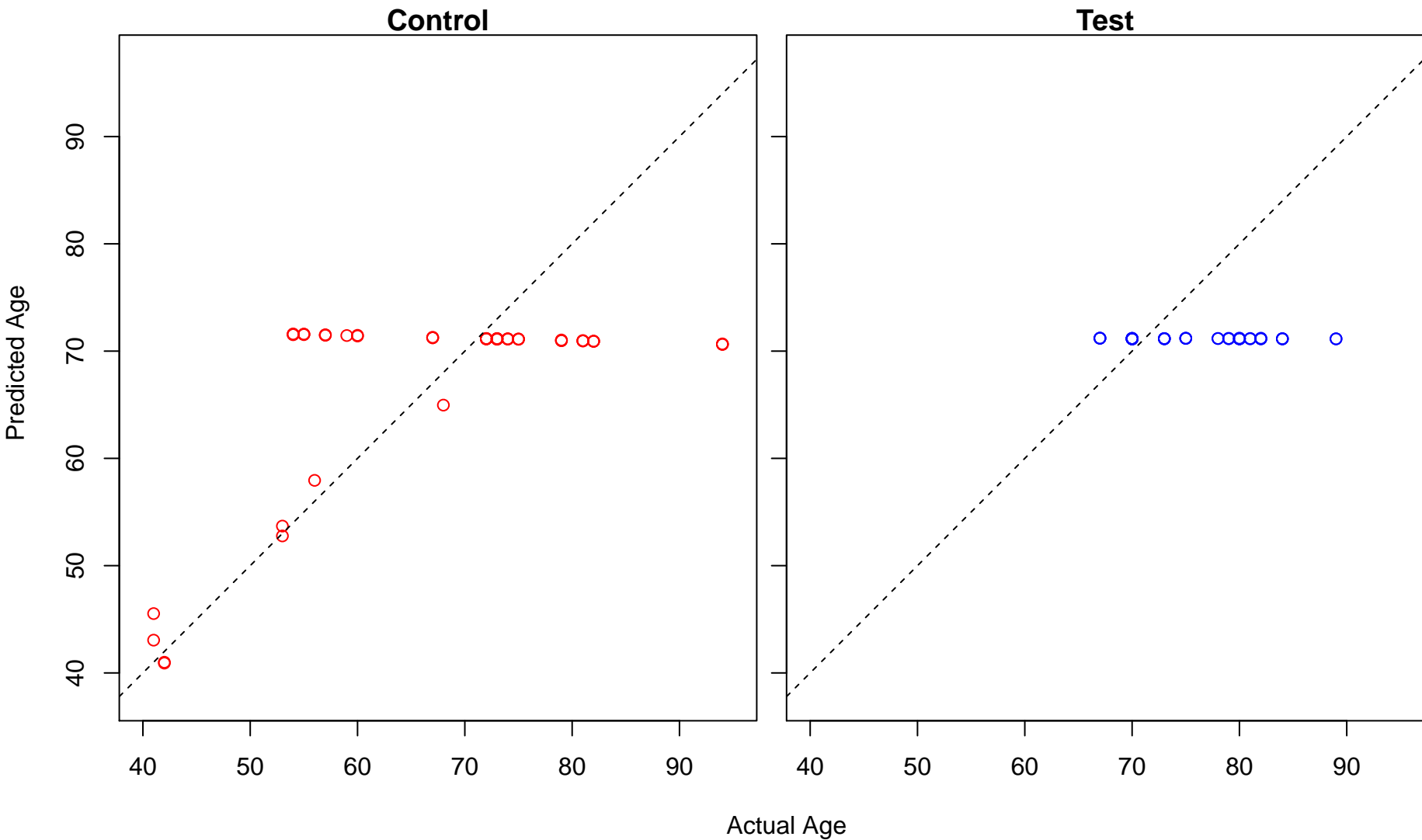
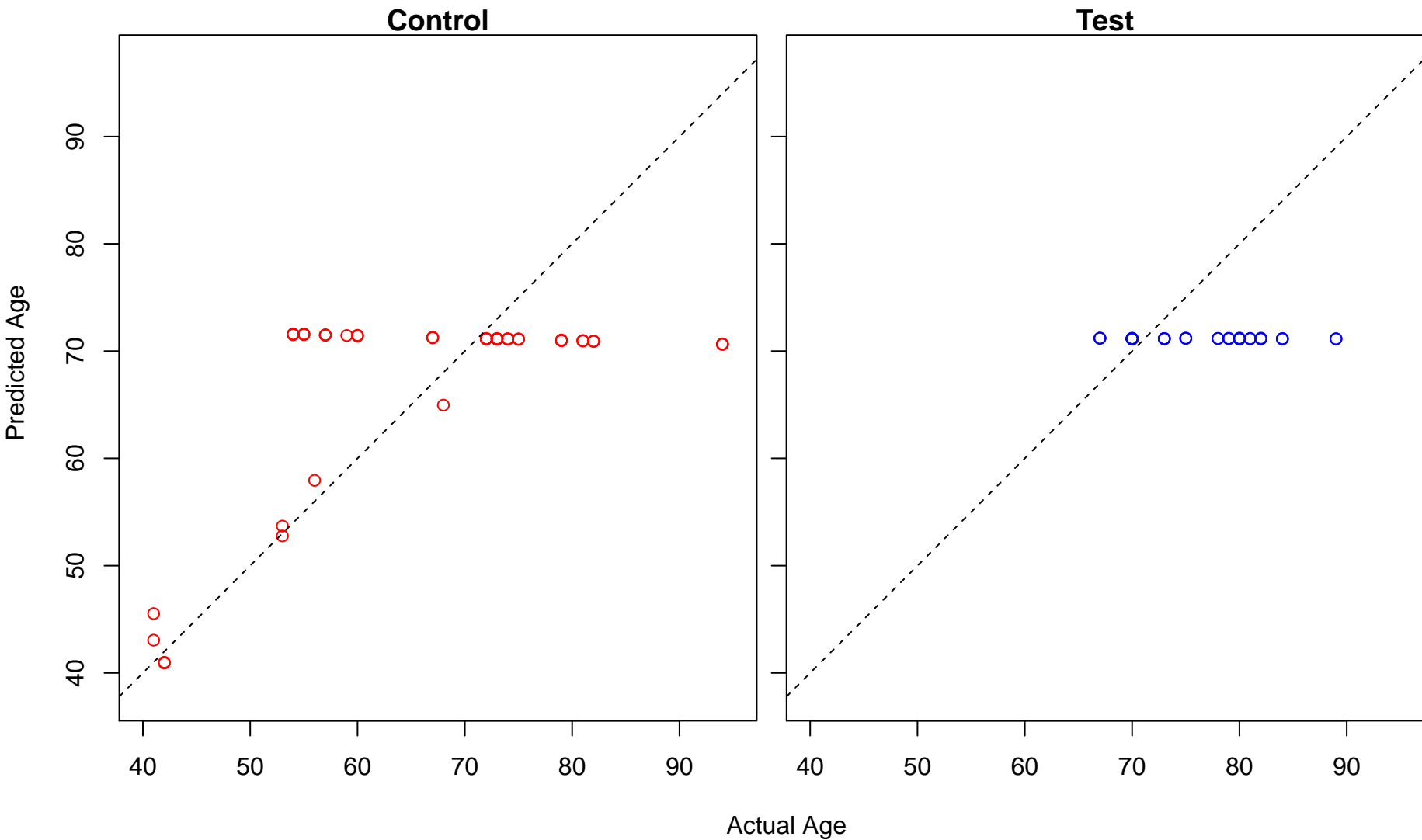


interleukin-12-mediated signaling pathway (Score: 0.860591)

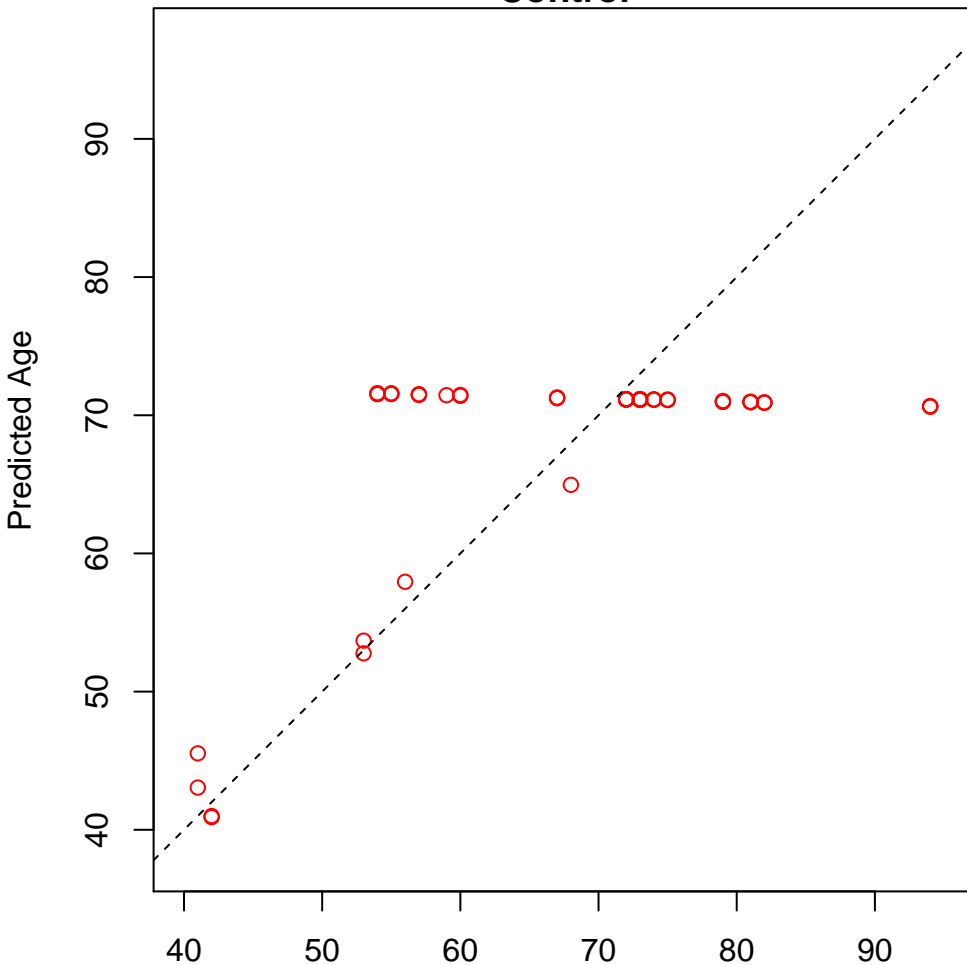


response to interleukin-12 (Score: 0.860591)

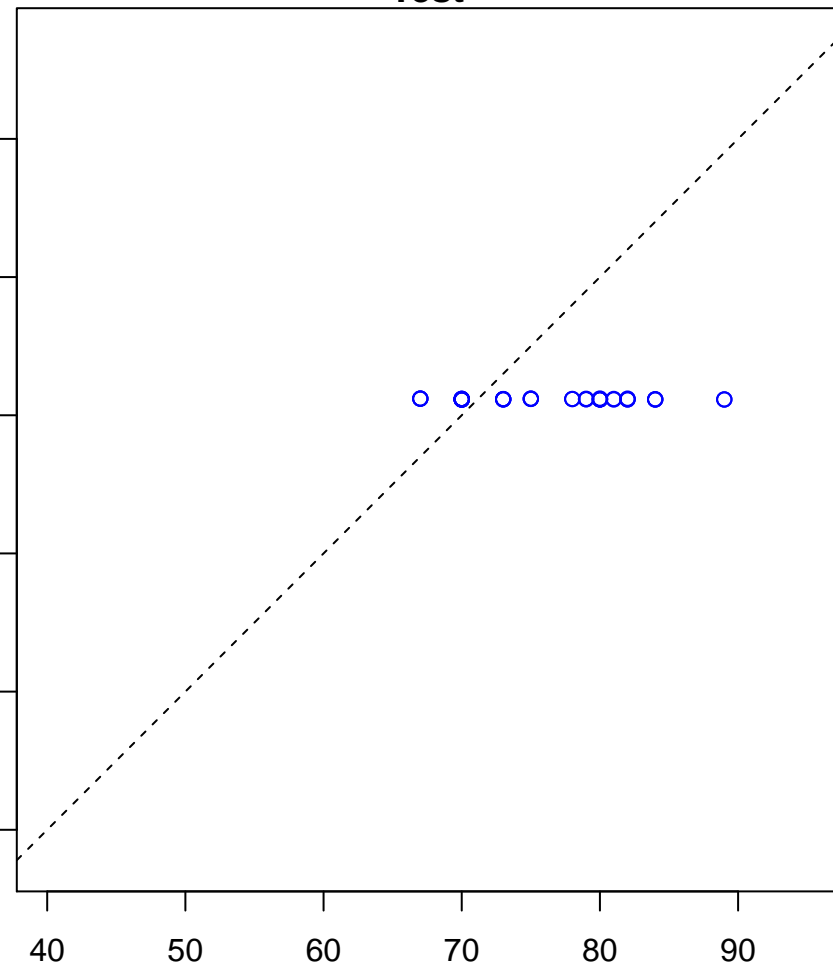


cellular response to interleukin-12 (Score: 0.860591)

Control



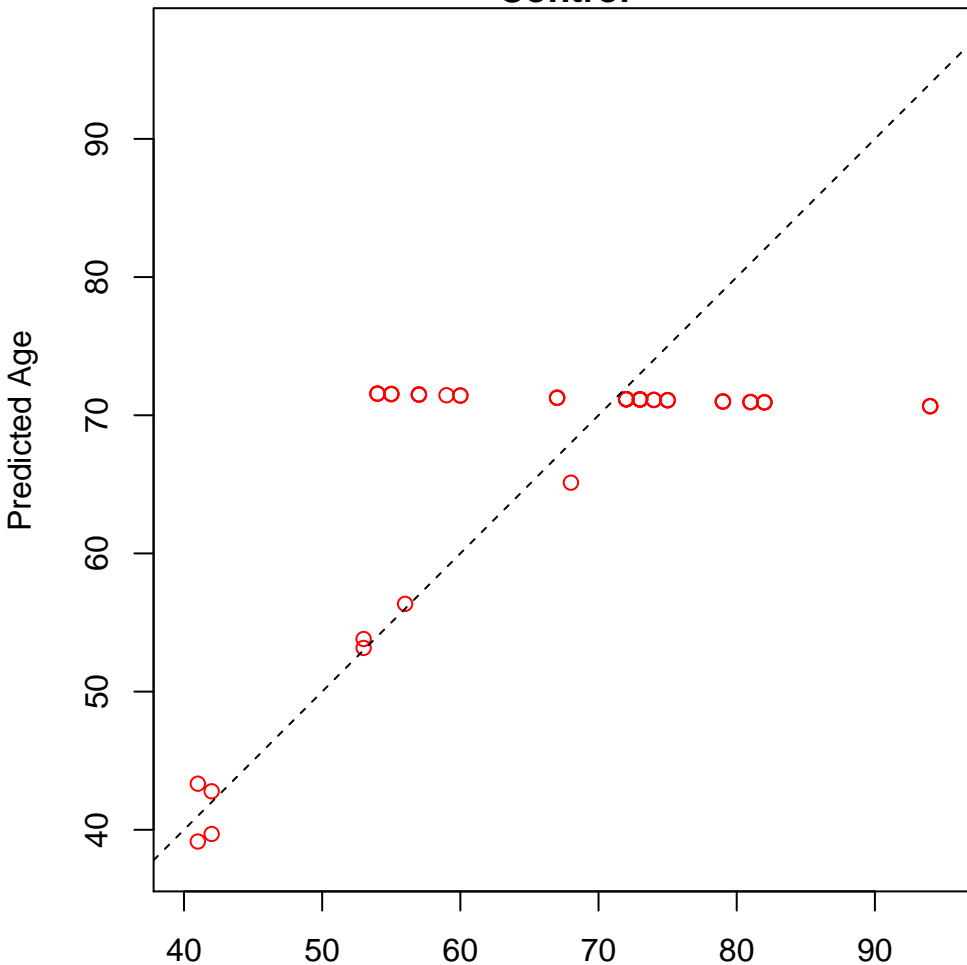
Test



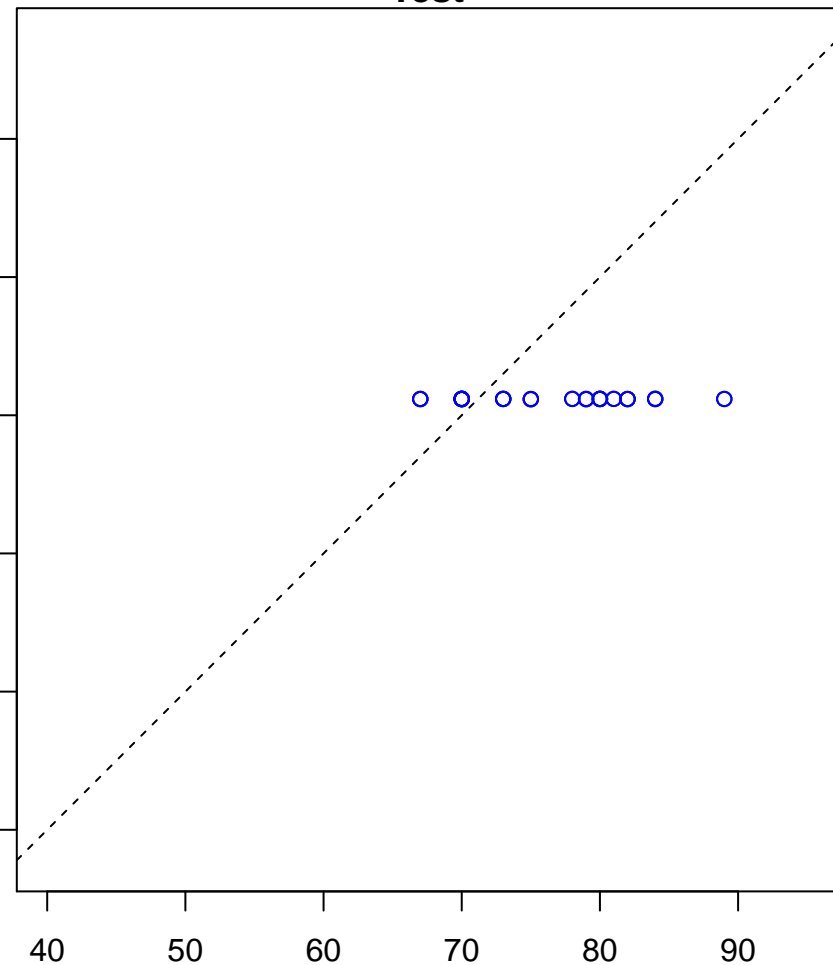
Actual Age

protein polyubiquitination (Score: 0.858895)

Control



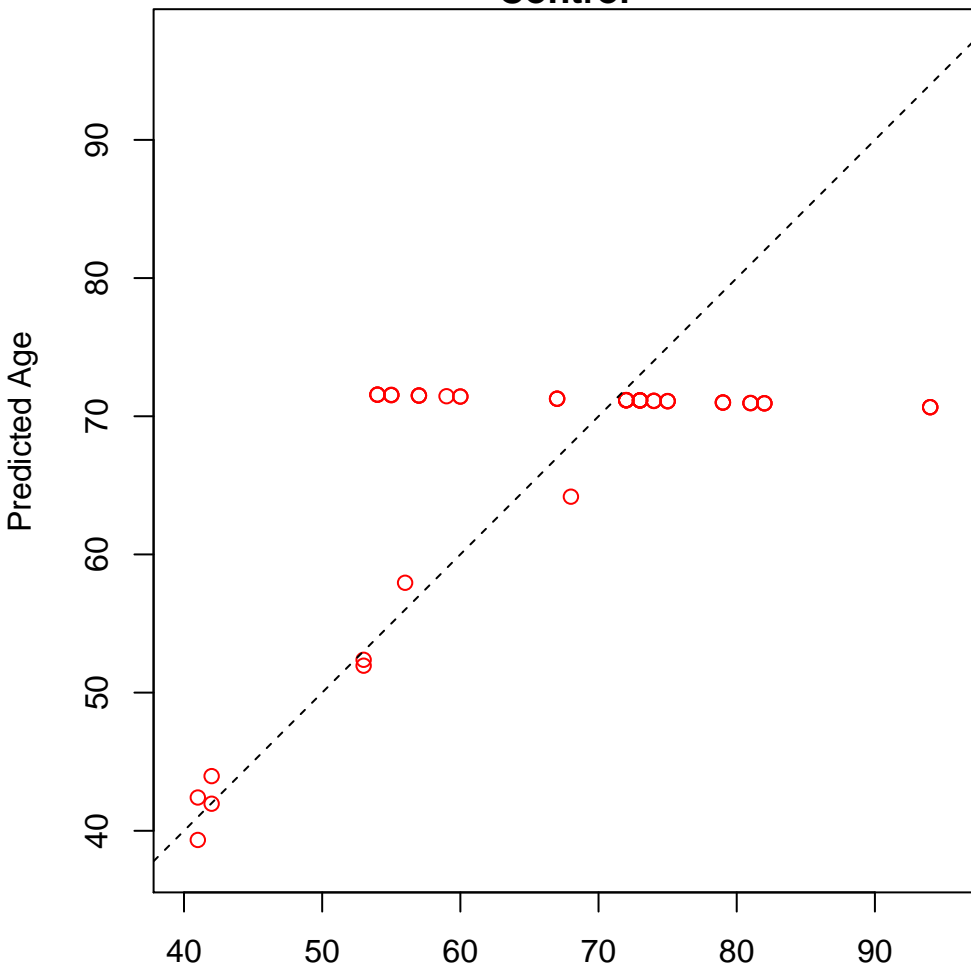
Test



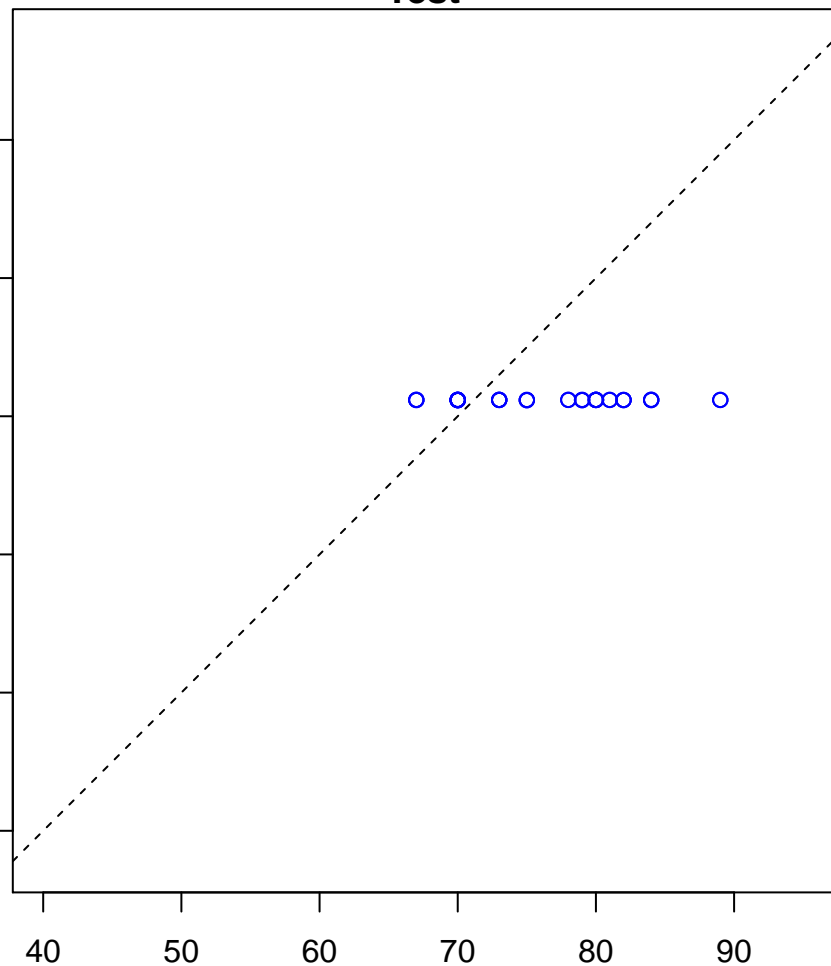
Actual Age

proteasomal protein catabolic process (Score: 0.858544)

Control

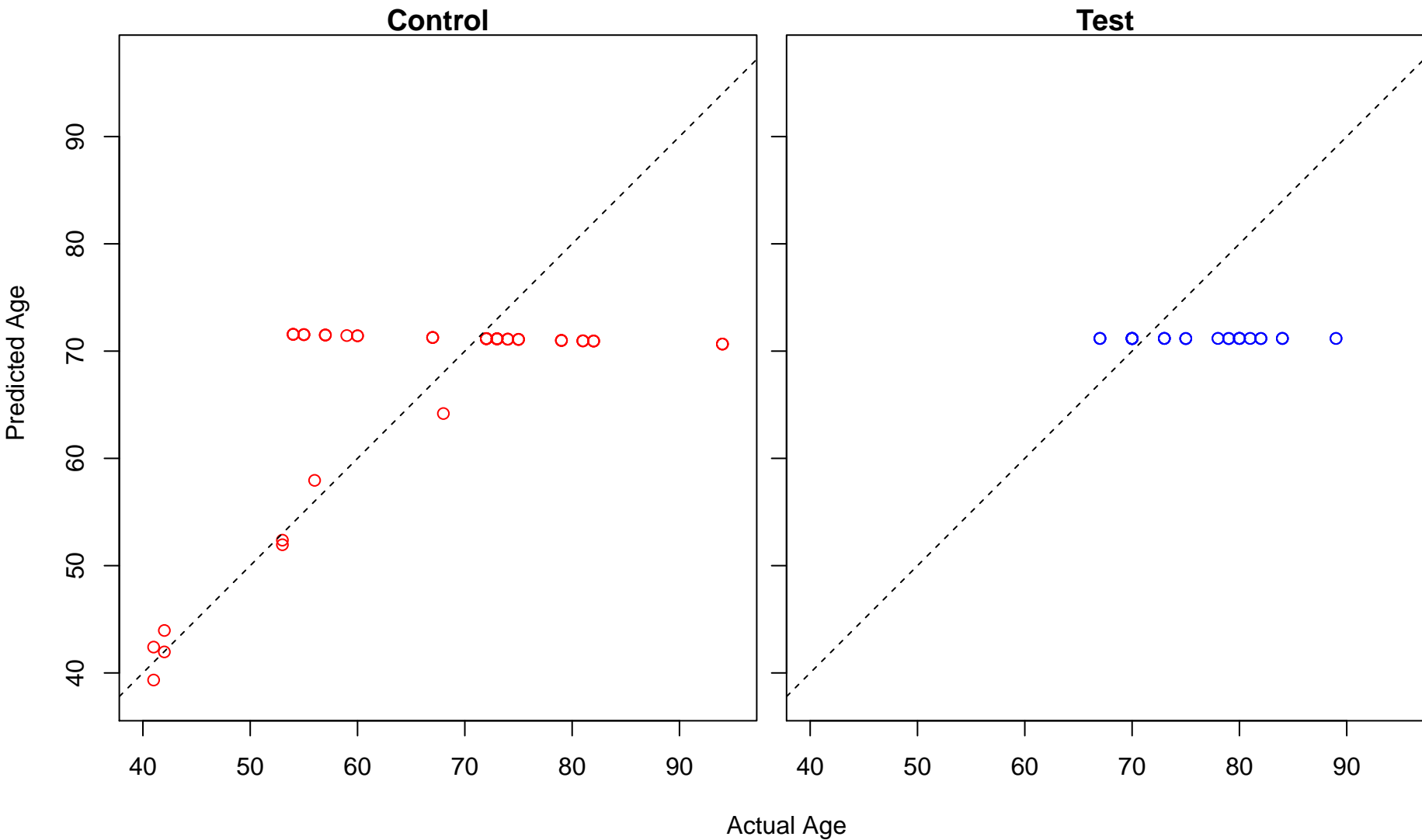


Test

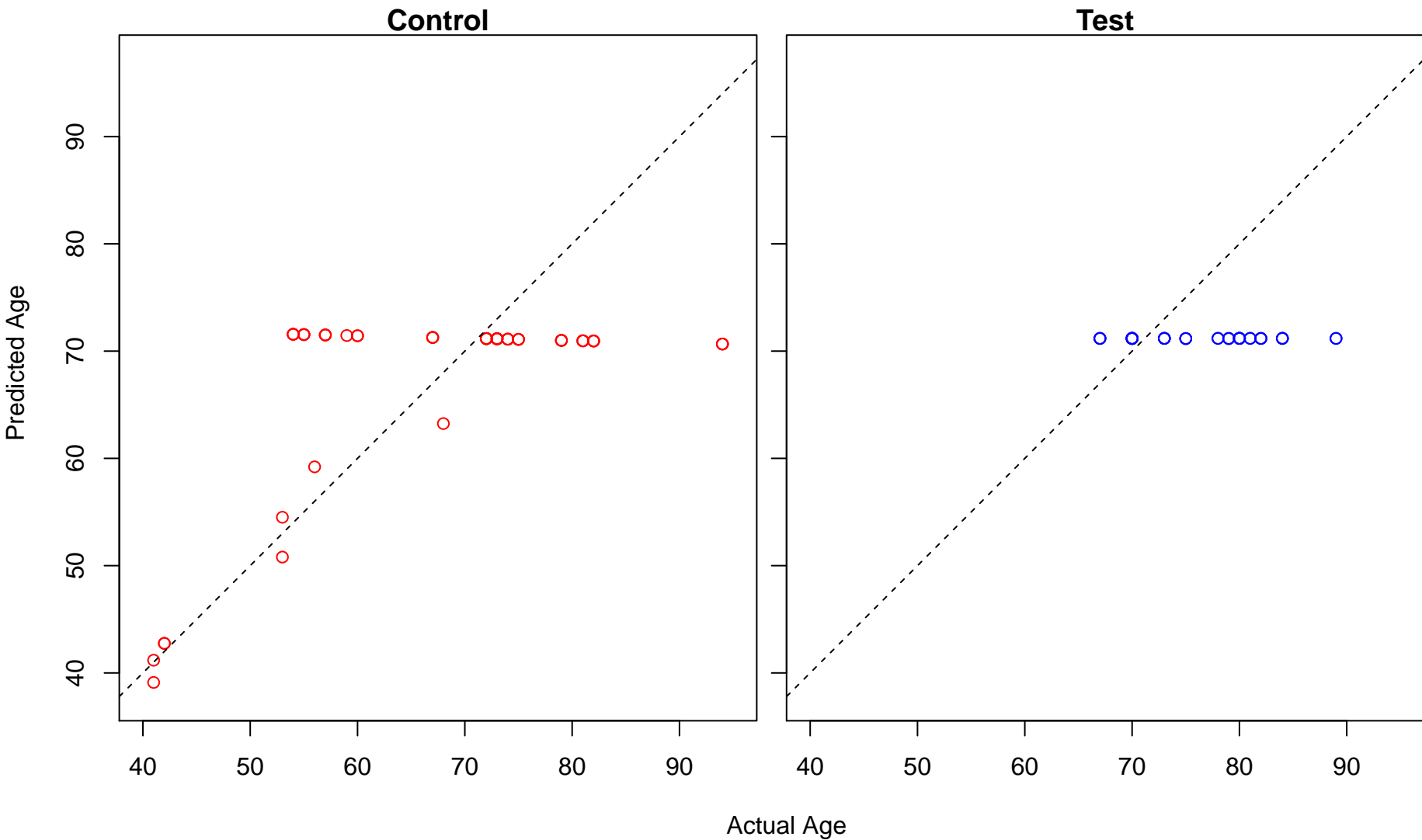


Actual Age

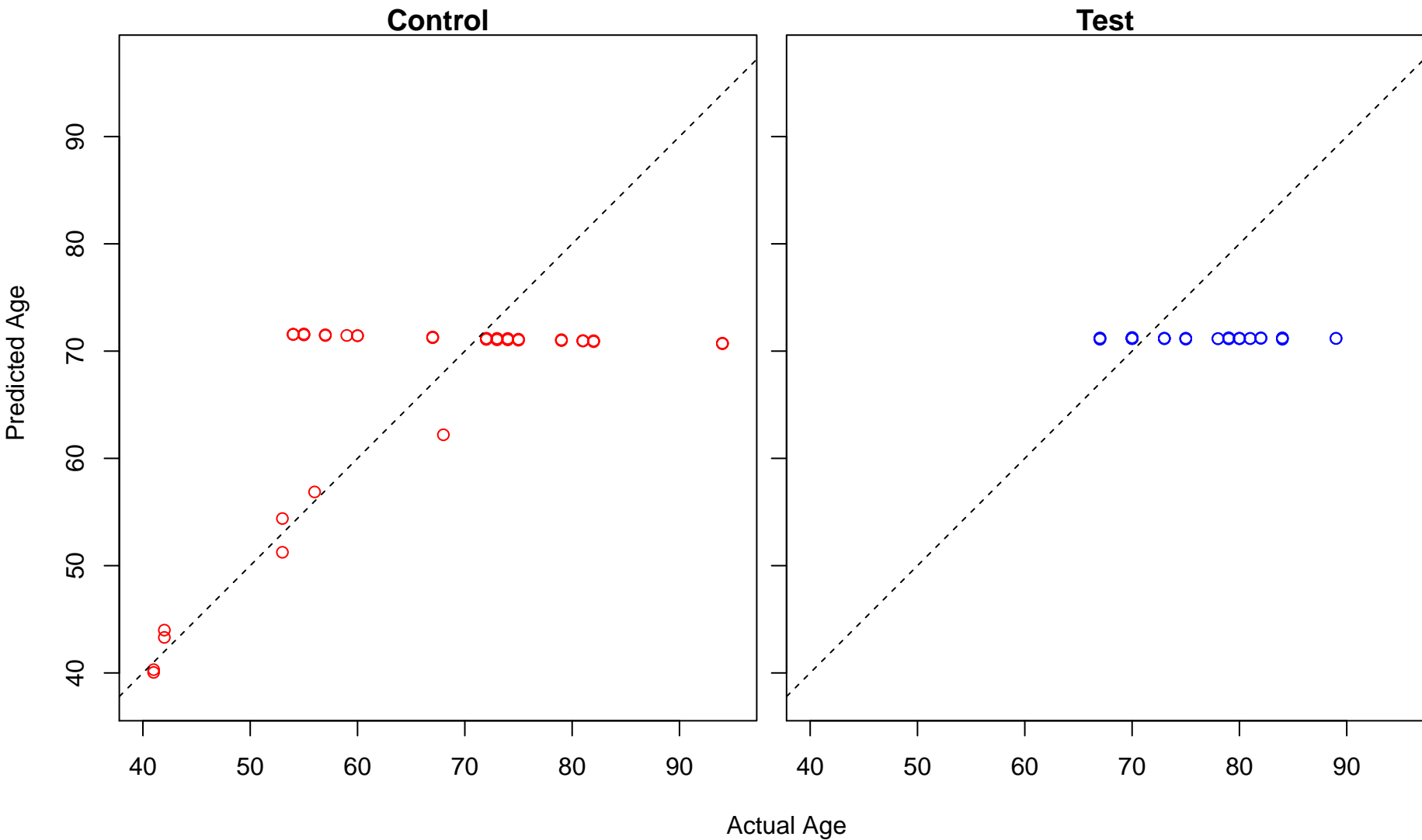
proteasome-mediated ubiquitin-dependent protein catabolic process (Score: 0.858544)



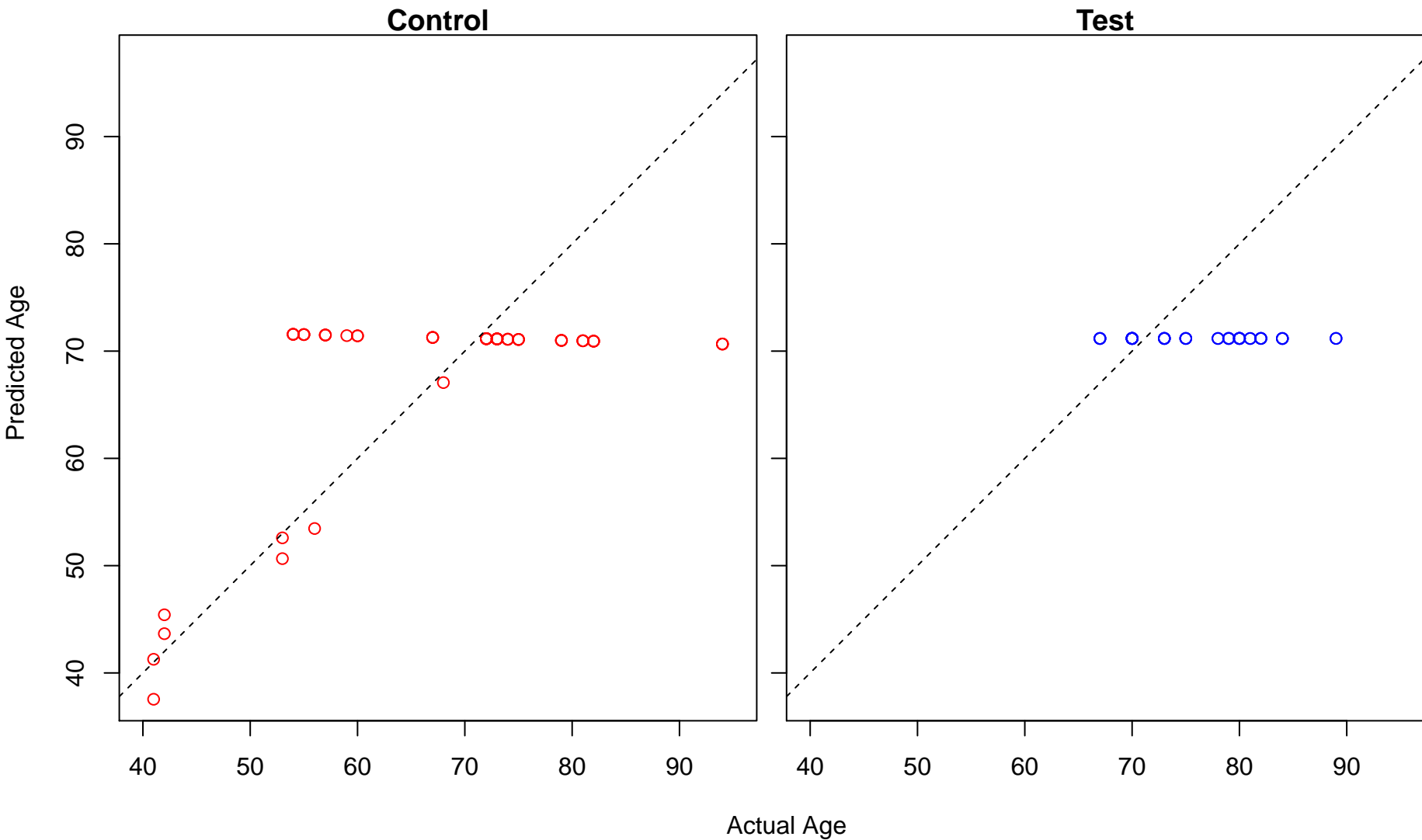
innate immune response-activating signal transduction (Score: 0.855669)



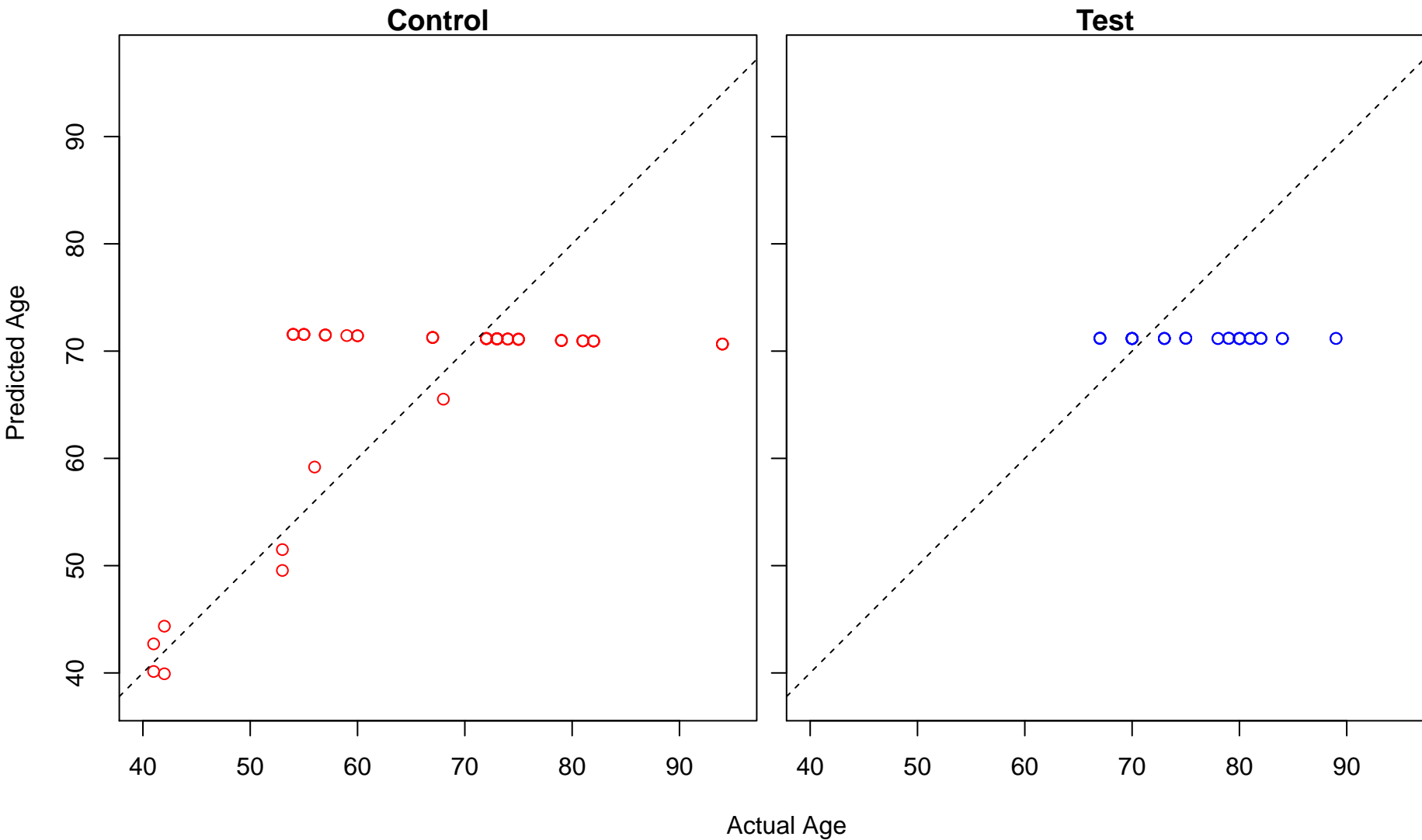
system process (Score: 0.855385)



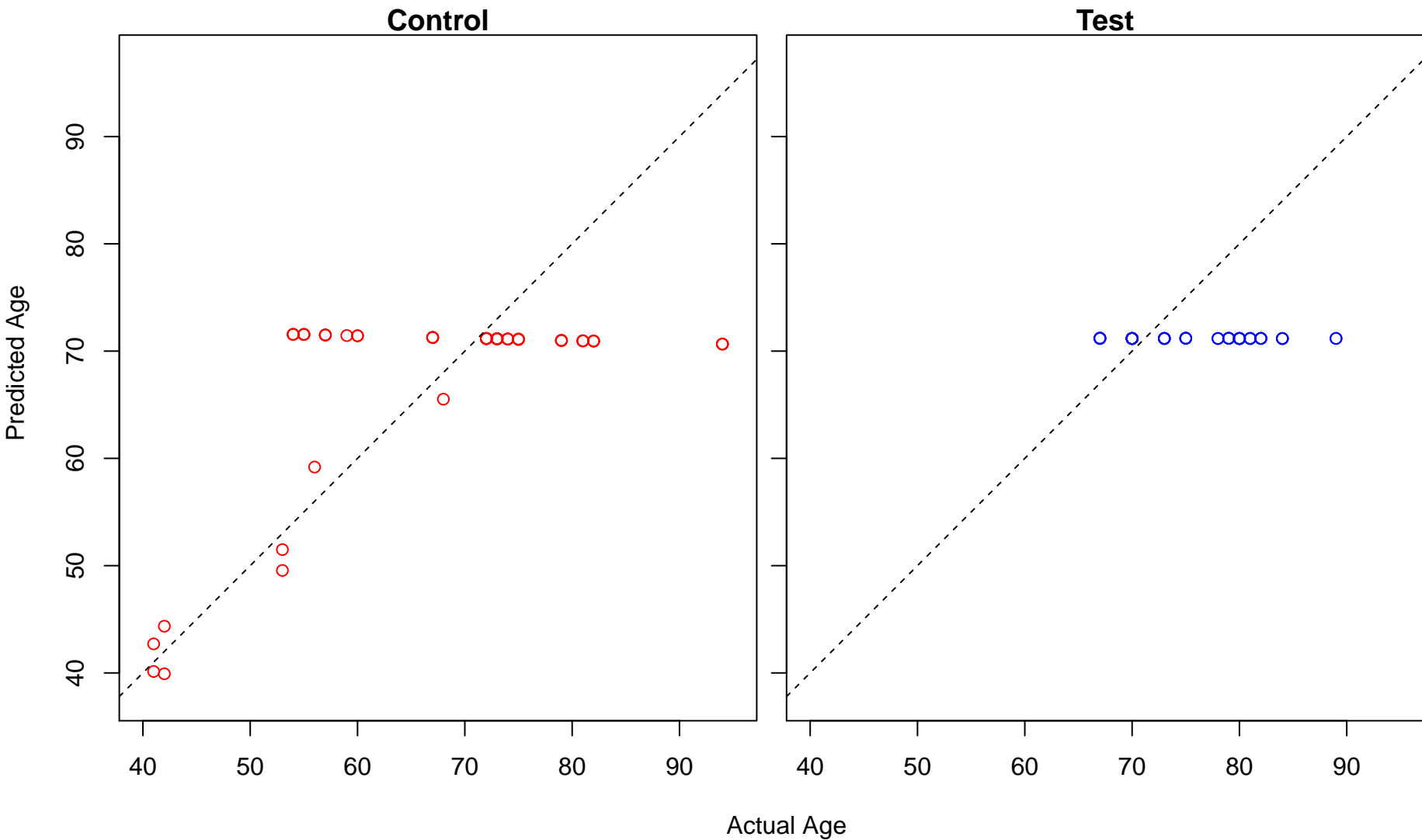
regulation of body fluid levels (Score: 0.854892)



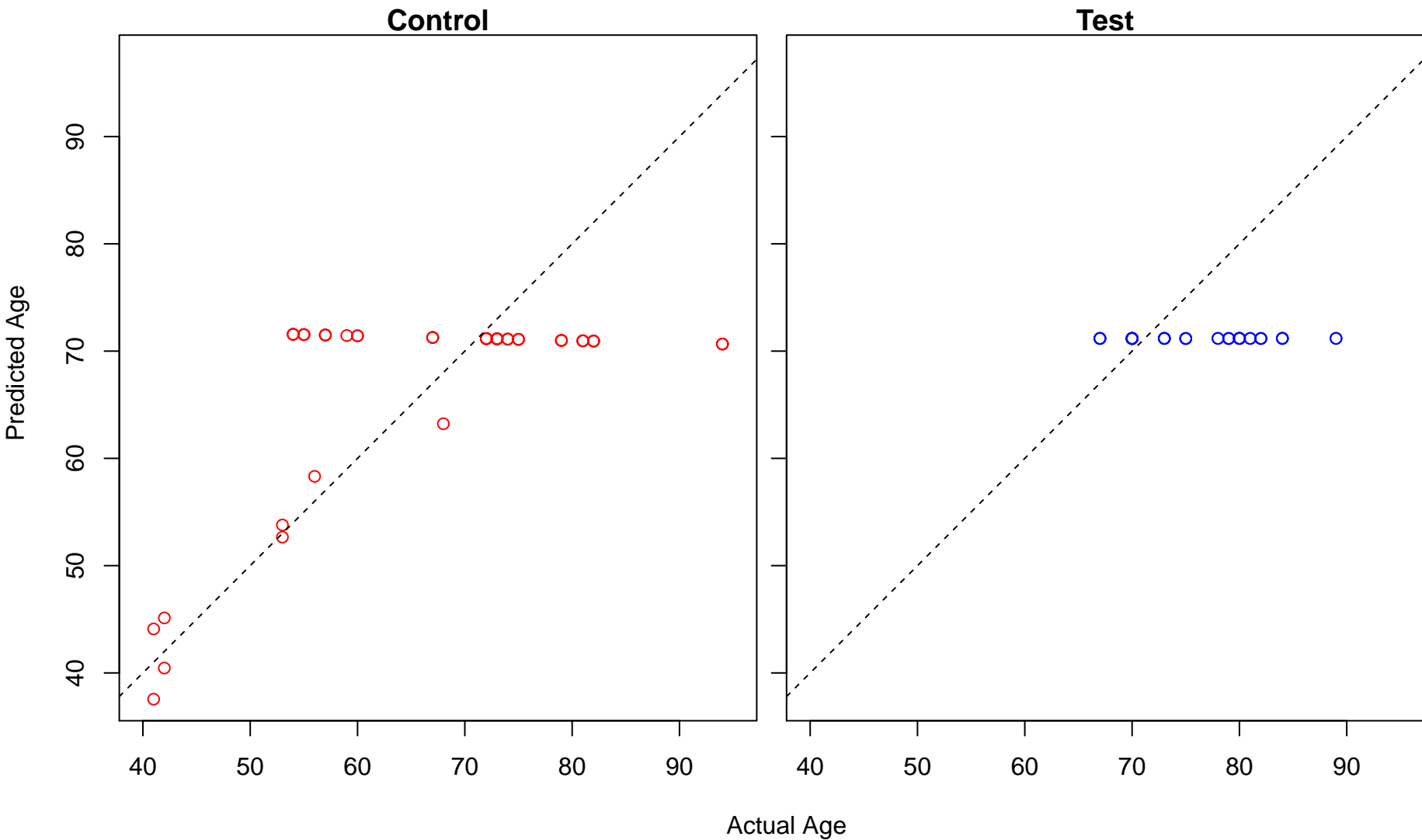
maintenance of location (Score: 0.853736)



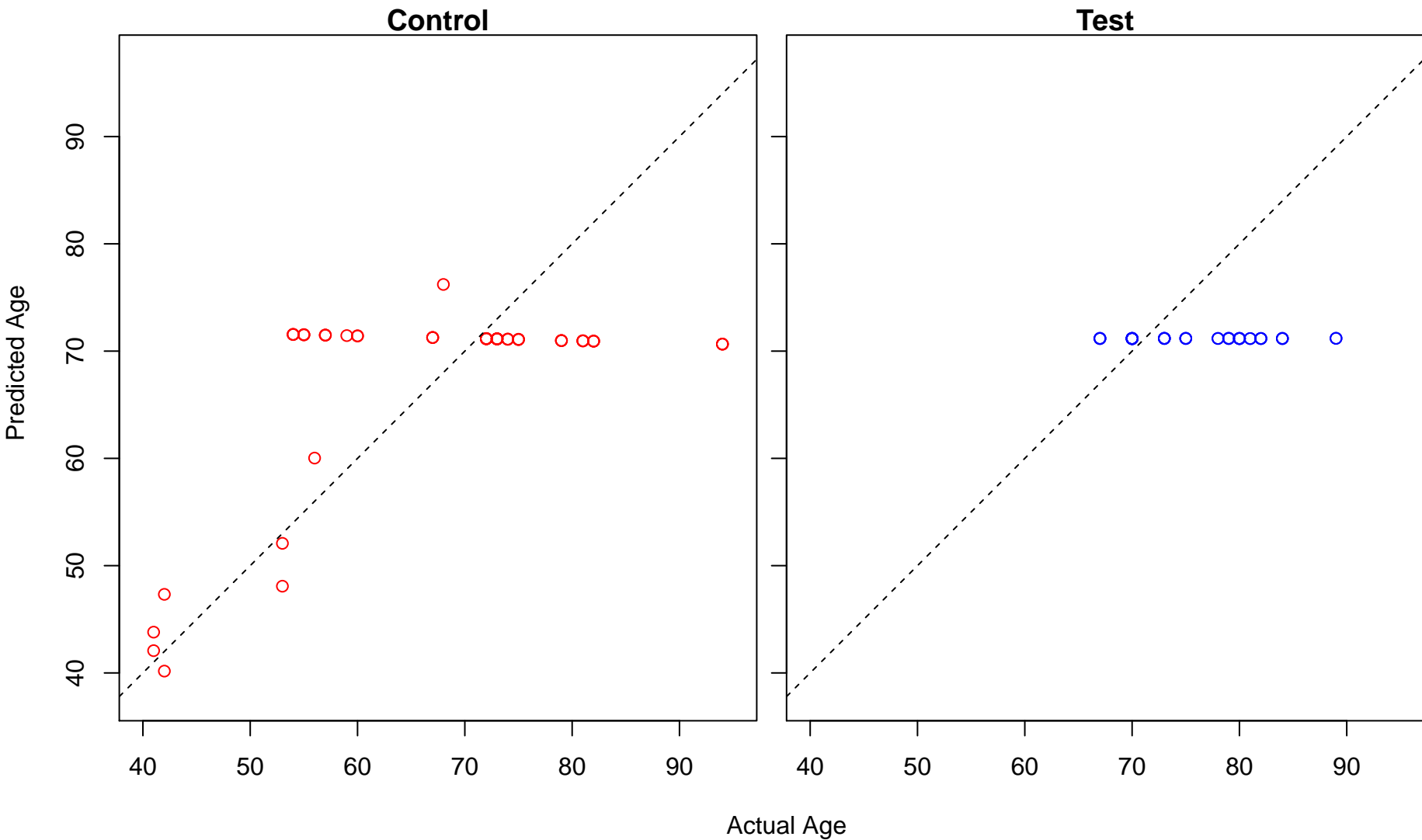
maintenance of location in cell (Score: 0.853736)



protein ubiquitination (Score: 0.853115)

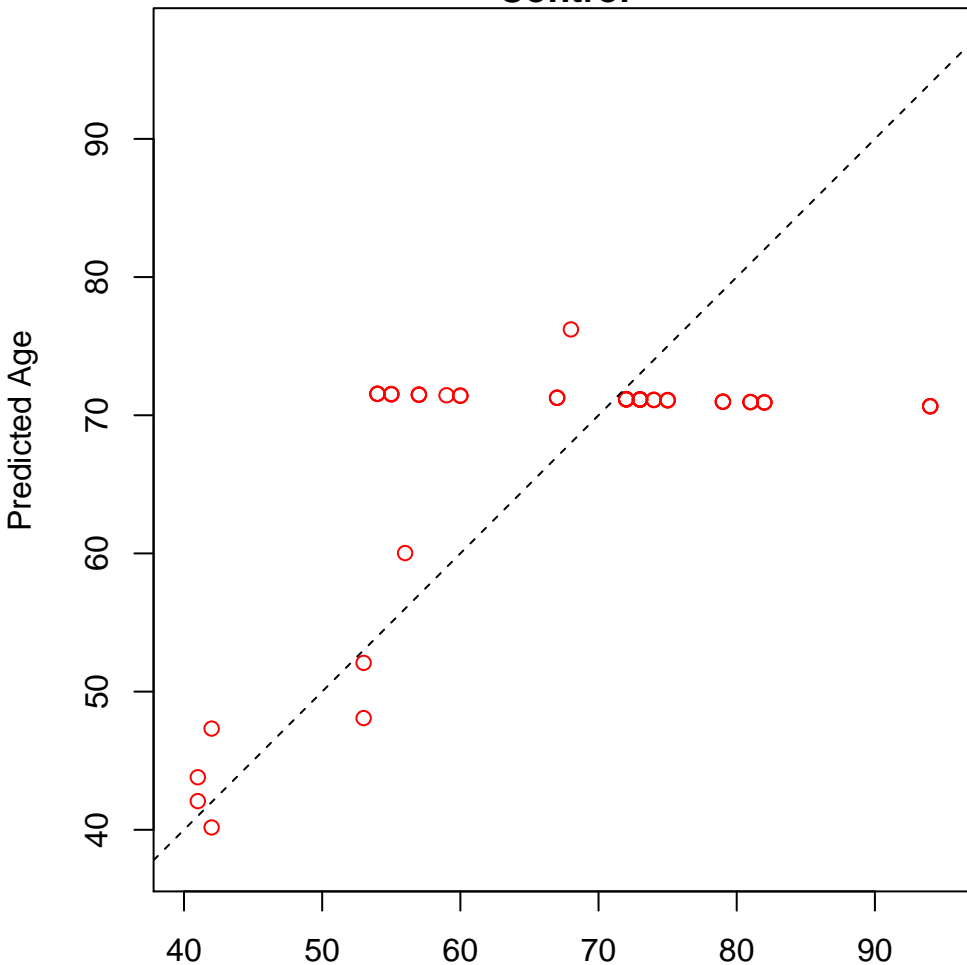


antigen processing and presentation of exogenous peptide antigen (Score: 0.852644)

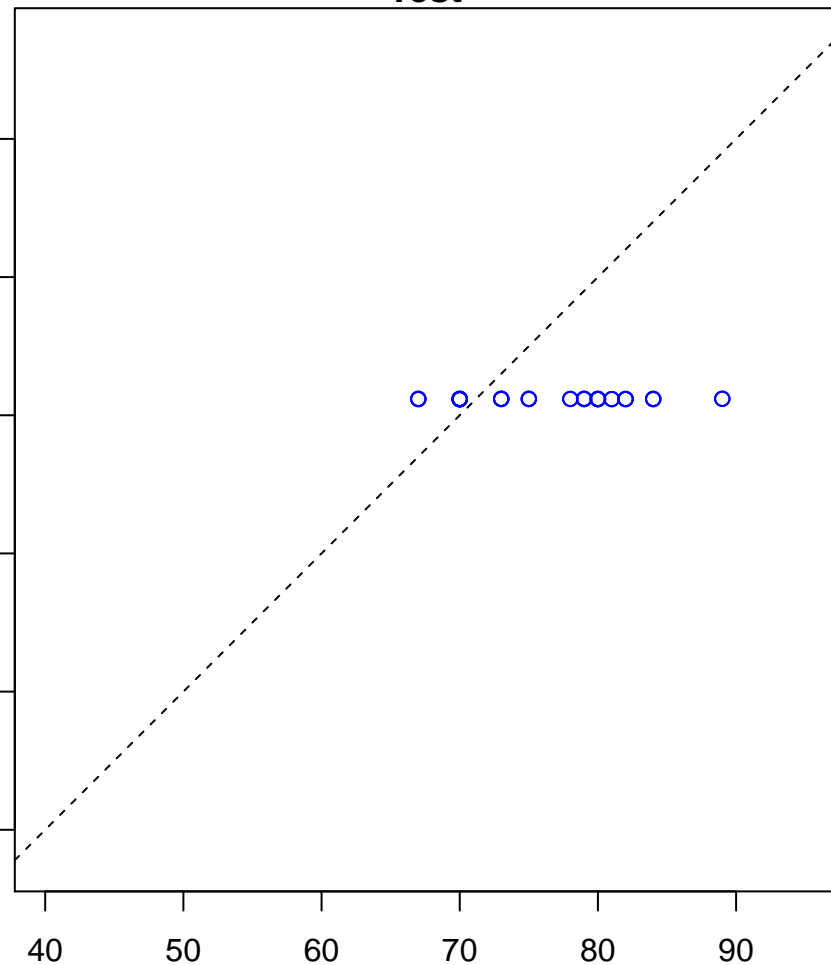


antigen processing and presentation (Score: 0.852644)

Control

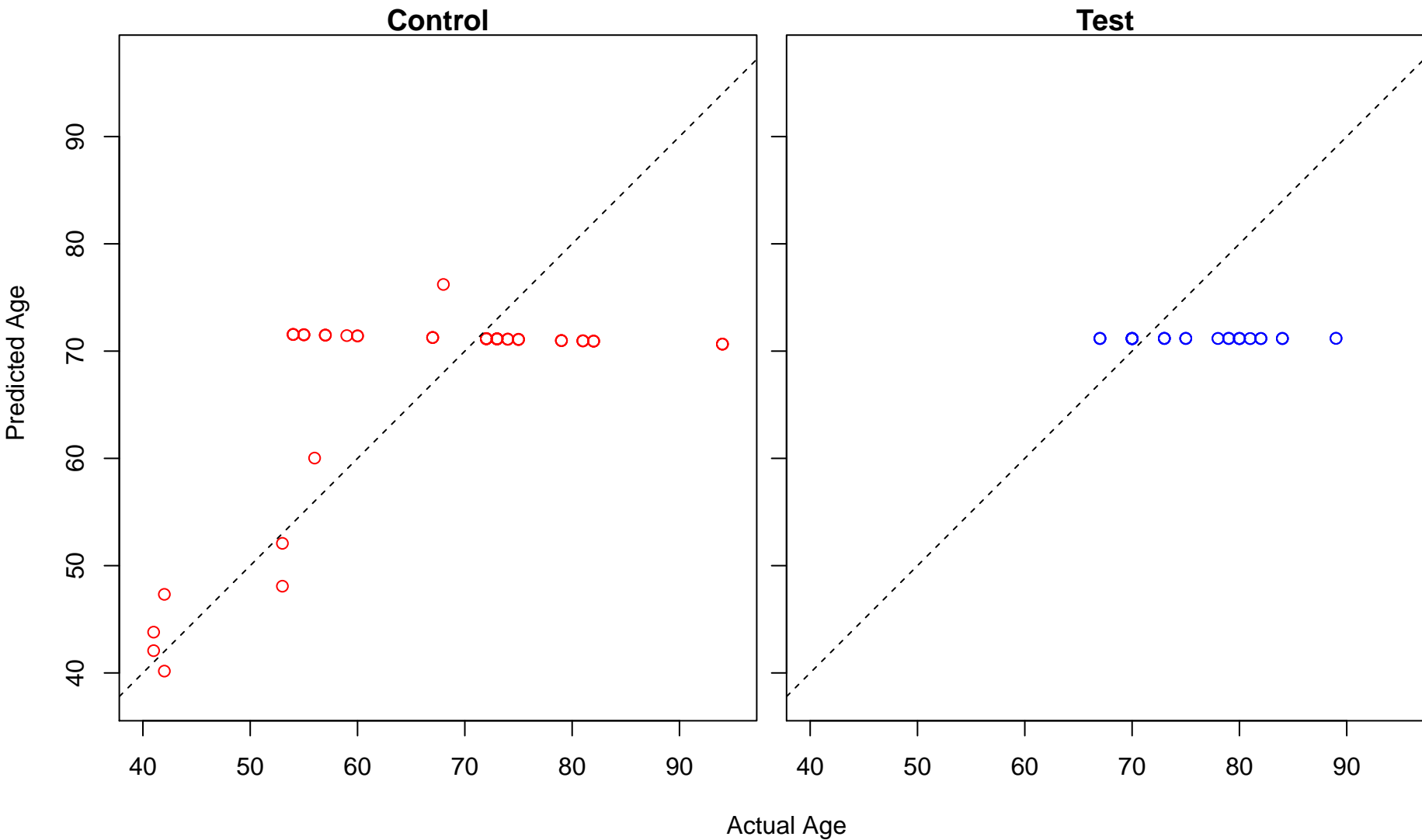


Test

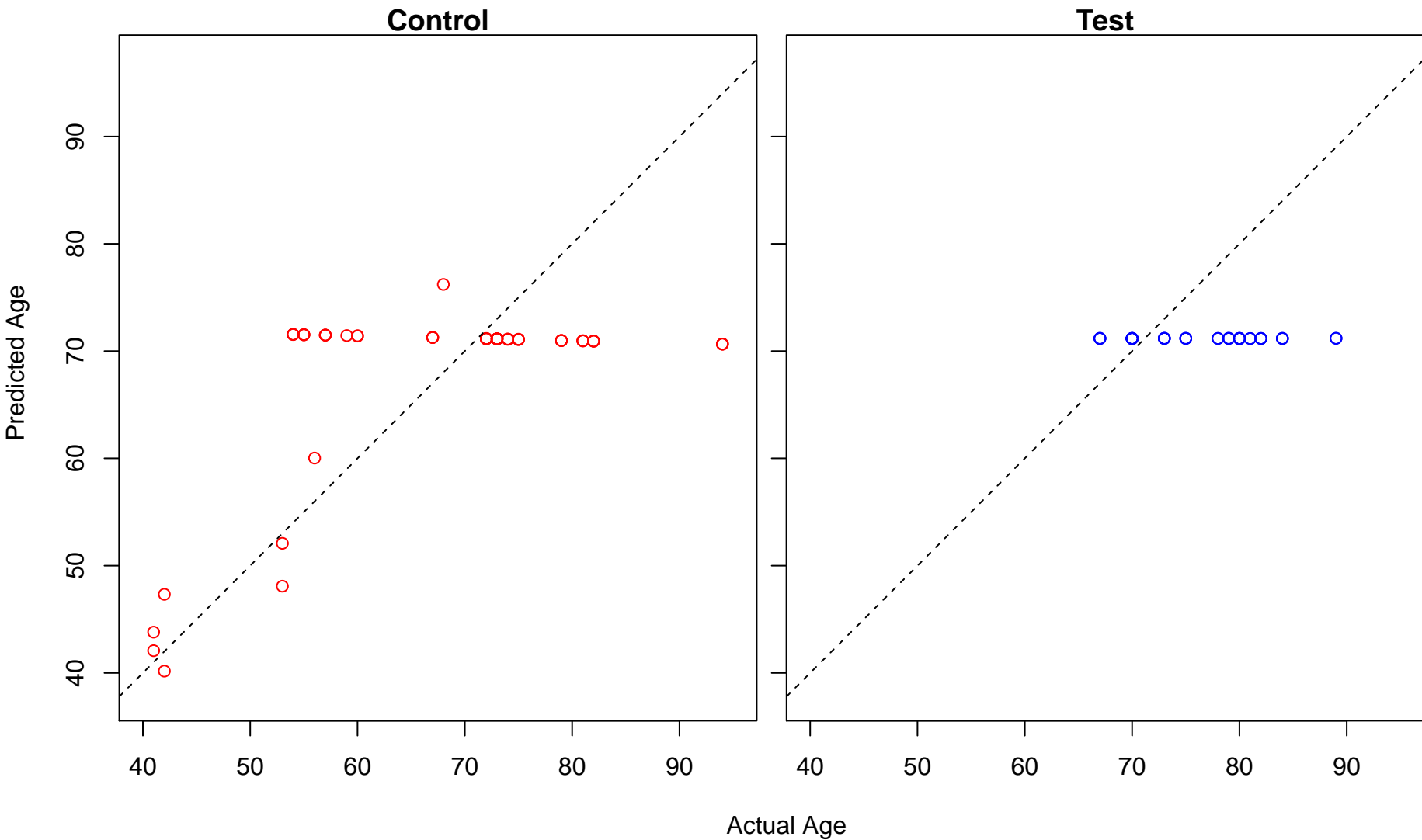


Actual Age

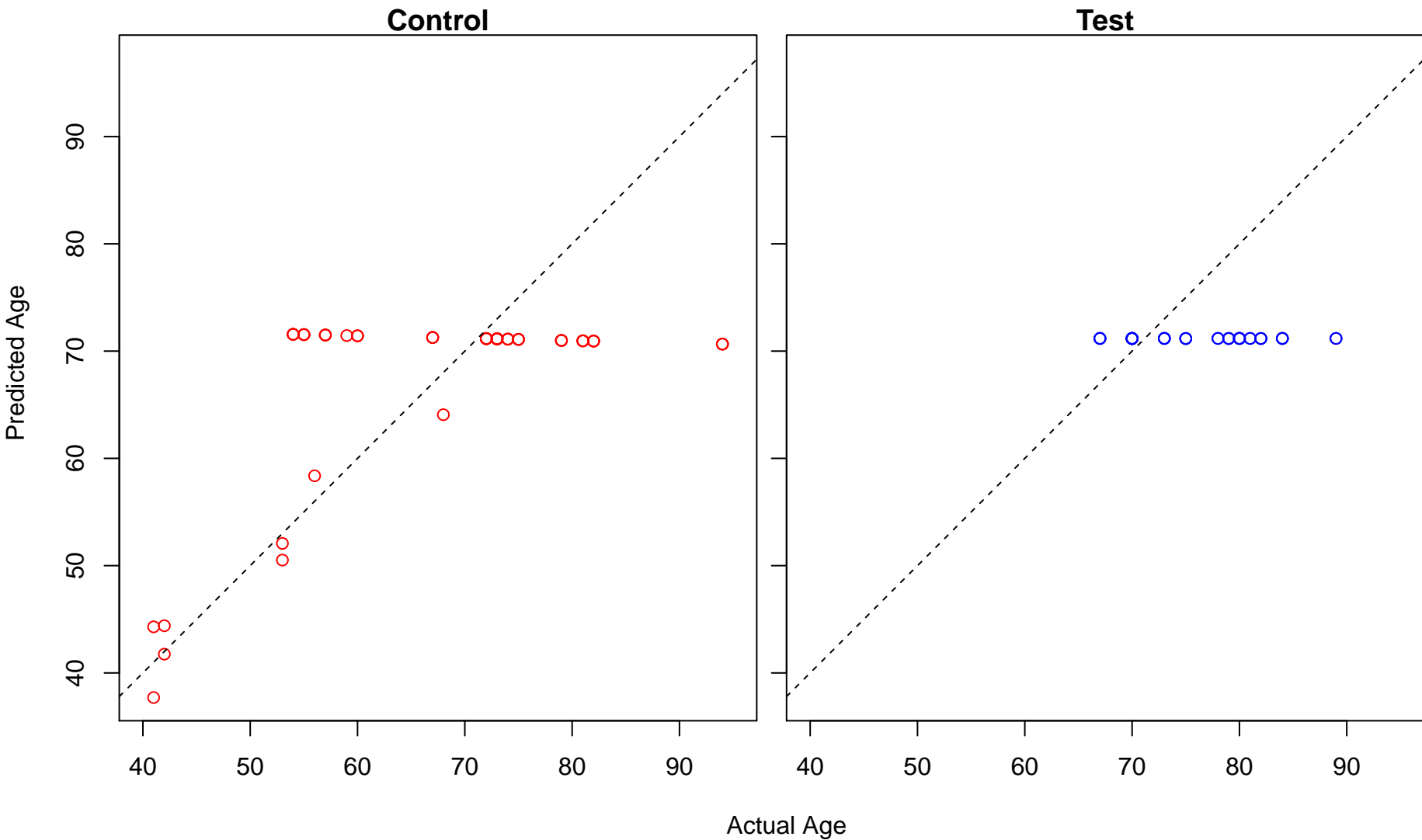
antigen processing and presentation of exogenous antigen (Score: 0.852644)



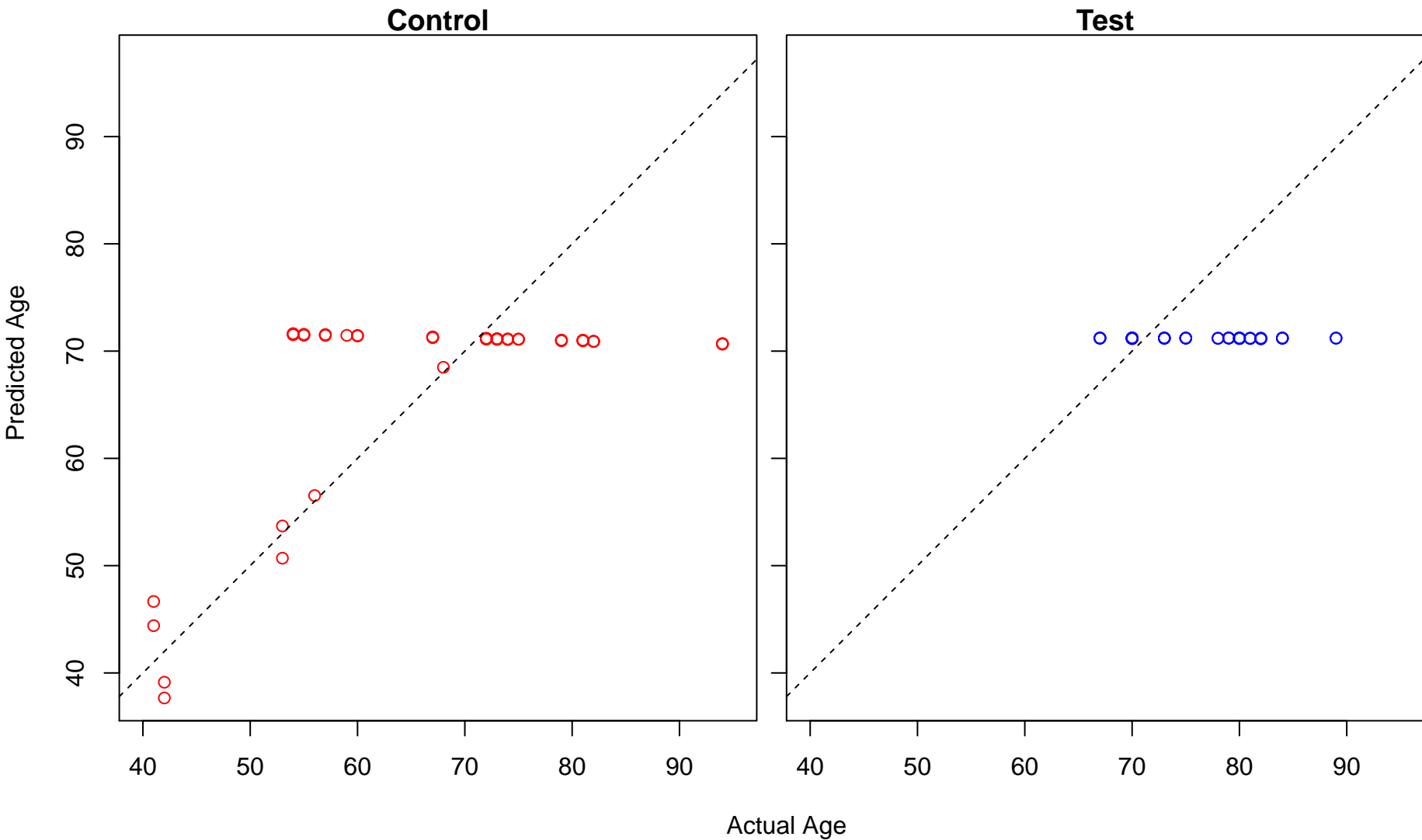
antigen processing and presentation of peptide antigen (Score: 0.852644)



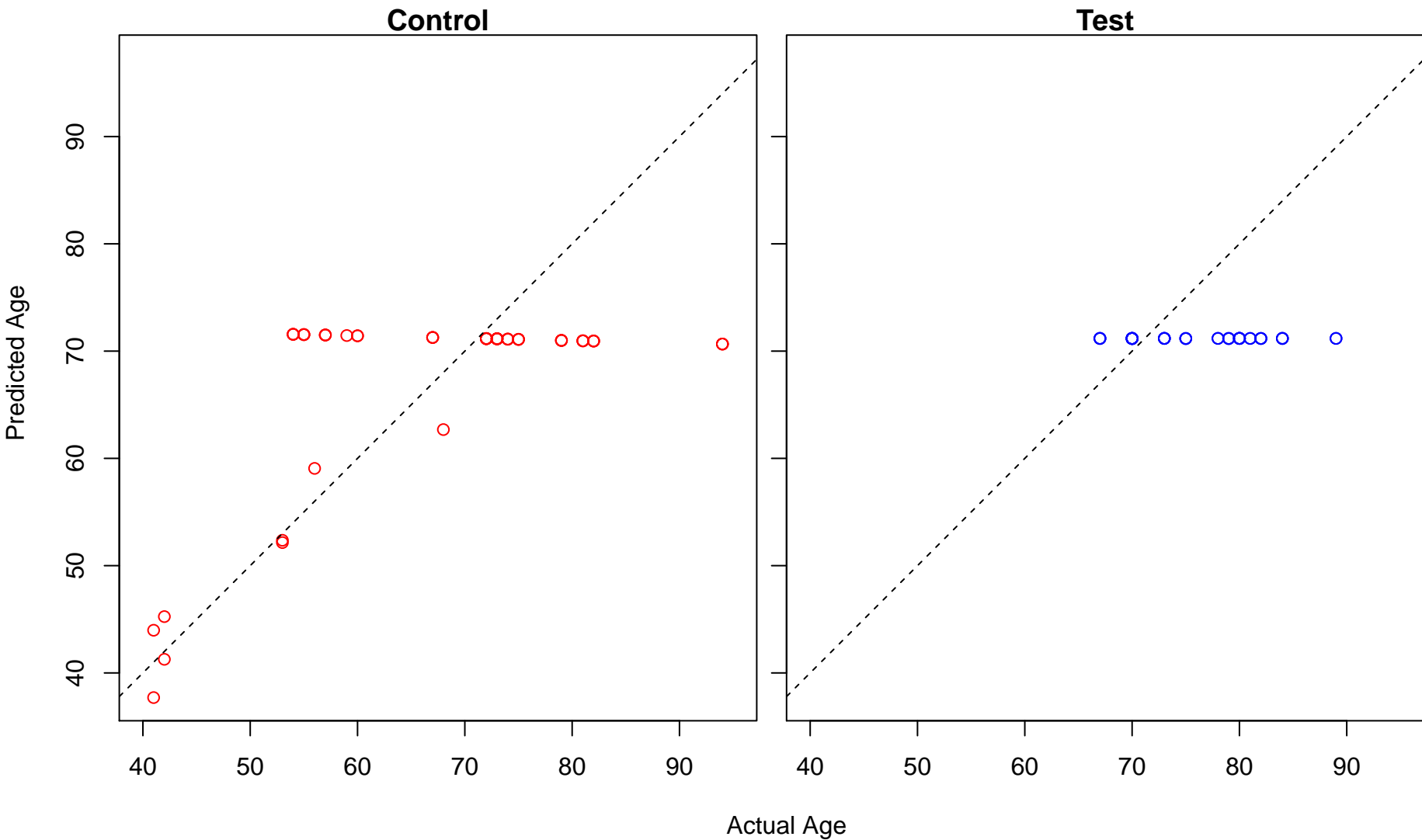
protein modification by small protein conjugation (Score: 0.852594)



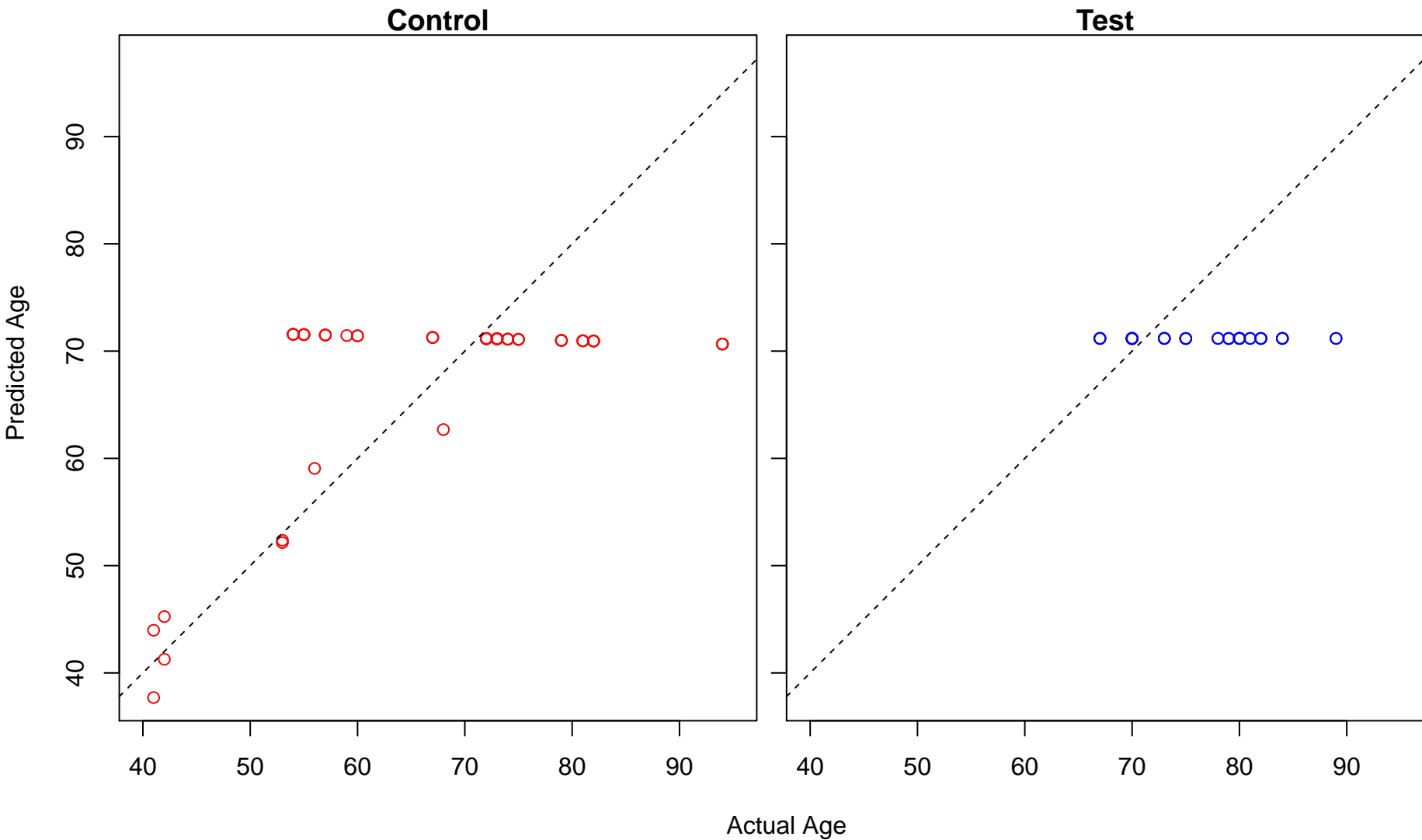
positive regulation of cellular component biogenesis (Score: 0.852367)



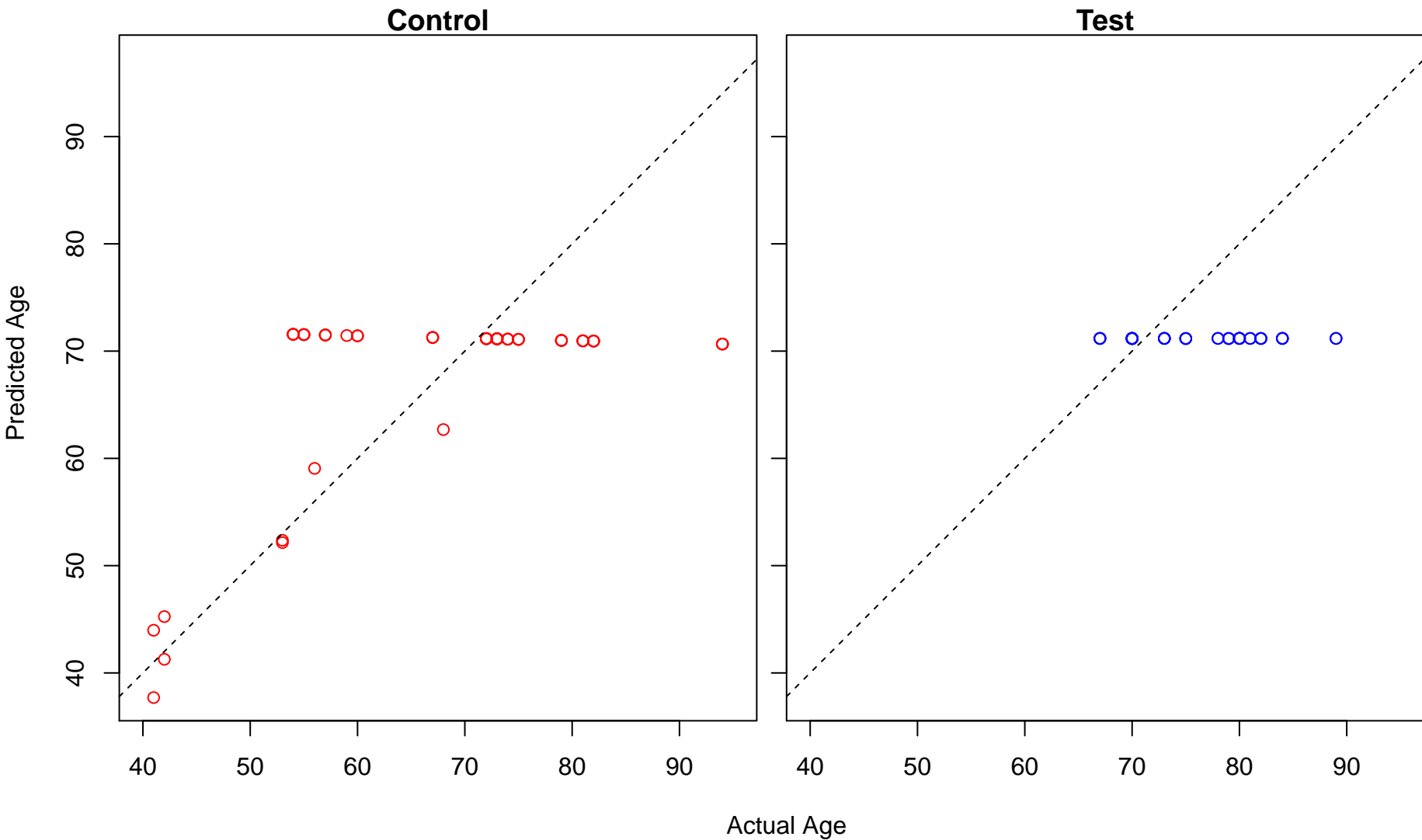
ubiquitin-dependent protein catabolic process (Score: 0.852101)



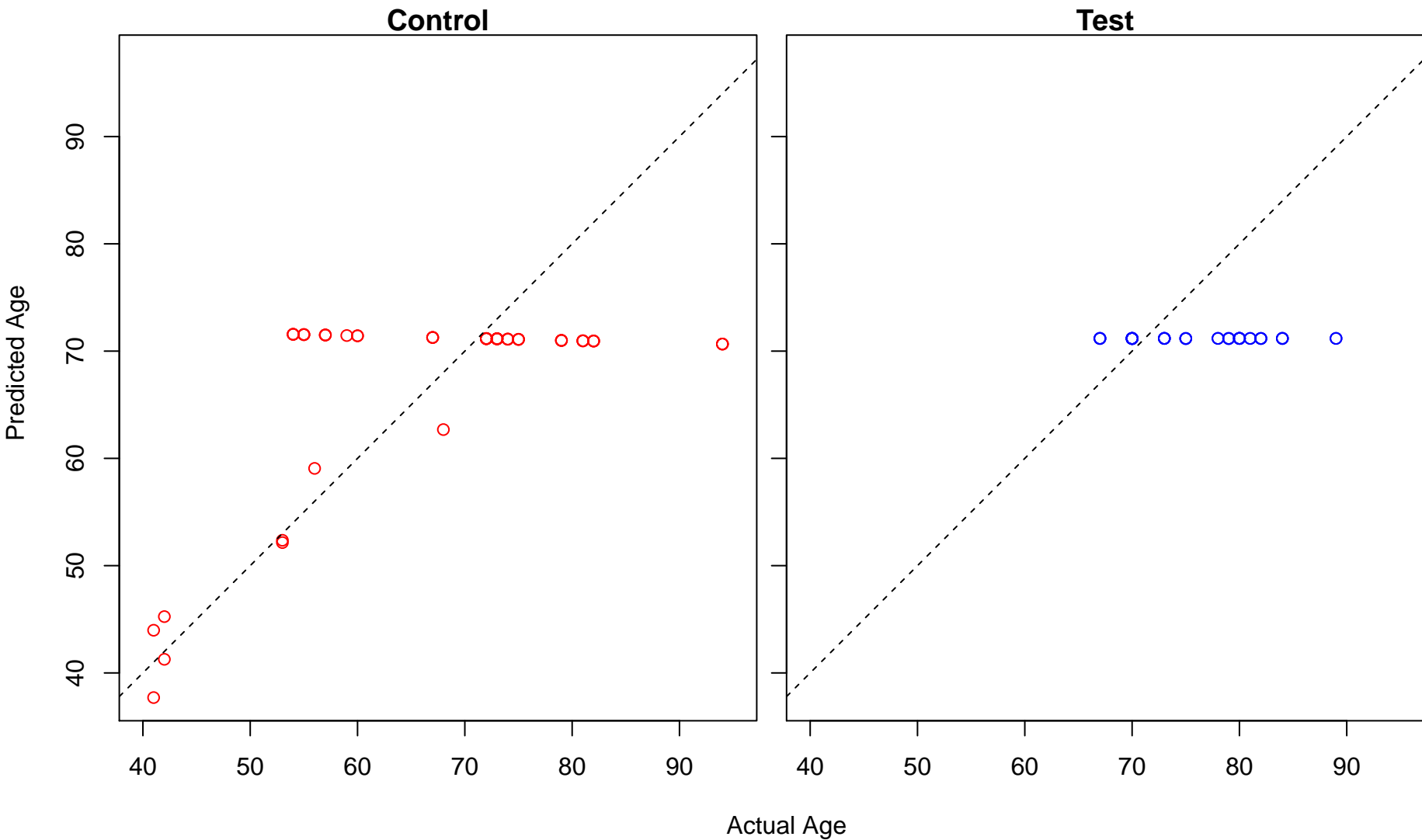
modification-dependent protein catabolic process (Score: 0.852101)



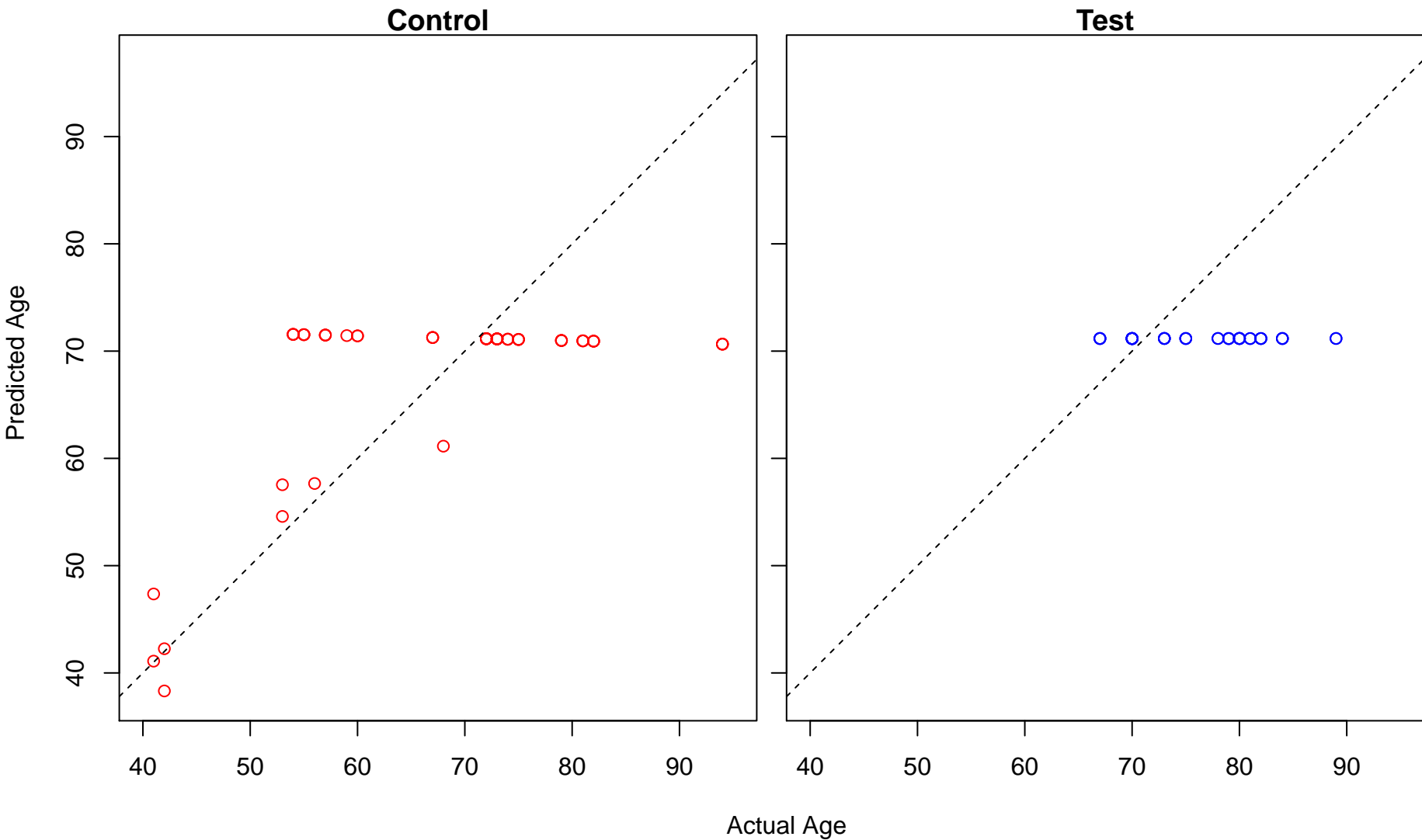
modification-dependent macromolecule catabolic process (Score: 0.852101)



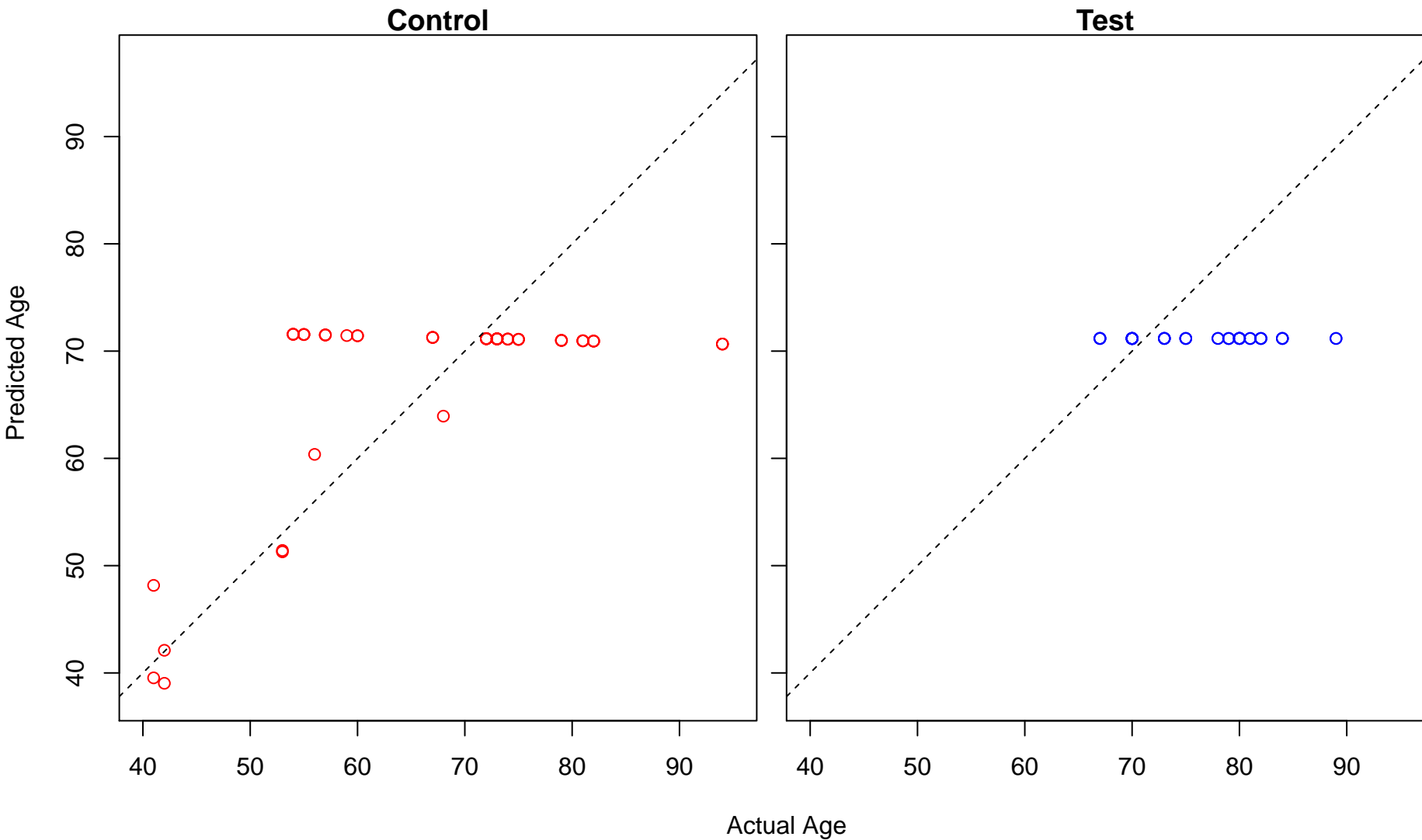
proteolysis involved in cellular protein catabolic process (Score: 0.852101)



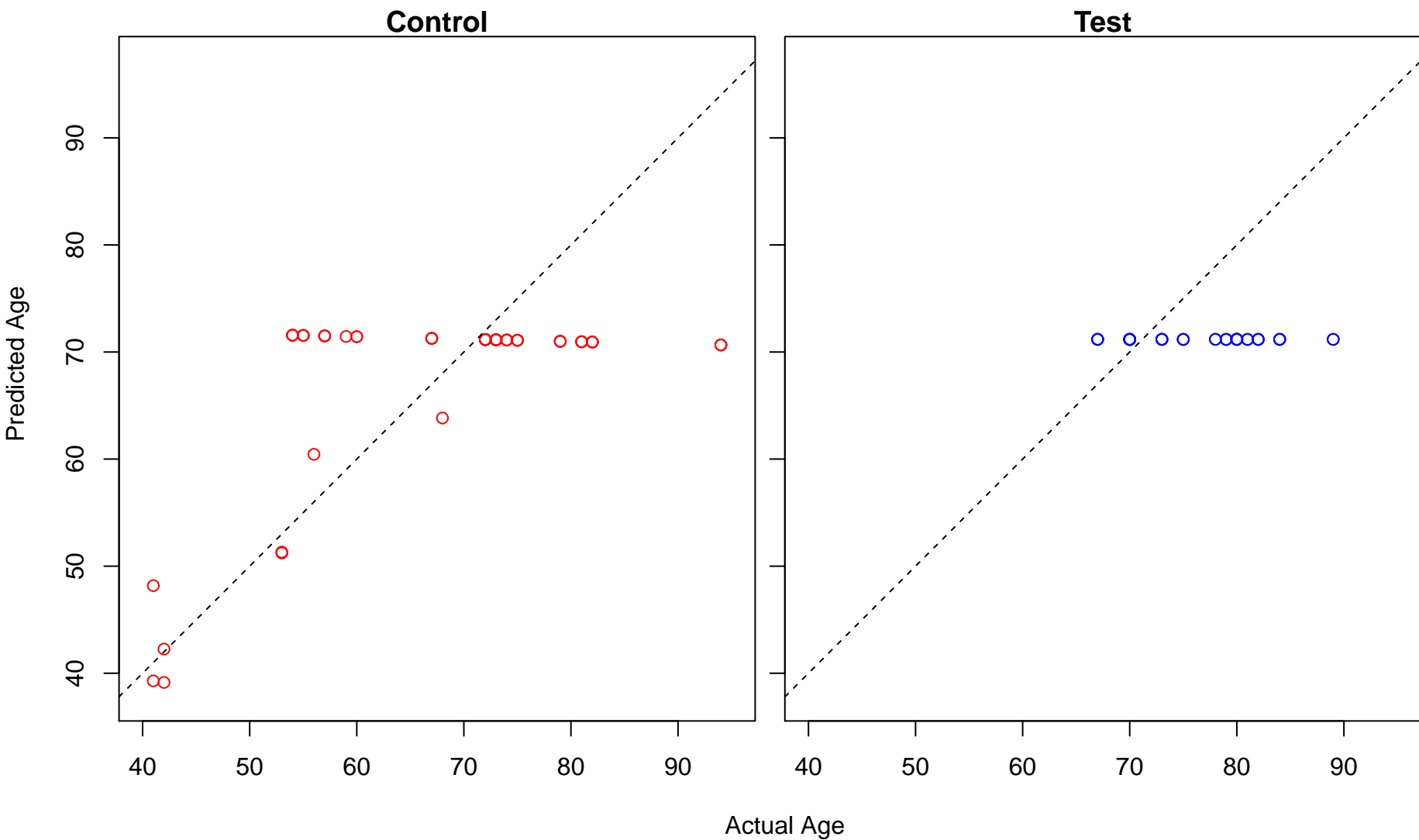
regulation of proteolysis involved in cellular protein catabolic process (Score: 0.850370)



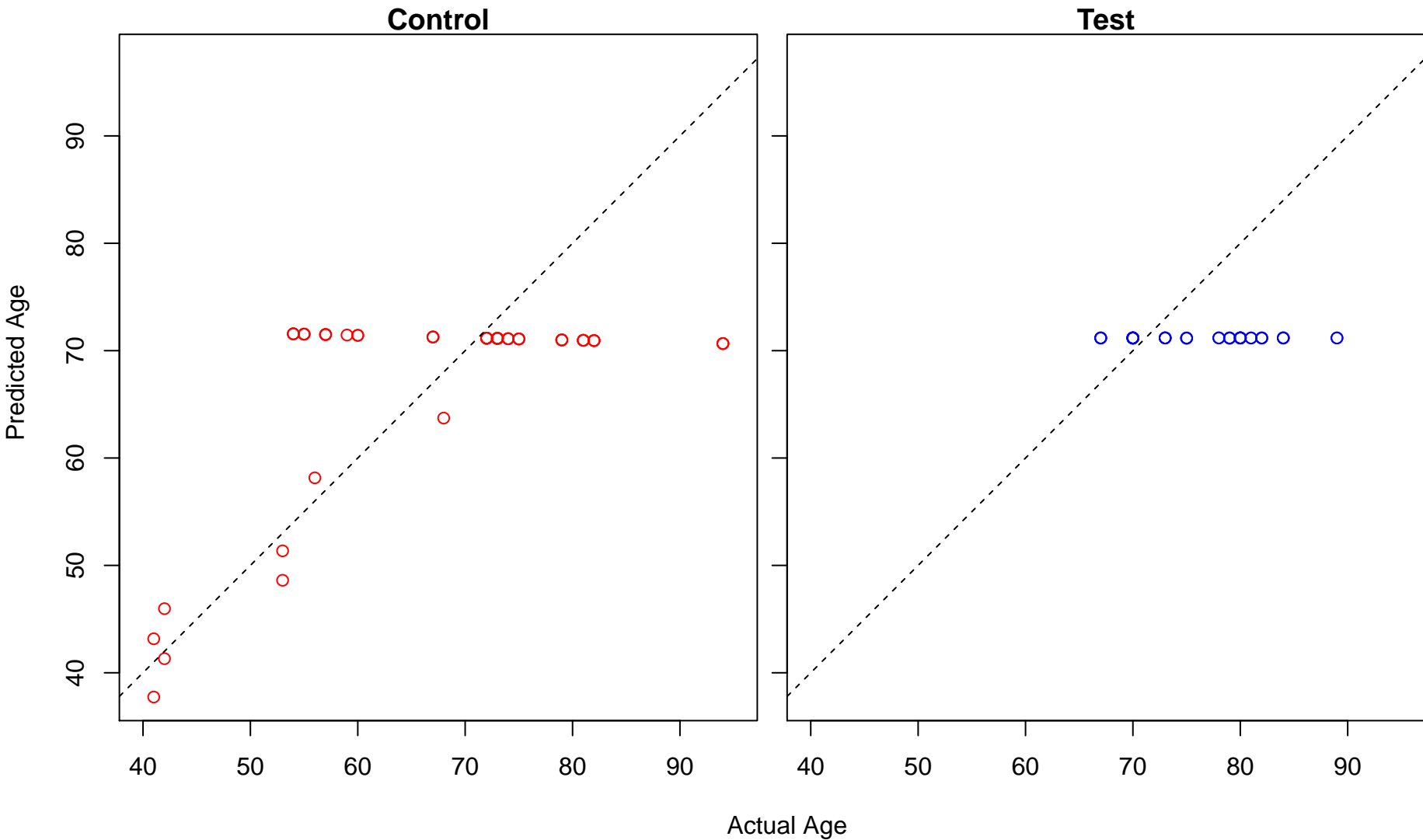
positive regulation of protein ubiquitination (Score: 0.849595)



positive regulation of protein modification by small protein conjugation or removal (Score: 0.84896)

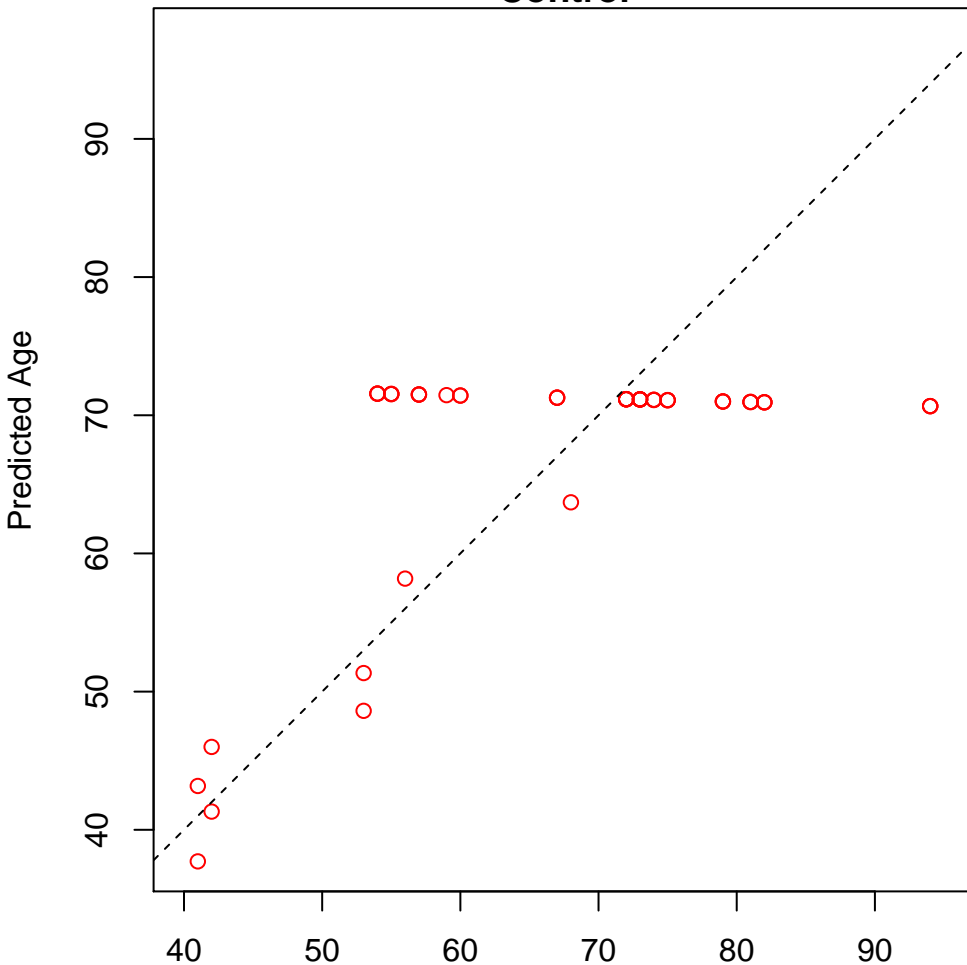


positive regulation of innate immune response (Score: 0.847767)

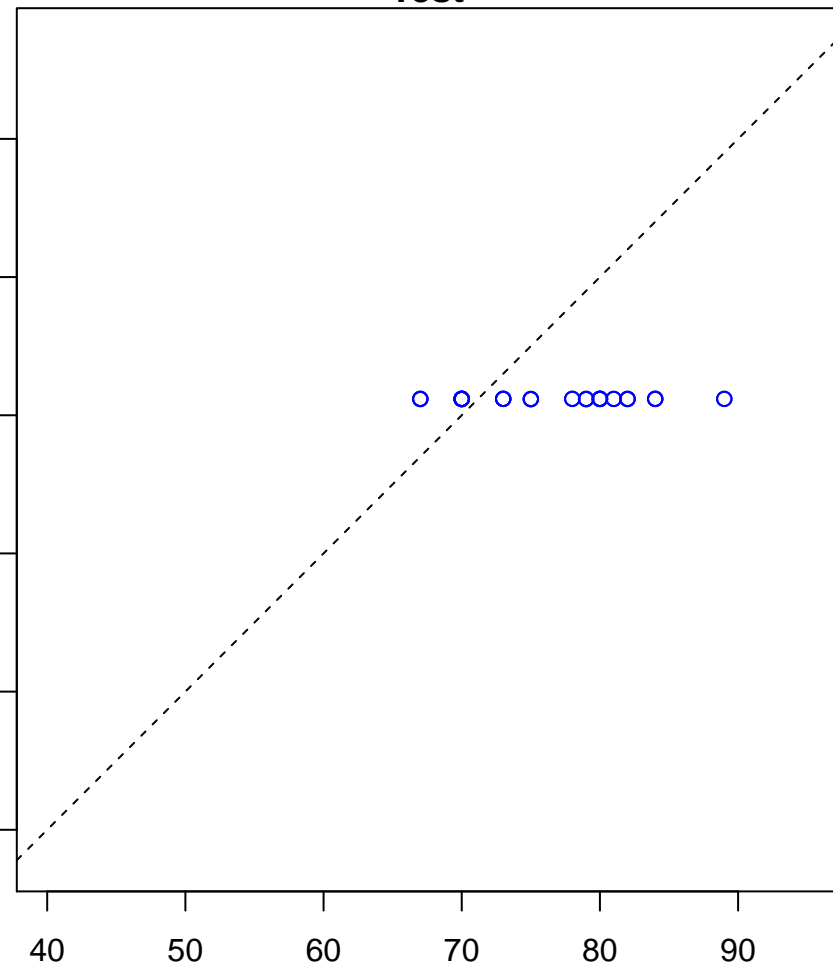


activation of innate immune response (Score: 0.847655)

Control

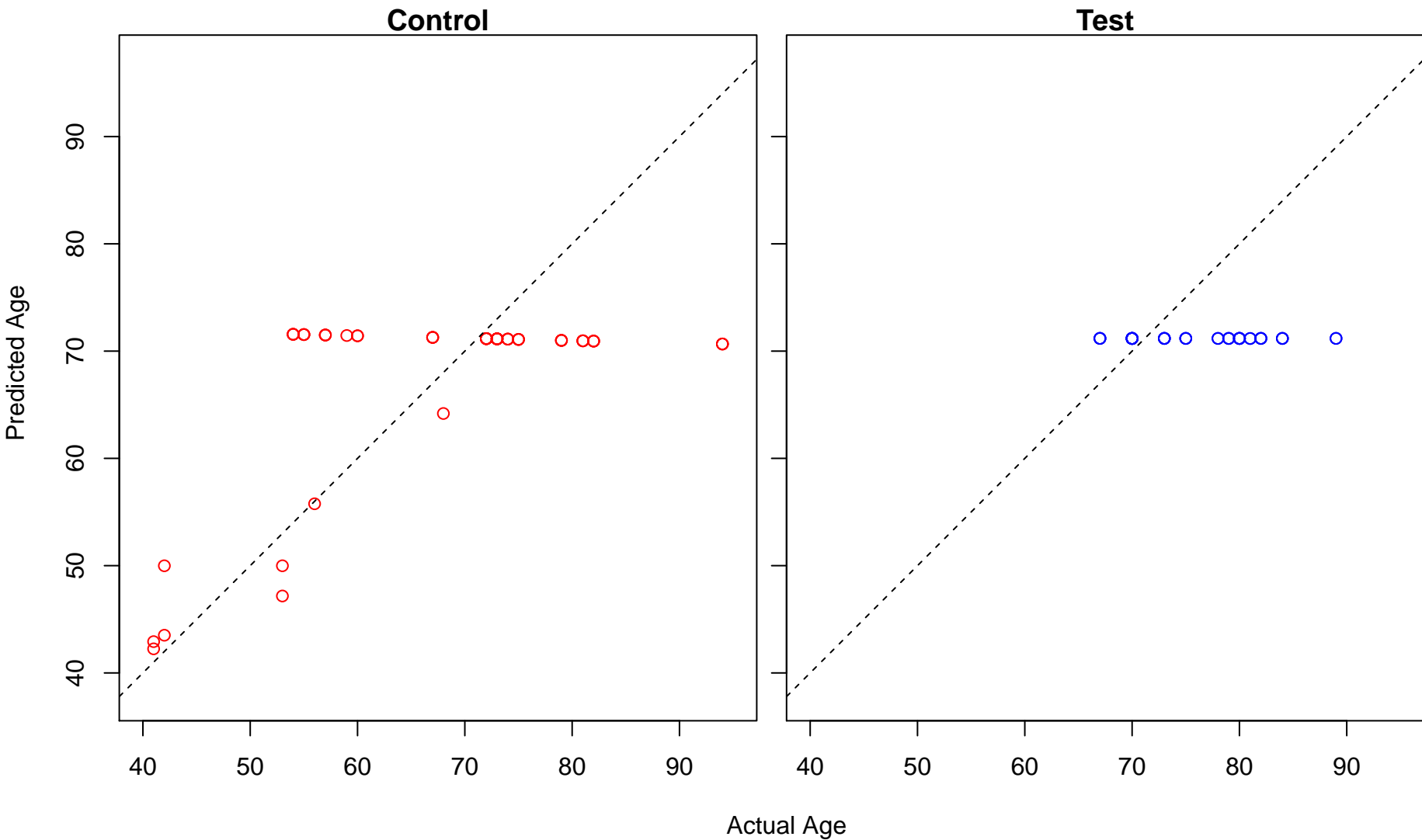


Test



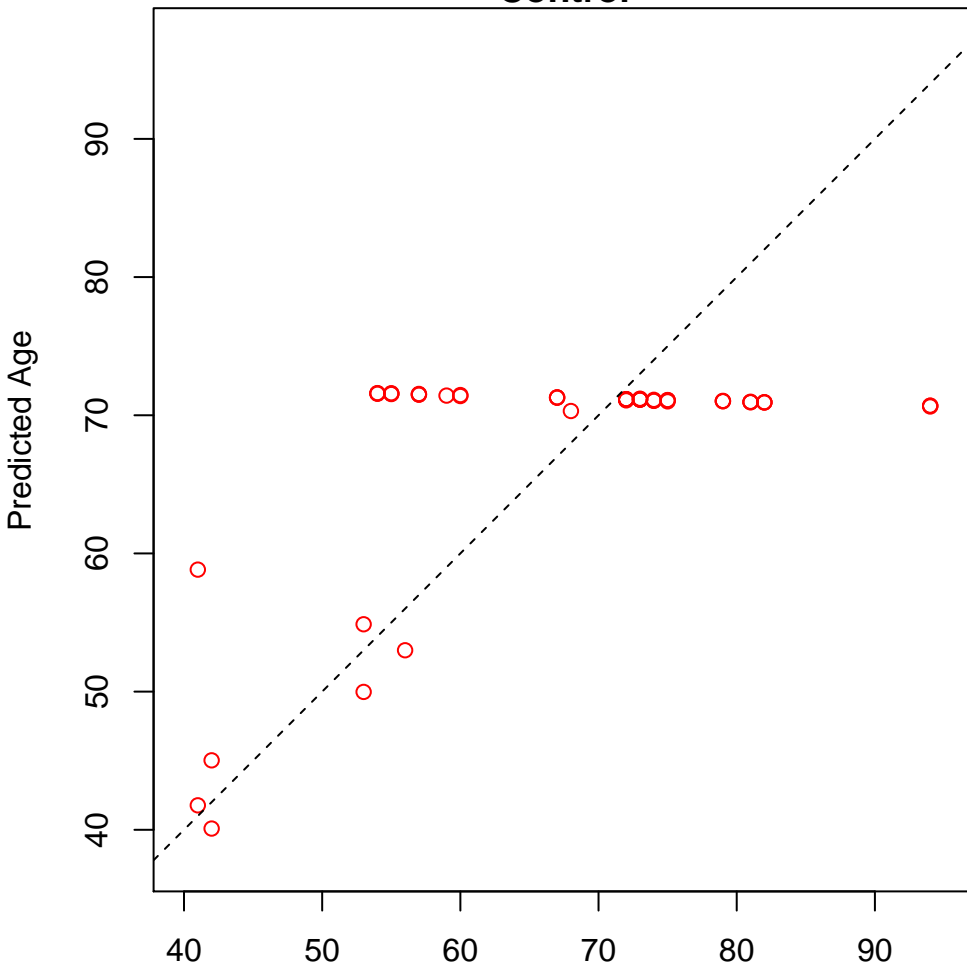
Actual Age

tissue development (Score: 0.847442)

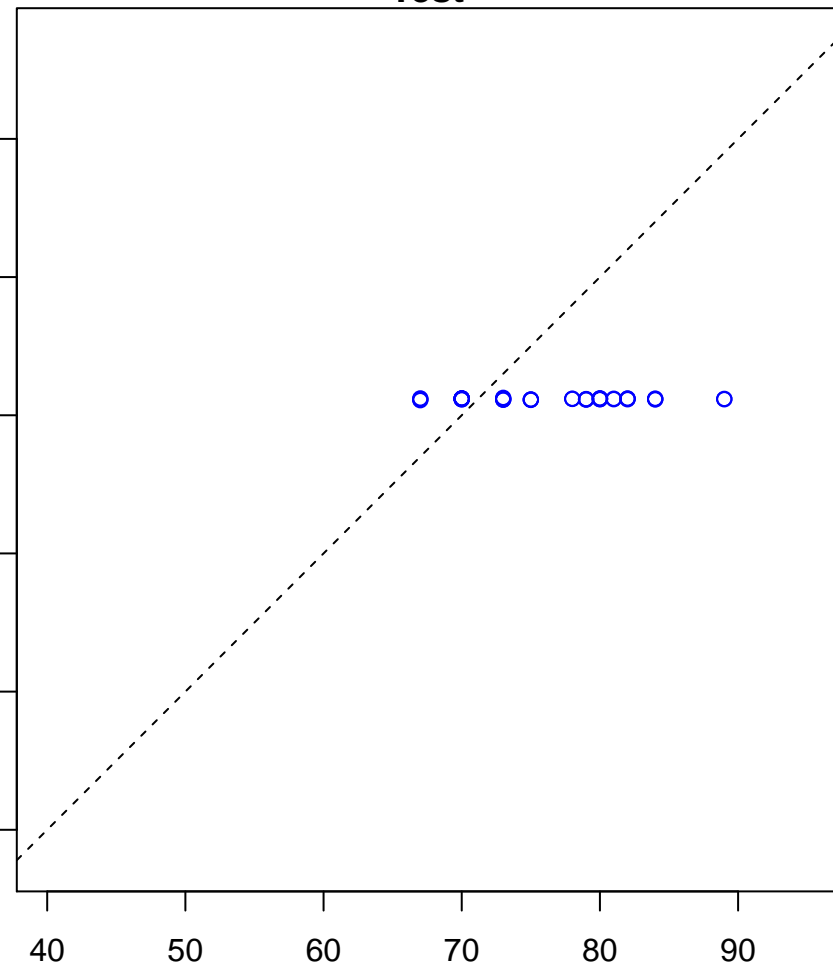


intrinsic apoptotic signaling pathway (Score: 0.847166)

Control

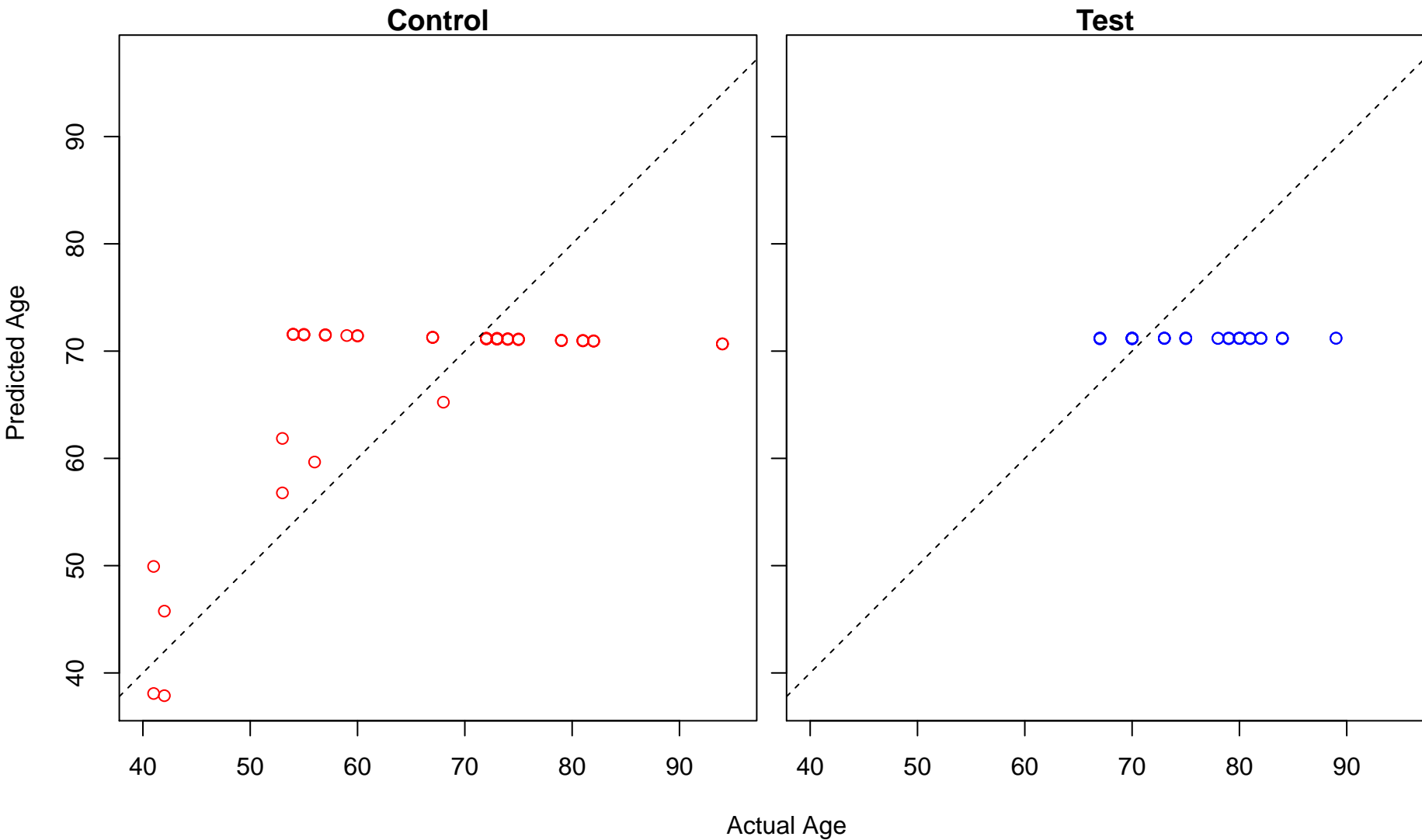


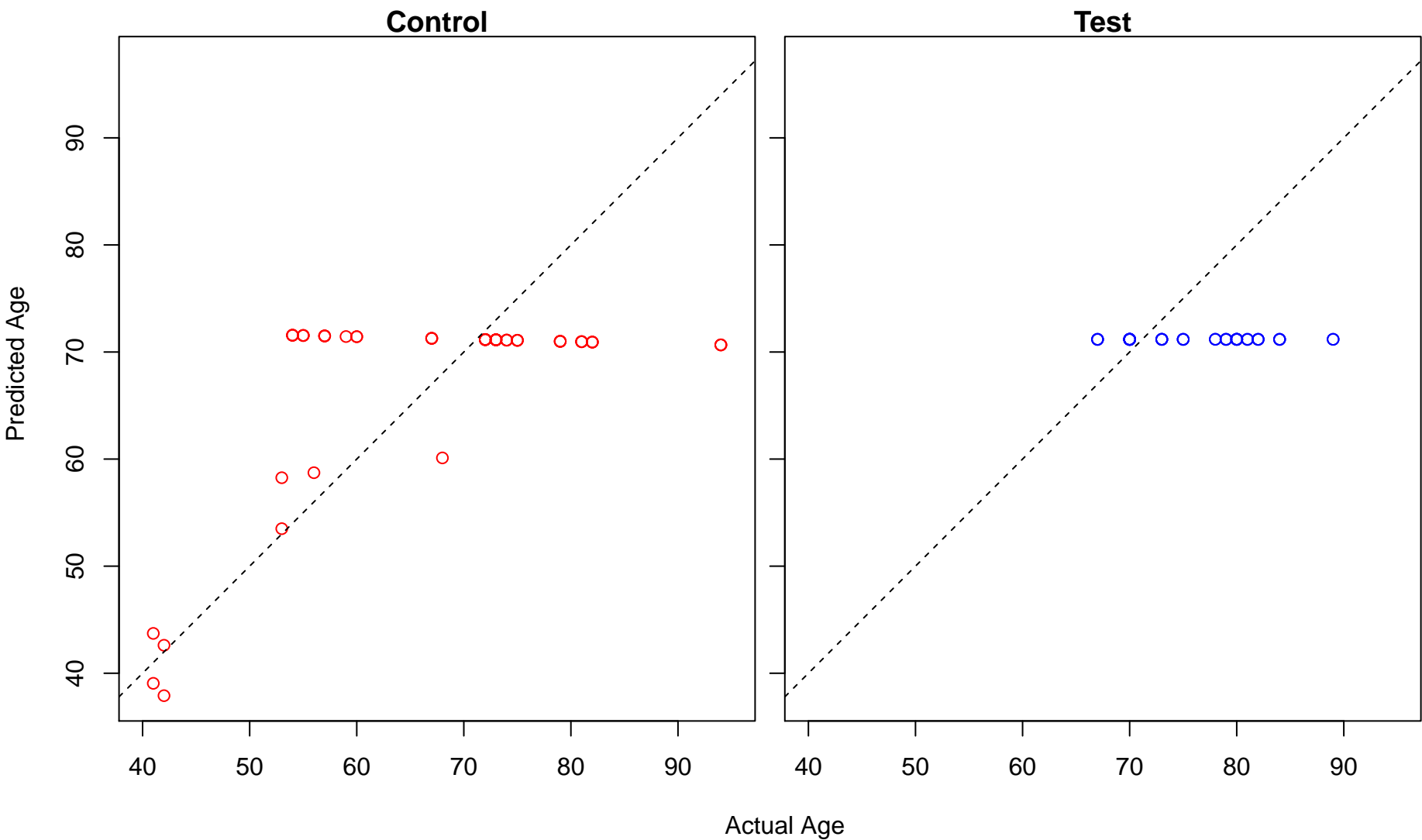
Test



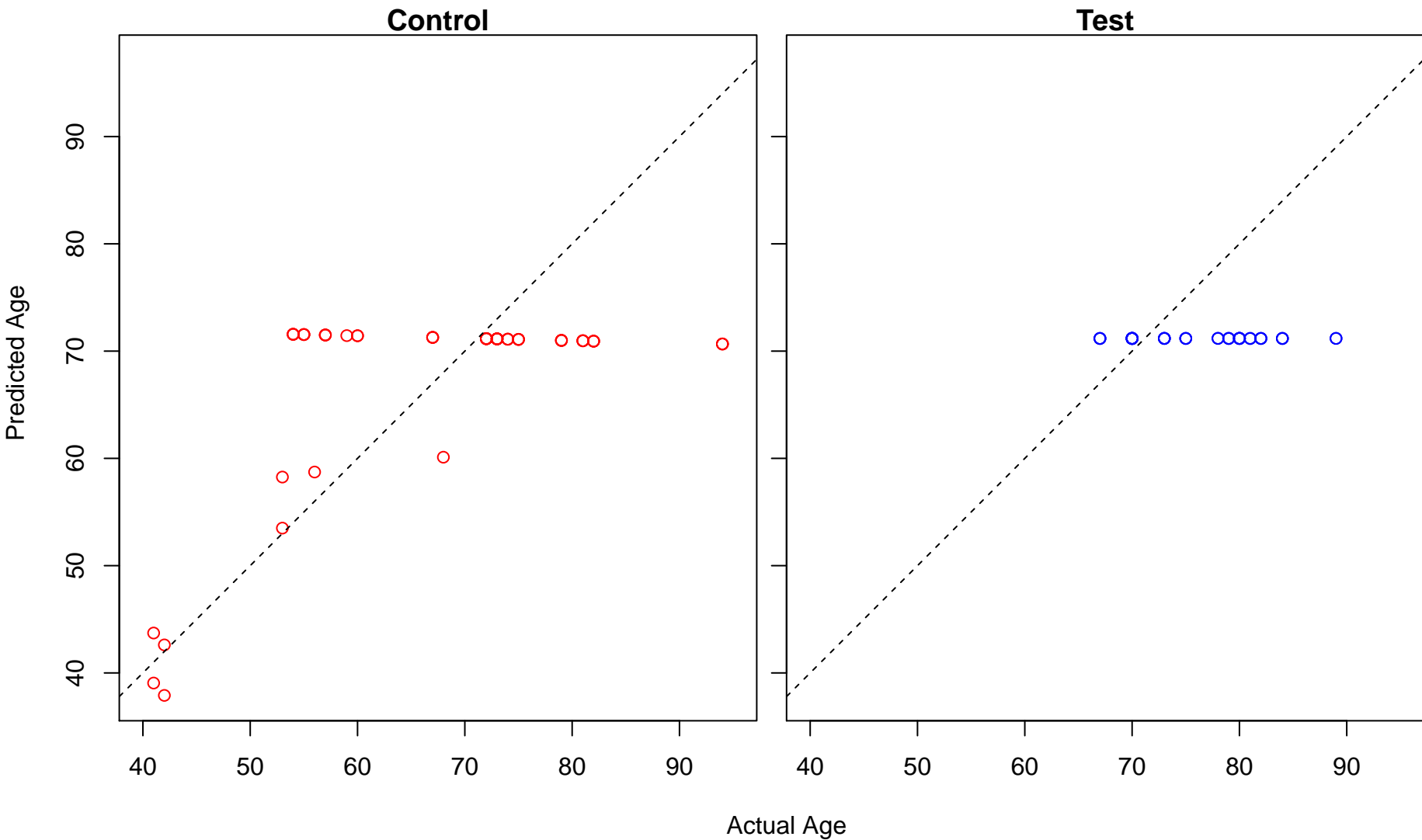
Actual Age

positive regulation of intracellular protein transport (Score: 0.847089)

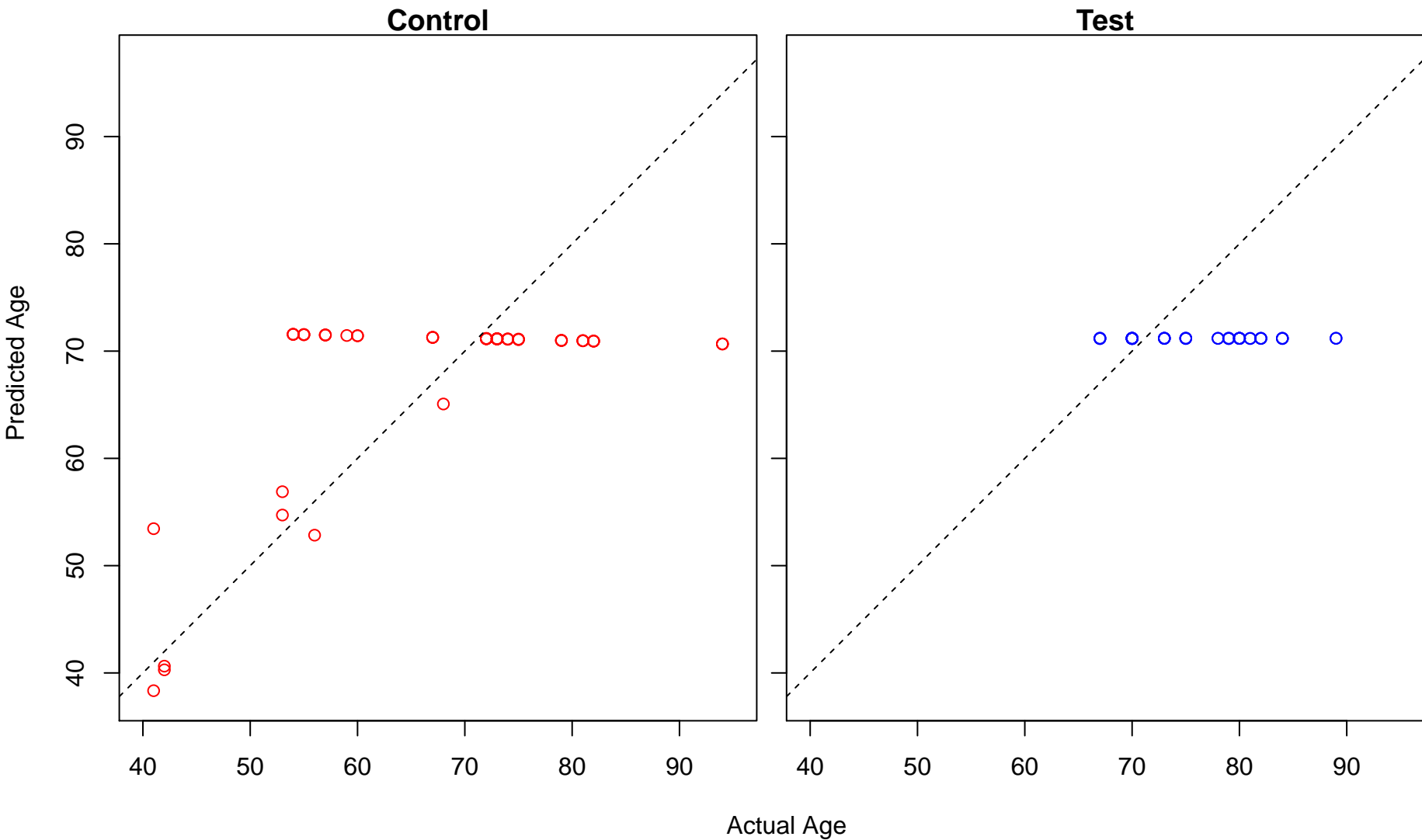




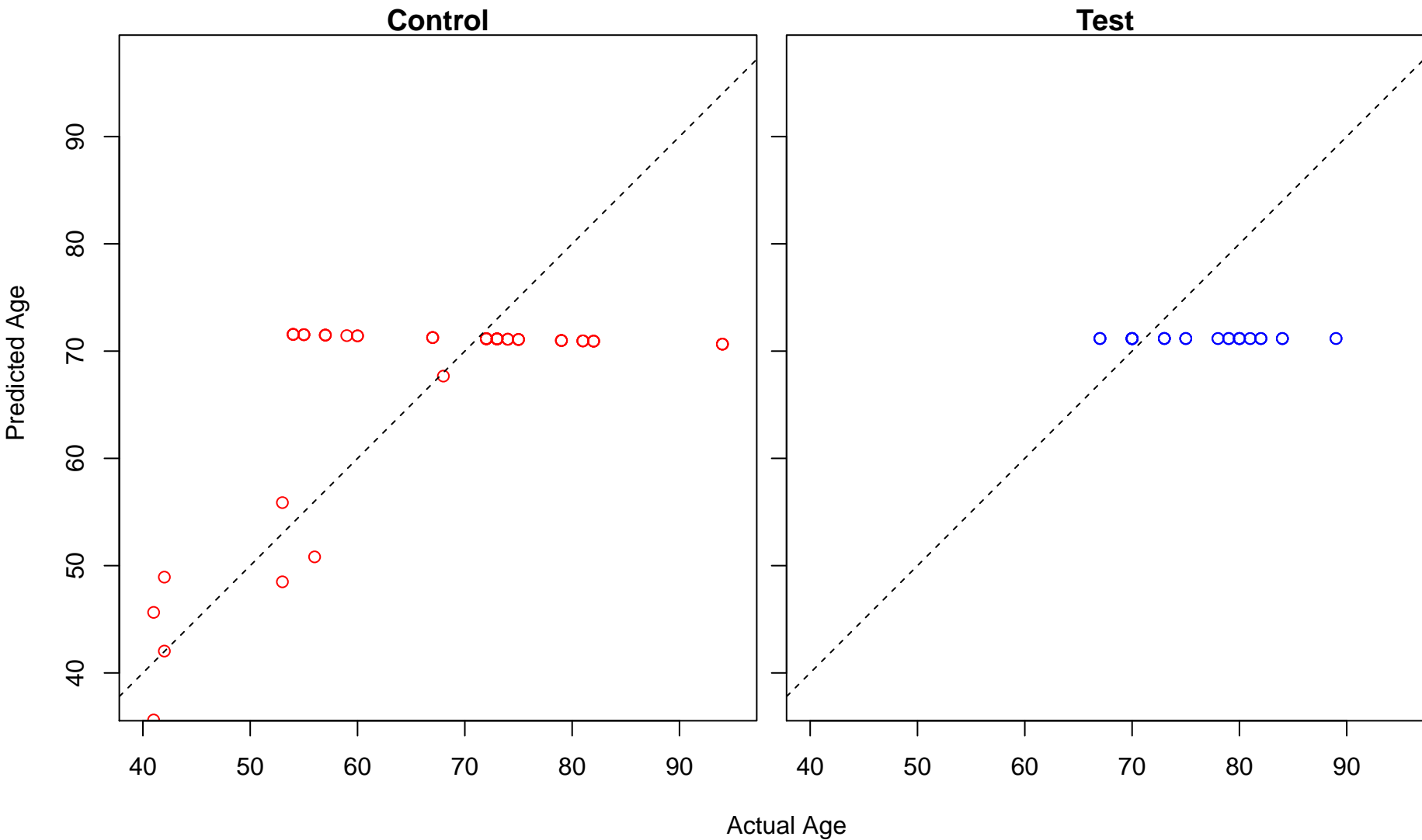
regulation of ubiquitin protein ligase activity (Score: 0.846122)



regulation of intracellular protein transport (Score: 0.845859)

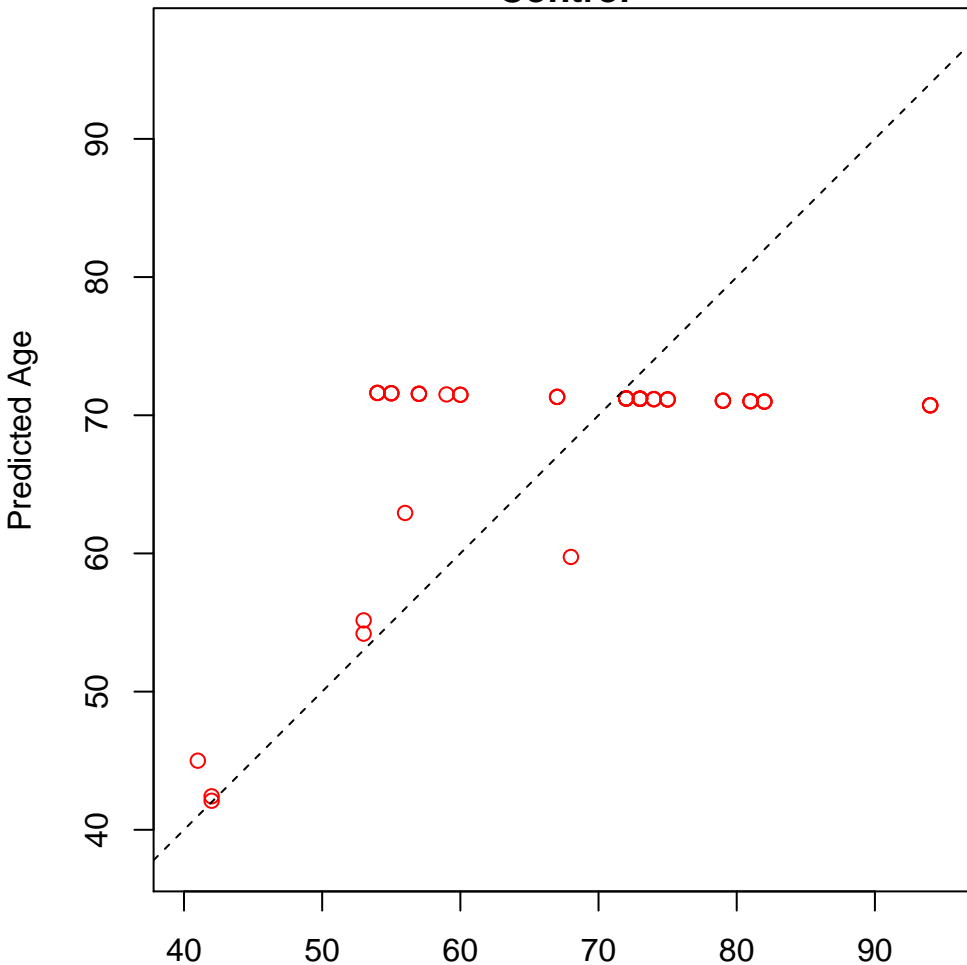


ion transport (Score: 0.843442)

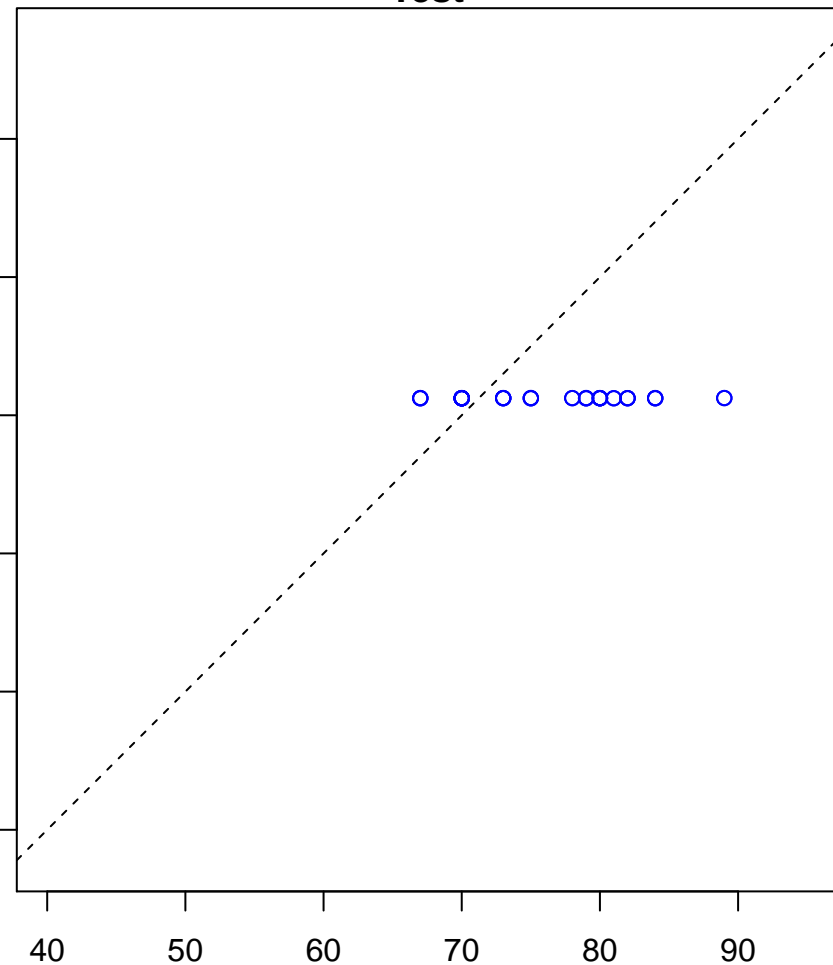


response to tumor necrosis factor (Score: 0.843318)

Control



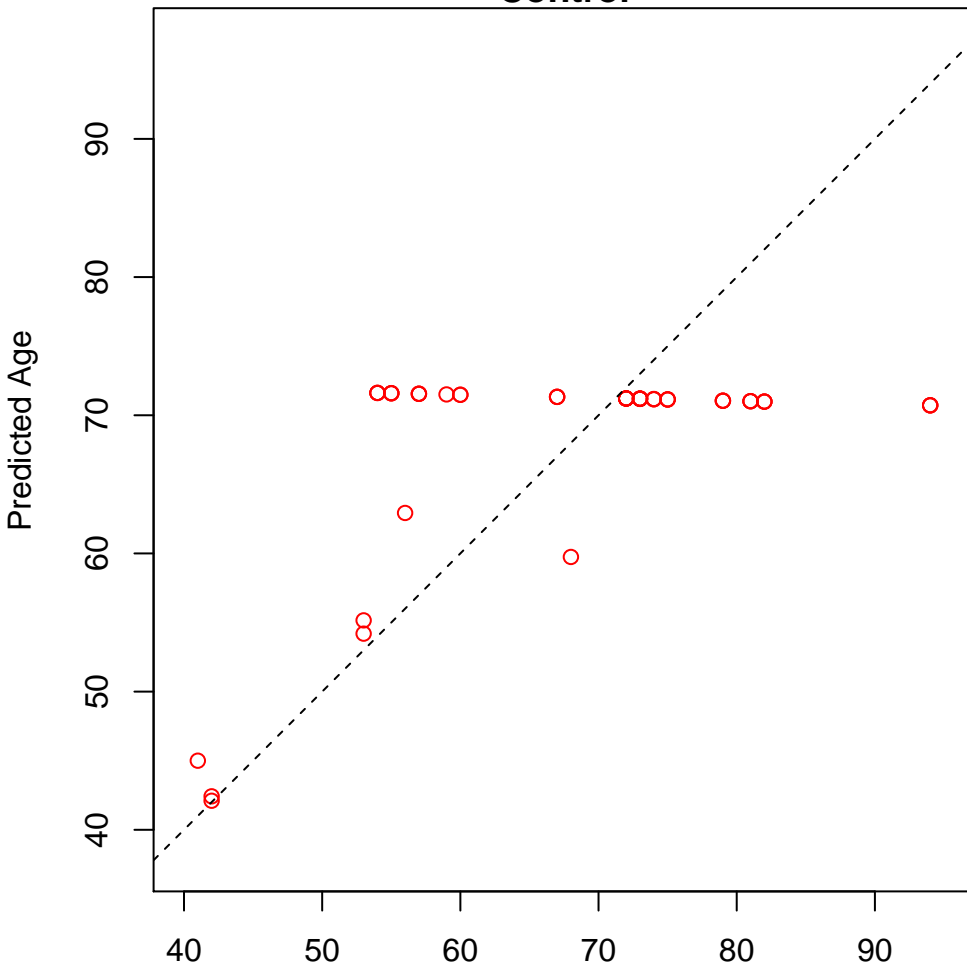
Test



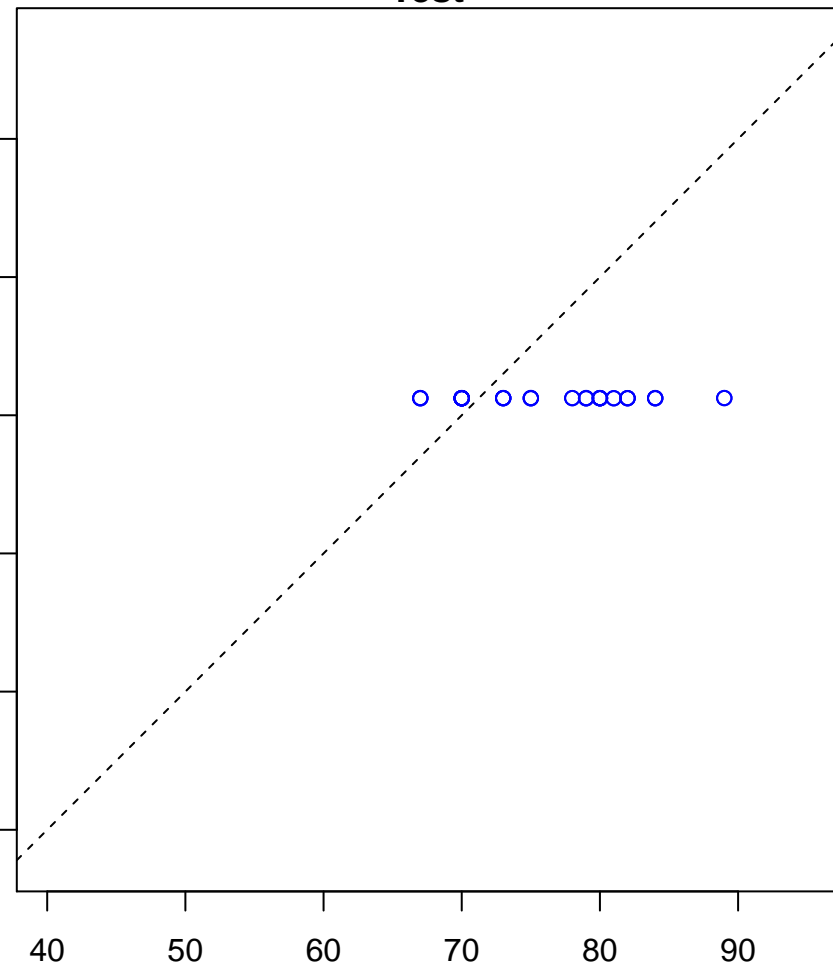
Actual Age

cellular response to tumor necrosis factor (Score: 0.843318)

Control

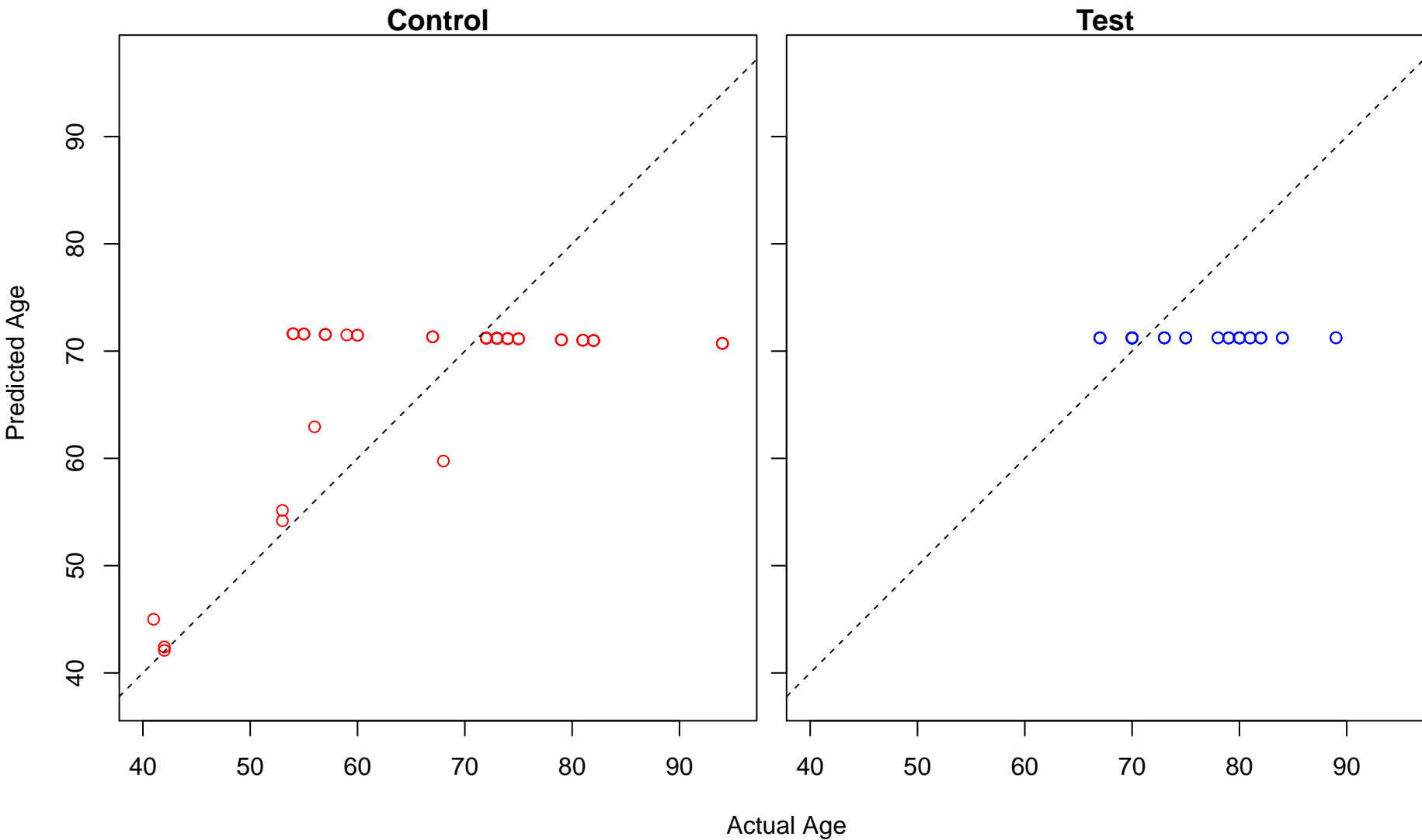


Test

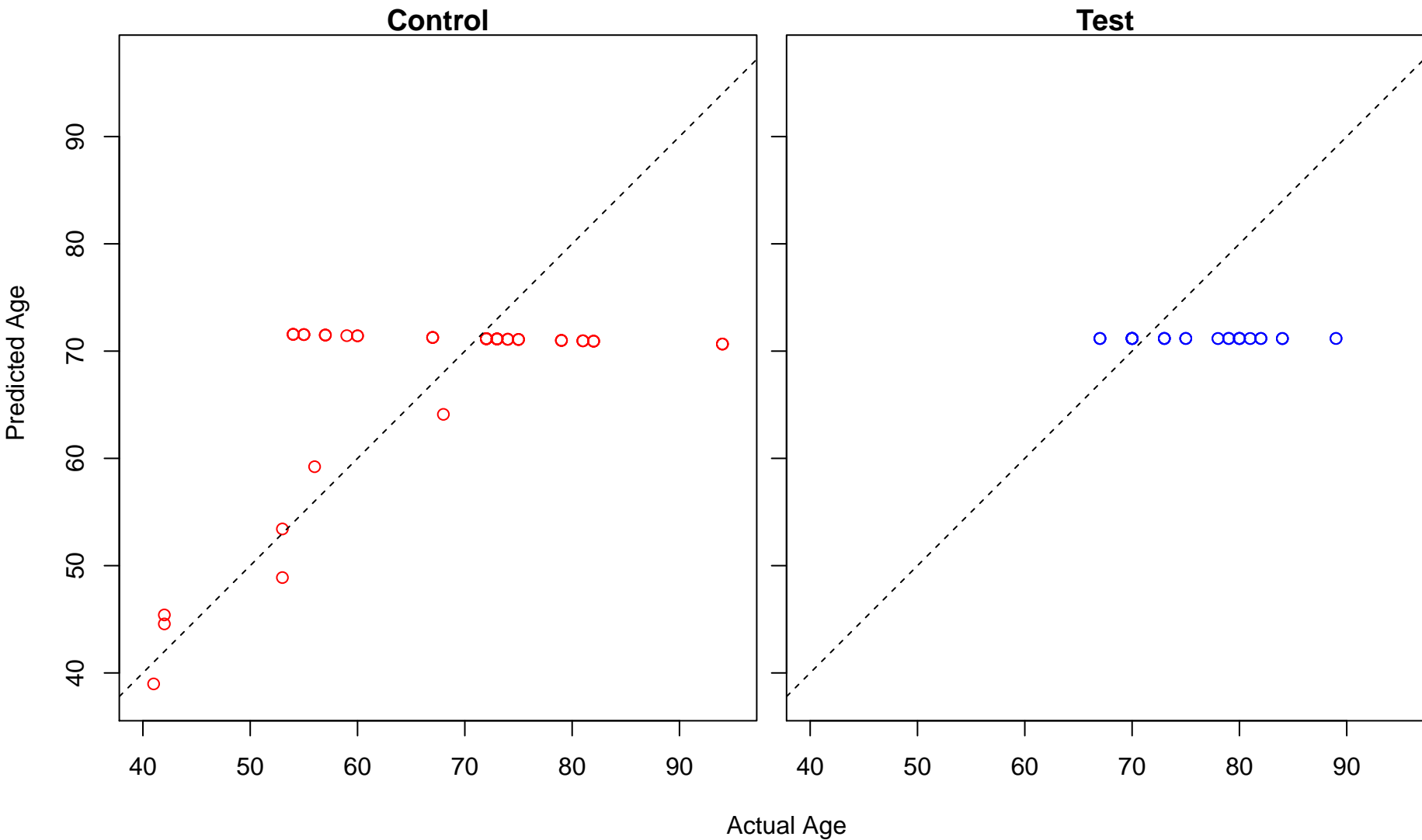


Actual Age

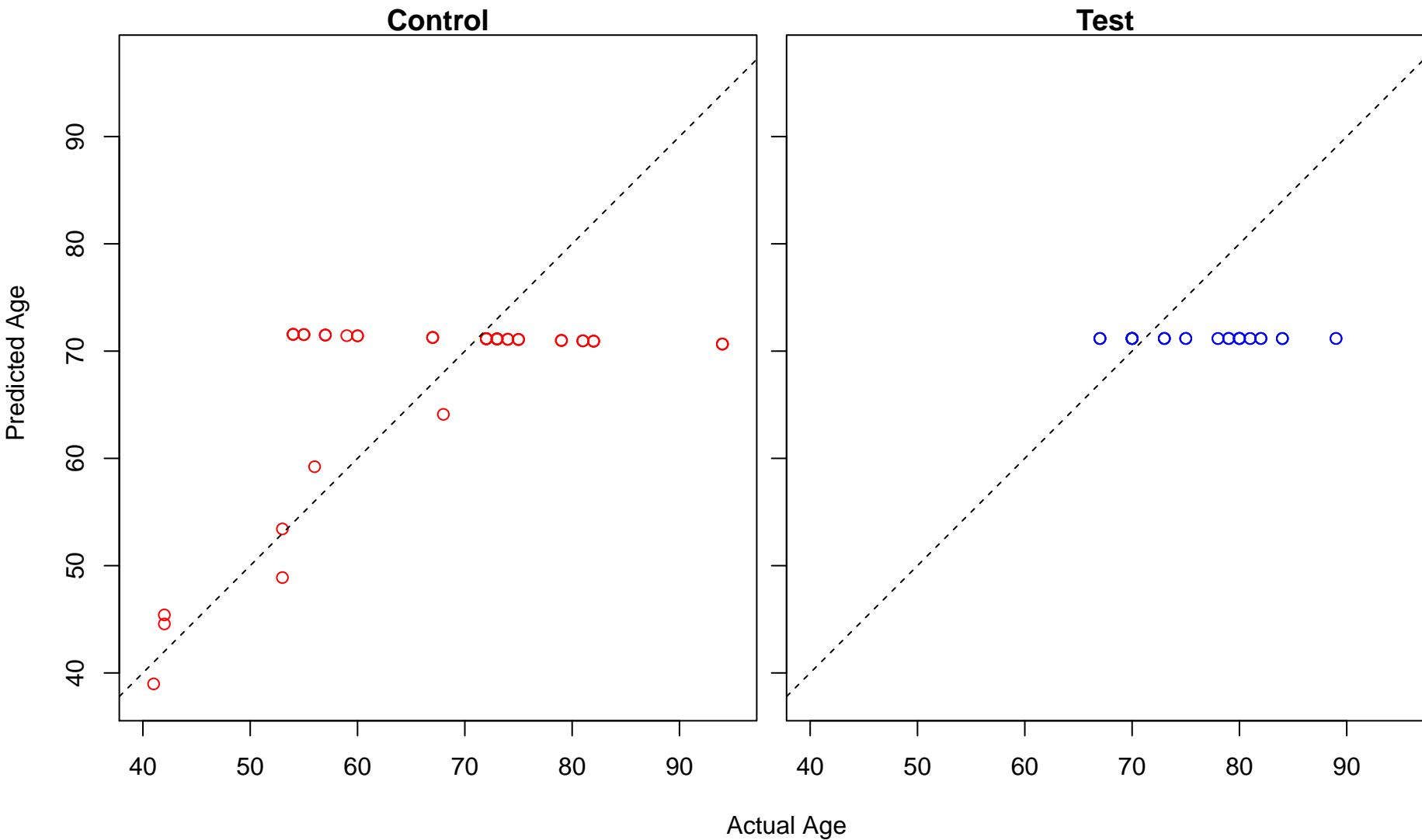
tumor necrosis factor-mediated signaling pathway (Score: 0.843307)



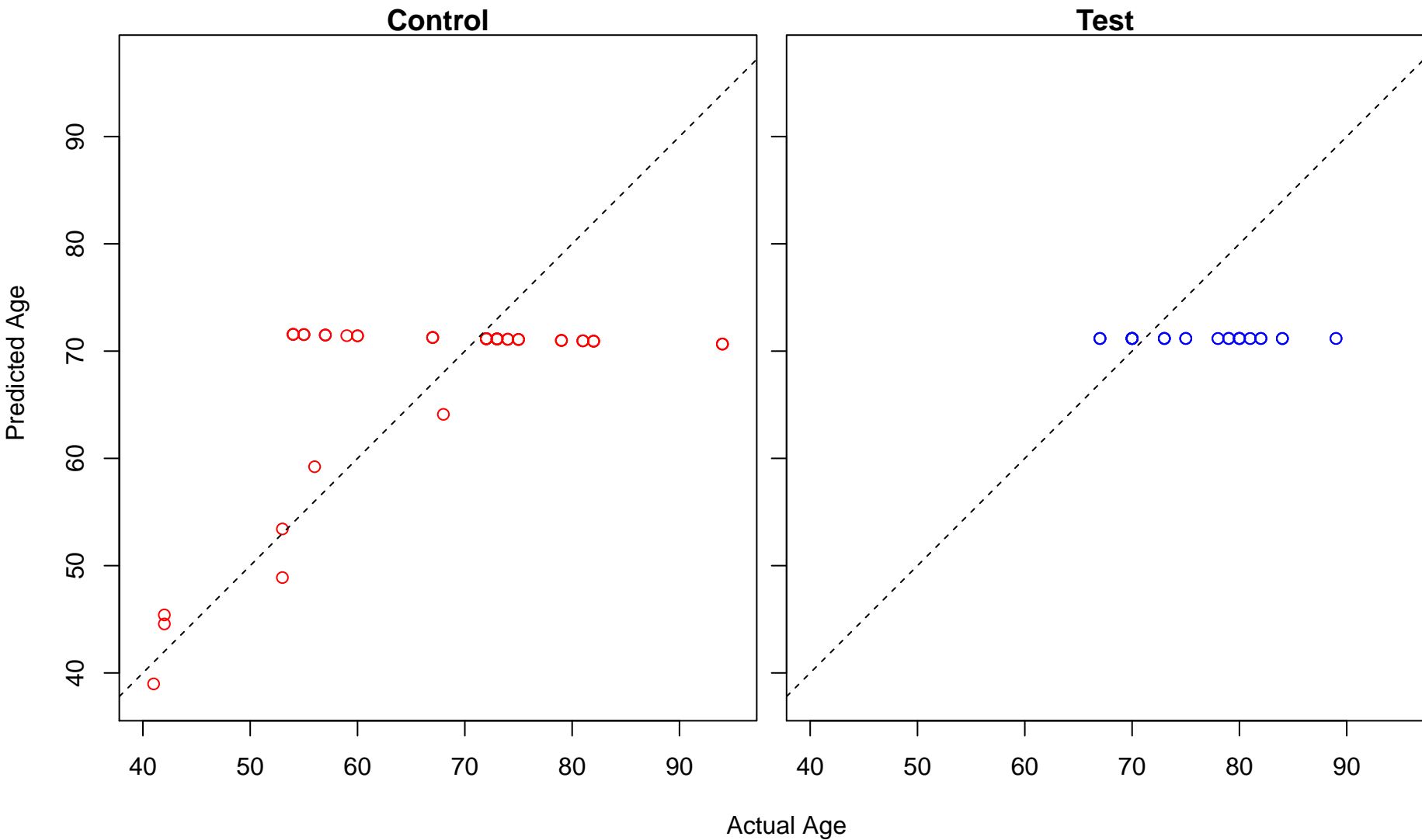
blood coagulation (Score: 0.842740)



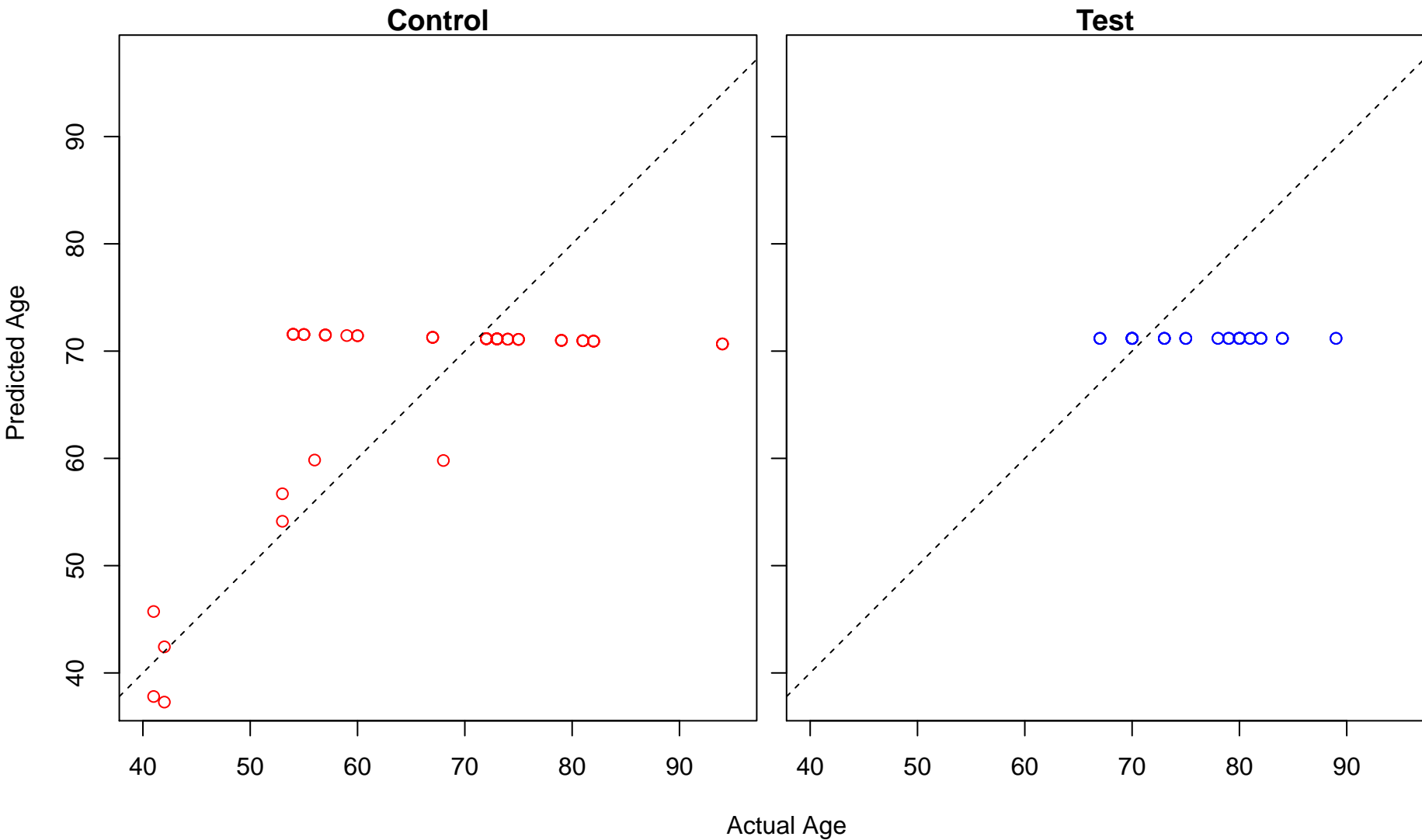
hemostasis (Score: 0.842740)



coagulation (Score: 0.842740)

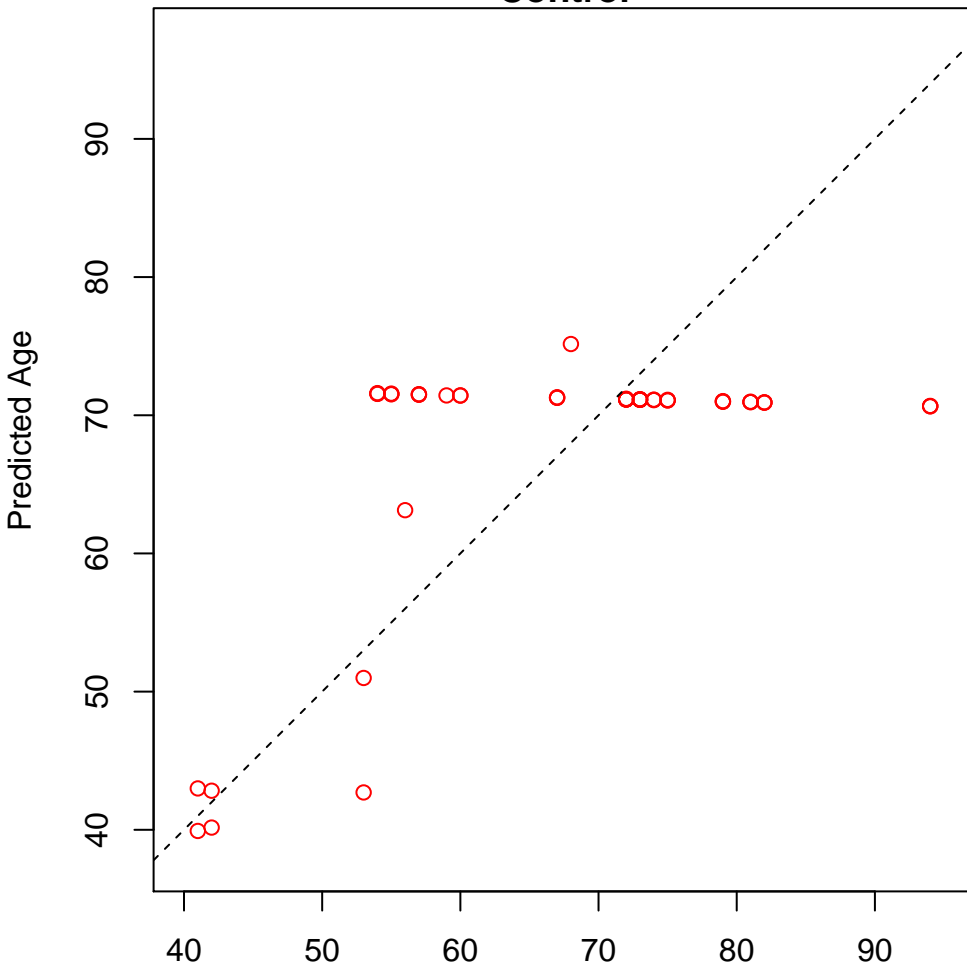


negative regulation of ubiquitin protein ligase activity (Score: 0.842296)

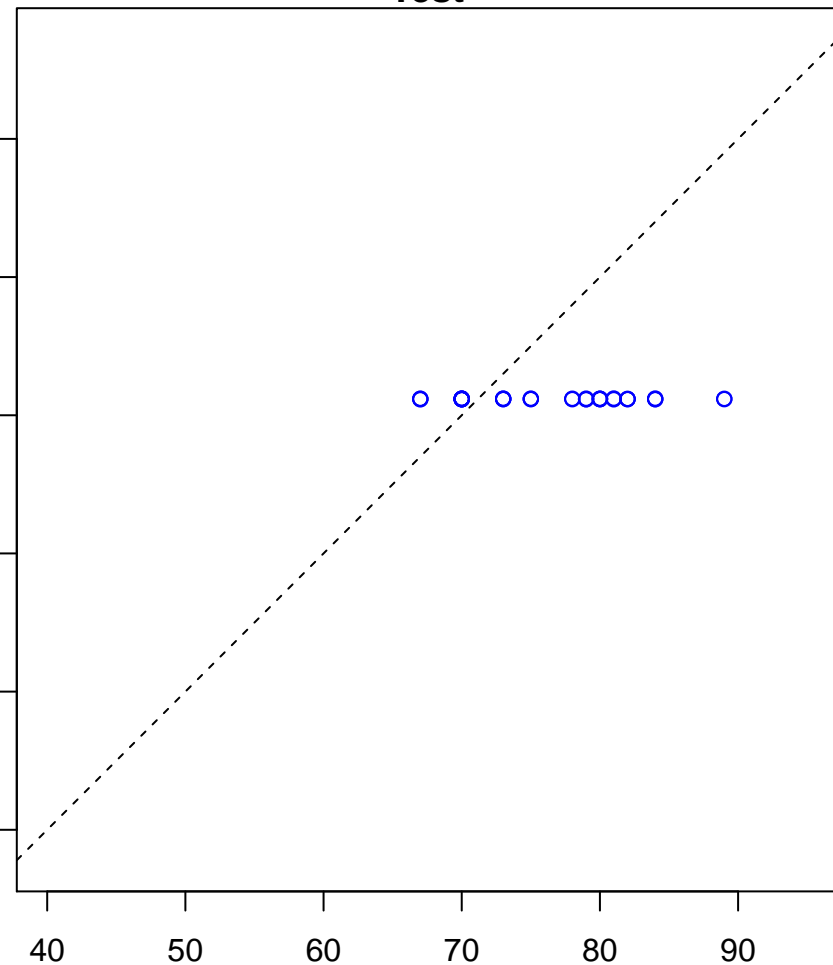


negative regulation of mitotic cell cycle (Score: 0.841634)

Control

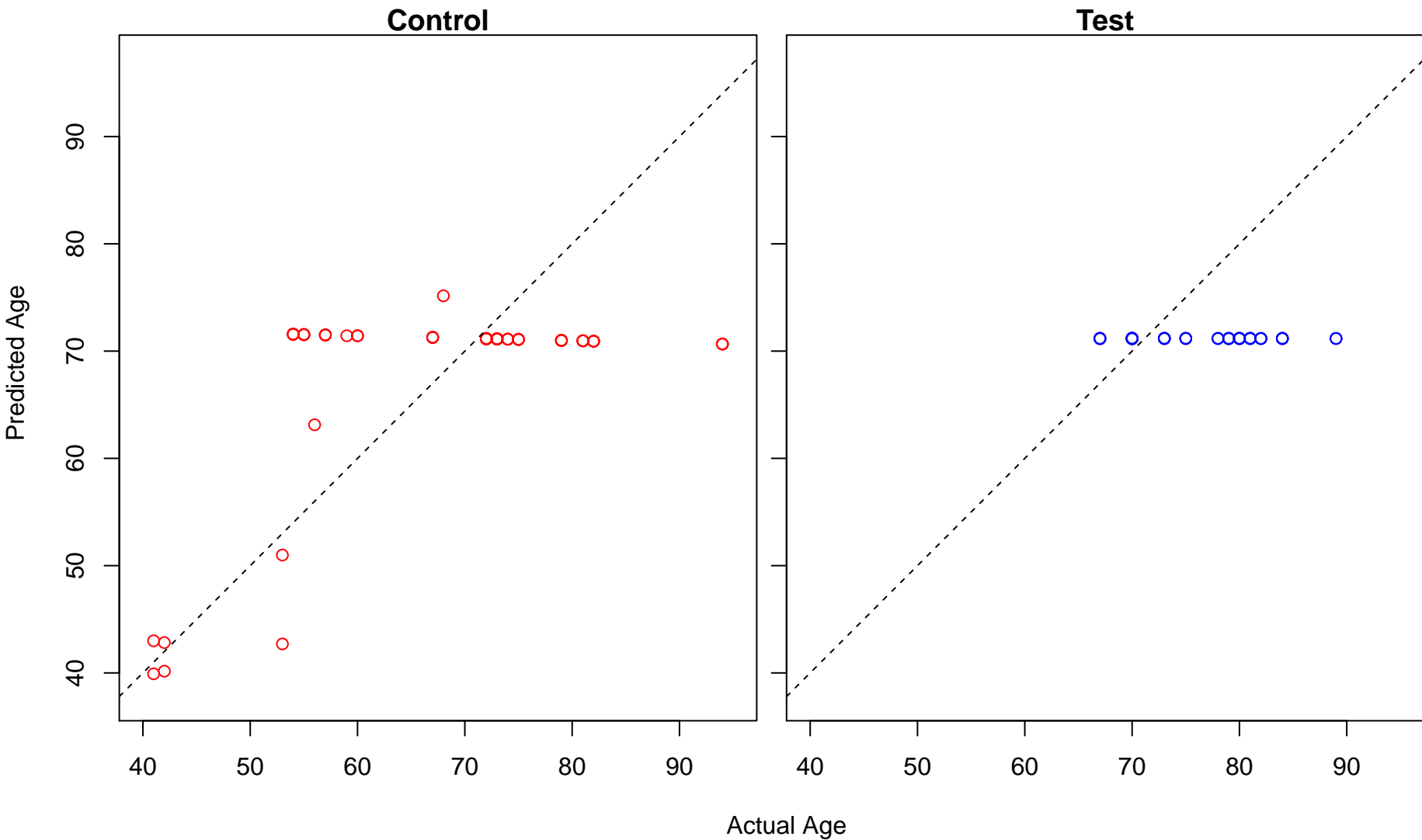


Test

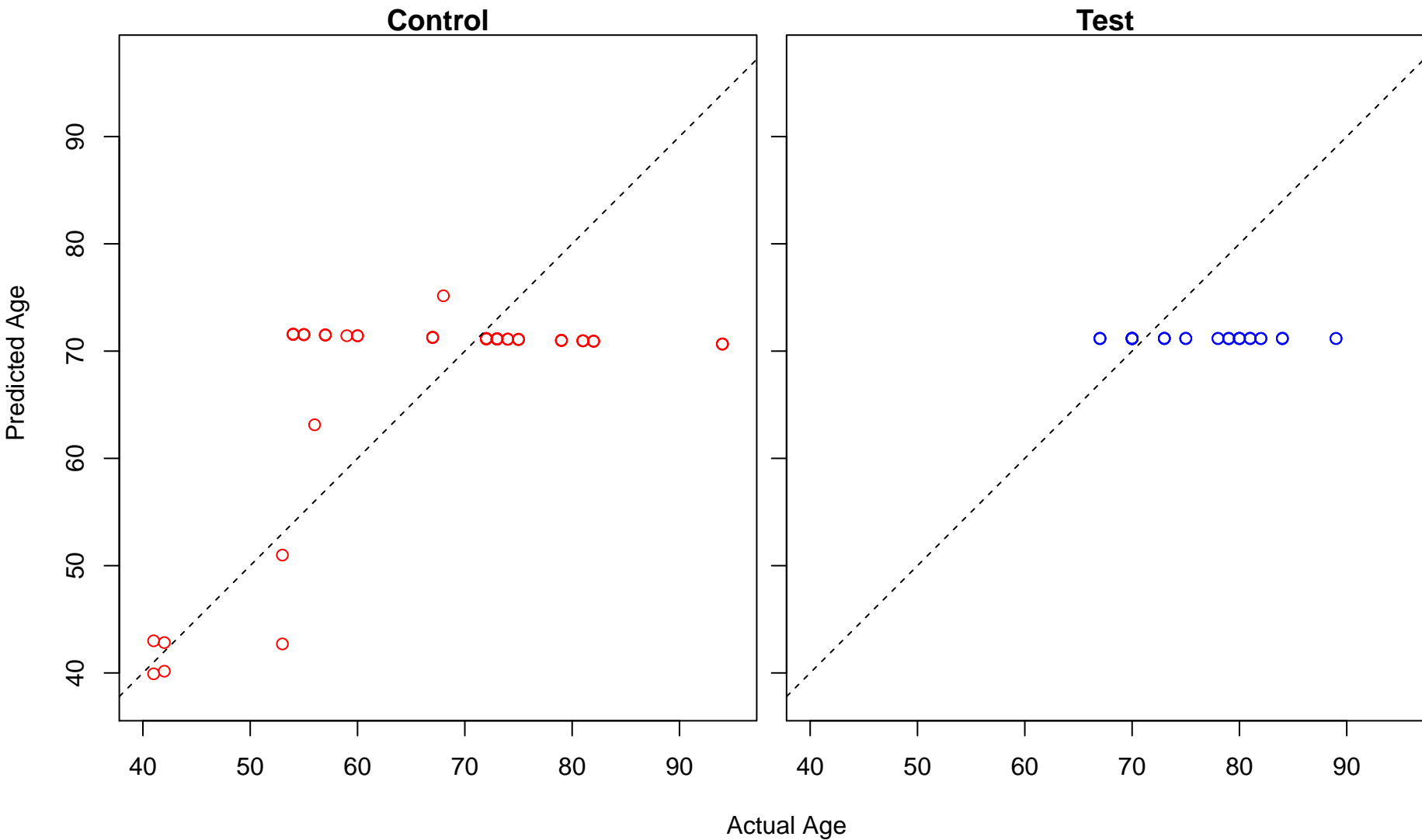


Actual Age

negative regulation of cell cycle phase transition (Score: 0.841634)

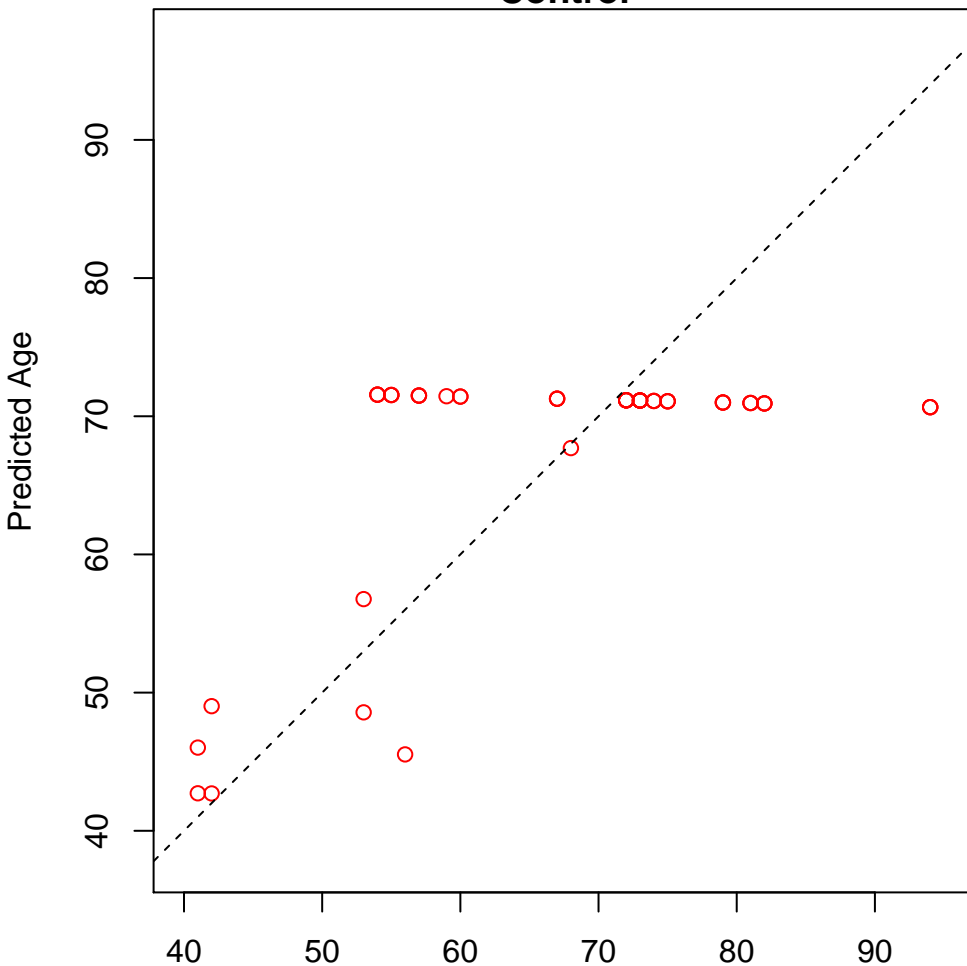


negative regulation of mitotic cell cycle phase transition (Score: 0.841634)

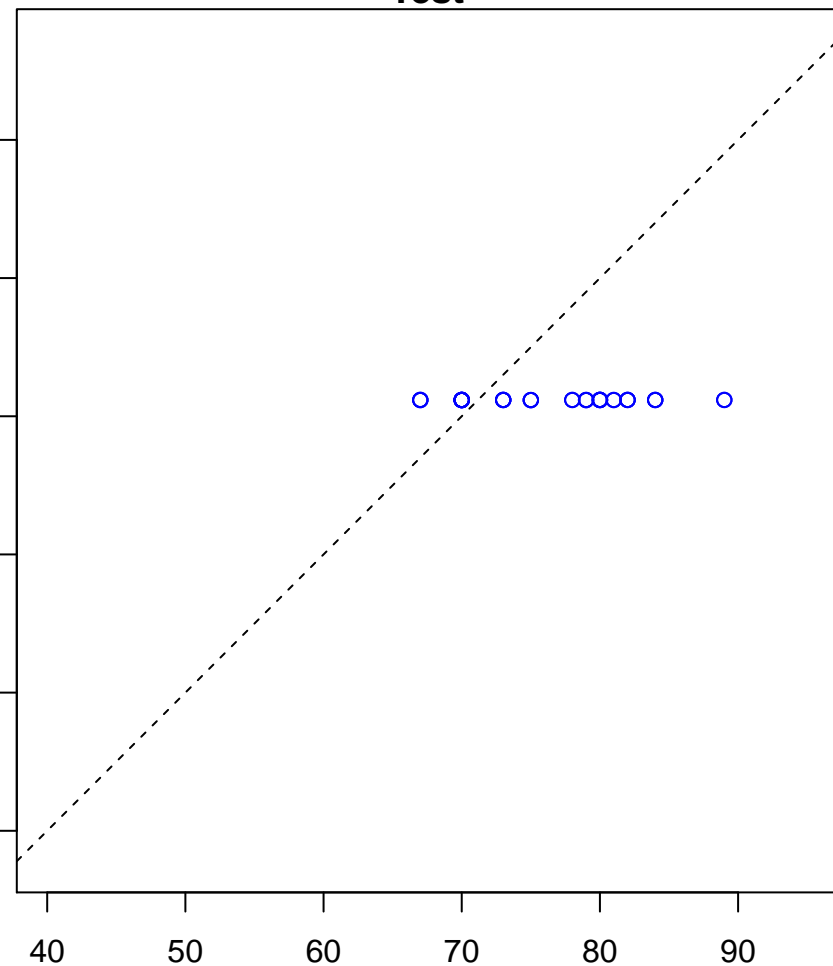


regulation of apoptotic signaling pathway (Score: 0.841623)

Control

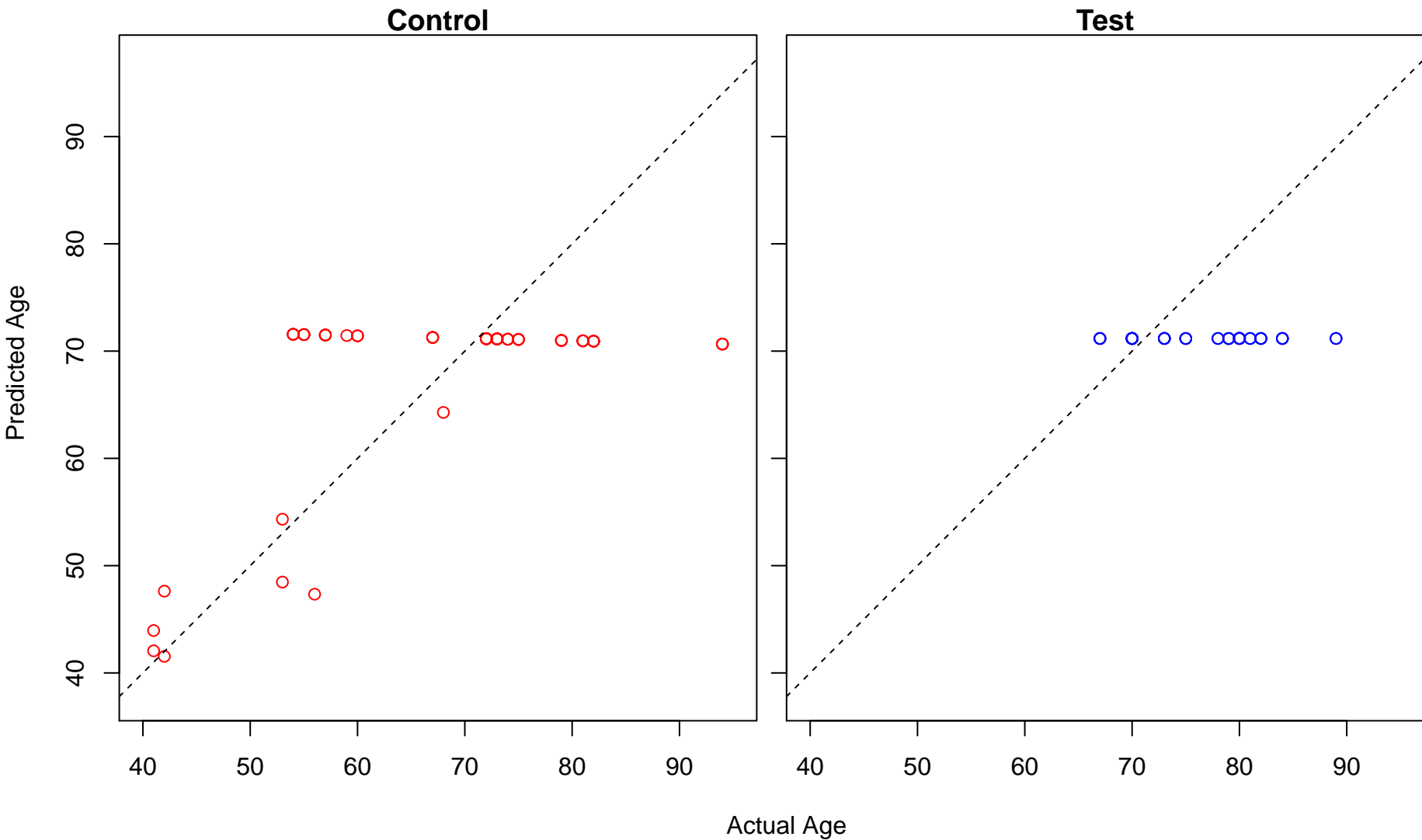


Test

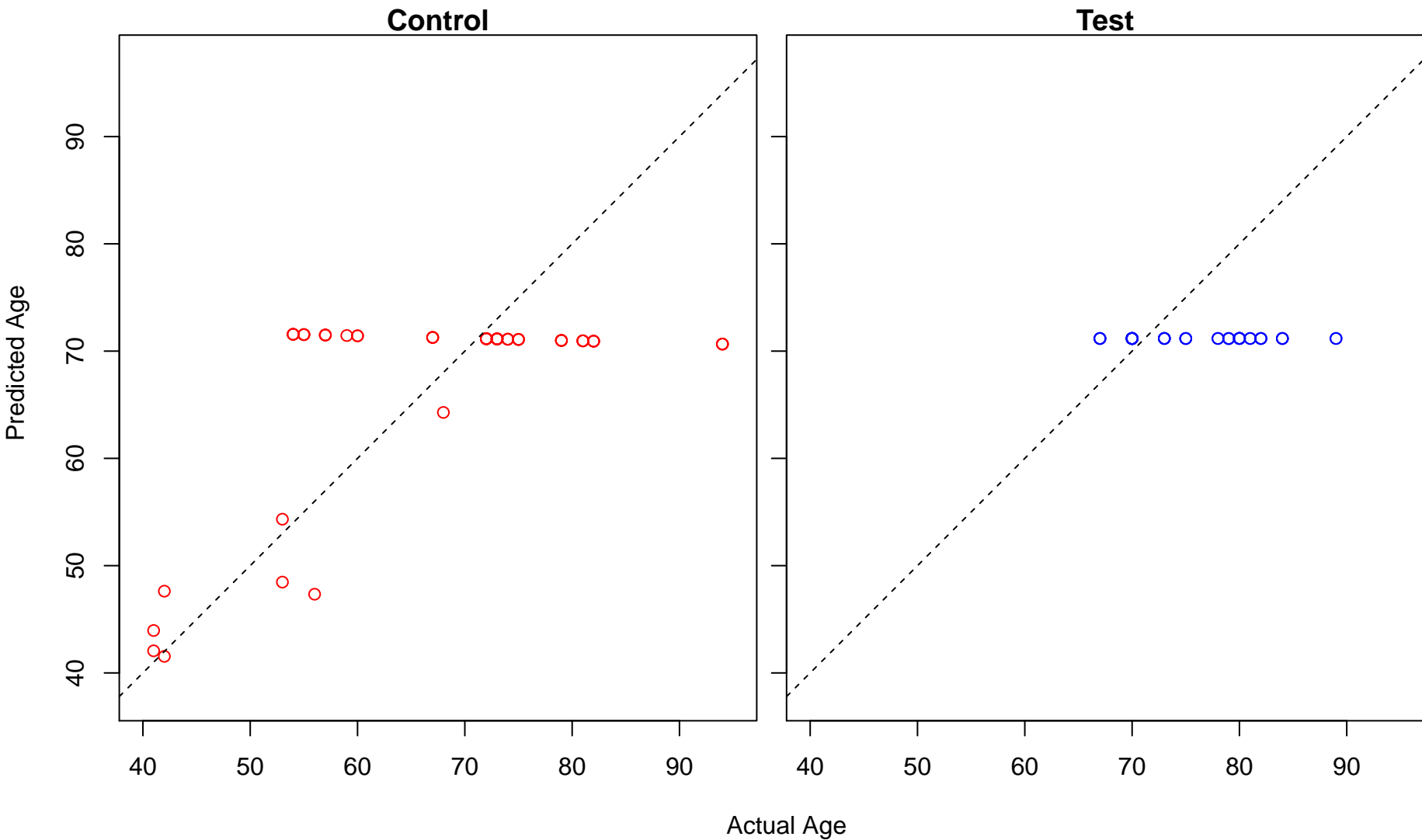


Actual Age

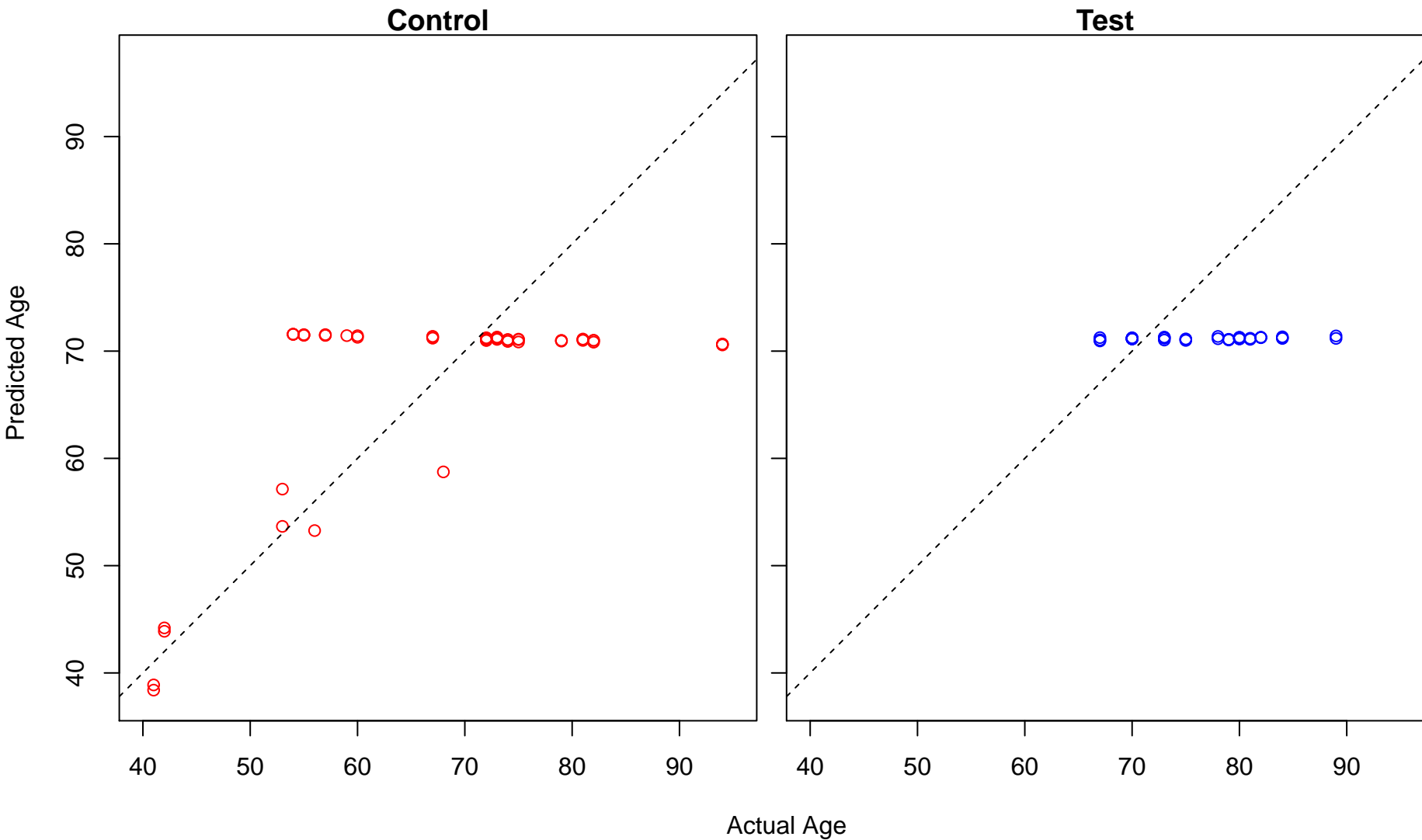
negative regulation of cell communication (Score: 0.841383)



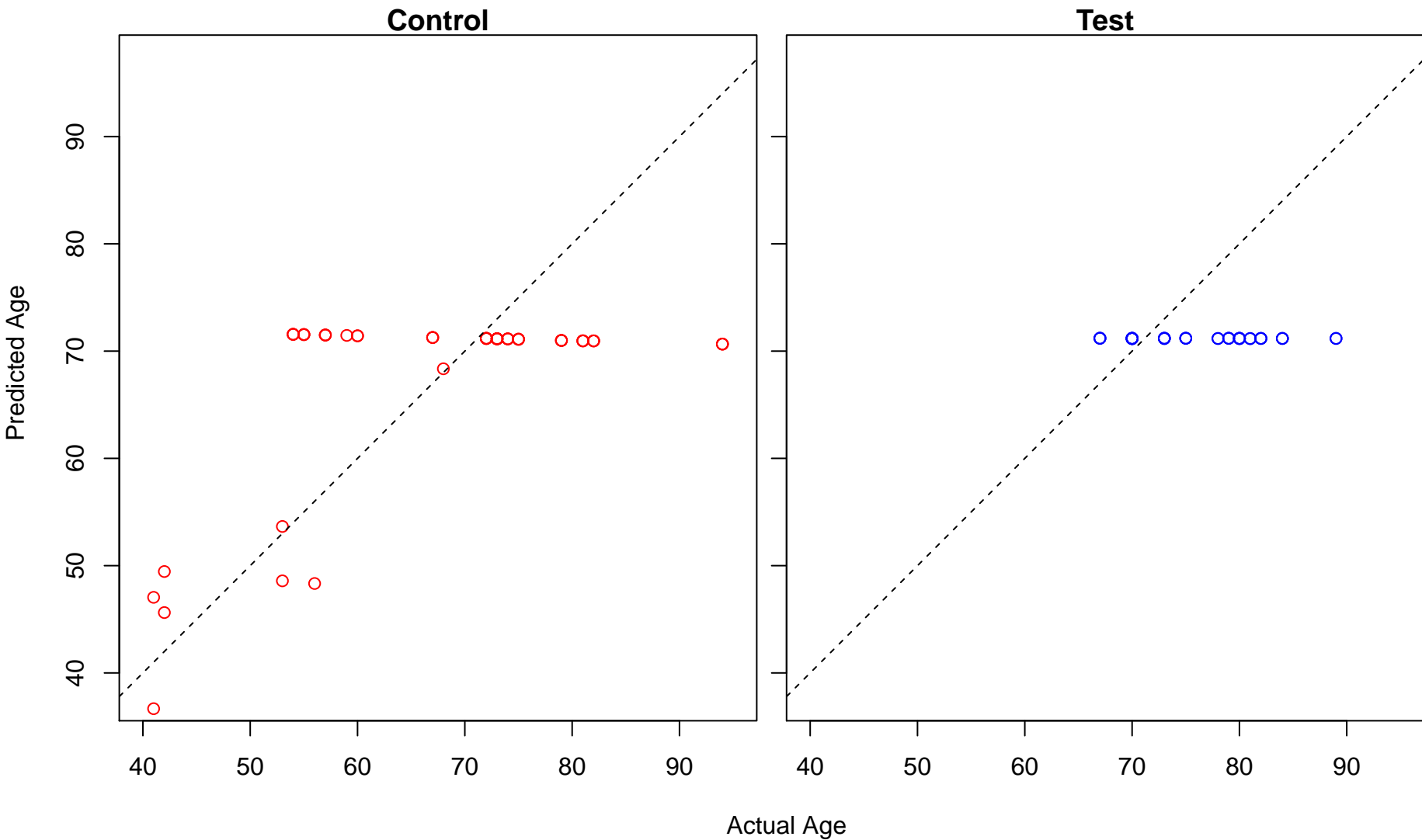
negative regulation of signaling (Score: 0.841383)



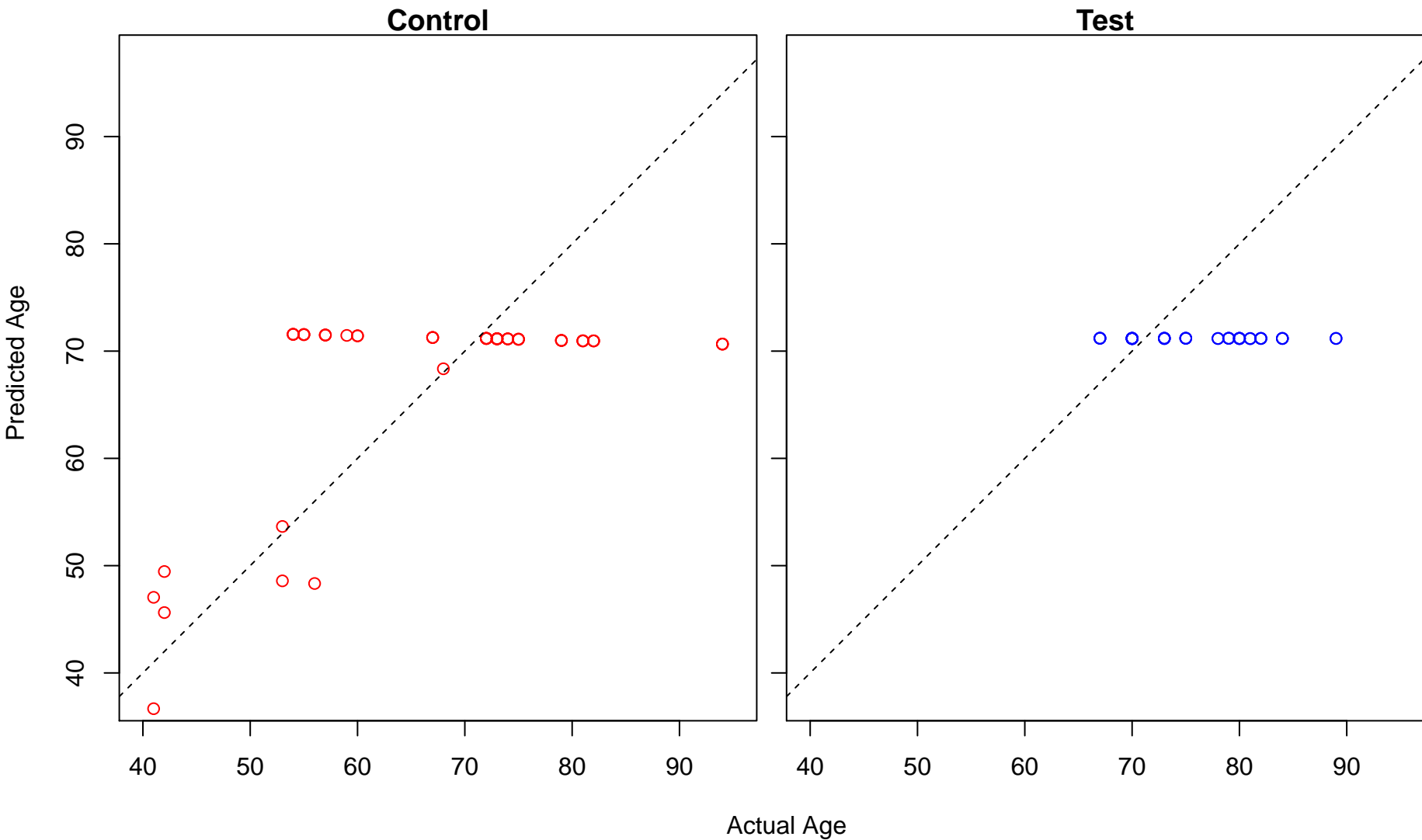
regulation of cell growth (Score: 0.841048)



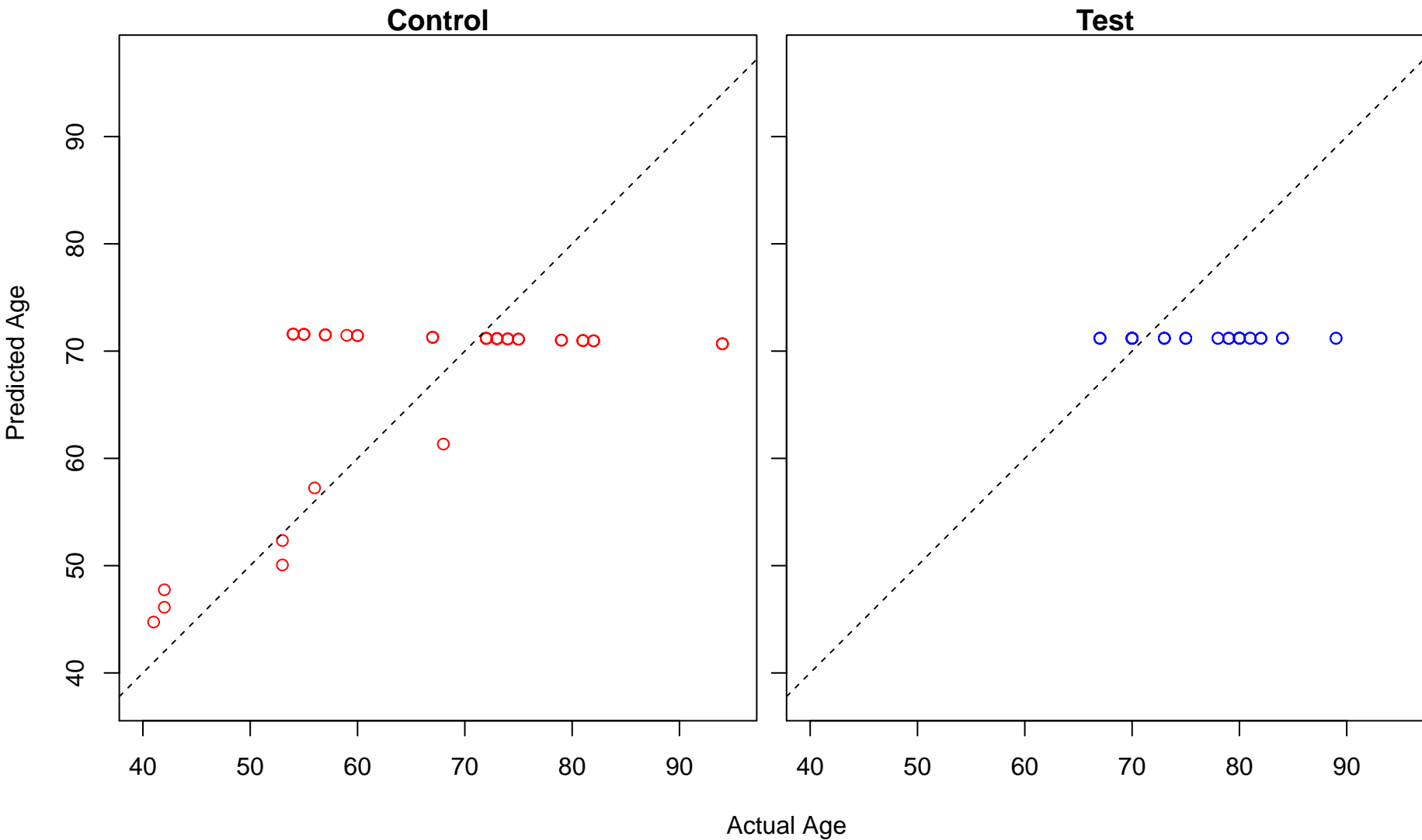
negative regulation of proteolysis involved in cellular protein catabolic process (Score: 0.840966)



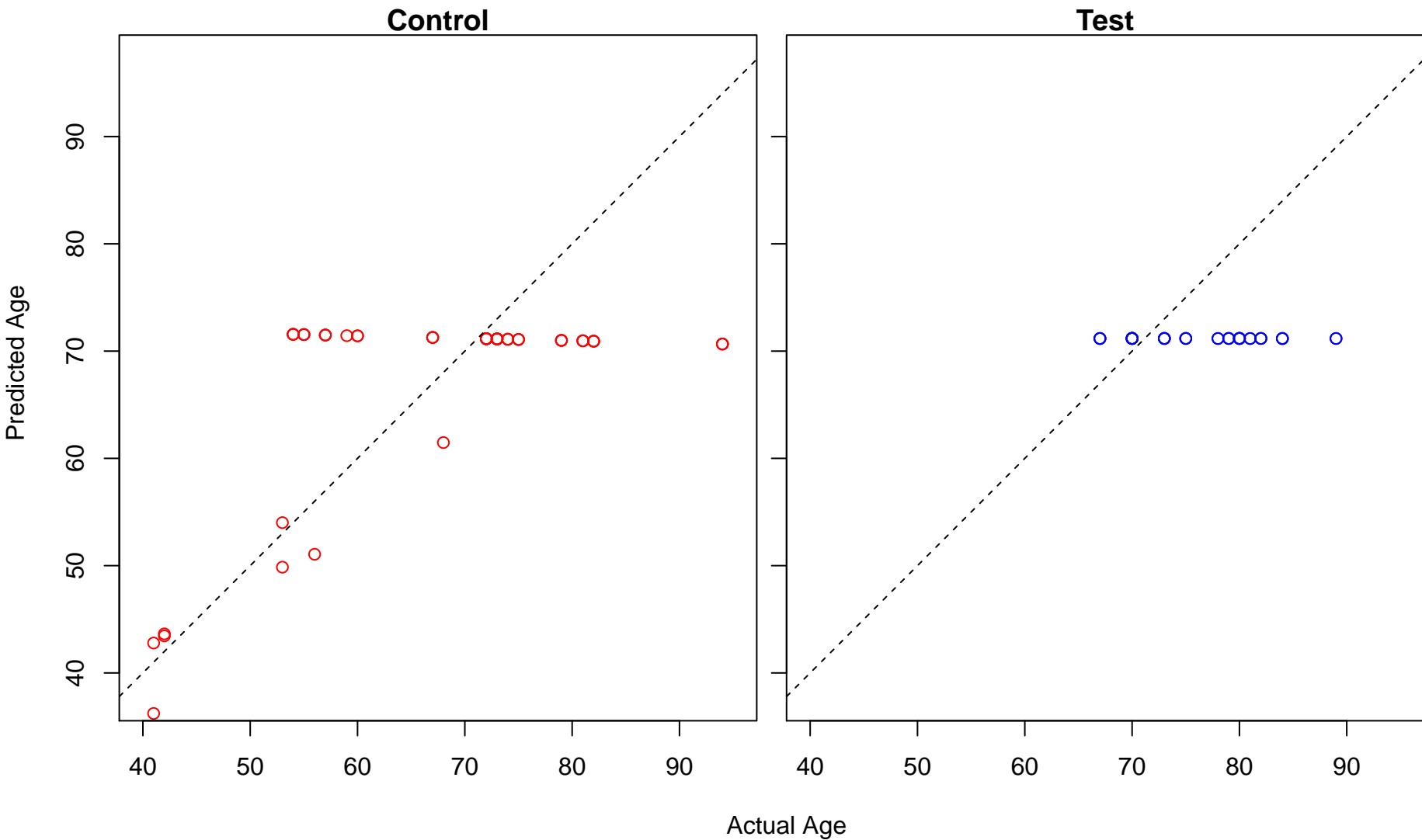
negative regulation of cellular protein catabolic process (Score: 0.840966)



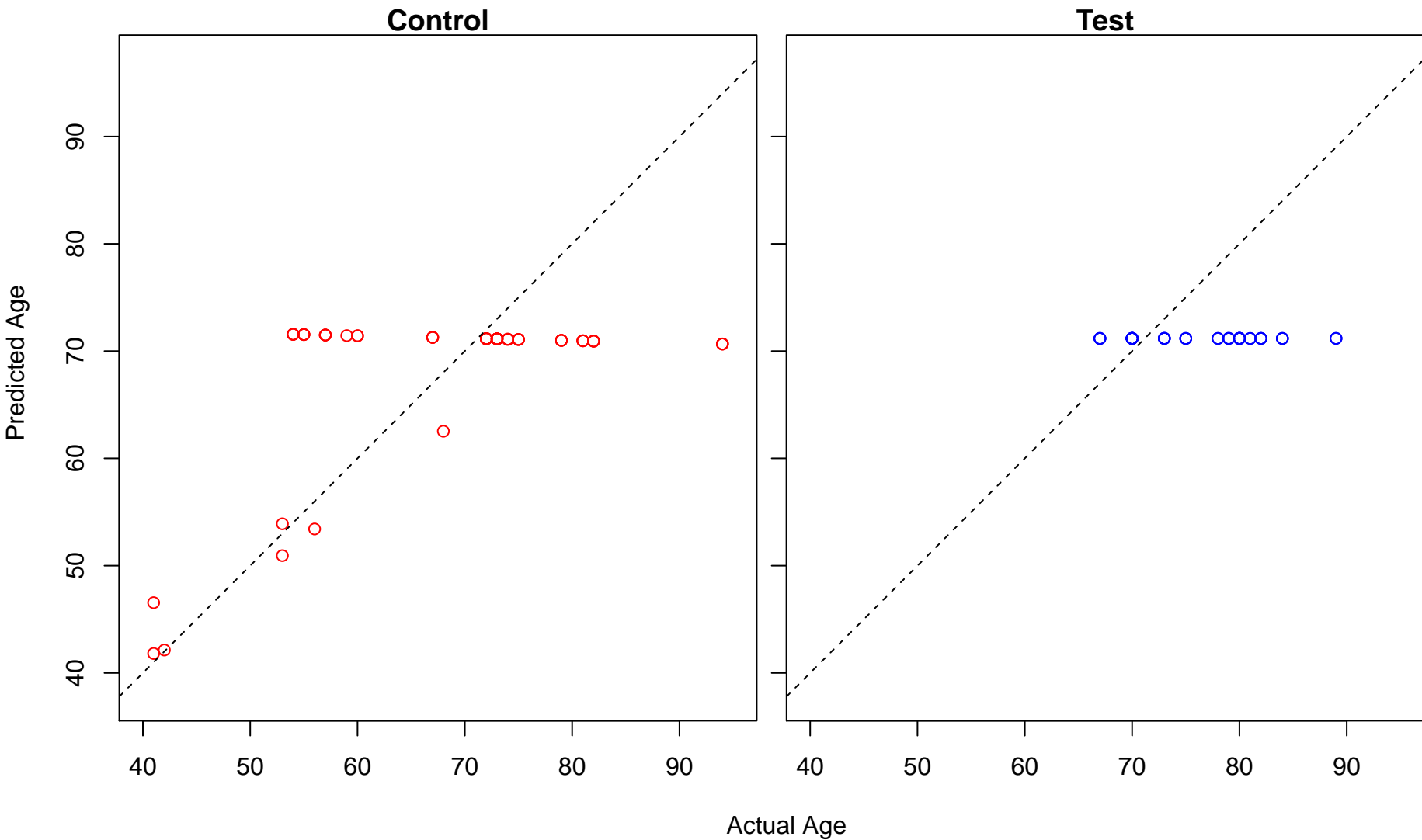
carbohydrate metabolic process (Score: 0.840837)



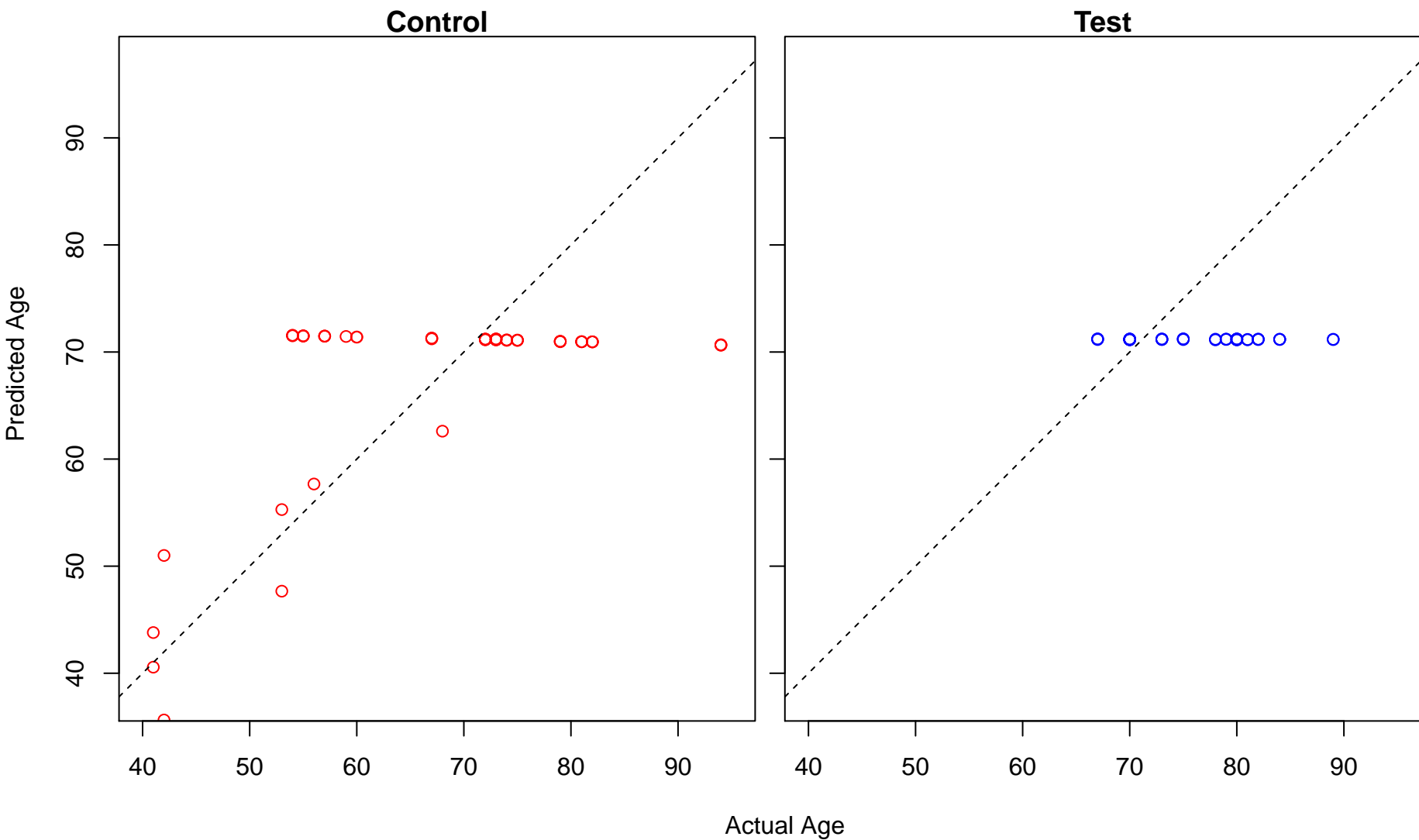
wound healing (Score: 0.840748)



response to wounding (Score: 0.840398)

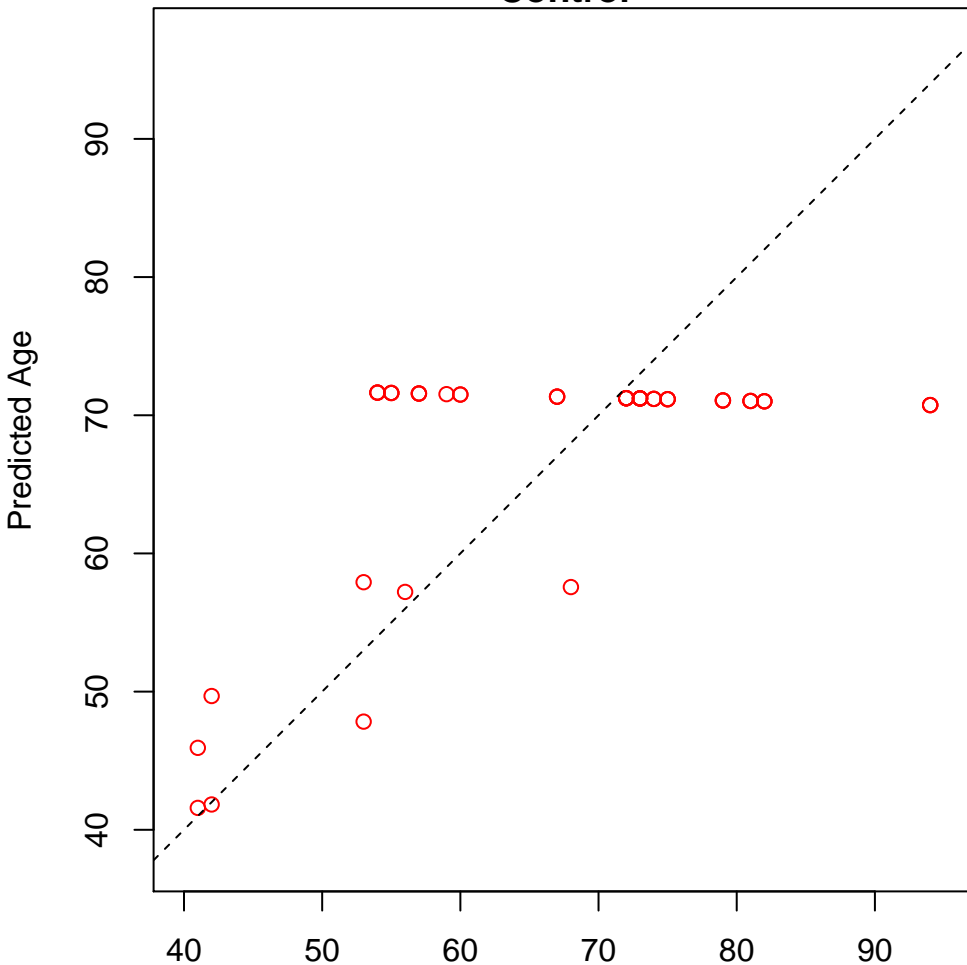


regulation of GTPase activity (Score: 0.840362)

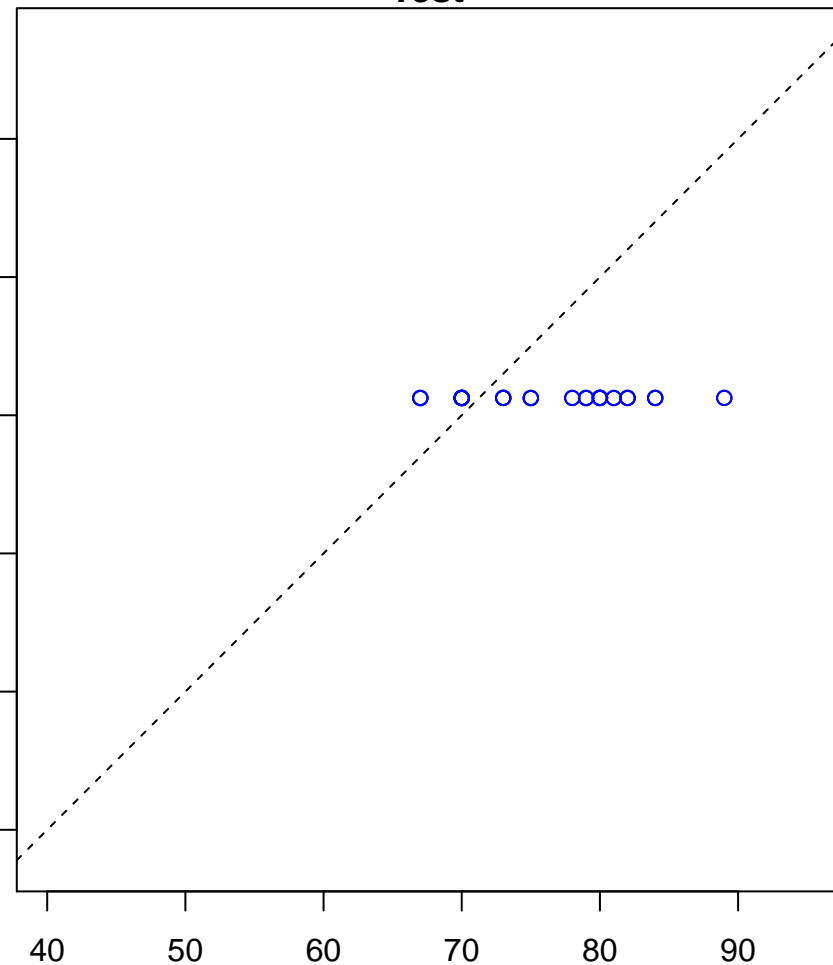


carbohydrate biosynthetic process (Score: 0.840183)

Control



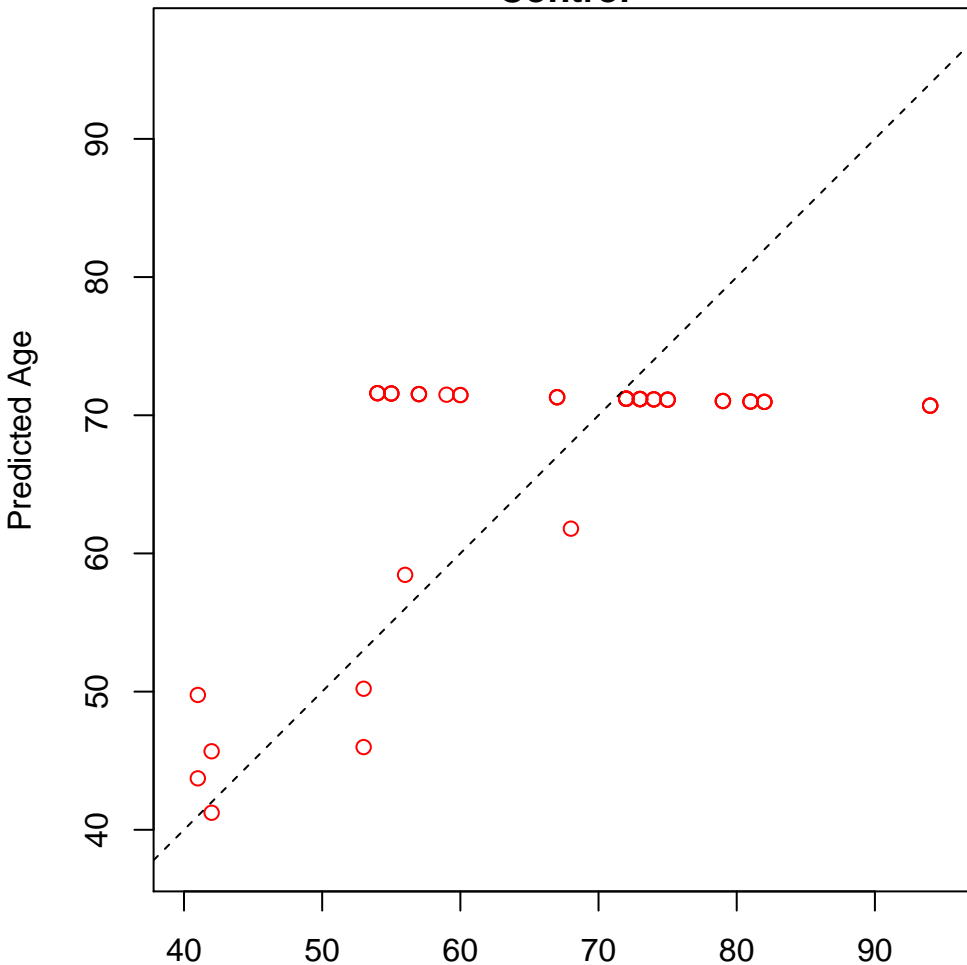
Test



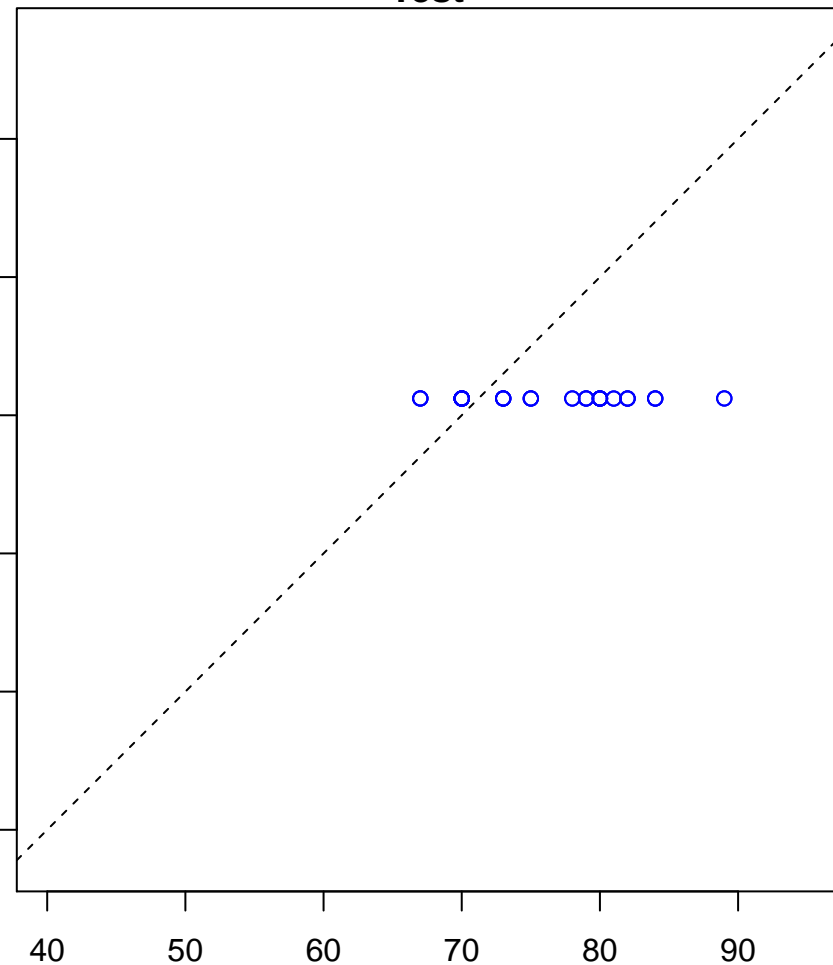
Actual Age

epithelial cell differentiation (Score: 0.840018)

Control

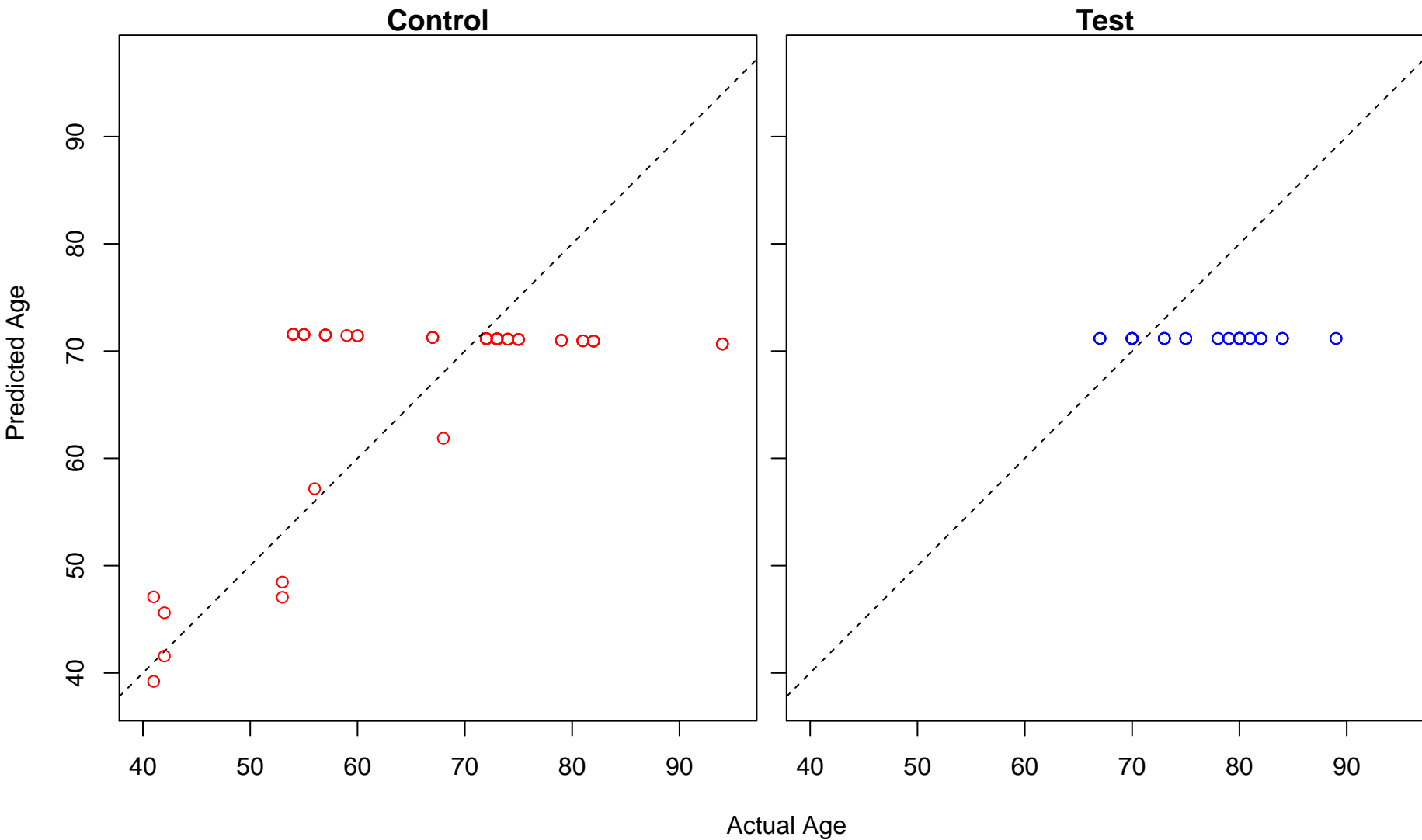


Test



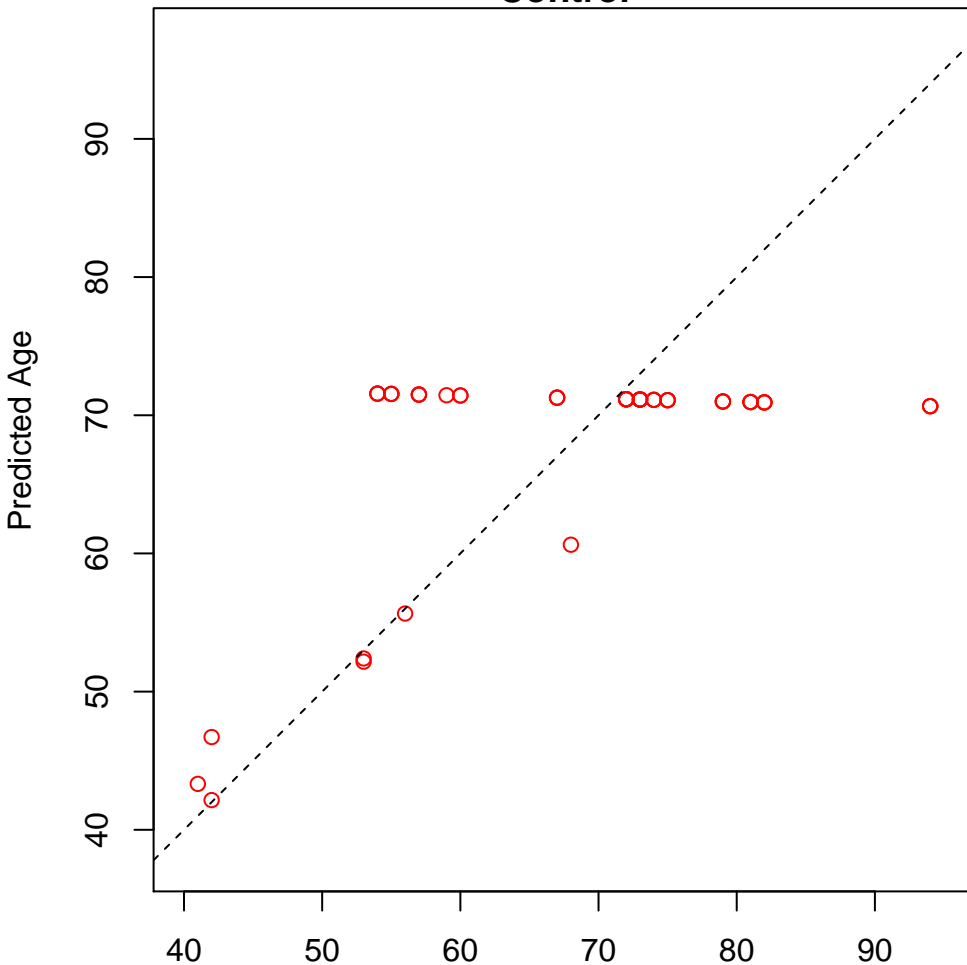
Actual Age

positive regulation of protein serine/threonine kinase activity (Score: 0.839959)

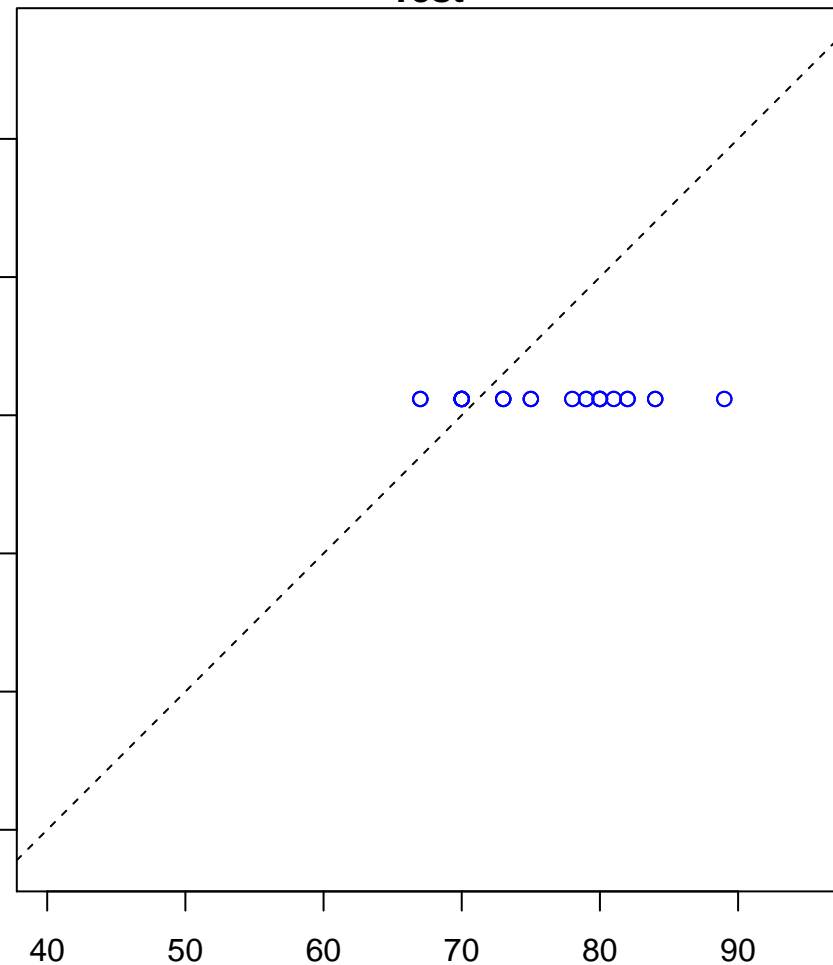


oxidation-reduction process (Score: 0.839915)

Control



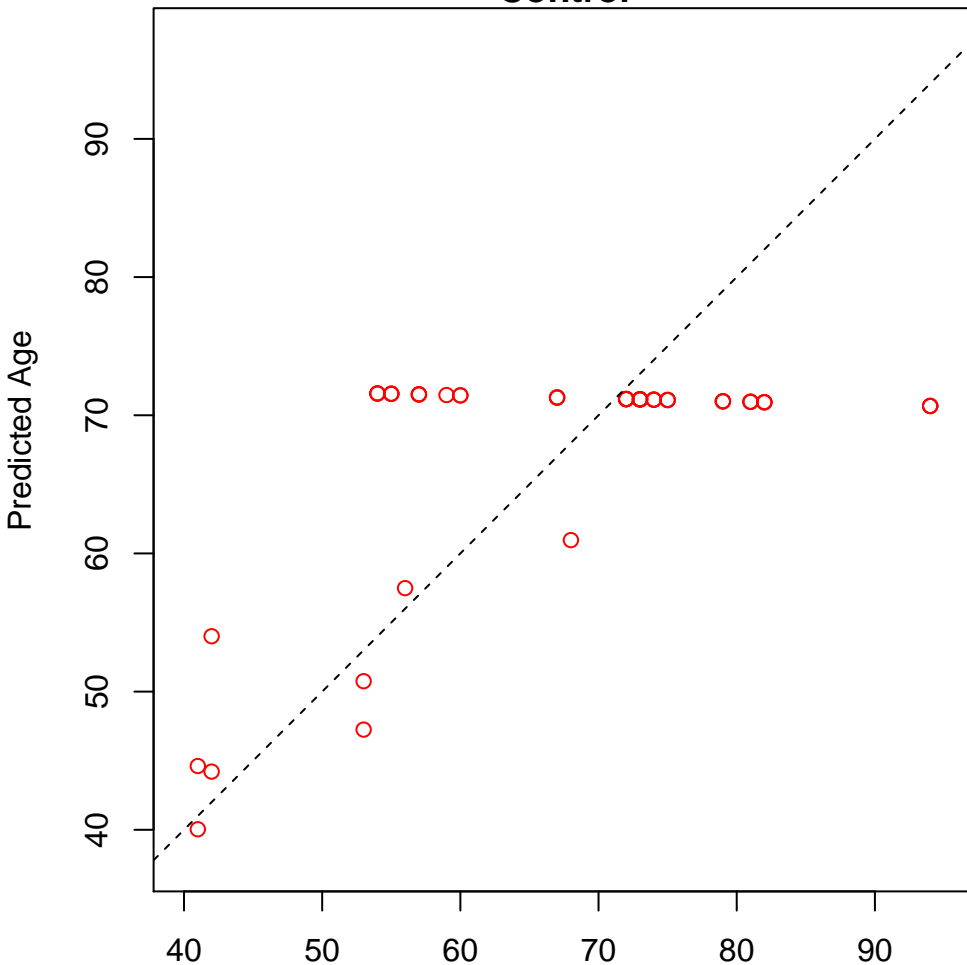
Test



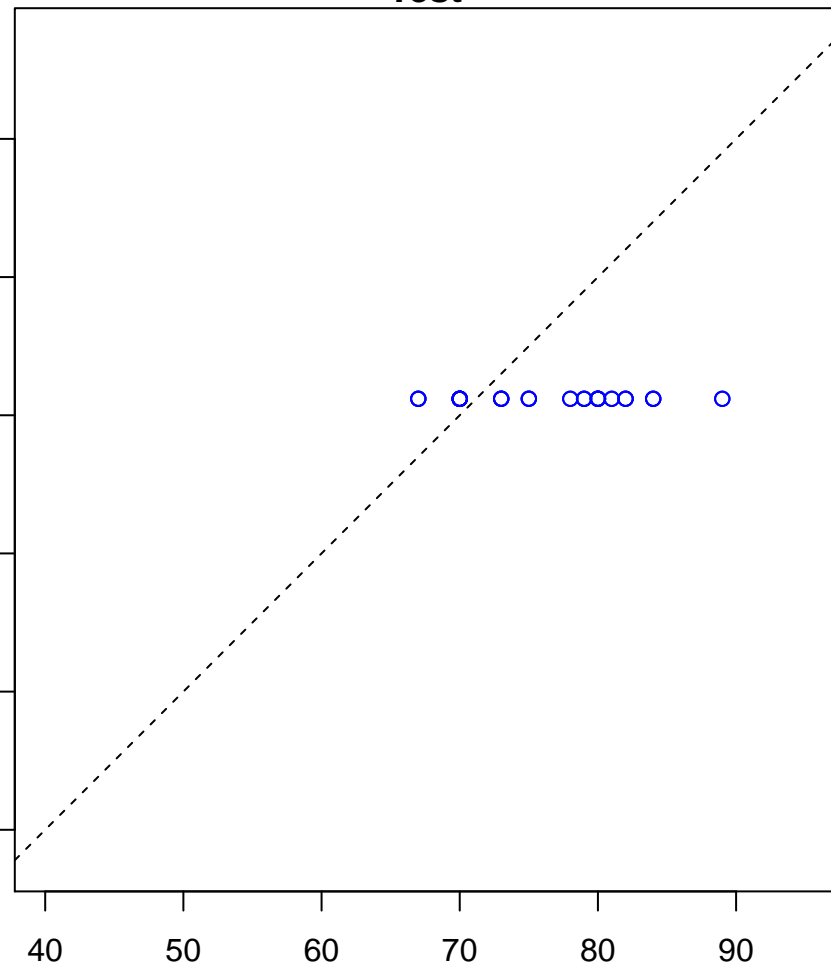
Actual Age

purine nucleotide metabolic process (Score: 0.839701)

Control

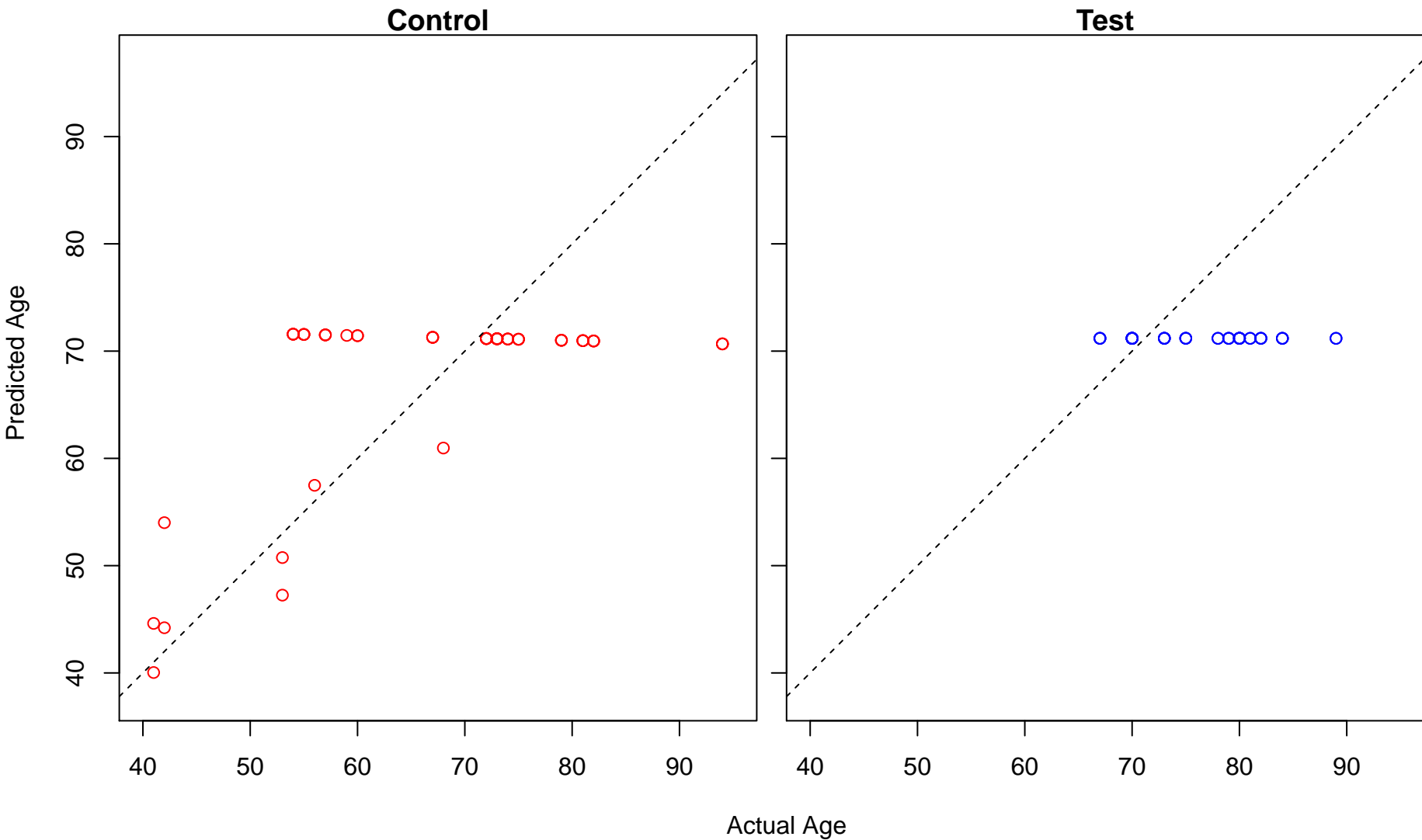


Test

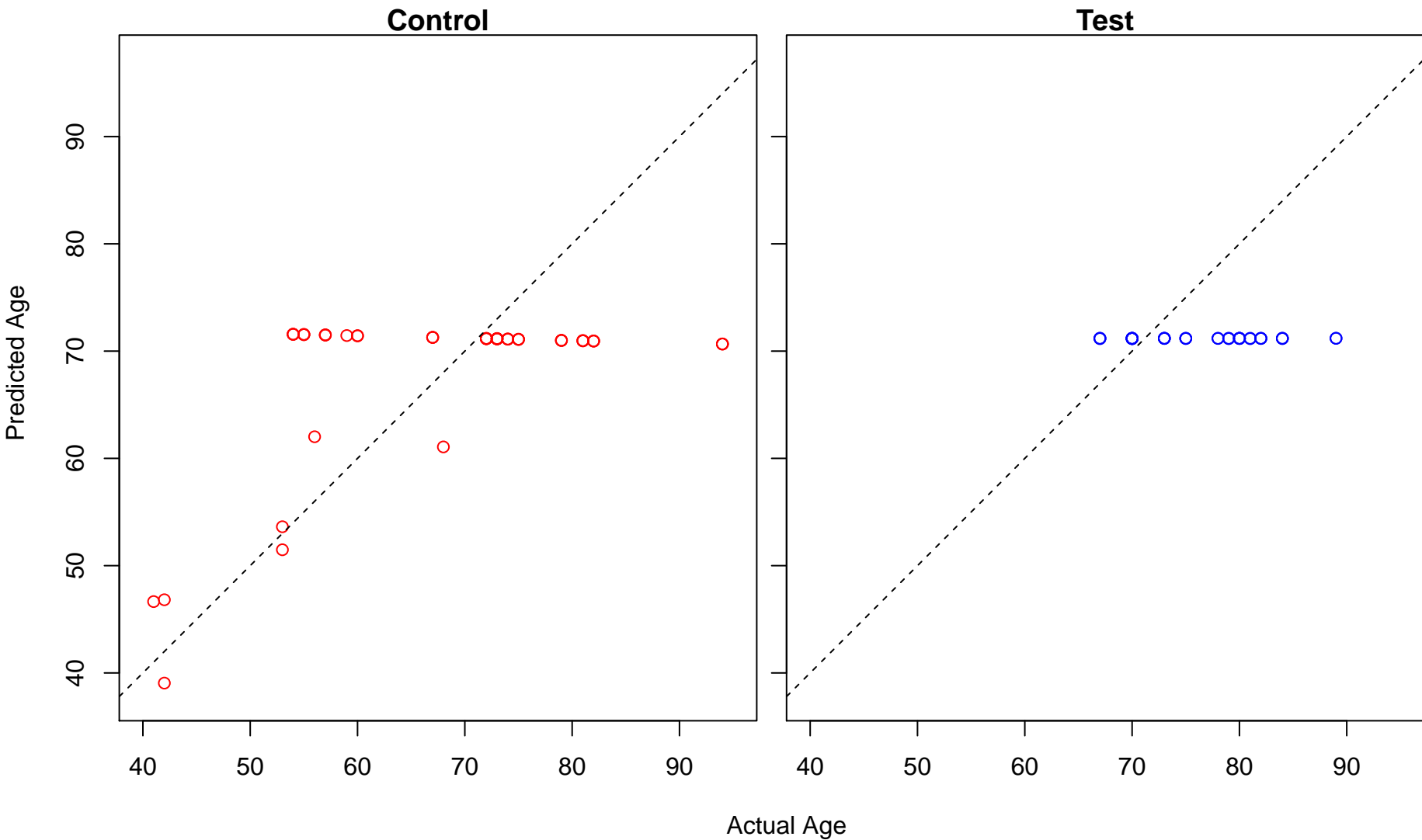


Actual Age

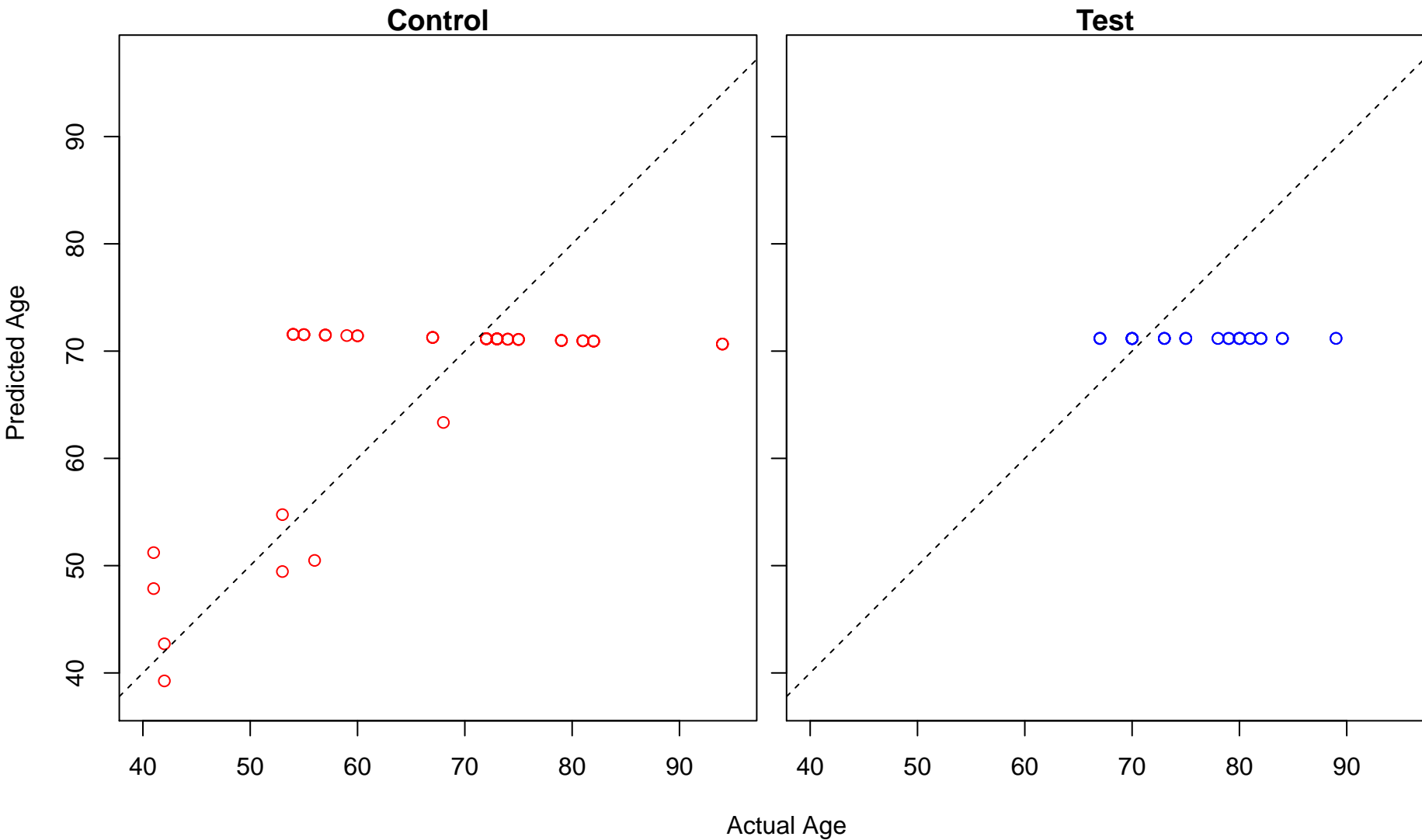
purine-containing compound metabolic process (Score: 0.839701)



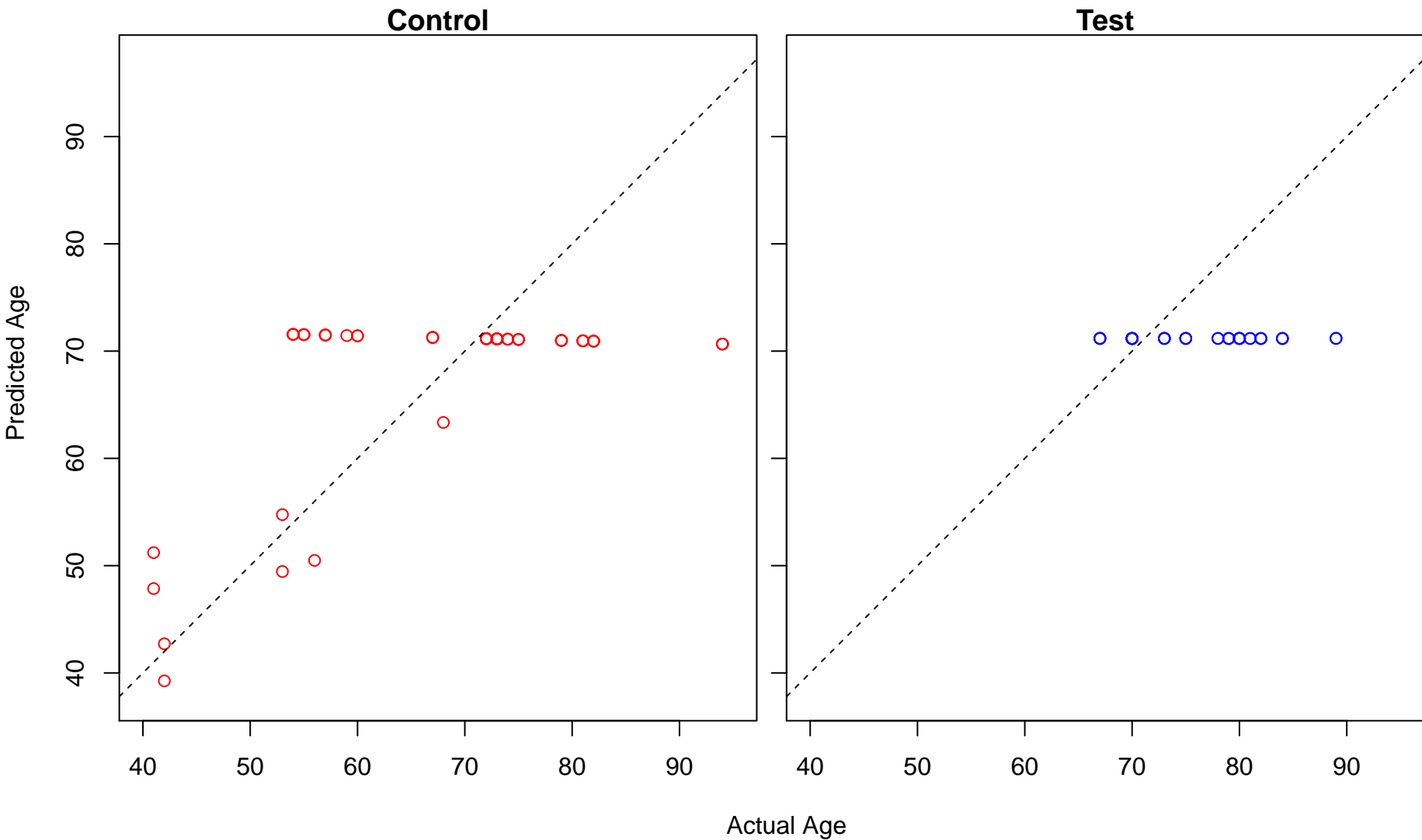
positive regulation of ubiquitin–protein transferase activity (Score: 0.839635)



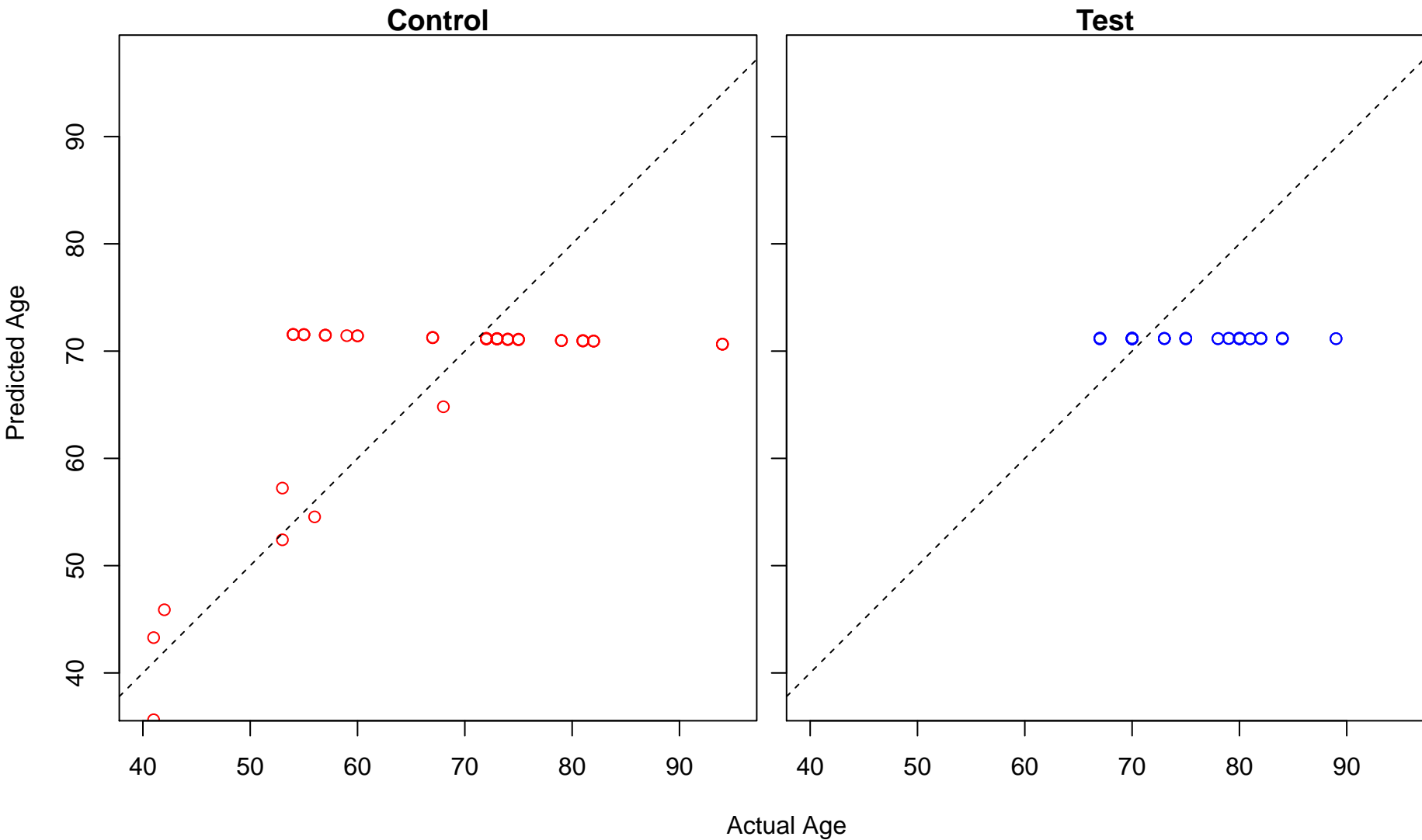
protein deubiquitination (Score: 0.839530)



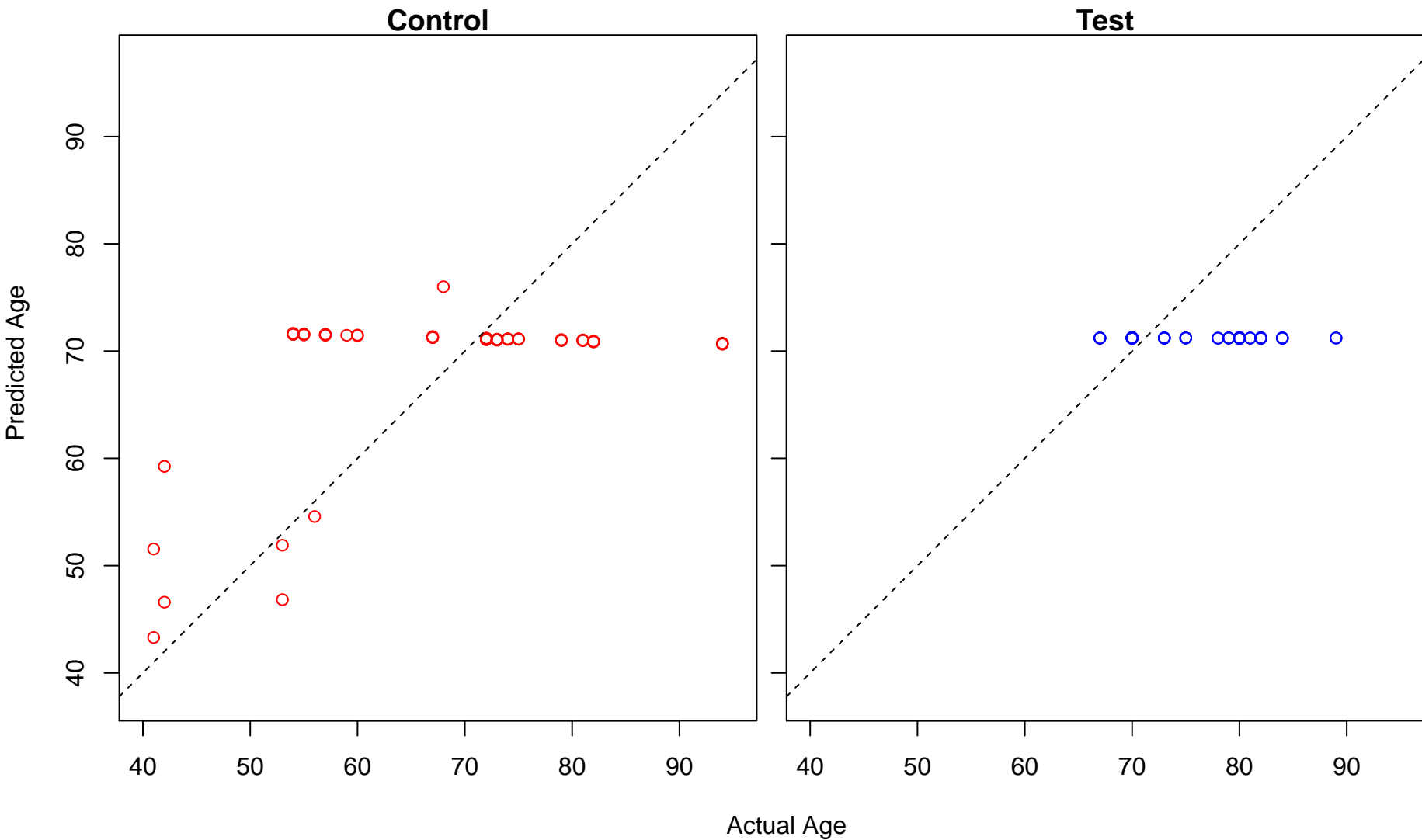
protein modification by small protein removal (Score: 0.839530)



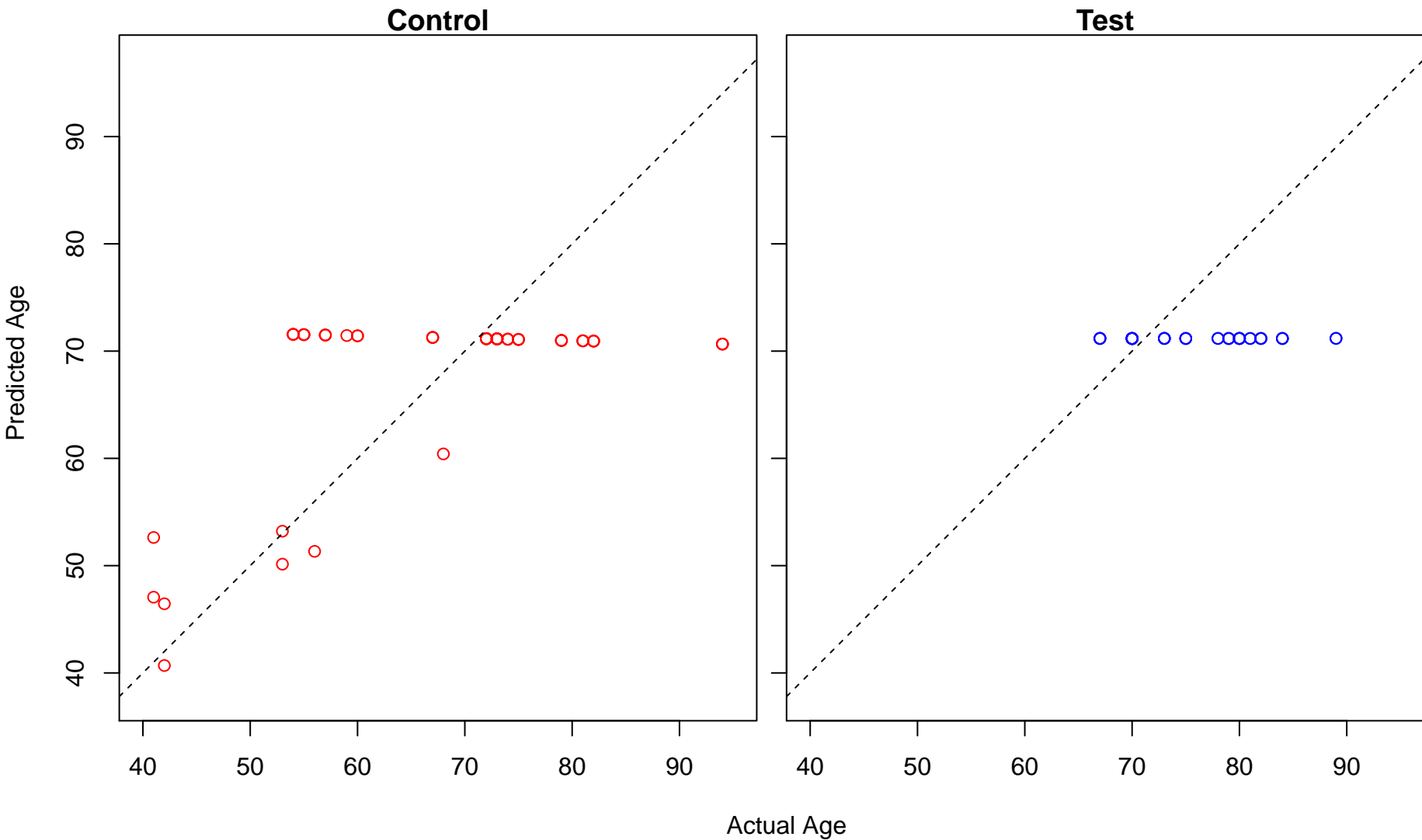
mitochondrial transport (Score: 0.839054)



positive regulation of supramolecular fiber organization (Score: 0.838976)

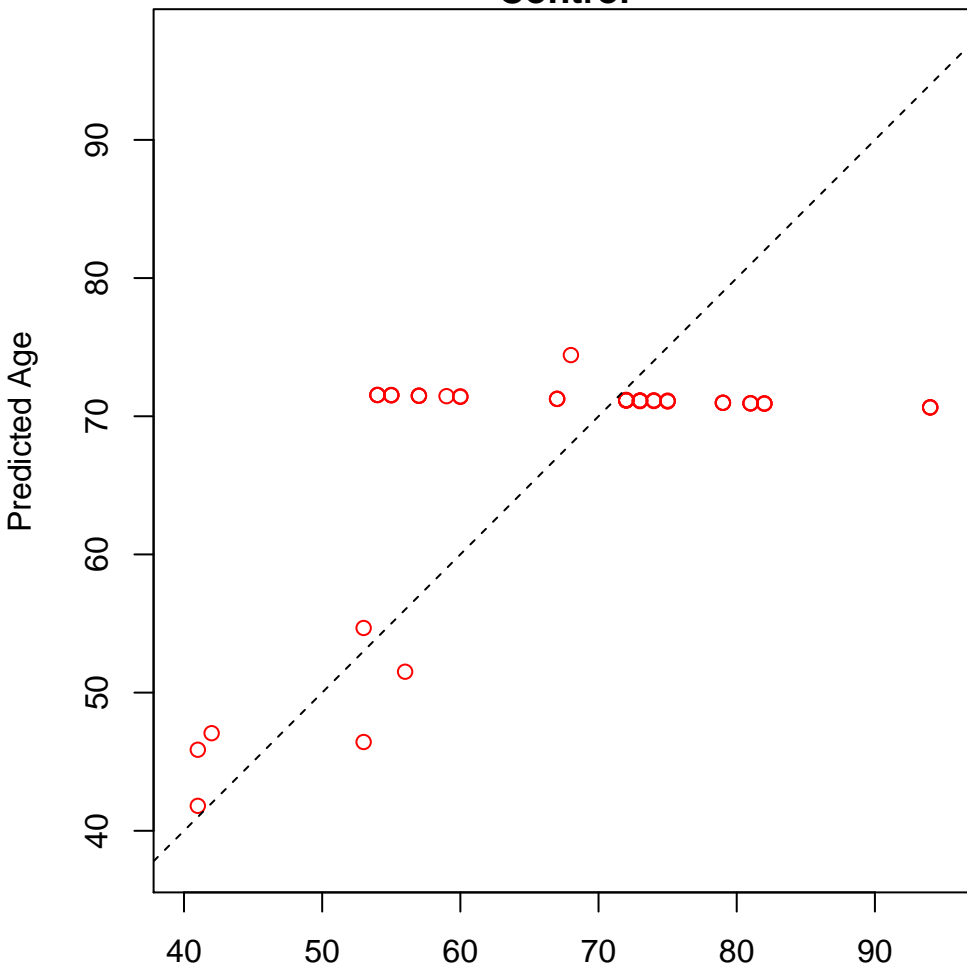


protein modification by small protein conjugation or removal (Score: 0.838115)

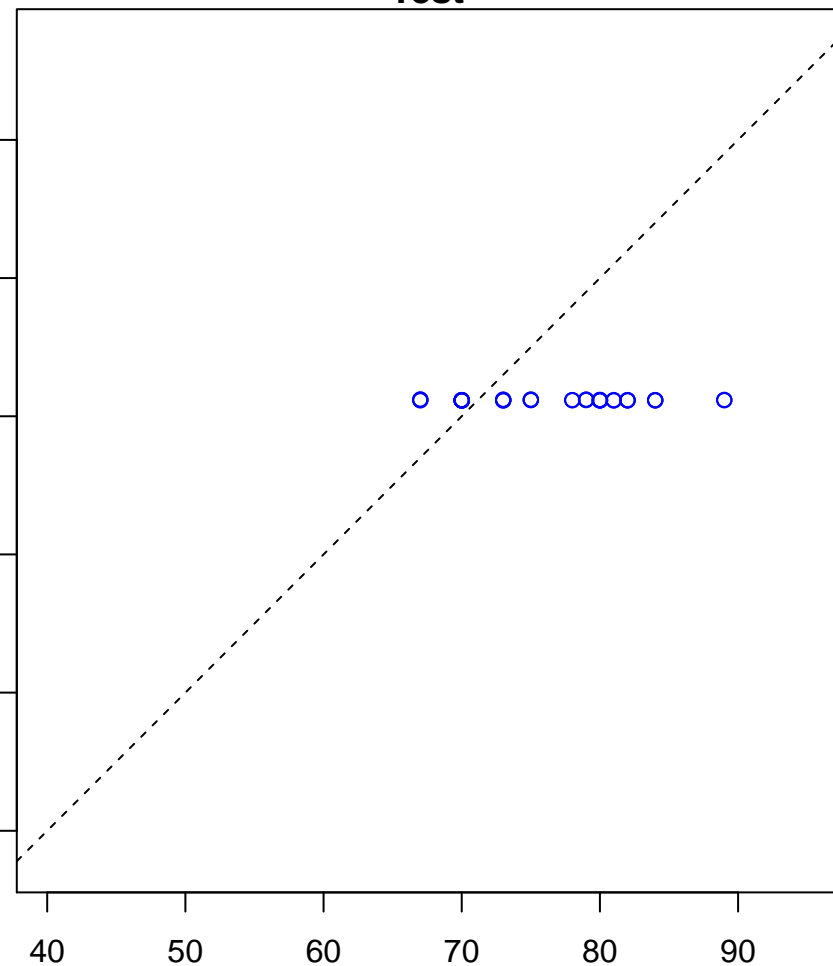


regulation of Wnt signaling pathway (Score: 0.838090)

Control

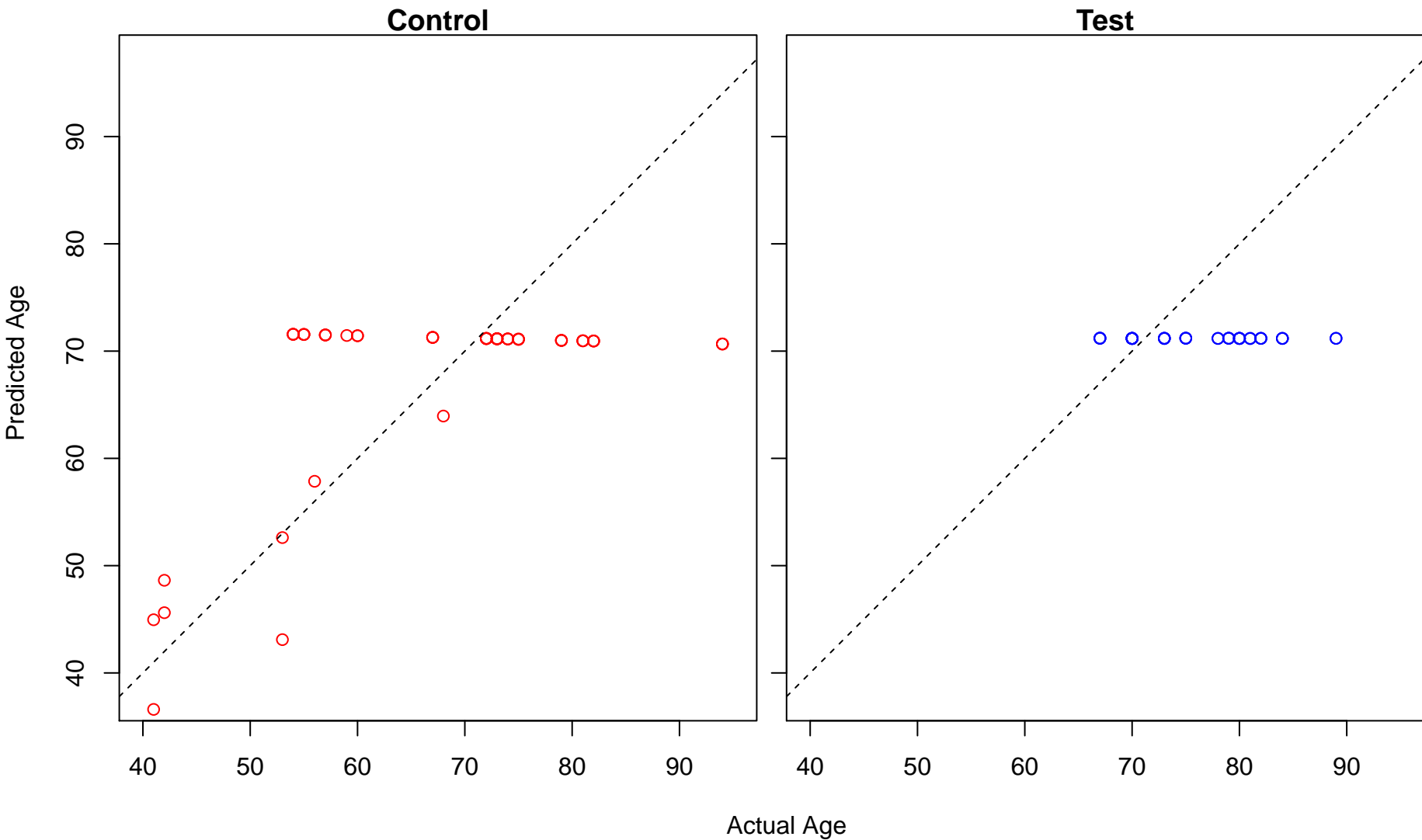


Test



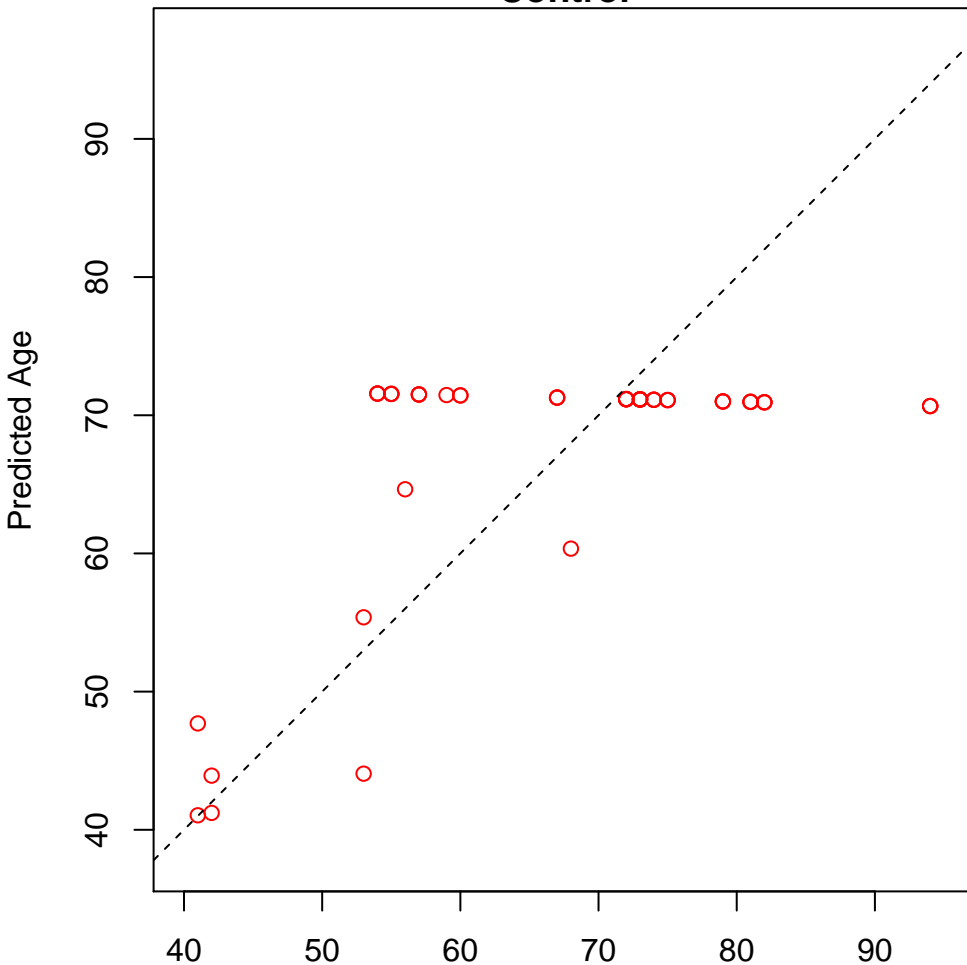
Actual Age

maintenance of protein localization in organelle (Score: 0.837786)

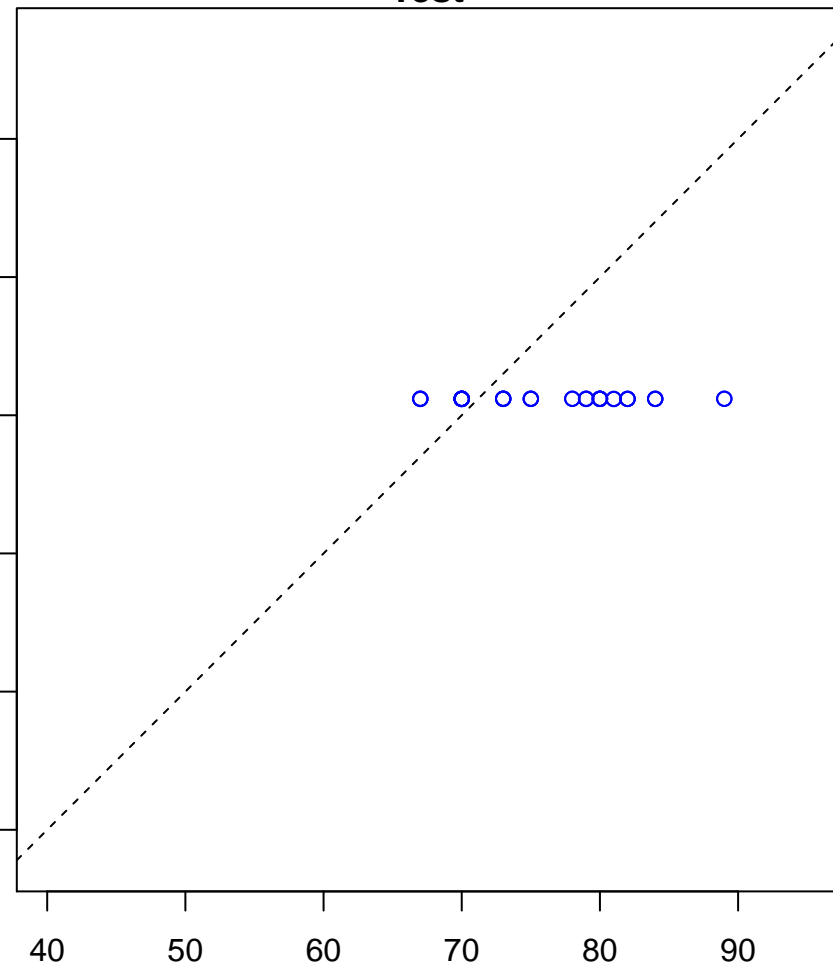


post-translational protein modification (Score: 0.837706)

Control

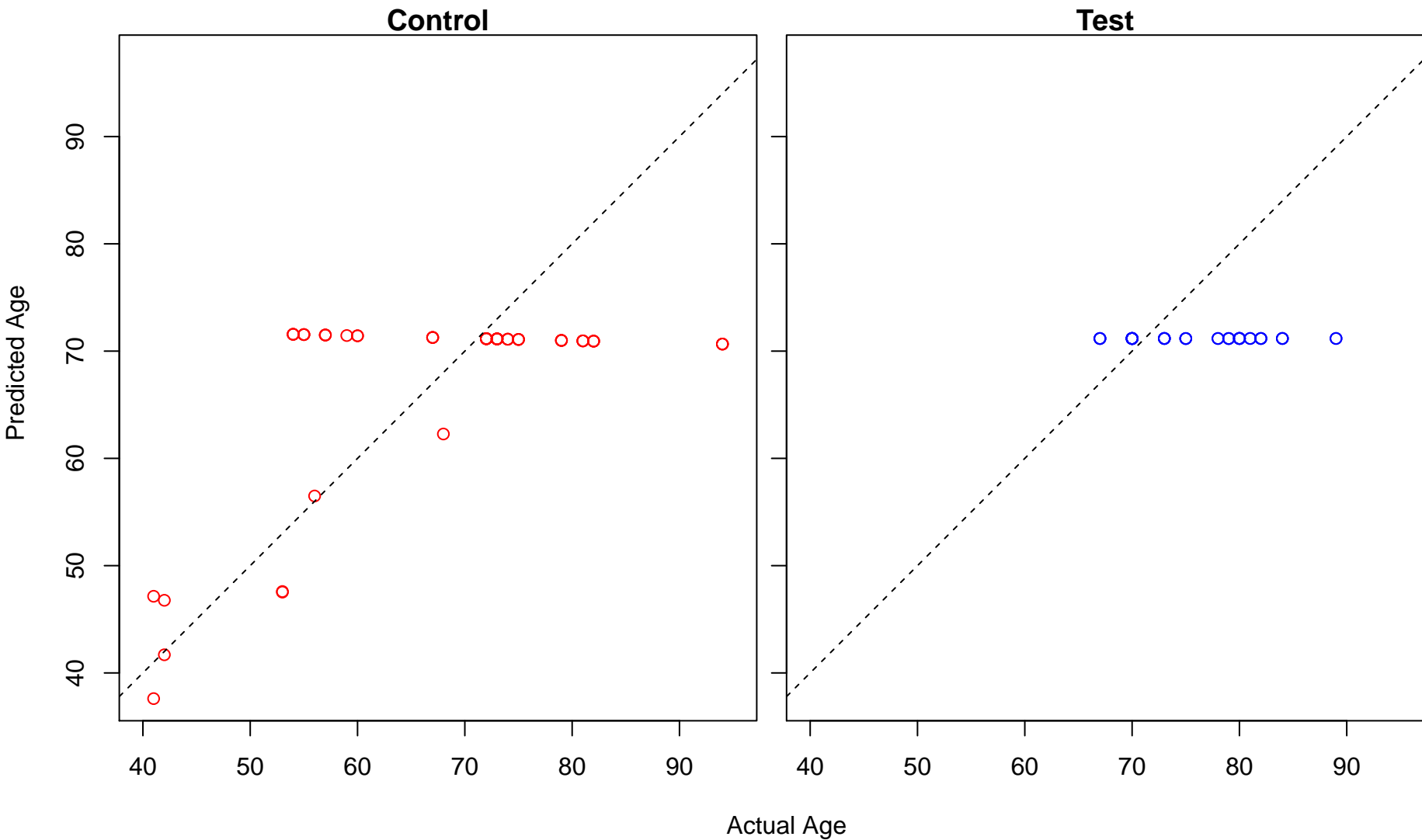


Test



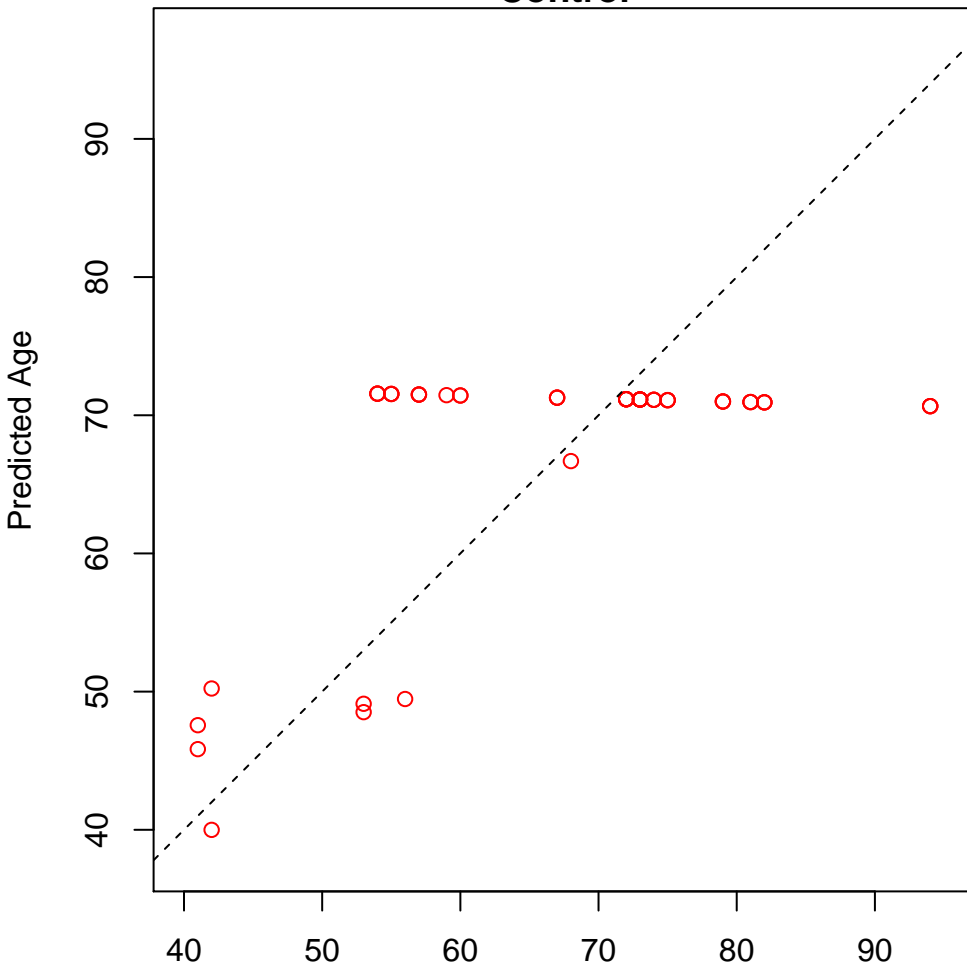
Actual Age

regulation of protein serine/threonine kinase activity (Score: 0.837670)

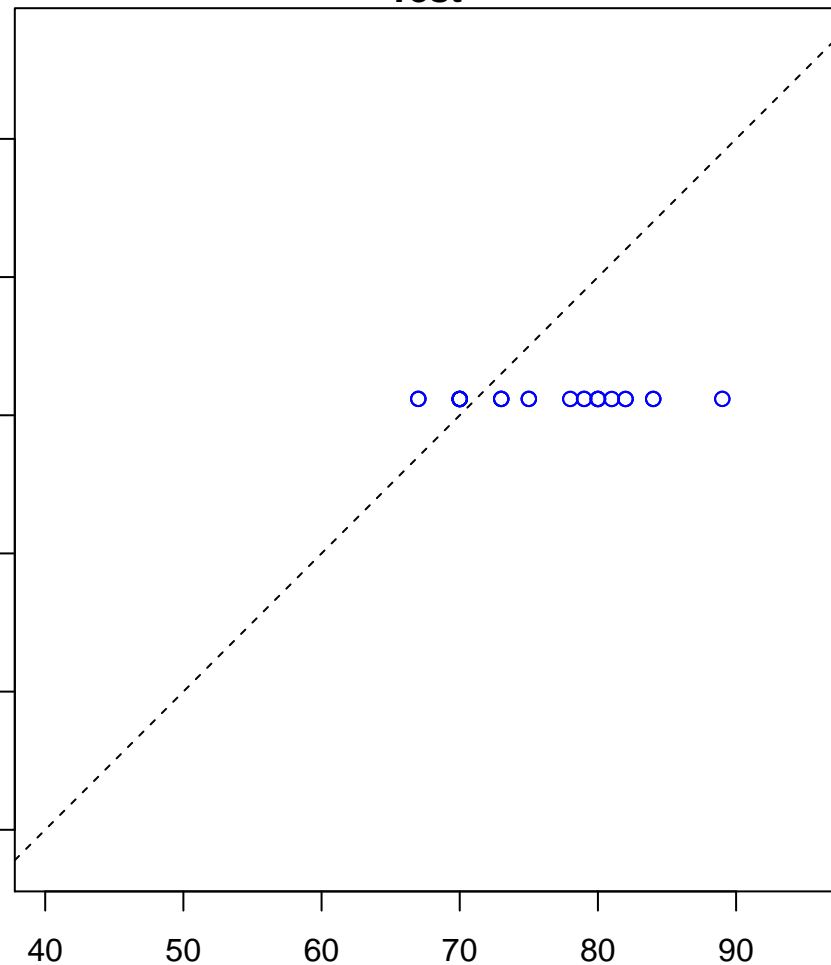


epithelium development (Score: 0.837584)

Control

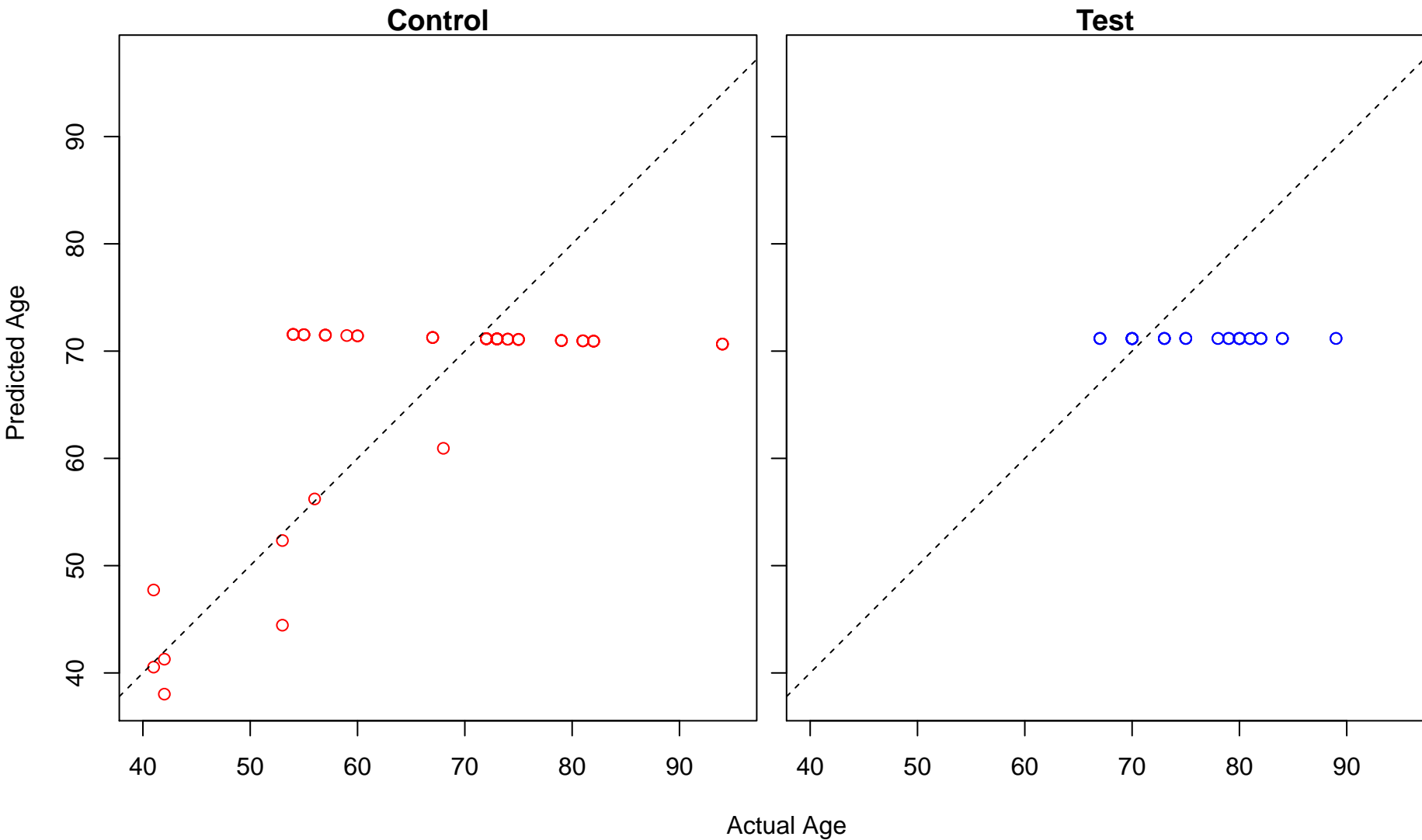


Test

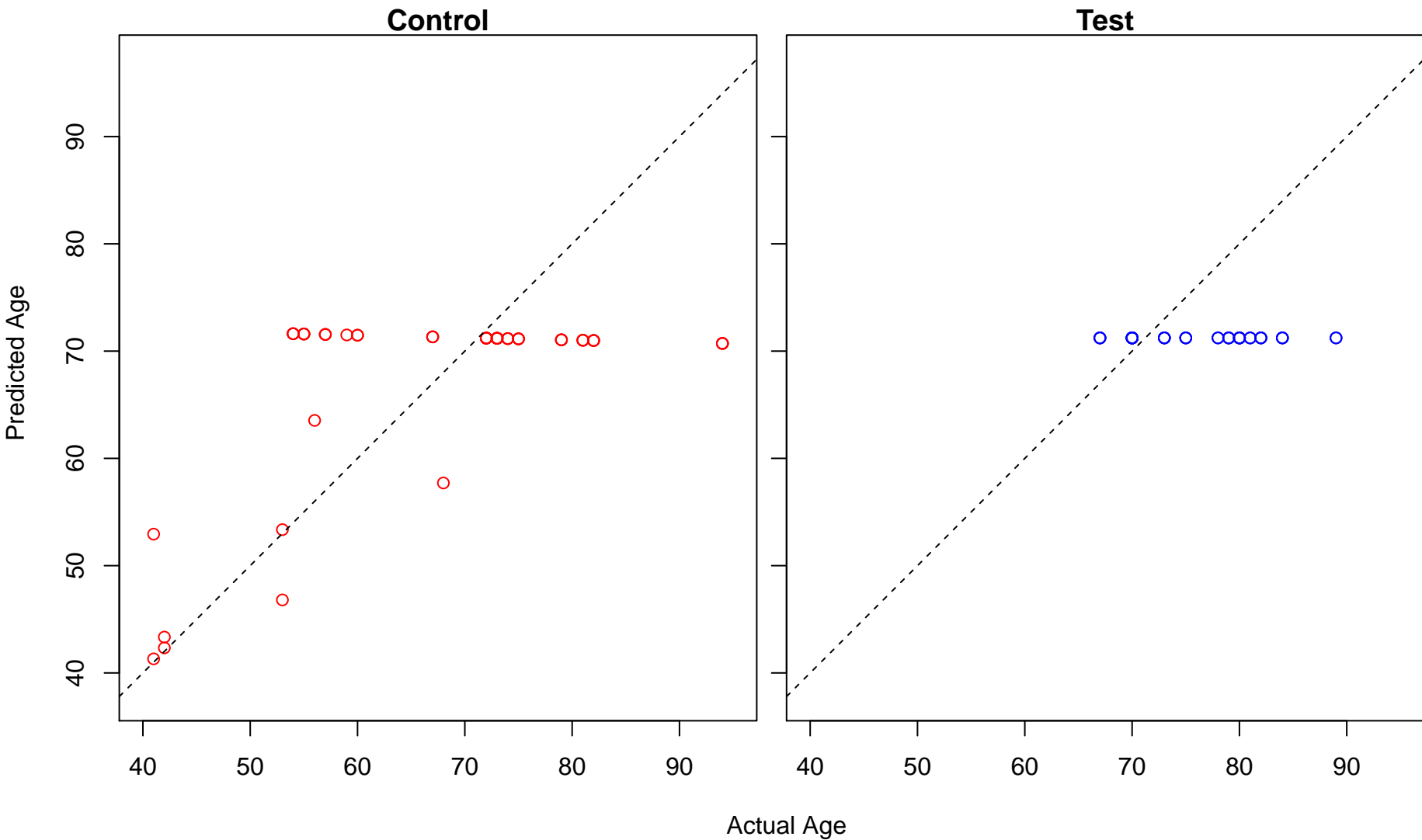


Actual Age

regulation of G2/M transition of mitotic cell cycle (Score: 0.837299)

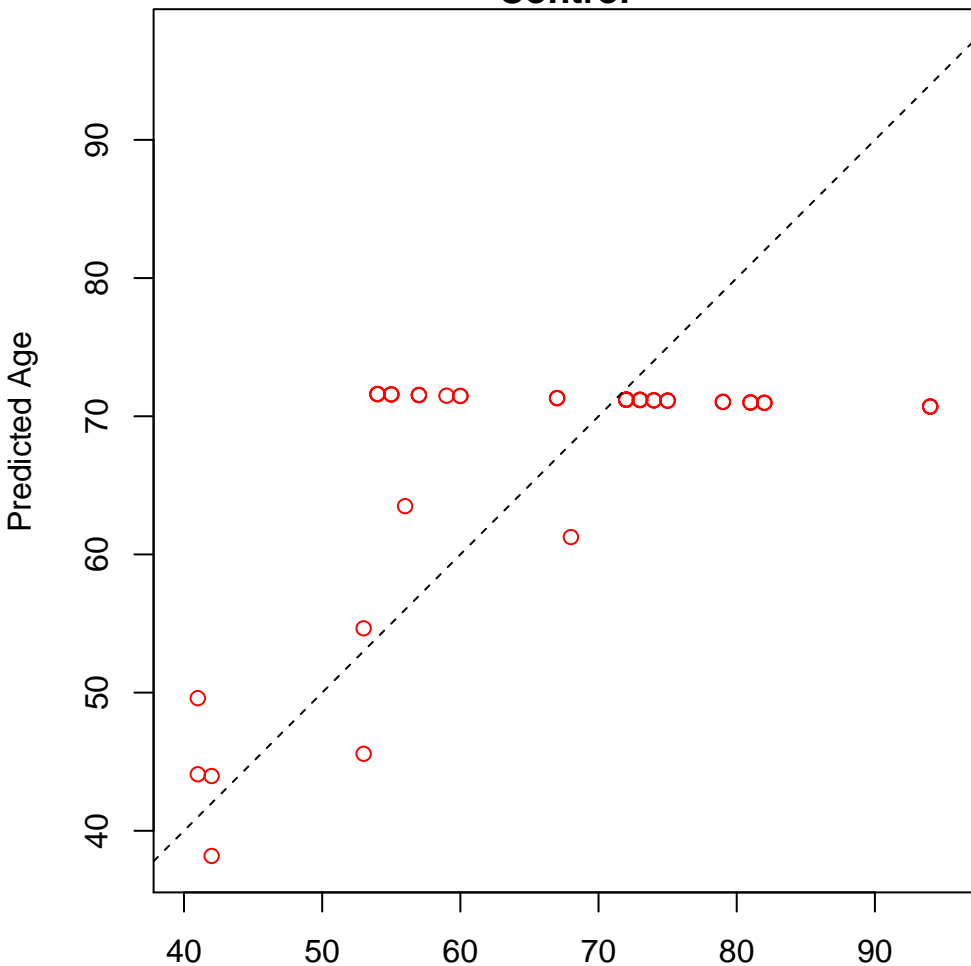


generation of precursor metabolites and energy (Score: 0.837143)

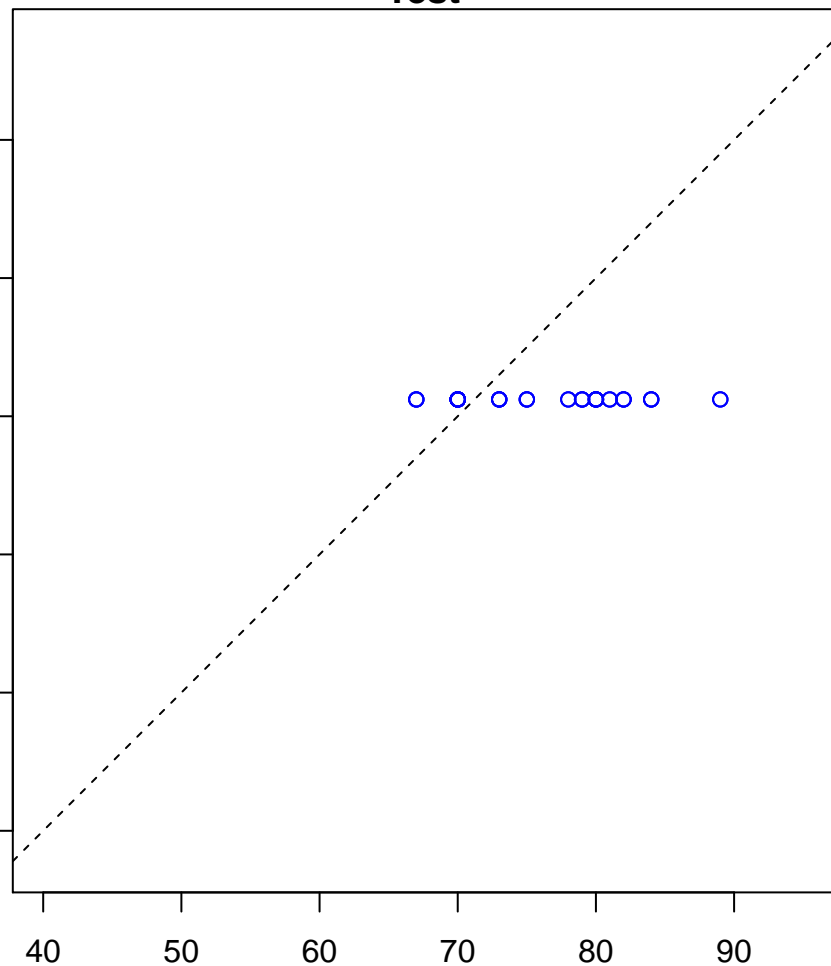


cellular carbohydrate metabolic process (Score: 0.836630)

Control

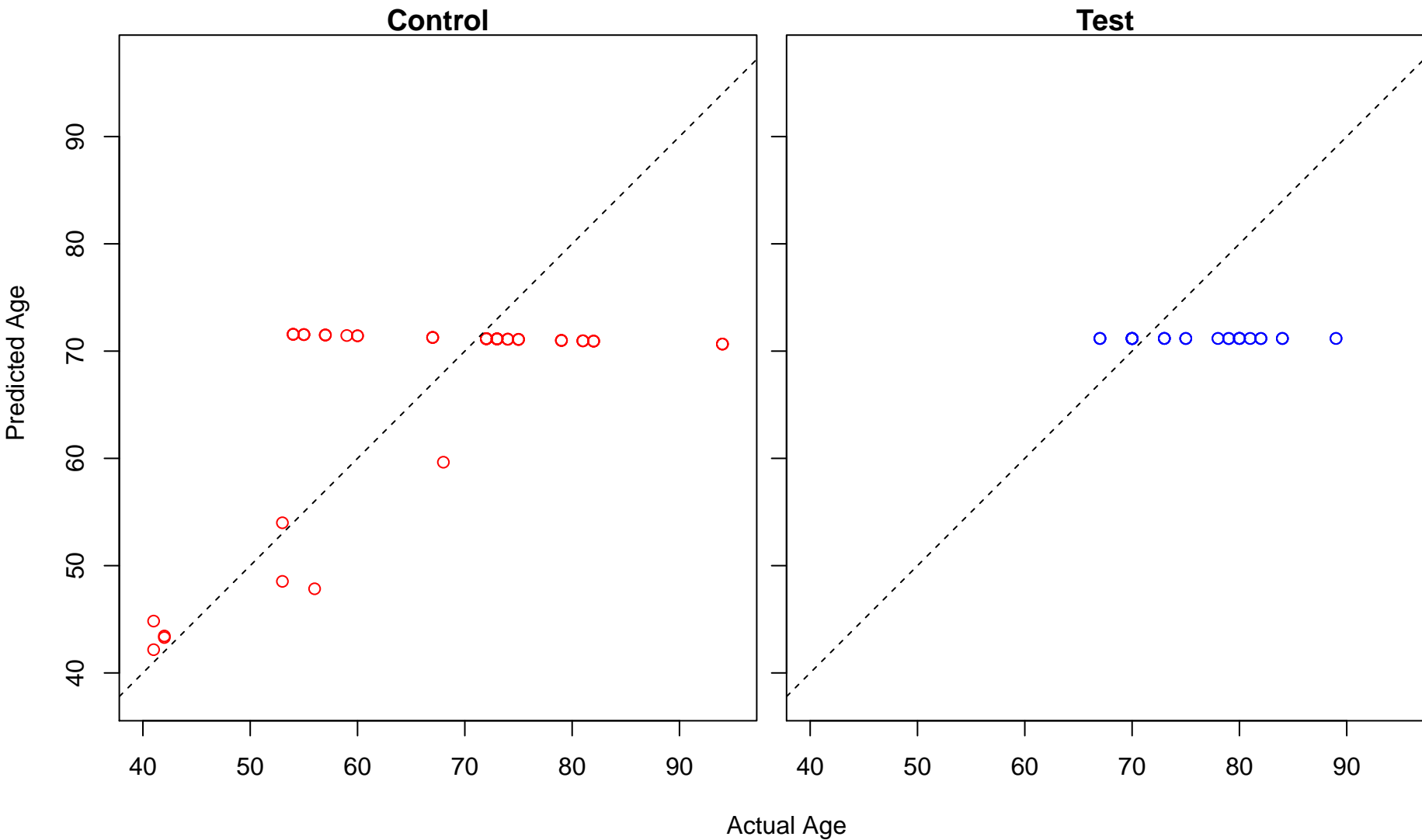


Test

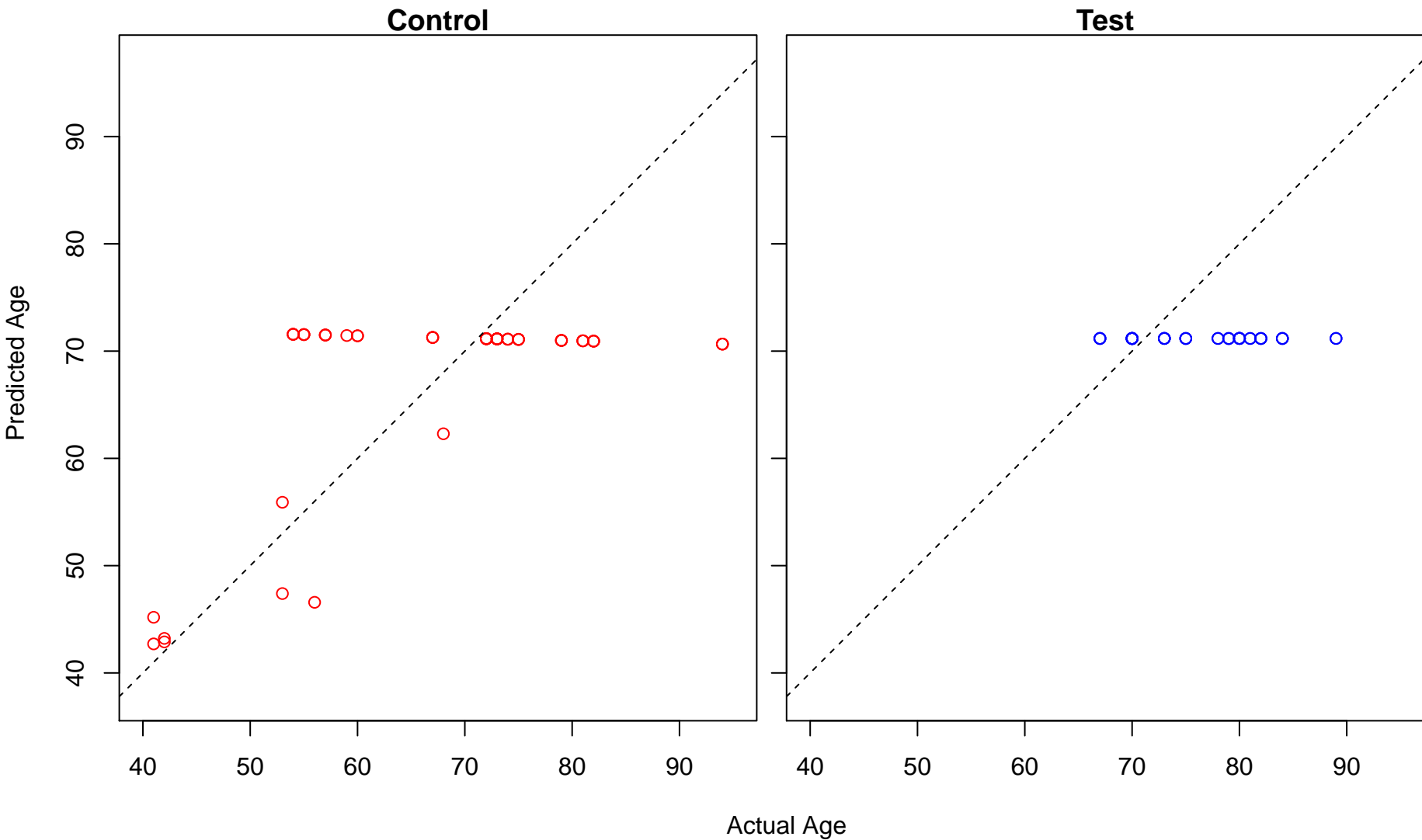


Actual Age

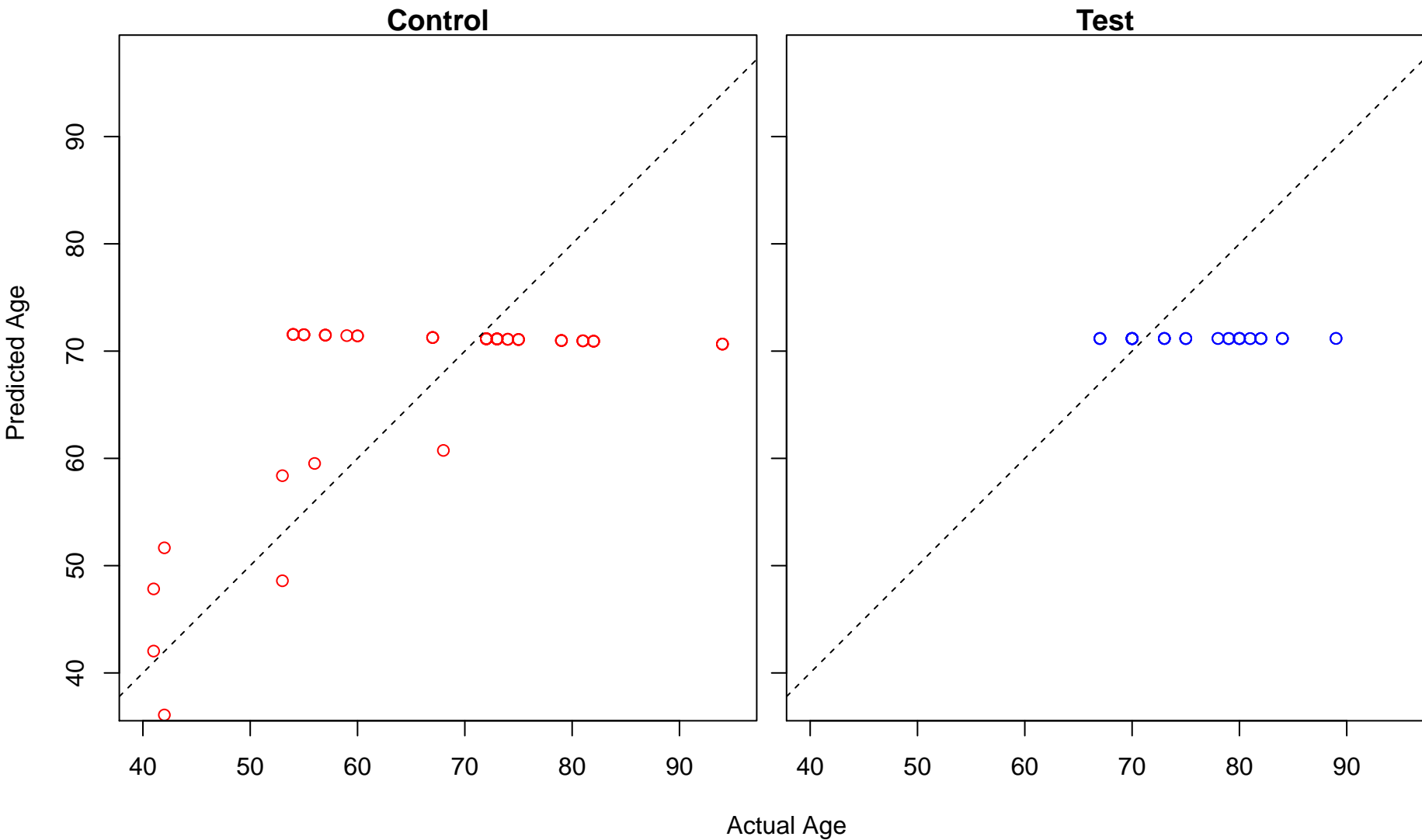
negative regulation of response to stimulus (Score: 0.836446)



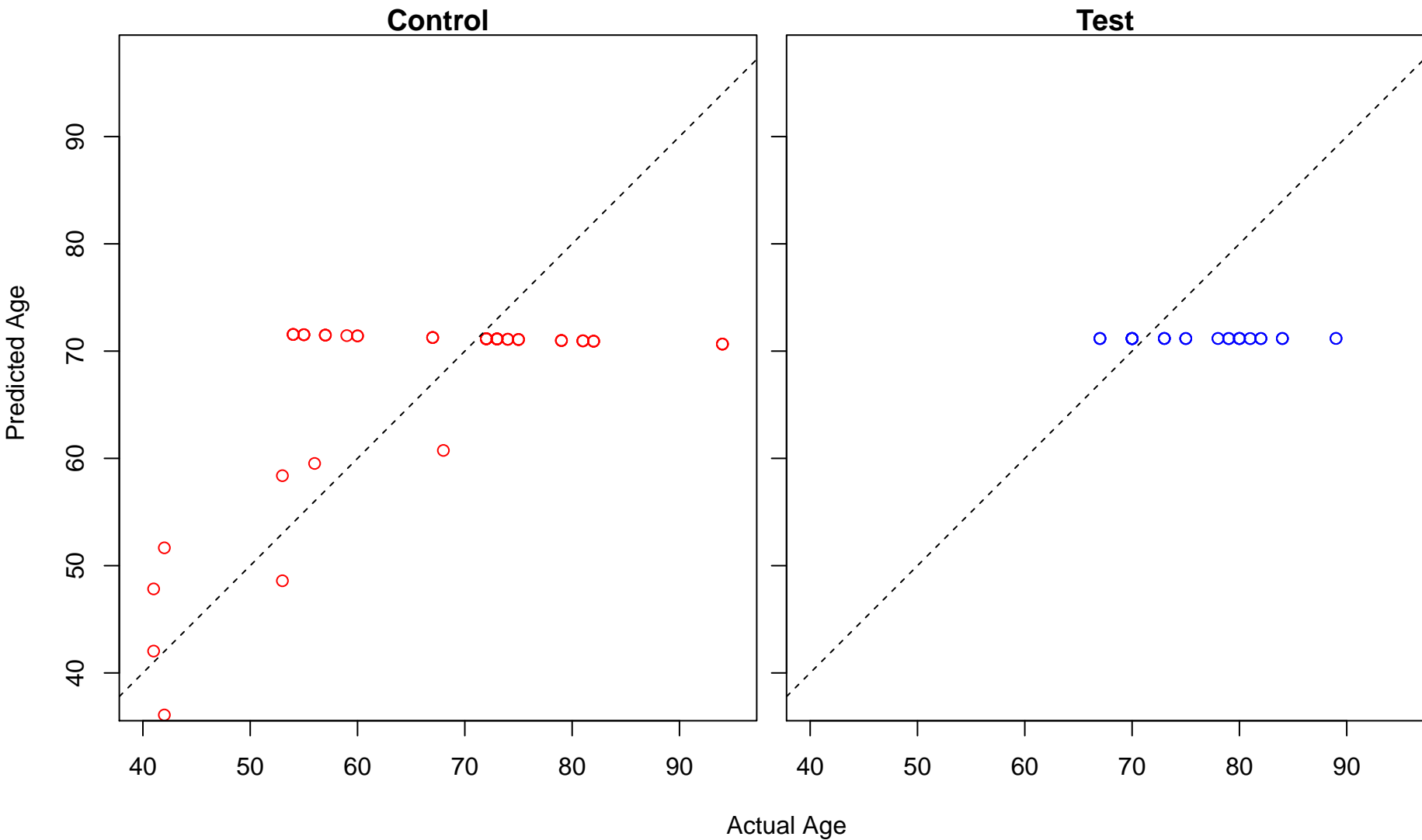
negative regulation of signal transduction (Score: 0.836258)



regulation of cellular amino acid metabolic process (Score: 0.836088)

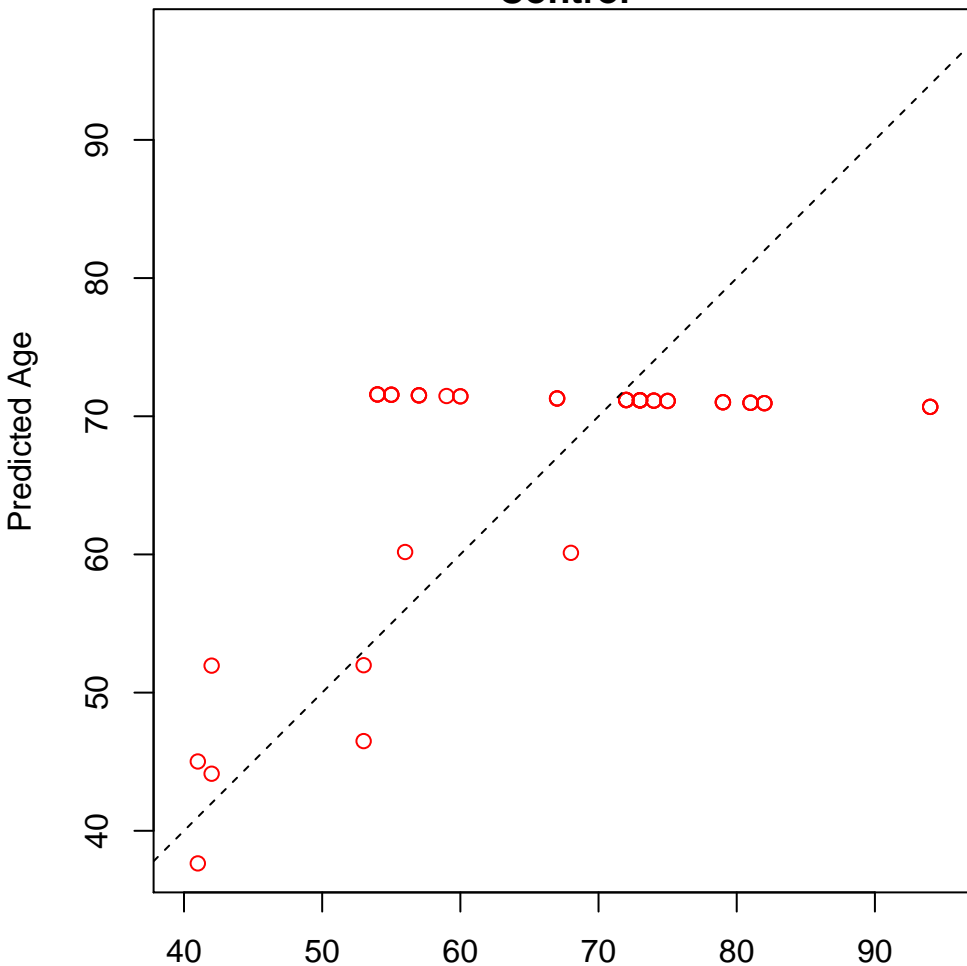


regulation of cellular amine metabolic process (Score: 0.836088)

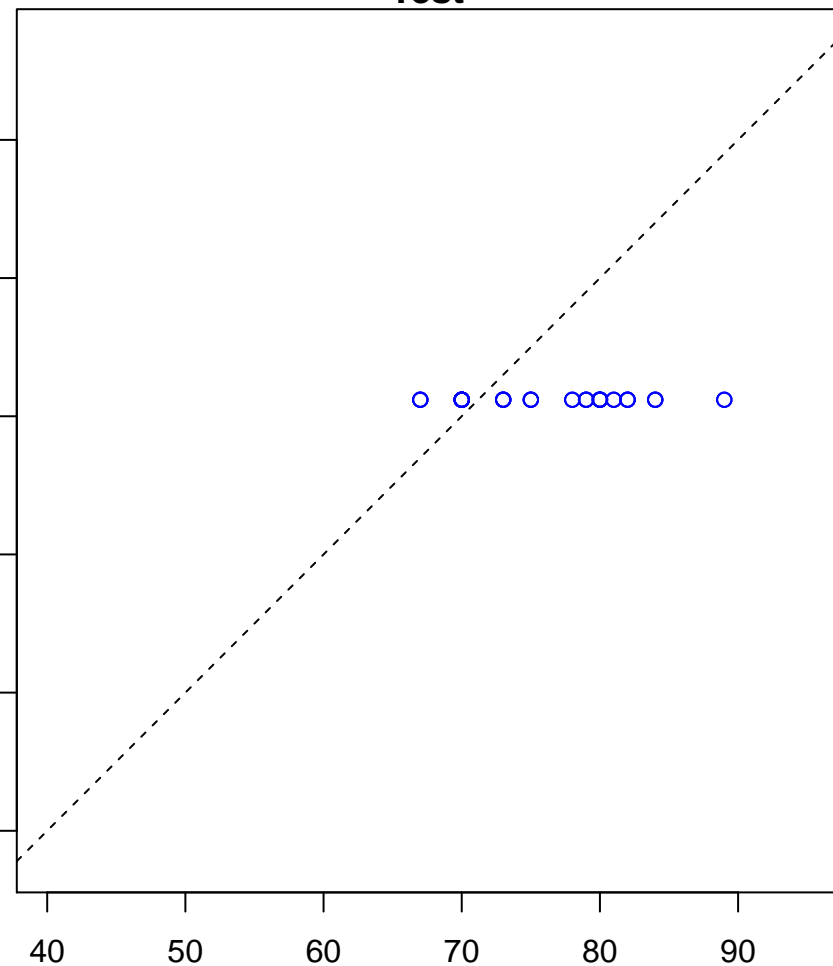


purine ribonucleotide metabolic process (Score: 0.836044)

Control



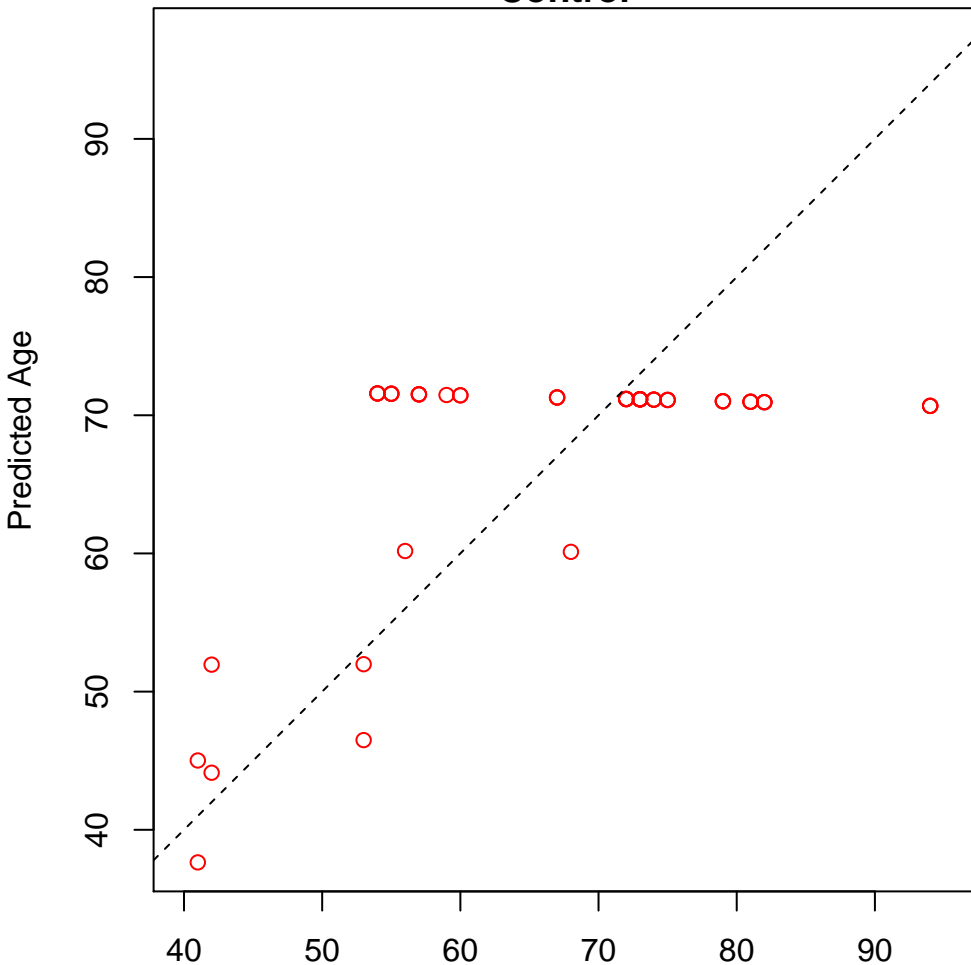
Test



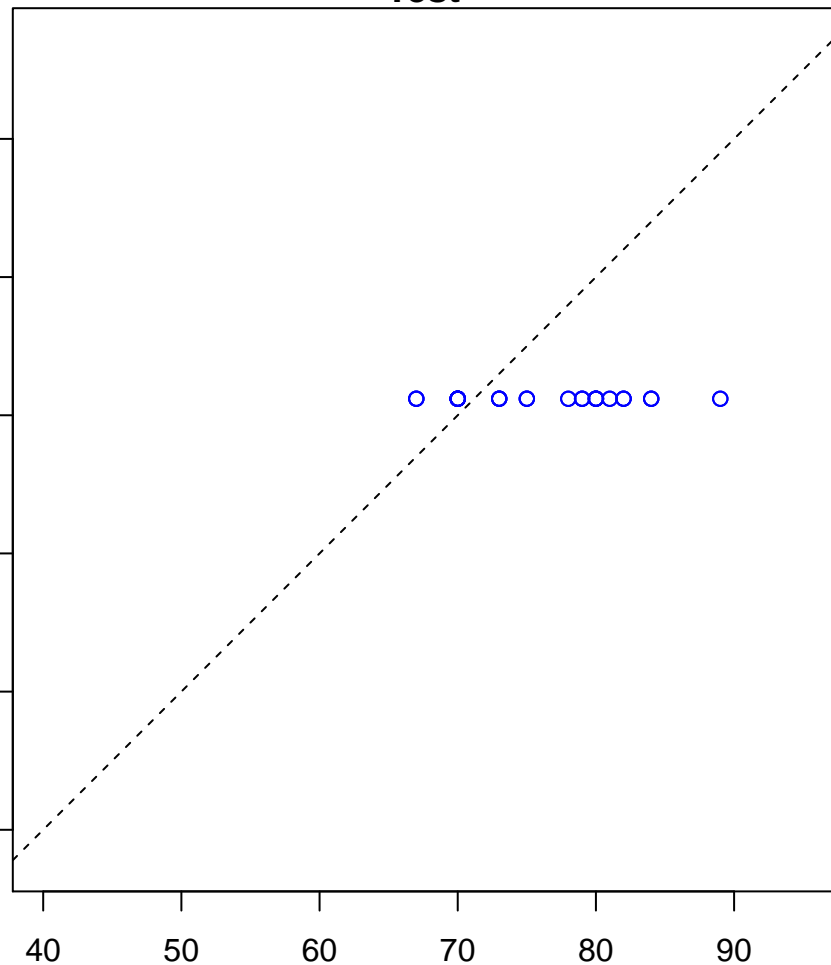
Actual Age

ribonucleotide metabolic process (Score: 0.836044)

Control



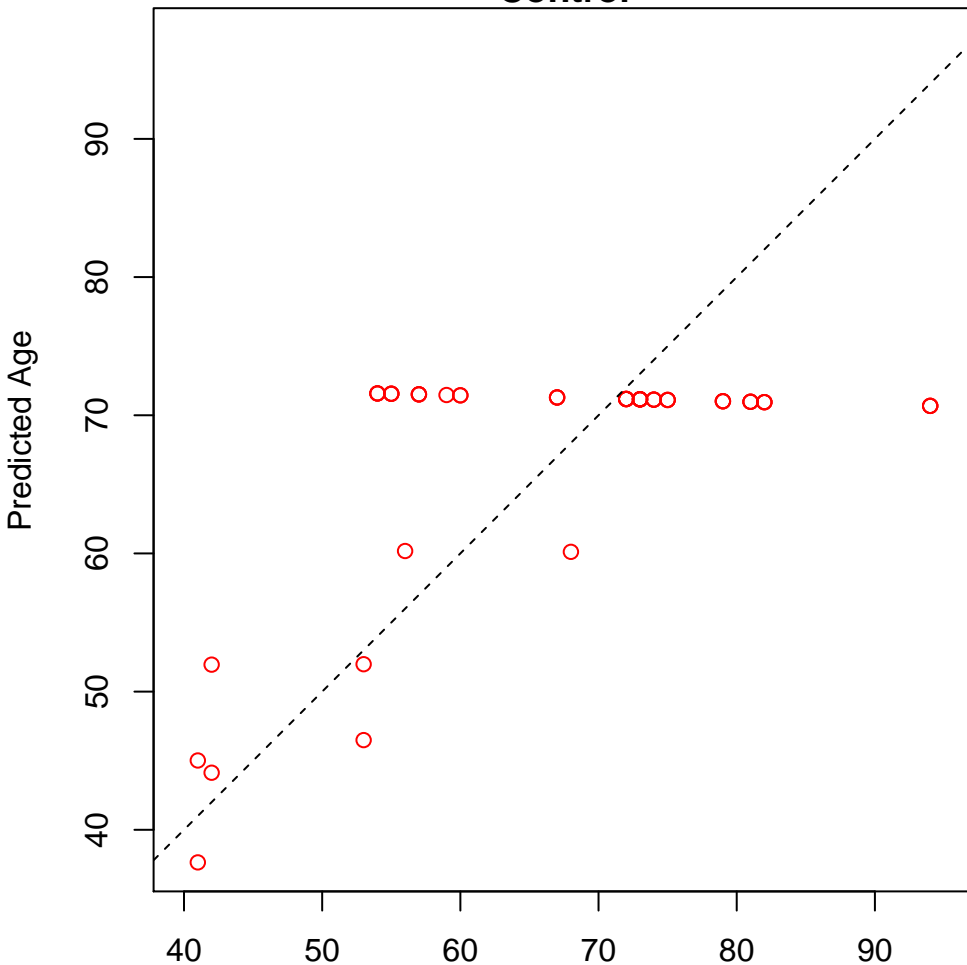
Test



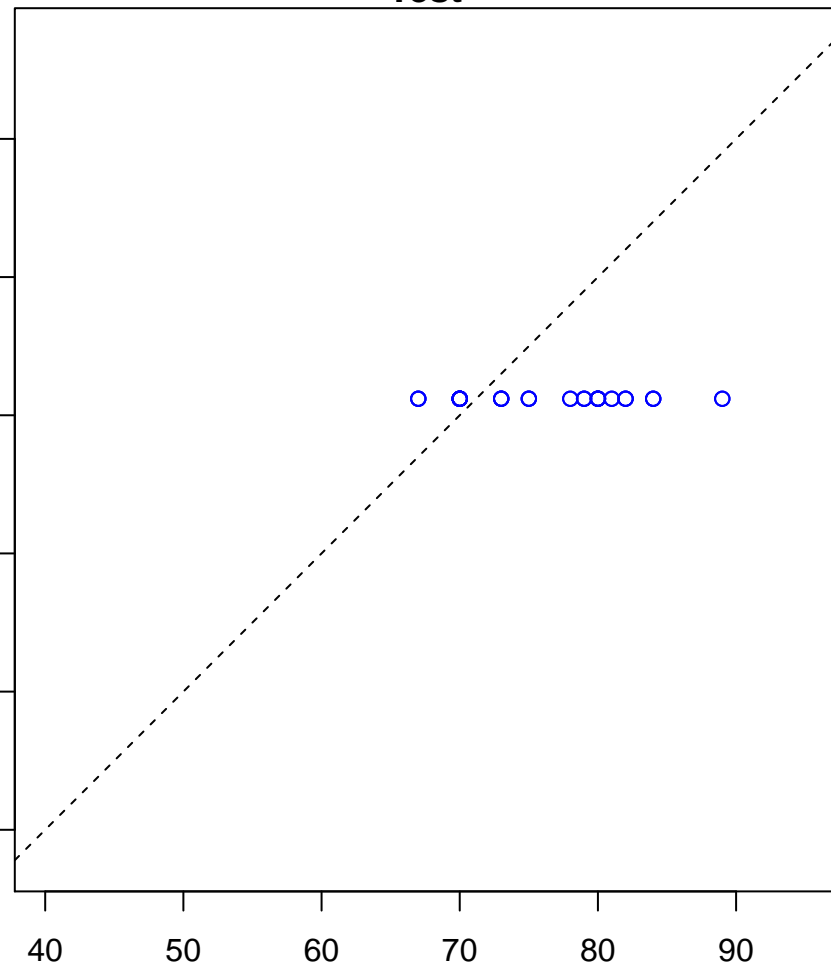
Actual Age

ribose phosphate metabolic process (Score: 0.836044)

Control

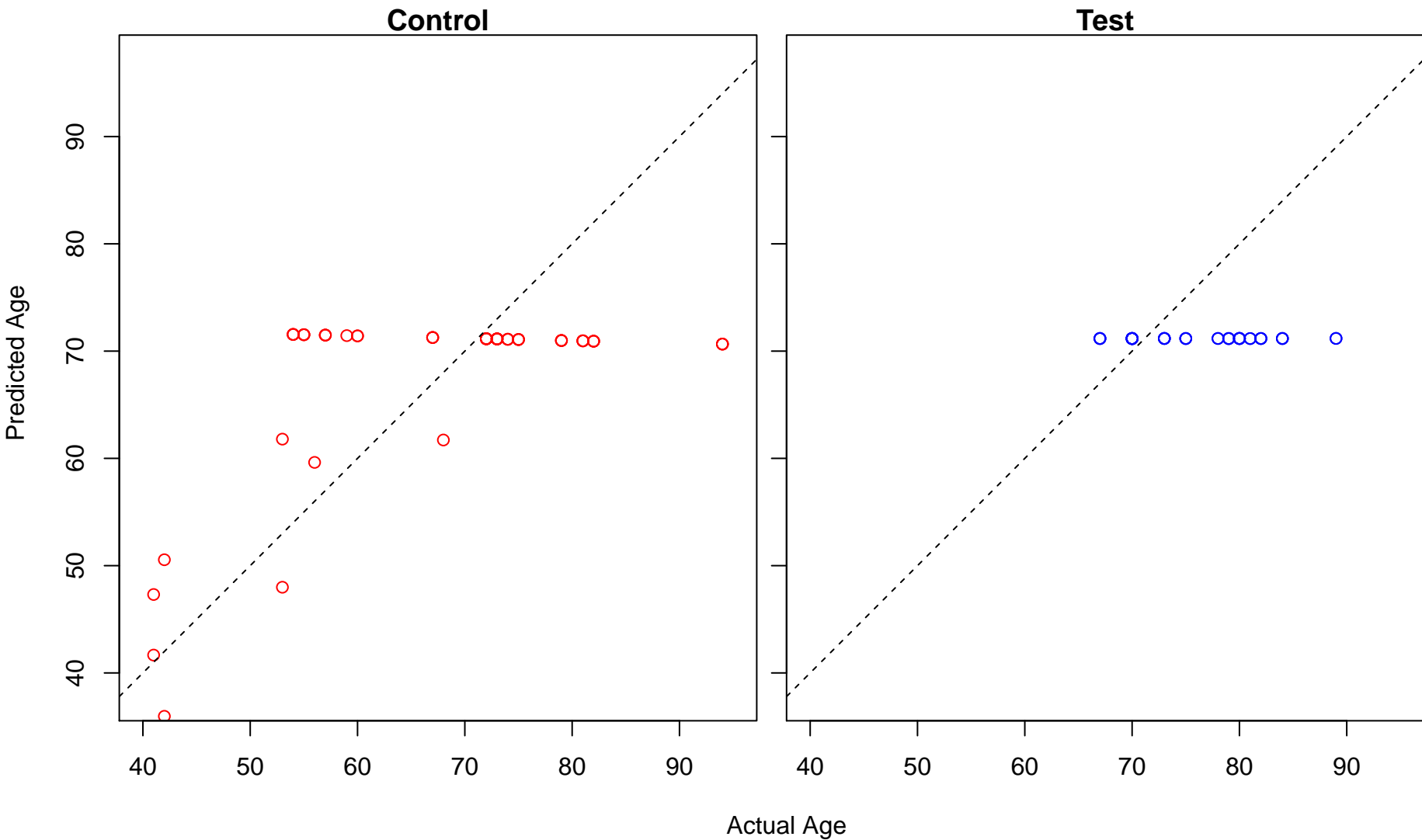


Test

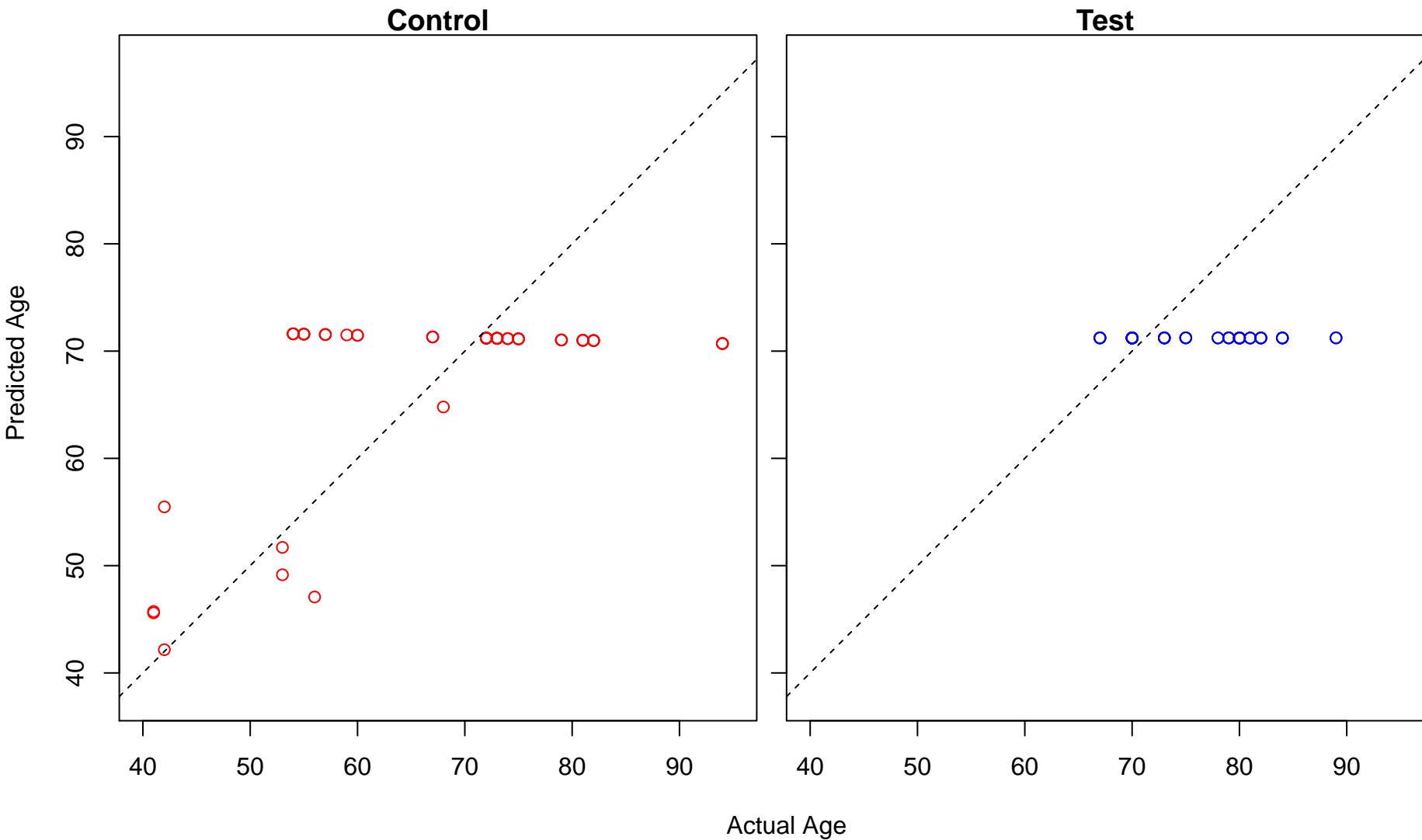


Actual Age

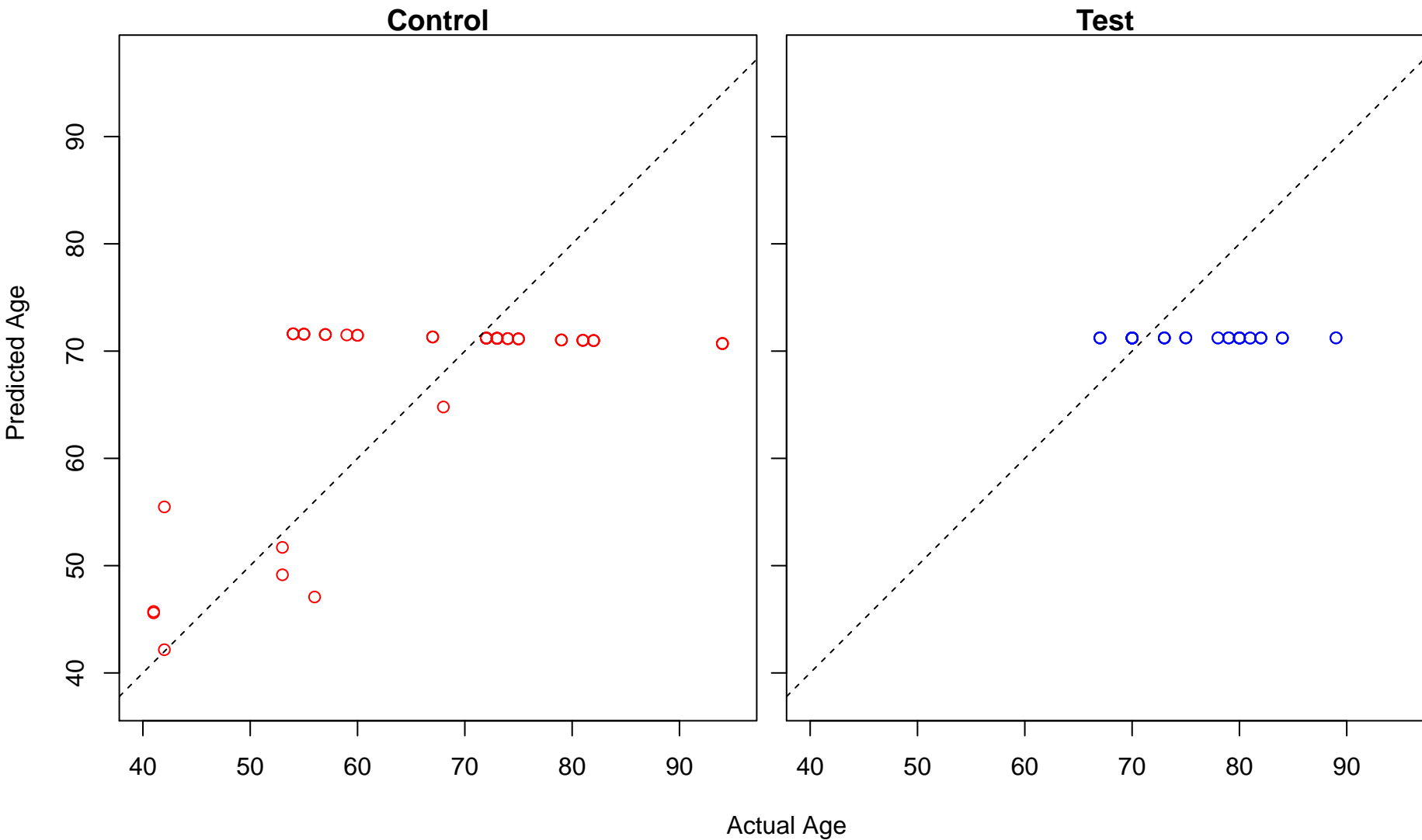
regulation of cellular ketone metabolic process (Score: 0.835937)



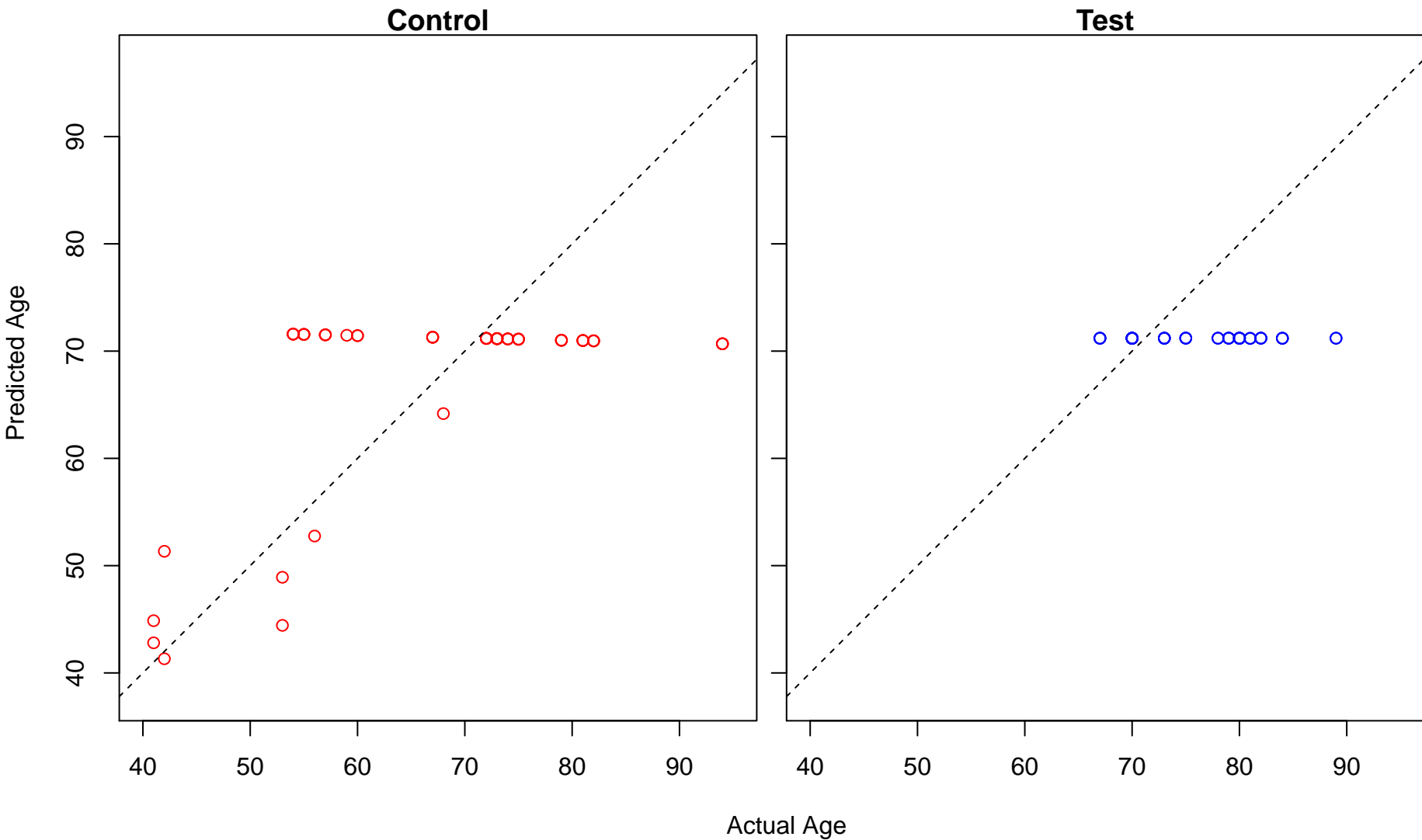
ciliary basal body-plasma membrane docking (Score: 0.835789)



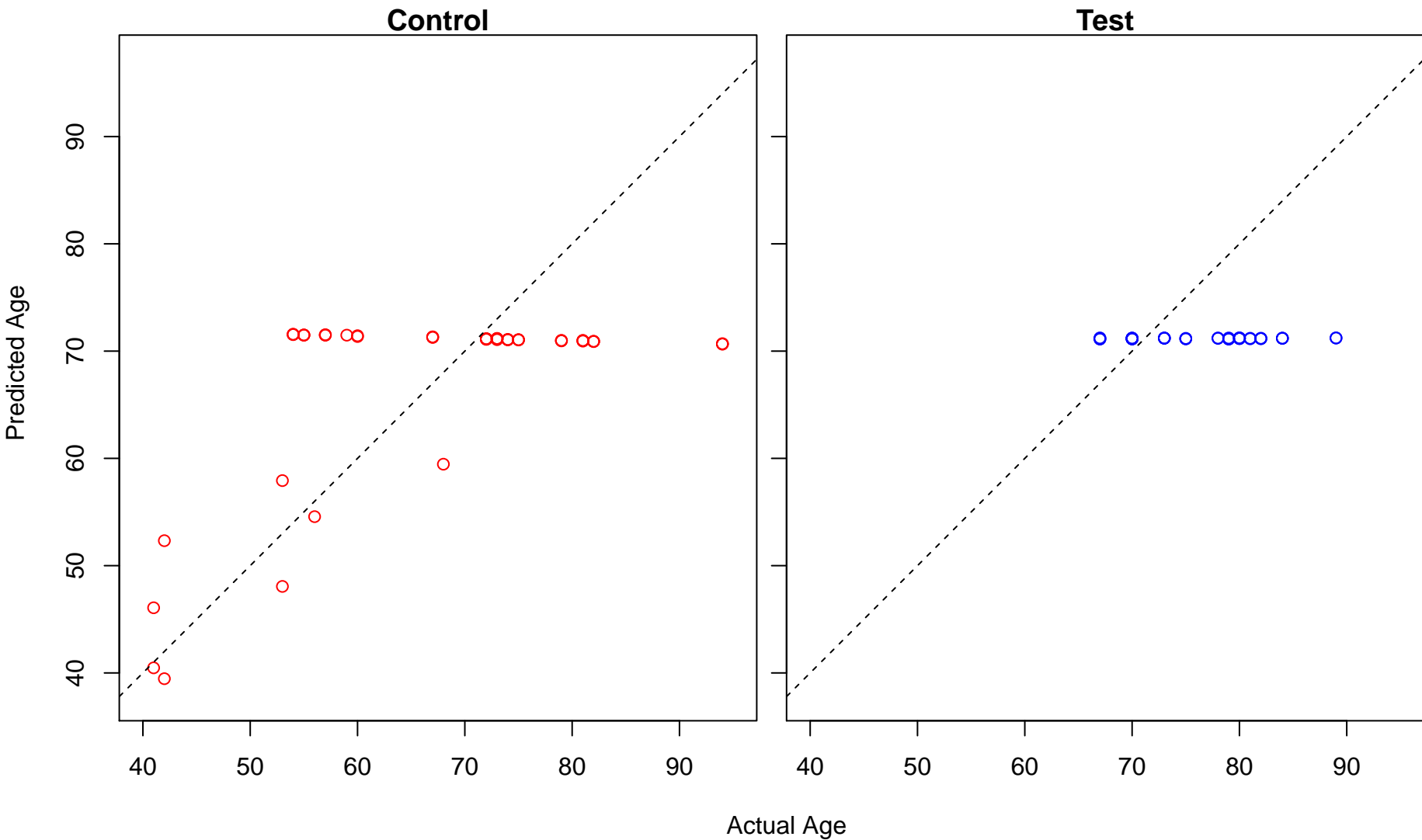
organelle localization by membrane tethering (Score: 0.835789)



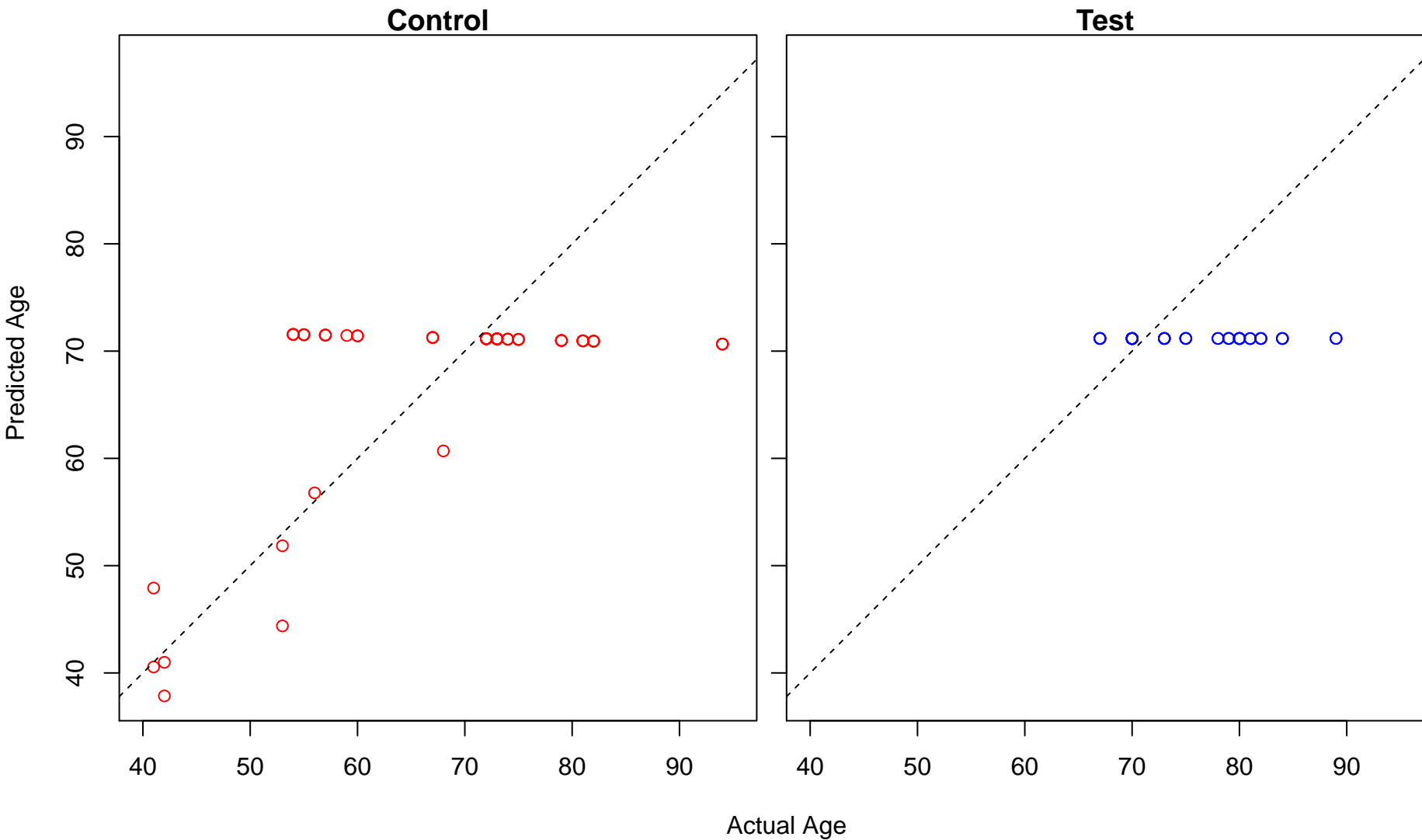
Golgi vesicle transport (Score: 0.835650)



positive regulation of DNA metabolic process (Score: 0.835558)

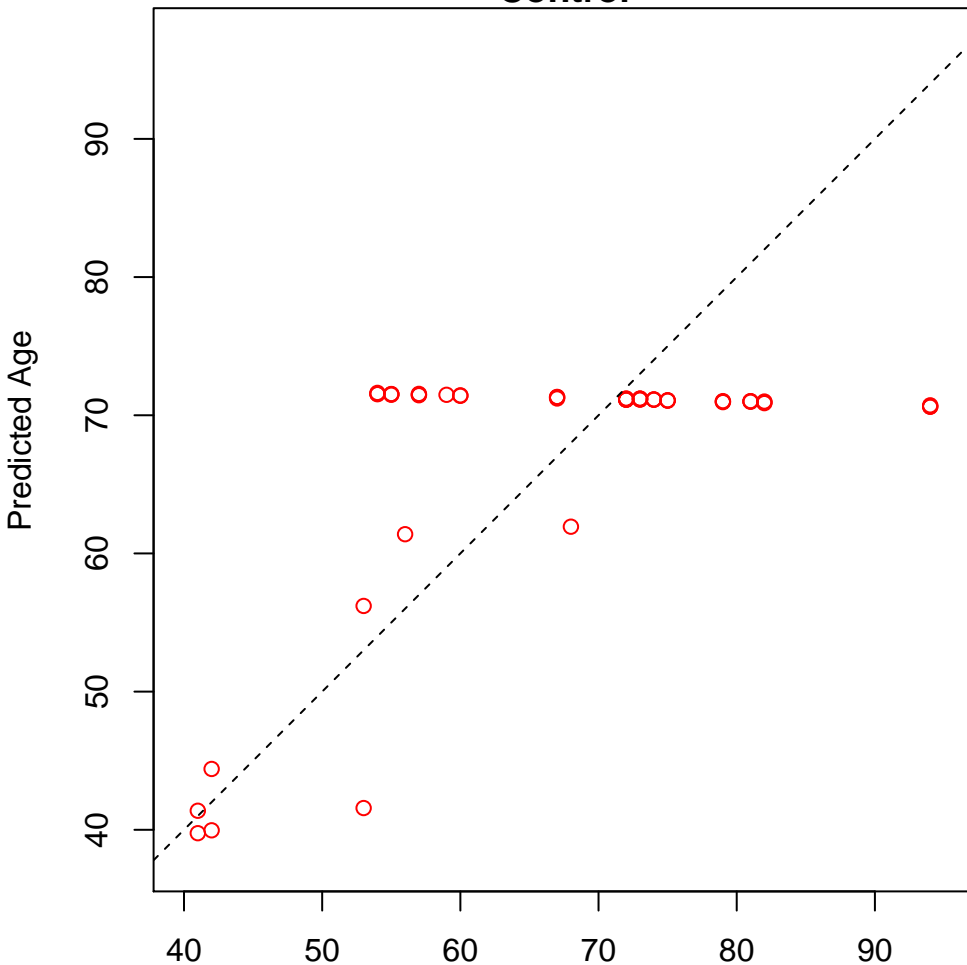


regulation of cell cycle G2/M phase transition (Score: 0.835415)

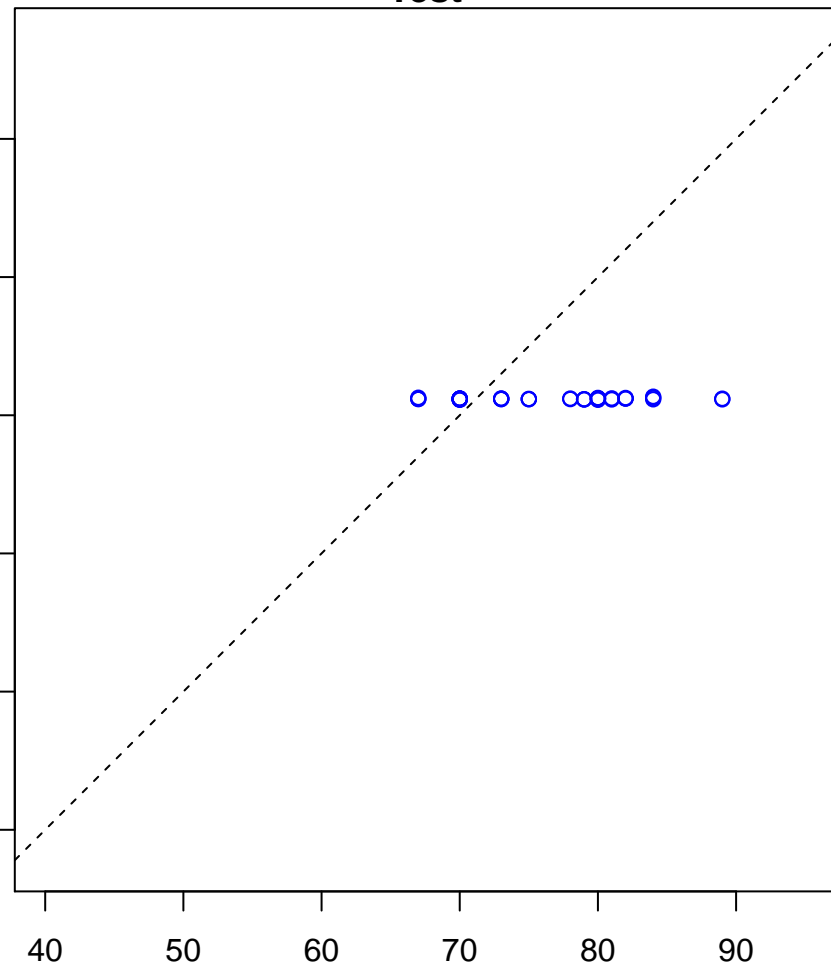


regulation of leukocyte chemotaxis (Score: 0.835386)

Control

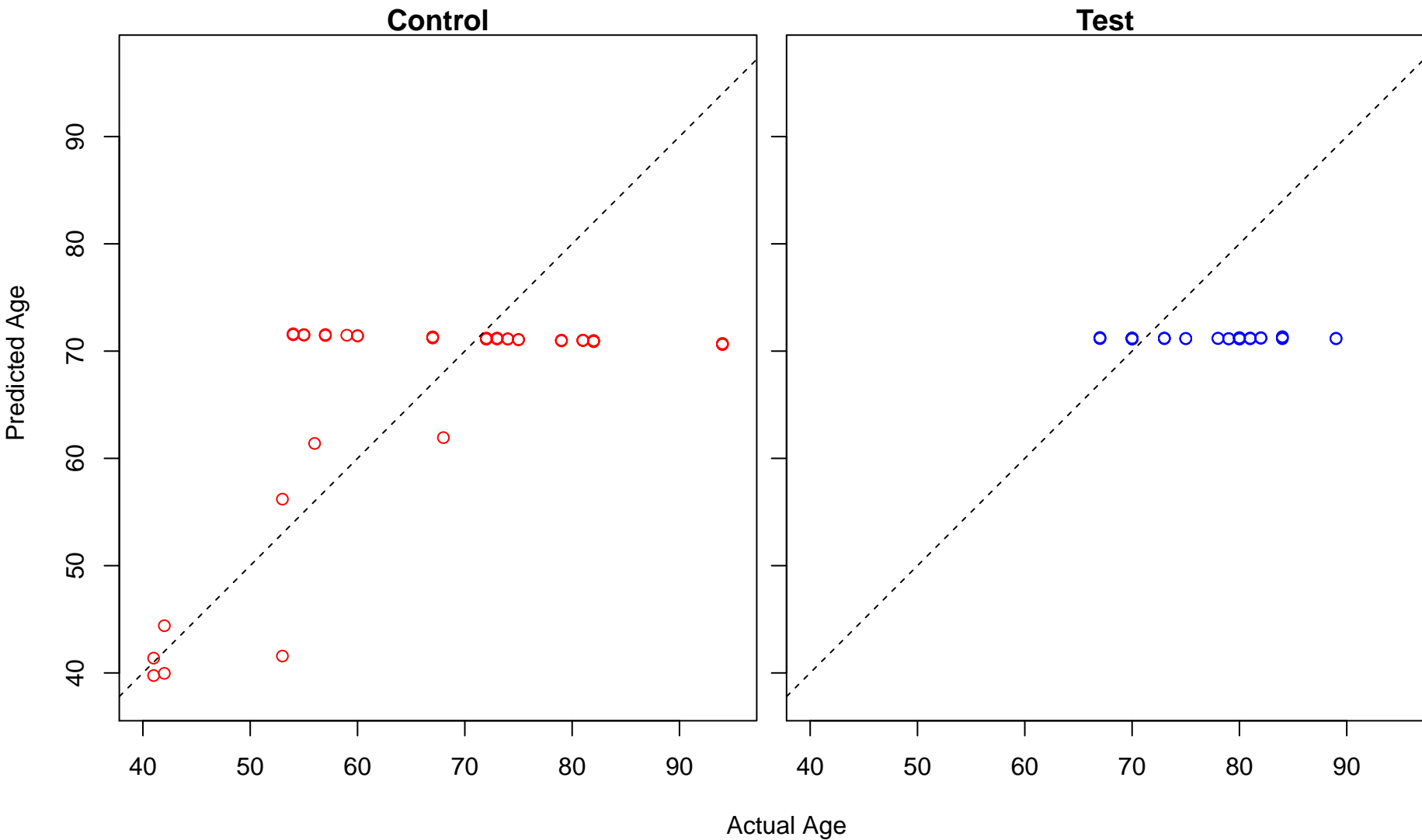


Test

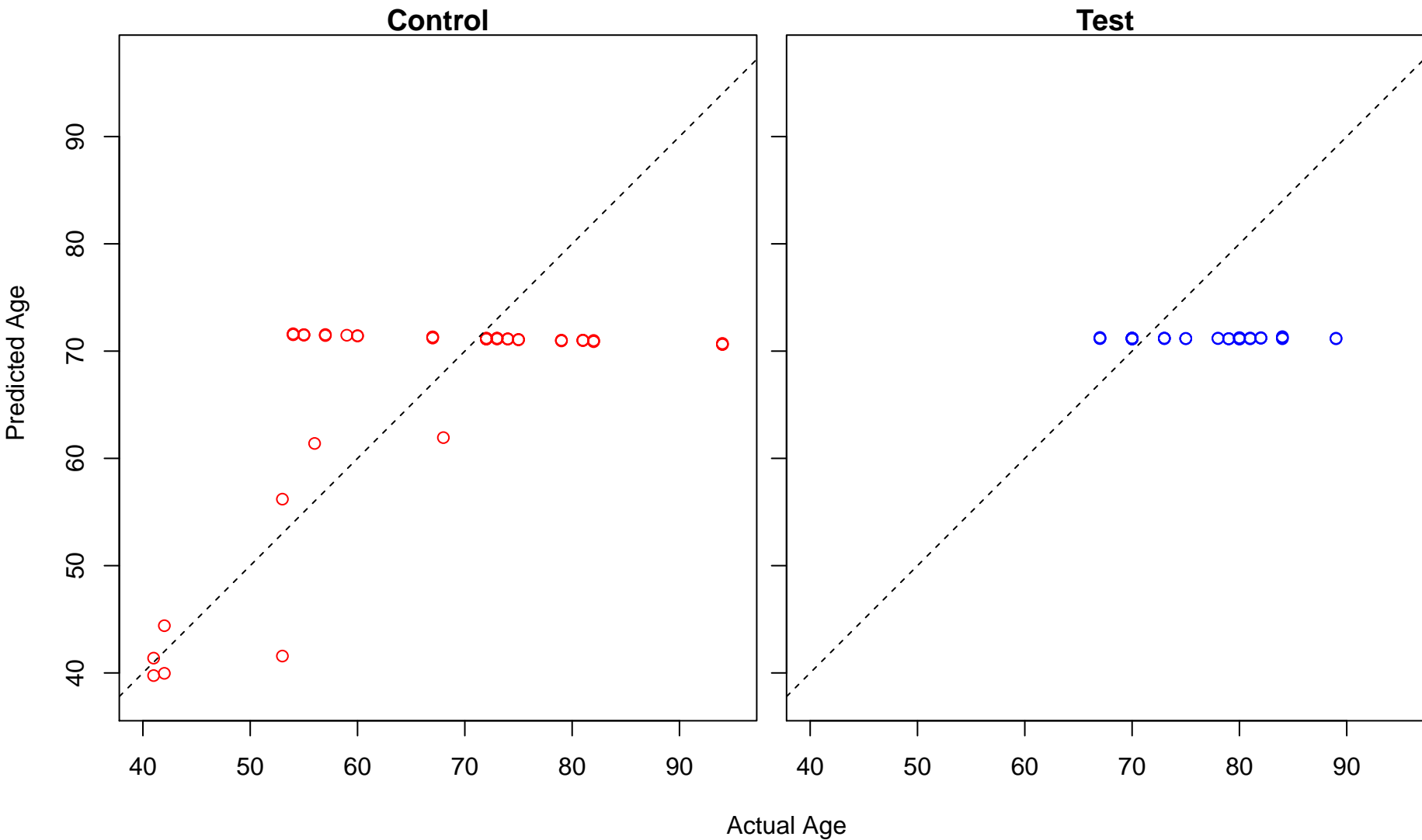


Actual Age

positive regulation of leukocyte chemotaxis (Score: 0.835386)

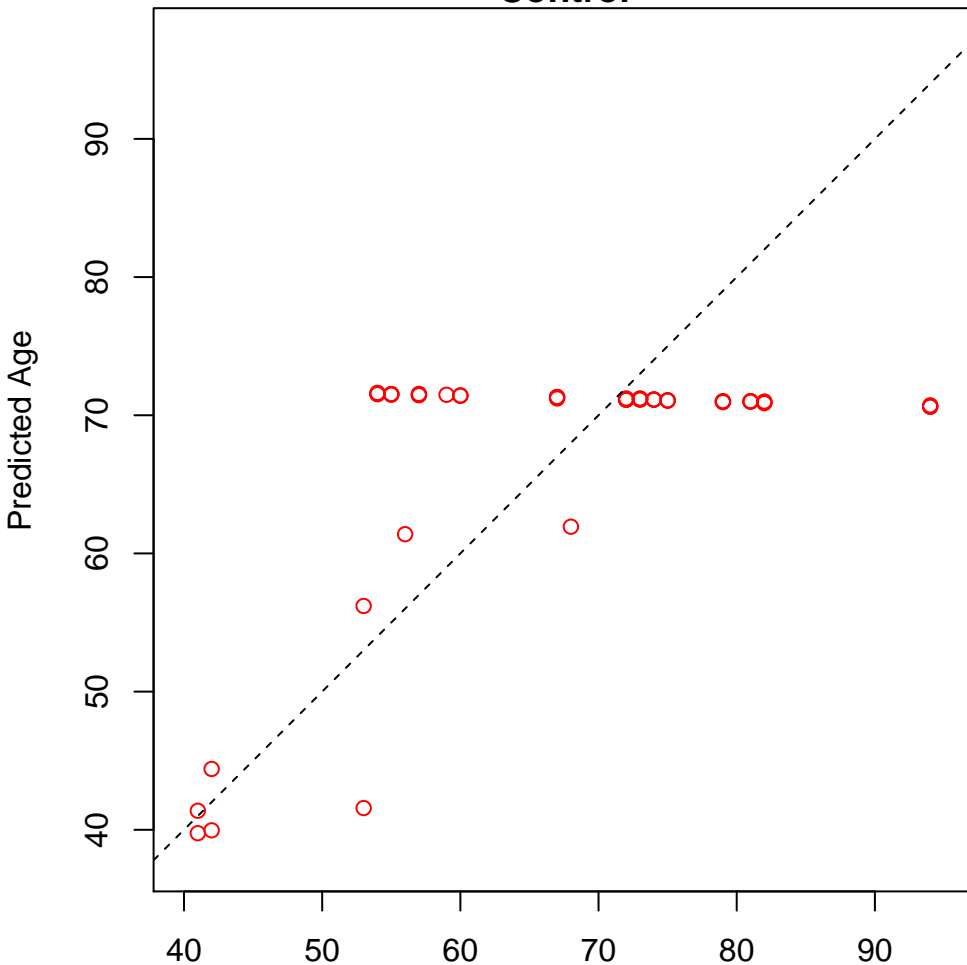


regulation of chemotaxis (Score: 0.835386)

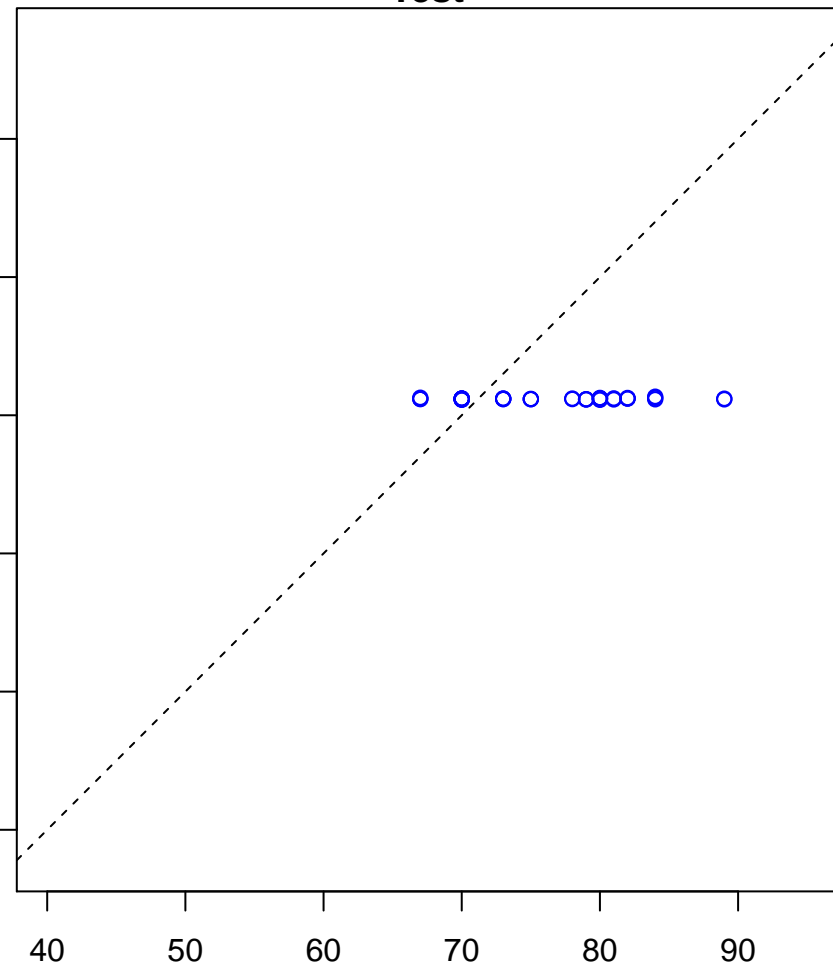


positive regulation of chemotaxis (Score: 0.835386)

Control

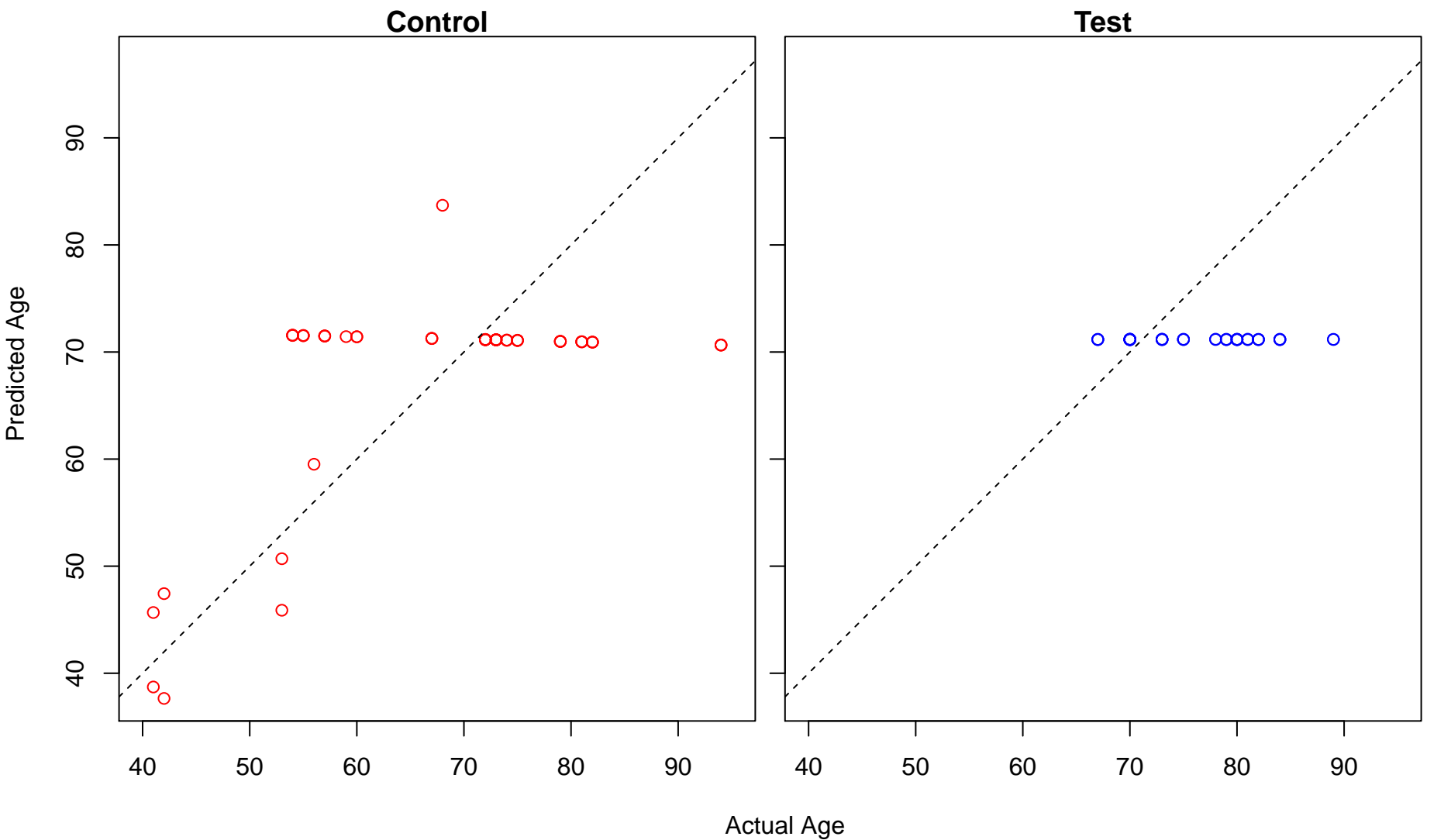


Test

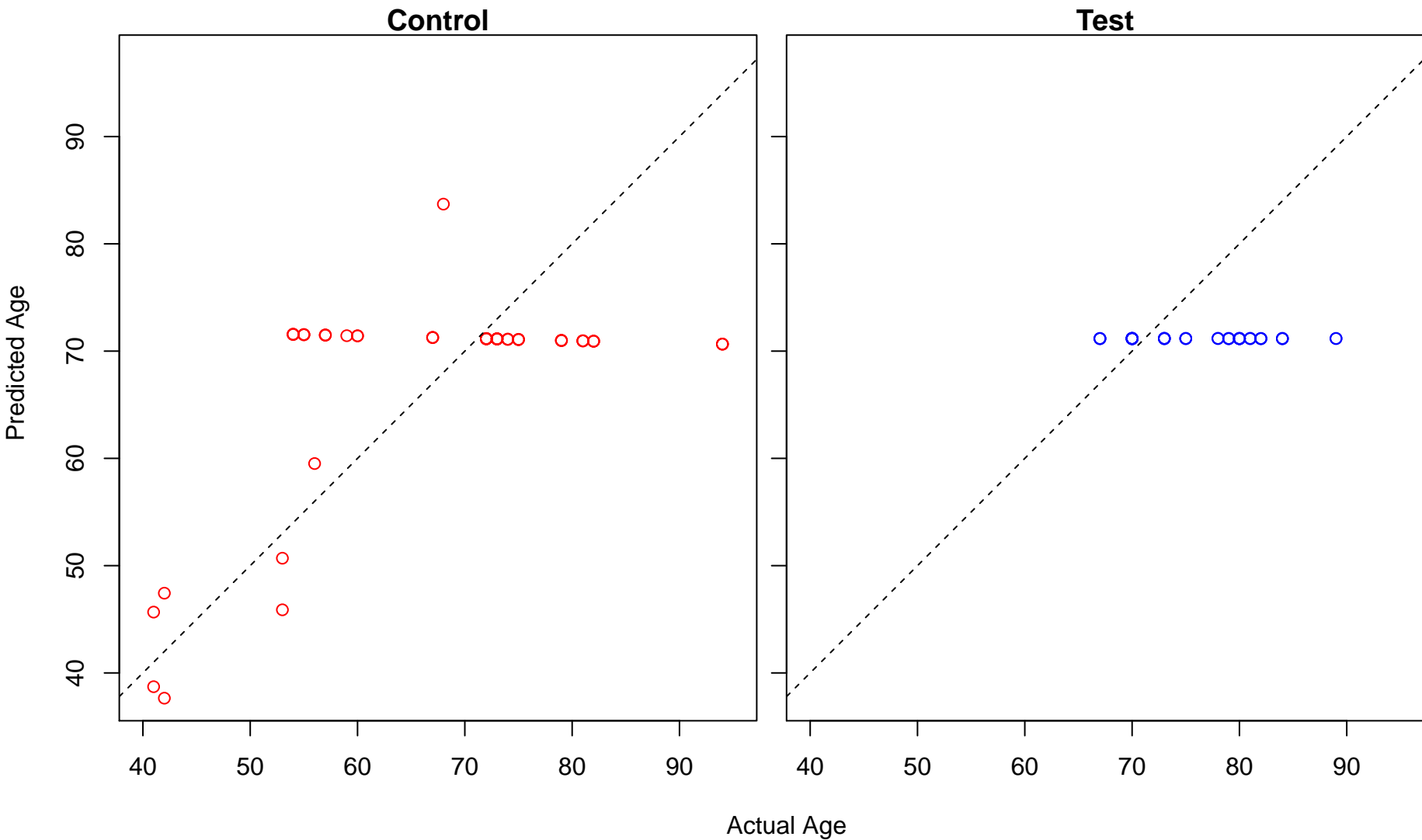


Actual Age

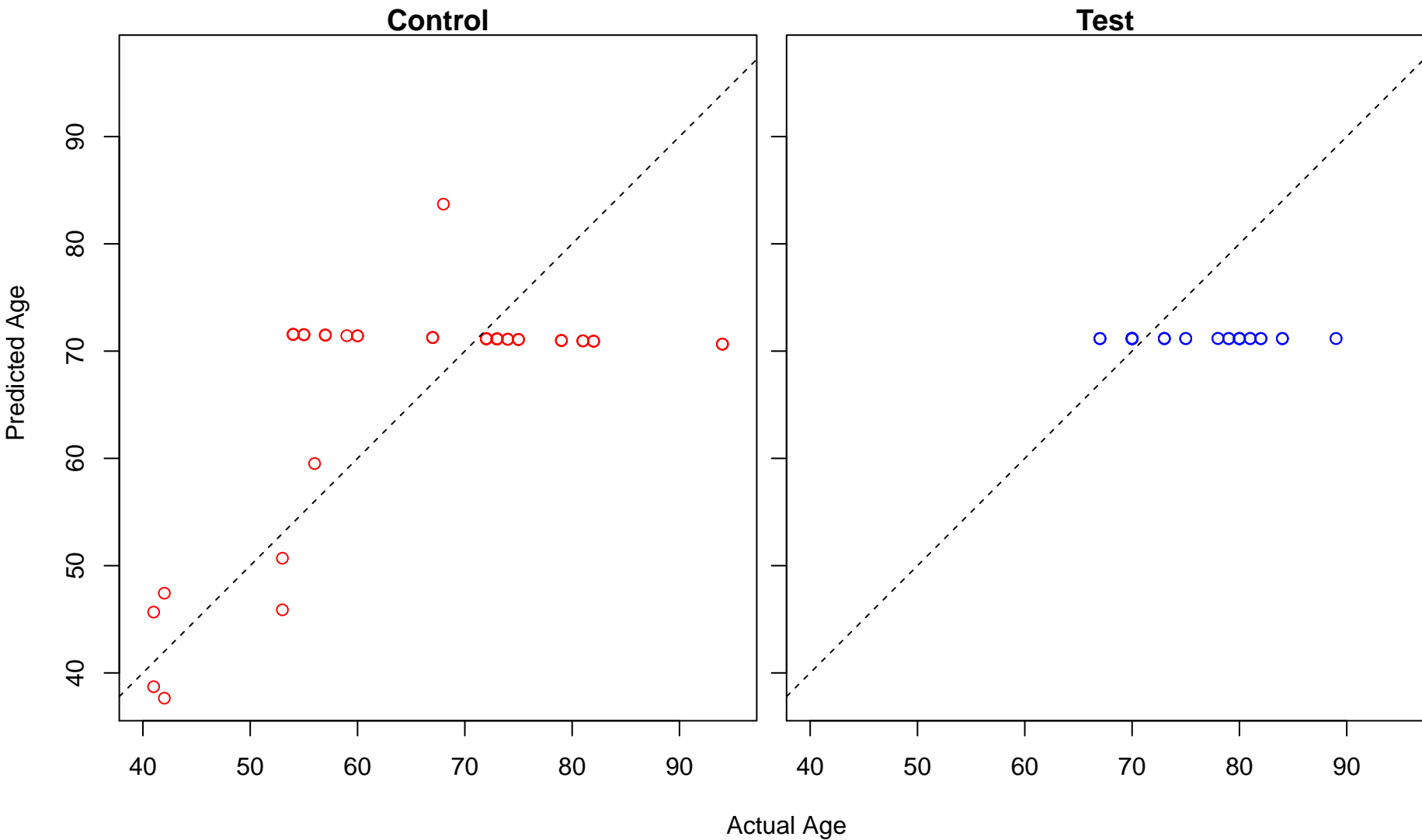
Positive regulation of ubiquitin–protein ligase activity involved in regulation of mitotic cell cycle transition (Scor



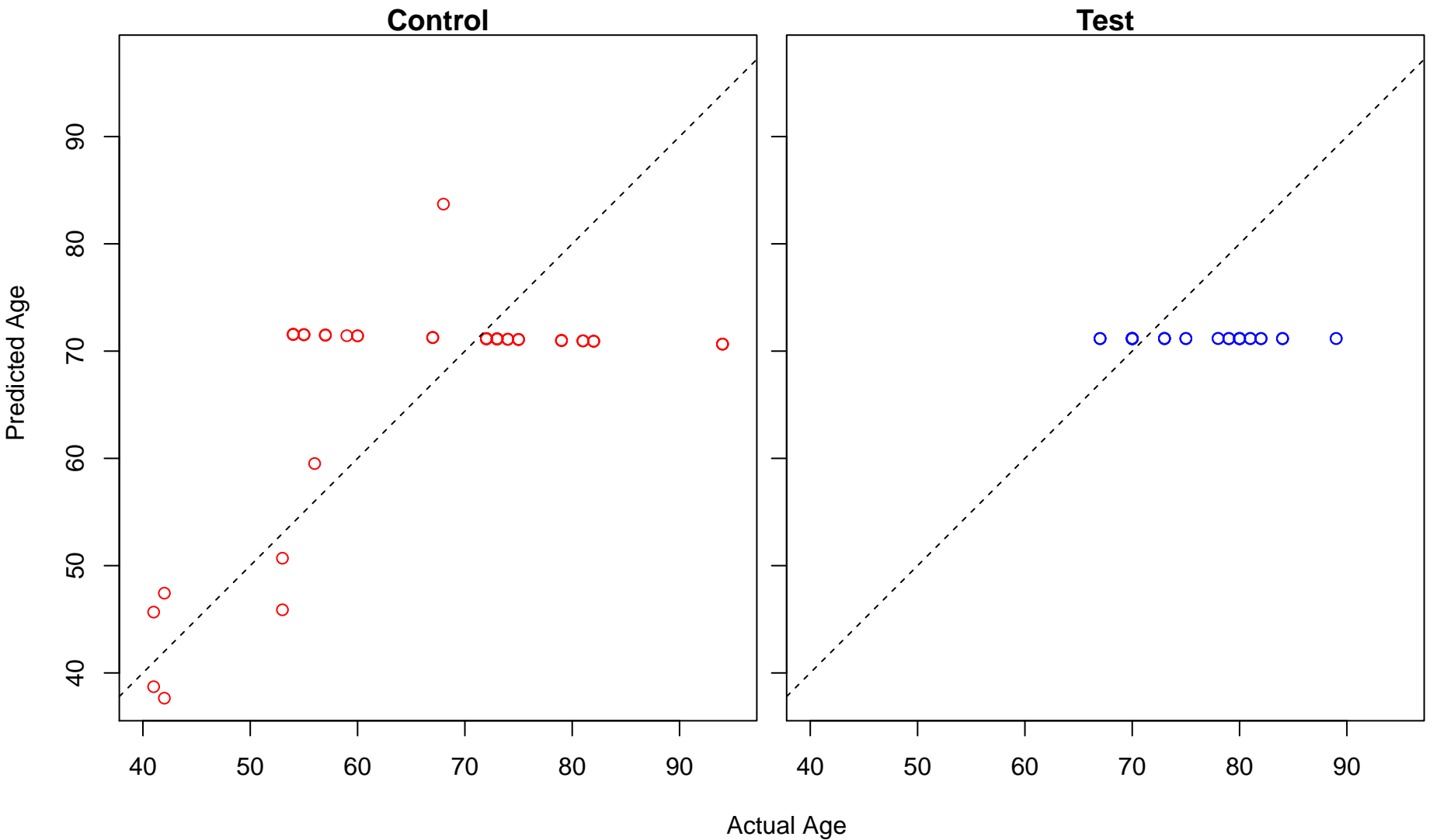
positive regulation of proteolysis involved in cellular protein catabolic process (Score: 0.835383)



positive regulation of ubiquitin protein ligase activity (Score: 0.835383)

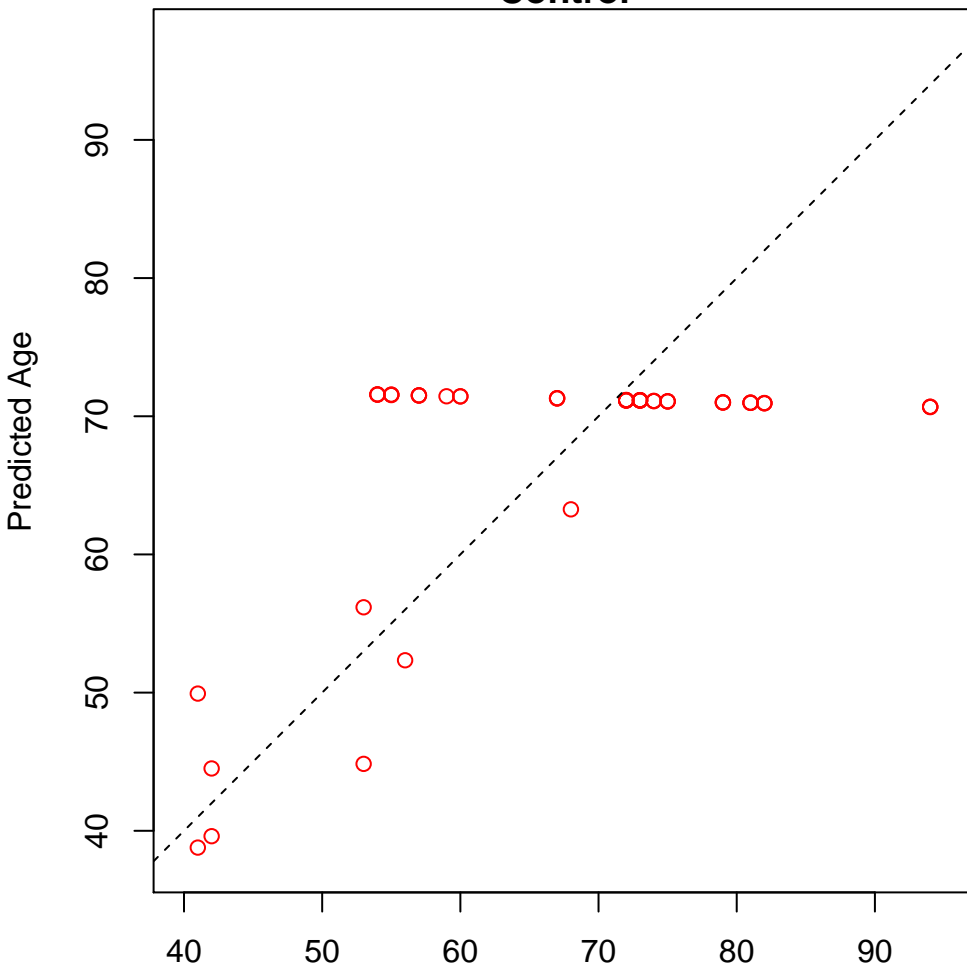


Positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score

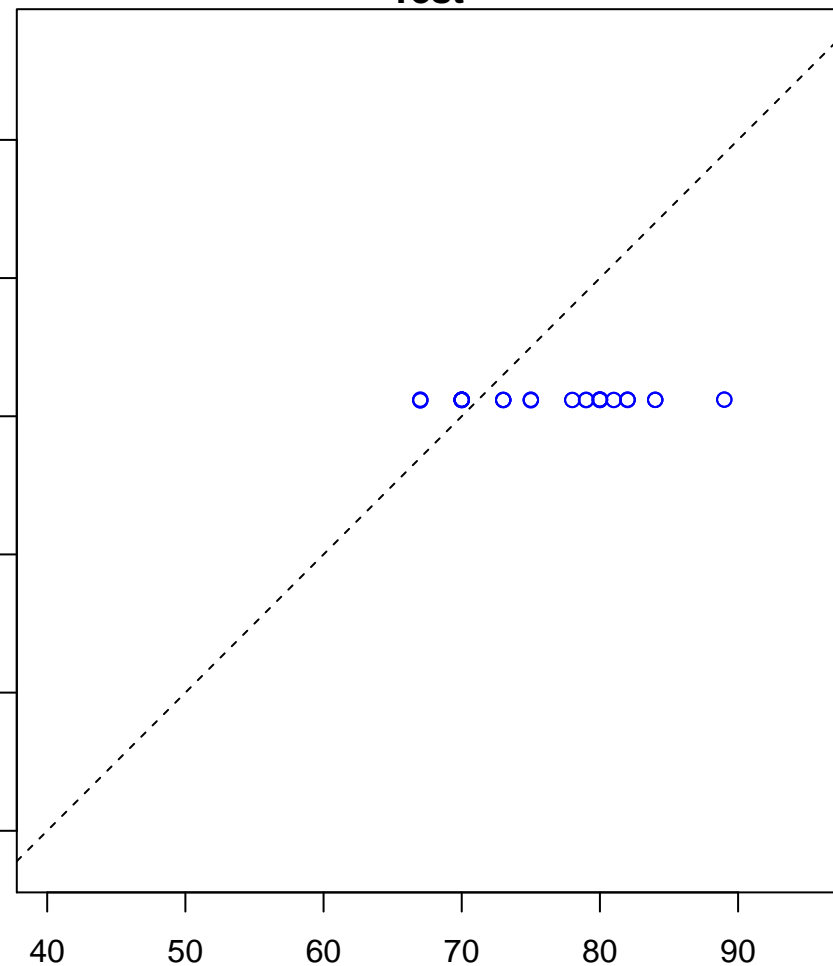


regulation of type I interferon production (Score: 0.834887)

Control



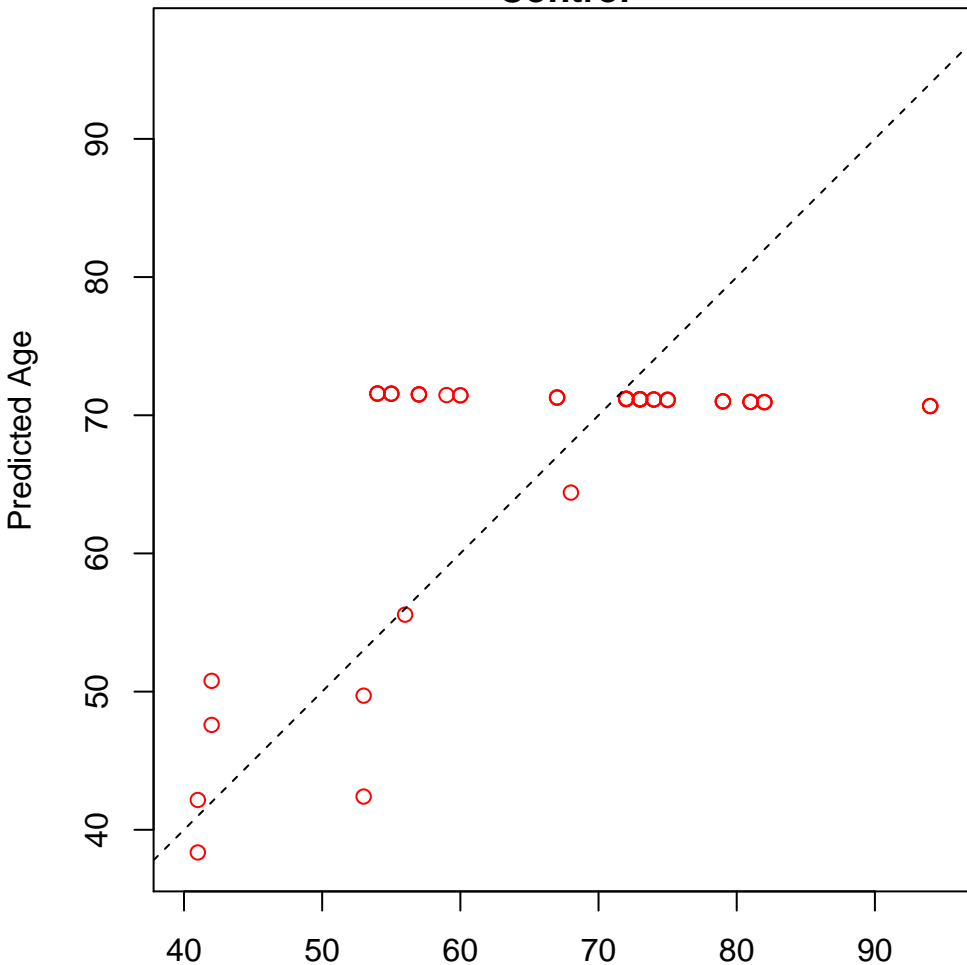
Test



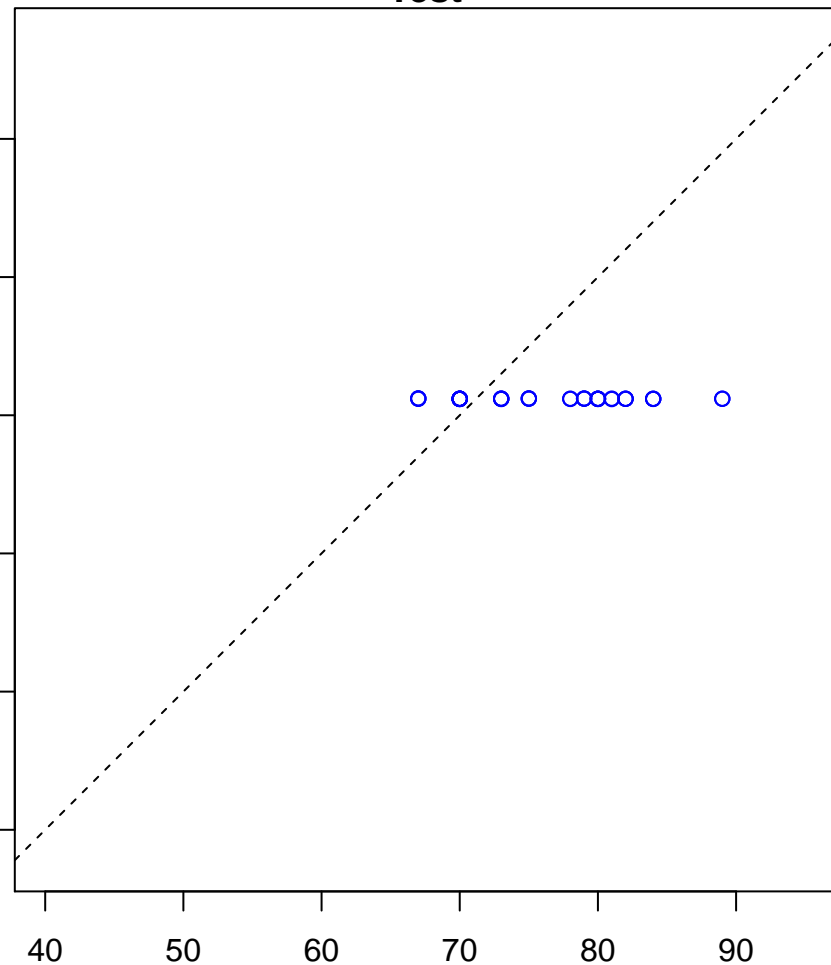
Actual Age

maintenance of protein location in cell (Score: 0.834852)

Control



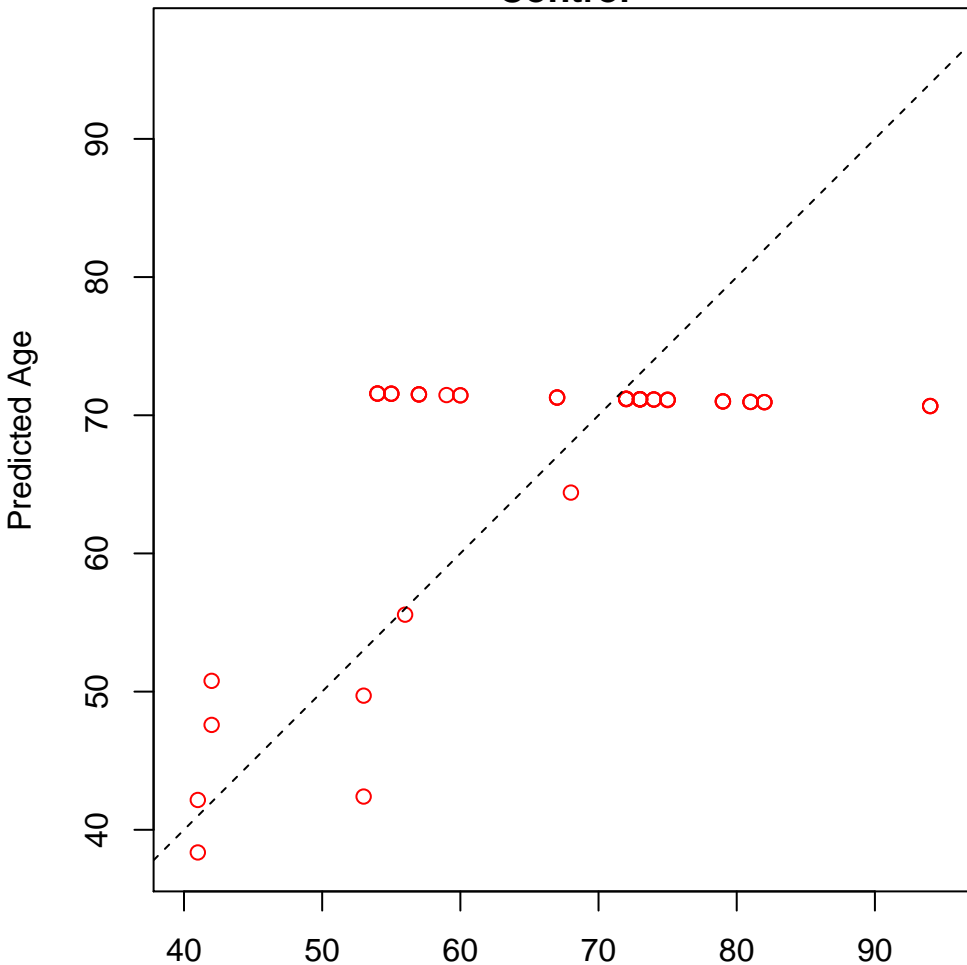
Test



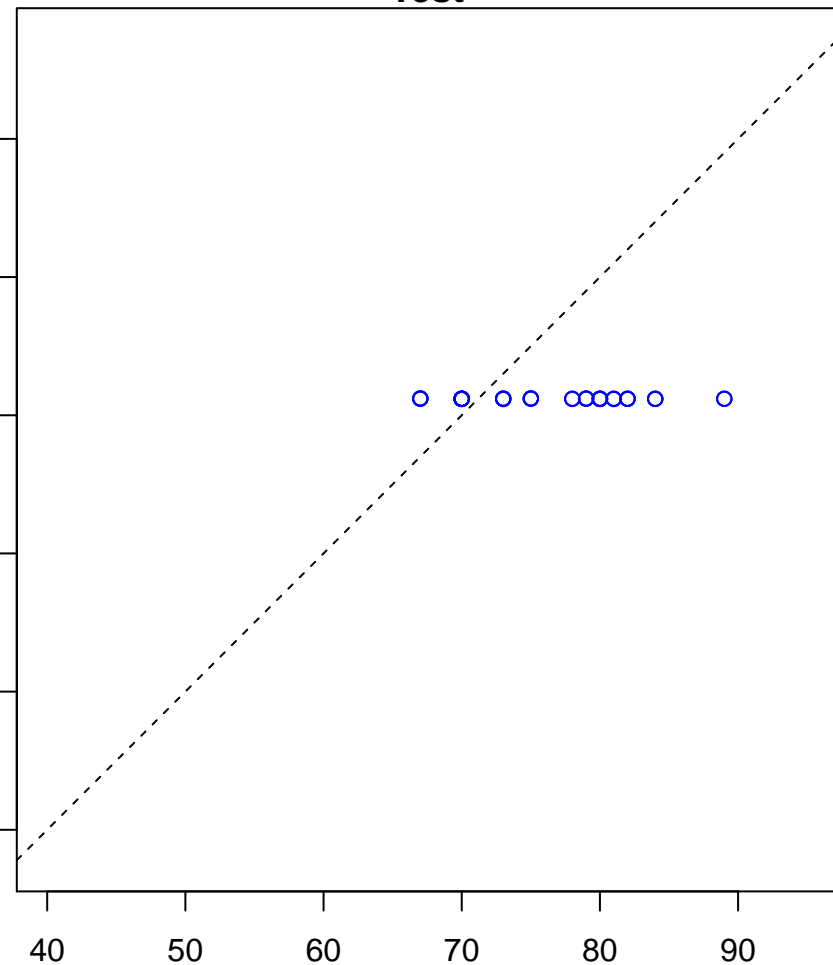
Actual Age

maintenance of protein location (Score: 0.834852)

Control



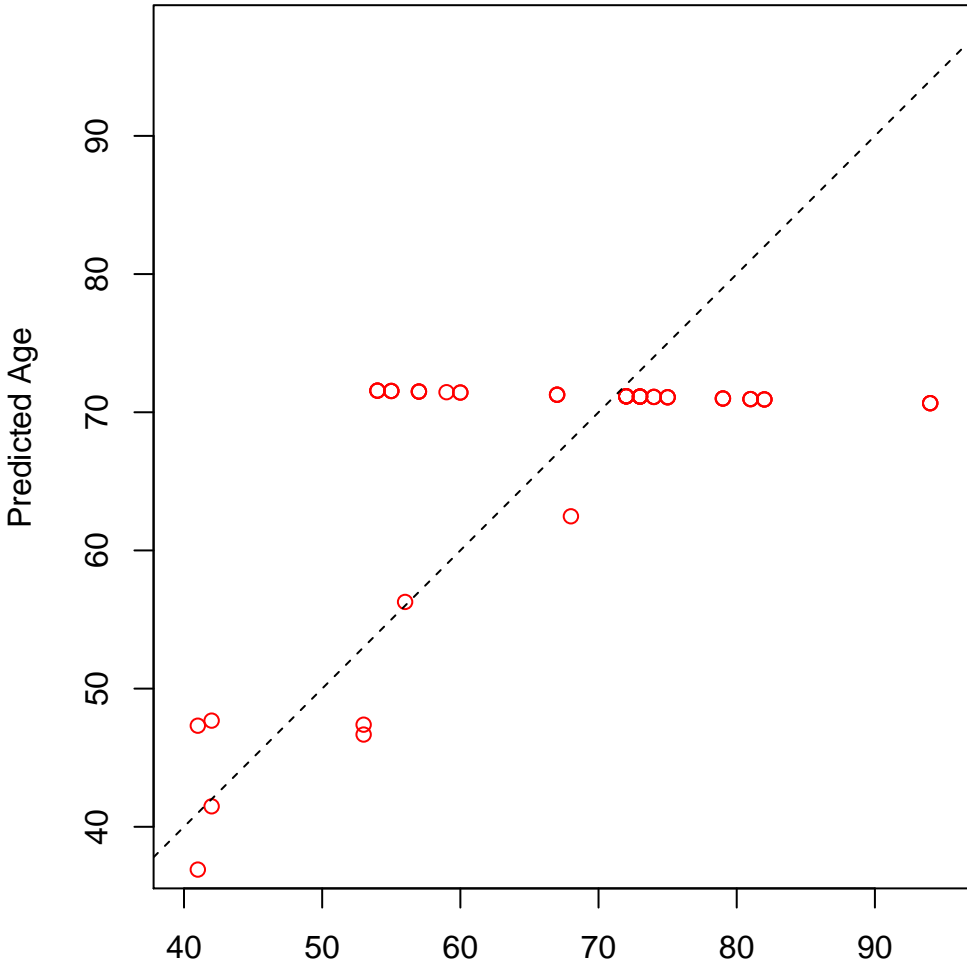
Test



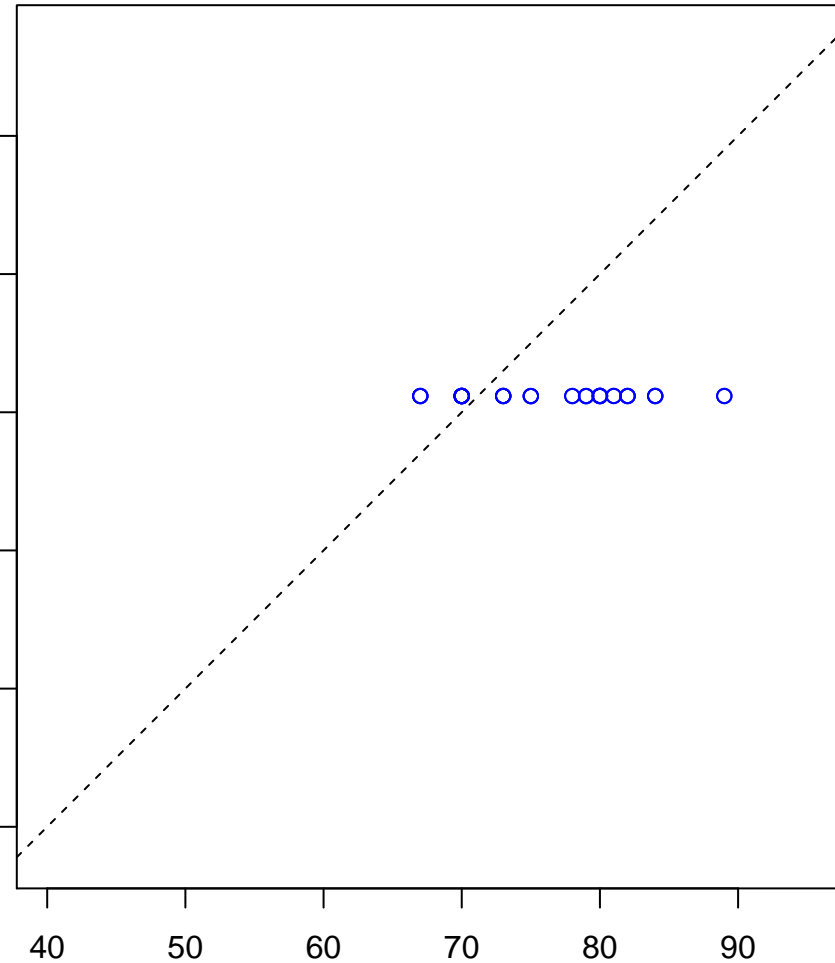
Actual Age

positive regulation of protein kinase activity (Score: 0.834795)

Control

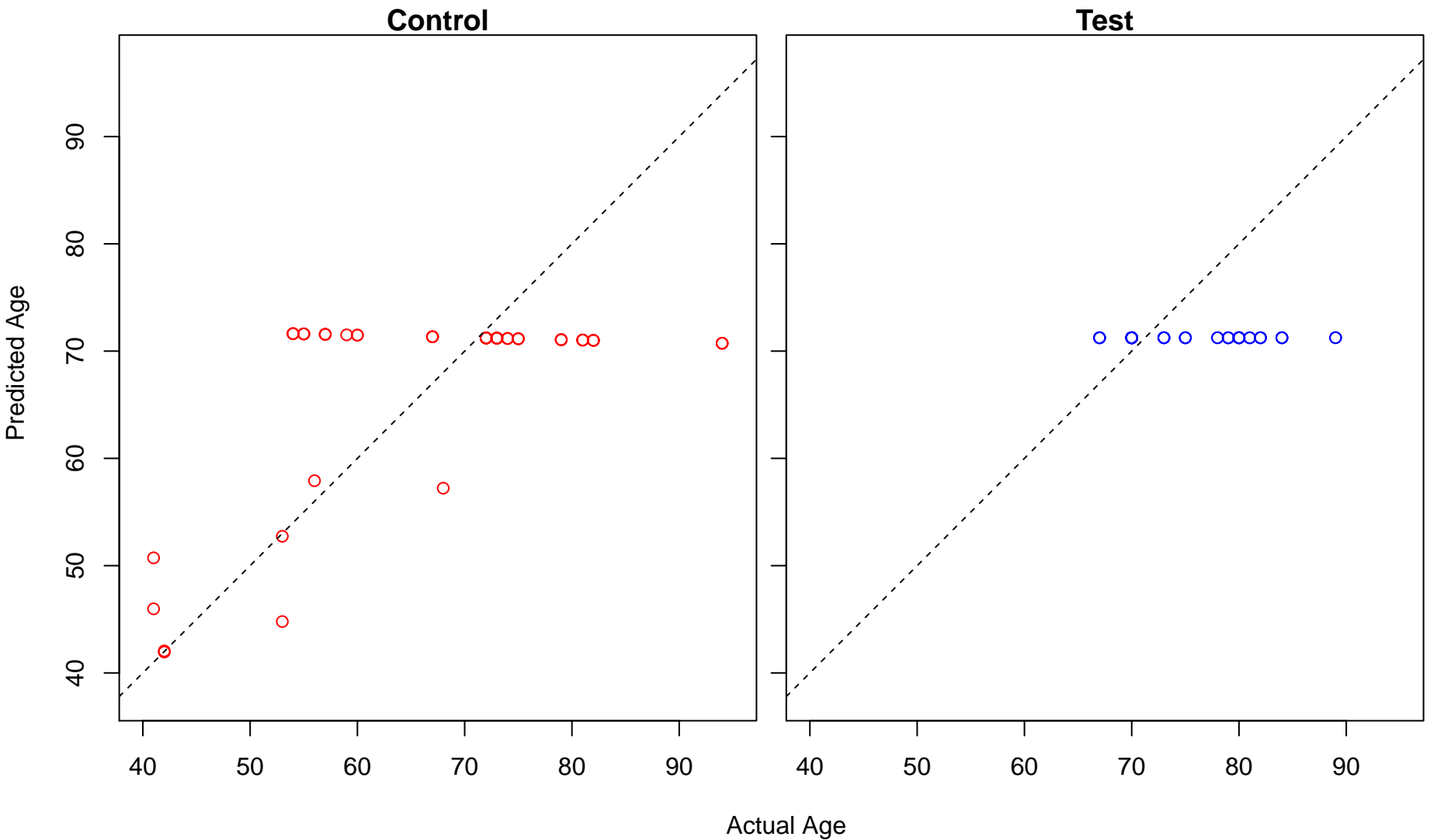


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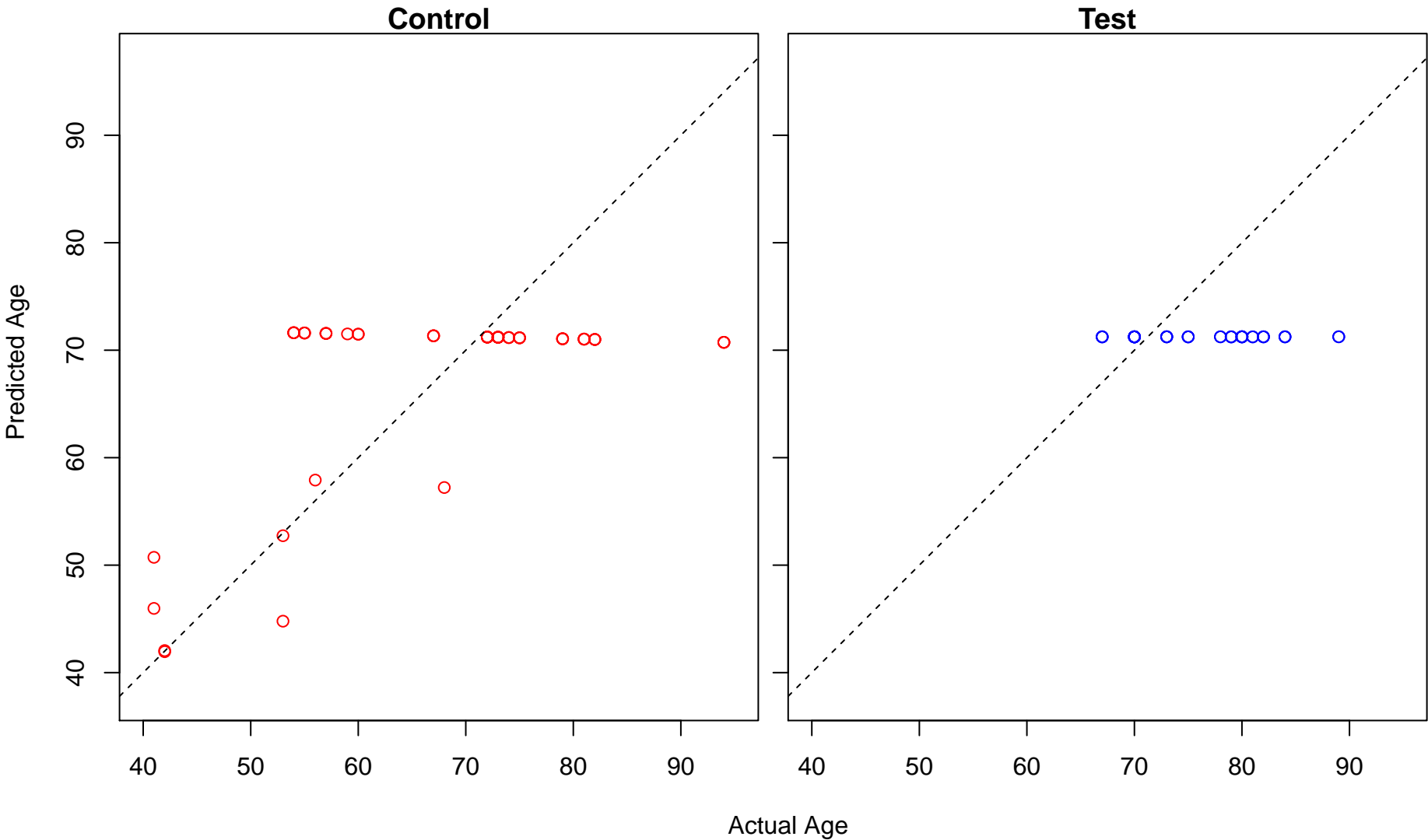


Actual Age

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

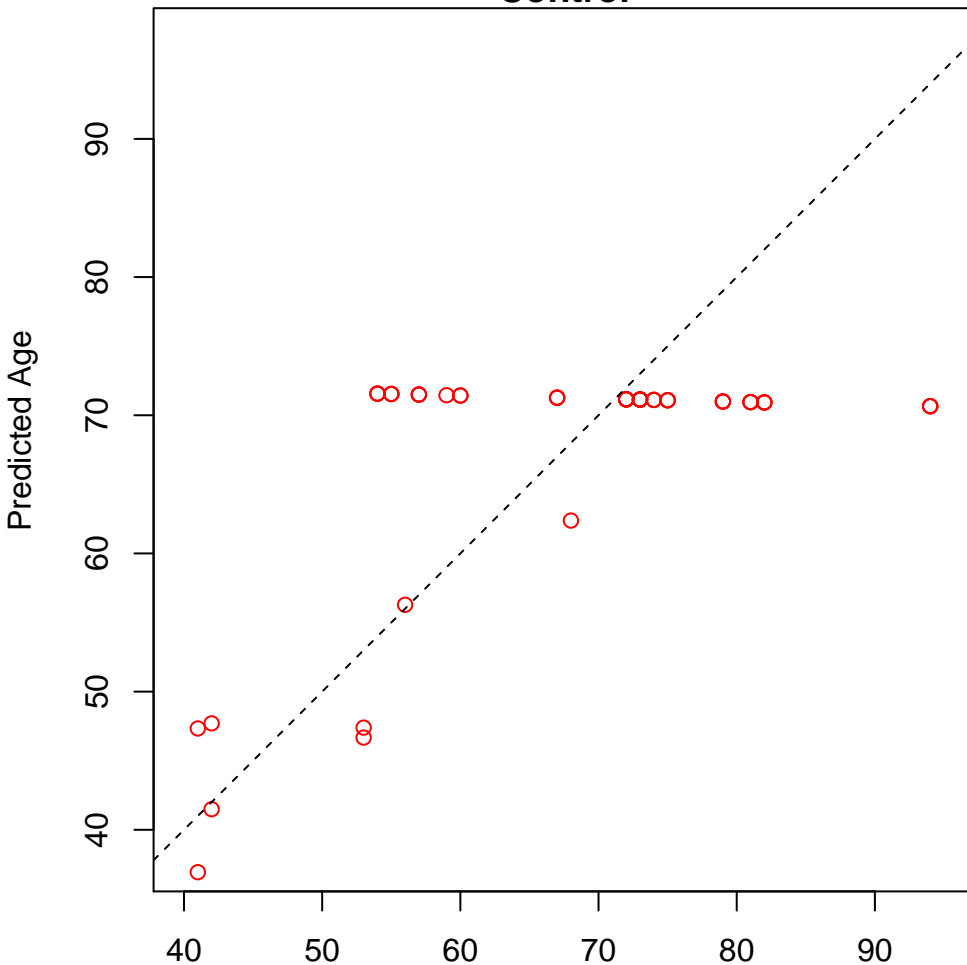


antigen processing and presentation of exogenous peptide antigen via MHC class I (Score: 0.83475)

