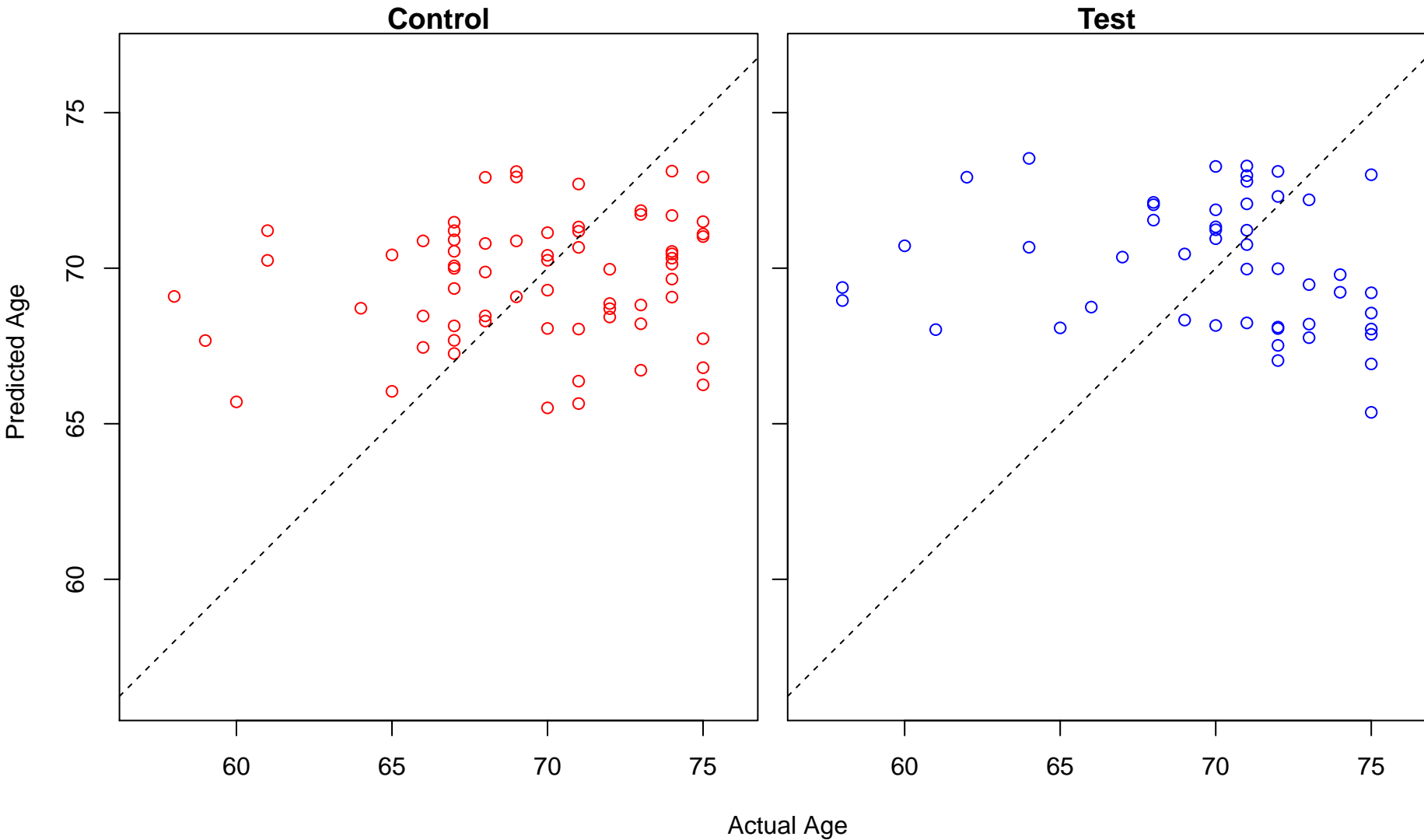
glomerular filtration (Score: 0.139893)



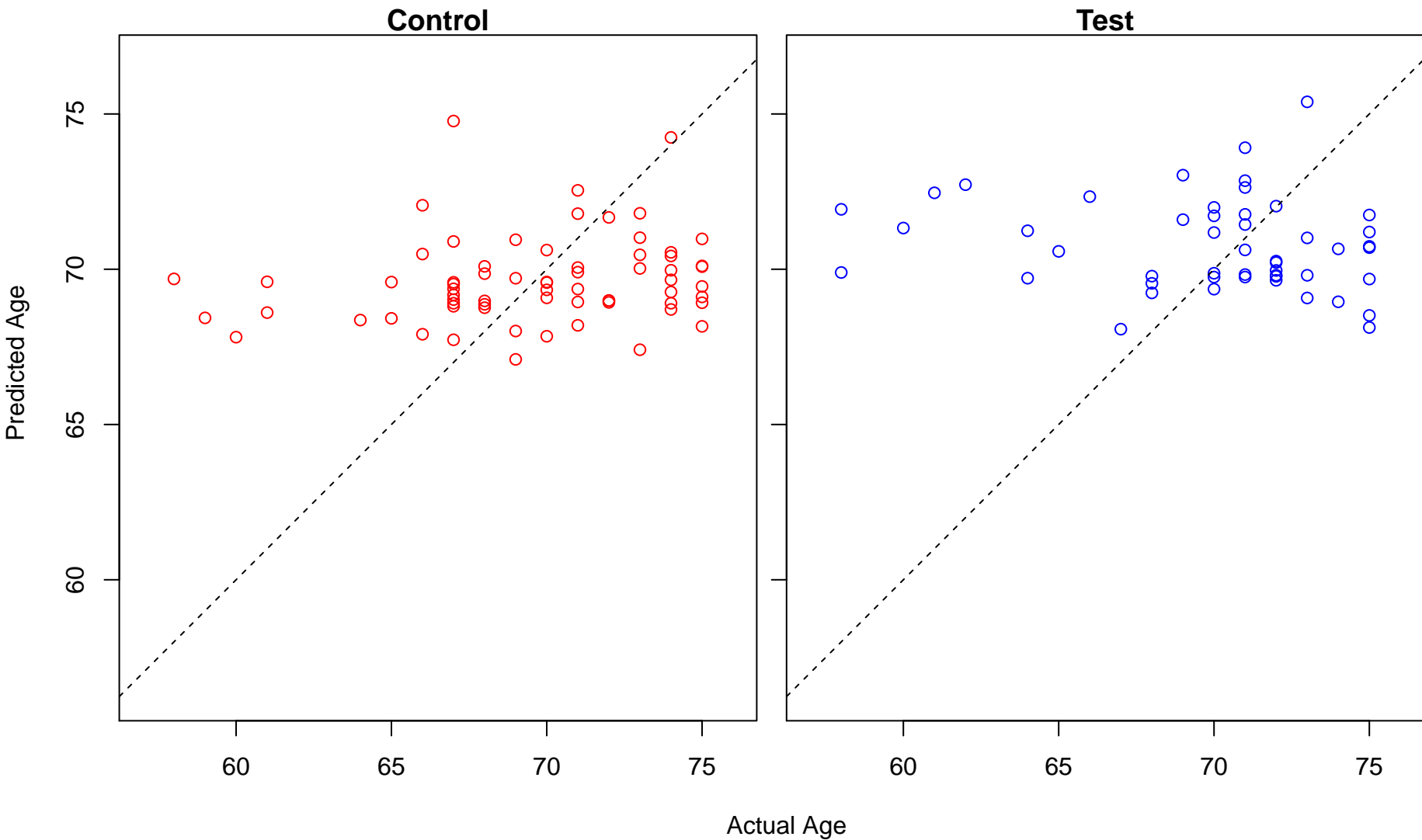
determination of digestive tract left/right asymmetry (Score: 0.139681)



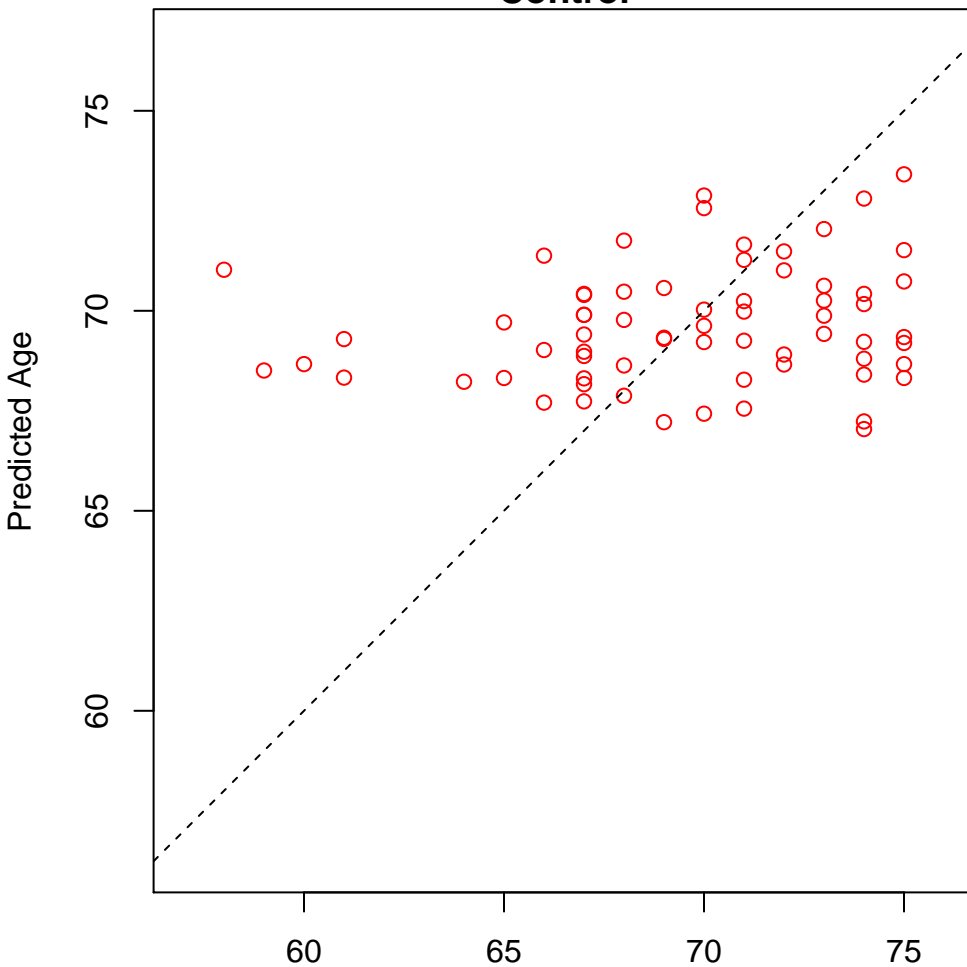
production of siRNA involved in RNA interference (Score: 0.139087)



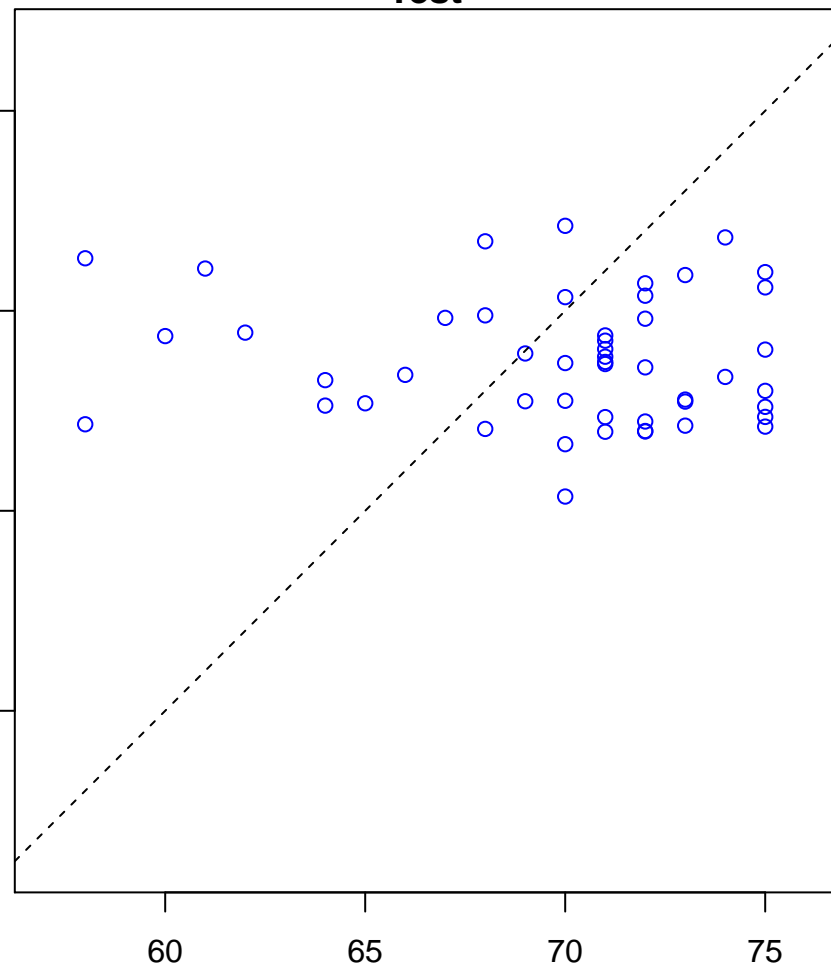
sulfate transport (Score: 0.137627)