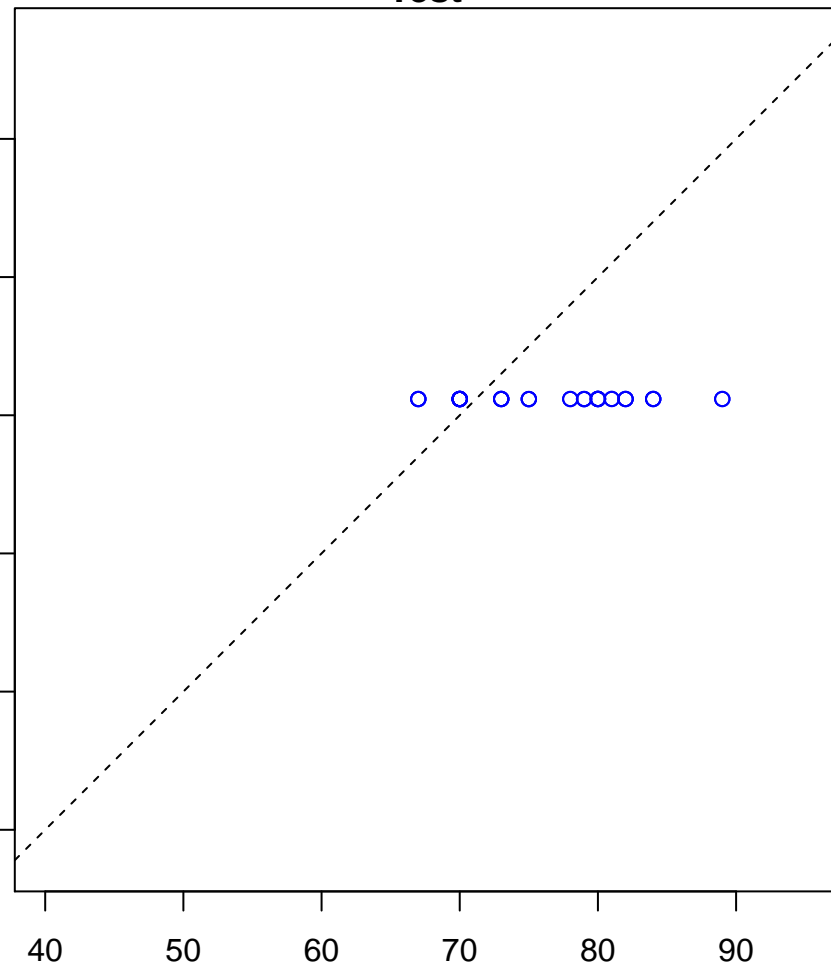


positive regulation of kinase activity (Score: 0.834699)

Control

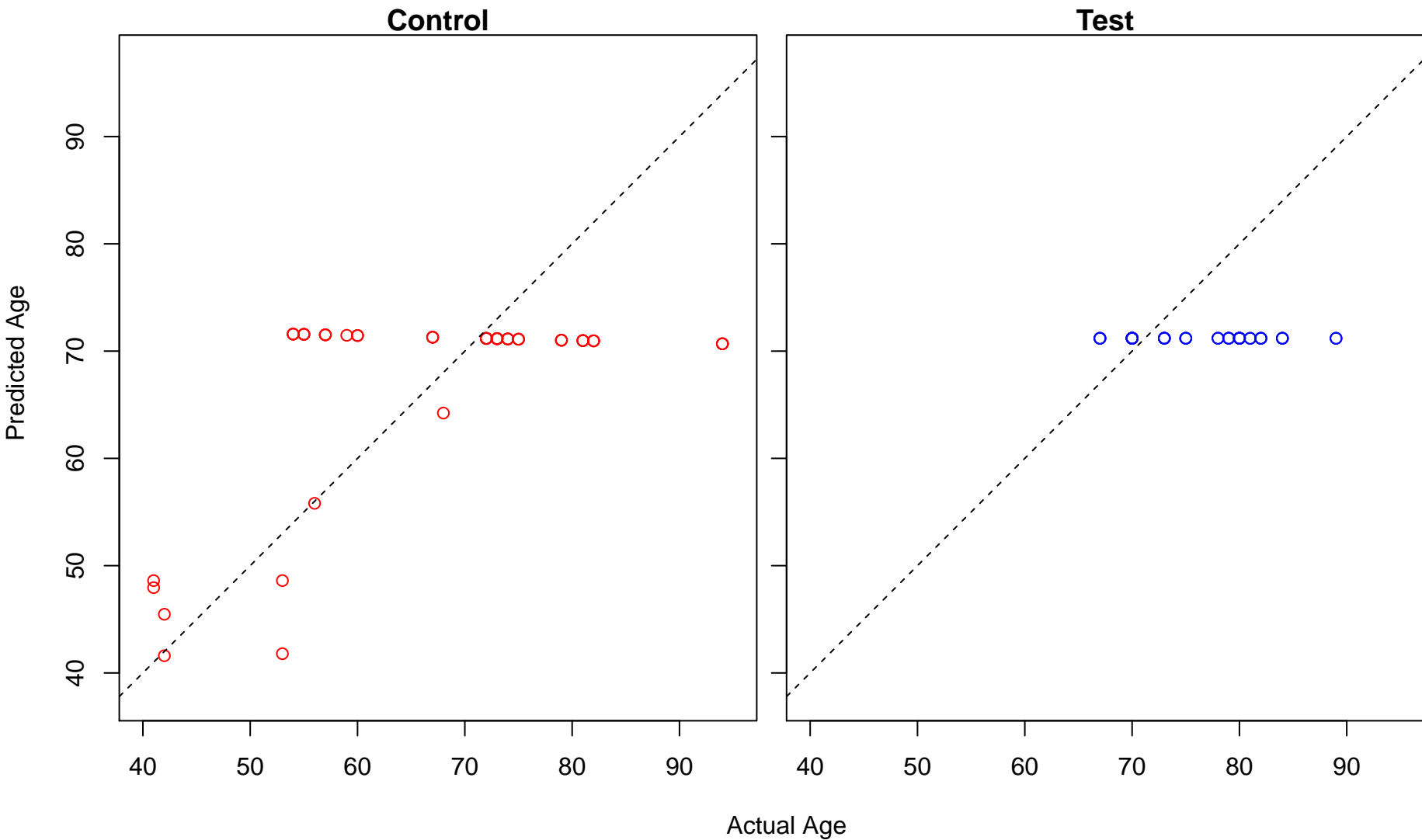


Test

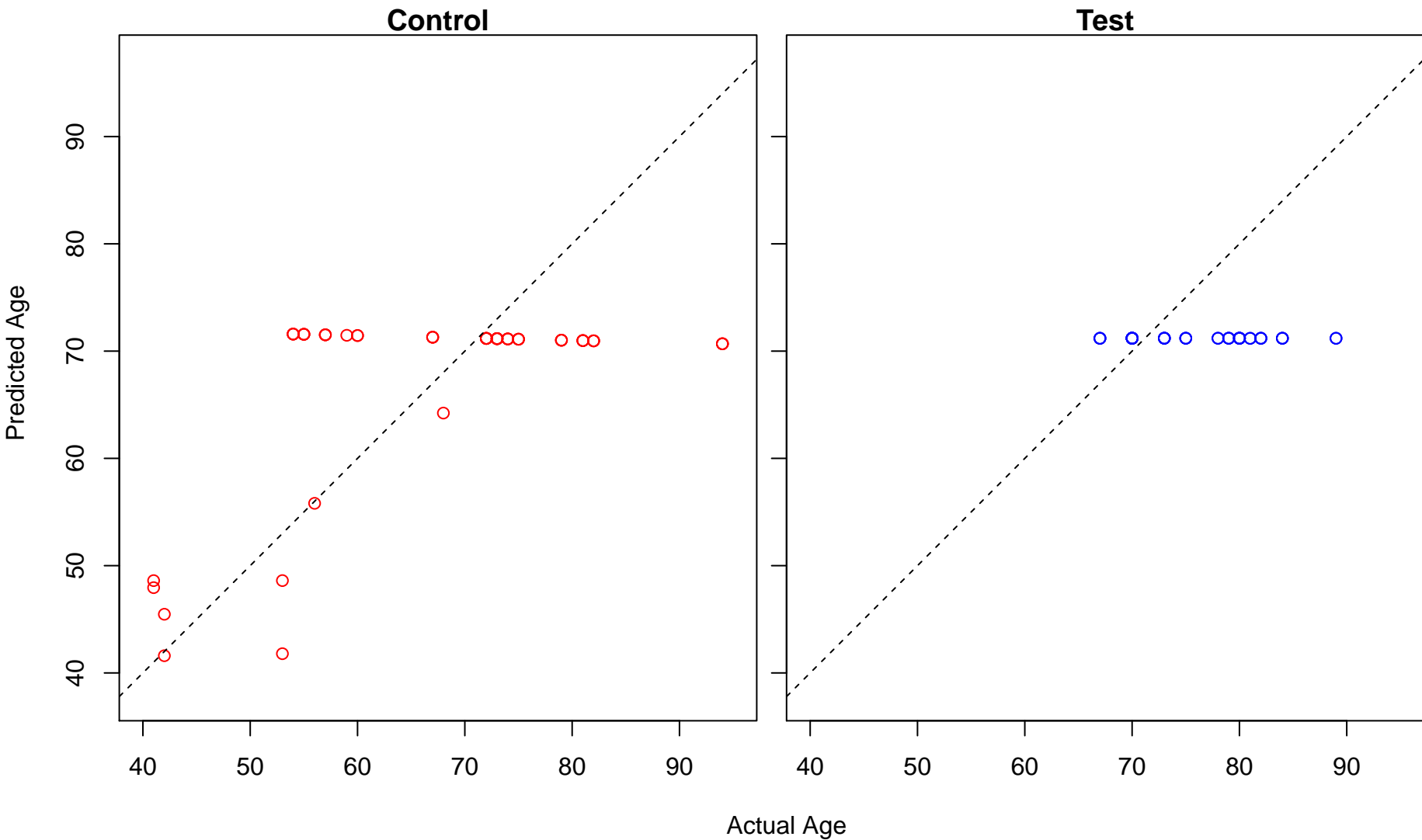


Actual Age

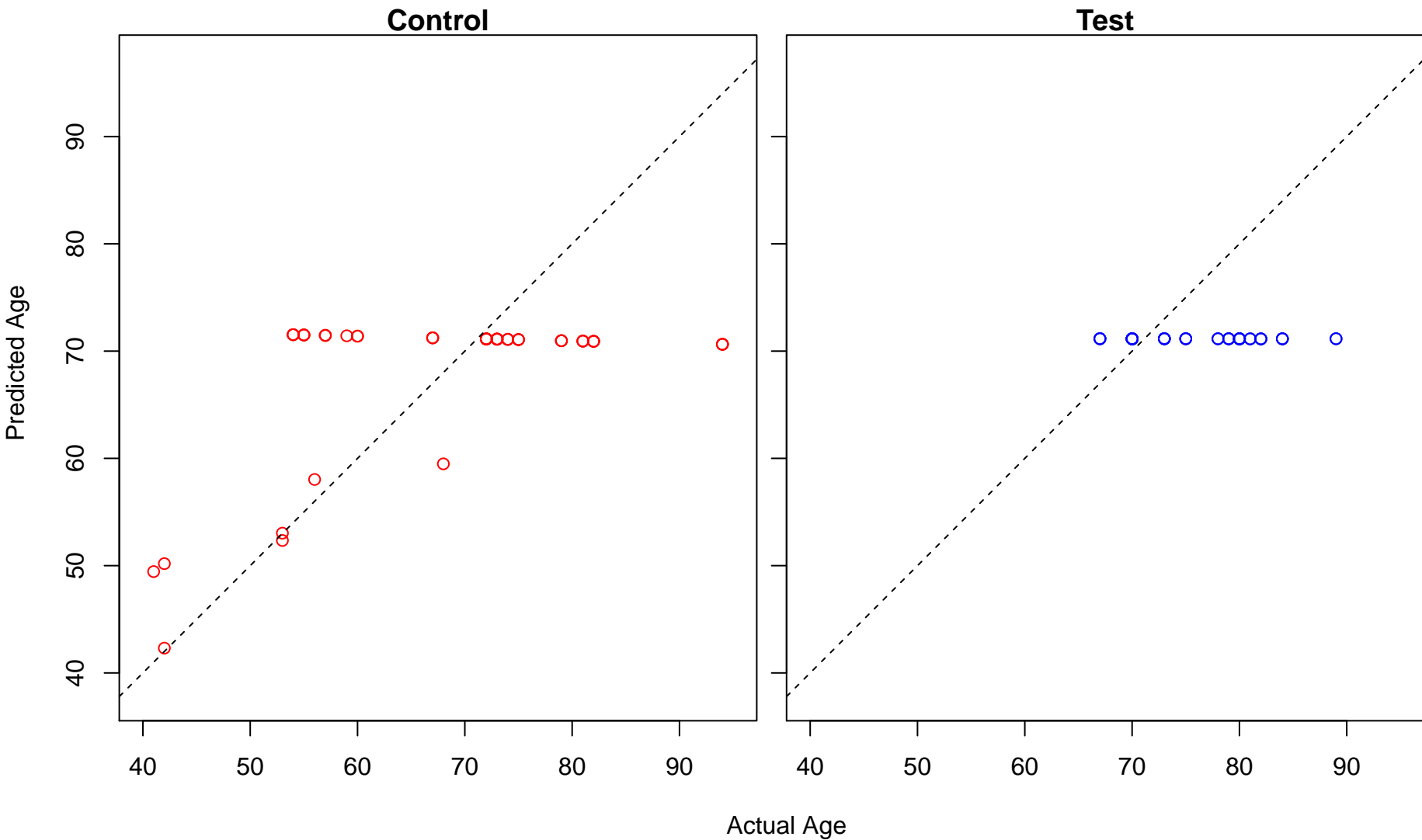
reproduction (Score: 0.834572)



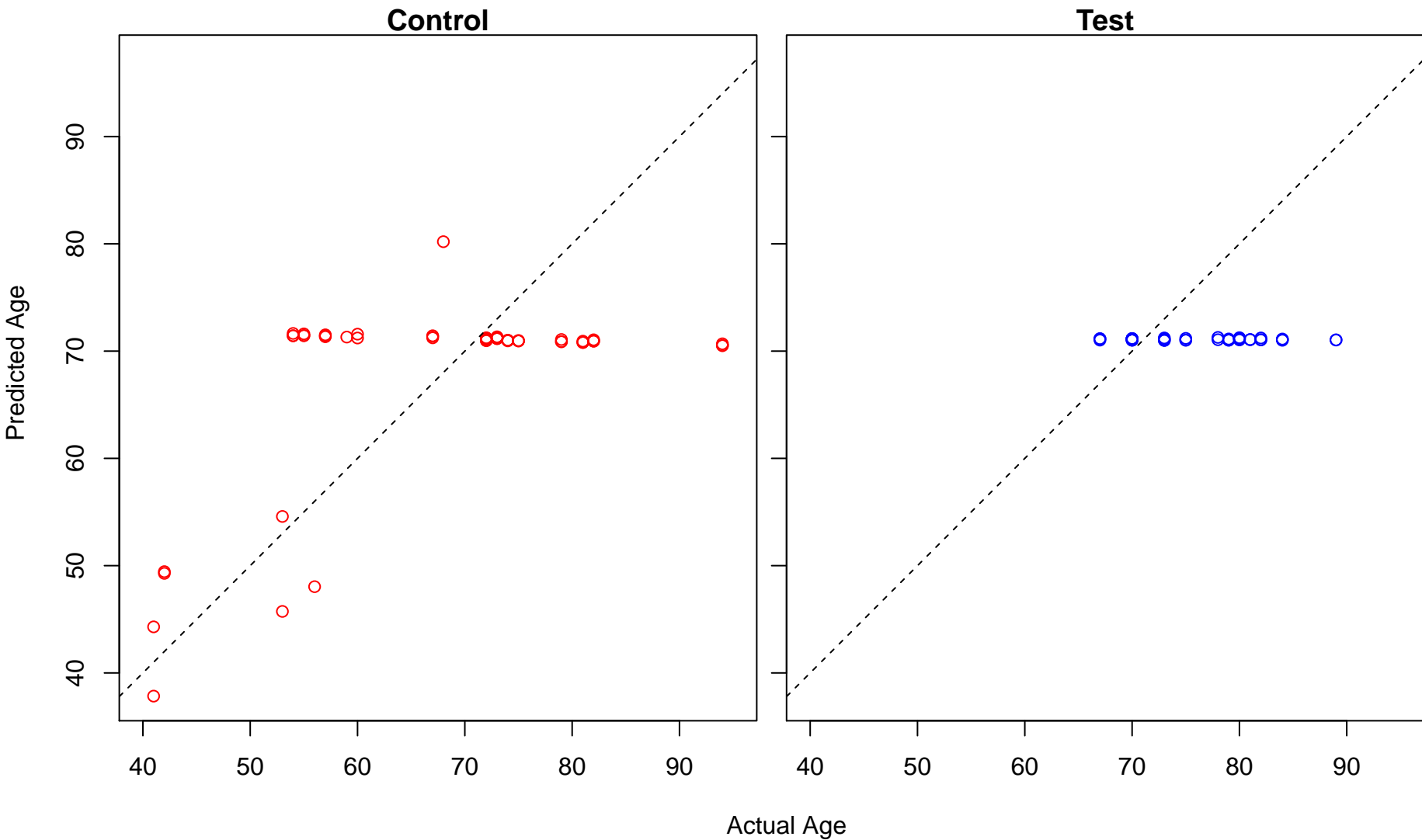
reproductive process (Score: 0.834572)



positive regulation of viral life cycle (Score: 0.834508)

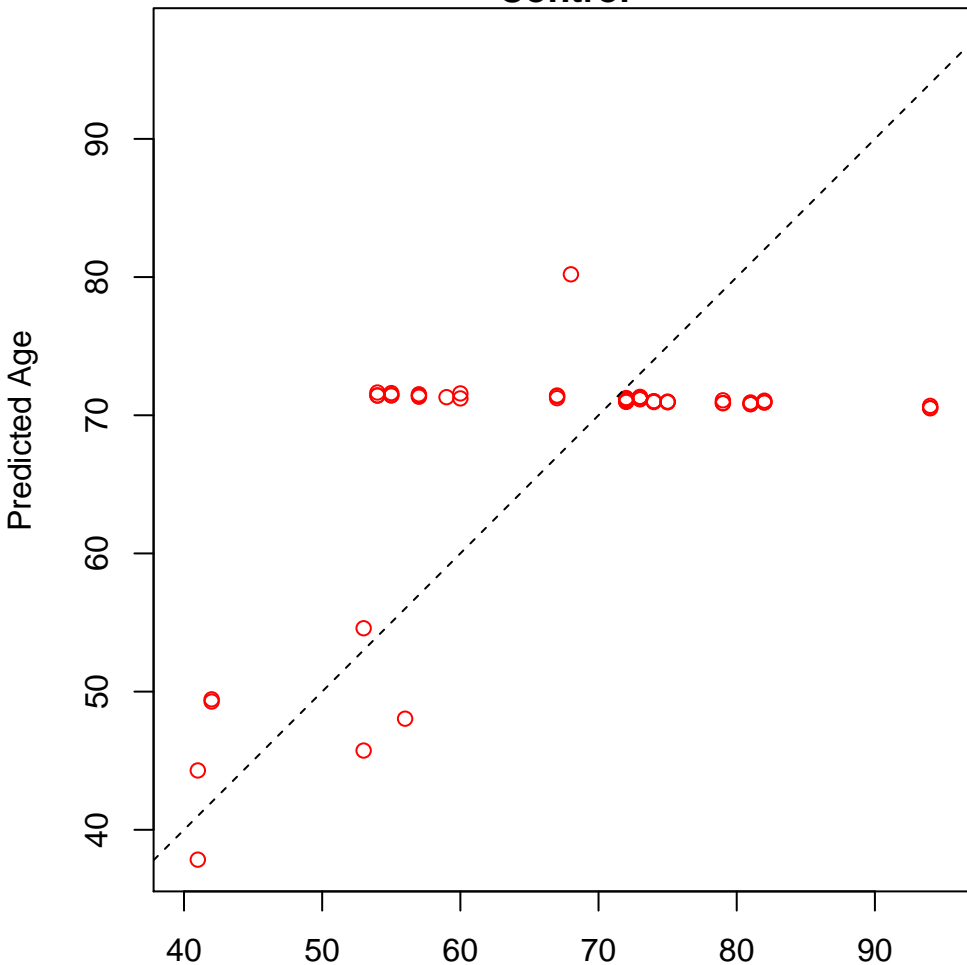


pattern recognition receptor signaling pathway (Score: 0.834307)

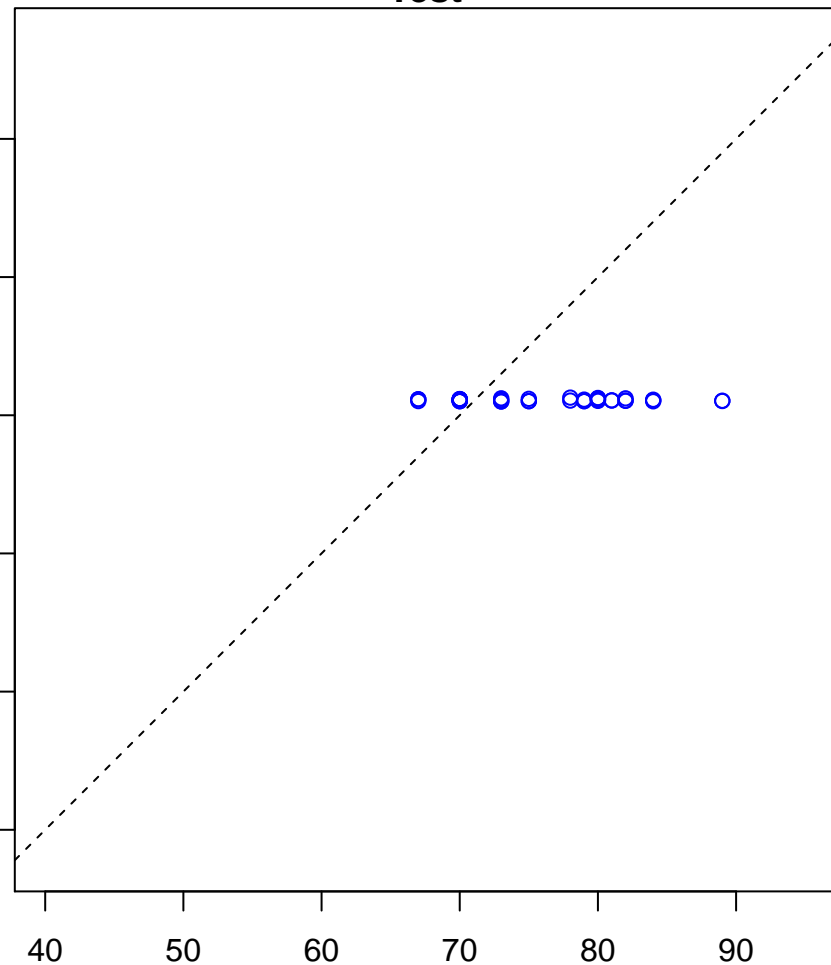


toll-like receptor signaling pathway (Score: 0.834307)

Control

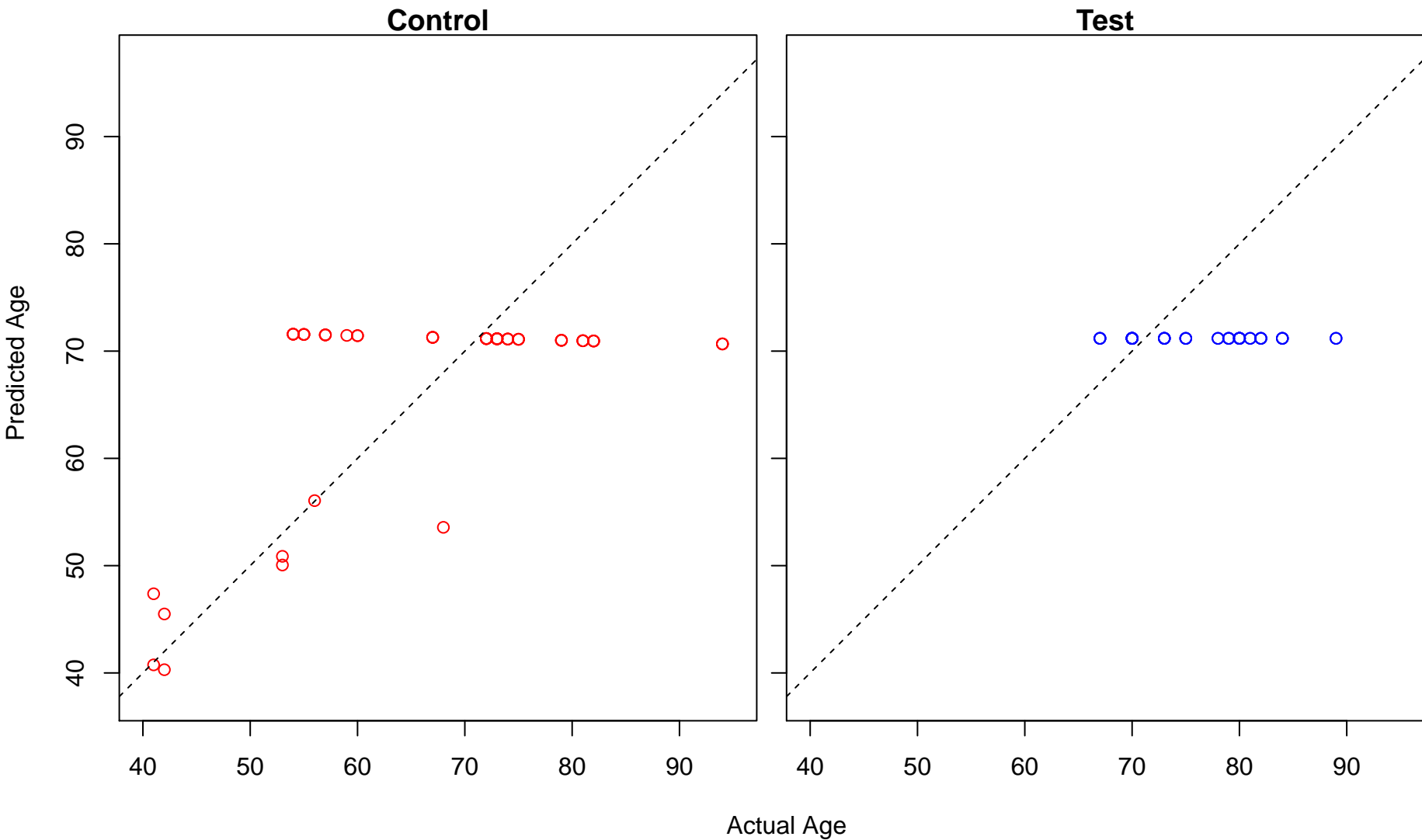


Test



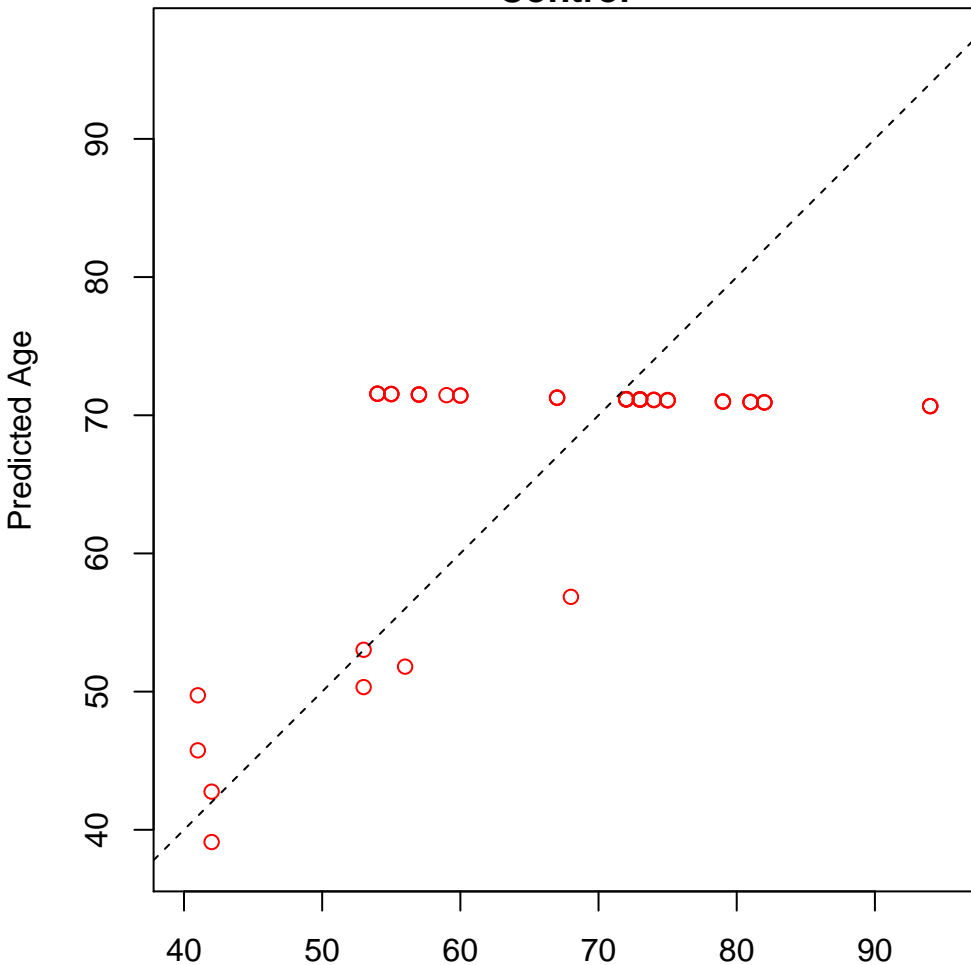
Actual Age

cellular homeostasis (Score: 0.834206)

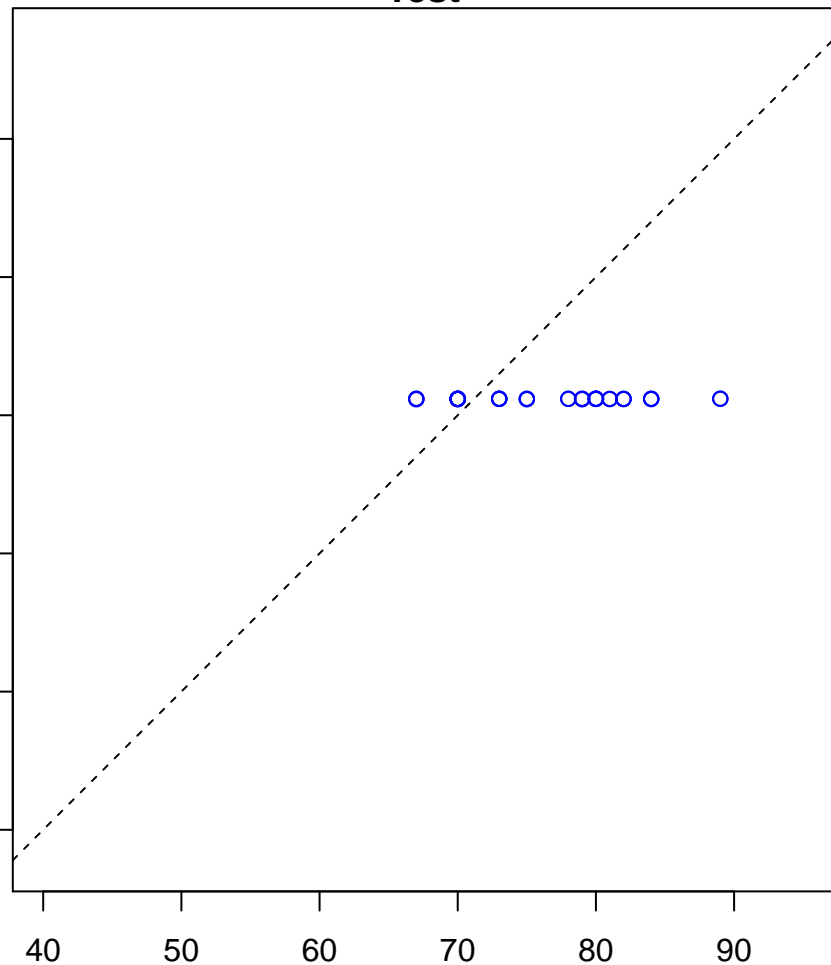


positive regulation of protein transport (Score: 0.834176)

Control

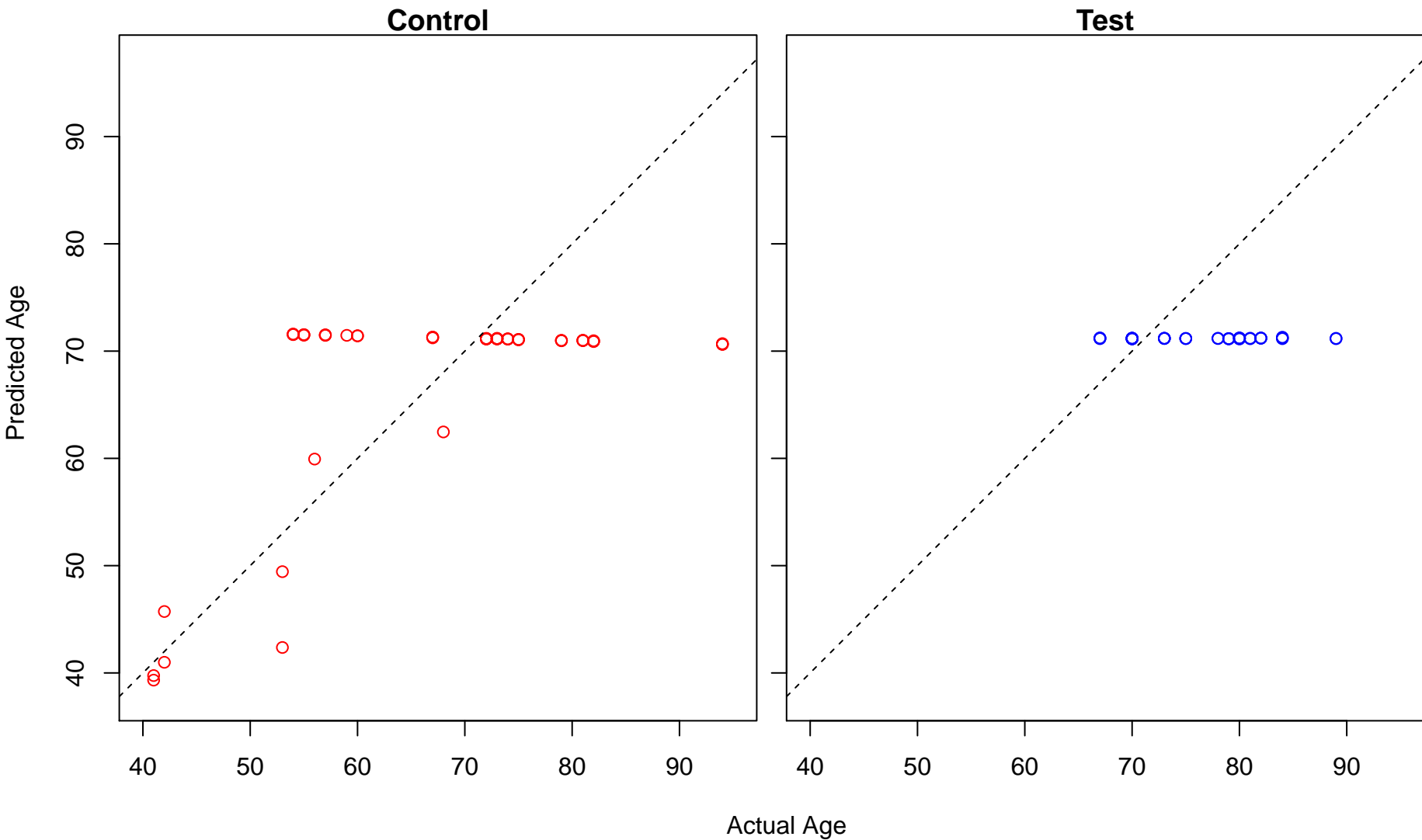


Test

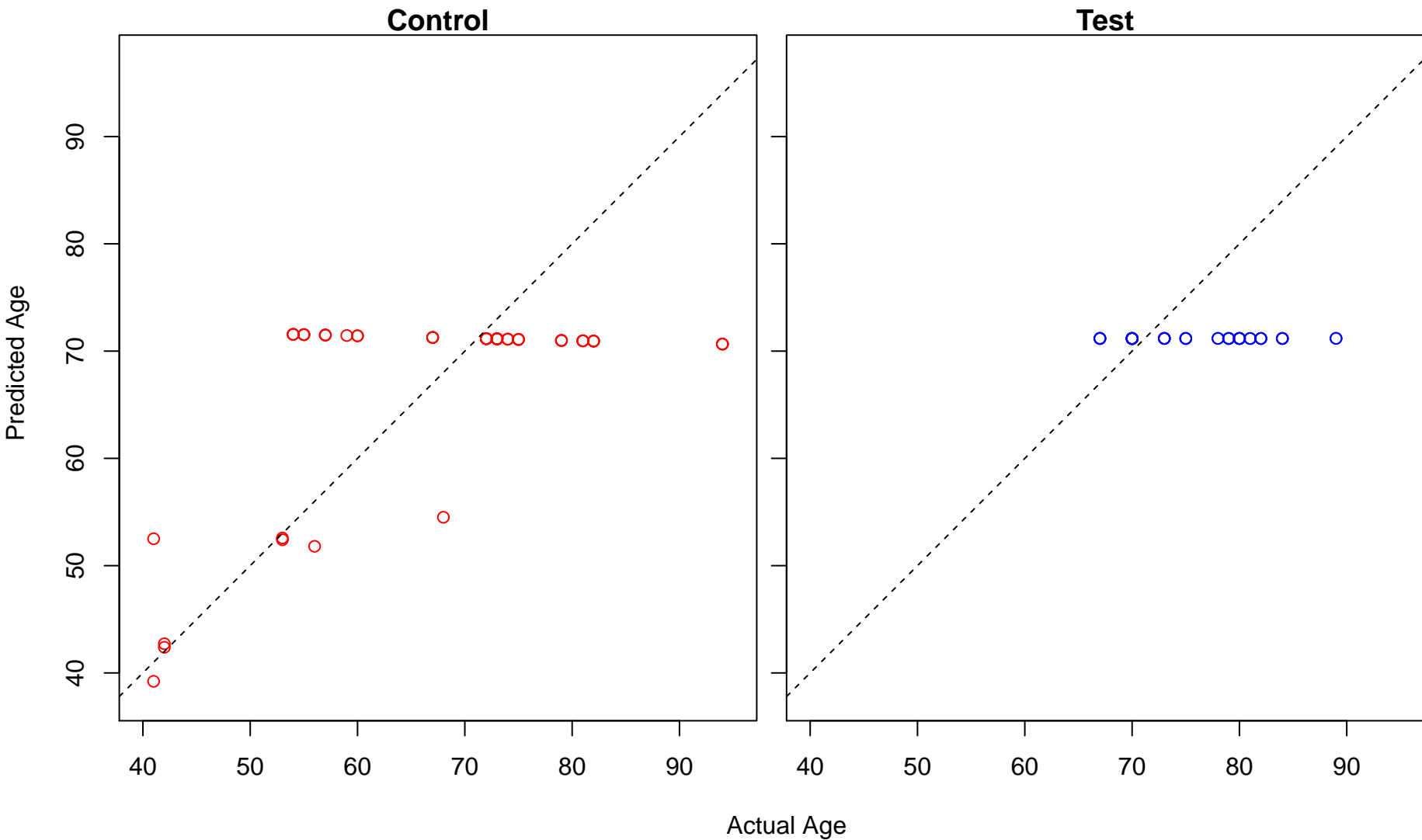


Actual Age

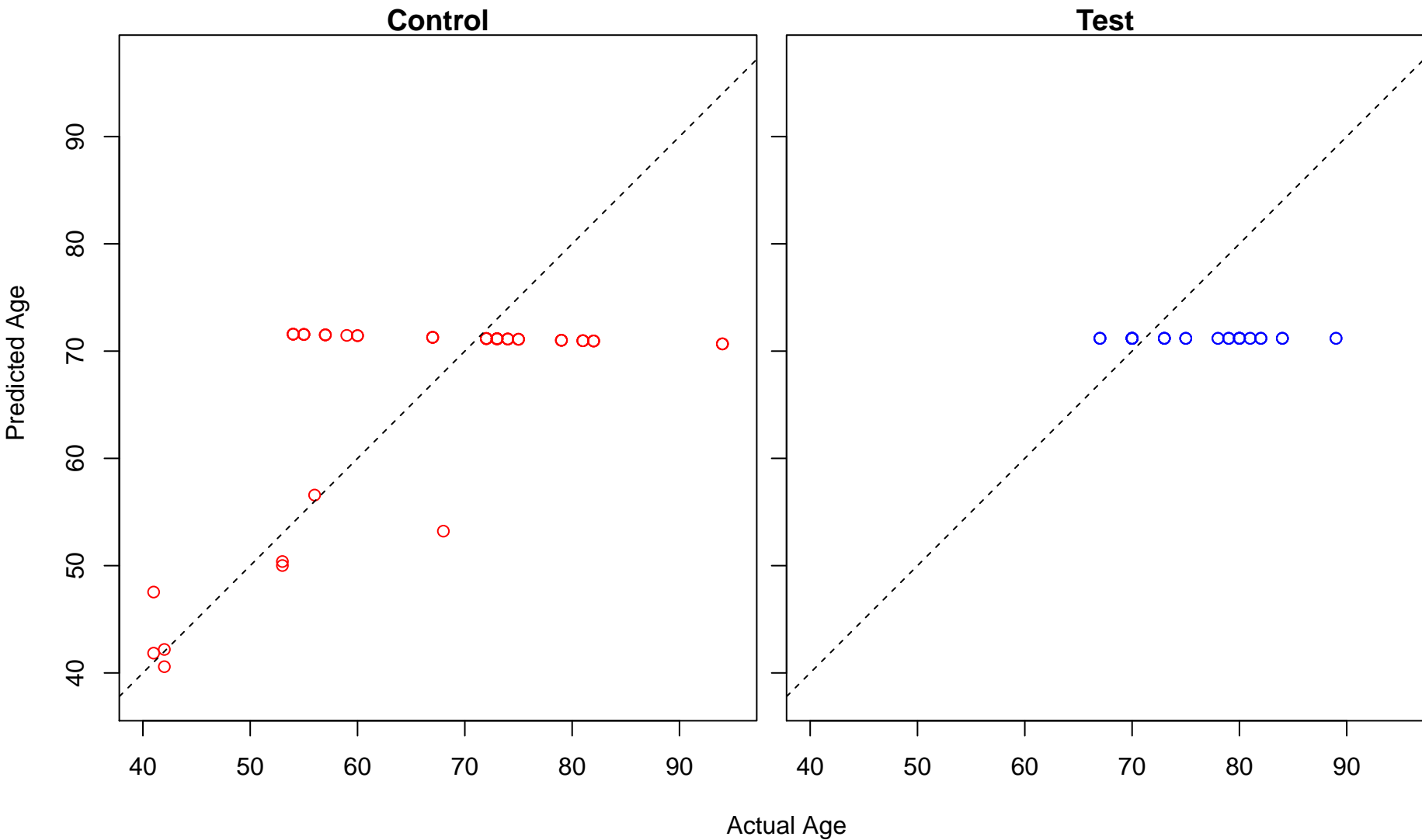
positive regulation of response to external stimulus (Score: 0.833990)



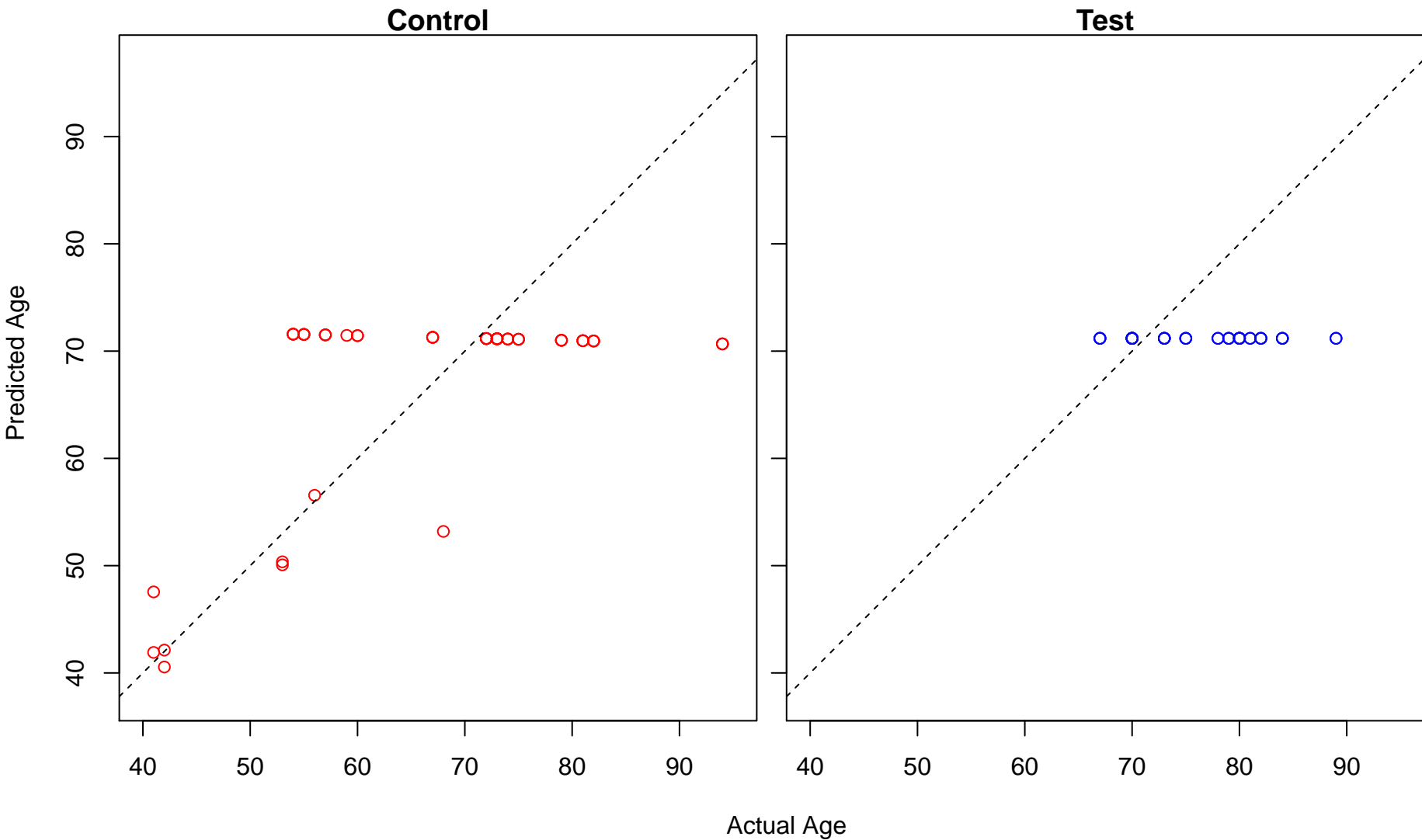
proteolysis (Score: 0.833737)



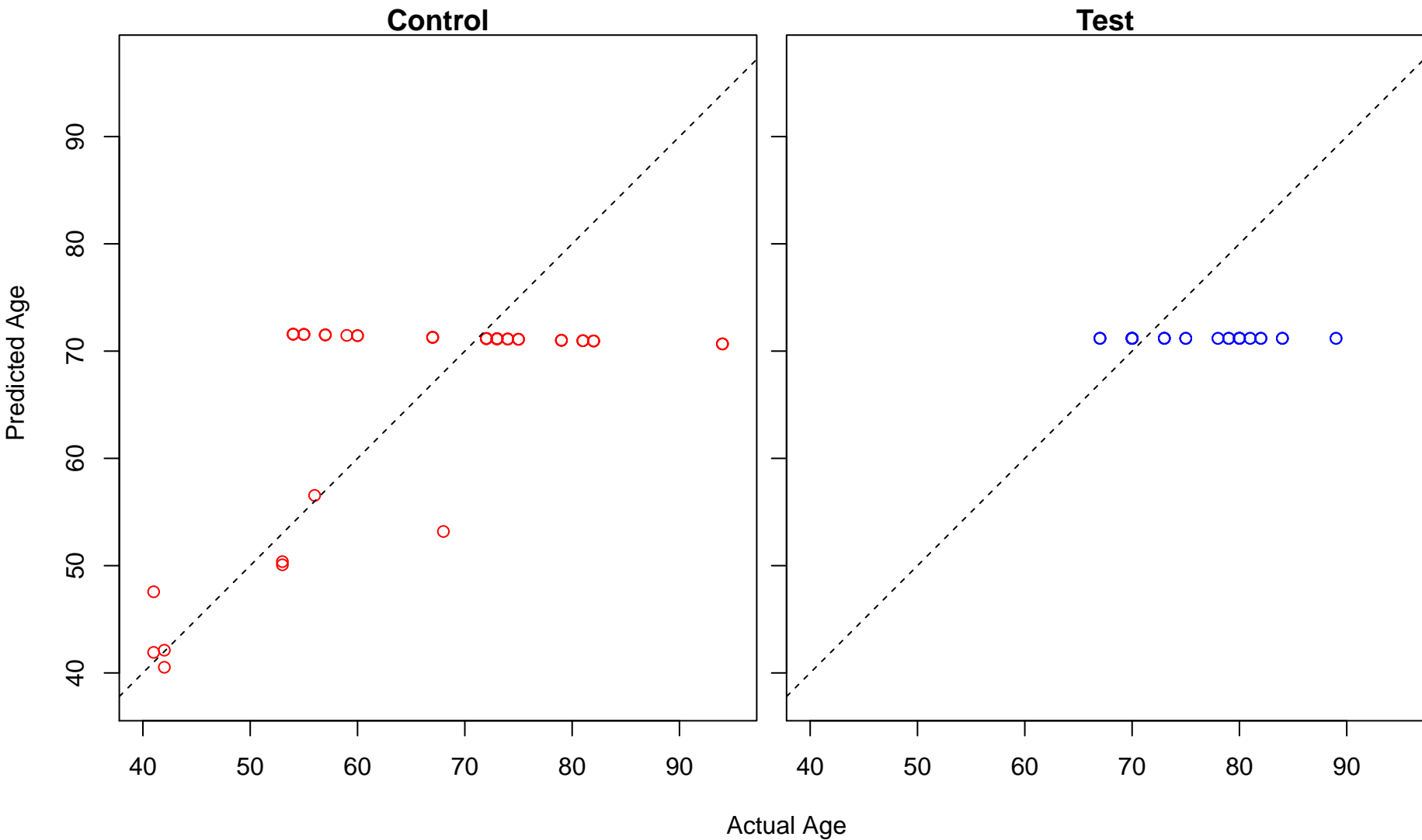
cellular chemical homeostasis (Score: 0.833719)



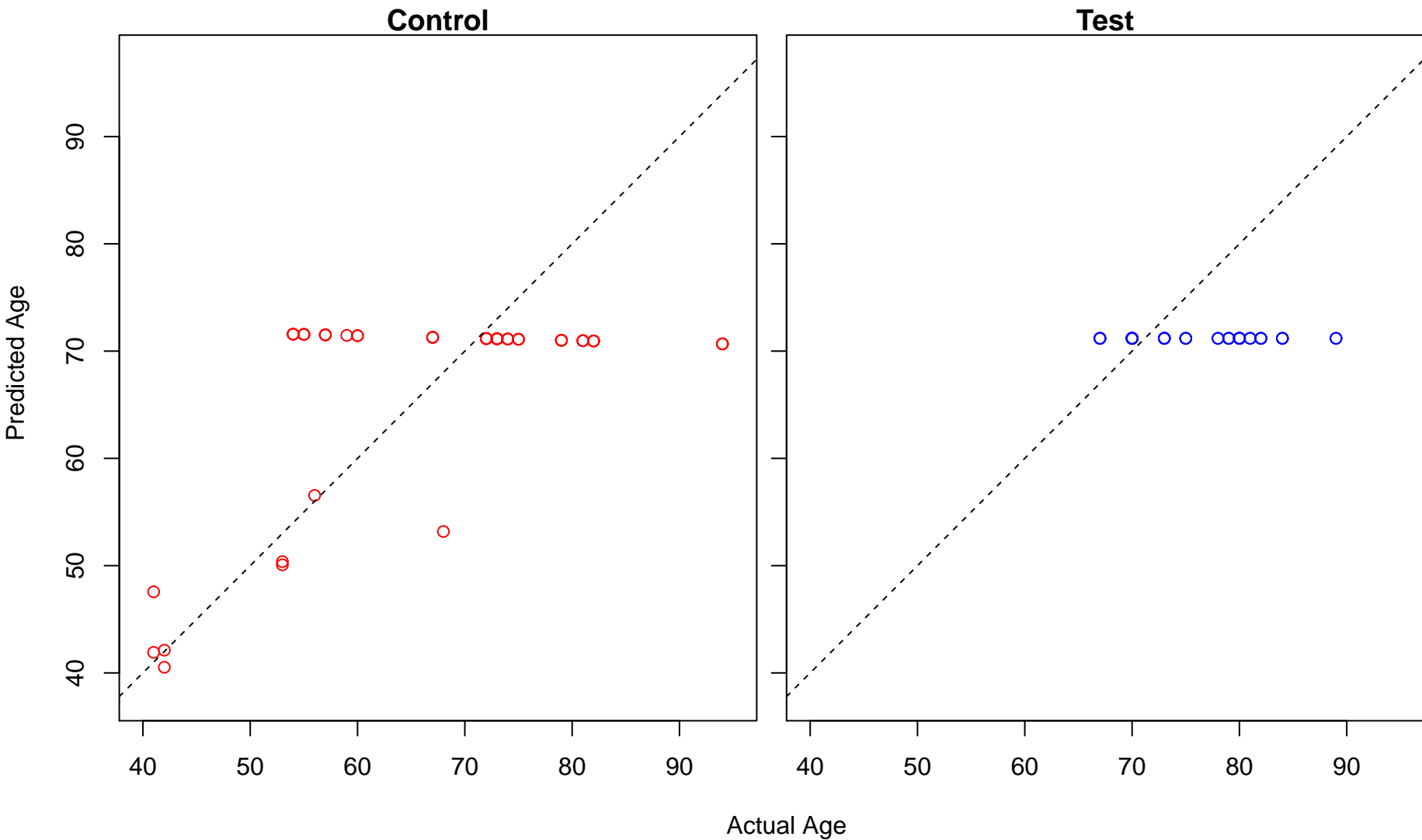
ion homeostasis (Score: 0.833671)



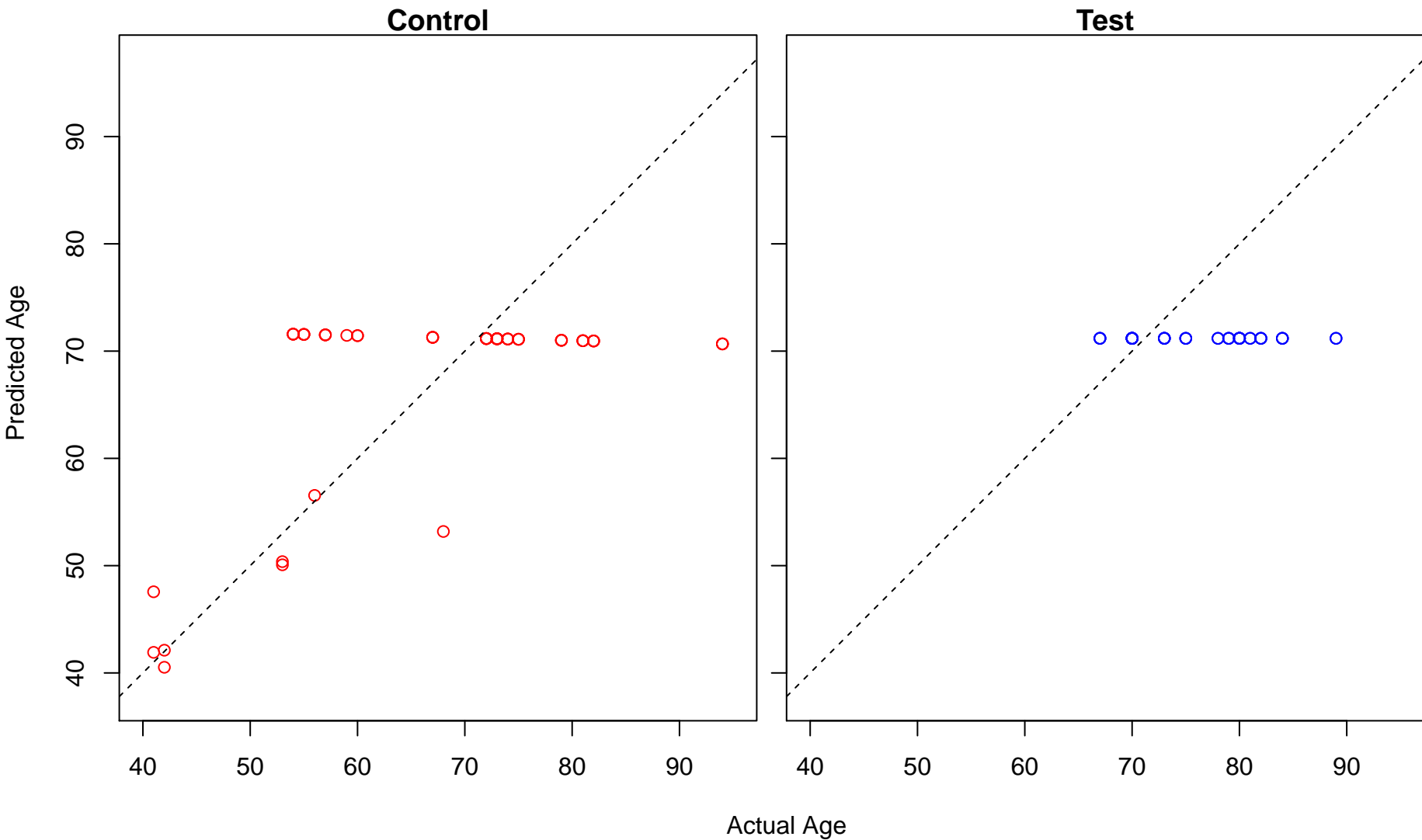
cellular ion homeostasis (Score: 0.833651)



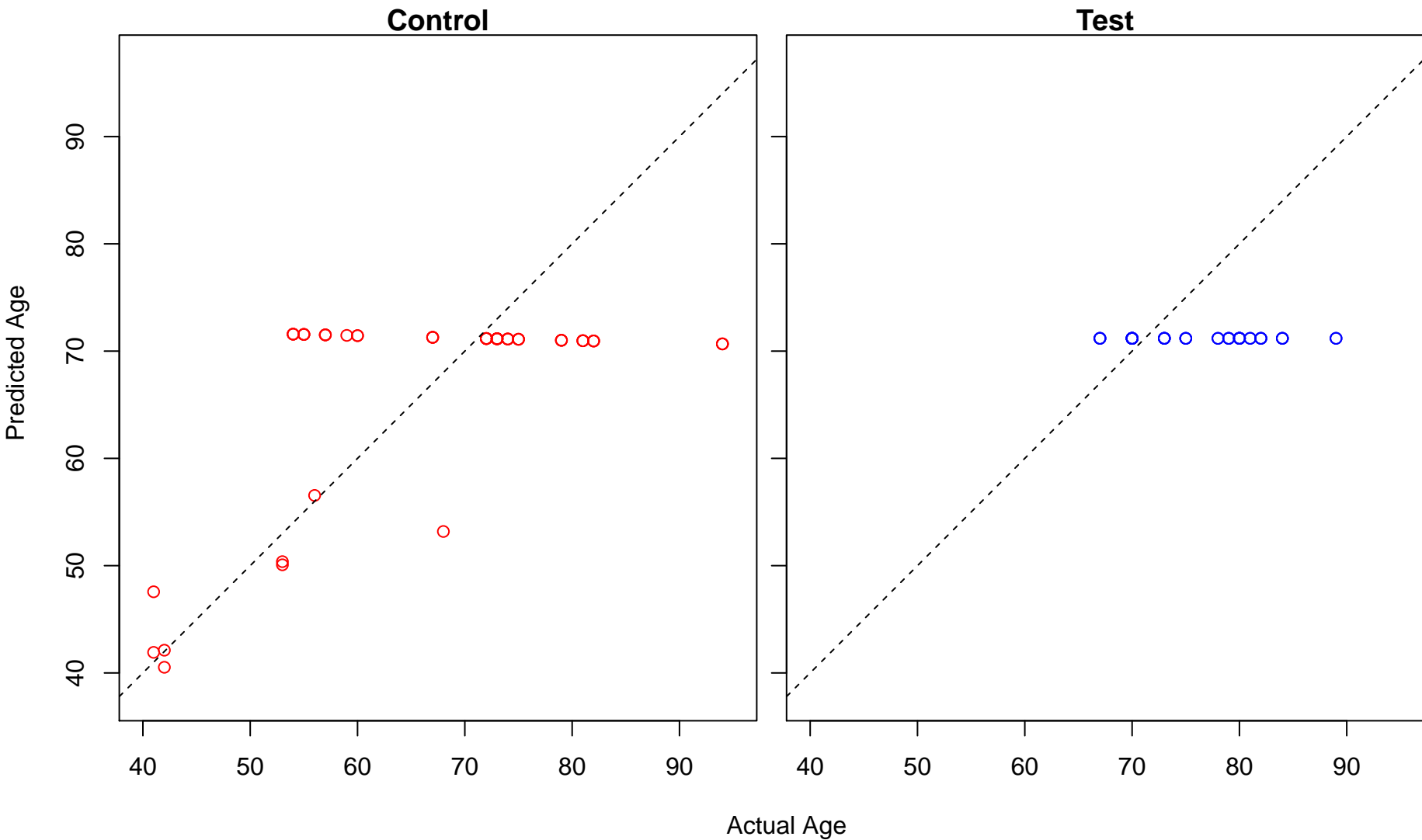
cellular cation homeostasis (Score: 0.833651)



cation homeostasis (Score: 0.833651)

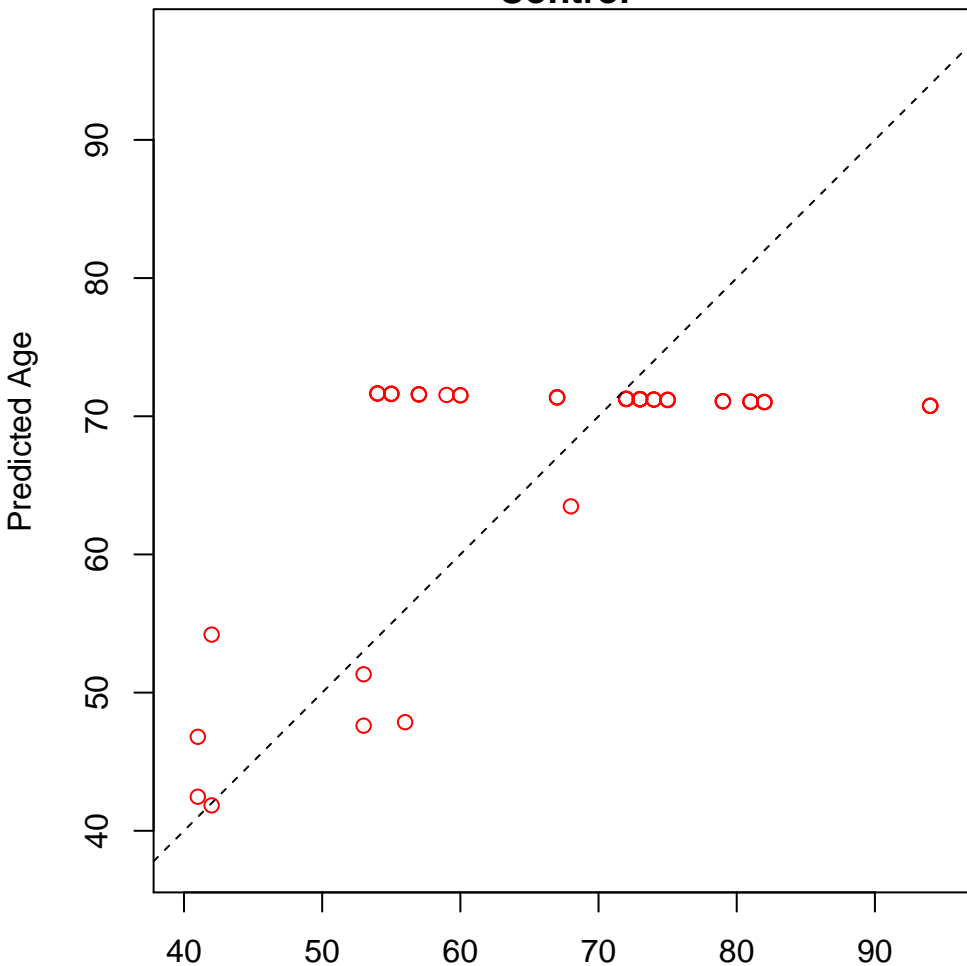


inorganic ion homeostasis (Score: 0.833651)

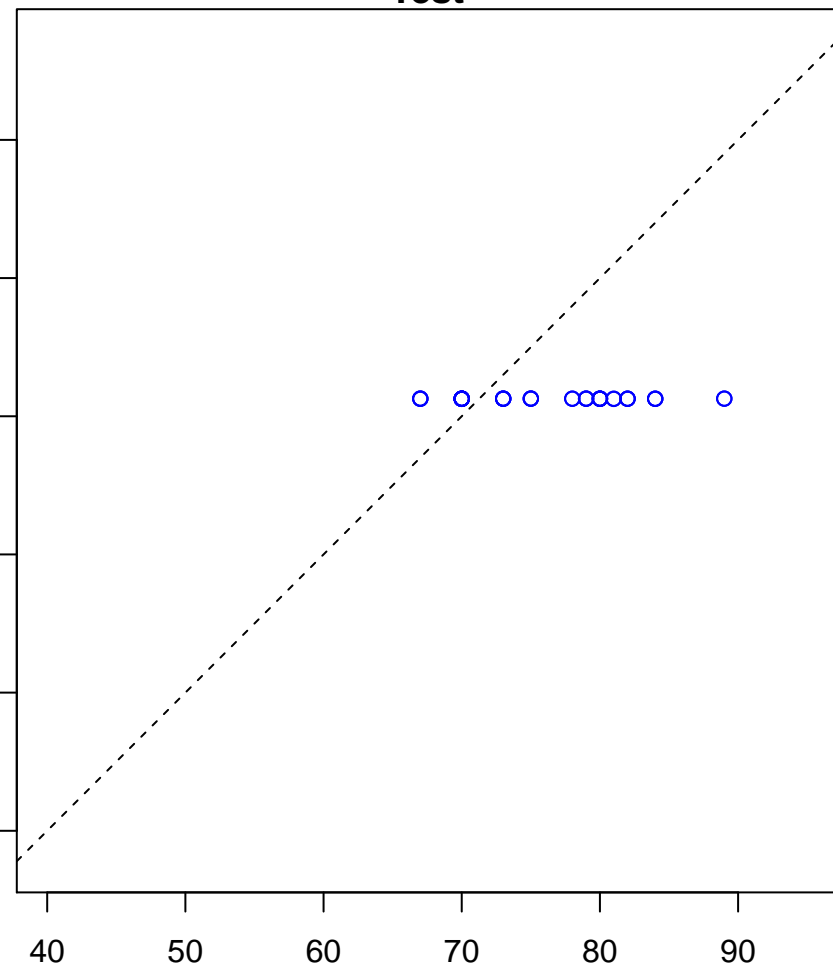


ER to Golgi vesicle-mediated transport (Score: 0.833509)

Control



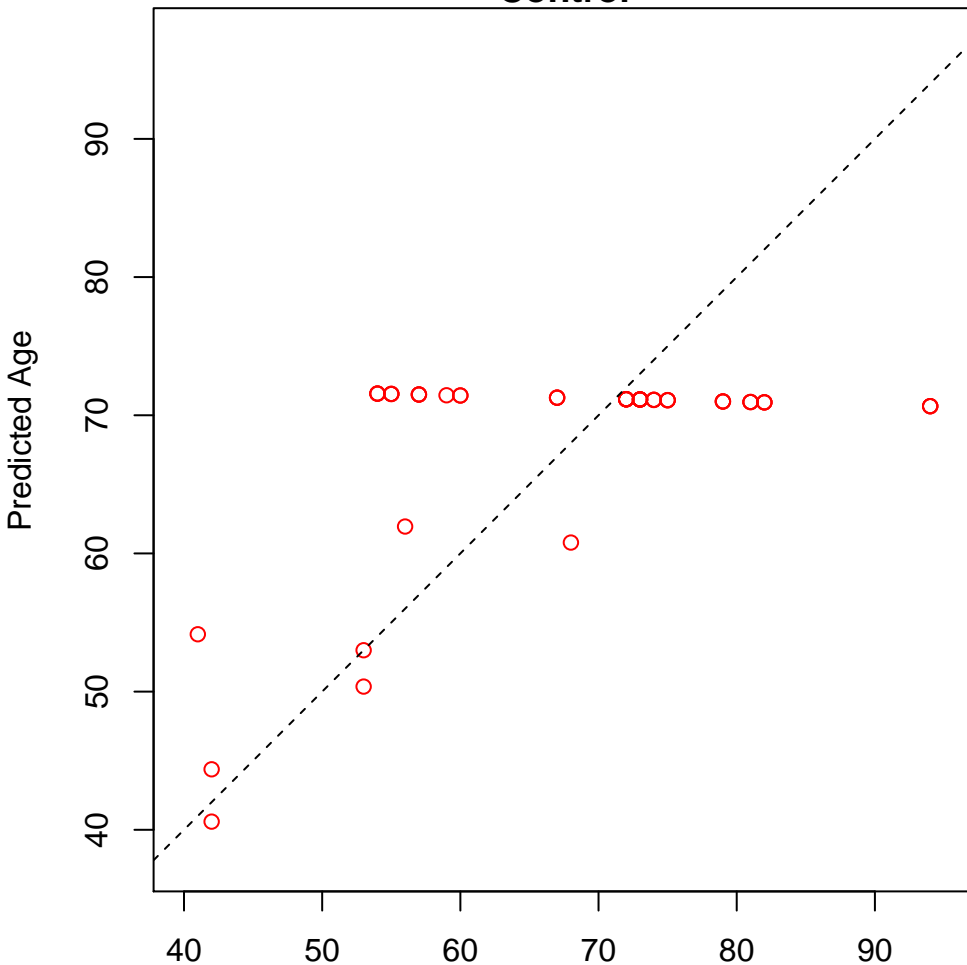
Test



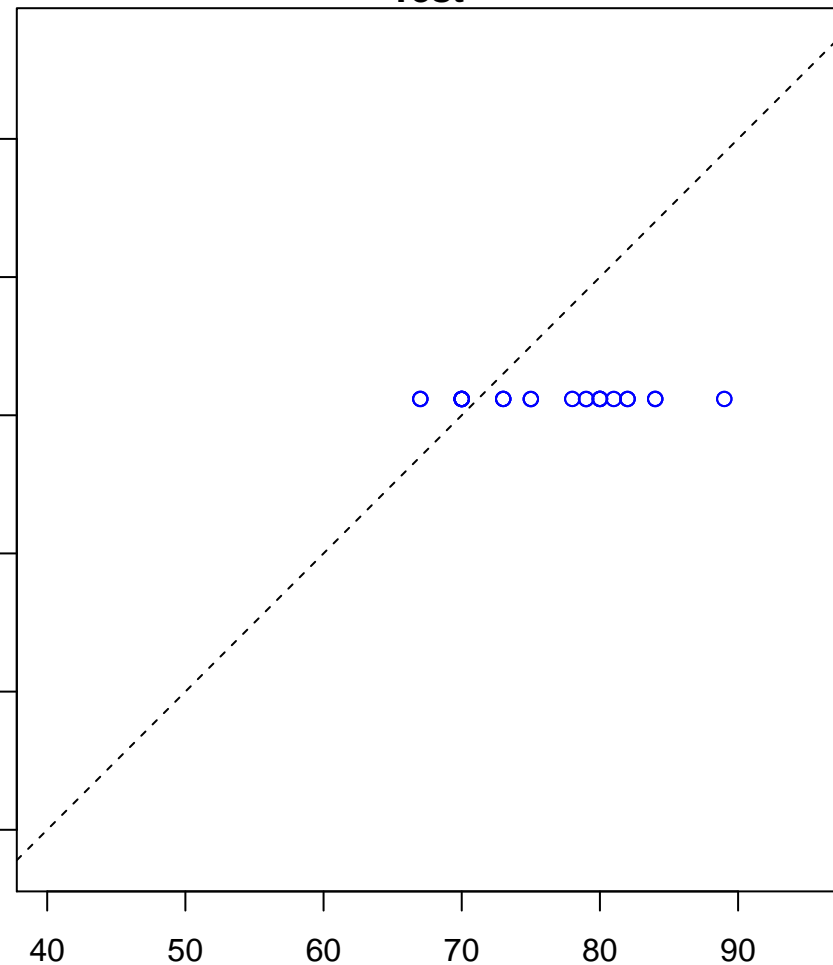
Actual Age

positive regulation of catabolic process (Score: 0.833324)

Control

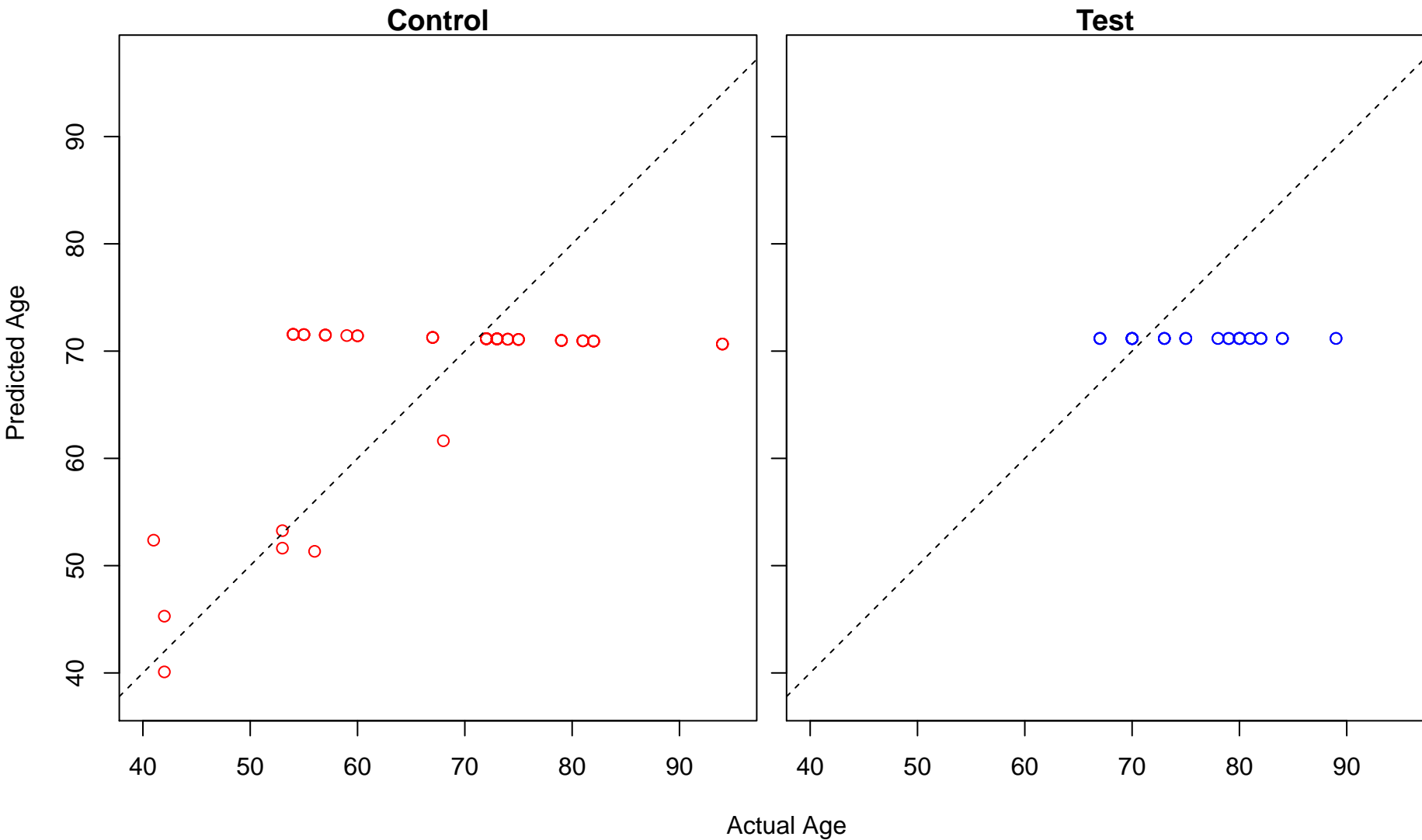


Test

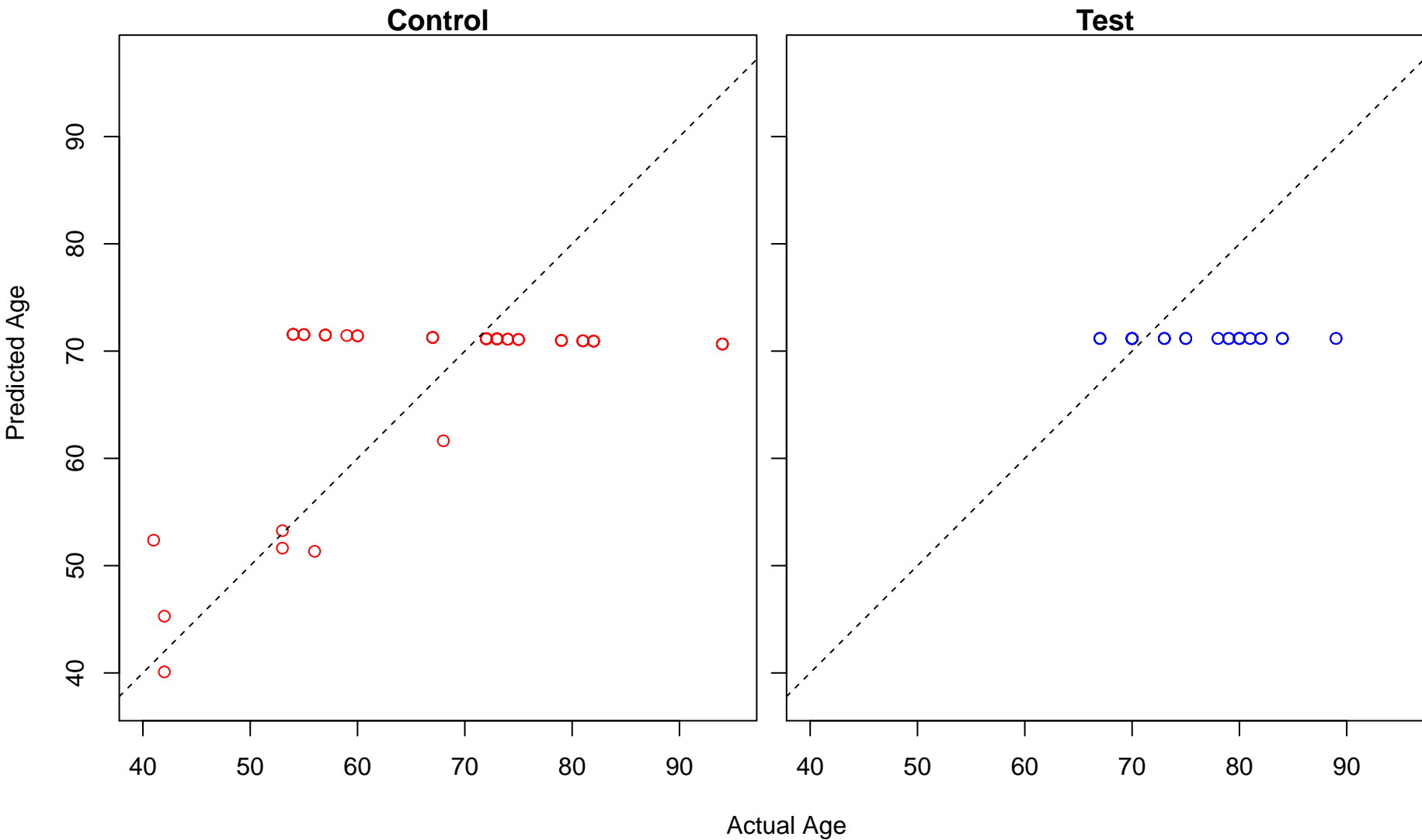


Actual Age

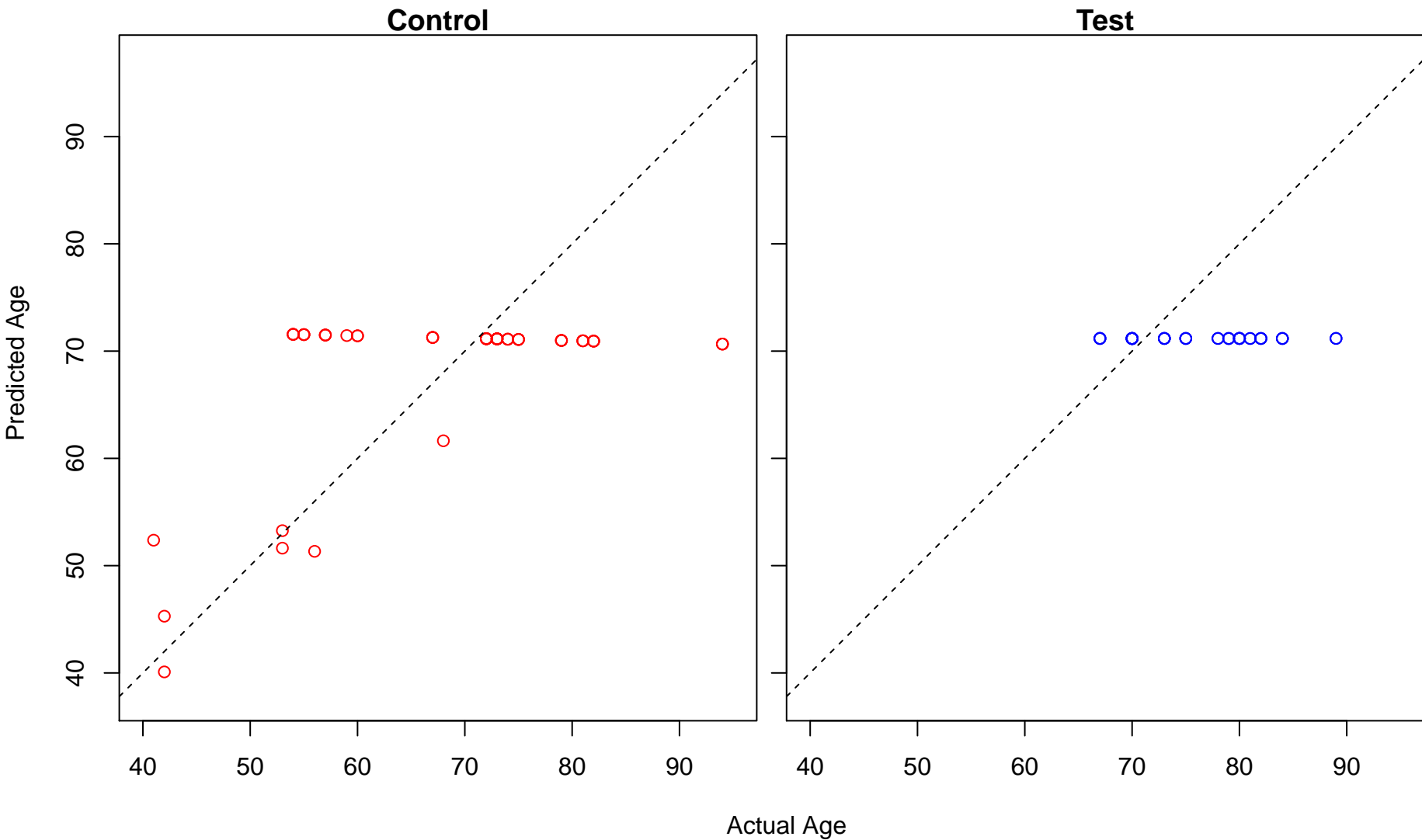
Wnt signaling pathway (Score: 0.833128)



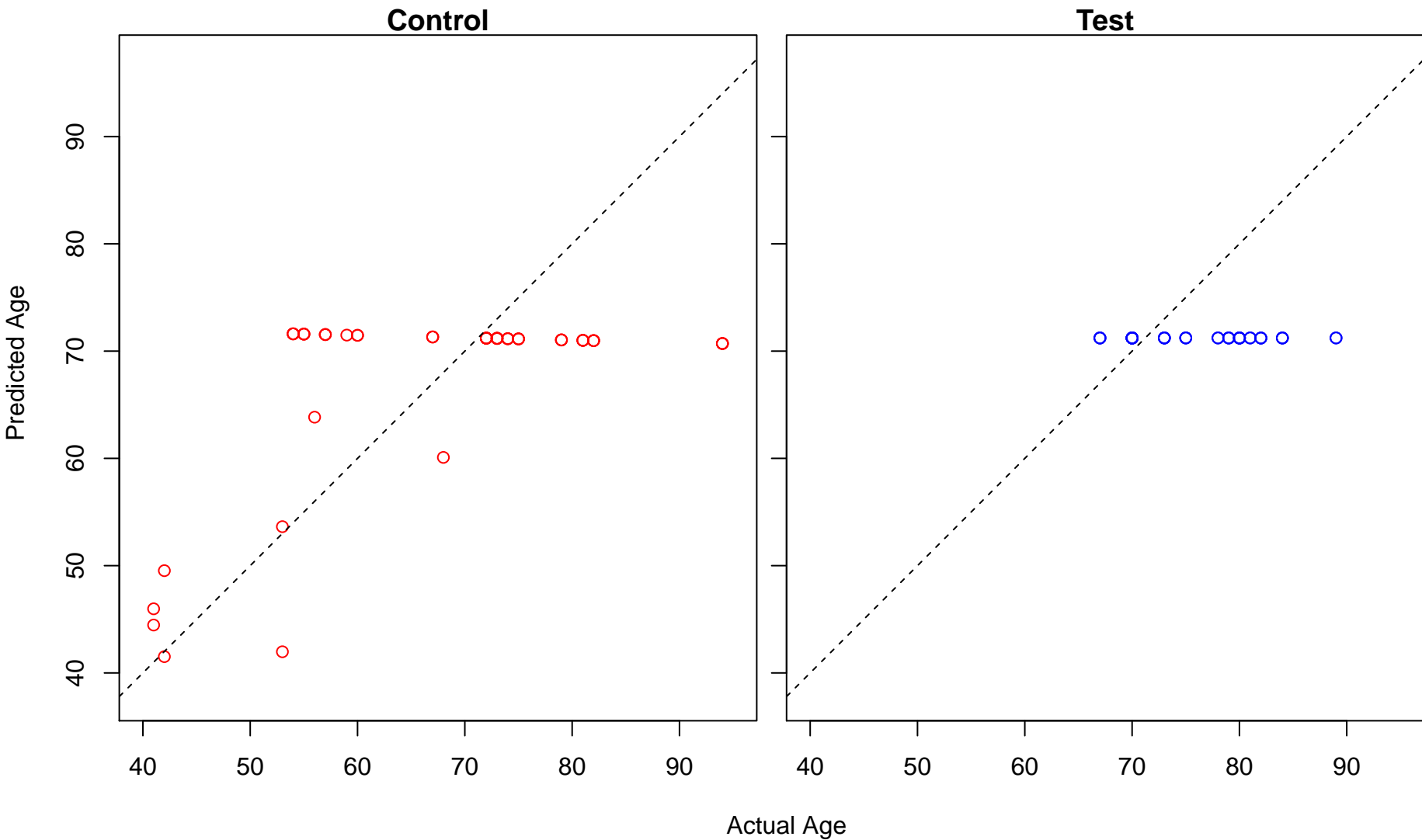
cell-cell signaling by wnt (Score: 0.833128)



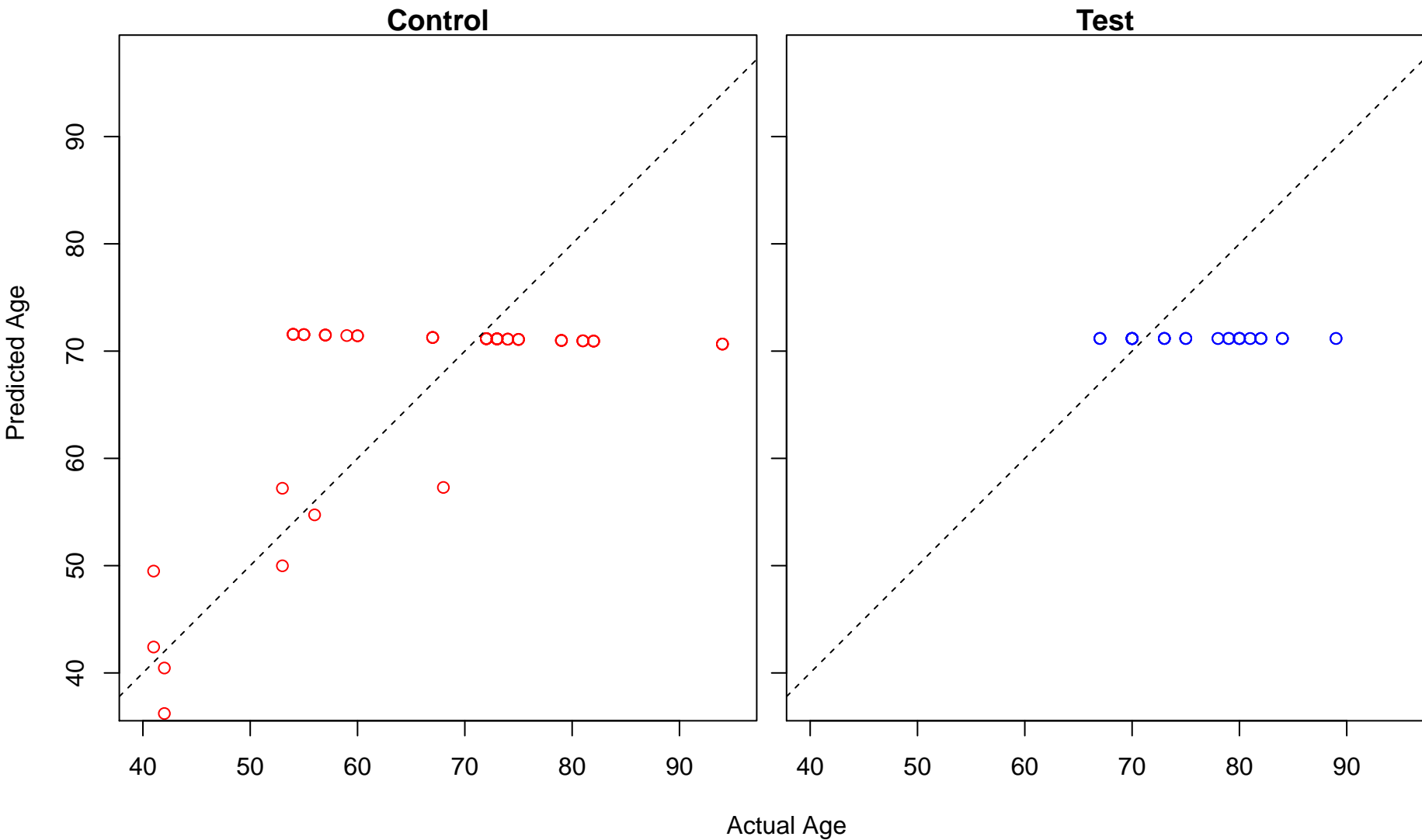
cell surface receptor signaling pathway involved in cell-cell signaling (Score: 0.833128)



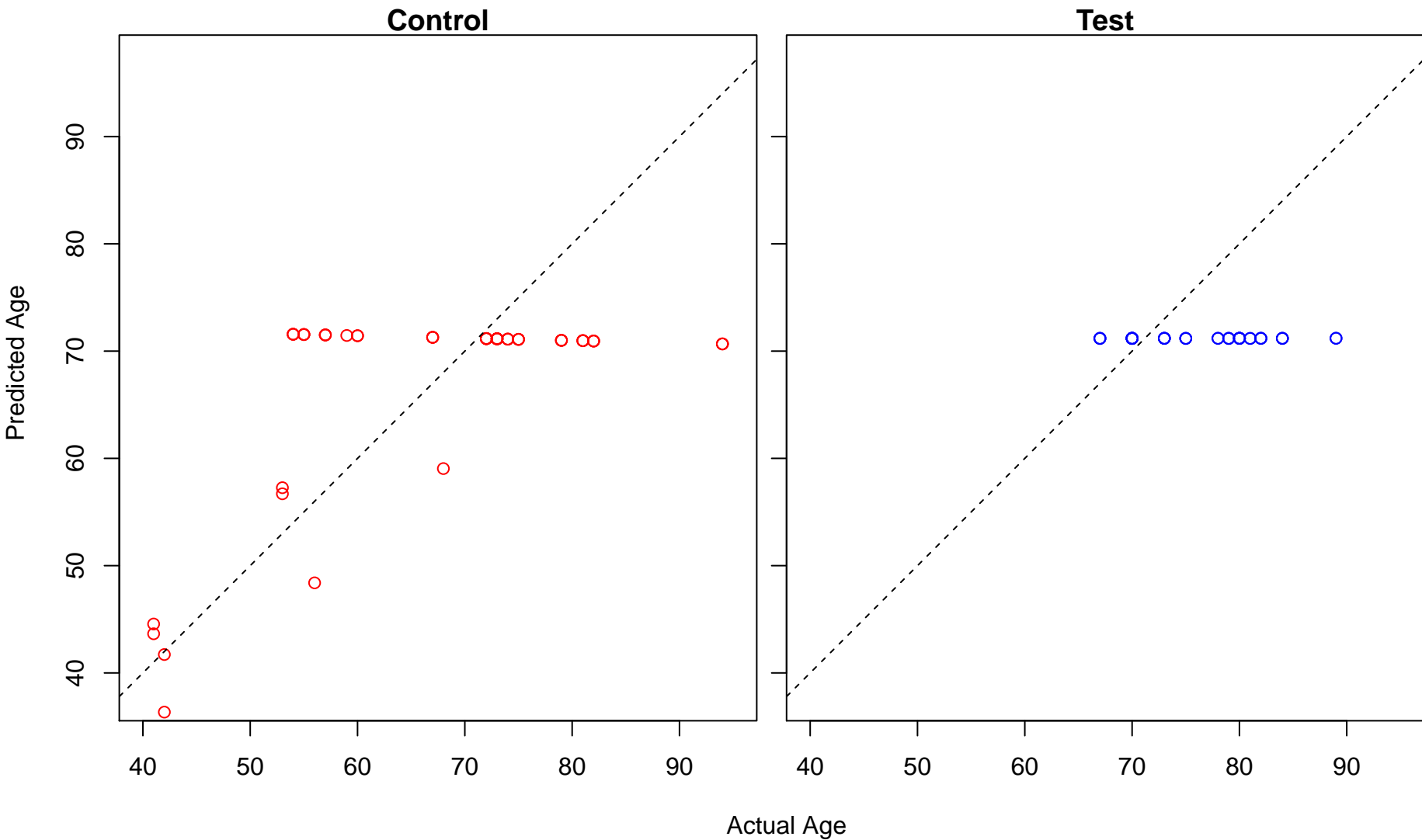
antigen processing and presentation of peptide antigen via MHC class I (Score: 0.832974)



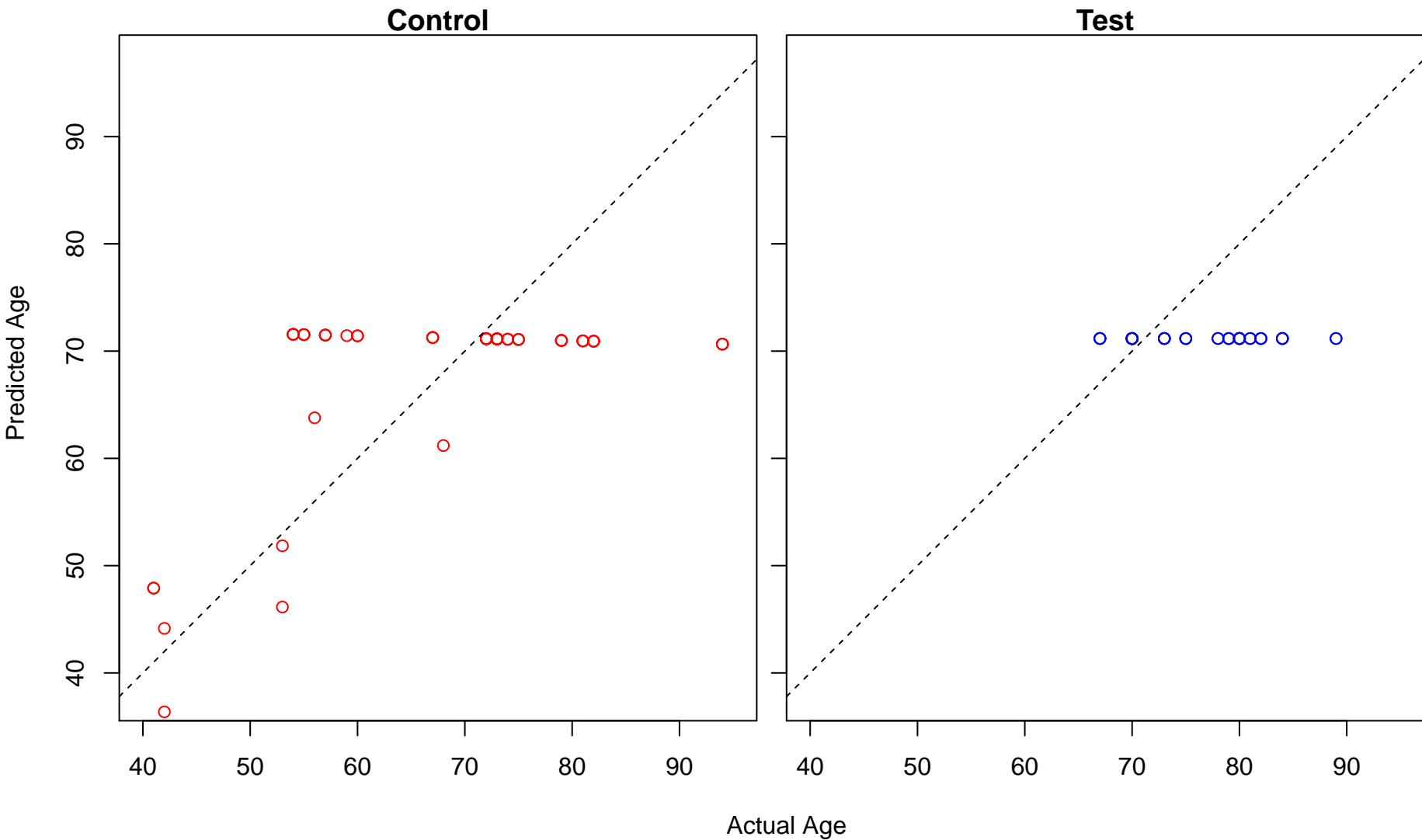
transmembrane transport (Score: 0.832969)



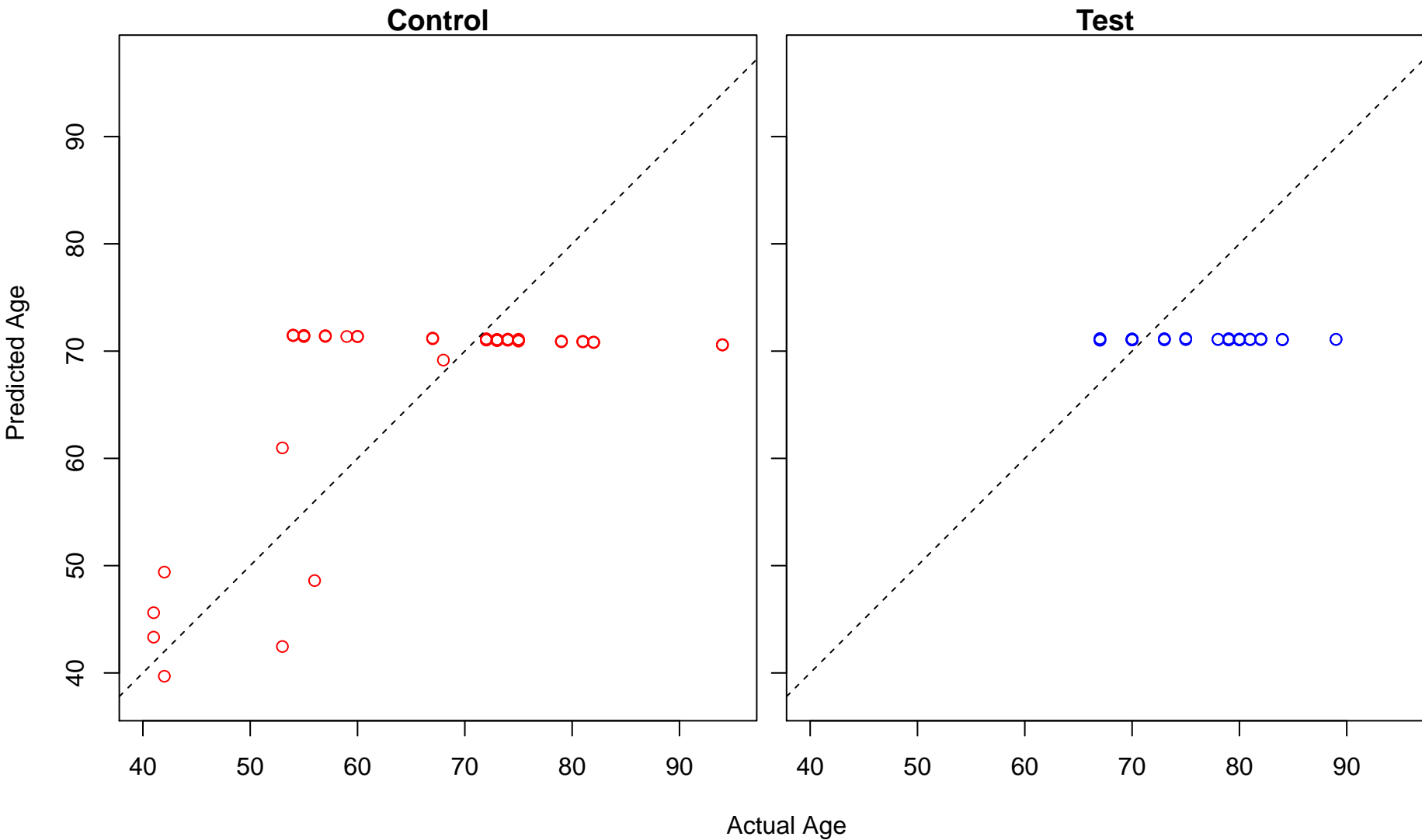
regulation of ubiquitin-protein transferase activity (Score: 0.832957)



positive regulation of cellular catabolic process (Score: 0.832852)

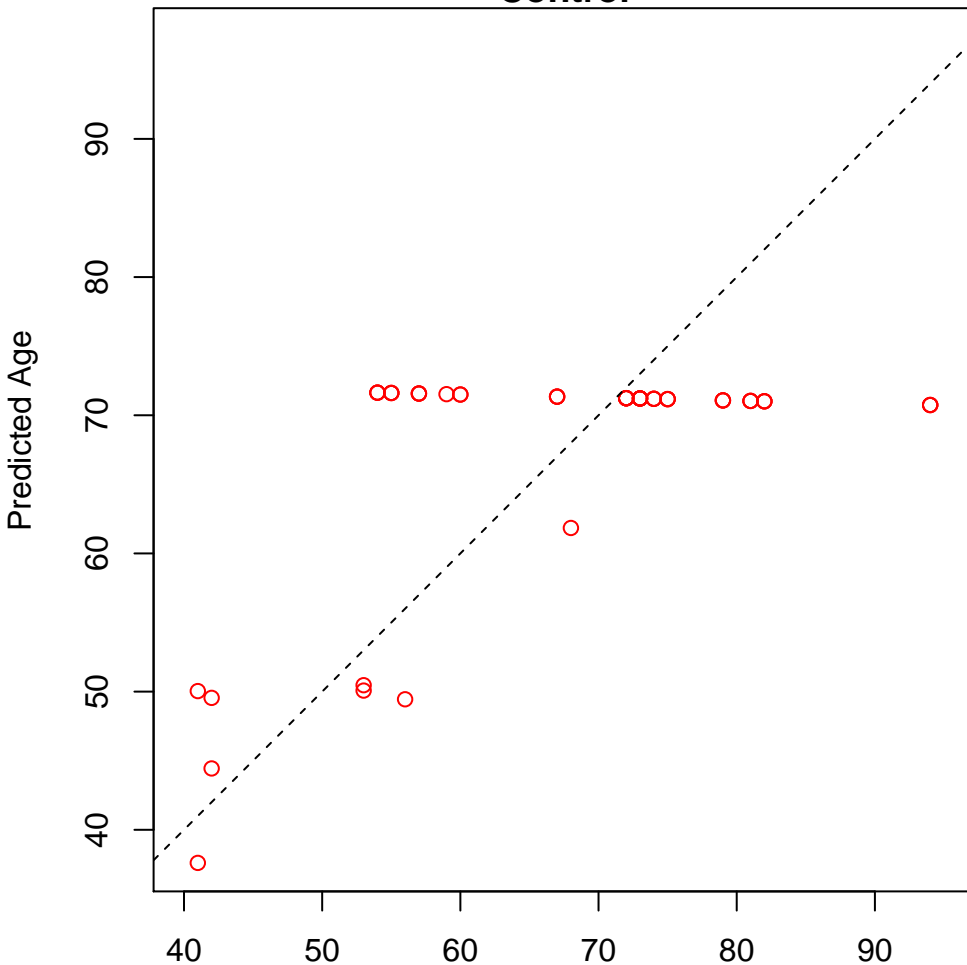


positive regulation of peptidyl-tyrosine phosphorylation (Score: 0.832652)

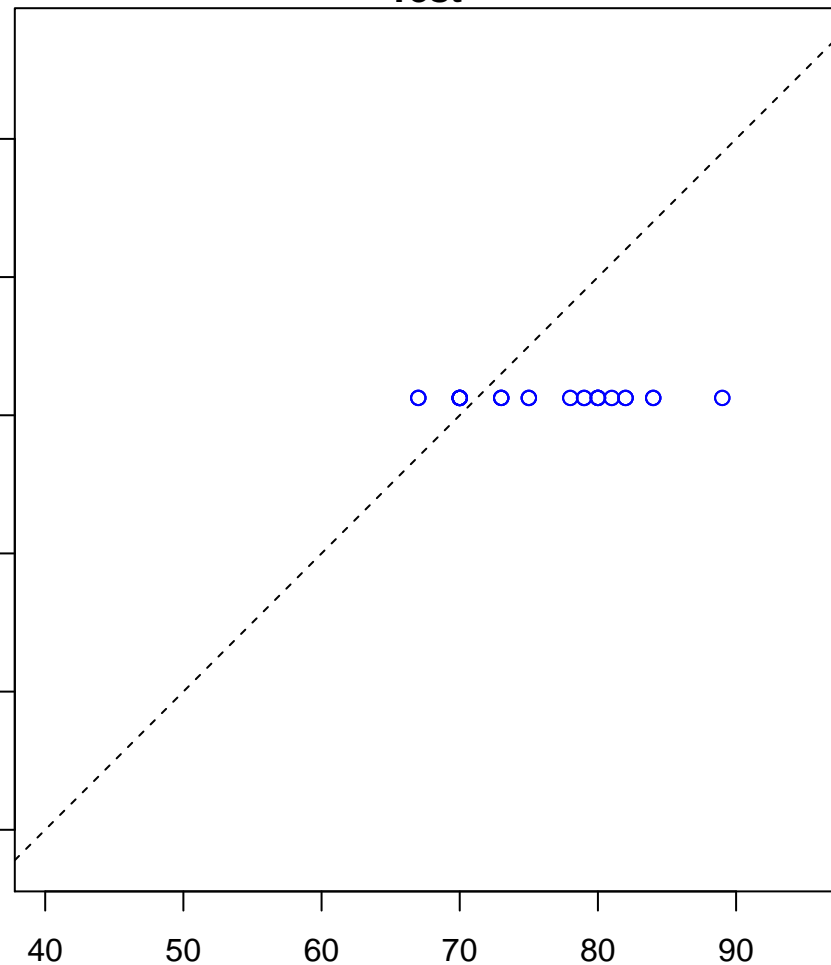


purine nucleotide catabolic process (Score: 0.832640)

Control

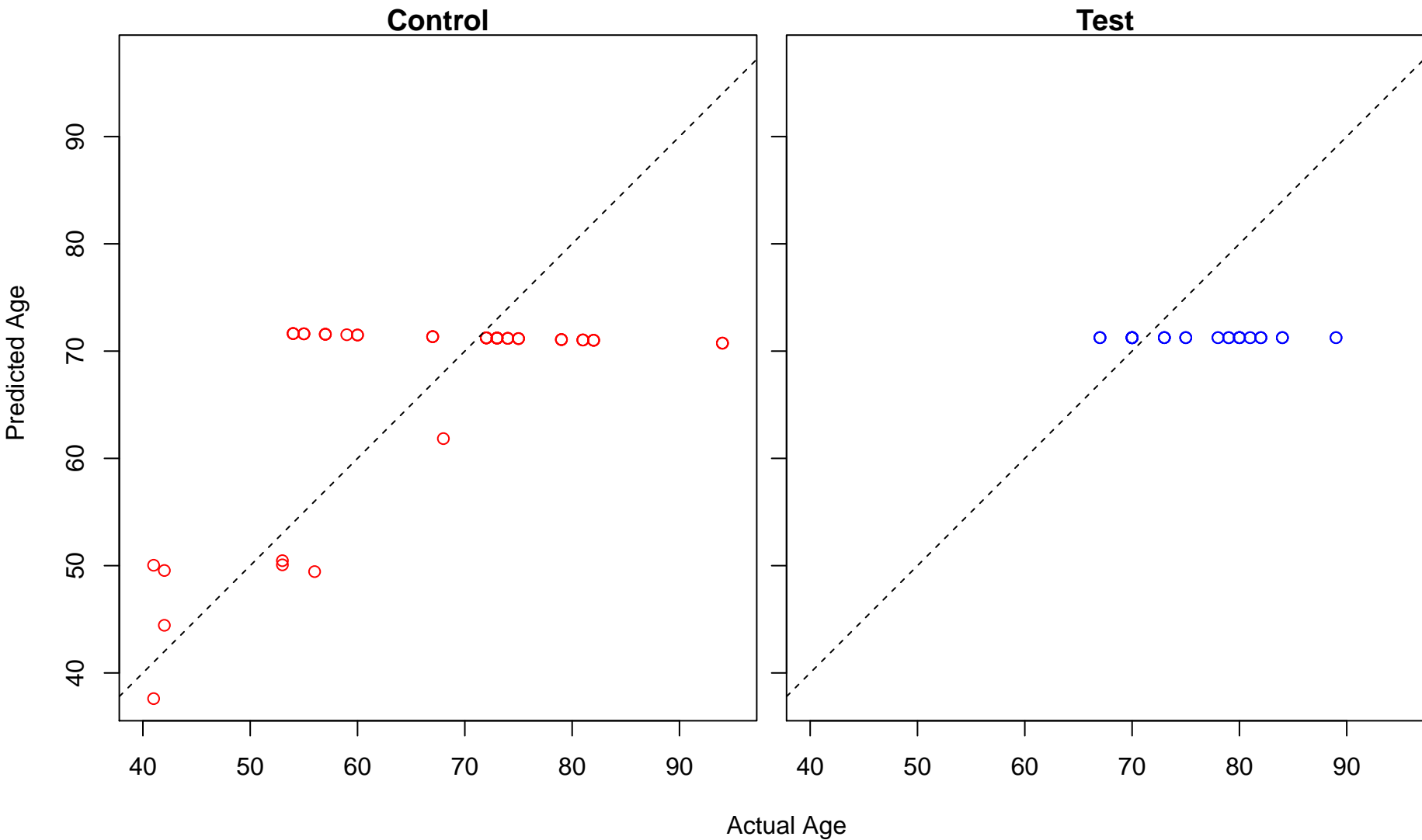


Test



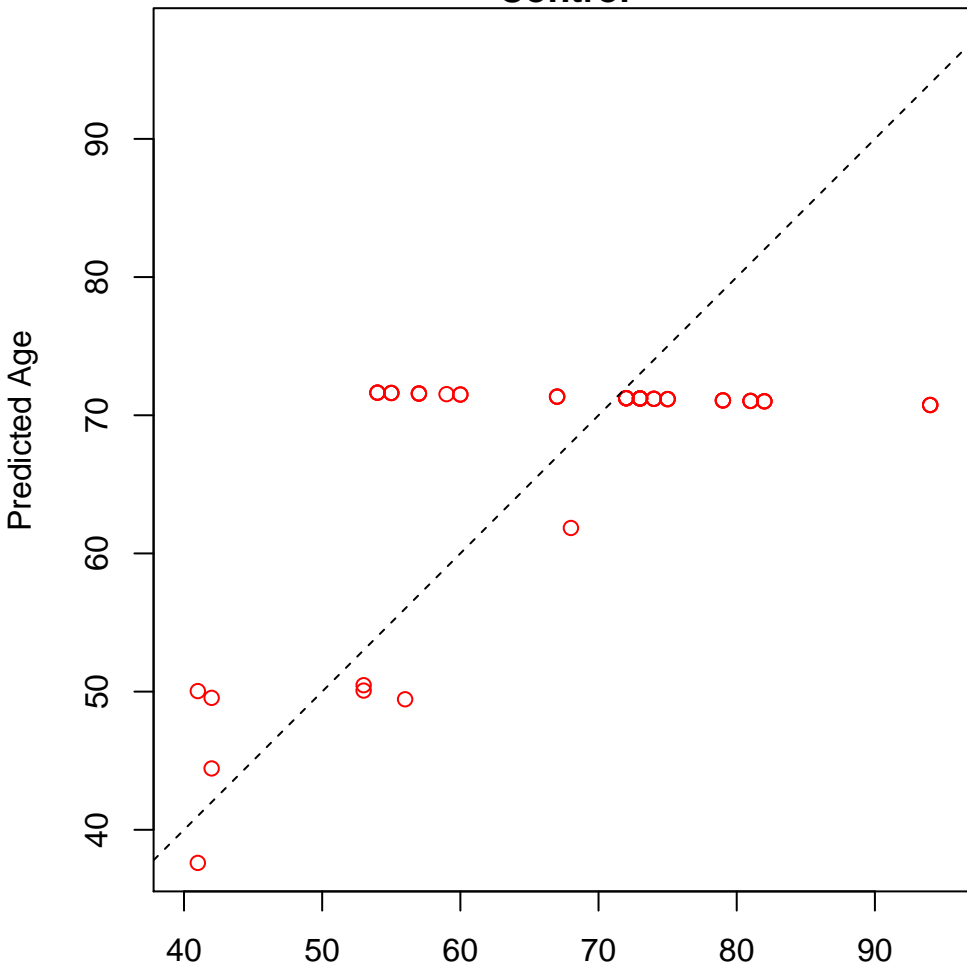
Actual Age

nucleotide catabolic process (Score: 0.832640)

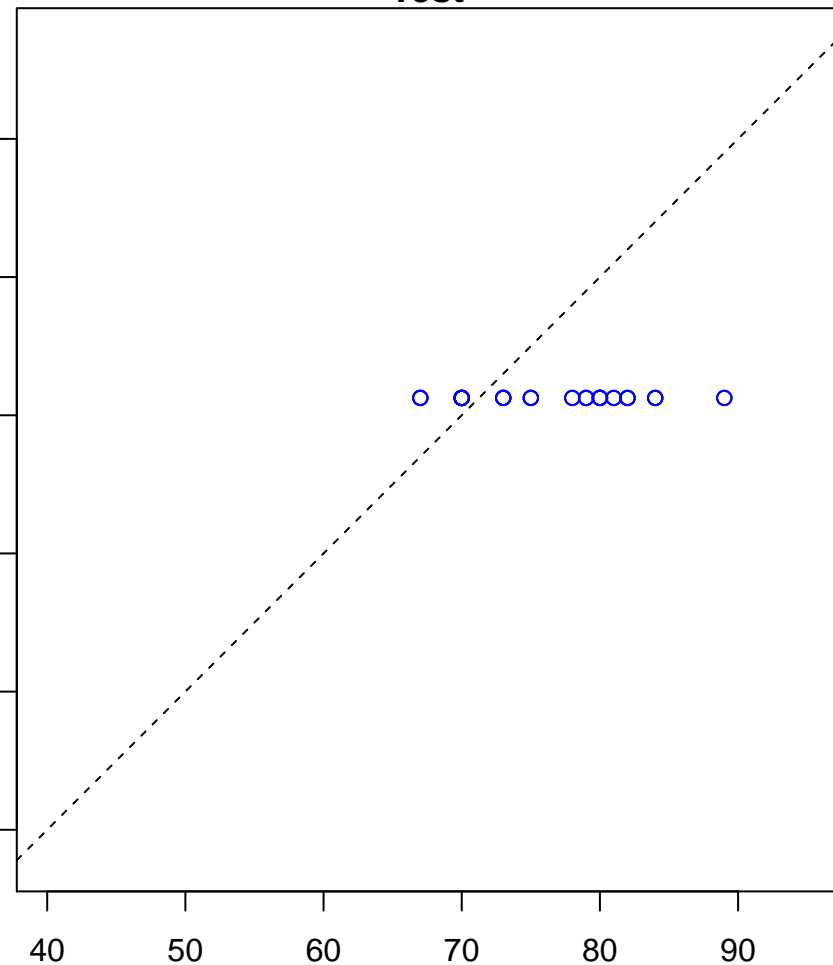


organophosphate catabolic process (Score: 0.832640)

Control

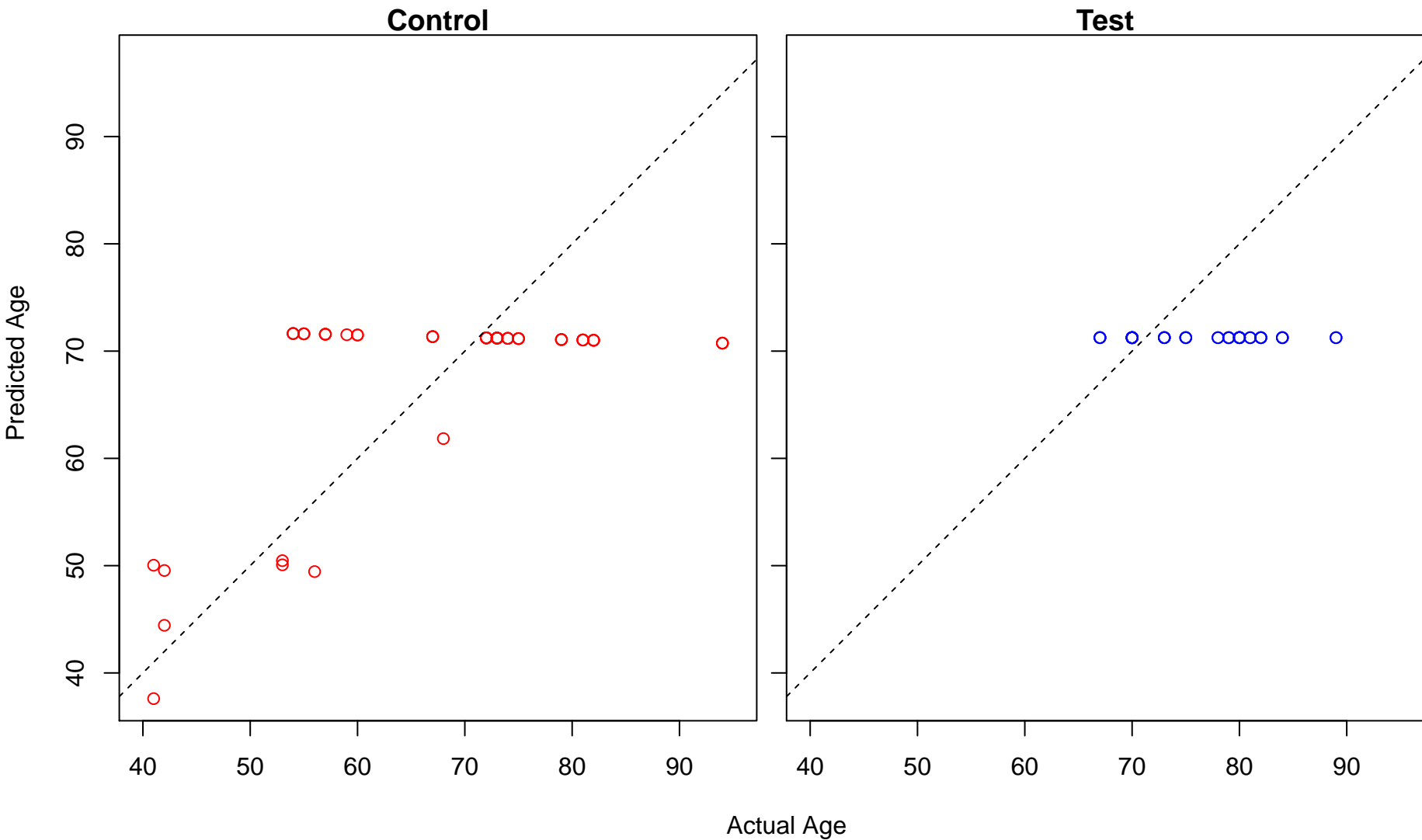


Test



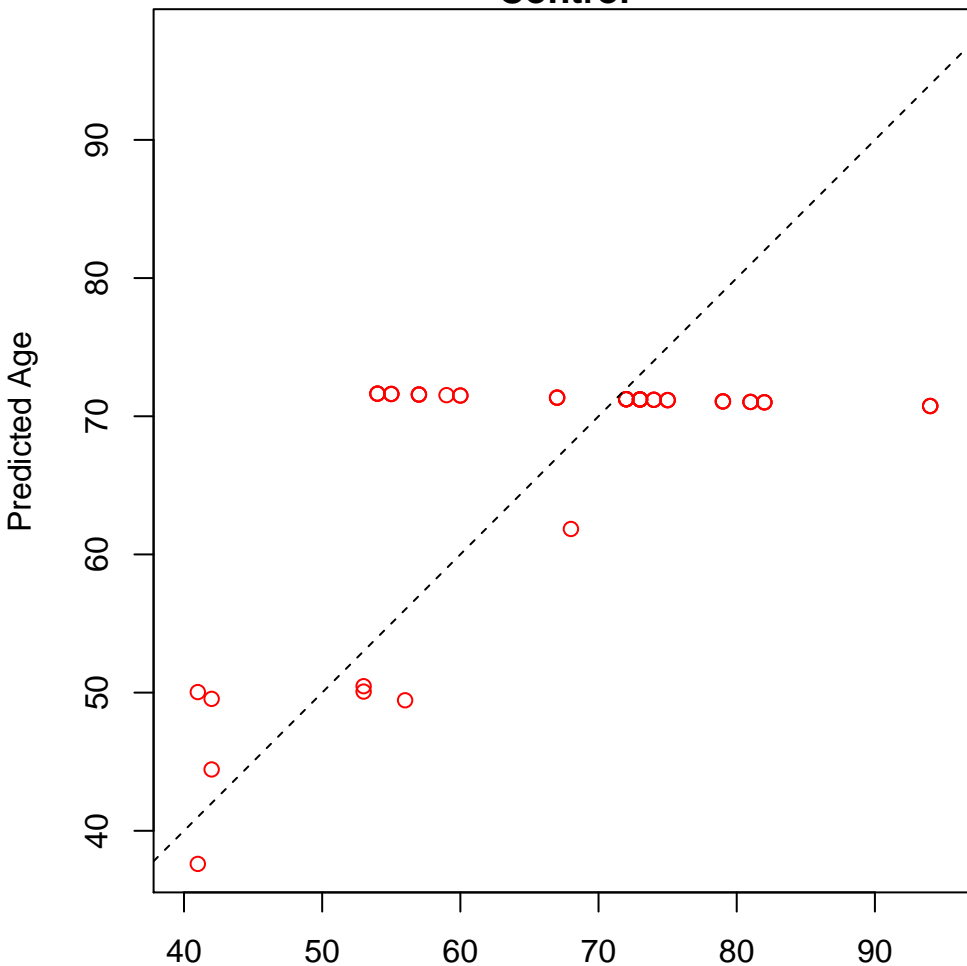
Actual Age

purine-containing compound catabolic process (Score: 0.832640)

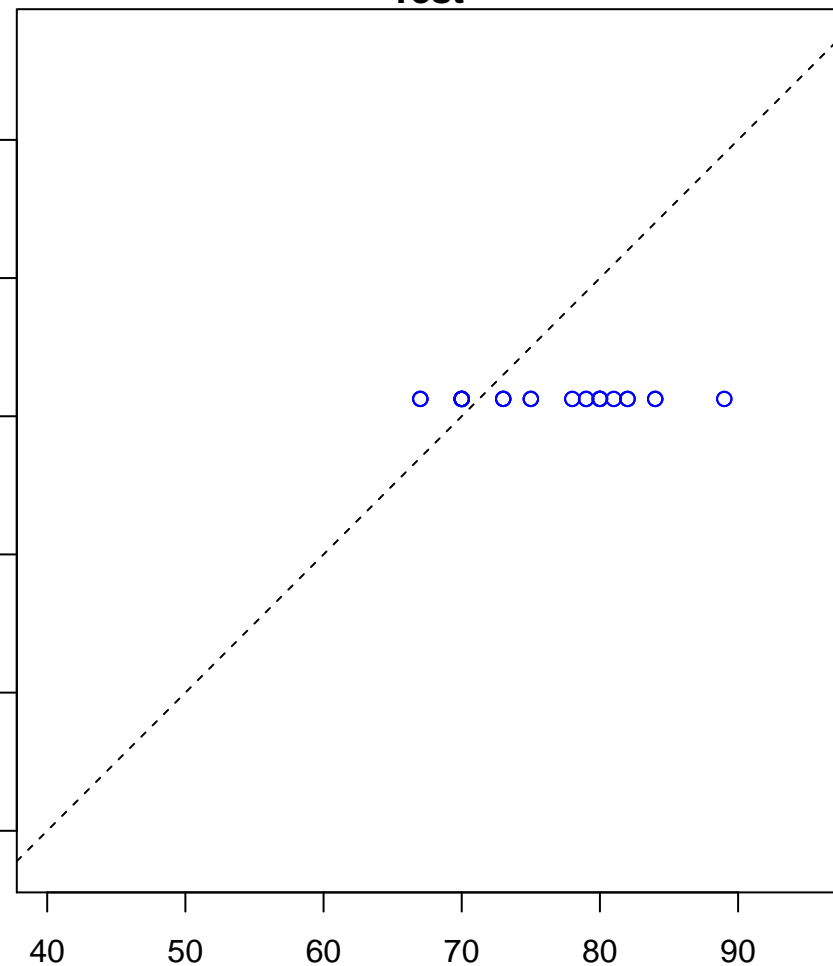


nucleoside phosphate catabolic process (Score: 0.832640)

Control



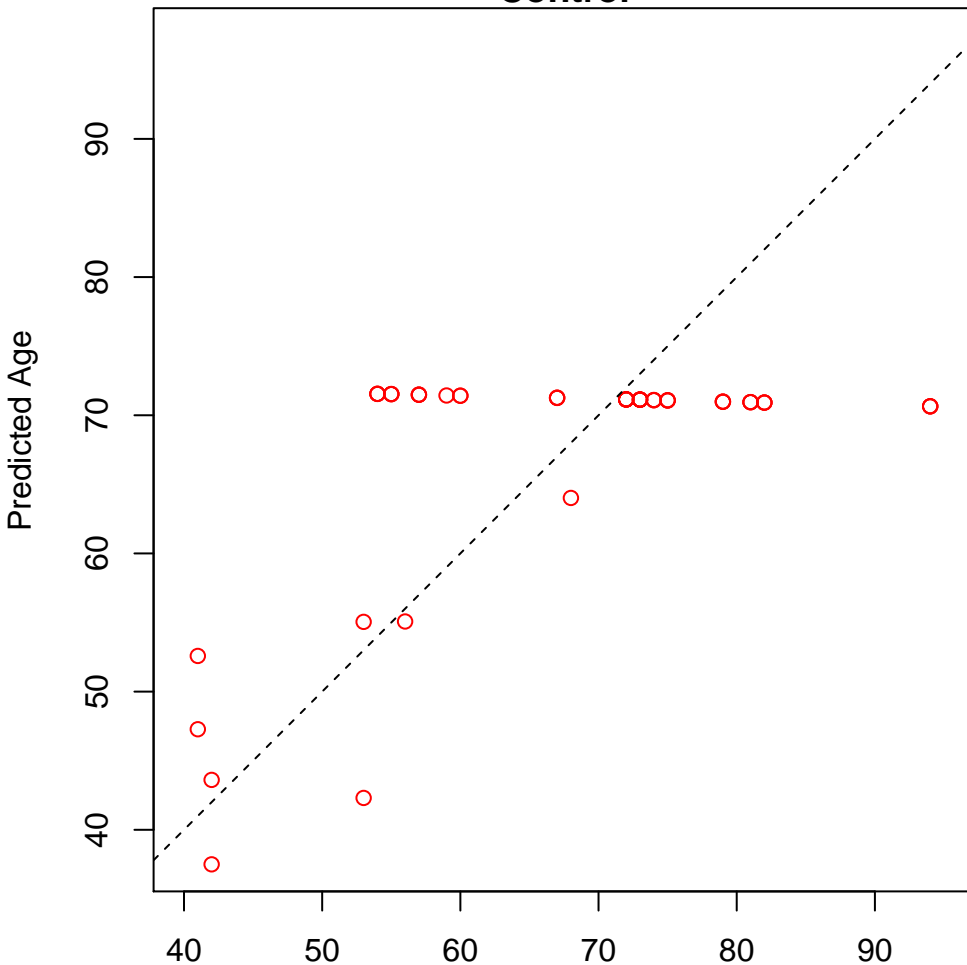
Test



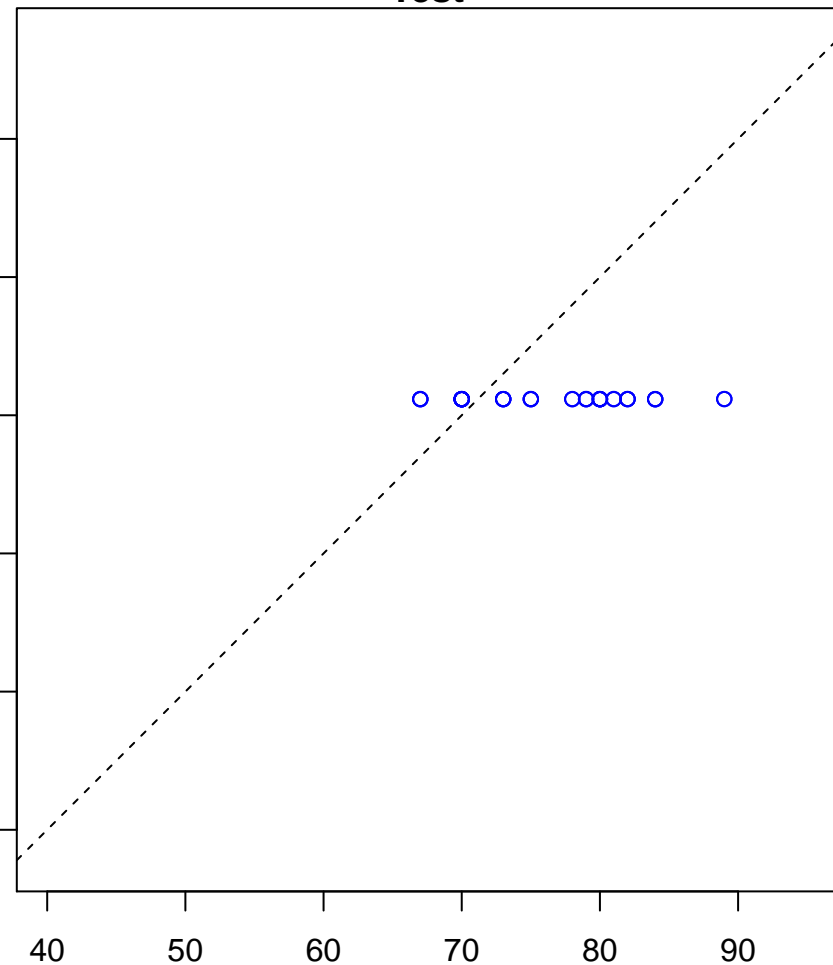
Actual Age

regulation of stem cell differentiation (Score: 0.832628)

Control

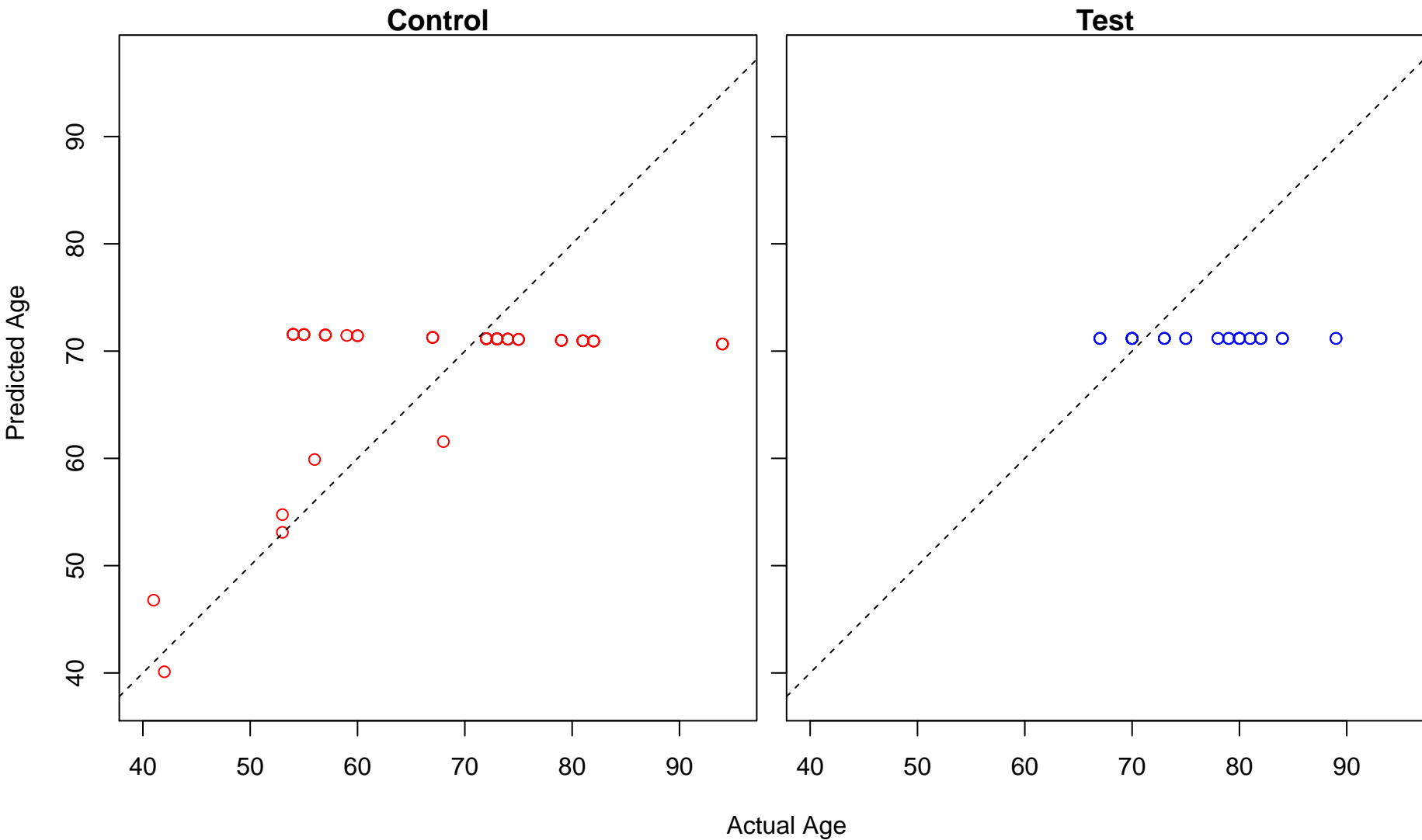


Test

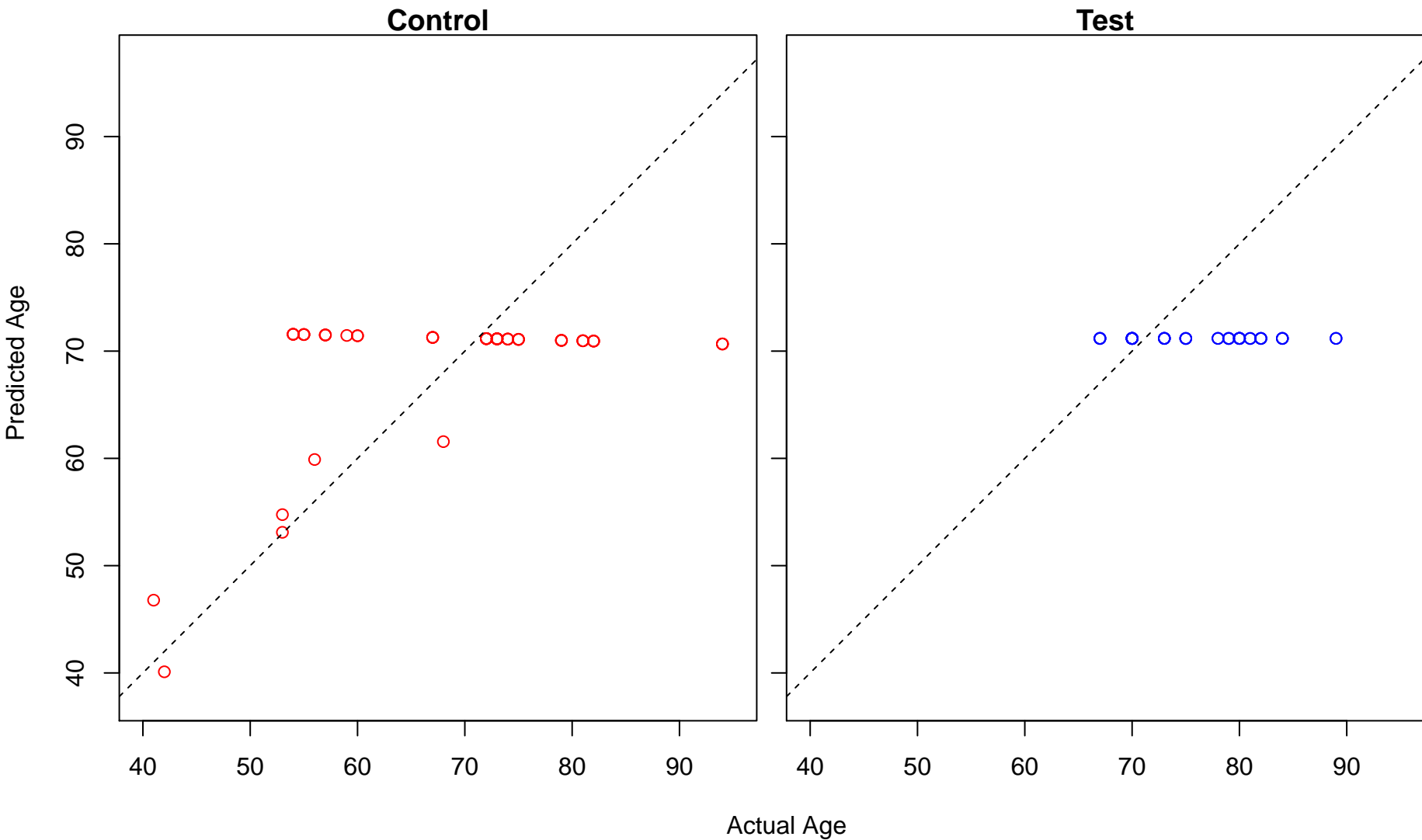


Actual Age

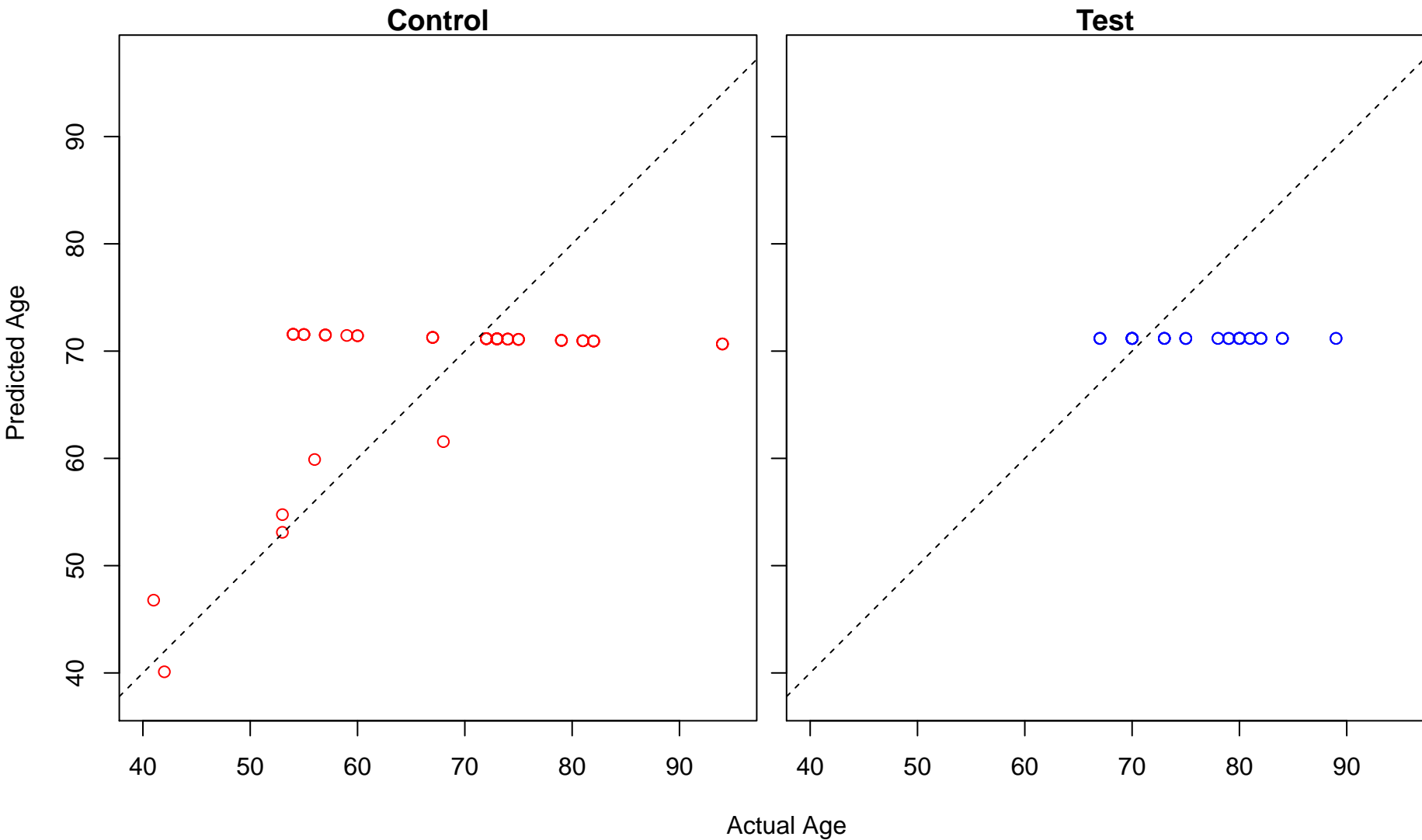
immune response-activating cell surface receptor signaling pathway (Score: 0.832618)



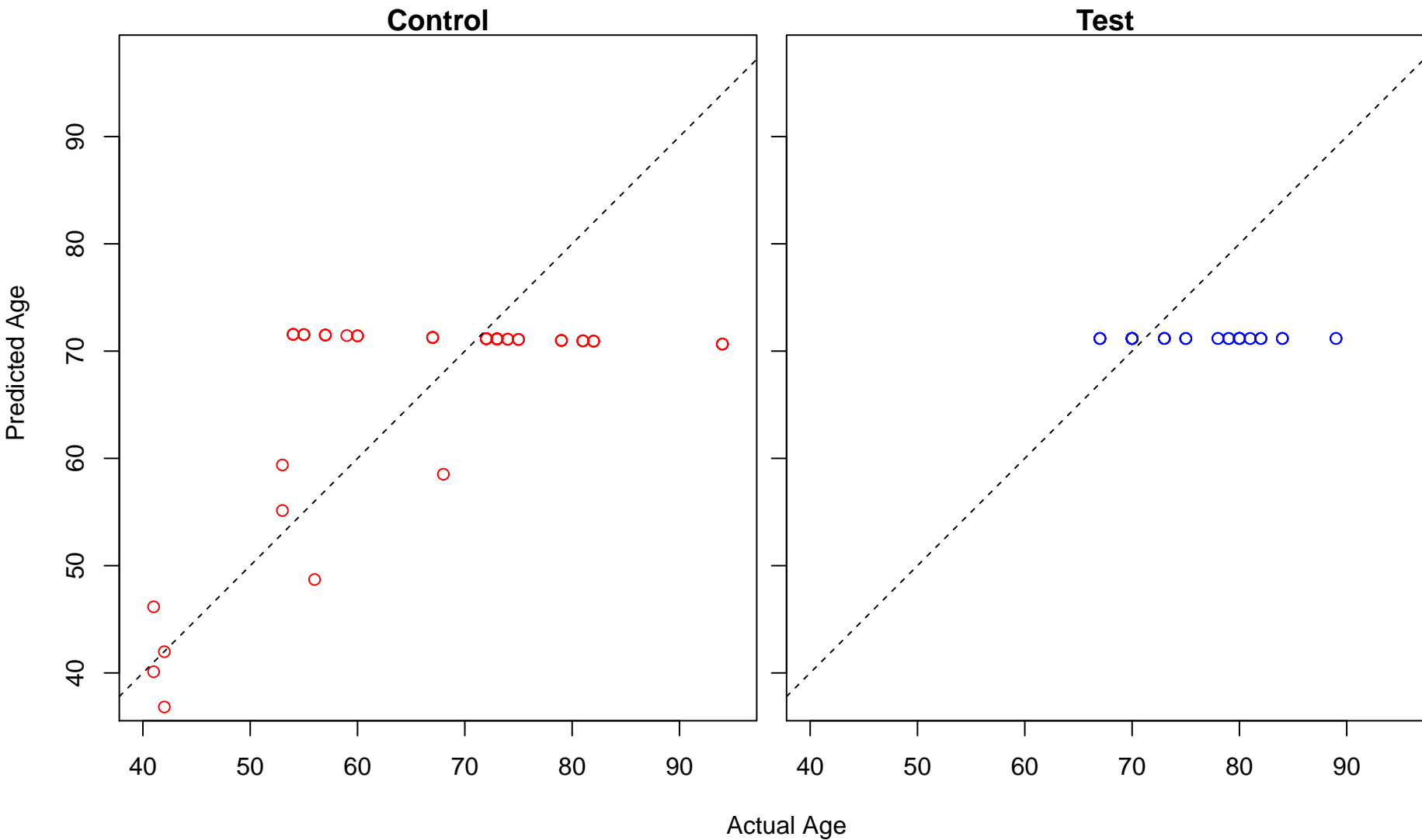
immune response–regulating cell surface receptor signaling pathway (Score: 0.832618)



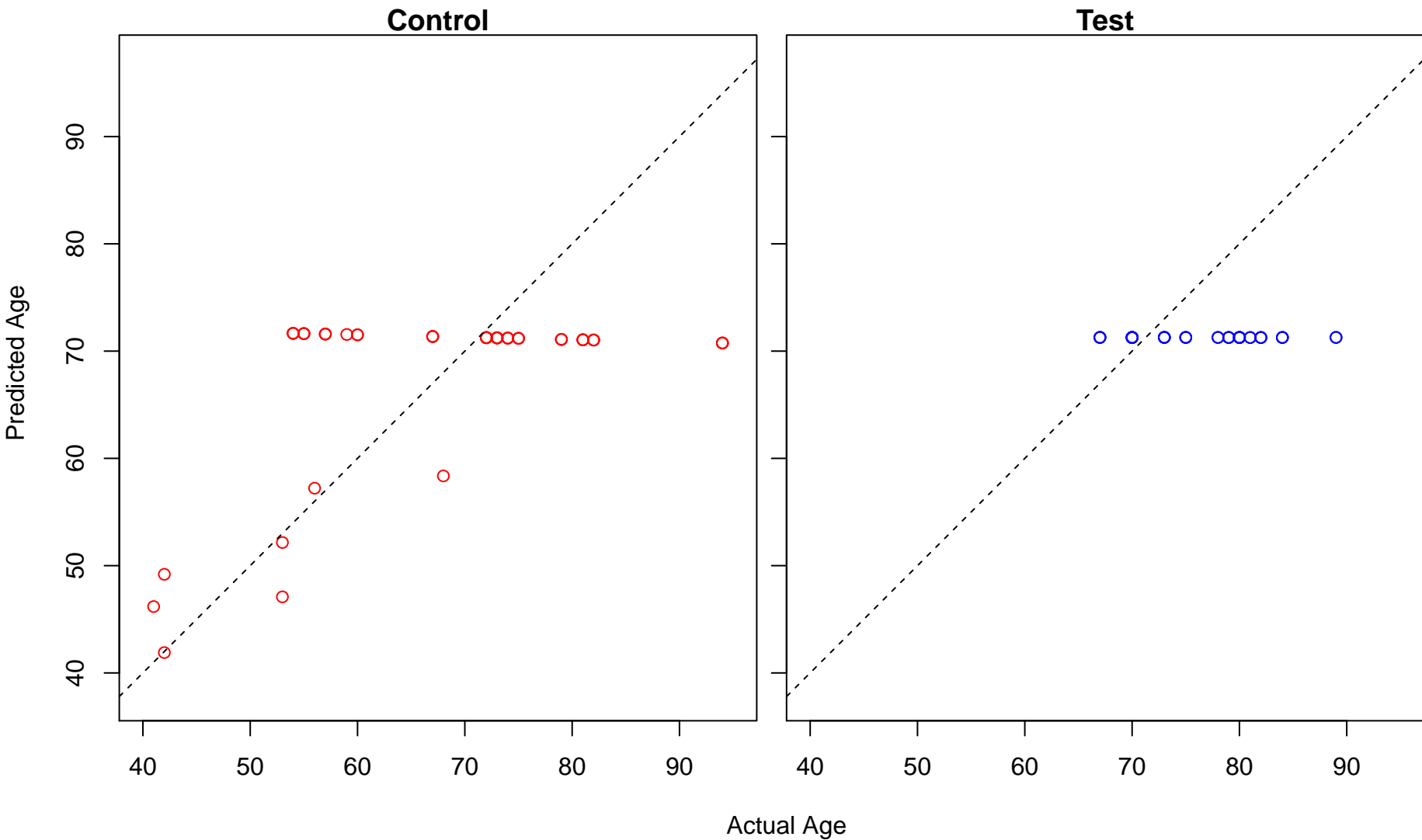
Fc receptor signaling pathway (Score: 0.832618)



regulation of protein modification by small protein conjugation or removal (Score: 0.832325)

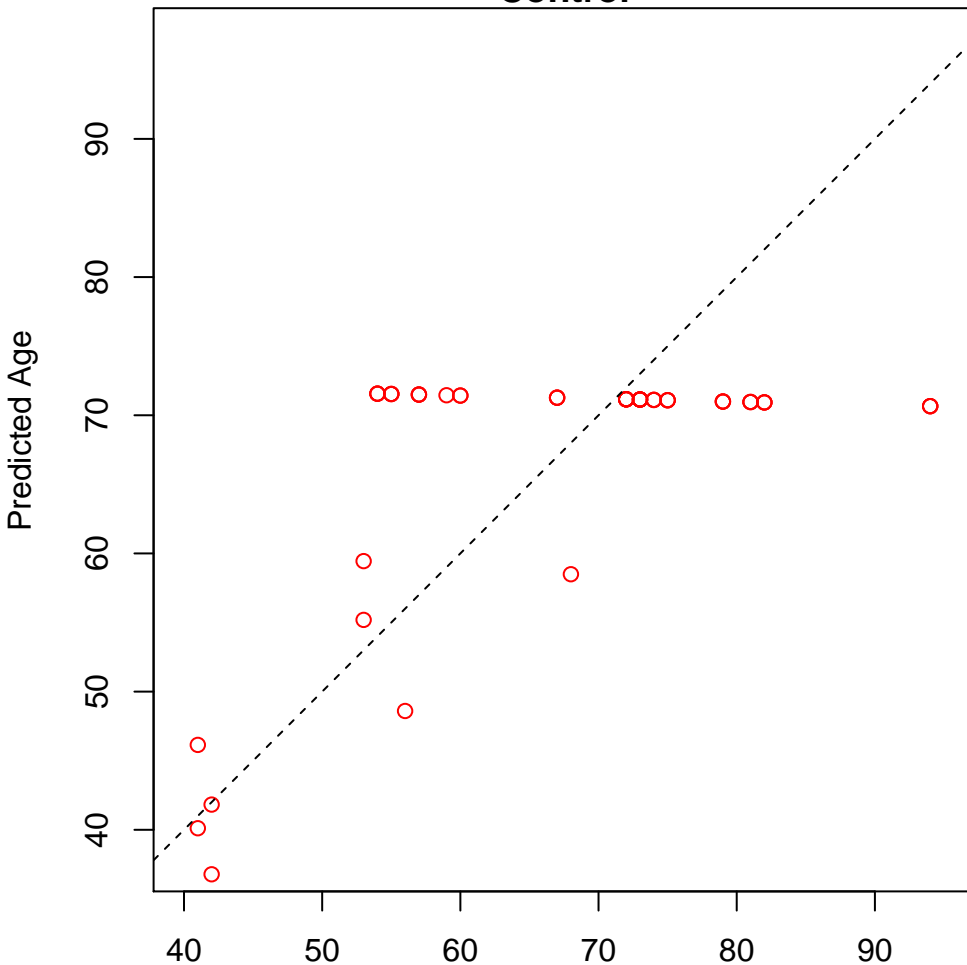


4-hydroxyproline metabolic process (Score: 0.832259)

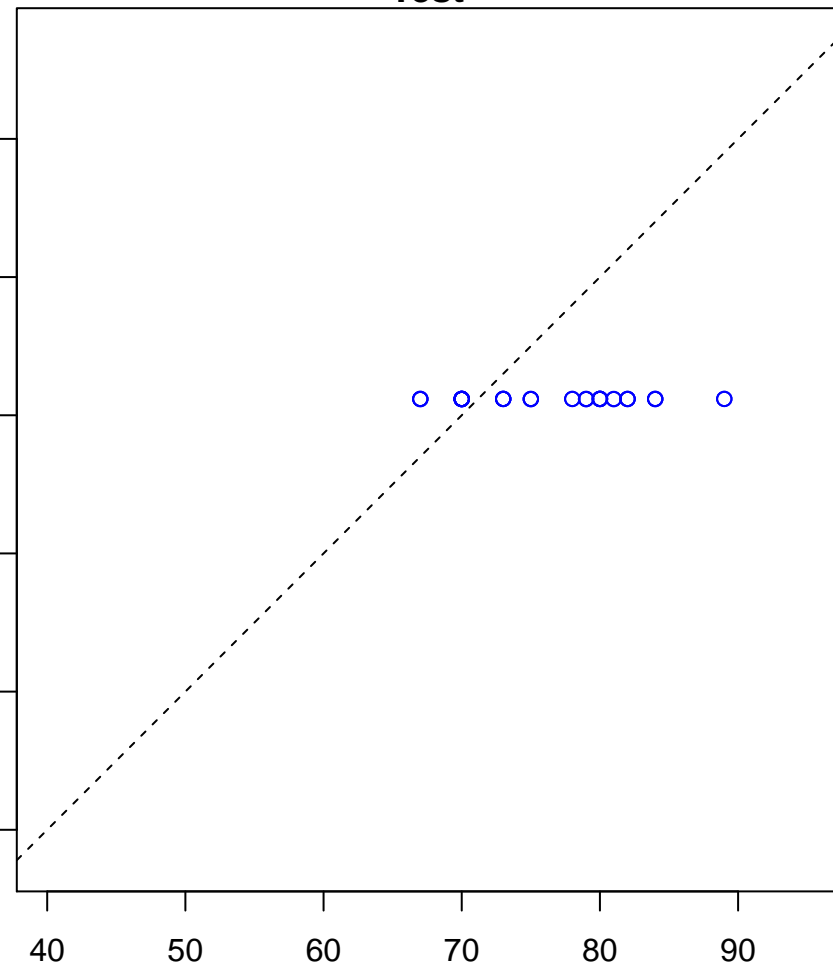


regulation of protein ubiquitination (Score: 0.832052)

Control

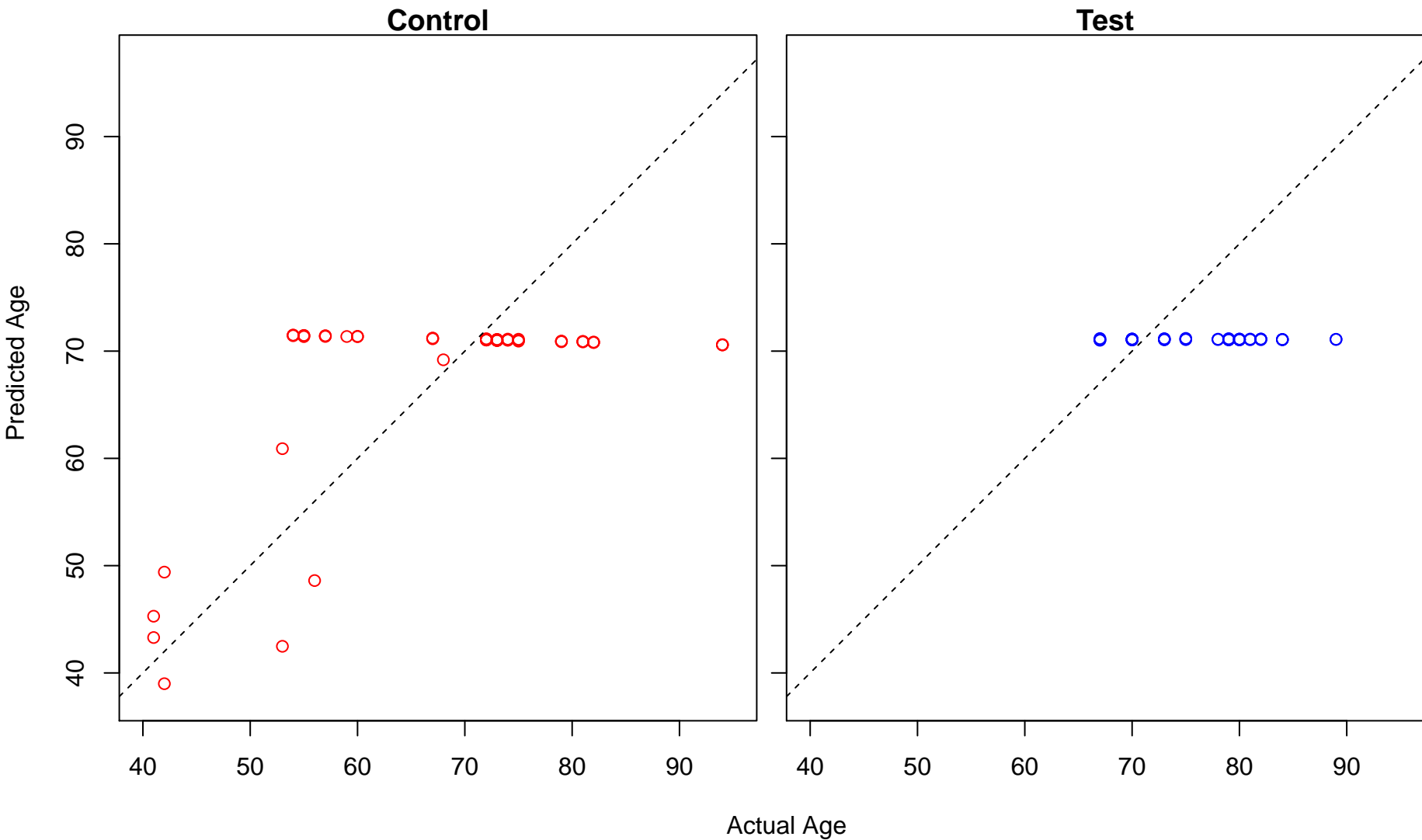


Test

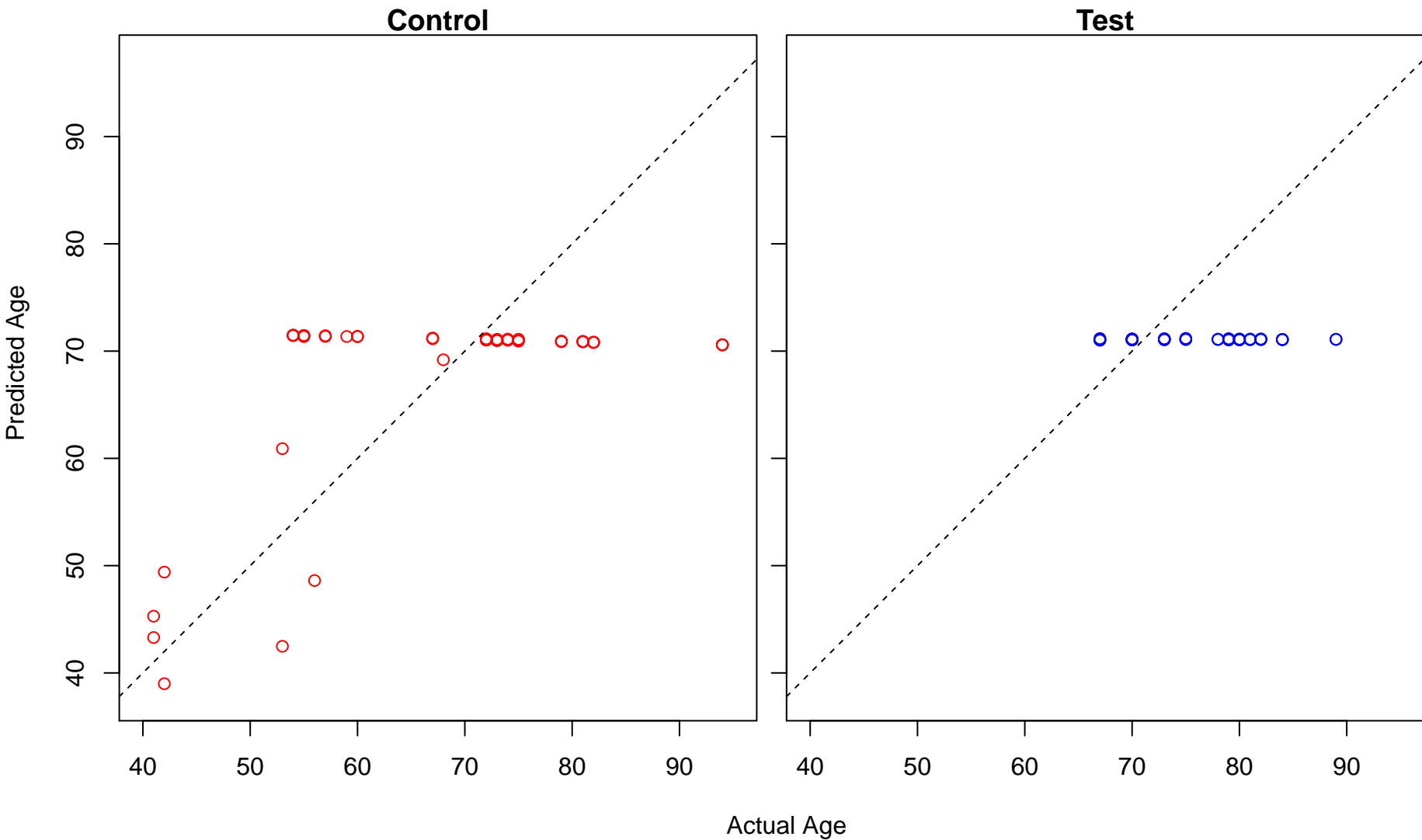


Actual Age

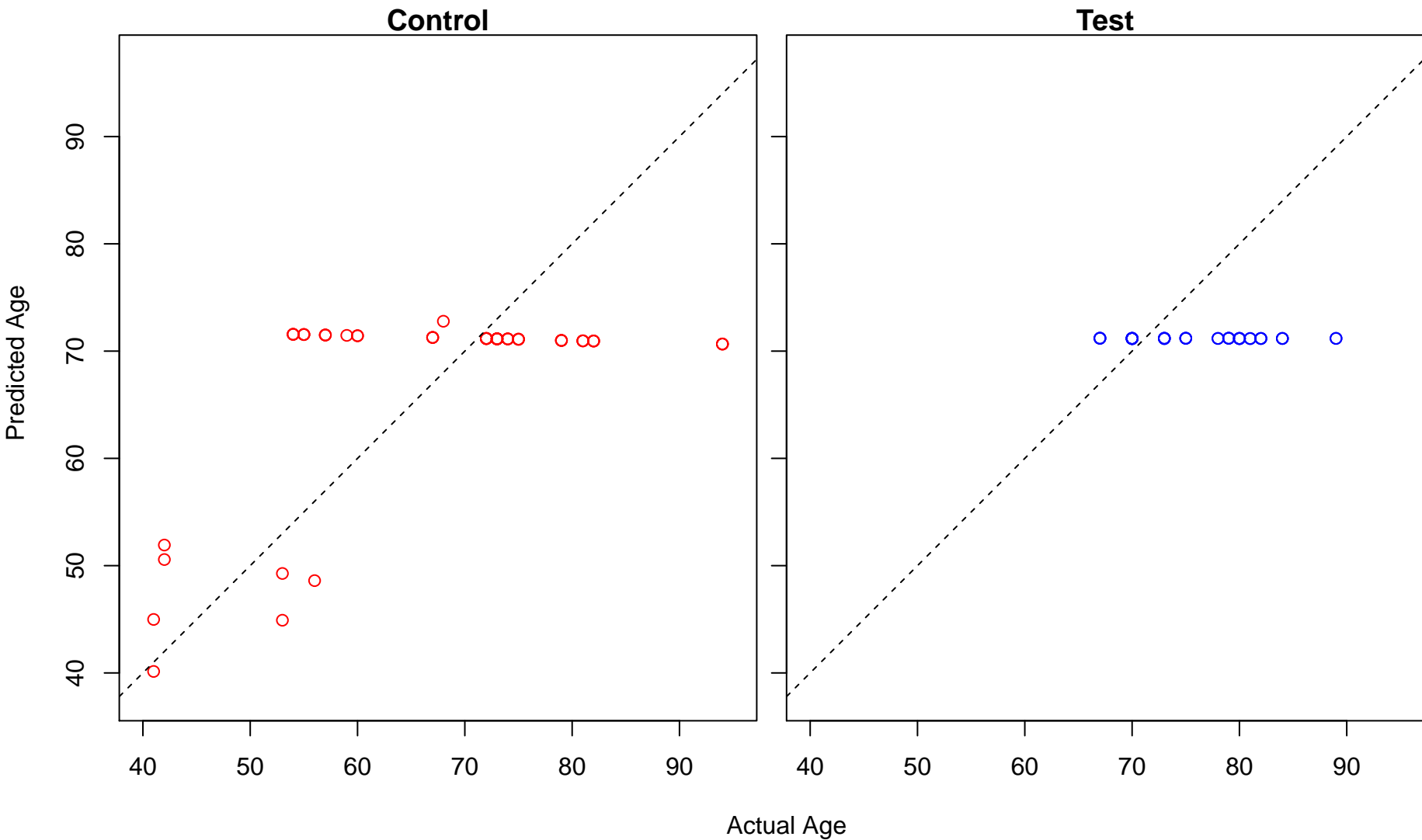
viral entry into host cell (Score: 0.831870)



receptor-mediated virion attachment to host cell (Score: 0.831870)

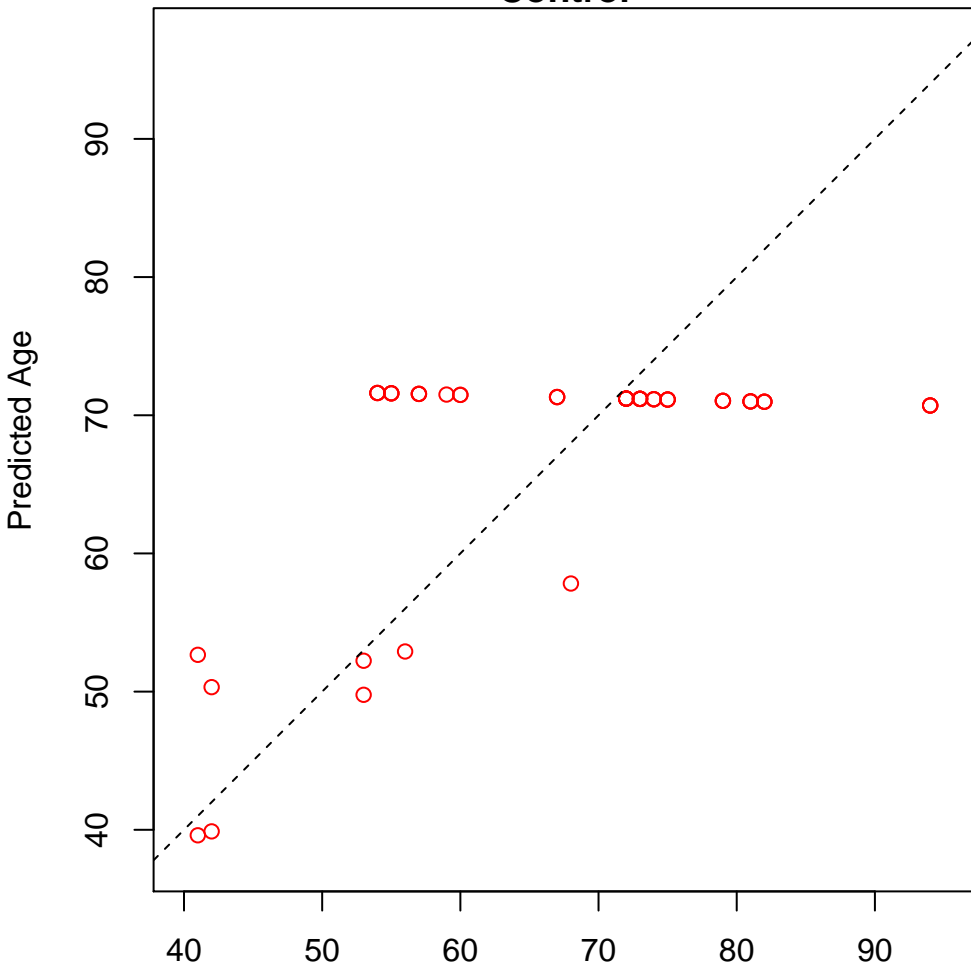


negative regulation of protein catabolic process (Score: 0.831848)

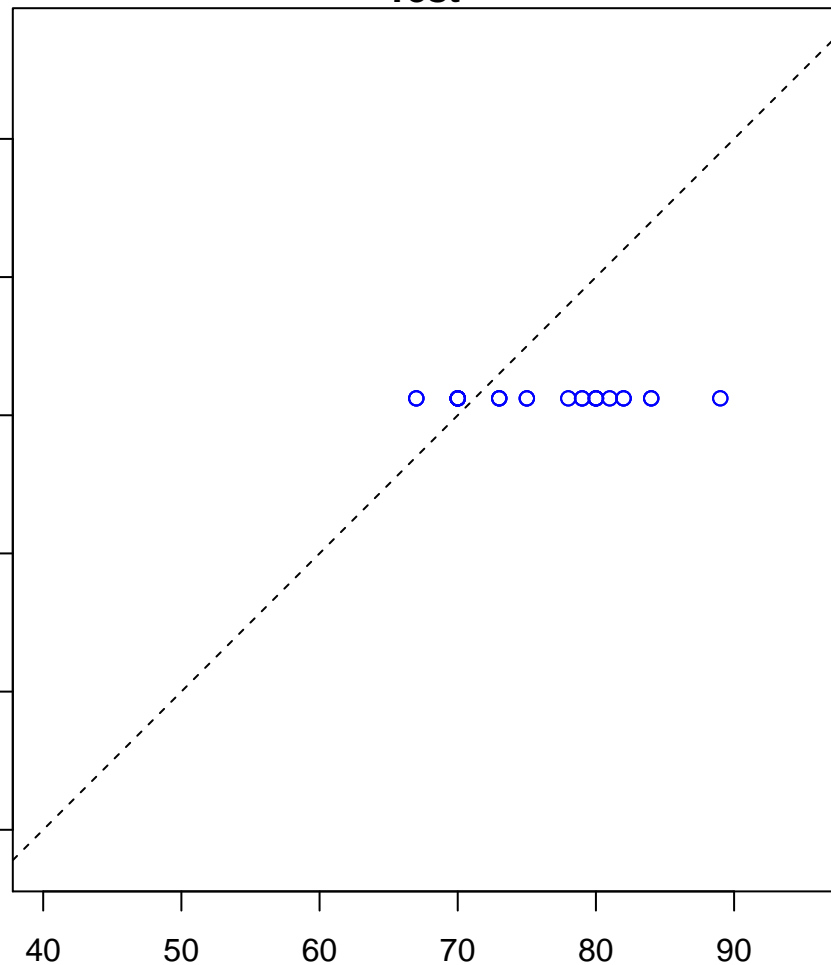


cytokine-mediated signaling pathway (Score: 0.831731)

Control



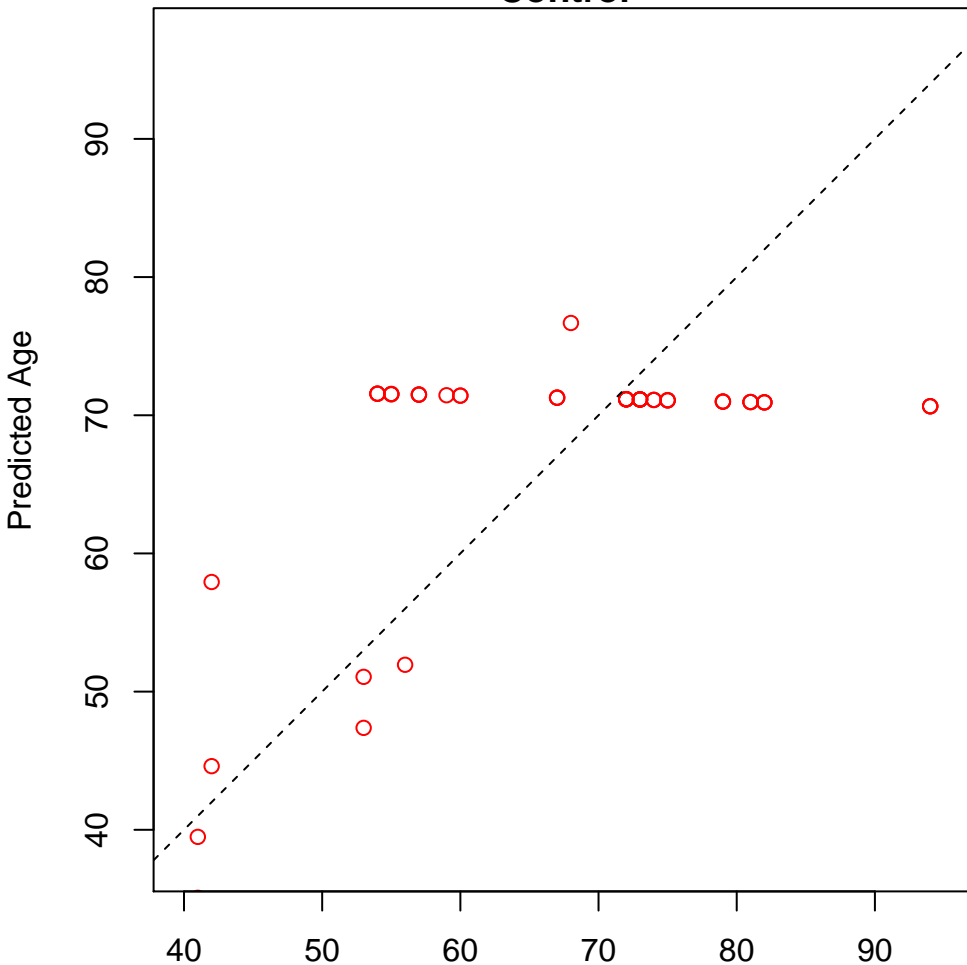
Test



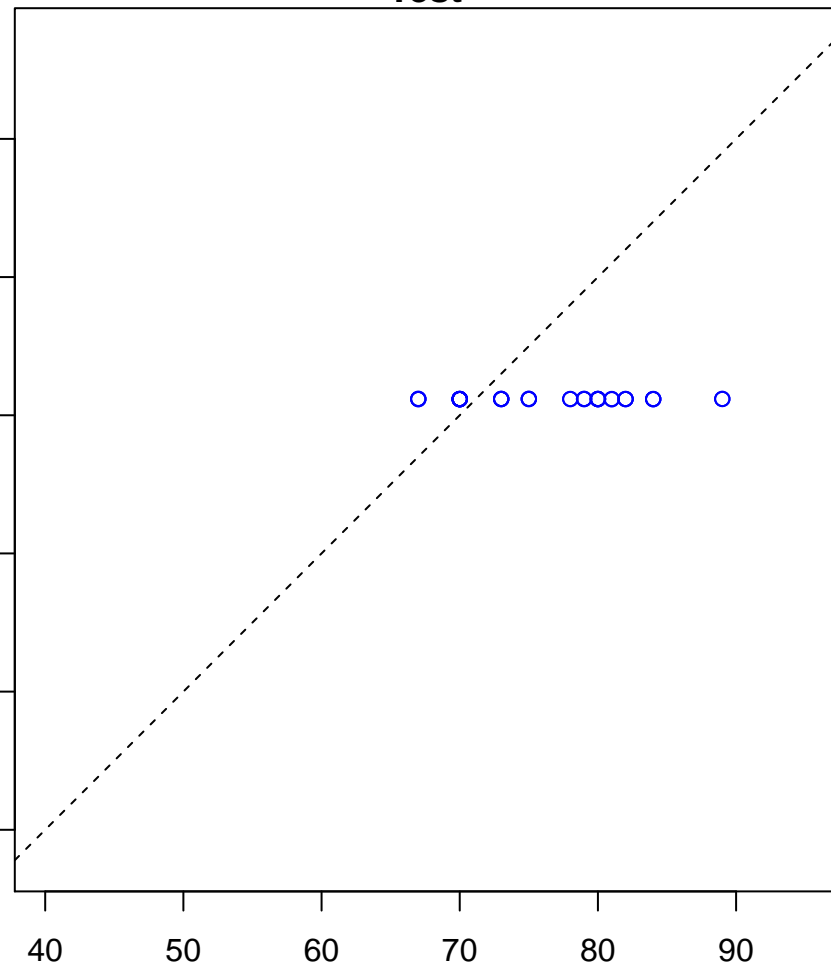
Actual Age

G2/M transition of mitotic cell cycle (Score: 0.831068)

Control



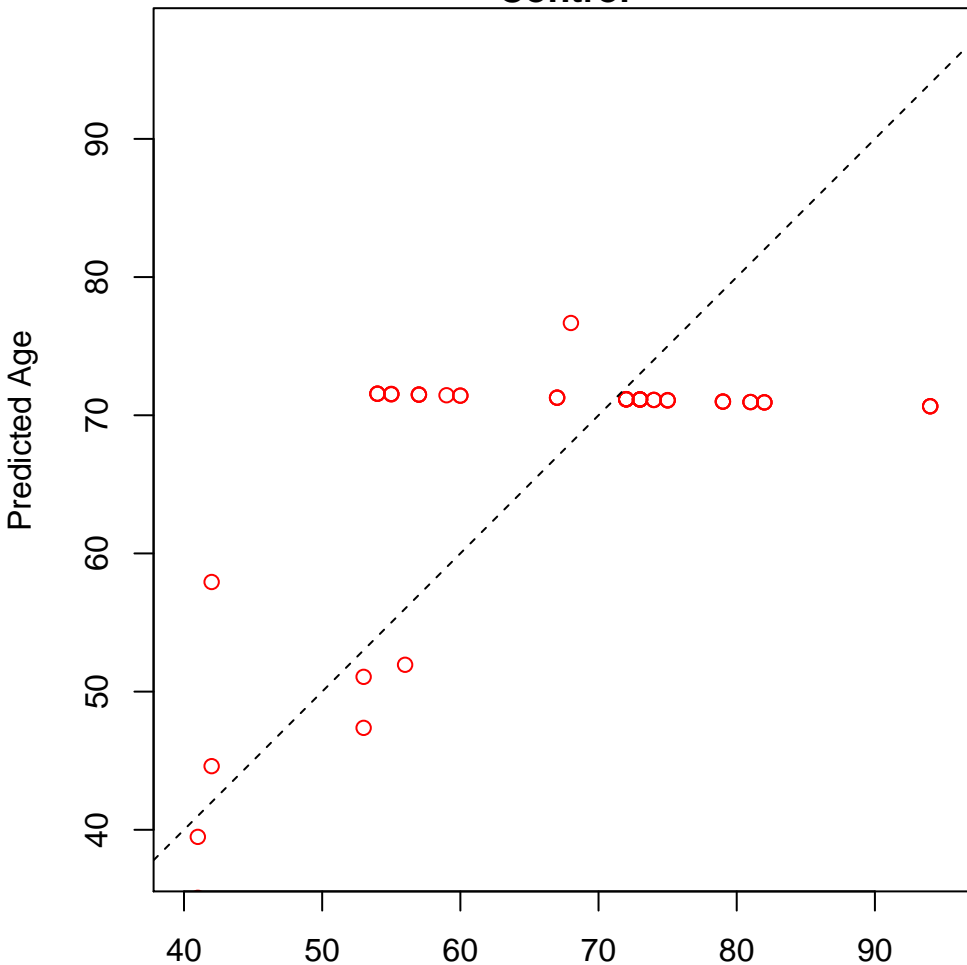
Test



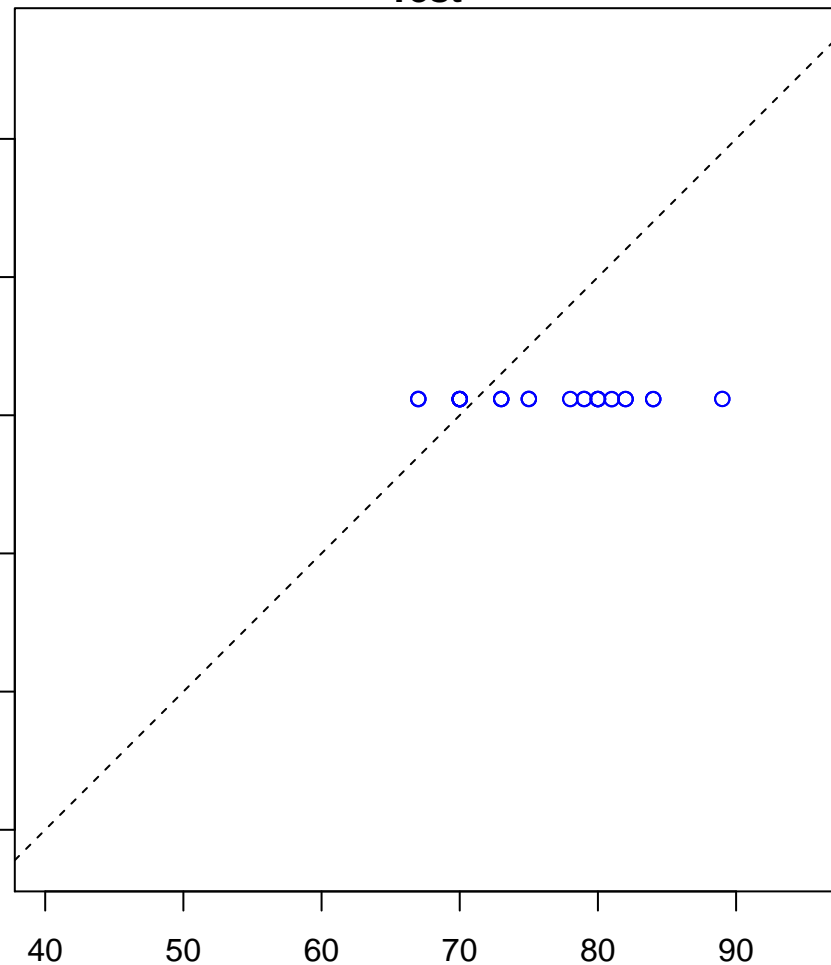
Actual Age

cell cycle G2/M phase transition (Score: 0.831068)

Control



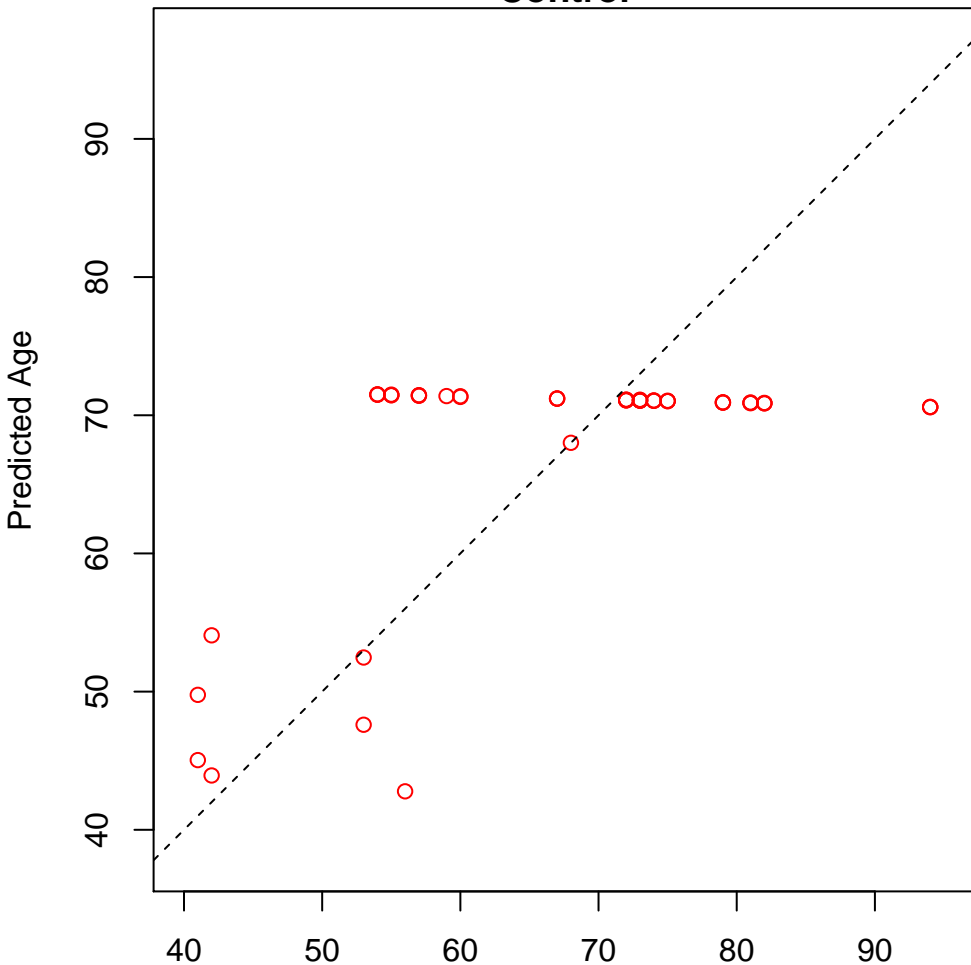
Test



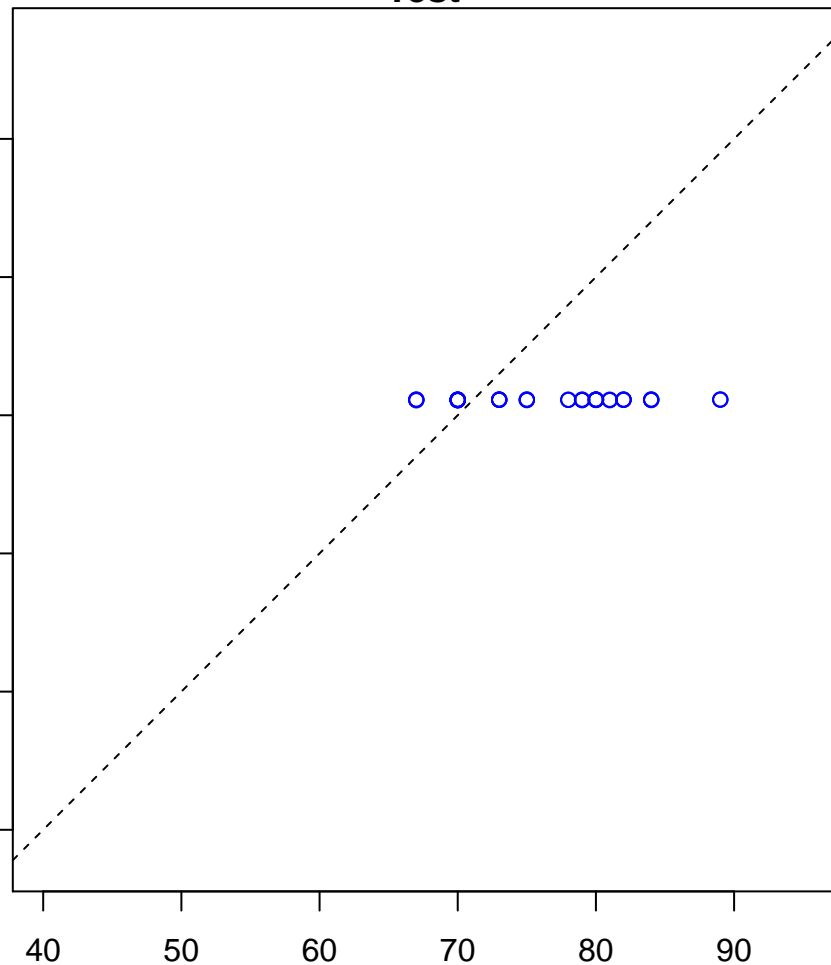
Actual Age

response to steroid hormone (Score: 0.830875)

Control

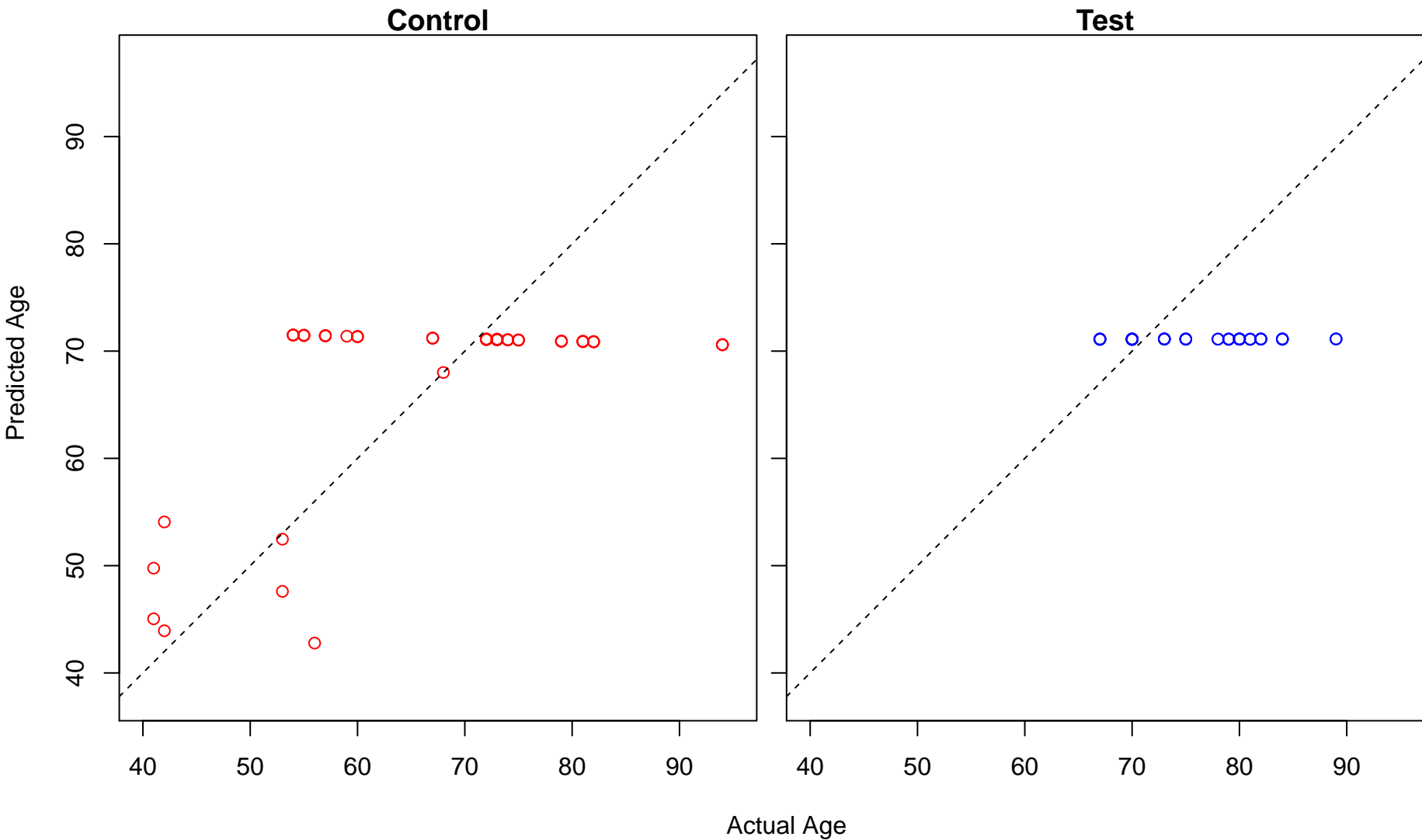


Test



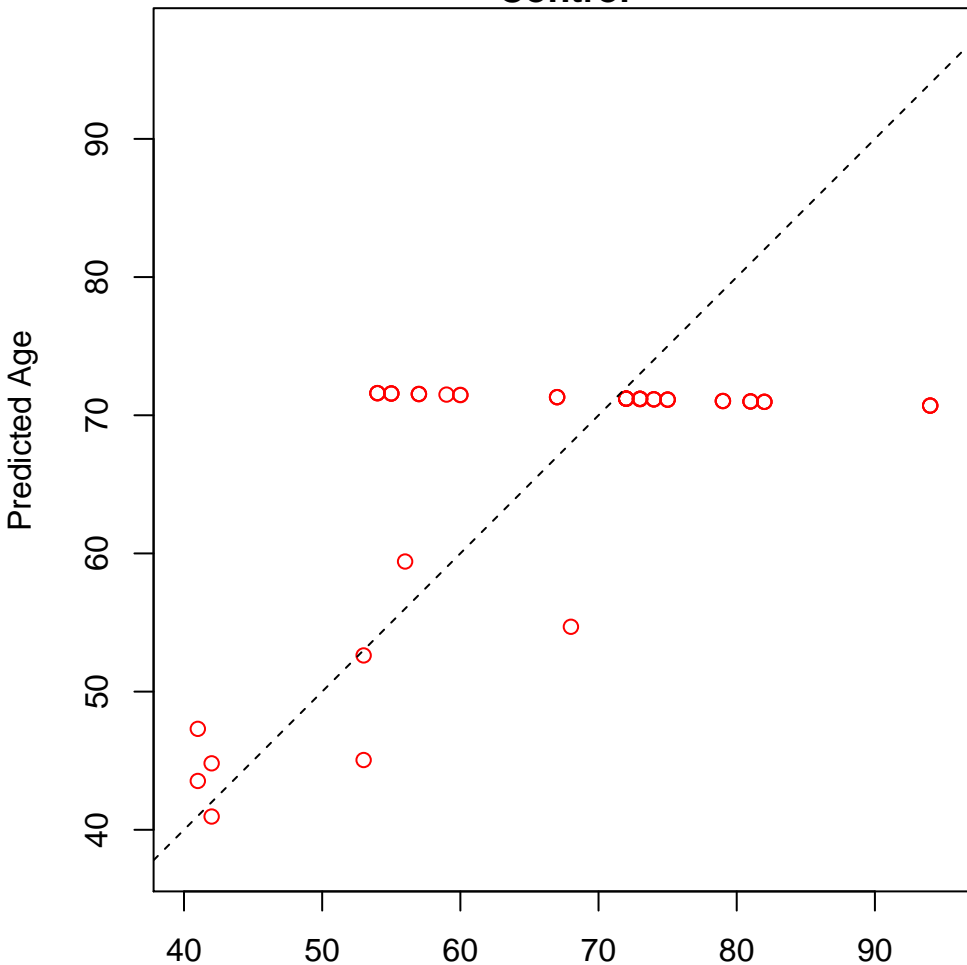
Actual Age

cellular response to steroid hormone stimulus (Score: 0.830875)

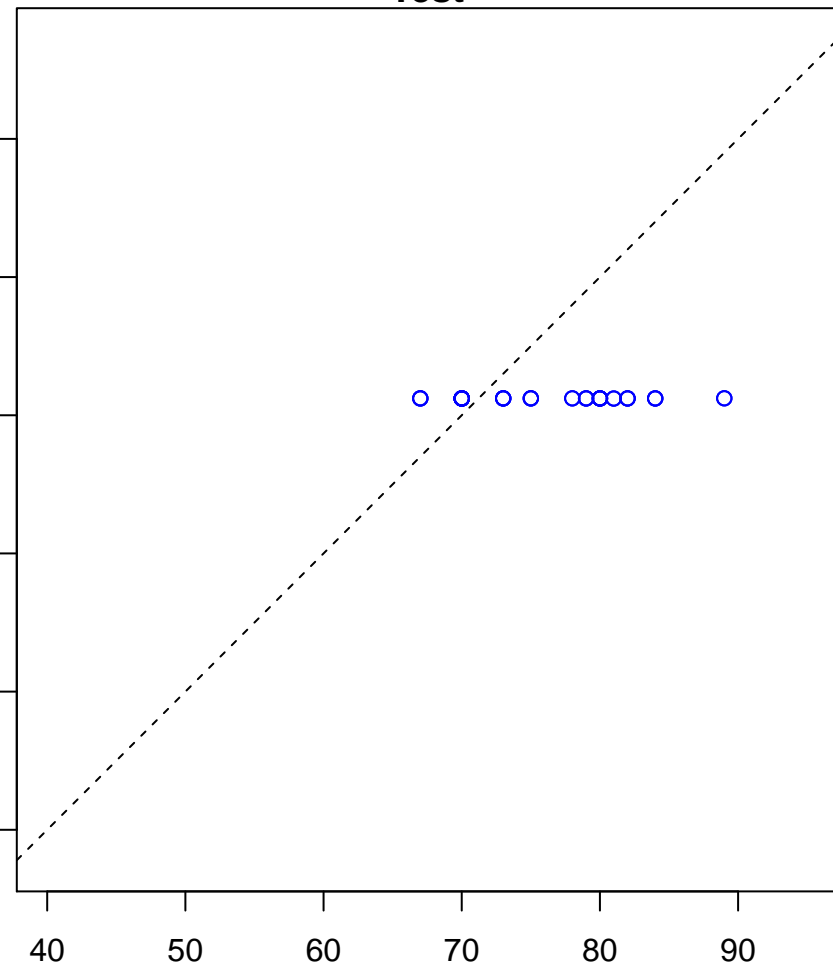


regulation of cell cycle phase transition (Score: 0.830759)

Control

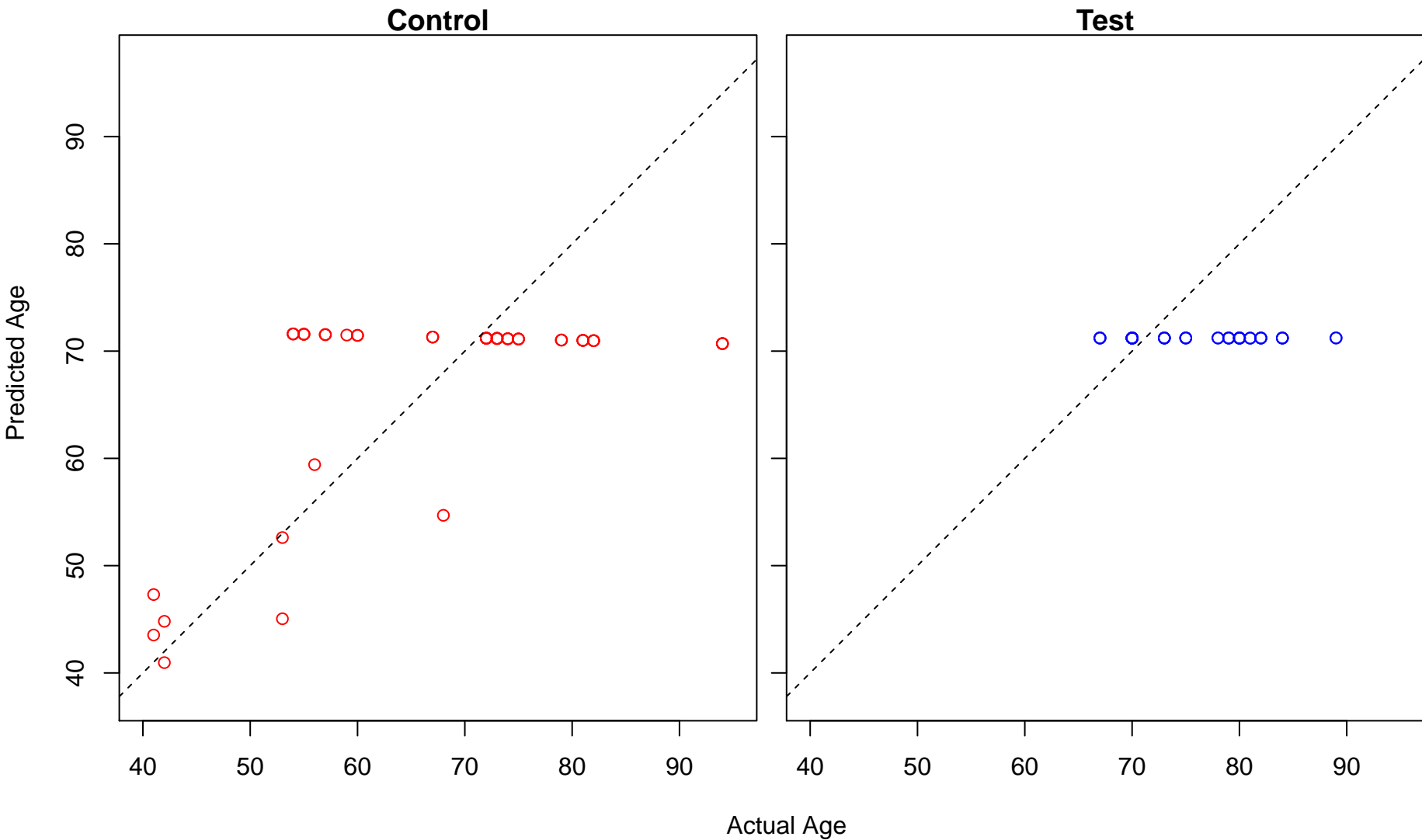


Test

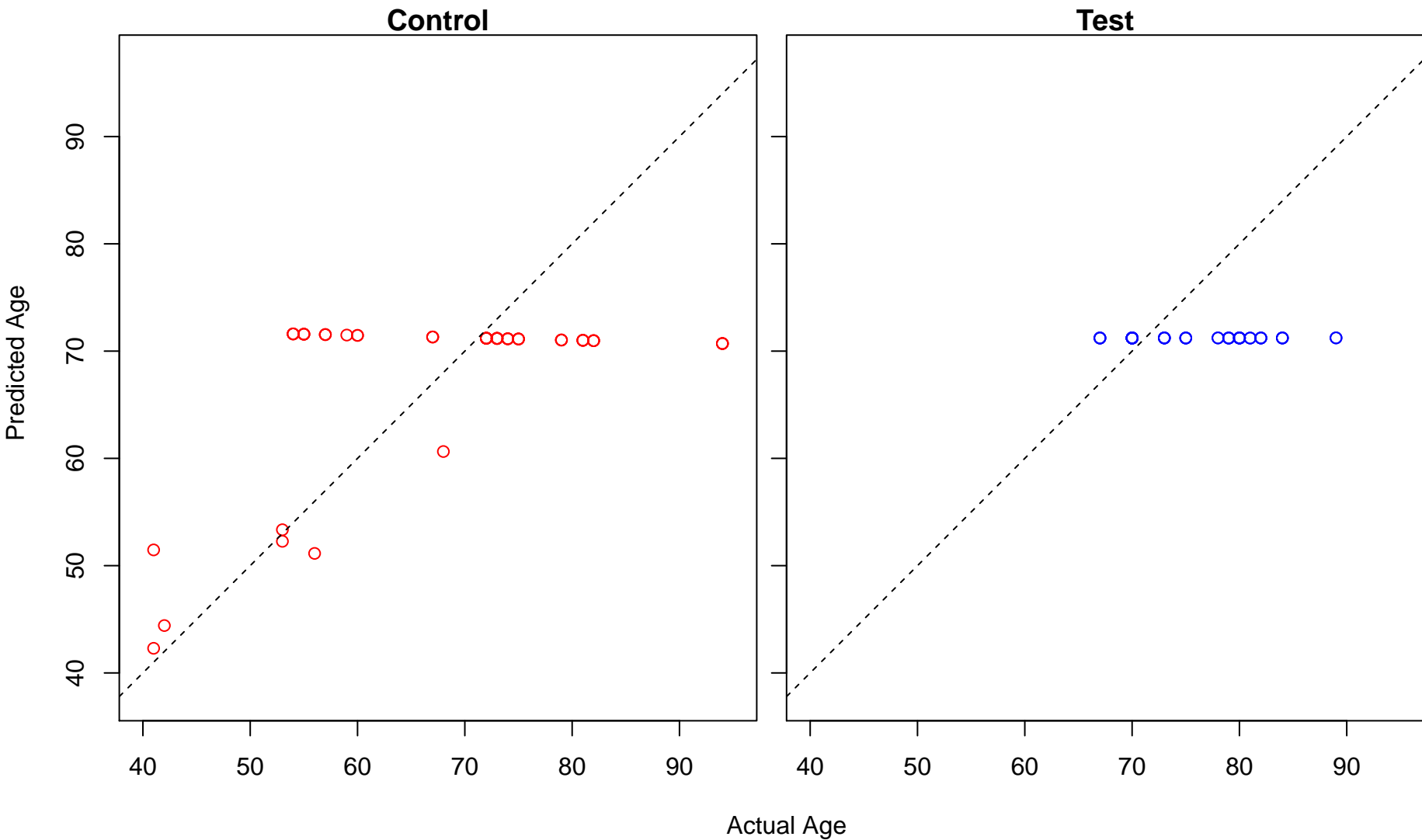


Actual Age

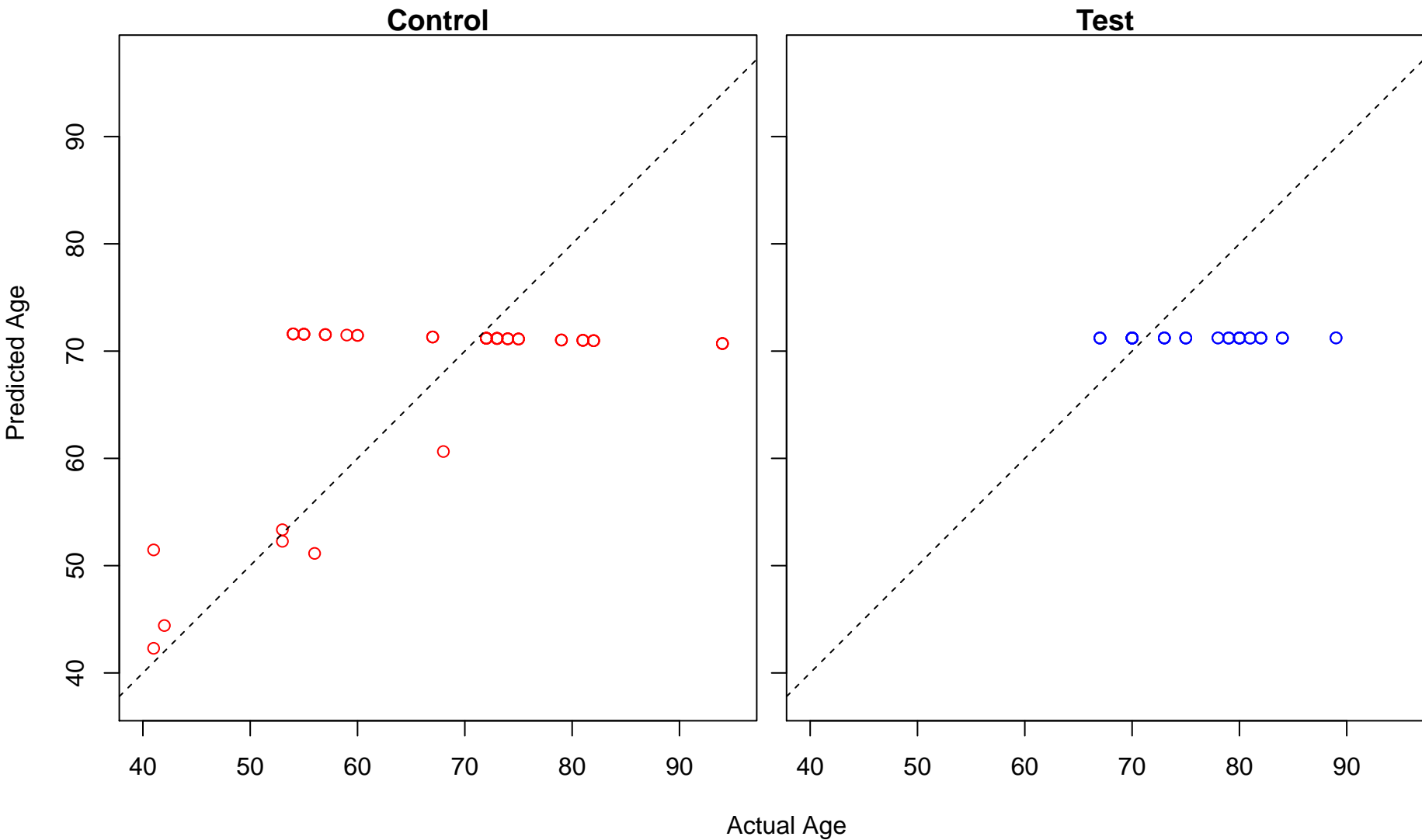
regulation of mitotic cell cycle phase transition (Score: 0.830759)



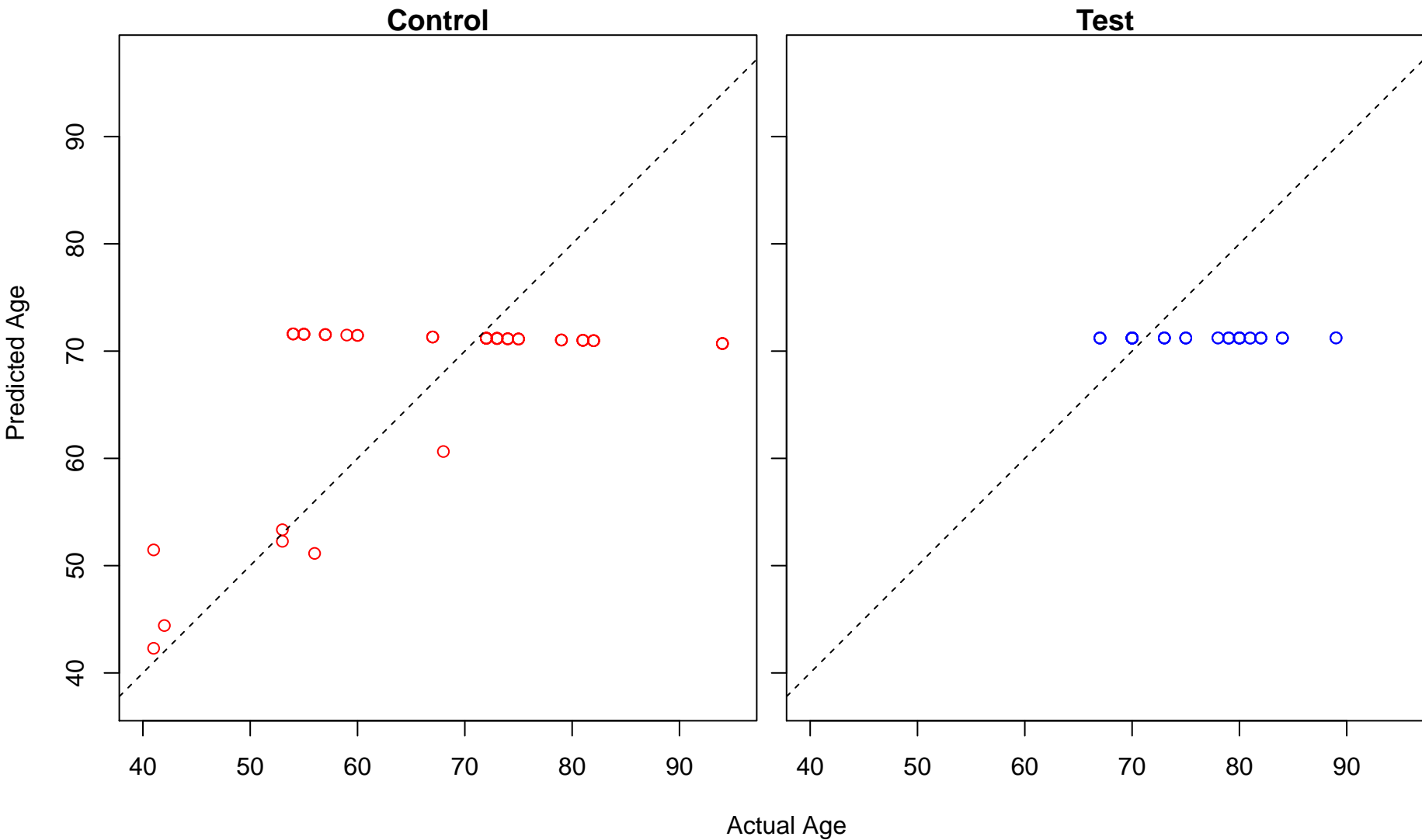
regulation of protein targeting to mitochondrion (Score: 0.830674)



regulation of protein targeting (Score: 0.830674)

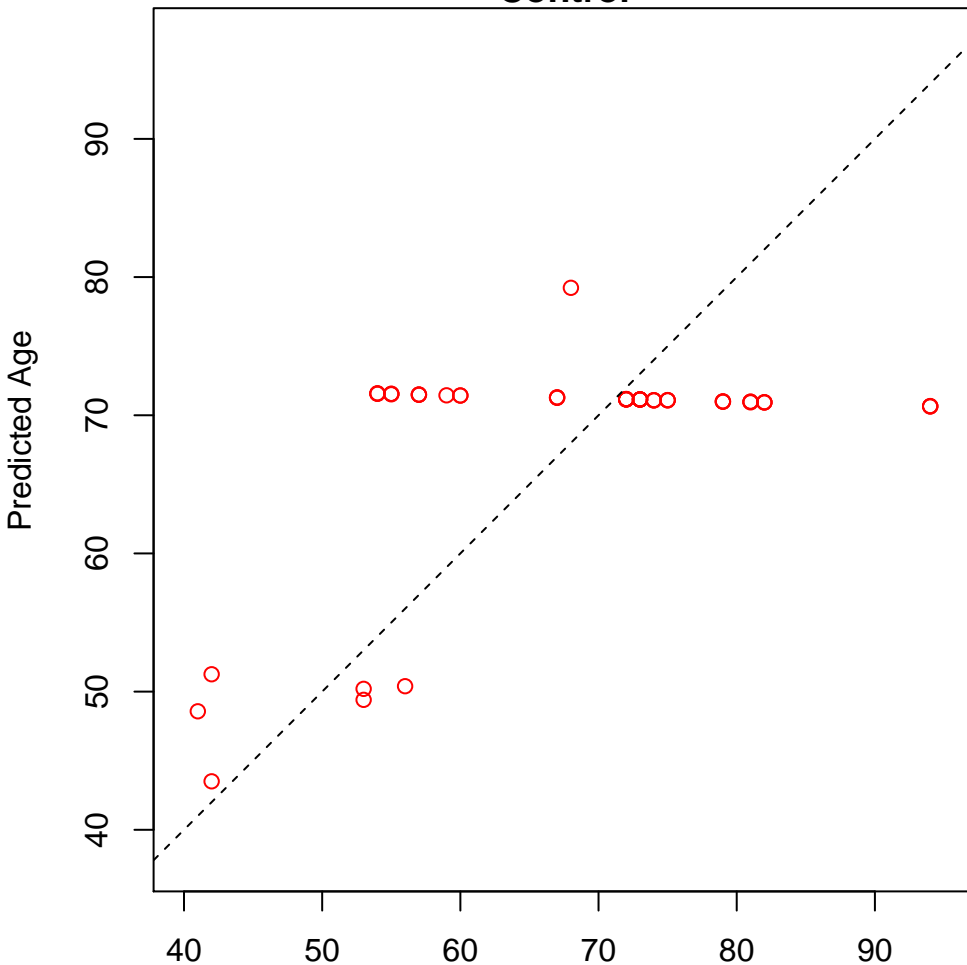


positive regulation of protein targeting to mitochondrion (Score: 0.830674)

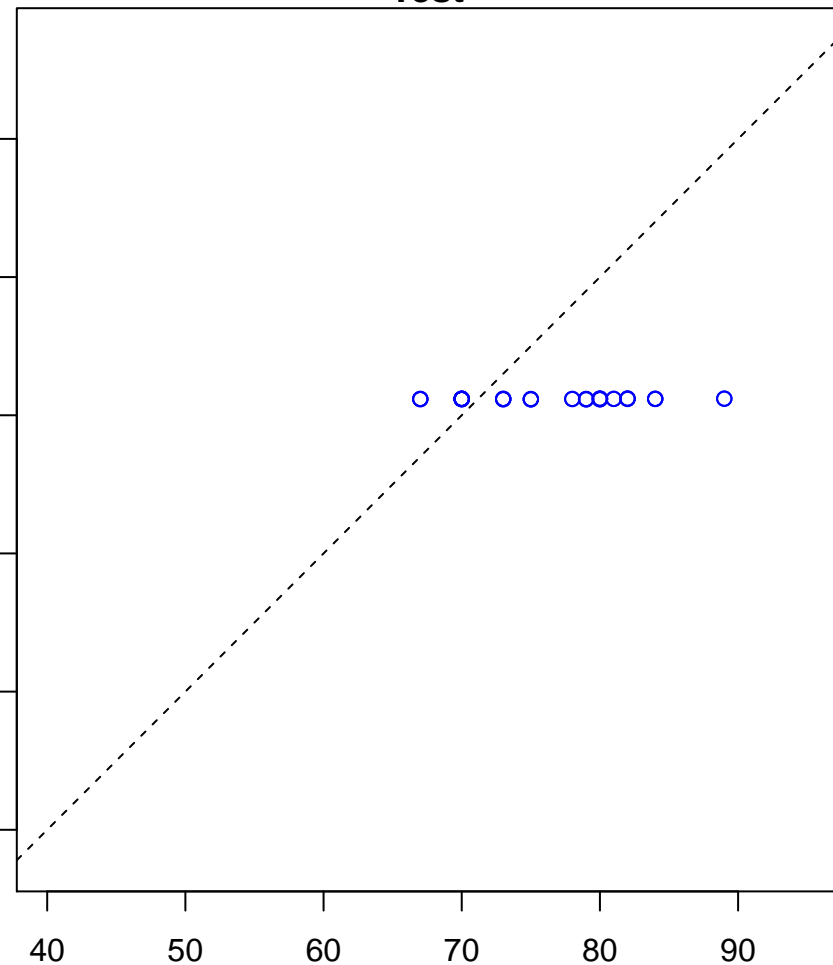


plasma lipoprotein particle clearance (Score: 0.830617)

Control

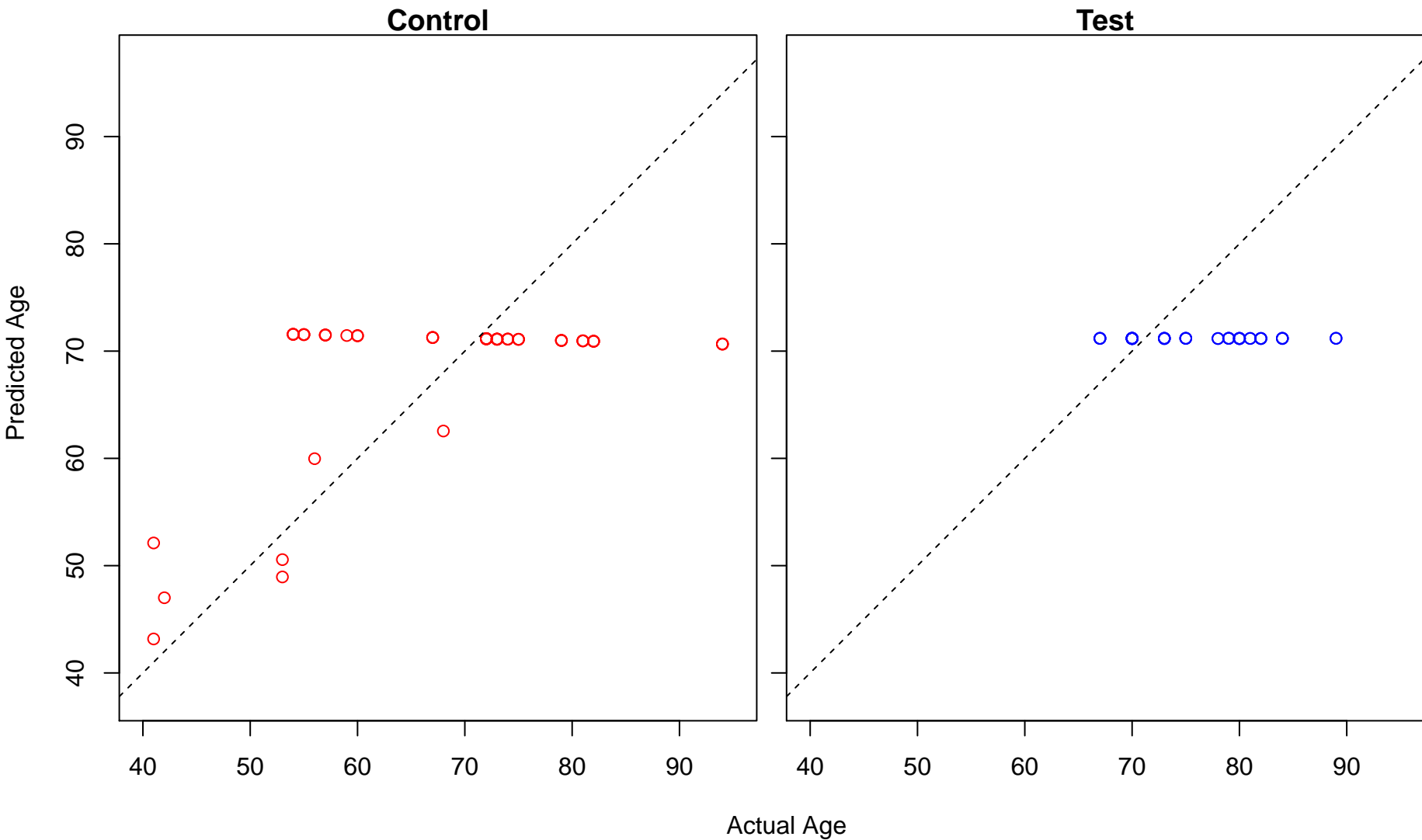


Test

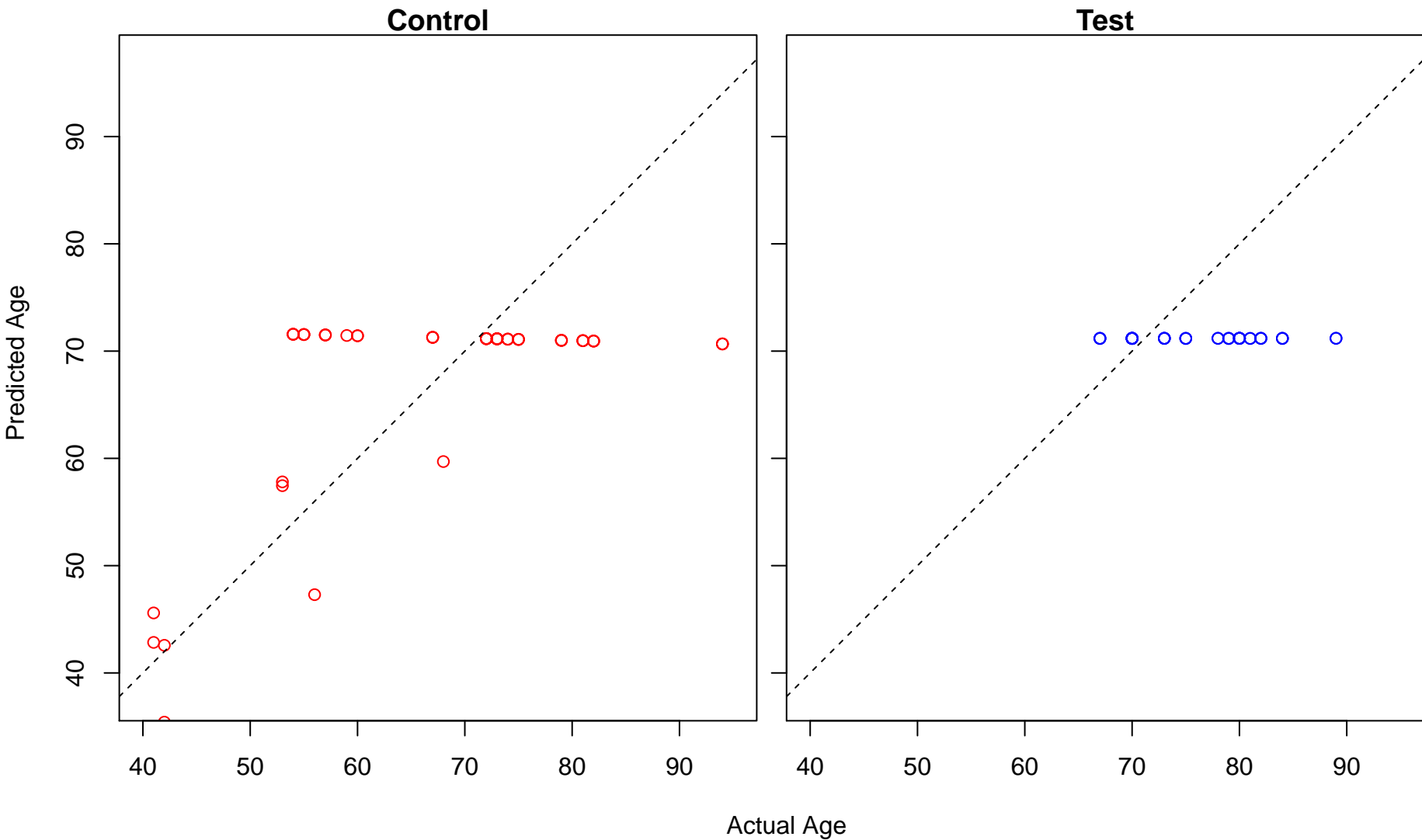


Actual Age

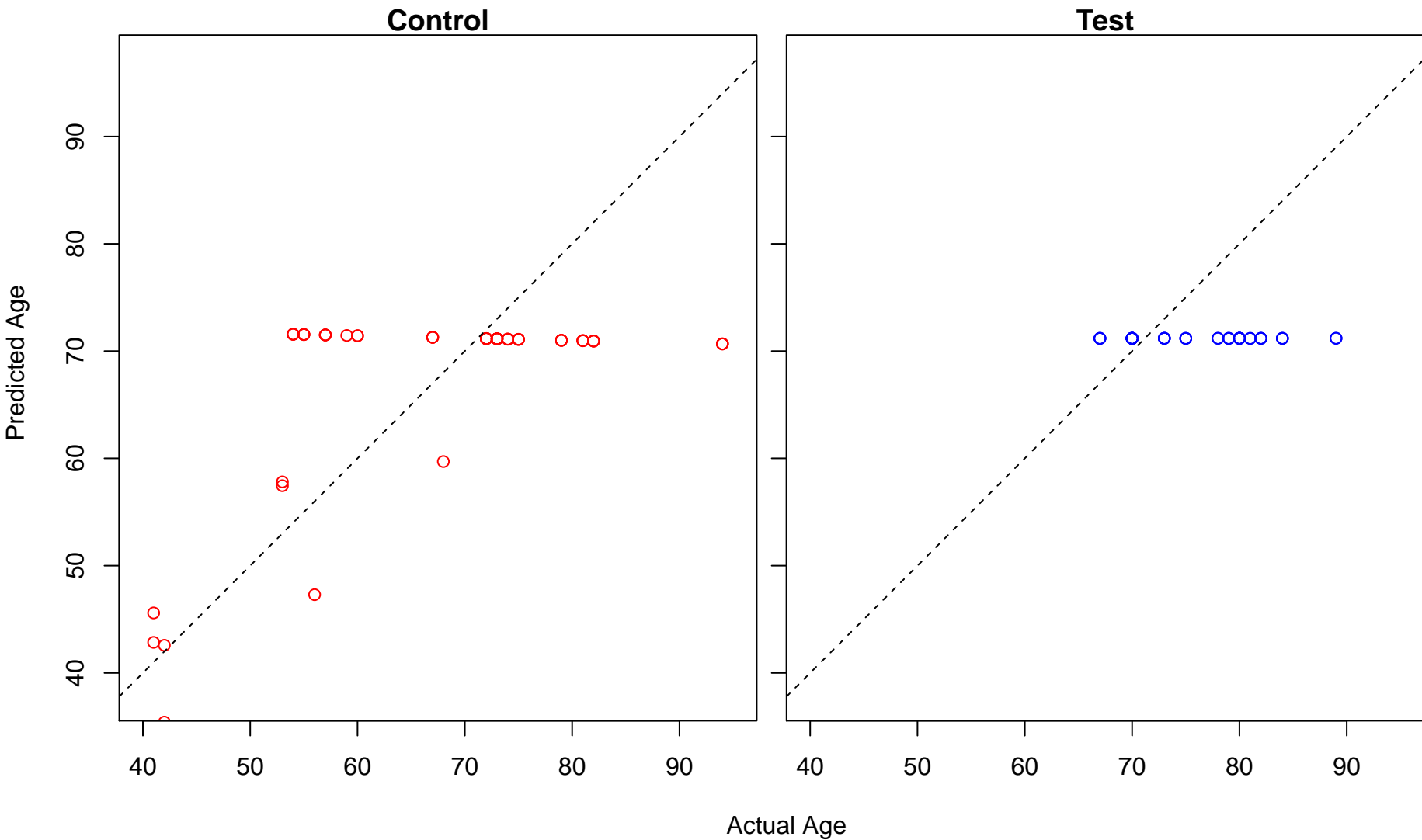
cytoskeleton organization (Score: 0.830582)



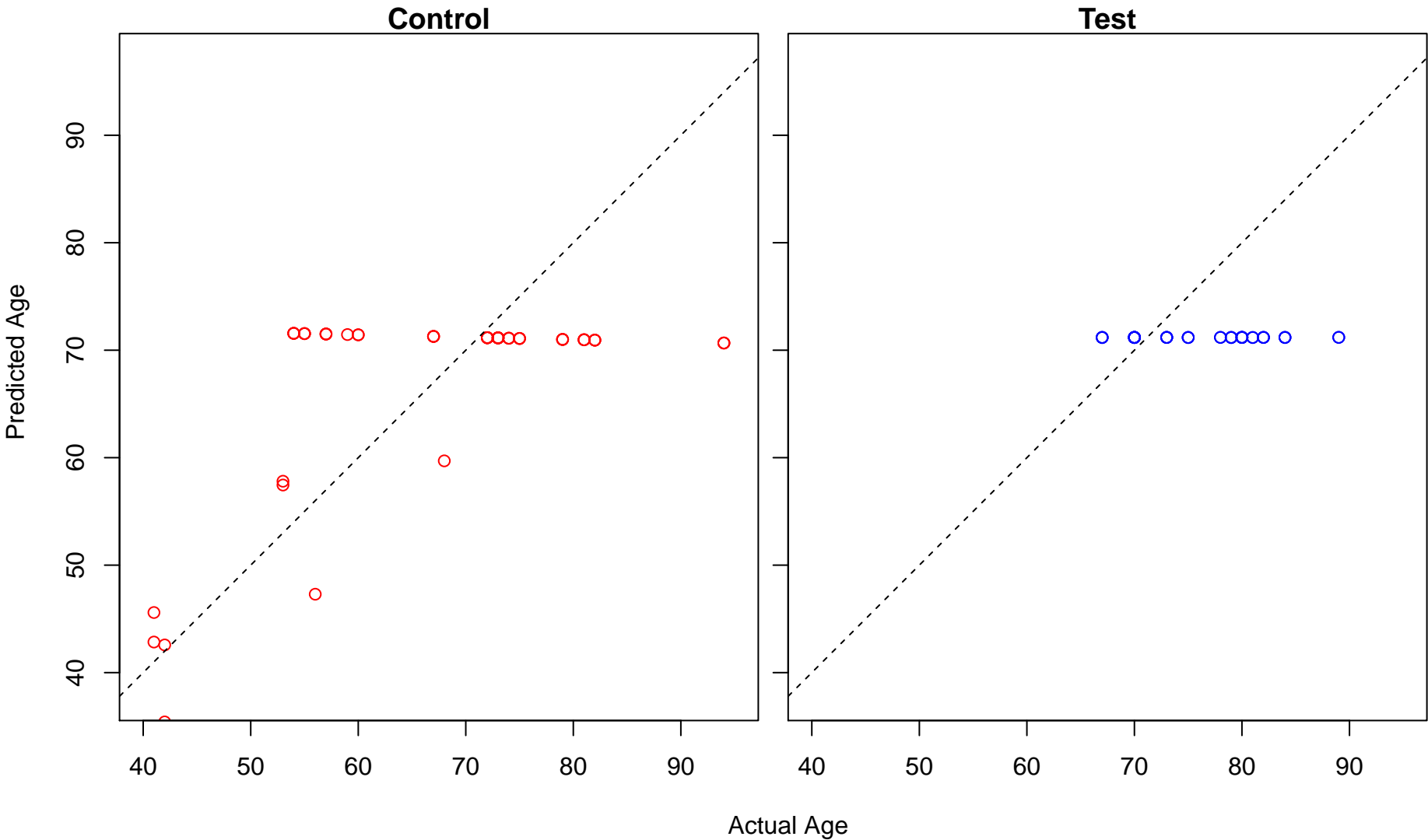
negative regulation of protein ubiquitination (Score: 0.830379)



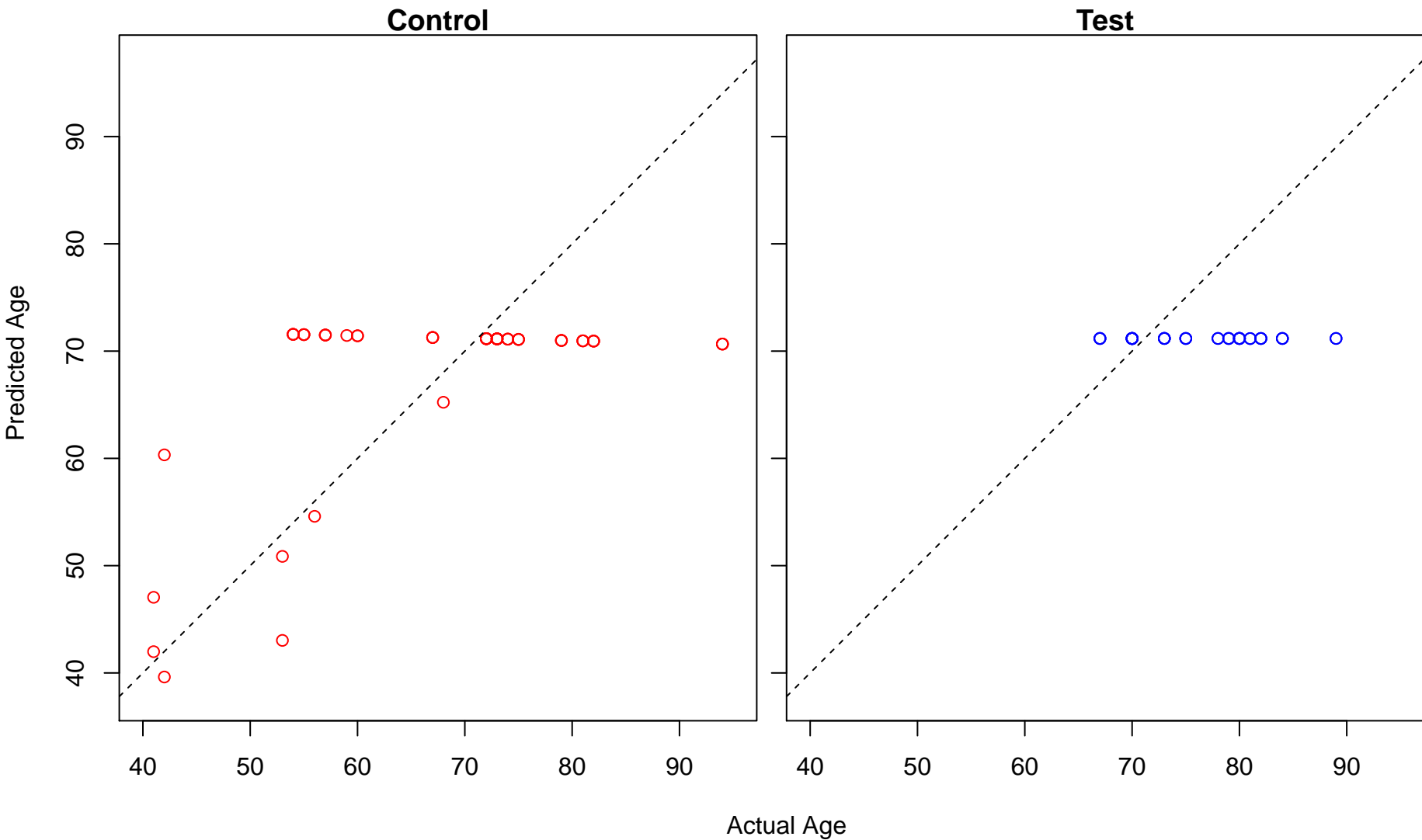
negative regulation of ubiquitin–protein transferase activity (Score: 0.830379)



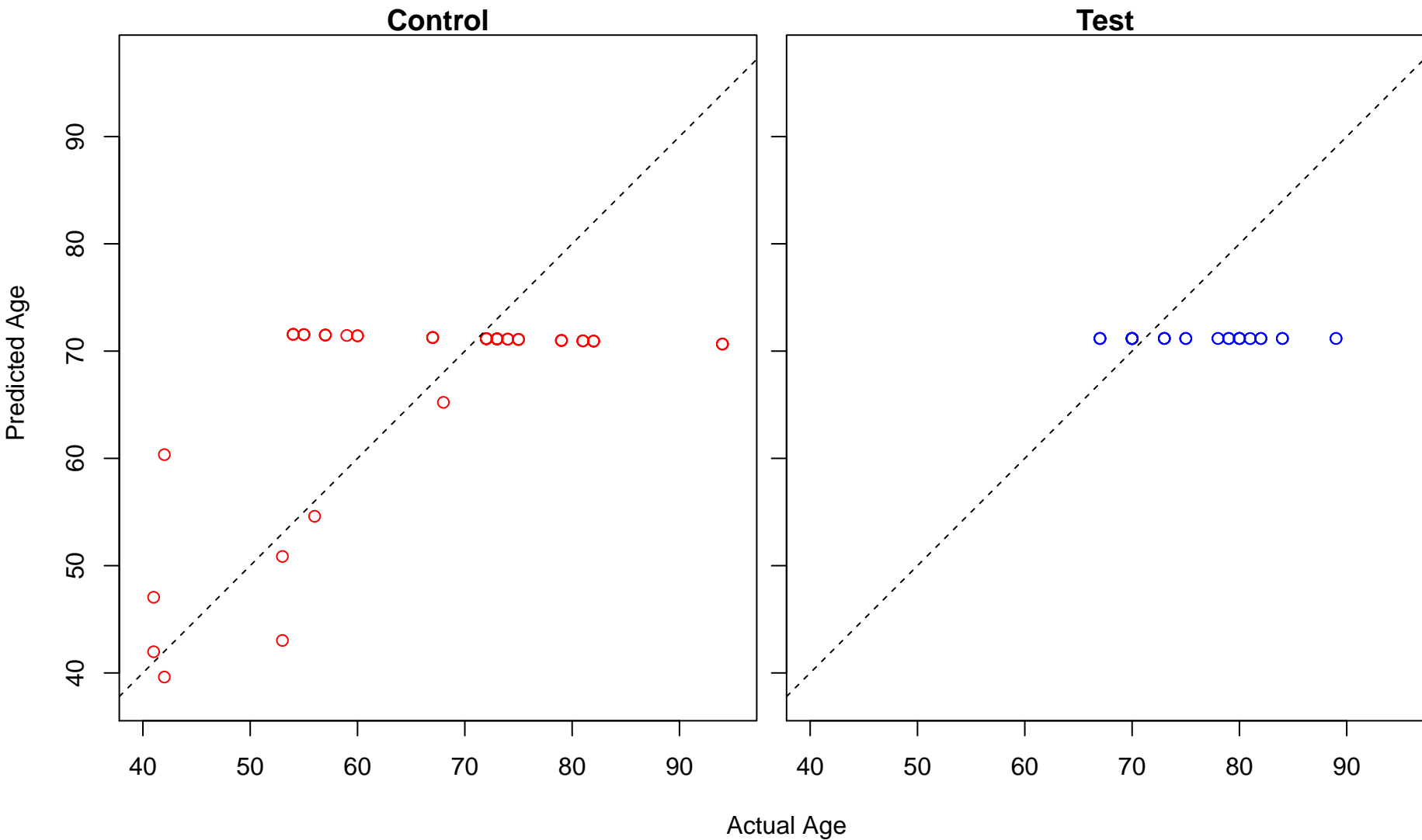
negative regulation of protein modification by small protein conjugation or removal (Score: 0.83037)



neutrophil activation (Score: 0.830345)

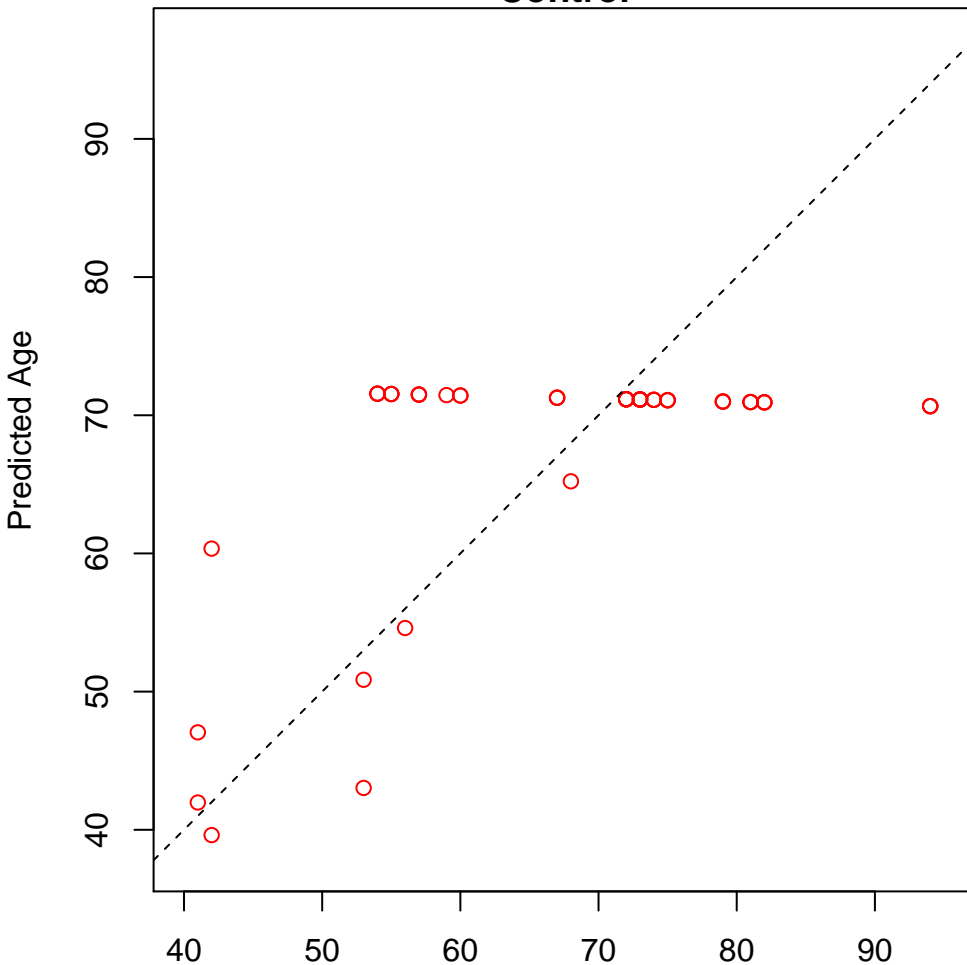


neutrophil activation involved in immune response (Score: 0.830299)

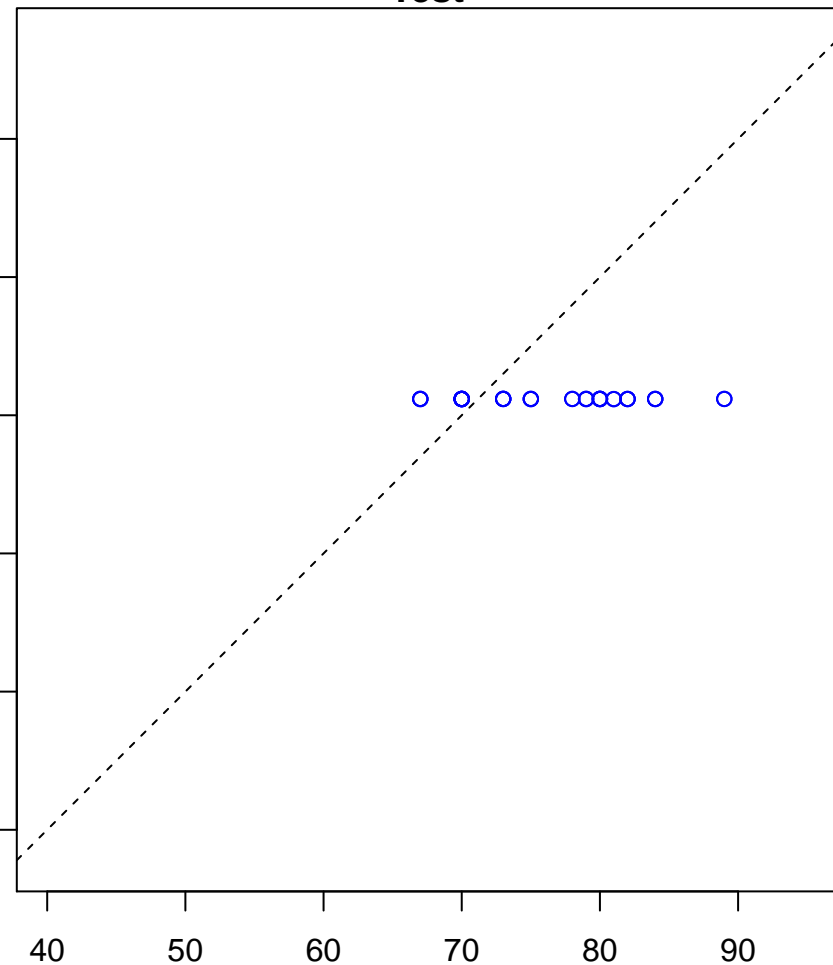


leukocyte mediated immunity (Score: 0.830299)

Control



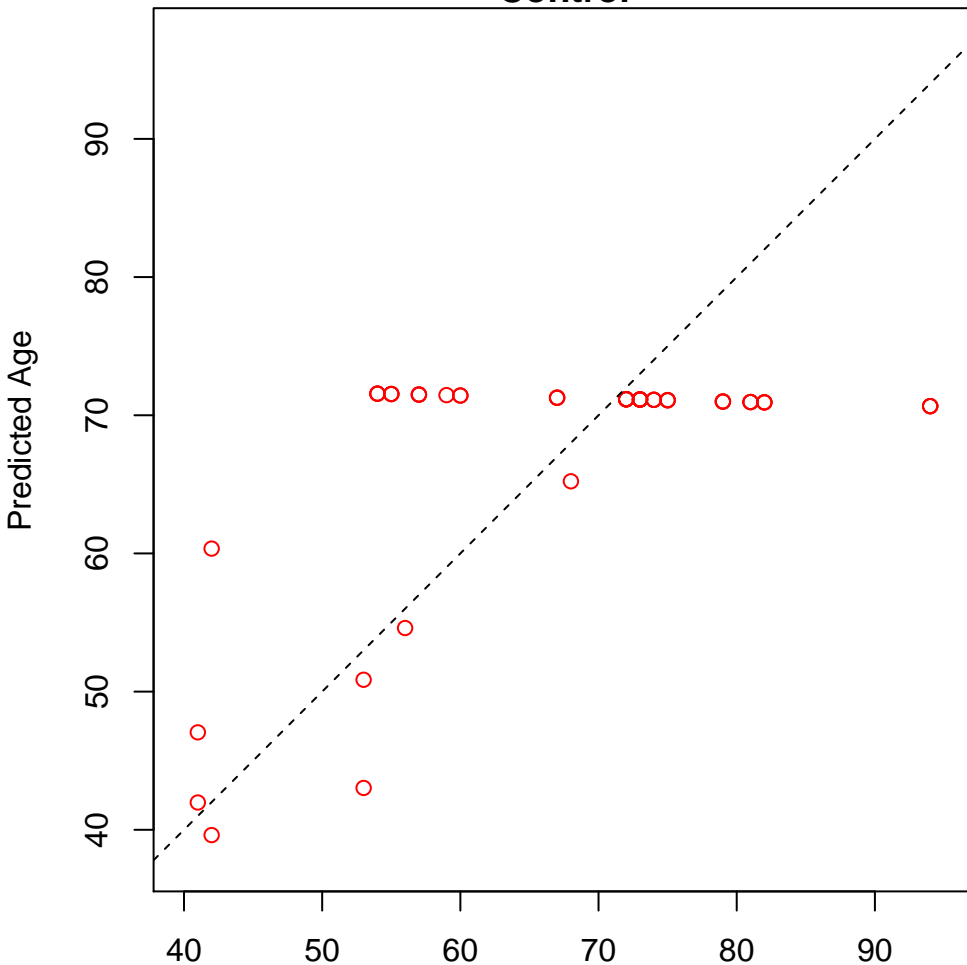
Test



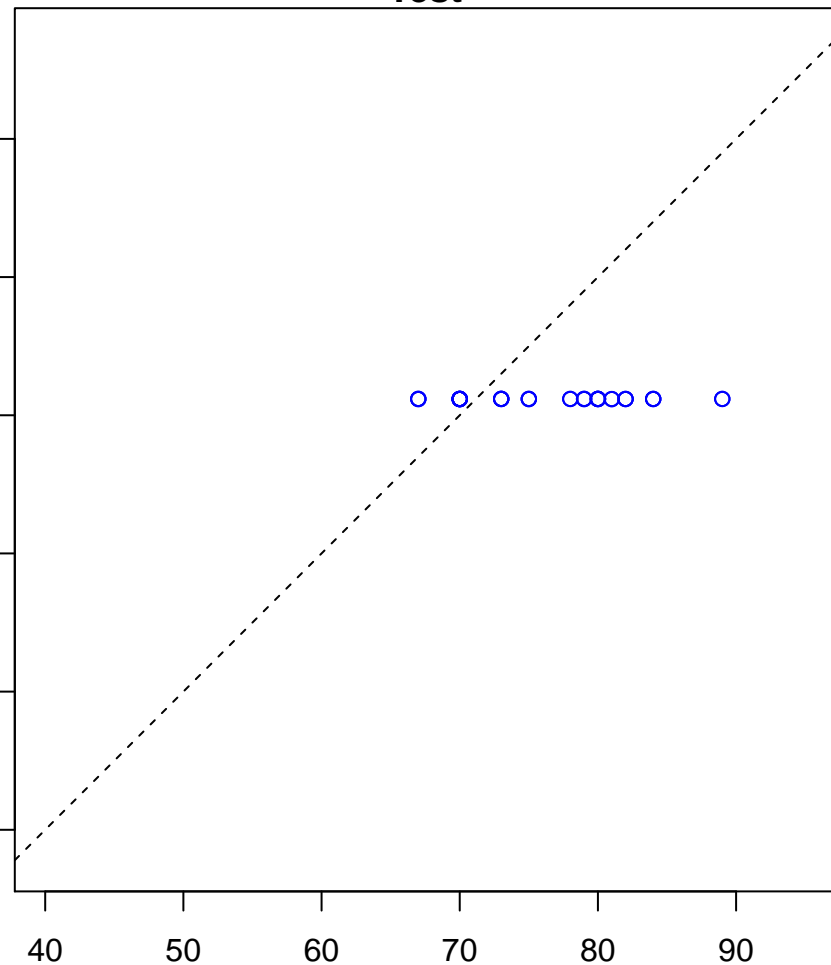
Actual Age

myeloid leukocyte mediated immunity (Score: 0.830299)

Control



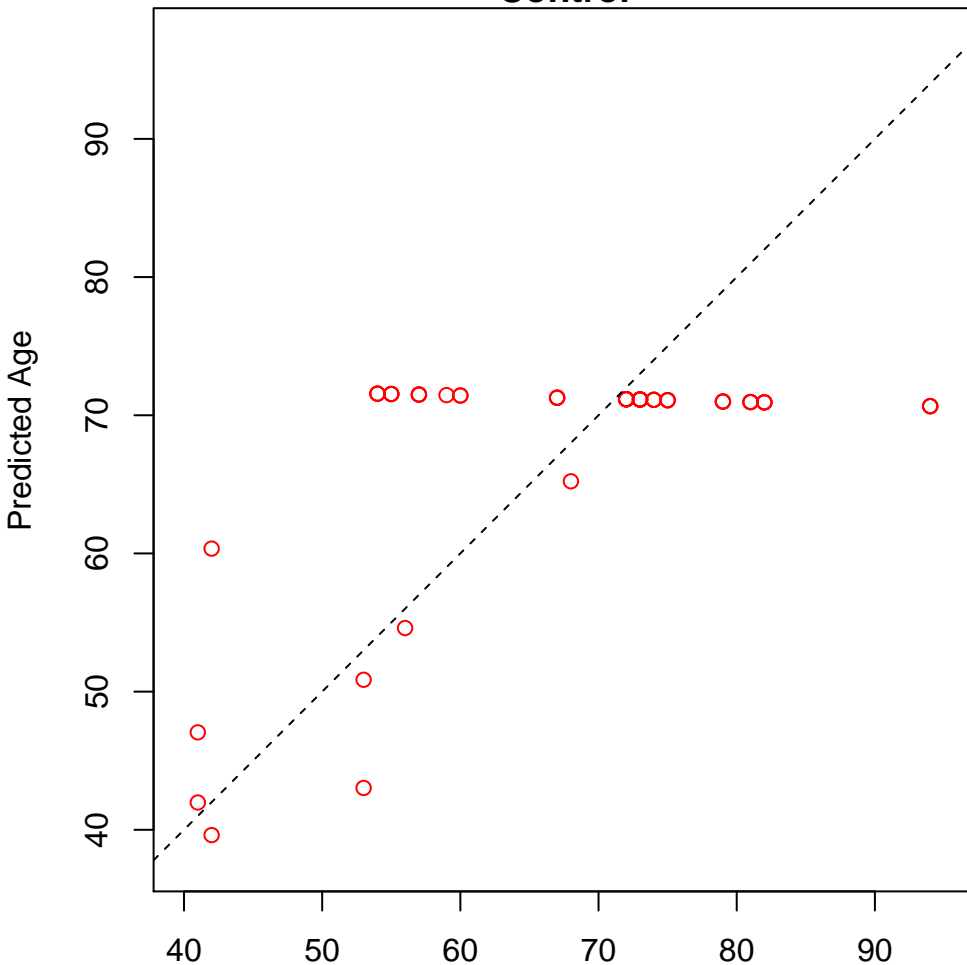
Test



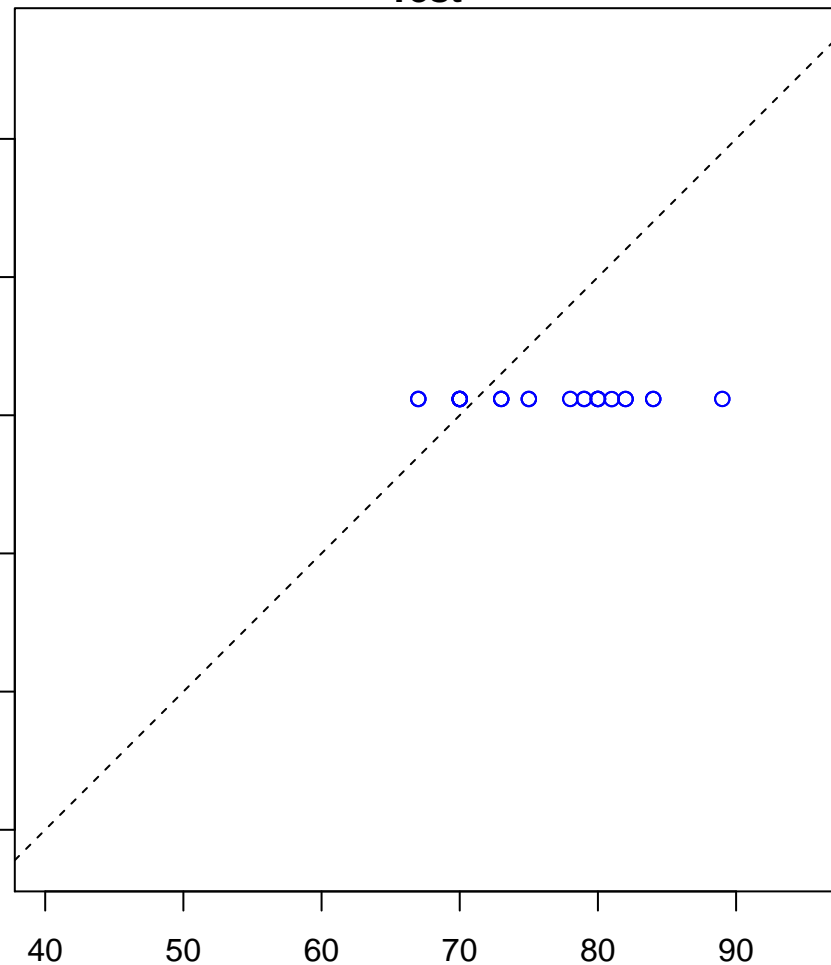
Actual Age

neutrophil mediated immunity (Score: 0.830299)

Control



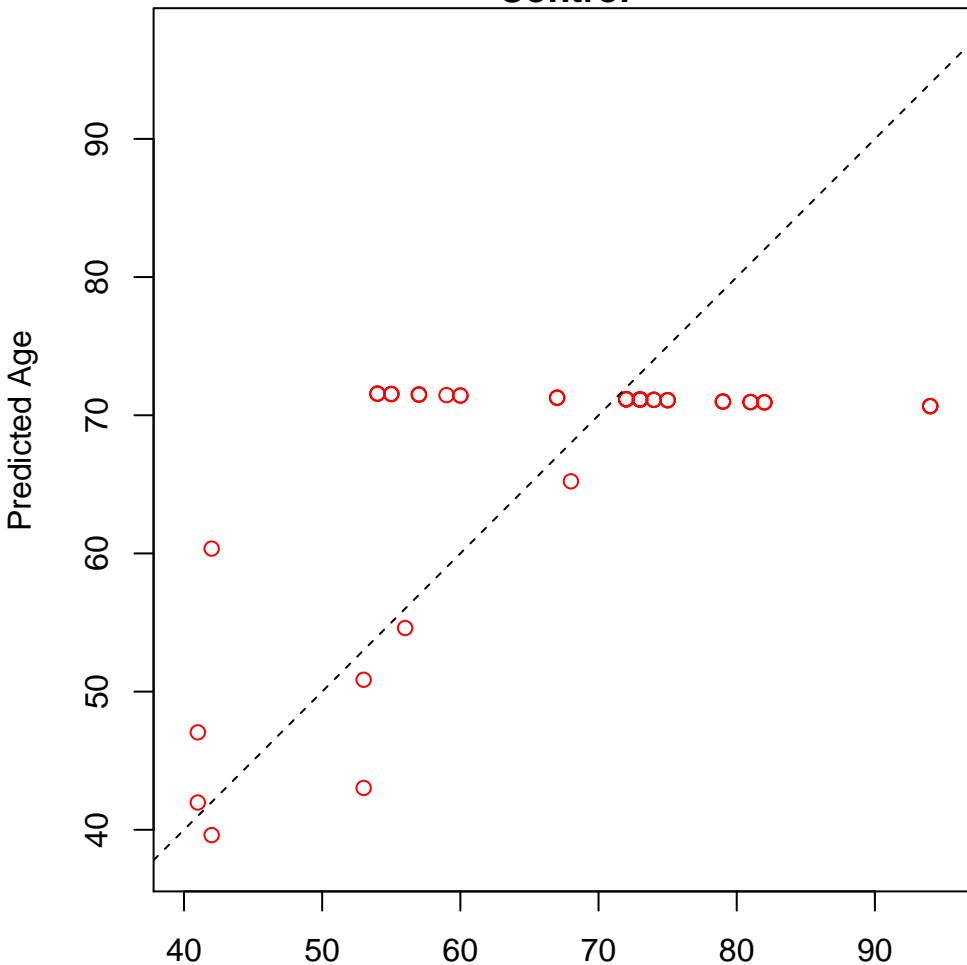
Test



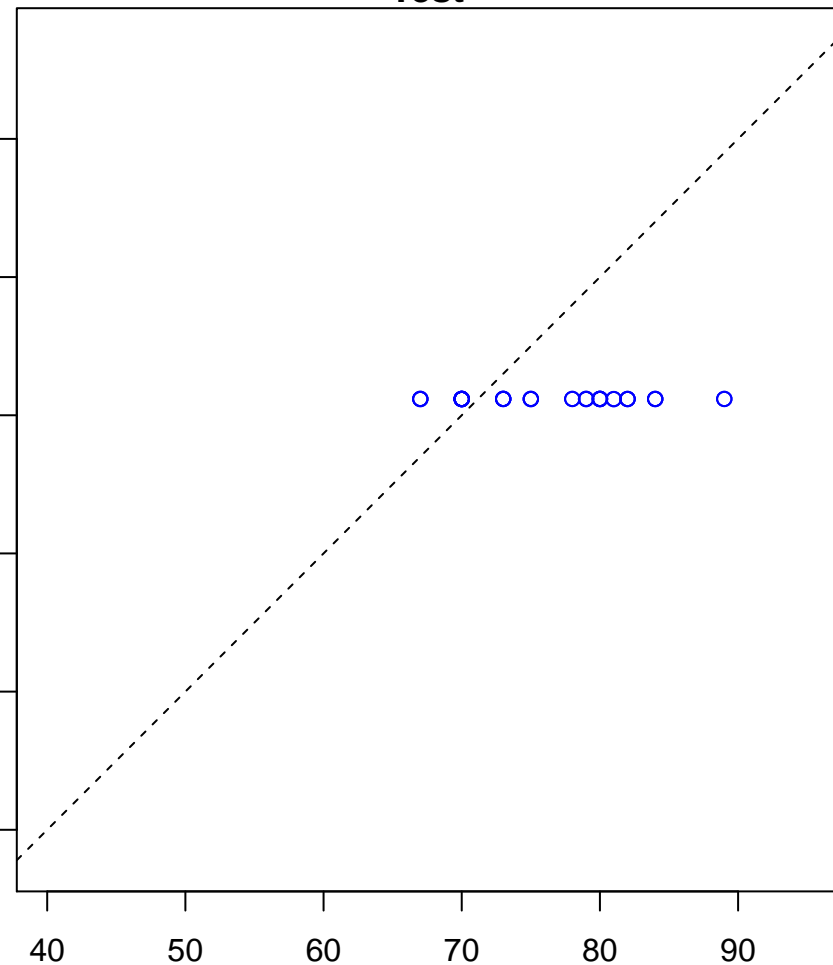
Actual Age

leukocyte degranulation (Score: 0.830299)

Control



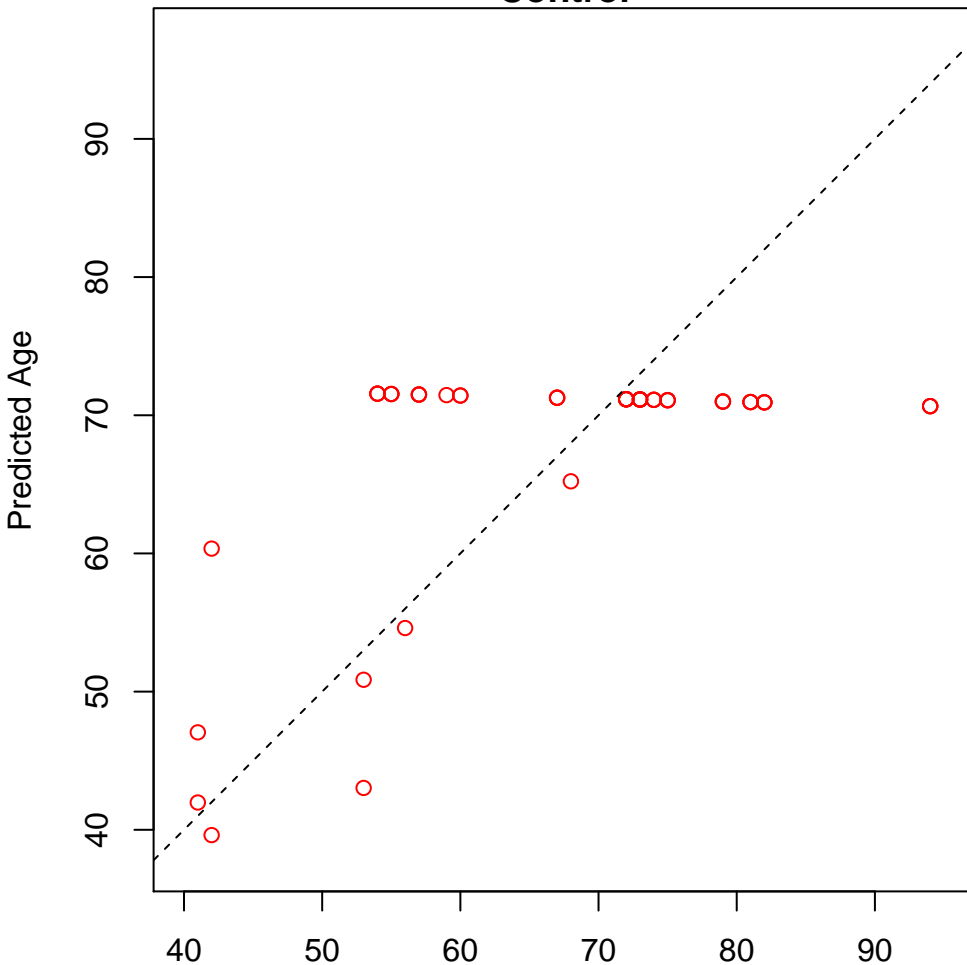
Test



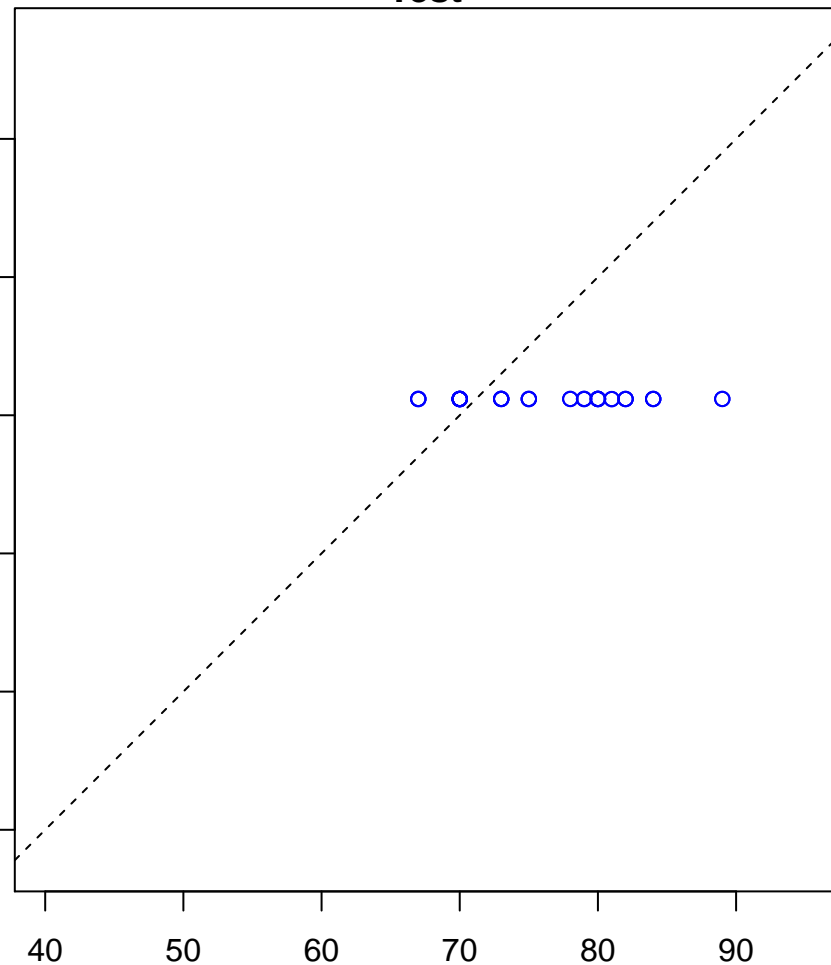
Actual Age

neutrophil degranulation (Score: 0.830299)

Control

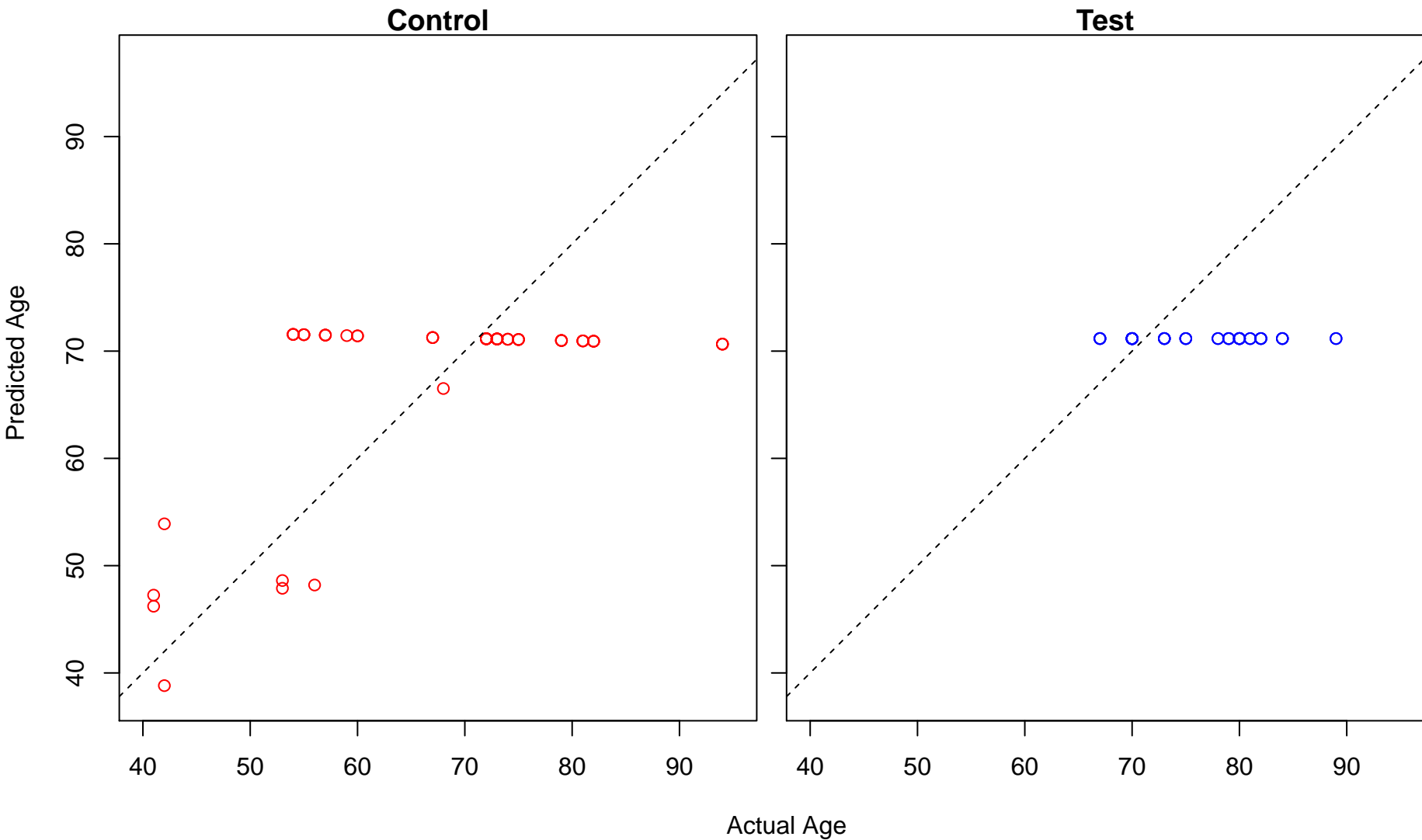


Test

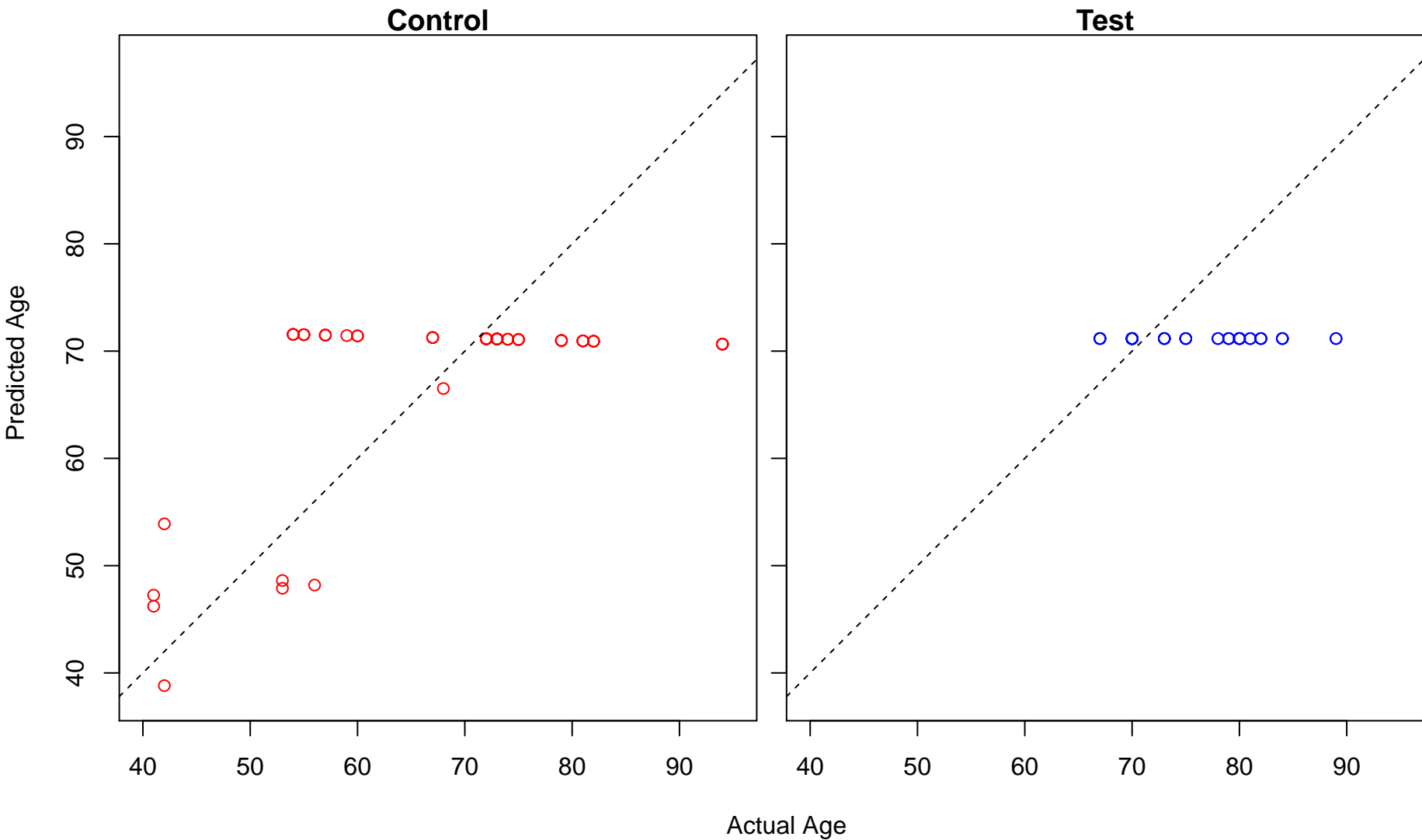


Actual Age

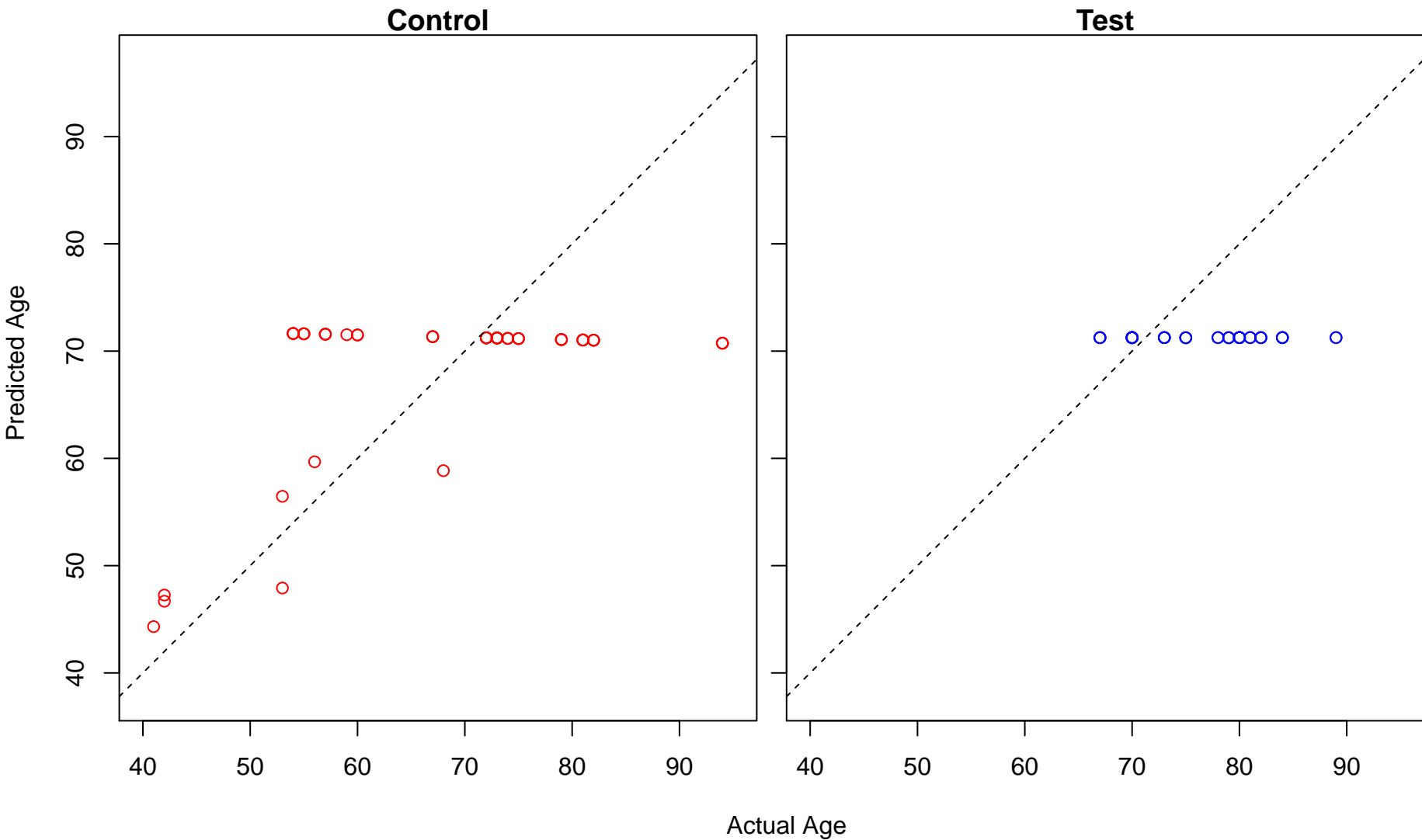
secretion by cell (Score: 0.830153)



secretion (Score: 0.830153)

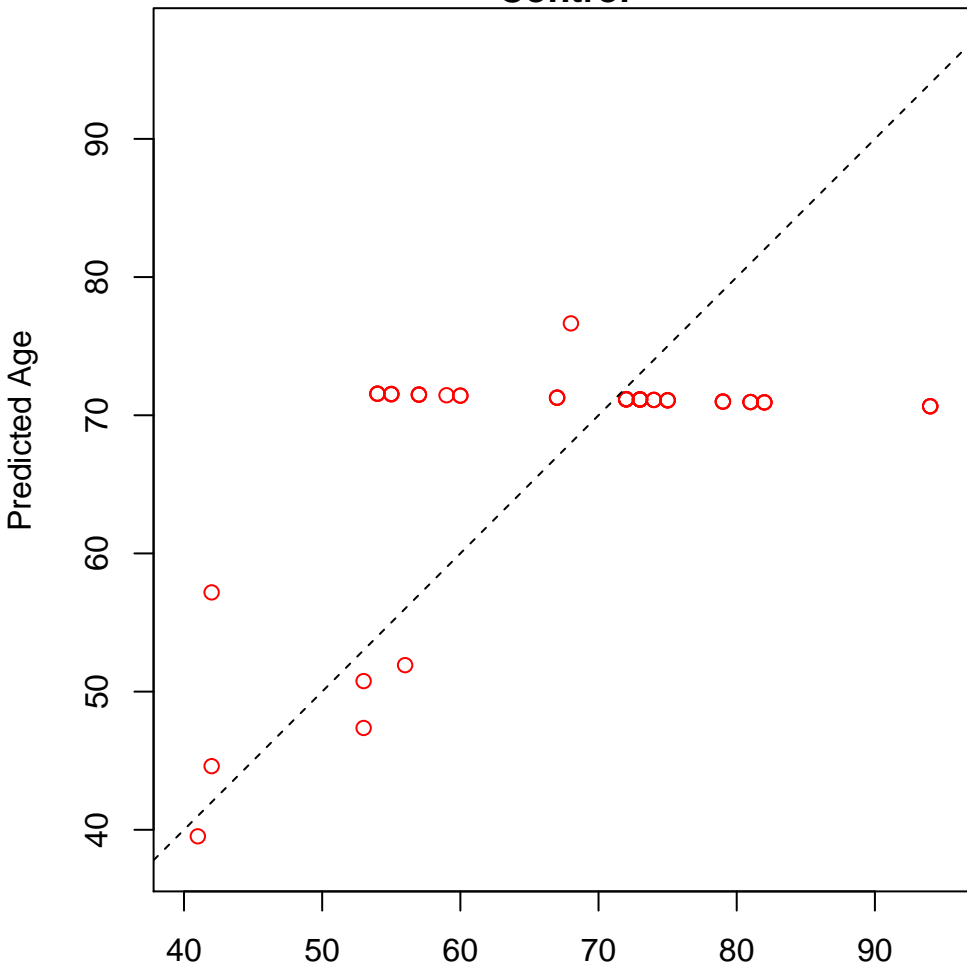


regulation of transcription from RNA polymerase II promoter in response to hypoxia (Score: 0.82993)

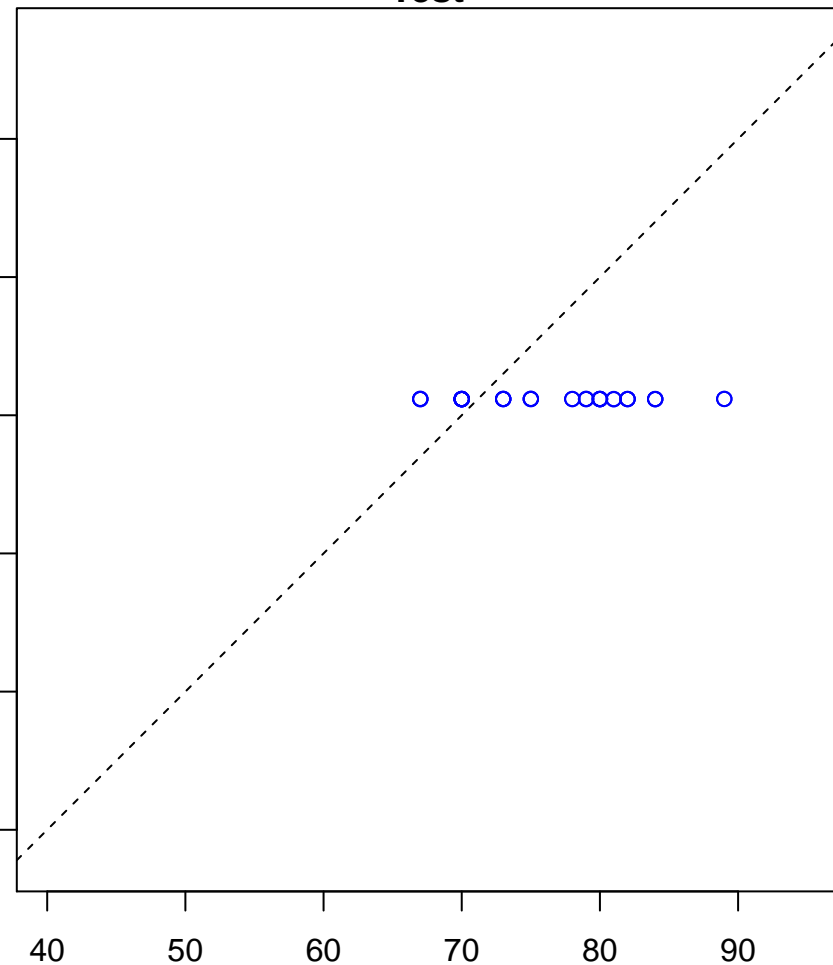


mitotic cell cycle phase transition (Score: 0.829889)

Control

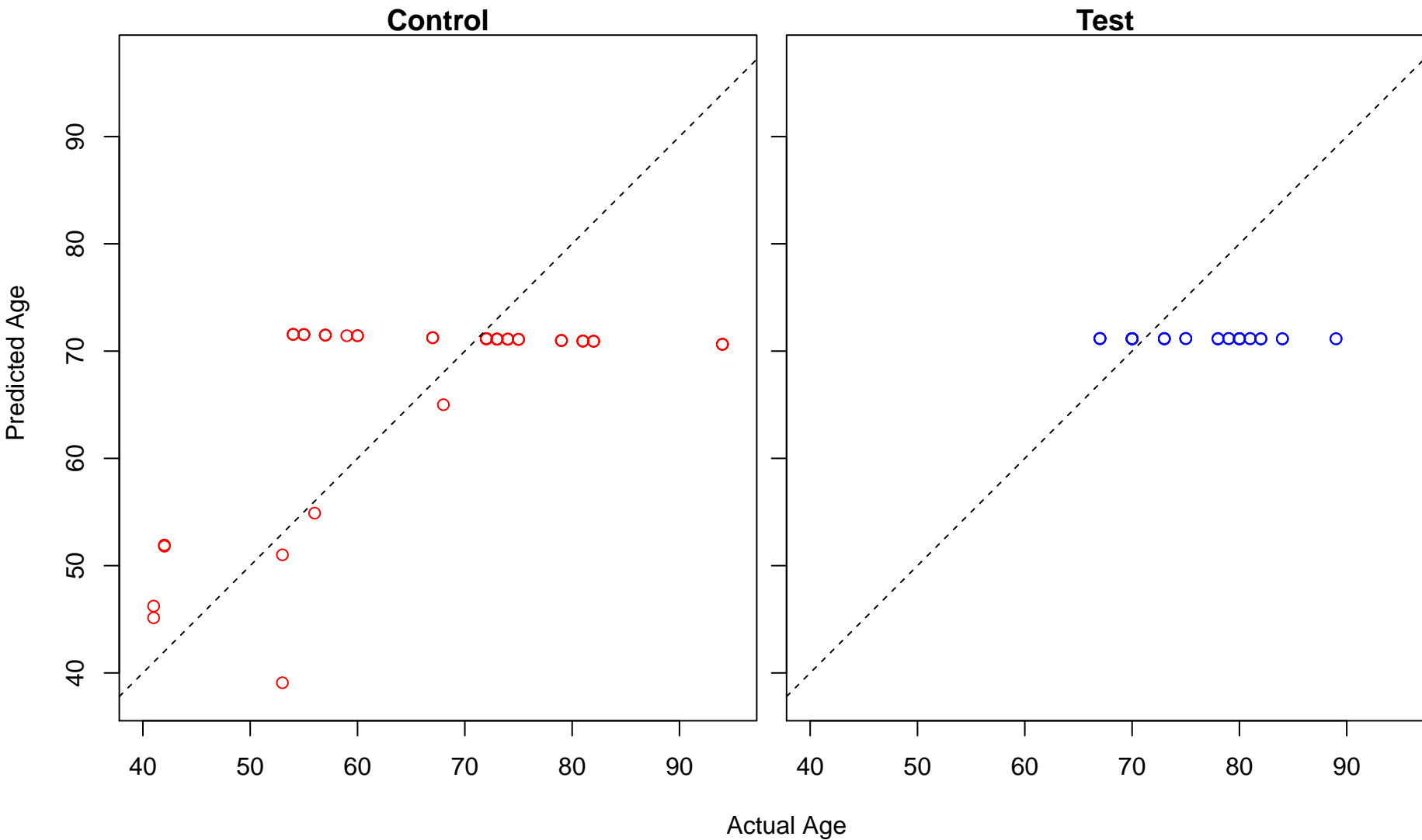


Test

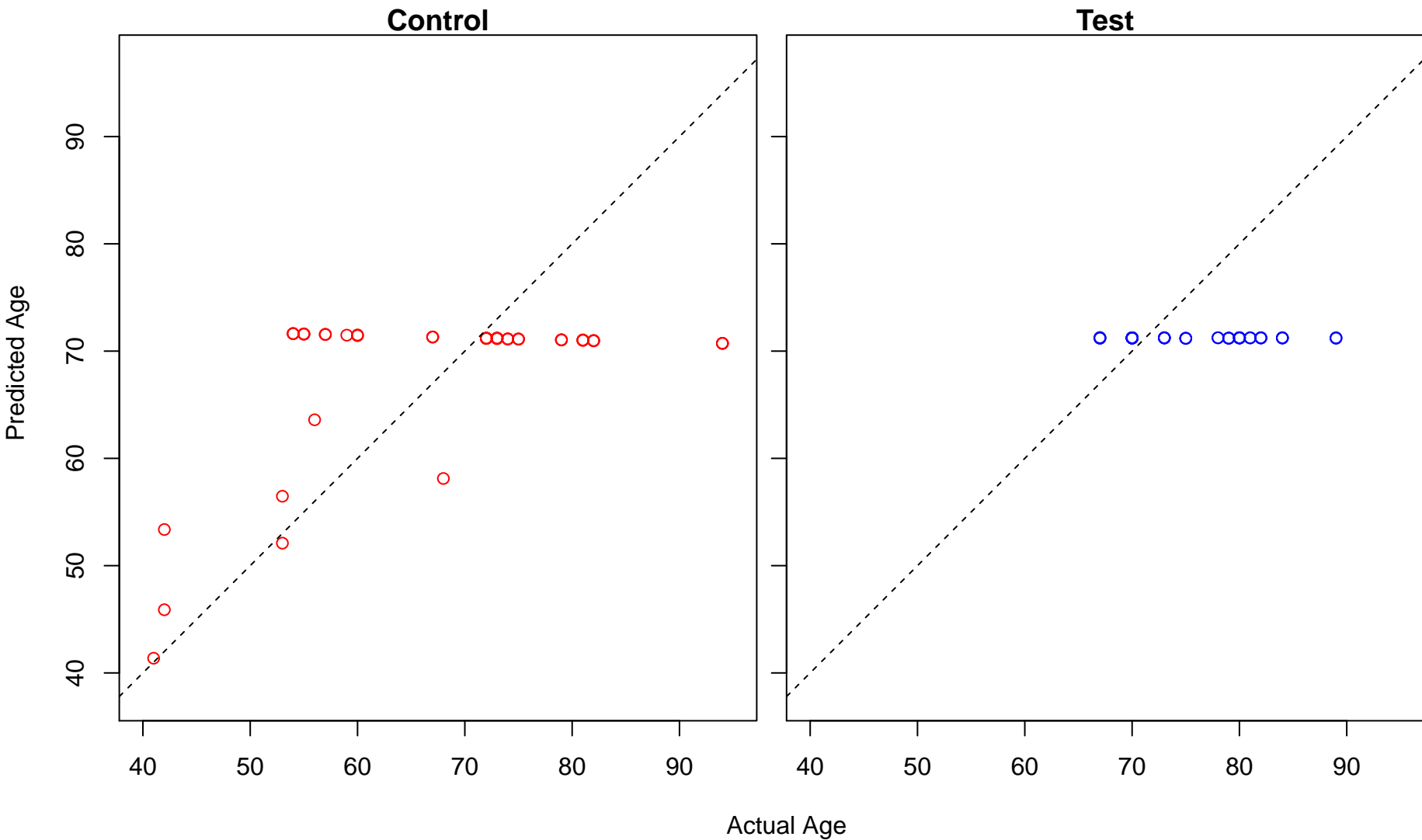


Actual Age

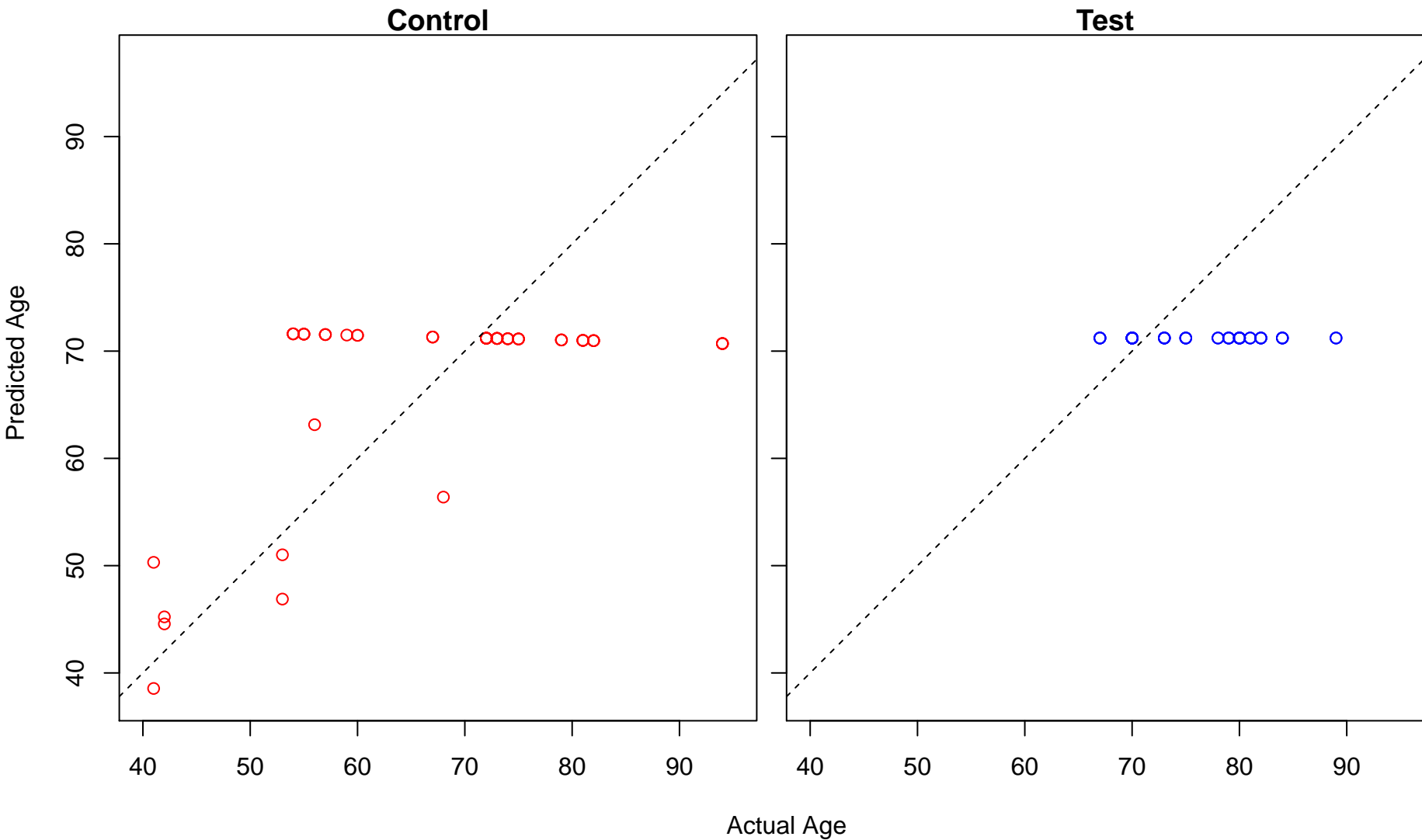
regulation of cell adhesion (Score: 0.829860)



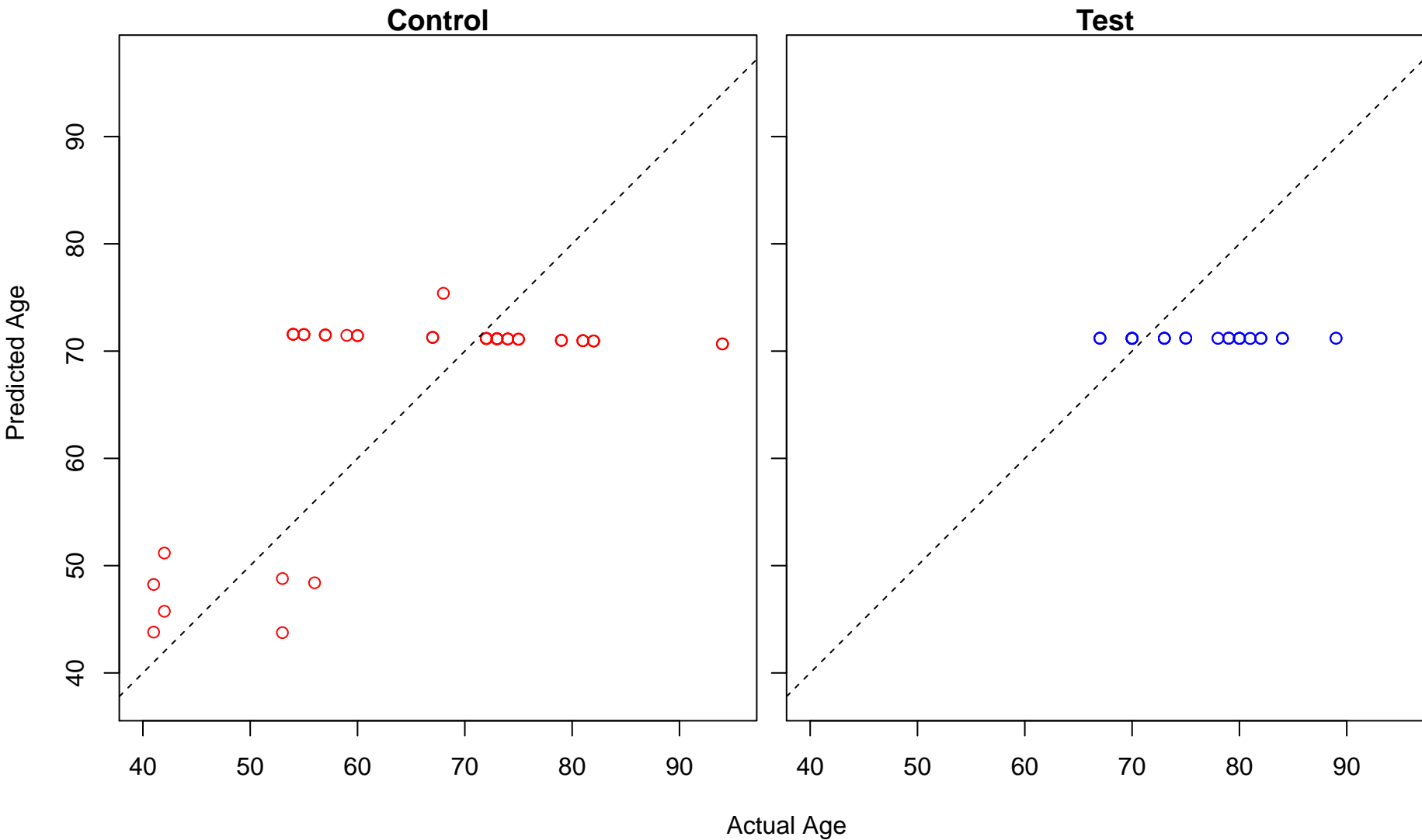
negative regulation of neuron apoptotic process (Score: 0.829800)



negative regulation of multicellular organismal process (Score: 0.829760)

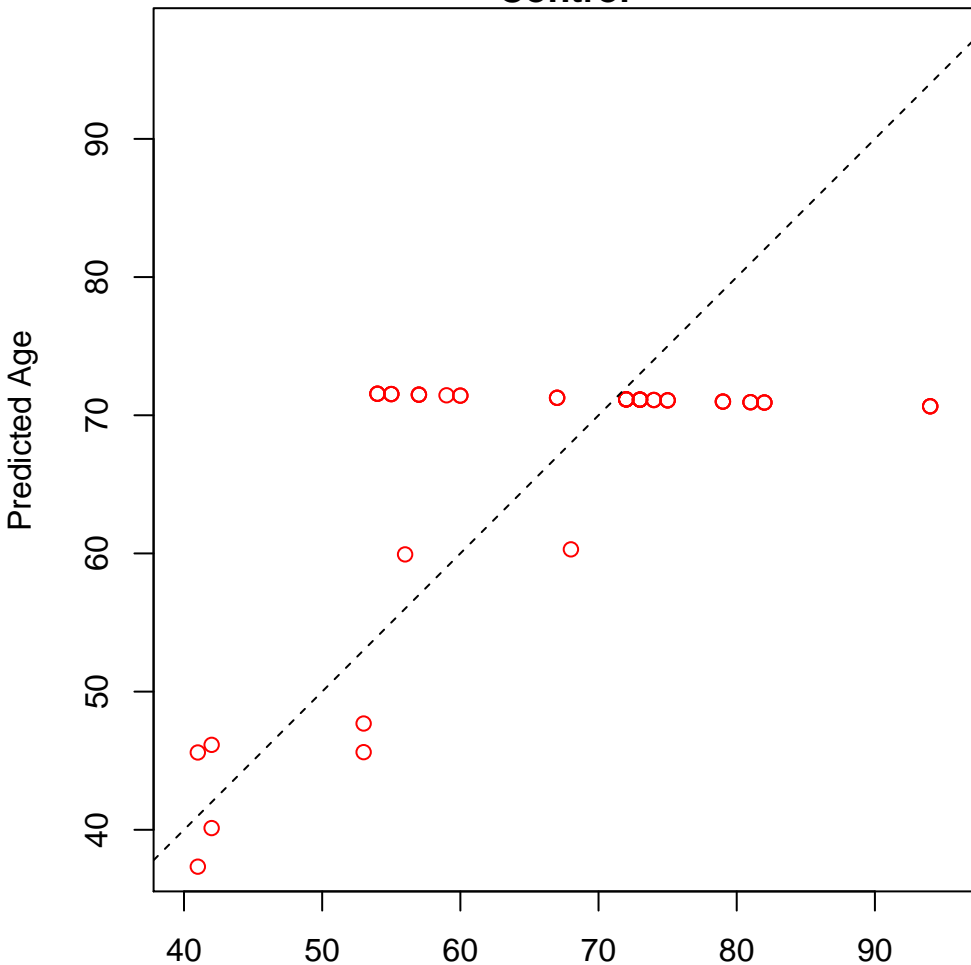


organelle assembly (Score: 0.829644)

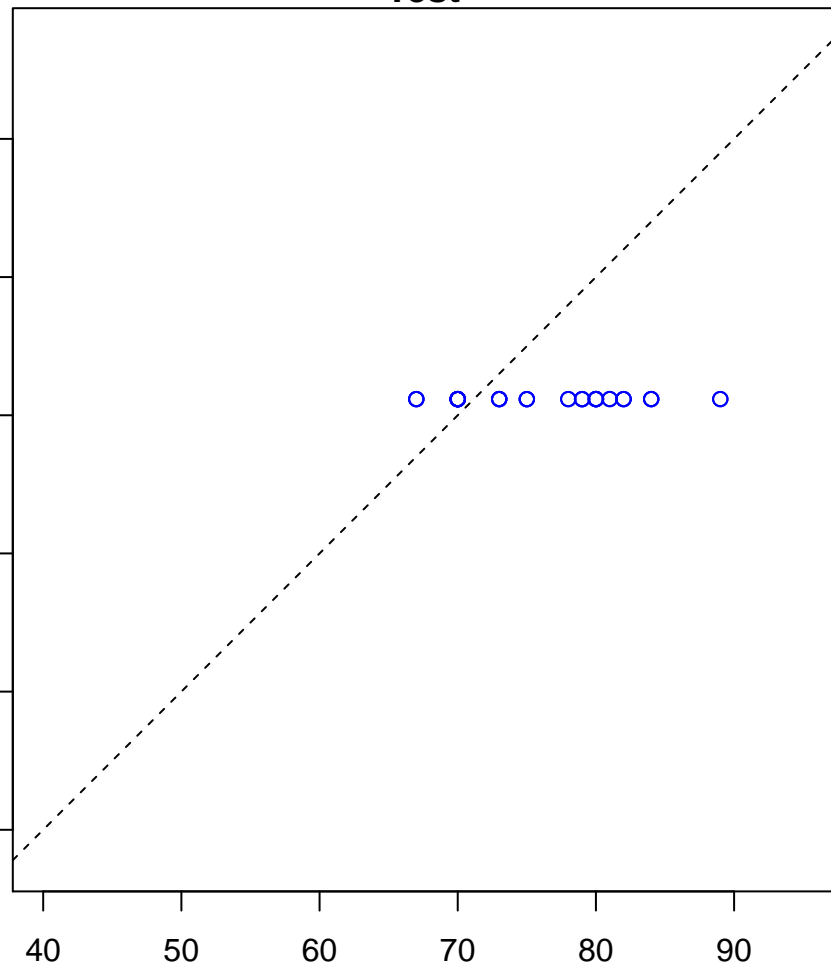


activation of protein kinase activity (Score: 0.829617)

Control



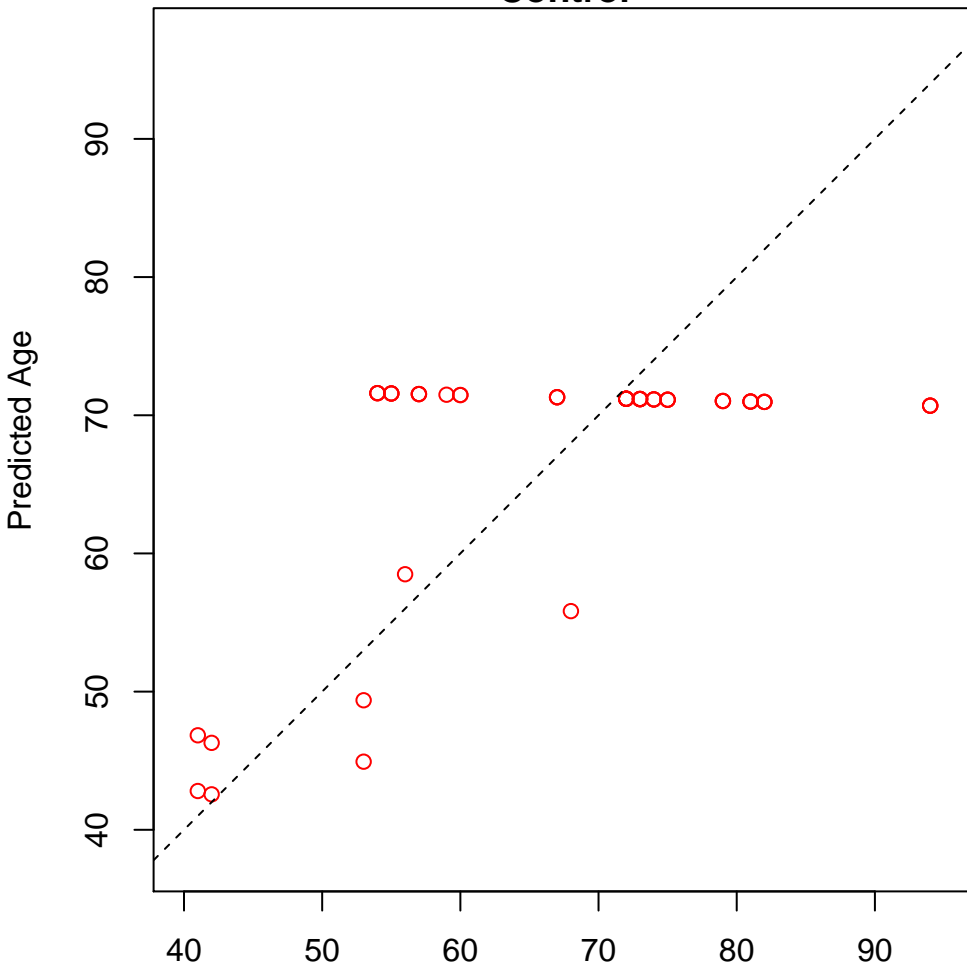
Test



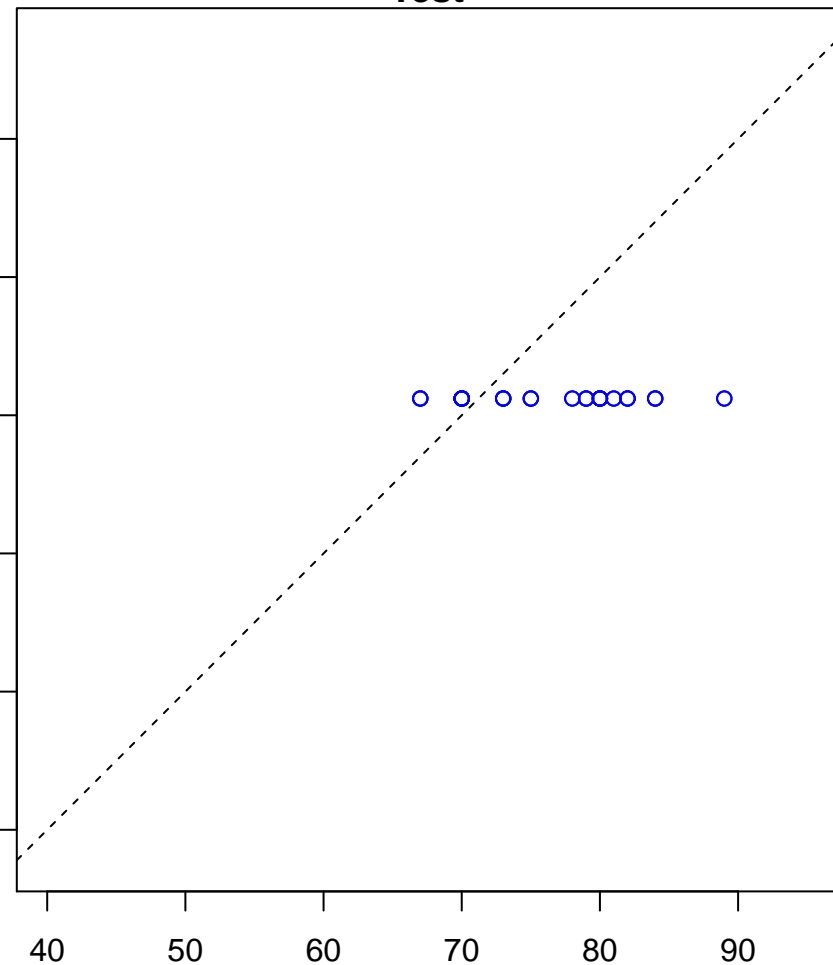
Actual Age

positive regulation of cell death (Score: 0.829571)

Control

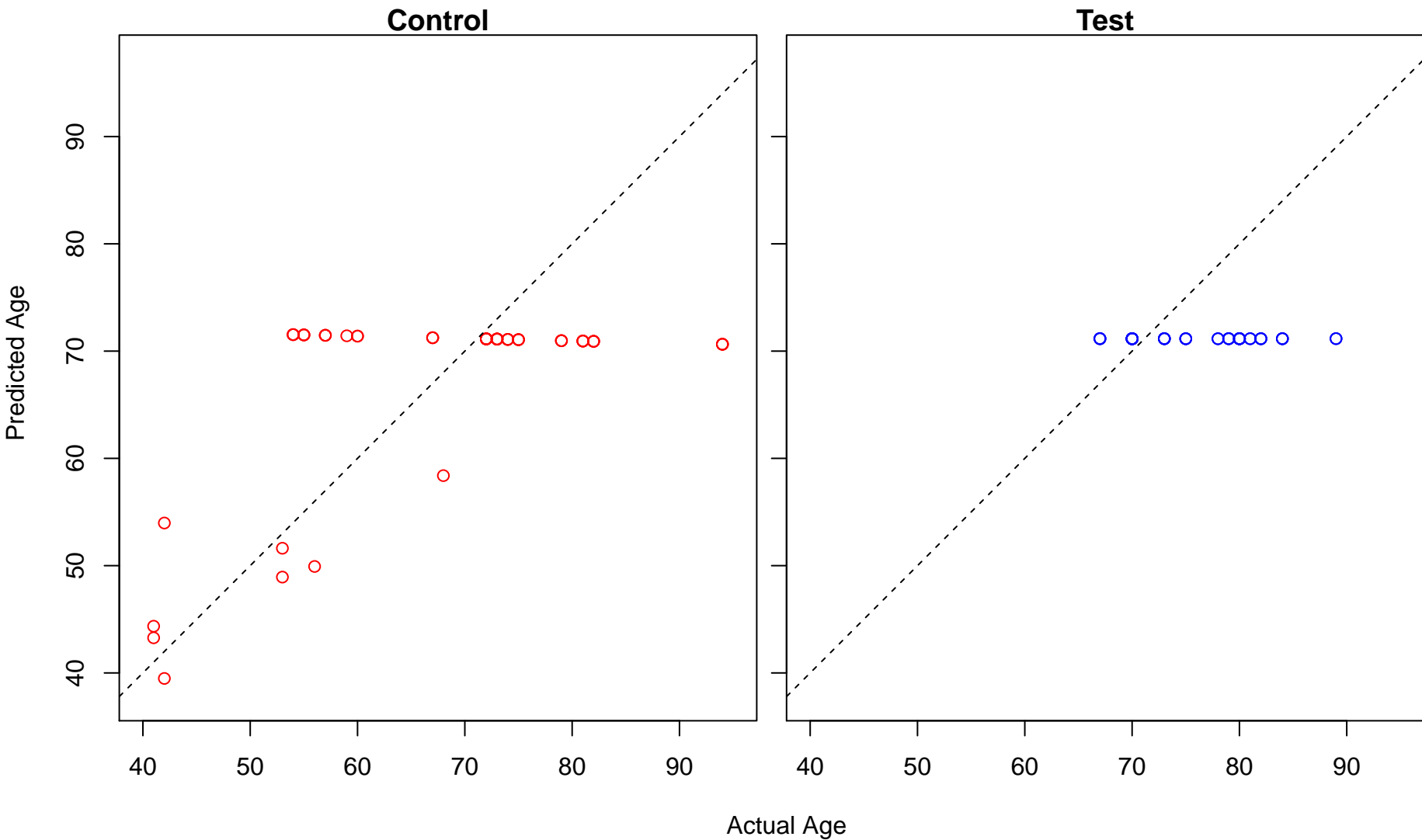


Test



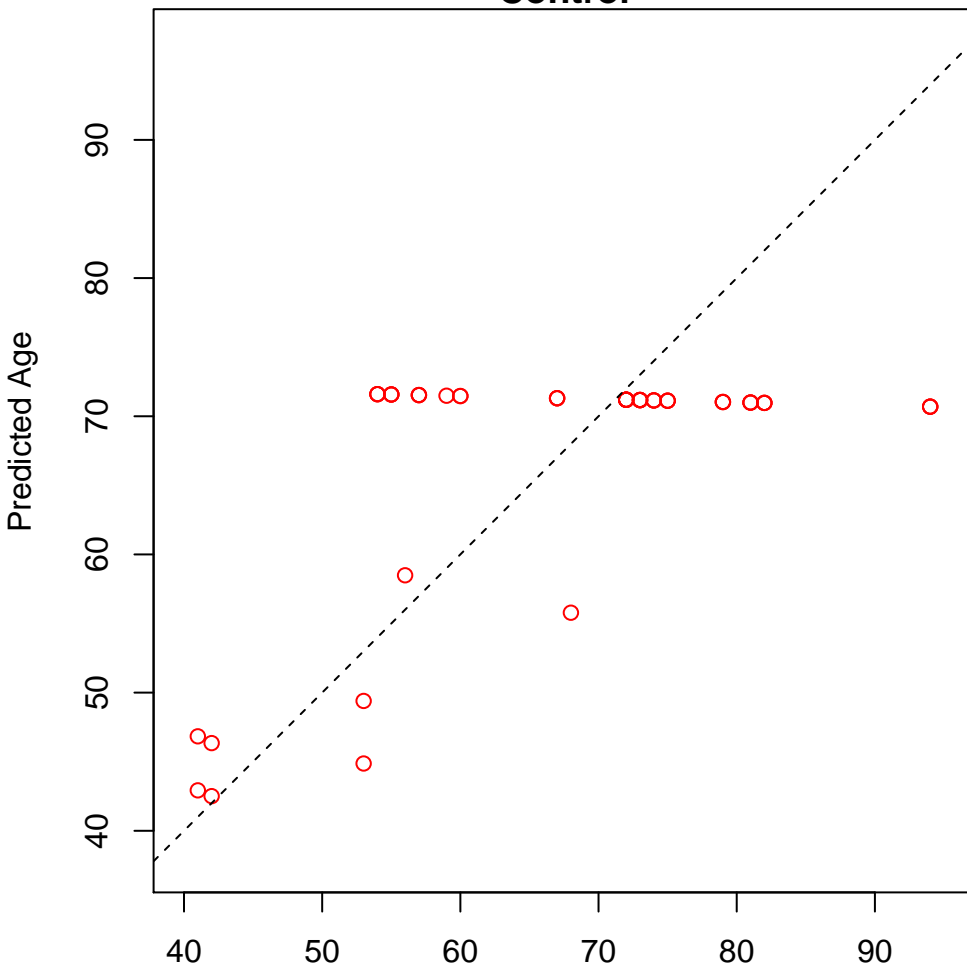
Actual Age

nuclear export (Score: 0.829566)

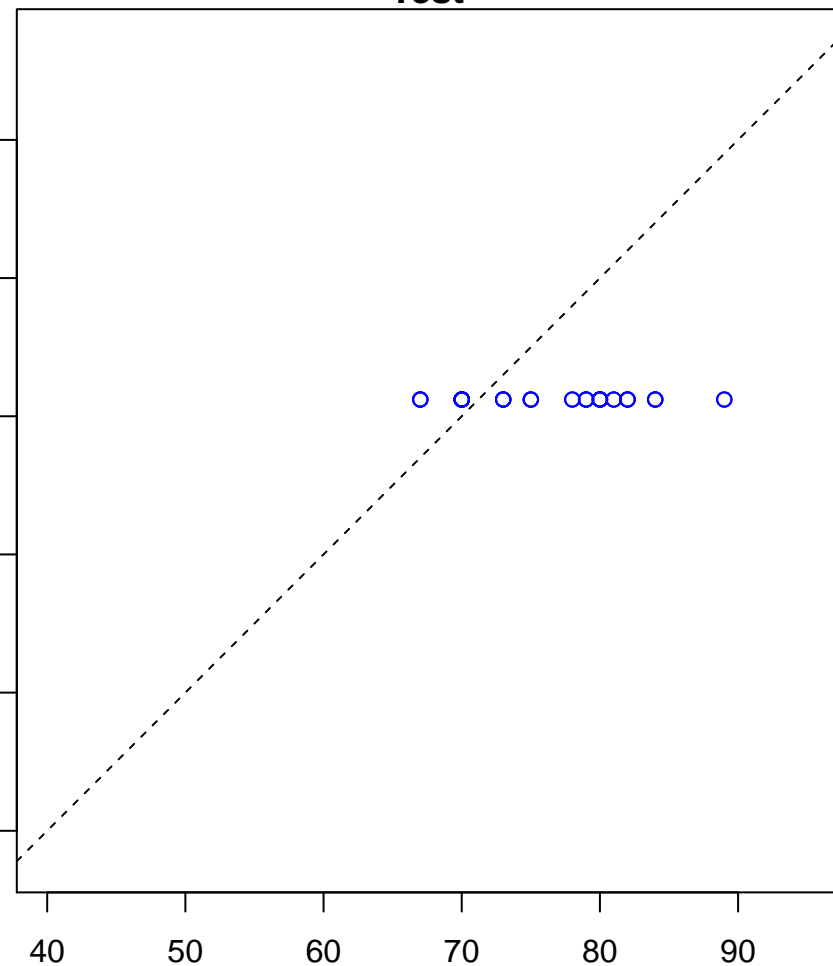


positive regulation of apoptotic process (Score: 0.829404)

Control

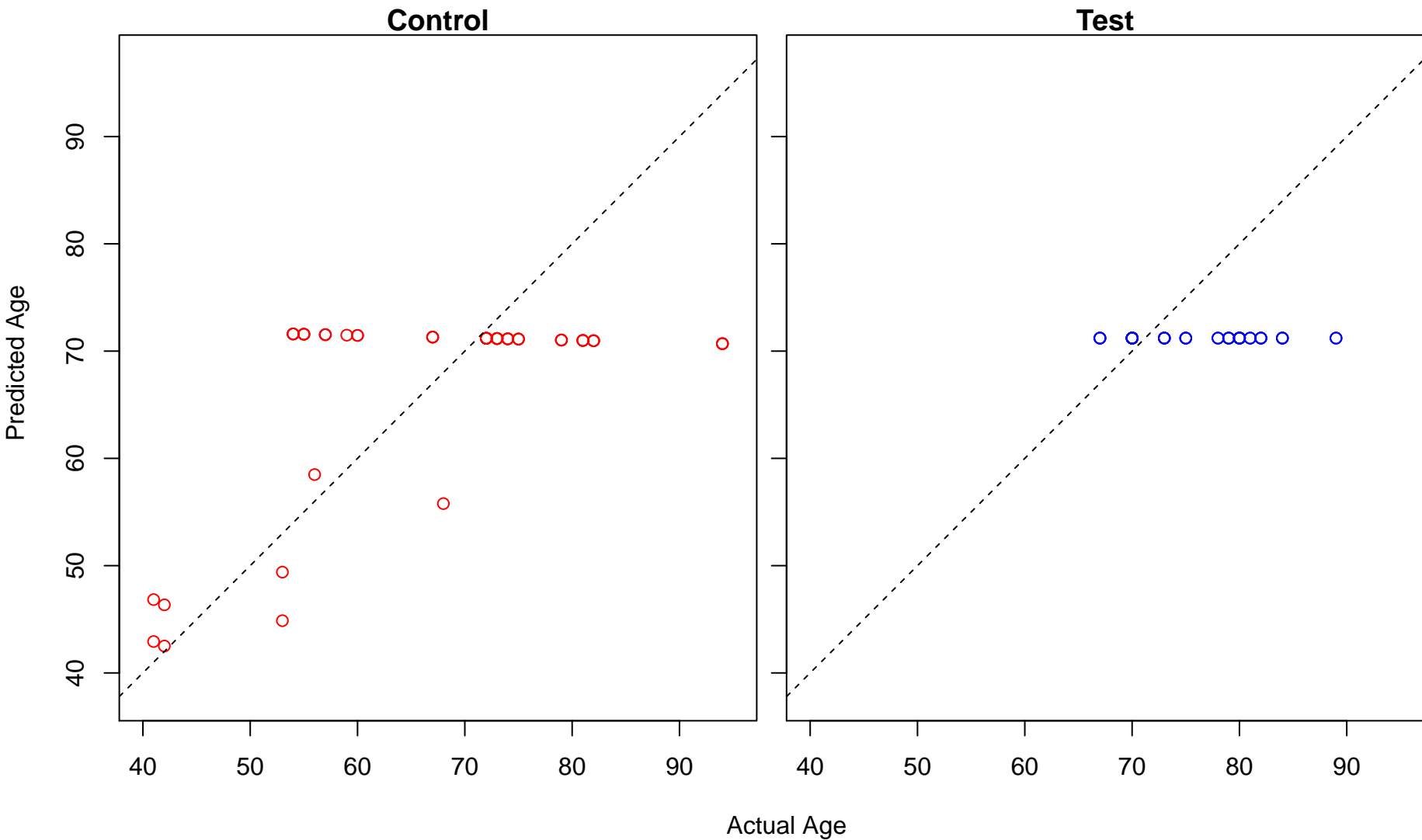


Test

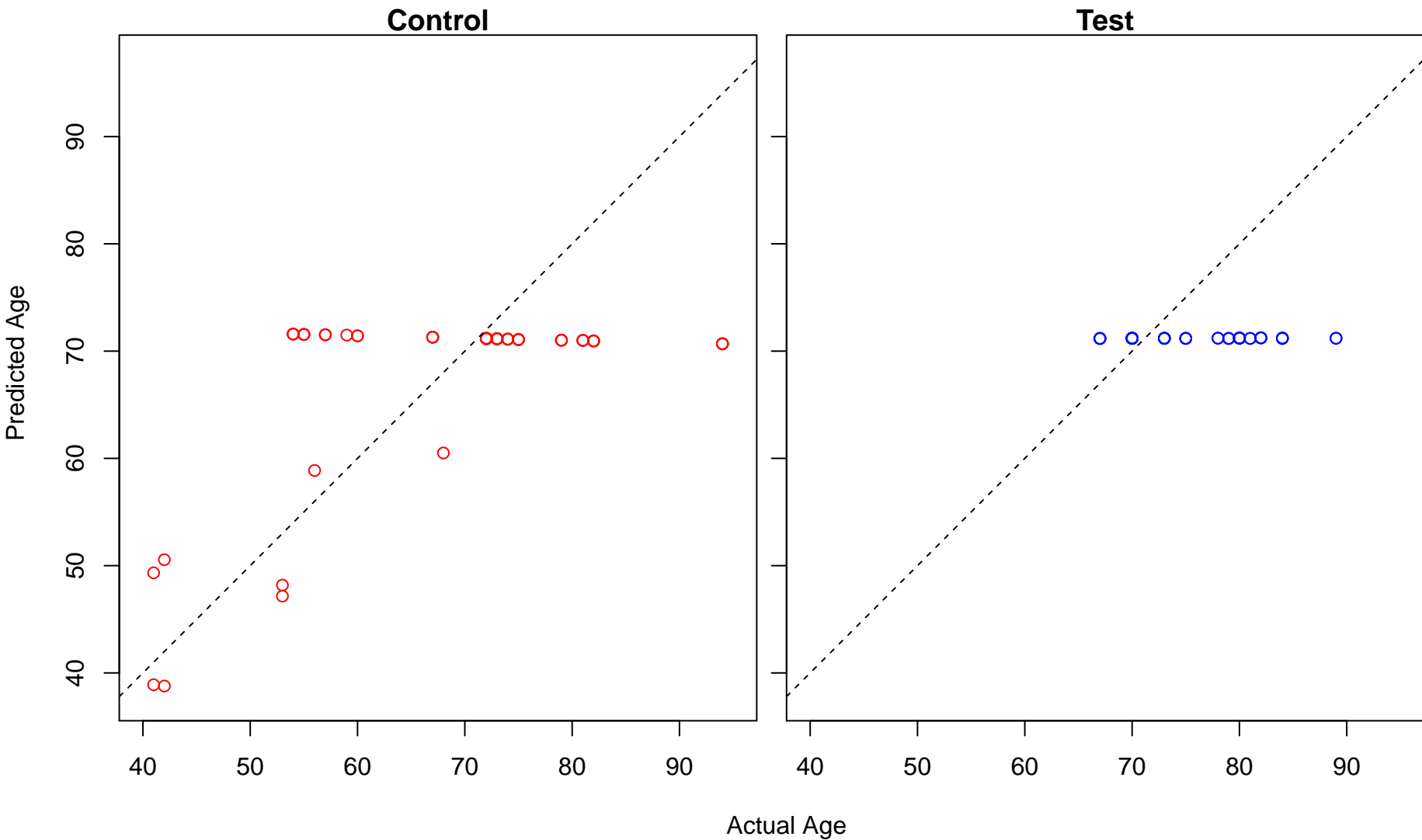


Actual Age

positive regulation of programmed cell death (Score: 0.829404)

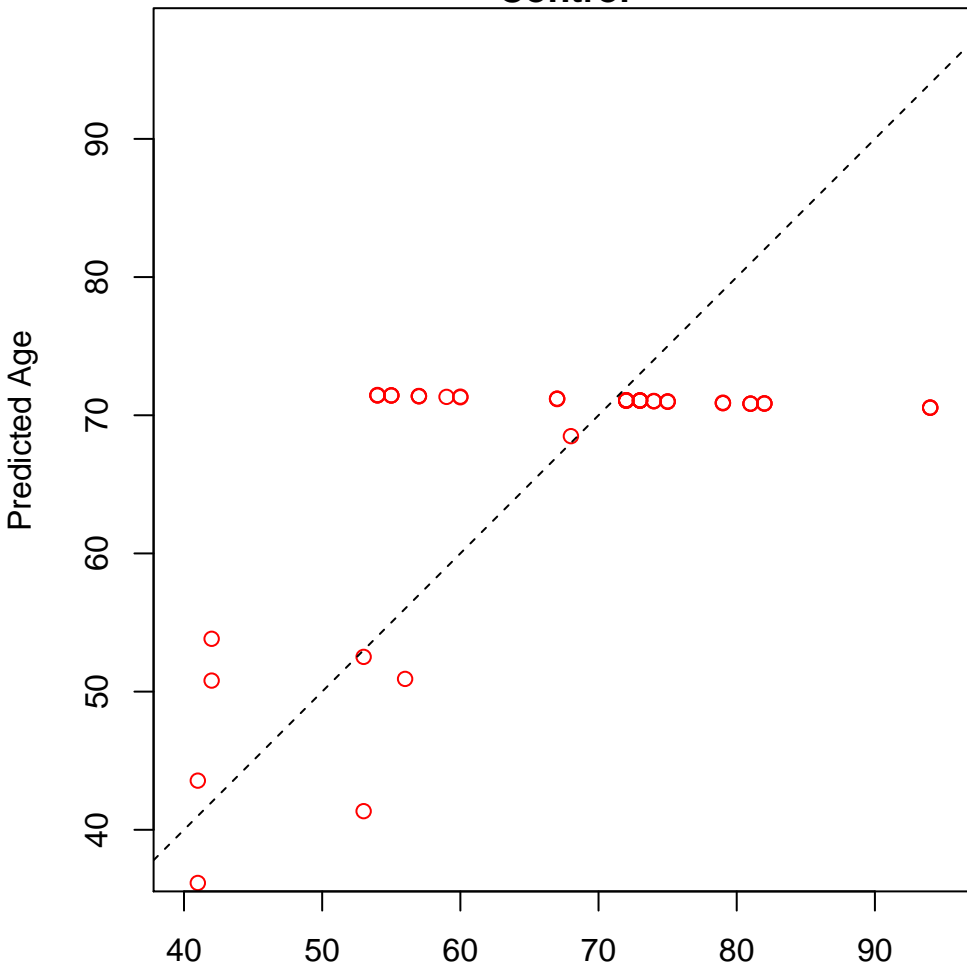


cell morphogenesis involved in differentiation (Score: 0.829377)

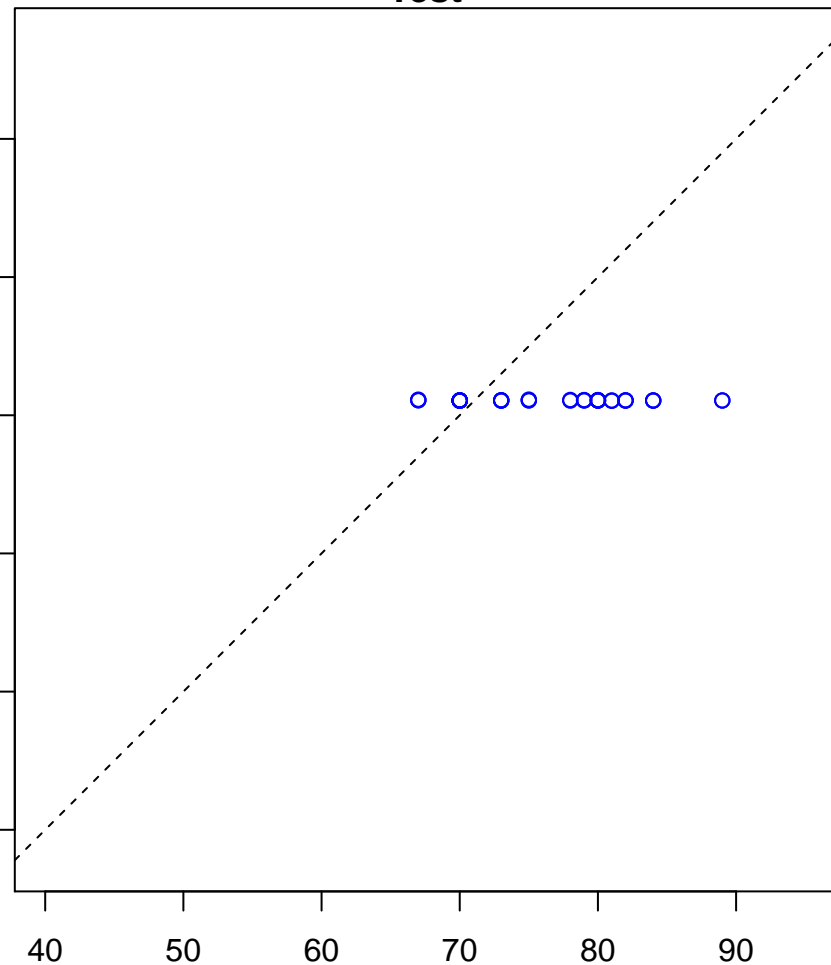


ubiquitin-dependent ERAD pathway (Score: 0.829355)

Control

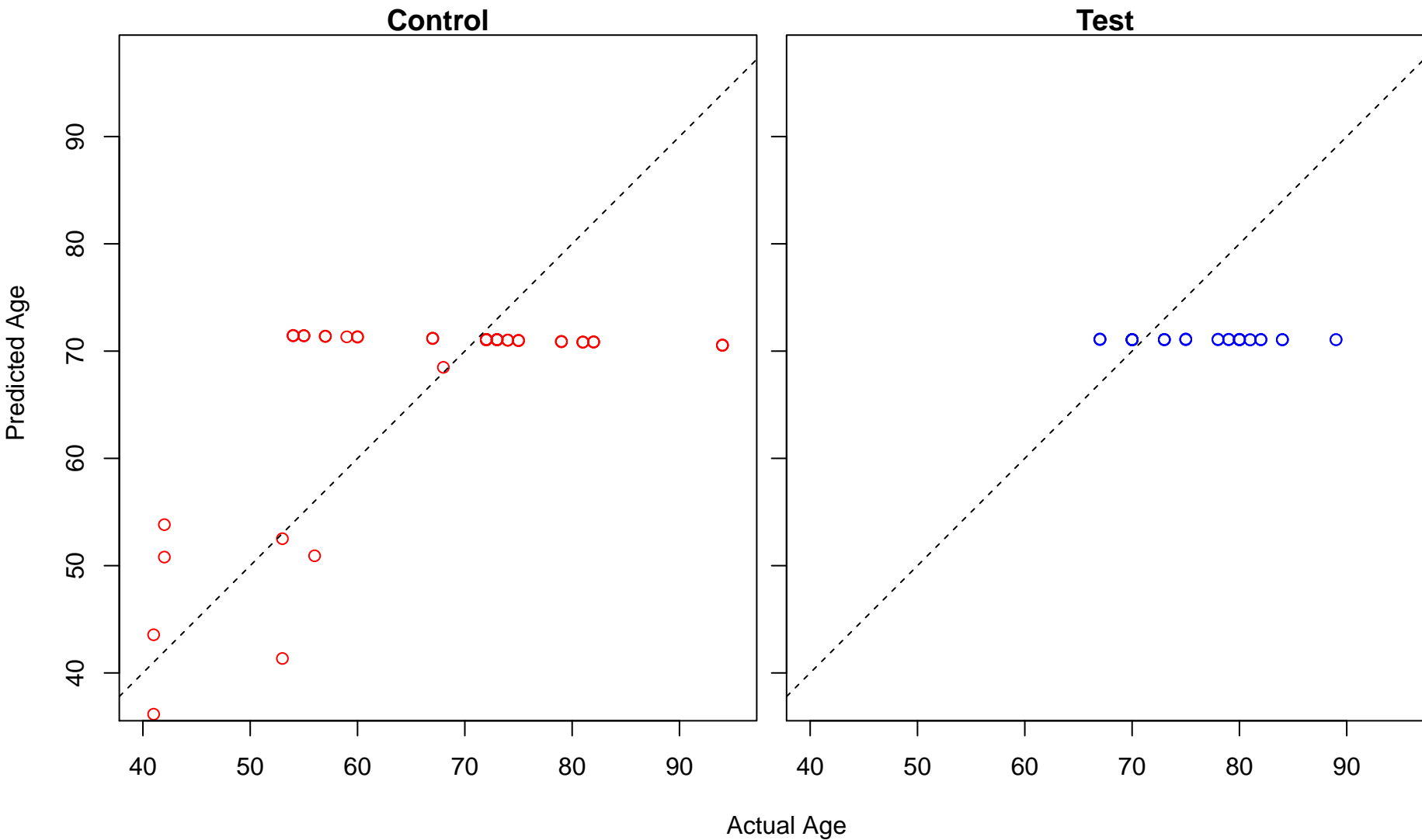


Test

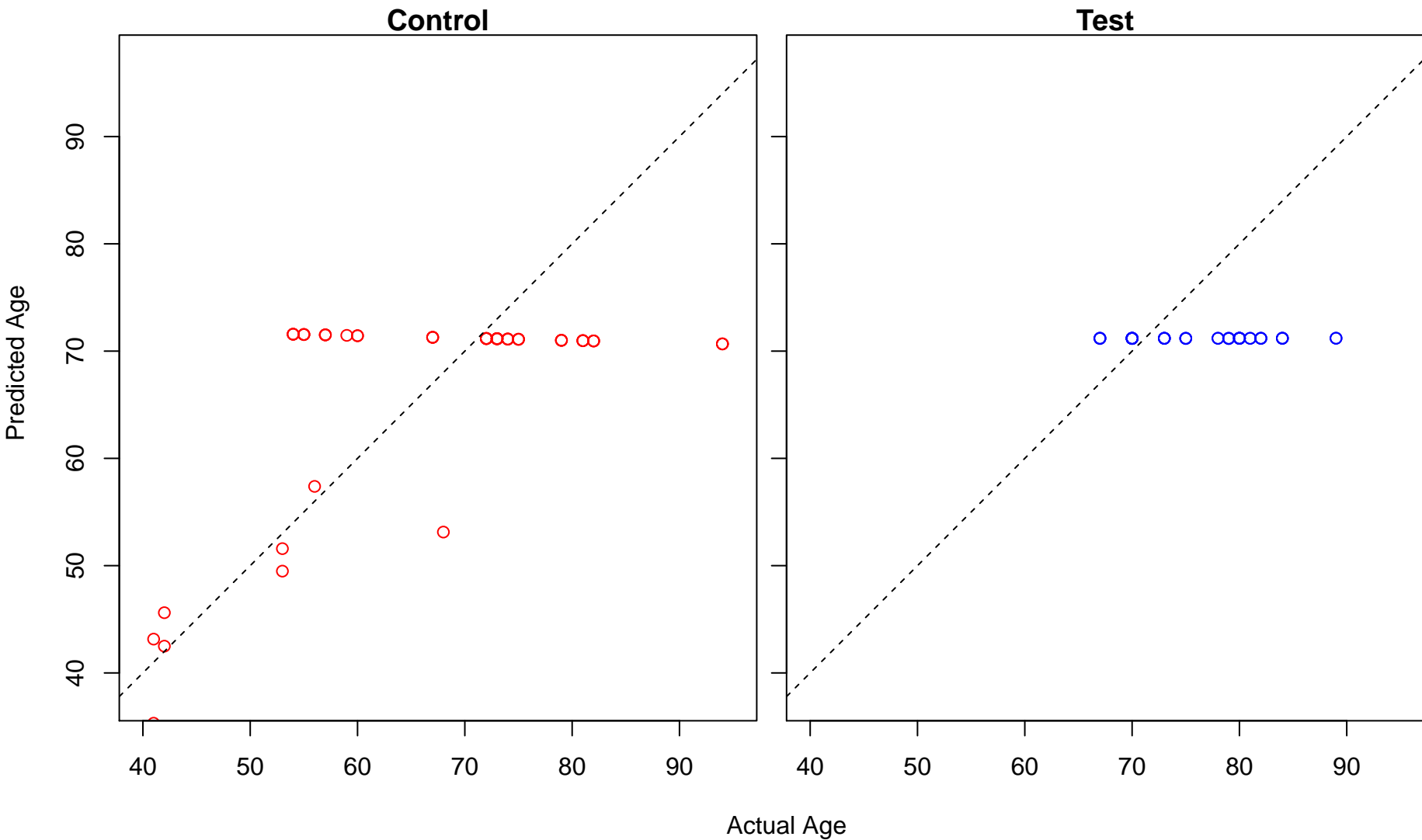


Actual Age

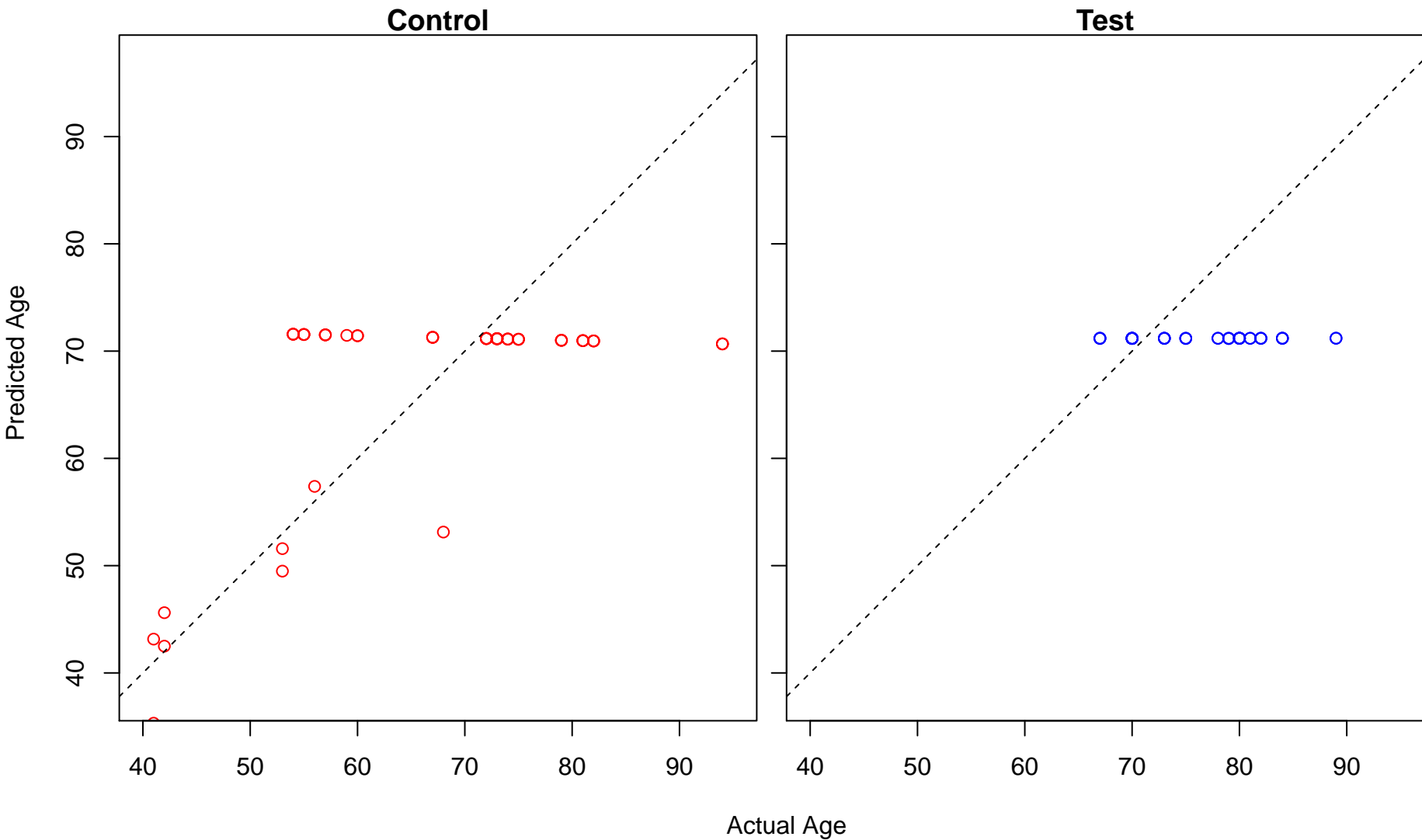
ERAD pathway (Score: 0.829355)



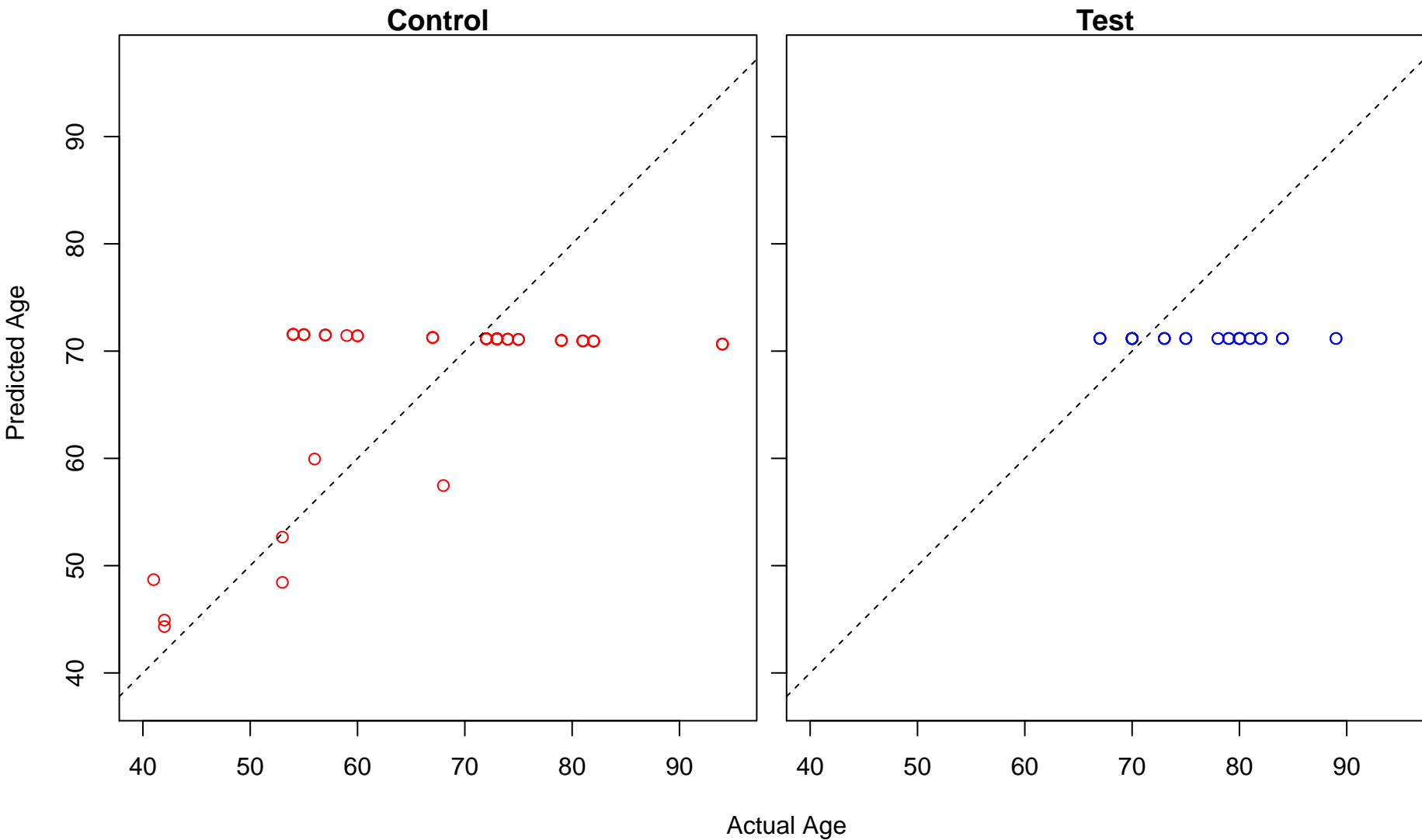
regulation of transcription from RNA polymerase II promoter in response to stress (Score: 0.829063)



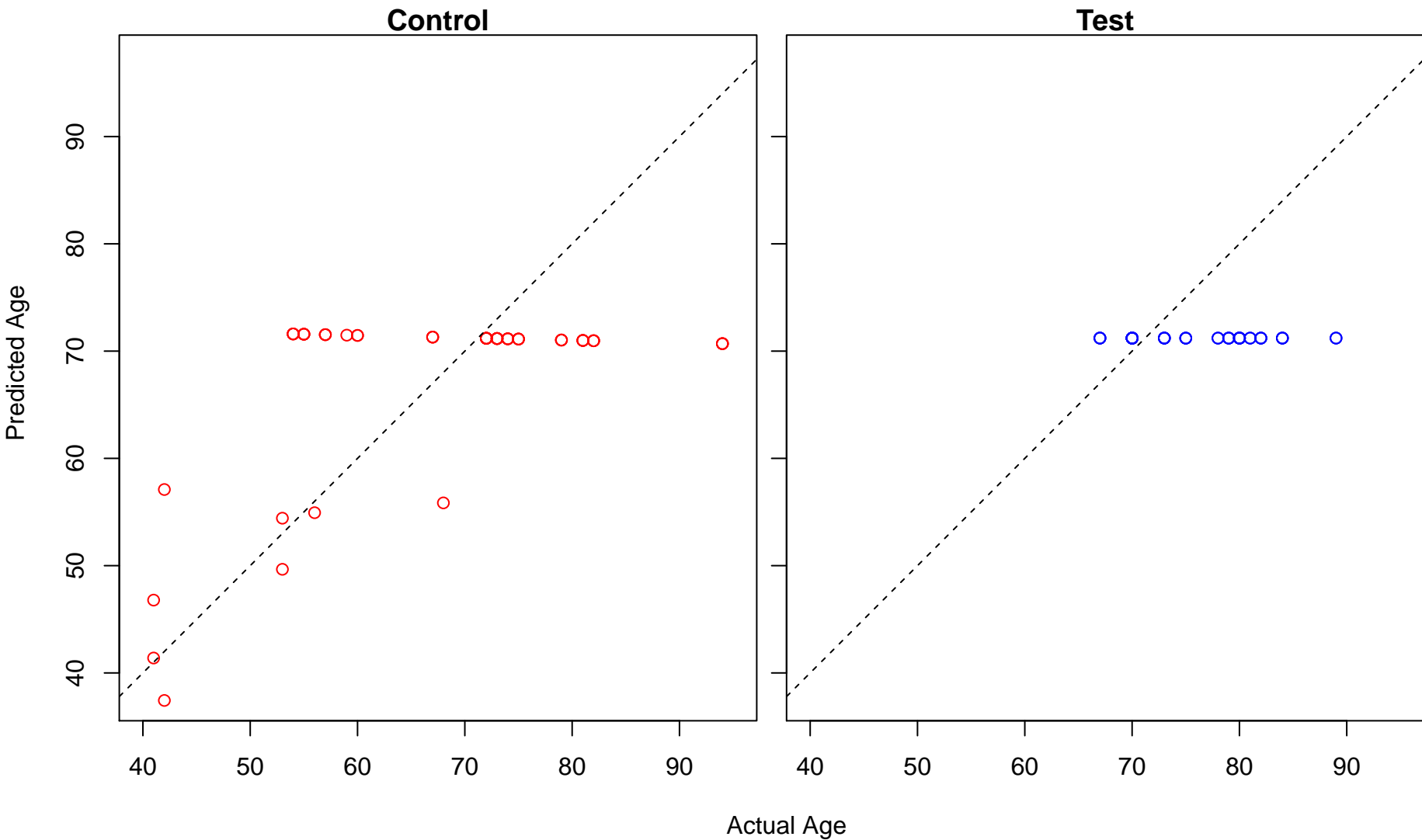
regulation of DNA-templated transcription in response to stress (Score: 0.829063)



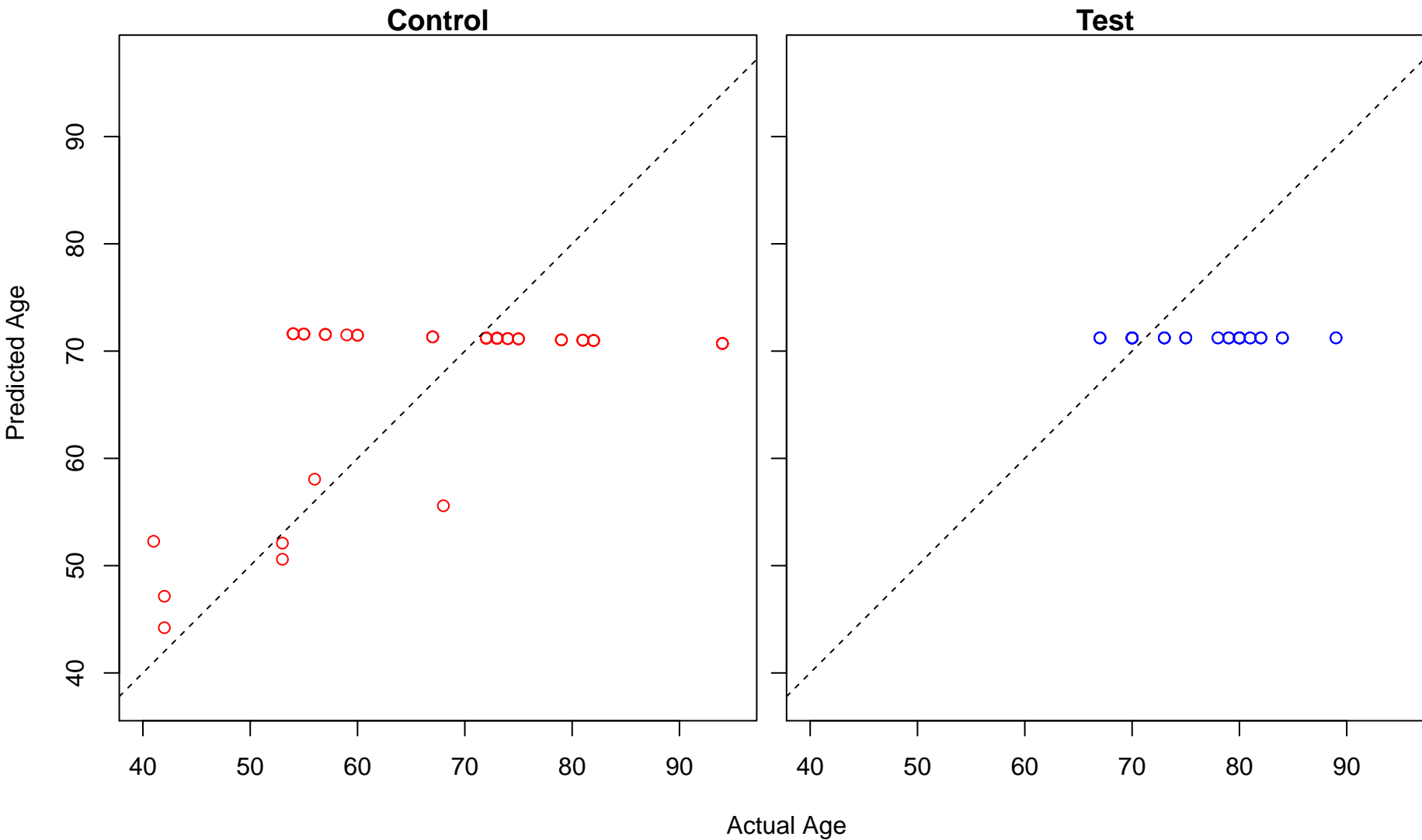
membrane organization (Score: 0.828832)



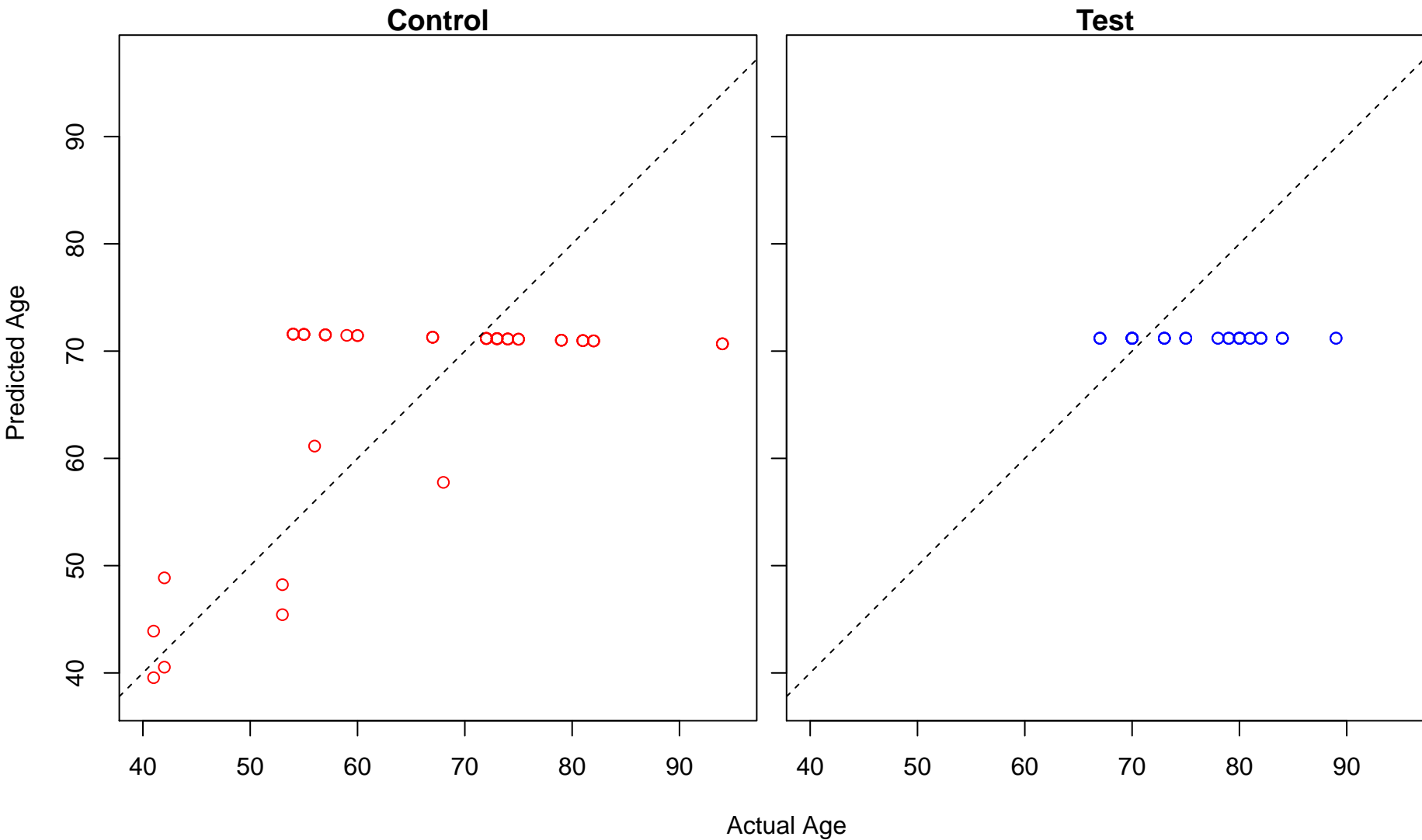
regulation of neuron death (Score: 0.828829)



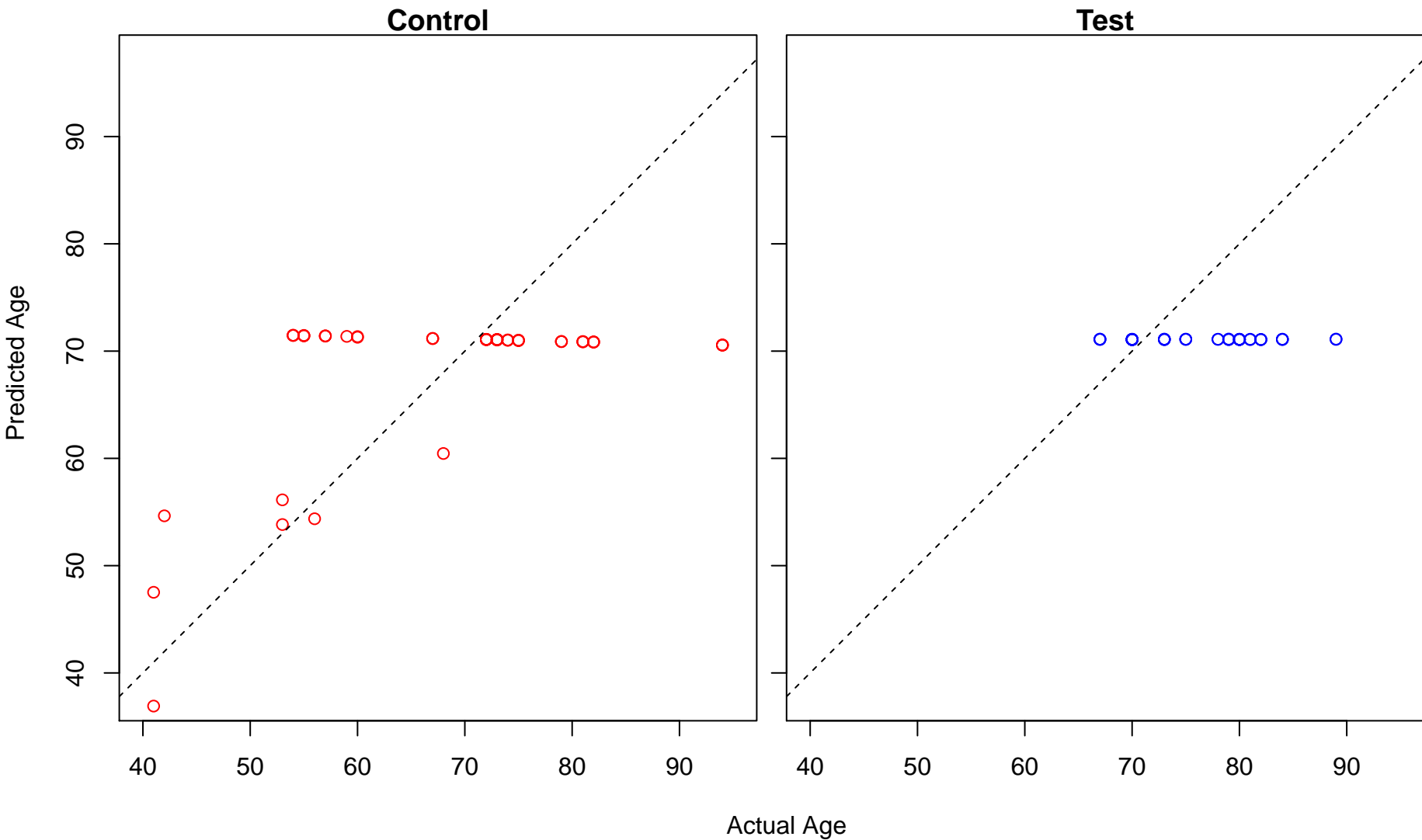
regulation of morphogenesis of an epithelium (Score: 0.828659)



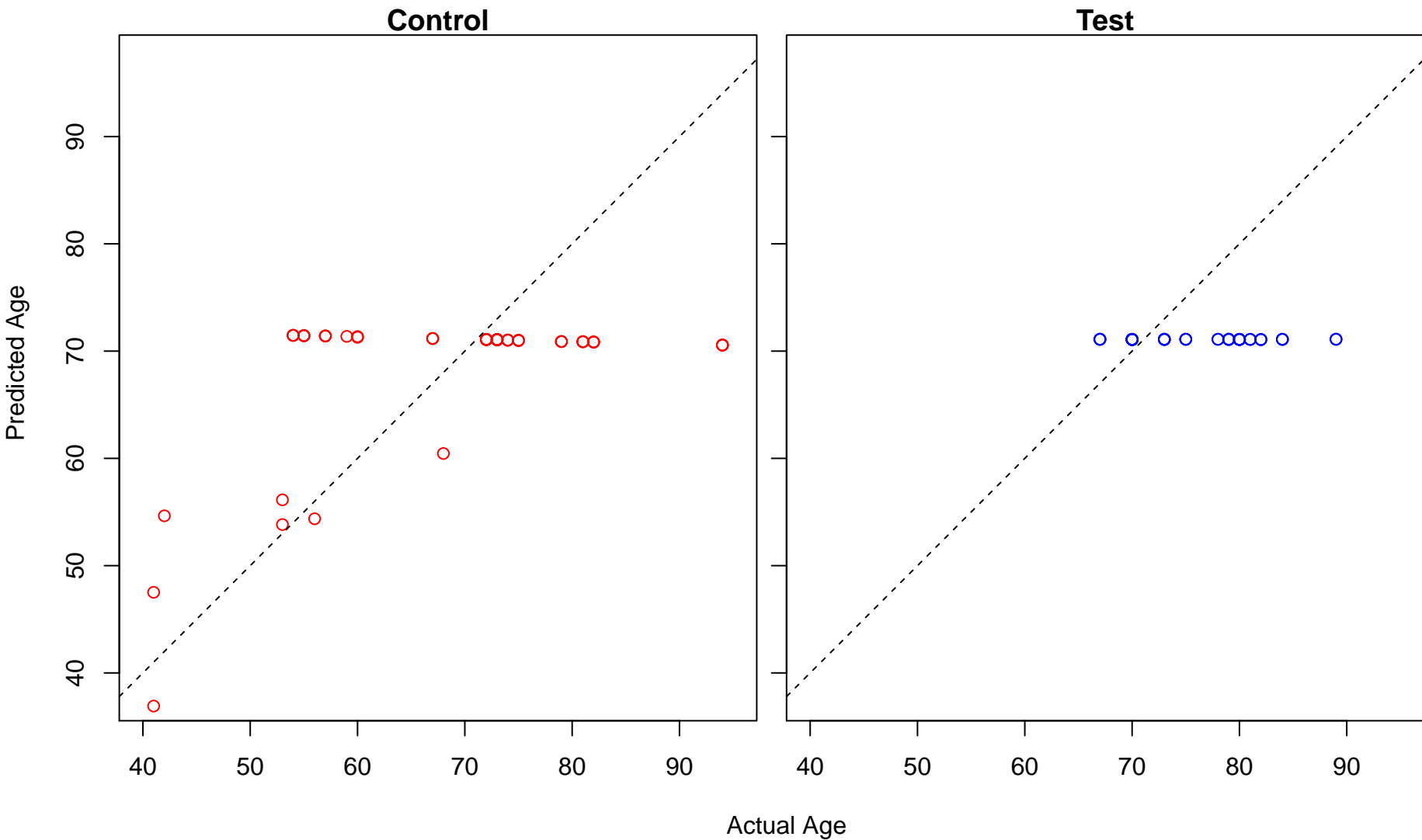
positive regulation of proteolysis (Score: 0.828449)



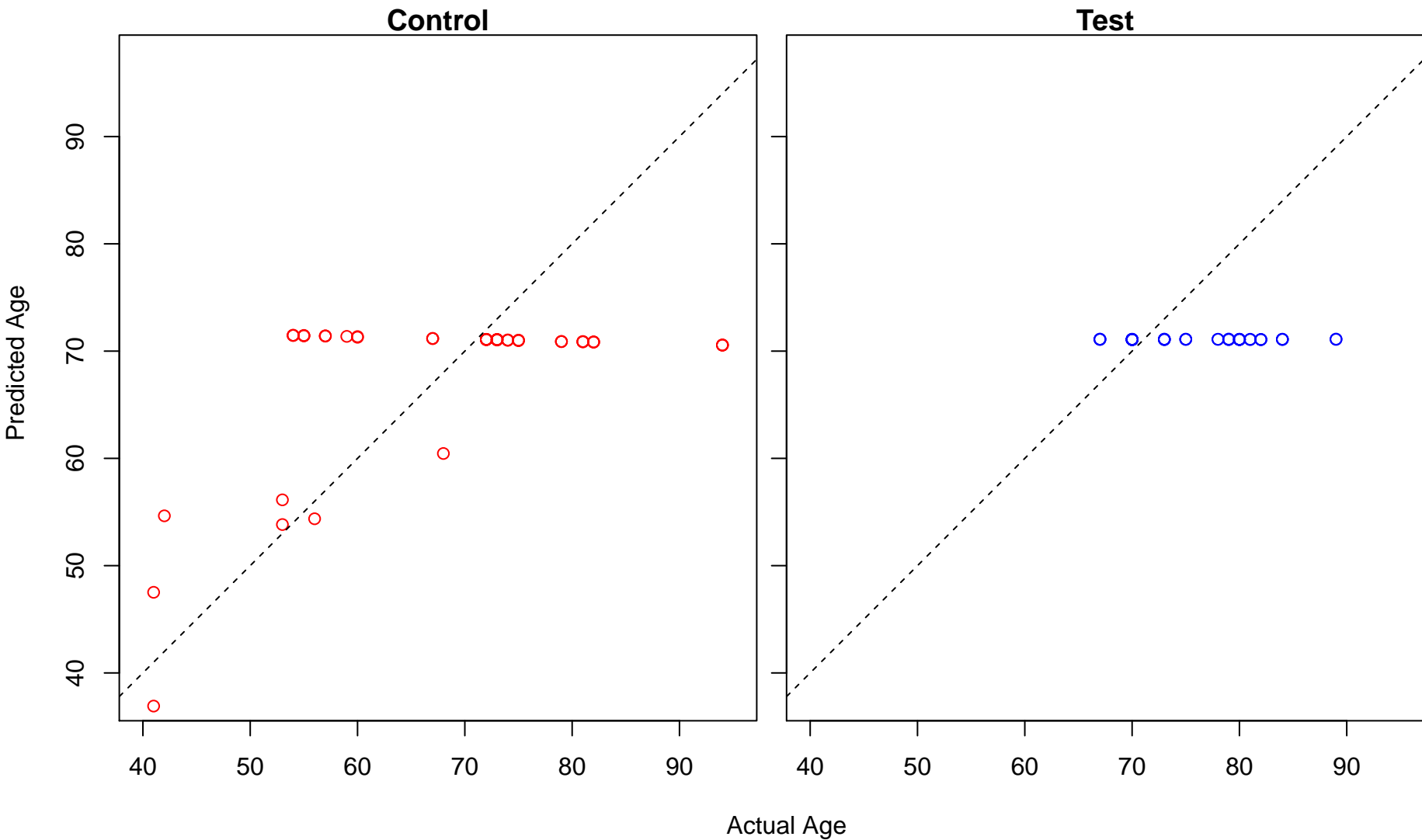
regulation of actin filament bundle assembly (Score: 0.828437)



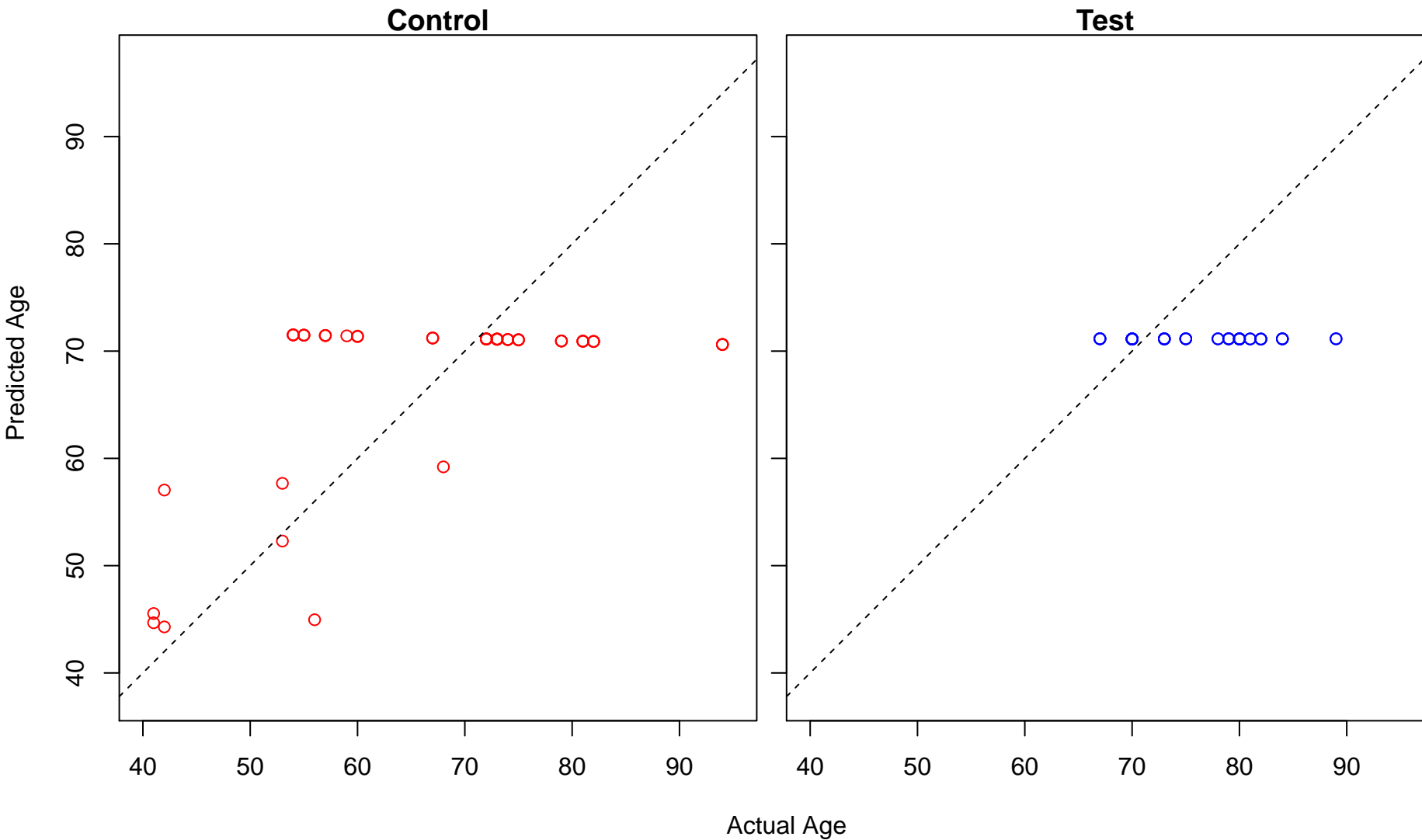
regulation of stress fiber assembly (Score: 0.828437)



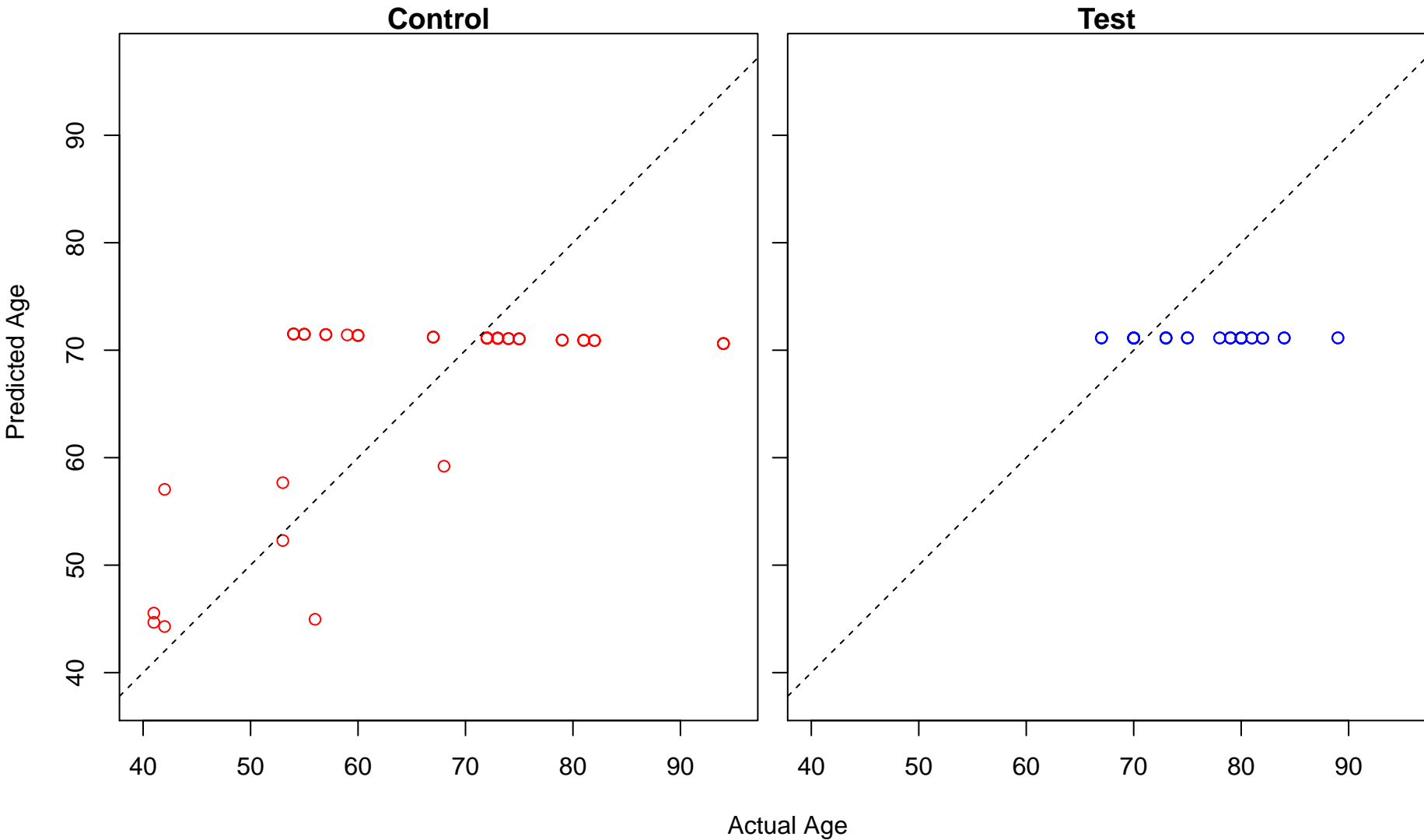
regulation of actomyosin structure organization (Score: 0.828437)



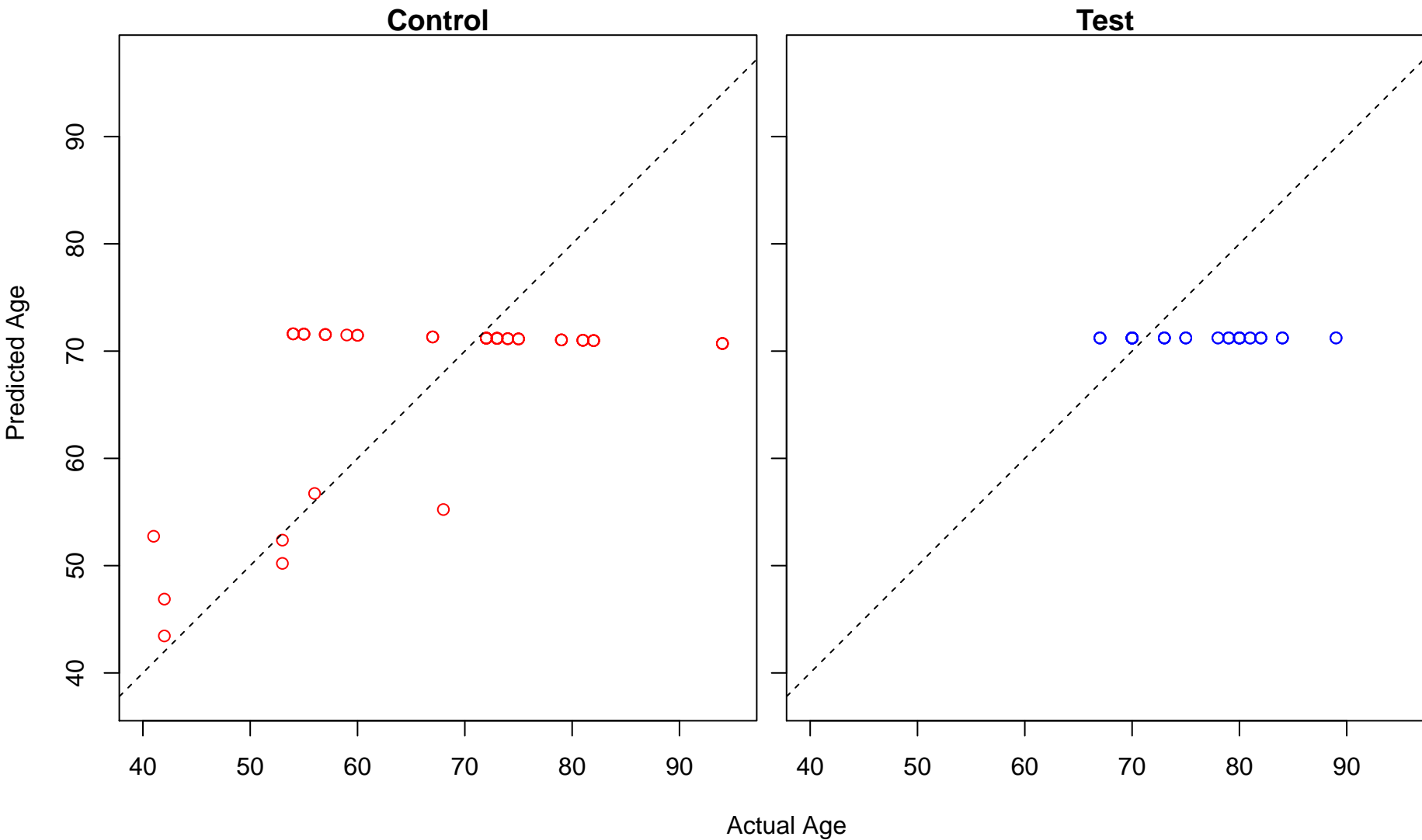
negative regulation of actin filament bundle assembly (Score: 0.828391)



negative regulation of stress fiber assembly (Score: 0.828391)

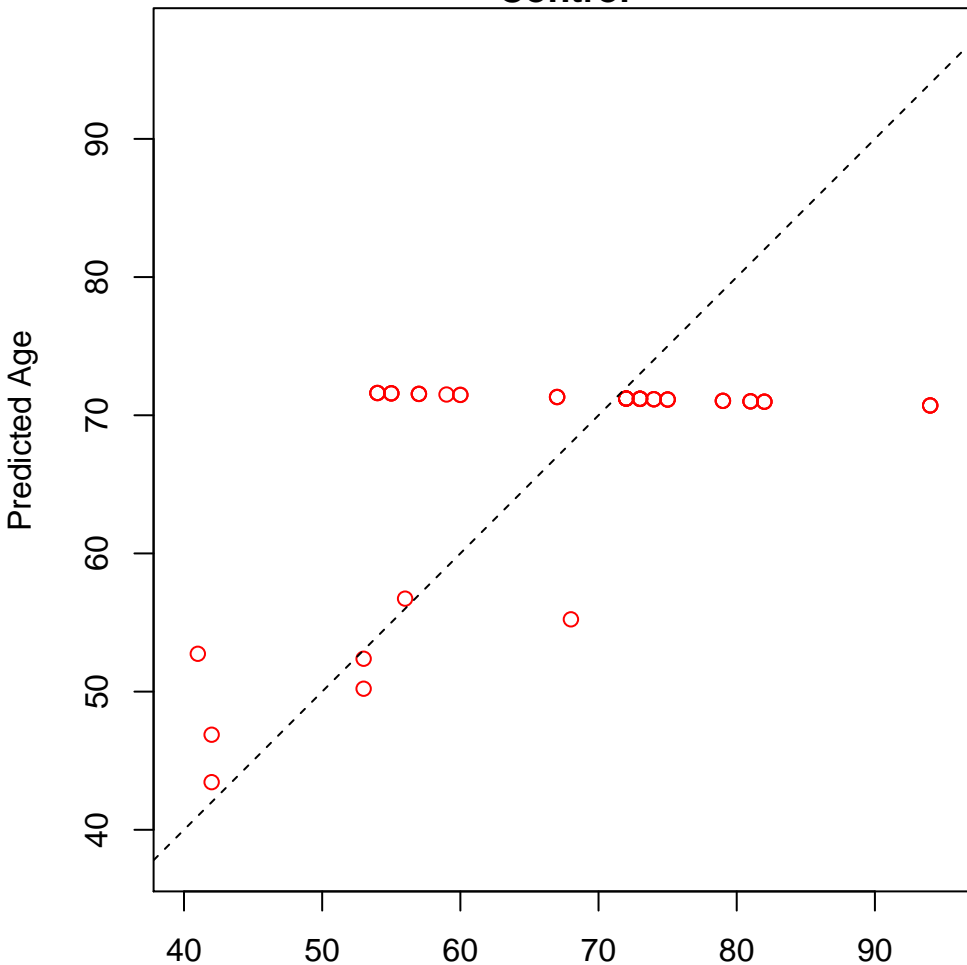


Wnt signaling pathway, planar cell polarity pathway (Score: 0.828266)

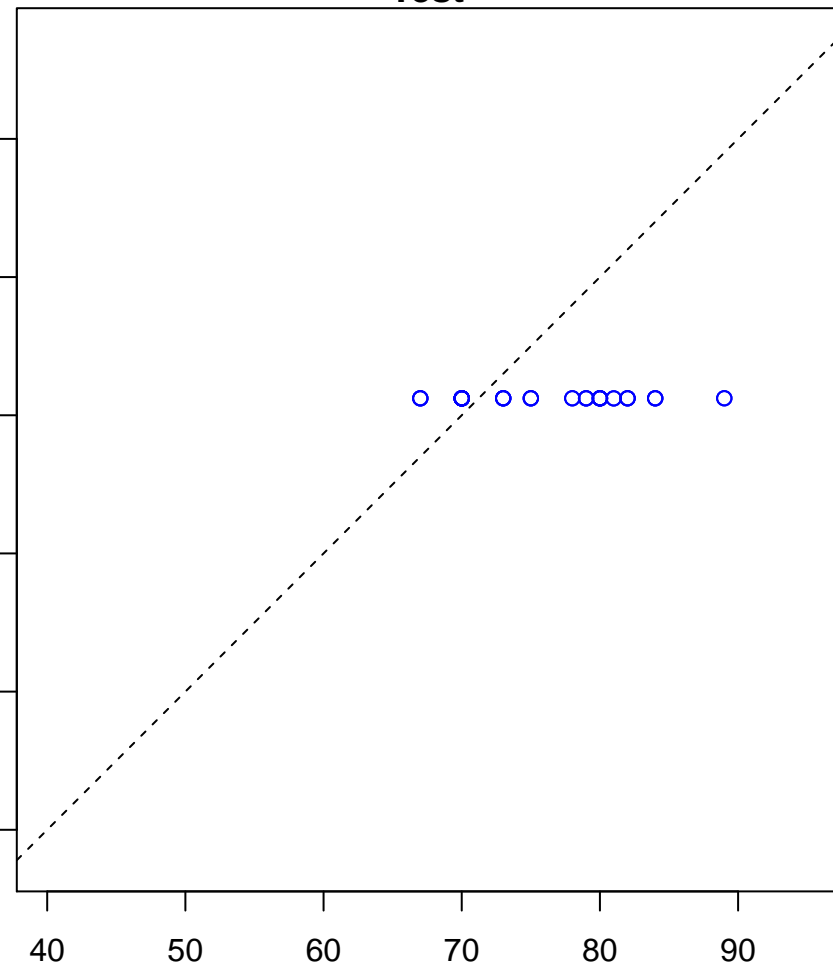


regulation of establishment of planar polarity (Score: 0.828266)

Control

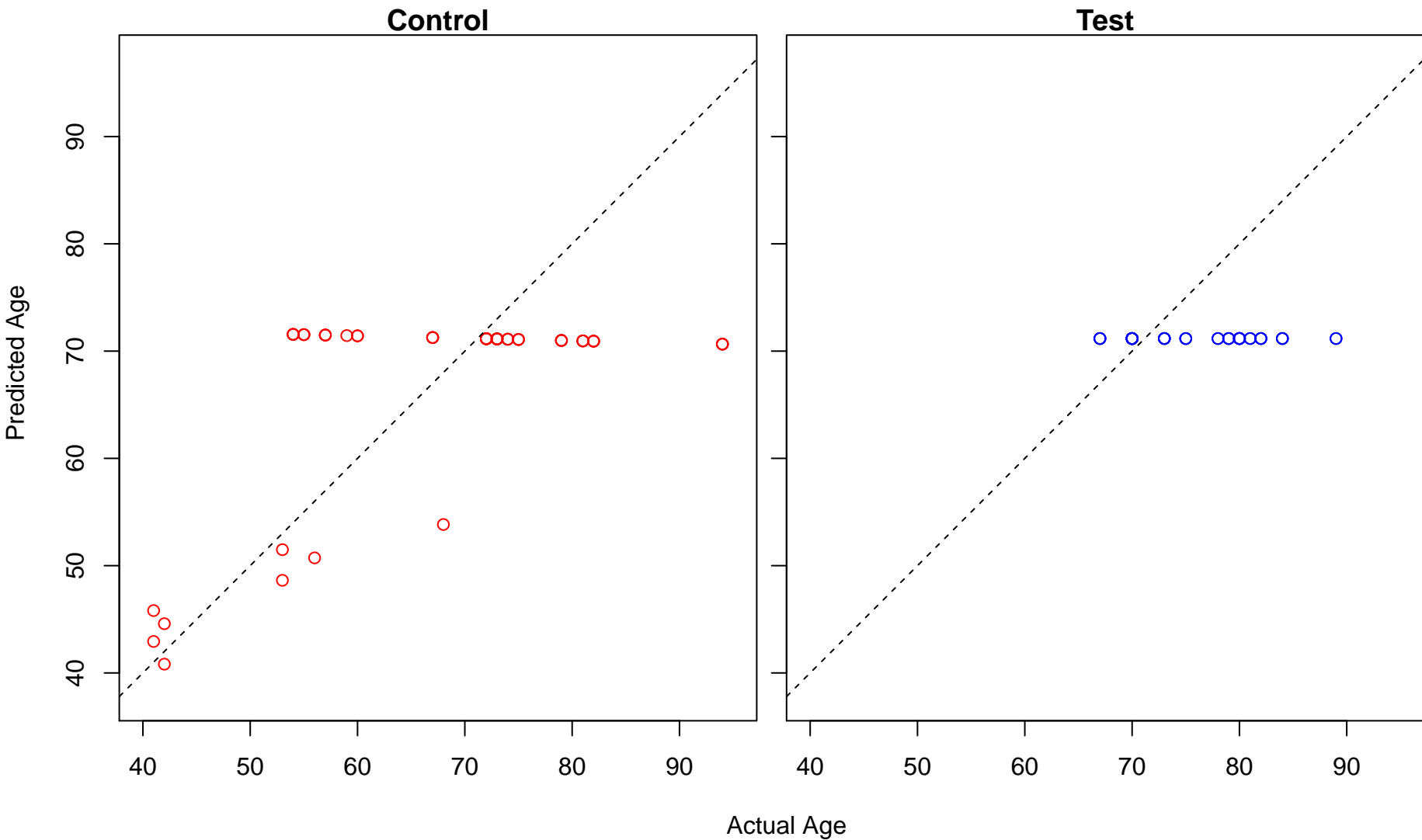


Test

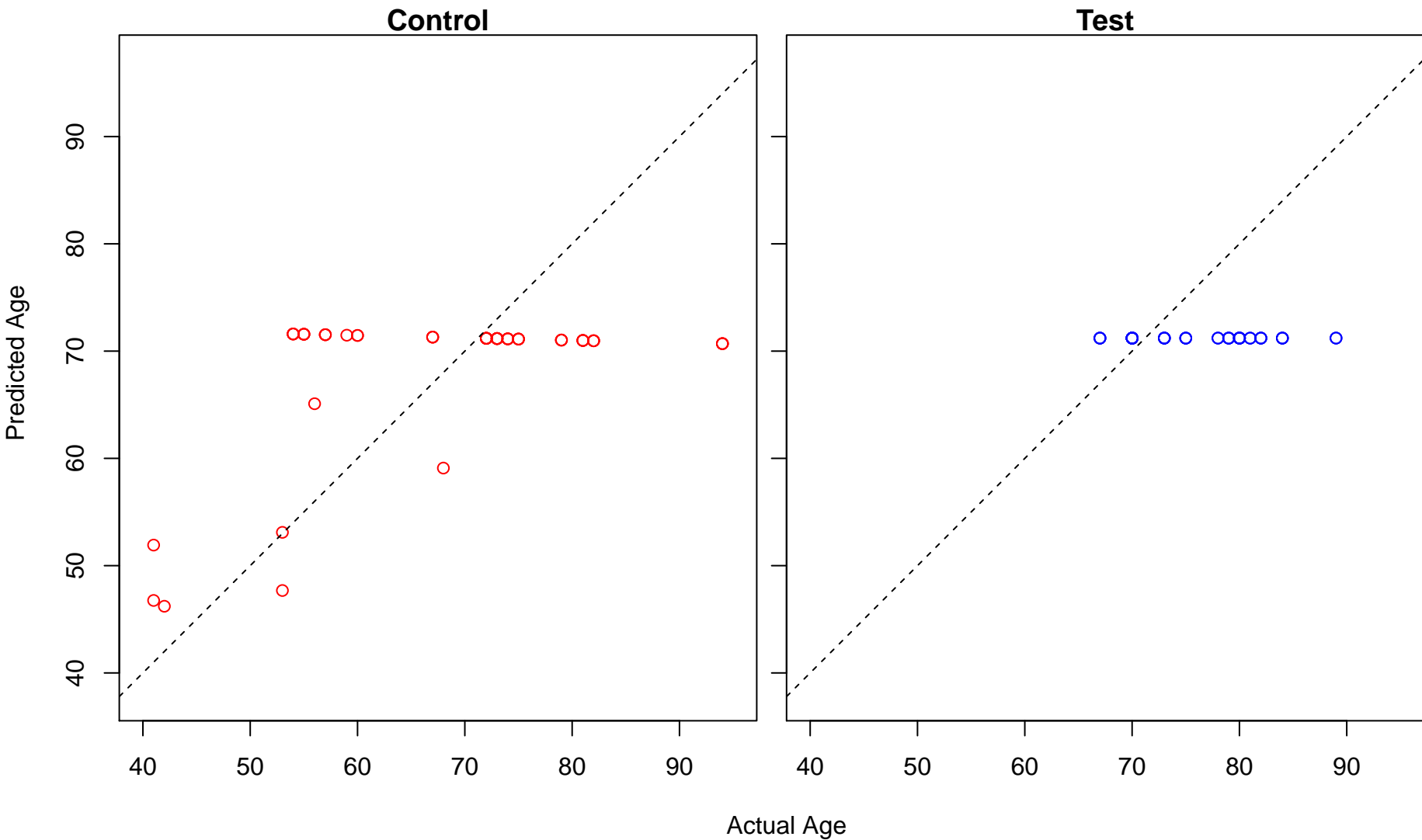


Actual Age

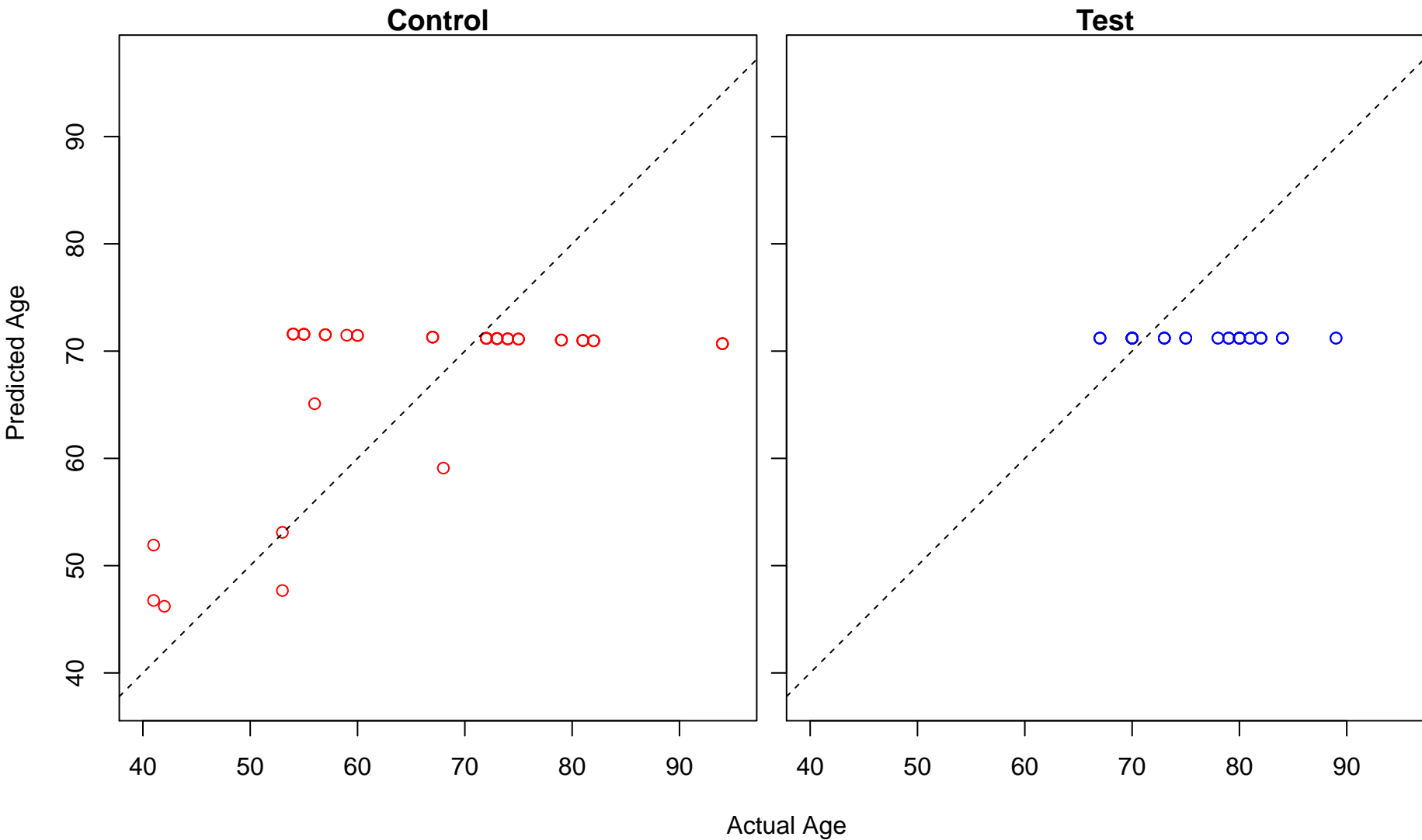
chemical homeostasis (Score: 0.828199)



regulation of hematopoietic progenitor cell differentiation (Score: 0.828174)

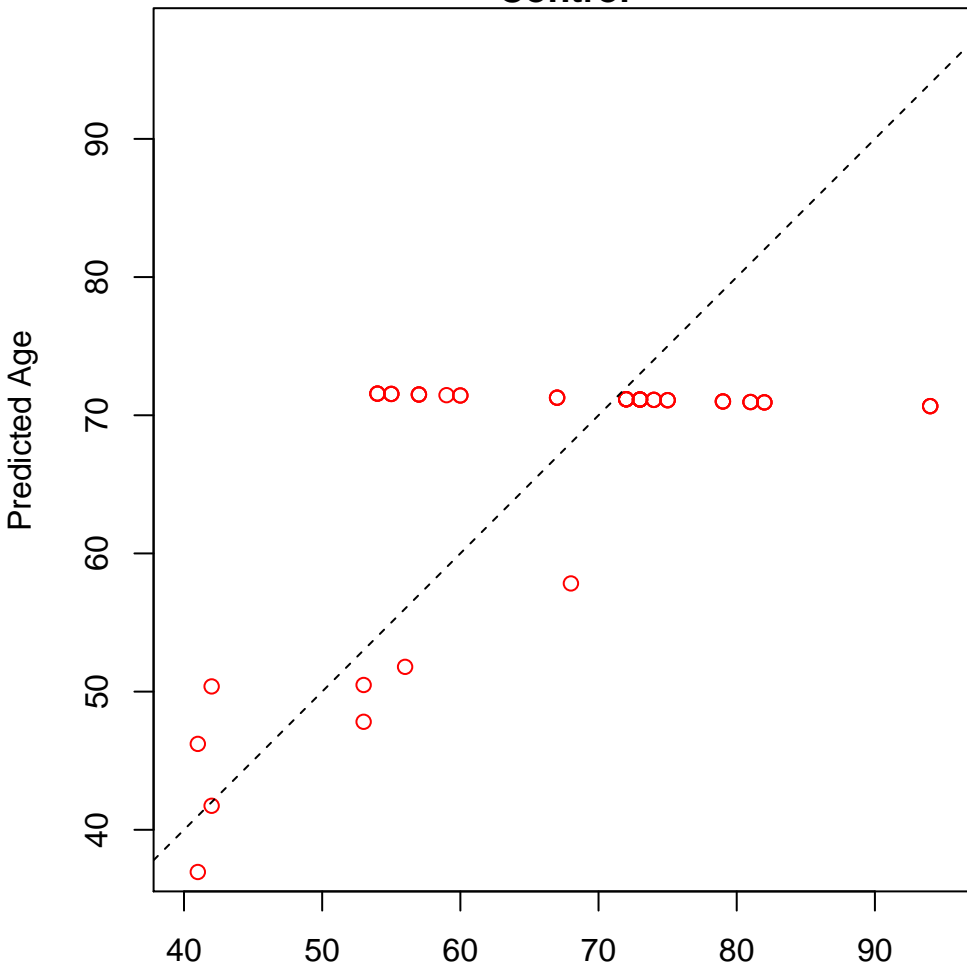


regulation of hematopoietic stem cell differentiation (Score: 0.828174)

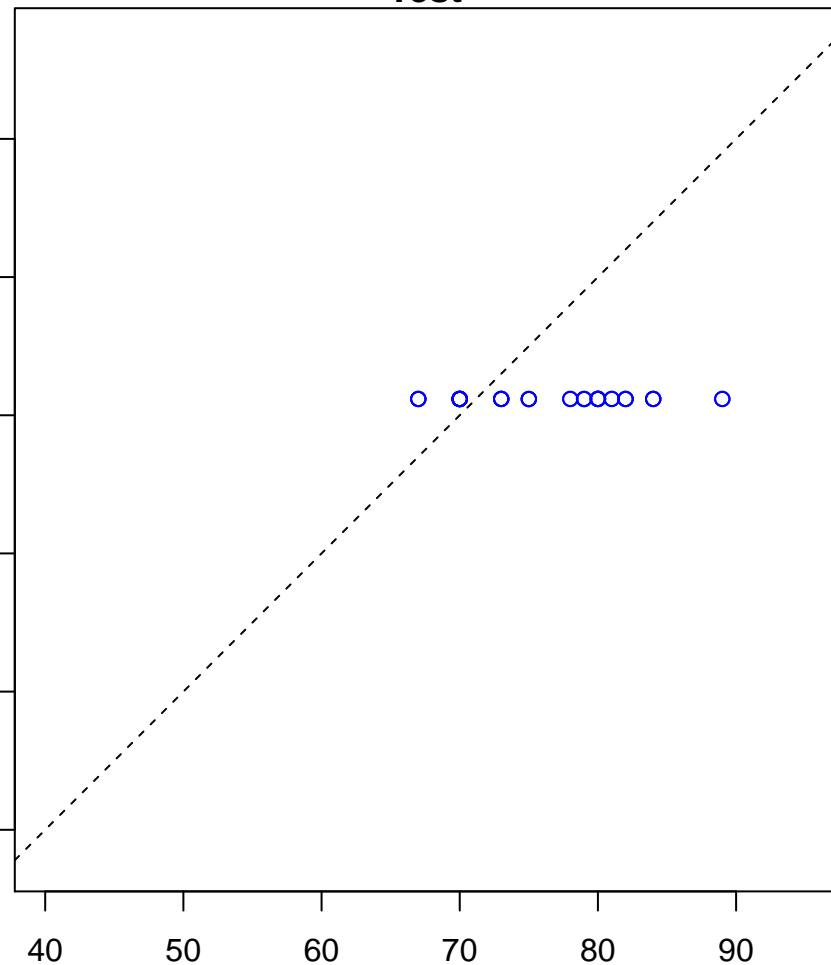


positive regulation of transferase activity (Score: 0.828148)

Control



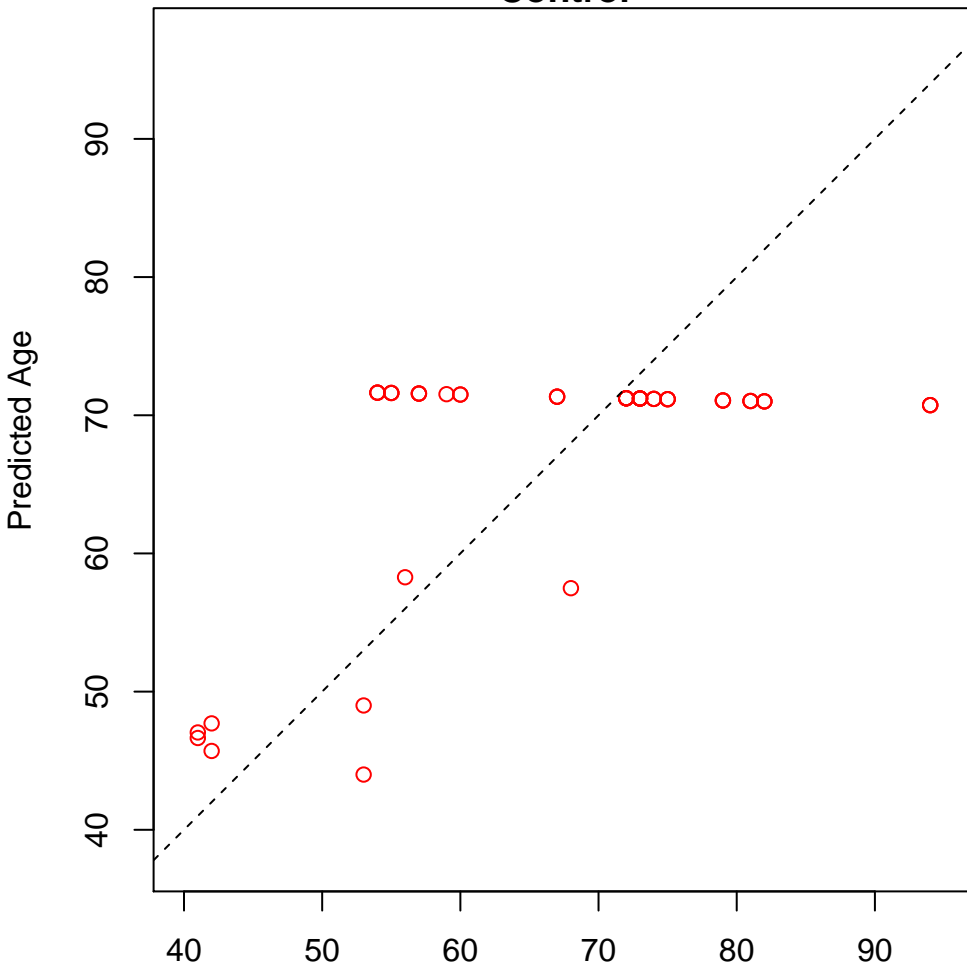
Test



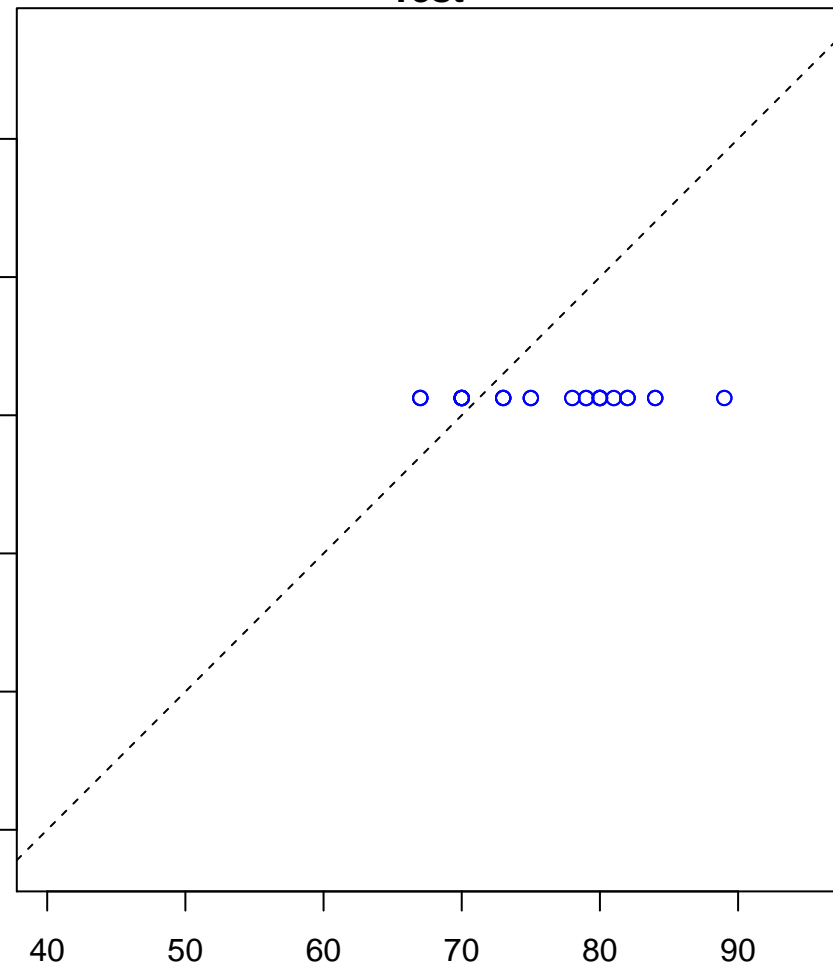
Actual Age

microtubule-based movement (Score: 0.828098)

Control



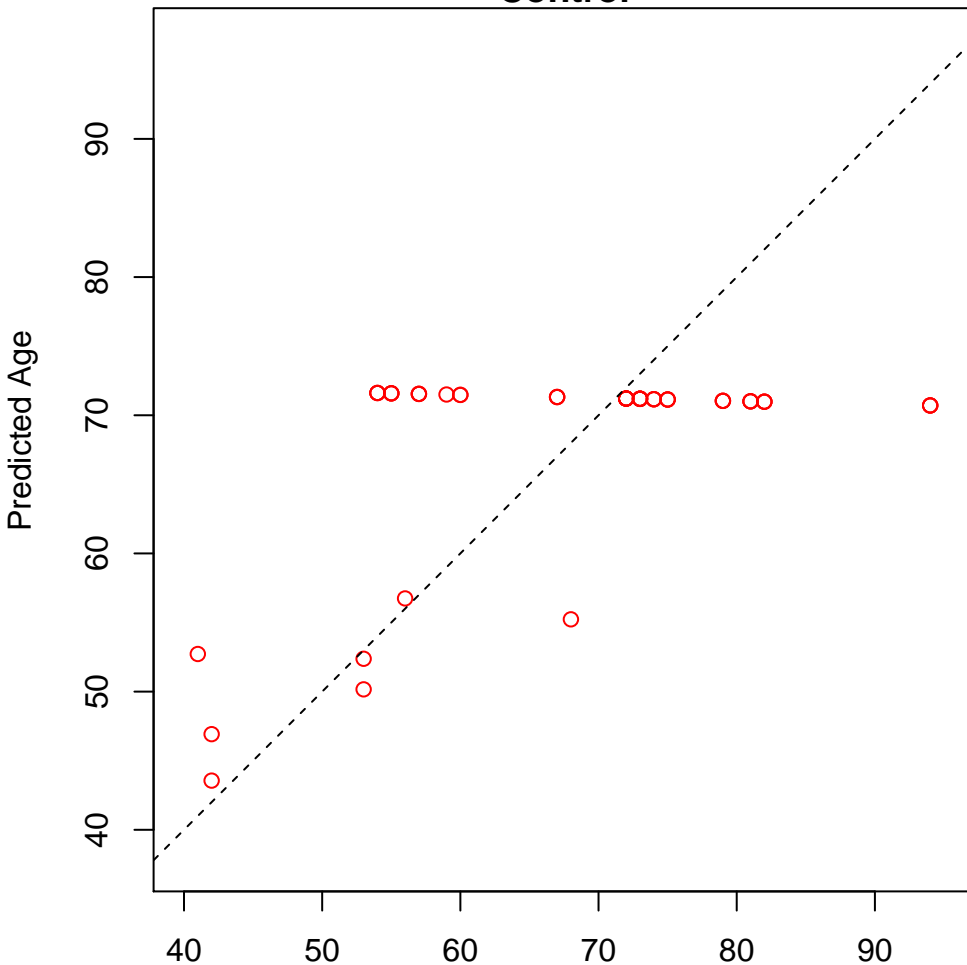
Test



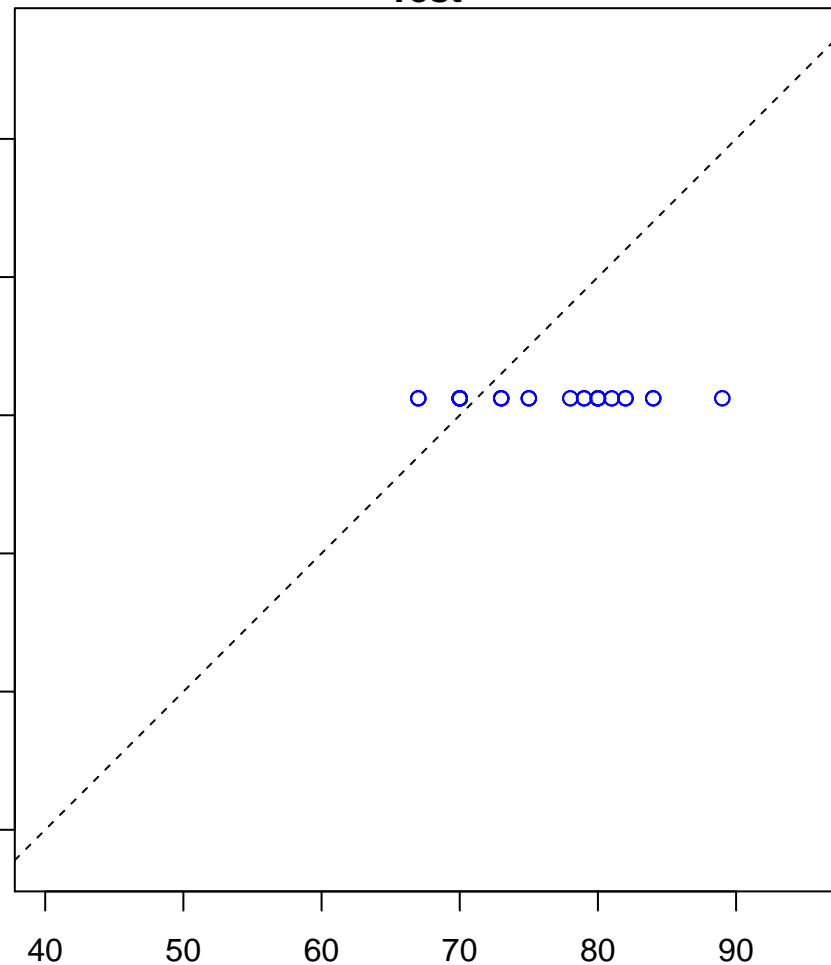
Actual Age

regulation of organ morphogenesis (Score: 0.828086)

Control

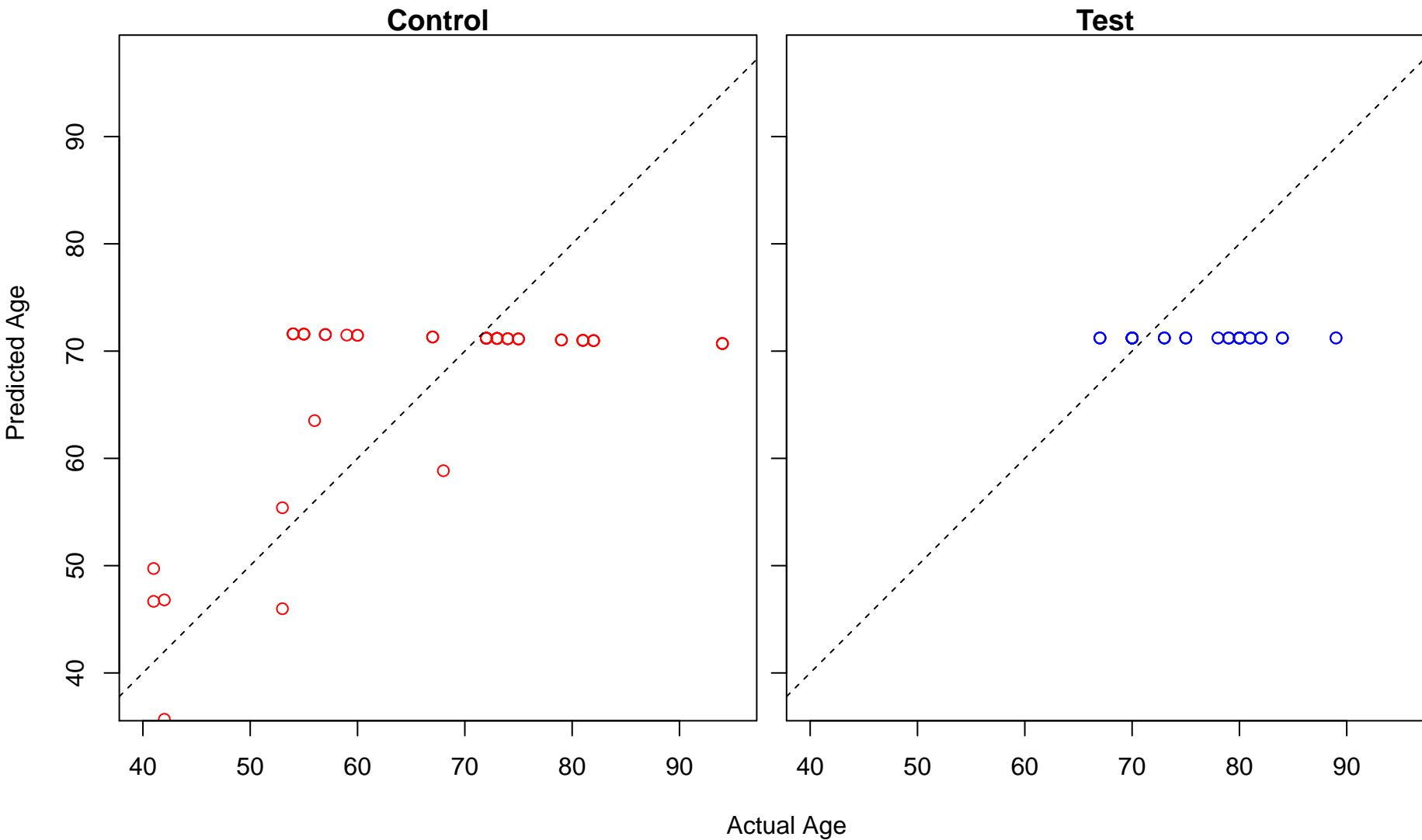


Test

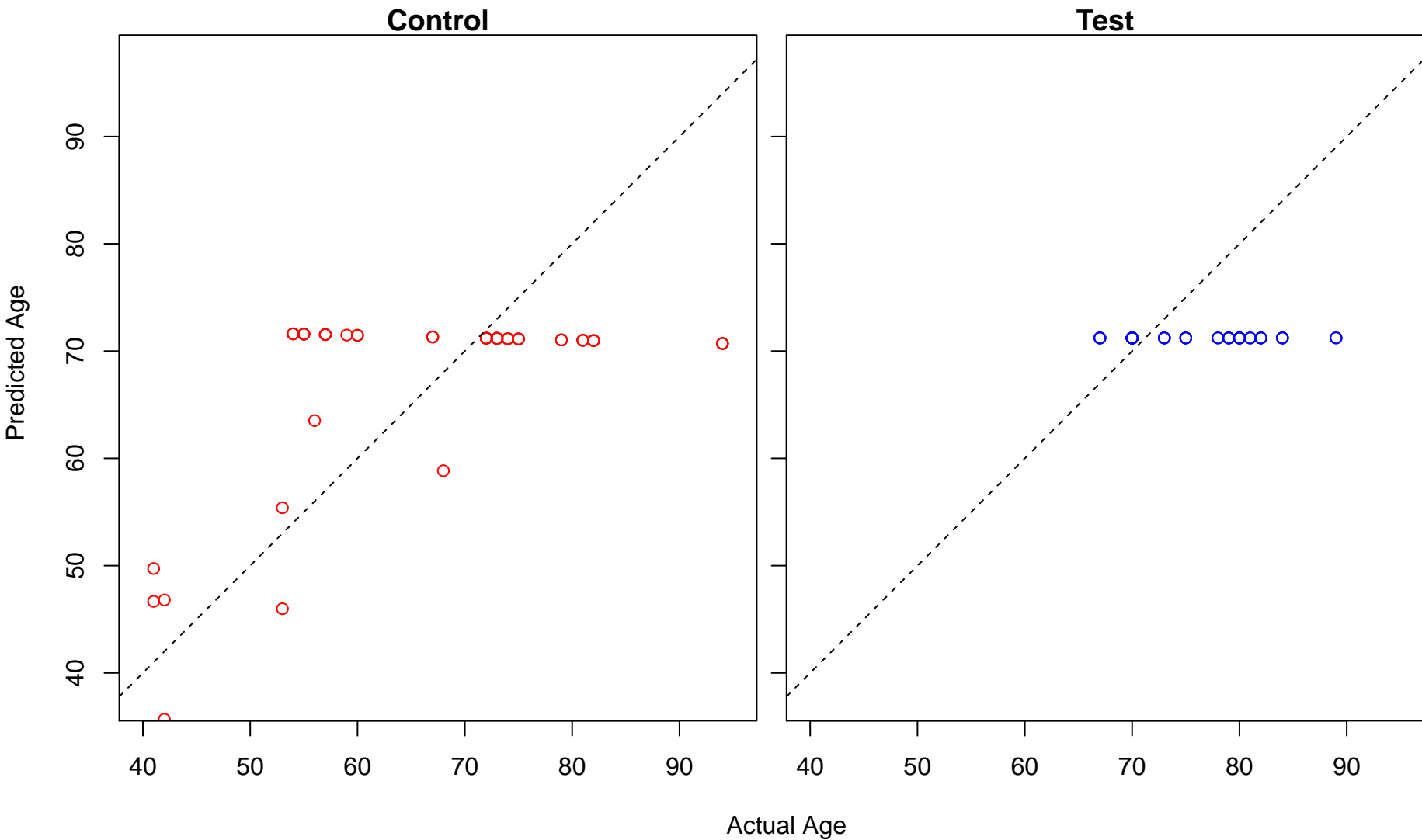


Actual Age

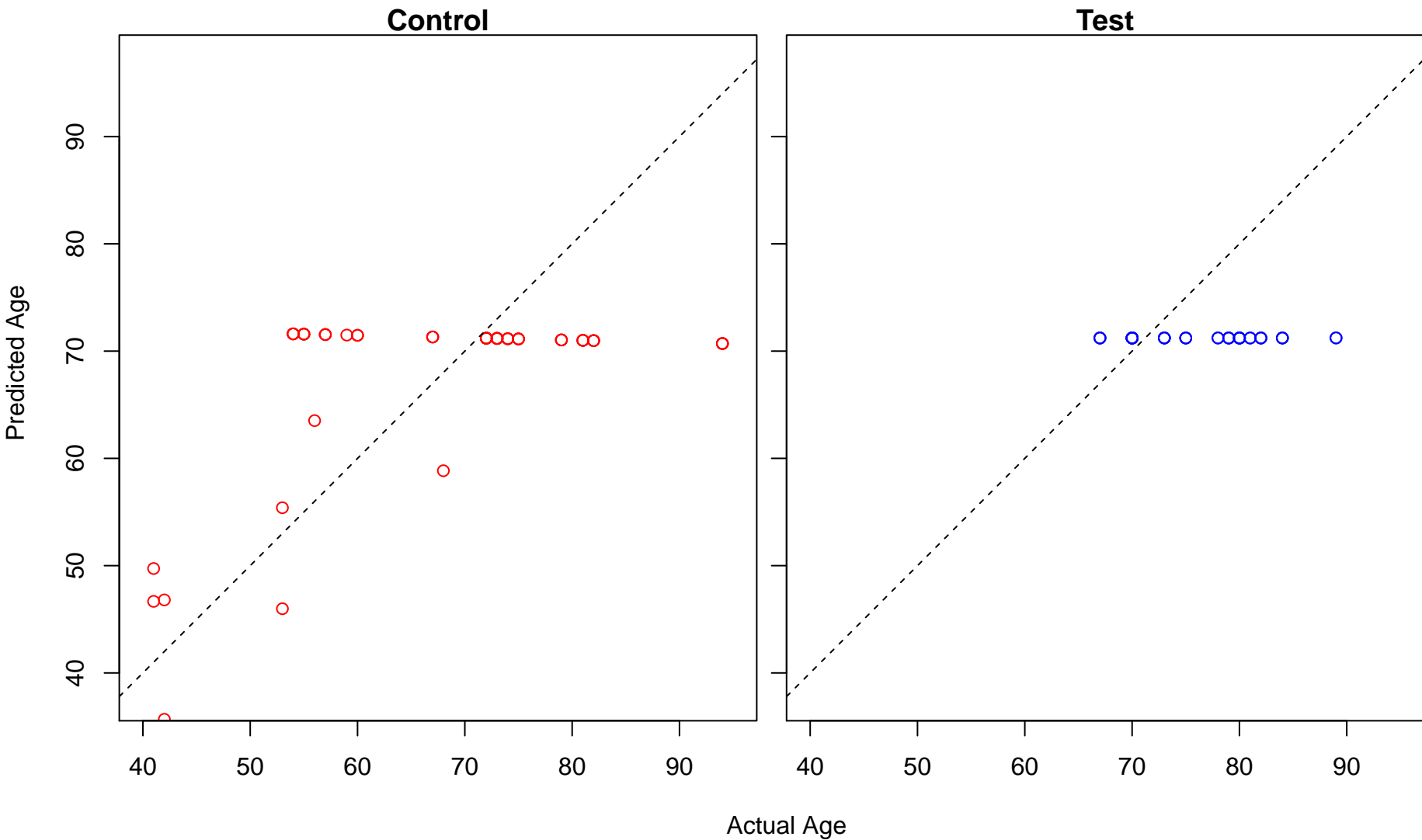
positive regulation of Wnt signaling pathway (Score: 0.827964)



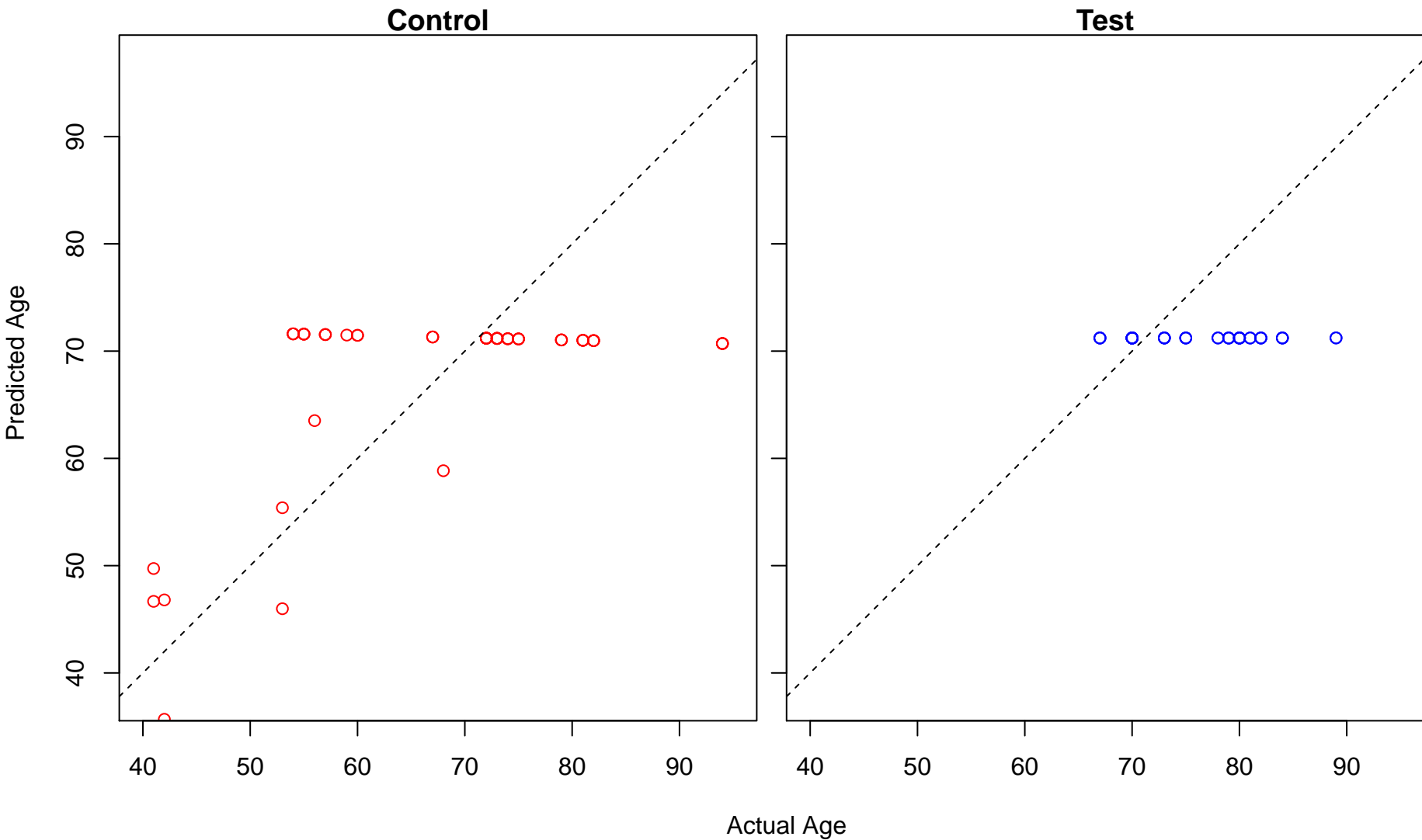
regulation of canonical Wnt signaling pathway (Score: 0.827964)



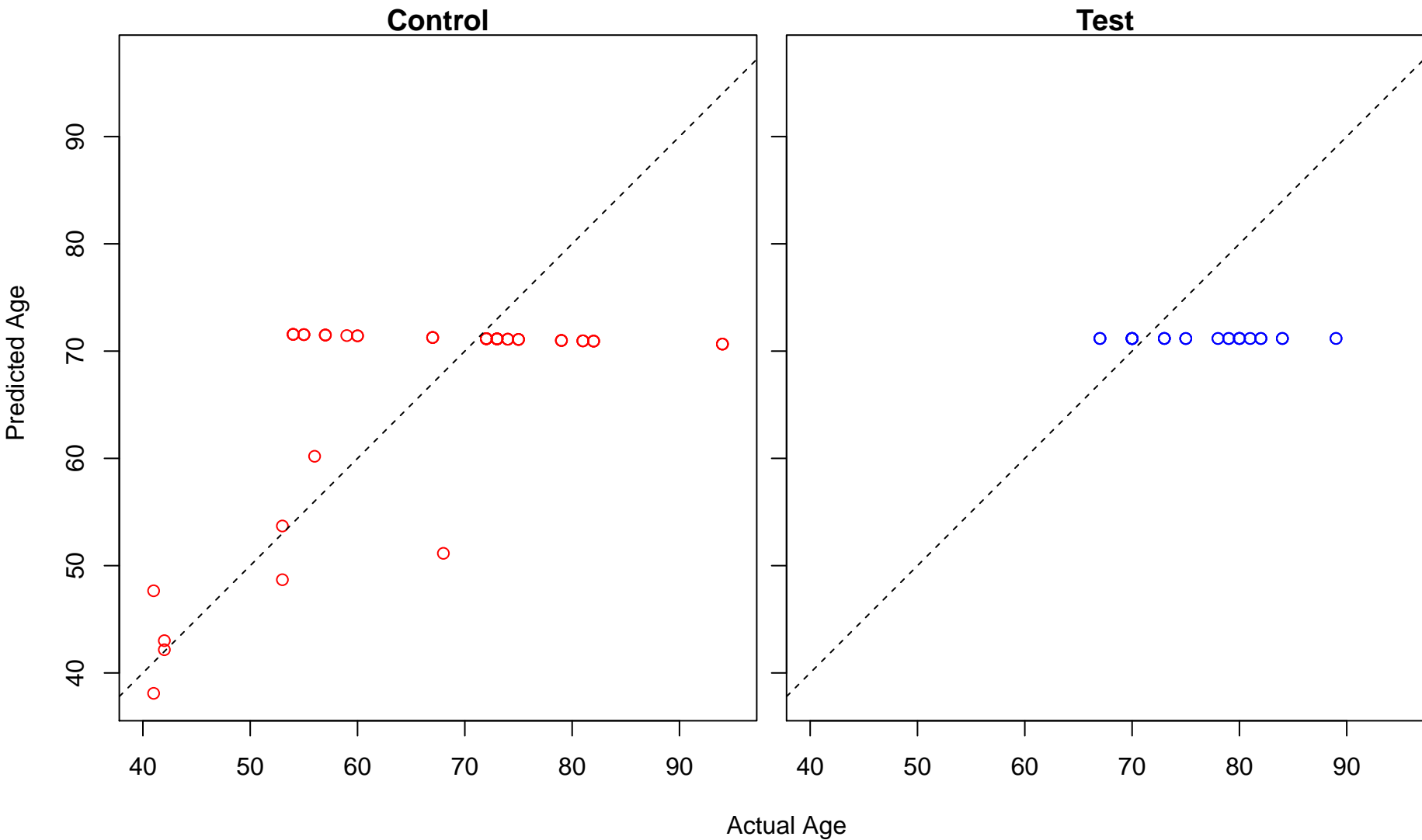
negative regulation of canonical Wnt signaling pathway (Score: 0.827964)



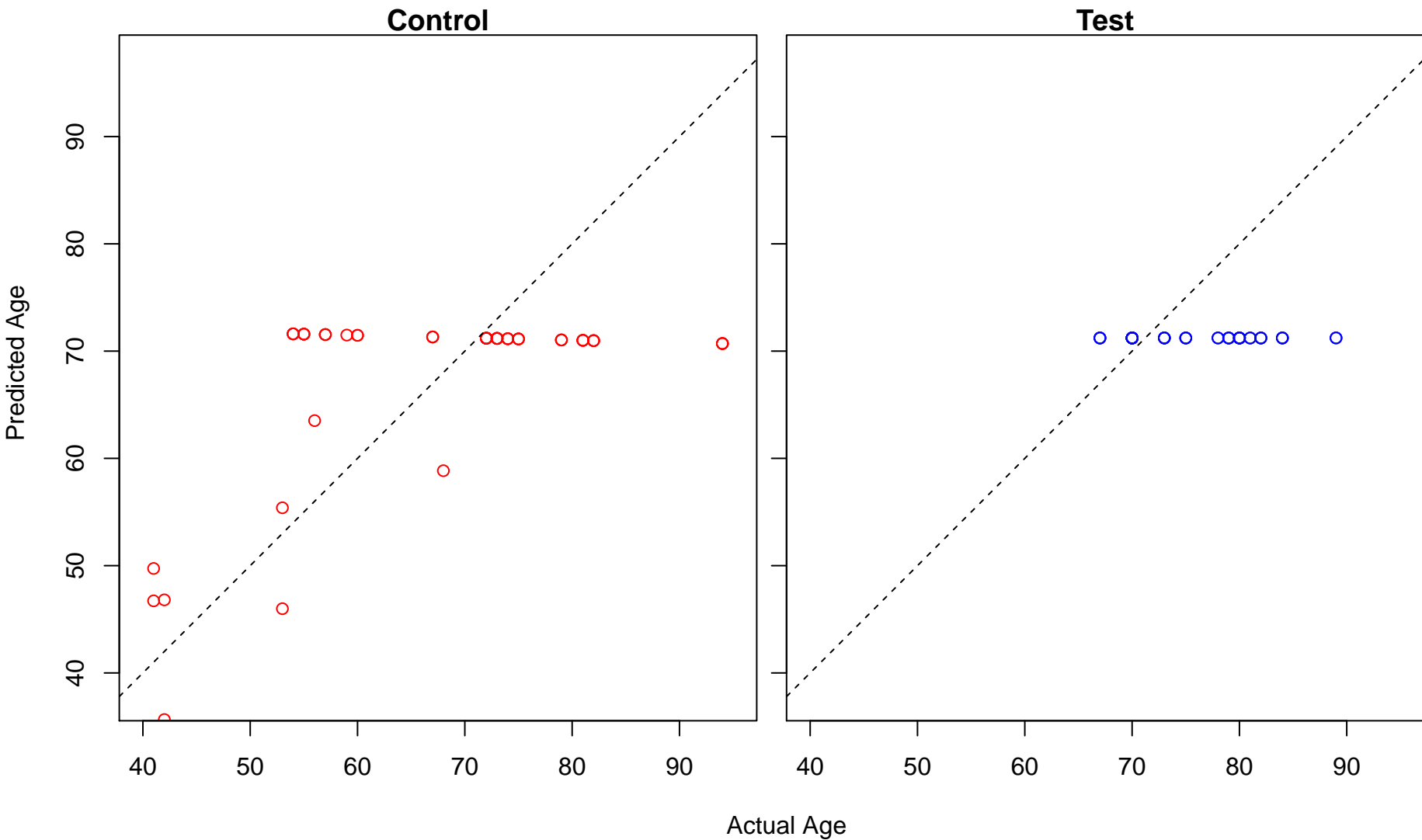
positive regulation of canonical Wnt signaling pathway (Score: 0.827964)



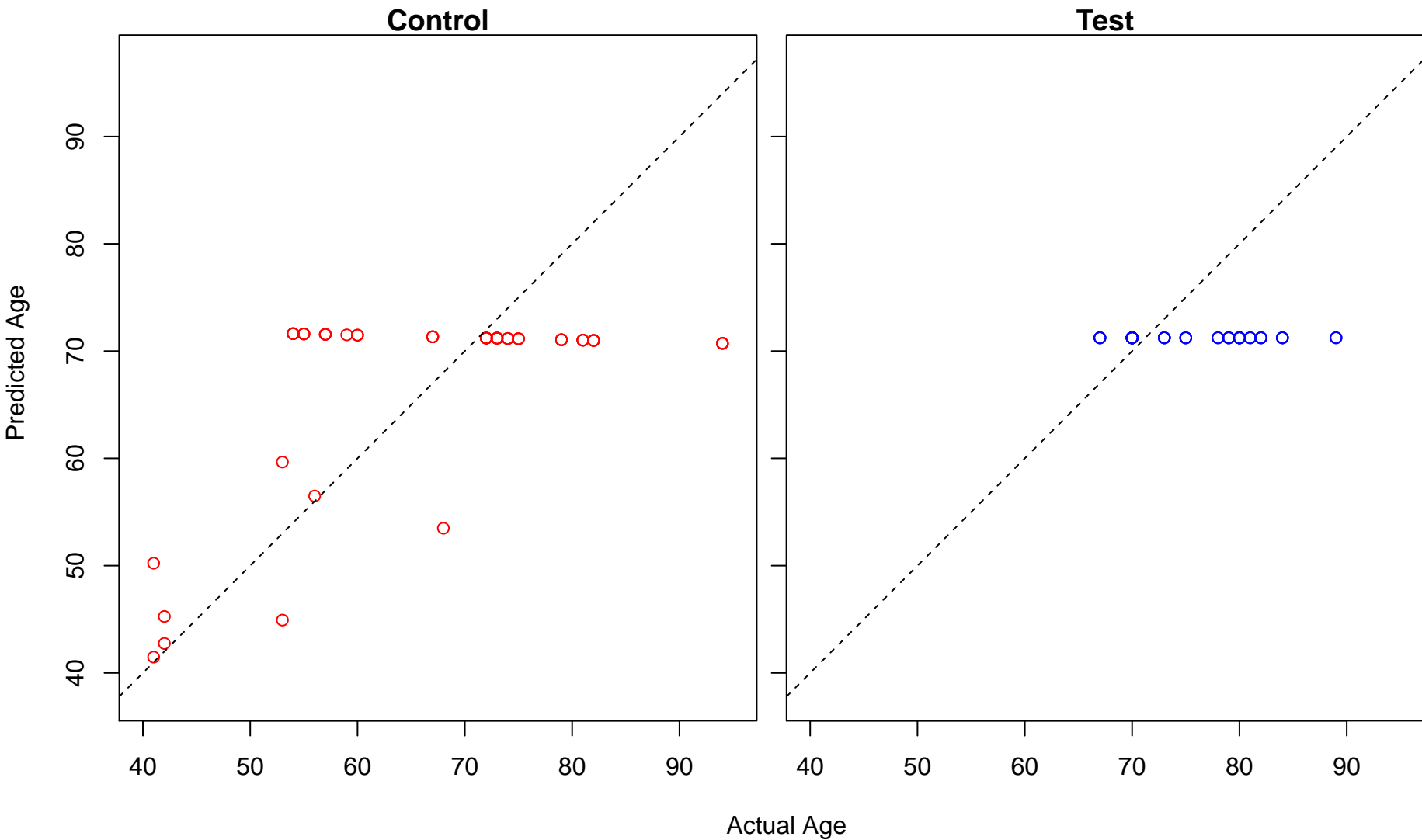
cellular response to stress (Score: 0.827925)



negative regulation of Wnt signaling pathway (Score: 0.827919)

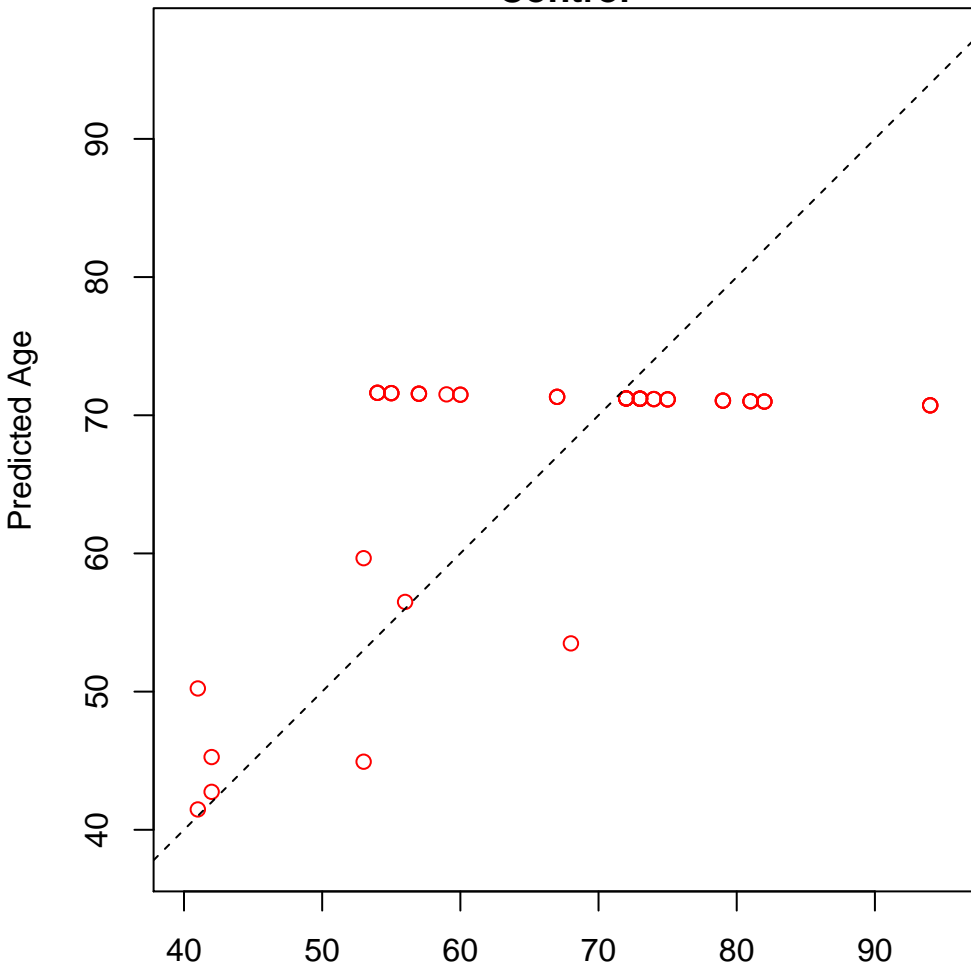


response to cytokine (Score: 0.827822)

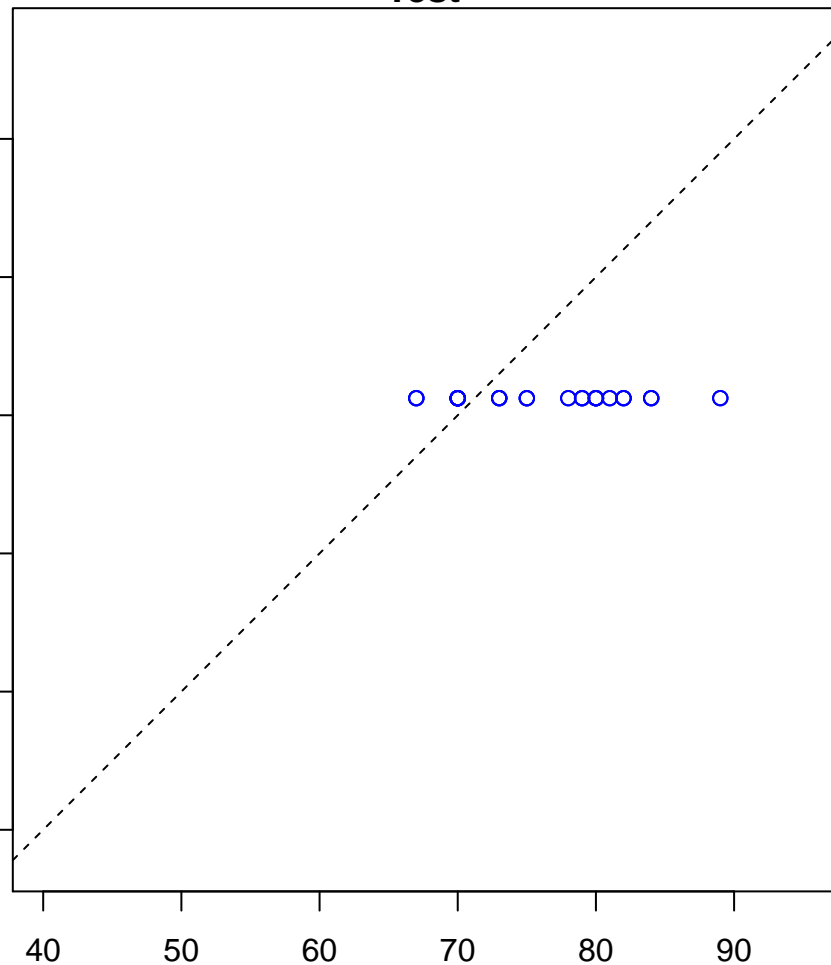


cellular response to cytokine stimulus (Score: 0.827822)

Control

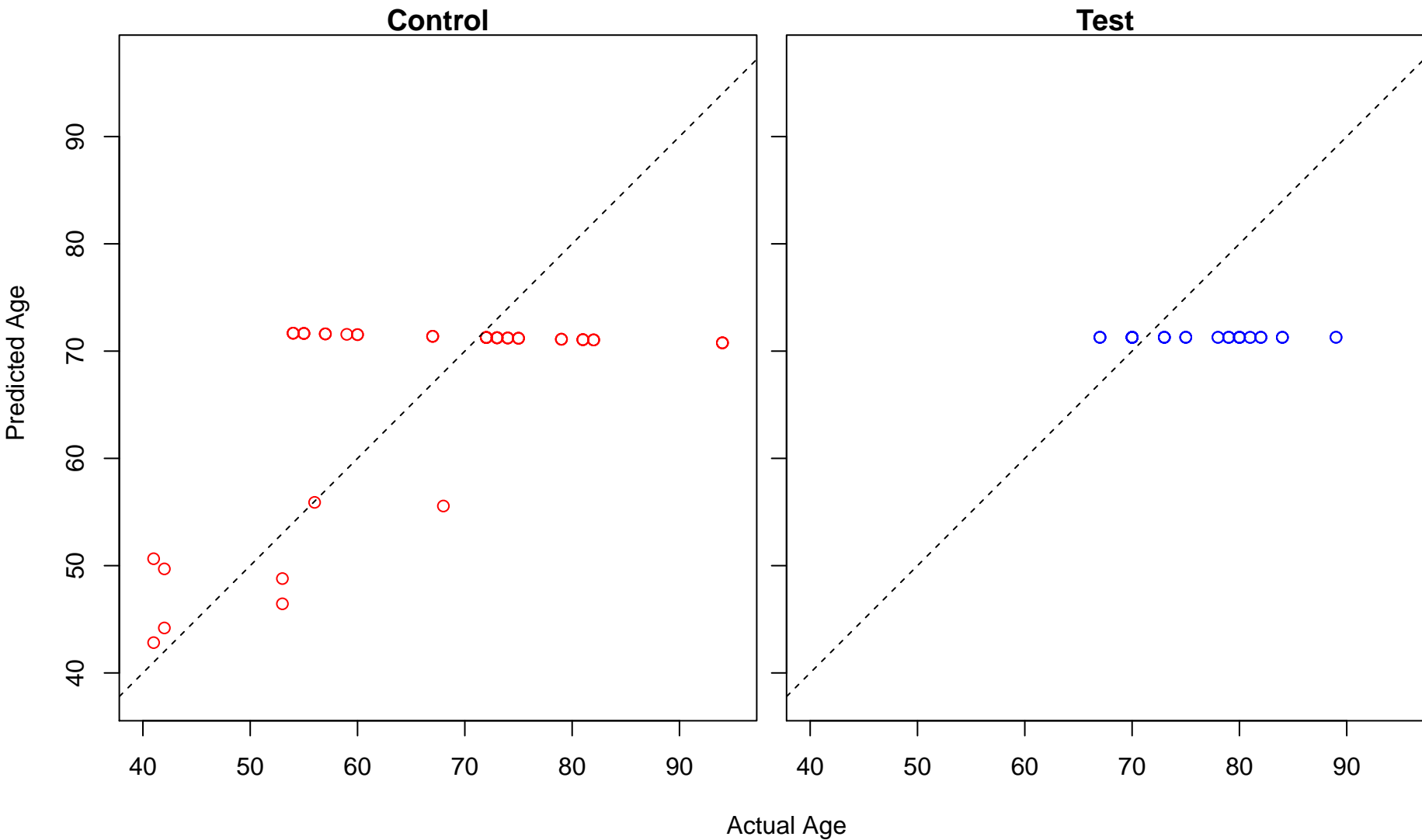


Test

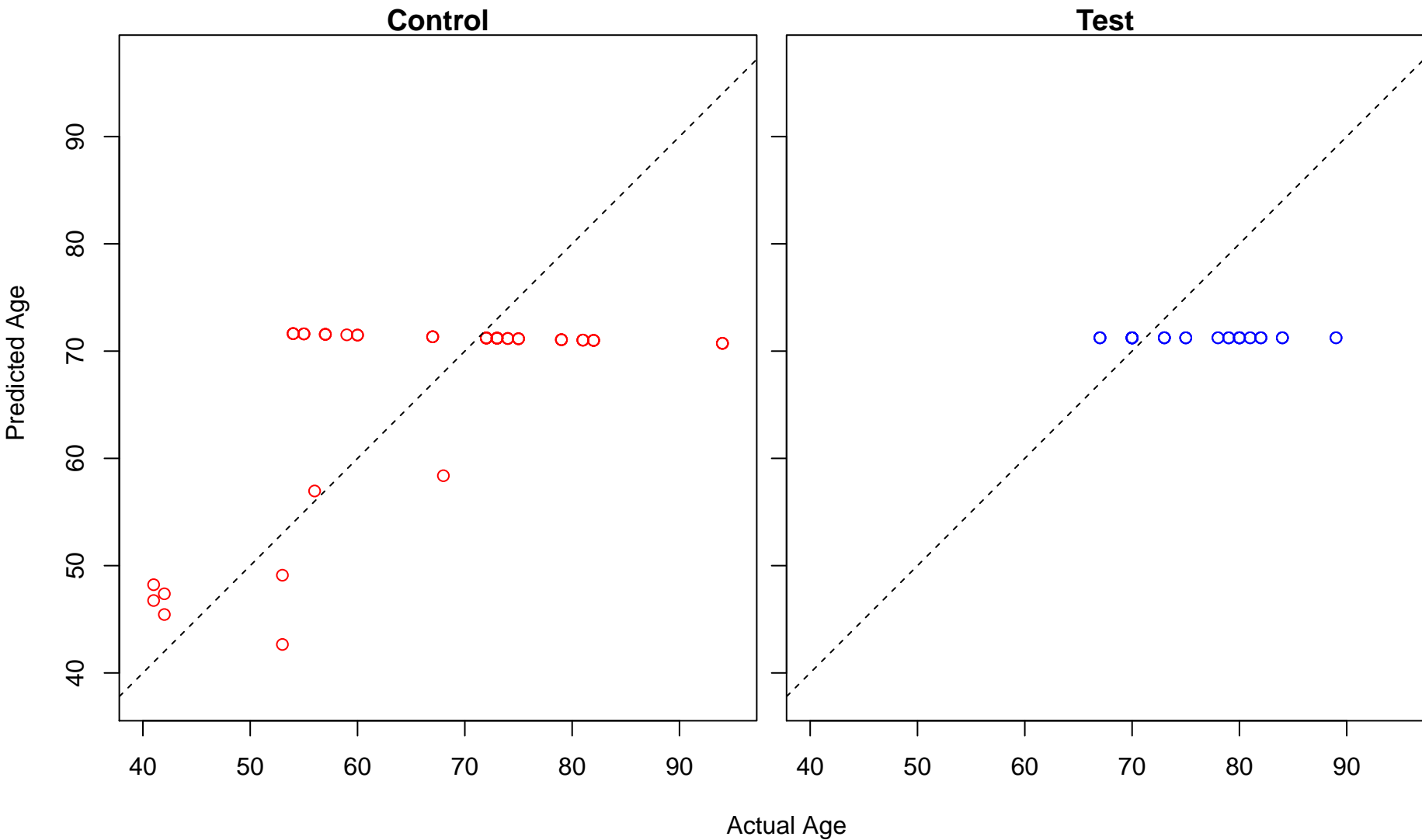


Actual Age

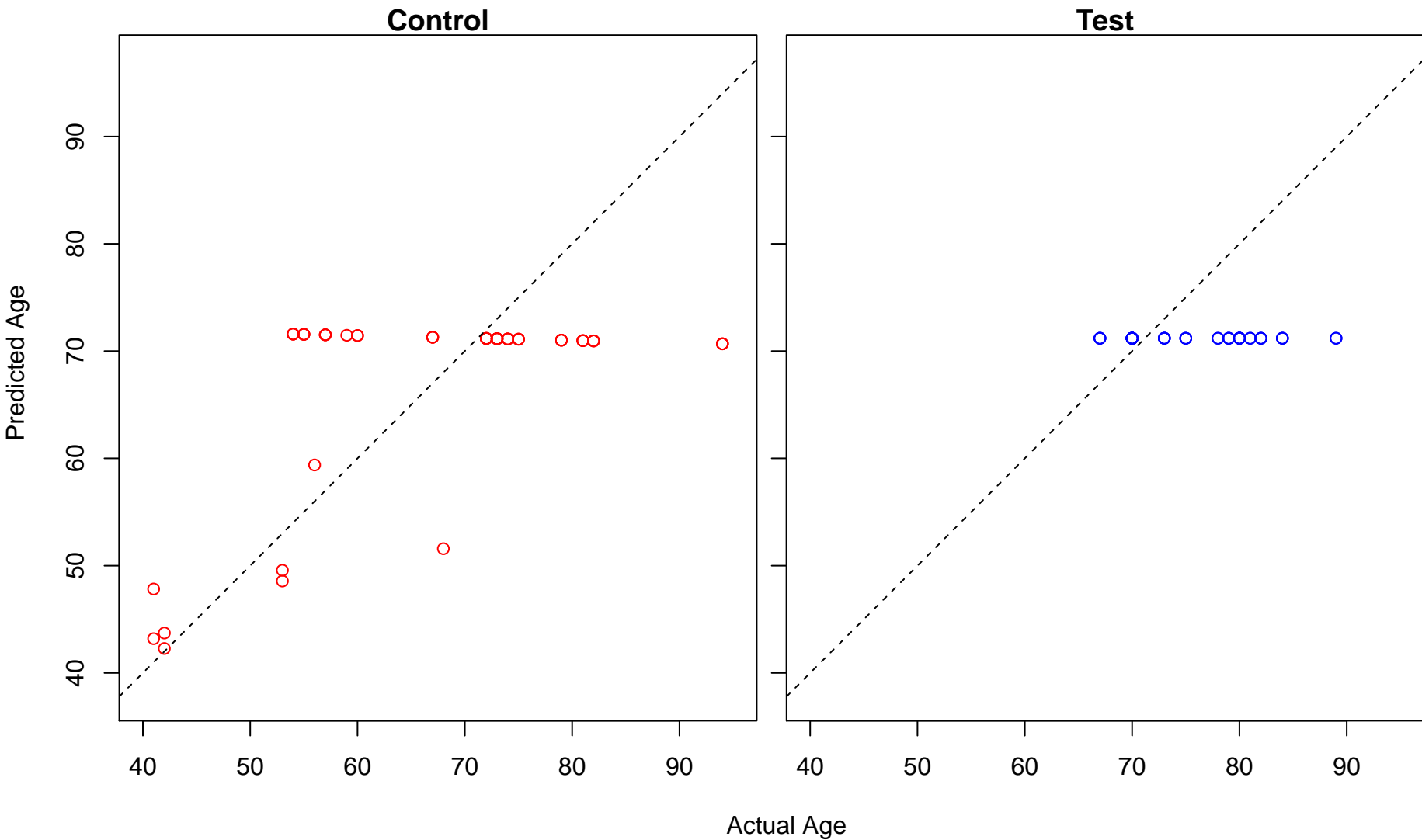
positive regulation of translation (Score: 0.827578)



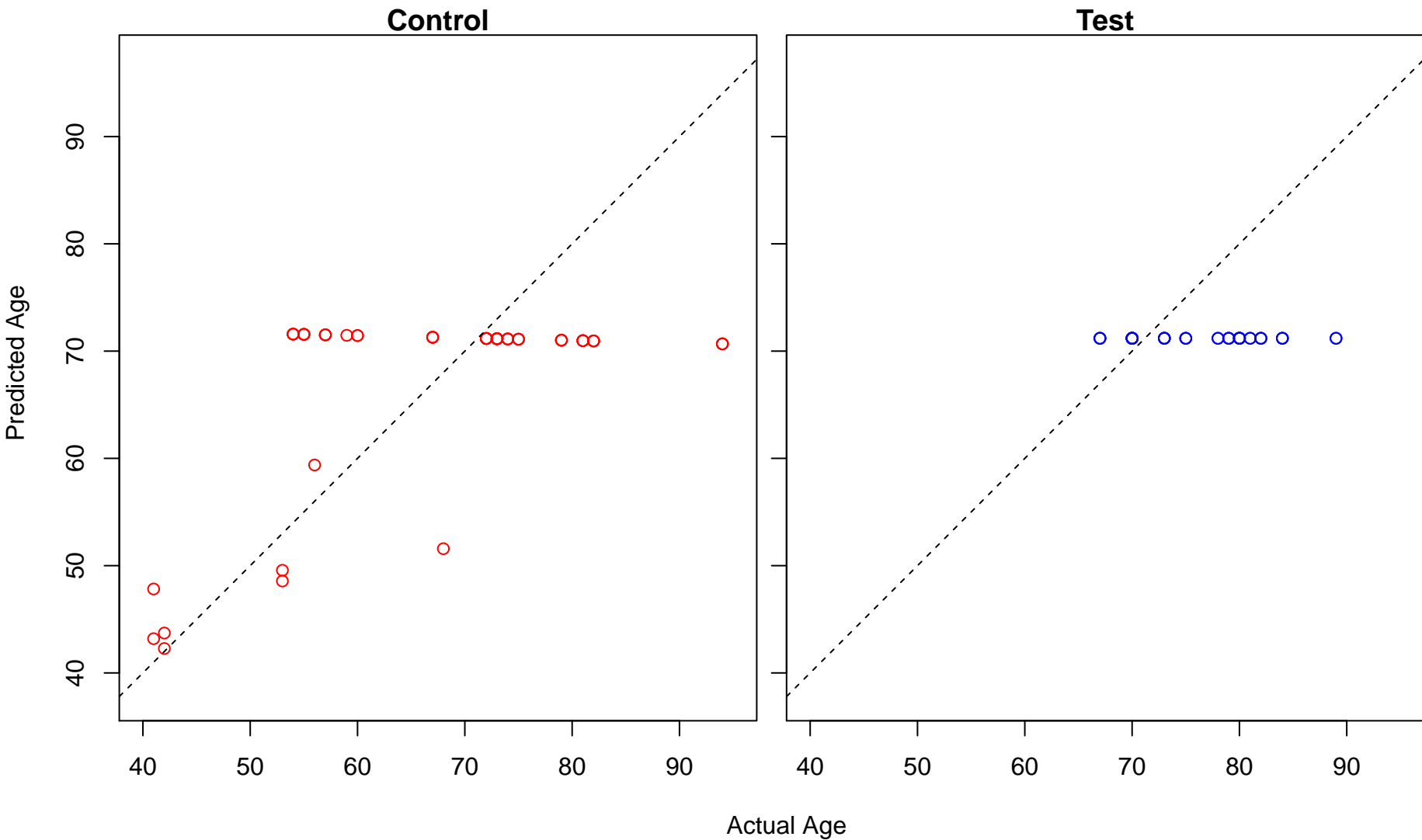
cytoskeleton-dependent intracellular transport (Score: 0.827508)



cellular metal ion homeostasis (Score: 0.827505)

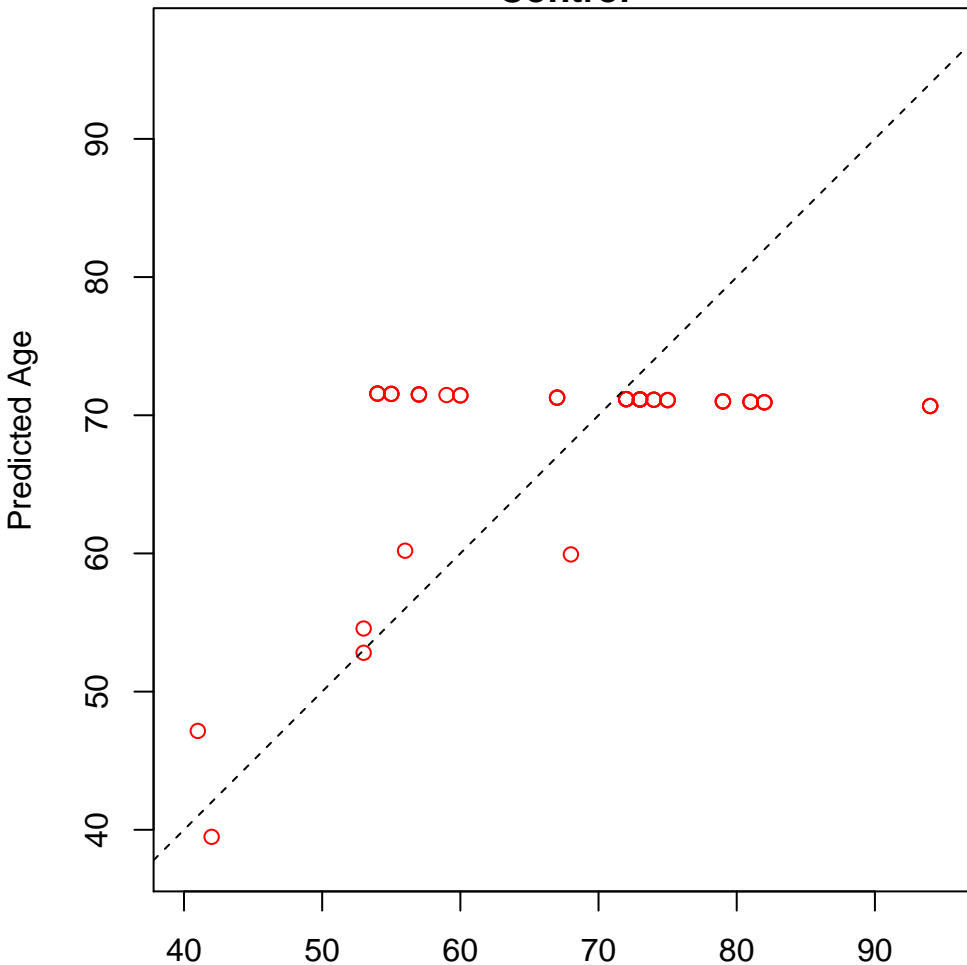


metal ion homeostasis (Score: 0.827505)

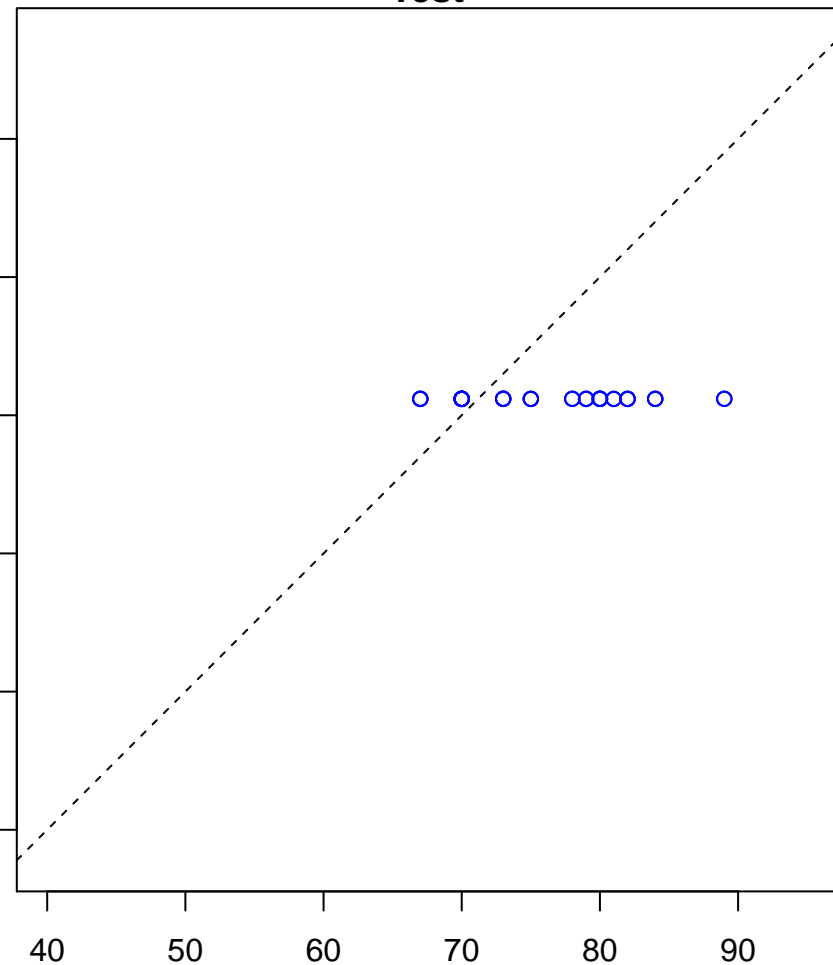


negative regulation of cell cycle process (Score: 0.827376)

Control

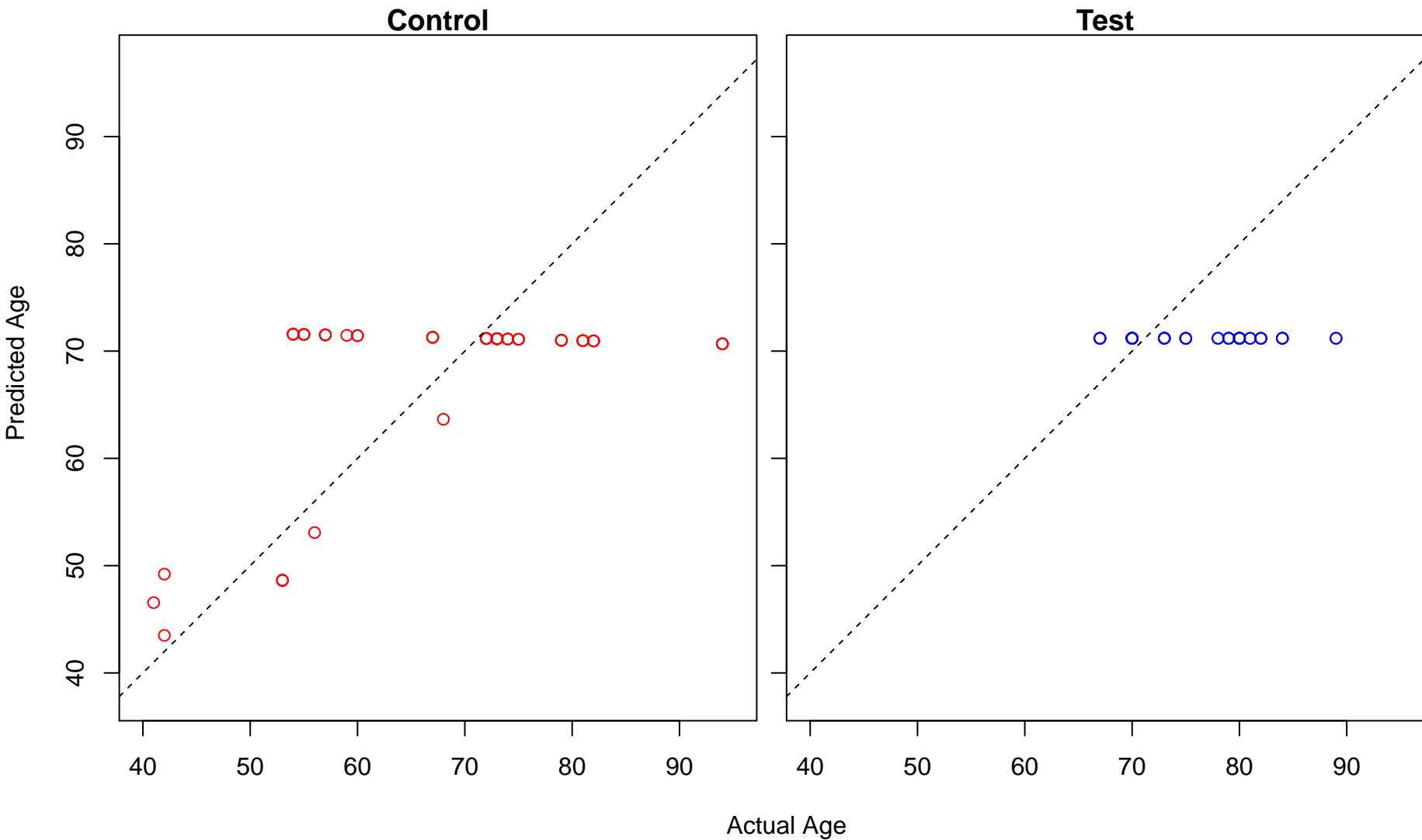


Test

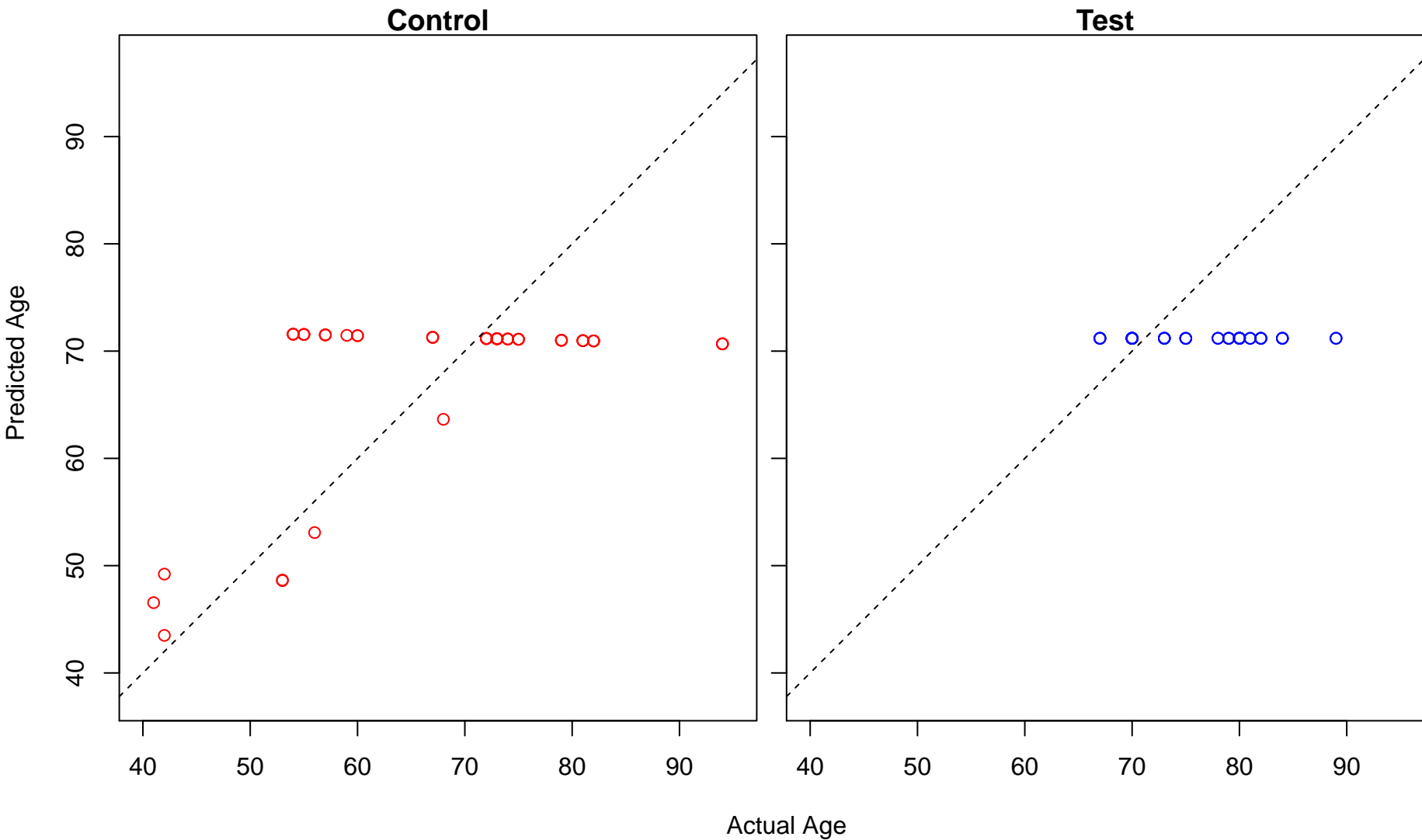


Actual Age

immune response-activating signal transduction (Score: 0.827242)

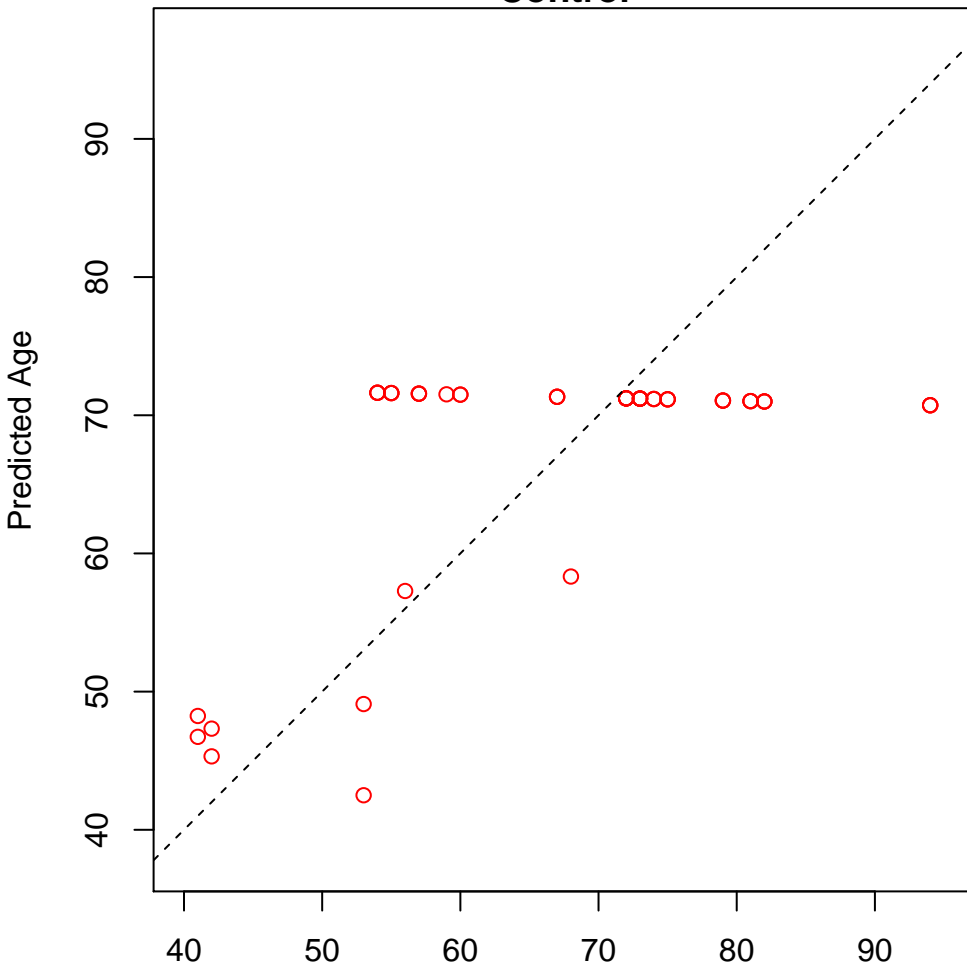


immune response-regulating signaling pathway (Score: 0.827242)

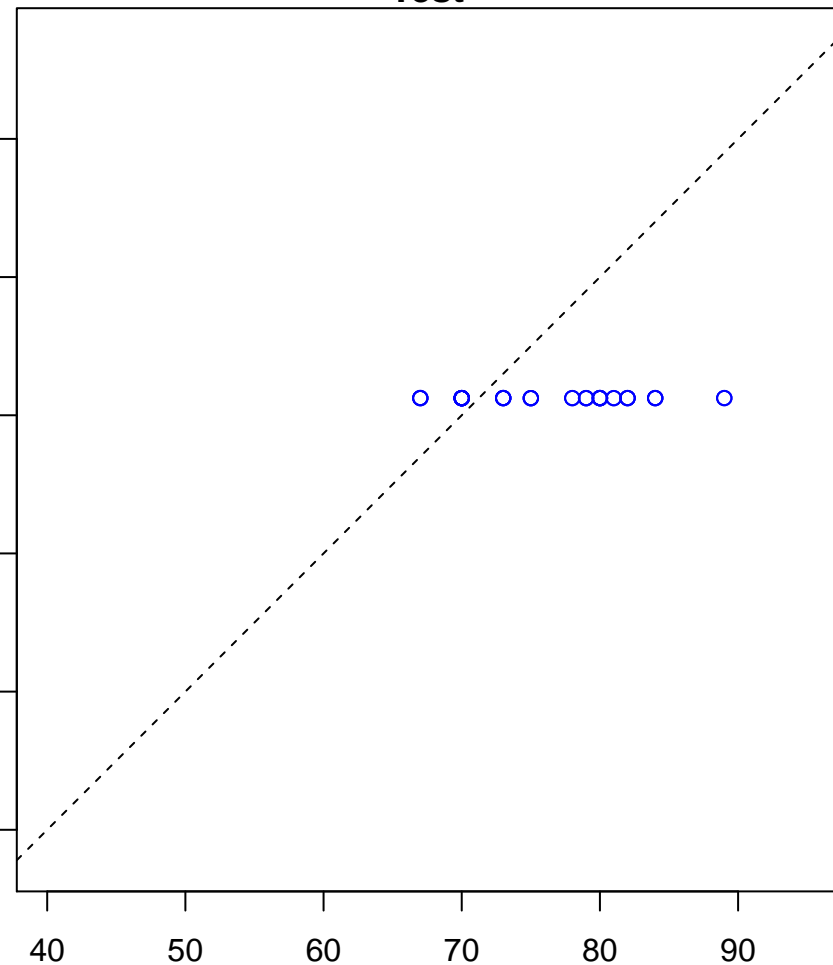


transport along microtubule (Score: 0.827144)

Control

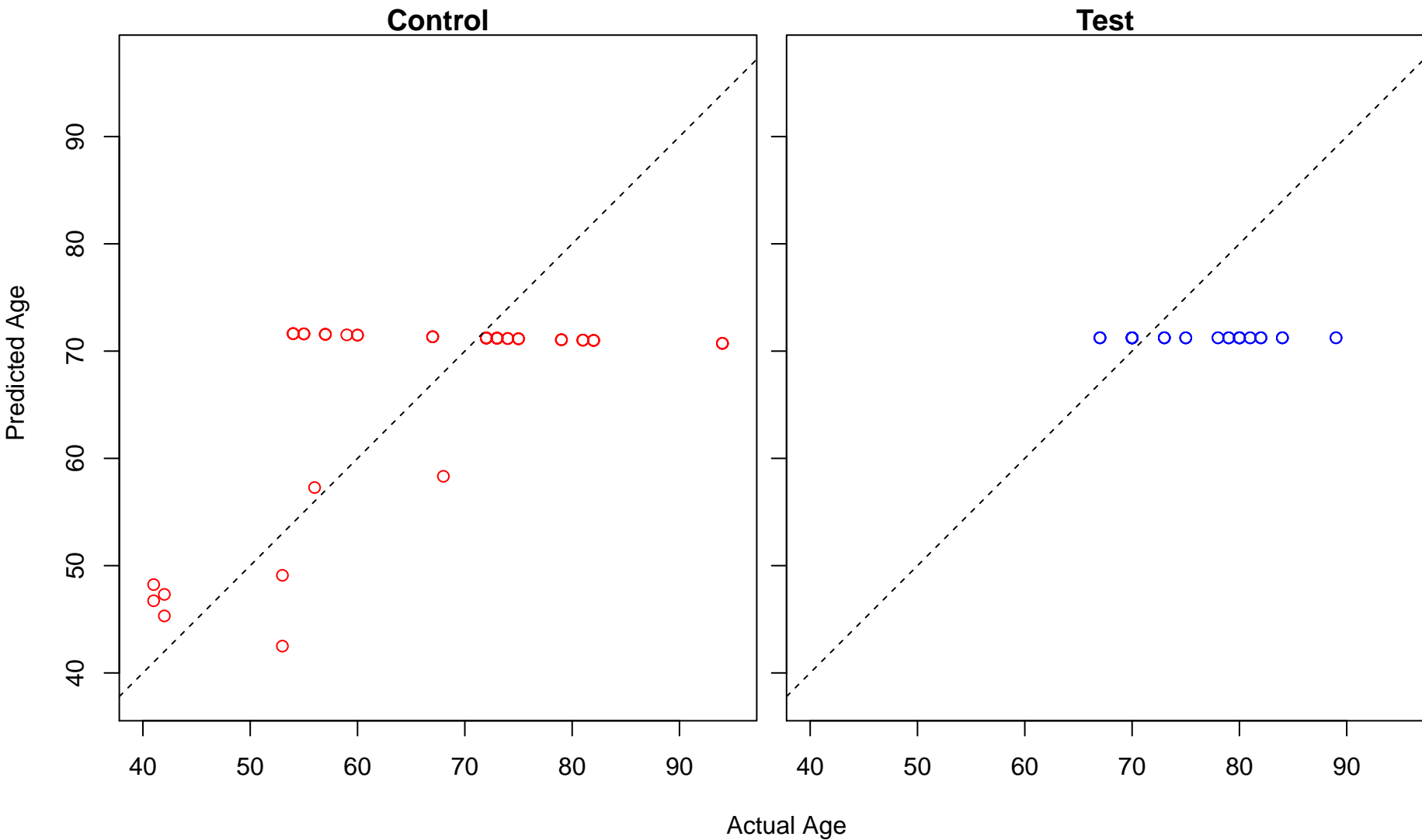


Test



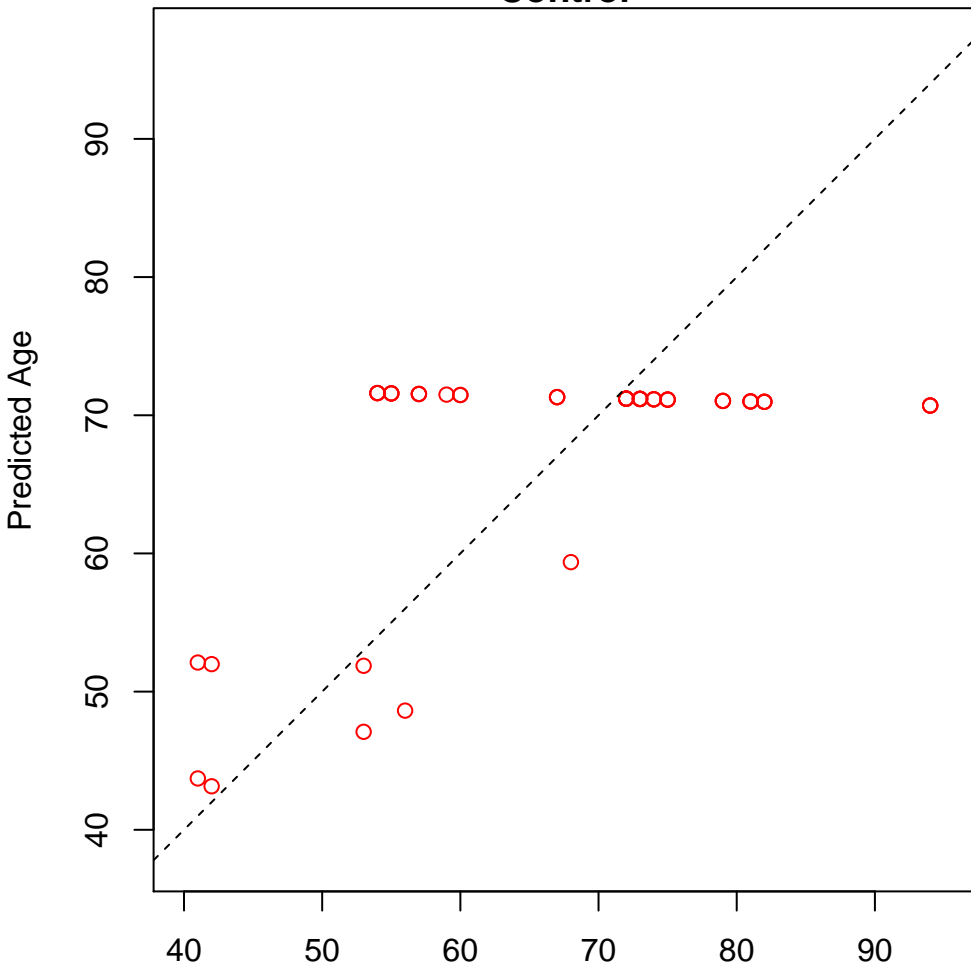
Actual Age

microtubule-based transport (Score: 0.827144)

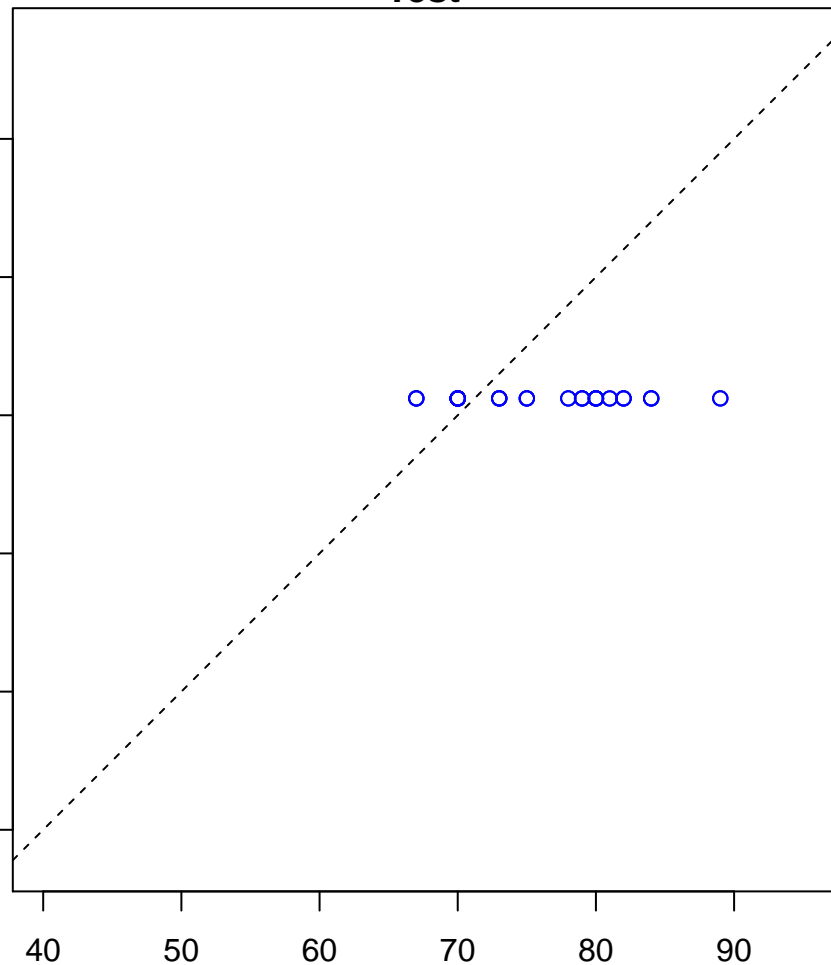


nucleoside phosphate metabolic process (Score: 0.827124)

Control

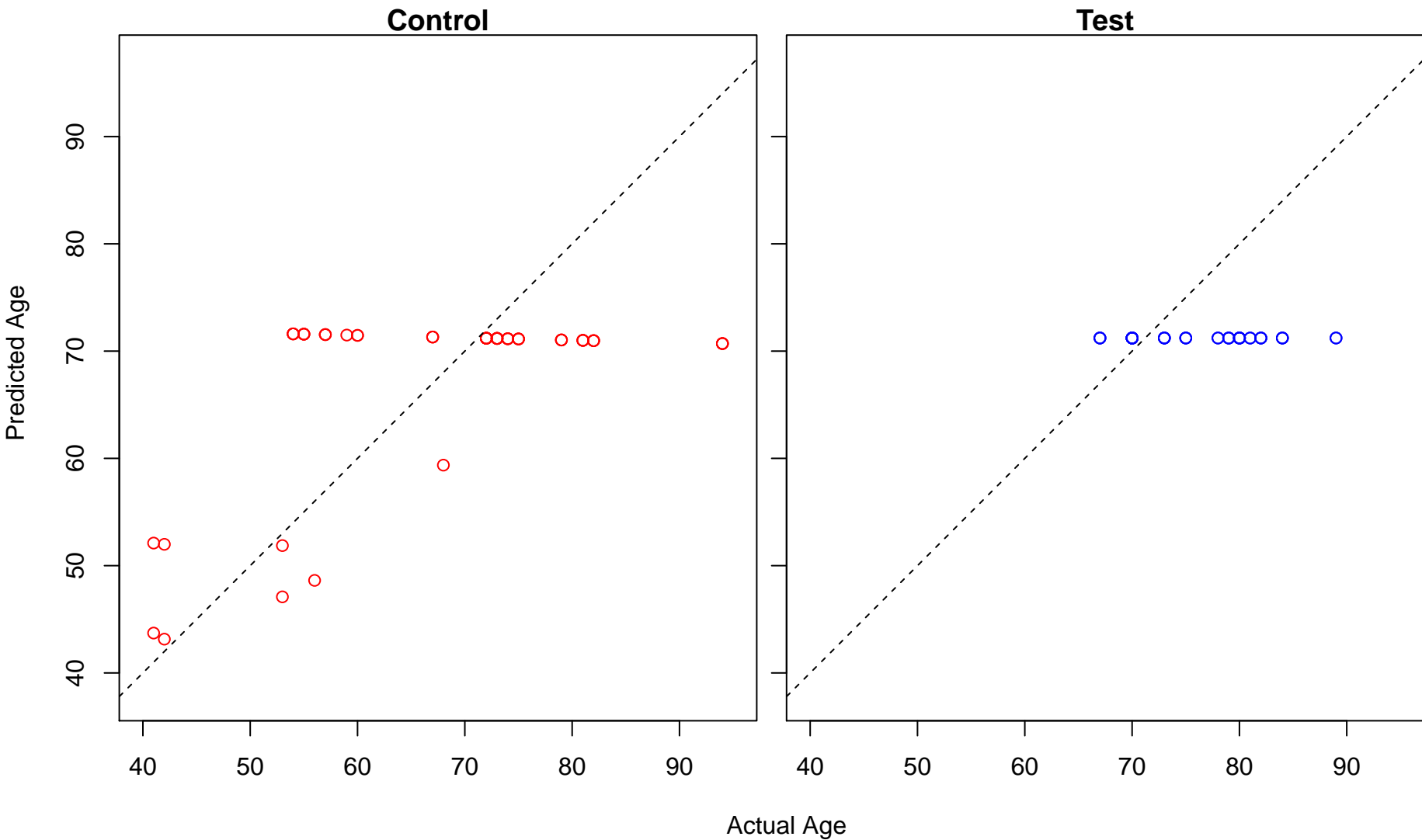


Test



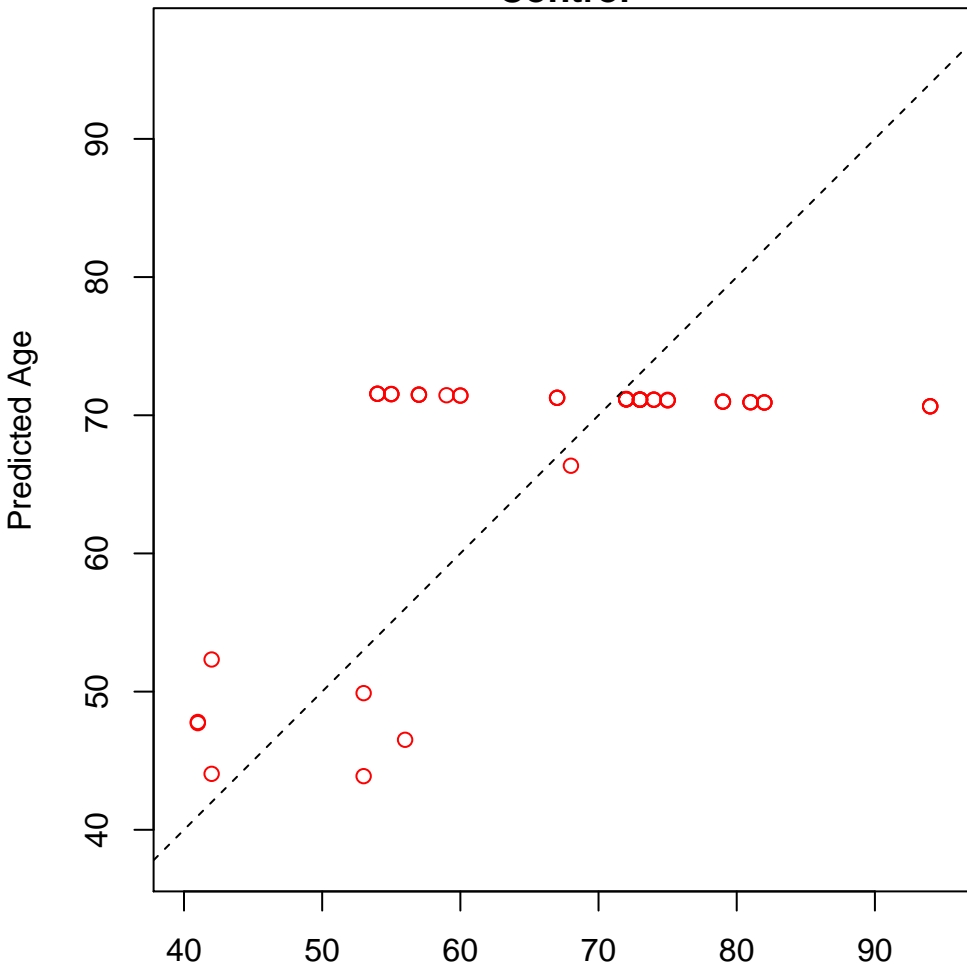
Actual Age

nucleotide metabolic process (Score: 0.827124)

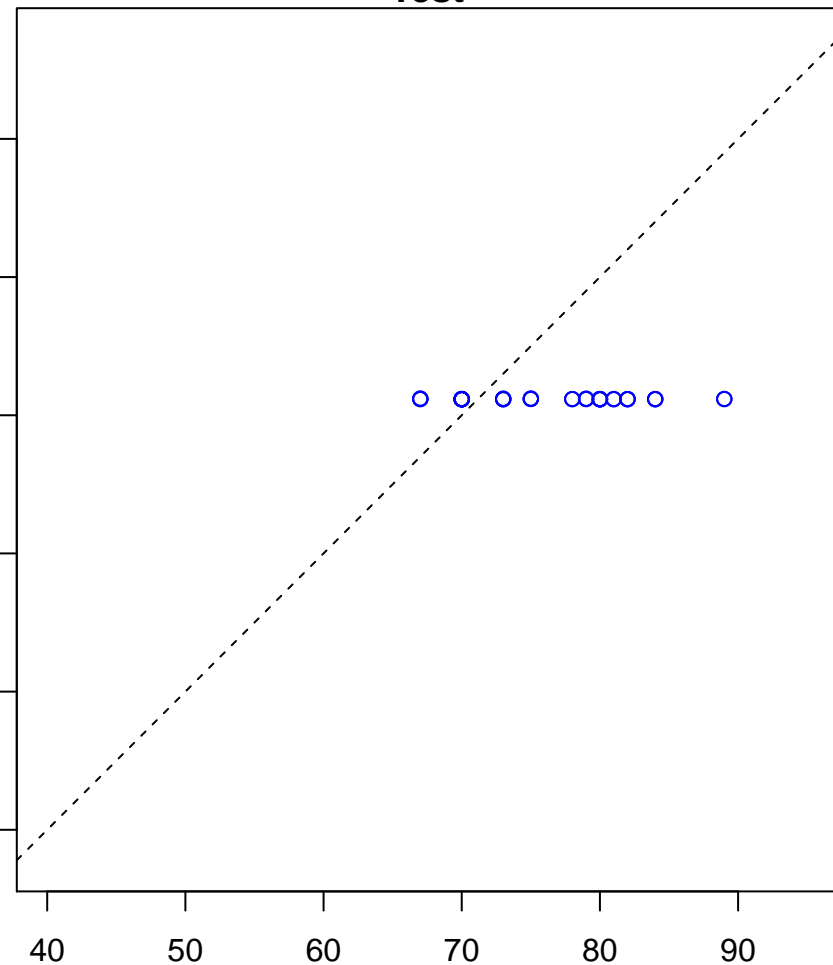


negative regulation of protein transport (Score: 0.827020)

Control

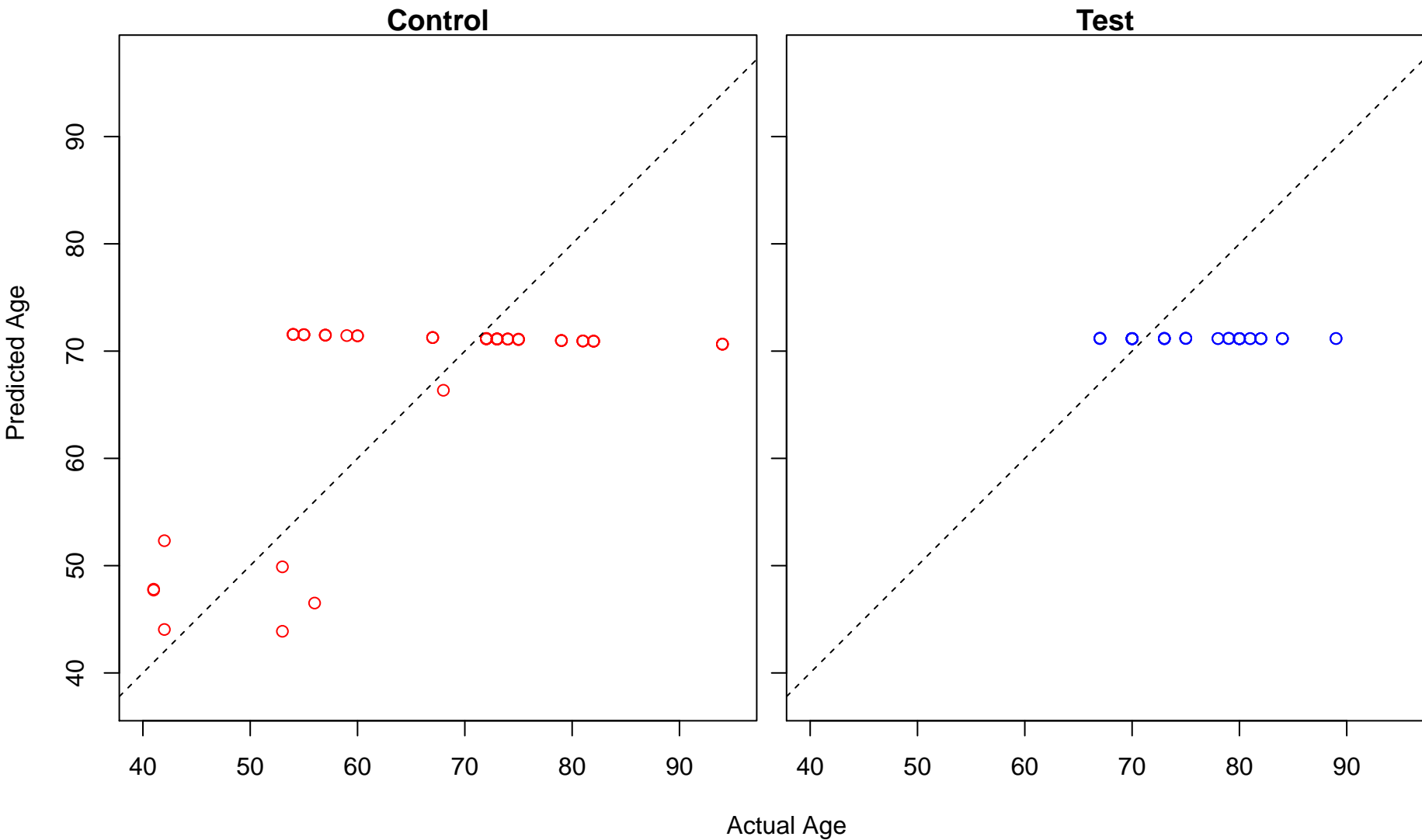


Test



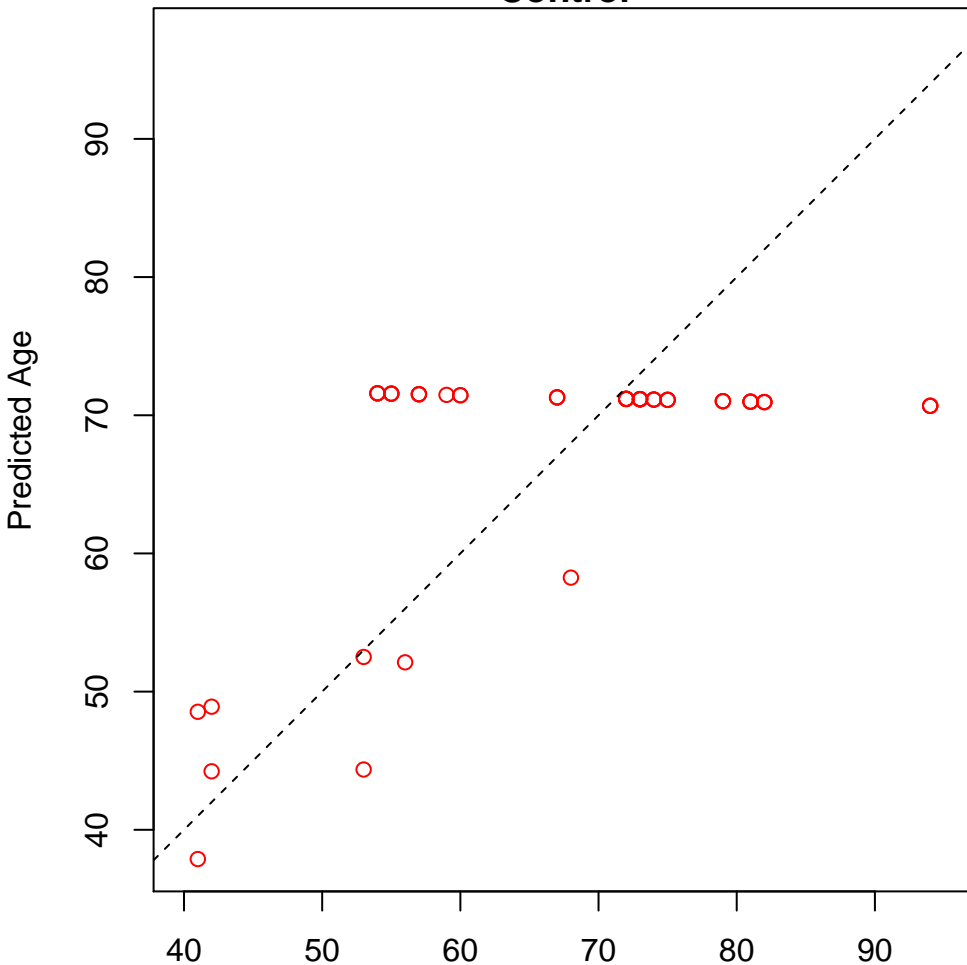
Actual Age

negative regulation of establishment of protein localization (Score: 0.827020)

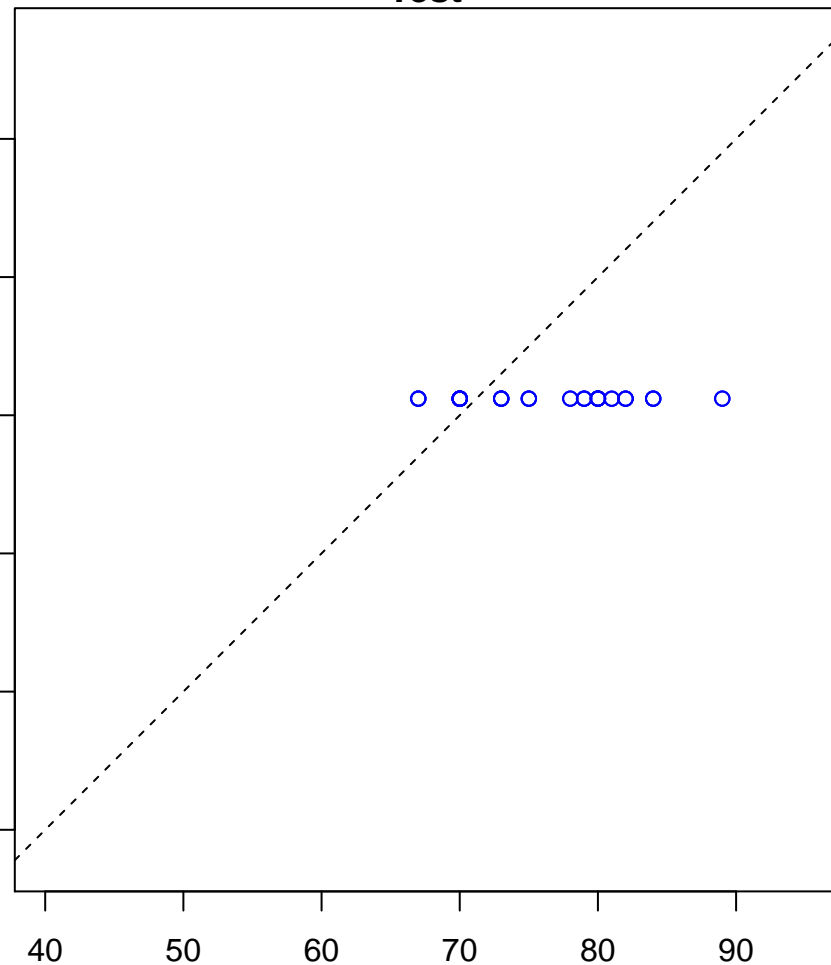


phosphorus metabolic process (Score: 0.826995)

Control

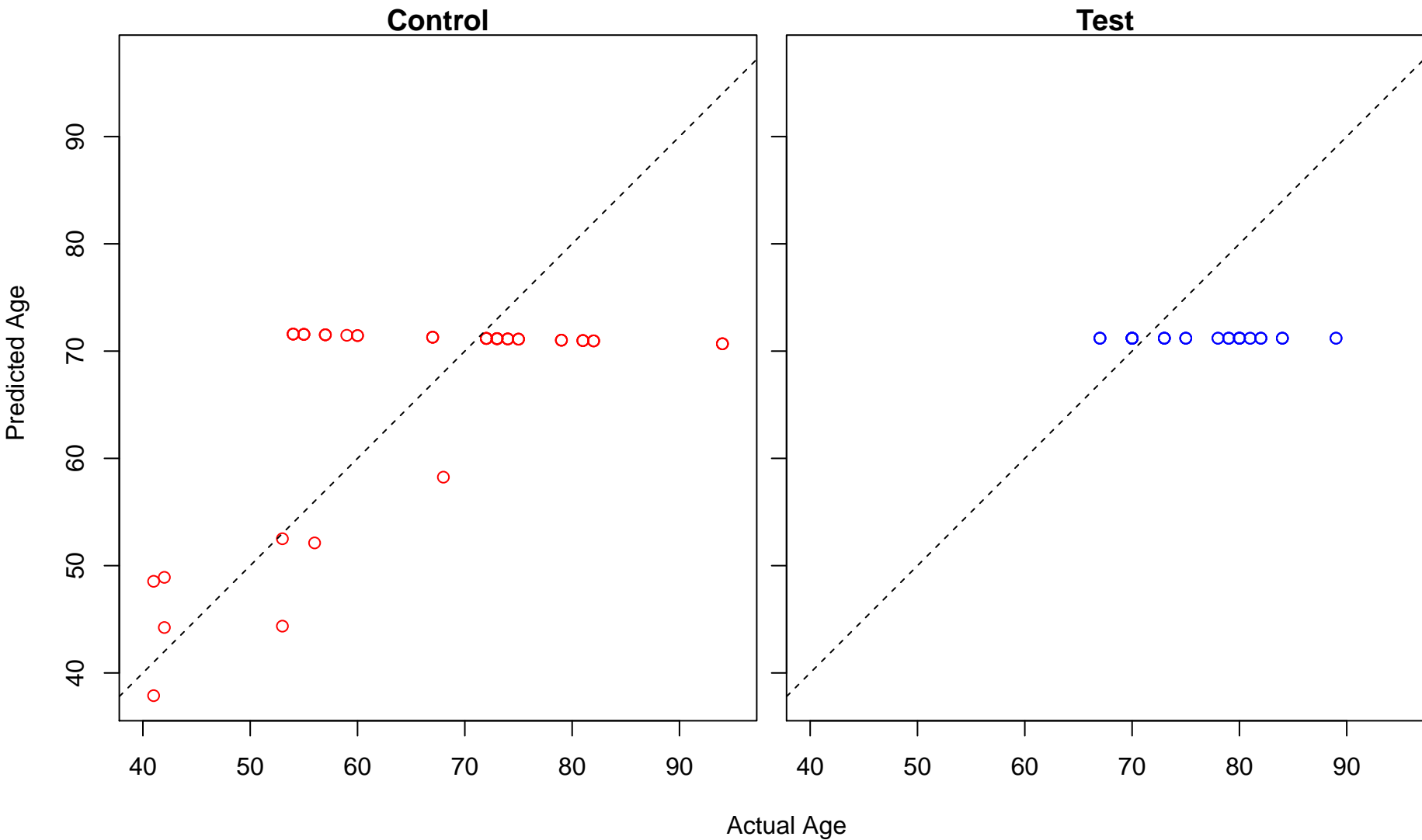


Test

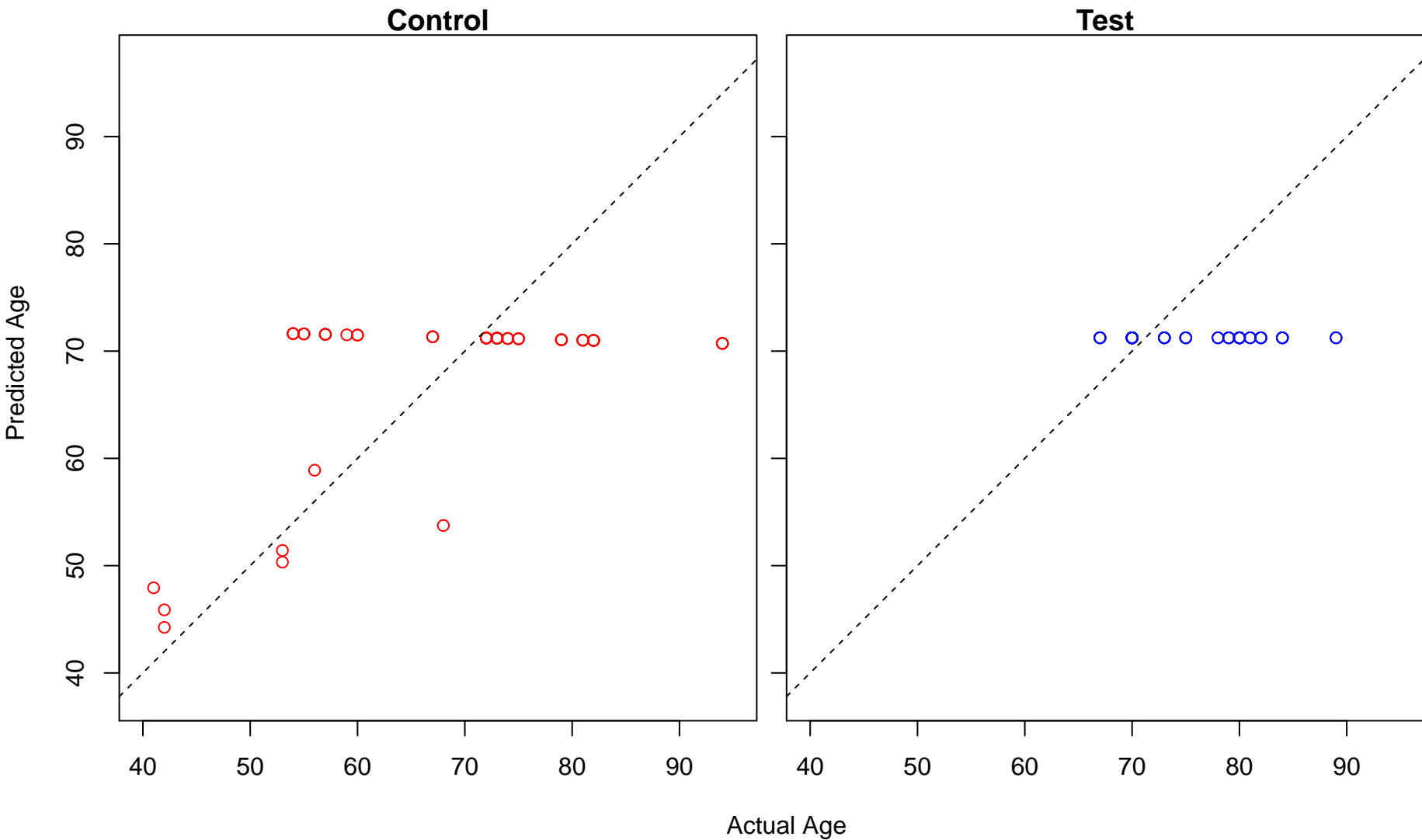


Actual Age

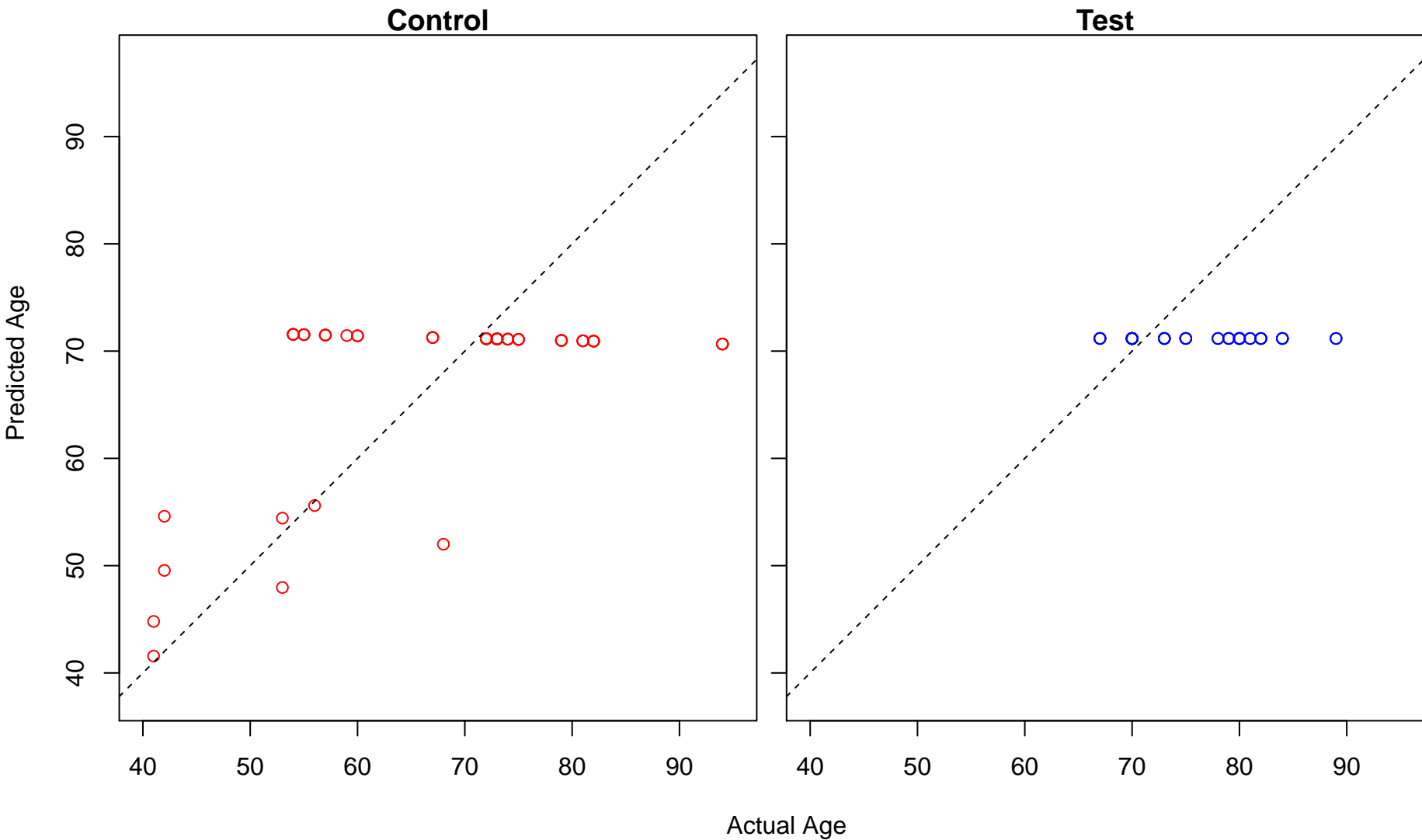
phosphate-containing compound metabolic process (Score: 0.826995)



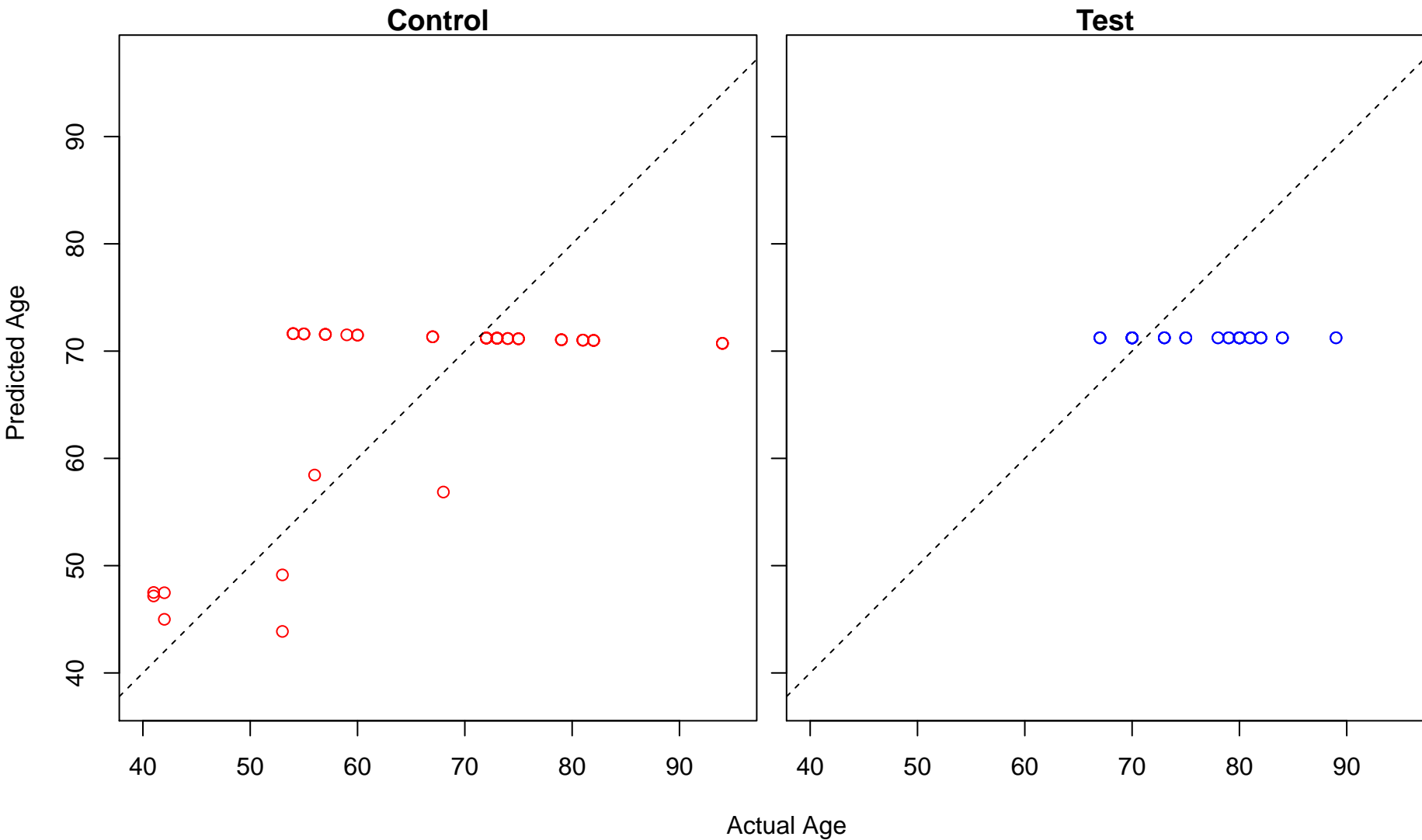
response to abiotic stimulus (Score: 0.826963)



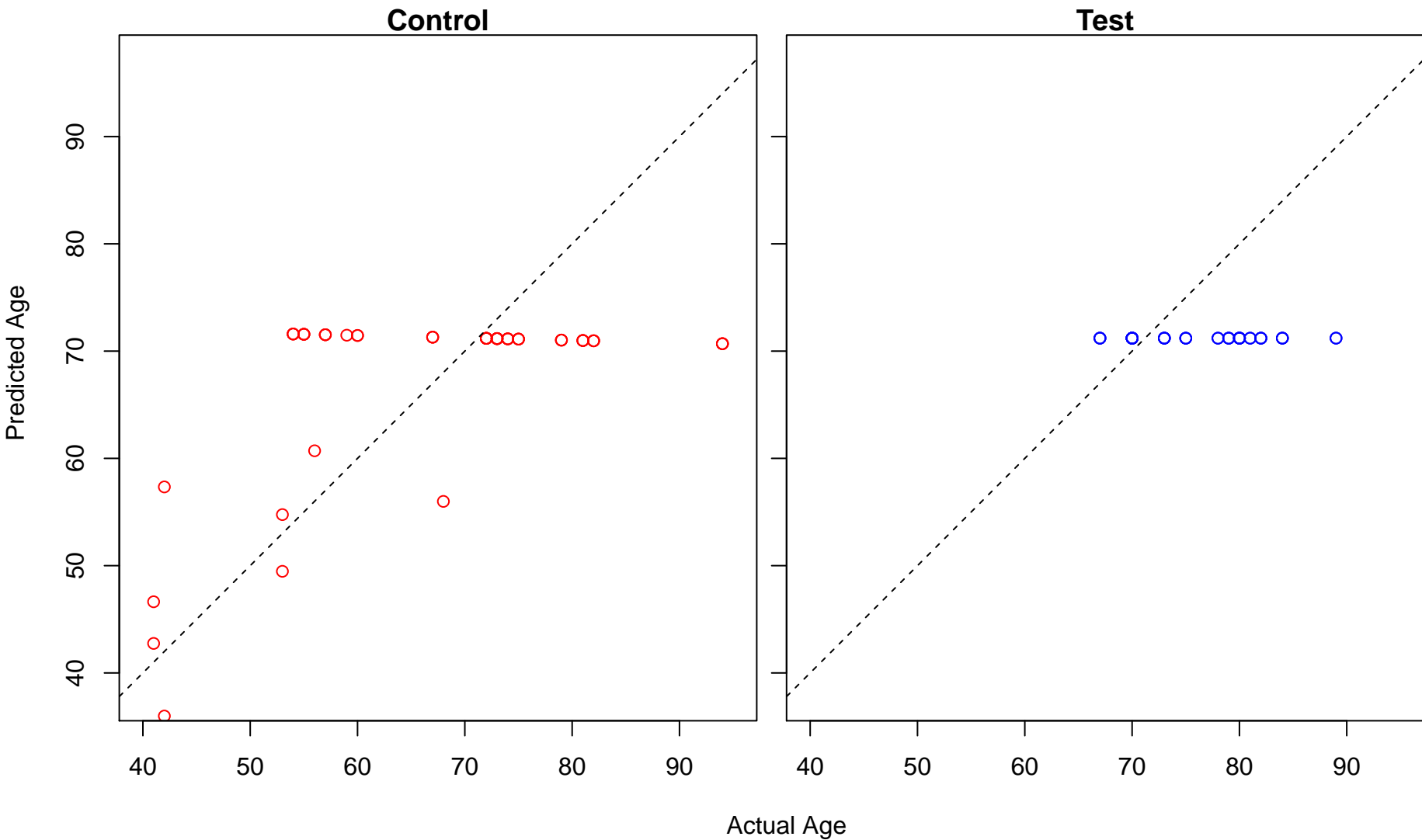
regulation of actin nucleation (Score: 0.826915)



microtubule-based process (Score: 0.826912)

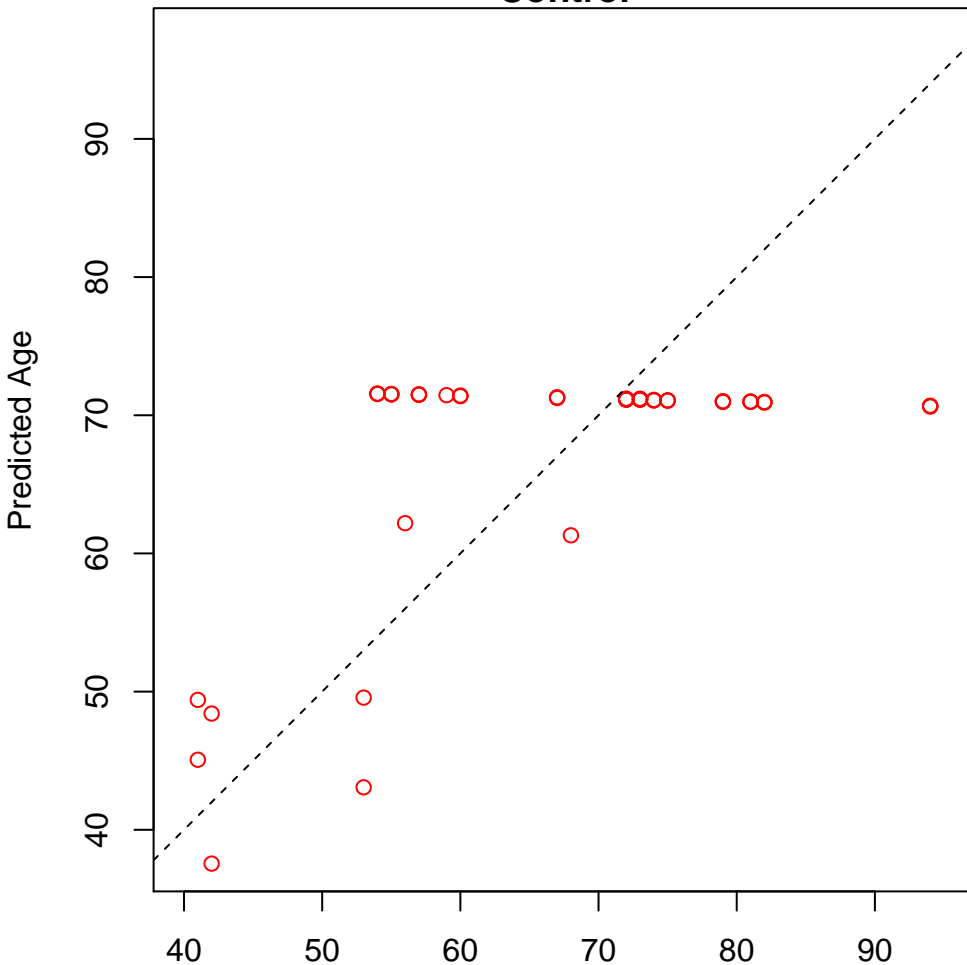


regulation of intrinsic apoptotic signaling pathway (Score: 0.826754)

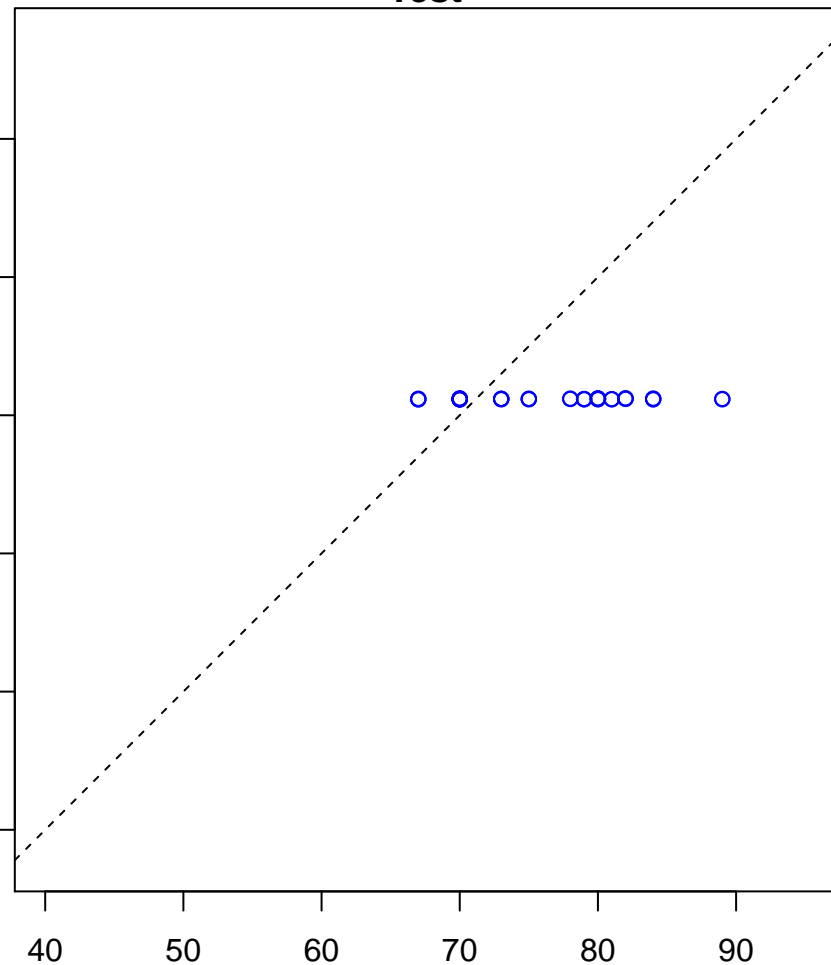


cell morphogenesis (Score: 0.826565)

Control



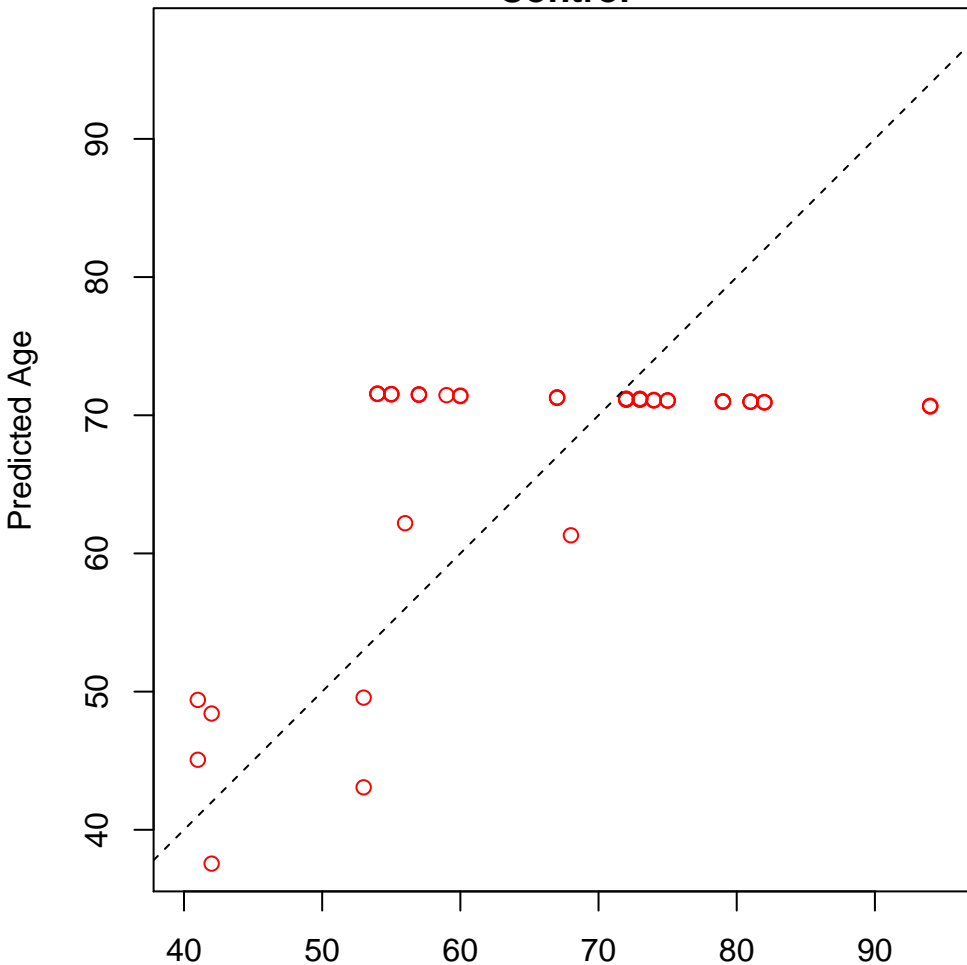
Test



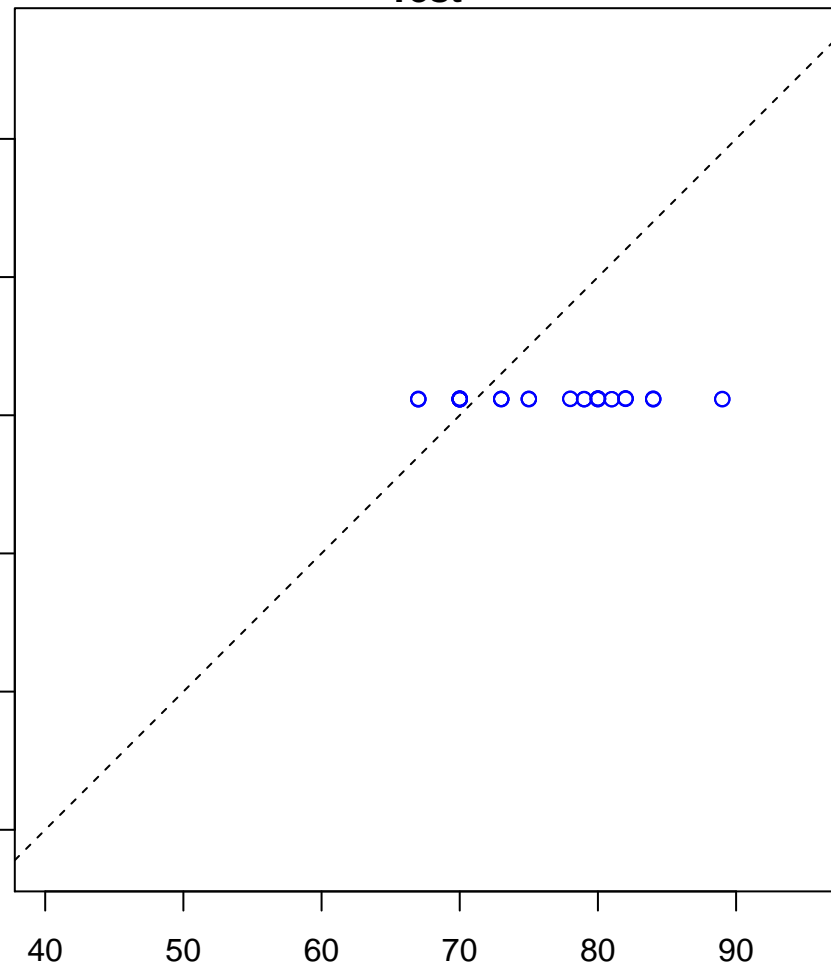
Actual Age

cellular component morphogenesis (Score: 0.826565)

Control



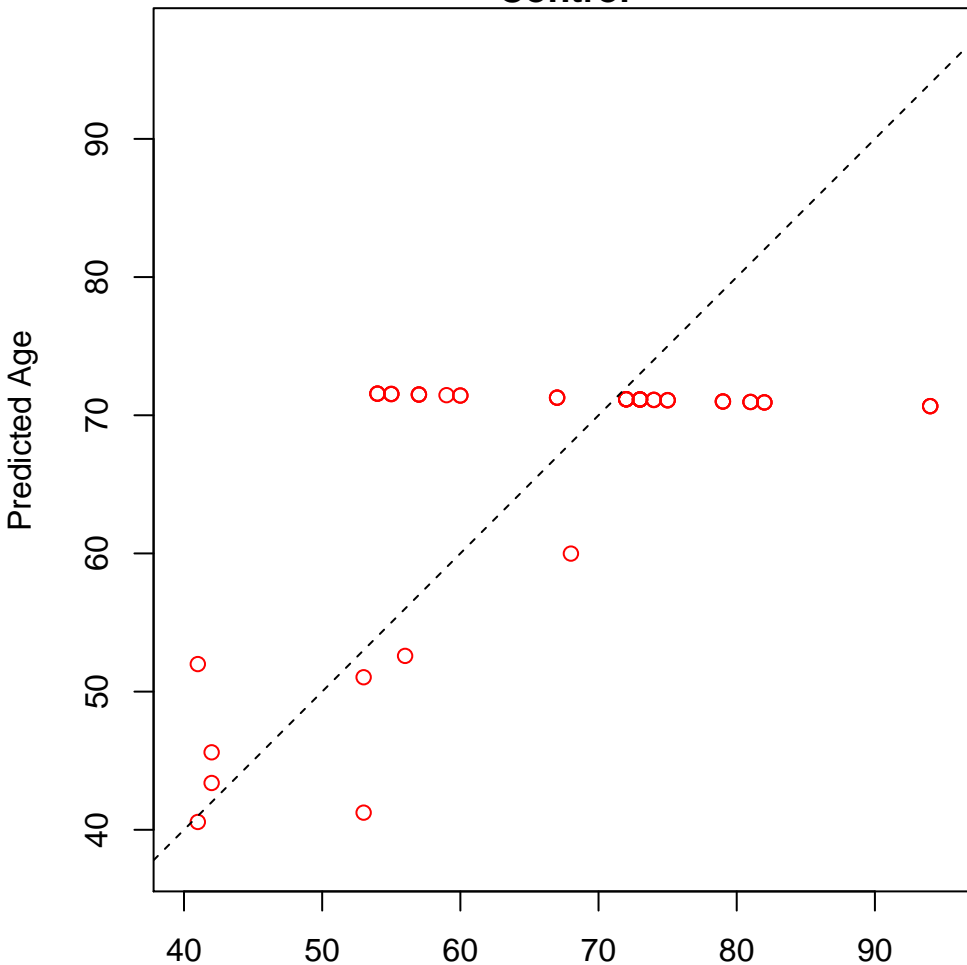
Test



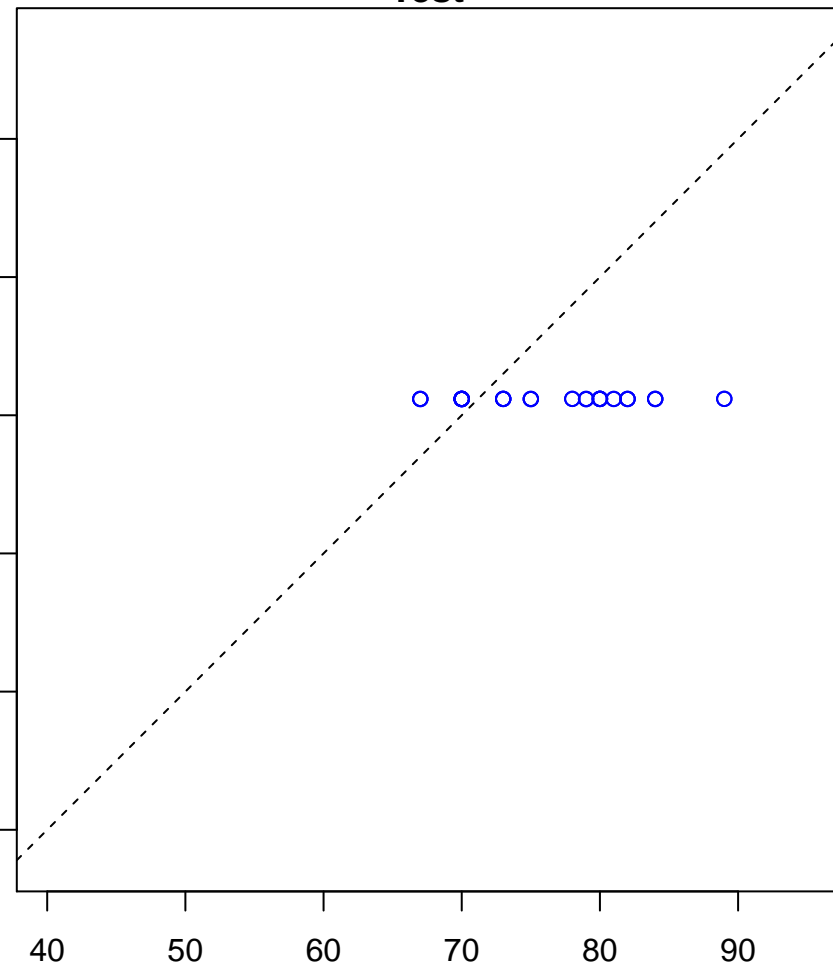
Actual Age

negative regulation of molecular function (Score: 0.826546)

Control



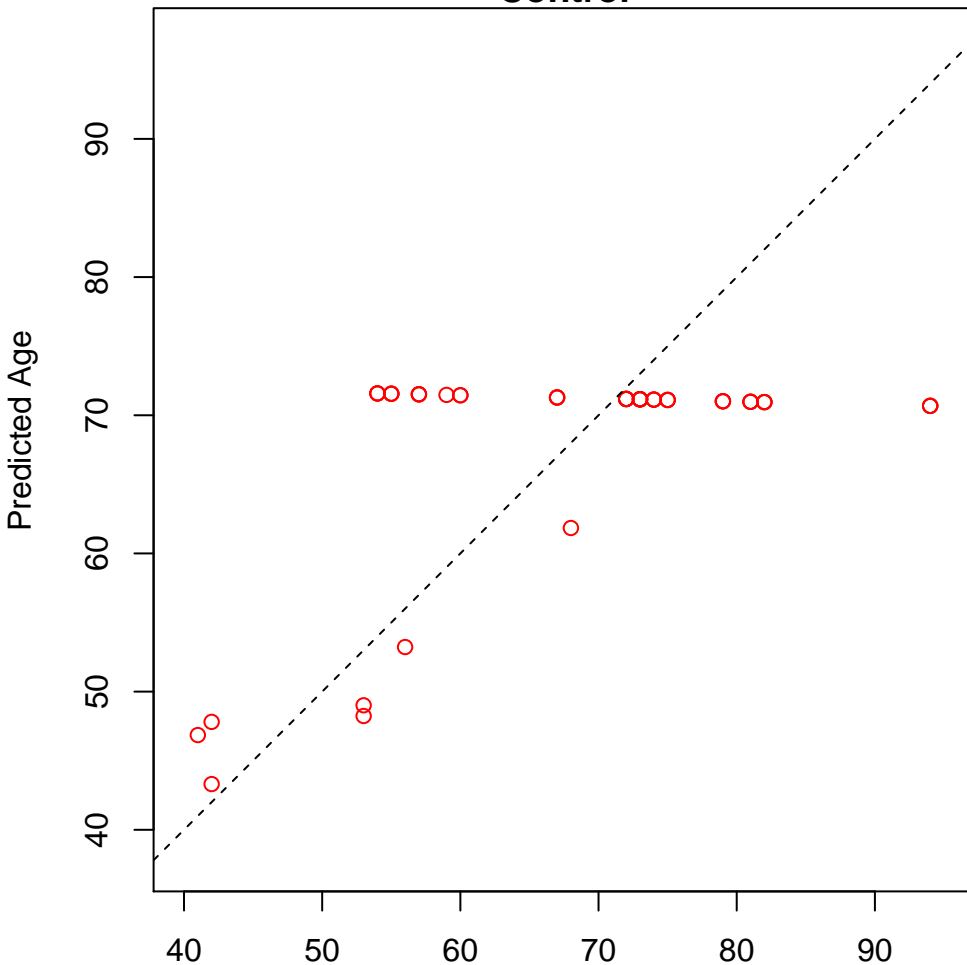
Test



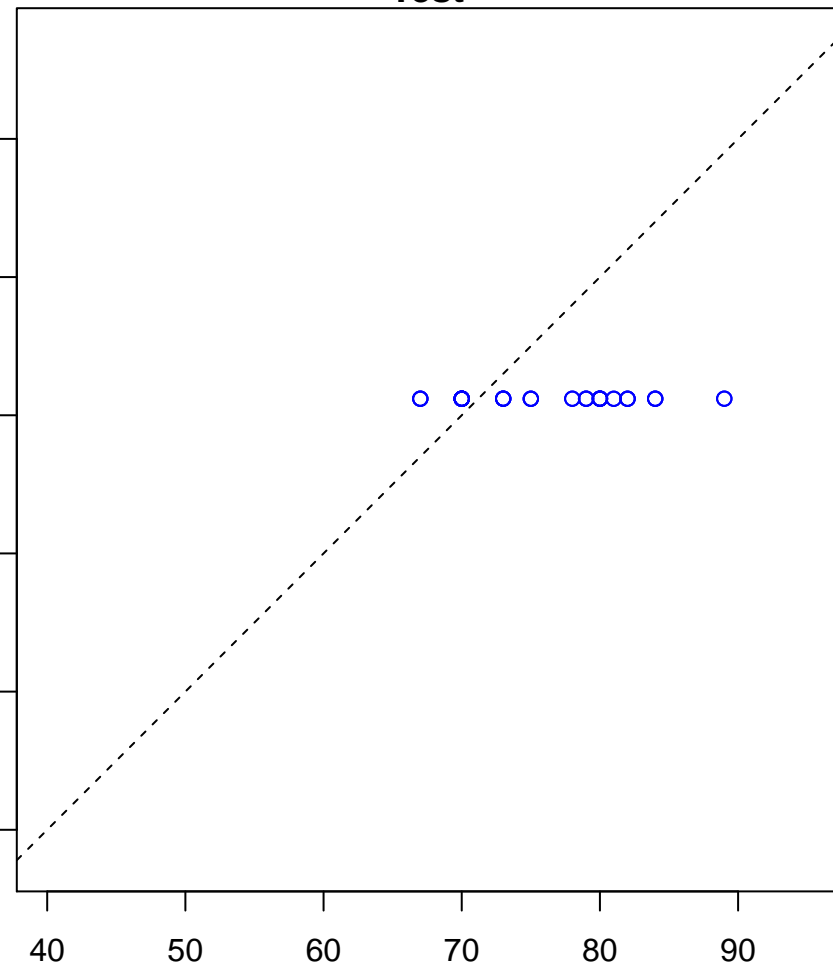
Actual Age

activation of immune response (Score: 0.826531)

Control

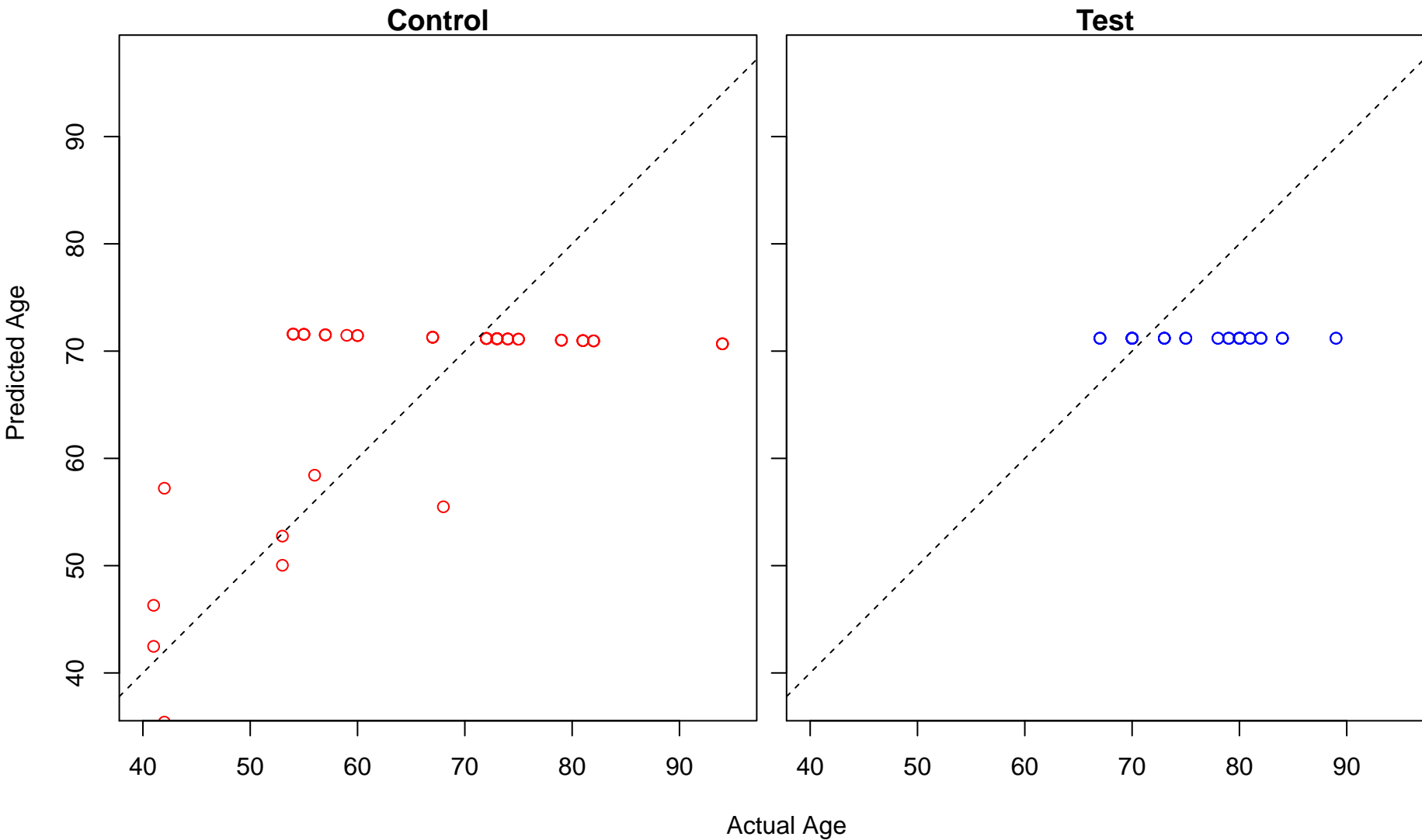


Test



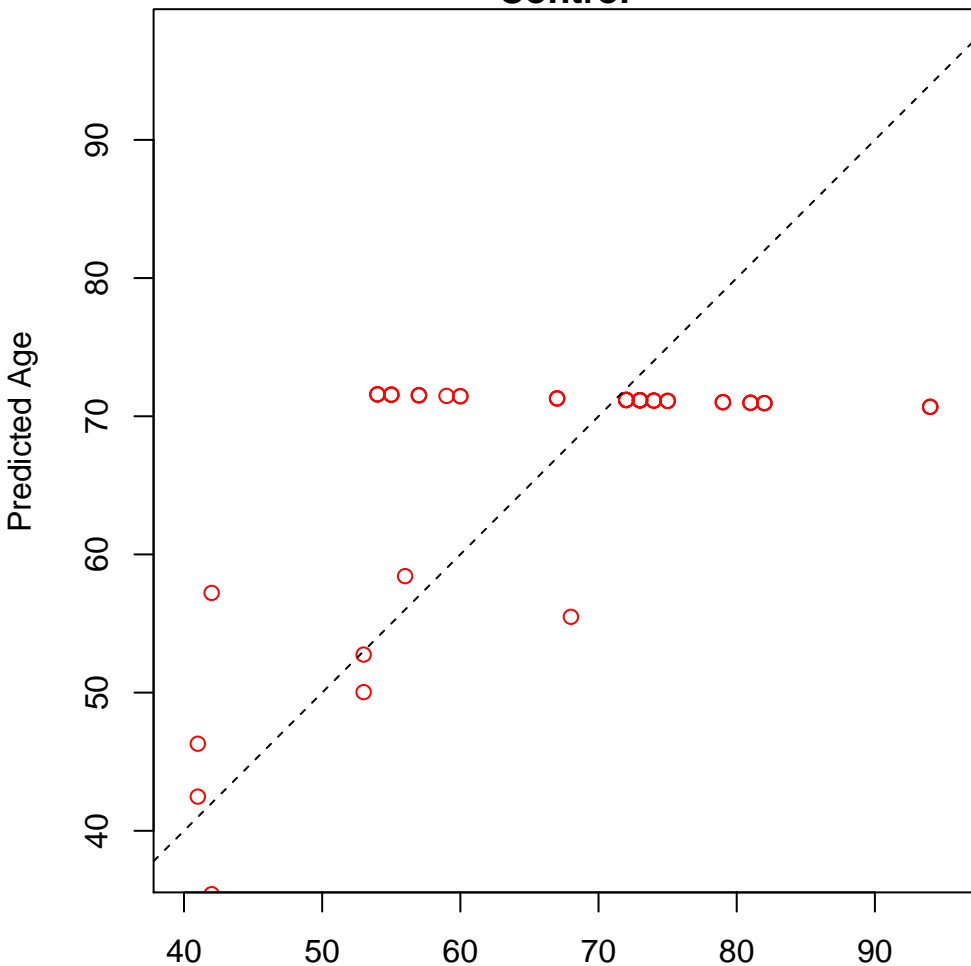
Actual Age

regulation of cellular response to oxidative stress (Score: 0.826514)

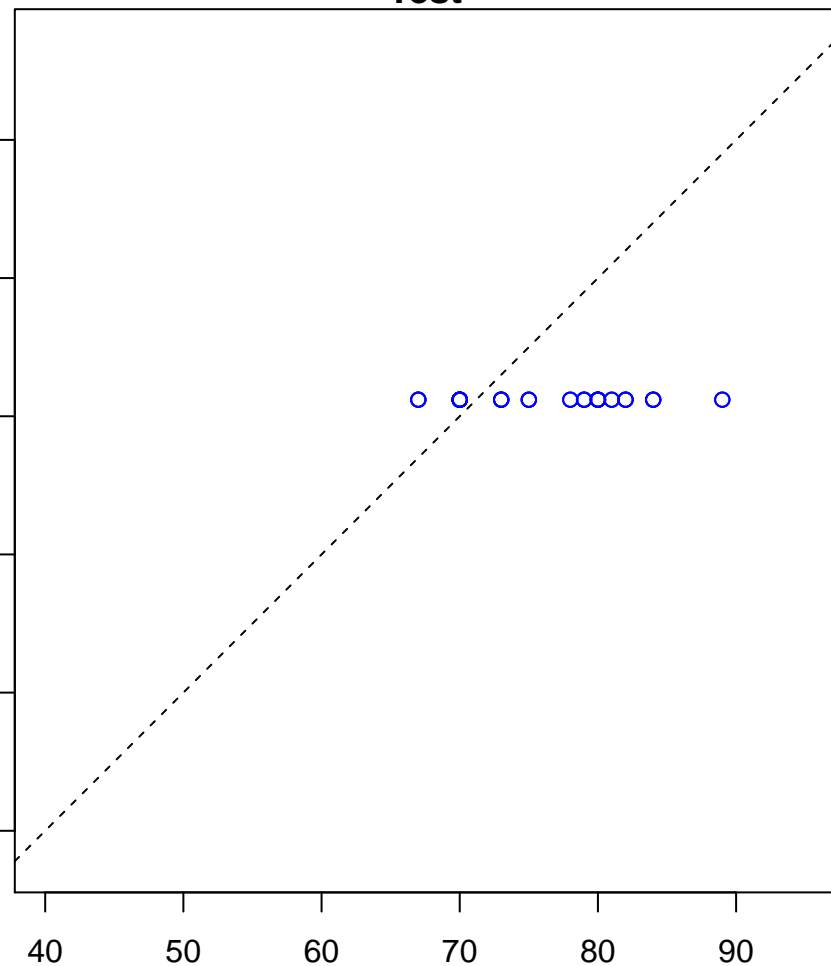


regulation of response to oxidative stress (Score: 0.826514)

Control

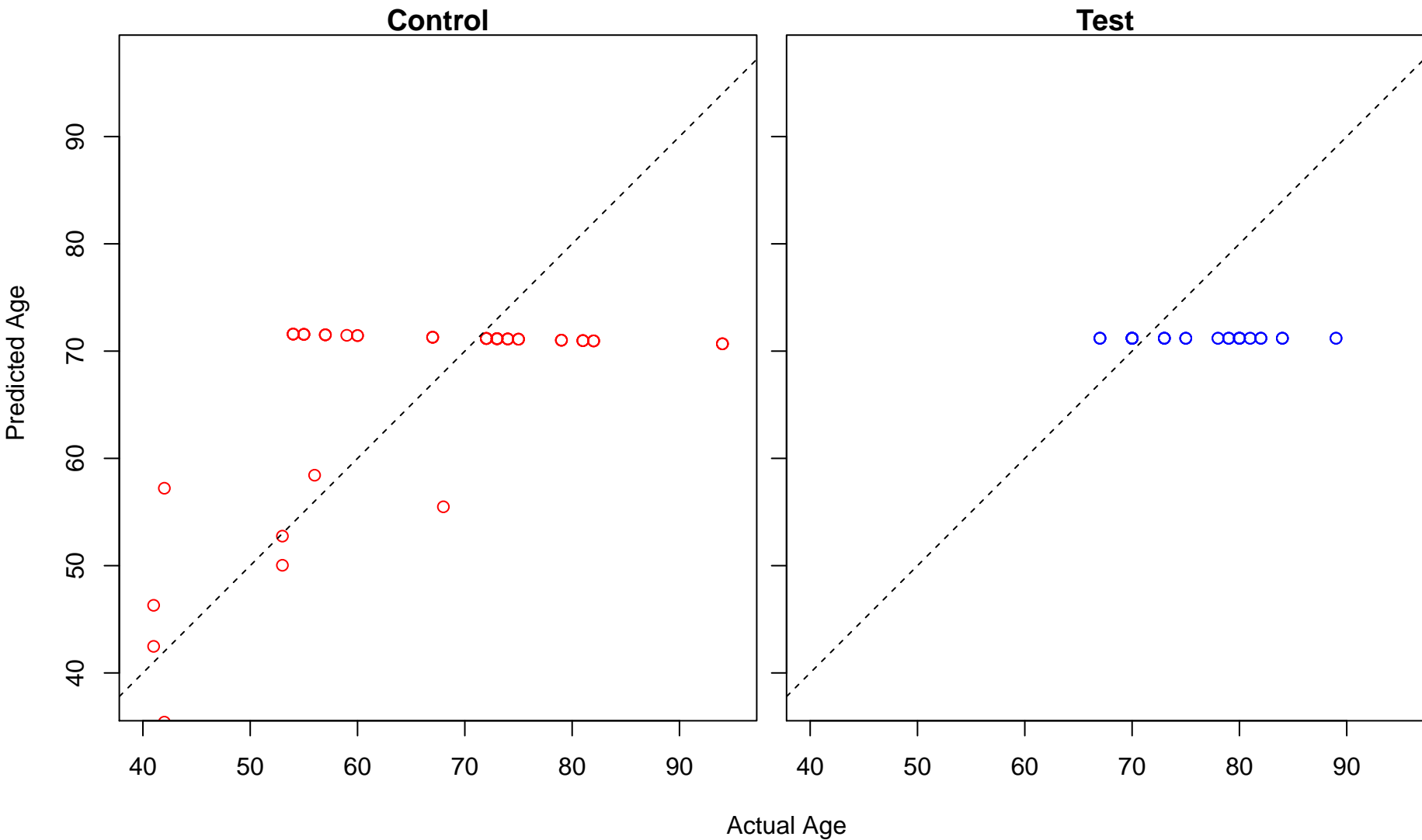


Test



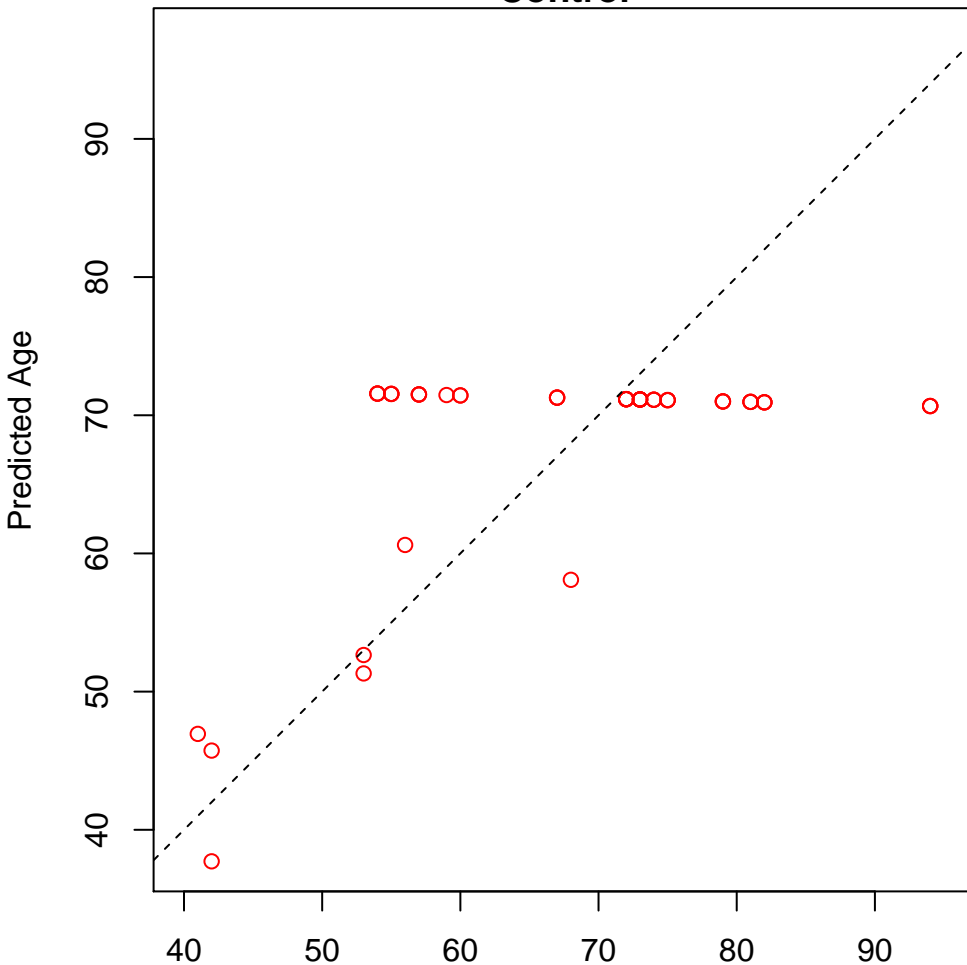
Actual Age

regulation of oxidative stress-induced cell death (Score: 0.826514)

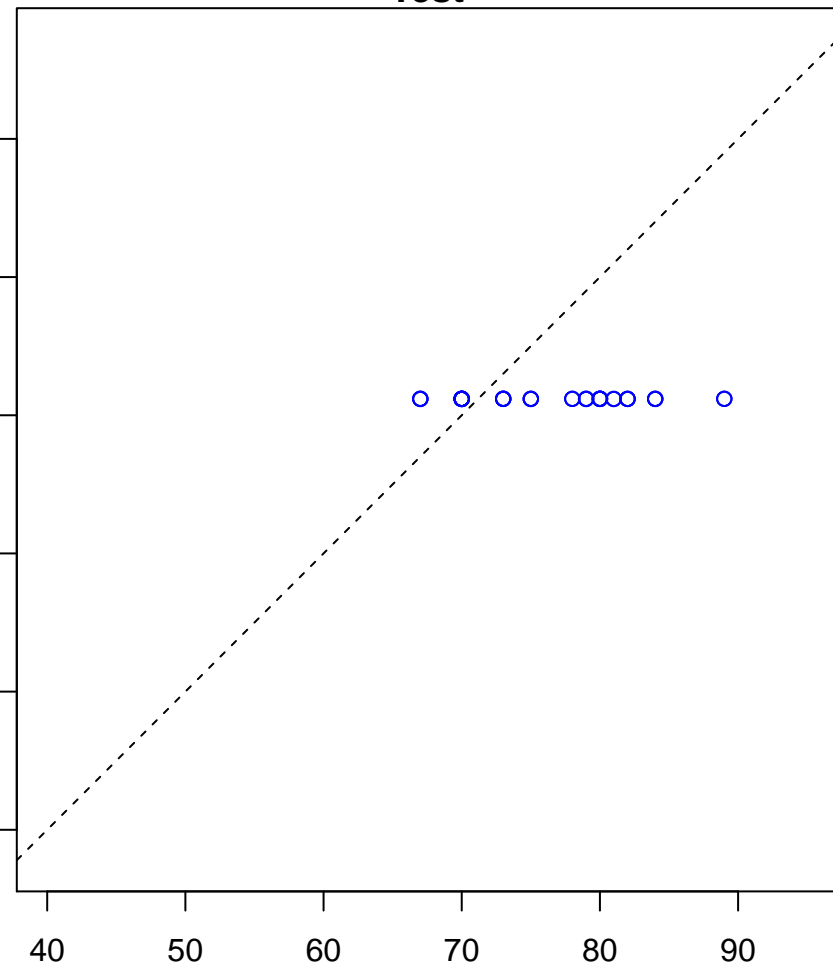


negative regulation of cell cycle (Score: 0.826317)

Control



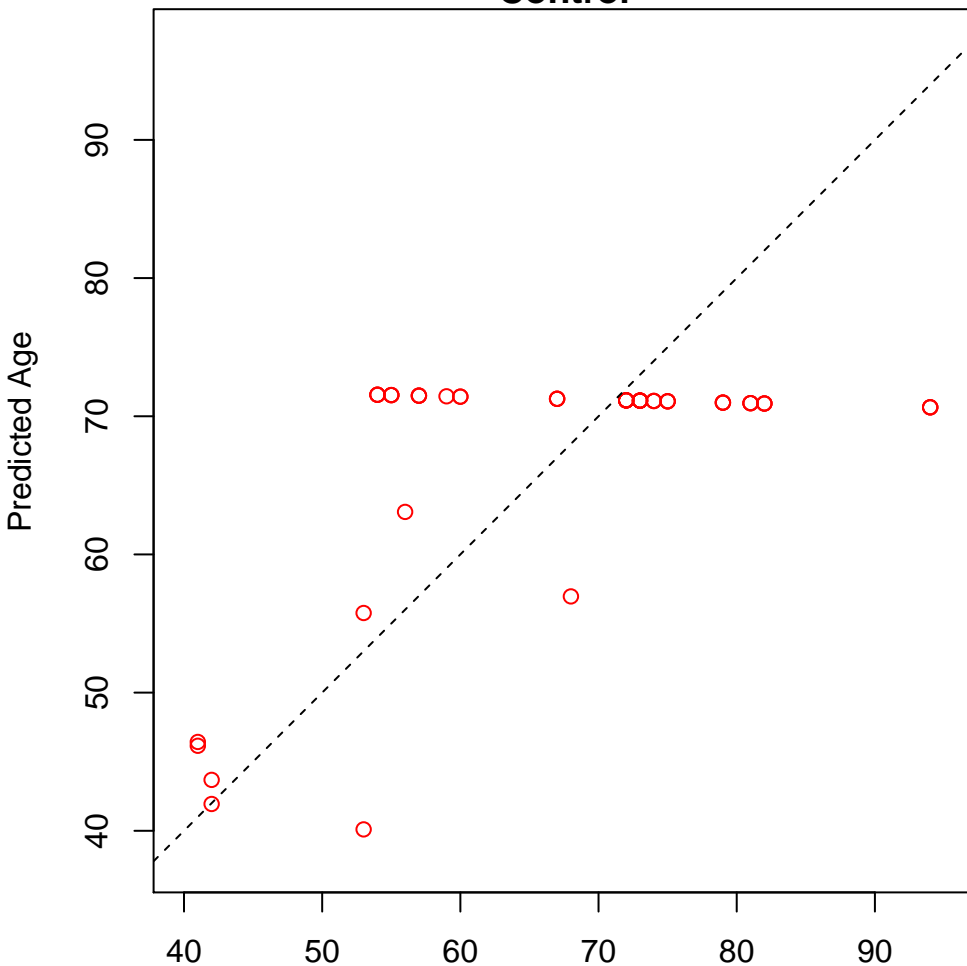
Test



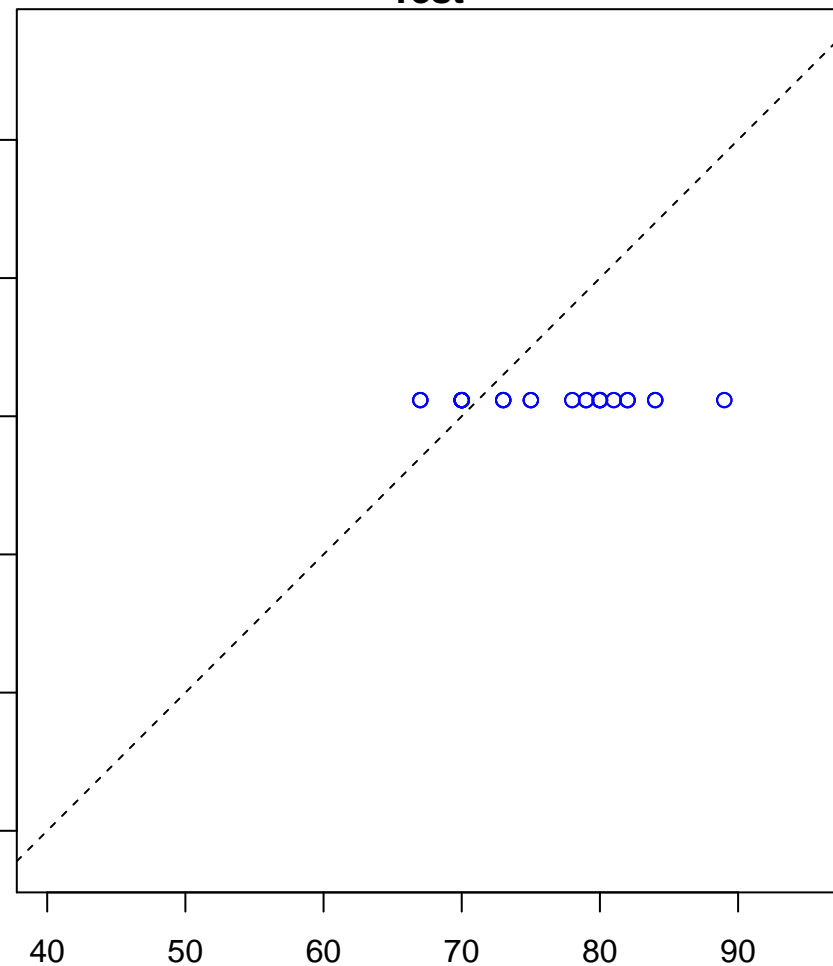
Actual Age

negative regulation of apoptotic process (Score: 0.826312)

Control

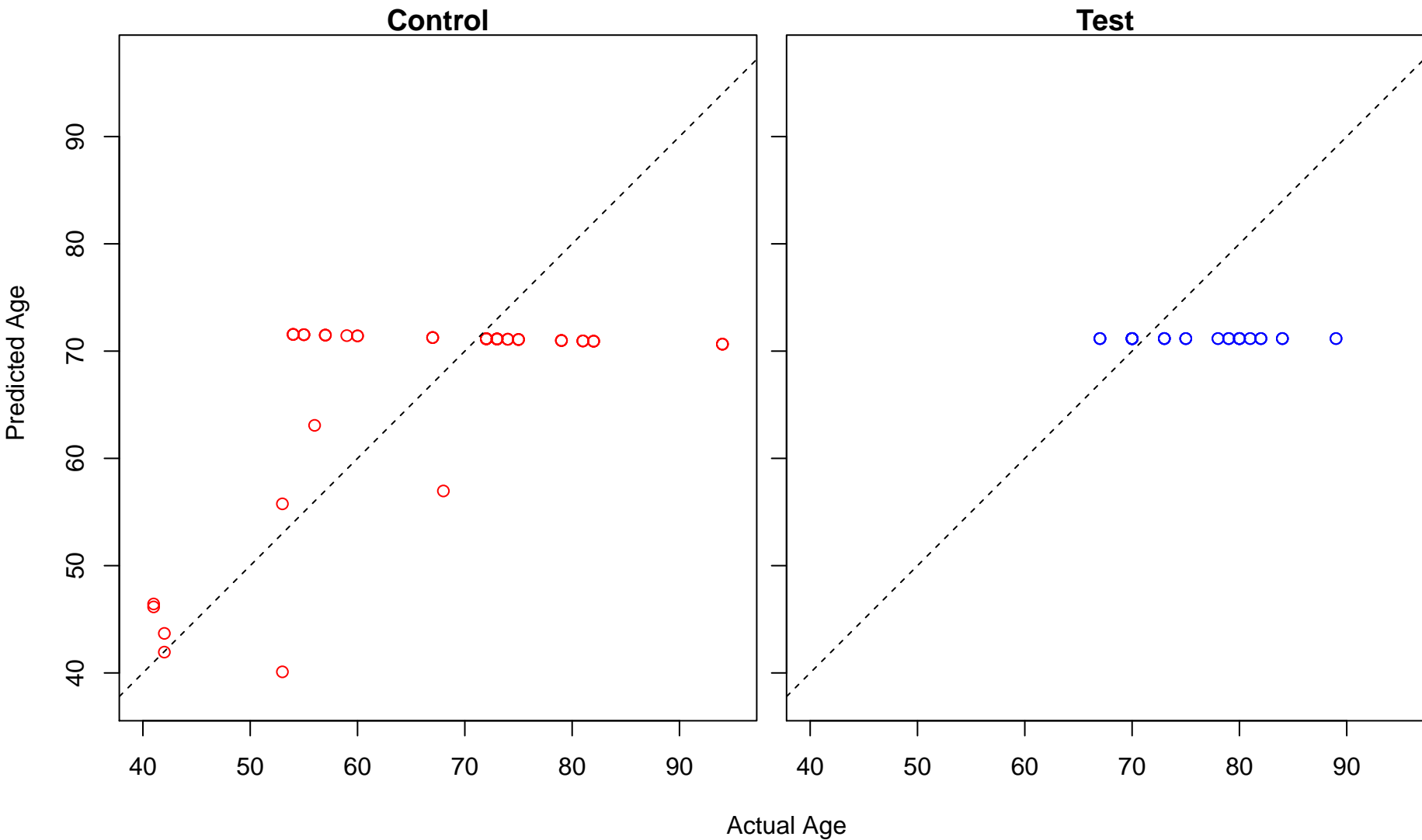


Test



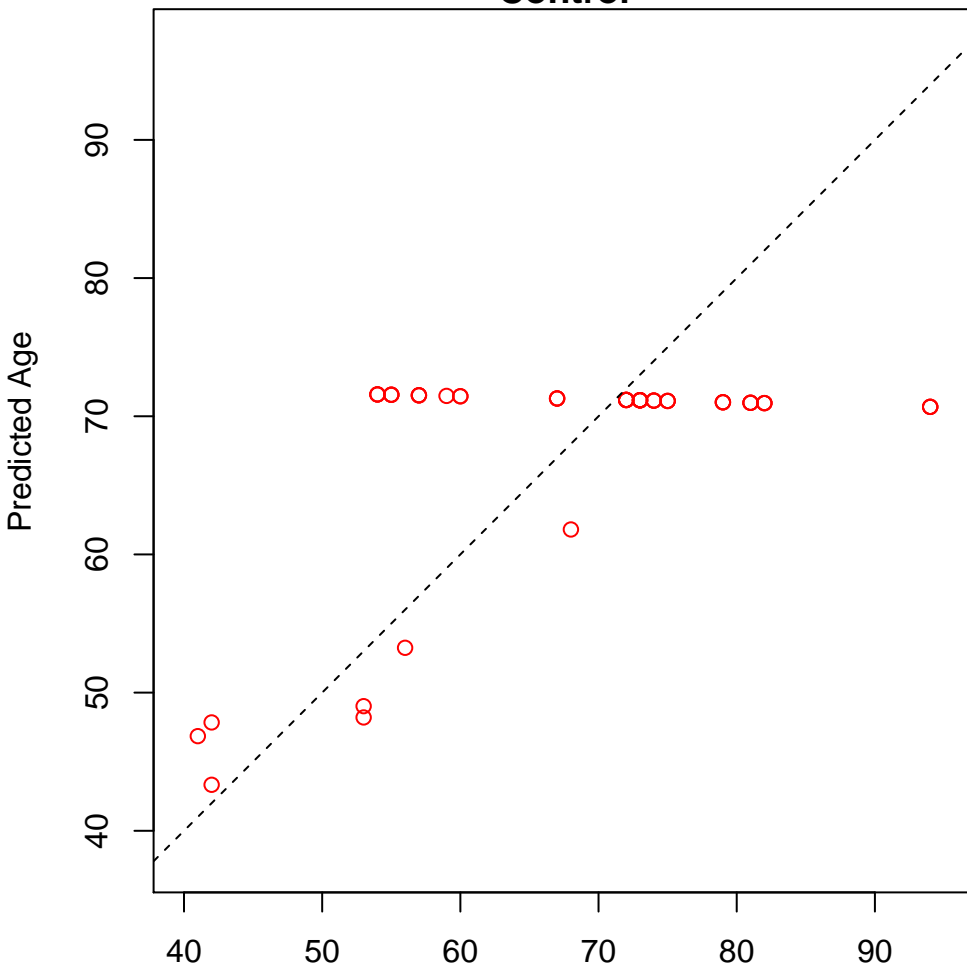
Actual Age

negative regulation of programmed cell death (Score: 0.826312)

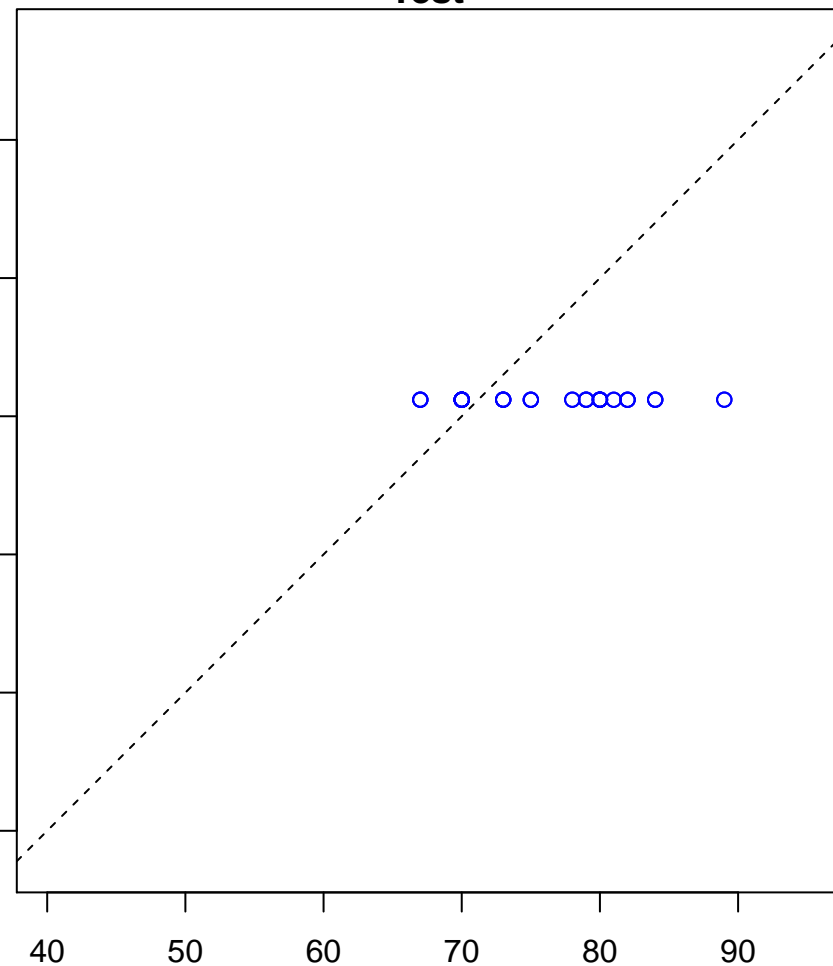


regulation of innate immune response (Score: 0.826289)

Control

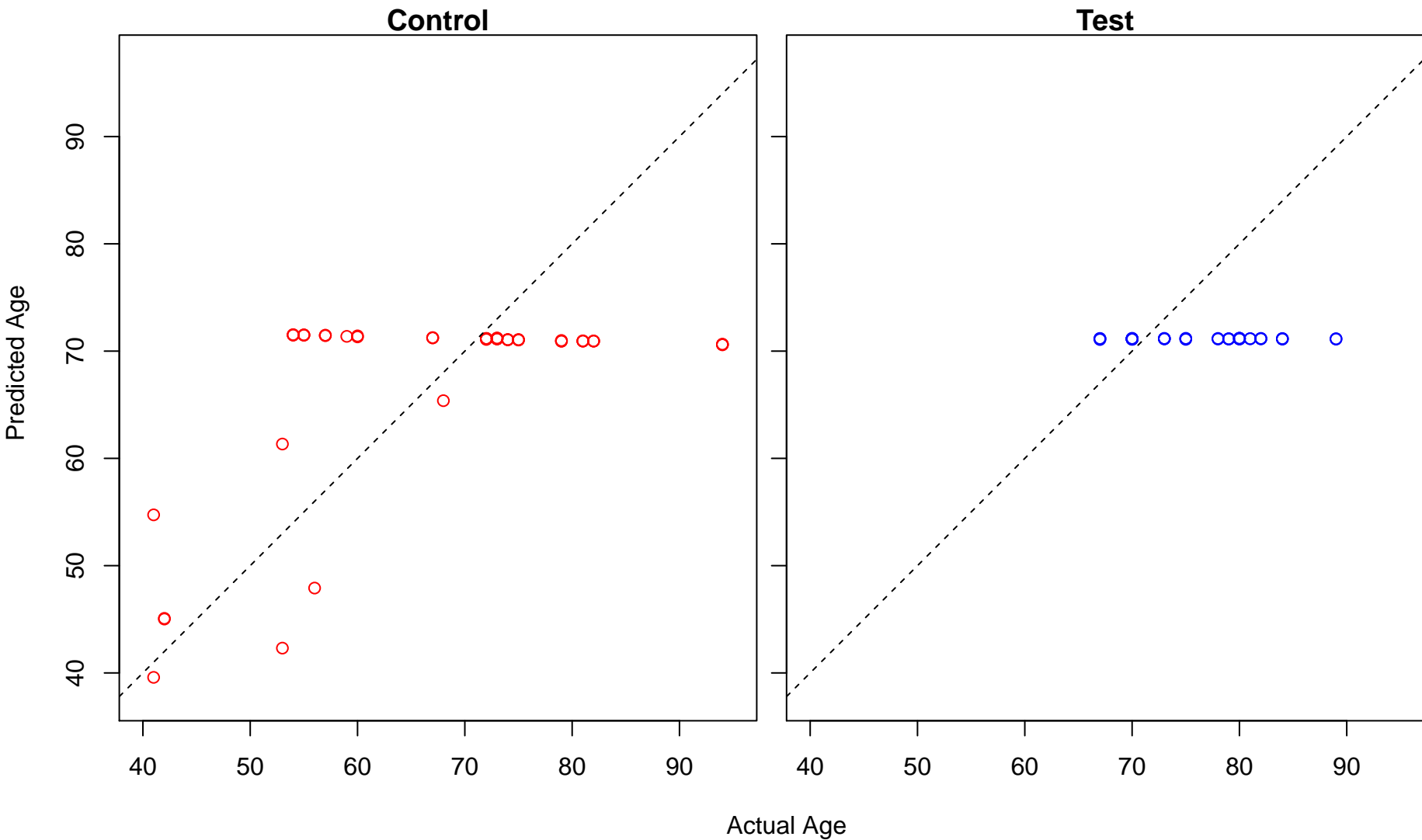


Test



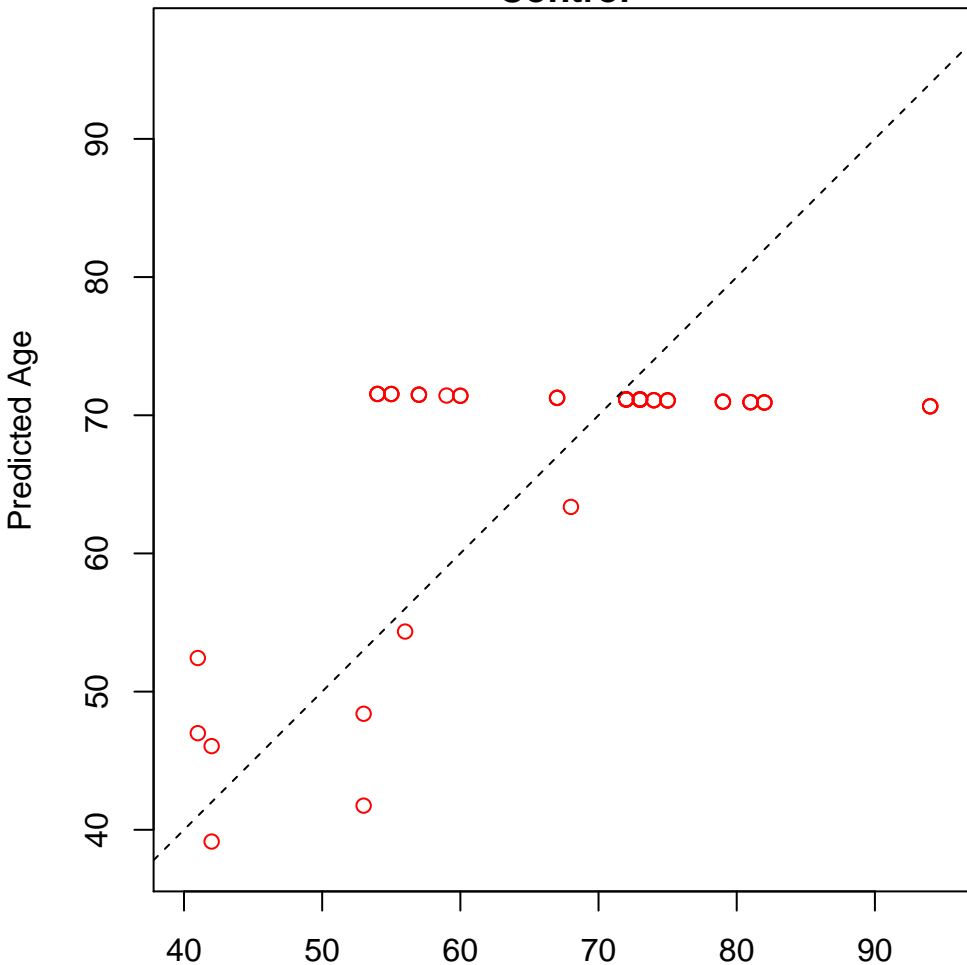
Actual Age

cell growth (Score: 0.826232)

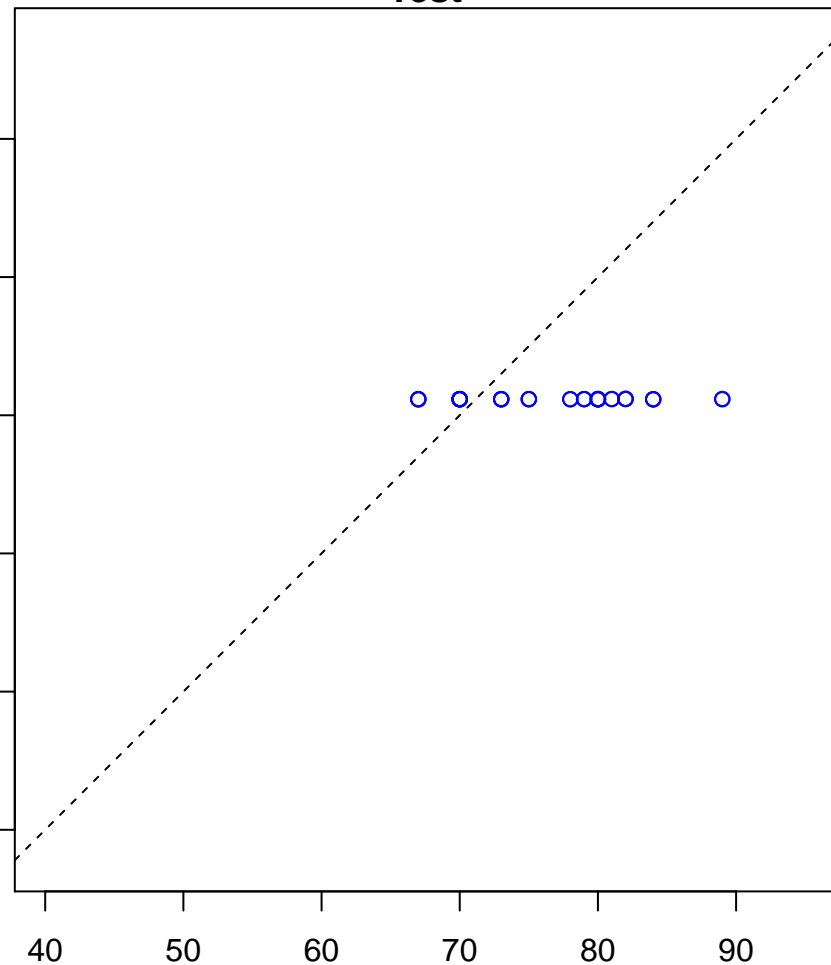


maintenance of protein location in nucleus (Score: 0.826203)

Control

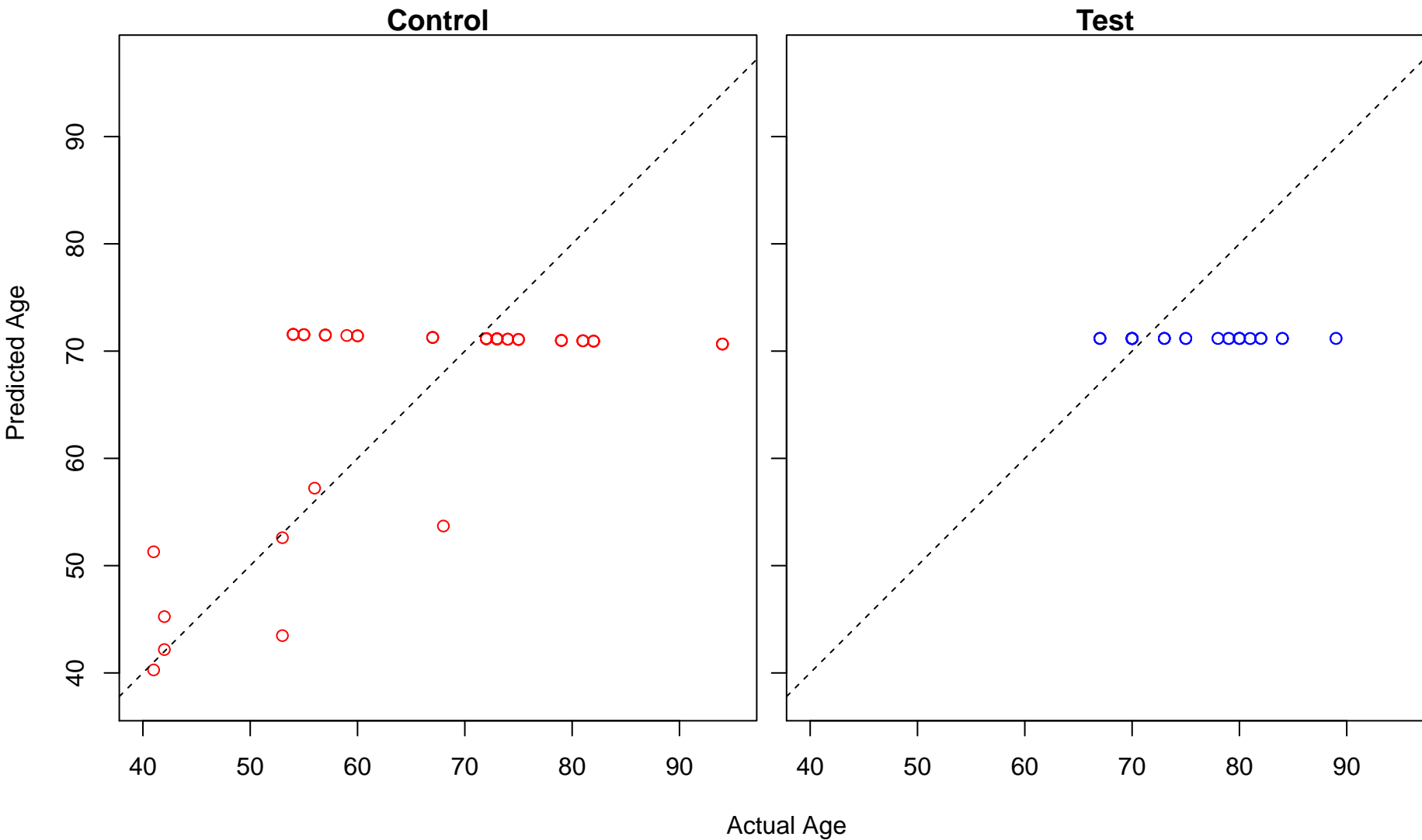


Test



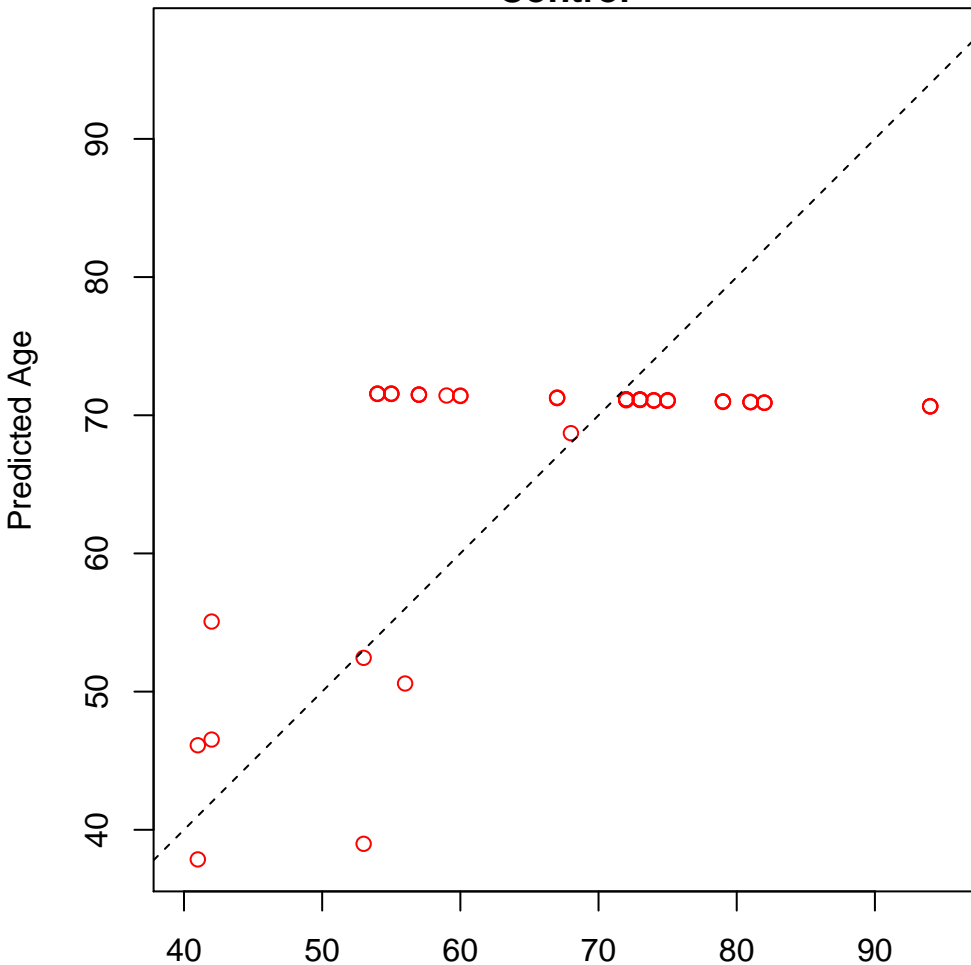
Actual Age

mitotic cell cycle process (Score: 0.826144)

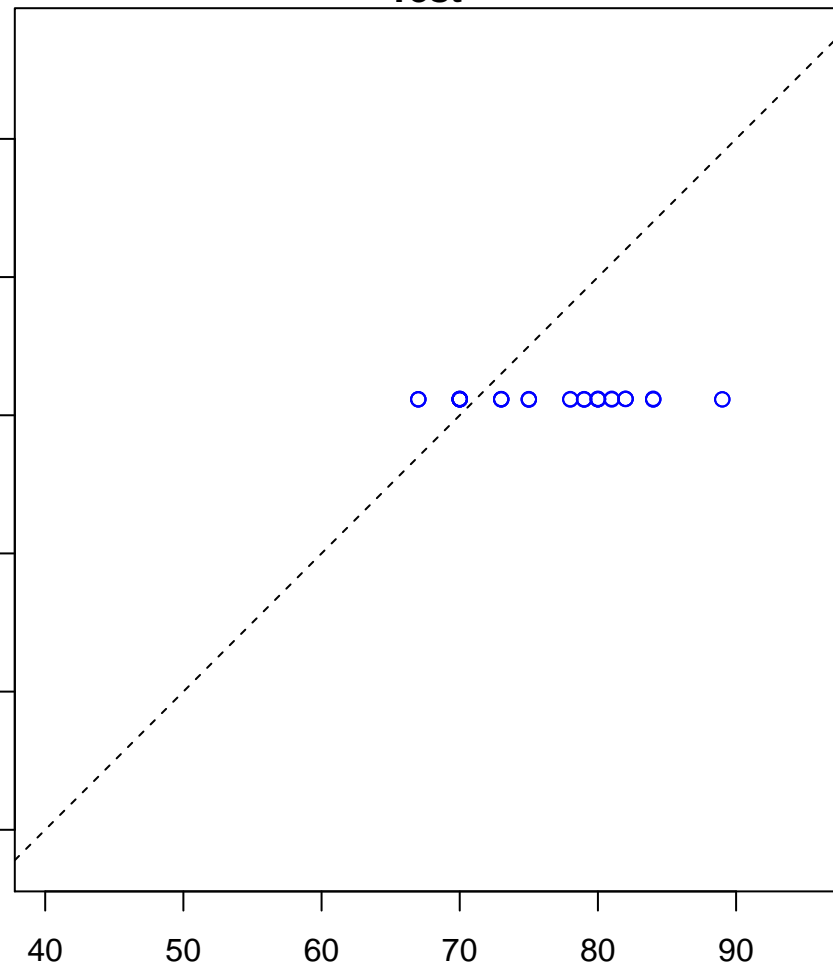


regulation of chromatin organization (Score: 0.826092)

Control

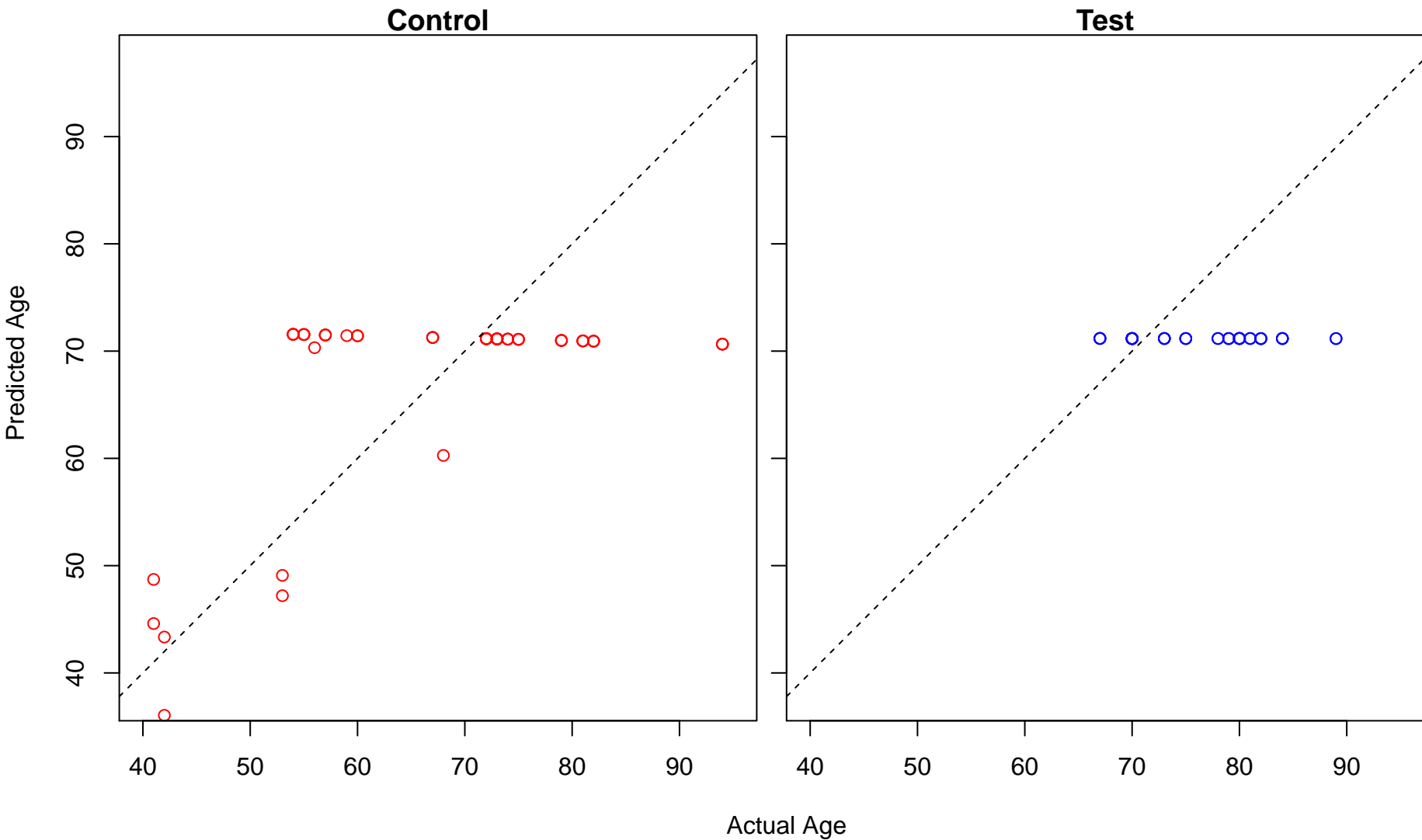


Test

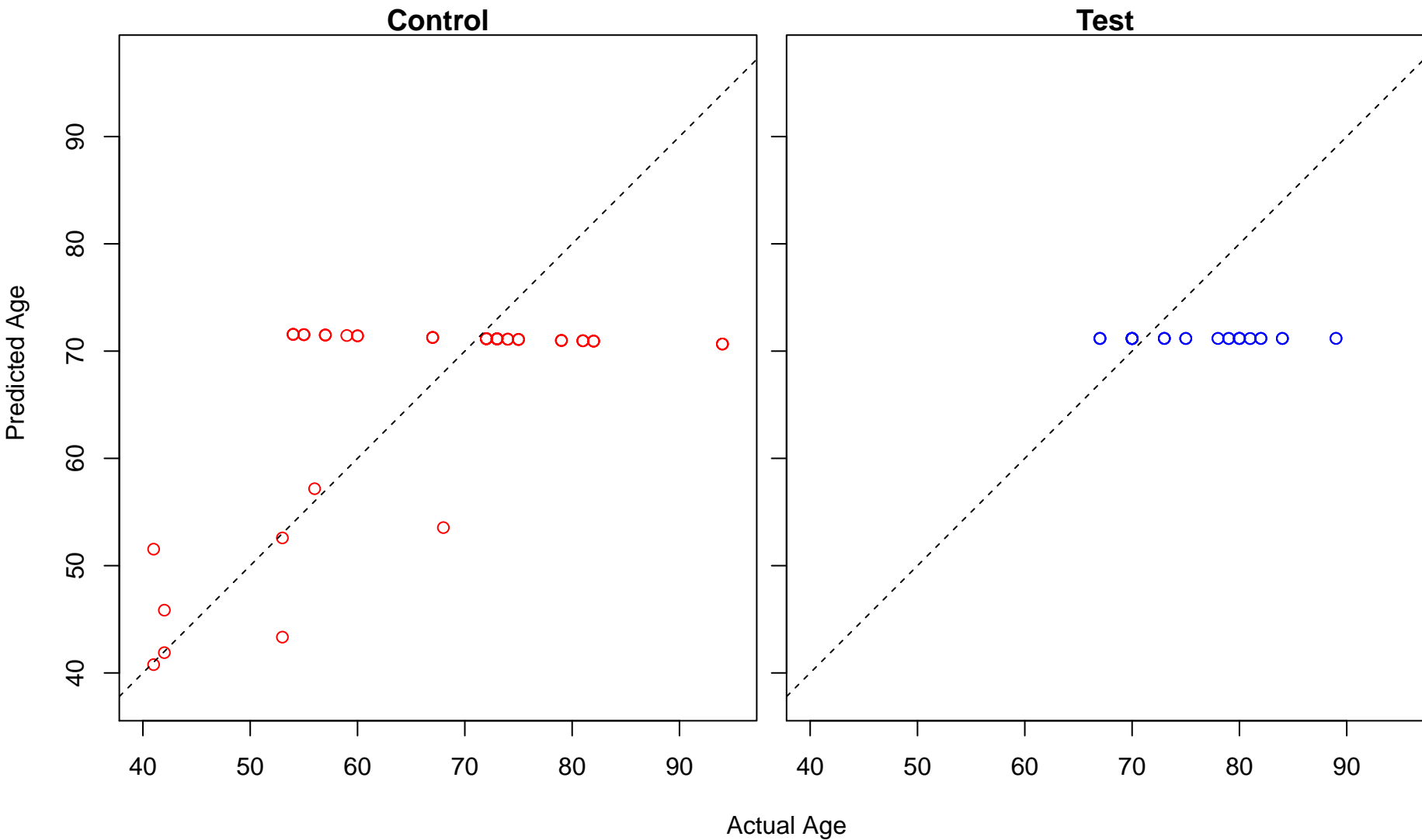


Actual Age

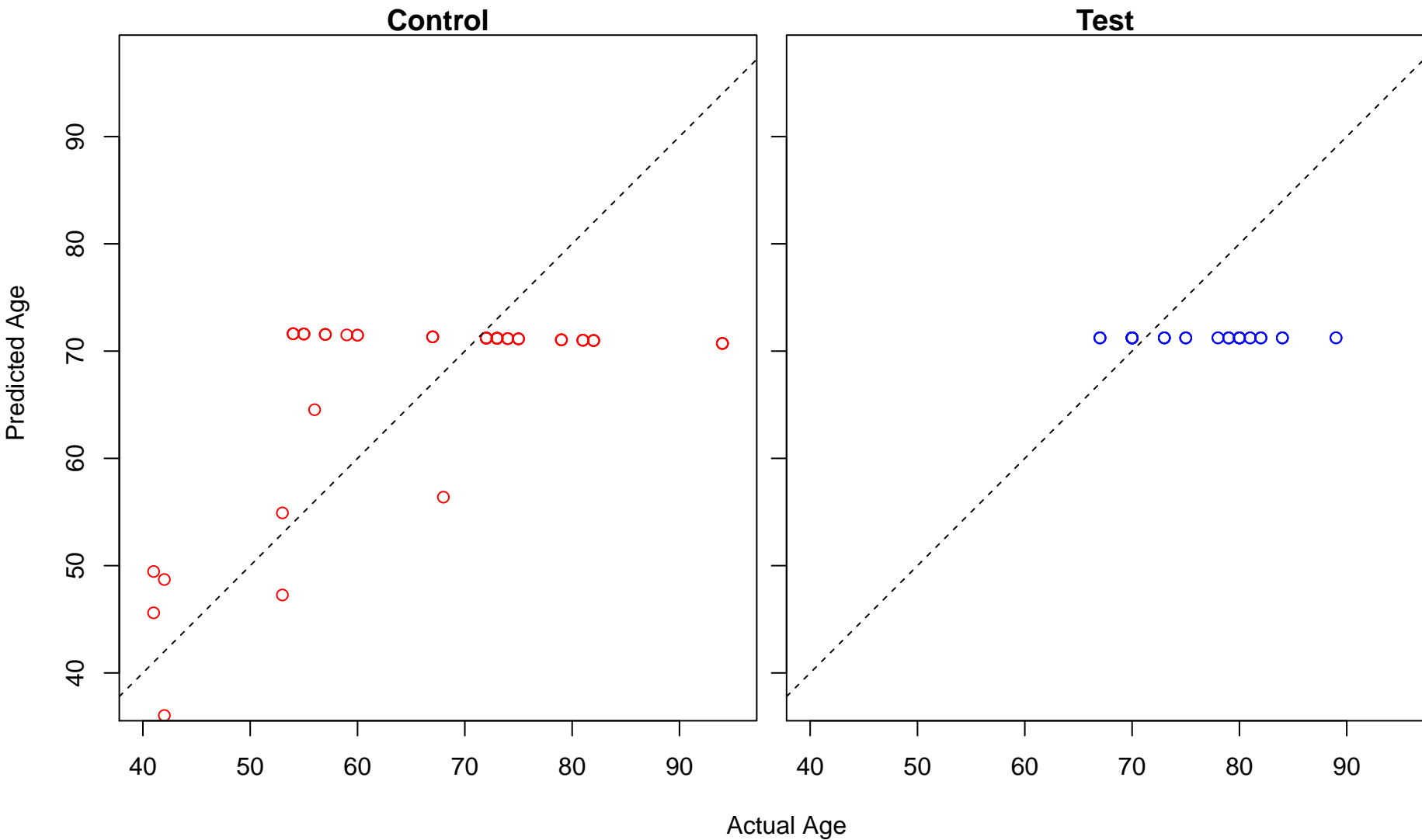
positive regulation of cellular protein catabolic process (Score: 0.826084)



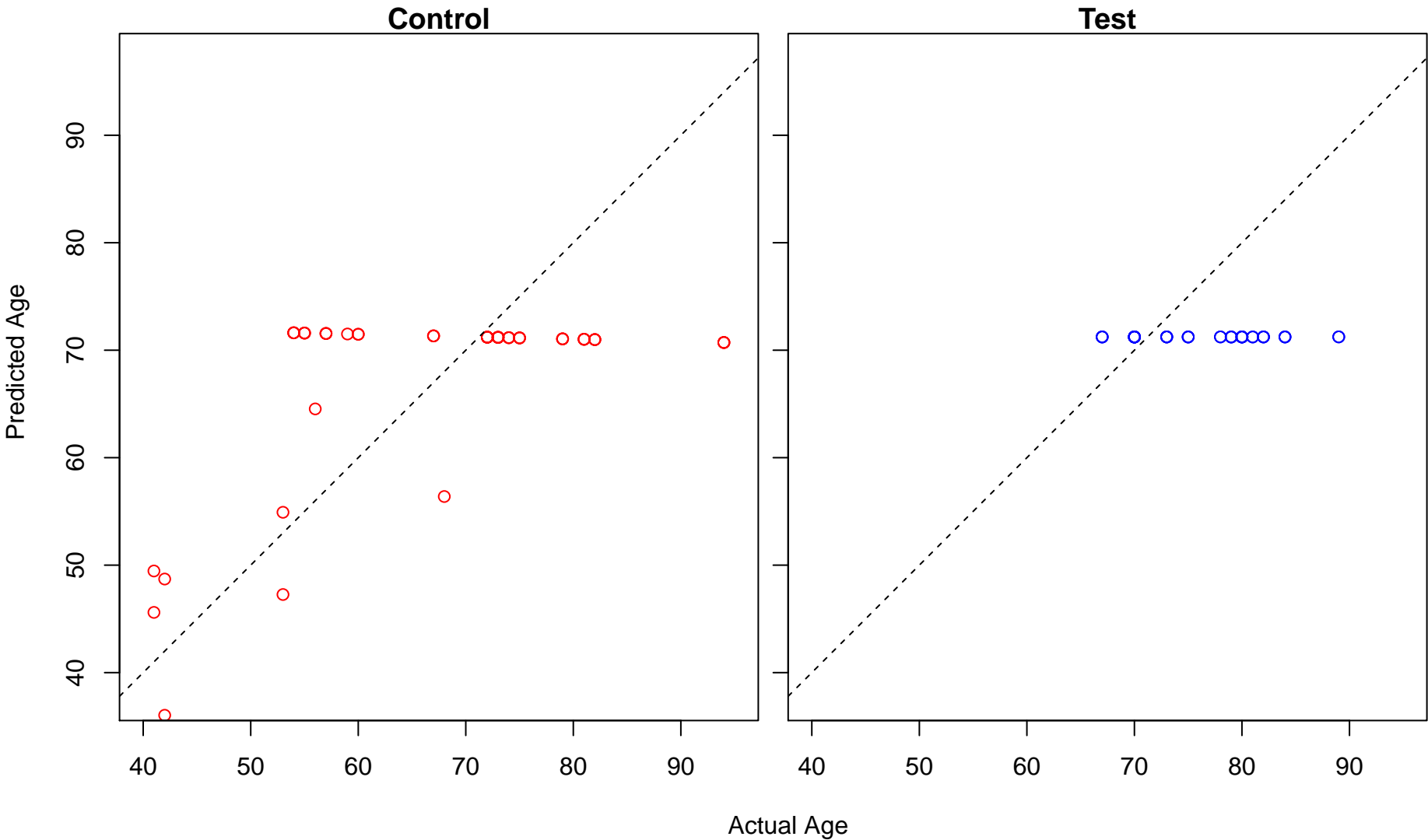
mitotic cell cycle (Score: 0.825981)



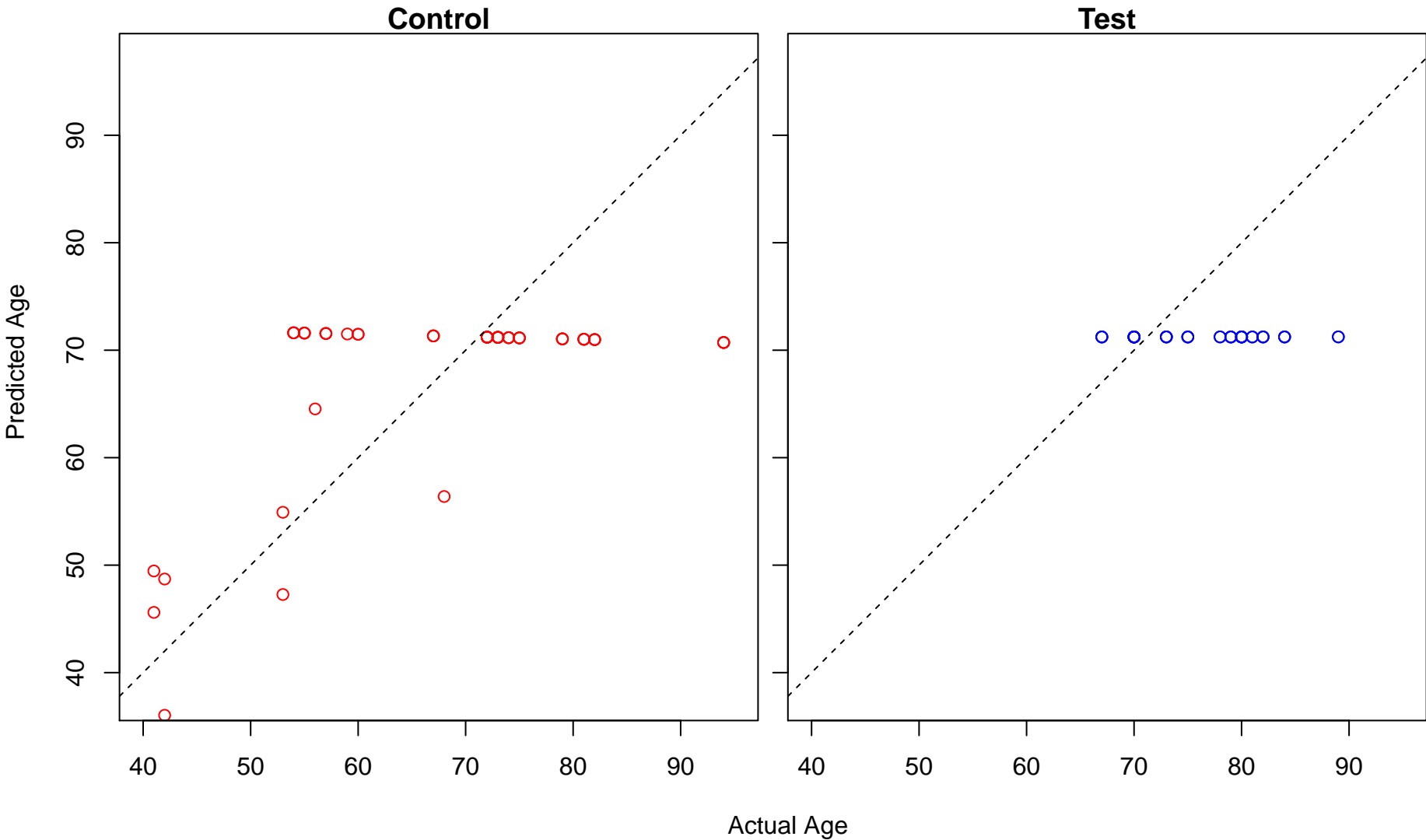
anaphase-promoting complex-dependent catabolic process (Score: 0.825782)



negative regulation of ubiquitin–protein ligase activity involved in mitotic cell cycle (Score: 0.82578)

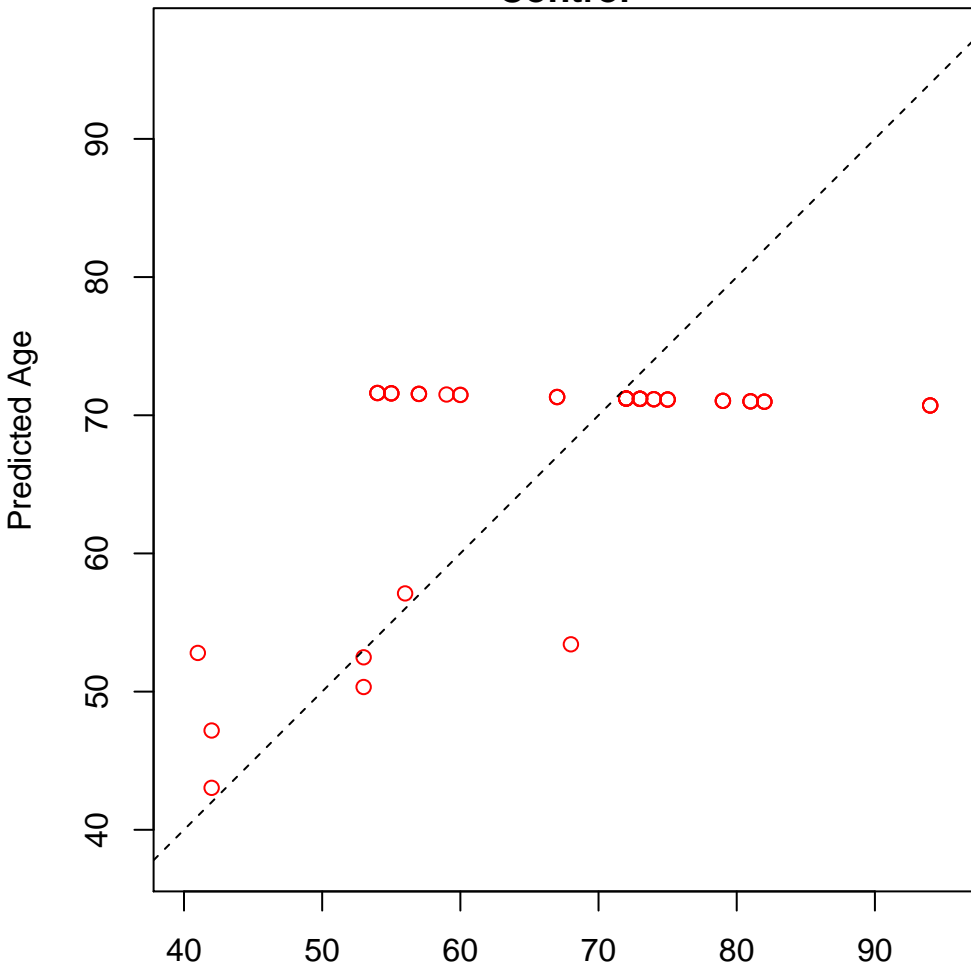


regulation of ubiquitin–protein ligase activity involved in mitotic cell cycle (Score: 0.825782)

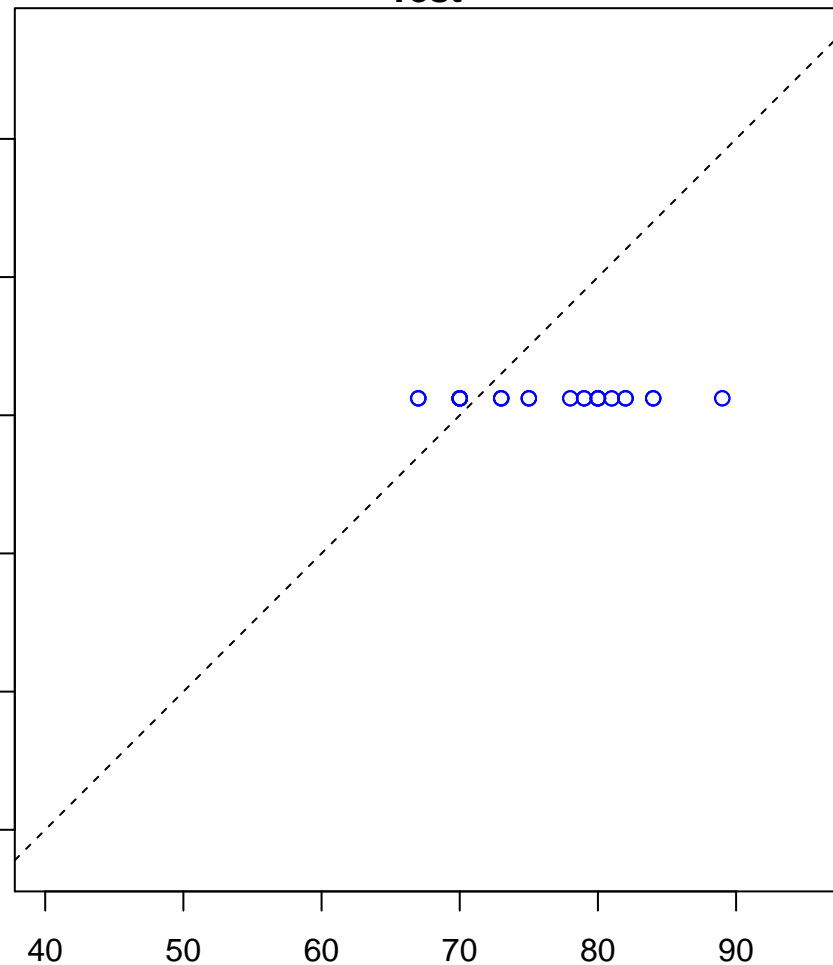


non-canonical Wnt signaling pathway (Score: 0.825768)

Control

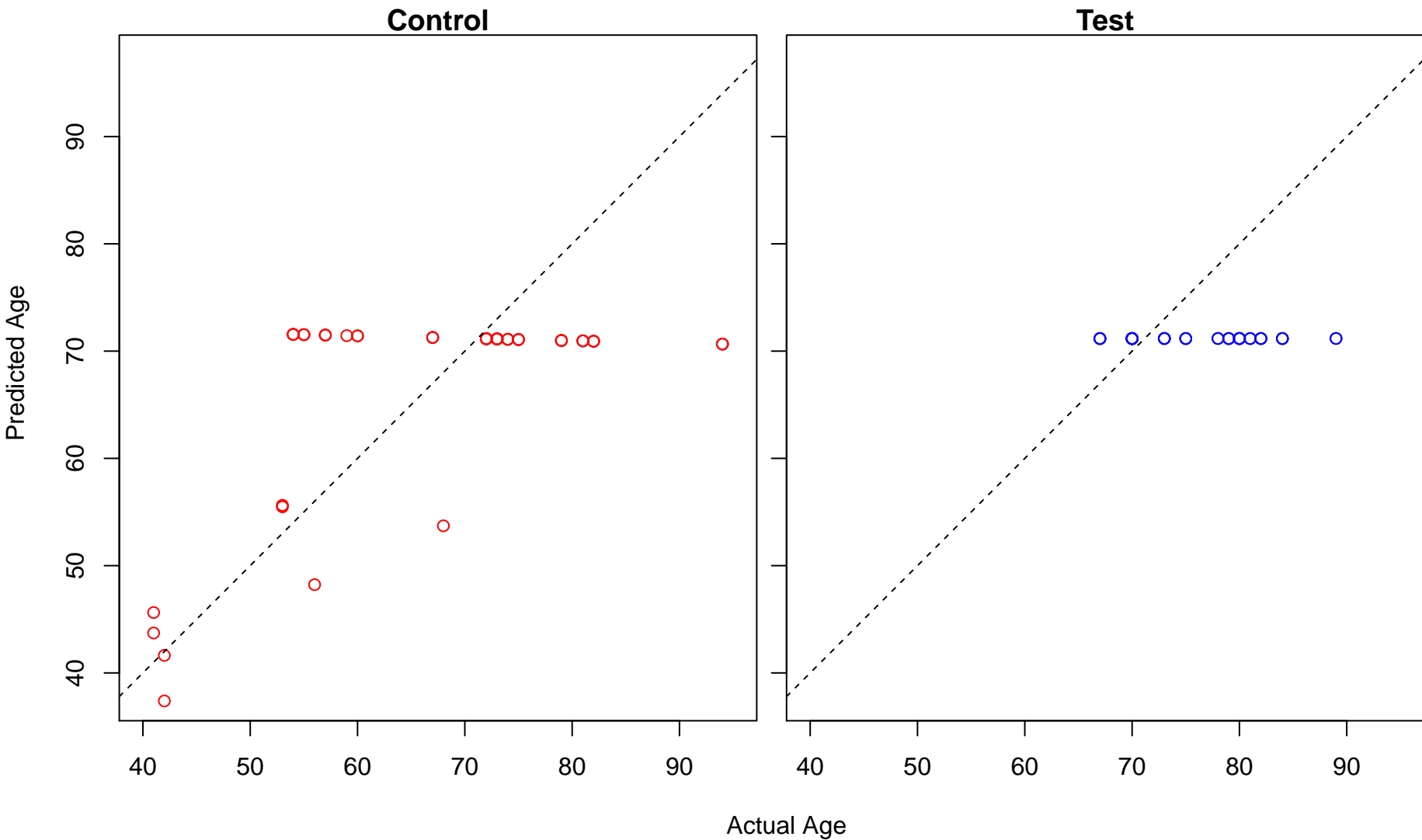


Test

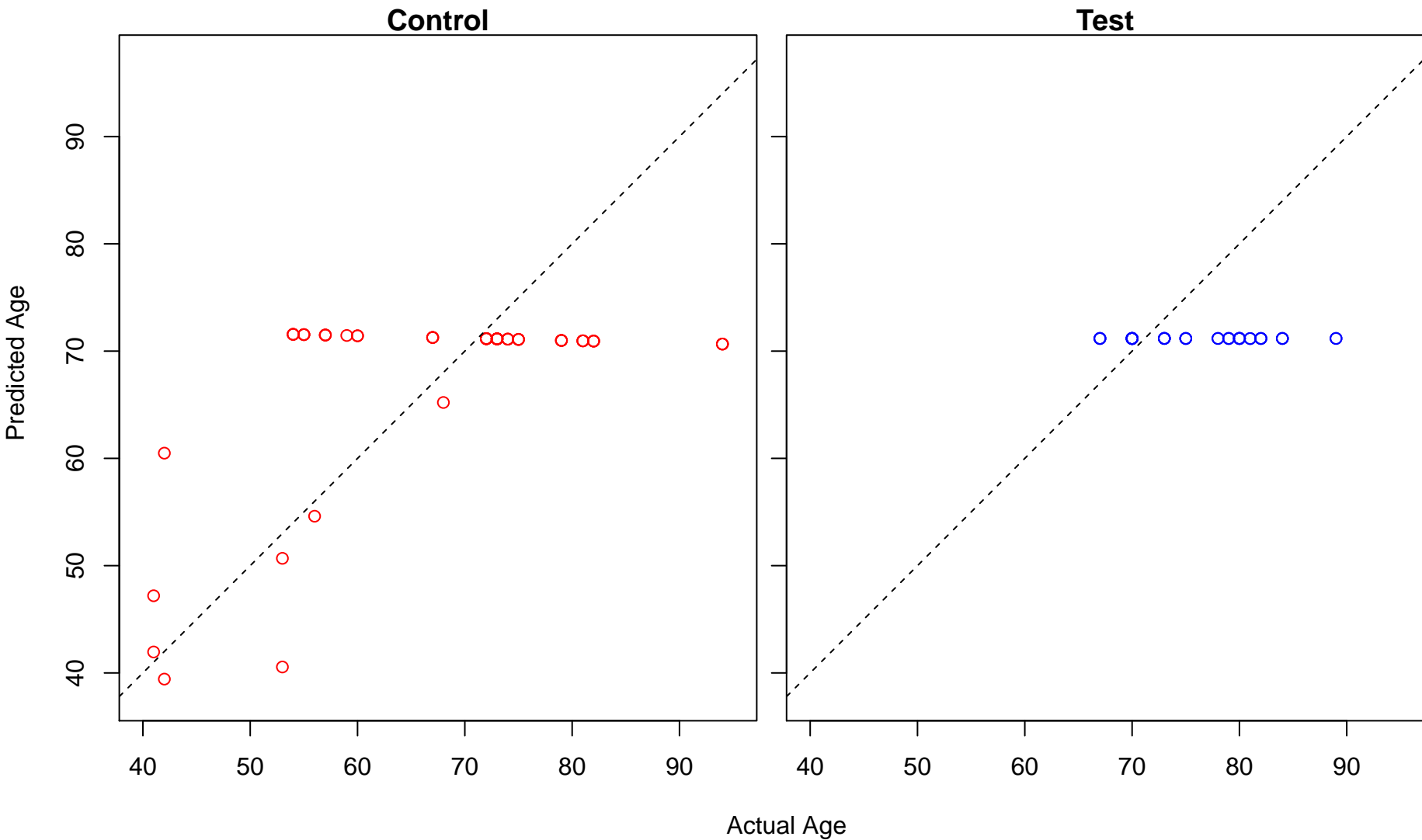


Actual Age

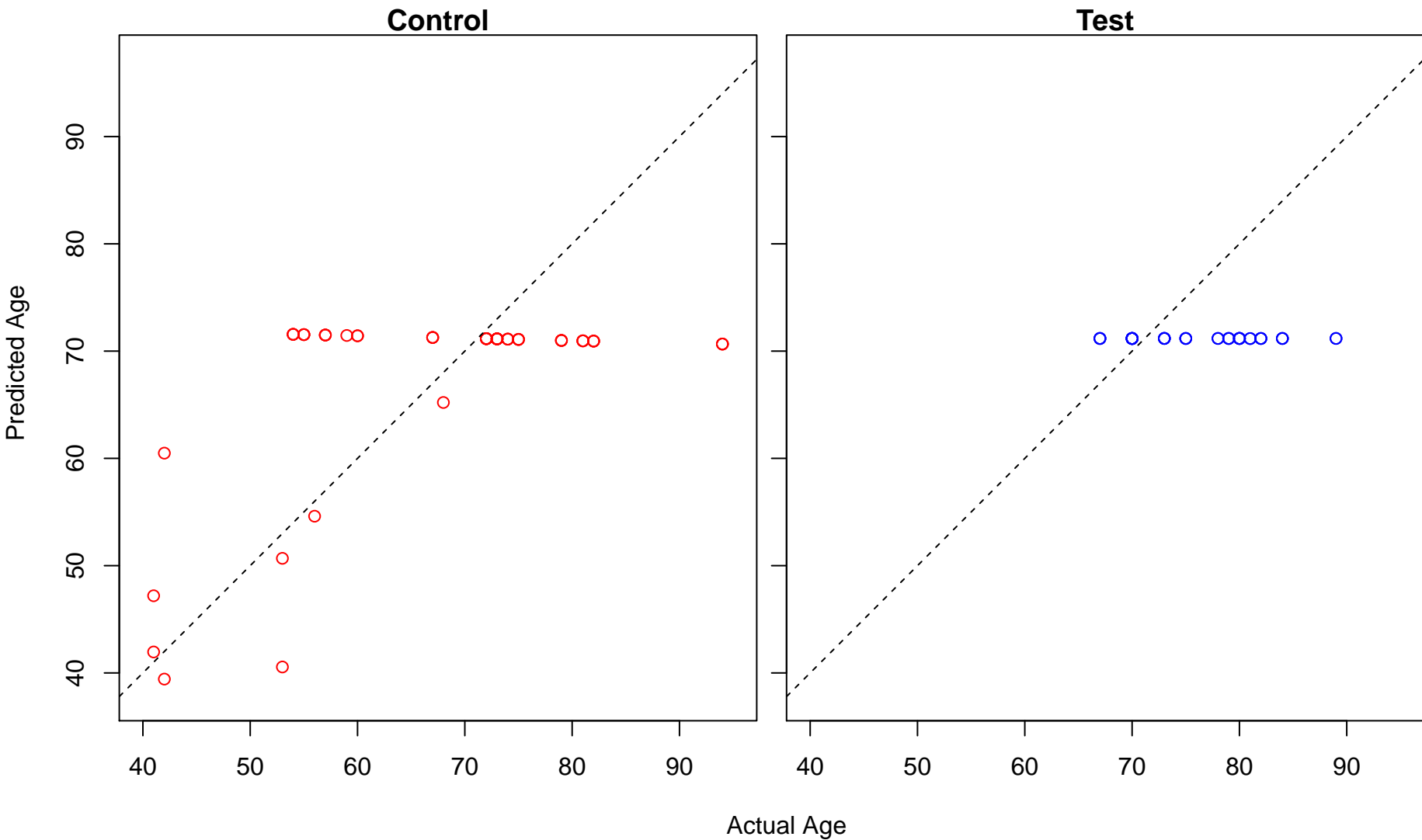
negative regulation of transferase activity (Score: 0.825649)



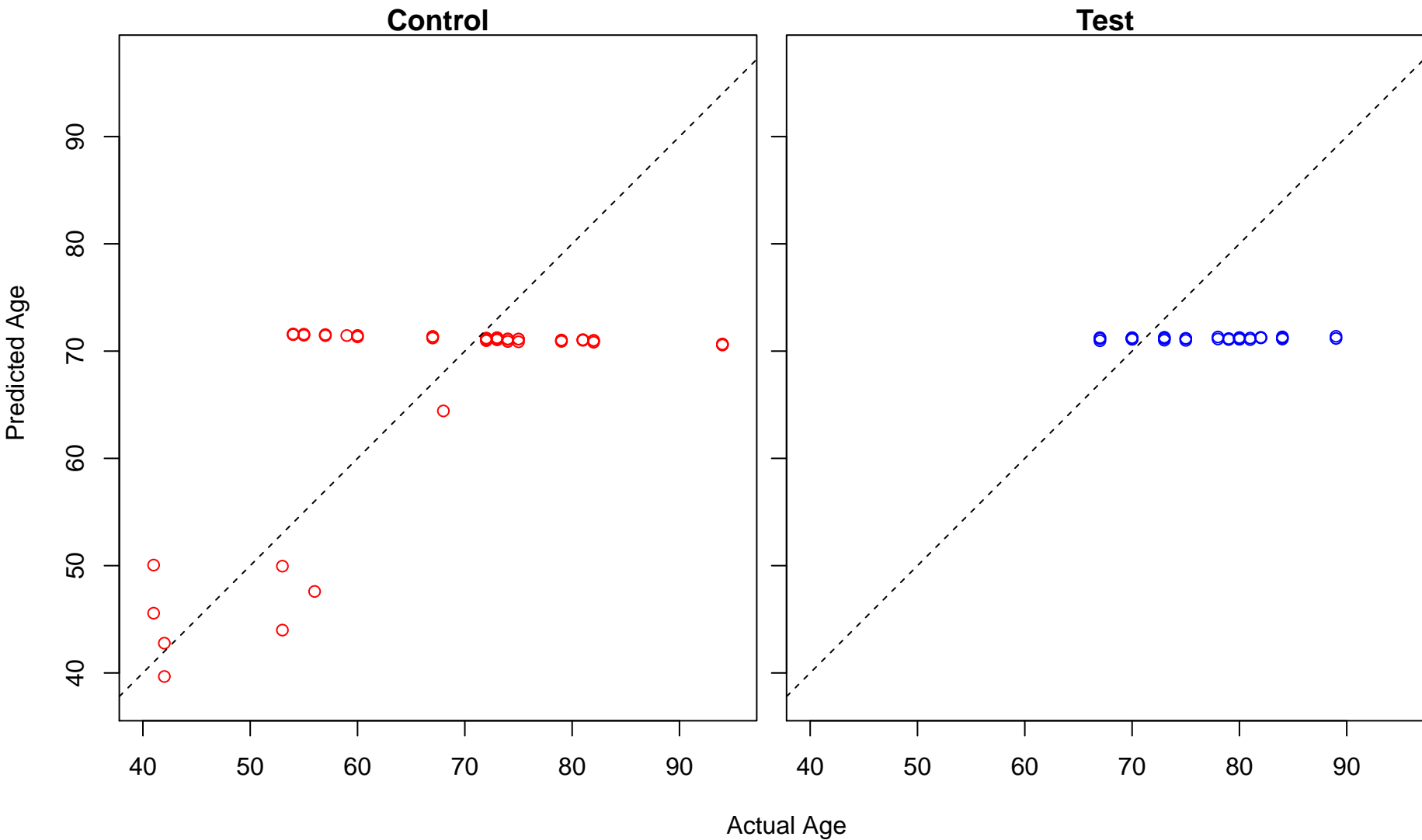
myeloid leukocyte activation (Score: 0.825608)



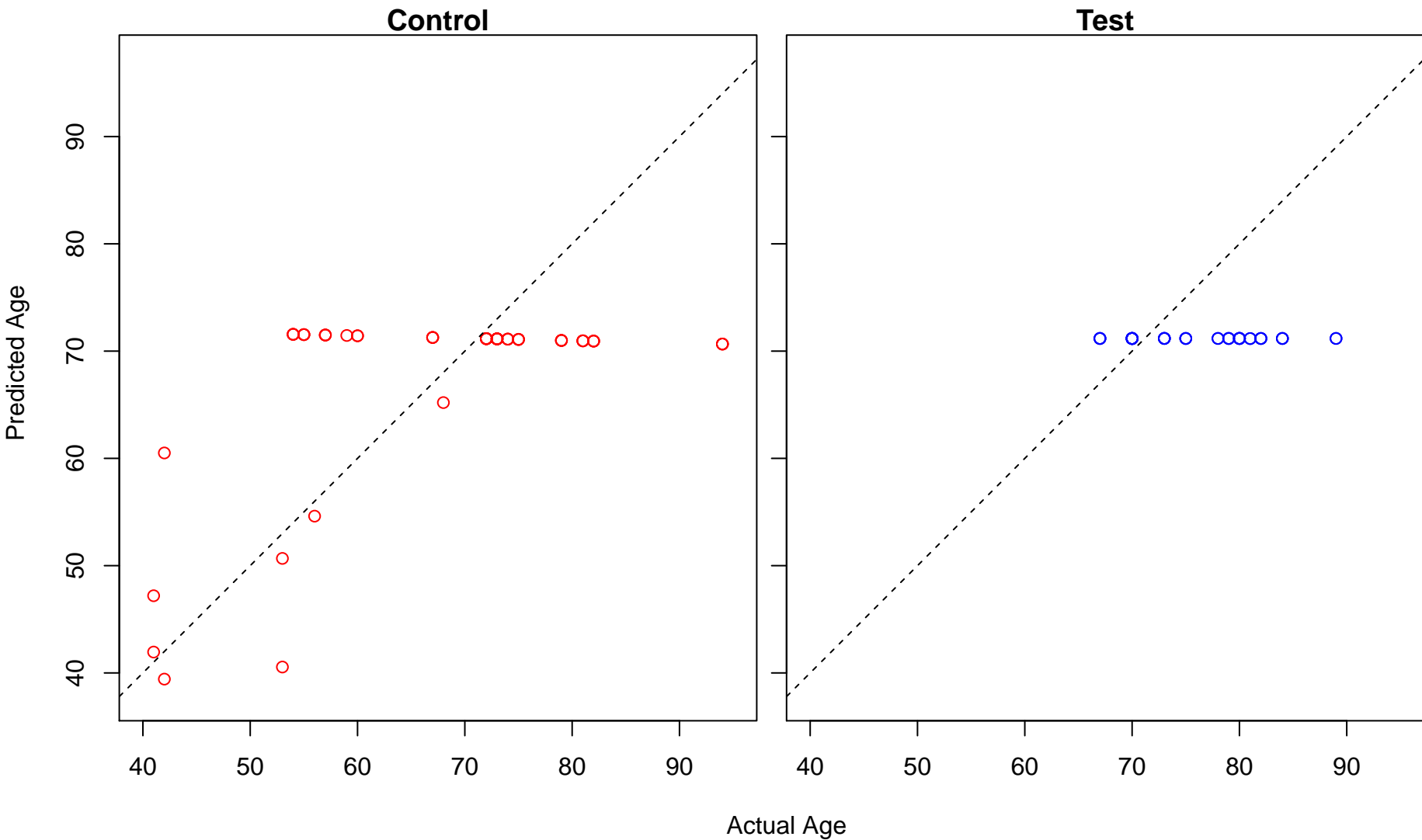
granulocyte activation (Score: 0.825608)



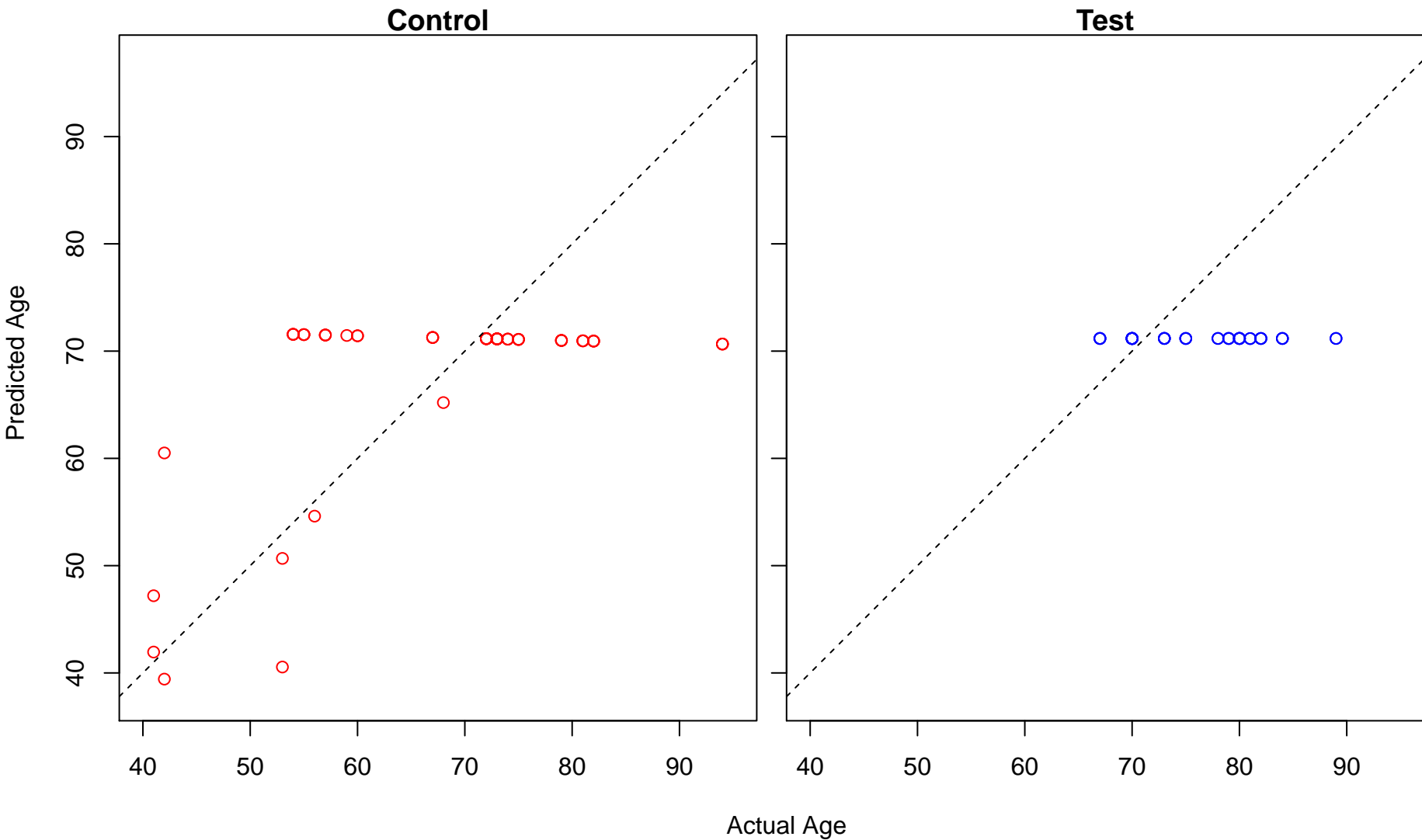
regulation of growth (Score: 0.825606)



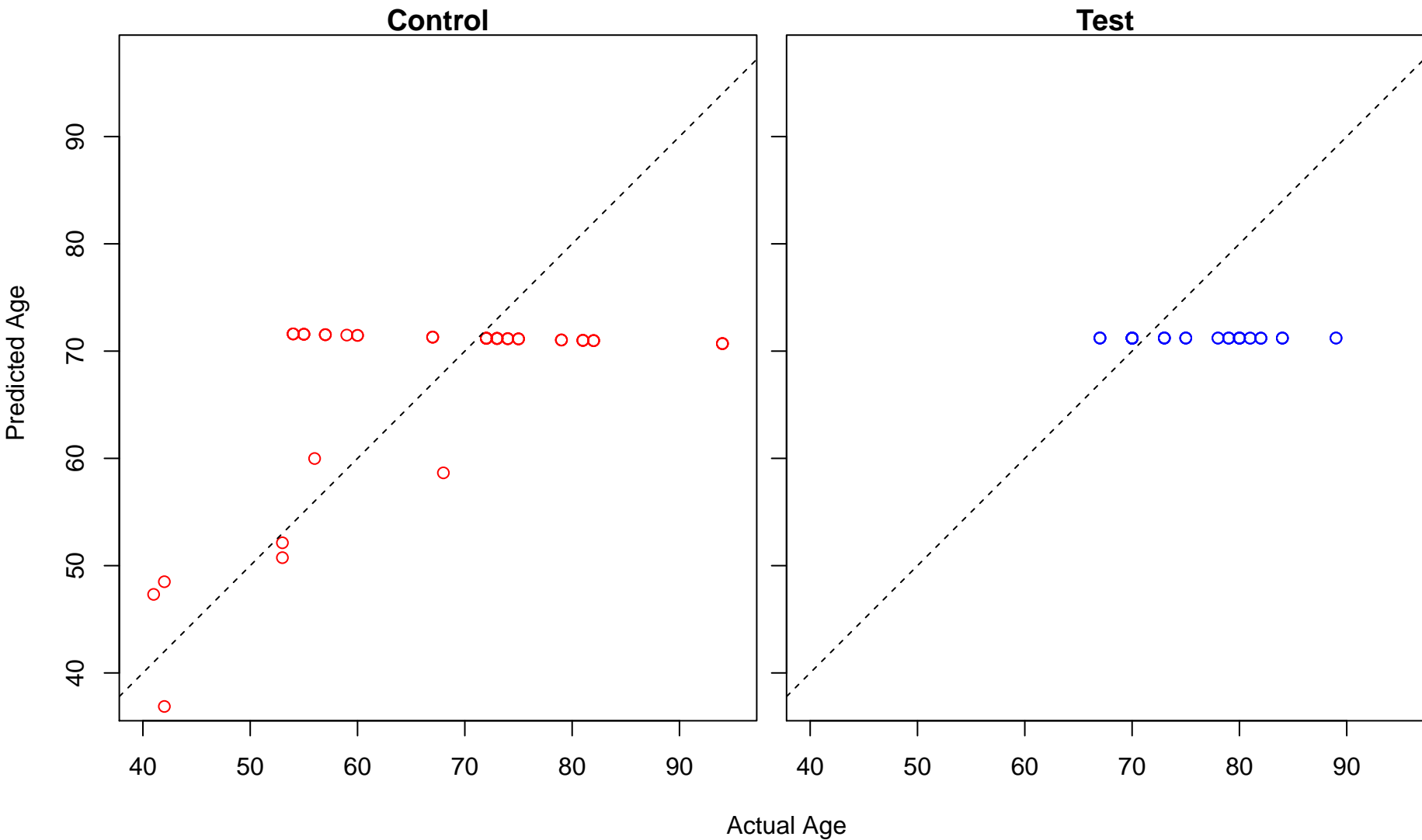
myeloid cell activation involved in immune response (Score: 0.825570)



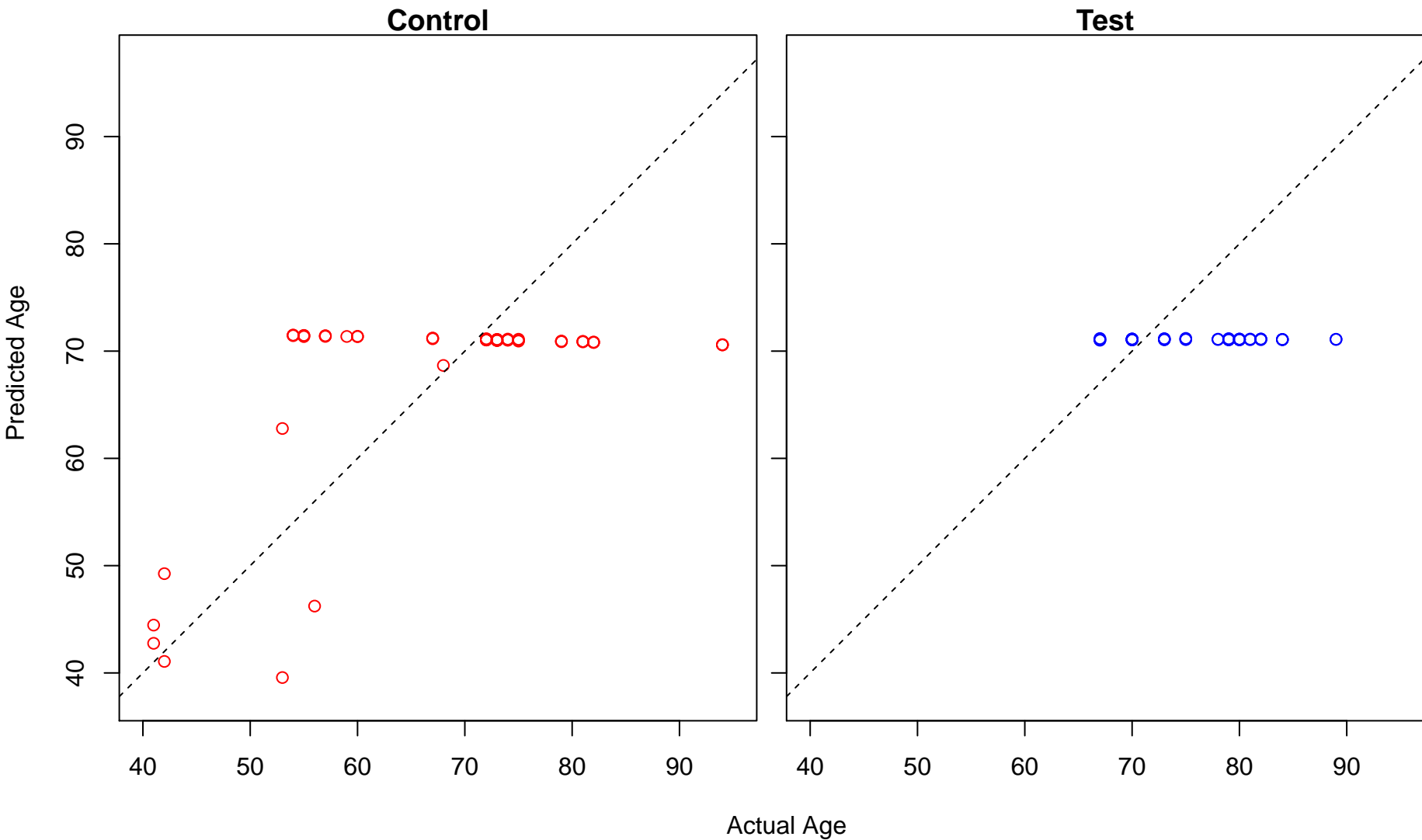
leukocyte activation involved in immune response (Score: 0.825570)



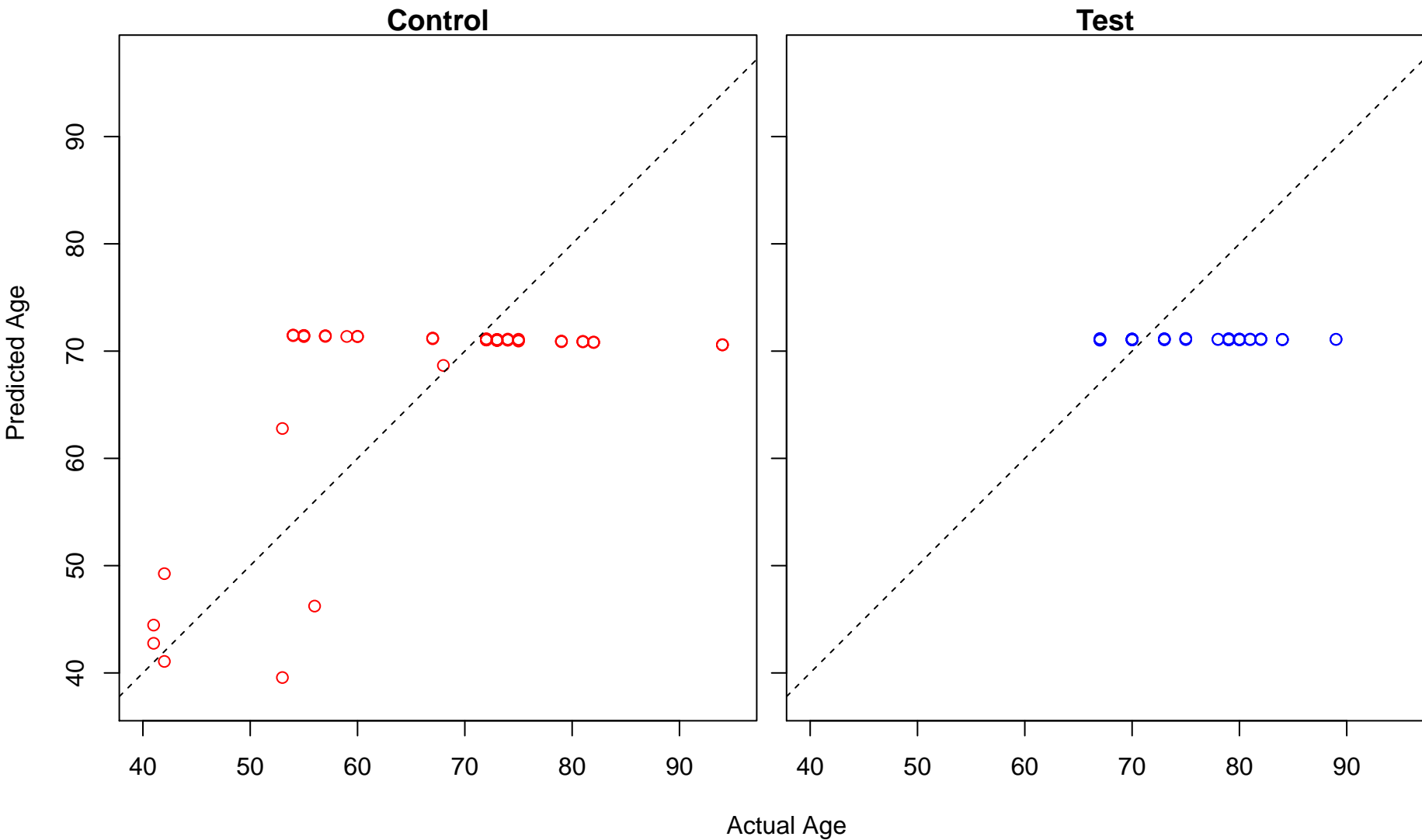
peptidyl-proline modification (Score: 0.825520)



virion attachment to host cell (Score: 0.825426)

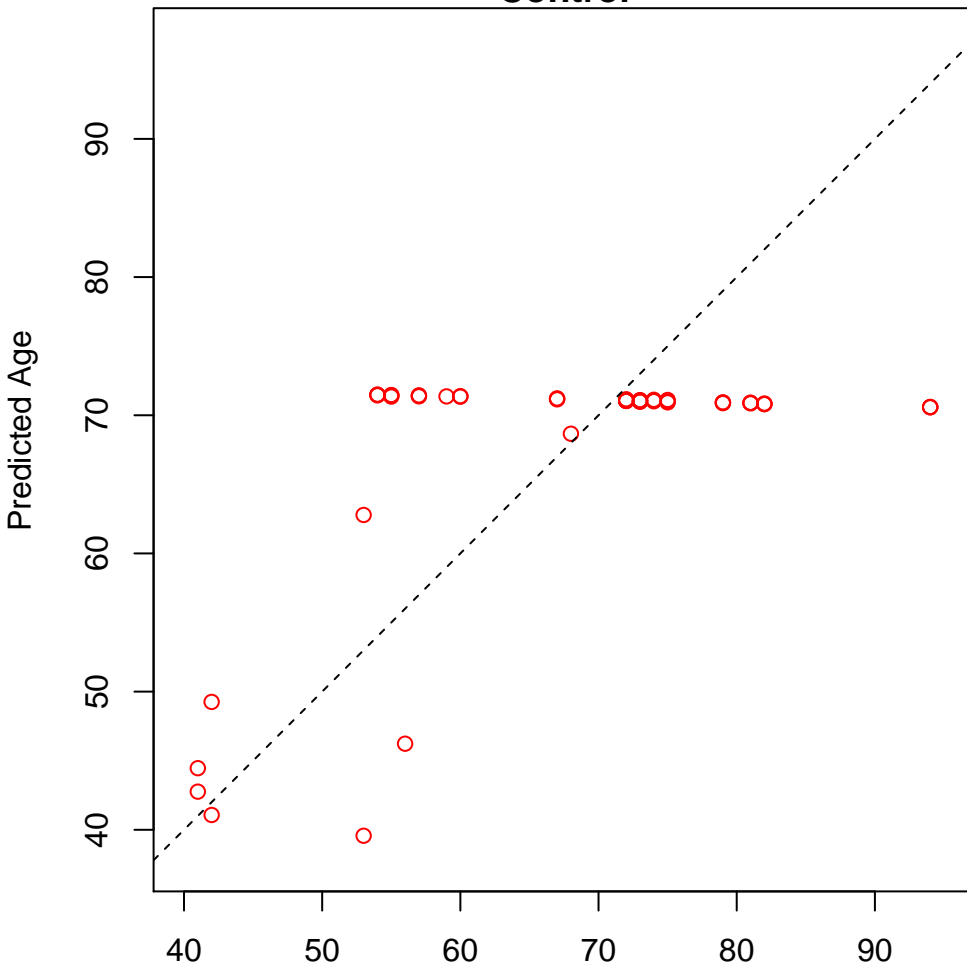


adhesion of symbiont to host (Score: 0.825426)

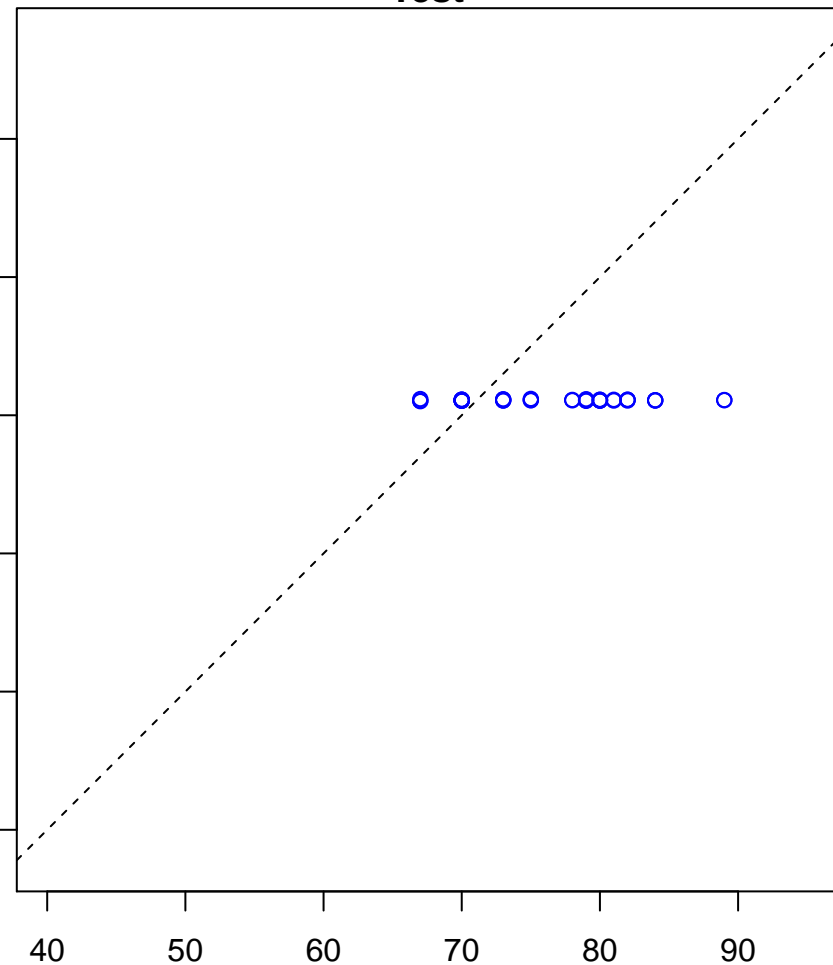


adhesion of symbiont to host cell (Score: 0.825426)

Control

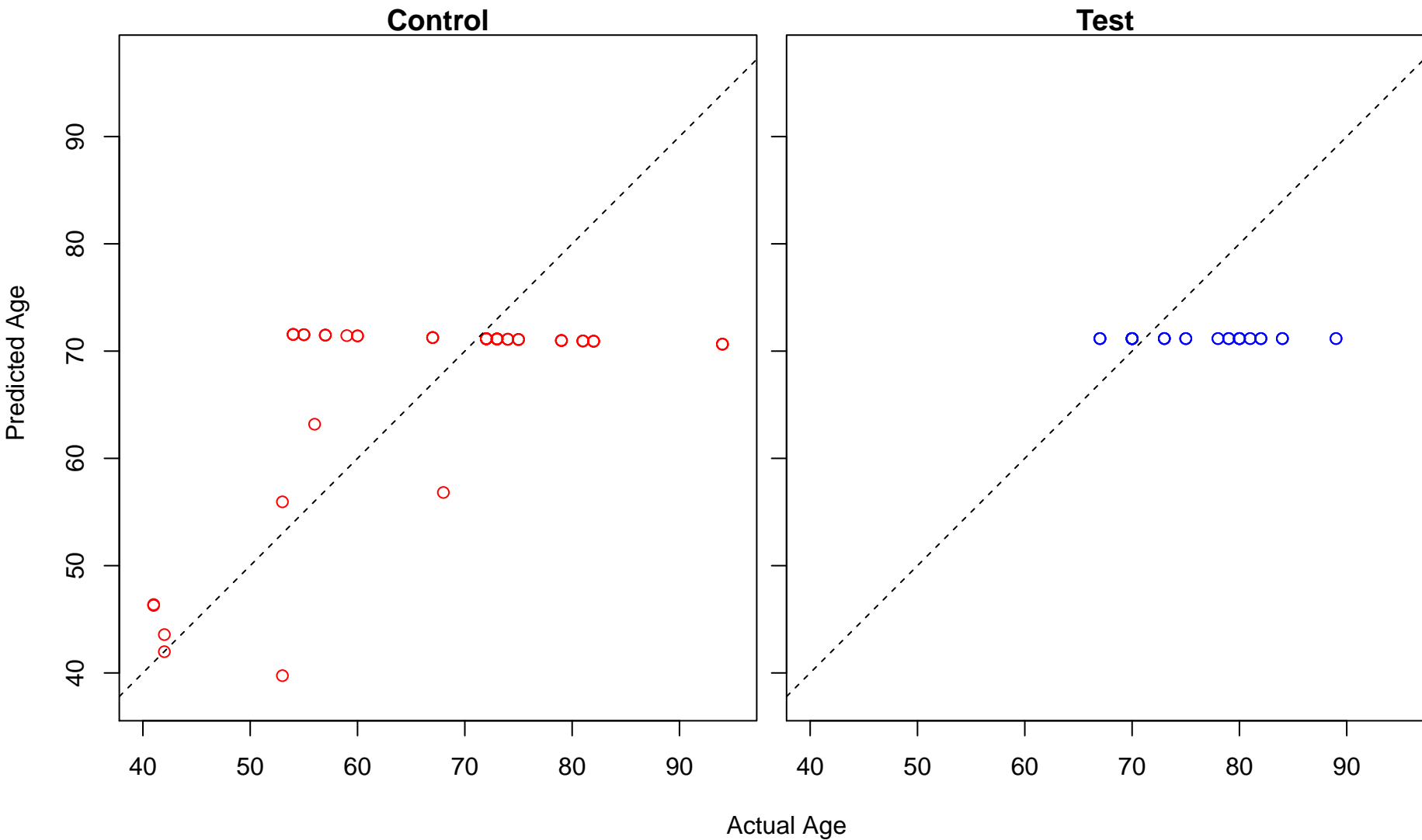


Test

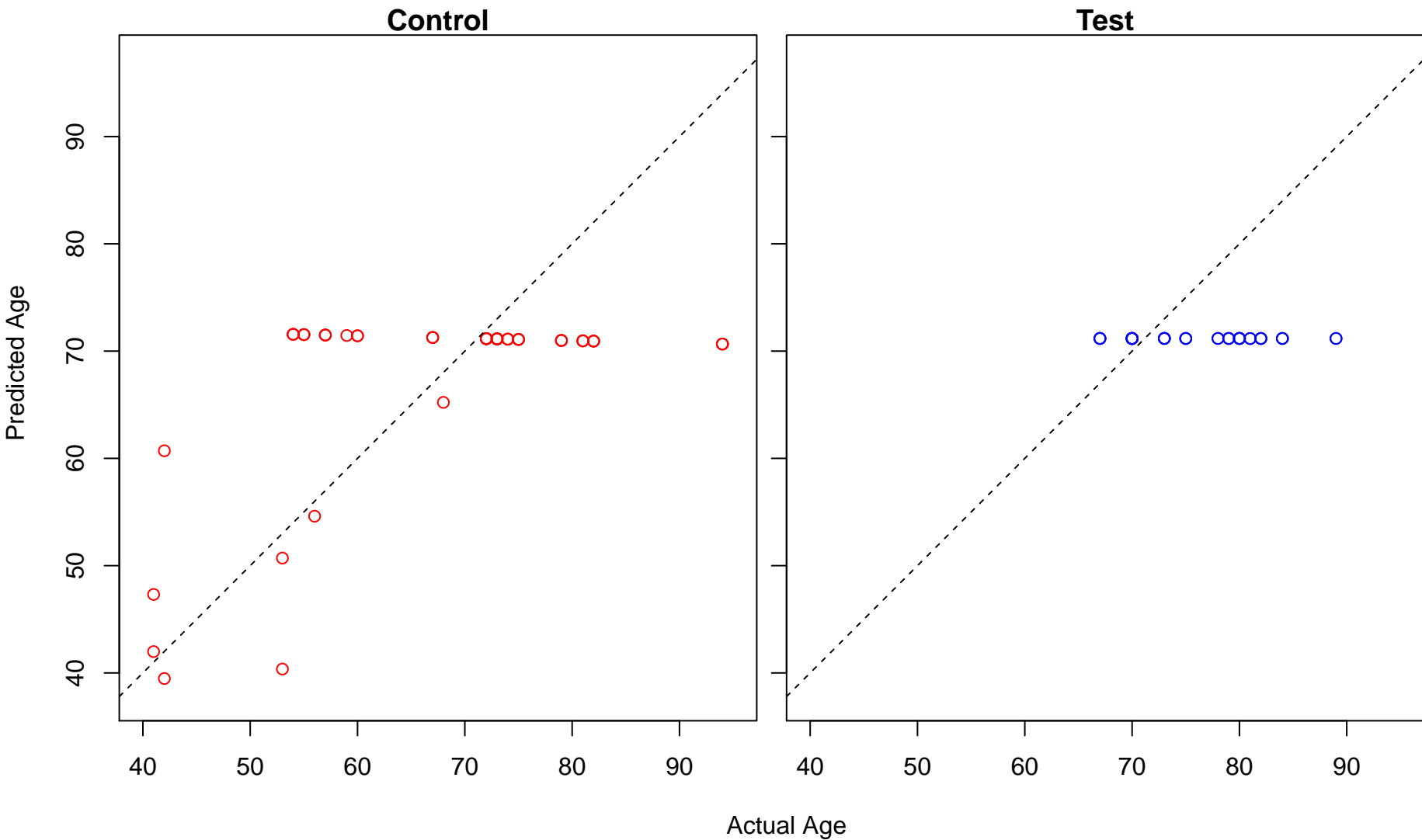


Actual Age

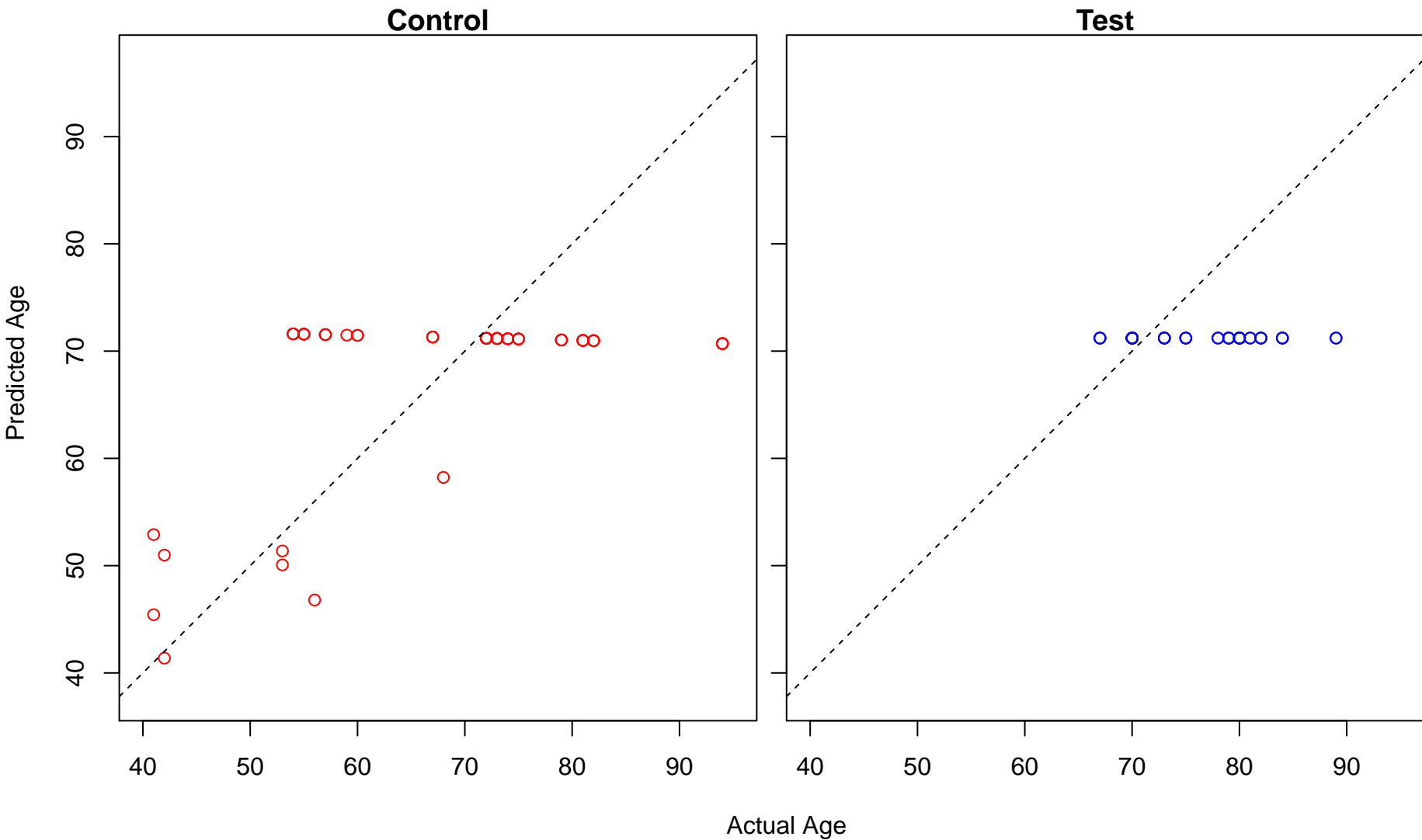
negative regulation of cell death (Score: 0.825377)



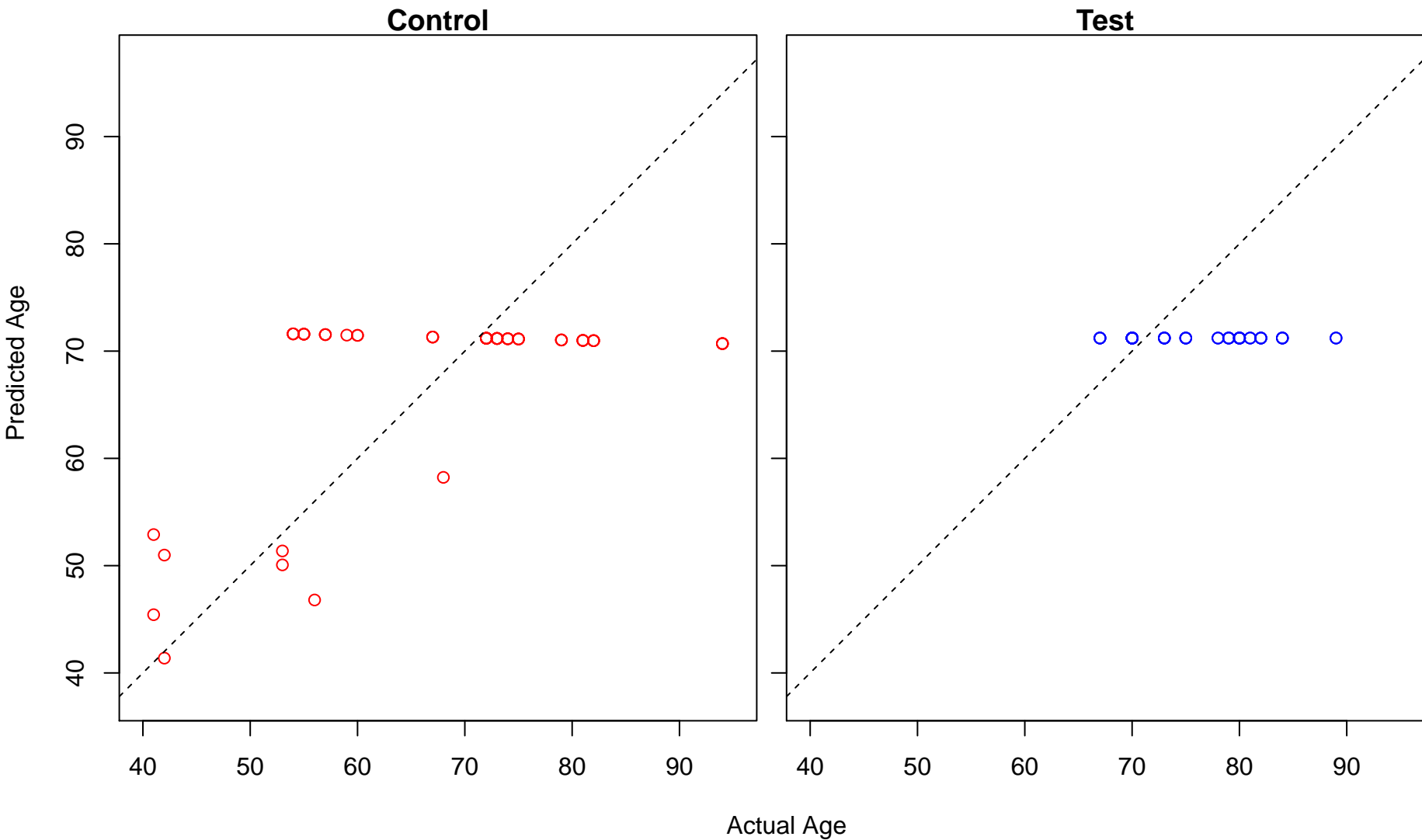
leukocyte activation (Score: 0.825148)



activation of MAPK activity (Score: 0.824964)

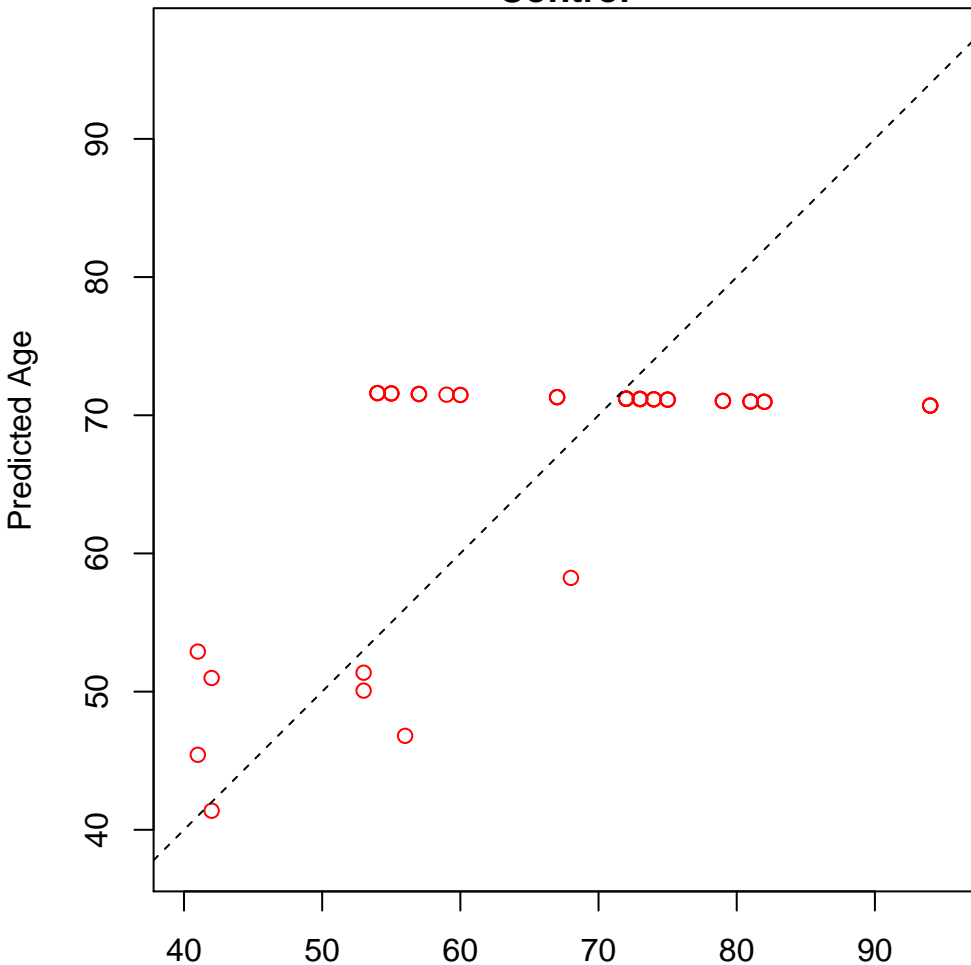


regulation of MAP kinase activity (Score: 0.824964)

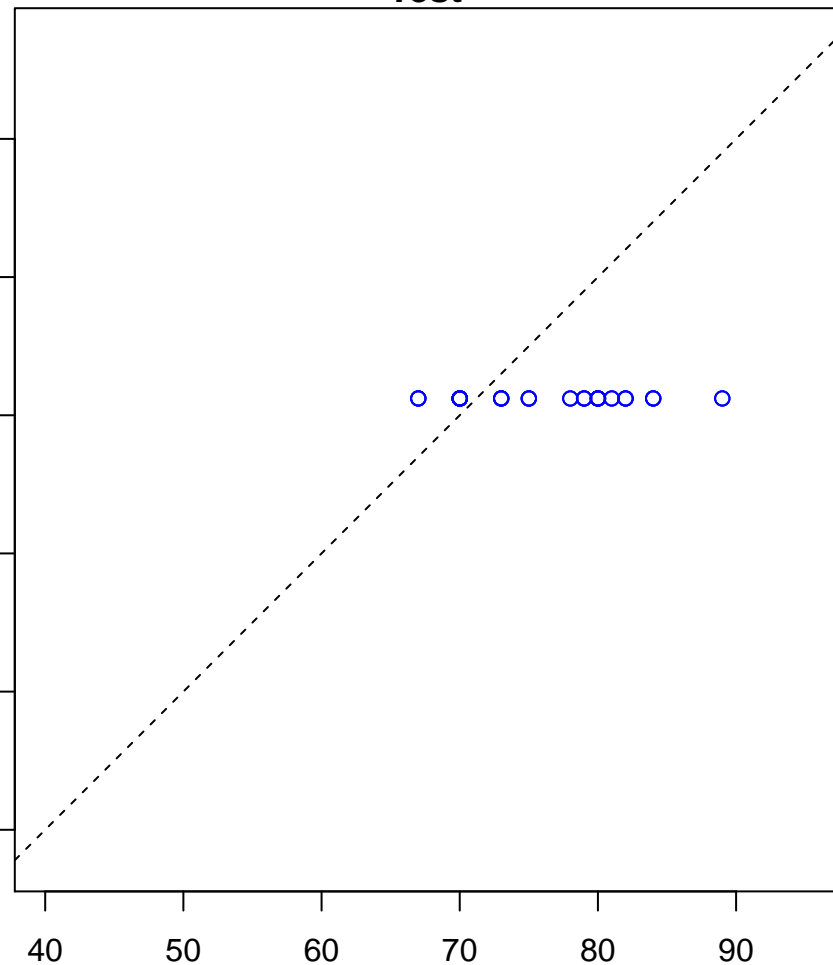


positive regulation of MAP kinase activity (Score: 0.824964)

Control

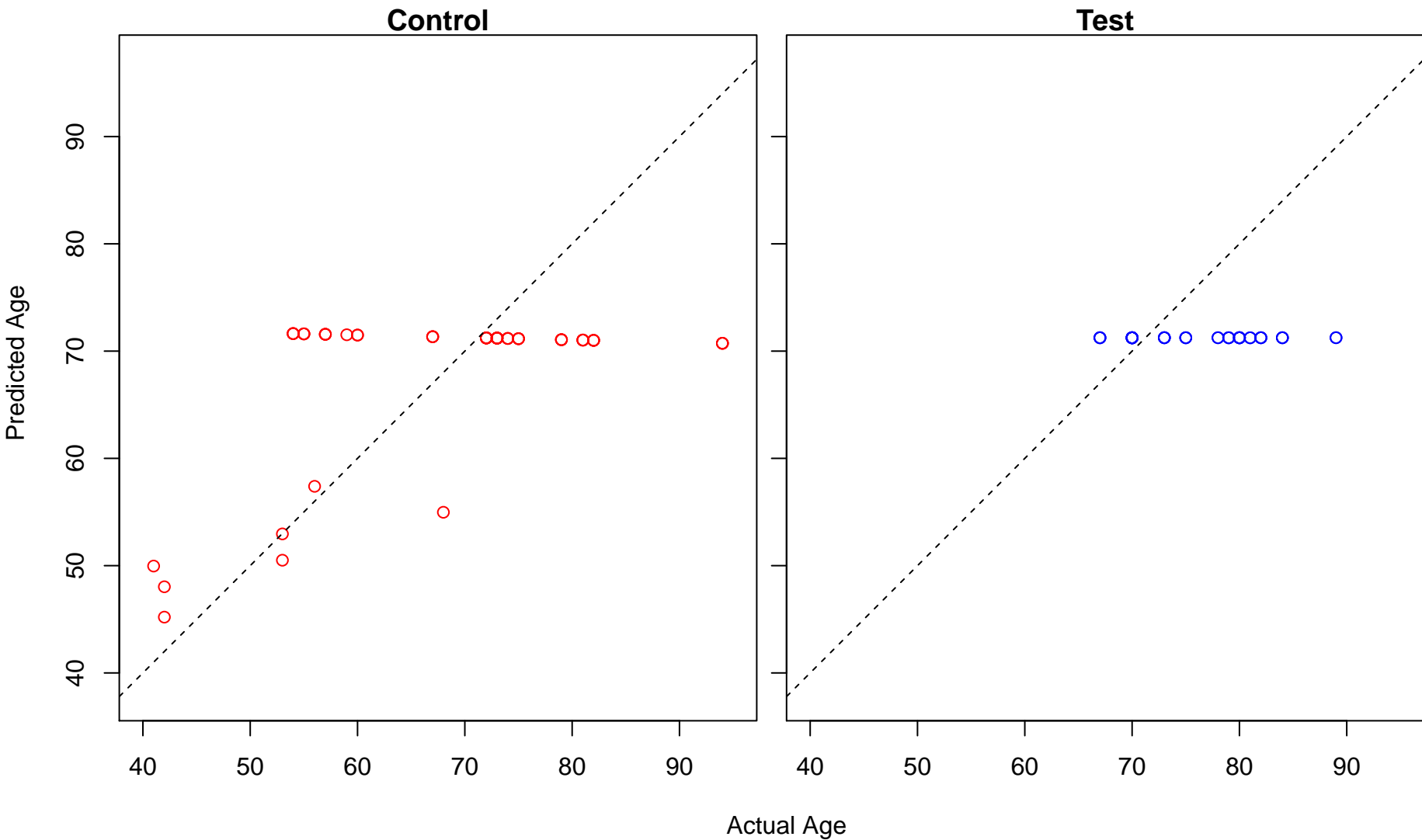


Test



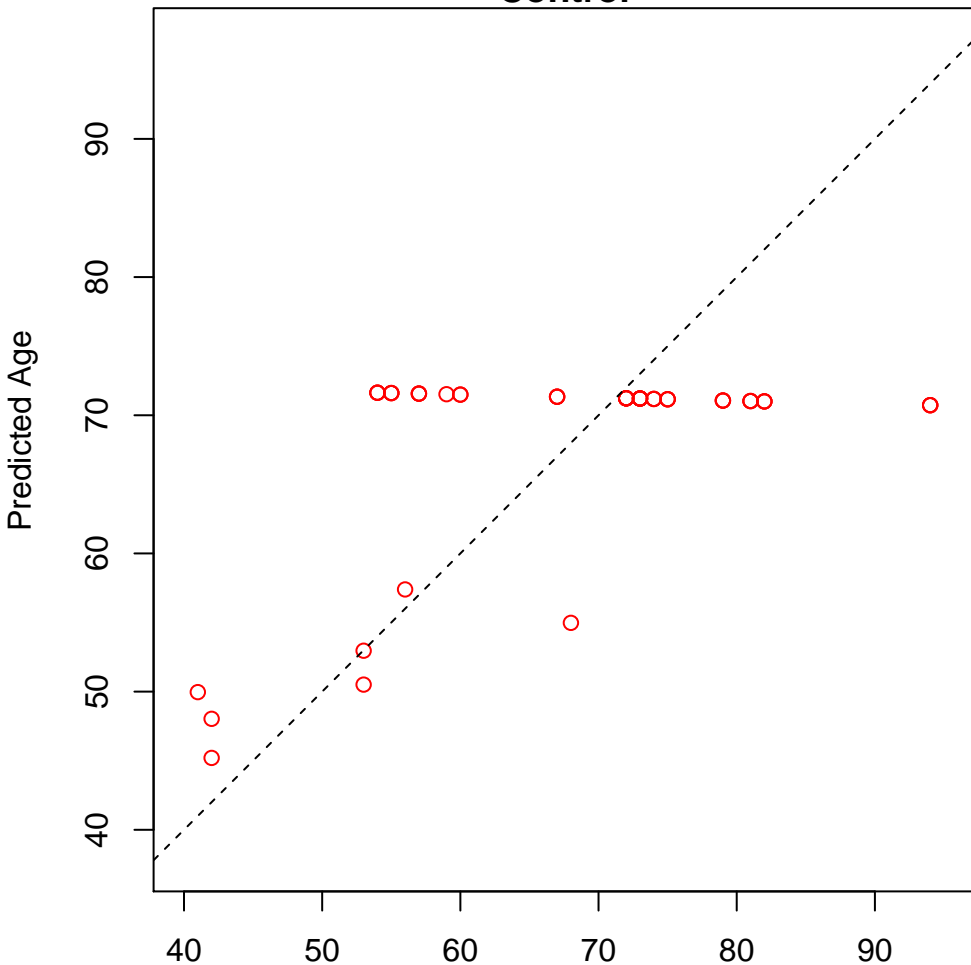
Actual Age

protein catabolic process (Score: 0.824946)

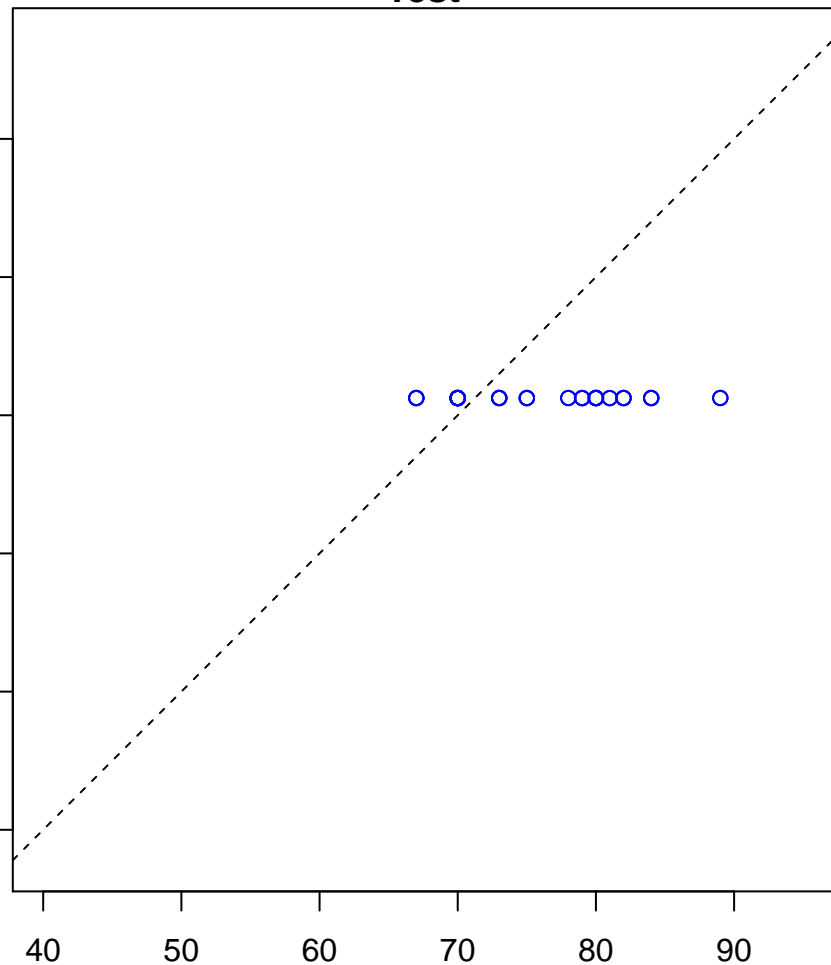


cellular protein catabolic process (Score: 0.824946)

Control

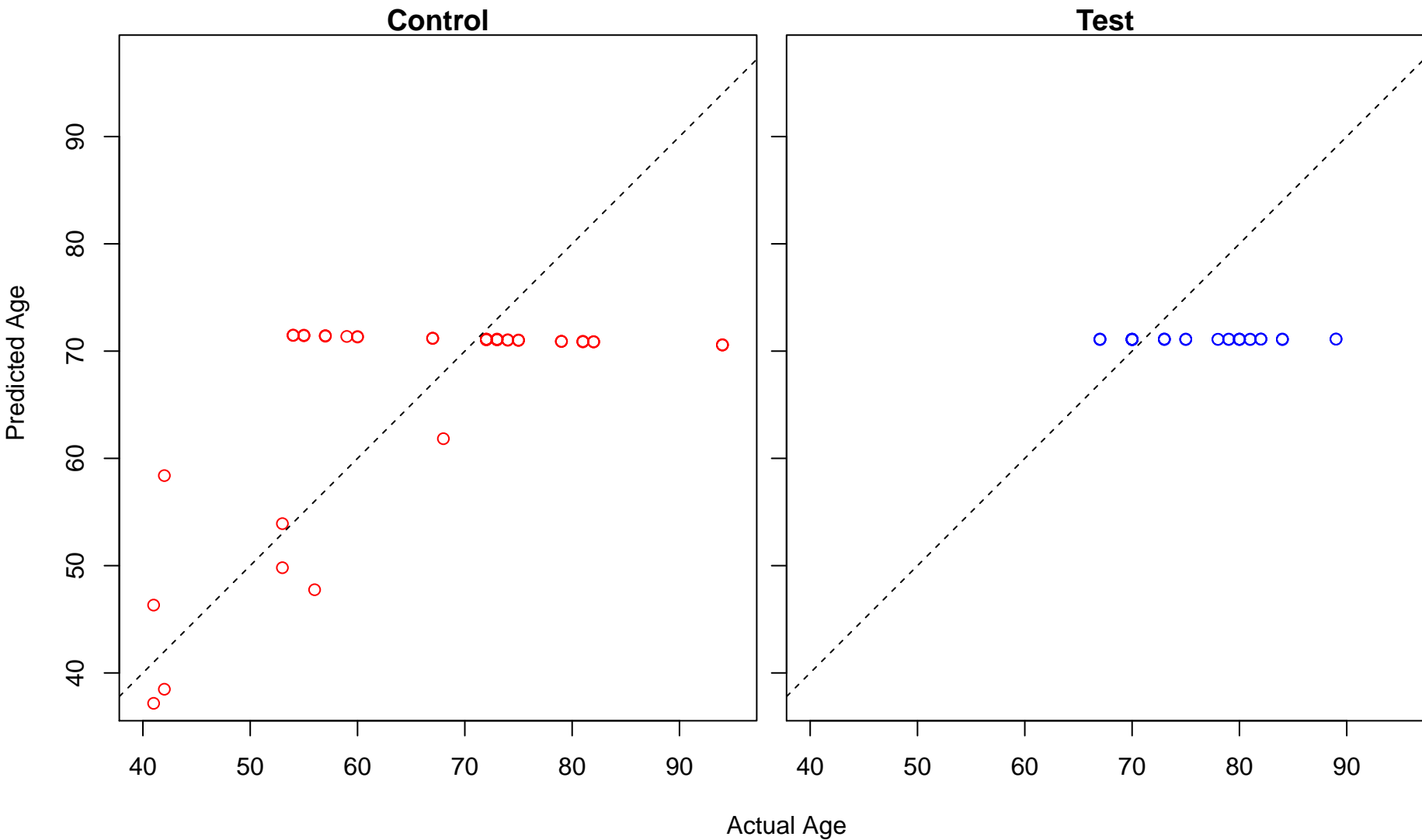


Test

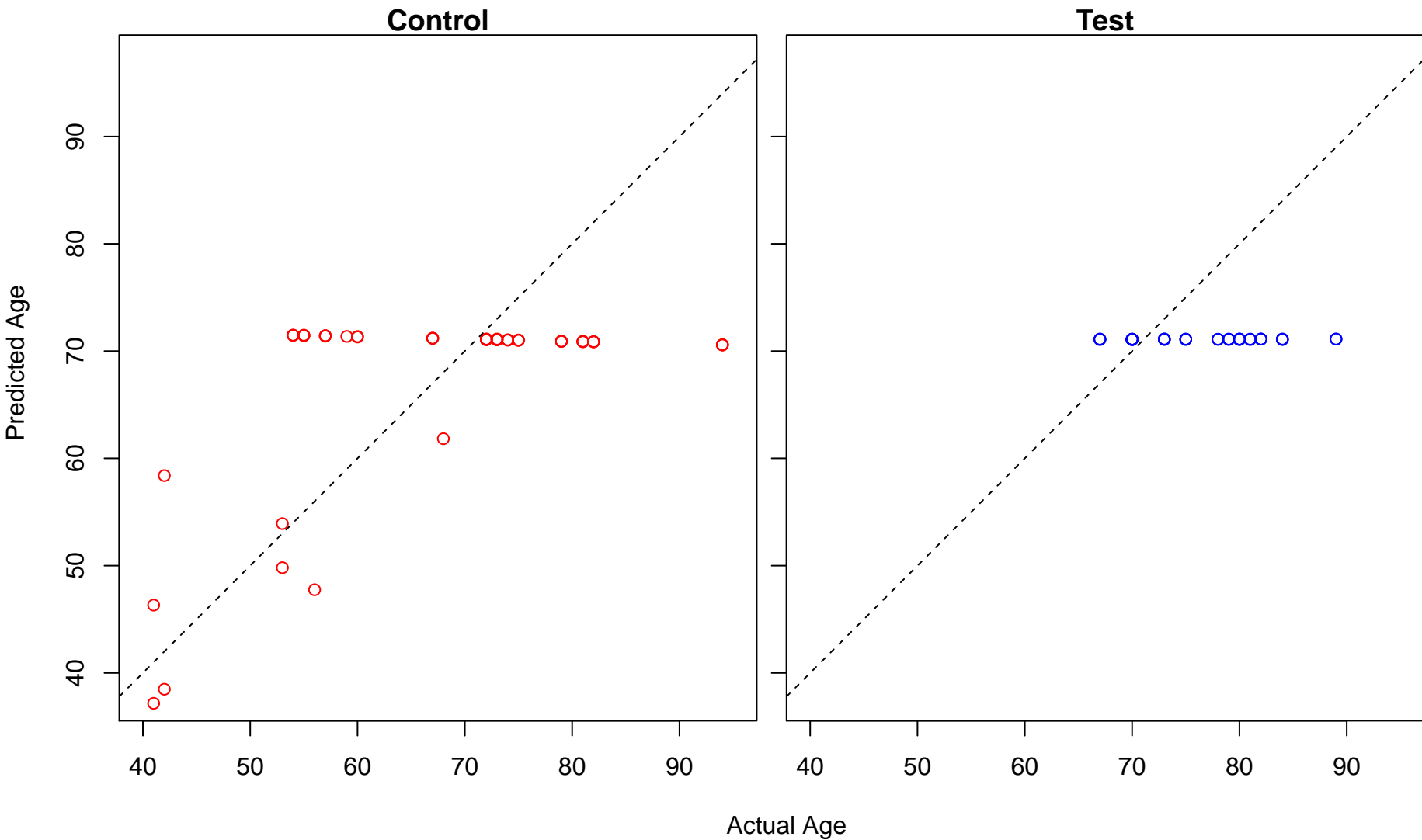


Actual Age

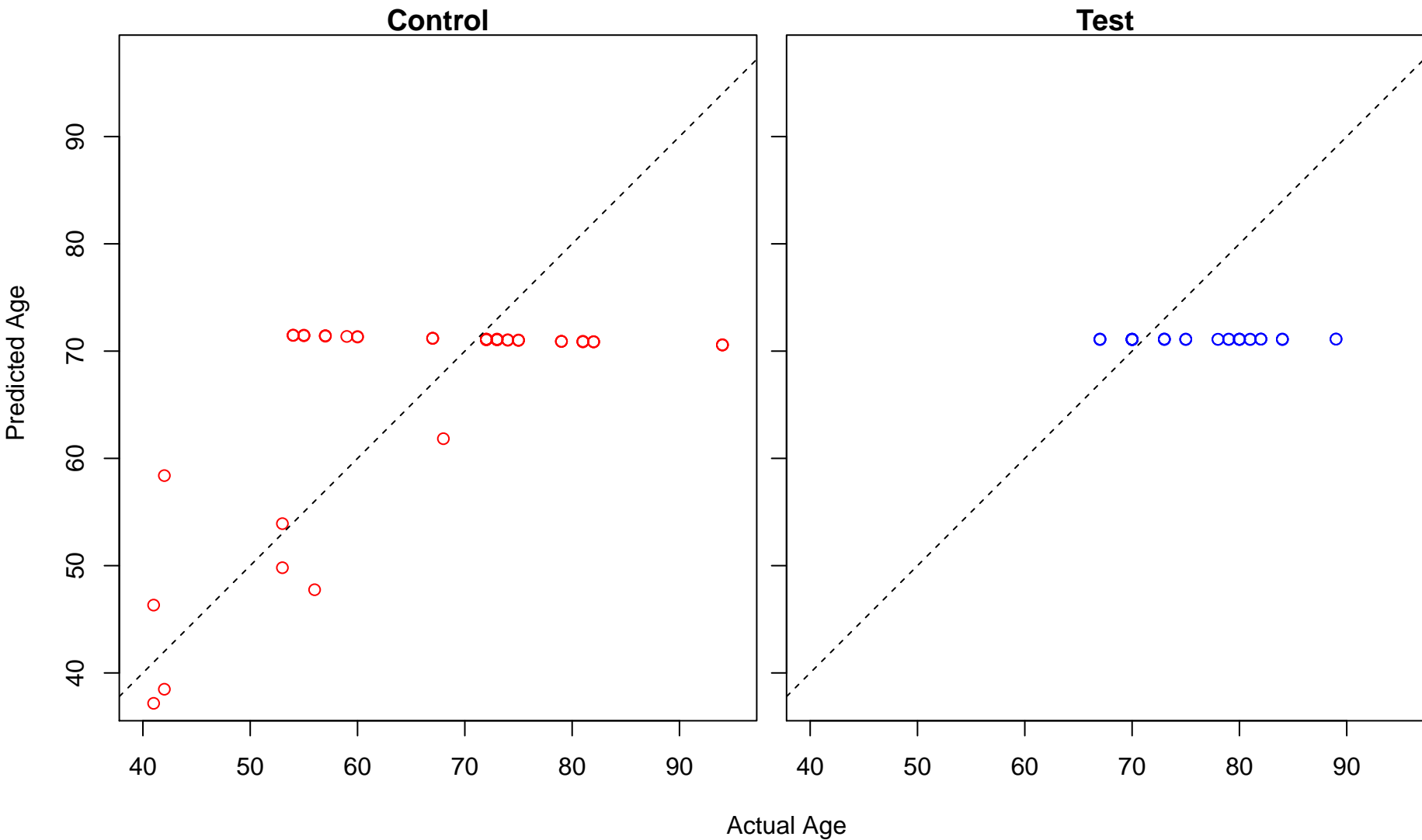
response to corticosteroid (Score: 0.824794)



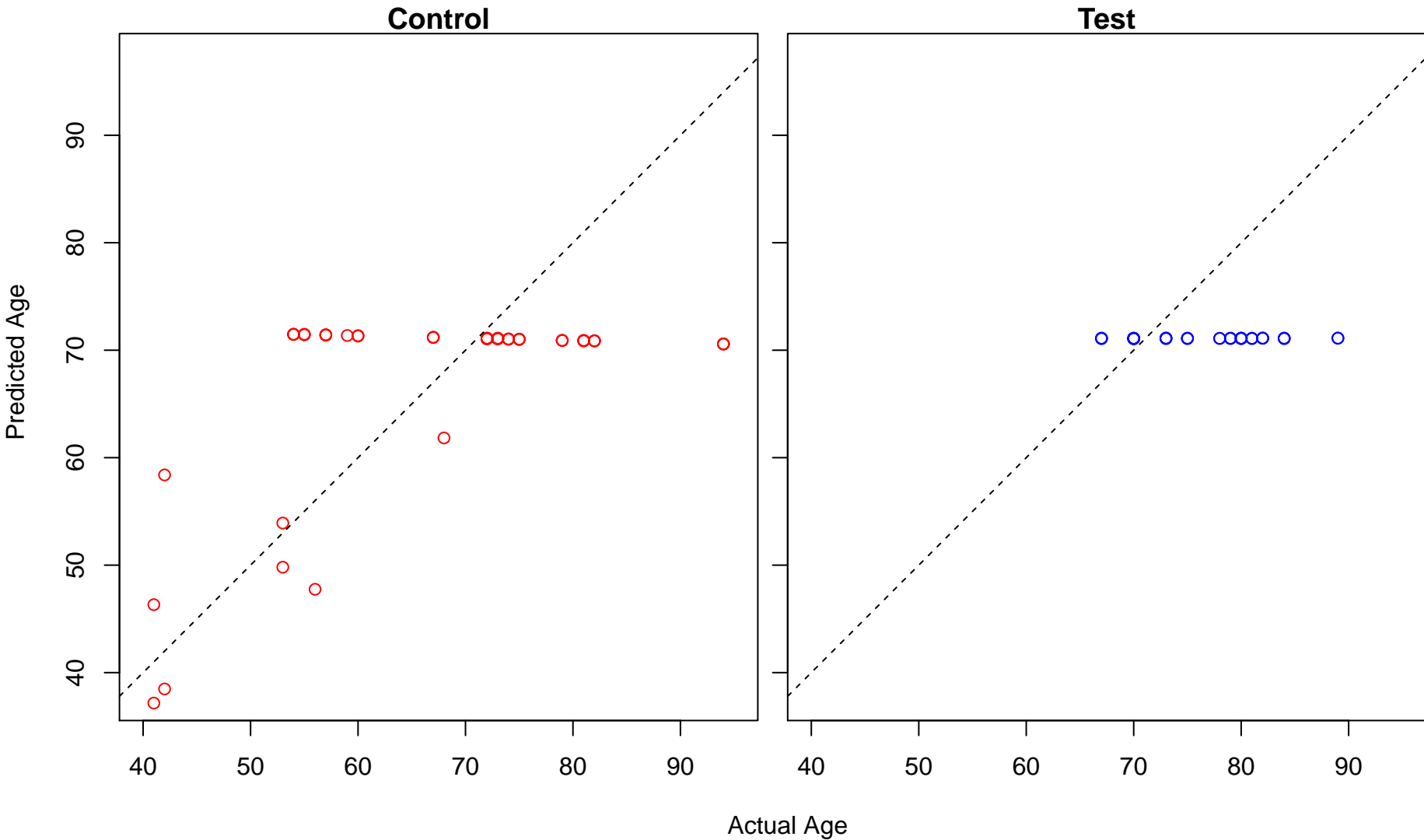
response to glucocorticoid (Score: 0.824794)



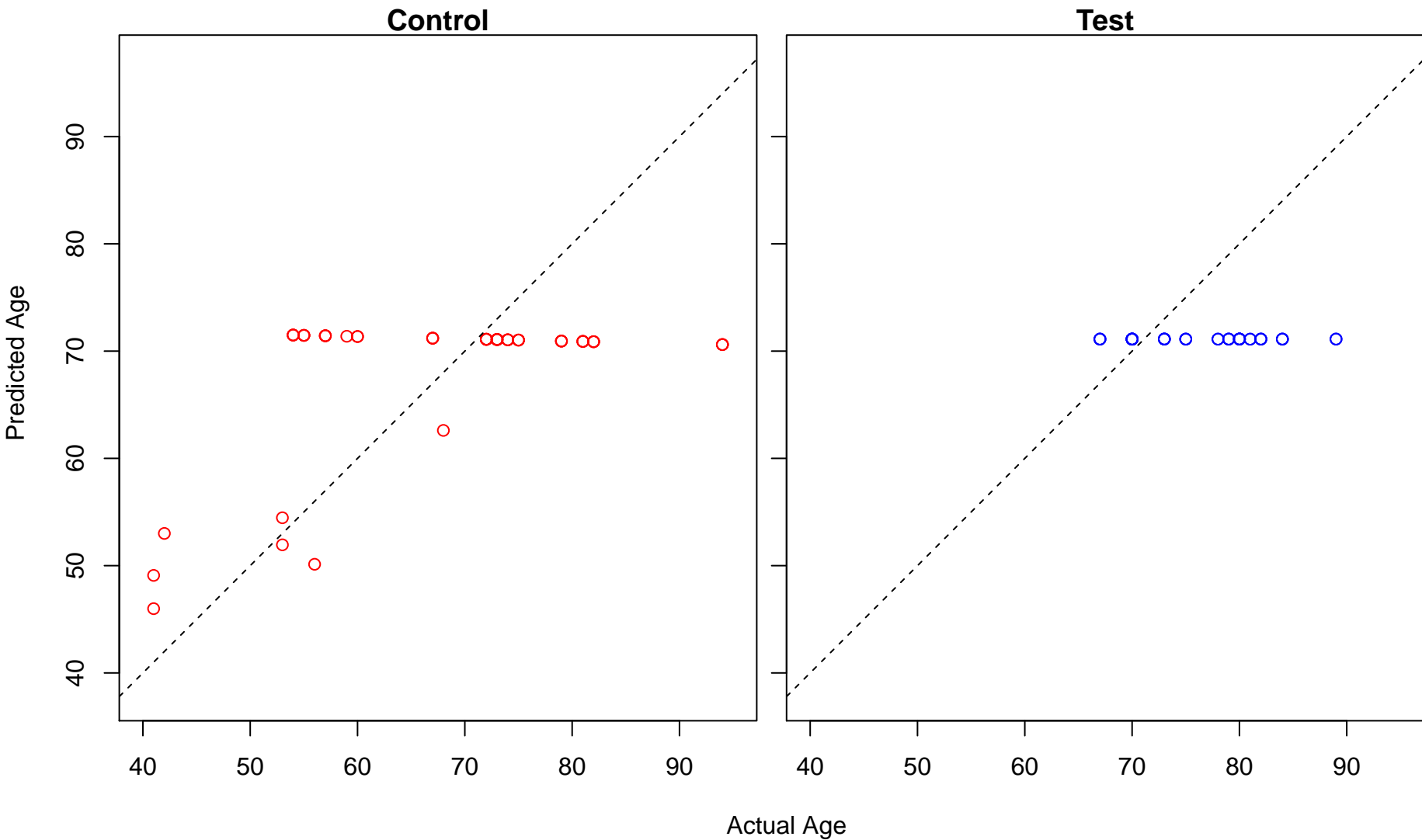
cellular response to corticosteroid stimulus (Score: 0.824794)



cellular response to glucocorticoid stimulus (Score: 0.824794)

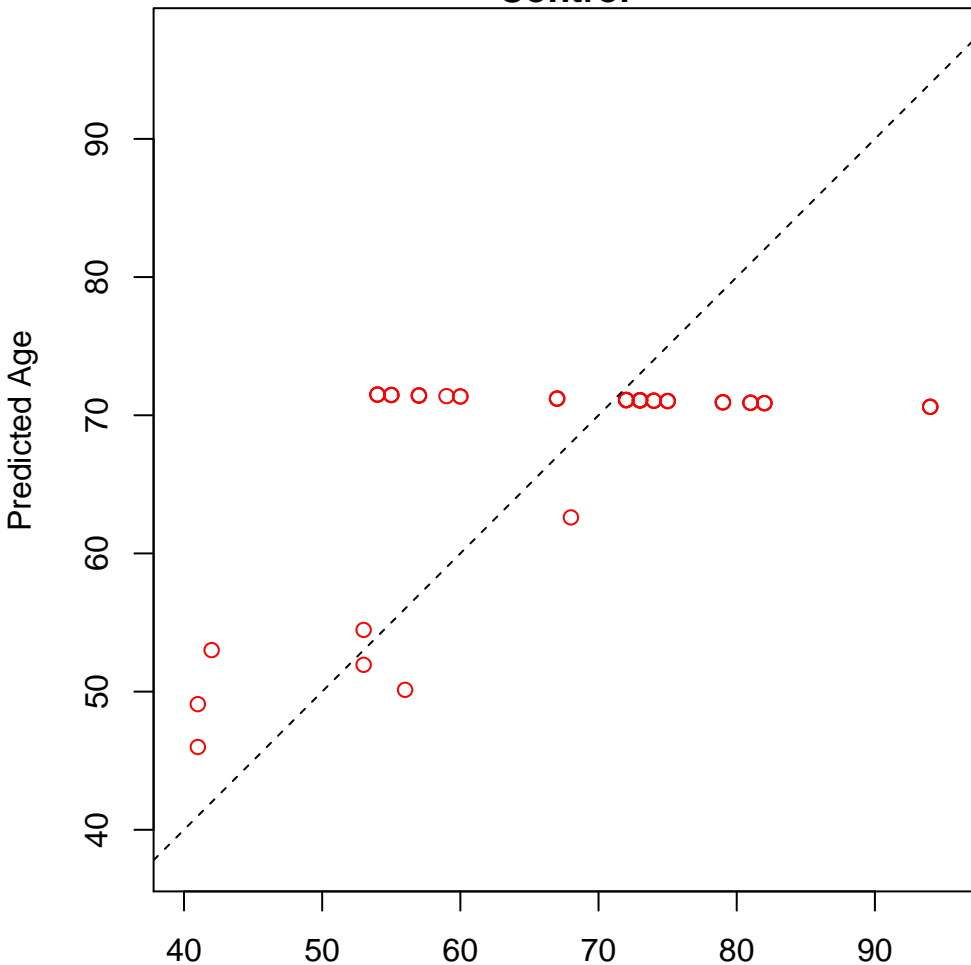


response to insulin (Score: 0.824662)

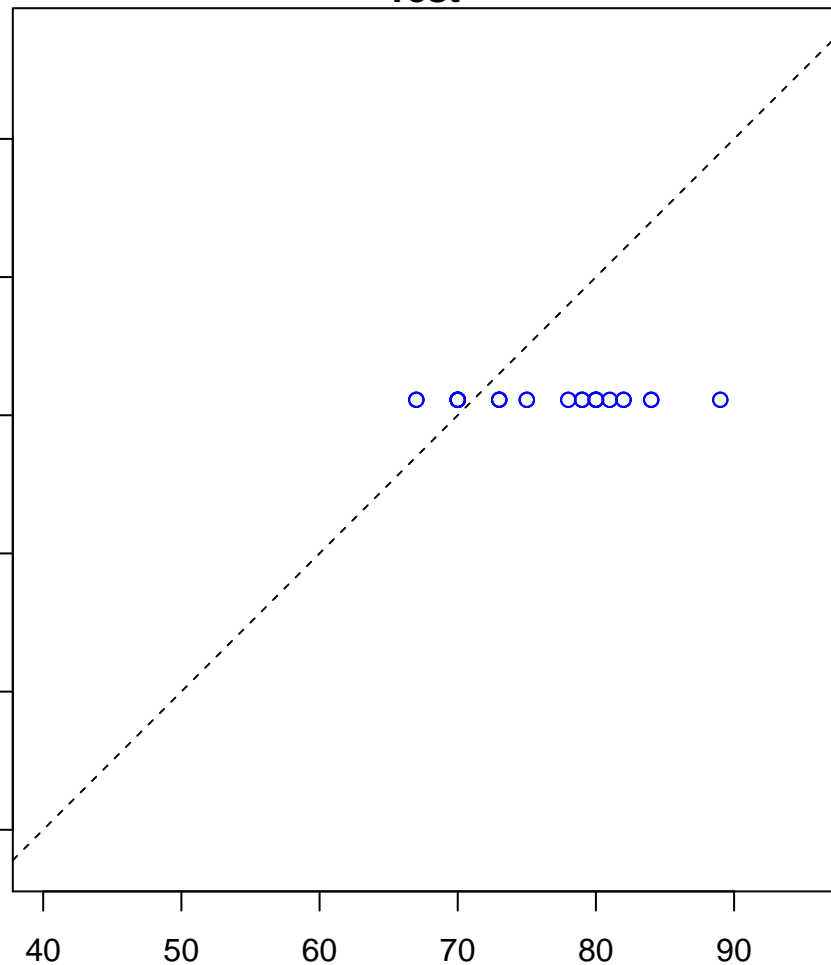


cellular response to insulin stimulus (Score: 0.824662)

Control

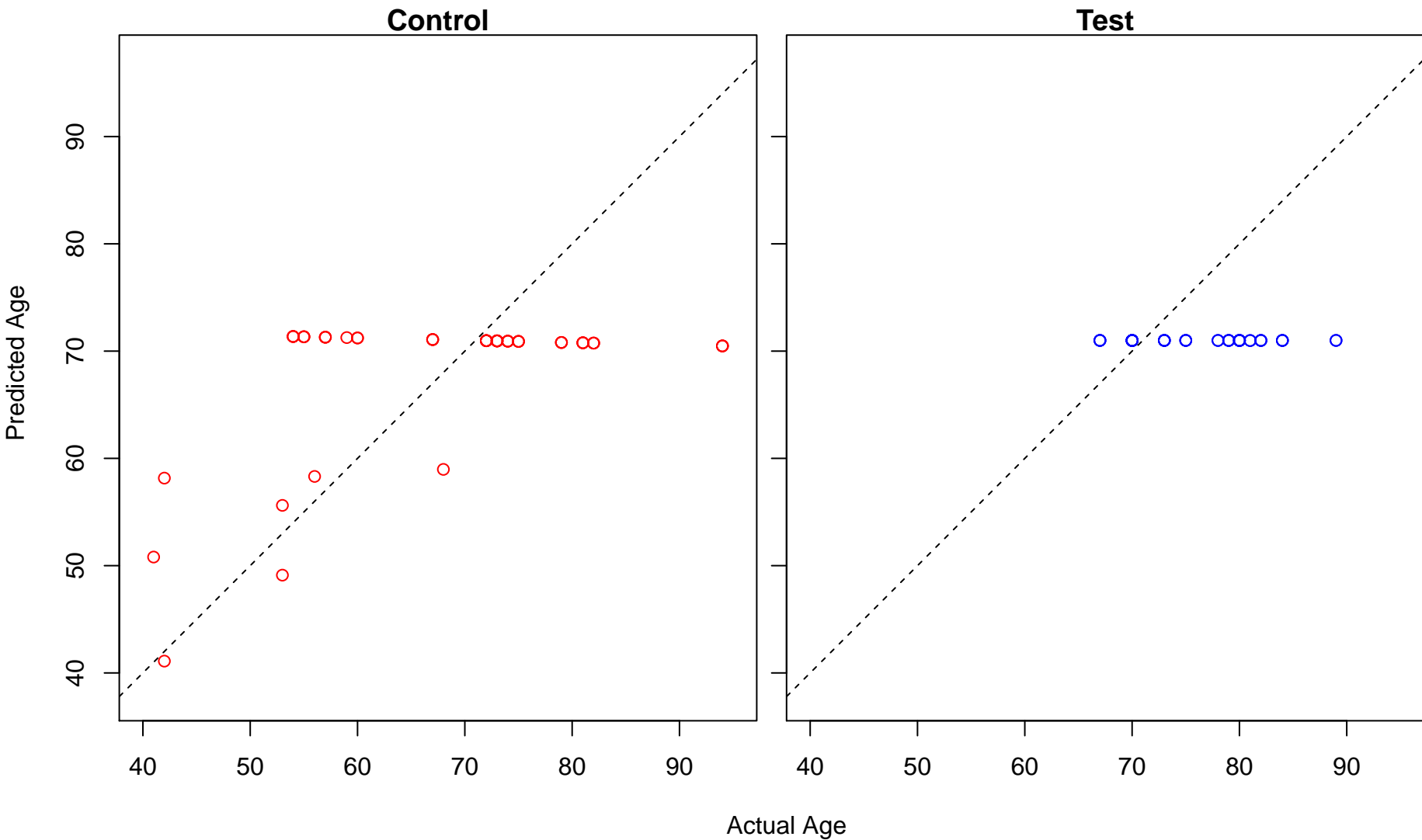


Test



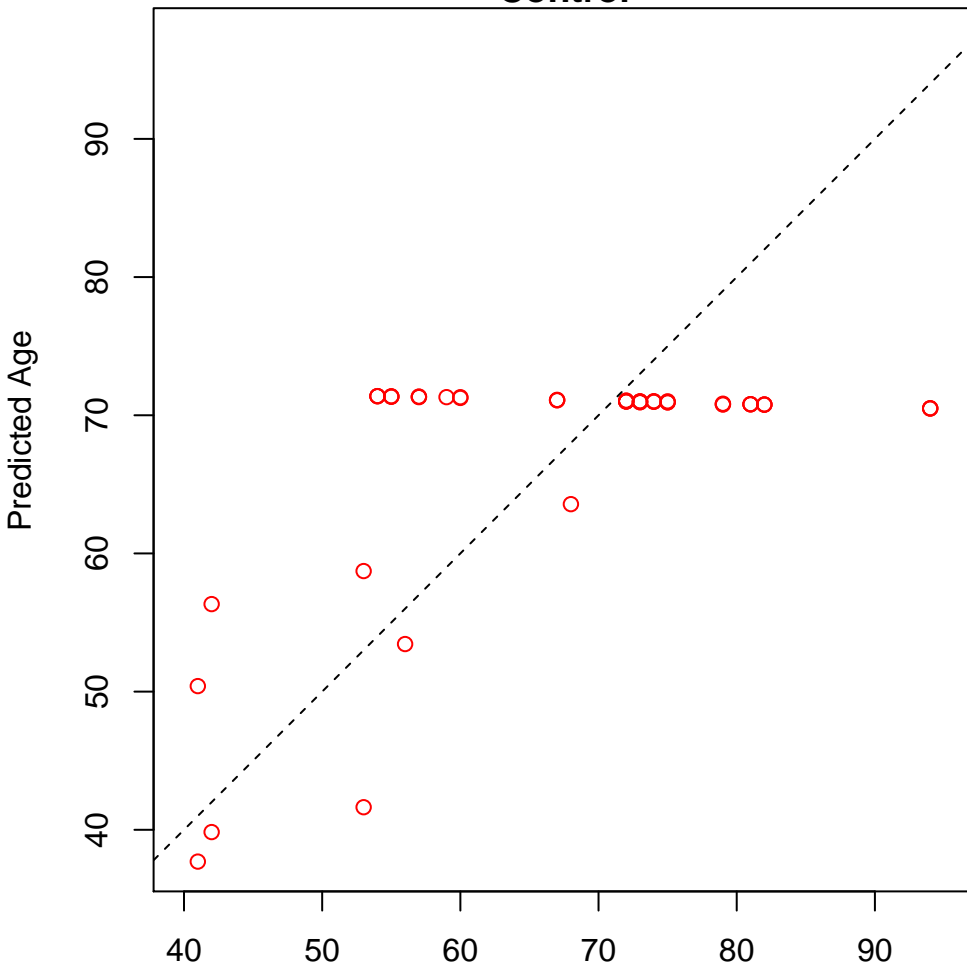
Actual Age

regulation of defense response to virus by virus (Score: 0.824121)

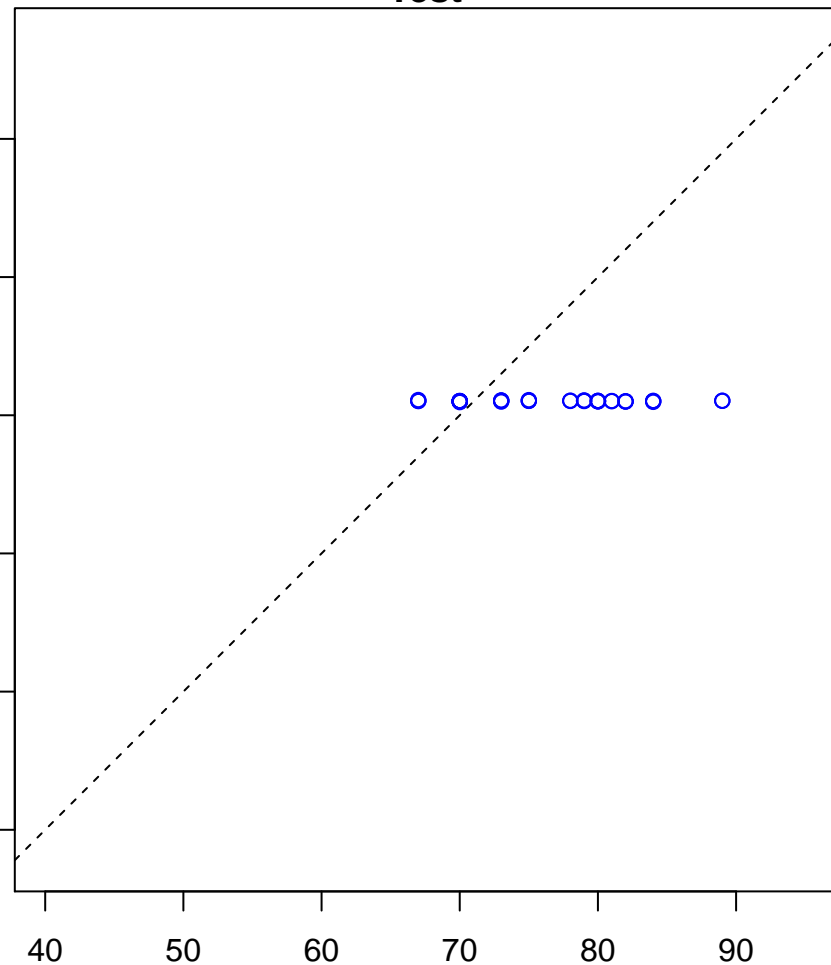


collagen catabolic process (Score: 0.824108)

Control



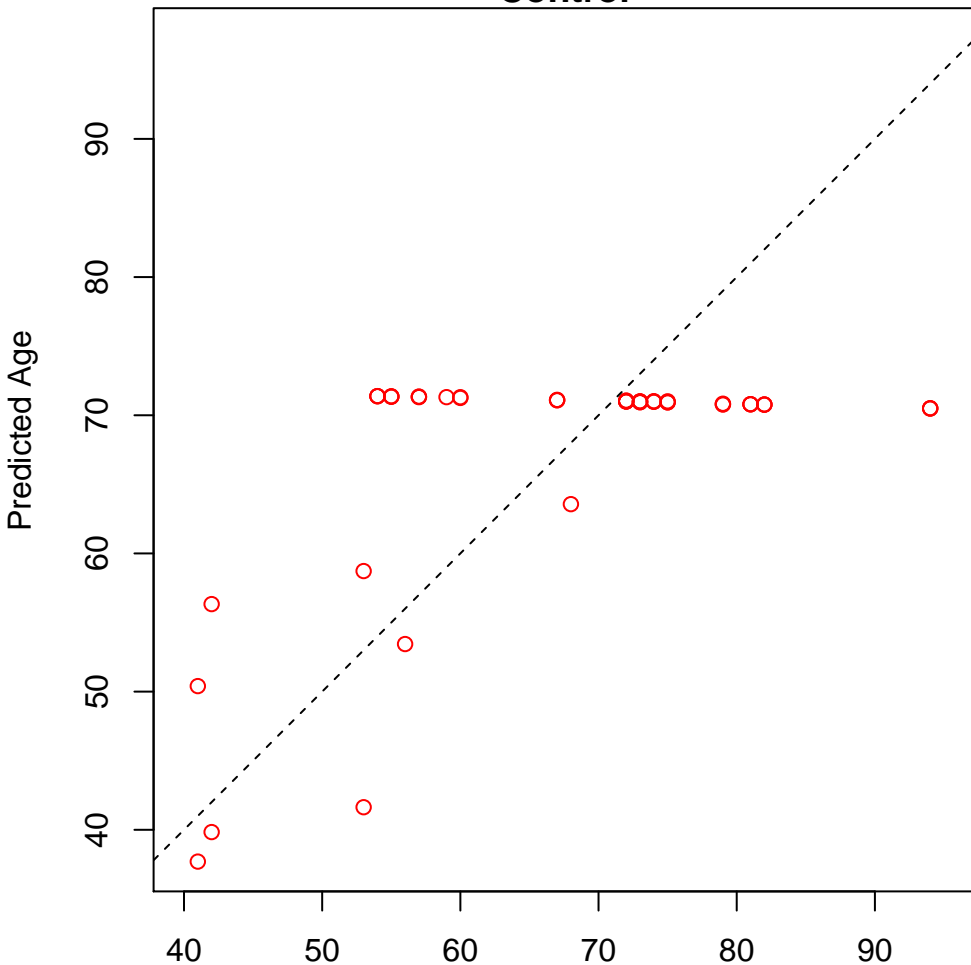
Test



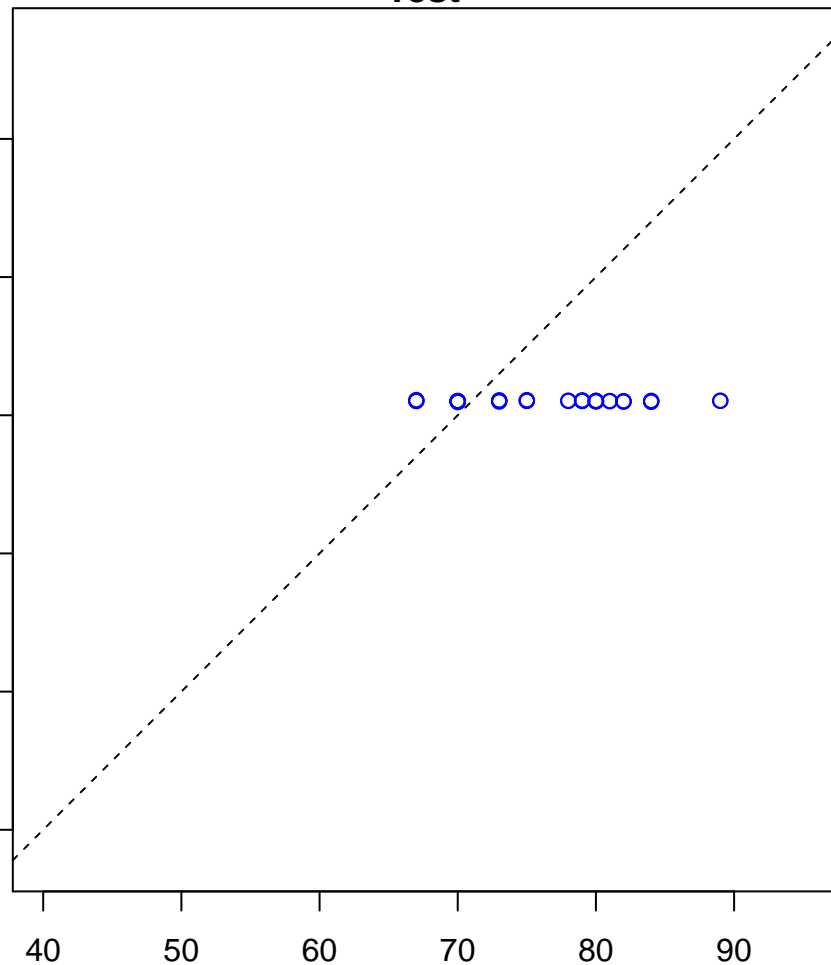
Actual Age

collagen metabolic process (Score: 0.824108)

Control

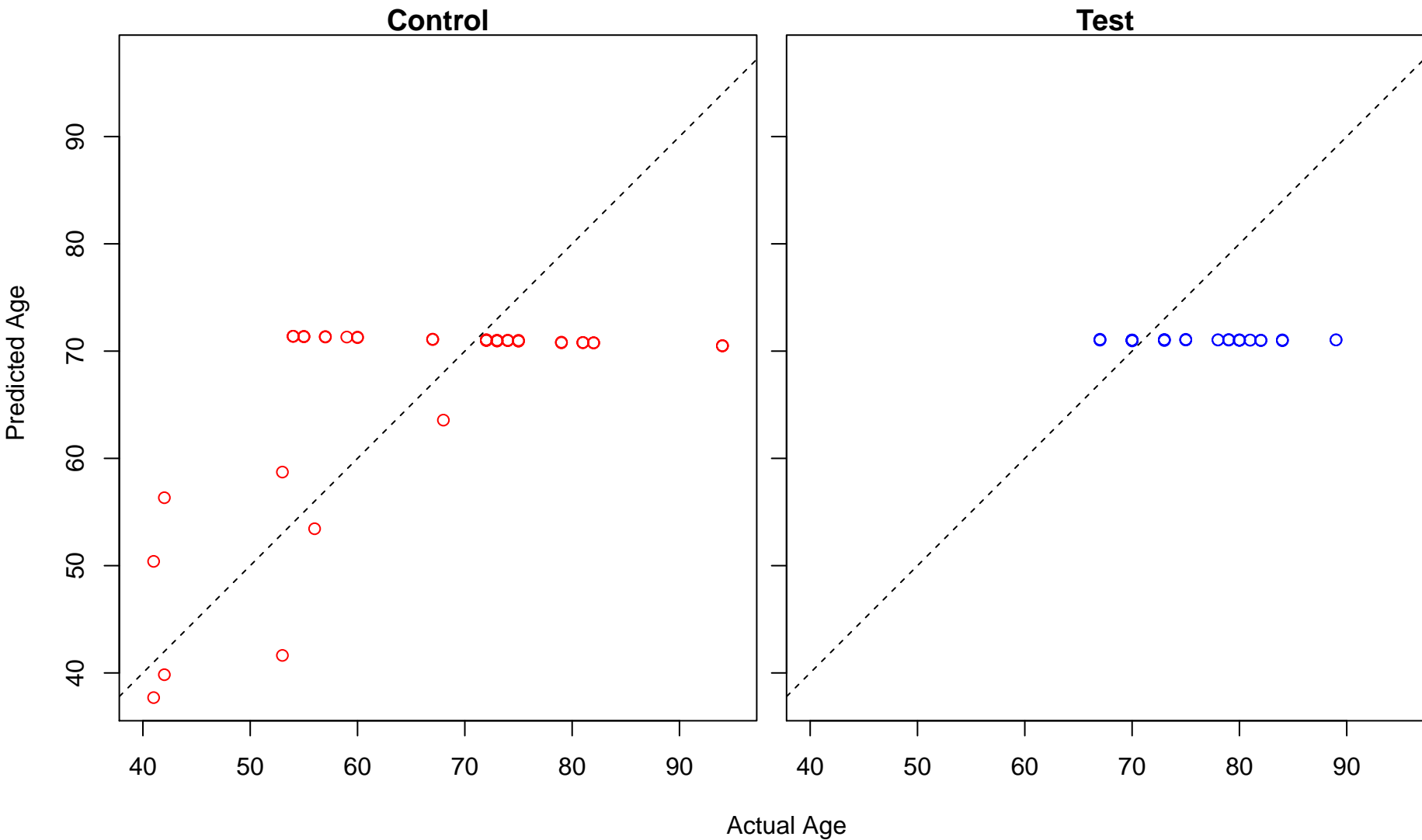


Test



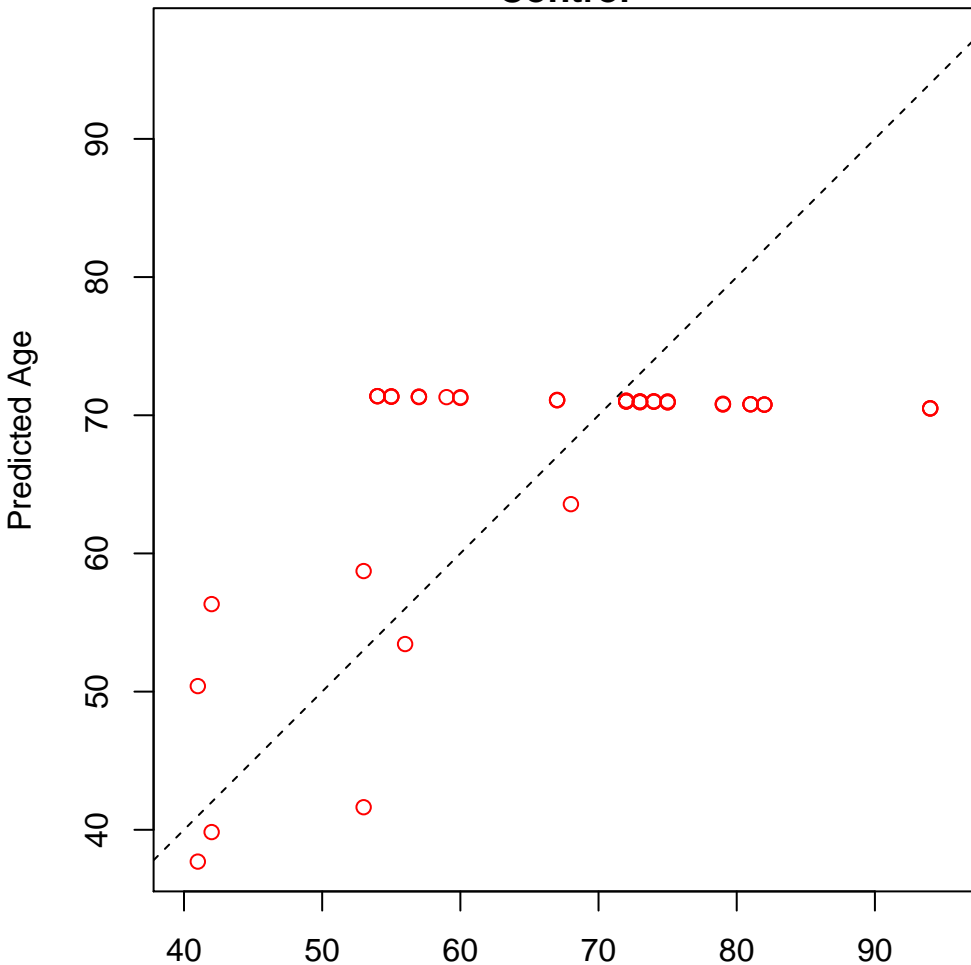
Actual Age

multicellular organism metabolic process (Score: 0.824108)

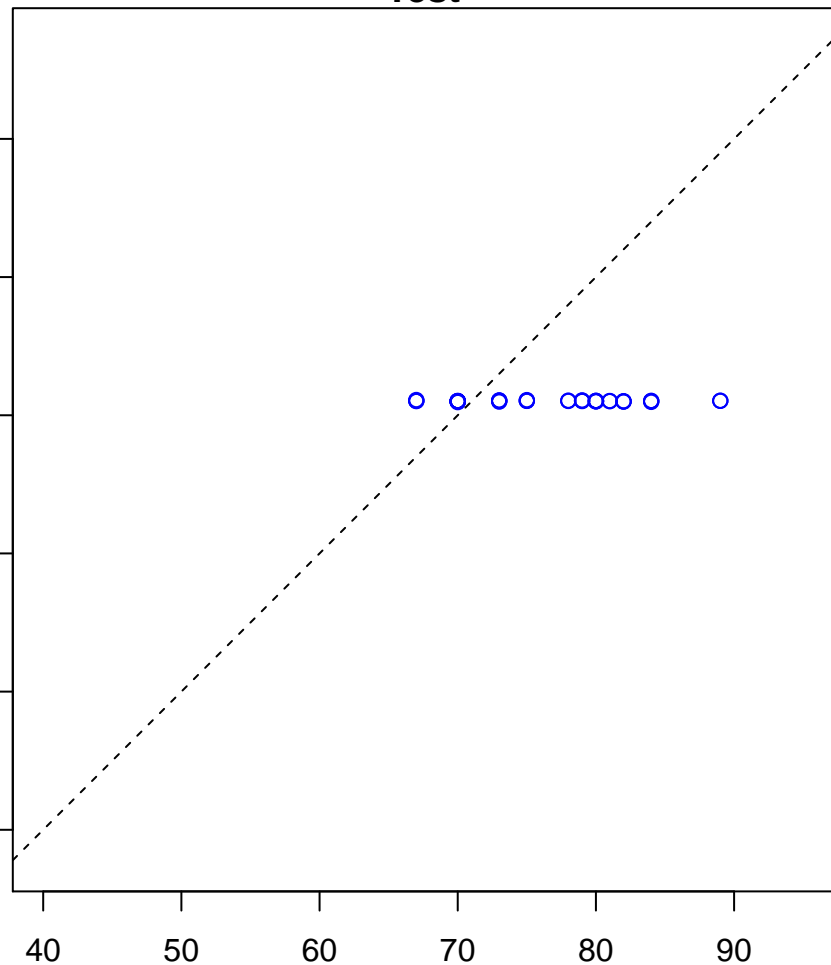


multicellular organismal catabolic process (Score: 0.824108)

Control

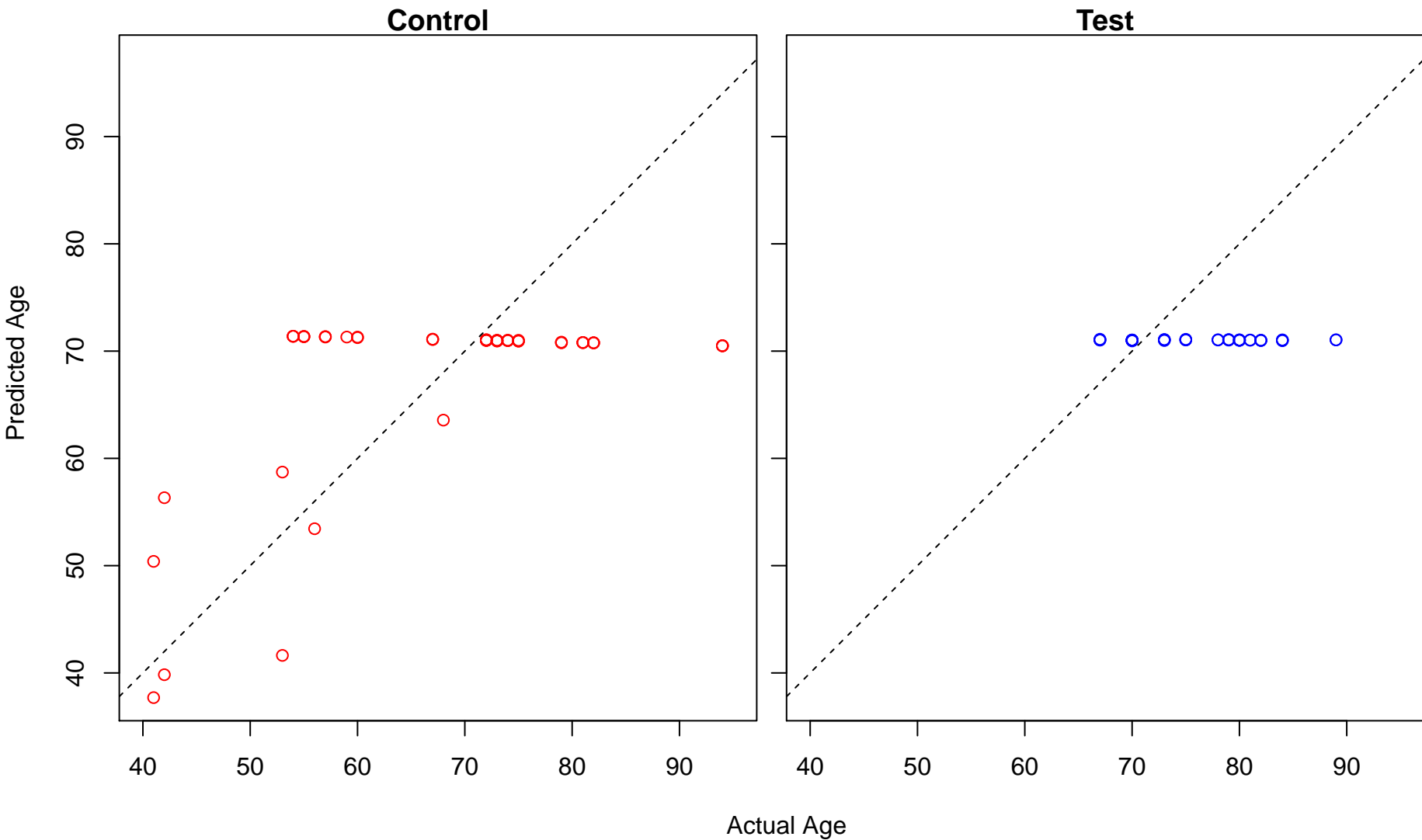


Test

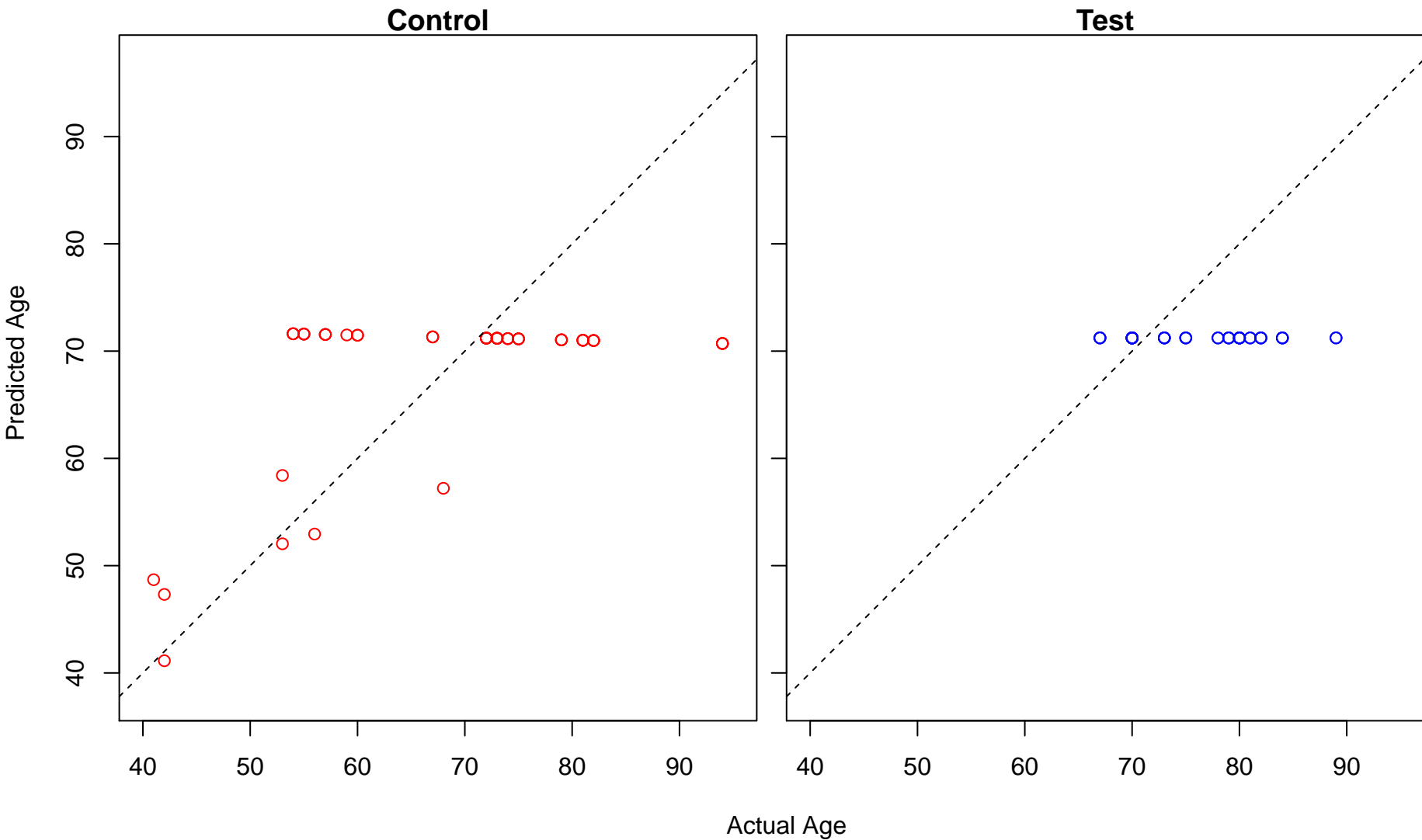


Actual Age

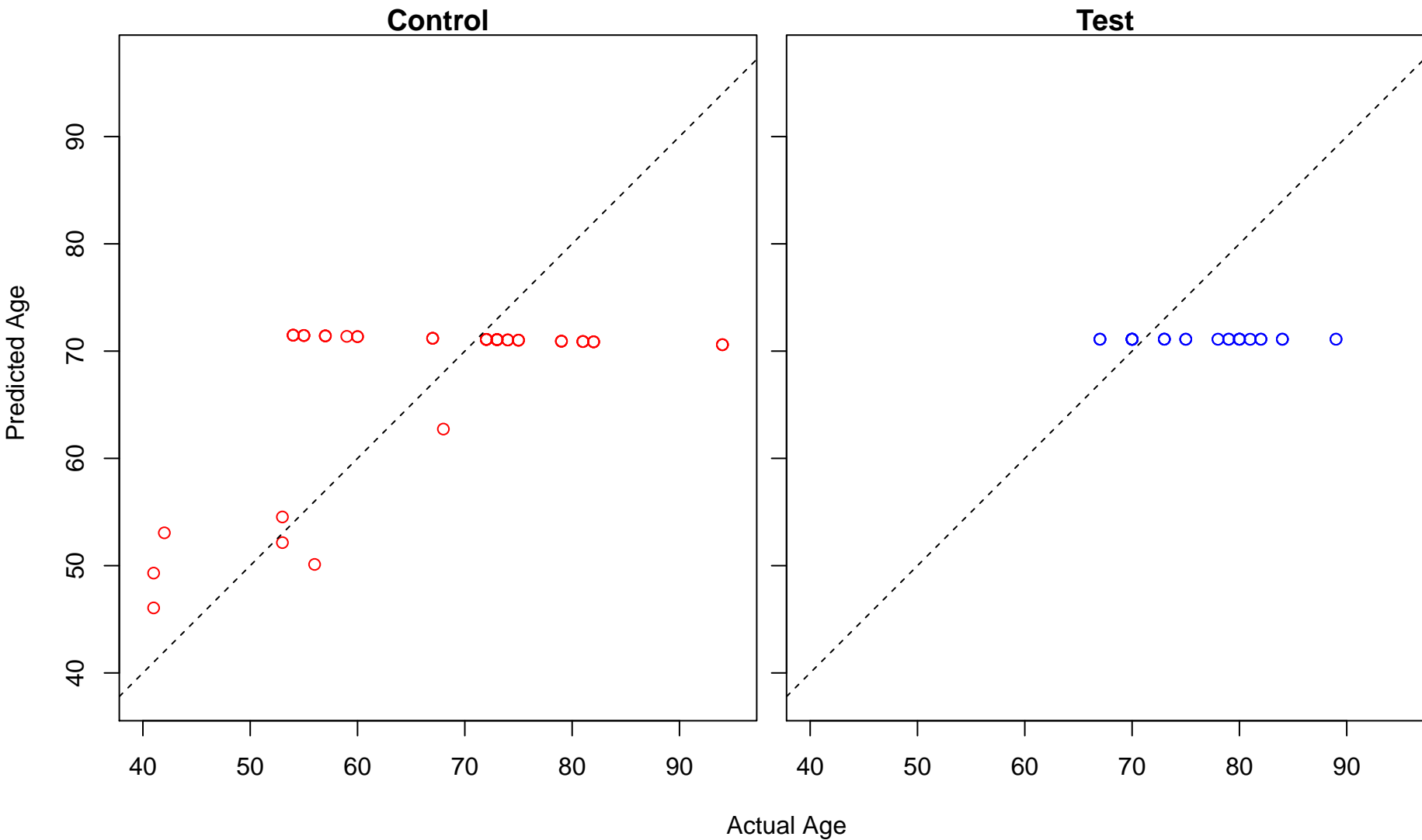
multicellular organismal macromolecule metabolic process (Score: 0.824108)



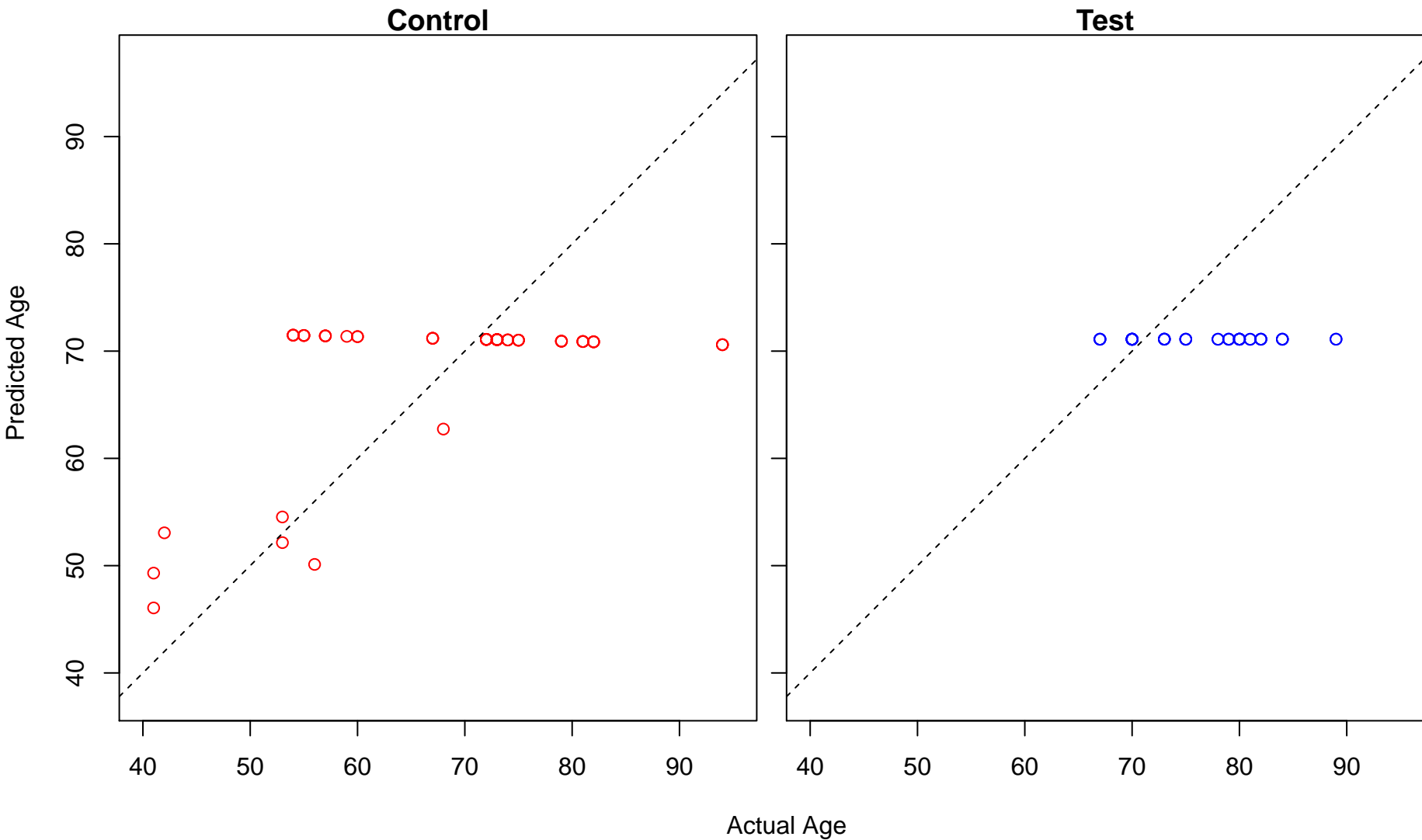
ion transmembrane transport (Score: 0.823957)



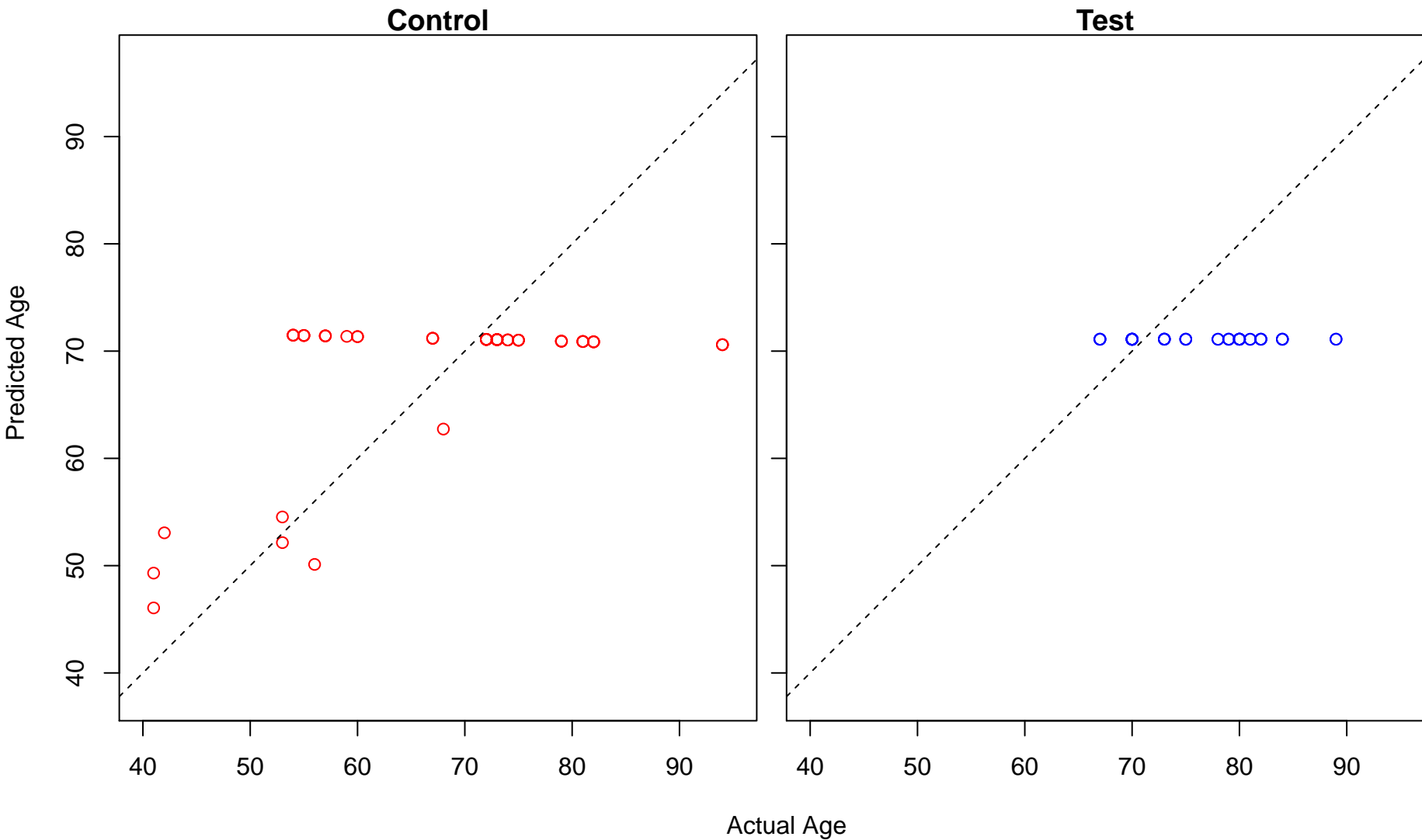
hydrogen transport (Score: 0.823913)



regulation of pH (Score: 0.823913)

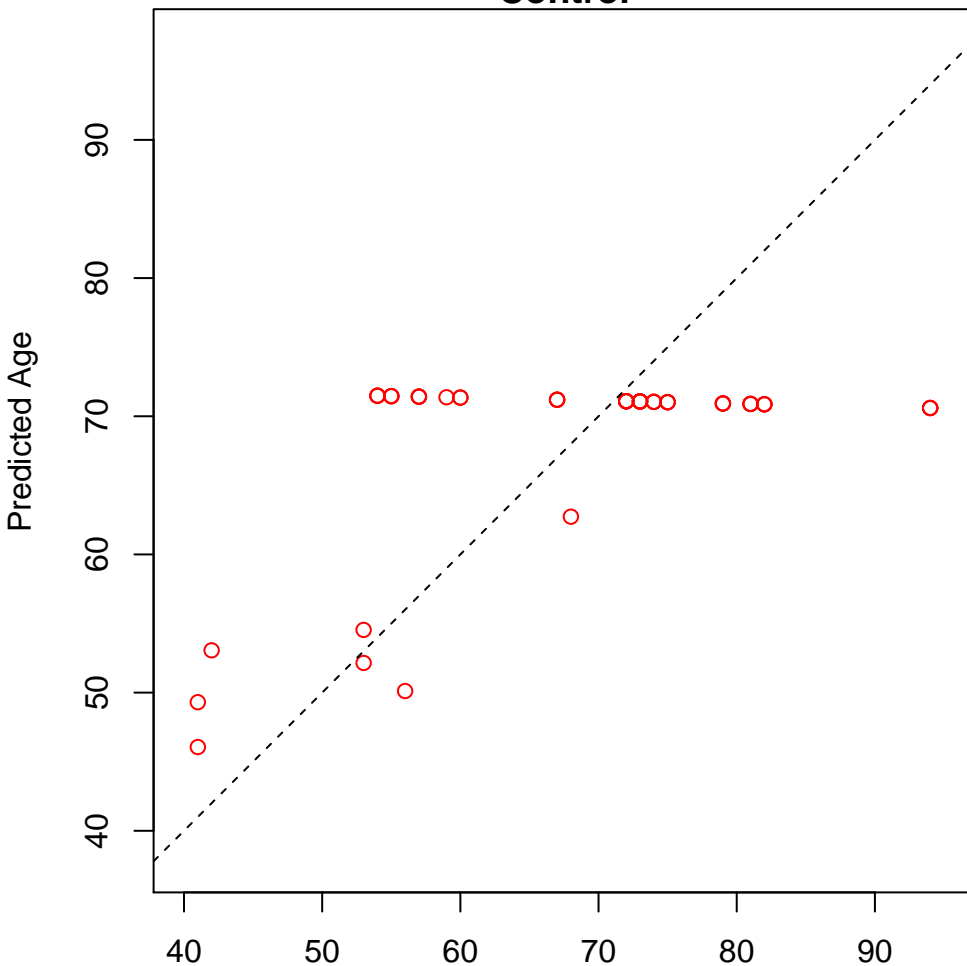


insulin receptor signaling pathway (Score: 0.823913)

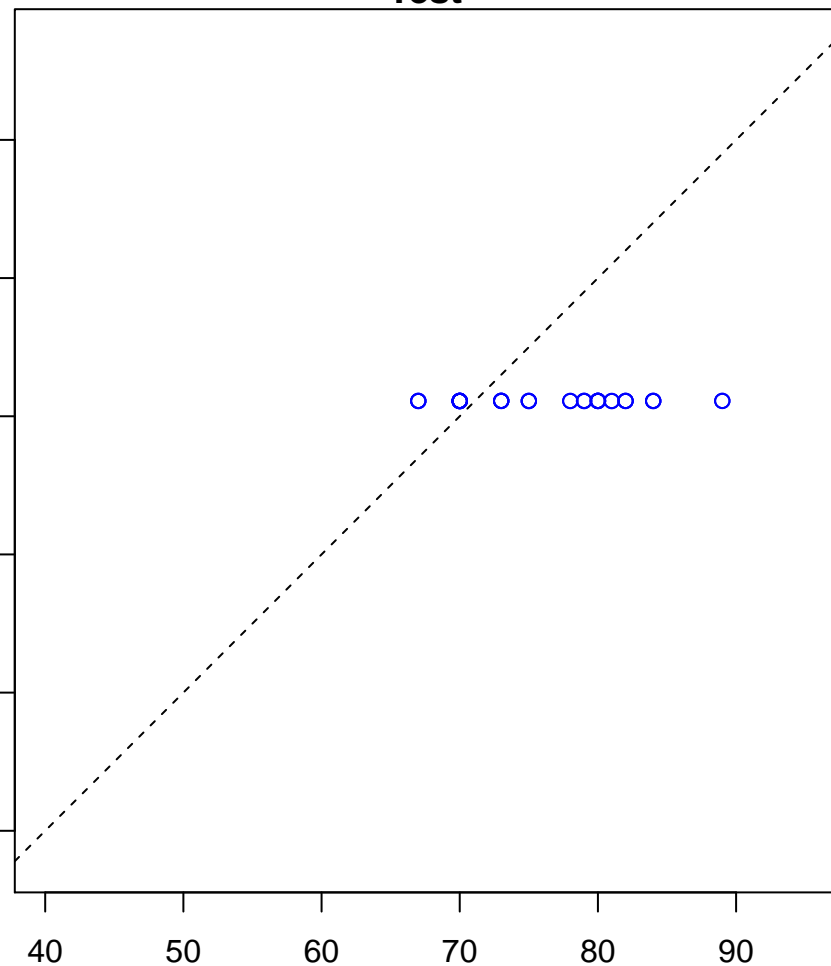


monovalent inorganic cation transport (Score: 0.823913)

Control

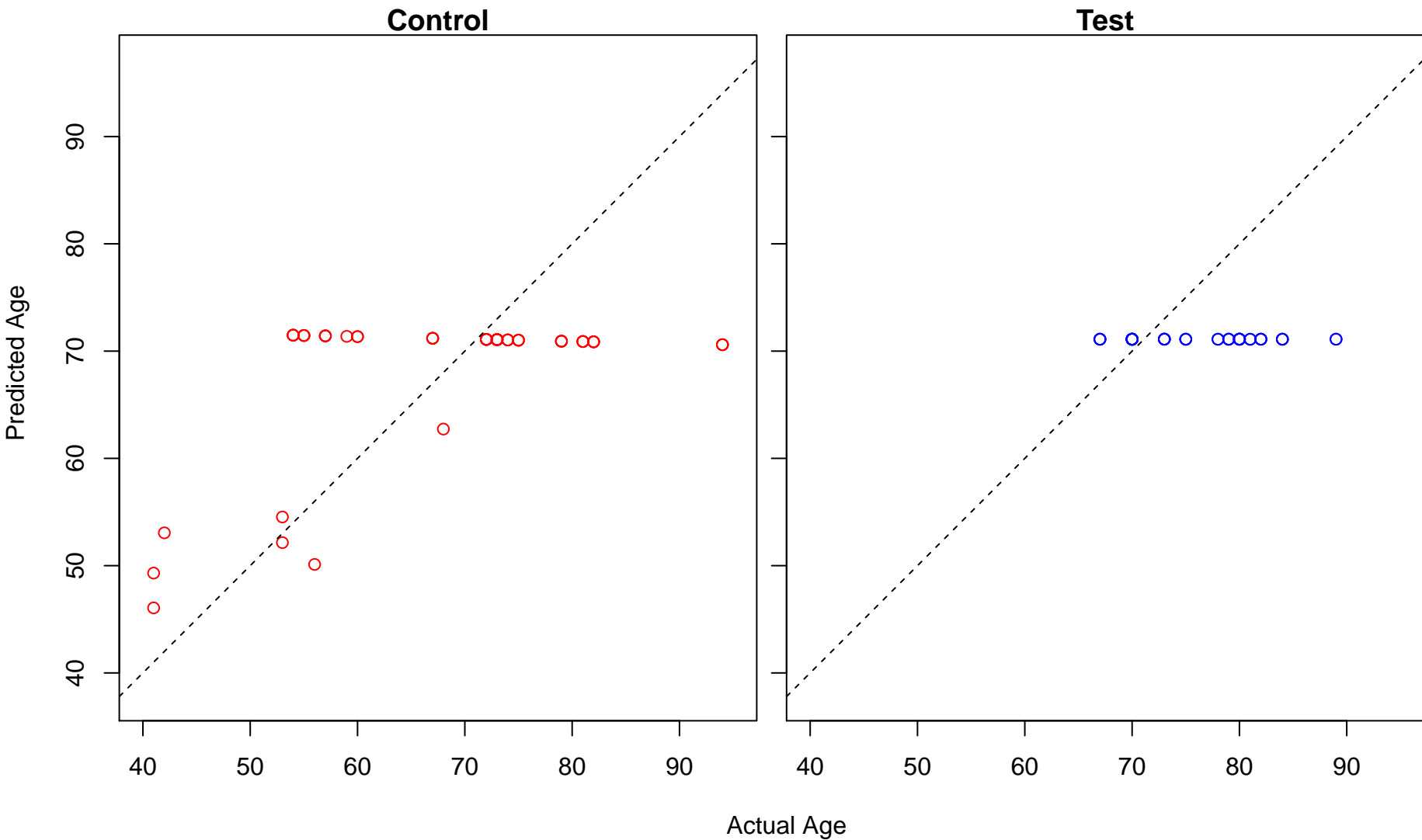


Test

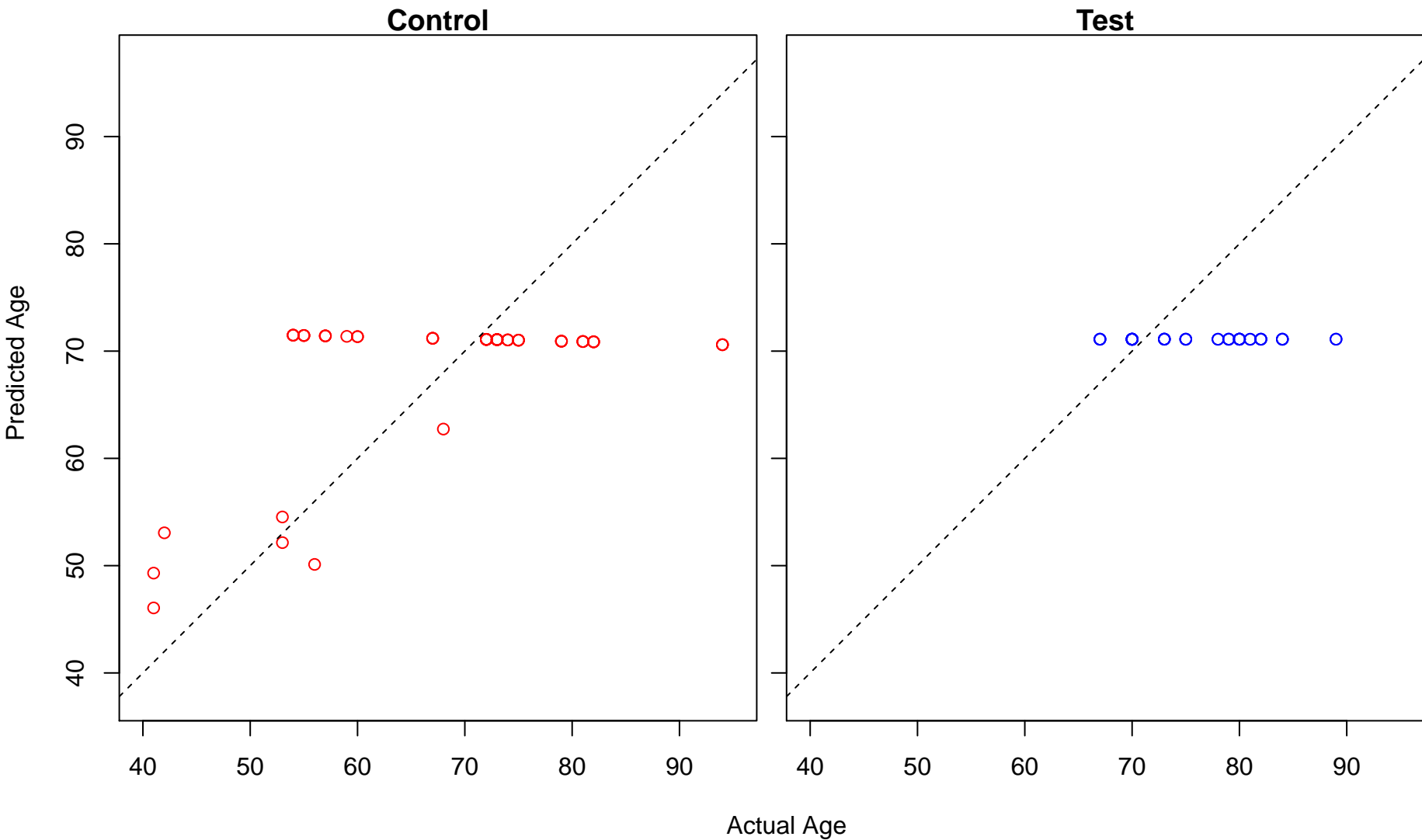


Actual Age

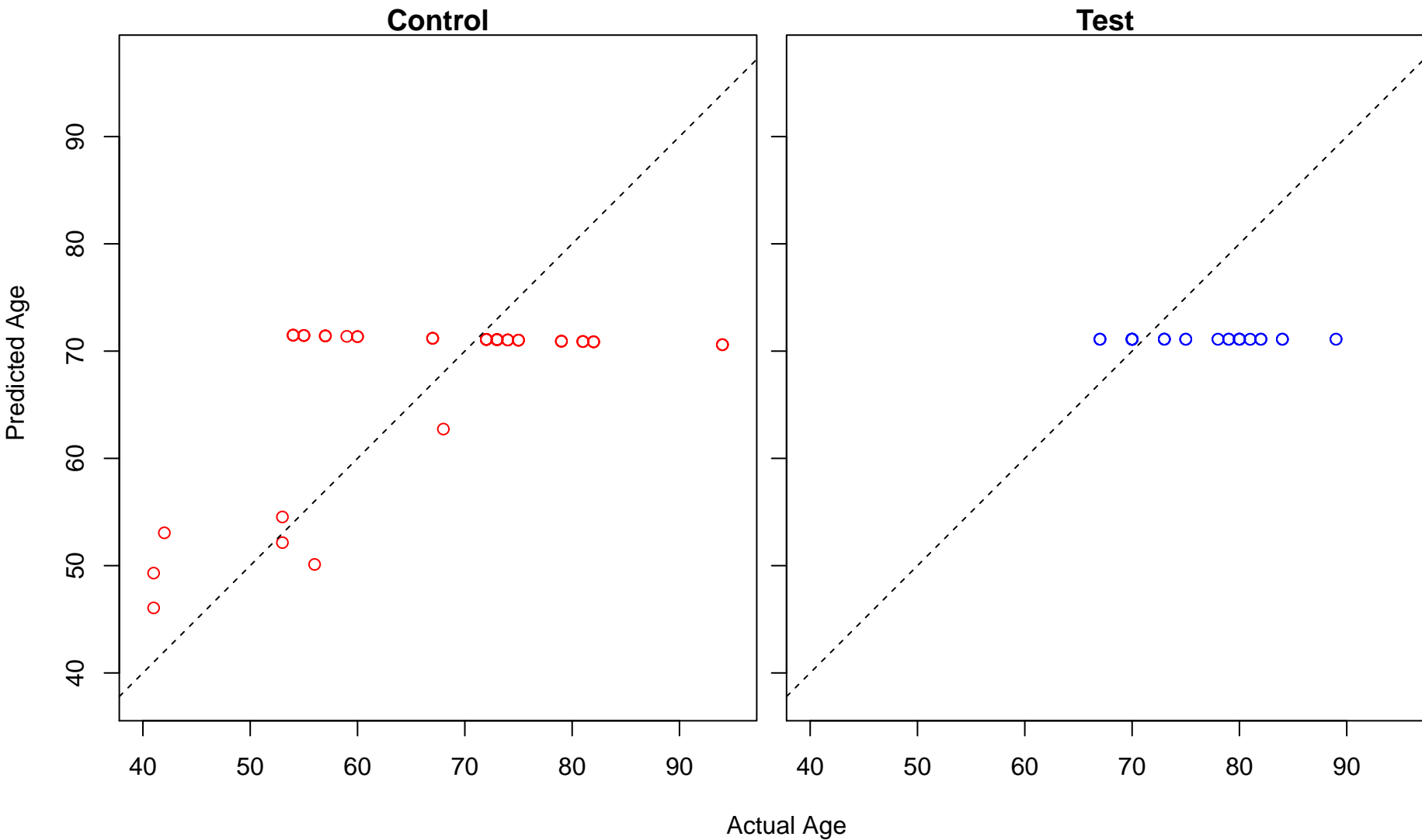
proton transport (Score: 0.823913)



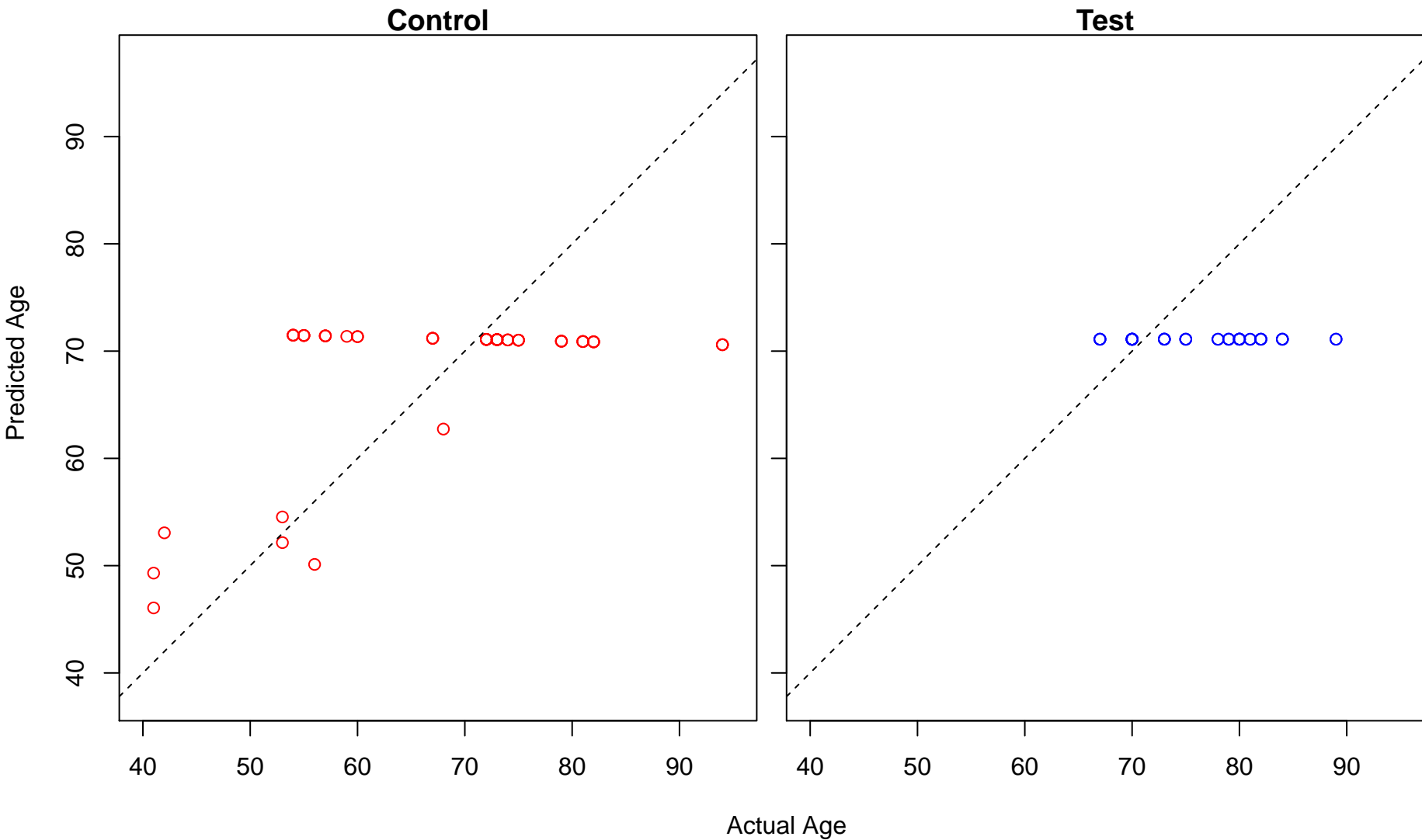
cellular monovalent inorganic cation homeostasis (Score: 0.823913)



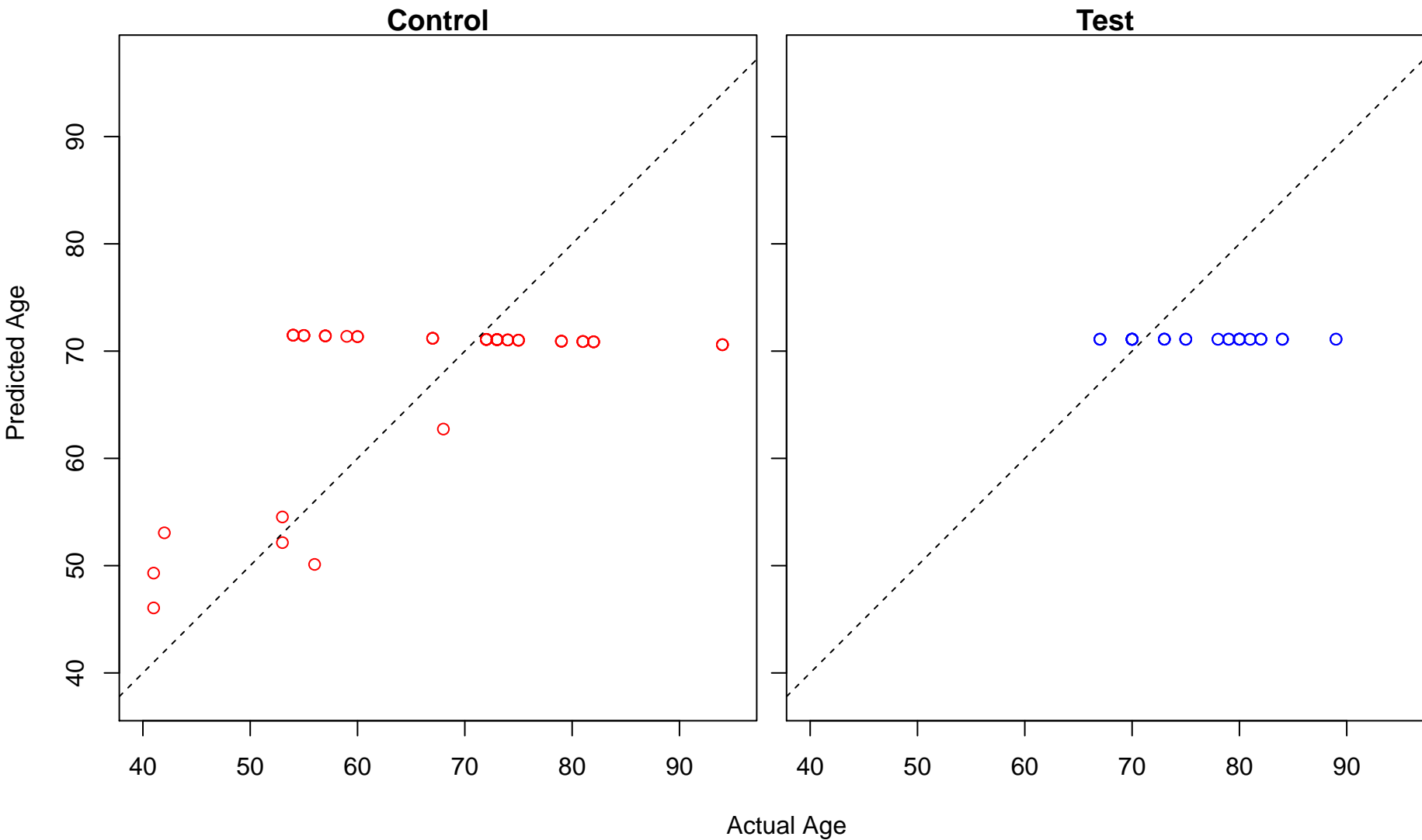
regulation of cellular pH (Score: 0.823913)



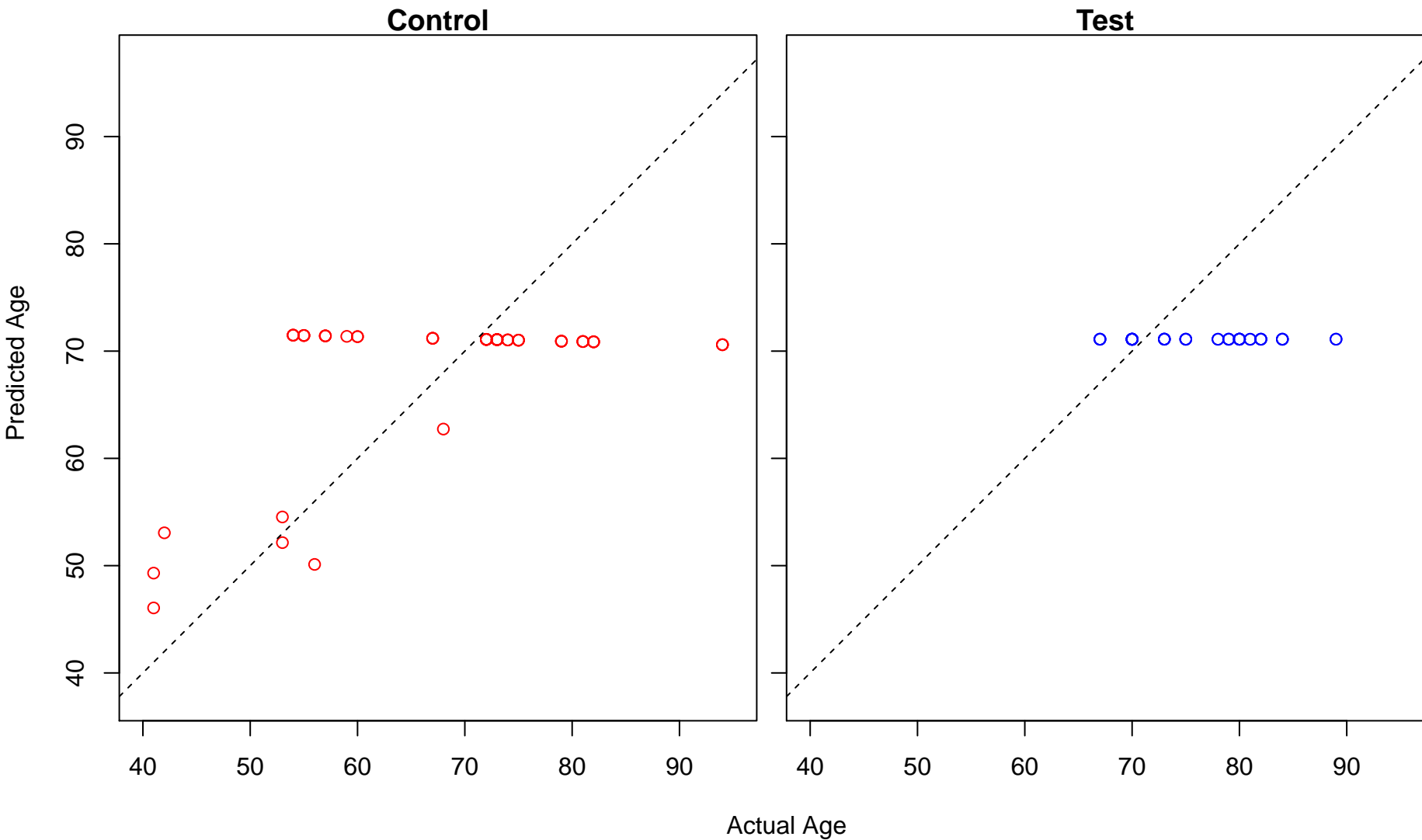
pH reduction (Score: 0.823913)



intracellular pH reduction (Score: 0.823913)

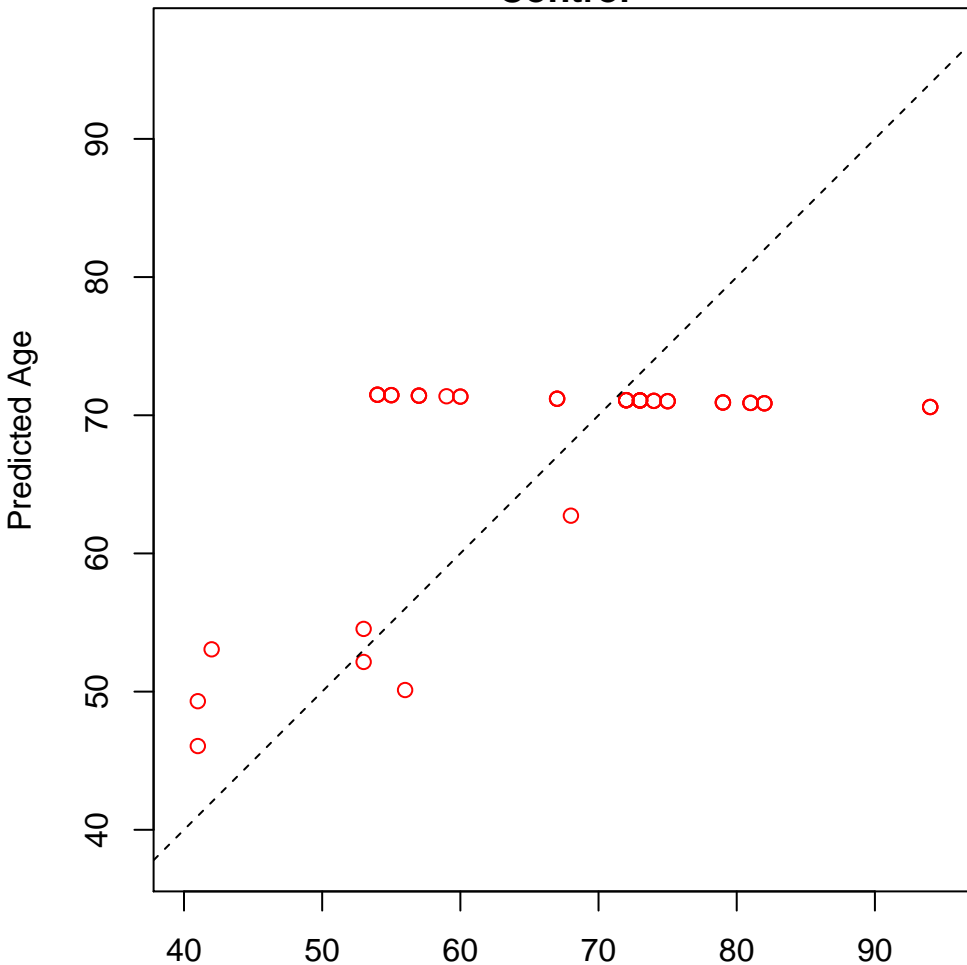


regulation of intracellular pH (Score: 0.823913)

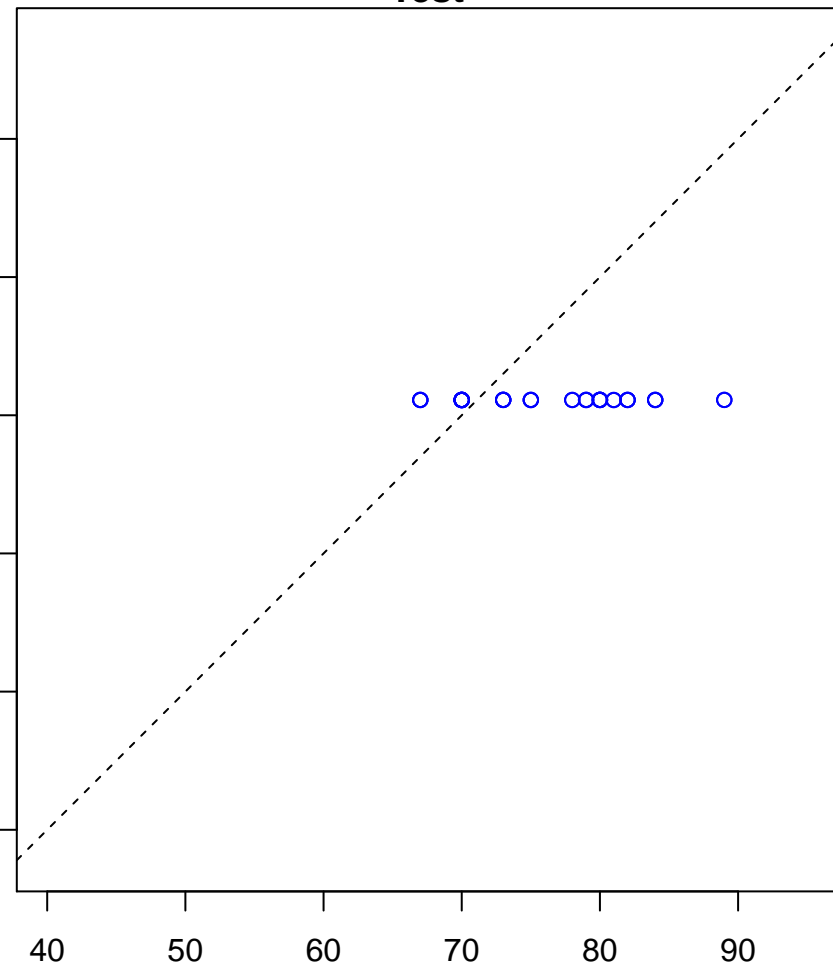


monovalent inorganic cation homeostasis (Score: 0.823913)

Control

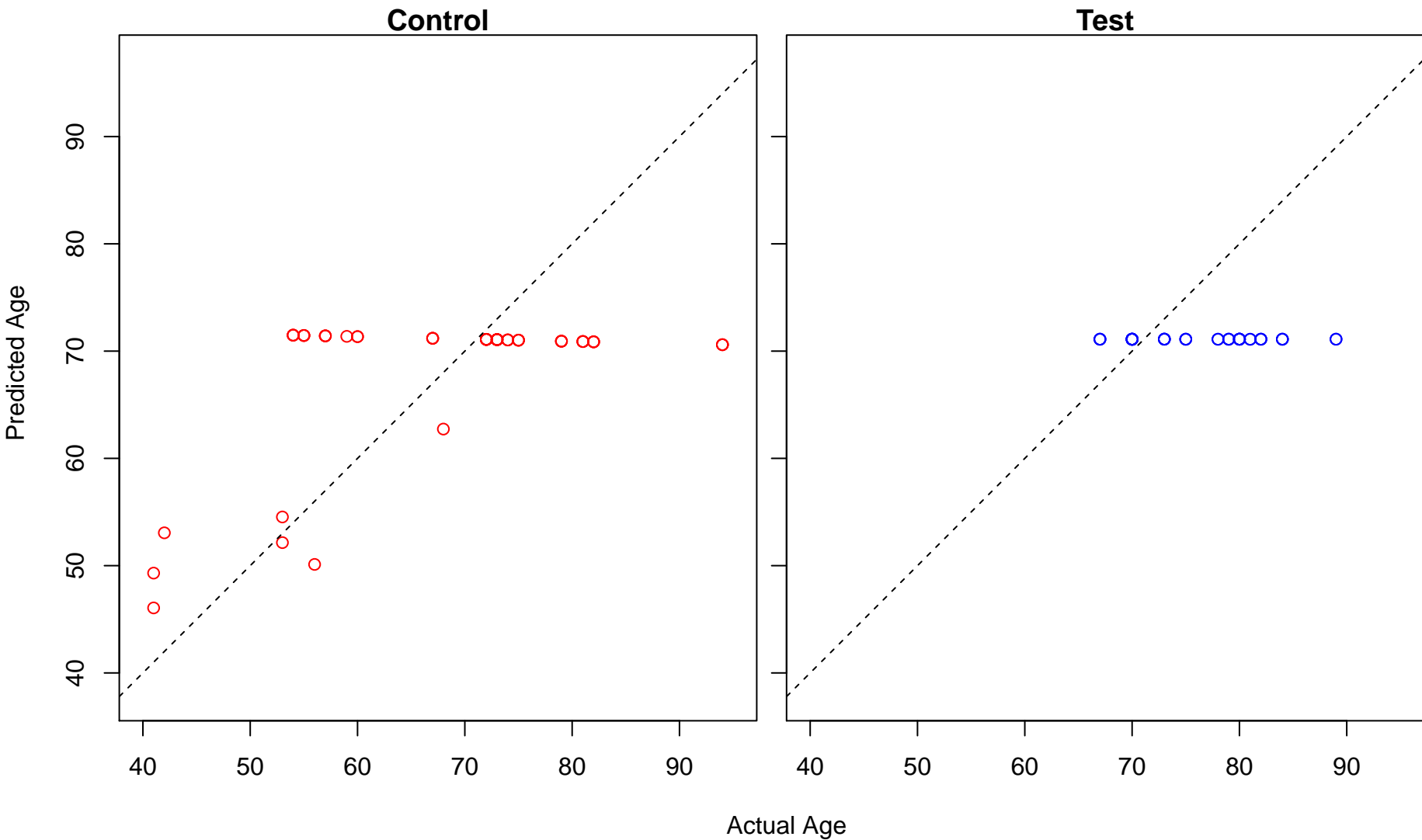


Test



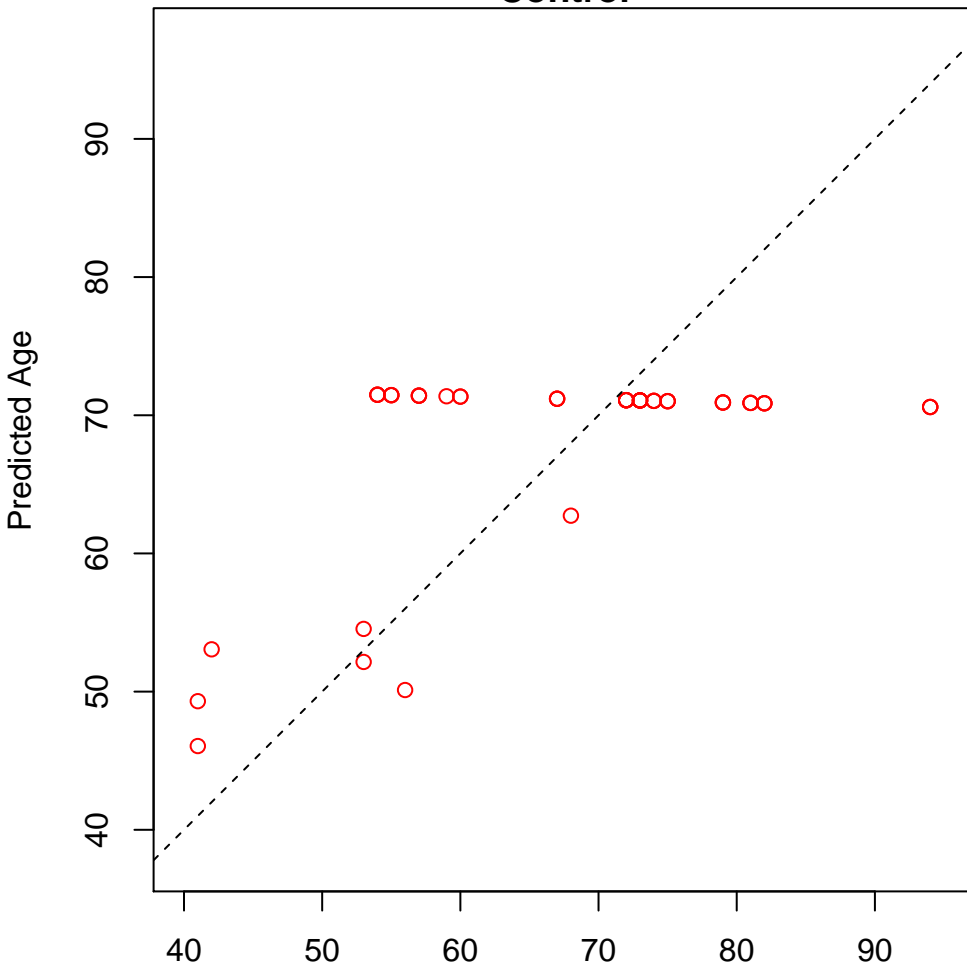
Actual Age

phagosome maturation (Score: 0.823913)

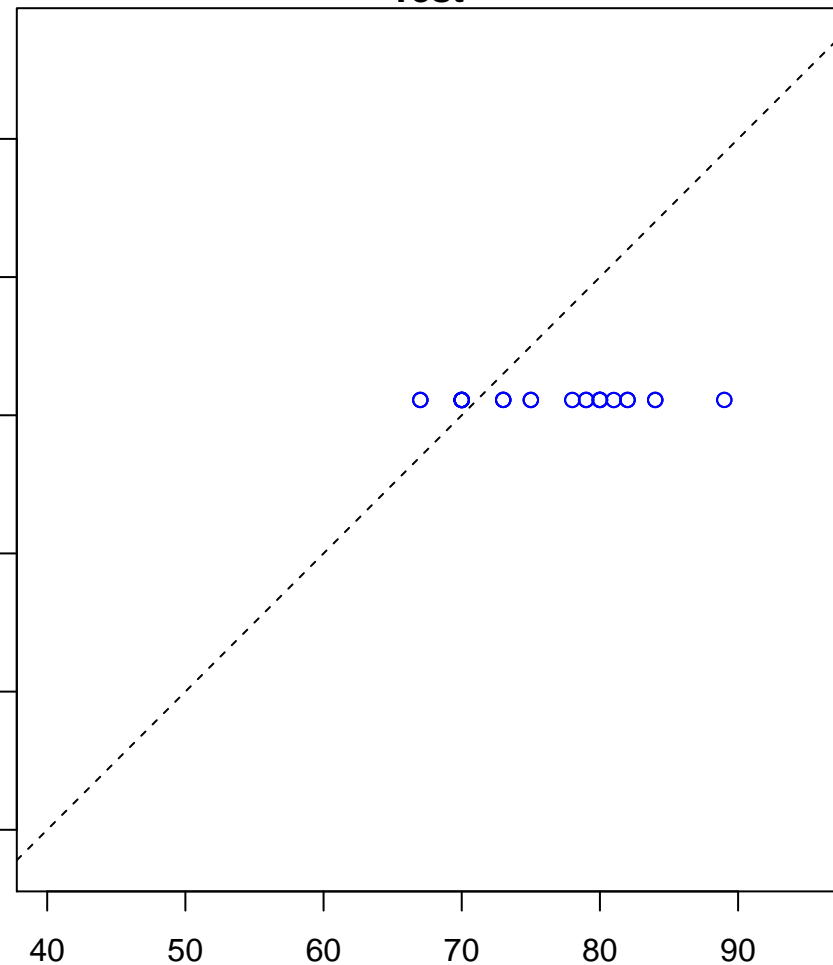


phagosome acidification (Score: 0.823913)

Control

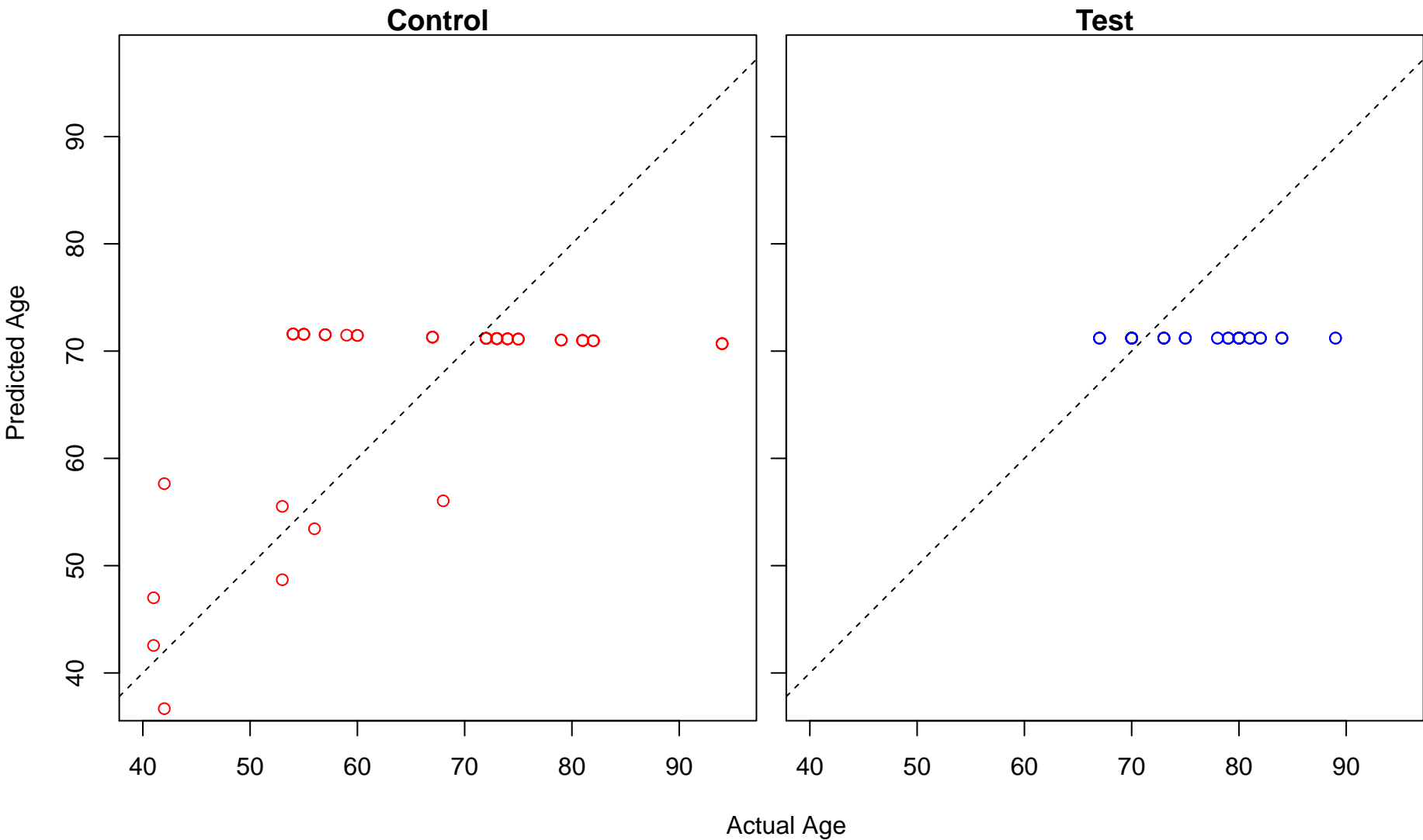


Test



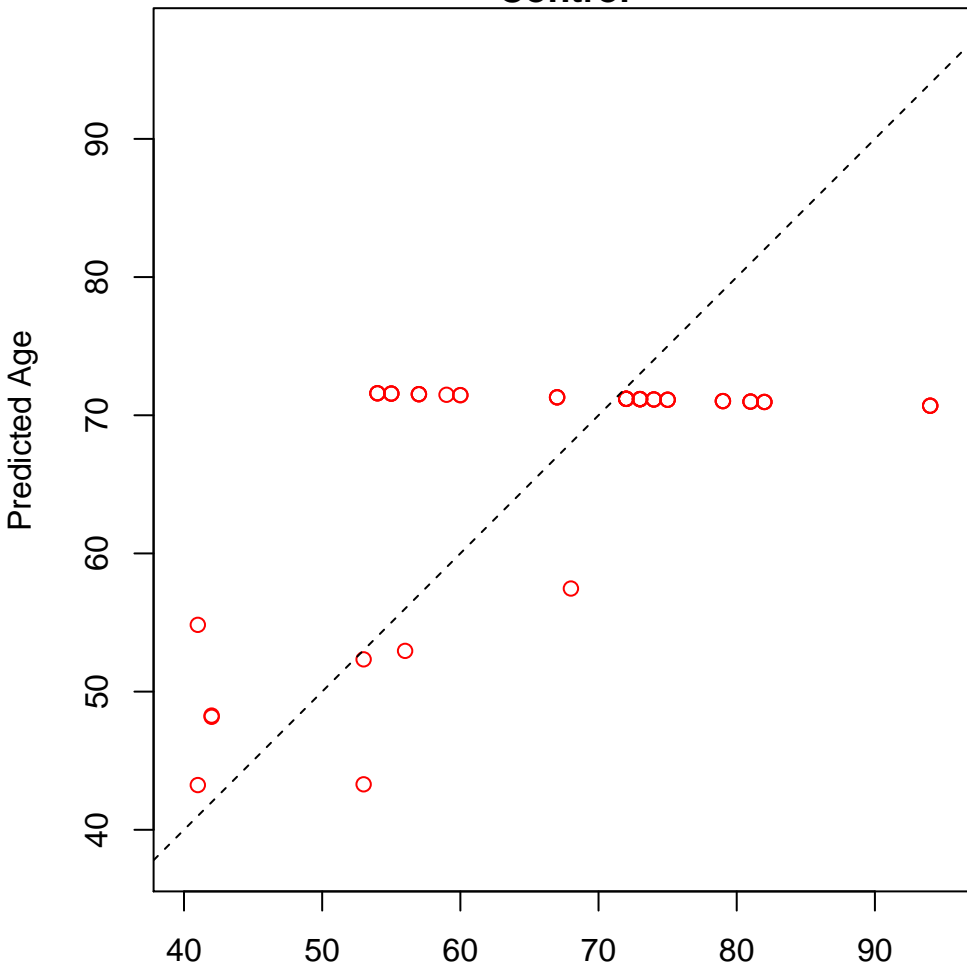
Actual Age

regulation of oxidative stress-induced intrinsic apoptotic signaling pathway (Score: 0.823858)

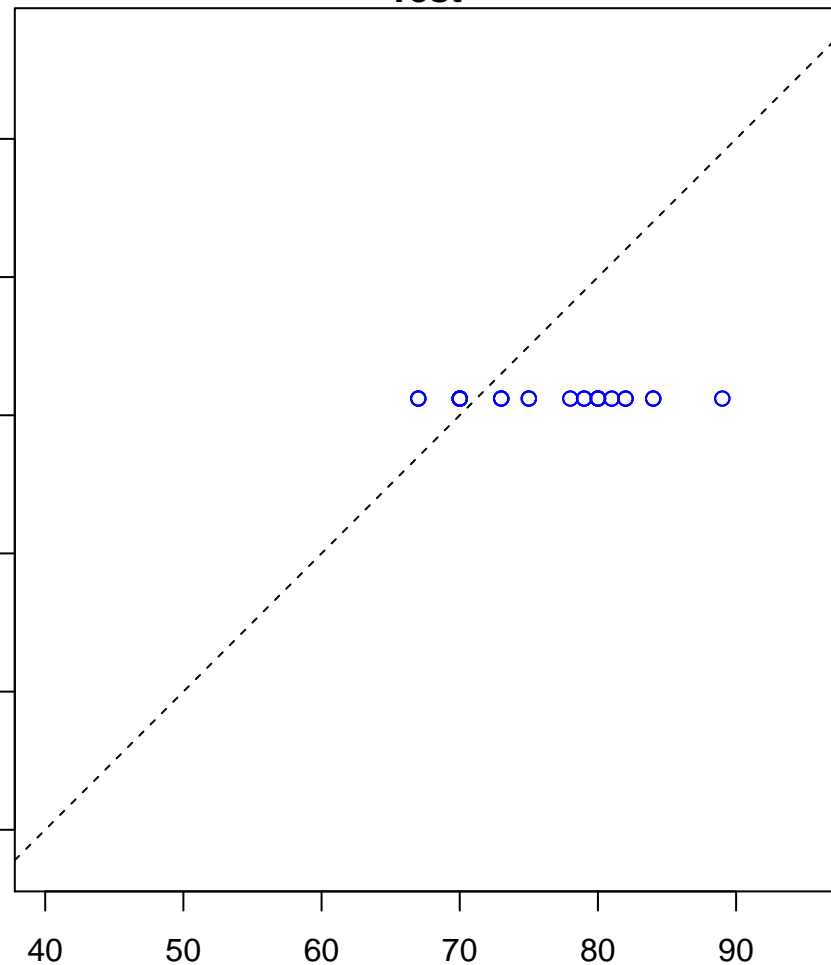


organophosphate metabolic process (Score: 0.823754)

Control

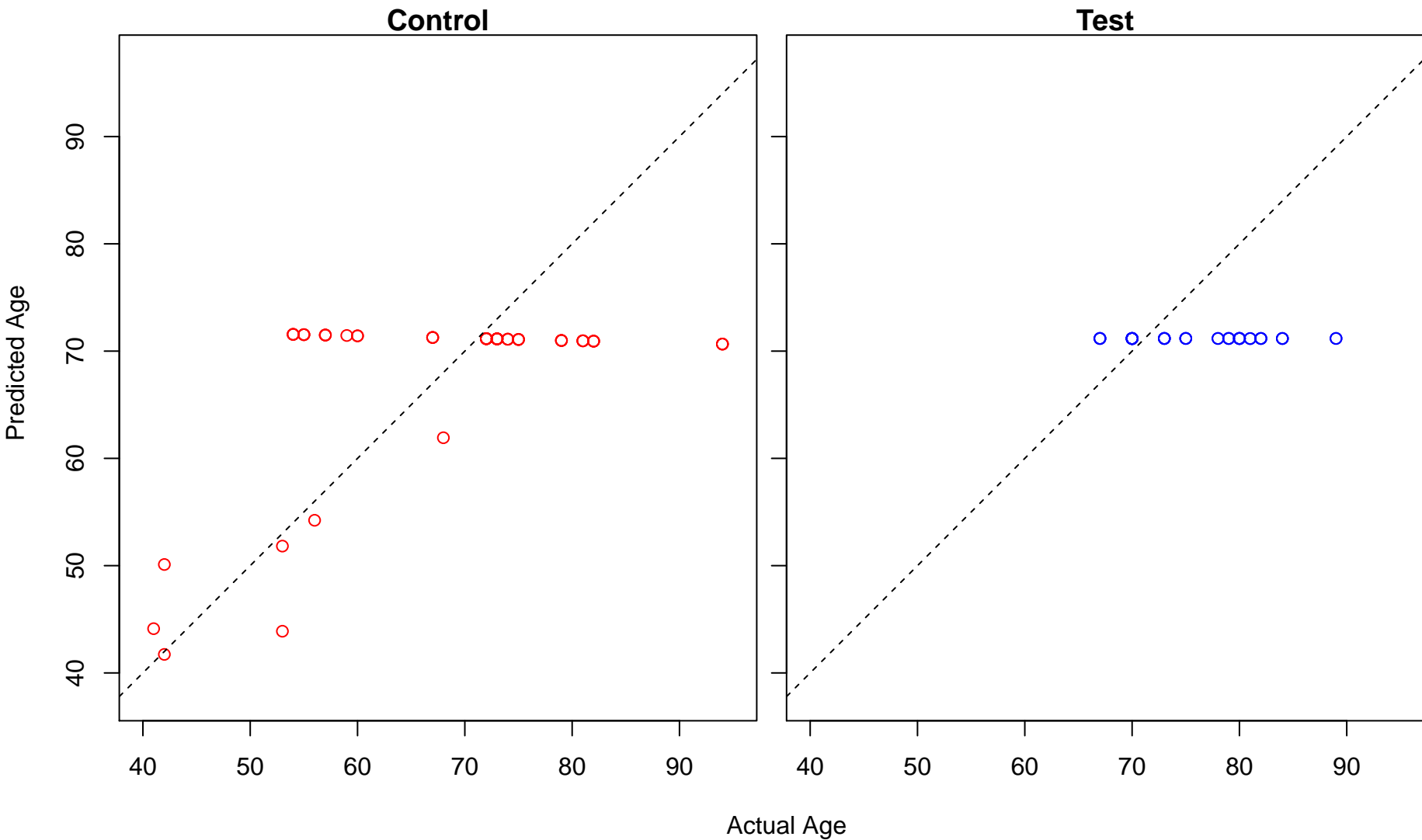


Test

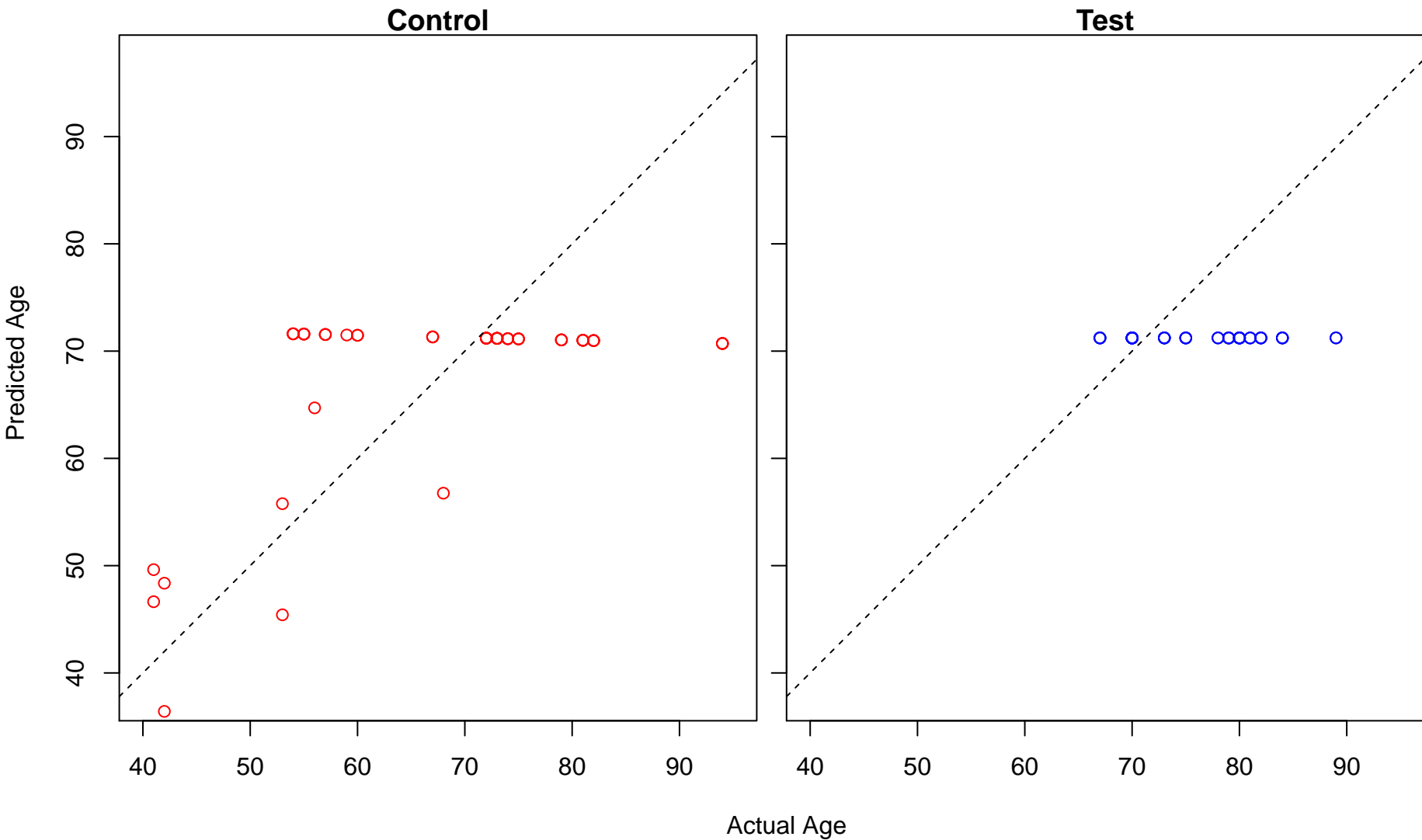


Actual Age

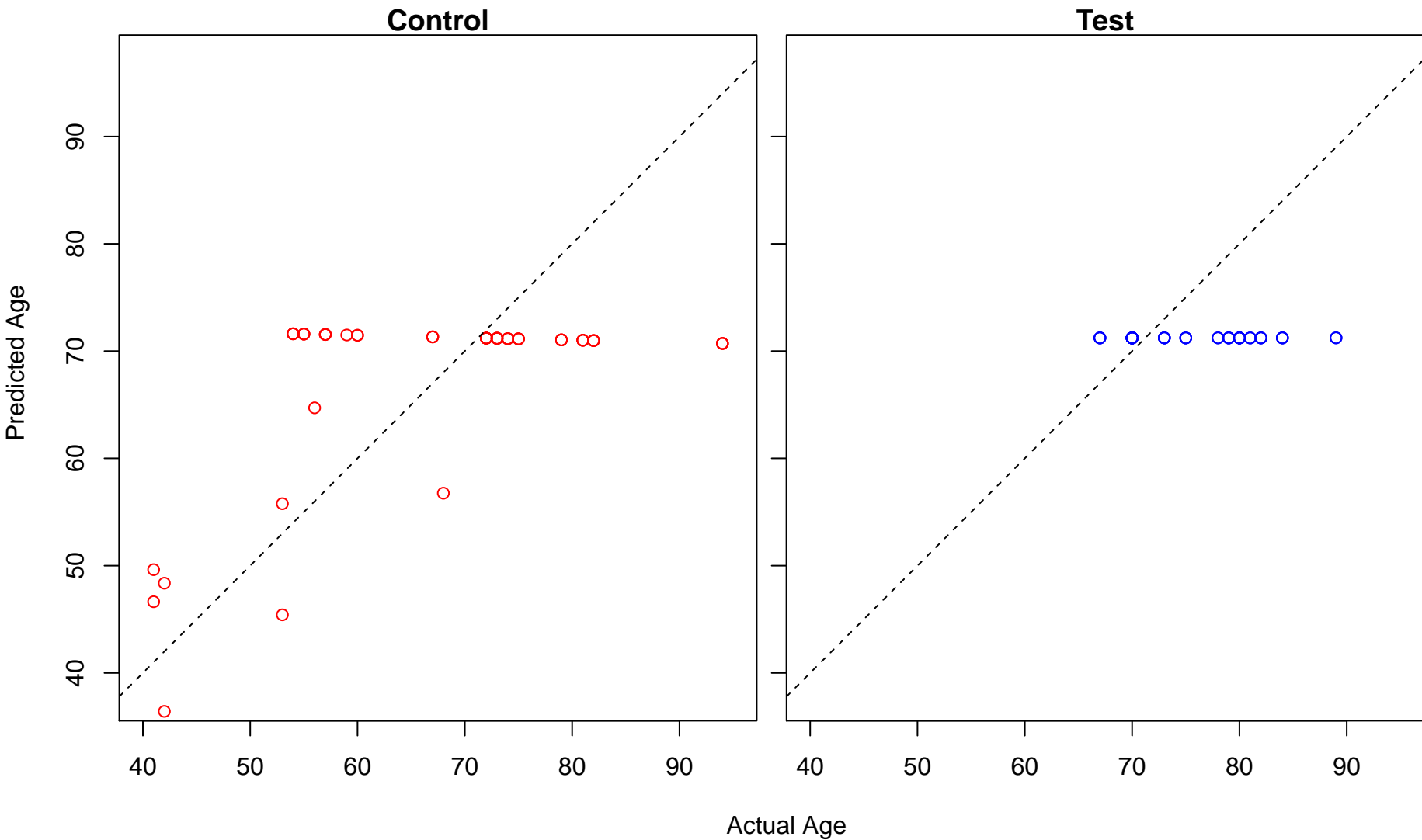
organelle localization (Score: 0.823711)



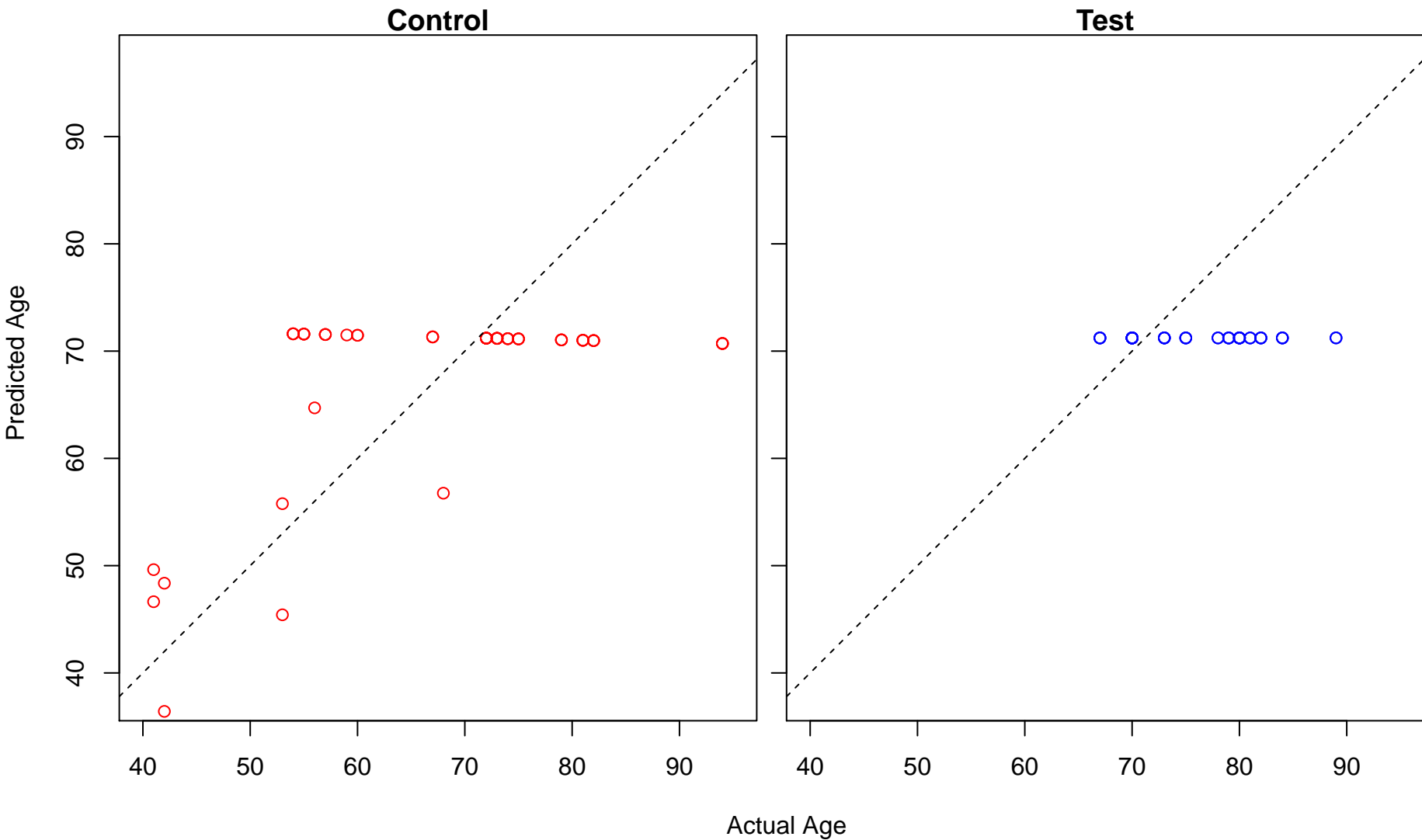
innate immune response activating cell surface receptor signaling pathway (Score: 0.823697)



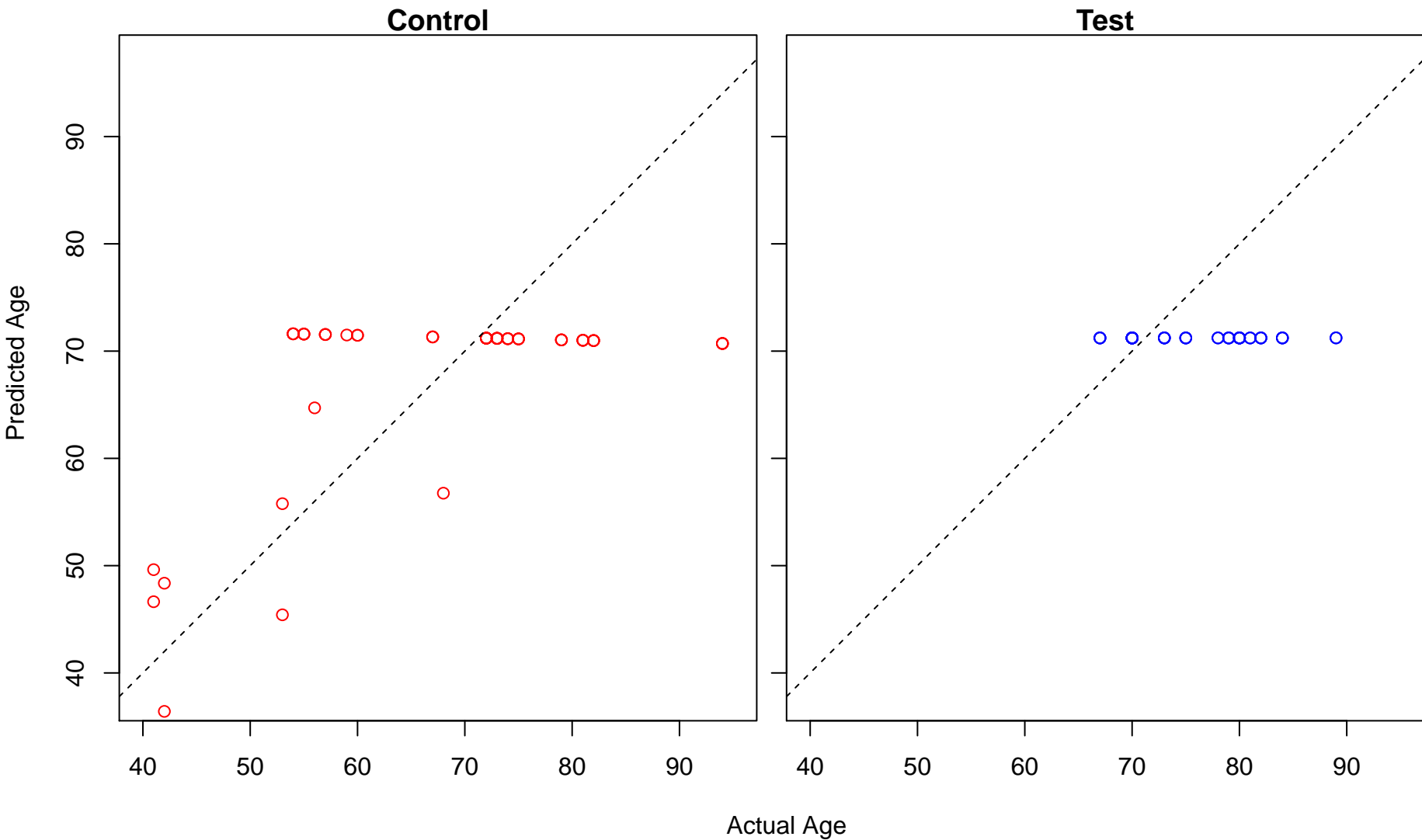
stimulatory C-type lectin receptor signaling pathway (Score: 0.823697)



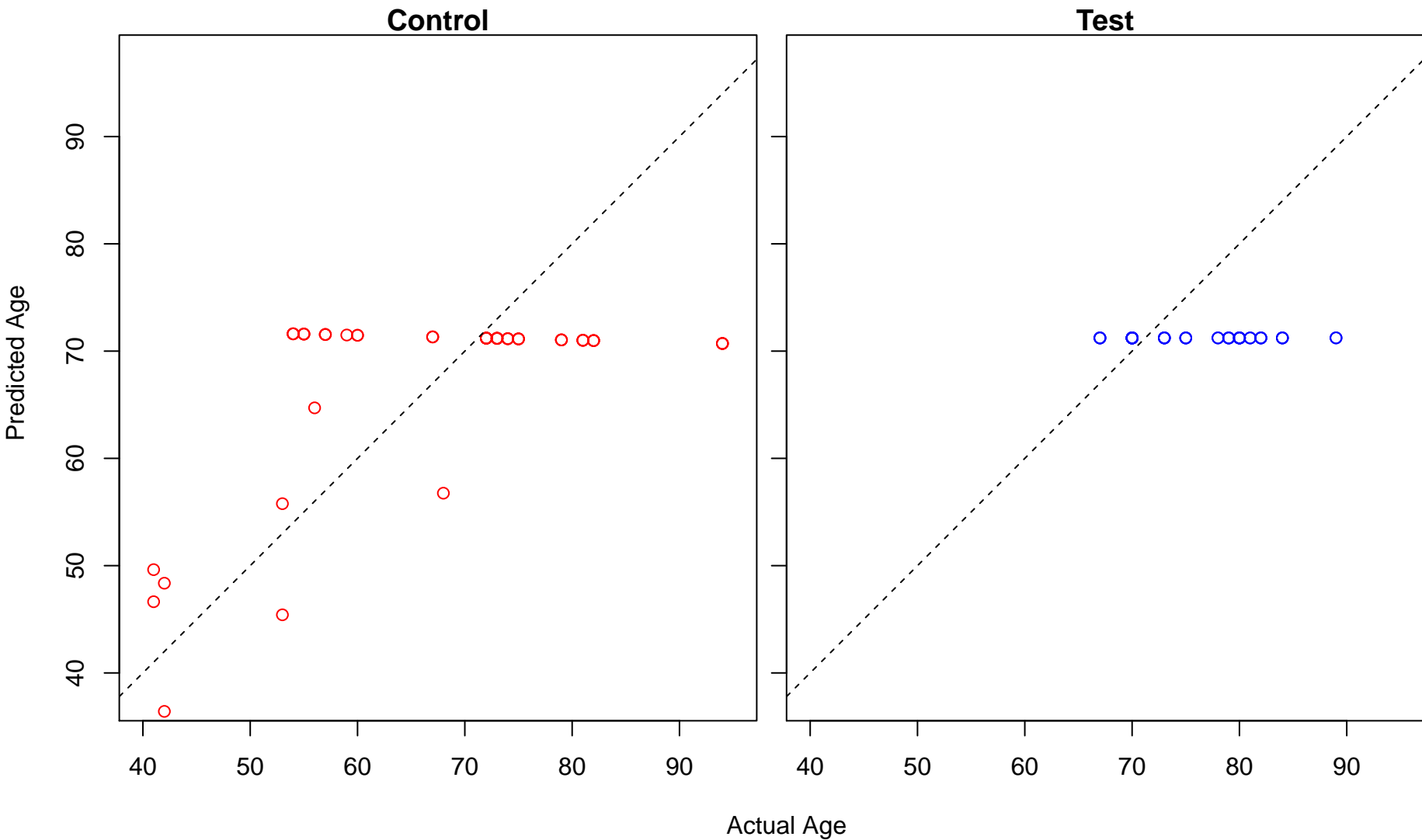
negative regulation of G2/M transition of mitotic cell cycle (Score: 0.823697)



SCF-dependent proteasomal ubiquitin-dependent protein catabolic process (Score: 0.823697)

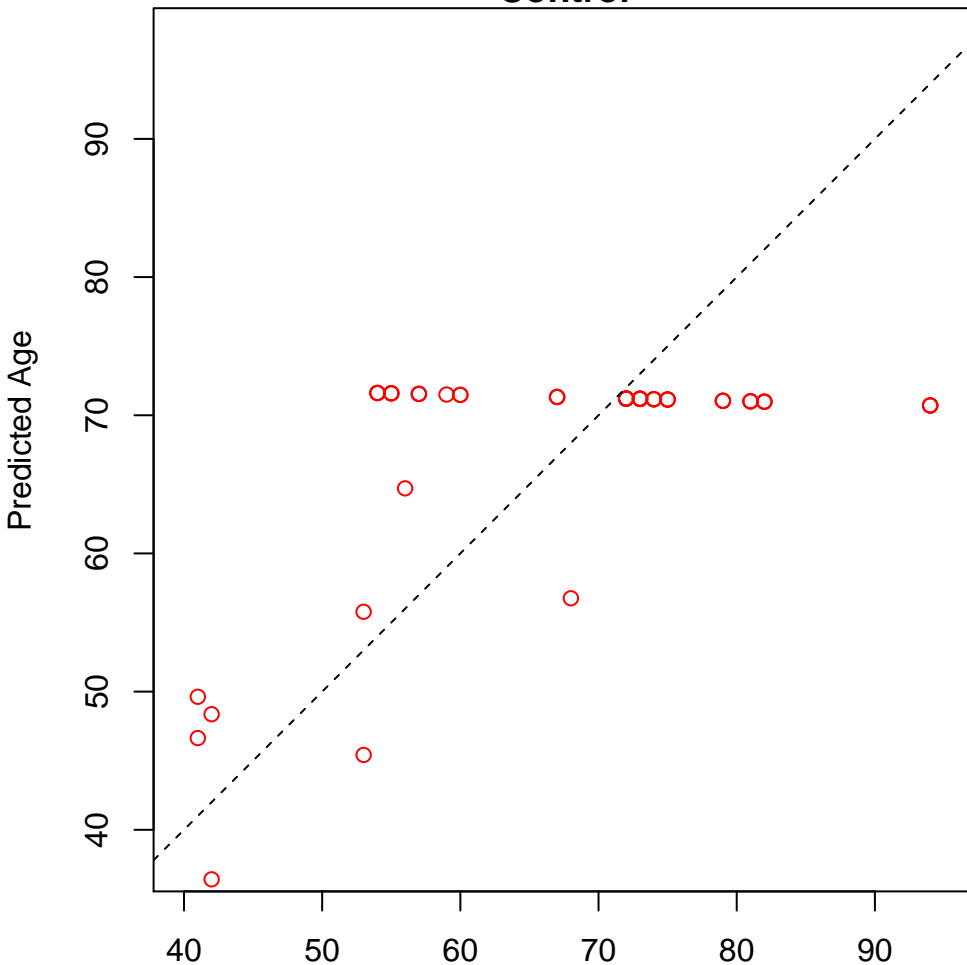


NIK/NF-kappaB signaling (Score: 0.823697)

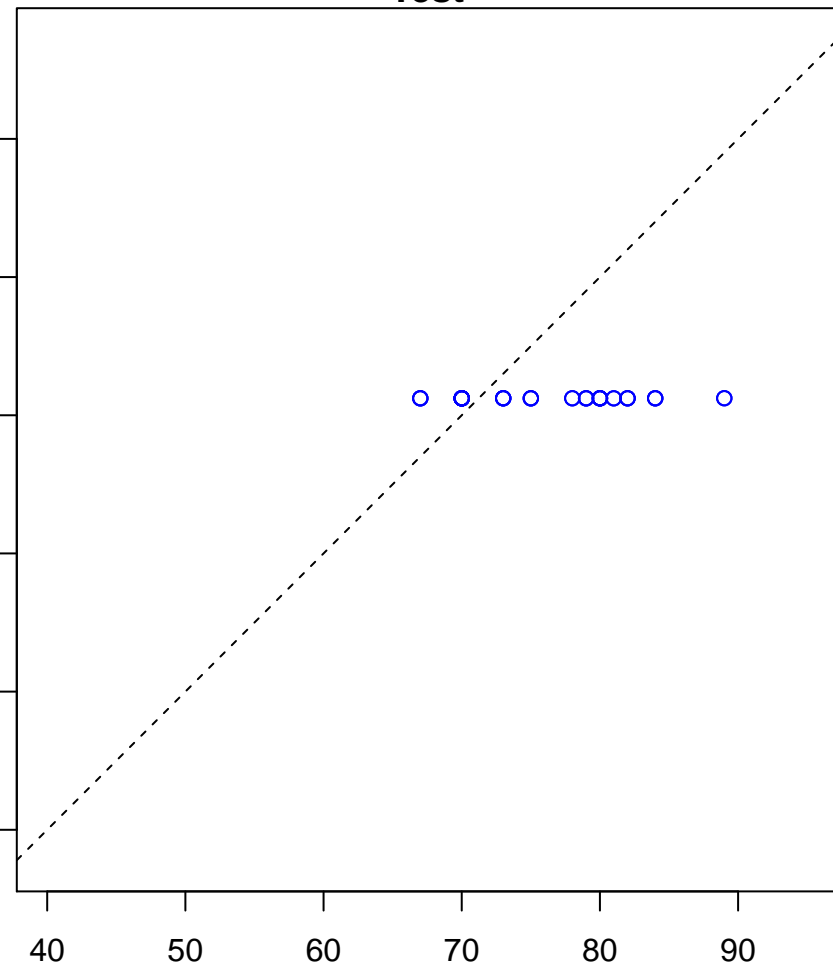


Fc-epsilon receptor signaling pathway (Score: 0.823697)

Control

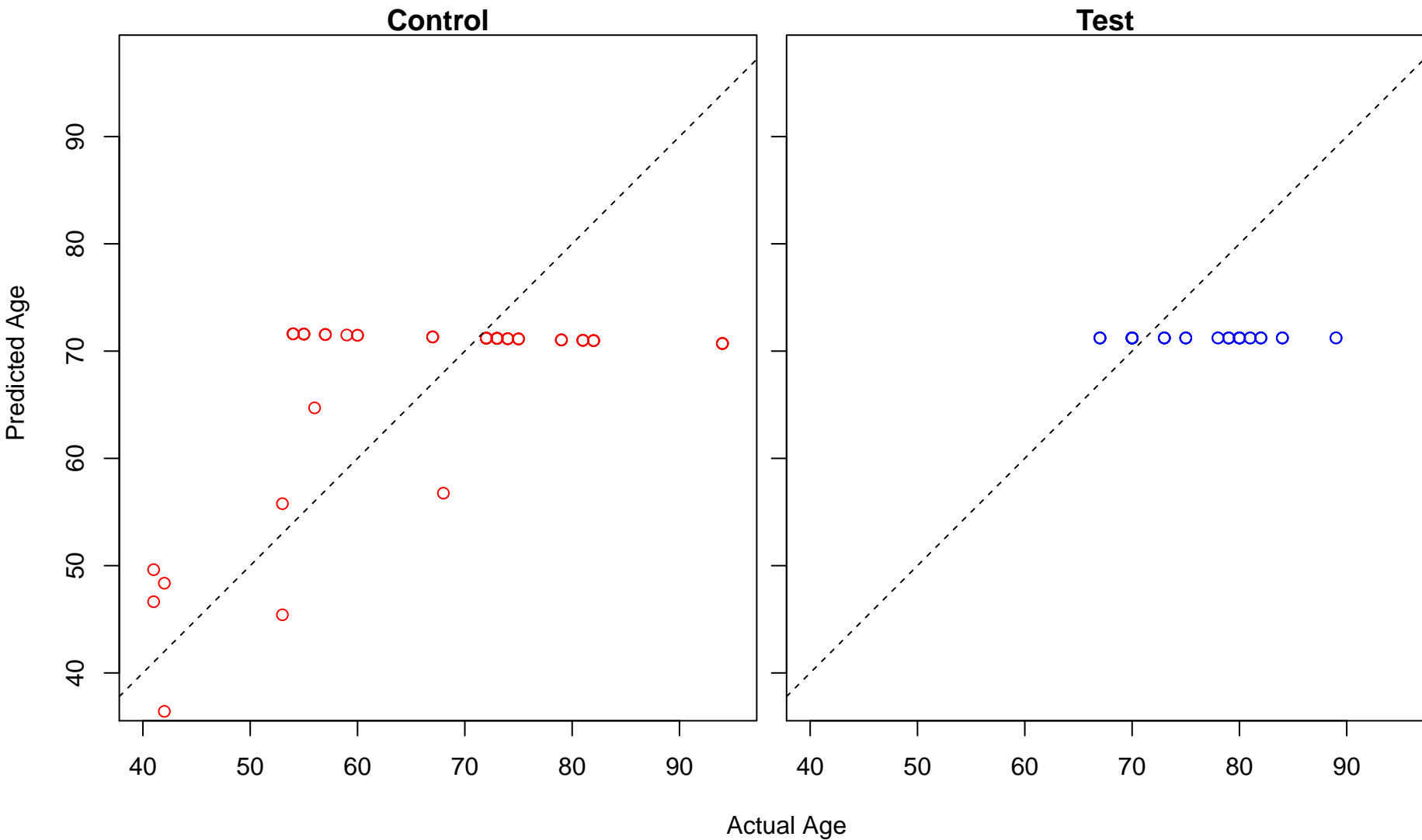


Test



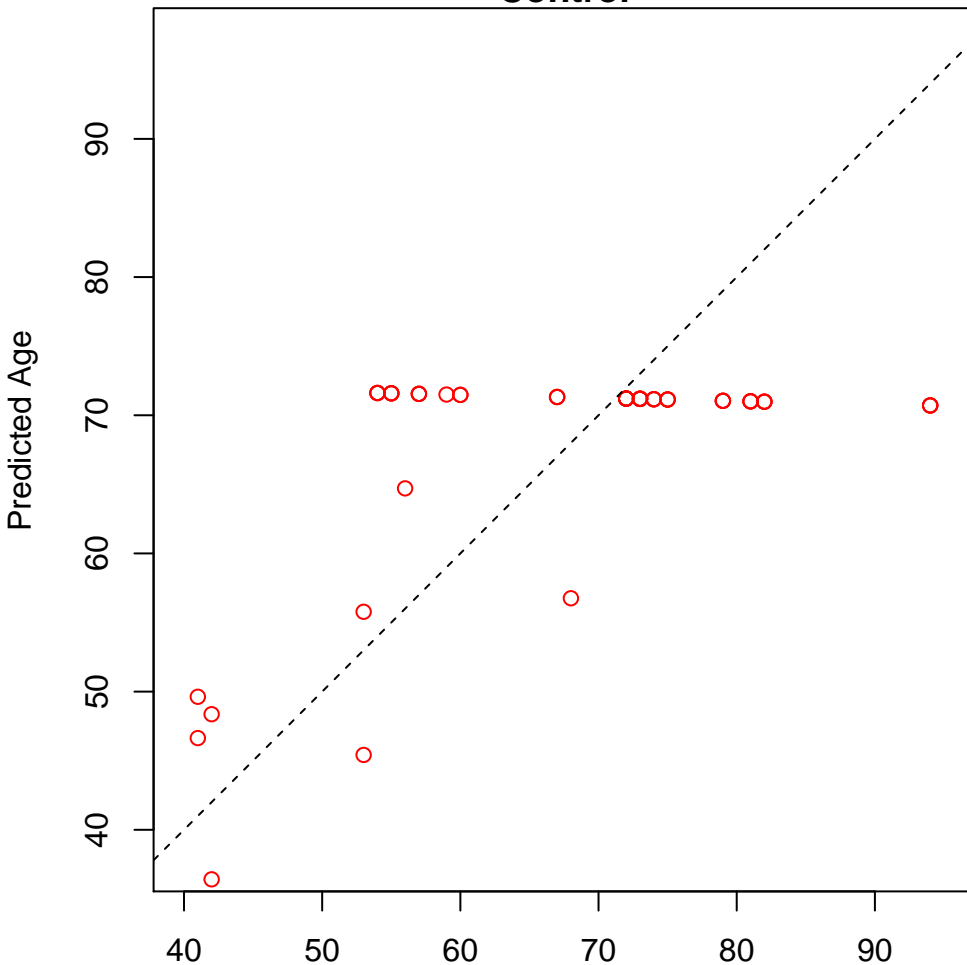
Actual Age

antigen receptor-mediated signaling pathway (Score: 0.823697)

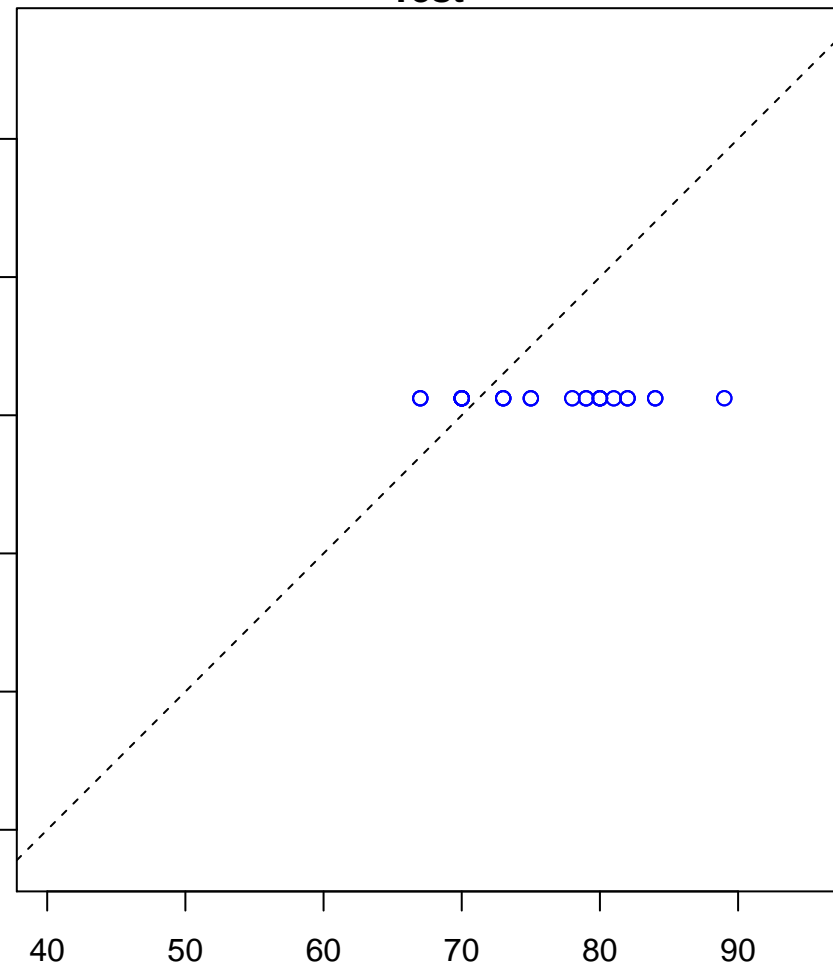


T cell receptor signaling pathway (Score: 0.823697)