Control

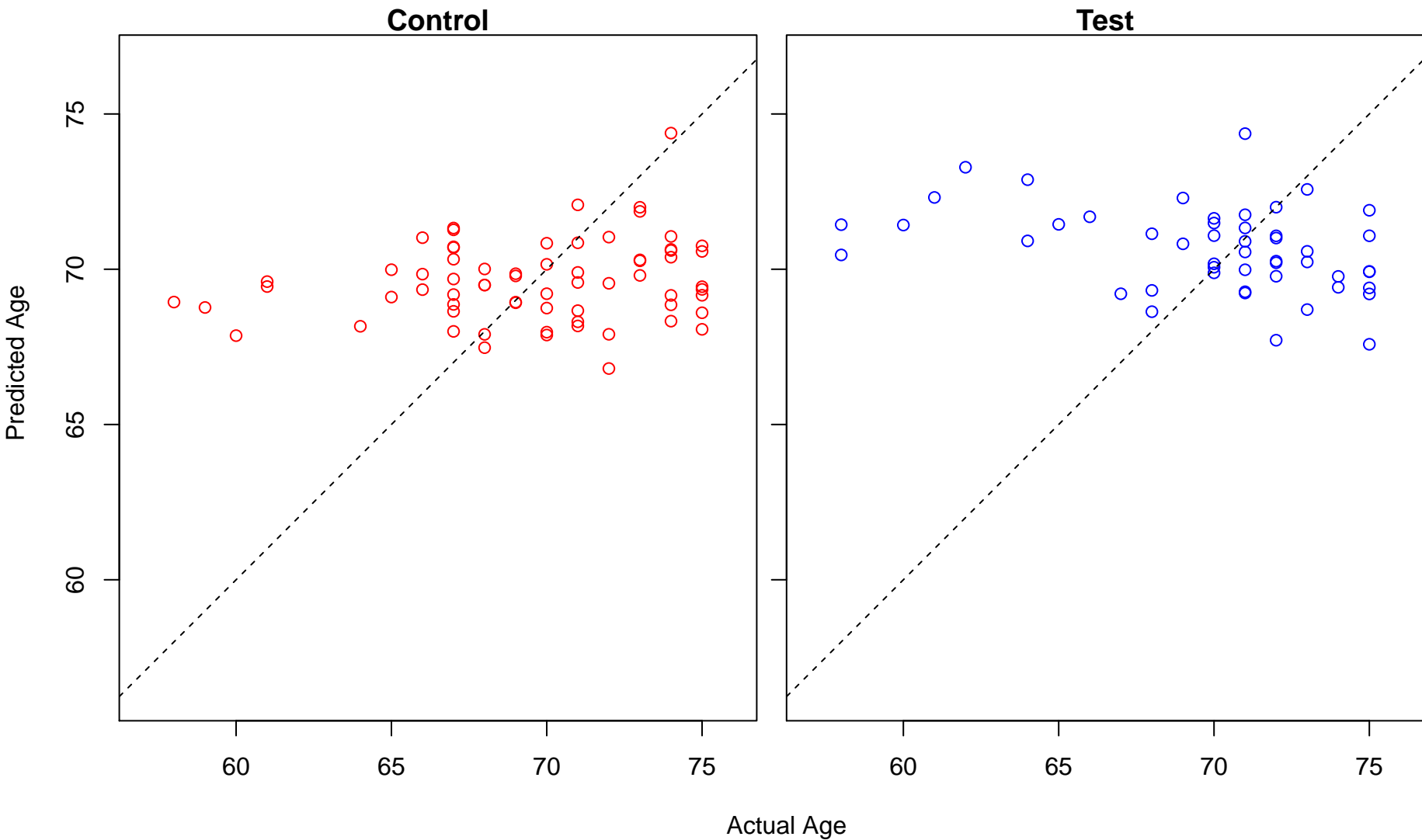


Test

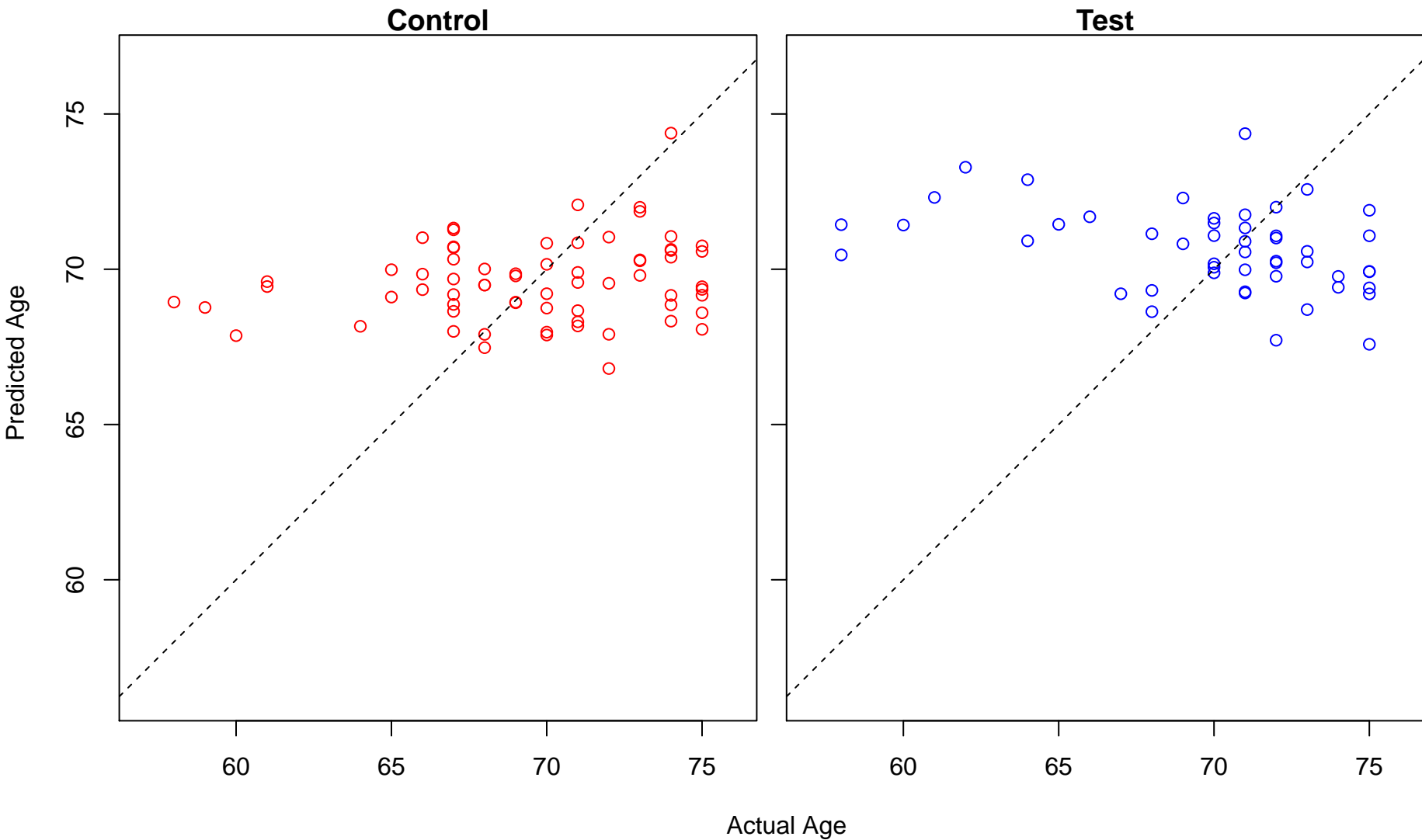


Actual Age

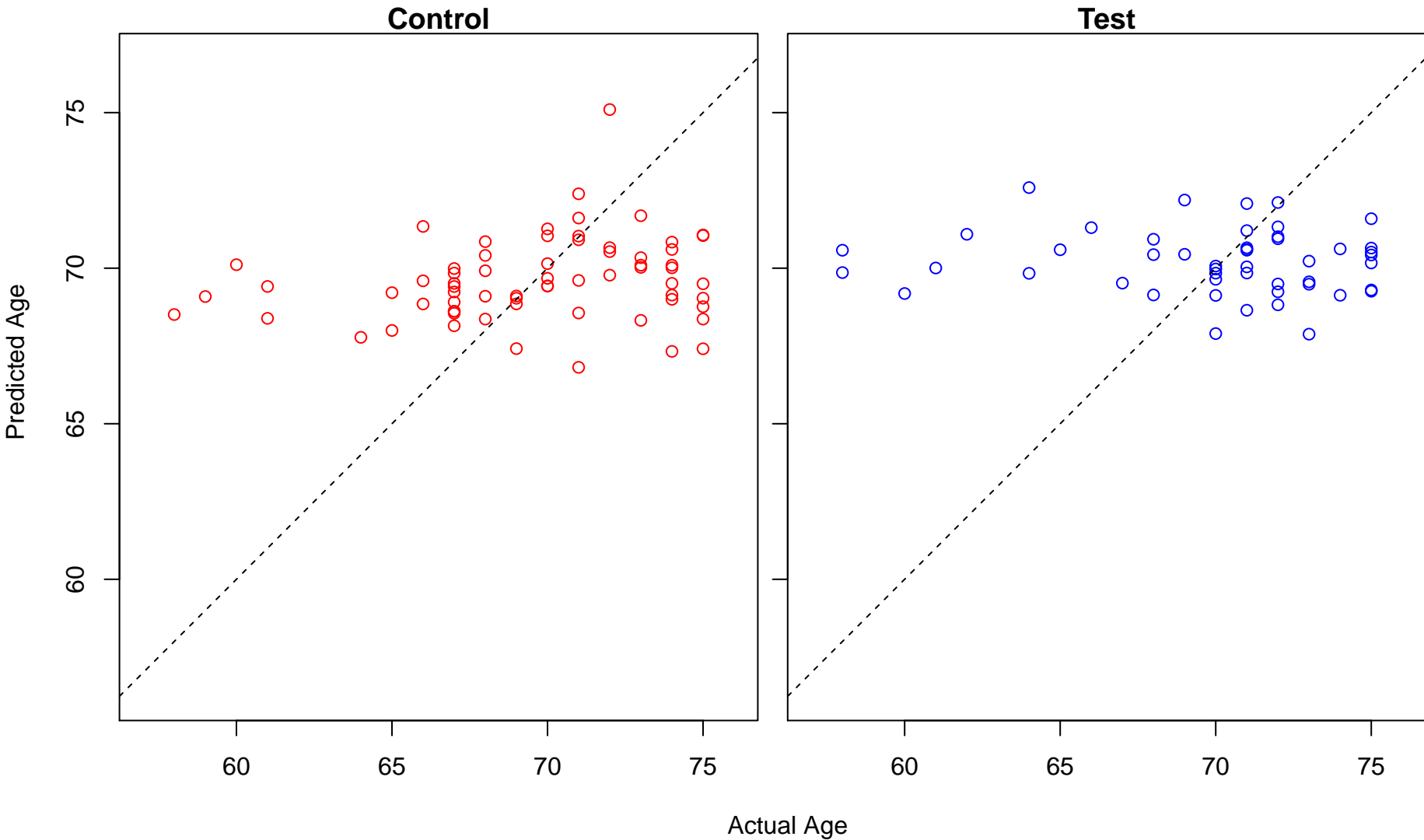
plasma membrane raft assembly (Score: 0.136565)



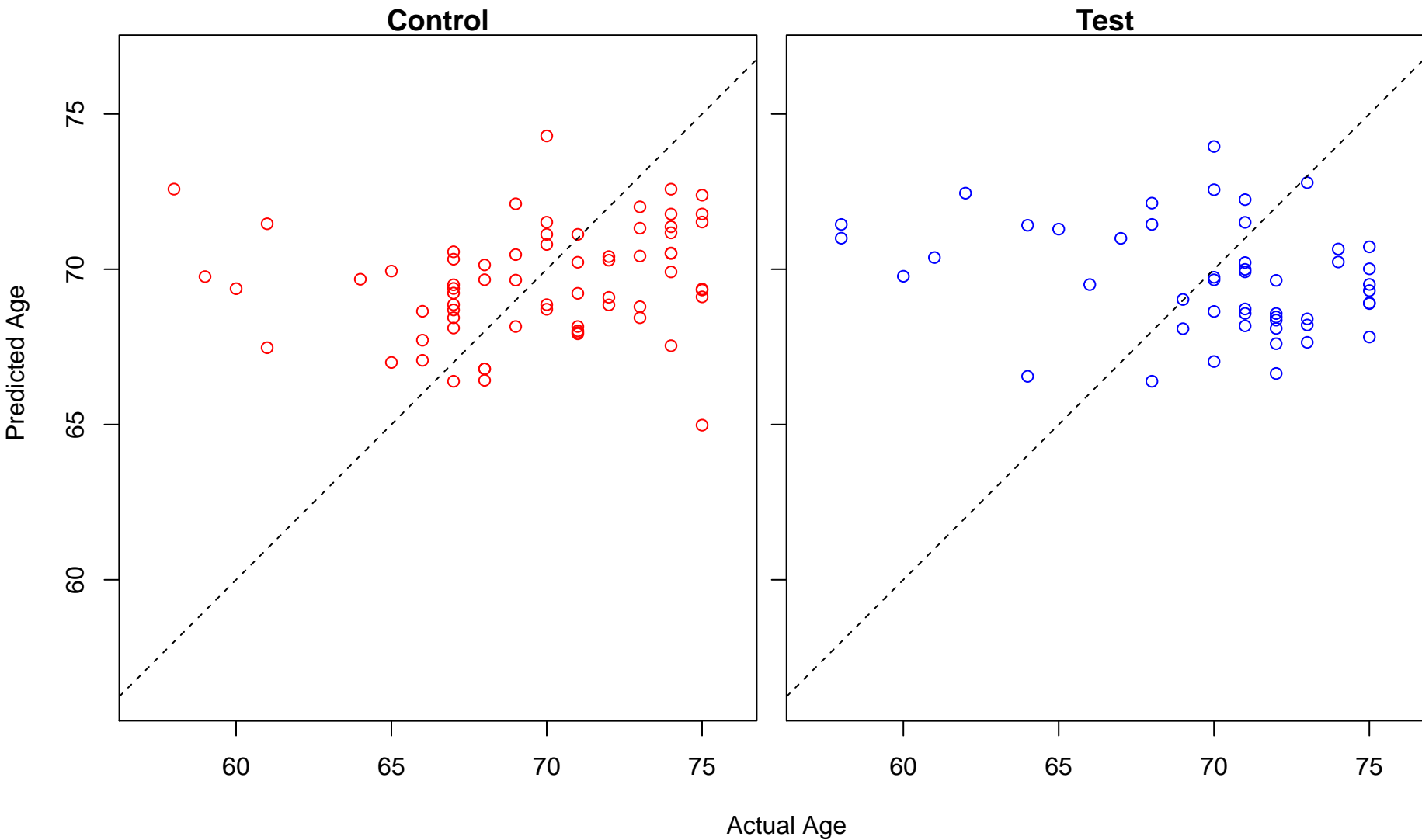
plasma membrane raft organization (Score: 0.136565)



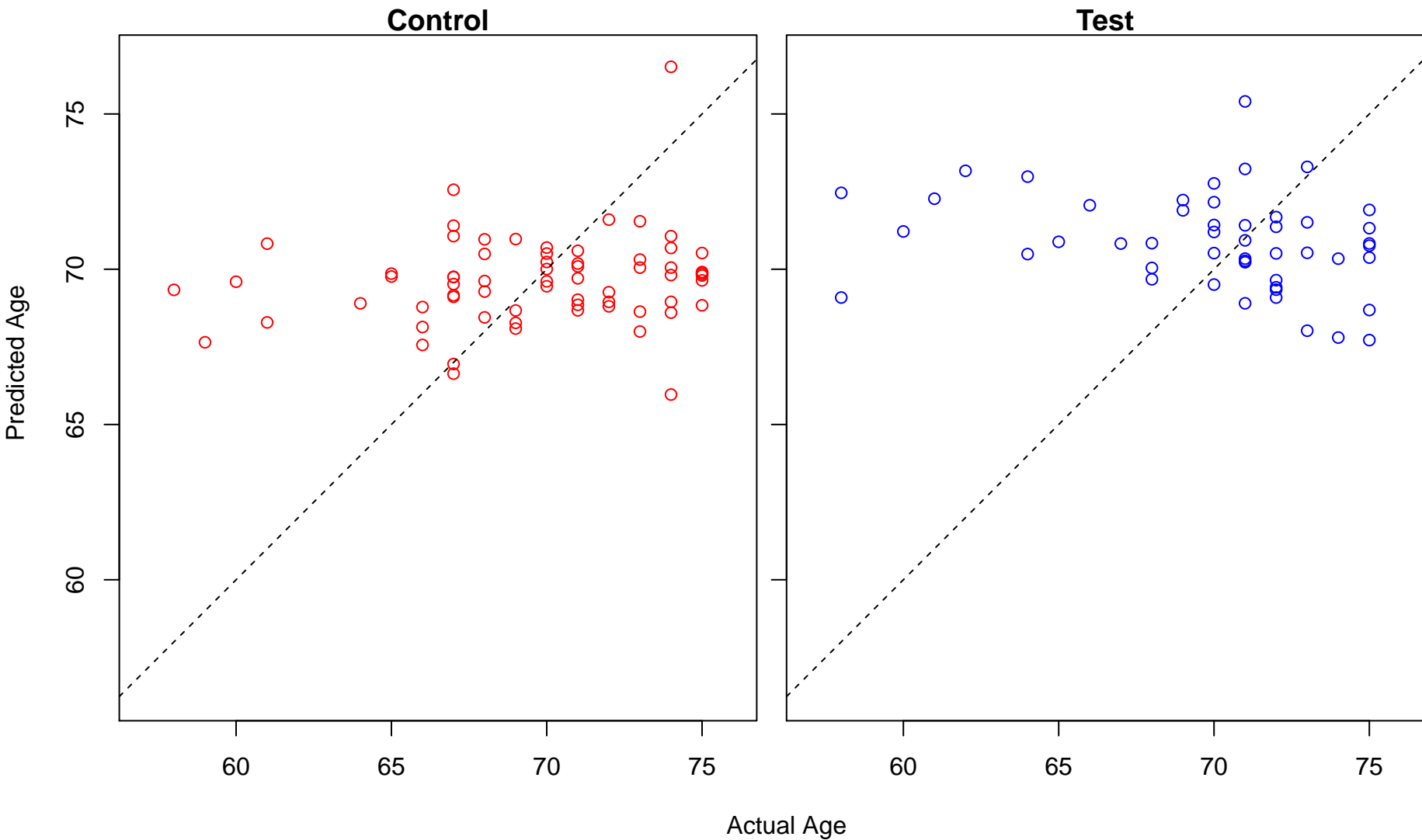
determination of liver left/right asymmetry (Score: 0.135641)



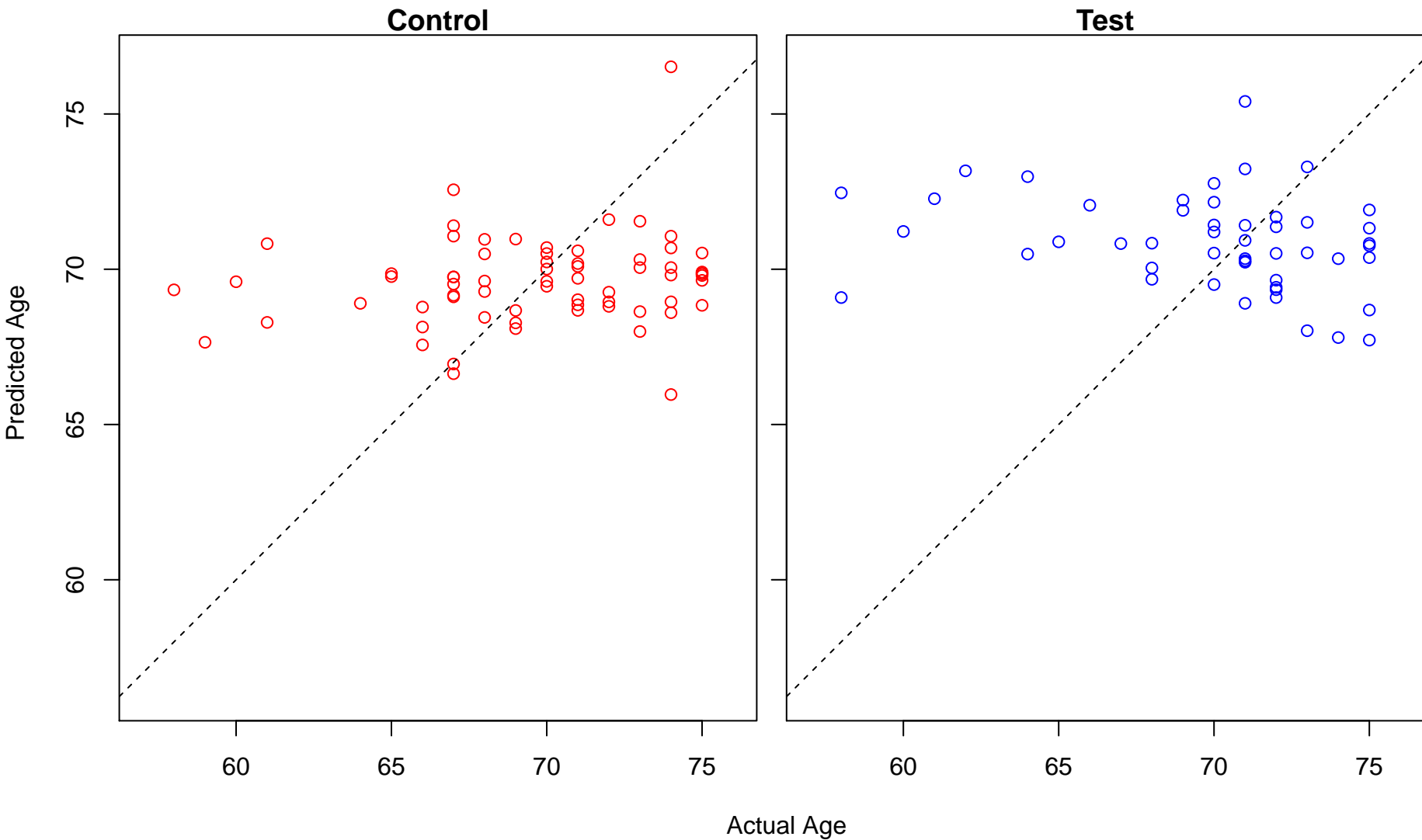
nitrogen cycle metabolic process (Score: 0.134315)



negative regulation of B cell mediated immunity (Score: 0.133706)

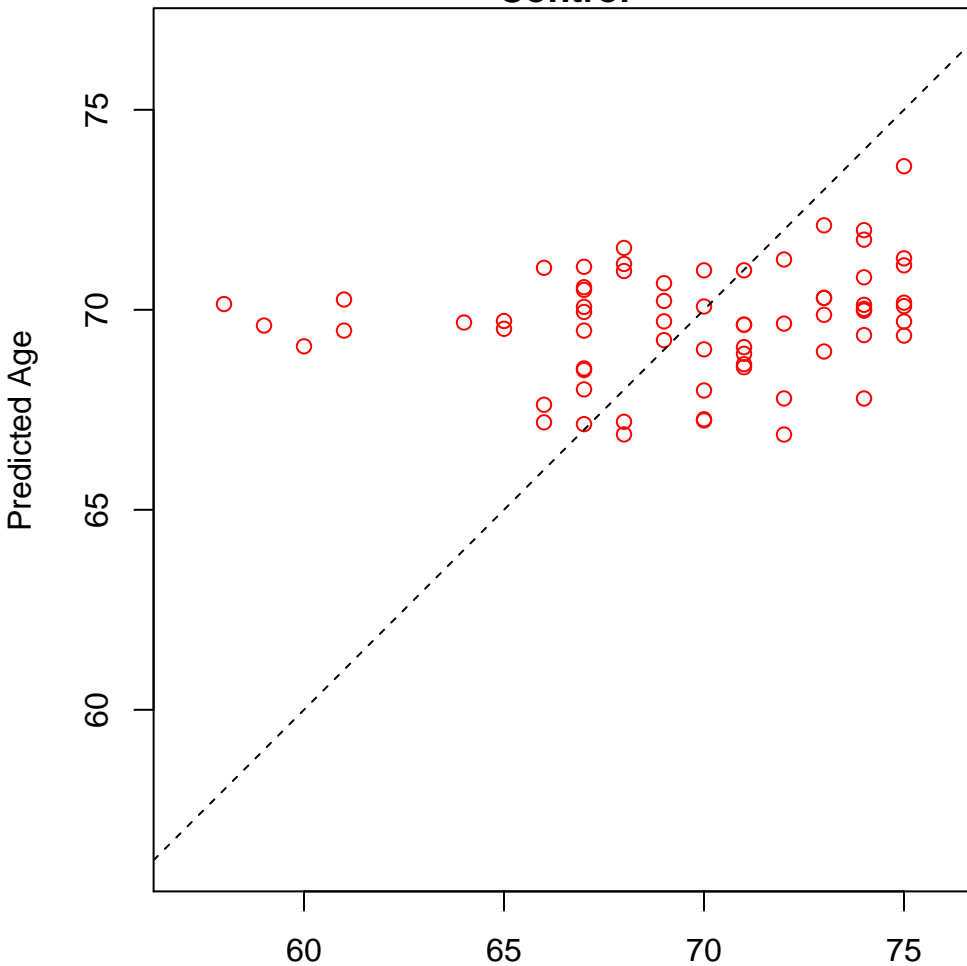


negative regulation of immunoglobulin mediated immune response (Score: 0.133706)

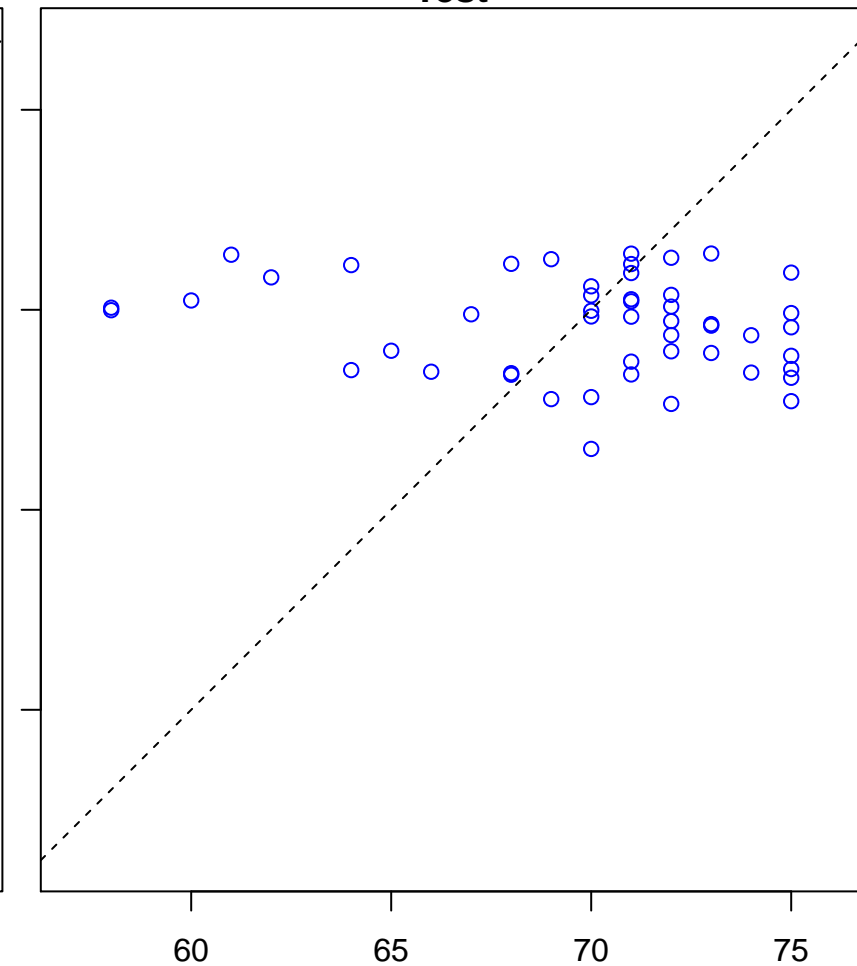


peptidyl-serine autophosphorylation (Score: 0.133207)

Control

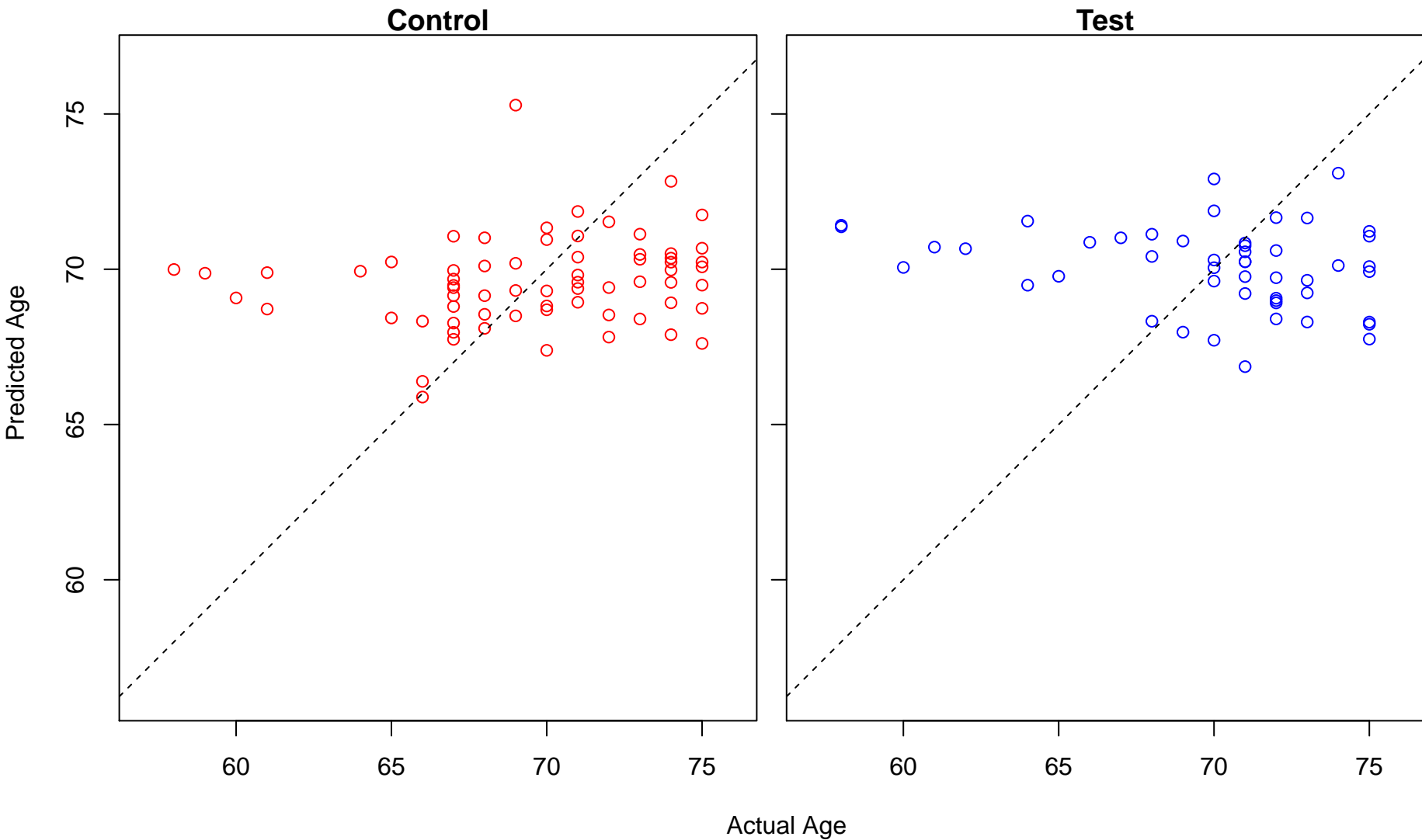


Test



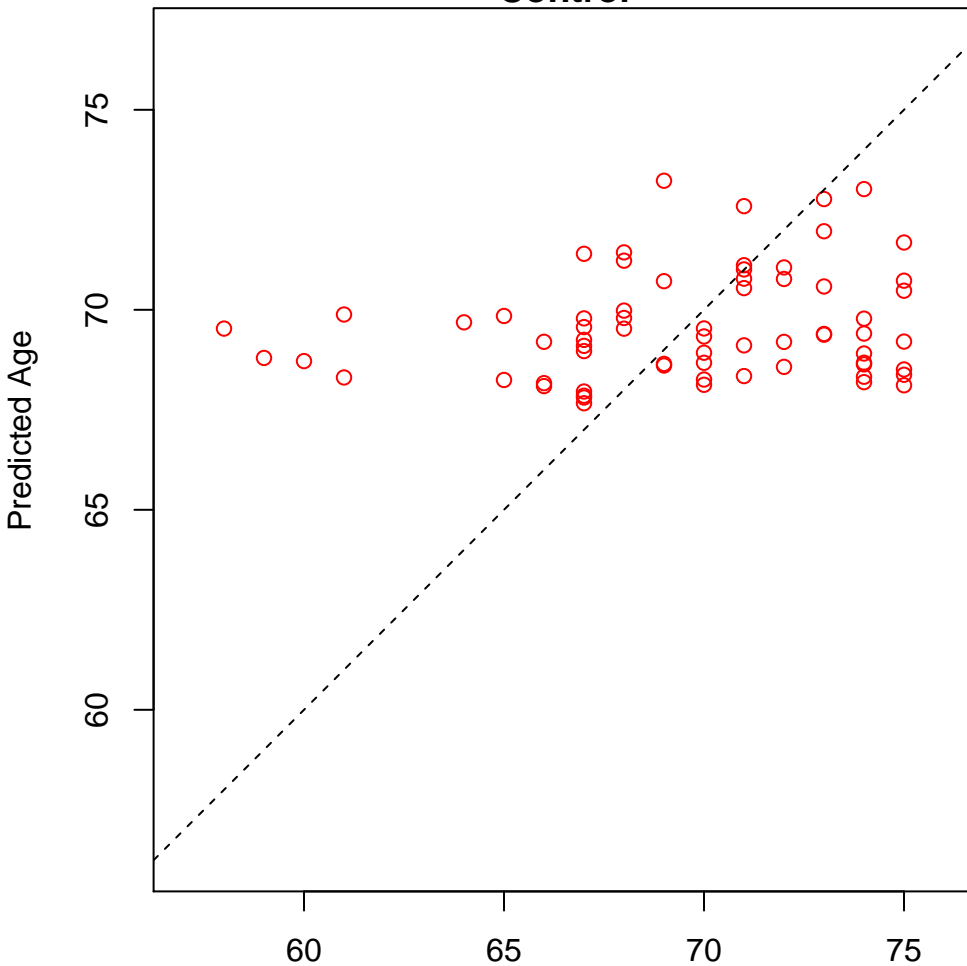
Actual Age

maturation of SSU-rRNA (Score: 0.132494)

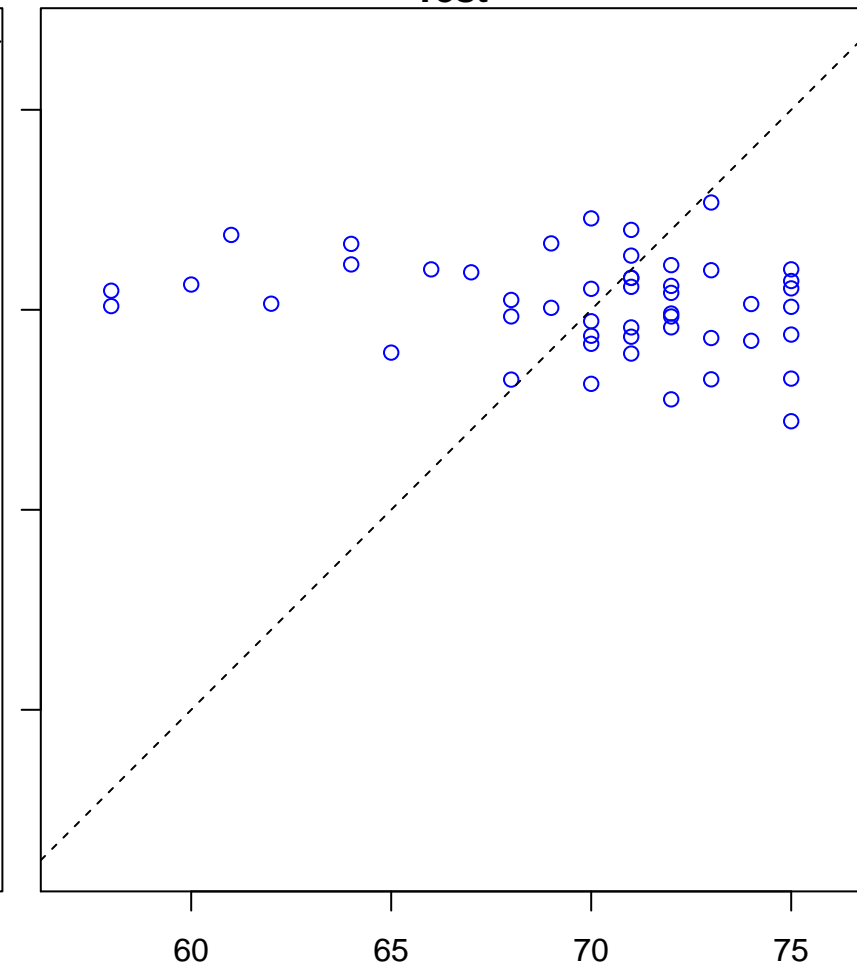


atrioventricular canal development (Score: 0.132157)