Control

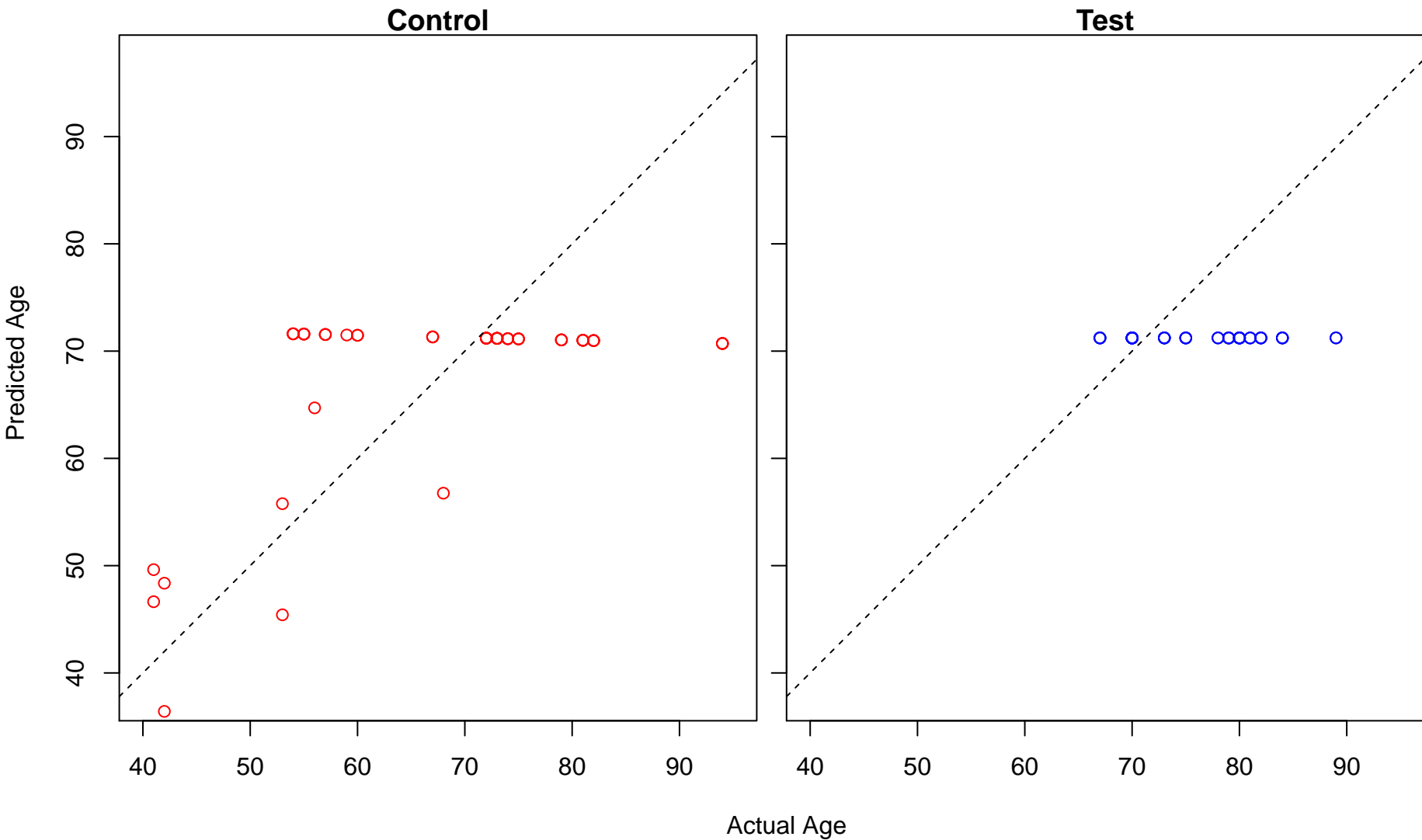


Test

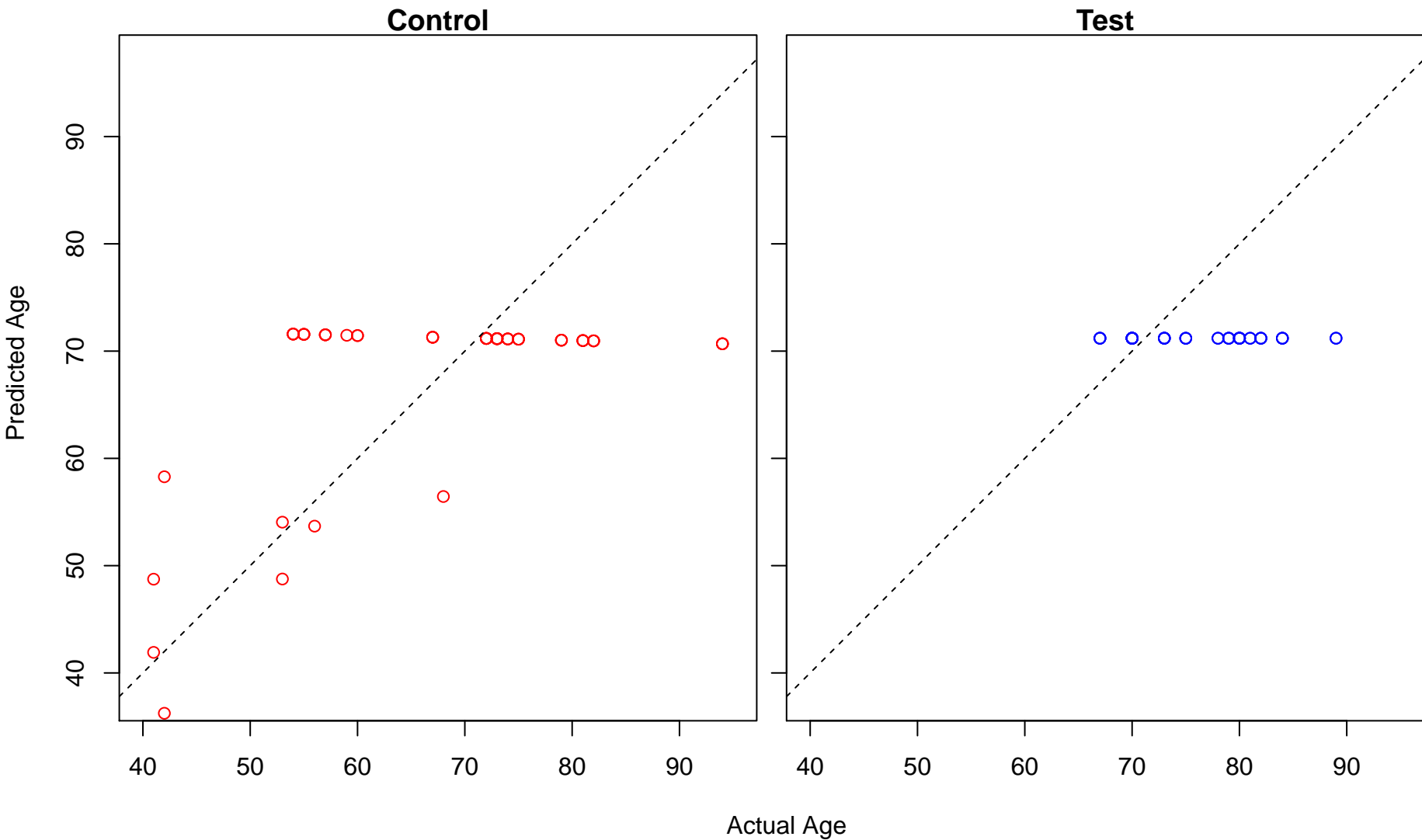


Actual Age

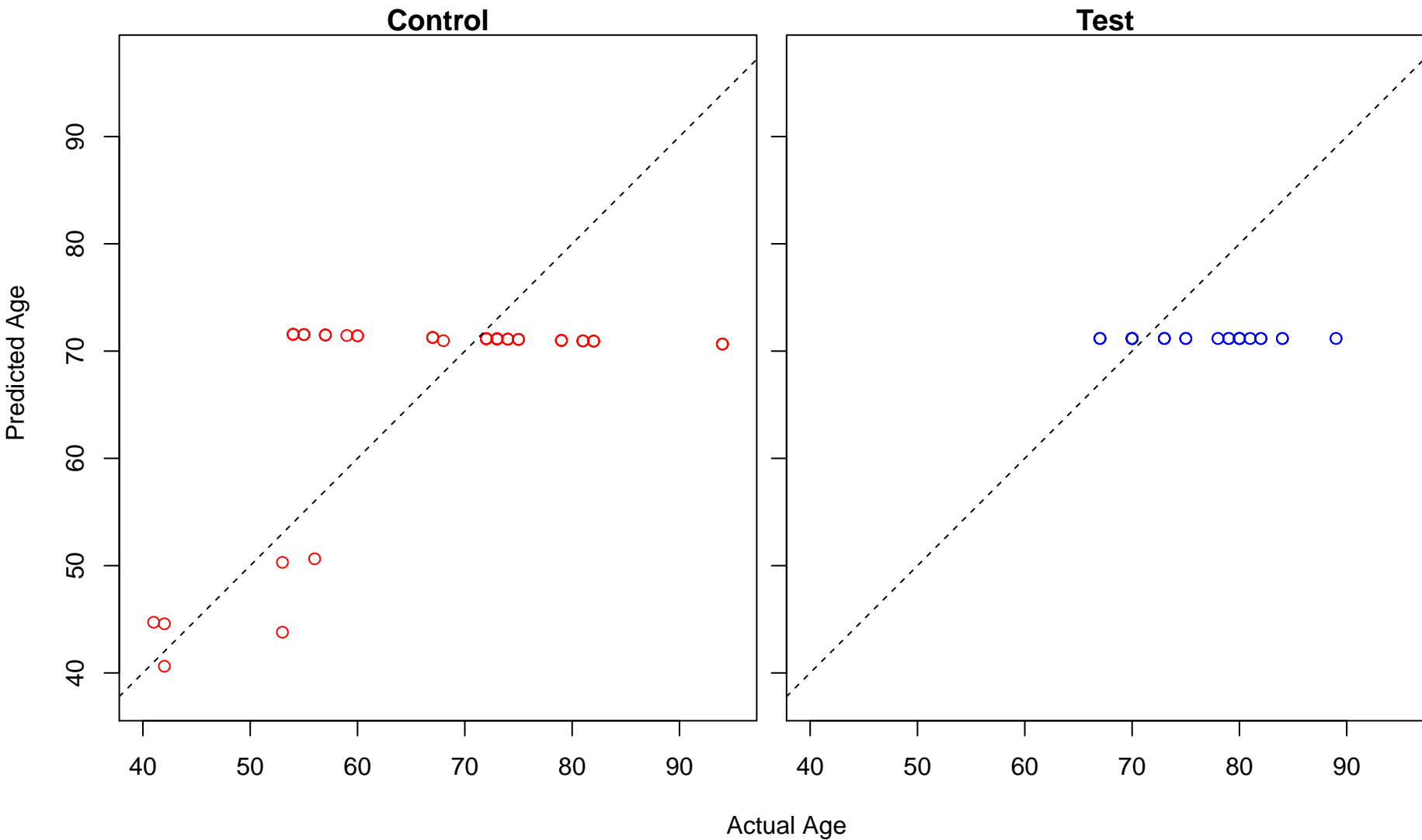
negative regulation of cell cycle G2/M phase transition (Score: 0.823697)



cellular modified amino acid metabolic process (Score: 0.823628)

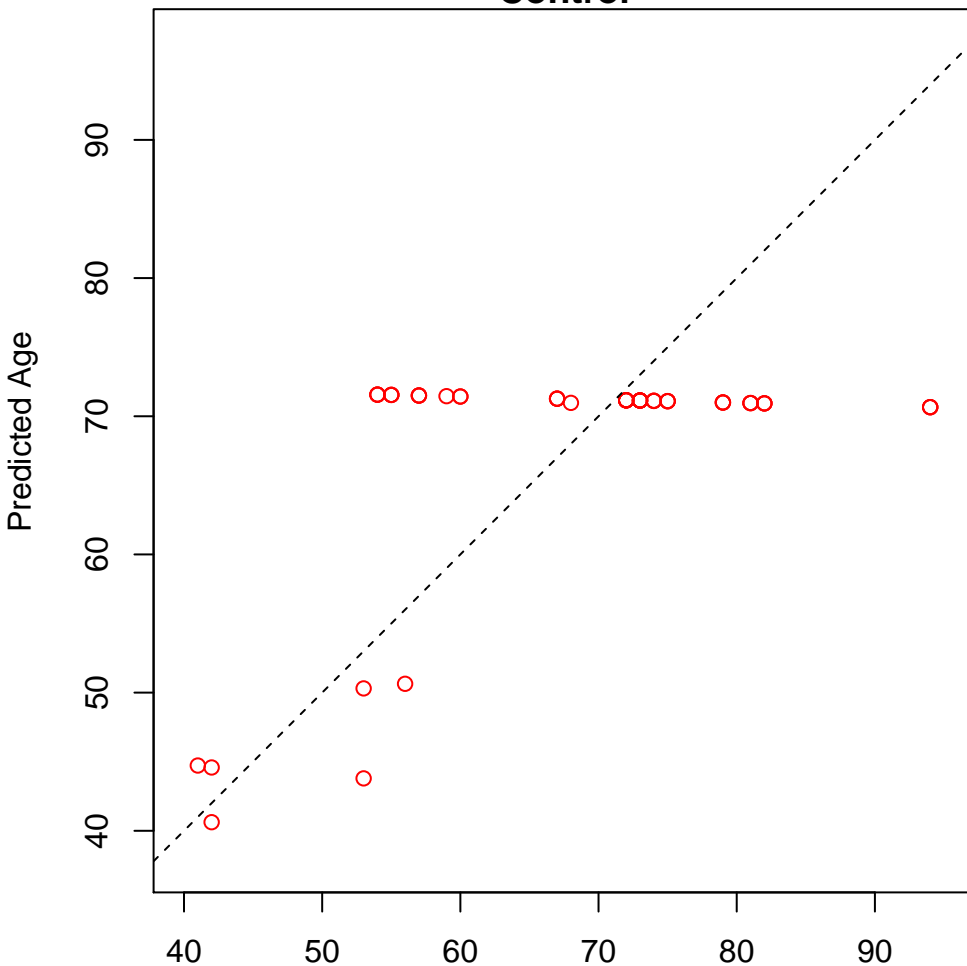


response to biotic stimulus (Score: 0.823467)

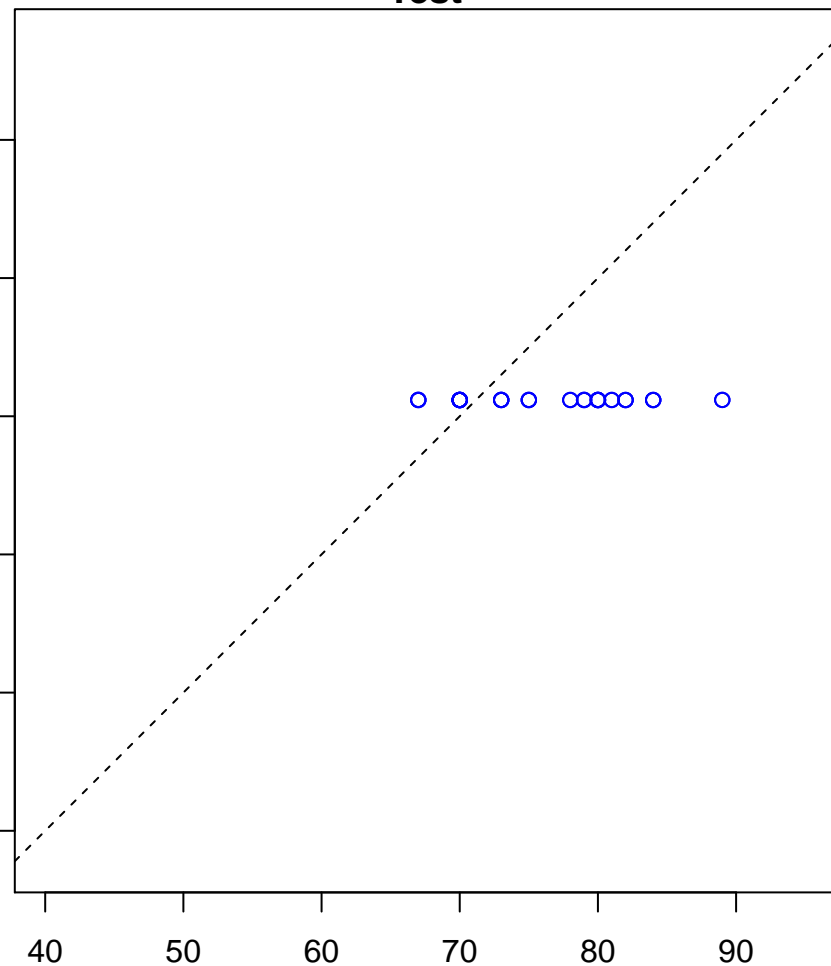


response to external biotic stimulus (Score: 0.823467)

Control



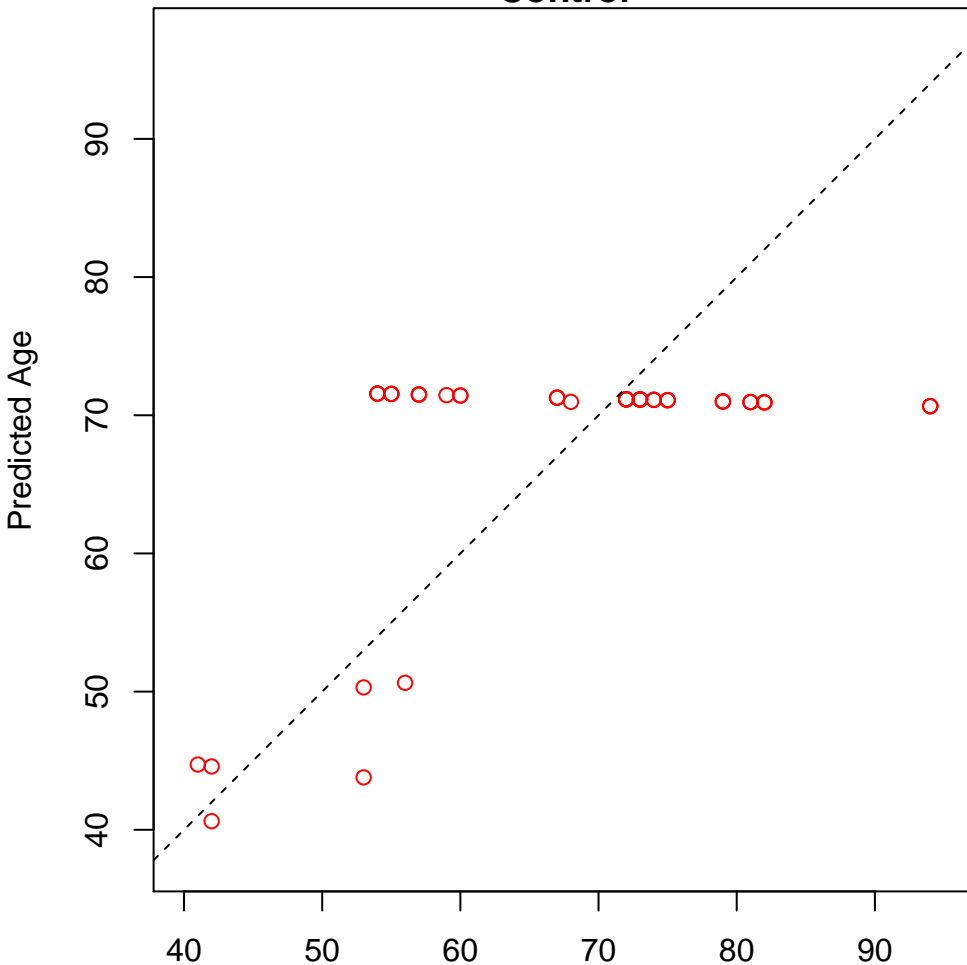
Test



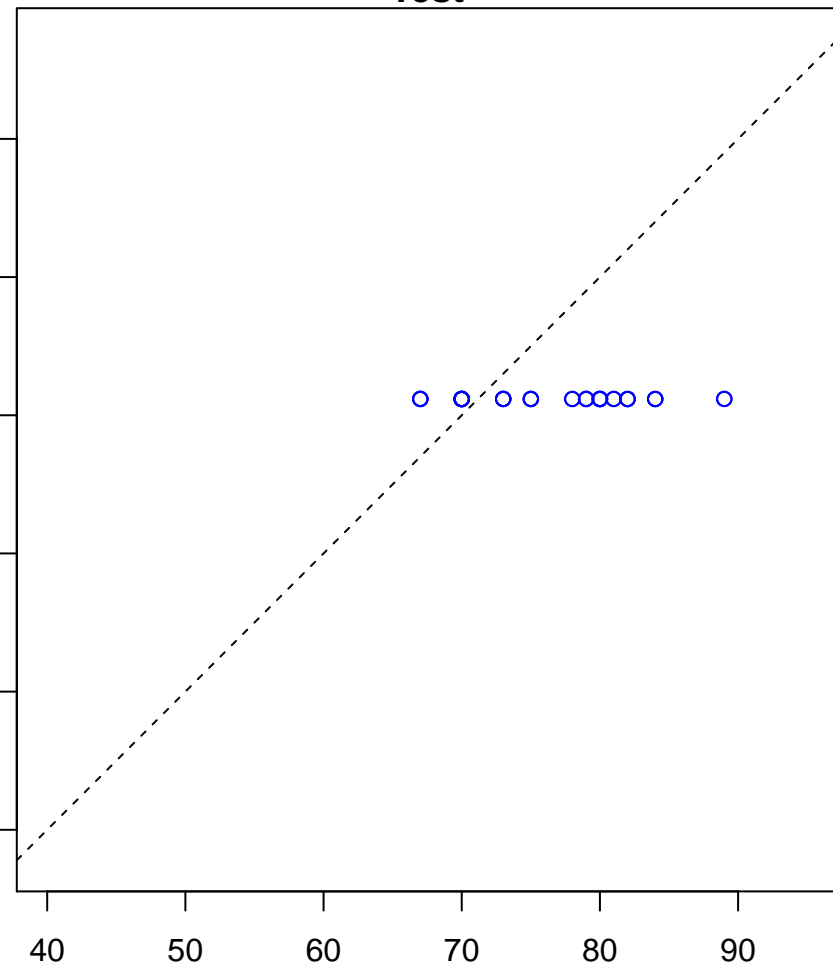
Actual Age

response to other organism (Score: 0.823467)

Control

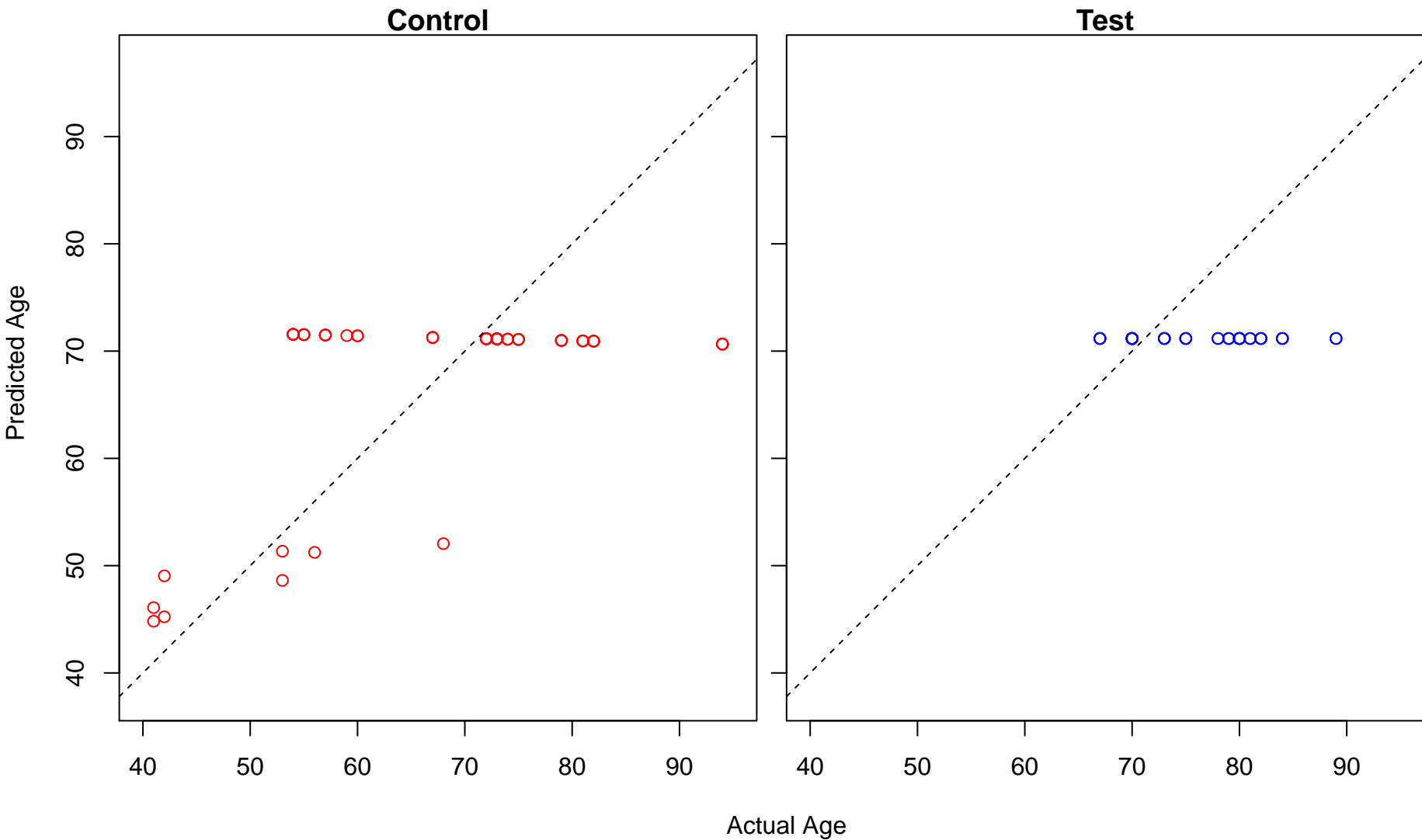


Test



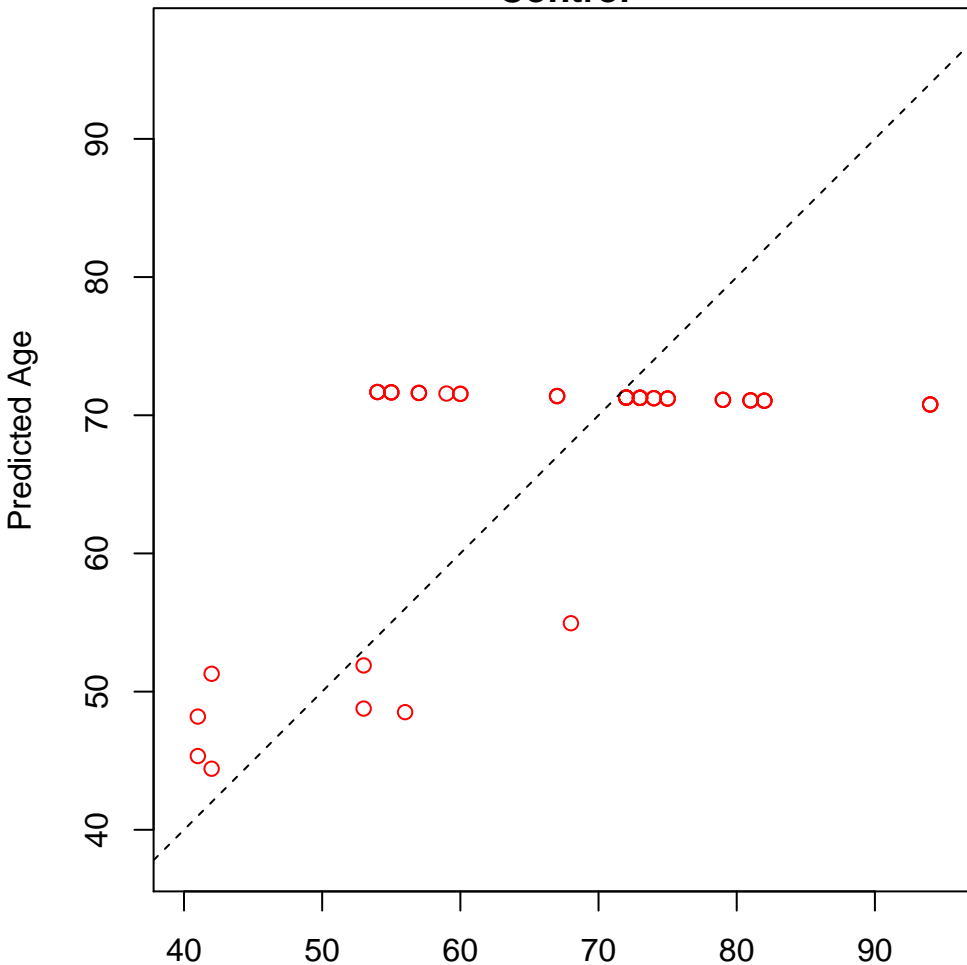
Actual Age

response to stress (Score: 0.823447)

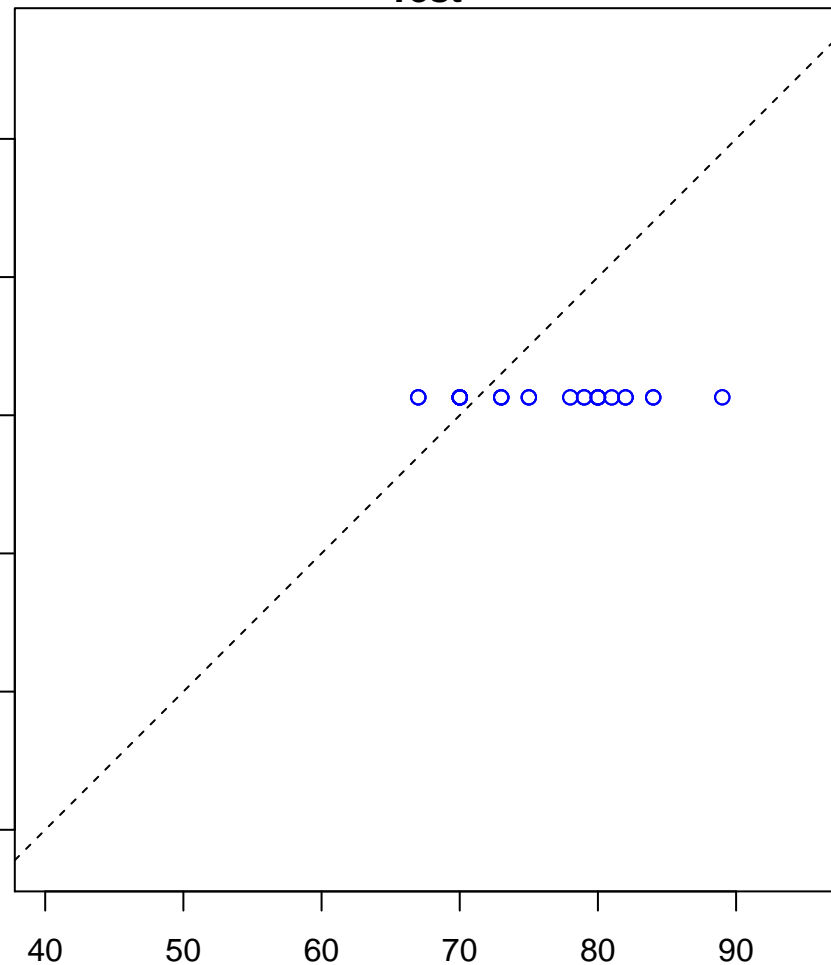


epidermal cell differentiation (Score: 0.823434)

Control

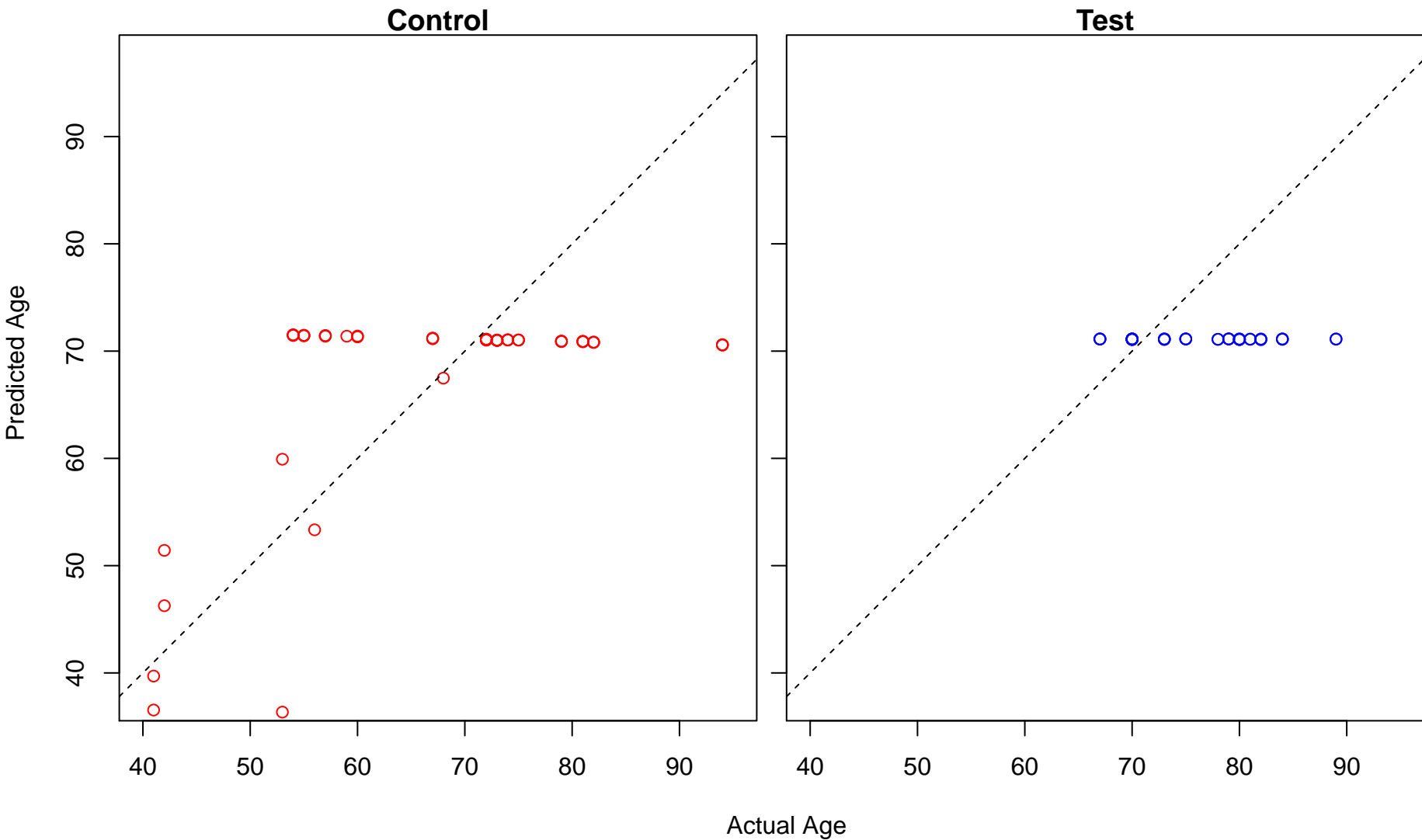


Test



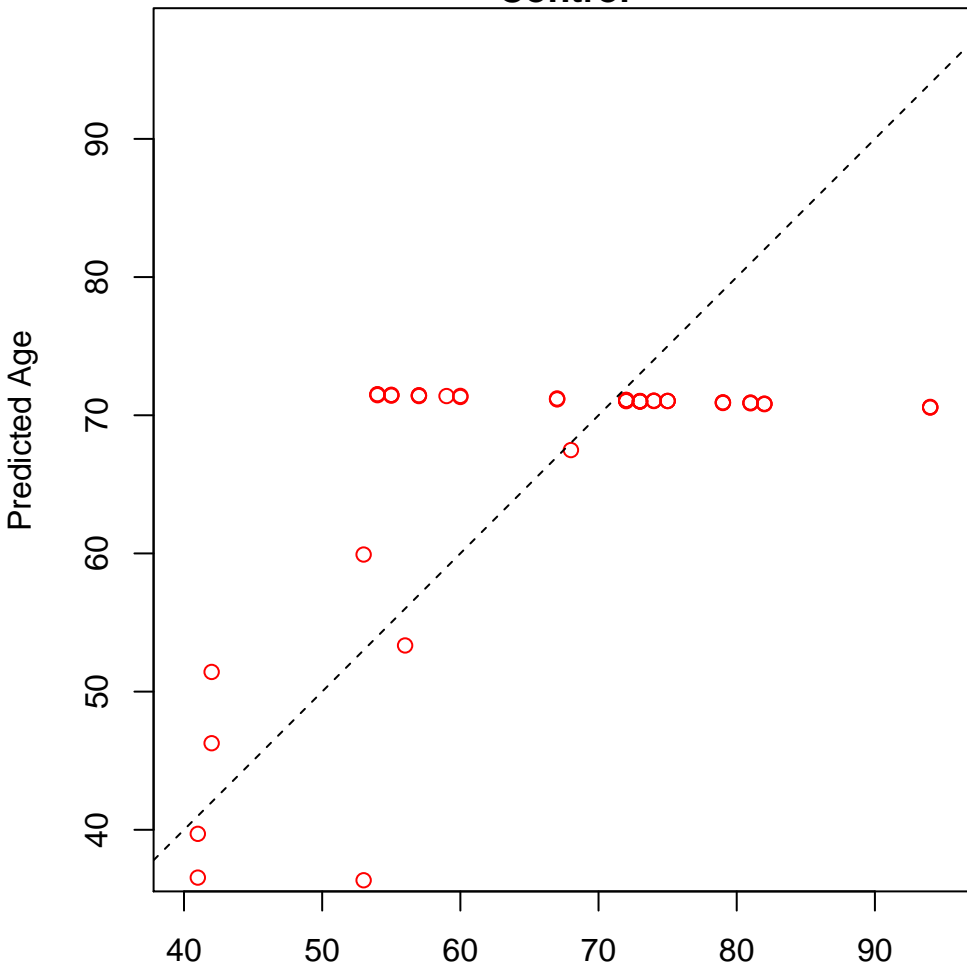
Actual Age

actin filament organization (Score: 0.823145)

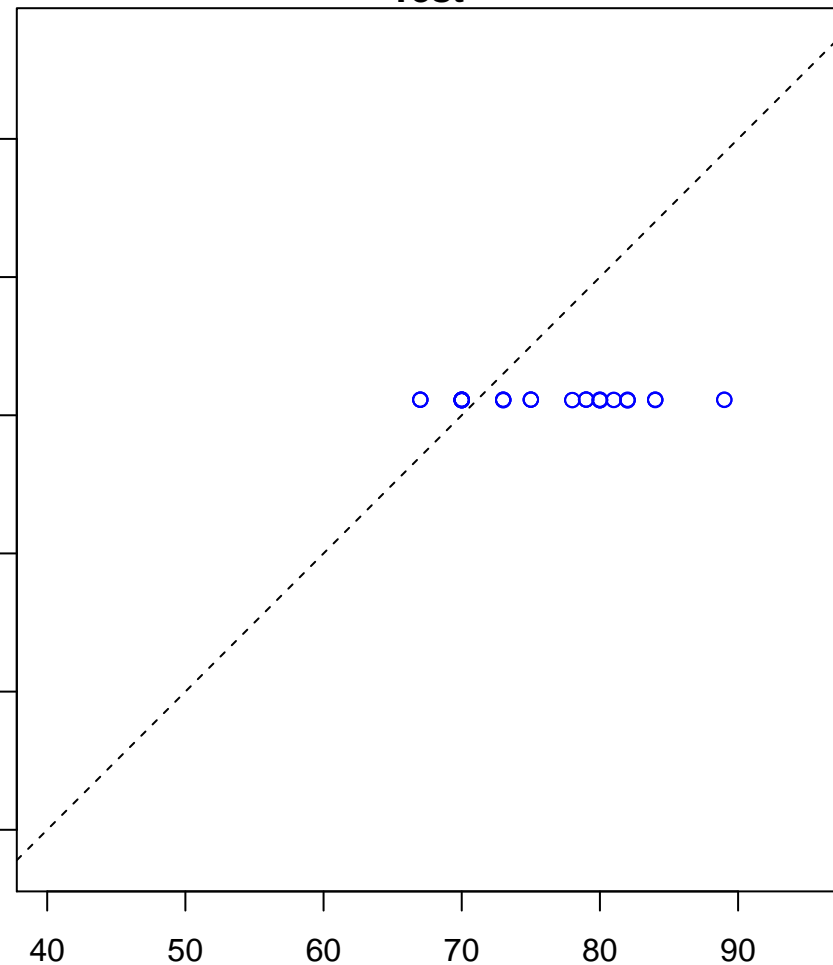


actin cytoskeleton organization (Score: 0.823145)

Control

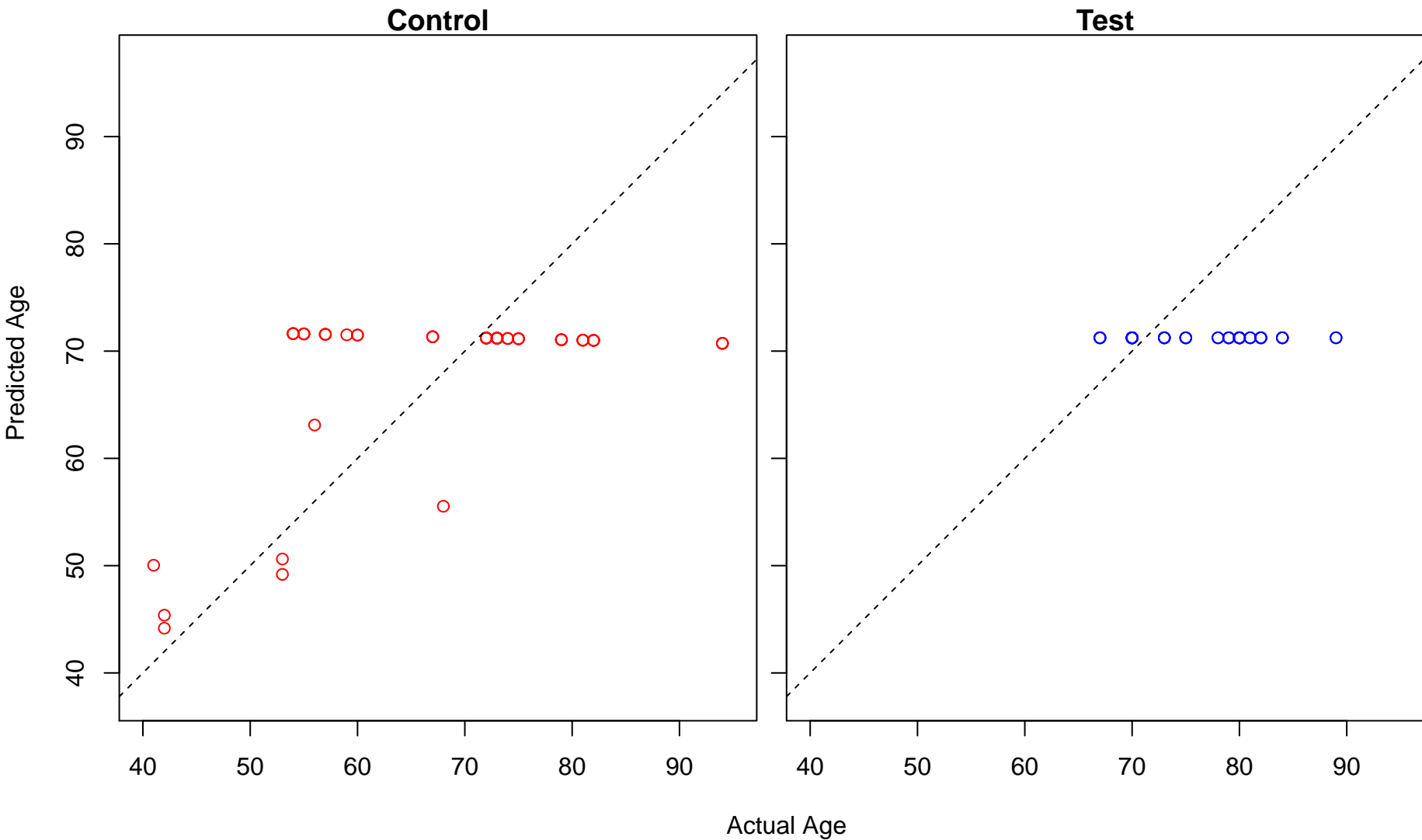


Test

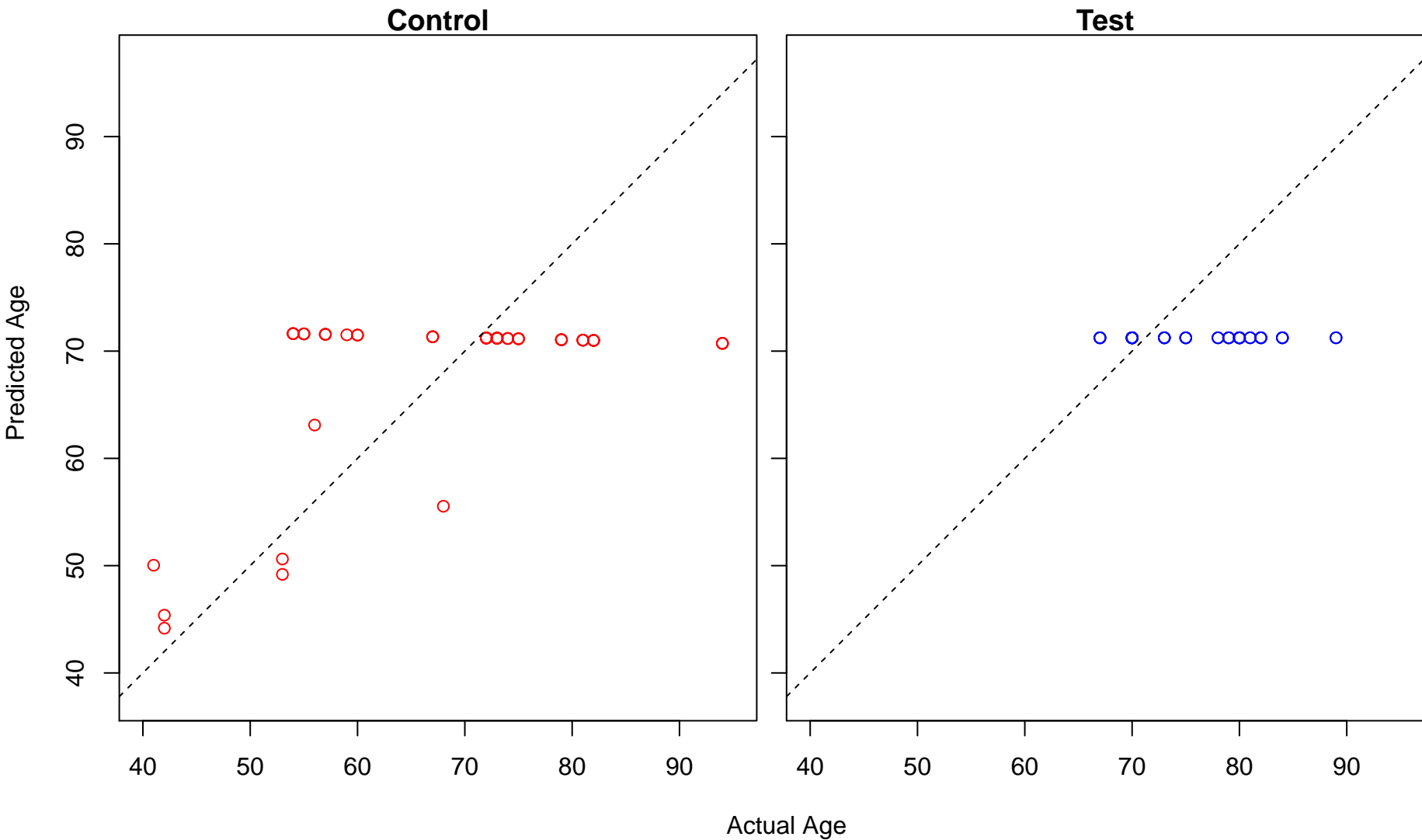


Actual Age

cellular iron ion homeostasis (Score: 0.823118)

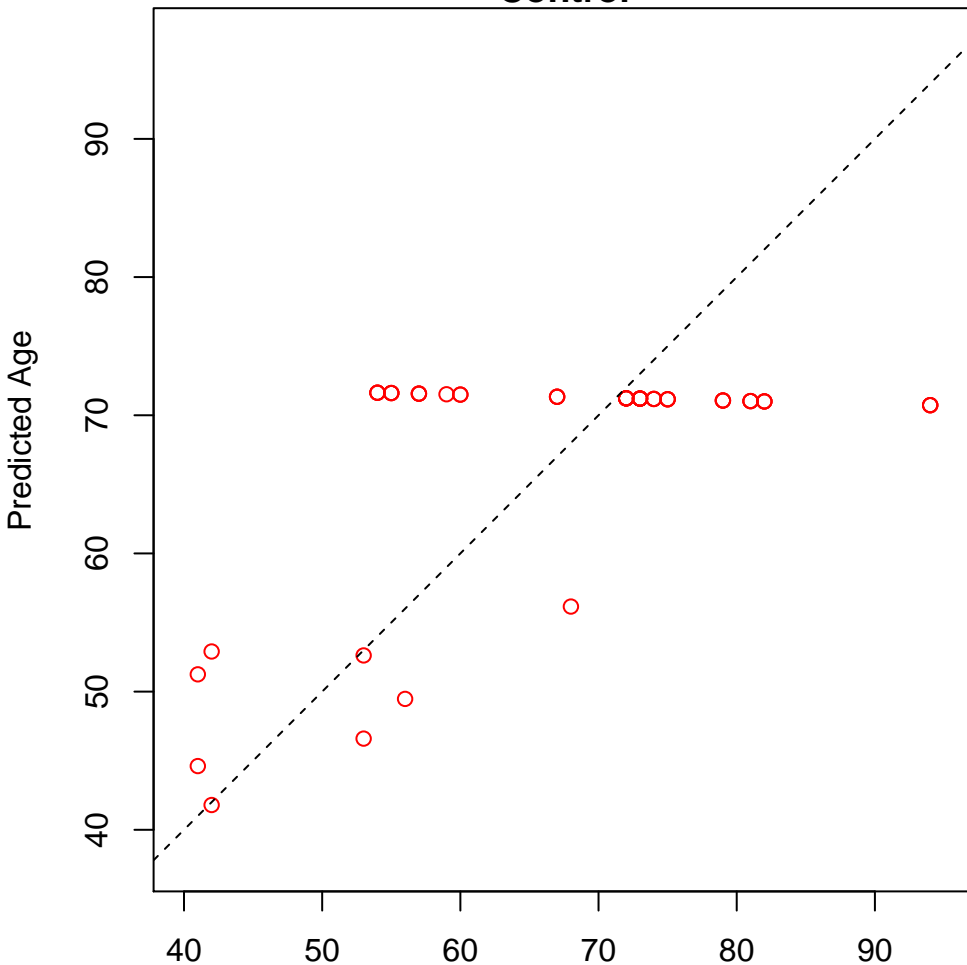


iron ion homeostasis (Score: 0.823118)

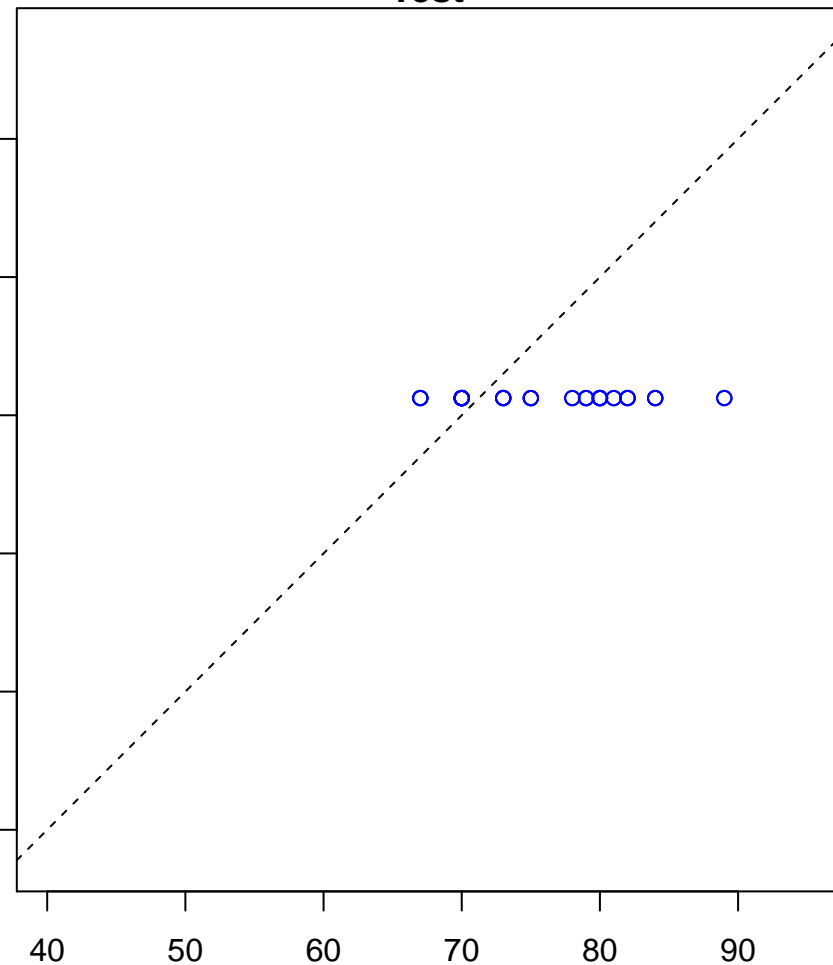


nervous system process (Score: 0.823040)

Control

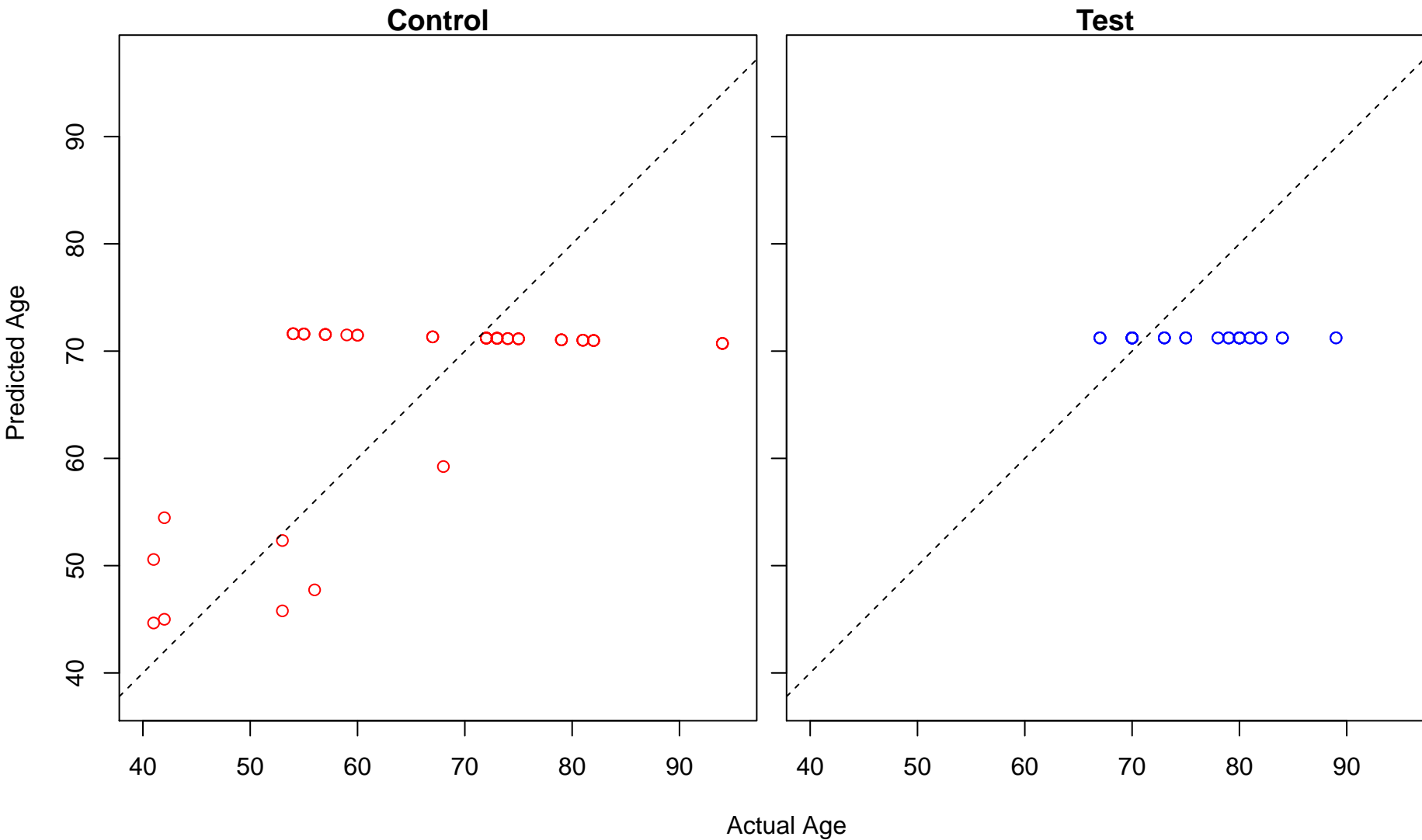


Test



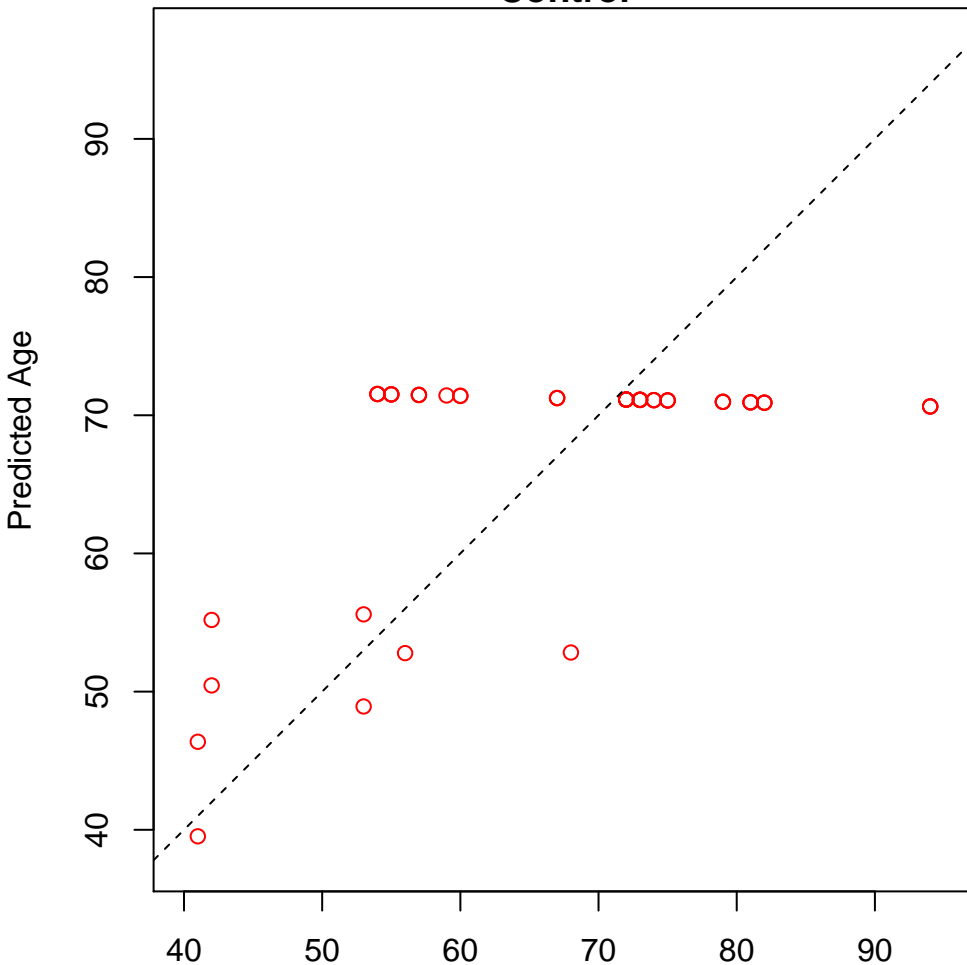
Actual Age

nucleobase-containing small molecule metabolic process (Score: 0.822956)

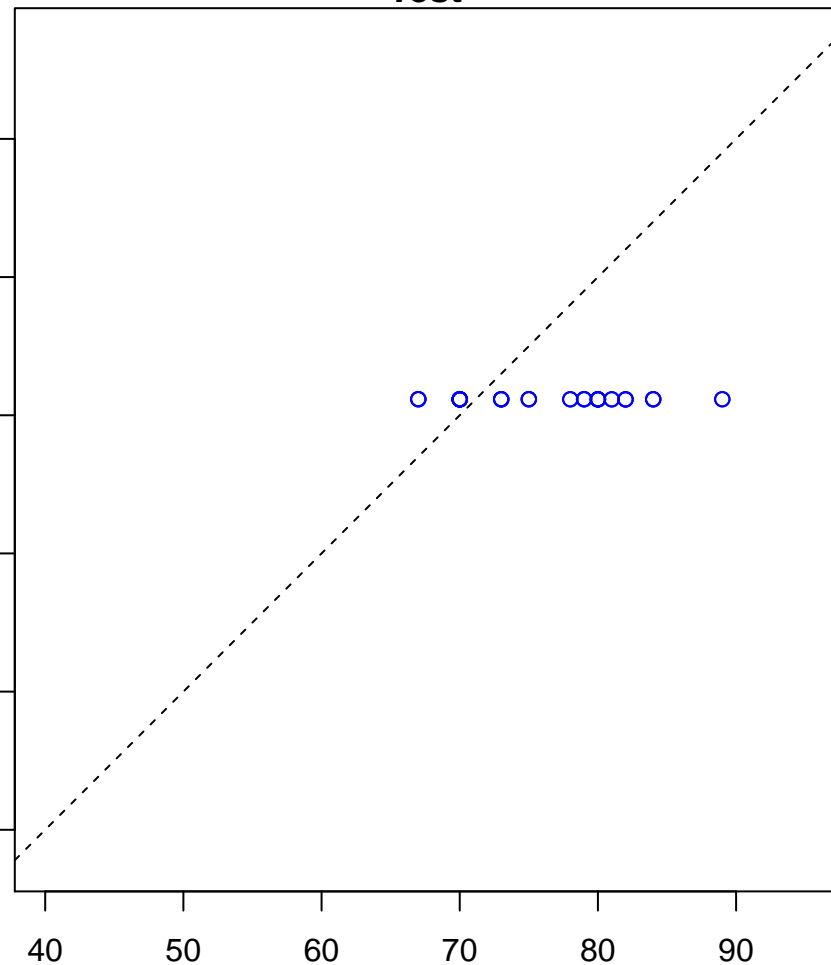


regulation of actin filament polymerization (Score: 0.822822)

Control



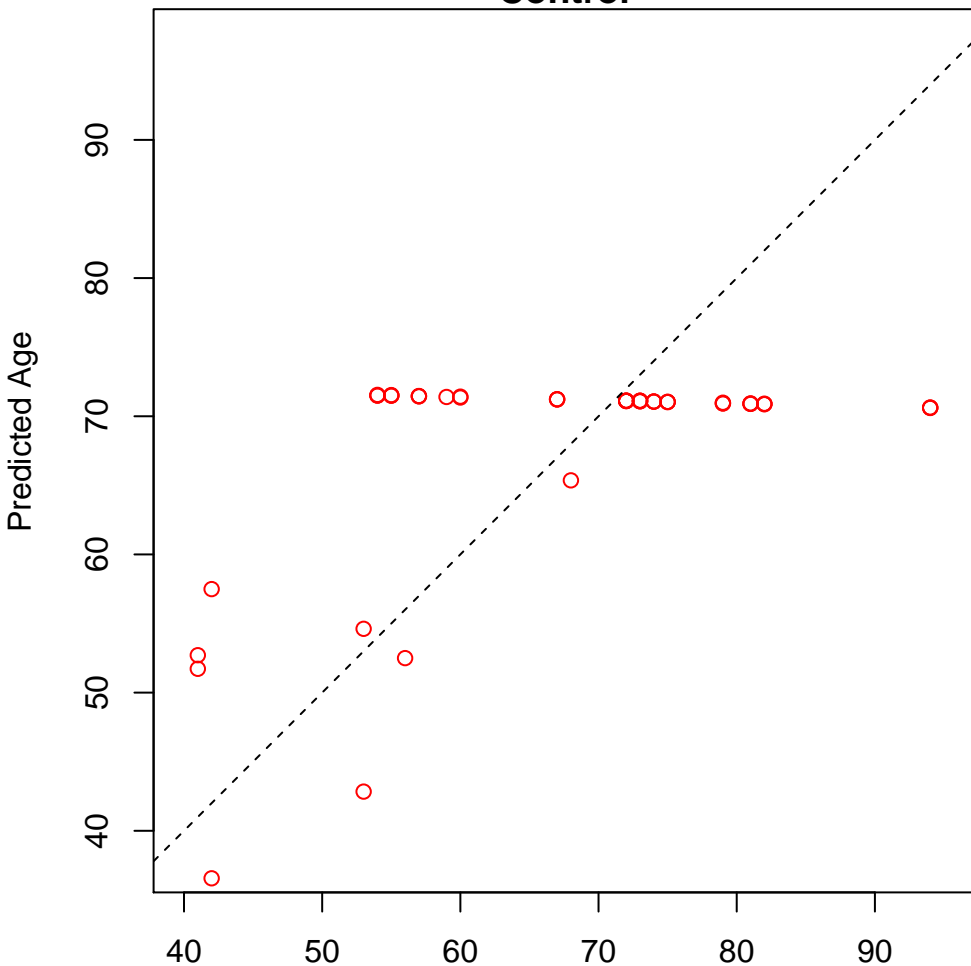
Test



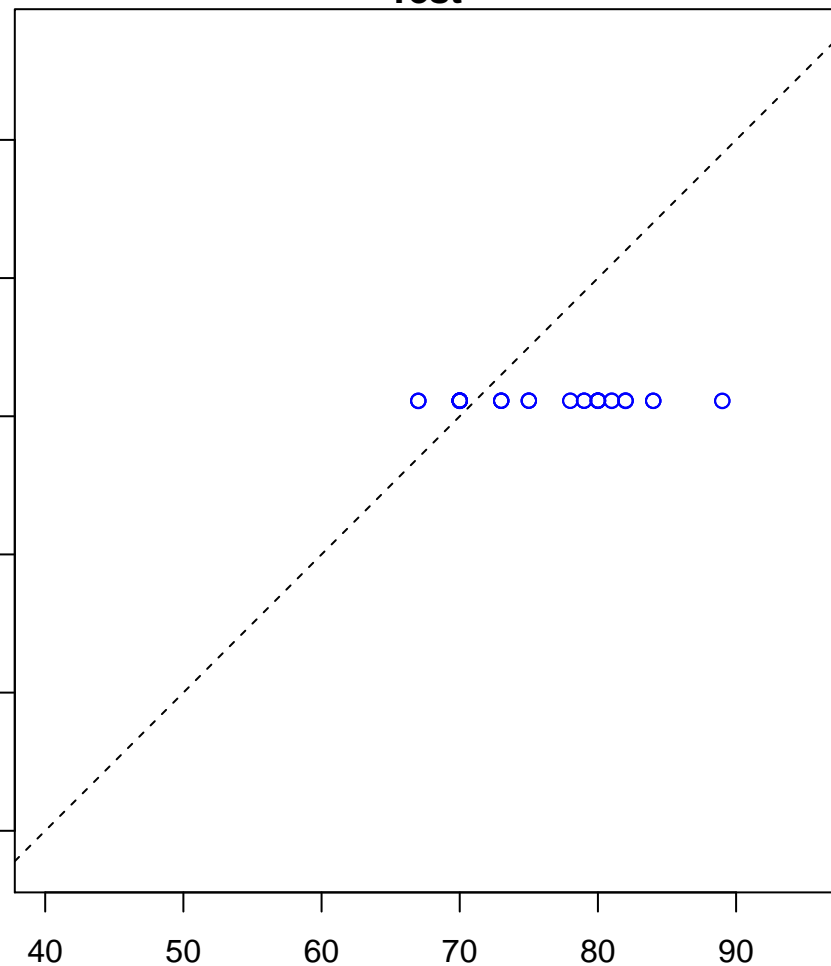
Actual Age

positive regulation of cell cycle process (Score: 0.822755)

Control

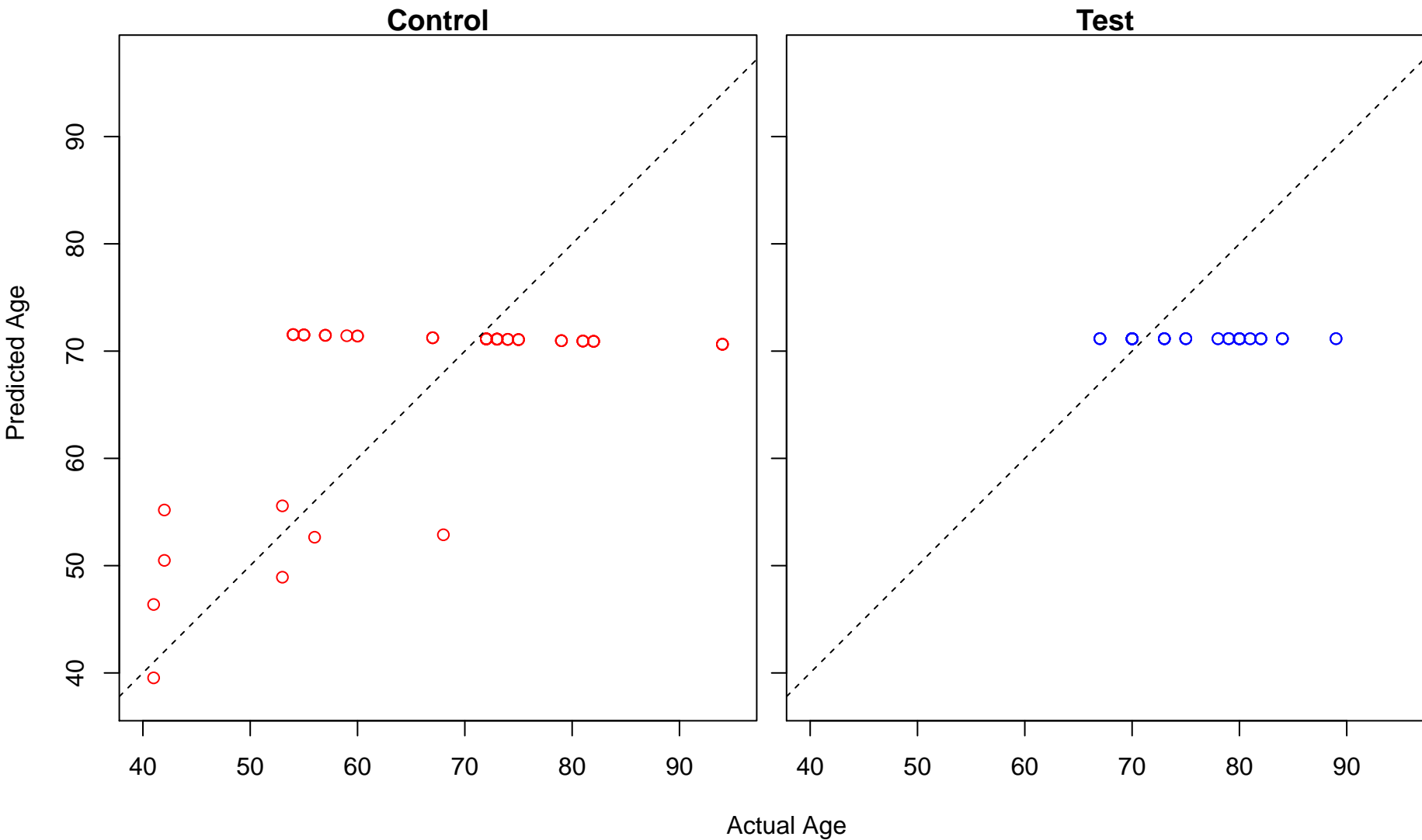


Test



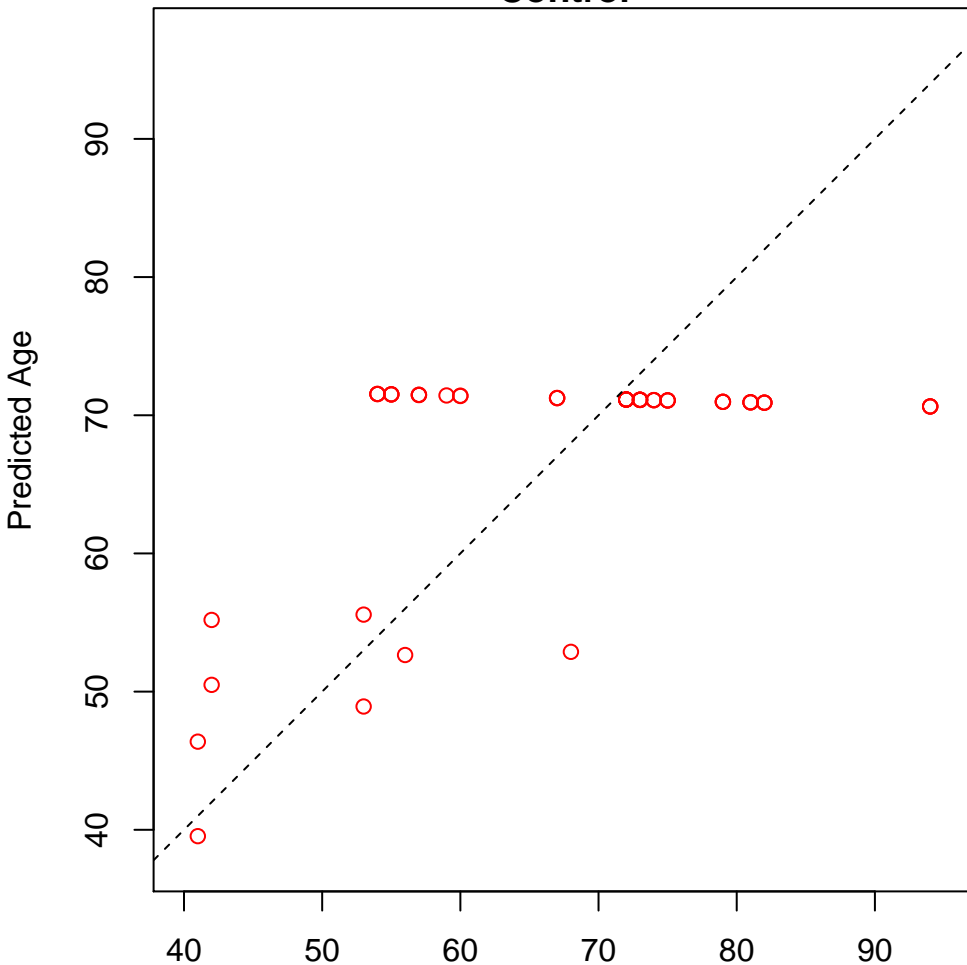
Actual Age

regulation of actin polymerization or depolymerization (Score: 0.822723)

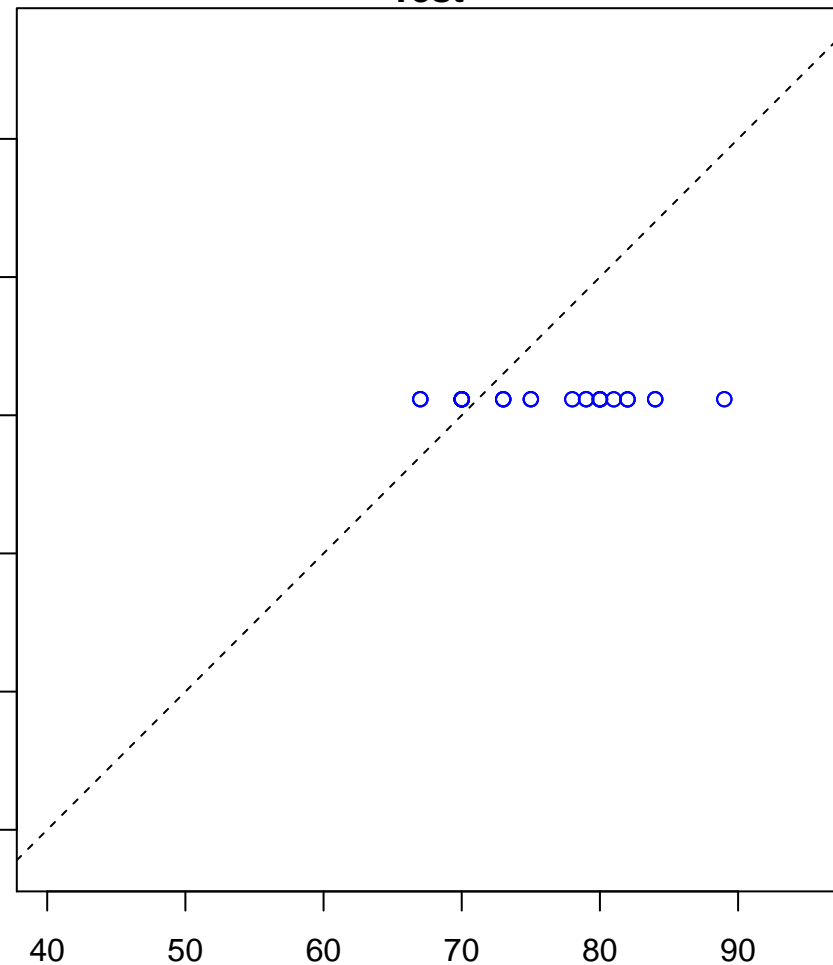


regulation of actin filament length (Score: 0.822723)

Control

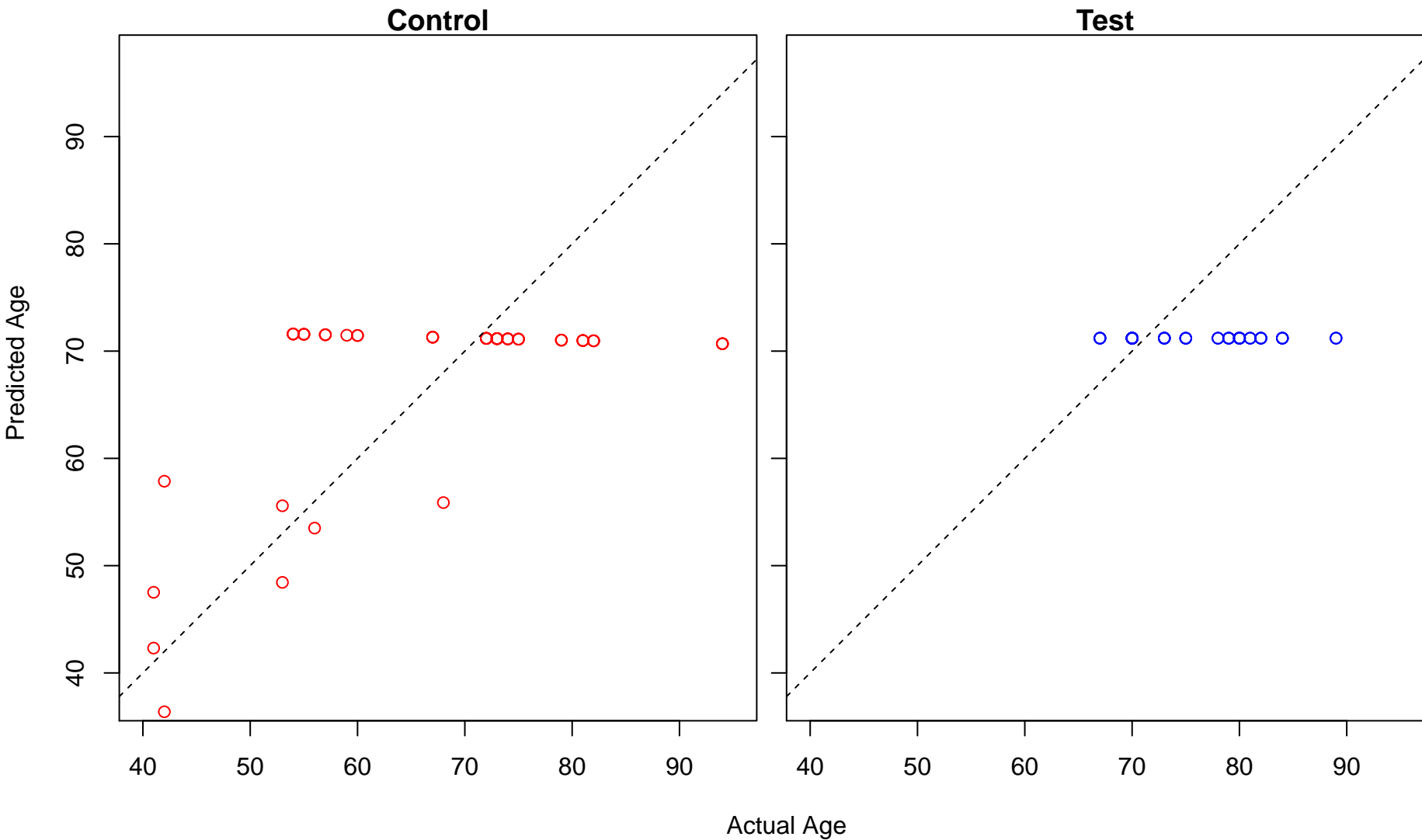


Test

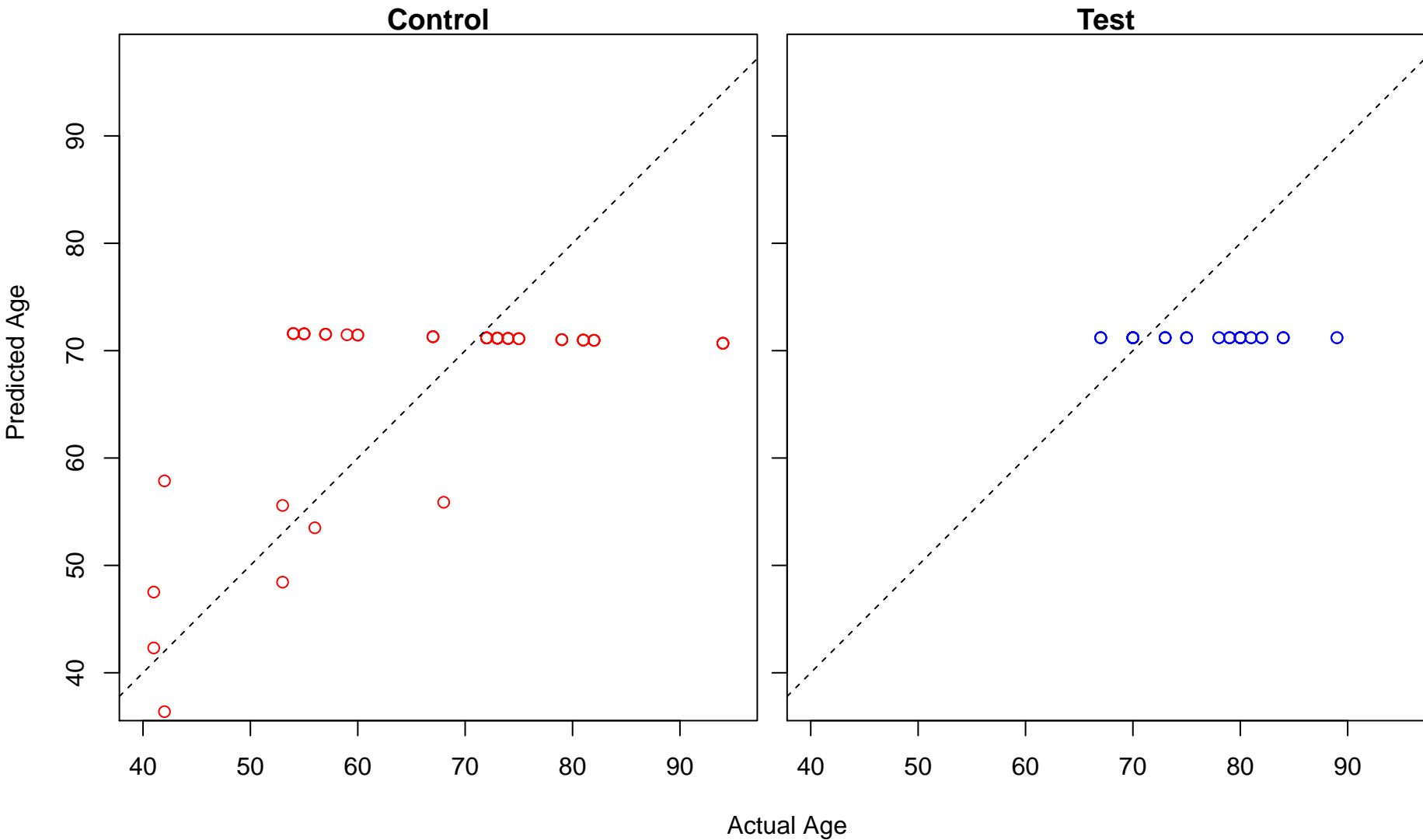


Actual Age

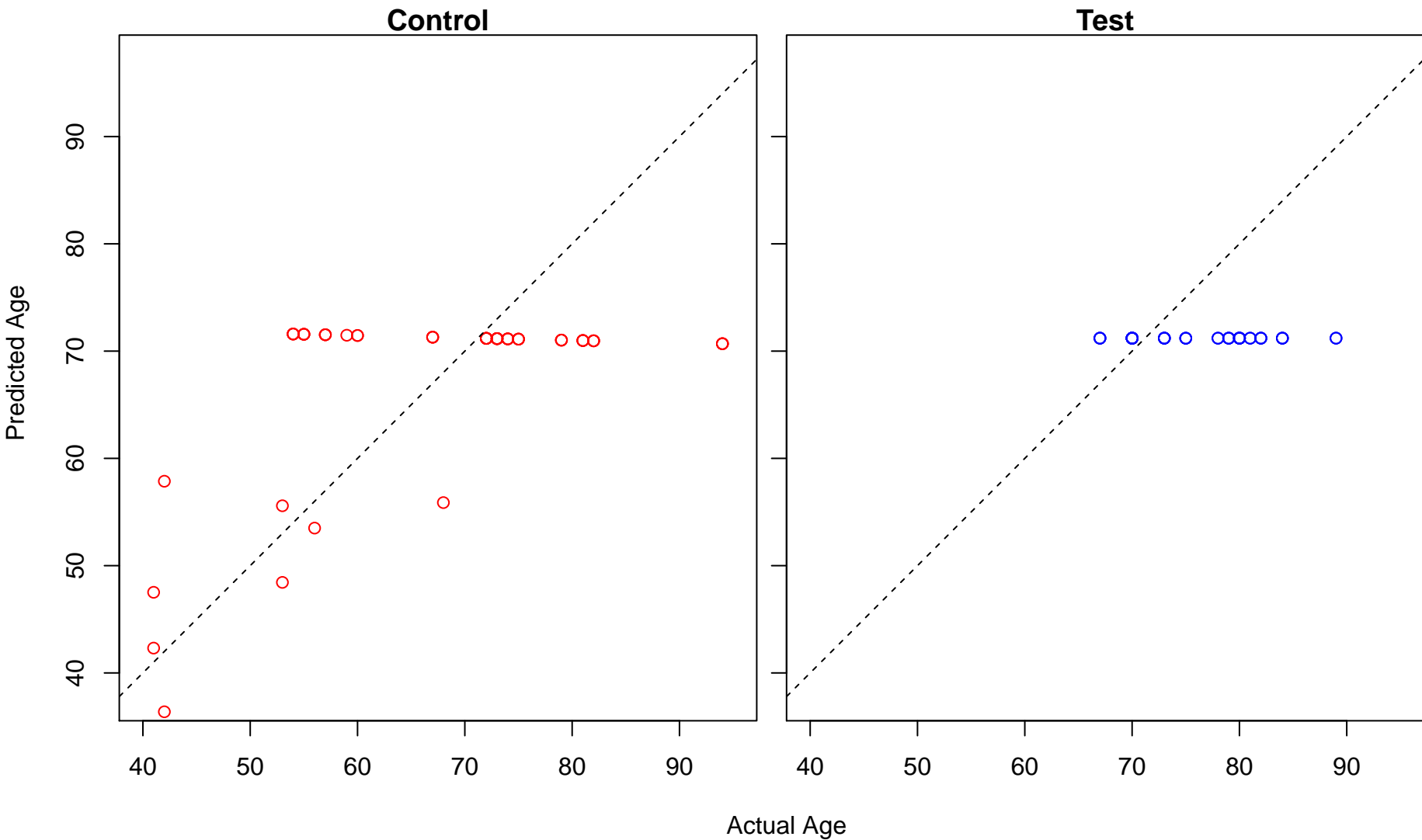
cellular response to reactive oxygen species (Score: 0.822594)



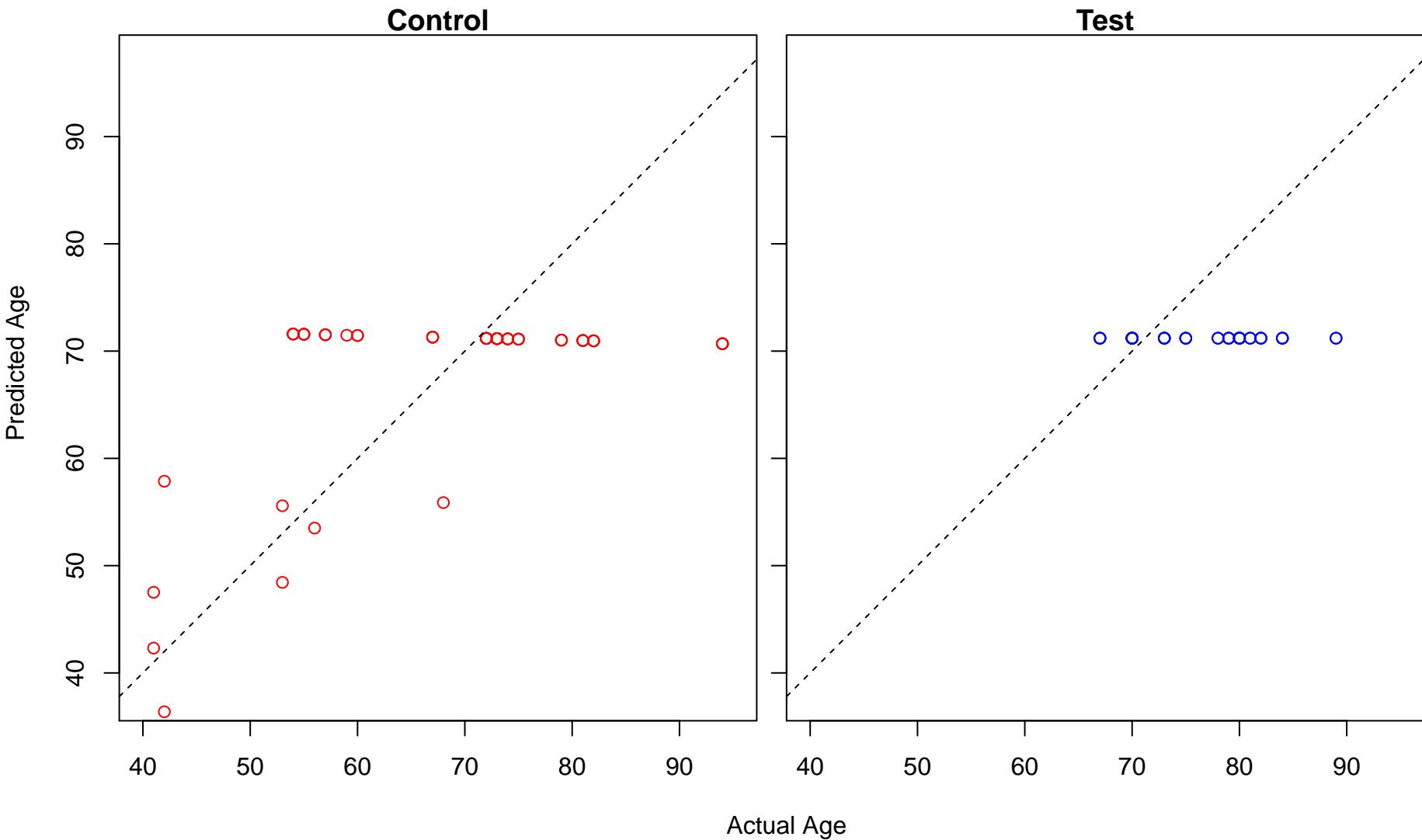
regulation of superoxide metabolic process (Score: 0.822594)



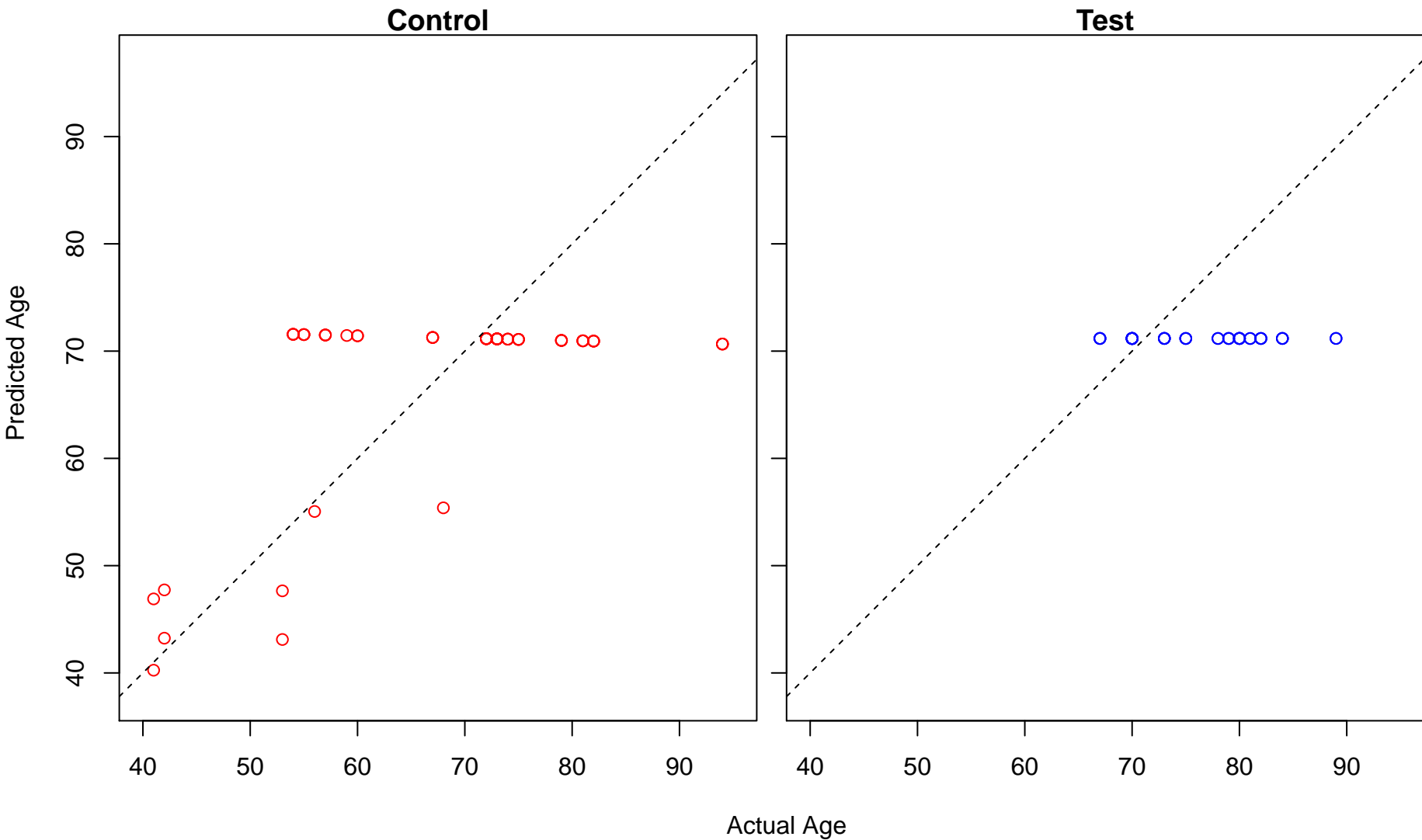
positive regulation of cellular response to oxidative stress (Score: 0.822594)



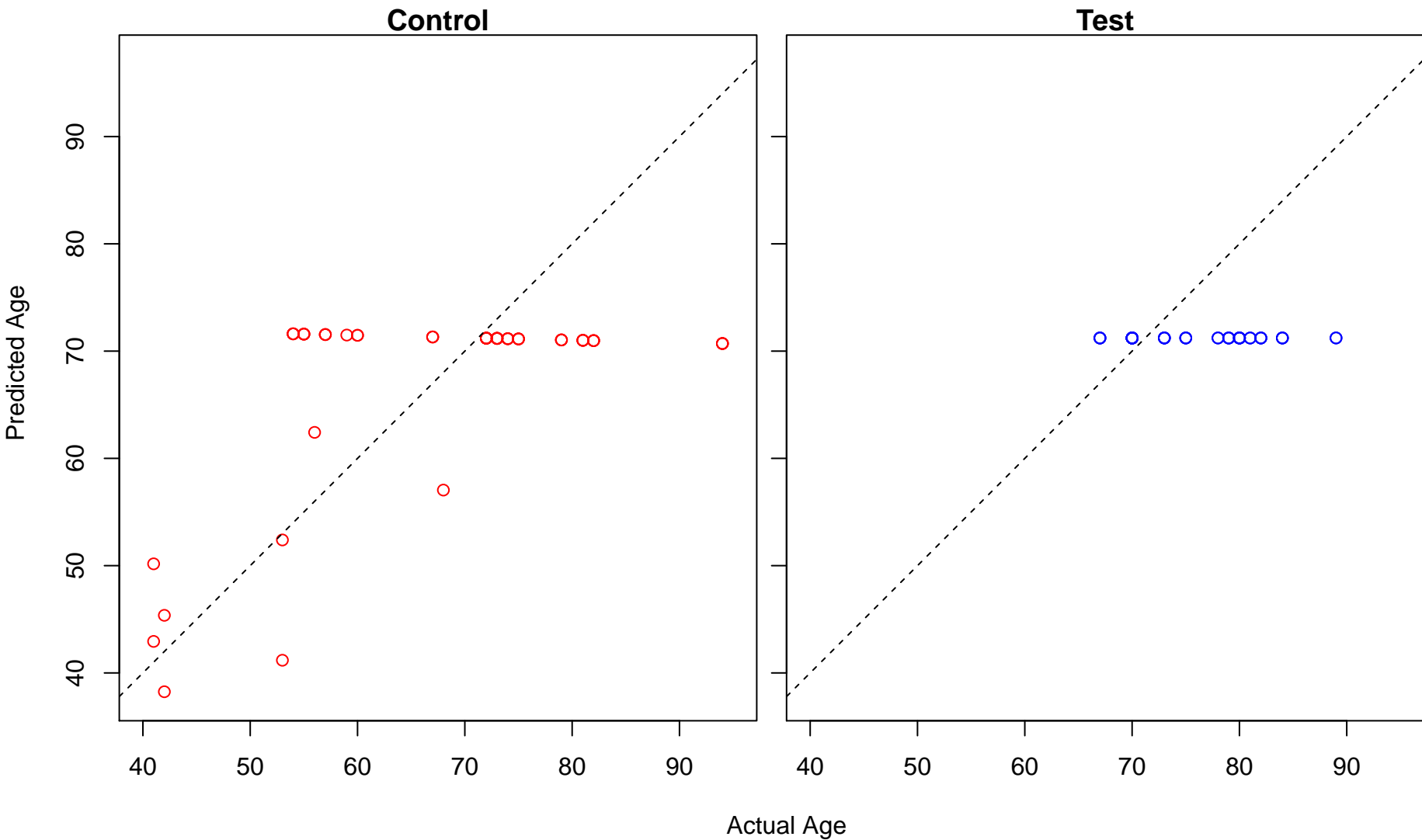
positive regulation of response to oxidative stress (Score: 0.822594)



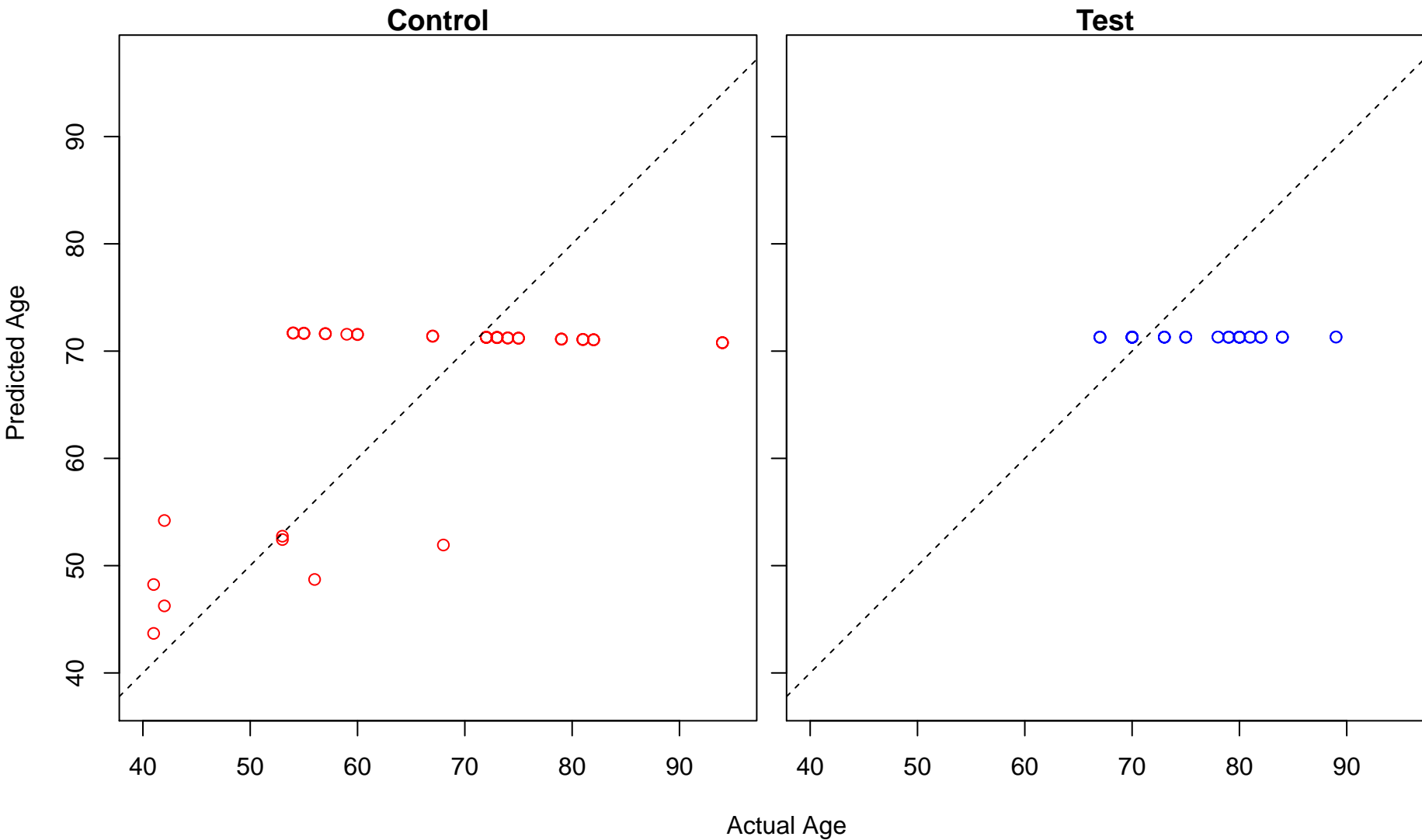
vesicle-mediated transport (Score: 0.822564)



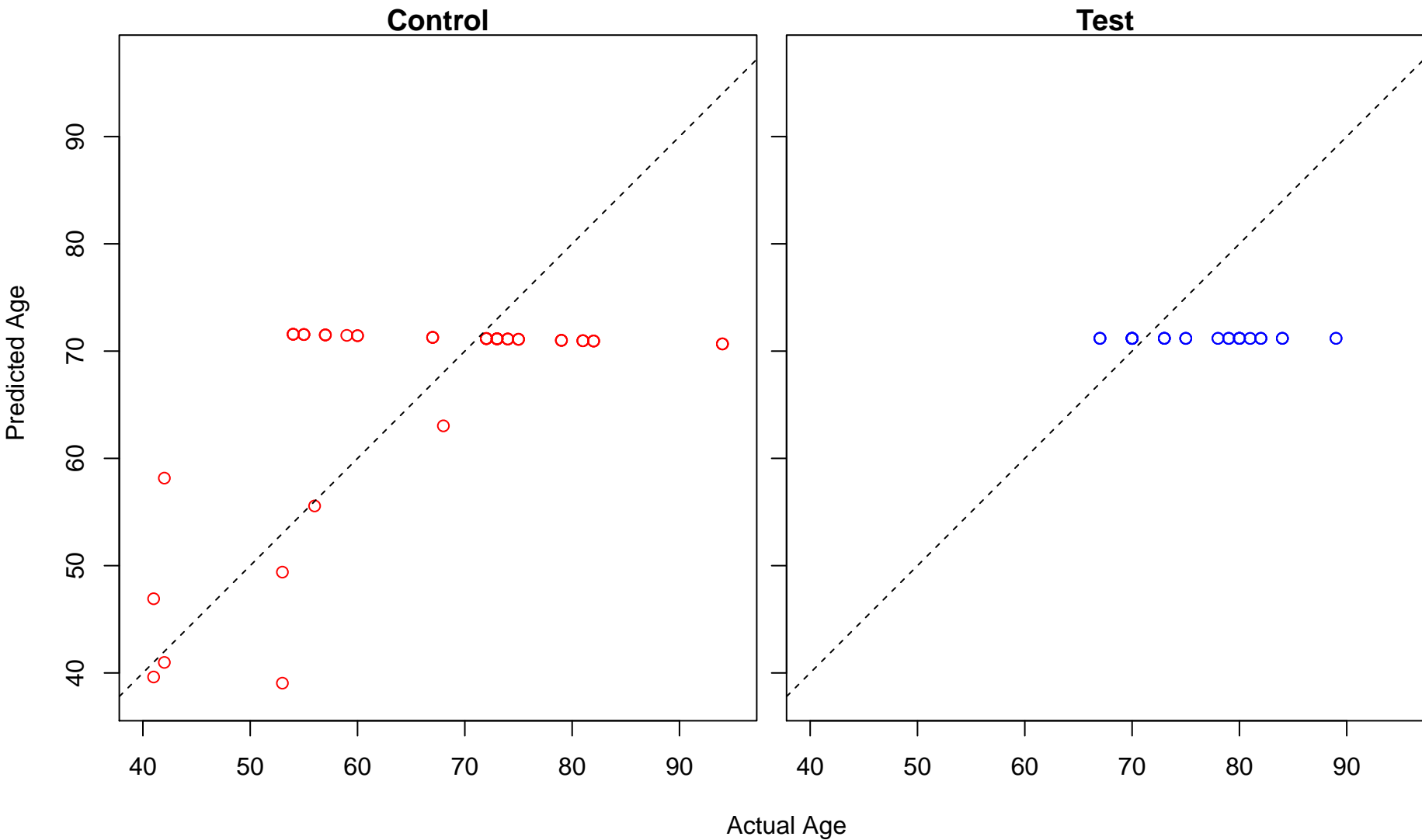
phosphorylation (Score: 0.822374)



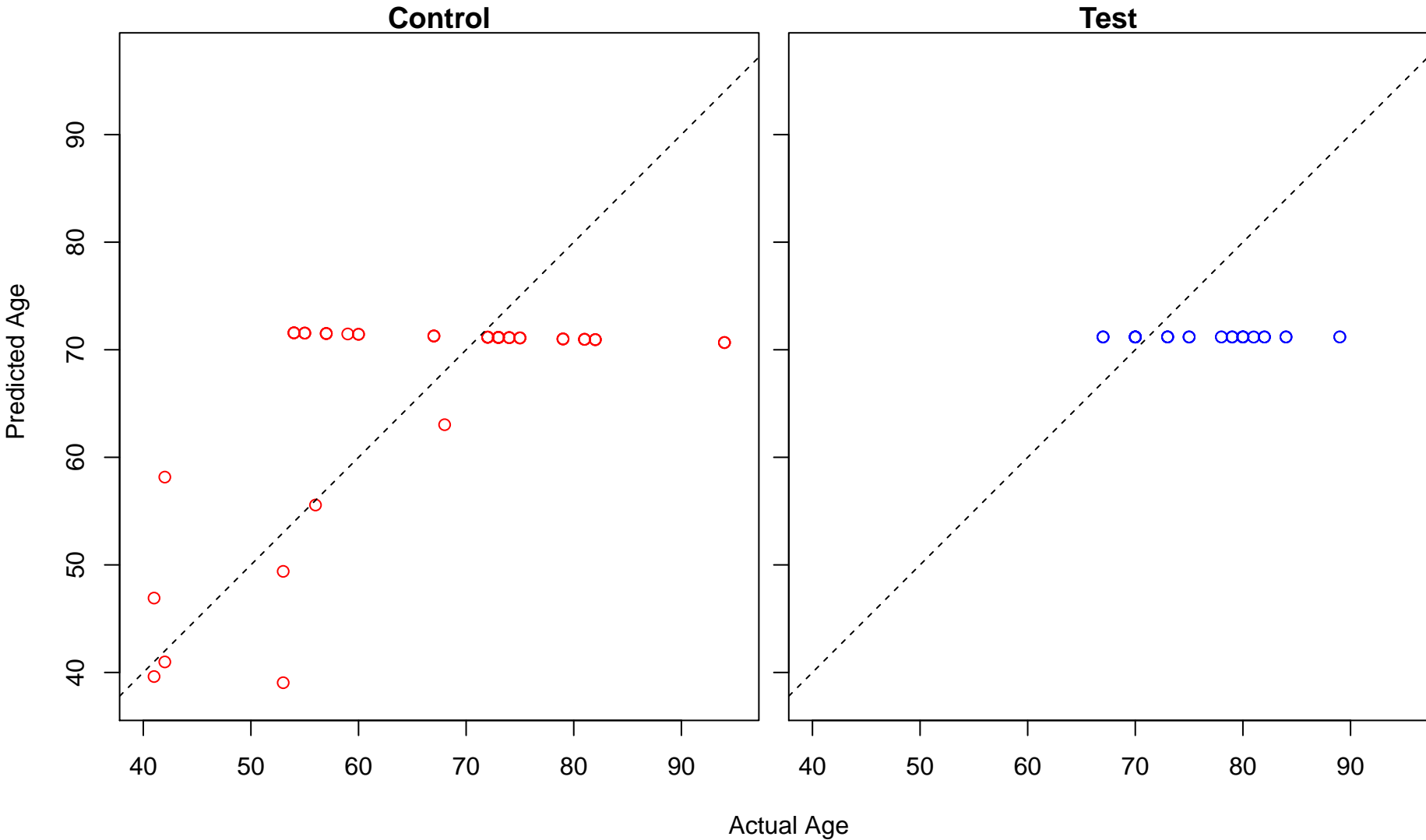
skin development (Score: 0.822315)



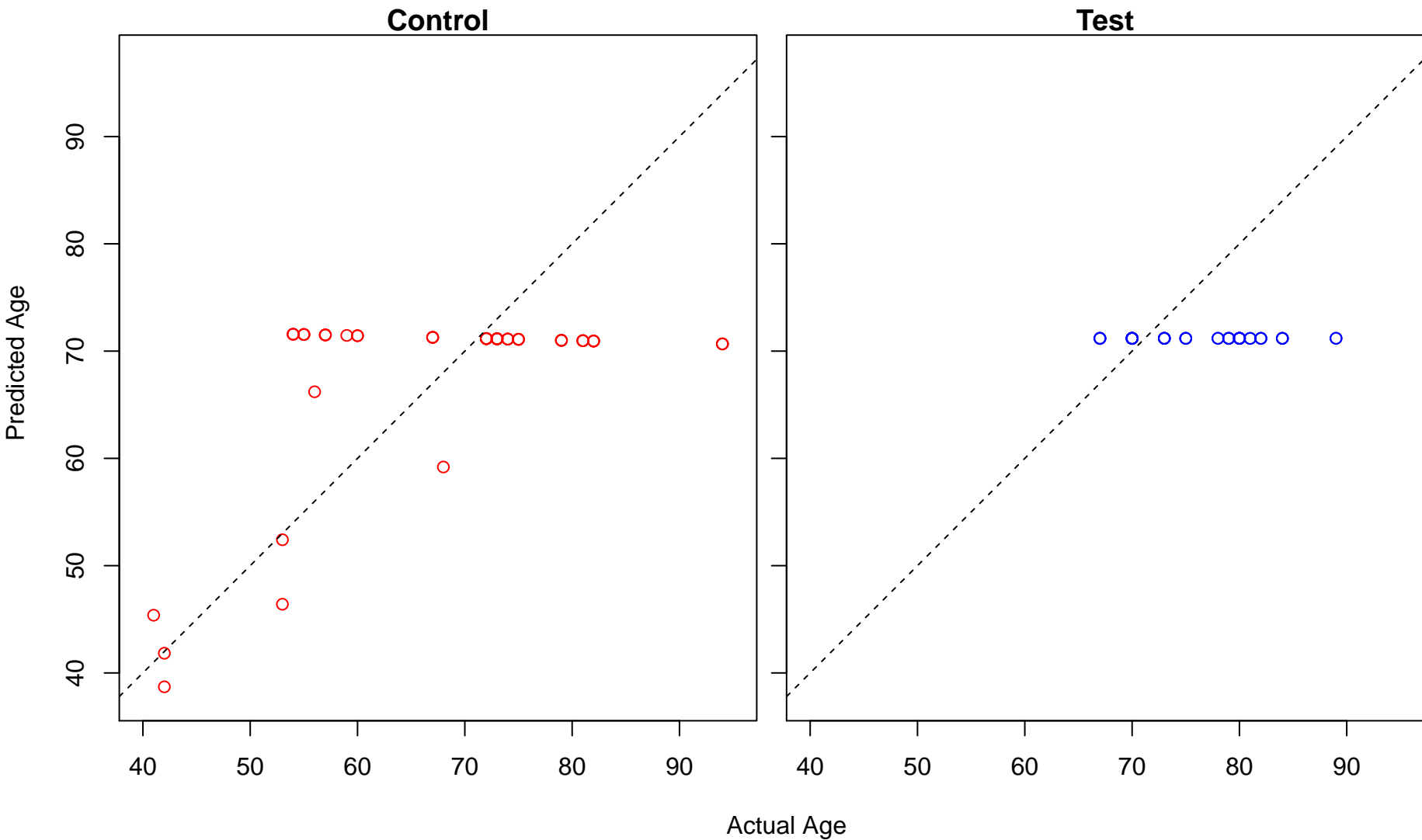
immune effector process (Score: 0.822279)



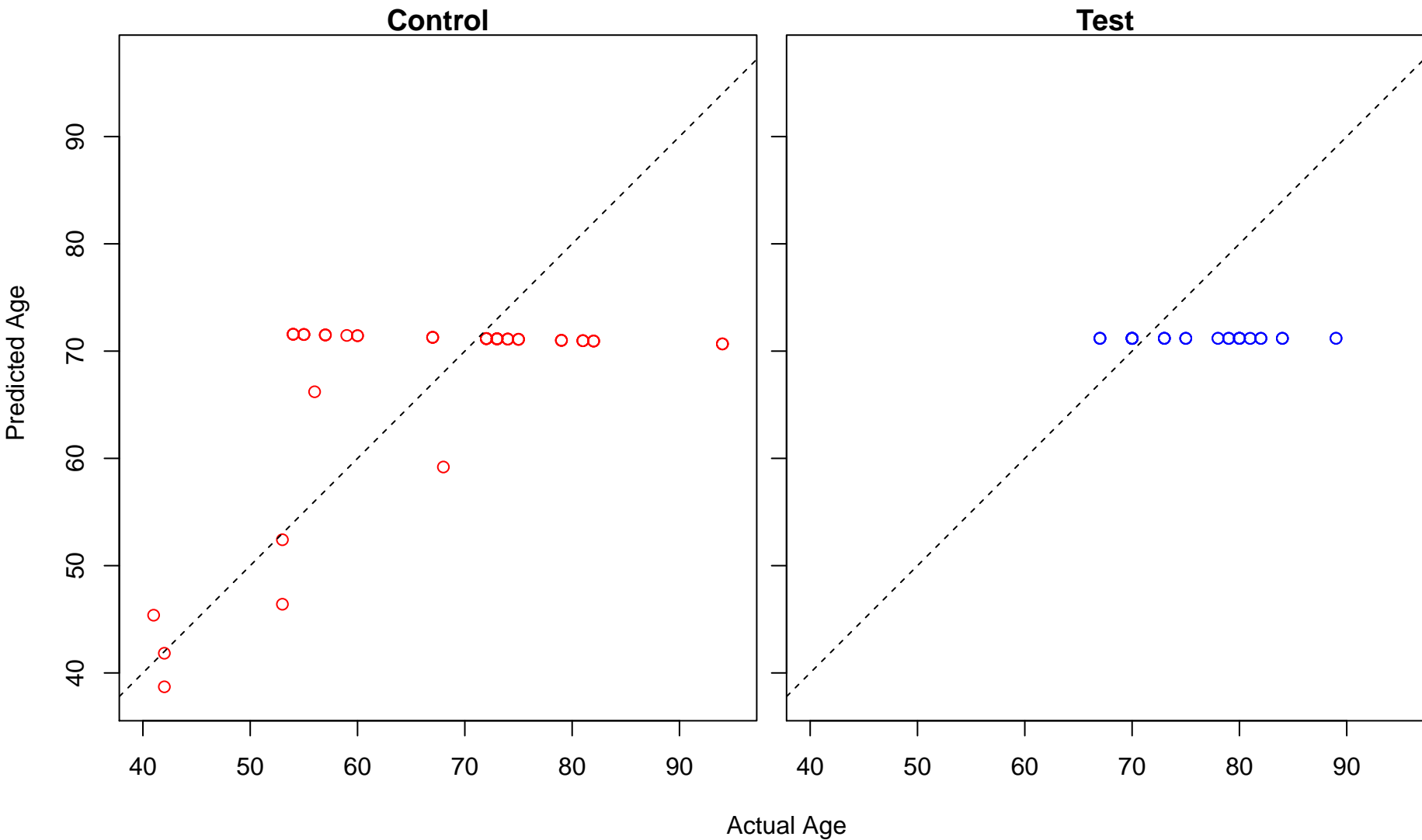
cell activation involved in immune response (Score: 0.822279)



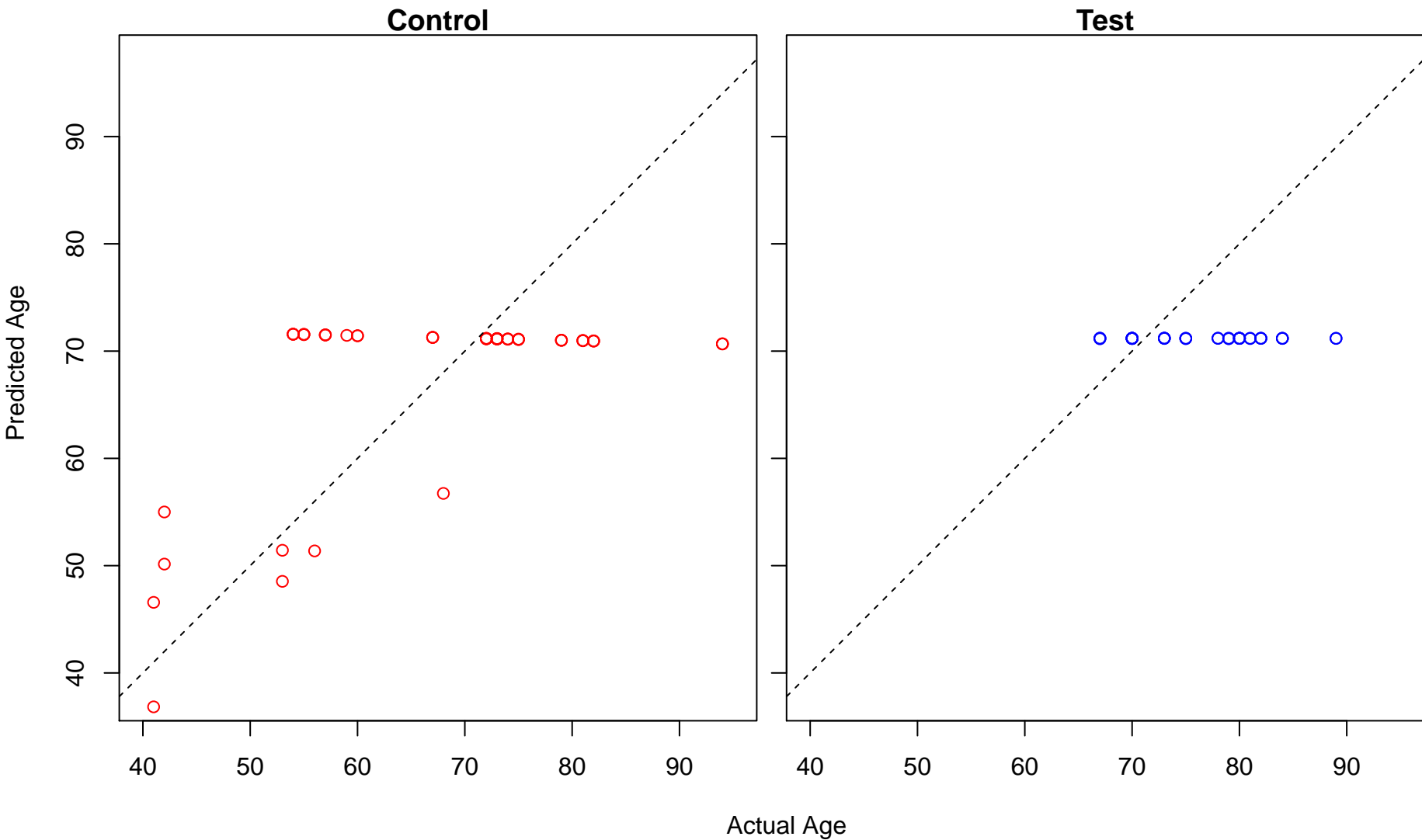
MAPK cascade (Score: 0.822156)



signal transduction by protein phosphorylation (Score: 0.822156)

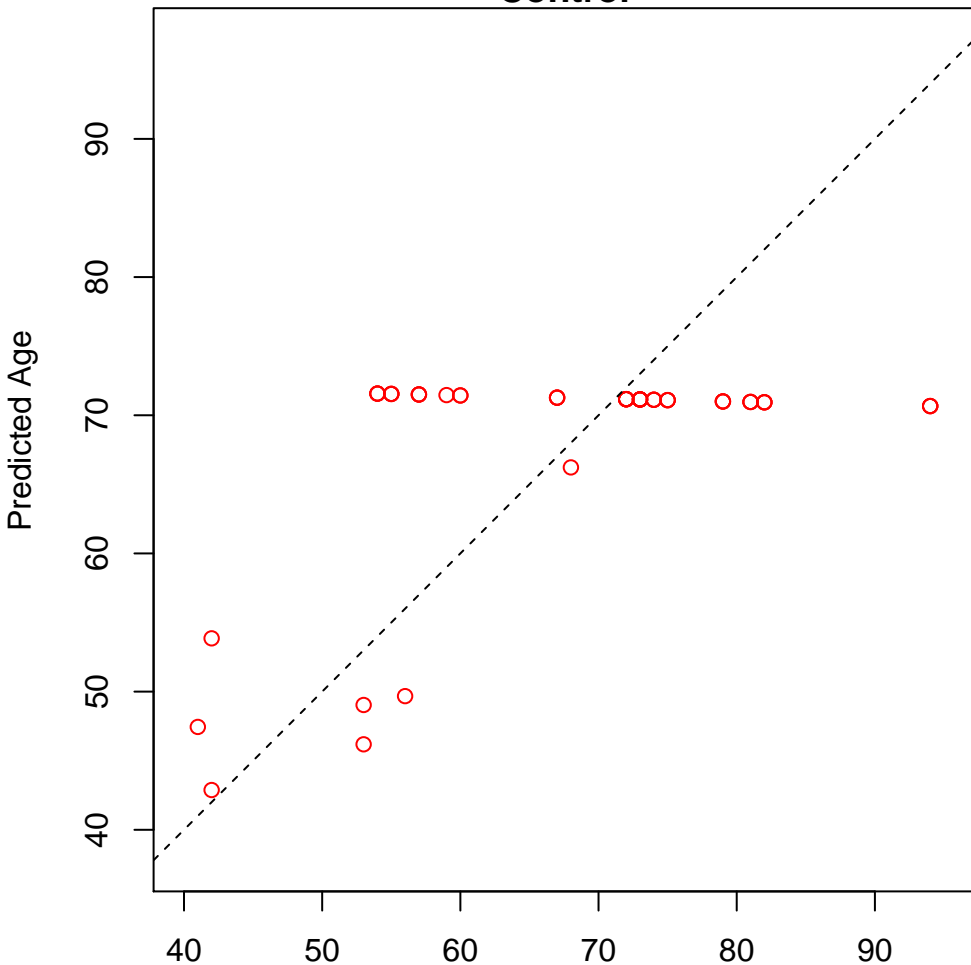


spliceosomal tri-snRNP complex assembly (Score: 0.822153)

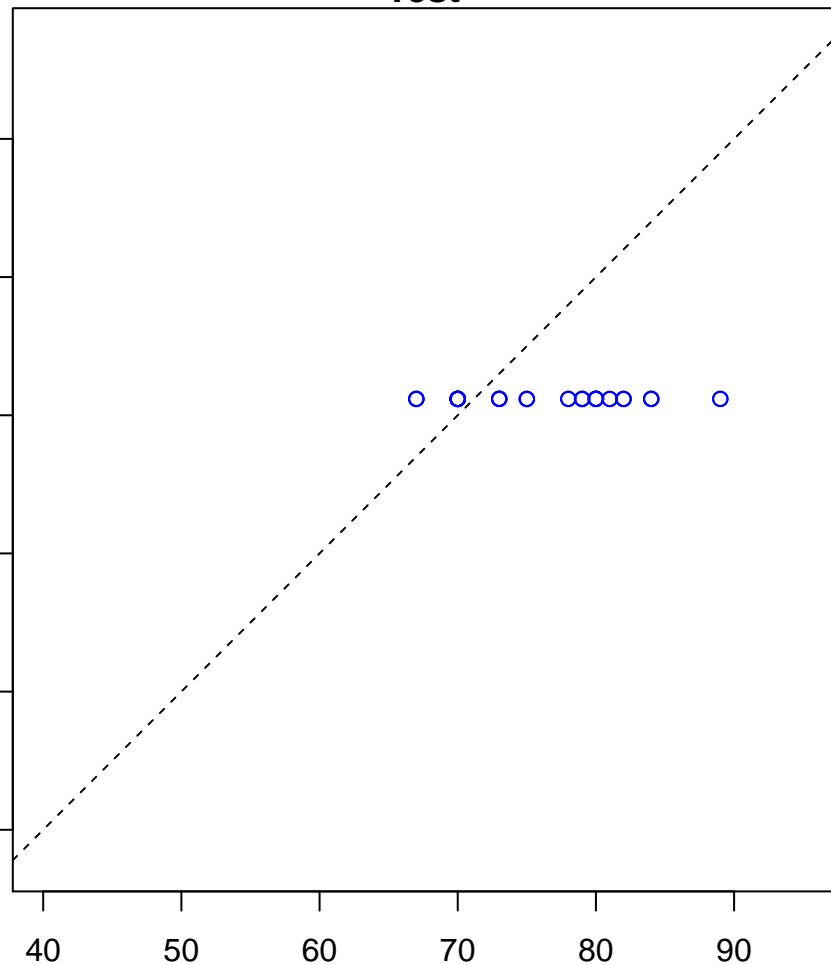


positive regulation of immune response (Score: 0.821974)

Control



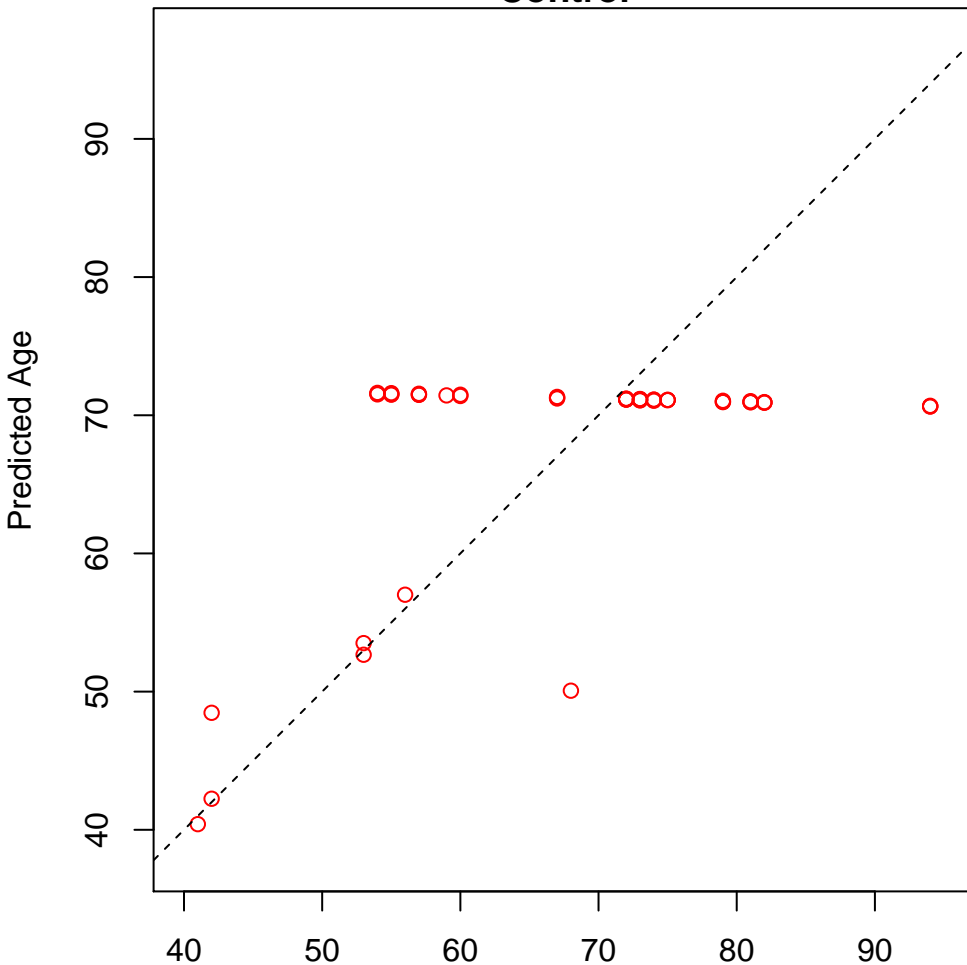
Test



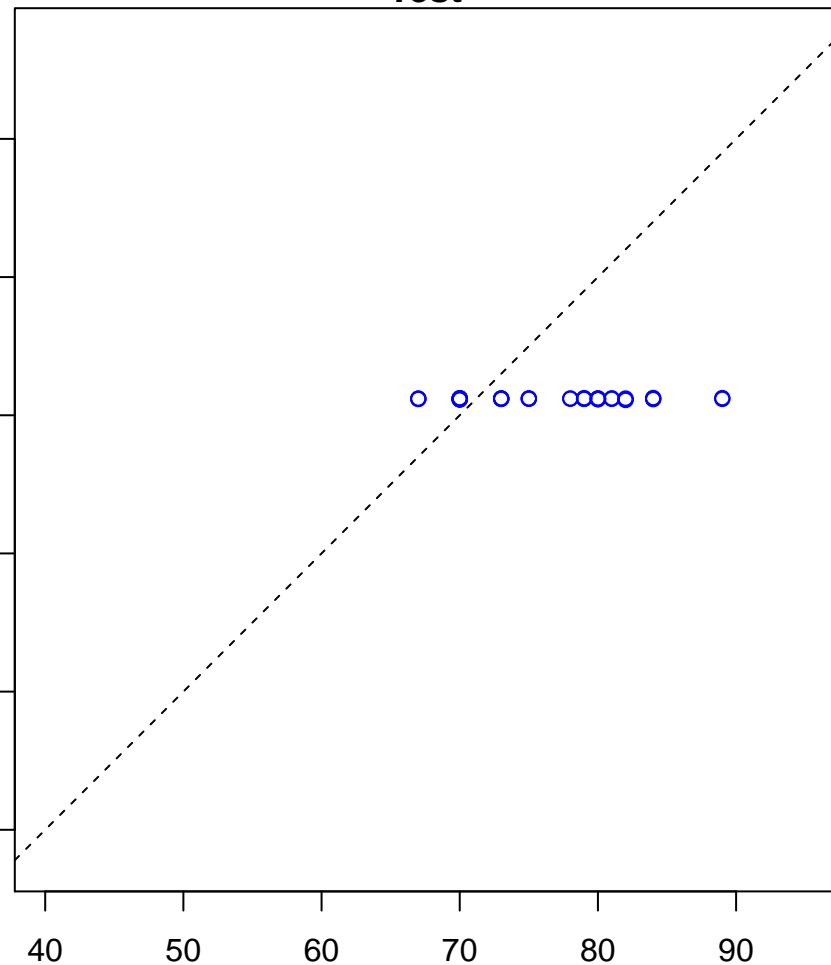
Actual Age

regulation of actin filament-based process (Score: 0.821915)

Control

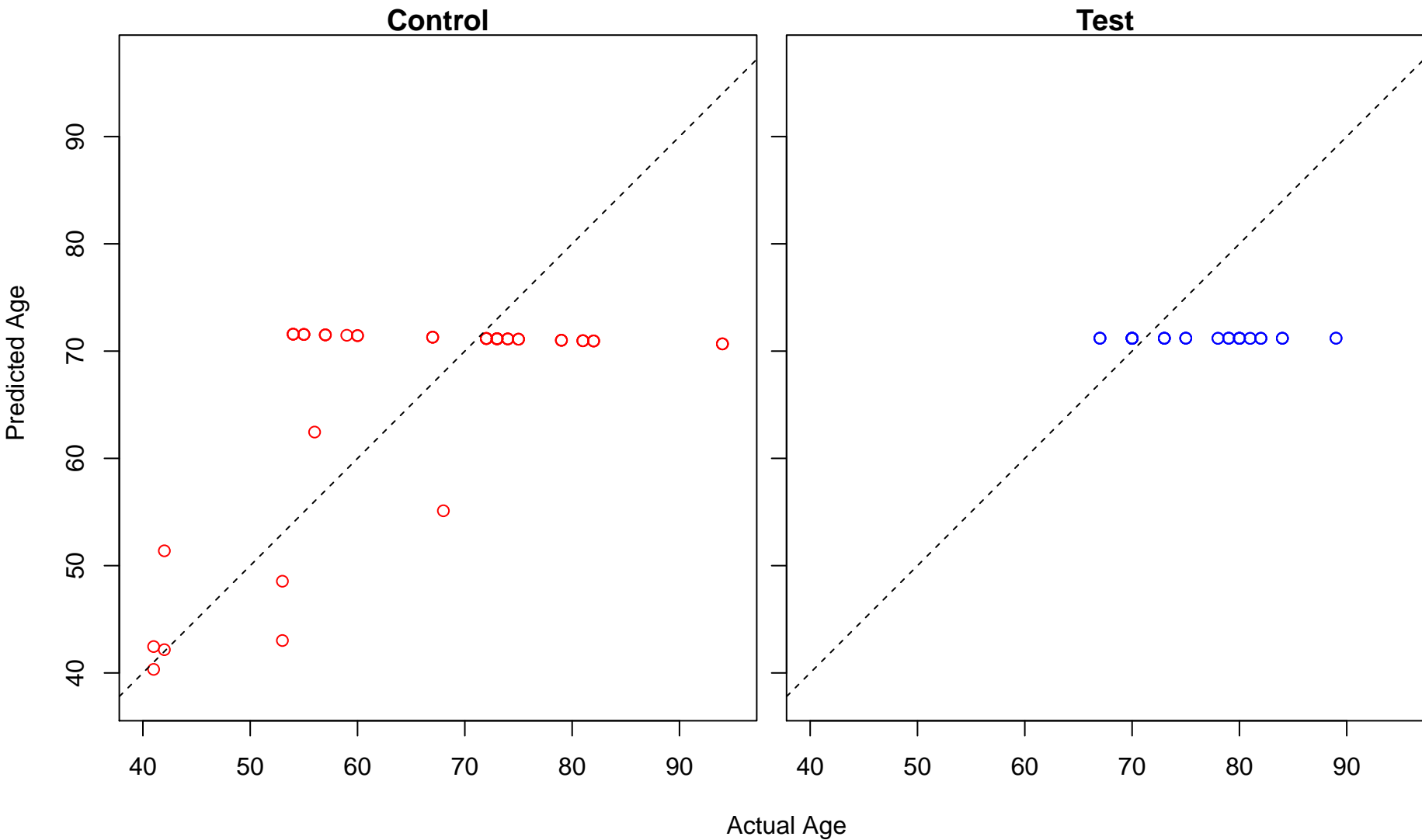


Test



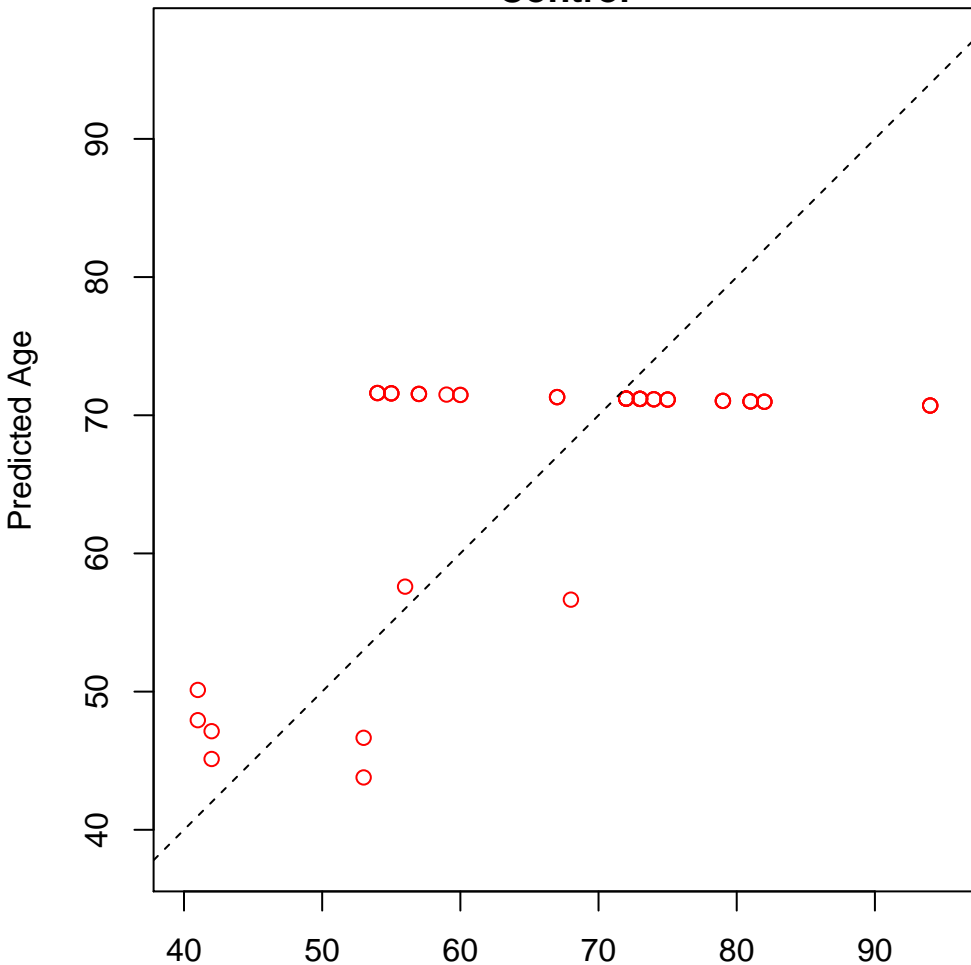
Actual Age

rhythmic process (Score: 0.821882)

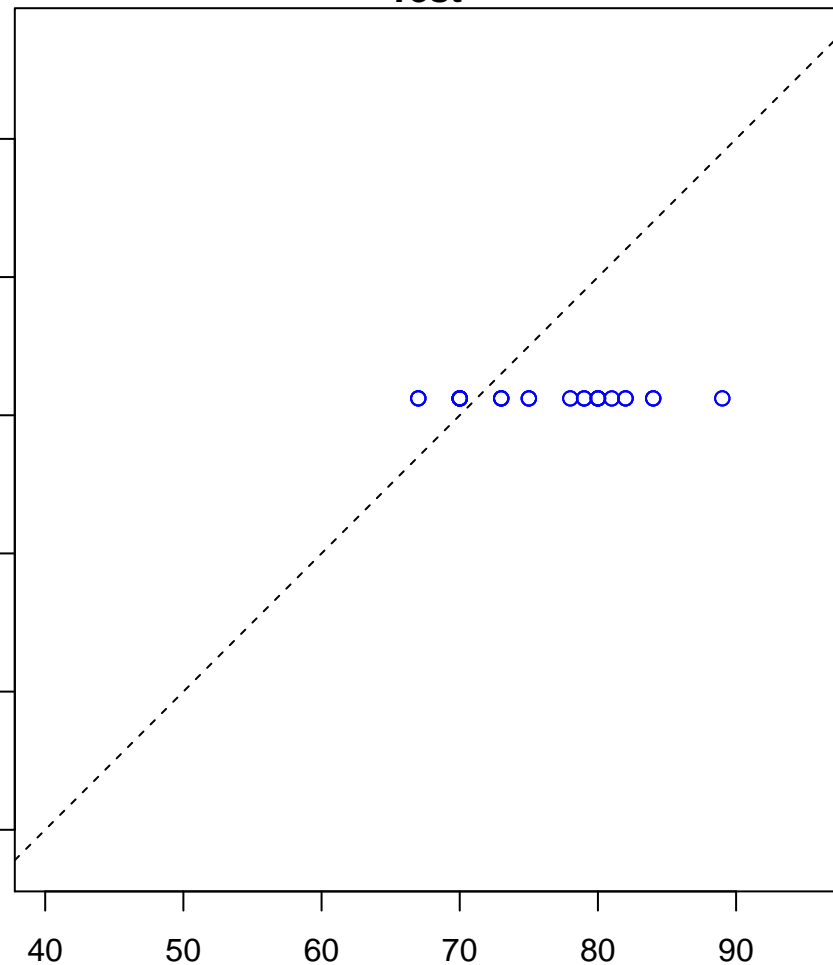


movement of cell or subcellular component (Score: 0.821819)

Control

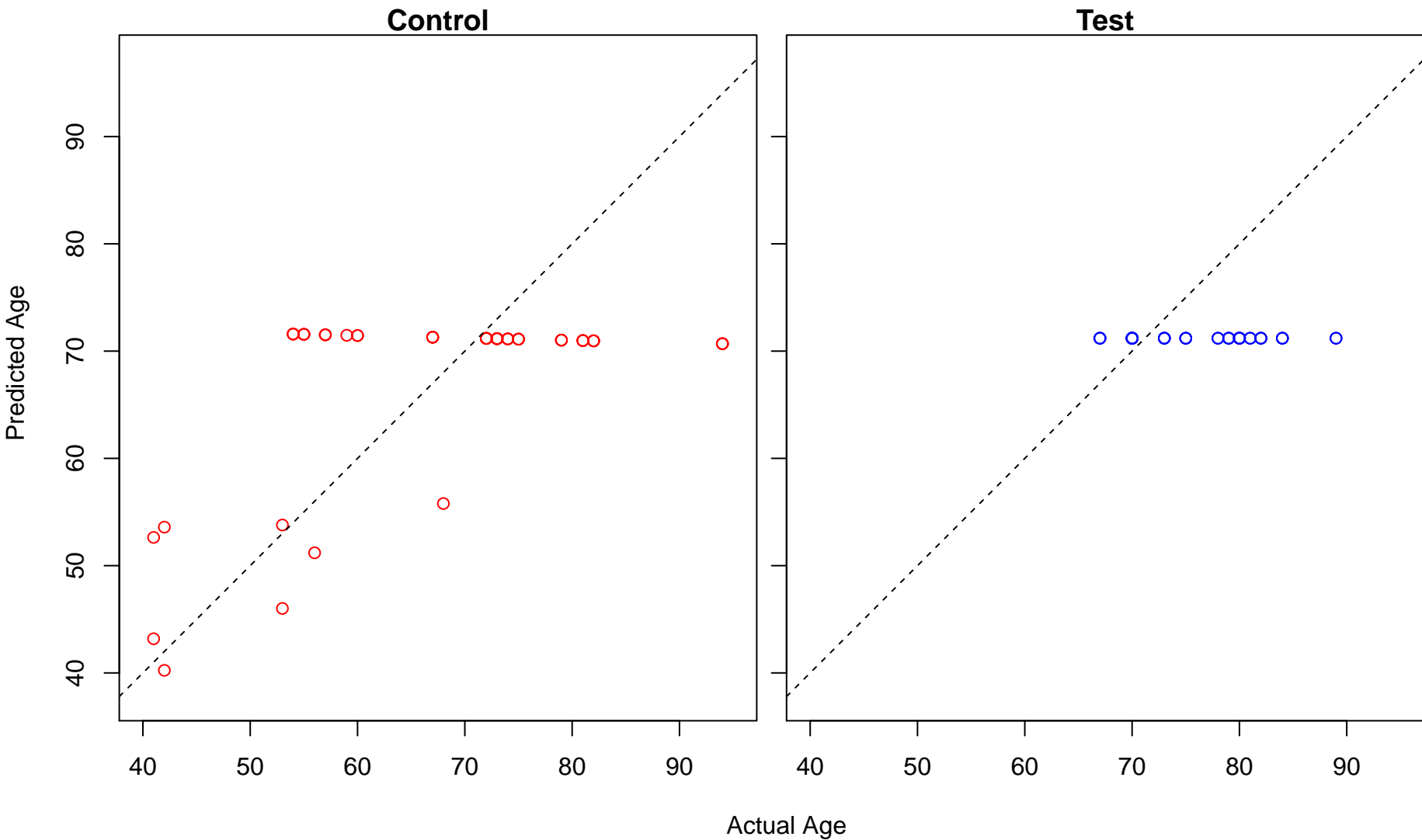


Test



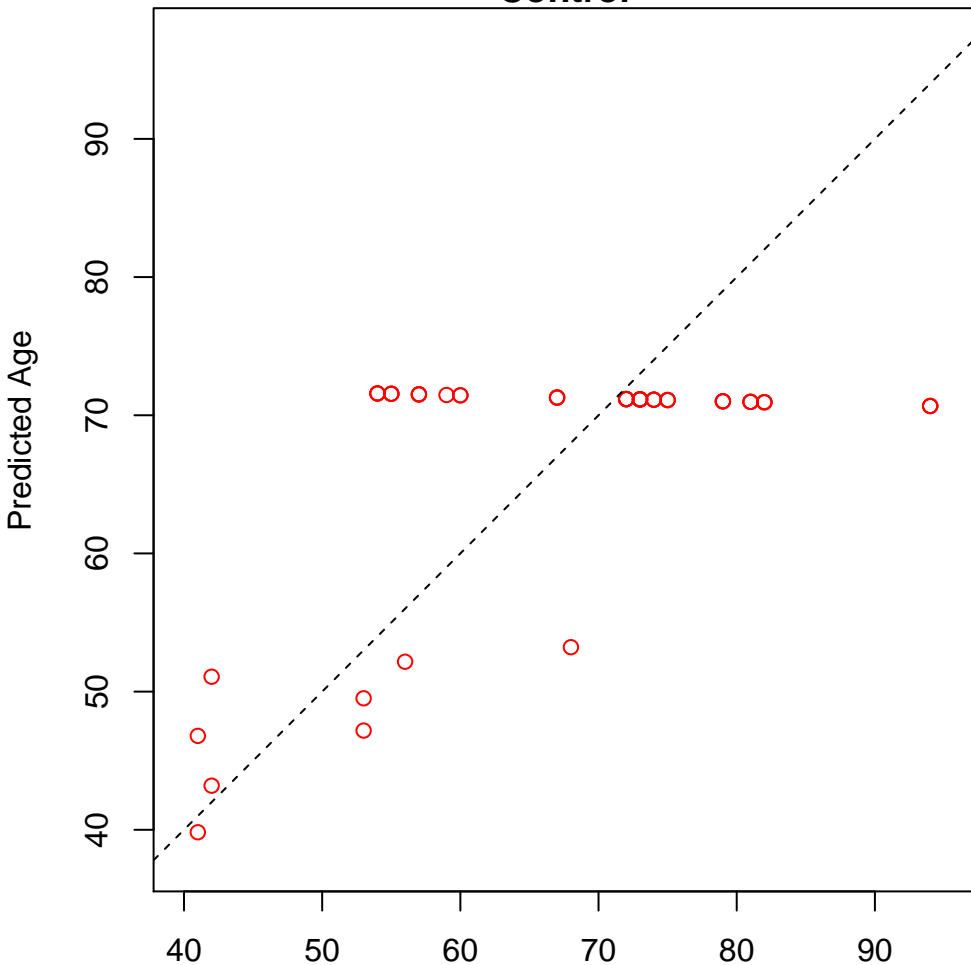
Actual Age

epidermis development (Score: 0.821813)

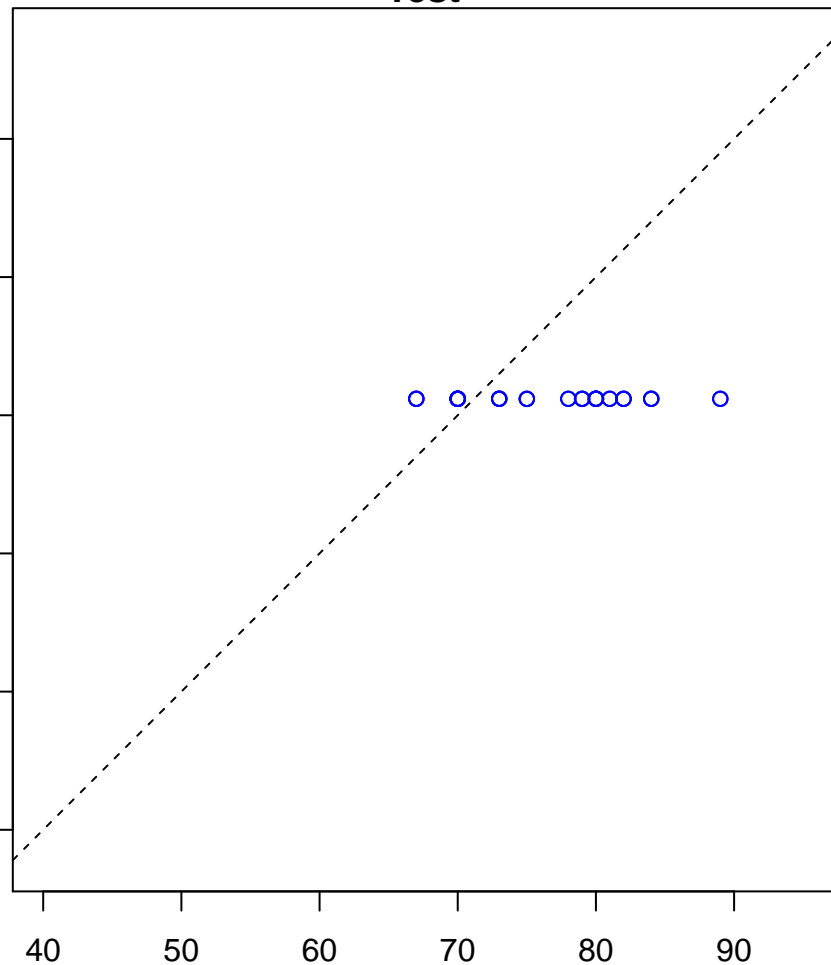


positive regulation of catalytic activity (Score: 0.821513)

Control

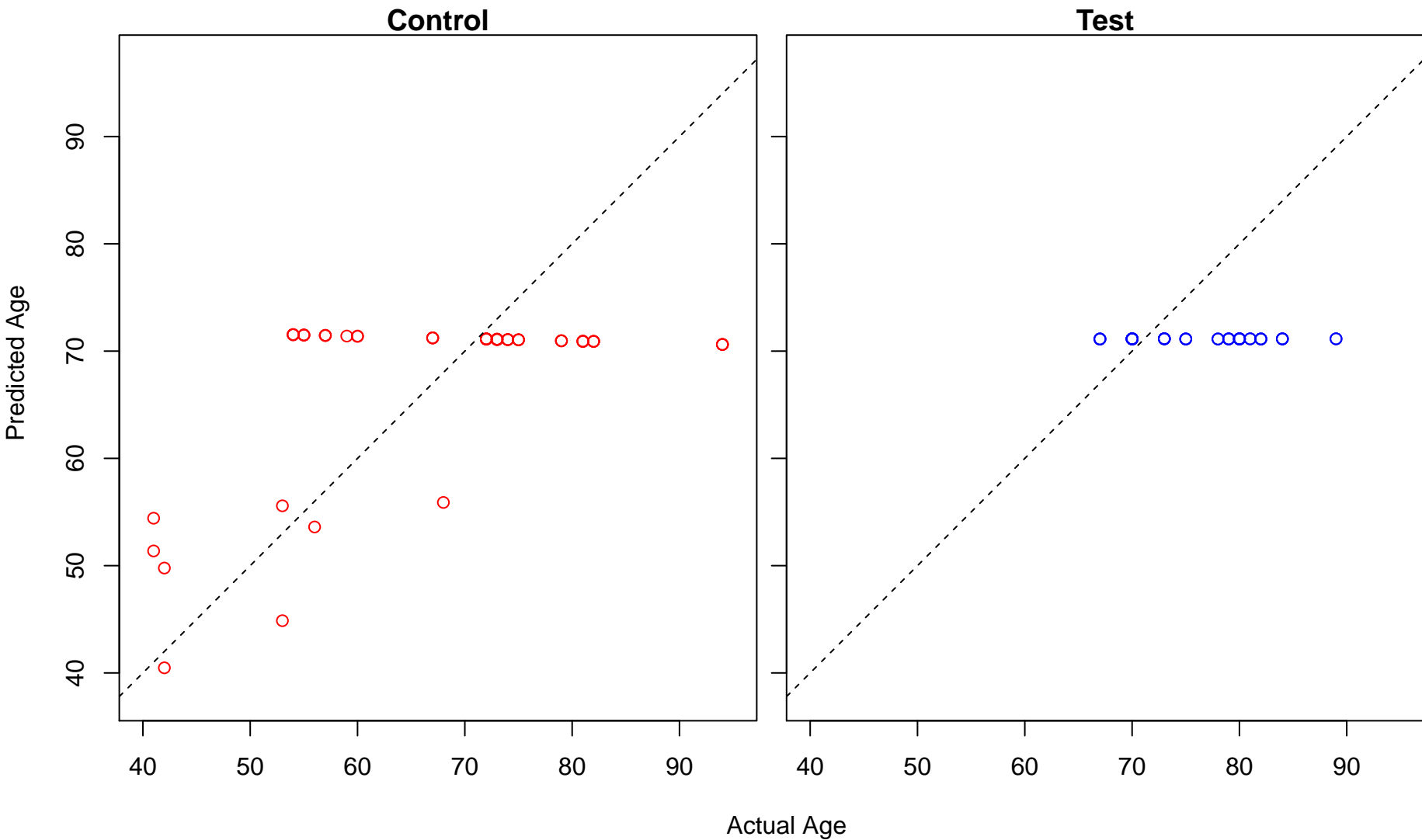


Test



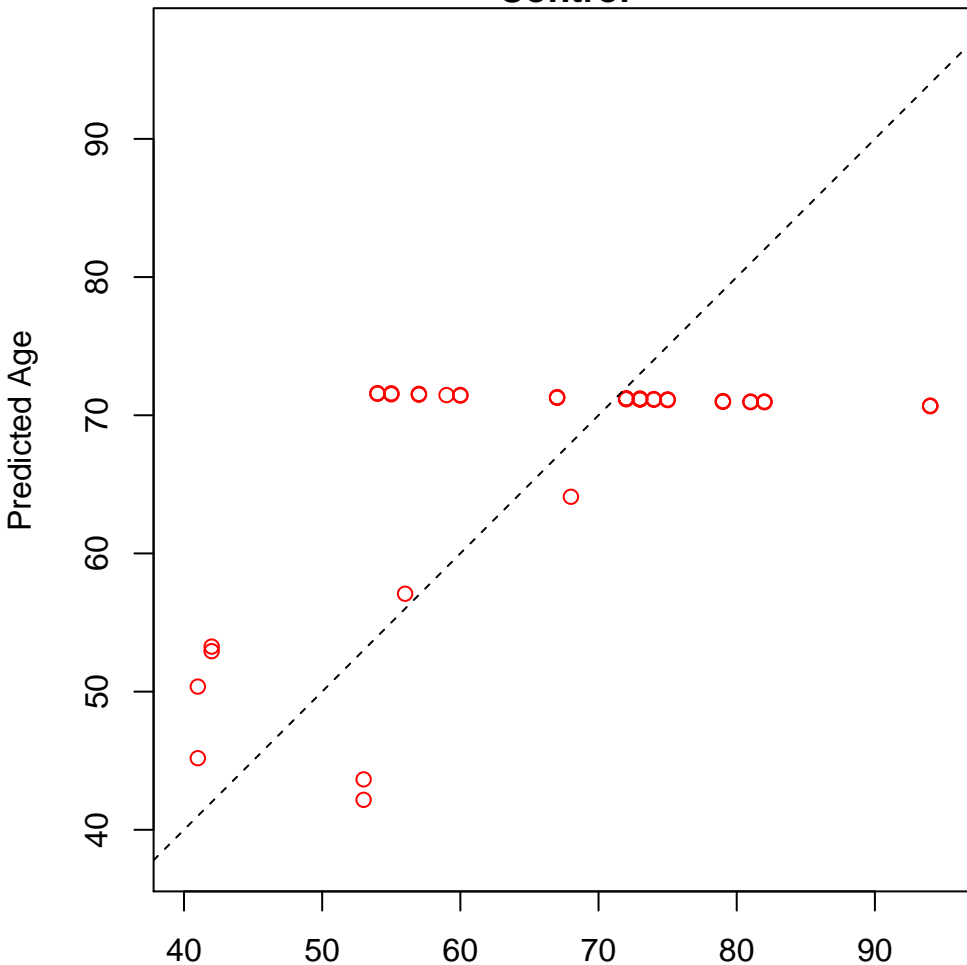
Actual Age

negative regulation of immune system process (Score: 0.821512)

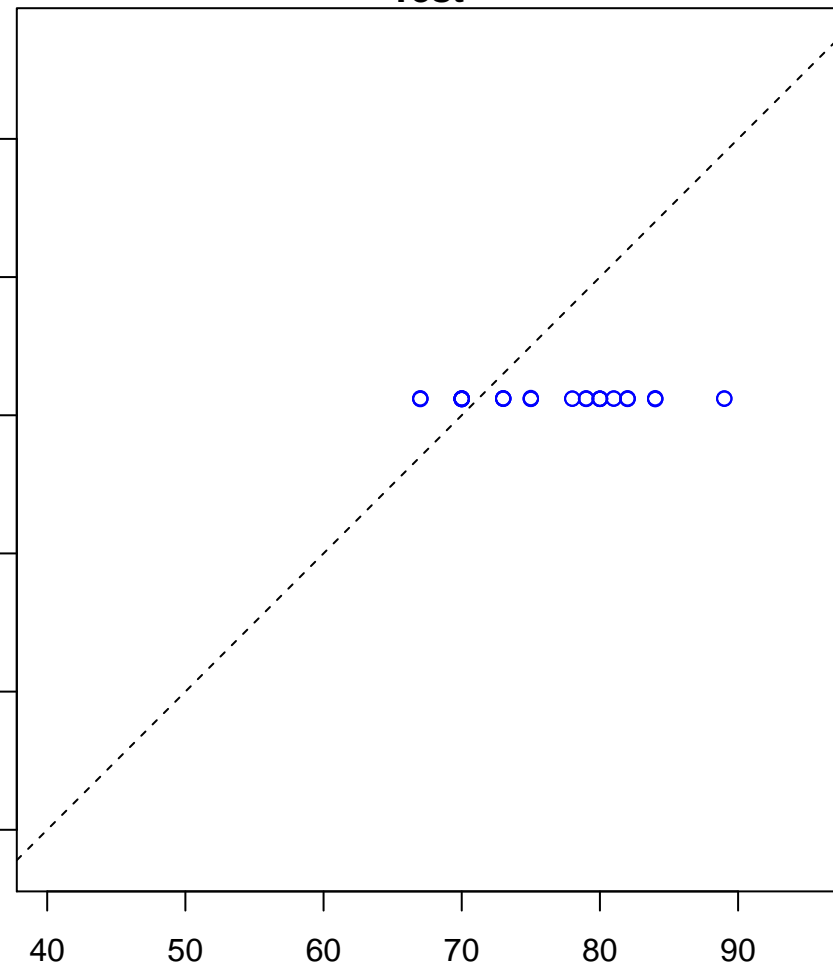


covalent chromatin modification (Score: 0.821462)

Control

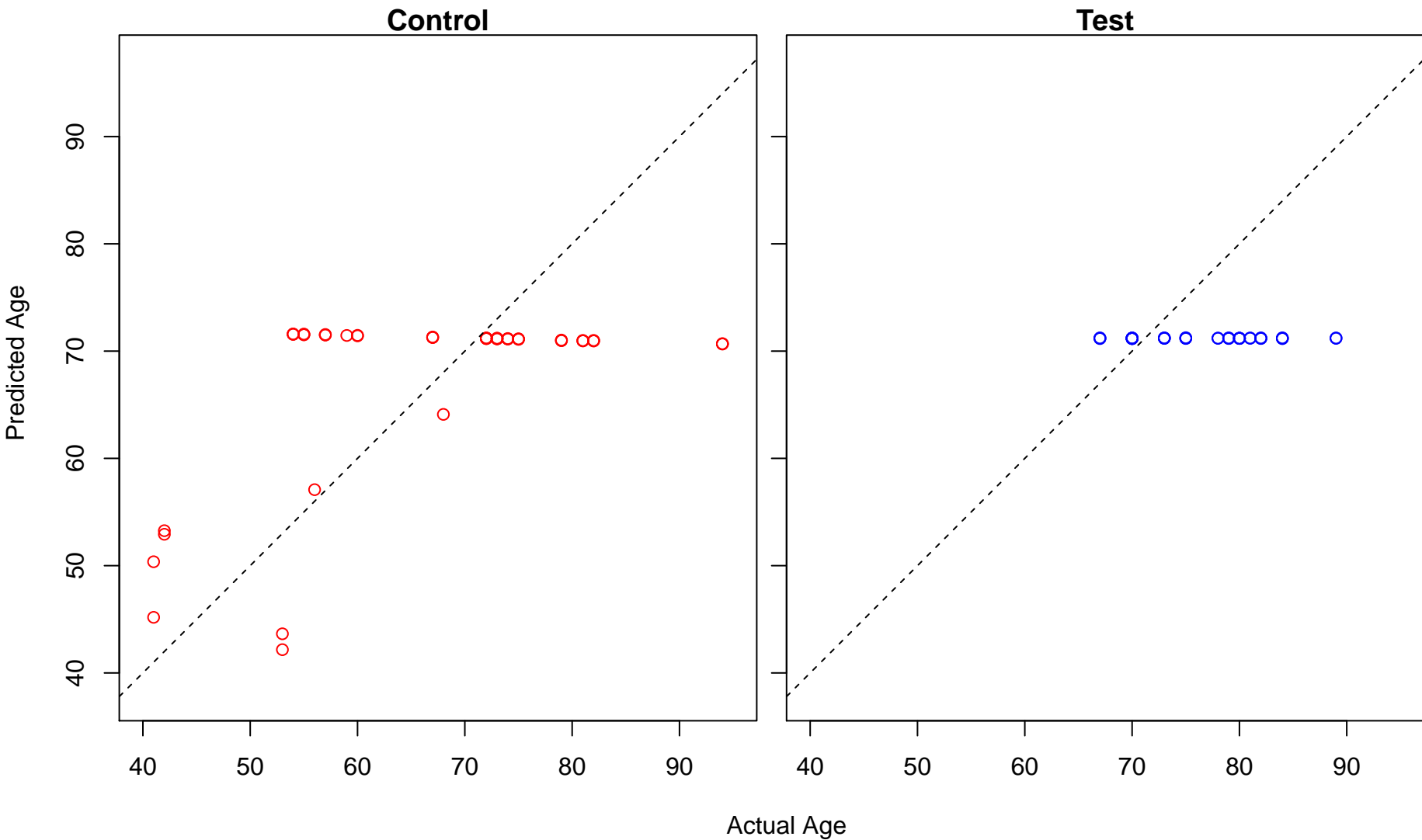


Test



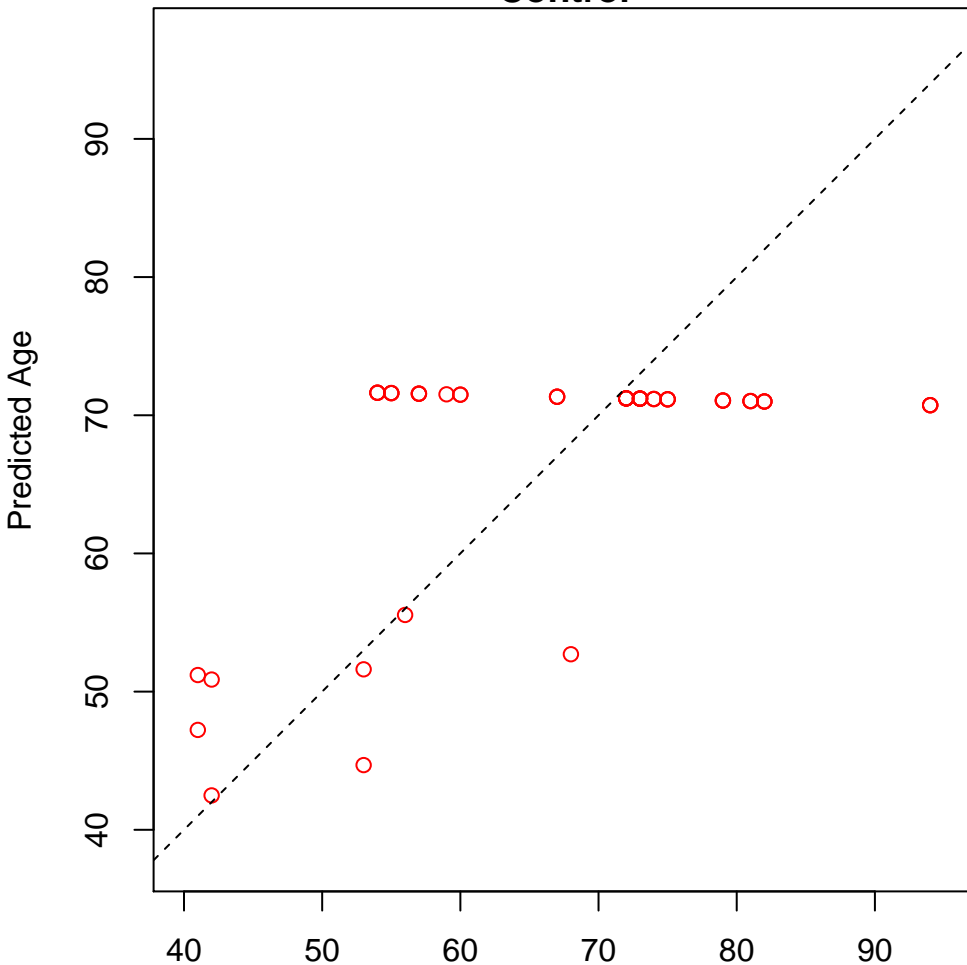
Actual Age

histone modification (Score: 0.821462)

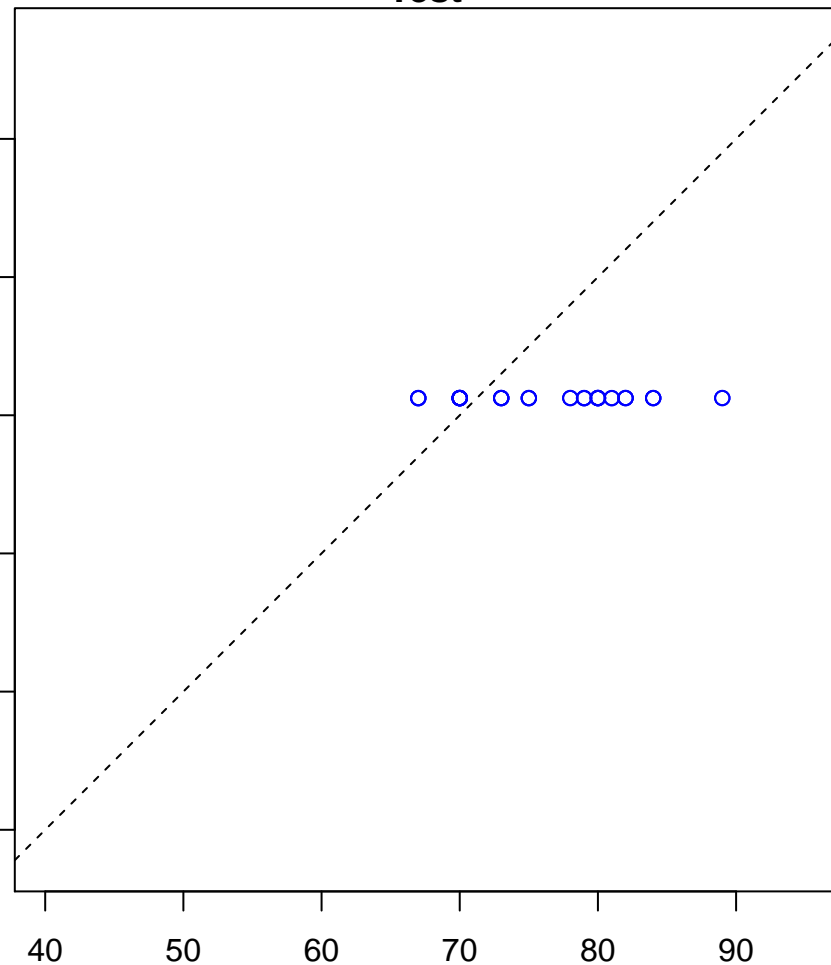


protein localization to mitochondrion (Score: 0.821447)

Control

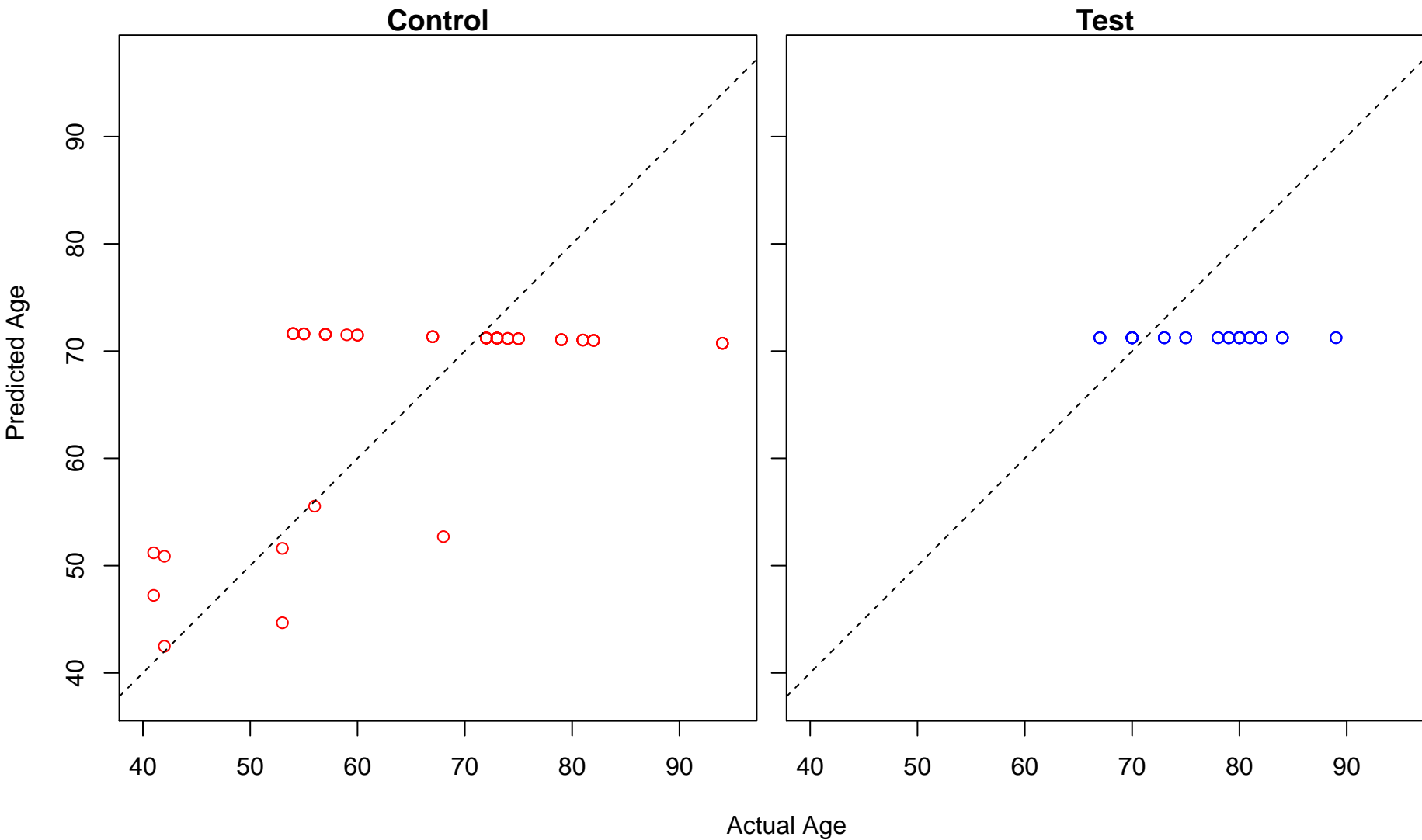


Test

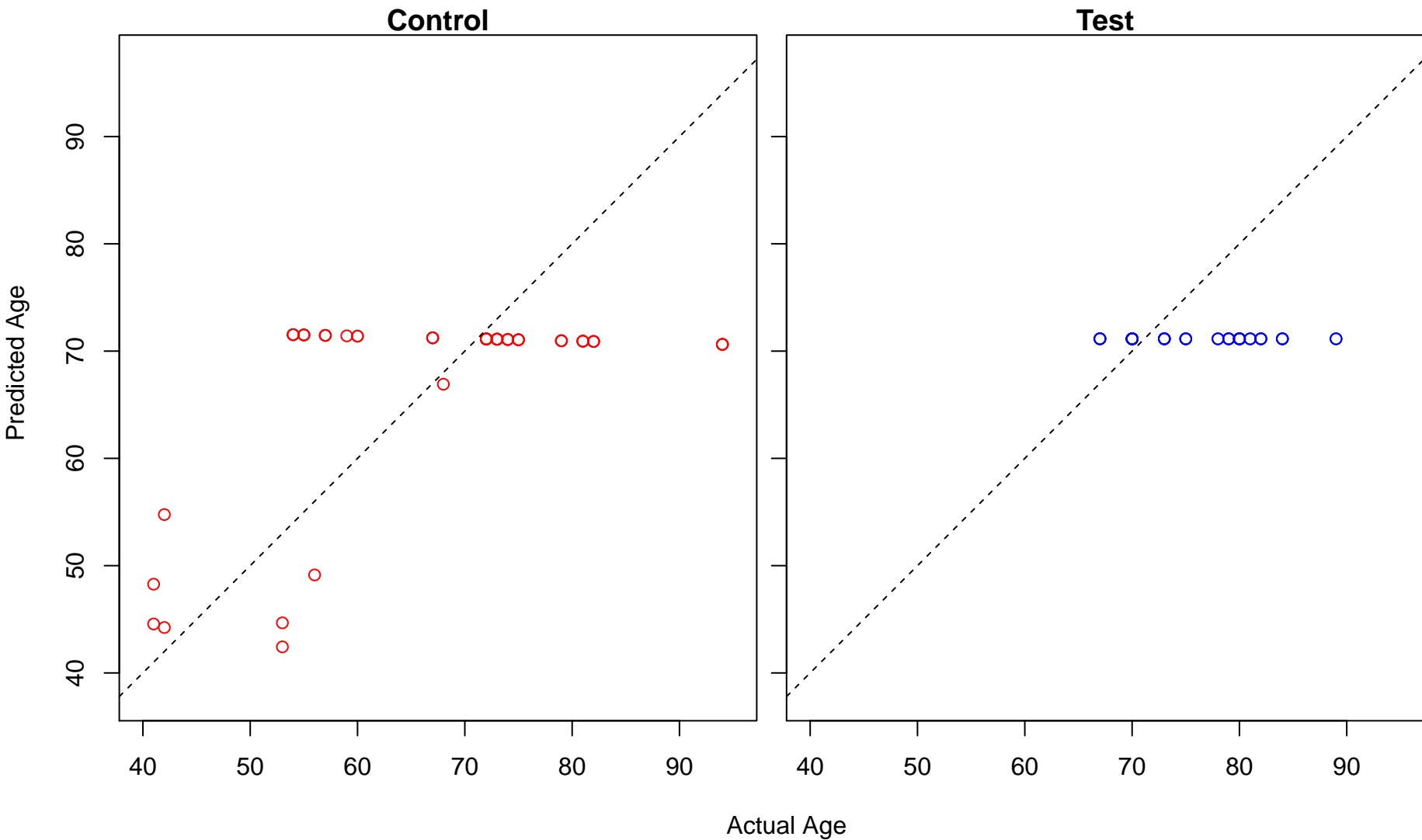


Actual Age

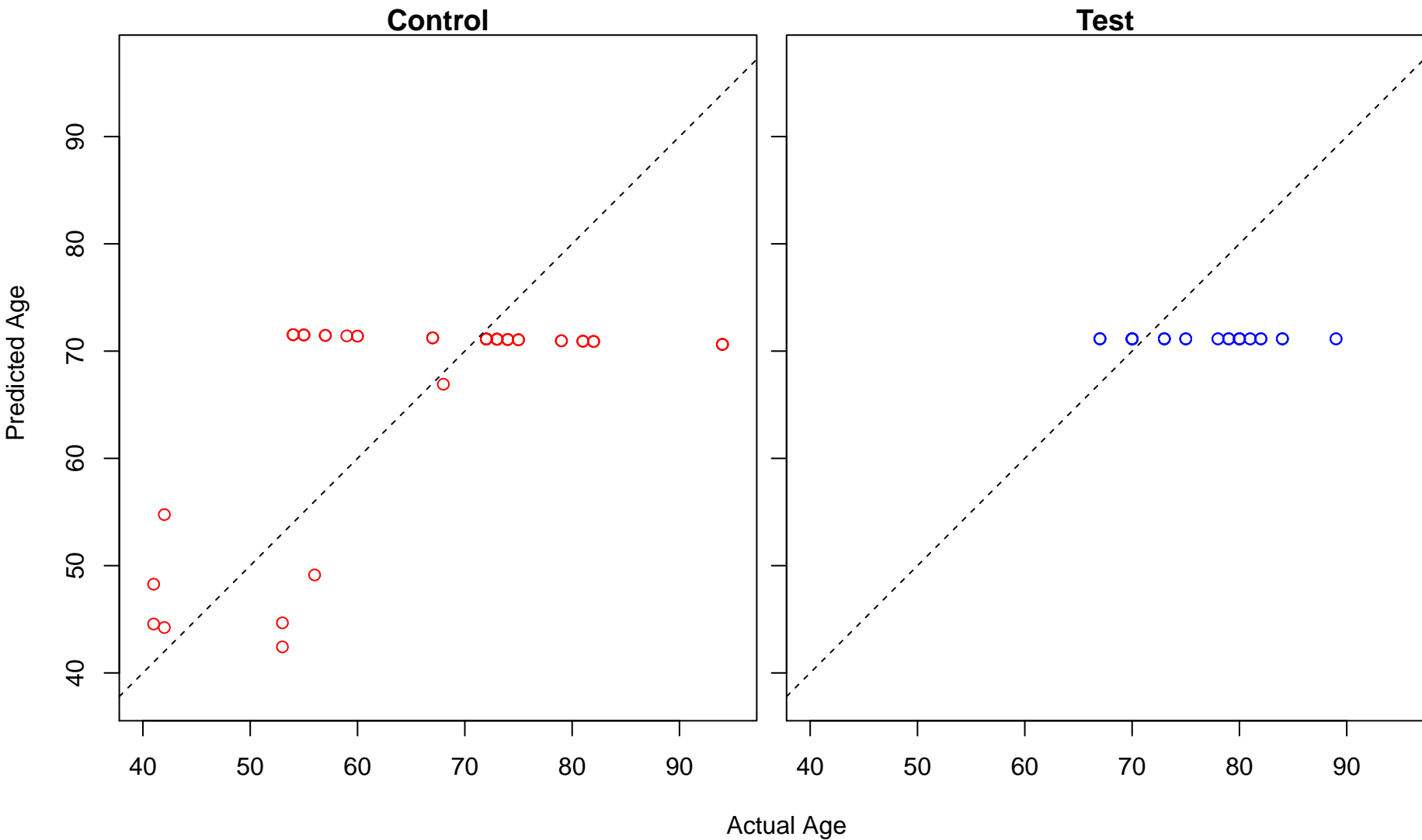
establishment of protein localization to mitochondrion (Score: 0.821447)



autophagy (Score: 0.821436)

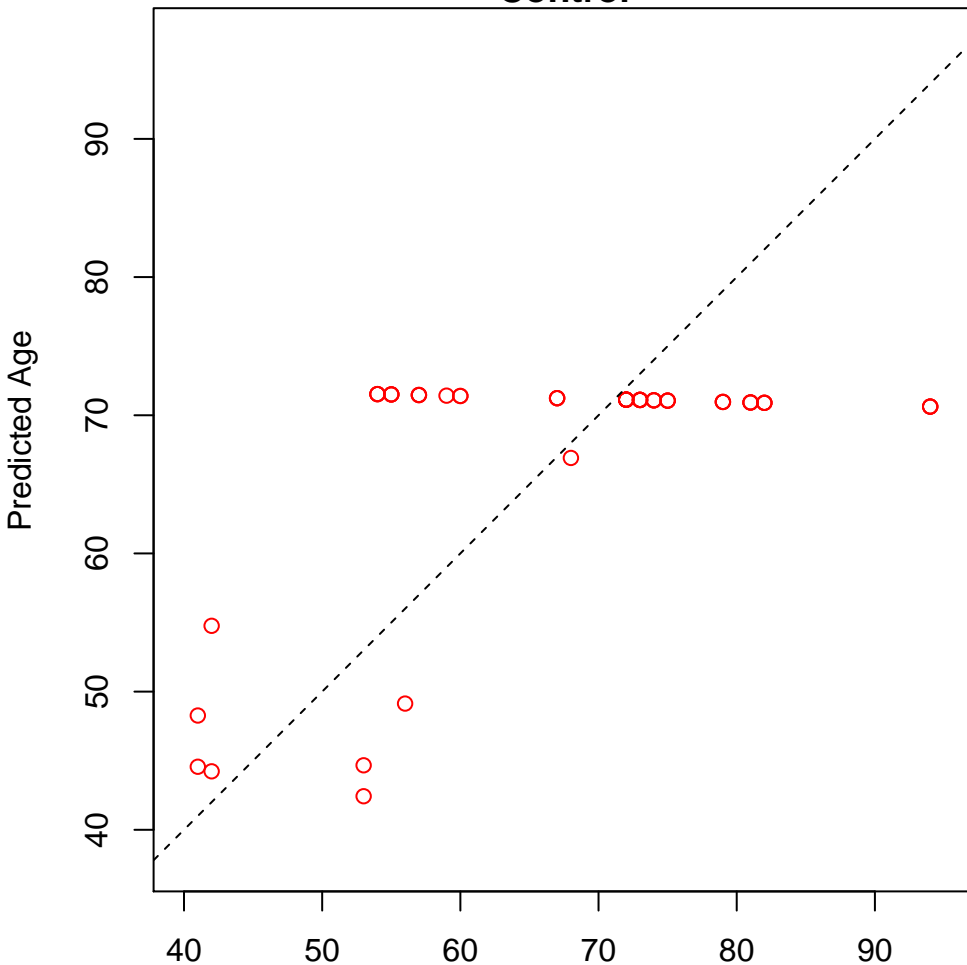


macroautophagy (Score: 0.821436)

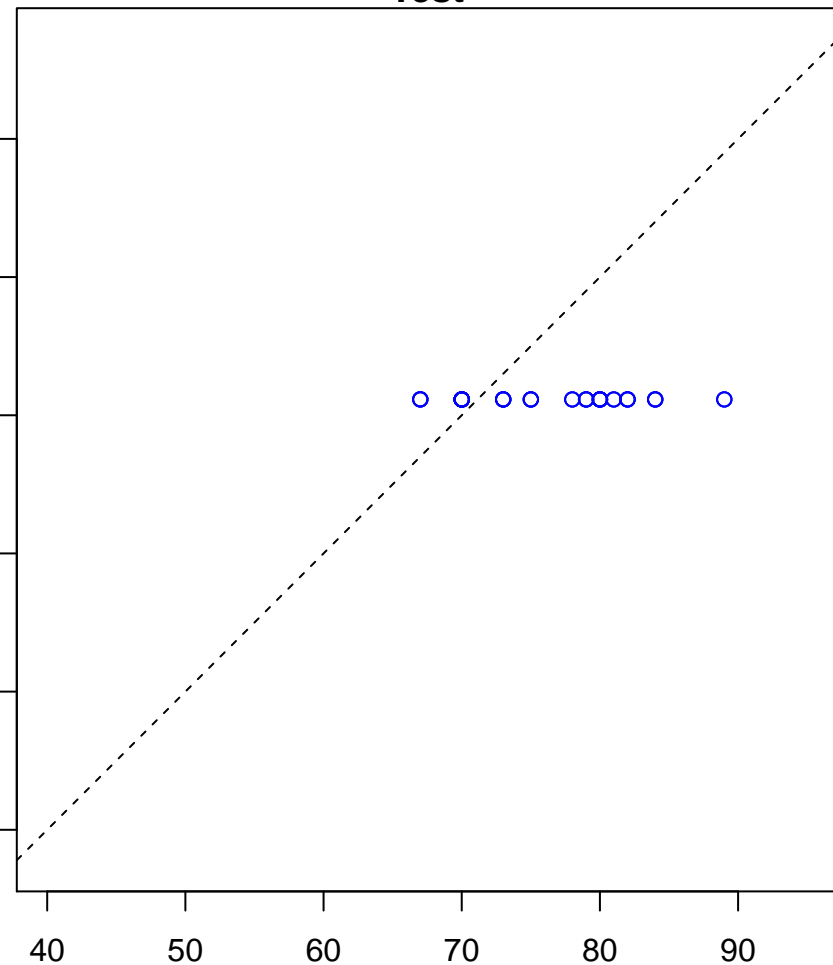


process utilizing autophagic mechanism (Score: 0.821436)

Control



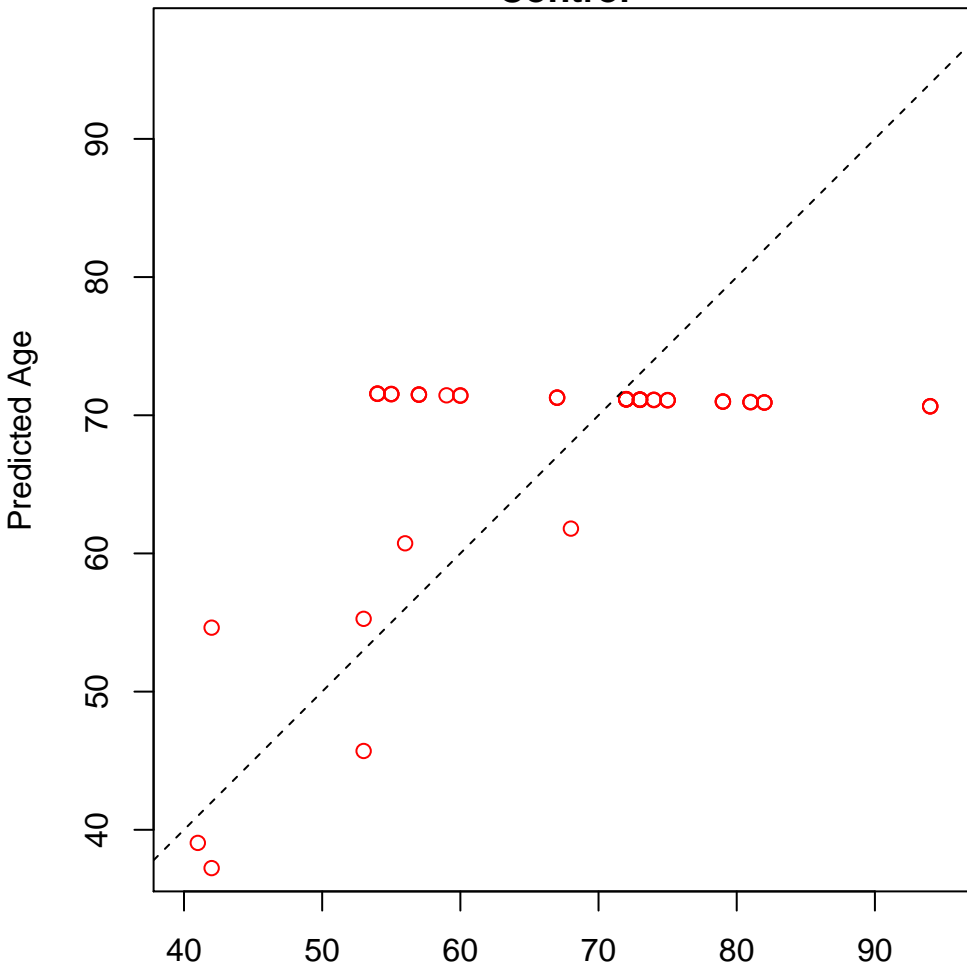
Test



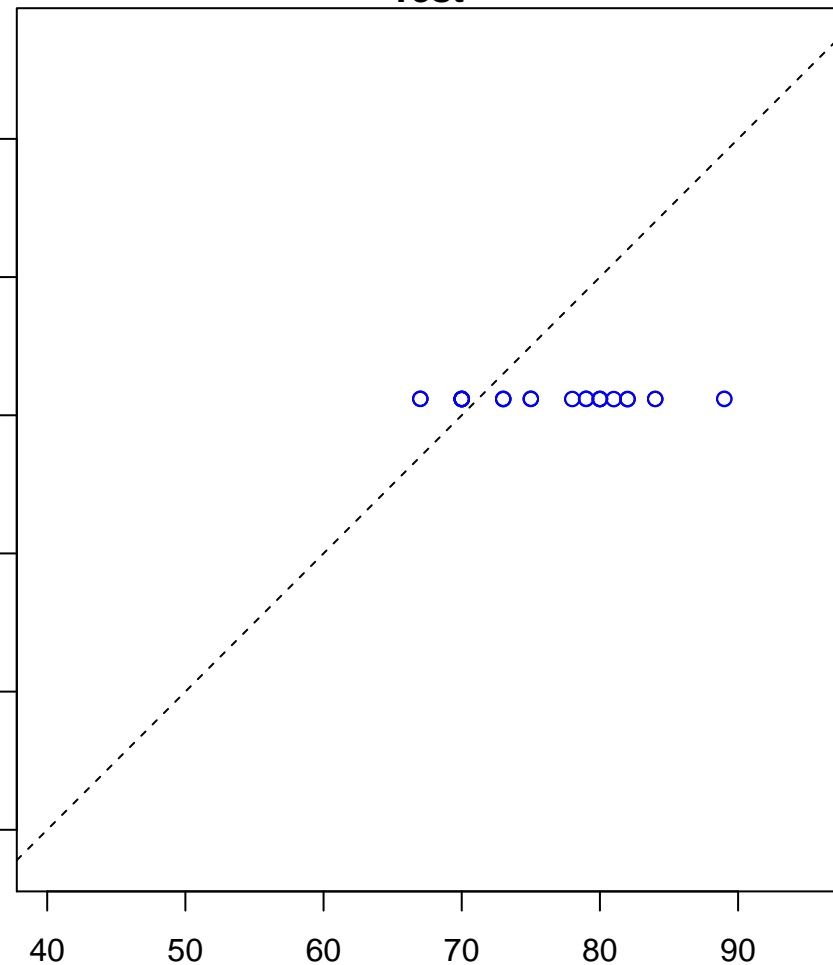
Actual Age

regulation of cytoskeleton organization (Score: 0.821217)

Control

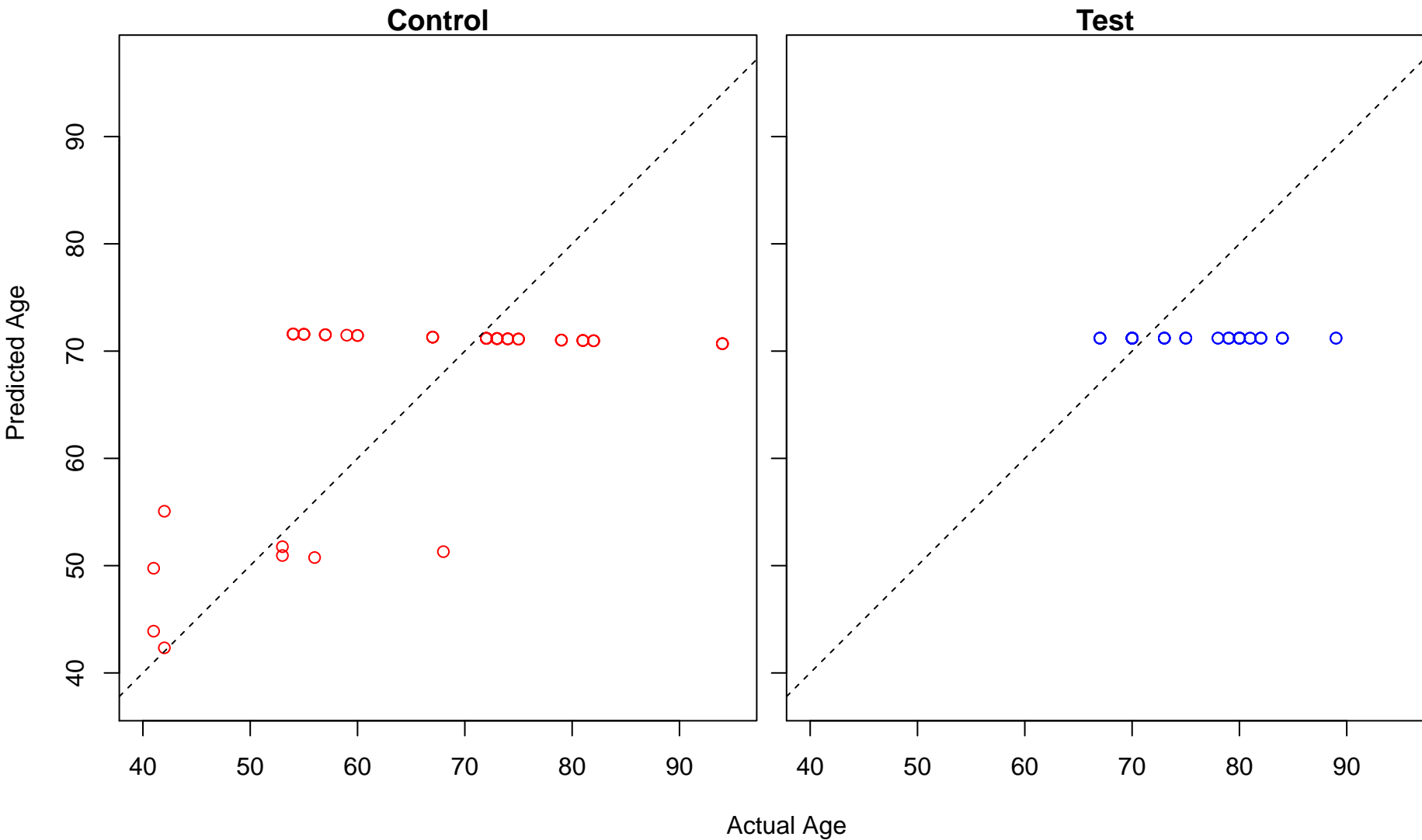


Test

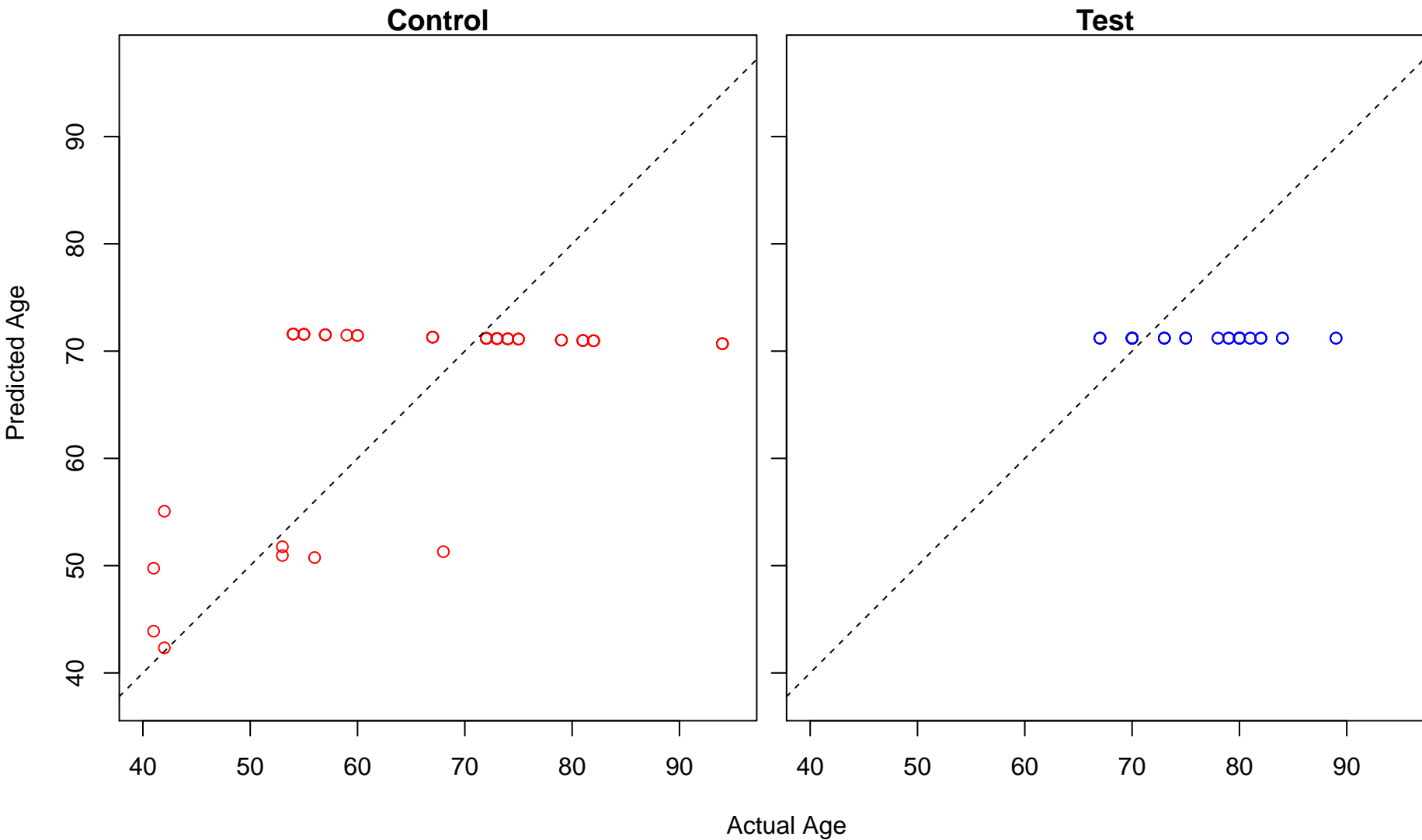


Actual Age

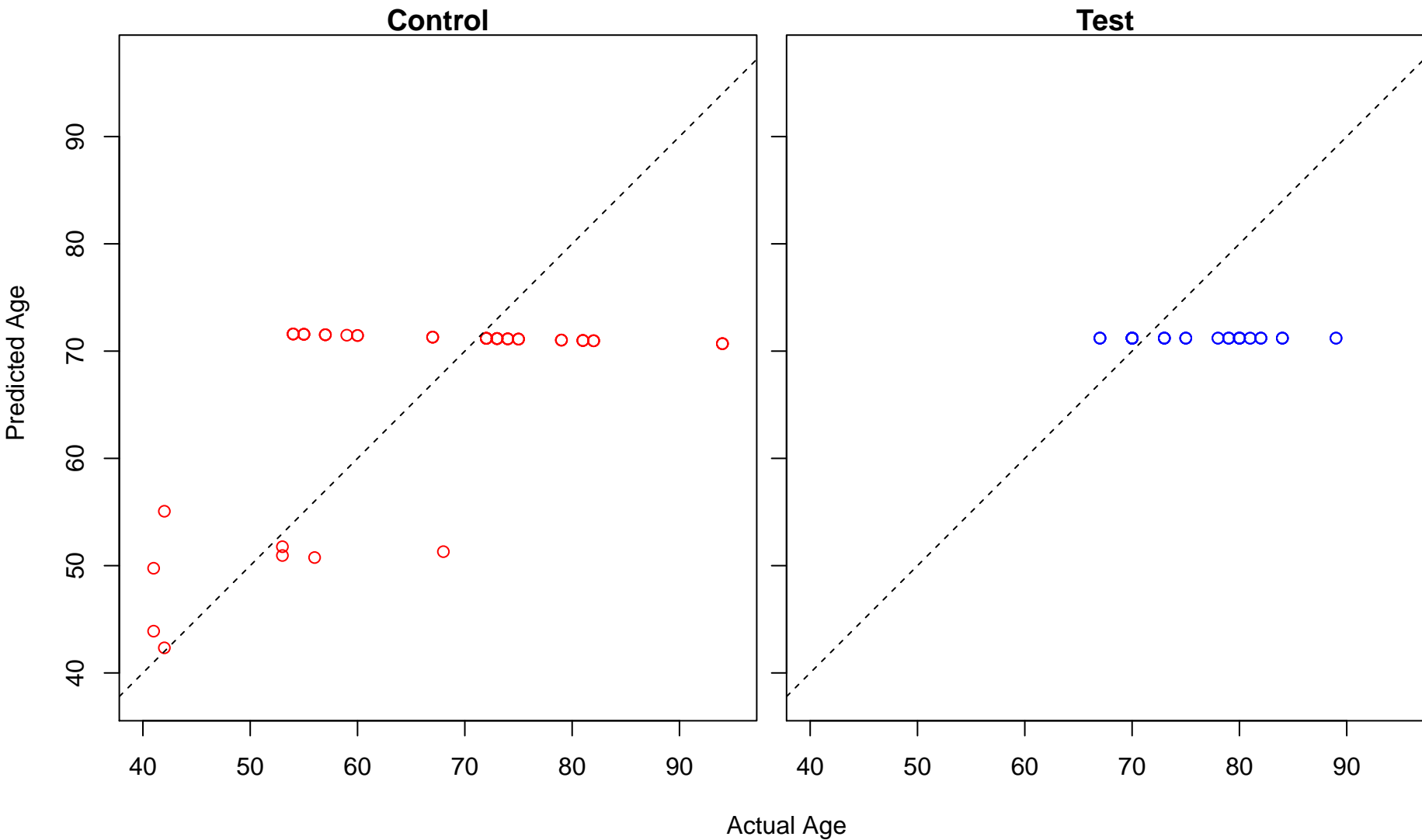
low-density lipoprotein receptor particle metabolic process (Score: 0.821188)



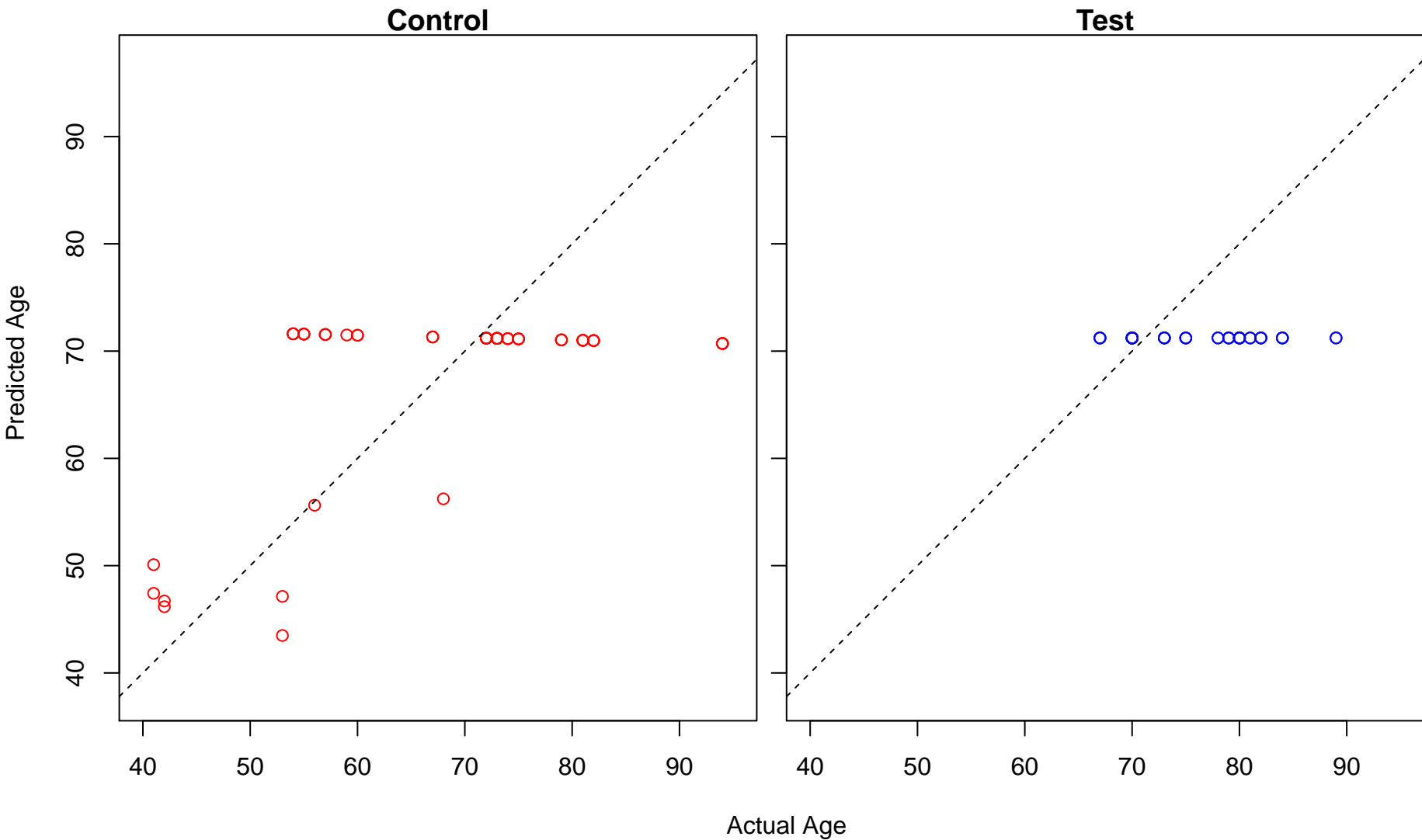
receptor catabolic process (Score: 0.821188)



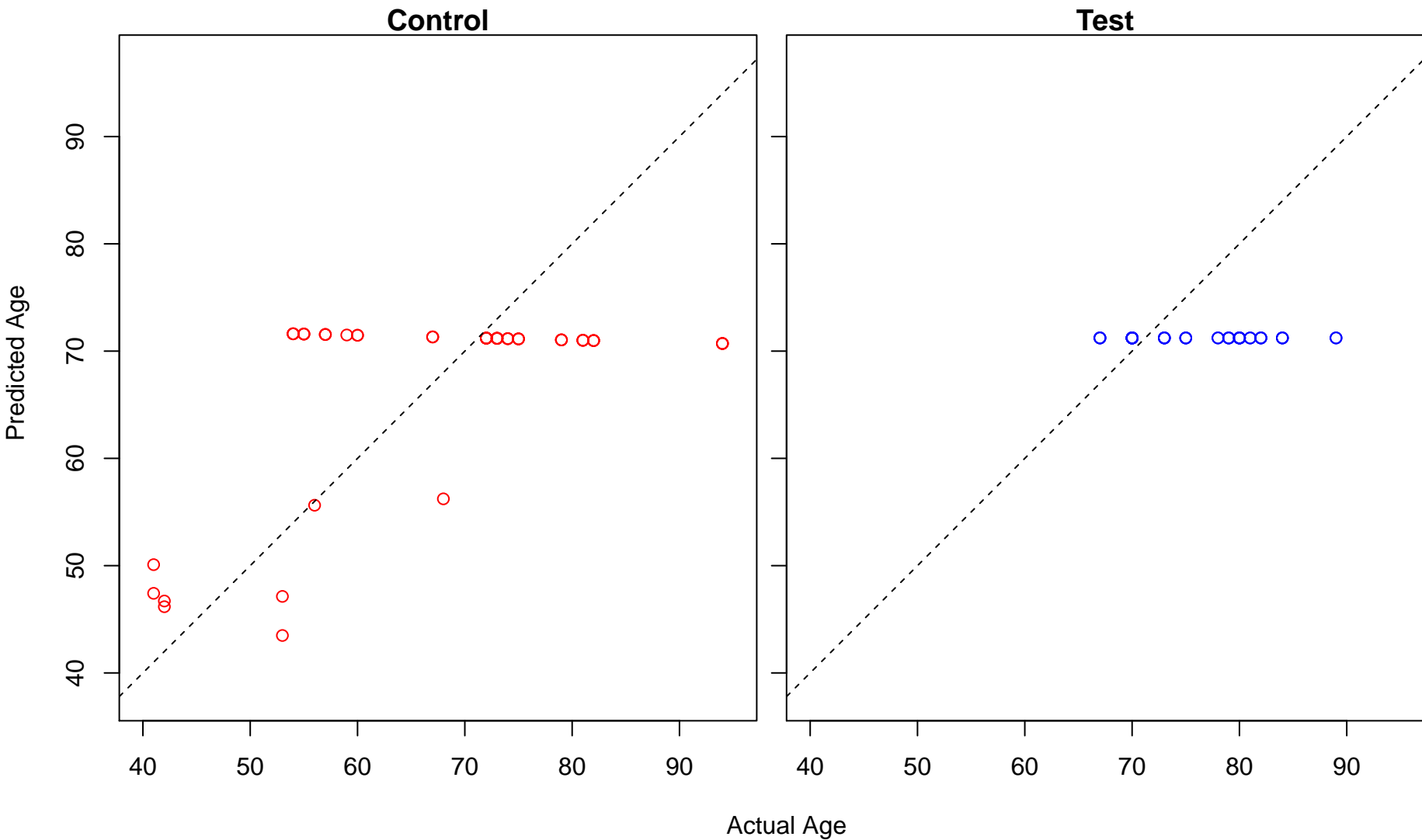
low-density lipoprotein particle receptor catabolic process (Score: 0.821188)



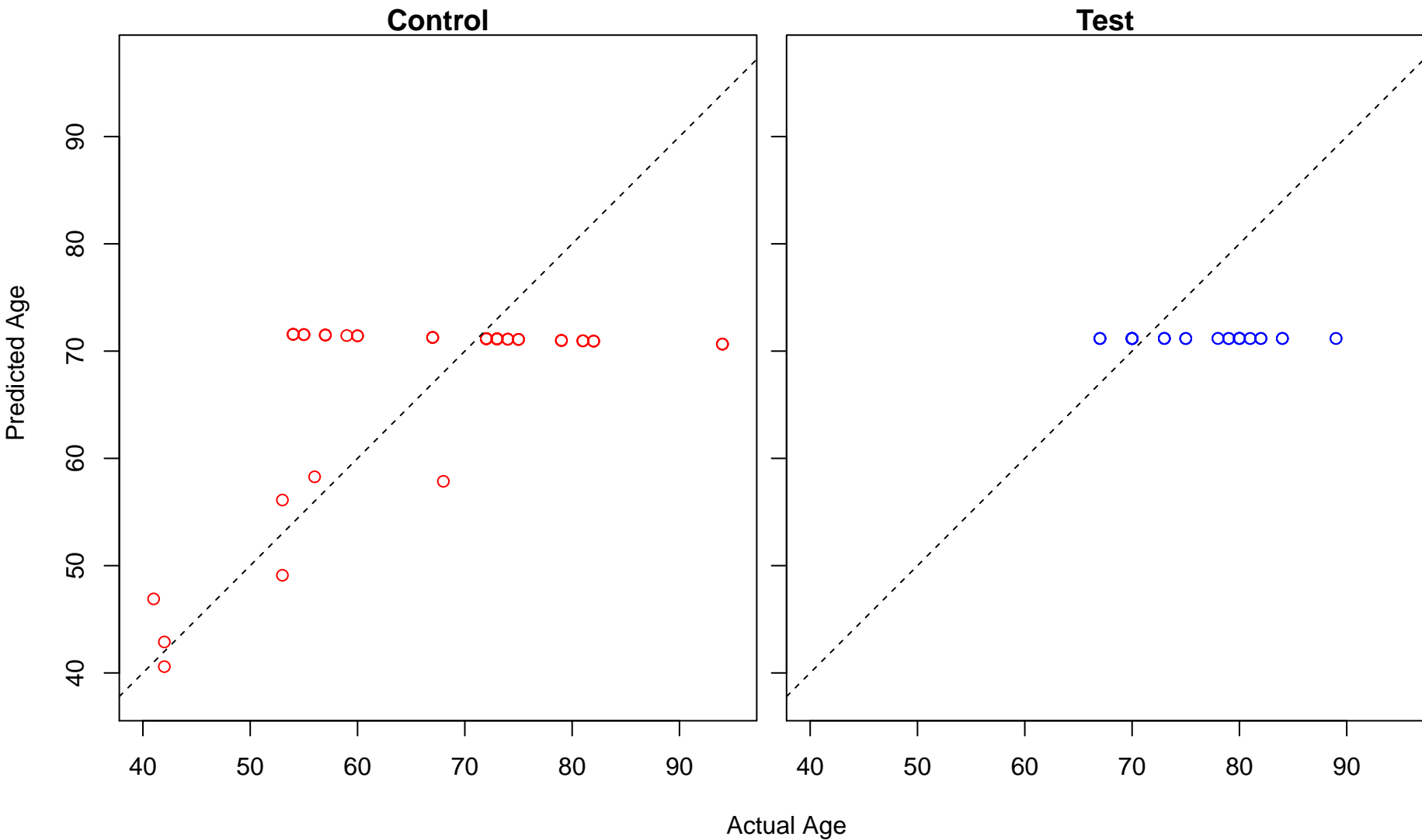
cell projection organization (Score: 0.821187)



plasma membrane bounded cell projection organization (Score: 0.821187)

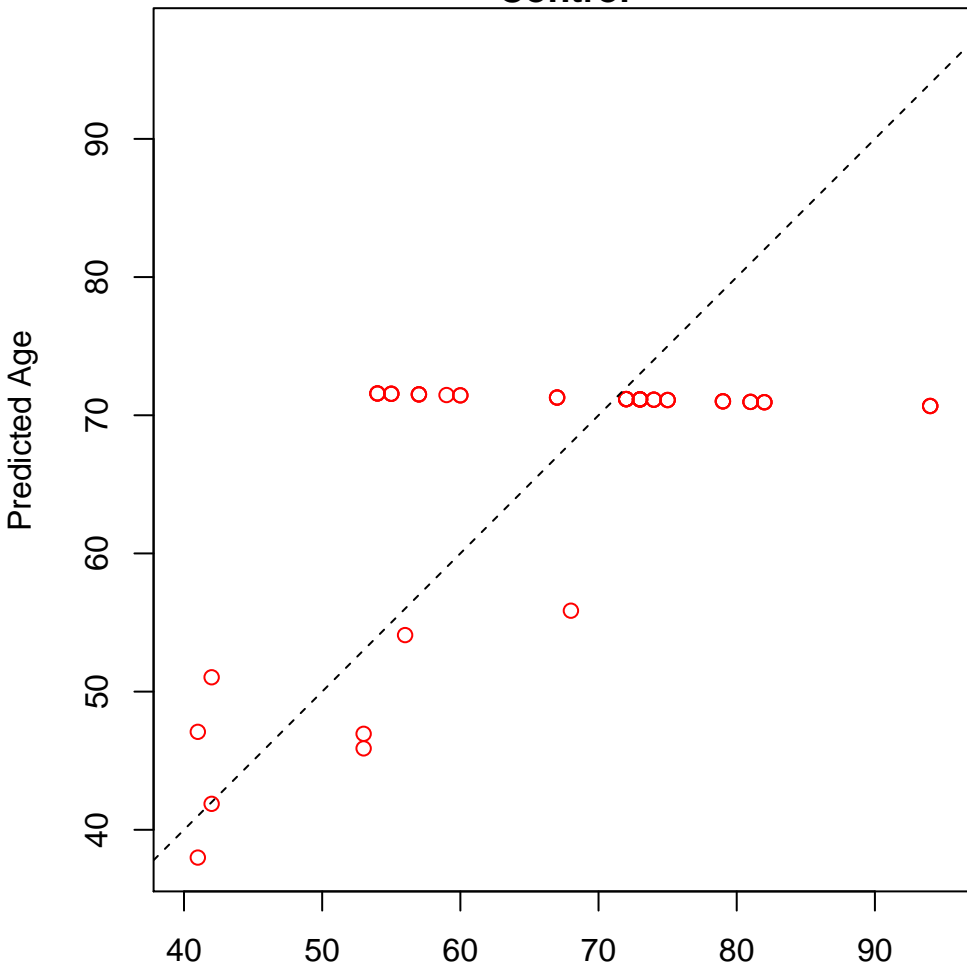


regulation of cellular protein catabolic process (Score: 0.821086)

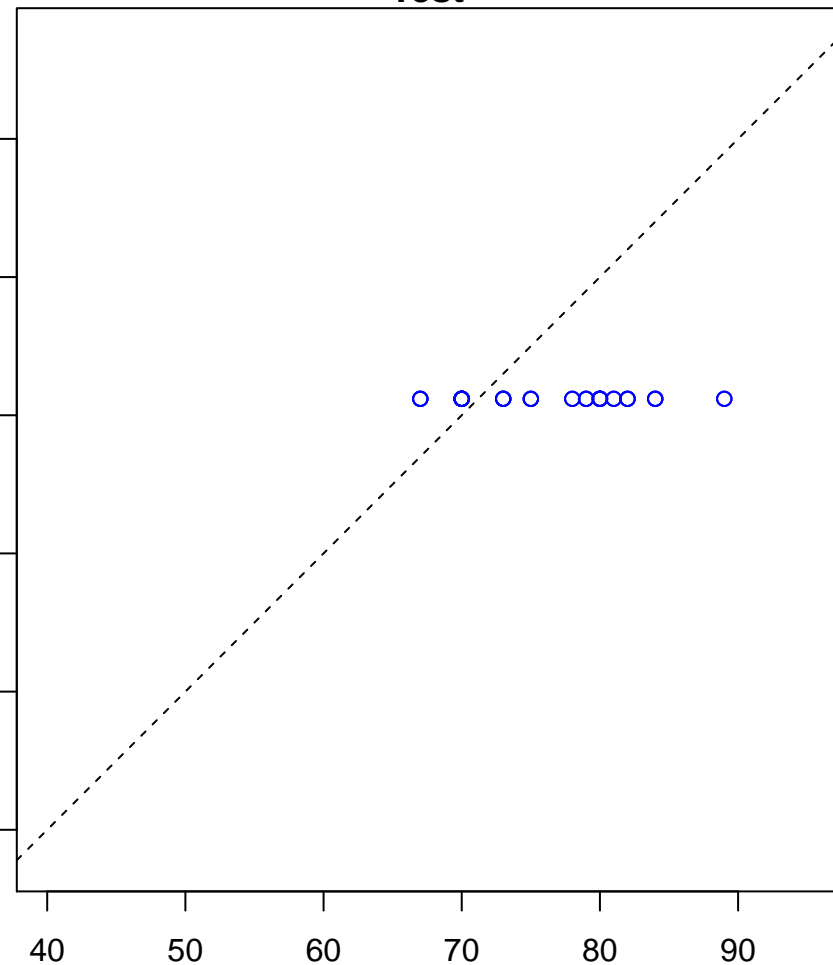


regulation of protein kinase activity (Score: 0.821080)

Control



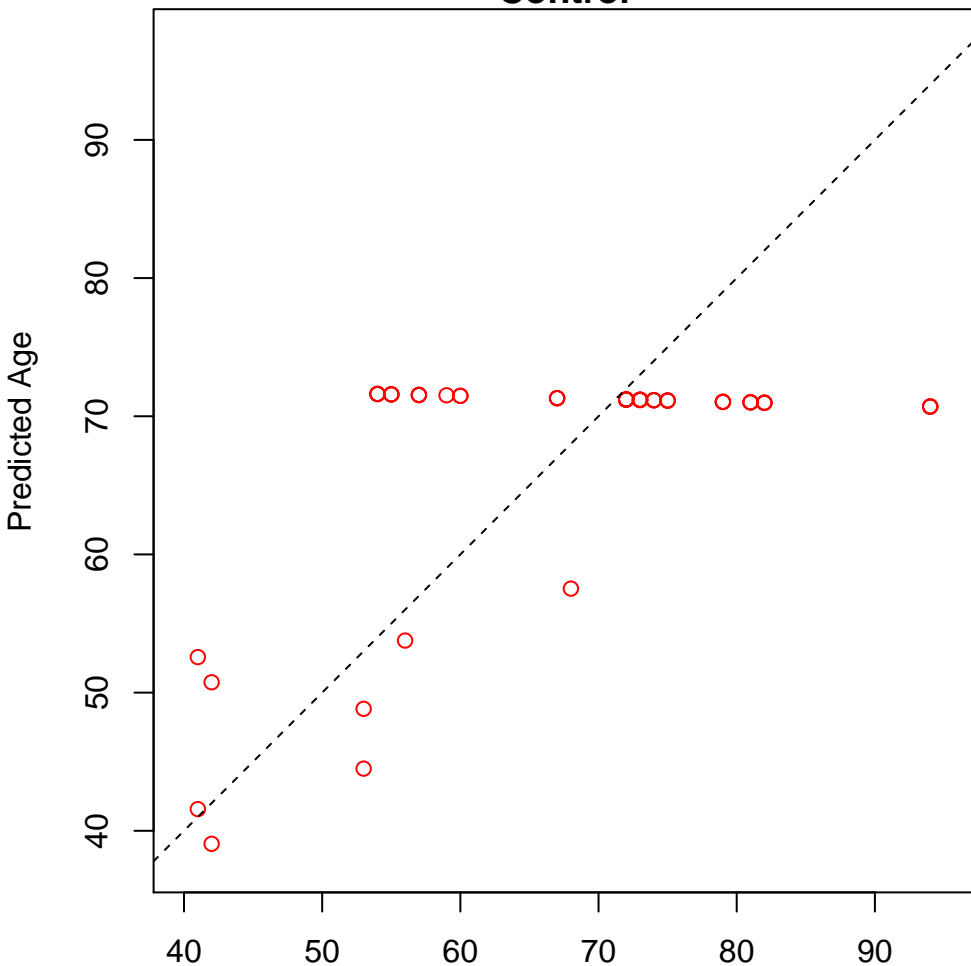
Test



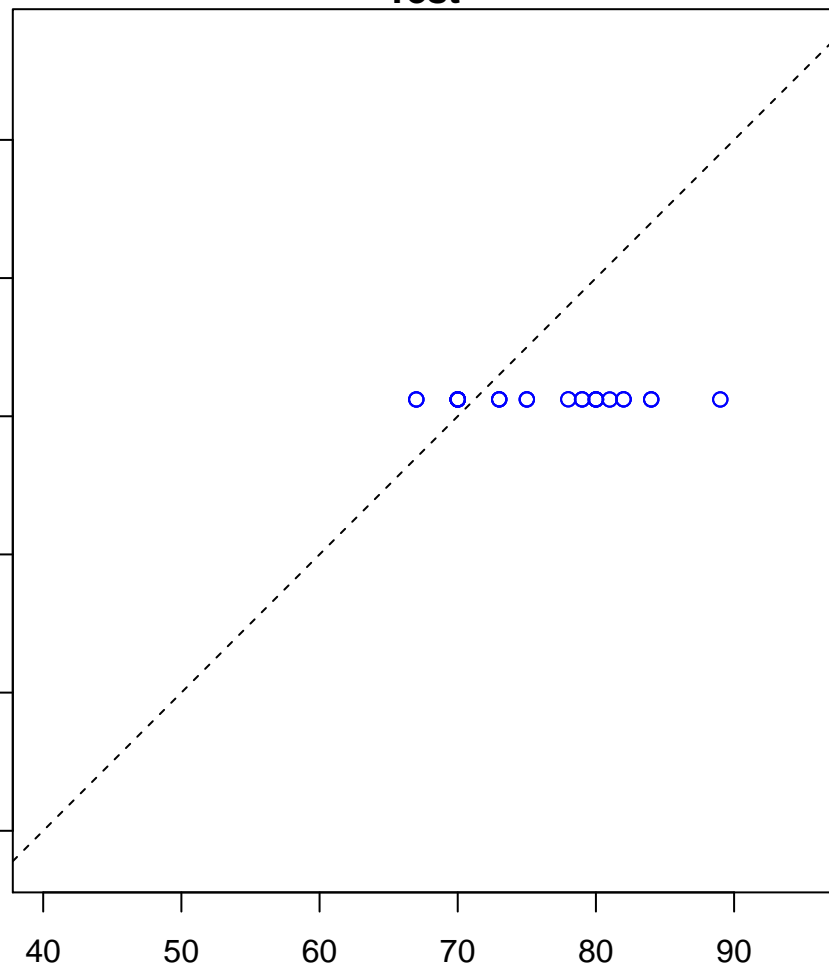
Actual Age

aging (Score: 0.821080)

Control



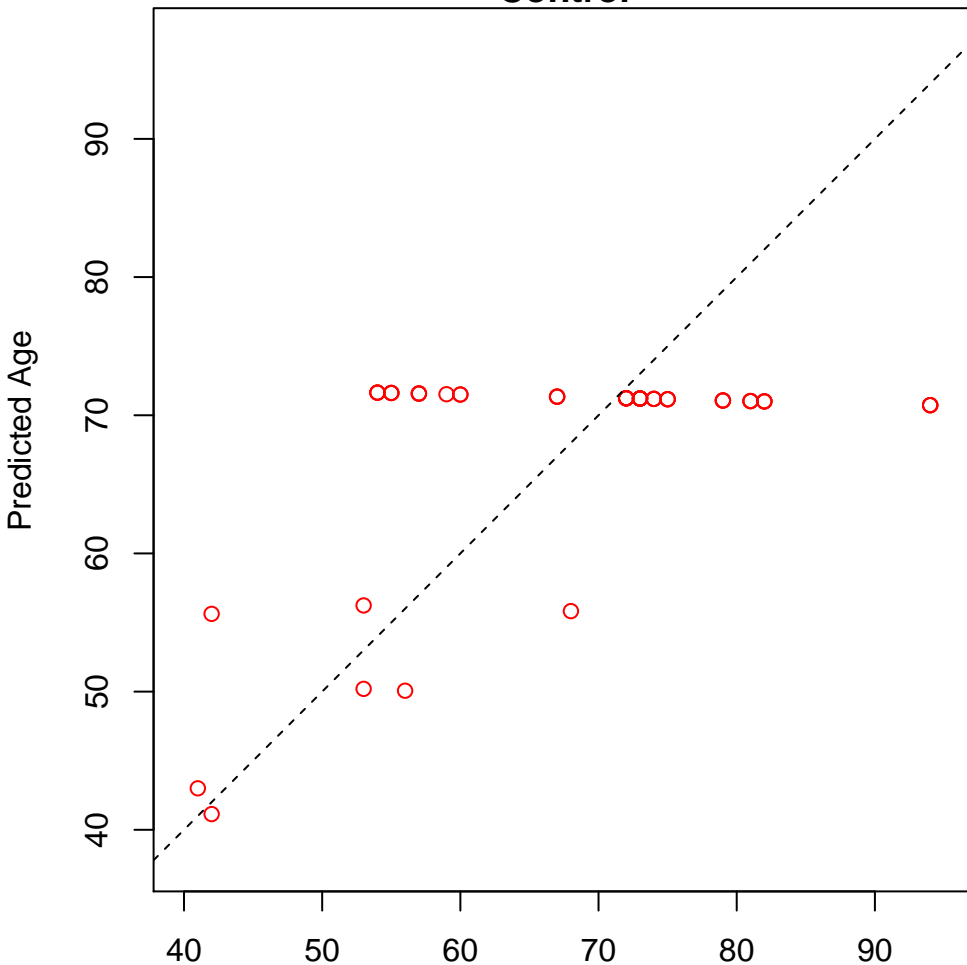
Test



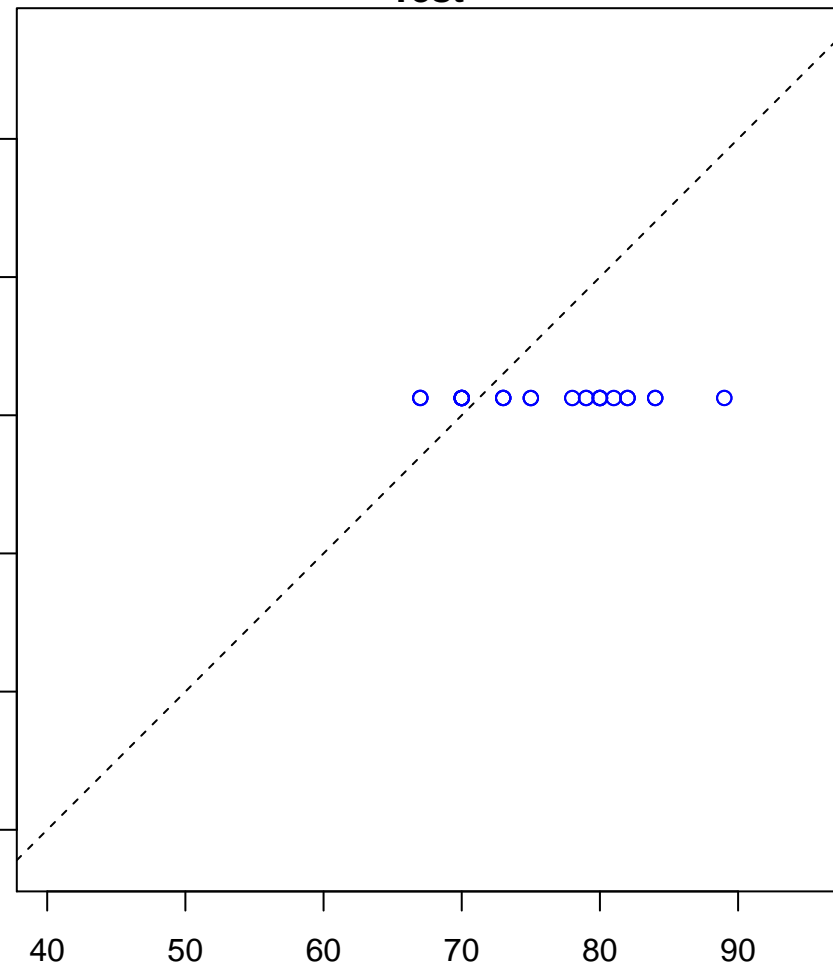
Actual Age

regulation of neuron apoptotic process (Score: 0.821046)

Control



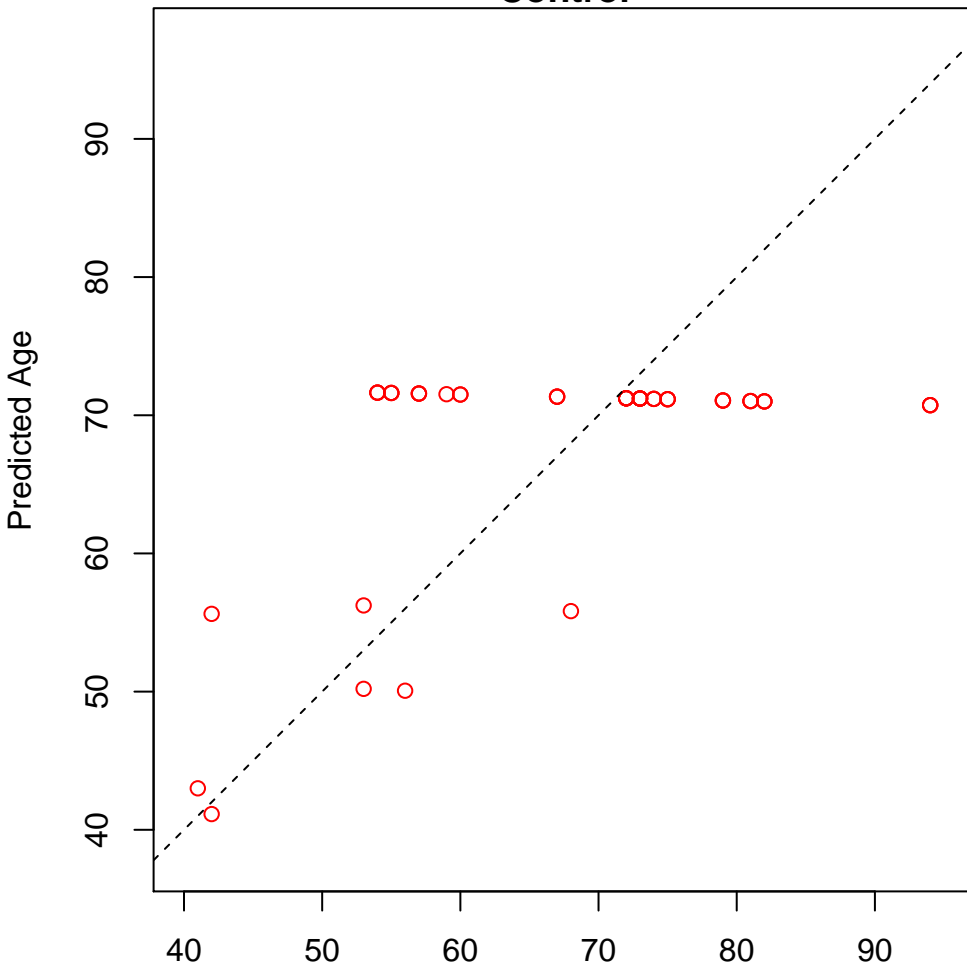
Test



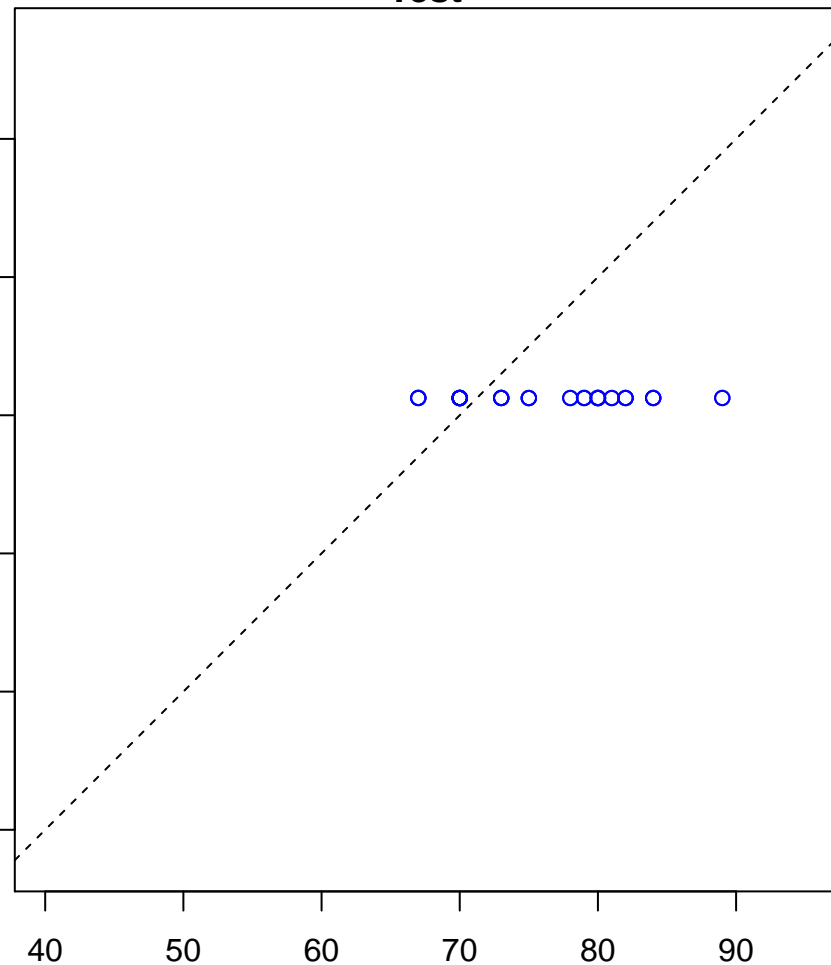
Actual Age

negative regulation of neuron death (Score: 0.821046)

Control

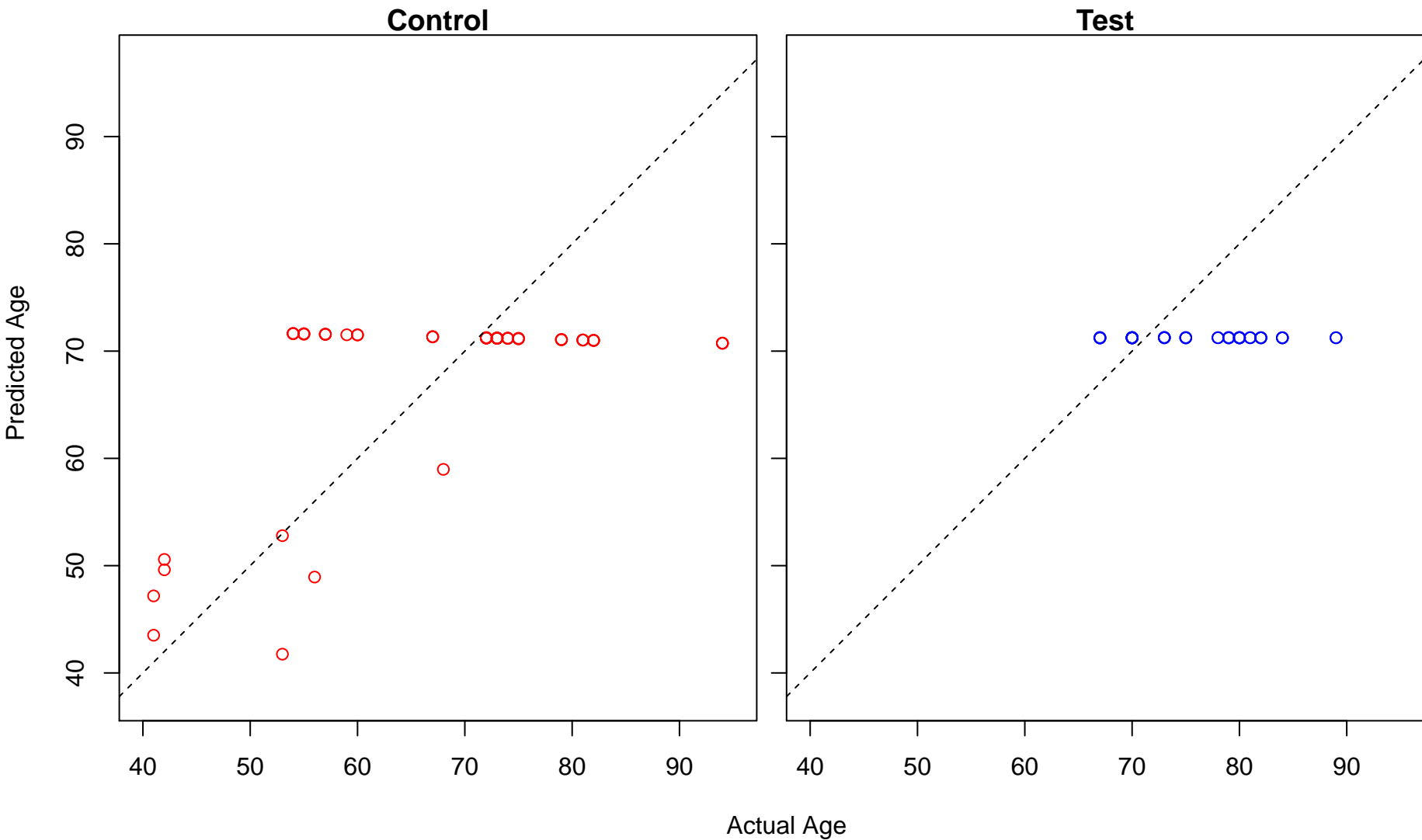


Test

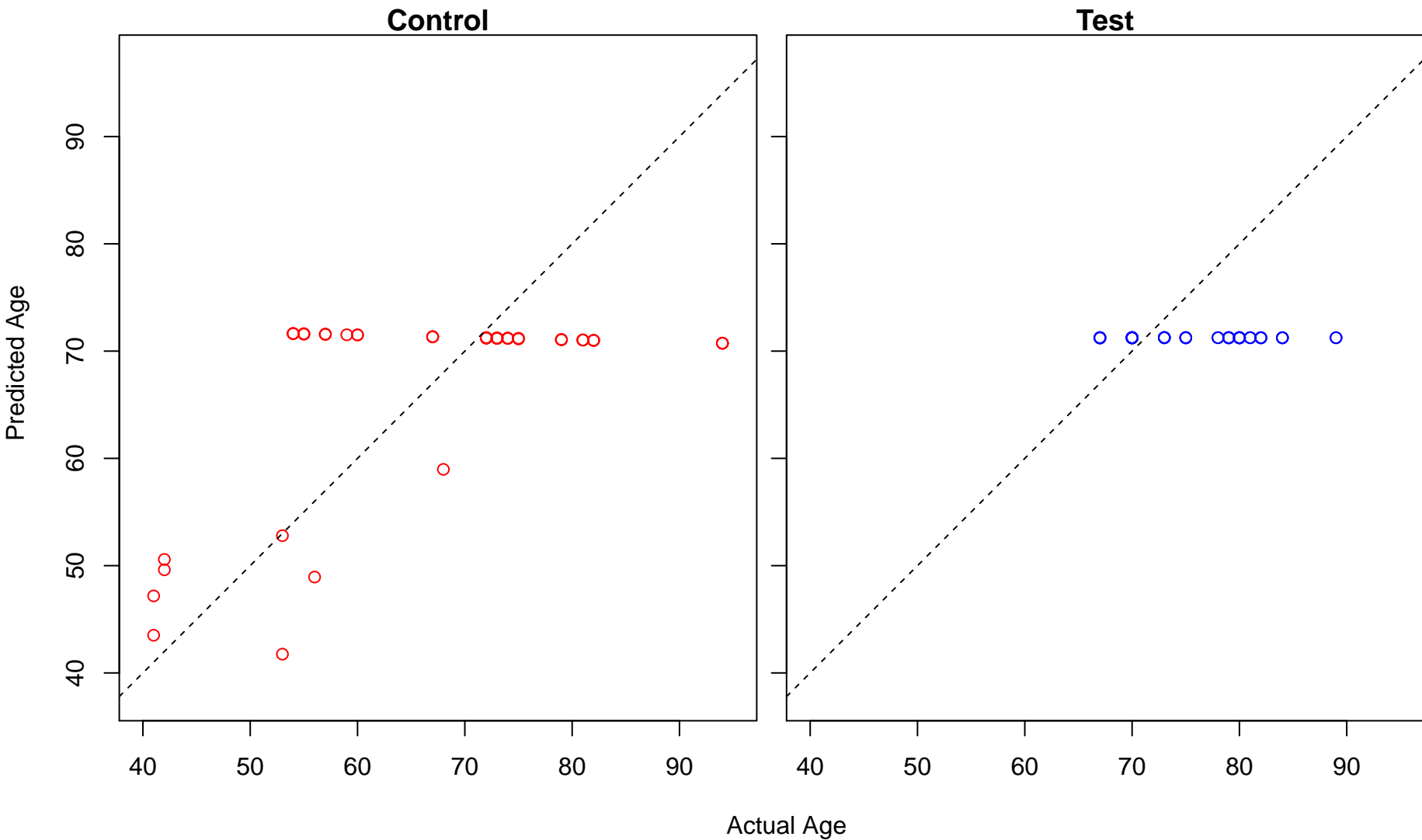


Actual Age

cellular glucose homeostasis (Score: 0.821014)

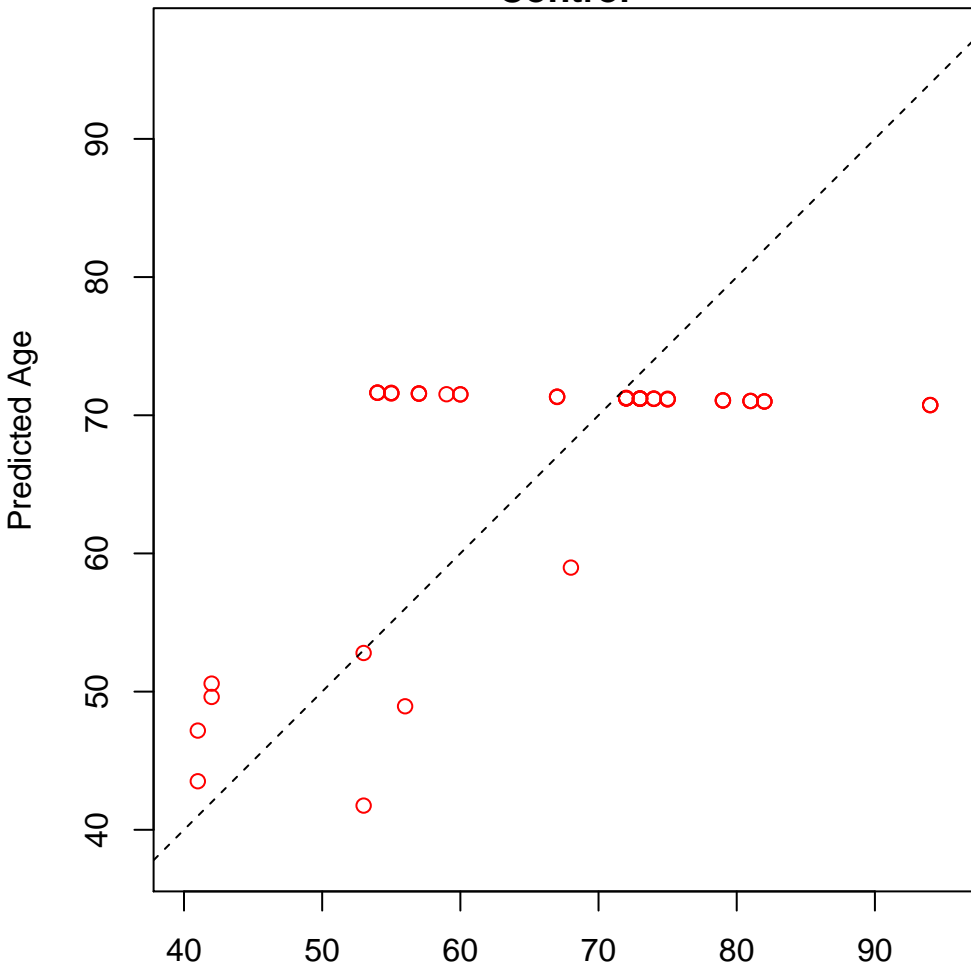


response to nutrient (Score: 0.821014)

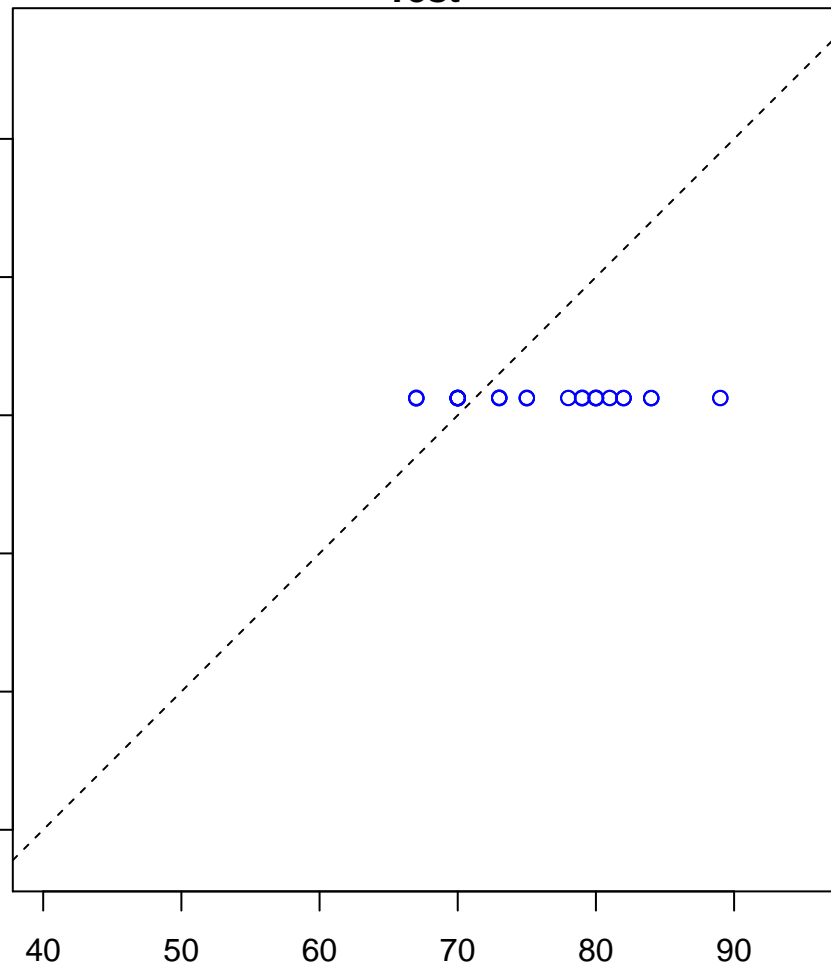


response to hexose (Score: 0.821014)

Control

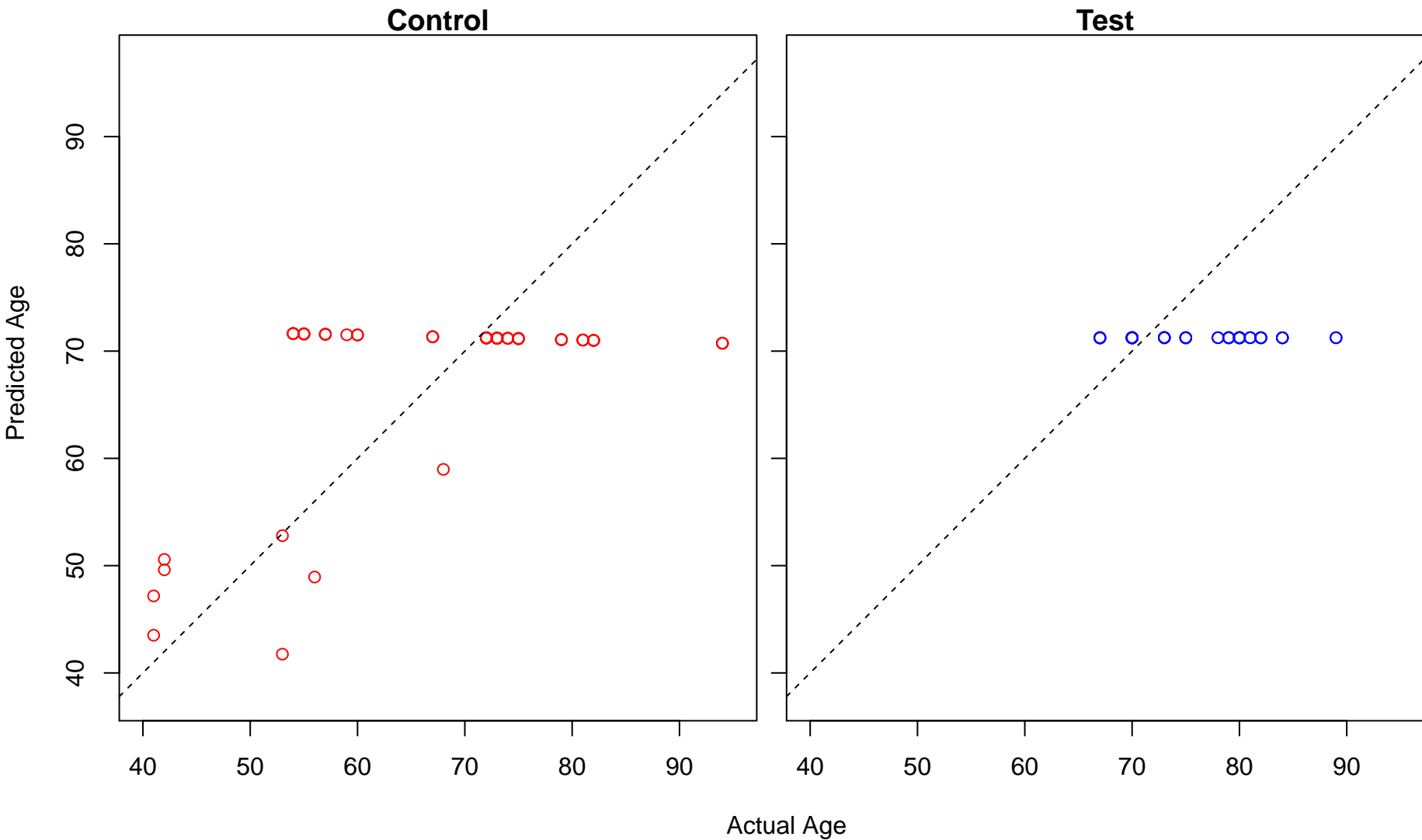


Test



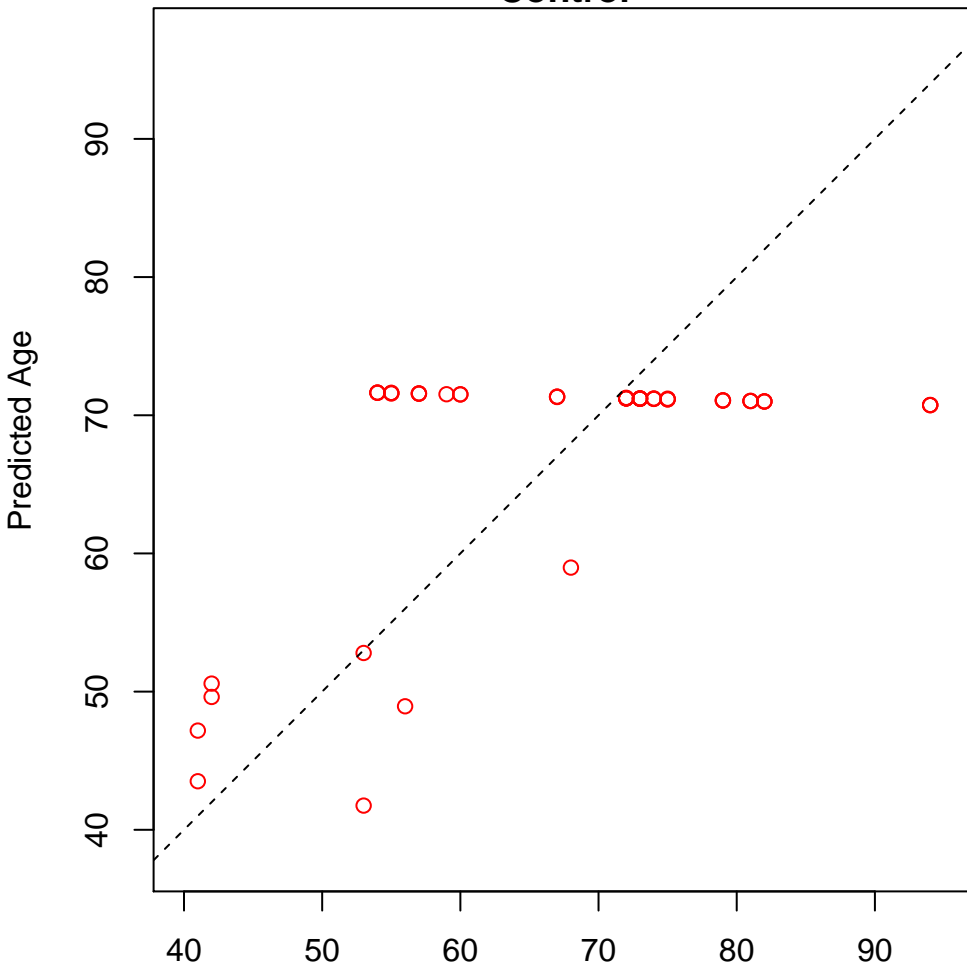
Actual Age

response to glucose (Score: 0.821014)

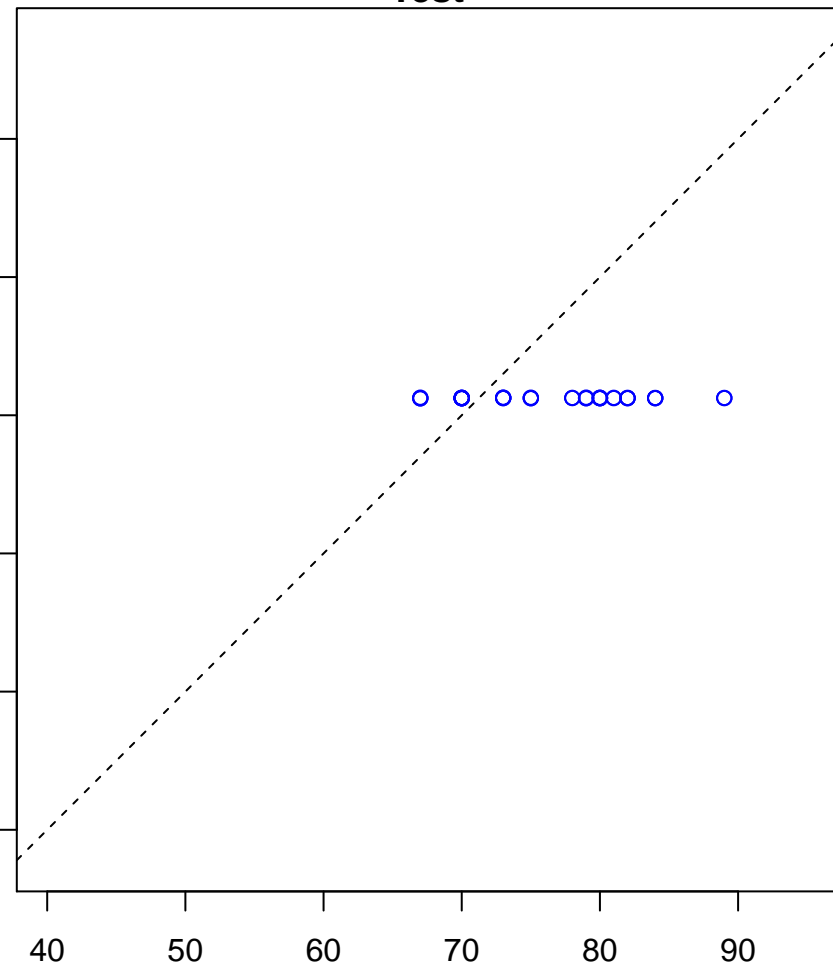


cellular response to nutrient (Score: 0.821014)

Control

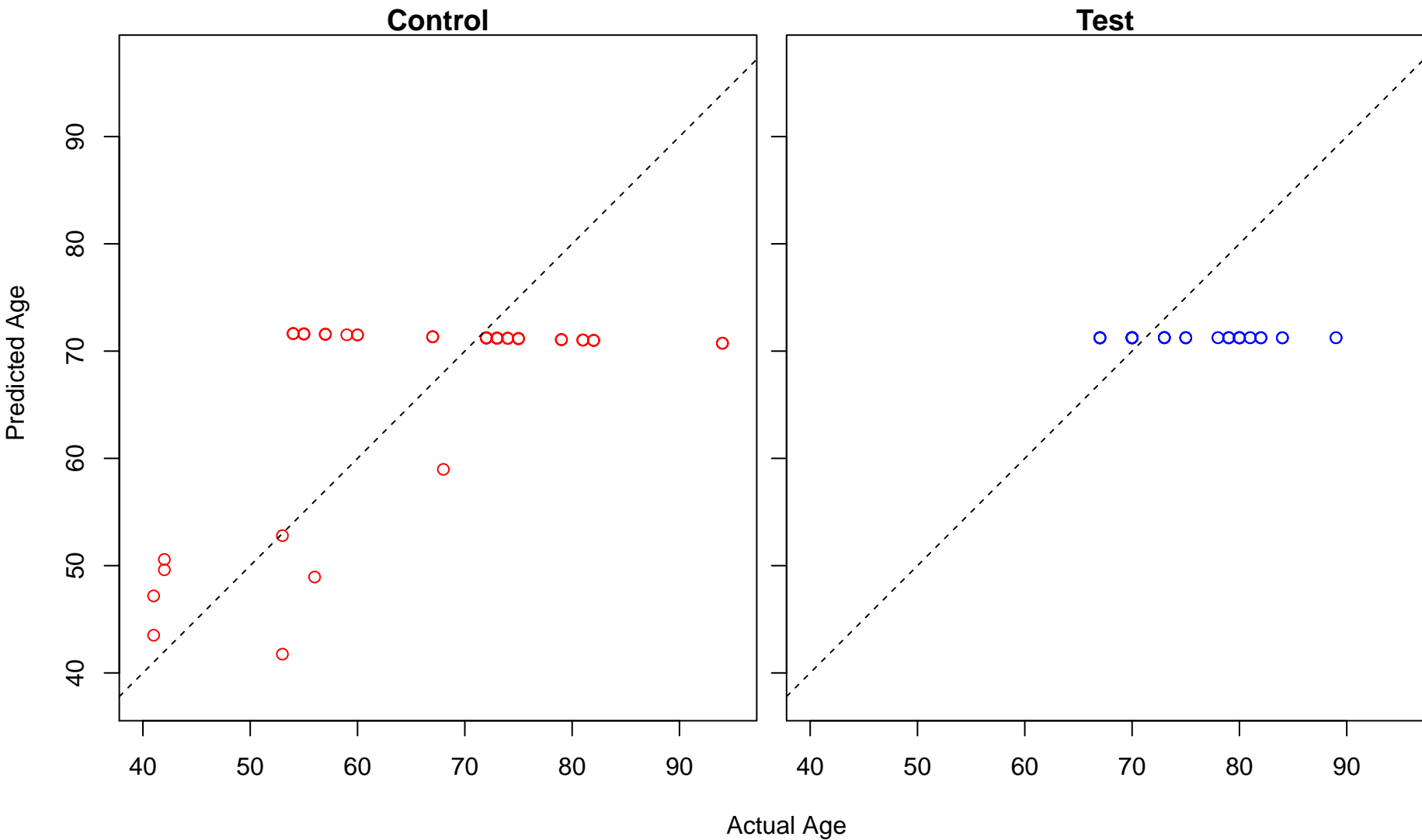


Test

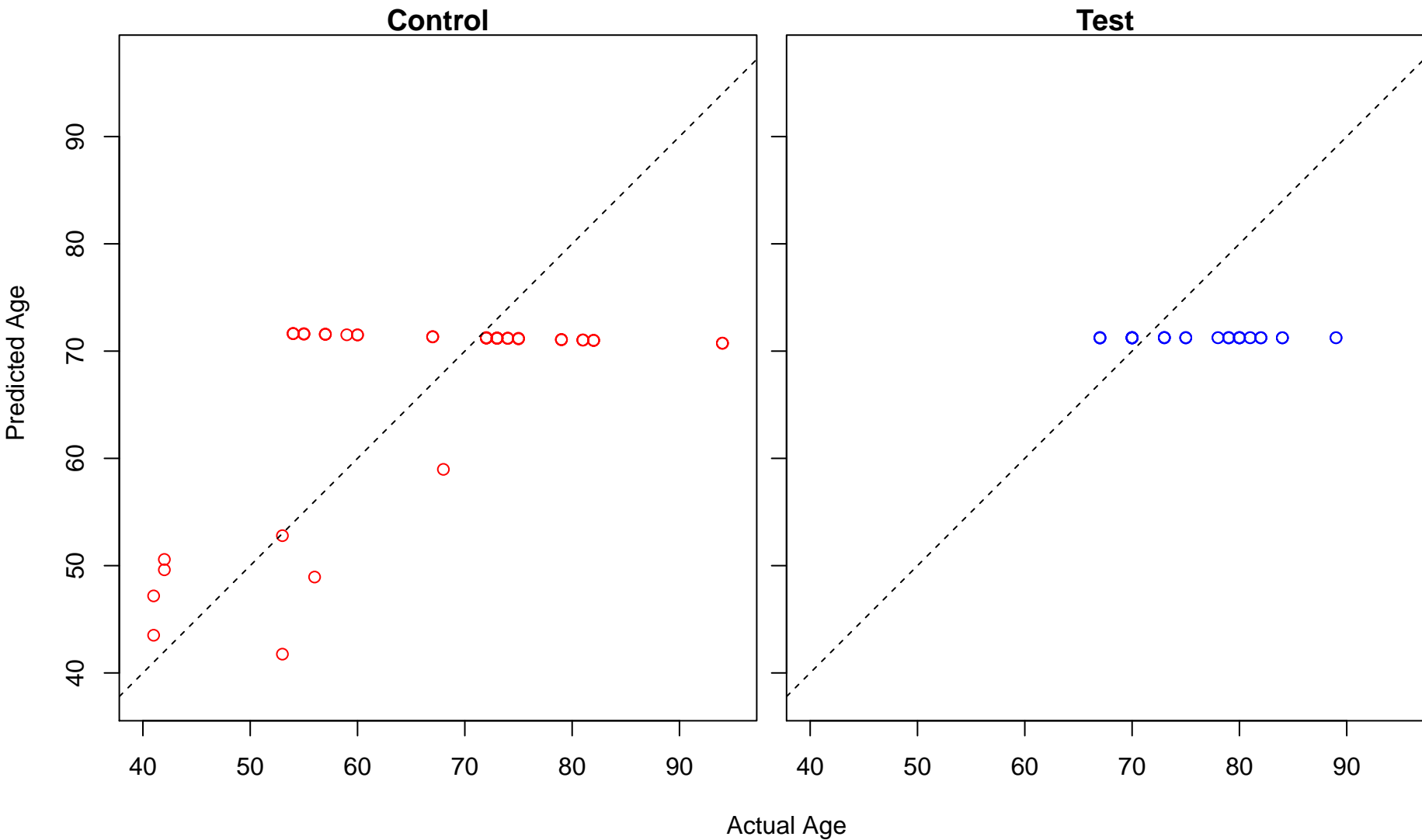


Actual Age

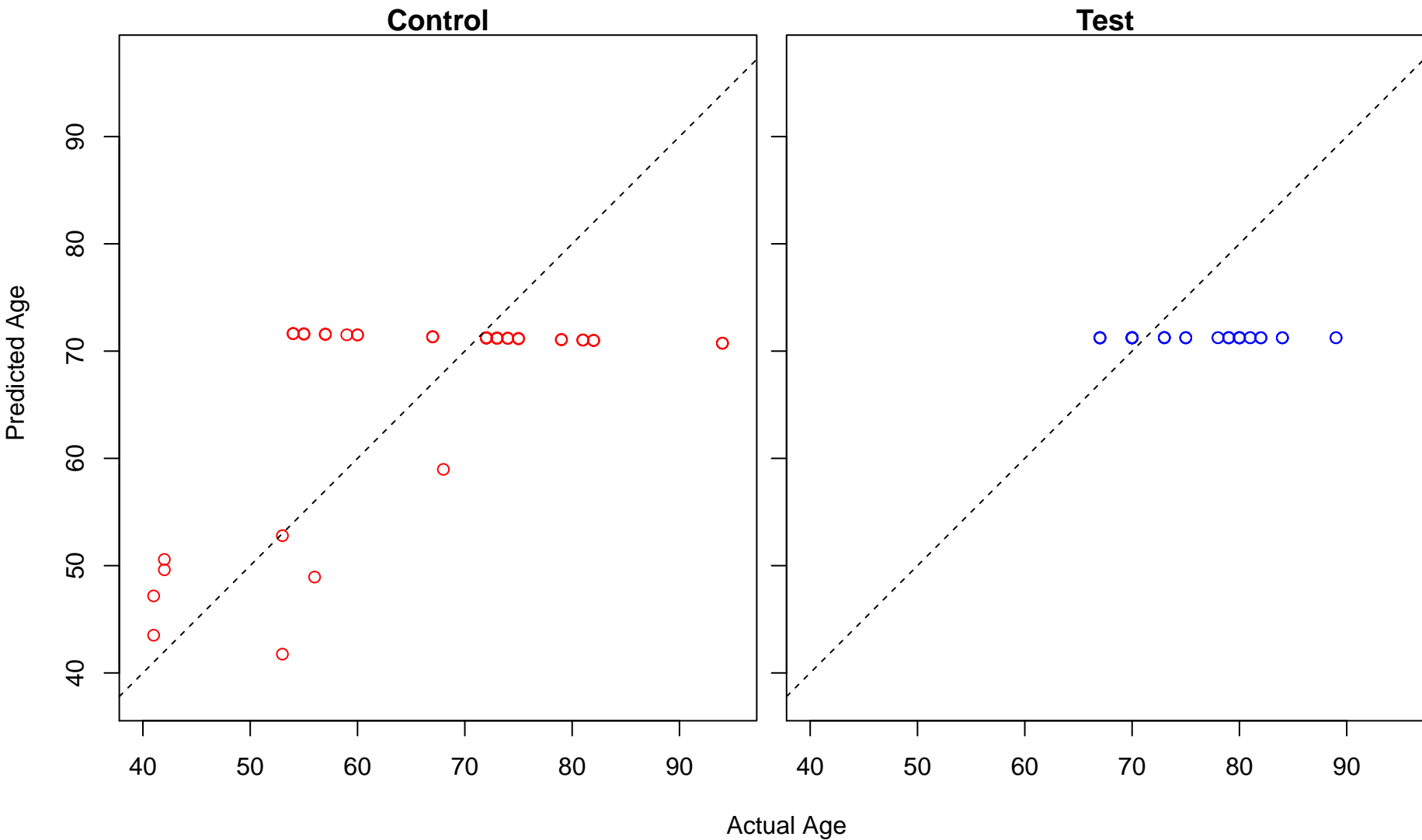
response to monosaccharide (Score: 0.821014)



cellular response to carbohydrate stimulus (Score: 0.821014)

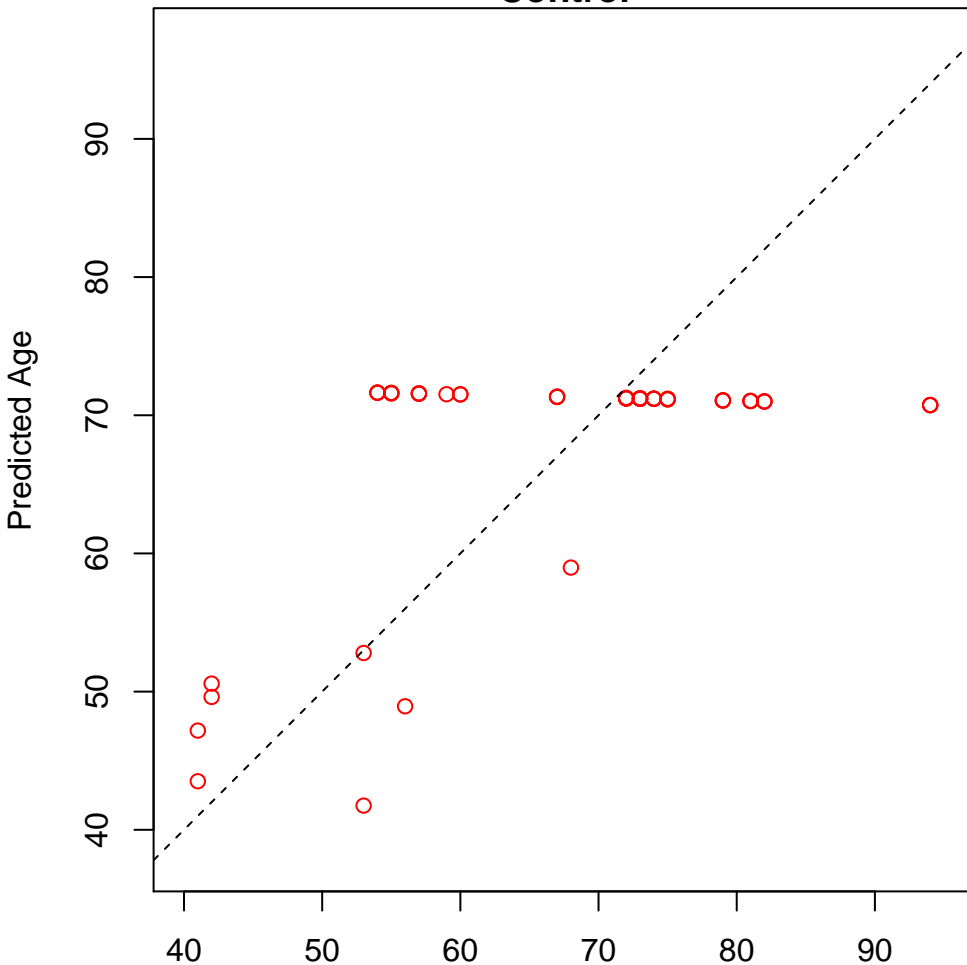


cellular response to monosaccharide stimulus (Score: 0.821014)

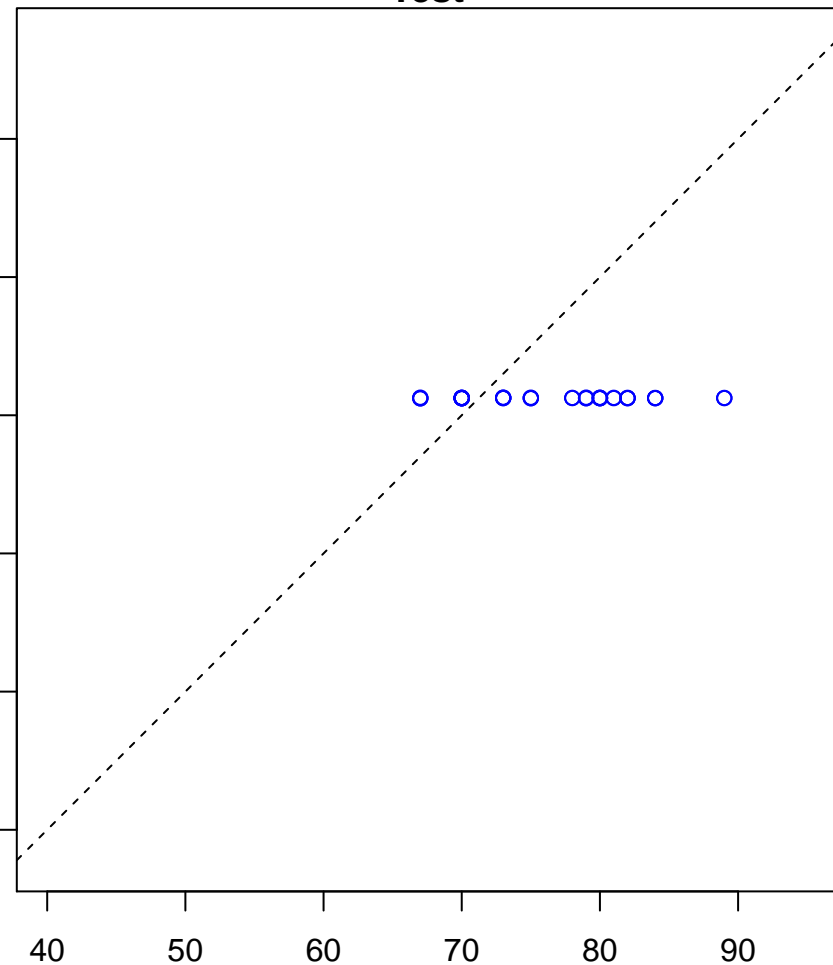


cellular response to hexose stimulus (Score: 0.821014)

Control



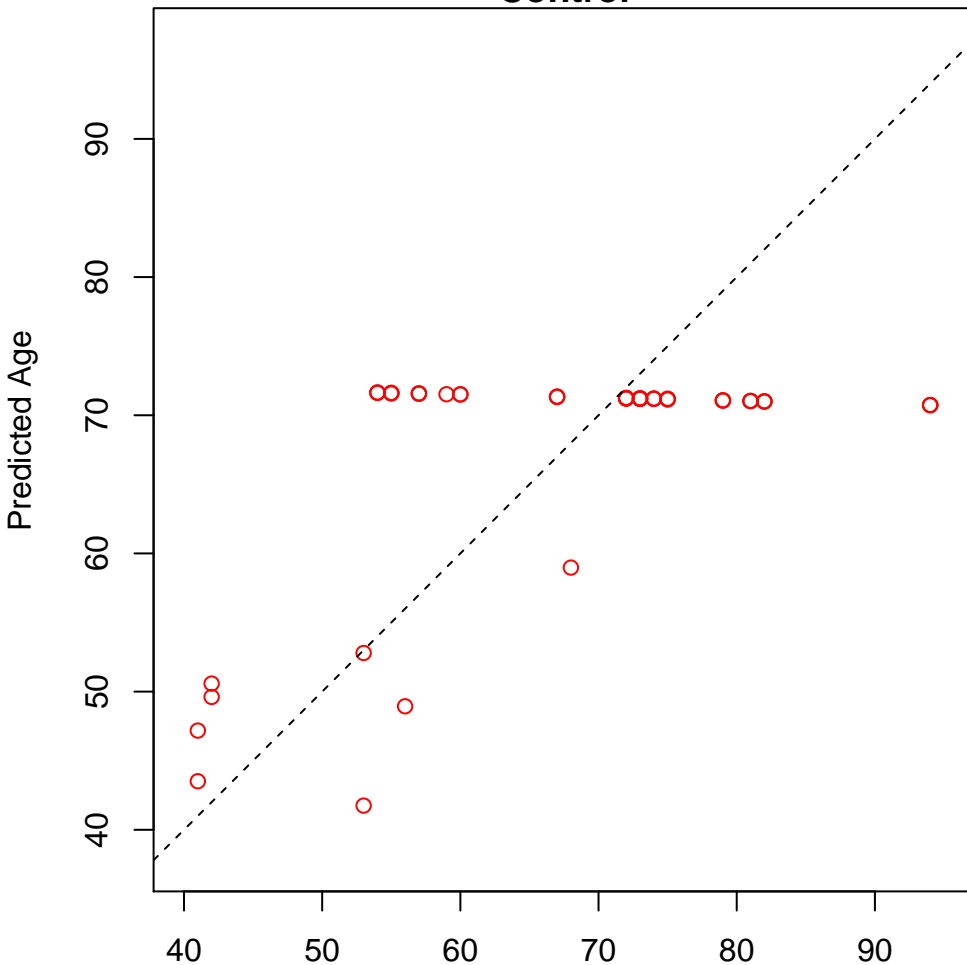
Test



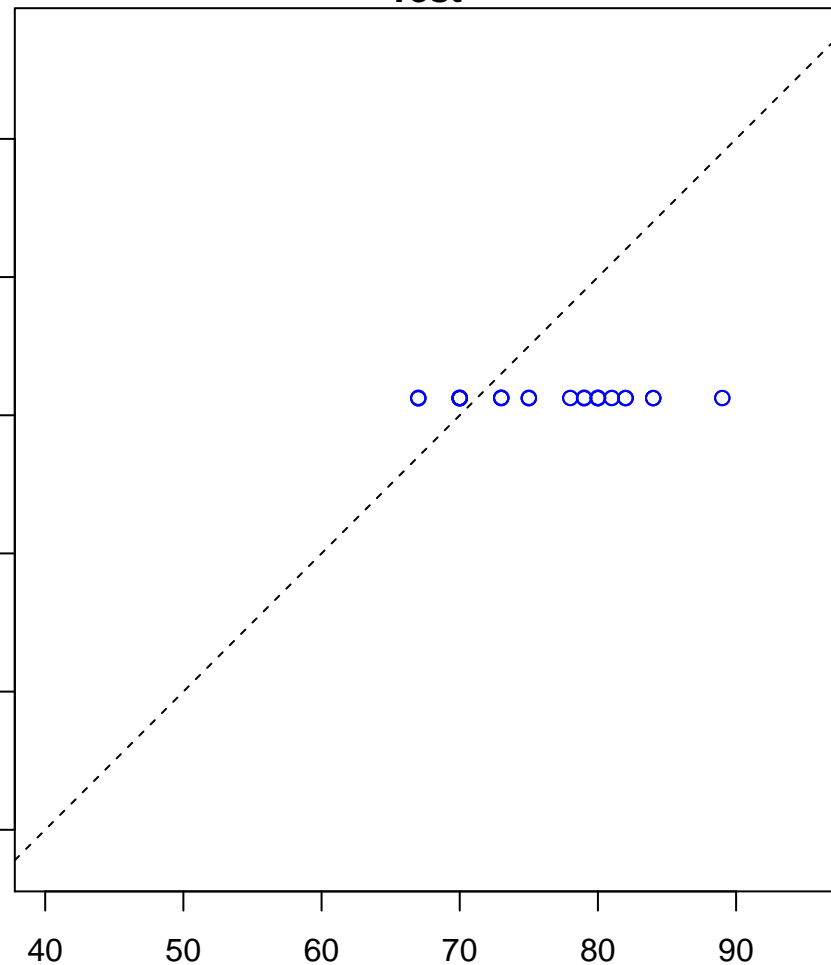
Actual Age

cellular response to glucose stimulus (Score: 0.821014)

Control



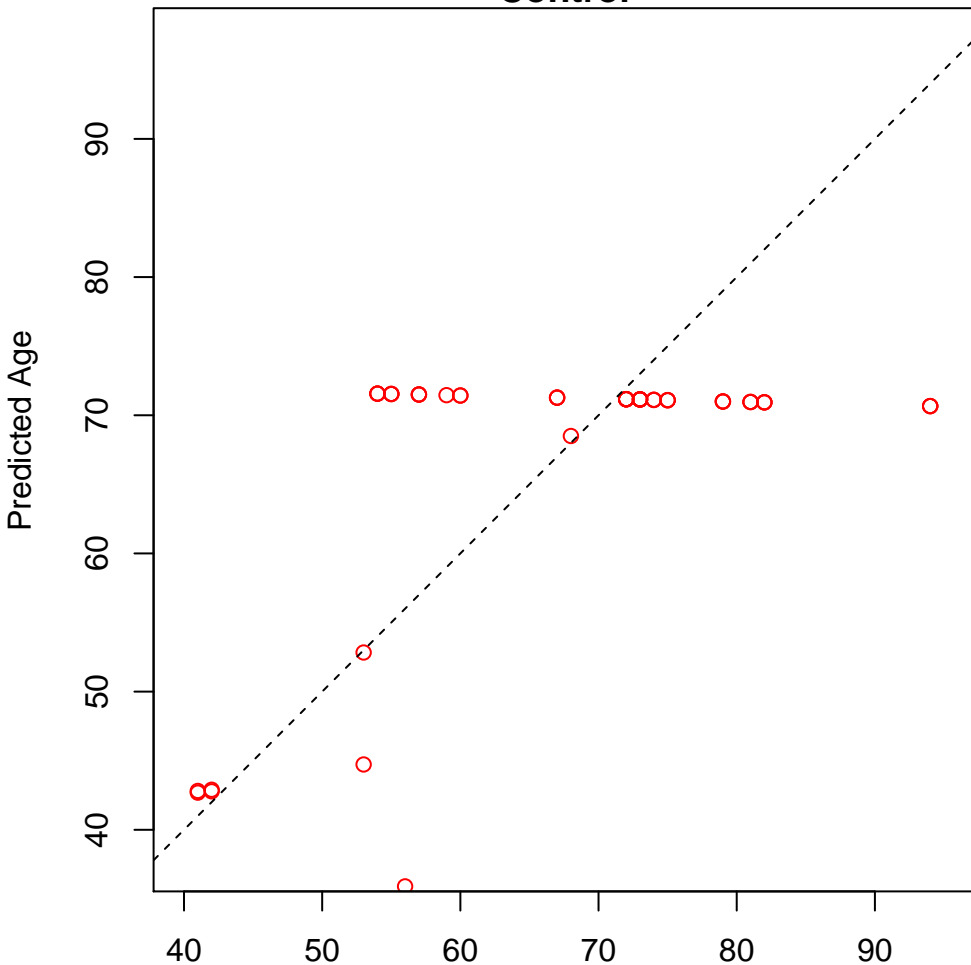
Test



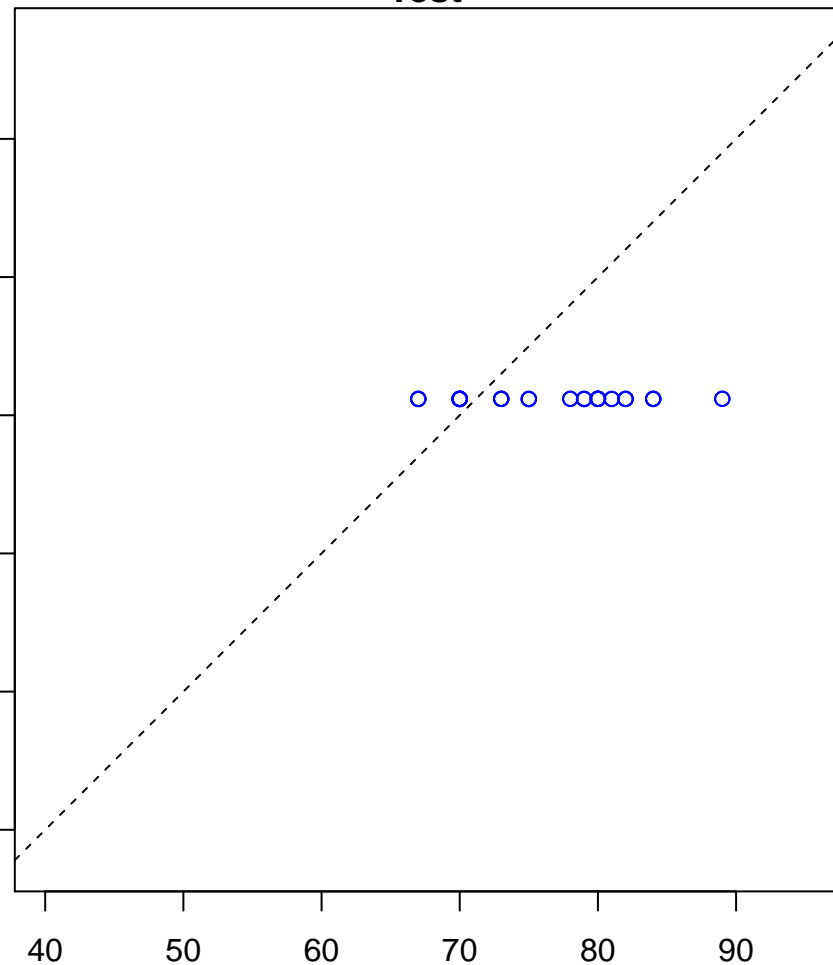
Actual Age

positive regulation of defense response (Score: 0.820997)

Control

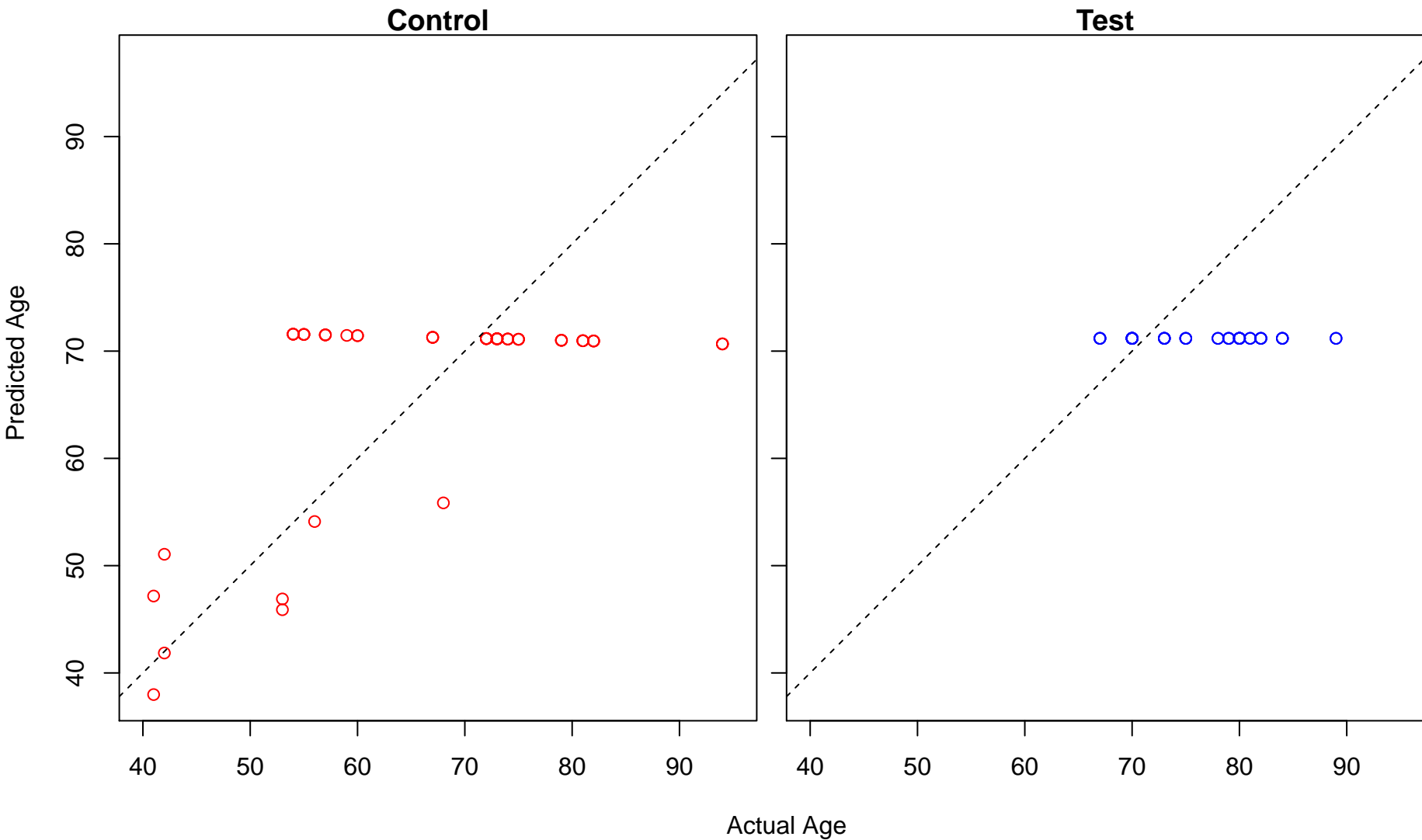


Test

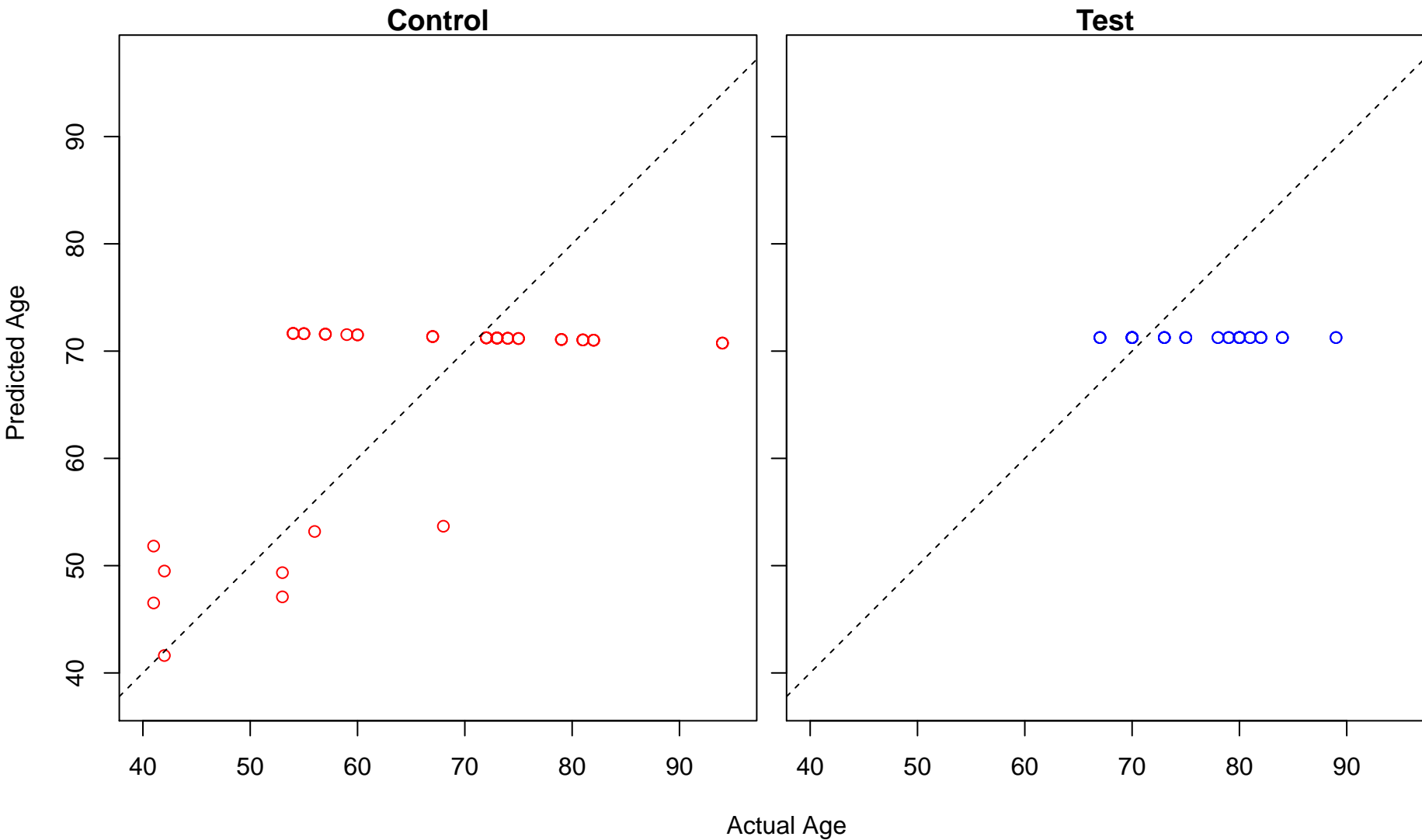


Actual Age

regulation of kinase activity (Score: 0.820977)

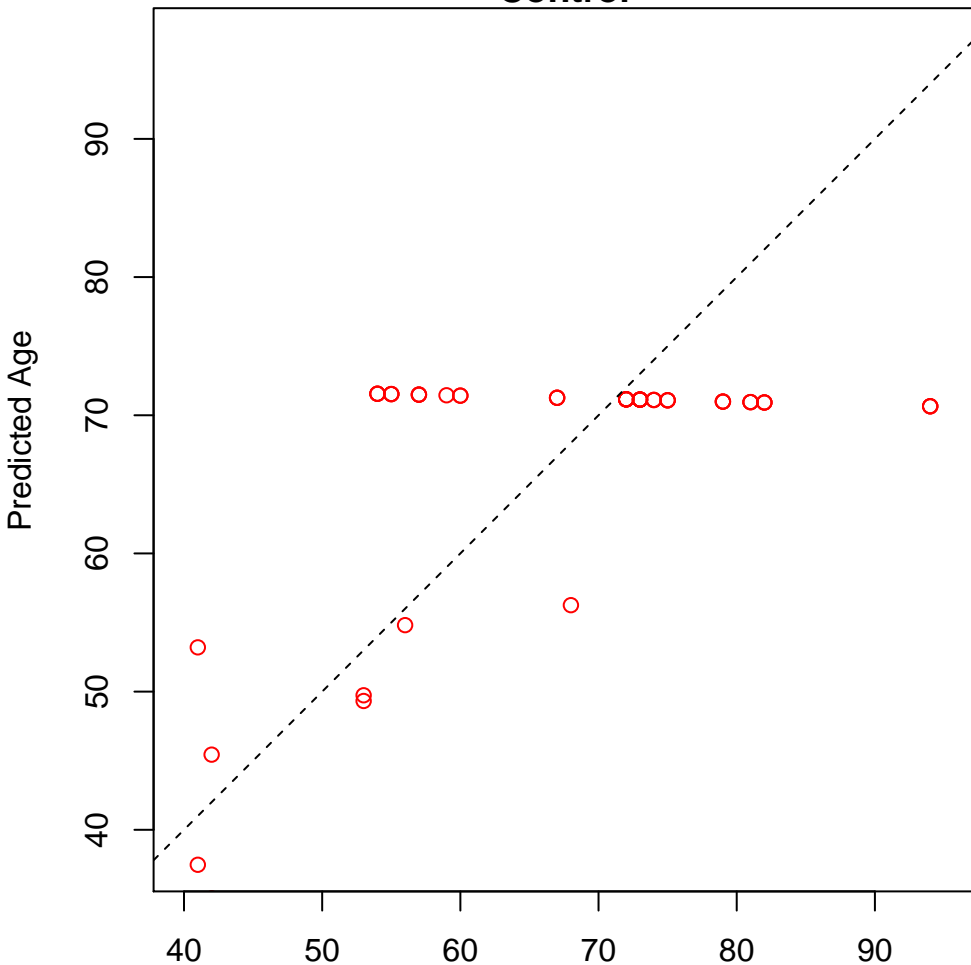


response to ethanol (Score: 0.820896)

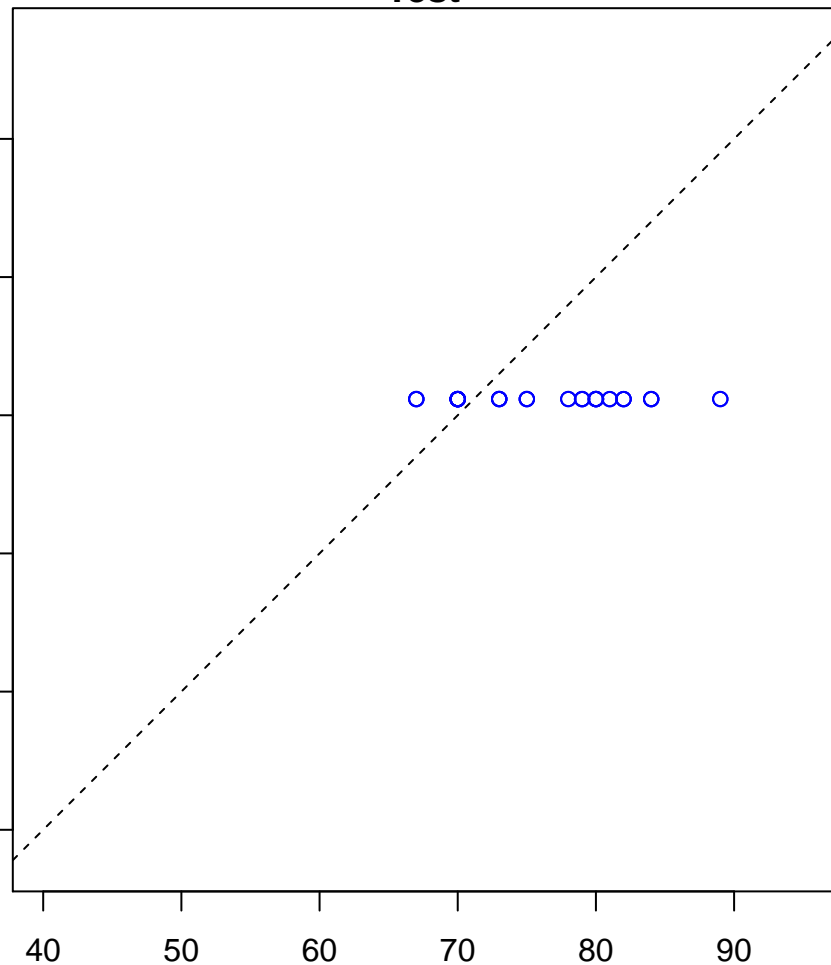


negative regulation of catalytic activity (Score: 0.820876)

Control



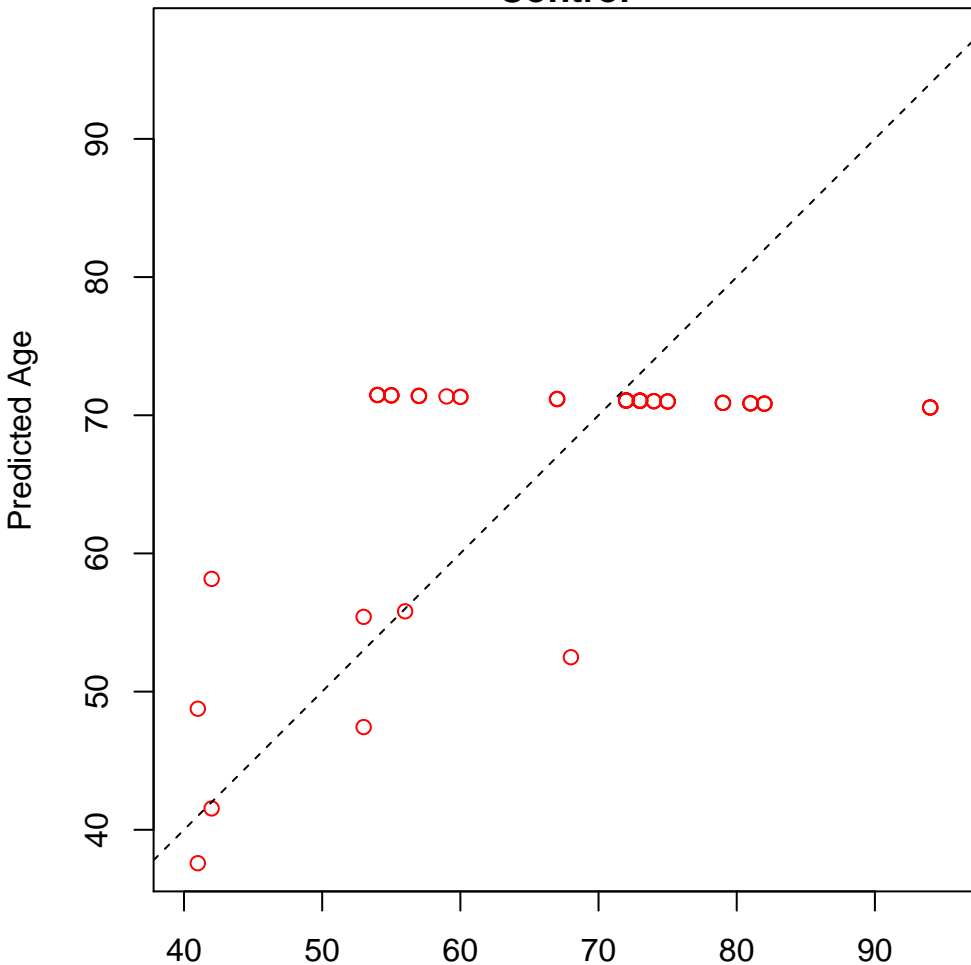
Test



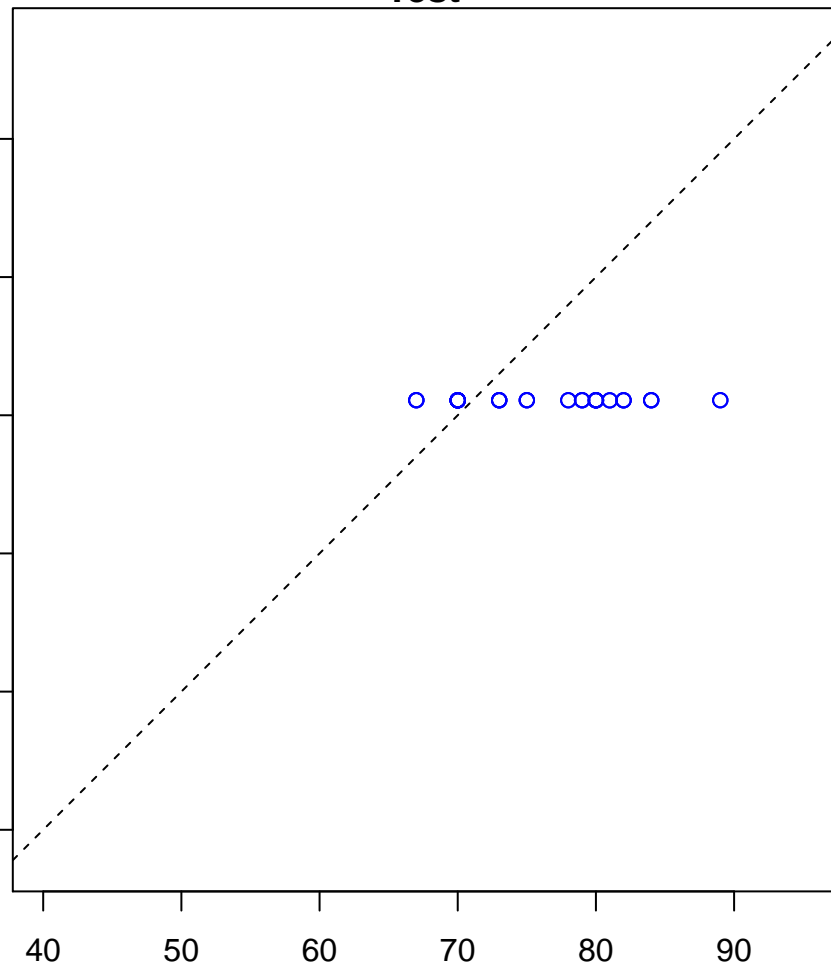
Actual Age

regulation of cellular component size (Score: 0.820804)

Control

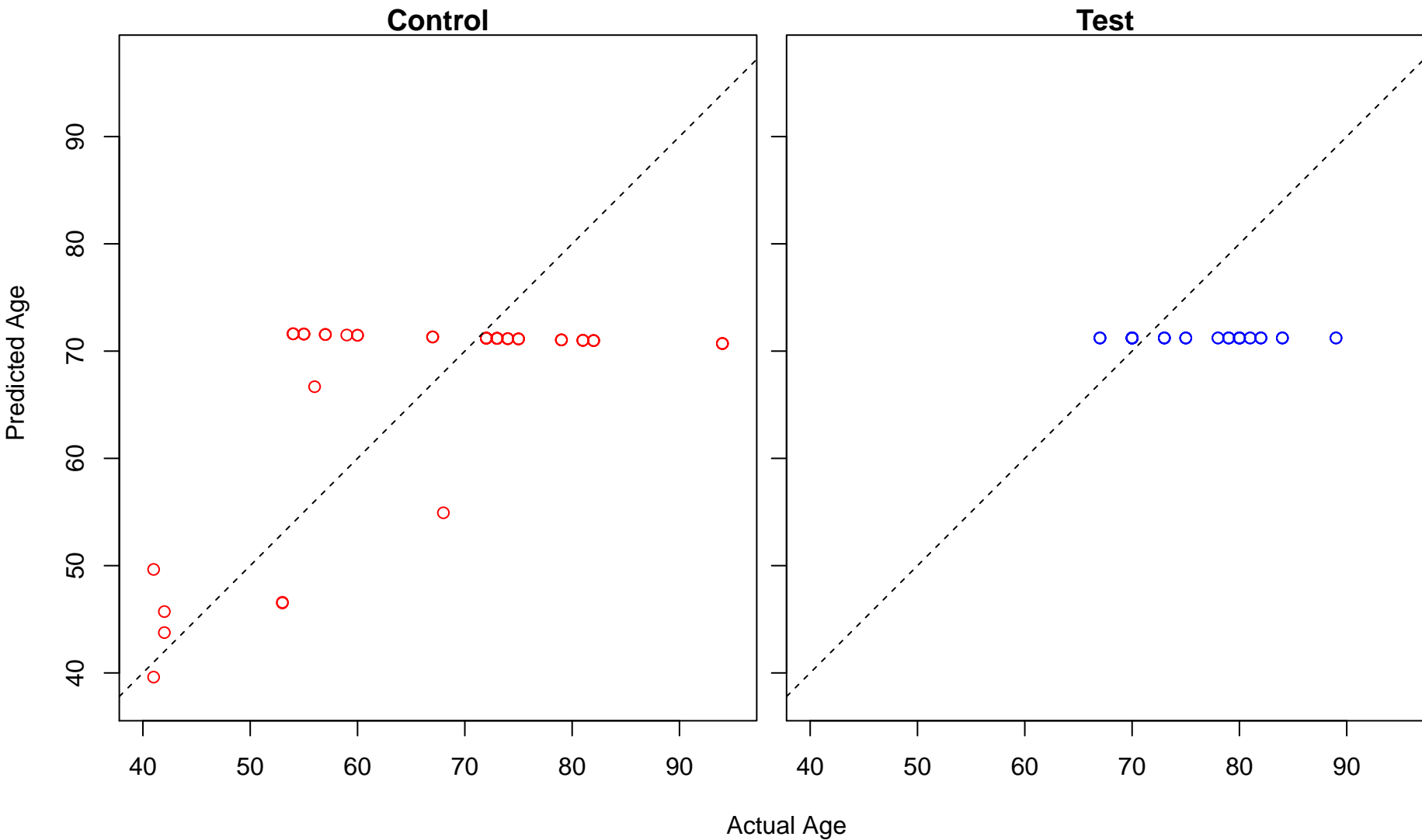


Test



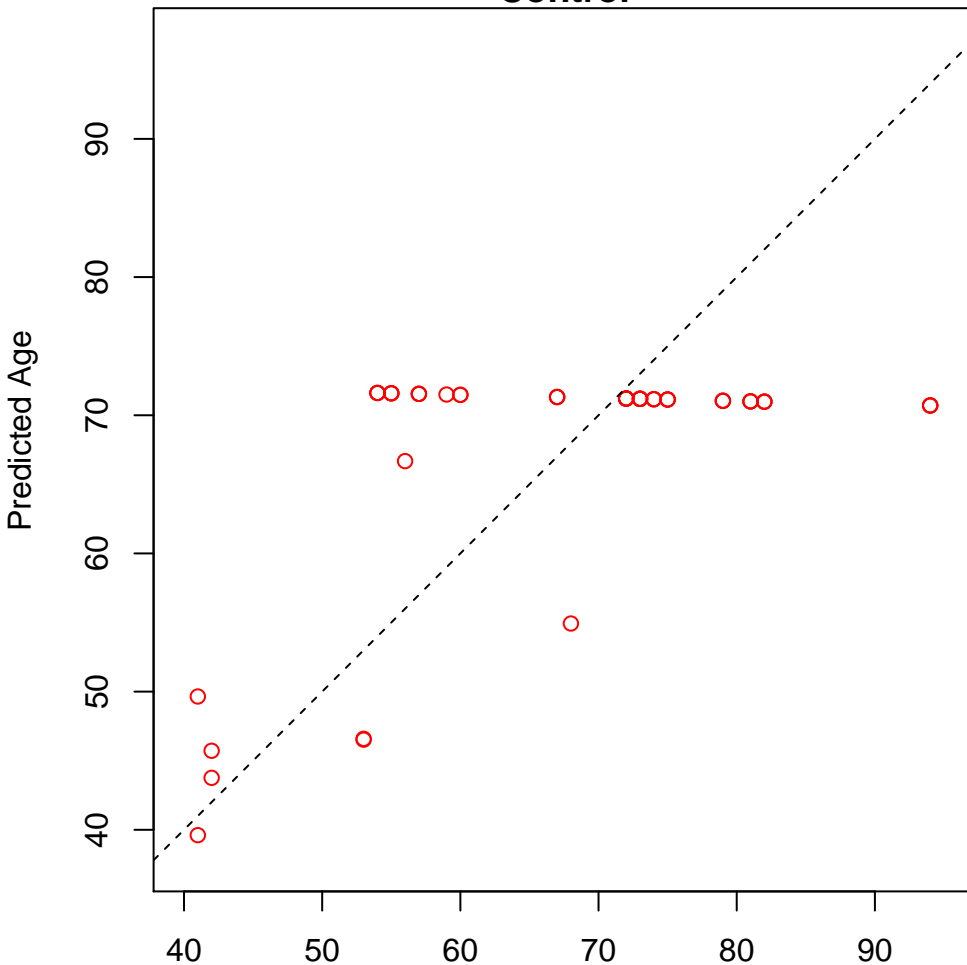
Actual Age

regulation of MAPK cascade (Score: 0.820638)

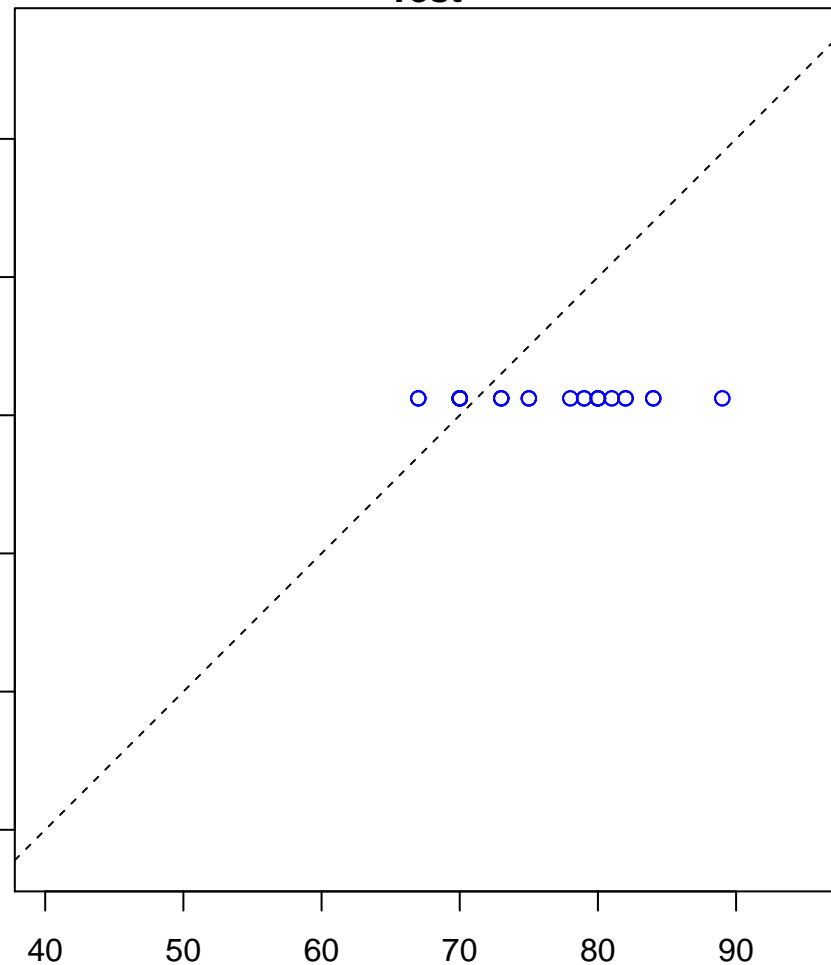


positive regulation of MAPK cascade (Score: 0.820638)

Control



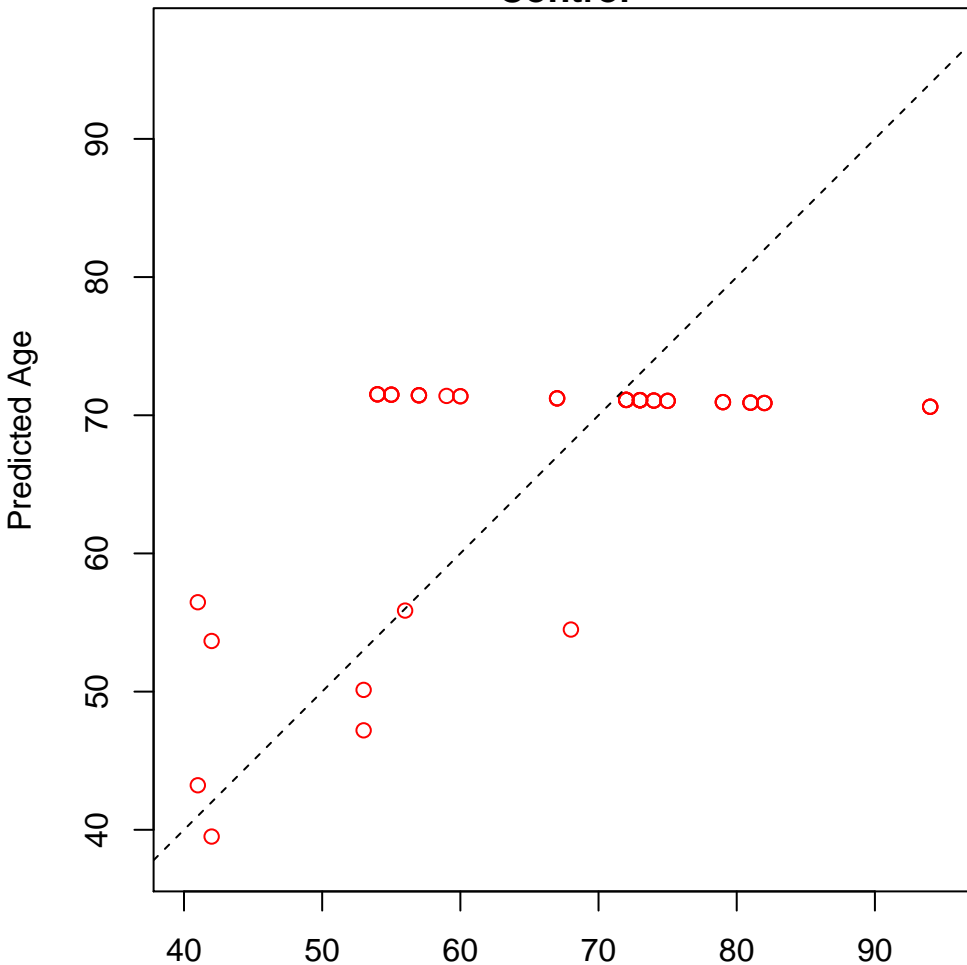
Test



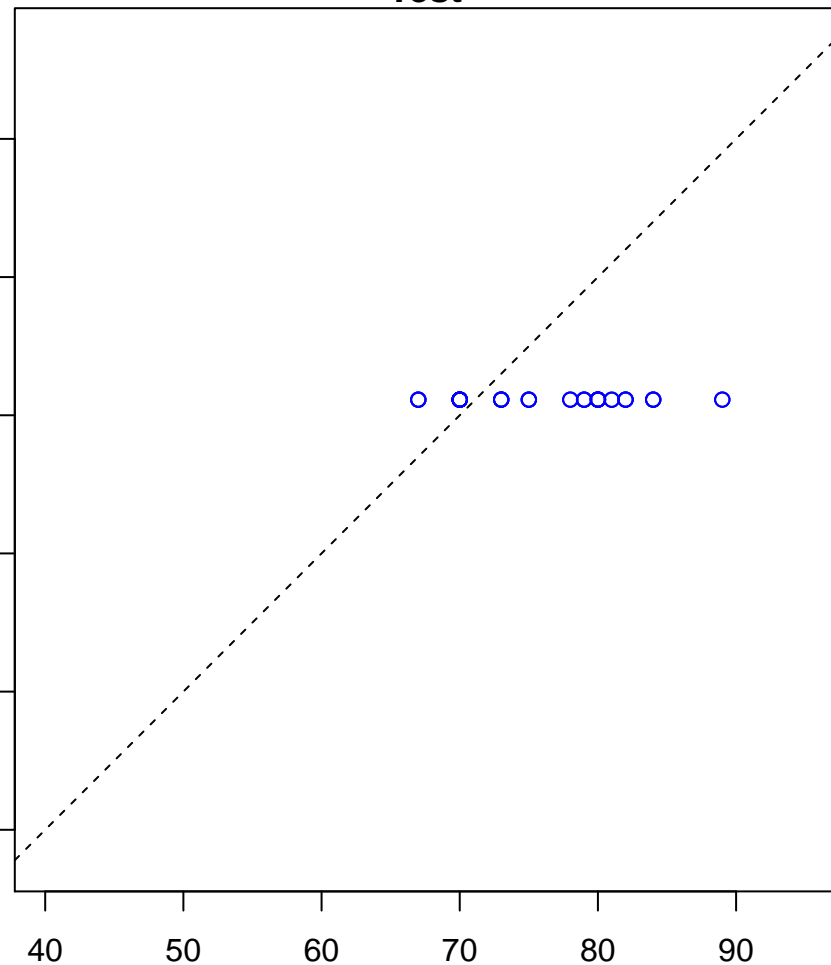
Actual Age

small molecule catabolic process (Score: 0.820571)

Control



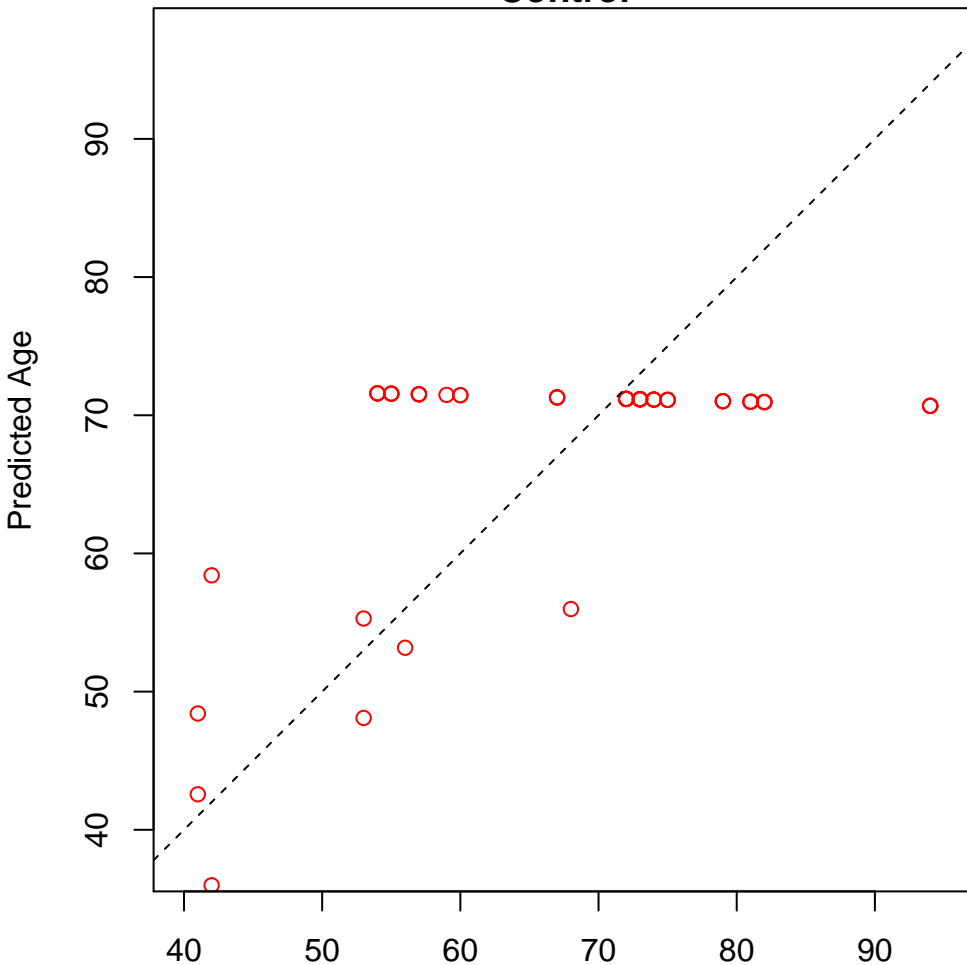
Test



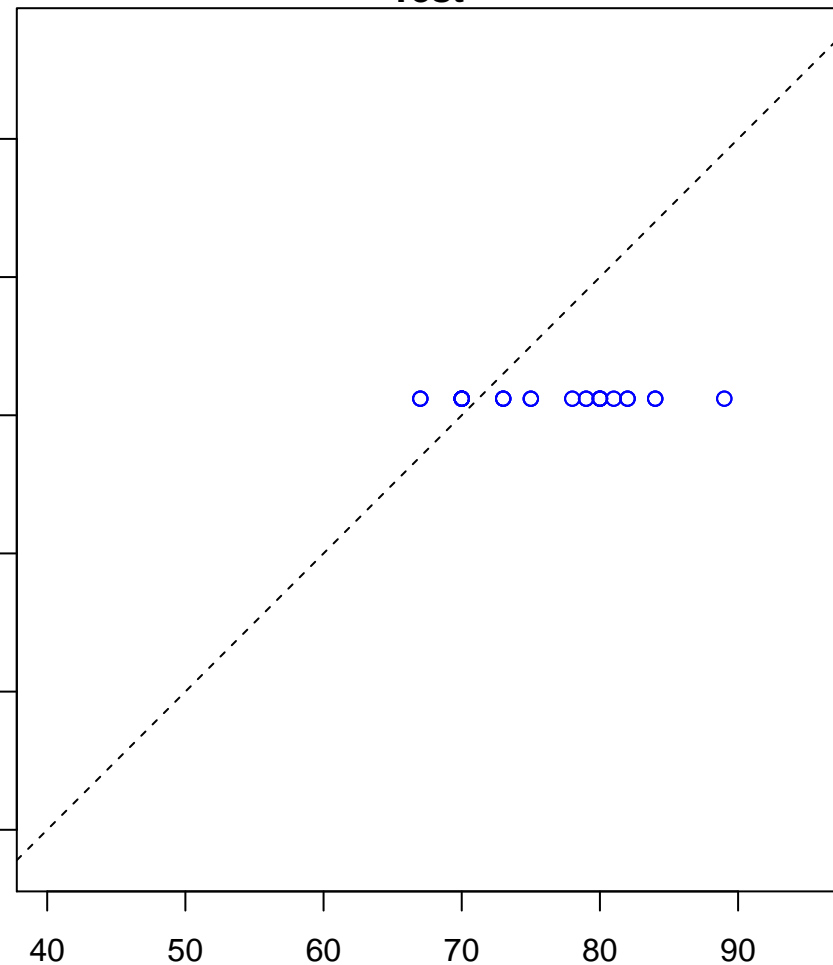
Actual Age

response to reactive oxygen species (Score: 0.820551)

Control

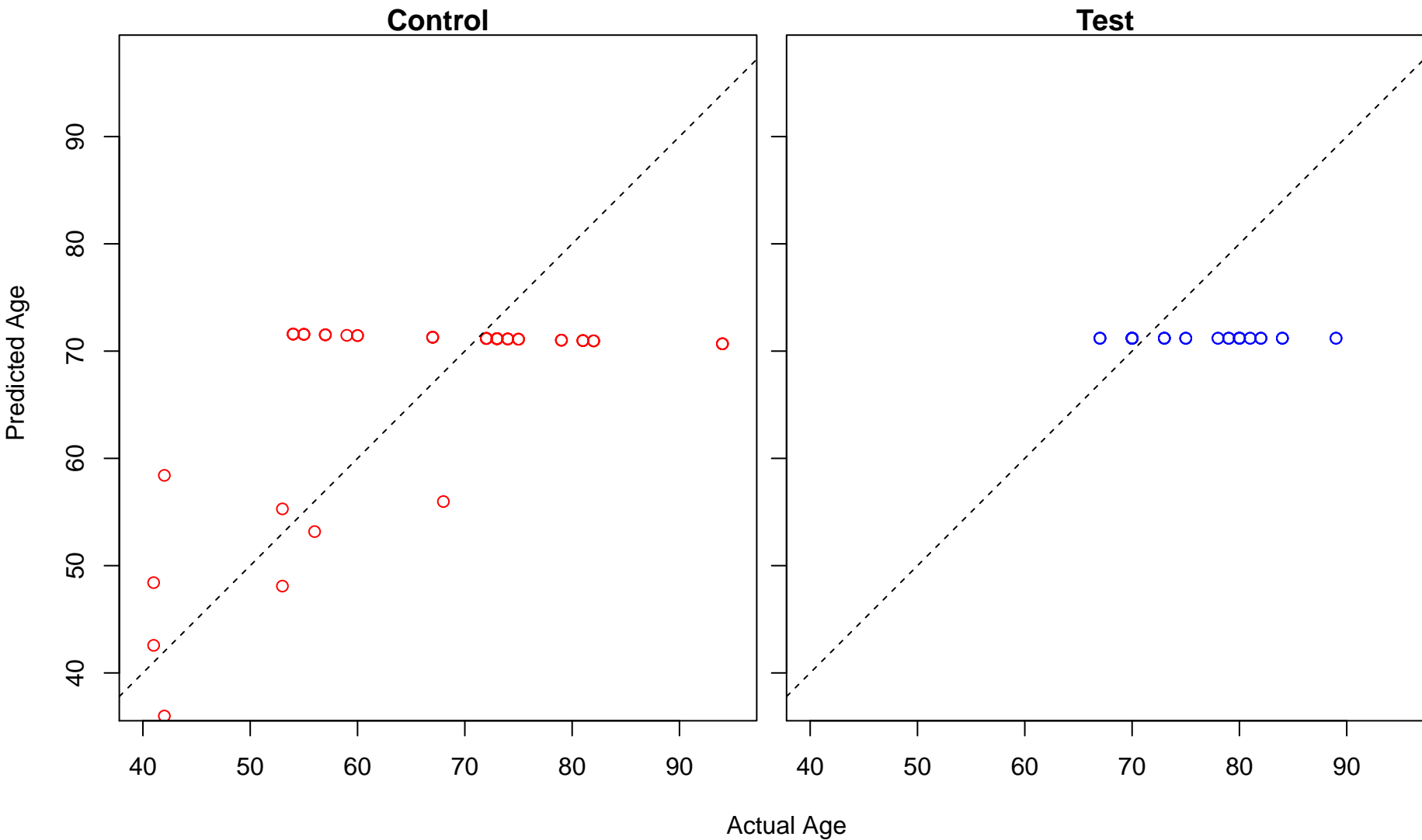


Test



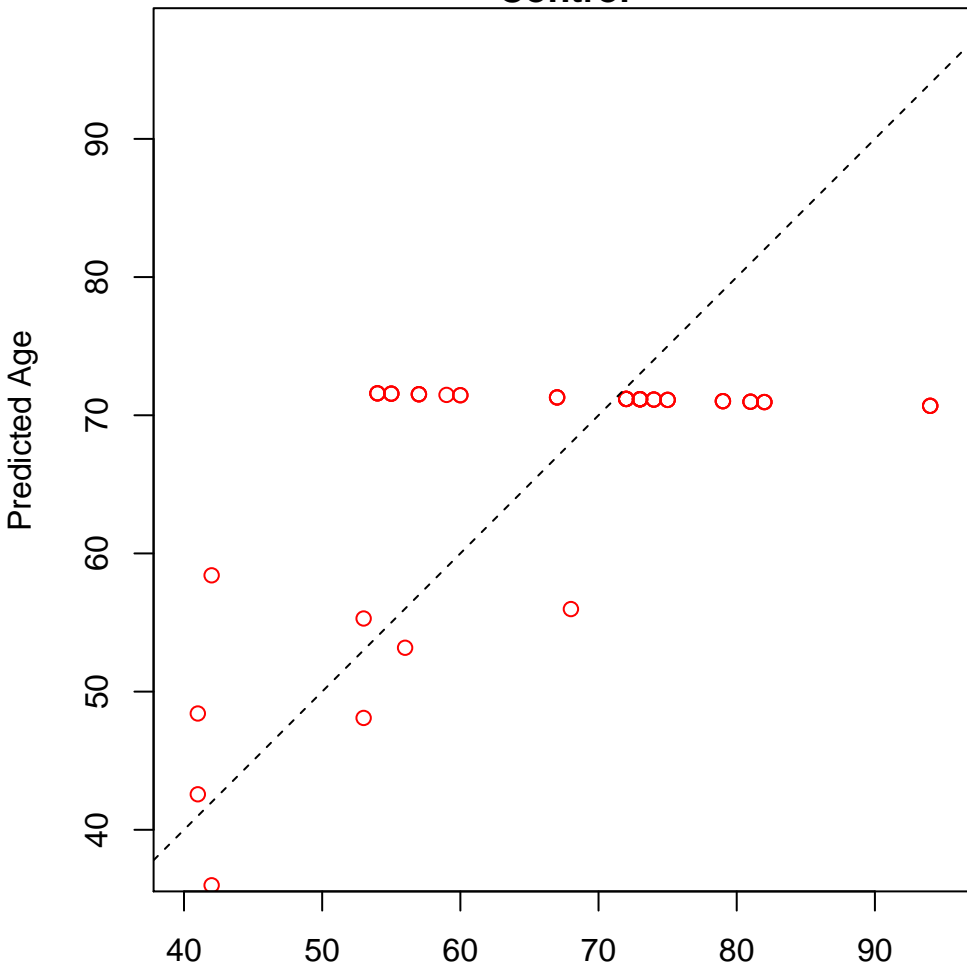
Actual Age

glutathione metabolic process (Score: 0.820551)

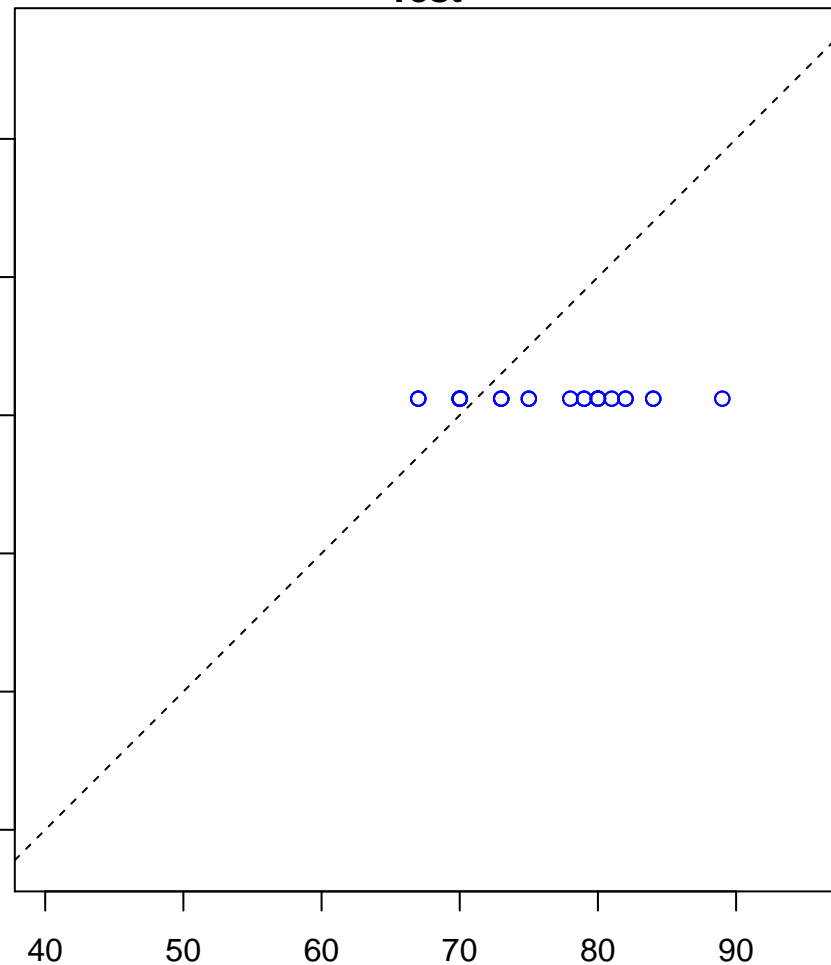


response to hydrogen peroxide (Score: 0.820551)

Control



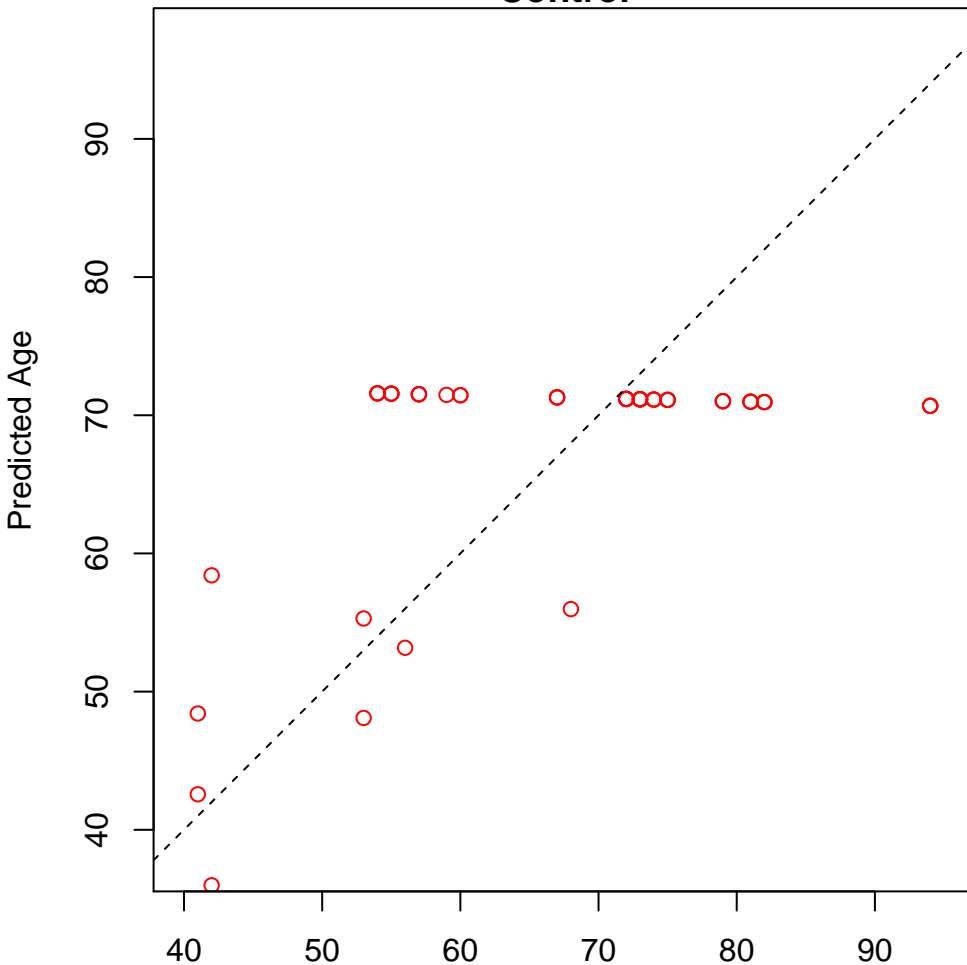
Test



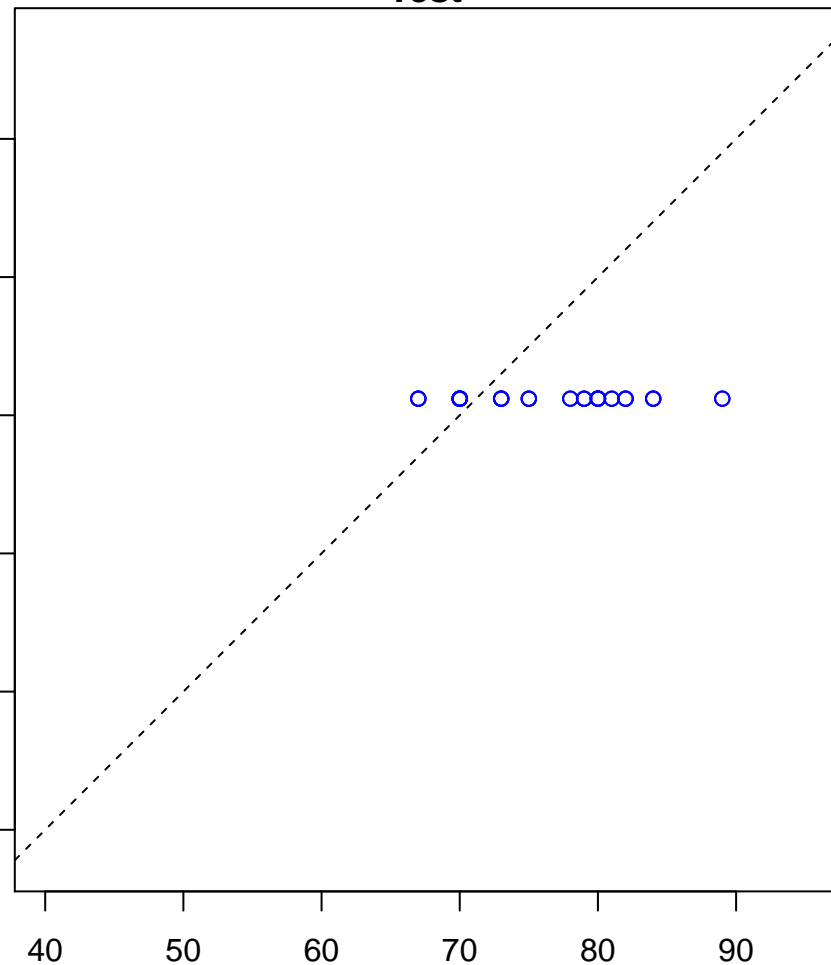
Actual Age

hydrogen peroxide metabolic process (Score: 0.820551)

Control



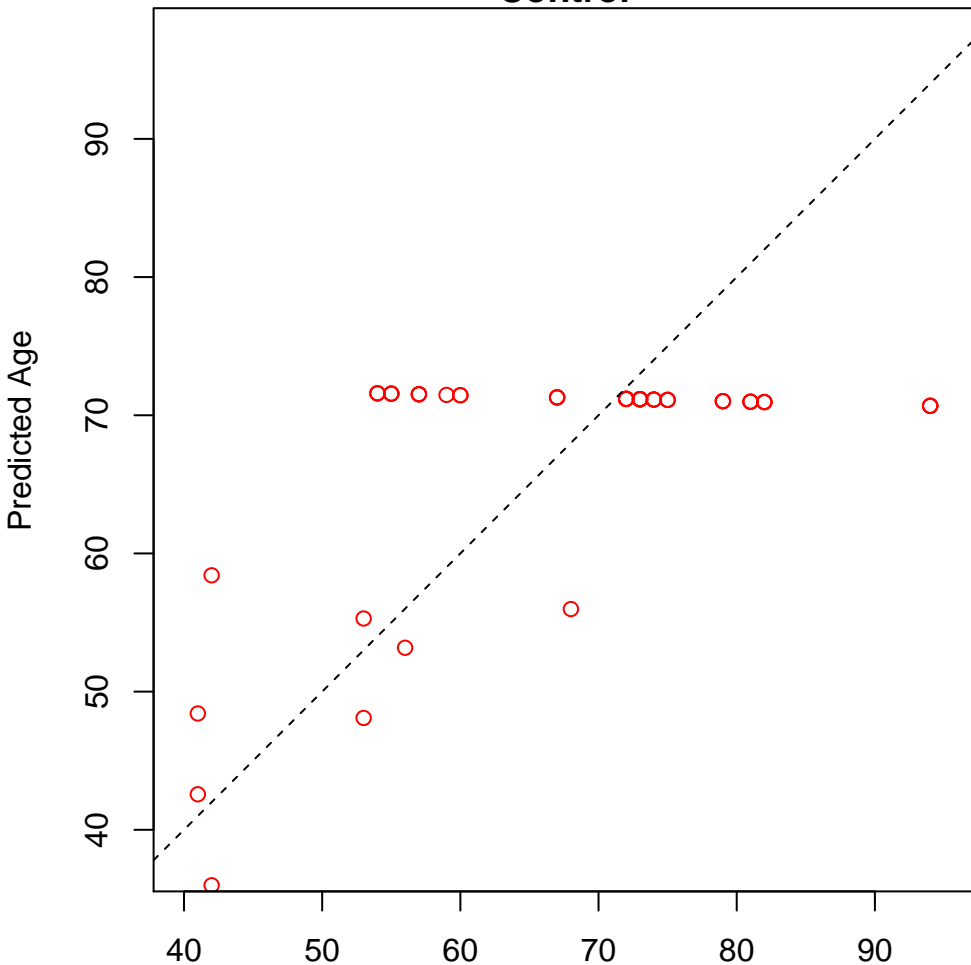
Test



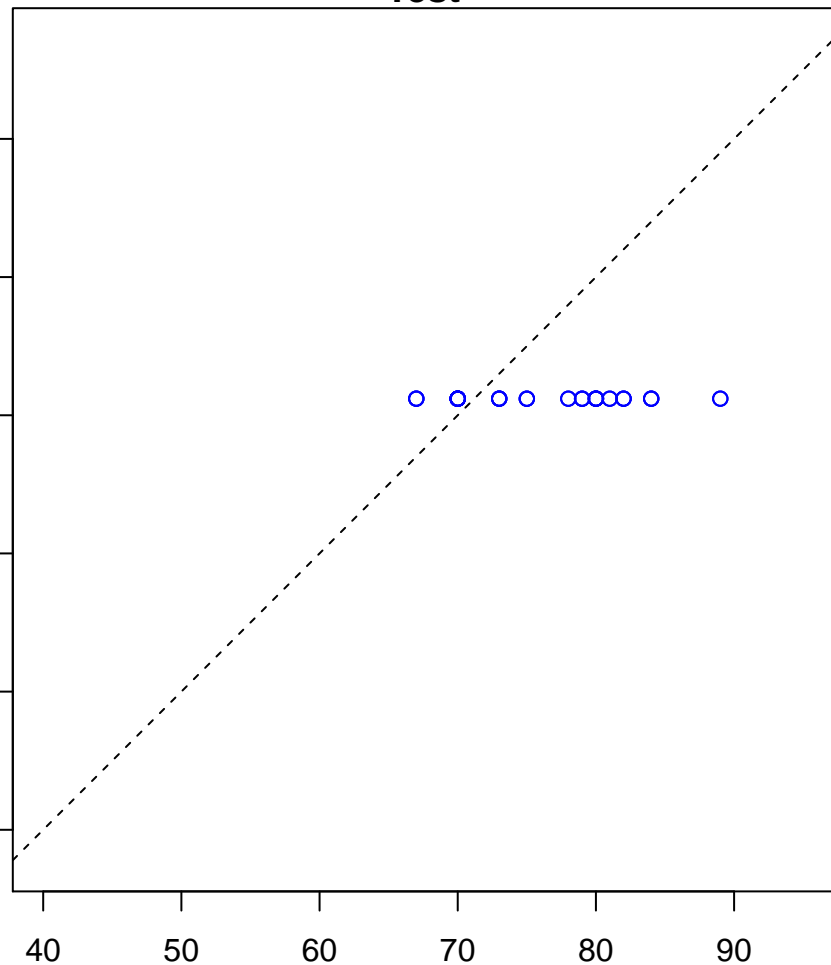
Actual Age

reactive oxygen species metabolic process (Score: 0.820551)

Control

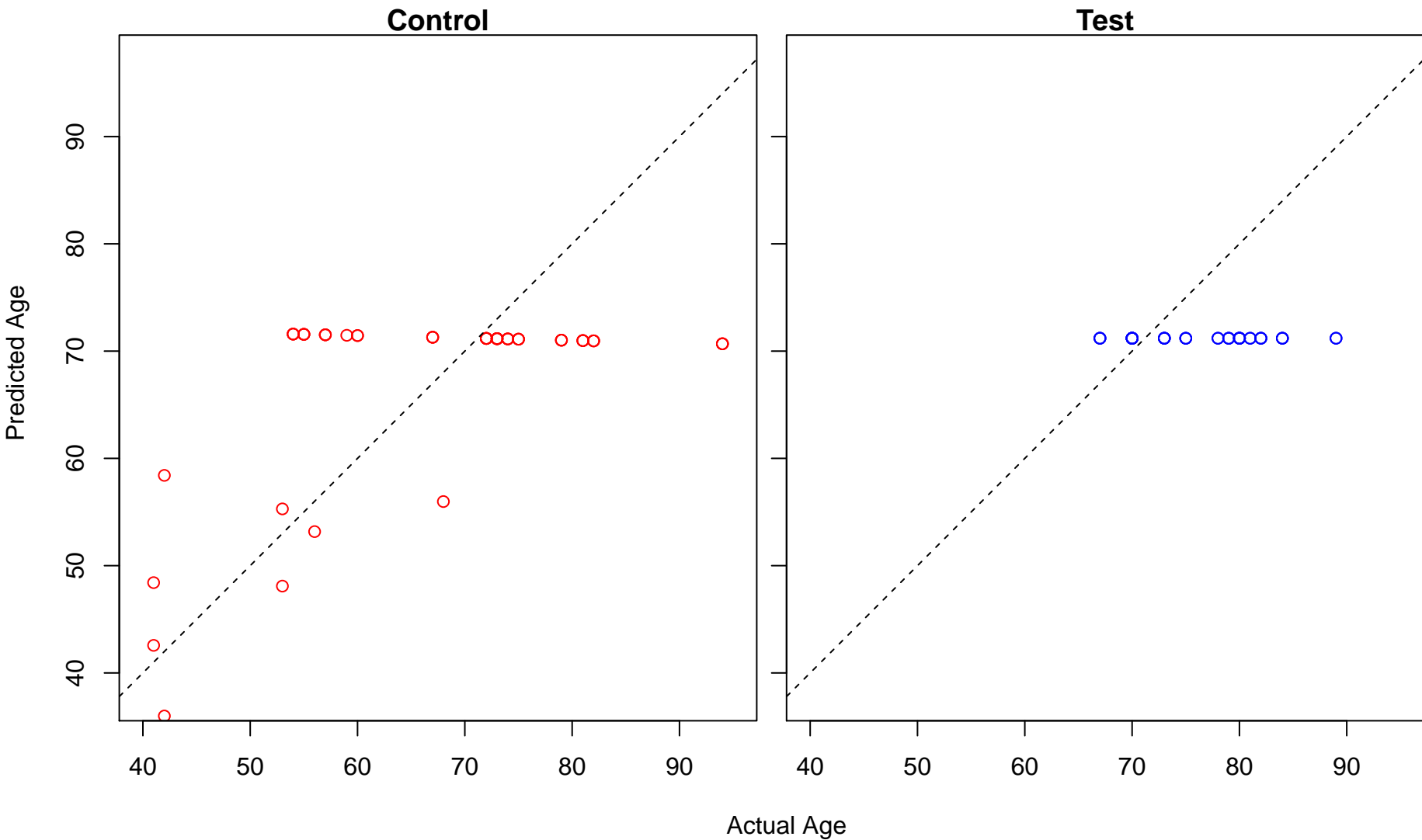


Test

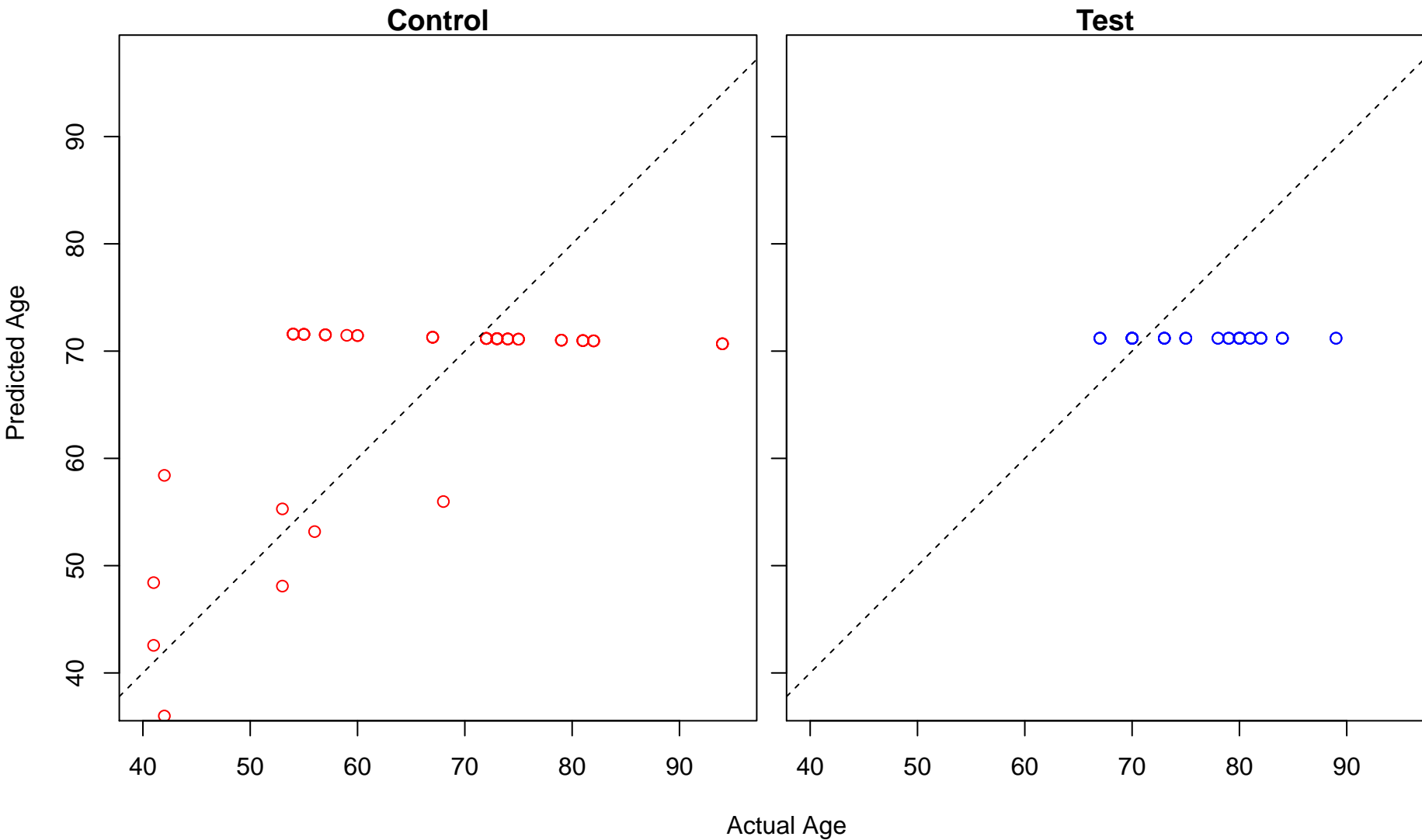


Actual Age

detoxification (Score: 0.820551)

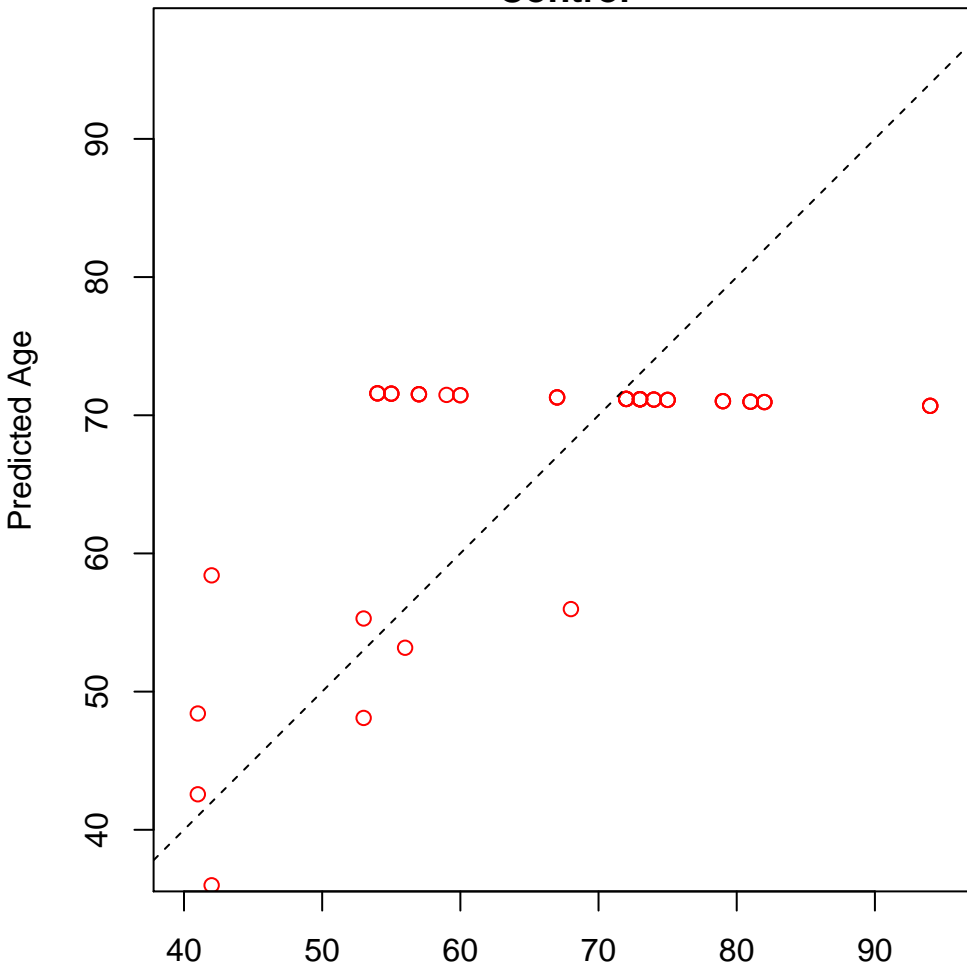


cellular detoxification (Score: 0.820551)

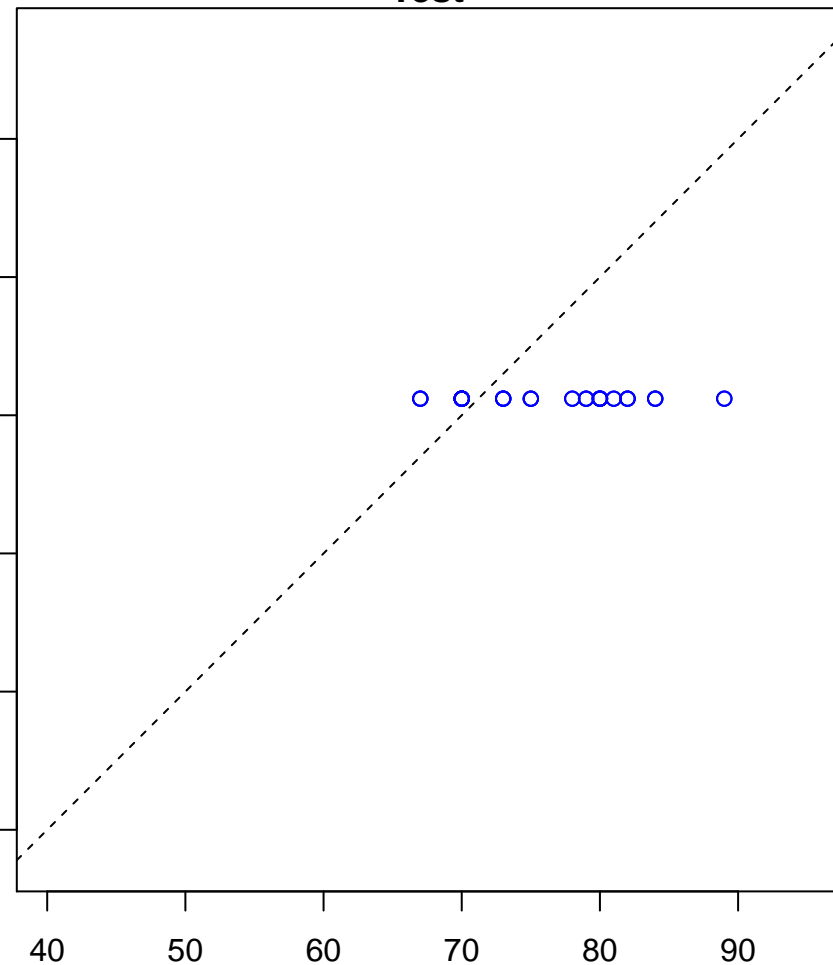


response to toxic substance (Score: 0.820550)

Control

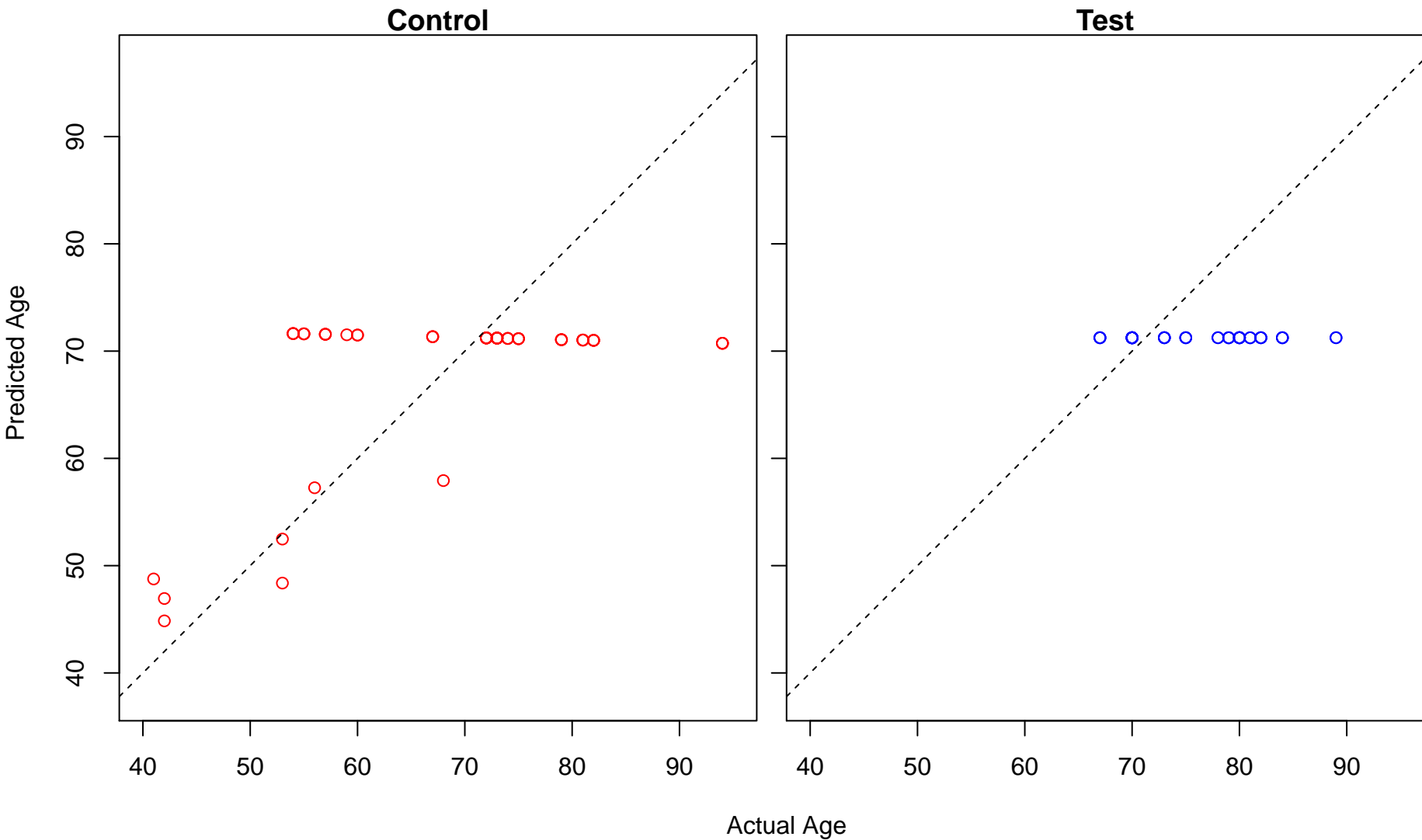


Test

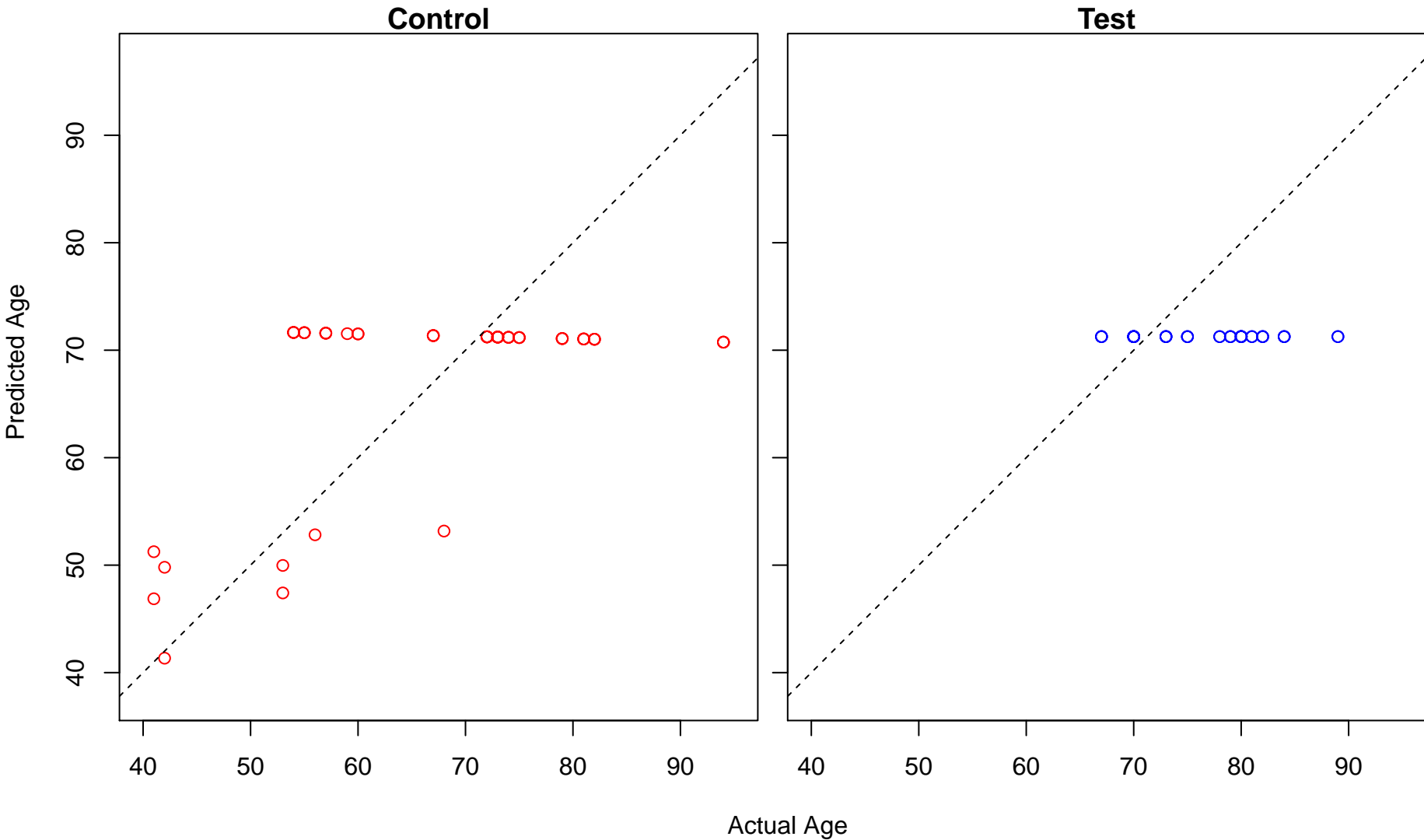


Actual Age

organonitrogen compound catabolic process (Score: 0.820549)

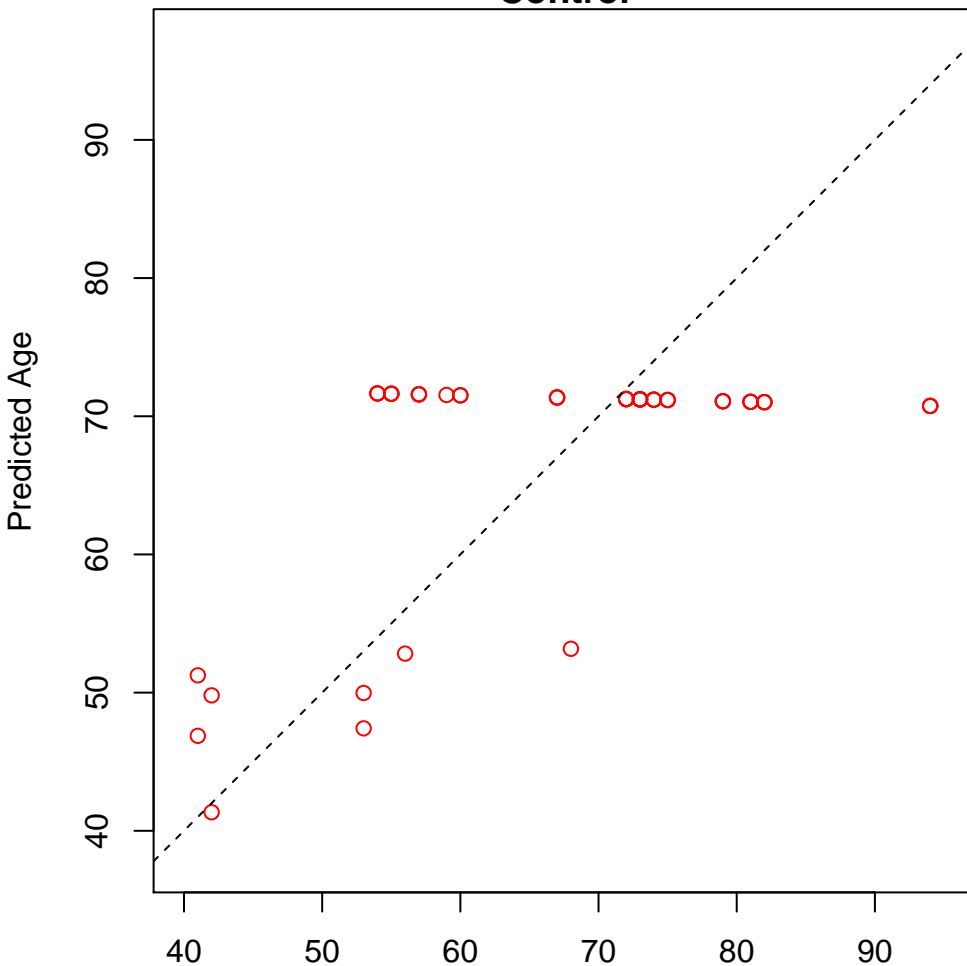


regulation of cholesterol biosynthetic process (Score: 0.820507)

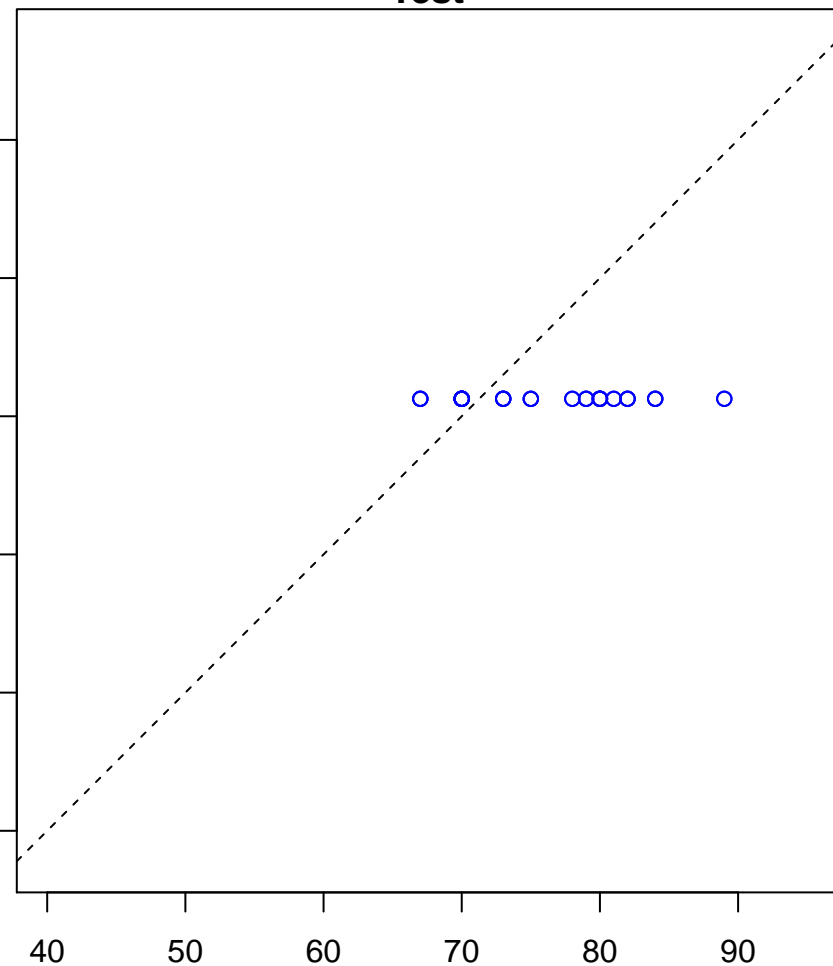


regulation of steroid biosynthetic process (Score: 0.820507)

Control



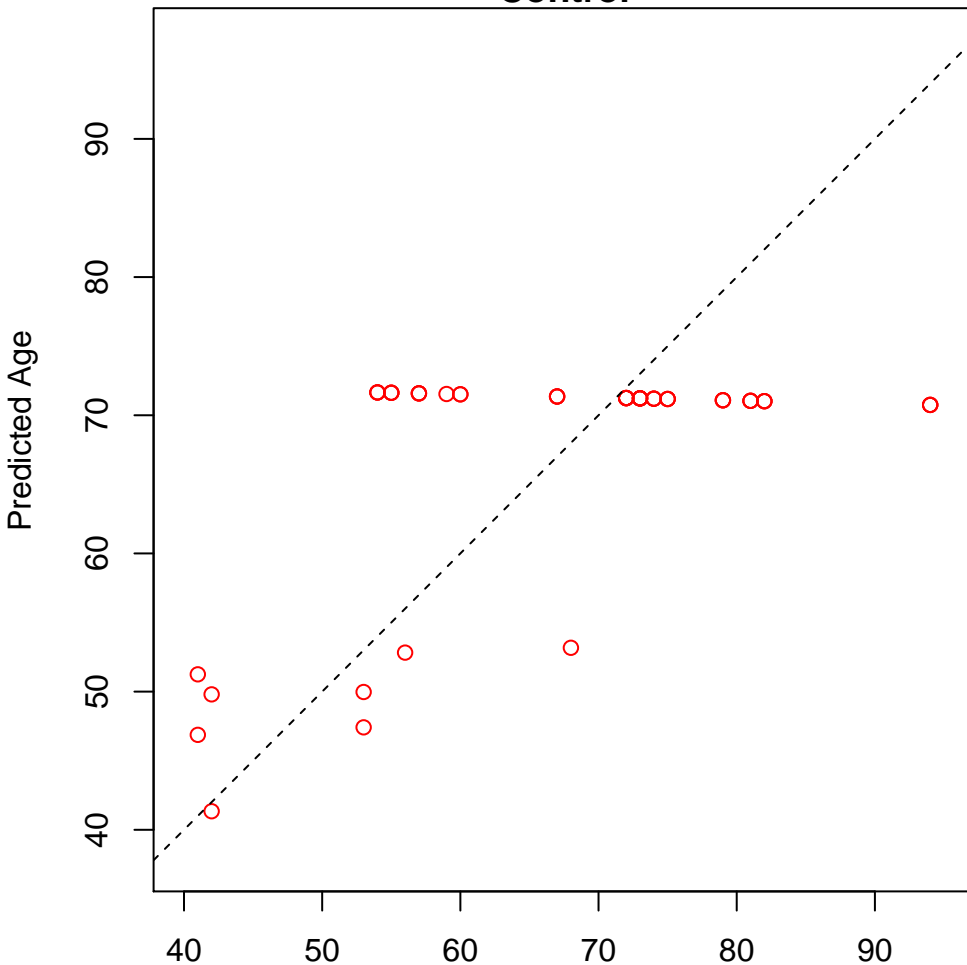
Test



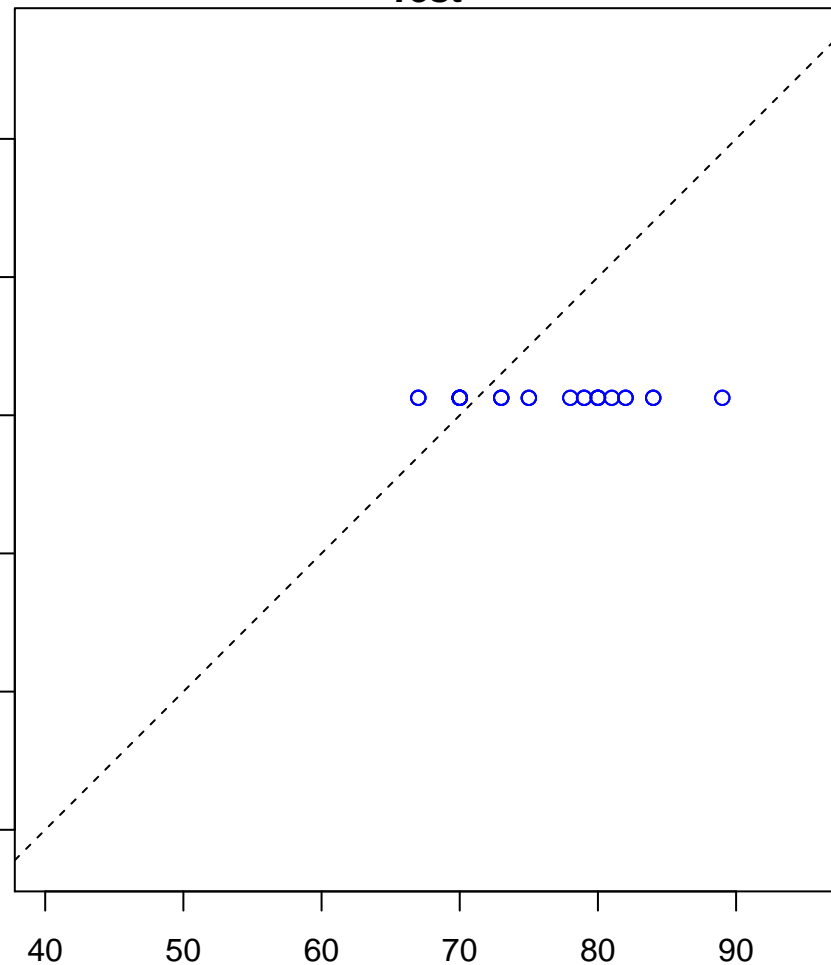
Actual Age

regulation of alcohol biosynthetic process (Score: 0.820507)

Control

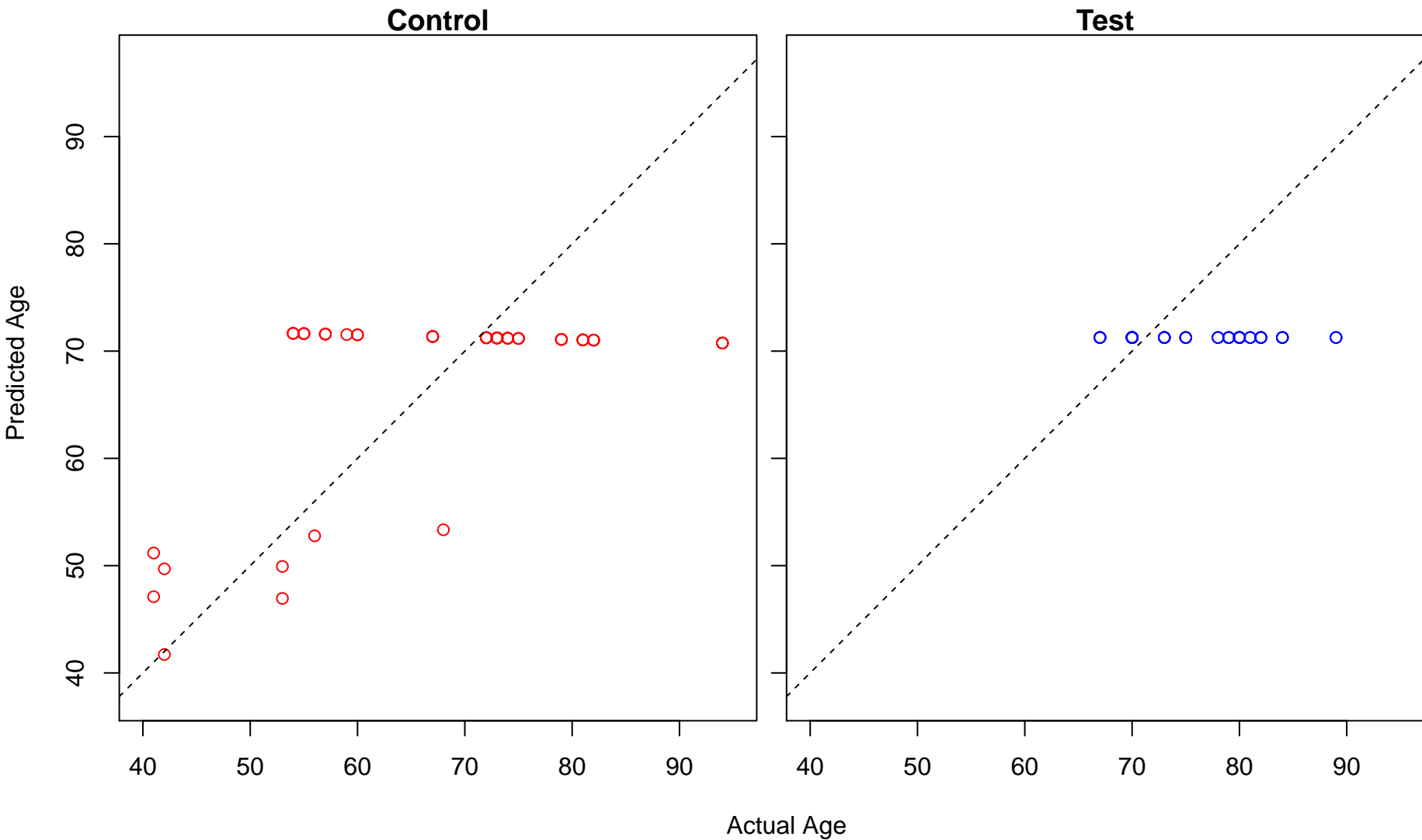


Test

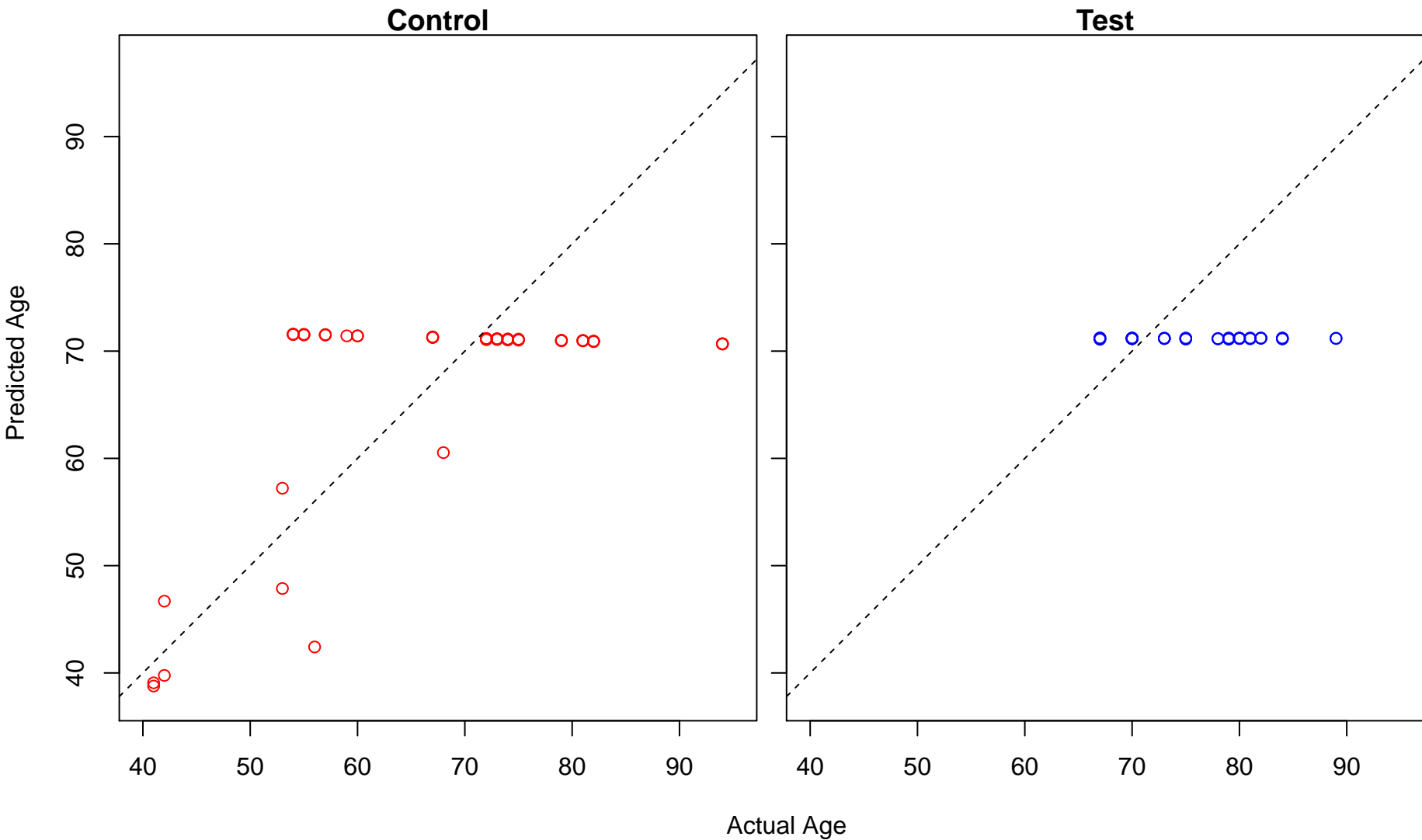


Actual Age

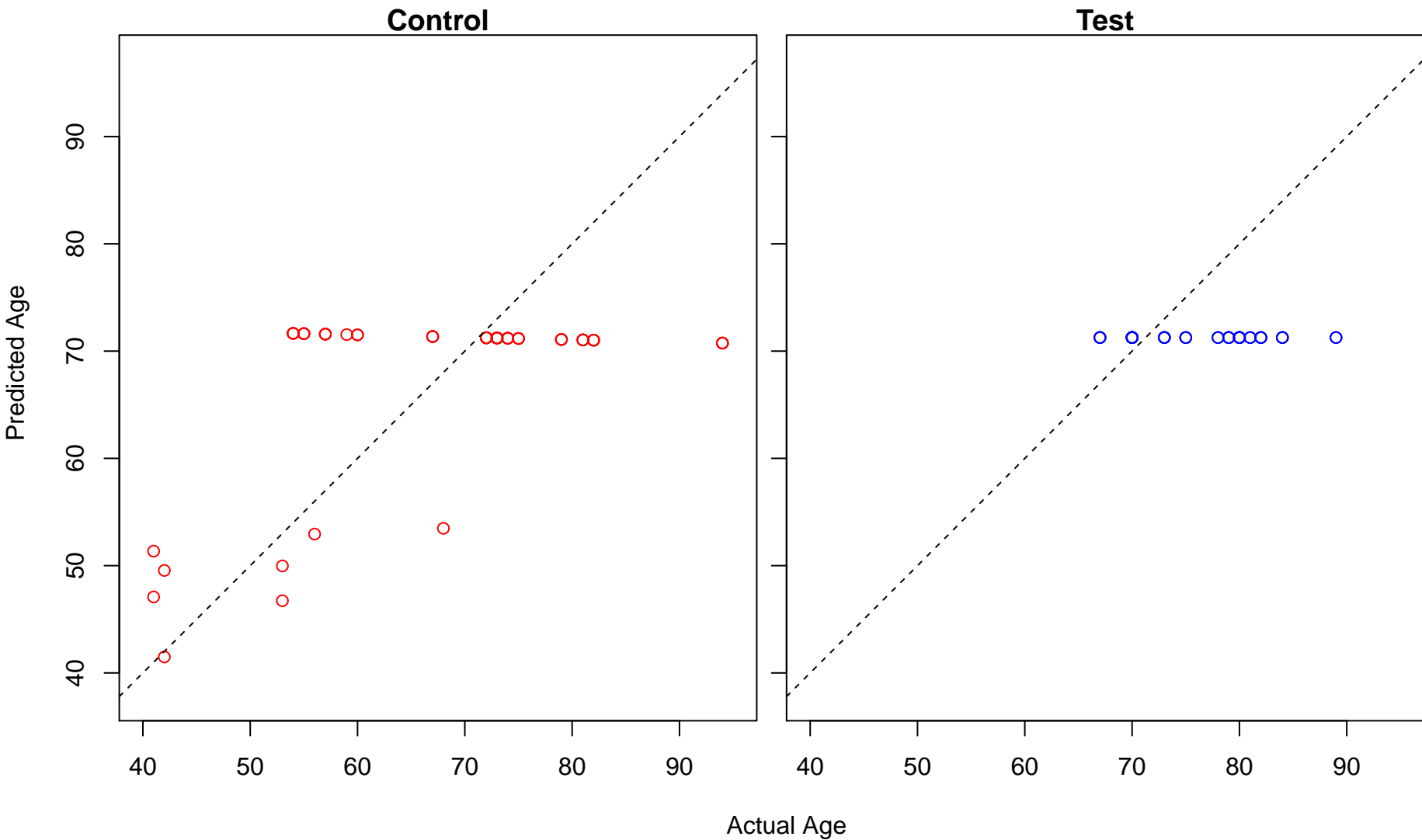
animal organ morphogenesis (Score: 0.820481)



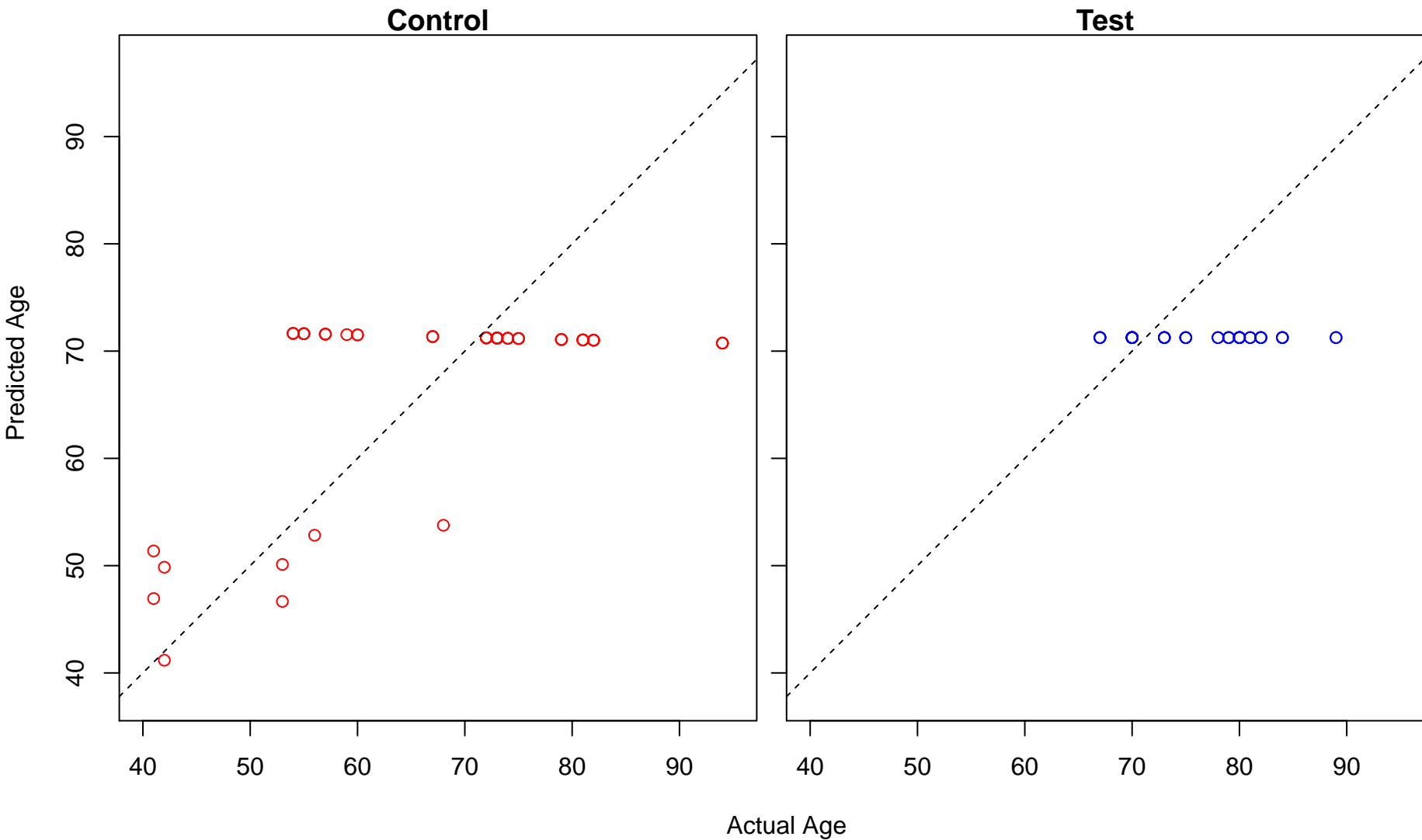
negative regulation of chromosome organization (Score: 0.820441)



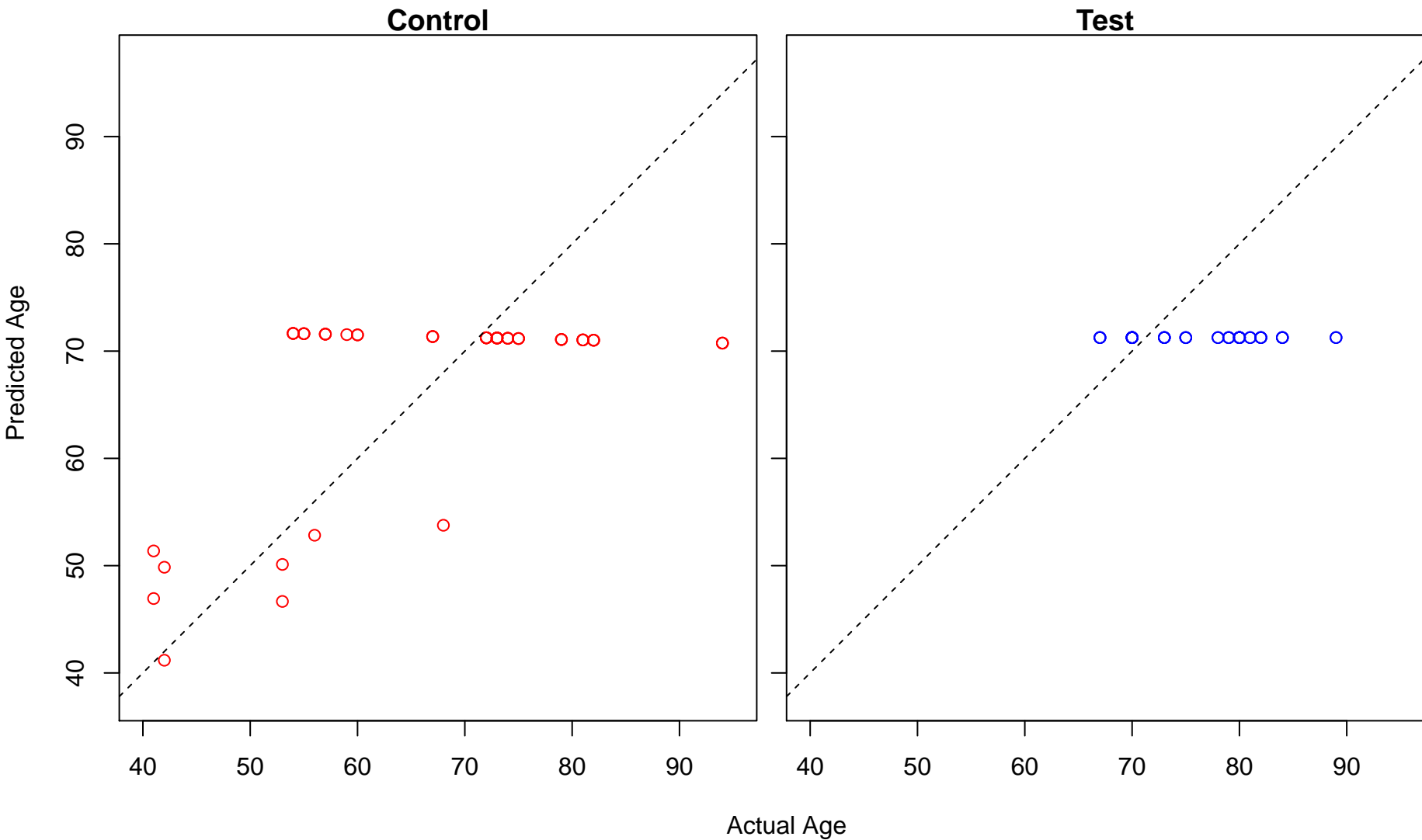
regulation of blood pressure (Score: 0.820420)



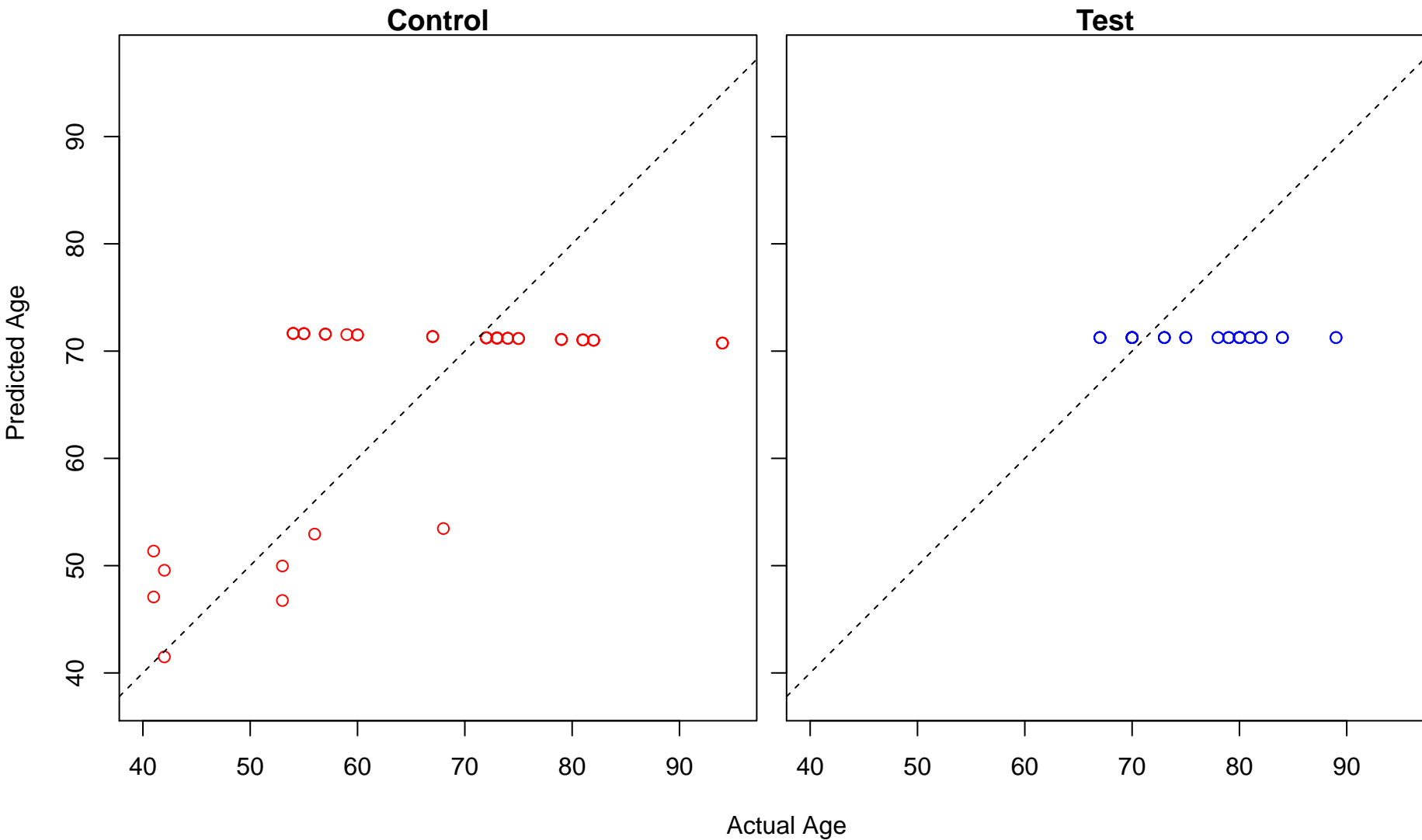
circulatory system process (Score: 0.820409)



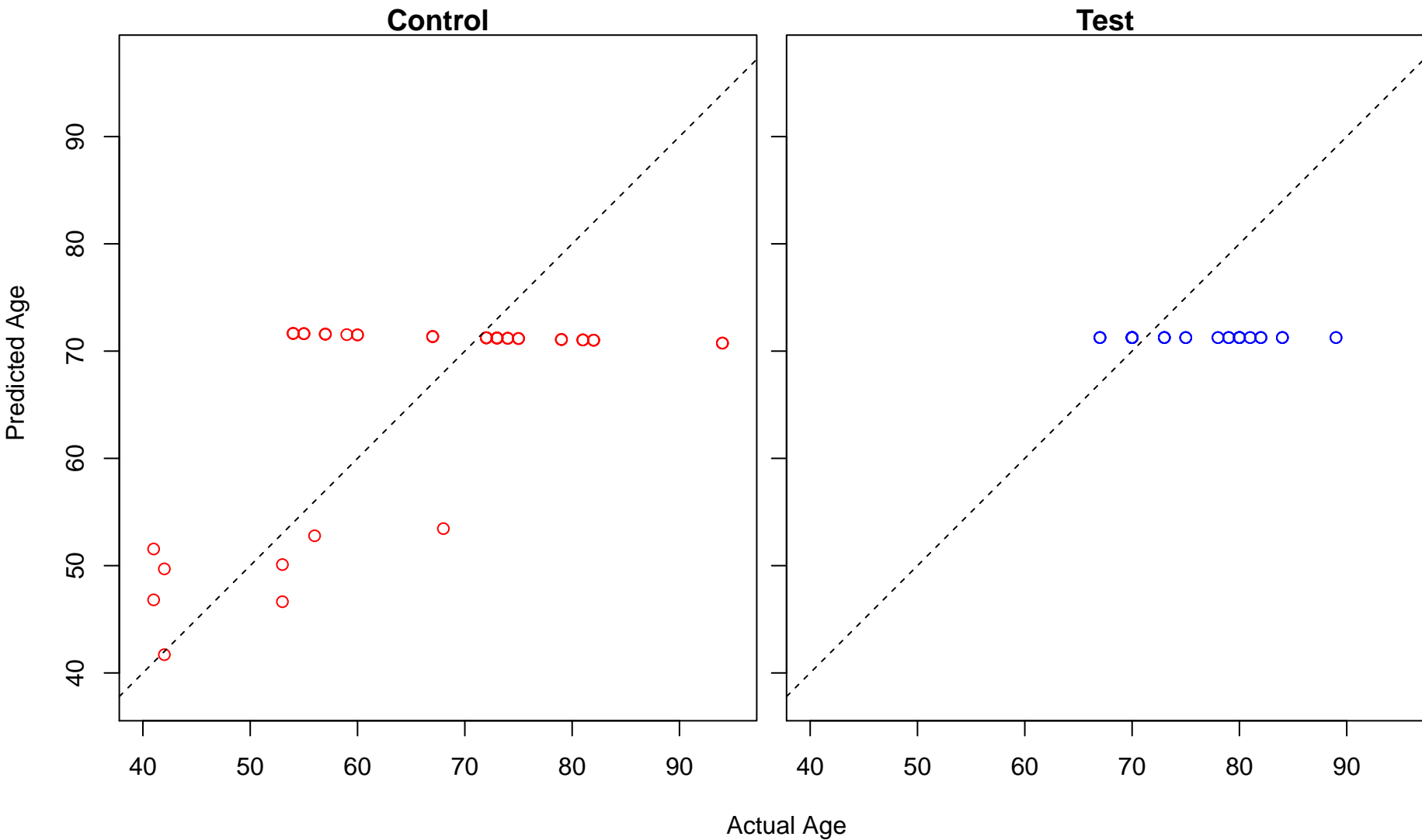
blood circulation (Score: 0.820409)



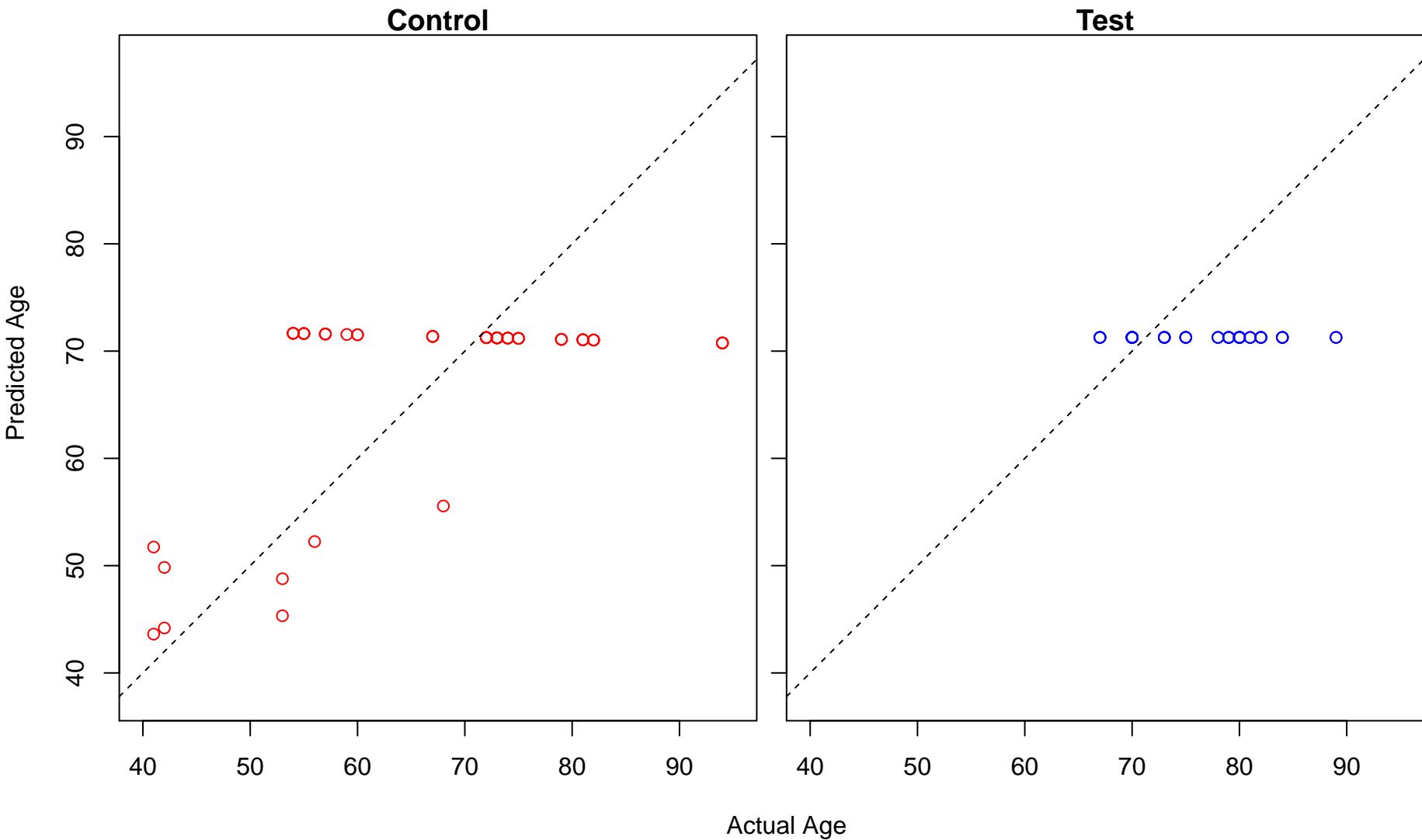
tissue homeostasis (Score: 0.820394)



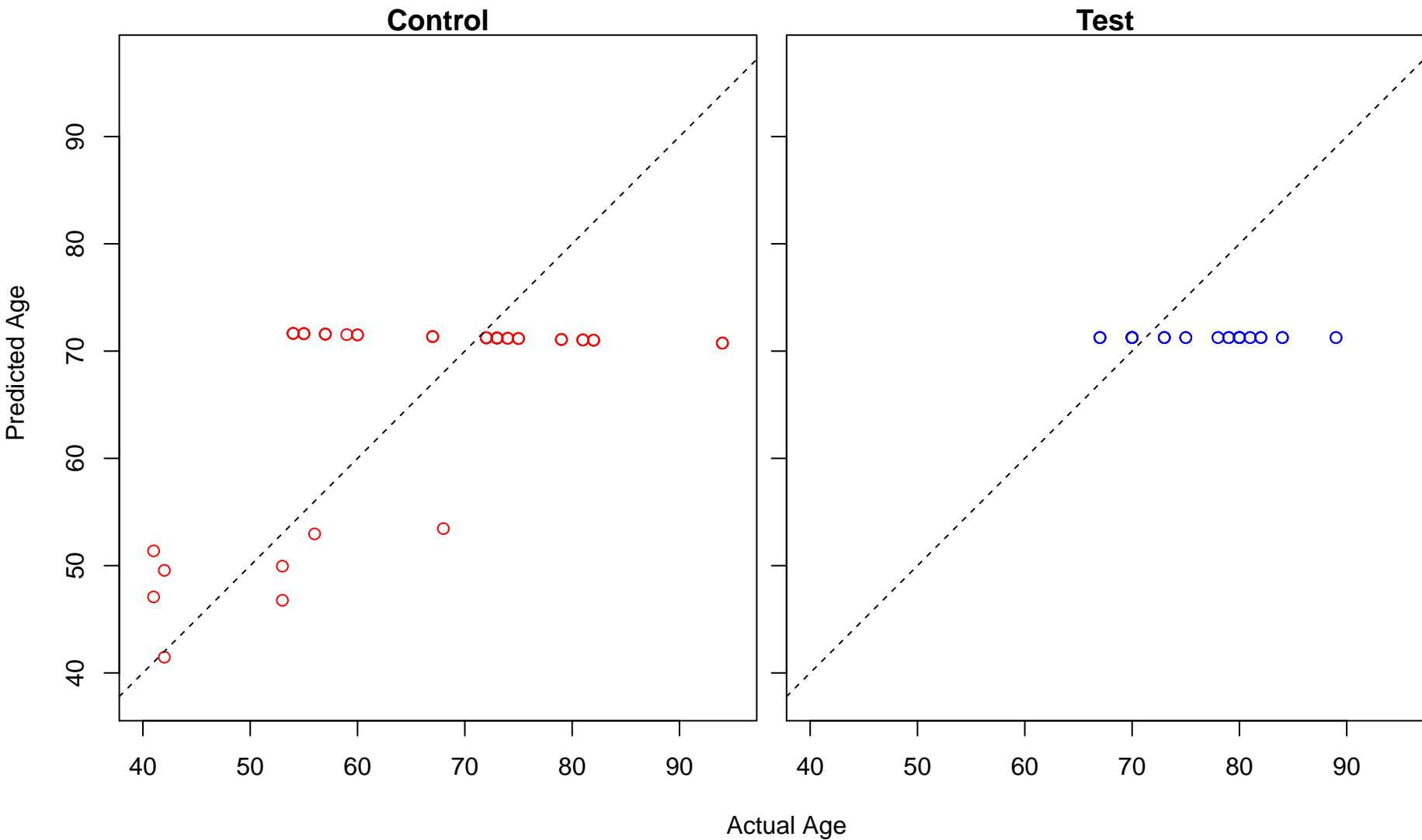
muscle system process (Score: 0.820385)



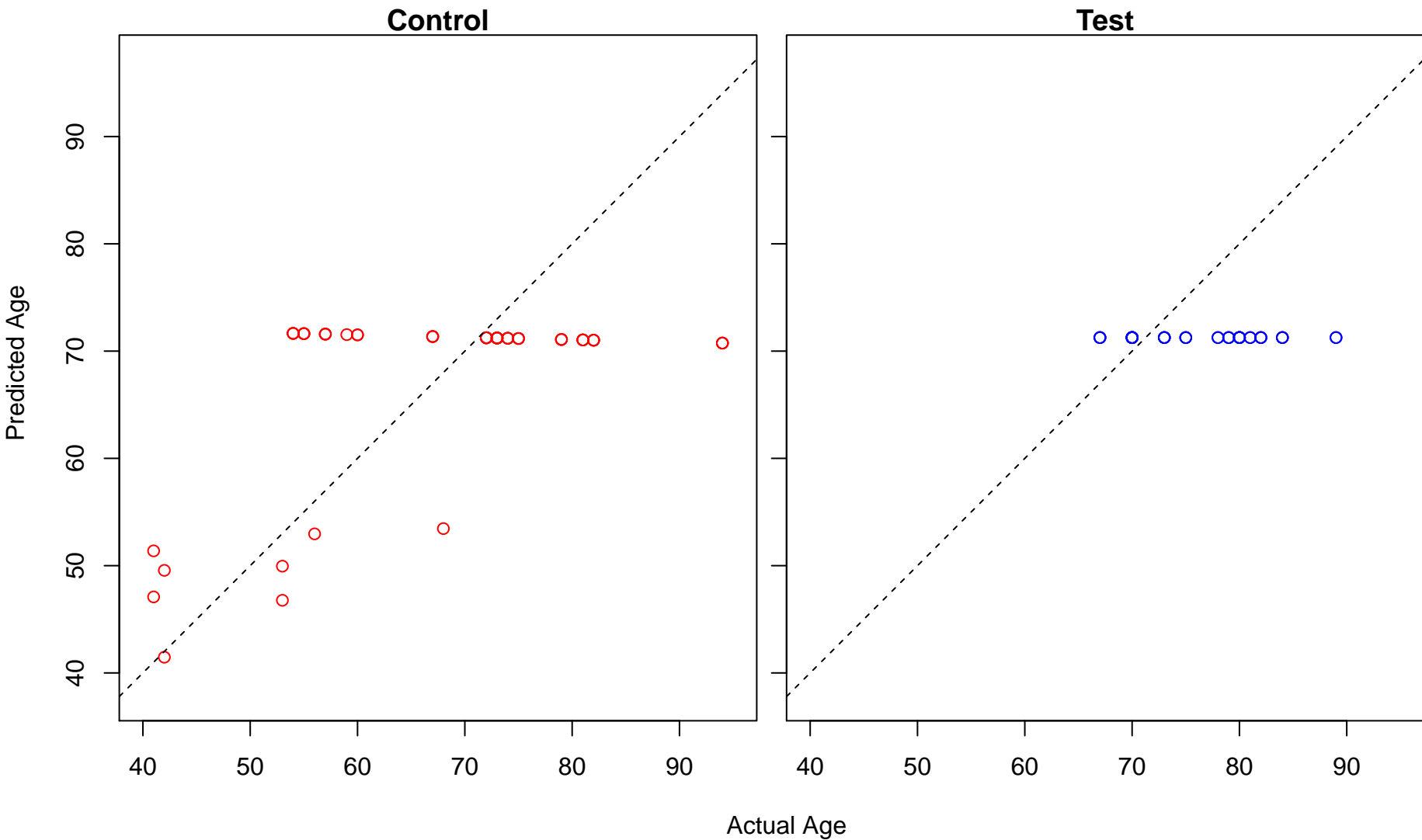
positive regulation of cellular amide metabolic process (Score: 0.820379)



sensory perception (Score: 0.820374)

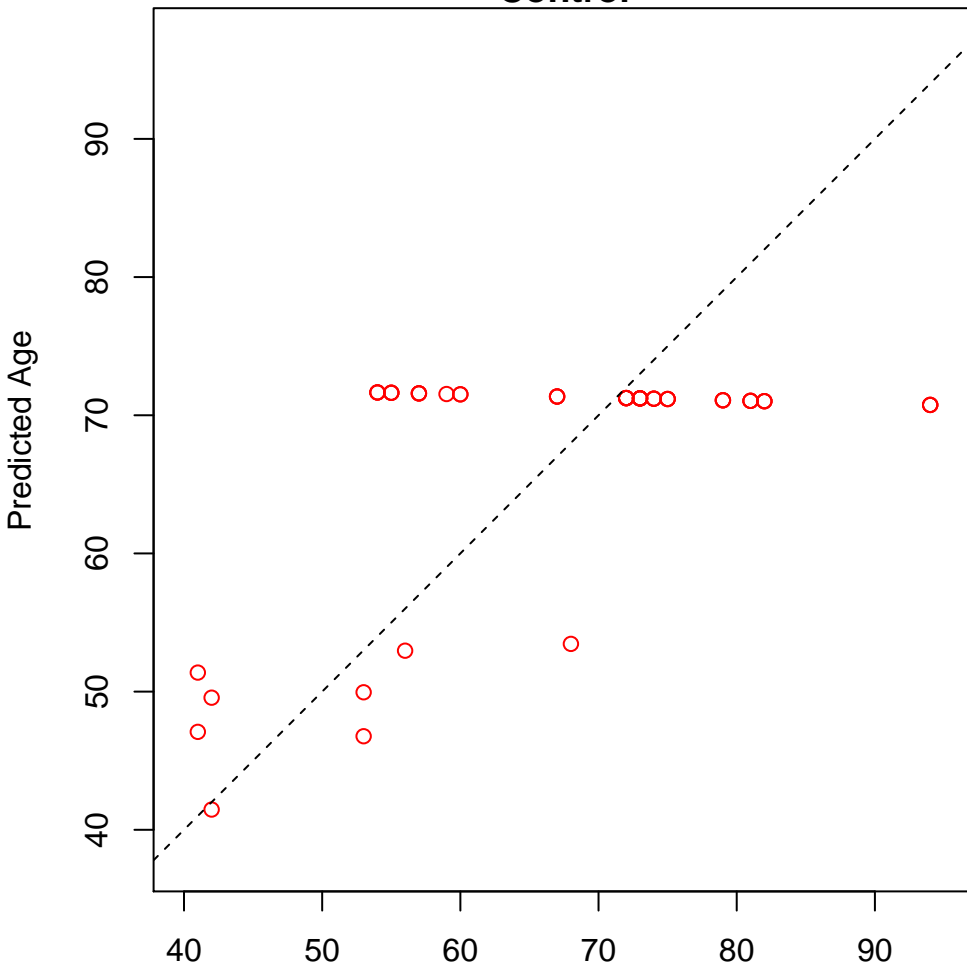


sensory perception of sound (Score: 0.820374)

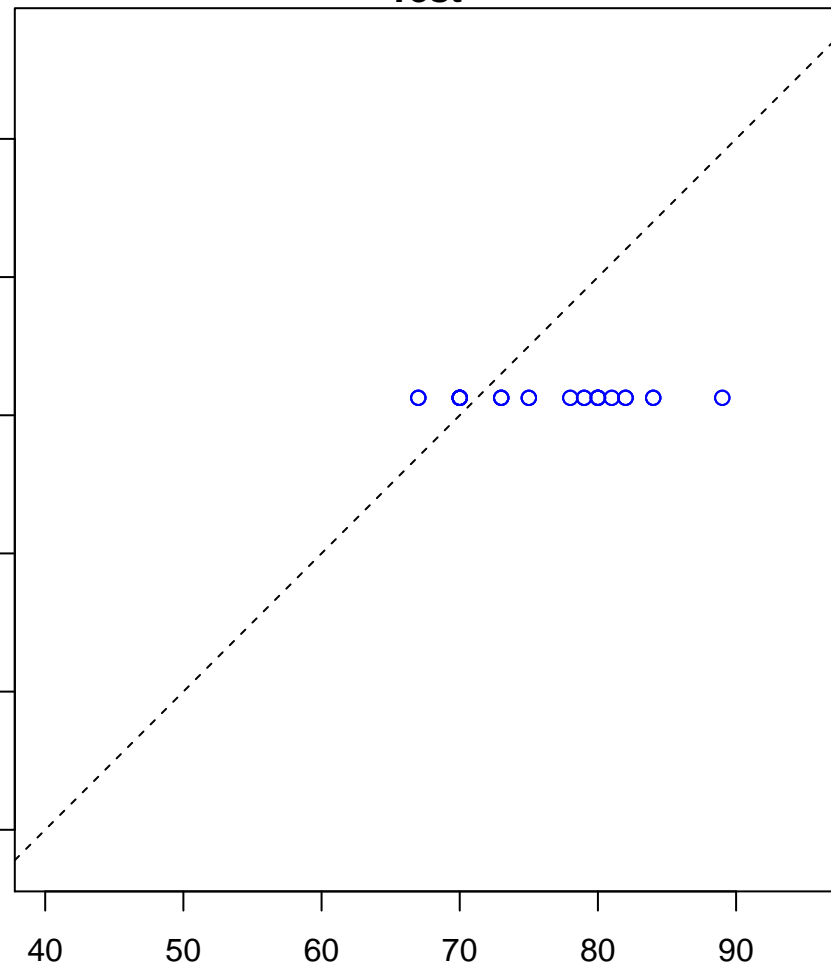


sensory perception of mechanical stimulus (Score: 0.820374)

Control

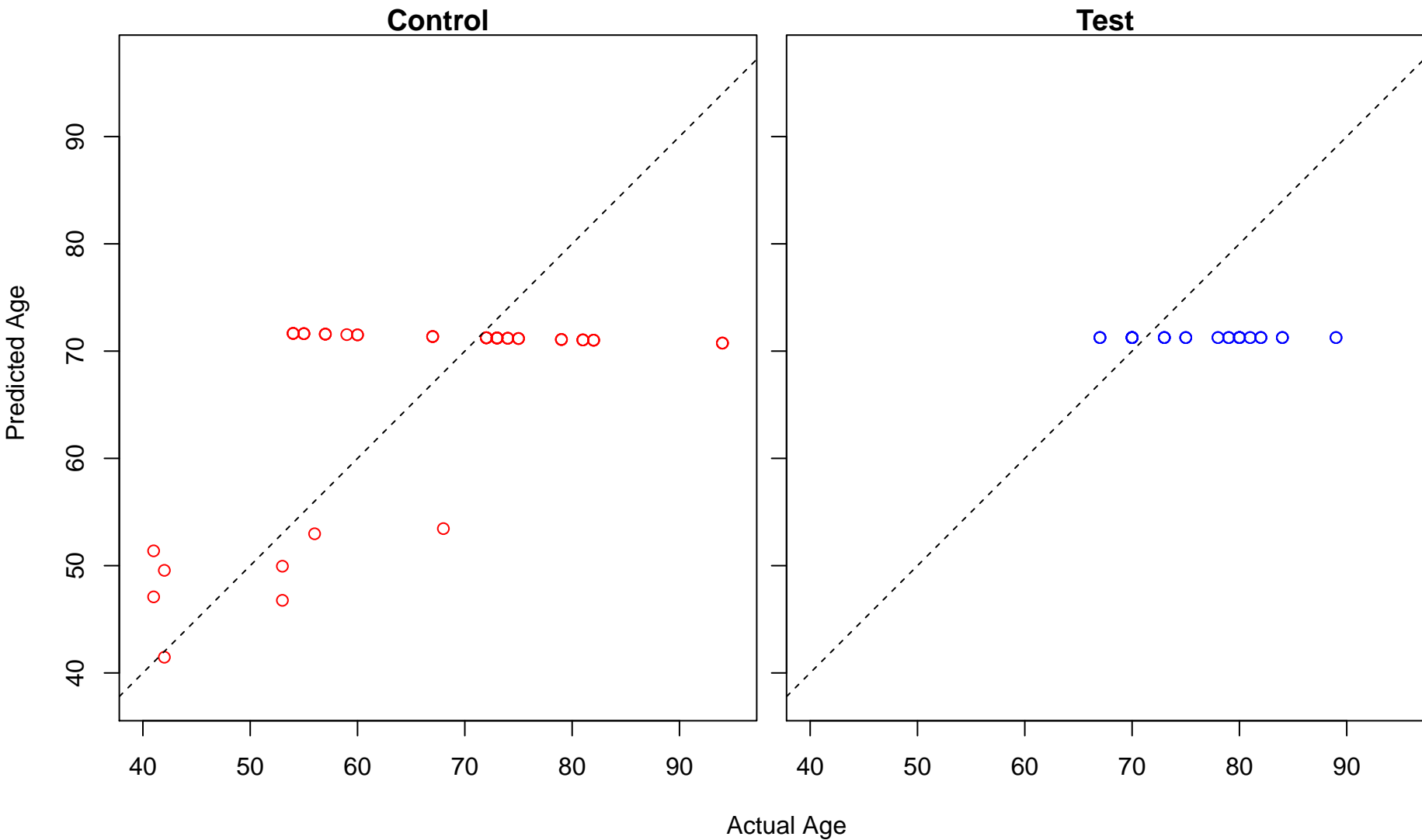


Test



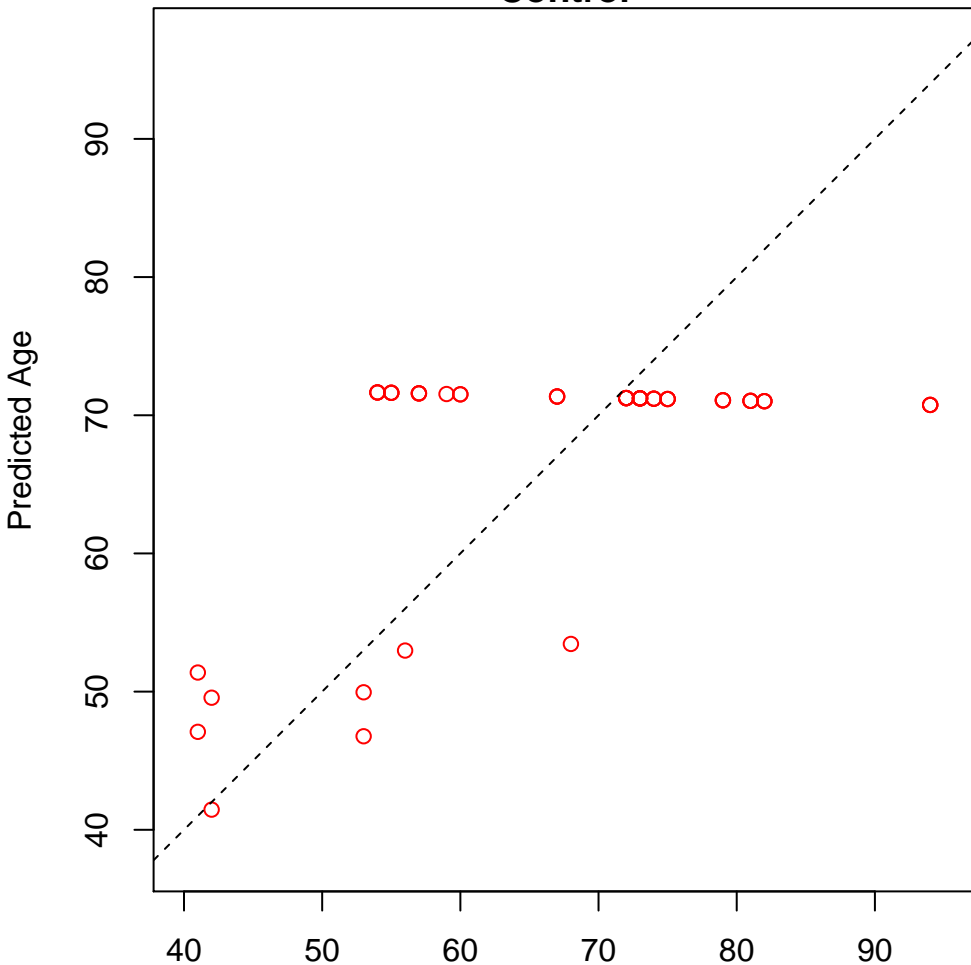
Actual Age

embryo development (Score: 0.820371)

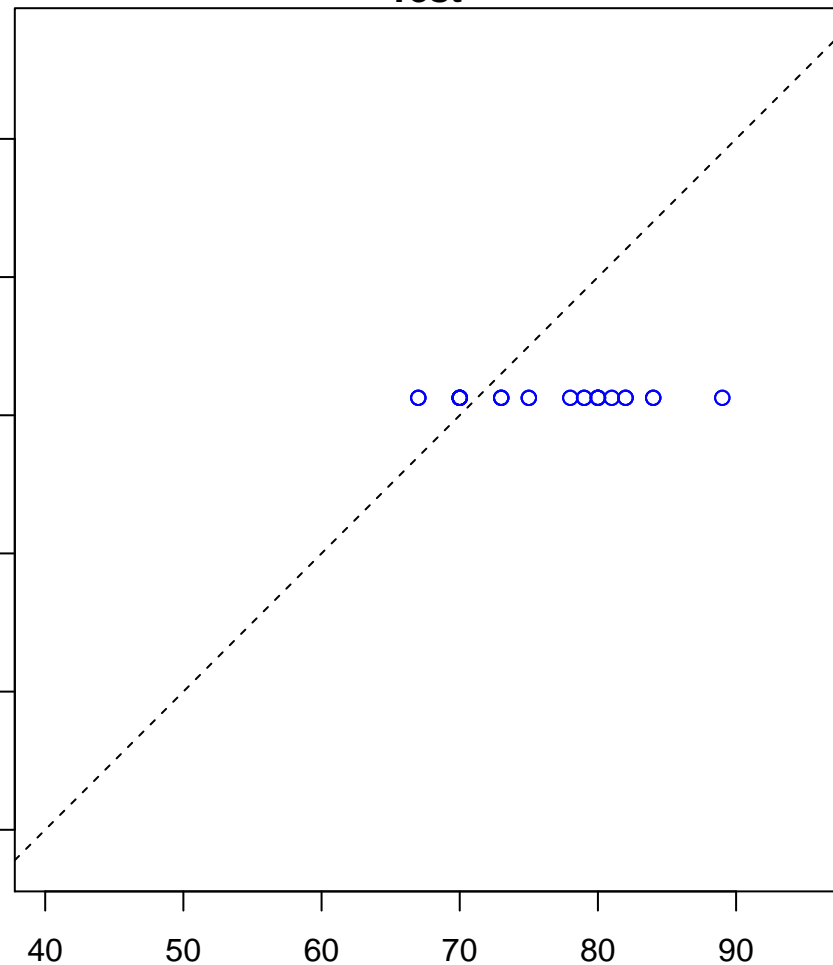


sensory organ development (Score: 0.820370)