Control

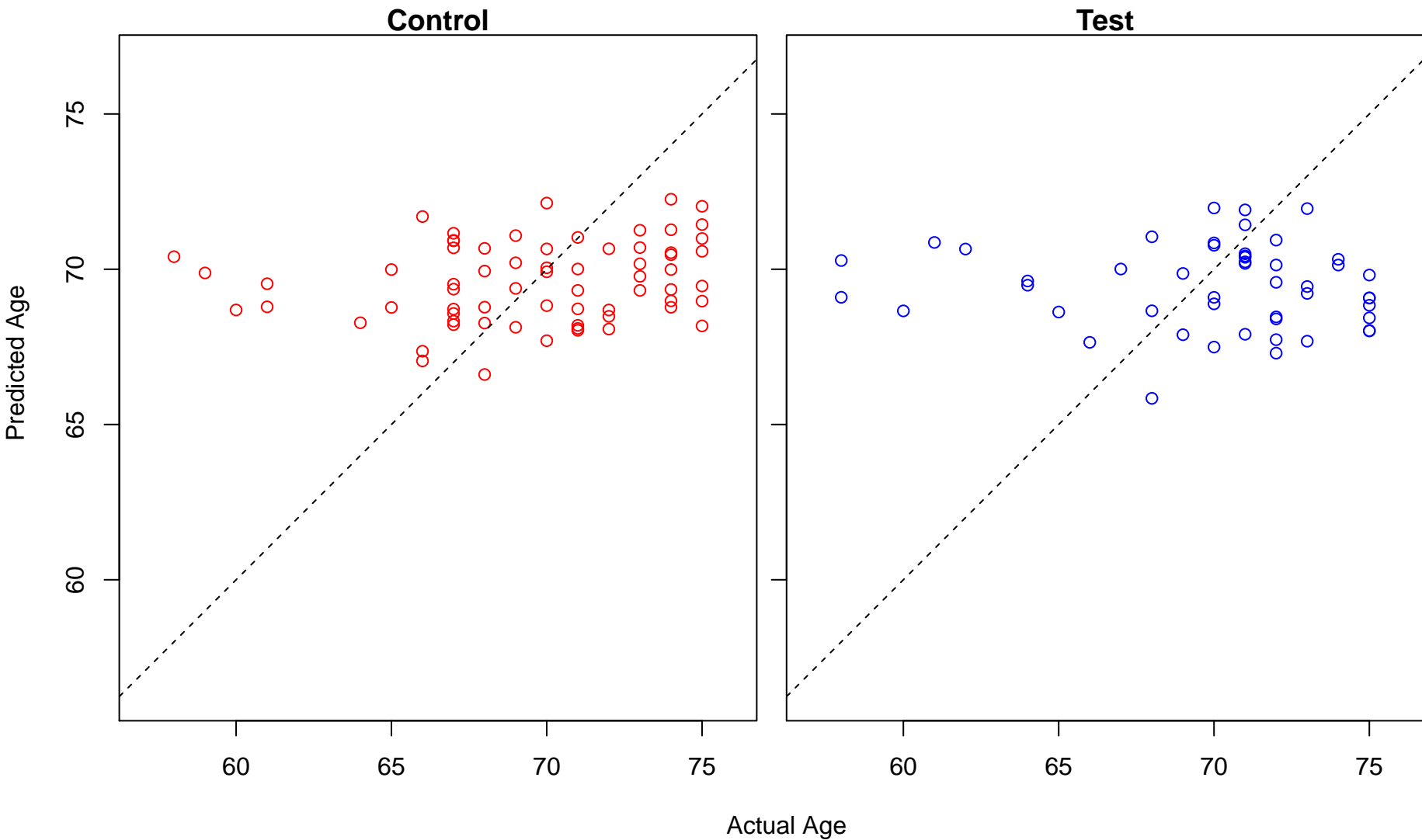


Test

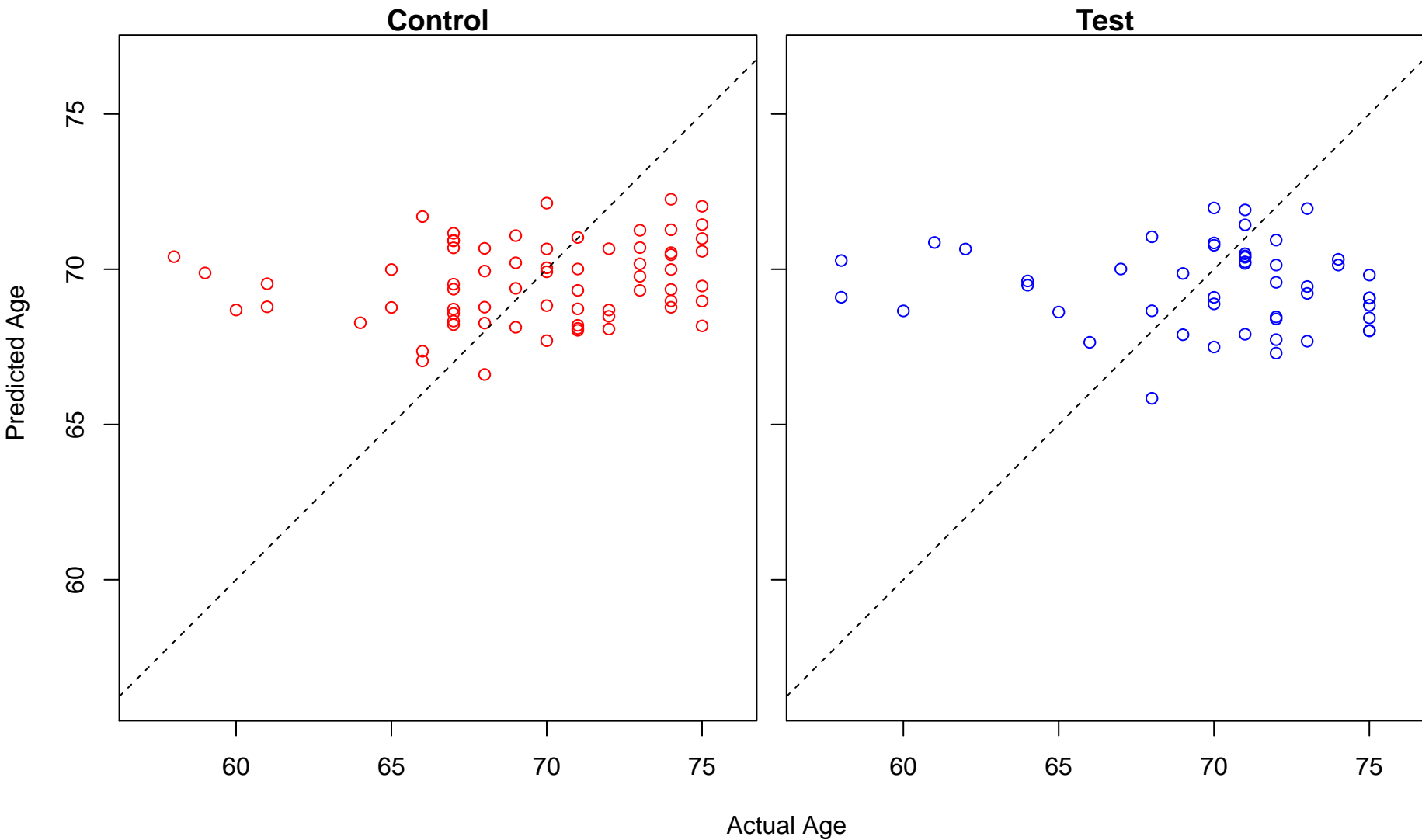


Actual Age

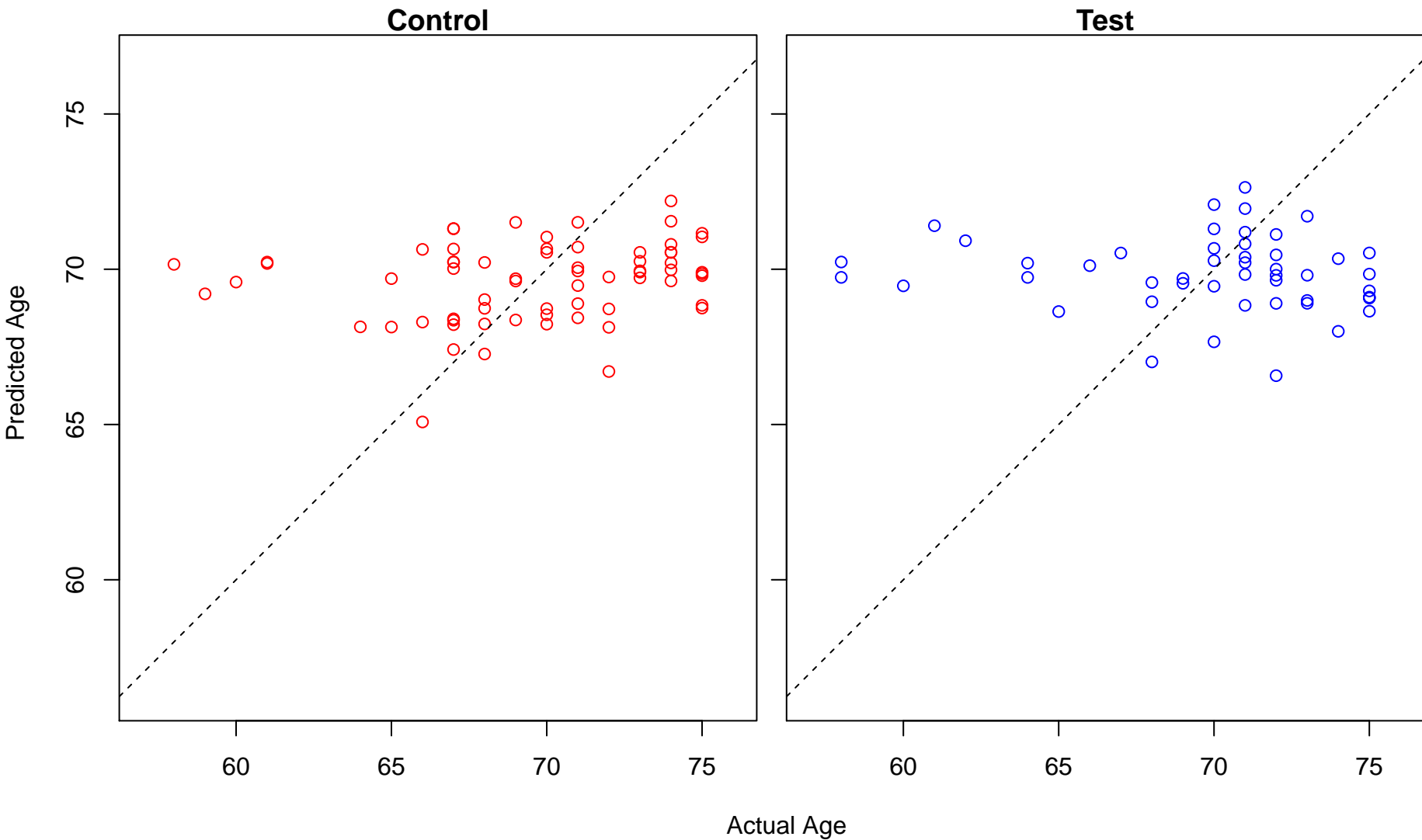
deoxyribonucleoside monophosphate biosynthetic process (Score: 0.131775)



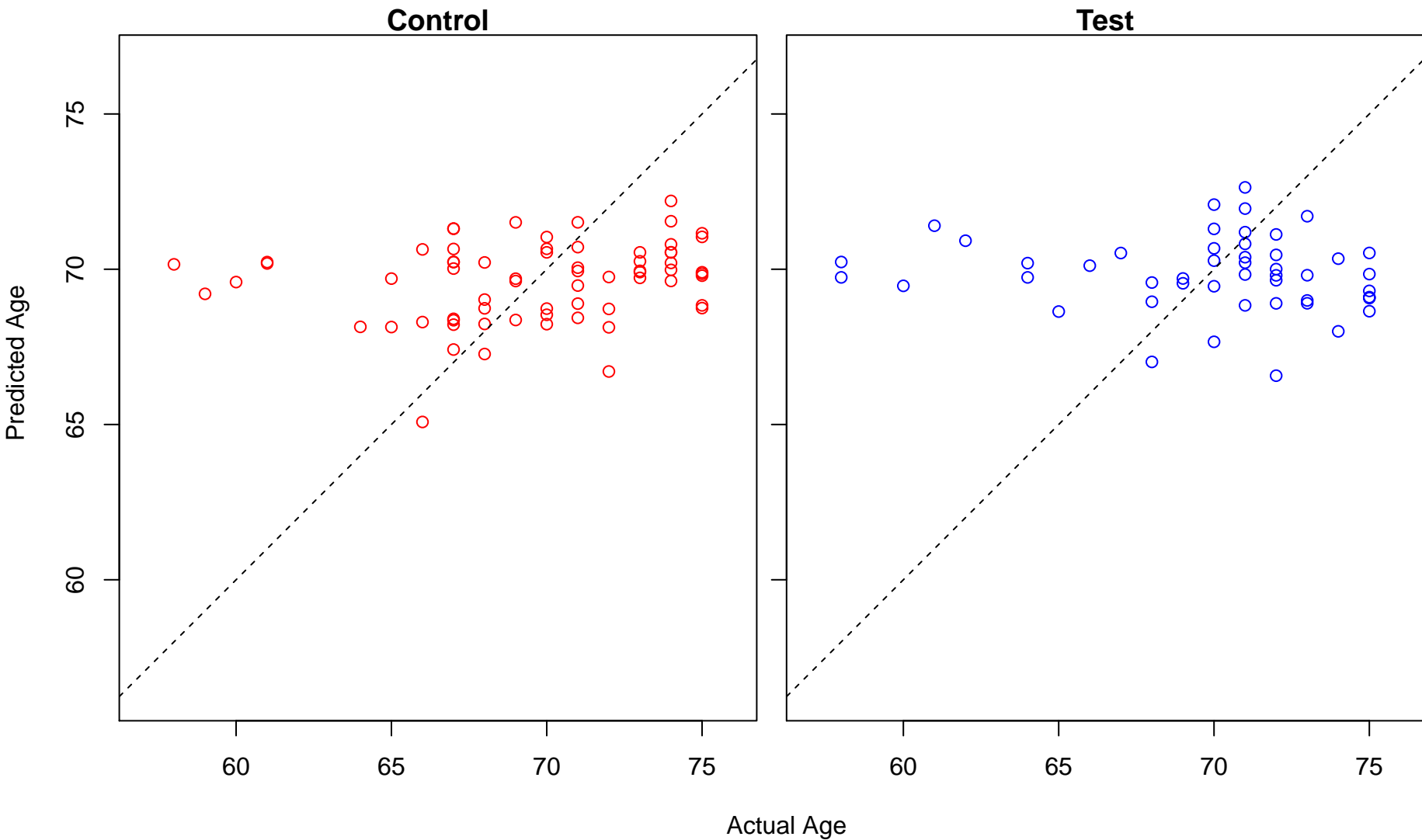
deoxyribonucleoside monophosphate metabolic process (Score: 0.131775)



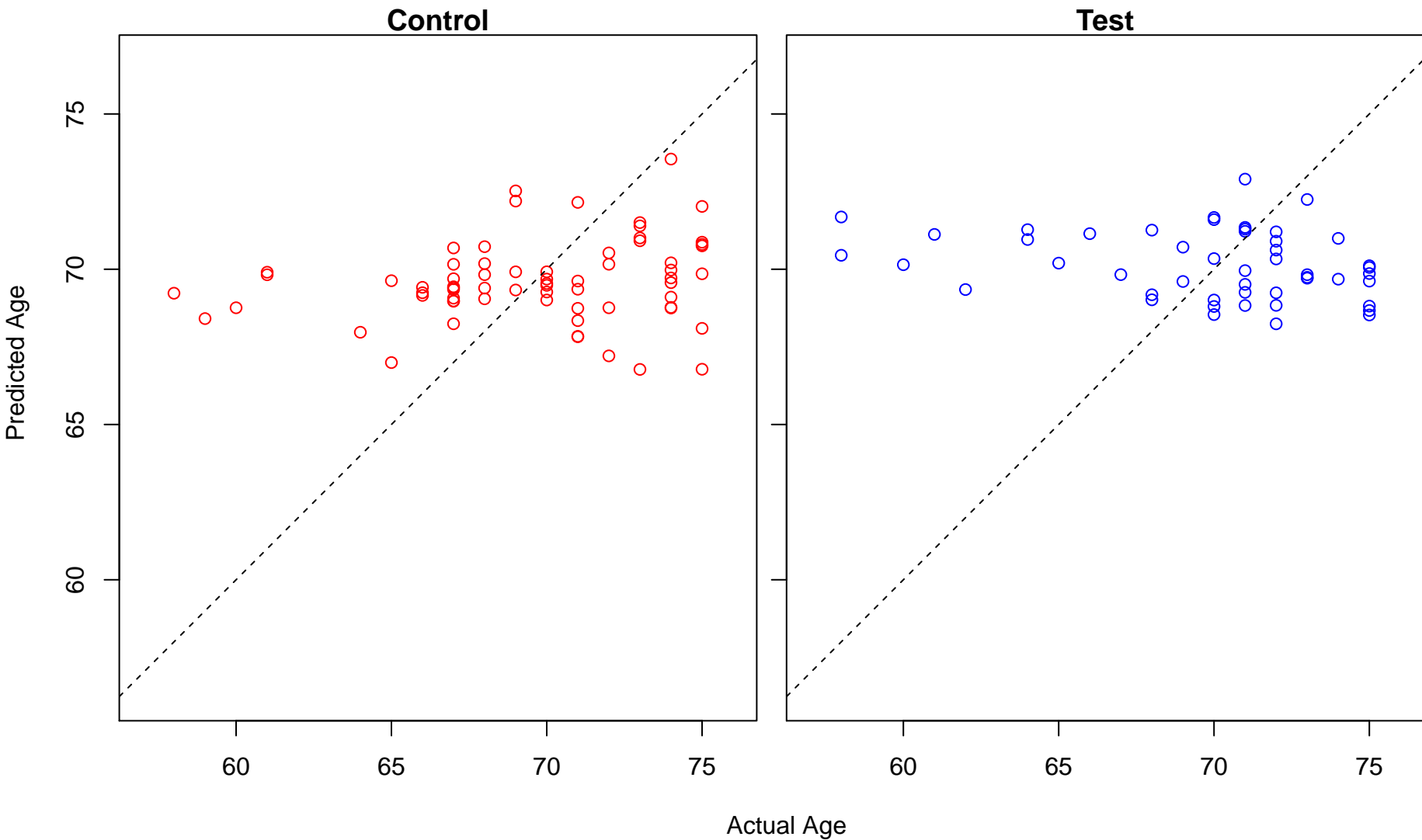
plus-end-directed vesicle transport along microtubule (Score: 0.131740)



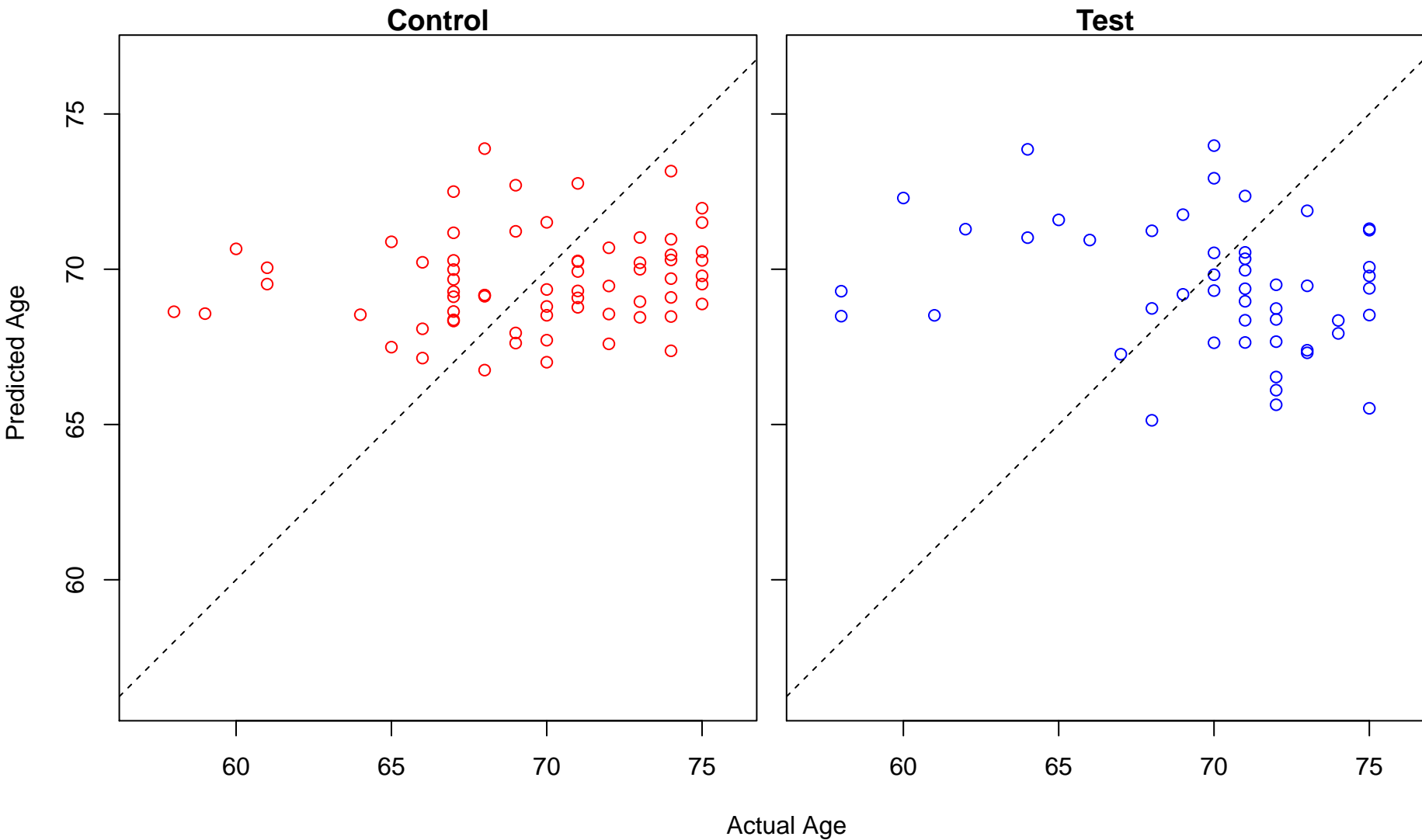
plus-end-directed organelle transport along microtubule (Score: 0.131740)



negative regulation of interleukin-2 production (Score: 0.125819)

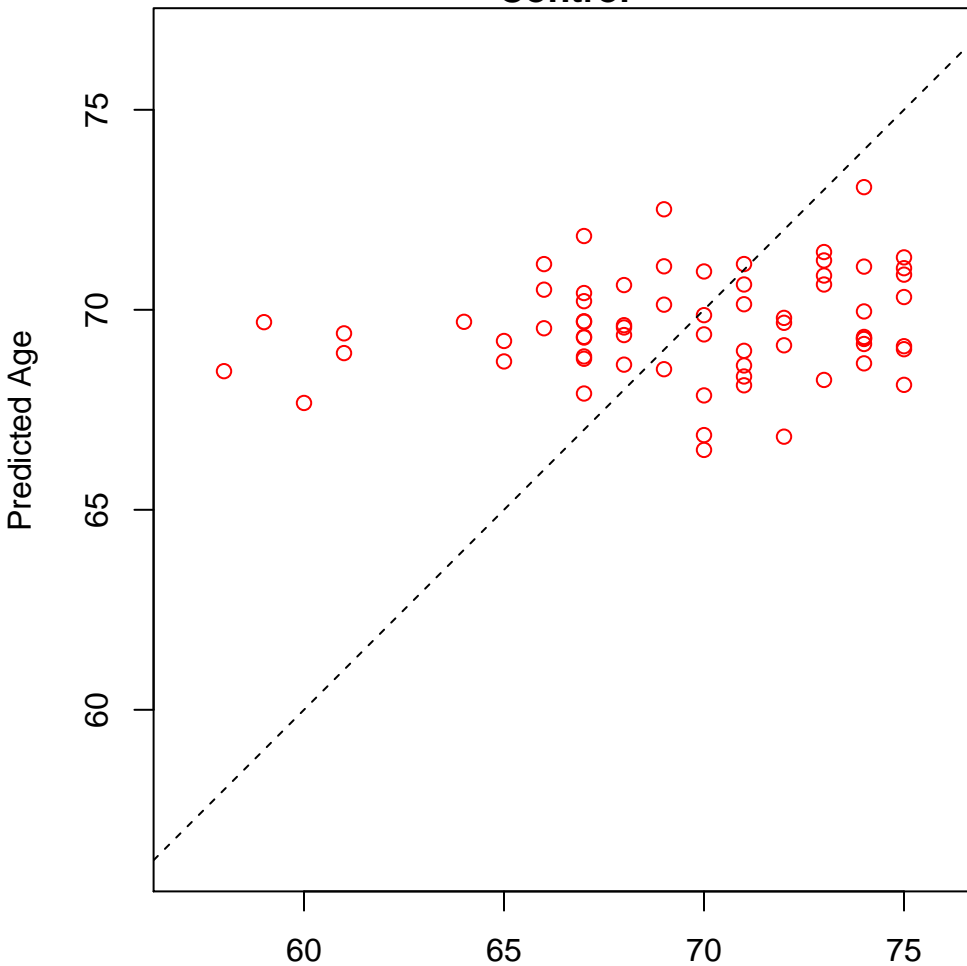


positive regulation of inositol phosphate biosynthetic process (Score: 0.116611)

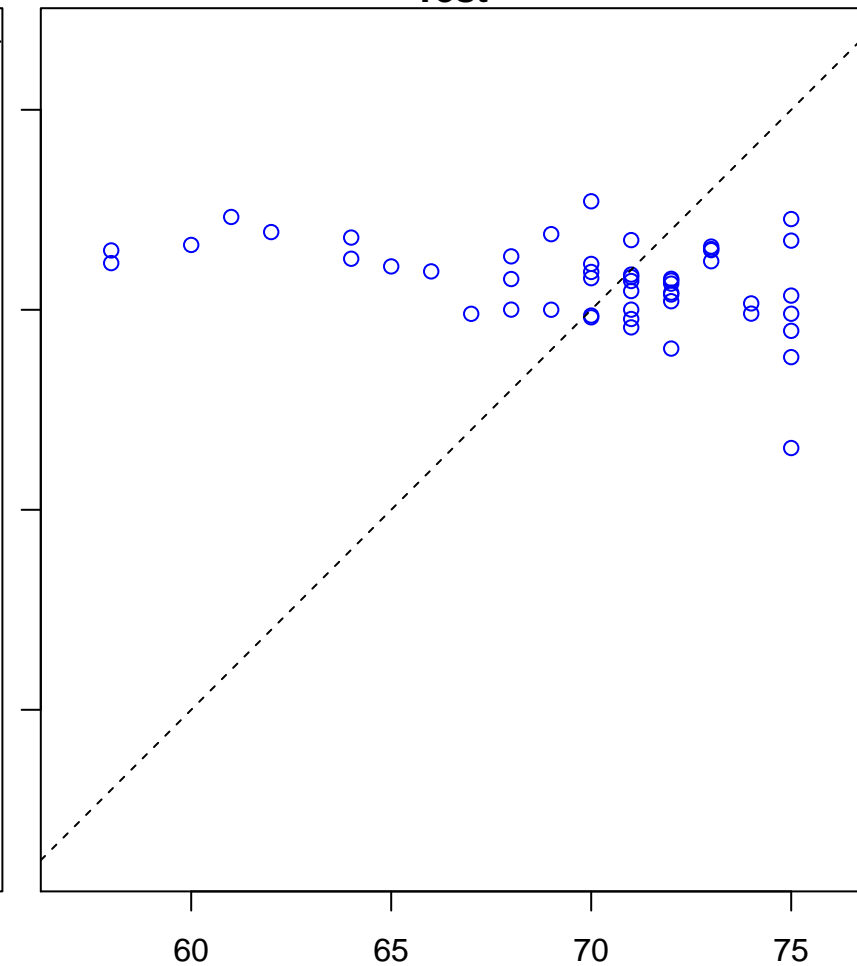


positive regulation of cholesterol storage (Score: 0.108034)

Control



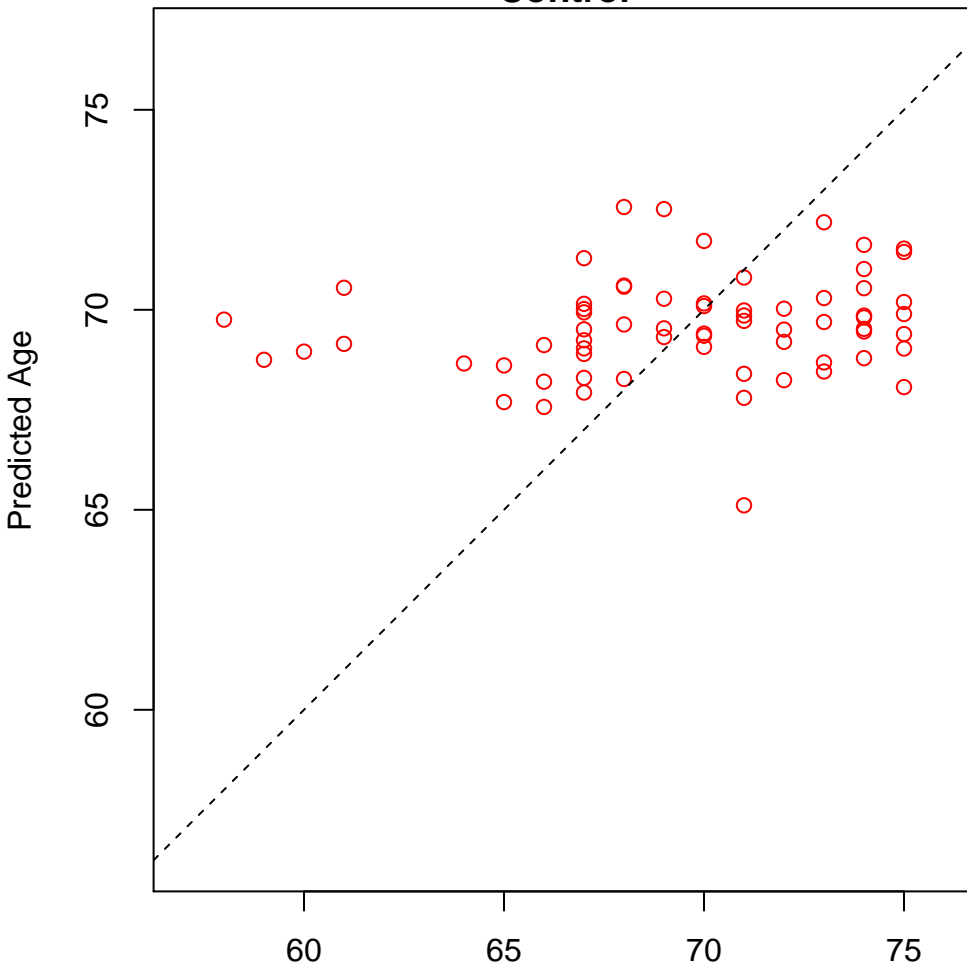
Test



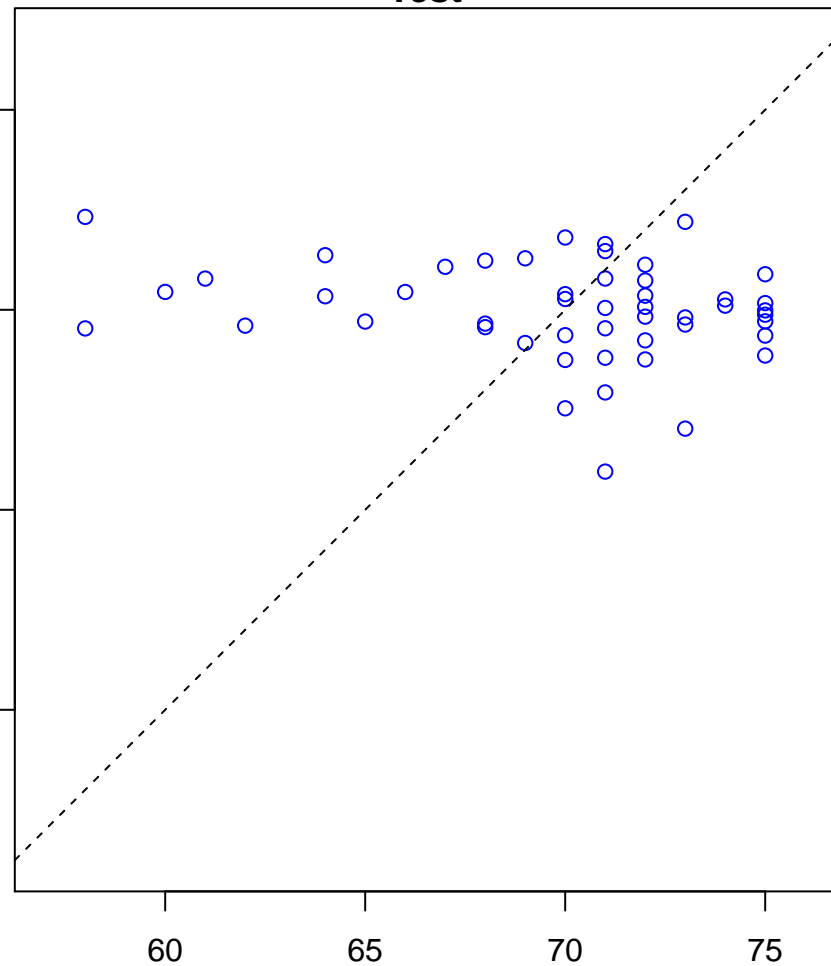
Actual Age

lens morphogenesis in camera-type eye (Score: 0.105757)