Control

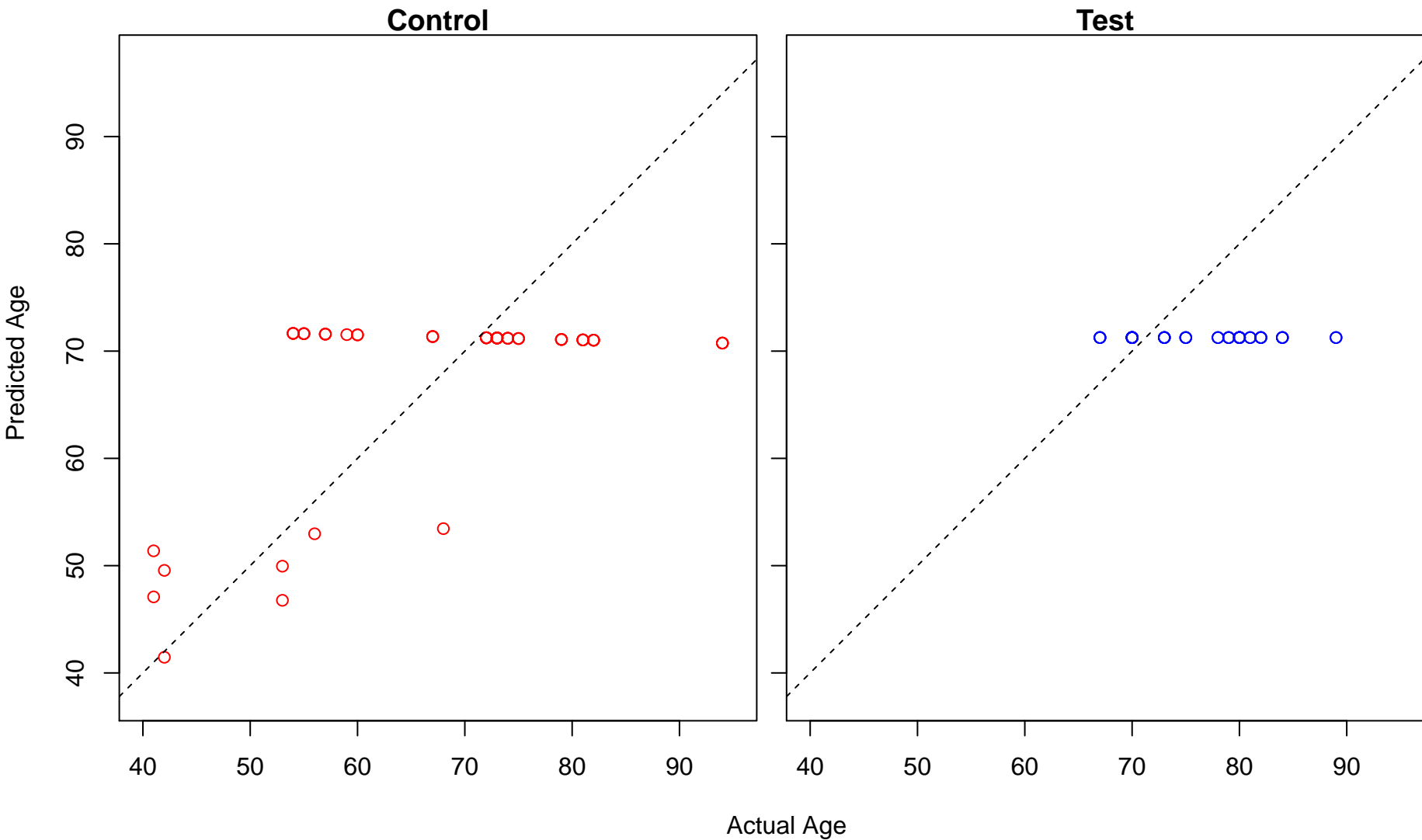


Test

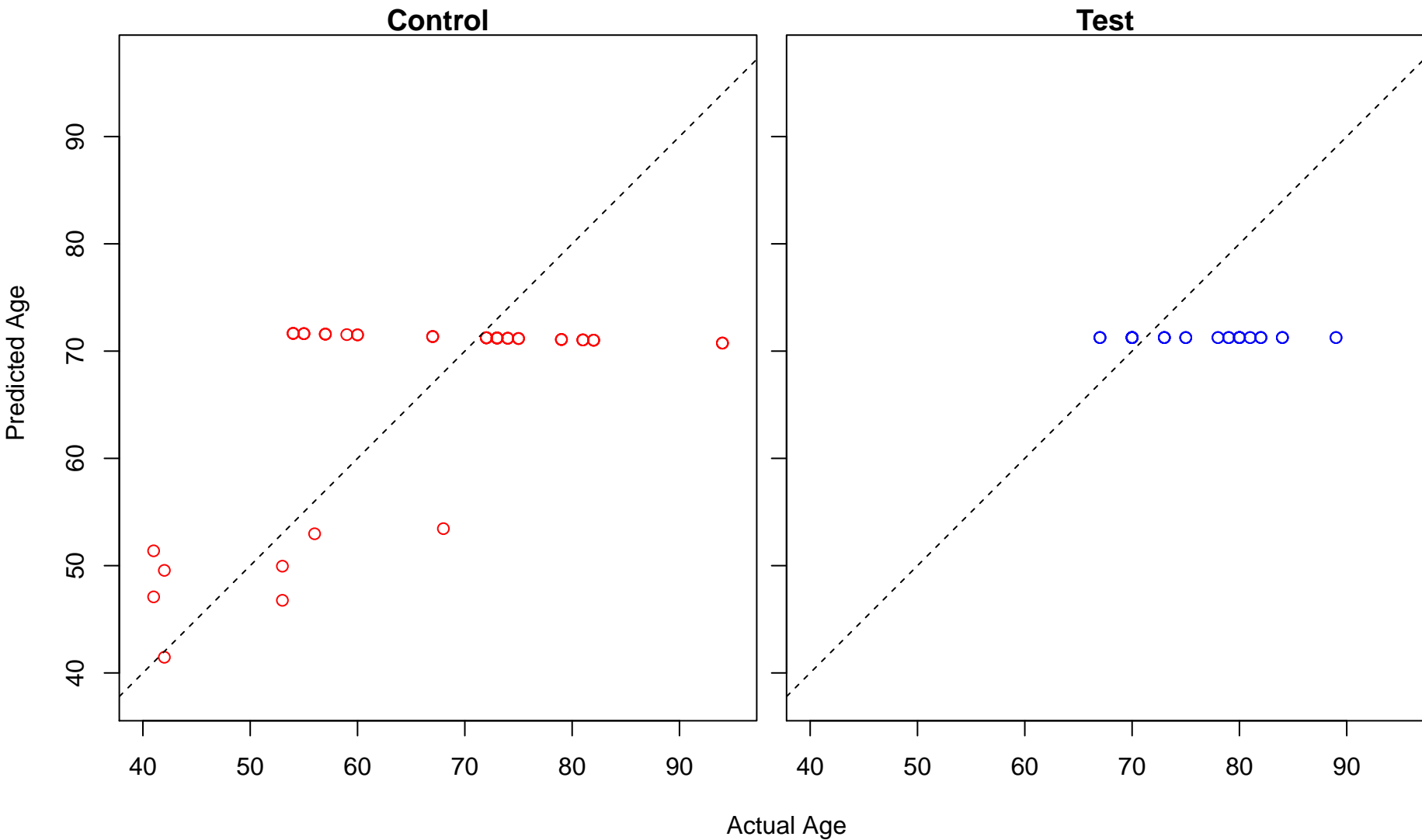


Actual Age

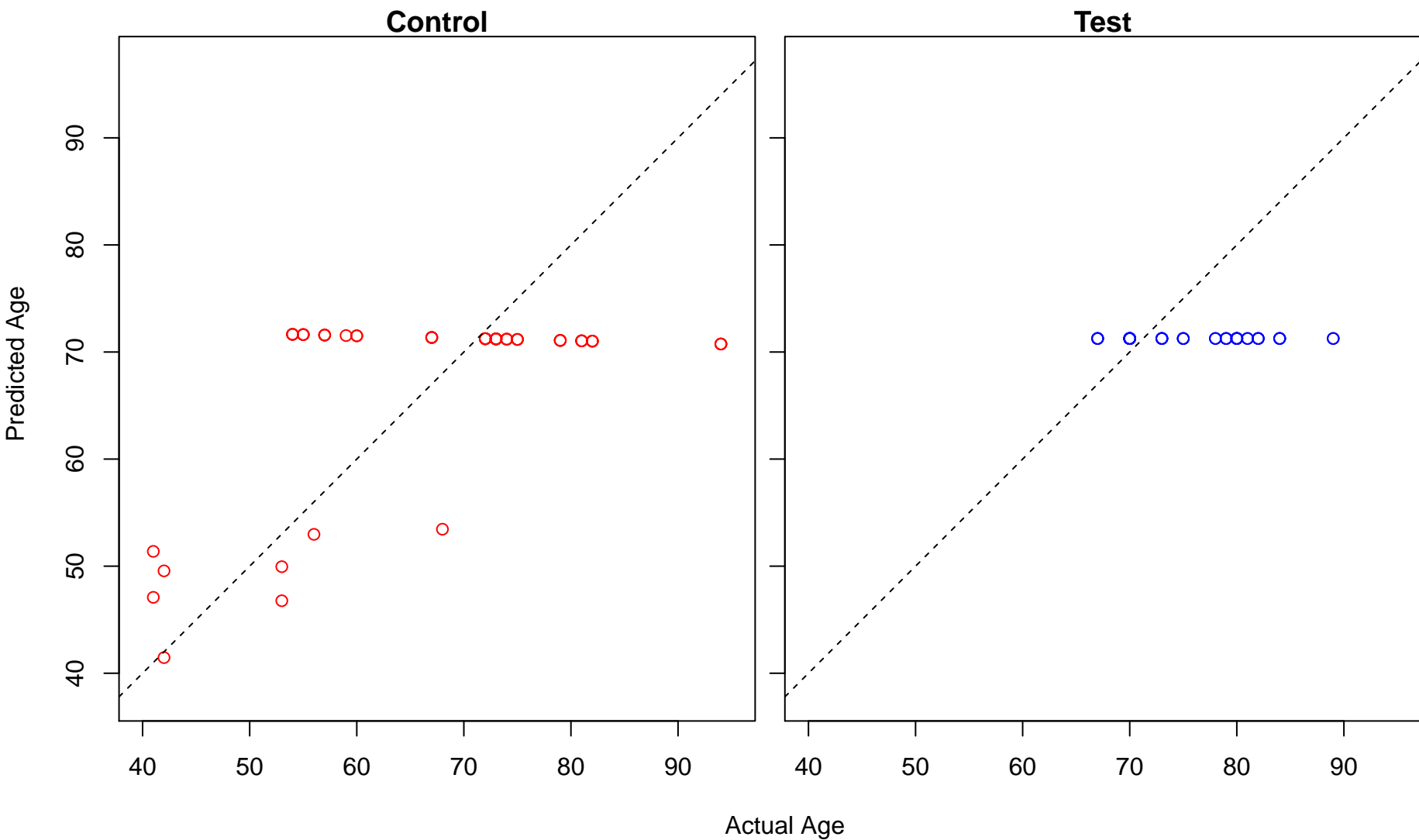
ear morphogenesis (Score: 0.820370)



inner ear morphogenesis (Score: 0.820370)

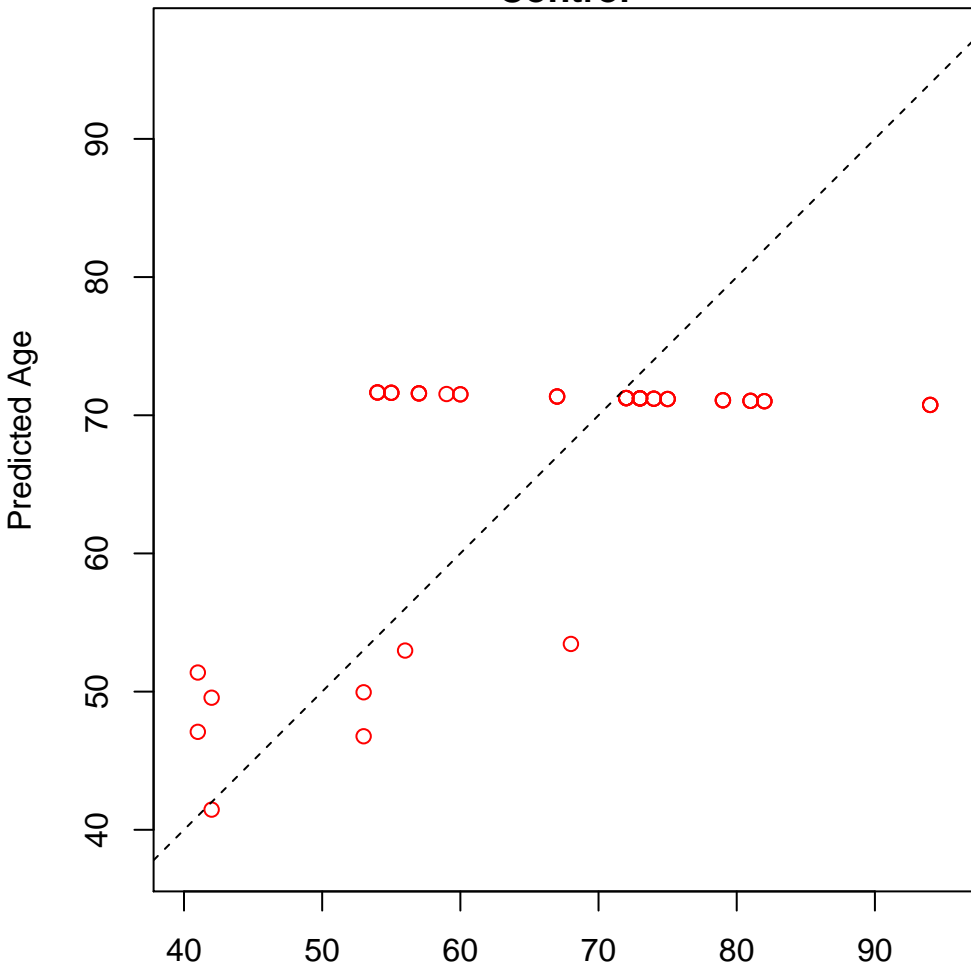


ear development (Score: 0.820370)

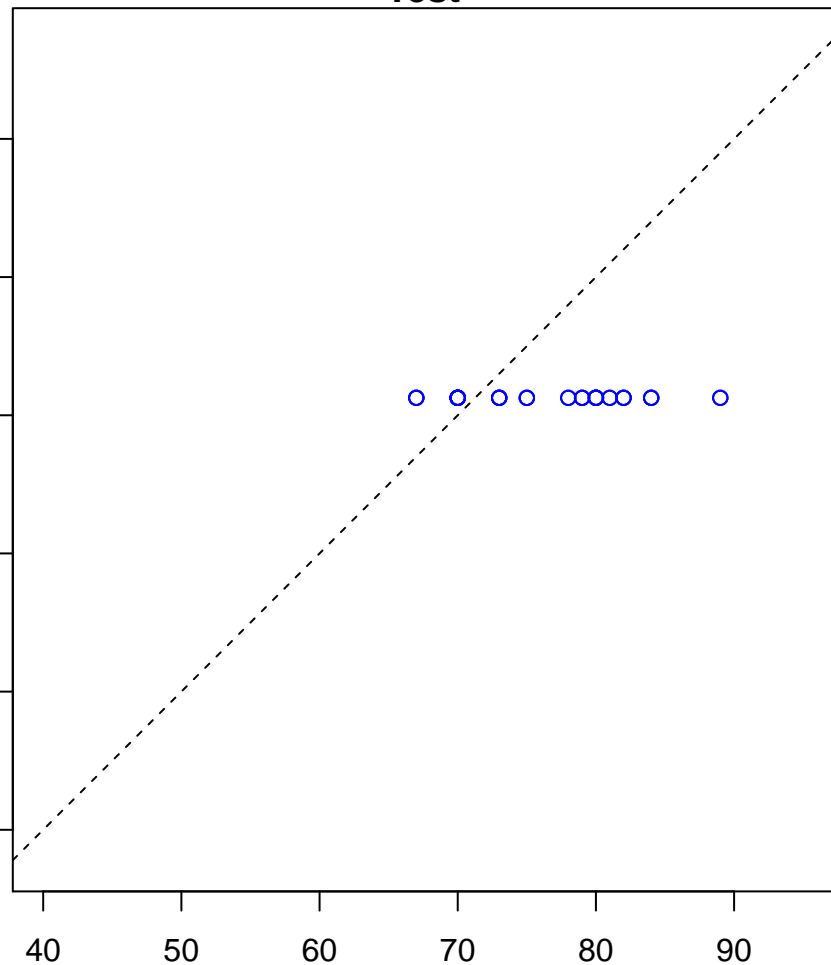


embryonic organ morphogenesis (Score: 0.820370)

Control

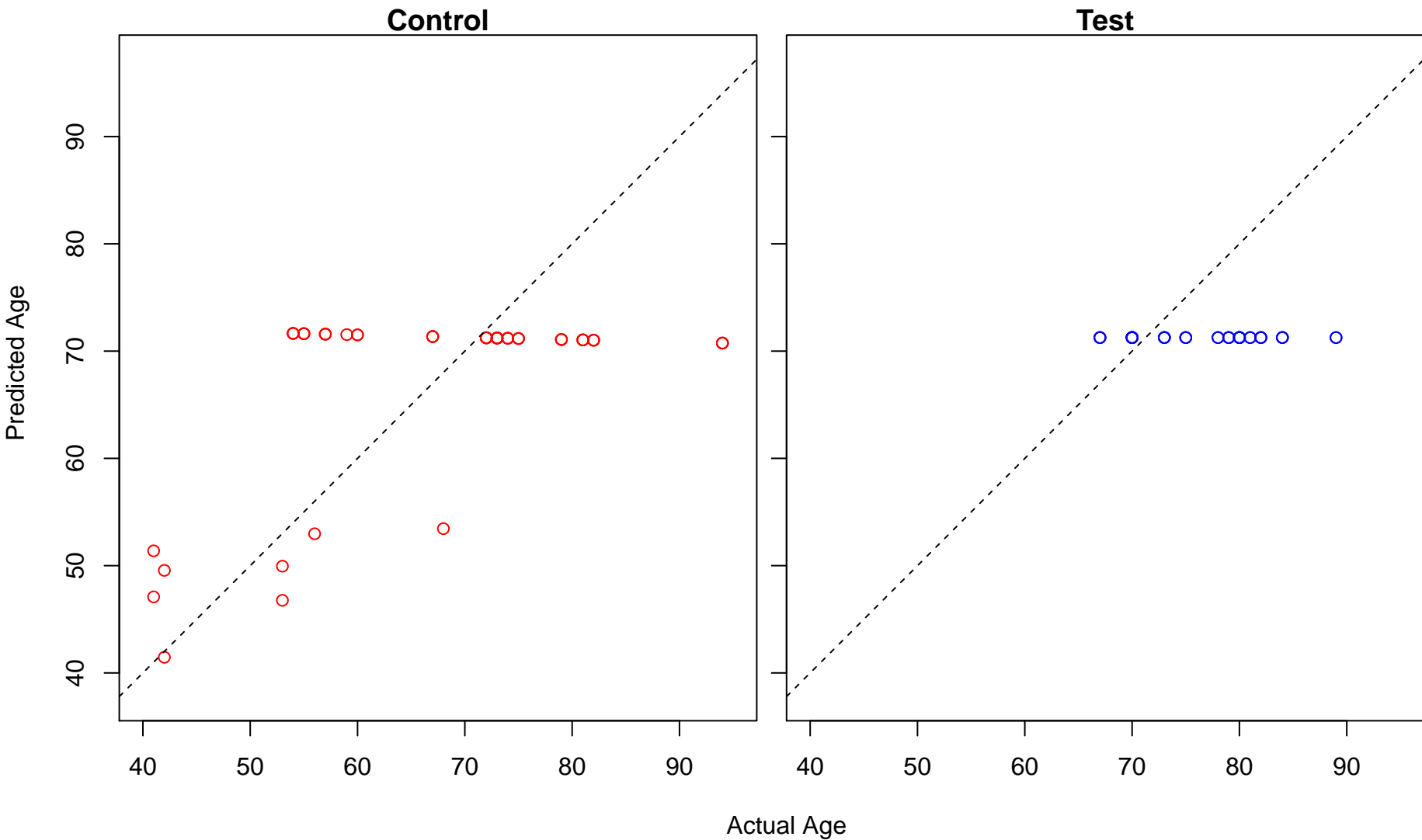


Test



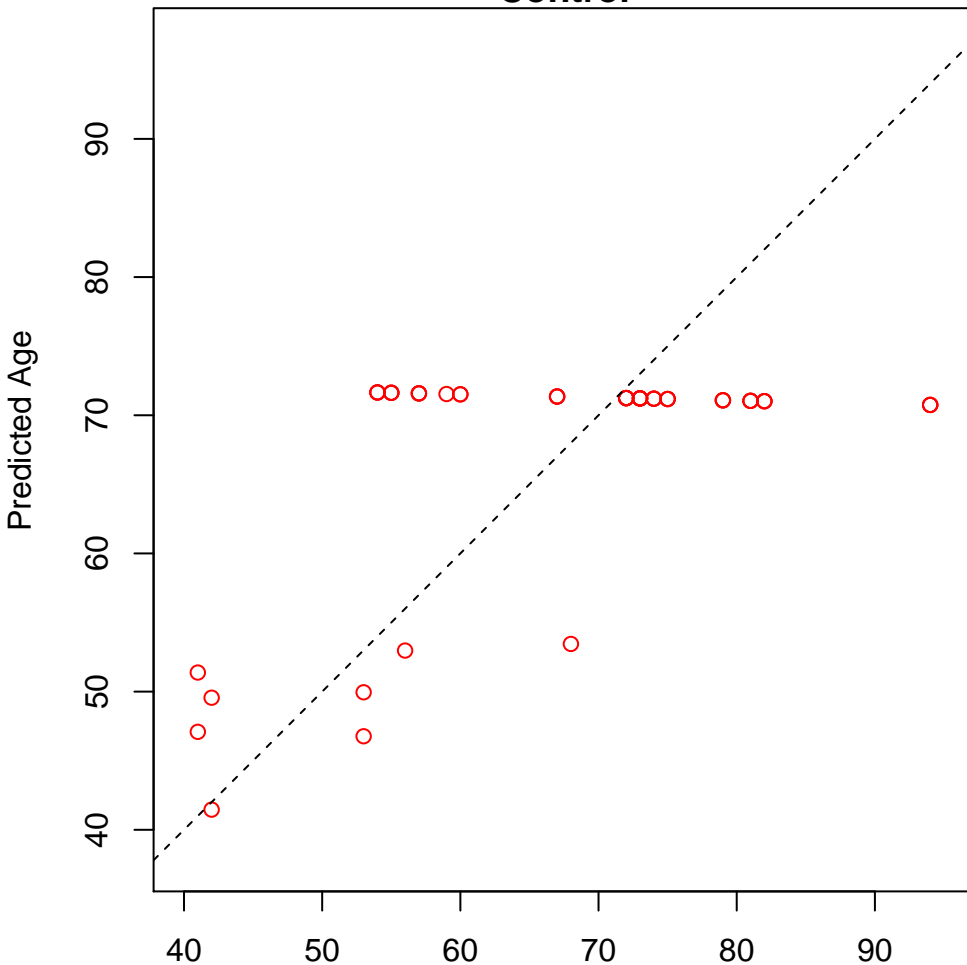
Actual Age

embryonic organ development (Score: 0.820370)

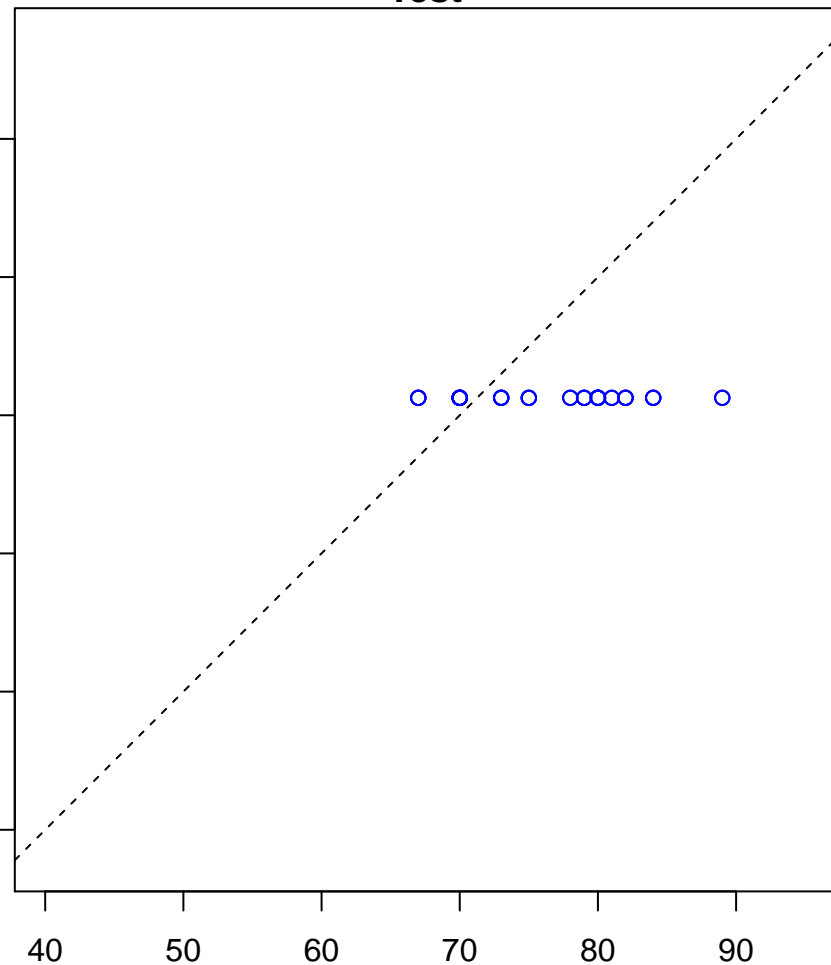


inner ear development (Score: 0.820370)

Control



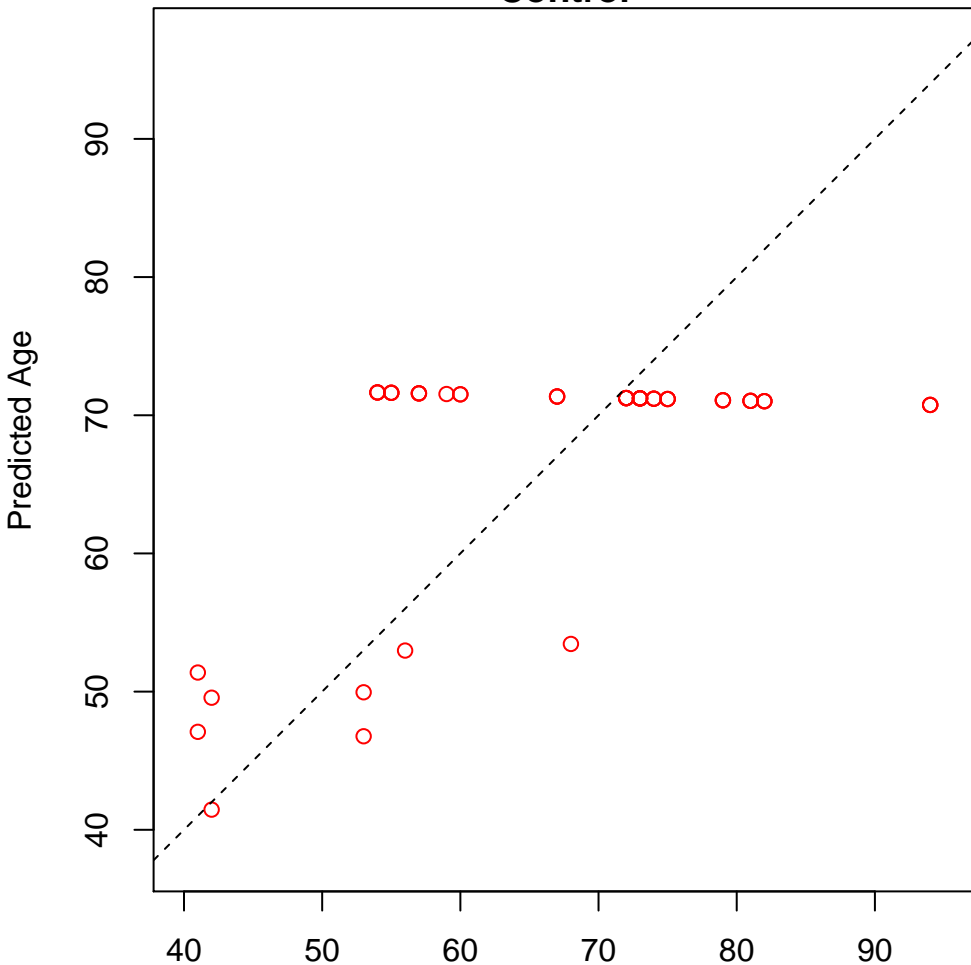
Test



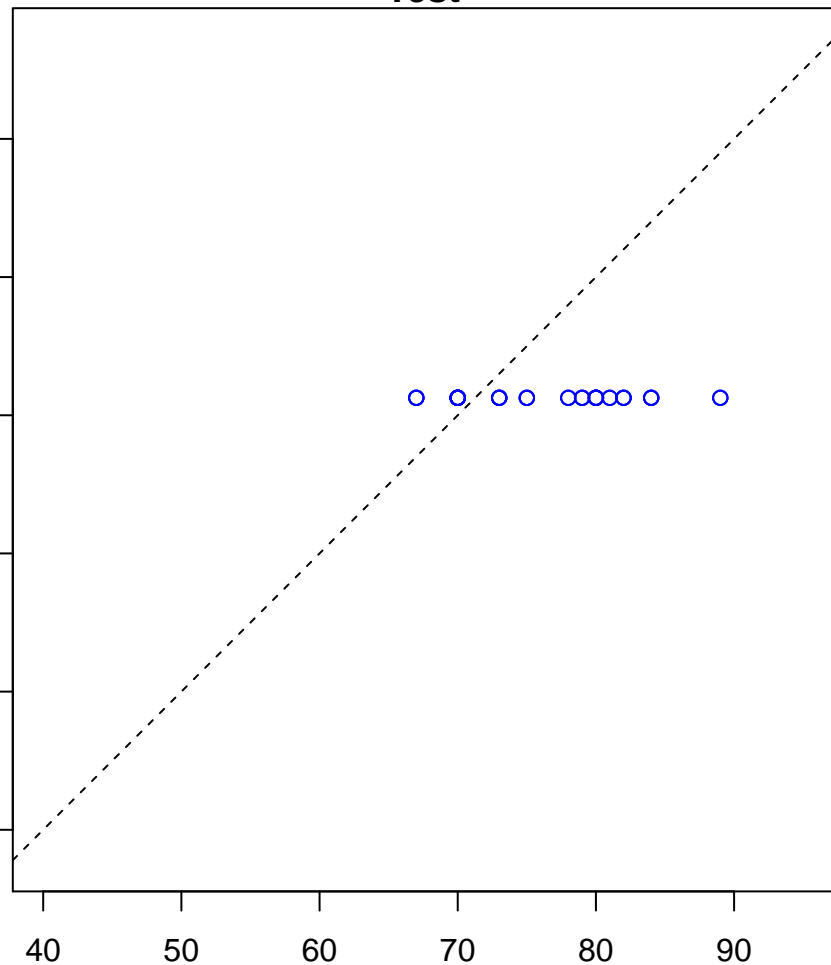
Actual Age

sensory organ morphogenesis (Score: 0.820370)

Control

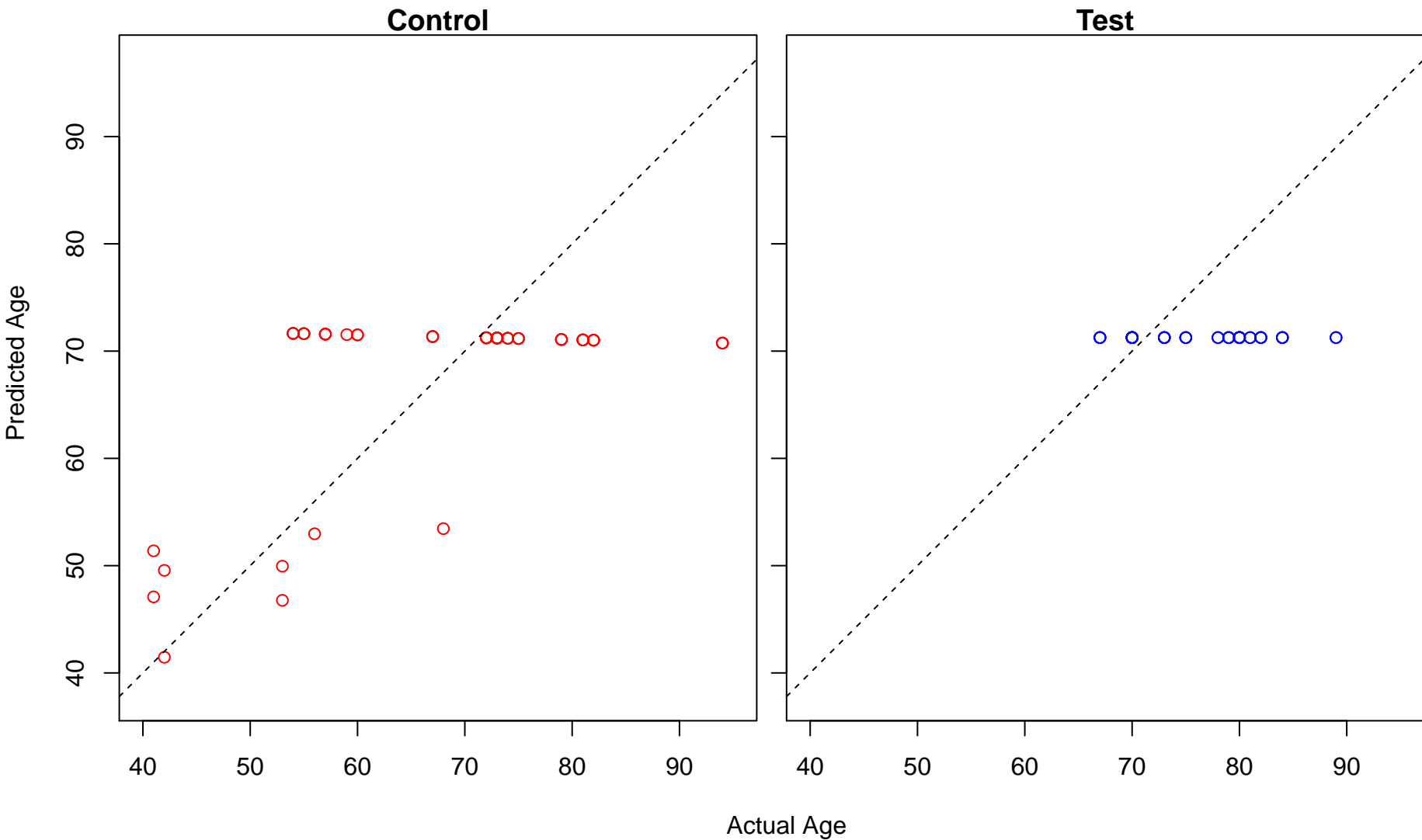


Test



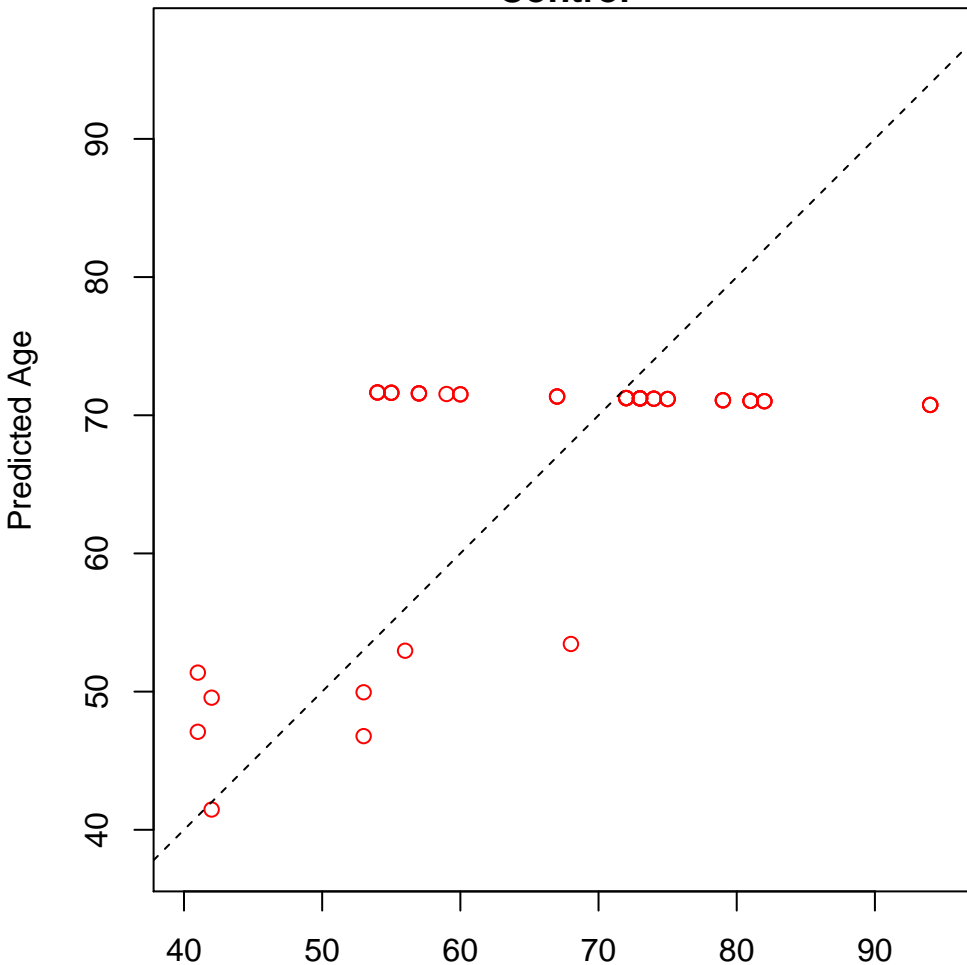
Actual Age

embryonic morphogenesis (Score: 0.820369)

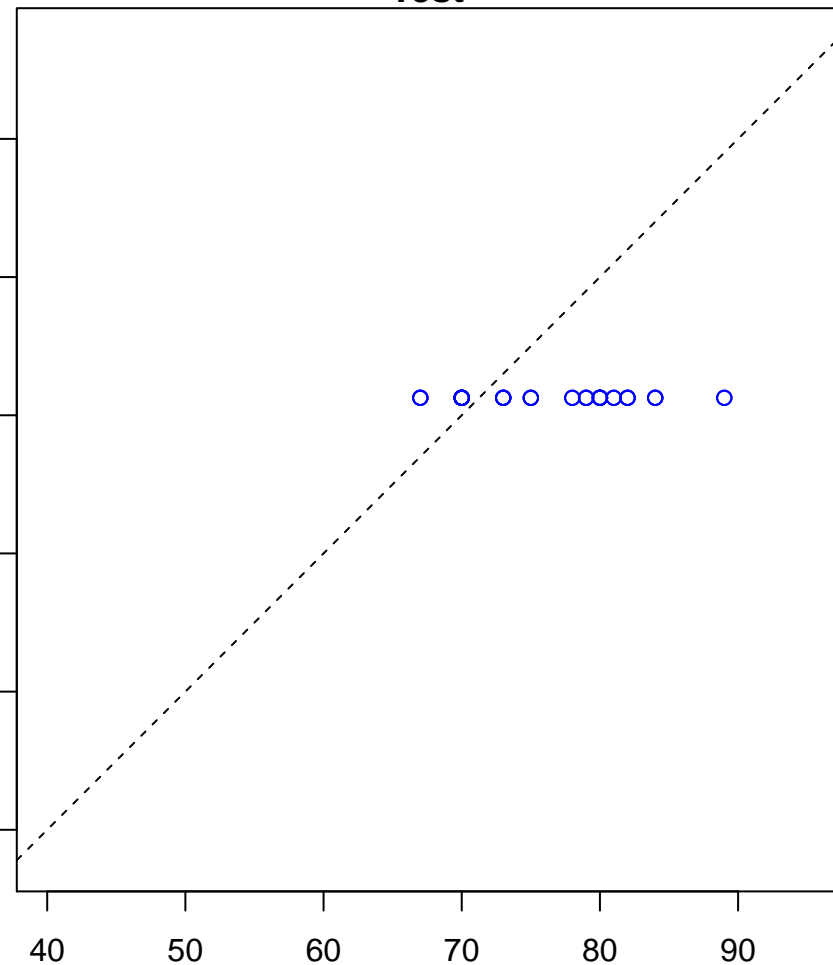


plasma membrane organization (Score: 0.820367)

Control



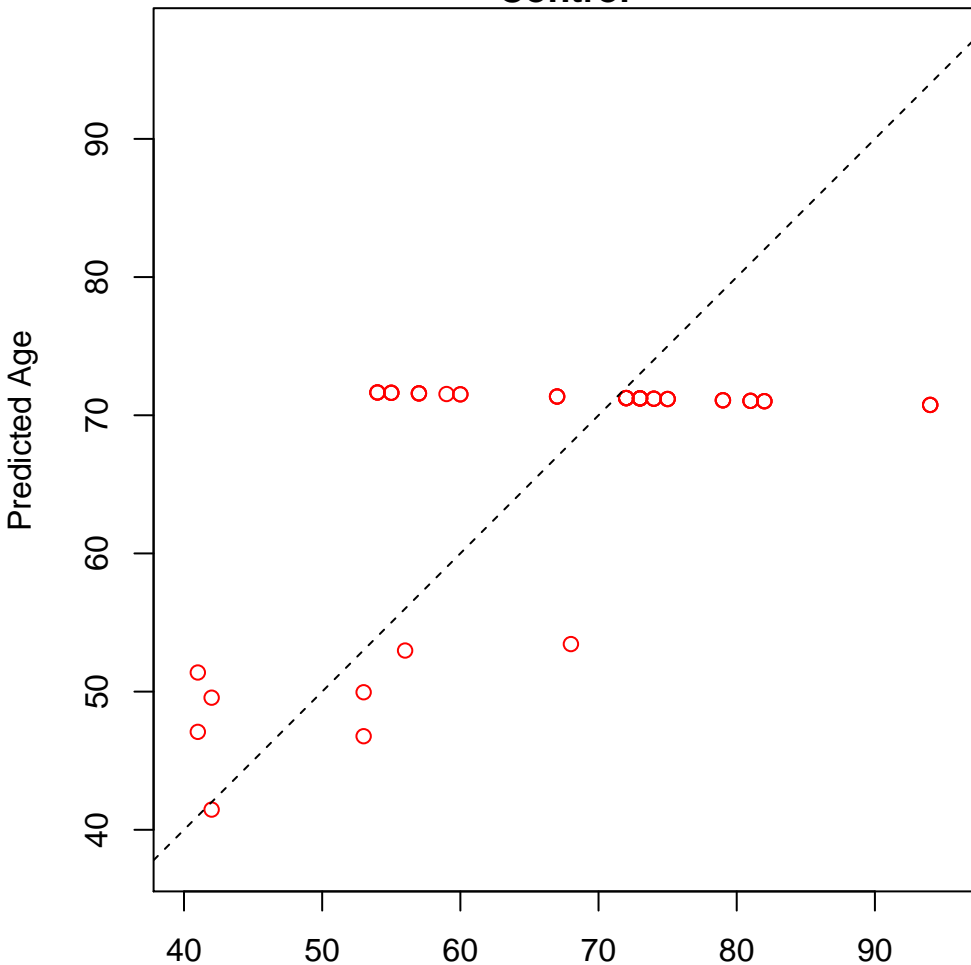
Test



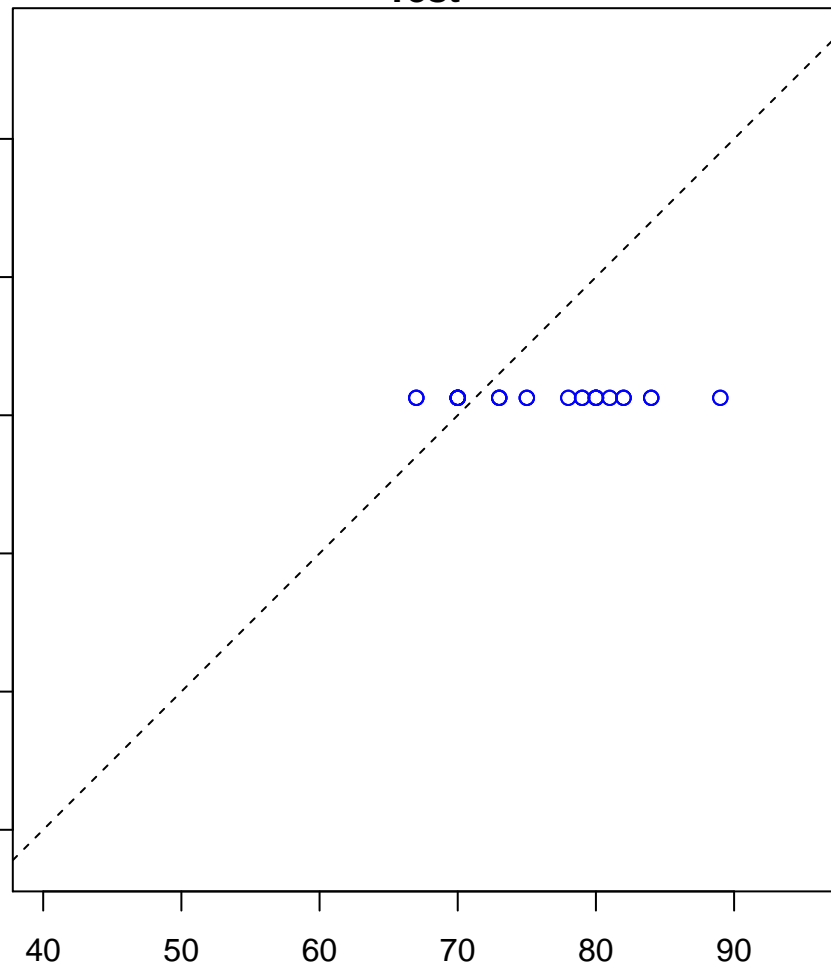
Actual Age

response to temperature stimulus (Score: 0.820364)

Control

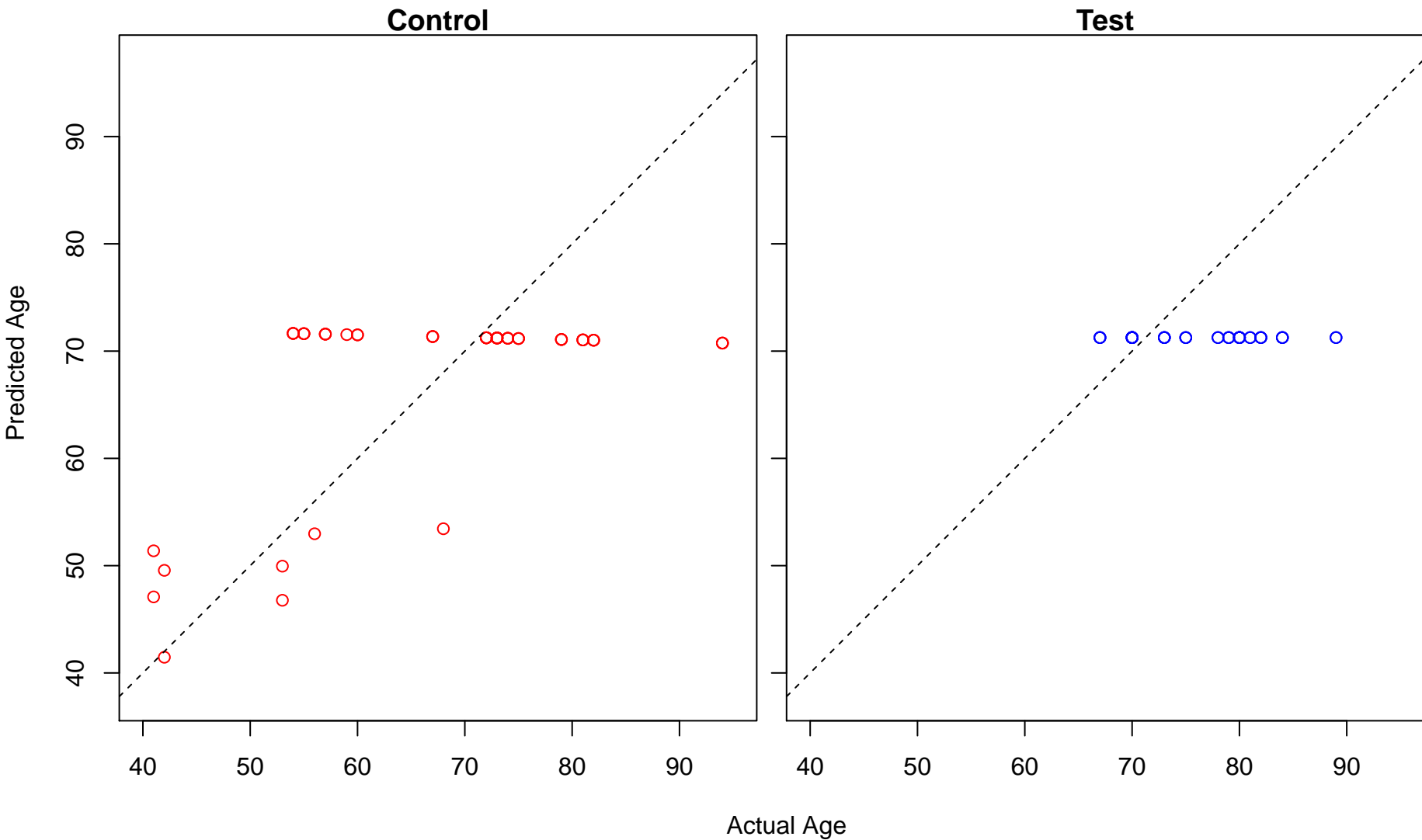


Test

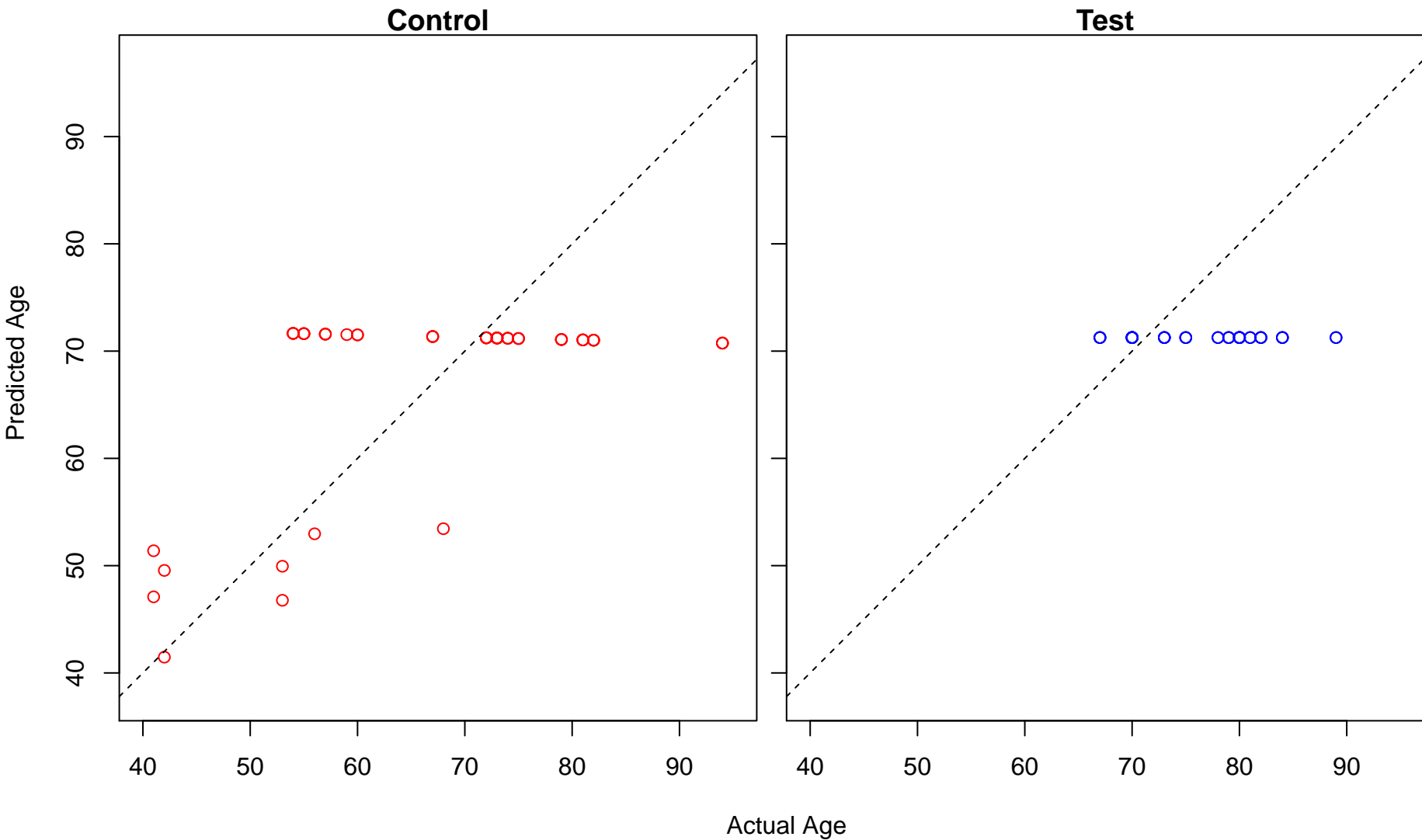


Actual Age

response to heat (Score: 0.820364)

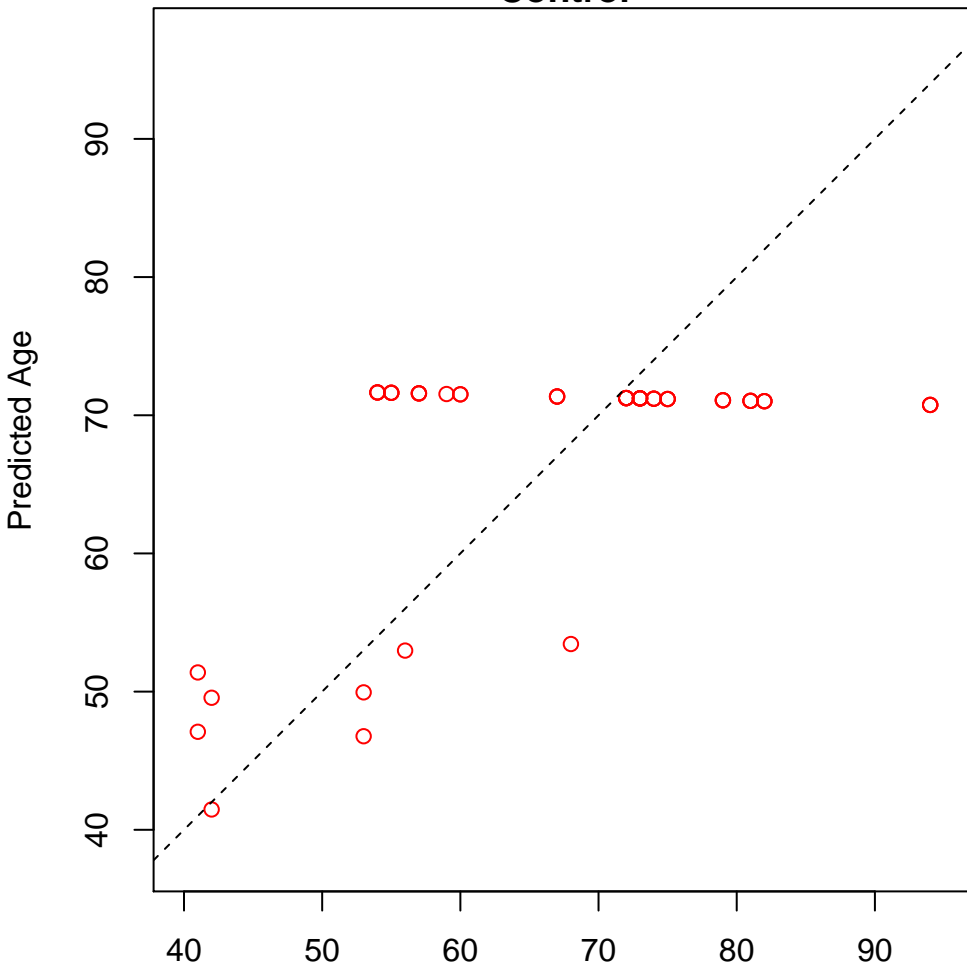


multicellular organismal signaling (Score: 0.820363)

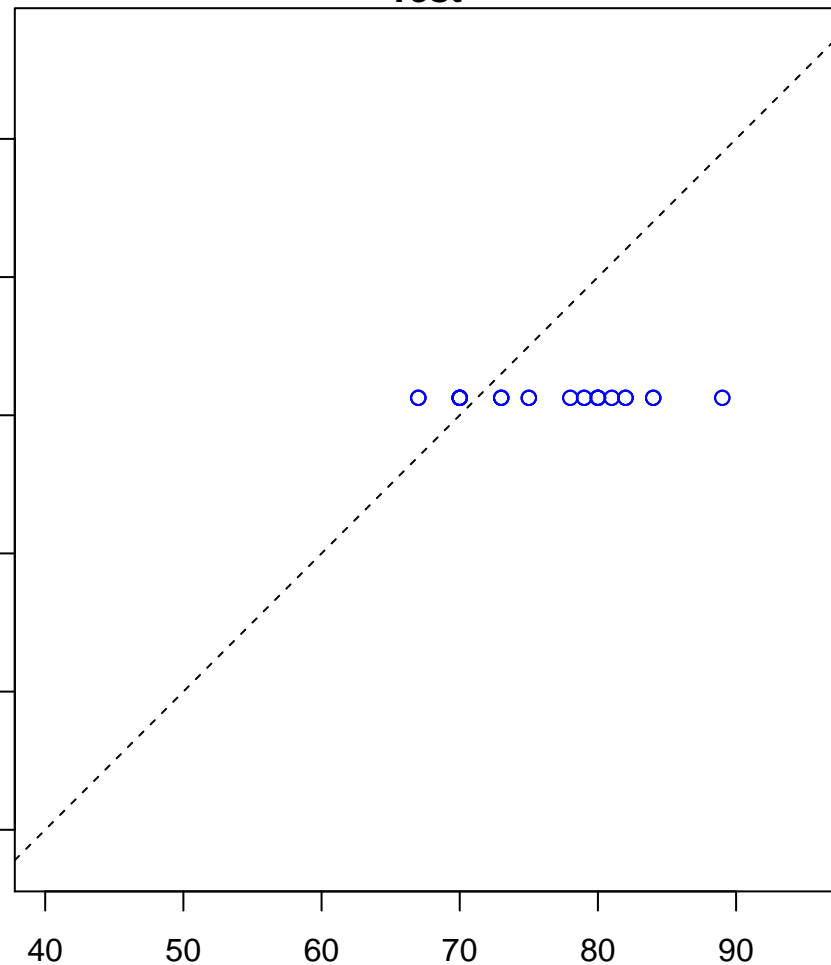


intermediate filament-based process (Score: 0.820363)

Control

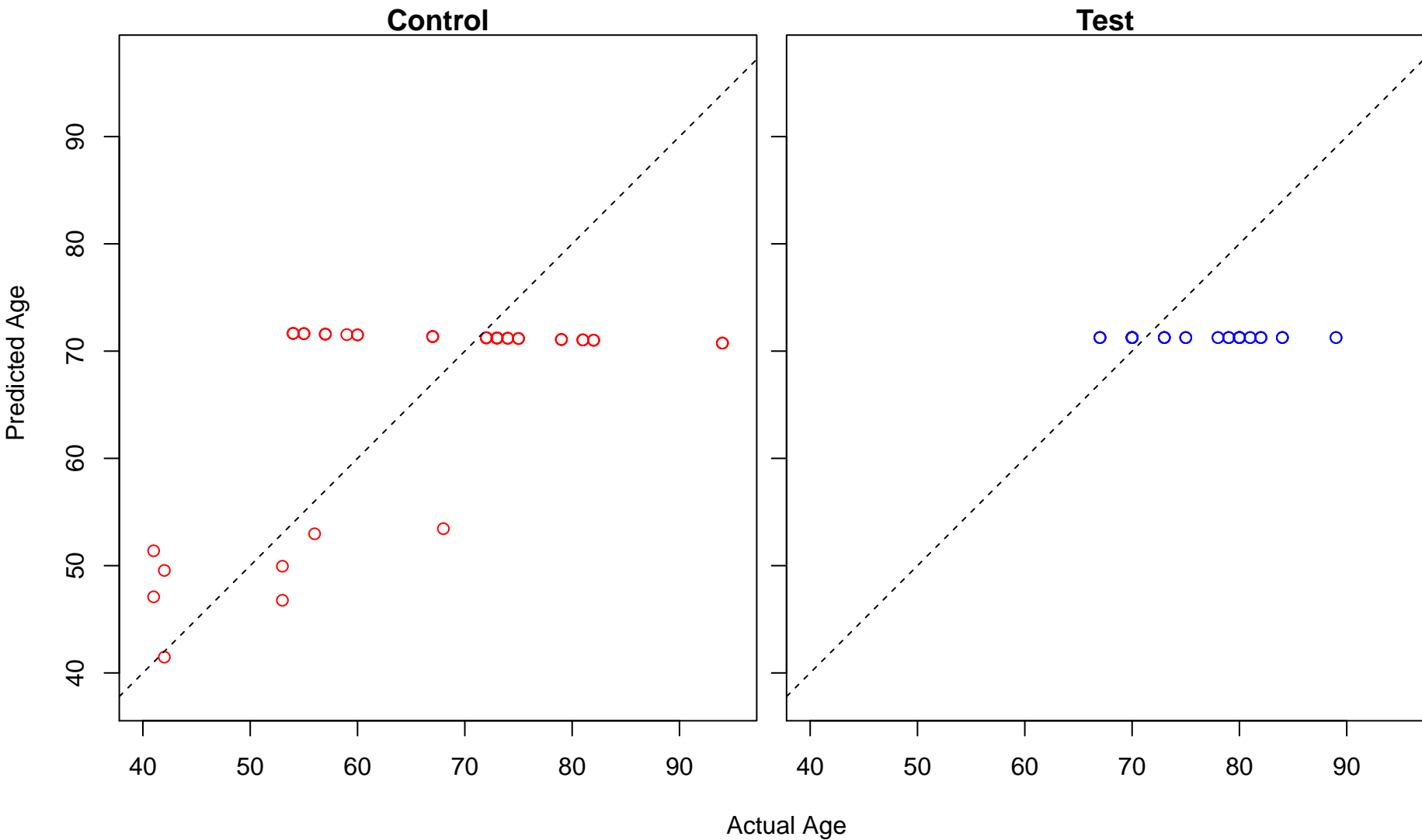


Test

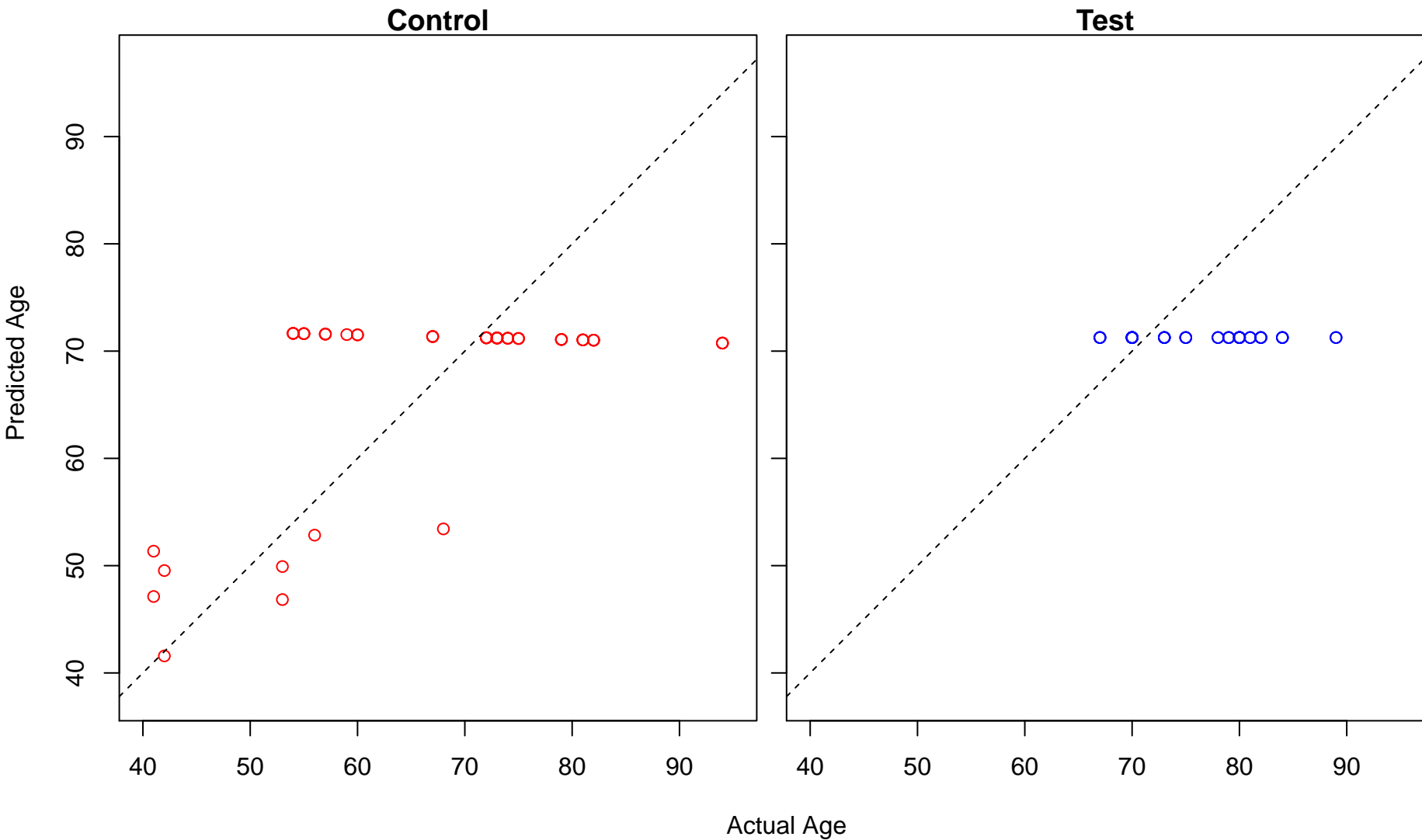


Actual Age

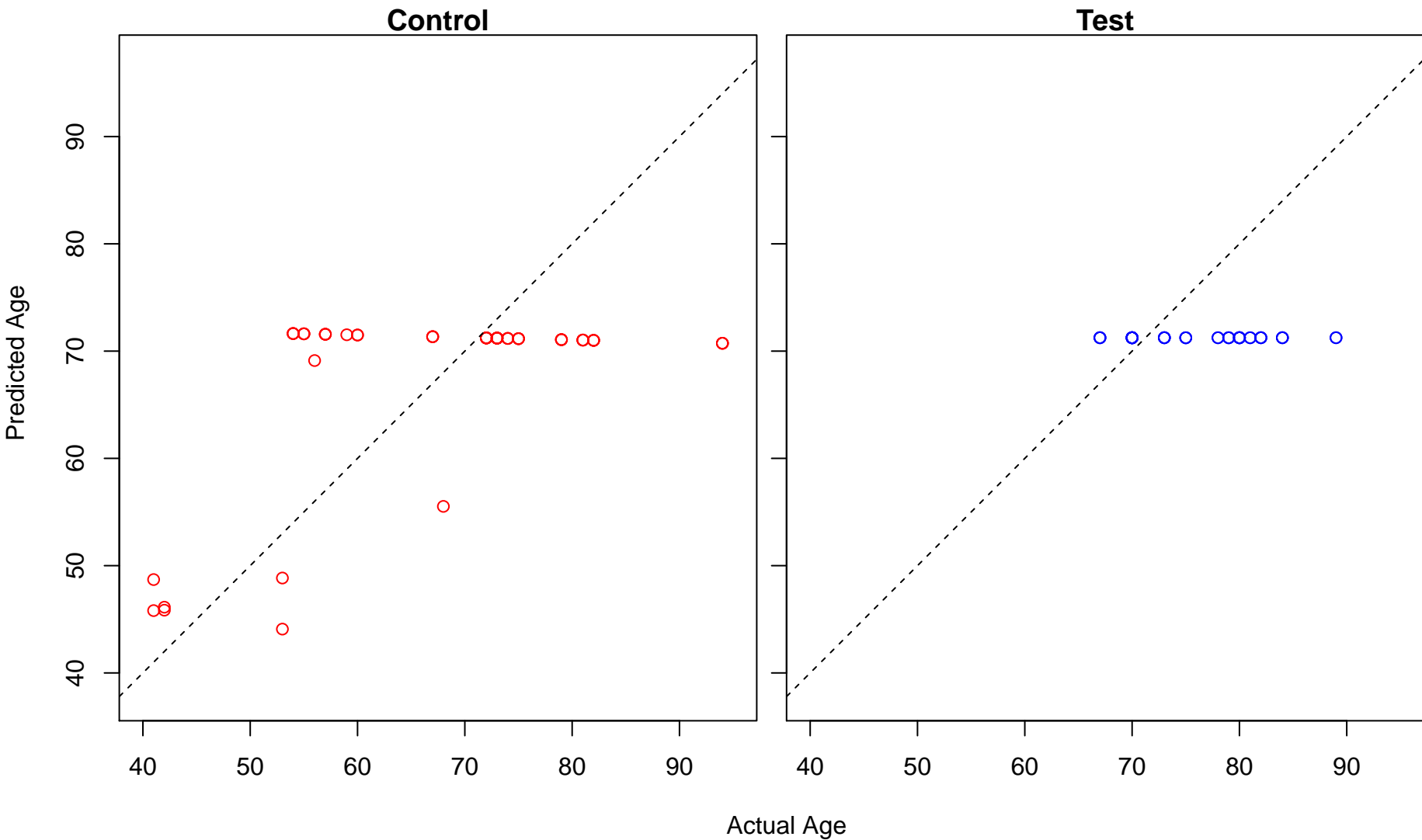
intermediate filament cytoskeleton organization (Score: 0.820363)



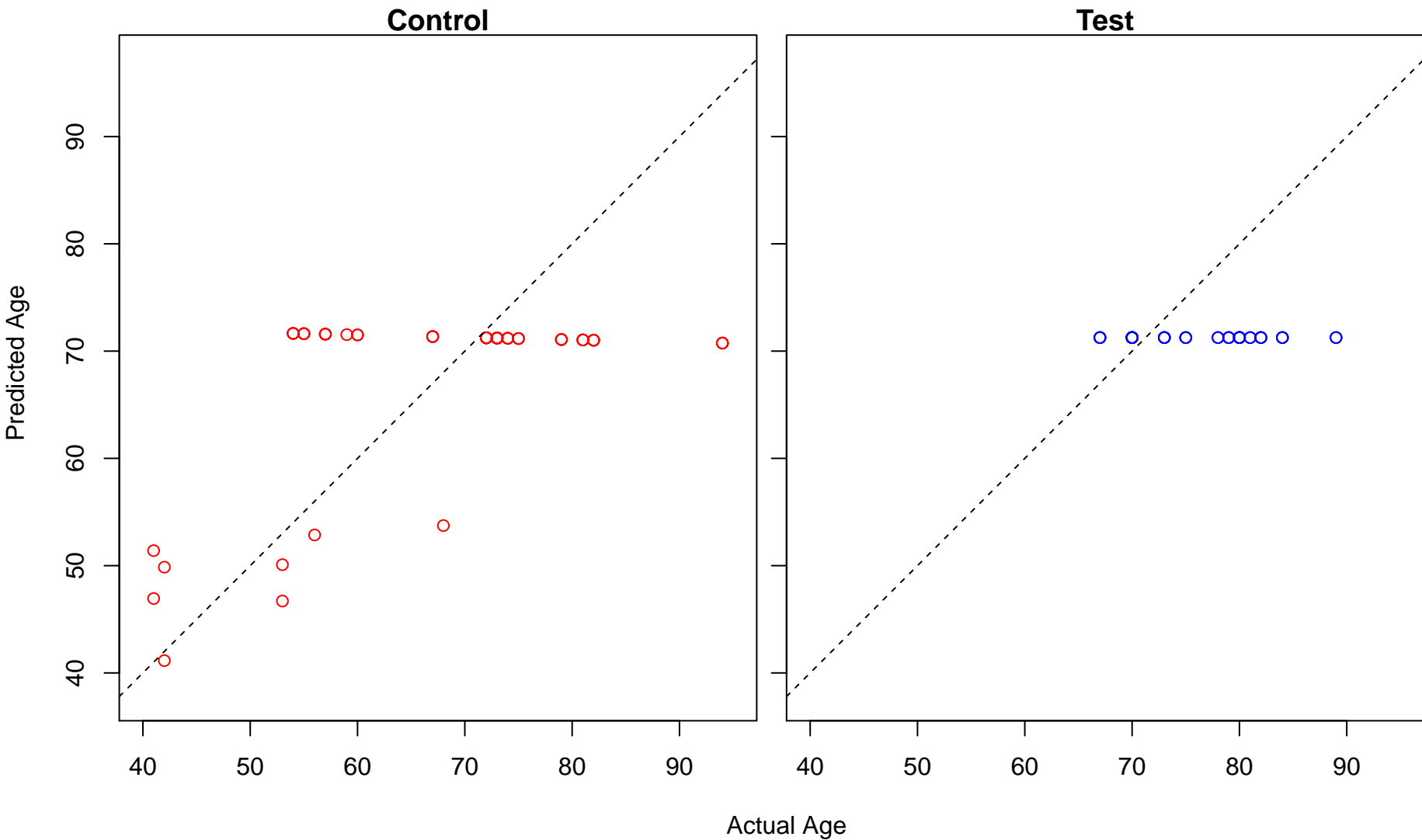
cell aging (Score: 0.820361)



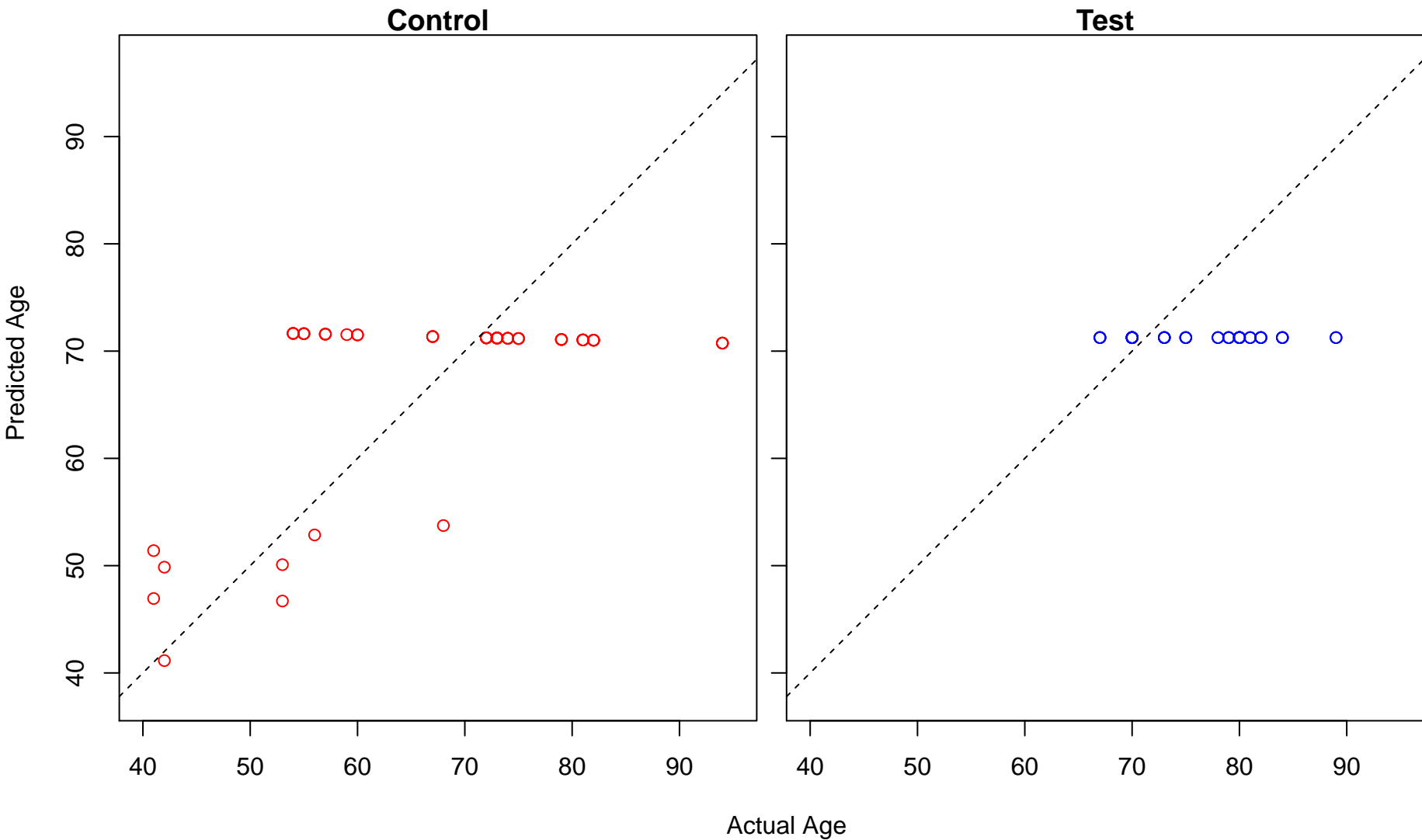
positive regulation of apoptotic signaling pathway (Score: 0.820360)



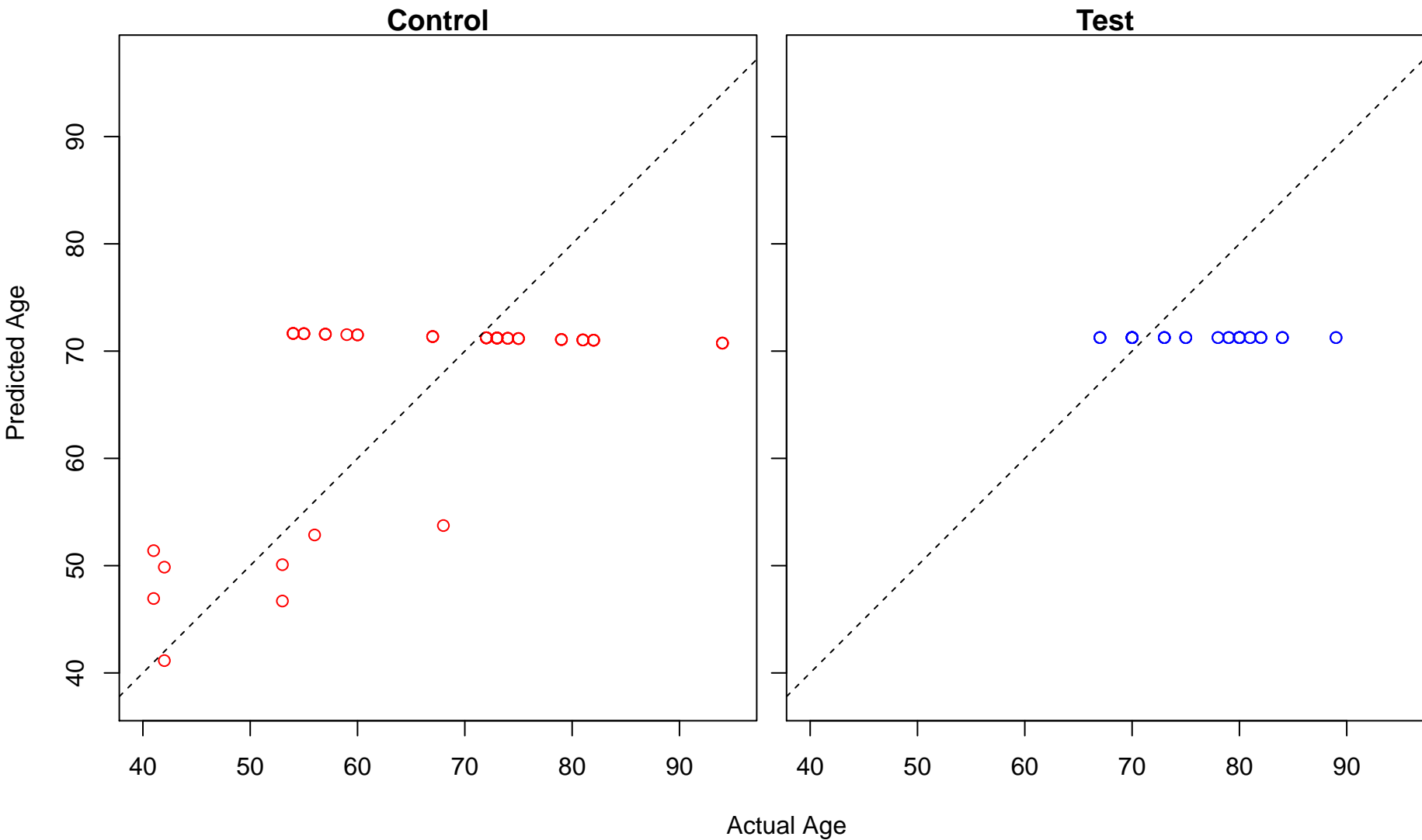
heart process (Score: 0.820360)



heart contraction (Score: 0.820360)

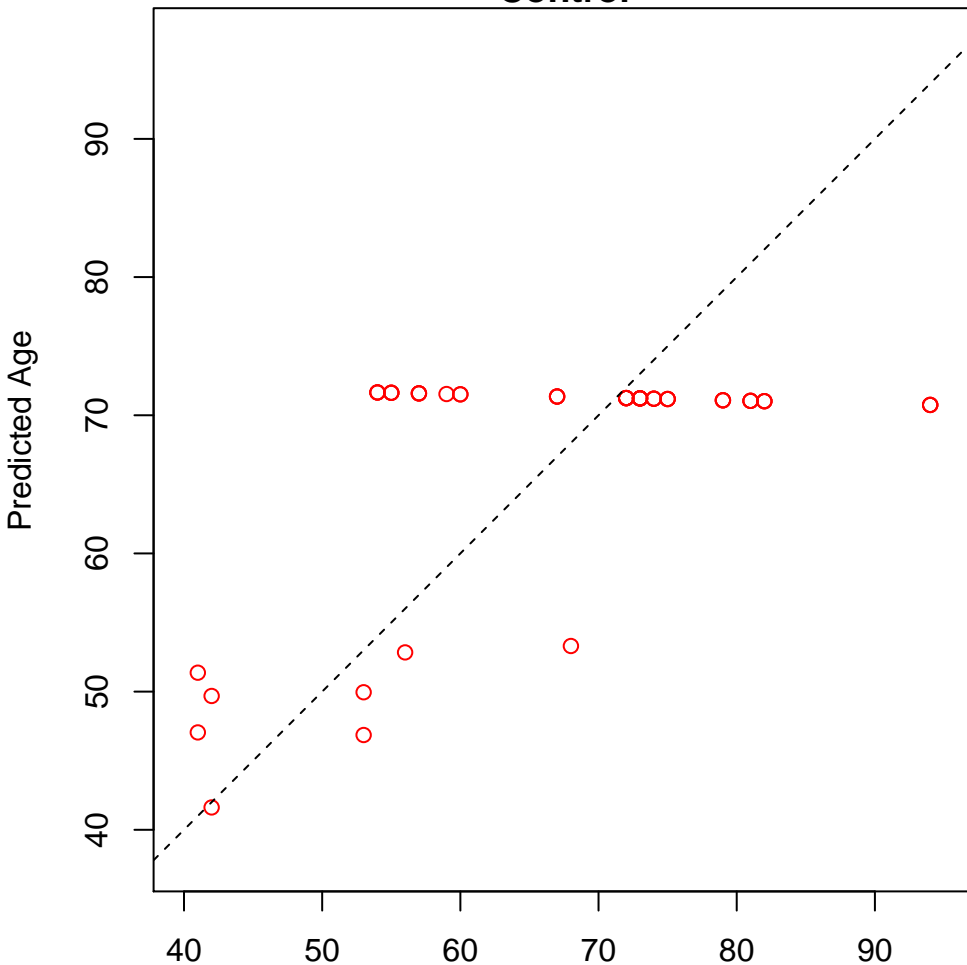


cellular oxidant detoxification (Score: 0.820360)

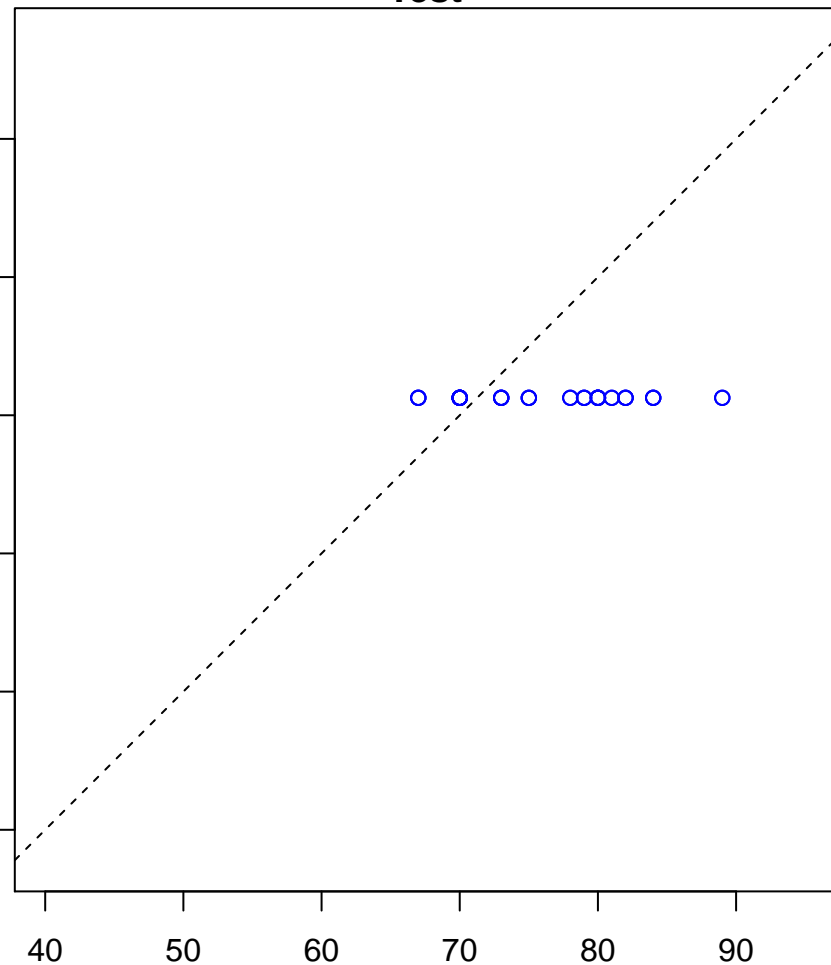


epithelial cell development (Score: 0.820226)

Control



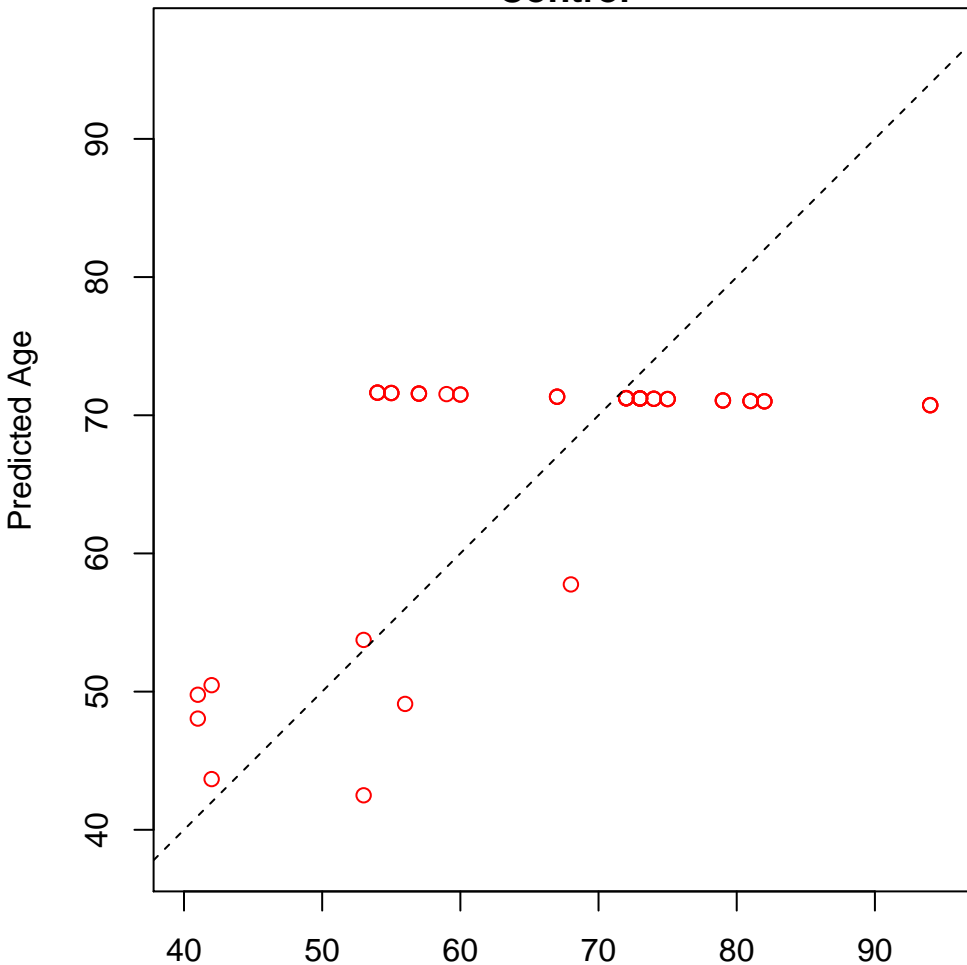
Test



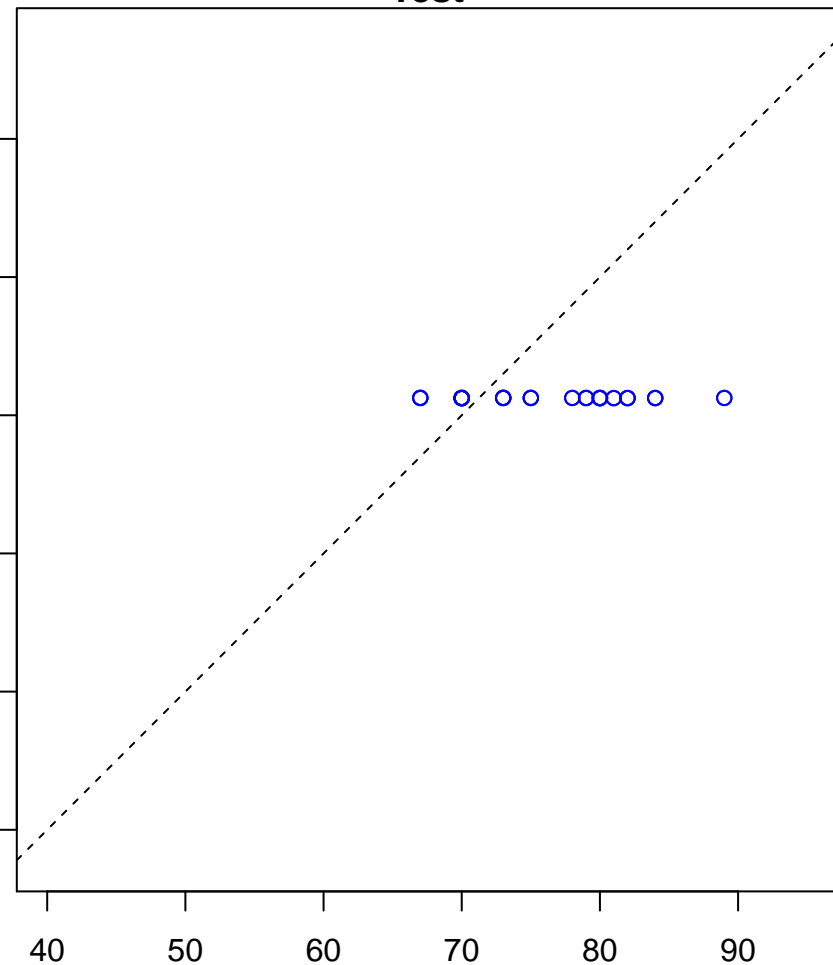
Actual Age

alpha-amino acid metabolic process (Score: 0.820209)

Control



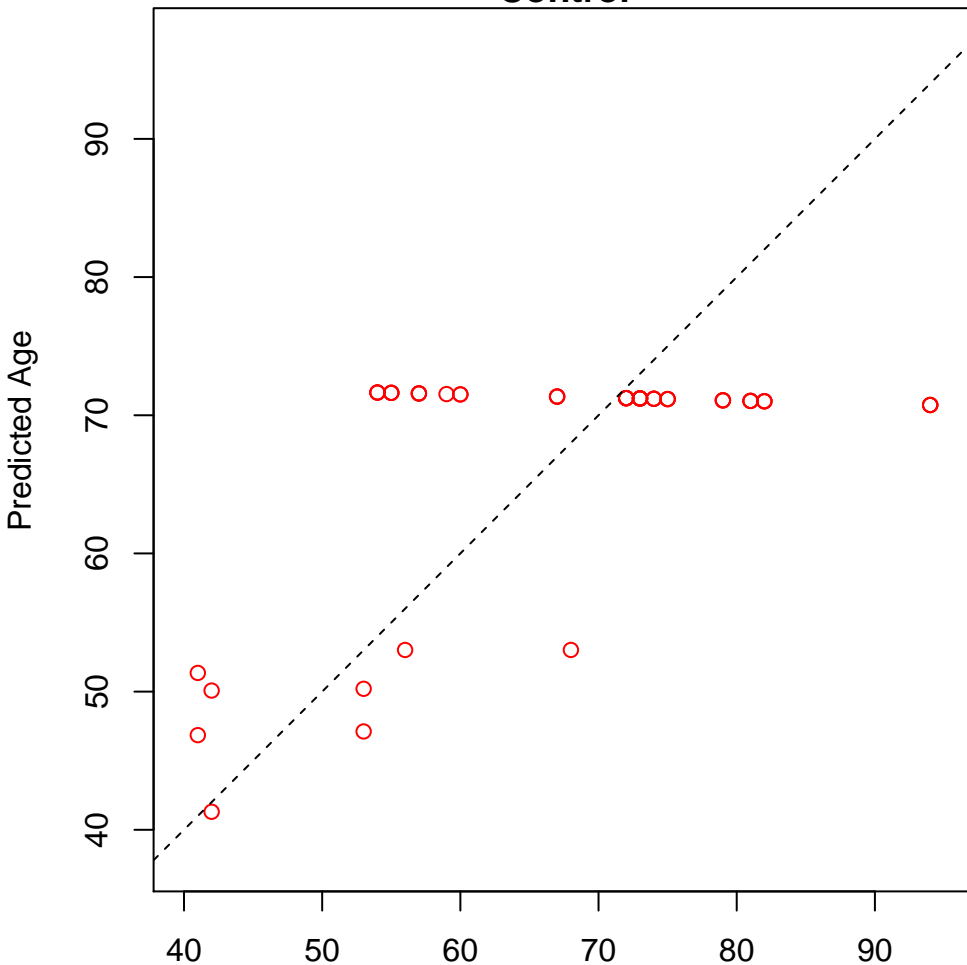
Test



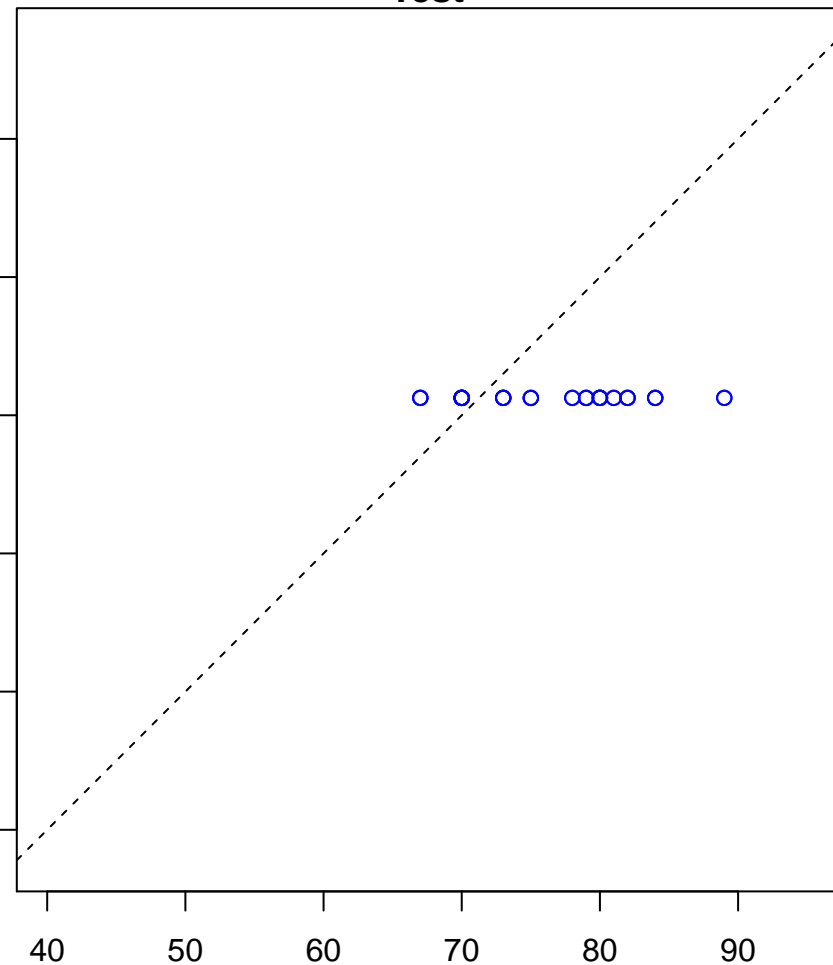
Actual Age

regulation of lipid biosynthetic process (Score: 0.820172)

Control



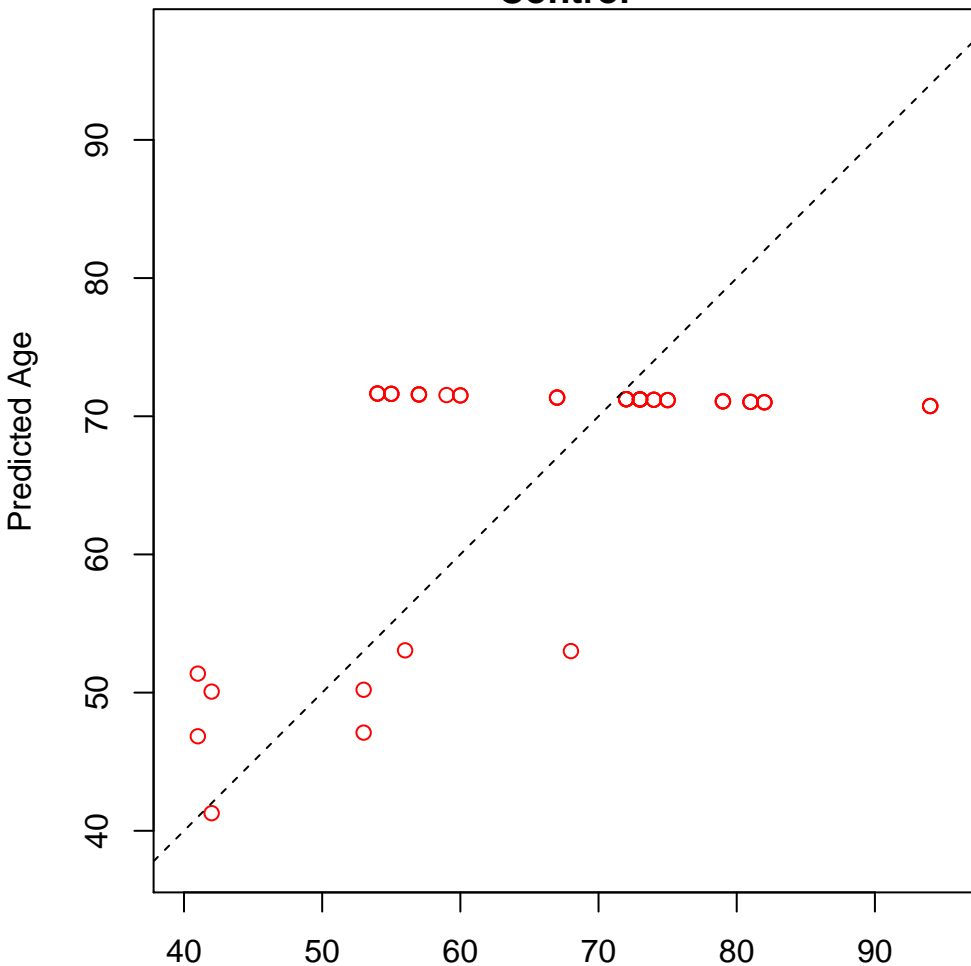
Test



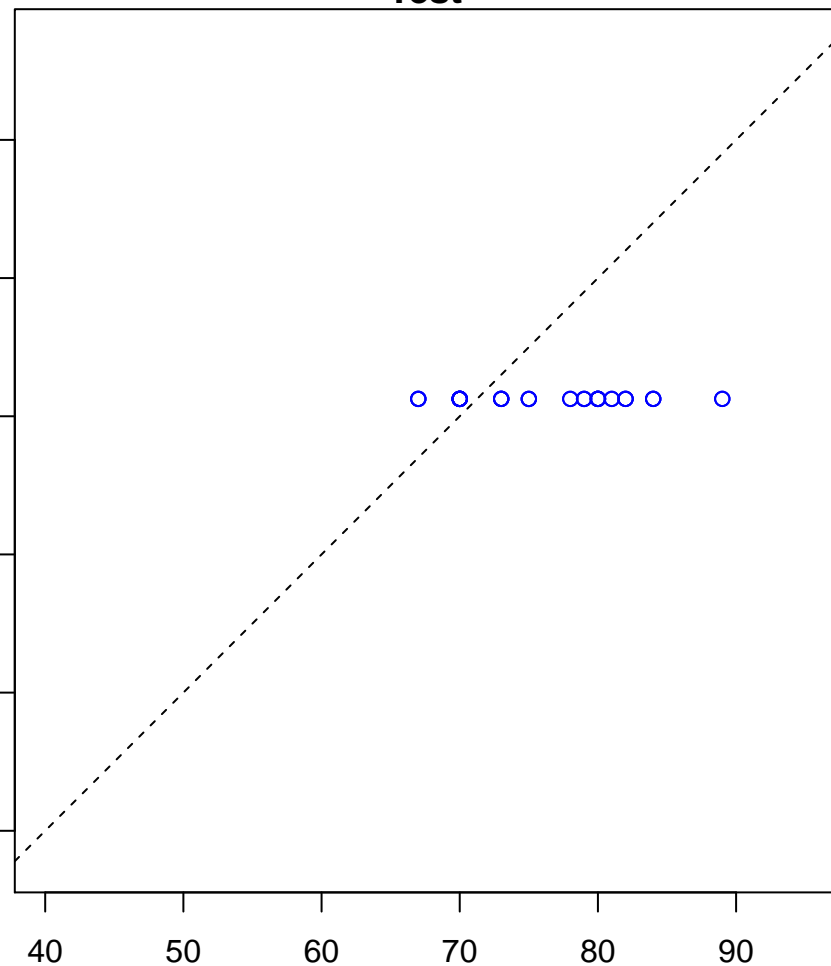
Actual Age

regulation of steroid metabolic process (Score: 0.820159)

Control

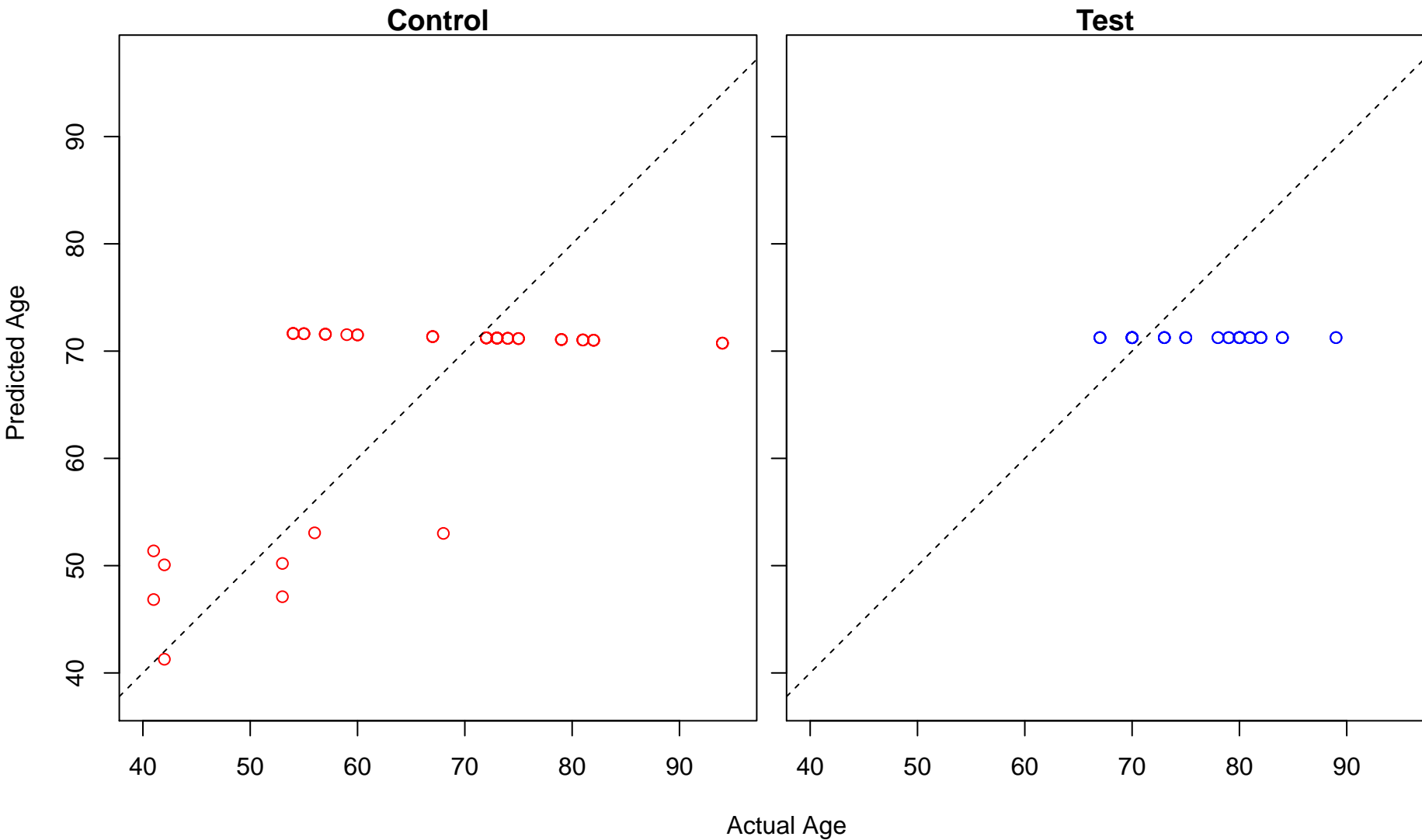


Test



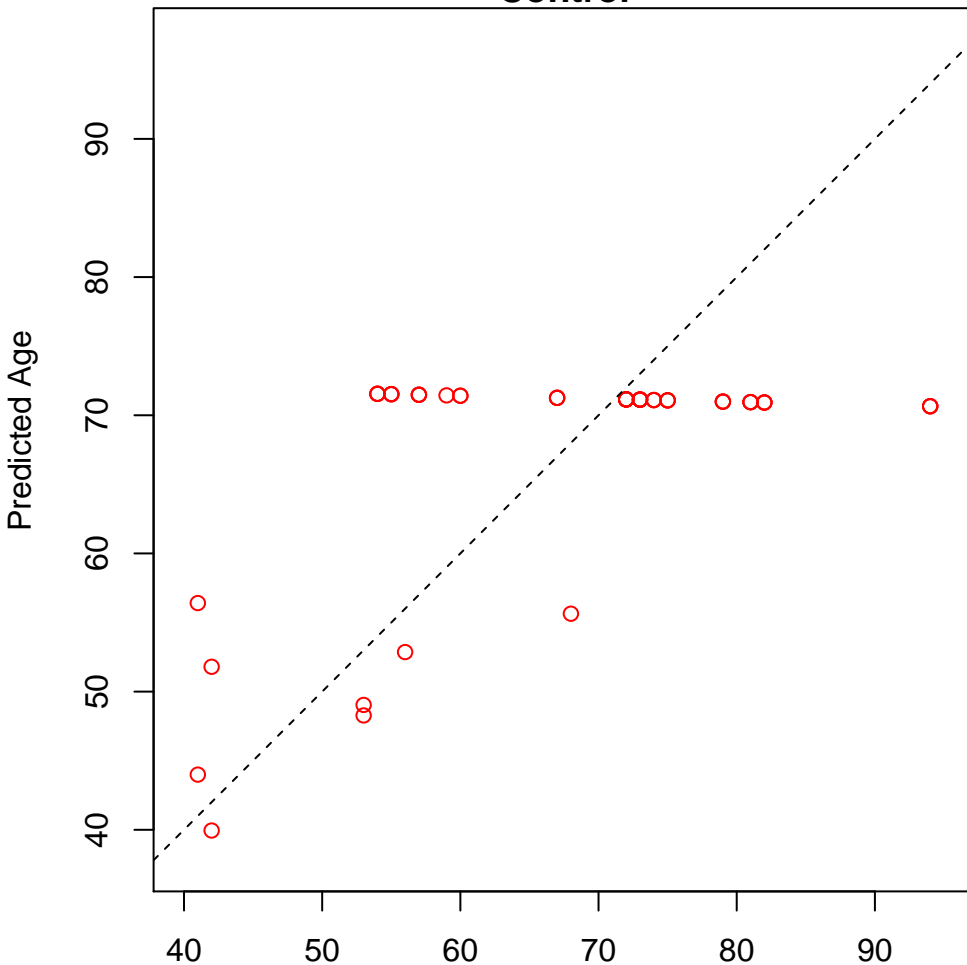
Actual Age

regulation of cholesterol metabolic process (Score: 0.820159)

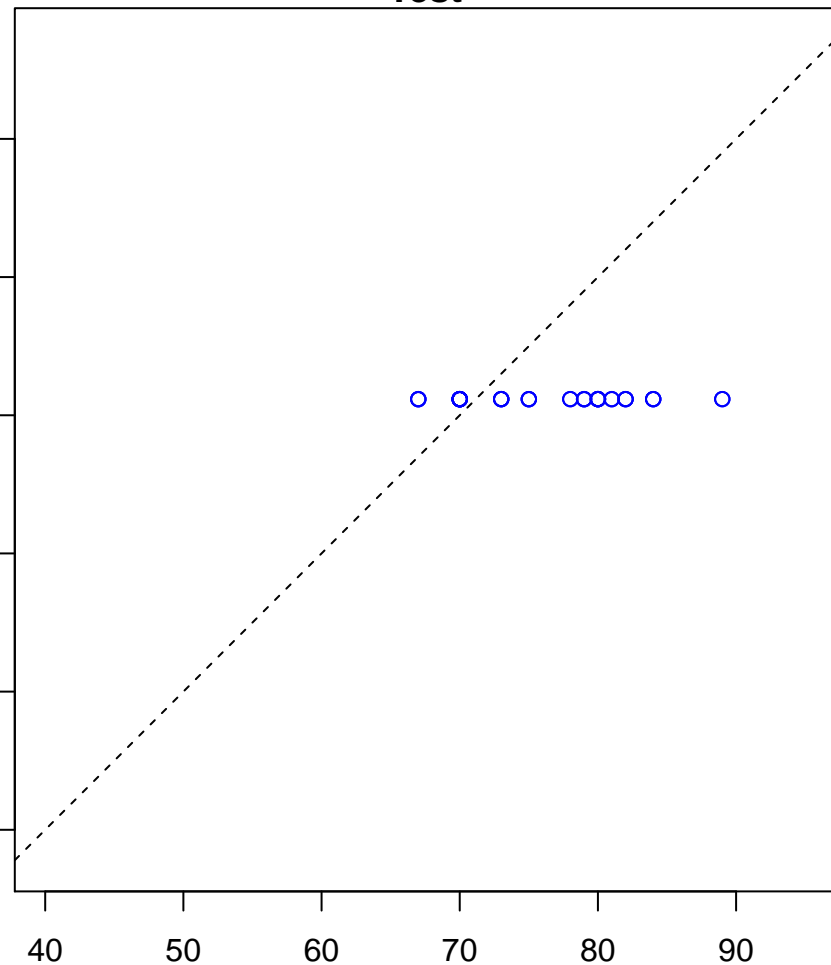


monosaccharide metabolic process (Score: 0.820089)

Control

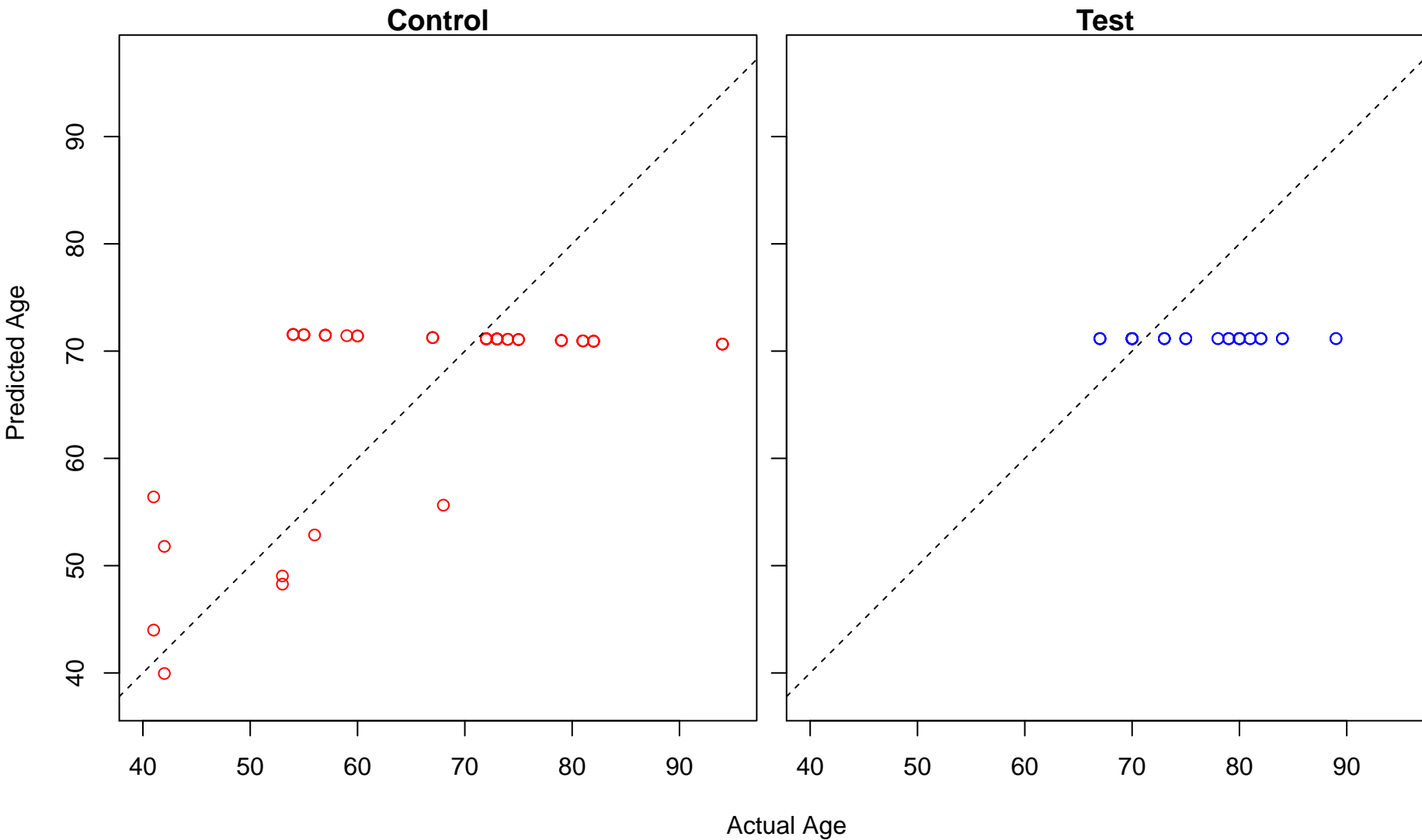


Test

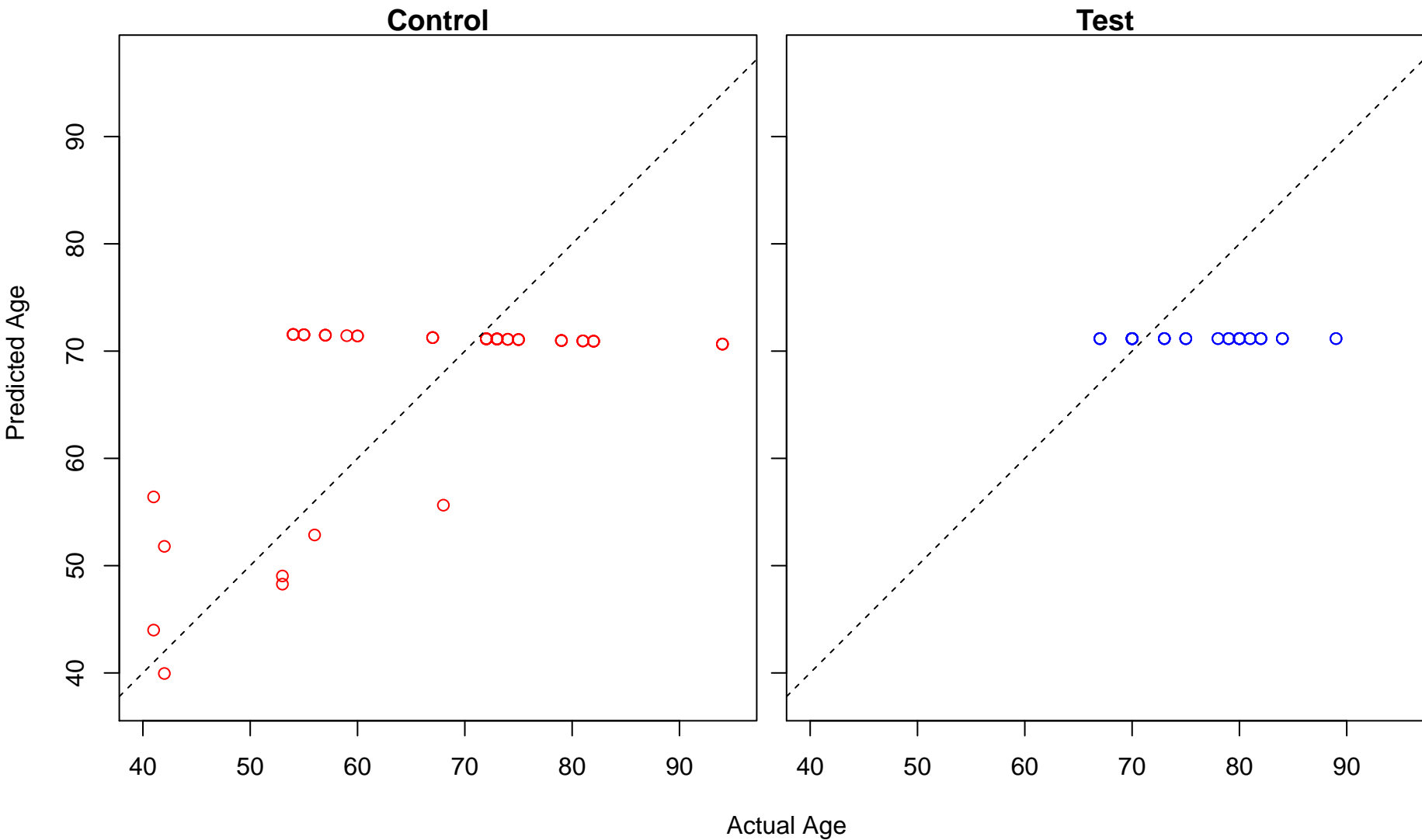


Actual Age

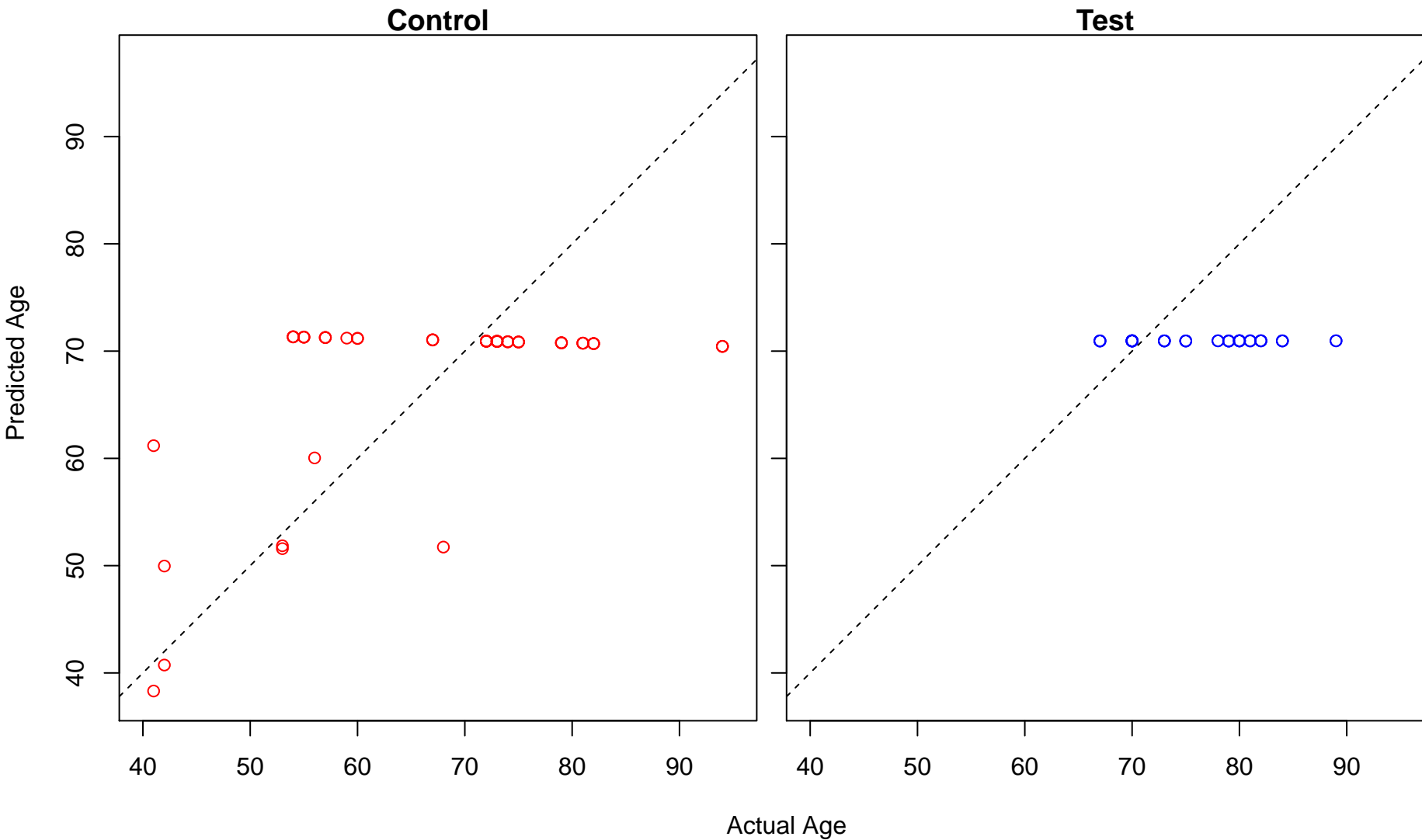
glucose metabolic process (Score: 0.820089)



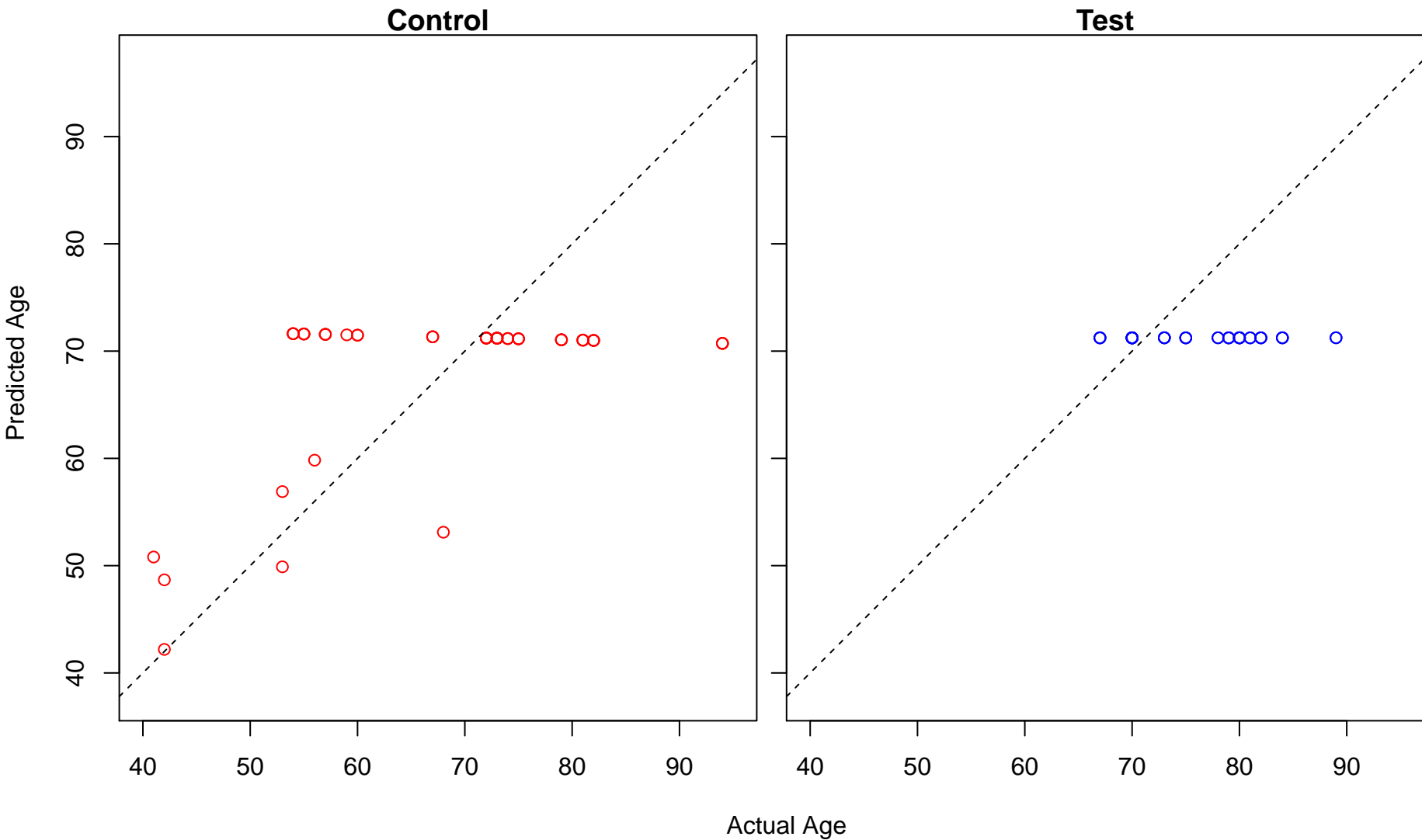
hexose metabolic process (Score: 0.820089)



negative regulation of G-protein coupled receptor protein signaling pathway (Score: 0.820064)

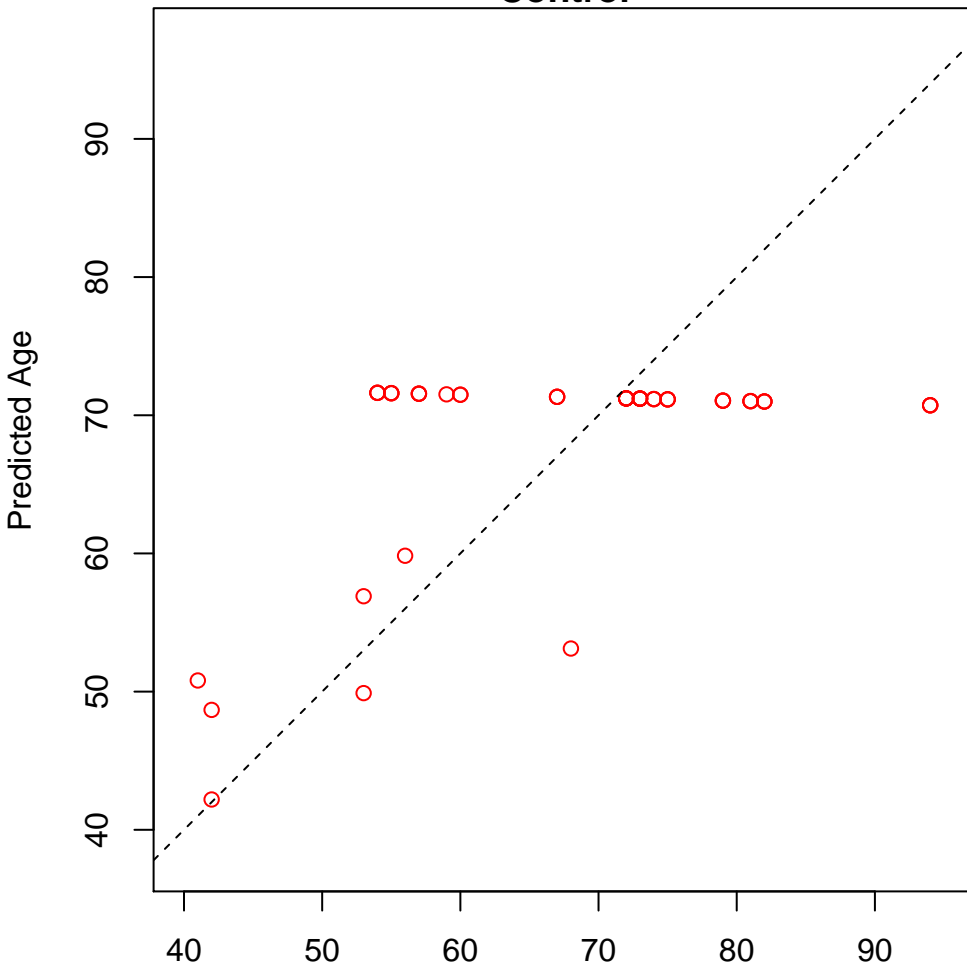


response to hypoxia (Score: 0.819964)

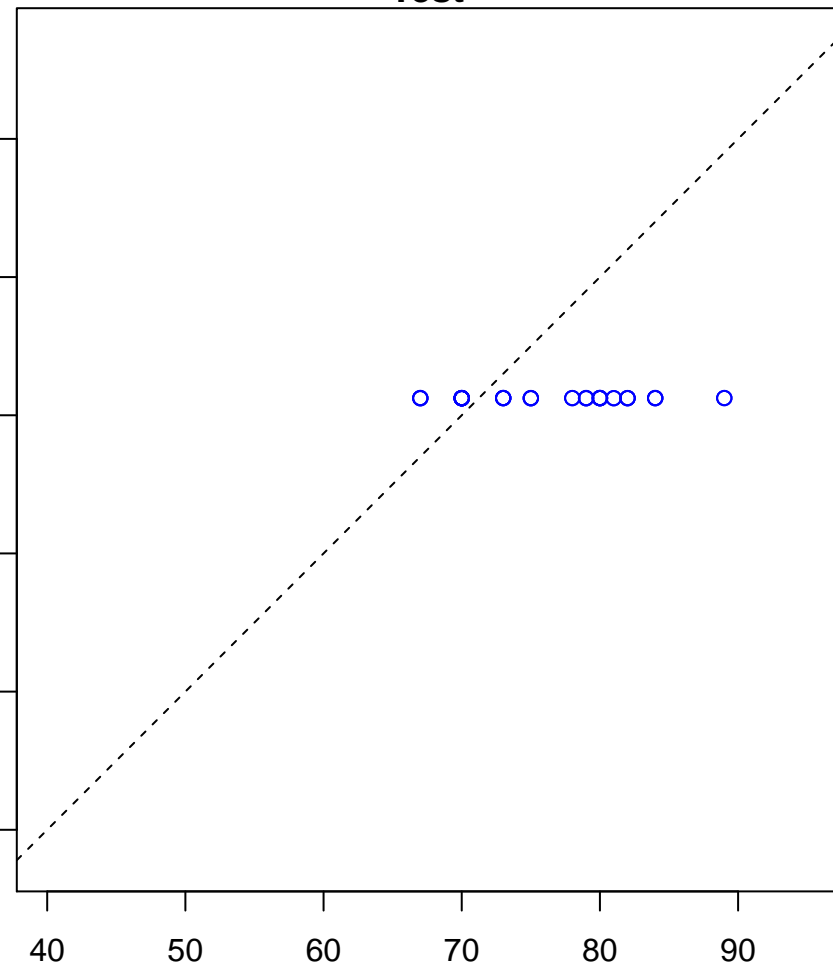


response to decreased oxygen levels (Score: 0.819964)

Control

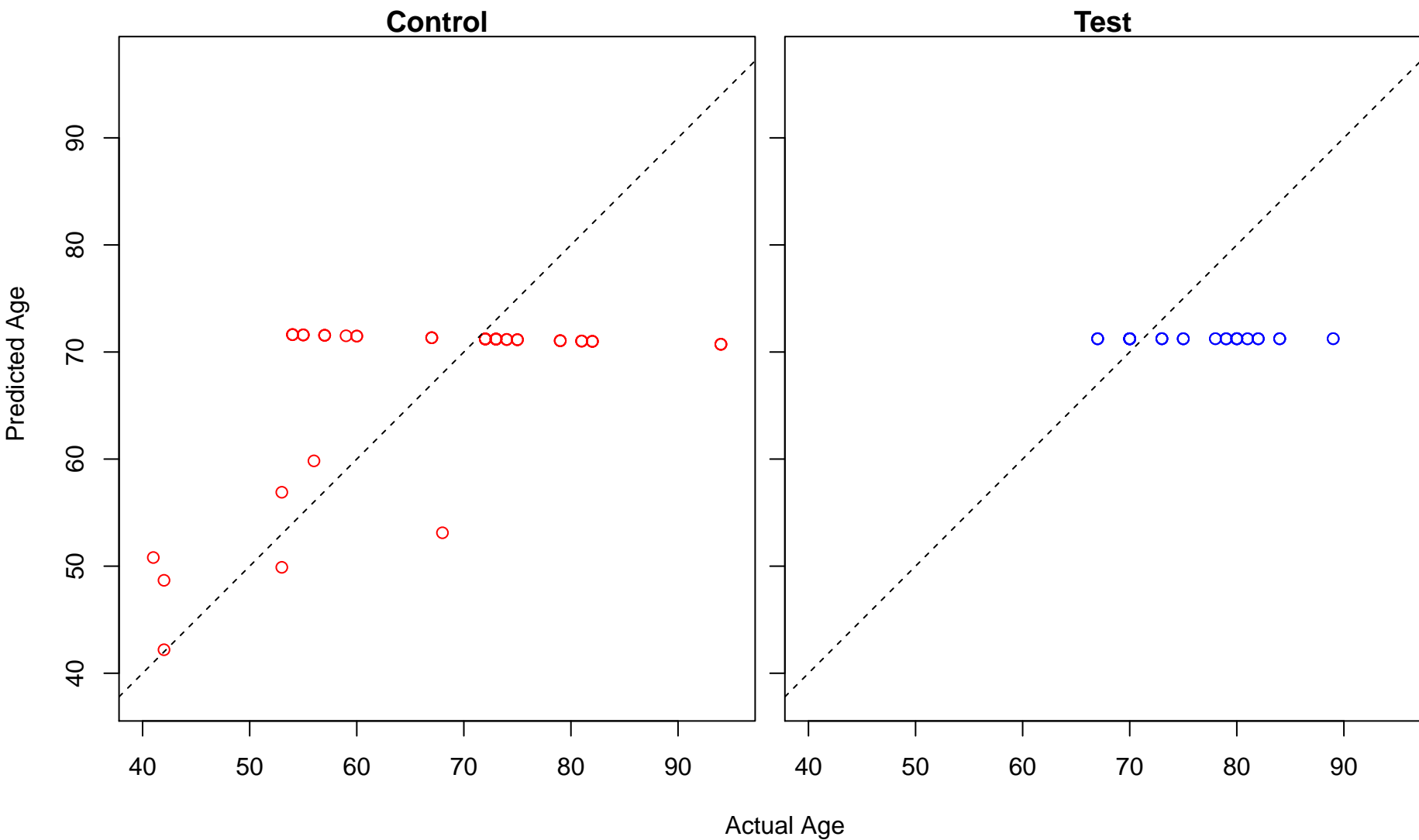


Test

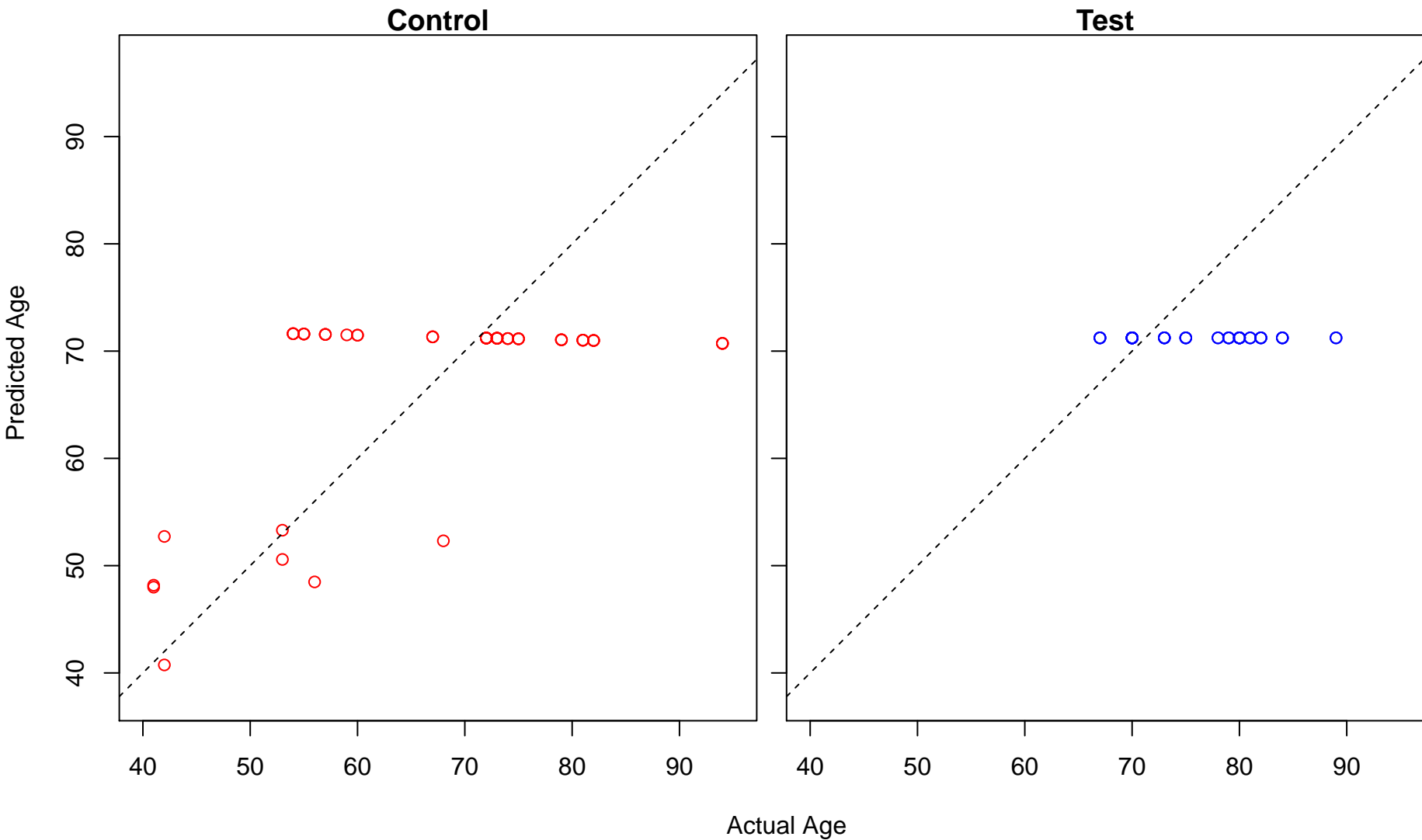


Actual Age

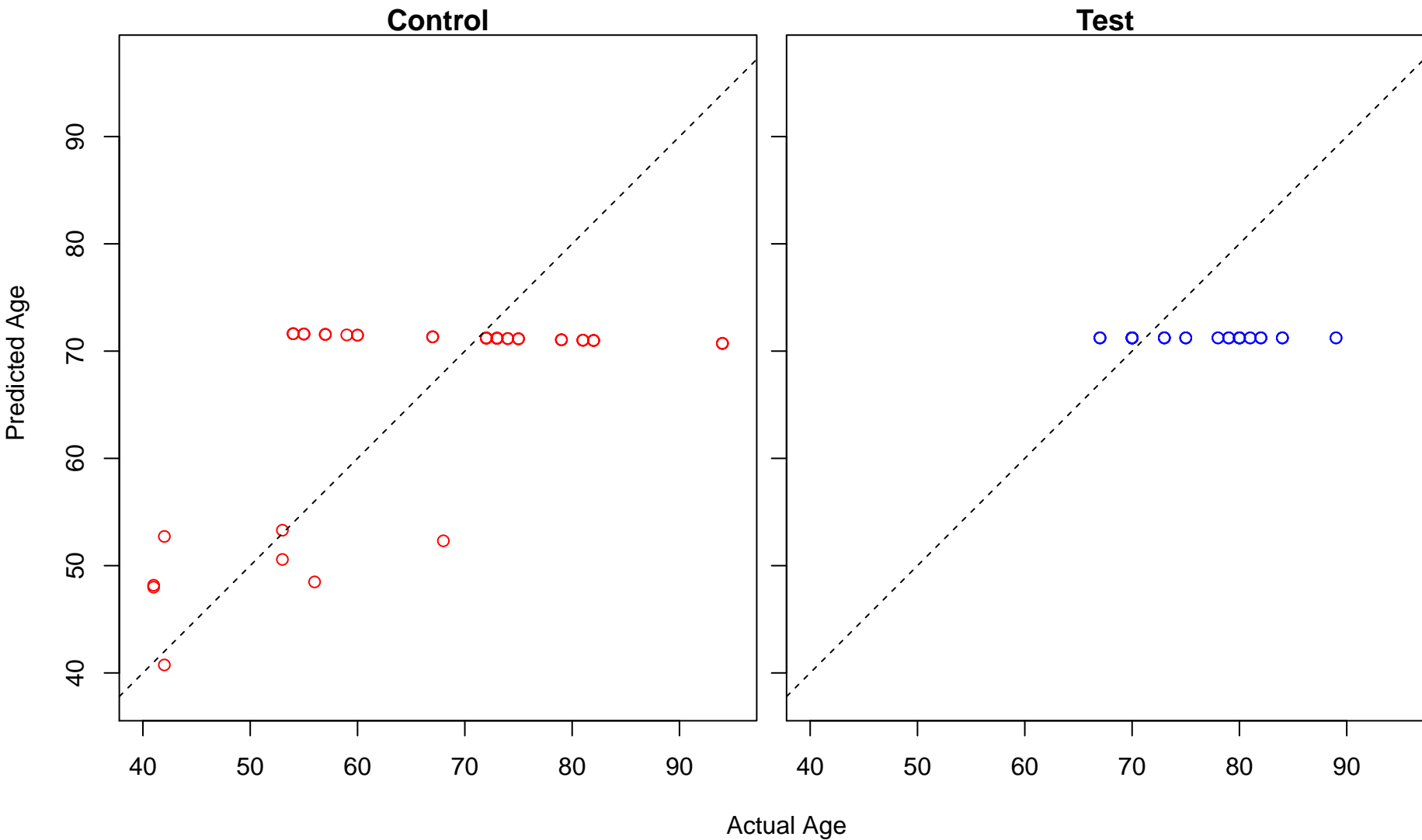
response to oxygen levels (Score: 0.819964)



cation transport (Score: 0.819952)

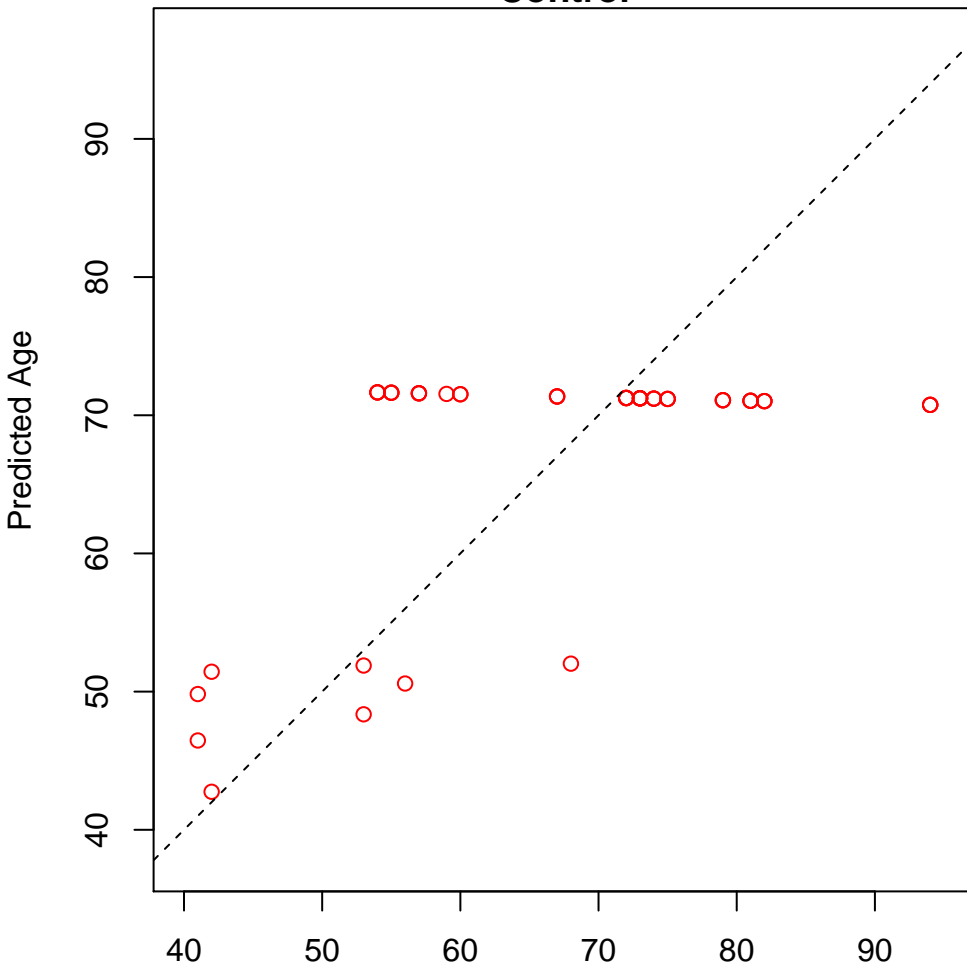


metal ion transport (Score: 0.819952)

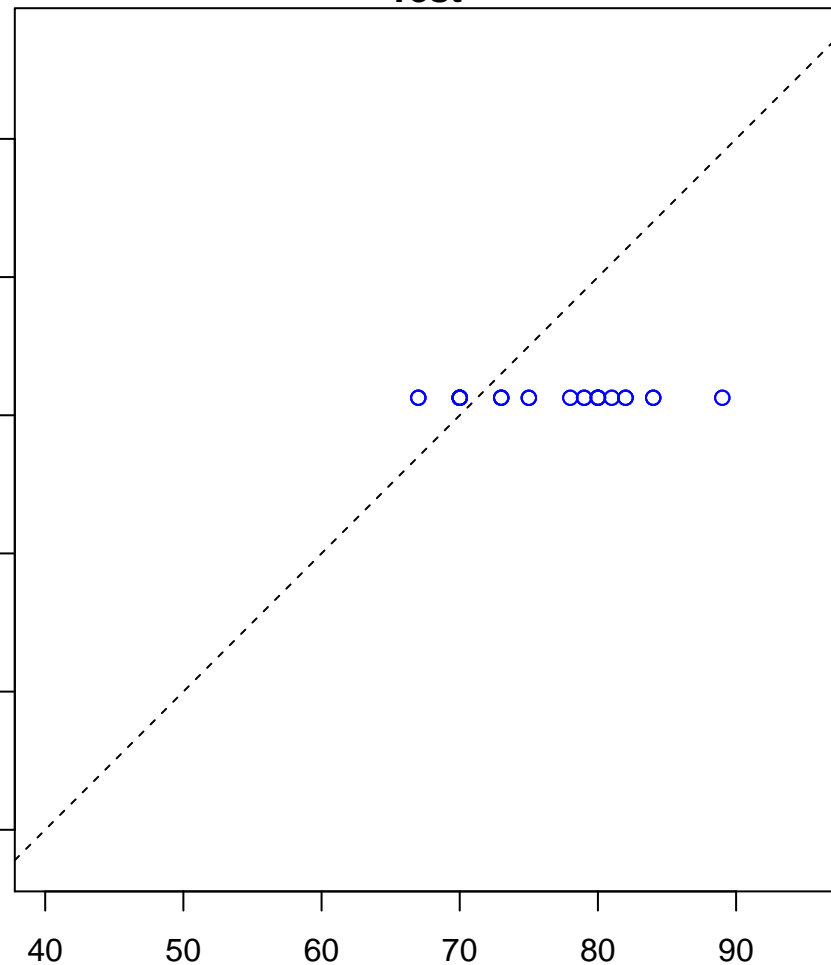


anatomical structure homeostasis (Score: 0.819940)

Control

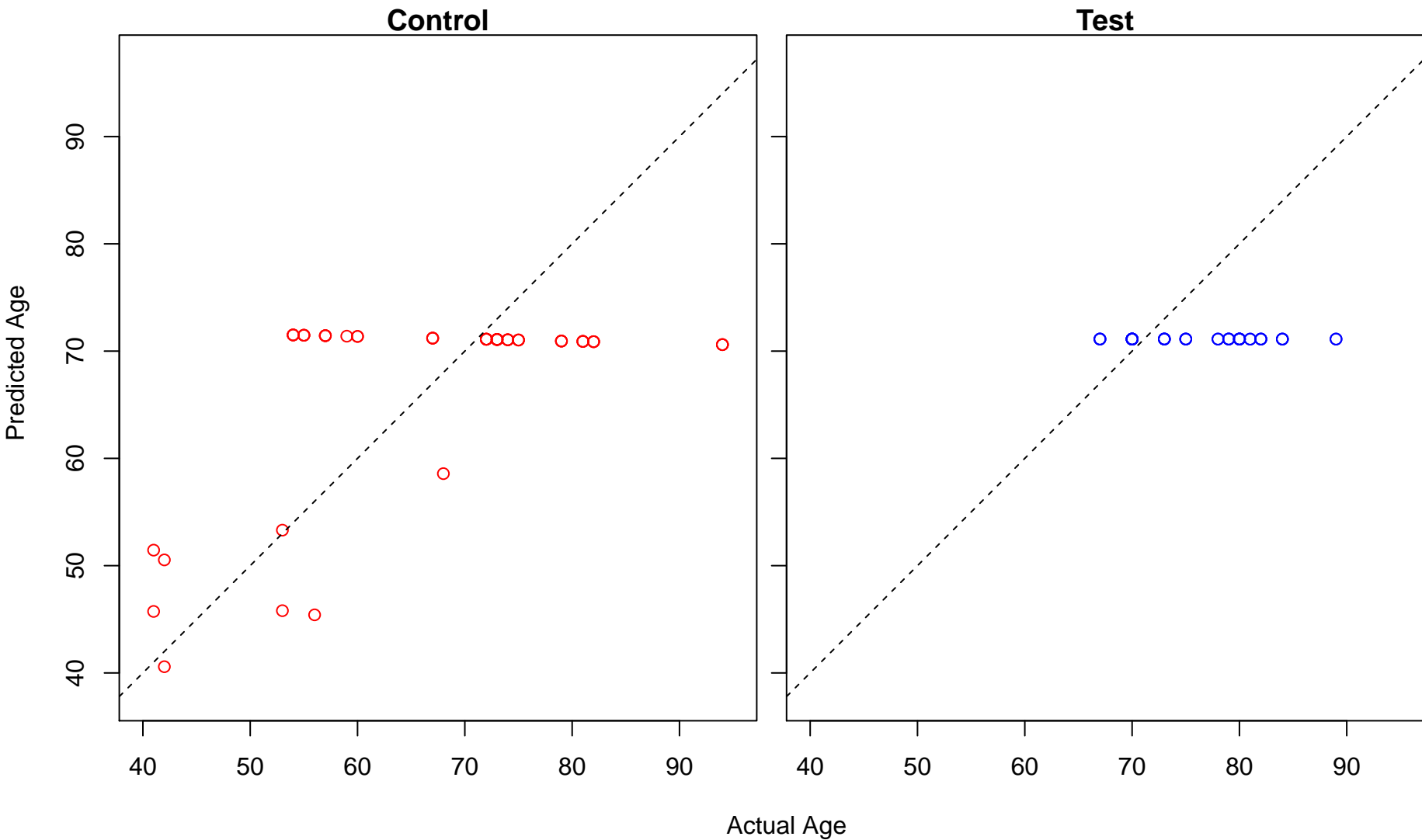


Test

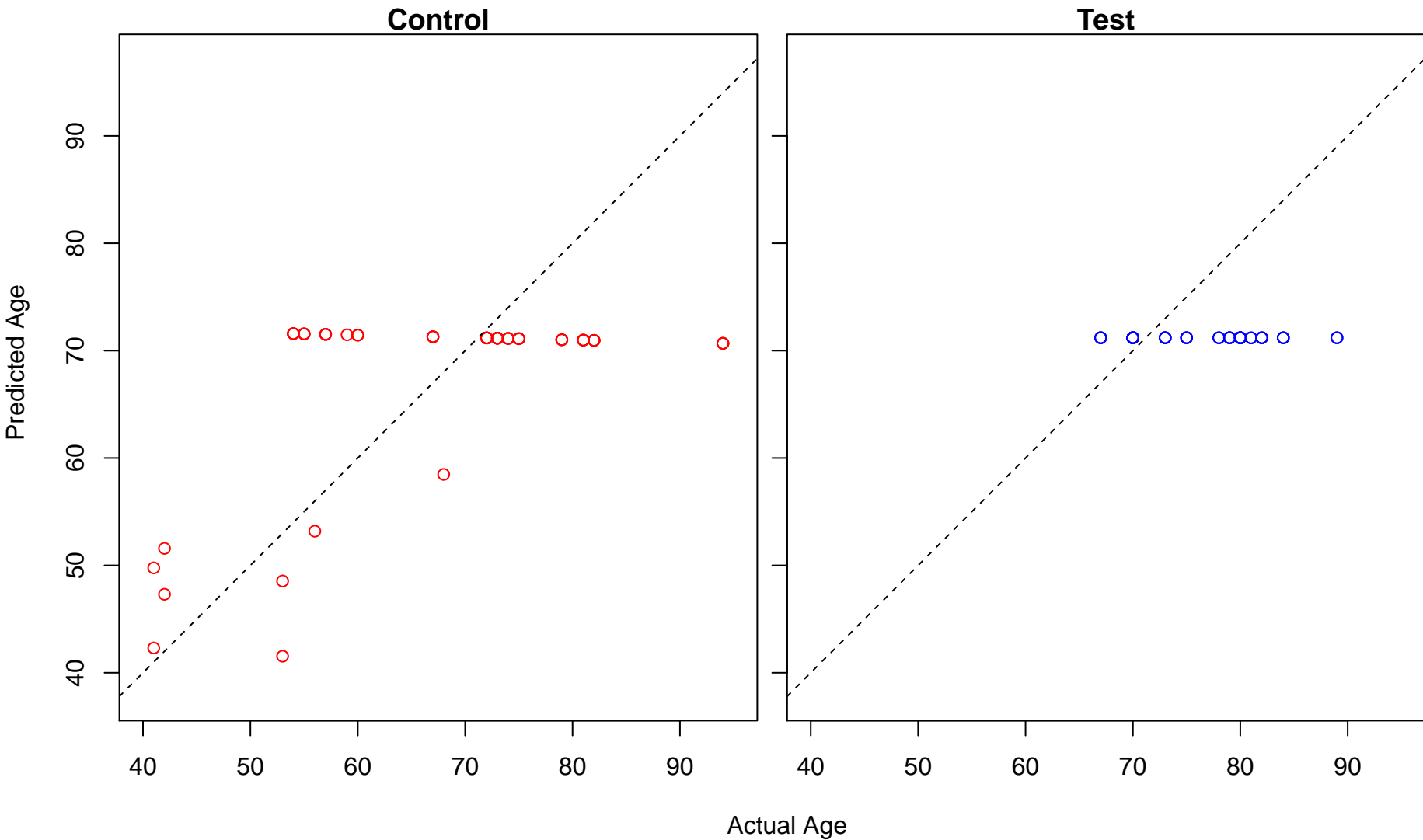


Actual Age

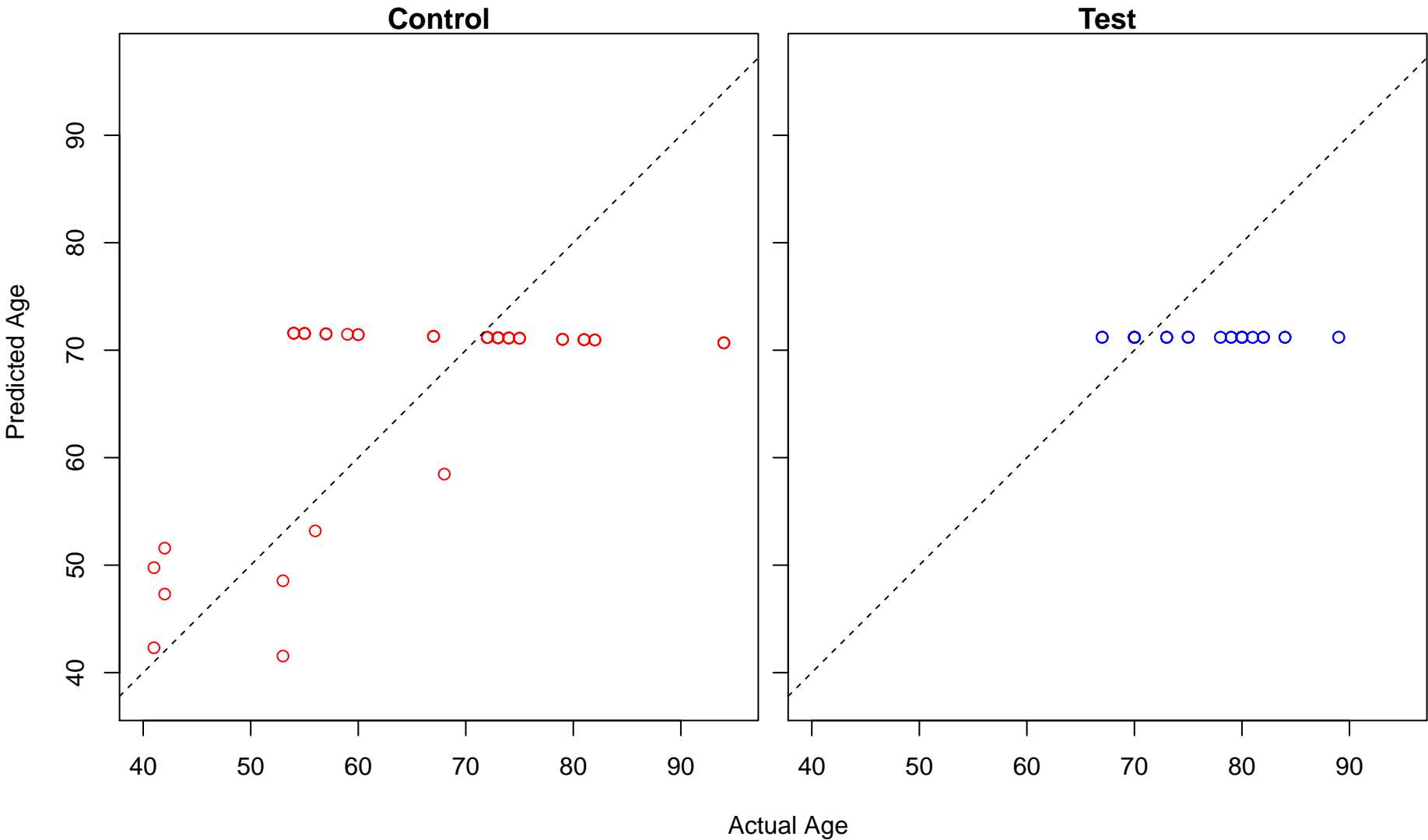
response to peptide (Score: 0.819924)



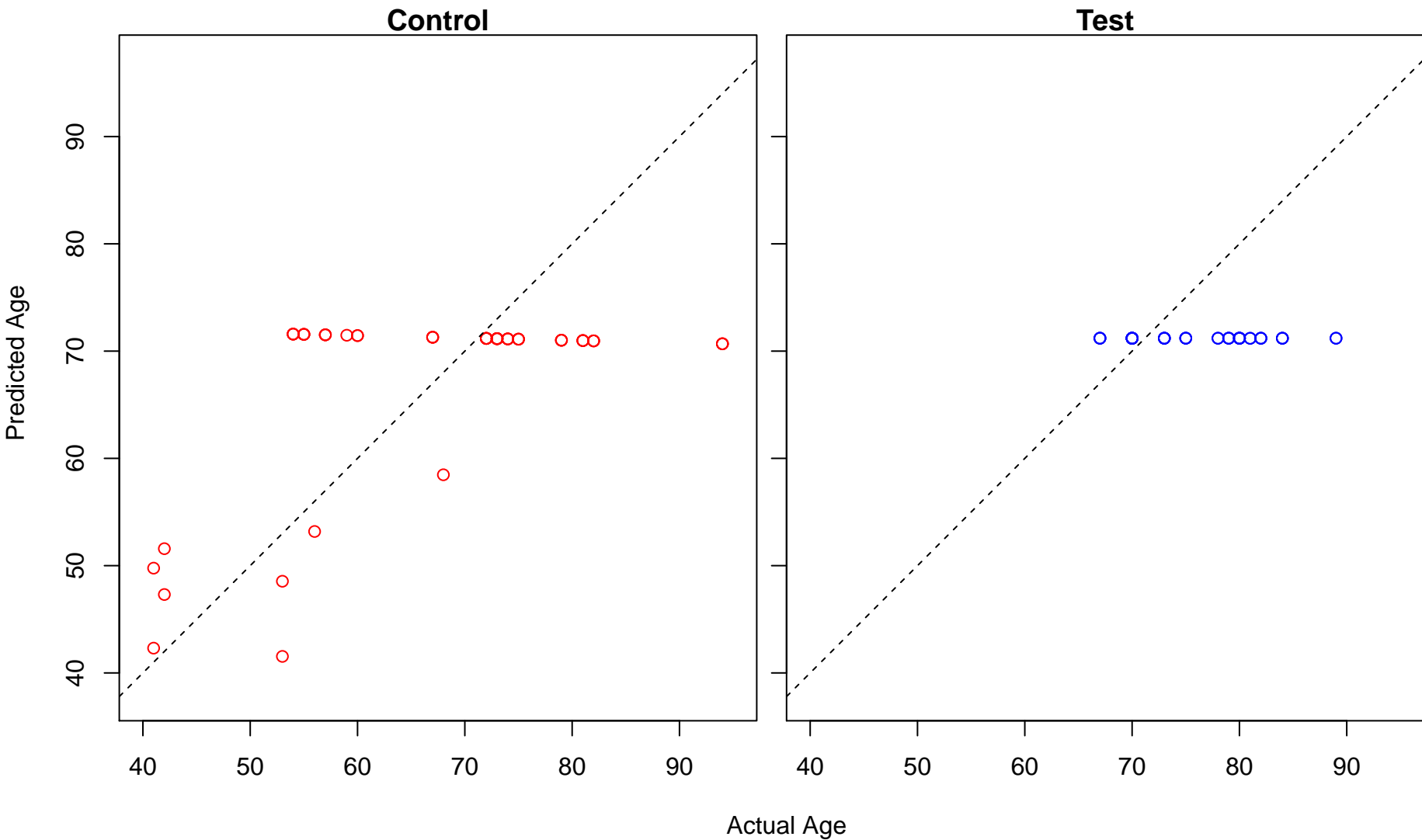
antigen processing and presentation of peptide antigen via MHC class II (Score: 0.819919)



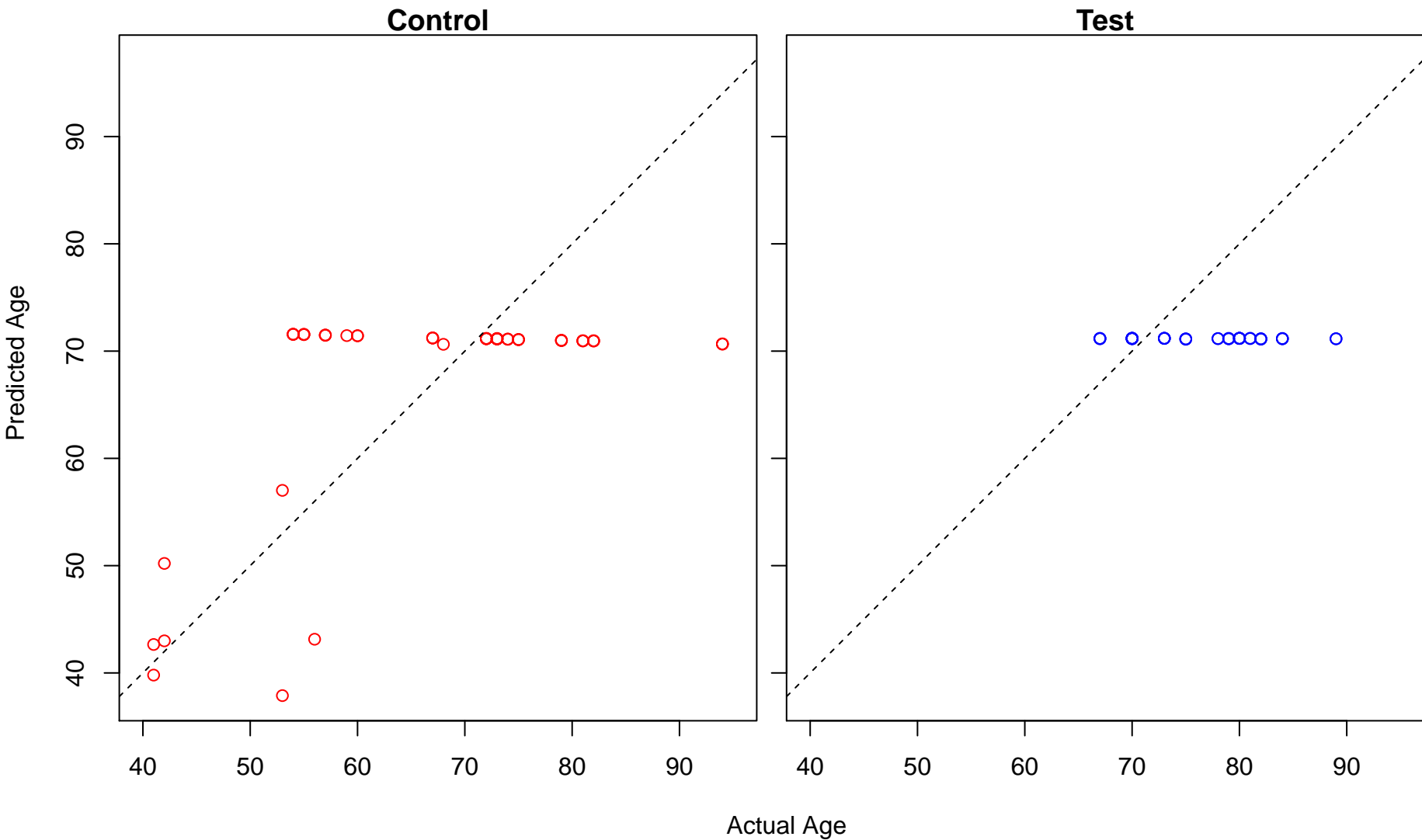
antigen processing and presentation of peptide or polysaccharide antigen via MHC class II (Score: 0.81)



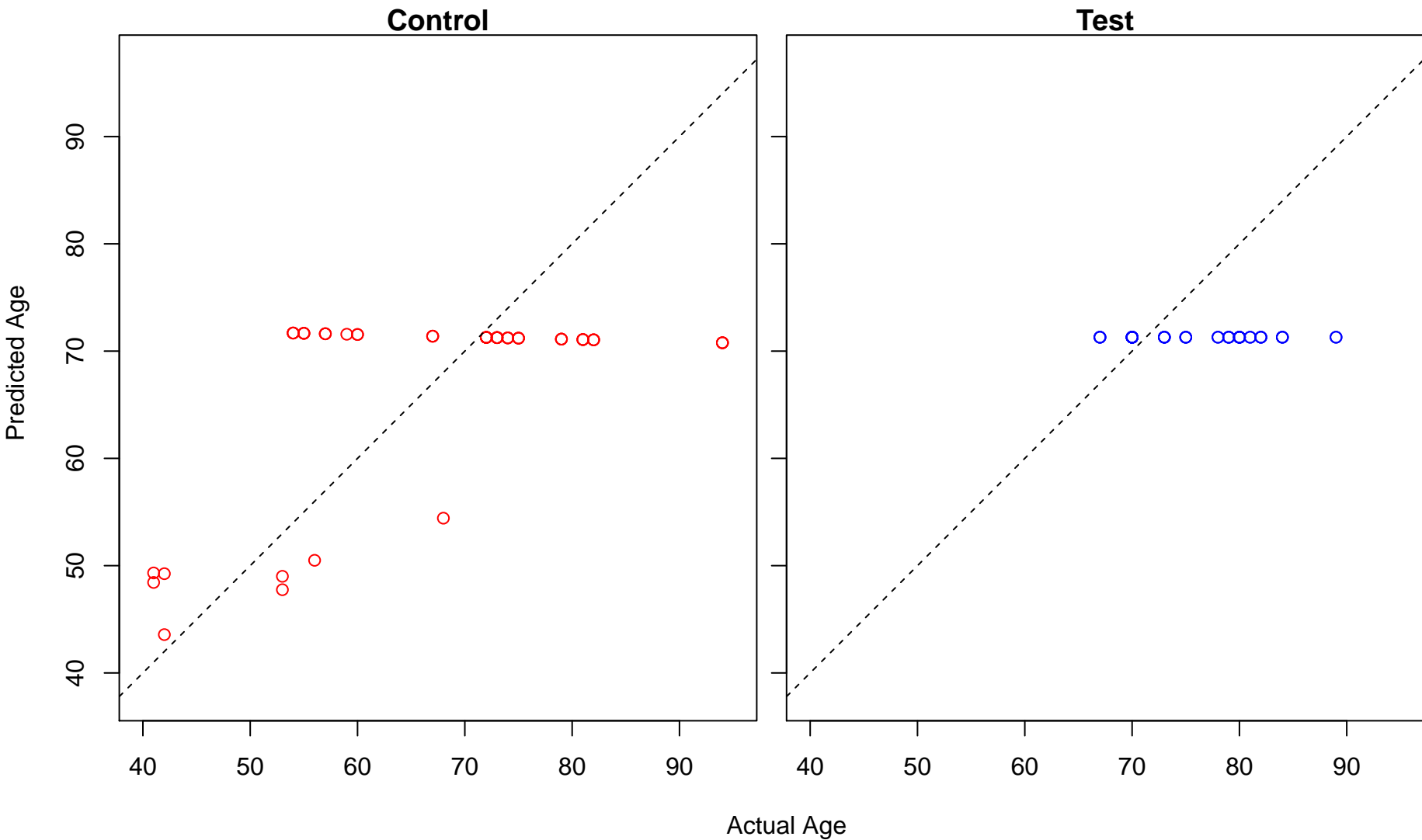
antigen processing and presentation of exogenous peptide antigen via MHC class II (Score: 0.81991)



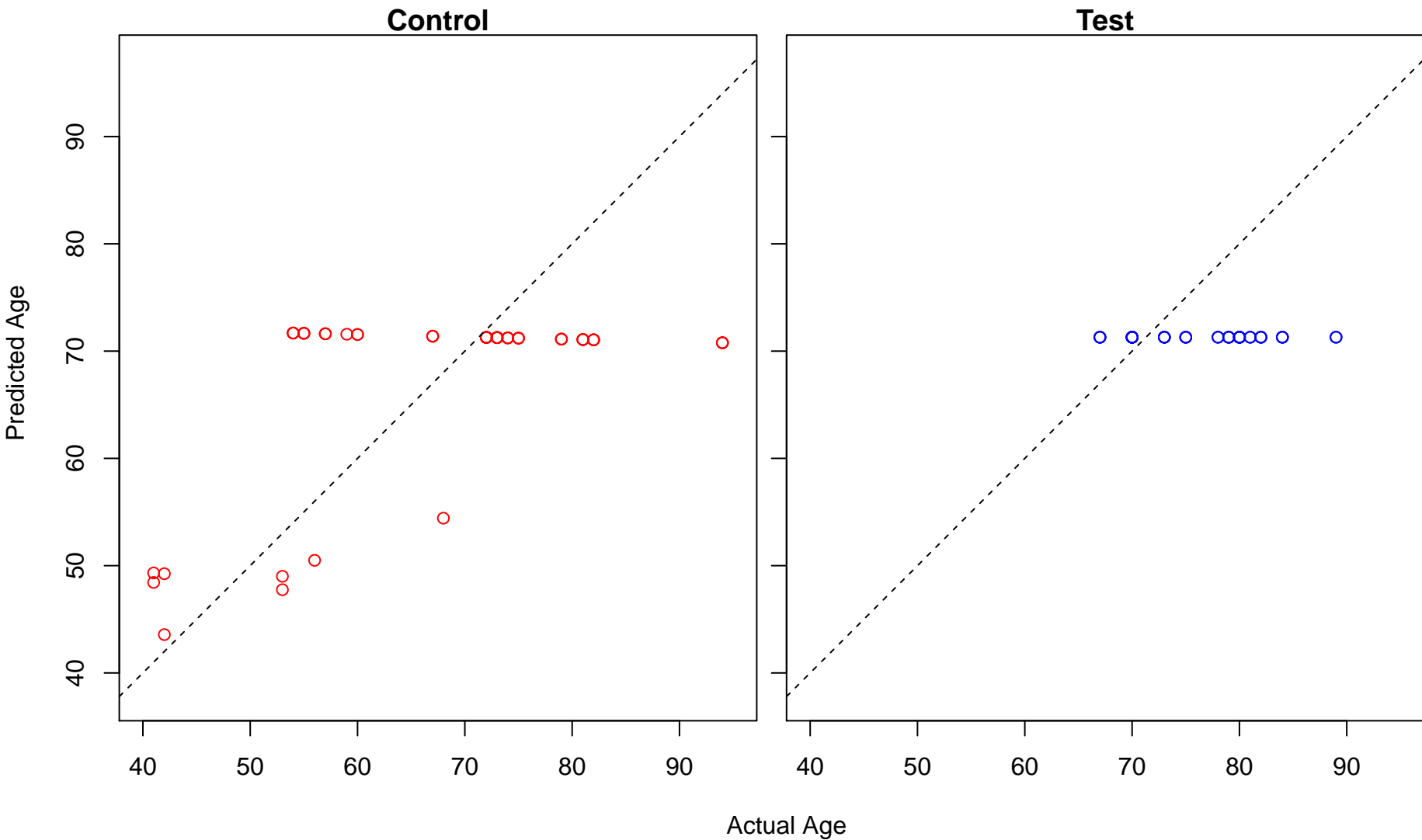
negative regulation of transcription from RNA polymerase II promoter (Score: 0.819848)



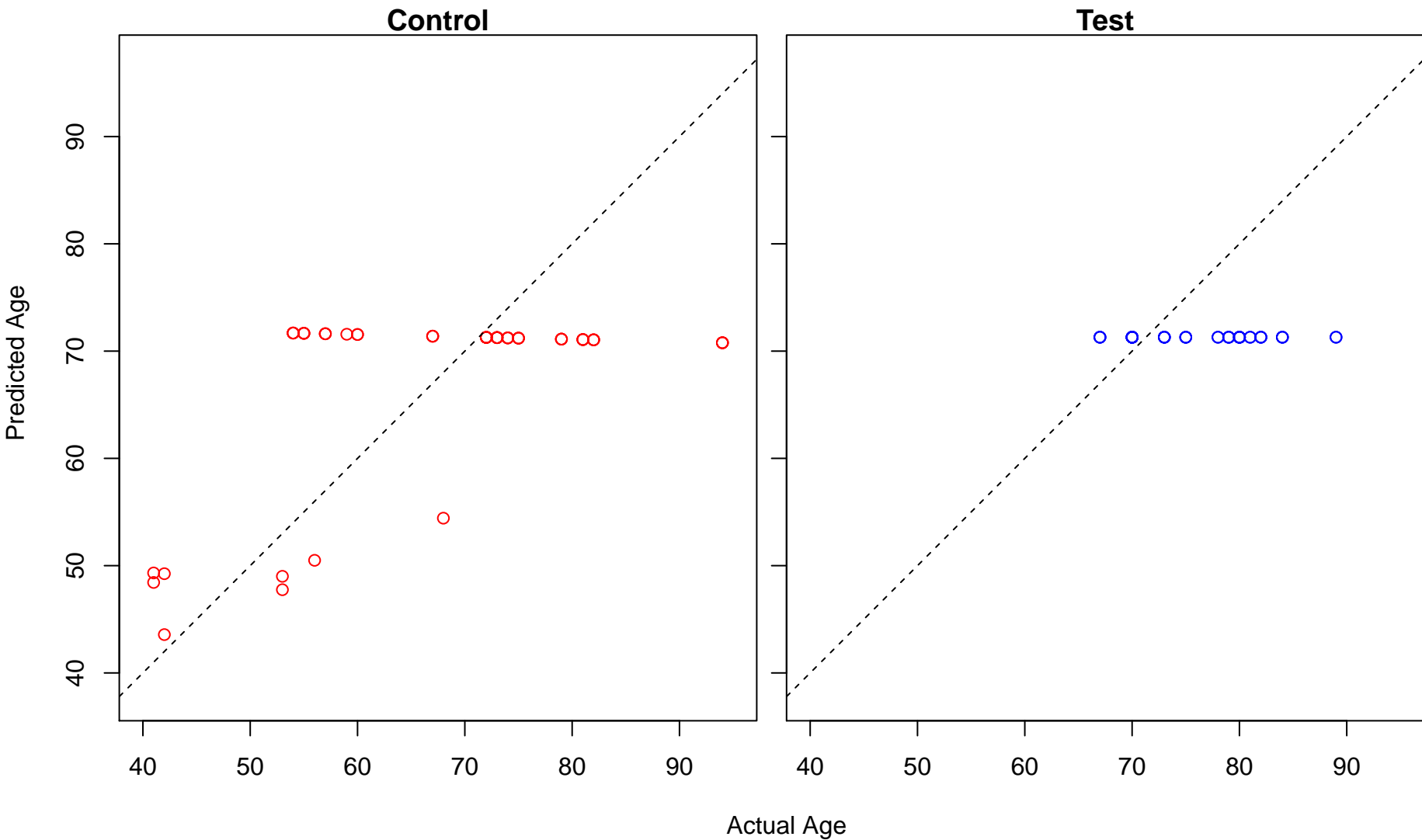
glial cell differentiation (Score: 0.819721)



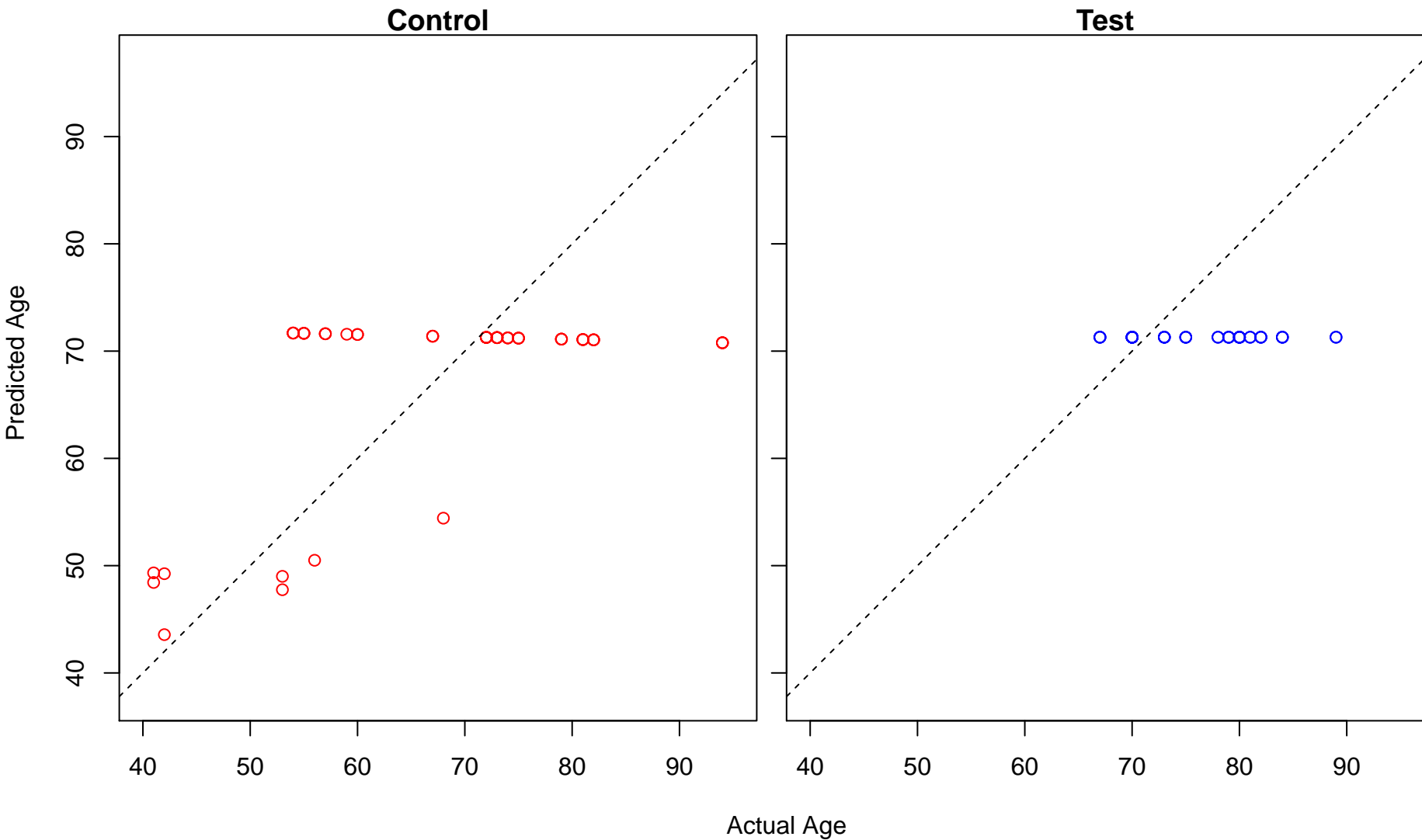
glial cell development (Score: 0.819721)



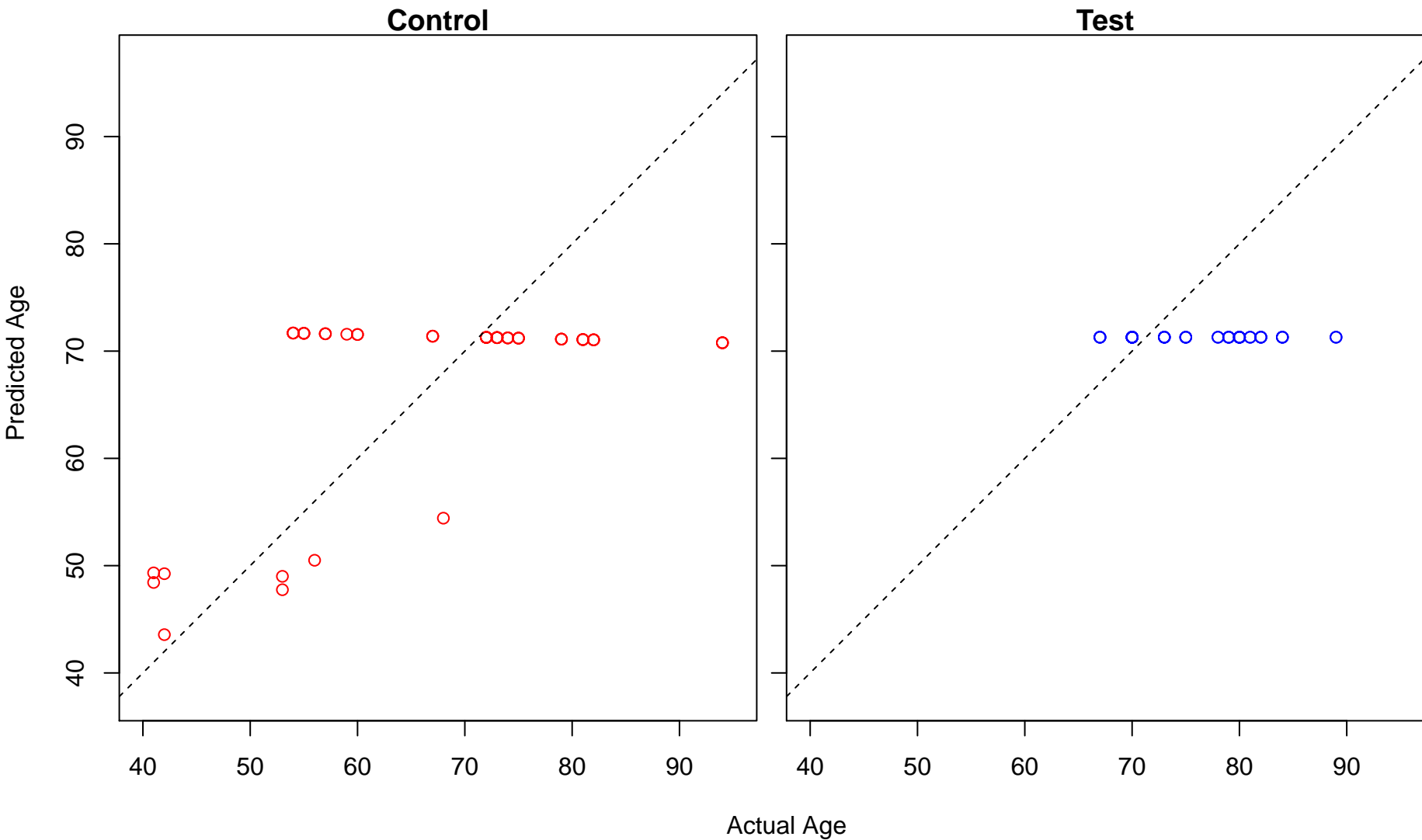
gliogenesis (Score: 0.819721)



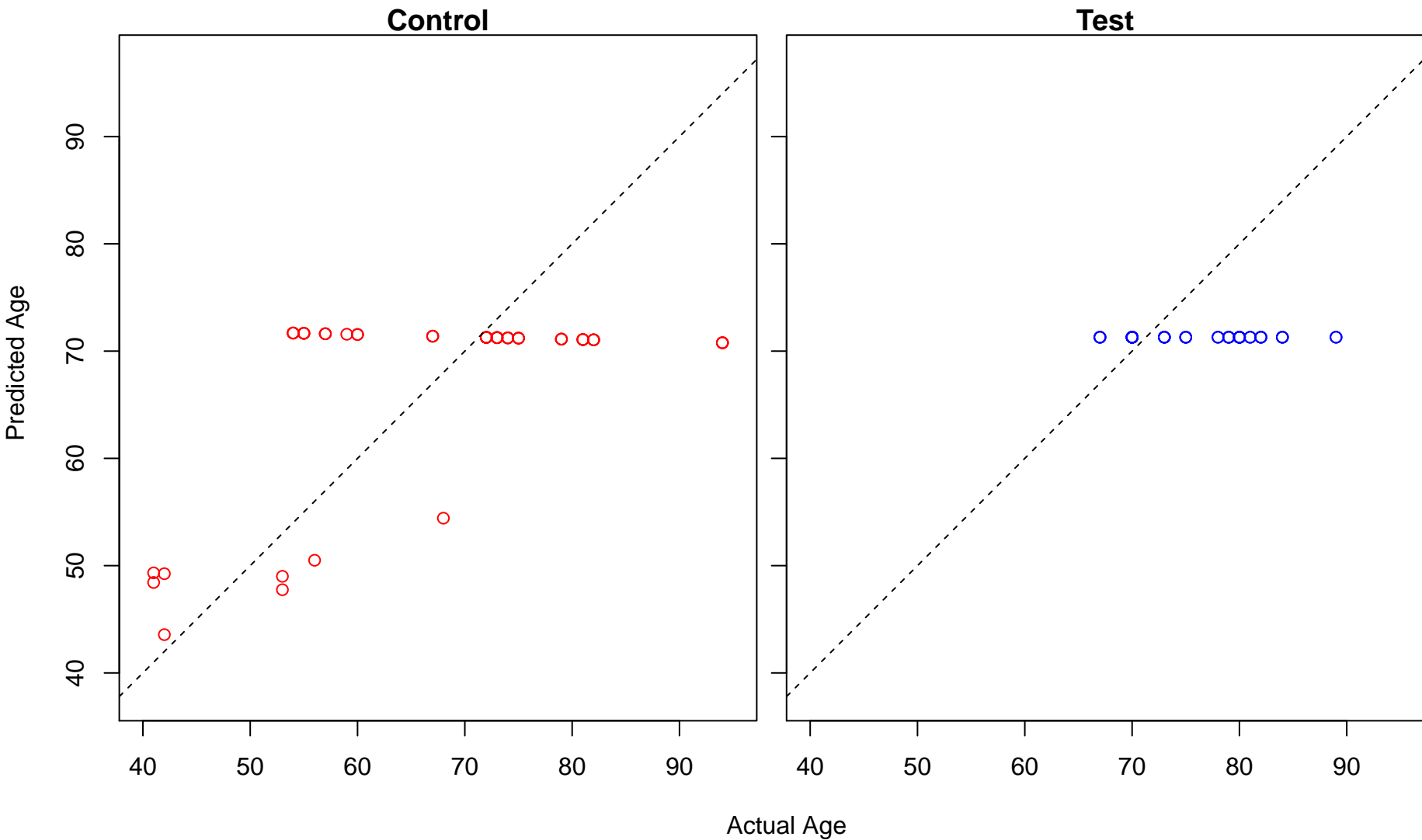
behavior (Score: 0.819720)



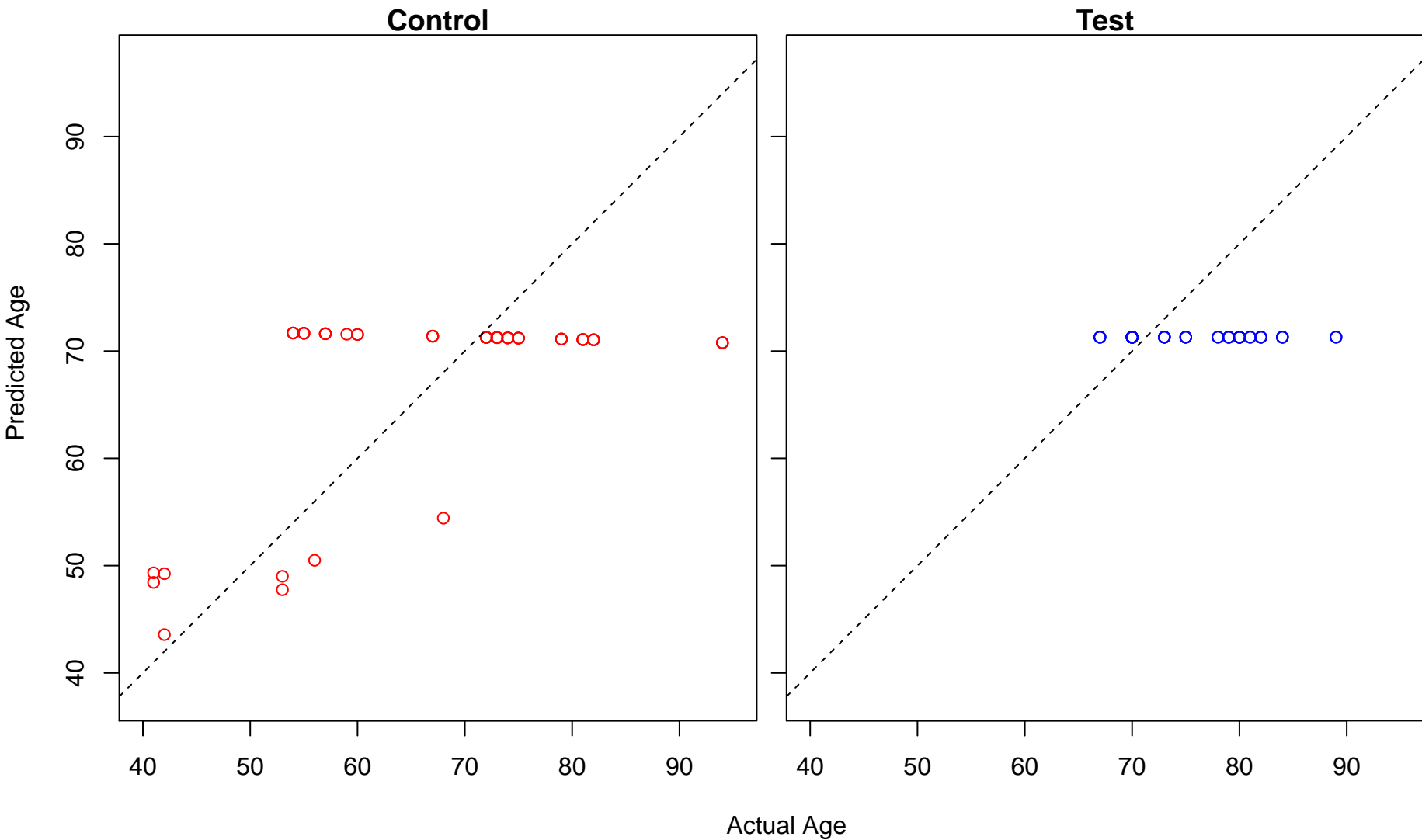
locomotory behavior (Score: 0.819720)



axo-dendritic transport (Score: 0.819720)

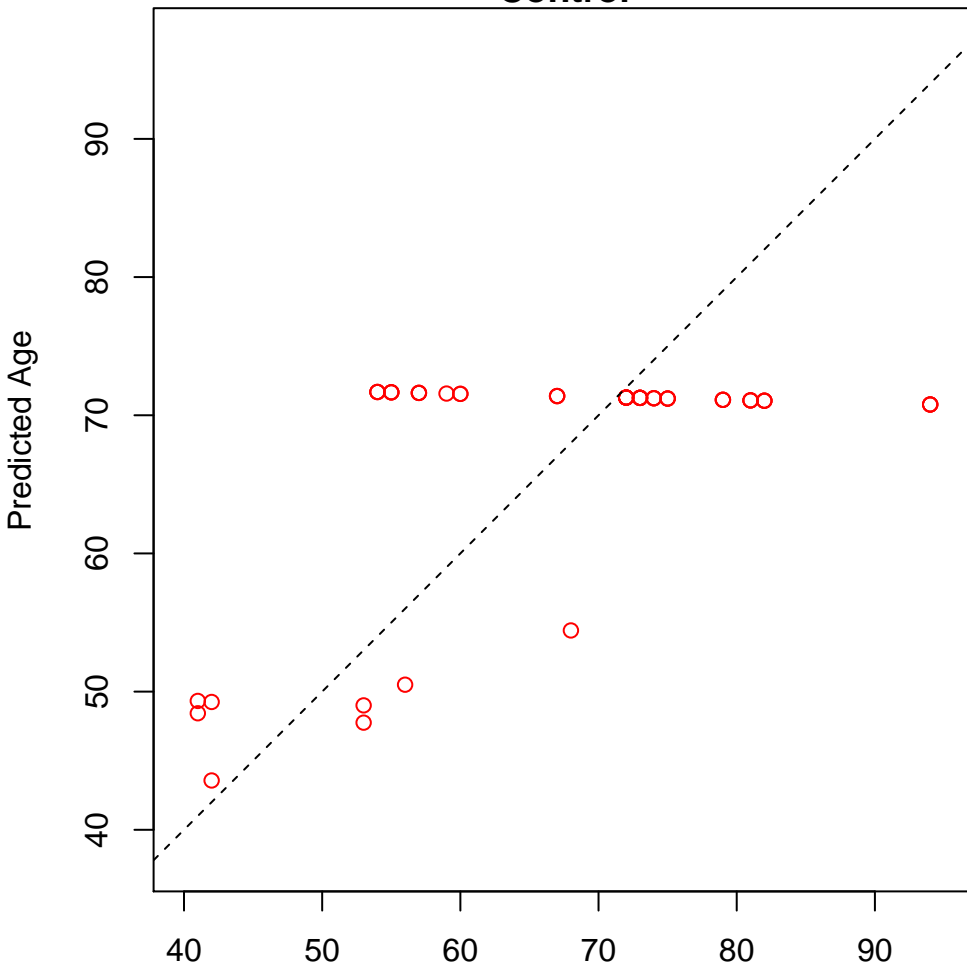


sexual reproduction (Score: 0.819720)

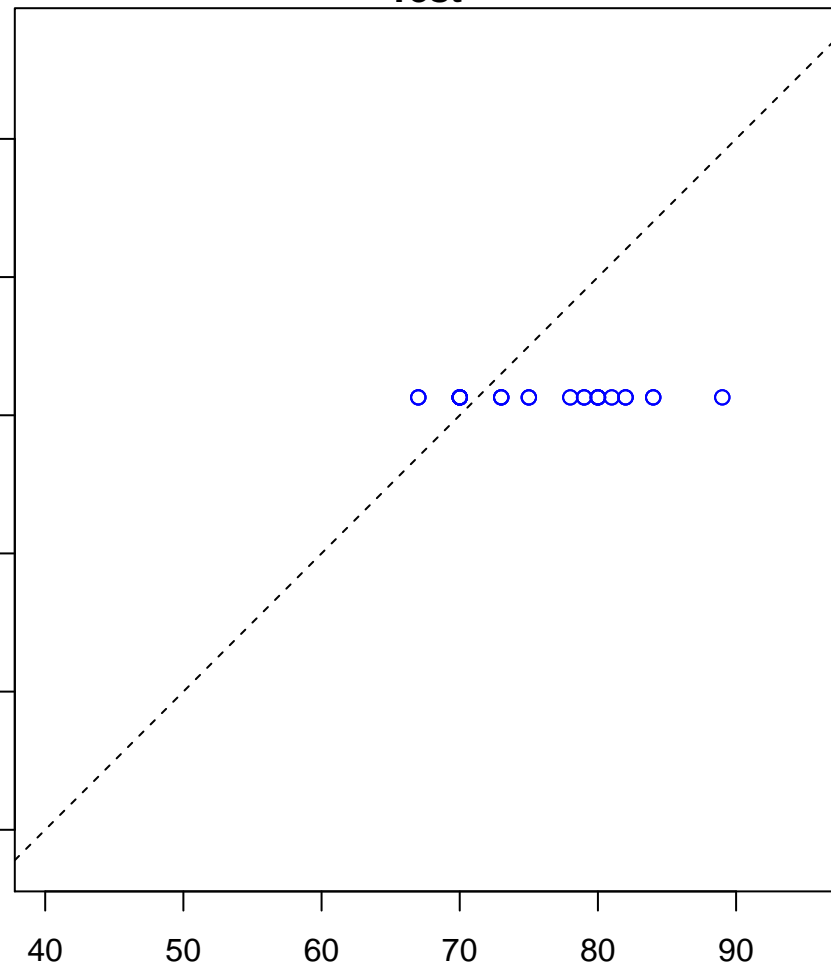


multicellular organism reproduction (Score: 0.819720)

Control

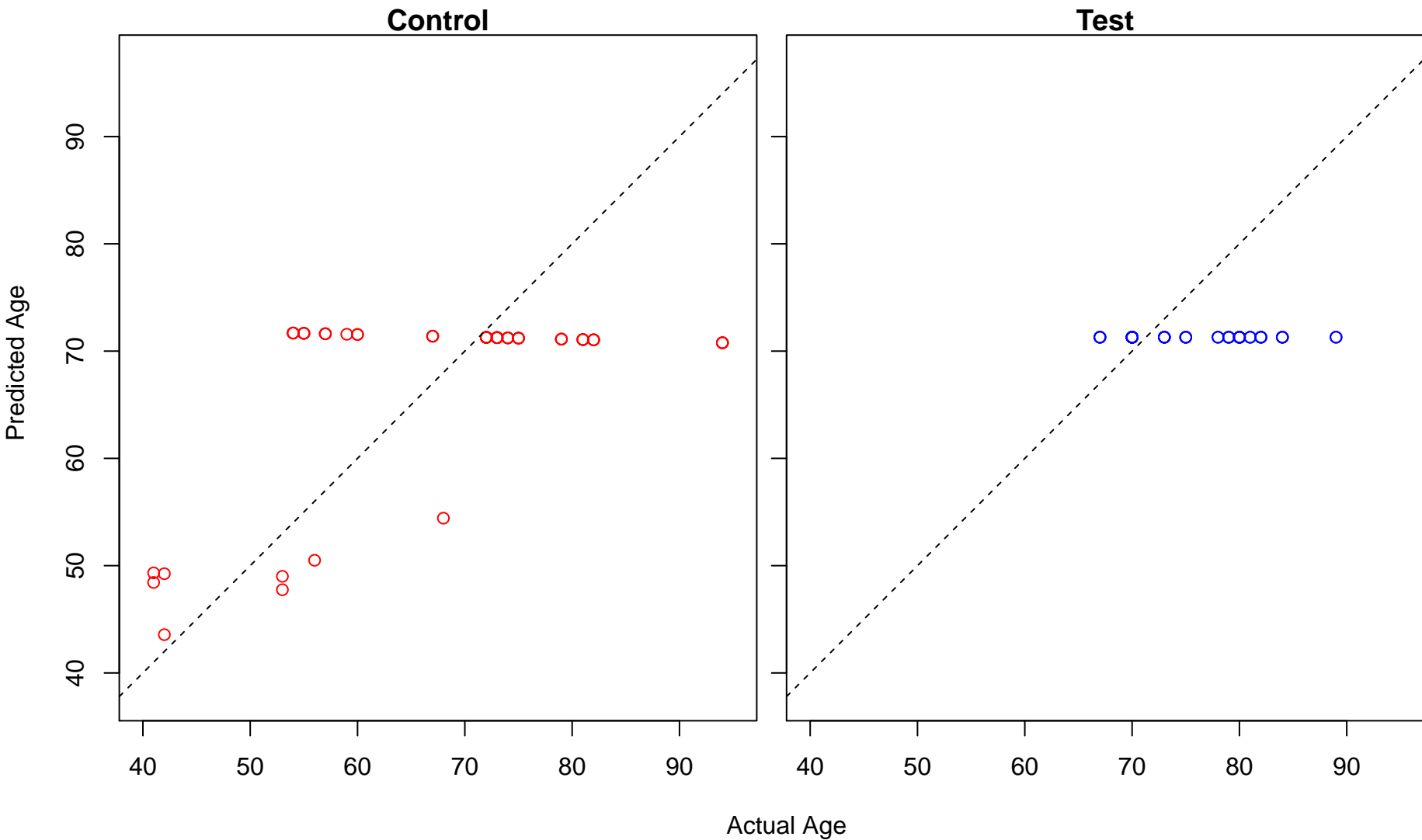


Test



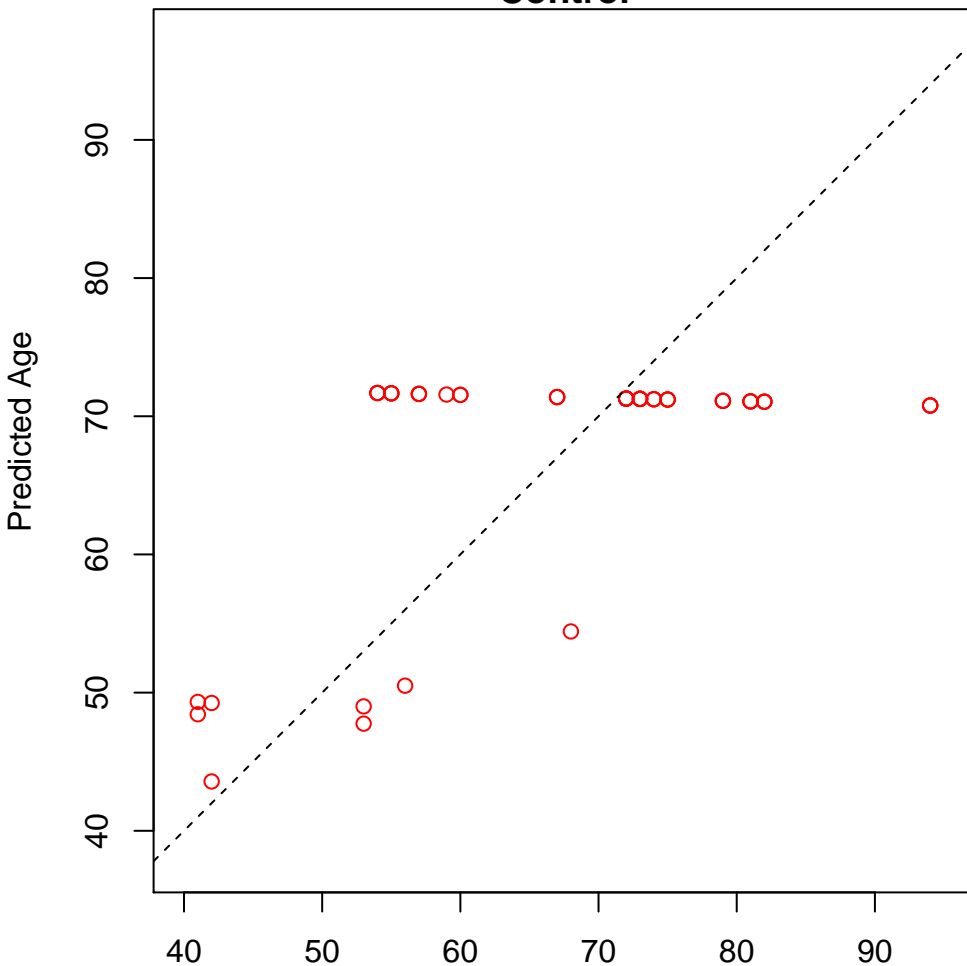
Actual Age

regulation of multicellular organism growth (Score: 0.819720)

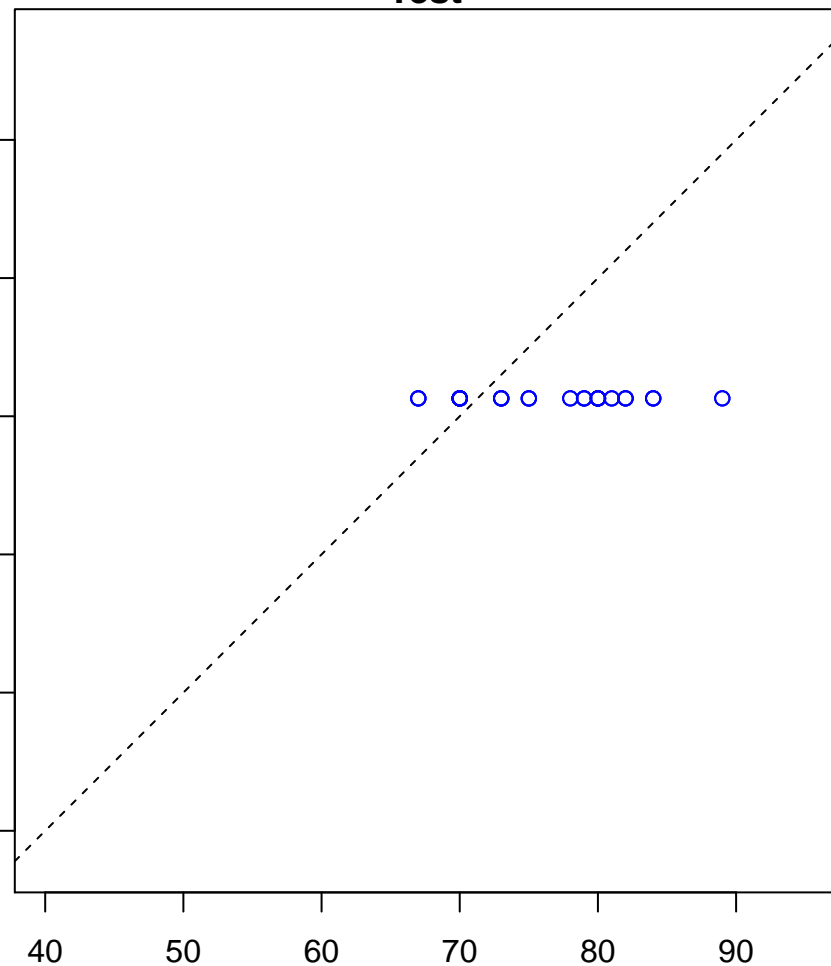


multi-organism reproductive process (Score: 0.819720)

Control

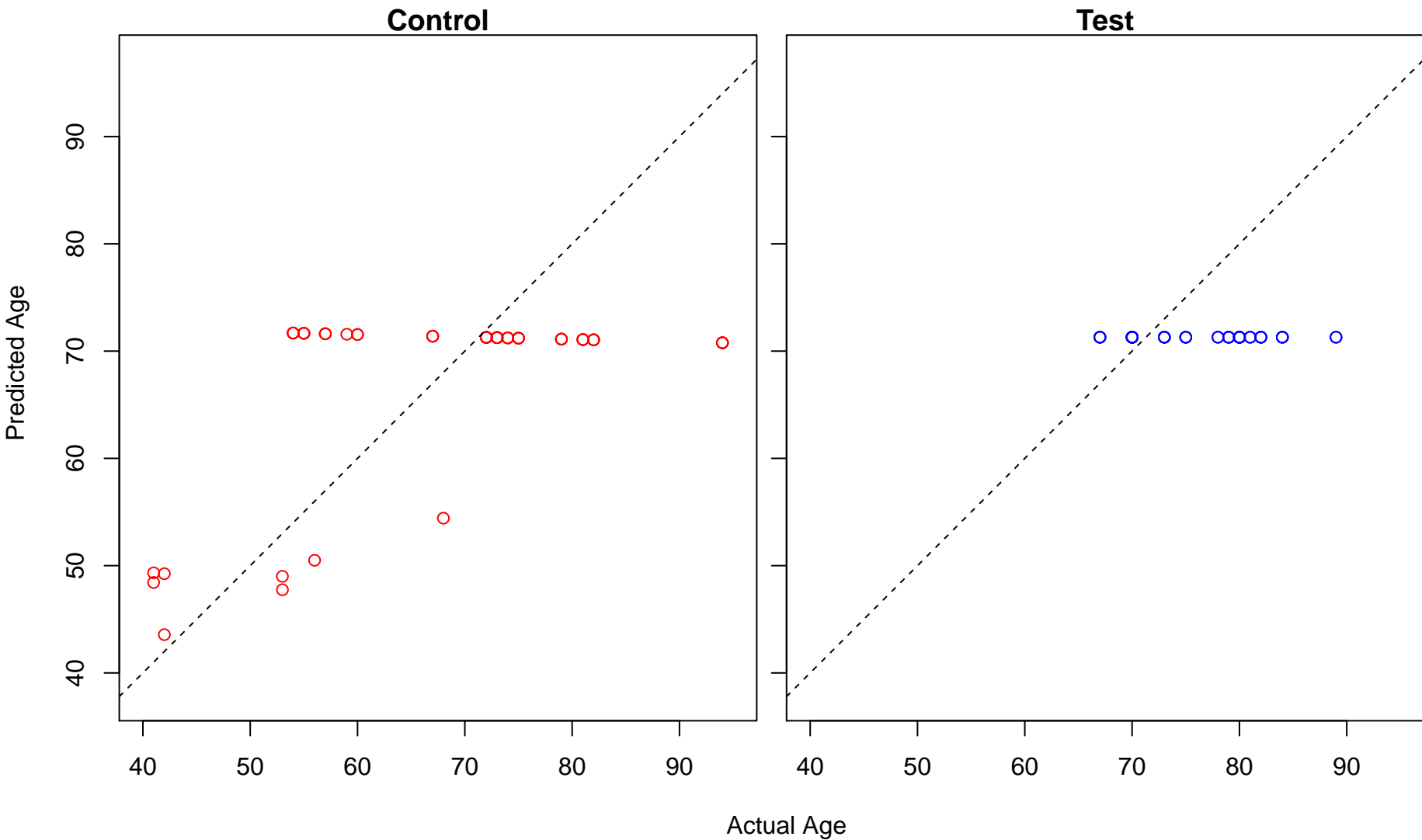


Test



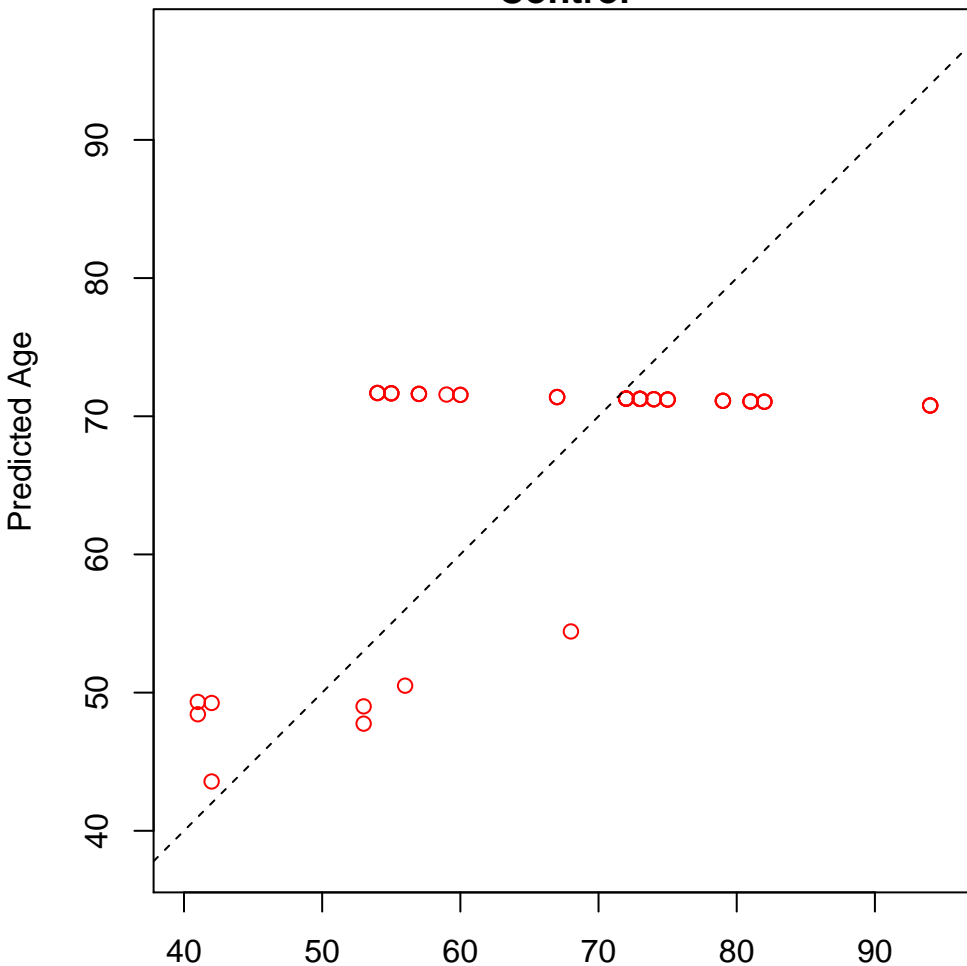
Actual Age

multicellular organismal reproductive process (Score: 0.819720)

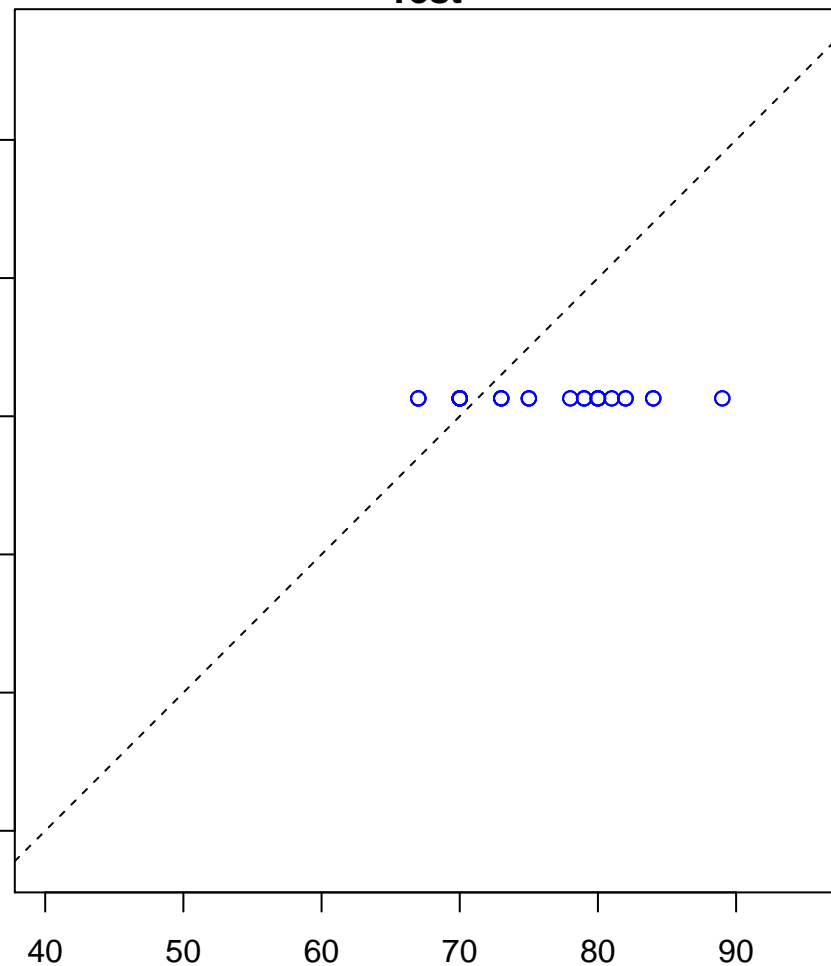


regulation of developmental growth (Score: 0.819720)

Control

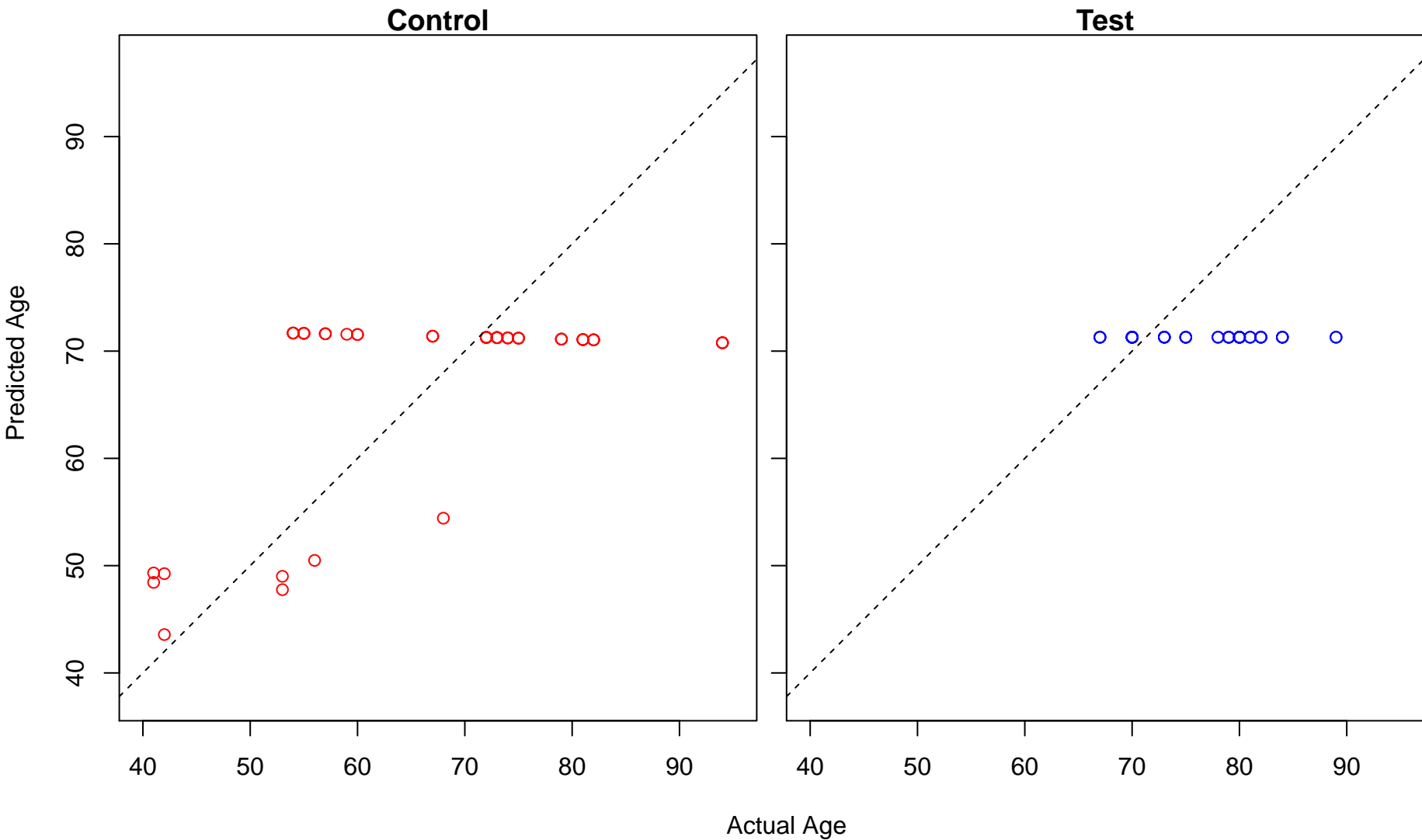


Test

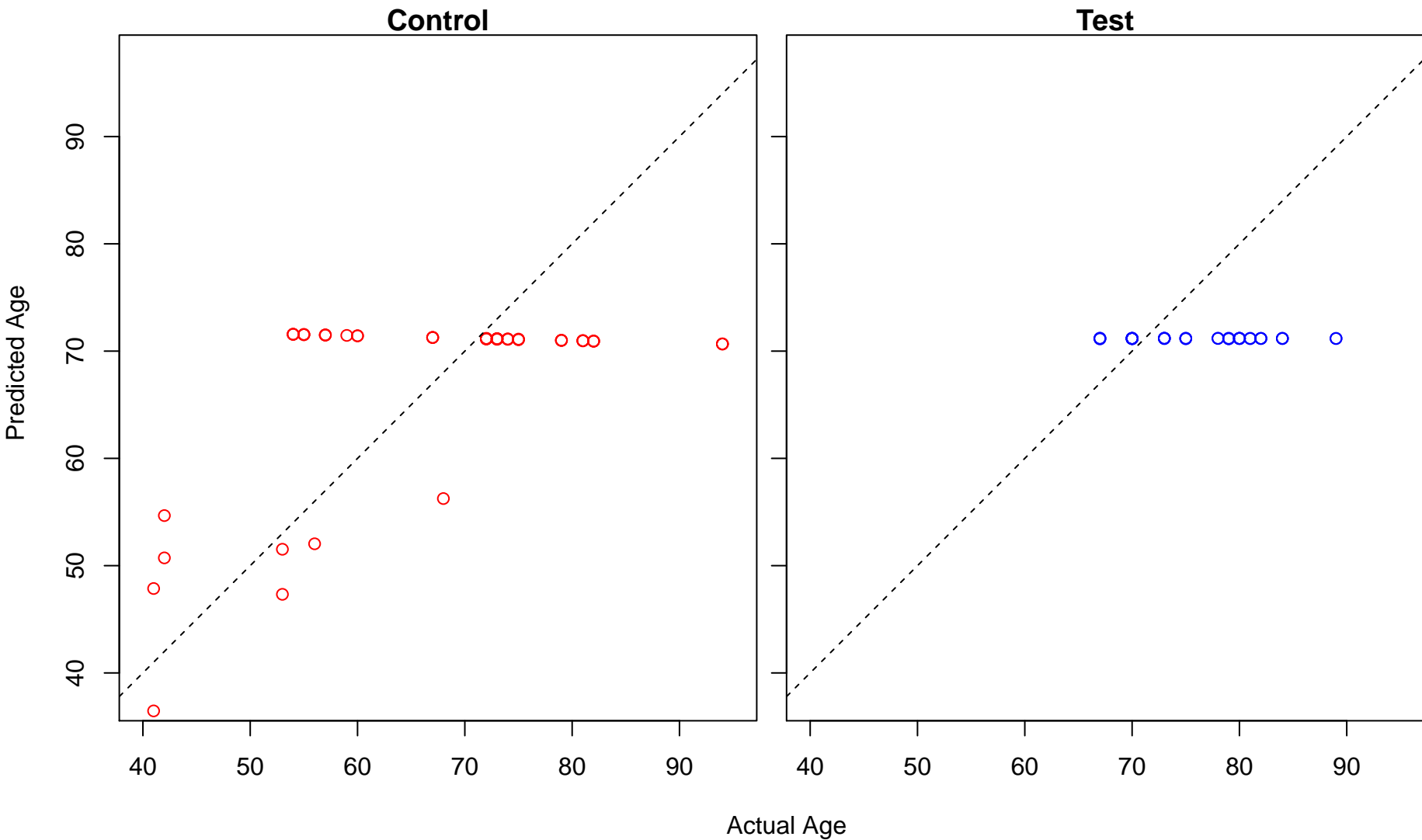


Actual Age

cell morphogenesis involved in neuron differentiation (Score: 0.819707)

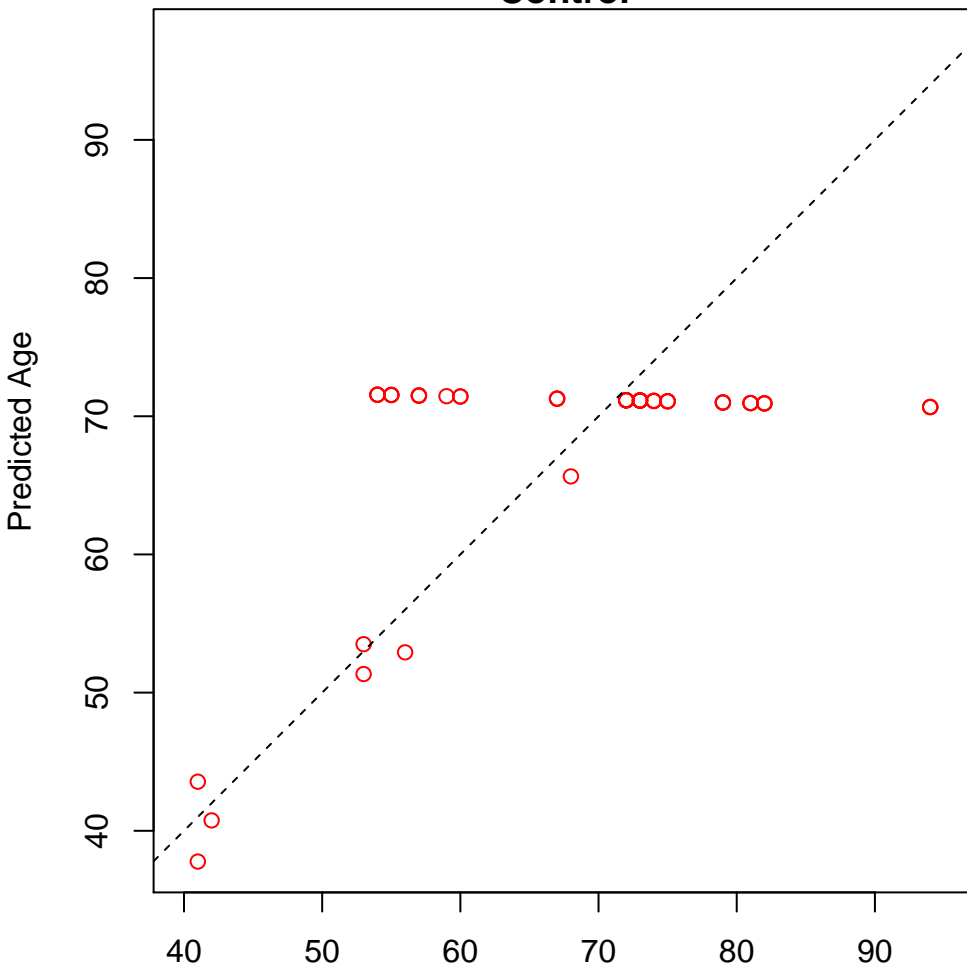


spliceosomal snRNP assembly (Score: 0.819651)

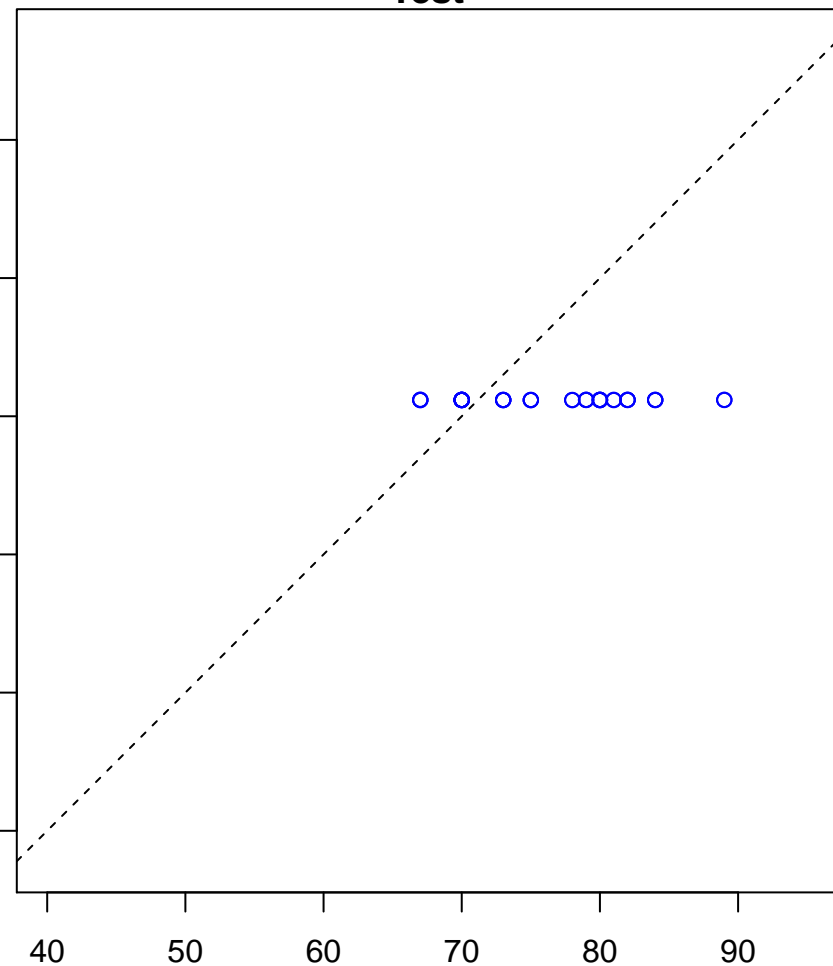


response to inorganic substance (Score: 0.819635)

Control



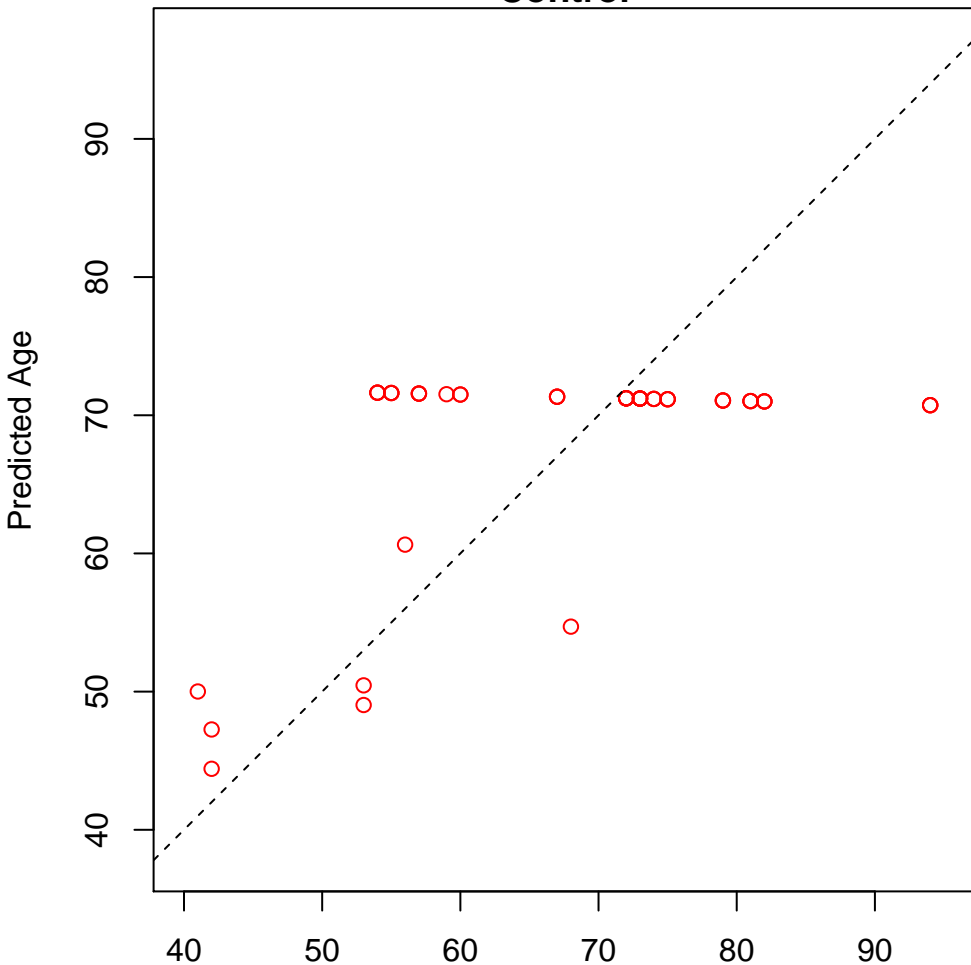
Test



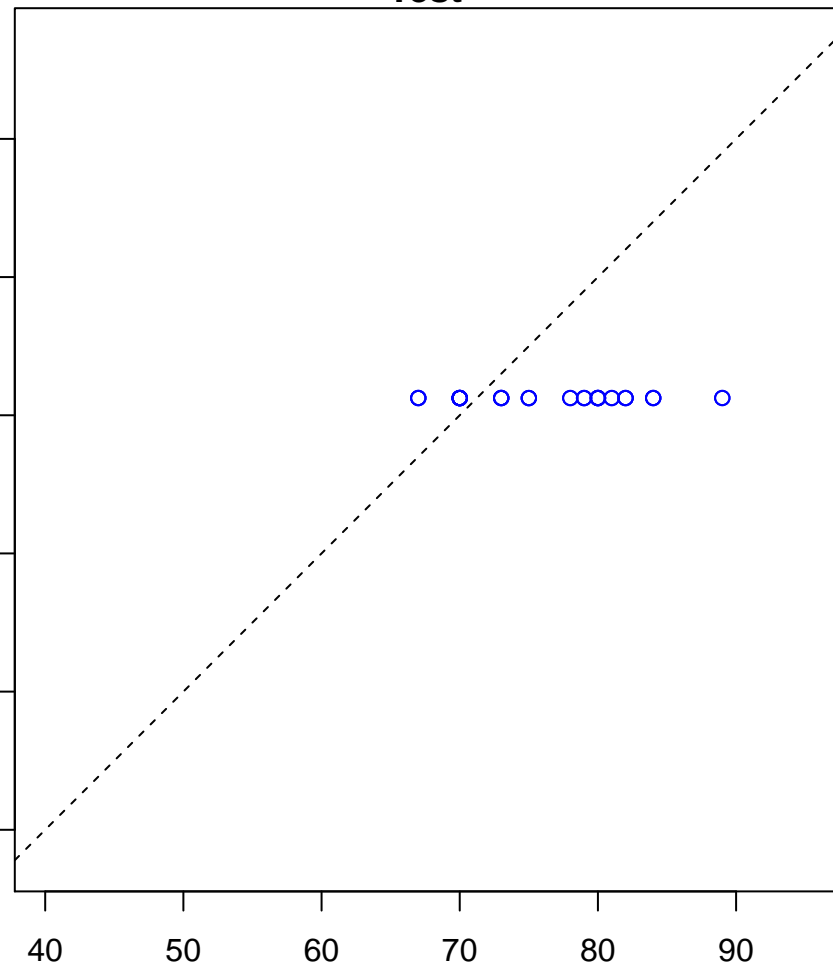
Actual Age

cellular transition metal ion homeostasis (Score: 0.819628)

Control



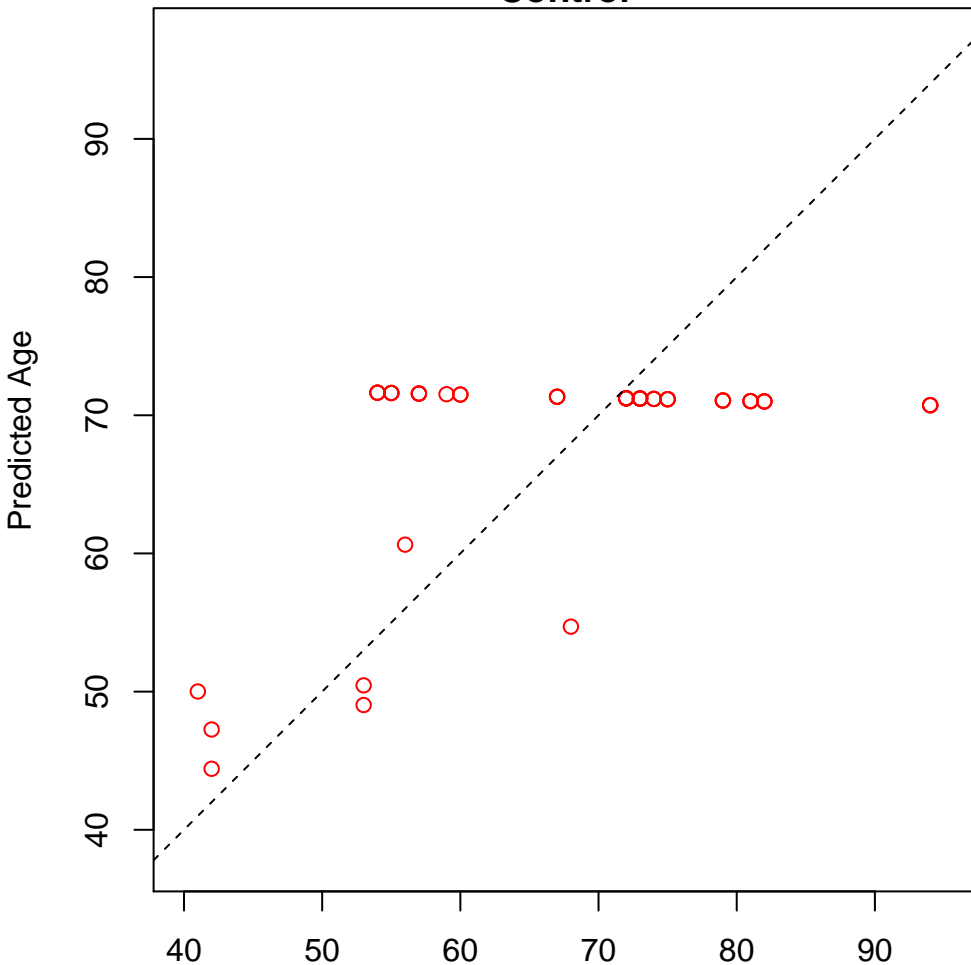
Test



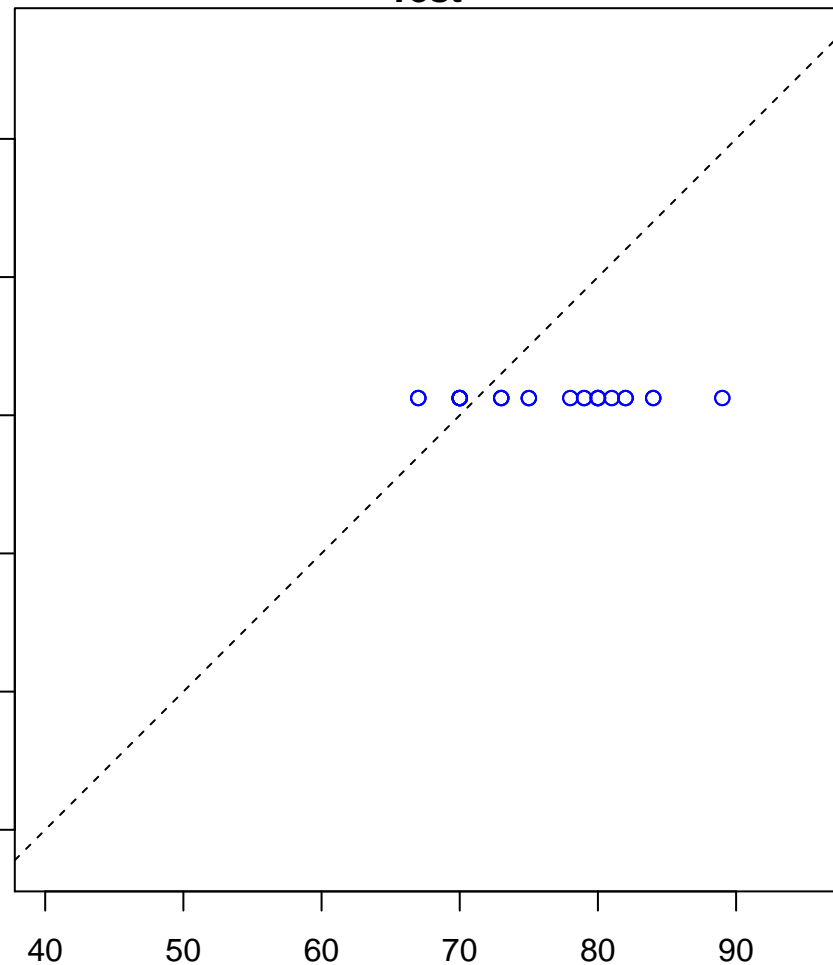
Actual Age

transition metal ion homeostasis (Score: 0.819628)

Control

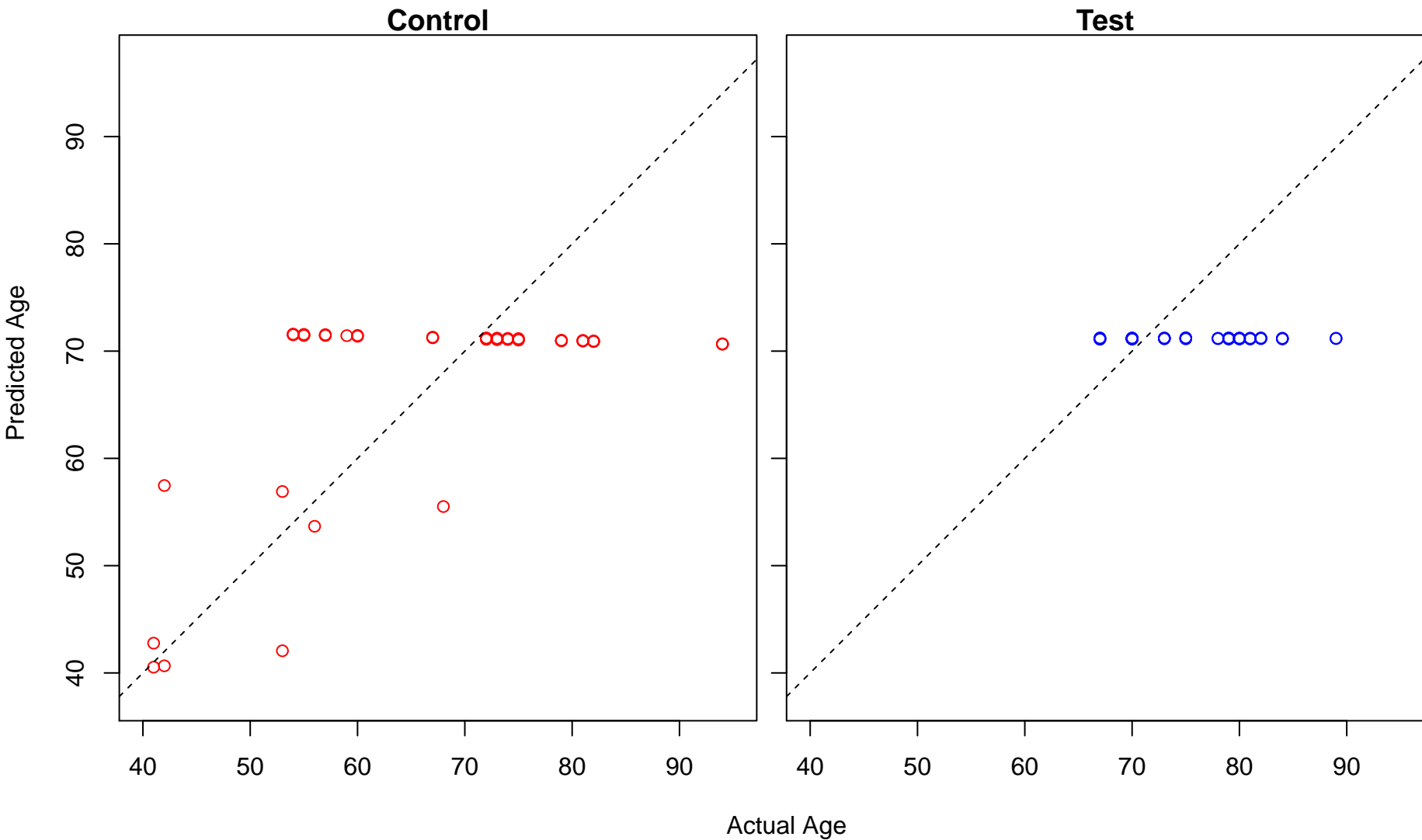


Test



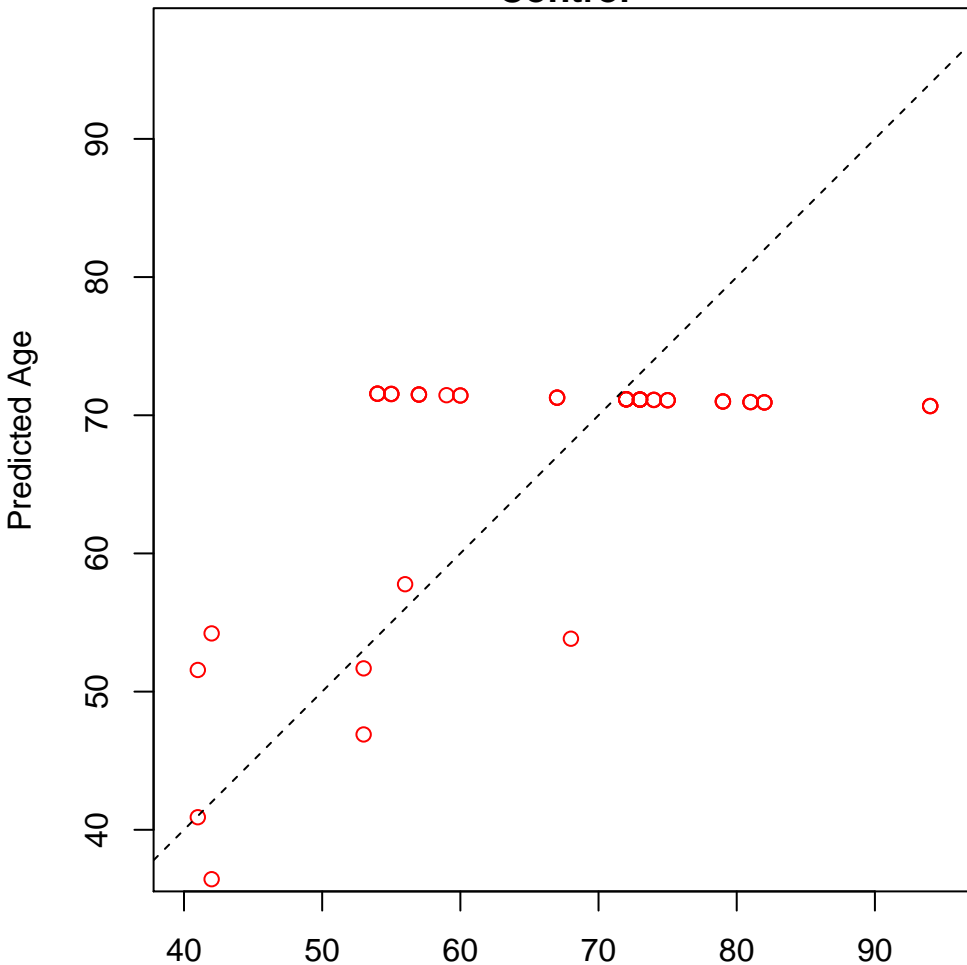
Actual Age

cell proliferation (Score: 0.819607)

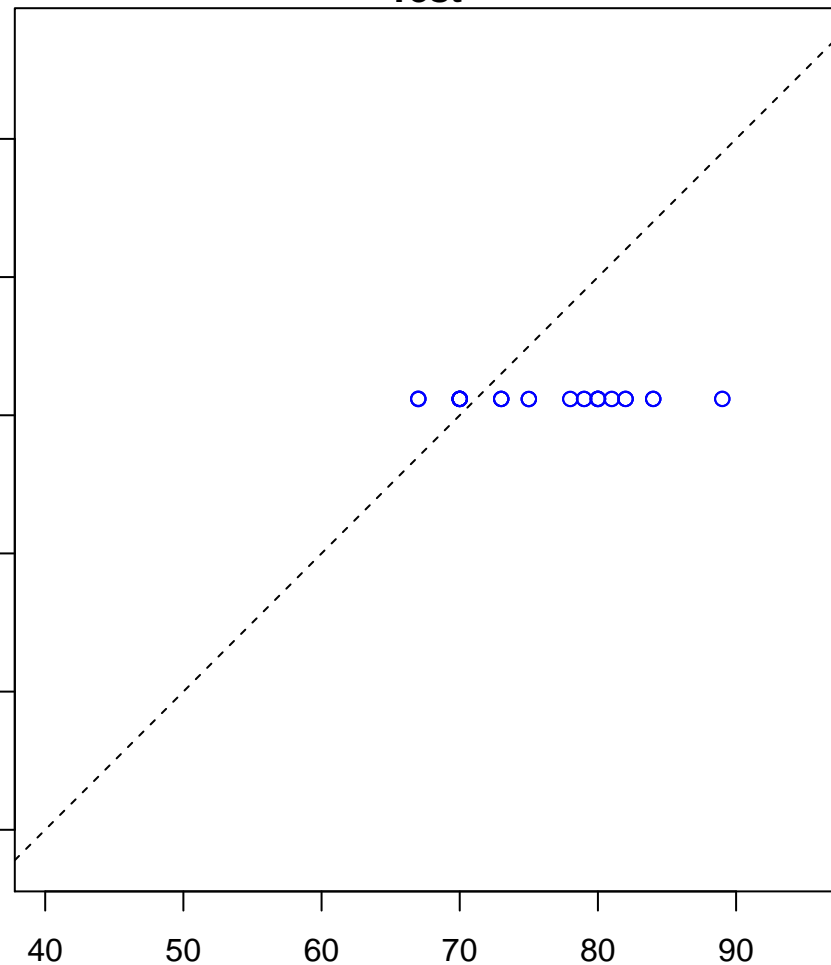


sulfur compound metabolic process (Score: 0.819577)

Control

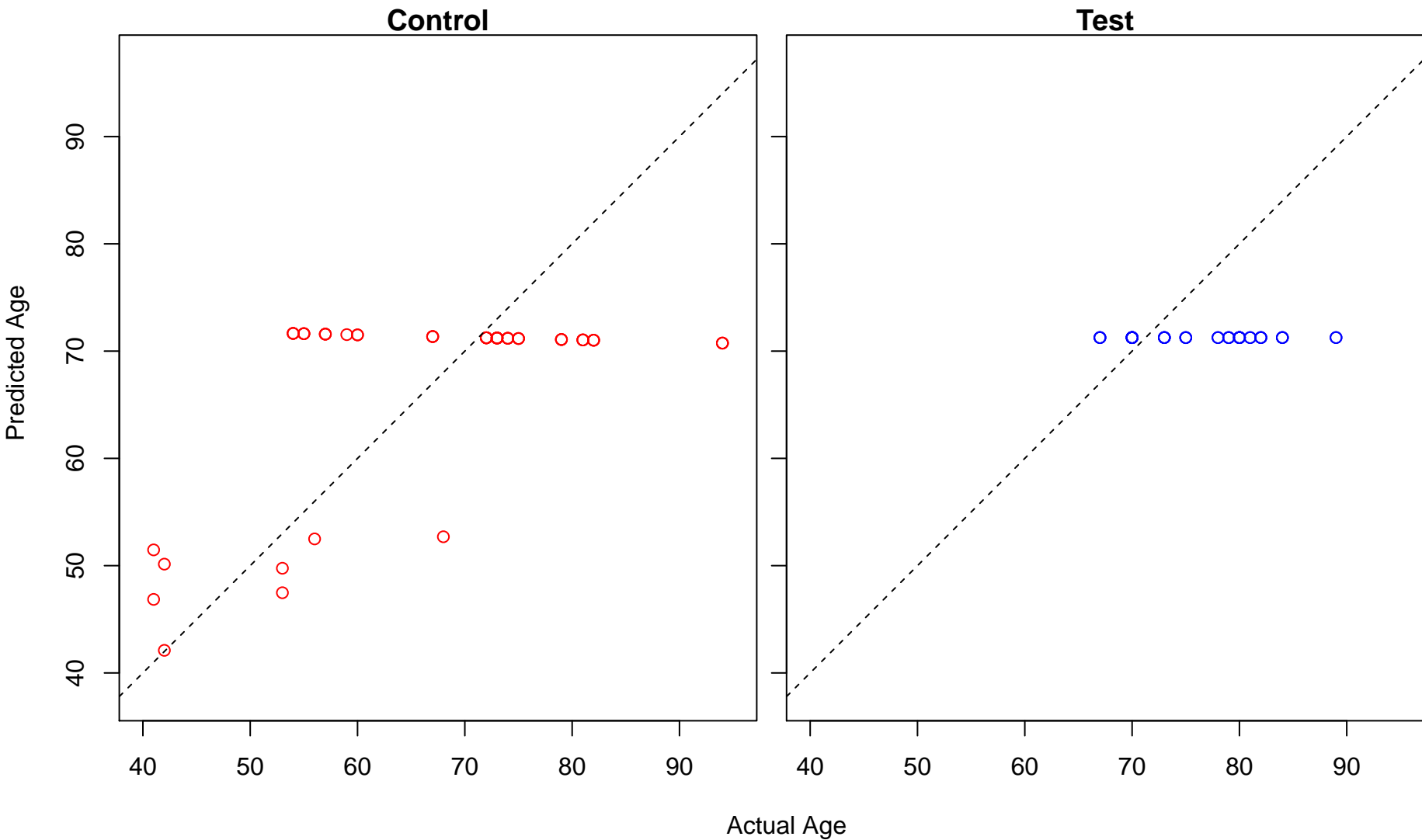


Test

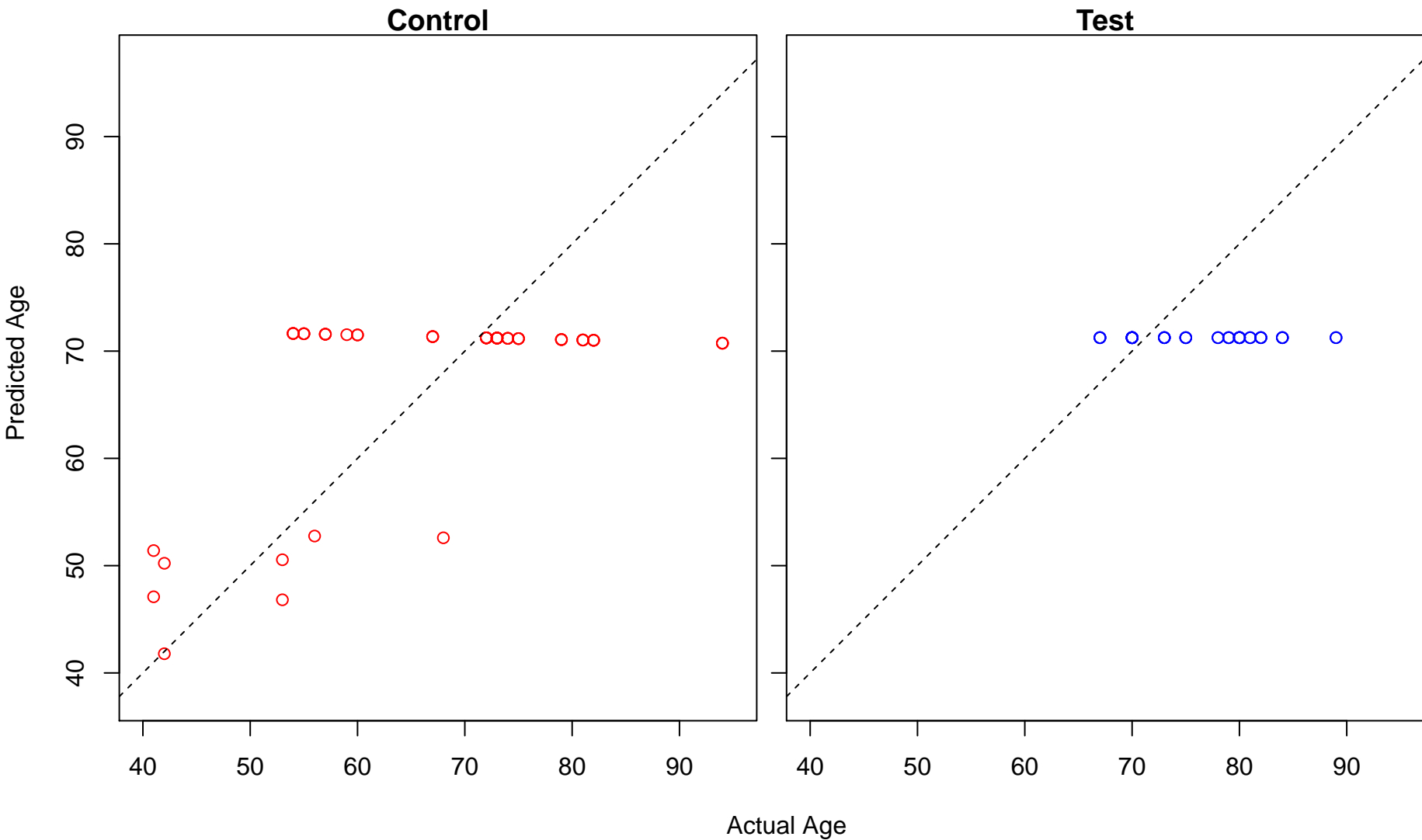


Actual Age

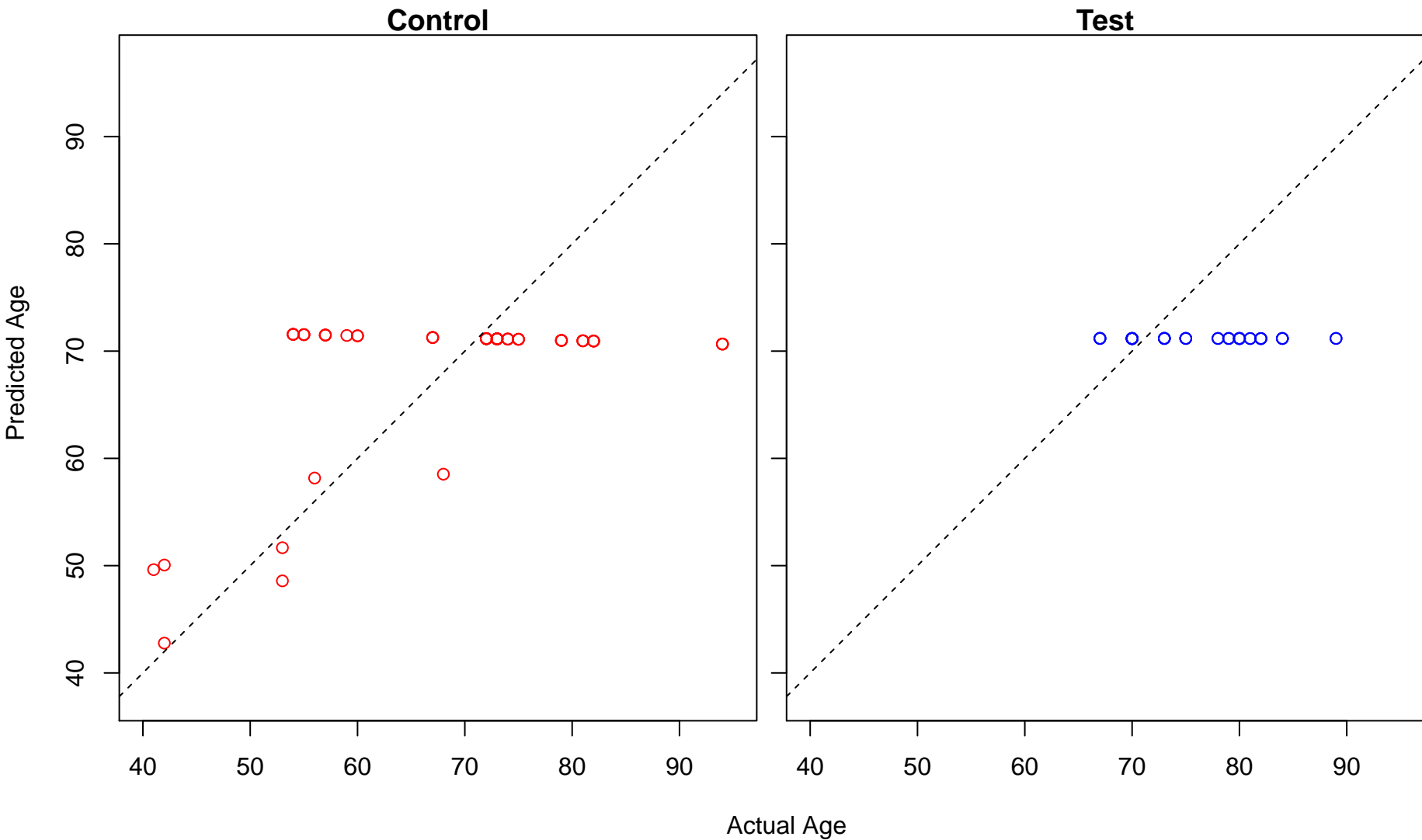
response to alcohol (Score: 0.819566)



multicellular organismal homeostasis (Score: 0.819527)

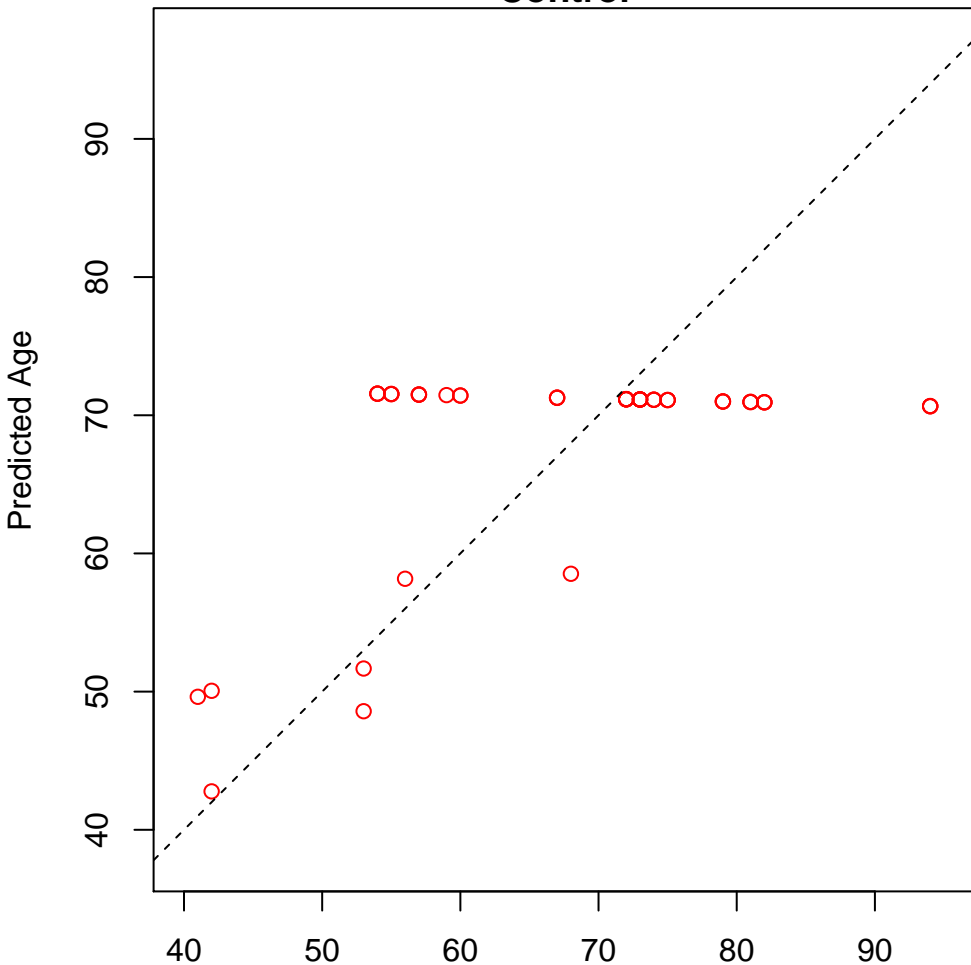


positive regulation of multi-organism process (Score: 0.819513)

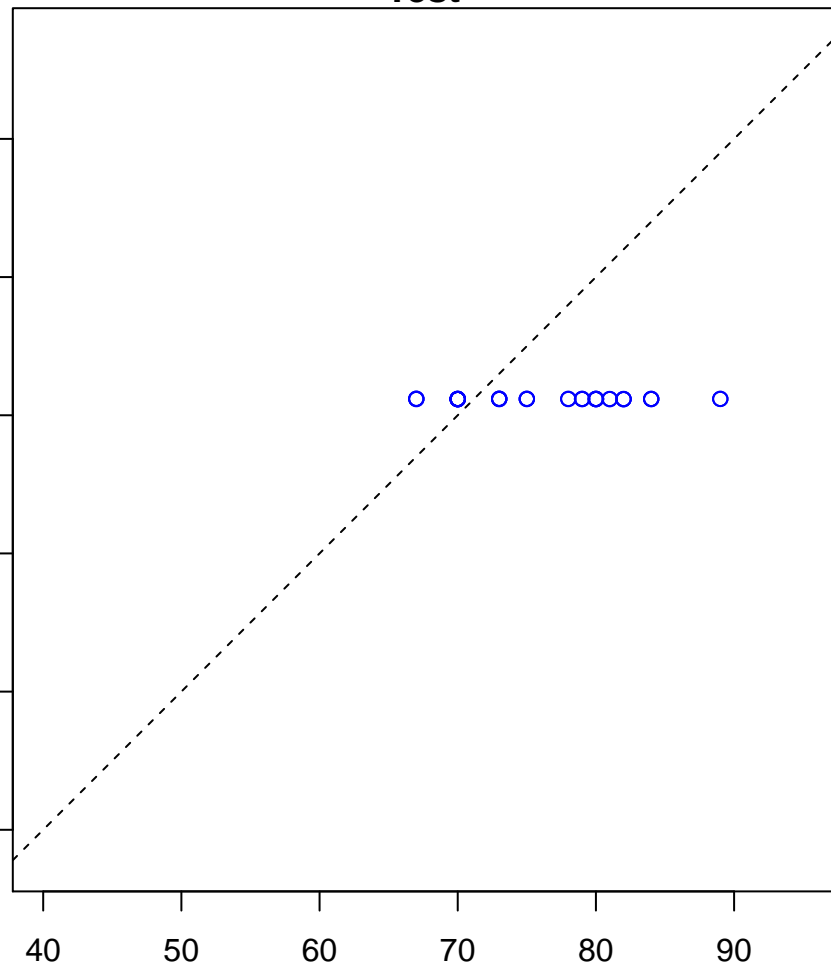


positive regulation of viral process (Score: 0.819513)

Control

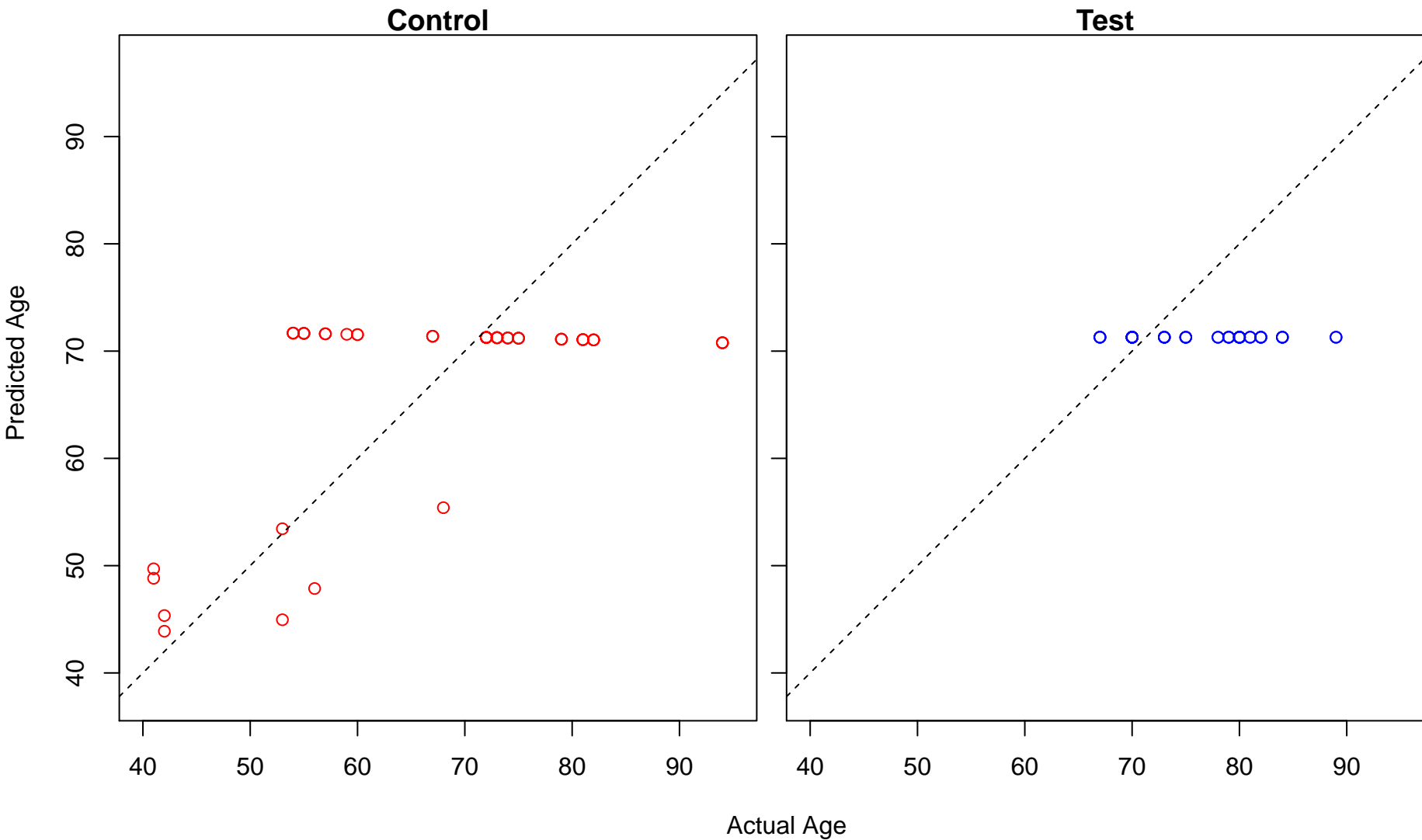


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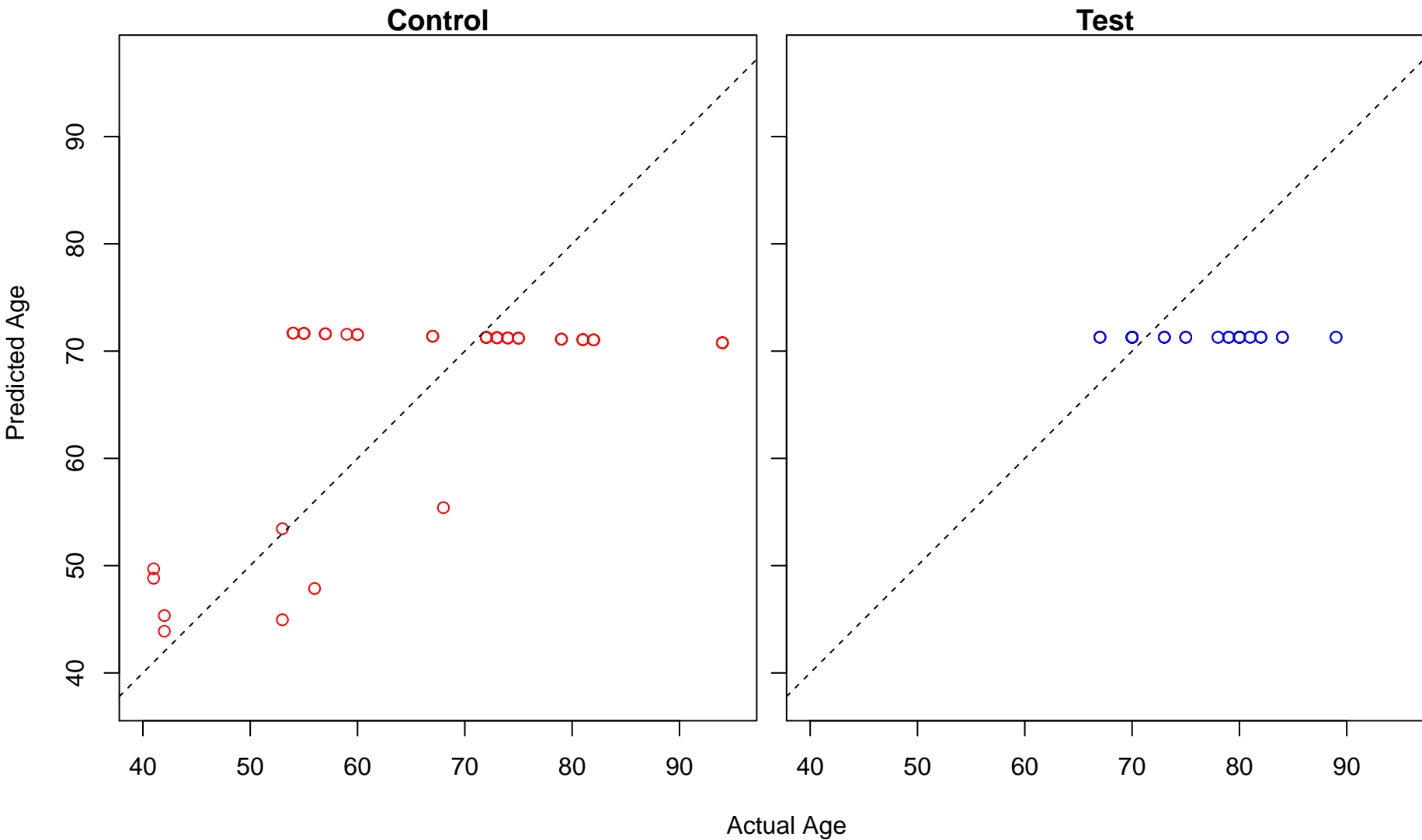


Actual Age

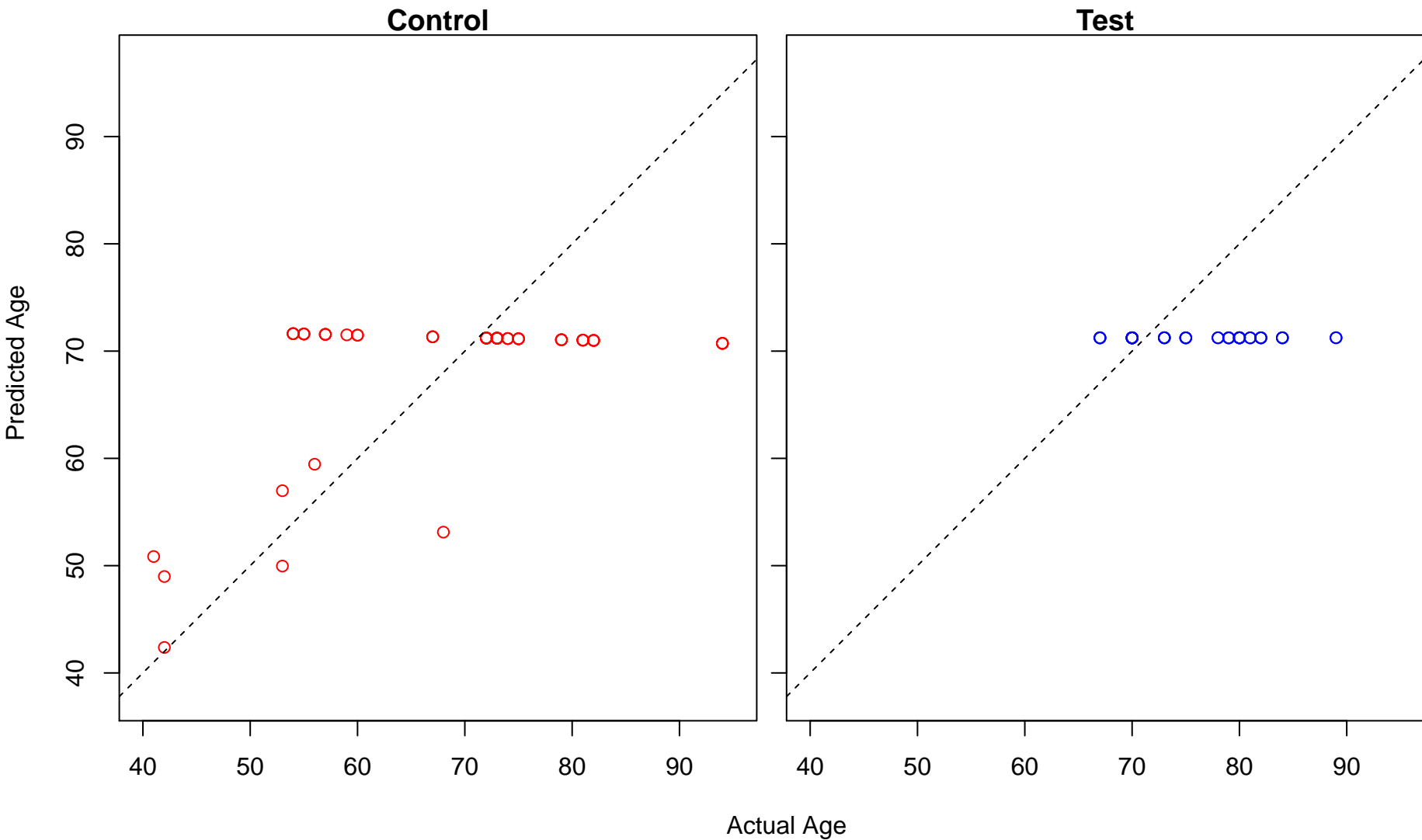
negative regulation of lipid metabolic process (Score: 0.819430)



negative regulation of lipid biosynthetic process (Score: 0.819430)

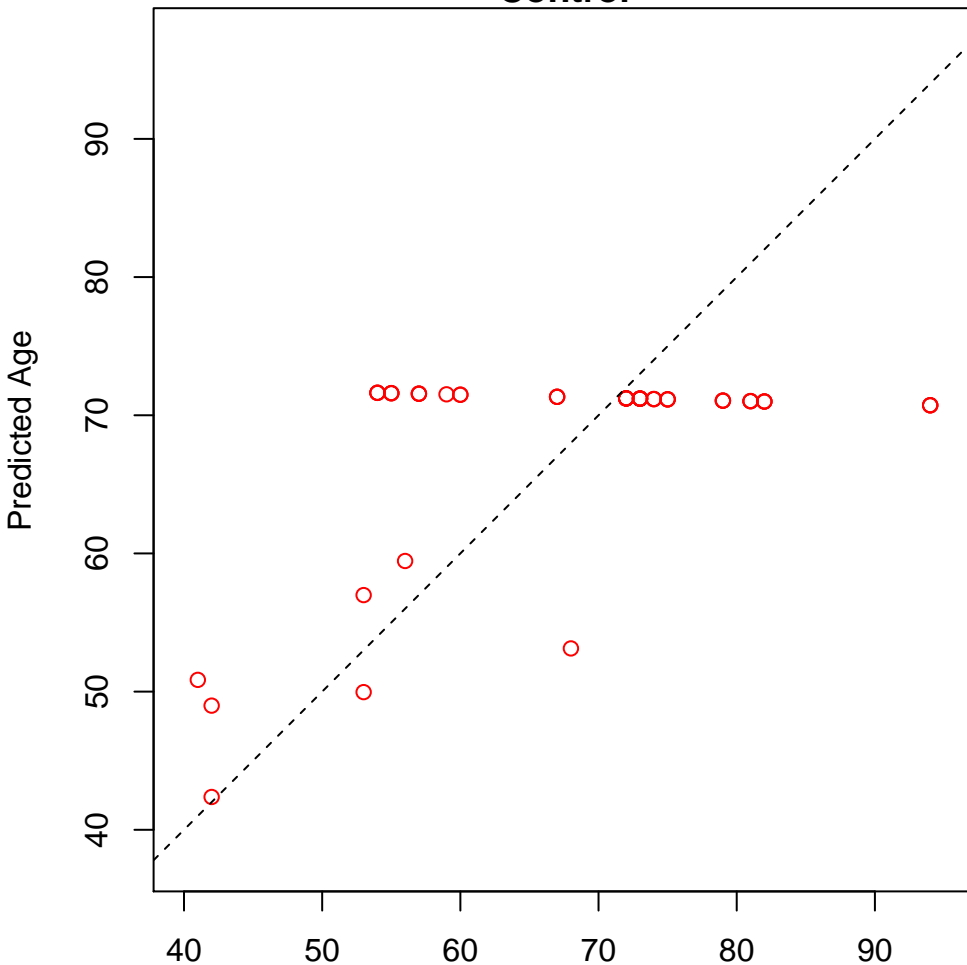


cellular response to decreased oxygen levels (Score: 0.819274)

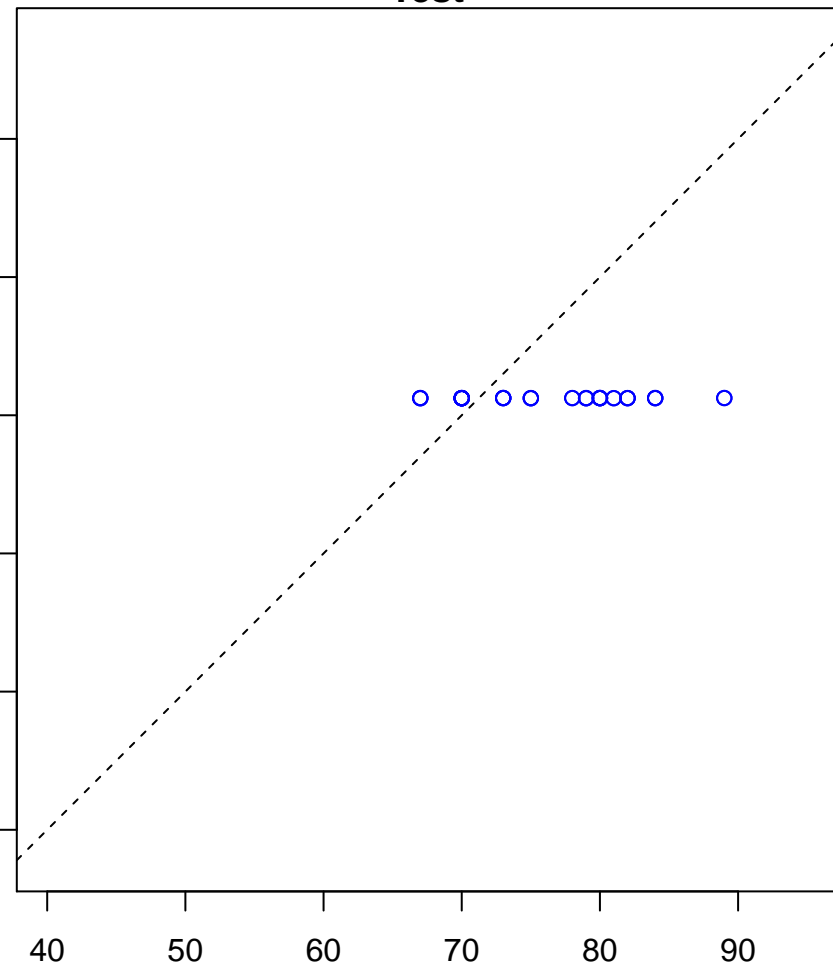


cellular response to oxygen levels (Score: 0.819274)

Control

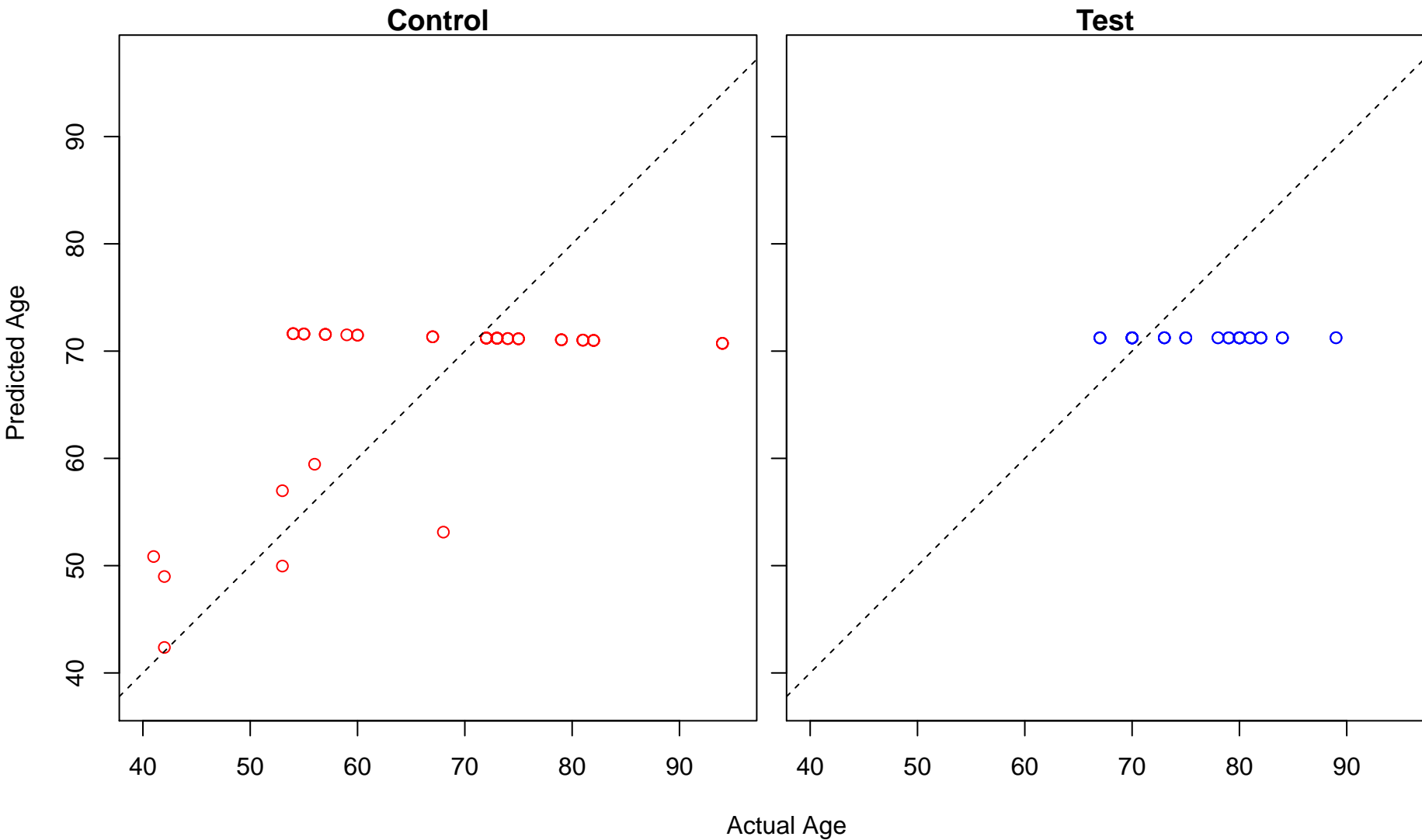


Test



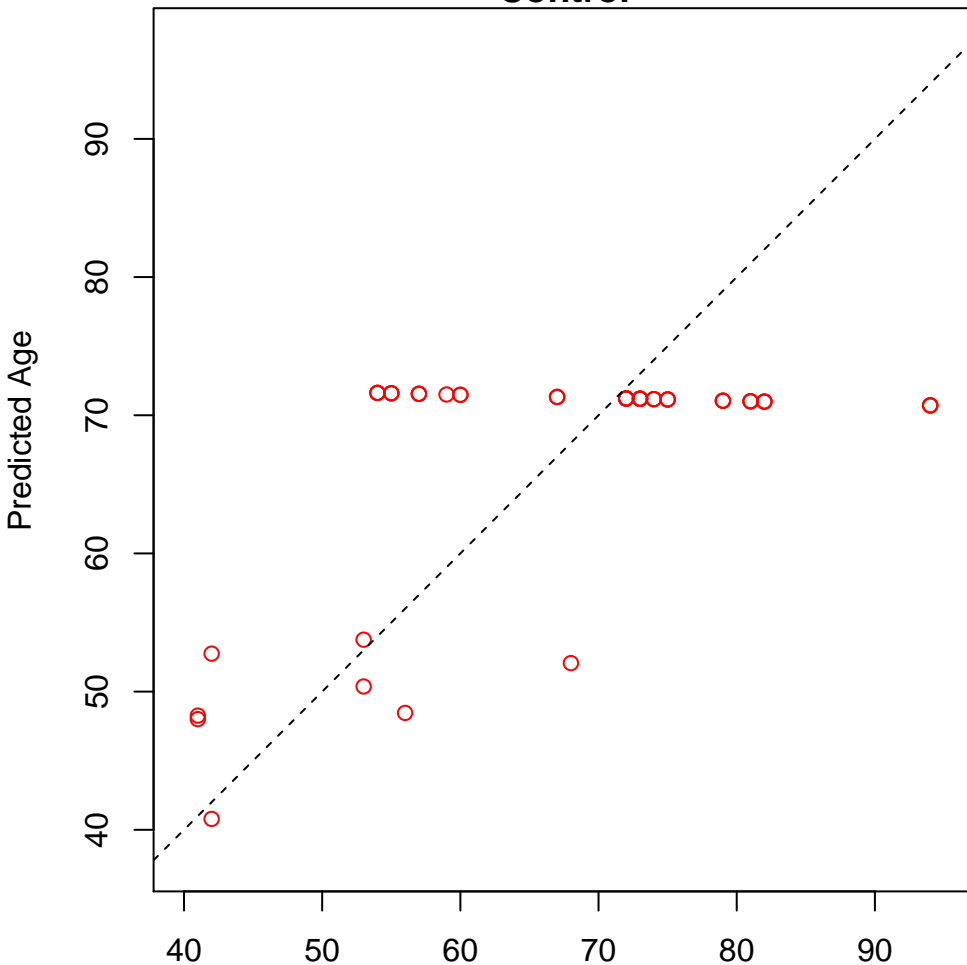
Actual Age

cellular response to hypoxia (Score: 0.819274)

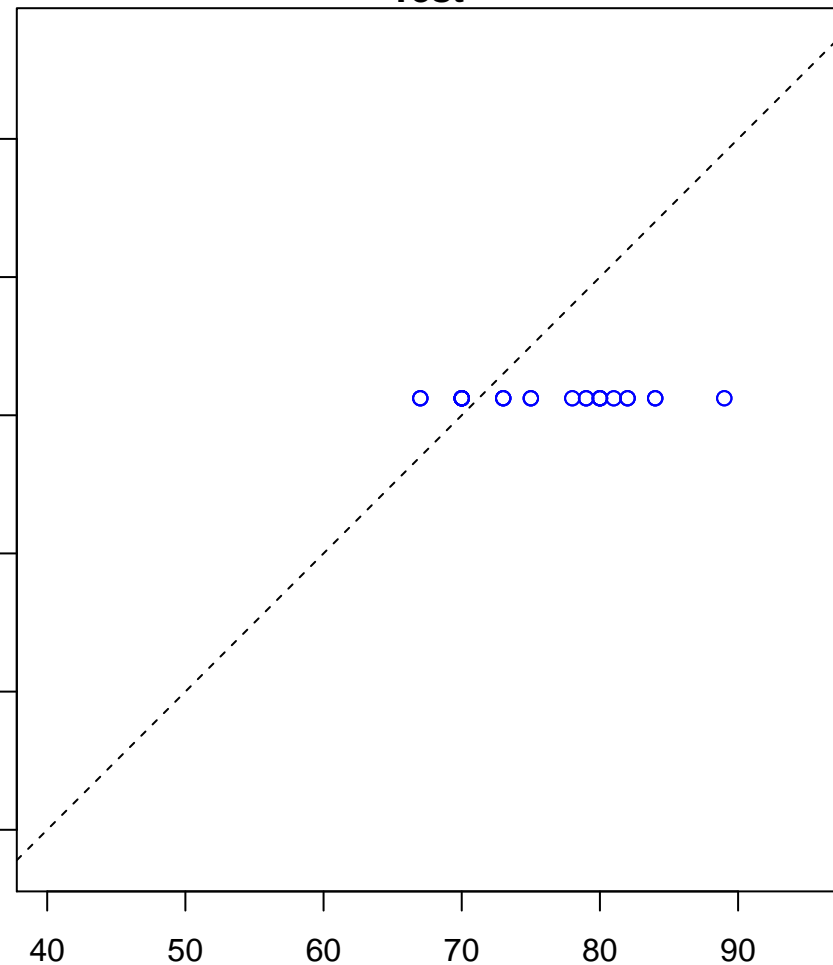


transition metal ion transport (Score: 0.819130)

Control

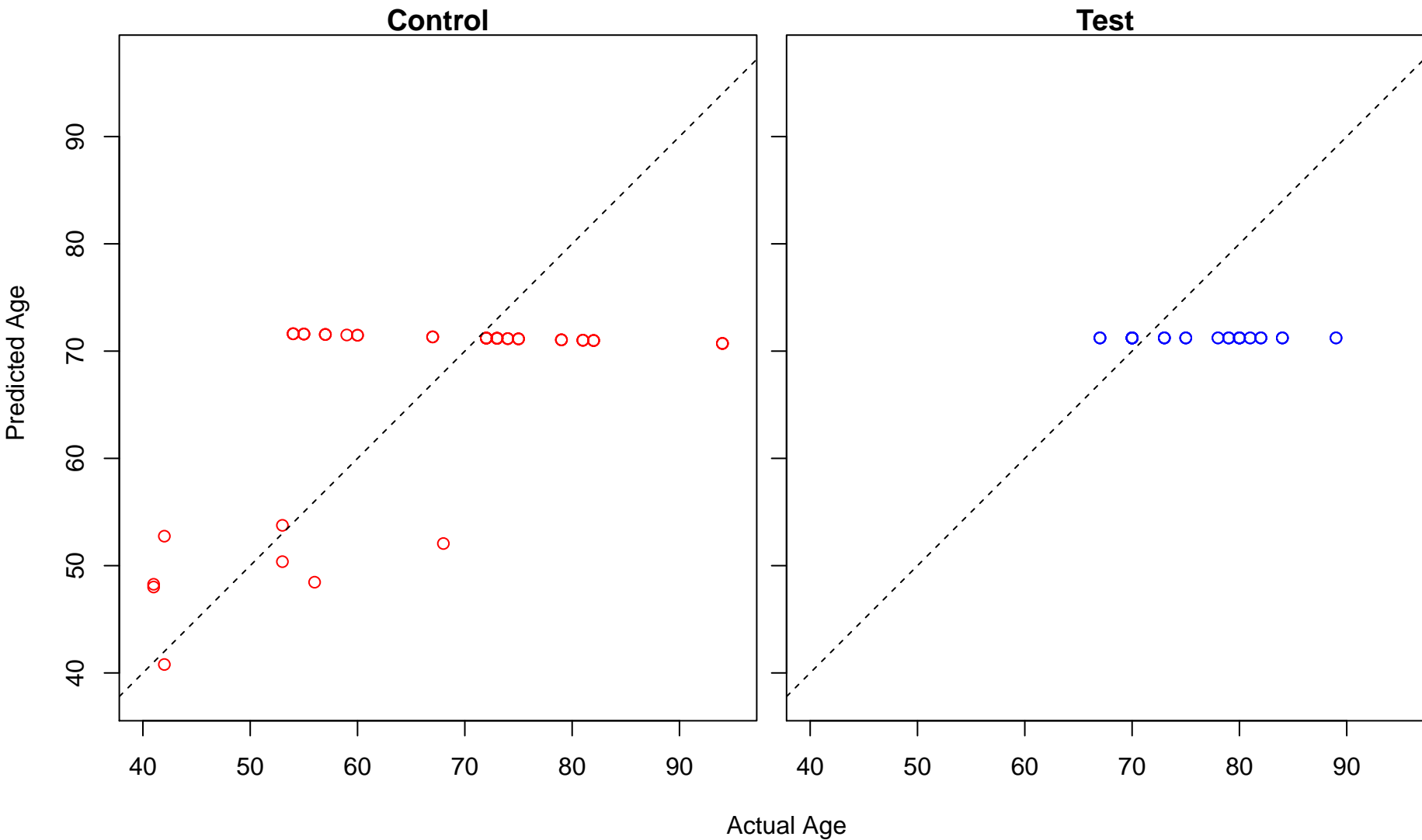


Test

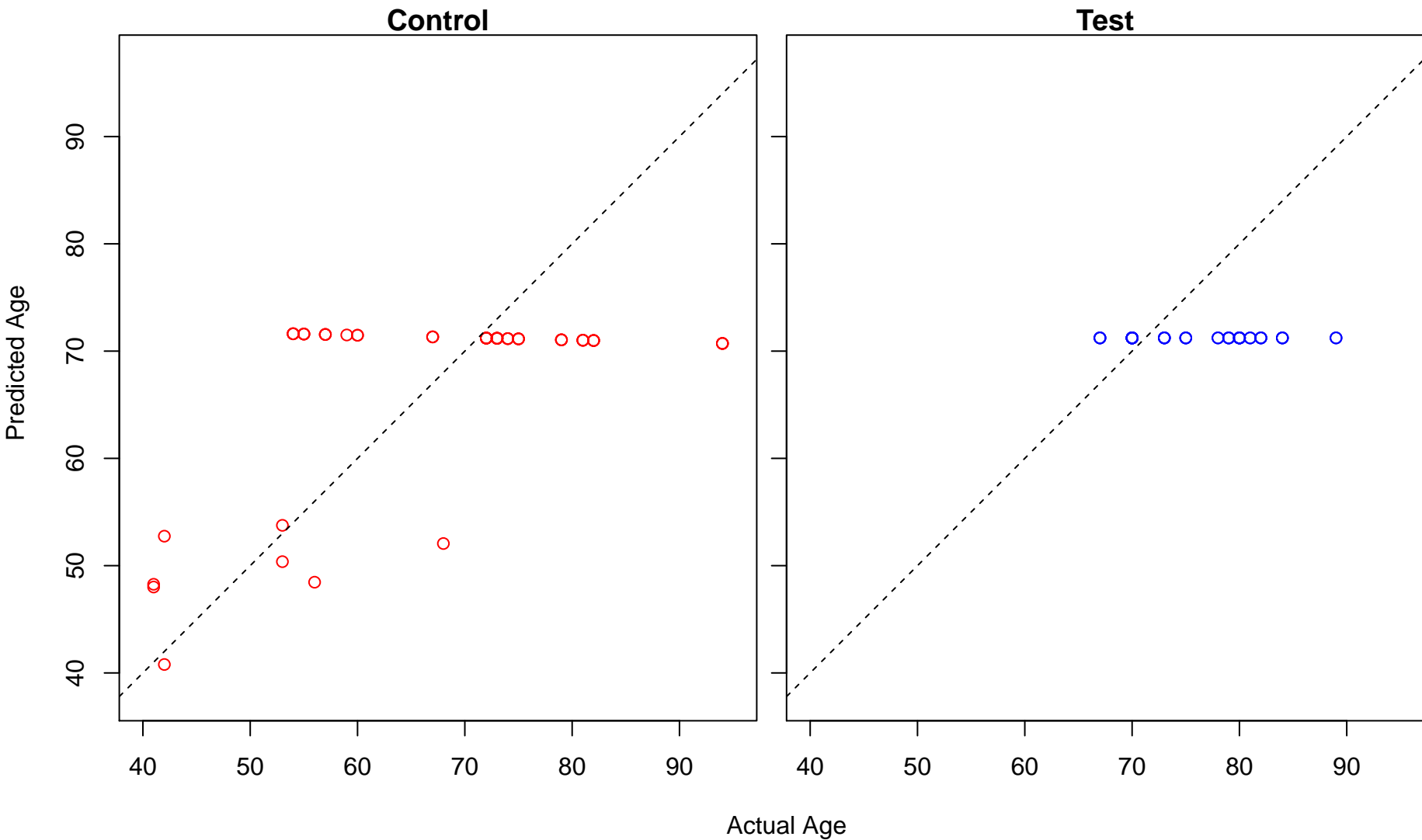


Actual Age

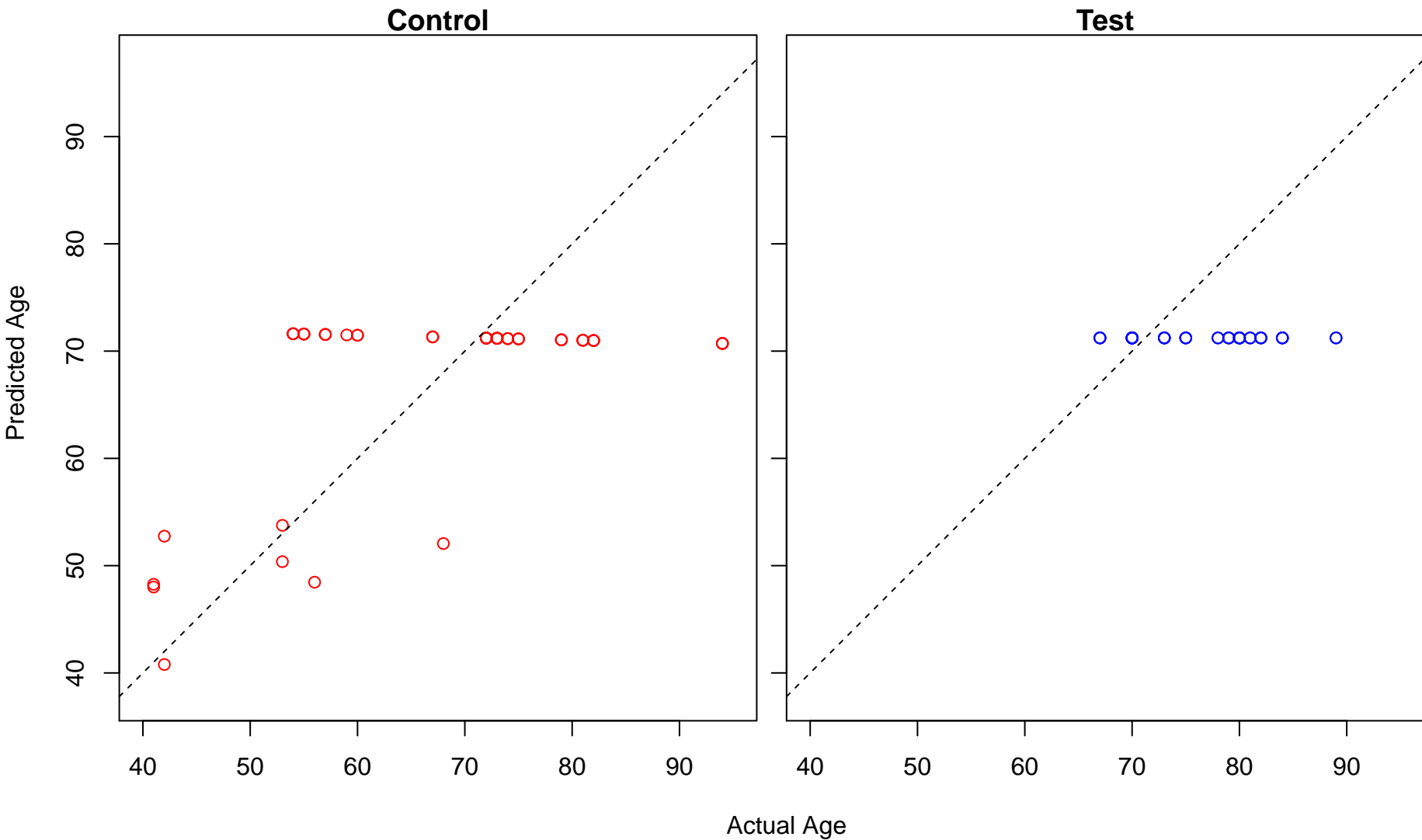
iron ion transport (Score: 0.819130)



ferric iron transport (Score: 0.819130)

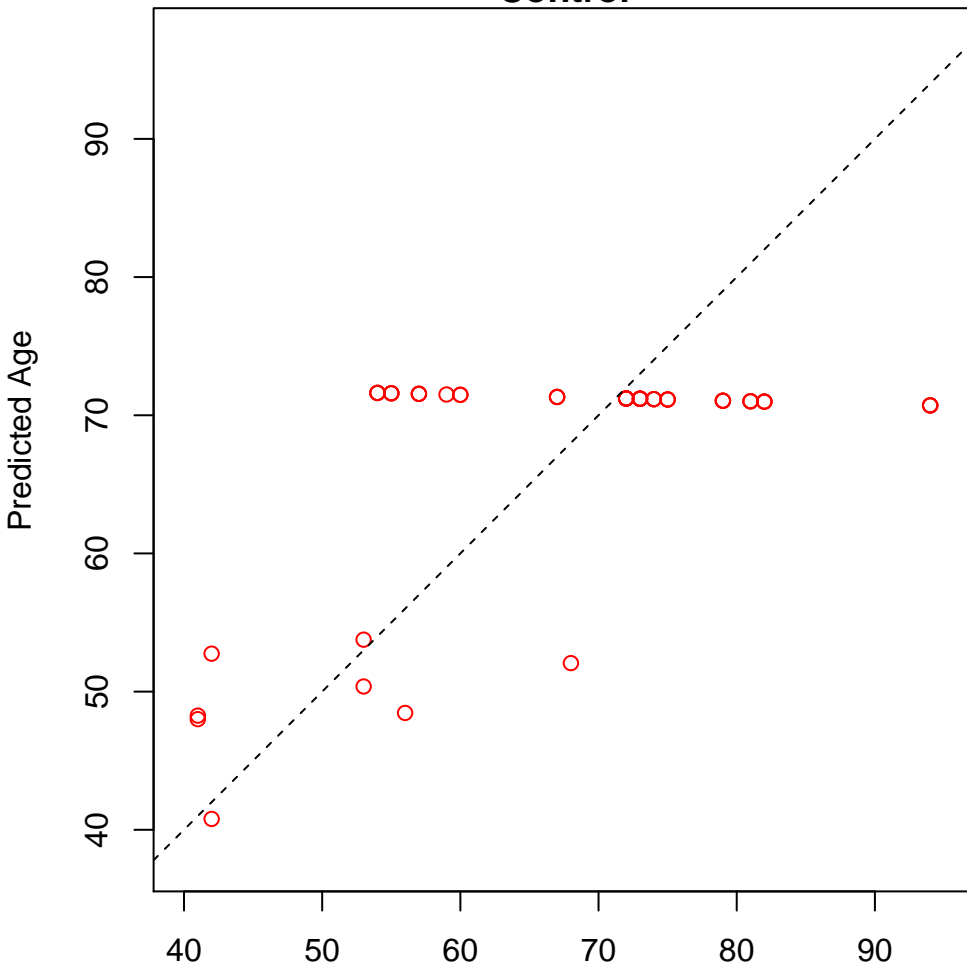


transferrin transport (Score: 0.819130)

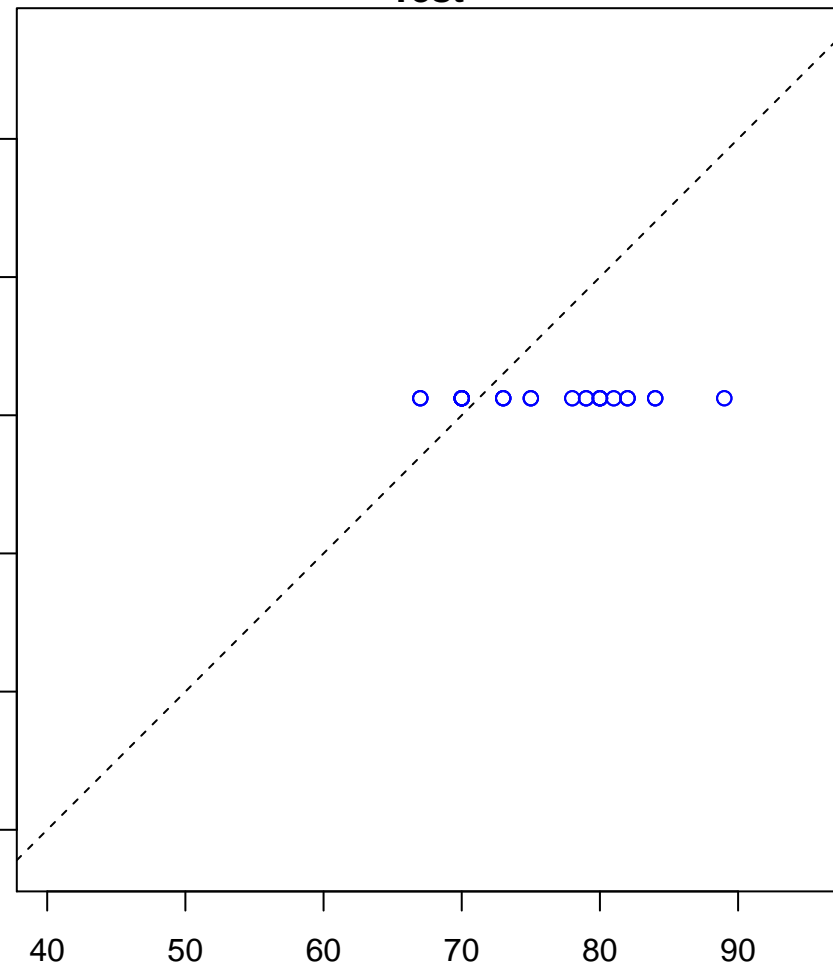


trivalent inorganic cation transport (Score: 0.819130)

Control

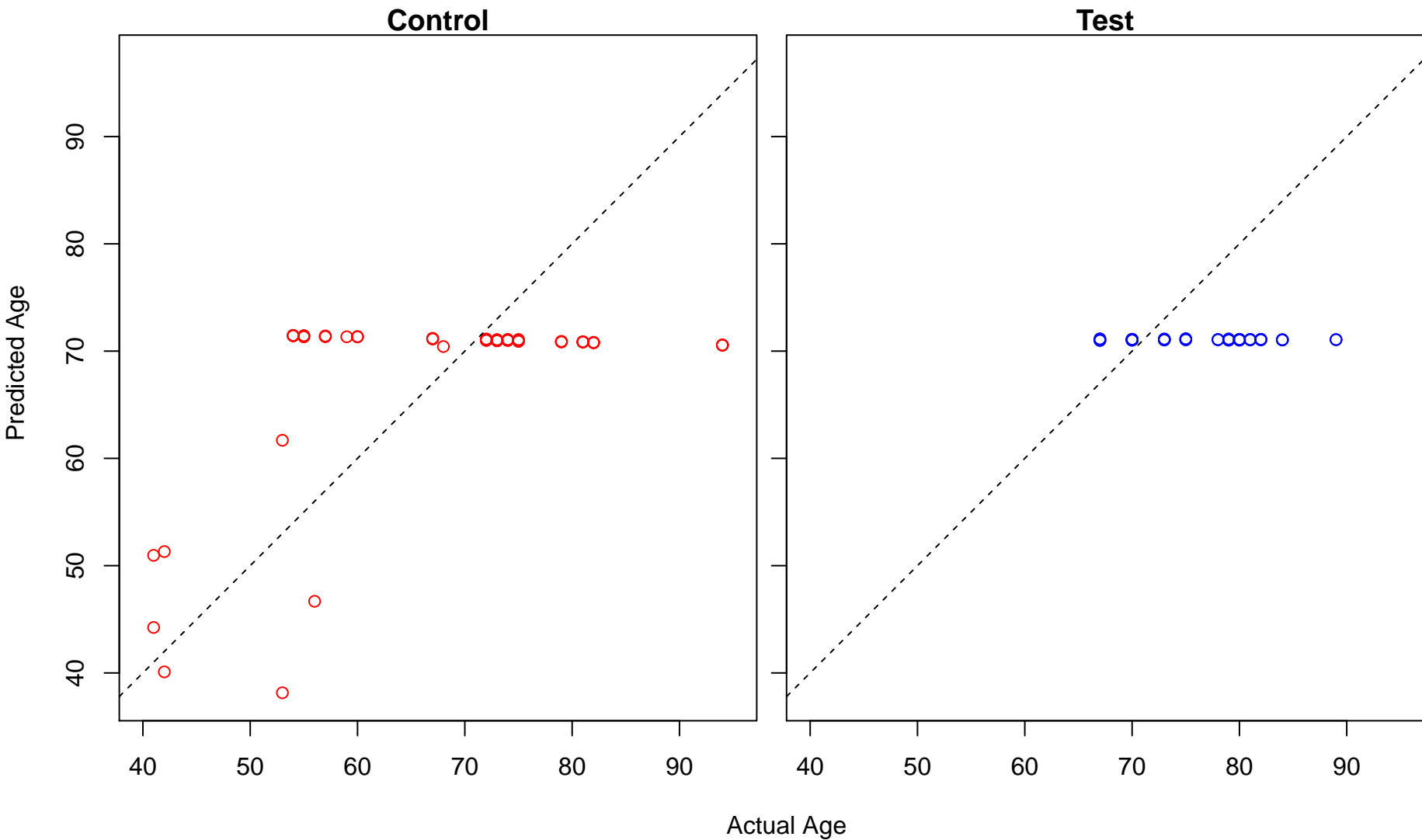


Test

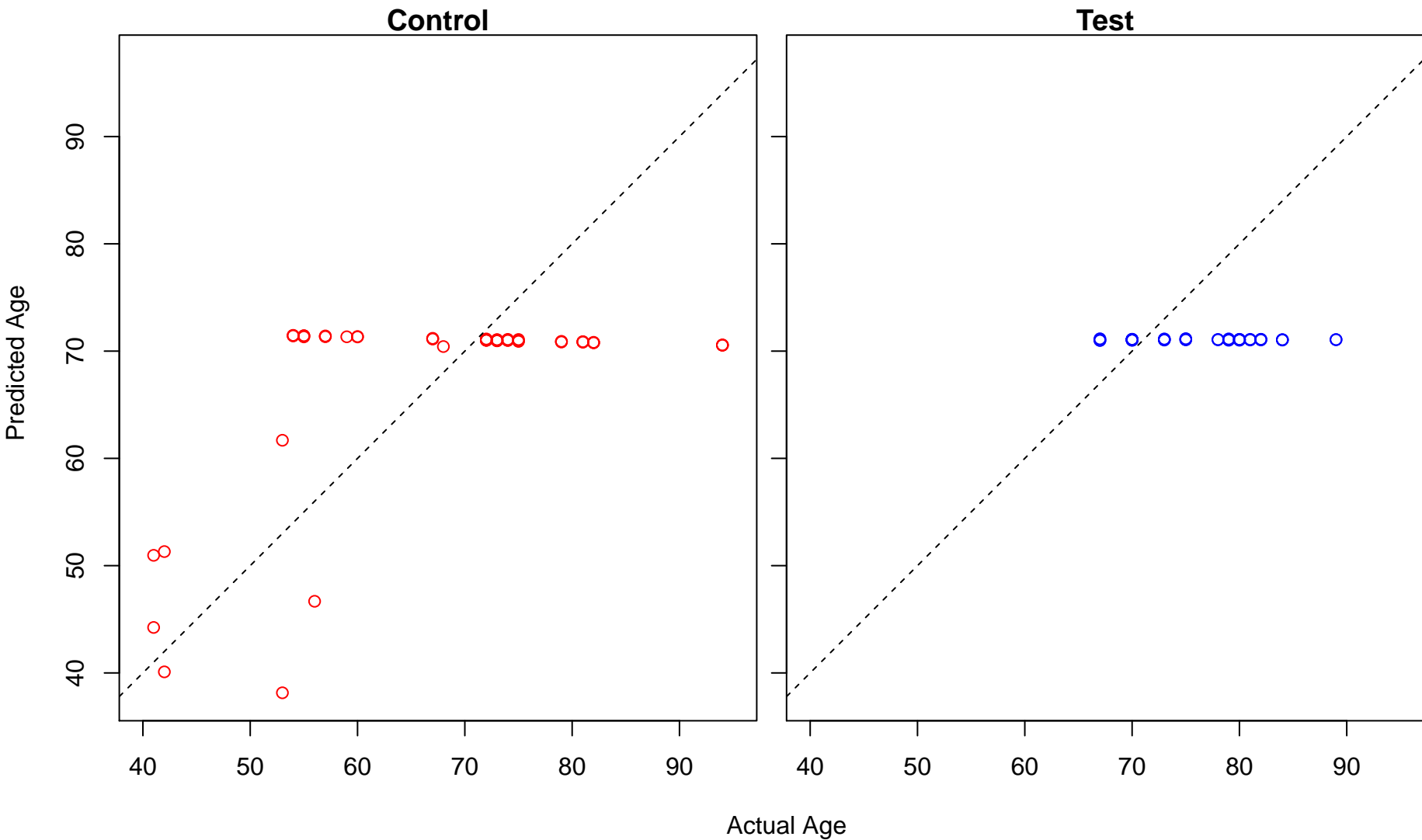


Actual Age

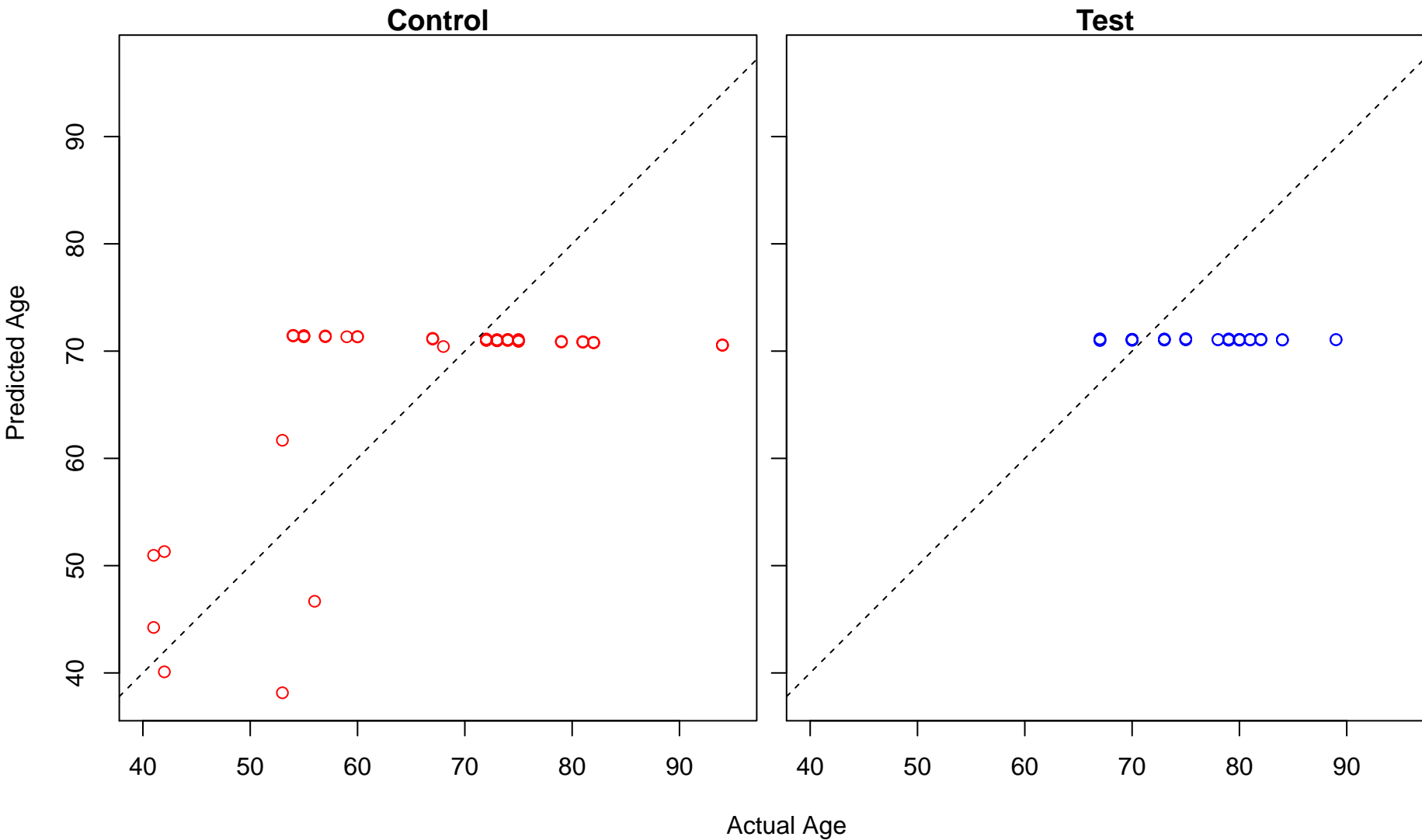
entry into host cell (Score: 0.819011)



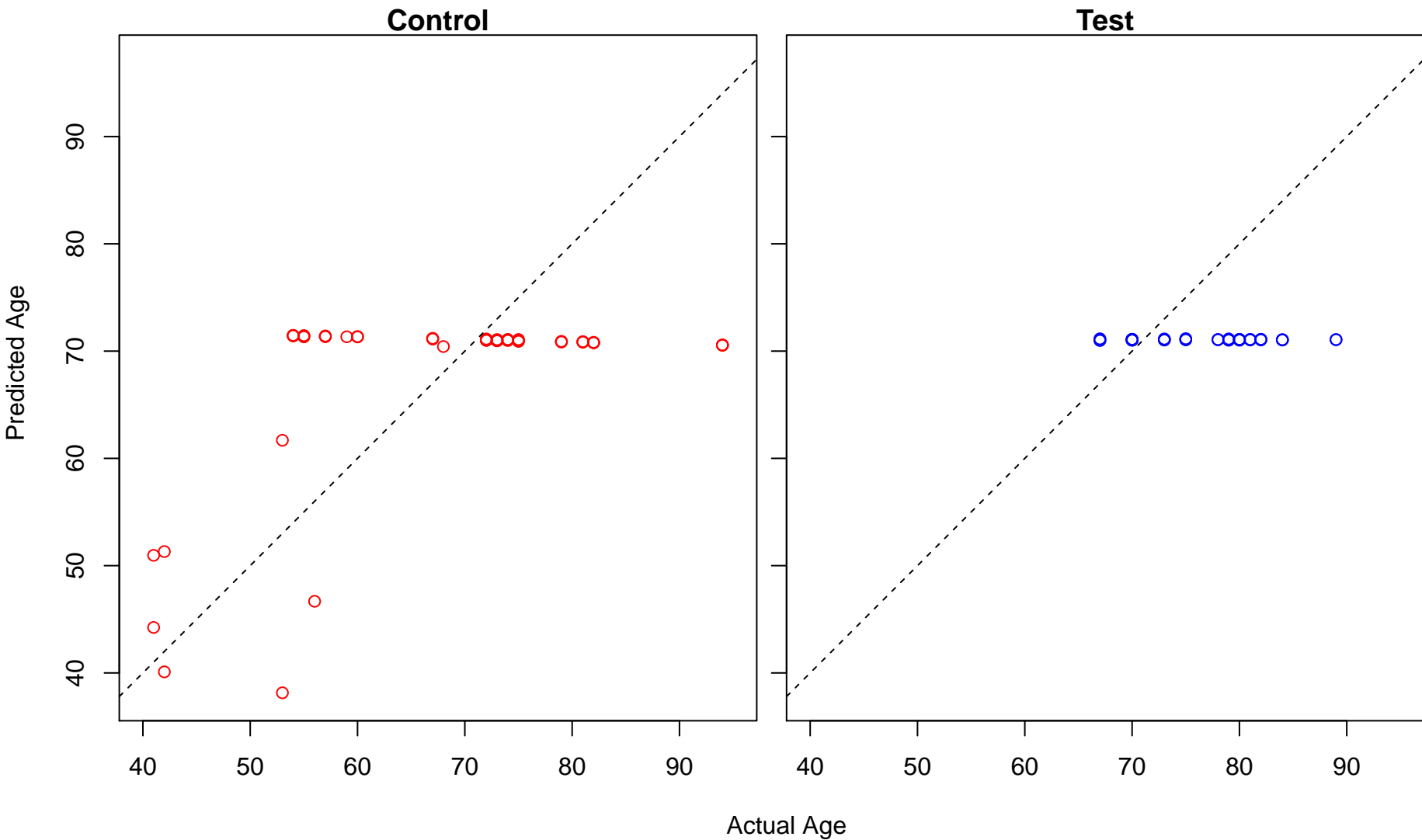
entry into host (Score: 0.819011)



entry into cell of other organism involved in symbiotic interaction (Score: 0.819011)

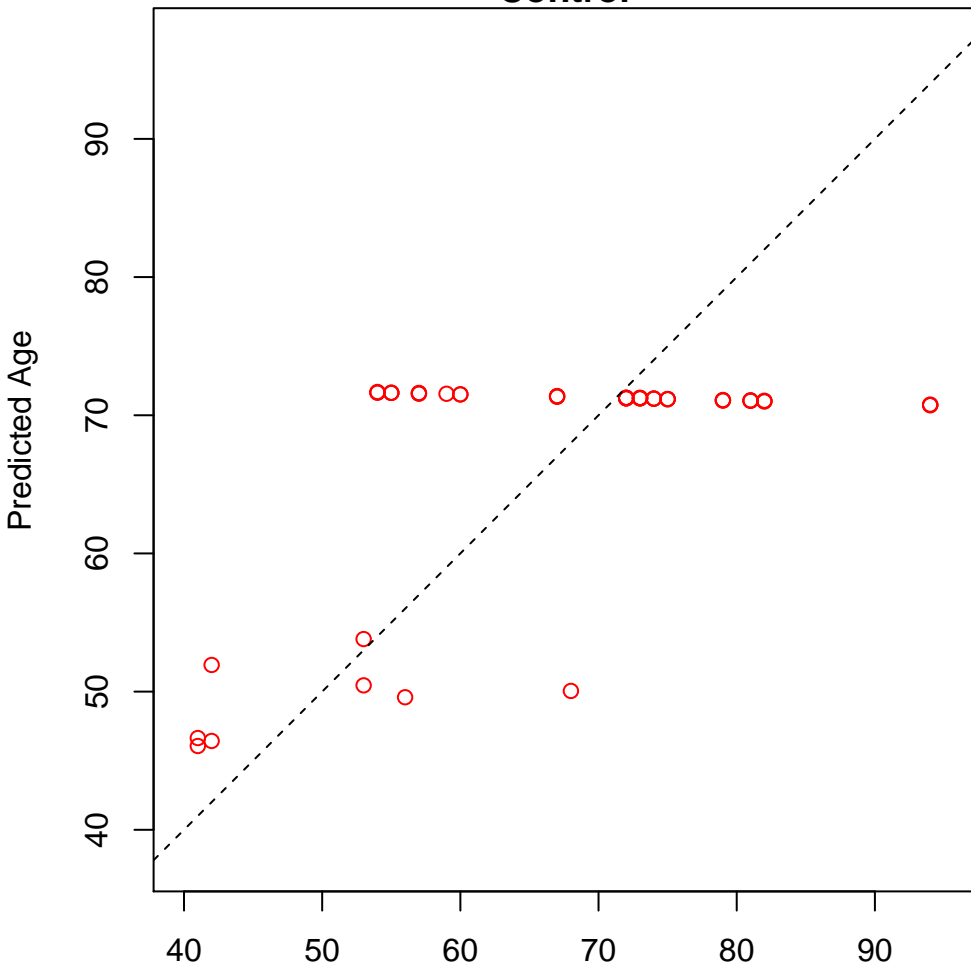


entry into other organism involved in symbiotic interaction (Score: 0.819011)

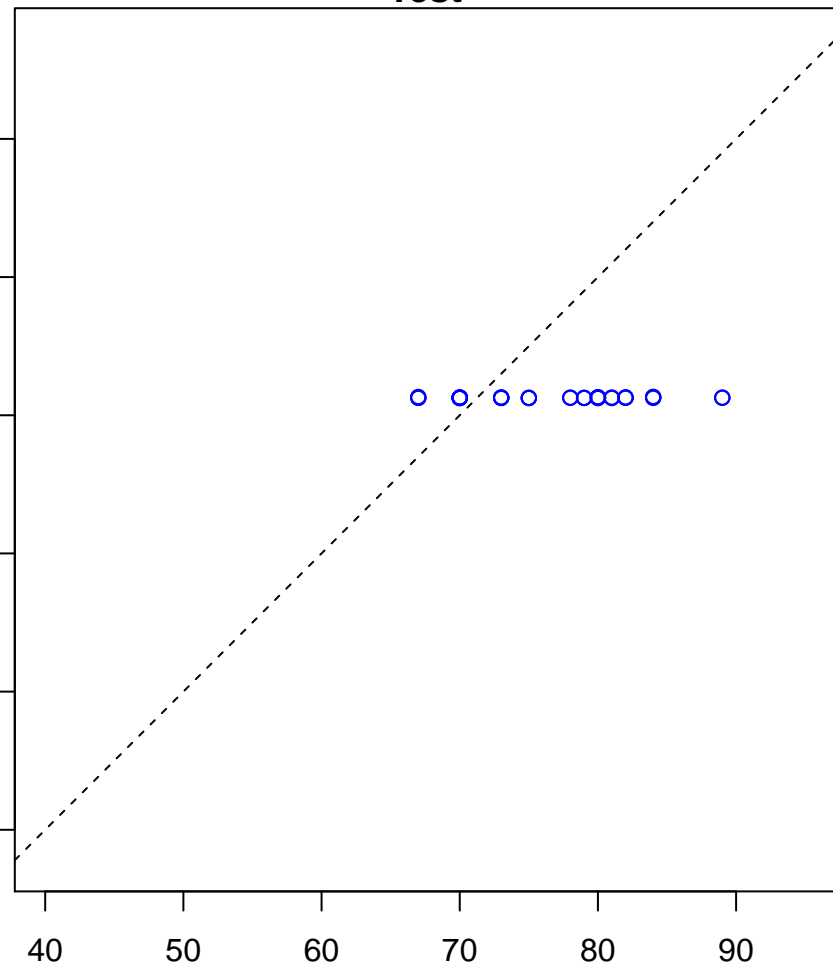


regulation of smooth muscle cell proliferation (Score: 0.818995)

Control

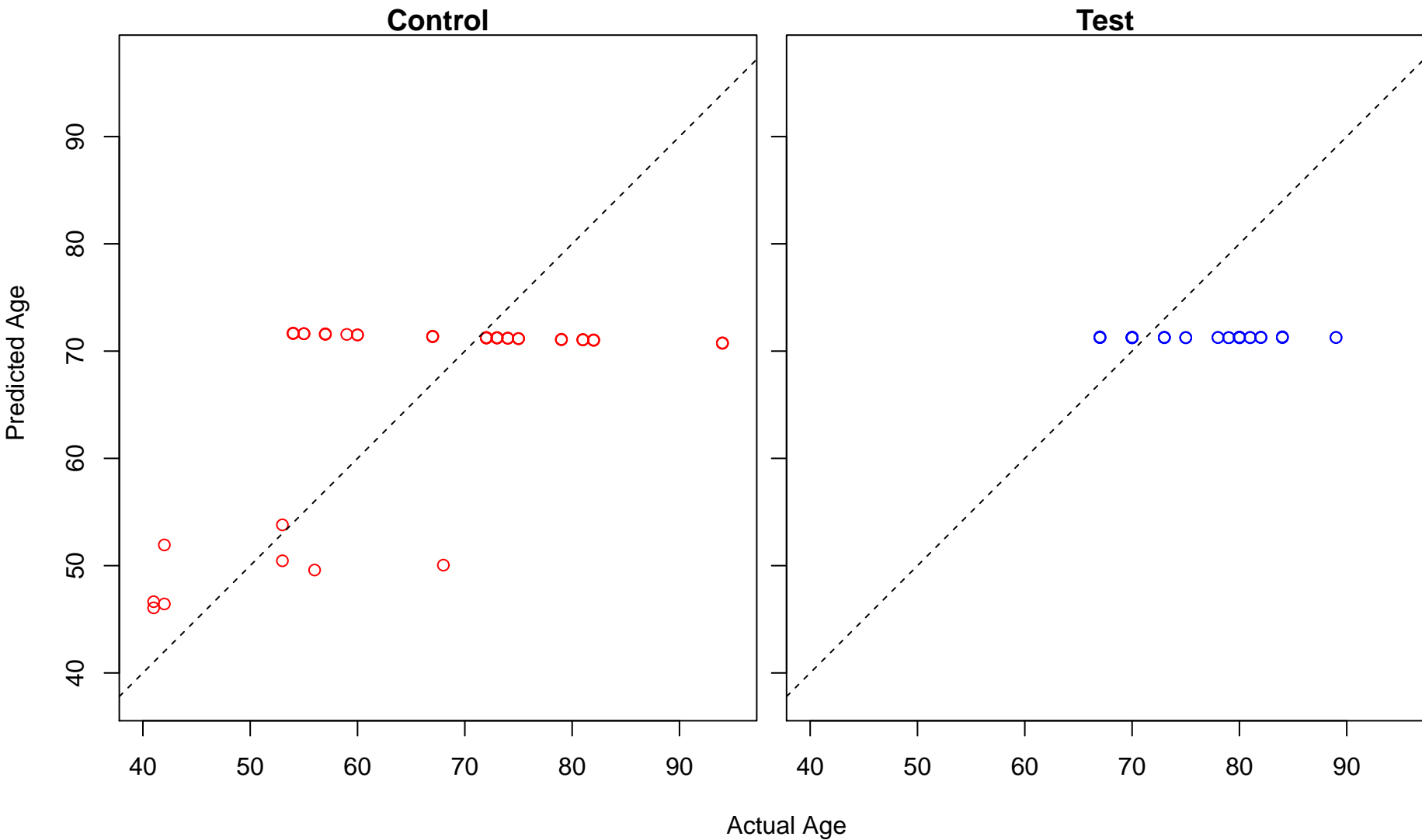


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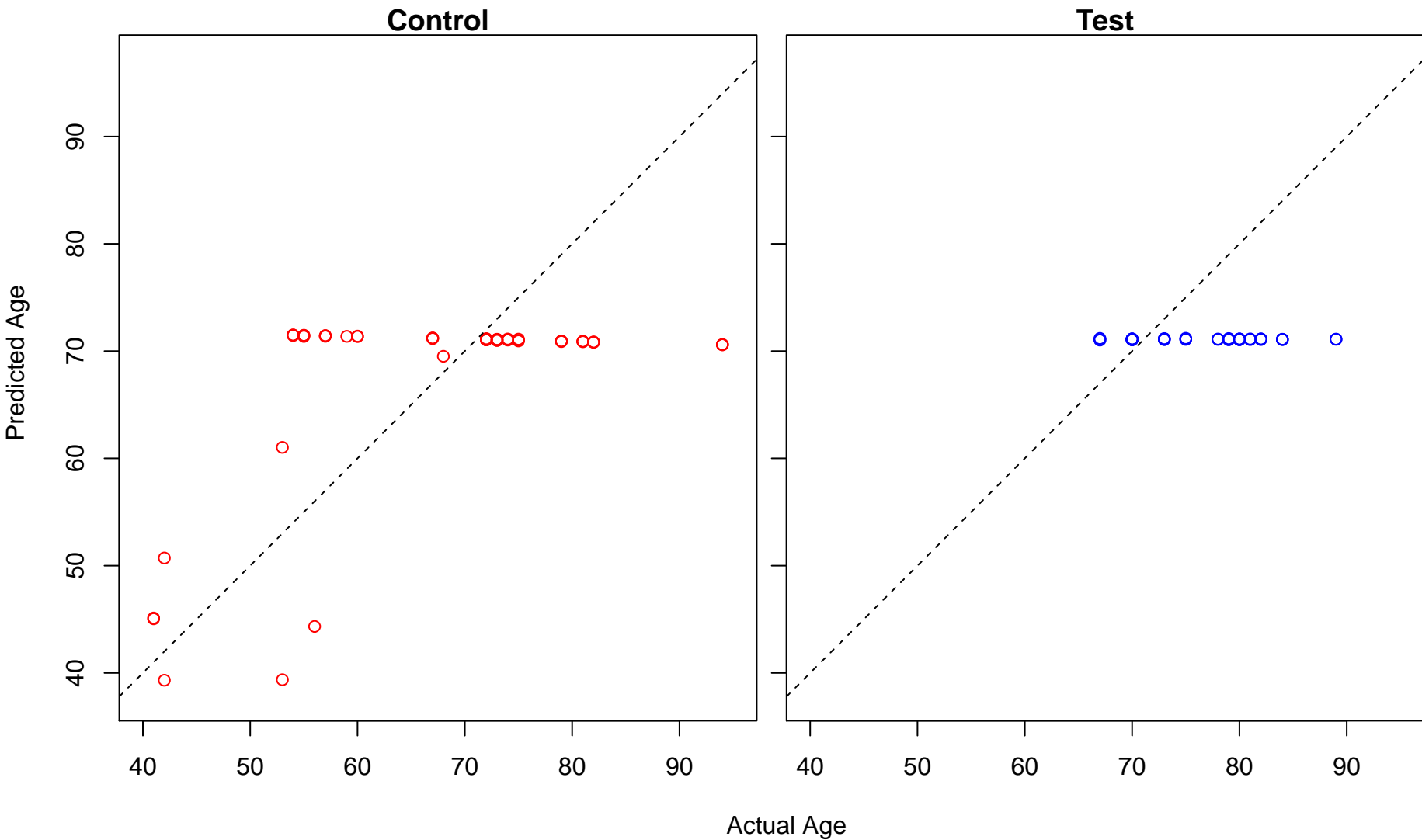


Actual Age

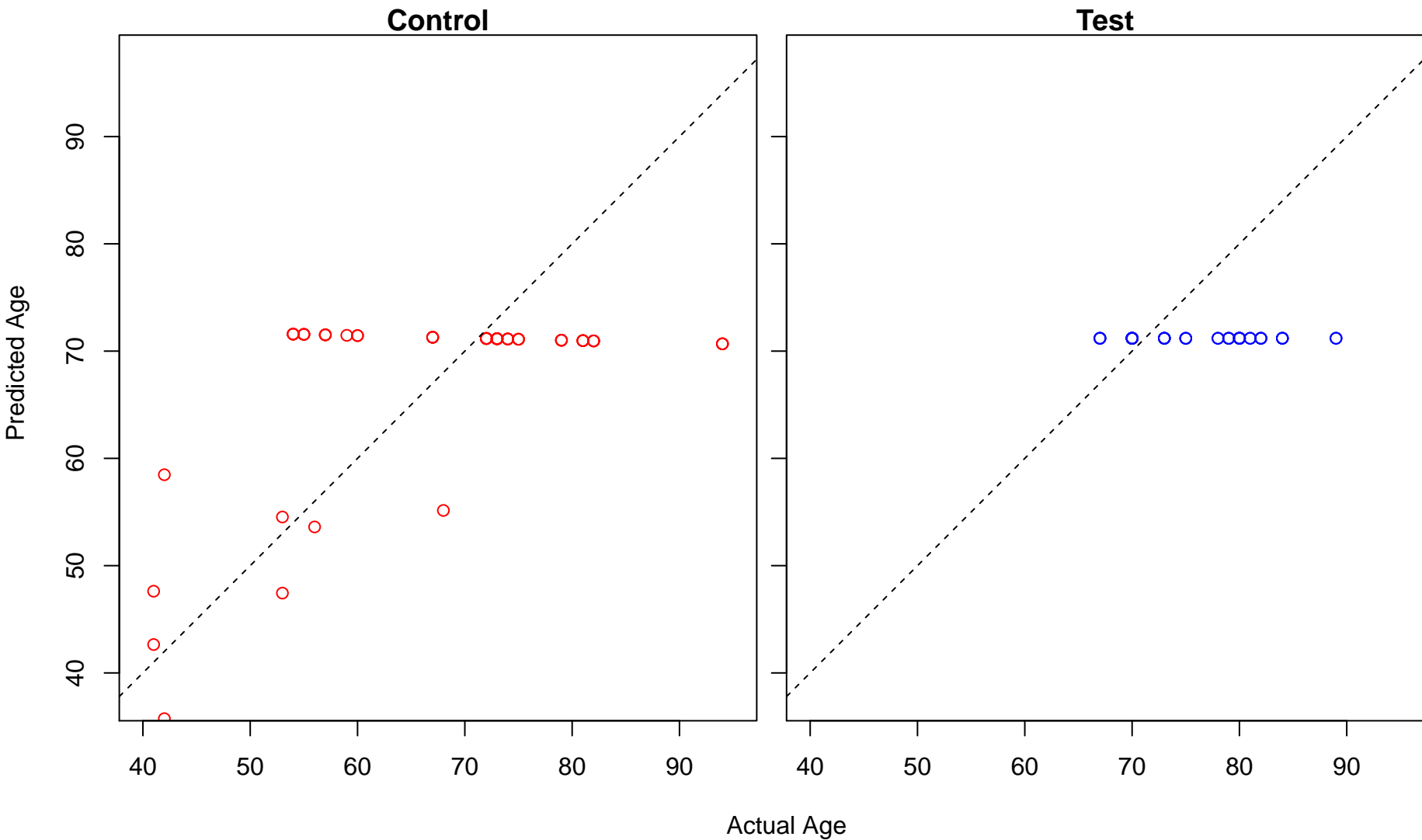
protein tetramerization (Score: 0.818995)



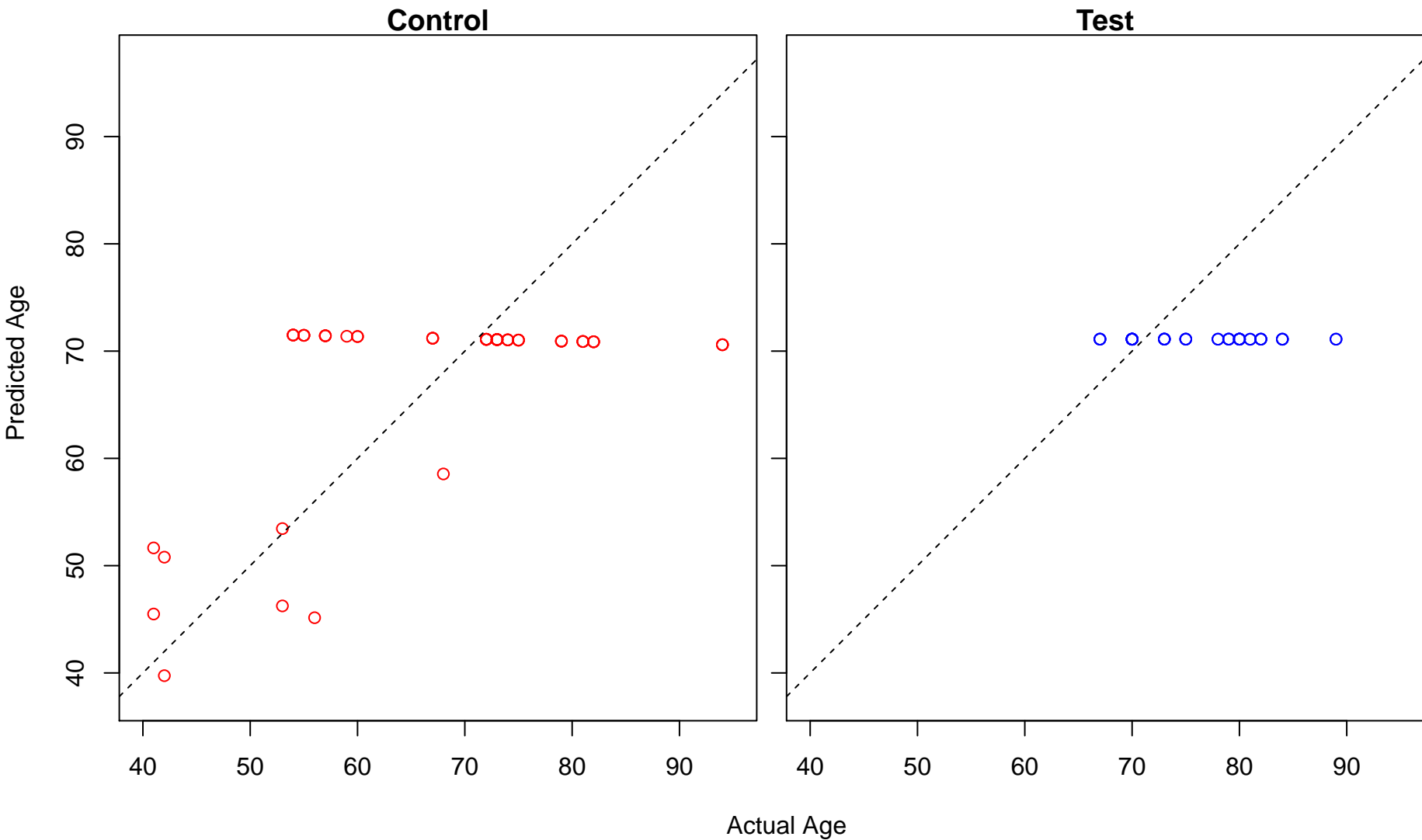
regulation of peptidyl-tyrosine phosphorylation (Score: 0.818993)



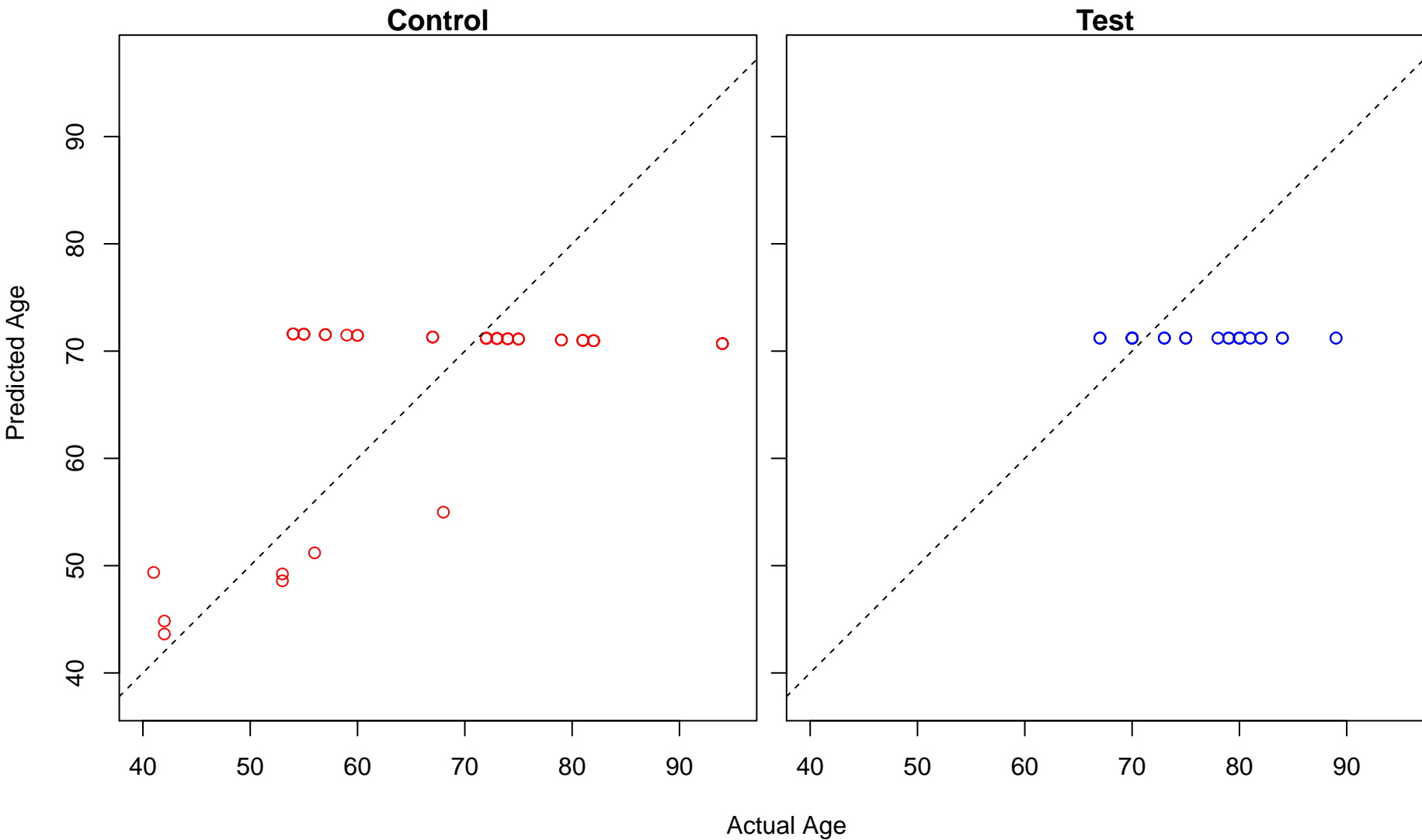
regulation of mitochondrial membrane potential (Score: 0.818913)



cellular response to peptide (Score: 0.818885)

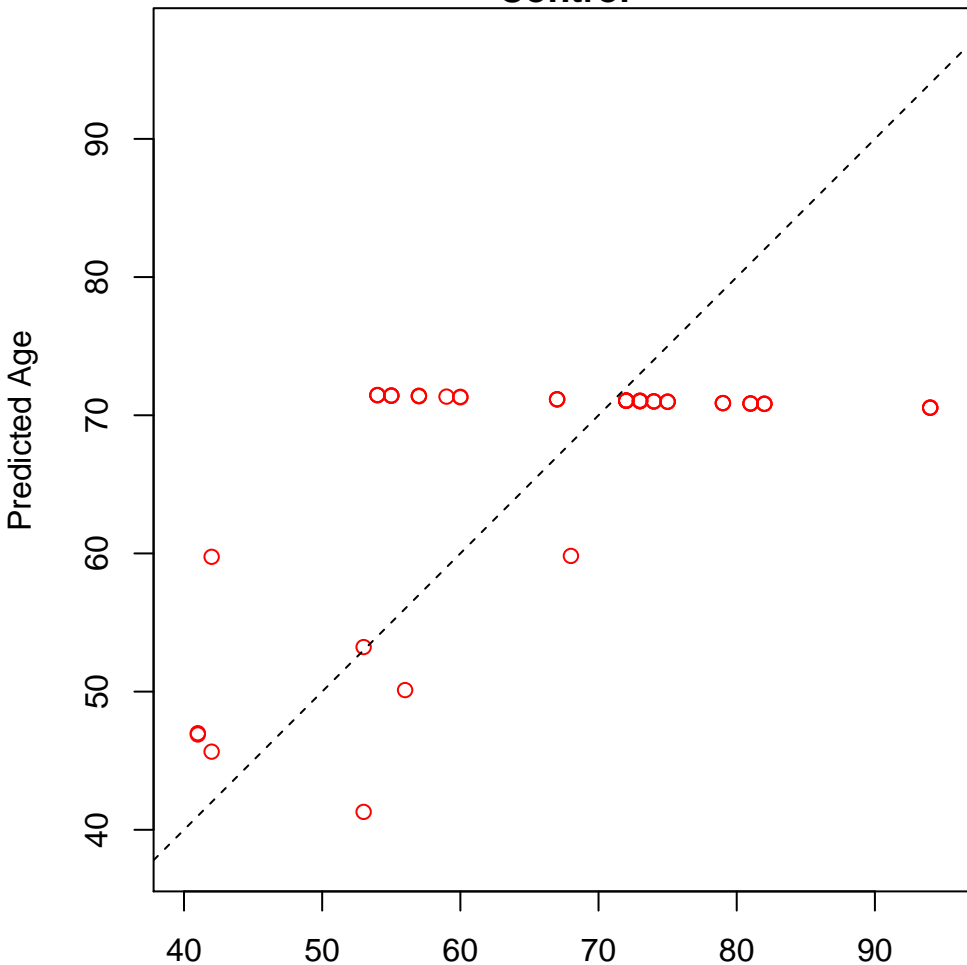


regulation of cytokine production (Score: 0.818701)

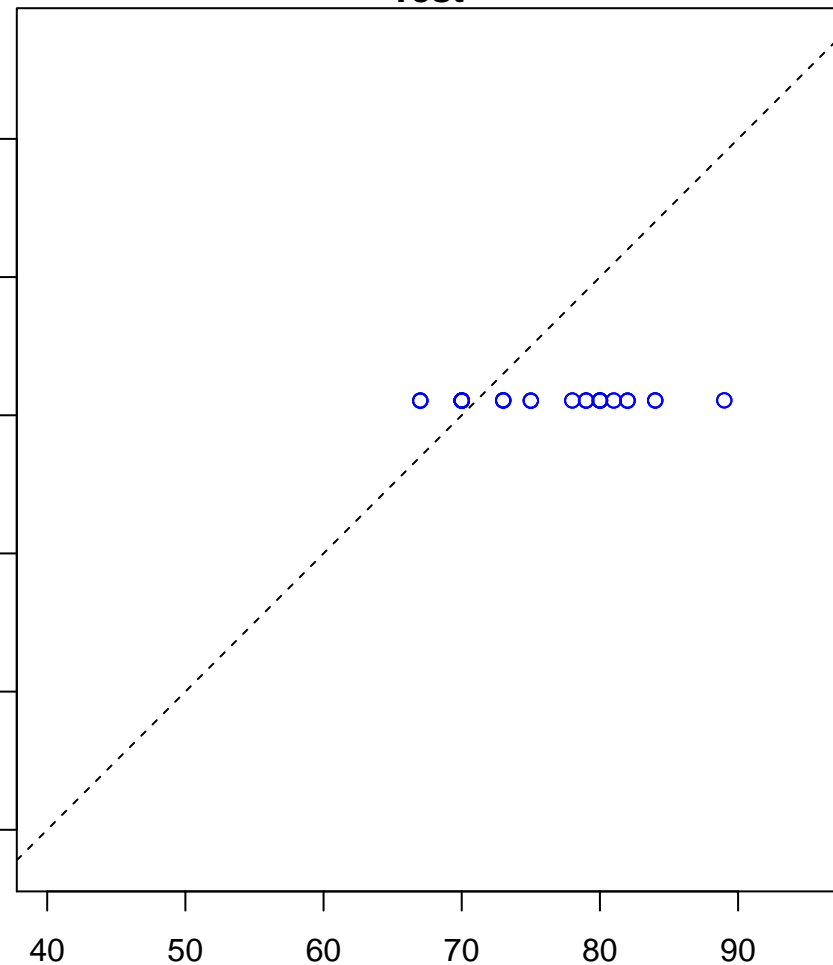


negative regulation of cell differentiation (Score: 0.818624)

Control

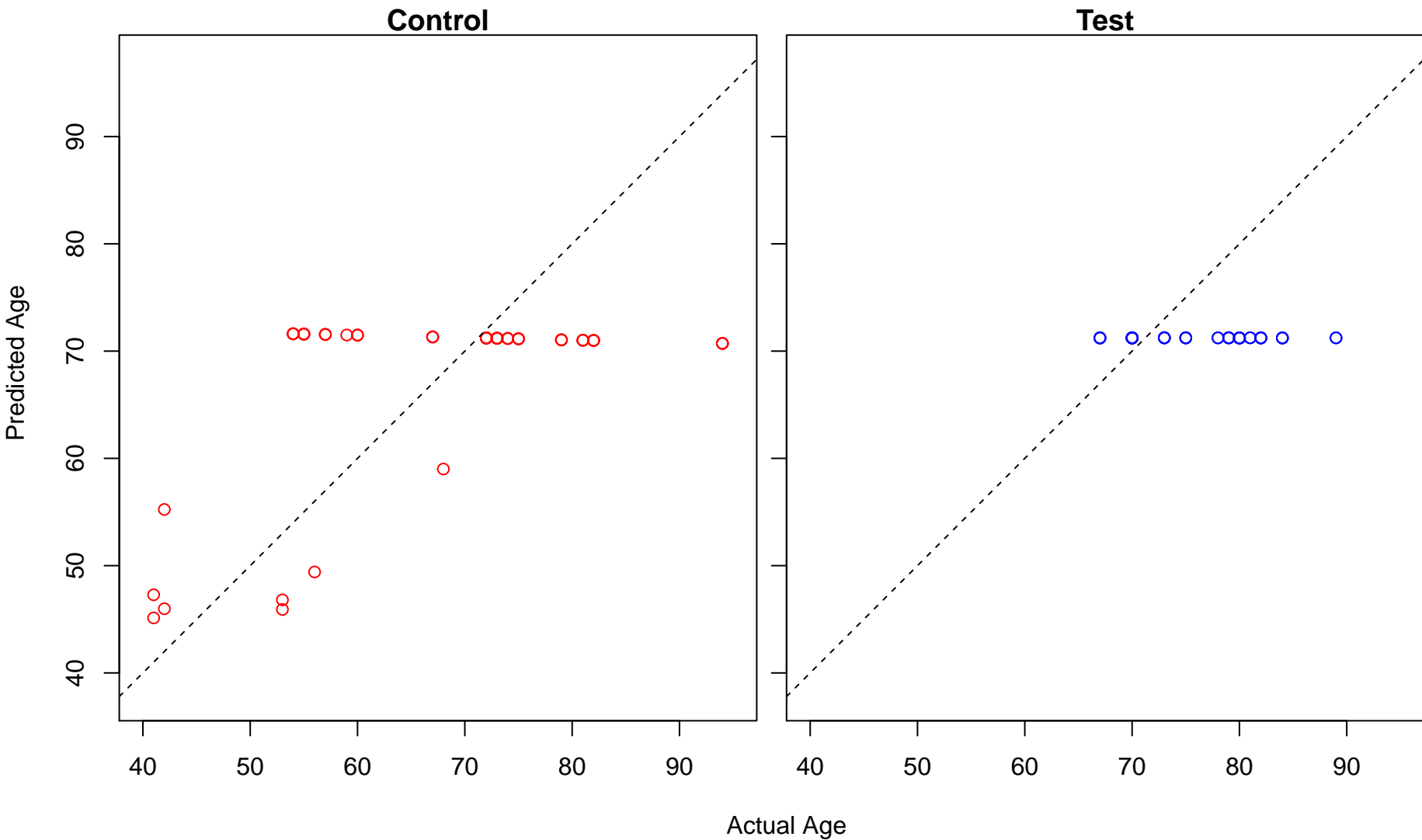


Test

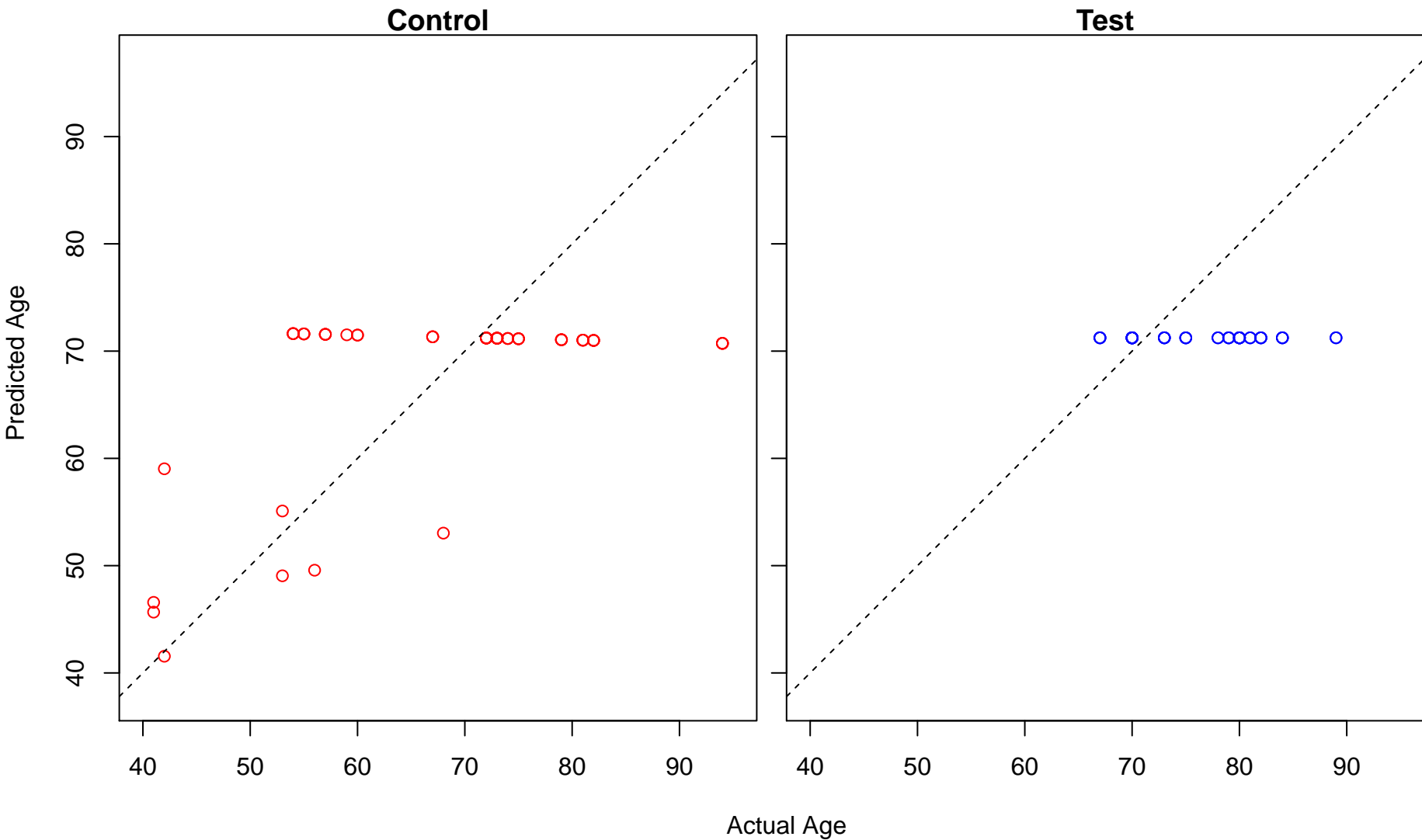


Actual Age

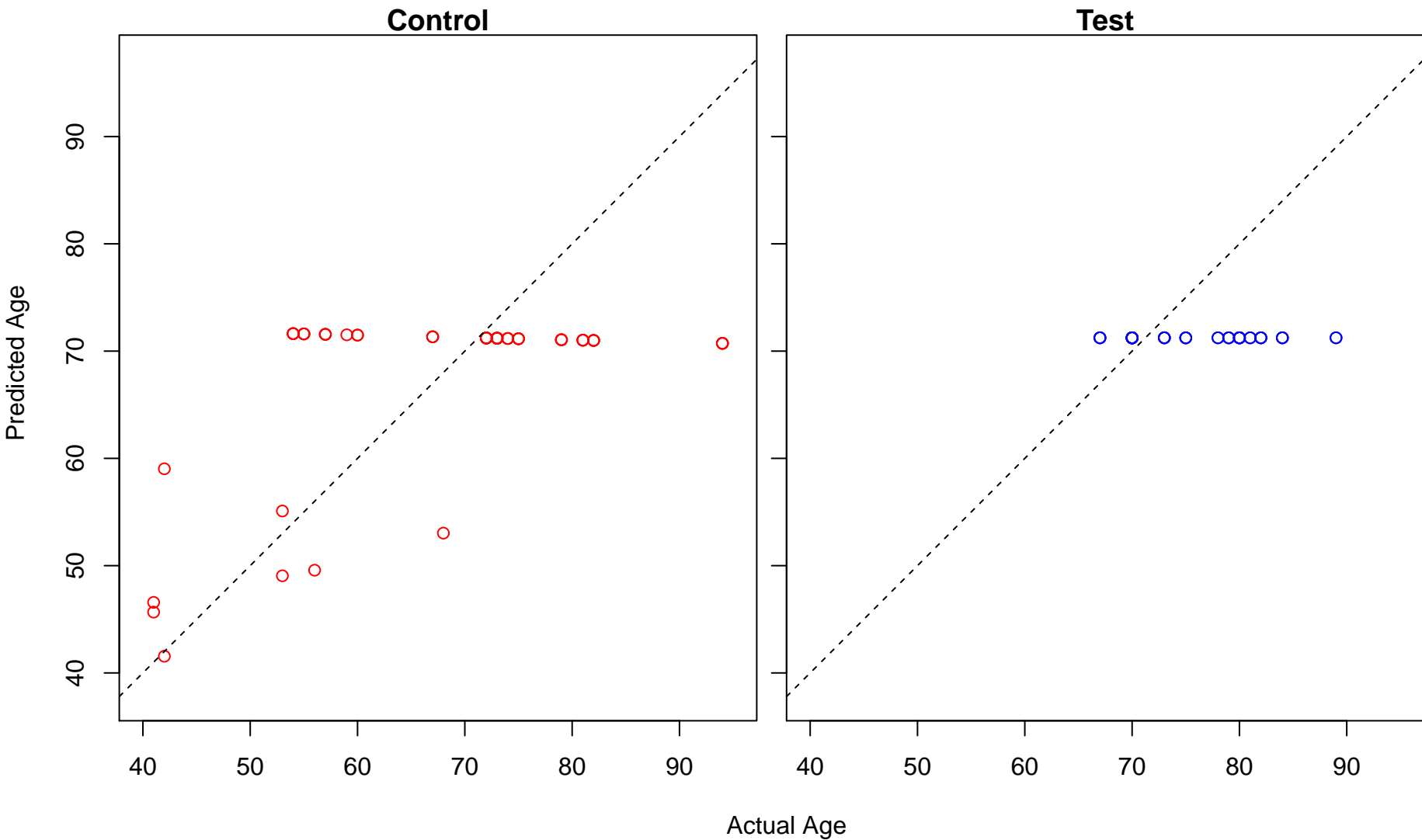
response to carbohydrate (Score: 0.818582)



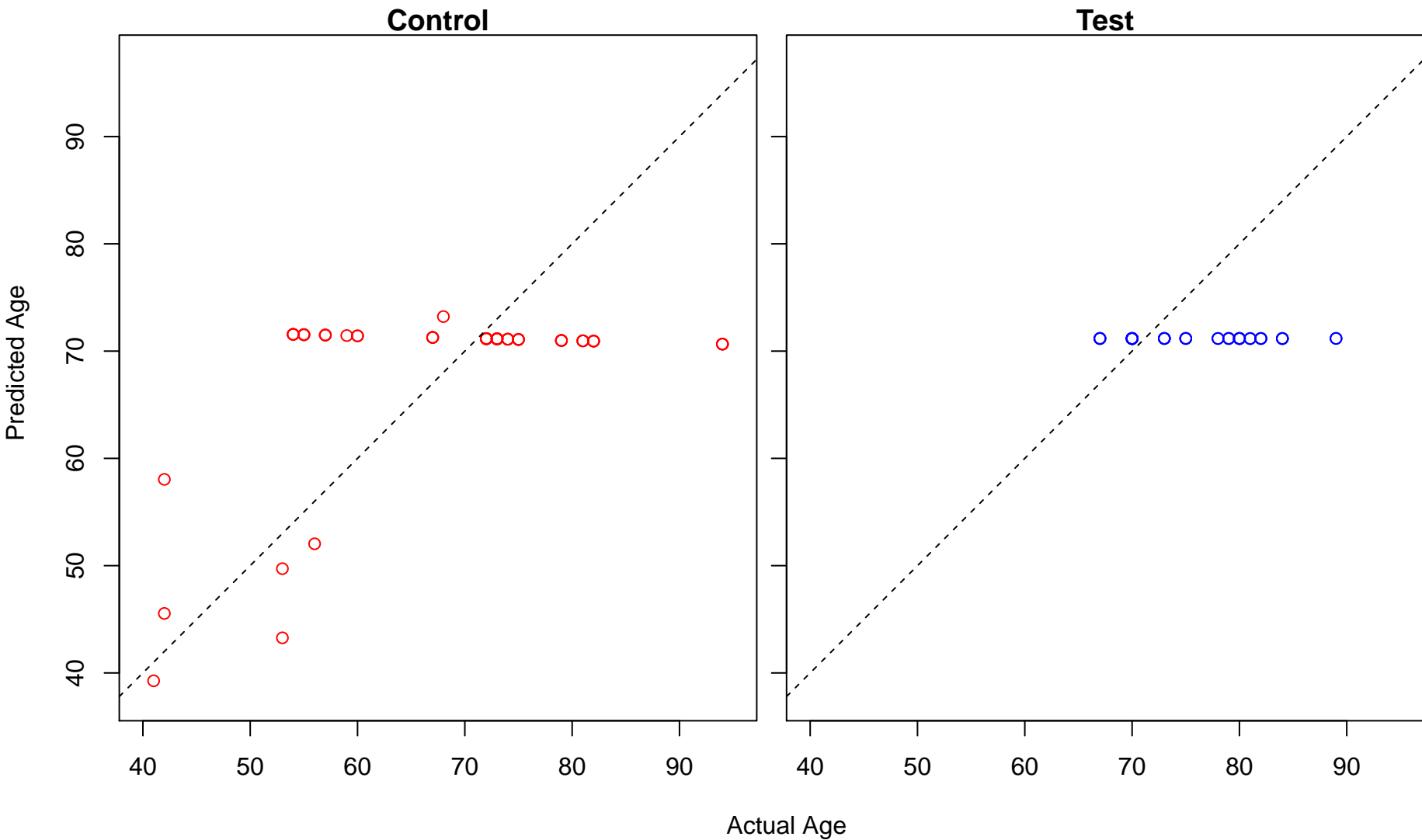
regulation of reactive oxygen species metabolic process (Score: 0.818581)



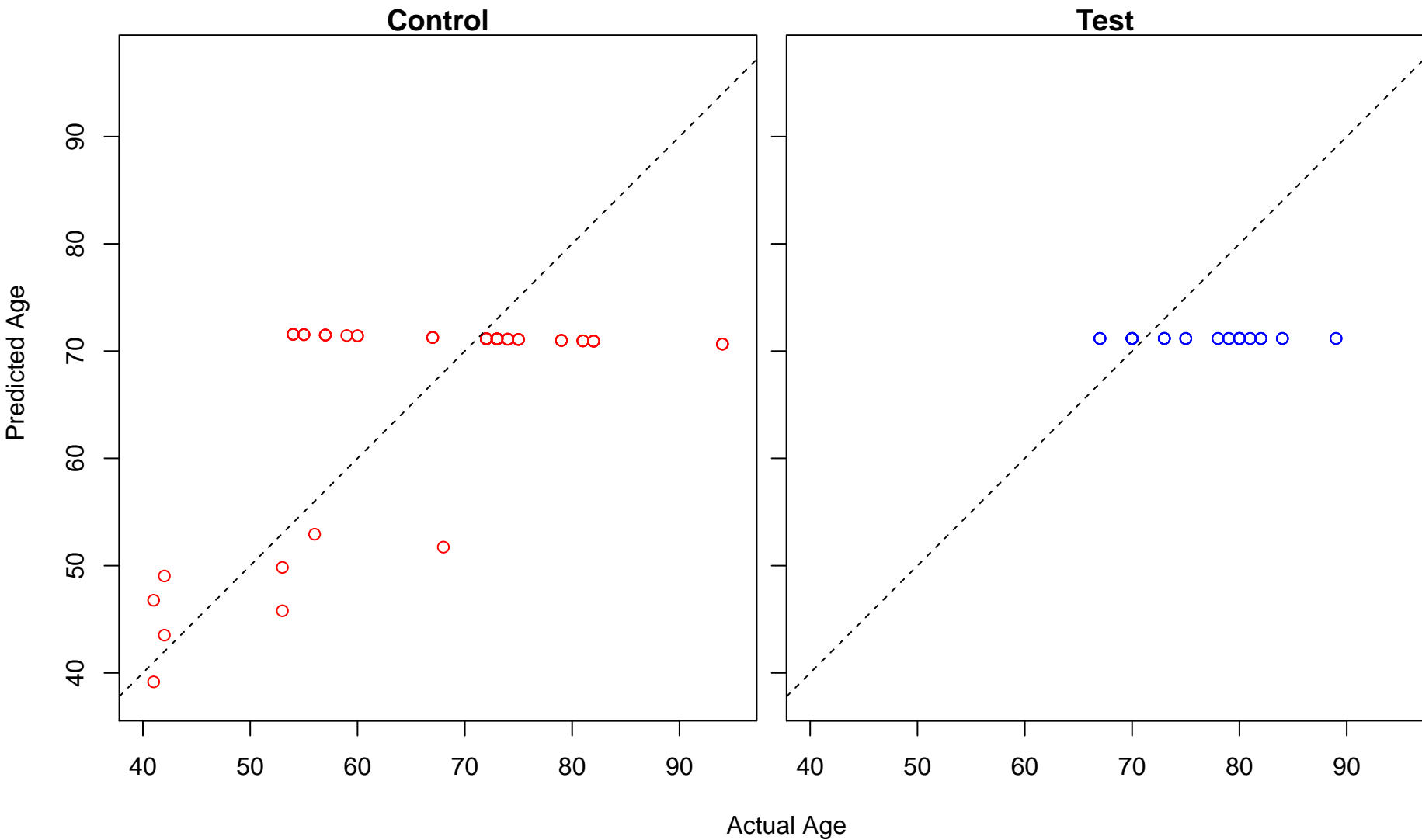
positive regulation of reactive oxygen species metabolic process (Score: 0.818581)



cell cycle phase transition (Score: 0.818560)

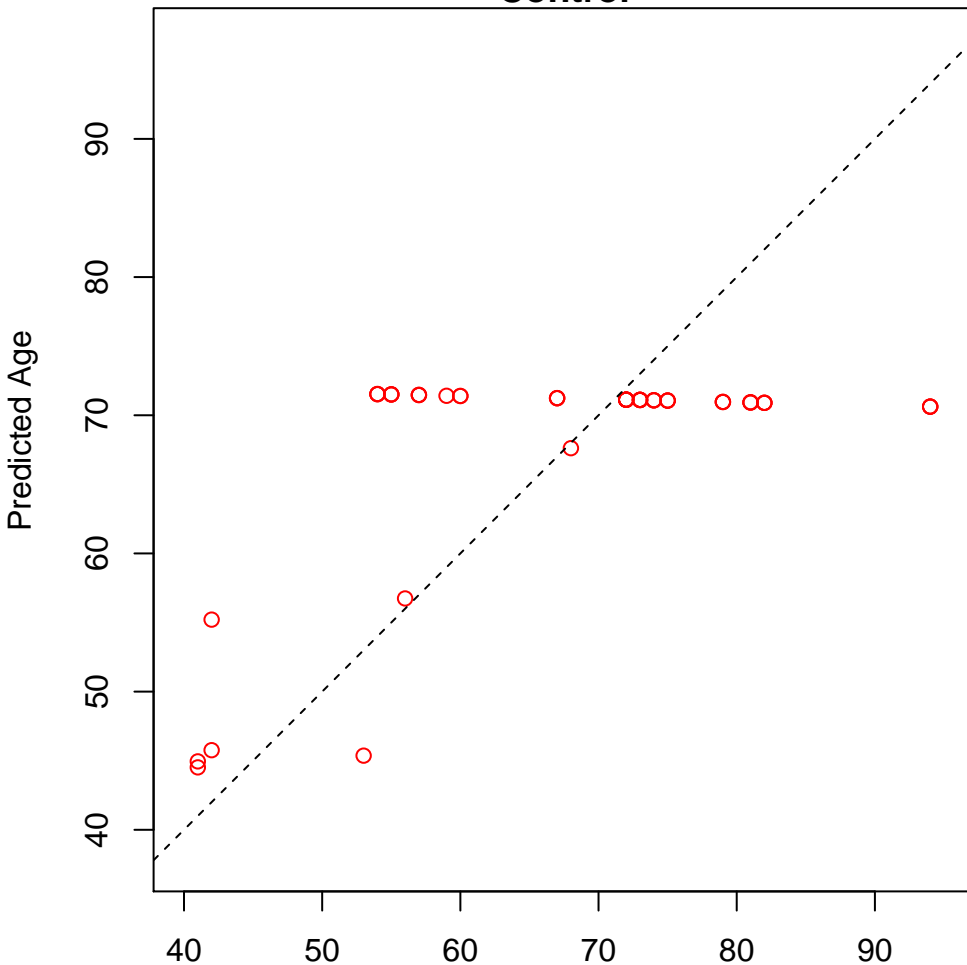


negative regulation of cellular protein metabolic process (Score: 0.818541)

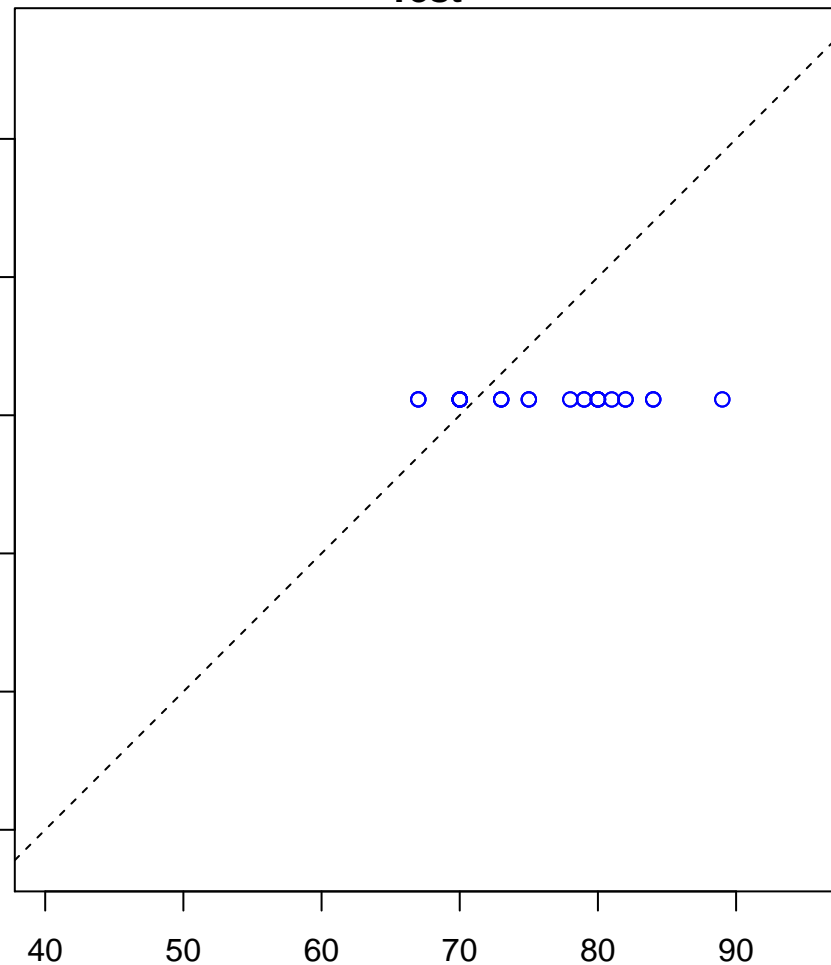


regulation of inflammatory response (Score: 0.818483)

Control



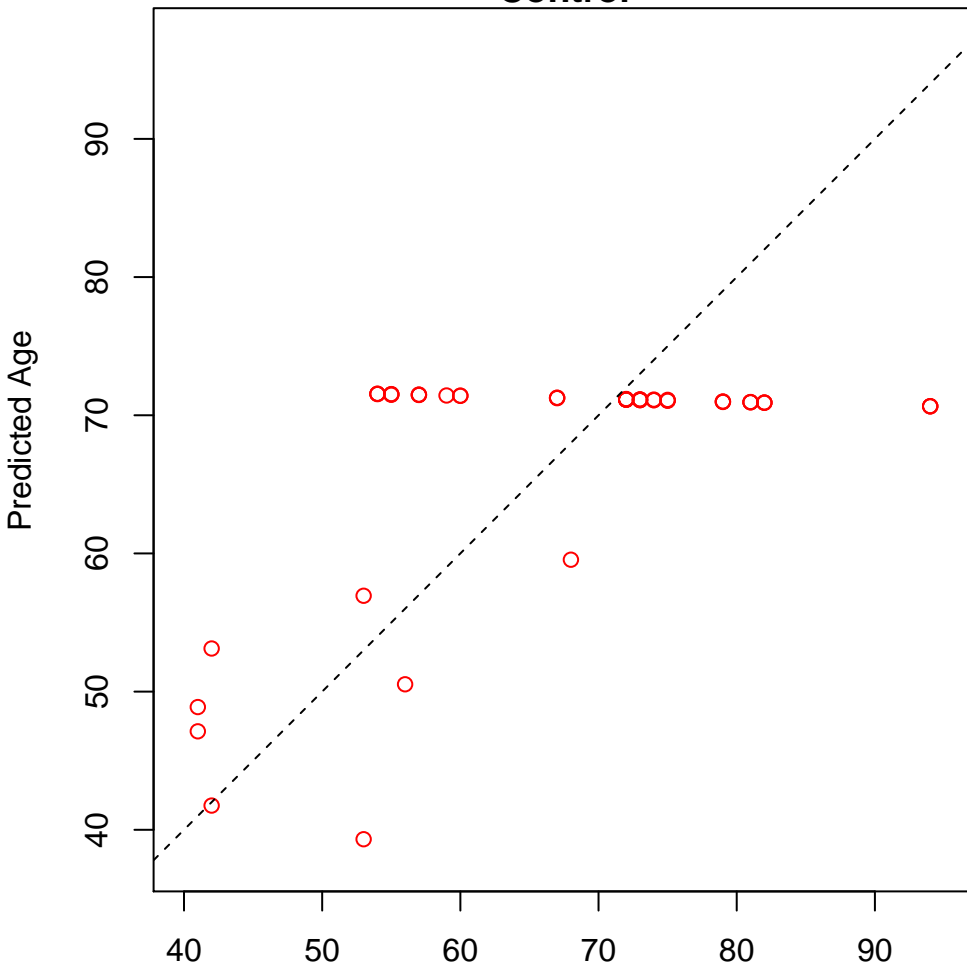
Test



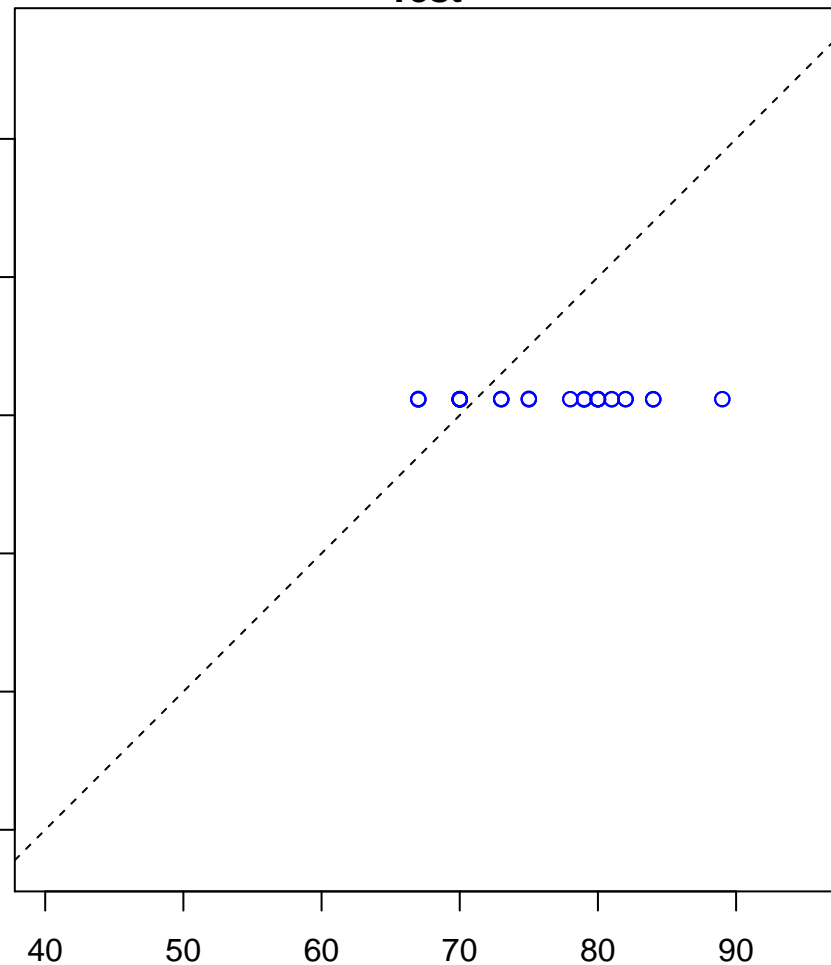
Actual Age

calcium ion transmembrane transport (Score: 0.818443)

Control



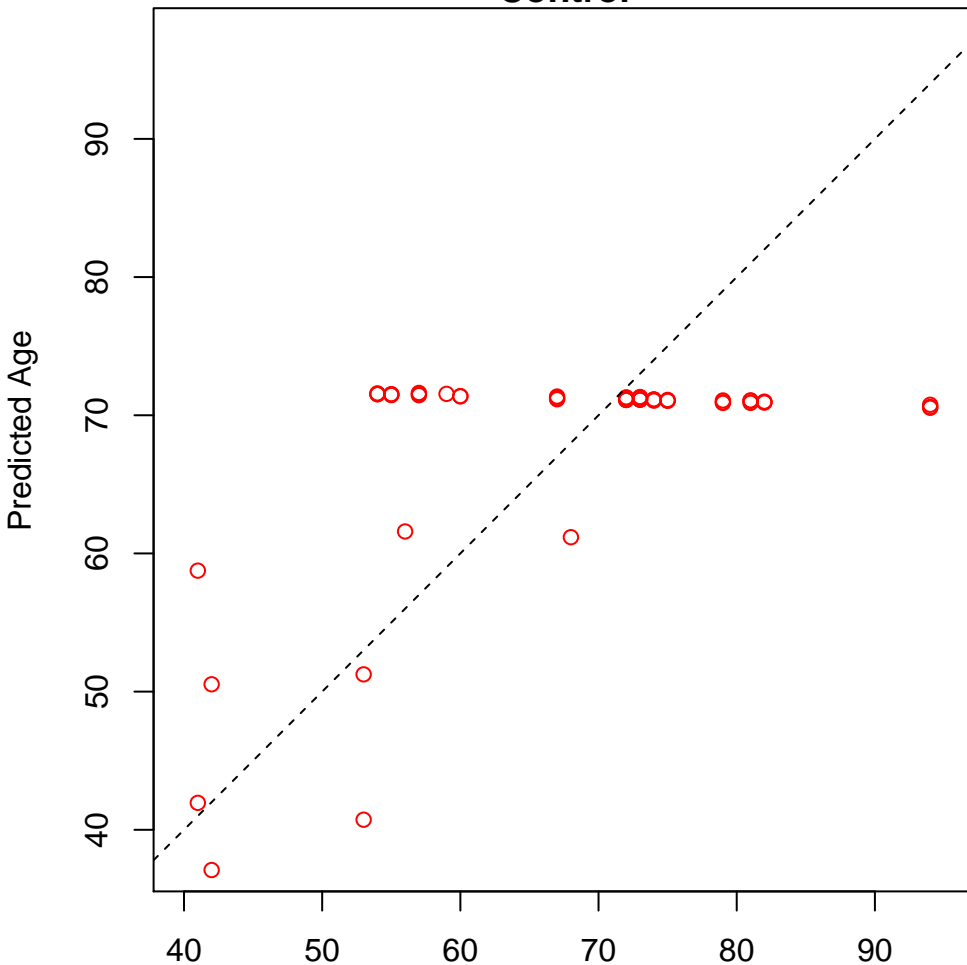
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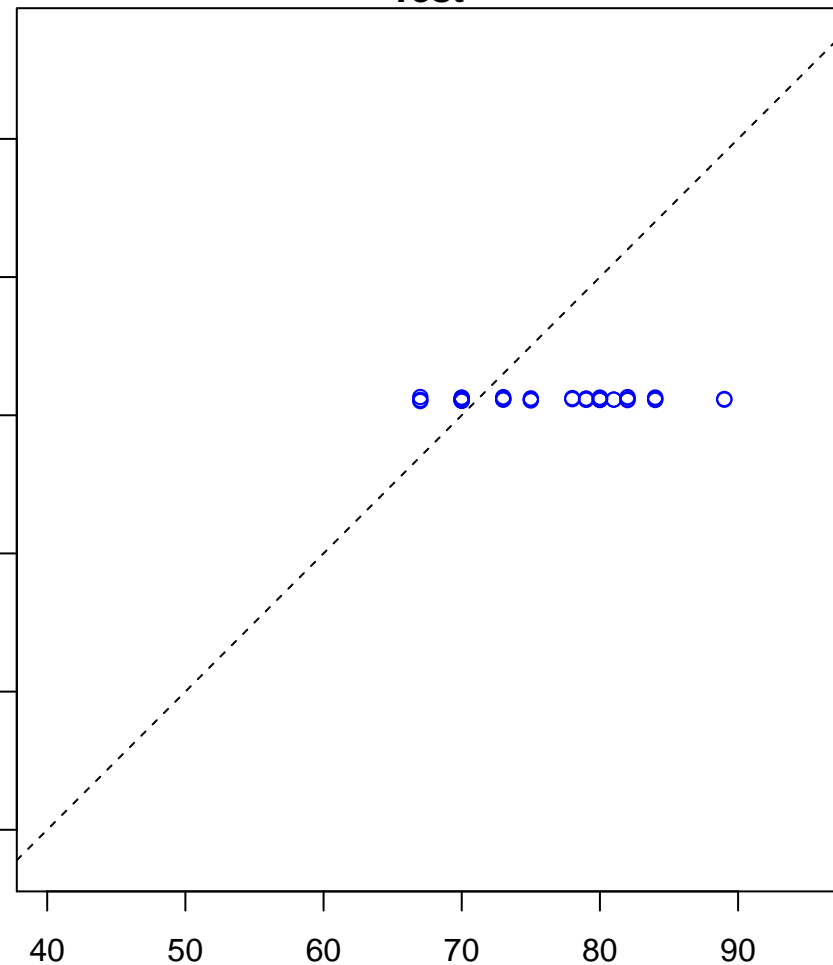
Actual Age

central nervous system development (Score: 0.818443)

Control



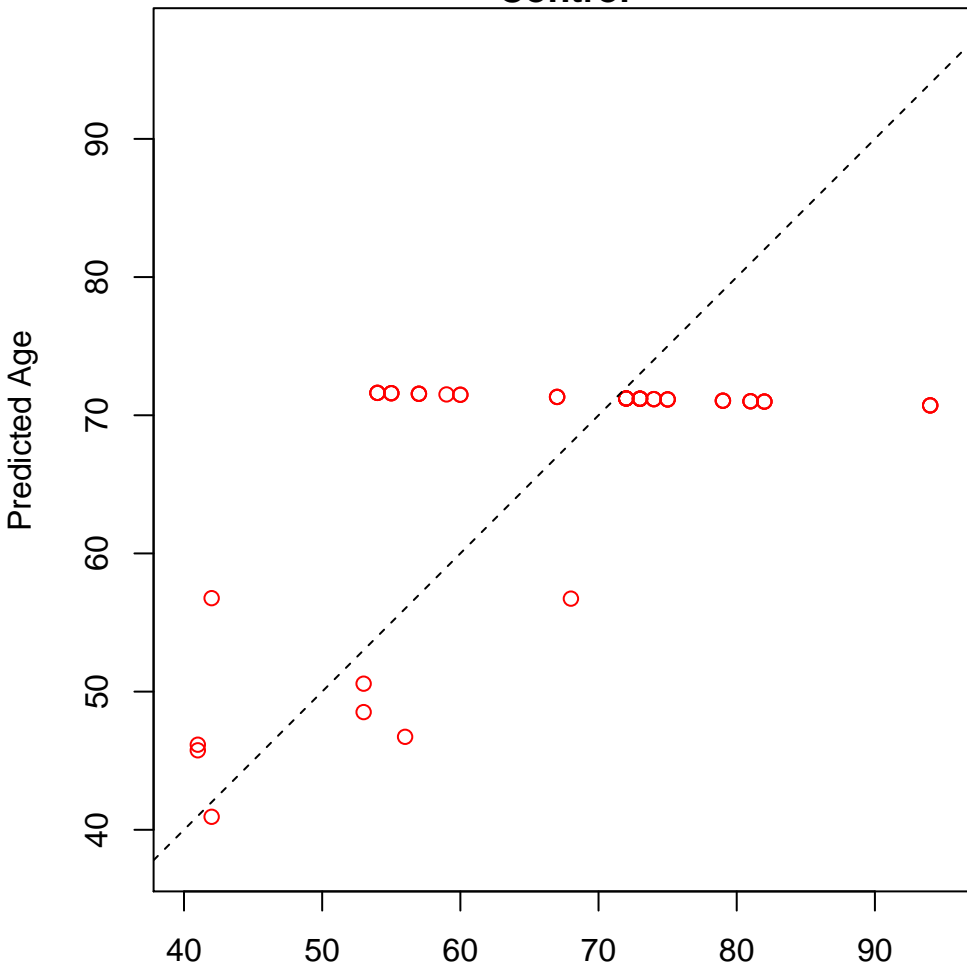
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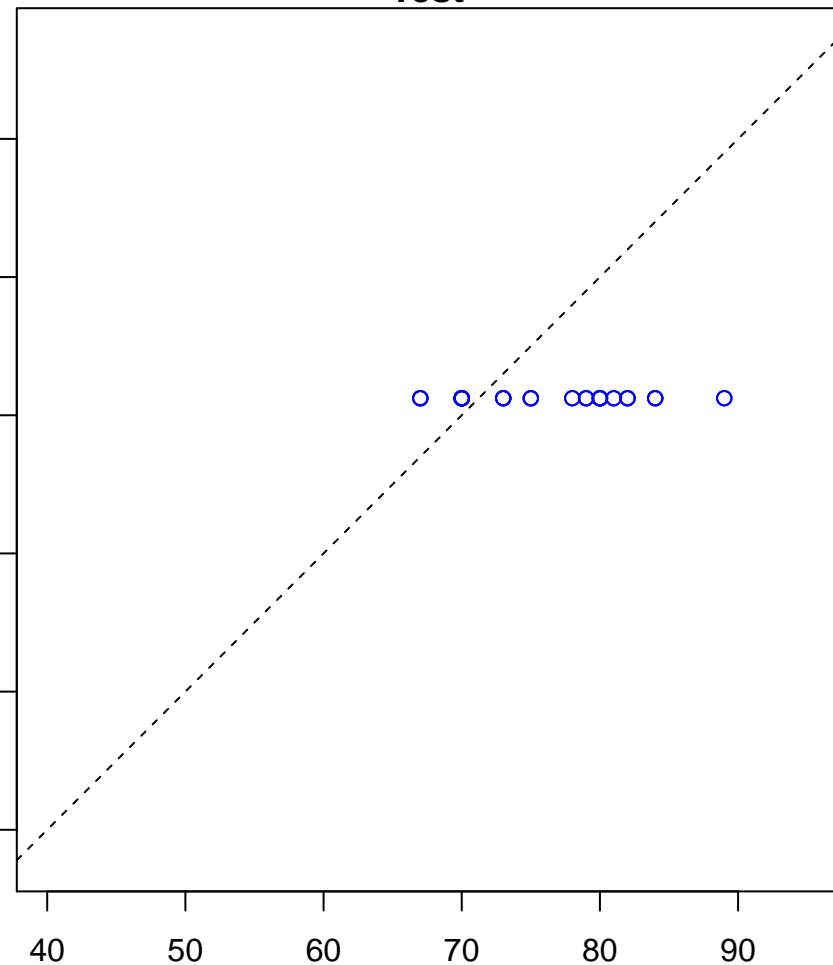
Actual Age

regulation of membrane potential (Score: 0.818389)

Control

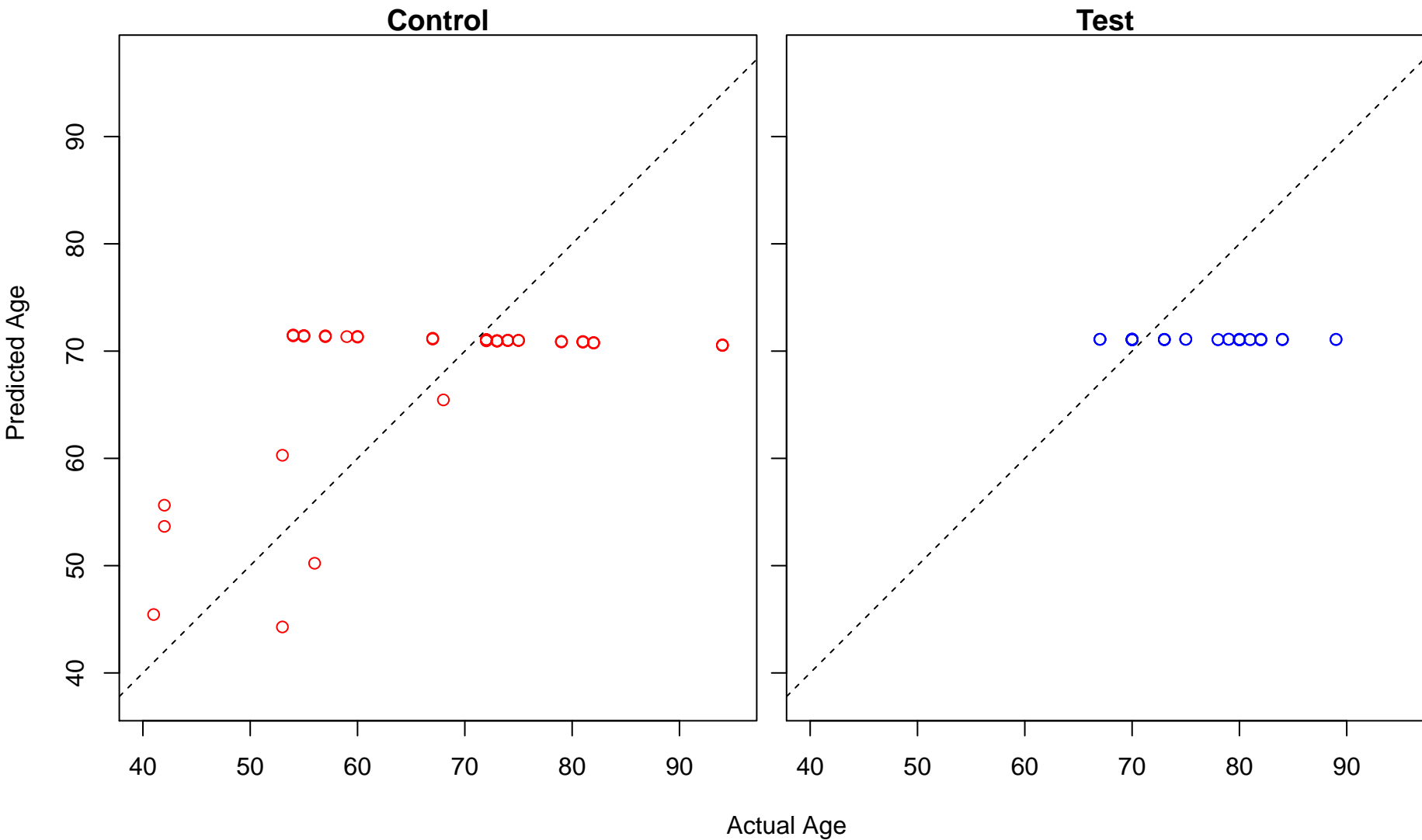


Test

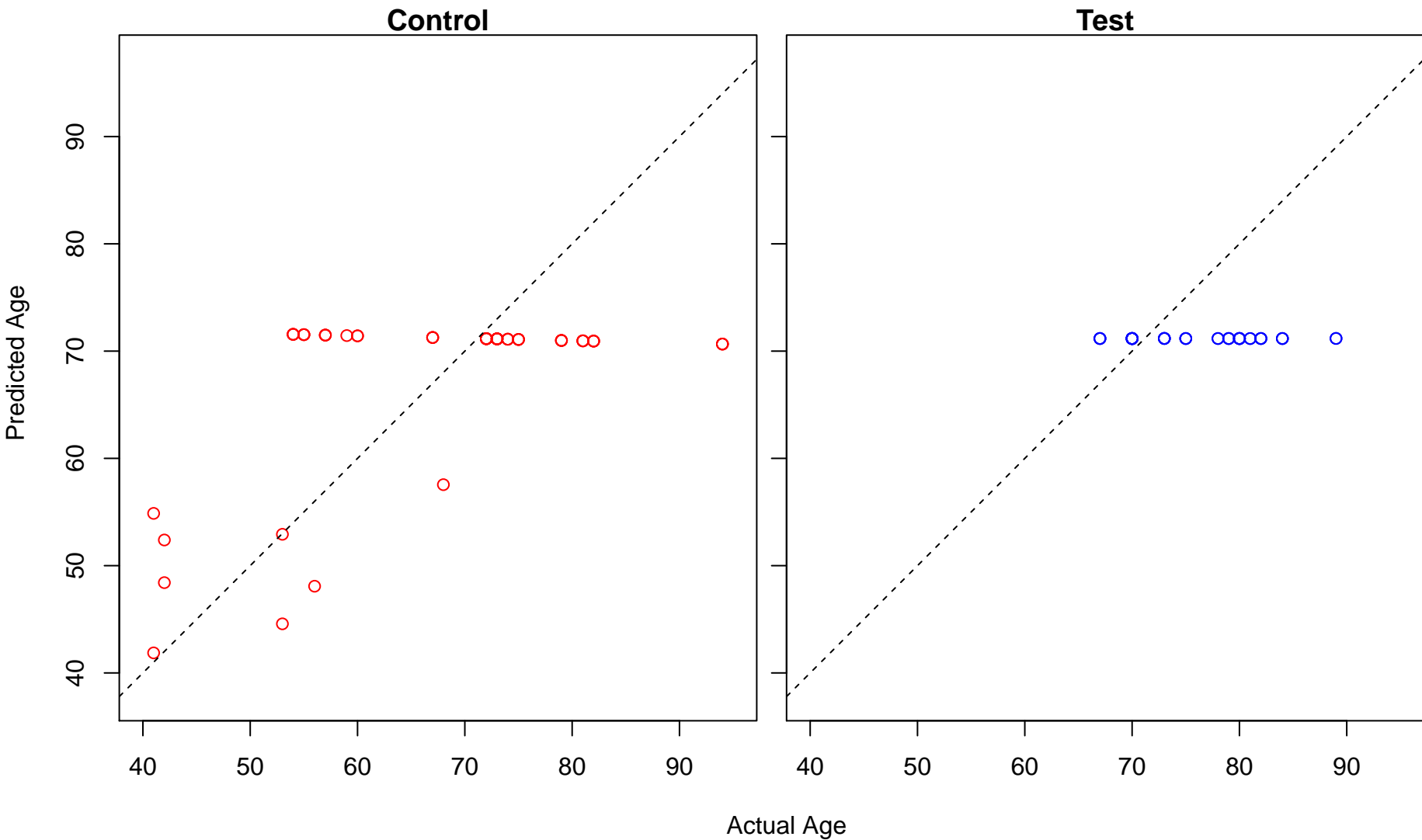


Actual Age

positive regulation of cytoskeleton organization (Score: 0.818366)

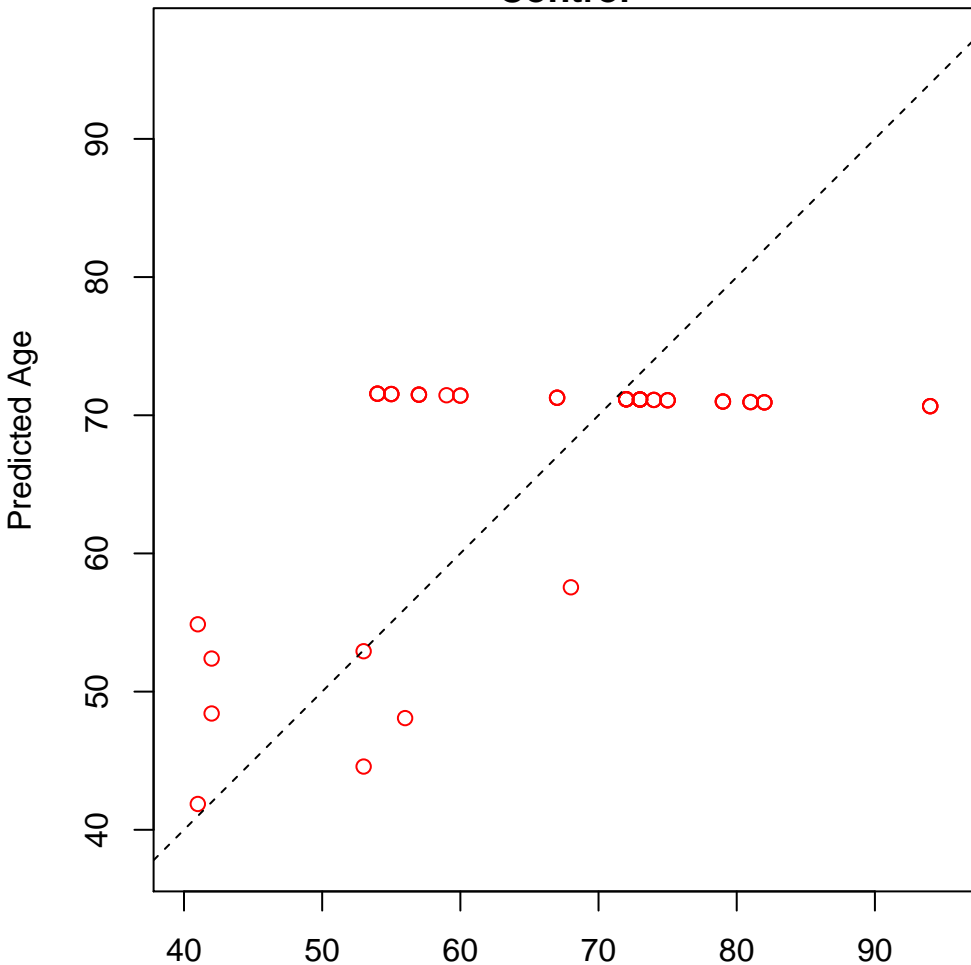


glutamate metabolic process (Score: 0.818341)

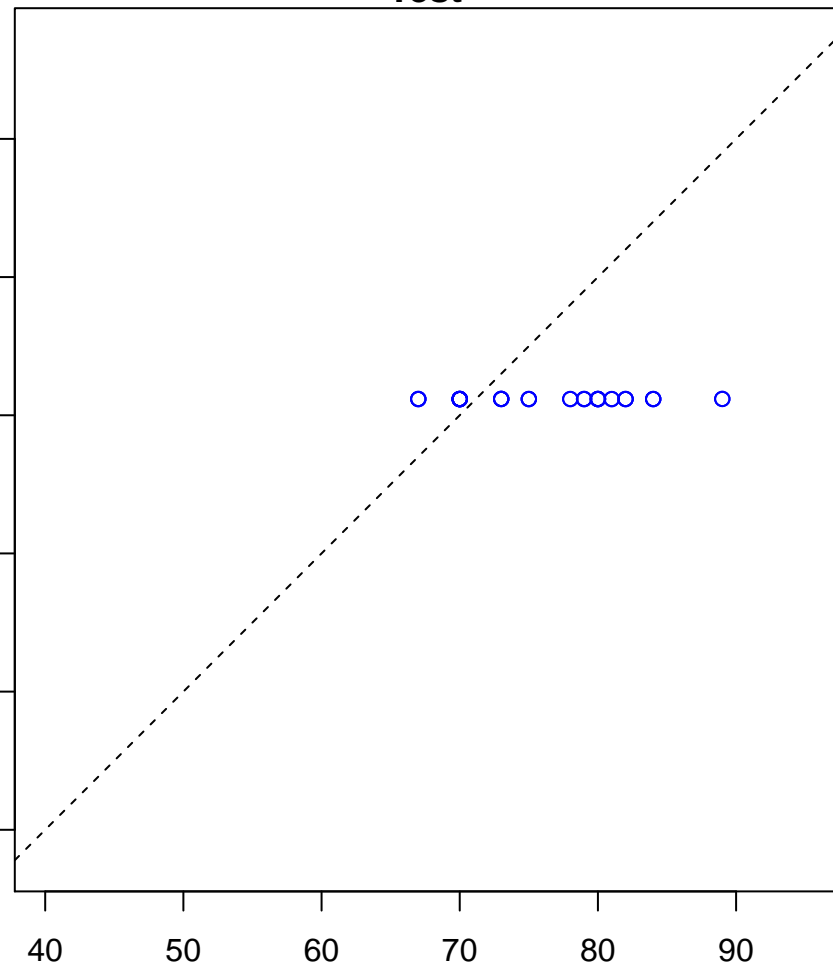


cellular amino acid biosynthetic process (Score: 0.818341)

Control



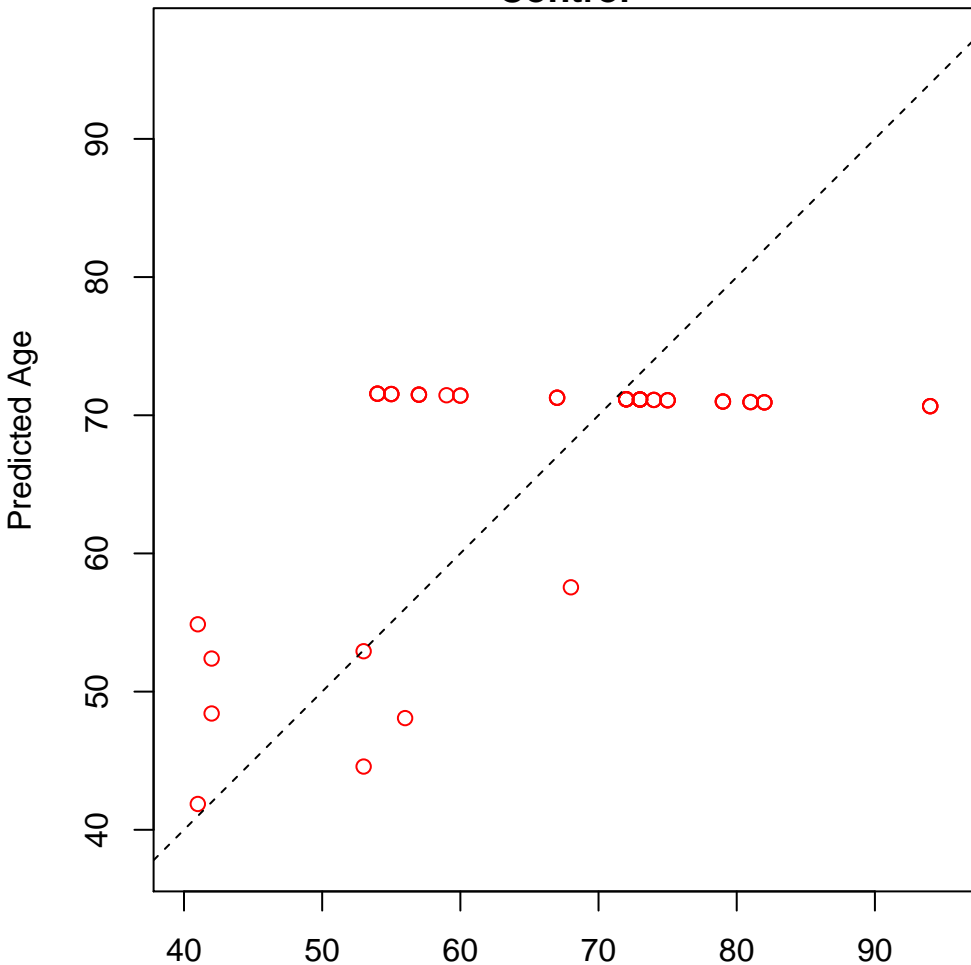
Test



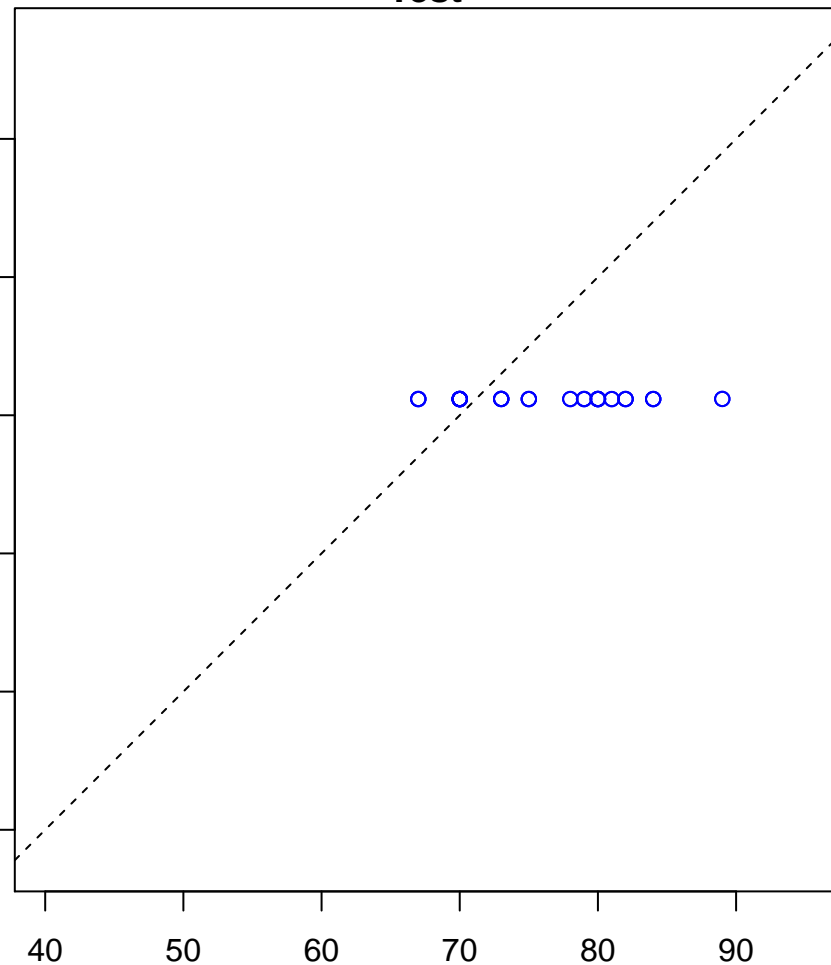
Actual Age

cellular amino acid catabolic process (Score: 0.818341)

Control

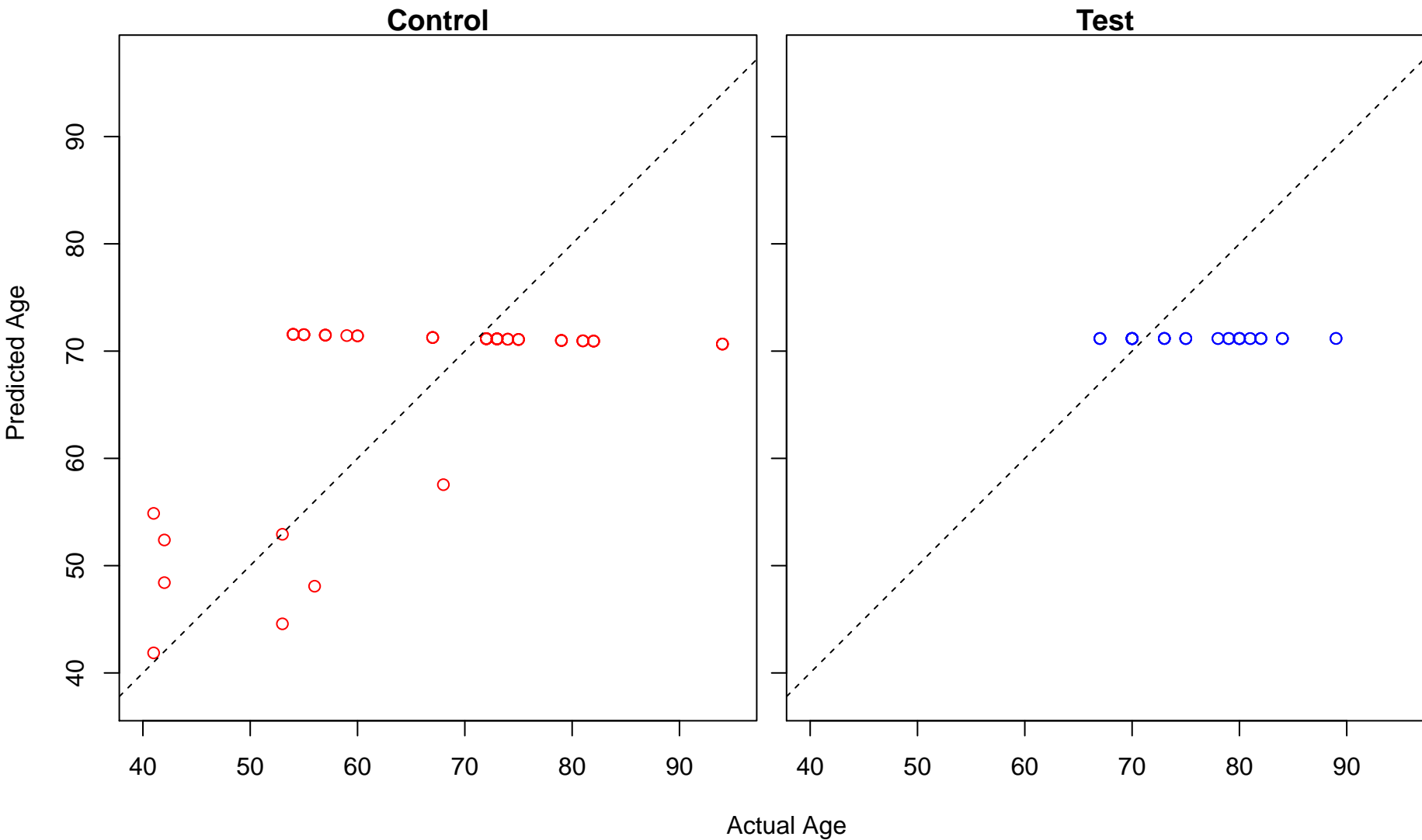


Test



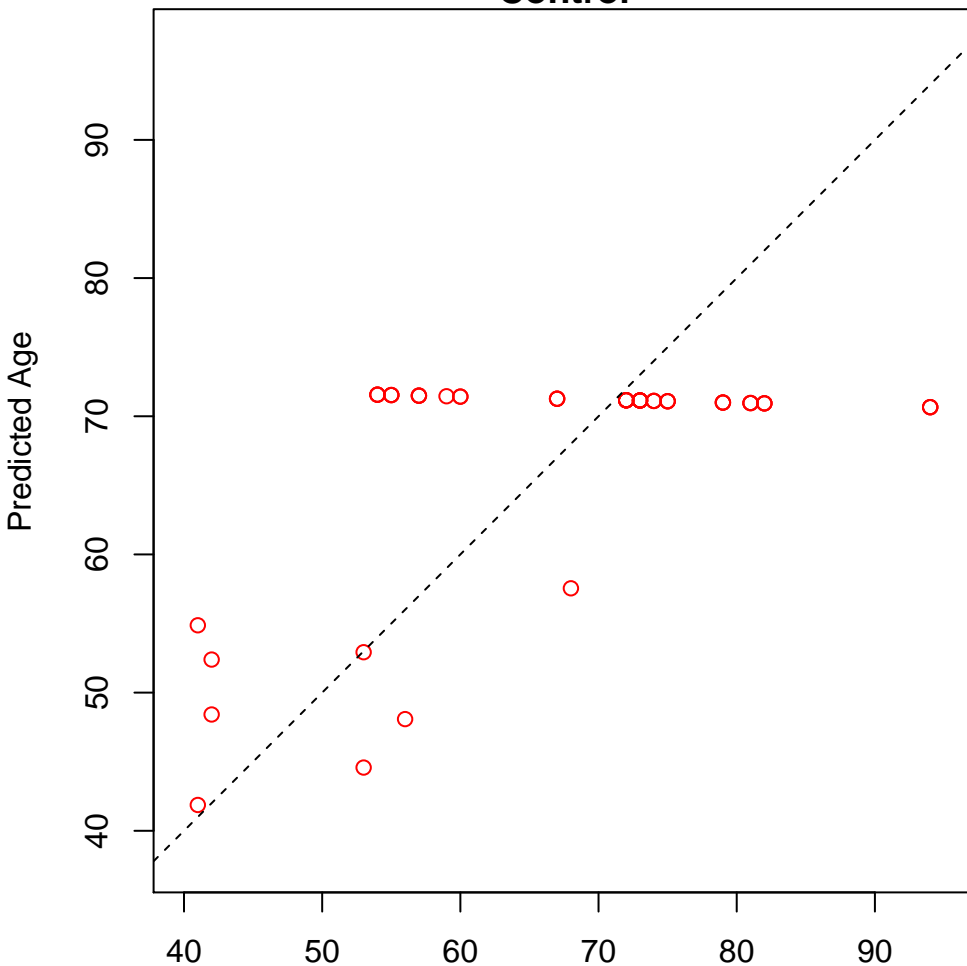
Actual Age

glutamine family amino acid metabolic process (Score: 0.818341)

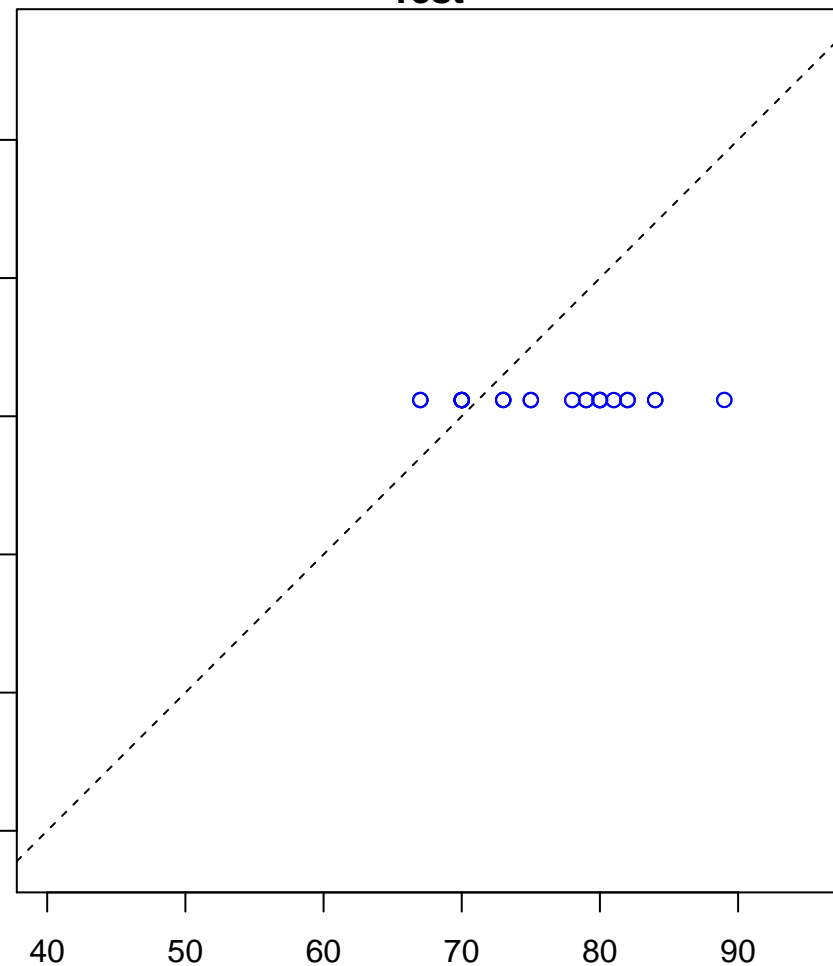


dicarboxylic acid metabolic process (Score: 0.818341)

Control



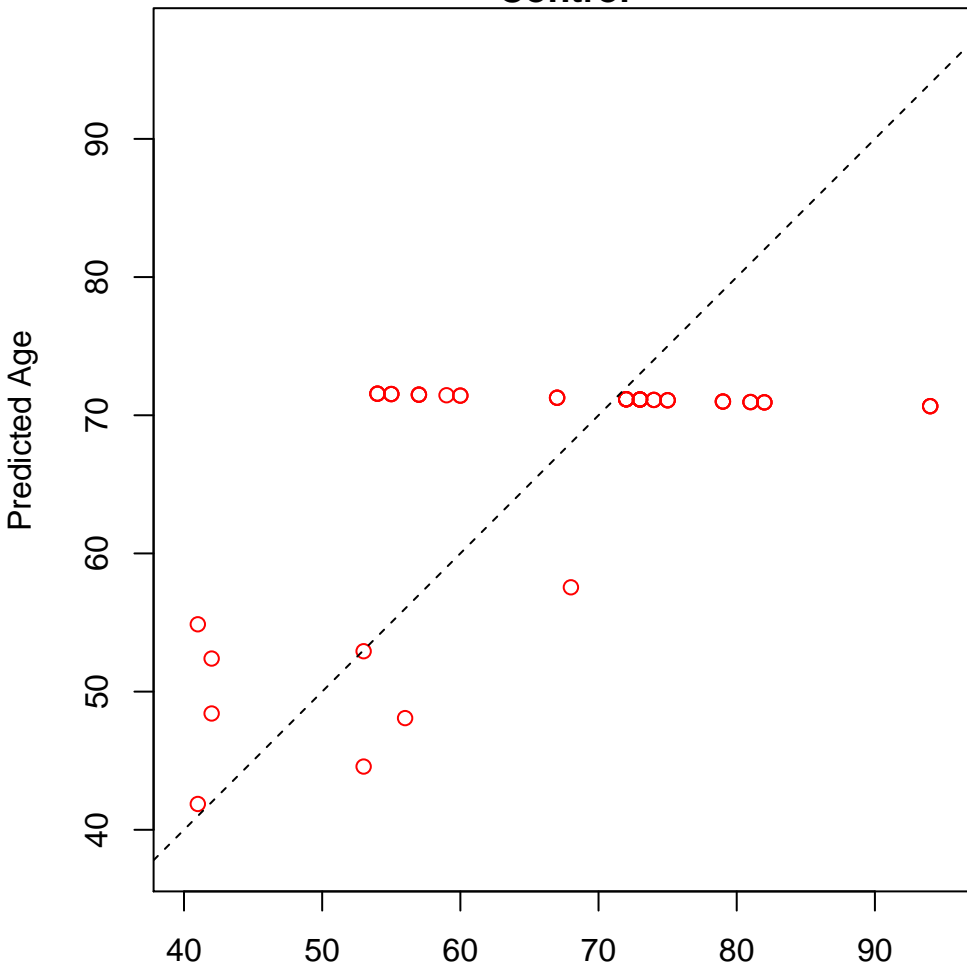
Test



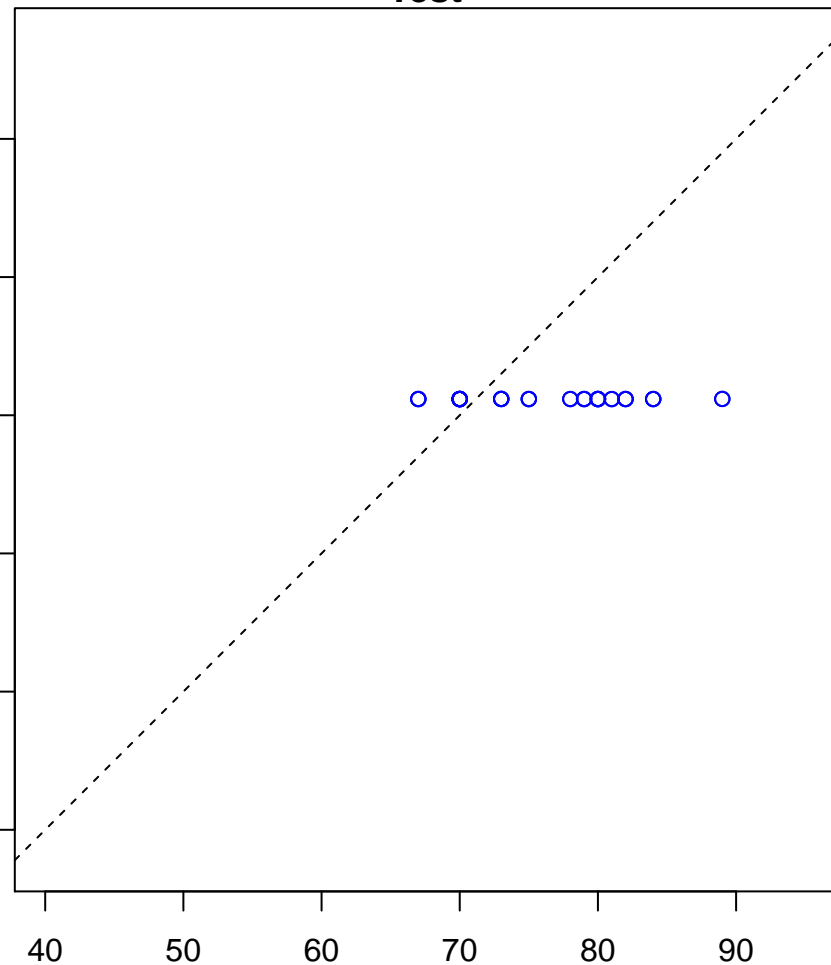
Actual Age

dicarboxylic acid catabolic process (Score: 0.818341)