Control

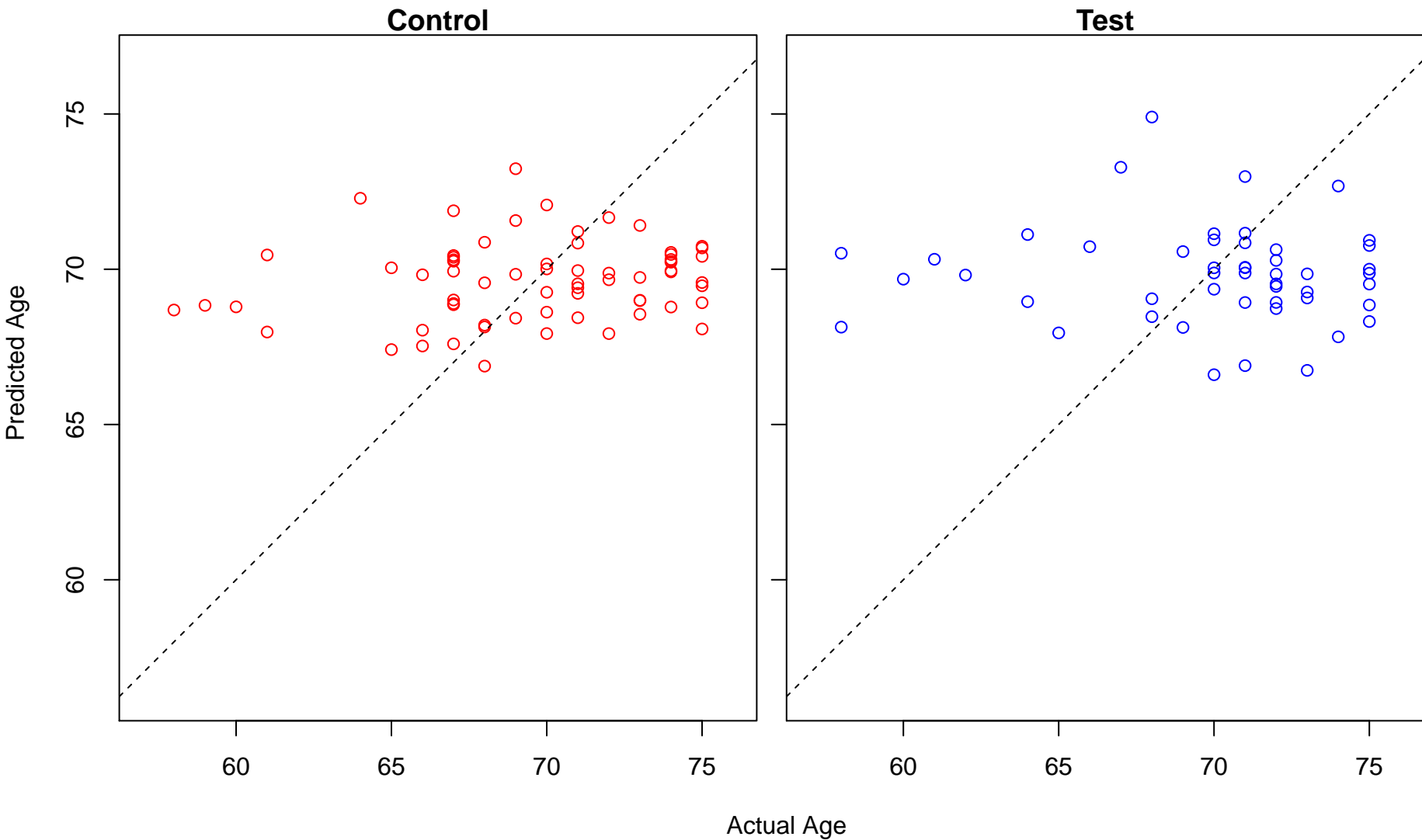


Test

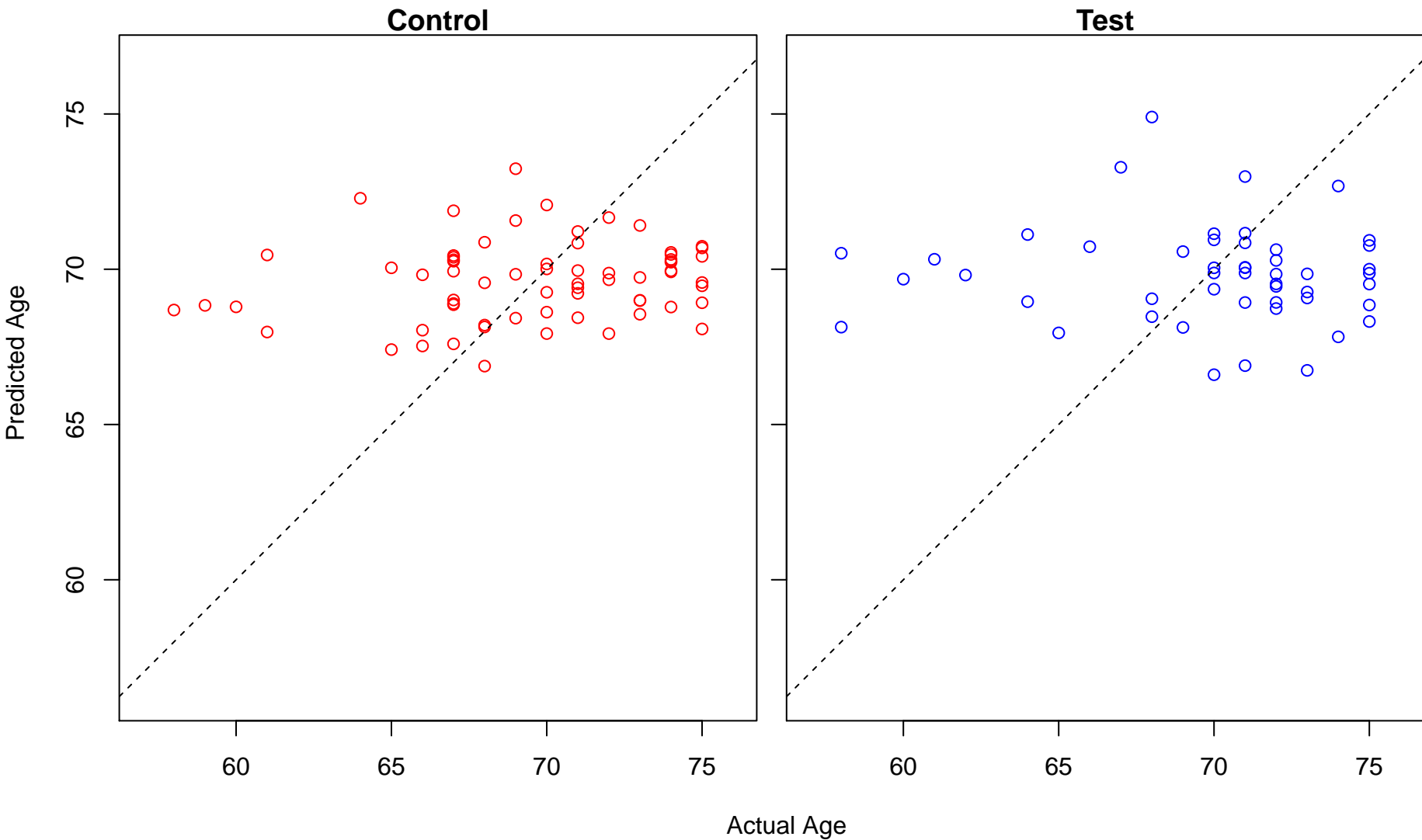


Actual Age

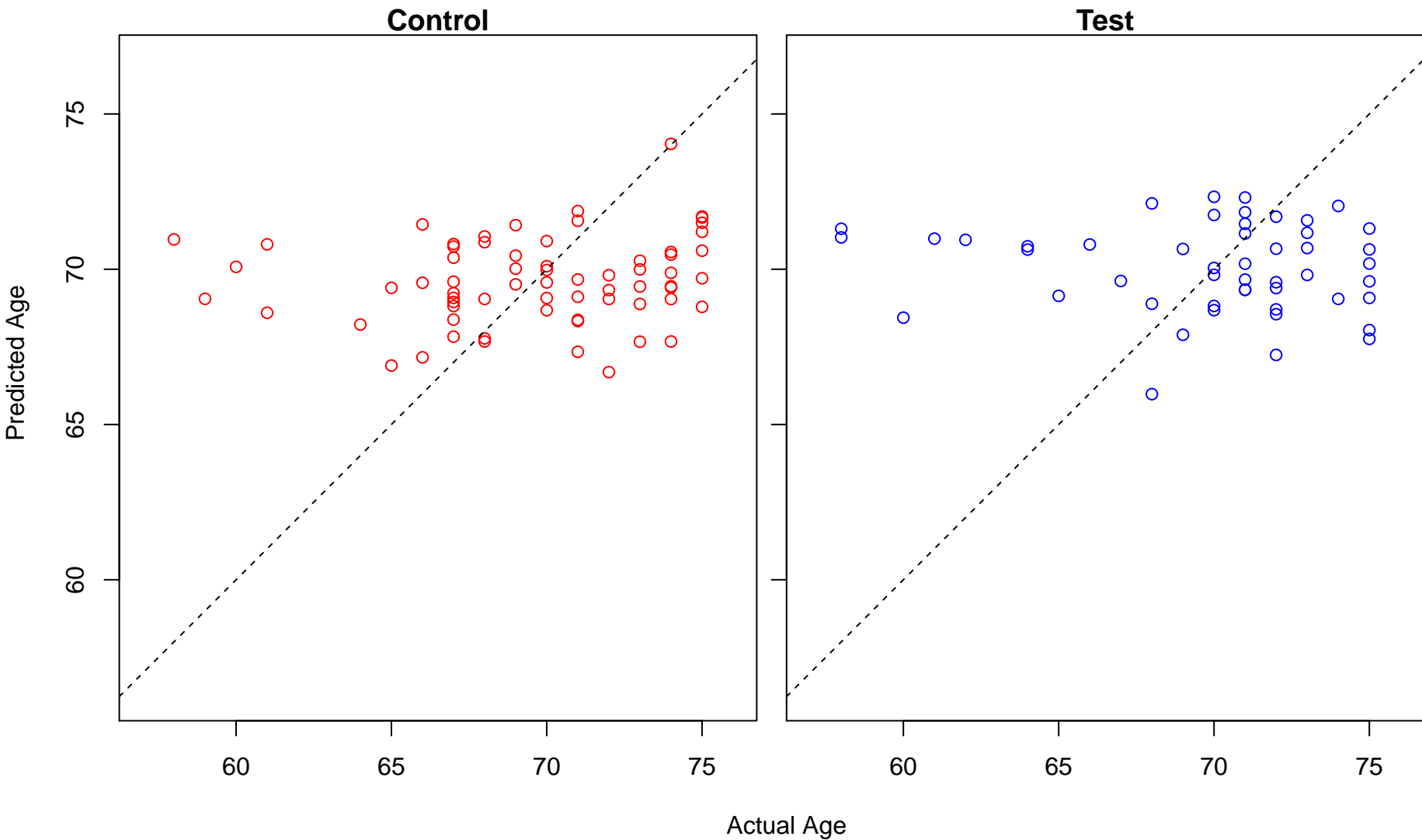
vitamin biosynthetic process (Score: 0.101452)



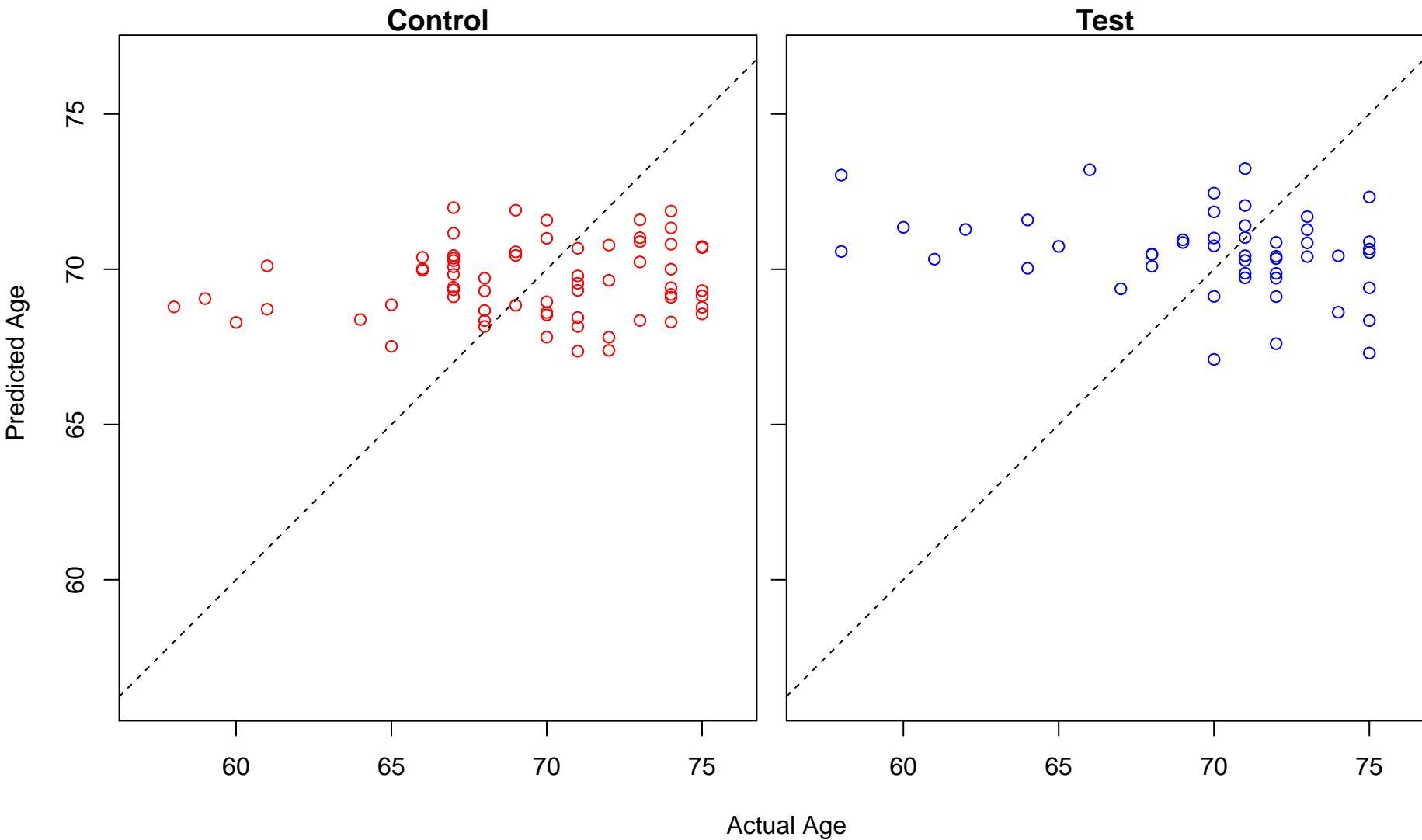
fat-soluble vitamin biosynthetic process (Score: 0.101452)



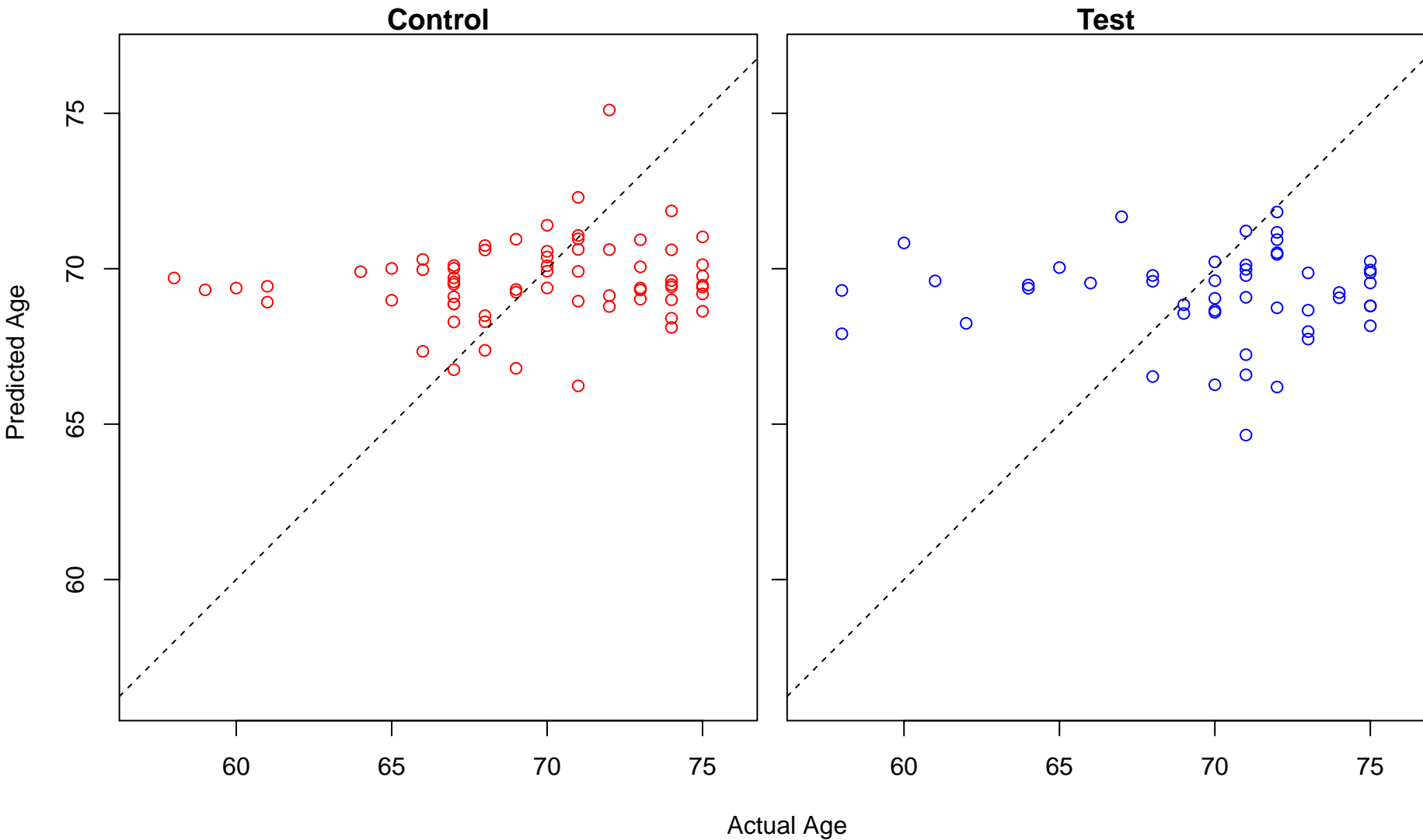
catecholamine biosynthetic process (Score: 0.088234)



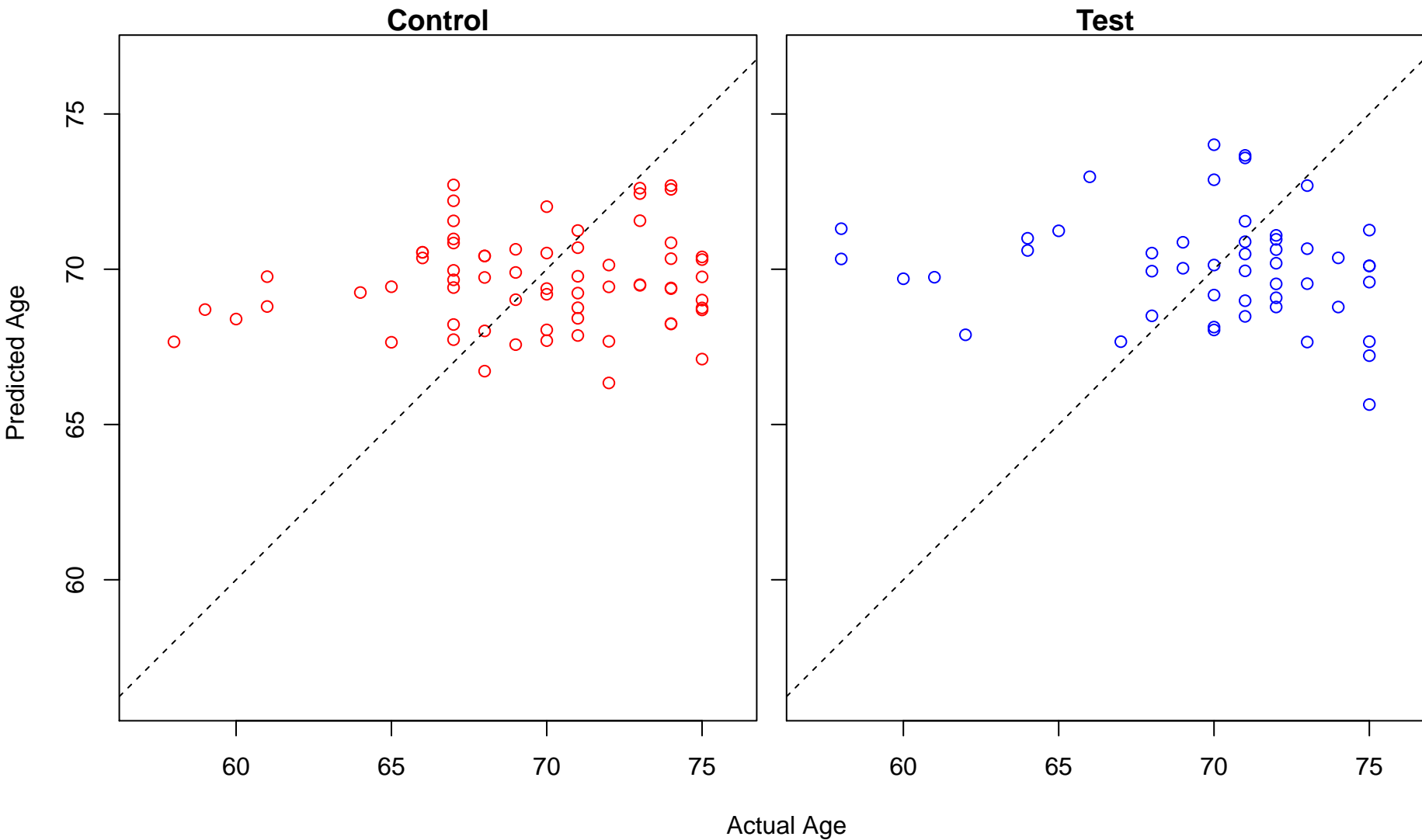
pentose metabolic process (Score: 0.087700)



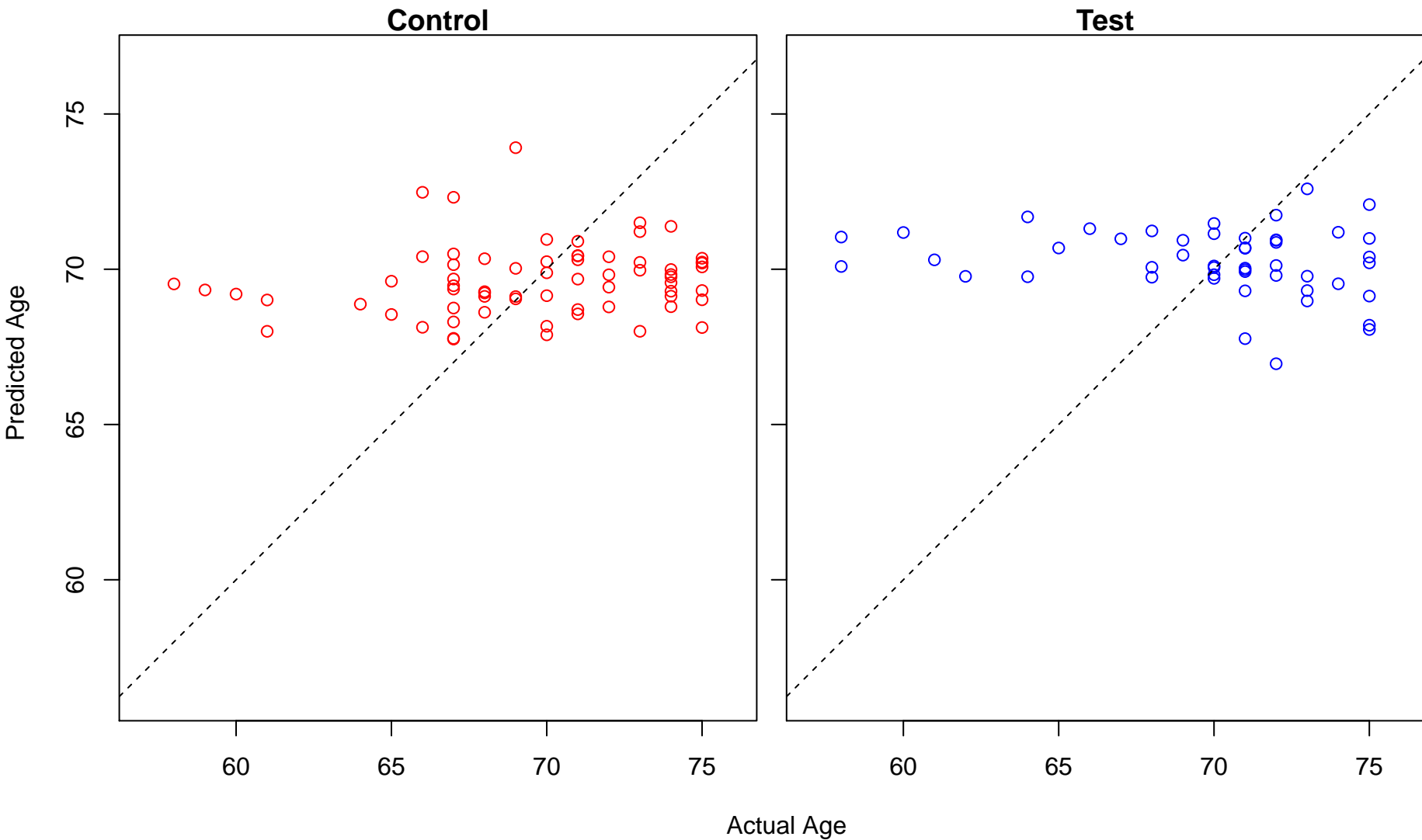
type B pancreatic cell development (Score: 0.085225)



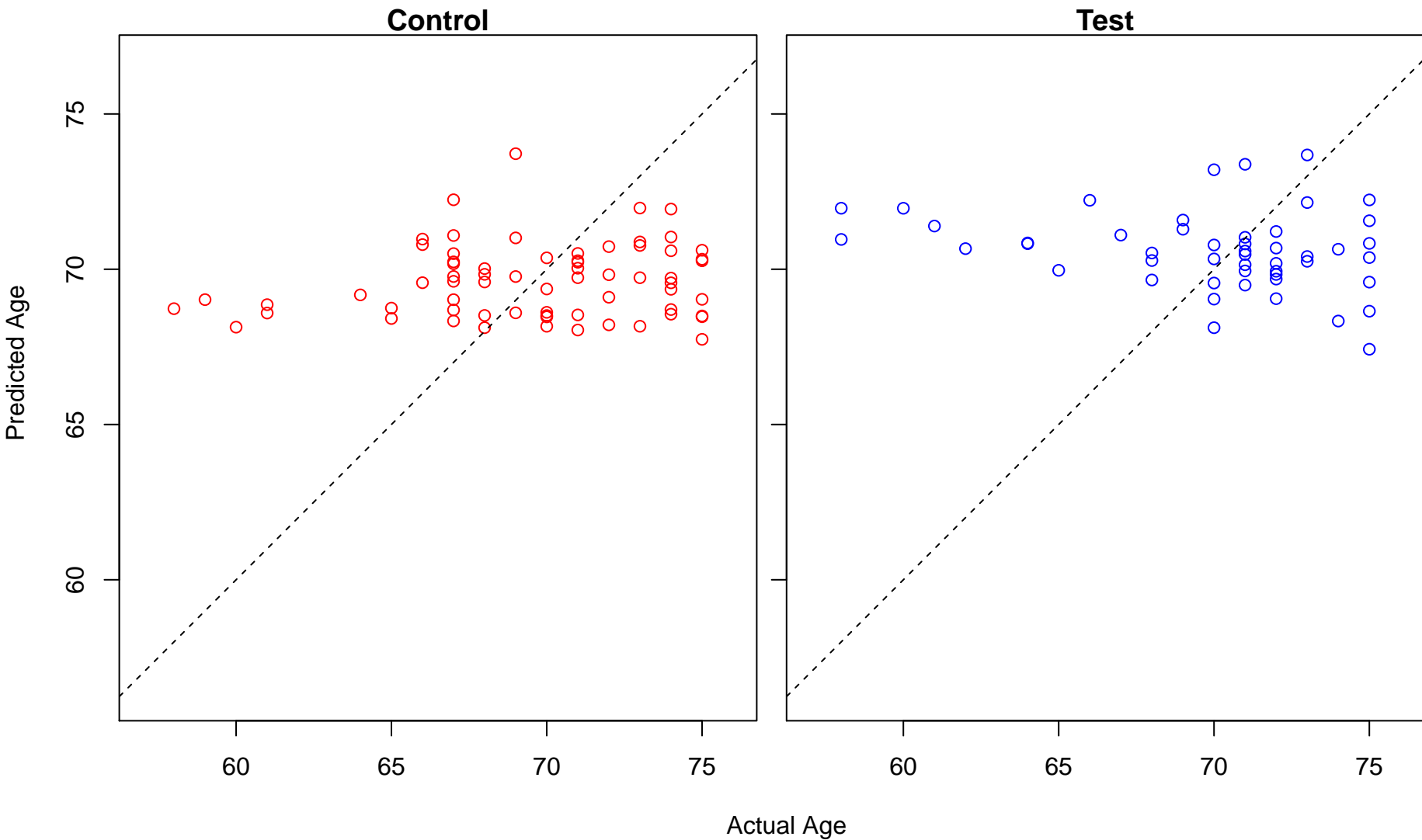
protein K27-linked ubiquitination (Score: 0.075895)



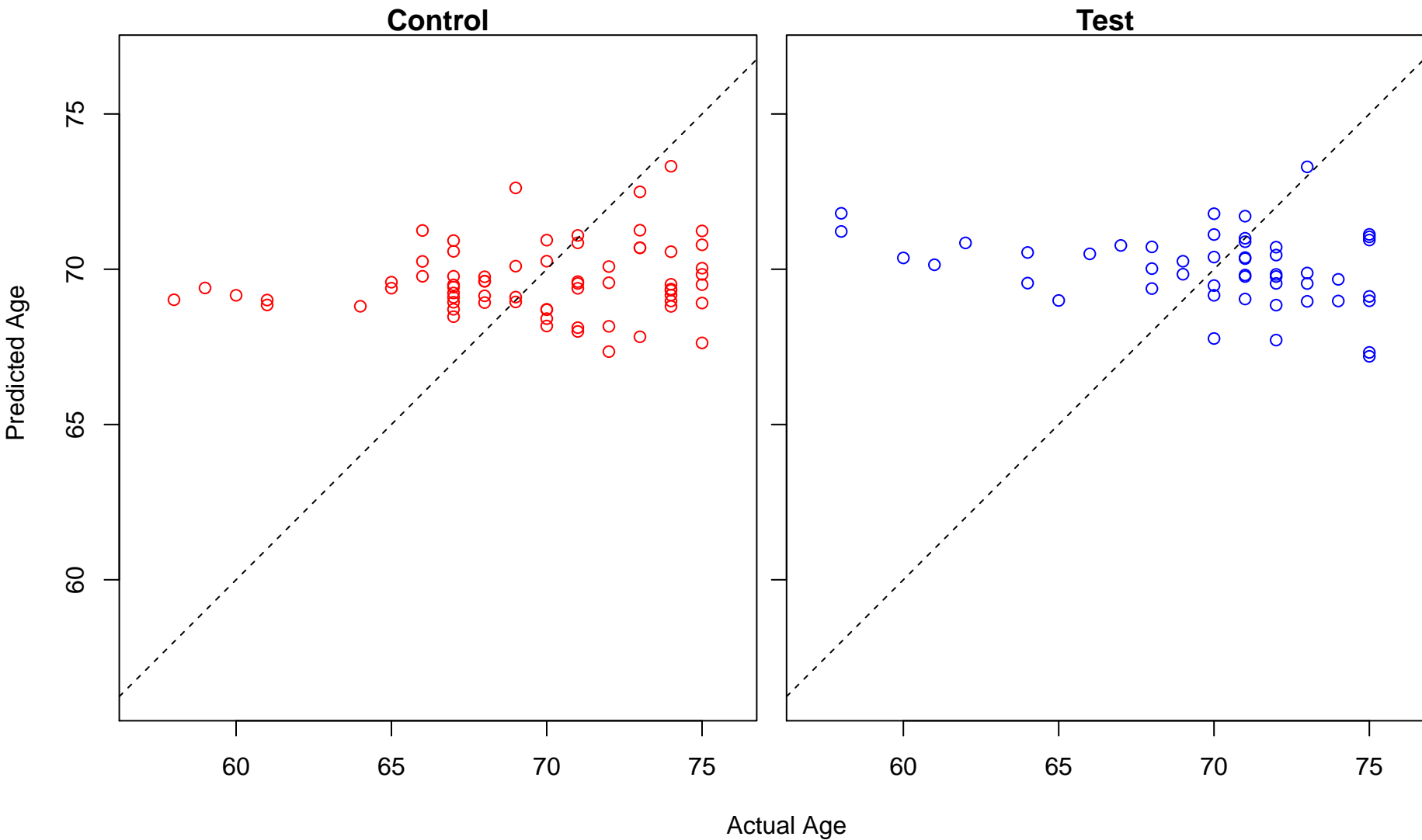
polyamine transport (Score: 0.075537)



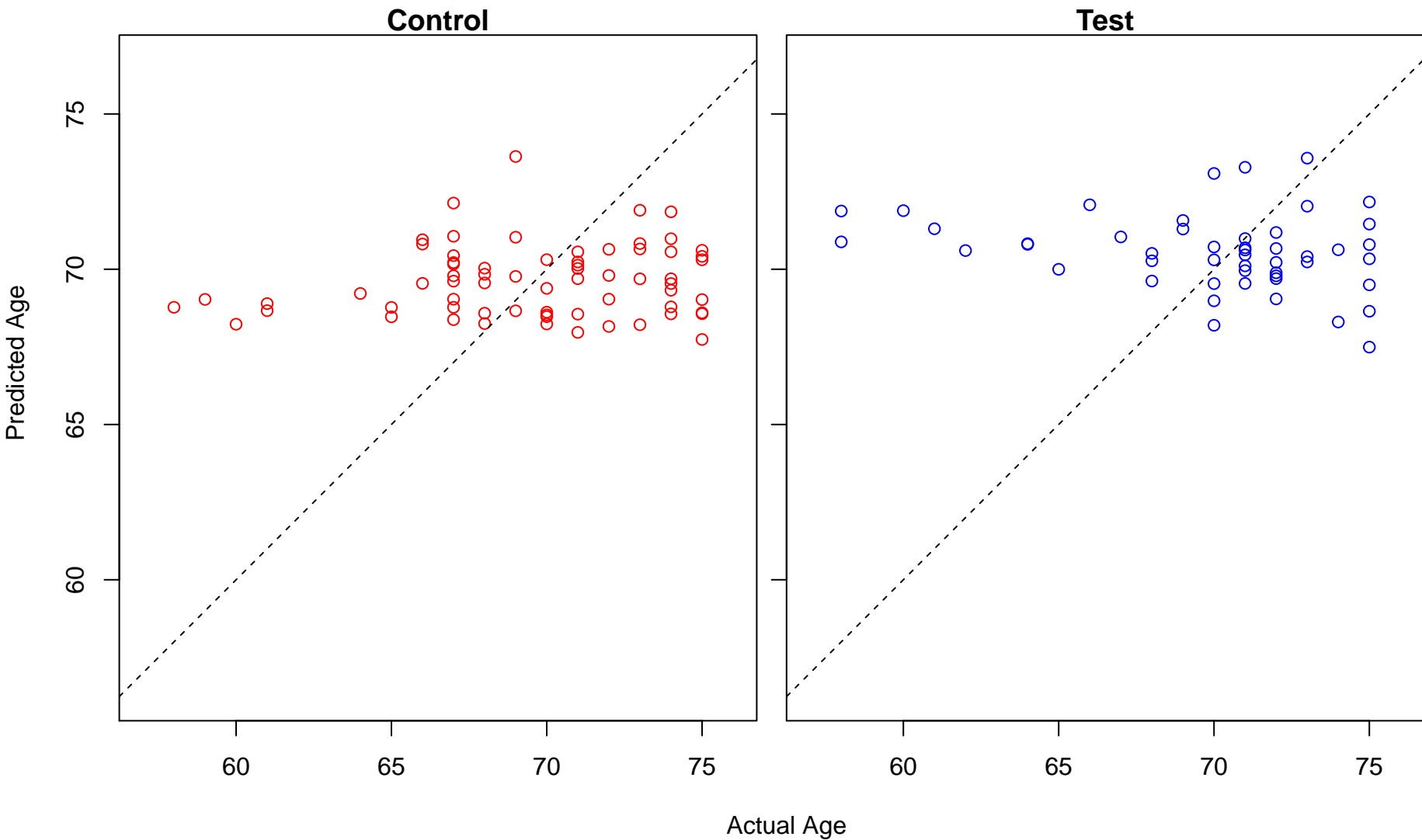
sphingoid metabolic process (Score: 0.071713)