Control



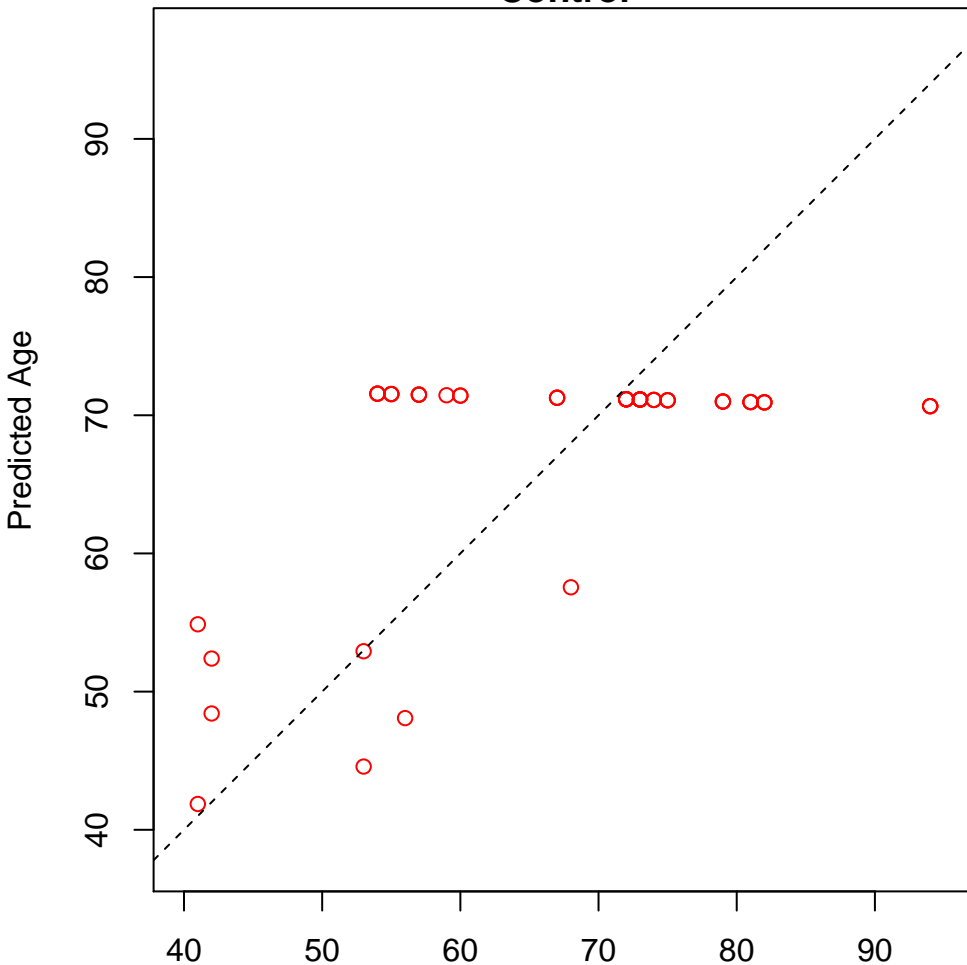
Test



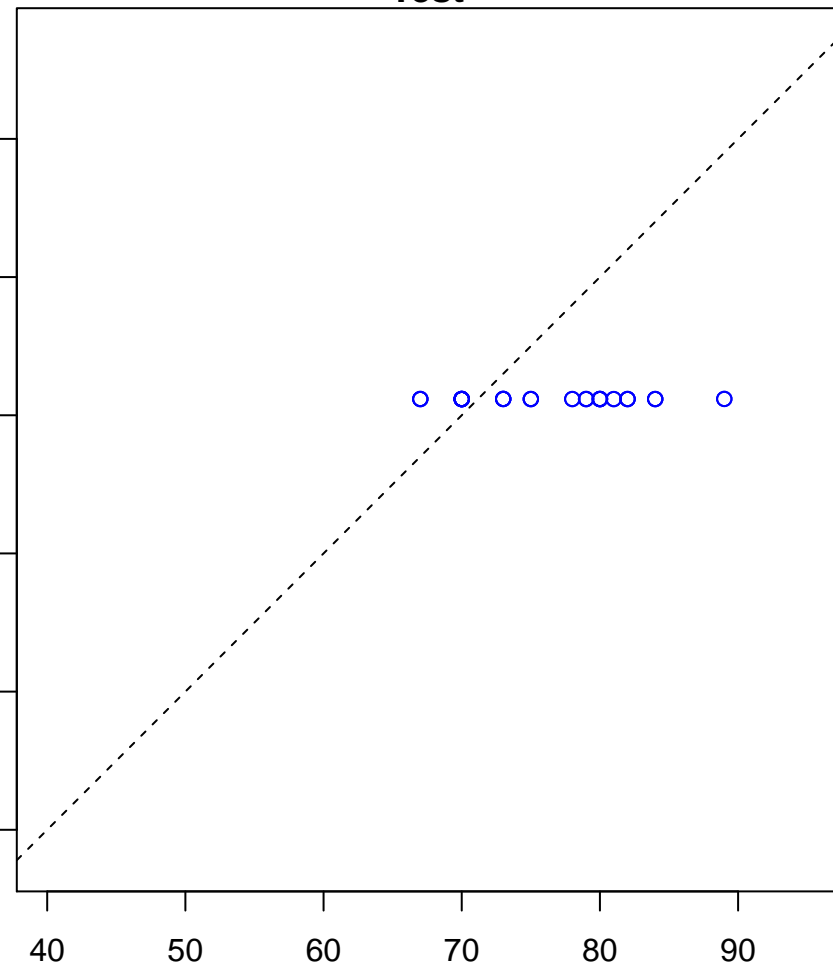
Actual Age

alpha-amino acid catabolic process (Score: 0.818341)

Control

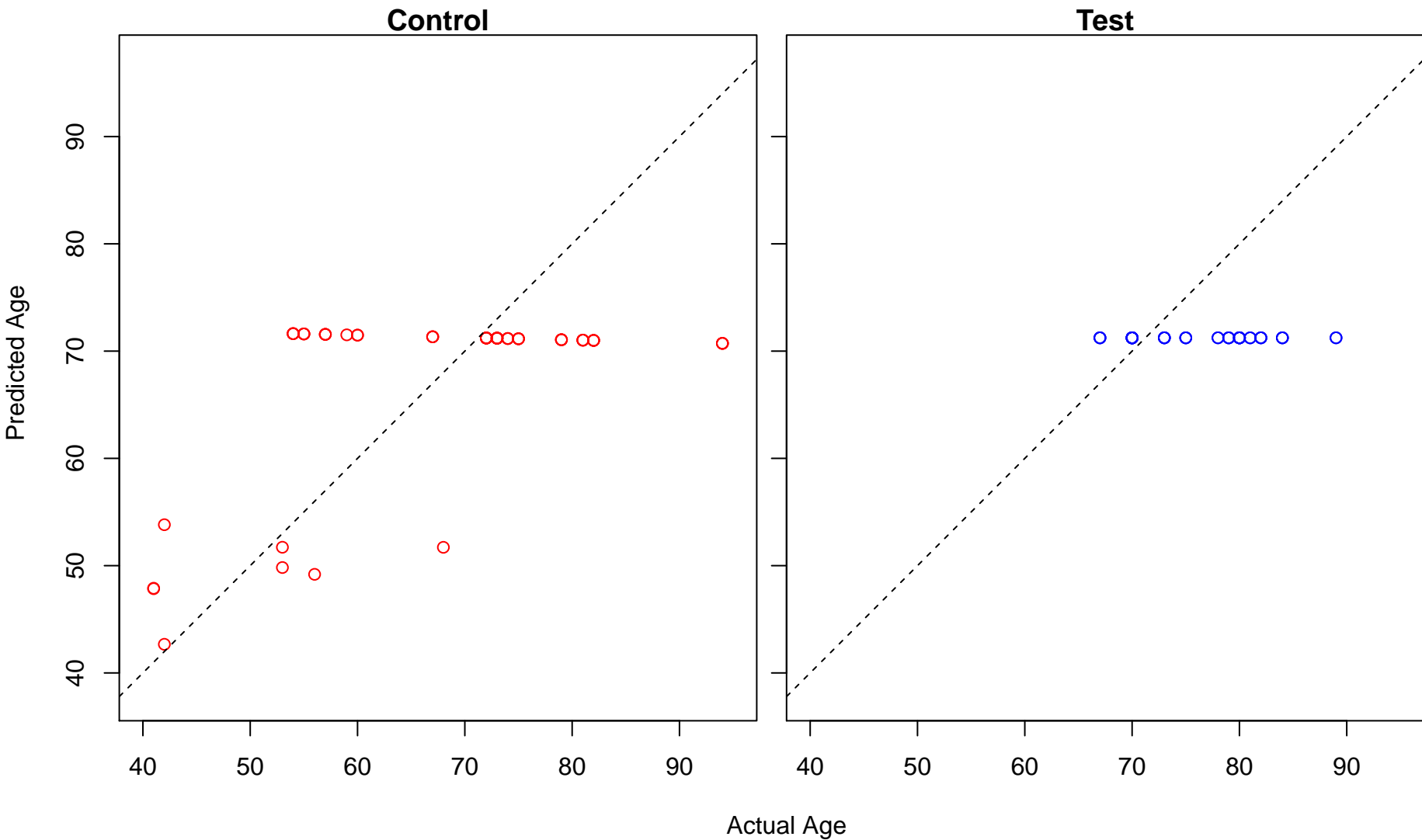


Test

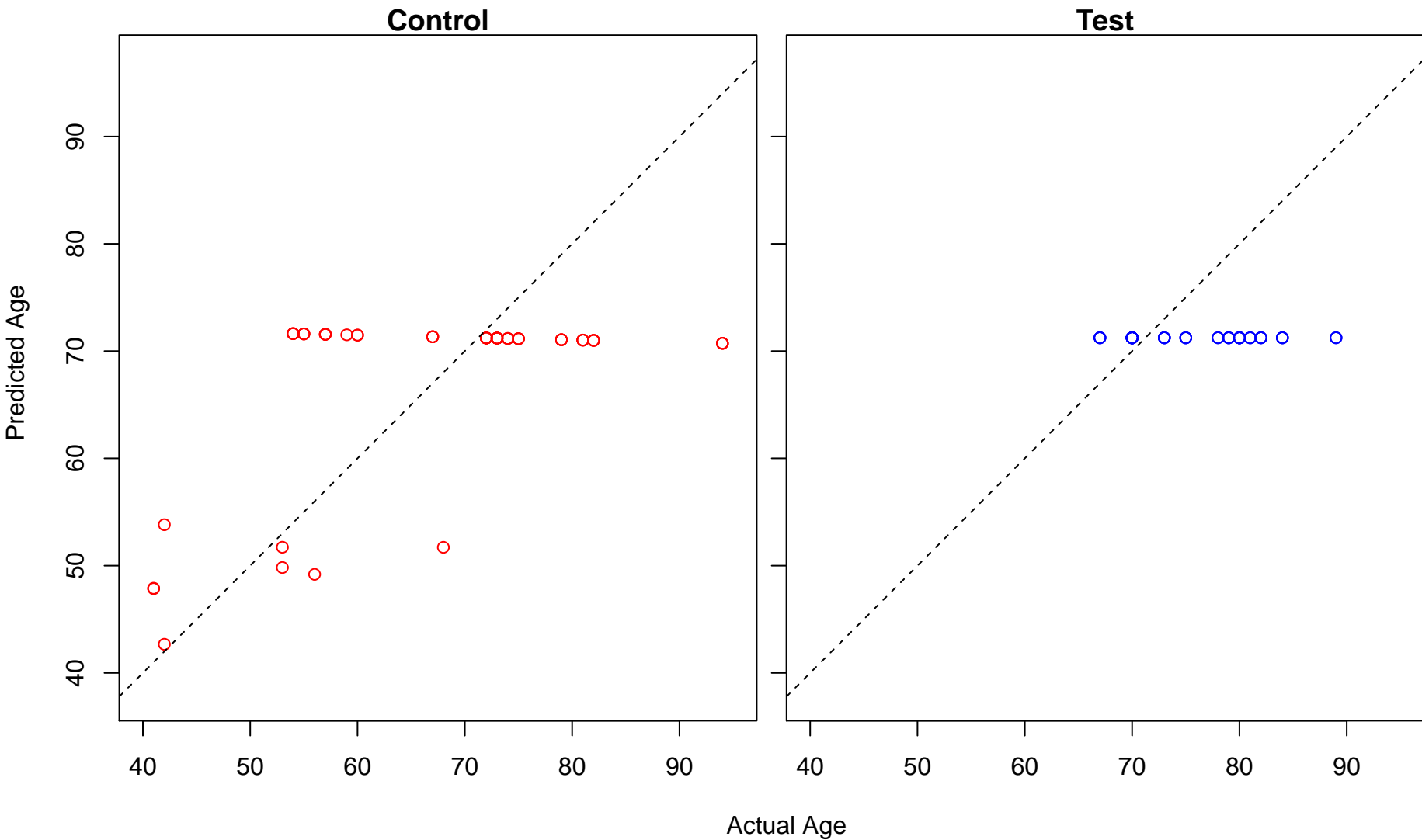


Actual Age

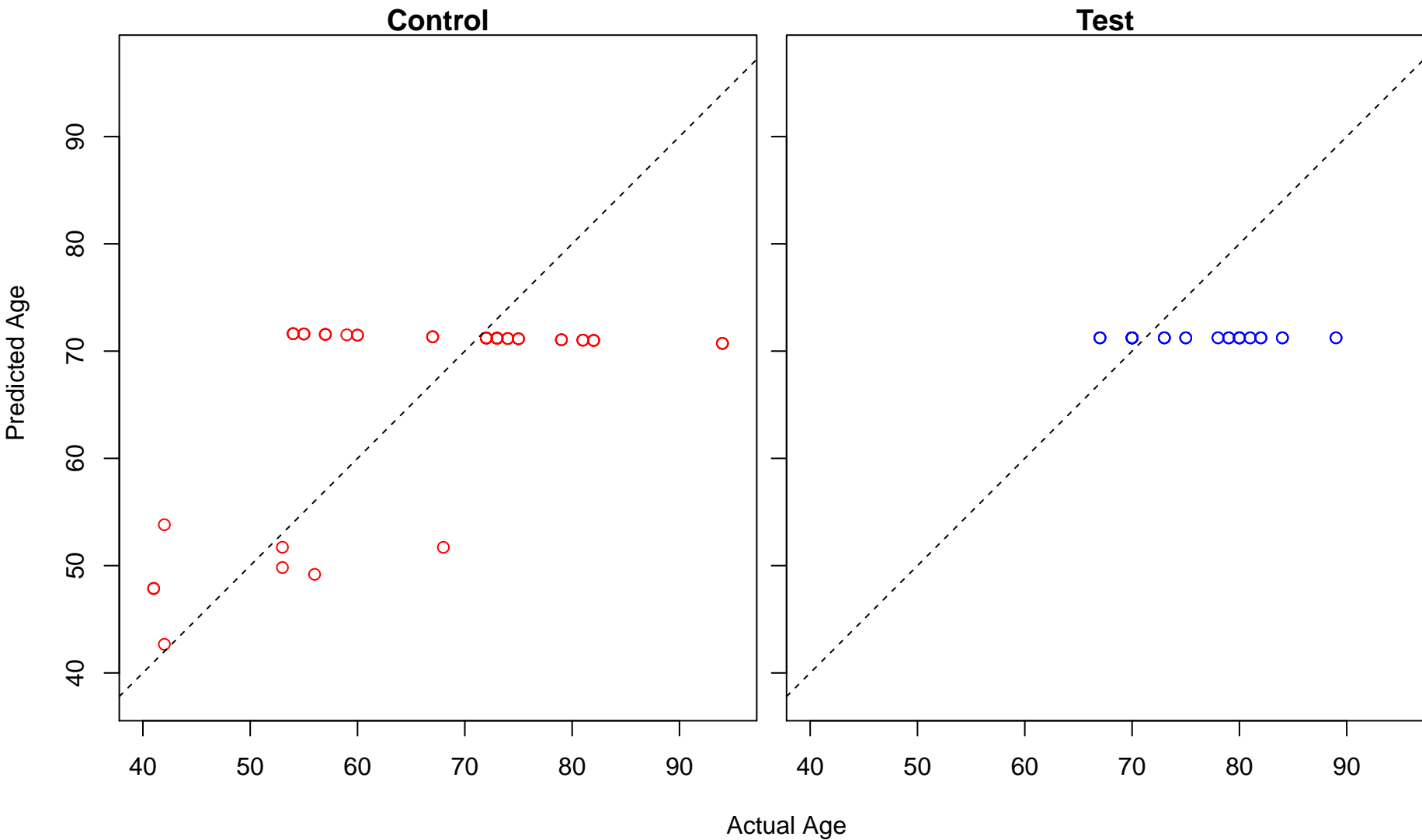
negative regulation of protein localization to plasma membrane (Score: 0.818324)



negative regulation of protein localization to cell periphery (Score: 0.818324)

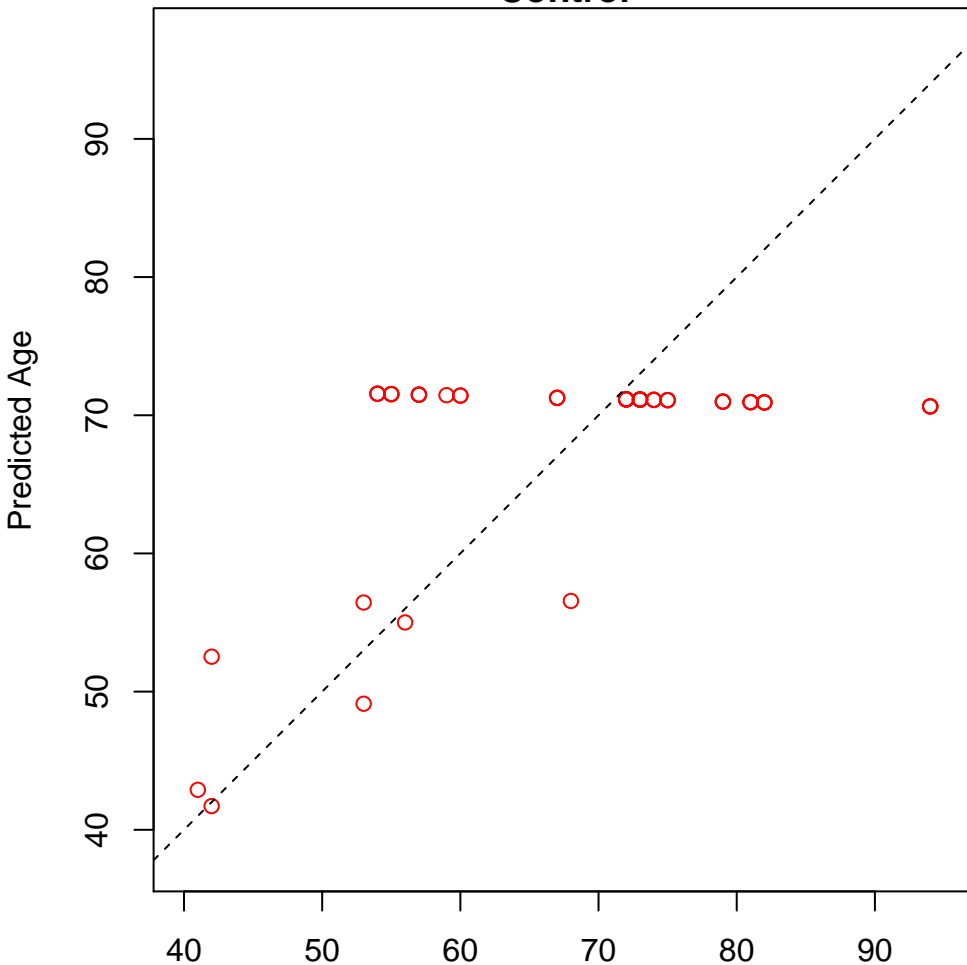


negative regulation of protein localization to membrane (Score: 0.818324)

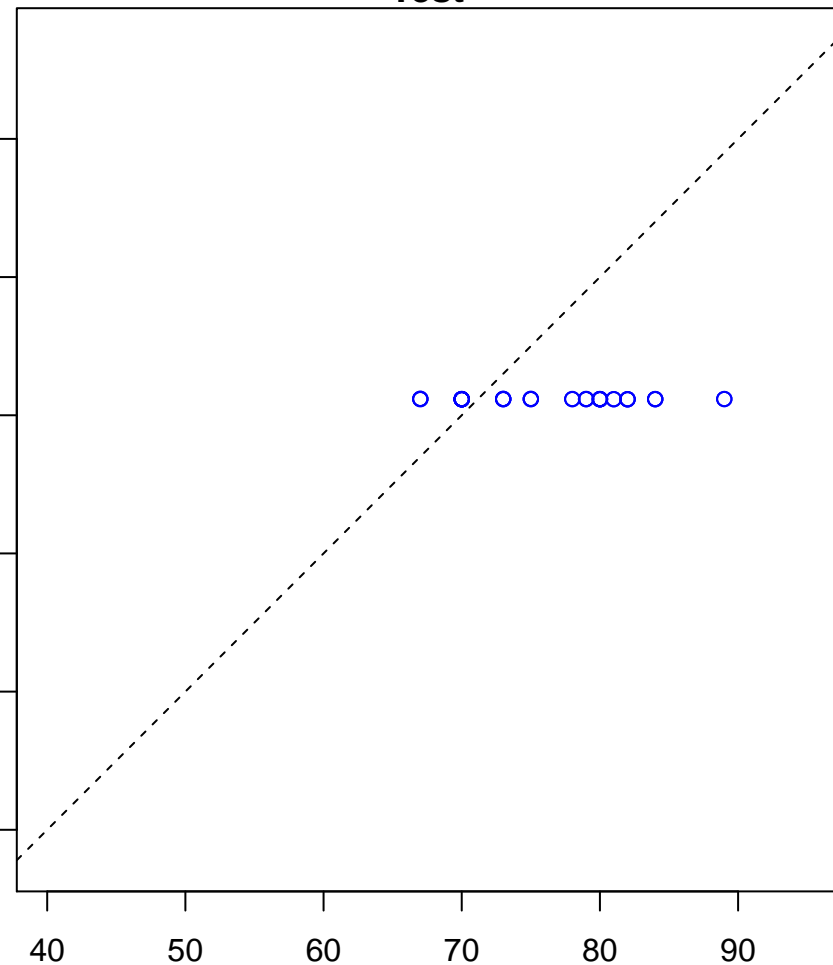


regulation of viral entry into host cell (Score: 0.818317)

Control

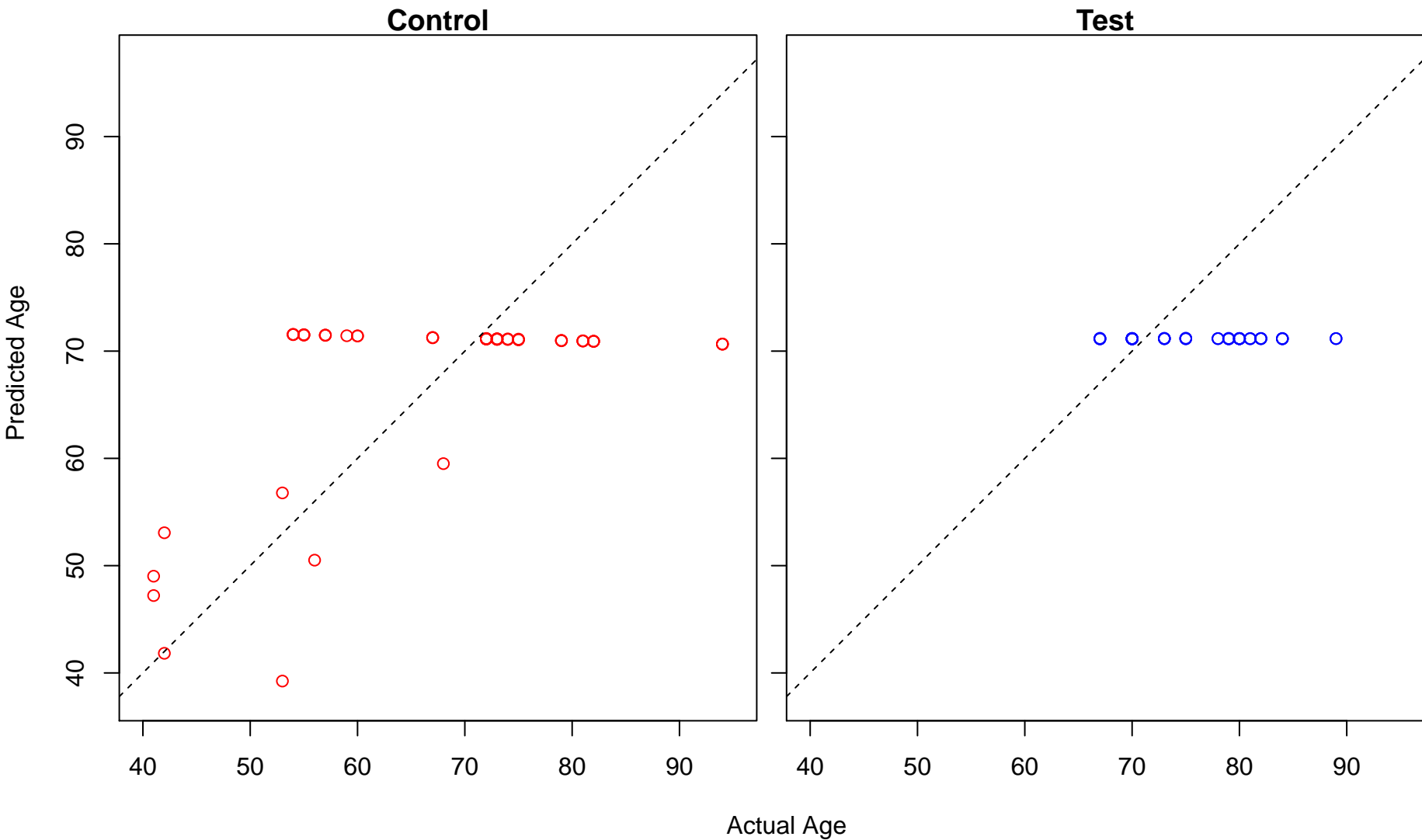


Test

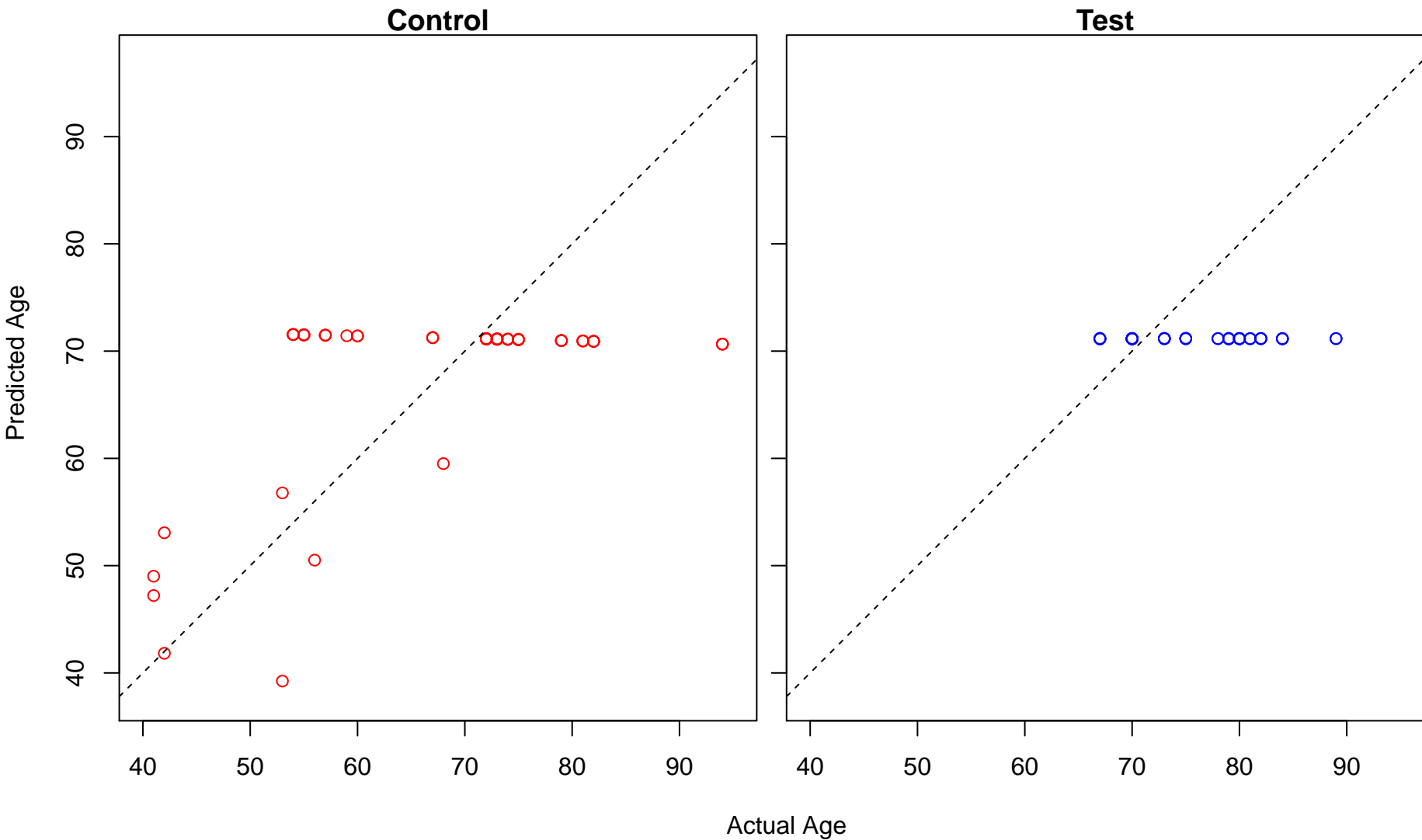


Actual Age

calcium ion transport (Score: 0.818308)

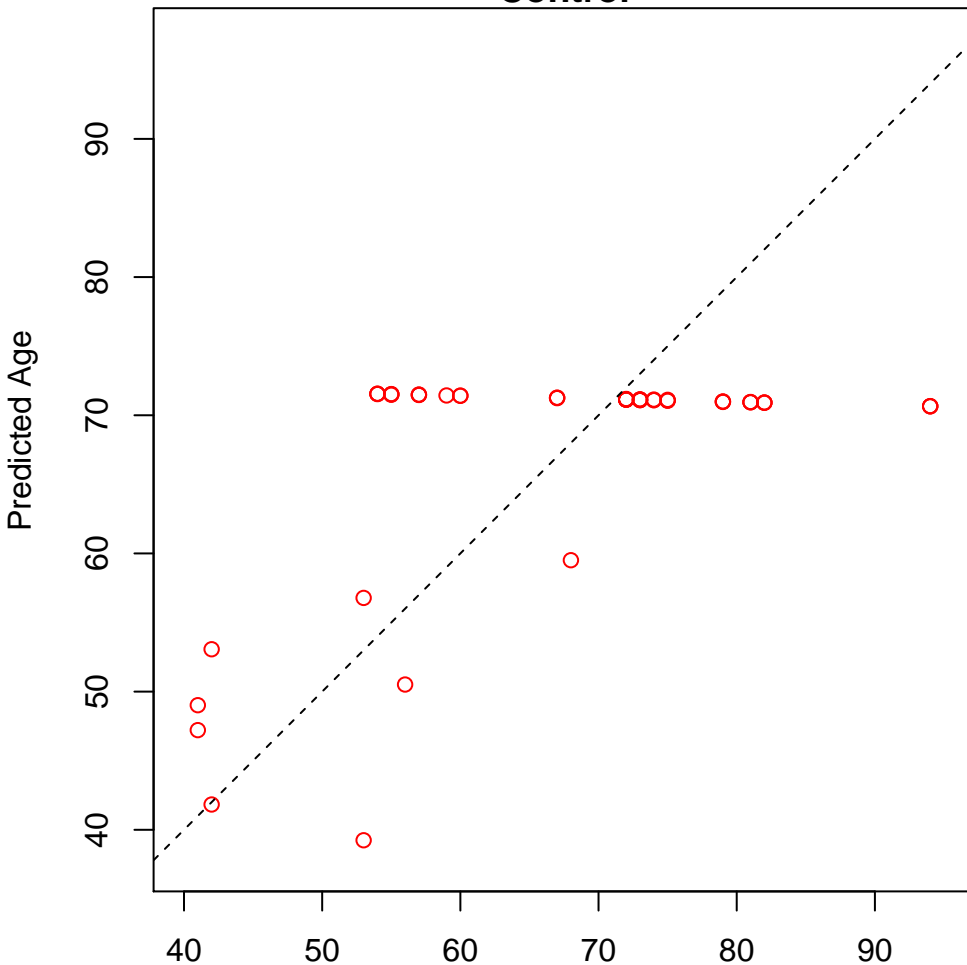


divalent metal ion transport (Score: 0.818308)

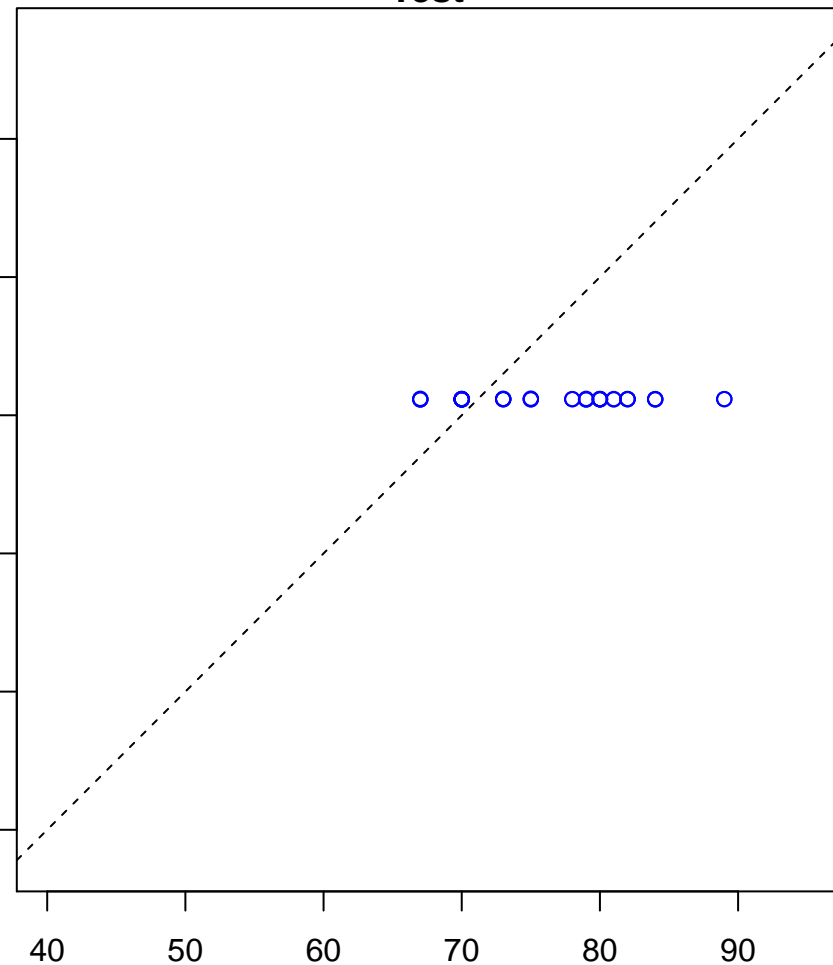


divalent inorganic cation transport (Score: 0.818308)

Control

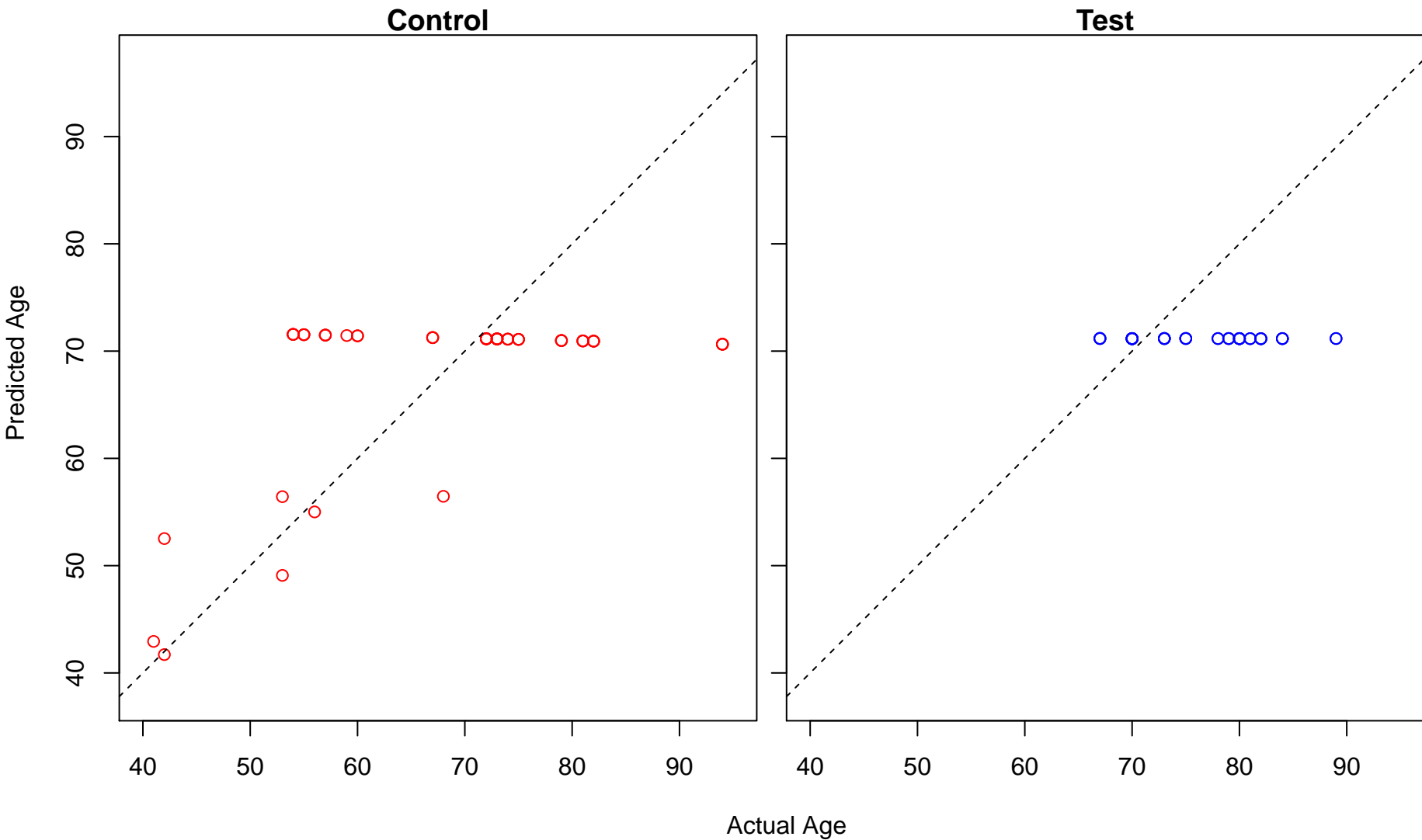


Test

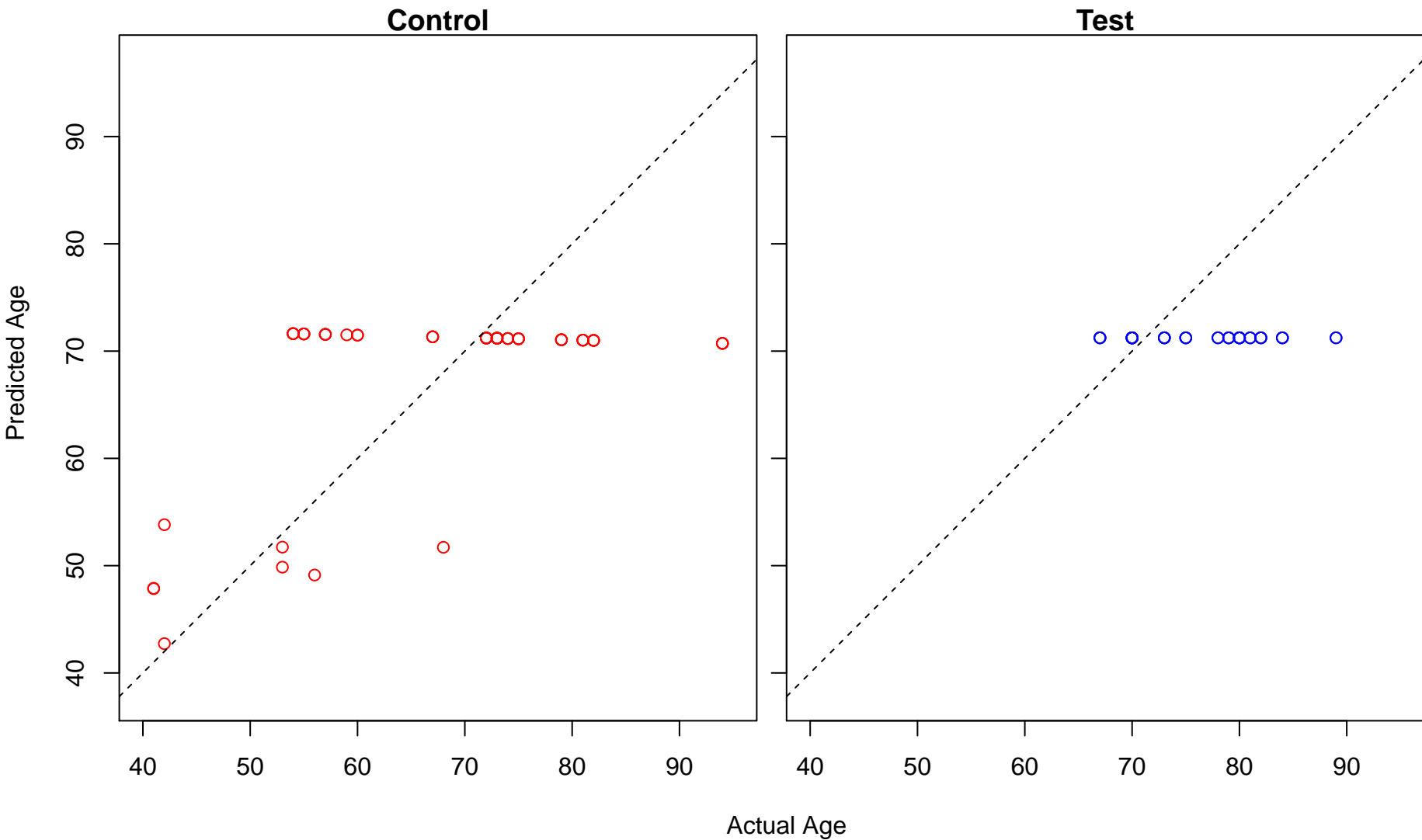


Actual Age

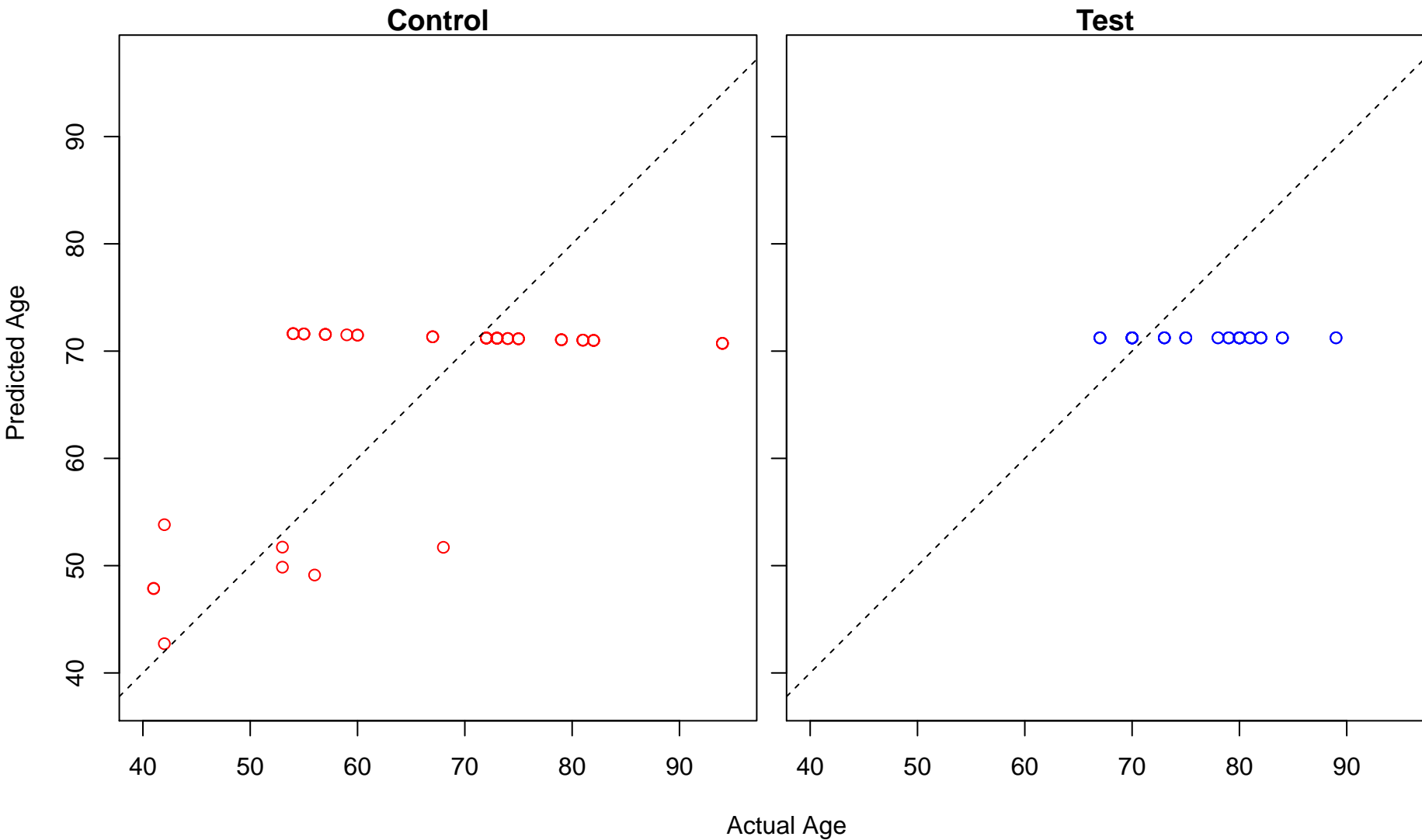
regulation of viral life cycle (Score: 0.818278)



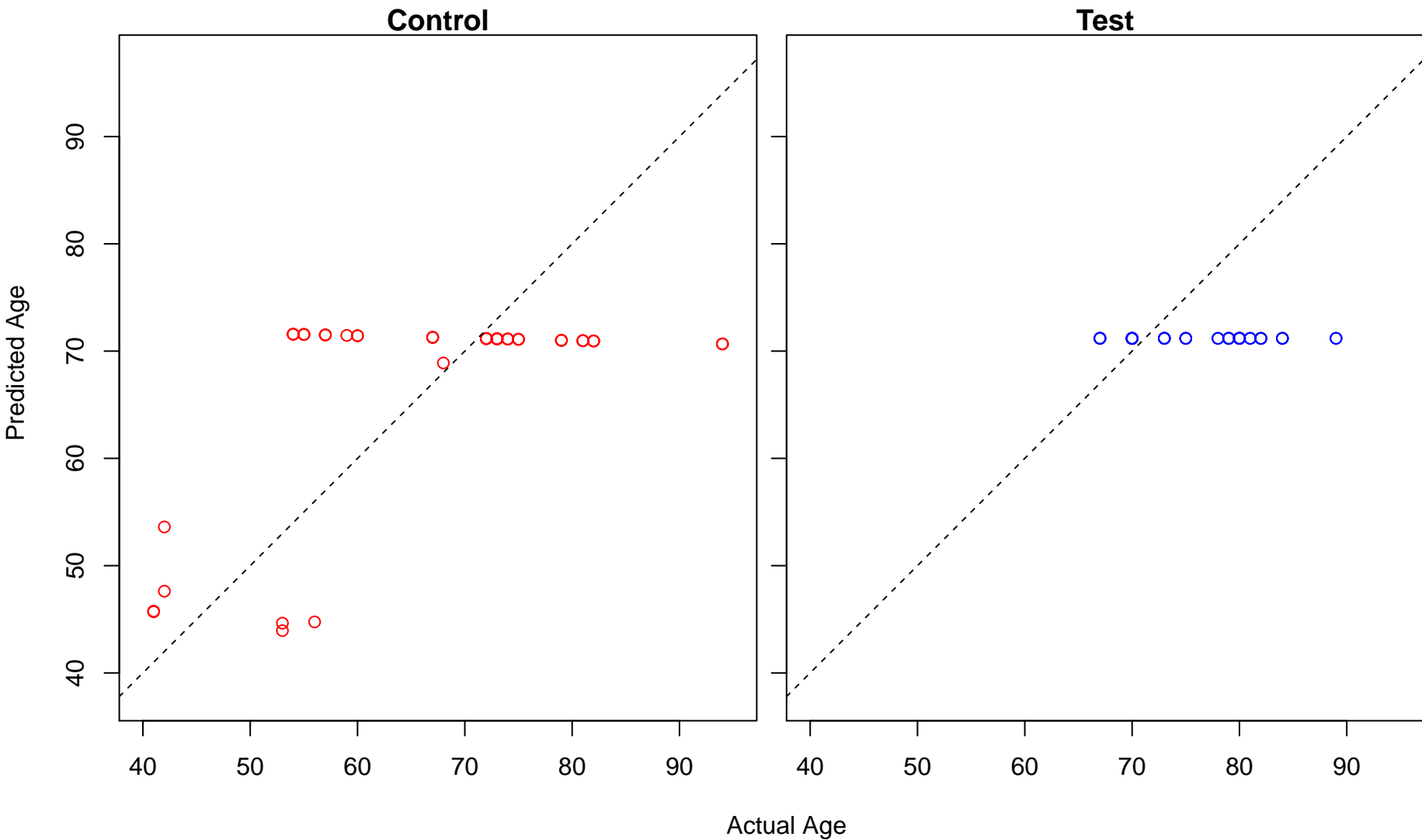
regulation of protein localization to cell periphery (Score: 0.818278)



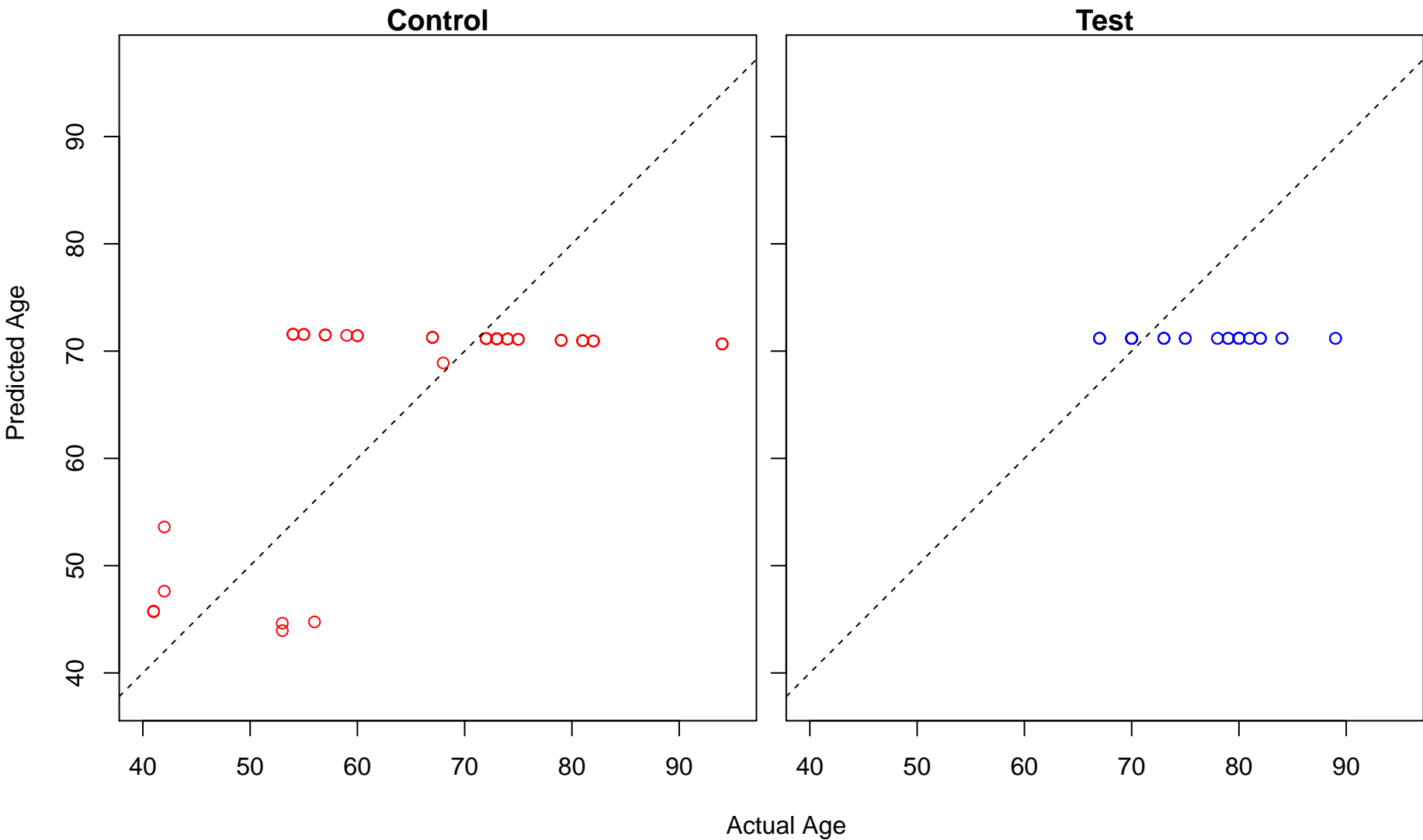
regulation of protein localization to plasma membrane (Score: 0.818277)



RNA splicing, via transesterification reactions (Score: 0.818258)

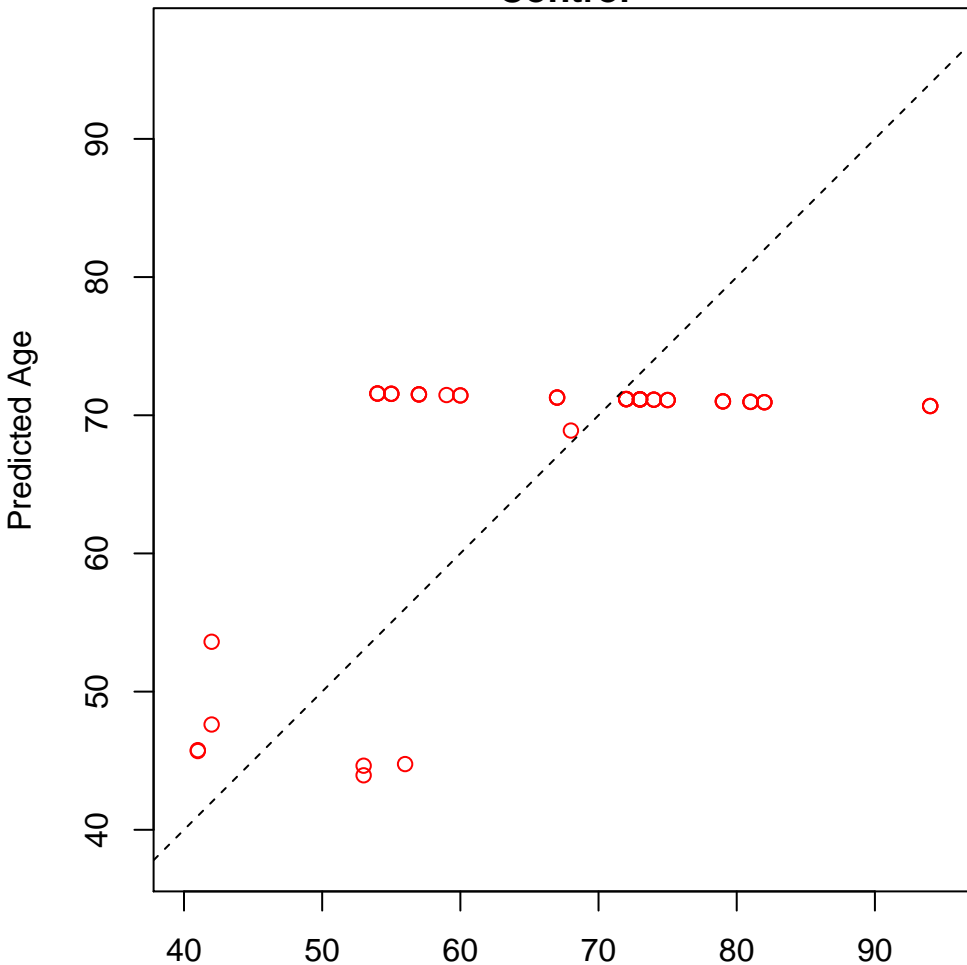


RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (Score: 0.8182)

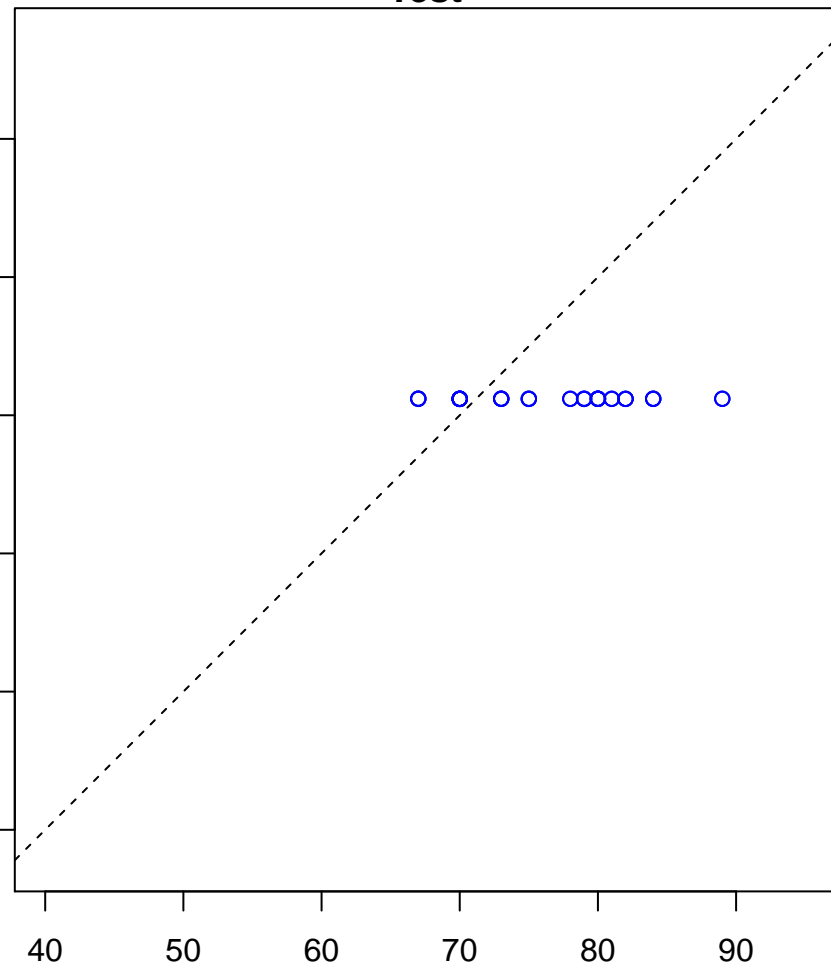


mRNA splicing, via spliceosome (Score: 0.818258)

Control

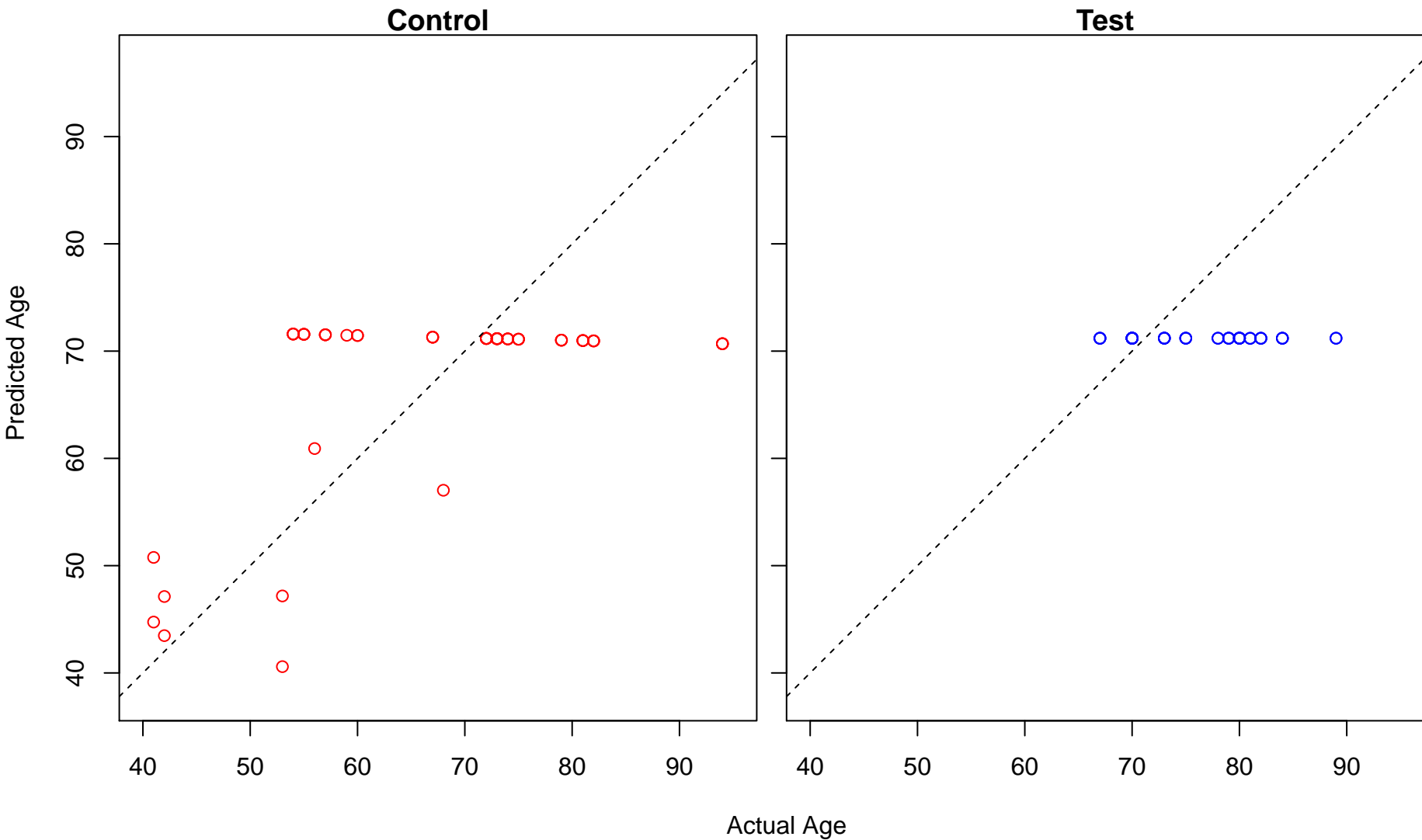


Test



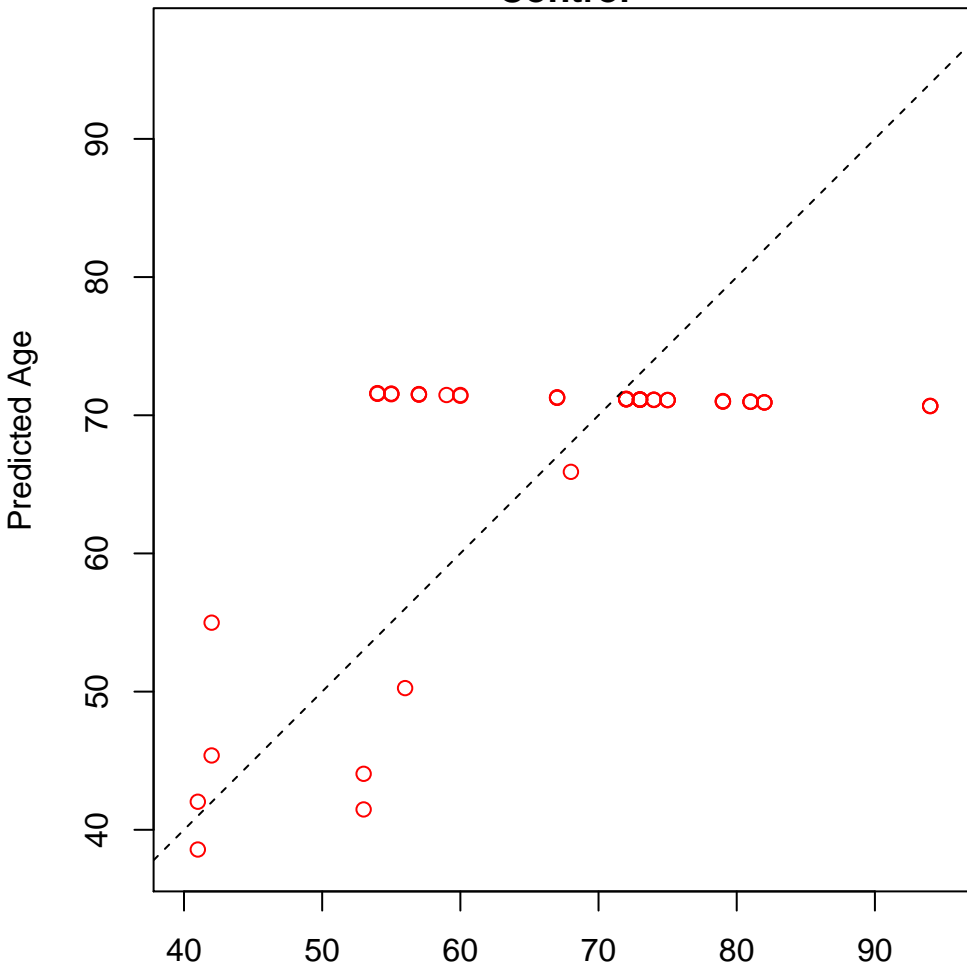
Actual Age

double-strand break repair (Score: 0.818229)

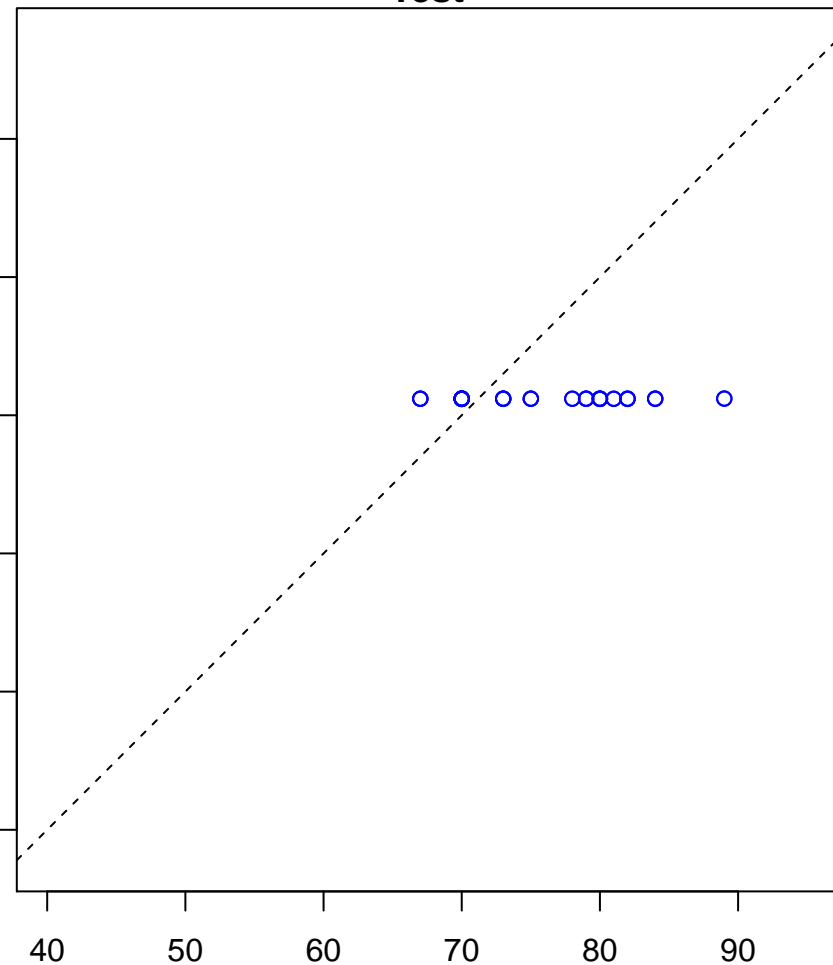


supramolecular fiber organization (Score: 0.818209)

Control

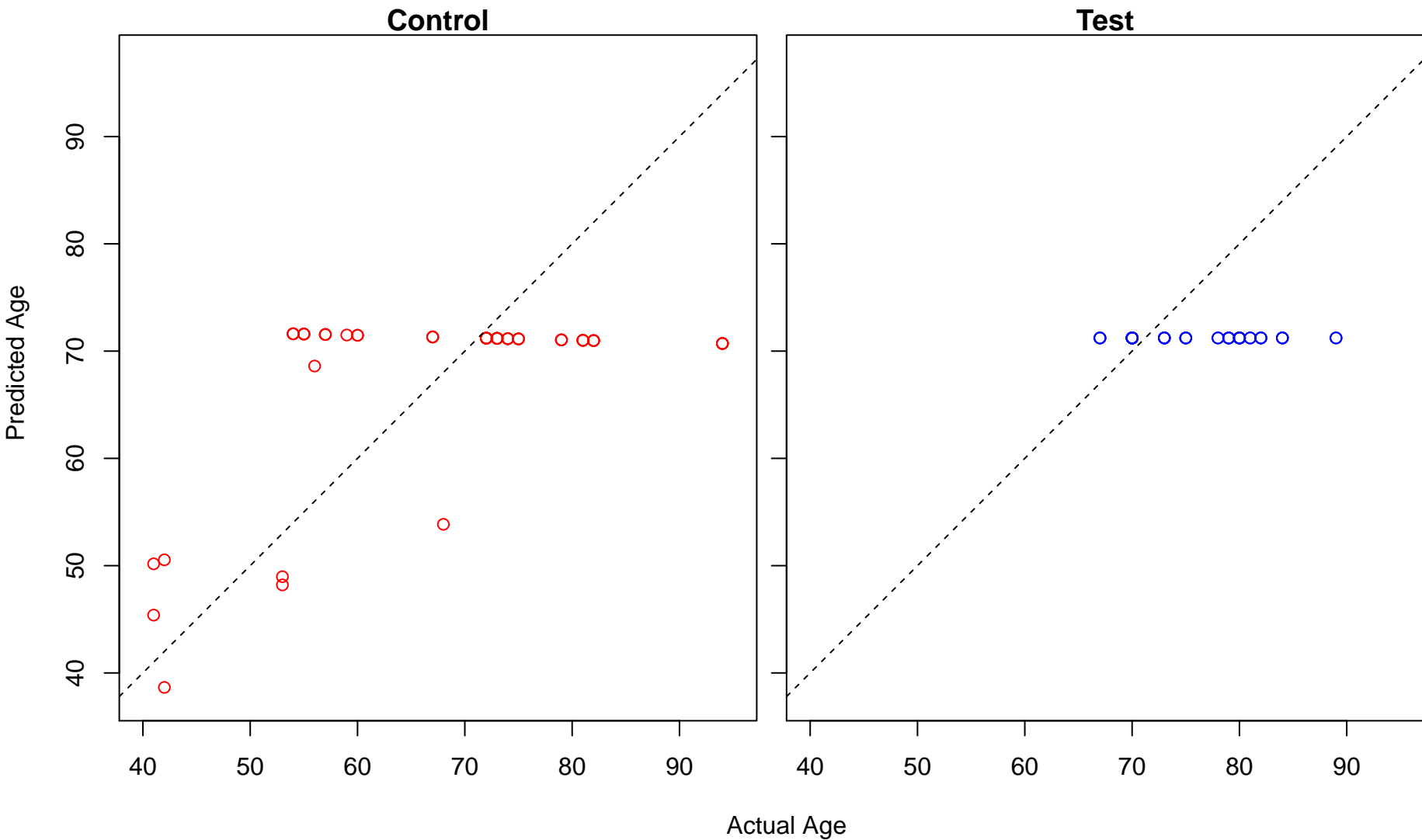


Test



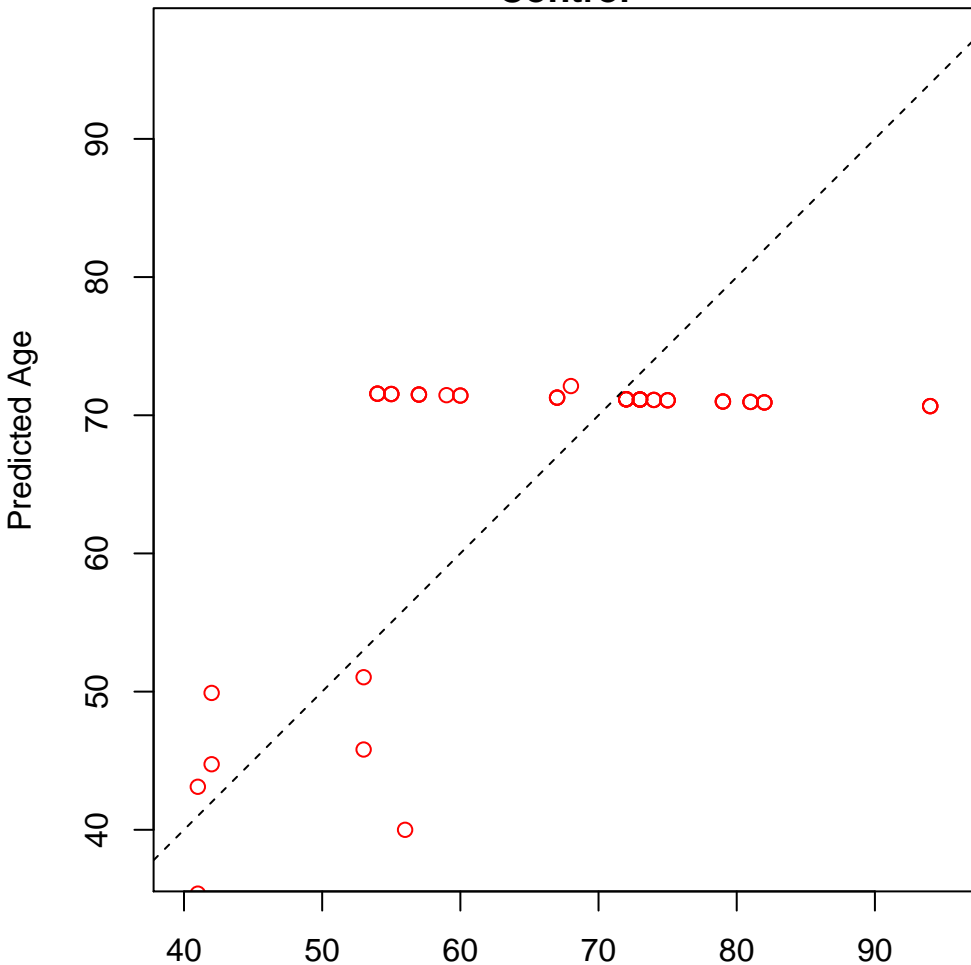
Actual Age

positive regulation of intrinsic apoptotic signaling pathway (Score: 0.818199)

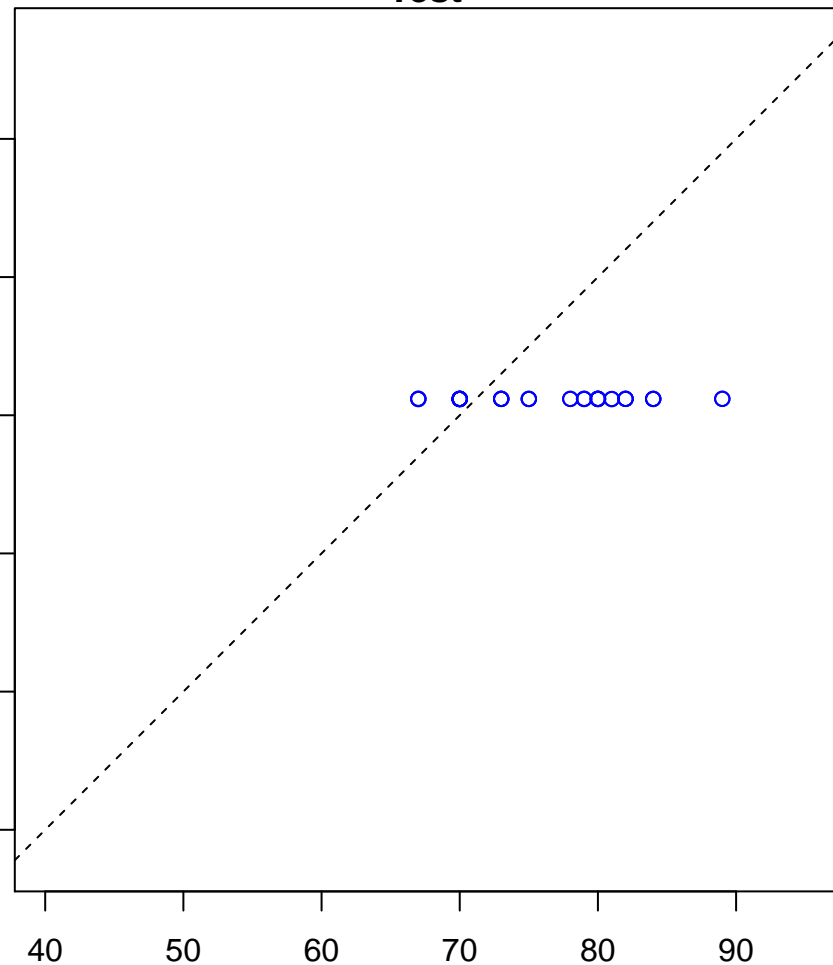


regulation of intracellular transport (Score: 0.818193)

Control

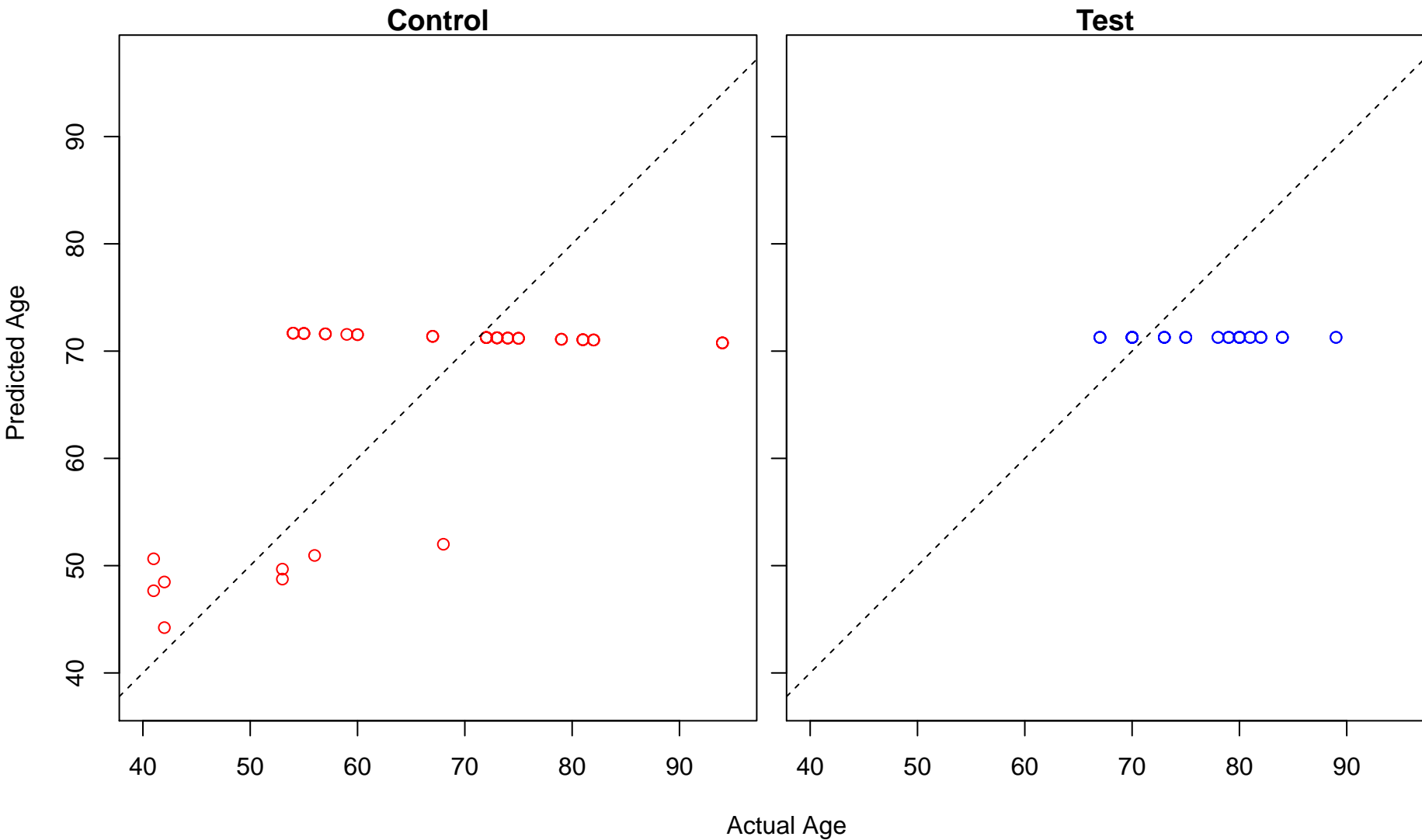


Test

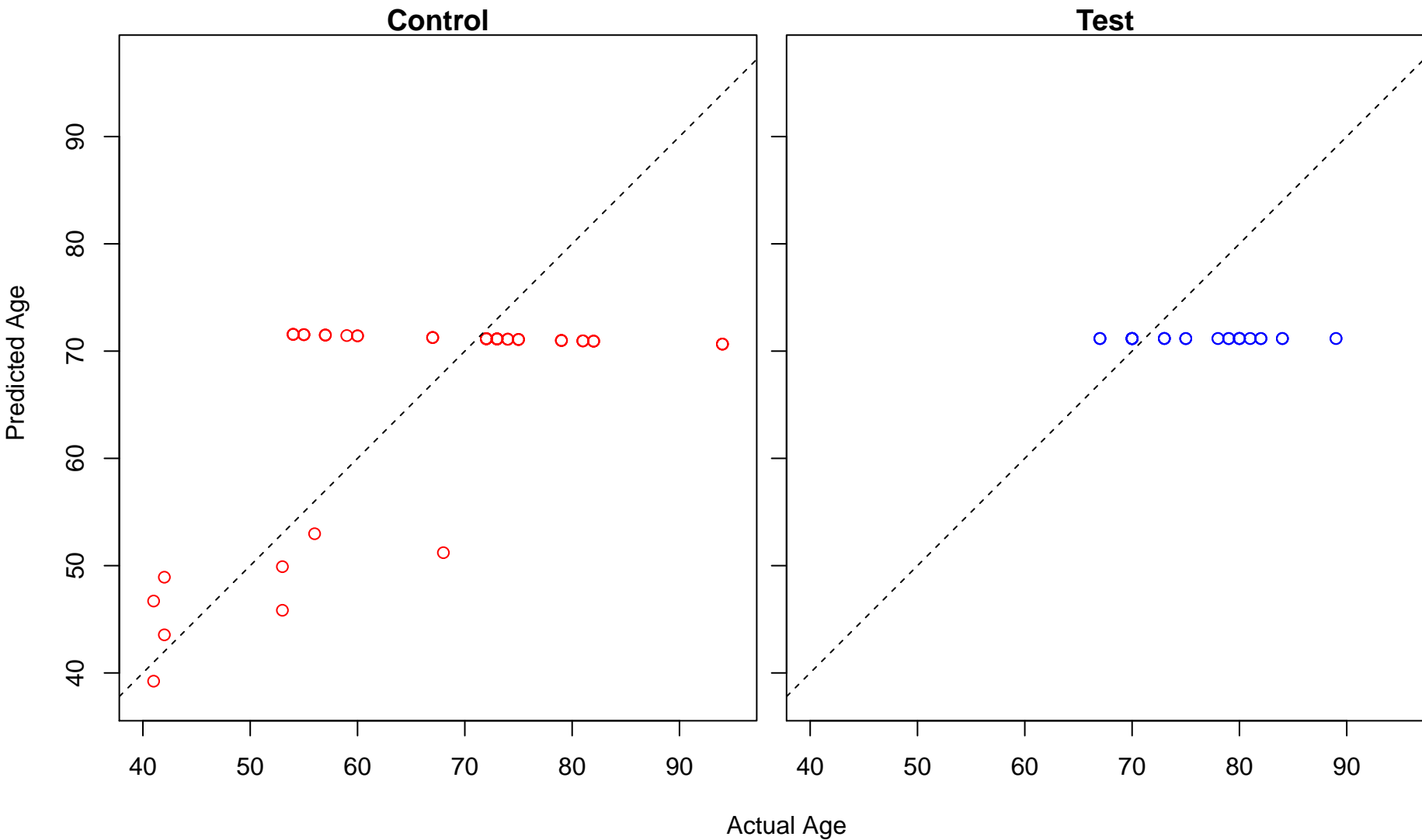


Actual Age

response to drug (Score: 0.818150)

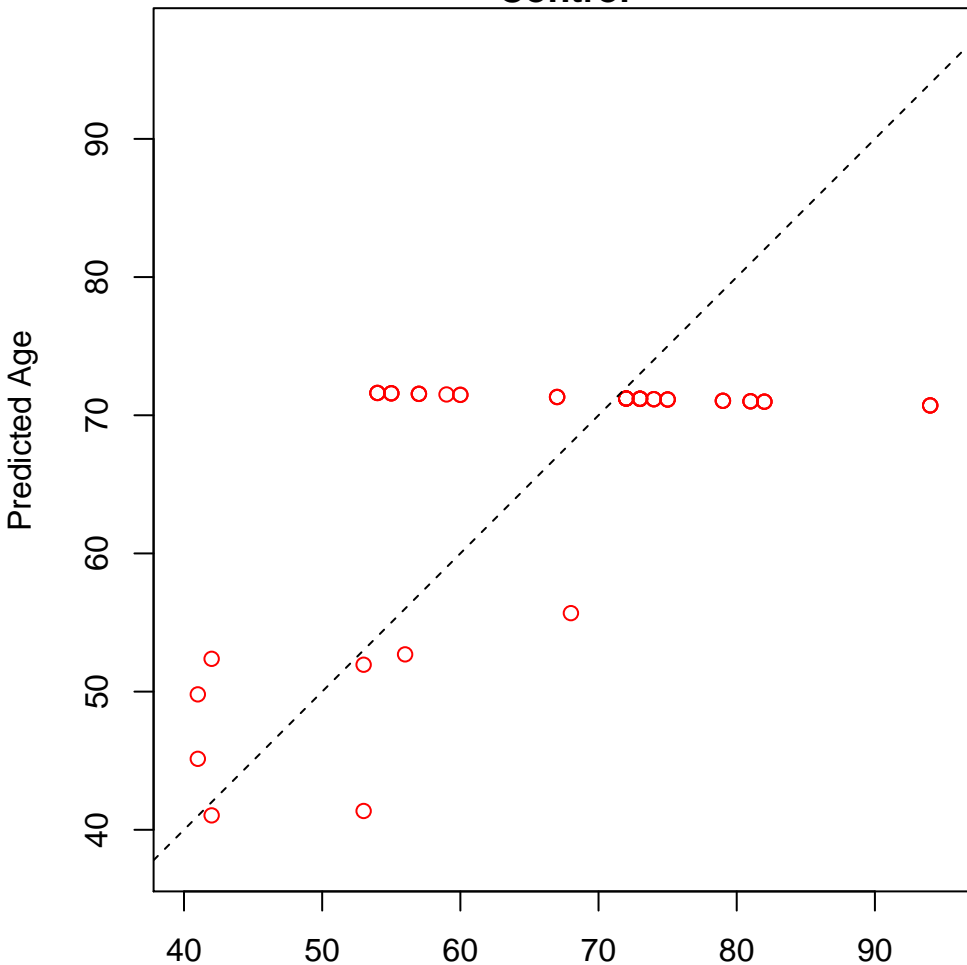


negative regulation of protein metabolic process (Score: 0.817972)

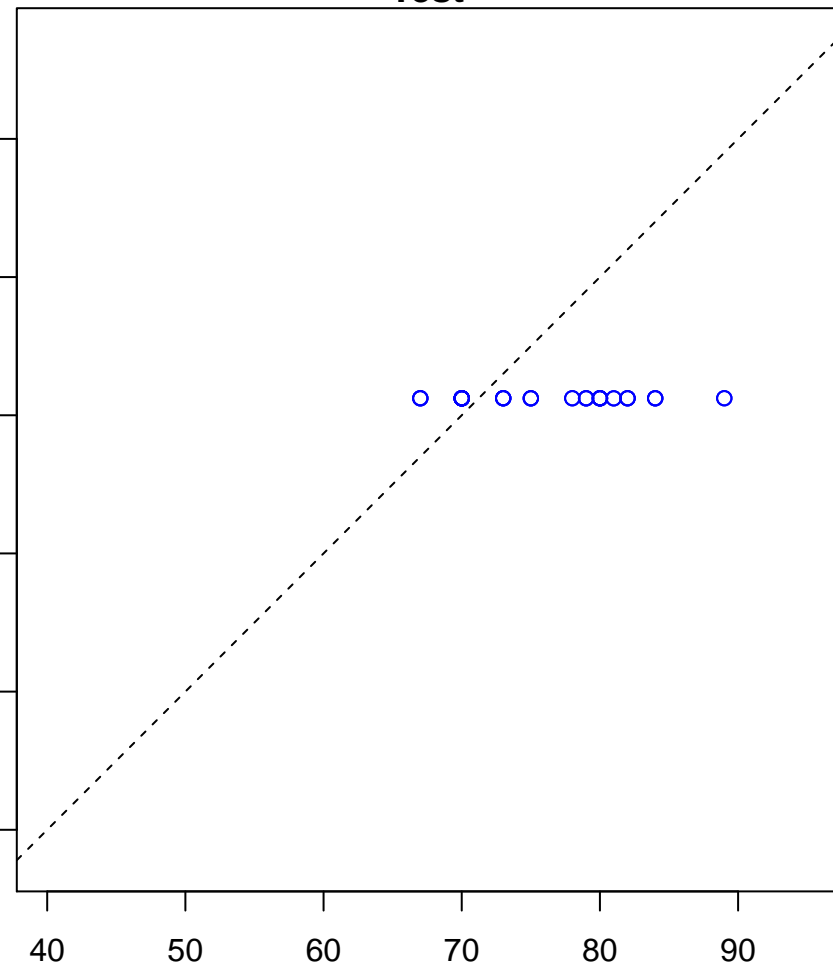


regulation of cell cycle process (Score: 0.817899)

Control



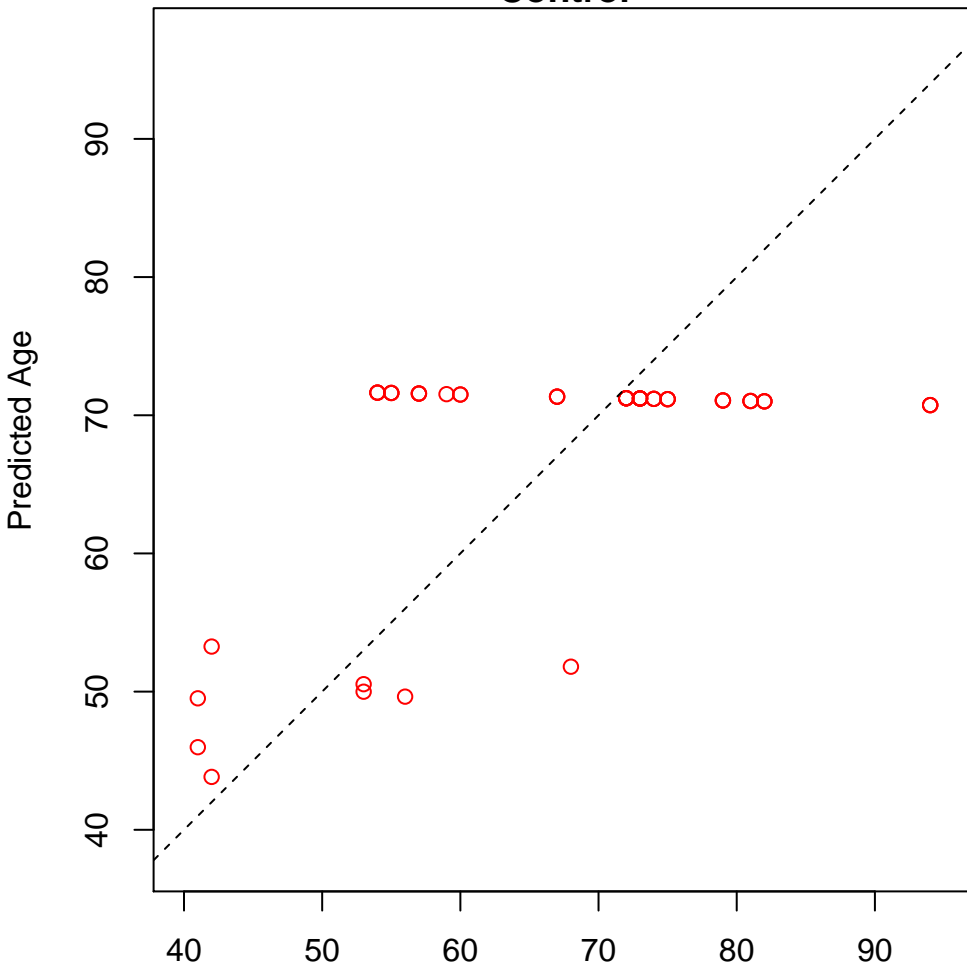
Test



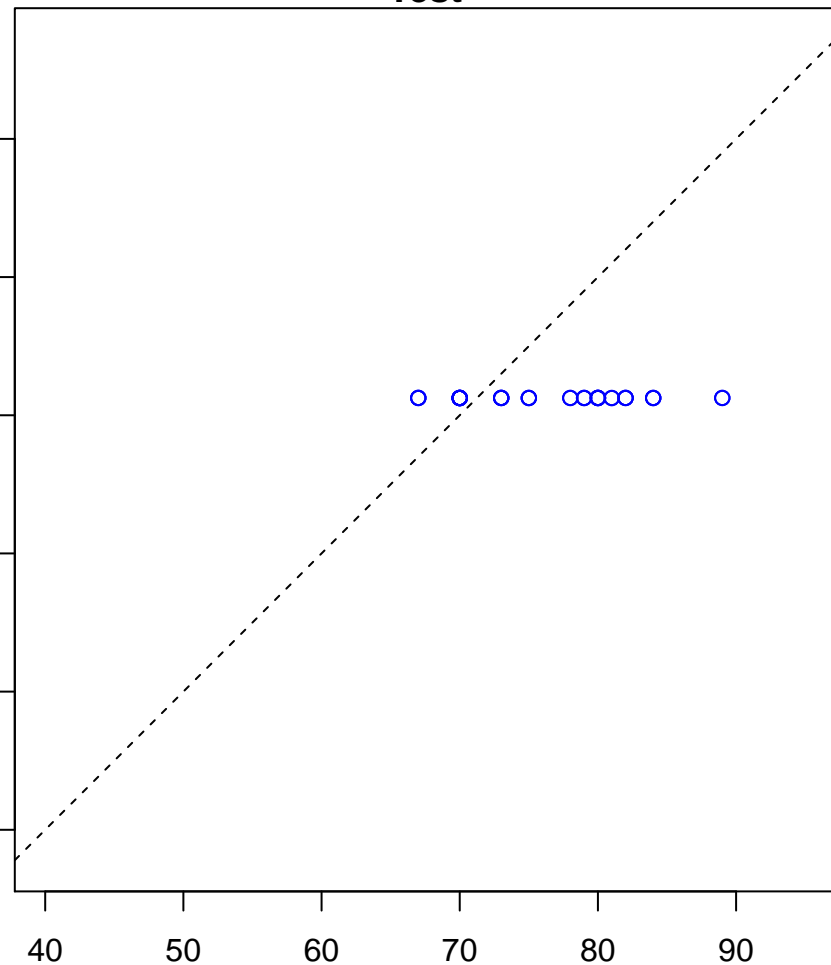
Actual Age

low-density lipoprotein particle clearance (Score: 0.817877)

Control



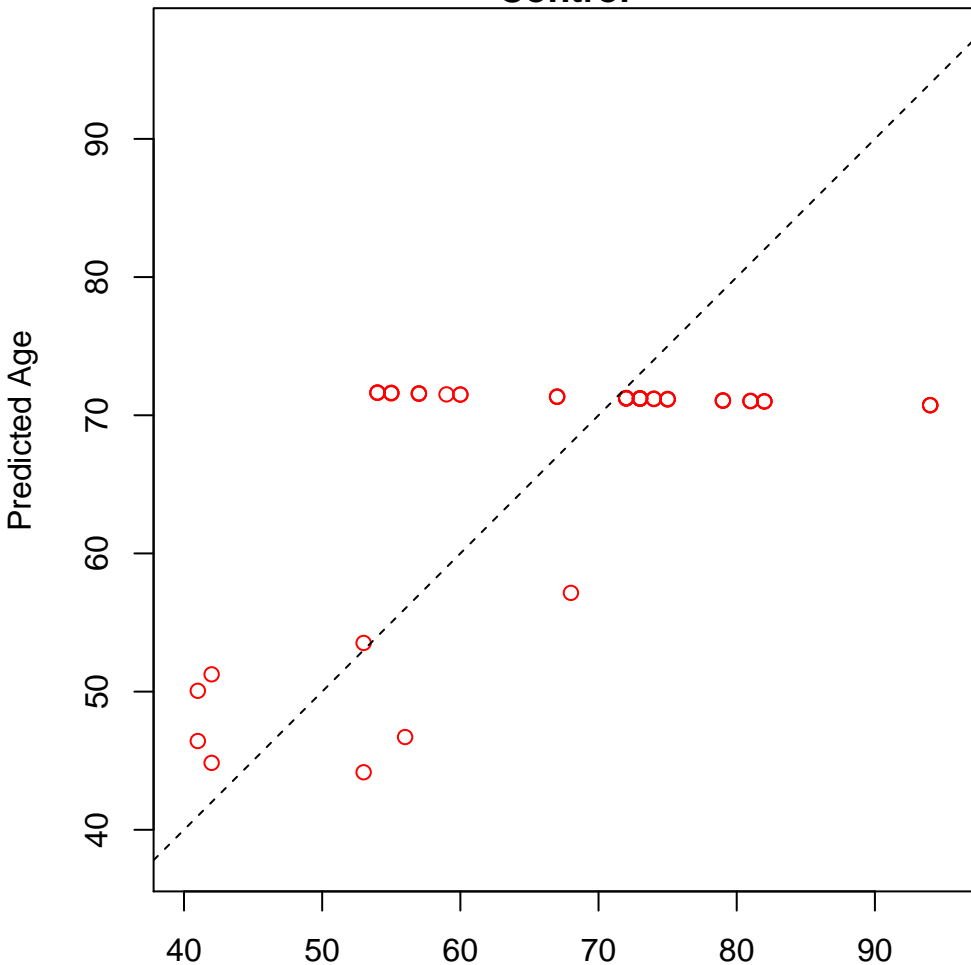
Test



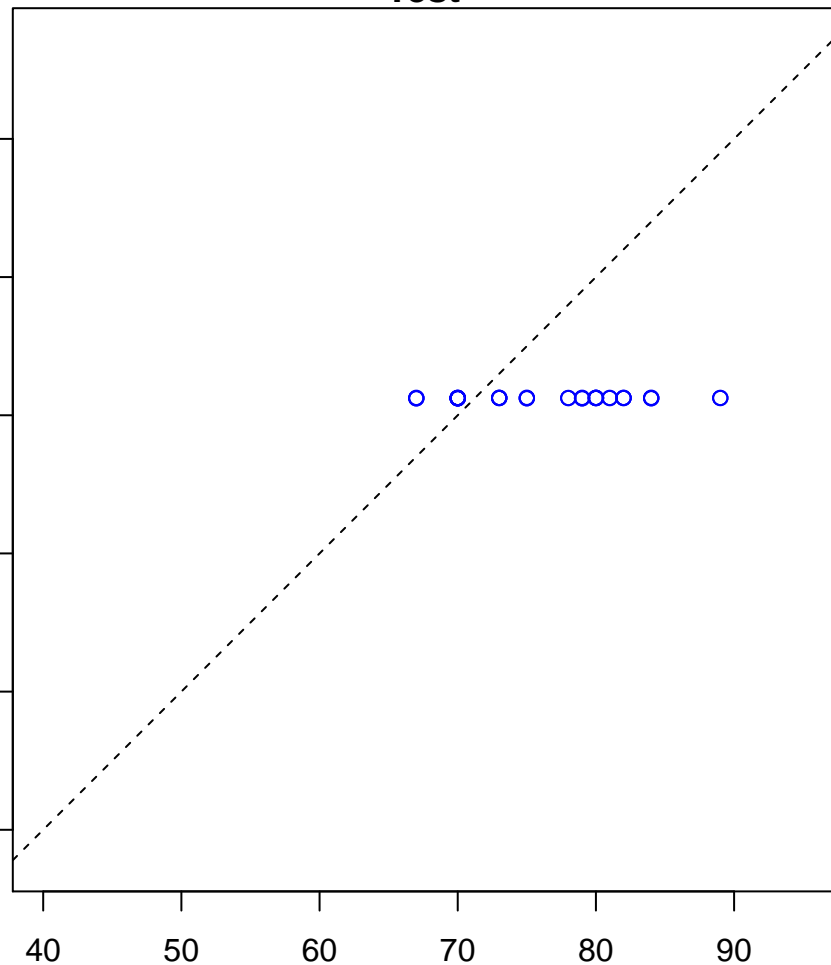
Actual Age

cation transmembrane transport (Score: 0.817808)

Control



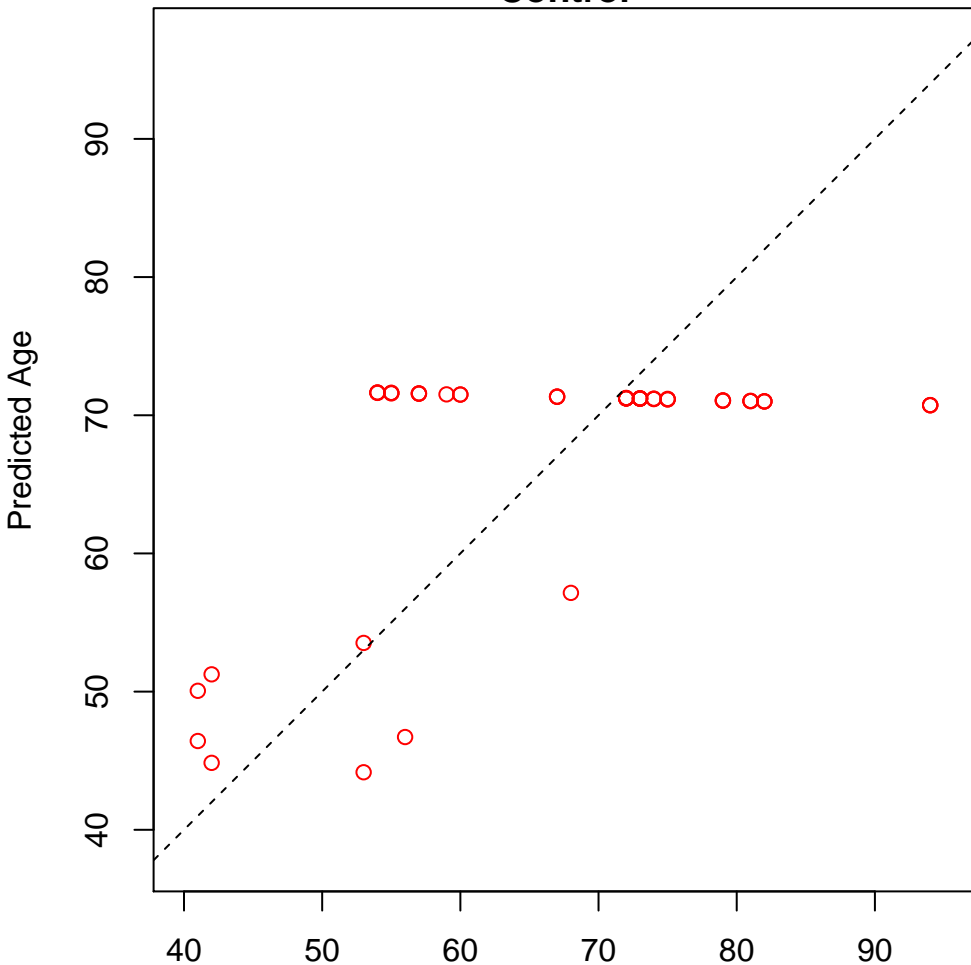
Test



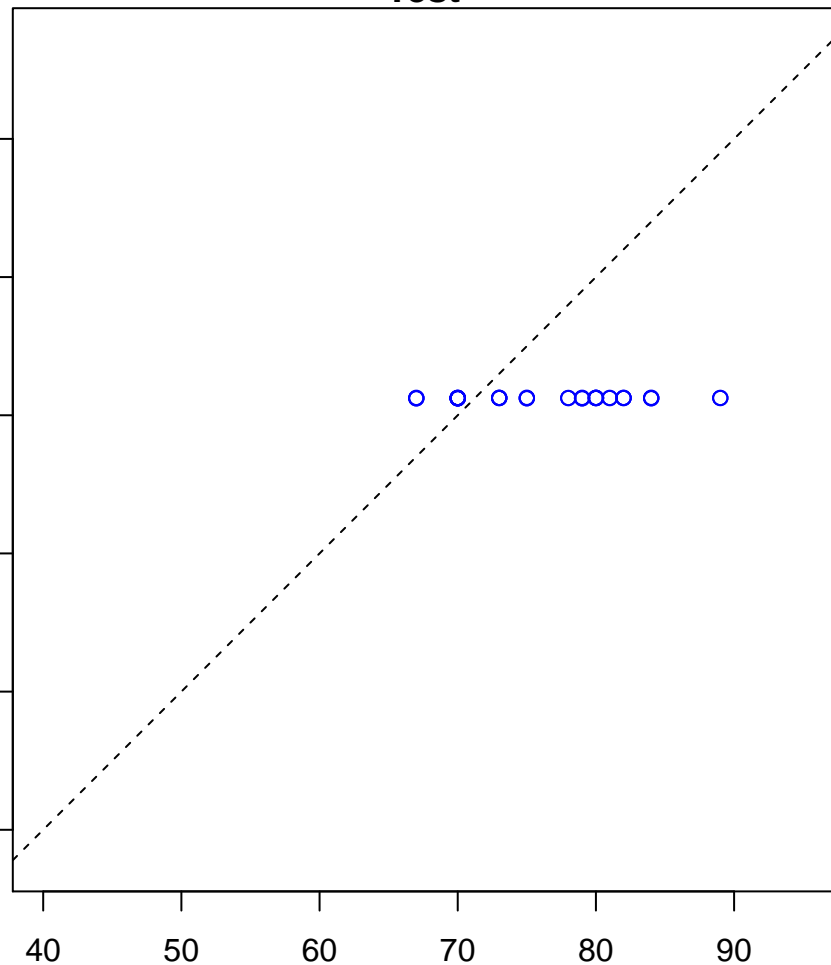
Actual Age

inorganic cation transmembrane transport (Score: 0.817808)

Control



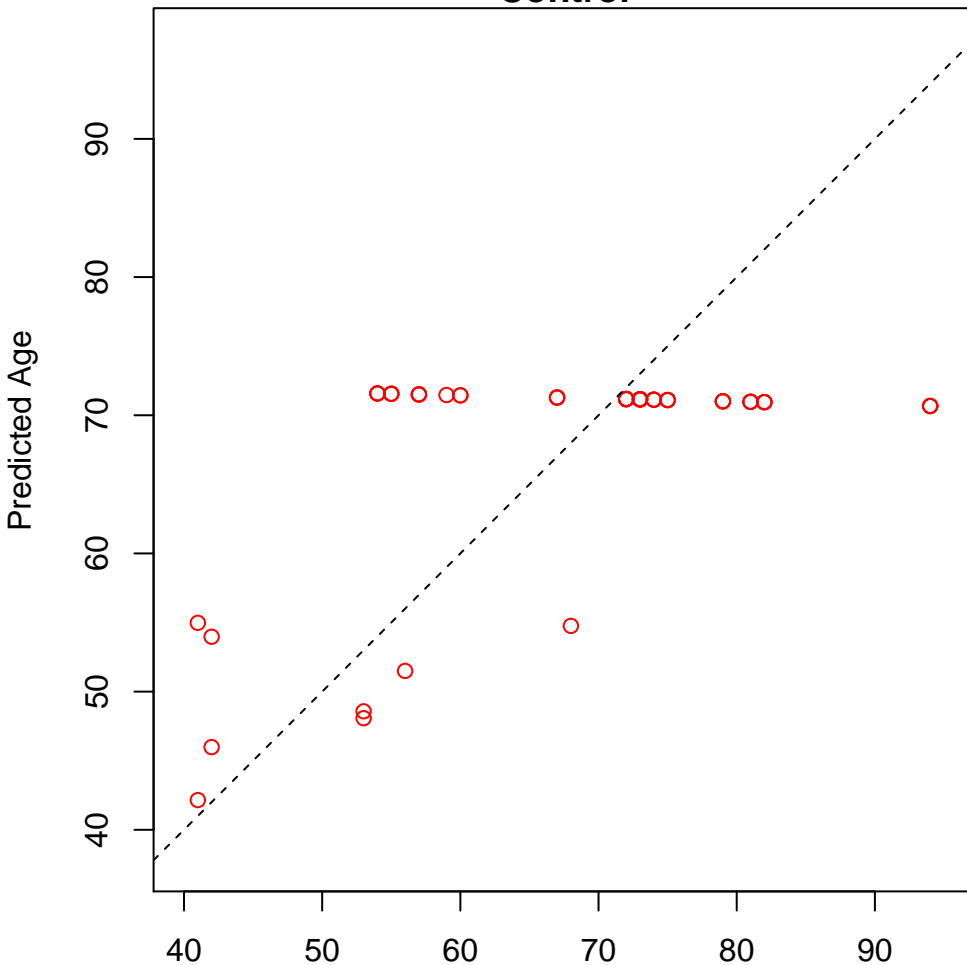
Test



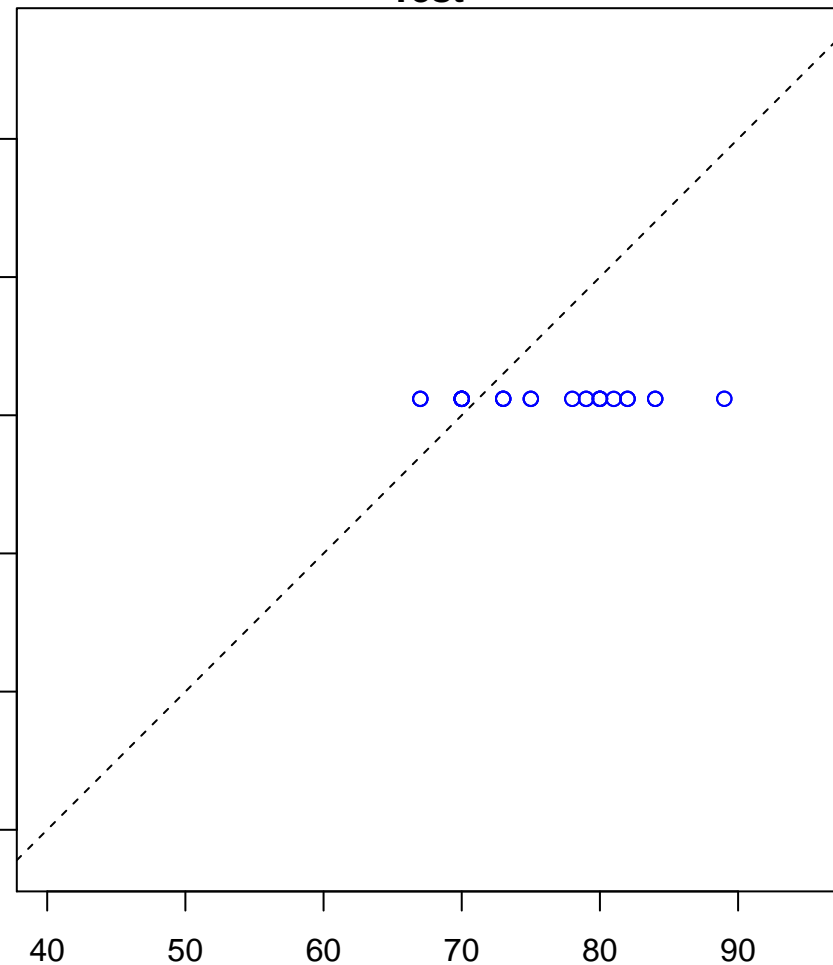
Actual Age

organic acid catabolic process (Score: 0.817781)

Control



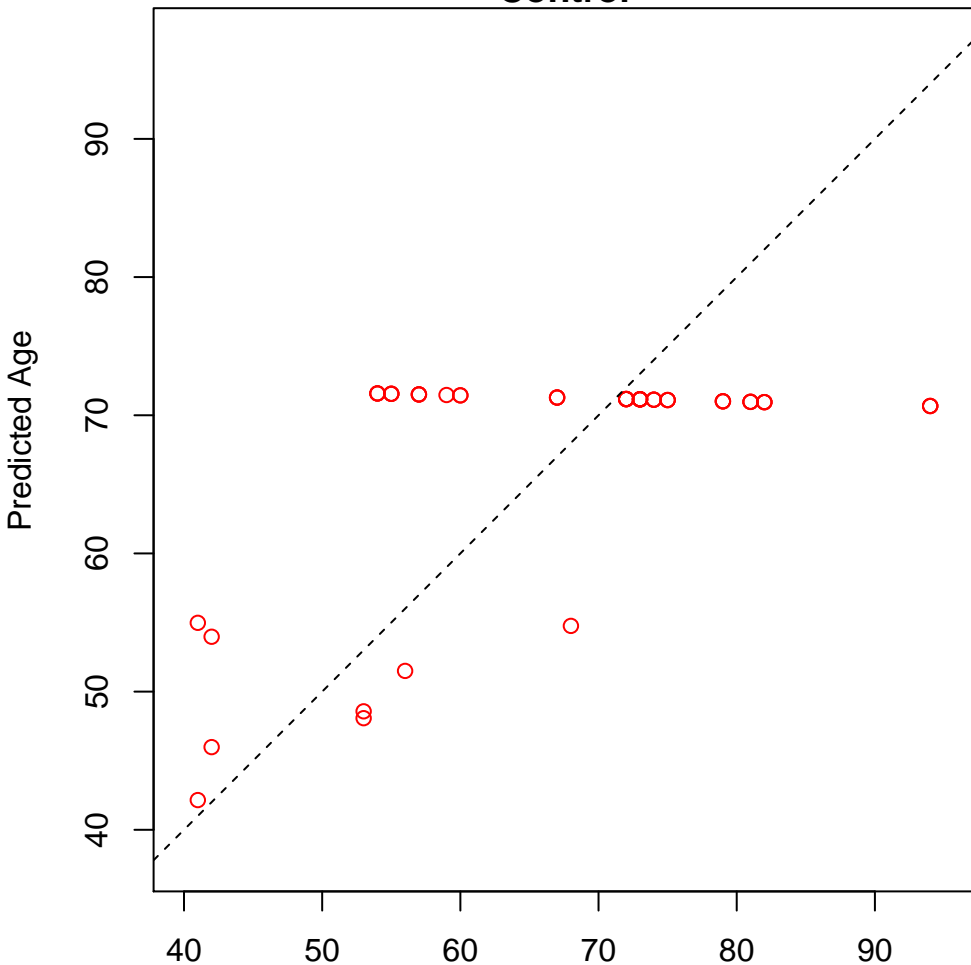
Test



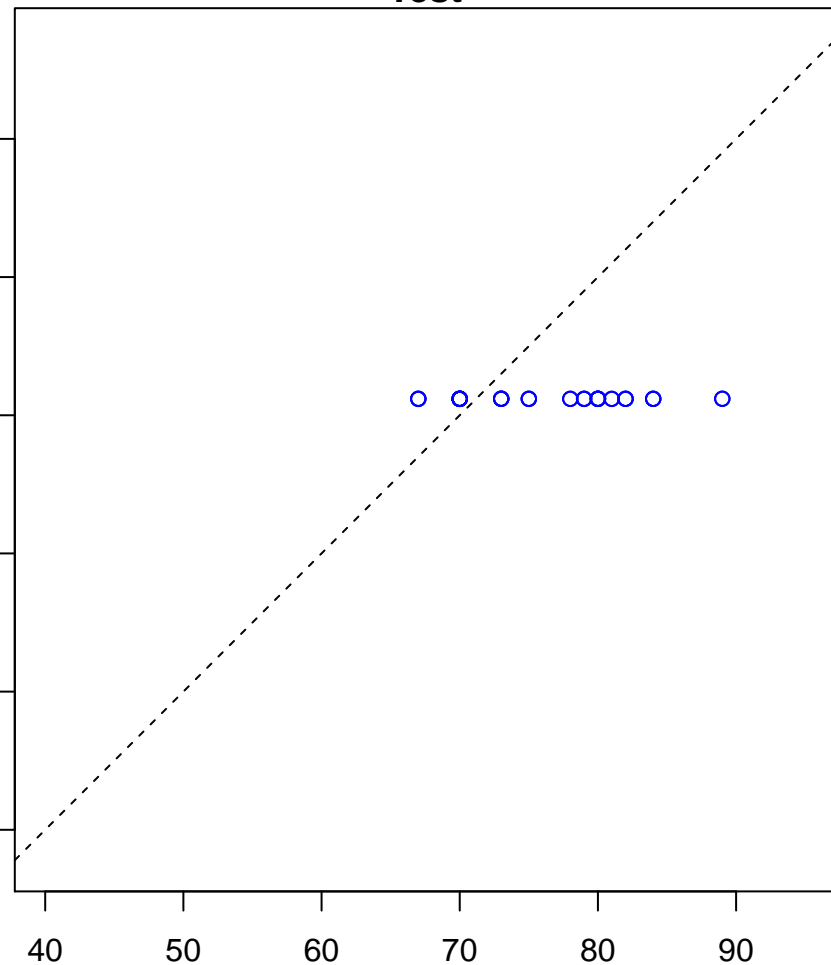
Actual Age

carboxylic acid catabolic process (Score: 0.817781)

Control



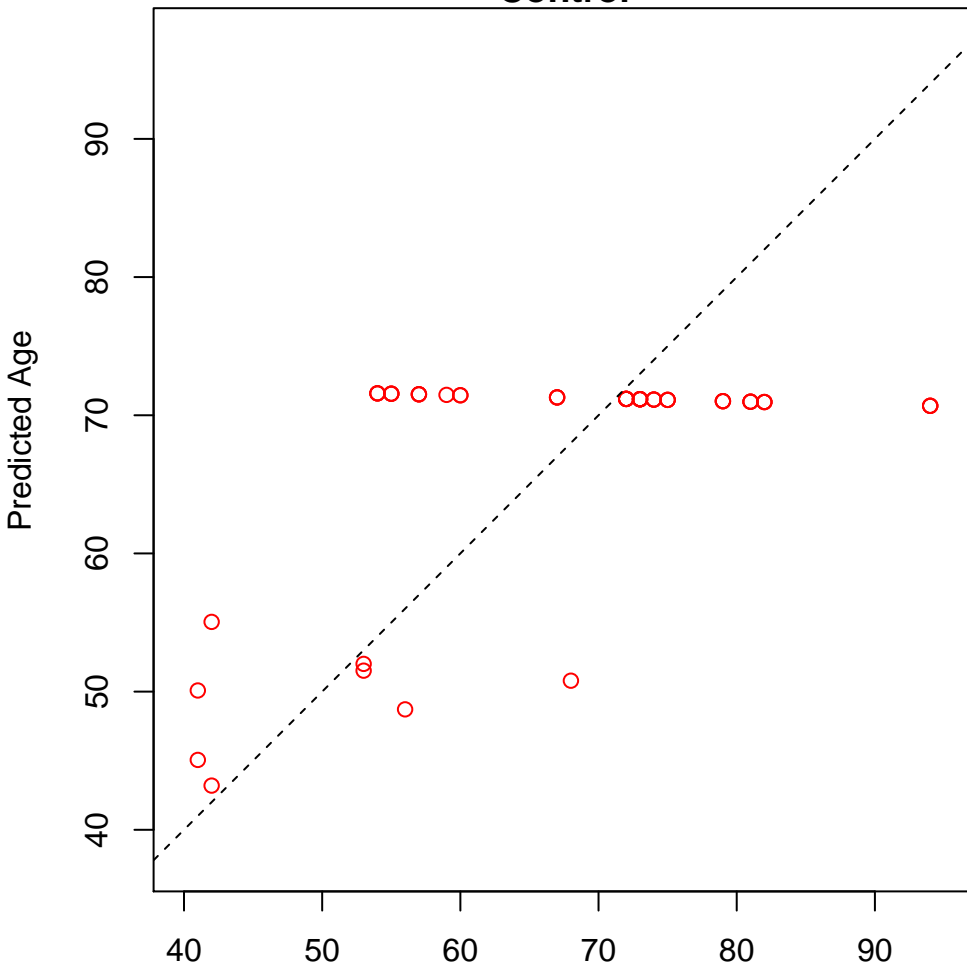
Test



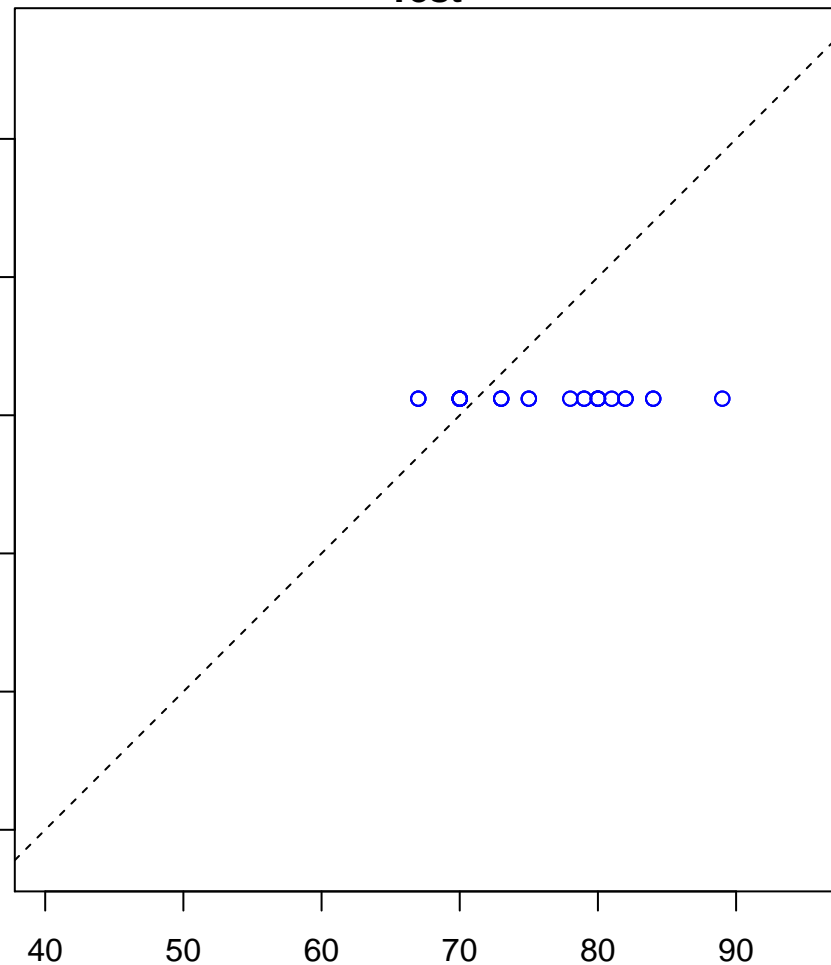
Actual Age

clathrin-dependent endocytosis (Score: 0.817779)

Control

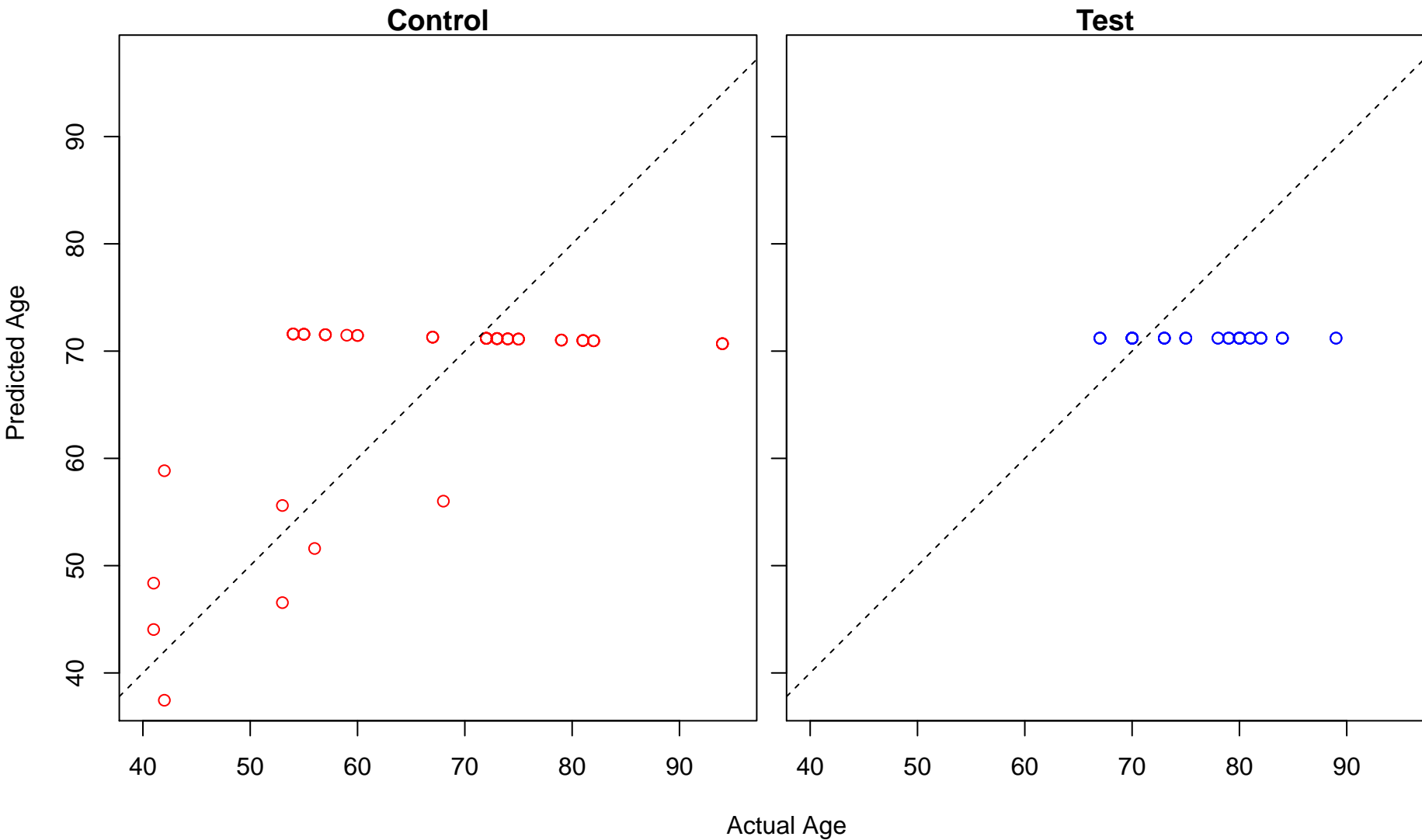


Test



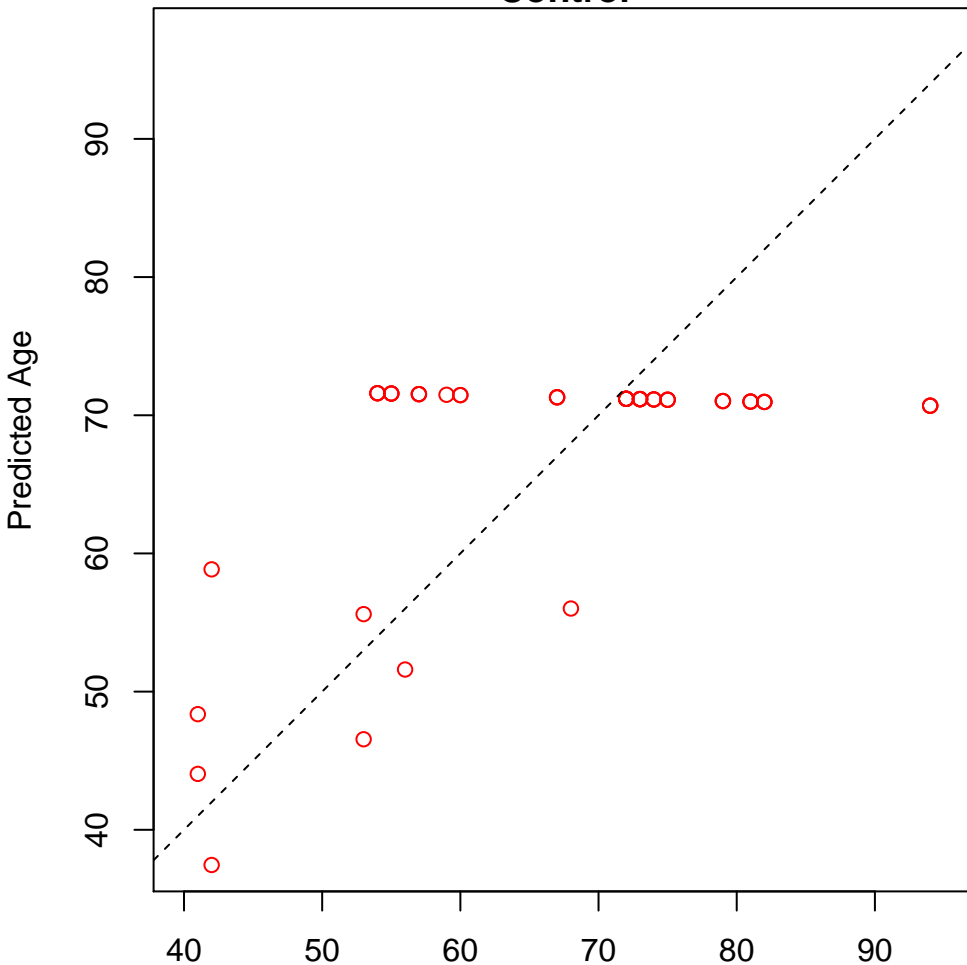
Actual Age

response to oxidative stress (Score: 0.817671)

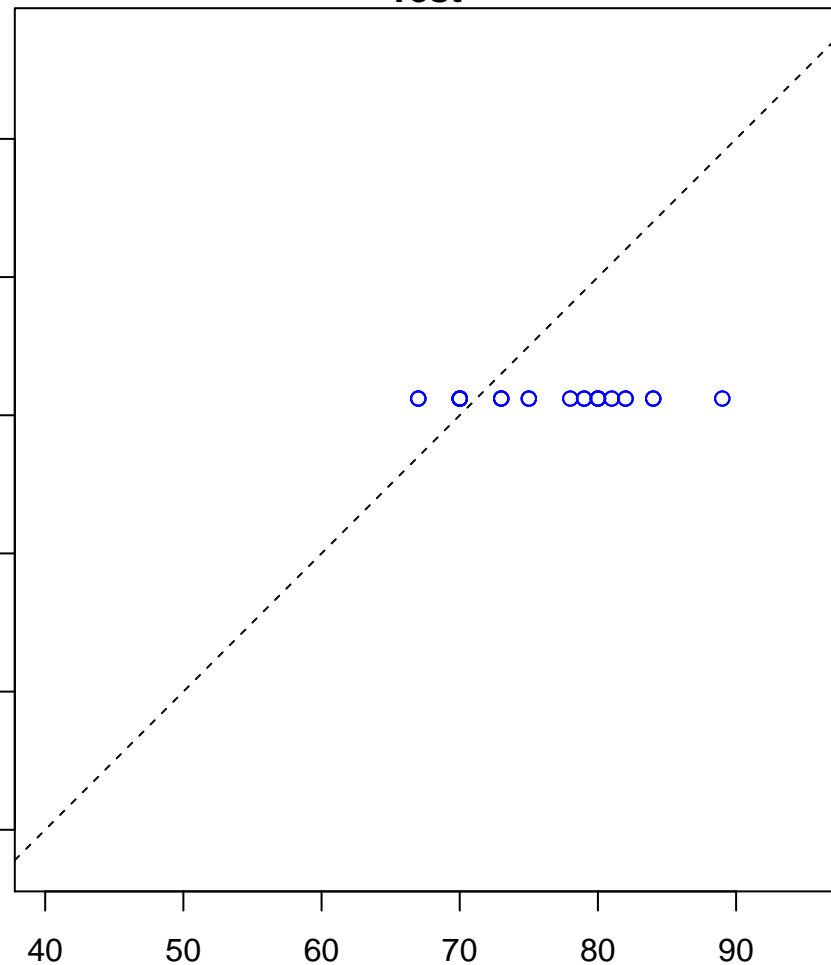


cellular response to oxidative stress (Score: 0.817671)

Control

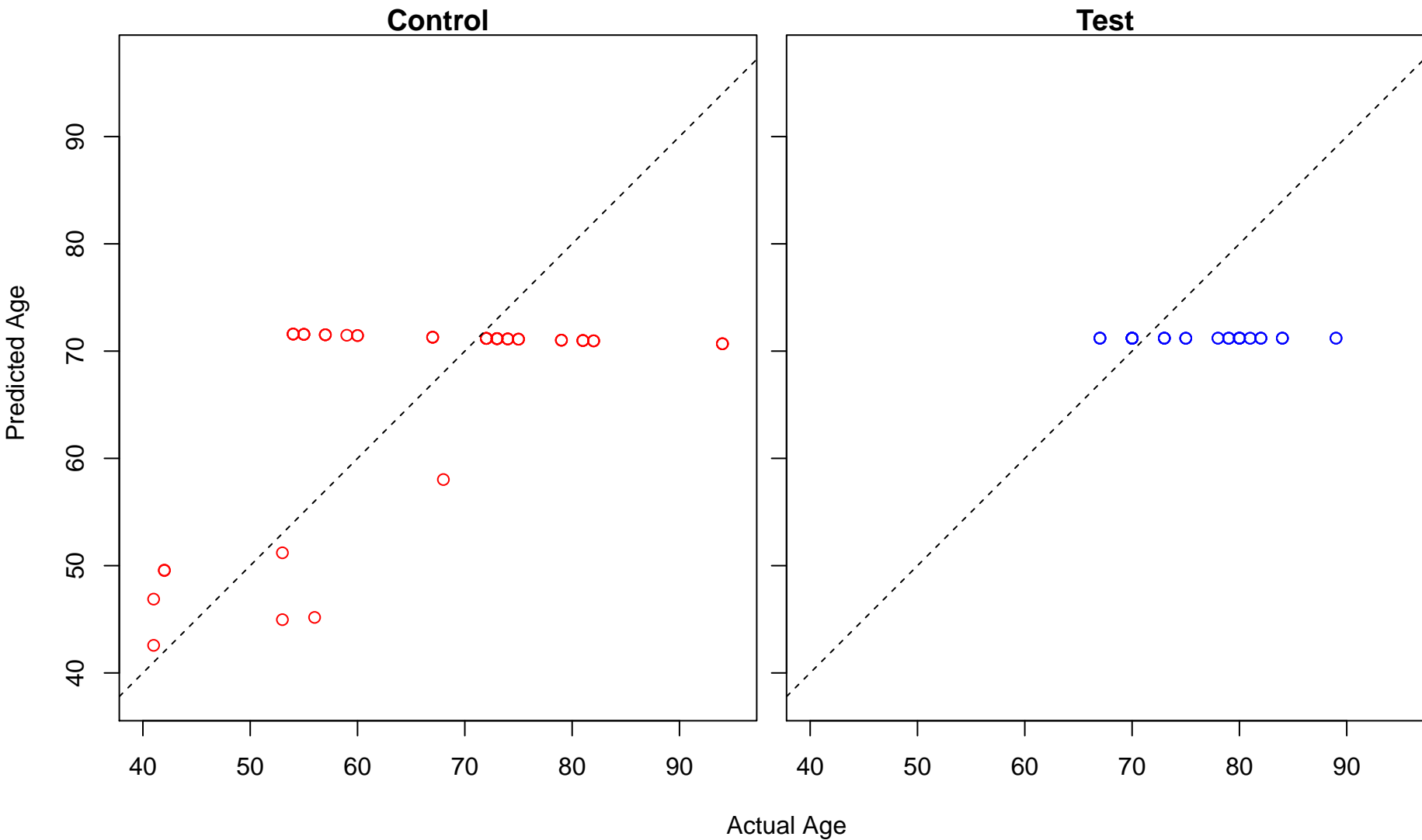


Test



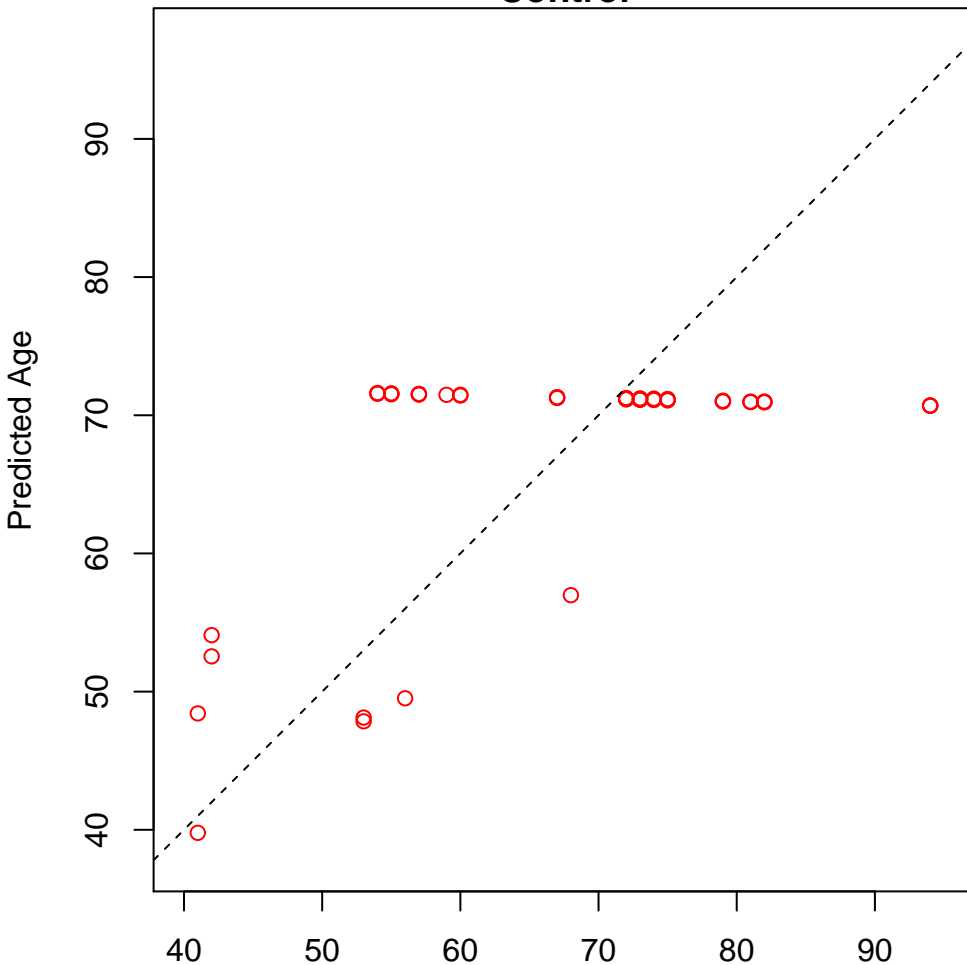
Actual Age

positive regulation of cellular protein localization (Score: 0.817619)

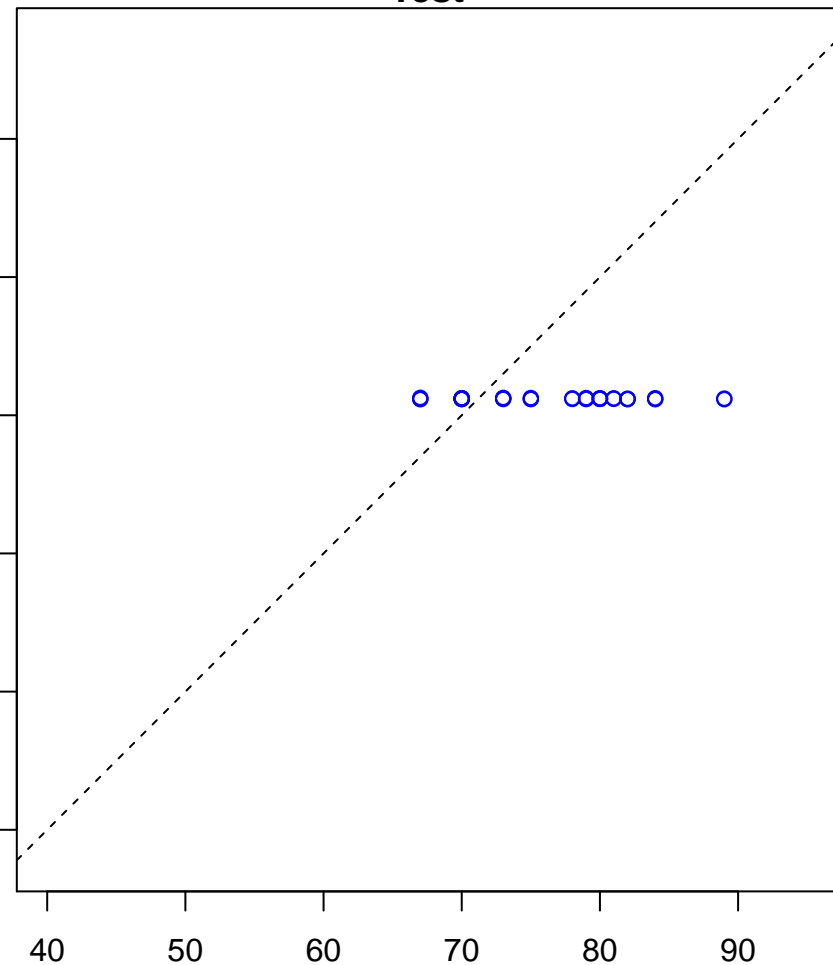


DNA-dependent DNA replication (Score: 0.817538)

Control

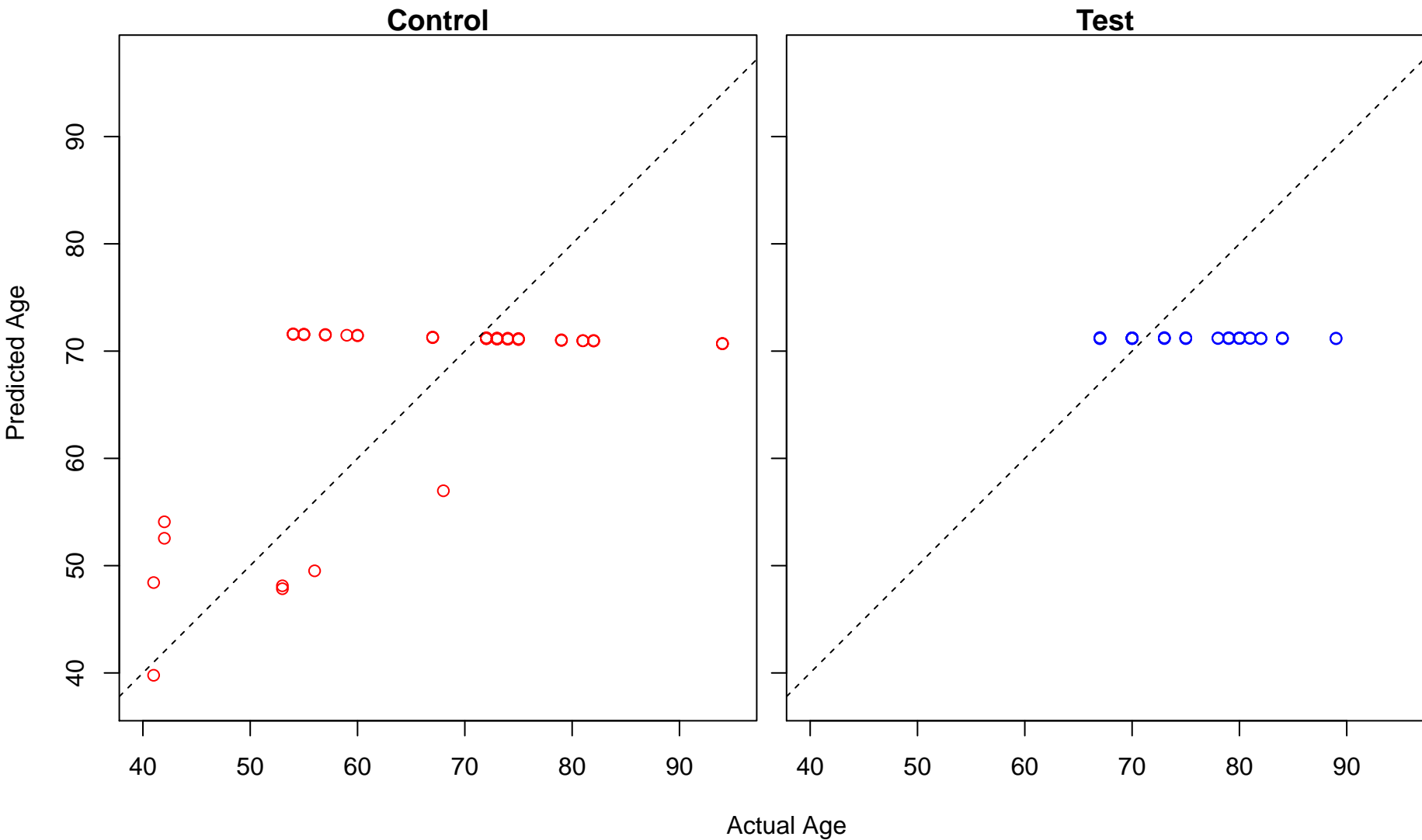


Test

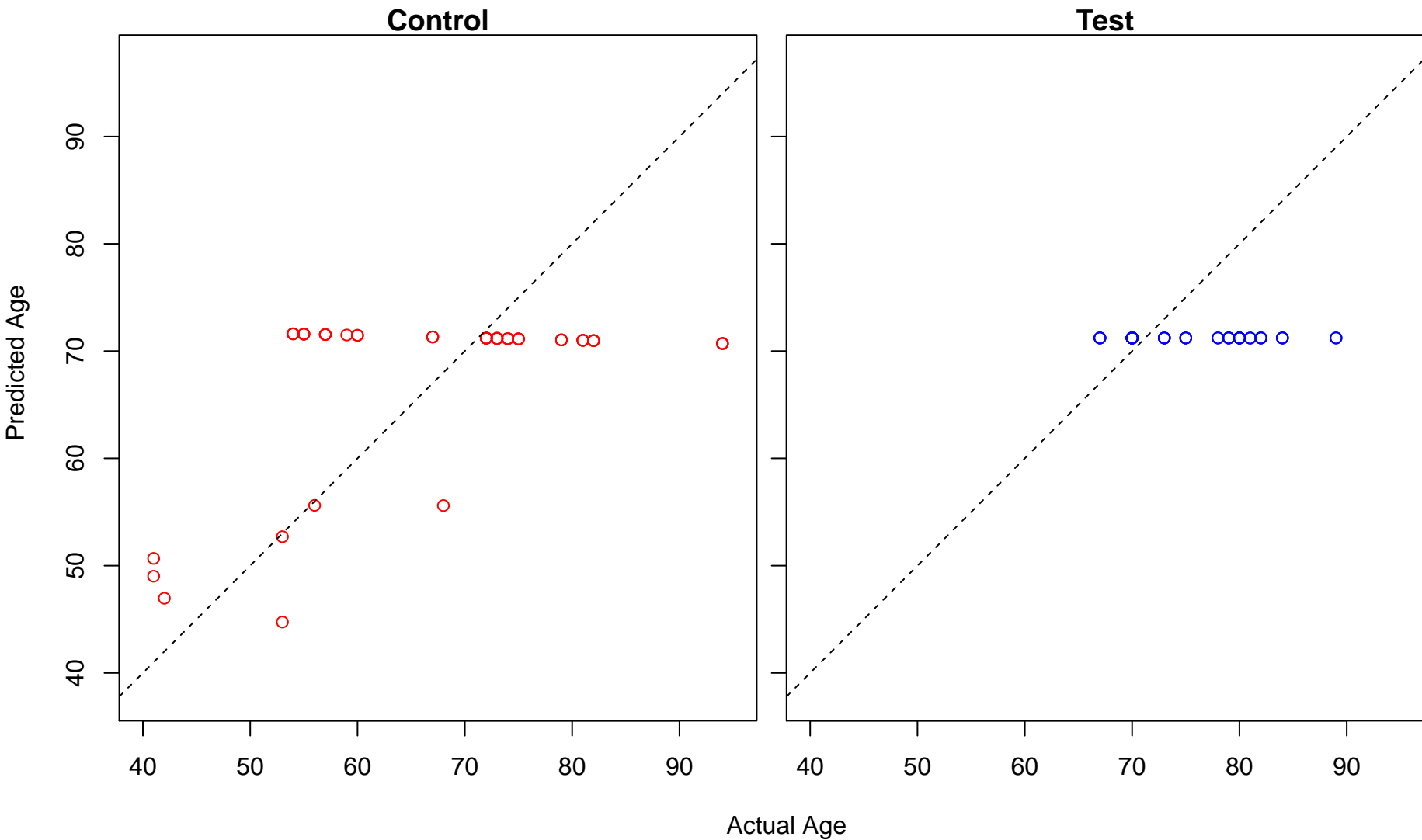


Actual Age

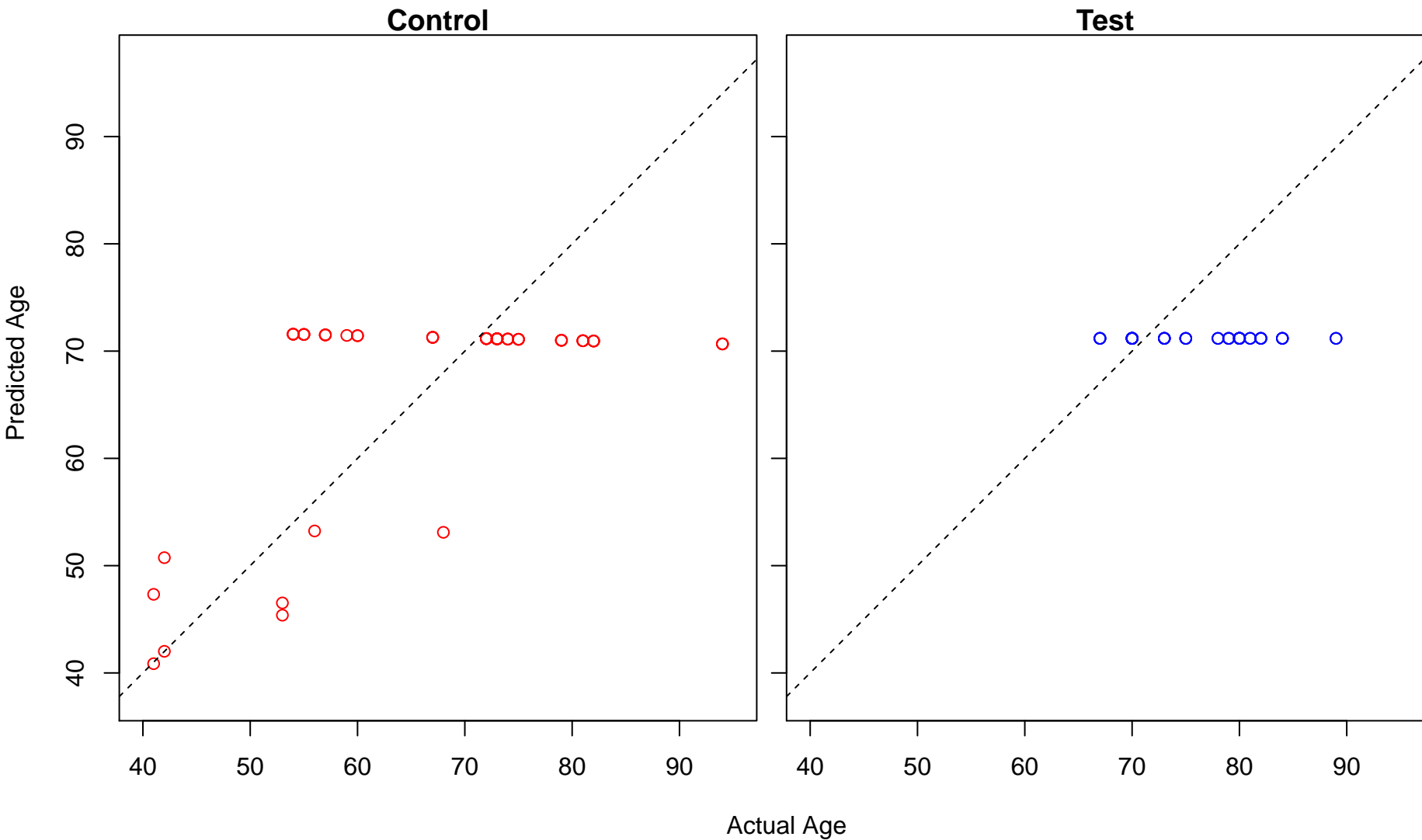
cell cycle DNA replication (Score: 0.817538)



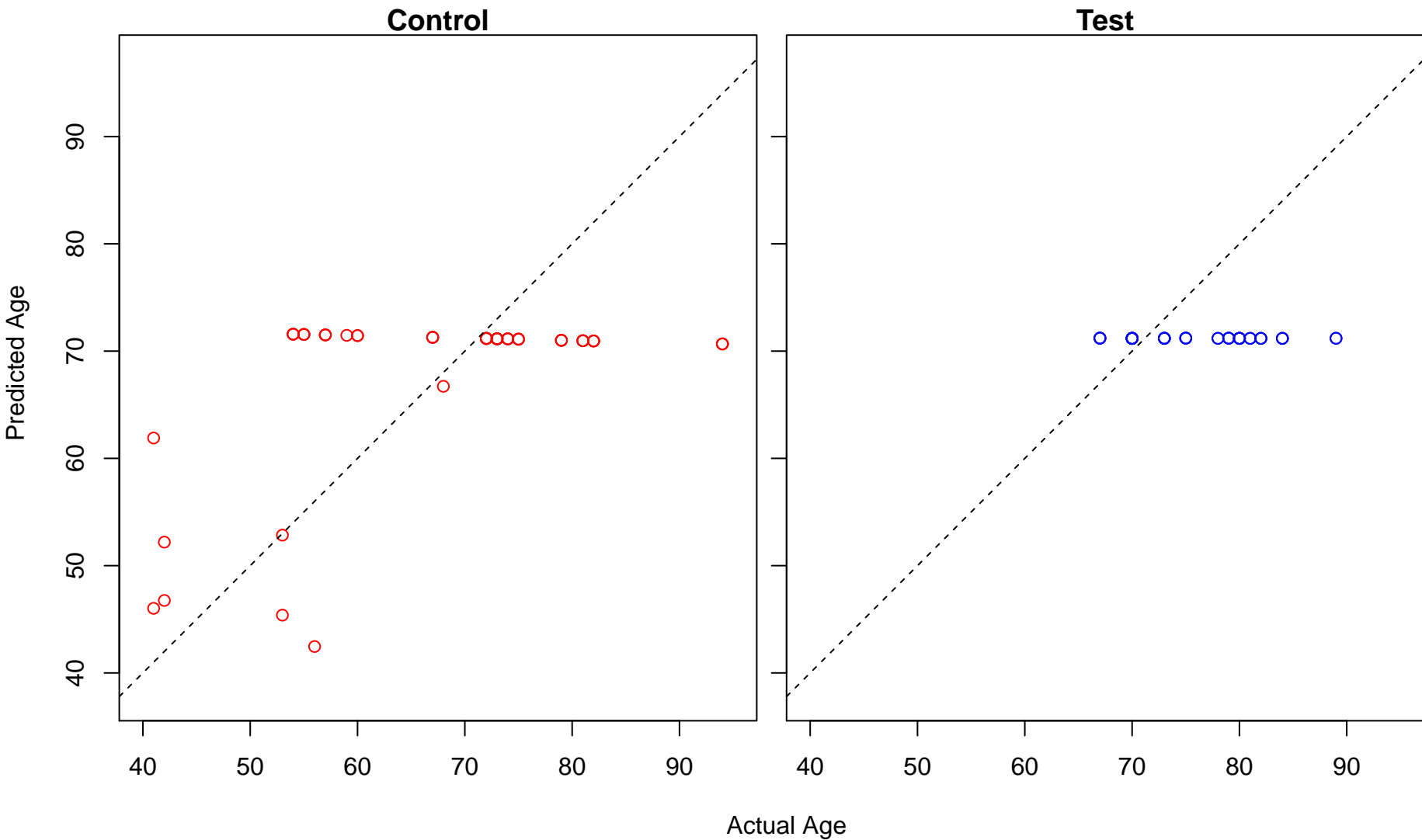
platelet degranulation (Score: 0.817493)



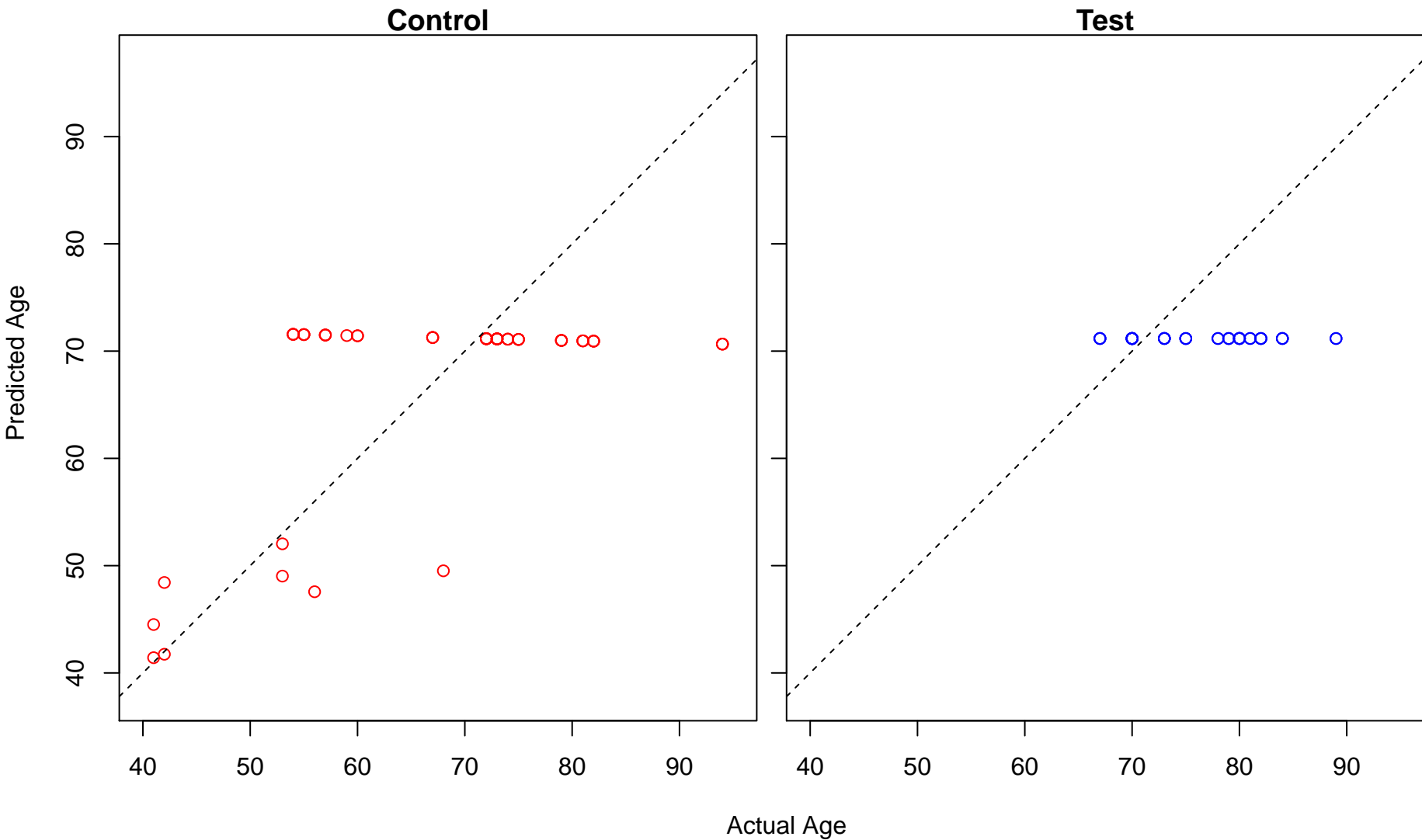
positive regulation of protein phosphorylation (Score: 0.817397)



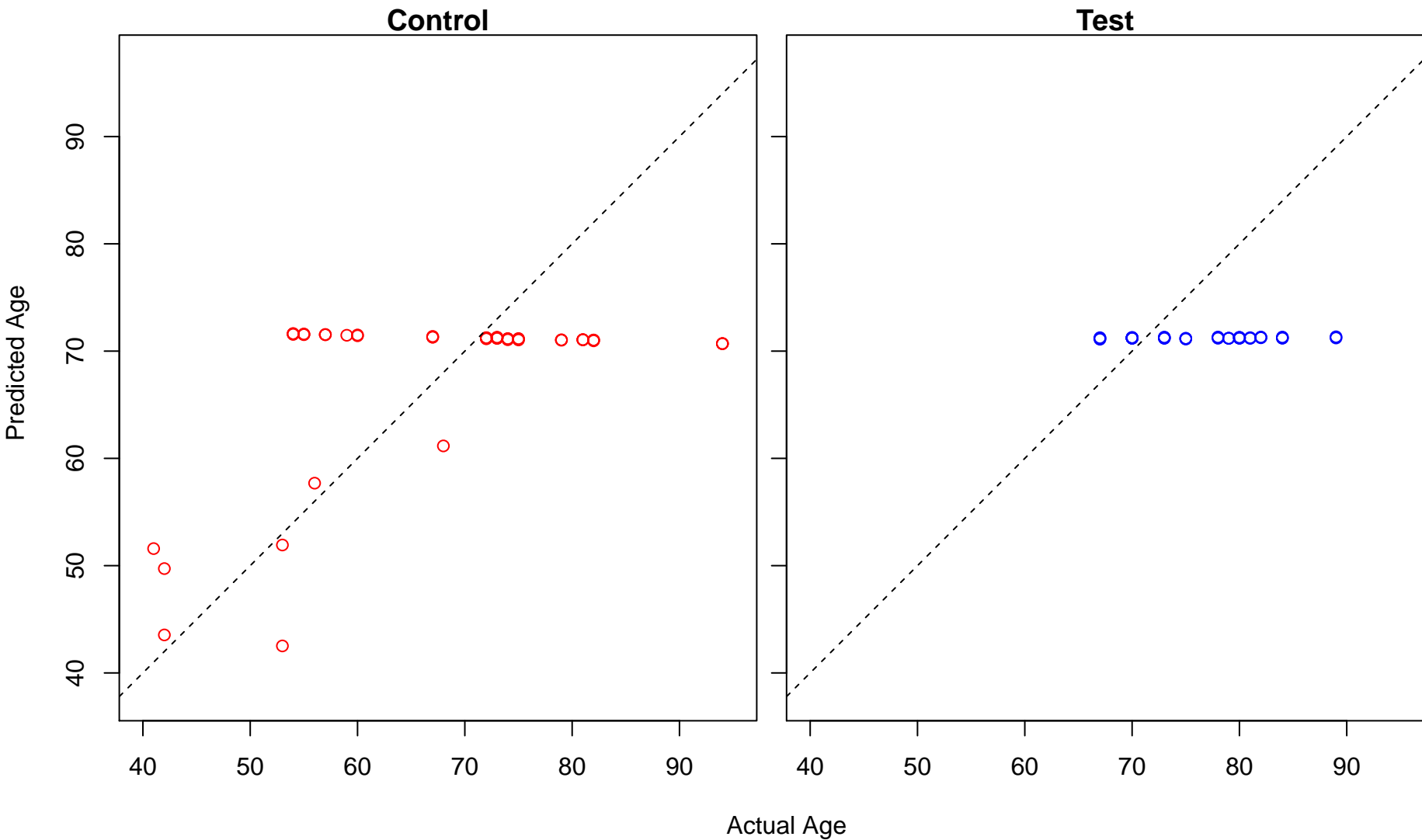
negative regulation of intracellular transport (Score: 0.817392)



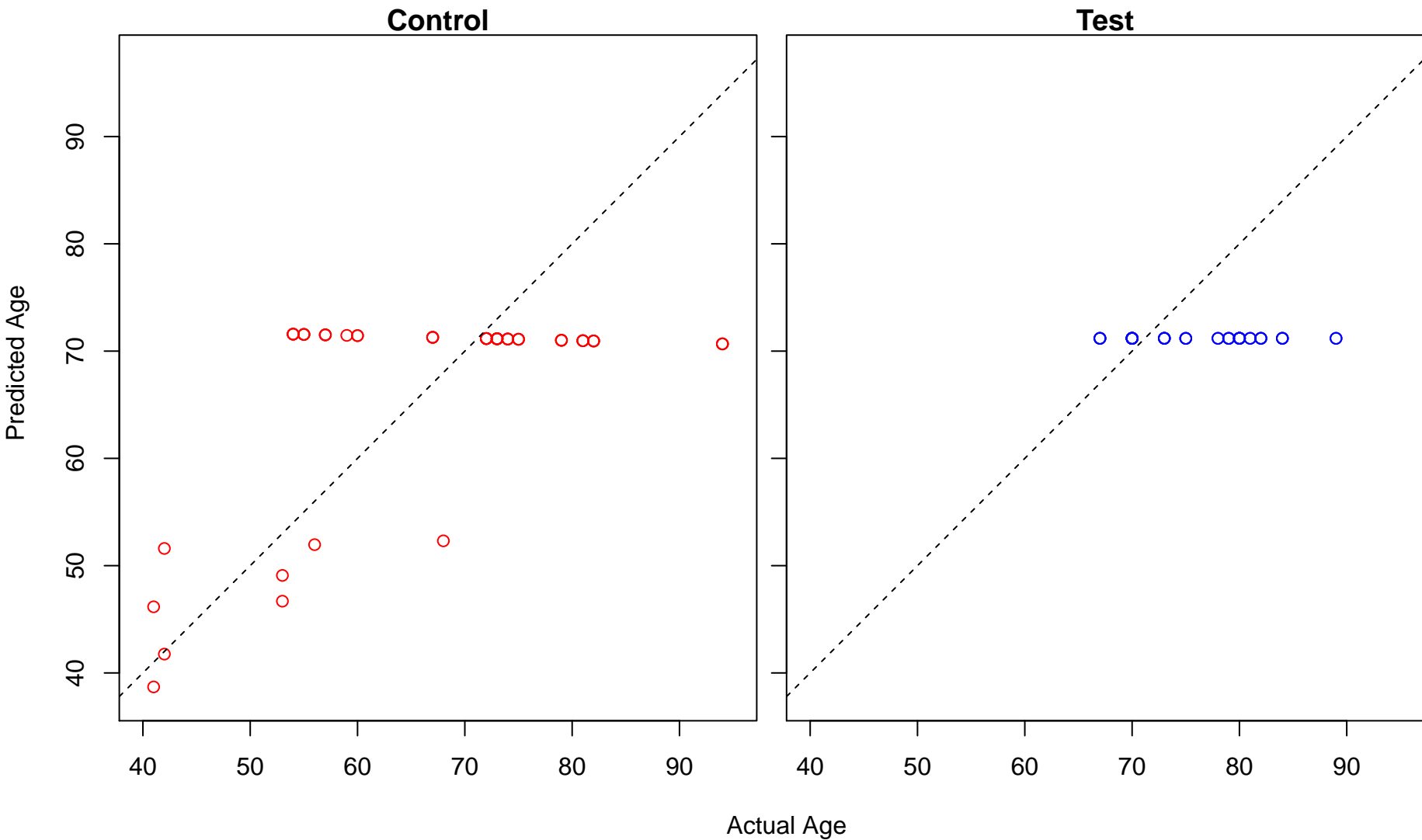
homeostatic process (Score: 0.817369)



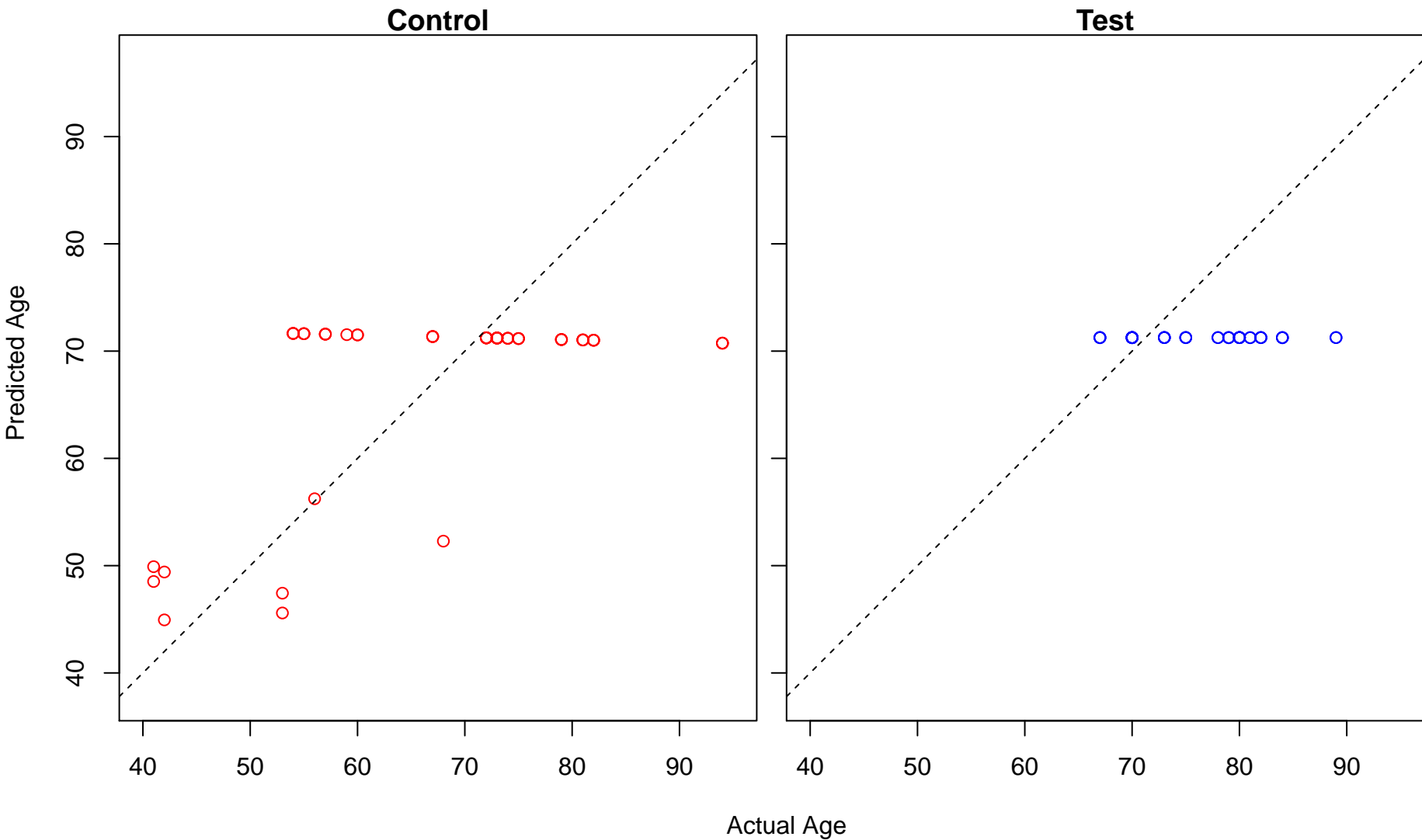
positive regulation of lymphocyte differentiation (Score: 0.817341)



regulation of transferase activity (Score: 0.817313)

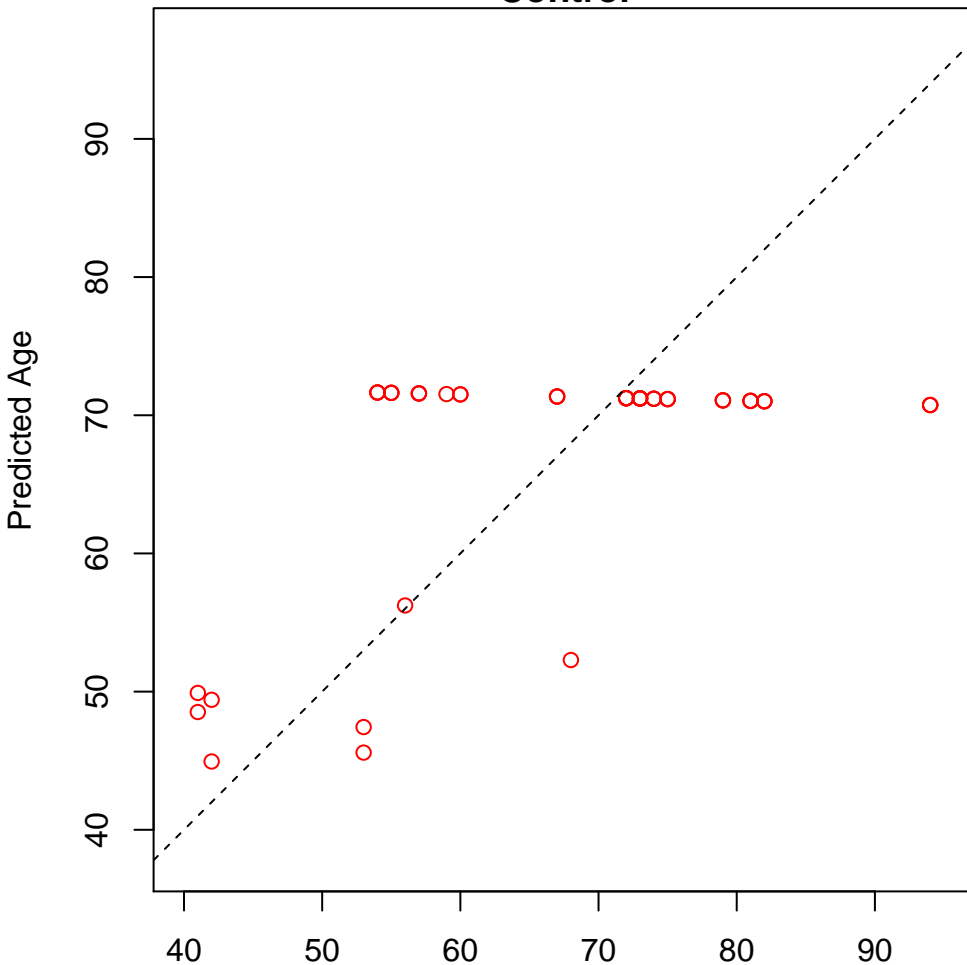


regulation of mRNA binding (Score: 0.817311)

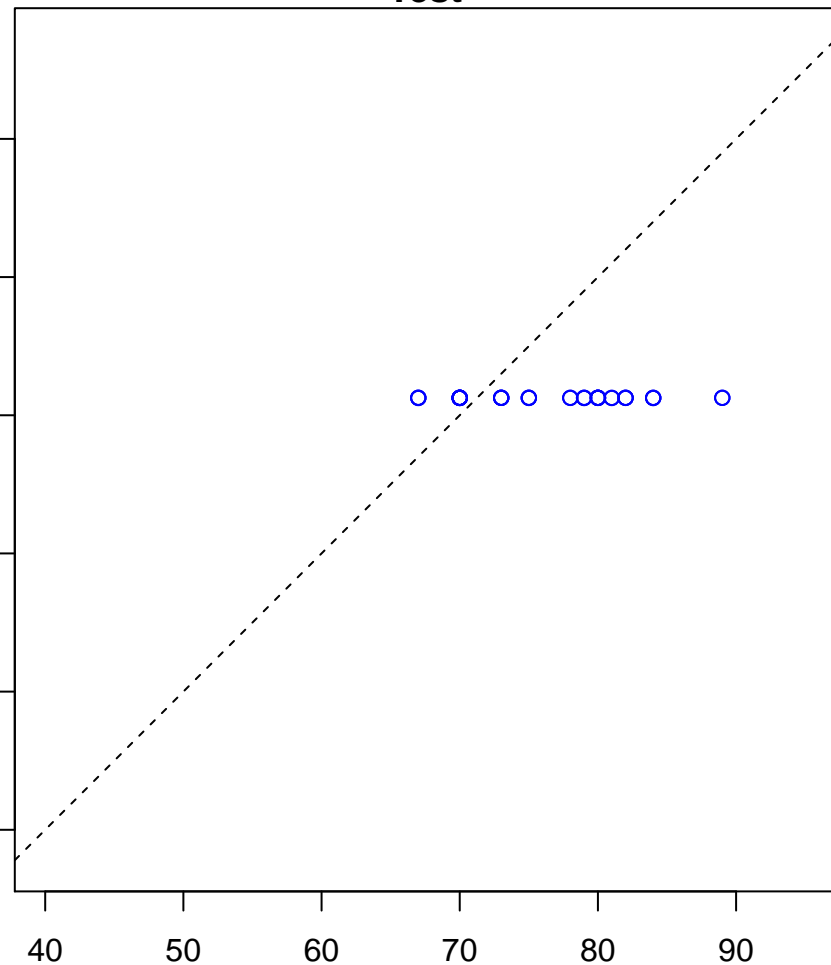


positive regulation of mRNA binding (Score: 0.817311)

Control

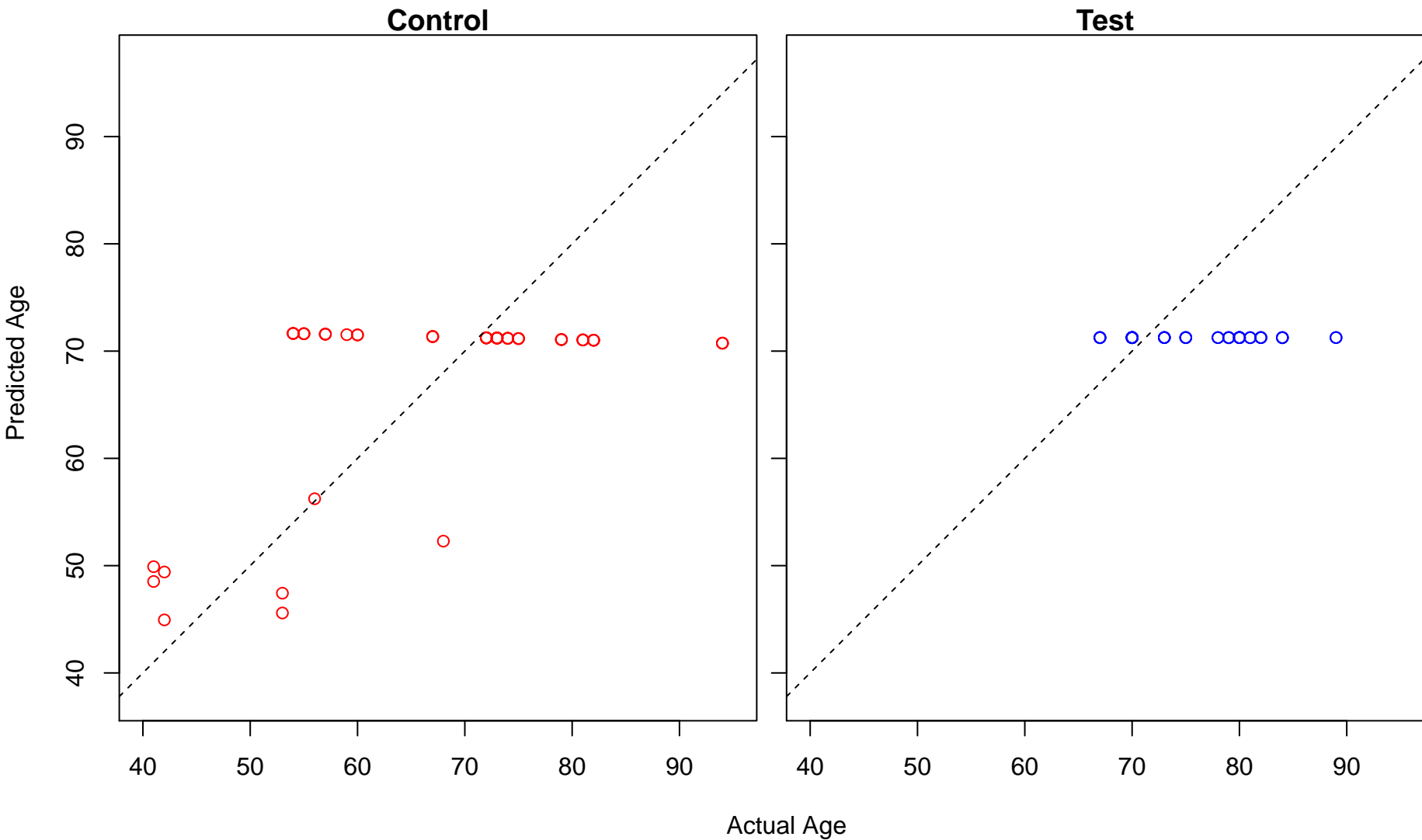


Test



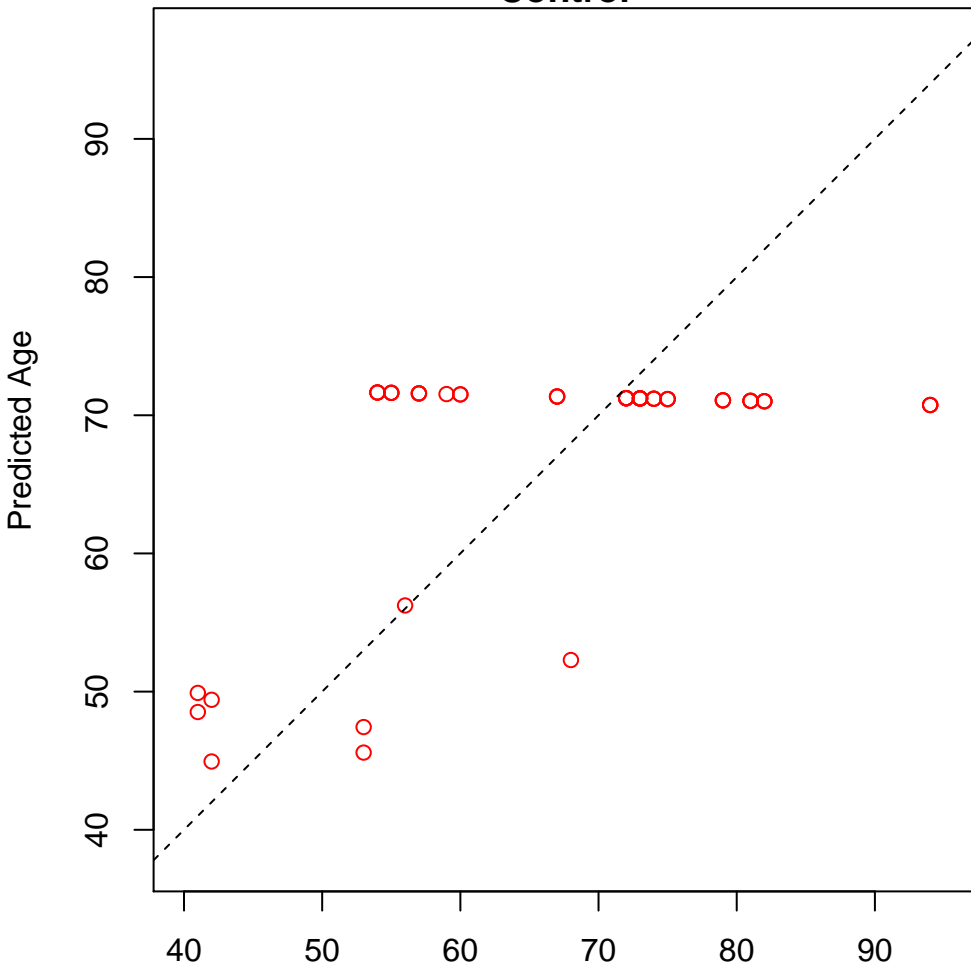
Actual Age

regulation of RNA binding (Score: 0.817311)

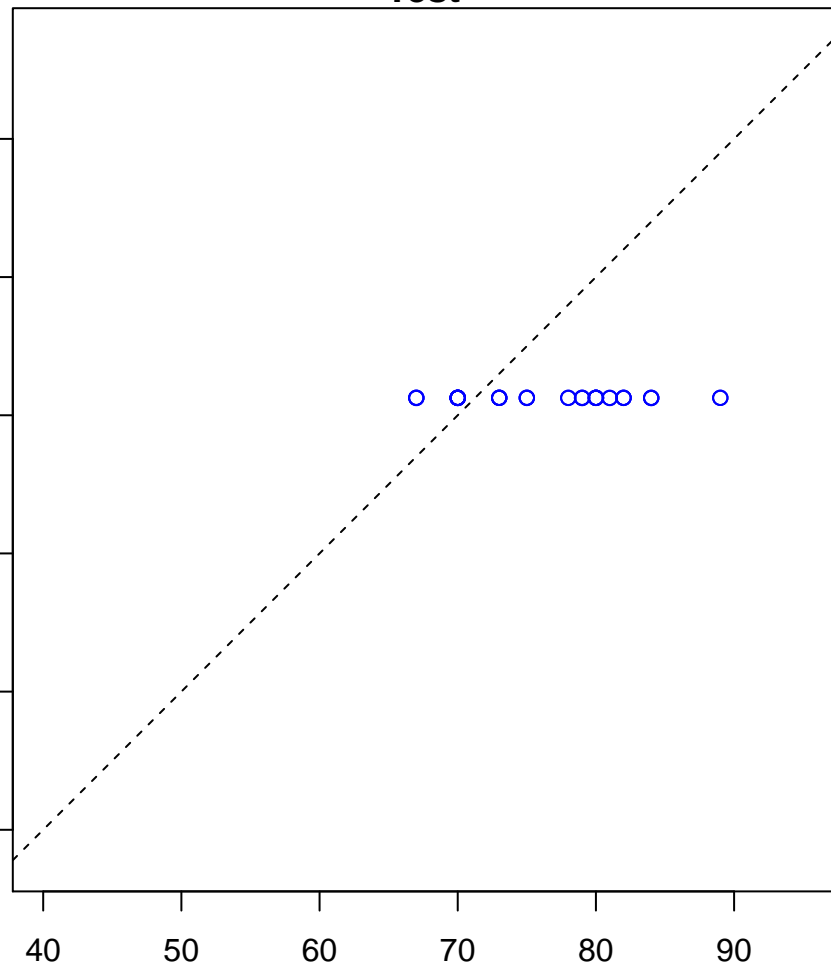


positive regulation of RNA binding (Score: 0.817311)

Control

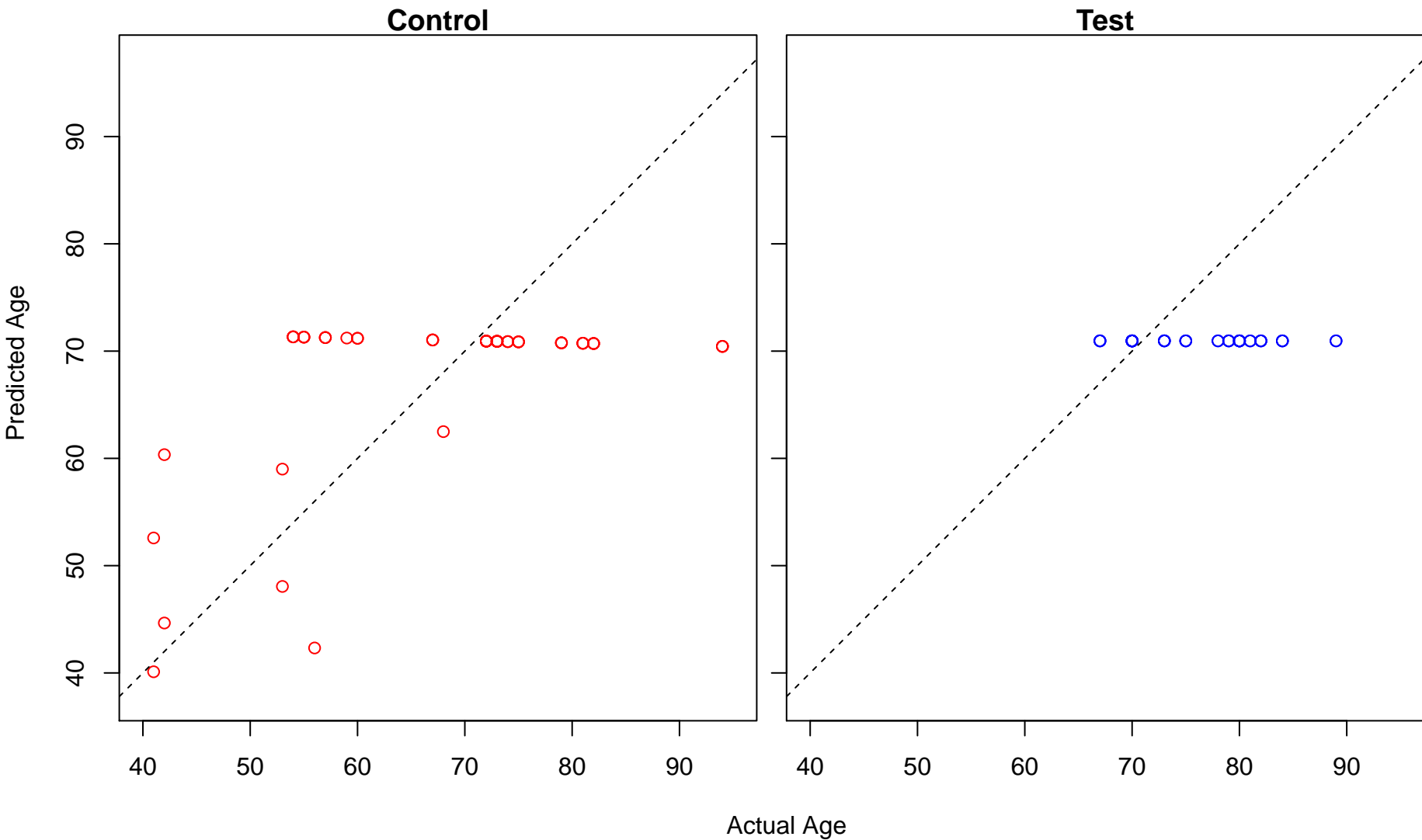


Test

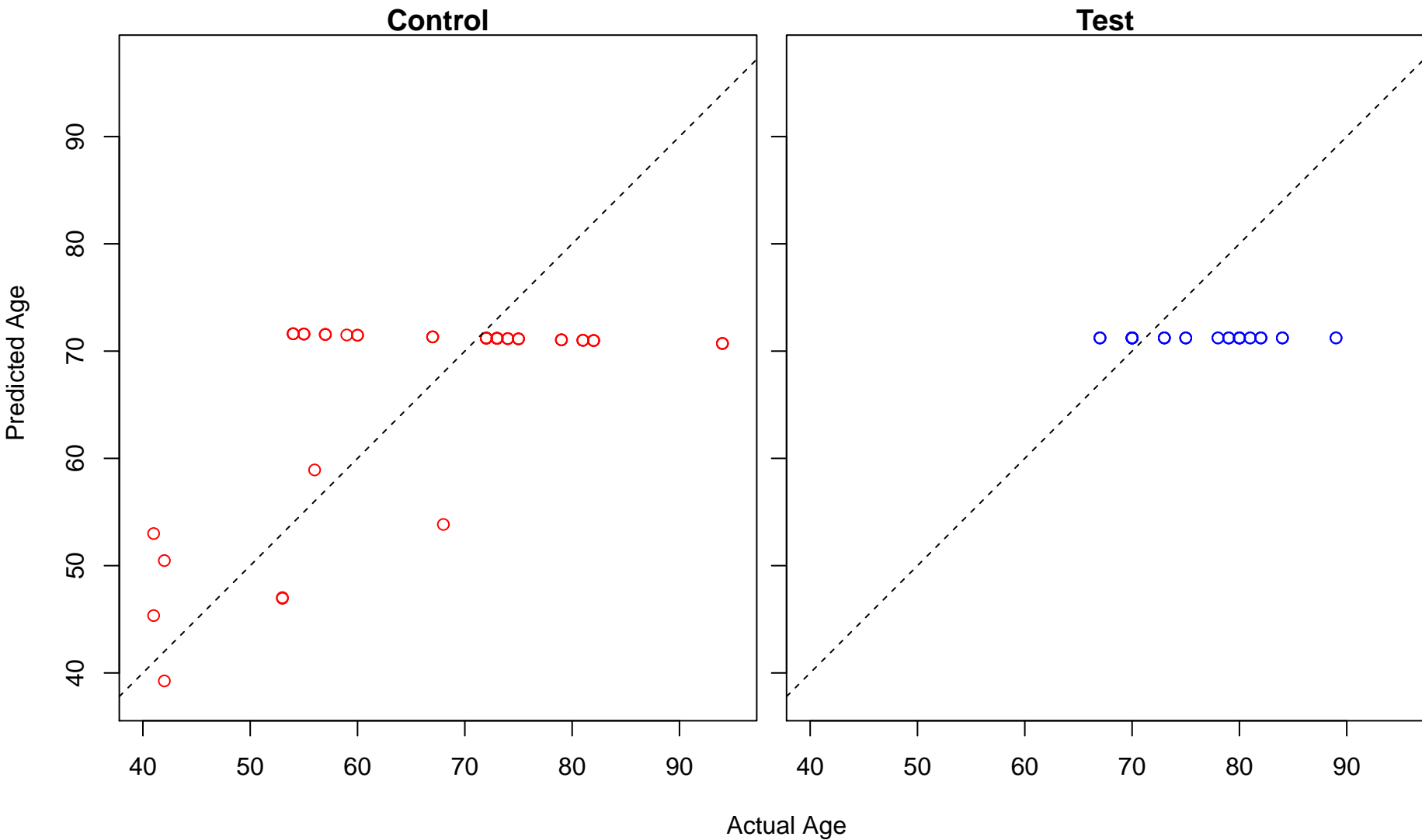


Actual Age

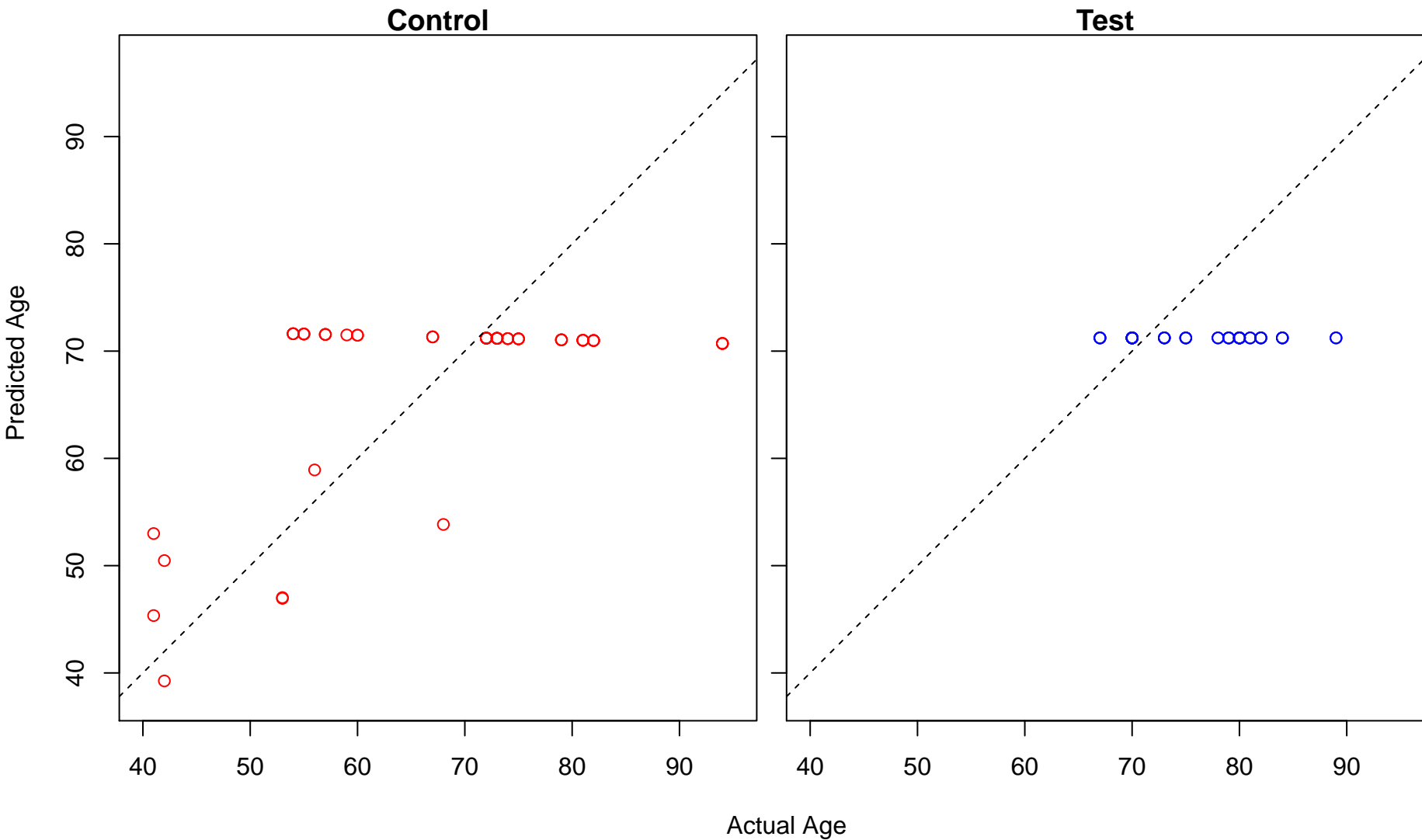
cognition (Score: 0.817136)



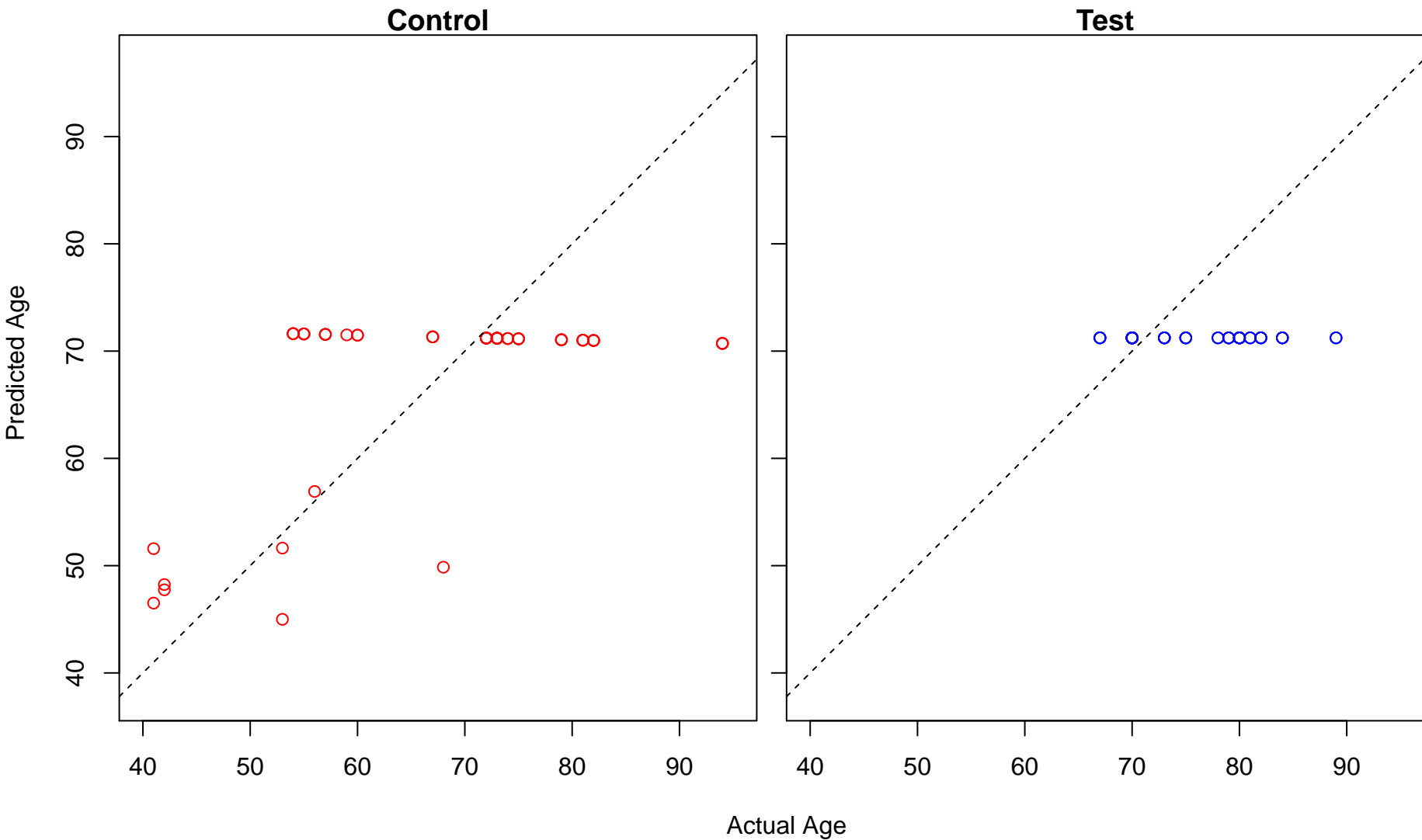
neuron differentiation (Score: 0.817133)



neuron development (Score: 0.817133)

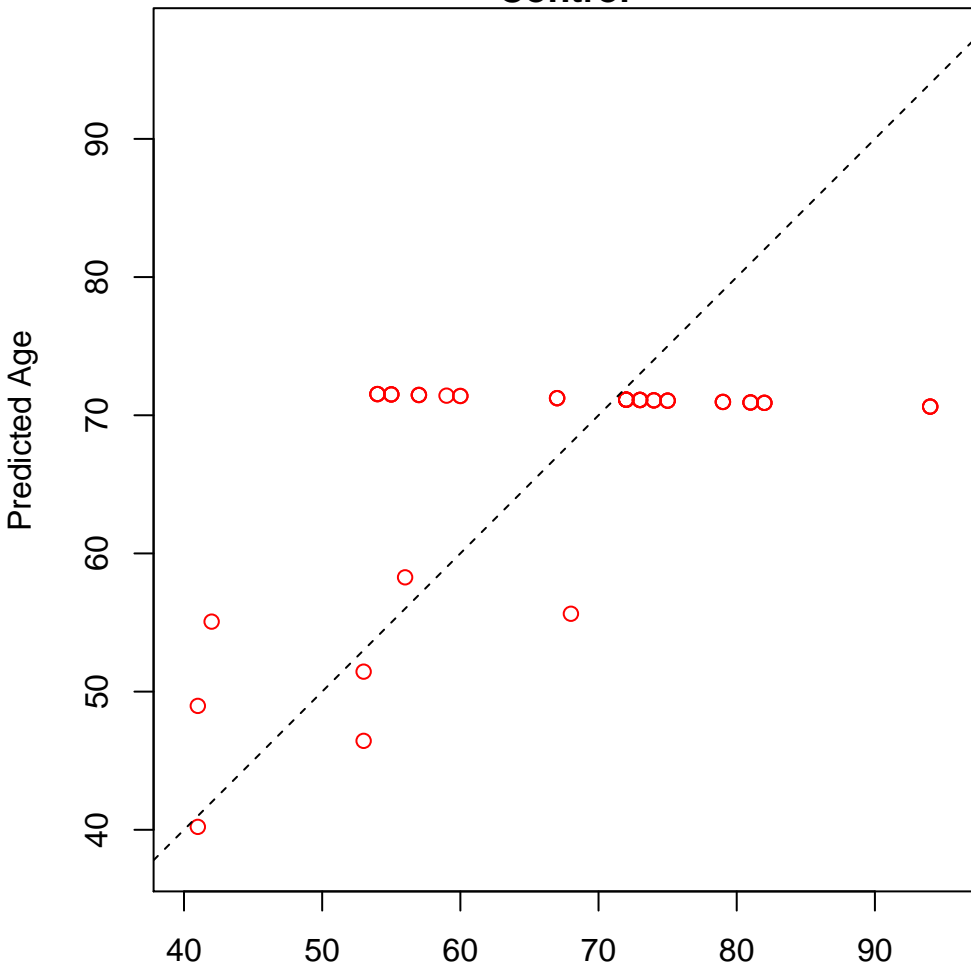


lipid metabolic process (Score: 0.817087)

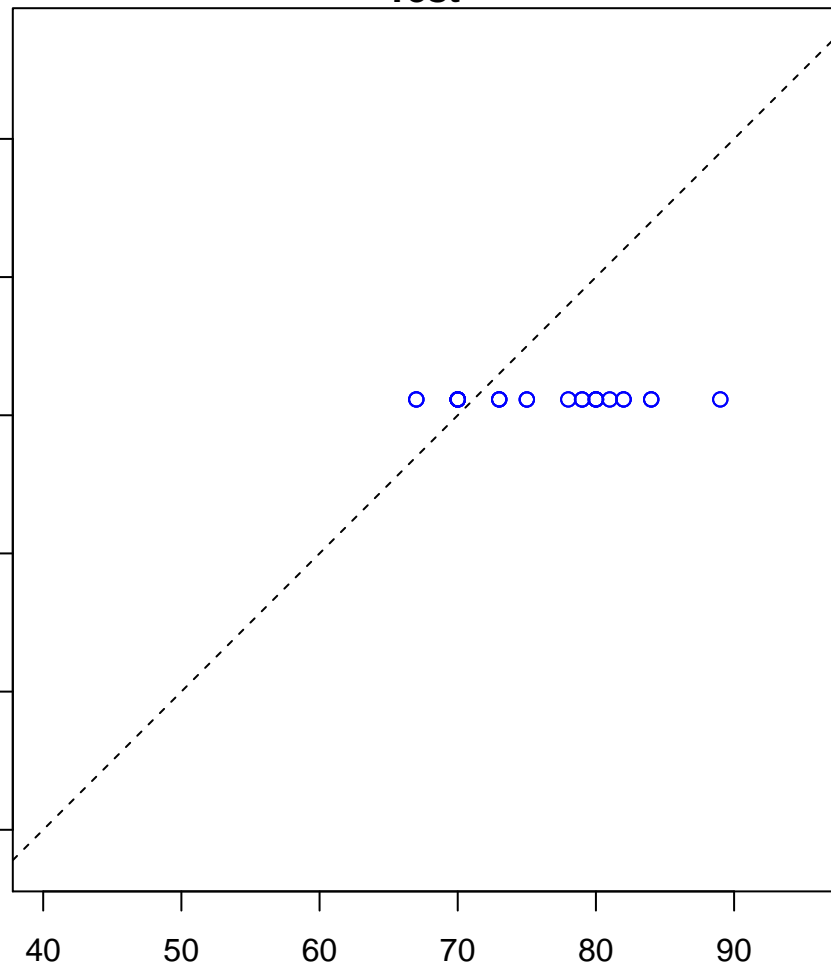


positive regulation of cytokine production (Score: 0.817050)

Control



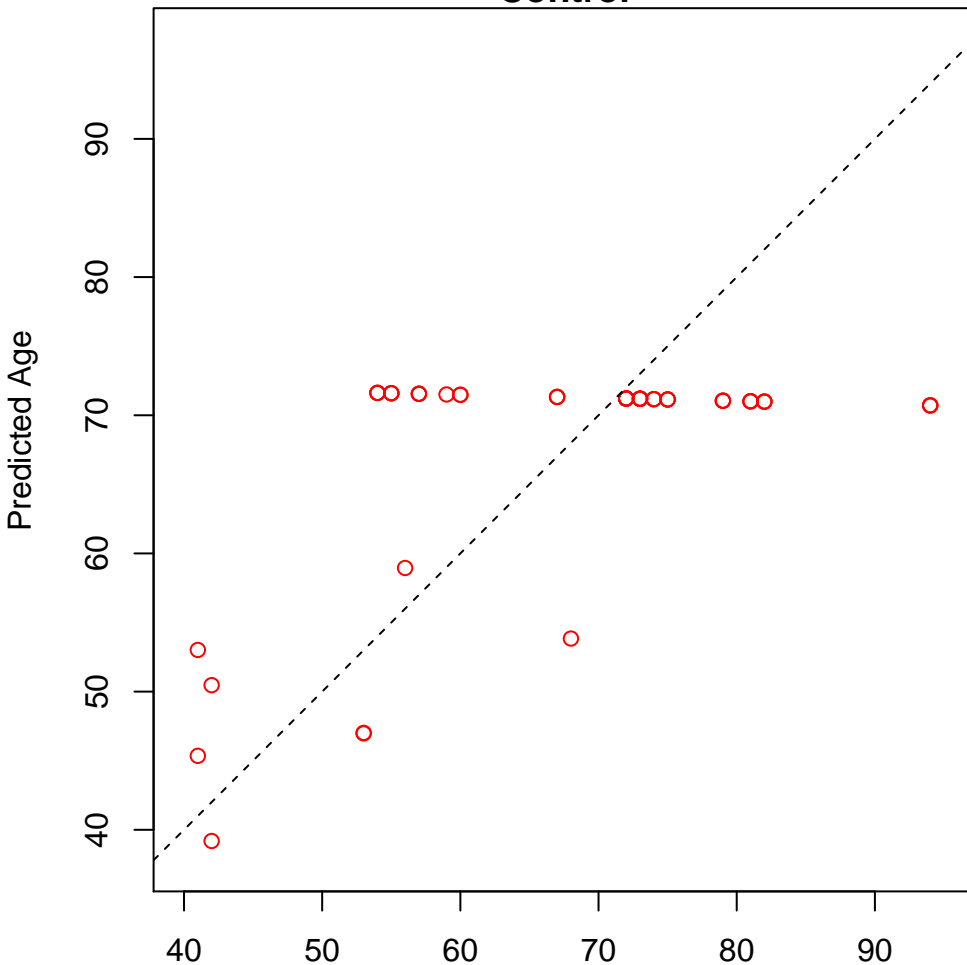
Test



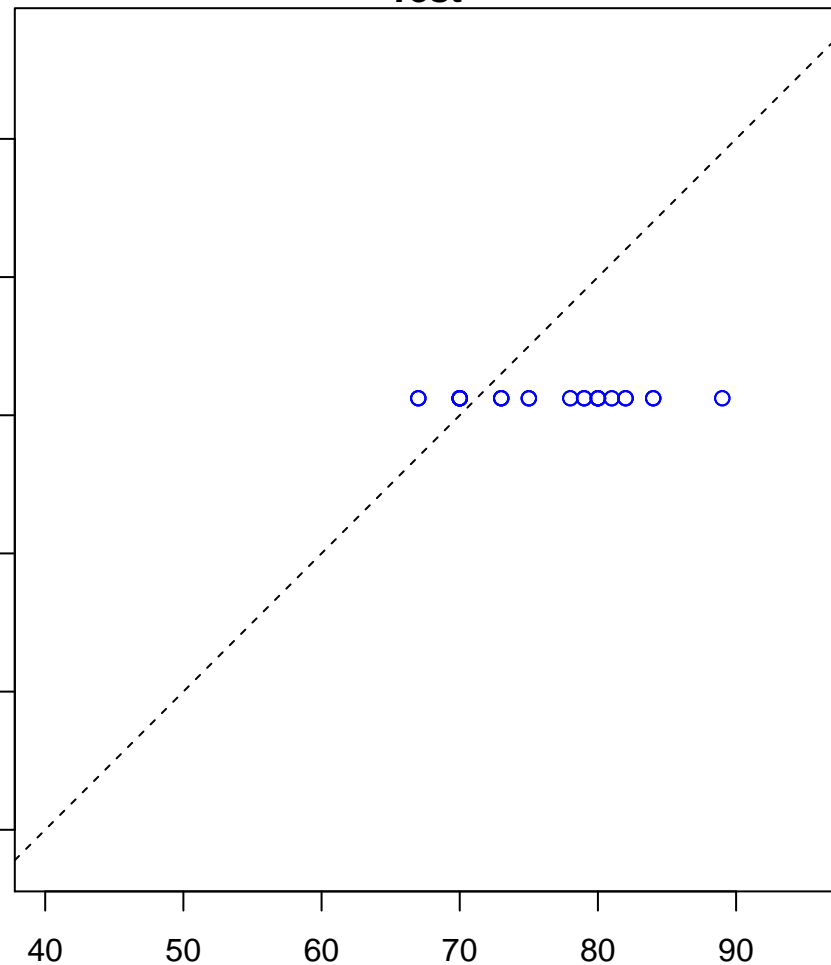
Actual Age

neuron projection development (Score: 0.817049)

Control



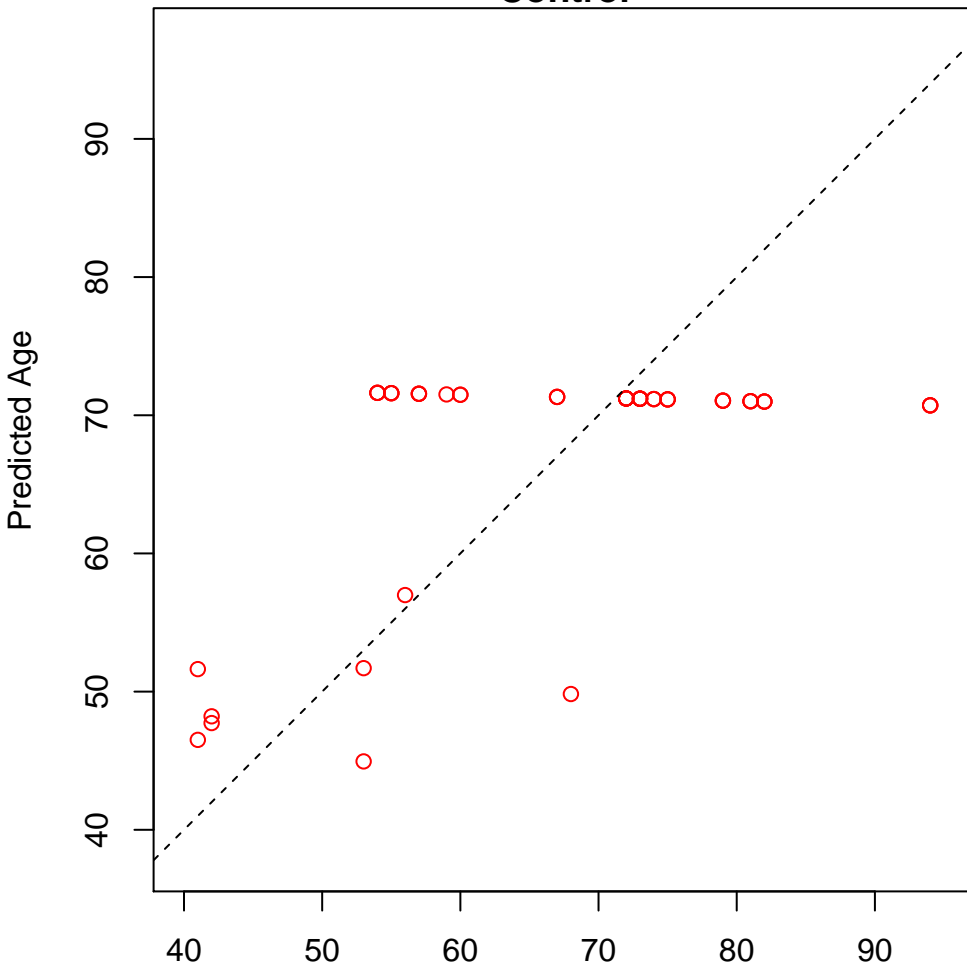
Test



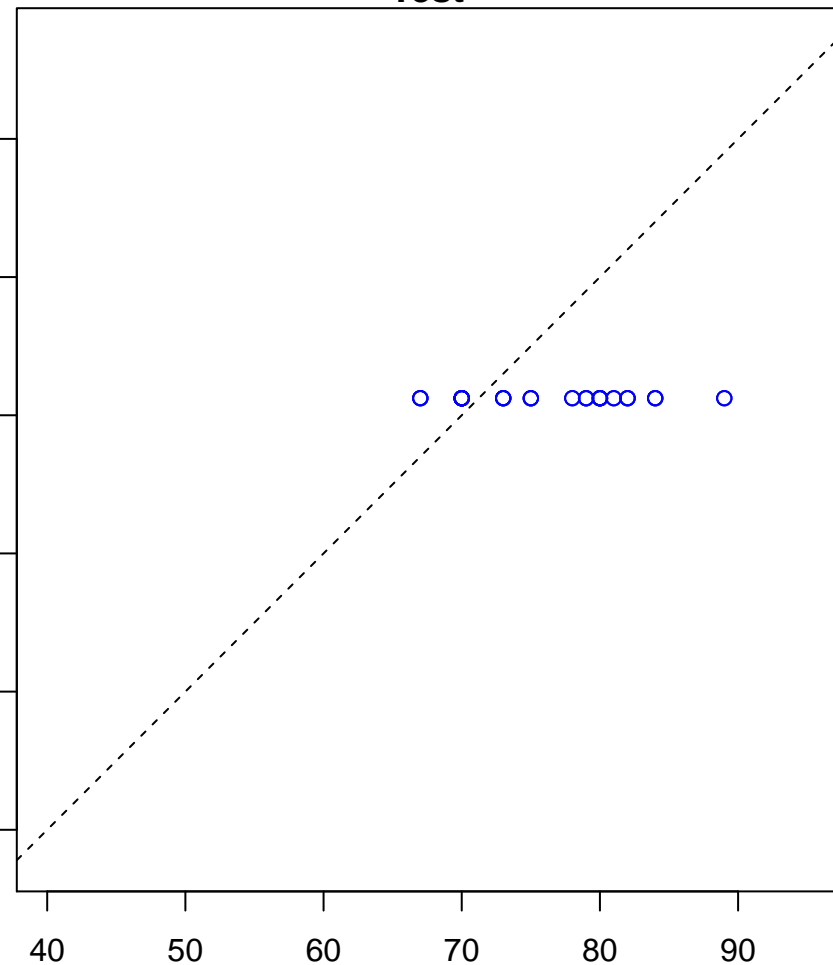
Actual Age

cellular lipid metabolic process (Score: 0.817021)

Control

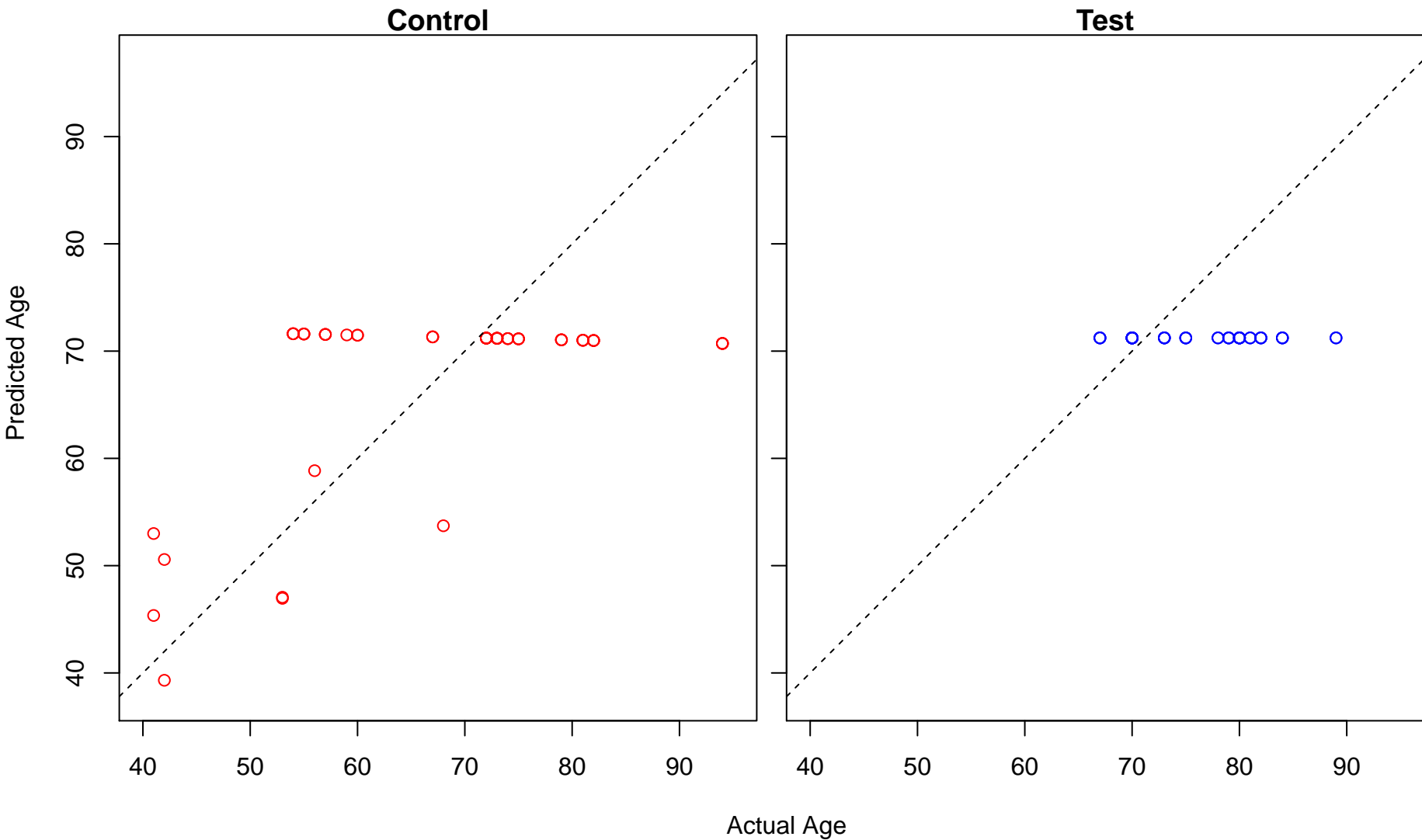


Test

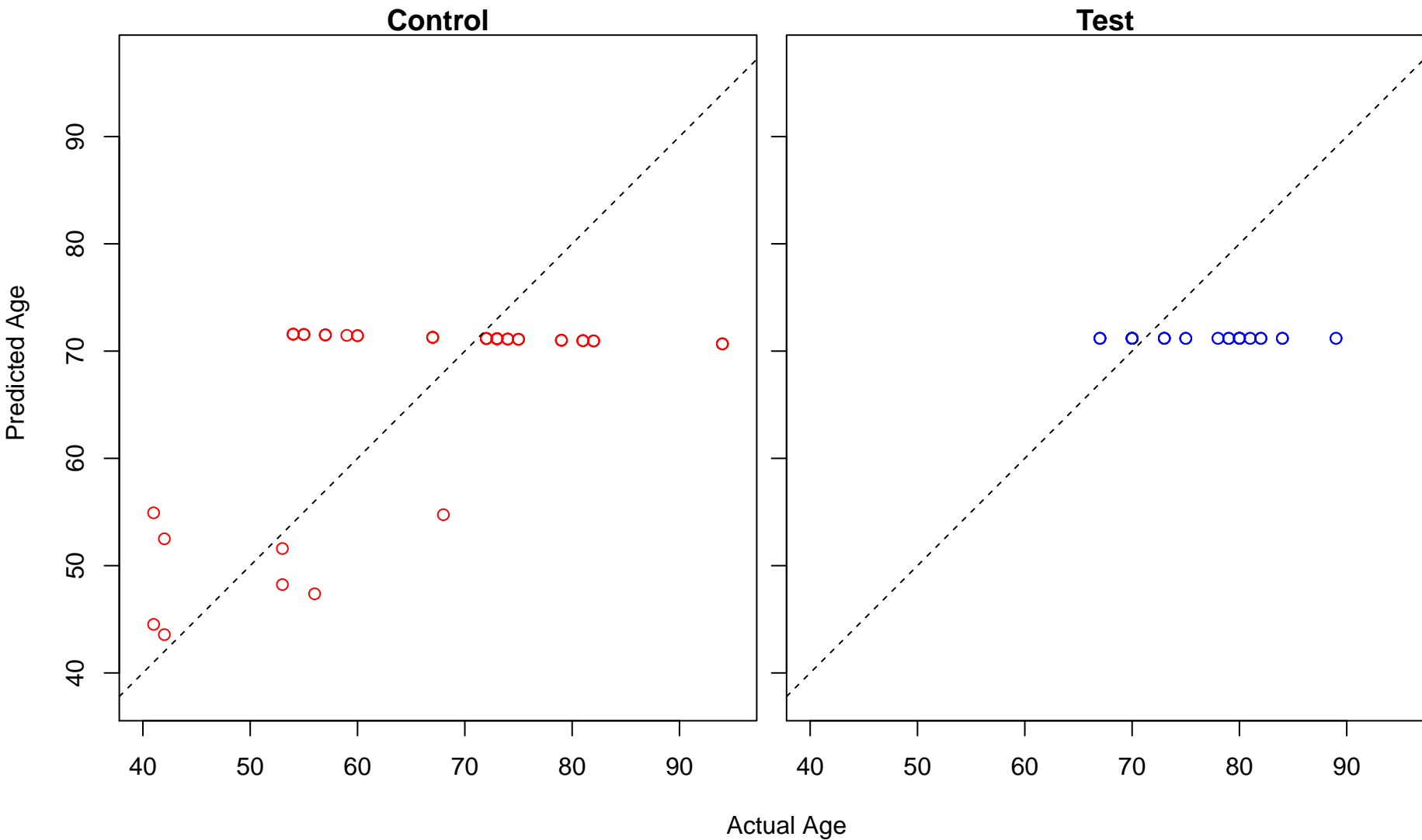


Actual Age

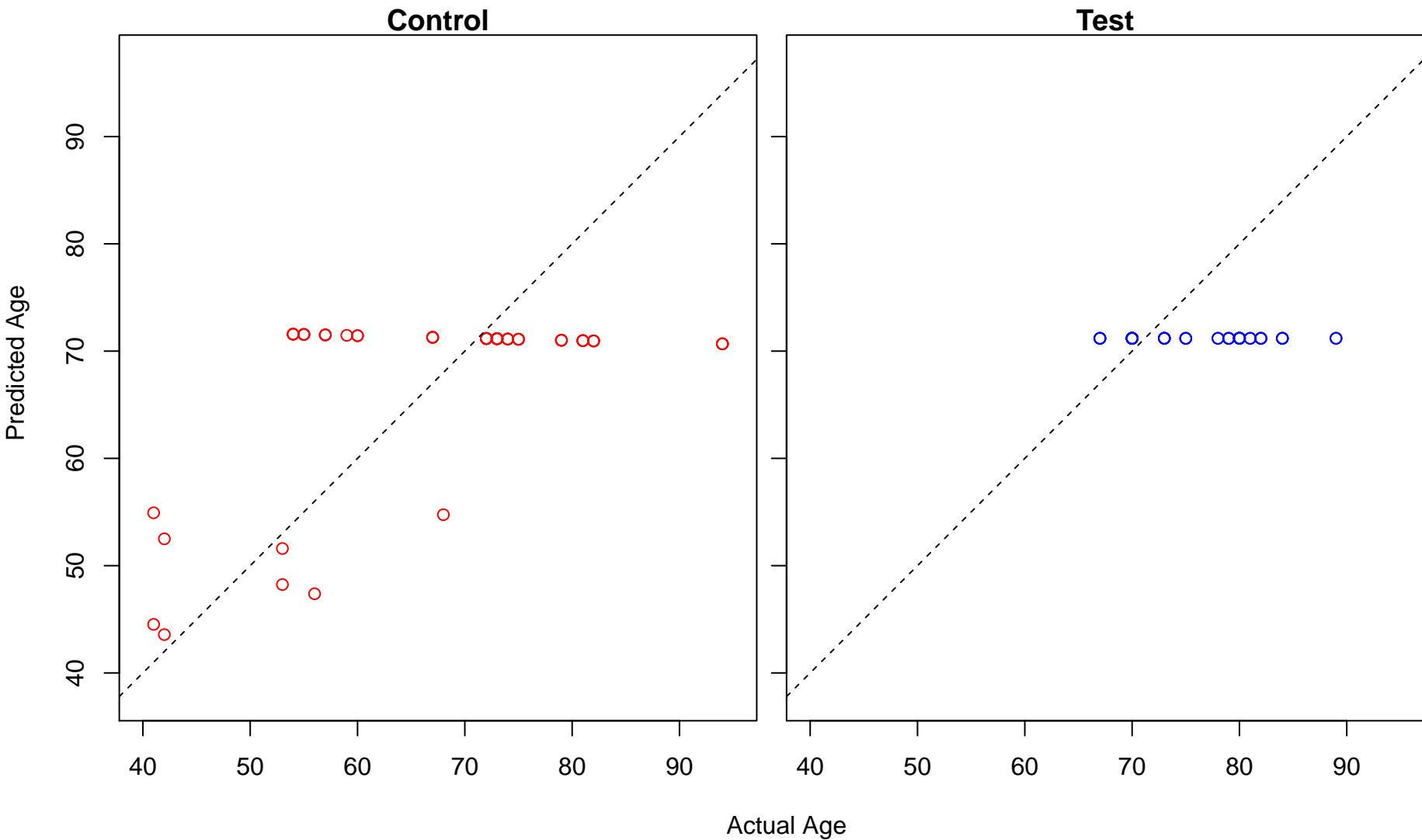
cell development (Score: 0.817009)



gluconeogenesis (Score: 0.816921)

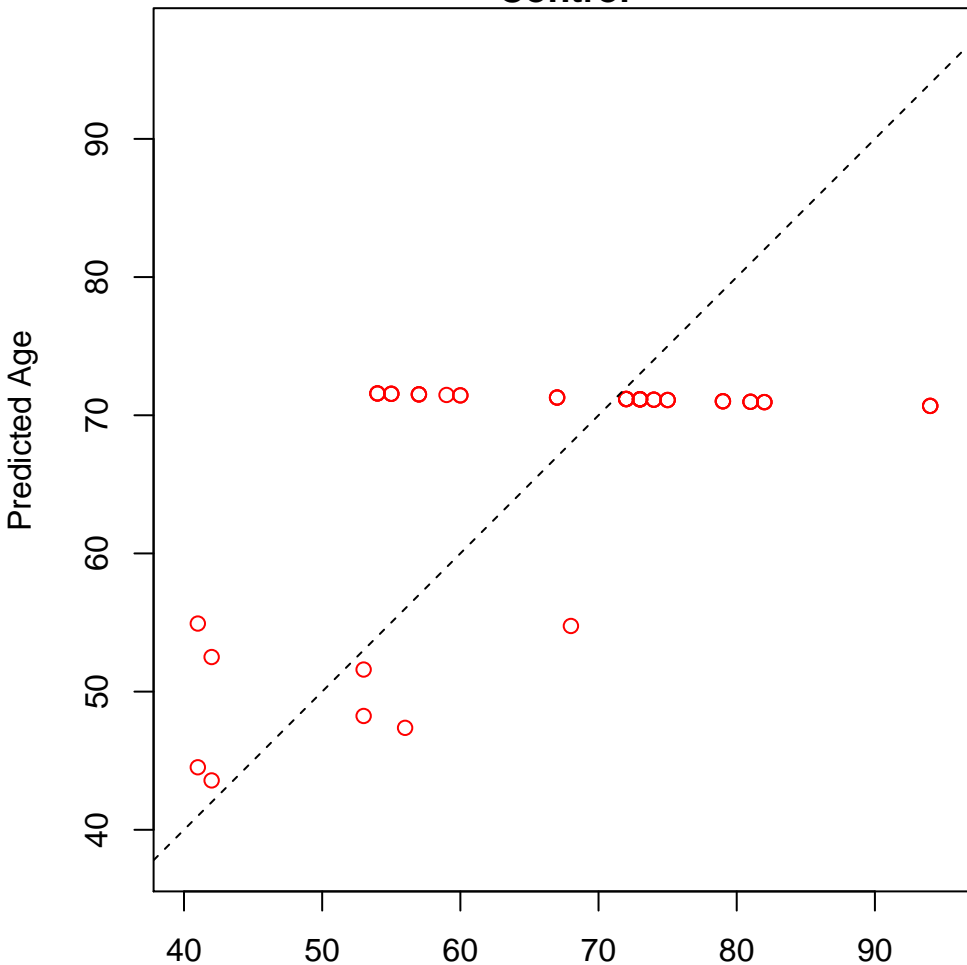


hexose biosynthetic process (Score: 0.816921)

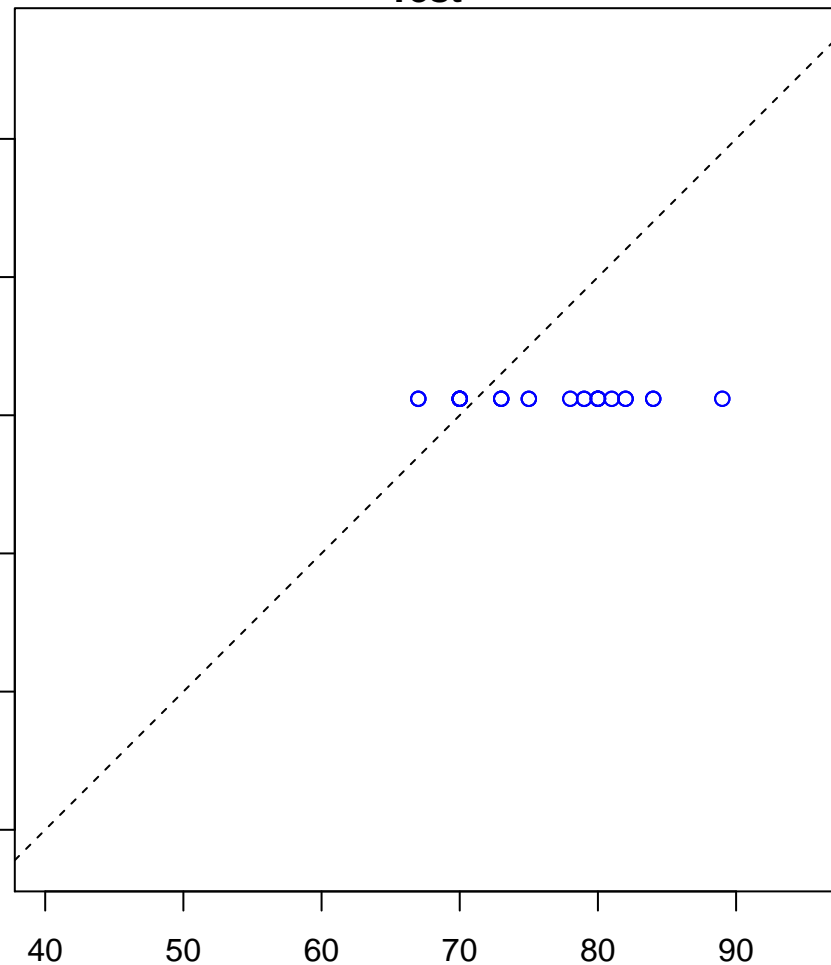


monosaccharide biosynthetic process (Score: 0.816921)

Control



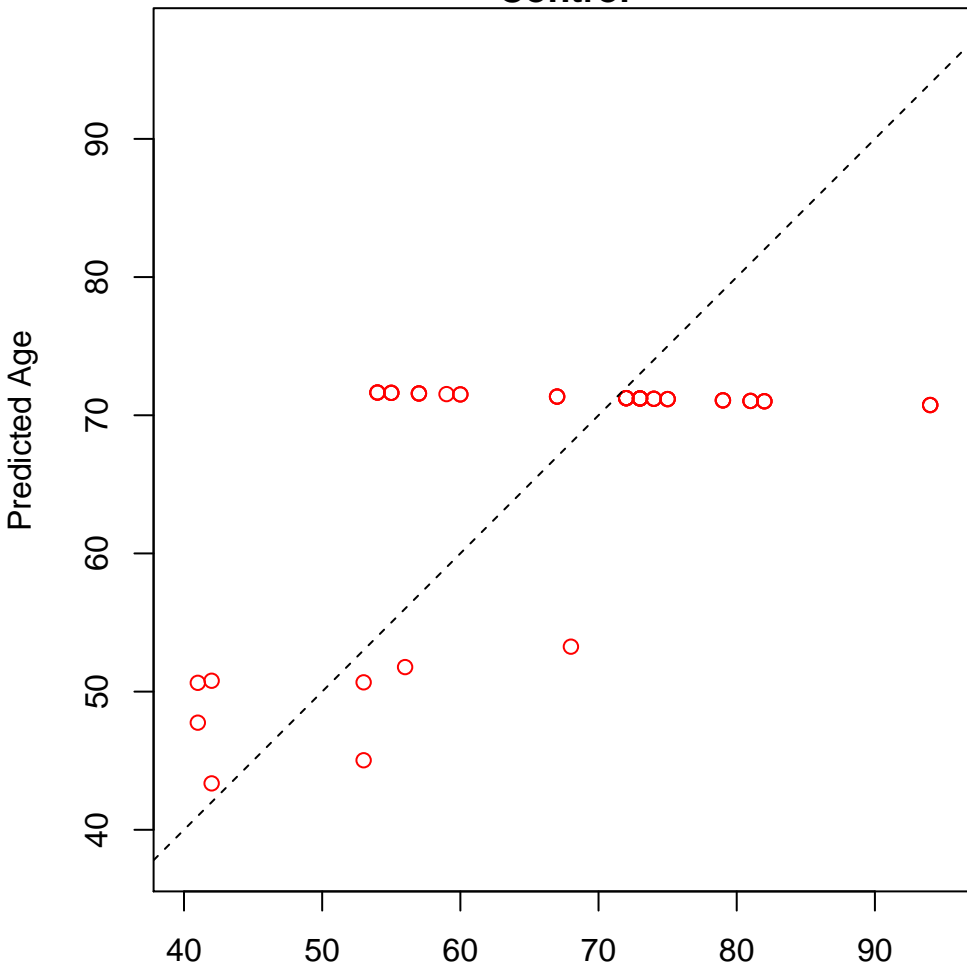
Test



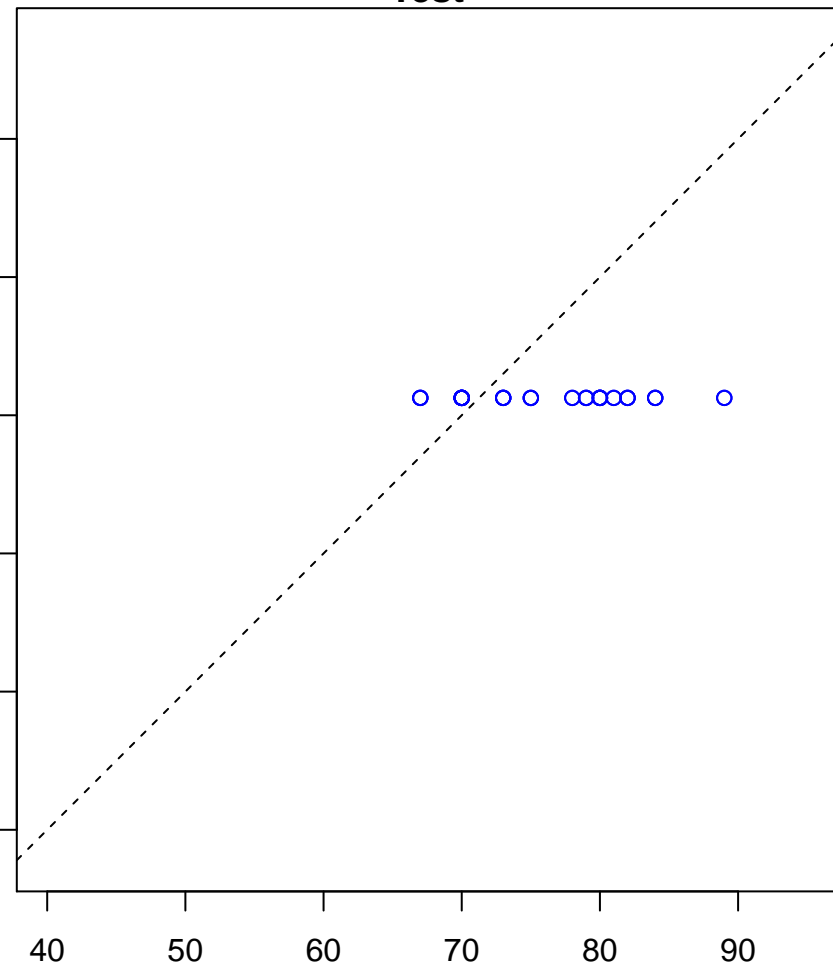
Actual Age

regulation of lipid metabolic process (Score: 0.816876)

Control

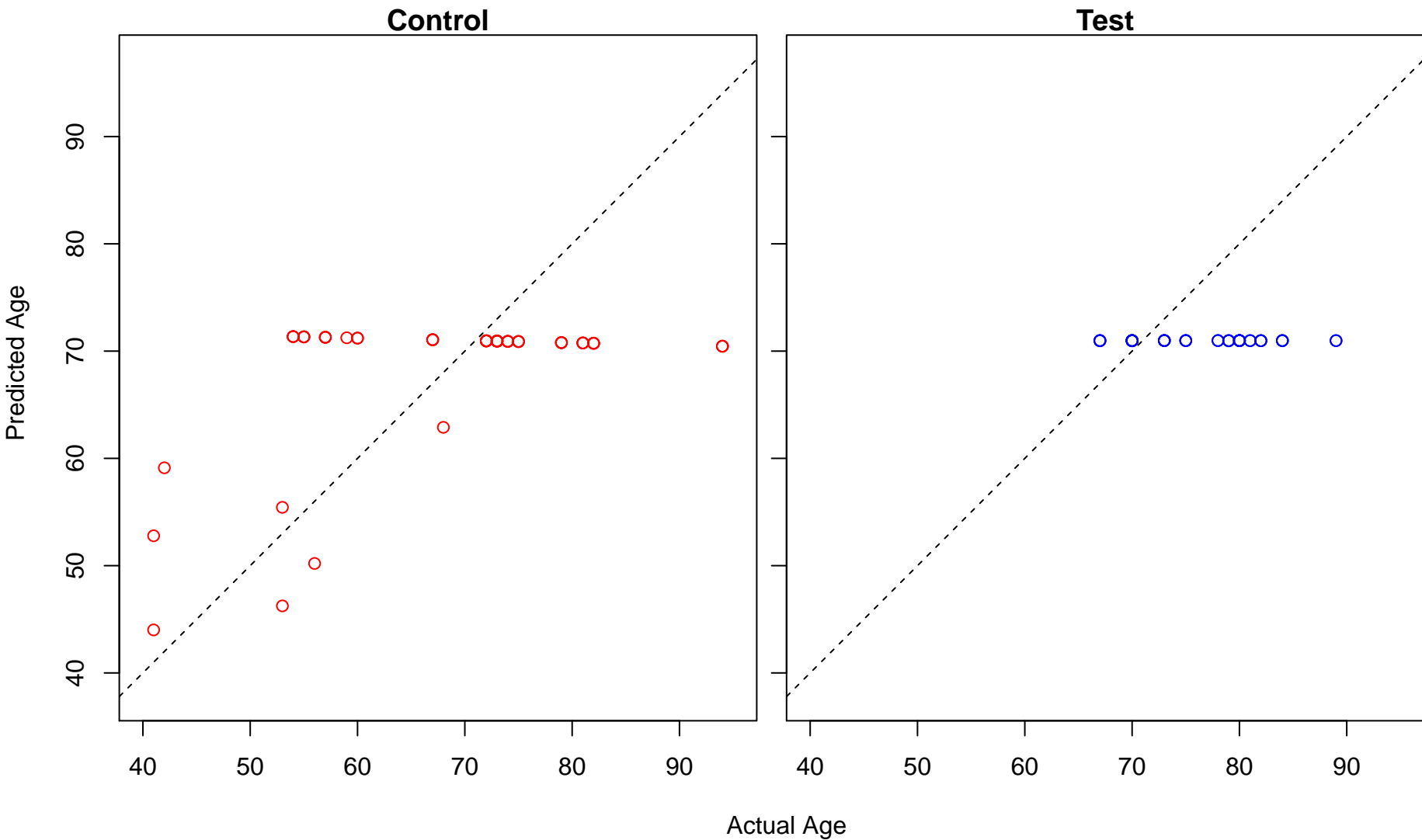


Test

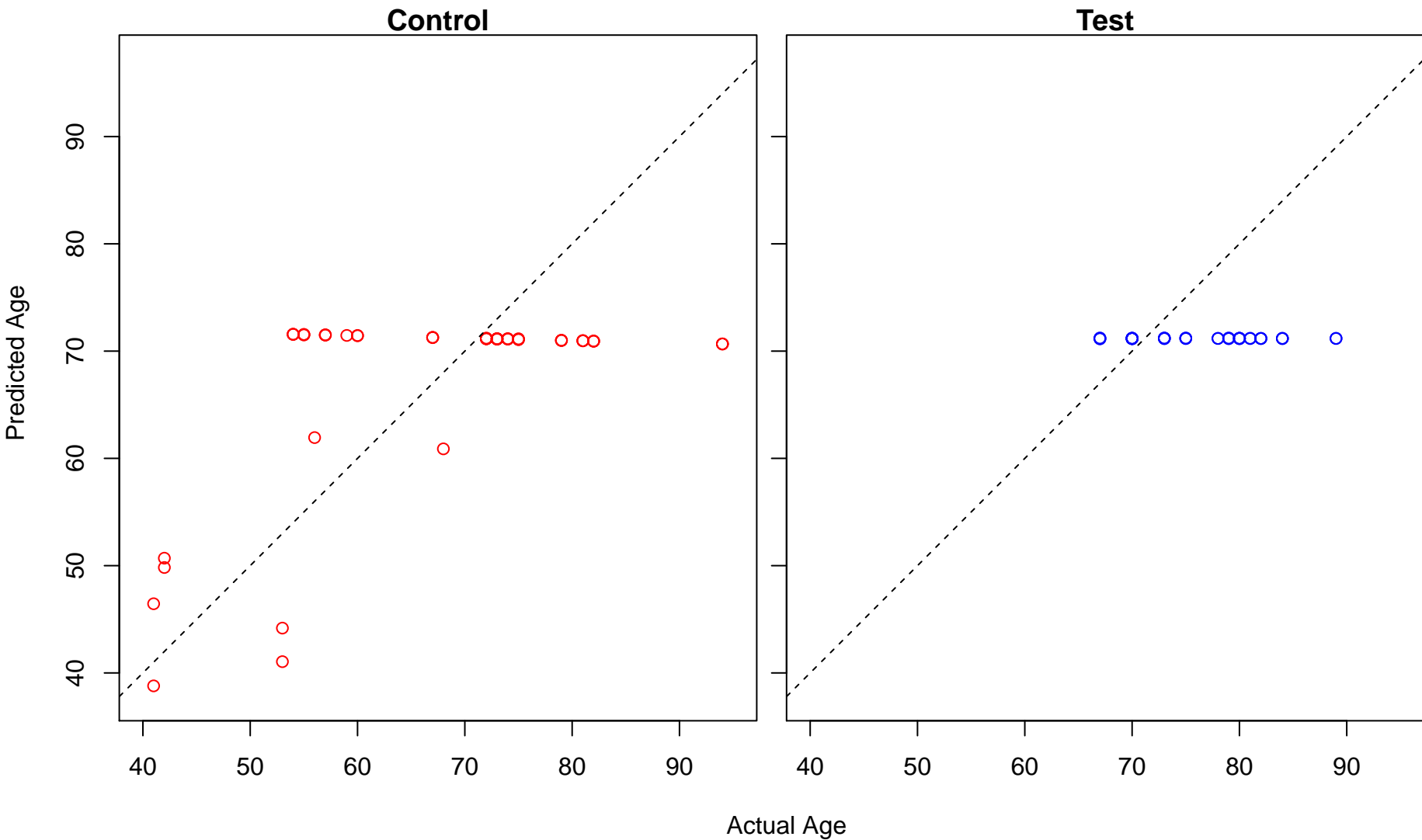


Actual Age

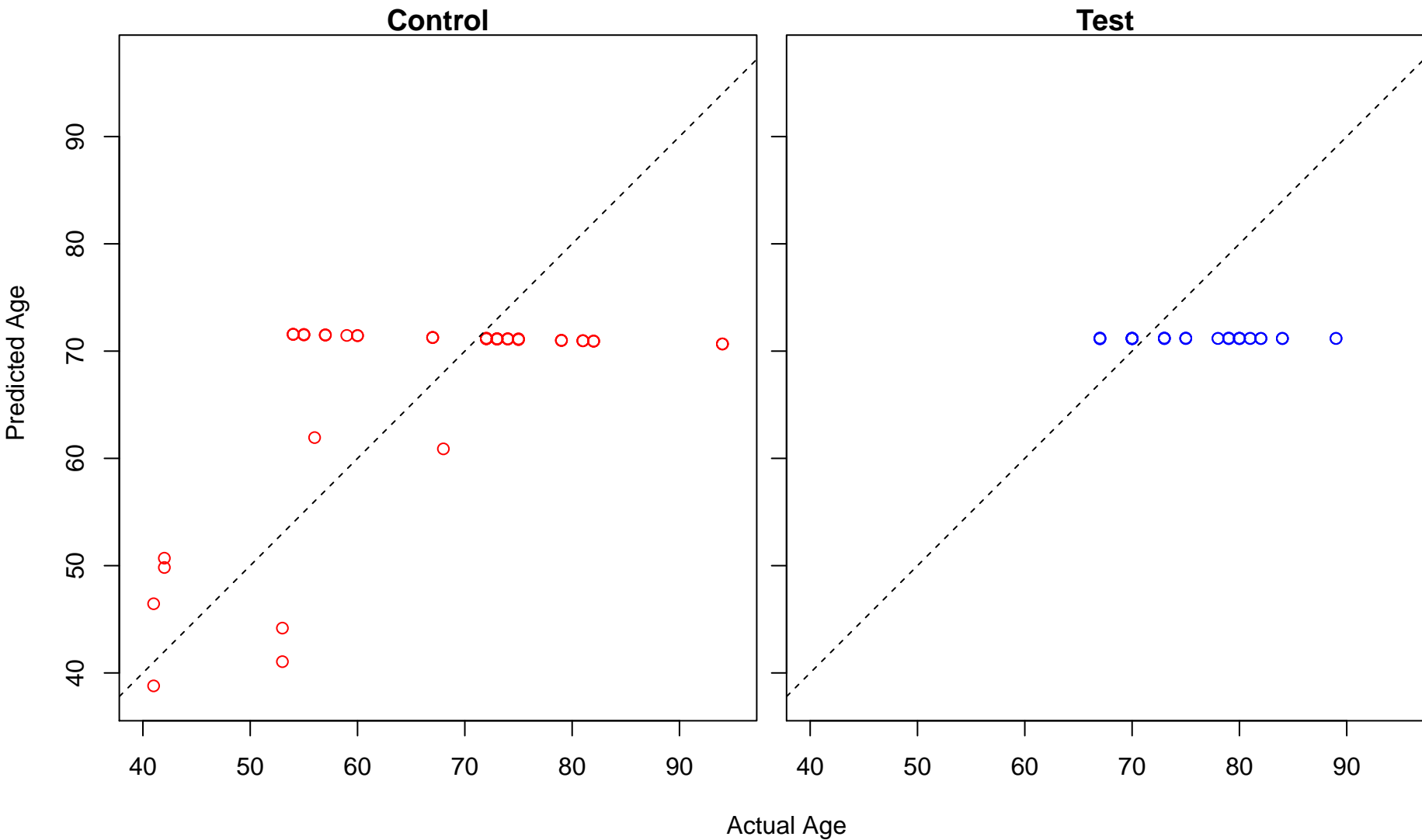
regulation of release of cytochrome c from mitochondria (Score: 0.816851)



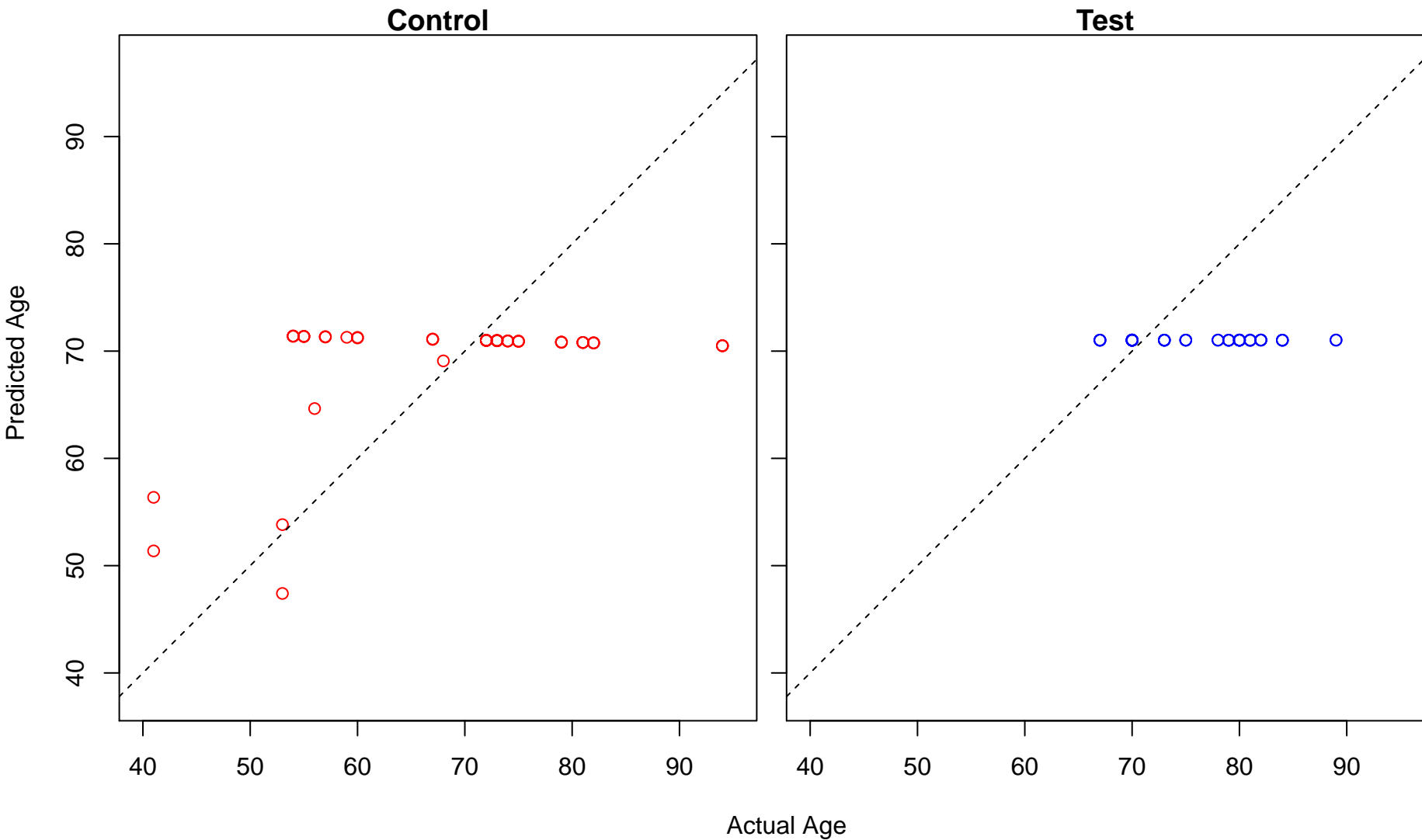
carbohydrate homeostasis (Score: 0.816837)



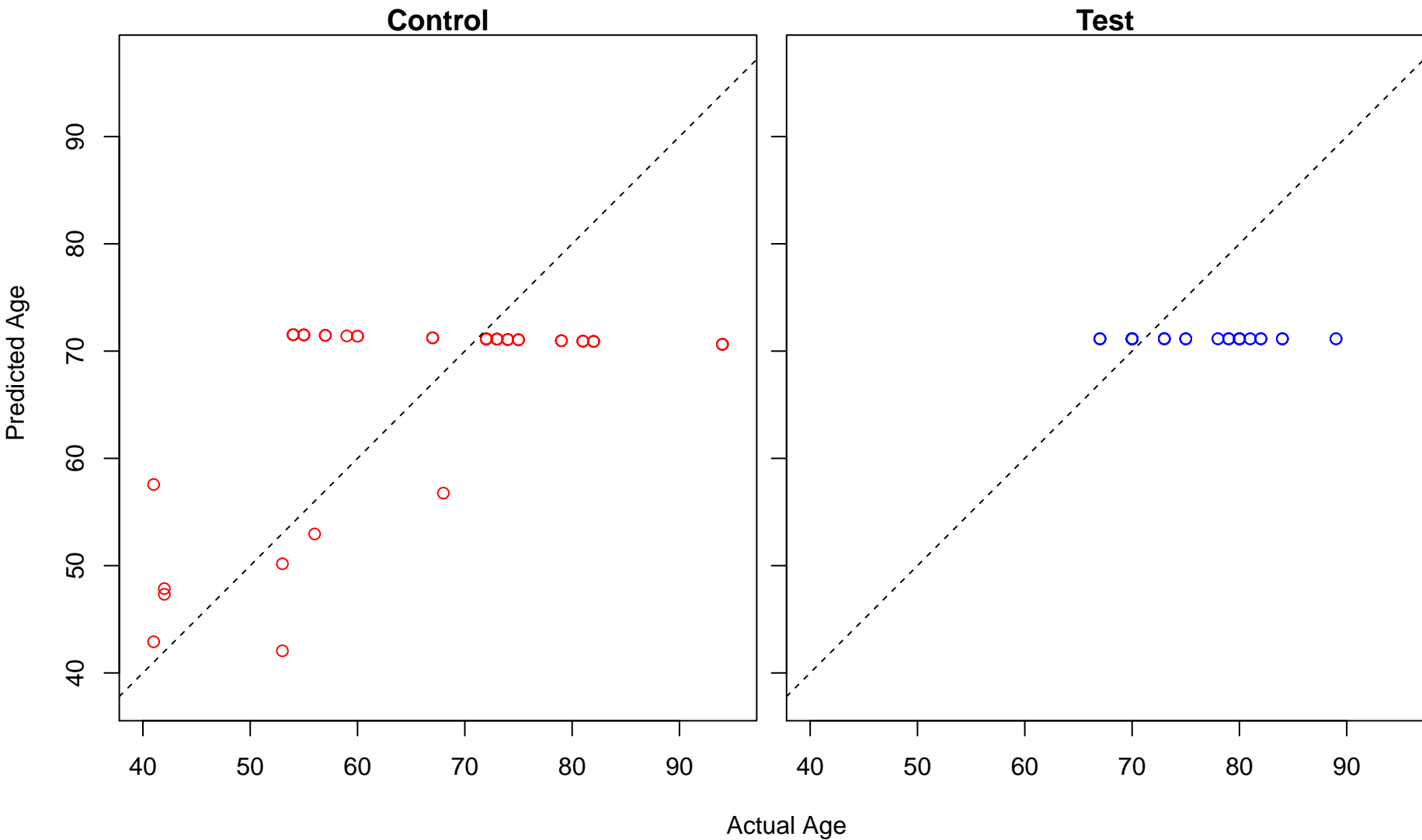
glucose homeostasis (Score: 0.816837)



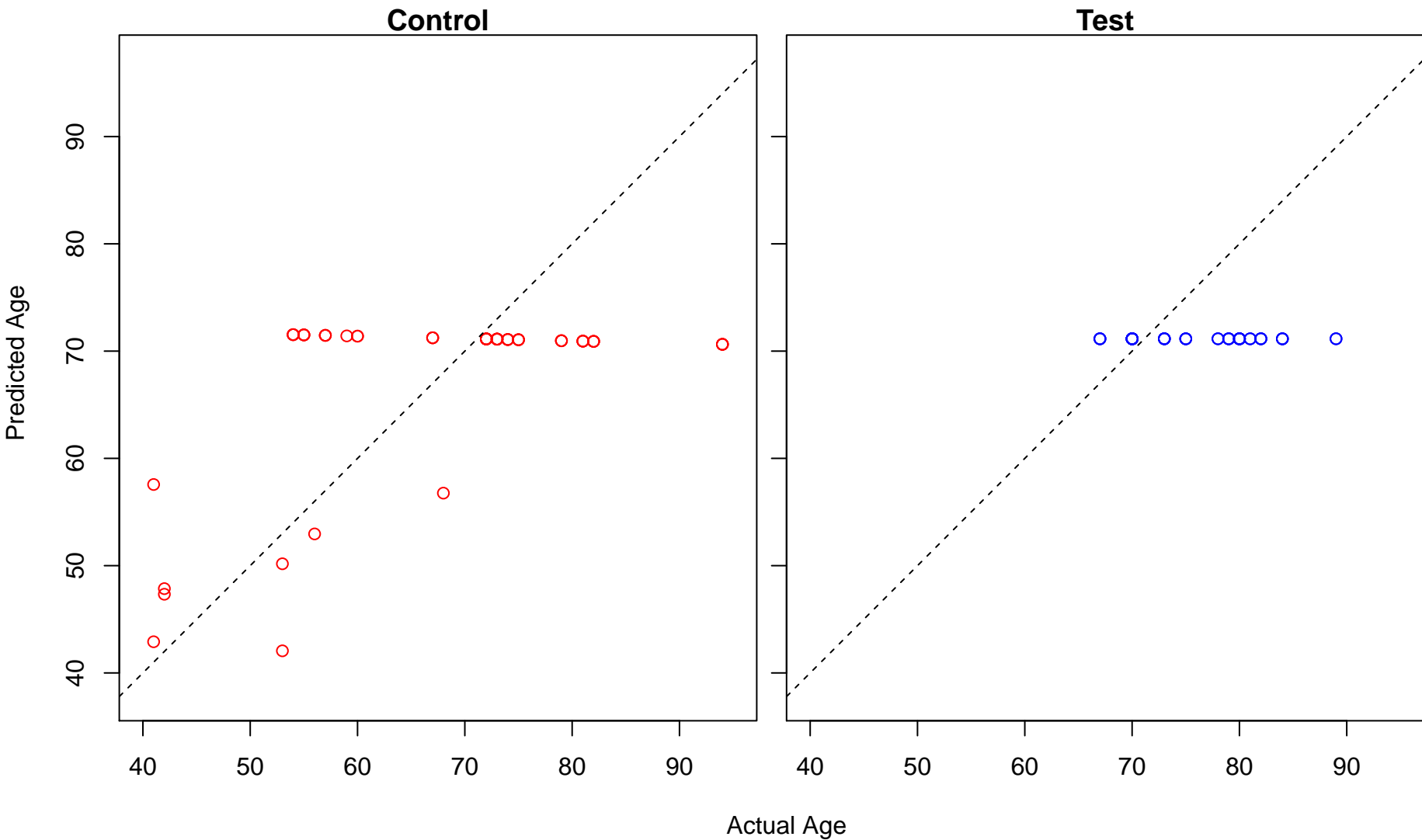
negative regulation of binding (Score: 0.816767)



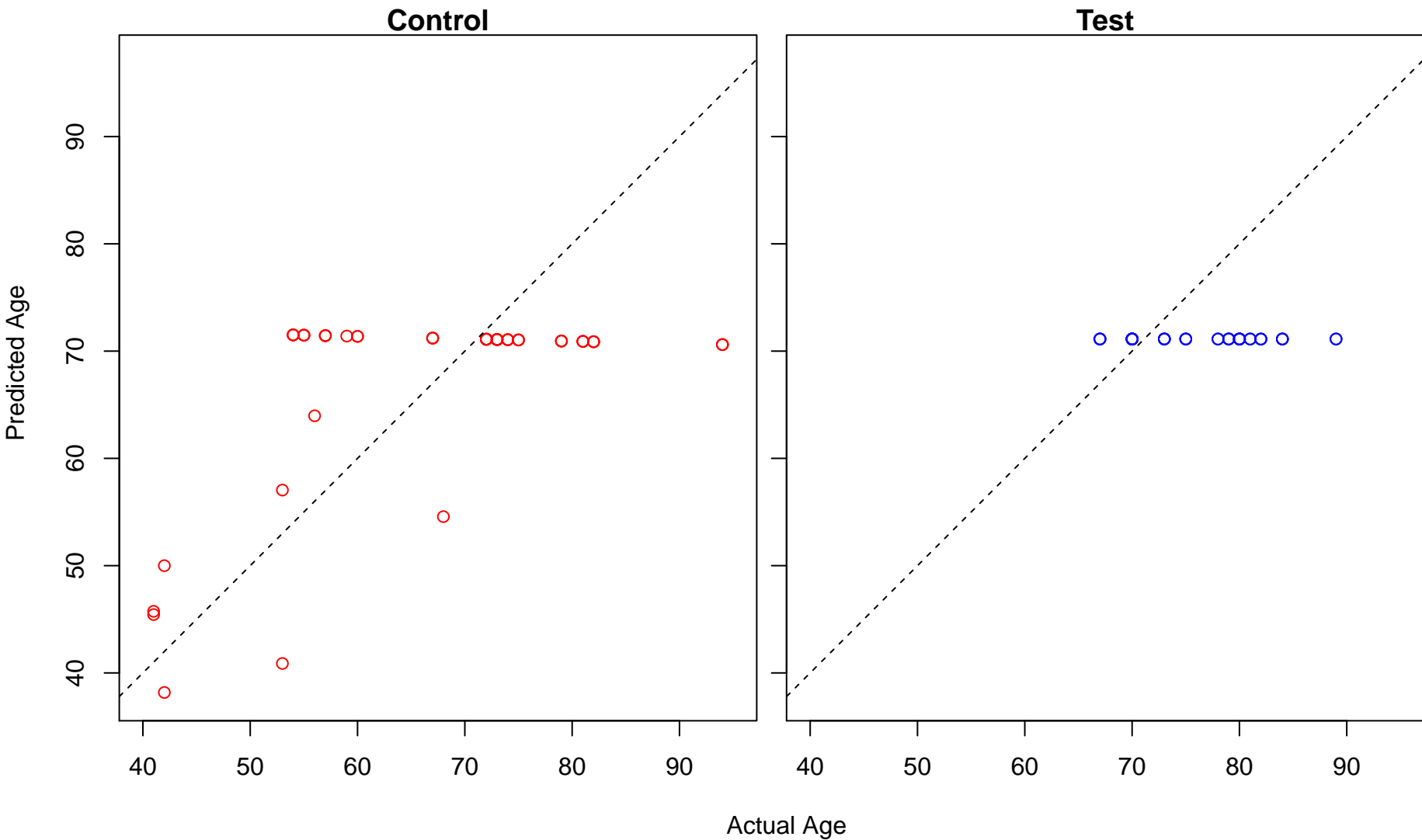
lipid transport (Score: 0.816753)



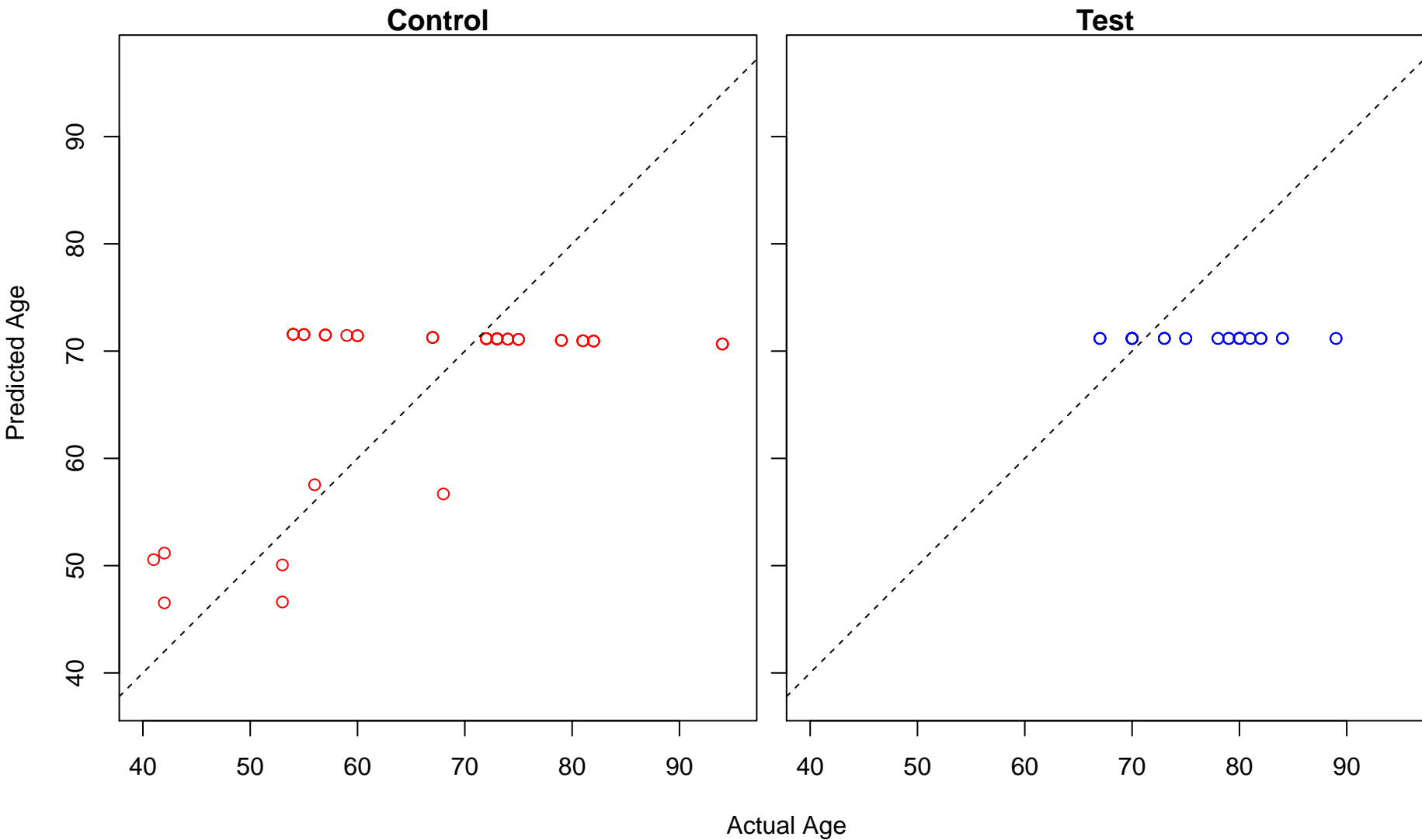
lipid localization (Score: 0.816753)



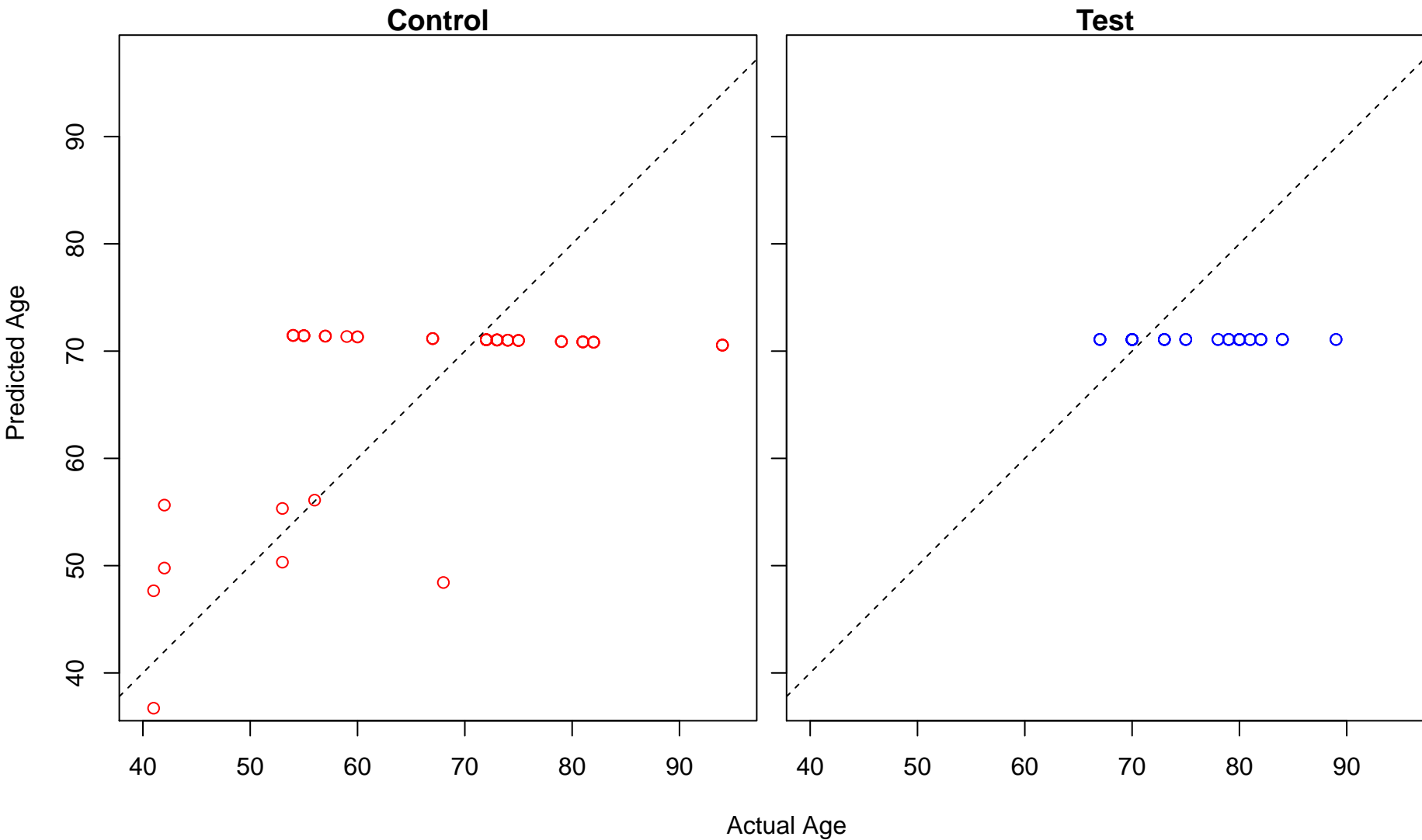
regulation of receptor-mediated endocytosis (Score: 0.81667)



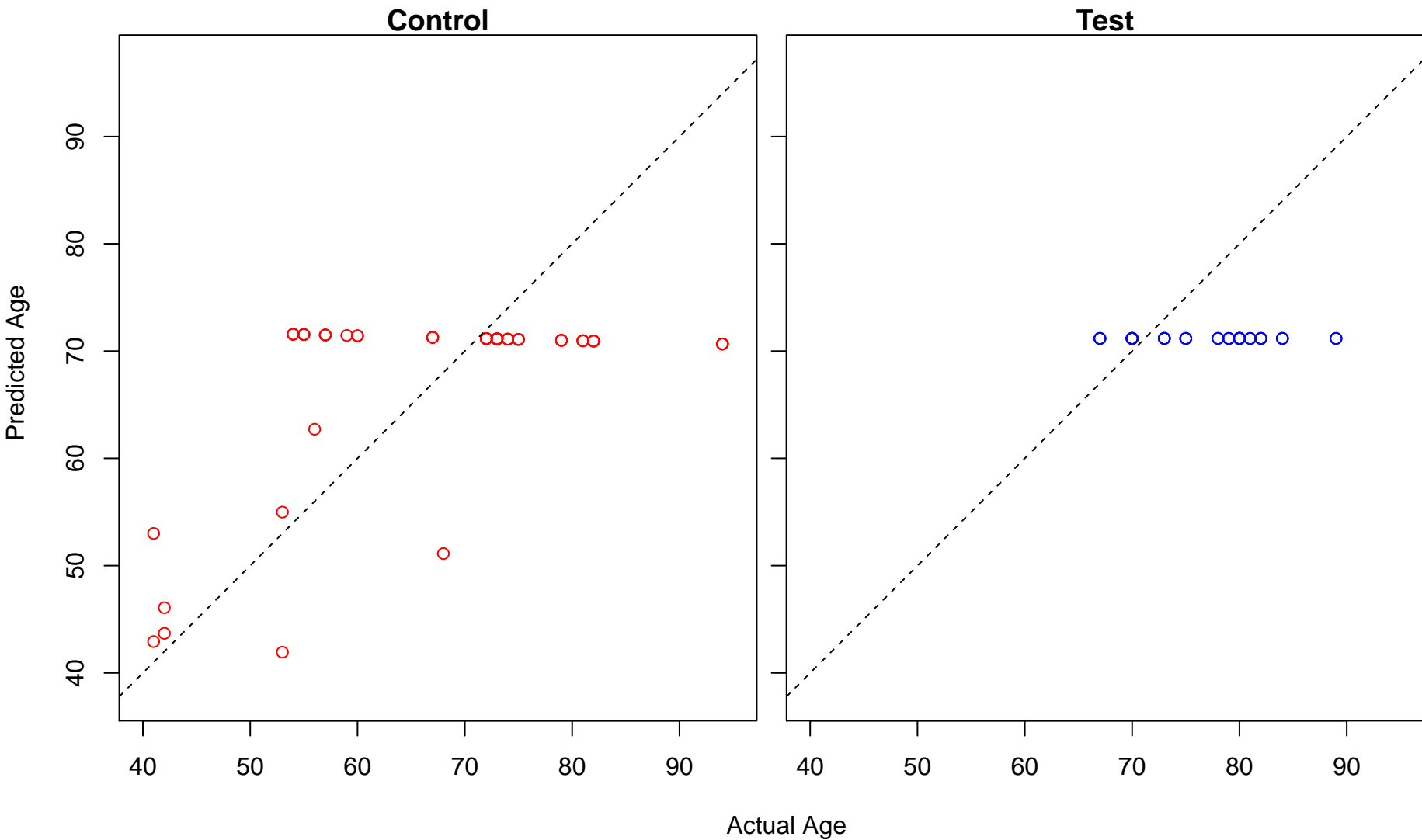
DNA metabolic process (Score: 0.816585)



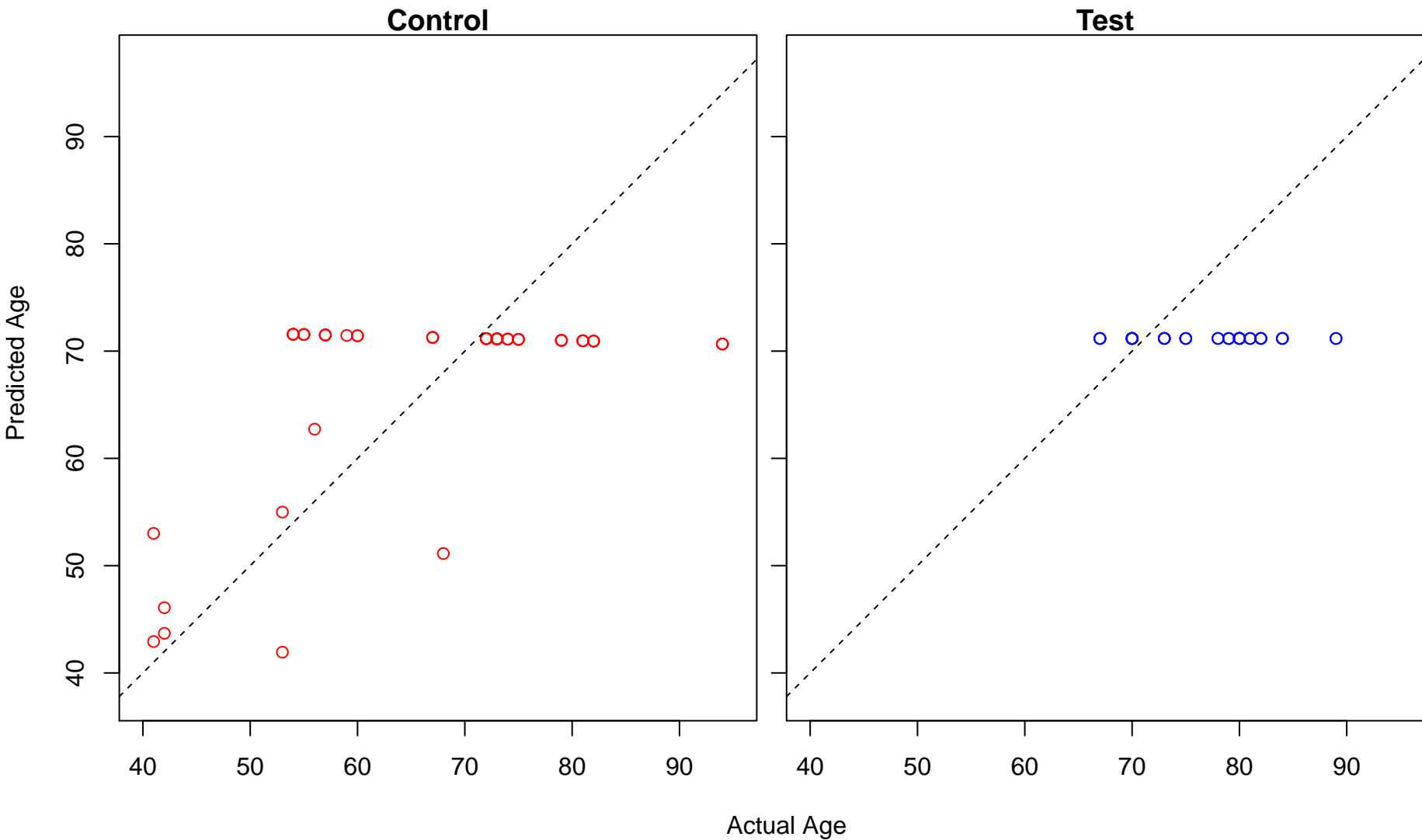
regulation of actin cytoskeleton organization (Score: 0.816580)



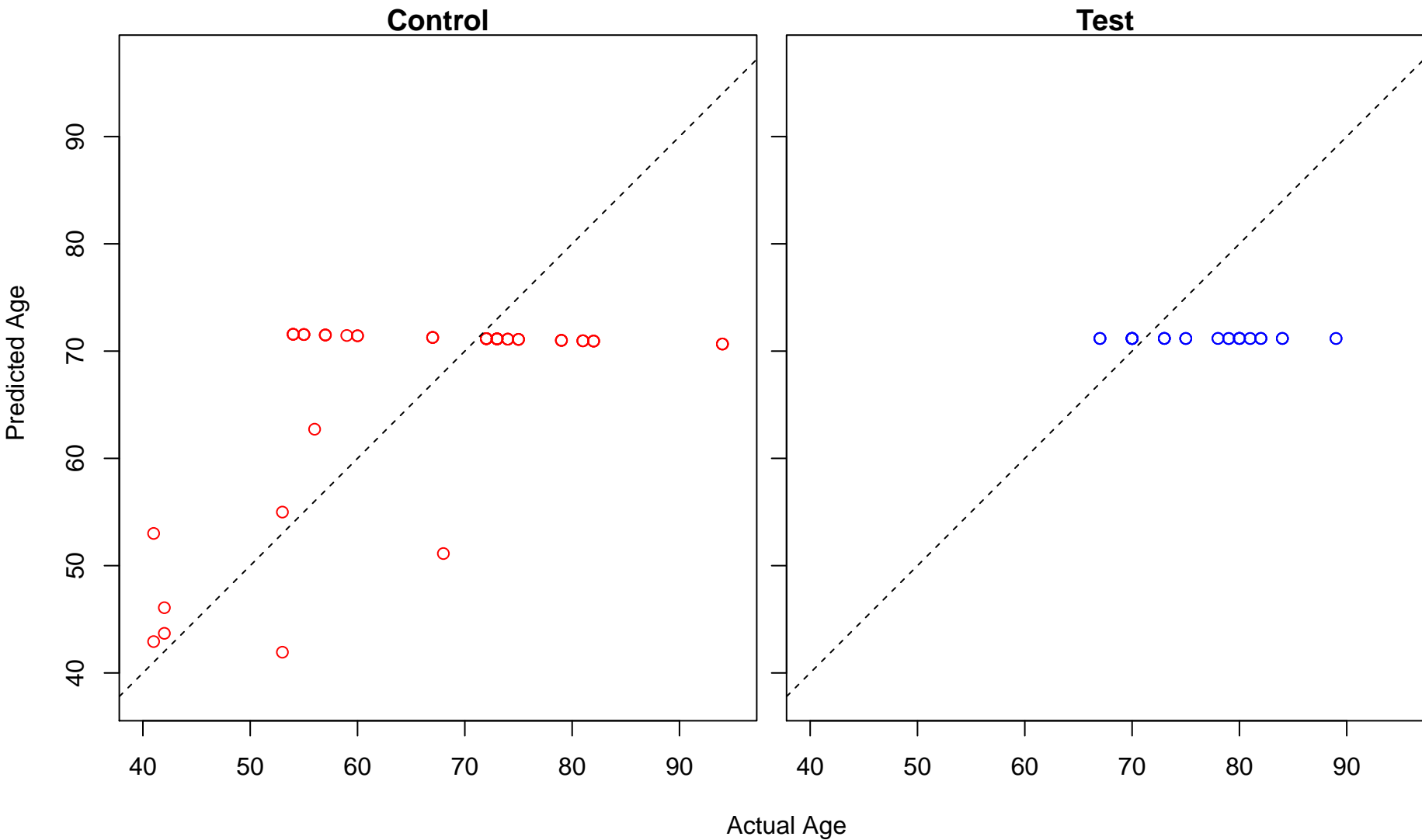
mitotic cytokinesis (Score: 0.816576)



cytokinesis (Score: 0.816576)

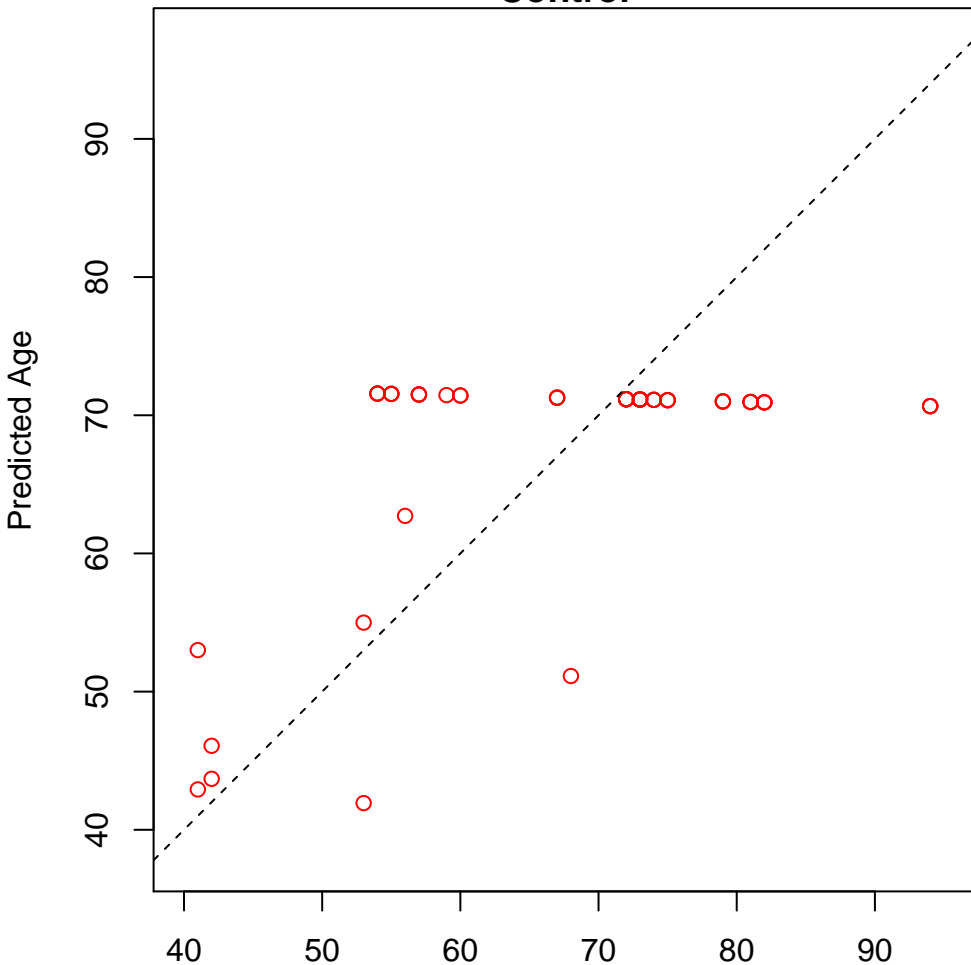


cell division (Score: 0.816576)

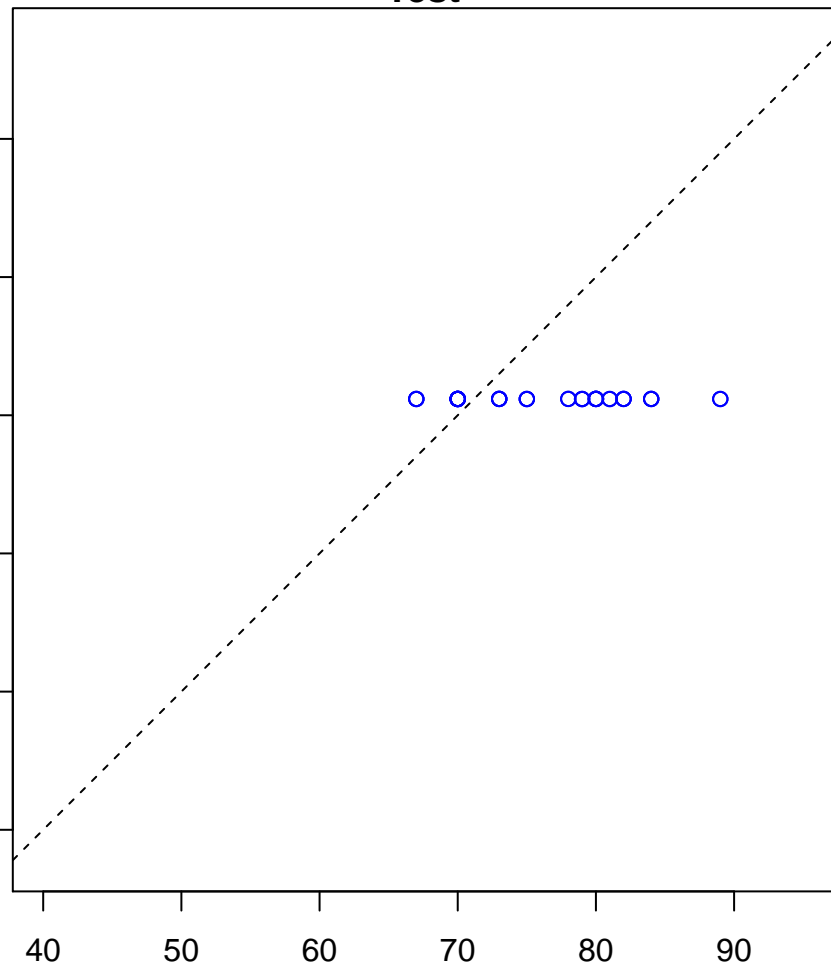


cytoskeleton-dependent cytokinesis (Score: 0.816576)

Control



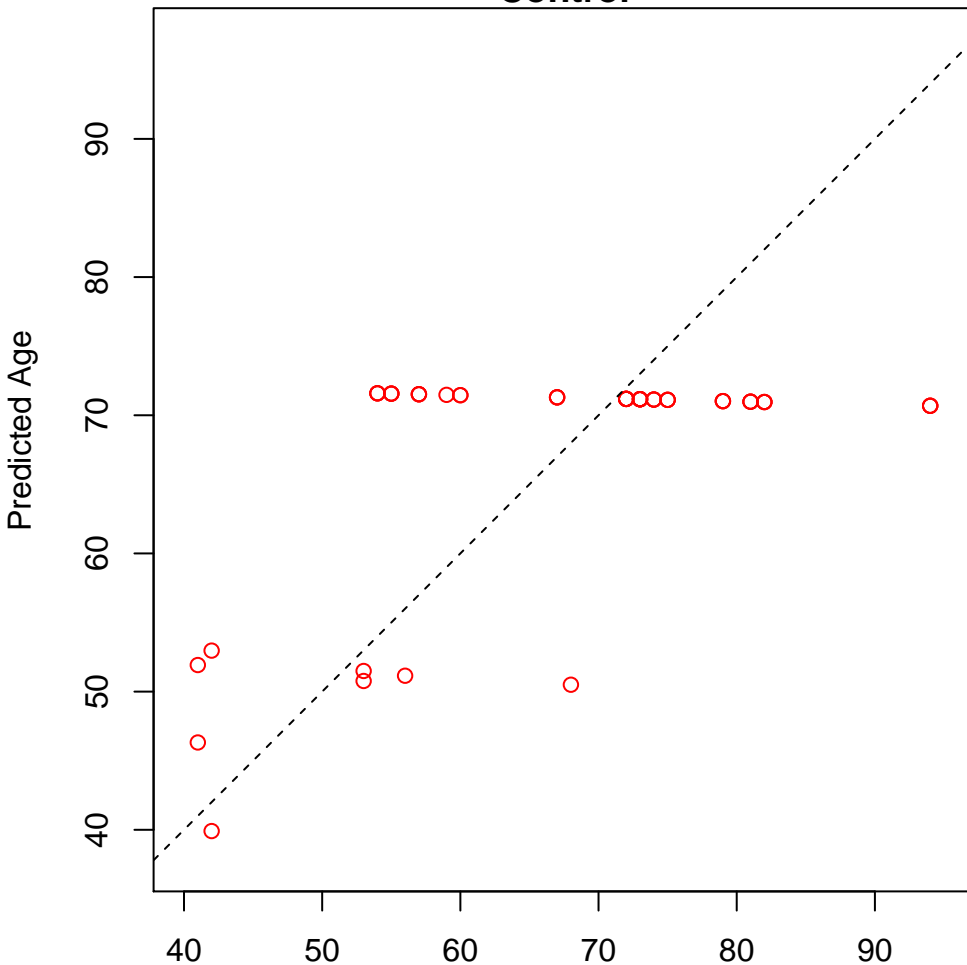
Test



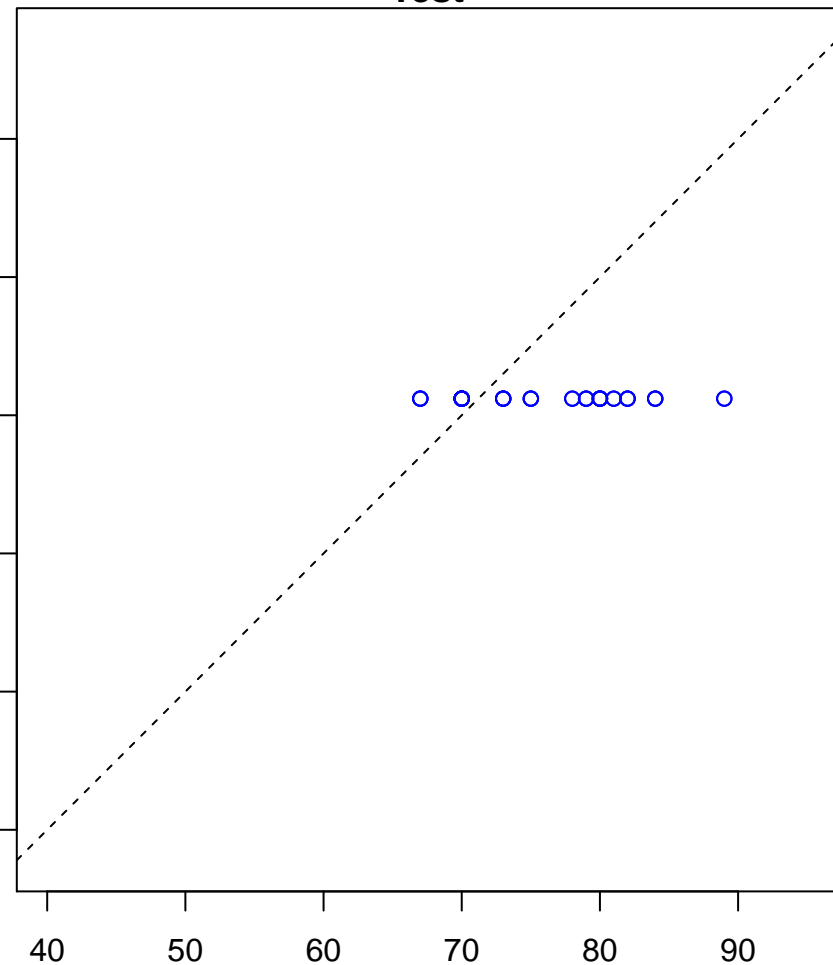
Actual Age

inorganic ion transmembrane transport (Score: 0.816561)

Control



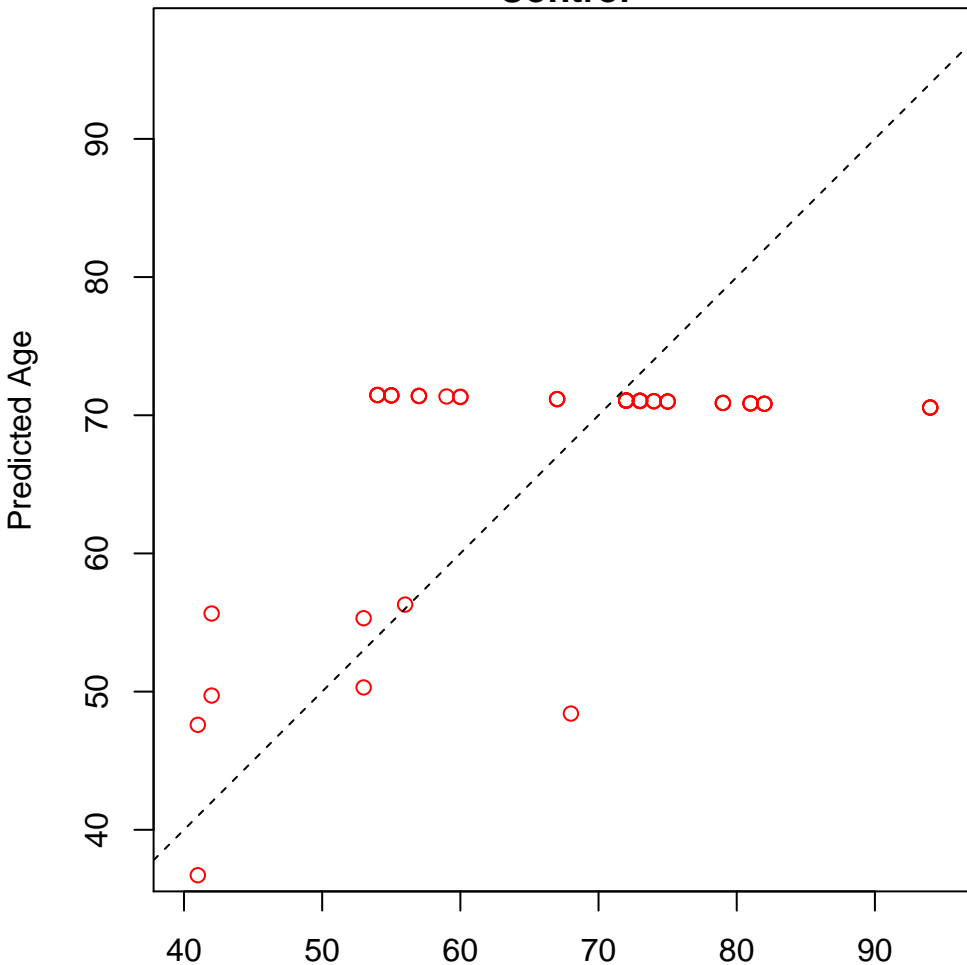
Test



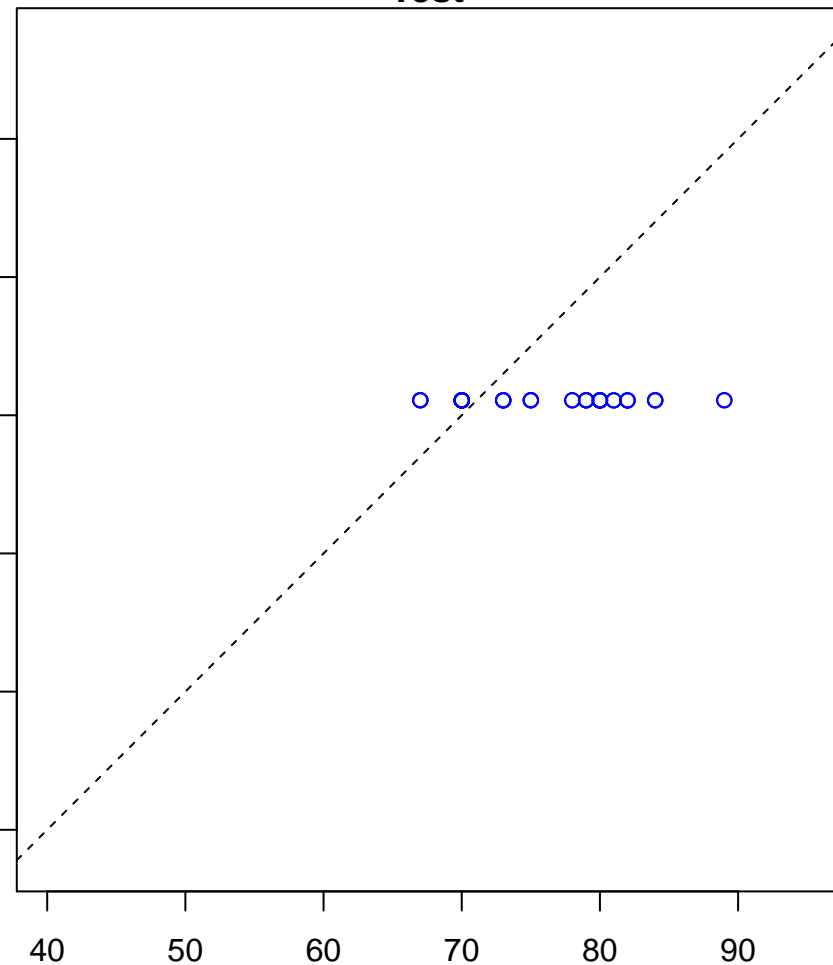
Actual Age

regulation of actin filament organization (Score: 0.816530)

Control



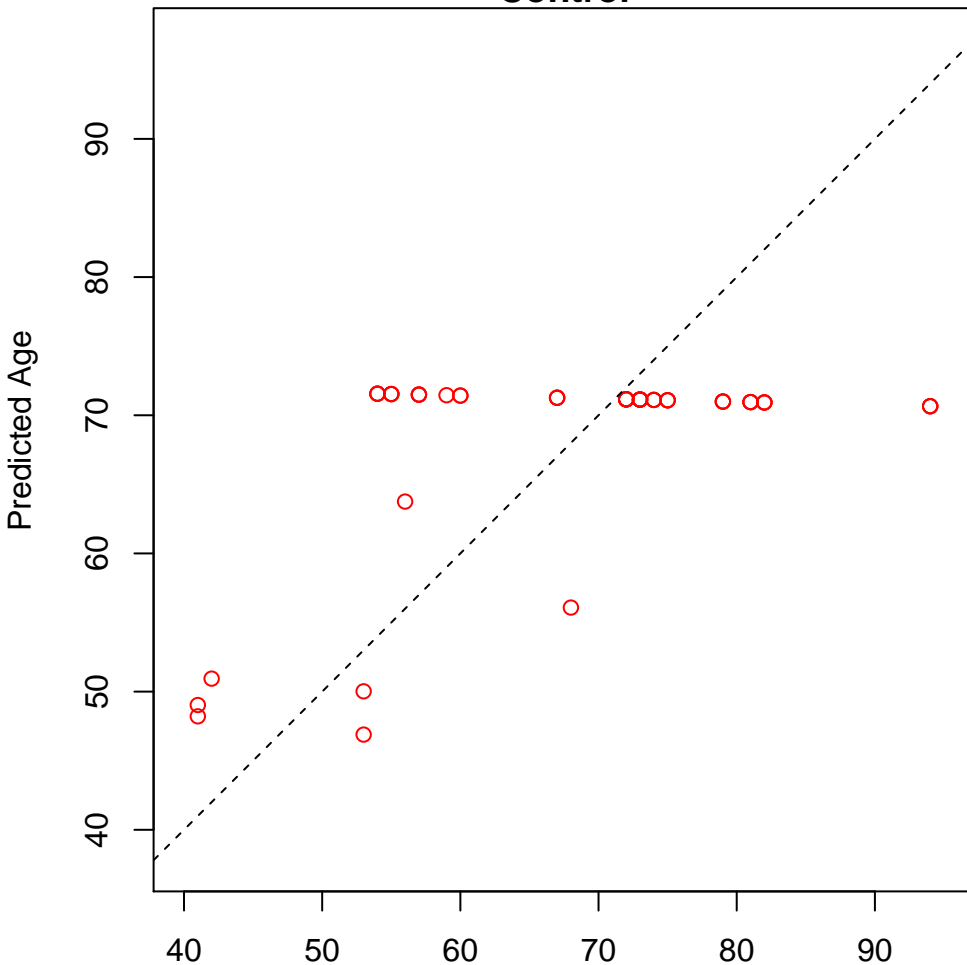
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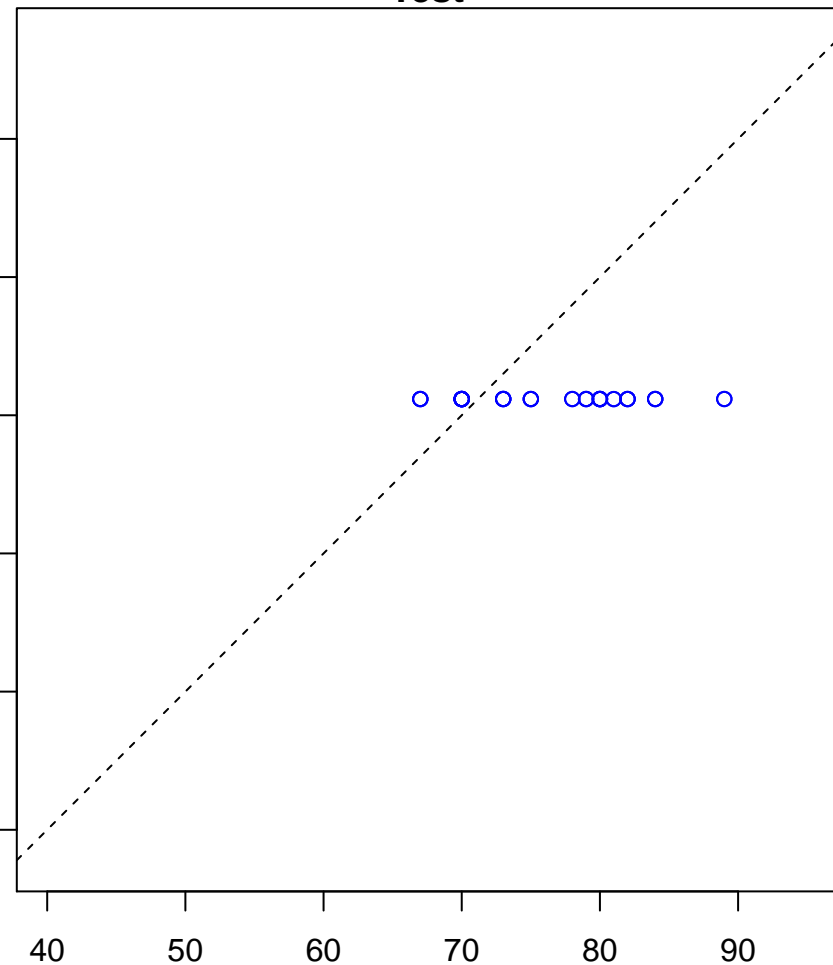
Actual Age

regulation of anatomical structure size (Score: 0.816464)

Control



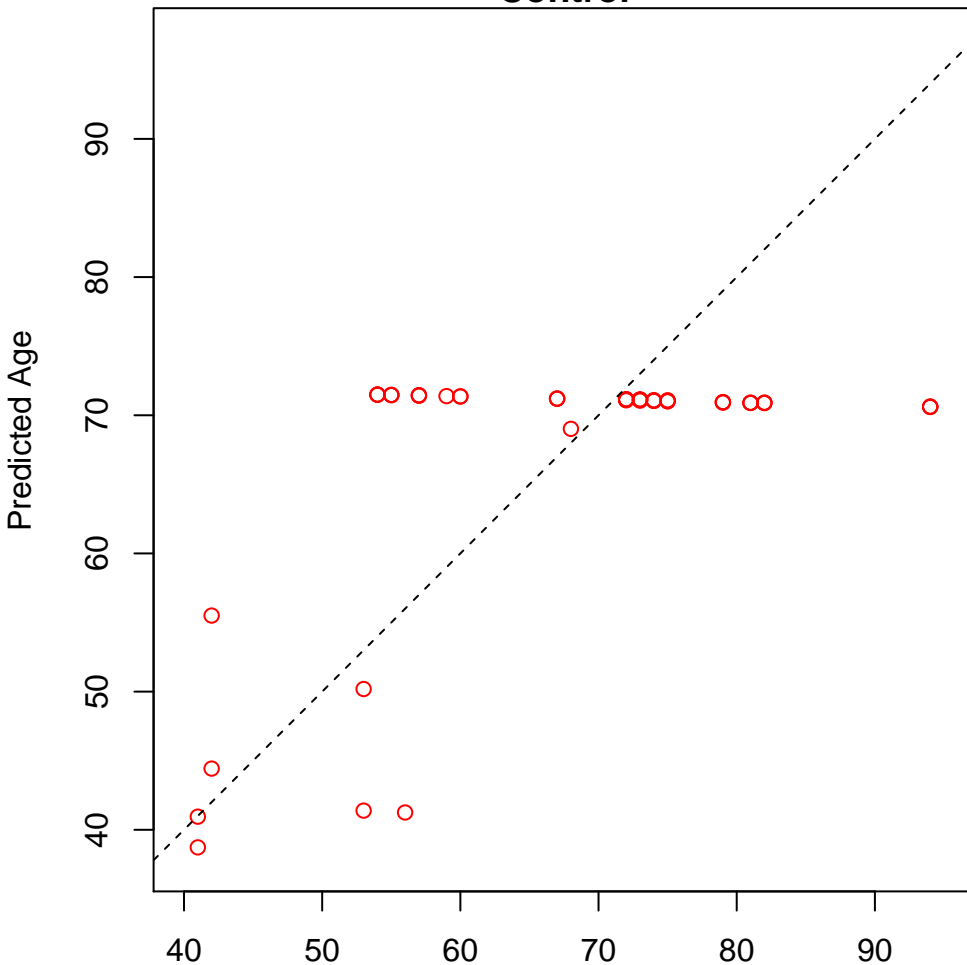
Test



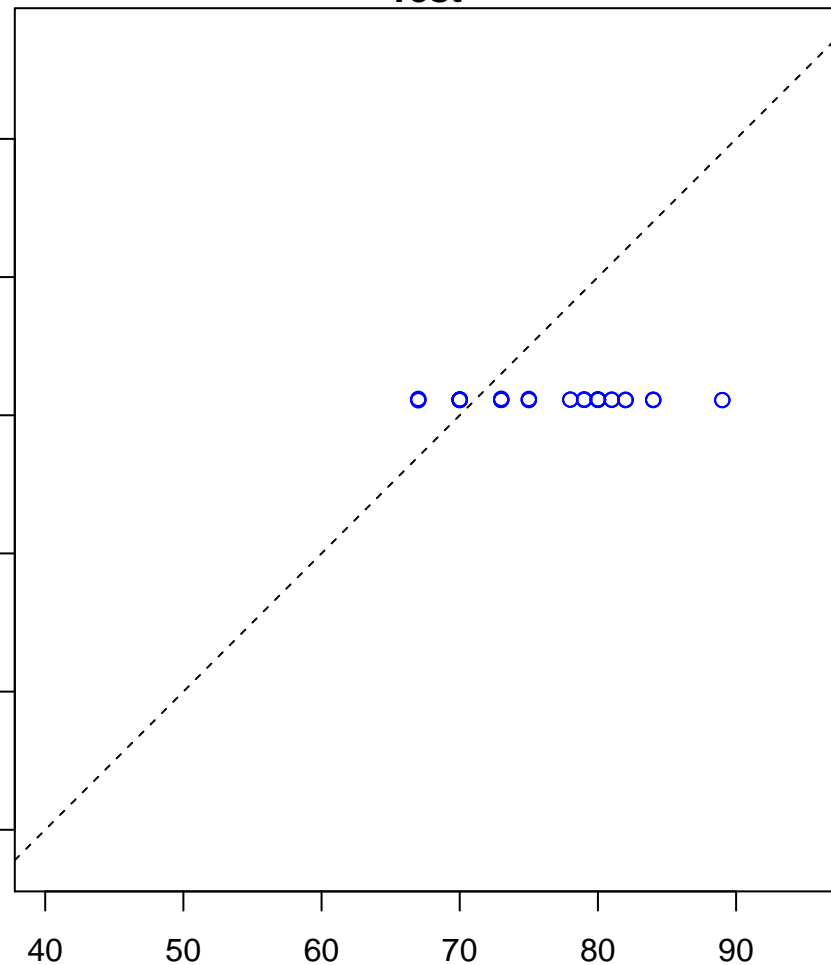
Actual Age

developmental growth (Score: 0.816455)

Control

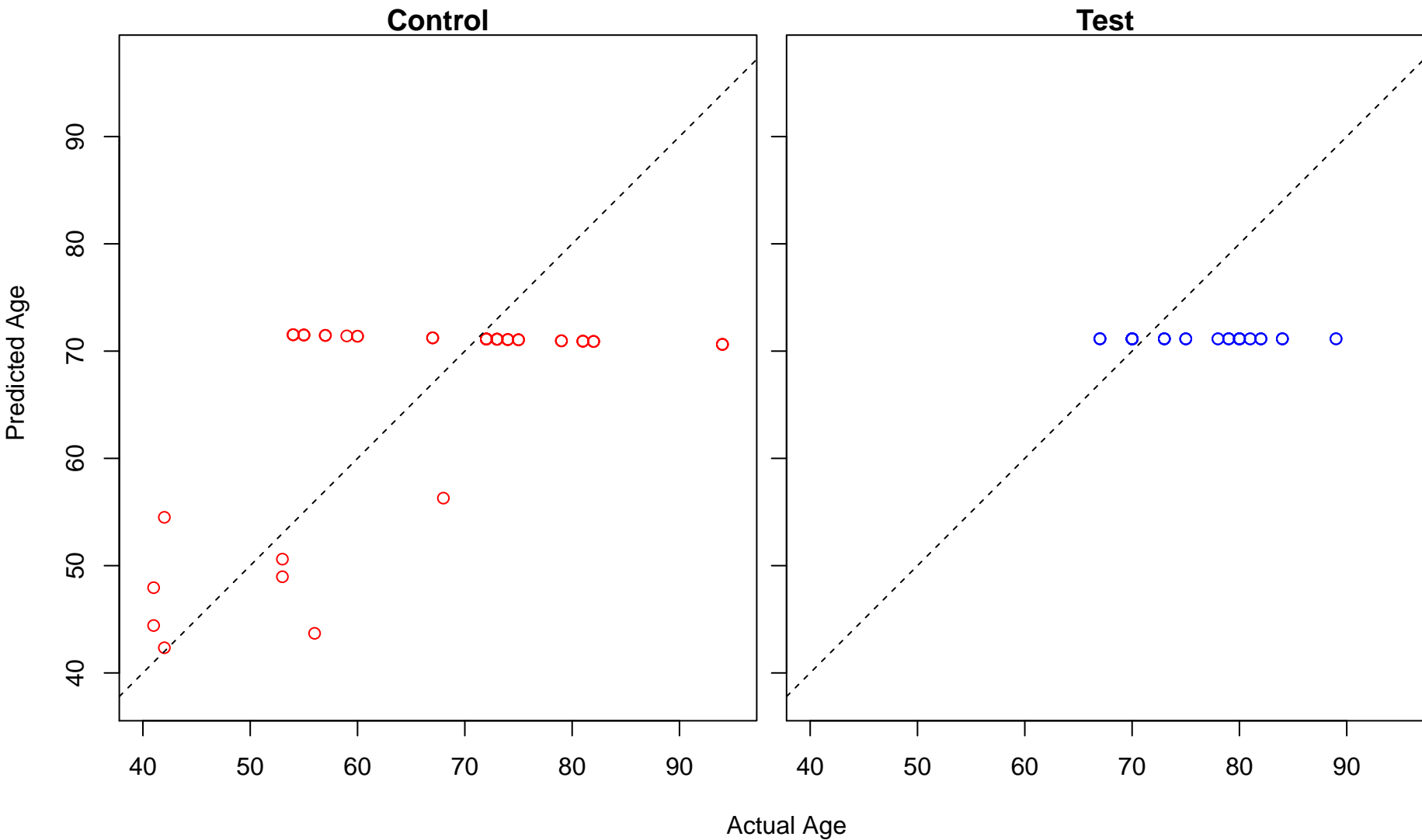


Test

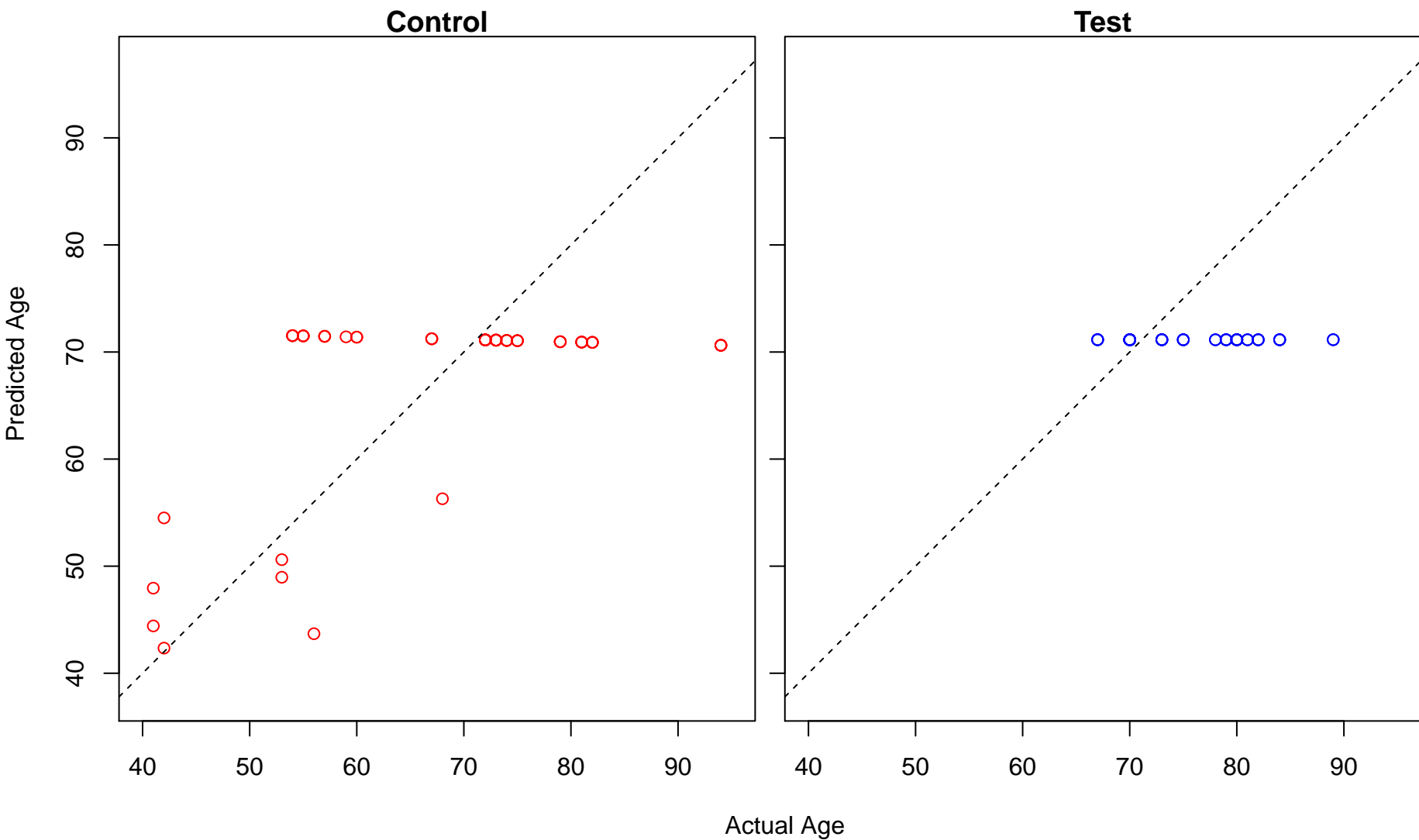


Actual Age

nucleocytoplasmic transport (Score: 0.816320)

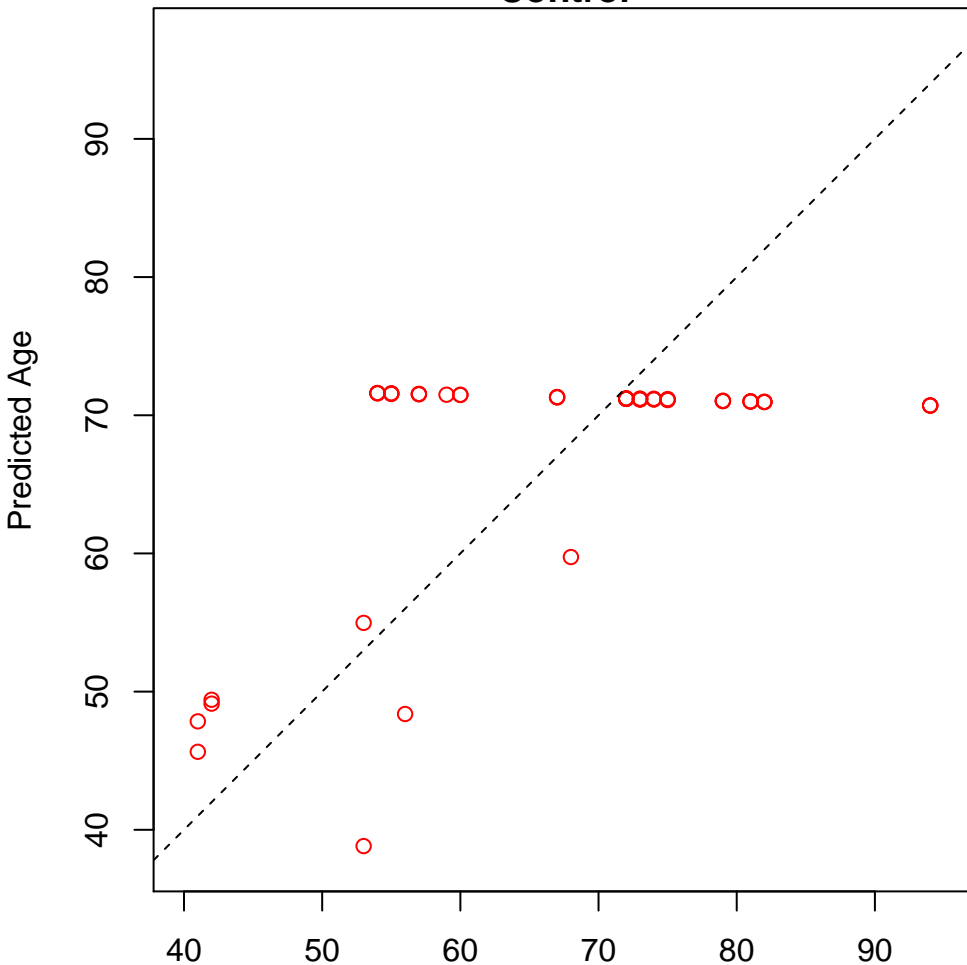


nuclear transport (Score: 0.816320)

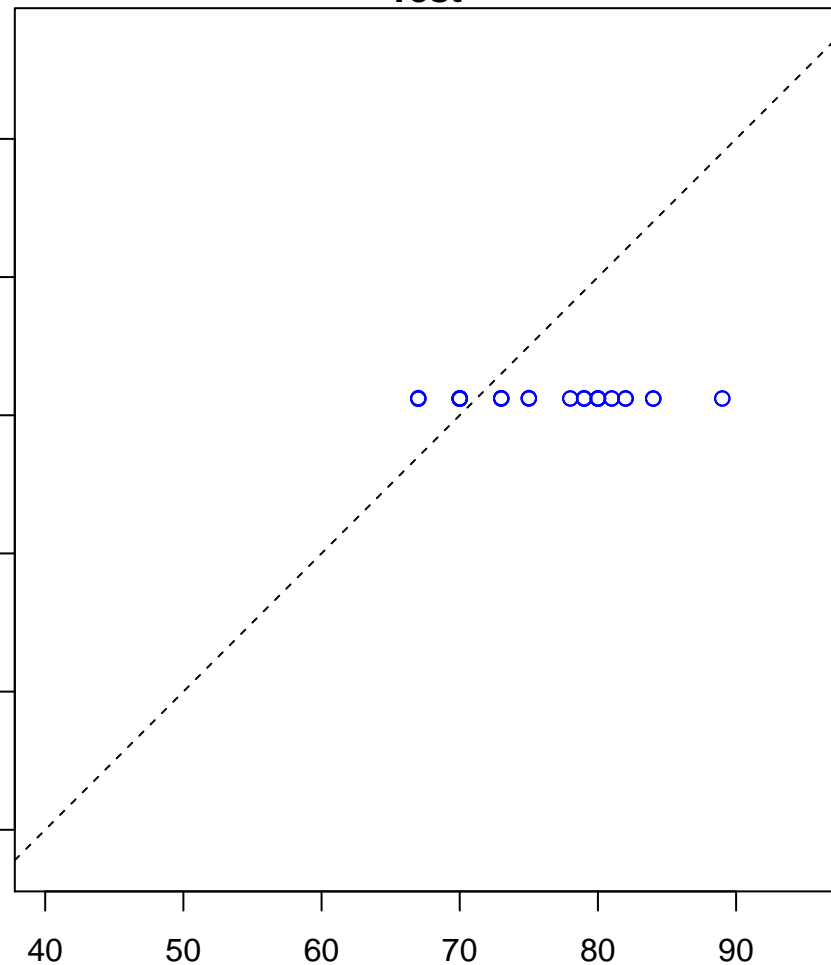


regulation of protein import into nucleus (Score: 0.816254)

Control

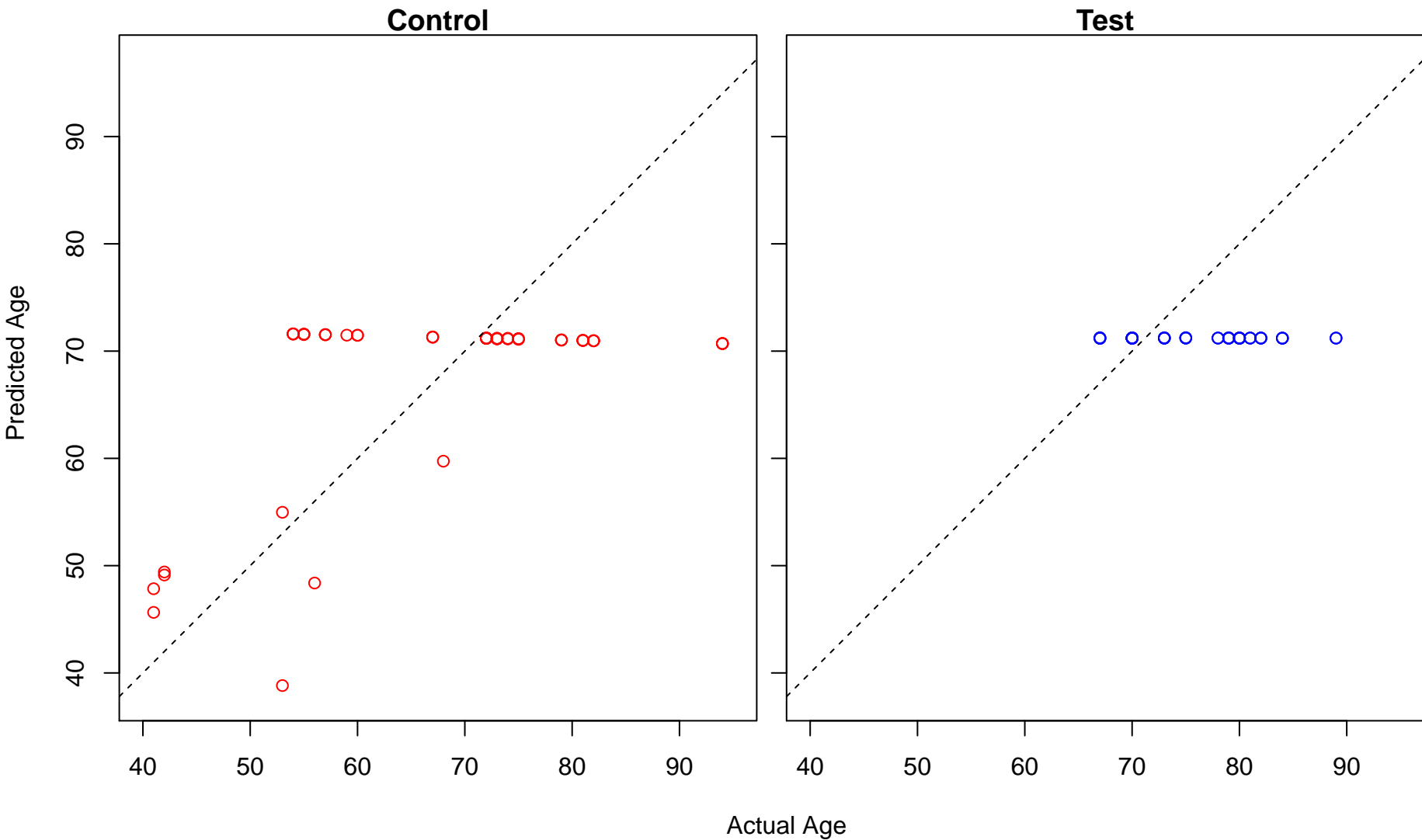


Test

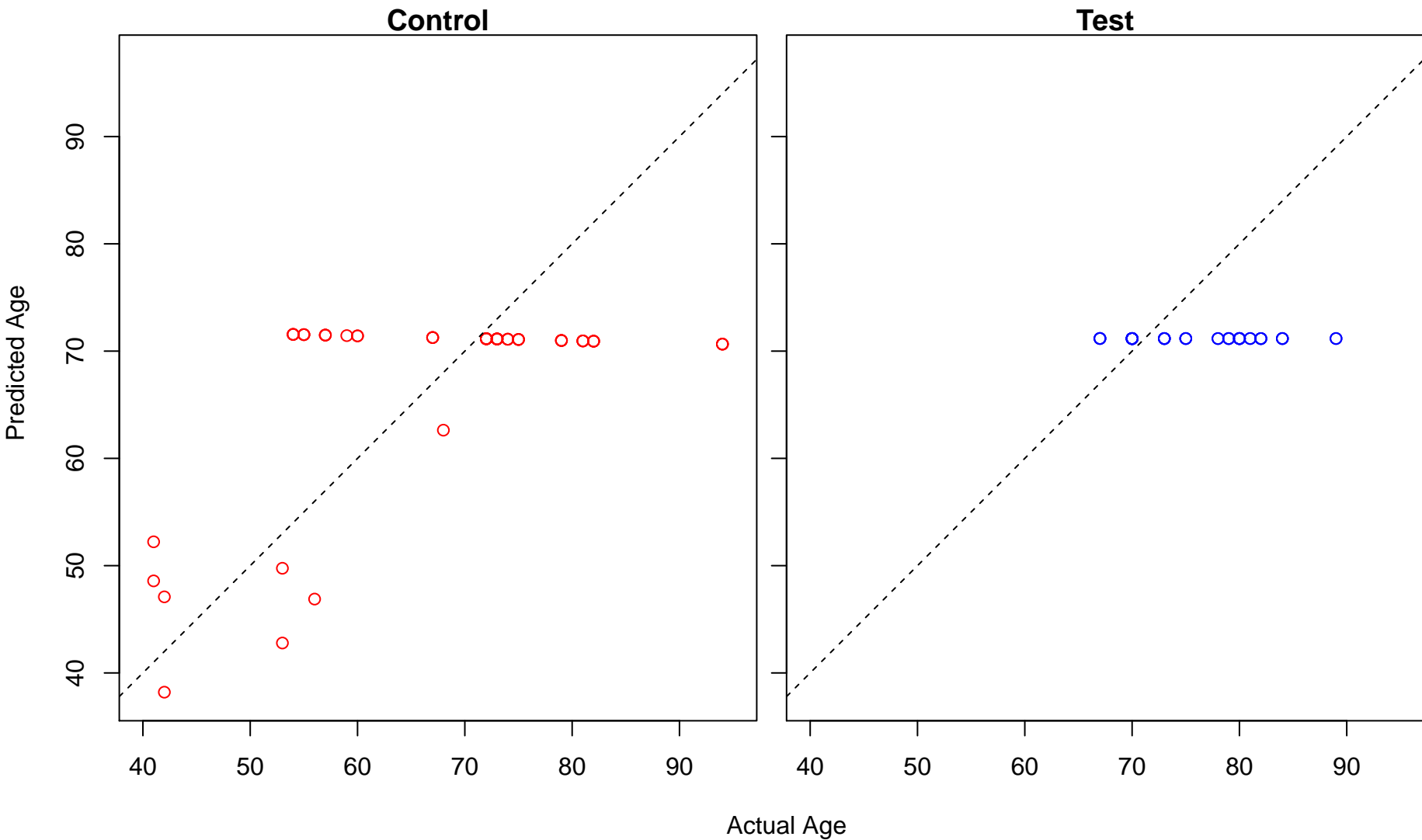


Actual Age

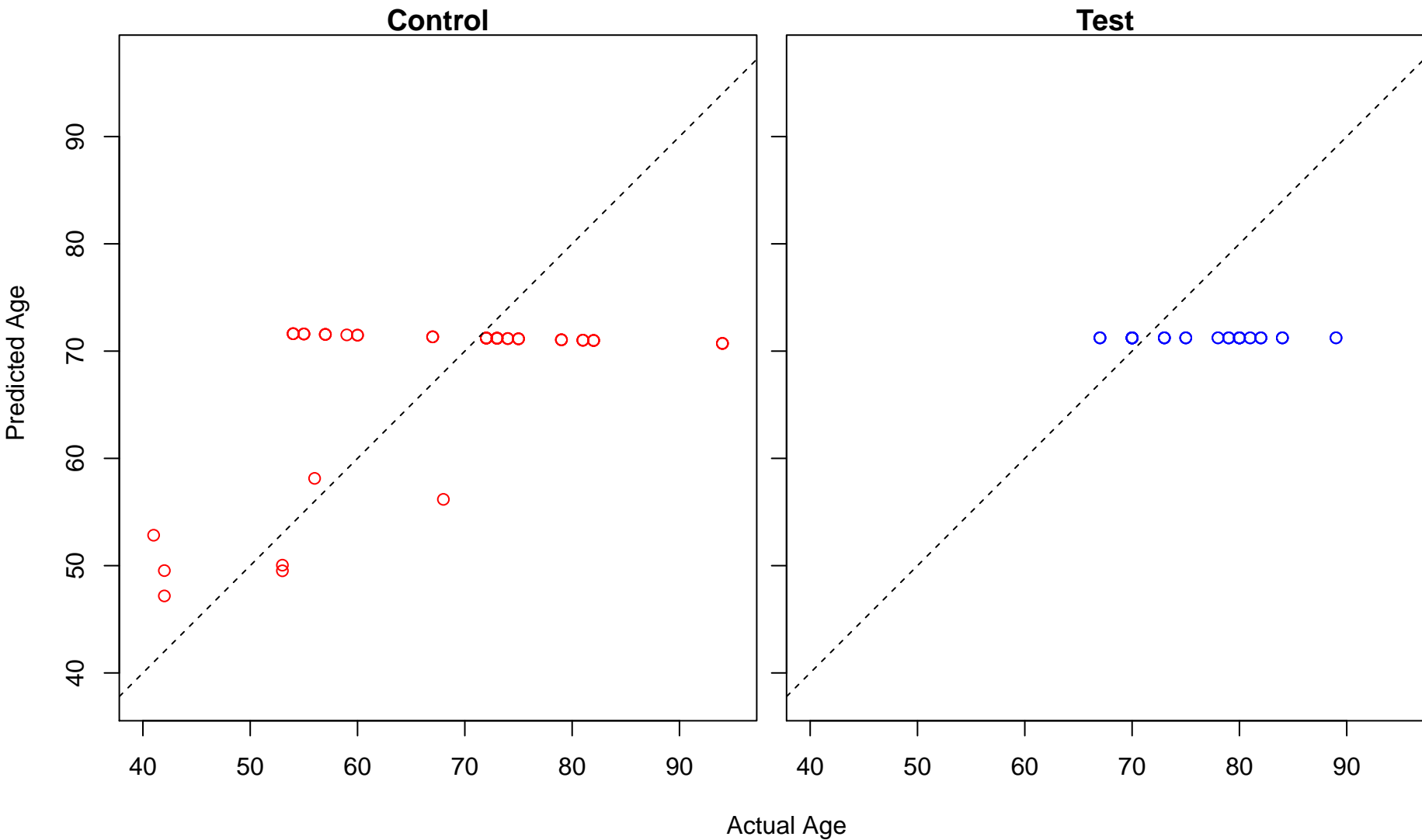
regulation of protein import (Score: 0.816254)



regulation of RNA splicing (Score: 0.816182)

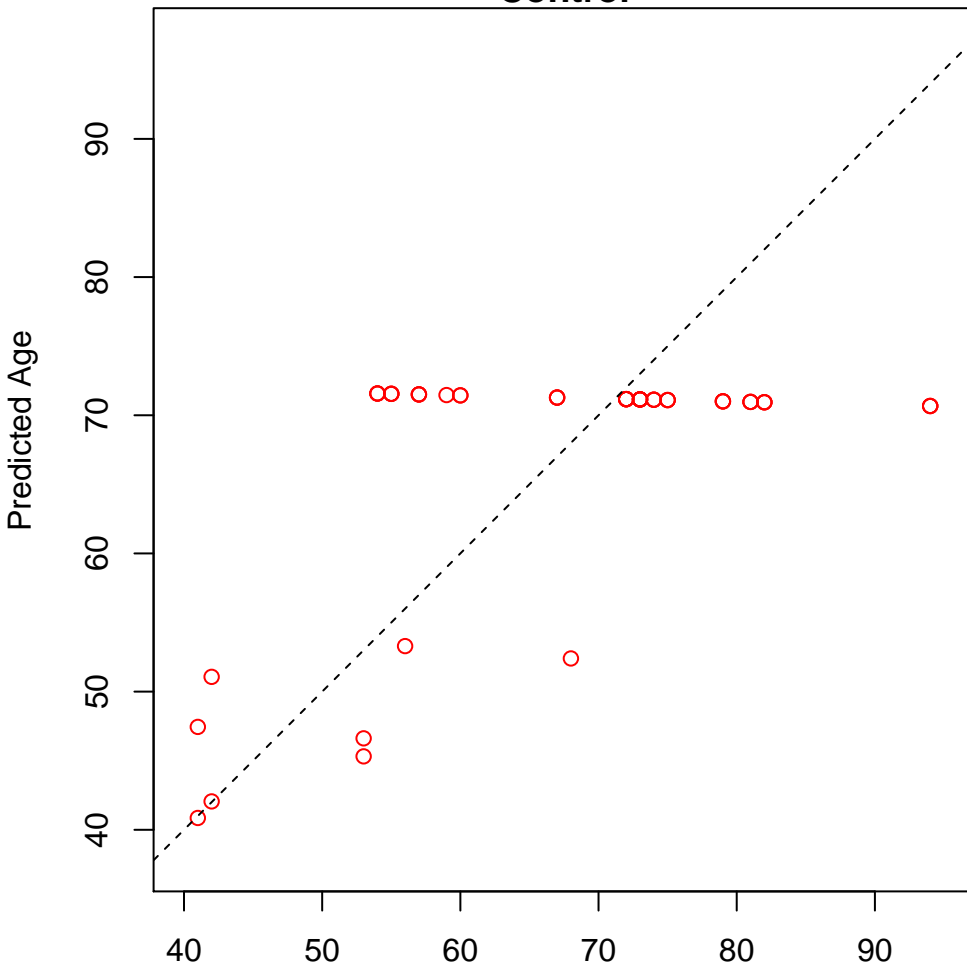


positive regulation of protein catabolic process (Score: 0.816092)

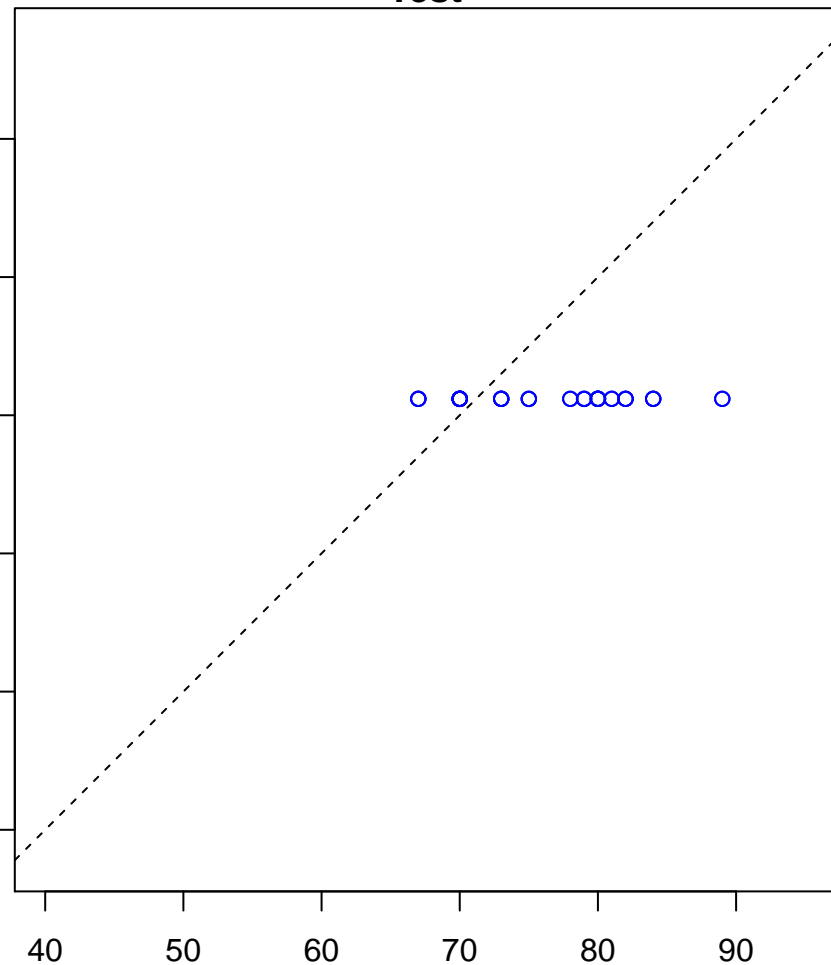


regulation of protein phosphorylation (Score: 0.816053)

Control

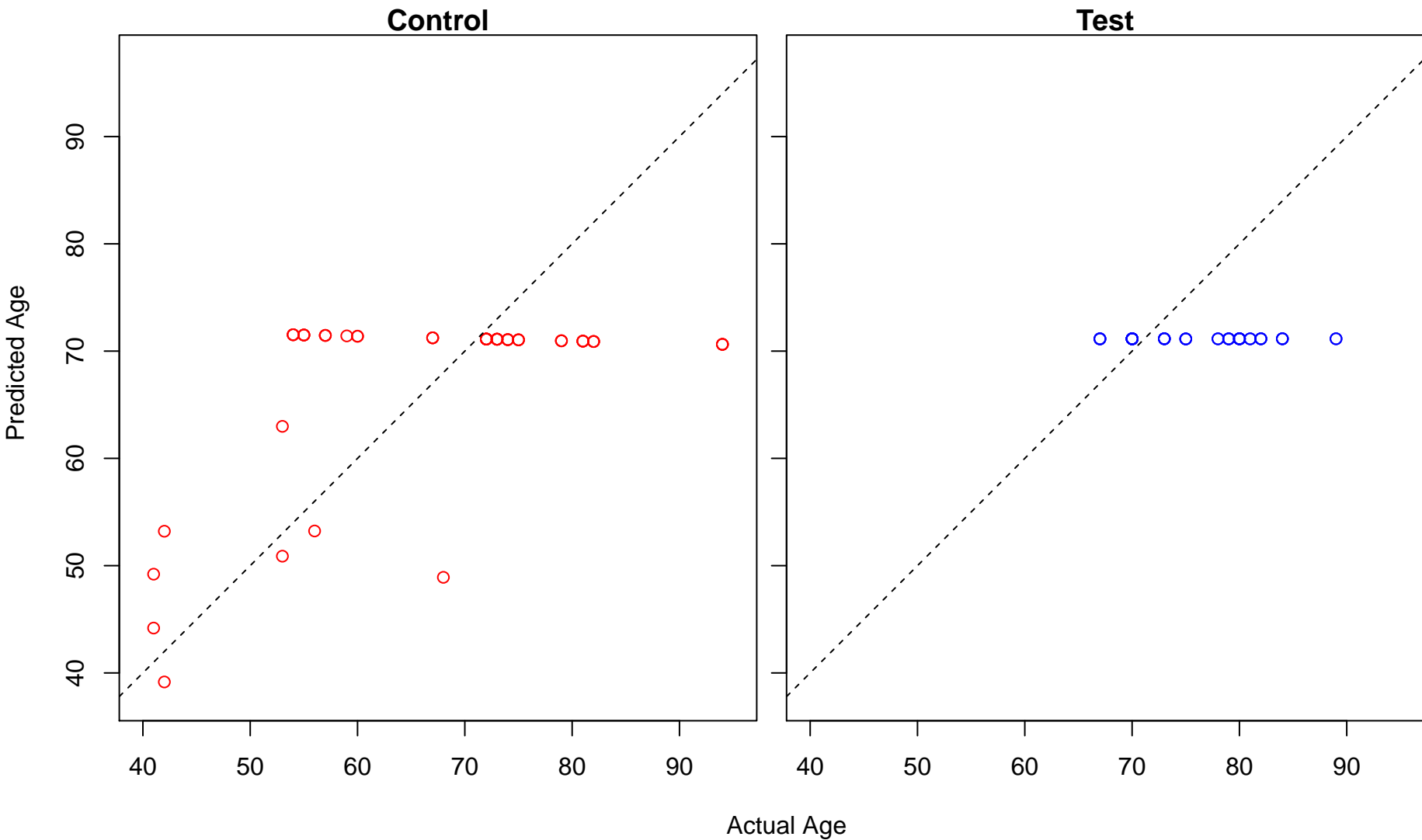


Test

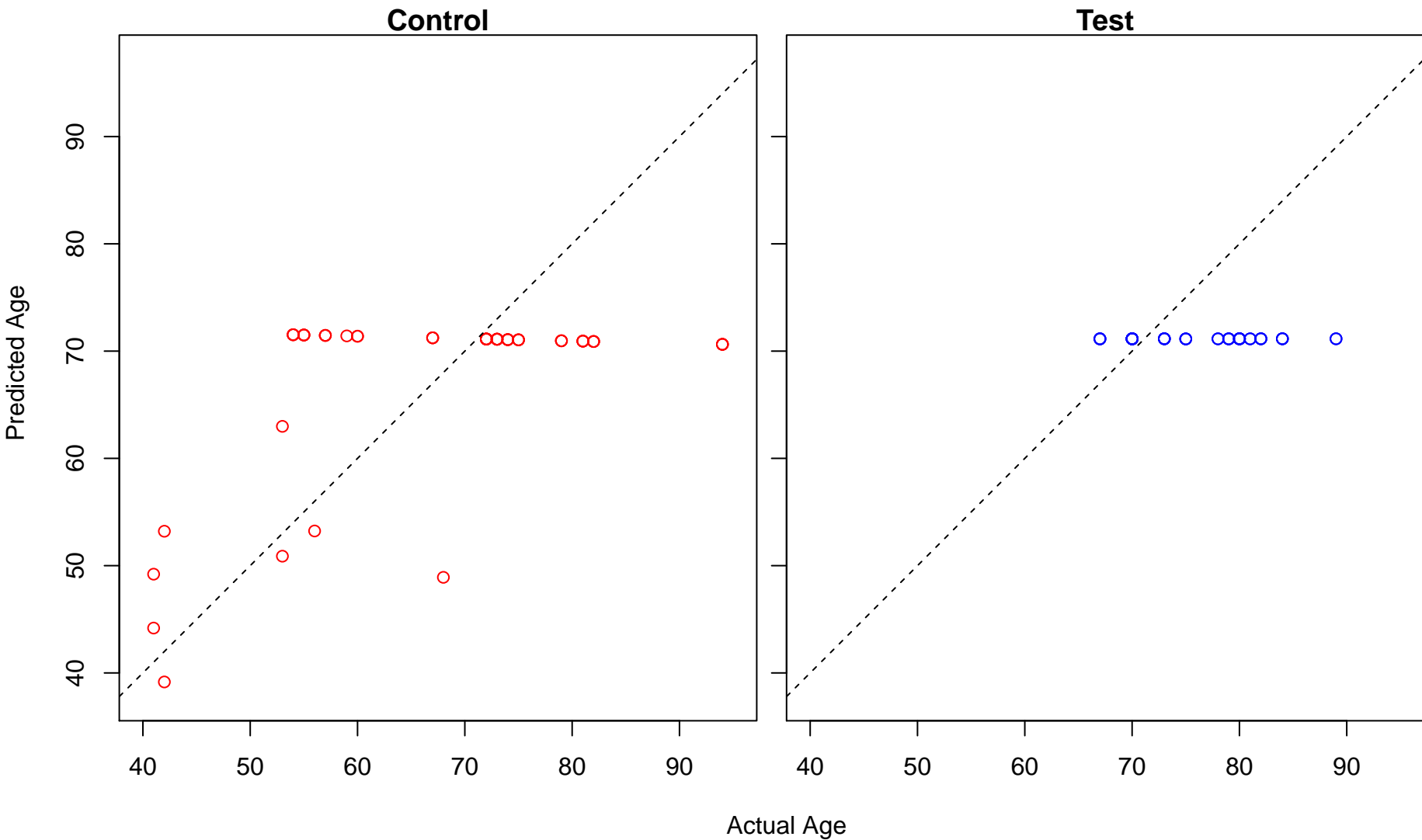


Actual Age

protein import into nucleus (Score: 0.816032)

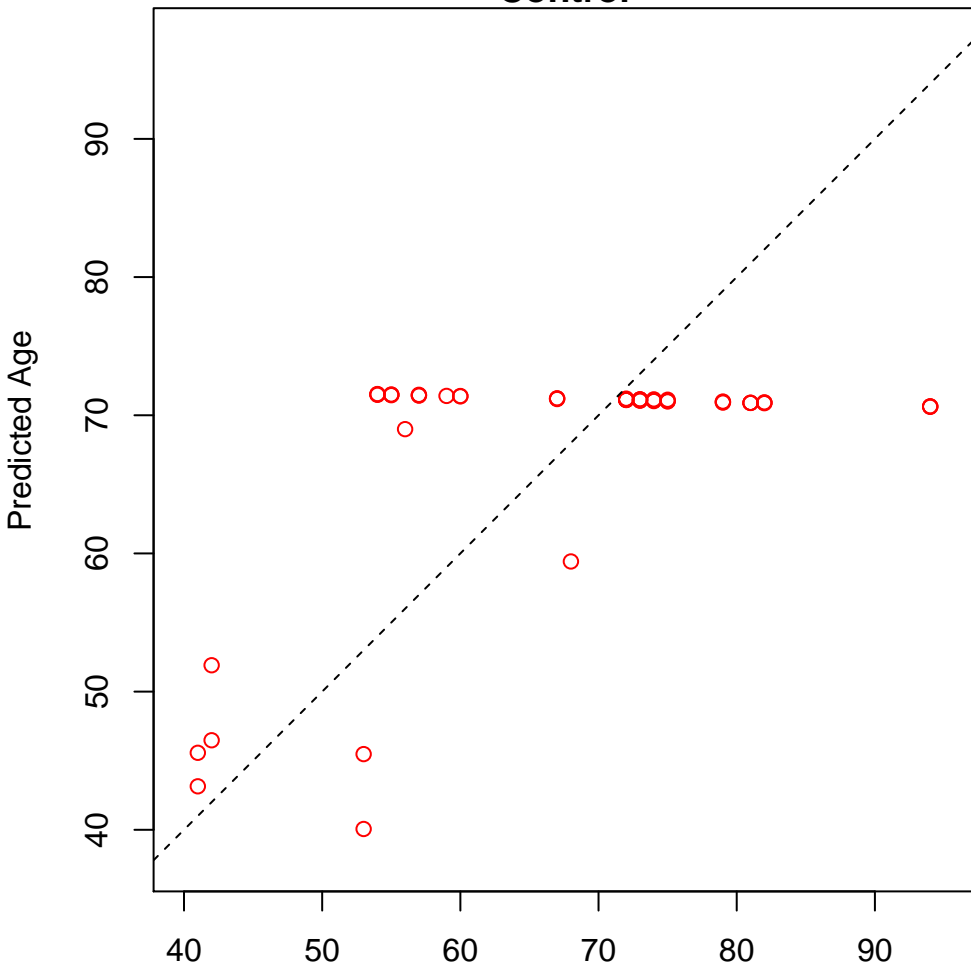


protein import (Score: 0.816032)

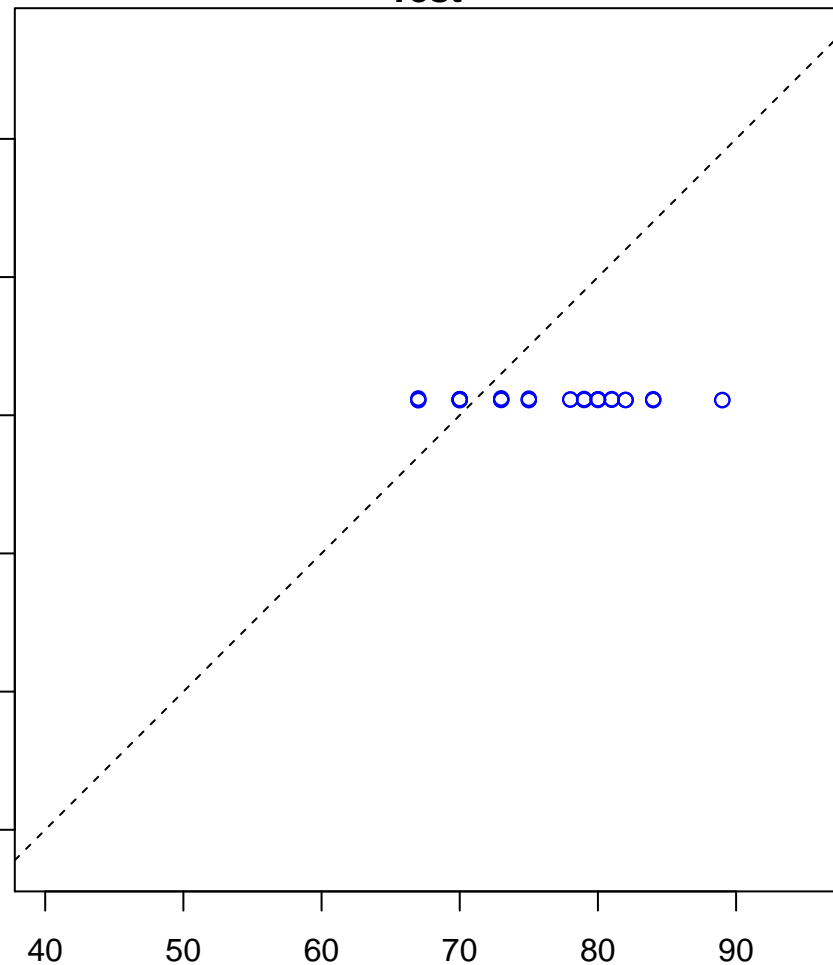


response to epidermal growth factor (Score: 0.815929)

Control

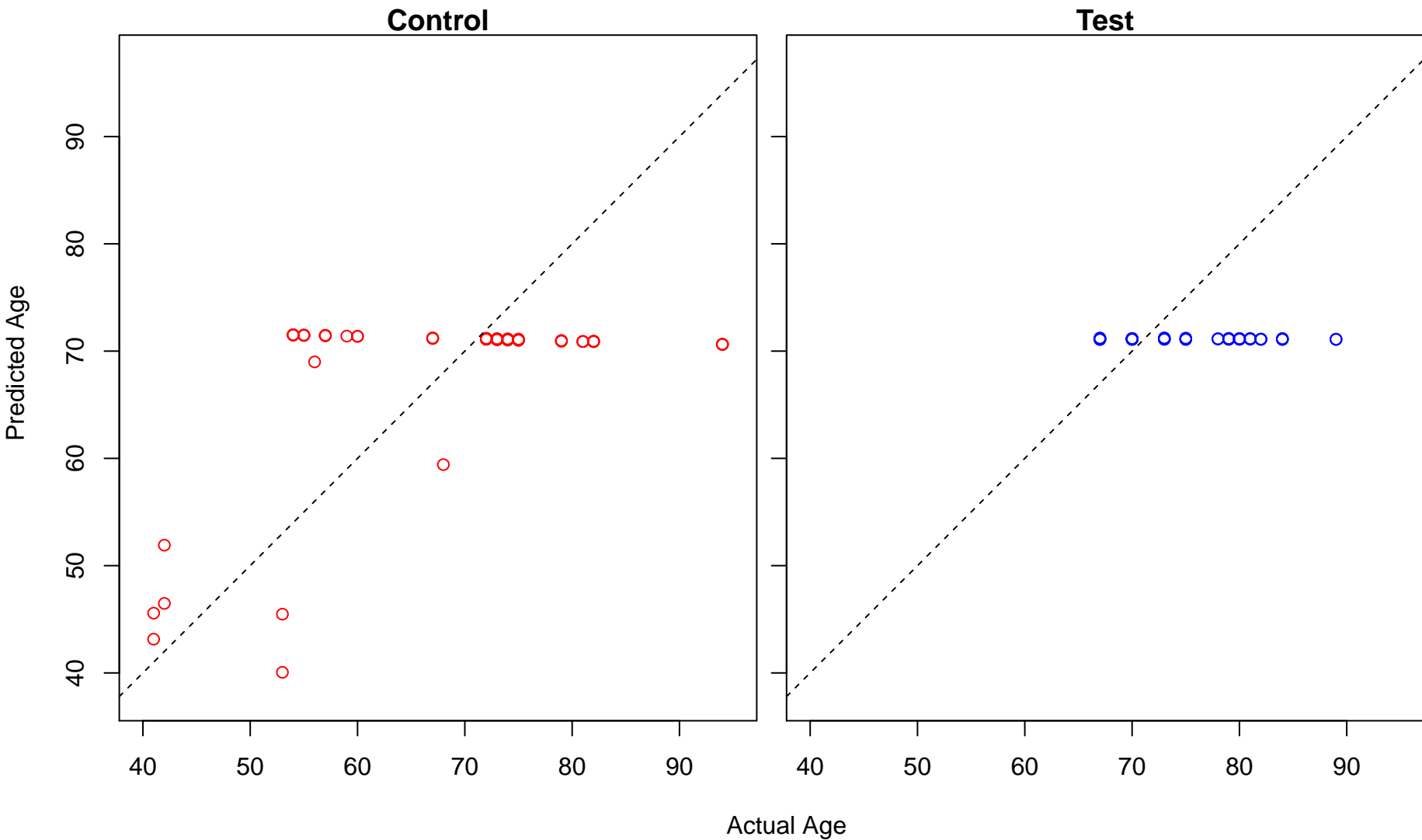


Test

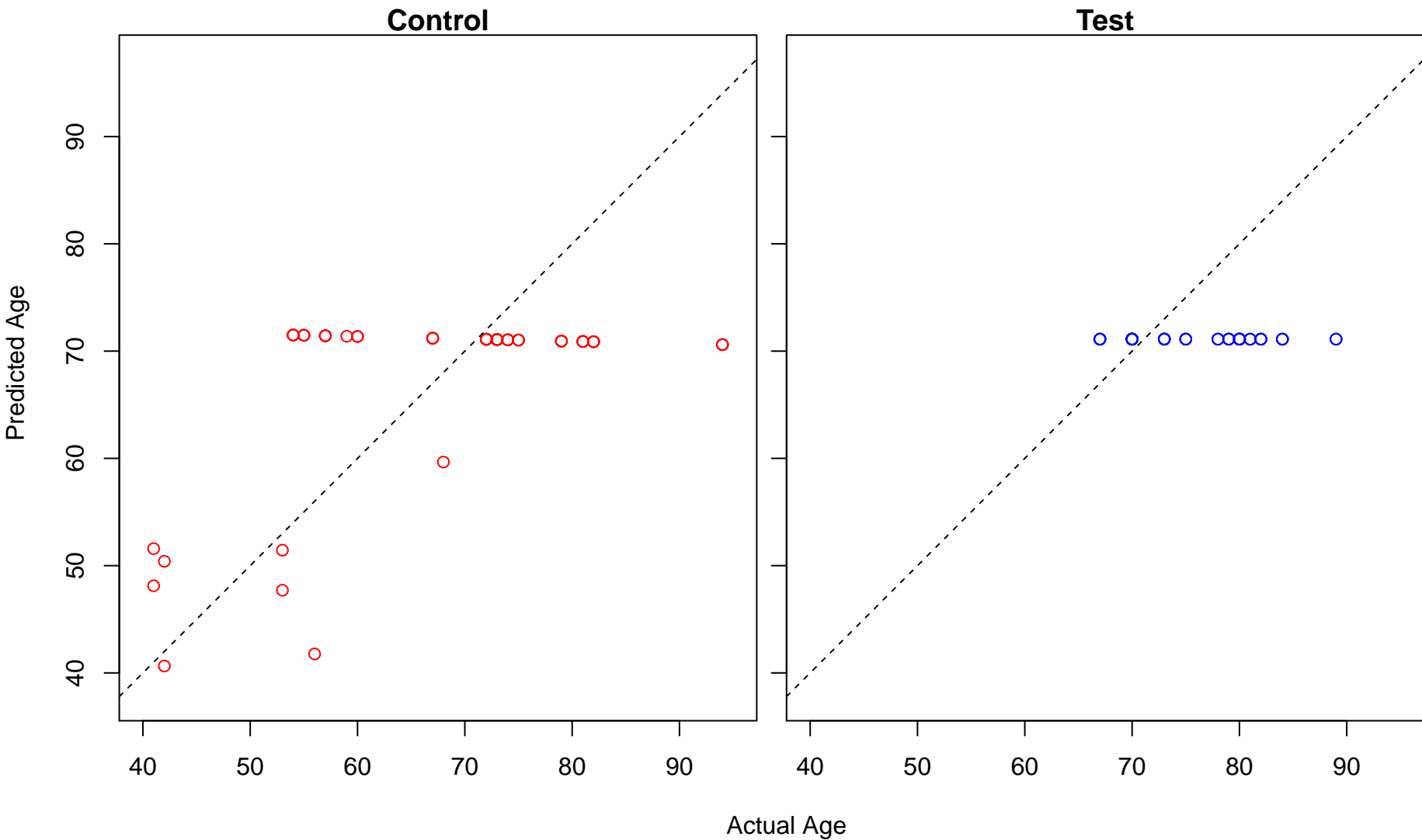


Actual Age

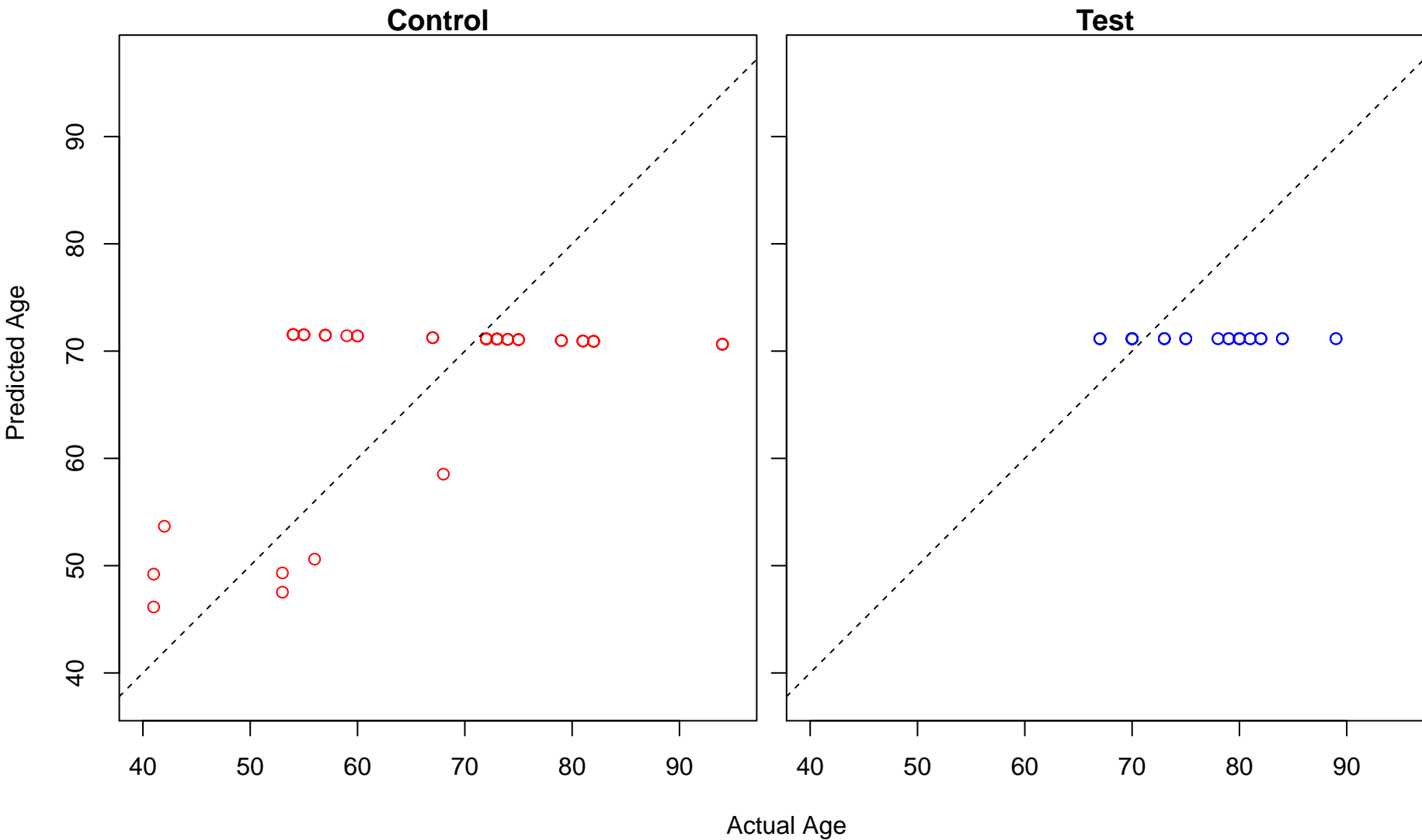
cellular response to epidermal growth factor stimulus (Score: 0.815929)



cellular response to organonitrogen compound (Score: 0.815793)

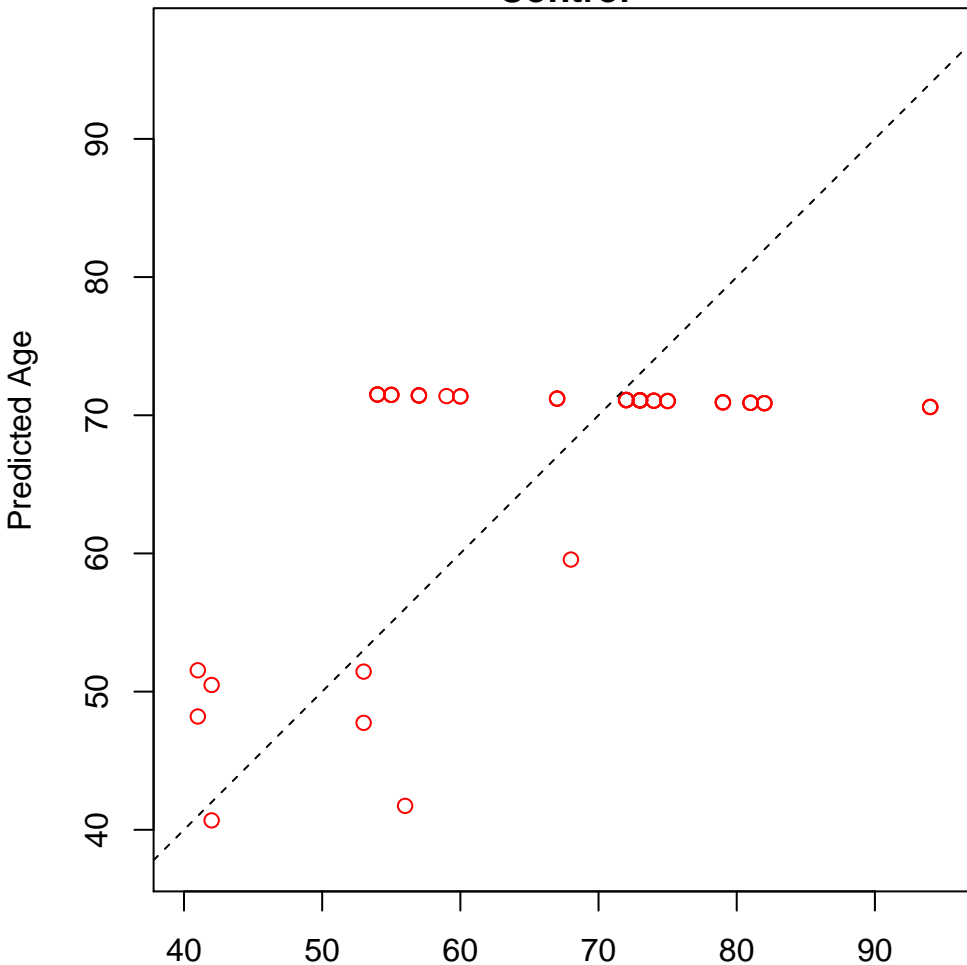


cellular response to oxygen-containing compound (Score: 0.815729)

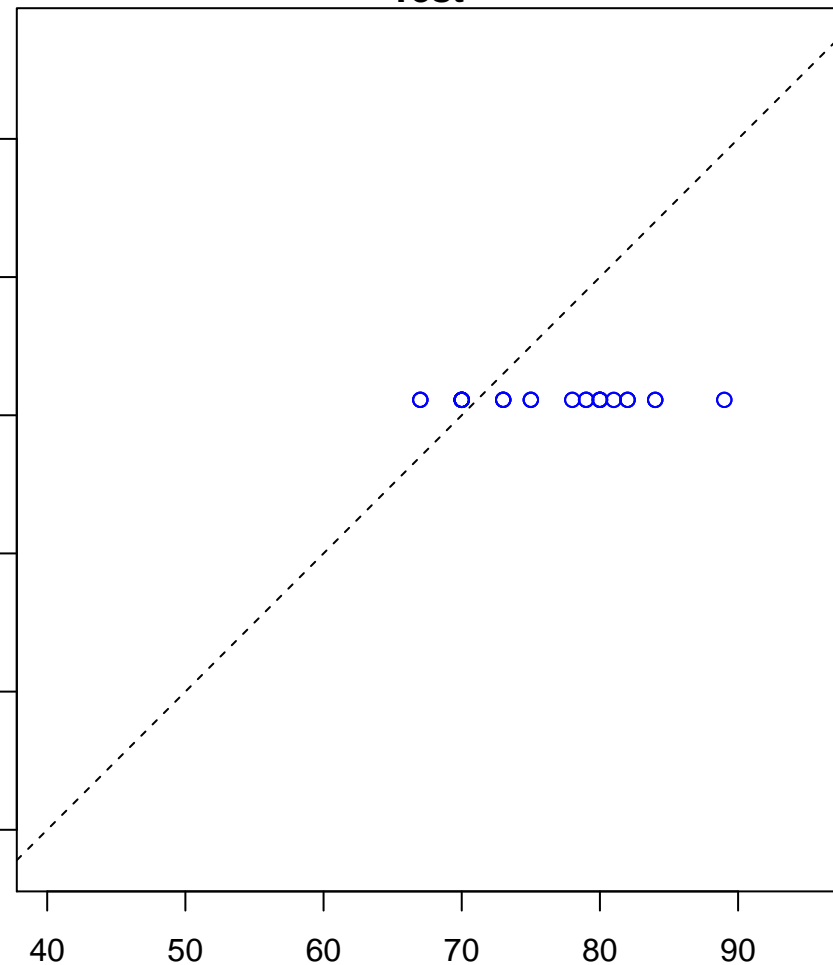


cellular response to nitrogen compound (Score: 0.815623)

Control

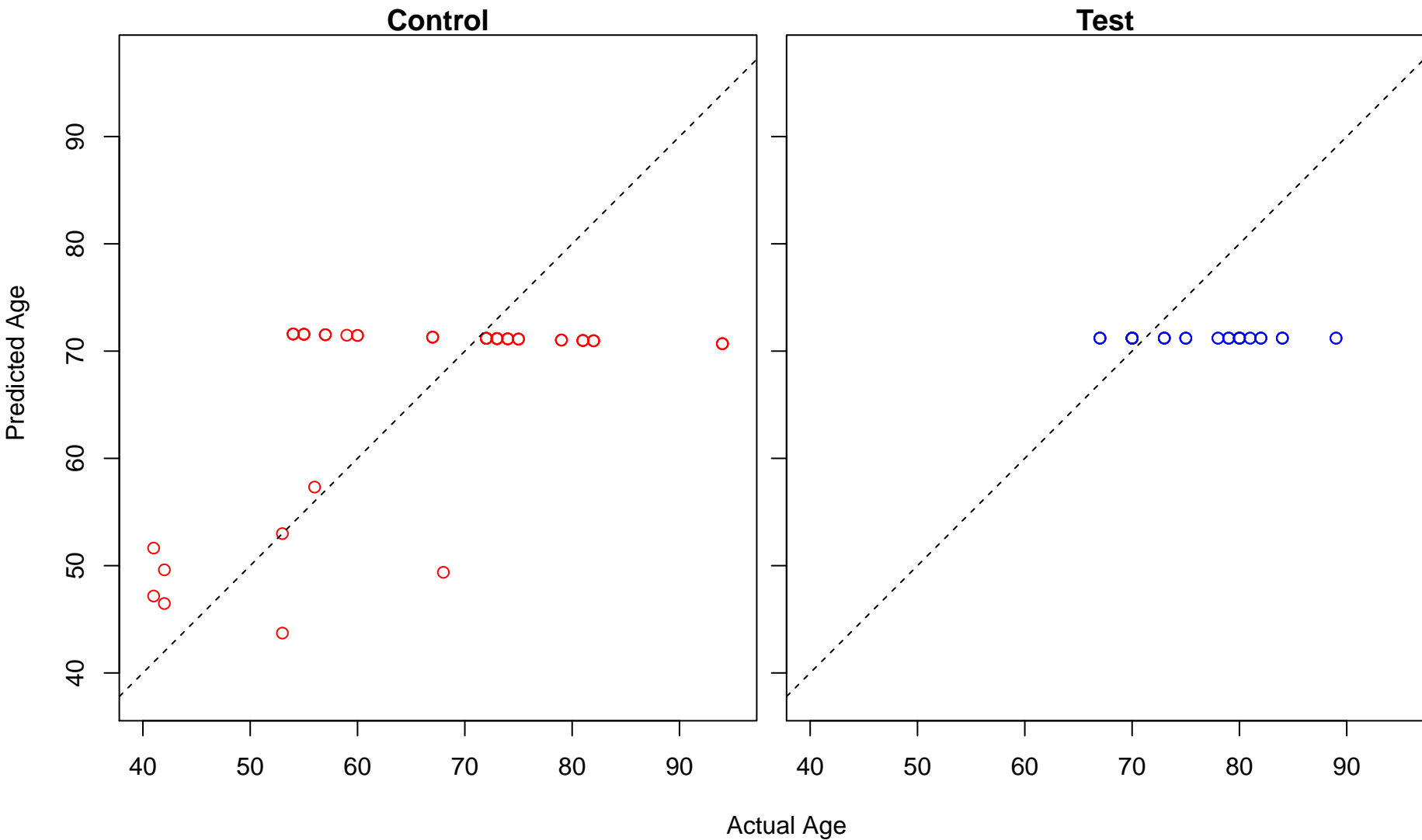


Test



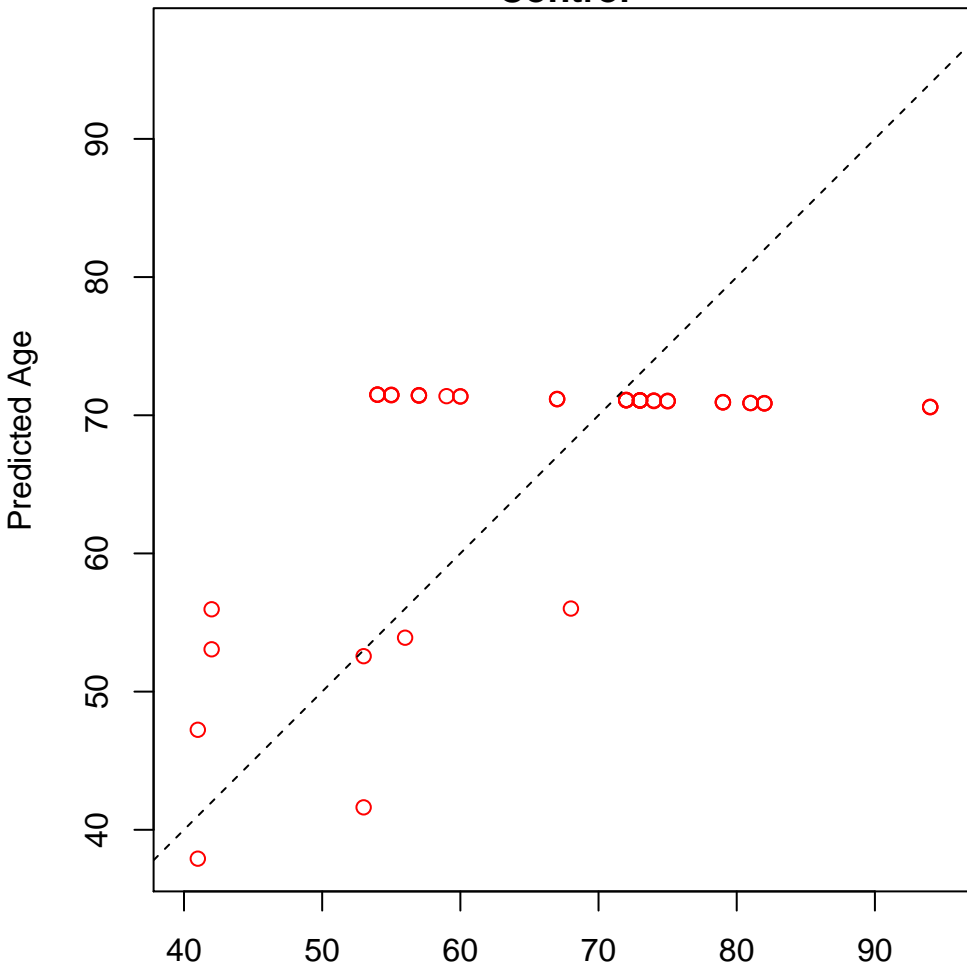
Actual Age

lipid biosynthetic process (Score: 0.815564)

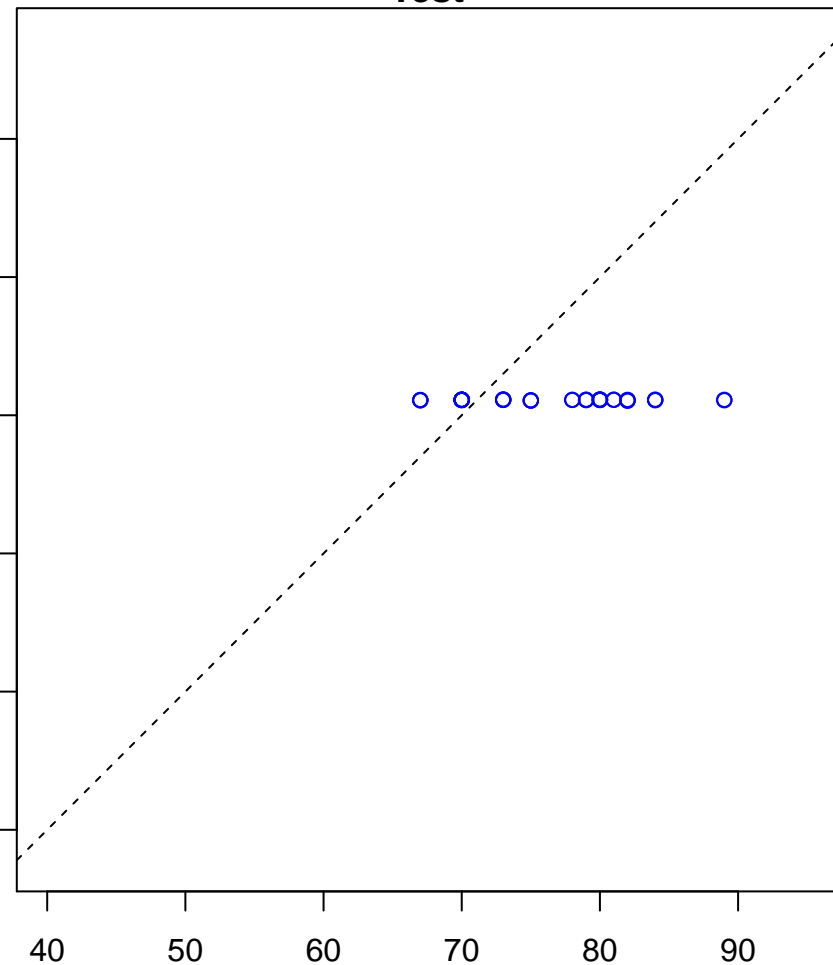


regulation of myotube differentiation (Score: 0.815360)

Control



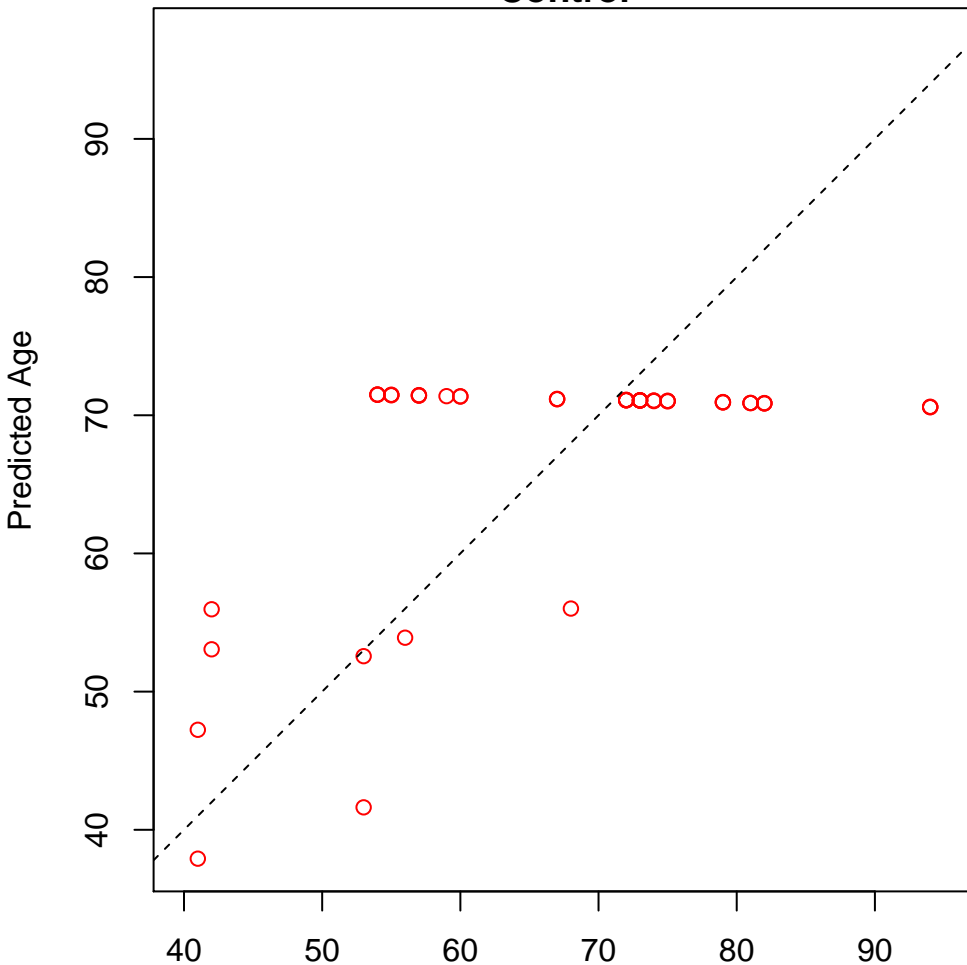
Test



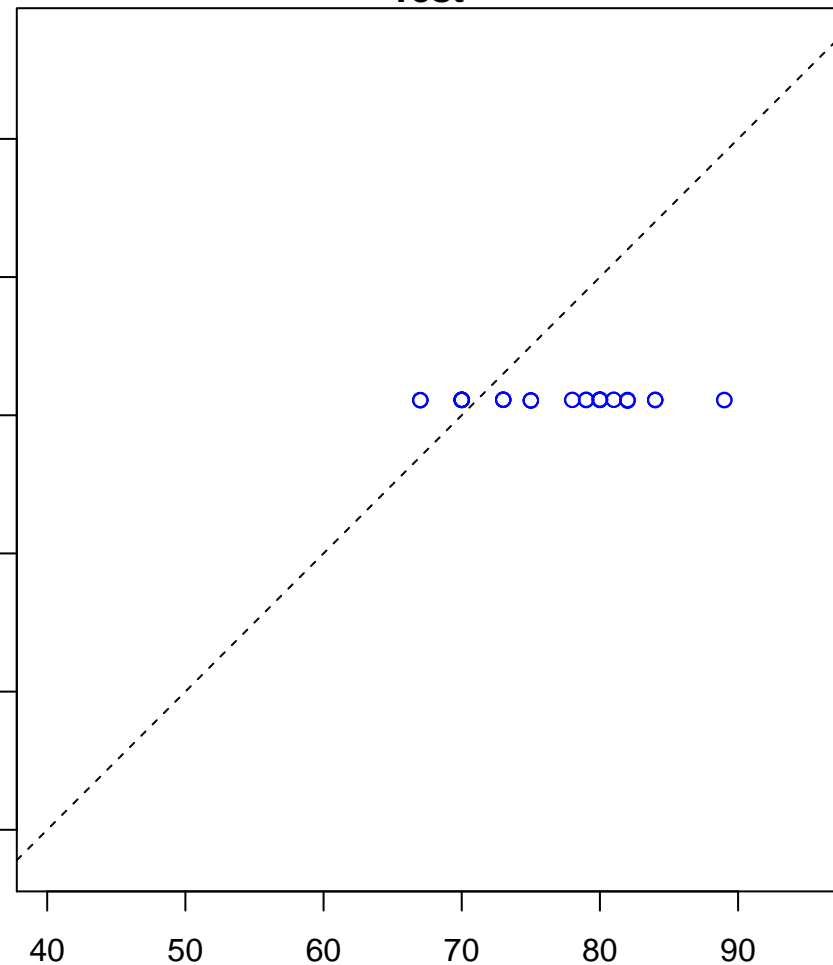
Actual Age

regulation of B cell differentiation (Score: 0.815360)

Control



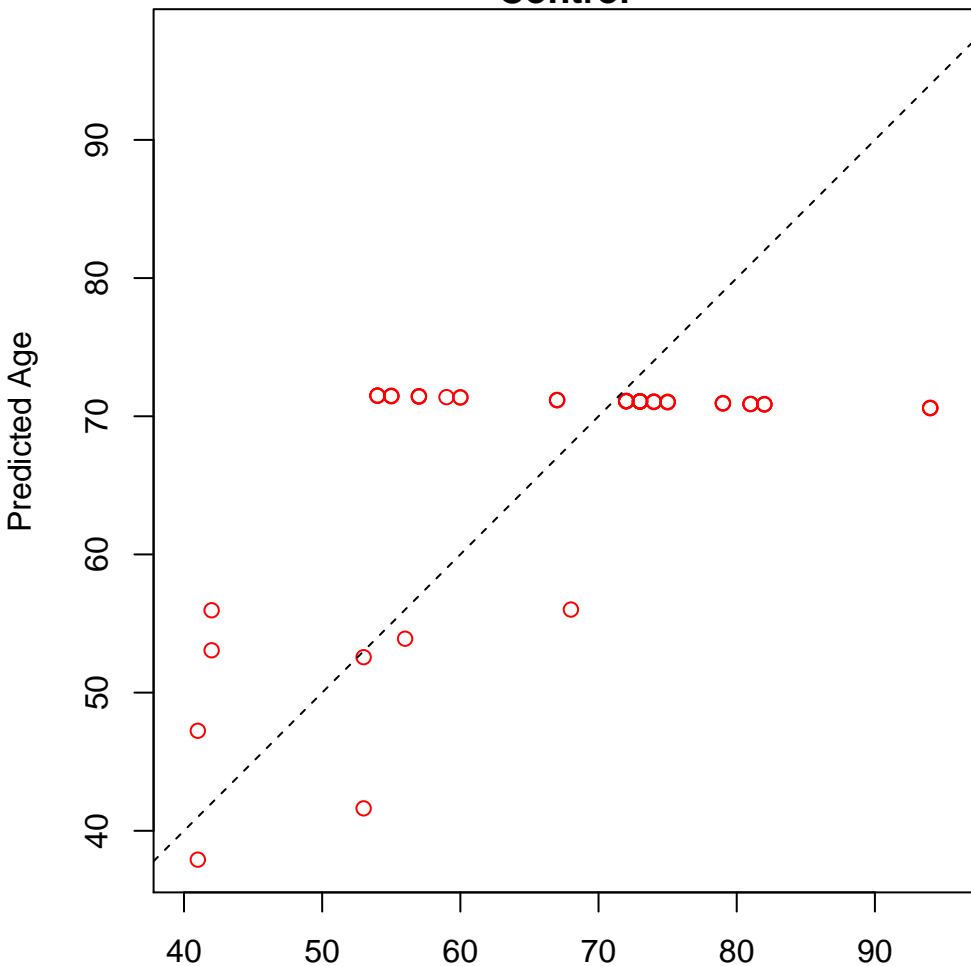
Test



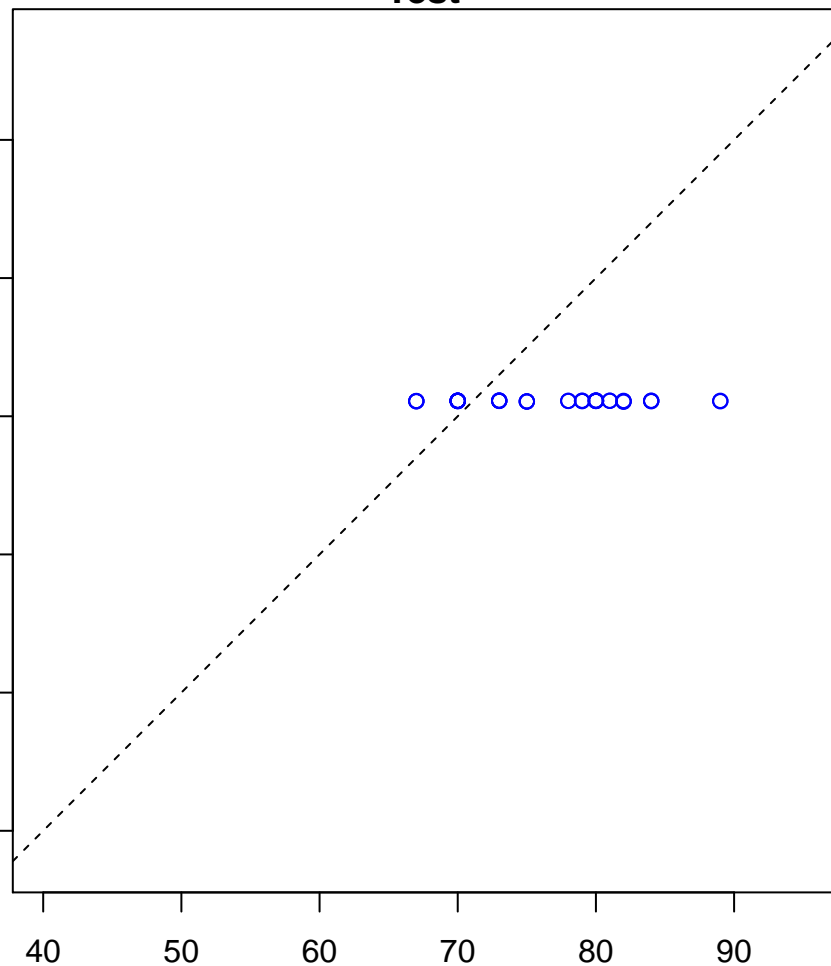
Actual Age

positive regulation of B cell differentiation (Score: 0.815360)

Control

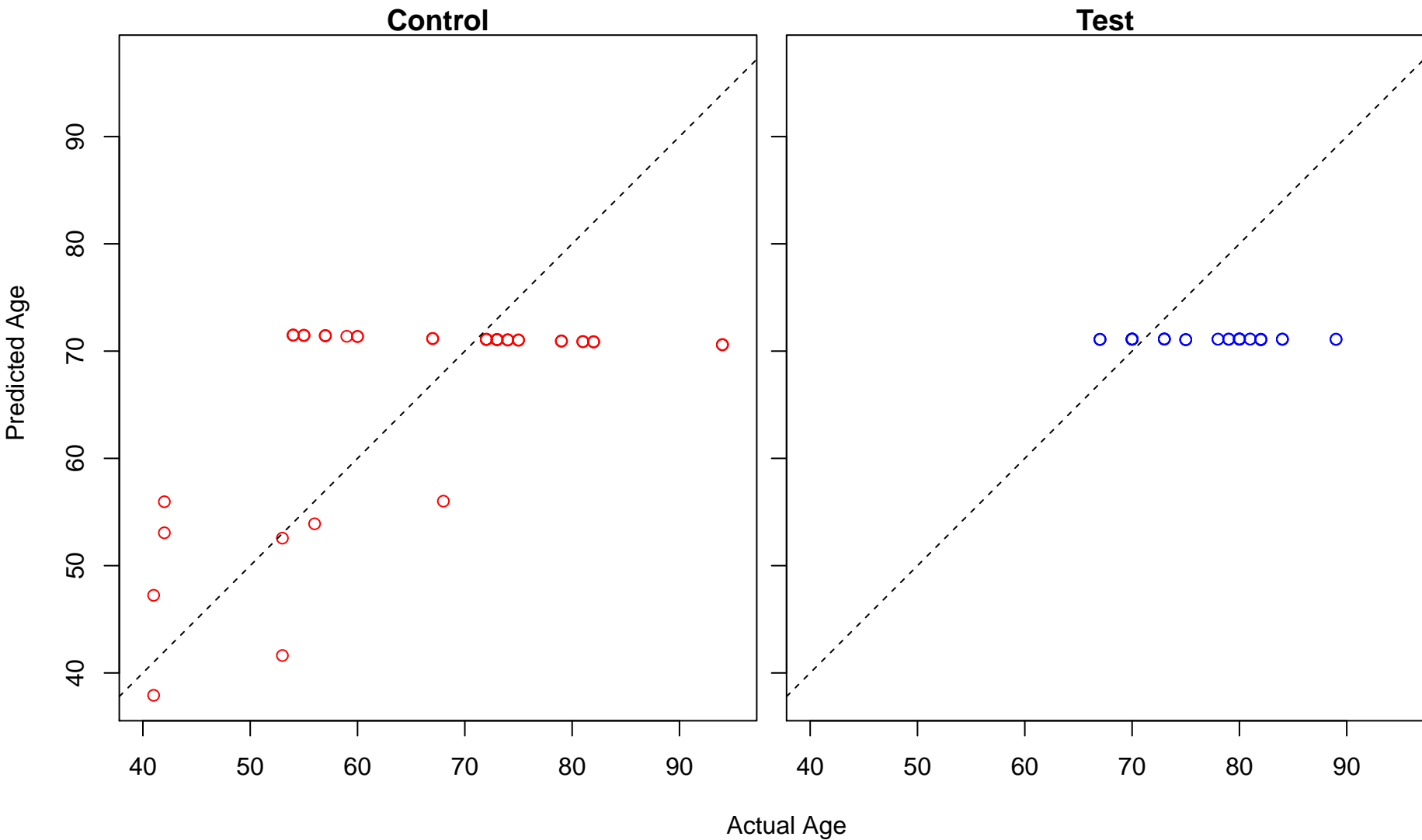


Test

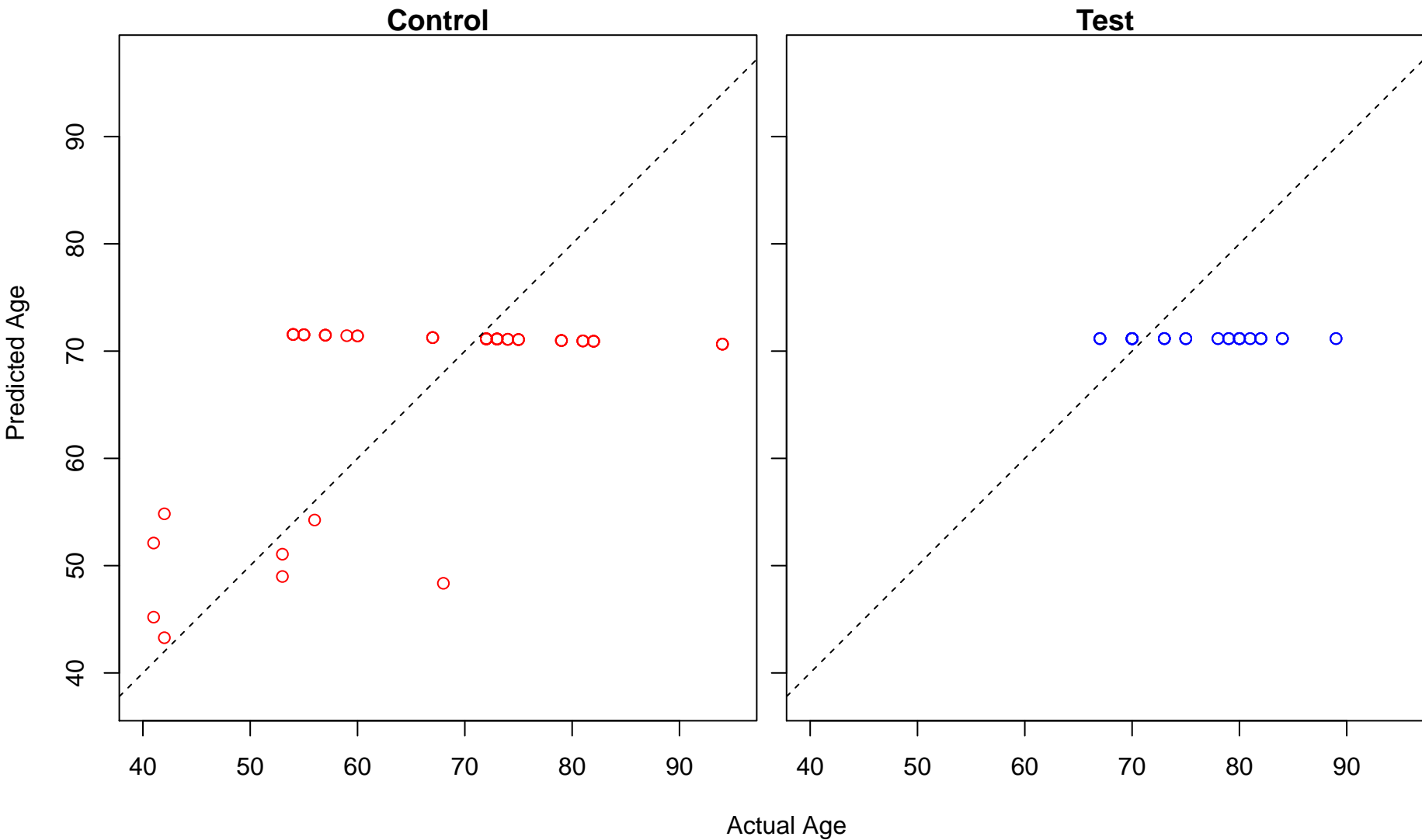


Actual Age

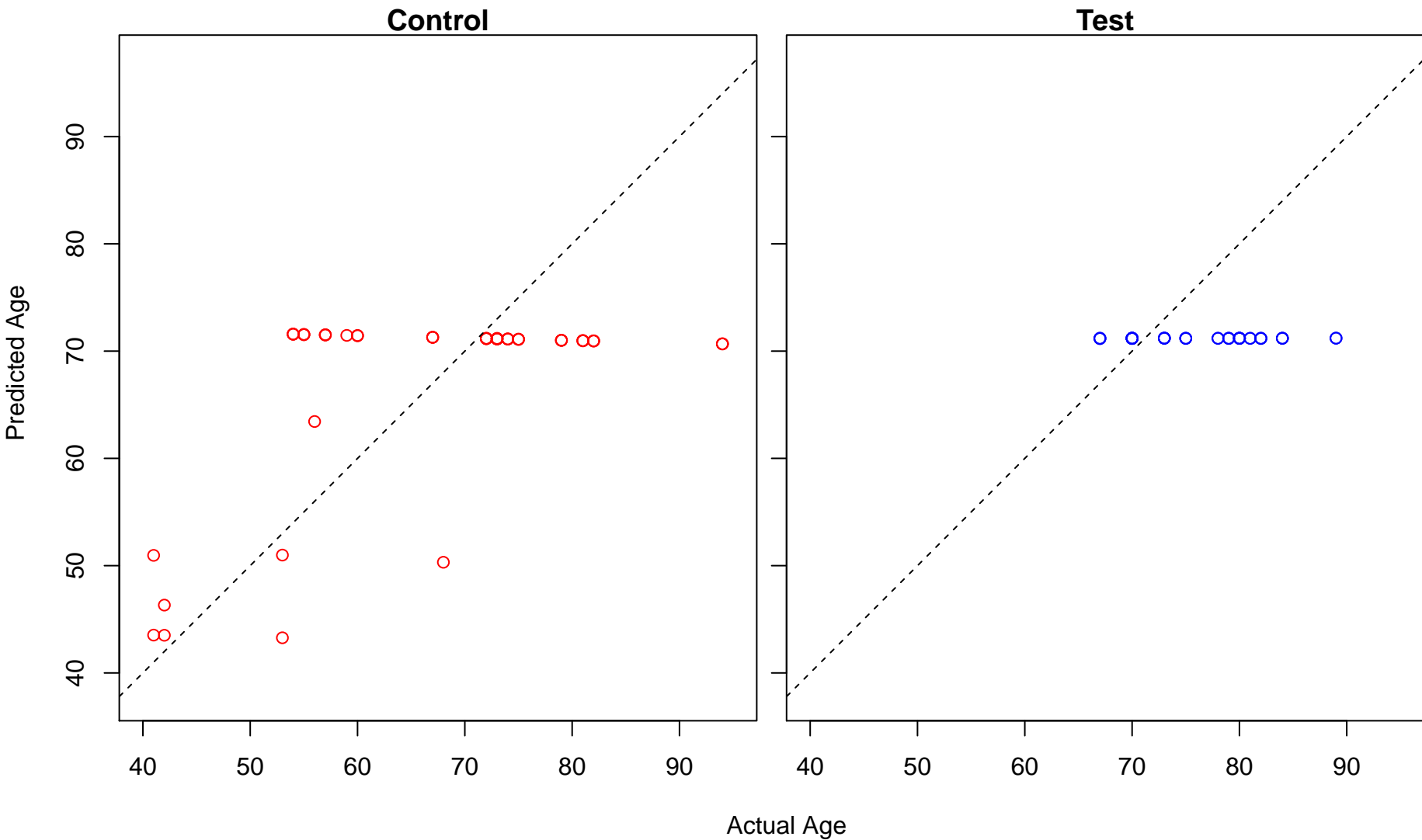
regulation of striated muscle cell differentiation (Score: 0.815360)



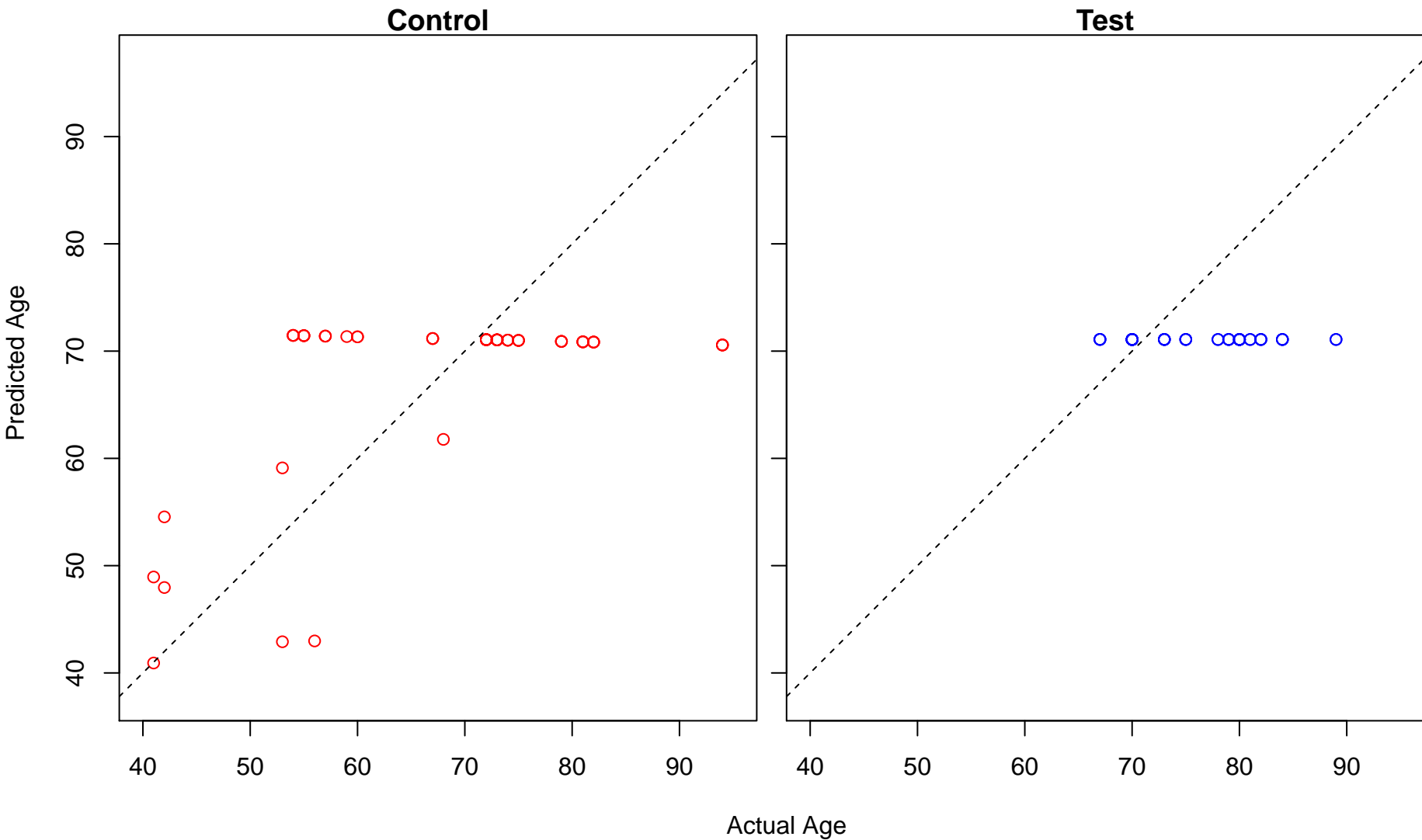
RNA localization (Score: 0.815319)



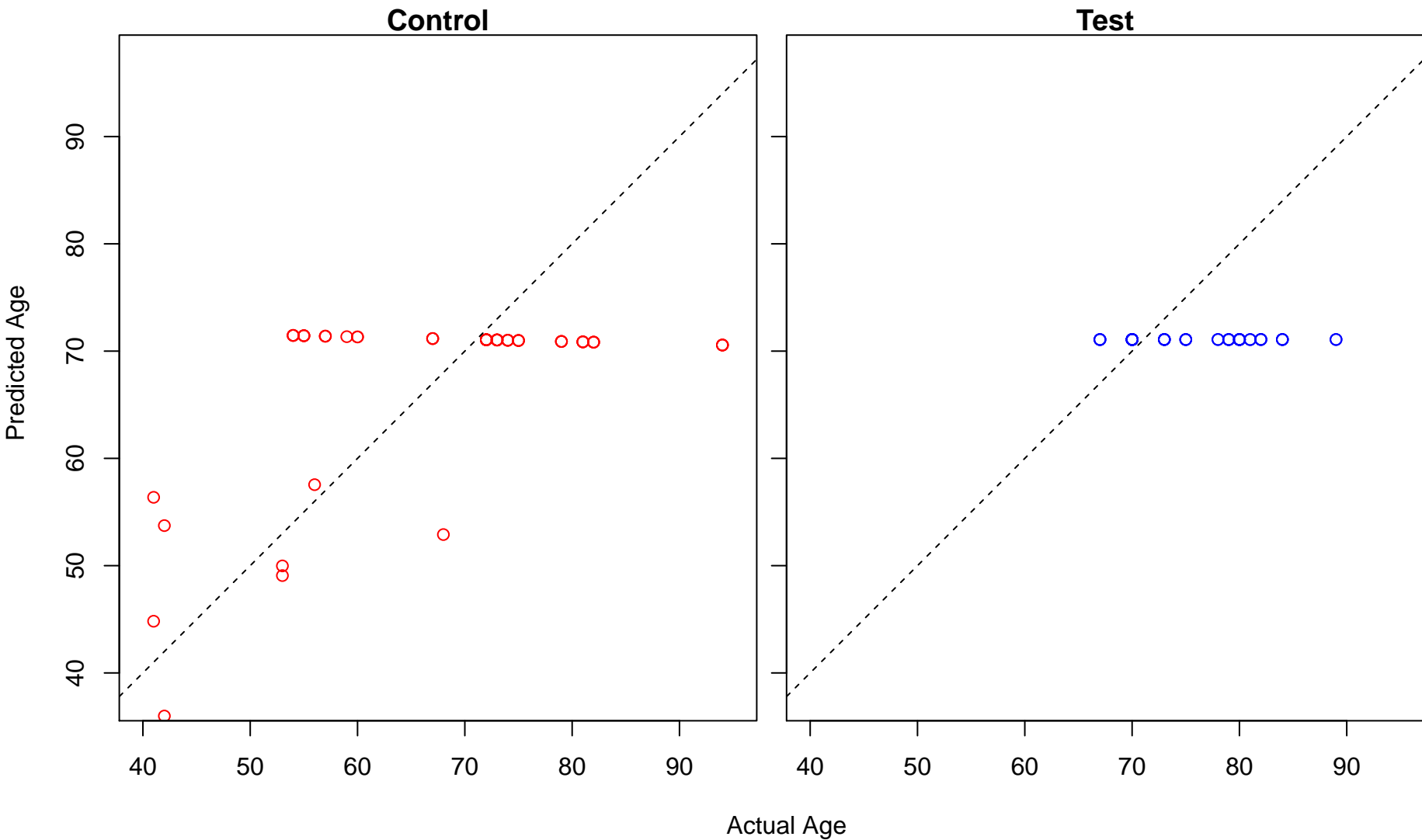
regulation of hemopoiesis (Score: 0.815317)



extrinsic apoptotic signaling pathway via death domain receptors (Score: 0.815243)

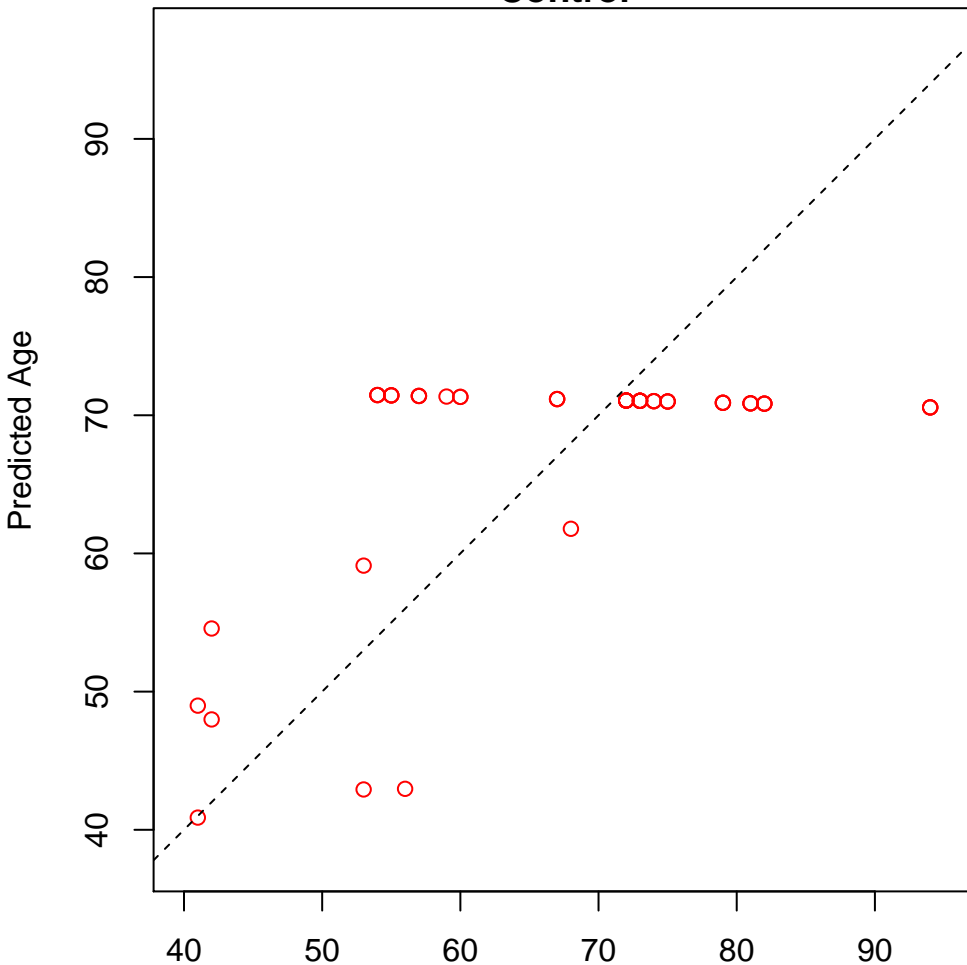


cofactor metabolic process (Score: 0.815212)

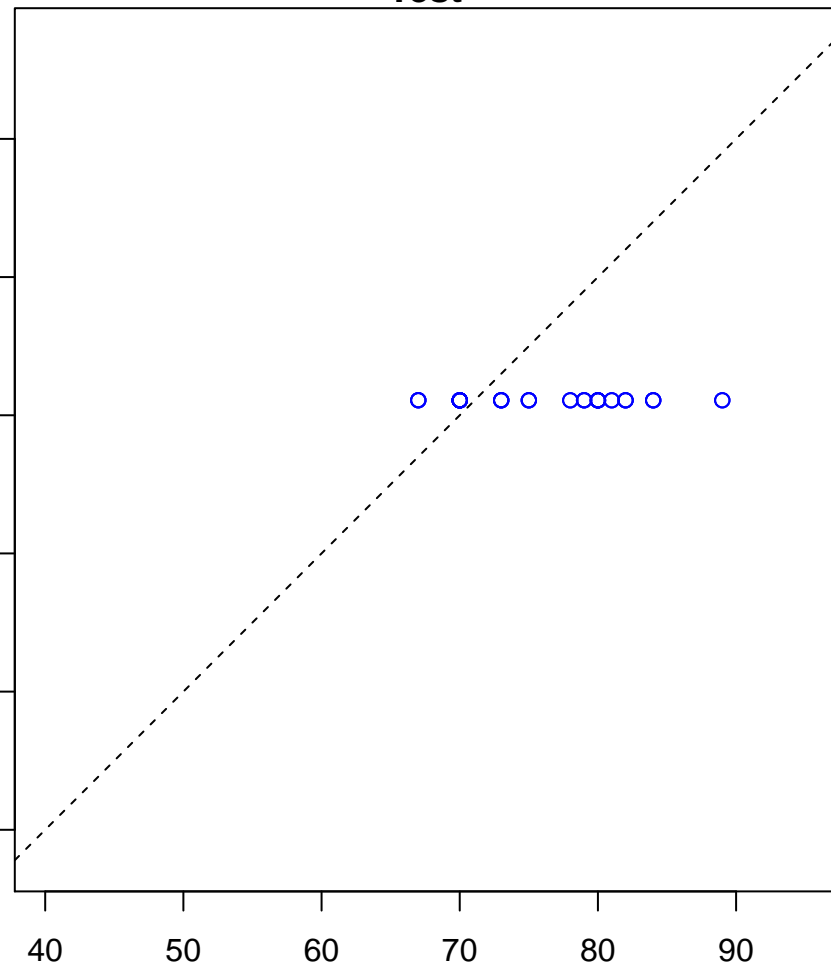


extrinsic apoptotic signaling pathway (Score: 0.815167)

Control



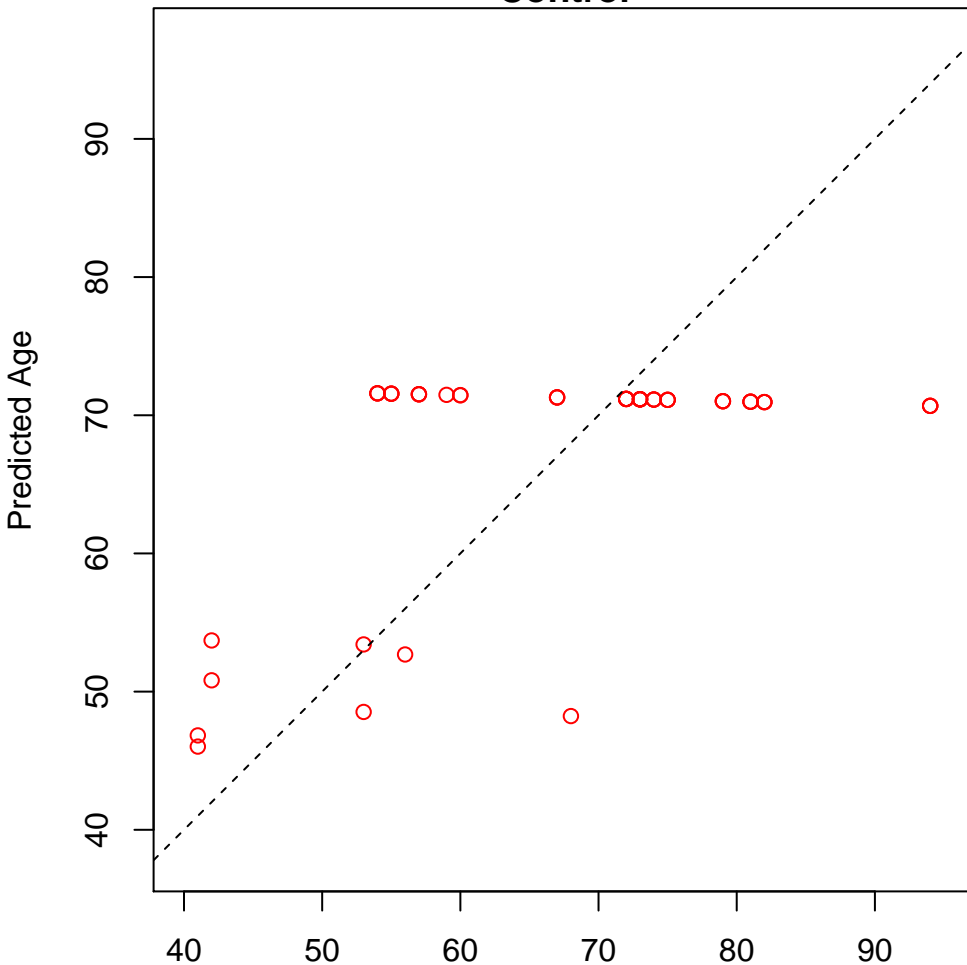
Test



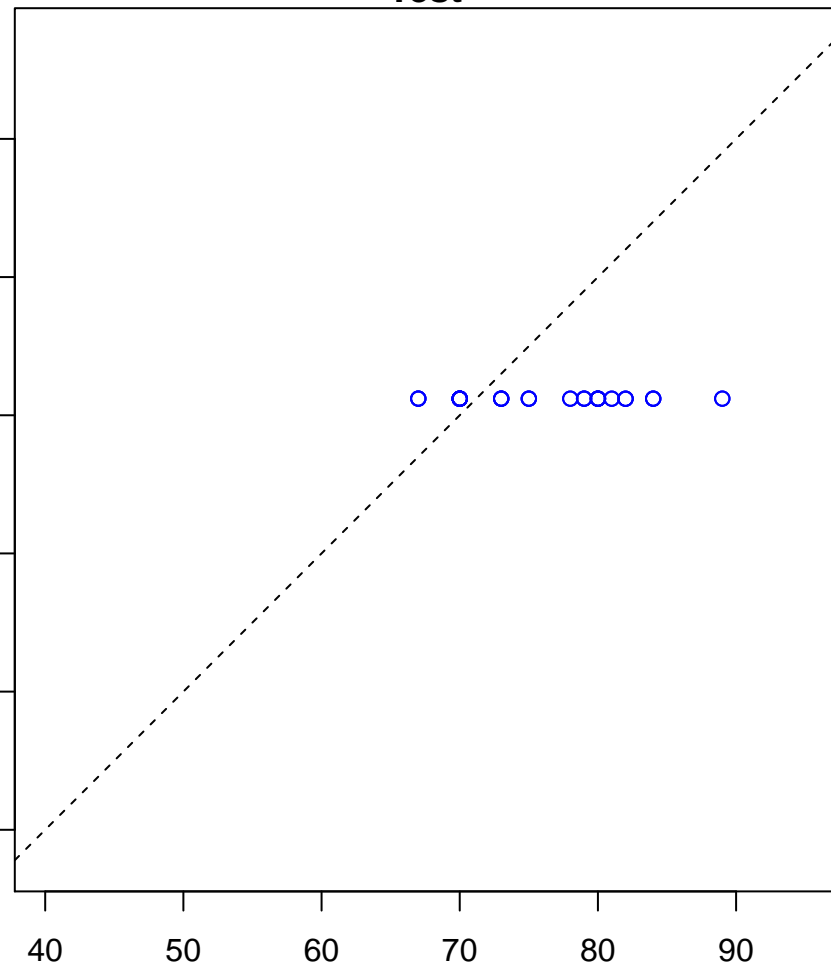
Actual Age

regulation of protein polymerization (Score: 0.815085)

Control



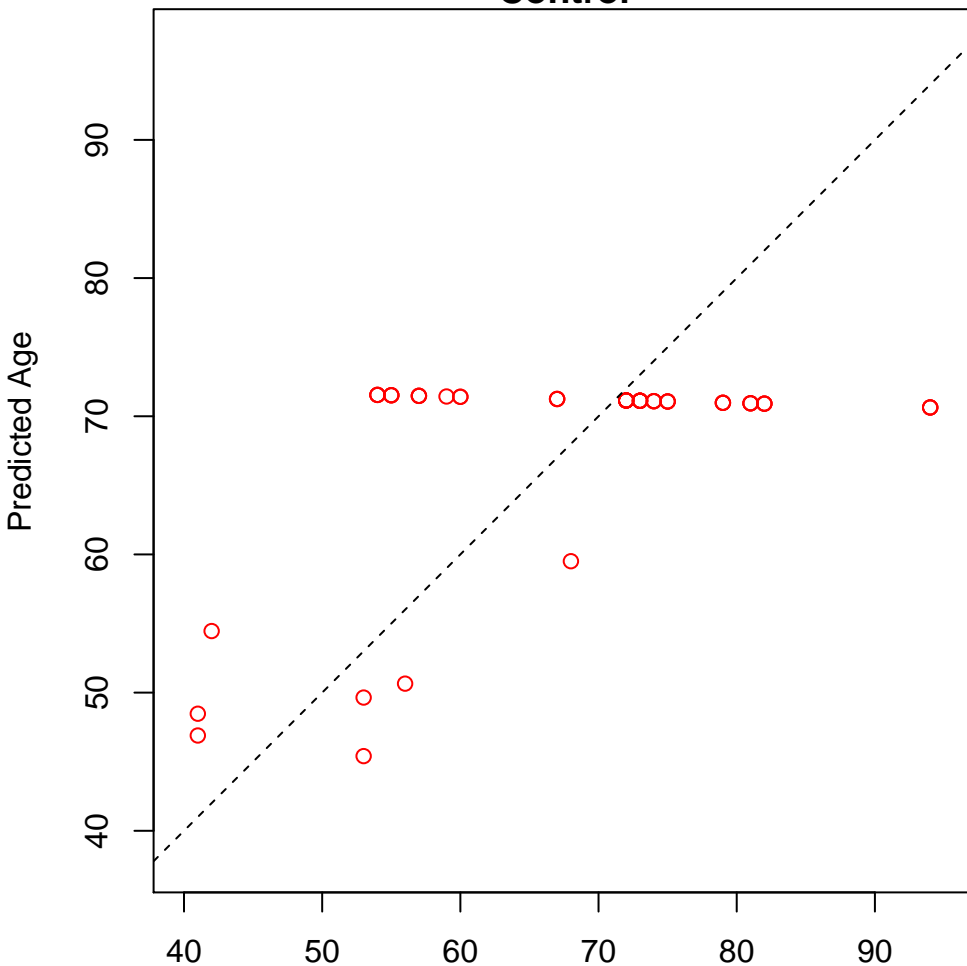
Test



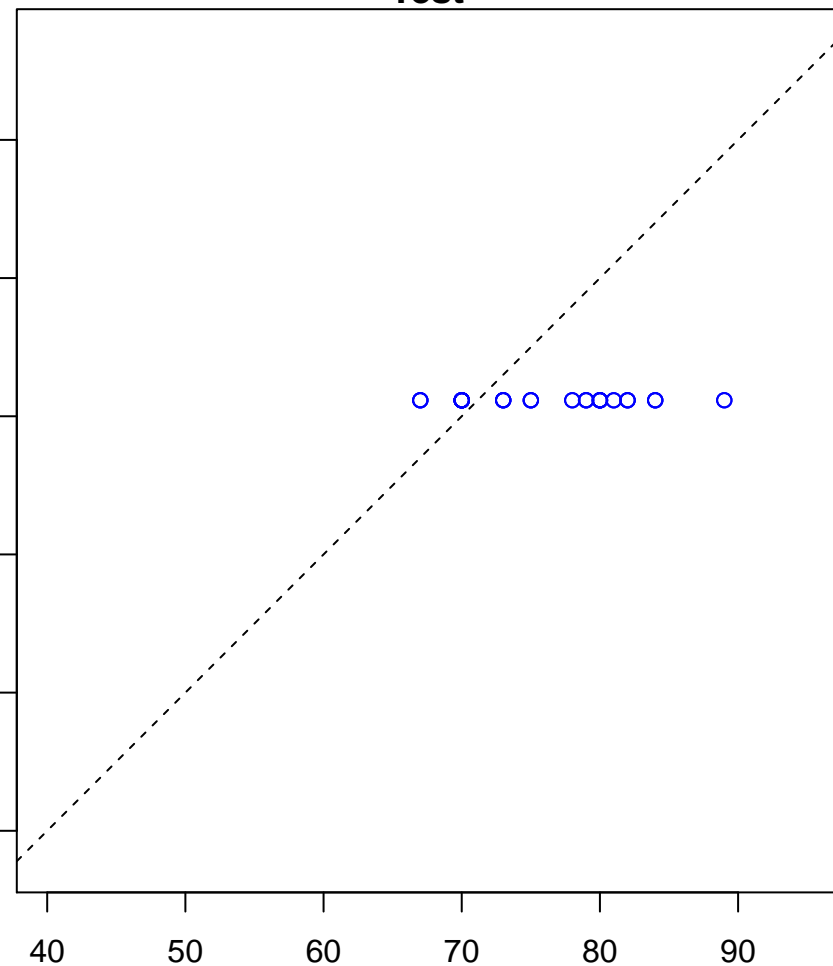
Actual Age

response to oxygen-containing compound (Score: 0.815066)

Control

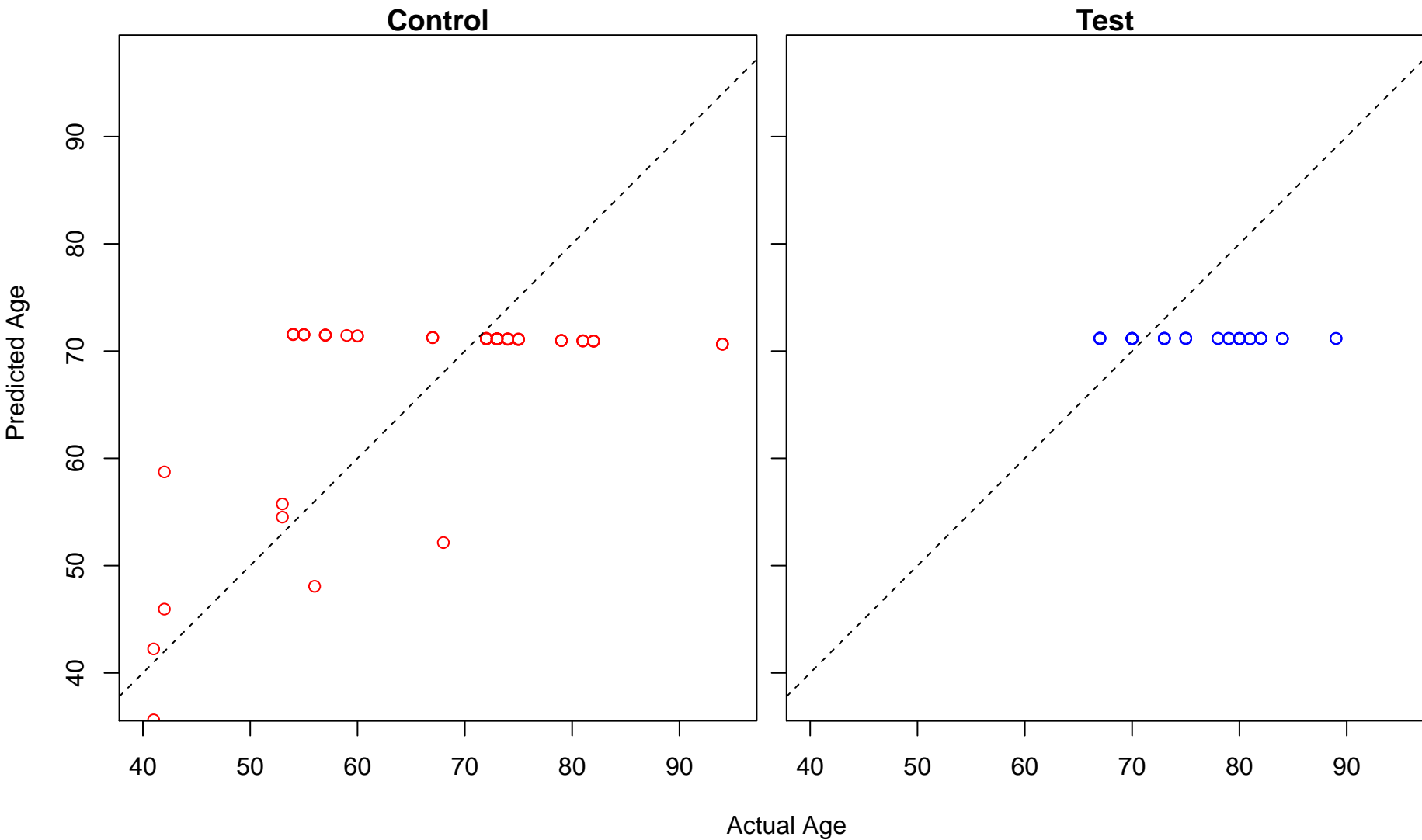


Test

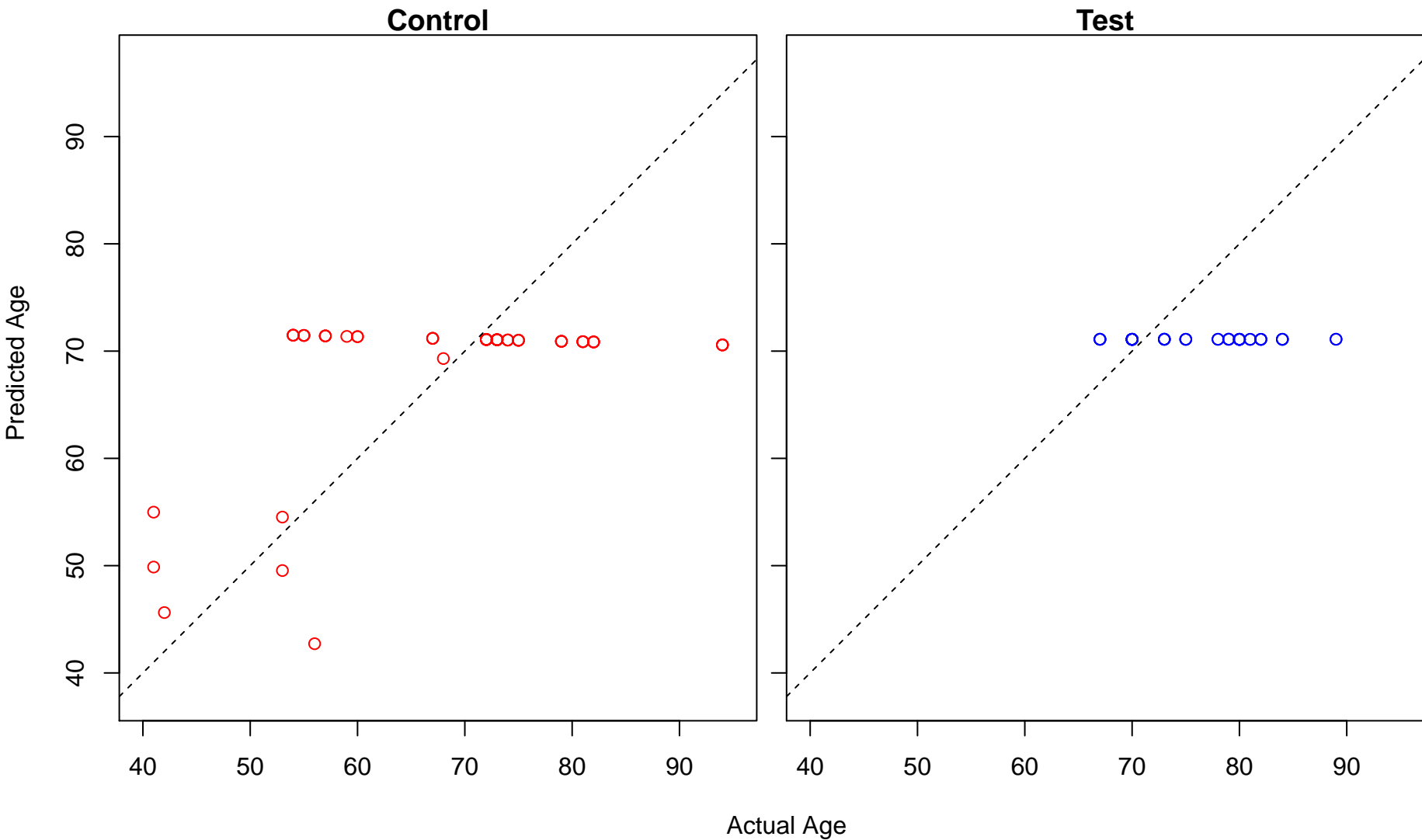


Actual Age

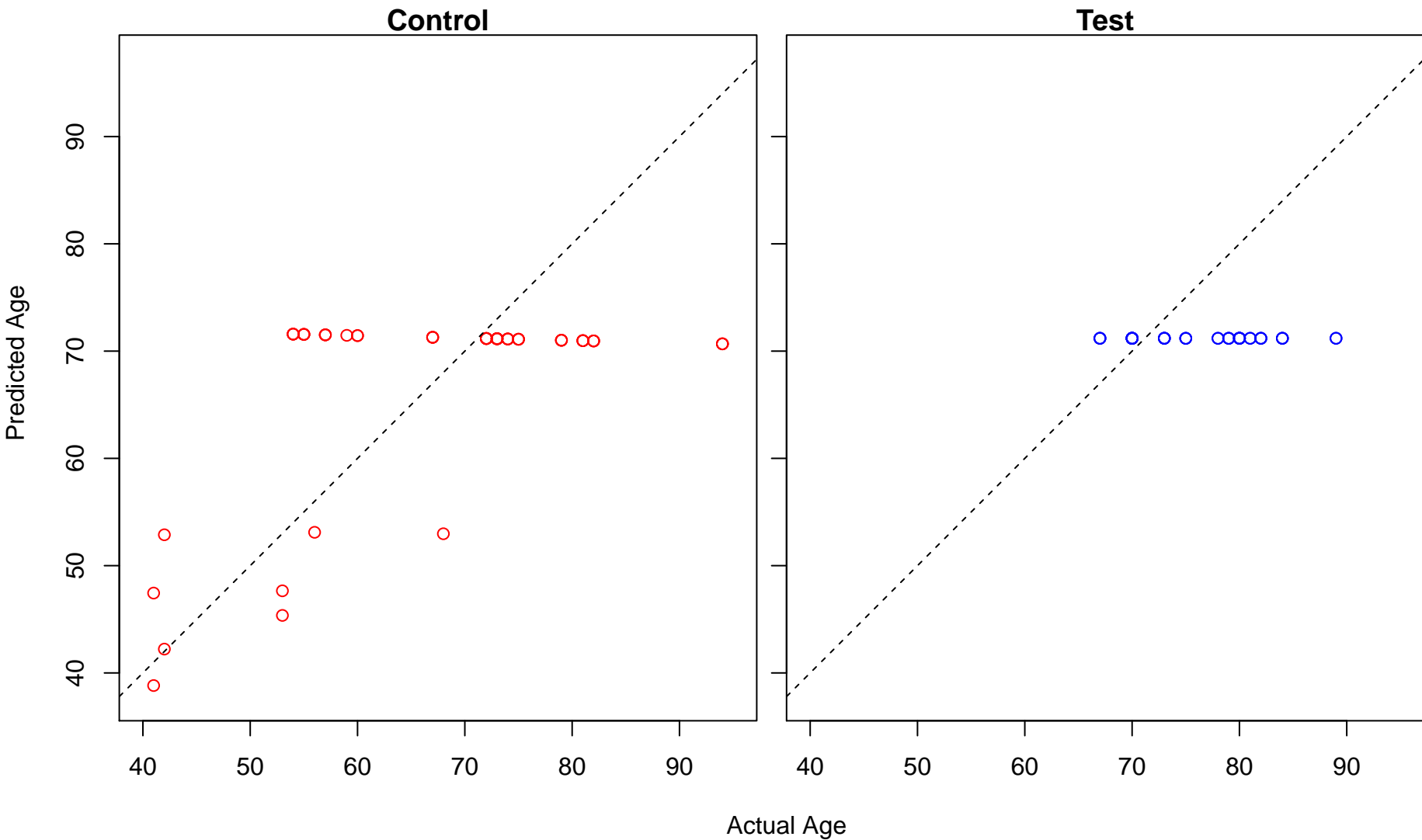
negative regulation of autophagy (Score: 0.815048)



developmental maturation (Score: 0.815019)

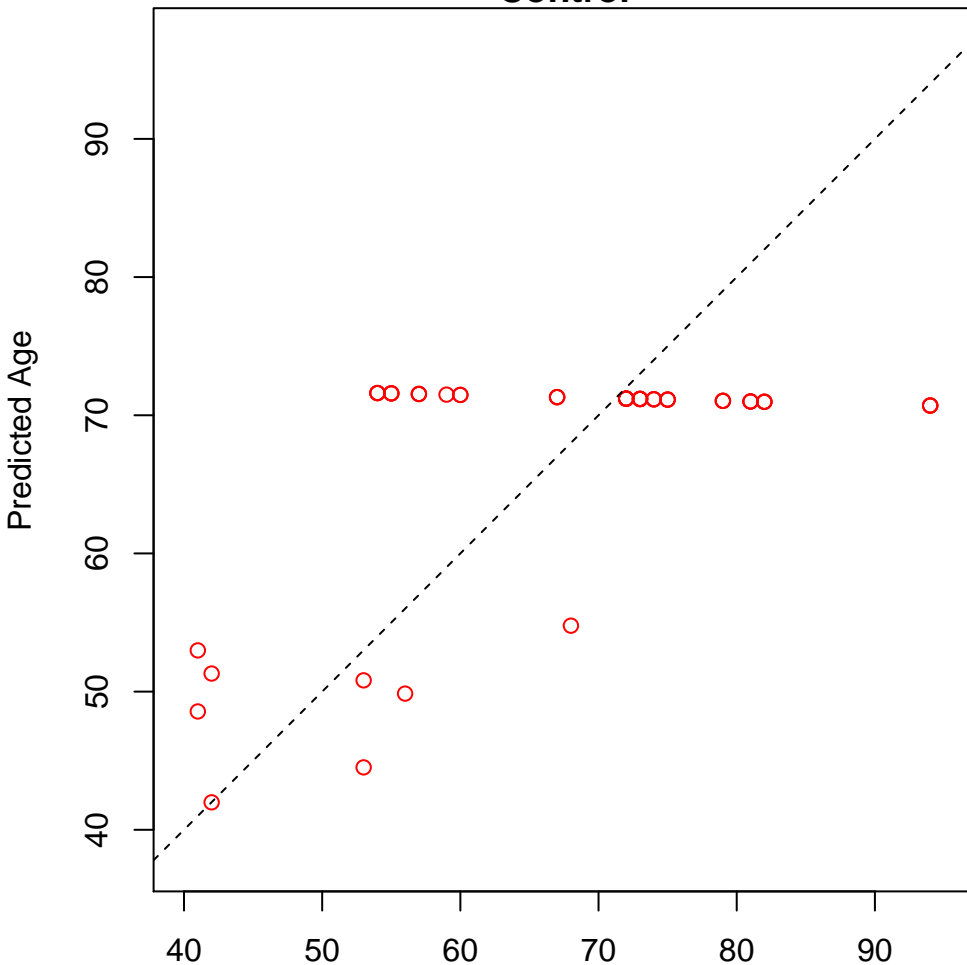


positive regulation of protein modification process (Score: 0.814965)

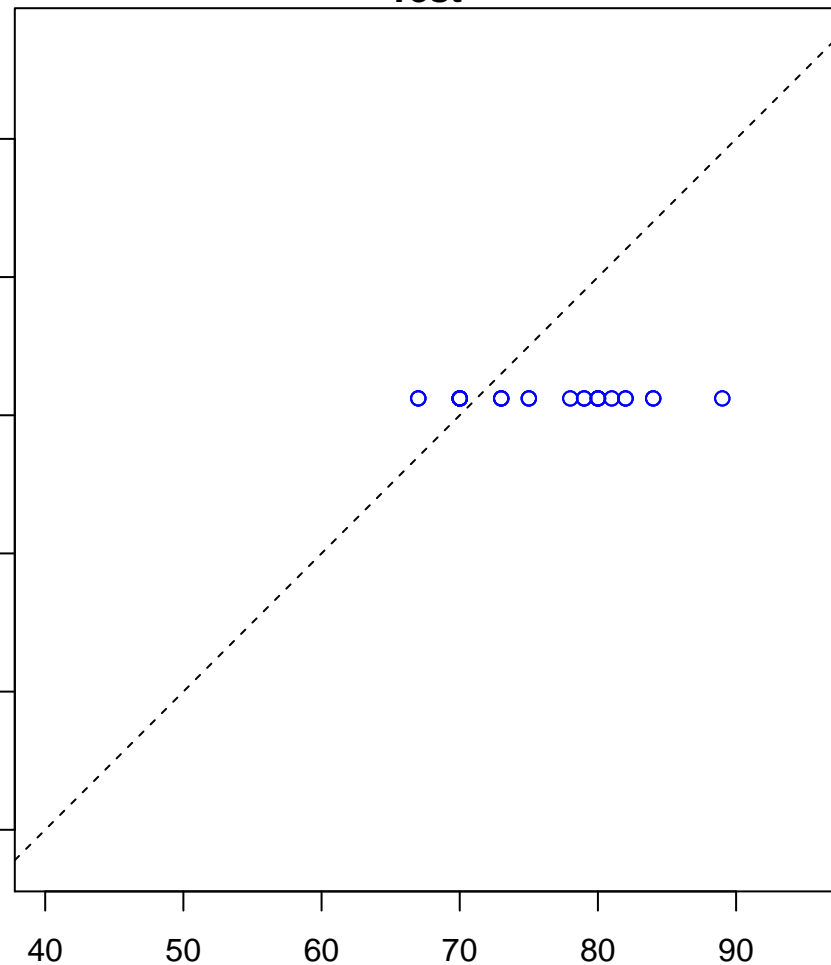


negative regulation of RNA splicing (Score: 0.814811)

Control

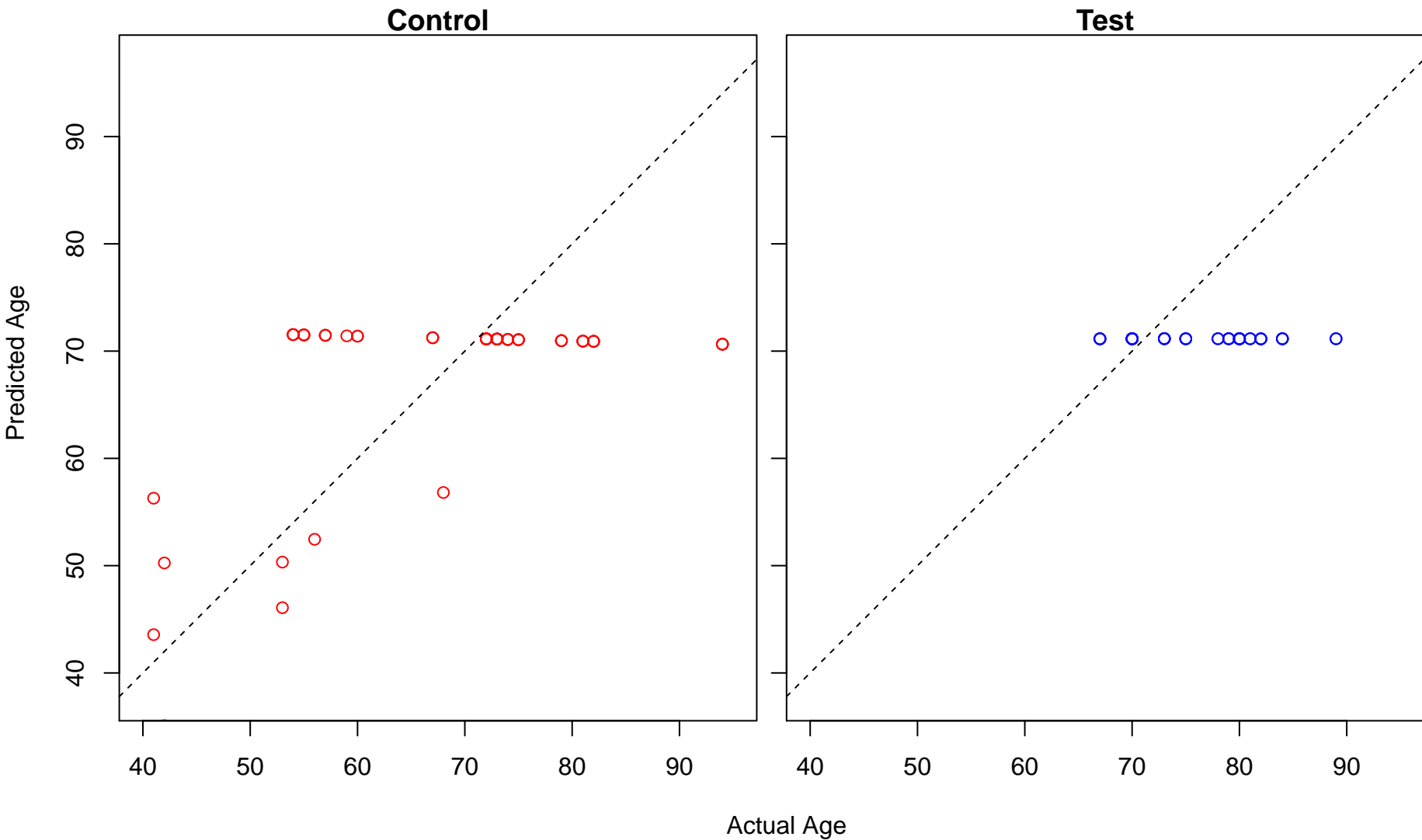


Test



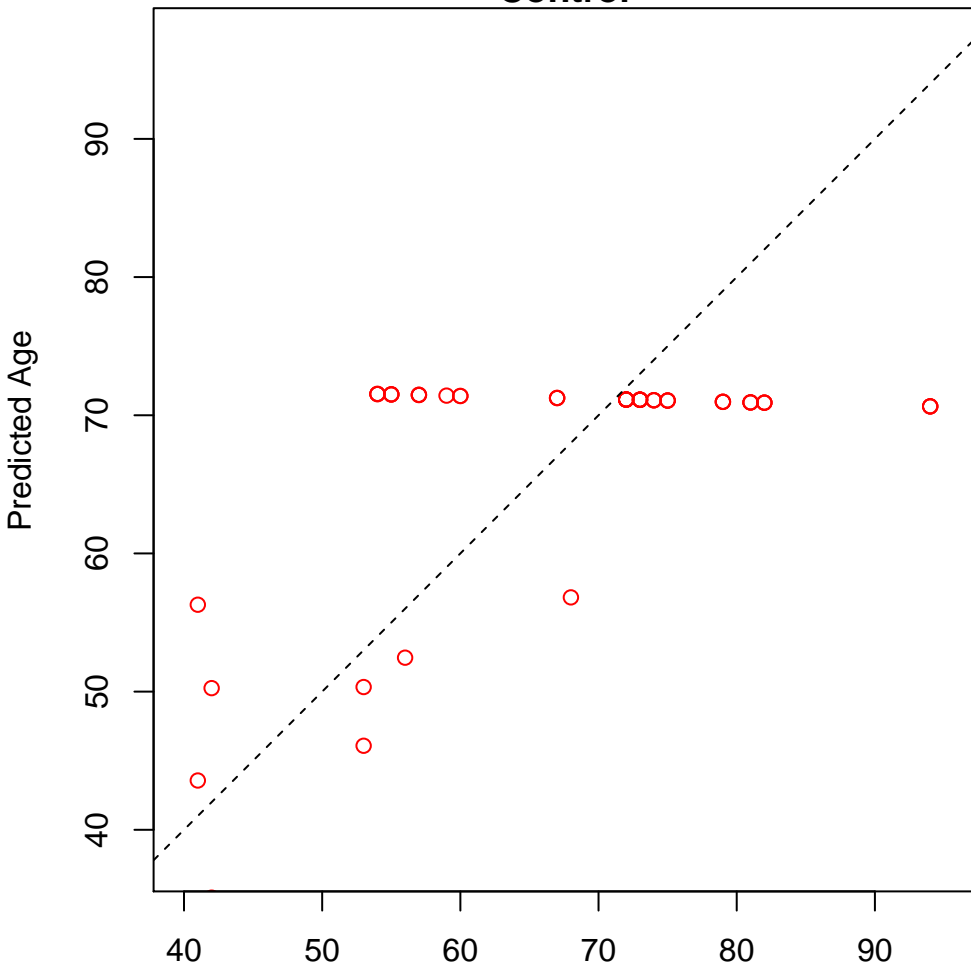
Actual Age

regulation of glycoprotein biosynthetic process (Score: 0.814761)

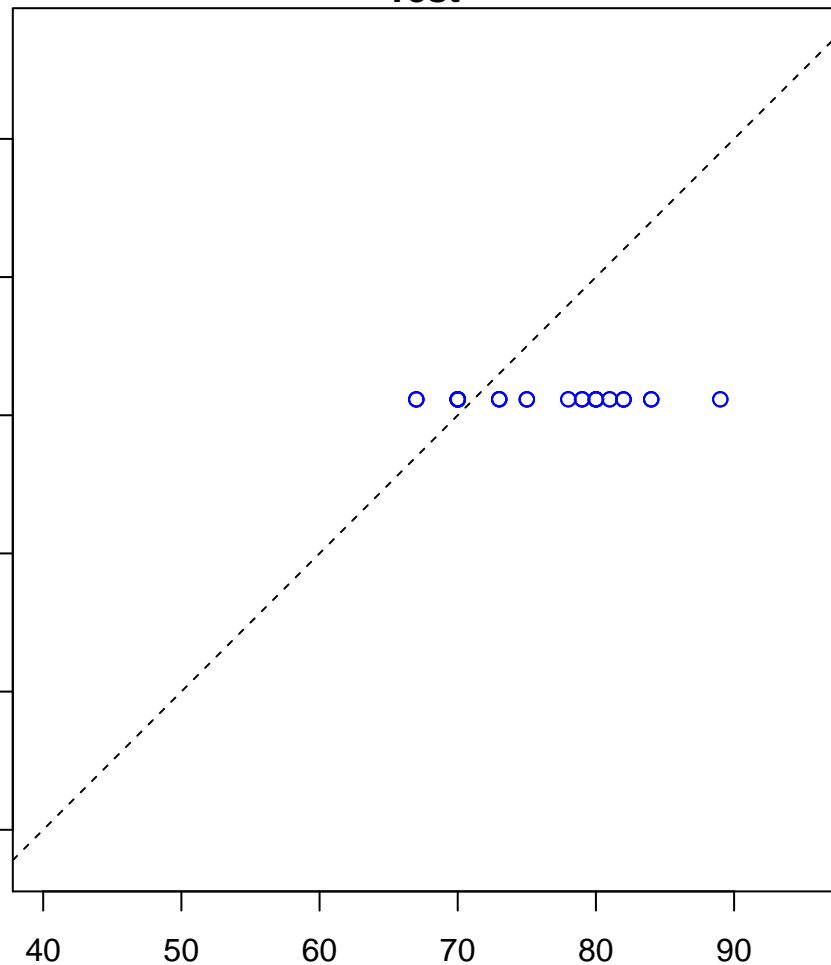


regulation of protein glycosylation (Score: 0.814761)

Control

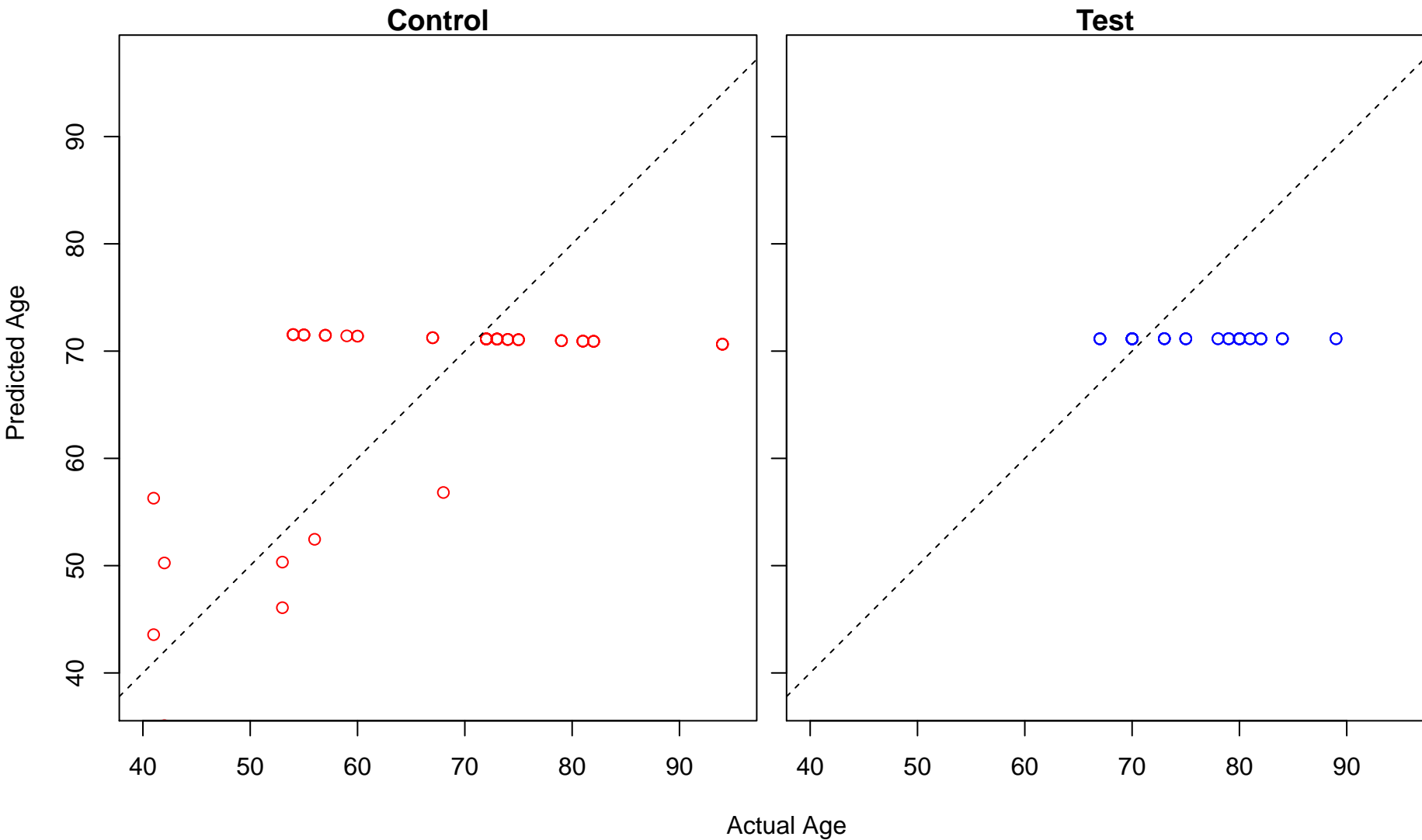


Test

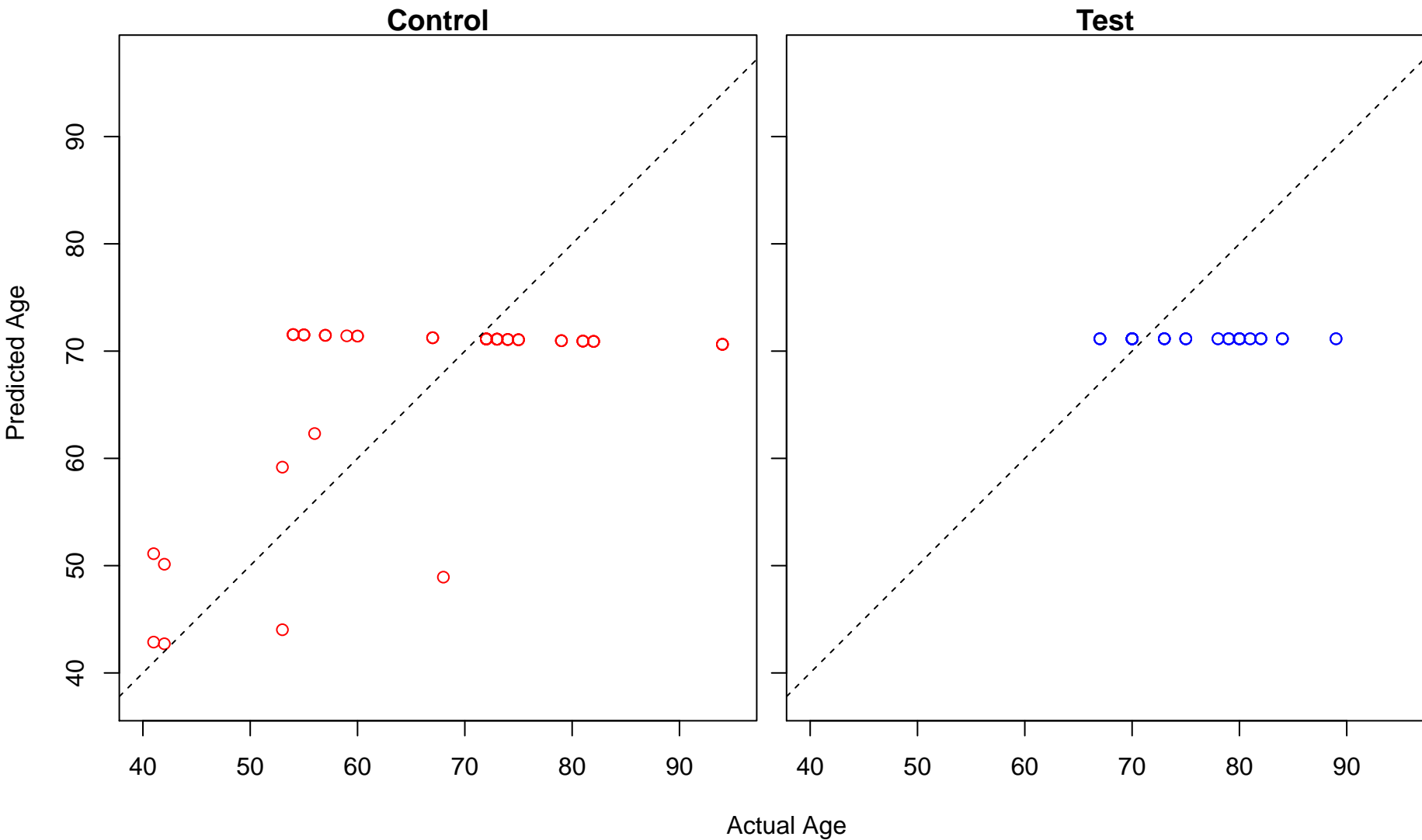


Actual Age

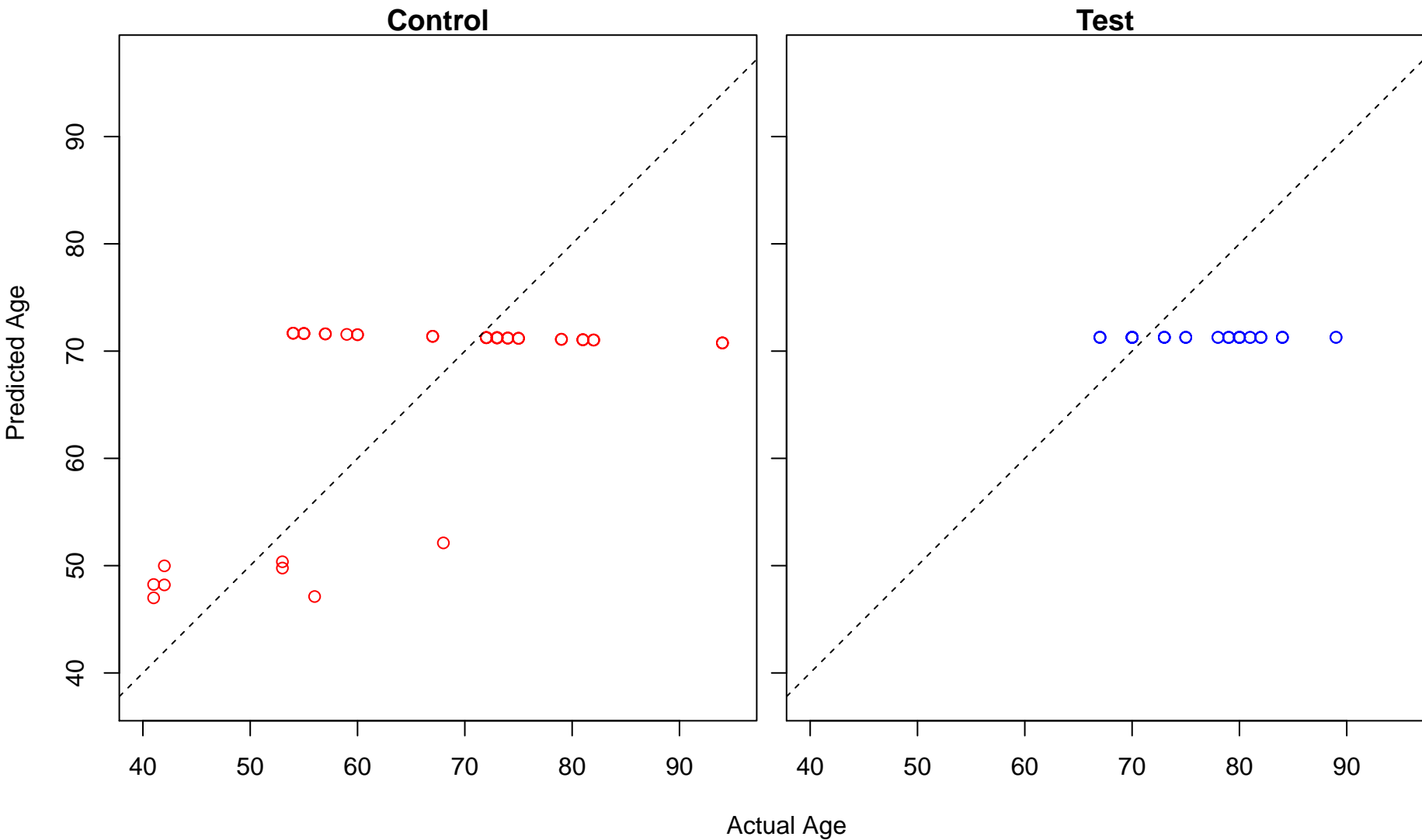
regulation of glycoprotein metabolic process (Score: 0.814761)



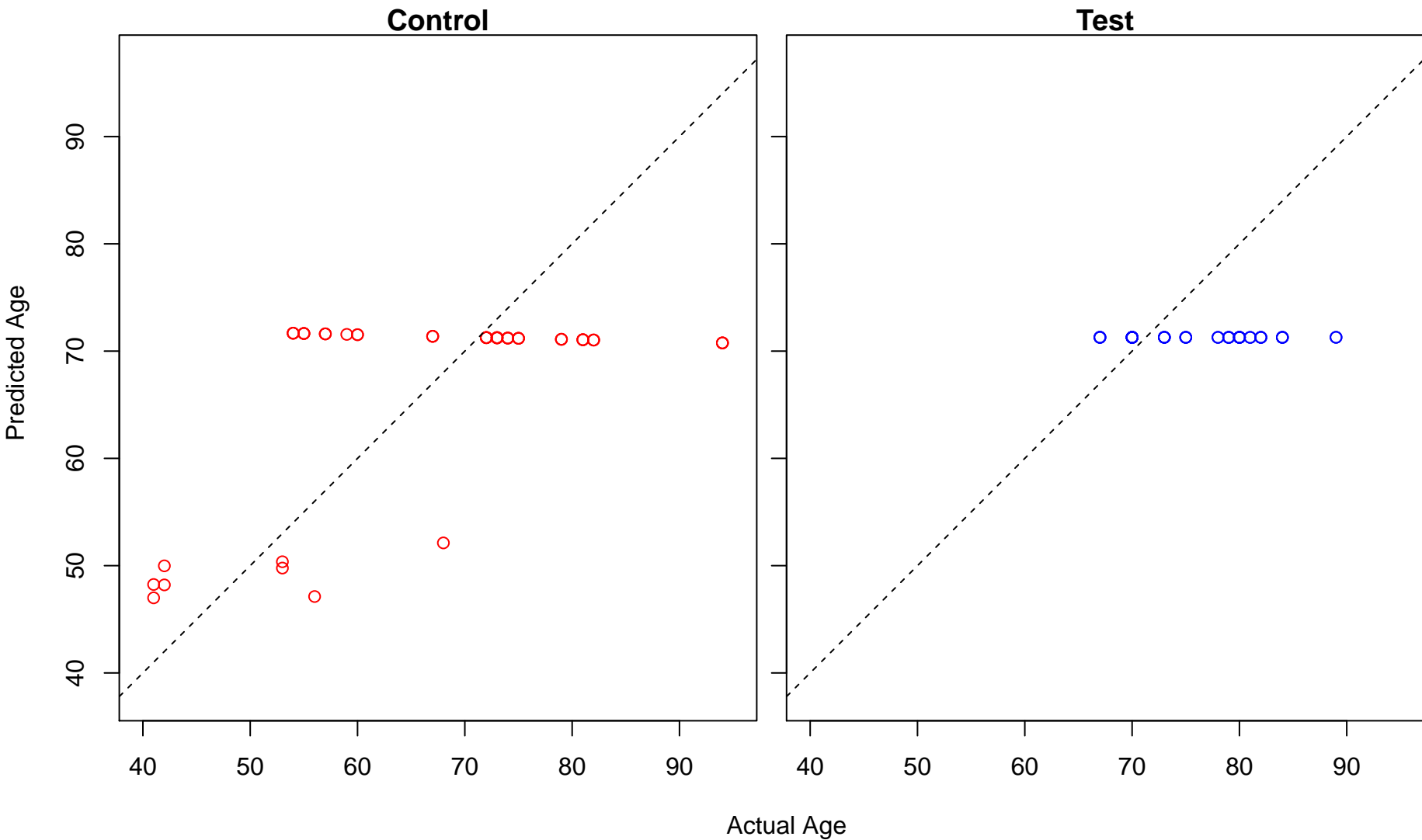
ossification (Score: 0.814627)



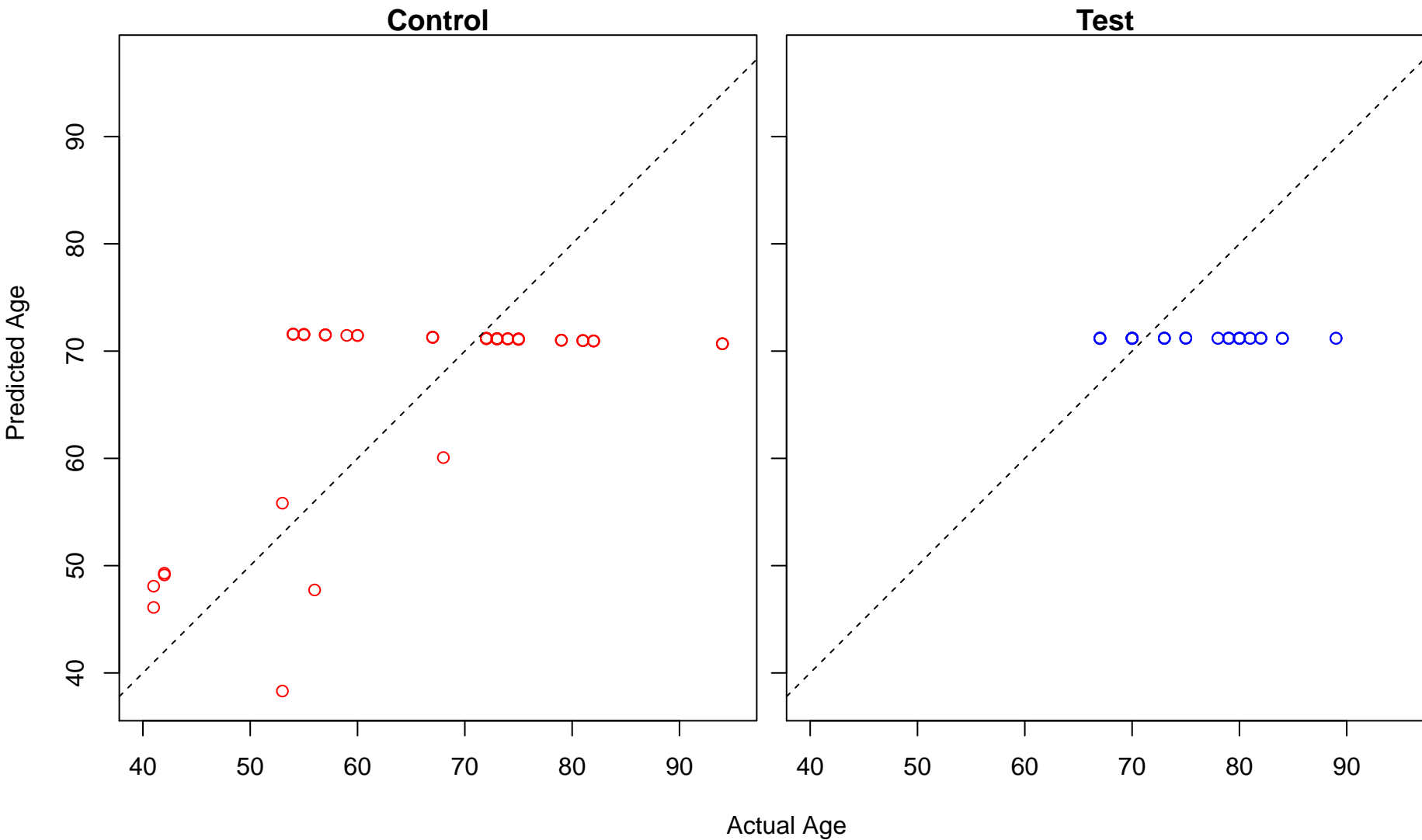
viral translation (Score: 0.814564)



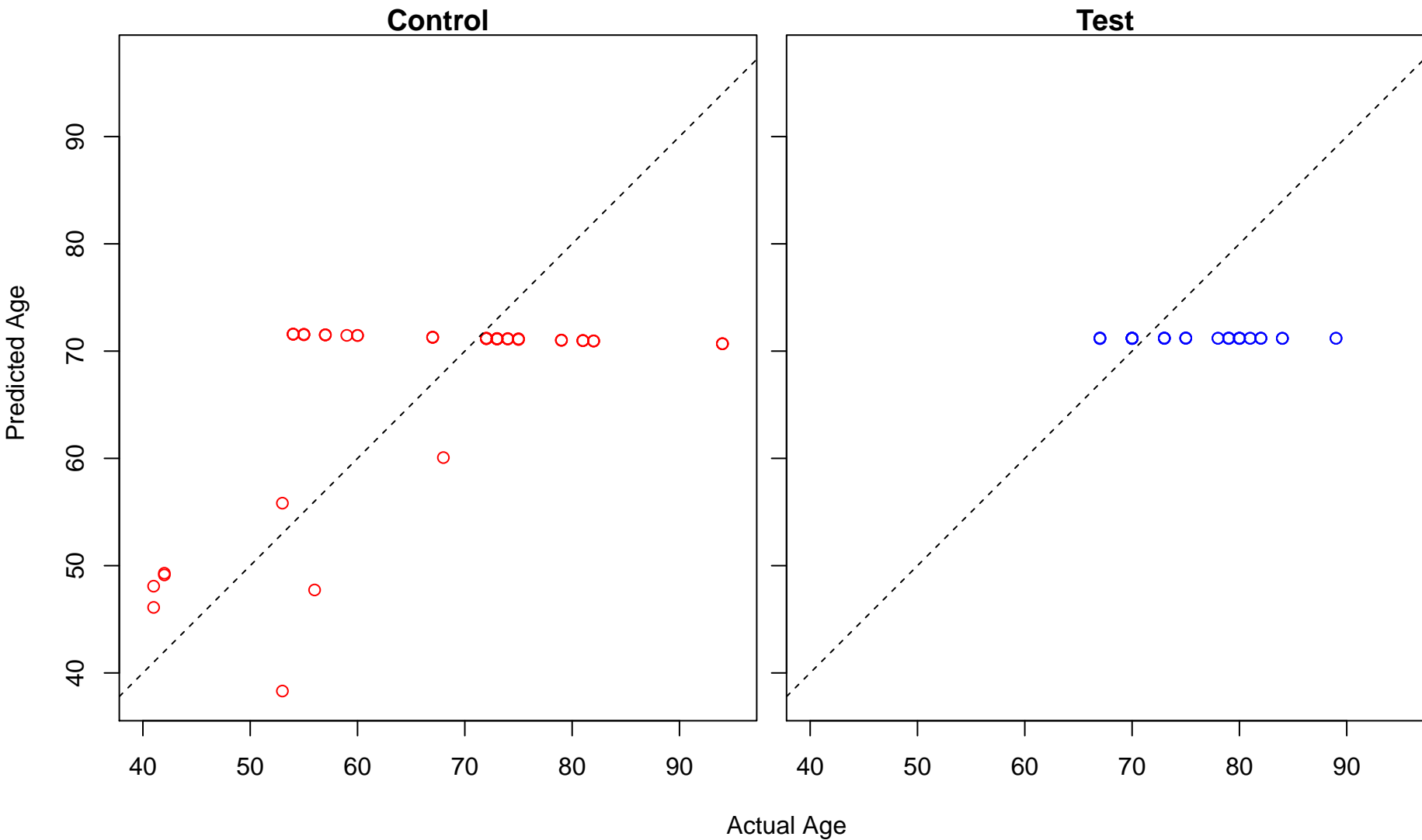
IRES-dependent viral translational initiation (Score: 0.814564)



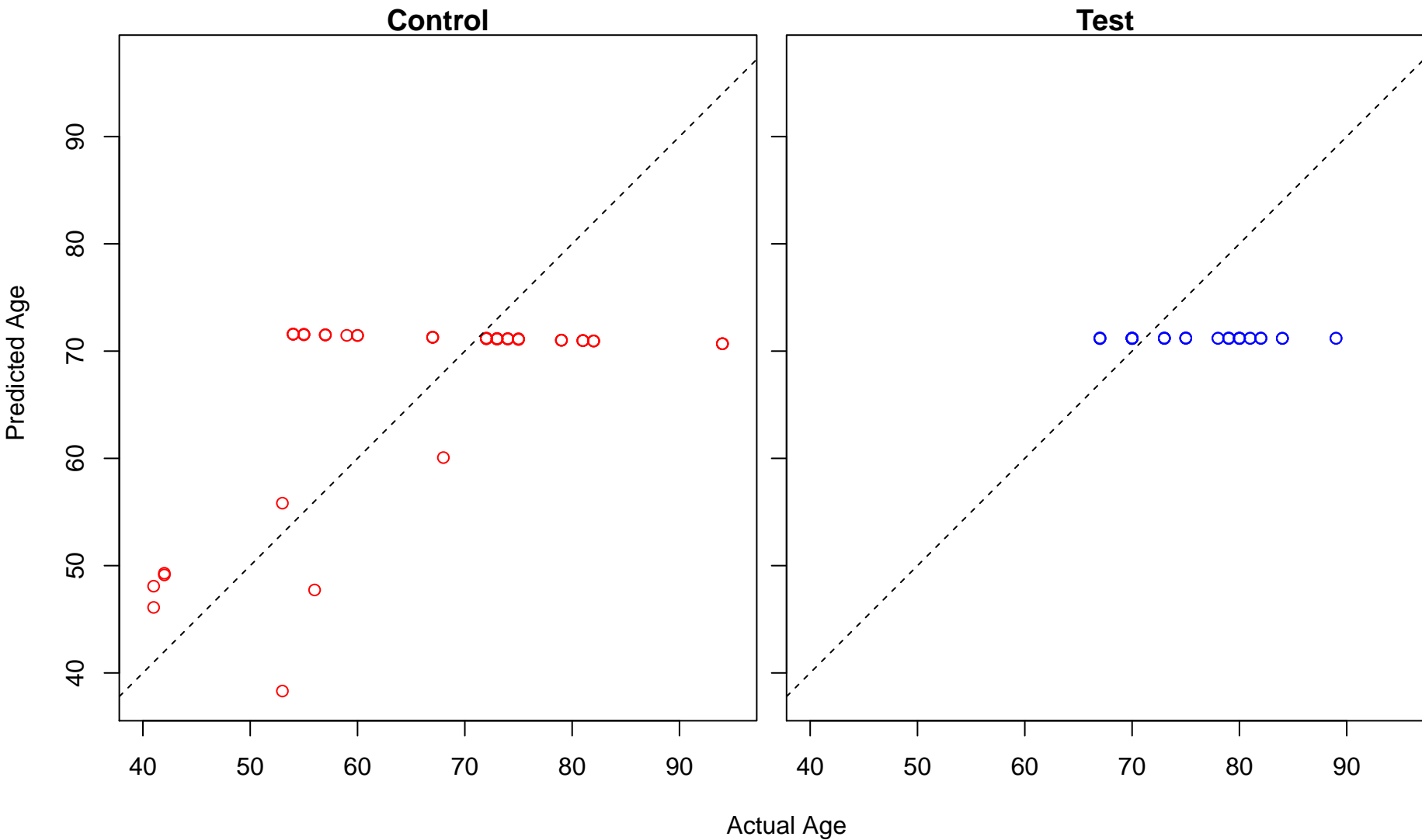
negative regulation of cytokine-mediated signaling pathway (Score: 0.814531)



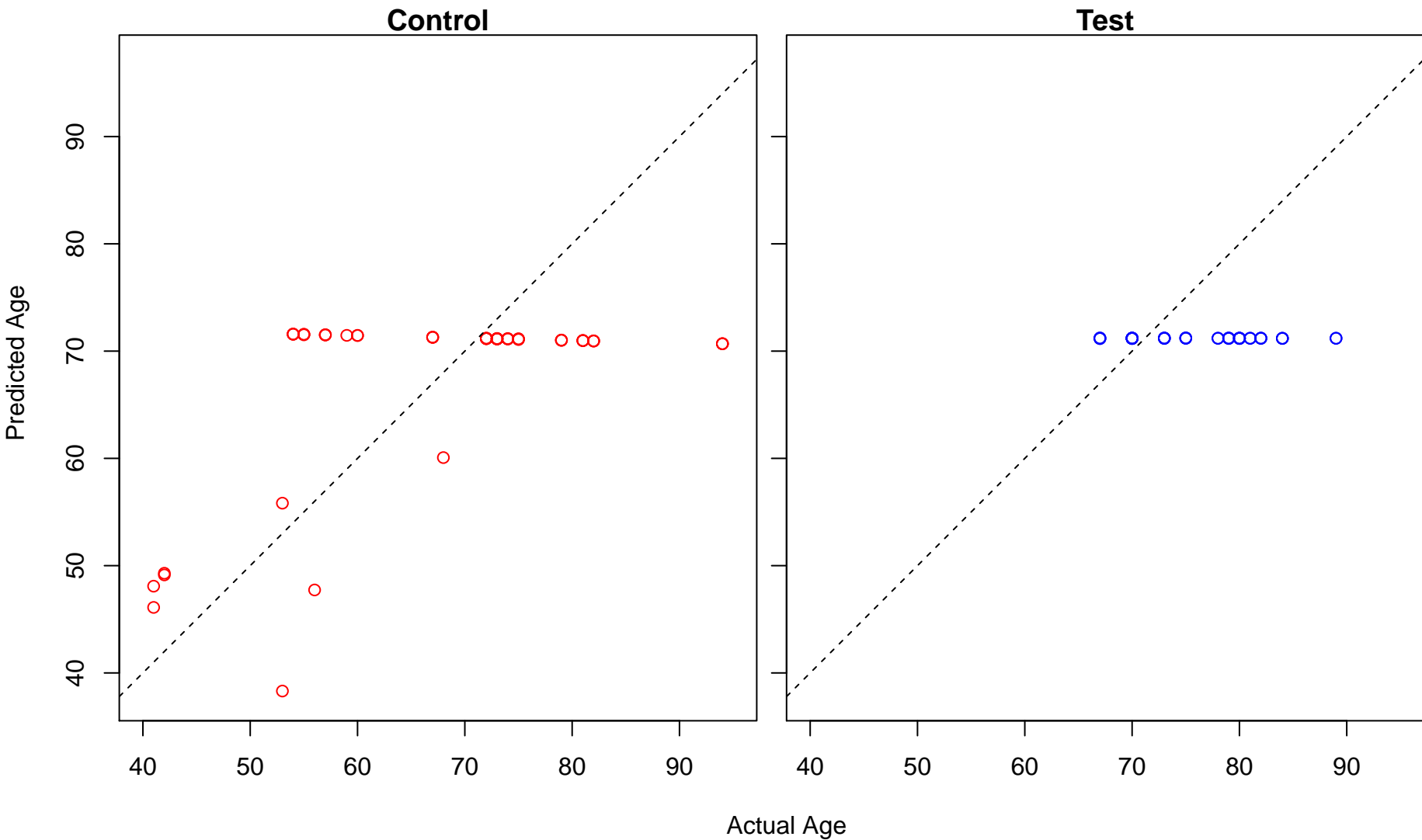
protein kinase B signaling (Score: 0.814531)



negative regulation of response to cytokine stimulus (Score: 0.814531)

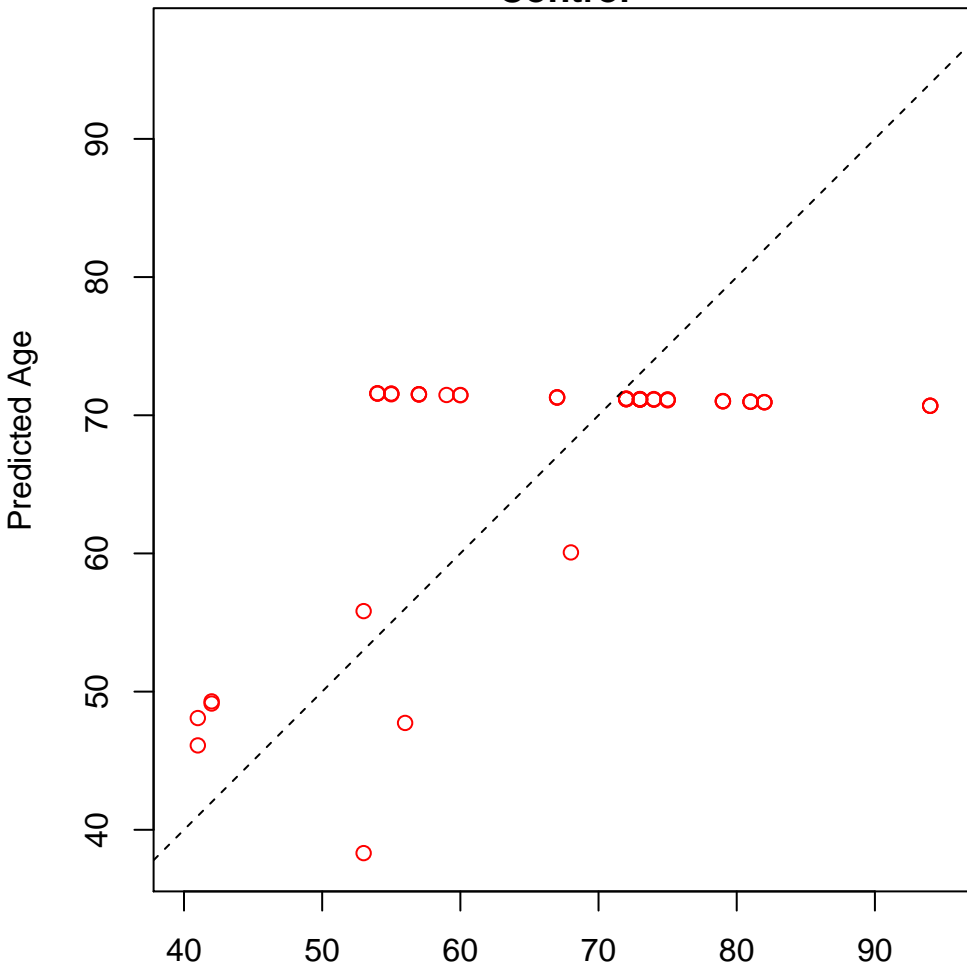


positive regulation of protein tyrosine kinase activity (Score: 0.814531)

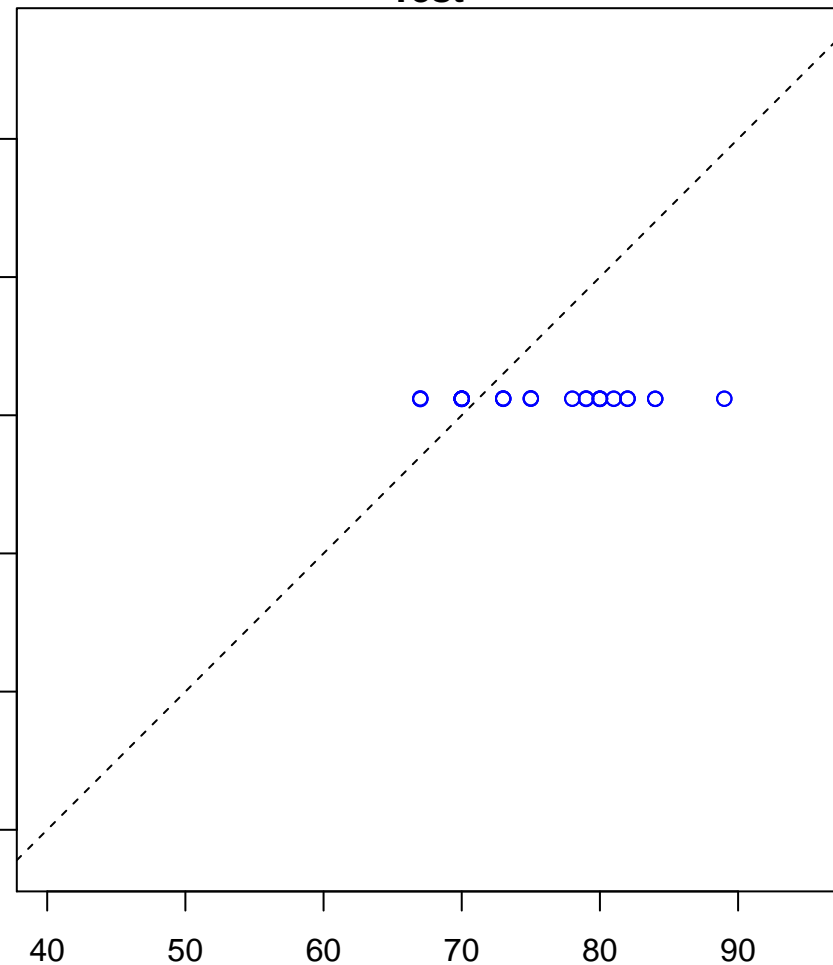


regulation of leukocyte apoptotic process (Score: 0.814531)

Control

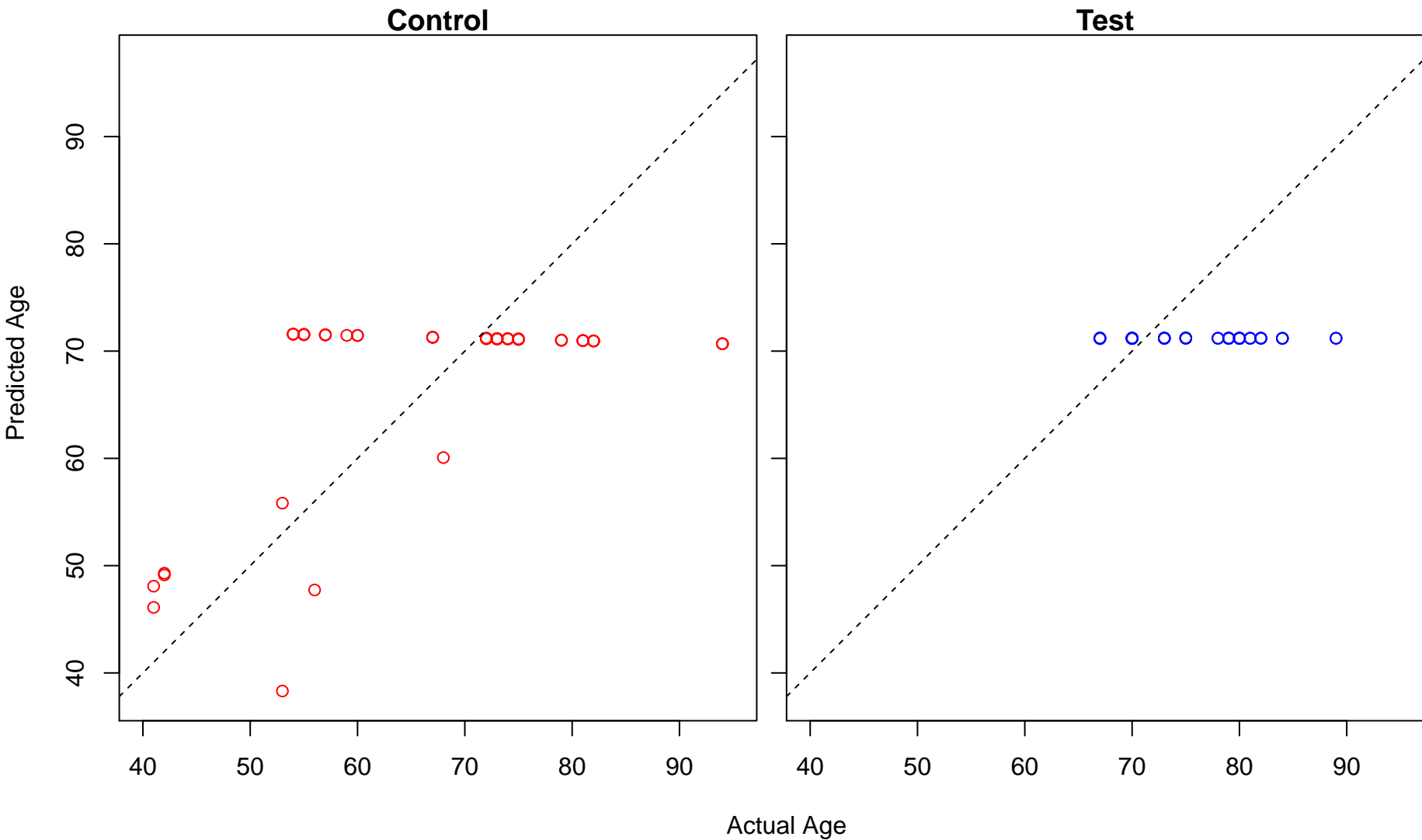


Test



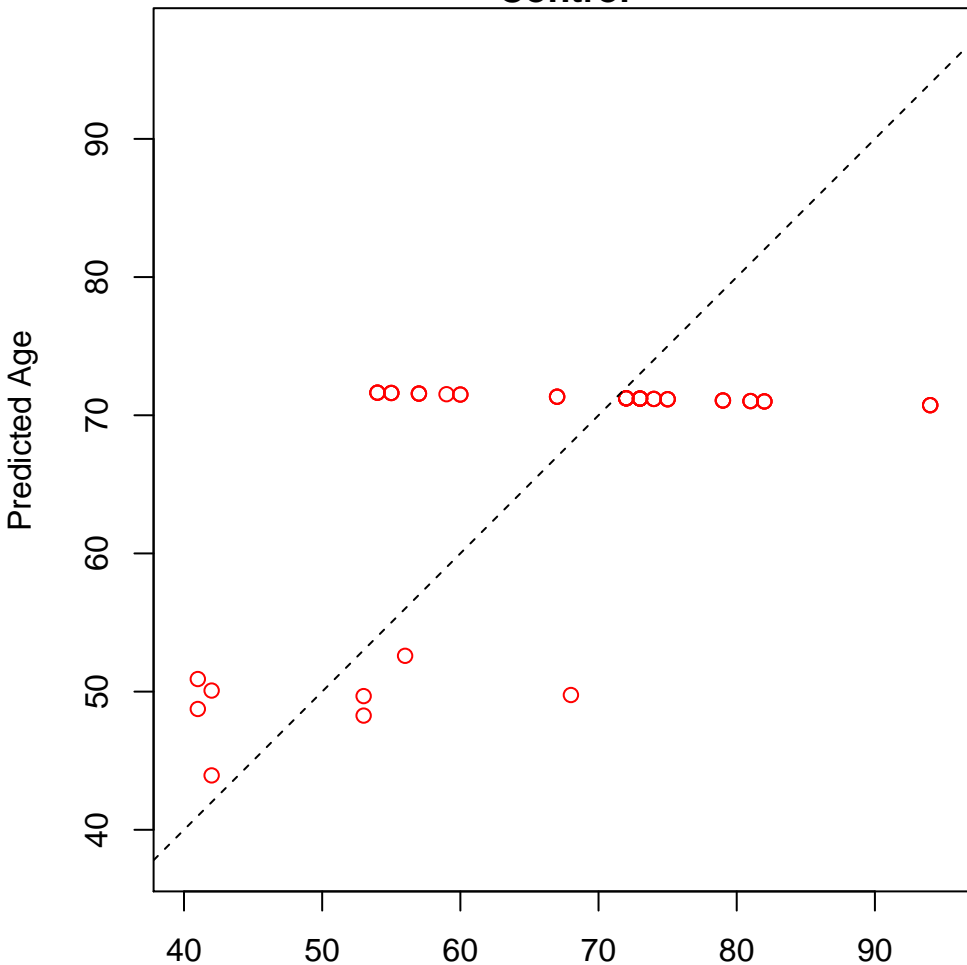
Actual Age

negative regulation of leukocyte apoptotic process (Score: 0.814531)

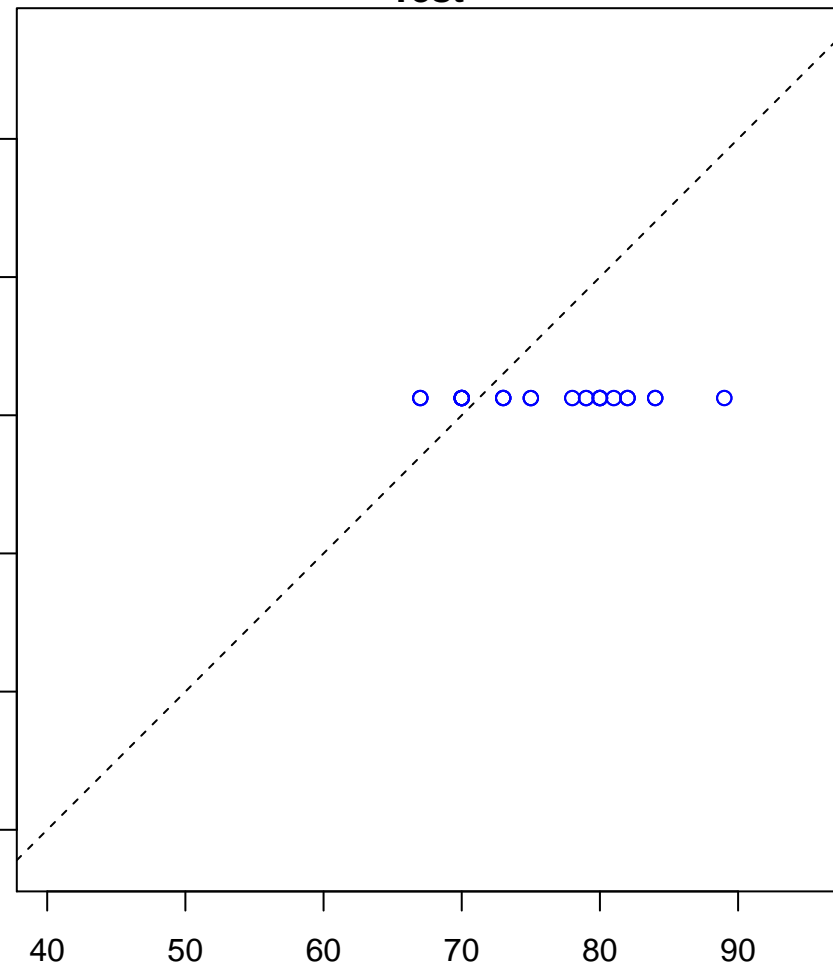


endomembrane system organization (Score: 0.814519)

Control

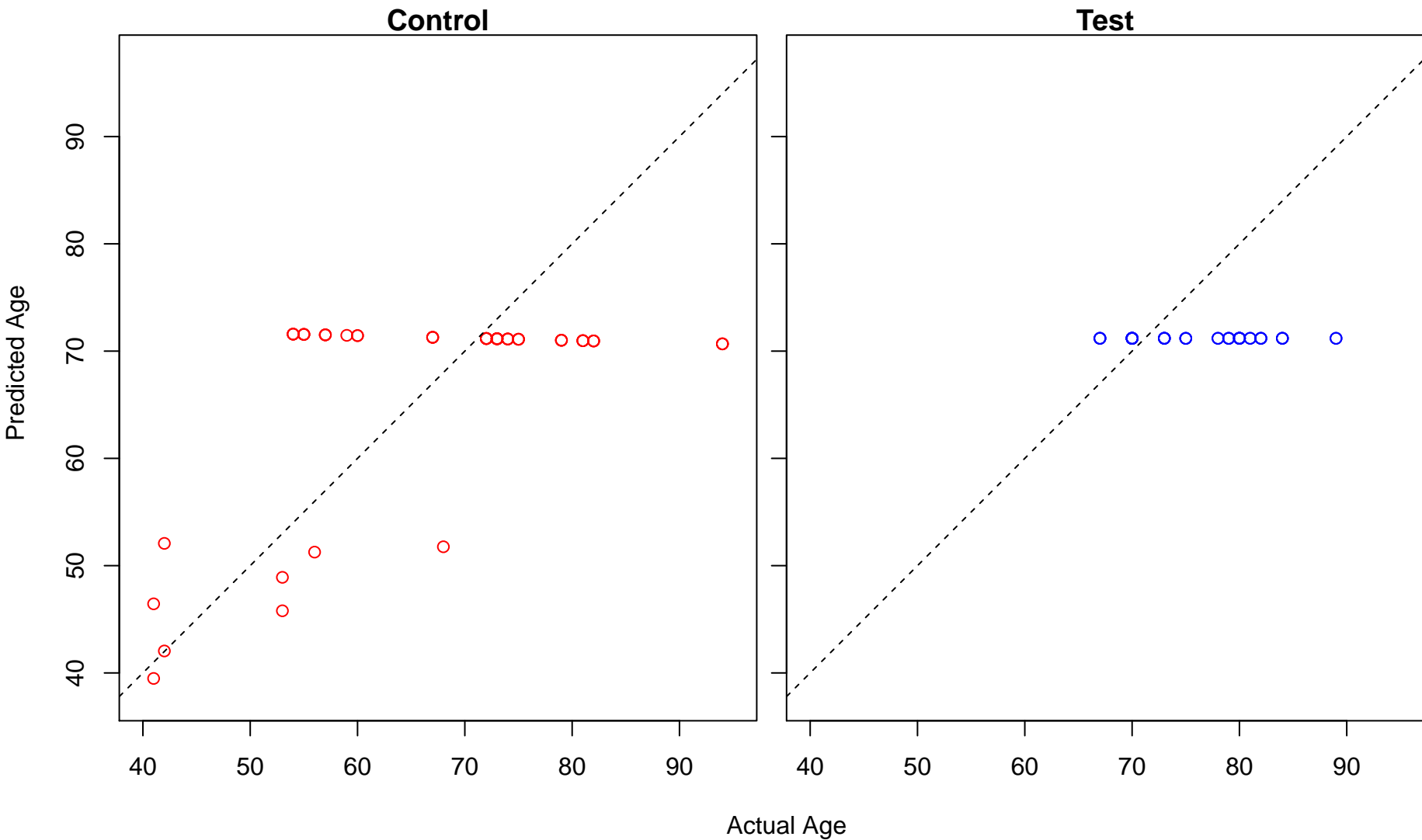


Test

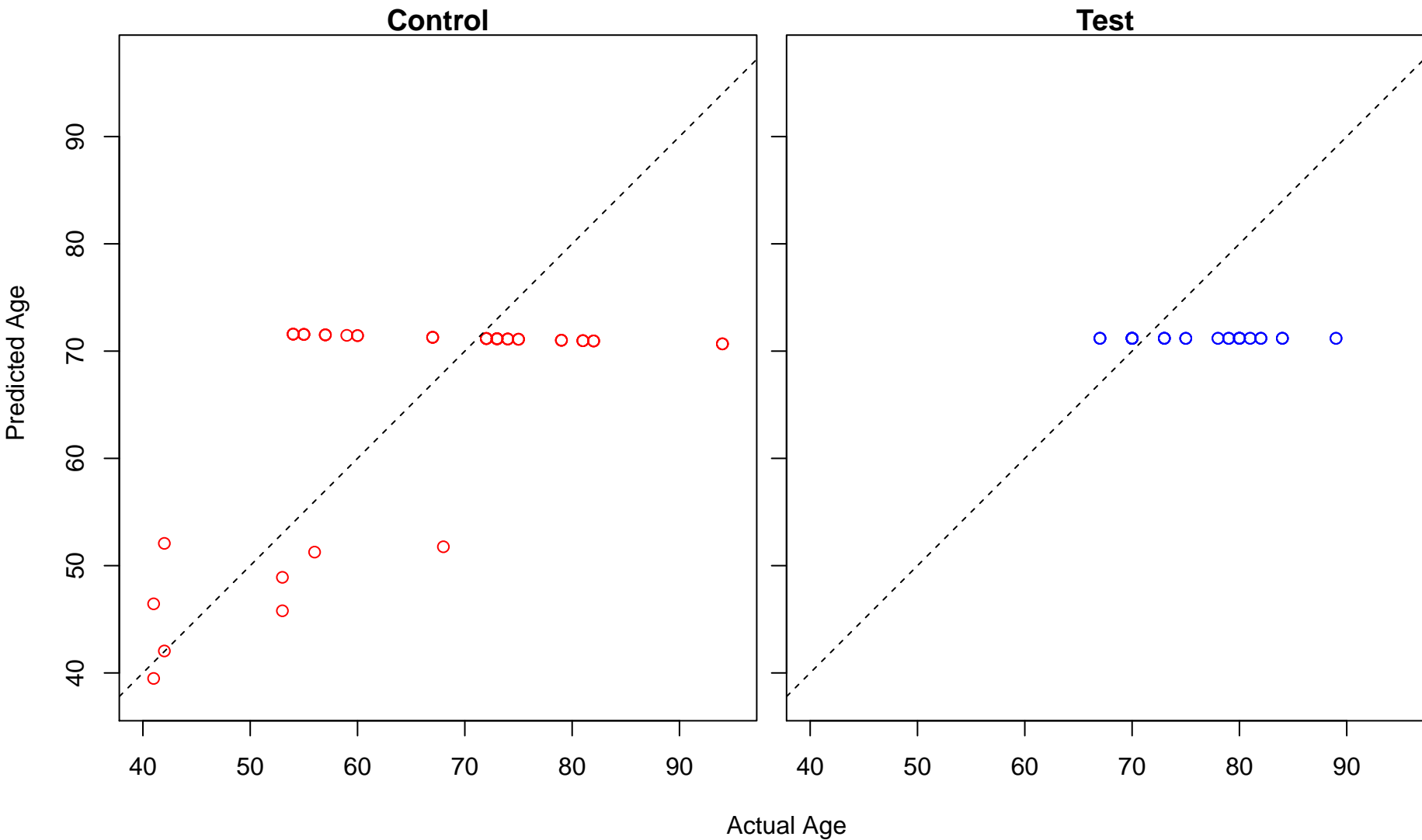


Actual Age

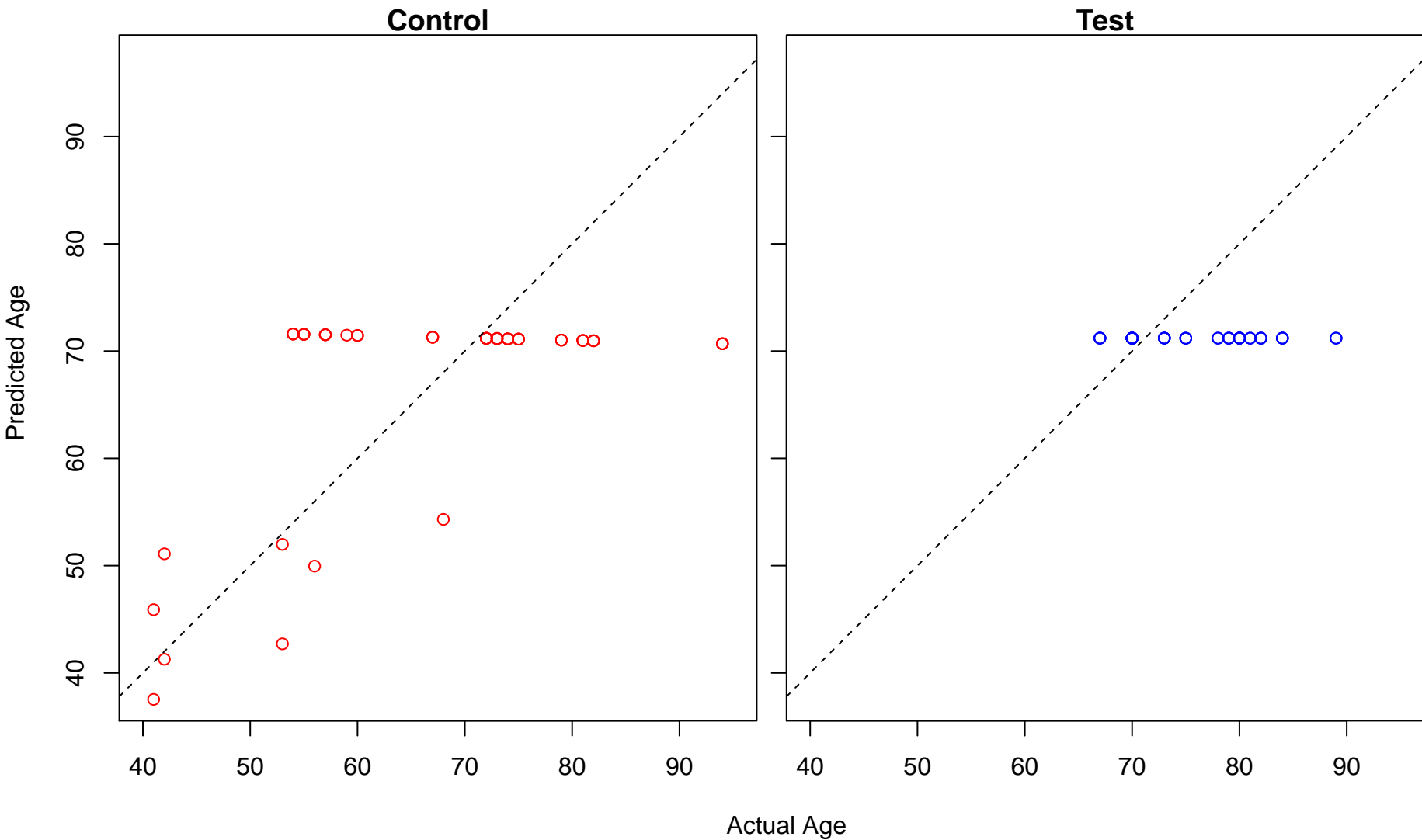
positive regulation of phosphorus metabolic process (Score: 0.814490)



positive regulation of phosphate metabolic process (Score: 0.814490)

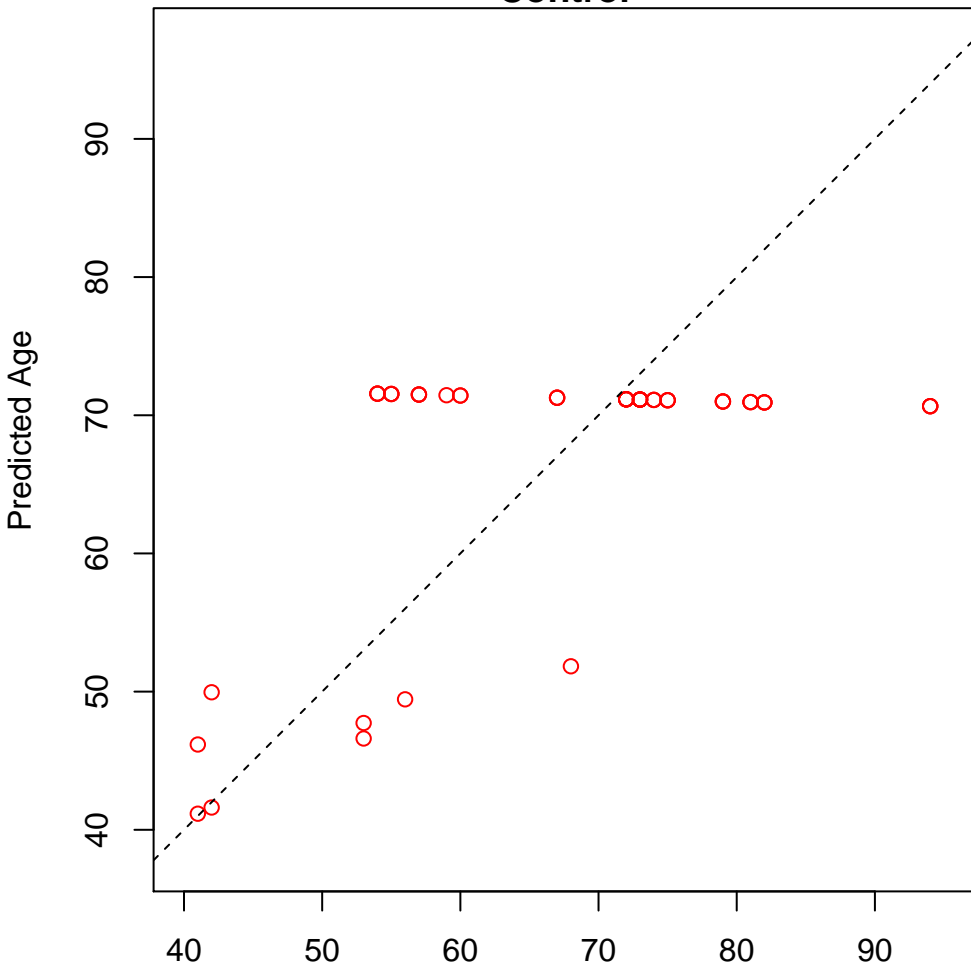


chromosome organization (Score: 0.814462)

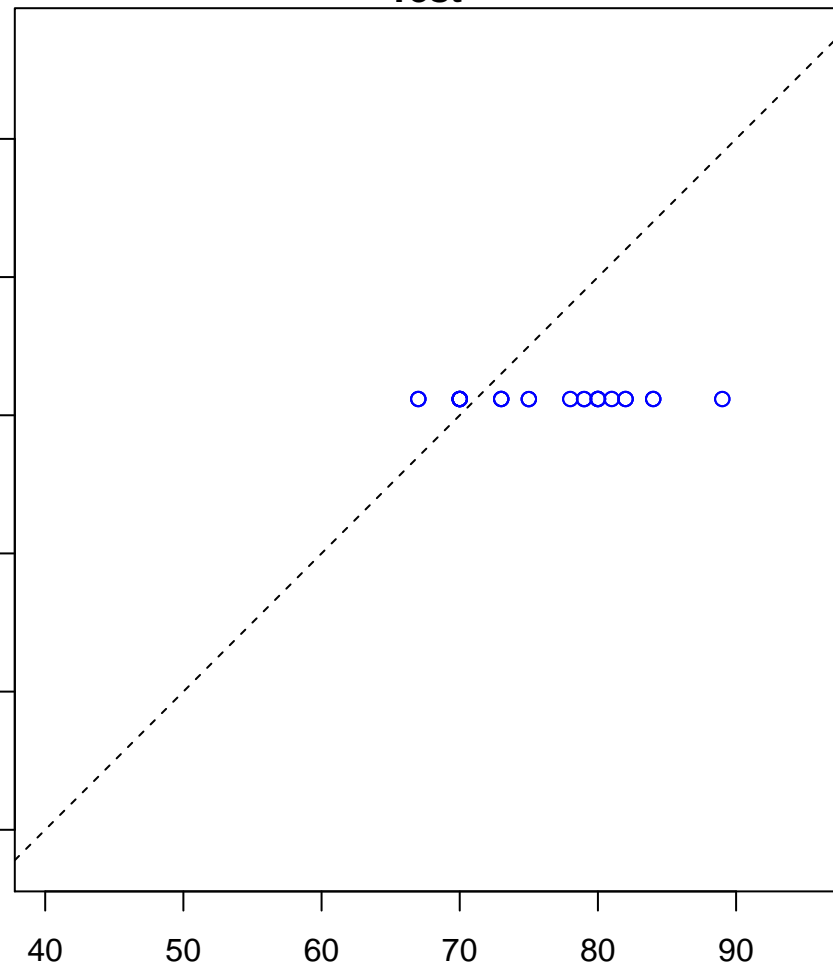


positive regulation of phosphorylation (Score: 0.814341)

Control

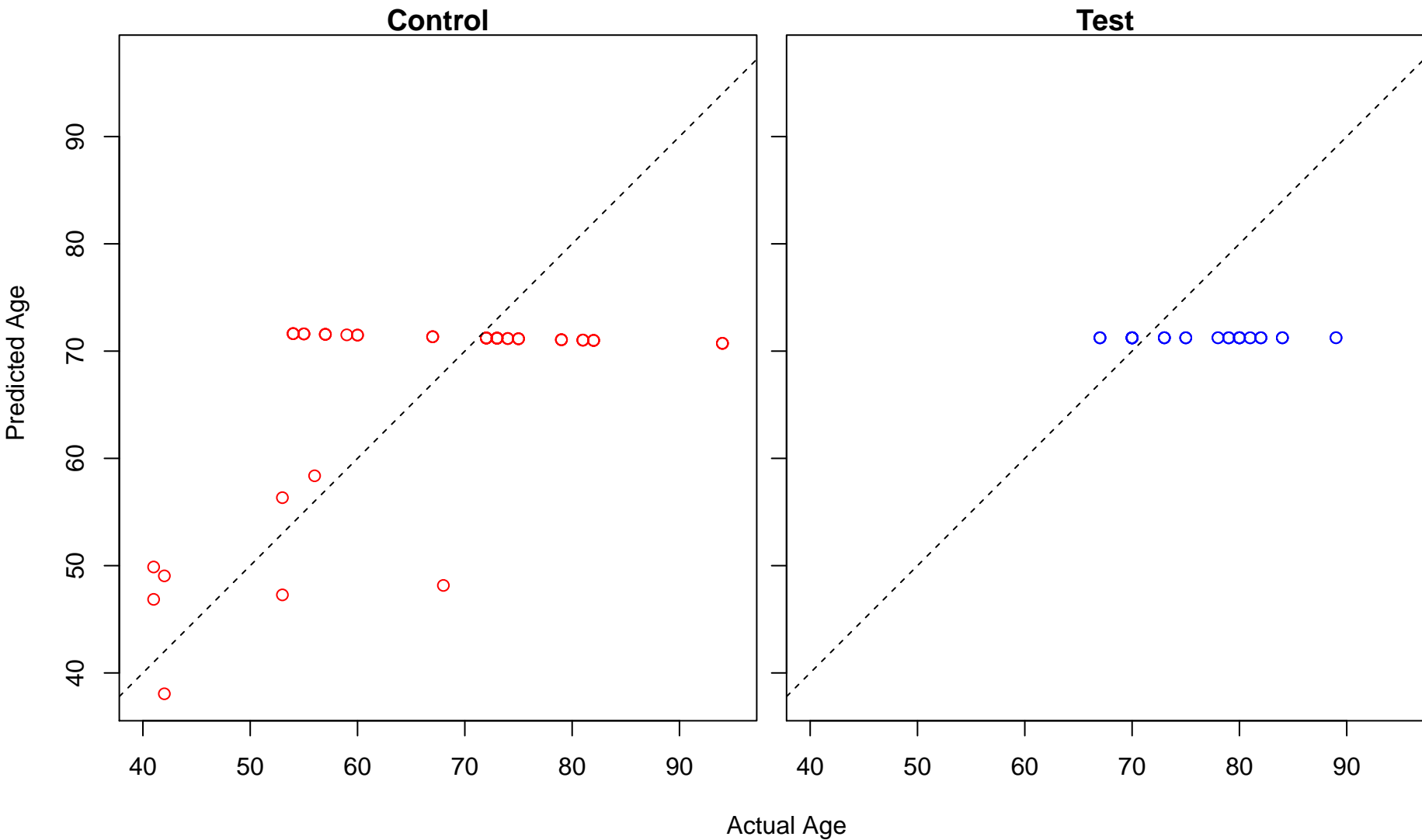


Test

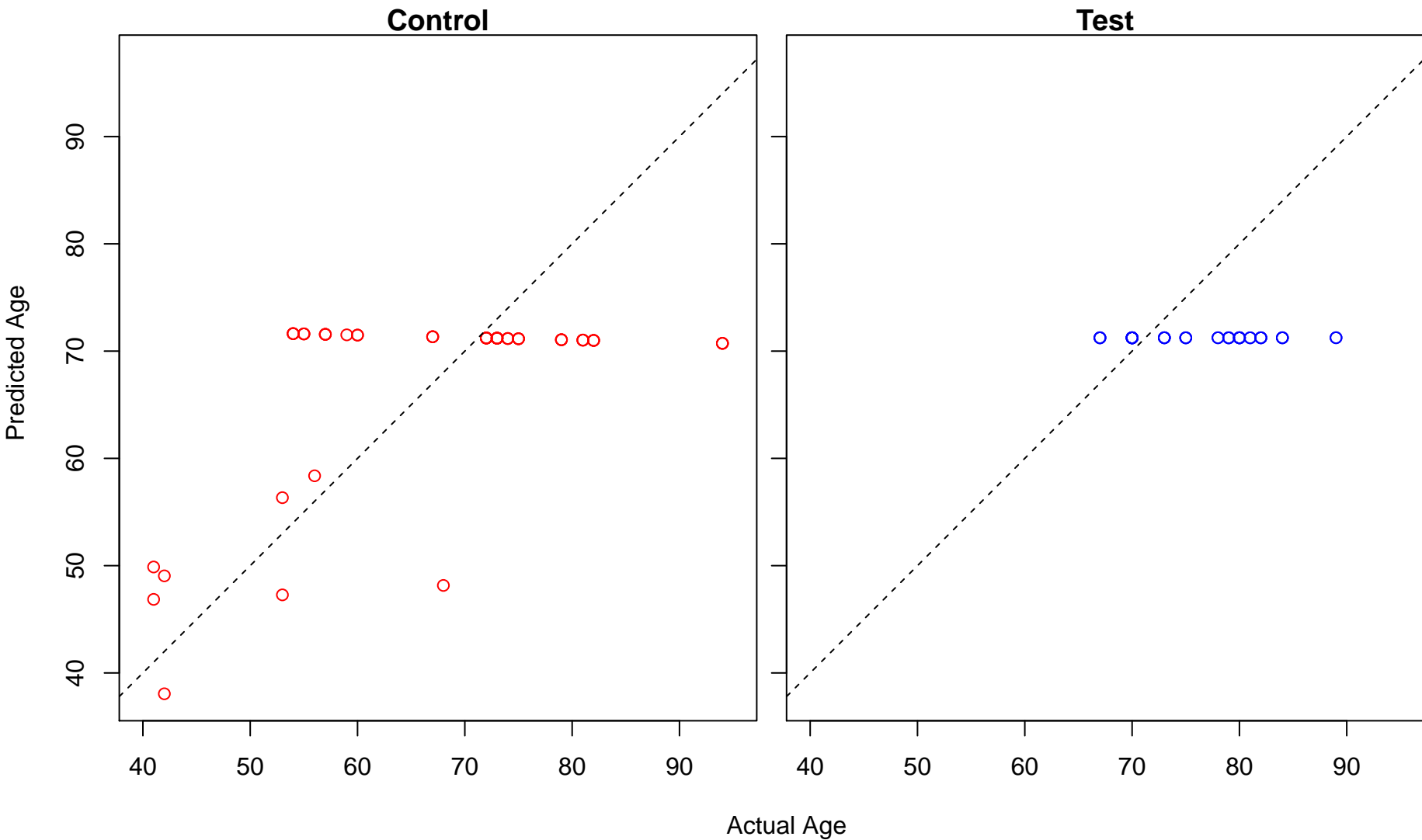


Actual Age

regulation of RNA stability (Score: 0.814313)

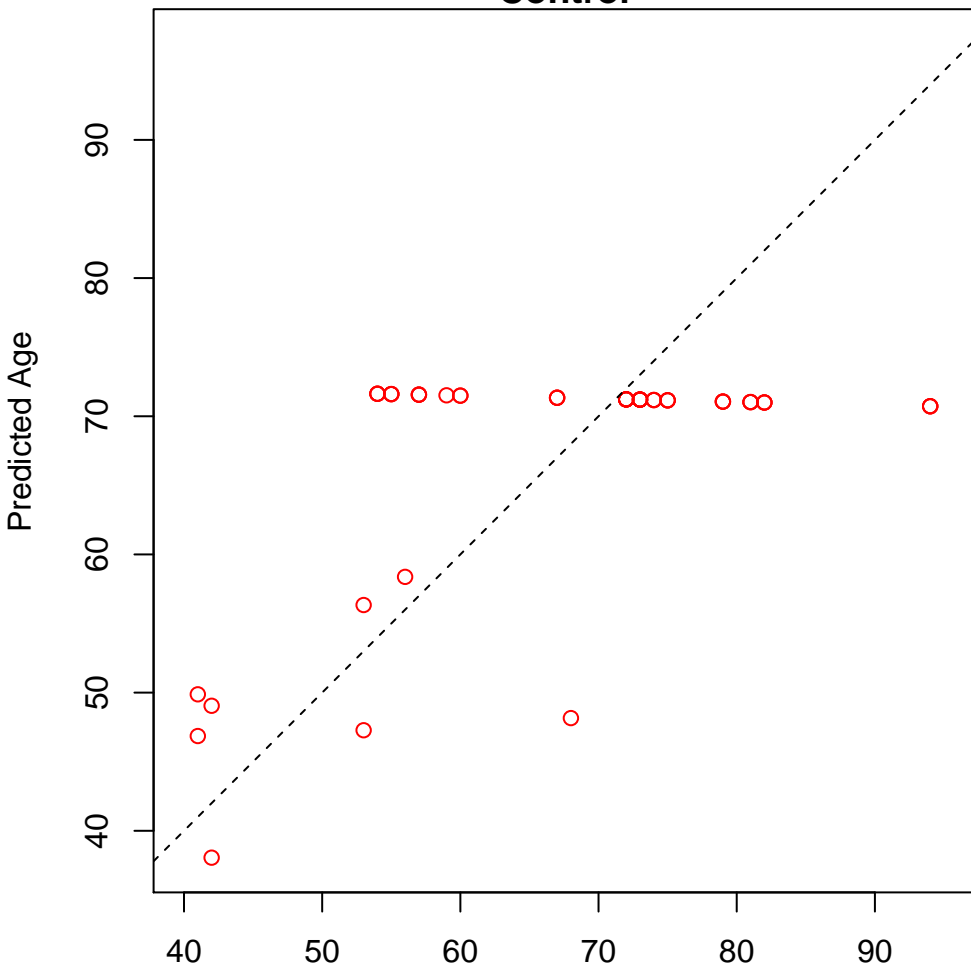


regulation of mRNA stability (Score: 0.814313)

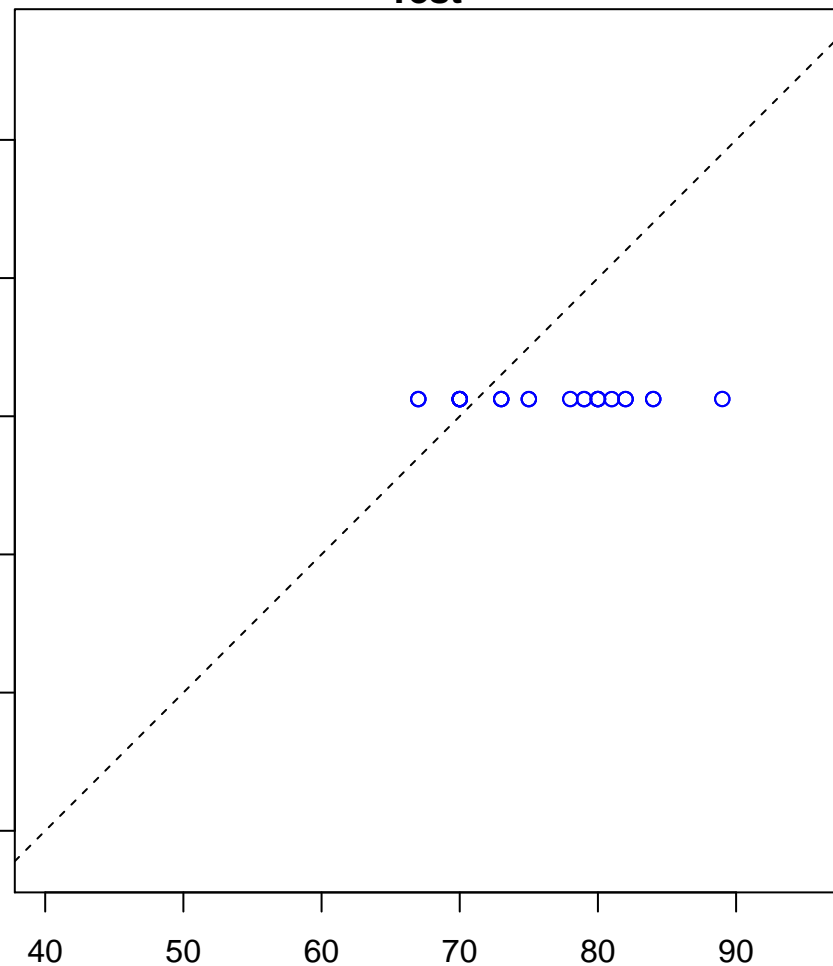


regulation of mRNA catabolic process (Score: 0.814313)

Control

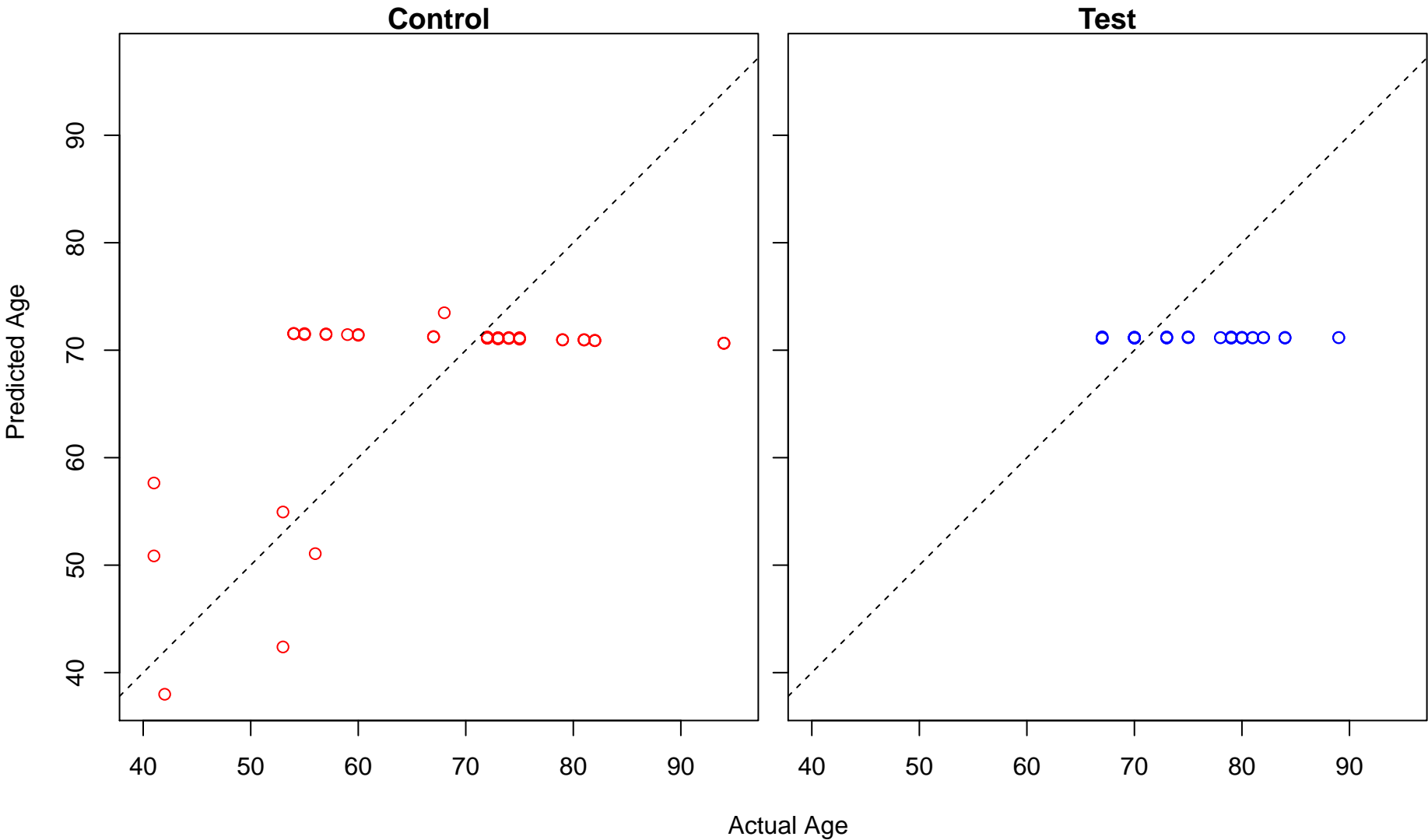


Test

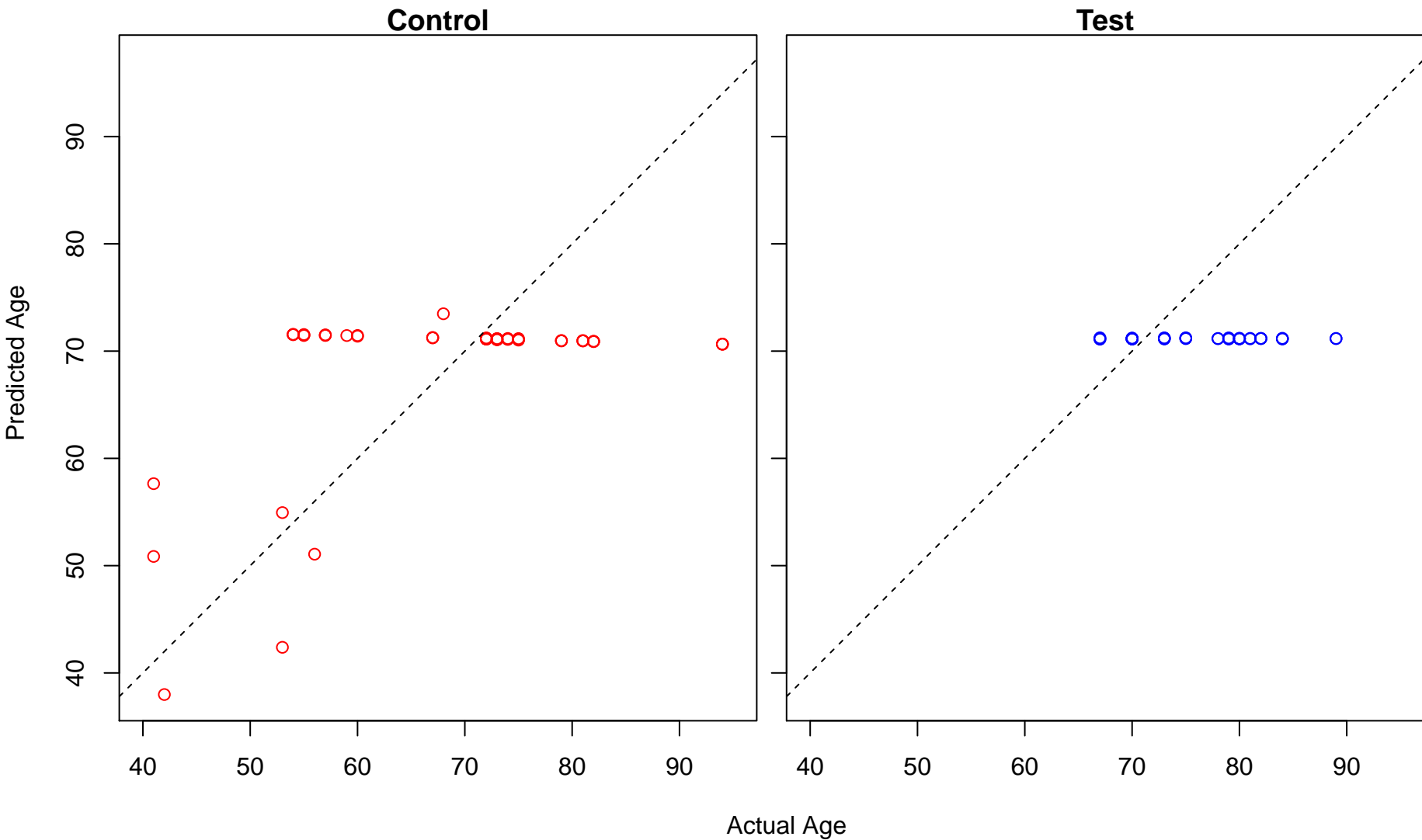


Actual Age

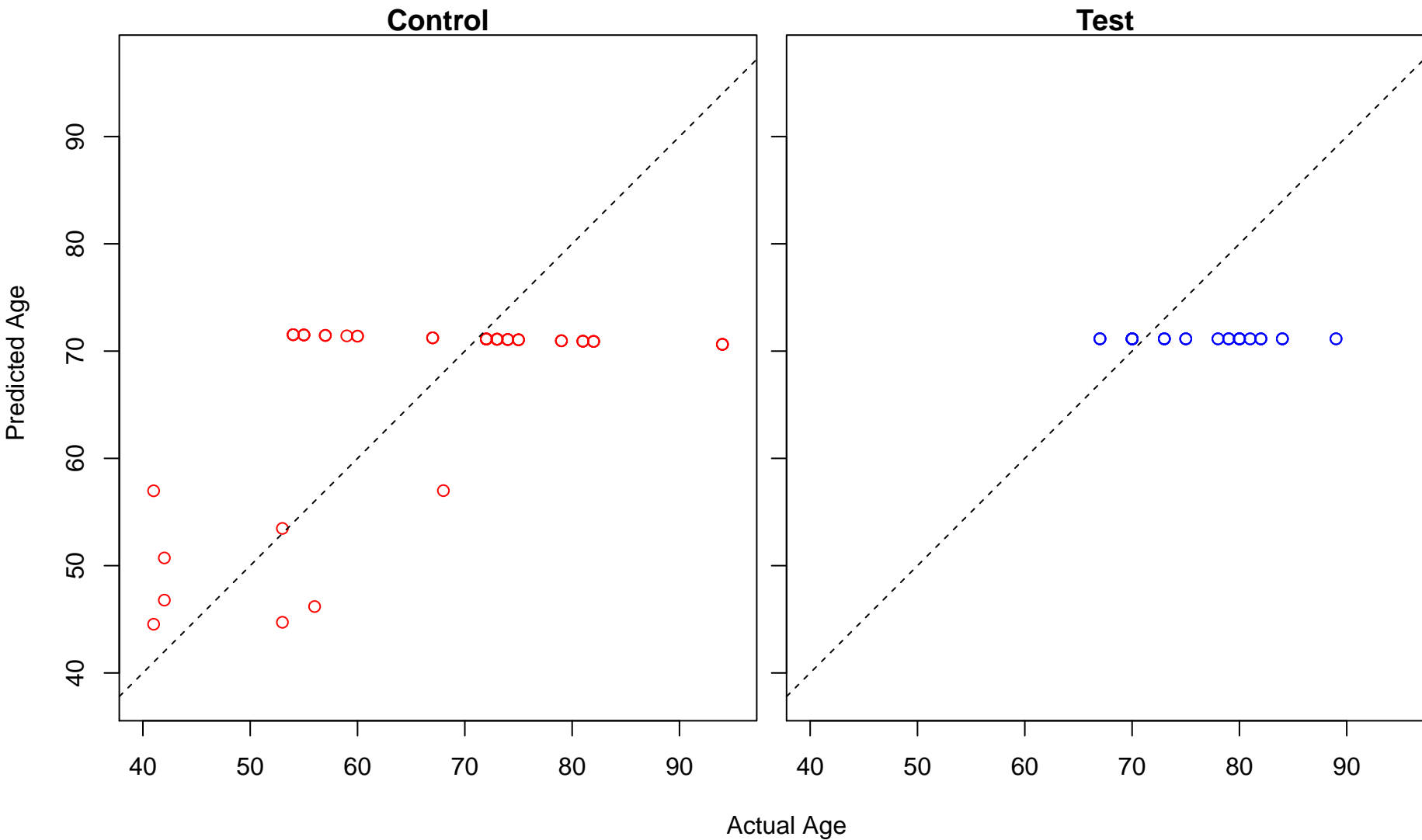
regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 0.814292)



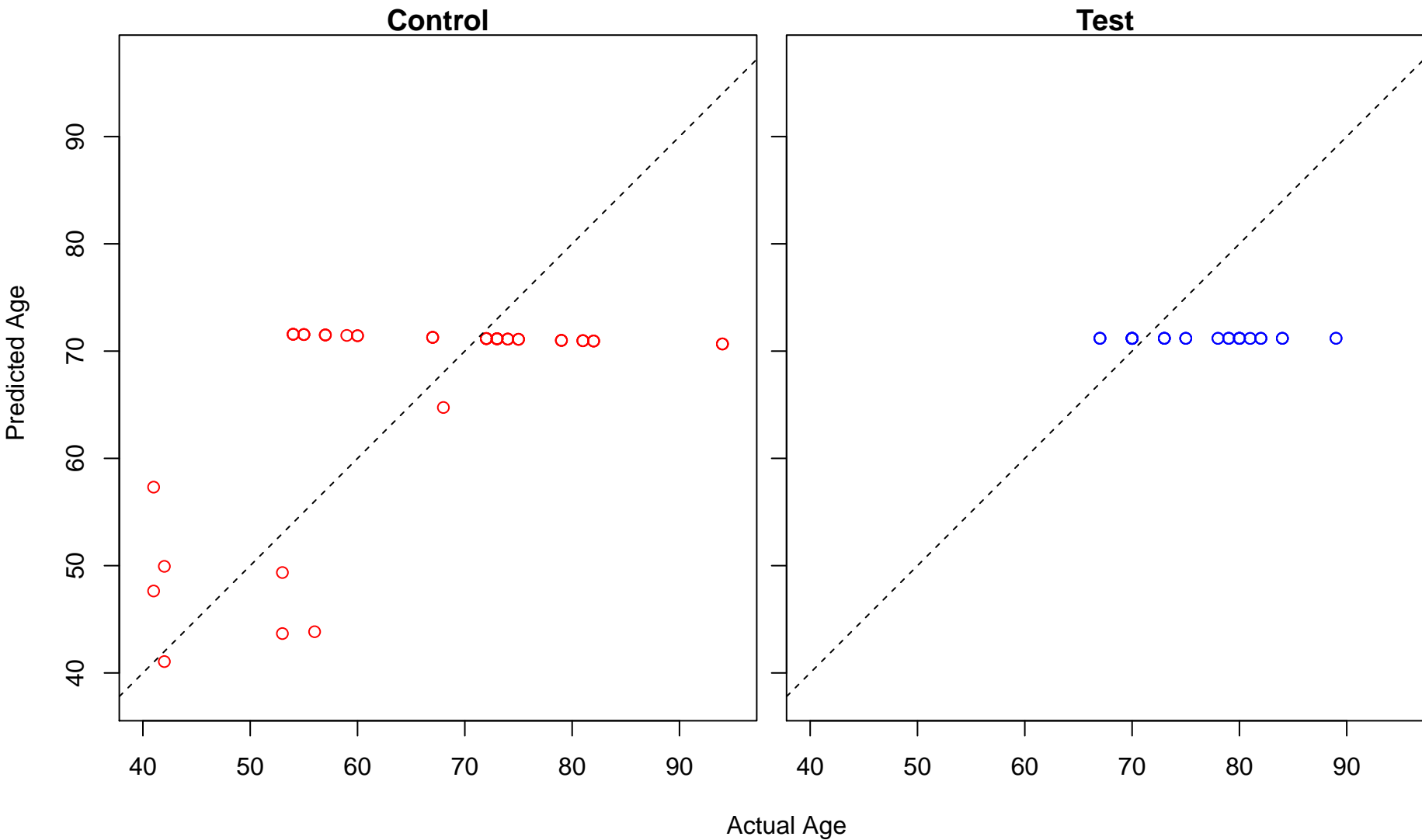
regulation of cysteine-type endopeptidase activity (Score: 0.814292)



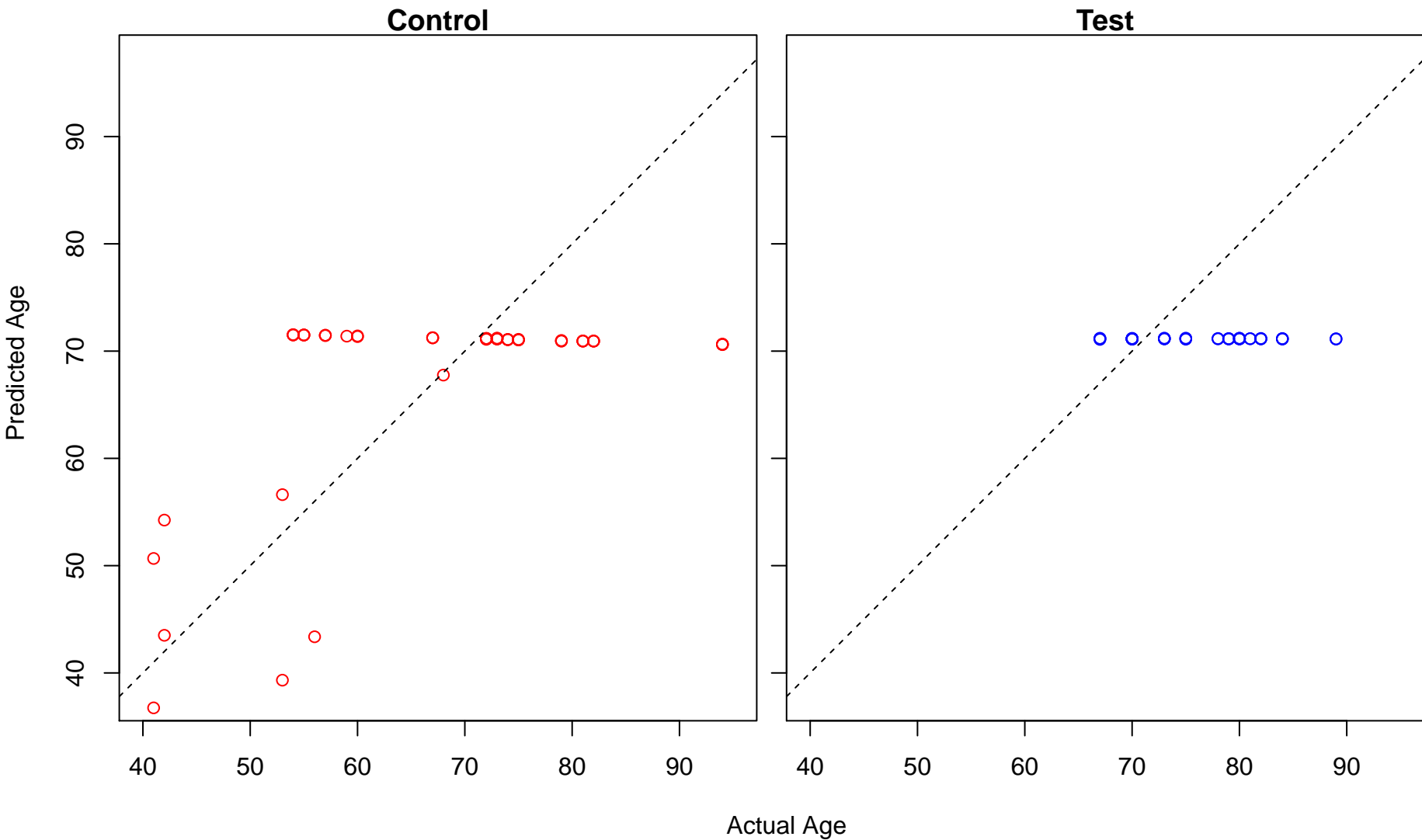
cellular respiration (Score: 0.814248)



positive regulation of cellular component organization (Score: 0.814215)

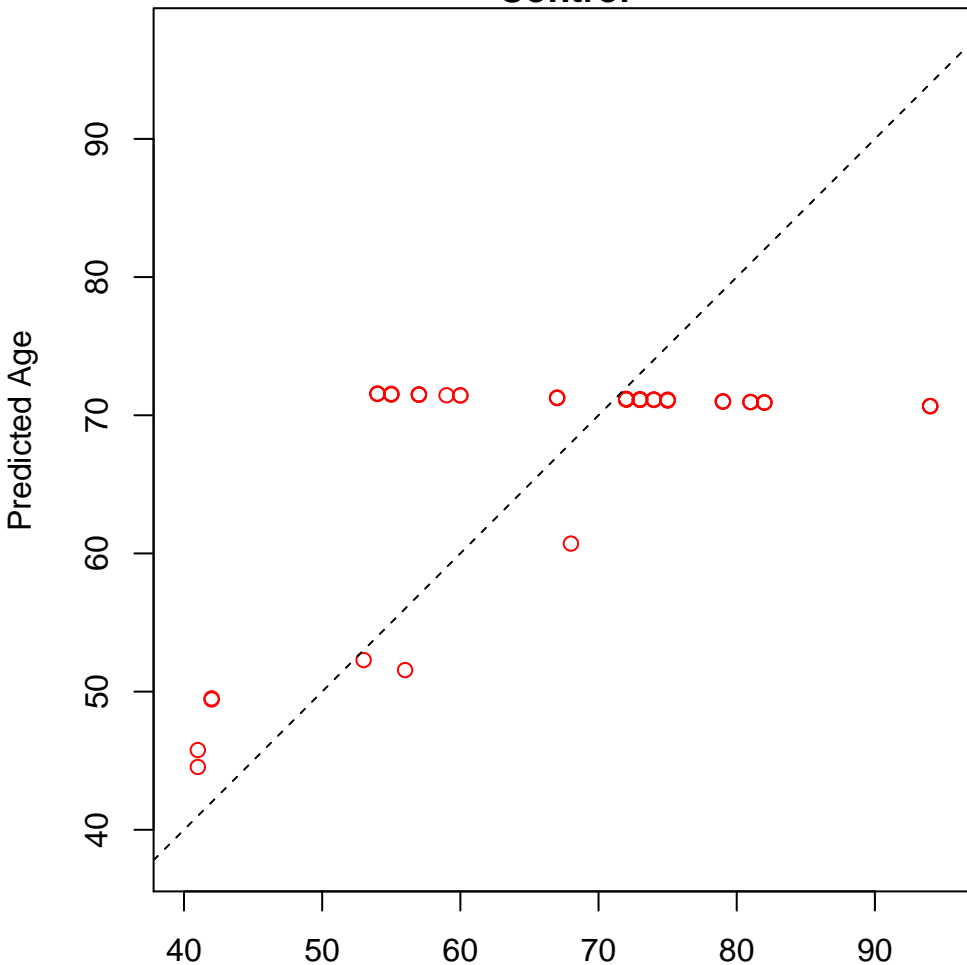


growth (Score: 0.814065)

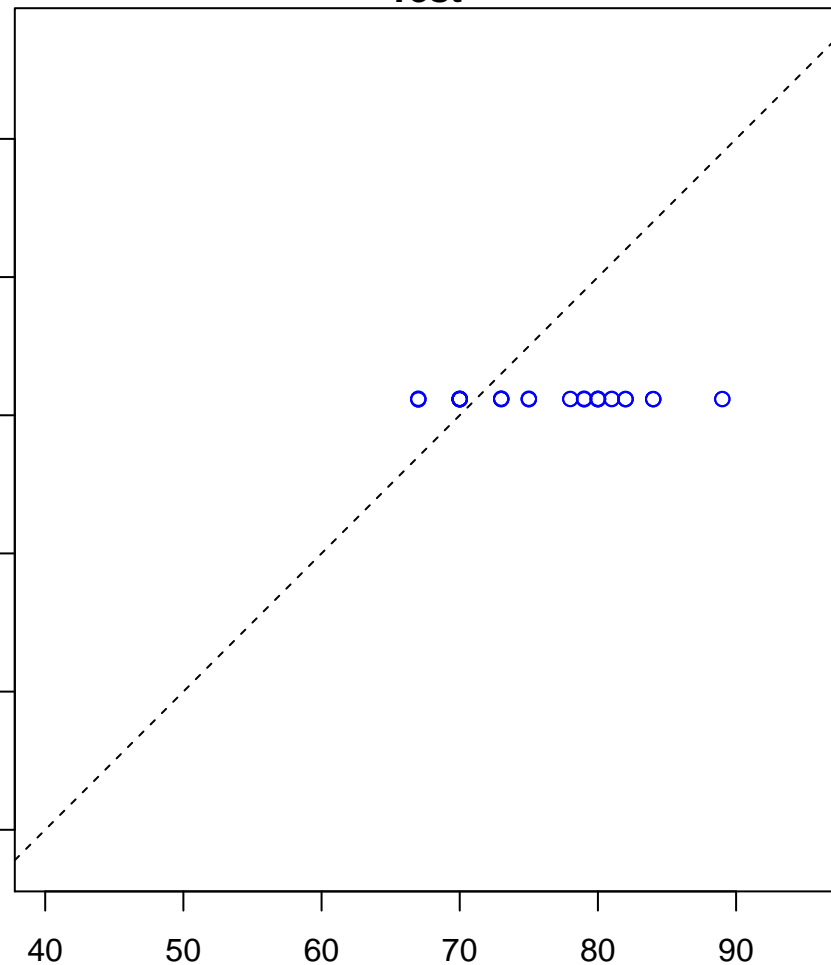


regulation of interleukin-6 production (Score: 0.814032)

Control



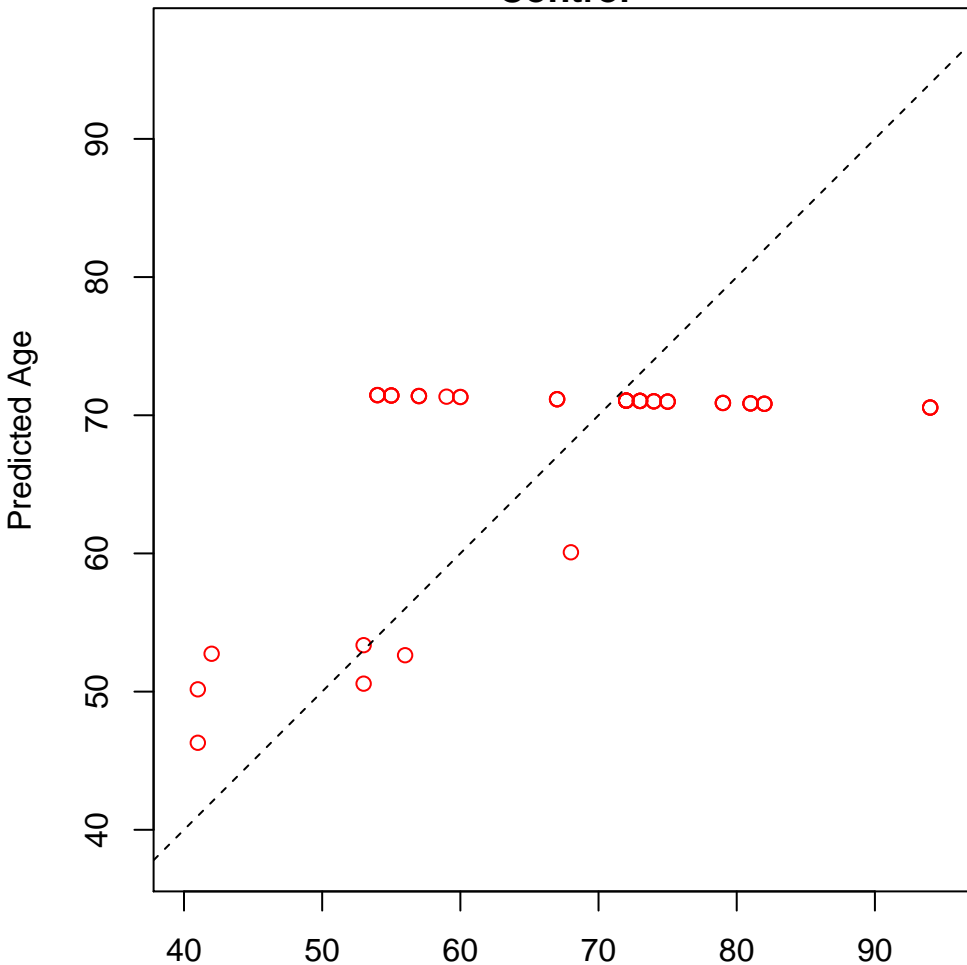
Test



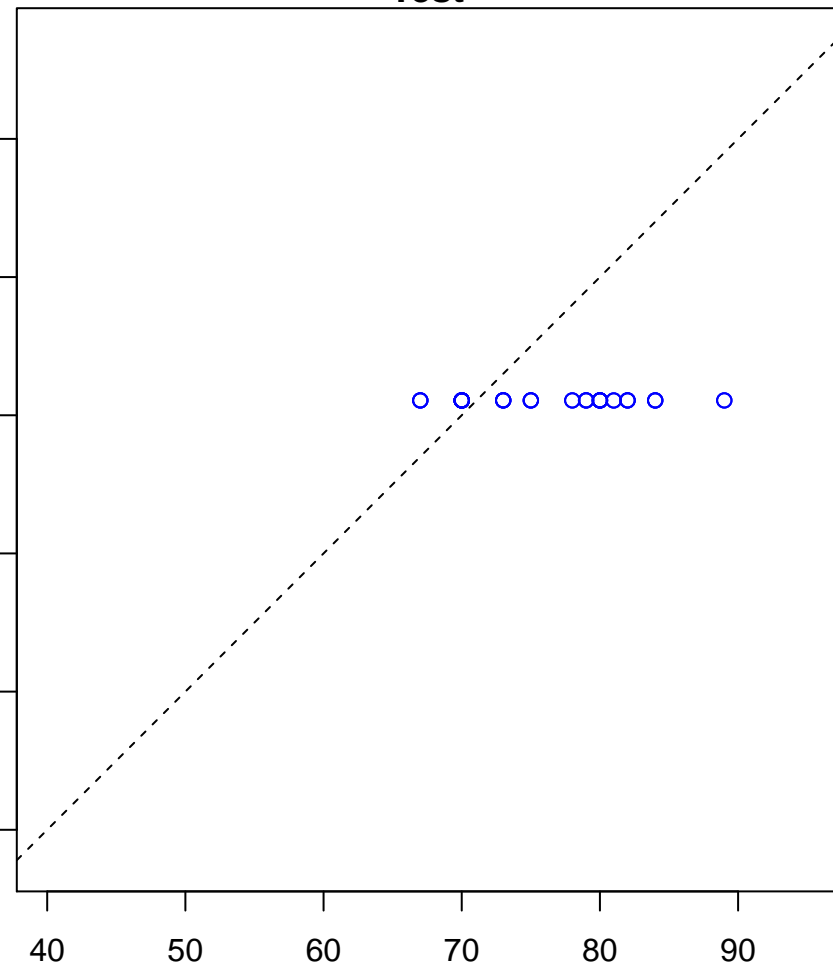
Actual Age

response to peptide hormone (Score: 0.814025)

Control

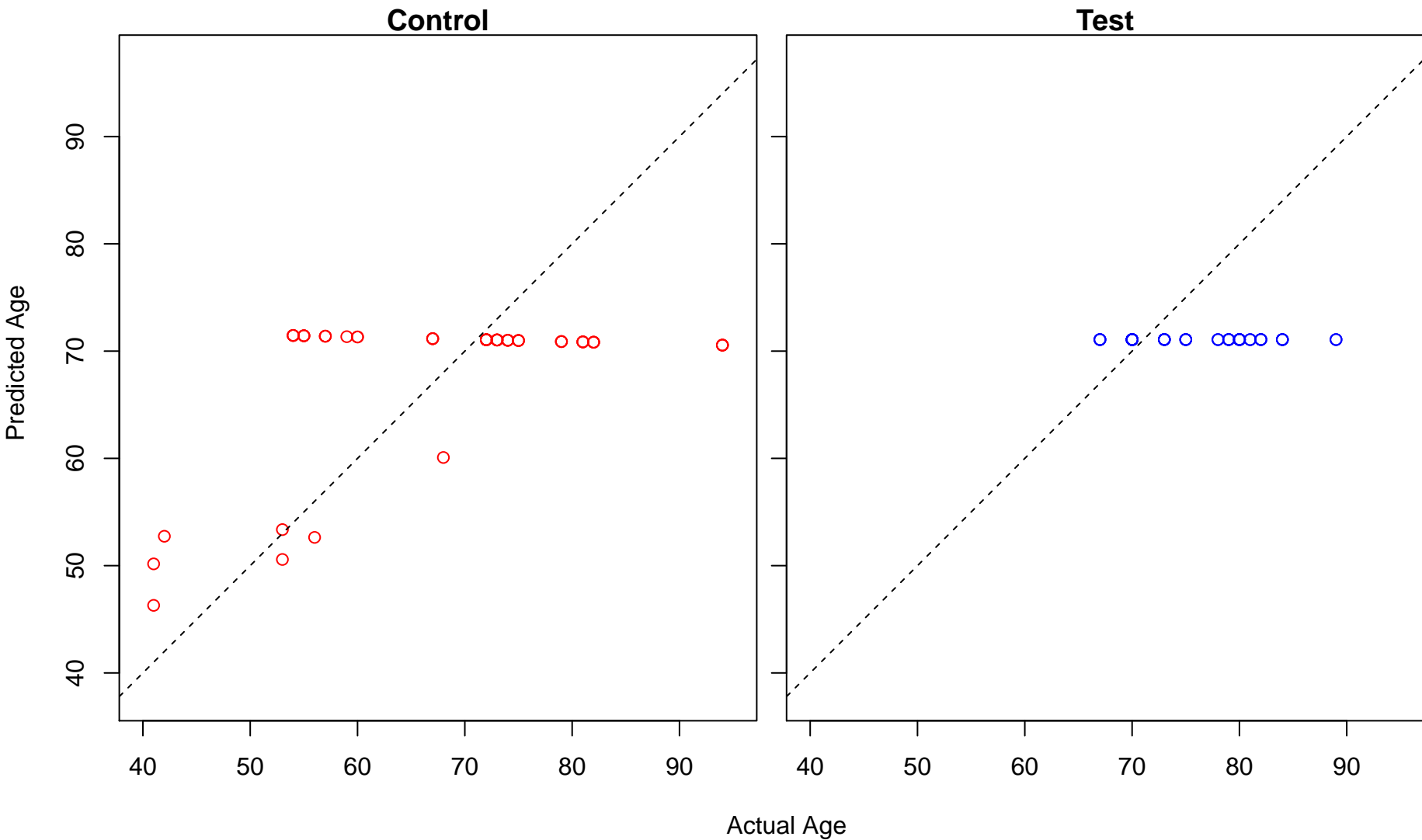


Test



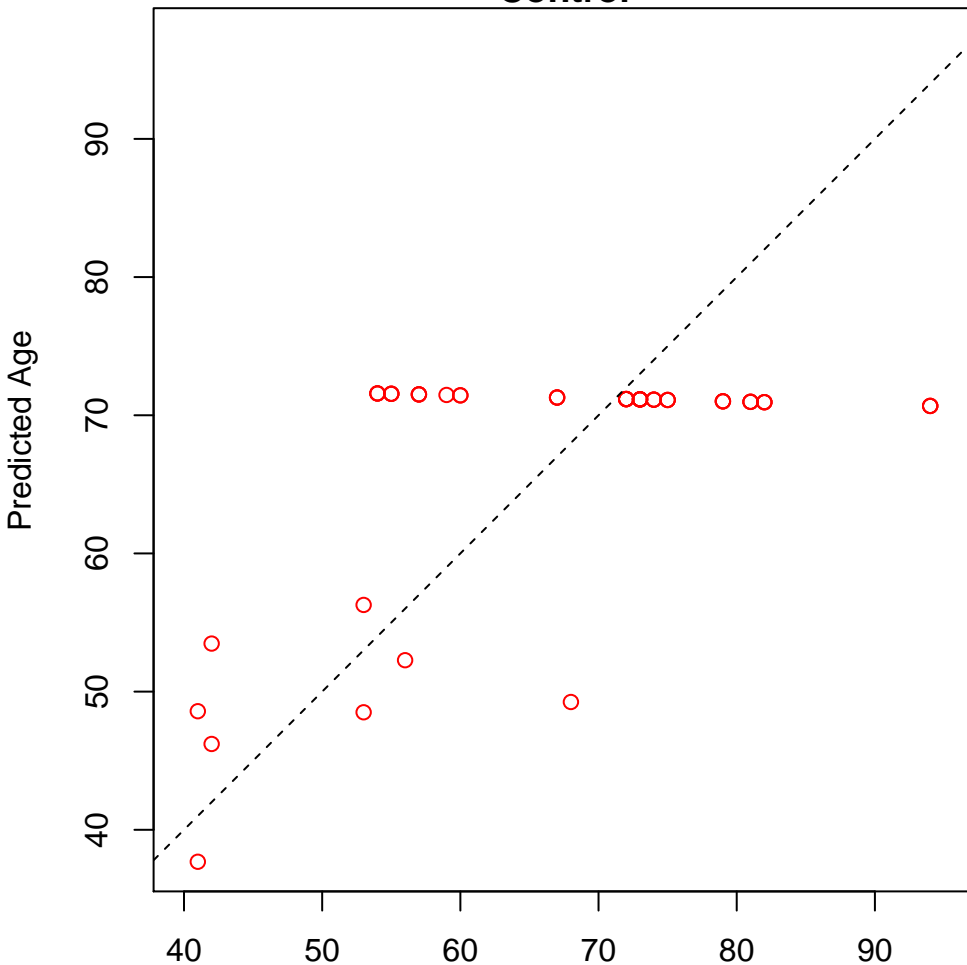
Actual Age

cellular response to peptide hormone stimulus (Score: 0.814025)

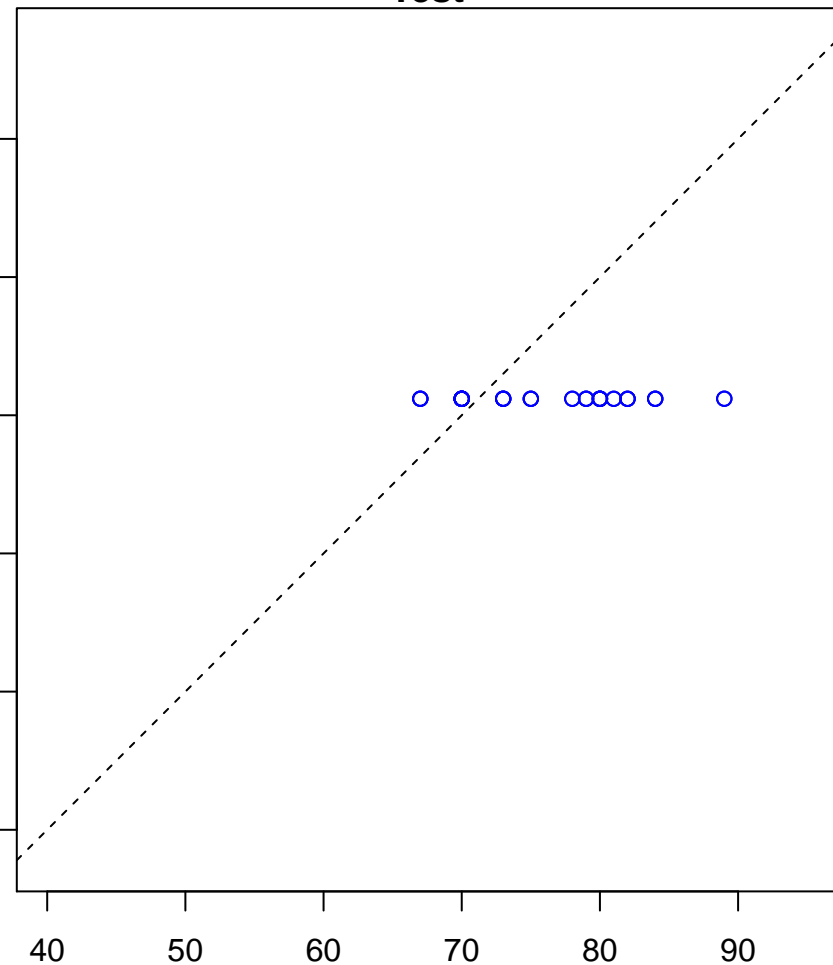


regulation of receptor internalization (Score: 0.814001)

Control

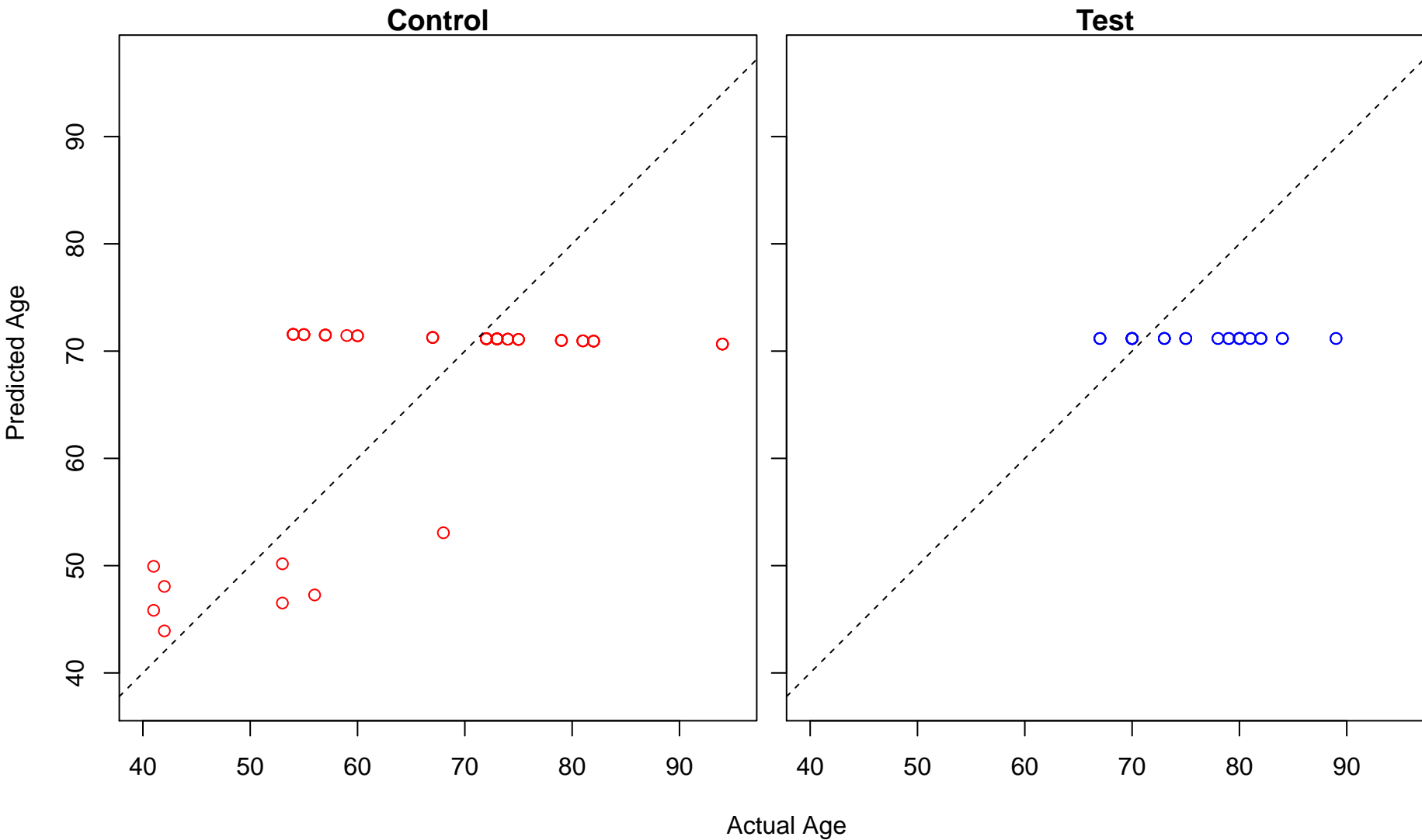


Test



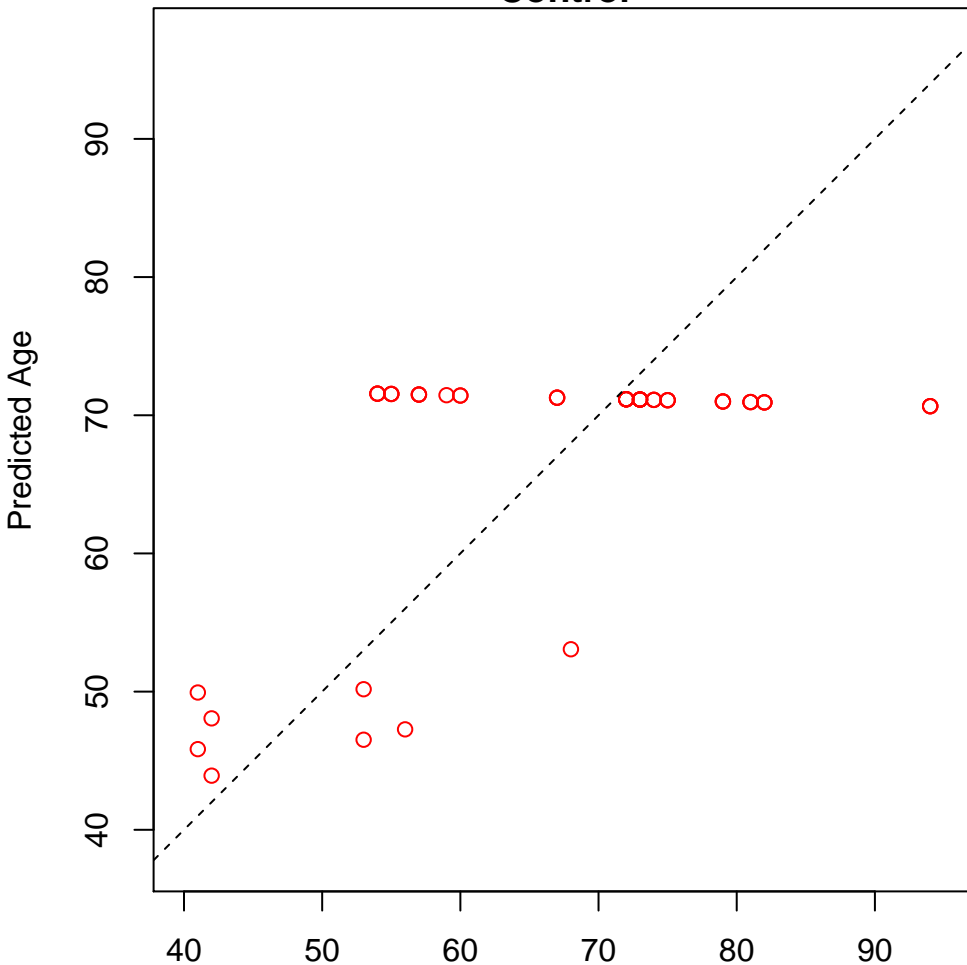
Actual Age

peptide metabolic process (Score: 0.813968)

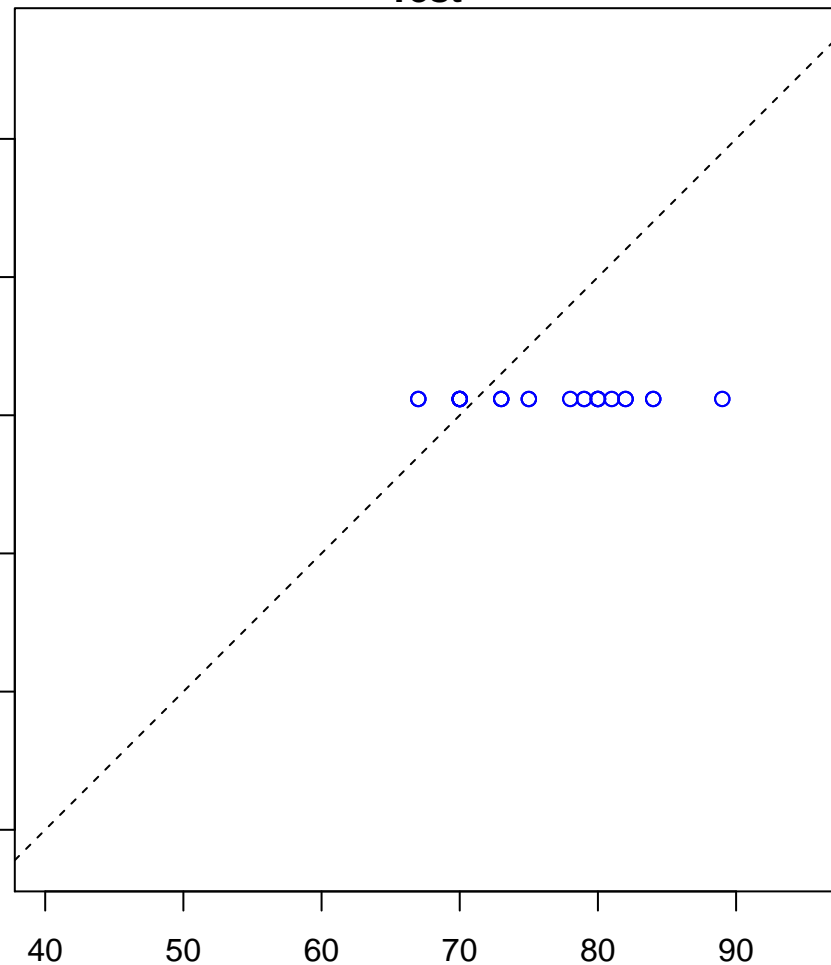


cellular amide metabolic process (Score: 0.813968)

Control



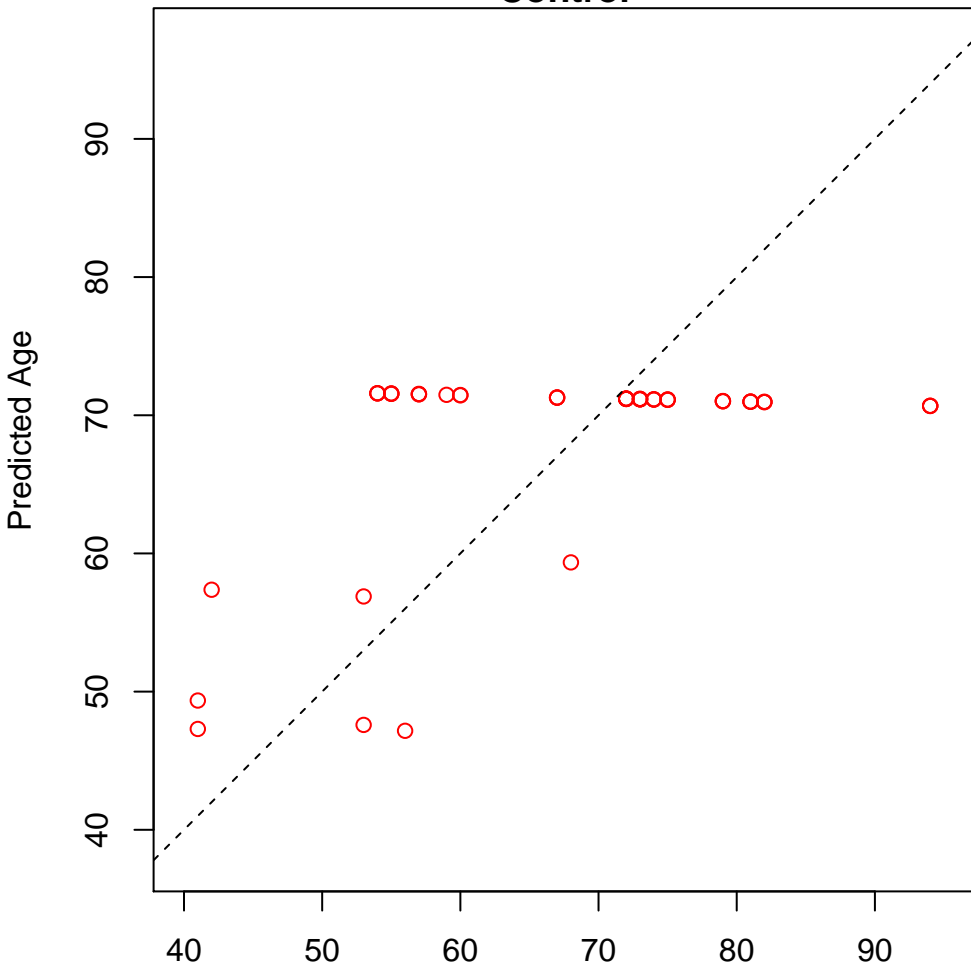
Test



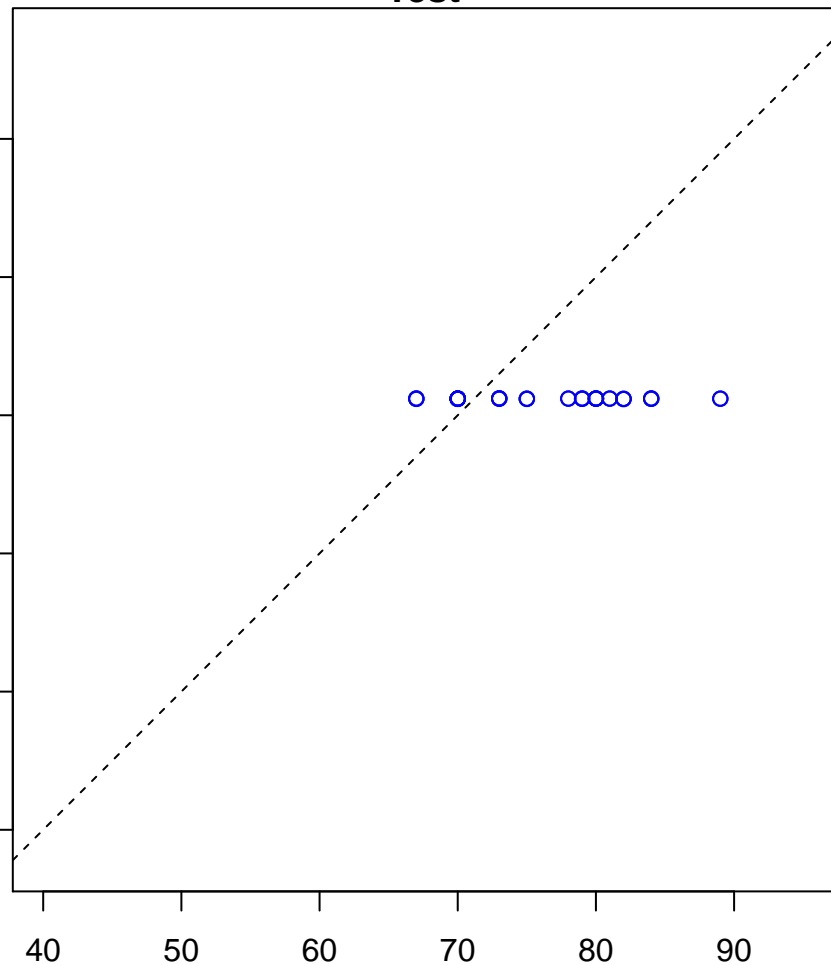
Actual Age

regulation of epithelial cell proliferation (Score: 0.813946)

Control

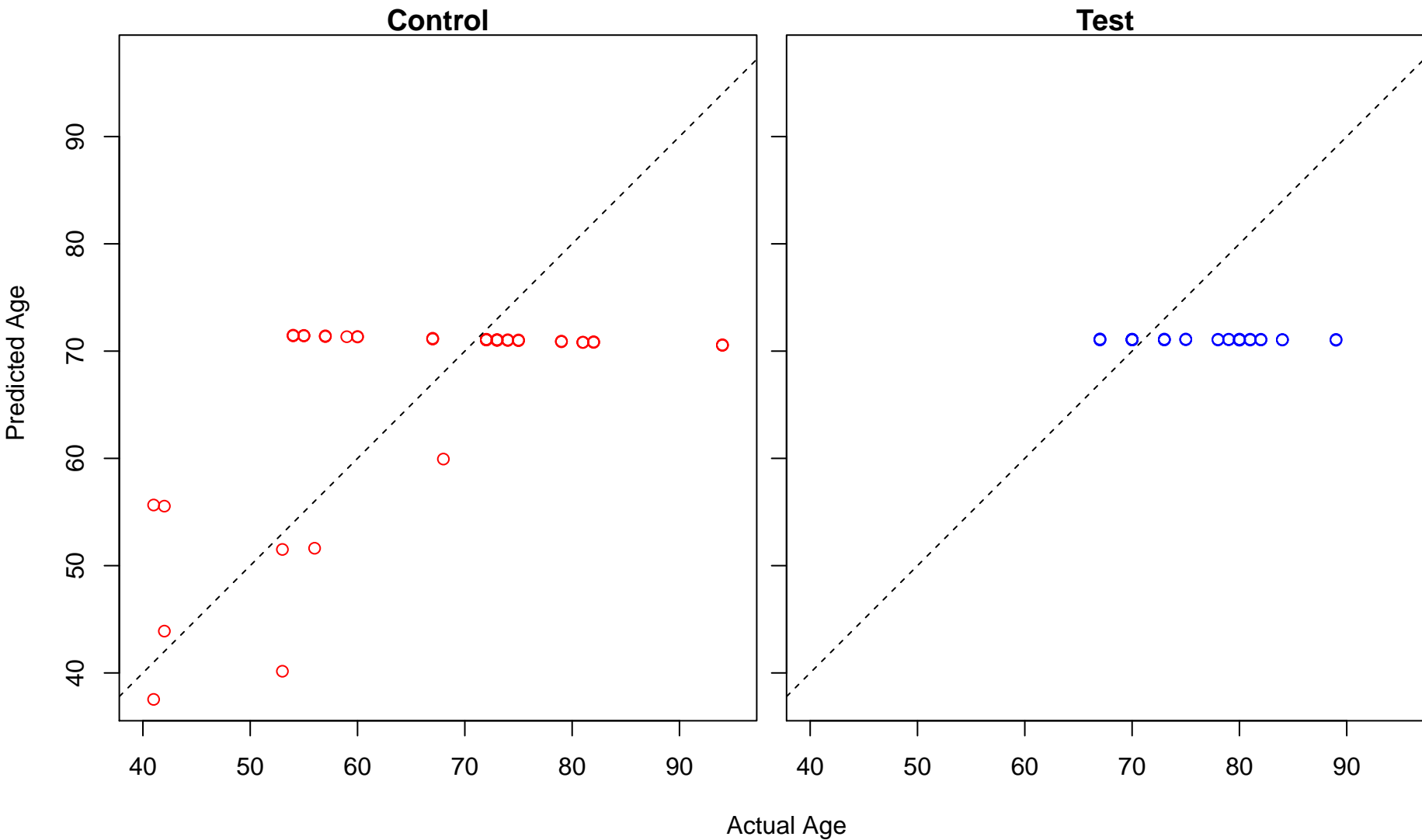


Test

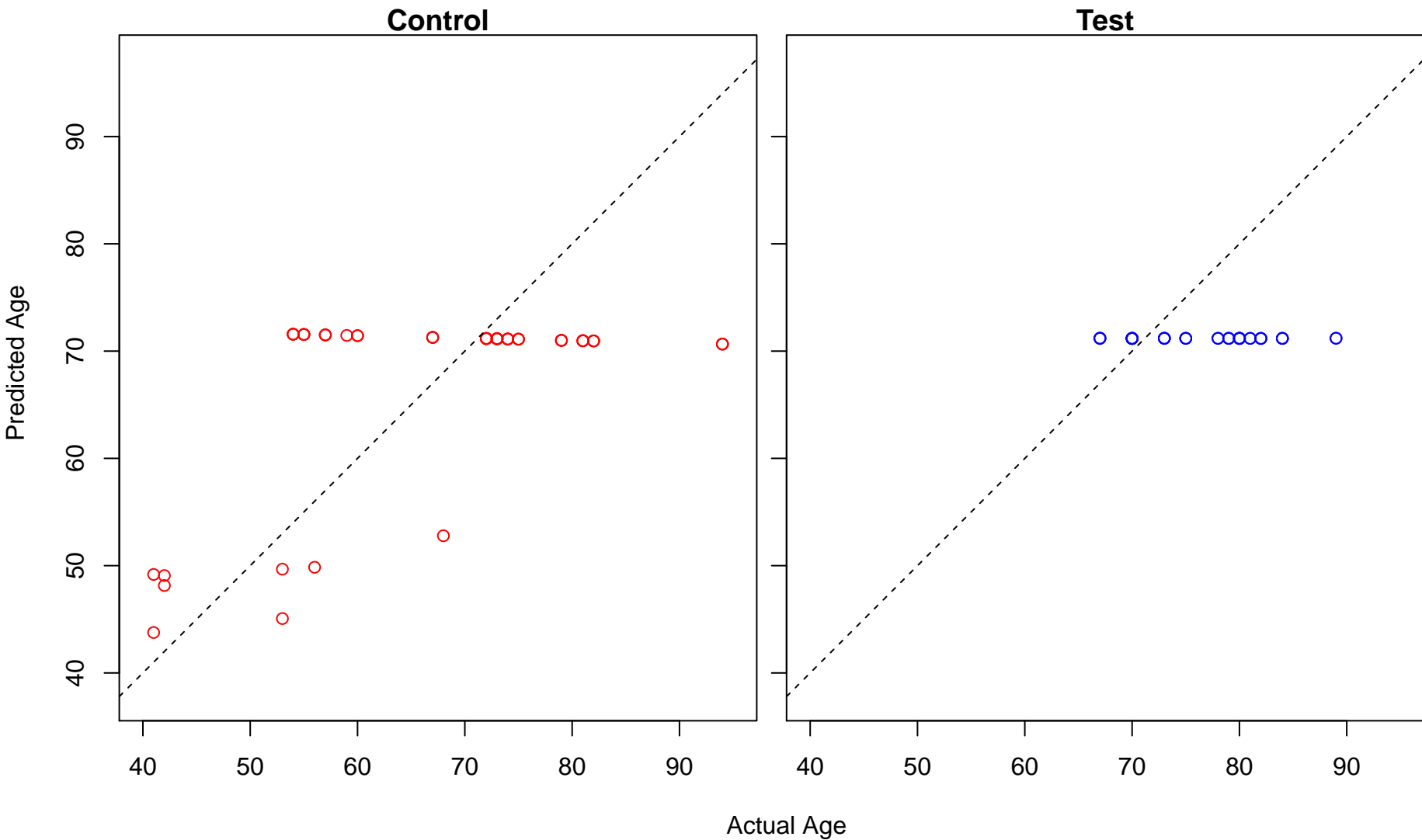


Actual Age

histone deubiquitination (Score: 0.813940)

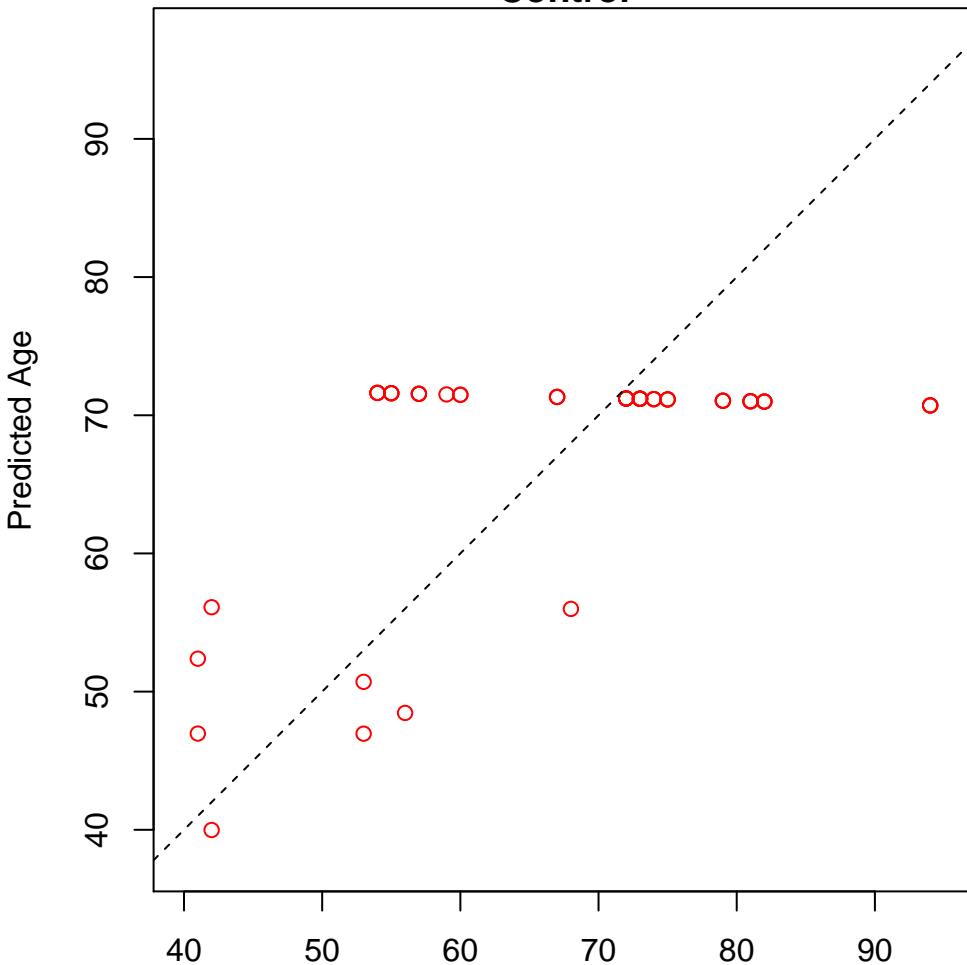


regulation of plasma lipoprotein particle levels (Score: 0.813797)

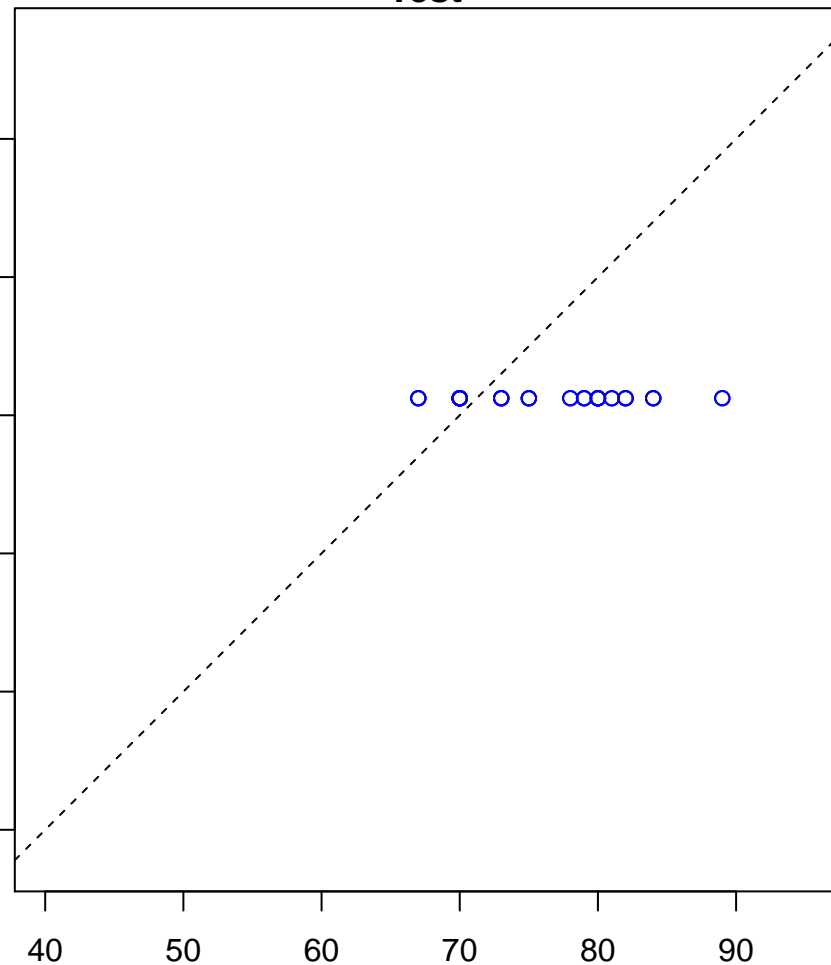


anatomical structure morphogenesis (Score: 0.813796)

Control

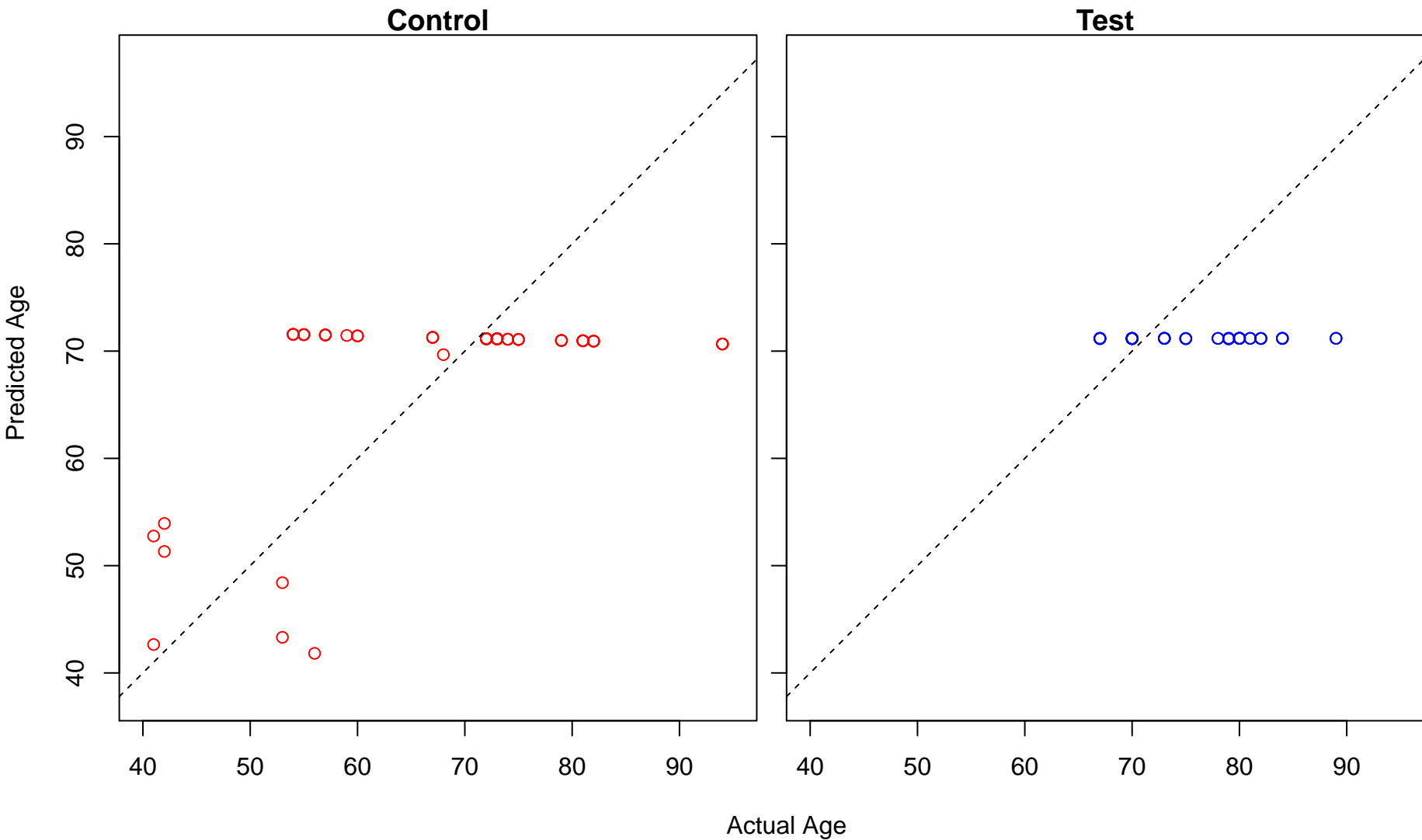


Test

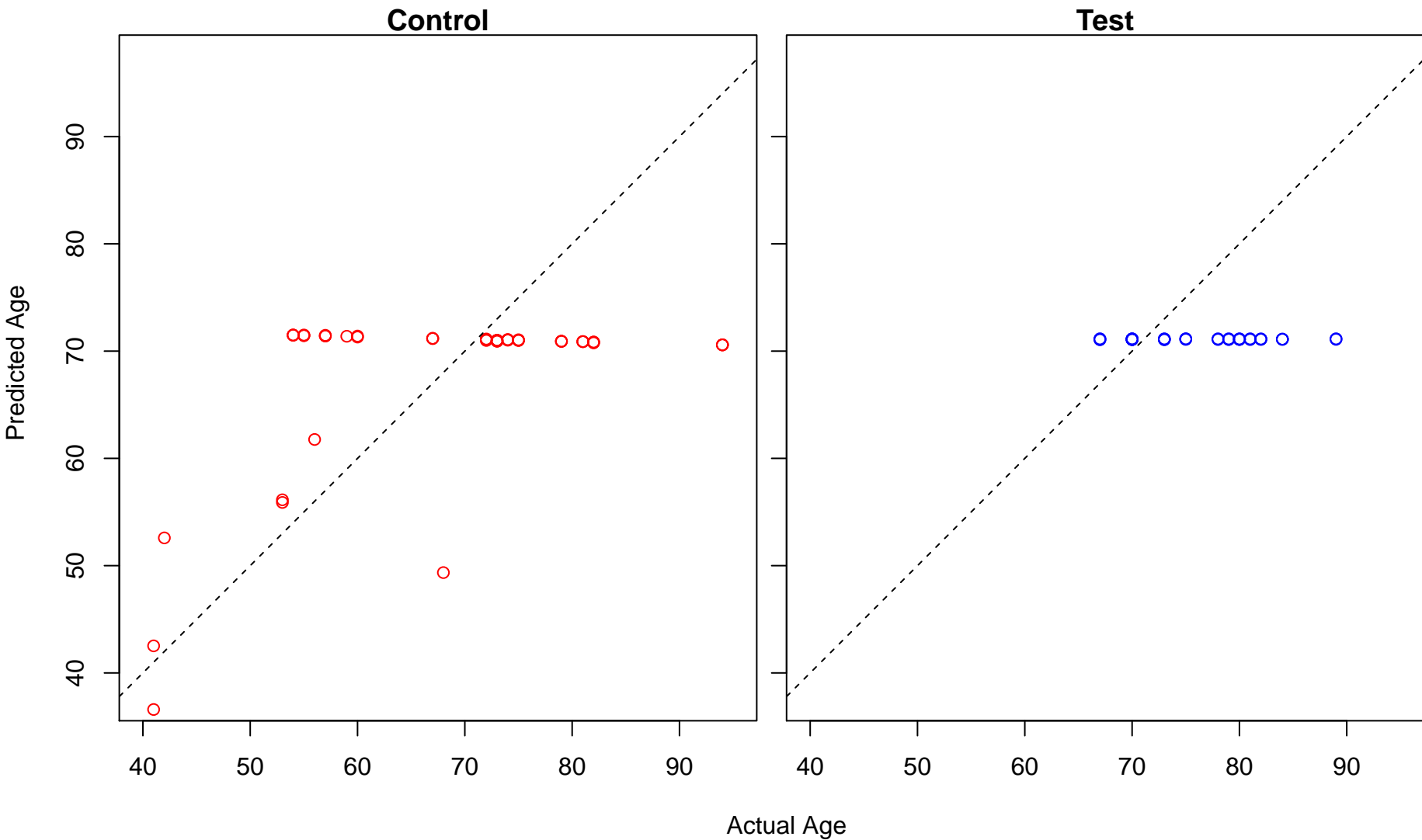


Actual Age

mRNA processing (Score: 0.813720)

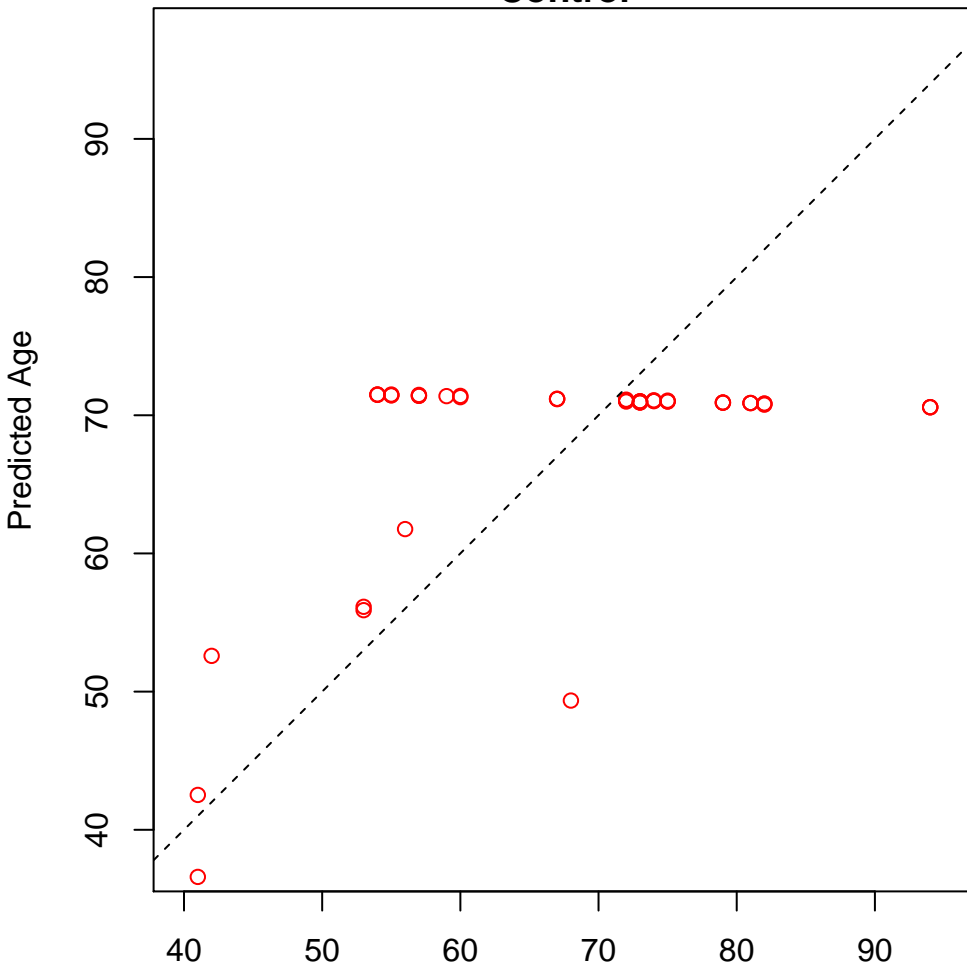


regulation of microtubule polymerization or depolymerization (Score: 0.813654)

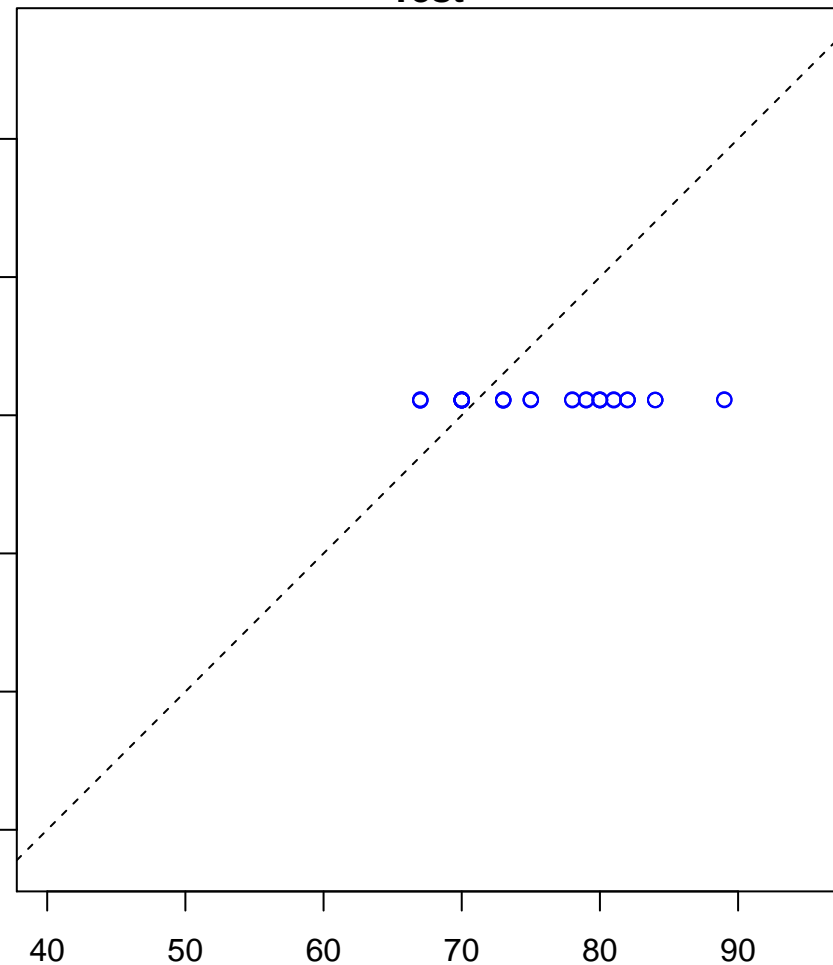


regulation of microtubule polymerization (Score: 0.813654)

Control

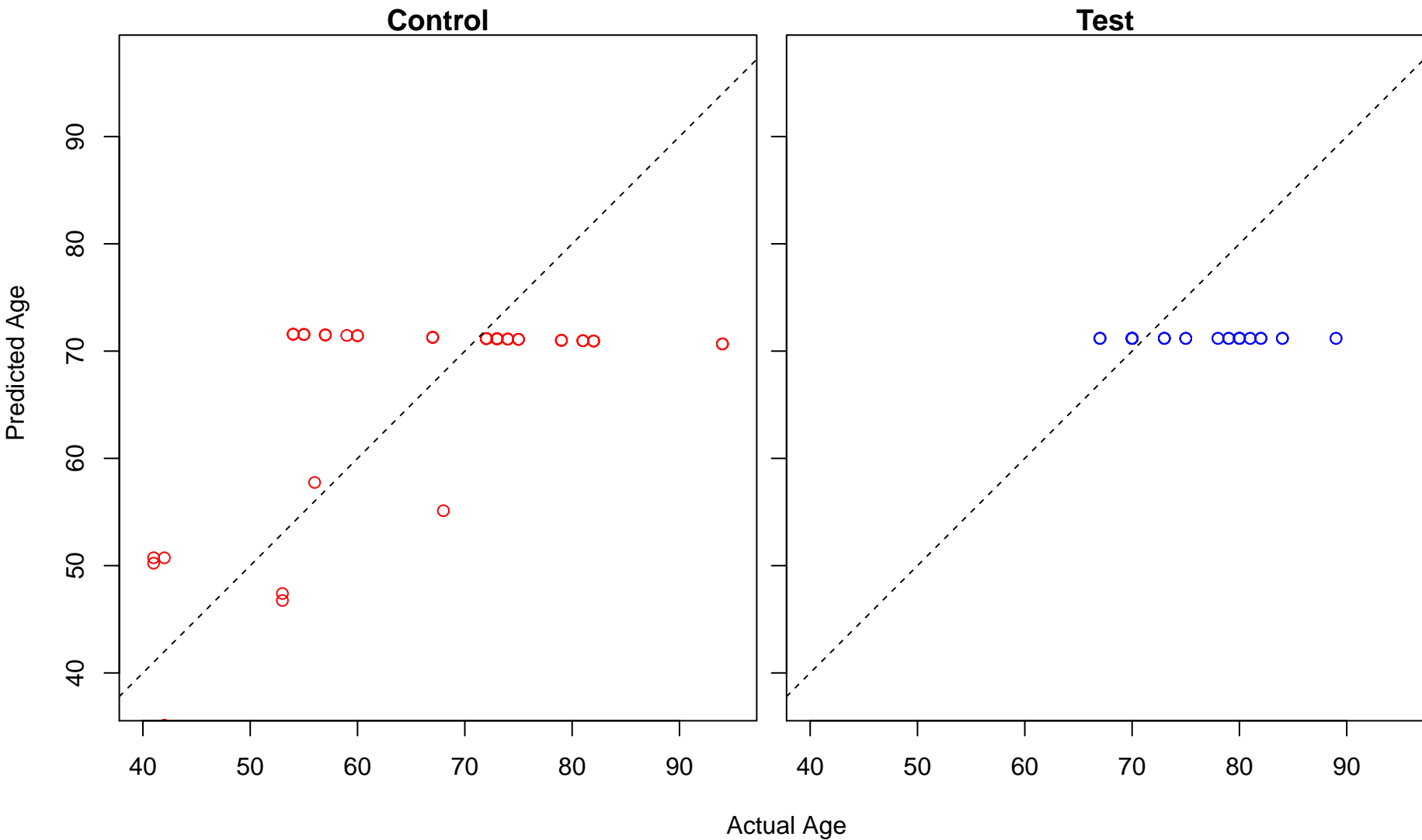


Test

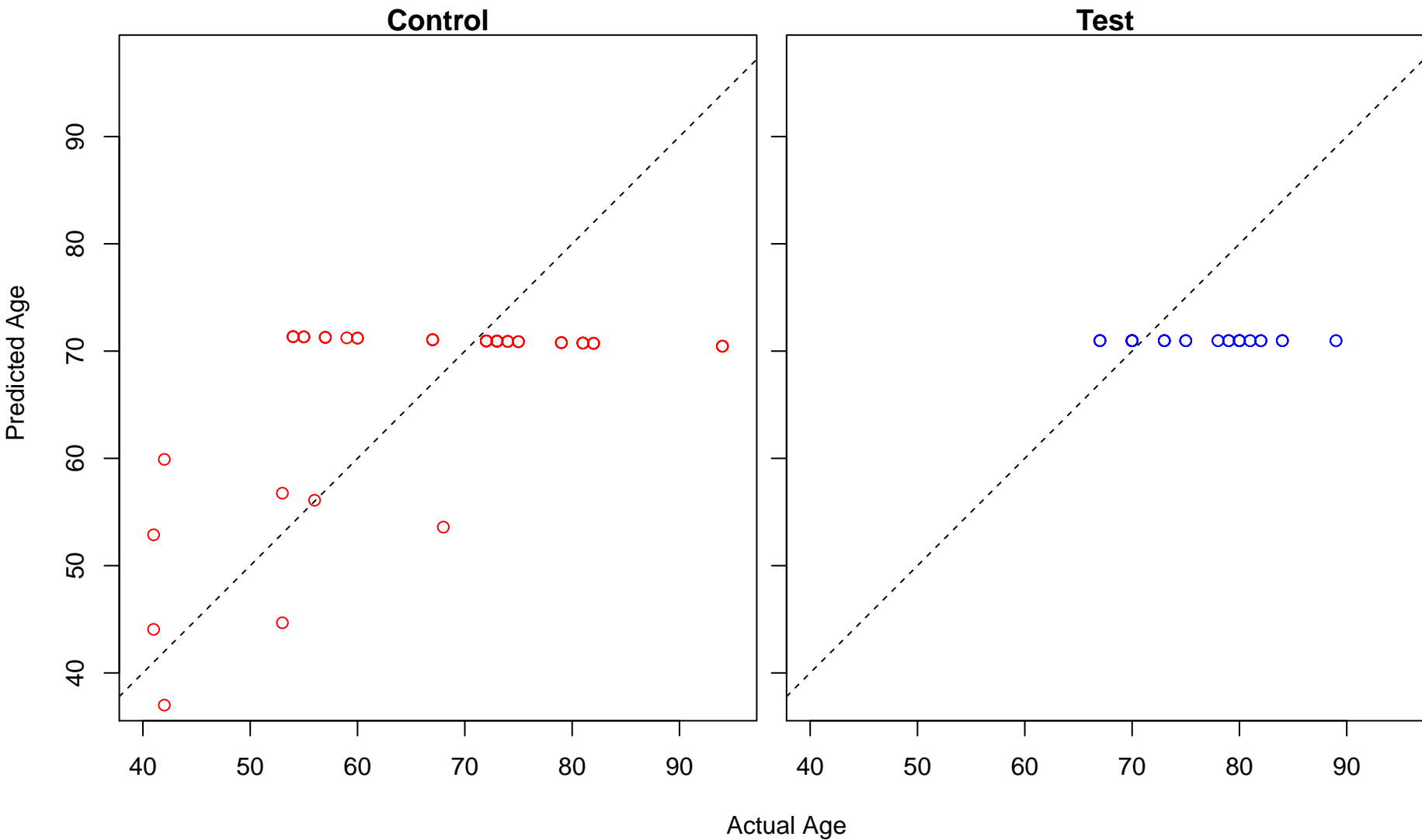


Actual Age

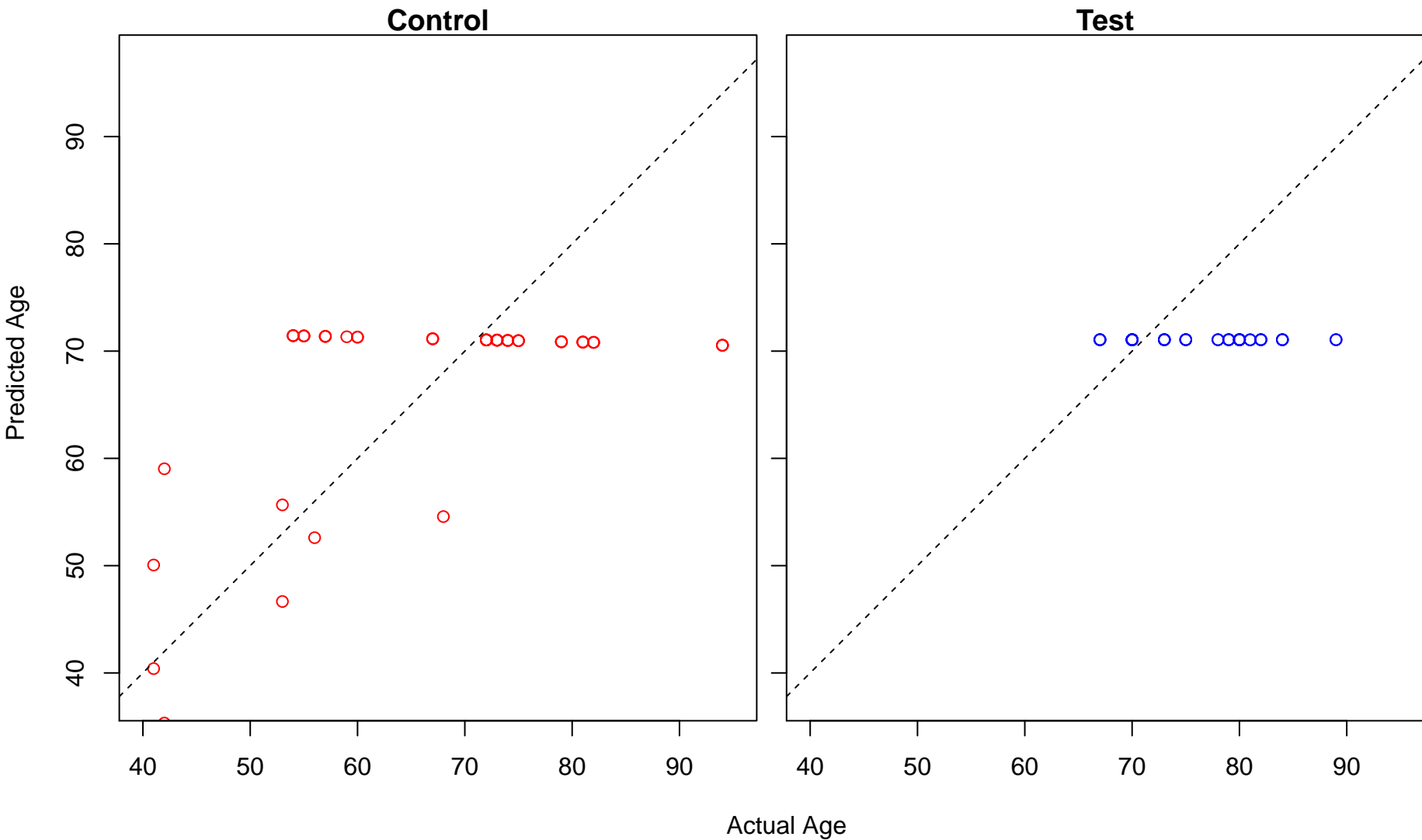
cell cycle (Score: 0.813594)



spliceosomal complex assembly (Score: 0.813566)

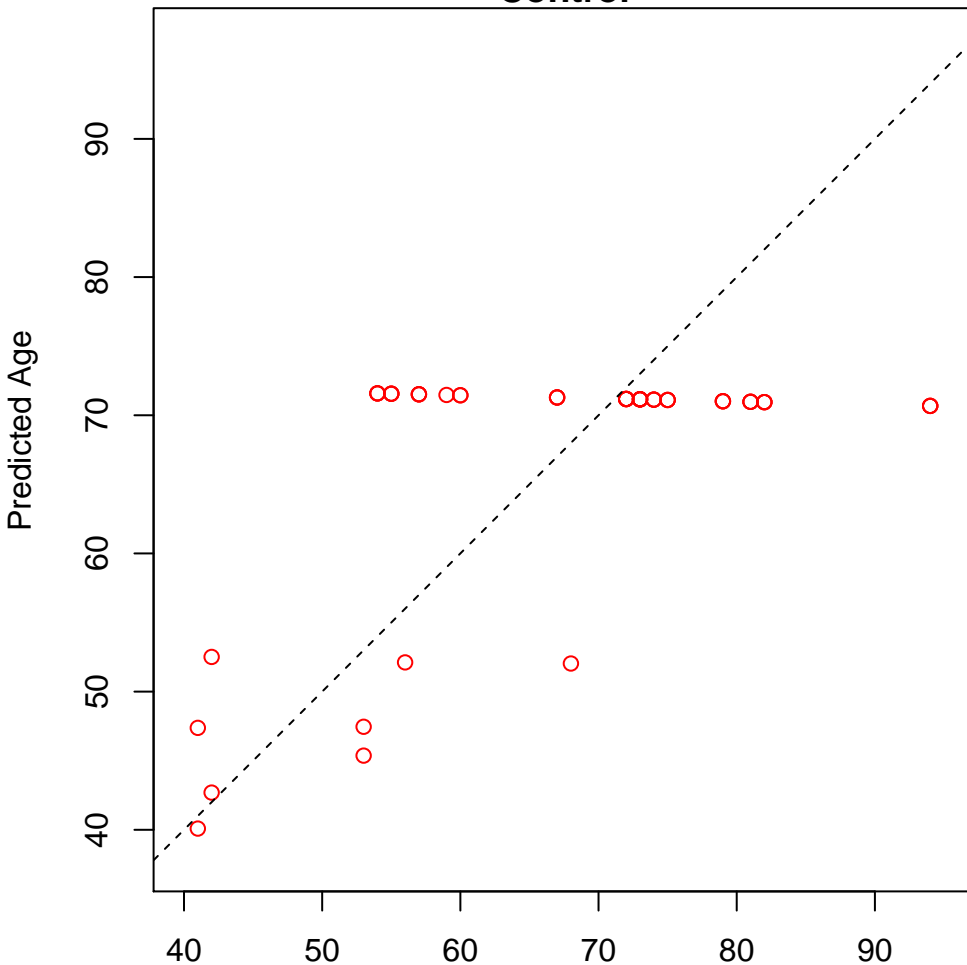


ephrin receptor signaling pathway (Score: 0.813559)

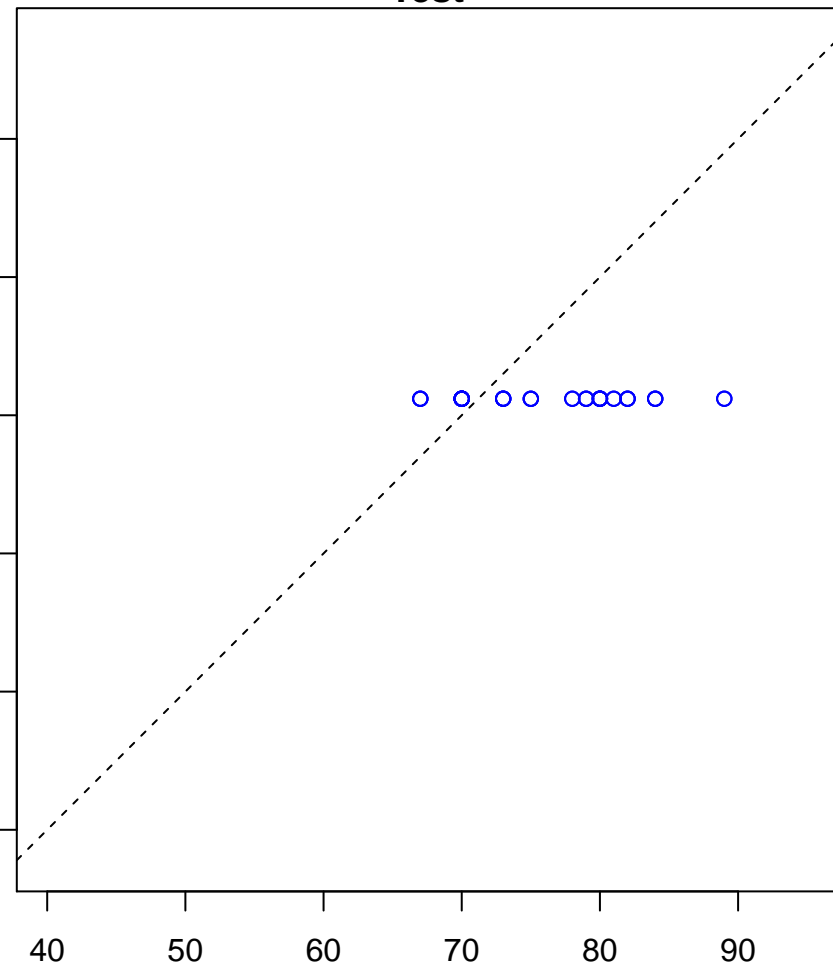


regulation of protein modification process (Score: 0.813497)

Control

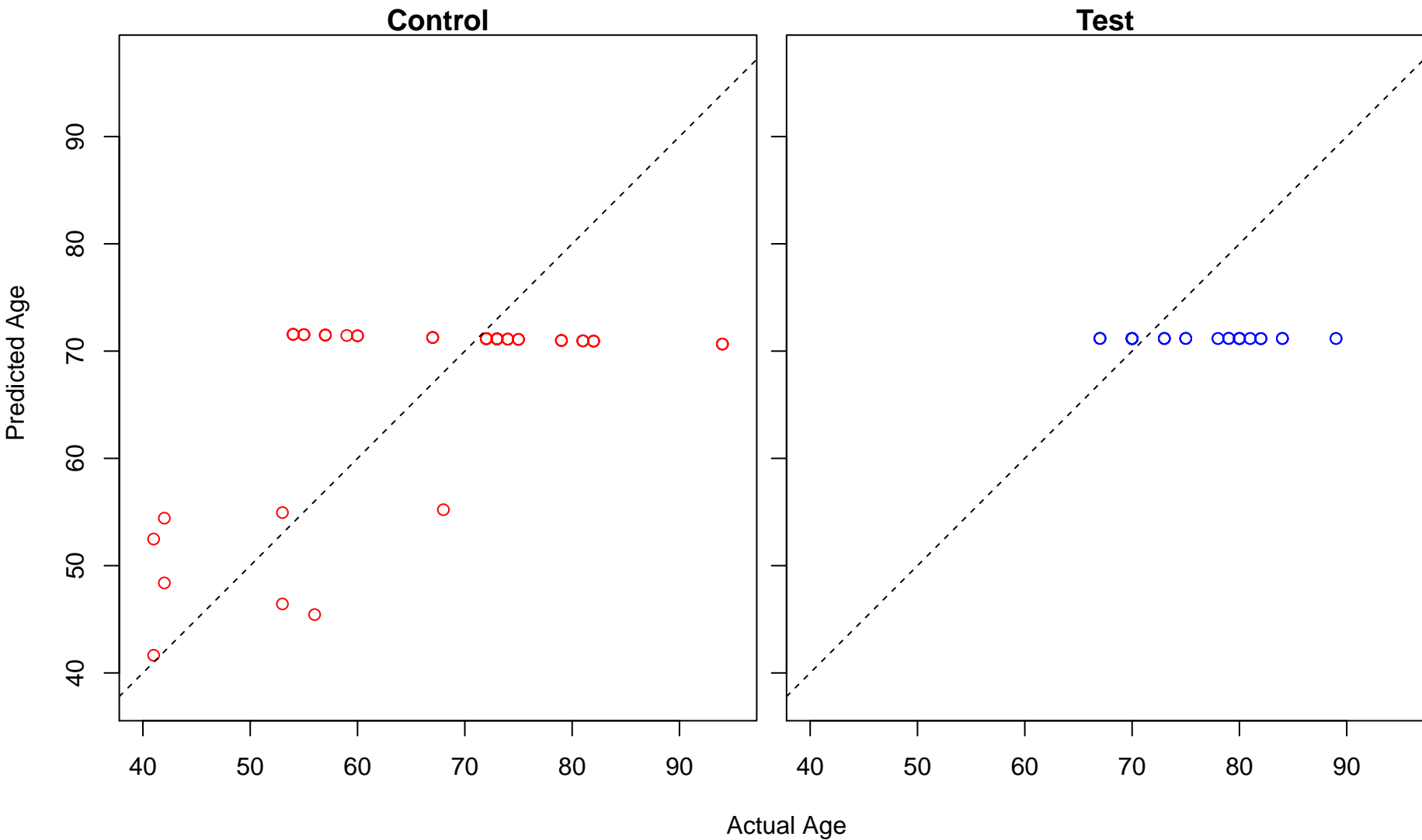


Test

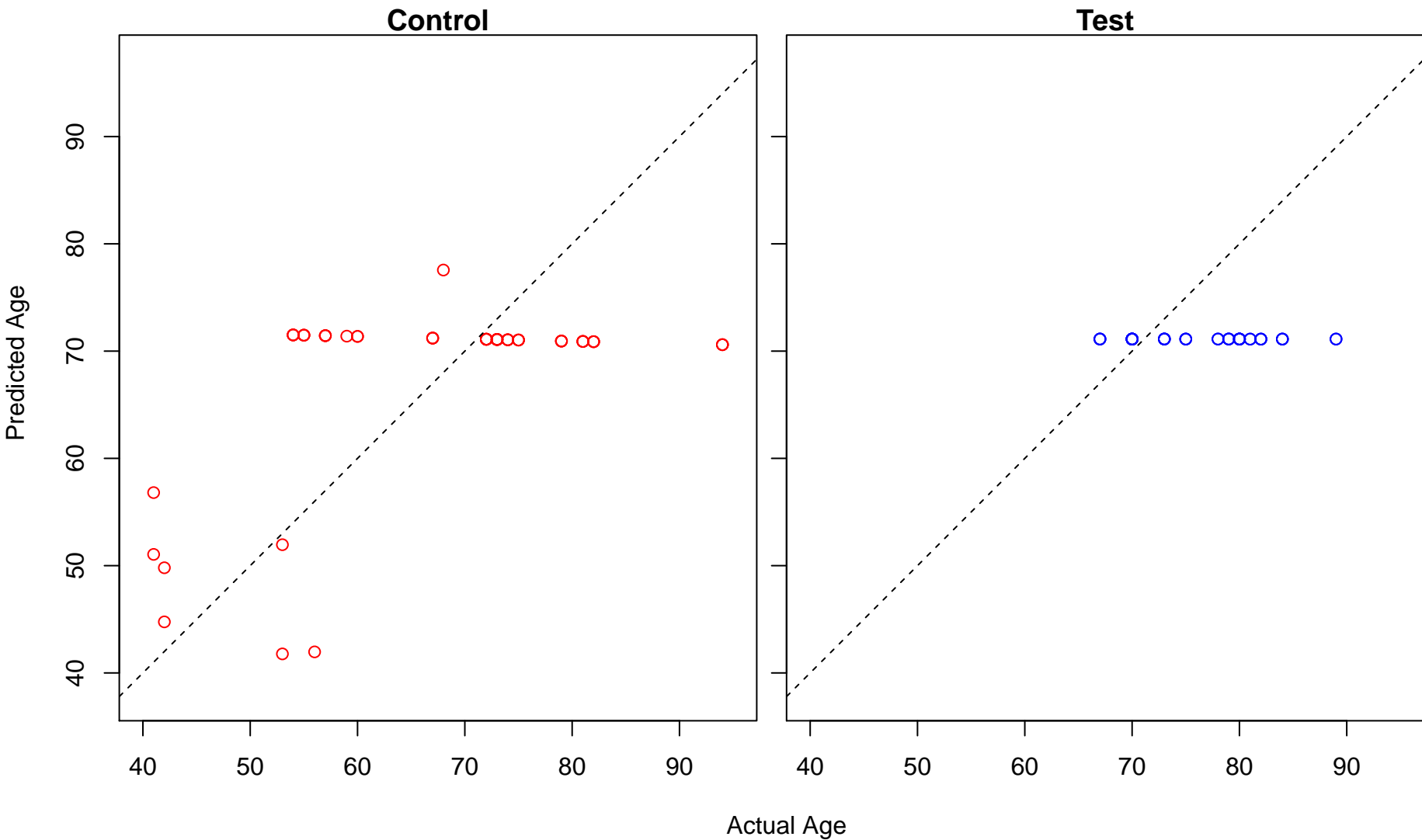


Actual Age

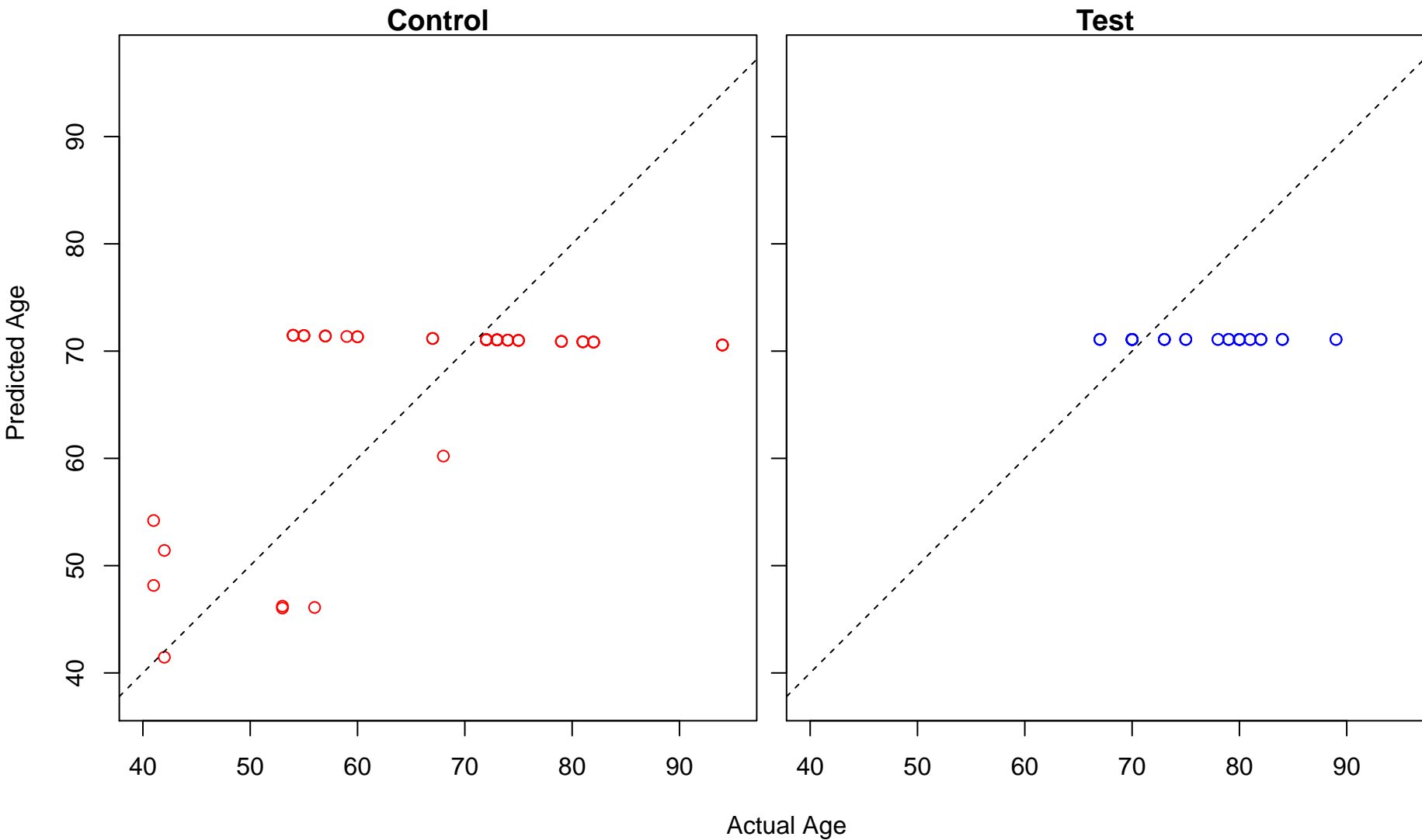
positive regulation of protein complex assembly (Score: 0.813394)



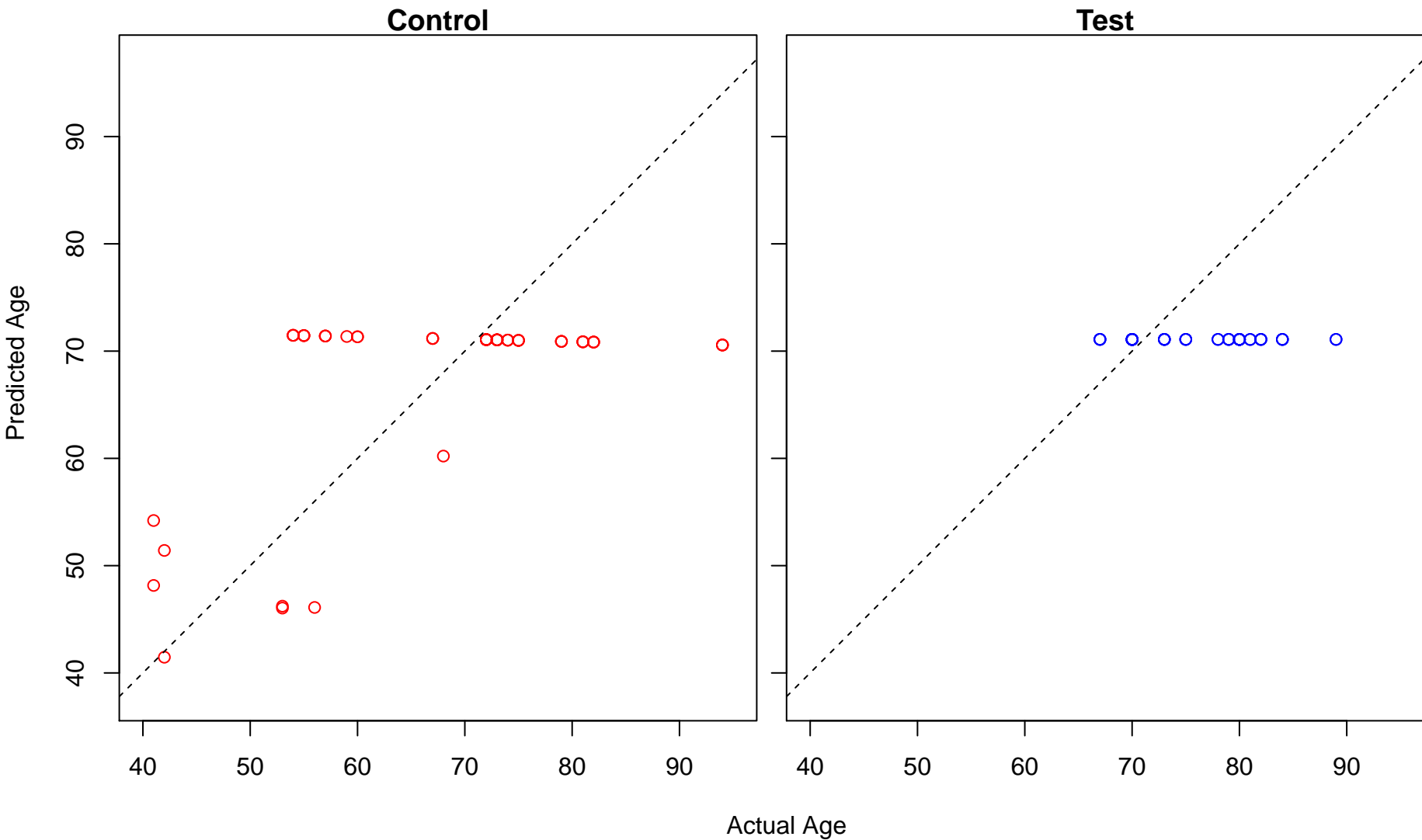
locomotion (Score: 0.813332)



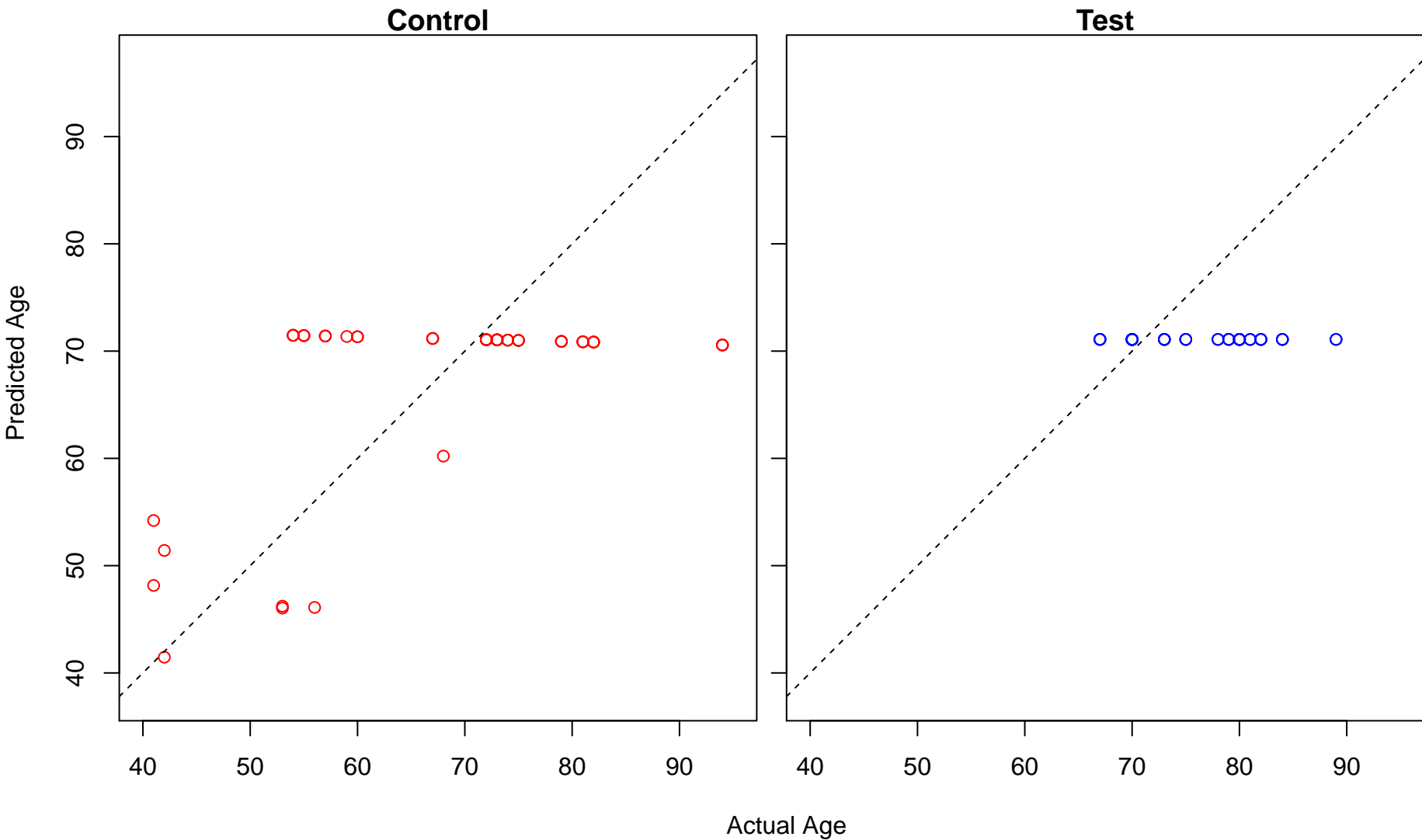
cell projection assembly (Score: 0.813265)



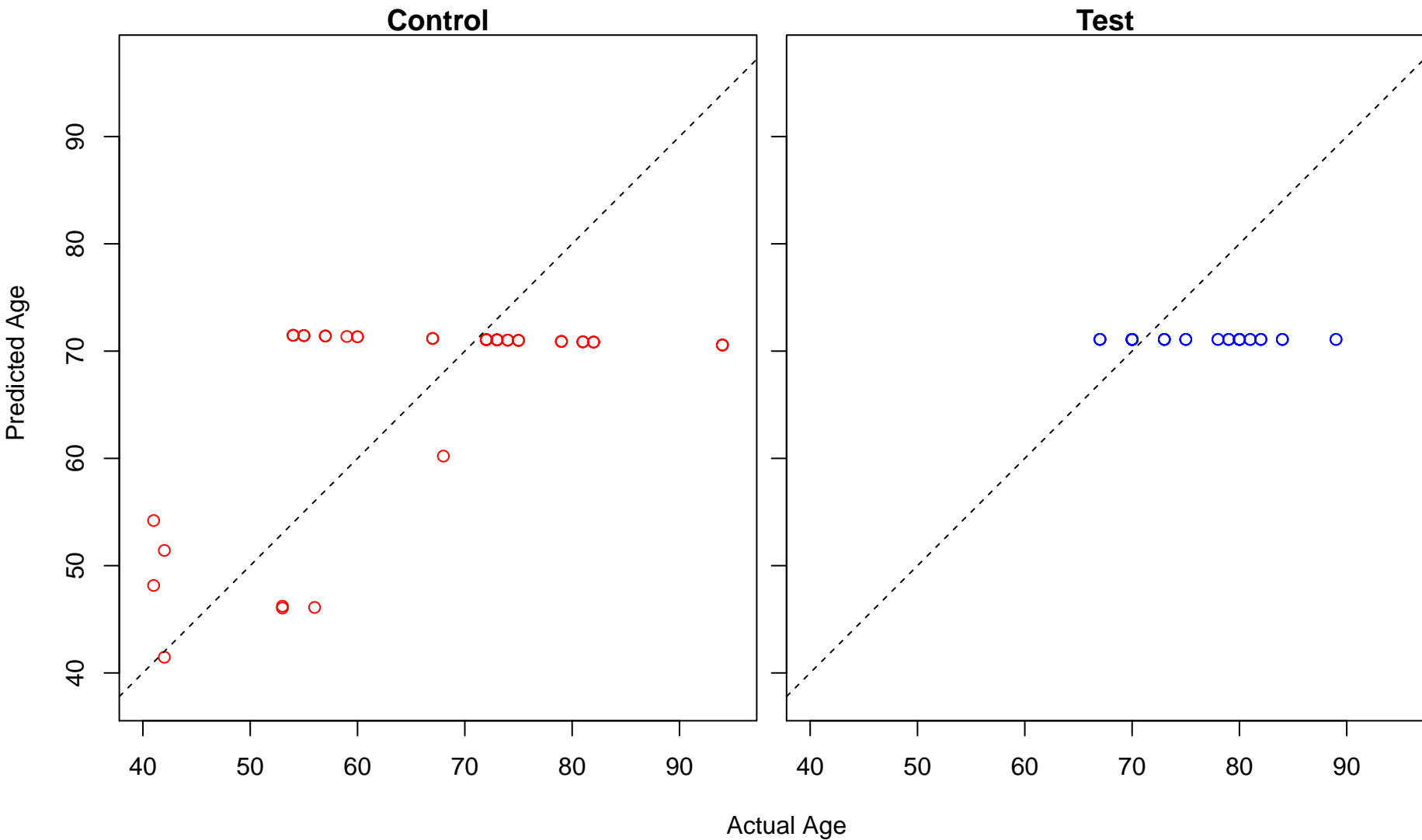
cilium organization (Score: 0.813265)



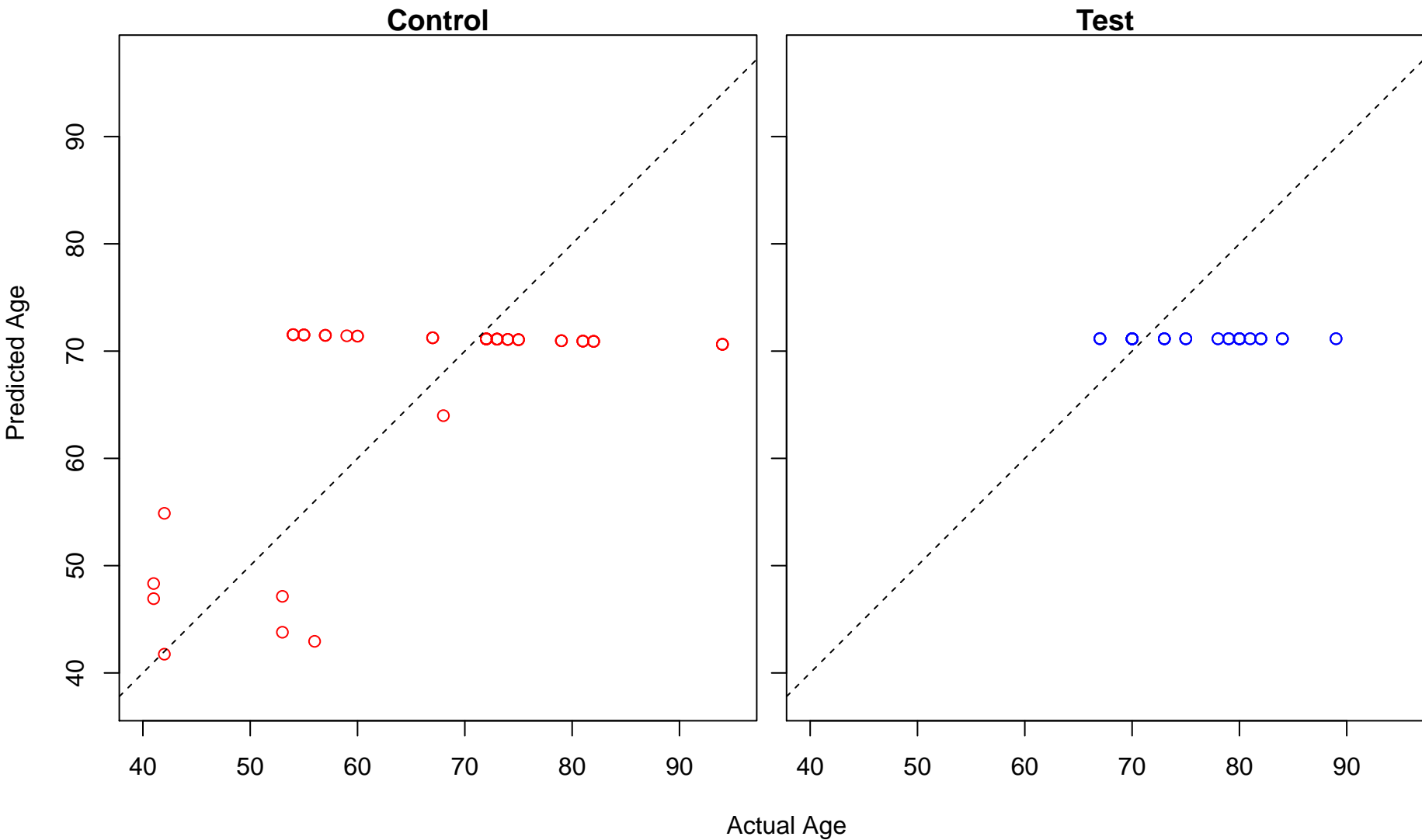
cilium assembly (Score: 0.813265)



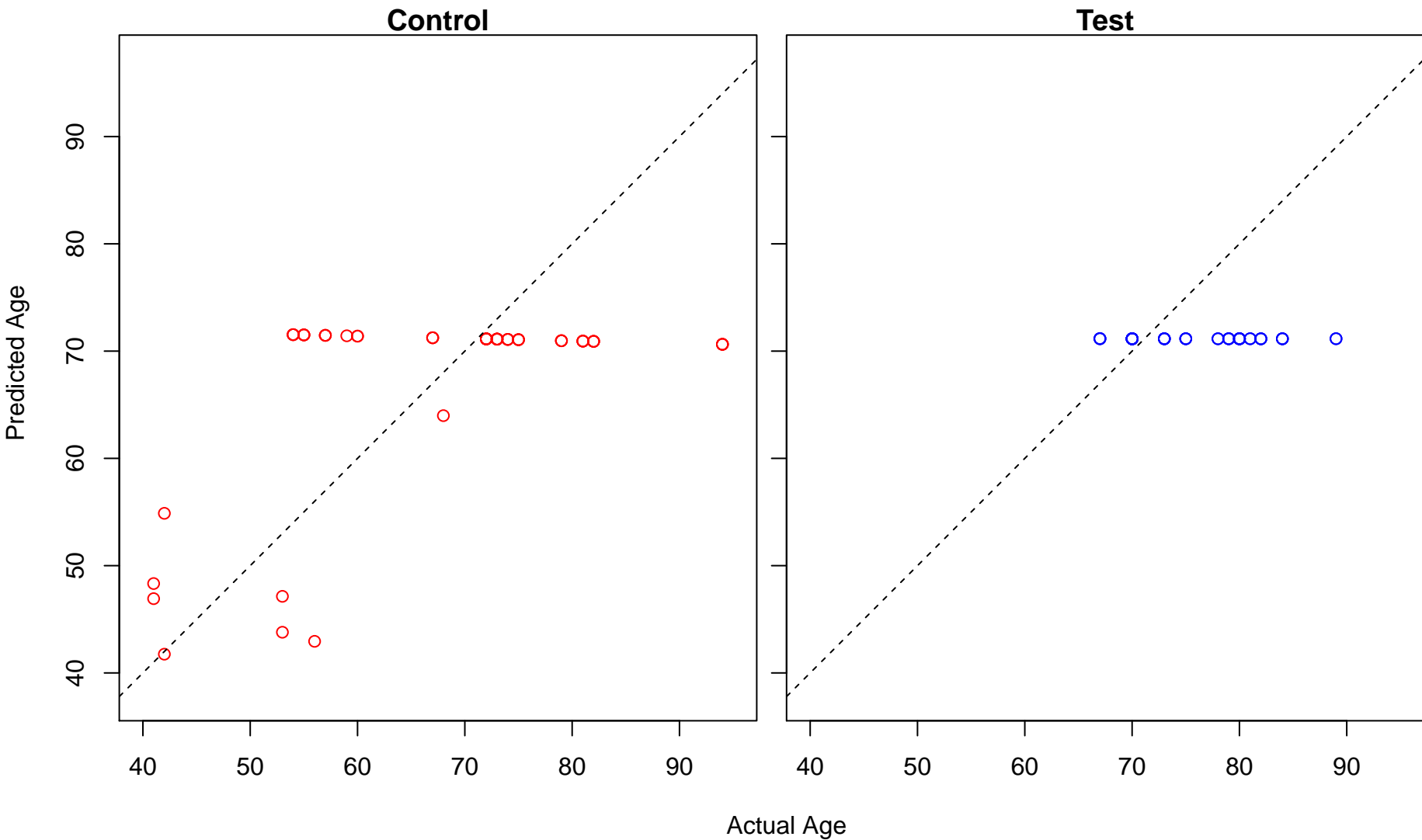
plasma membrane bounded cell projection assembly (Score: 0.813265)



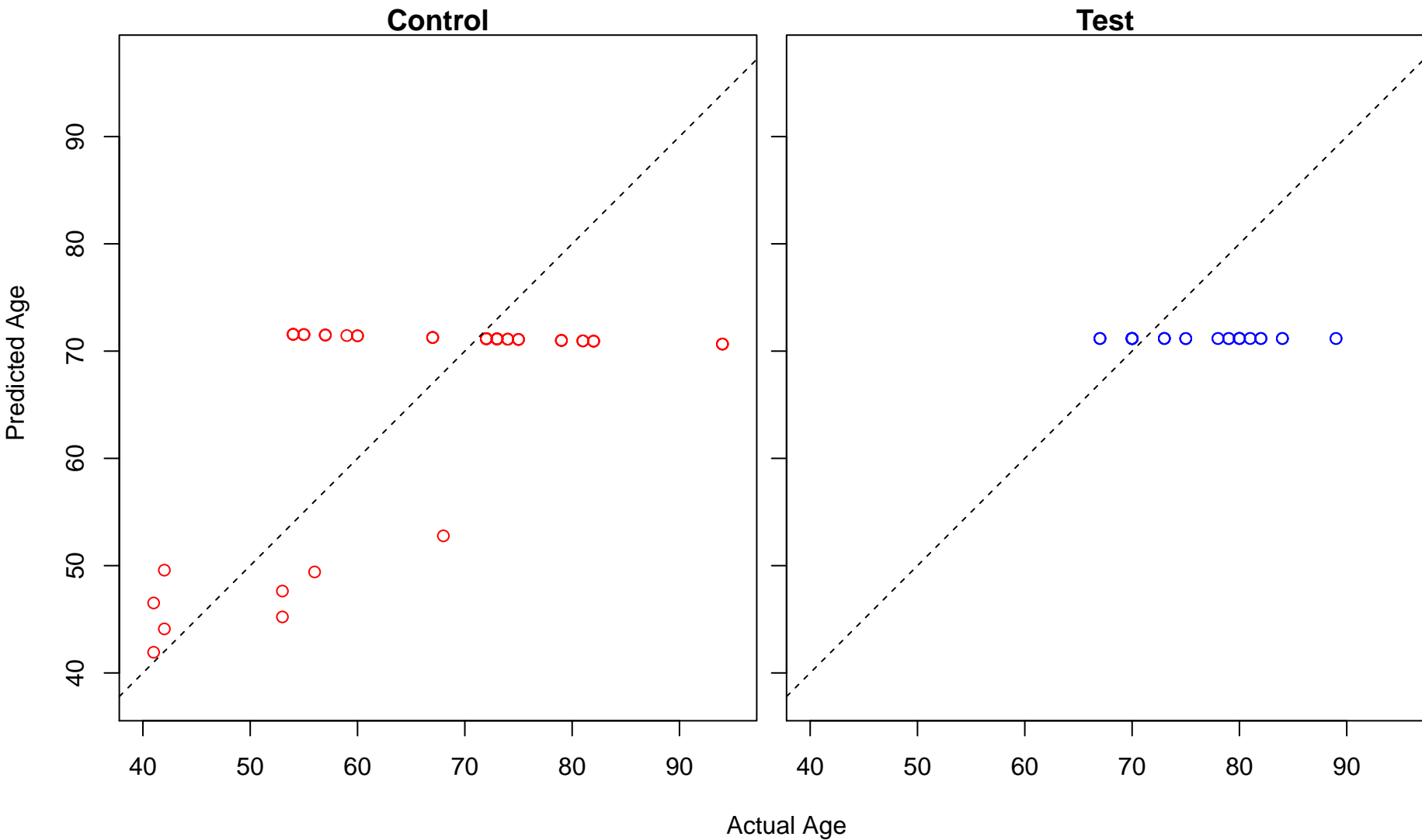
regulation of mRNA splicing, via spliceosome (Score: 0.813234)



regulation of mRNA processing (Score: 0.813234)

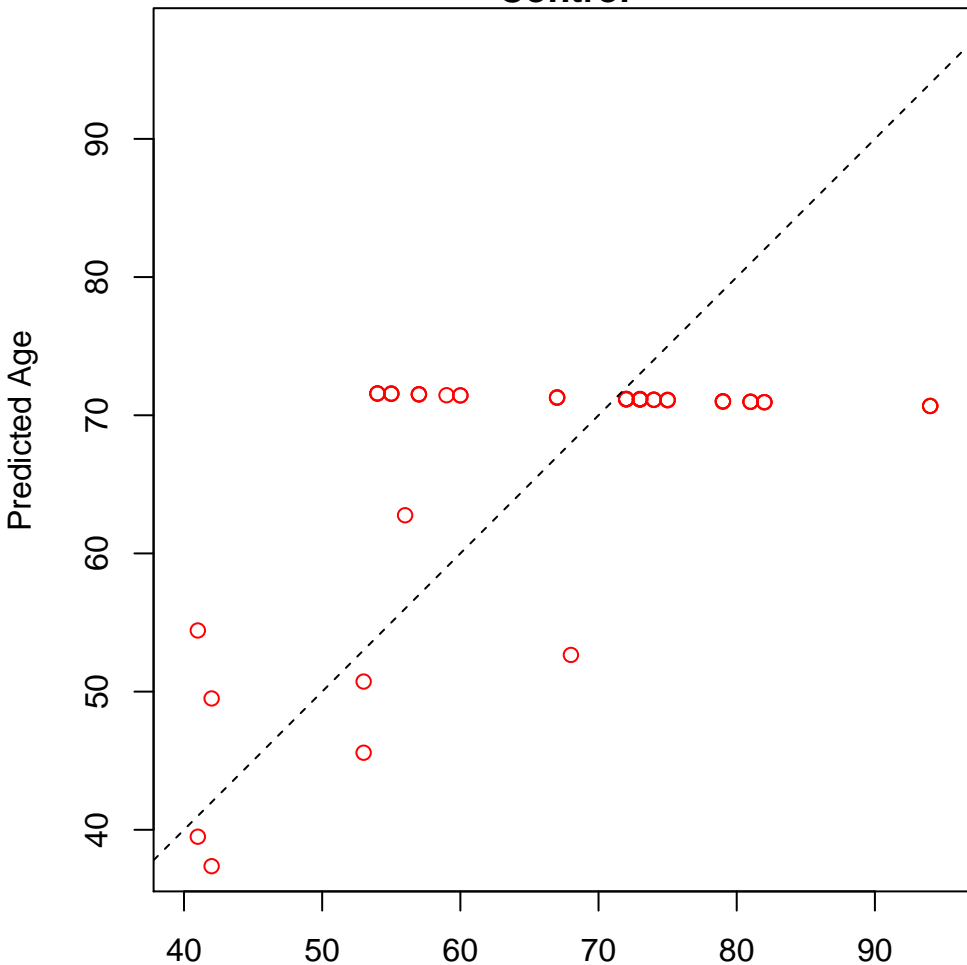


regulation of phosphorylation (Score: 0.813211)

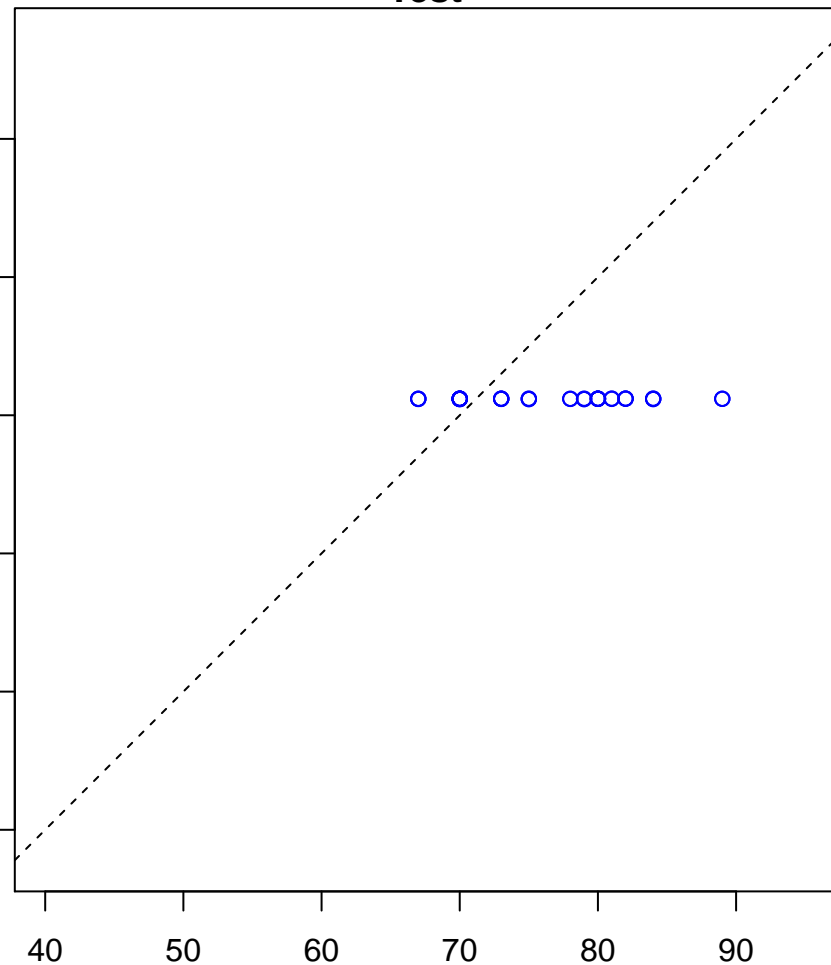


osteoblast differentiation (Score: 0.813192)

Control

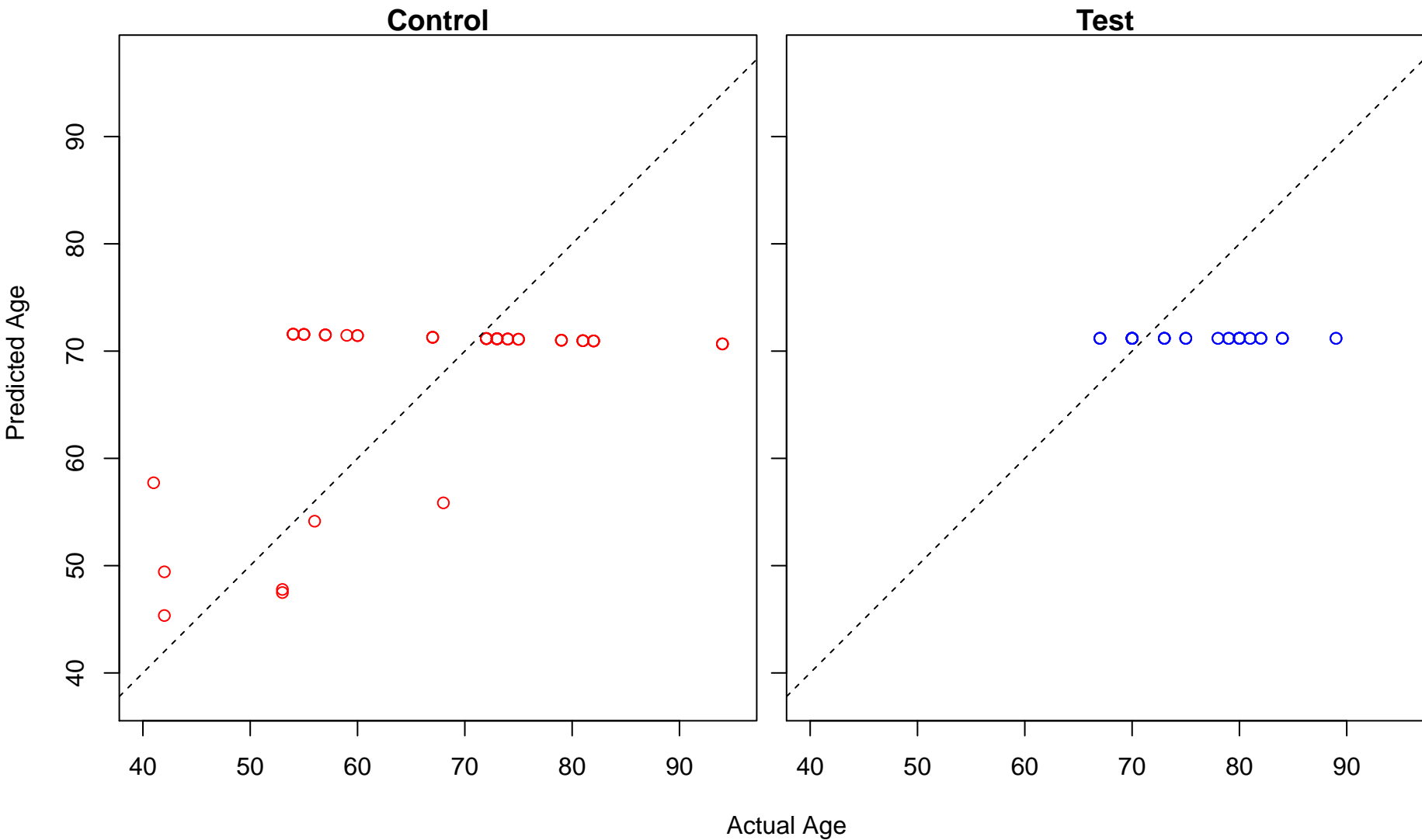


Test

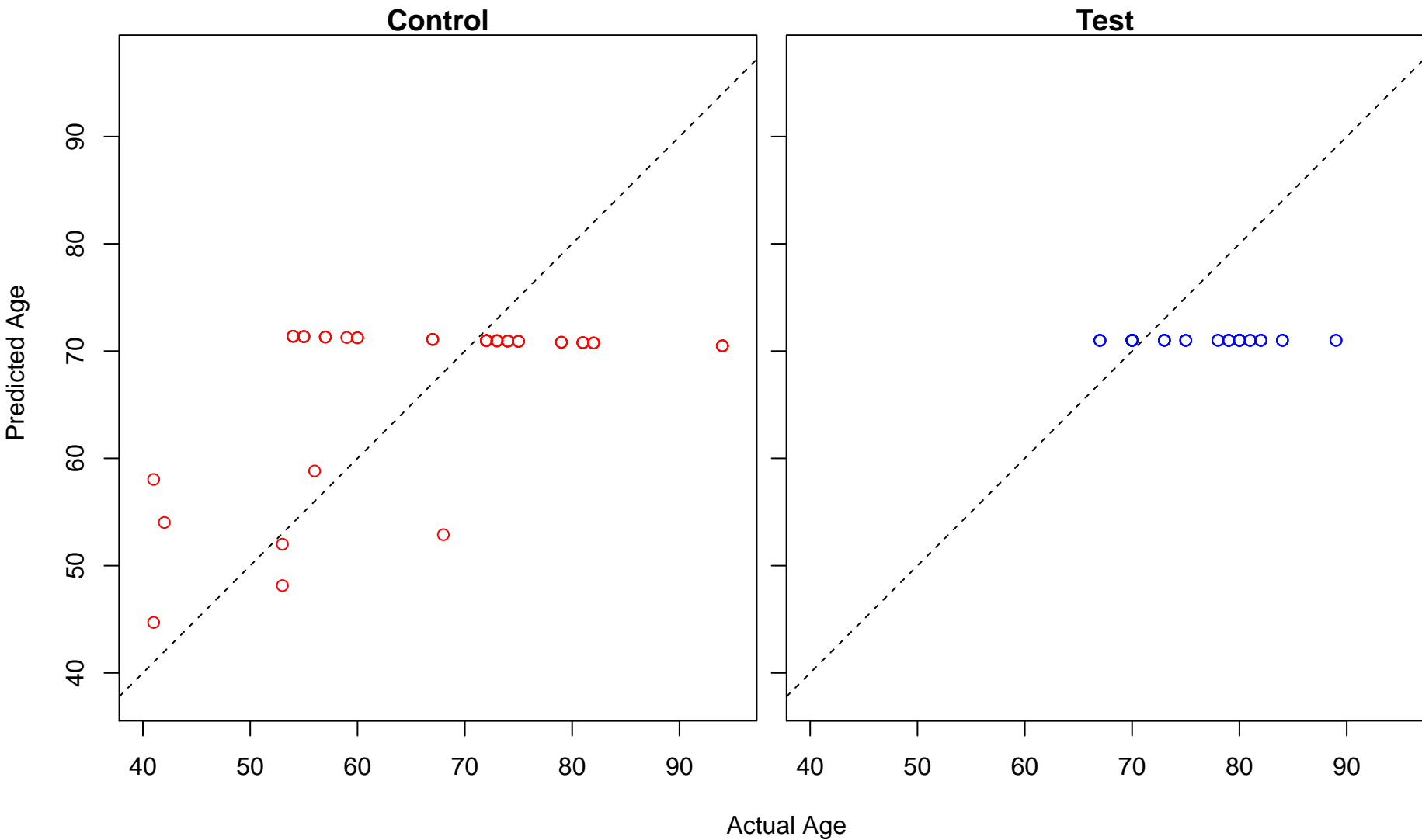


Actual Age

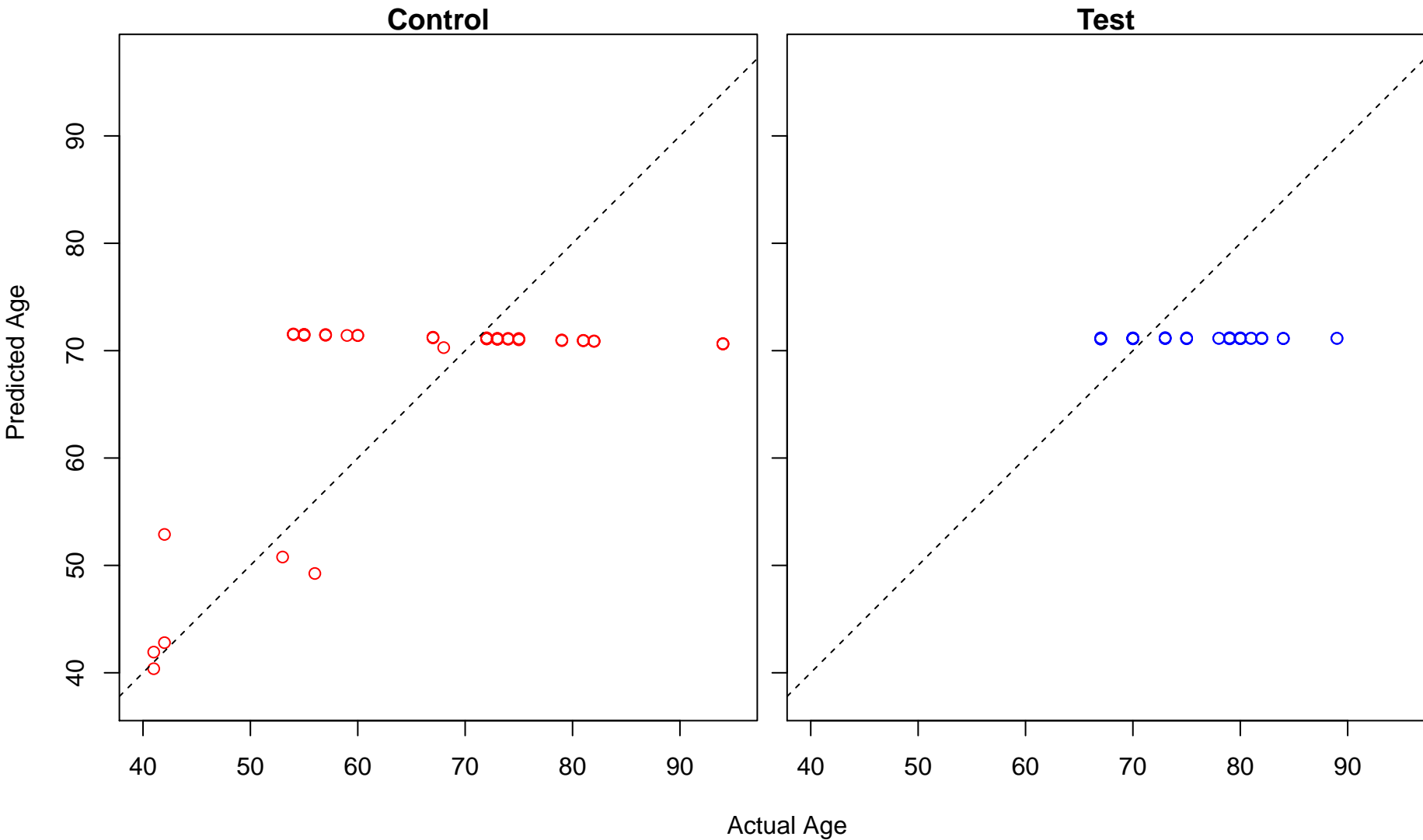
energy derivation by oxidation of organic compounds (Score: 0.813181)



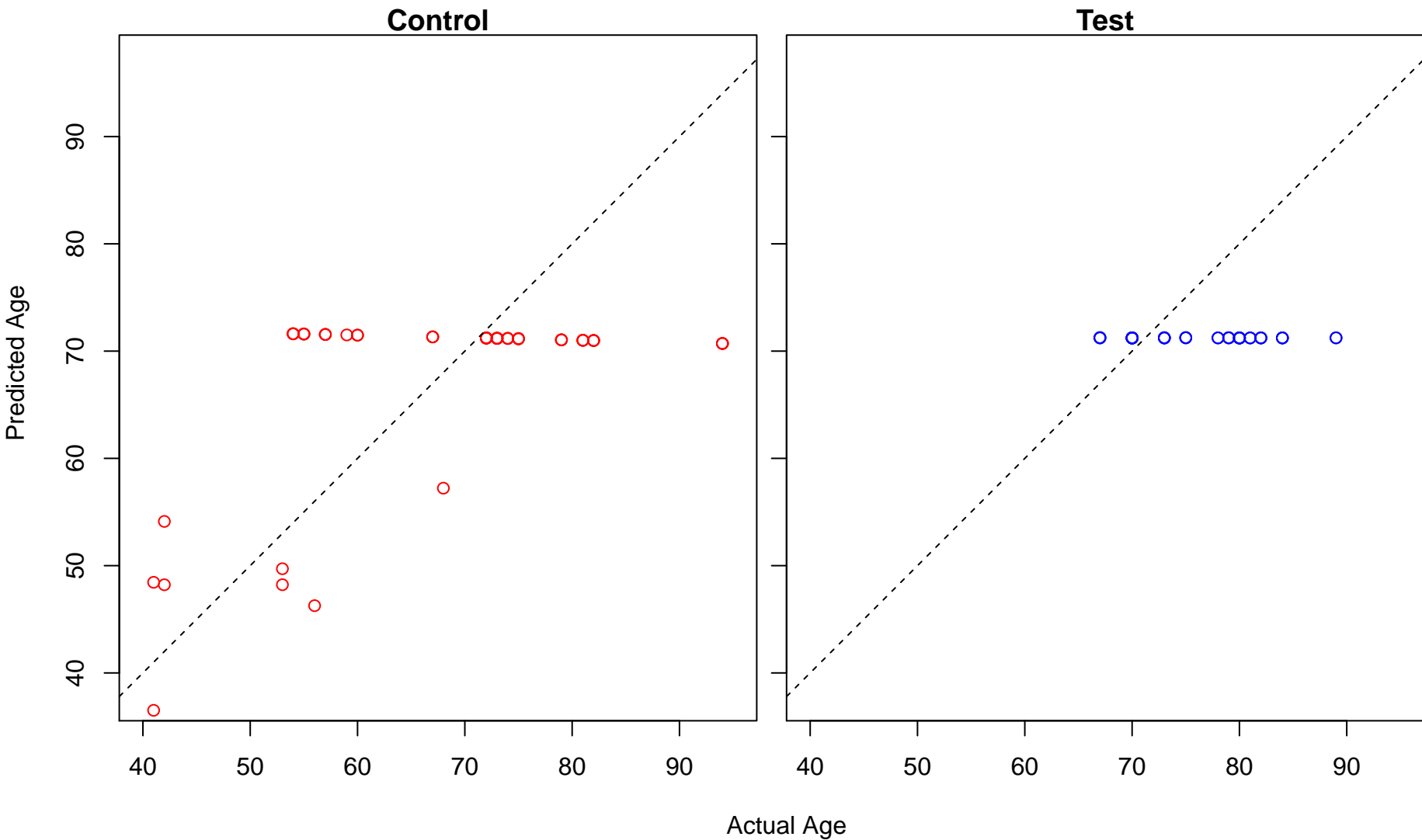
coenzyme metabolic process (Score: 0.813112)



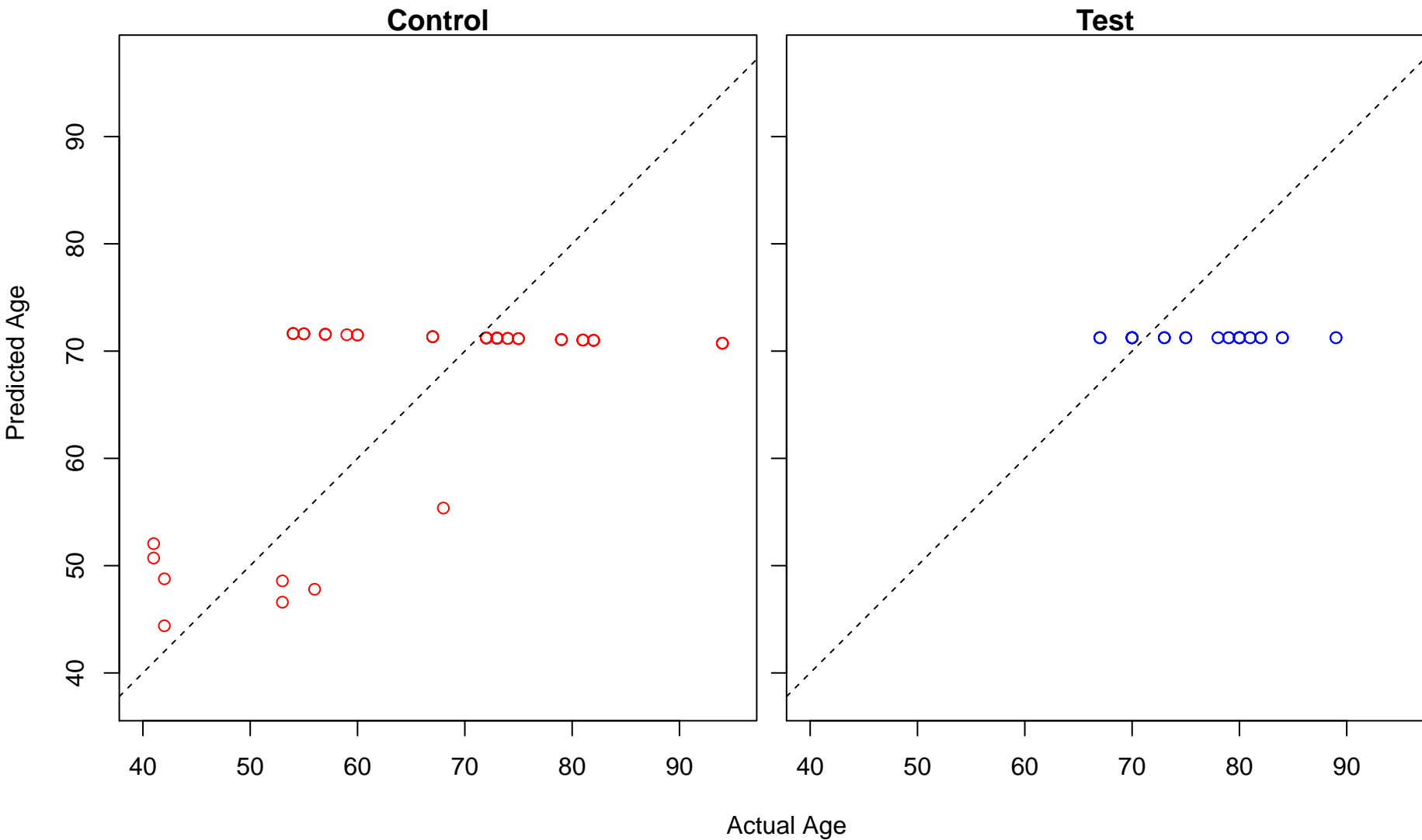
positive regulation of lymphocyte activation (Score: 0.813083)



negative regulation of intracellular protein transport (Score: 0.813057)

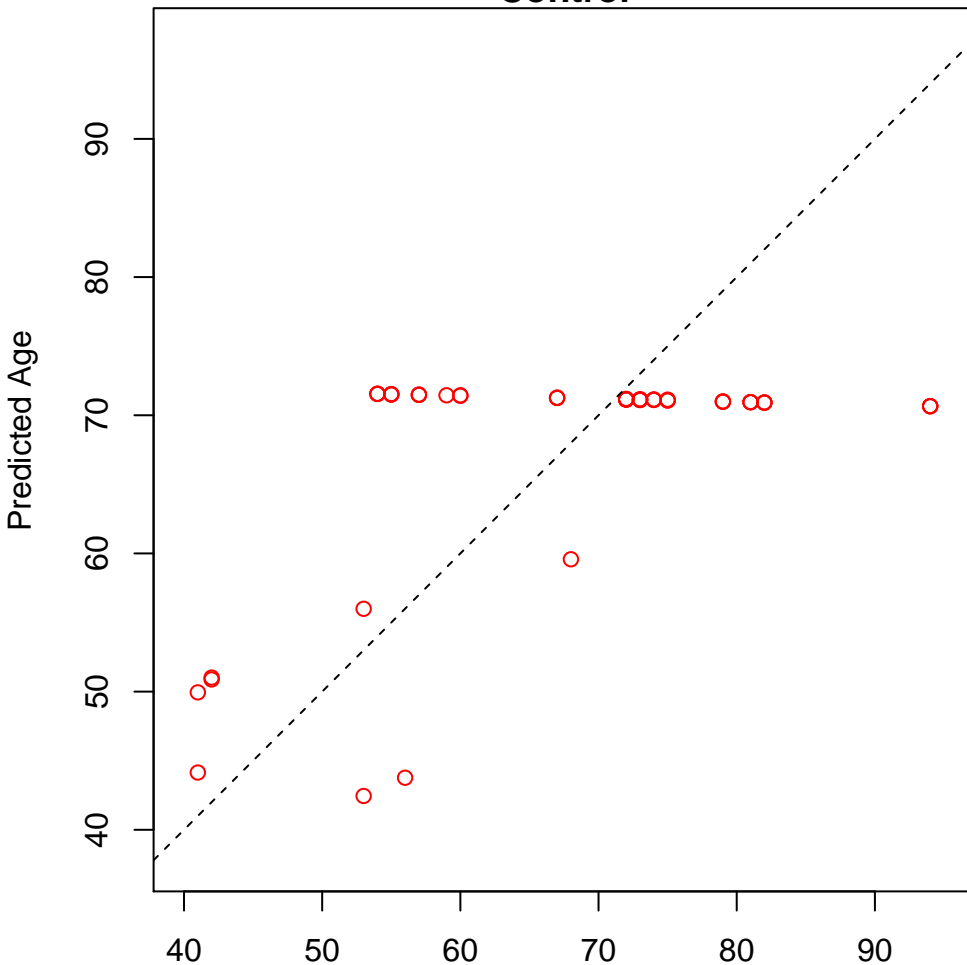


positive regulation of intracellular transport (Score: 0.813032)

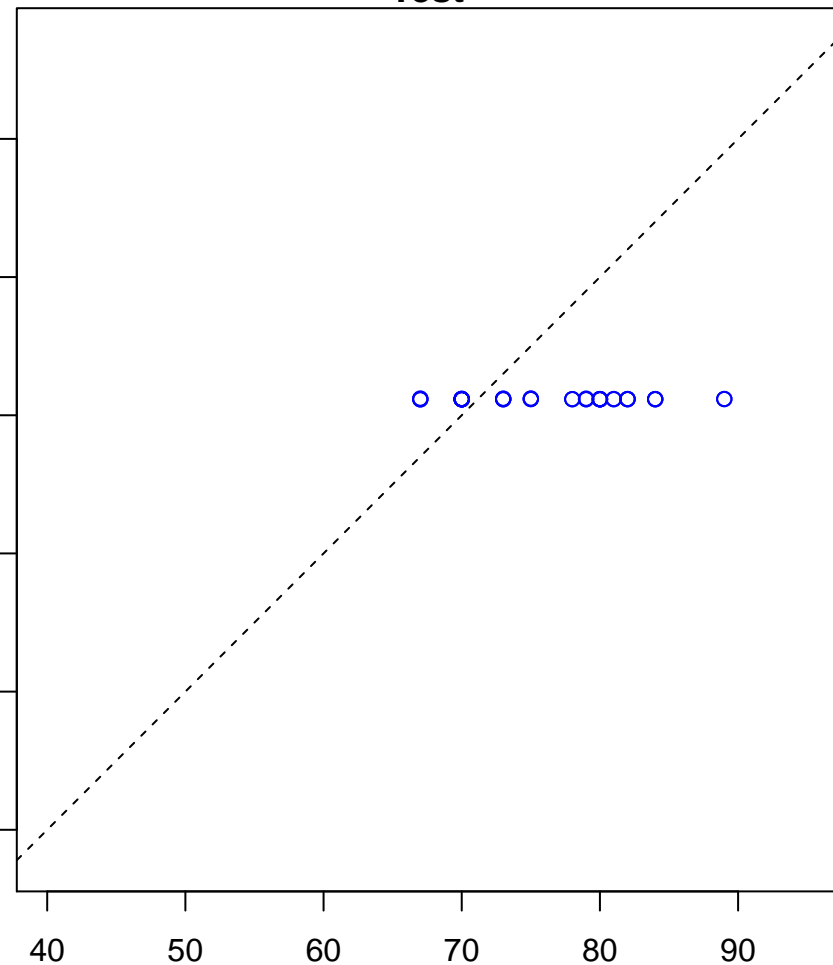


protein localization to plasma membrane (Score: 0.812960)

Control



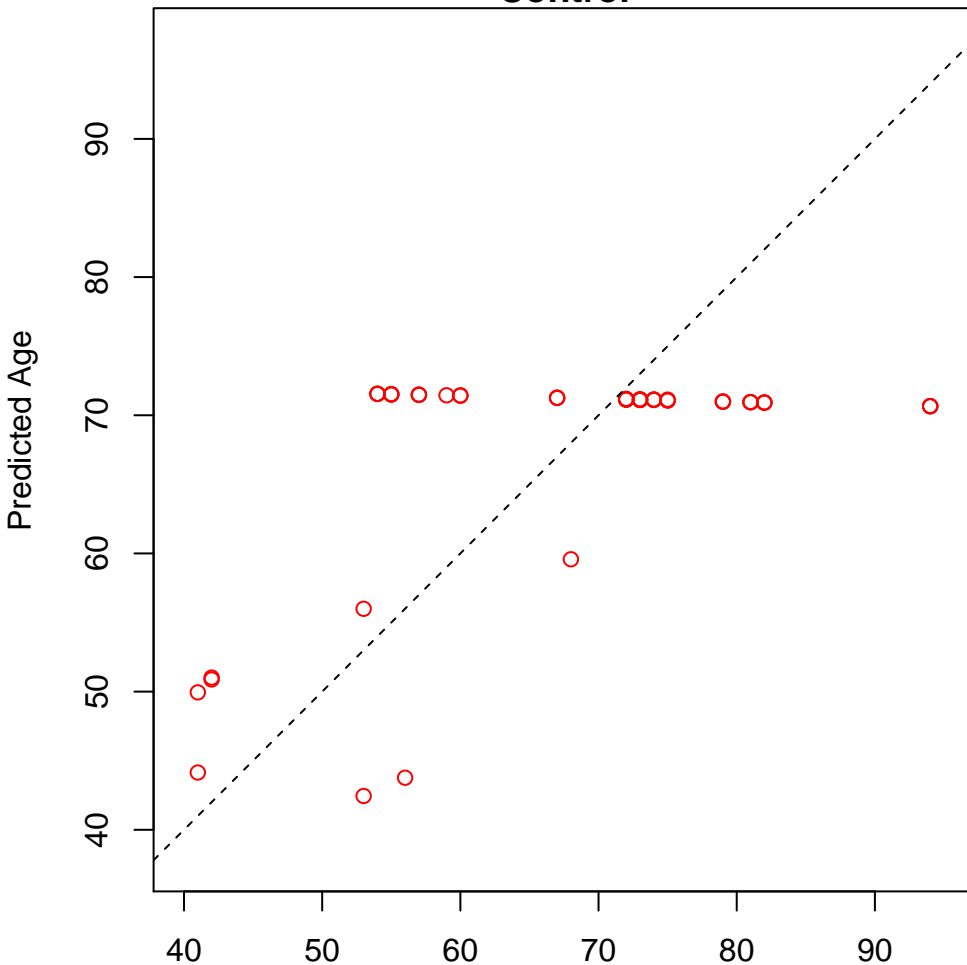
Test



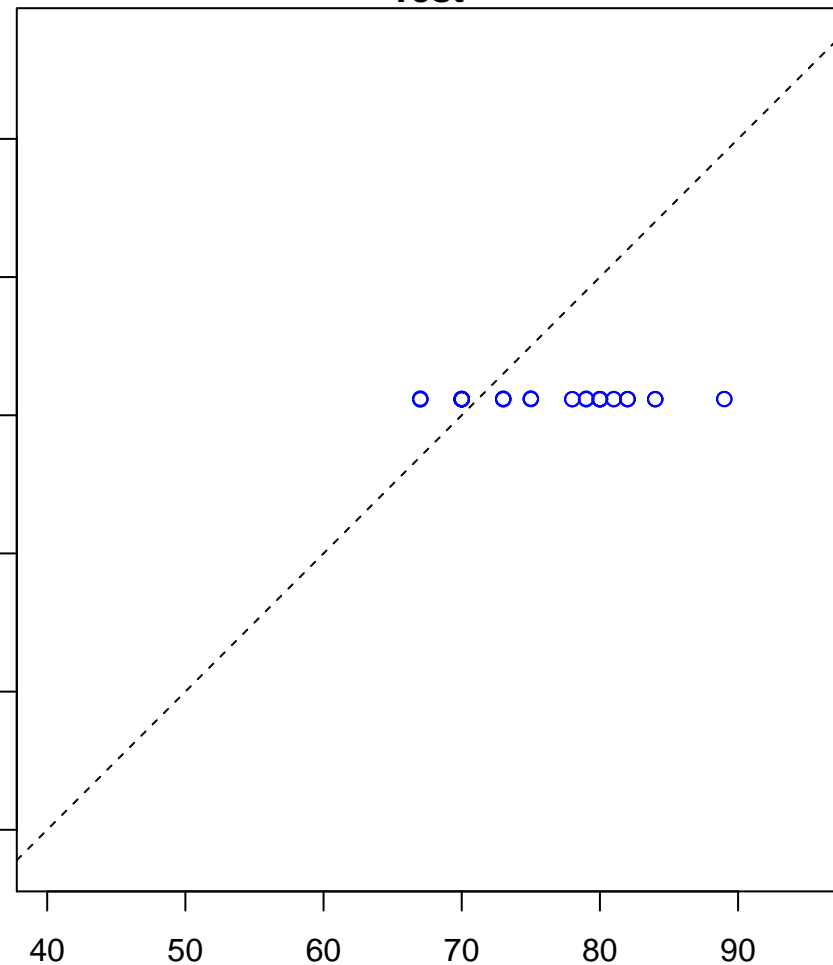
Actual Age

protein localization to cell periphery (Score: 0.812960)

Control

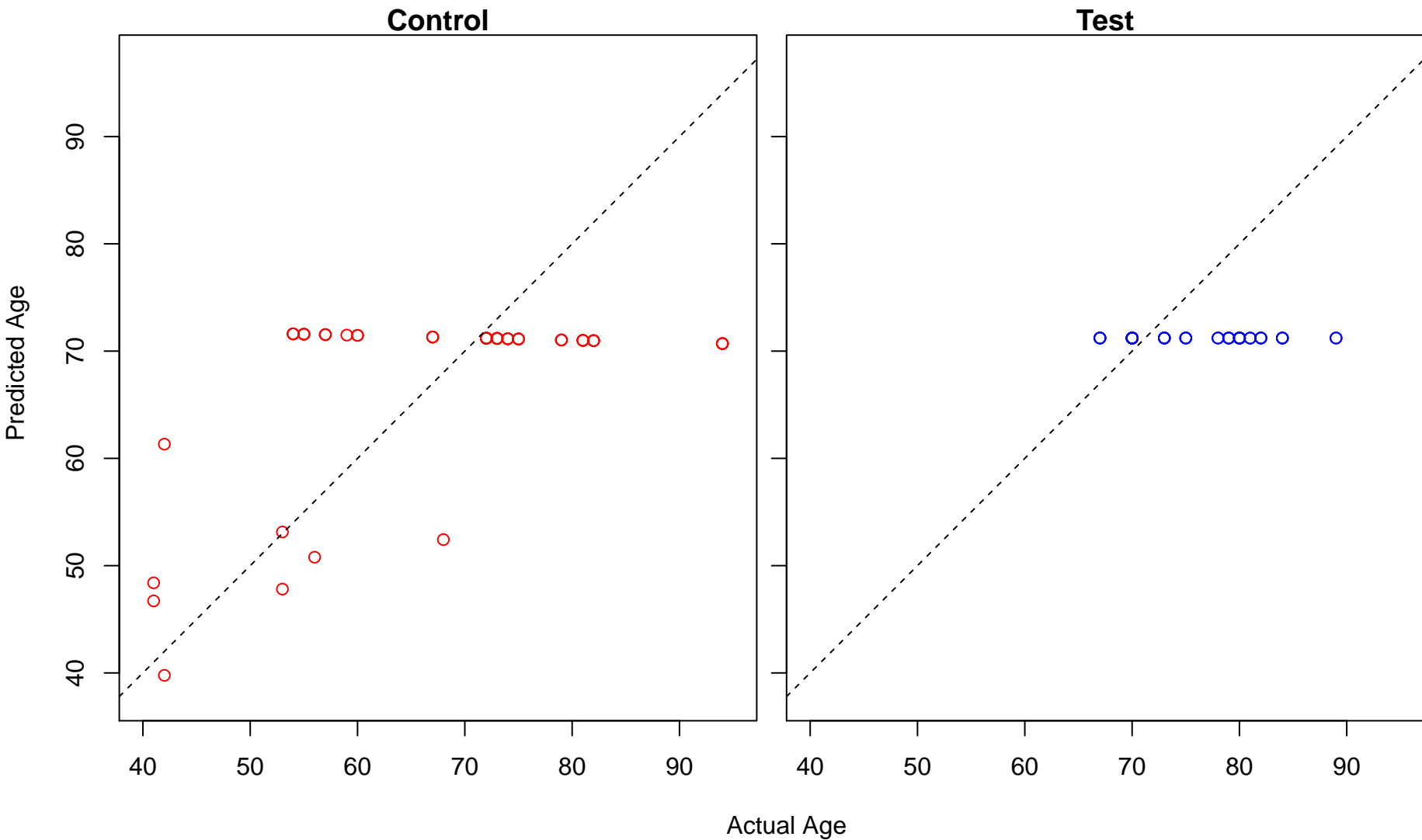


Test

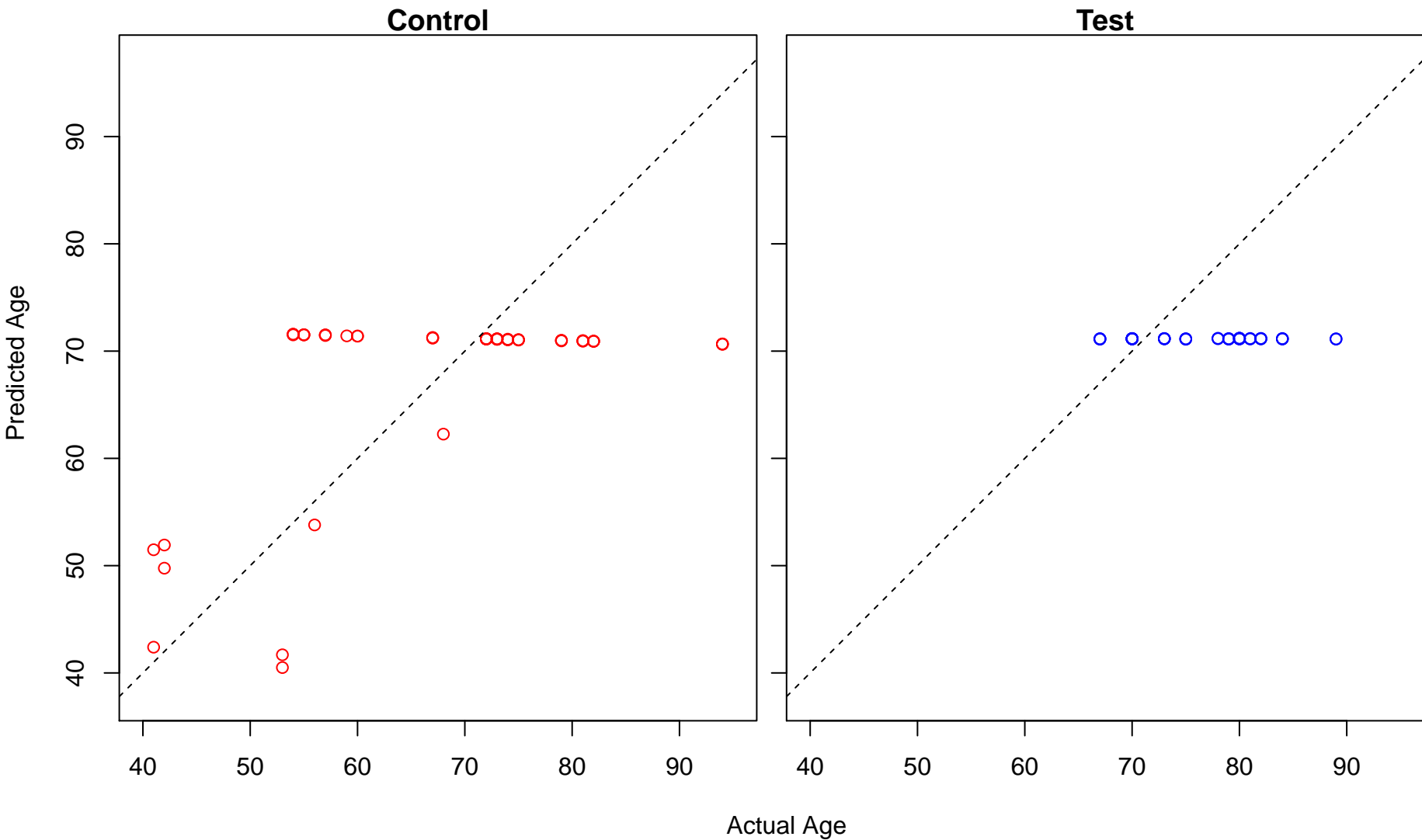


Actual Age

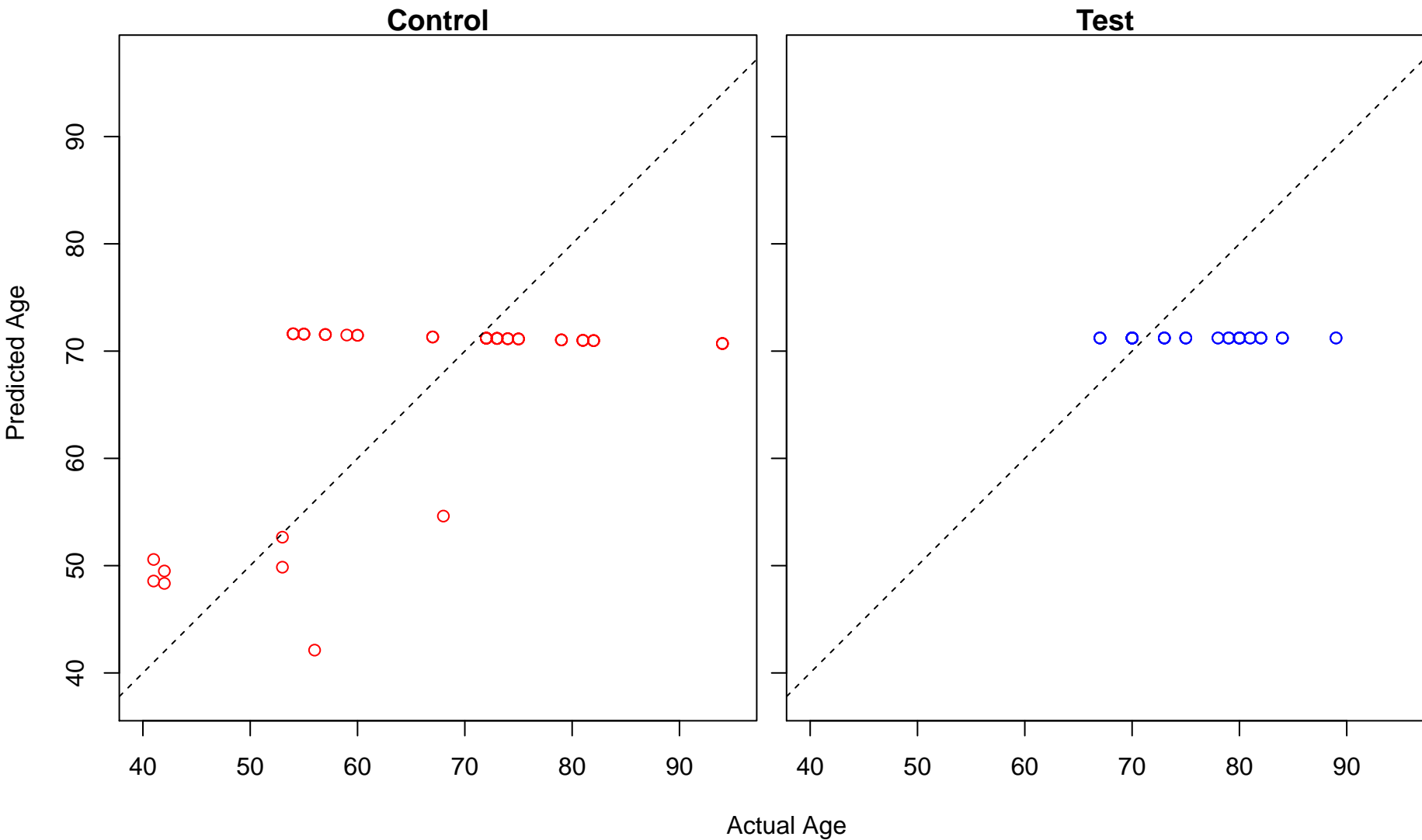
negative regulation of cellular protein localization (Score: 0.812923)



axon development (Score: 0.812888)

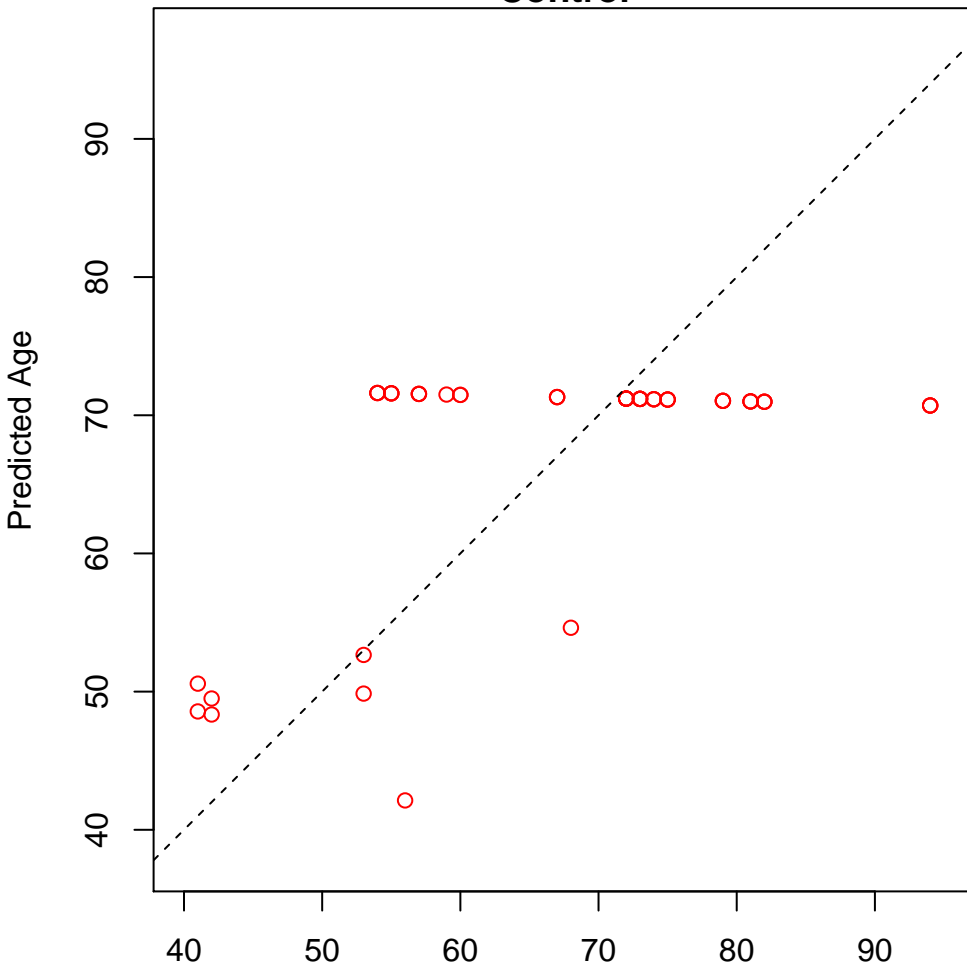


myeloid cell homeostasis (Score: 0.812781)

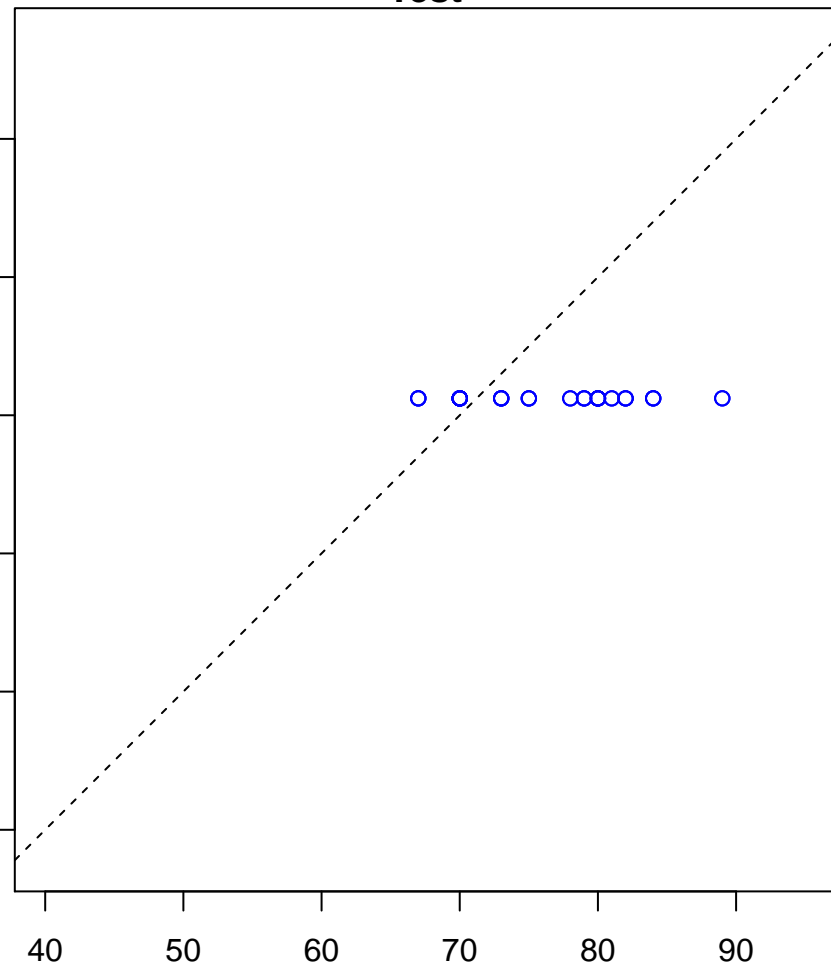


homeostasis of number of cells (Score: 0.812781)

Control

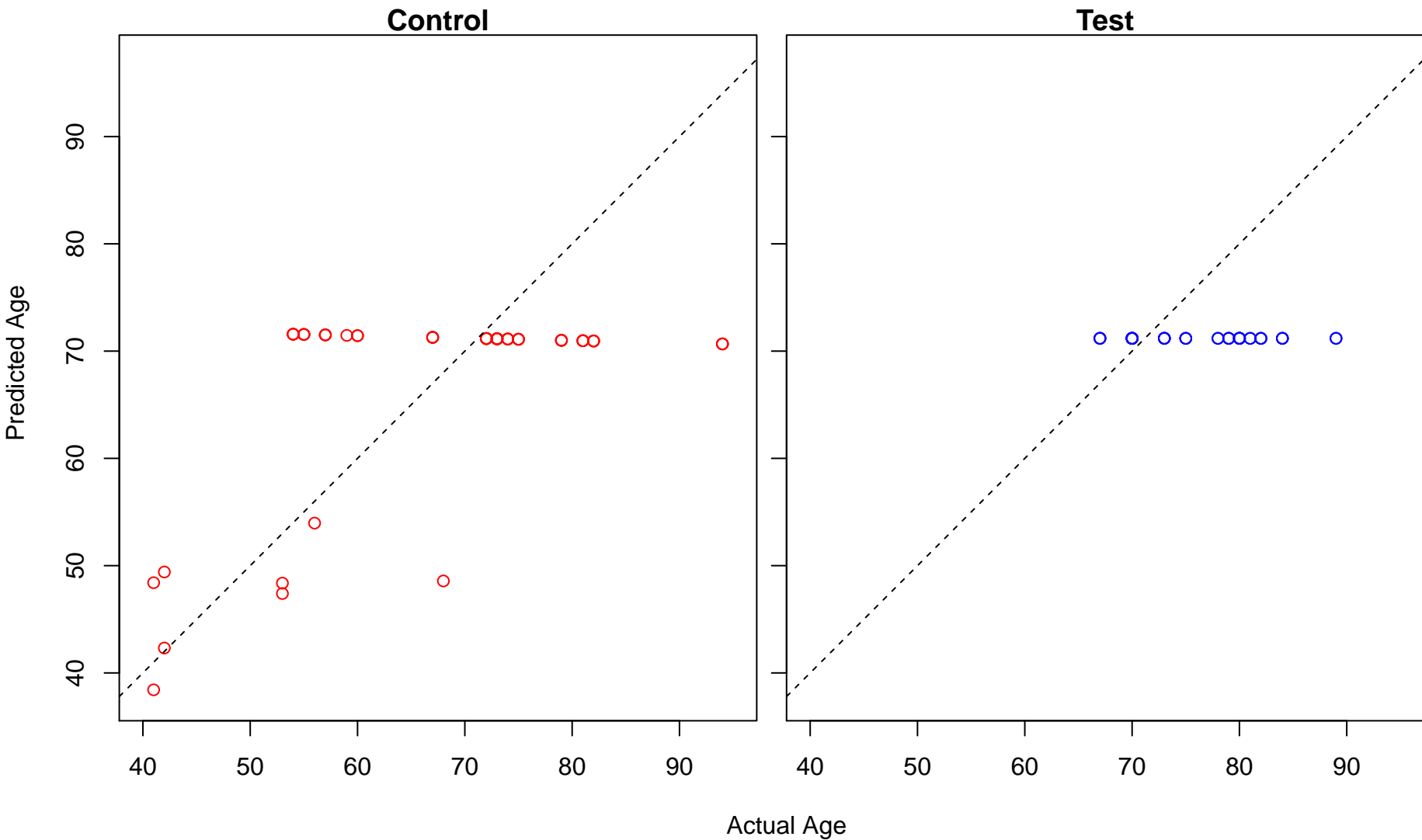


Test



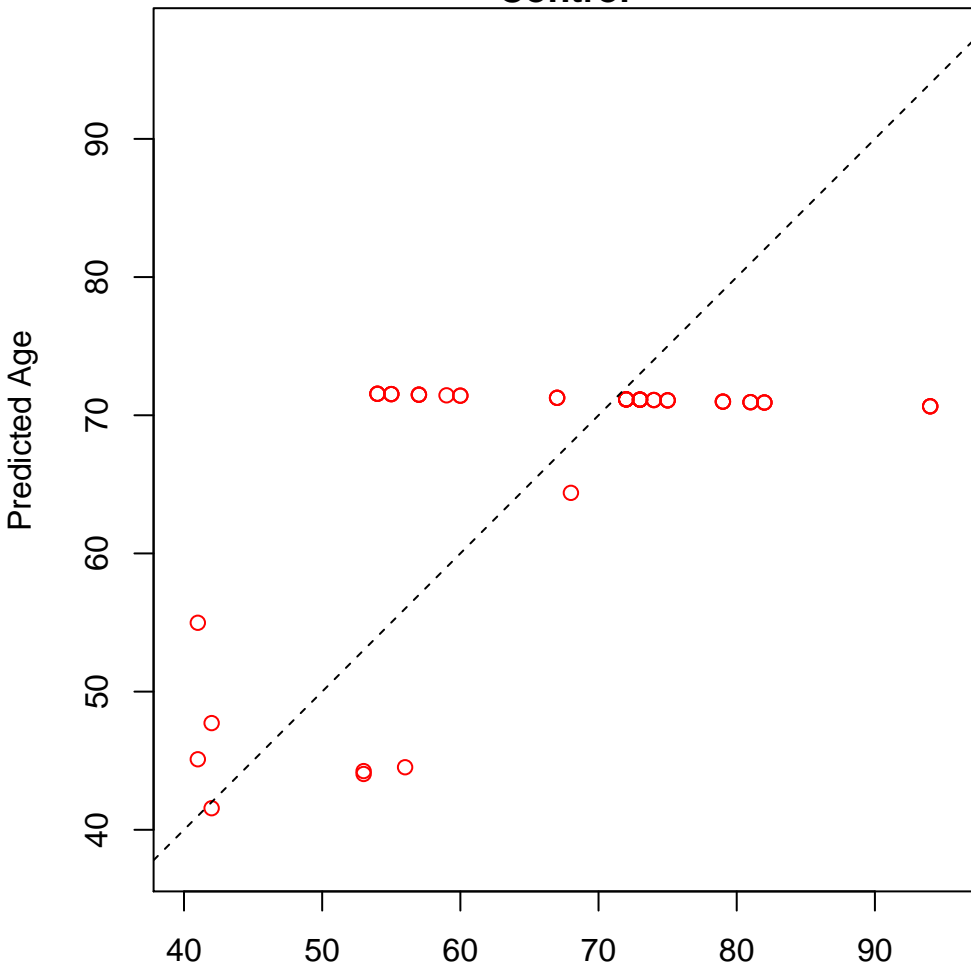
Actual Age

regulation of response to stress (Score: 0.812769)

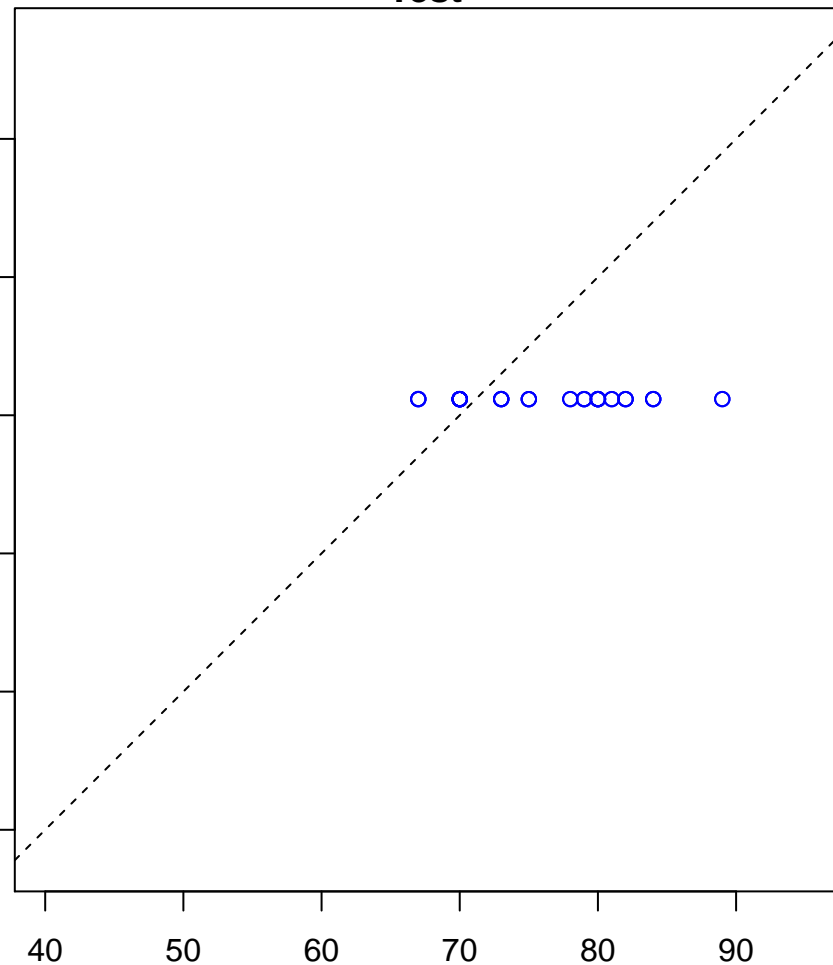


nervous system development (Score: 0.812699)

Control



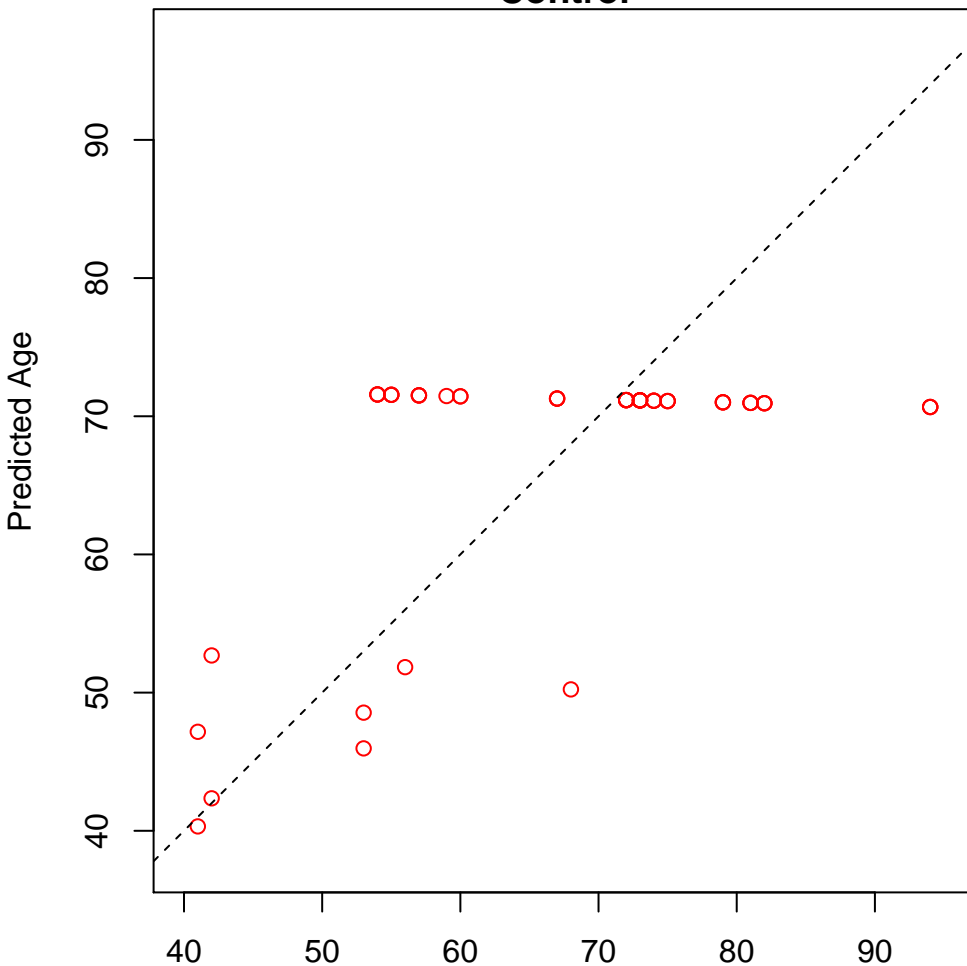
Test



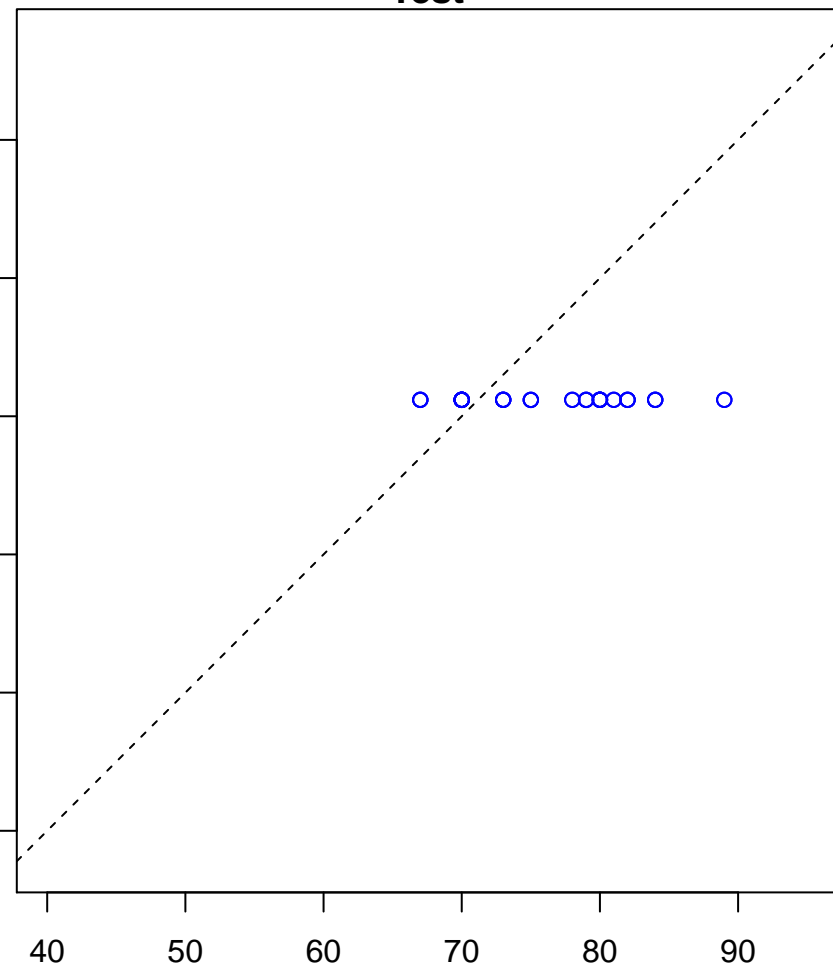
Actual Age

positive regulation of molecular function (Score: 0.812600)

Control

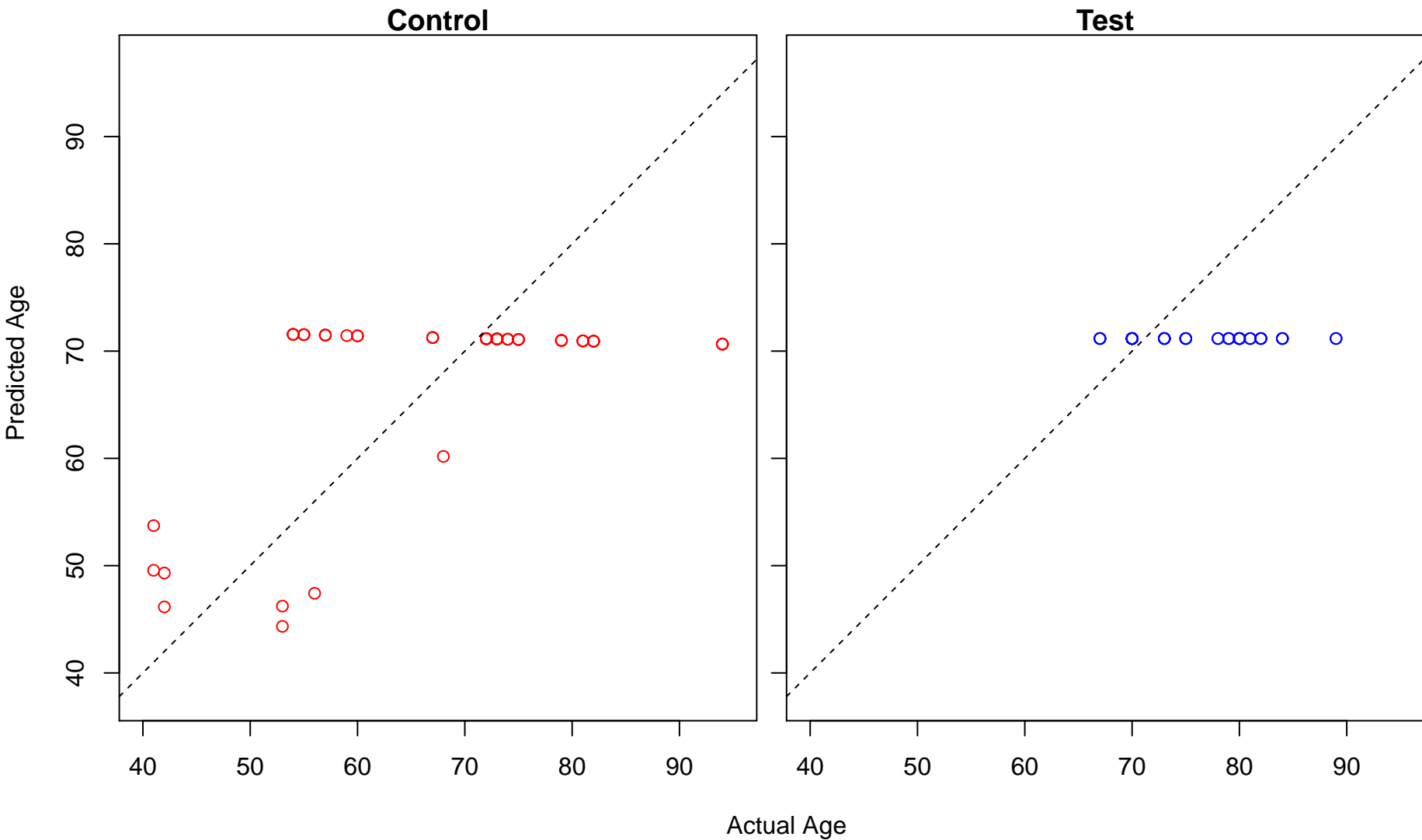


Test

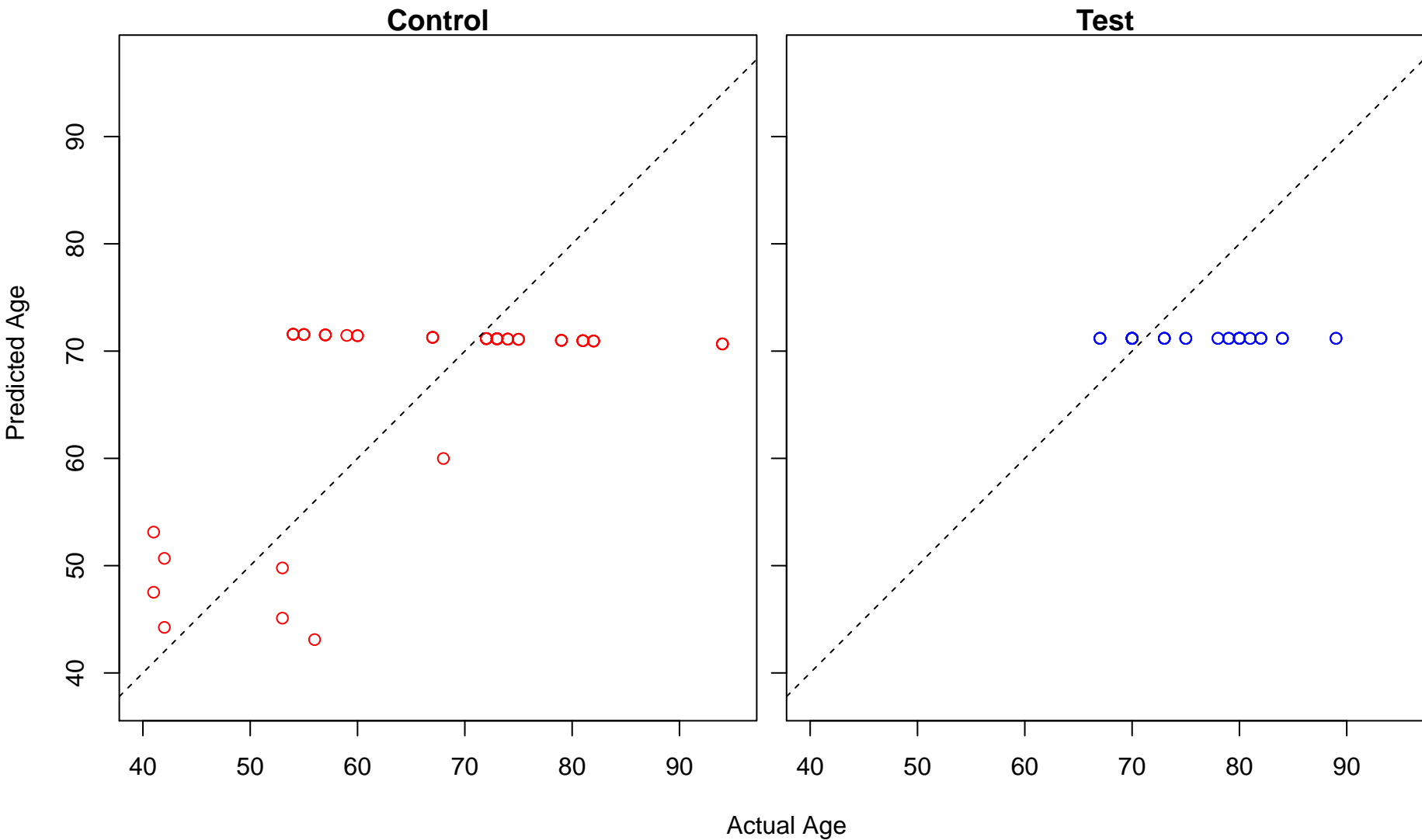


Actual Age

animal organ development (Score: 0.812596)

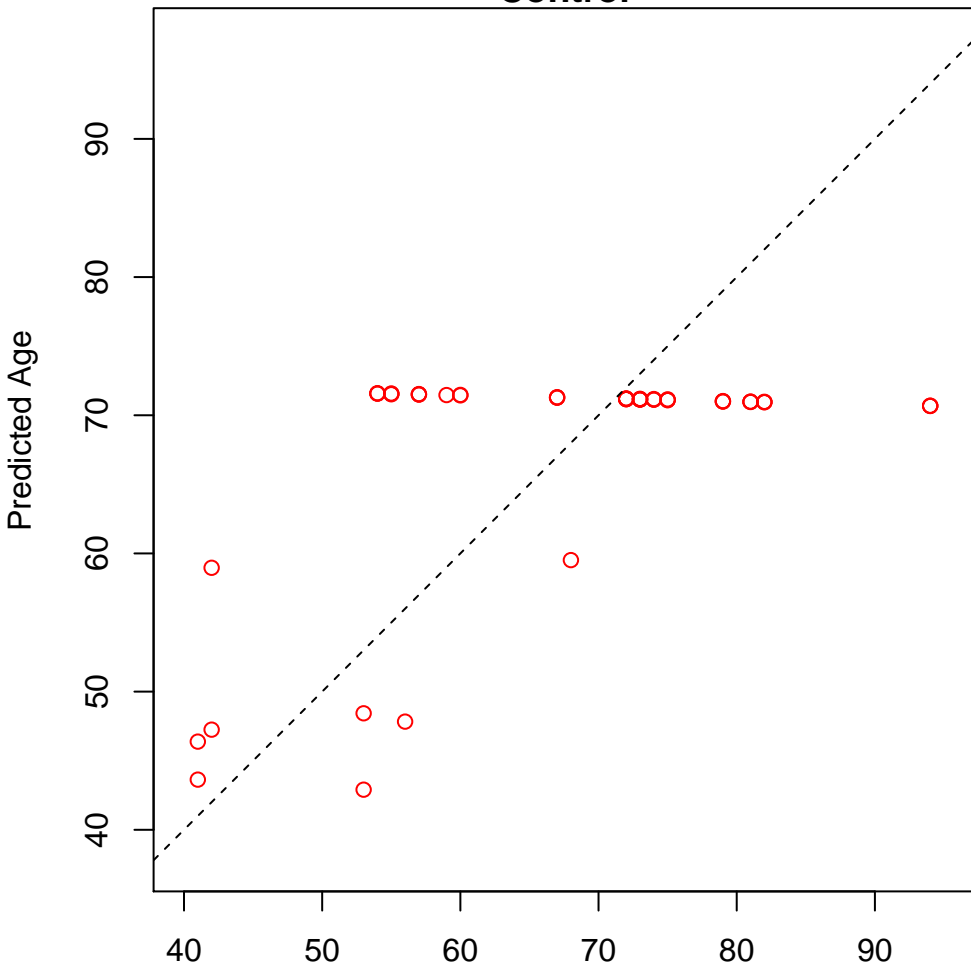


regulation of establishment of protein localization (Score: 0.812508)

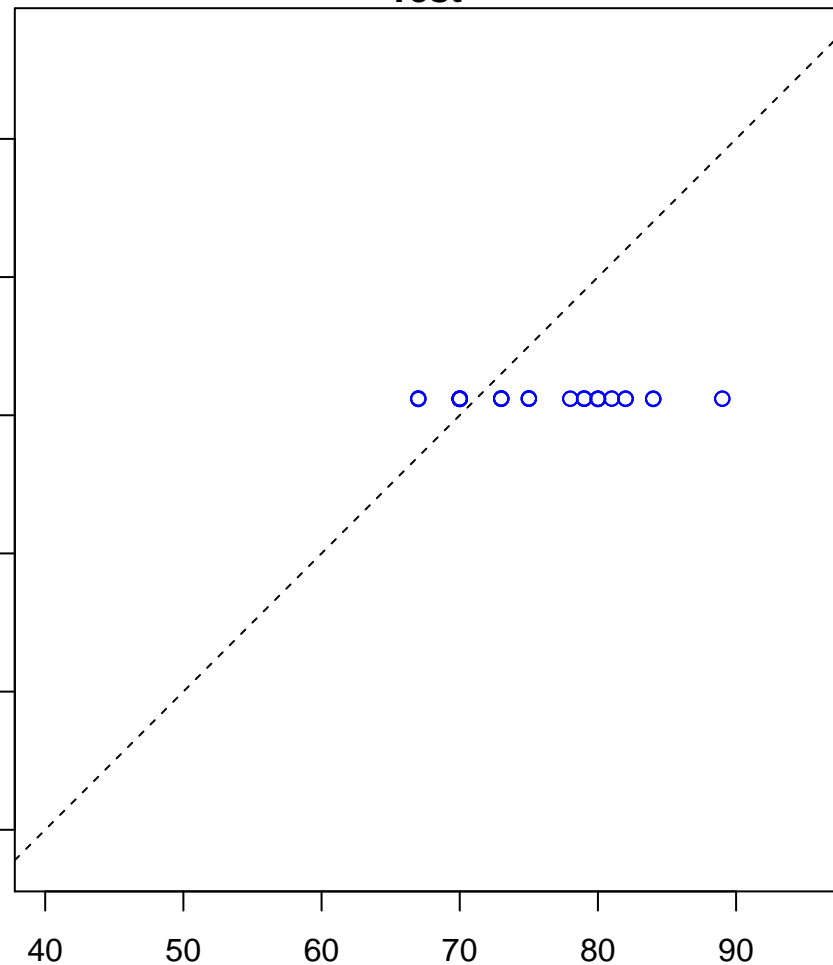


regulation of protein localization to nucleus (Score: 0.812506)

Control

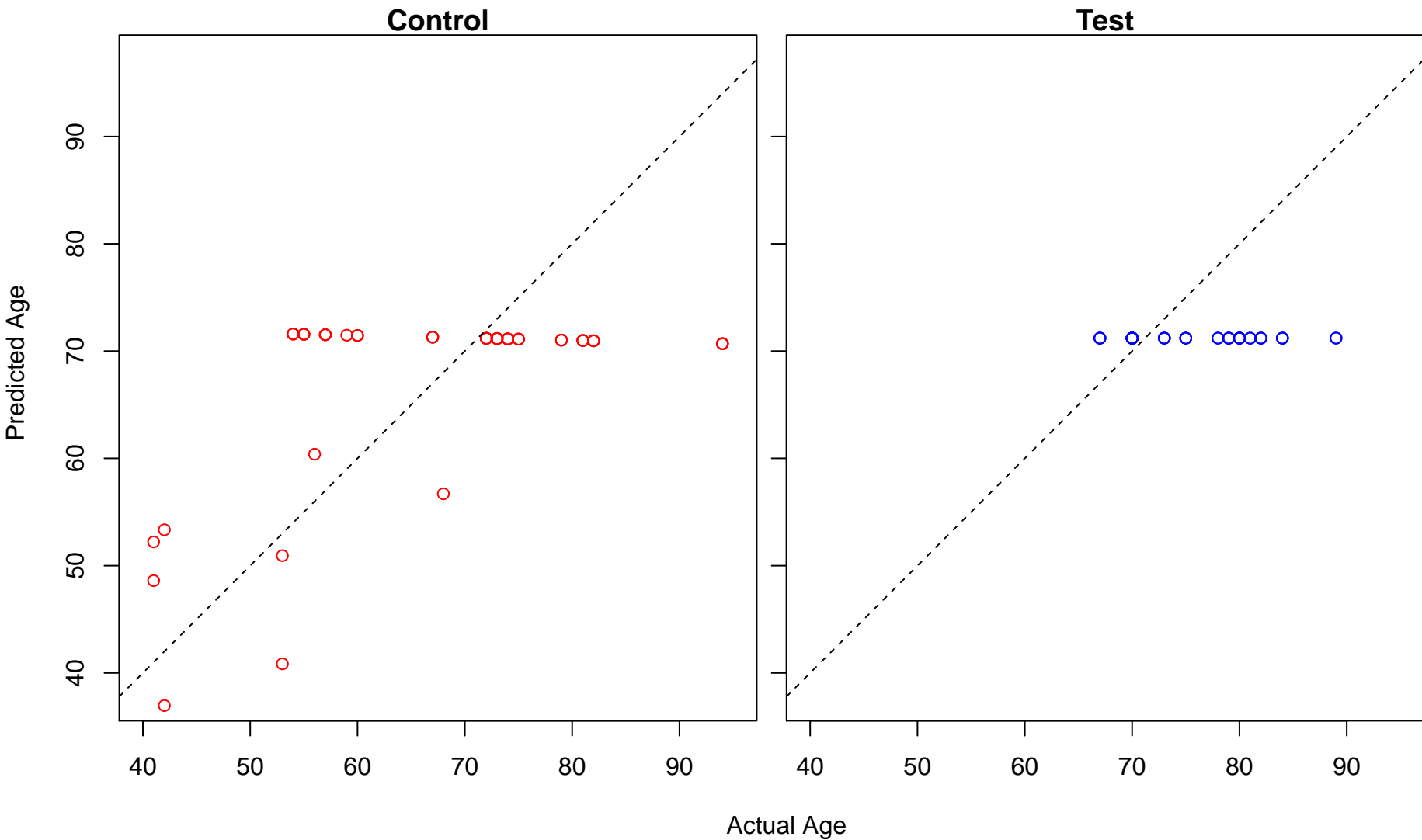


Test

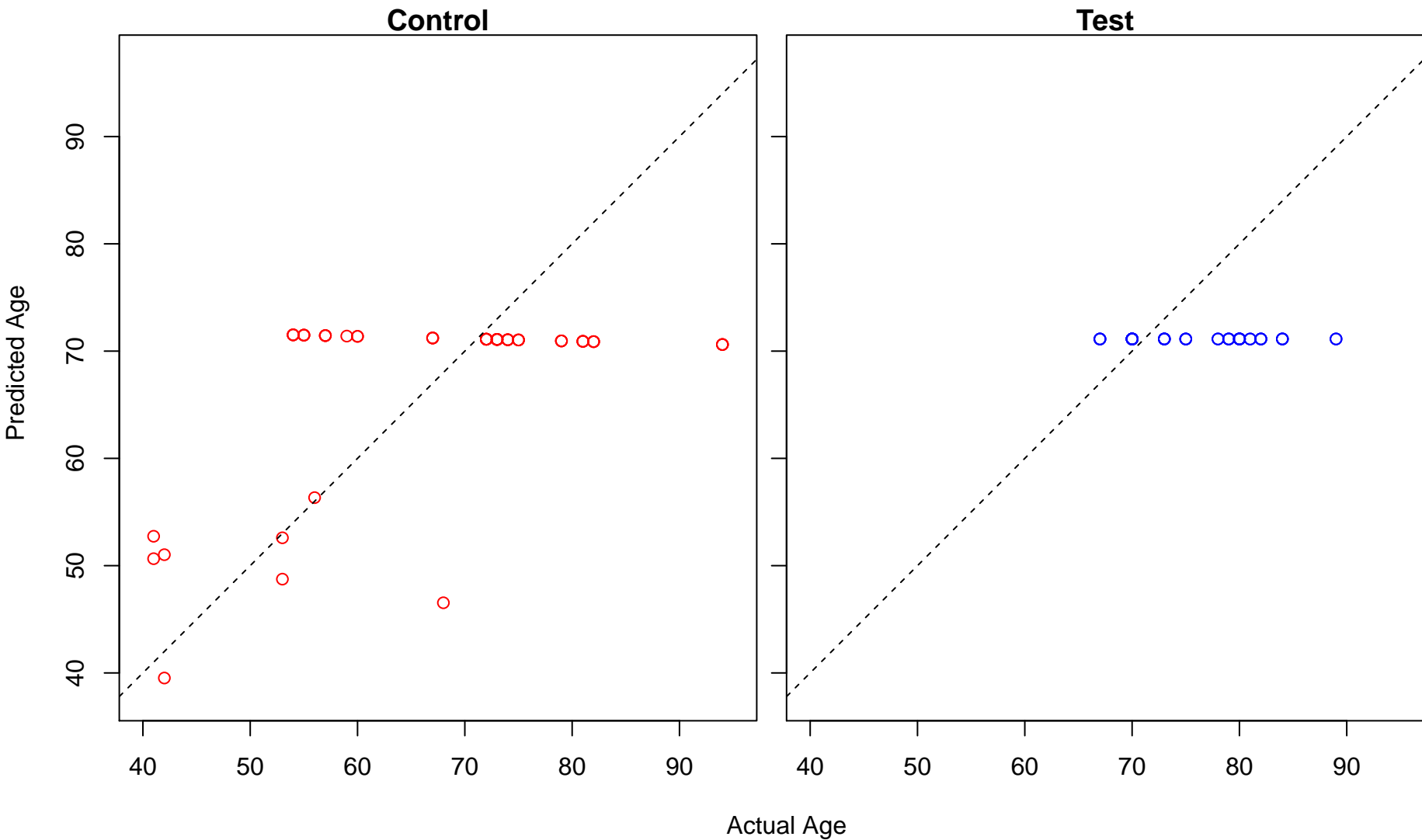


Actual Age

regulation of mitotic cell cycle (Score: 0.812375)

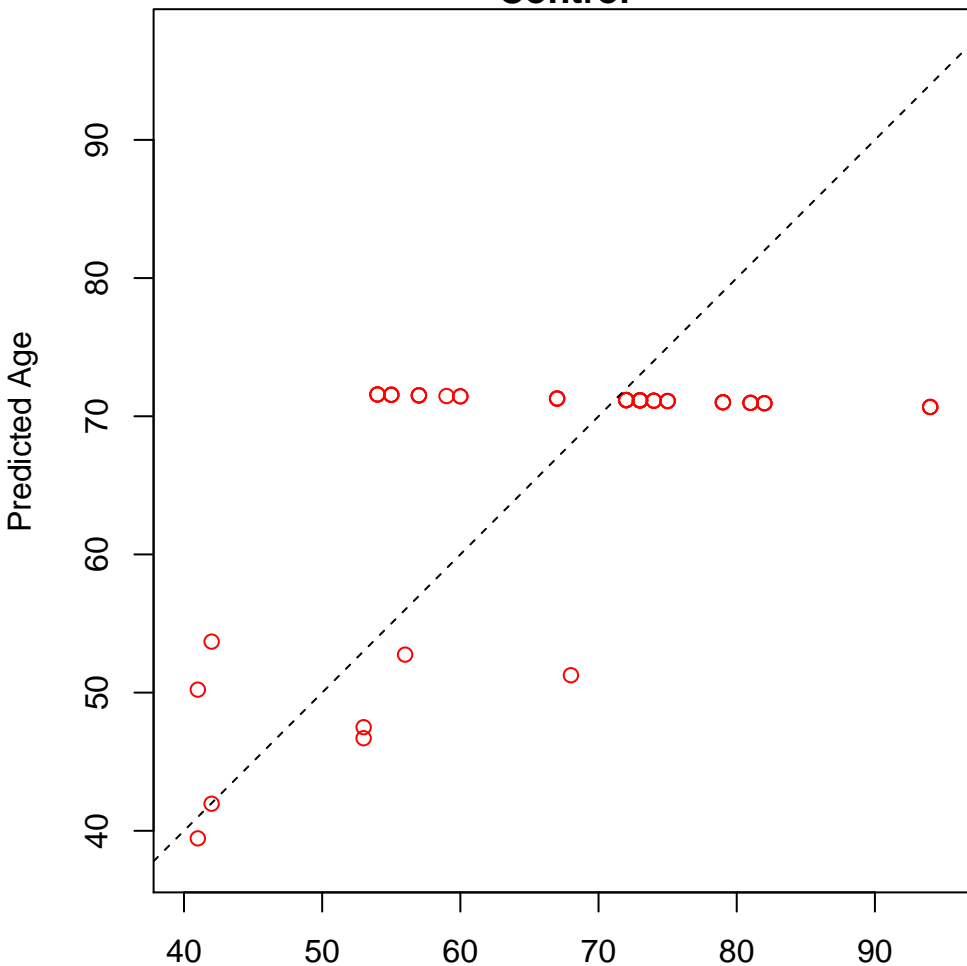


pyruvate metabolic process (Score: 0.812319)

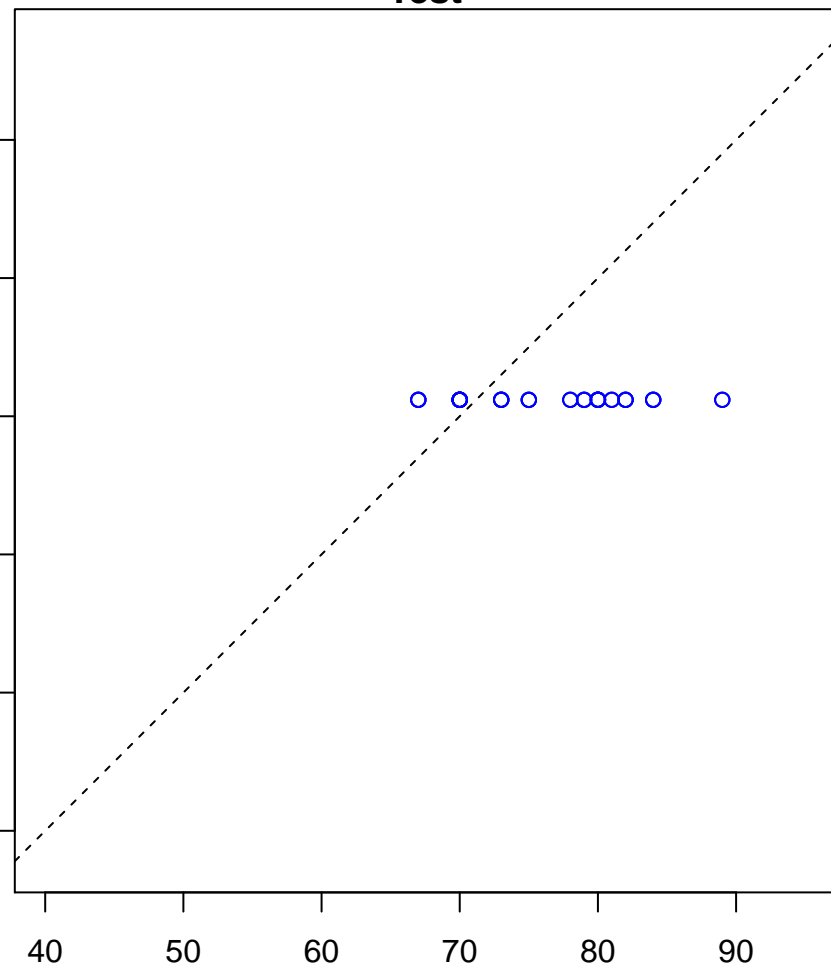


regulation of molecular function (Score: 0.812284)

Control

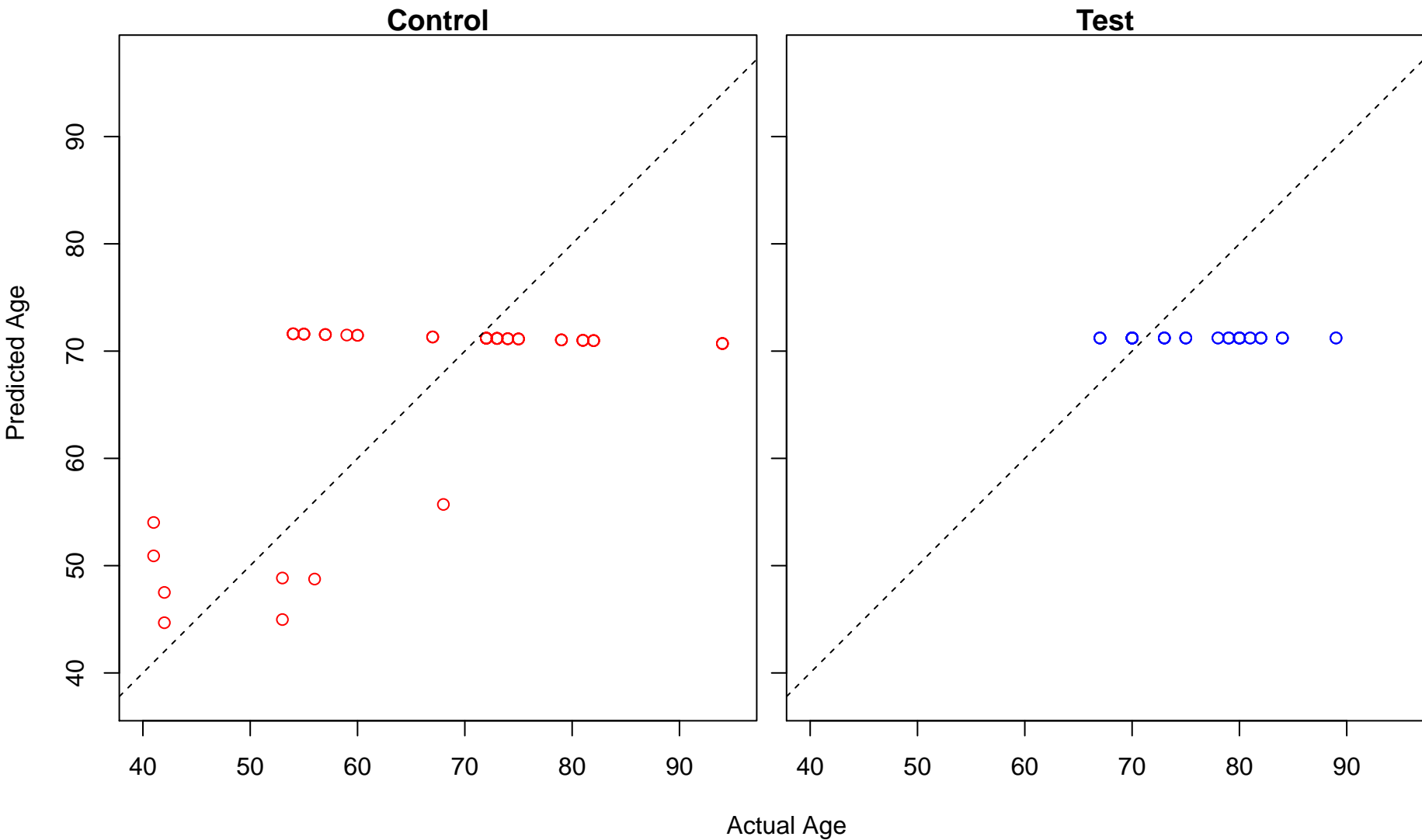


Test

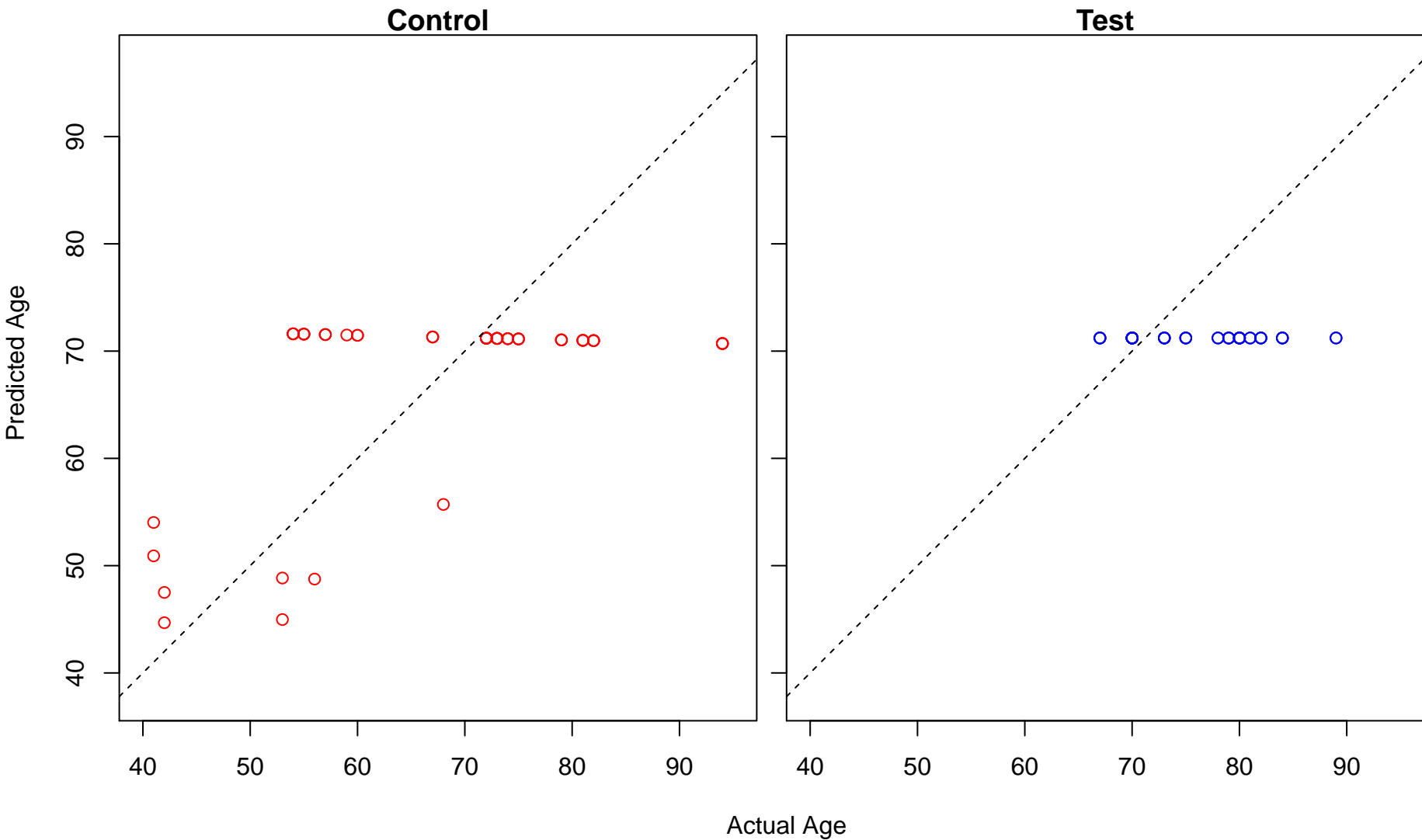


Actual Age

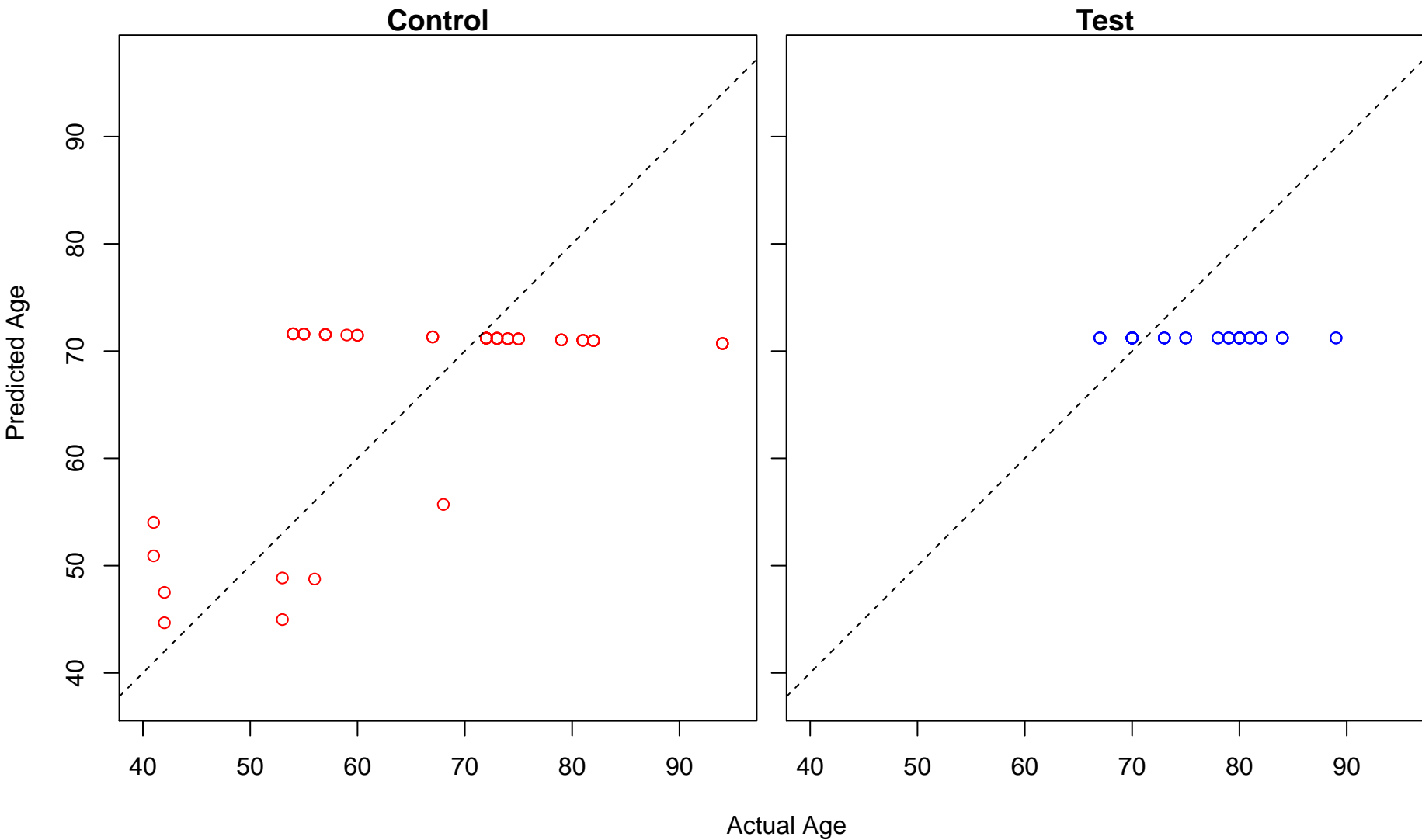
nucleoside monophosphate metabolic process (Score: 0.812237)



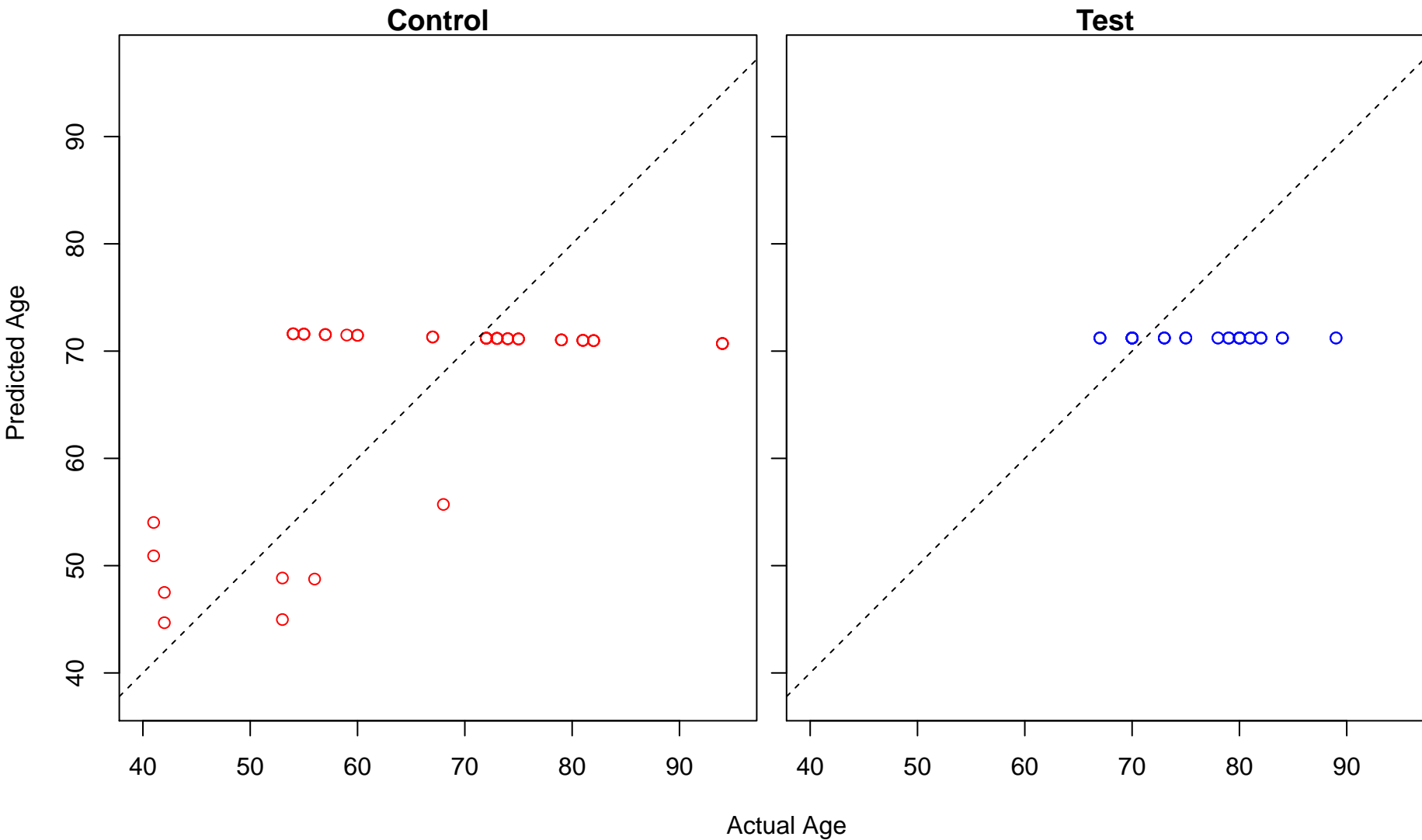
purine nucleoside monophosphate metabolic process (Score: 0.812237)



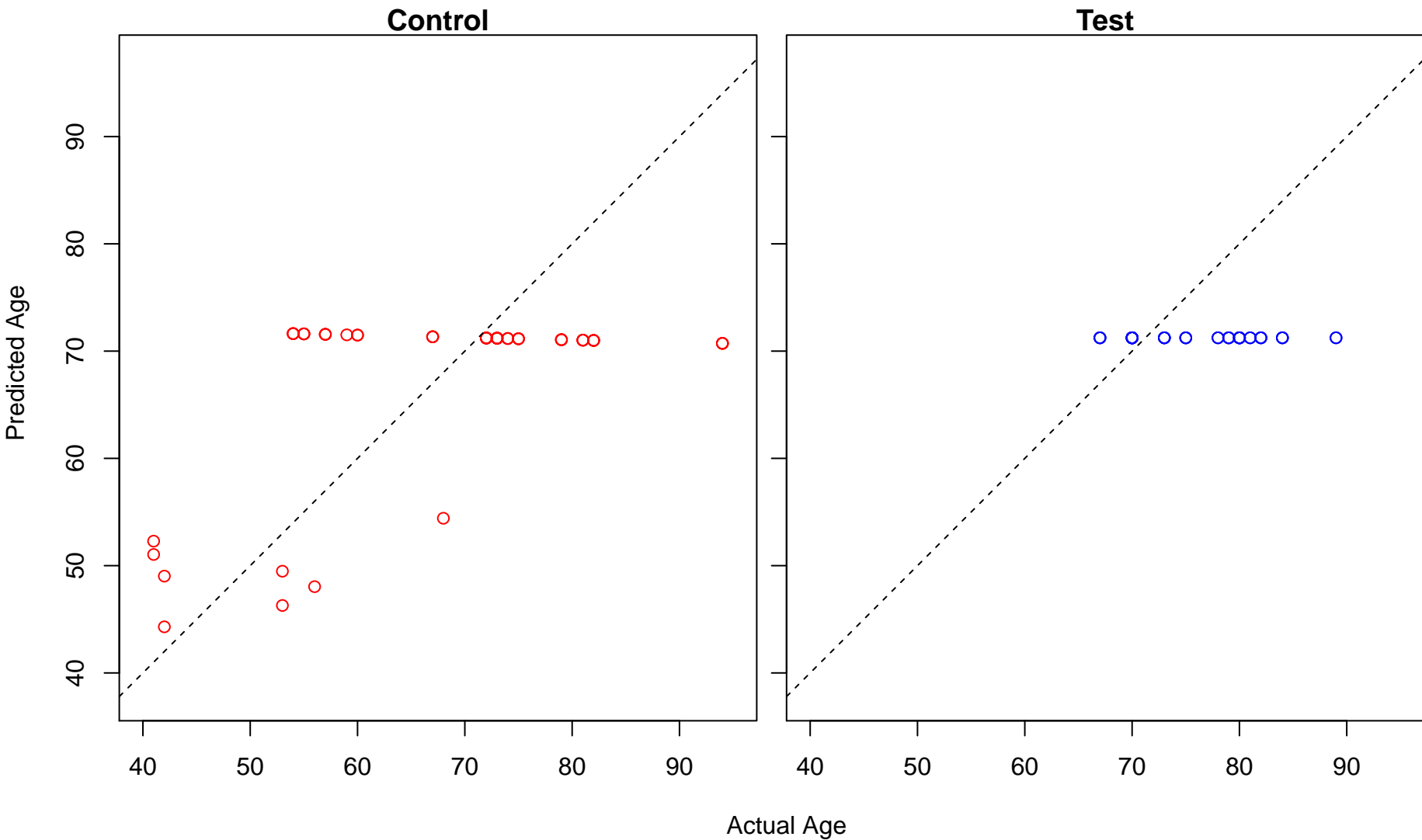
ribonucleoside monophosphate metabolic process (Score: 0.812237)



purine ribonucleoside monophosphate metabolic process (Score: 0.812237)

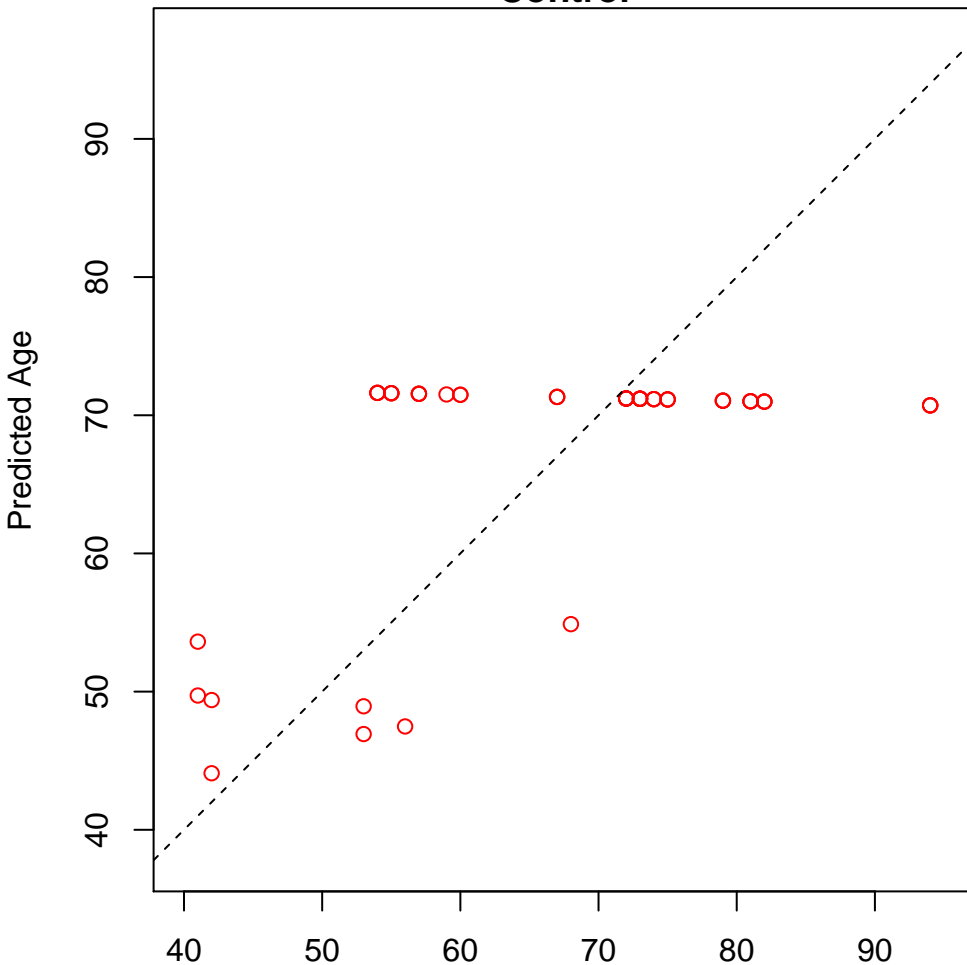


positive regulation of establishment of protein localization (Score: 0.812231)

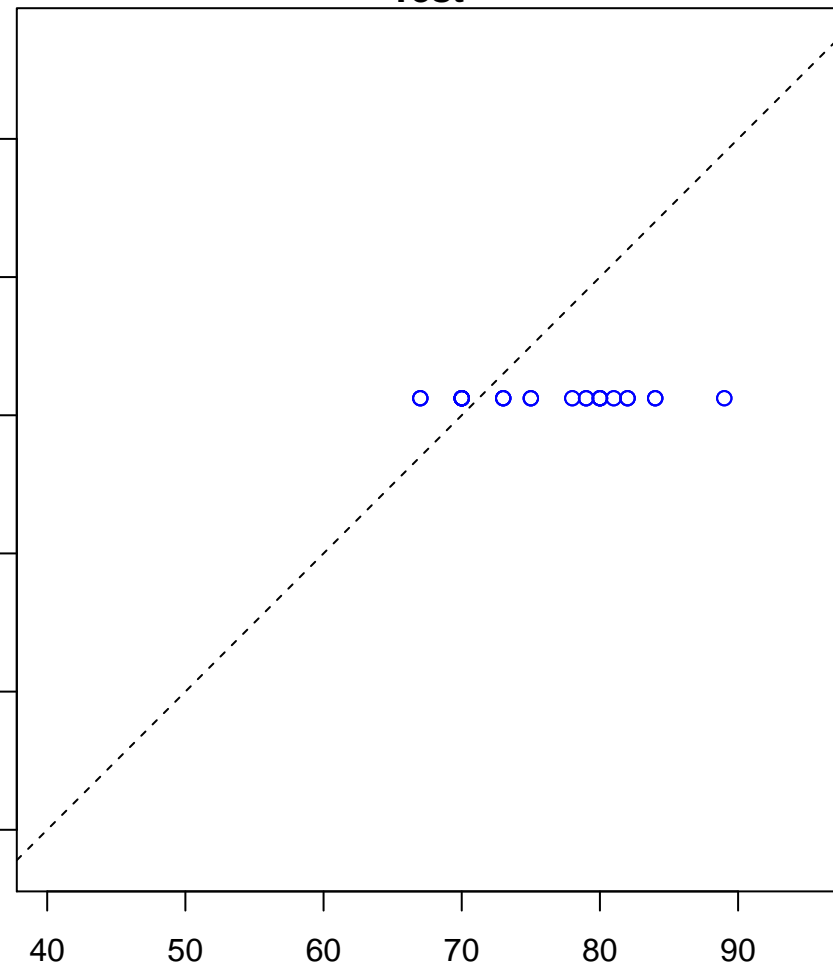


regulation of mitochondrion organization (Score: 0.812153)

Control



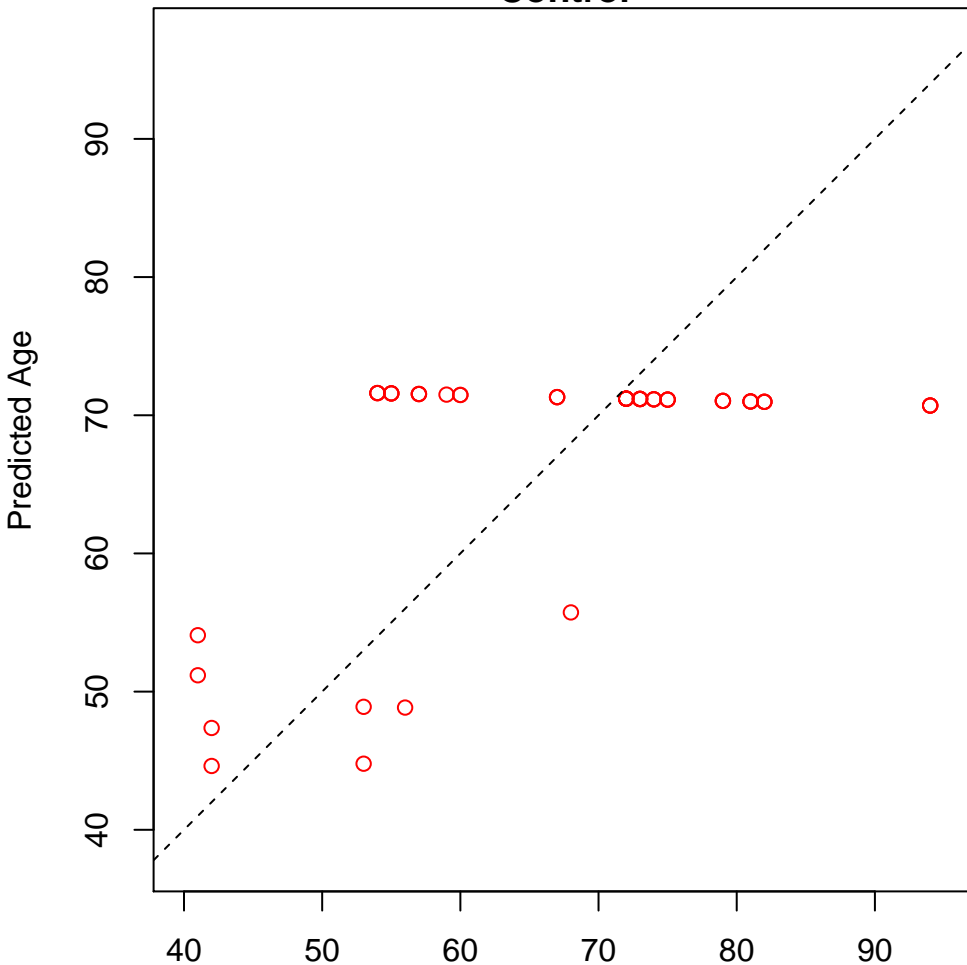
Test



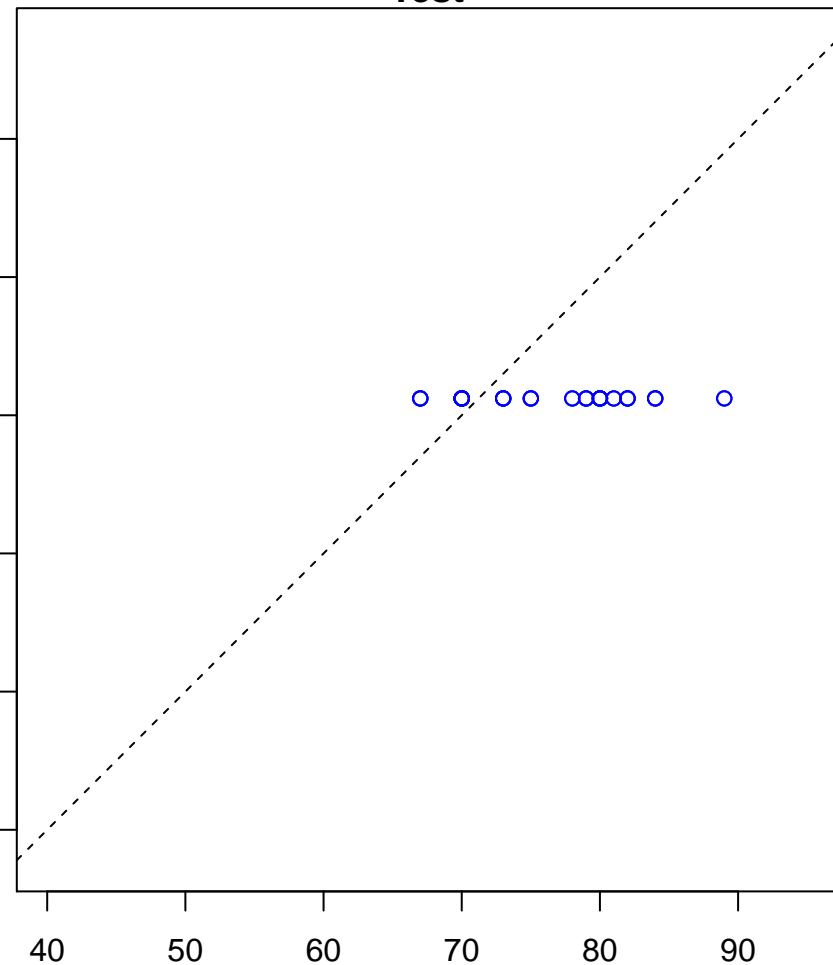
Actual Age

nucleoside triphosphate metabolic process (Score: 0.812108)

Control

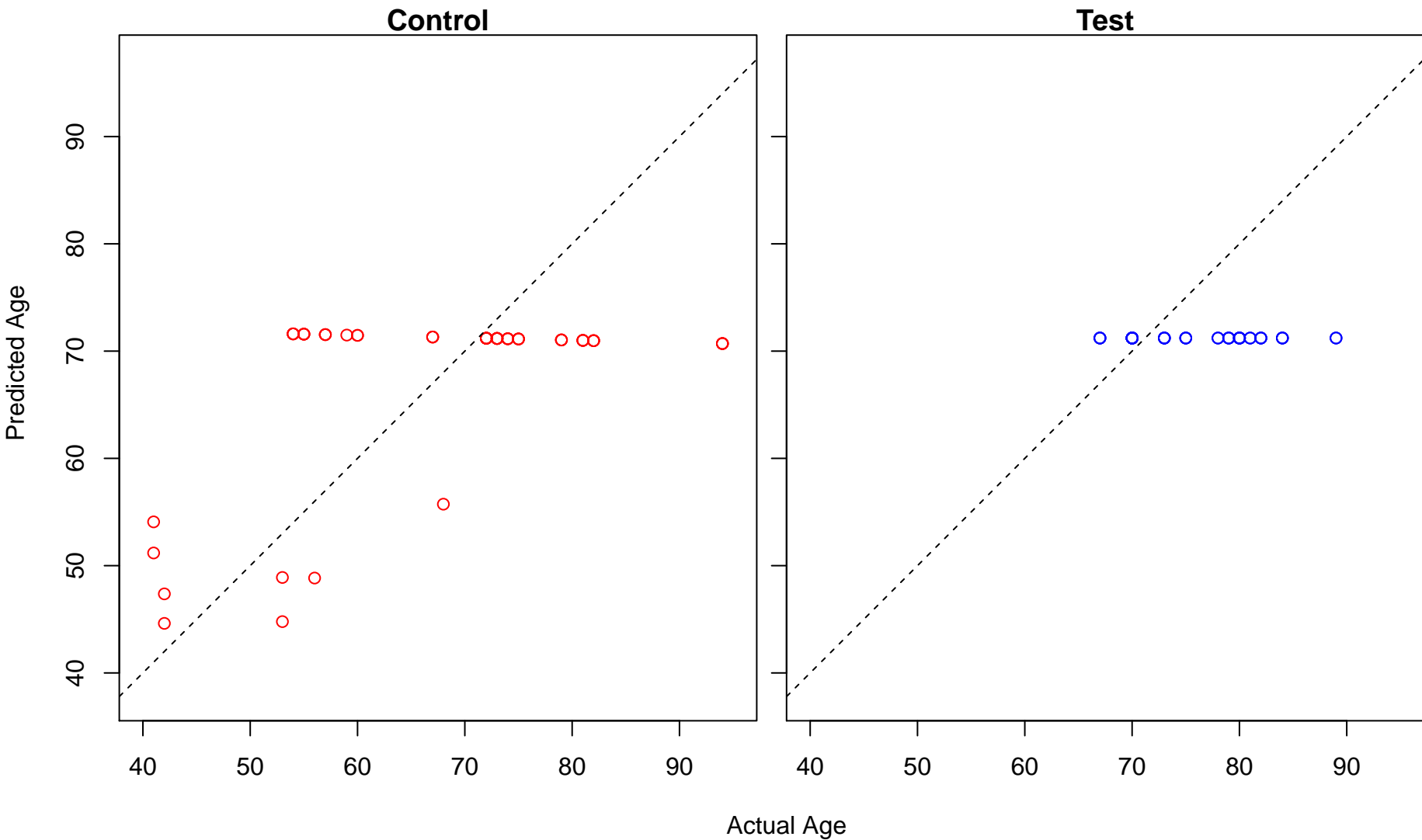


Test

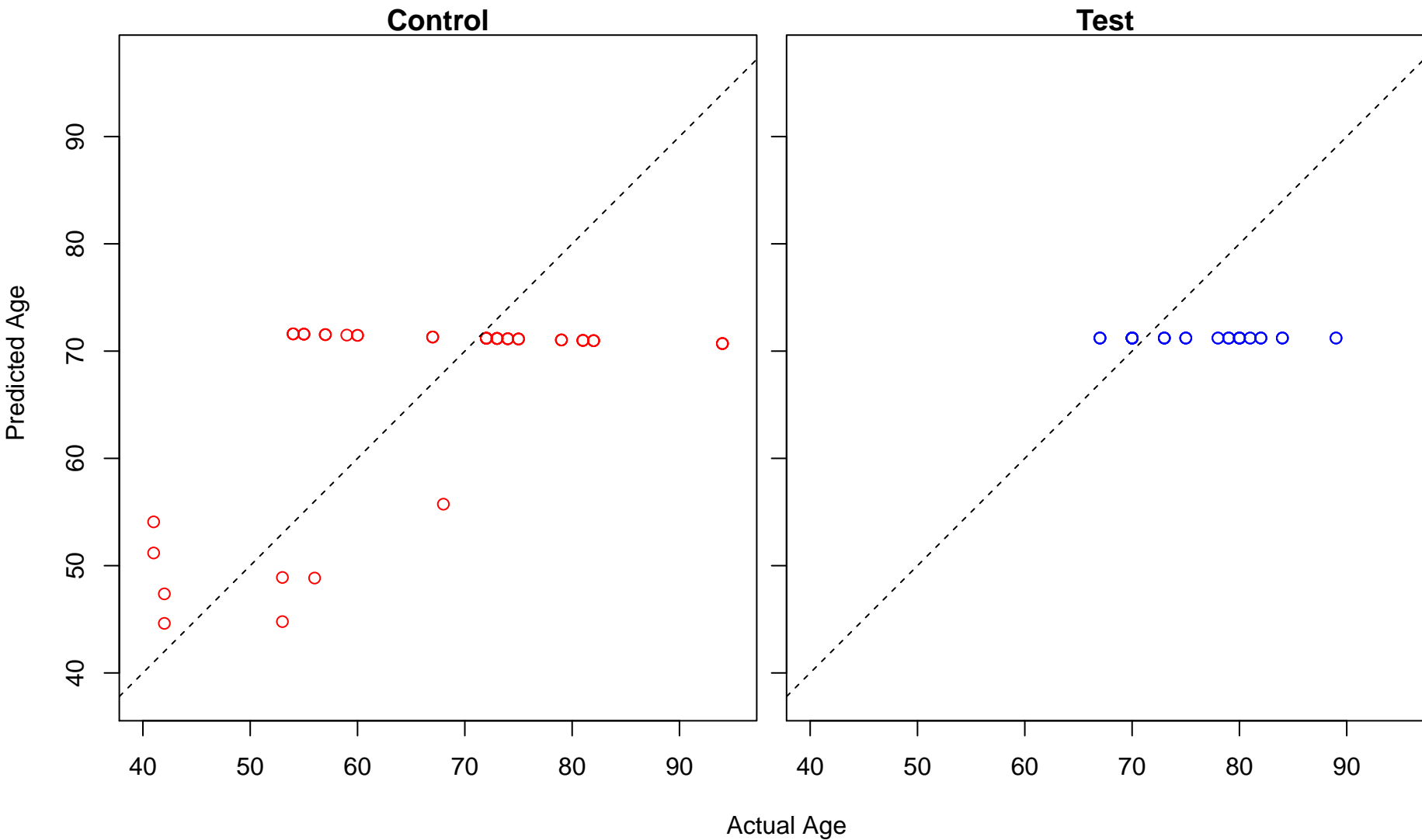


Actual Age

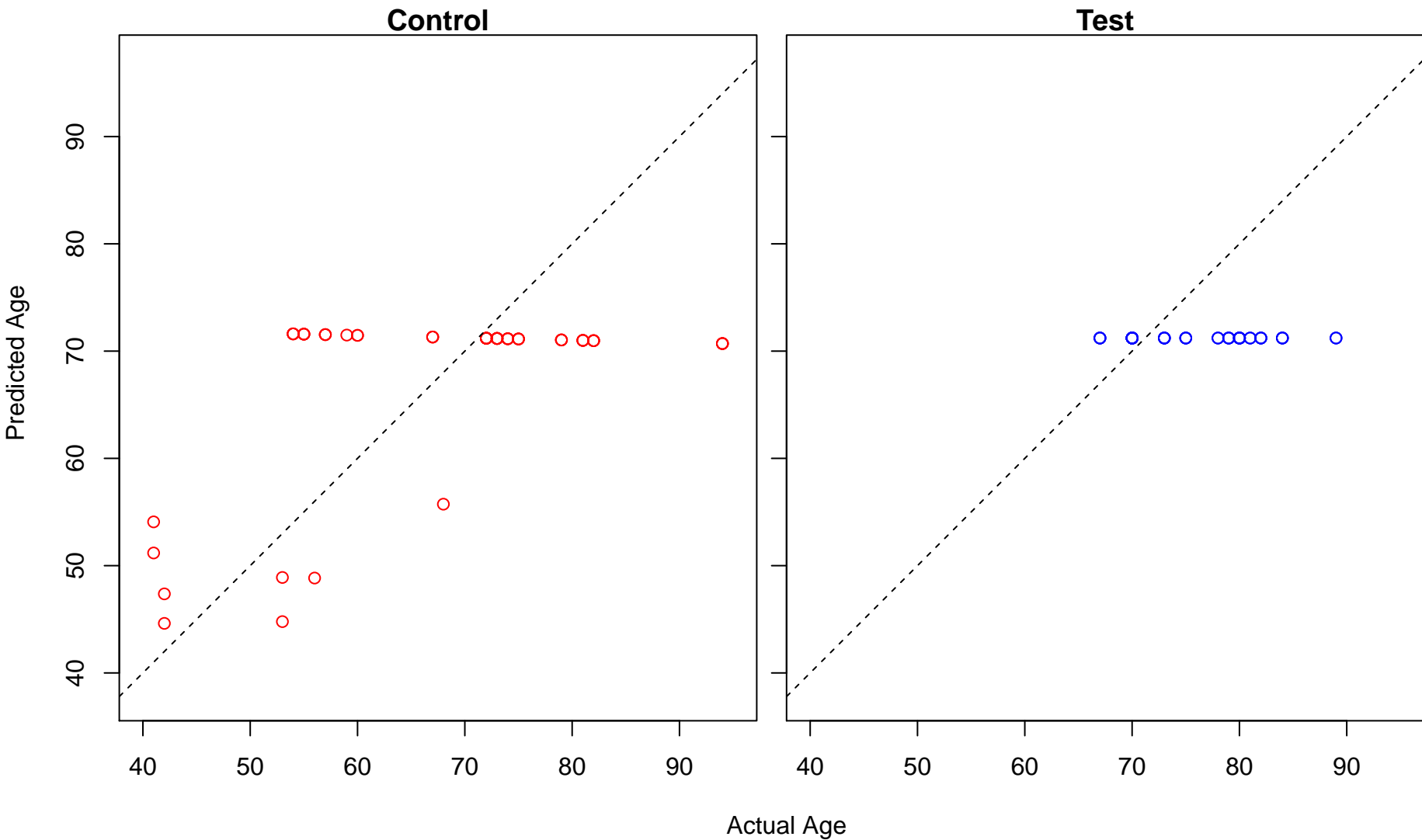
purine nucleoside triphosphate metabolic process (Score: 0.812108)



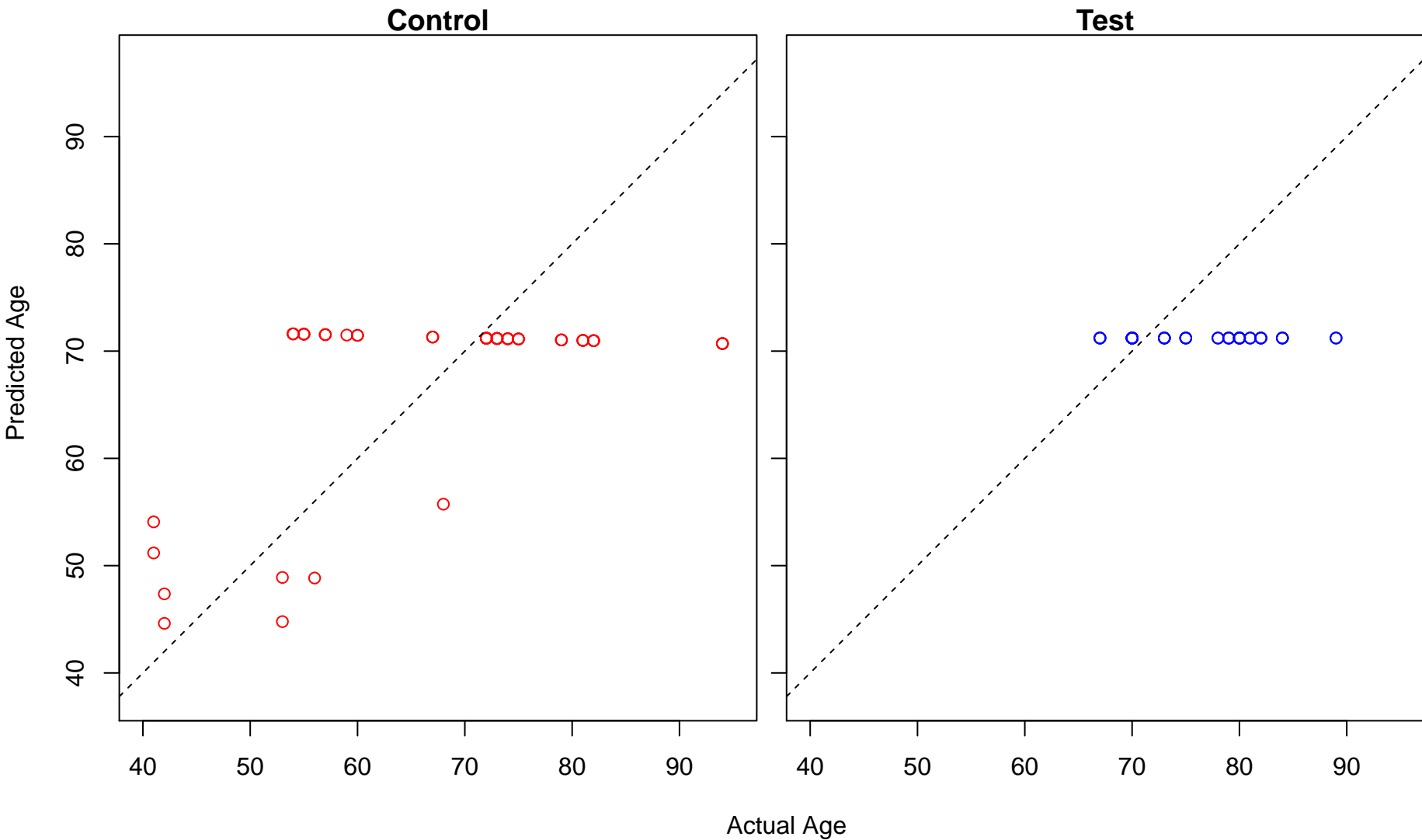
ribonucleoside triphosphate metabolic process (Score: 0.812108)



purine ribonucleoside triphosphate metabolic process (Score: 0.812108)

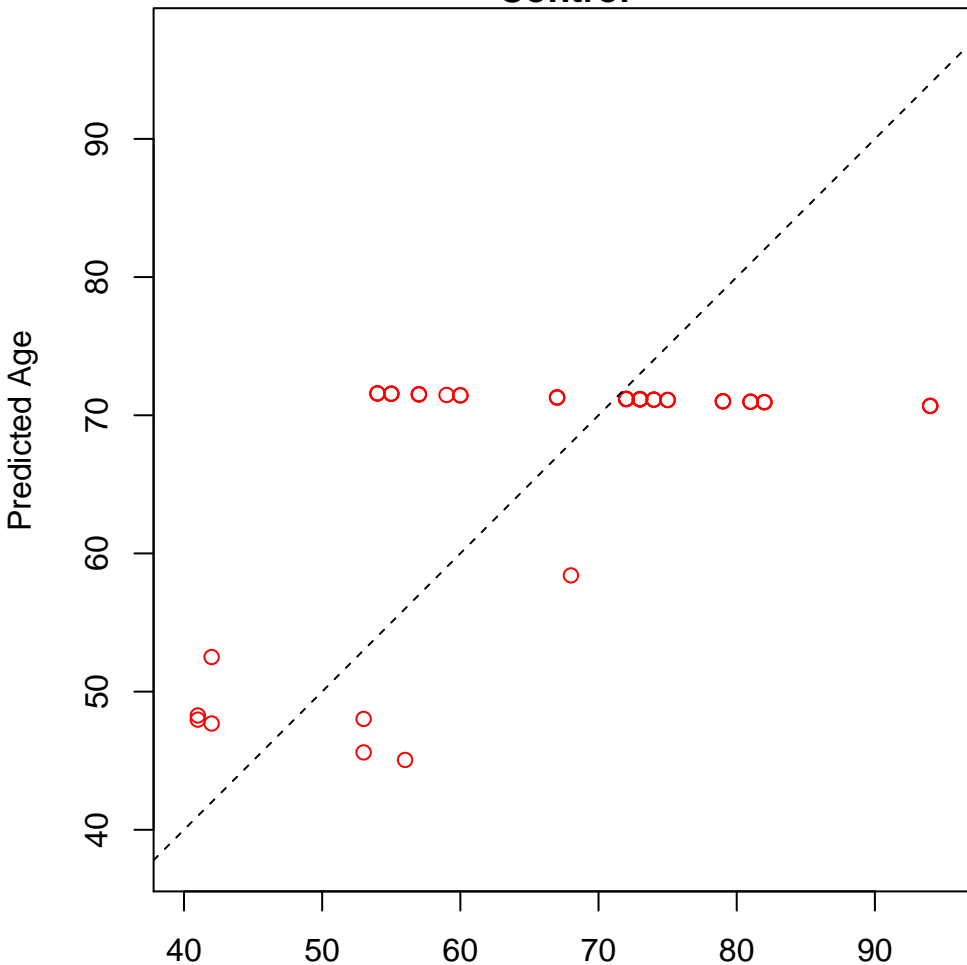


ATP metabolic process (Score: 0.812108)

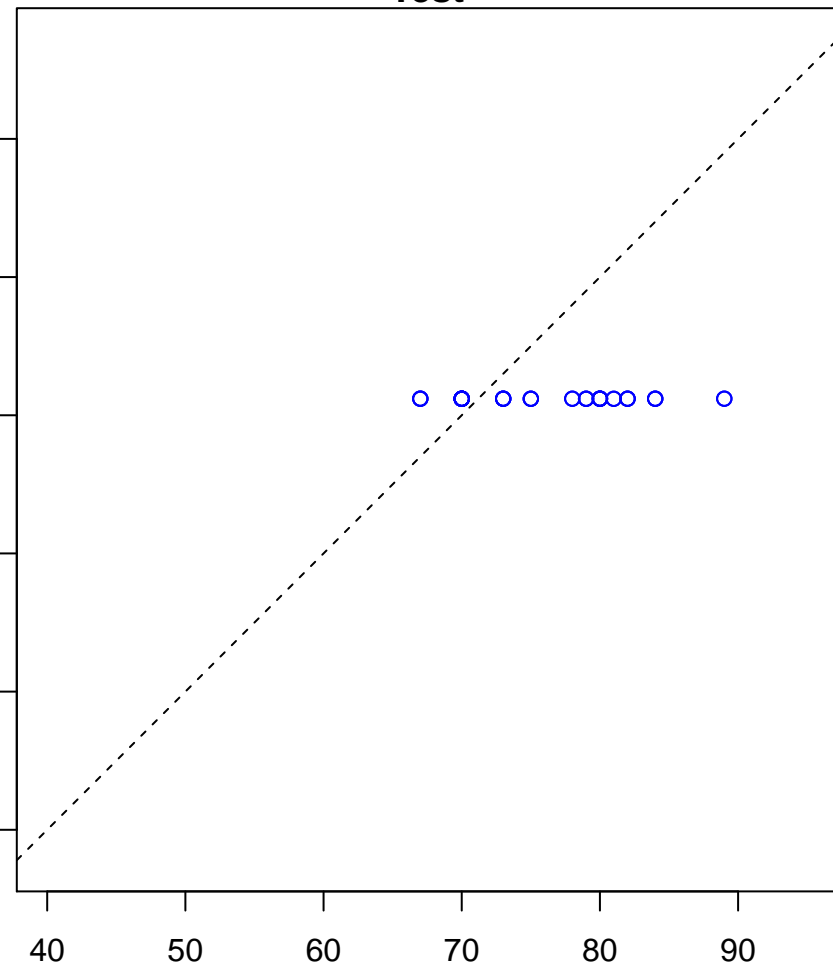


regulation of cellular protein localization (Score: 0.812025)

Control



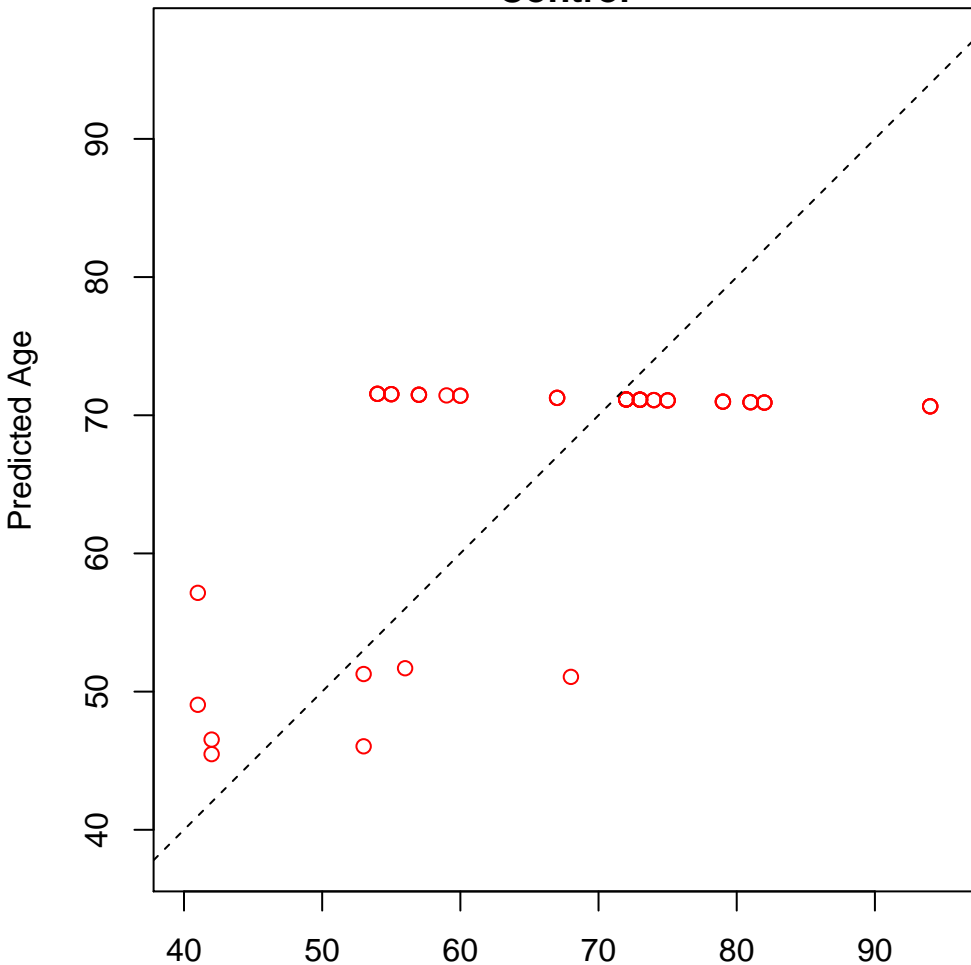
Test



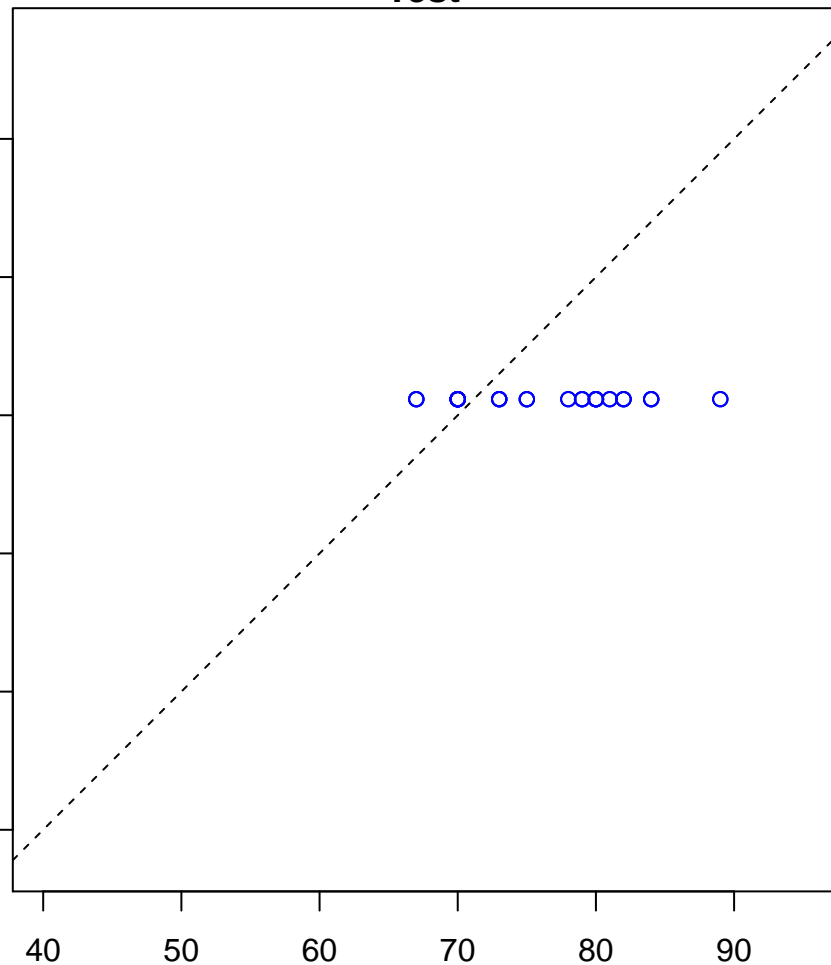
Actual Age

cellular amino acid metabolic process (Score: 0.812020)

Control

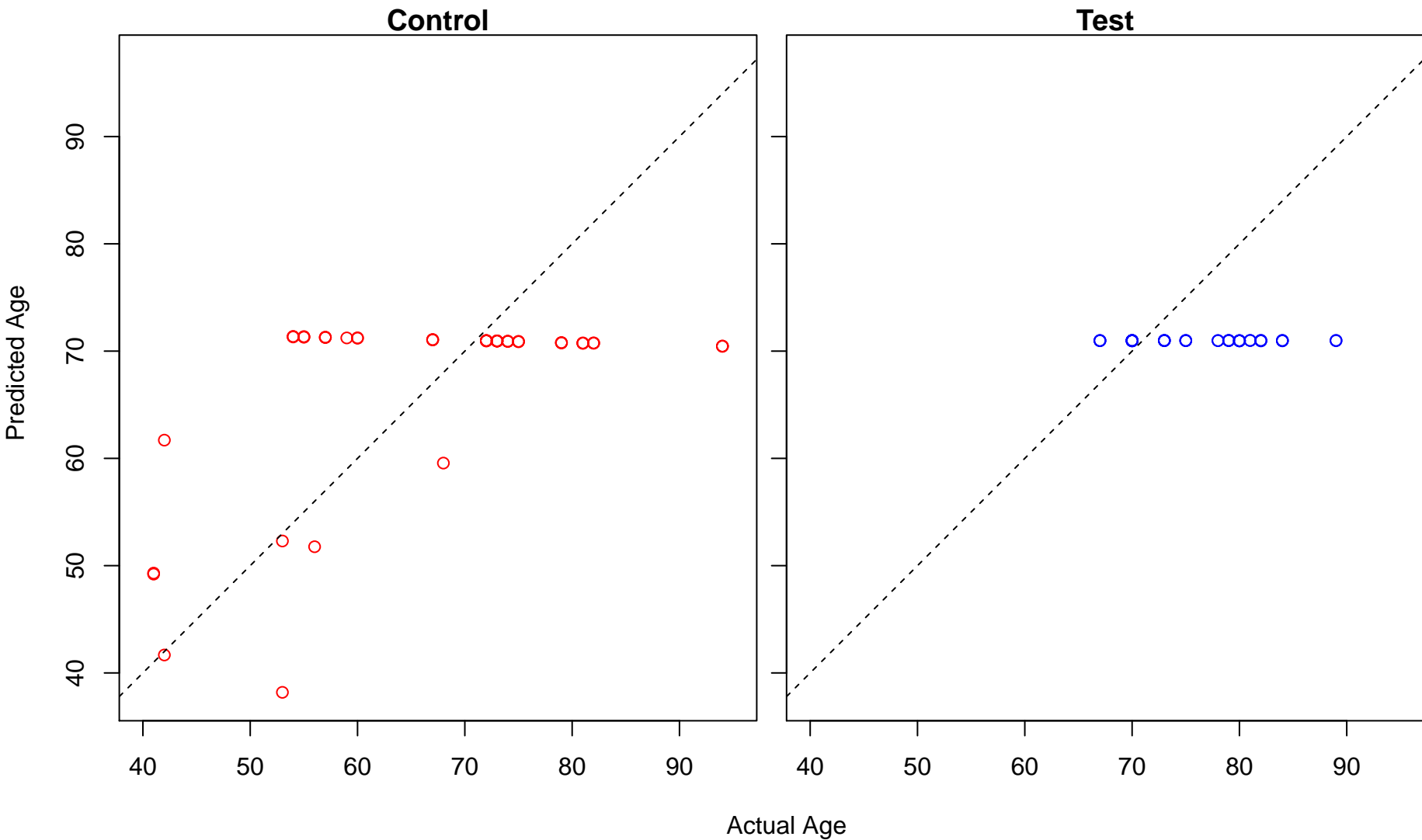


Test

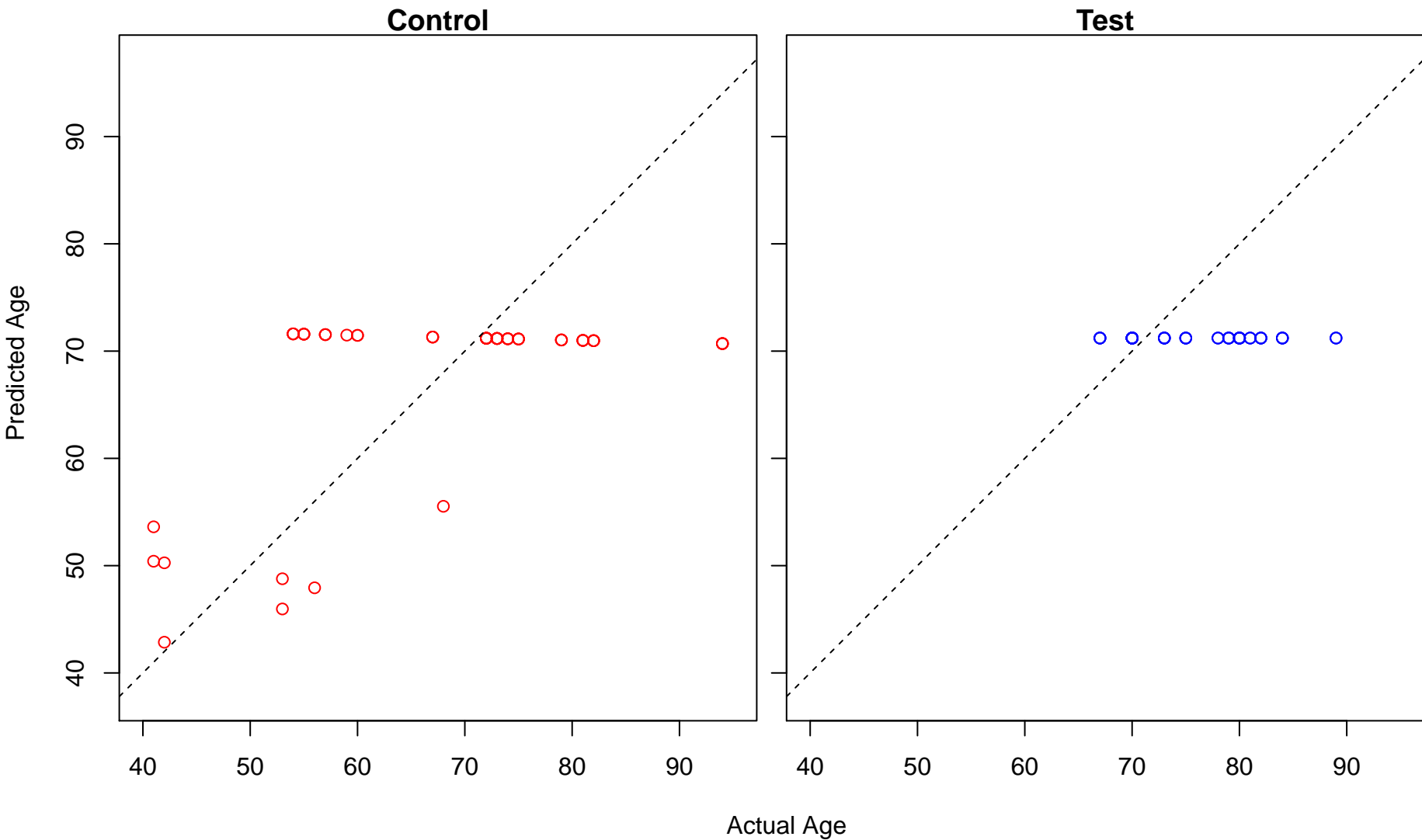


Actual Age

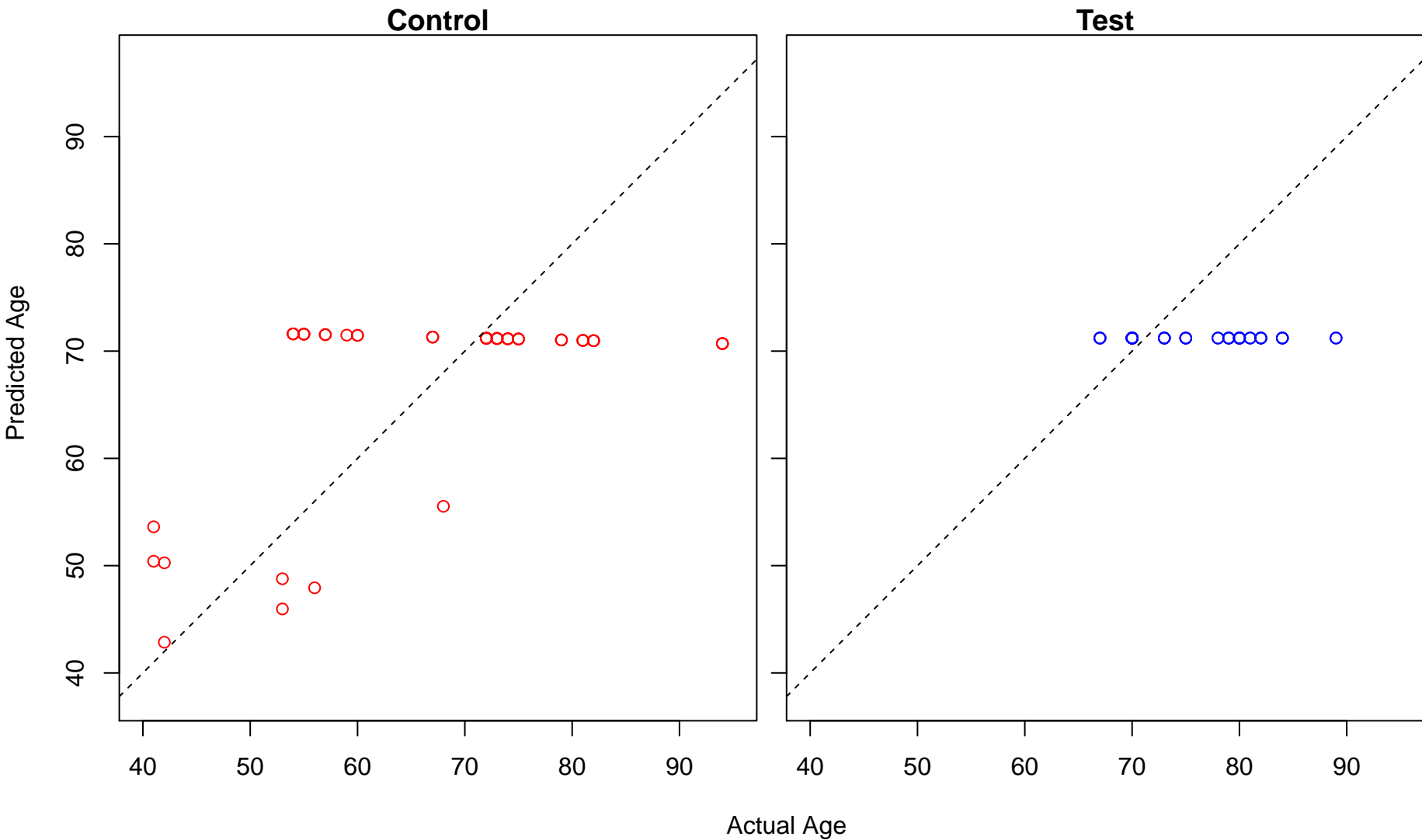
histone H4 acetylation (Score: 0.812011)



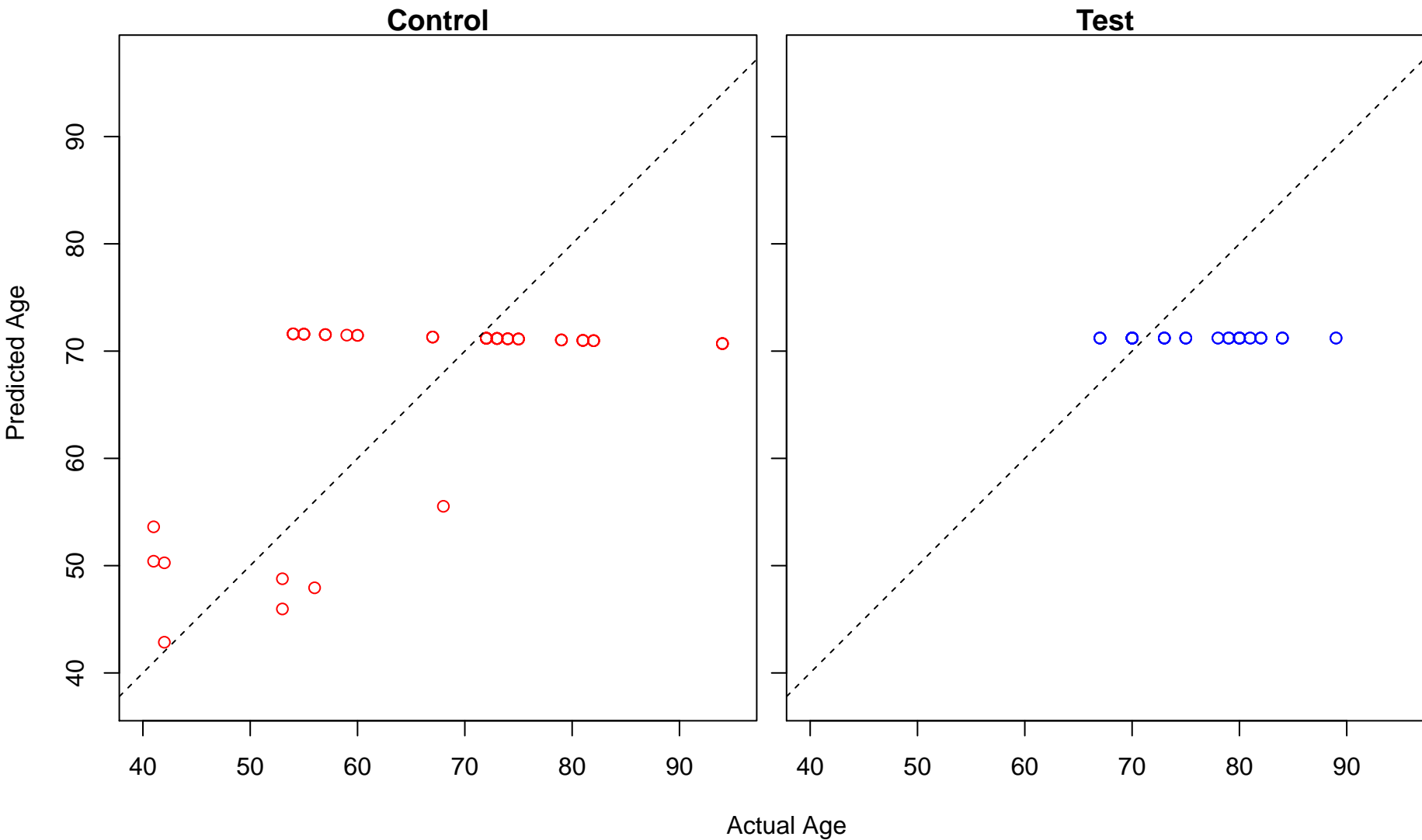
positive regulation of mitochondrion organization (Score: 0.81962)



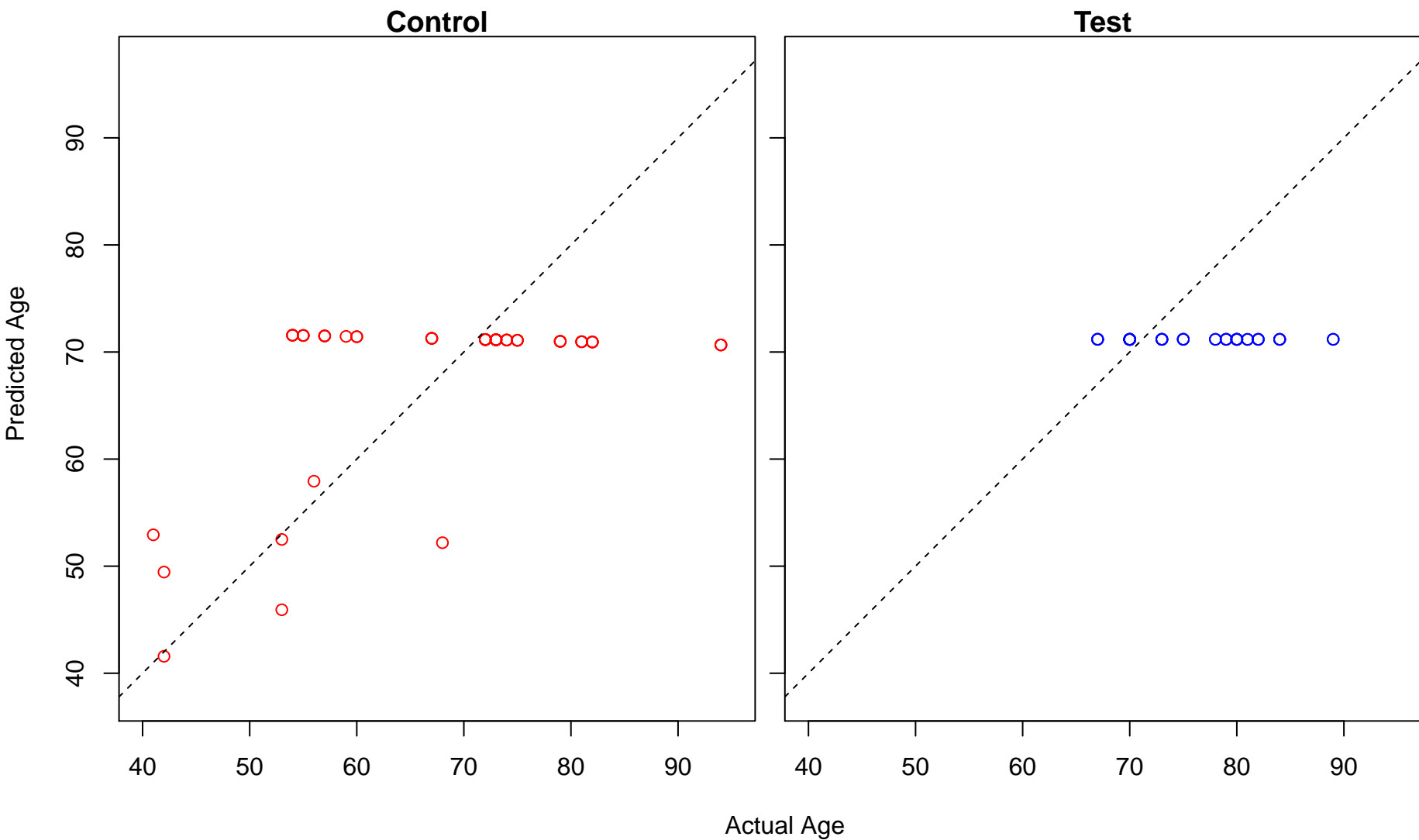
regulation of establishment of protein localization to mitochondrion (Score: 0.811962)



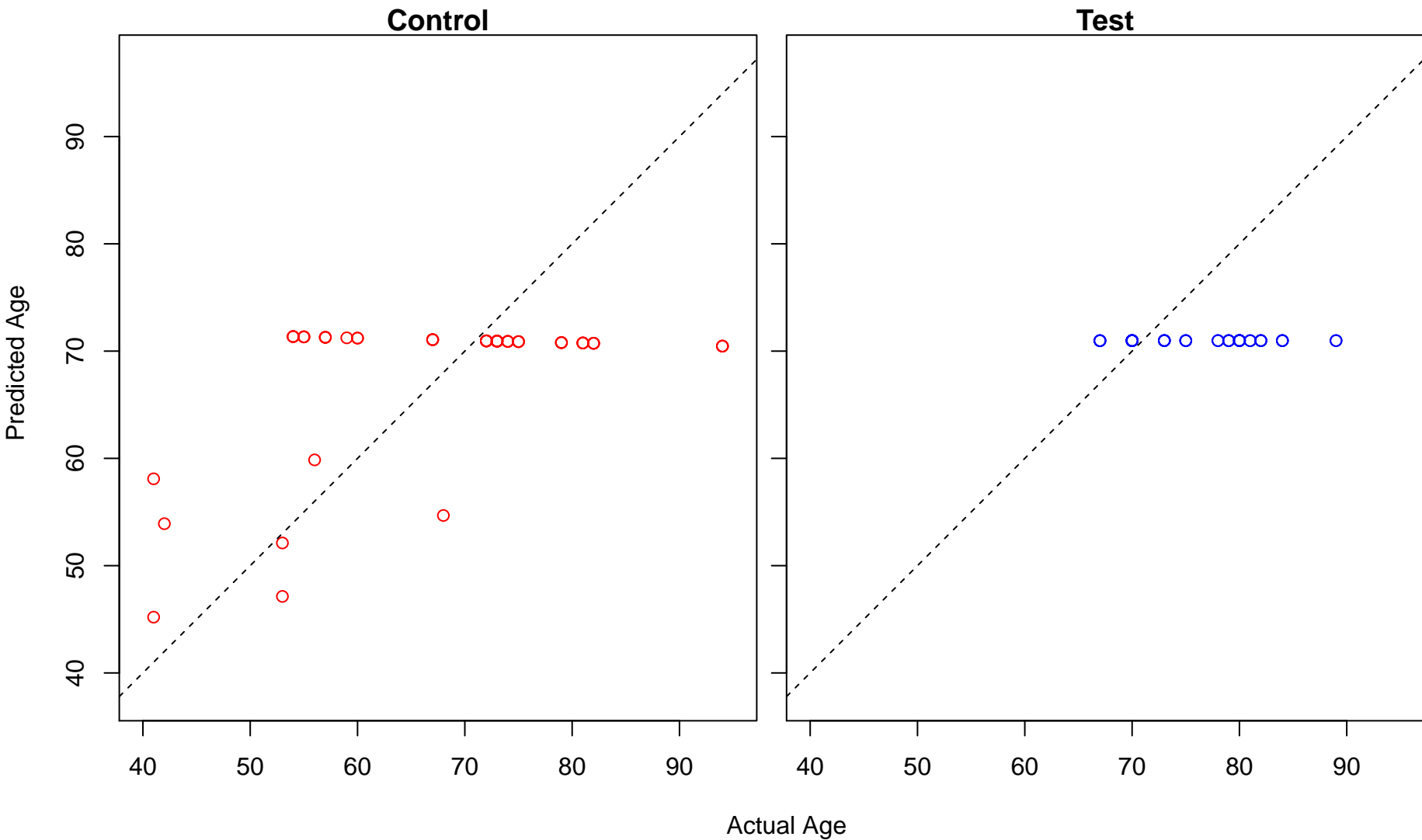
positive regulation of establishment of protein localization to mitochondrion (Score: 0.811962)



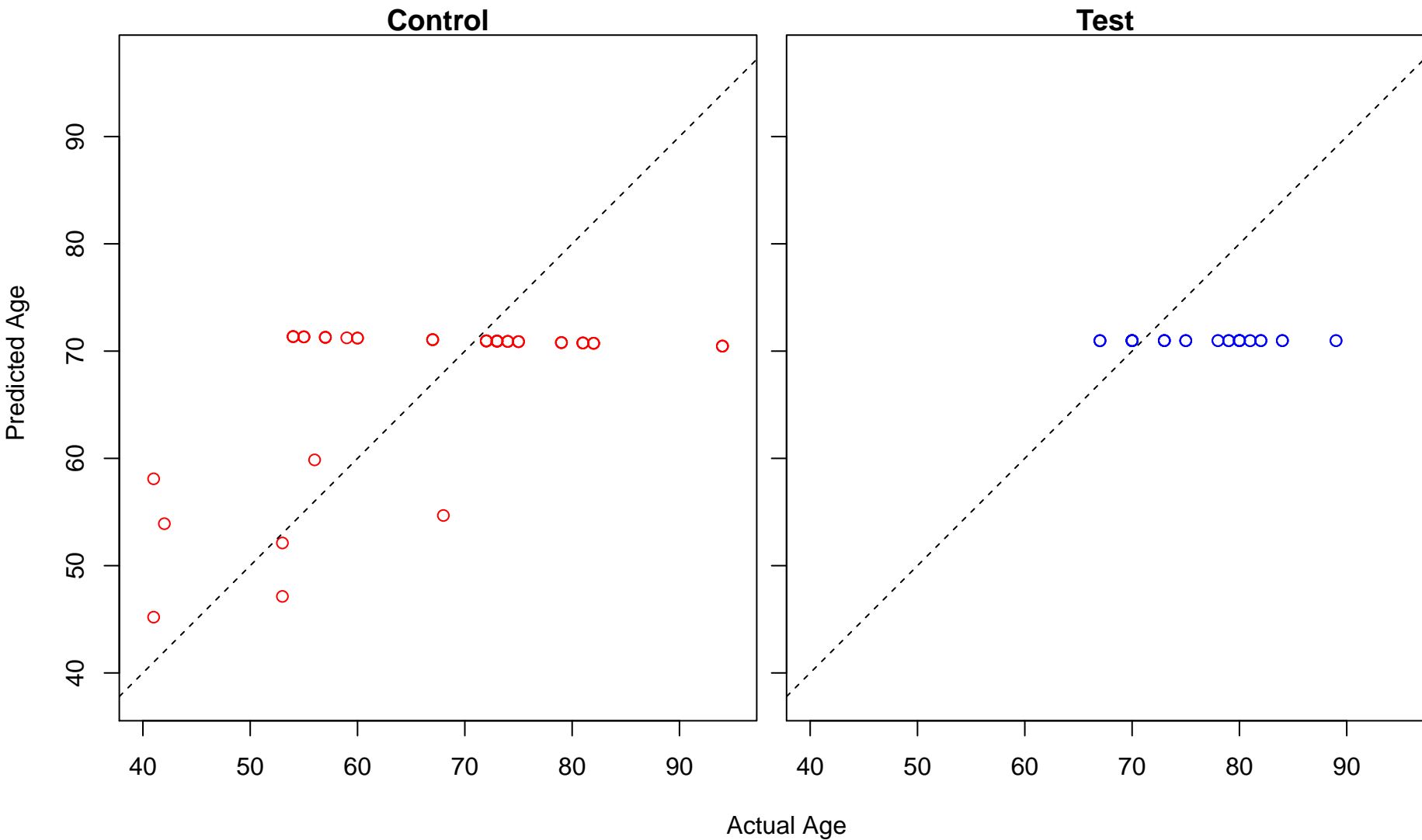
cell-cell signaling (Score: 0.811958)



glucose catabolic process (Score: 0.811949)

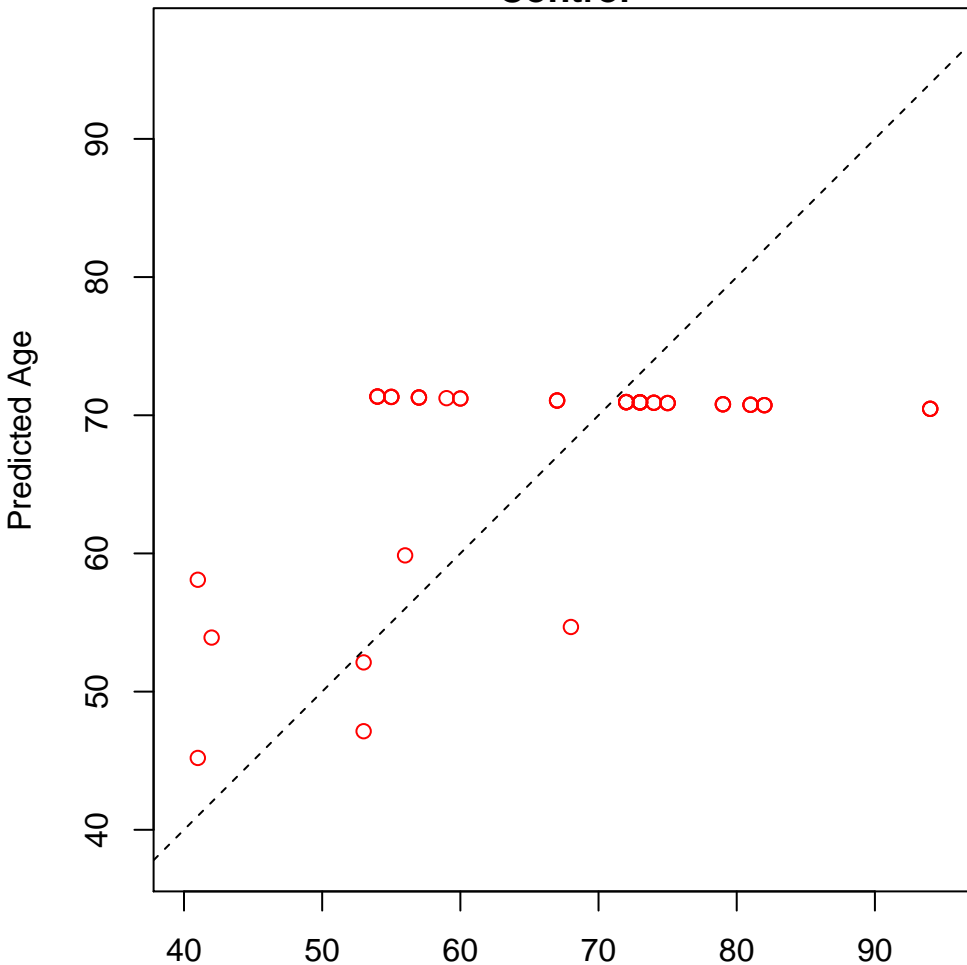


glycolytic process (Score: 0.811949)

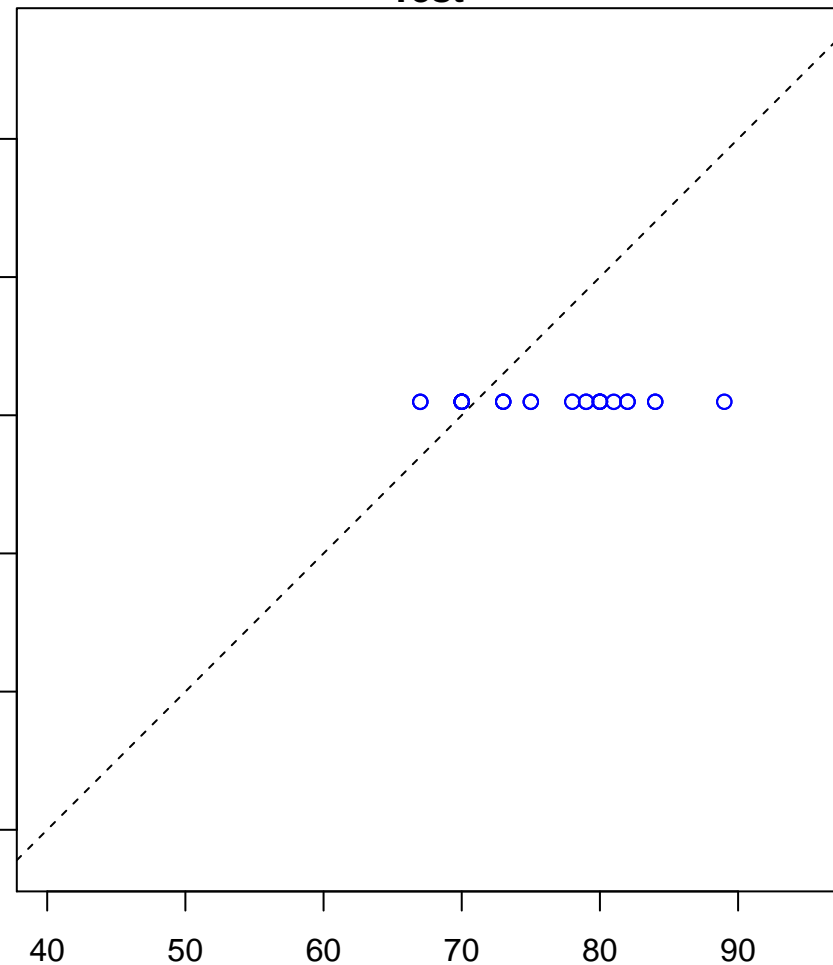


nucleoside diphosphate phosphorylation (Score: 0.811949)

Control

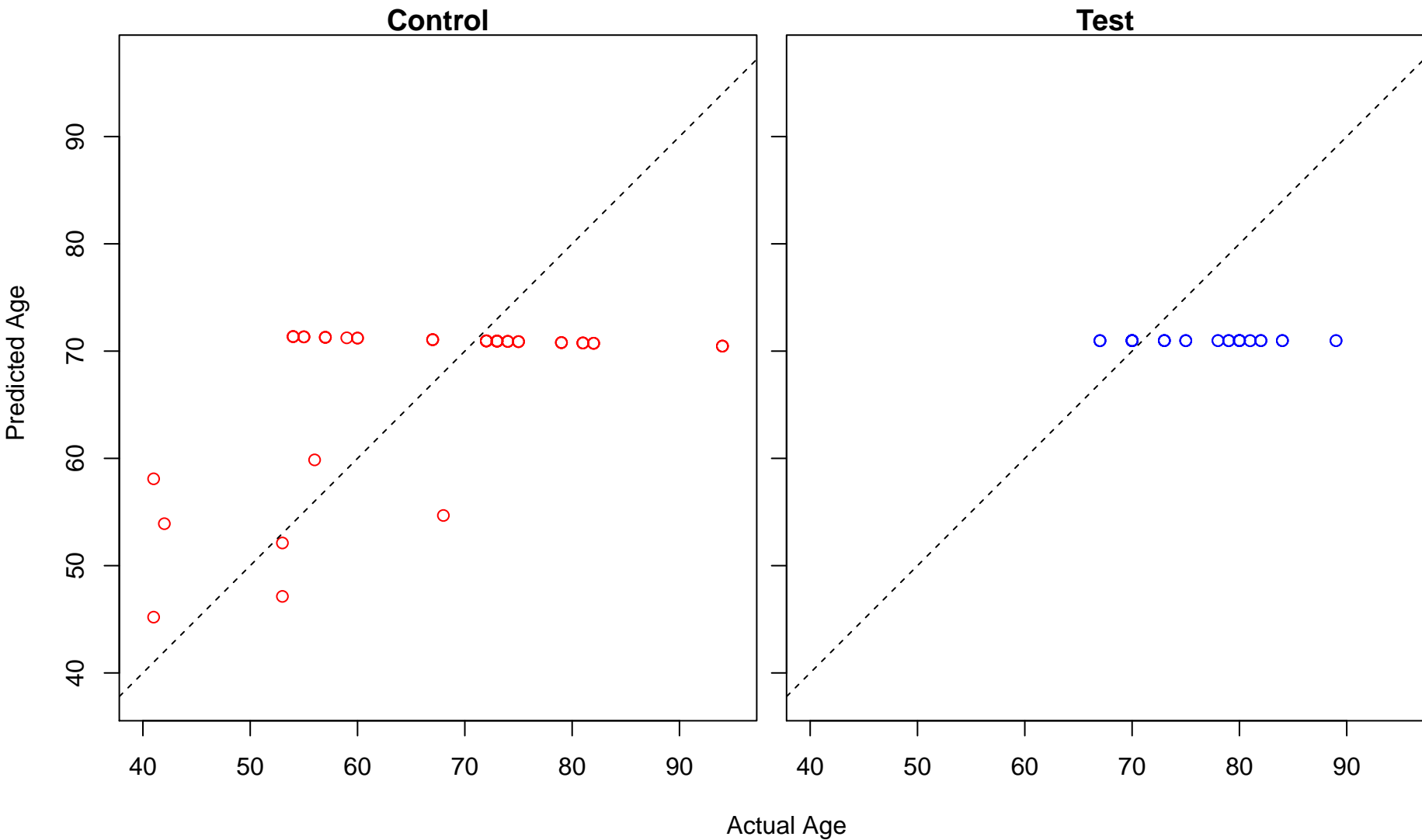


Test

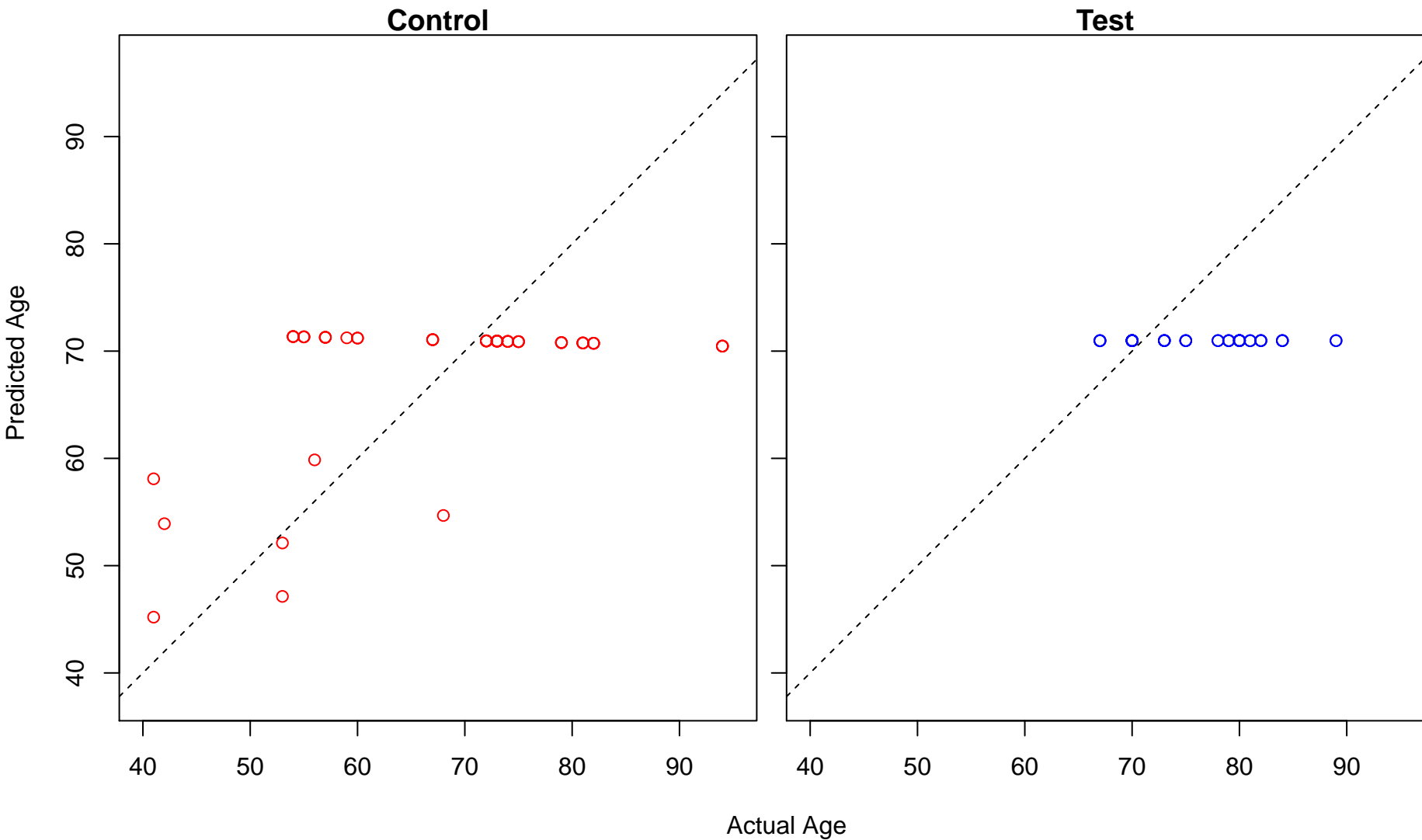


Actual Age

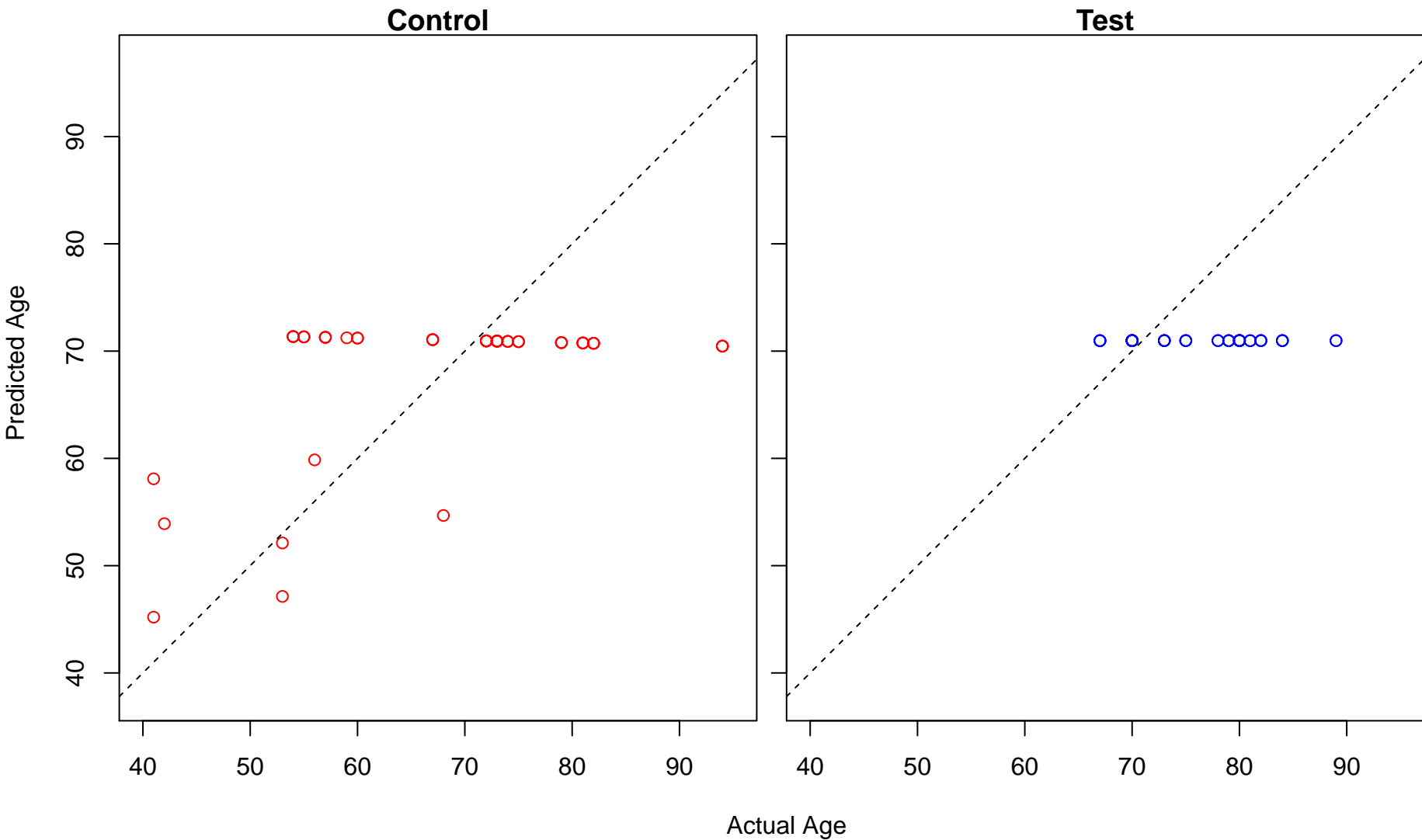
oxidoreduction coenzyme metabolic process (Score: 0.811949)



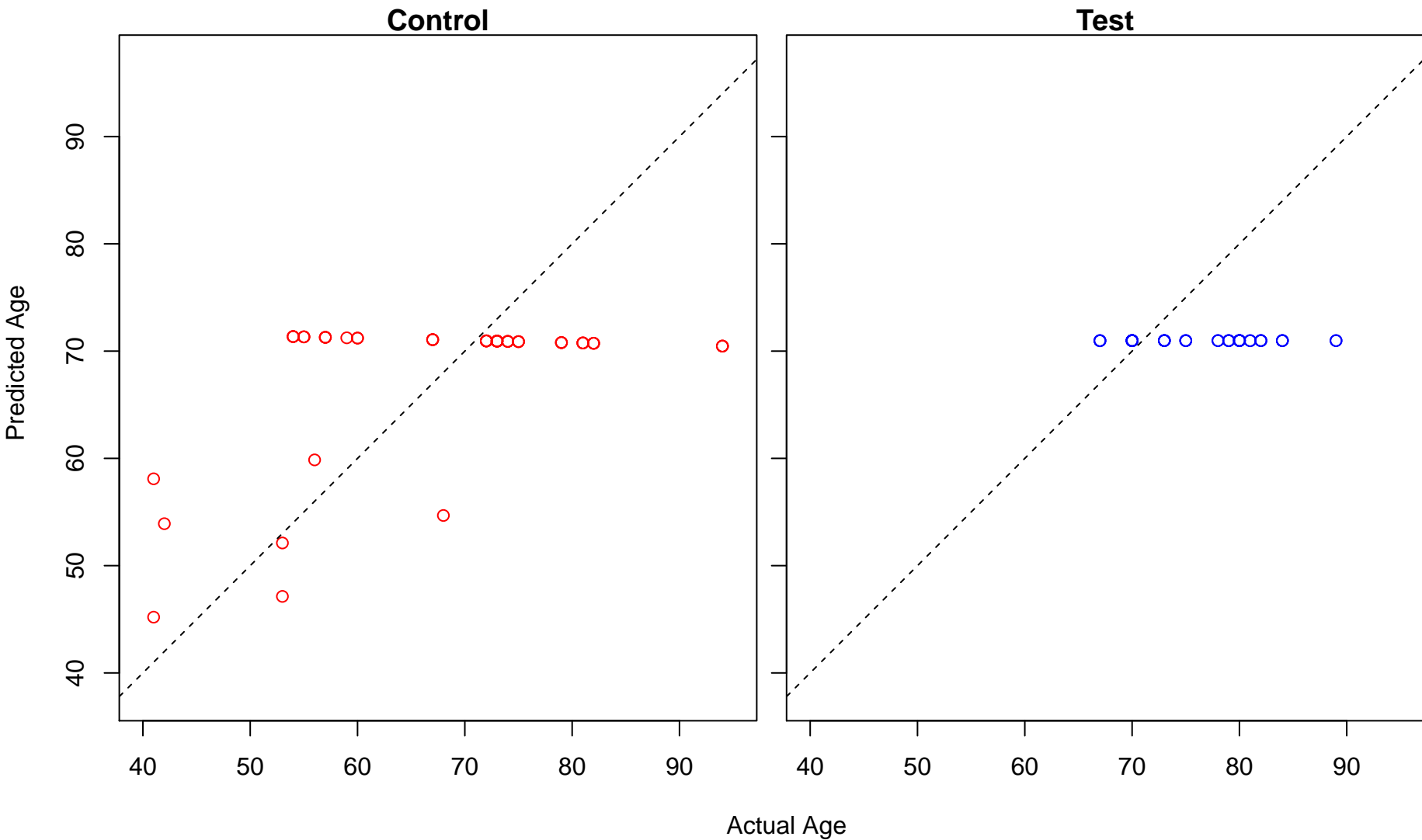
NADH metabolic process (Score: 0.811949)



NADH regeneration (Score: 0.811949)

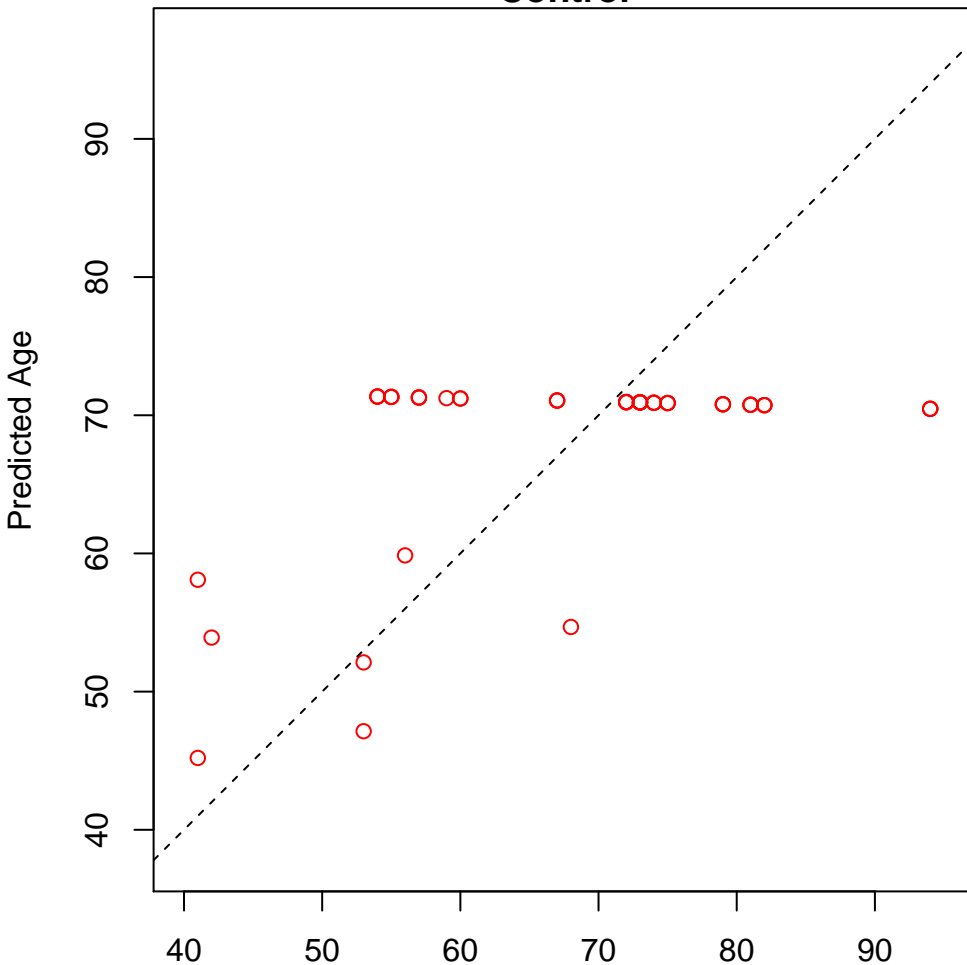


ATP generation from ADP (Score: 0.811949)