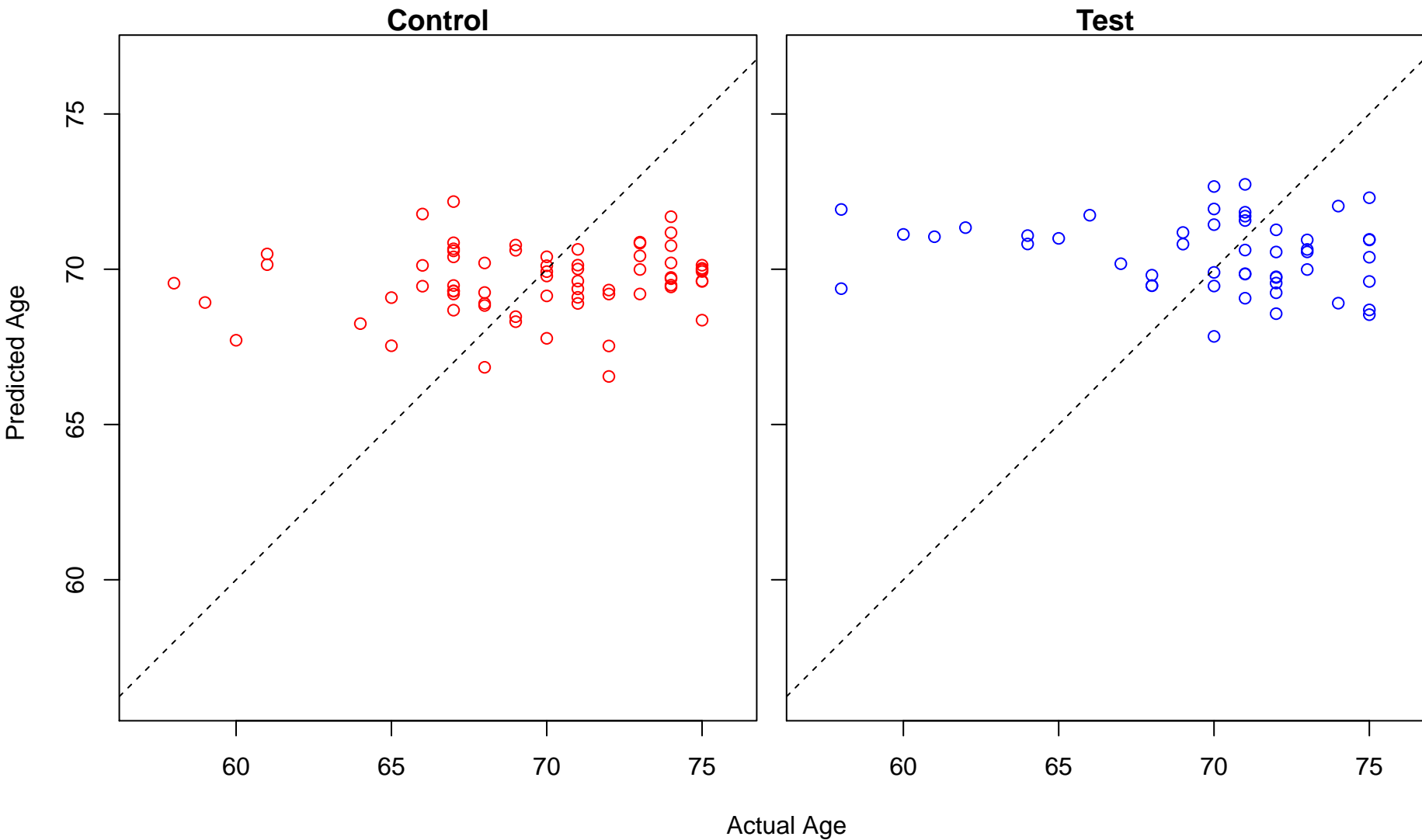
morphogenesis of a polarized epithelium (Score: 0.069422)



sphingoid biosynthetic process (Score: 0.063650)

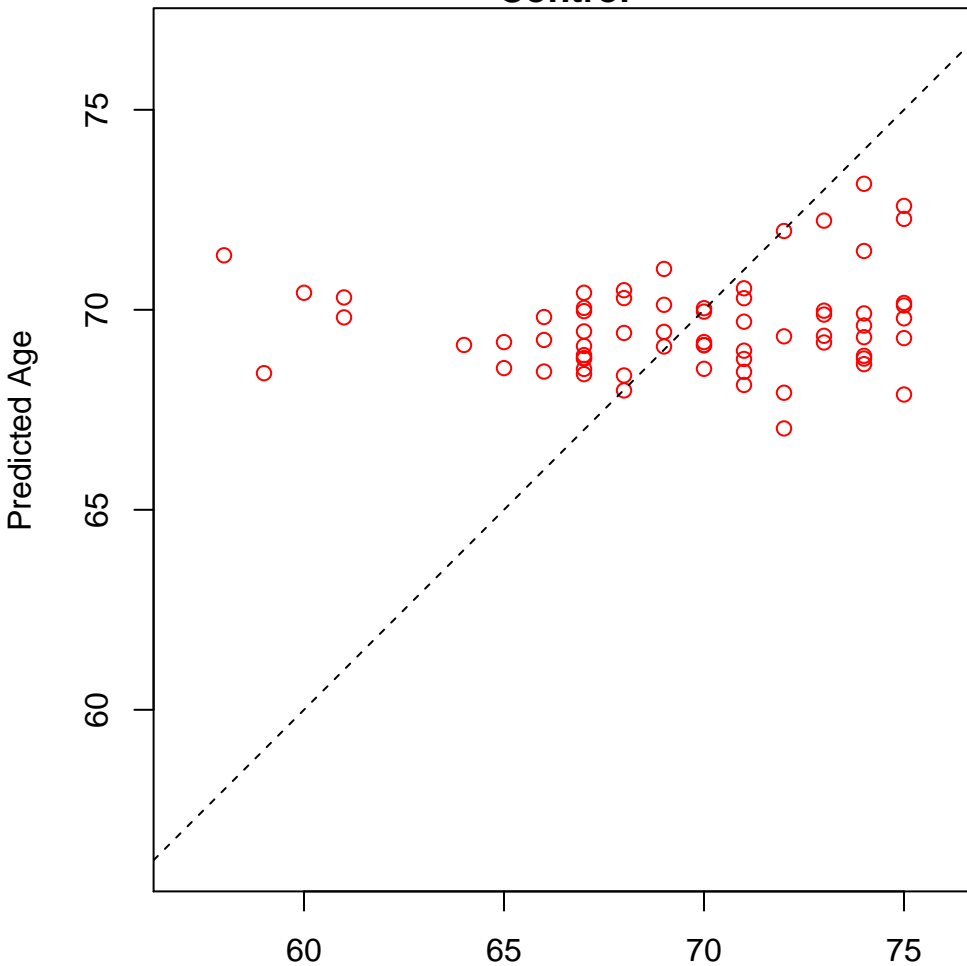


citrulline biosynthetic process (Score: 0.061620)

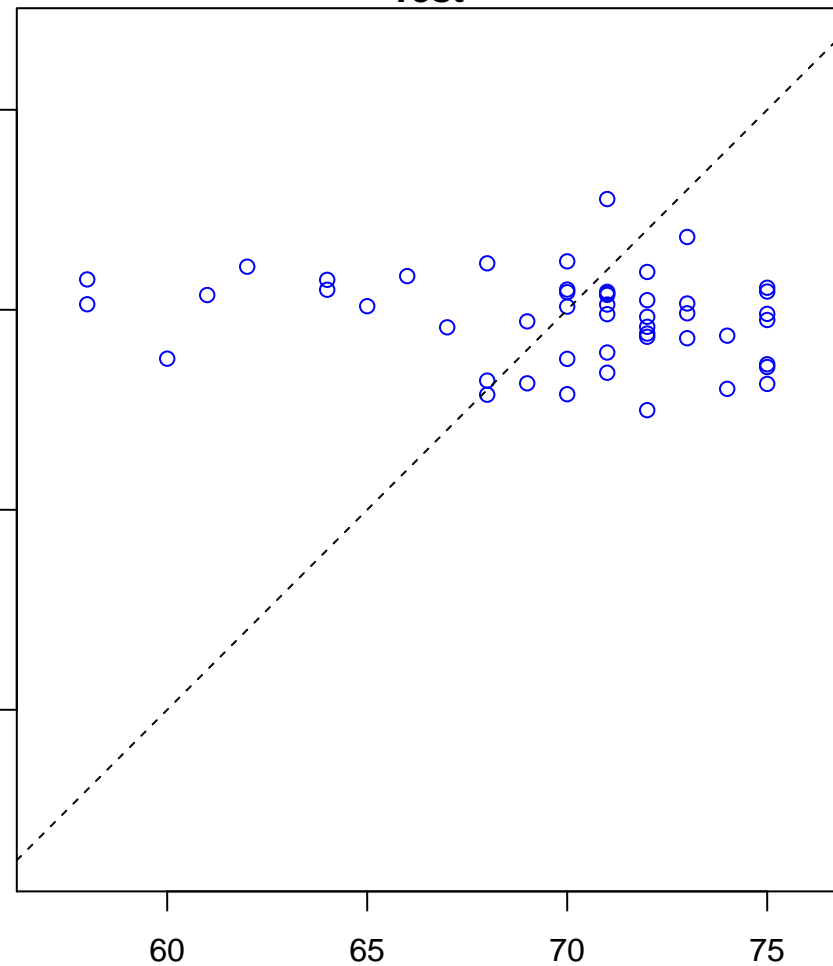


negative regulation of amine transport (Score: 0.055056)

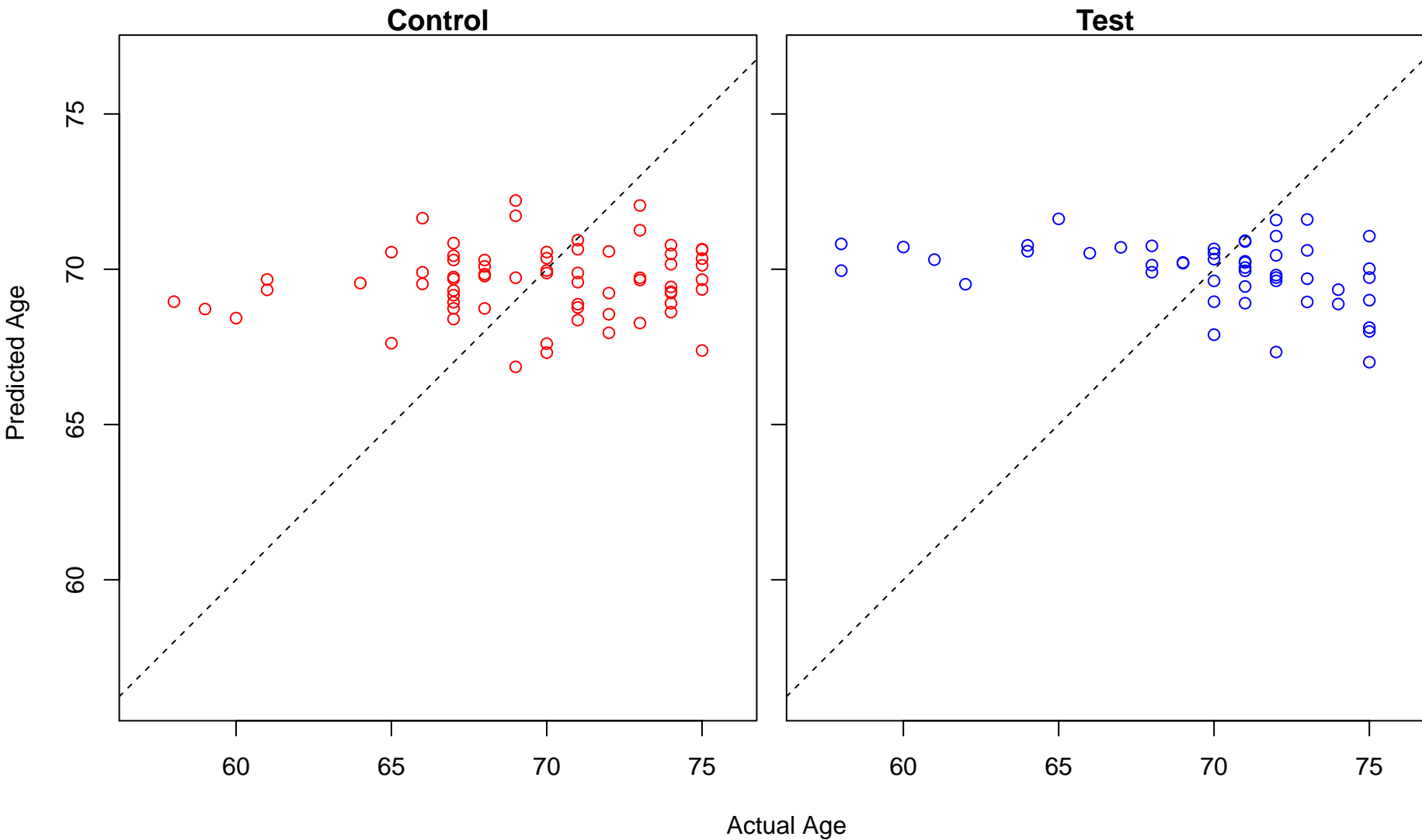
Control



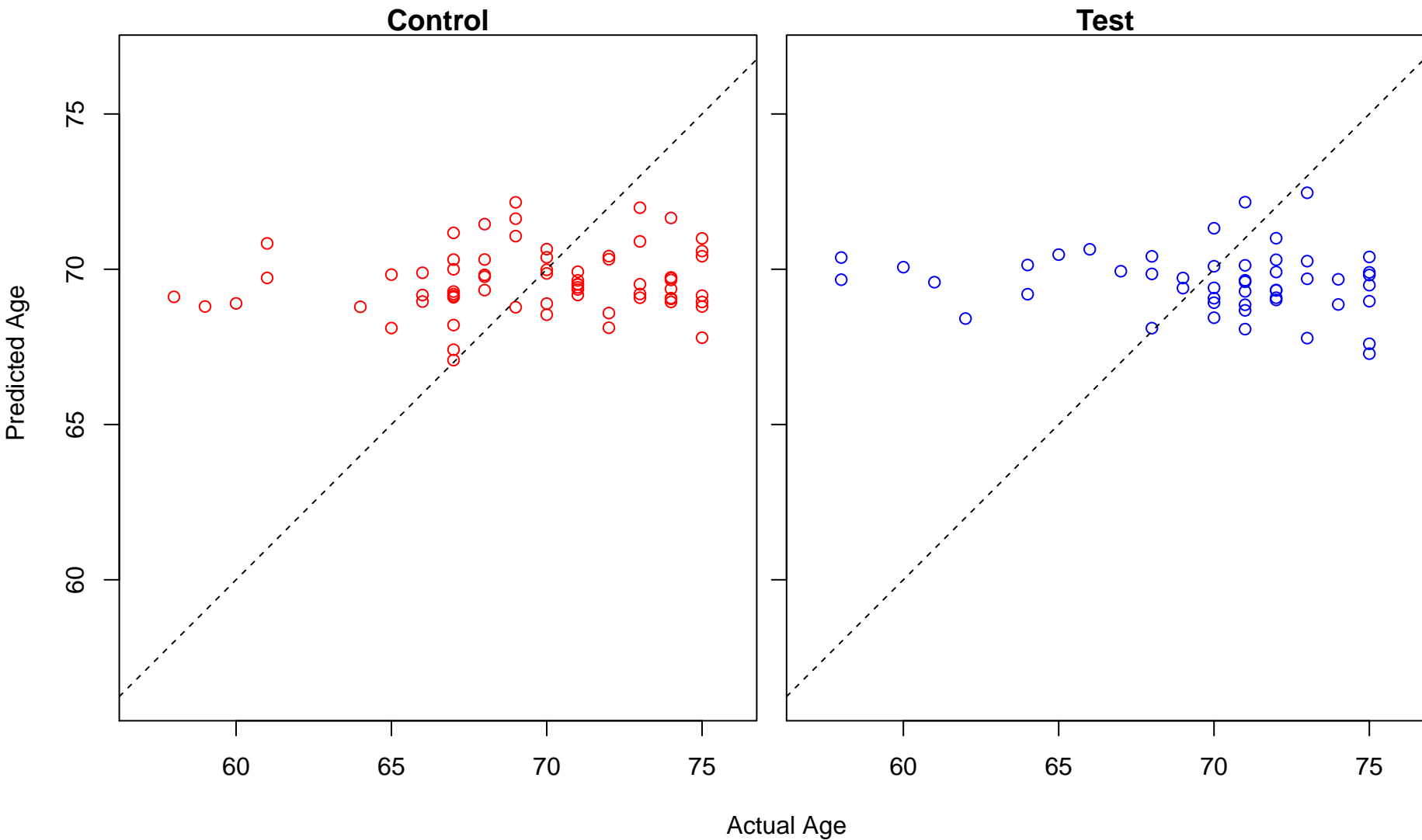
Test



regulation of smooth muscle cell apoptotic process (Score: 0.043643)



cellular phosphate ion homeostasis (Score: 0.042397)



cellular trivalent inorganic anion homeostasis (Score: 0.042397)