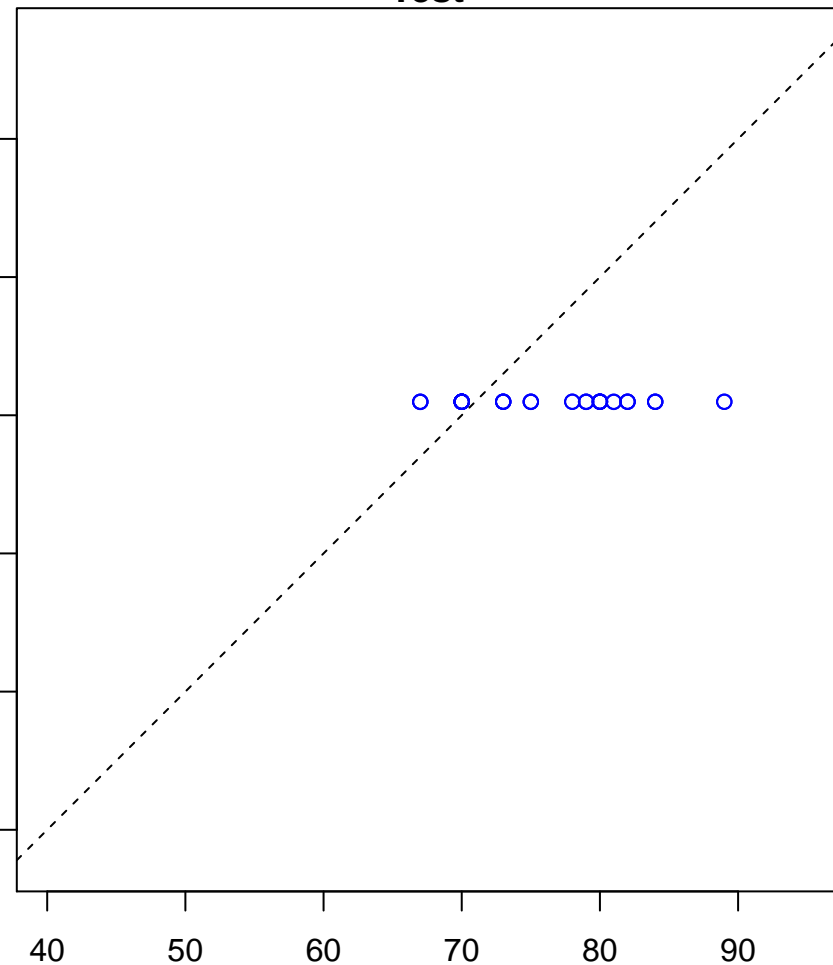


carbohydrate catabolic process (Score: 0.811949)

Control

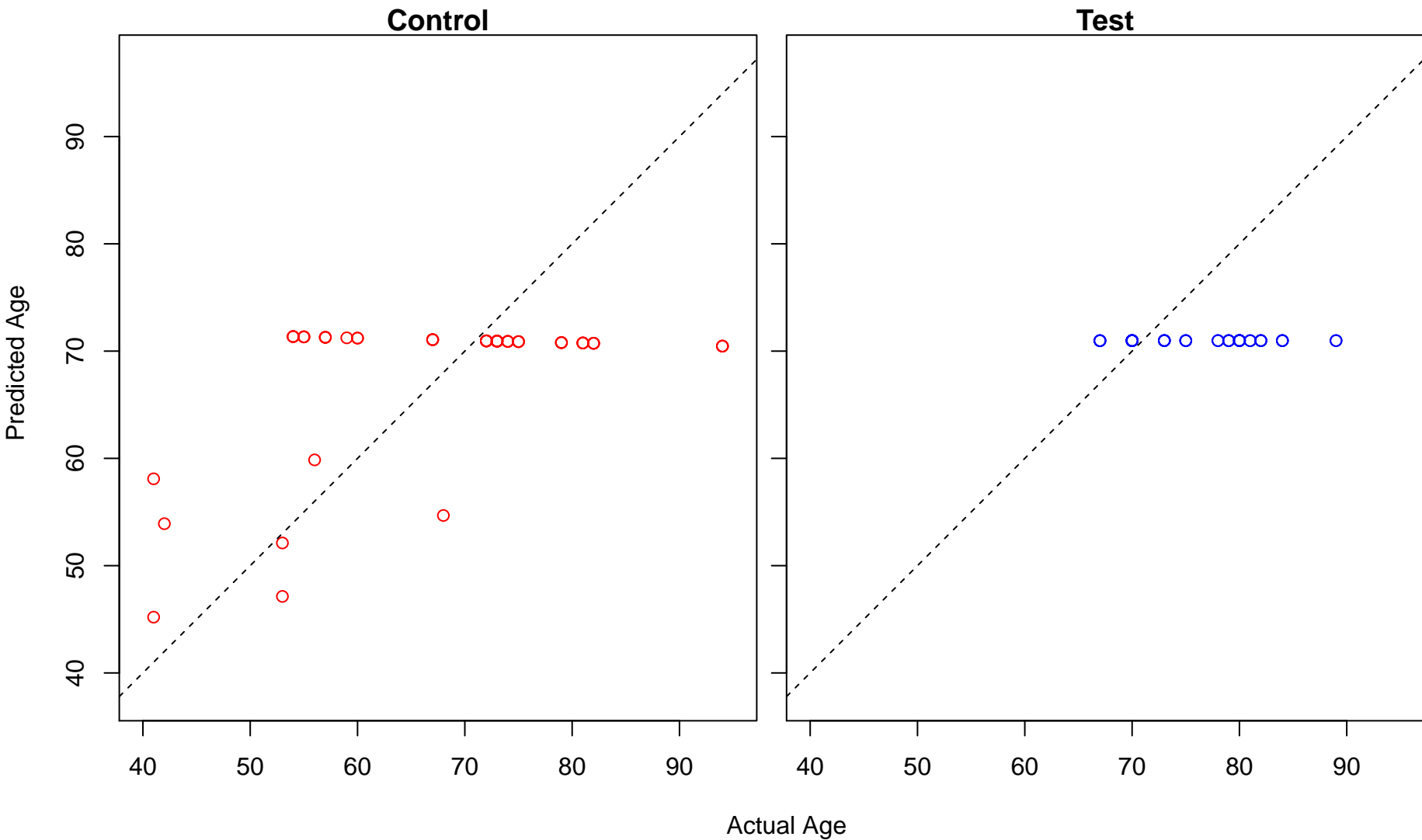


Test



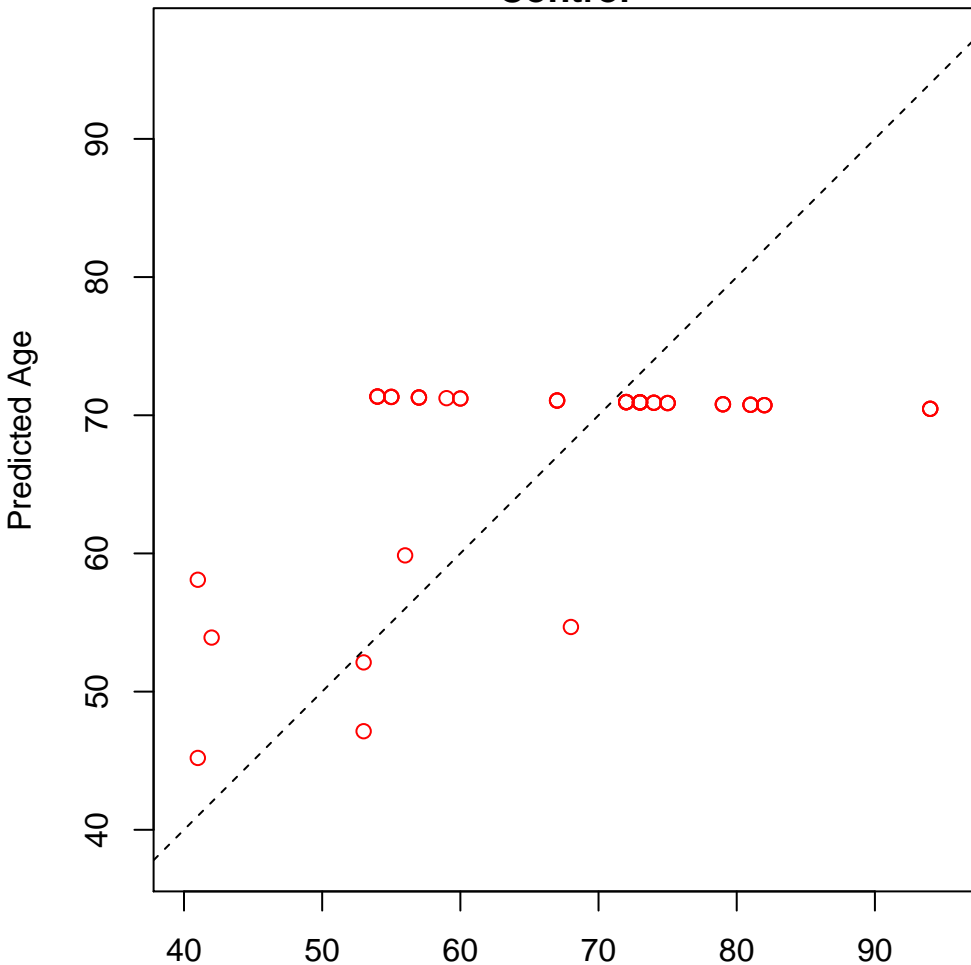
Actual Age

hexose catabolic process (Score: 0.811949)

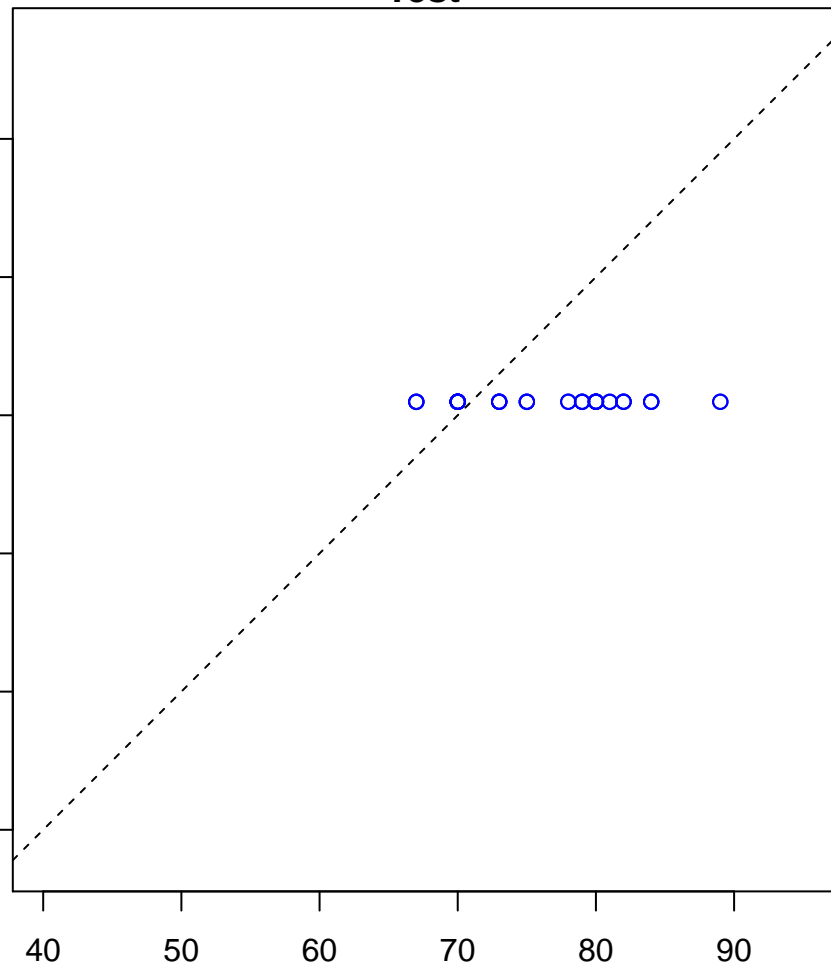


pyridine nucleotide metabolic process (Score: 0.811949)

Control

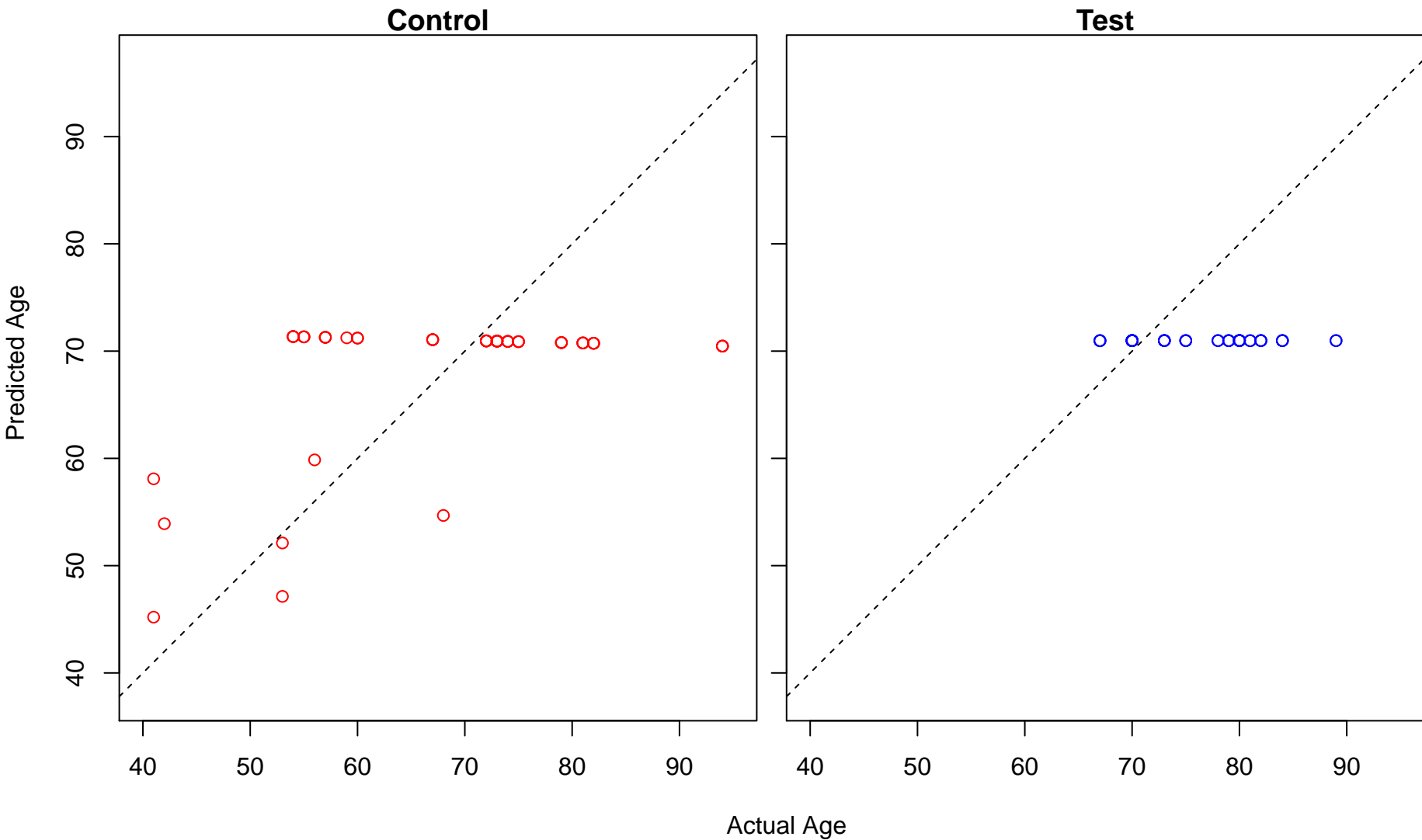


Test



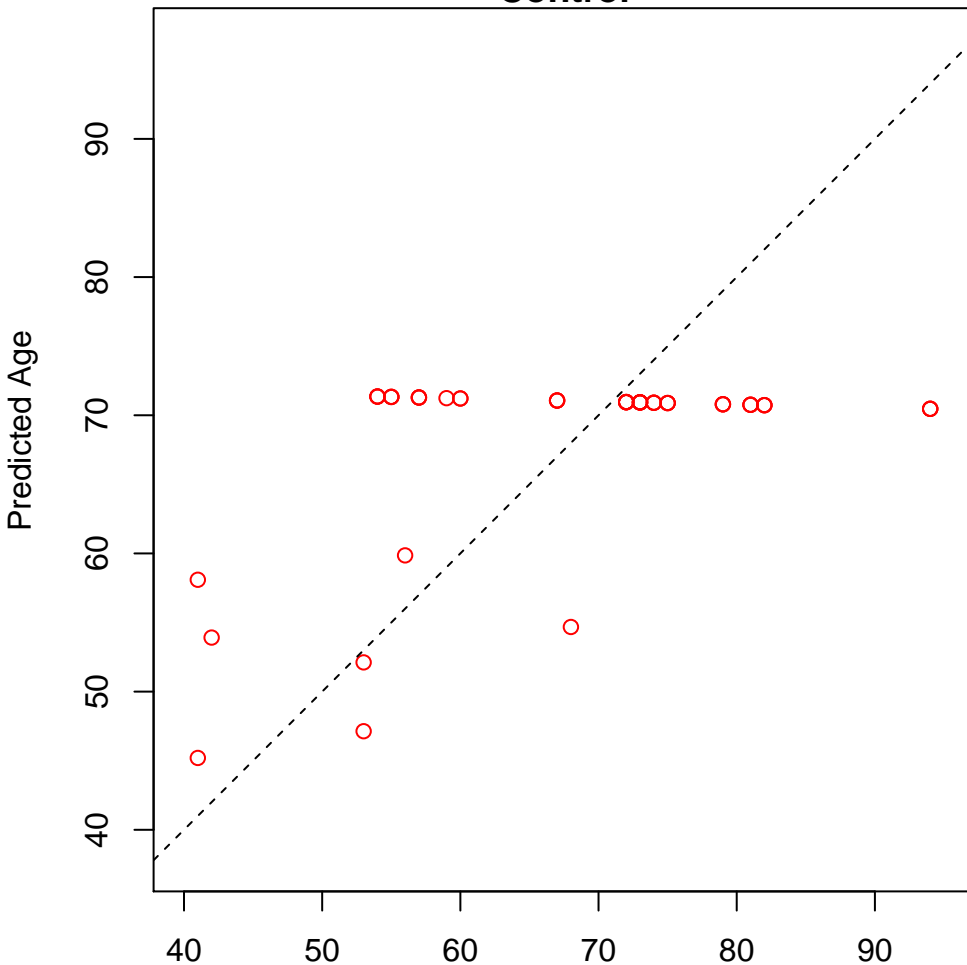
Actual Age

NAD metabolic process (Score: 0.811949)

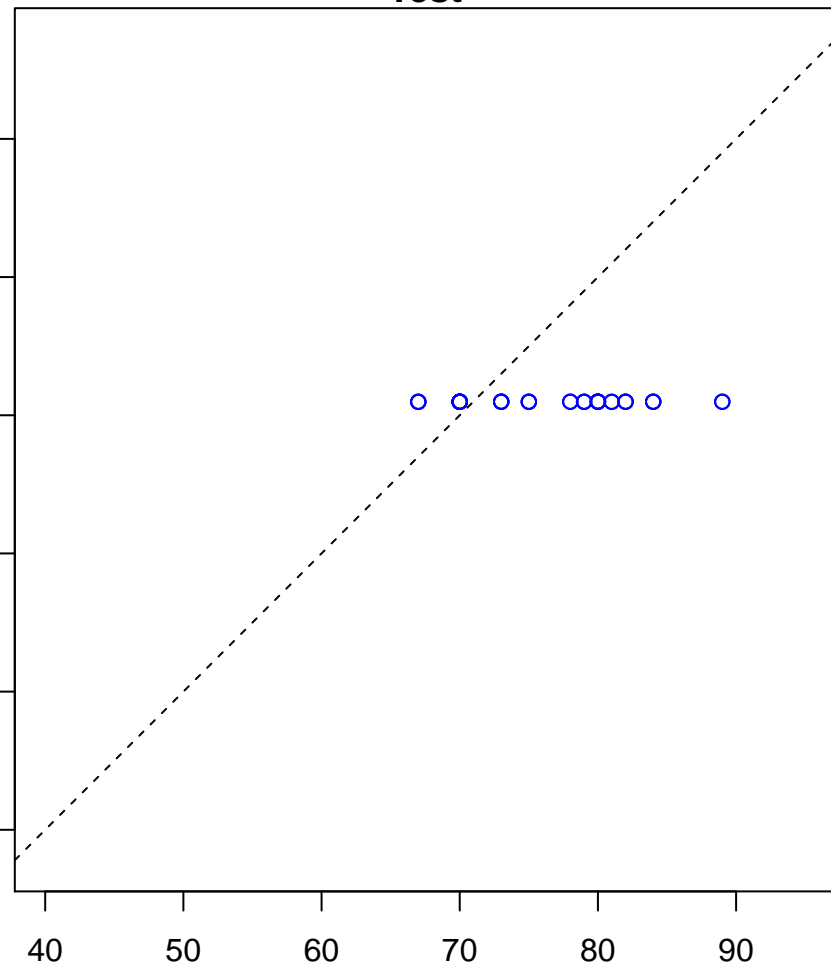


monosaccharide catabolic process (Score: 0.811949)

Control



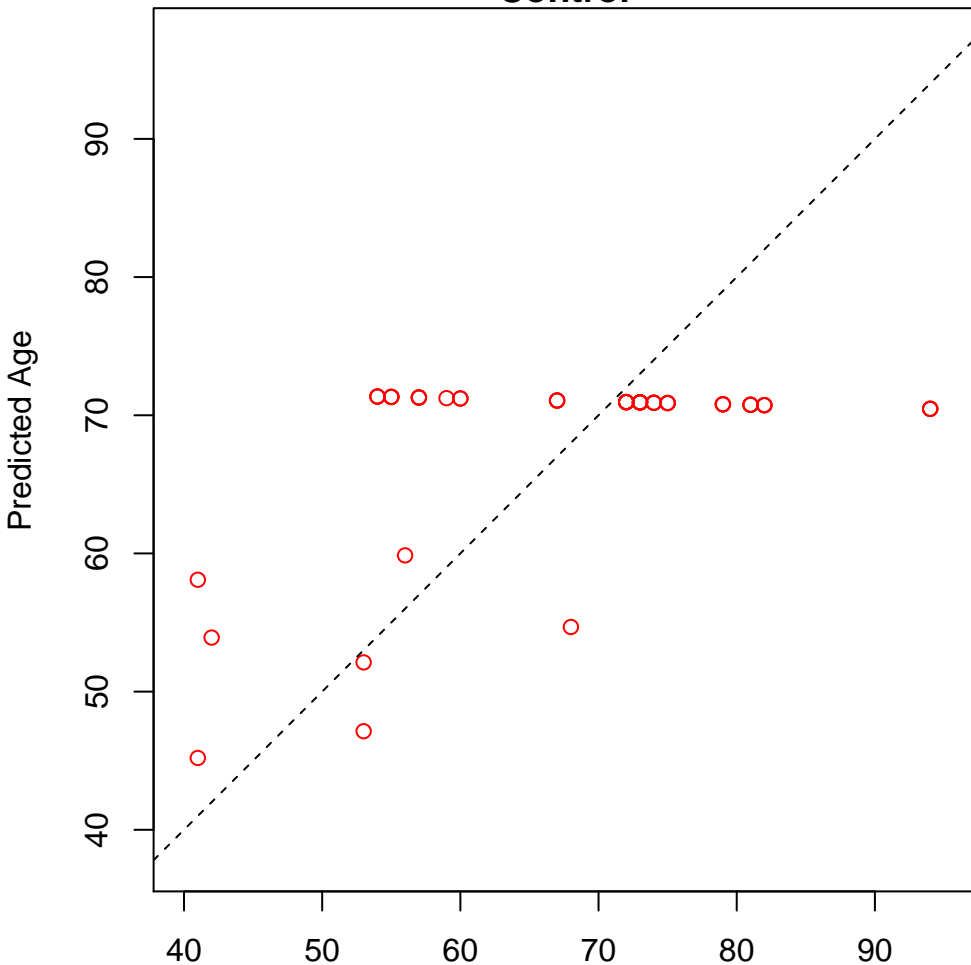
Test



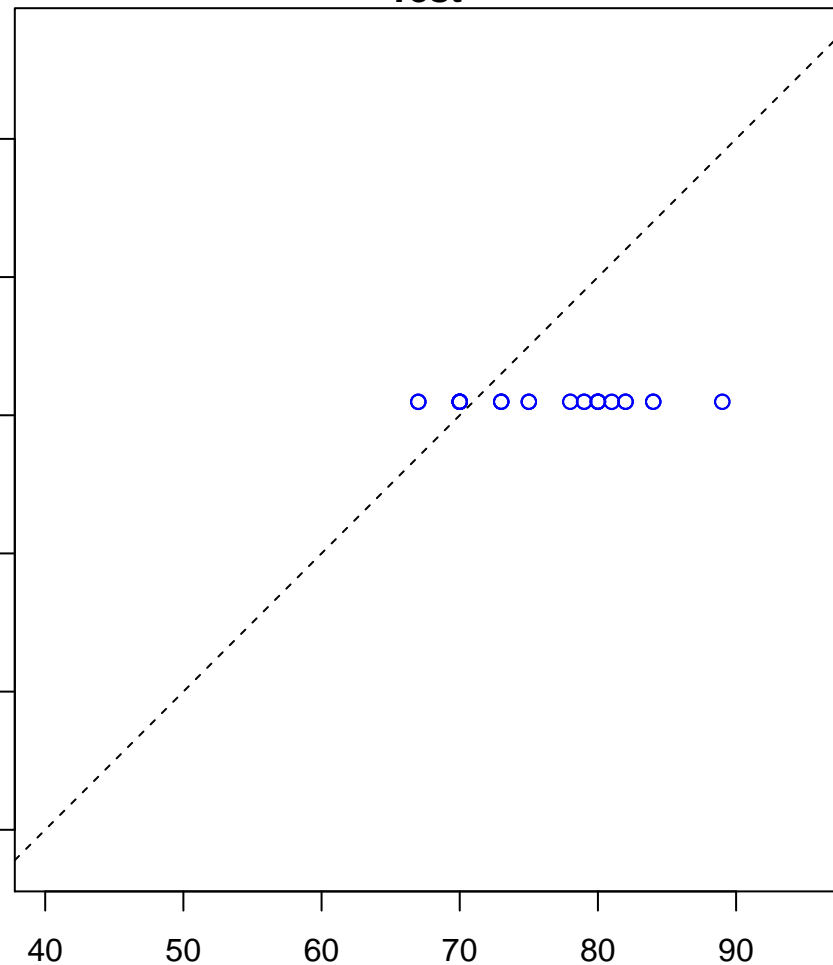
Actual Age

nicotinamide nucleotide metabolic process (Score: 0.811949)

Control

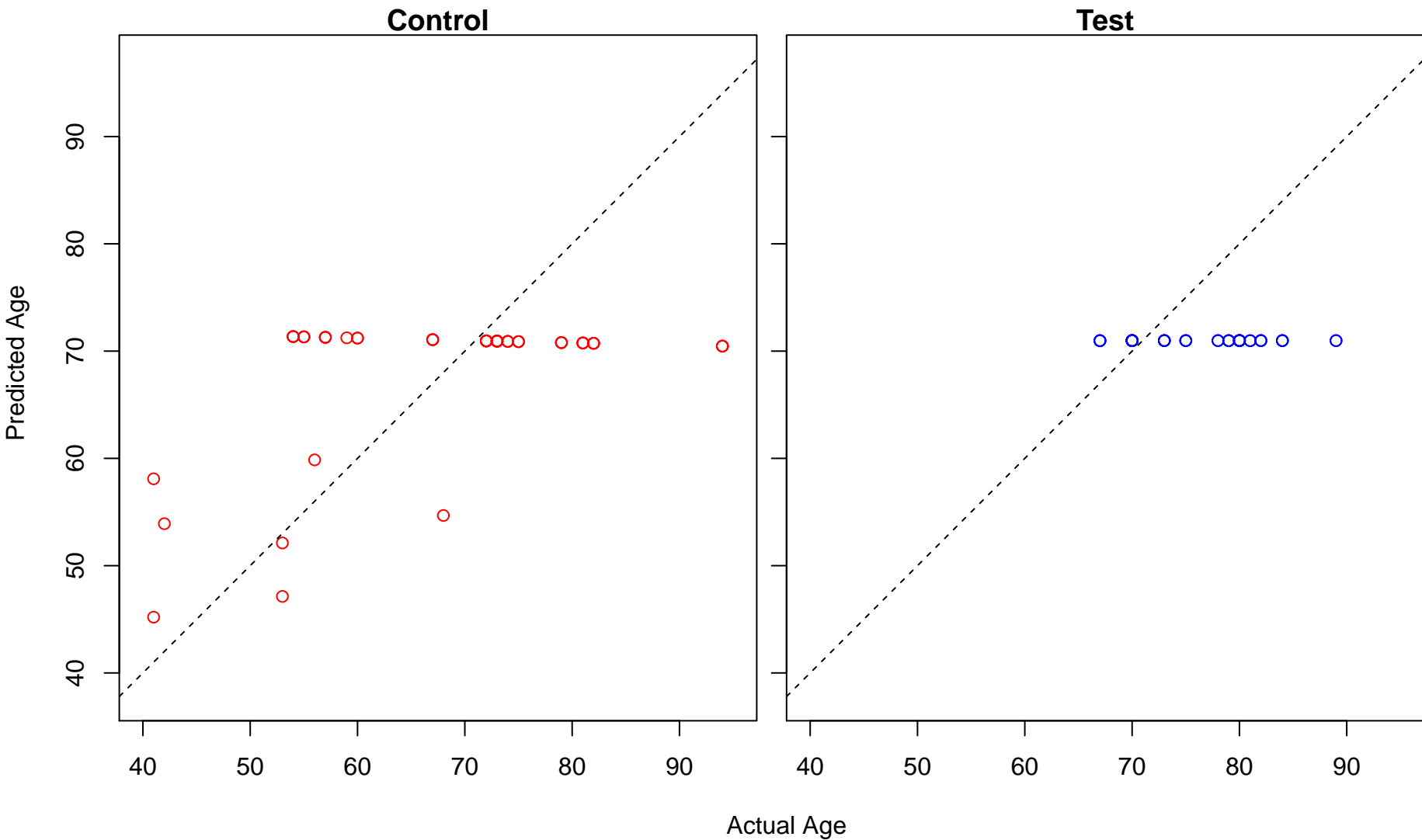


Test

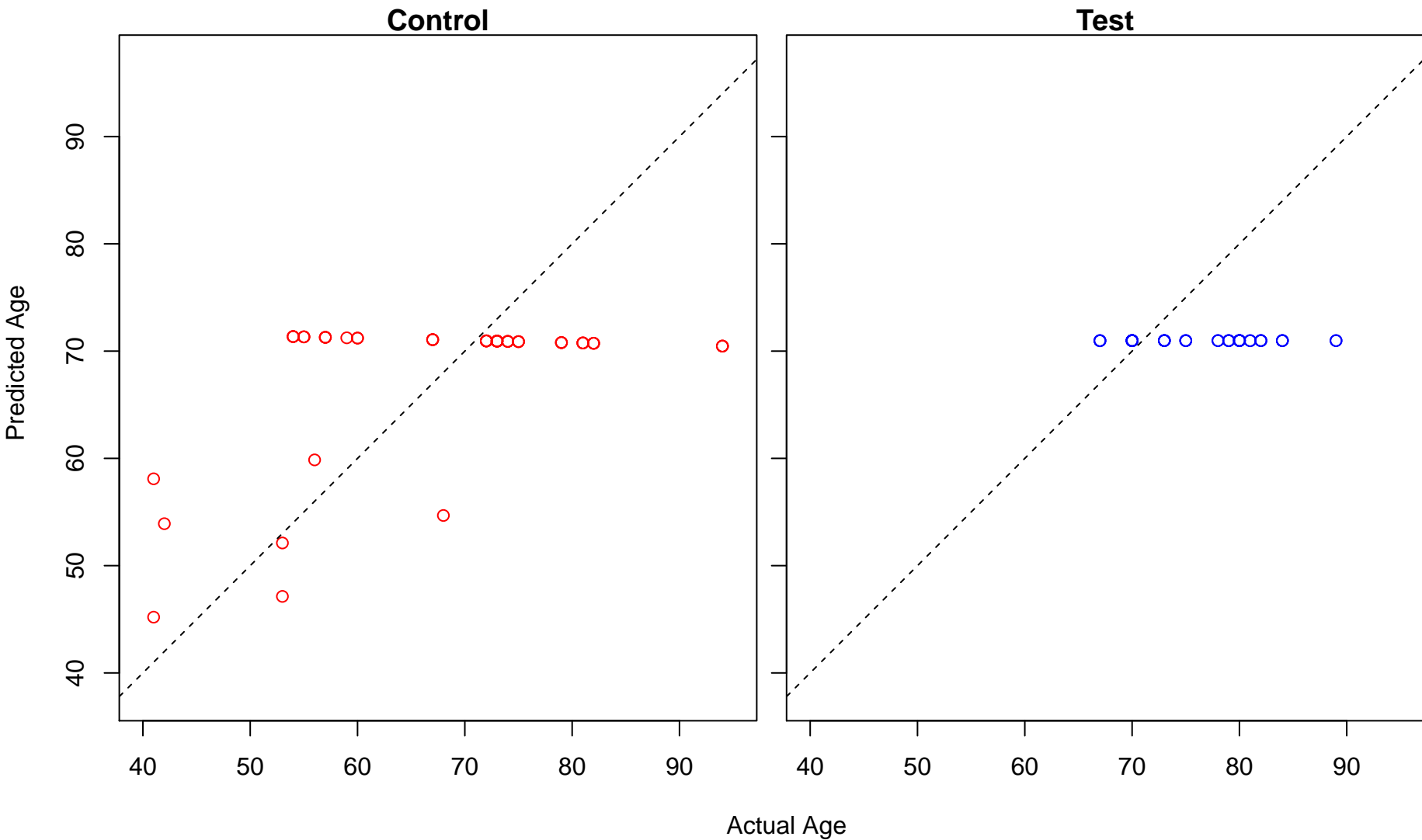


Actual Age

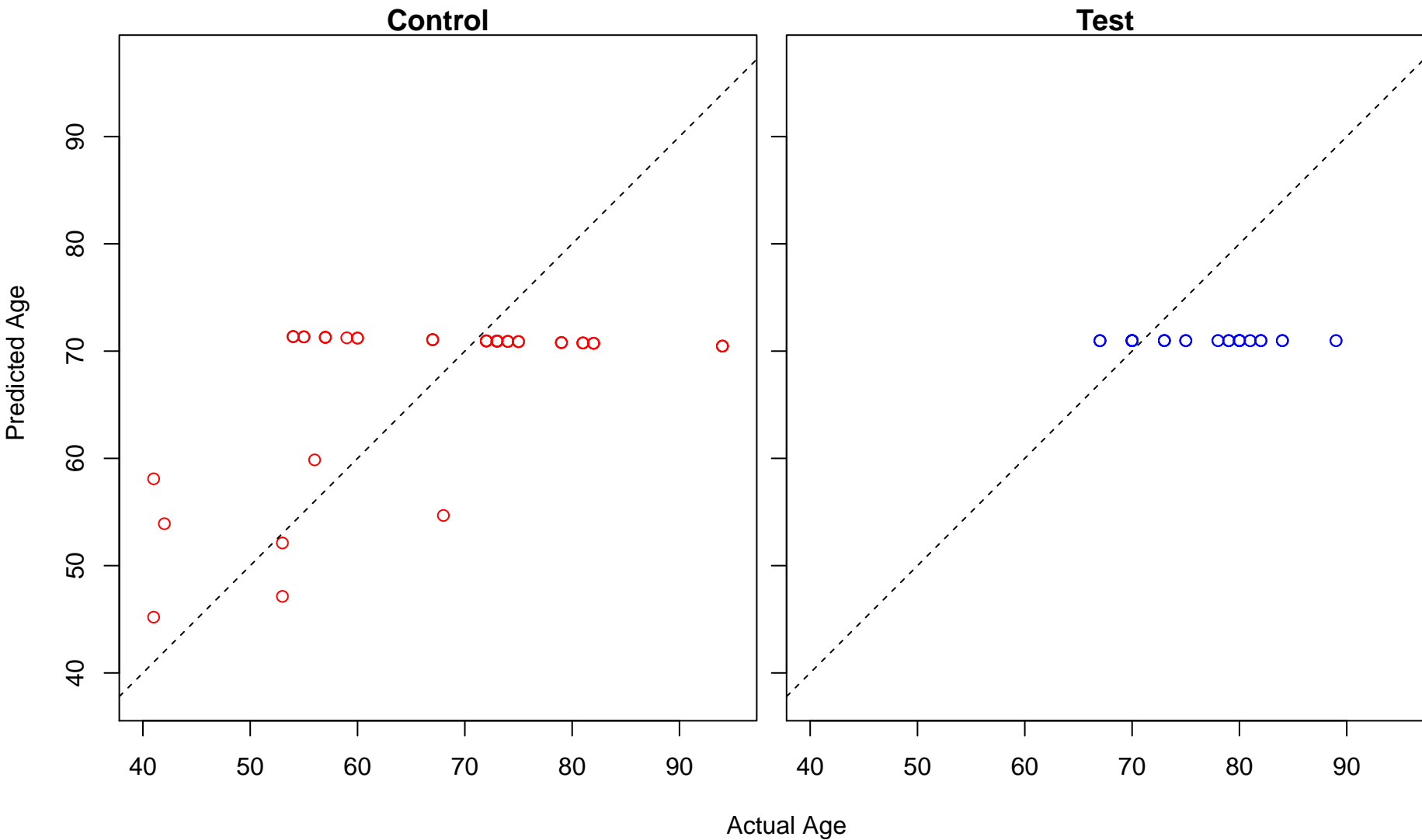
glycolytic process through fructose-6-phosphate (Score: 0.811949)



glycolytic process through glucose-6-phosphate (Score: 0.811949)

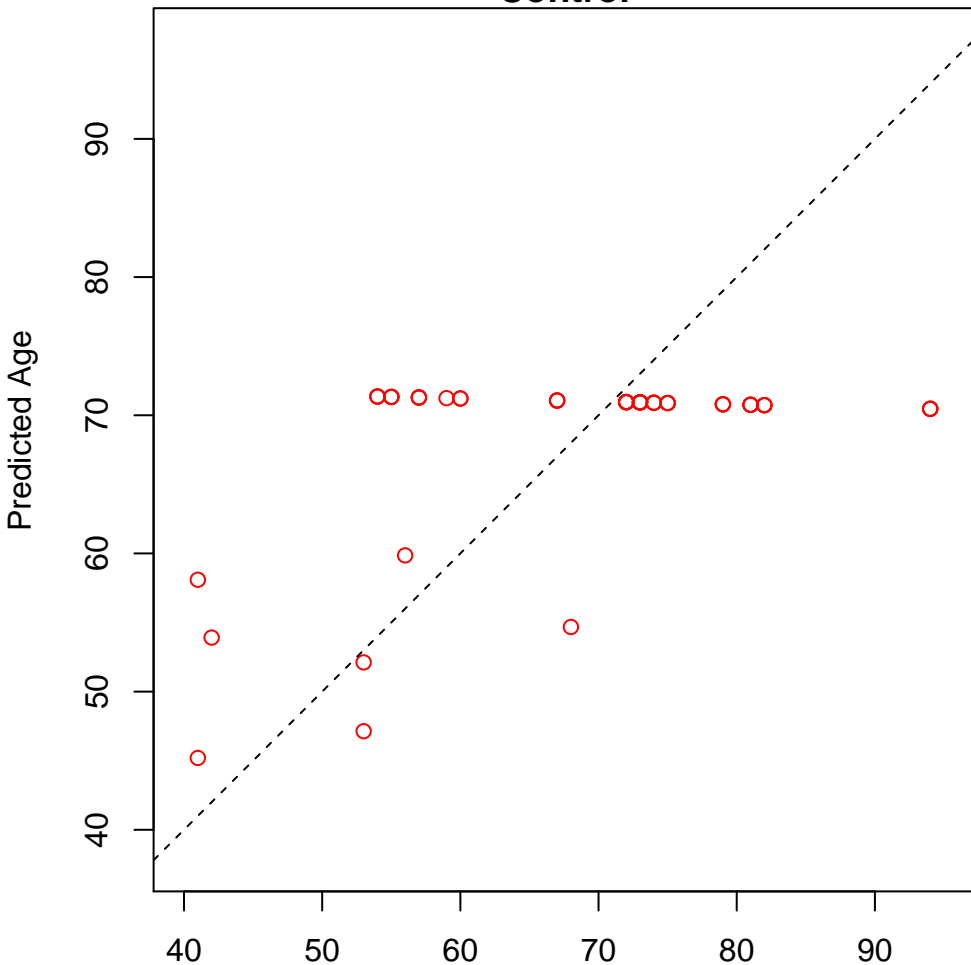


canonical glycolysis (Score: 0.811949)

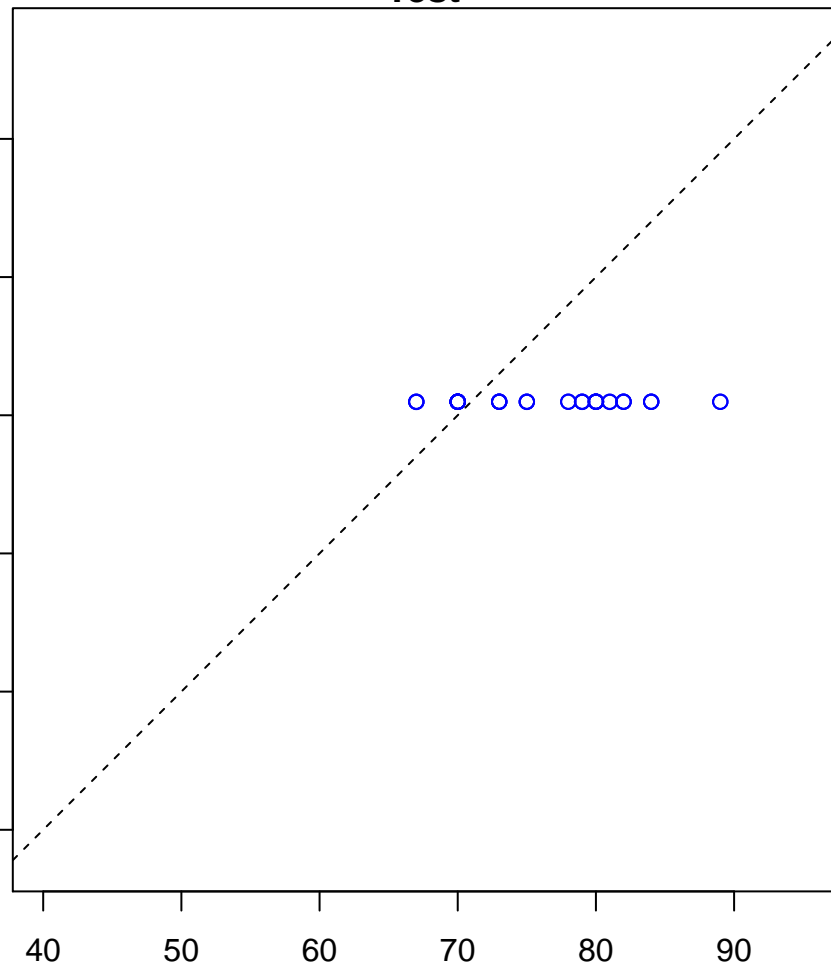


glucose catabolic process to pyruvate (Score: 0.811949)

Control

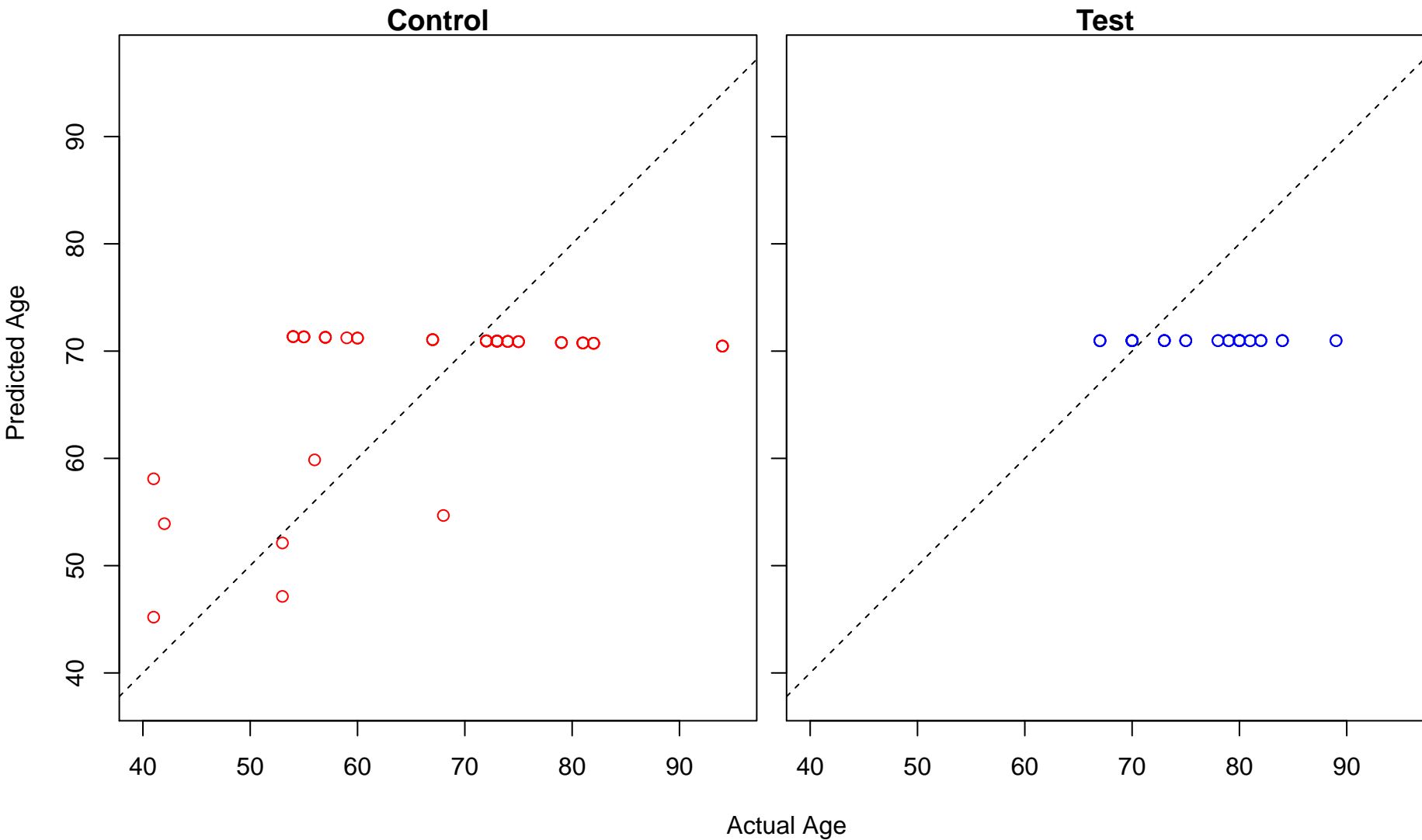


Test



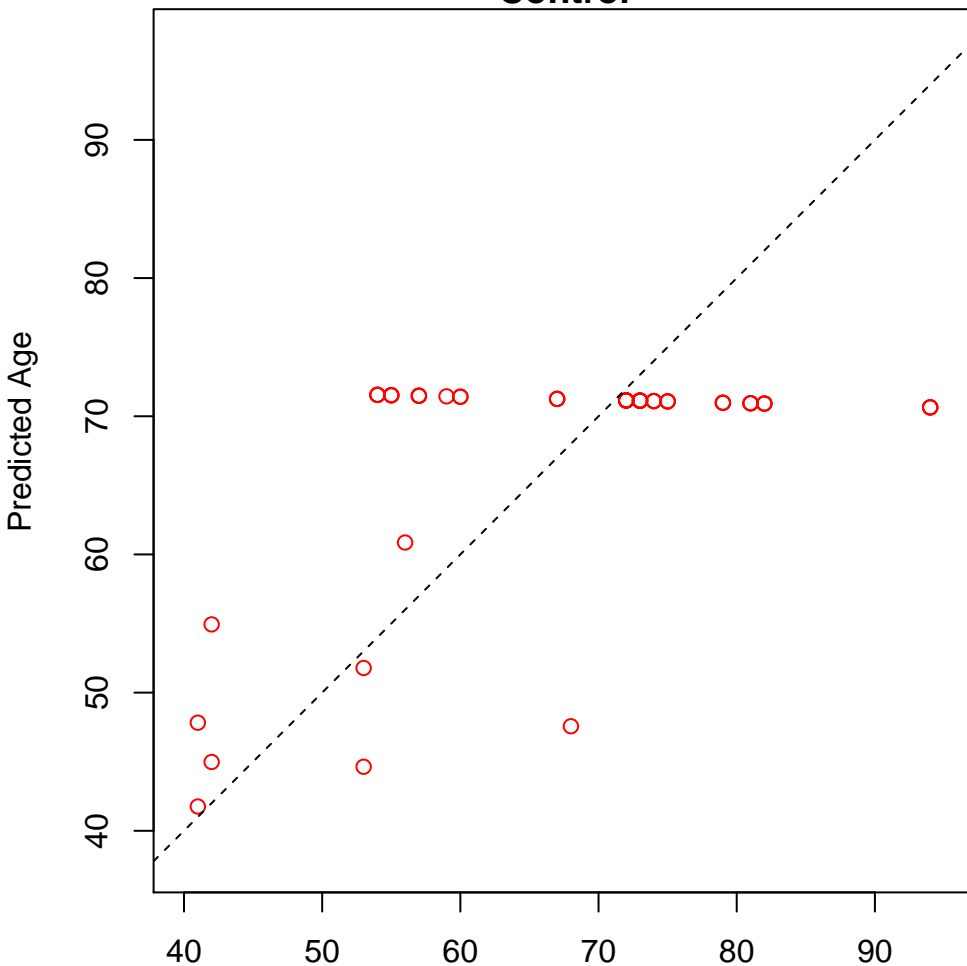
Actual Age

pyridine-containing compound metabolic process (Score: 0.811949)

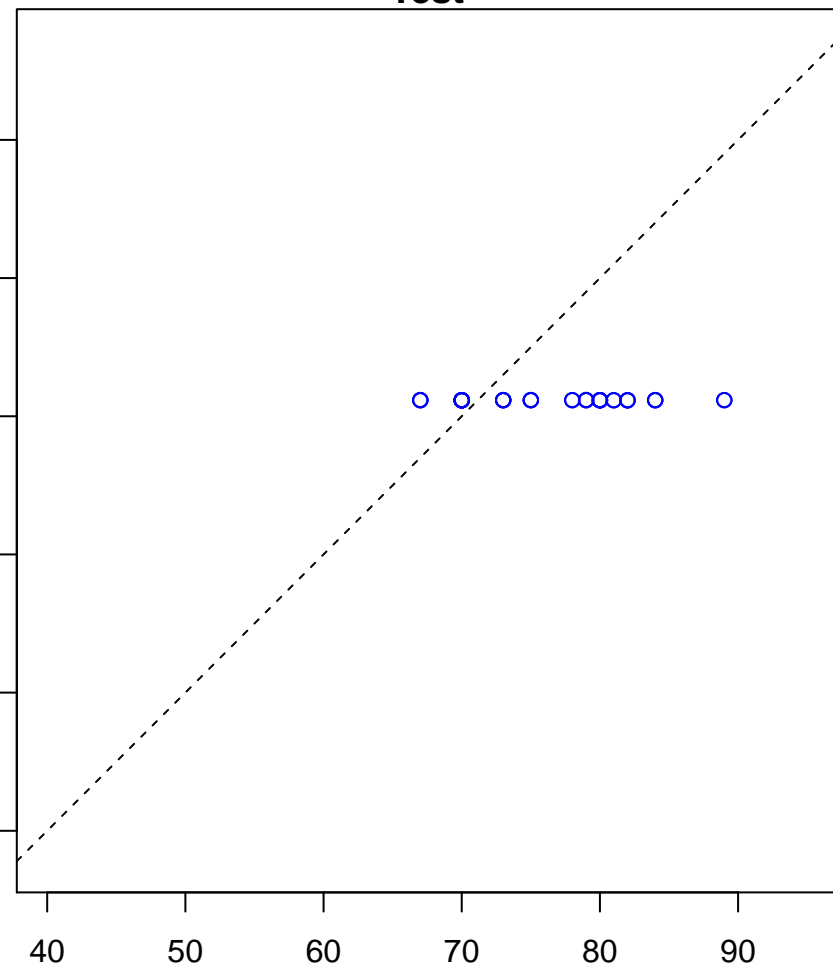


regulation of protein complex assembly (Score: 0.811930)

Control

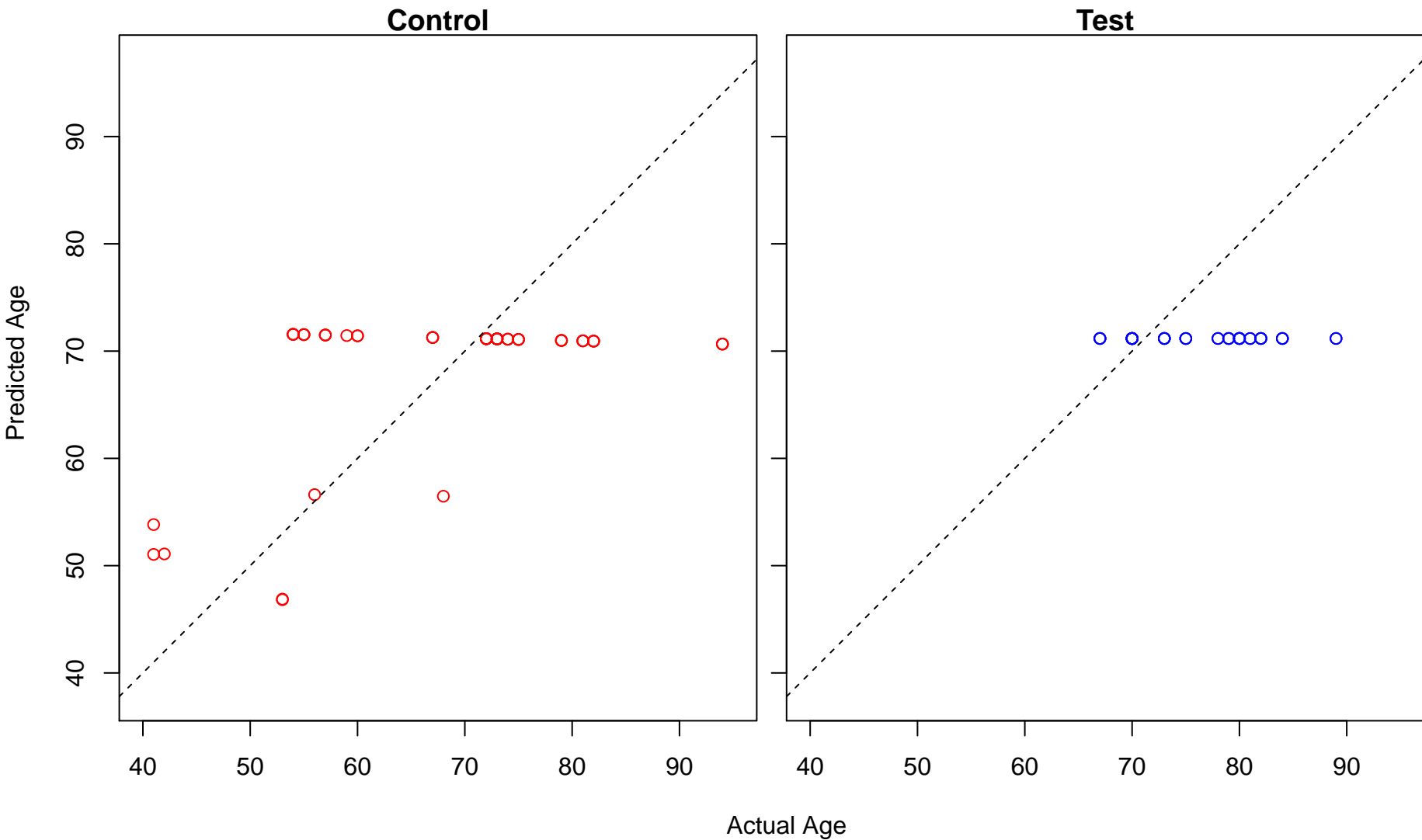


Test

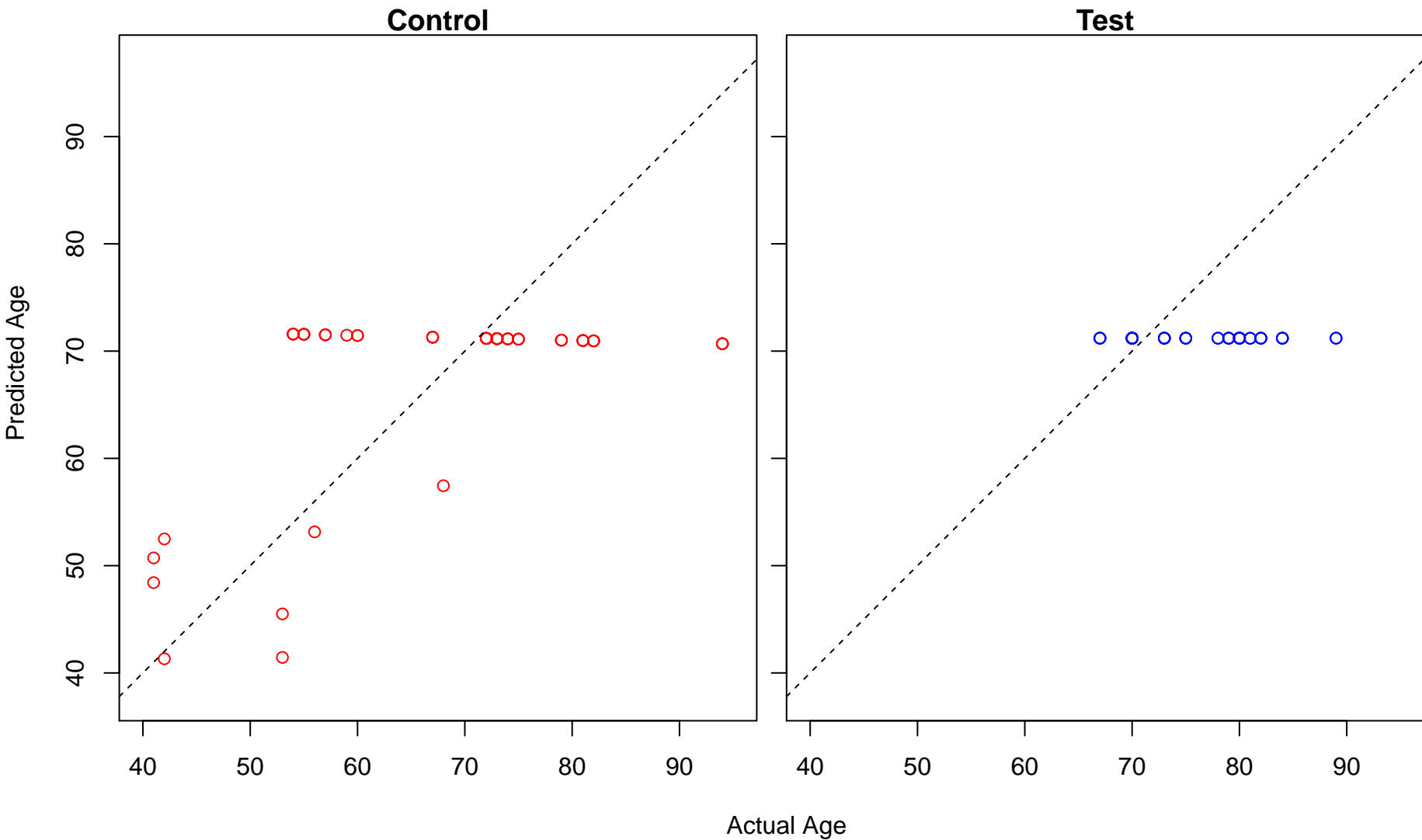


Actual Age

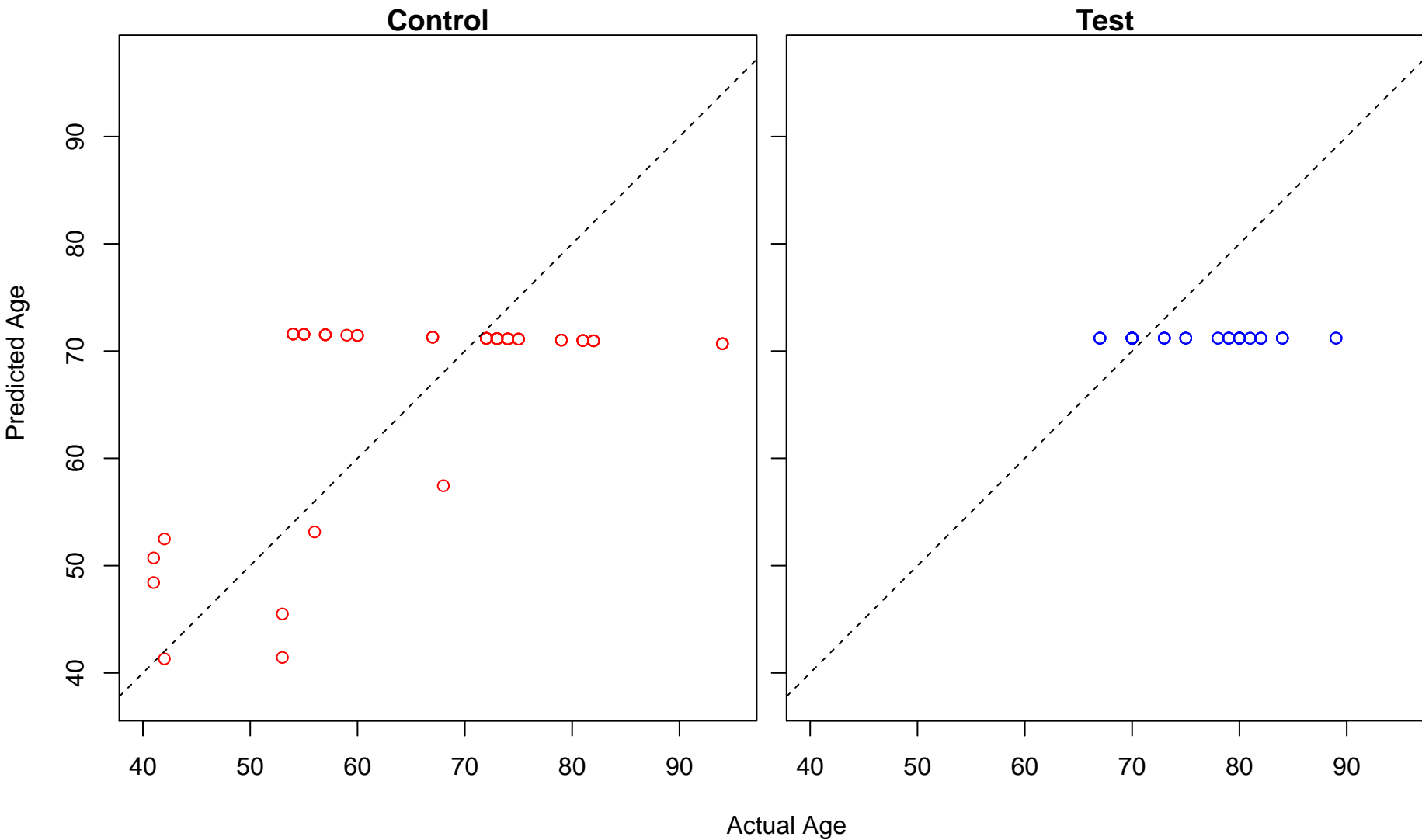
cell cycle process (Score: 0.811732)



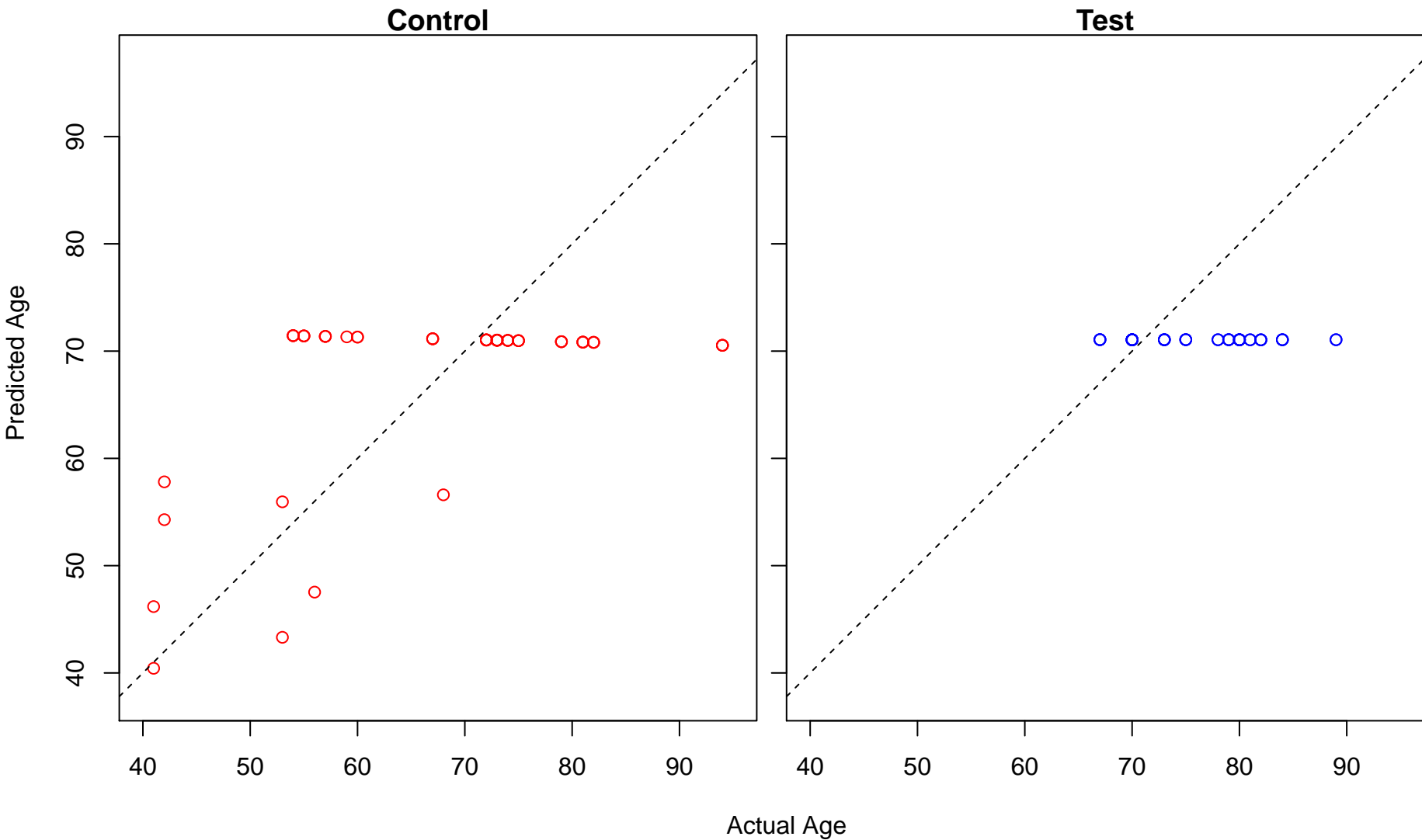
exocytosis (Score: 0.811661)



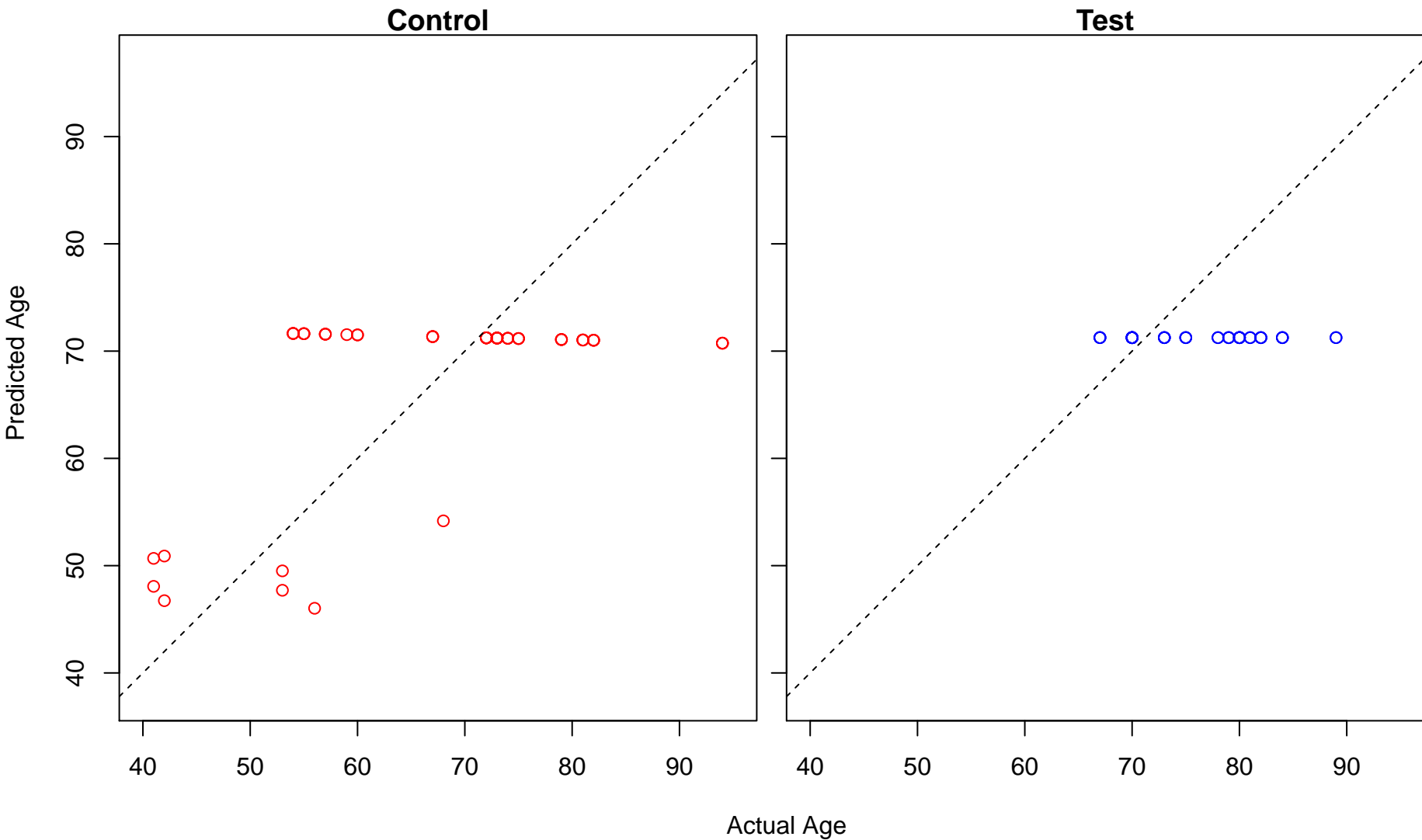
regulated exocytosis (Score: 0.811655)



regulation of DNA-templated transcription, elongation (Score: 0.811633)

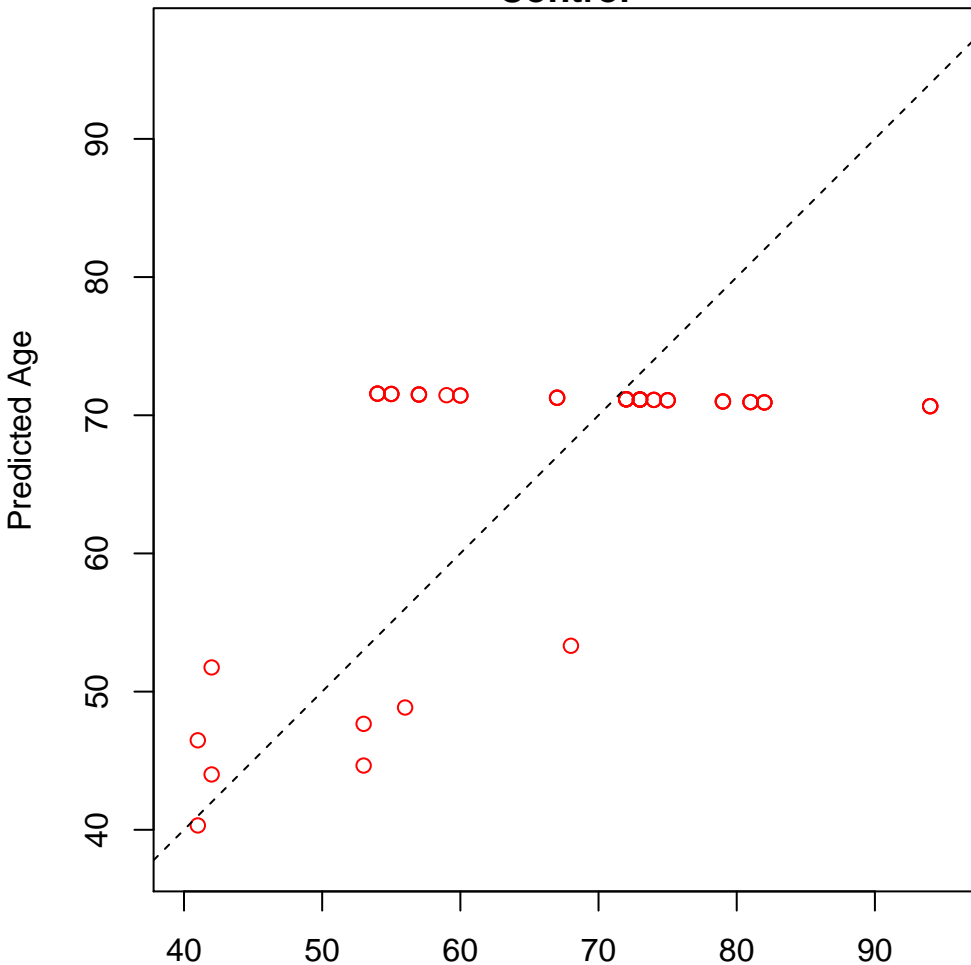


translational elongation (Score: 0.811468)

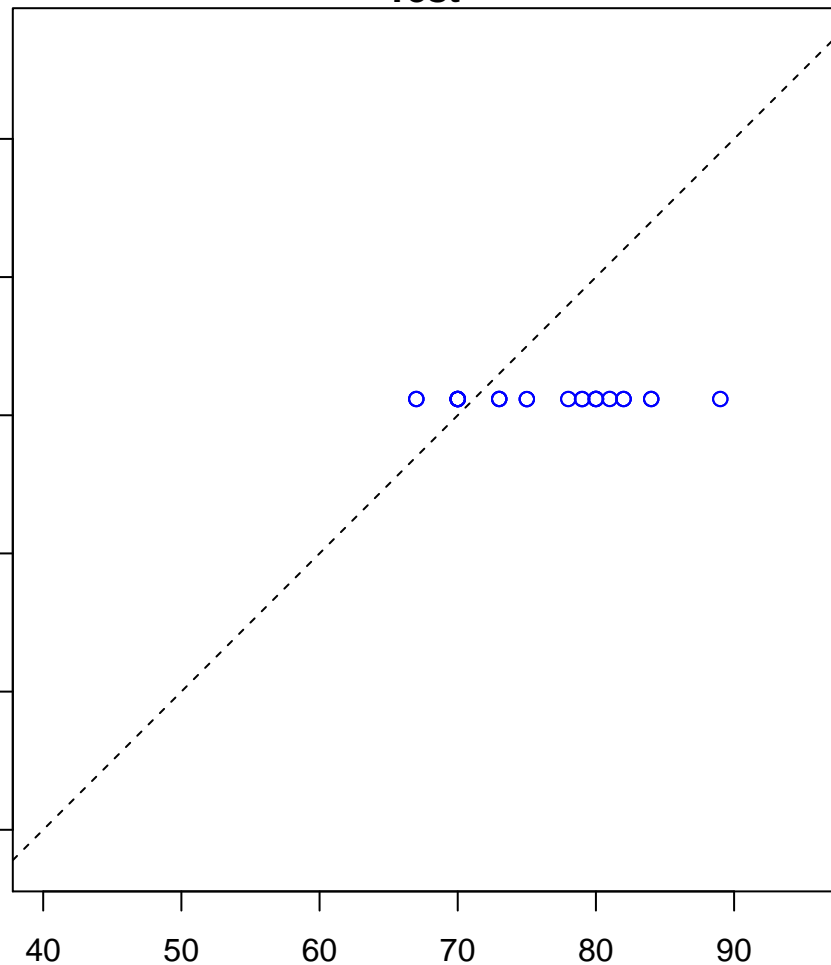


regulation of phosphate metabolic process (Score: 0.811443)

Control

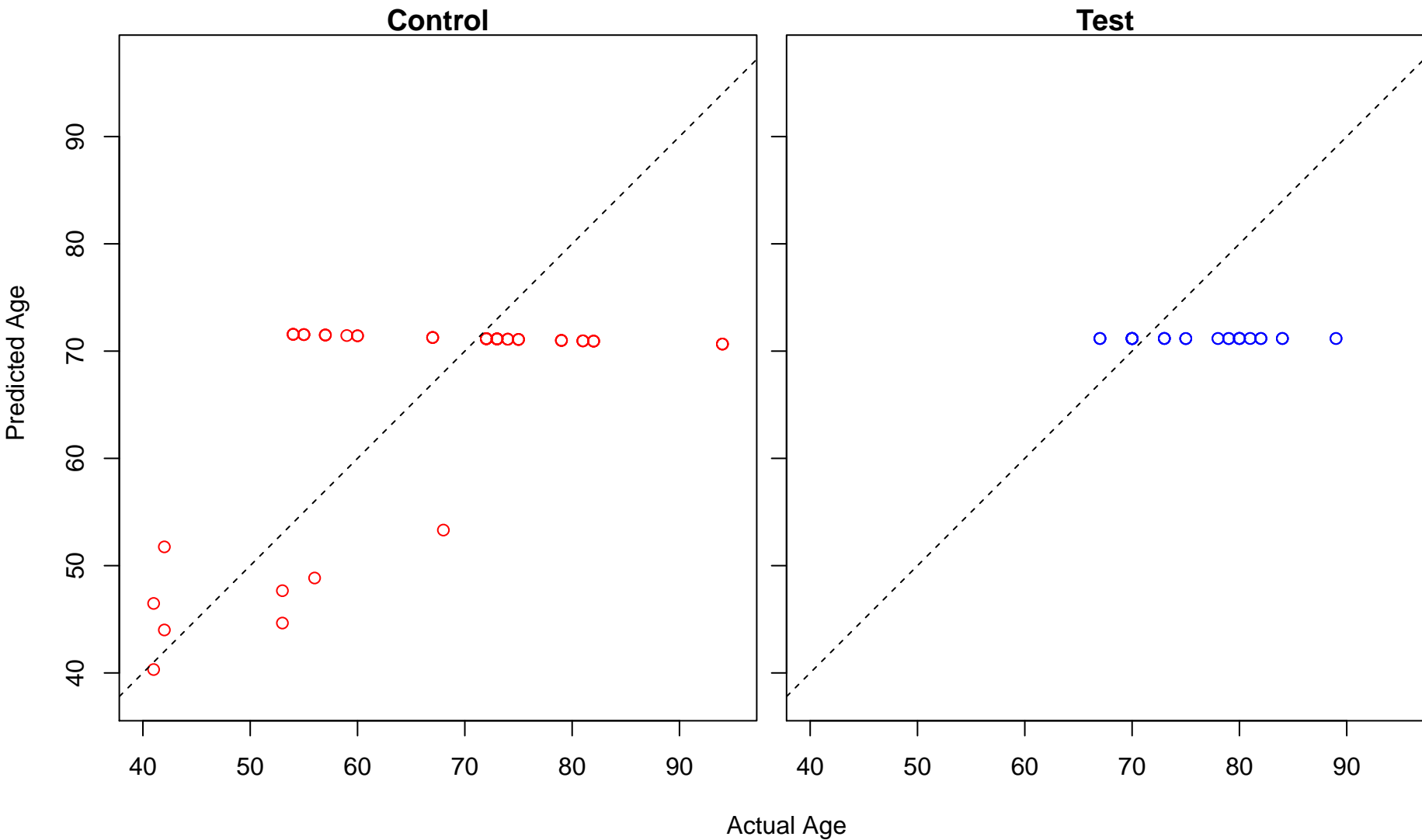


Test



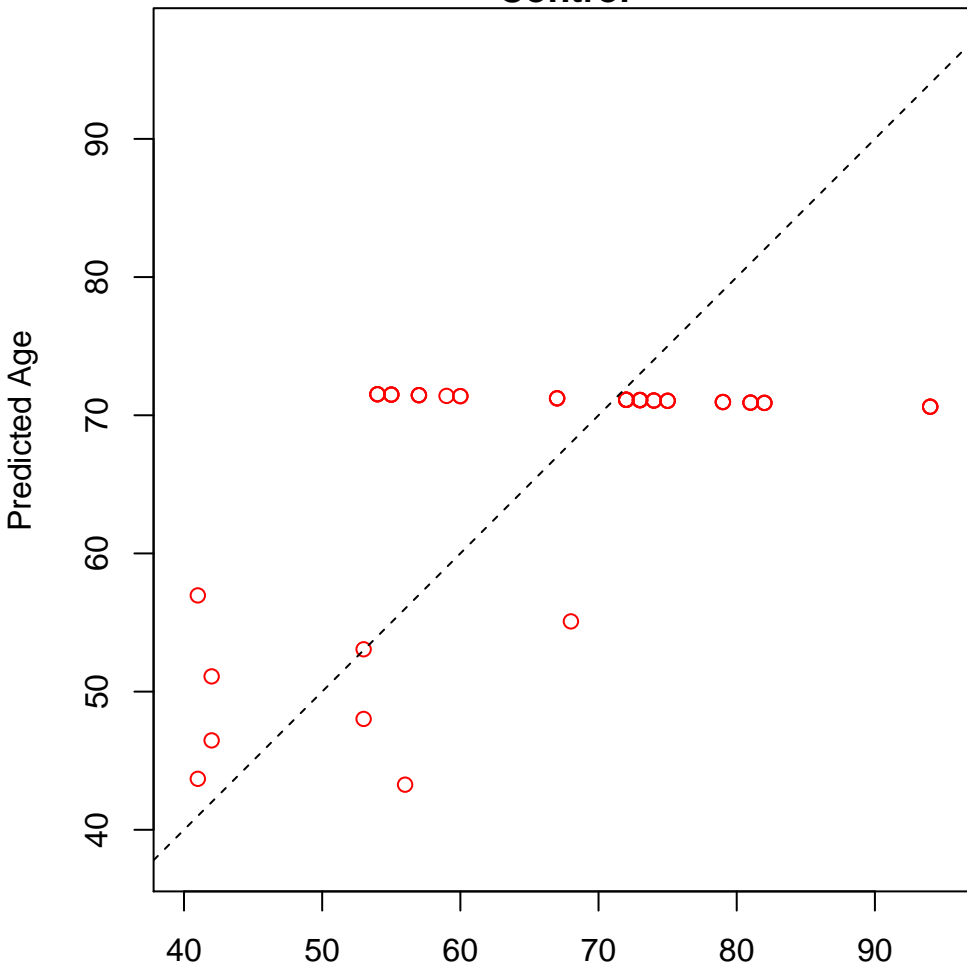
Actual Age

regulation of phosphorus metabolic process (Score: 0.811443)

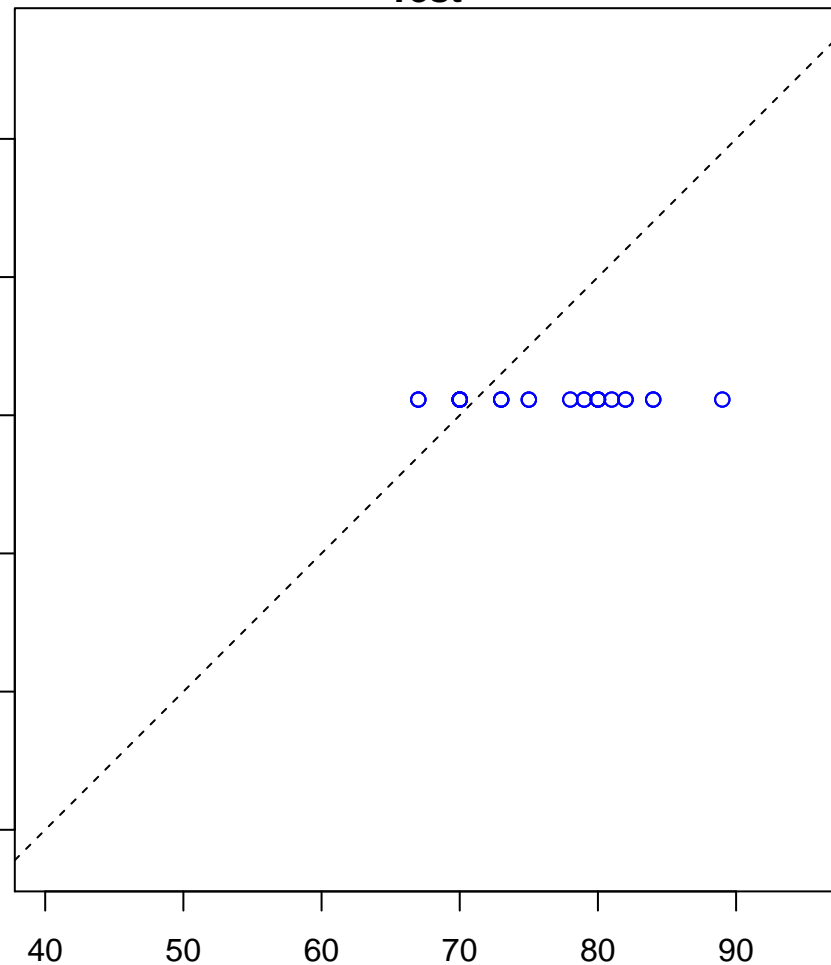


positive regulation of autophagy (Score: 0.811405)

Control

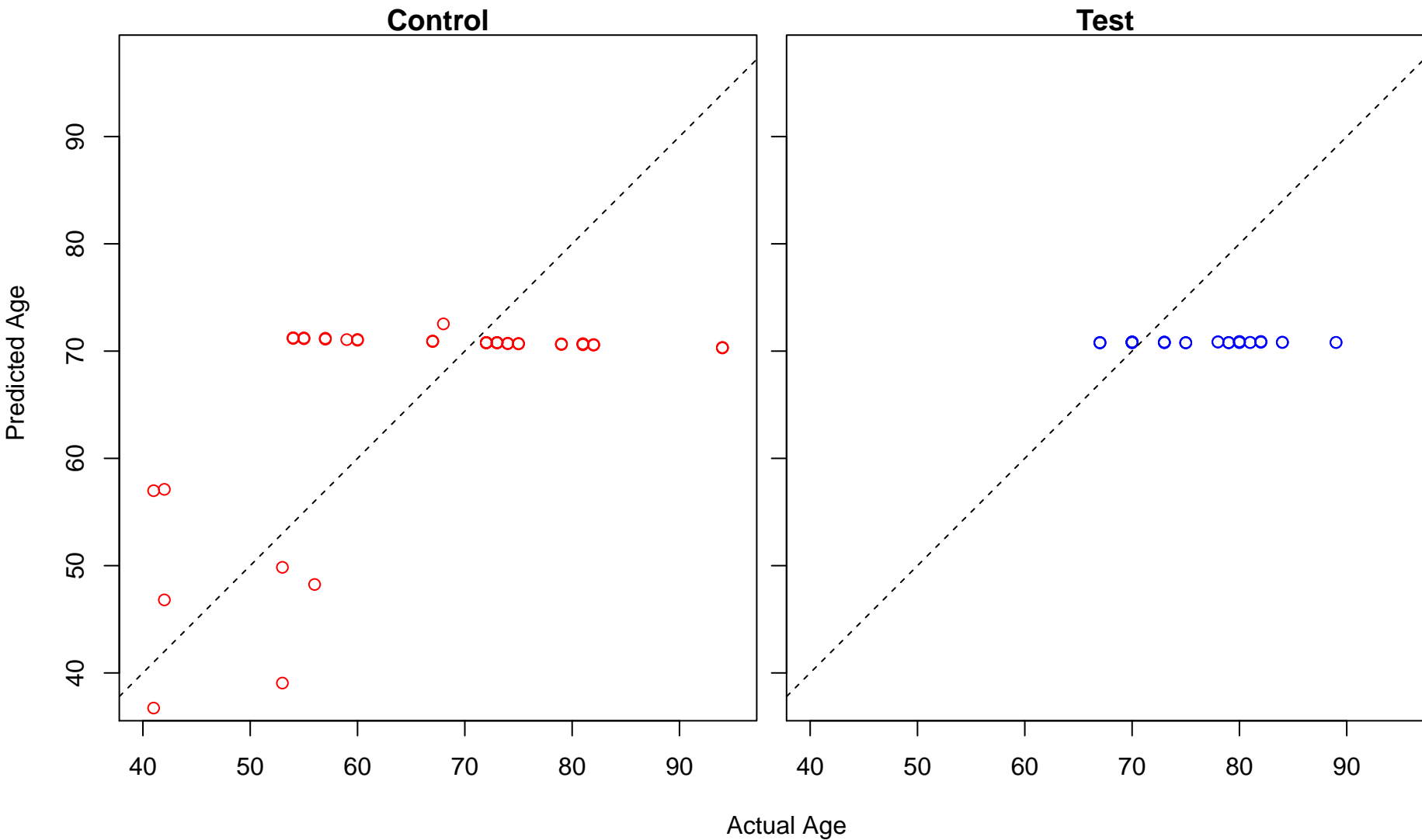


Test

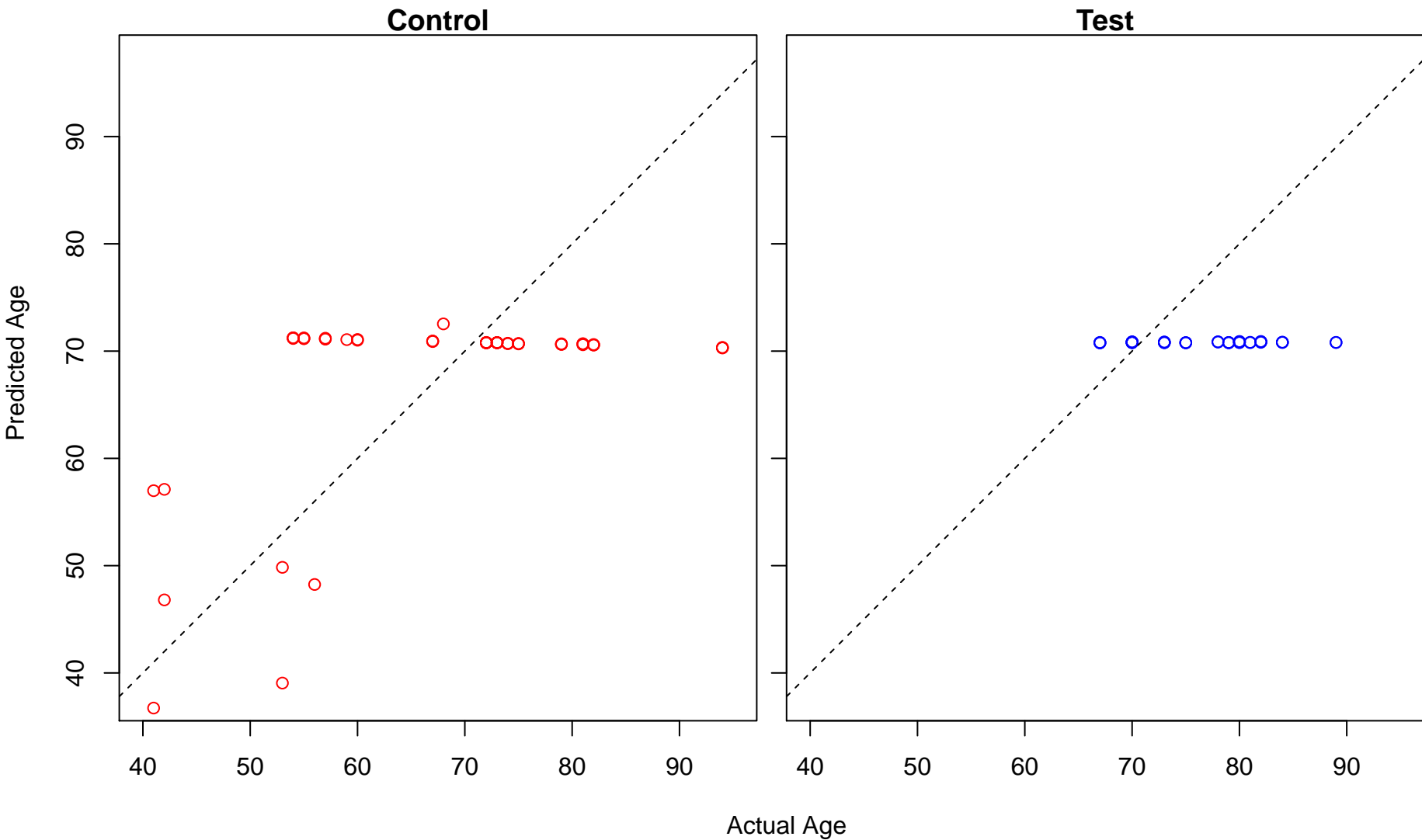


Actual Age

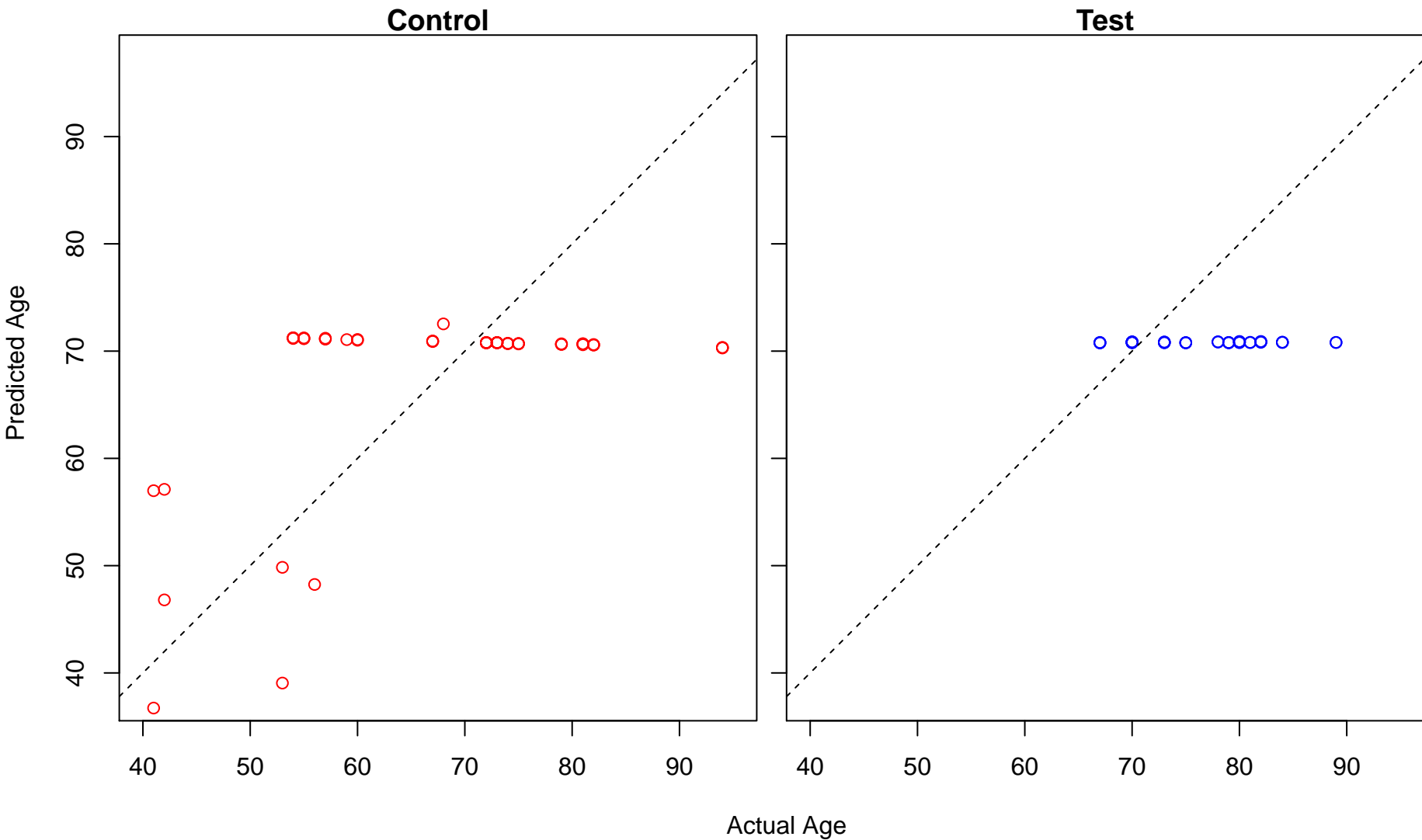
axonogenesis (Score: 0.811247)



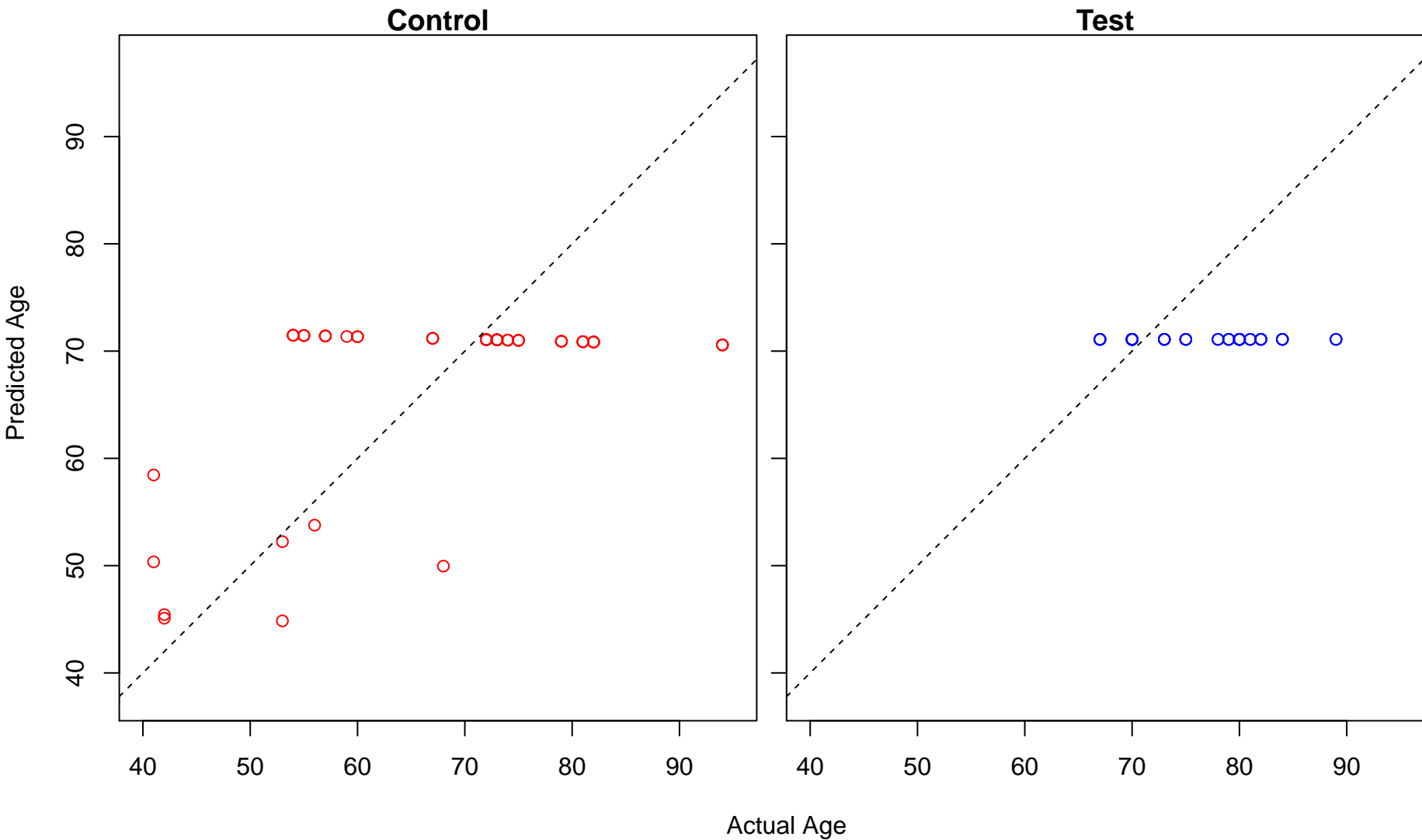
axon guidance (Score: 0.811247)



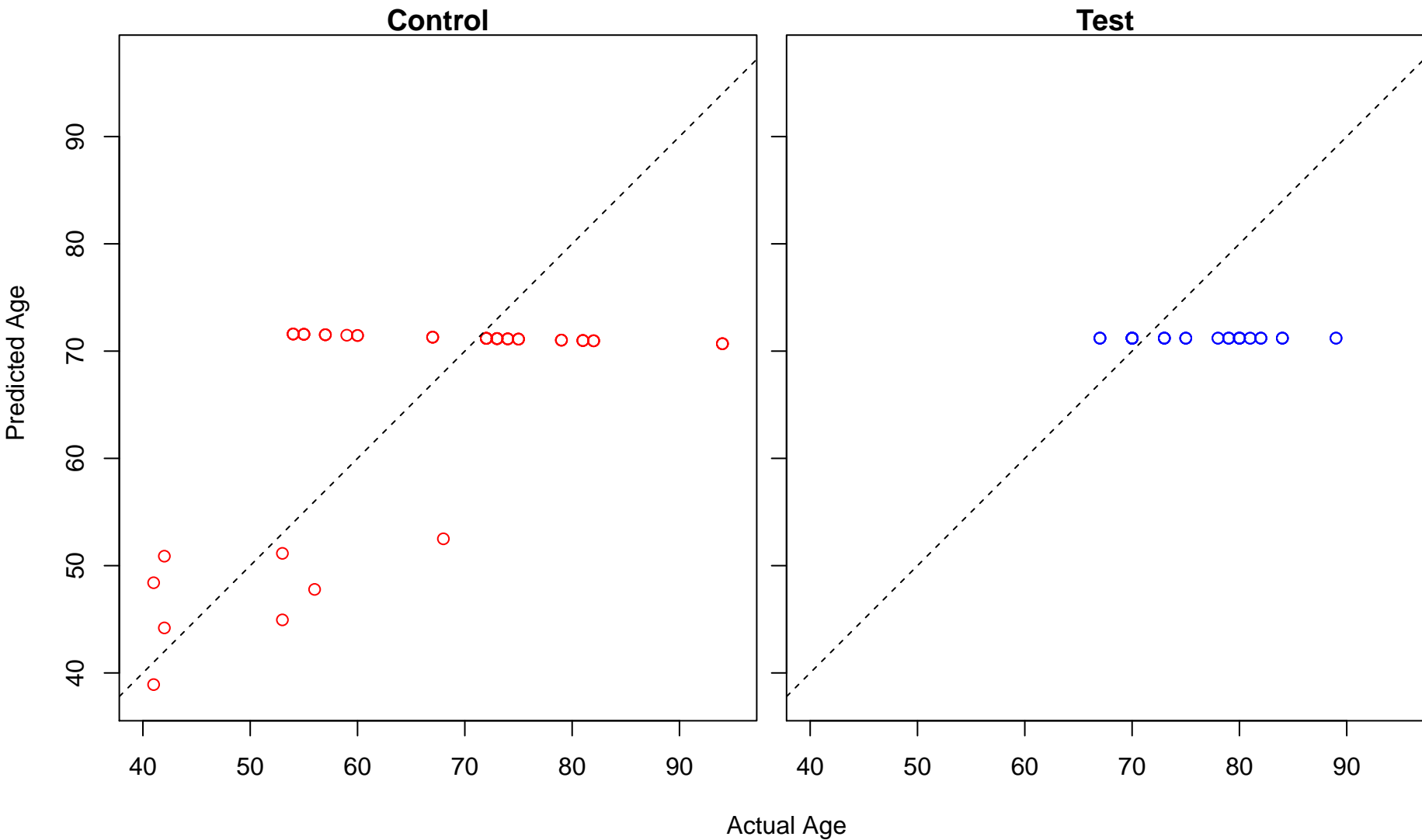
neuron projection guidance (Score: 0.811247)



tRNA metabolic process (Score: 0.811238)

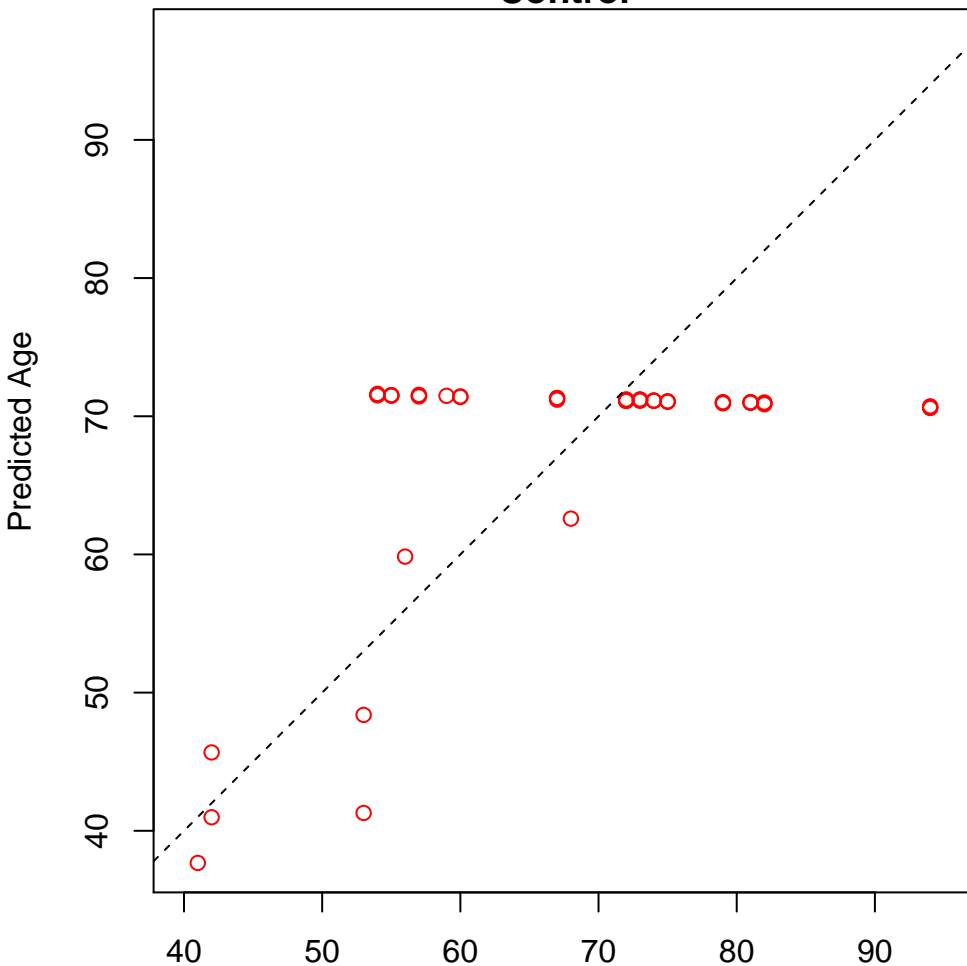


immune system process (Score: 0.811183)

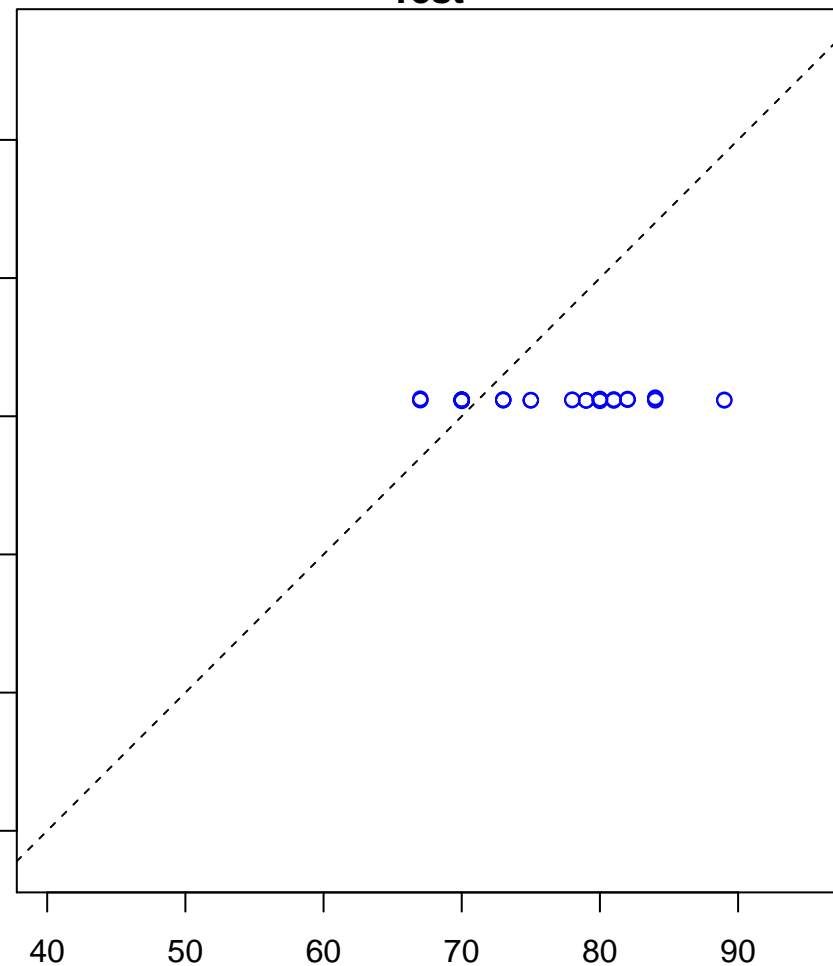


positive regulation of leukocyte migration (Score: 0.81169)

Control

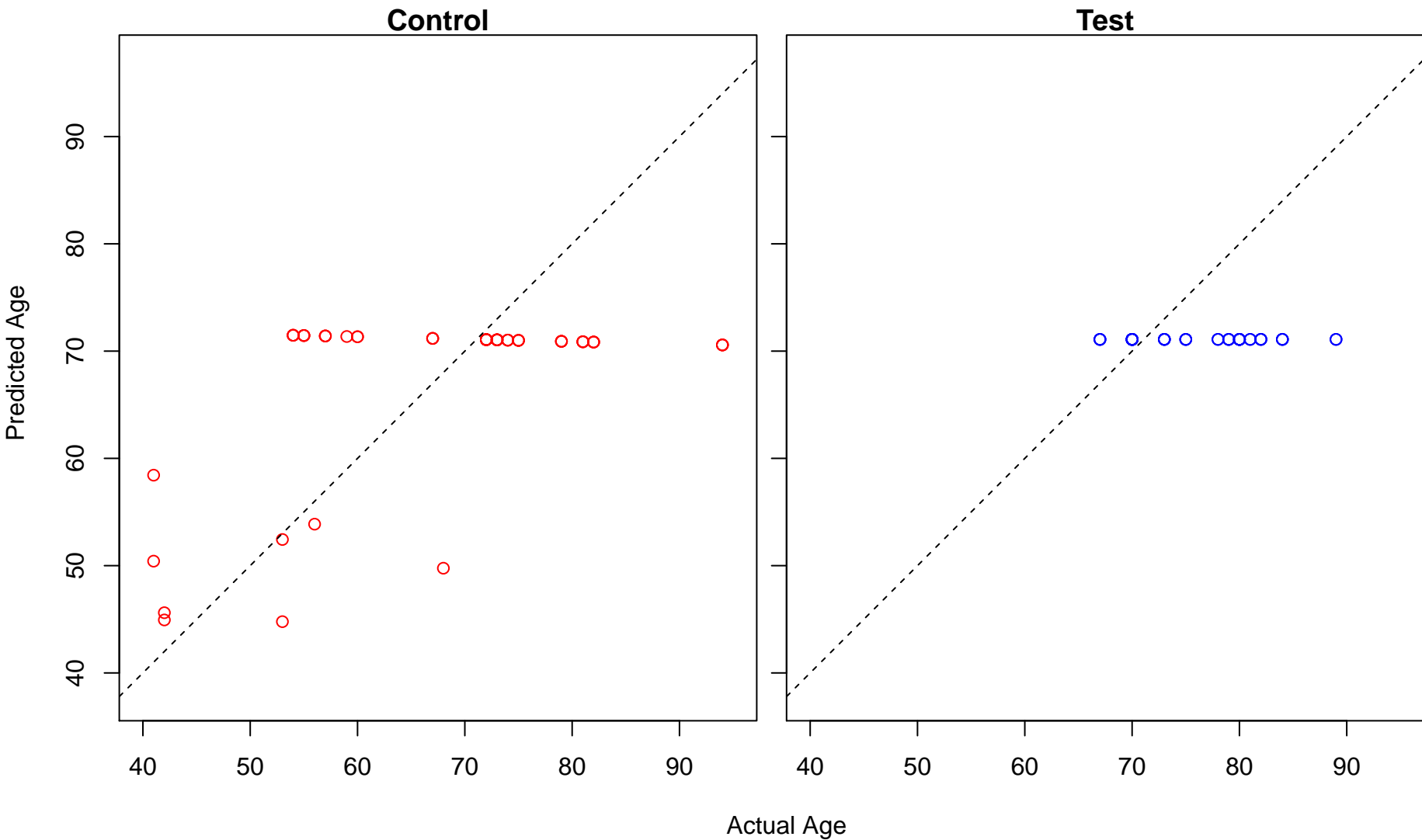


Test

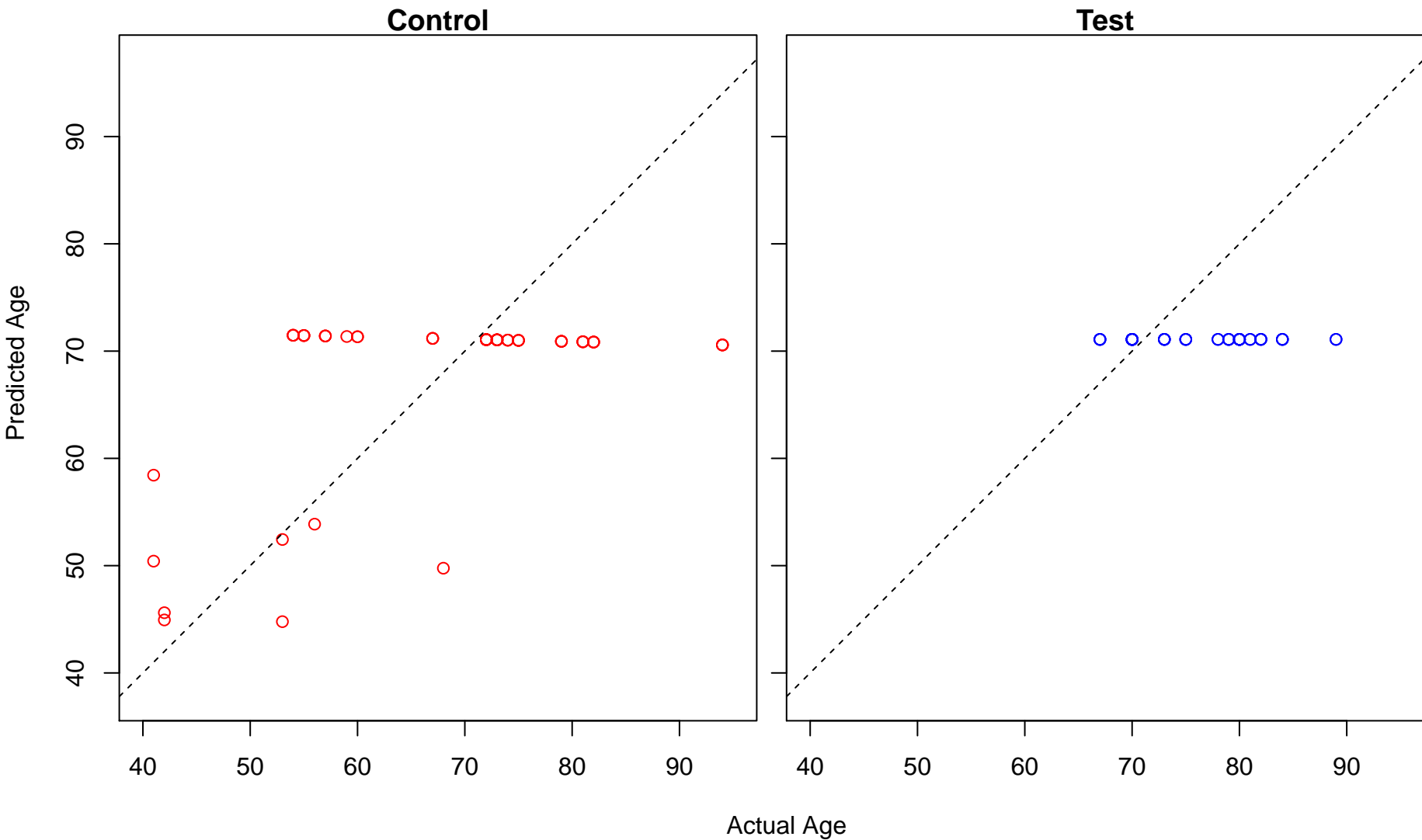


Actual Age

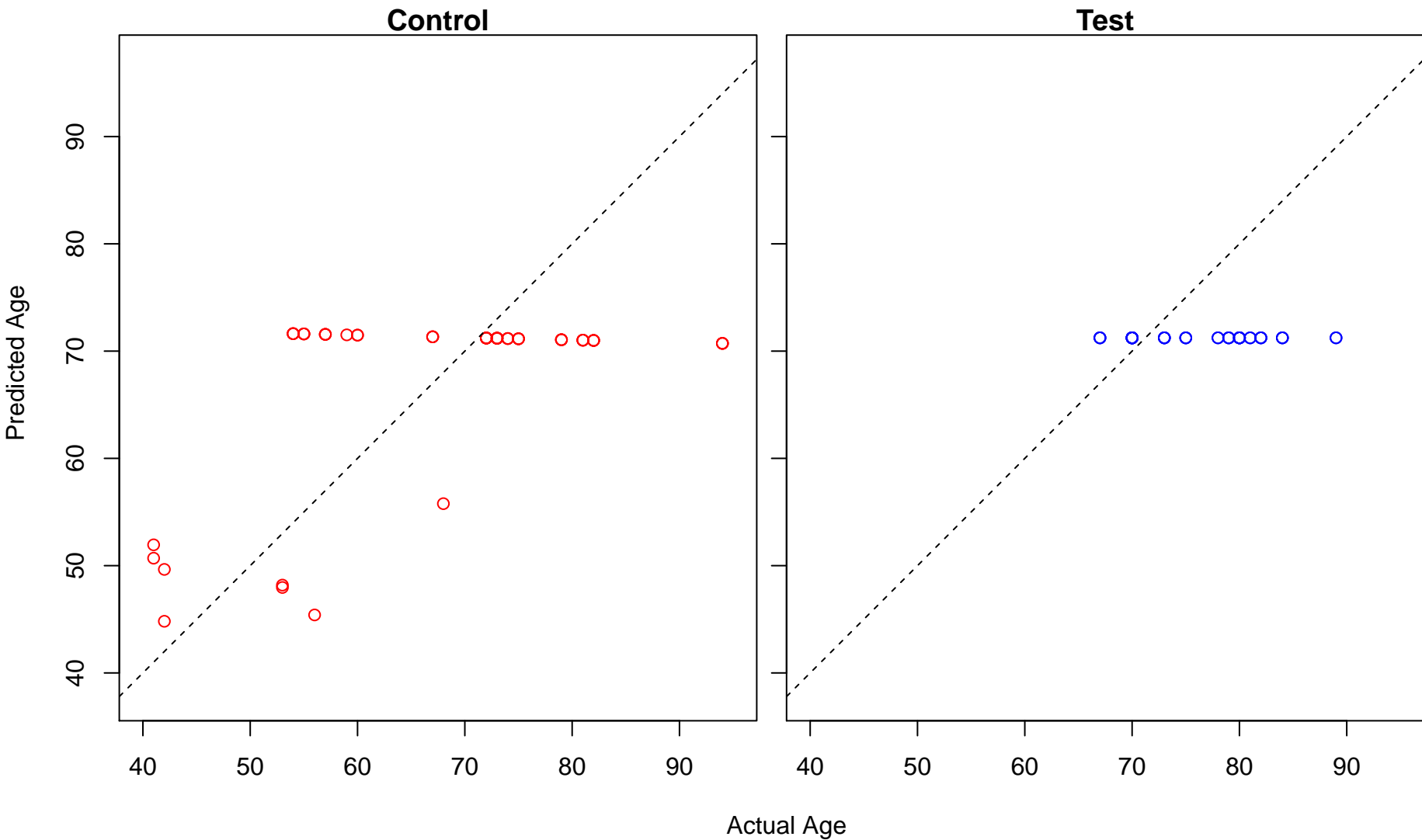
amino acid activation (Score: 0.811132)



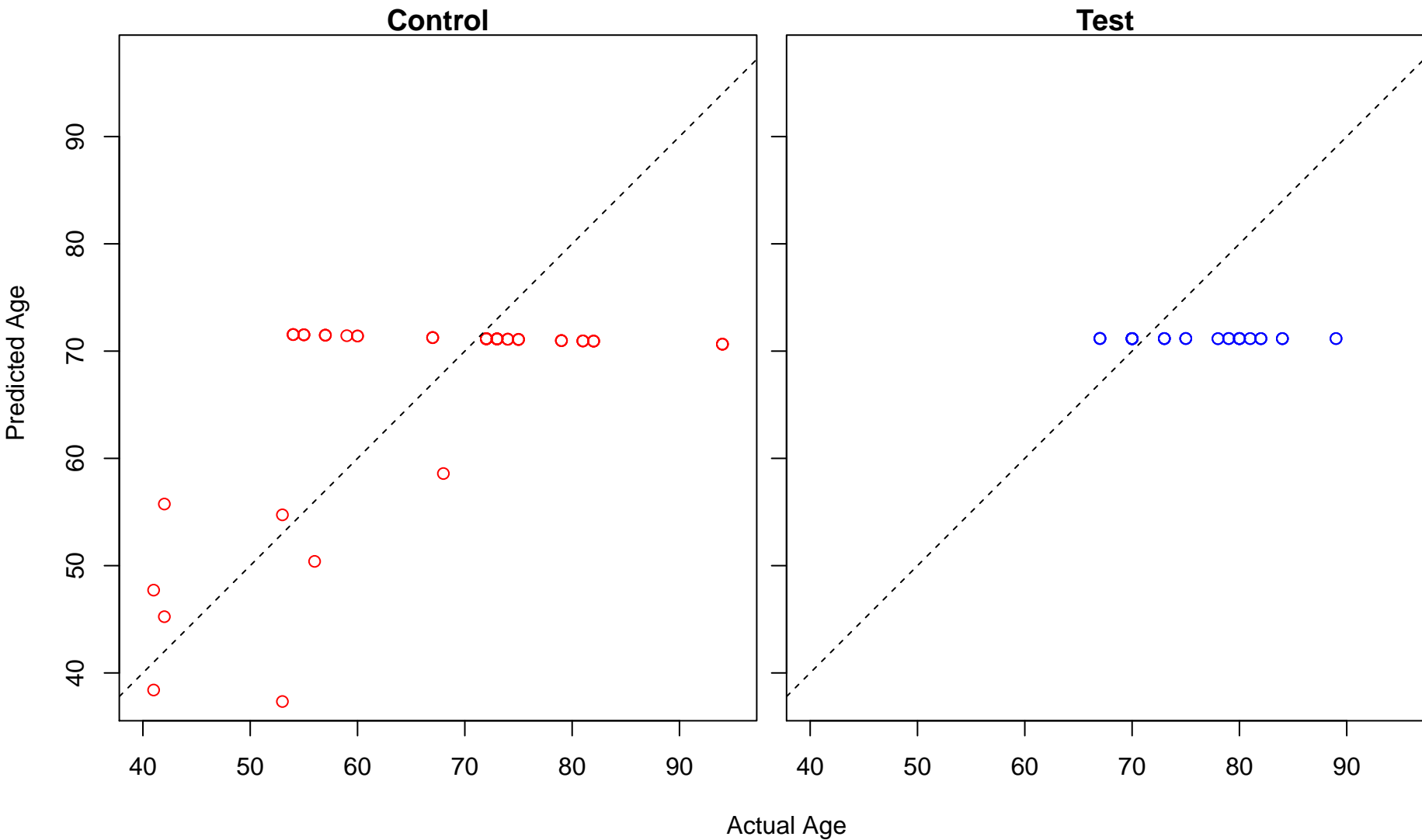
tRNA aminoacylation (Score: 0.811132)



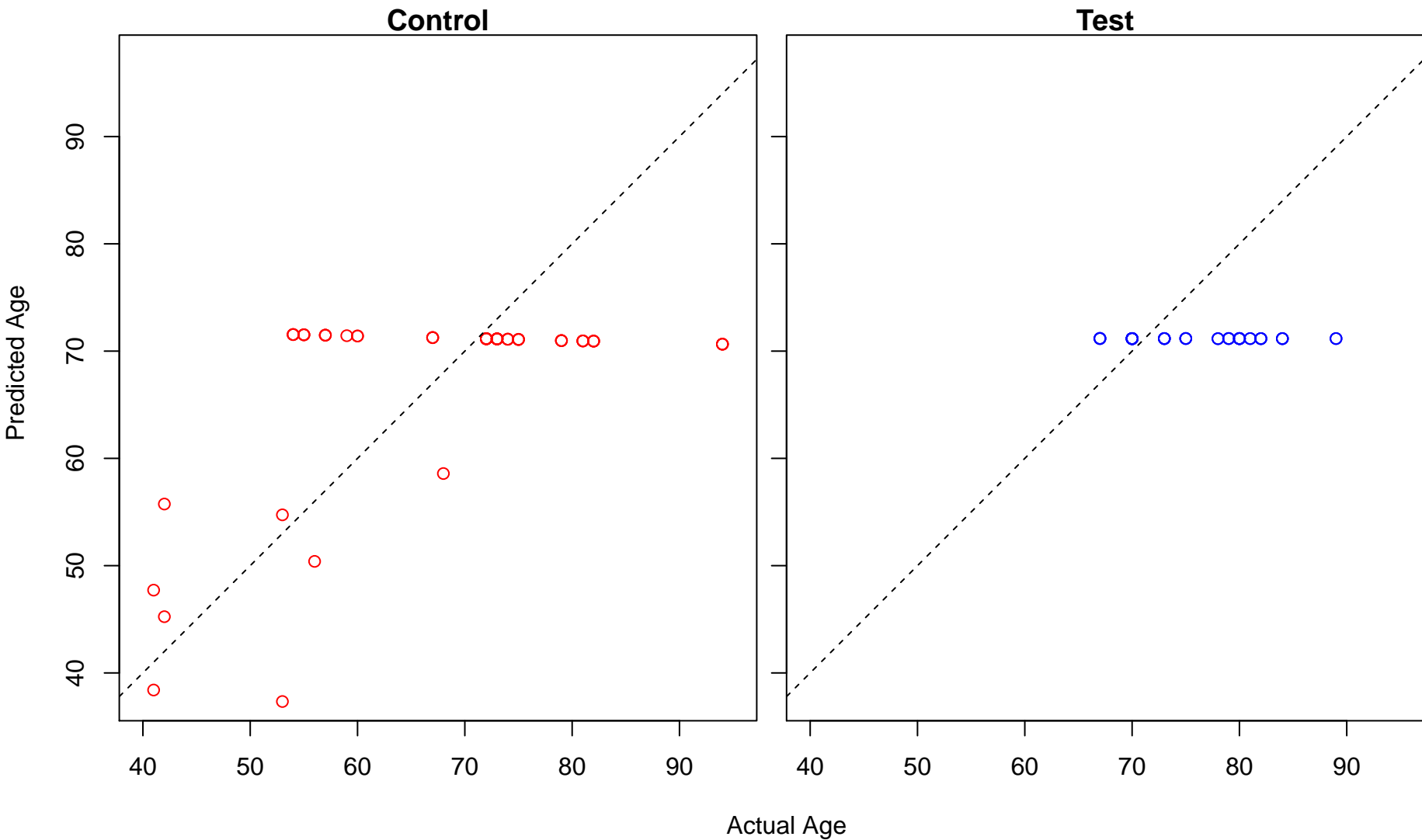
regulation of protein localization to membrane (Score: 0.811119)



RNA export from nucleus (Score: 0.811045)

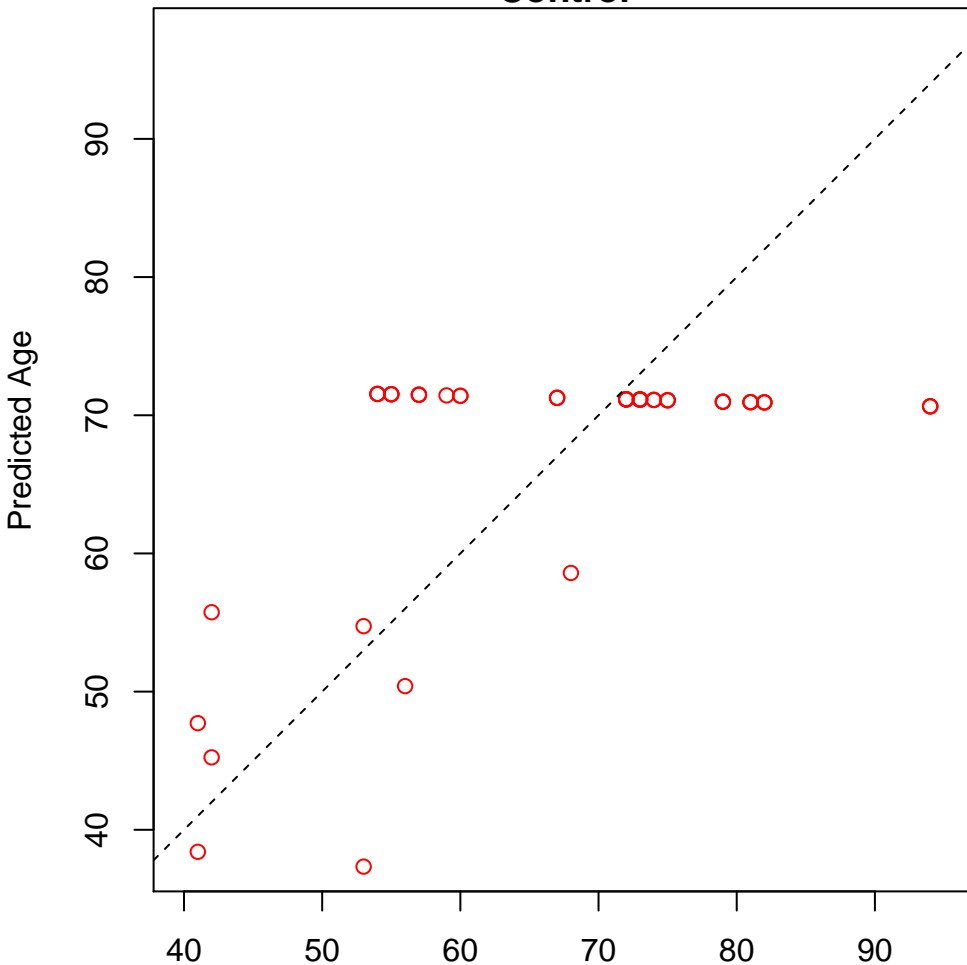


protein export from nucleus (Score: 0.811045)

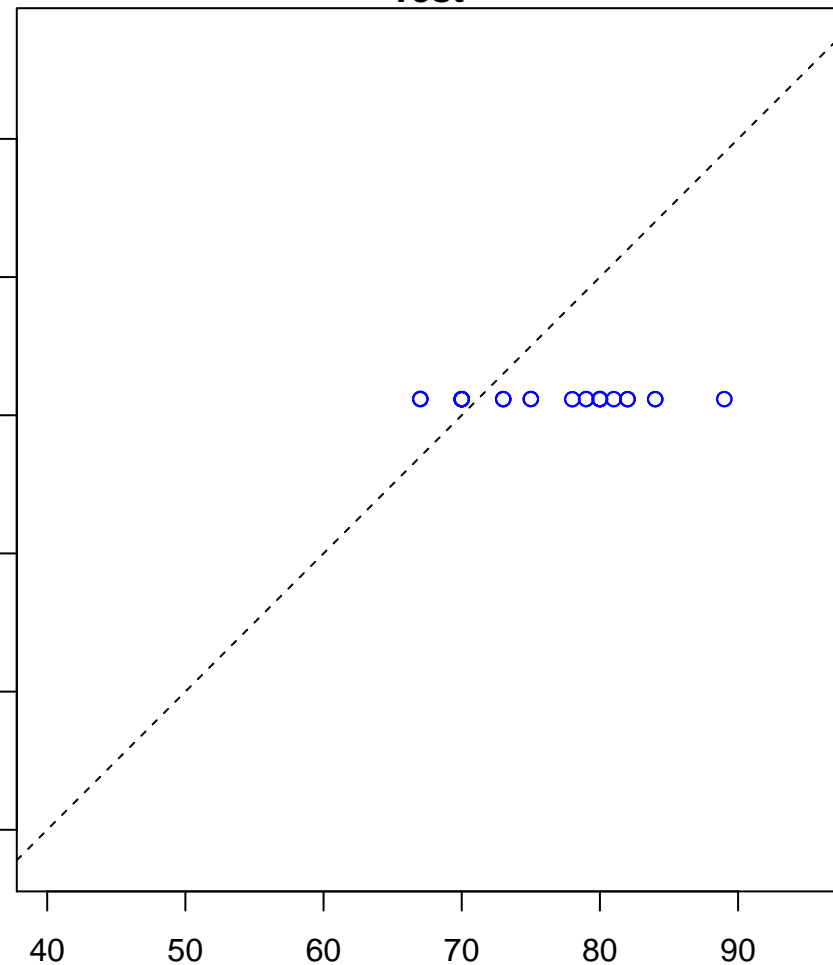


nucleobase-containing compound transport (Score: 0.811045)

Control

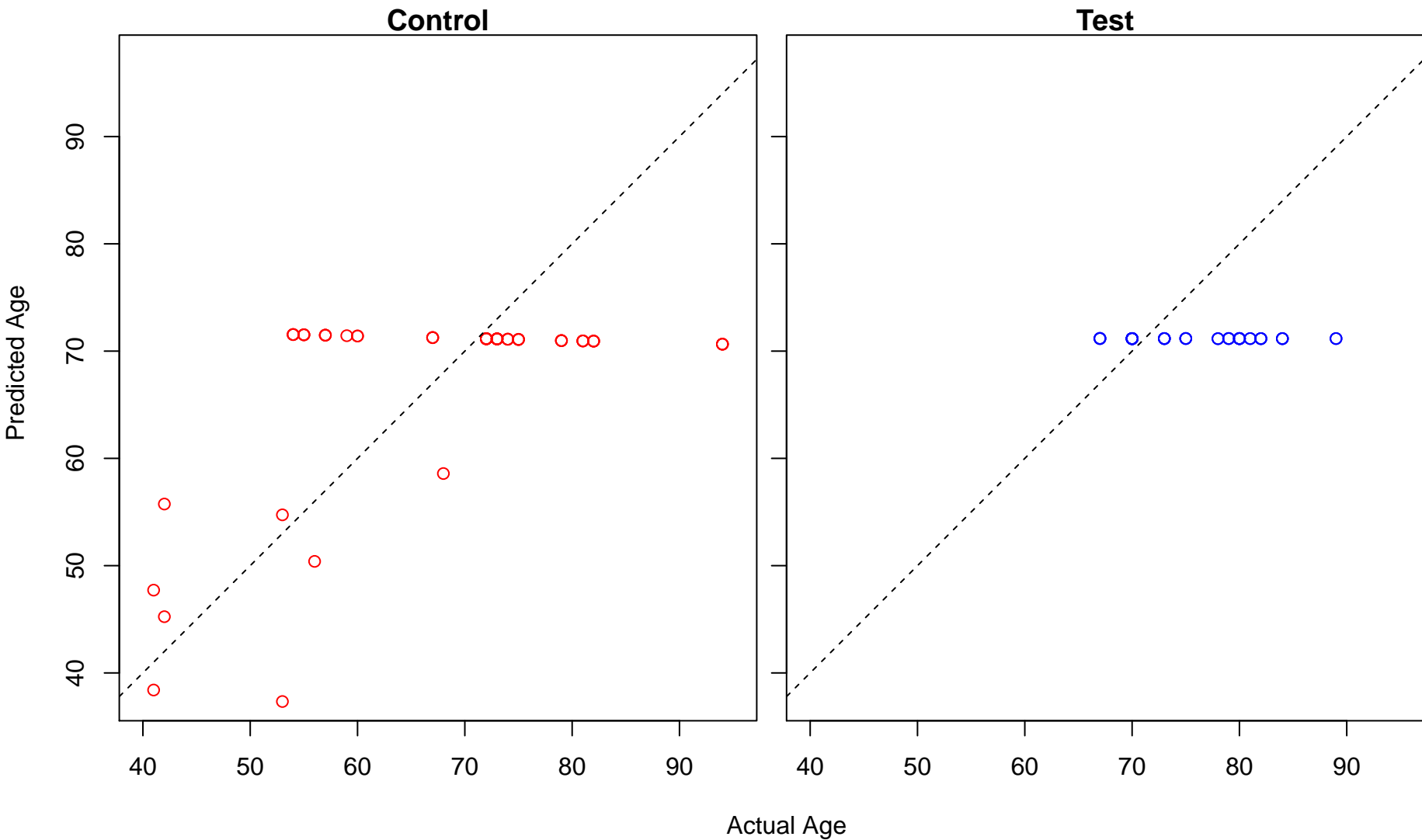


Test

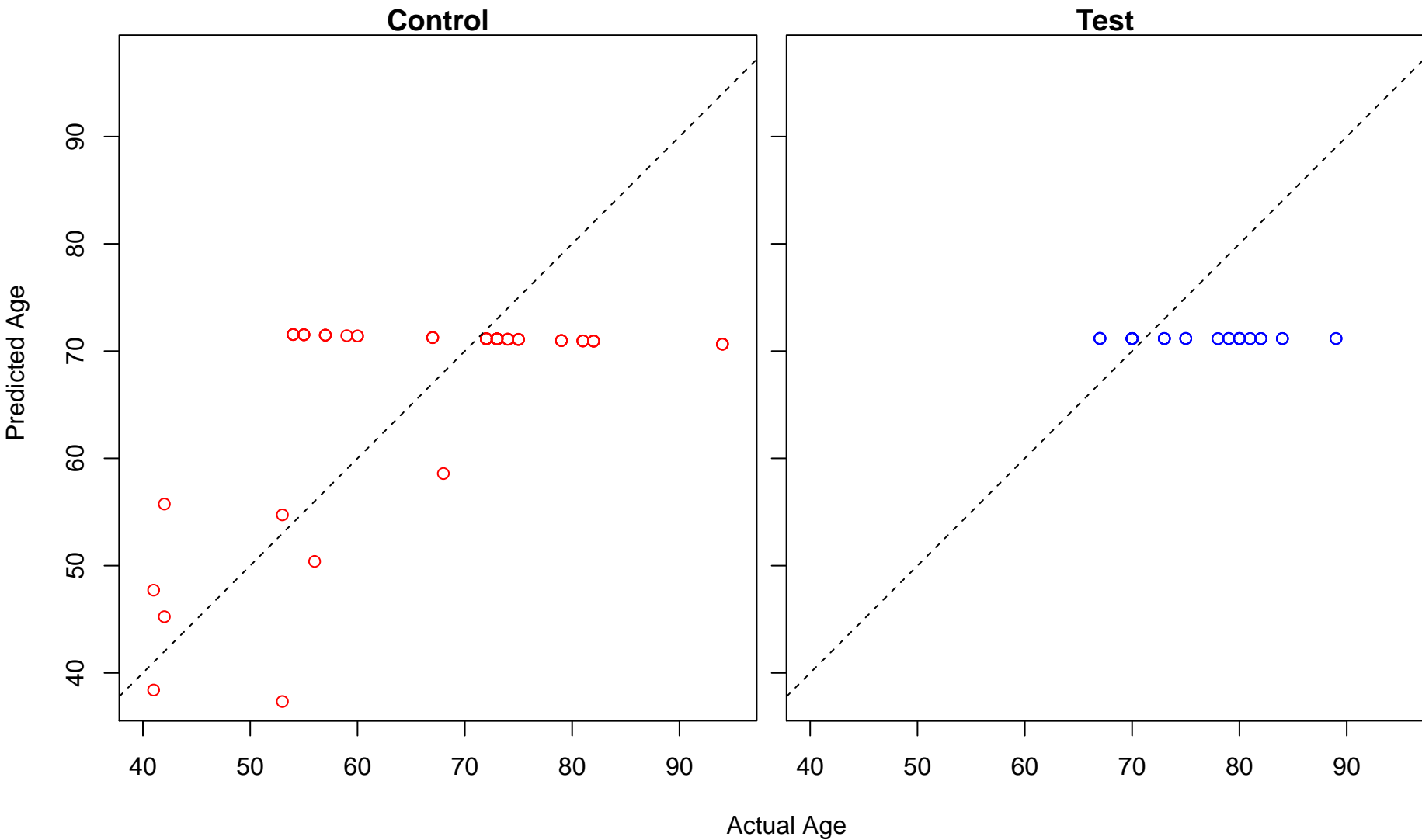


Actual Age

nucleic acid transport (Score: 0.811045)

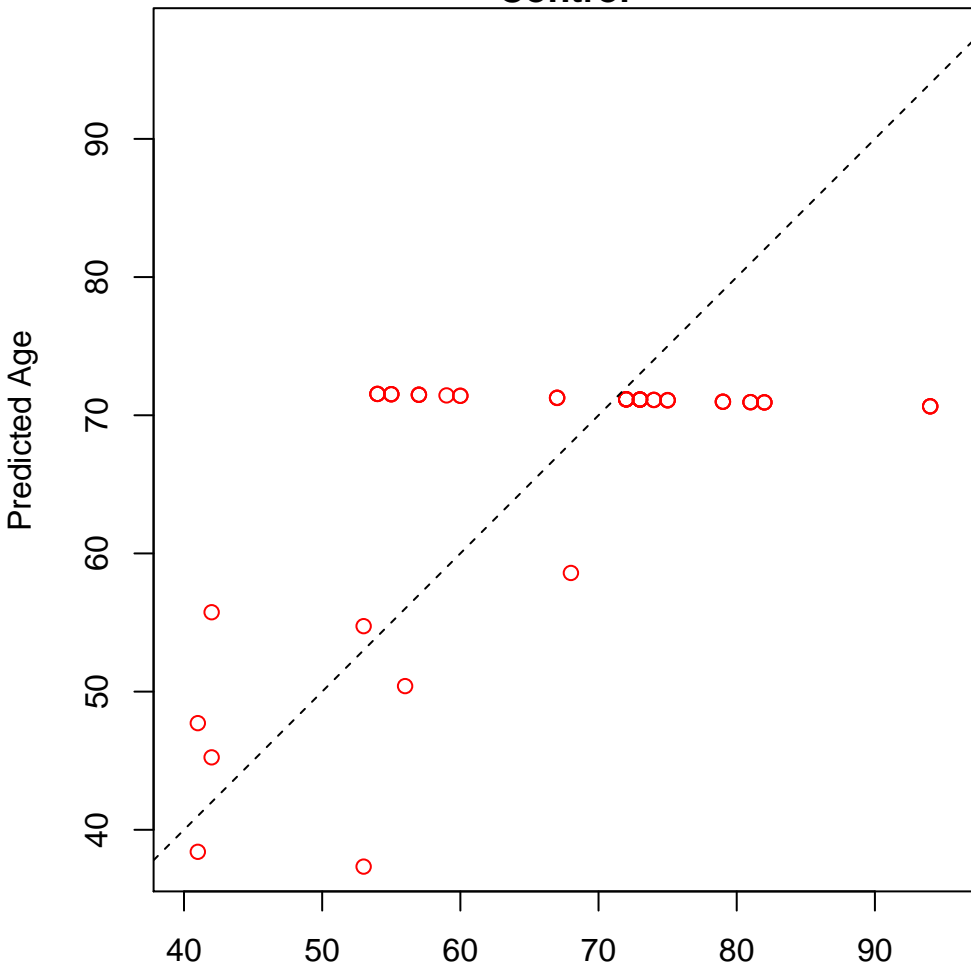


RNA transport (Score: 0.811045)

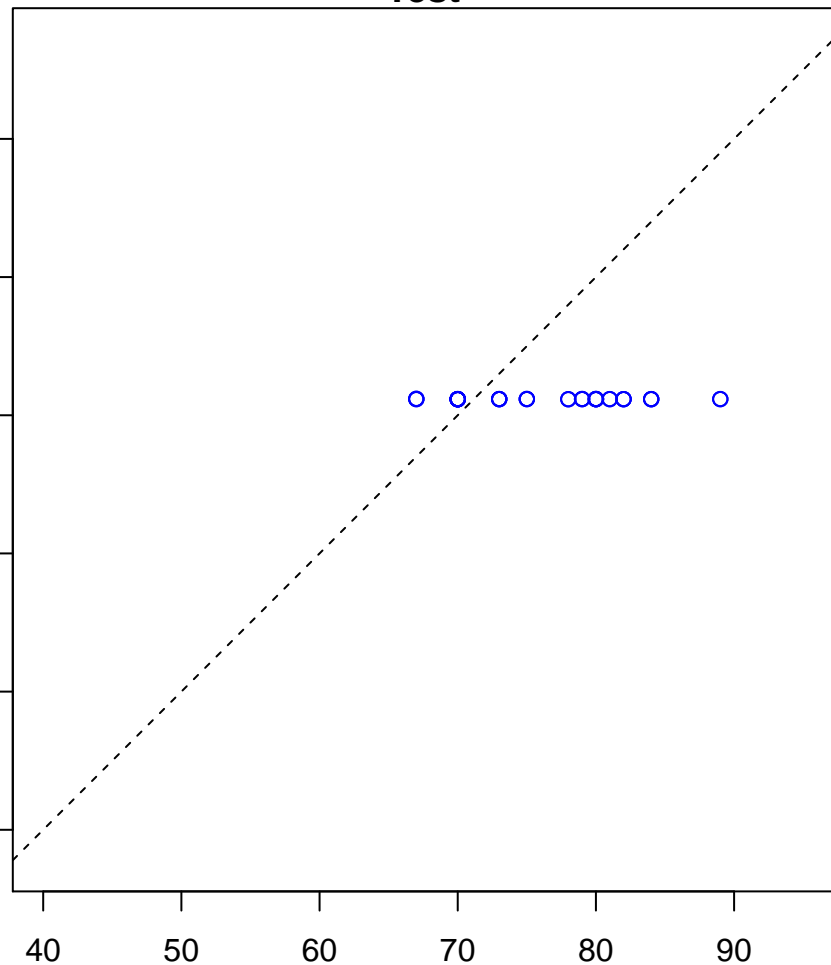


establishment of RNA localization (Score: 0.811045)

Control



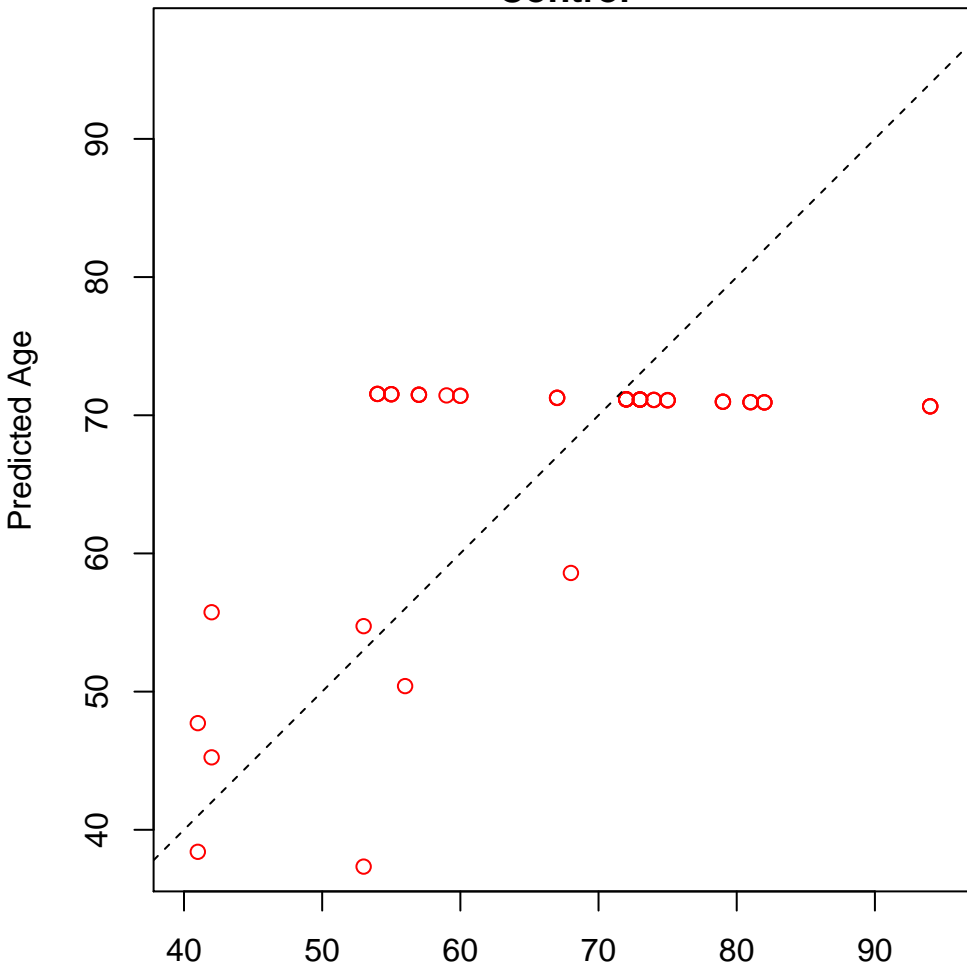
Test



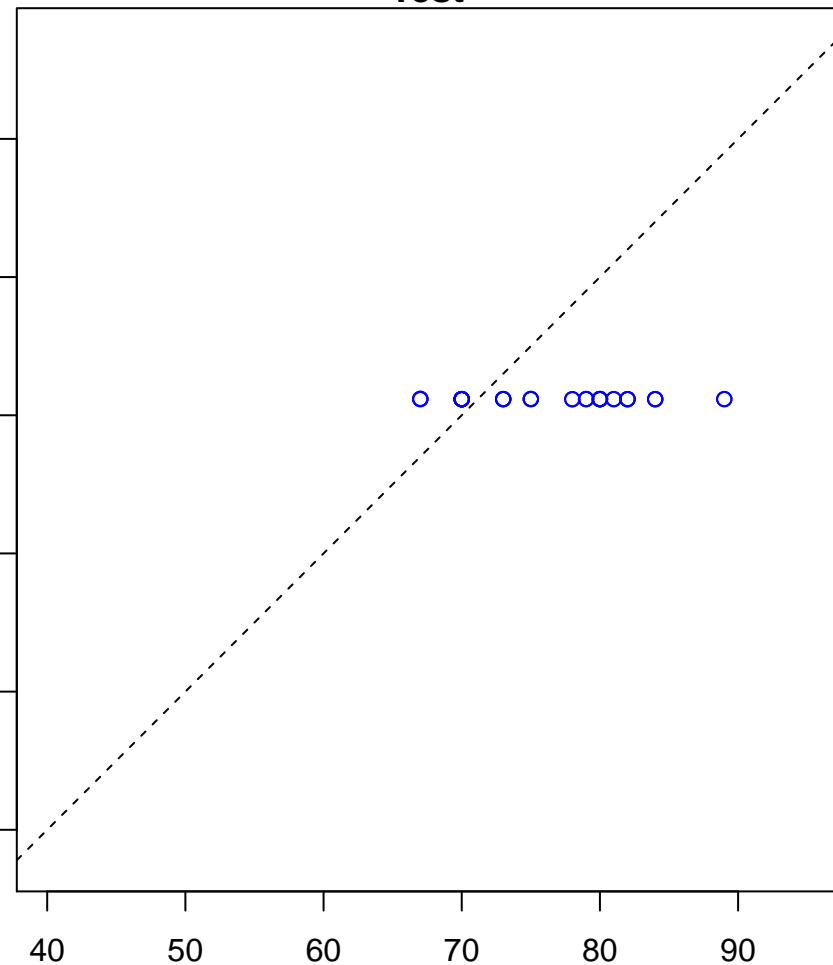
Actual Age

ribonucleoprotein complex localization (Score: 0.811045)

Control

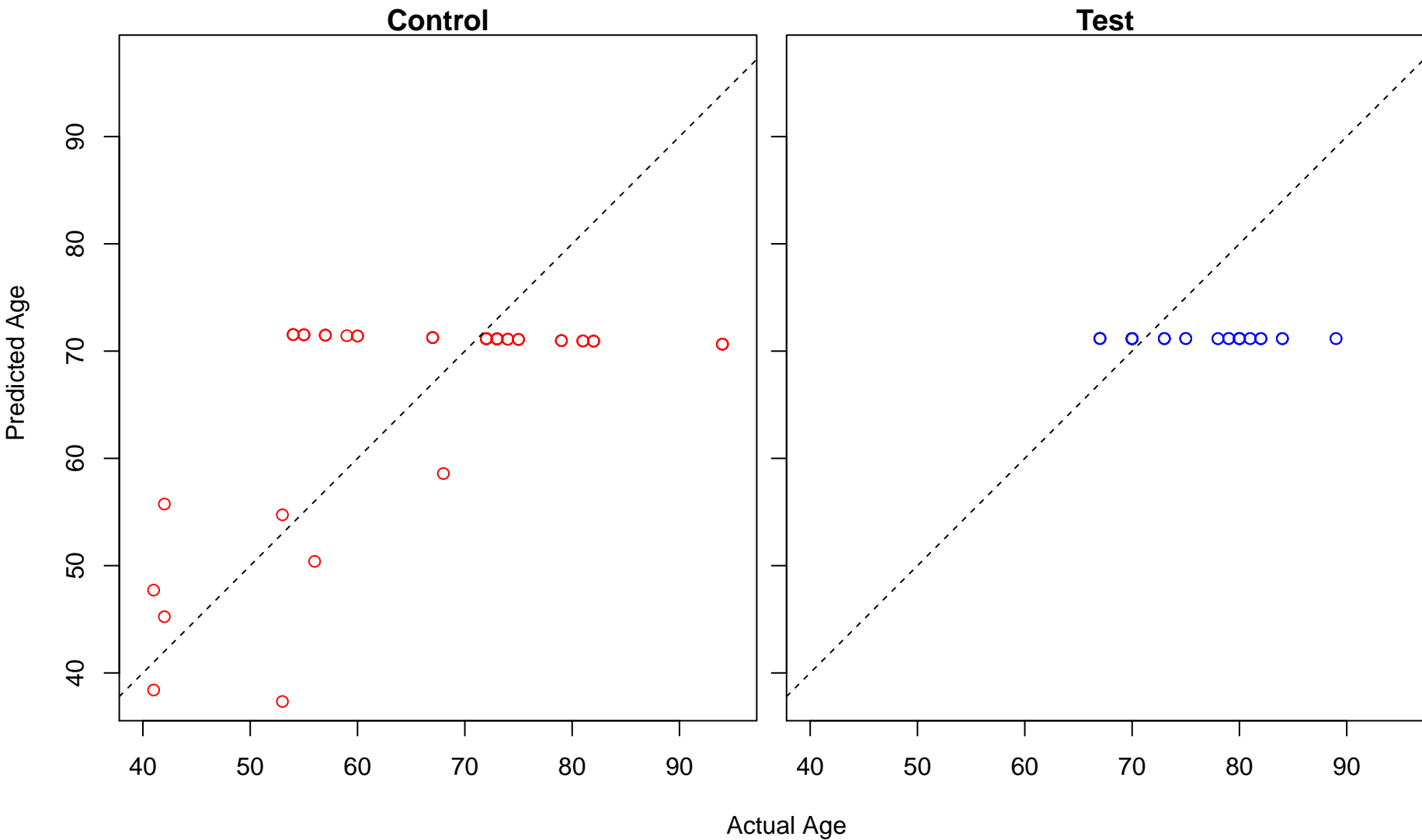


Test

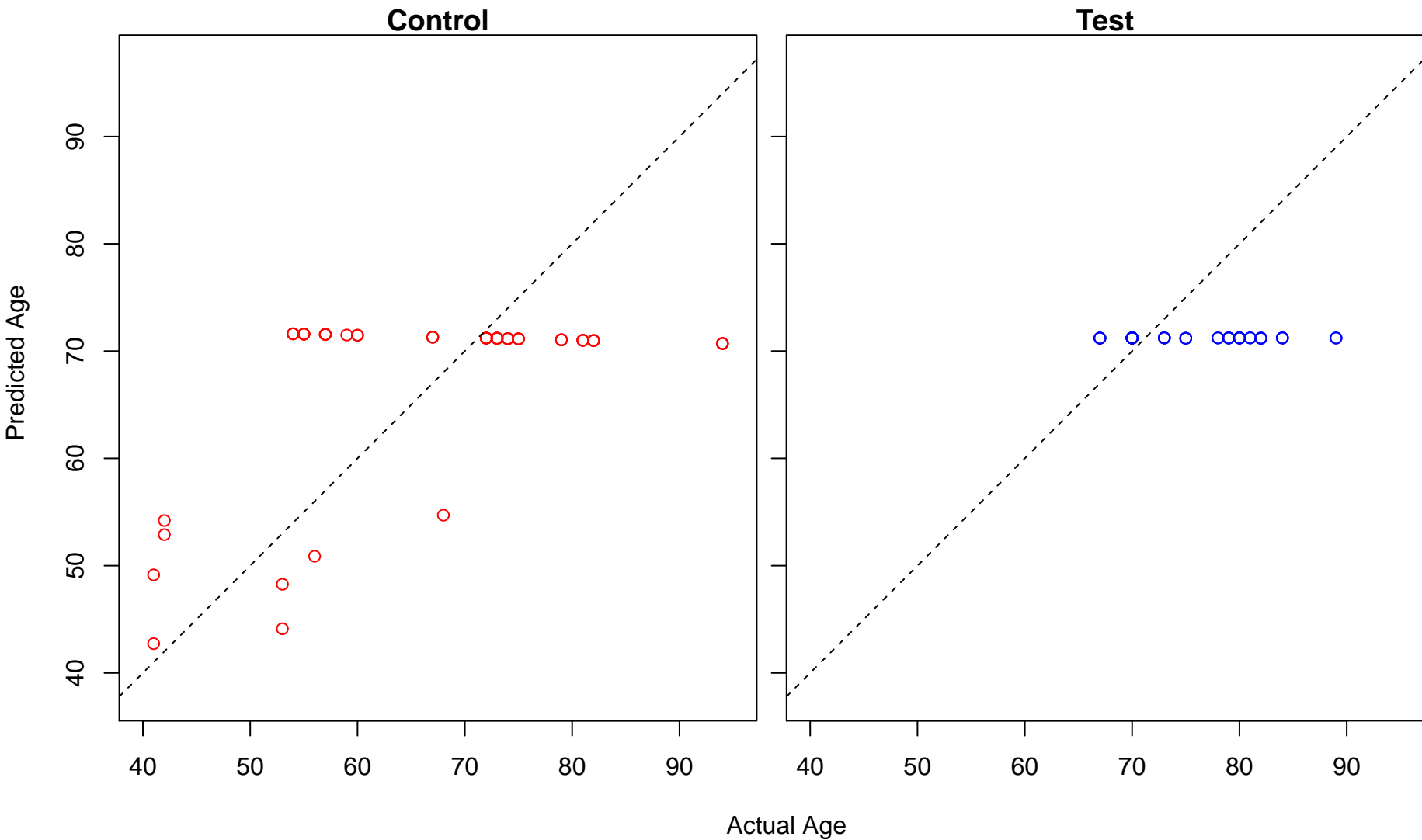


Actual Age

ribonucleoprotein complex export from nucleus (Score: 0.811045)

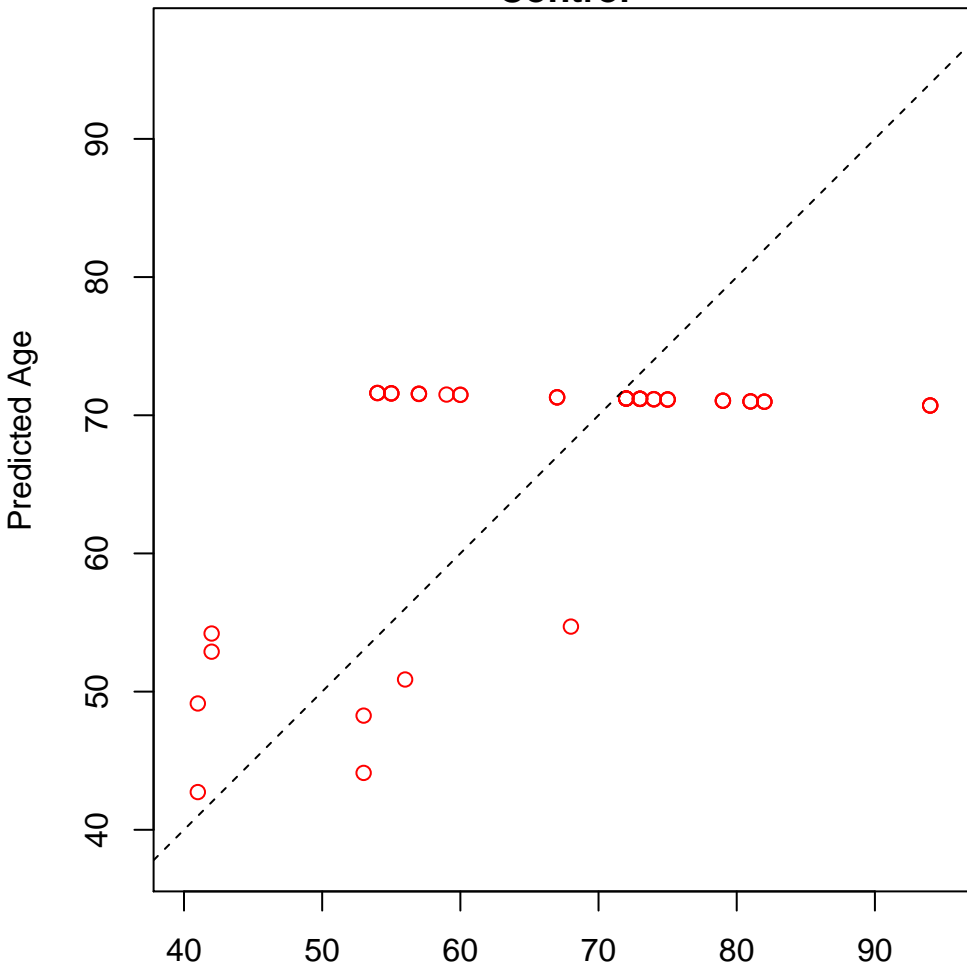


regulation of wound healing (Score: 0.811016)

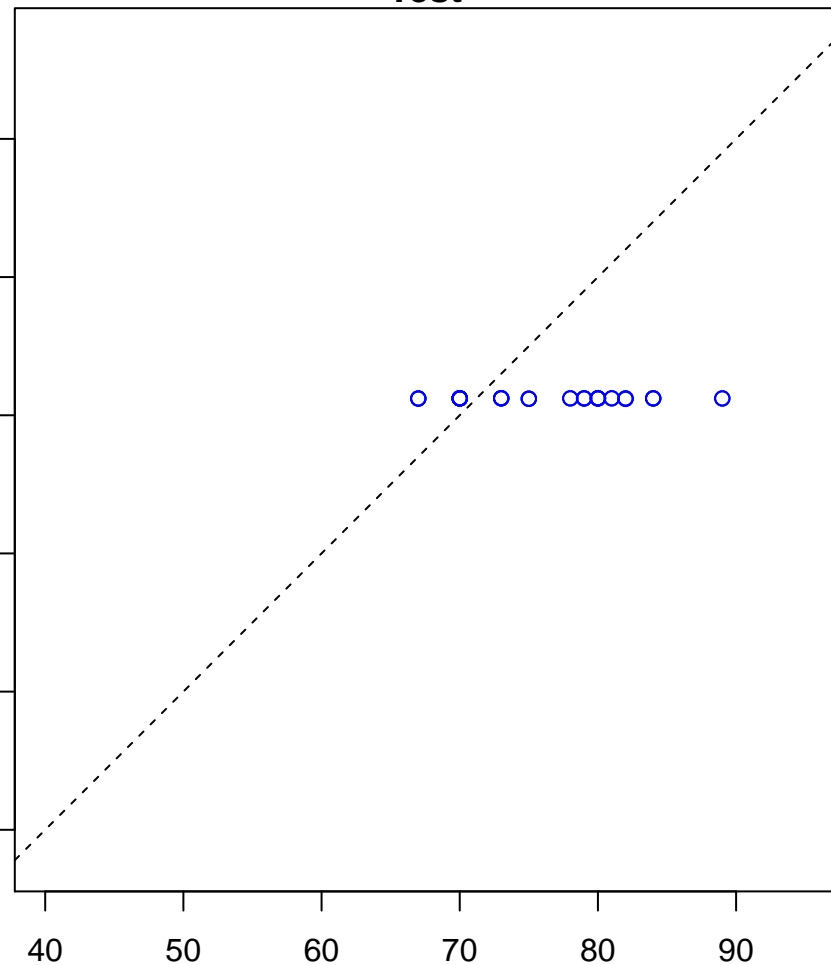


regulation of response to wounding (Score: 0.811016)

Control



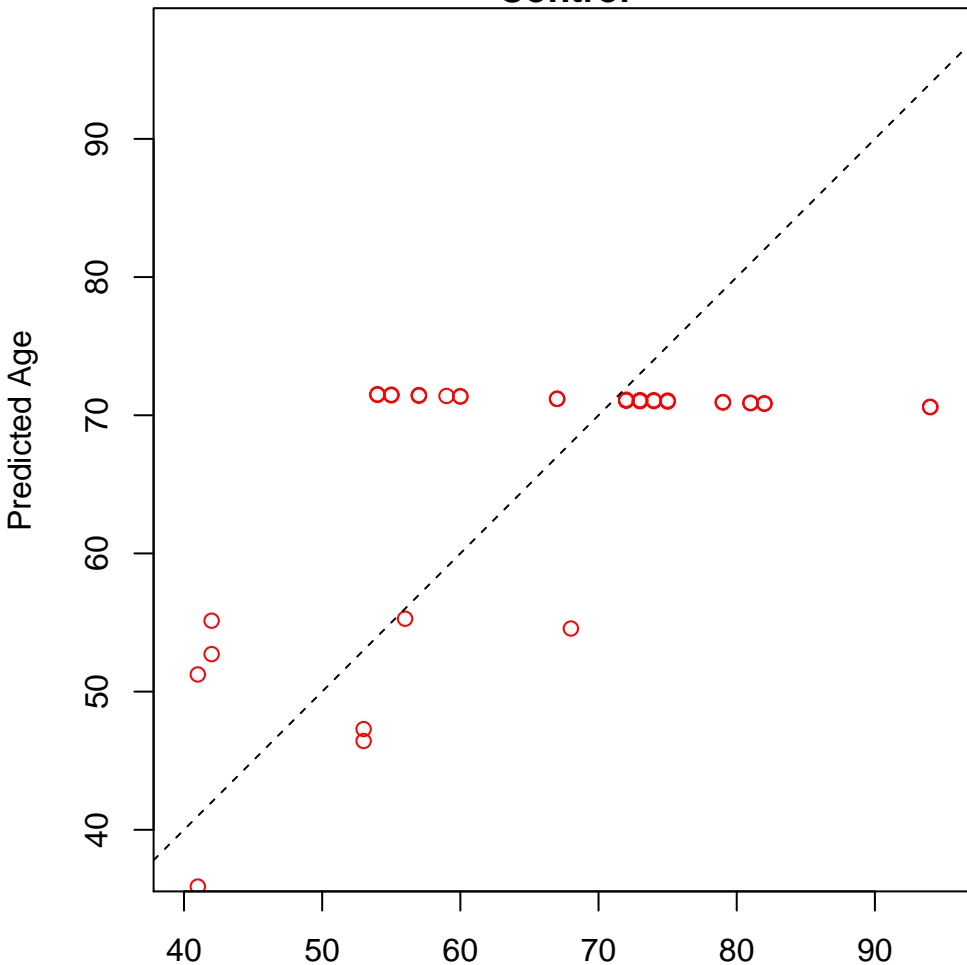
Test



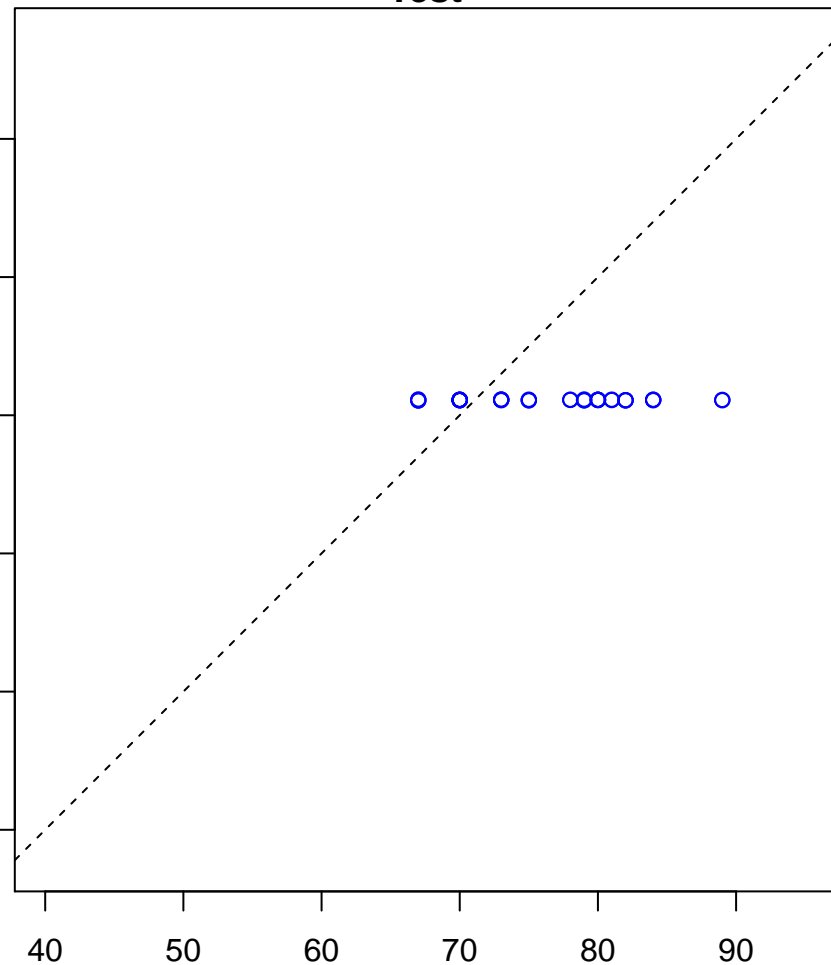
Actual Age

positive regulation of T cell differentiation (Score: 0.811005)

Control

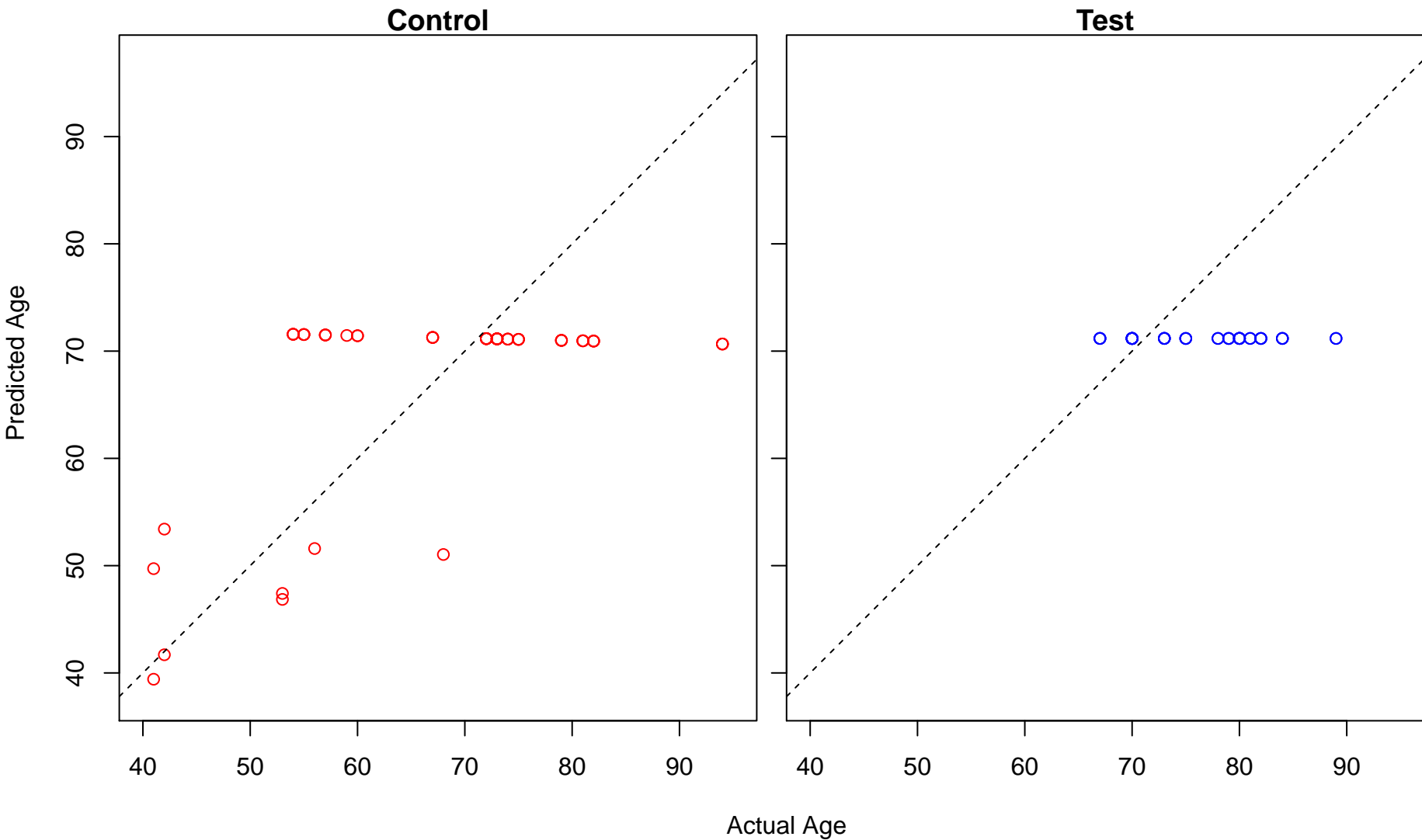


Test

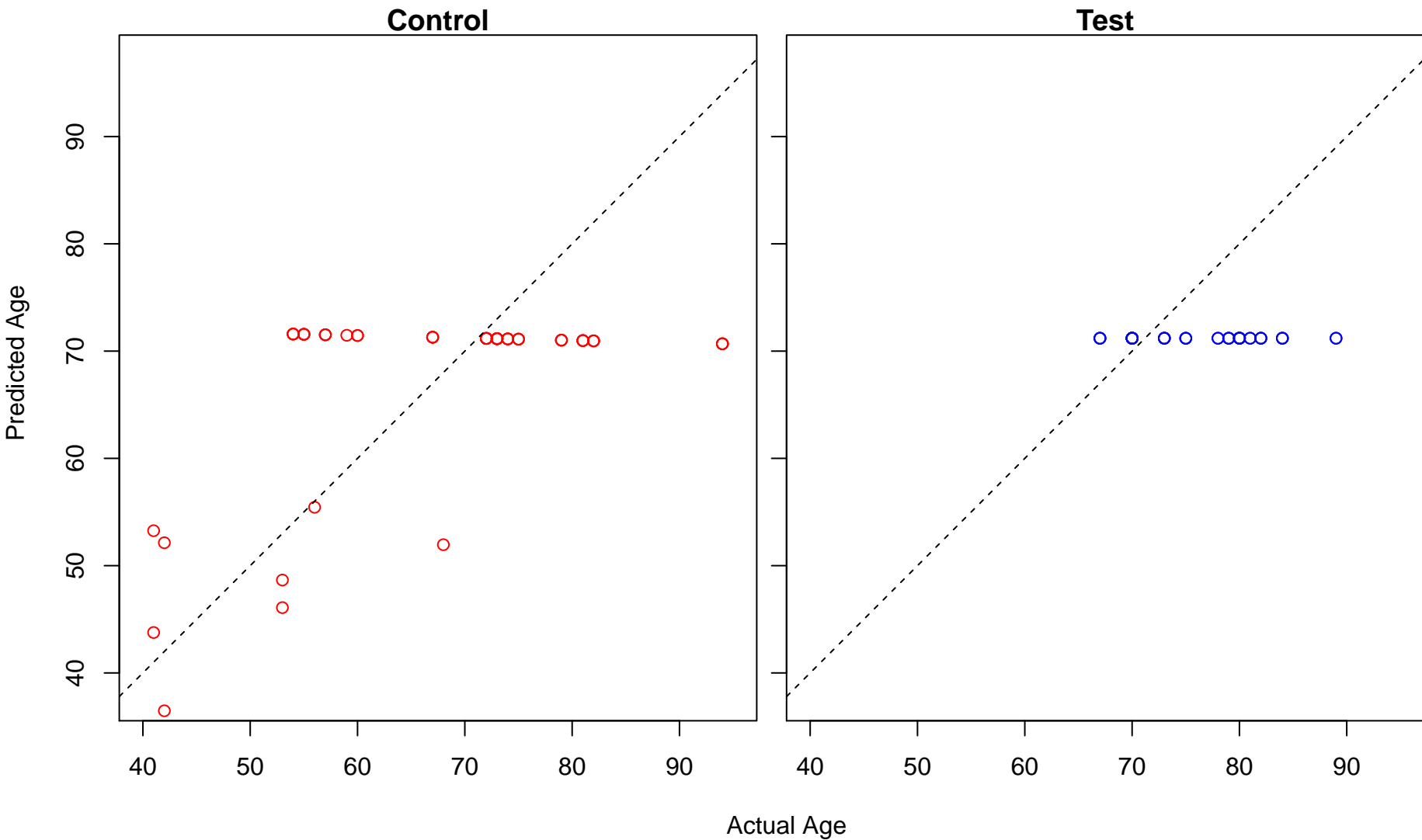


Actual Age

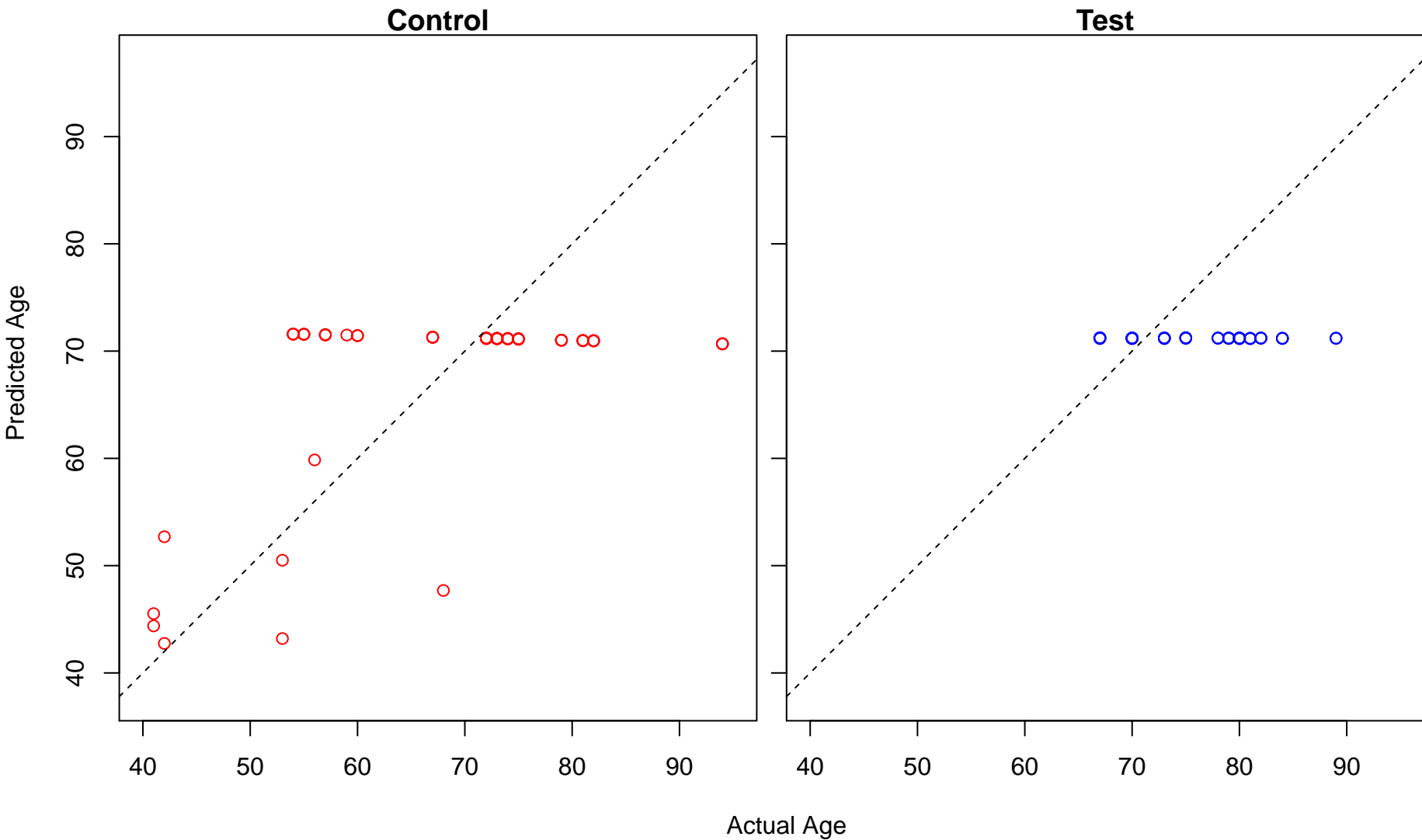
regulation of catalytic activity (Score: 0.810963)



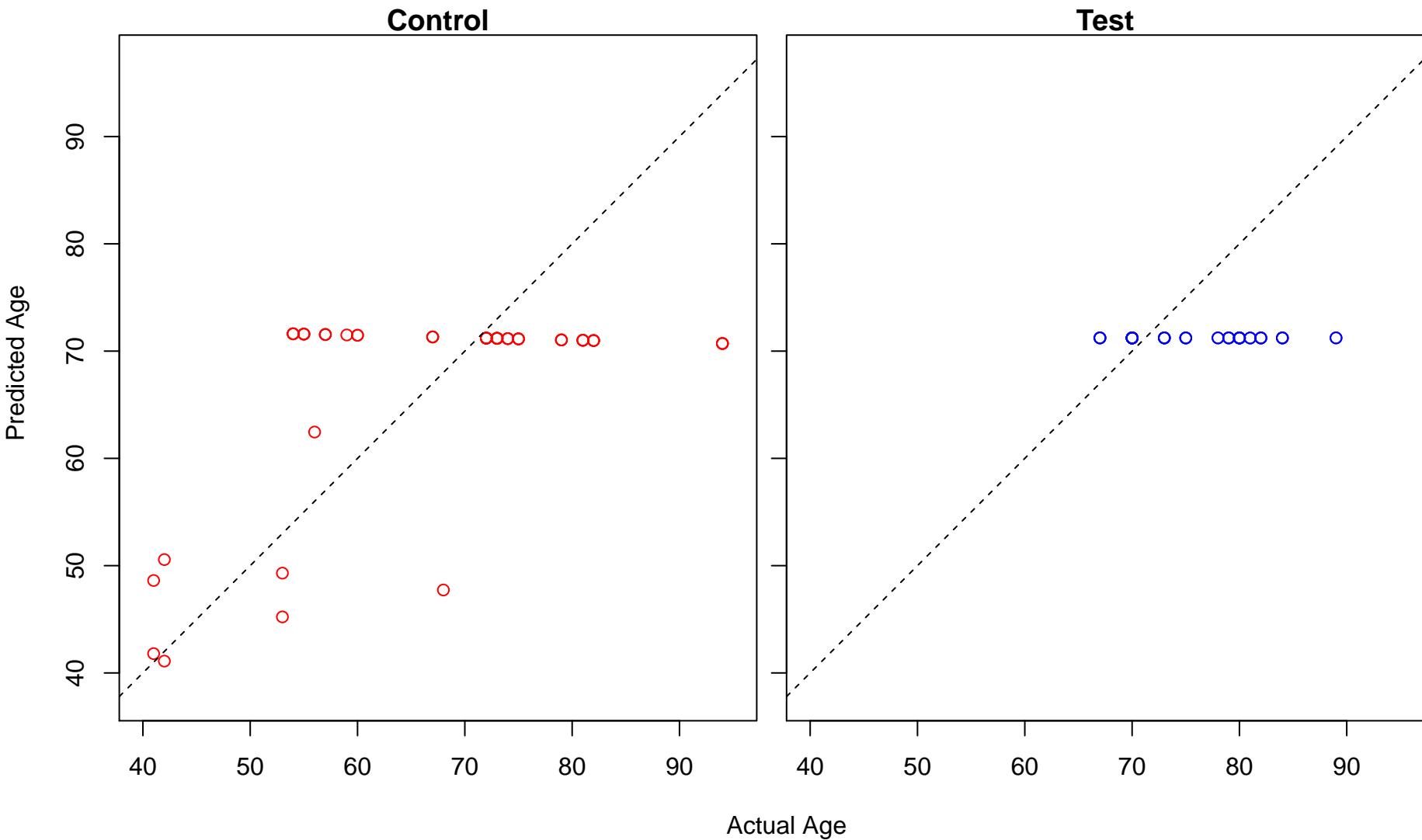
regulation of system process (Score: 0.810846)



regulation of autophagy (Score: 0.810813)

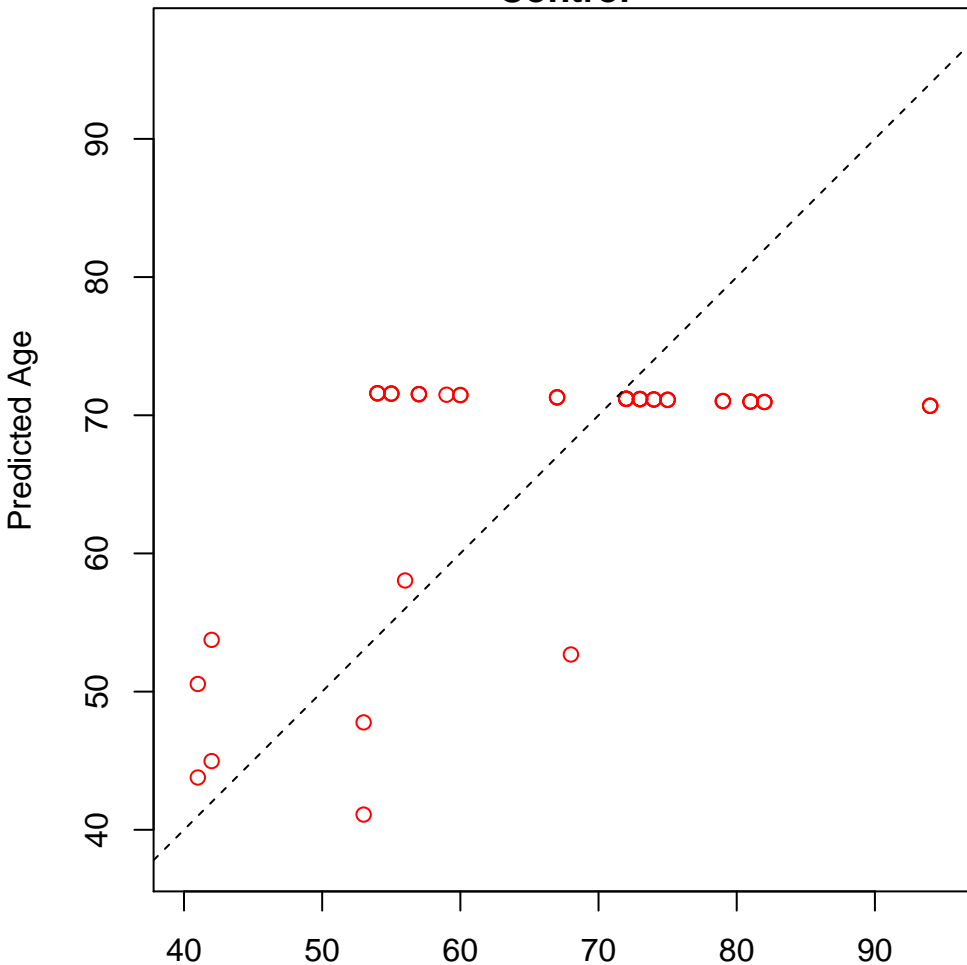


regulation of cell cycle (Score: 0.810791)

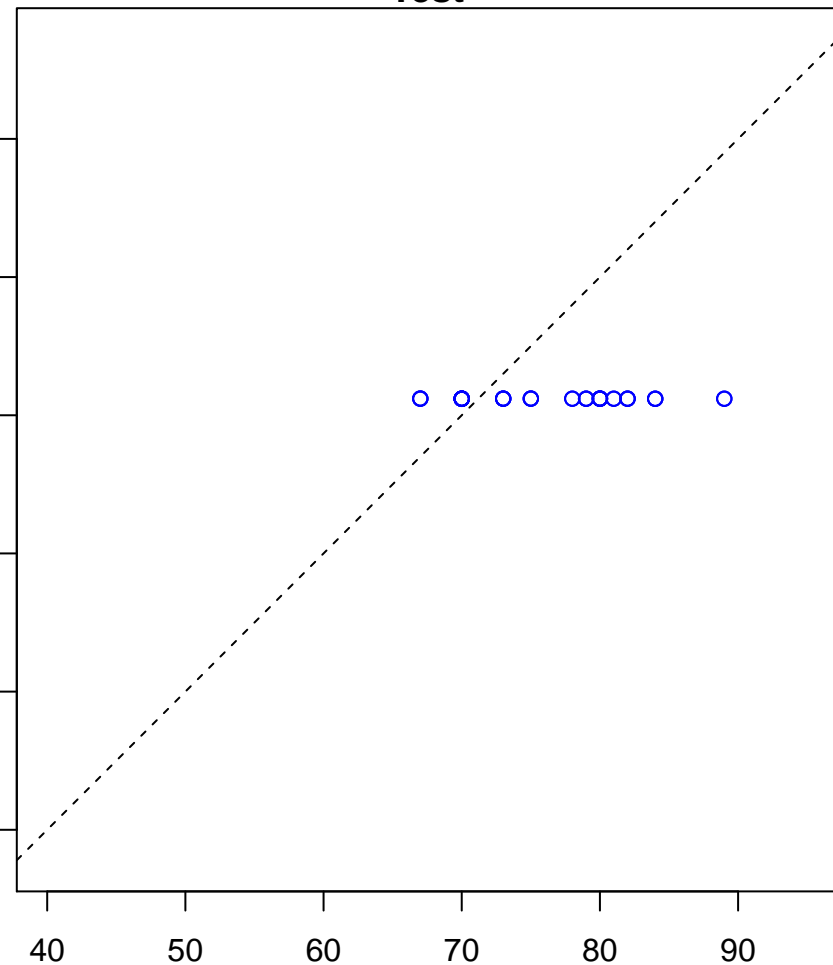


protein oligomerization (Score: 0.810783)

Control

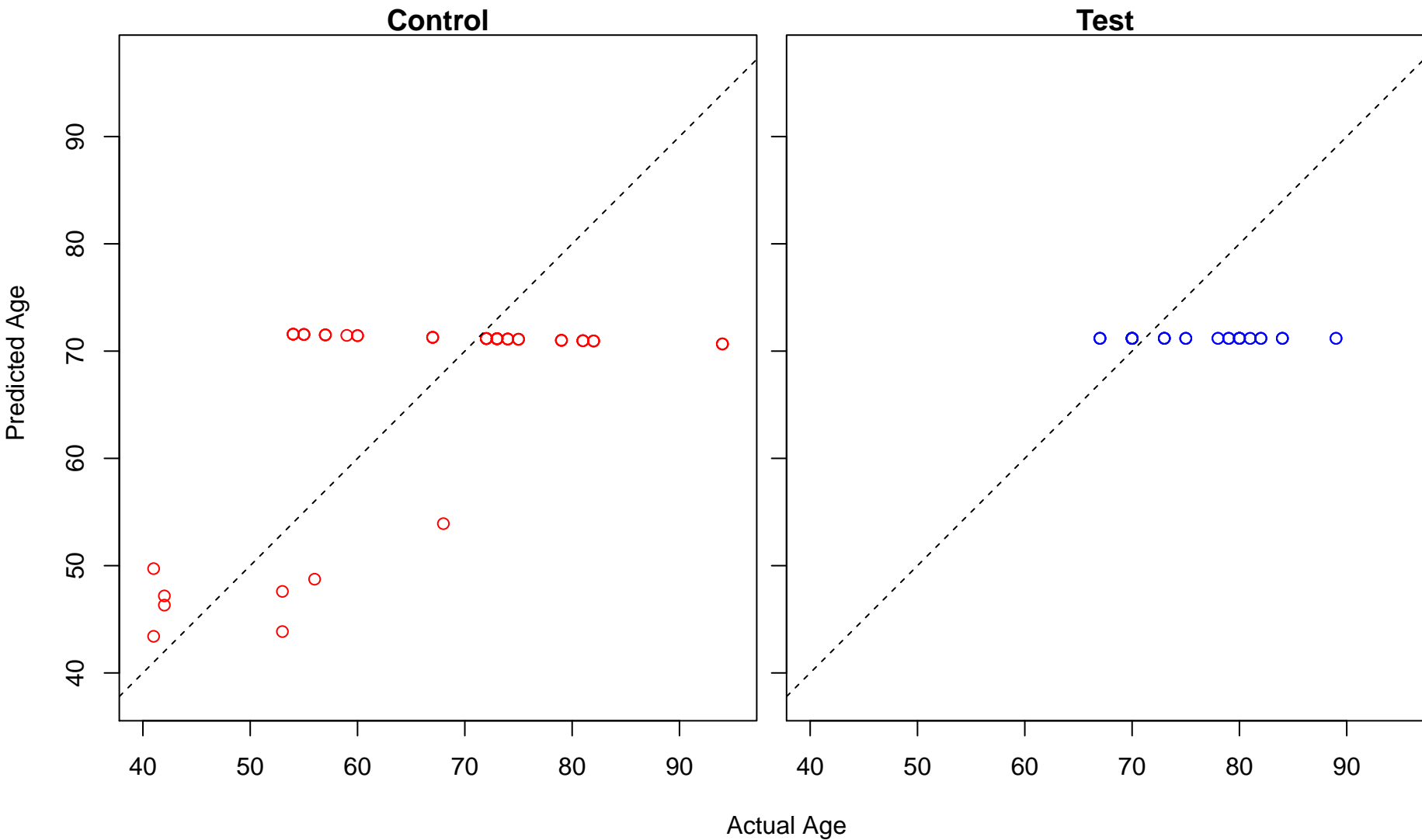


Test



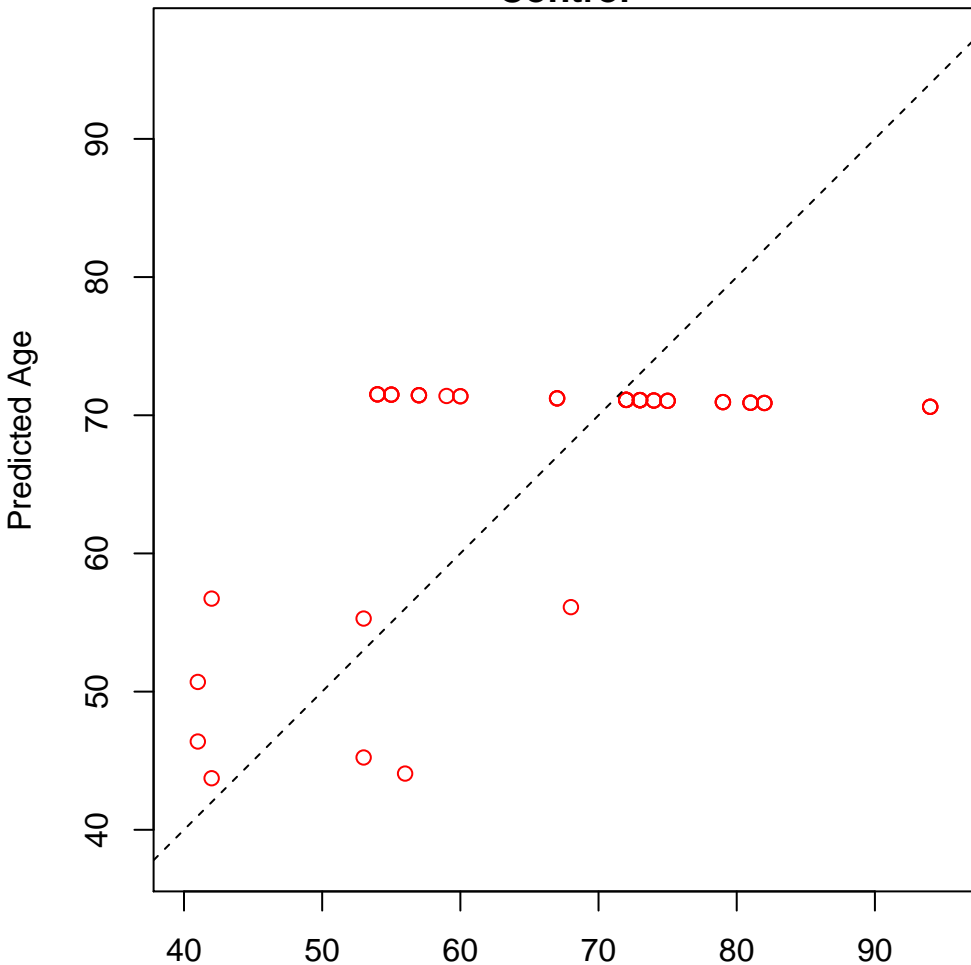
Actual Age

regulation of proteolysis (Score: 0.810767)

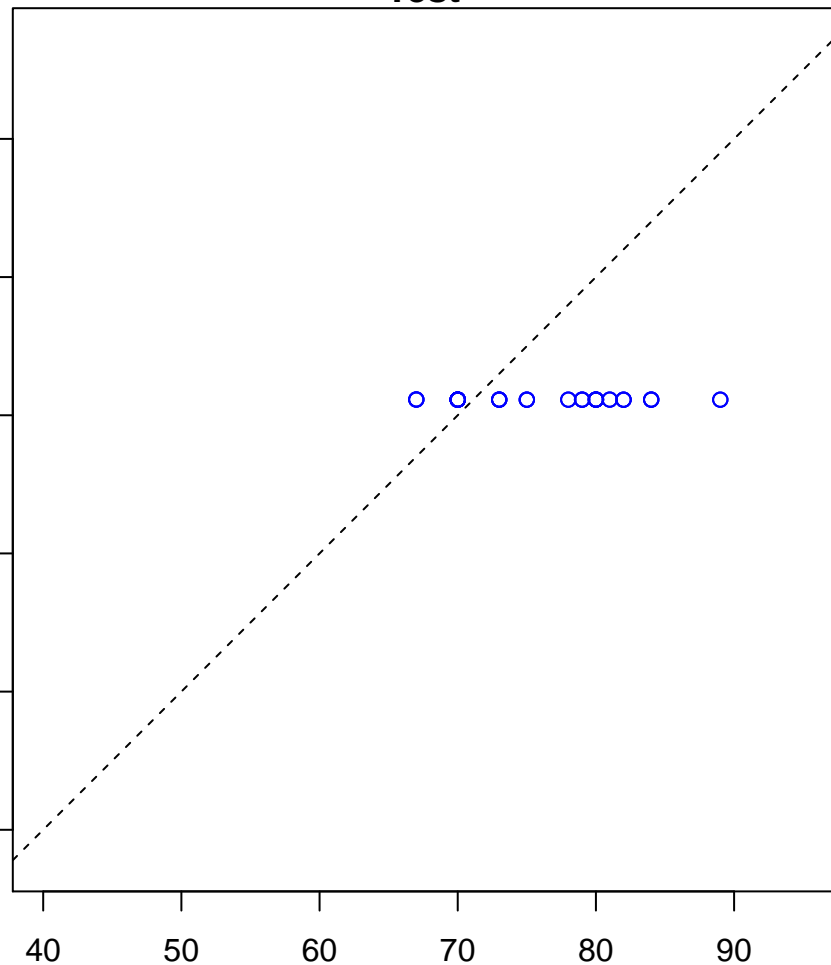


endothelial cell differentiation (Score: 0.810764)

Control



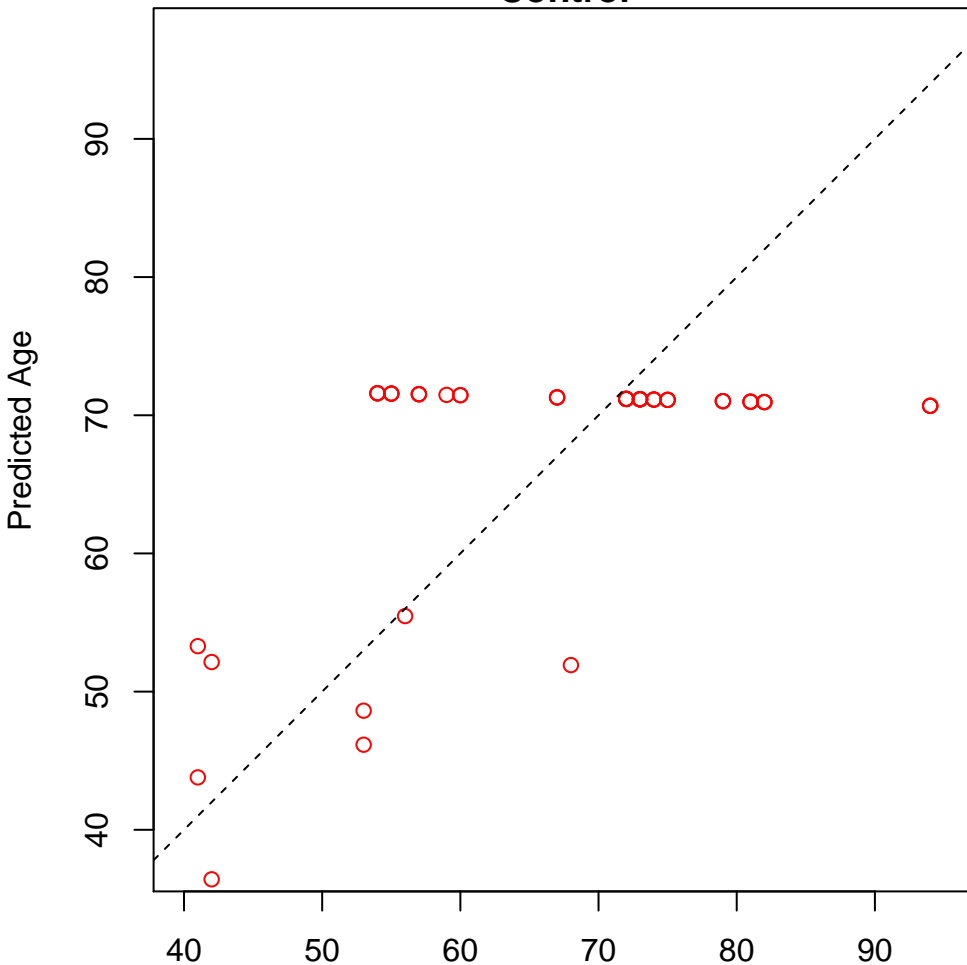
Test



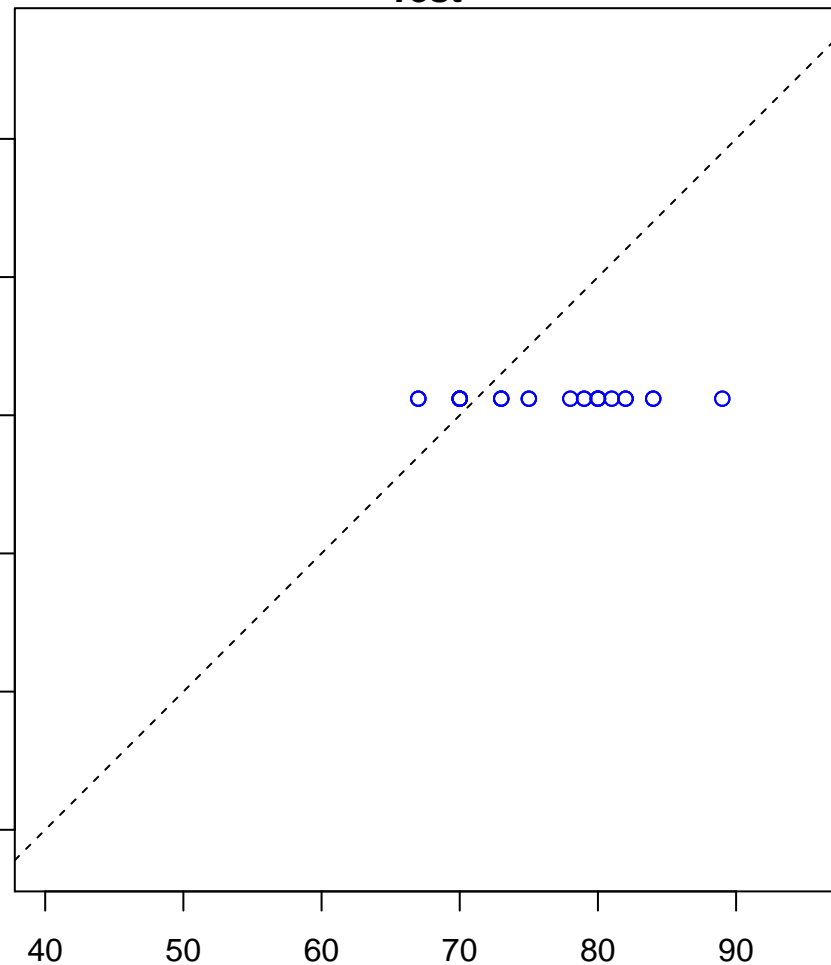
Actual Age

regulation of muscle contraction (Score: 0.810758)

Control



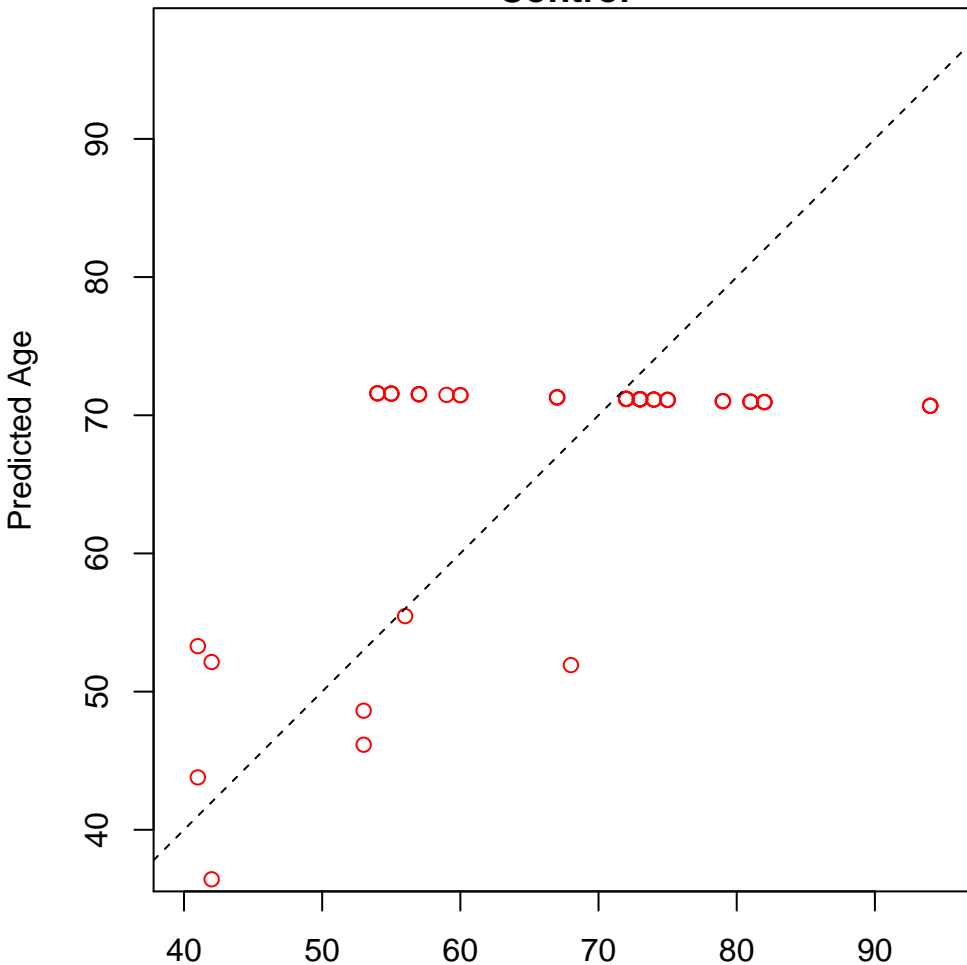
Test



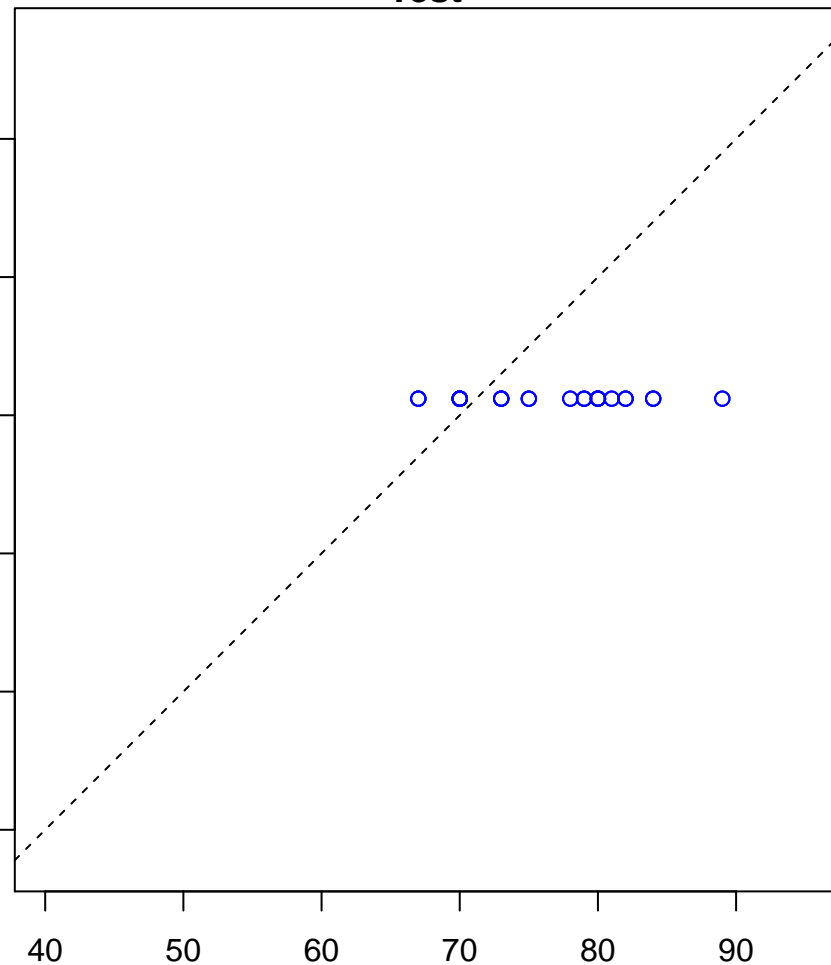
Actual Age

regulation of muscle system process (Score: 0.810758)

Control

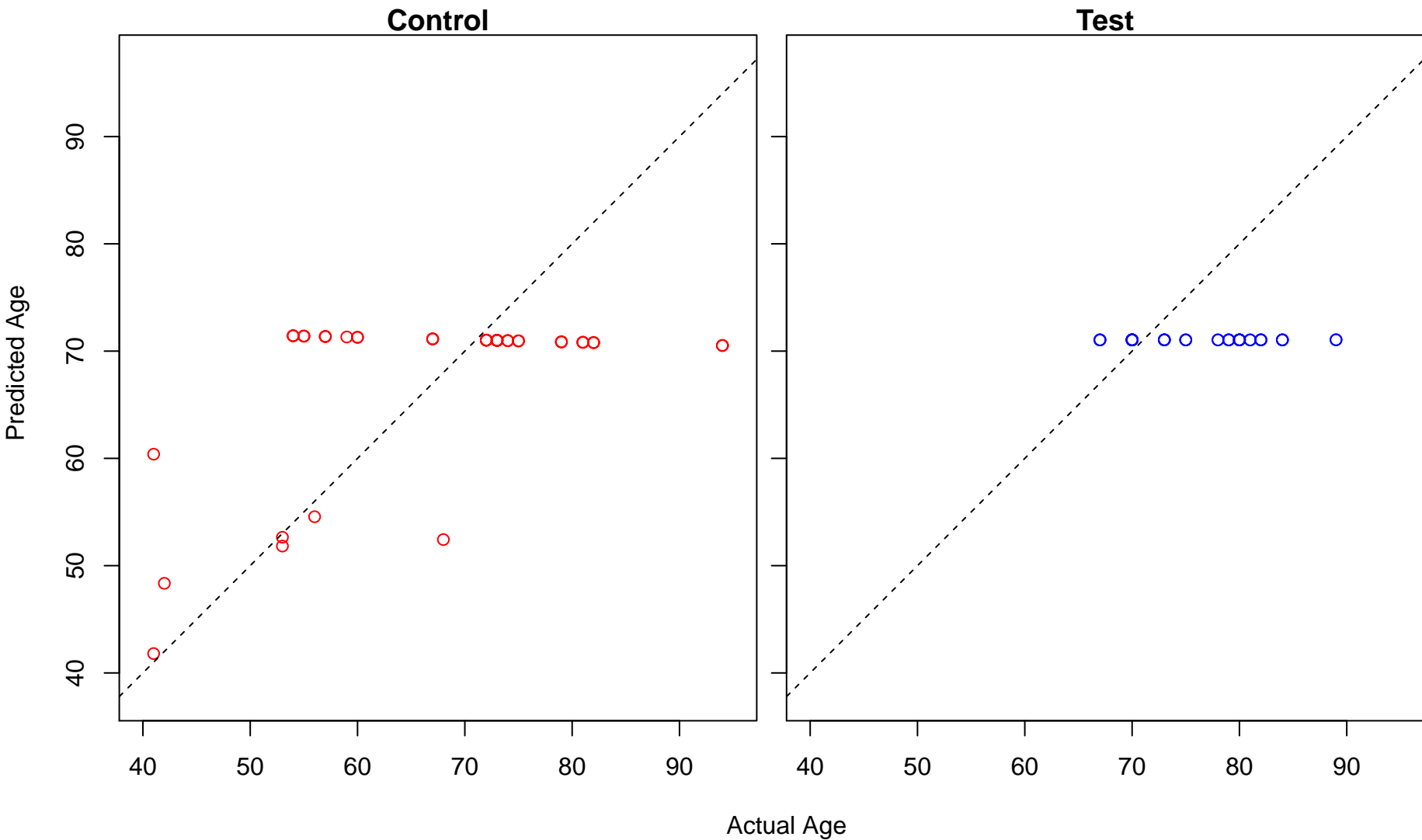


Test

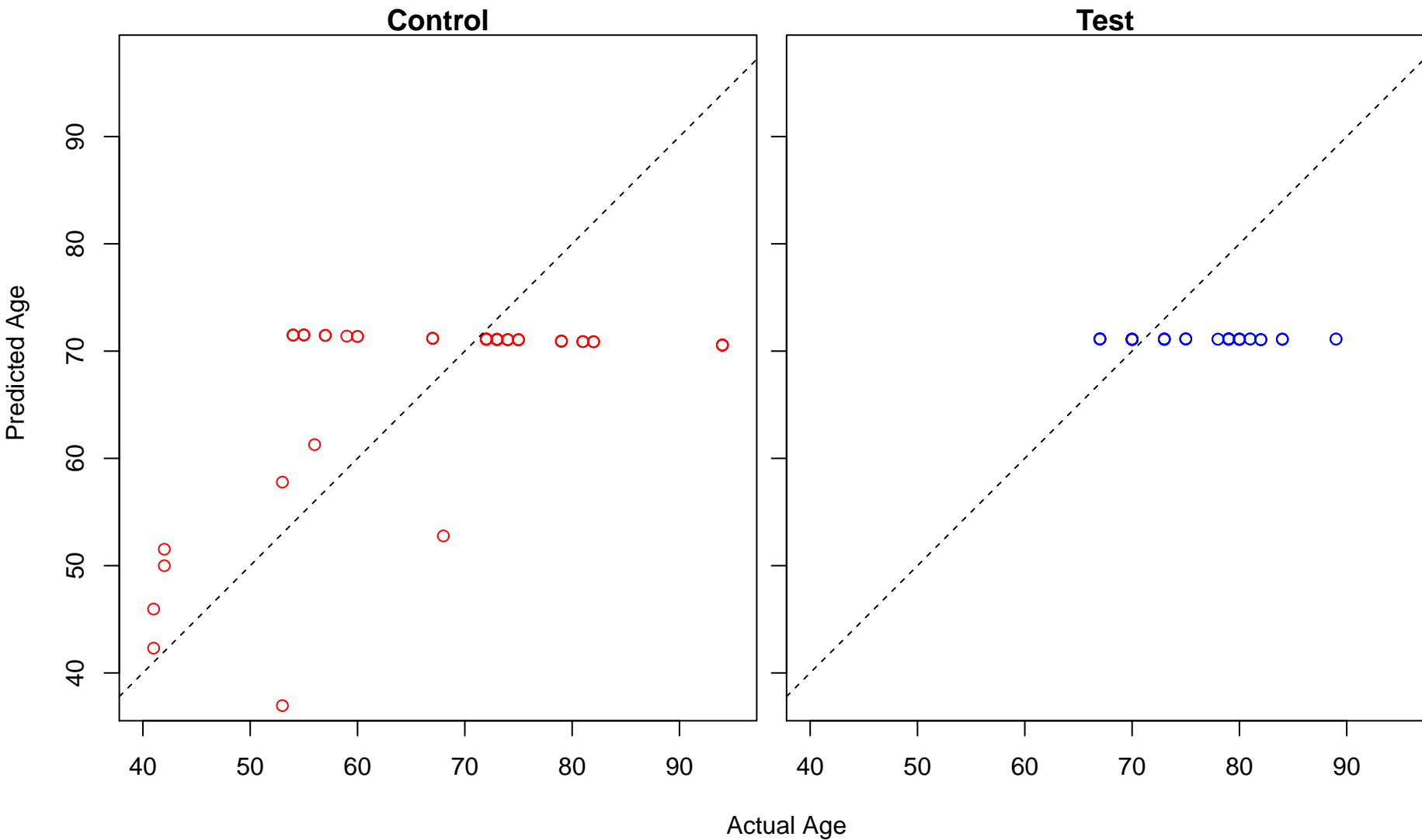


Actual Age

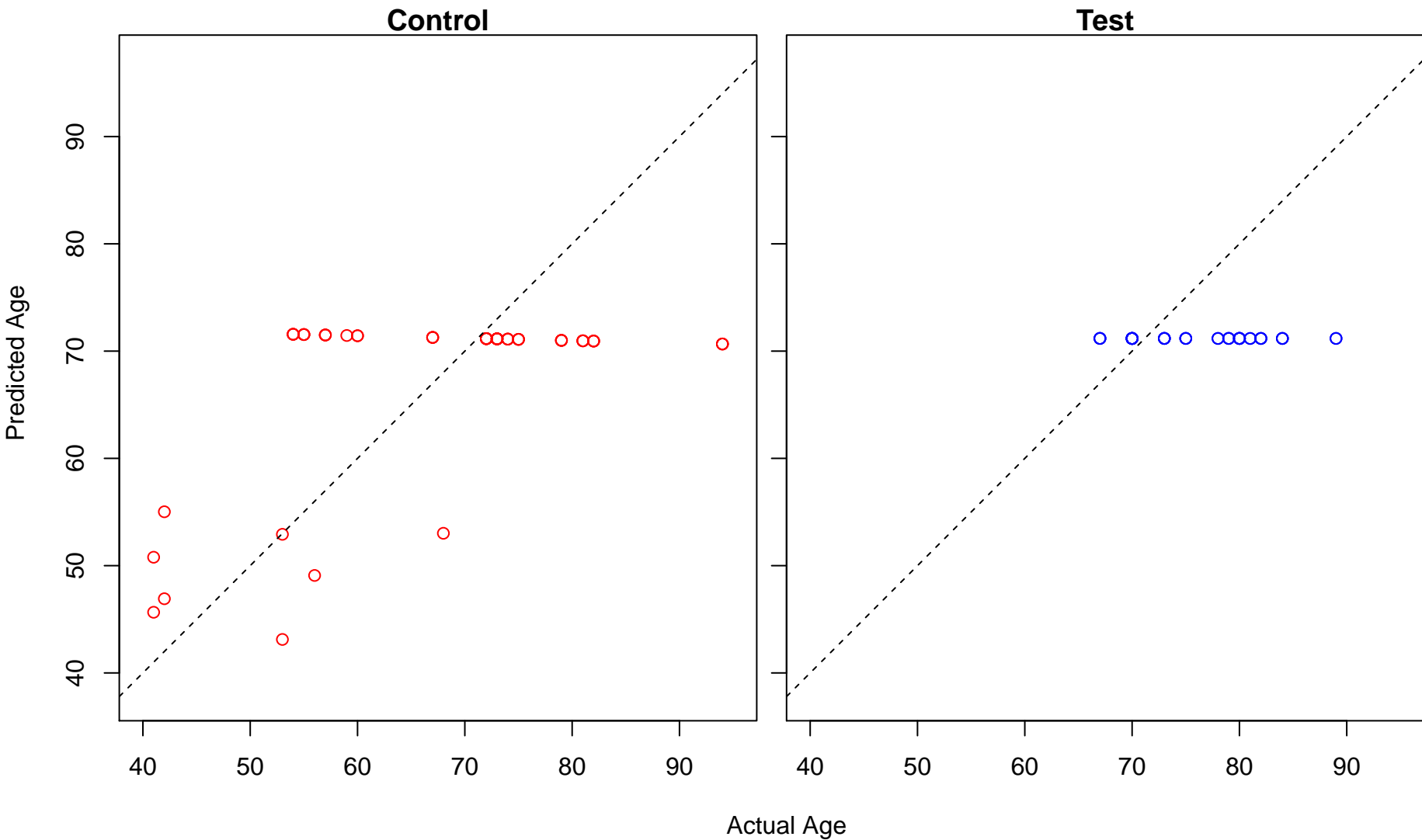
regulation of small GTPase mediated signal transduction (Score: 0.810752)



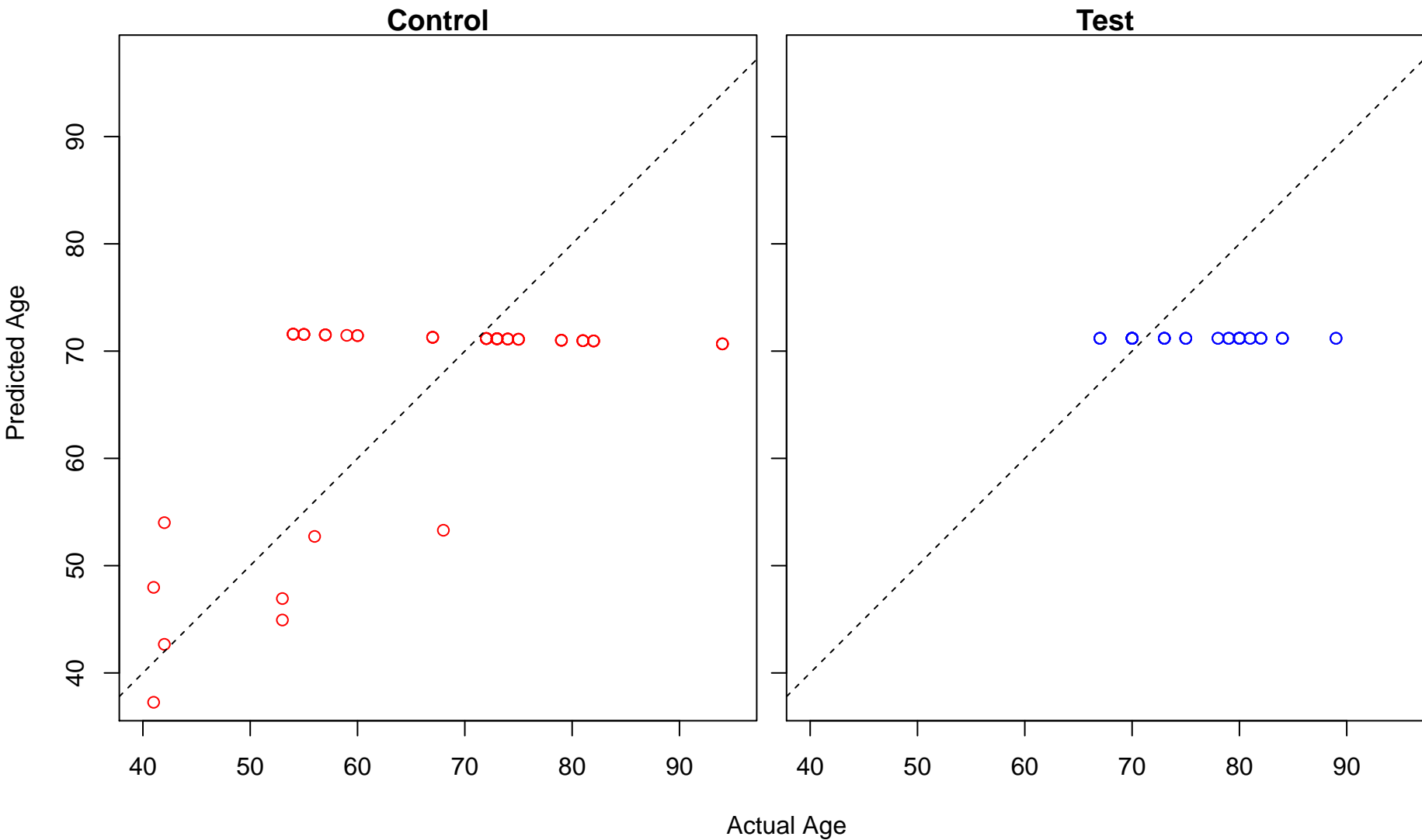
negative regulation of DNA metabolic process (Score: 0.810544)



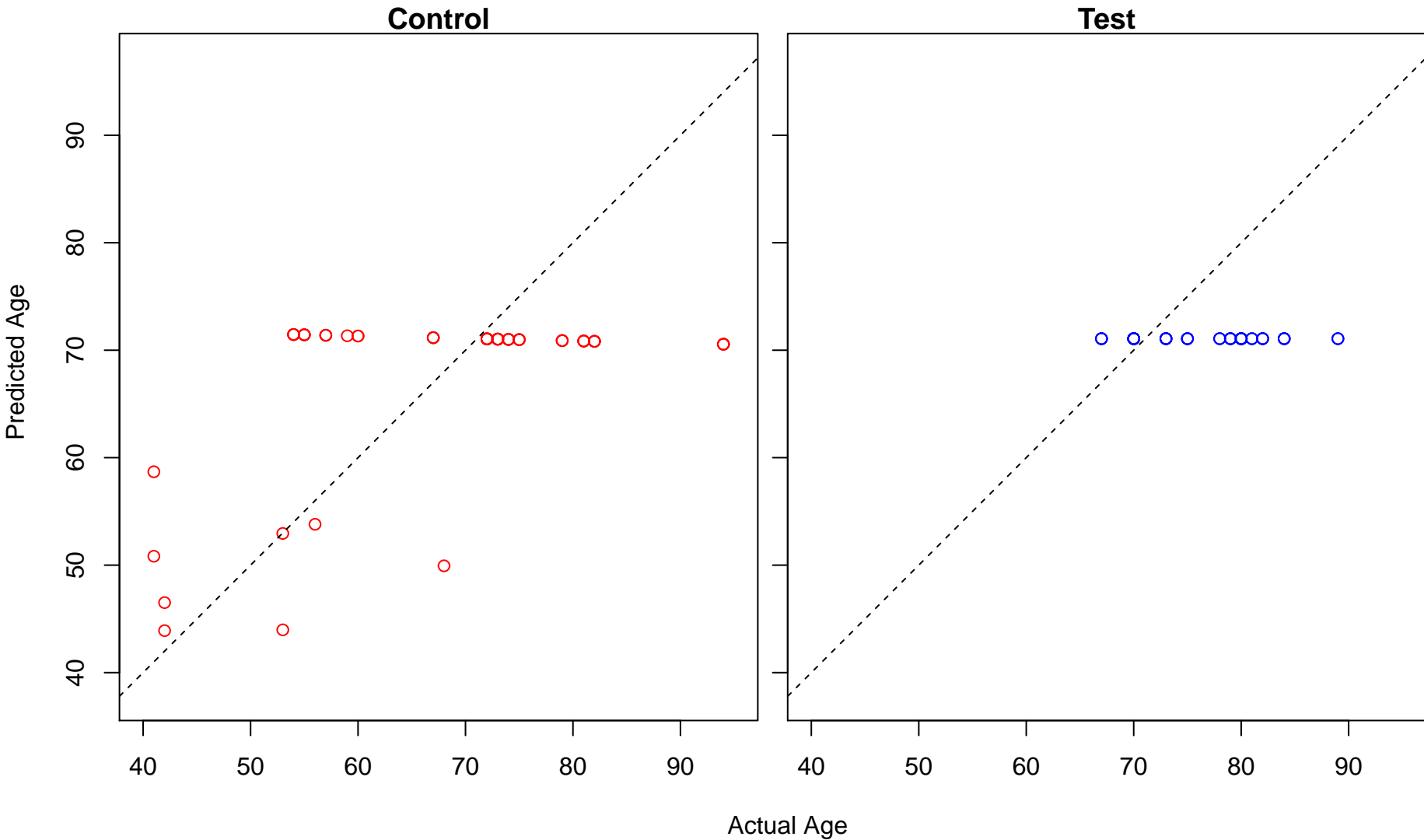
receptor metabolic process (Score: 0.810519)



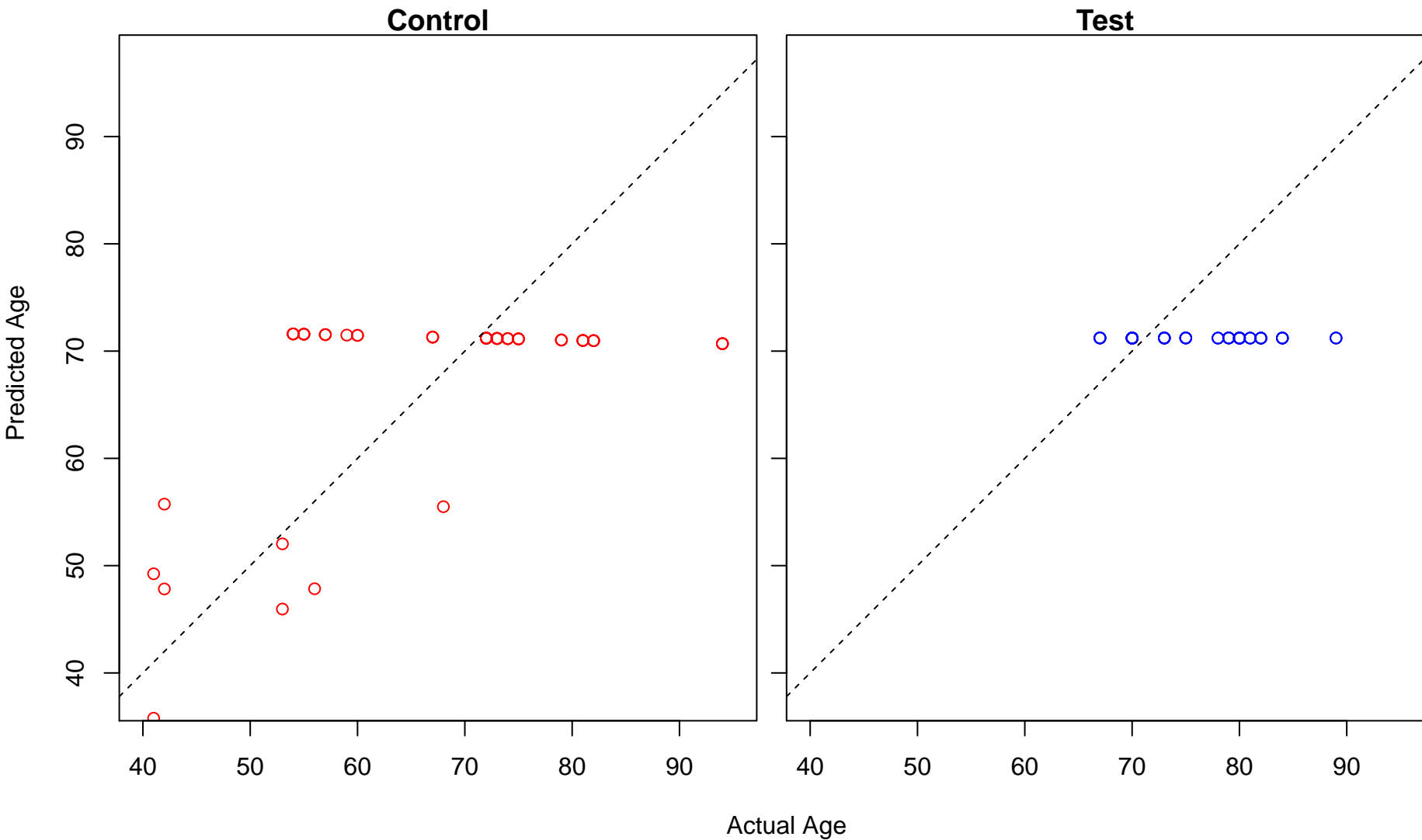
positive regulation of cellular protein metabolic process (Score: 0.810511)



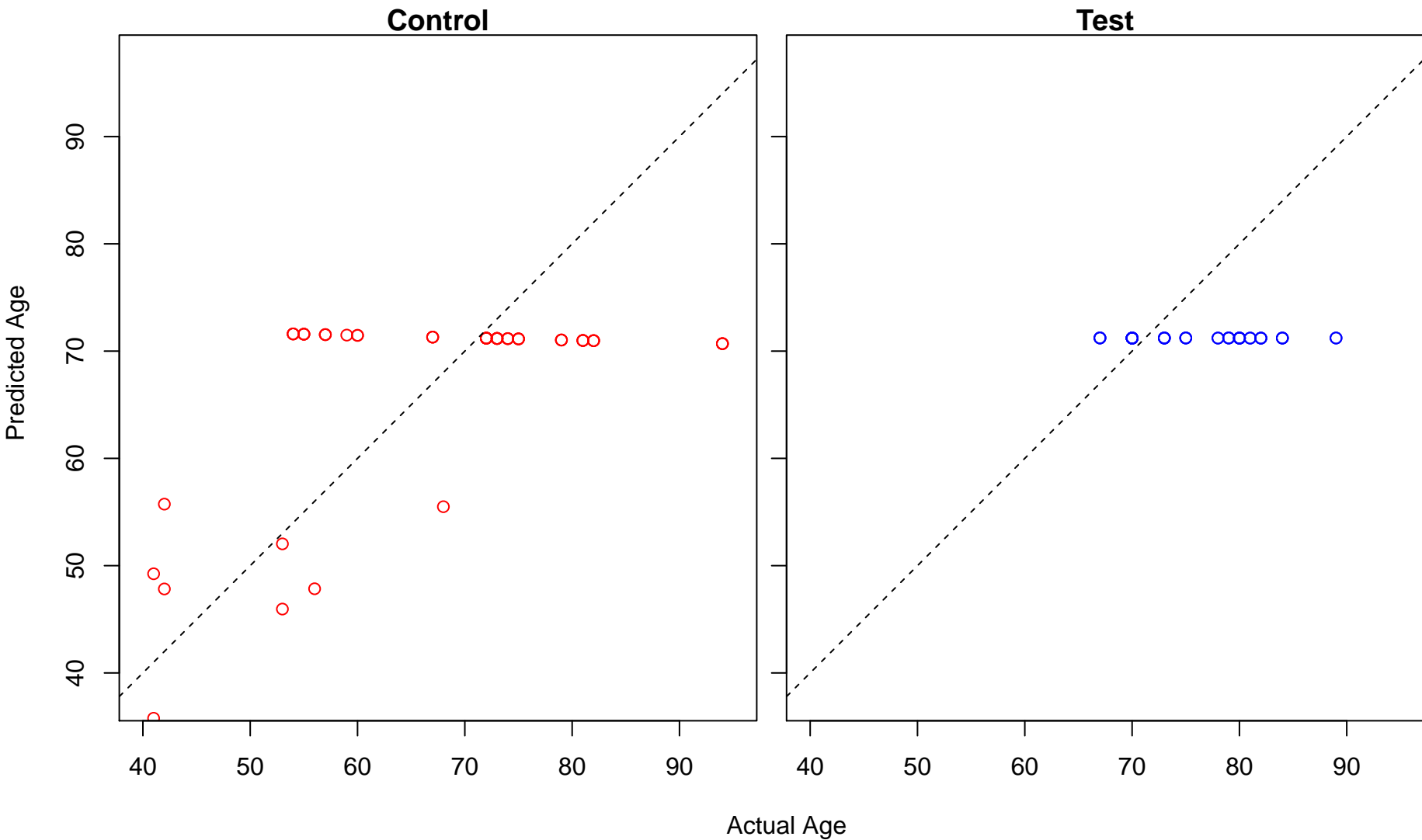
tRNA aminoacylation for protein translation (Score: 0.810479)



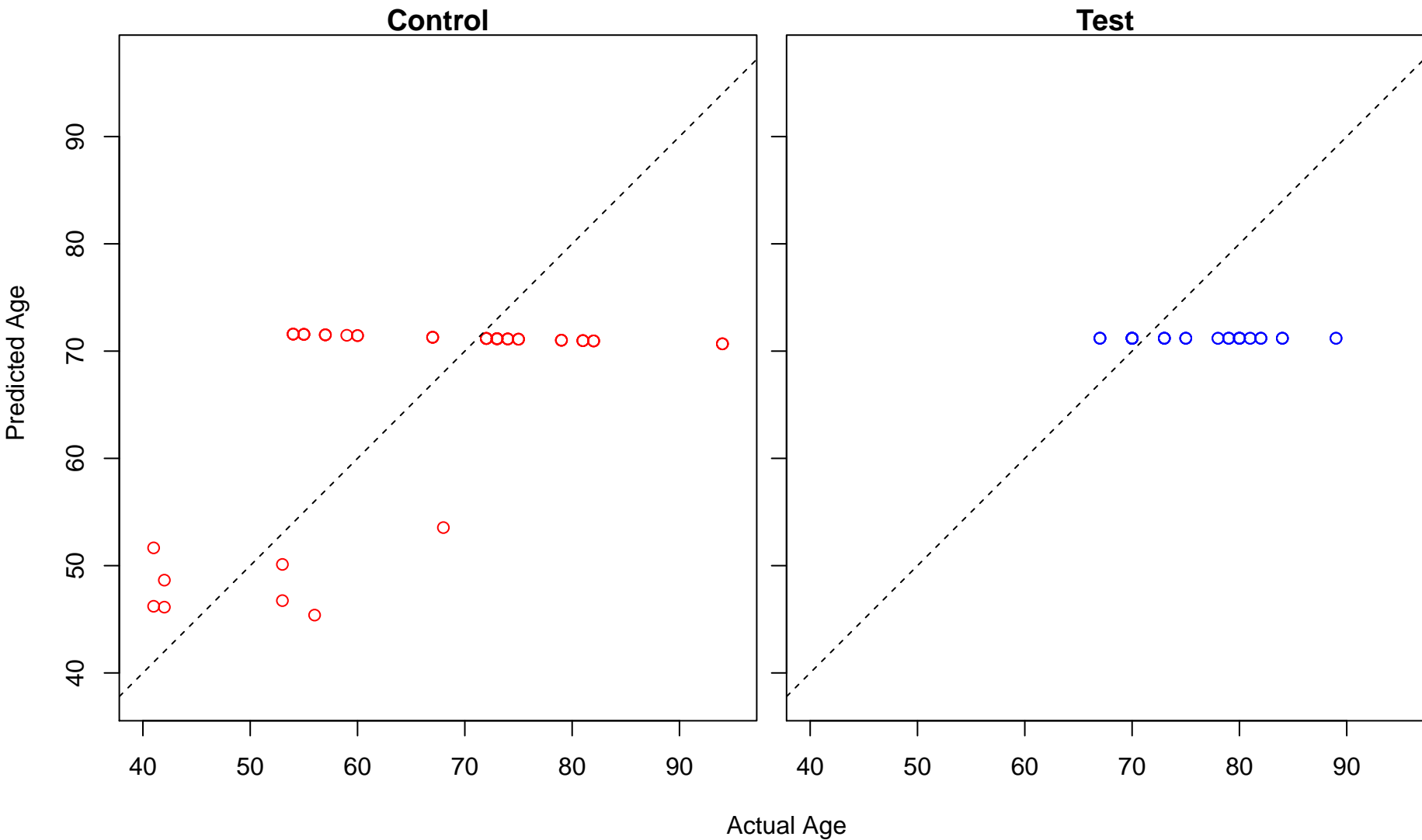
negative regulation of response to endoplasmic reticulum stress (Score: 0.810359)



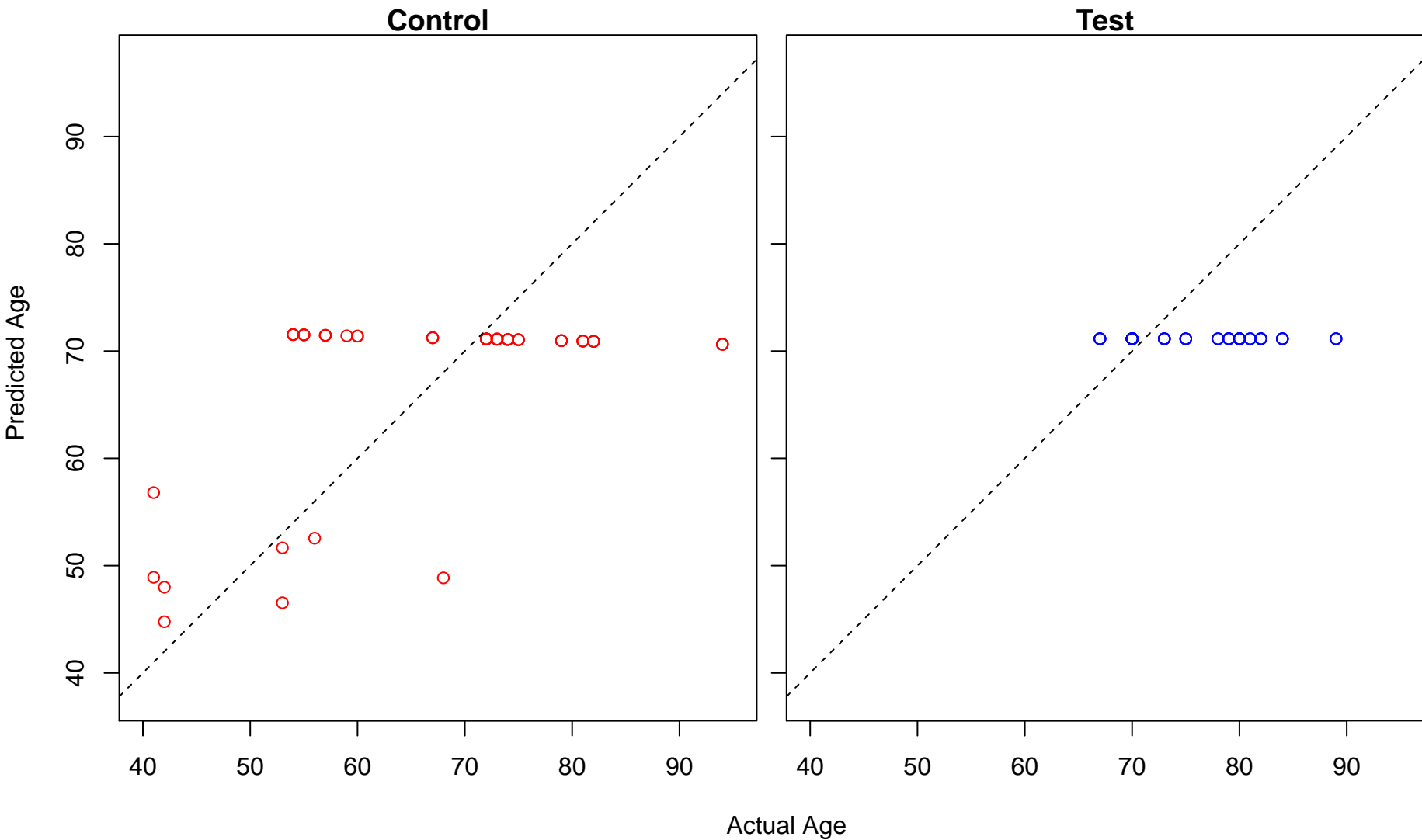
regulation of response to endoplasmic reticulum stress (Score: 0.810359)



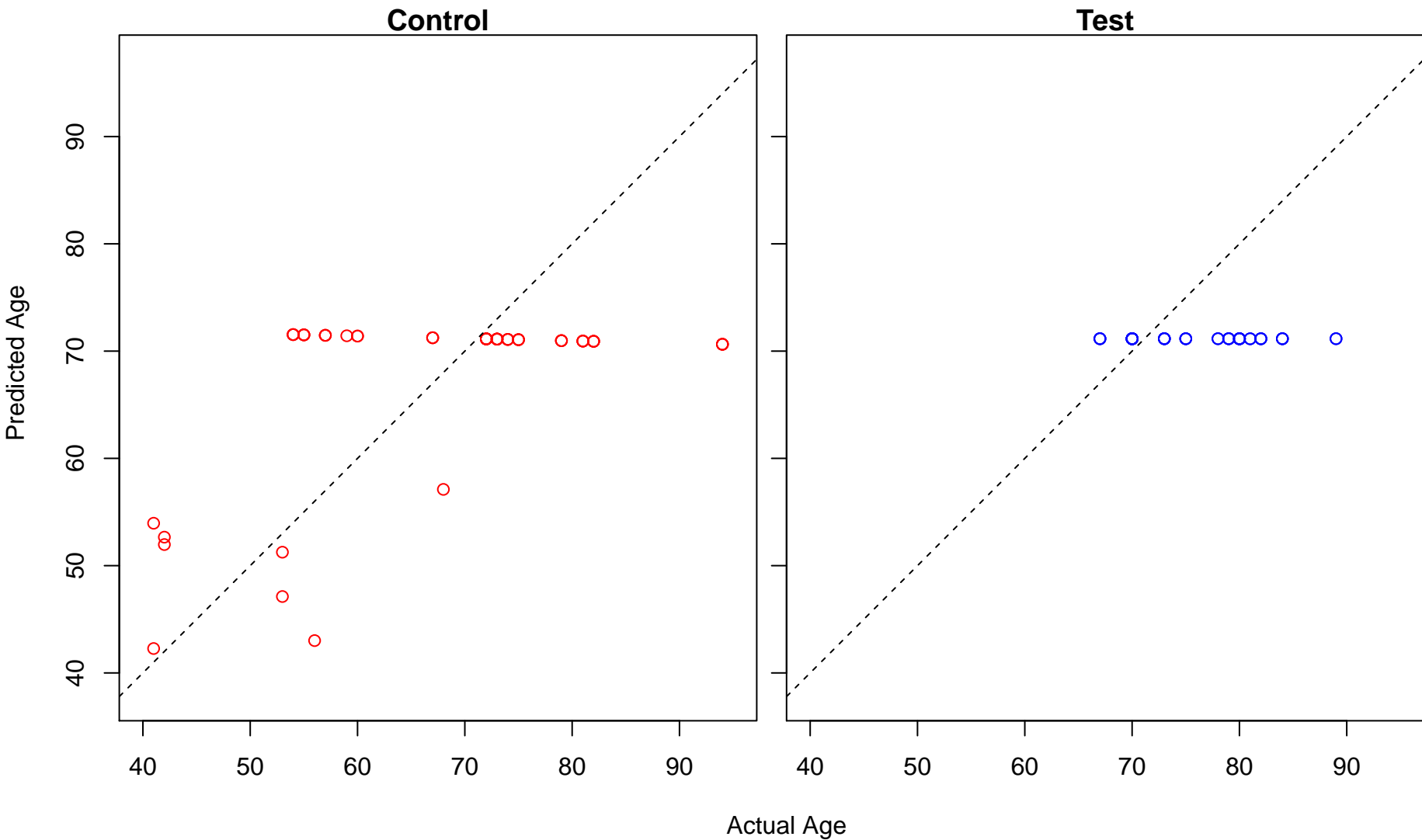
apoptotic signaling pathway (Score: 0.810325)



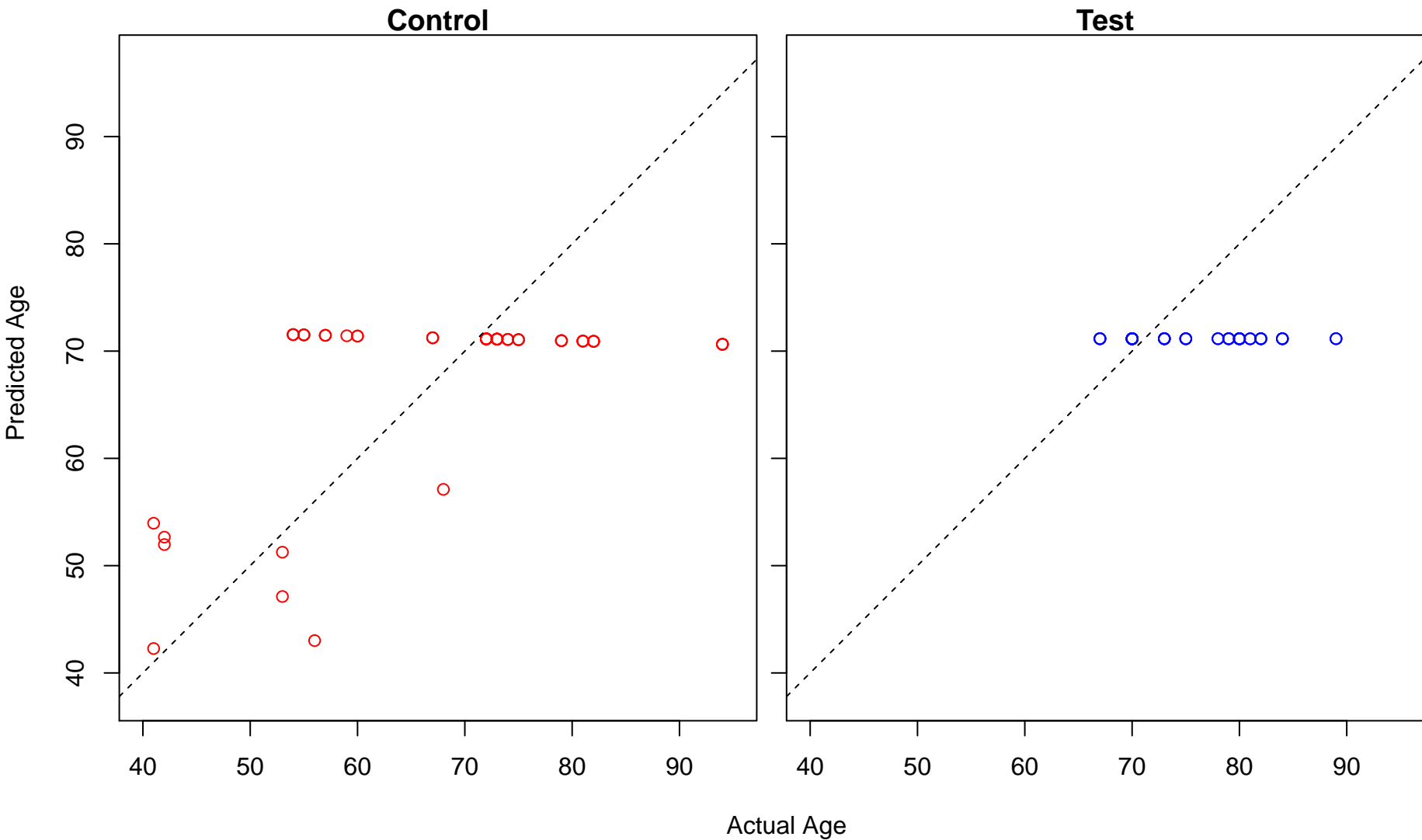
anion transport (Score: 0.810300)



RNA 3'-end processing (Score: 0.810295)

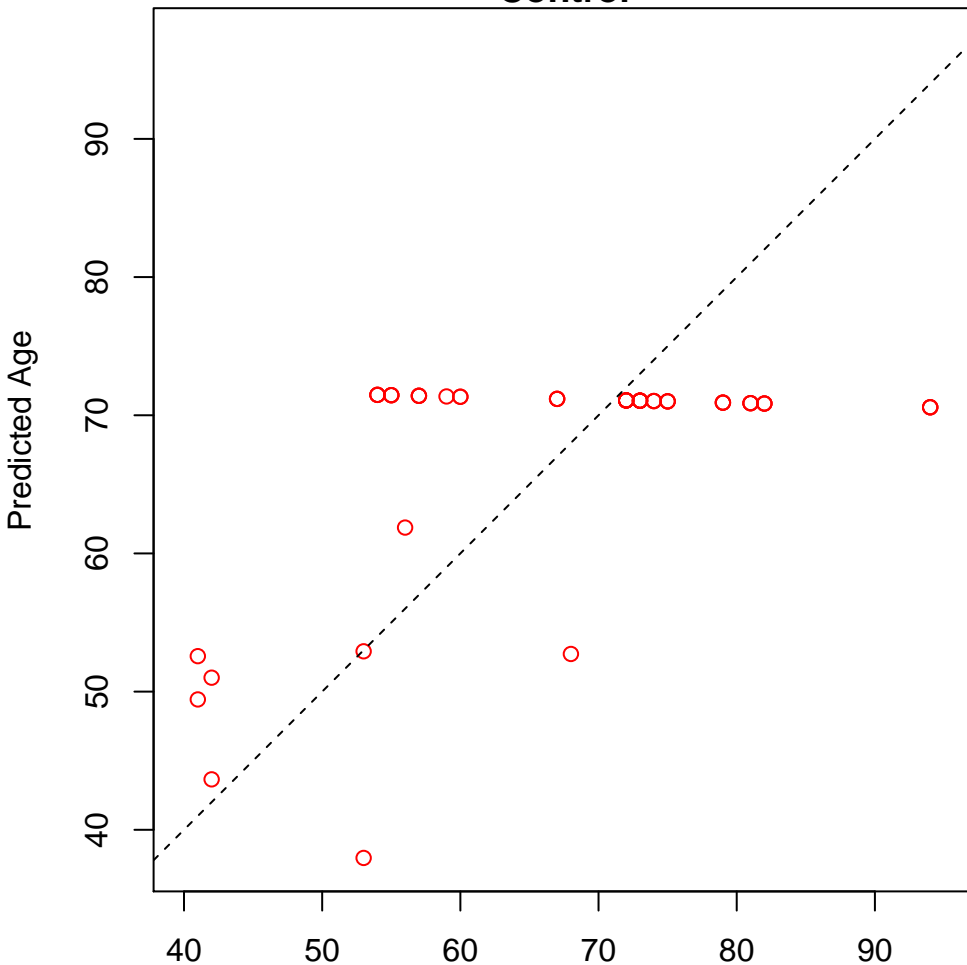


mRNA 3'-end processing (Score: 0.810295)

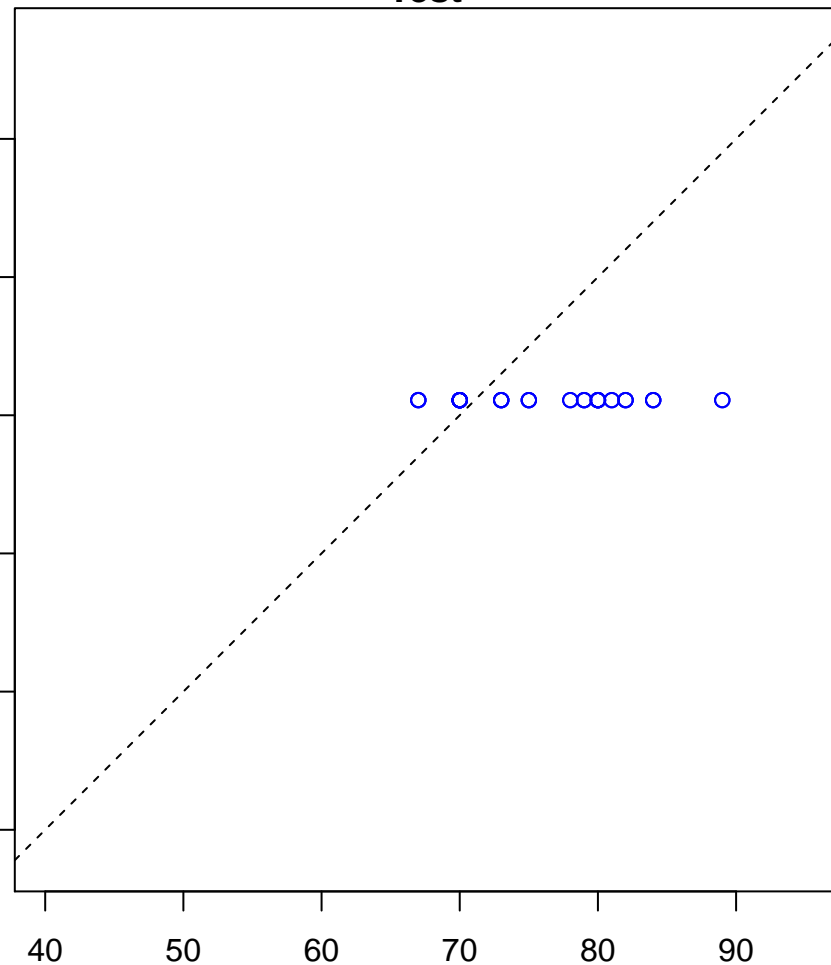


phospholipid metabolic process (Score: 0.810274)

Control



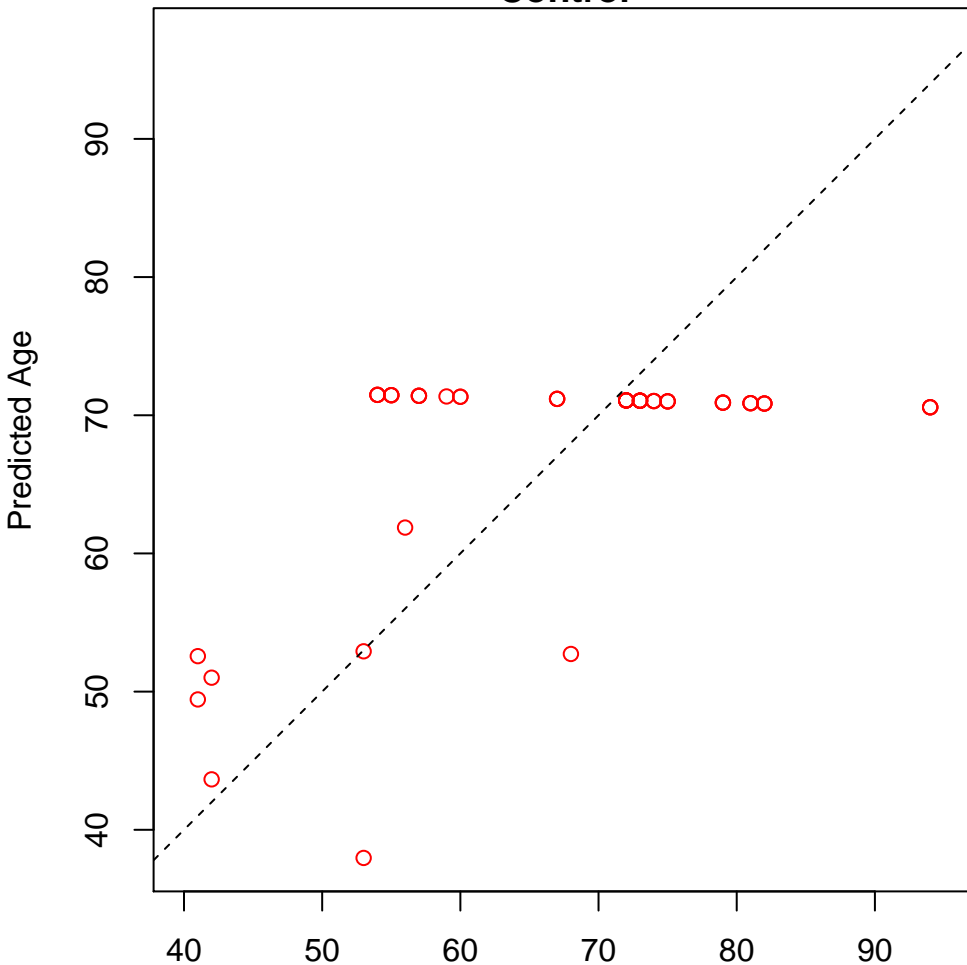
Test



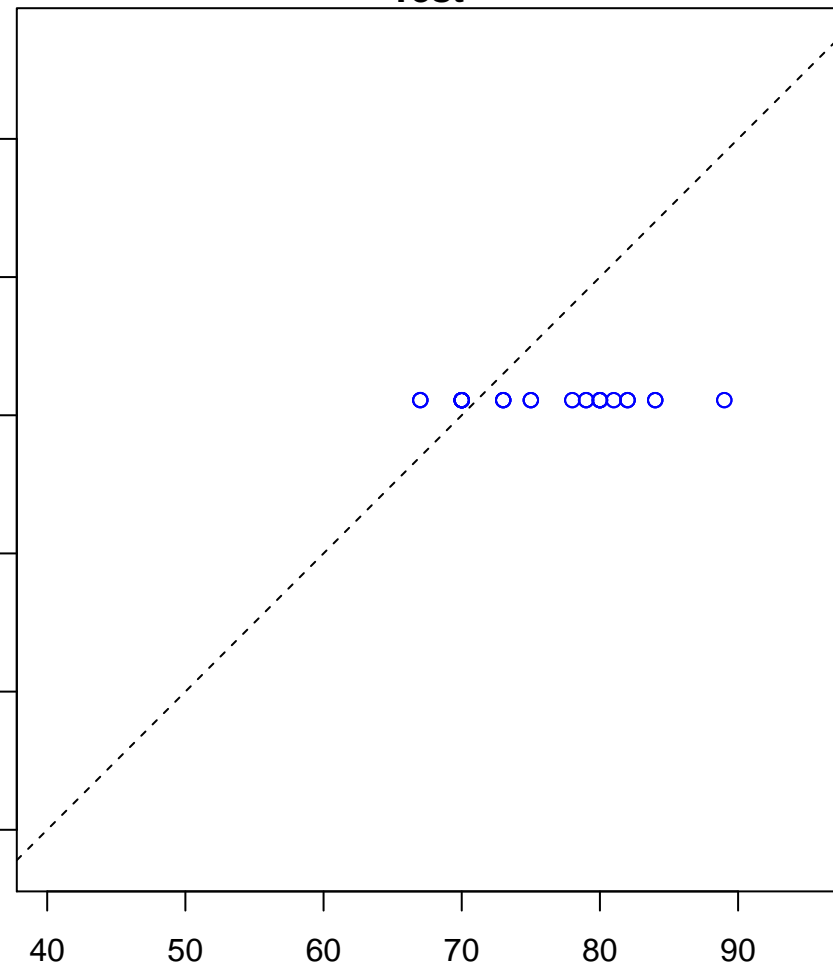
Actual Age

glycerophospholipid metabolic process (Score: 0.810274)

Control



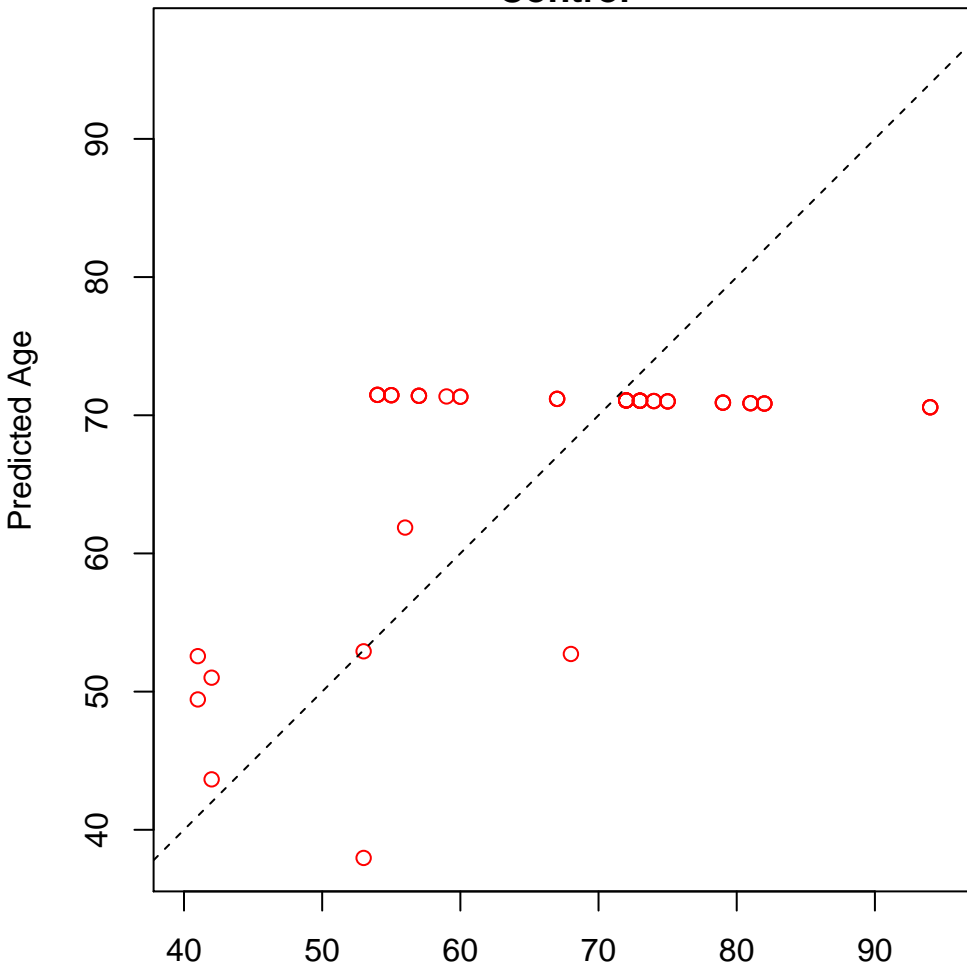
Test



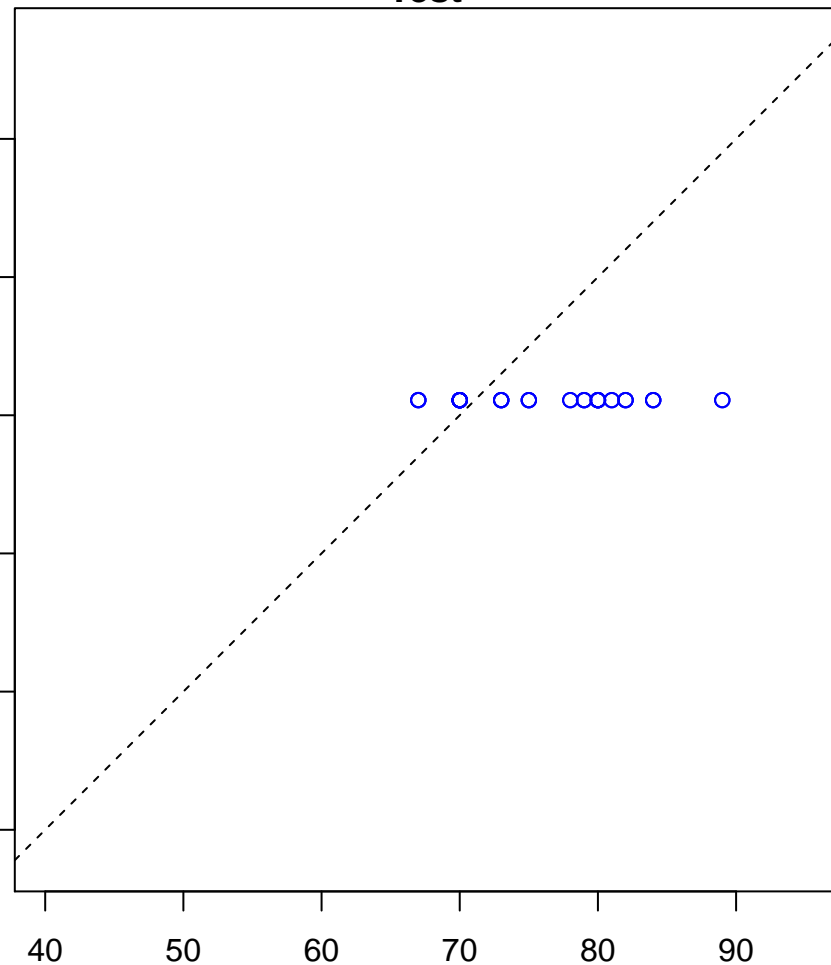
Actual Age

phospholipid biosynthetic process (Score: 0.810274)

Control



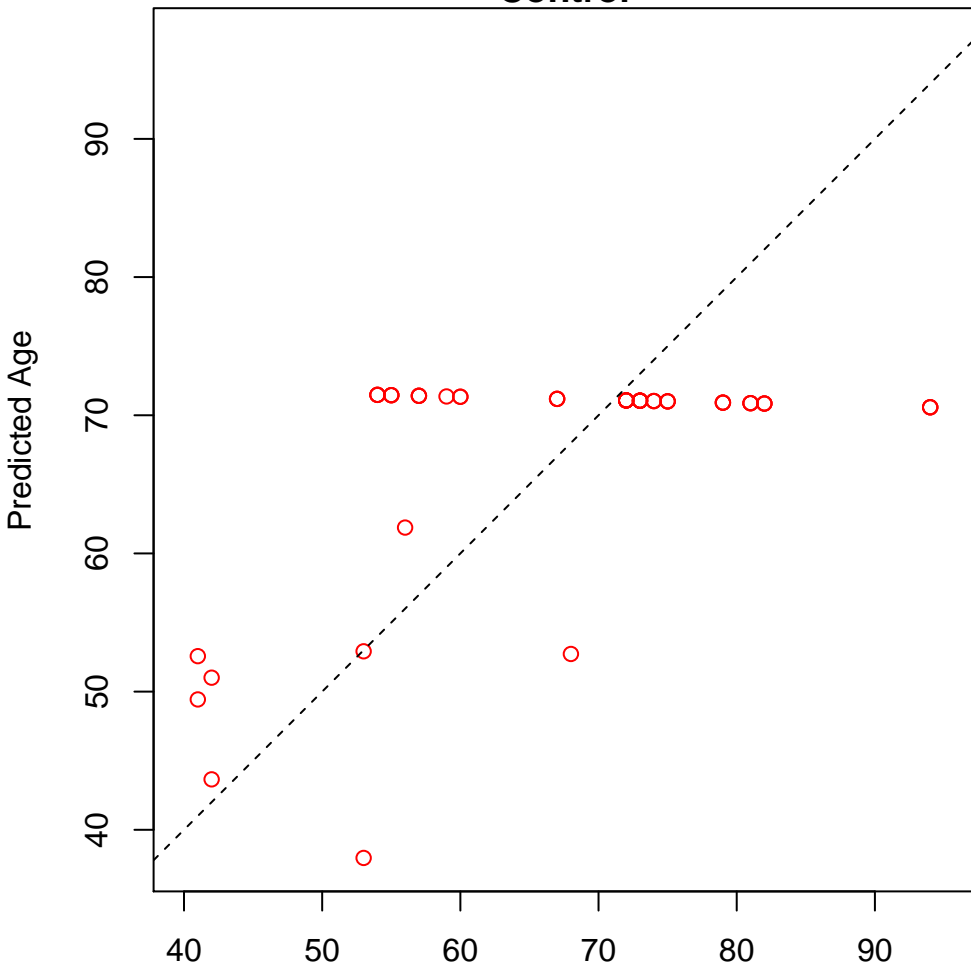
Test



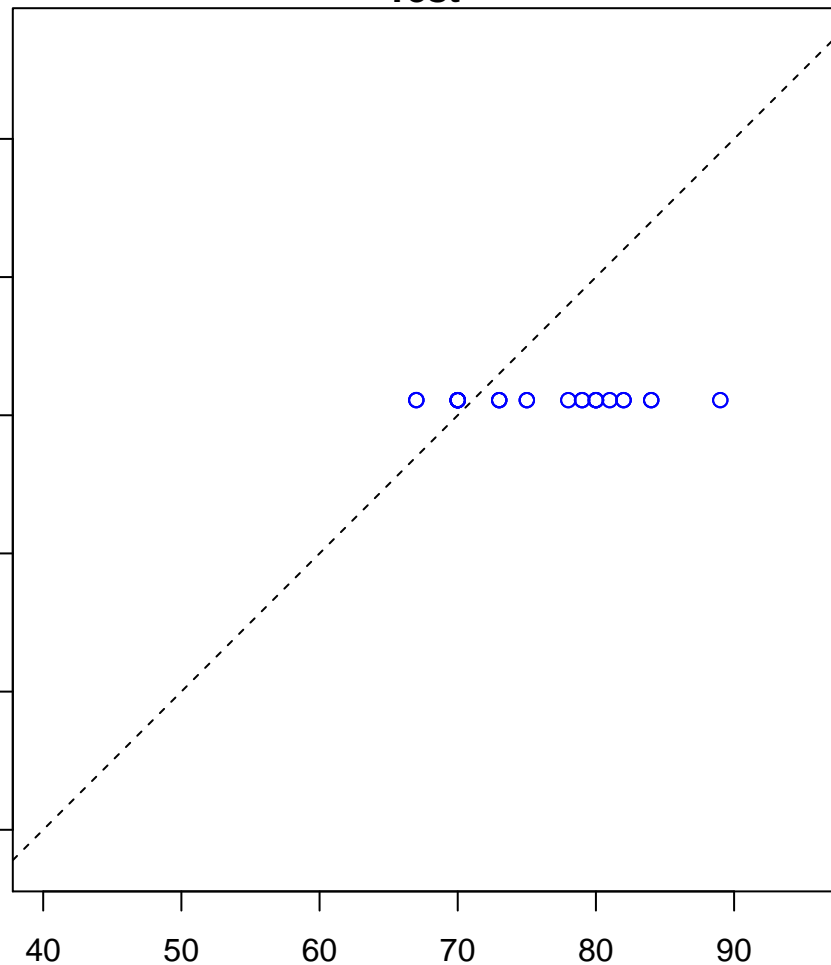
Actual Age

glycerolipid biosynthetic process (Score: 0.810274)

Control

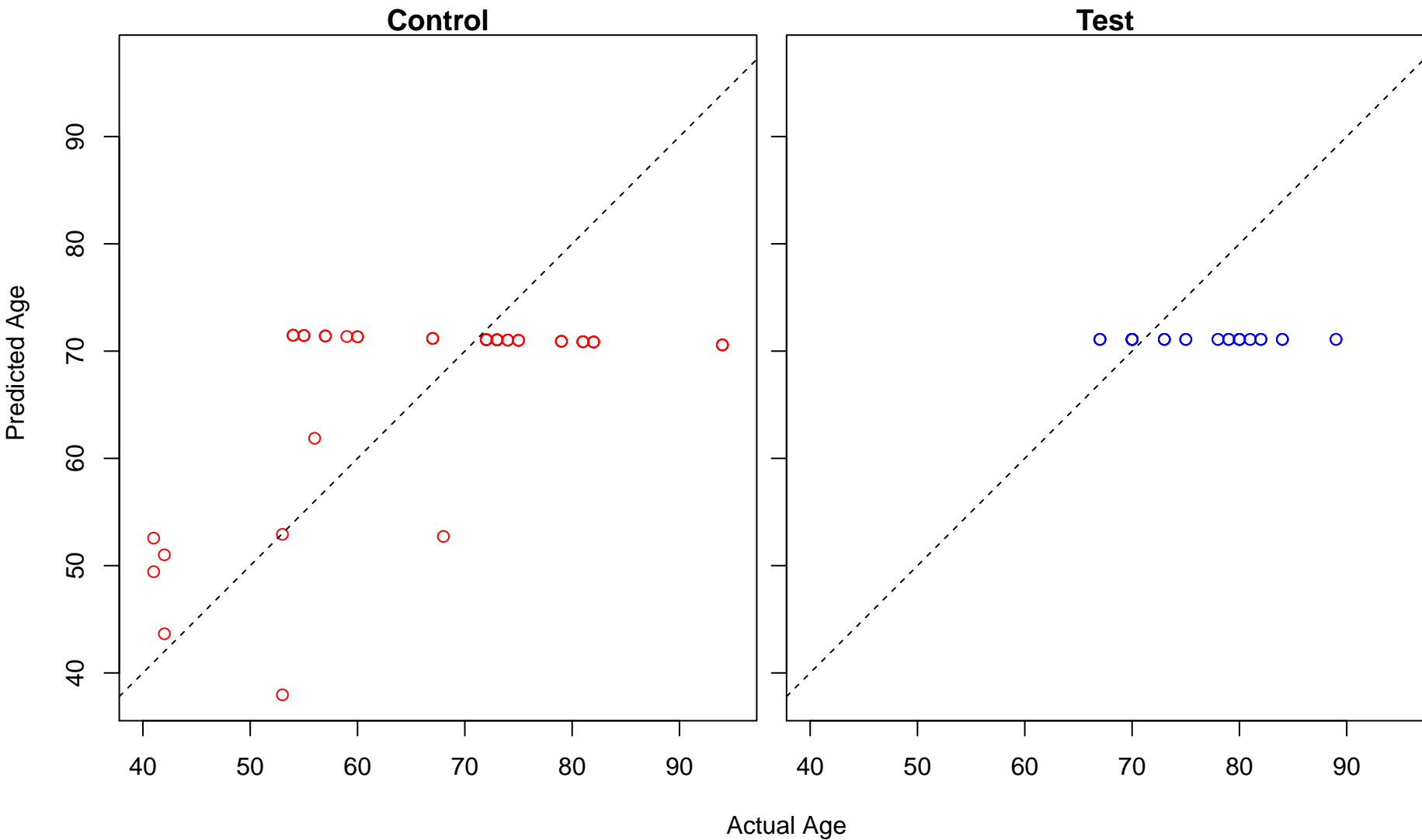


Test



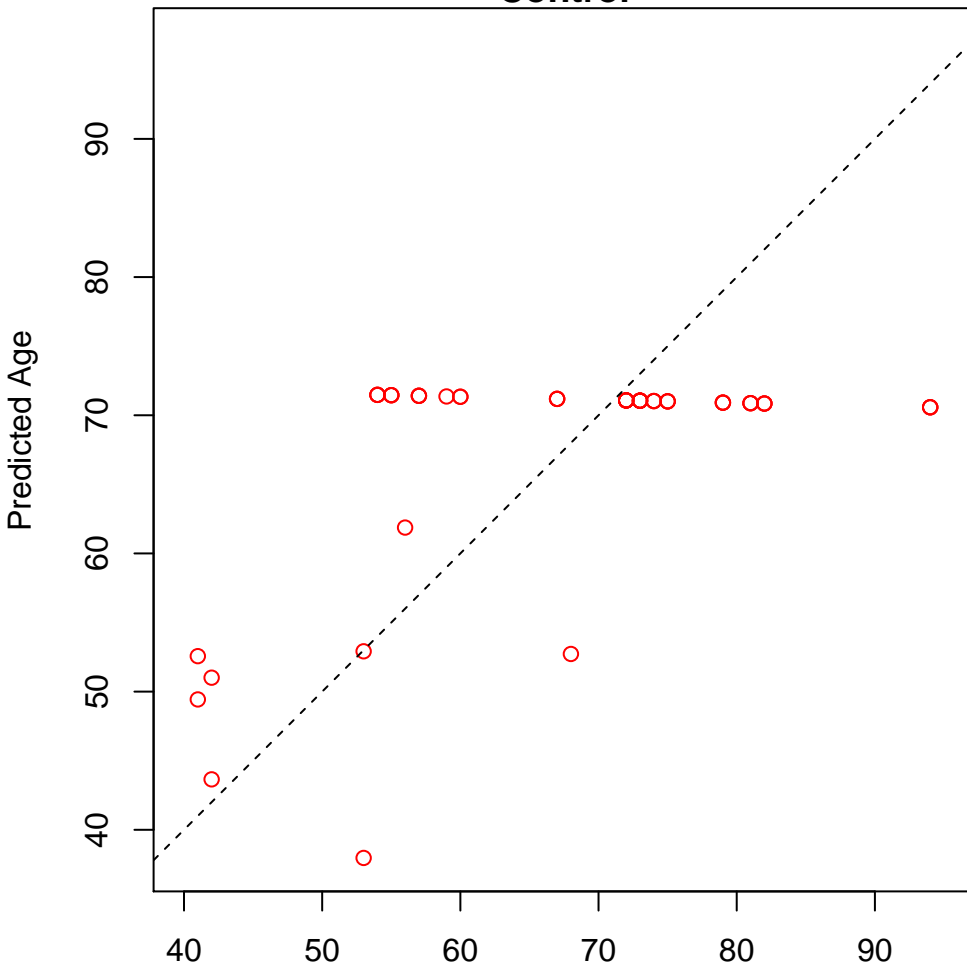
Actual Age

glycerophospholipid biosynthetic process (Score: 0.810274)

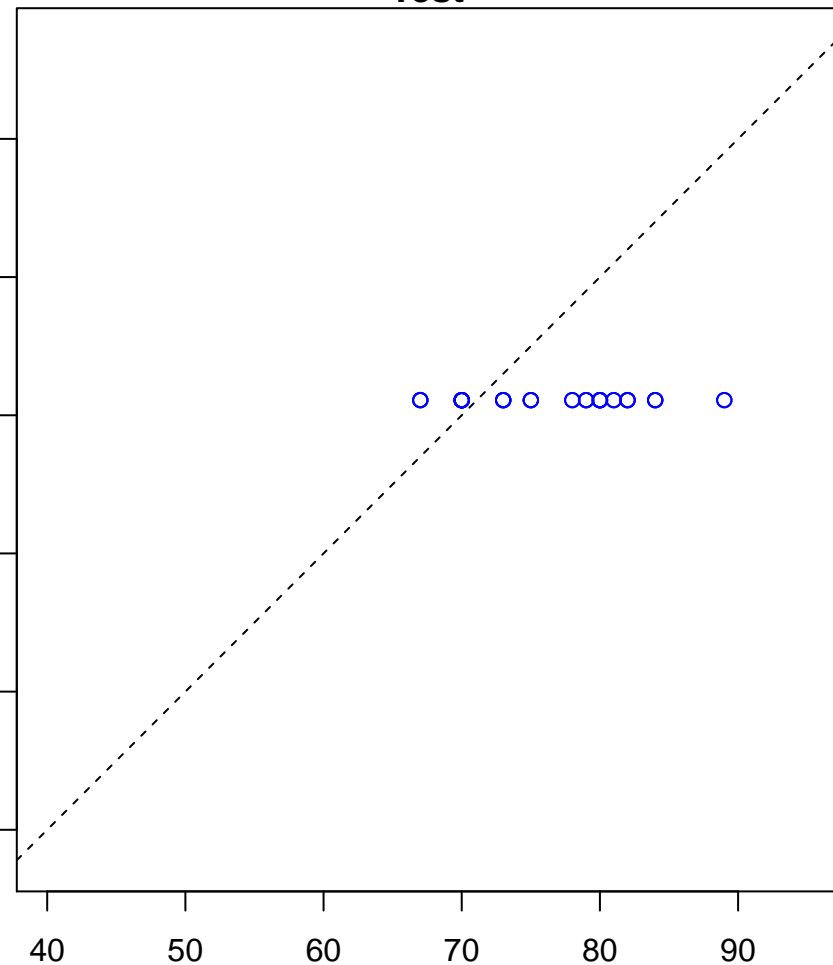


glycerolipid metabolic process (Score: 0.810274)

Control

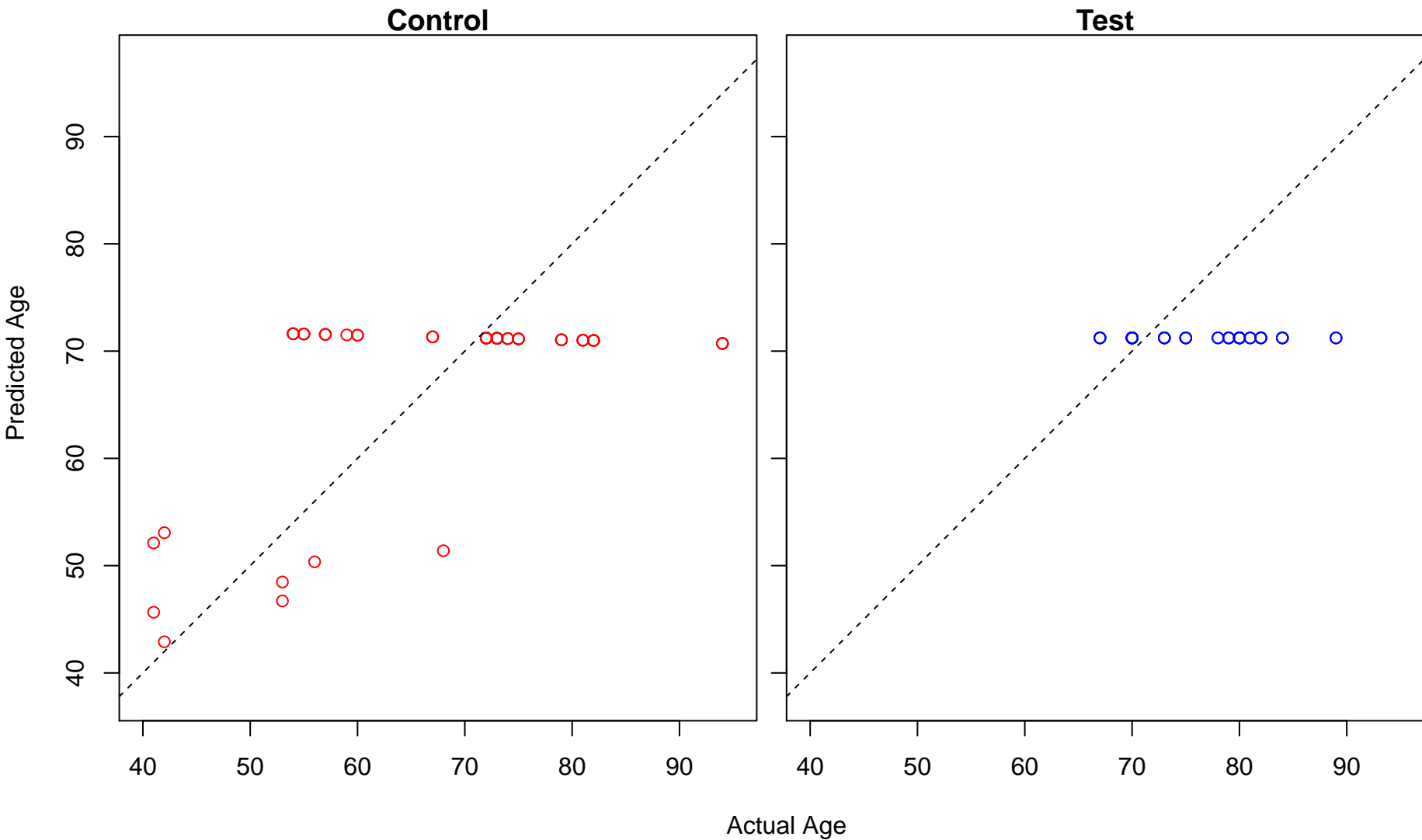


Test

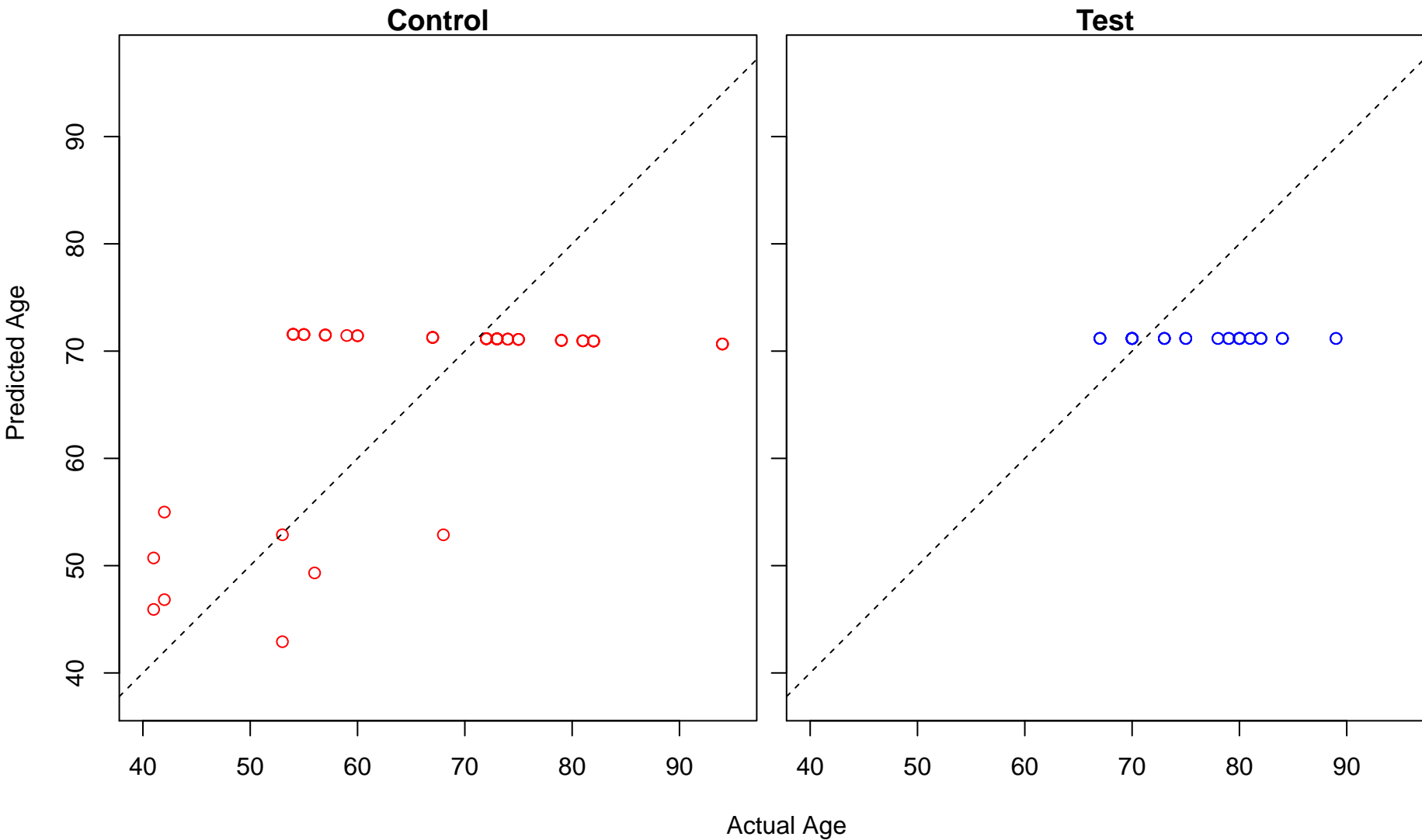


Actual Age

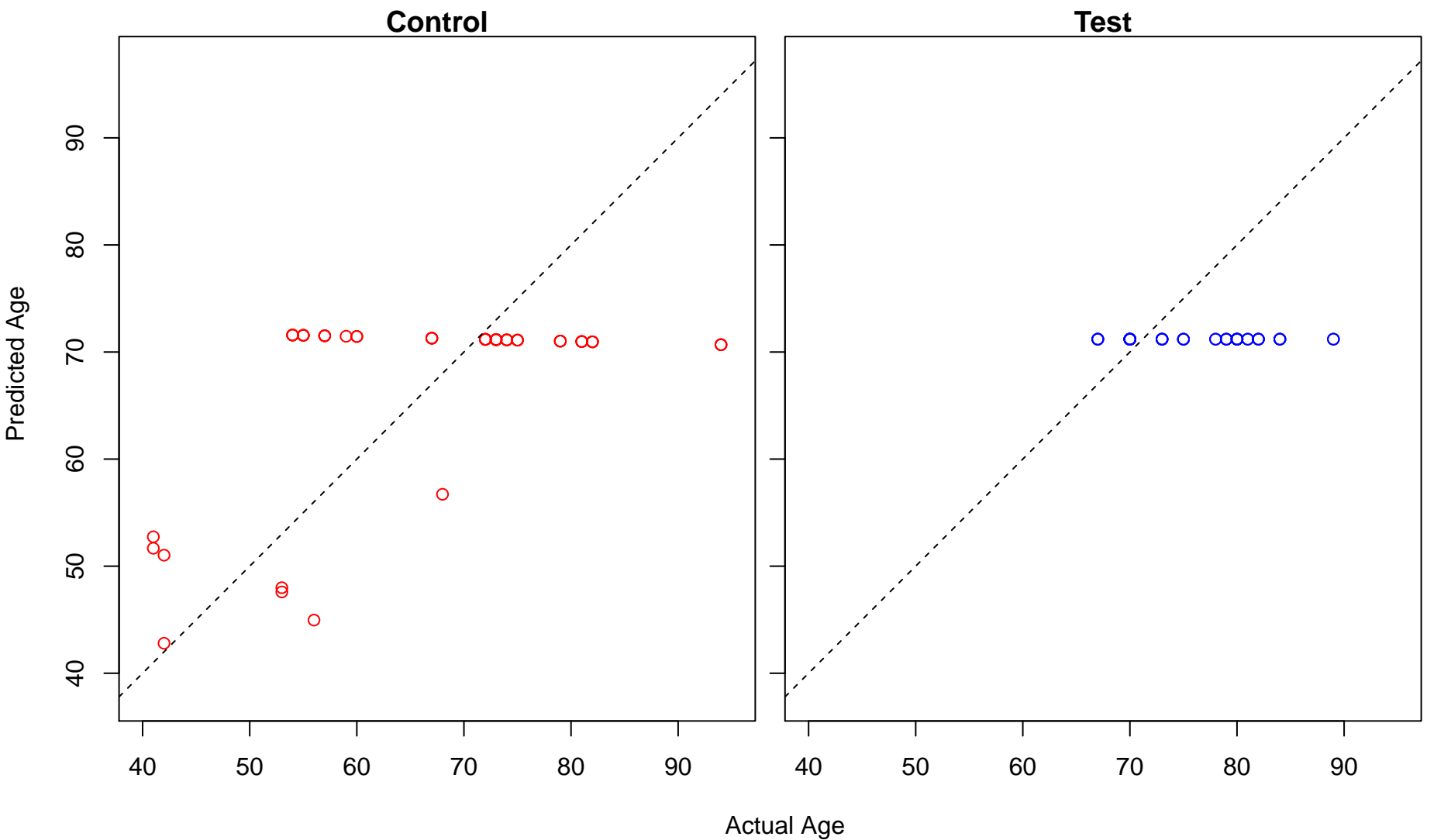
cellular component assembly (Score: 0.810254)



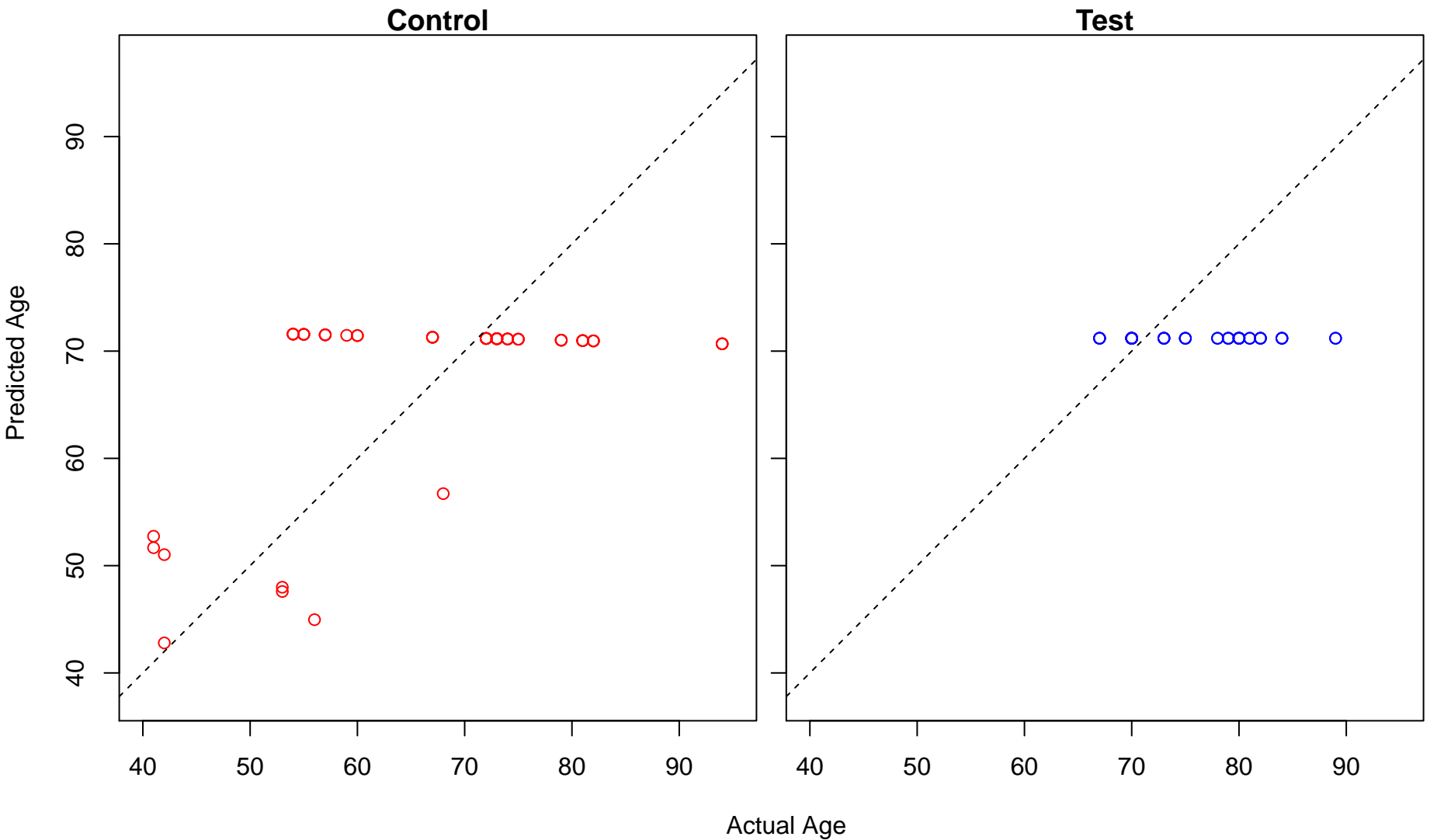
receptor internalization (Score: 0.810233)



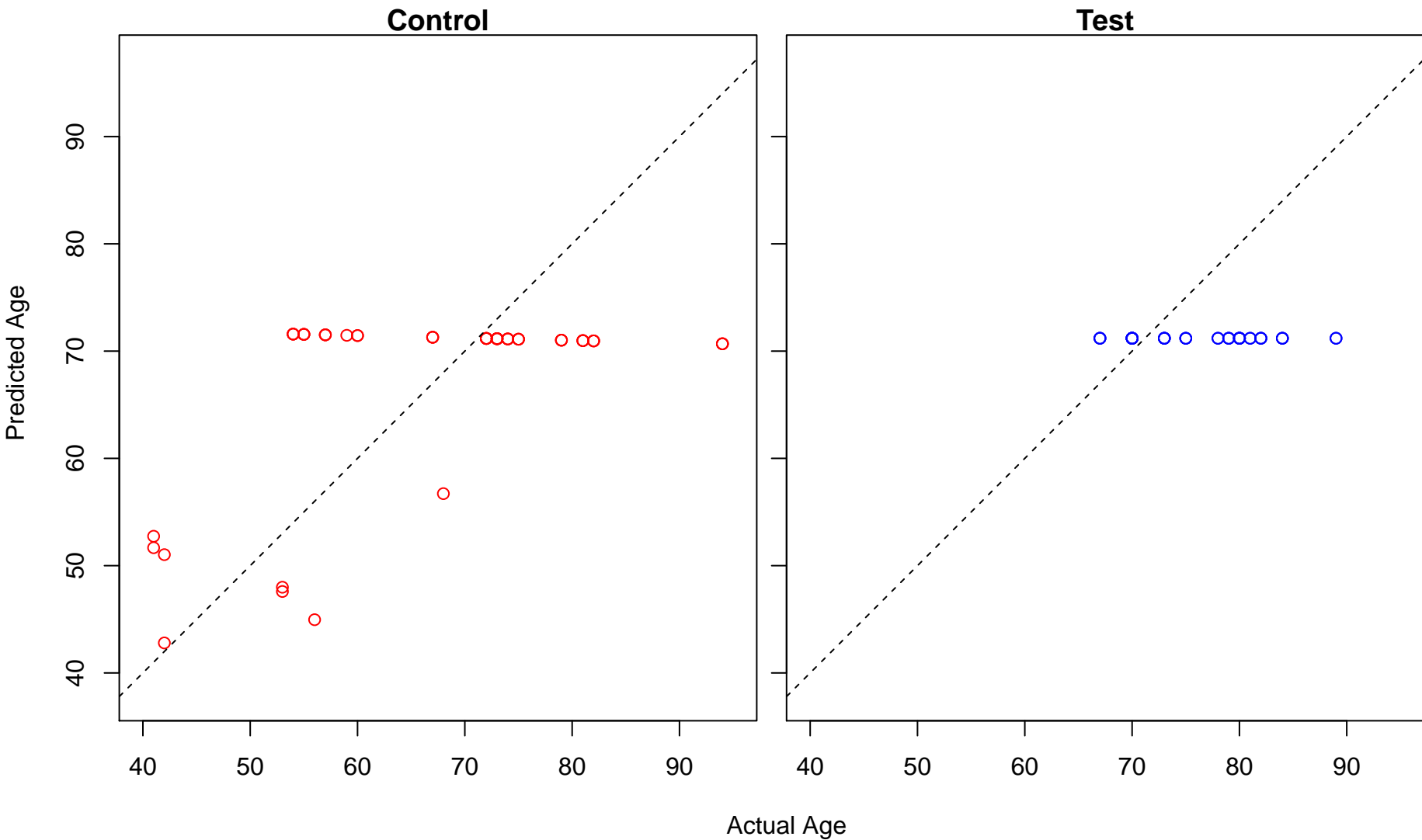
Regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (Score



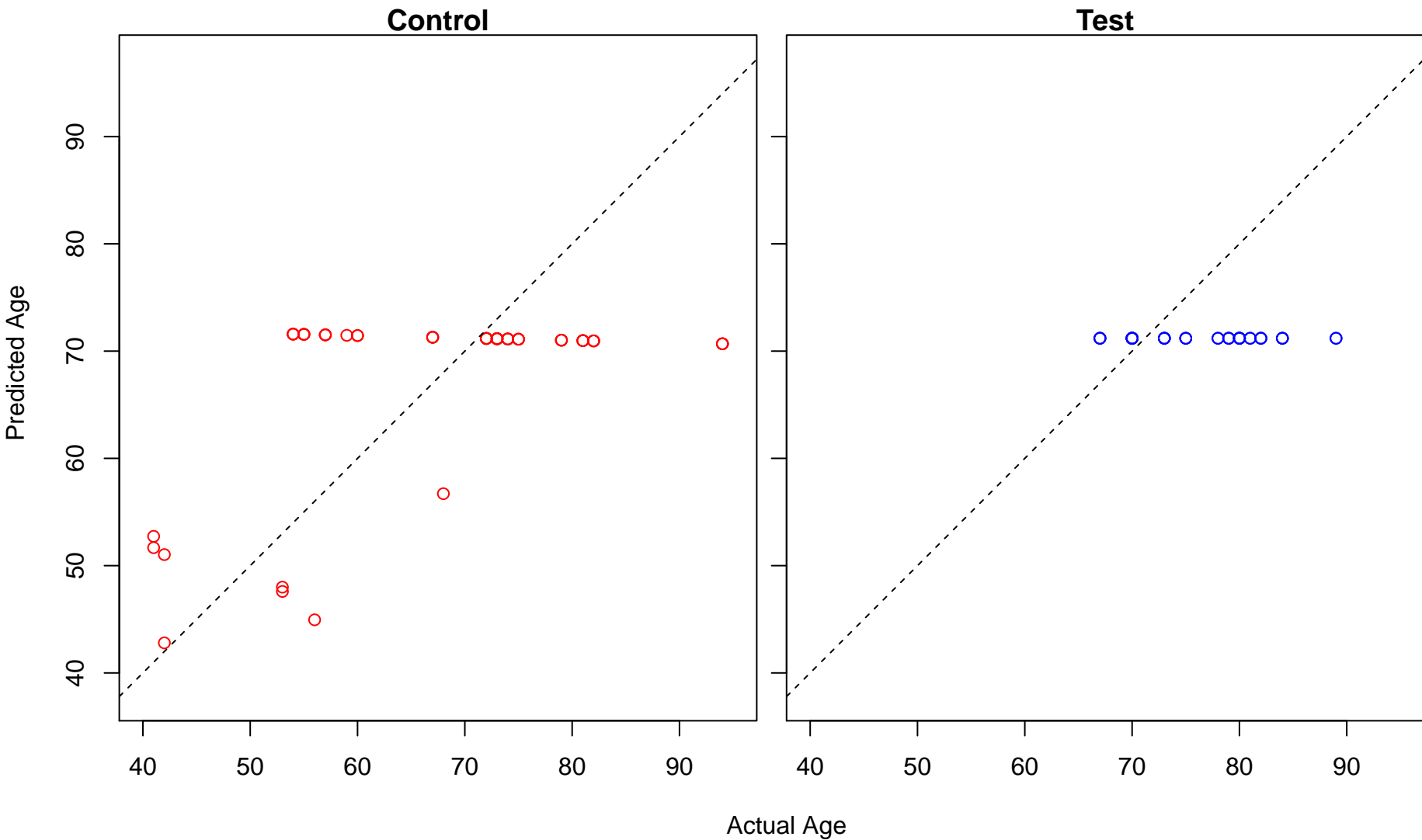
ve regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (S



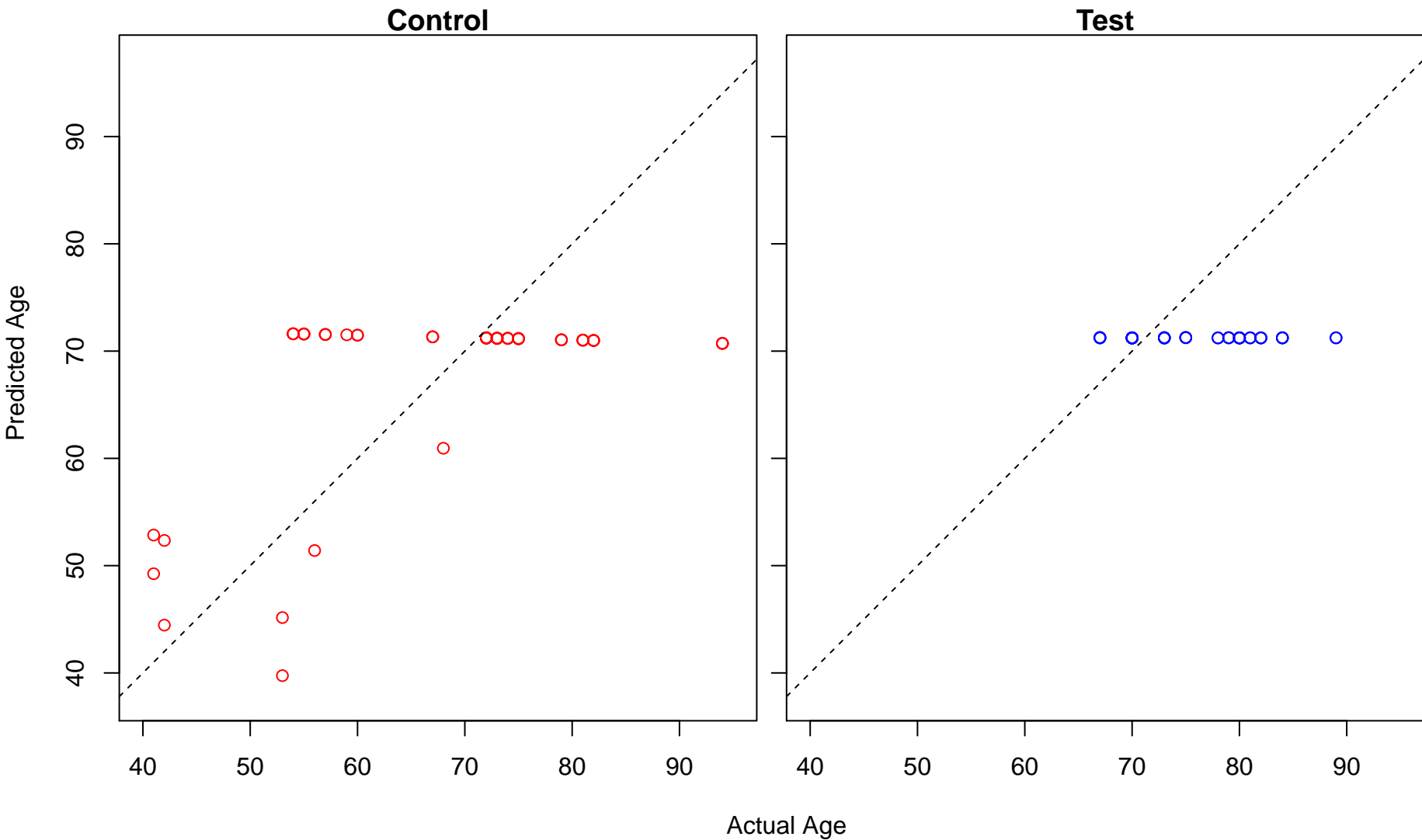
The regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (S



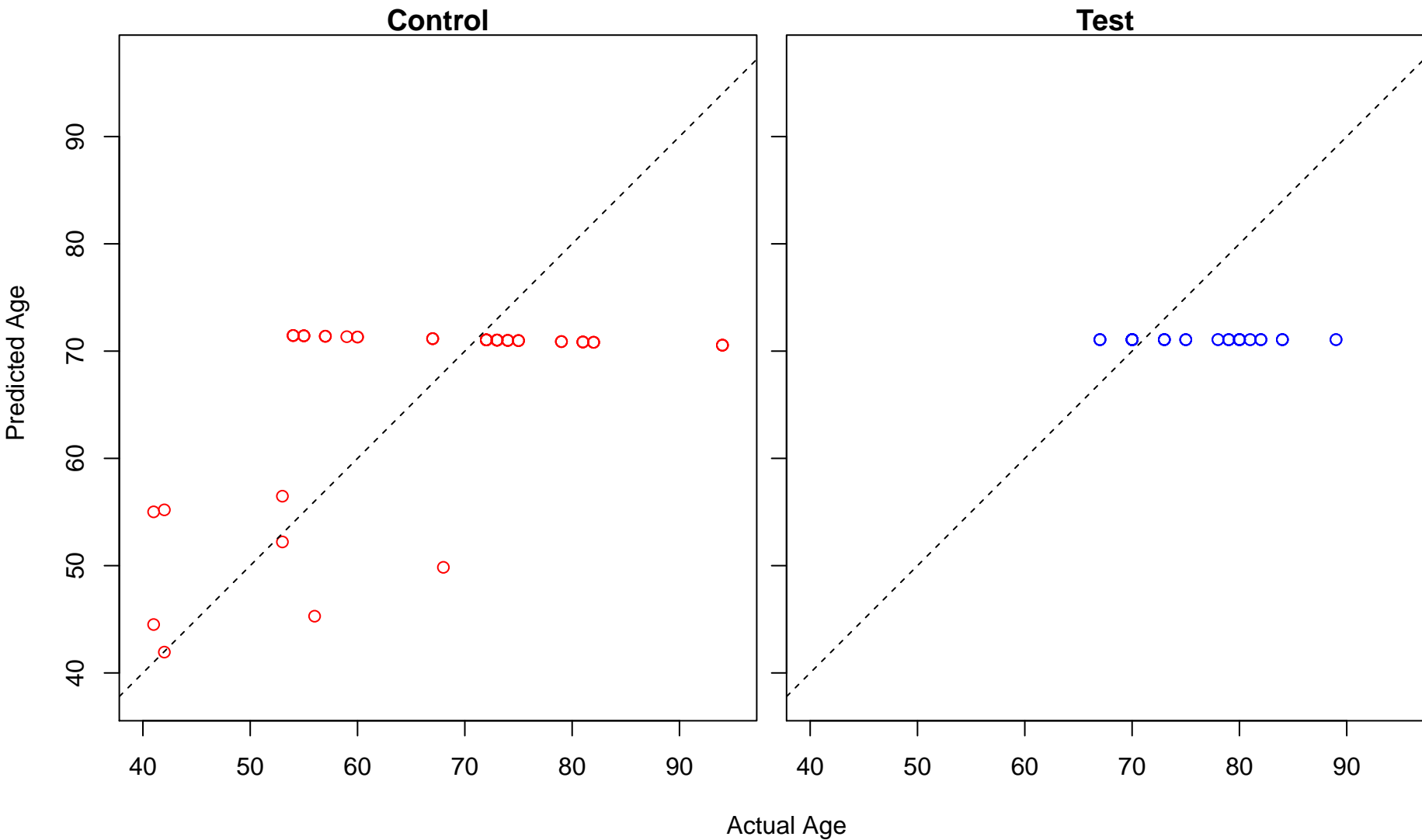
positive regulation of protein localization to membrane (Score: 0.810208)



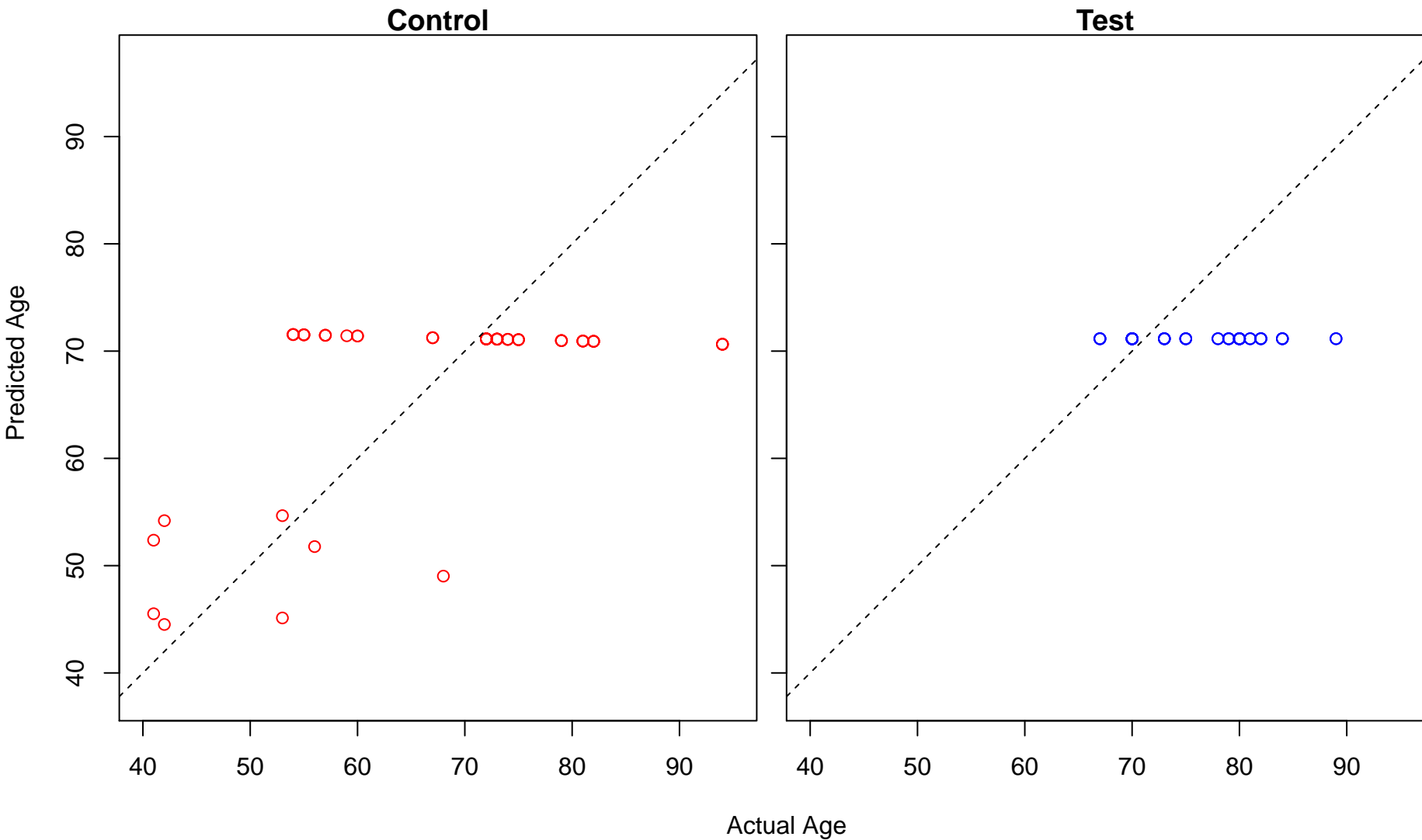
ADP metabolic process (Score: 0.810190)



negative regulation of mitochondrion organization (Score: 0.810185)

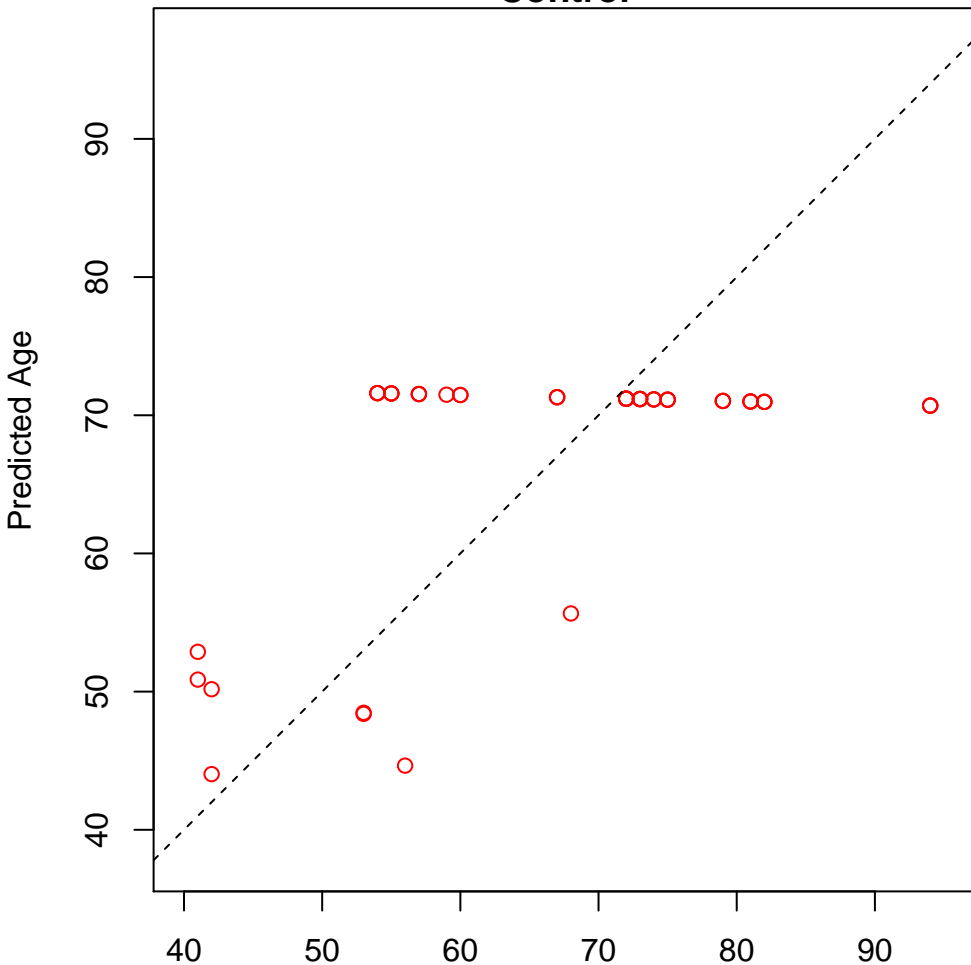


cofactor biosynthetic process (Score: 0.810169)

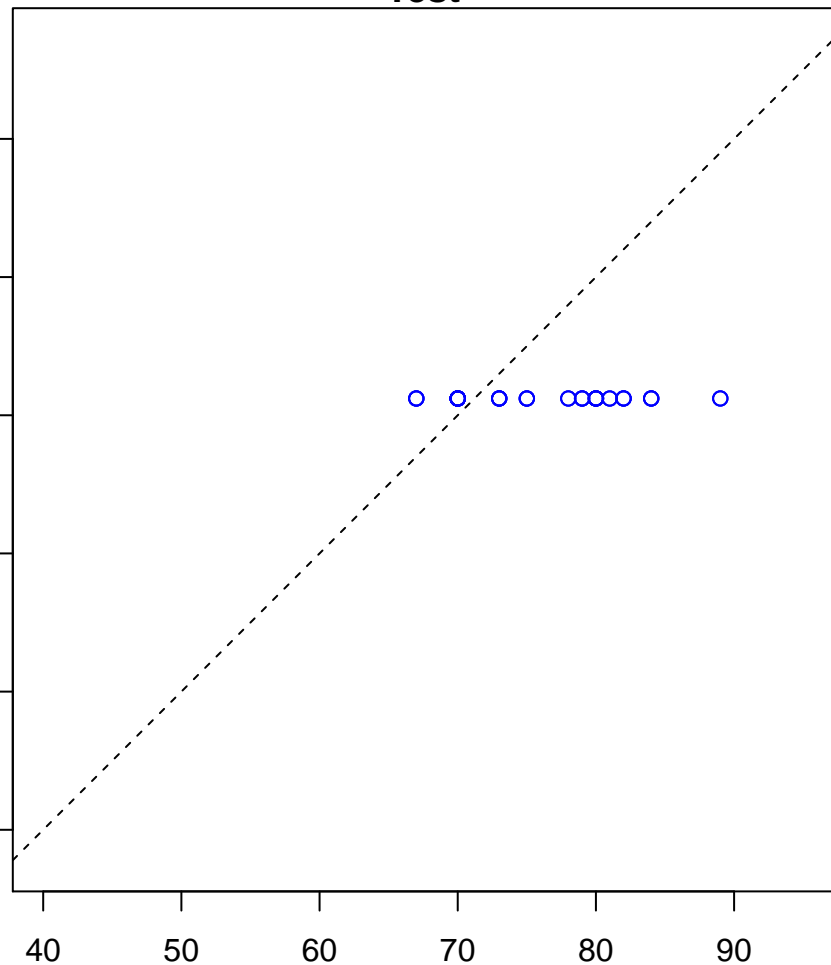


mitochondrial membrane organization (Score: 0.810119)

Control

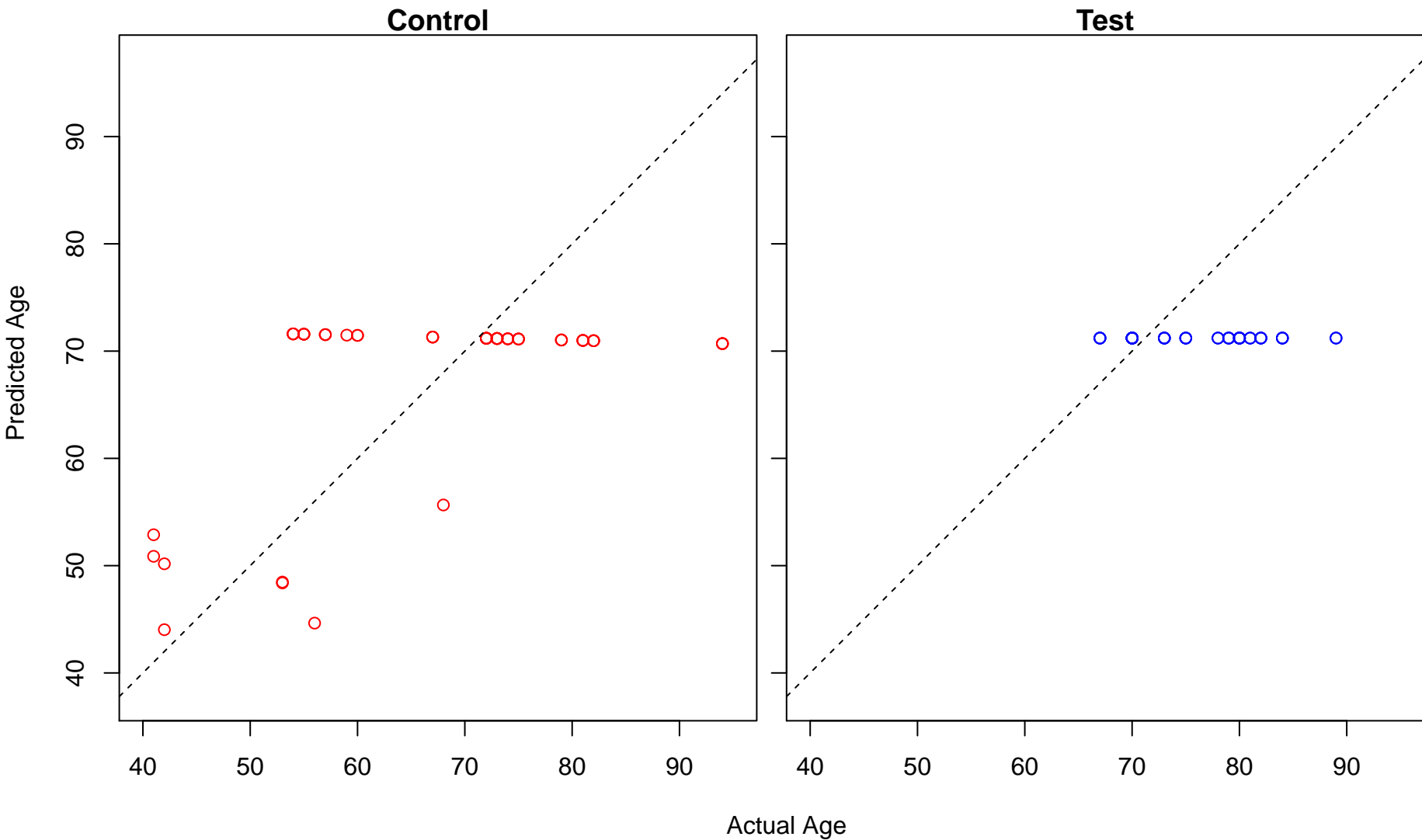


Test



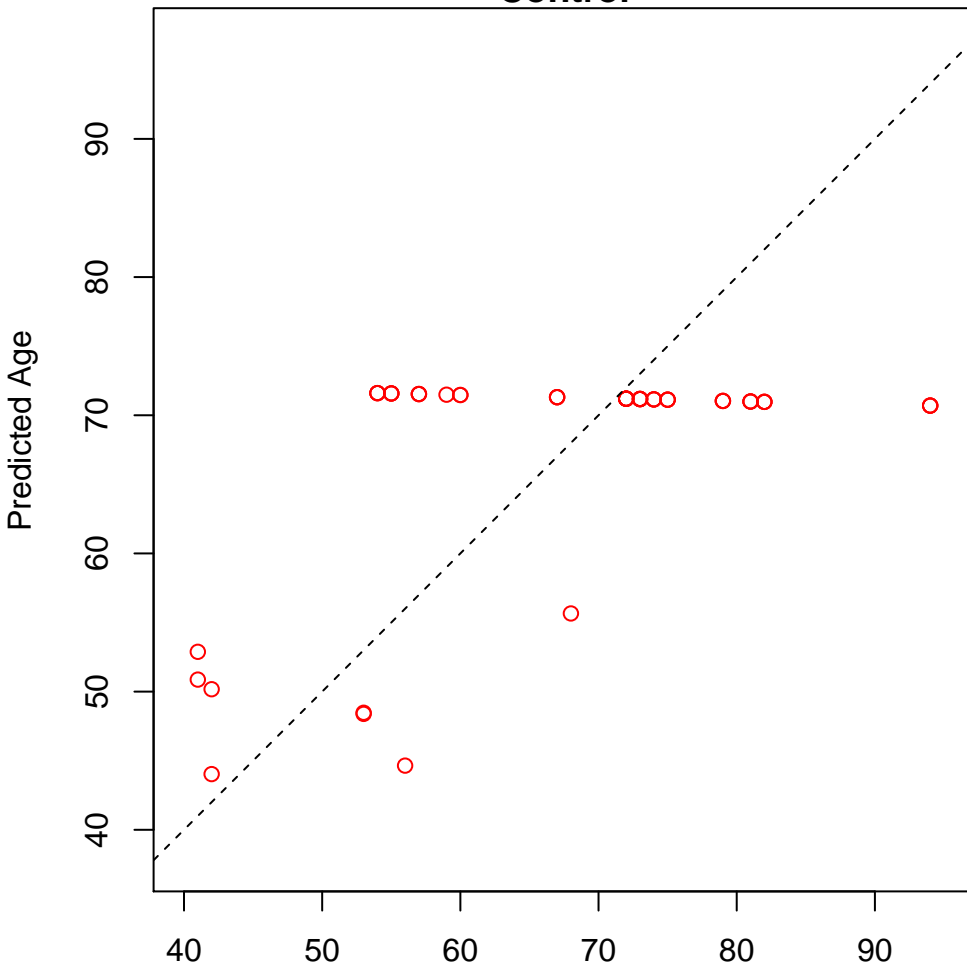
Actual Age

regulation of mitochondrial membrane permeability (Score: 0.810119)

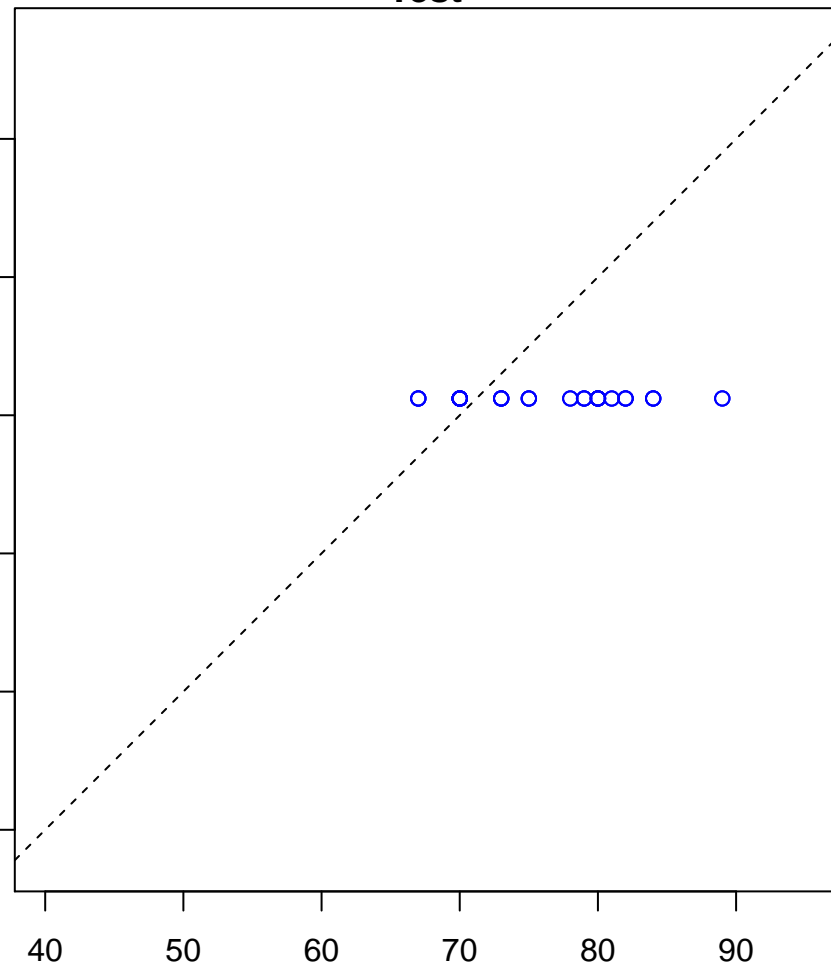


regulation of membrane permeability (Score: 0.810119)

Control

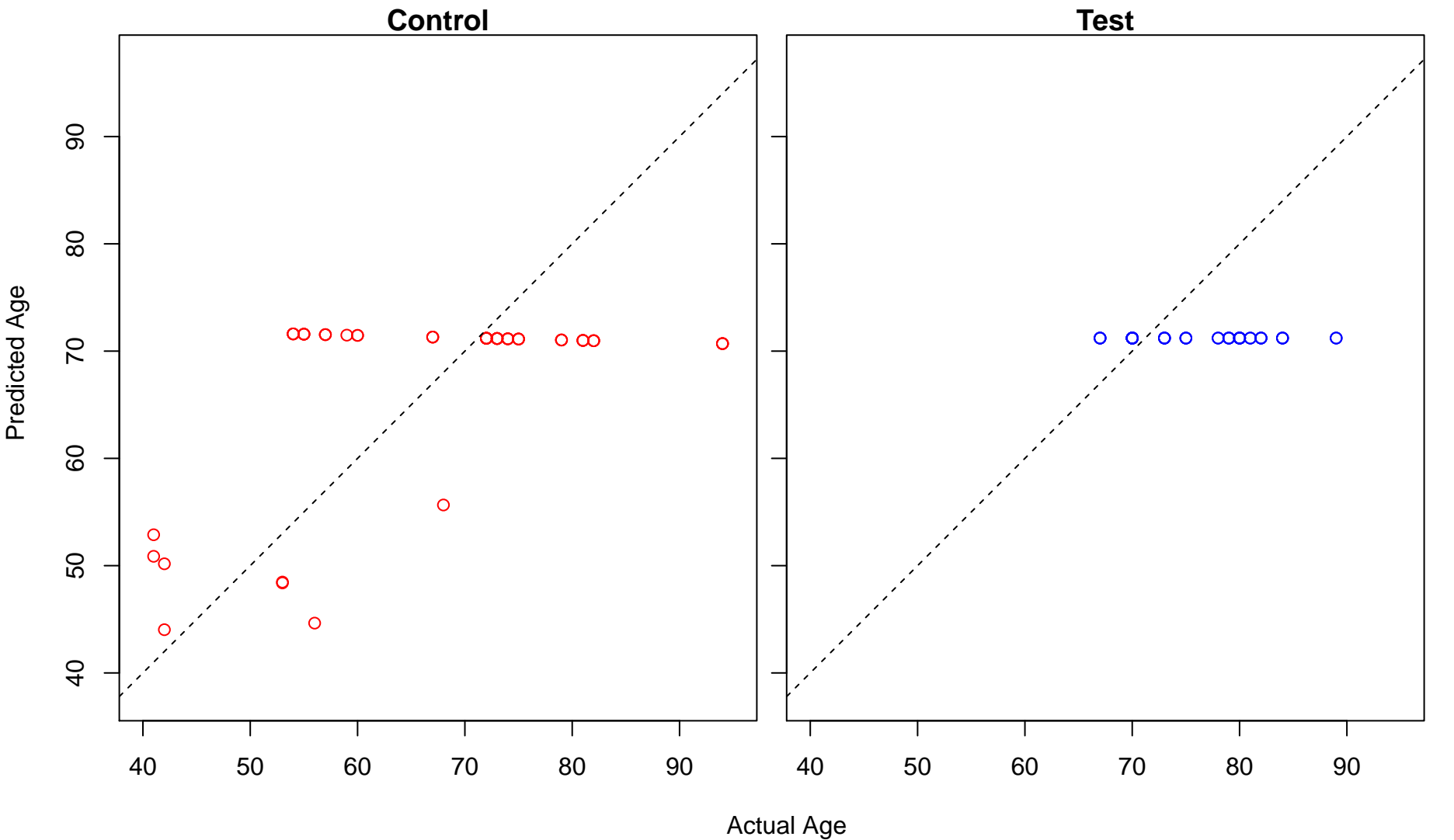


Test

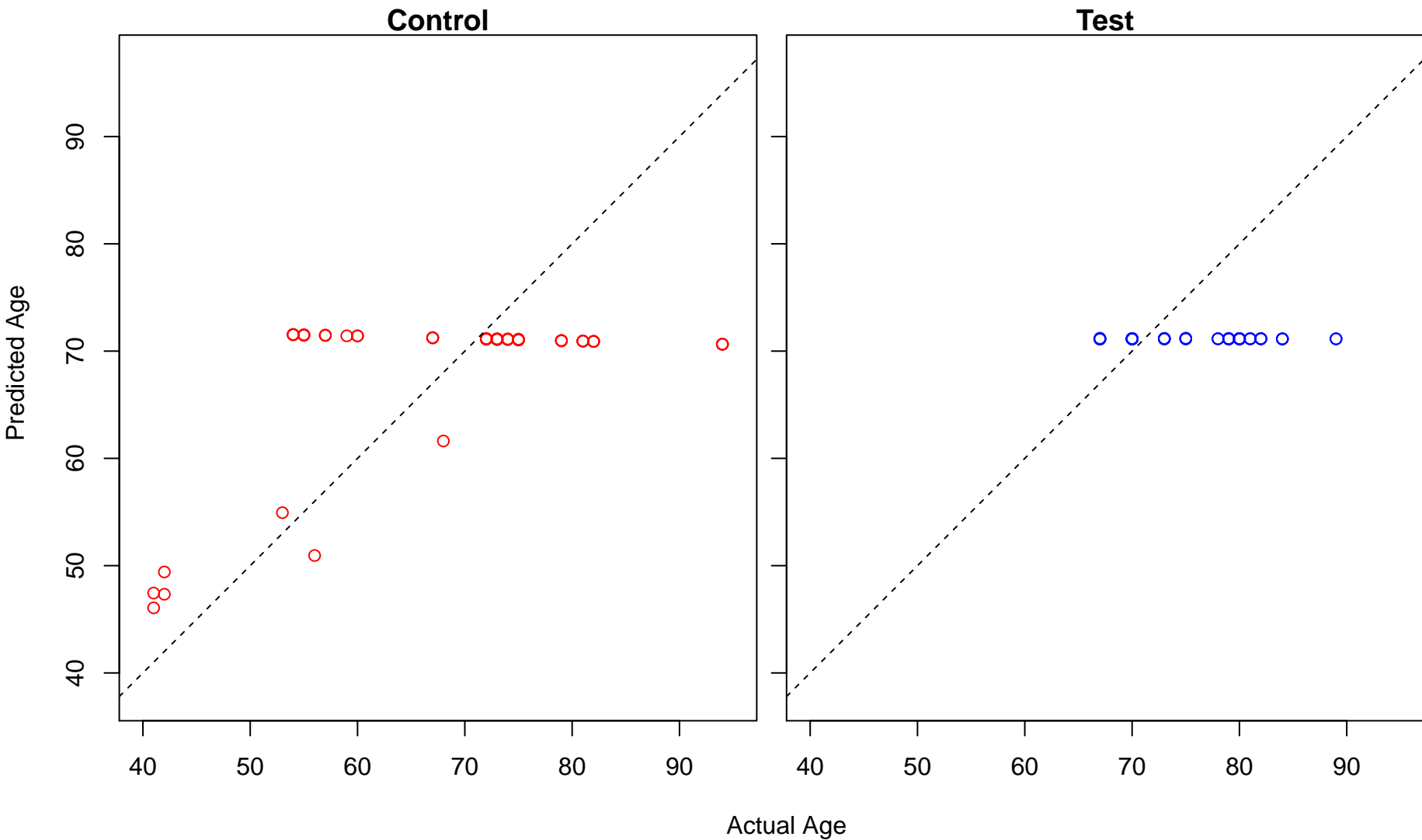


Actual Age

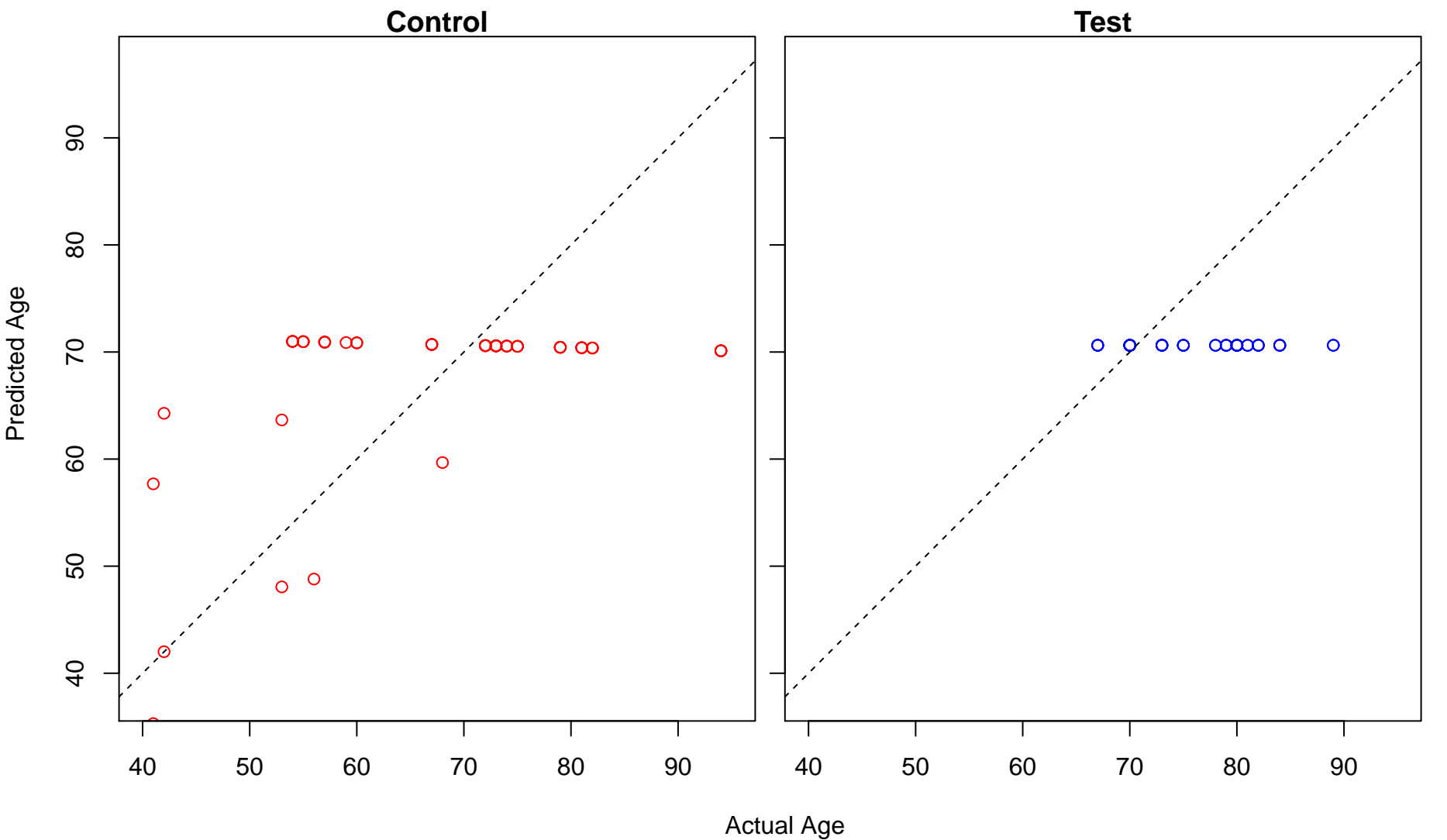
Regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (Score



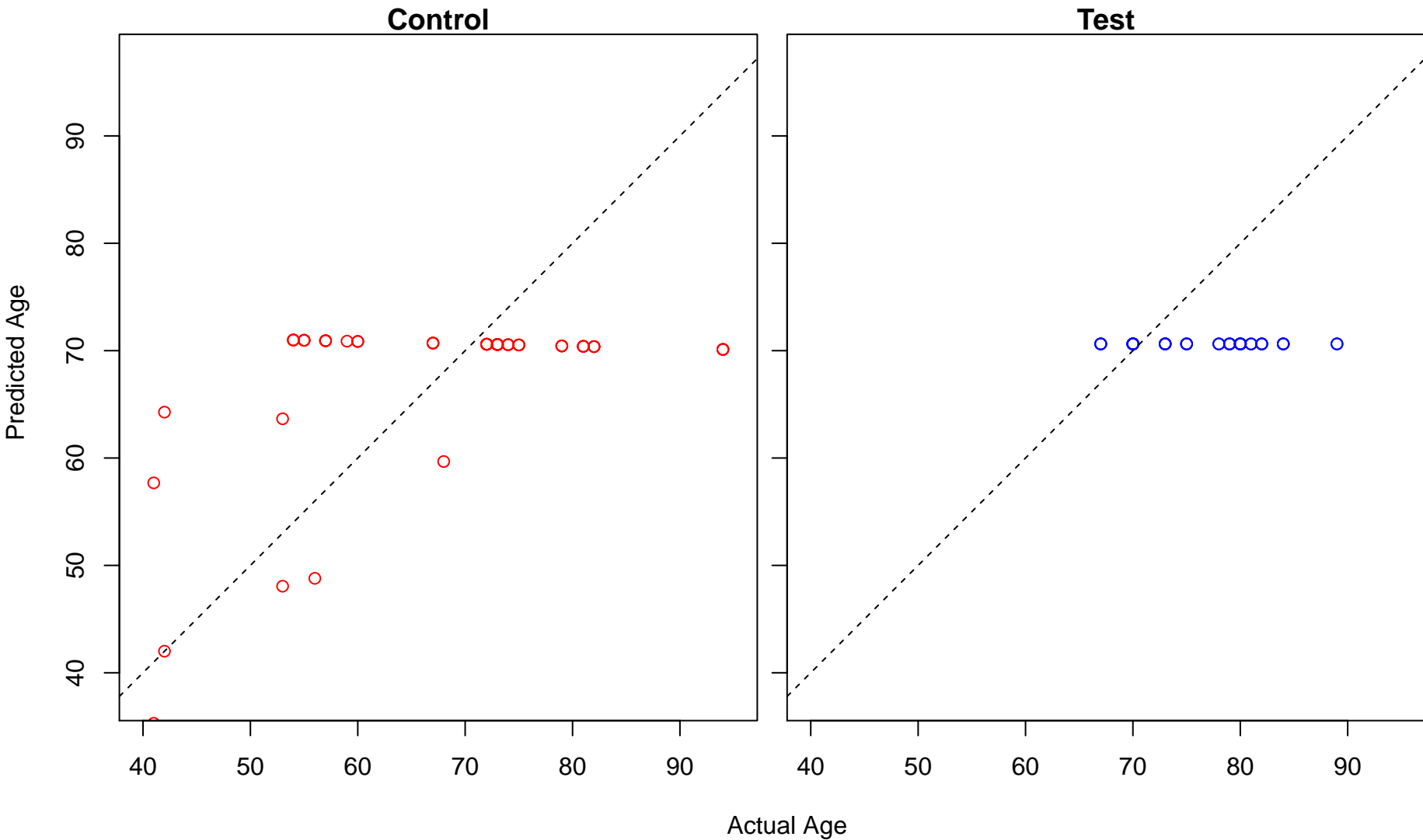
positive regulation of nucleocytoplasmic transport (Score: 0.810064)



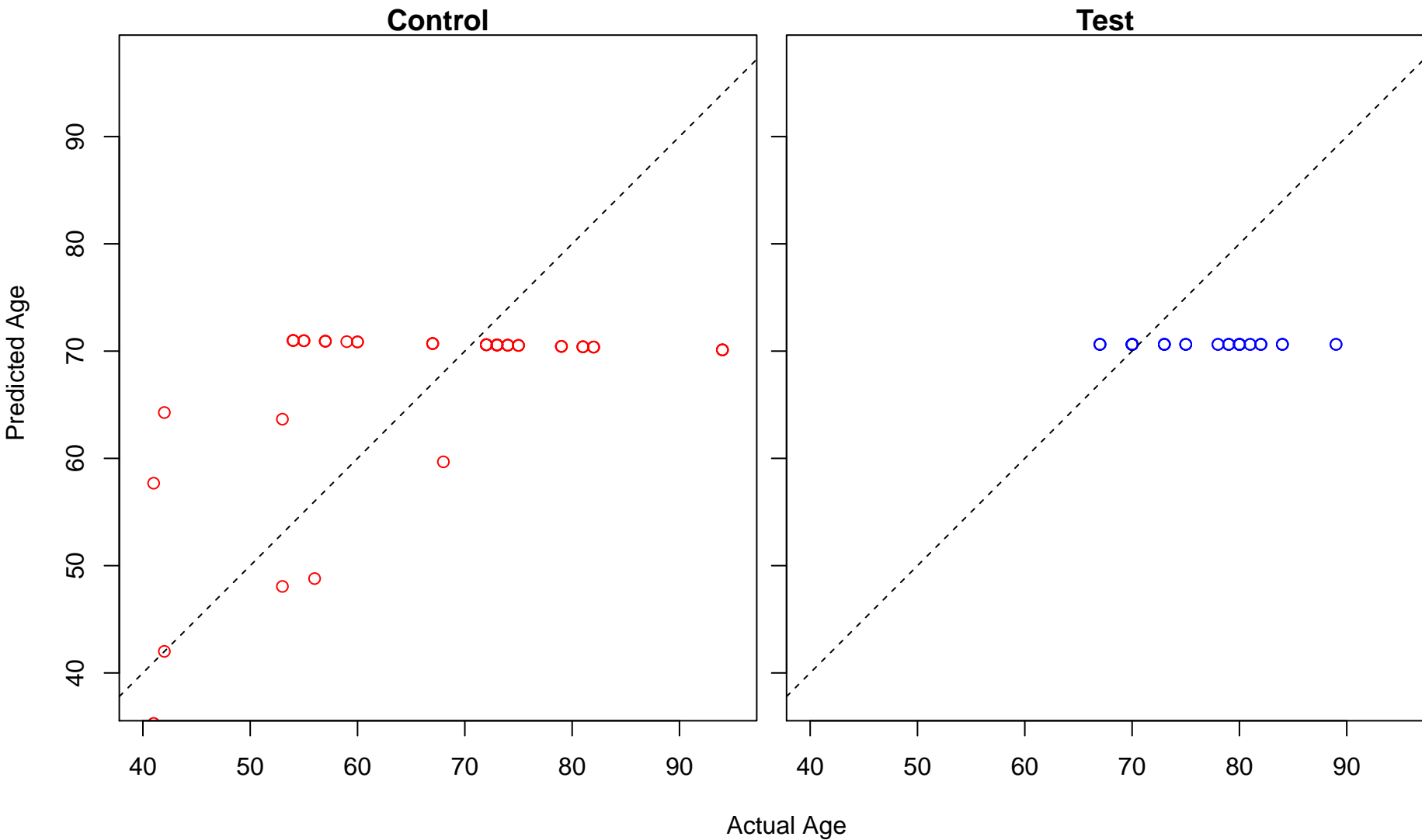
G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (Score: 0.0)



adenylate cyclase–modulating G–protein coupled receptor signaling pathway (Score: 0.809943)

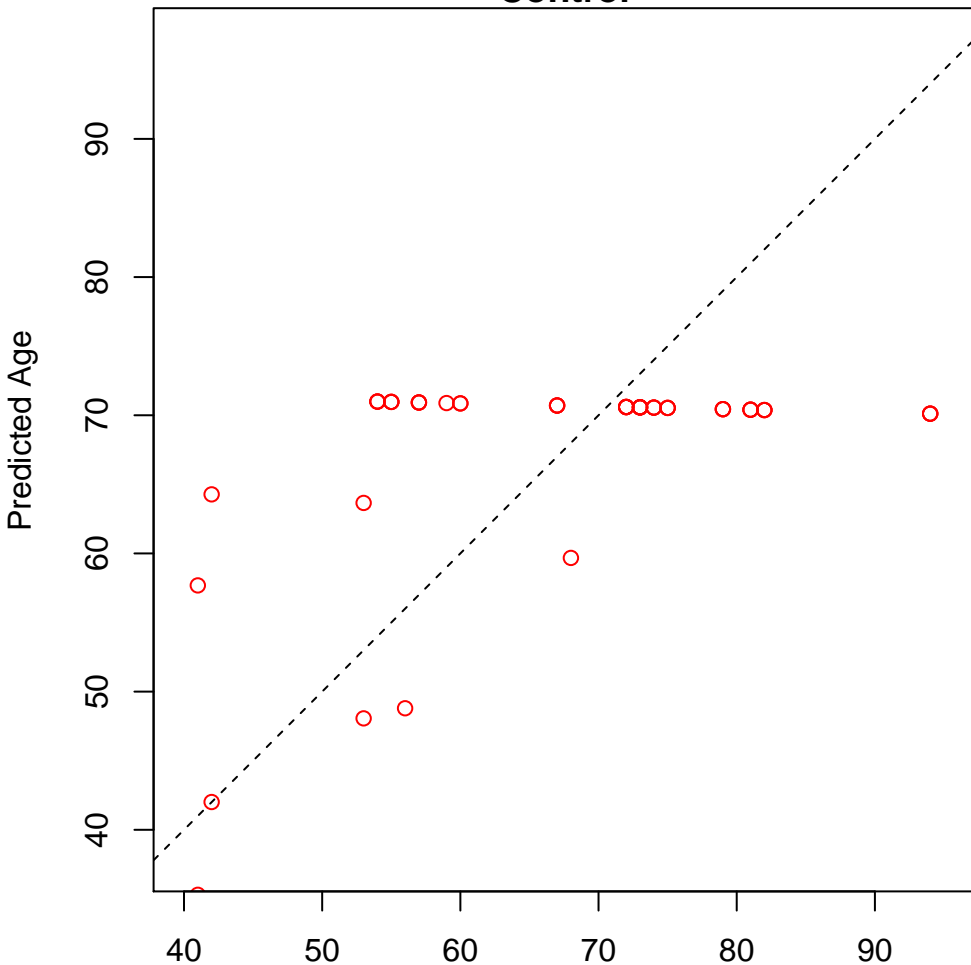


adenylate cyclase-activating G-protein coupled receptor signaling pathway (Score: 0.809943)

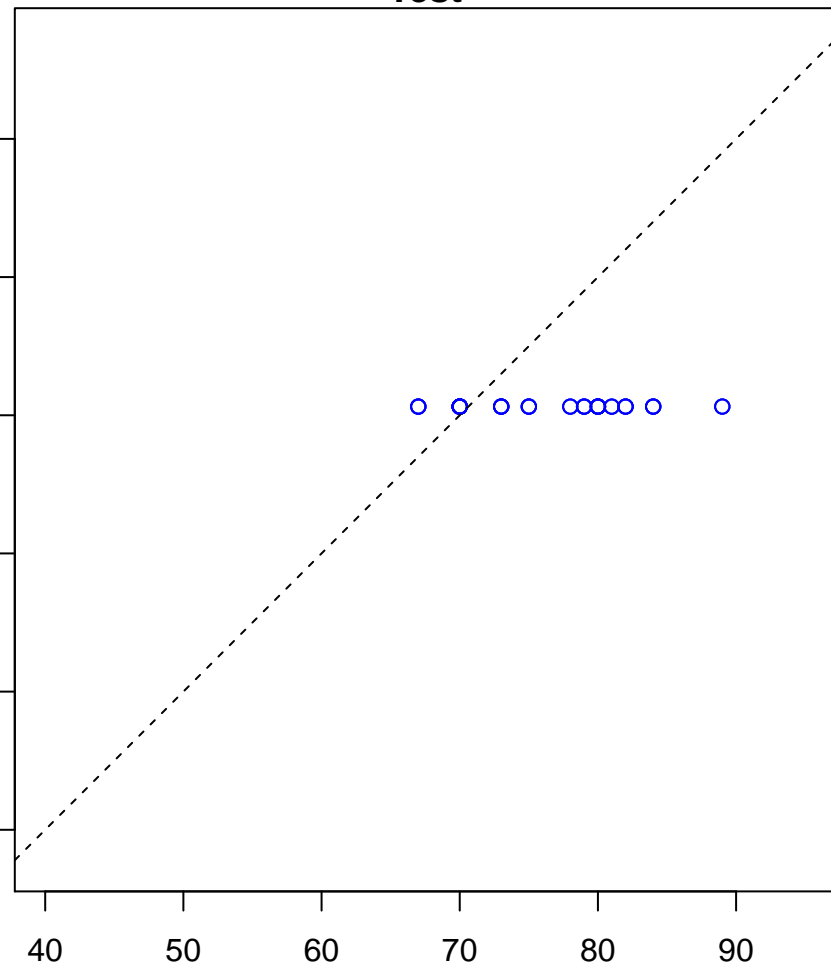


second-messenger-mediated signaling (Score: 0.809943)

Control

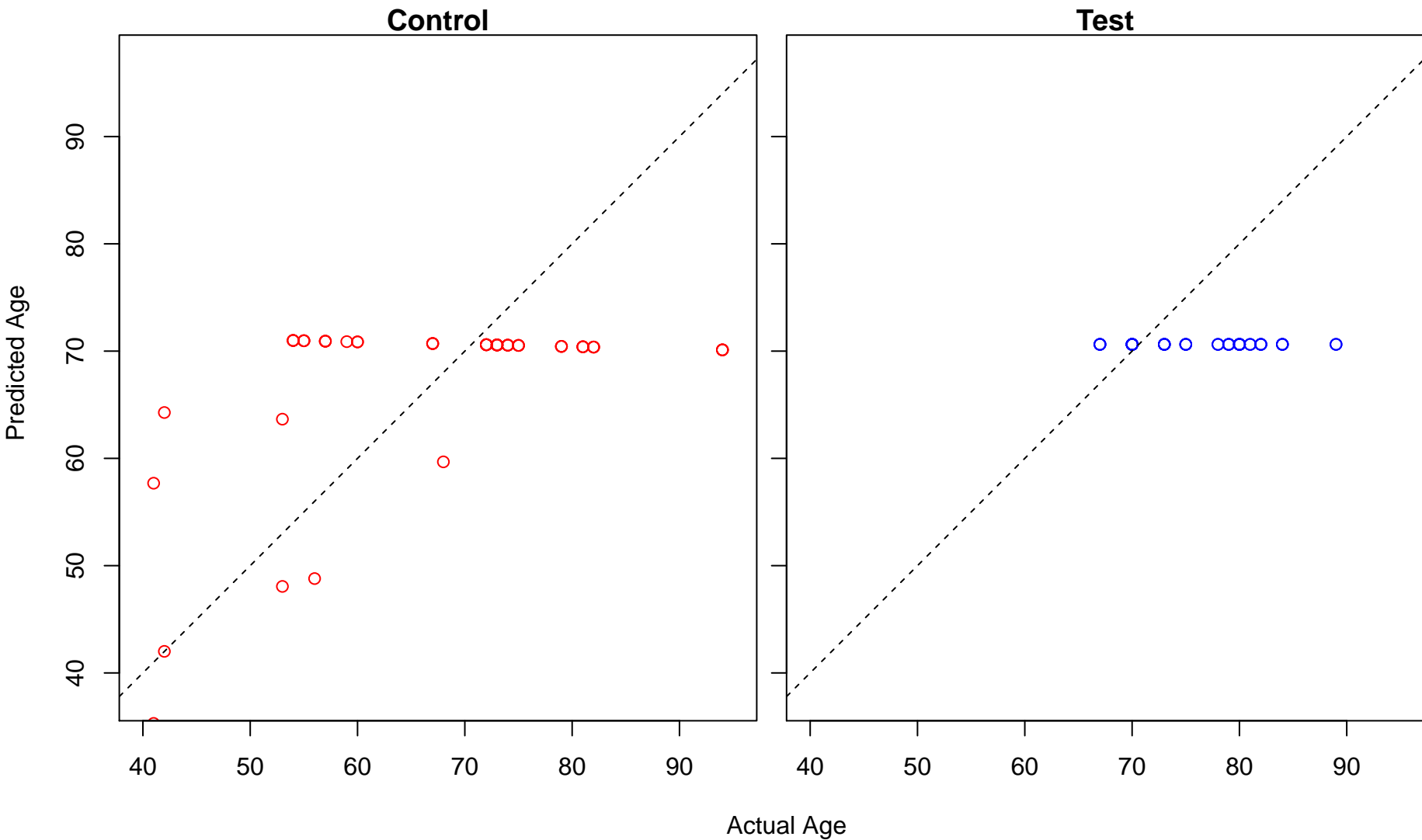


Test



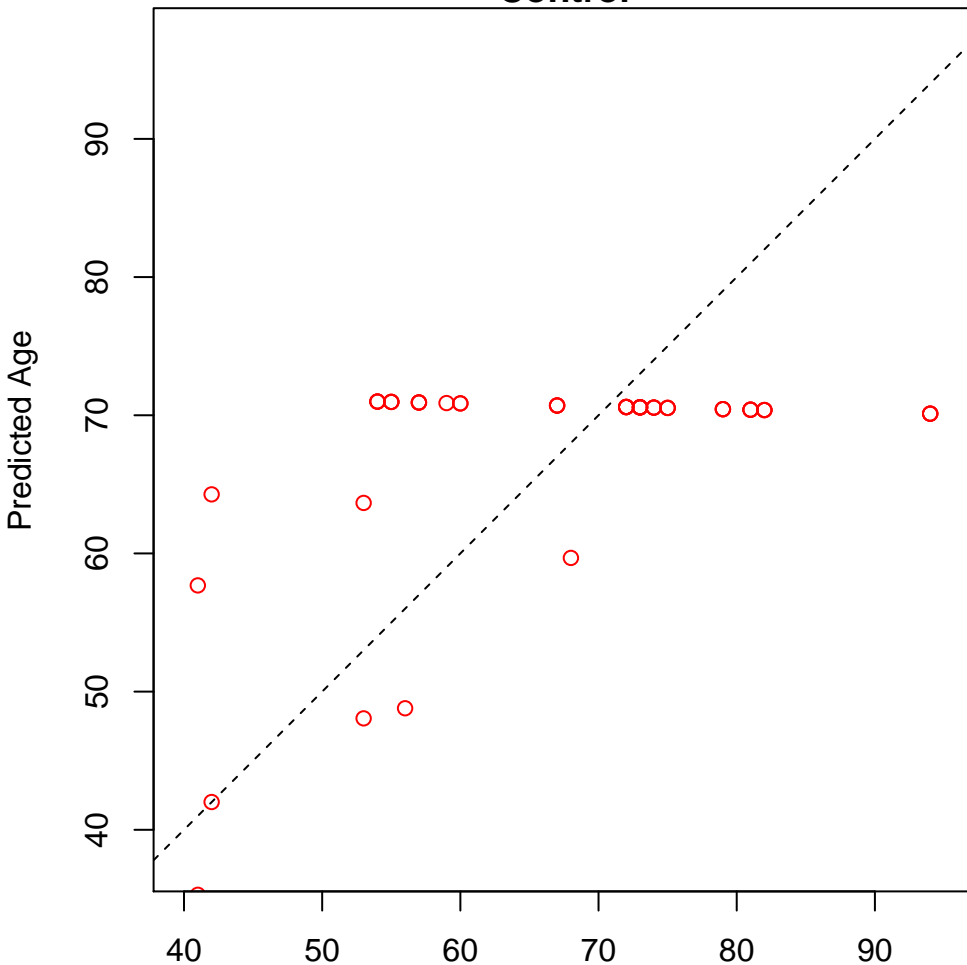
Actual Age

cAMP-mediated signaling (Score: 0.809943)

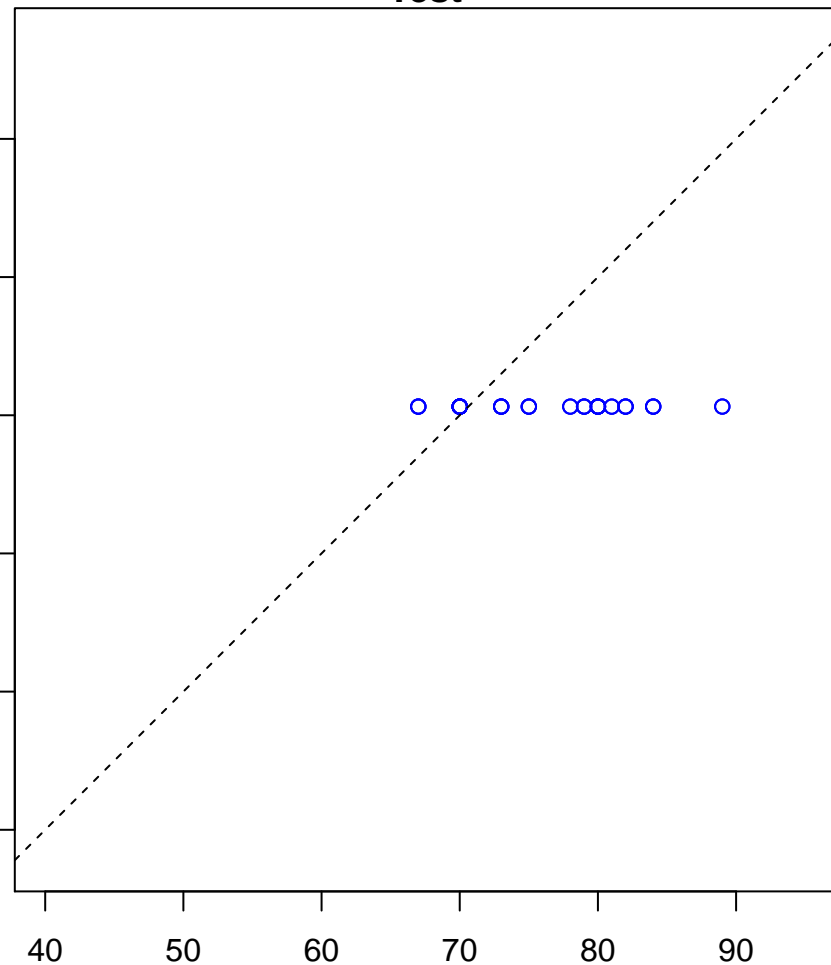


cyclic-nucleotide-mediated signaling (Score: 0.809943)

Control

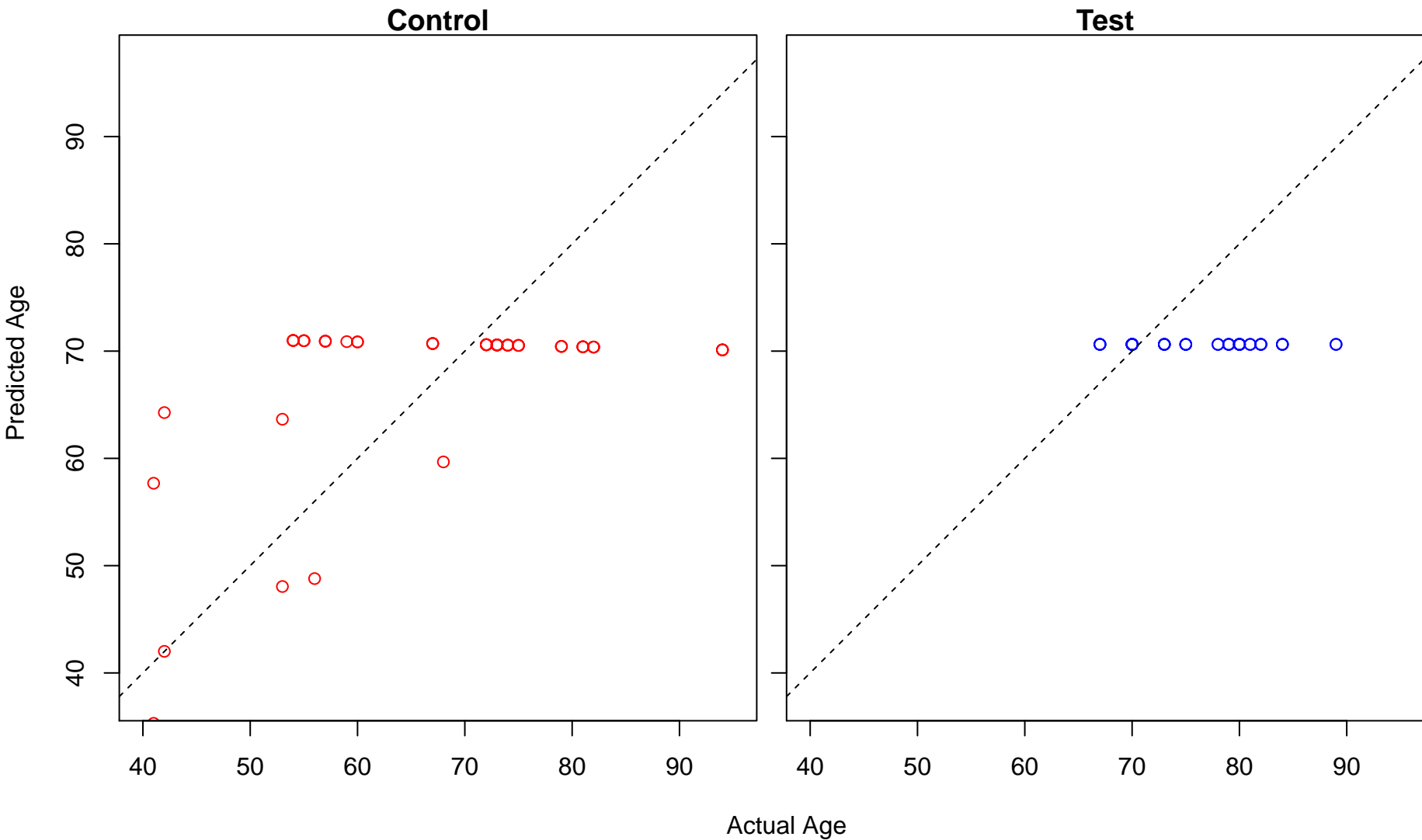


Test

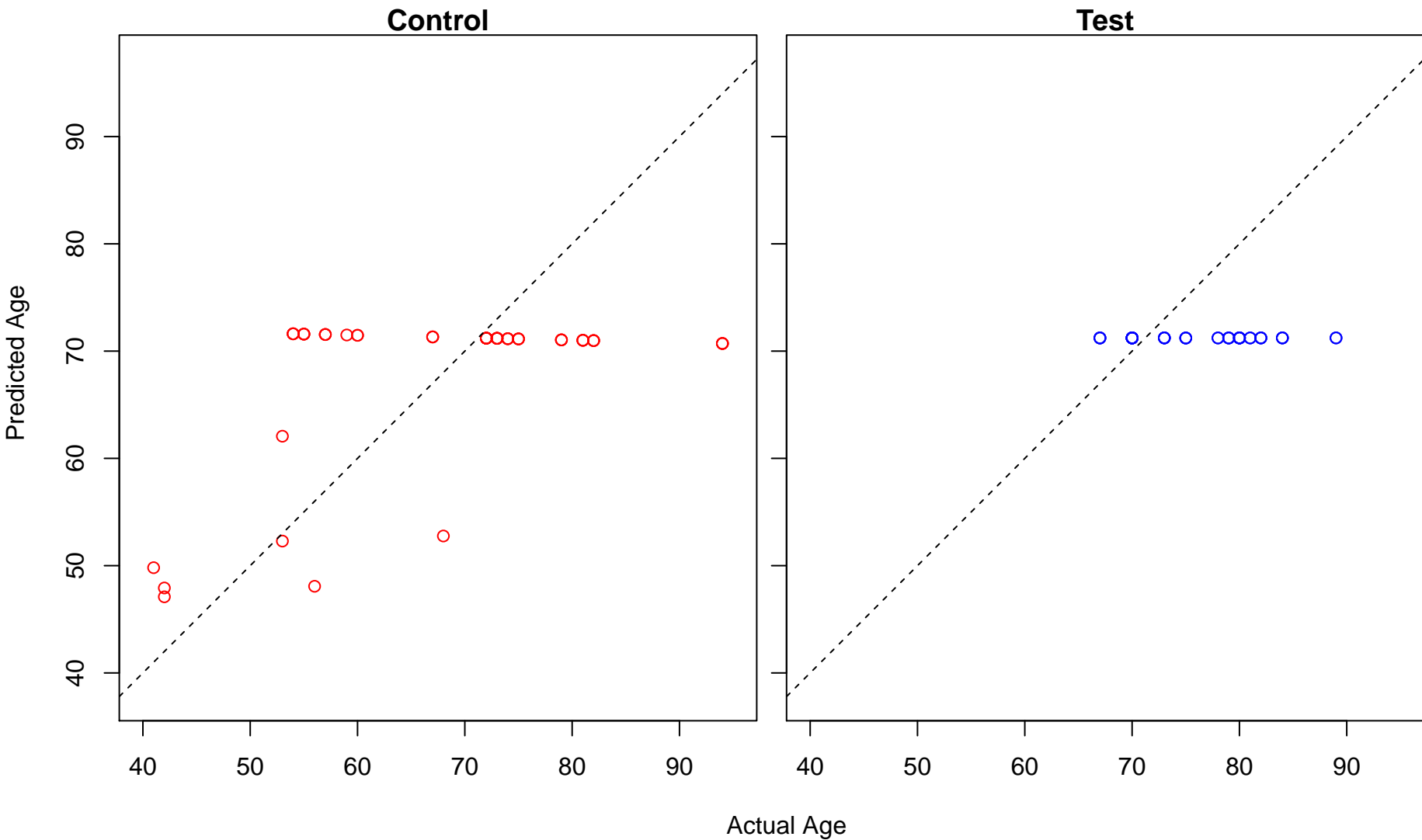


Actual Age

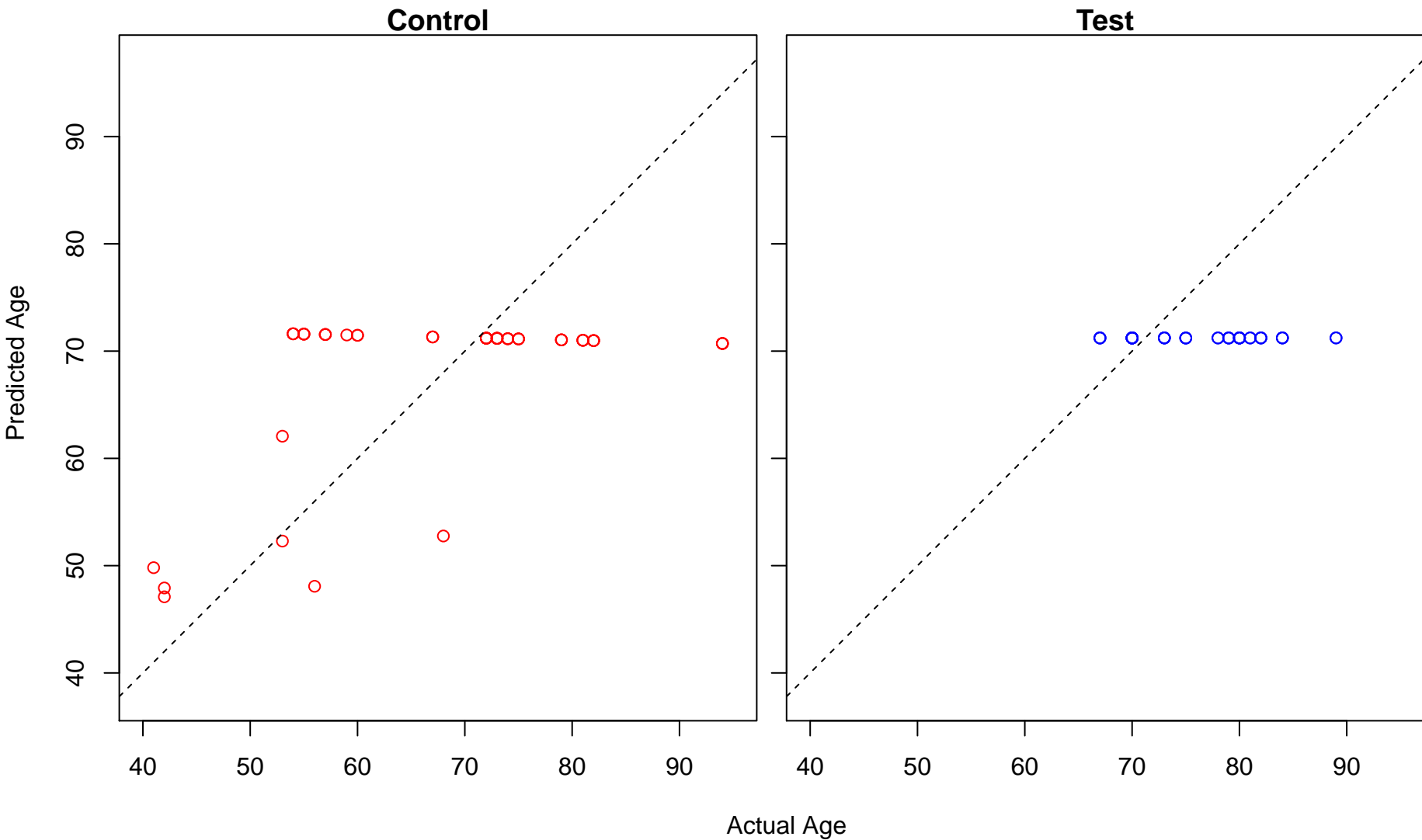
G-protein coupled receptor signaling pathway (Score: 0.809942)



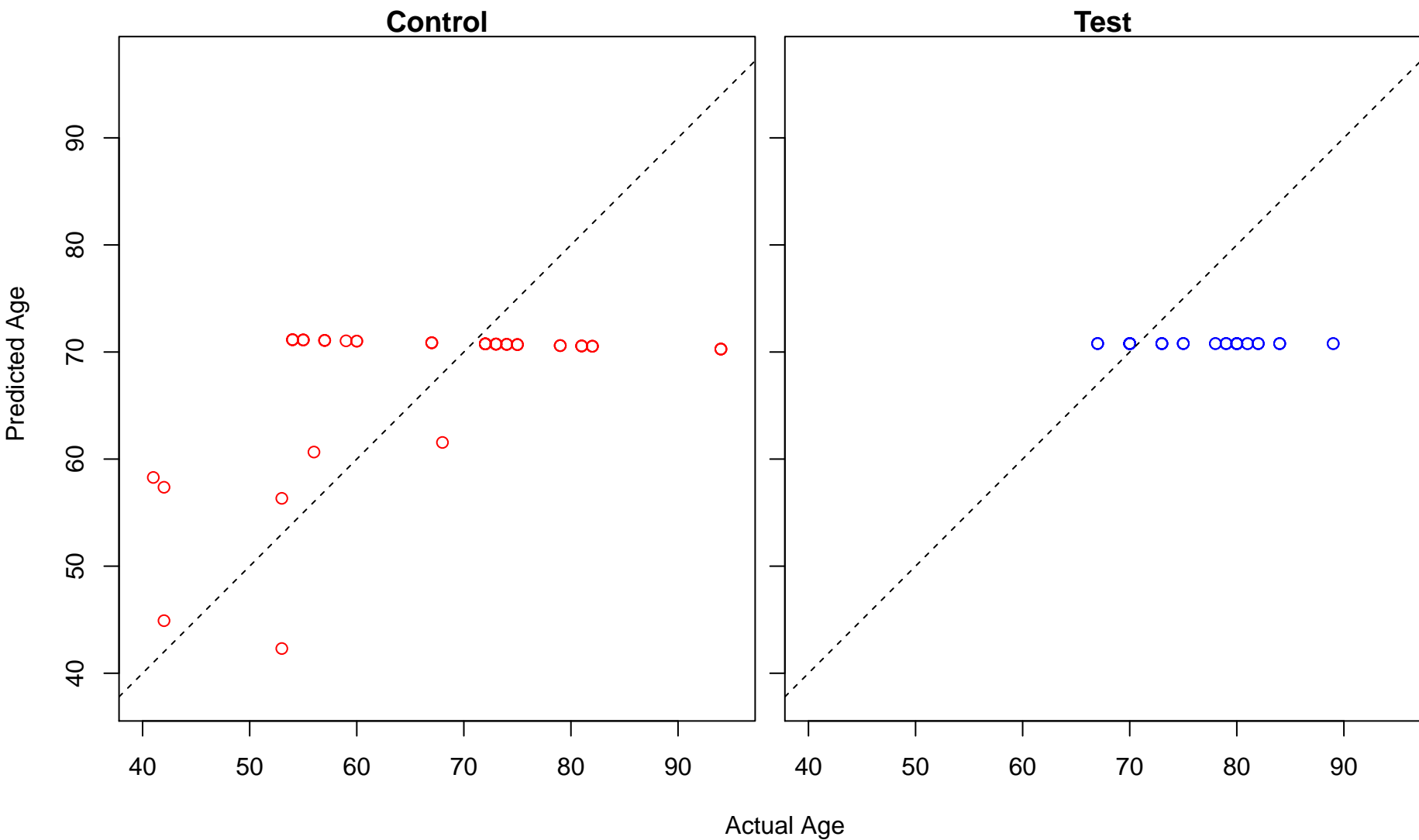
transport of virus (Score: 0.809928)



intracellular transport of virus (Score: 0.809928)

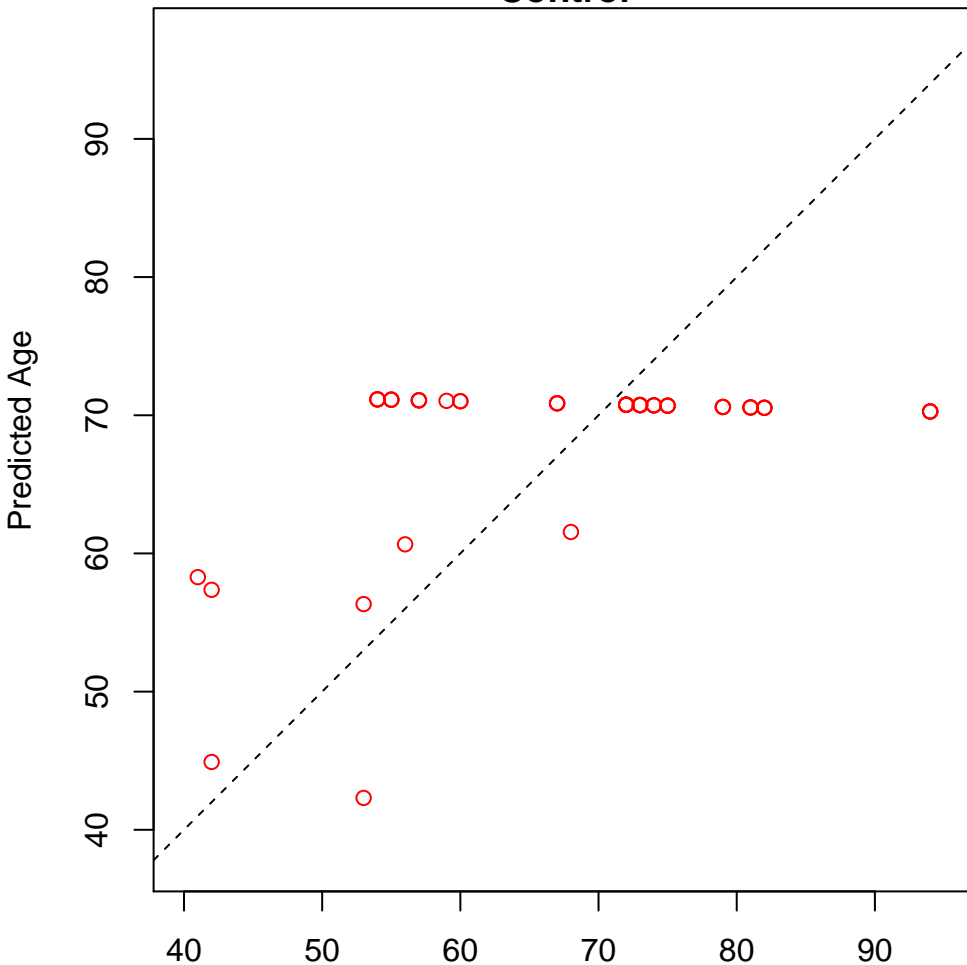


phosphatidylinositol biosynthetic process (Score: 0.809873)

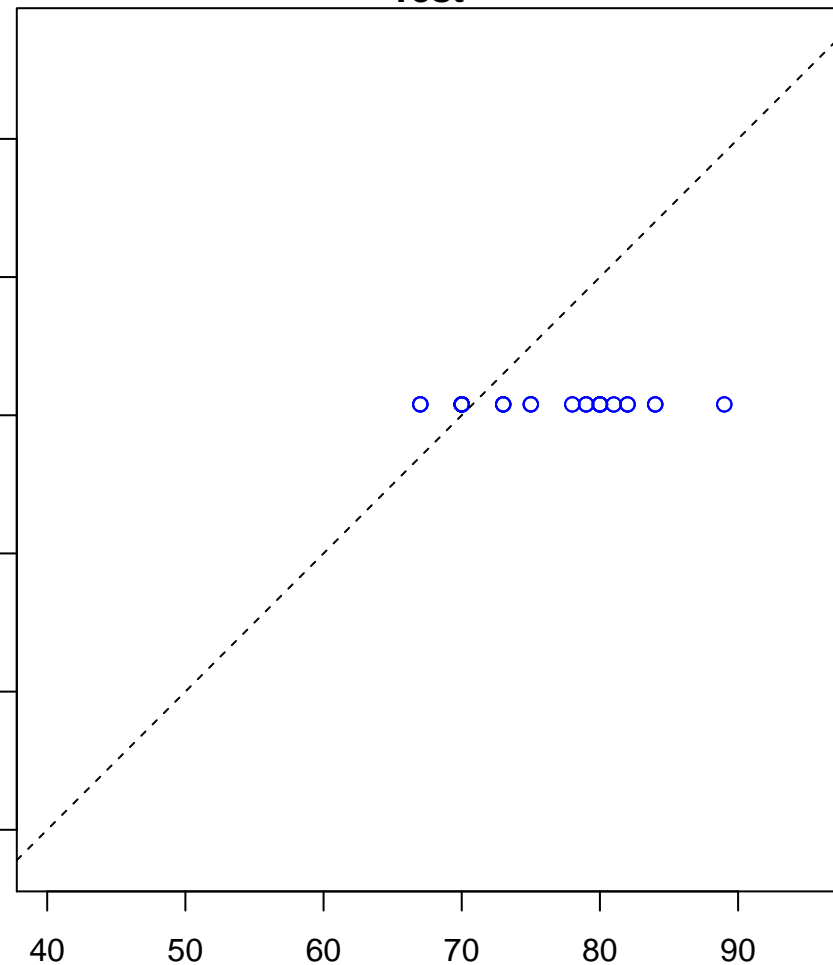


phosphatidylinositol metabolic process (Score: 0.809873)

Control



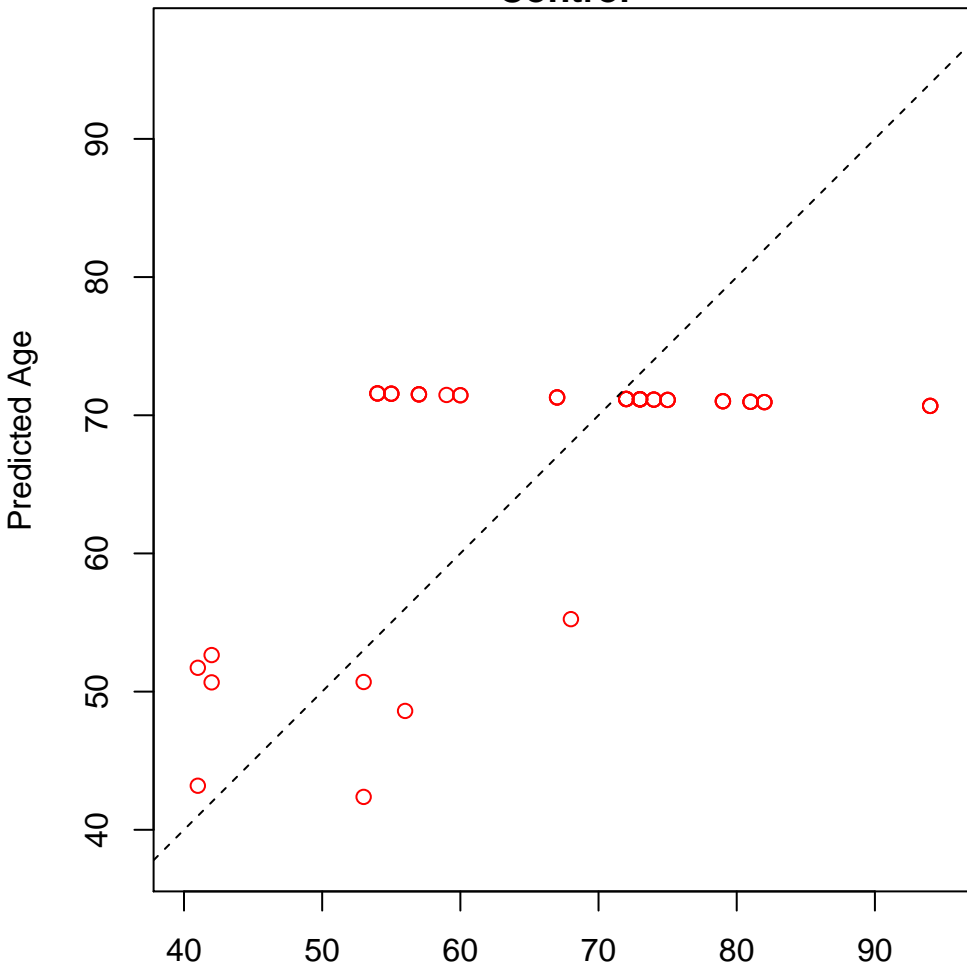
Test



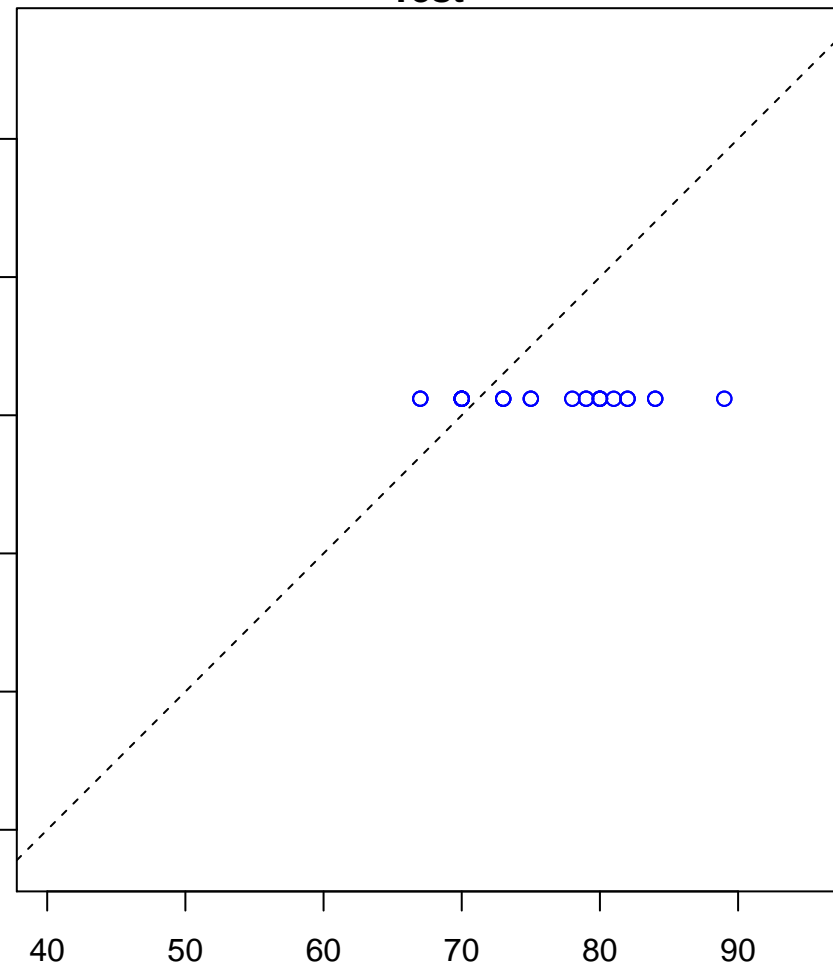
Actual Age

nucleoside metabolic process (Score: 0.809742)

Control



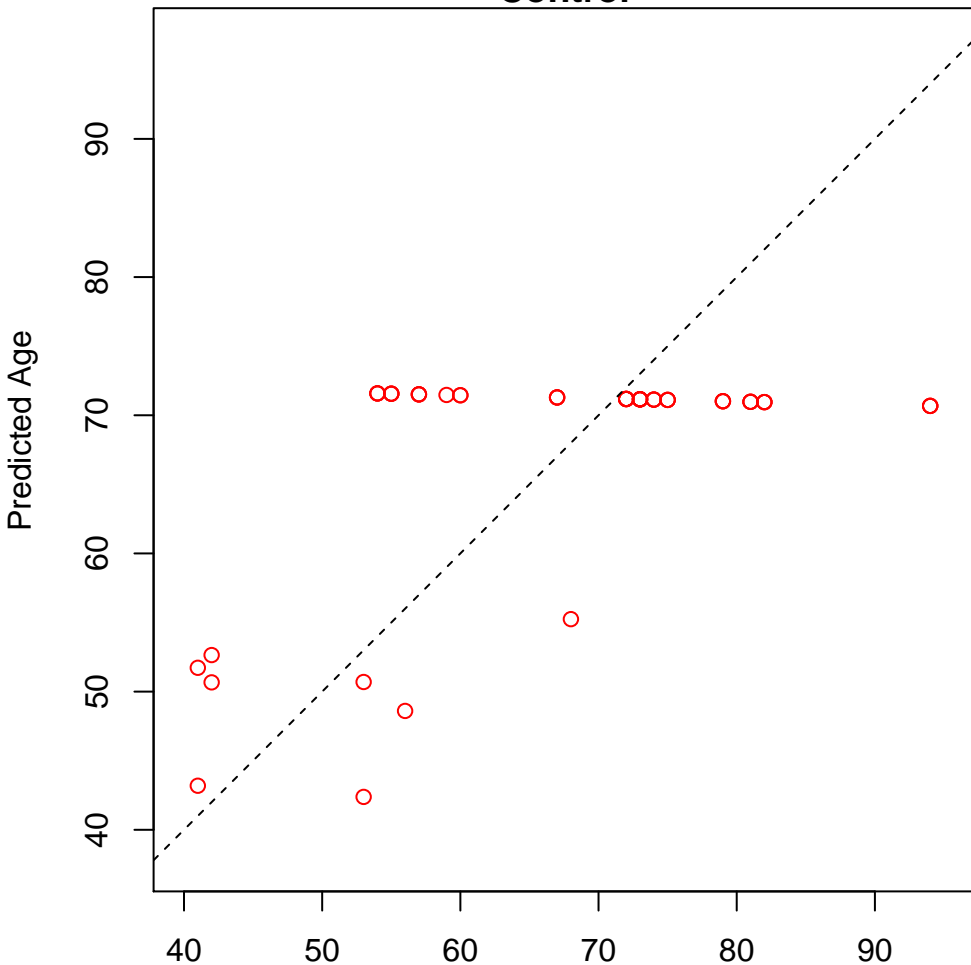
Test



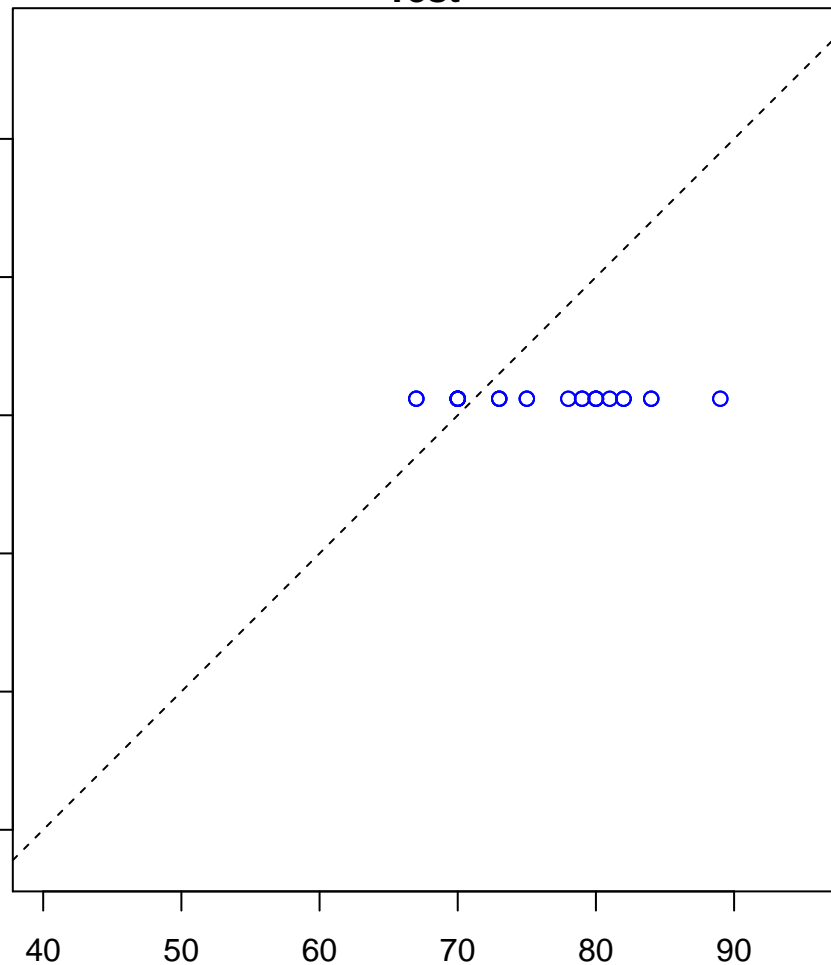
Actual Age

glycosyl compound metabolic process (Score: 0.809742)

Control

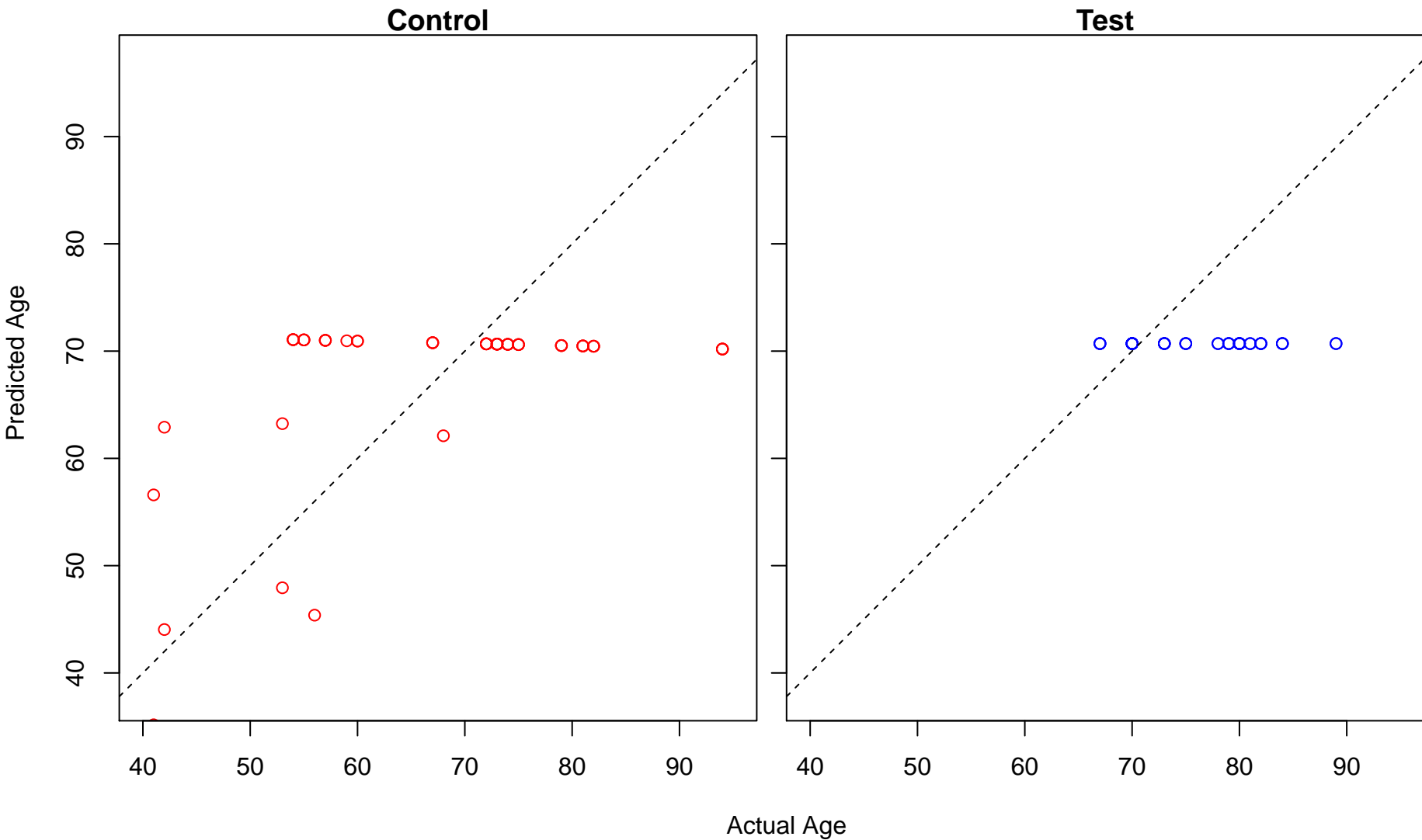


Test

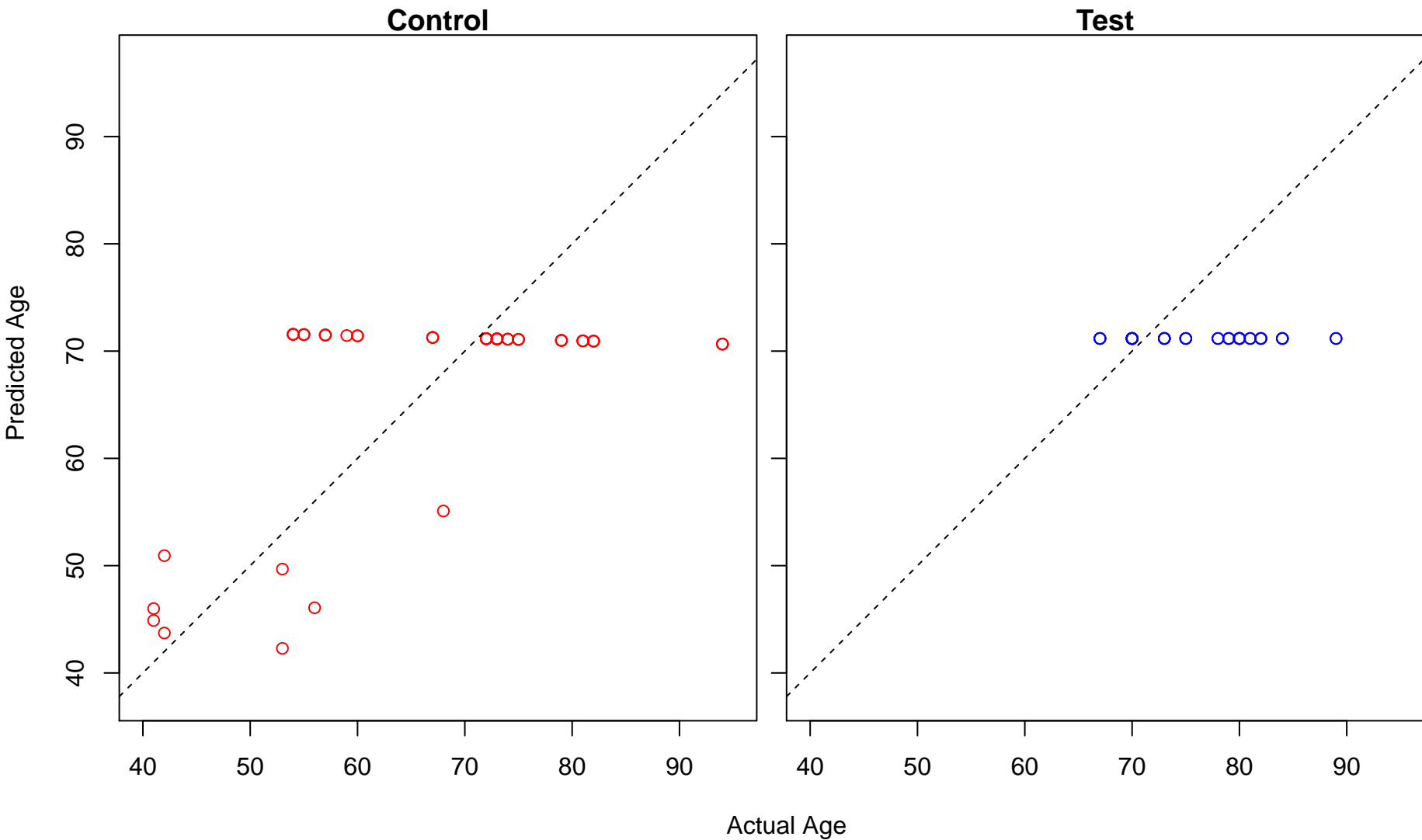


Actual Age

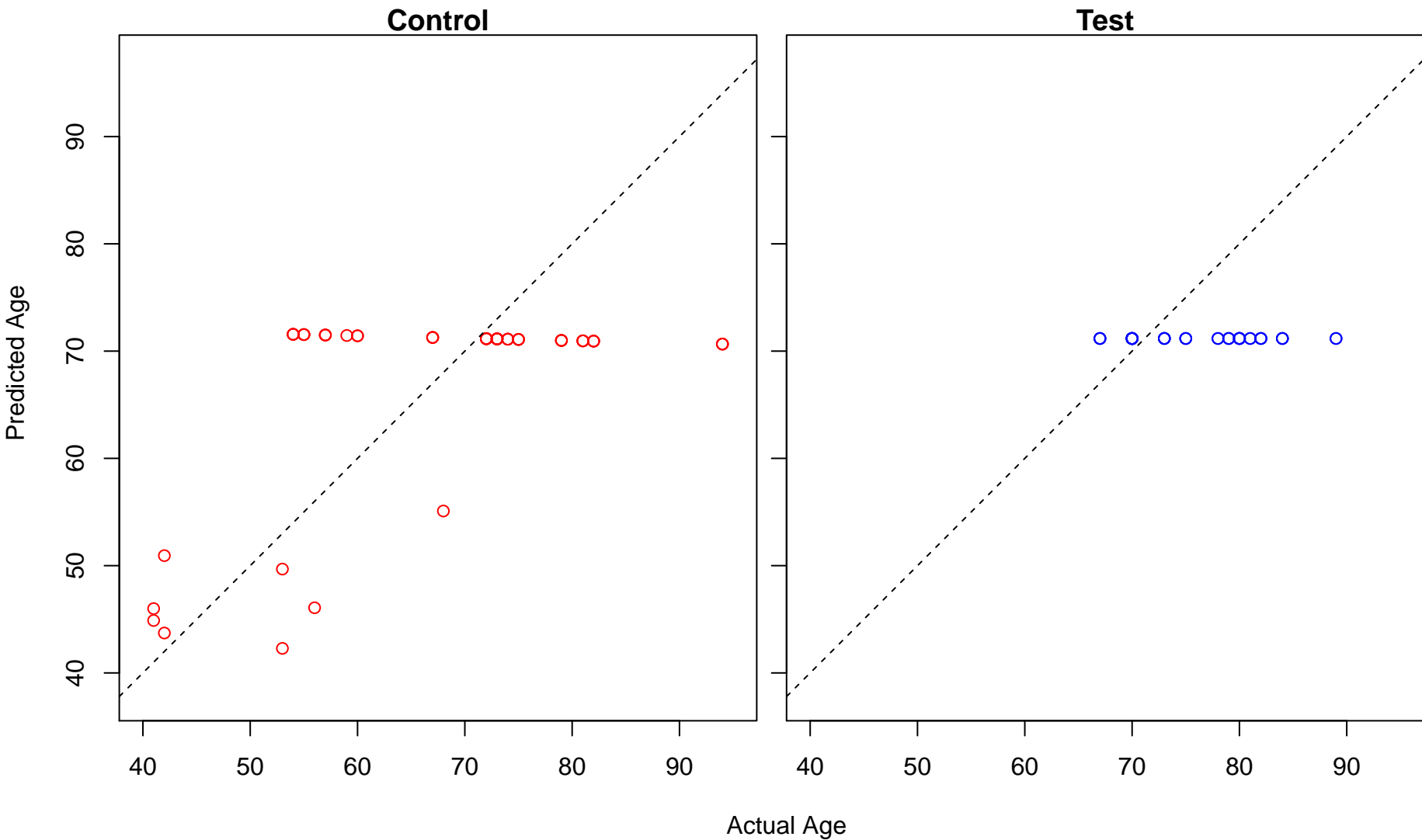
anatomical structure formation involved in morphogenesis (Score: 0.809696)



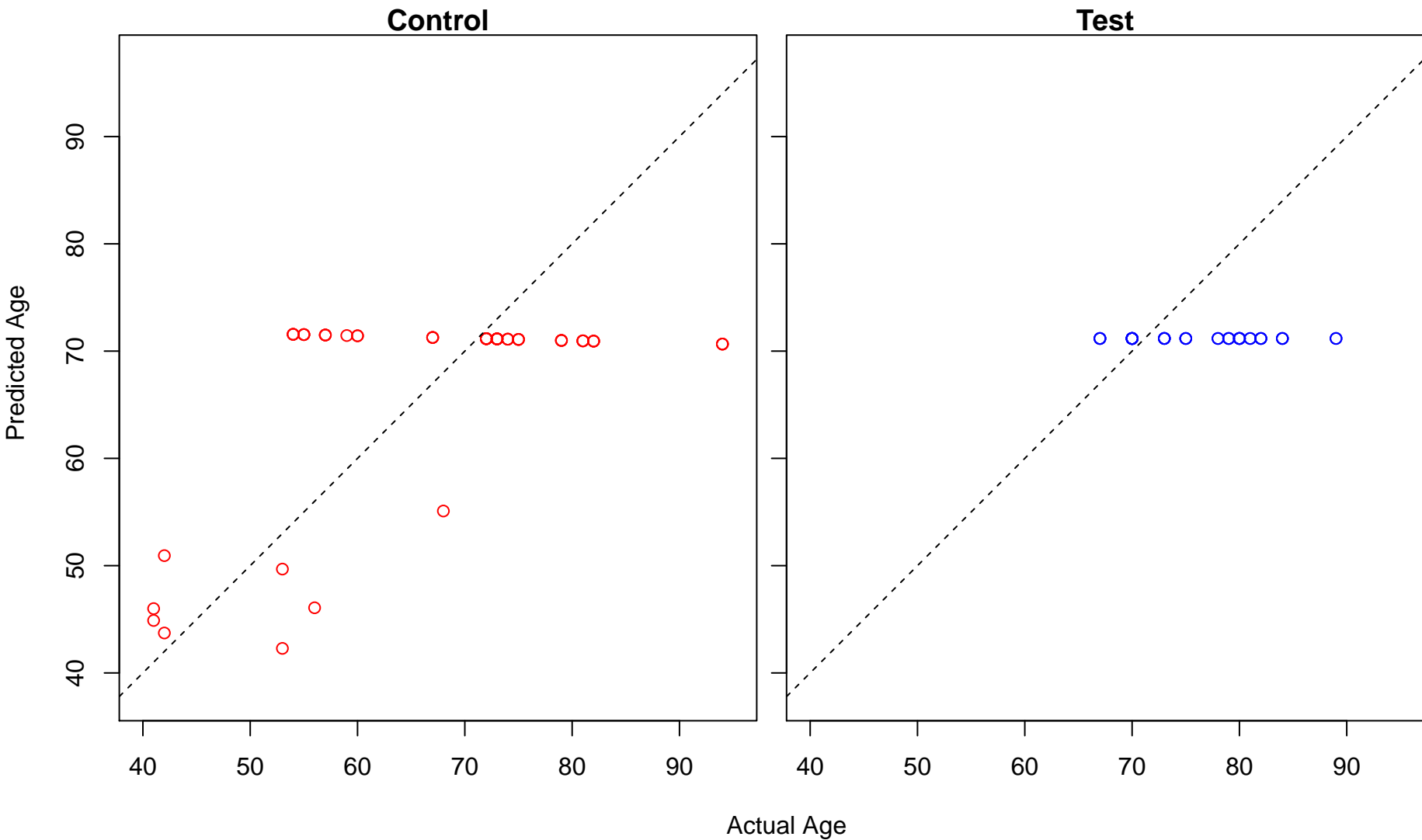
cell communication (Score: 0.809464)



signaling (Score: 0.809464)

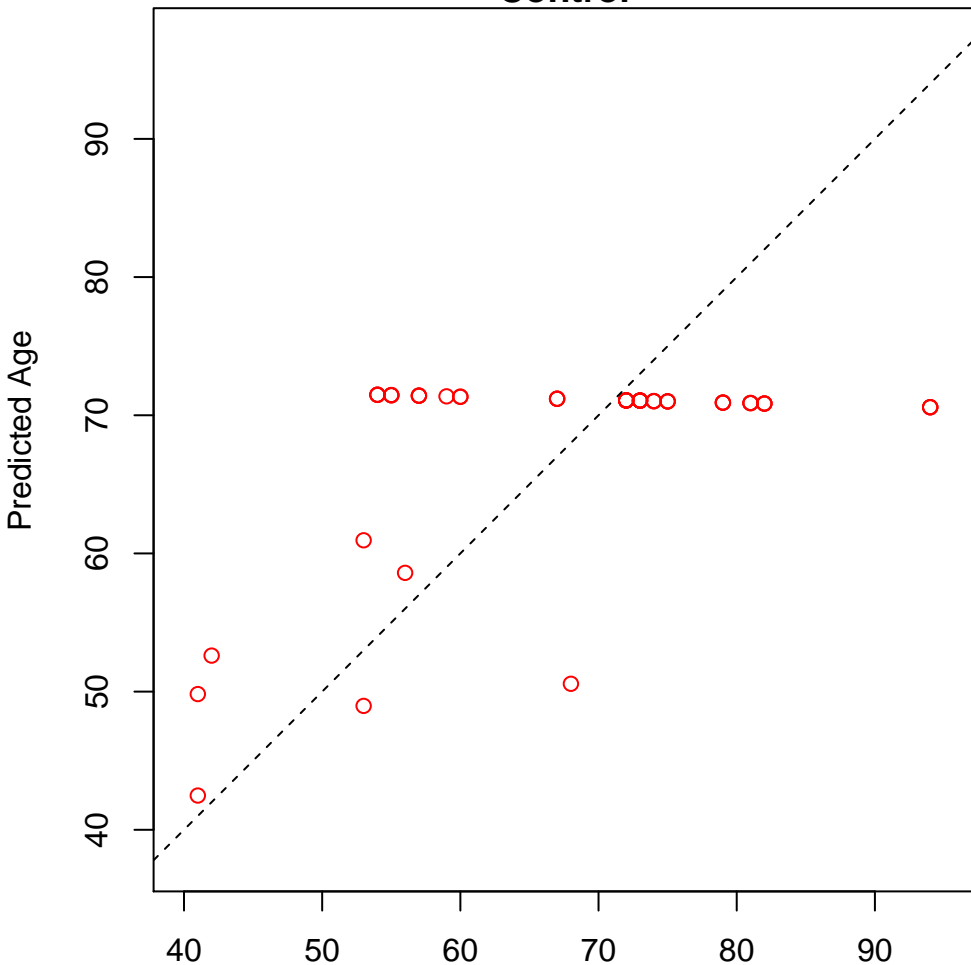


signal transduction (Score: 0.809462)

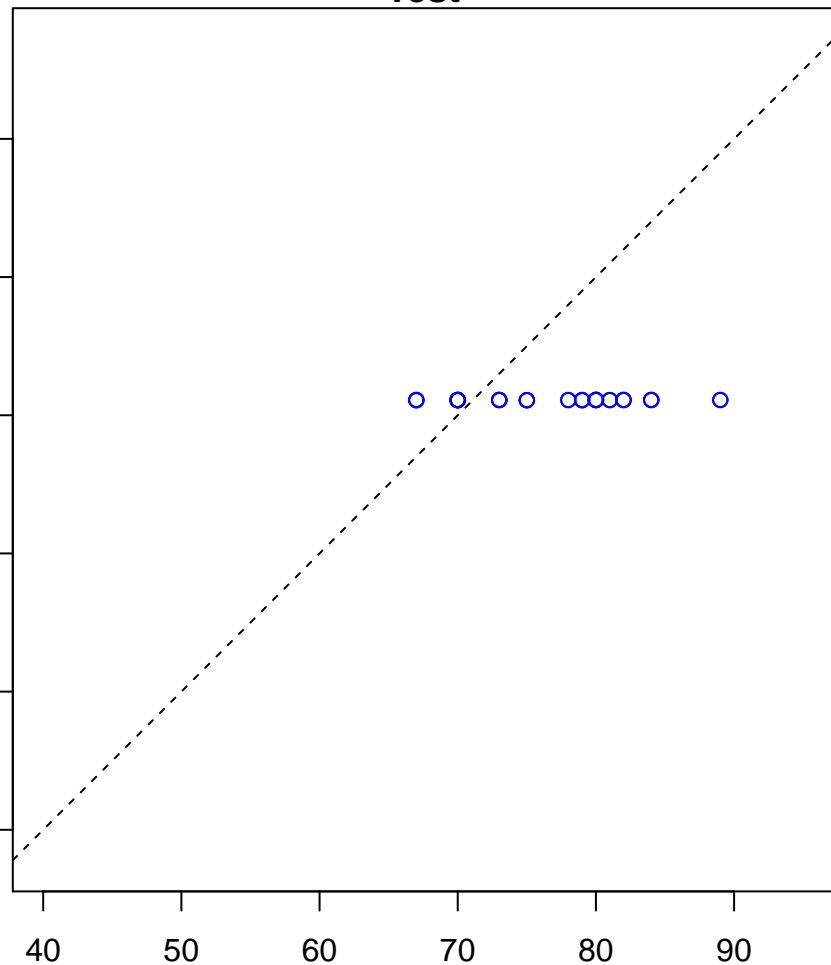


microtubule cytoskeleton organization (Score: 0.809426)

Control



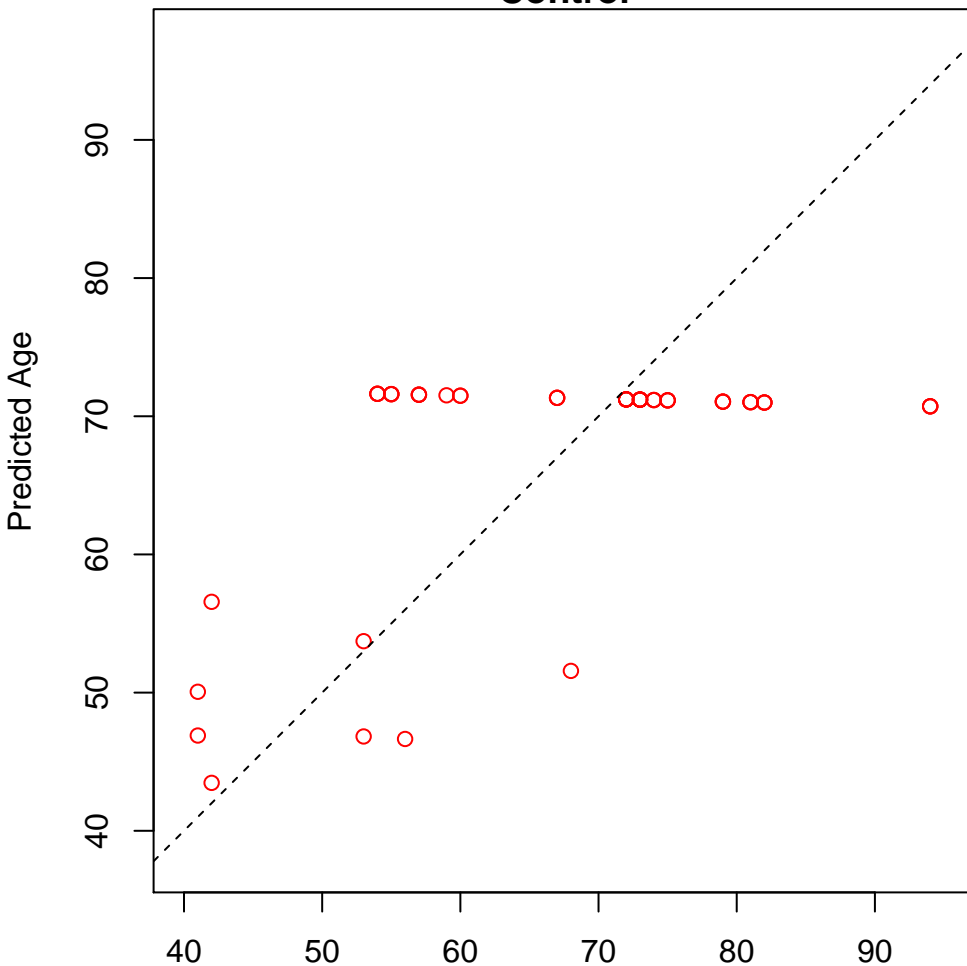
Test



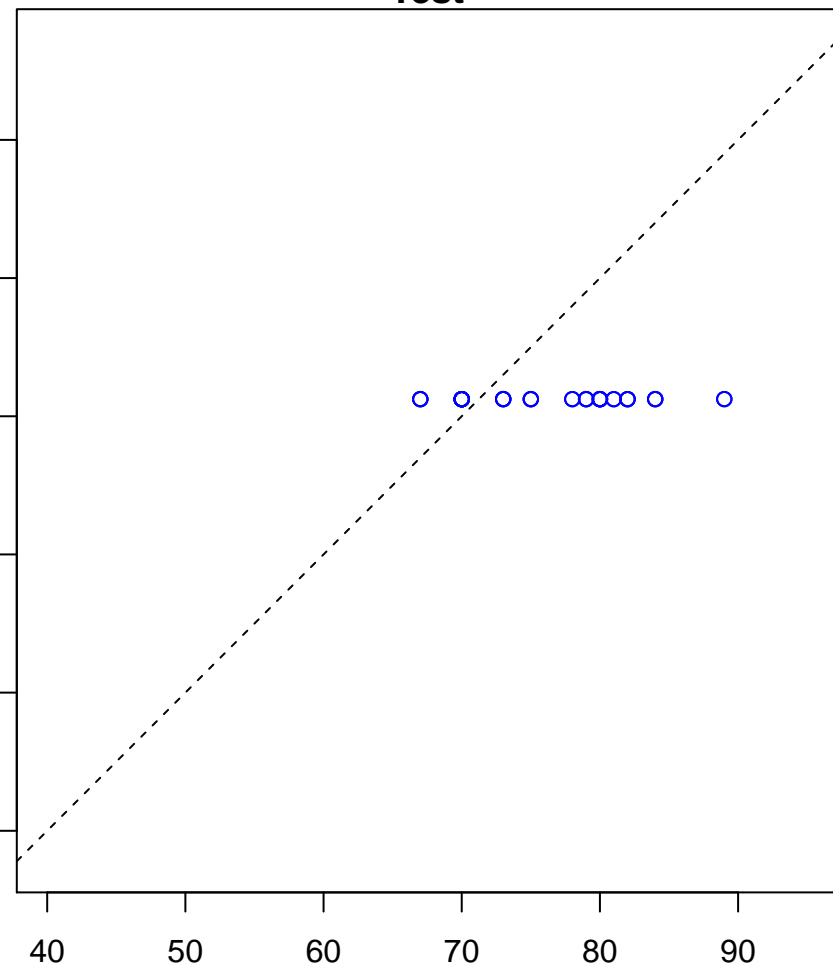
Actual Age

small molecule metabolic process (Score: 0.809410)

Control

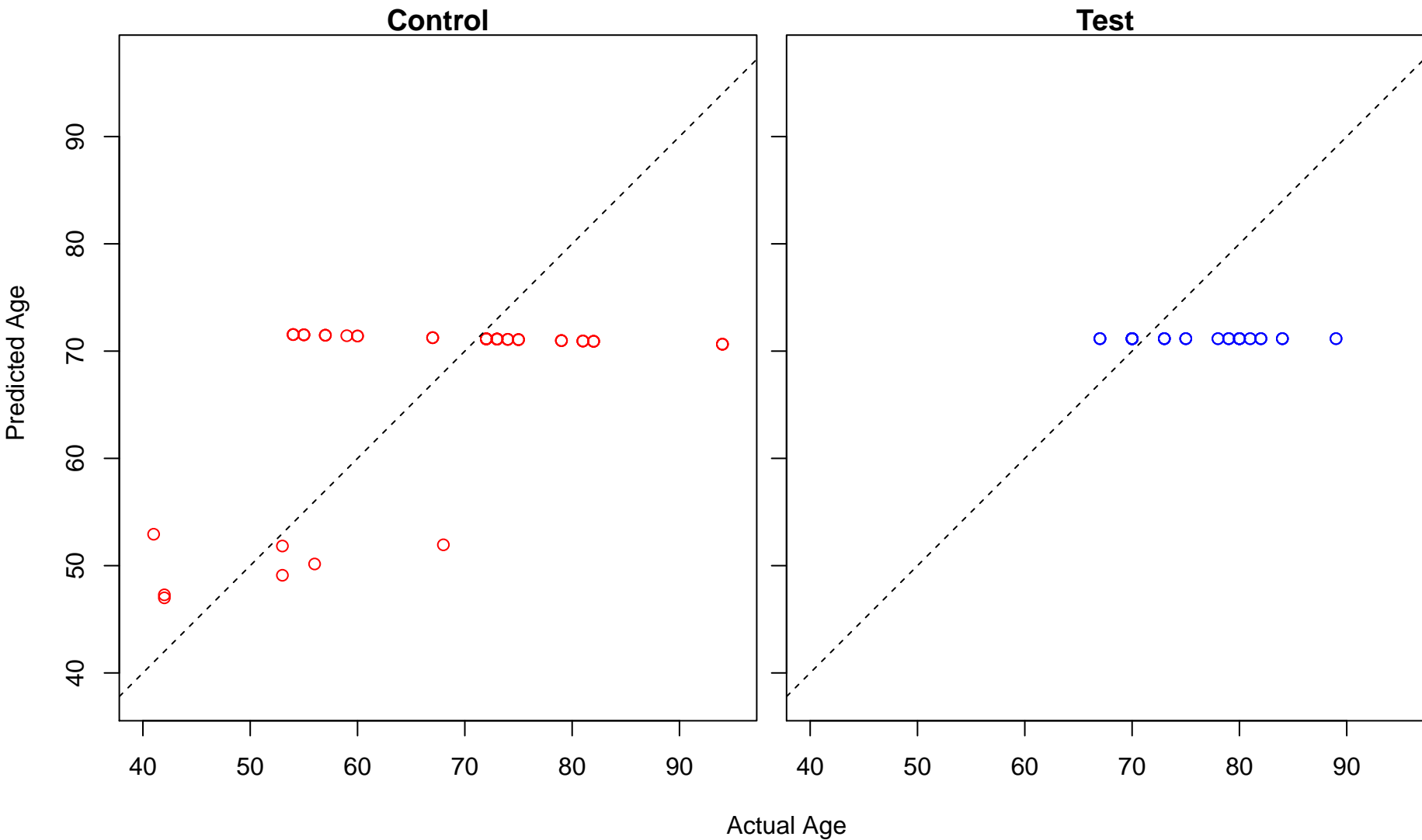


Test



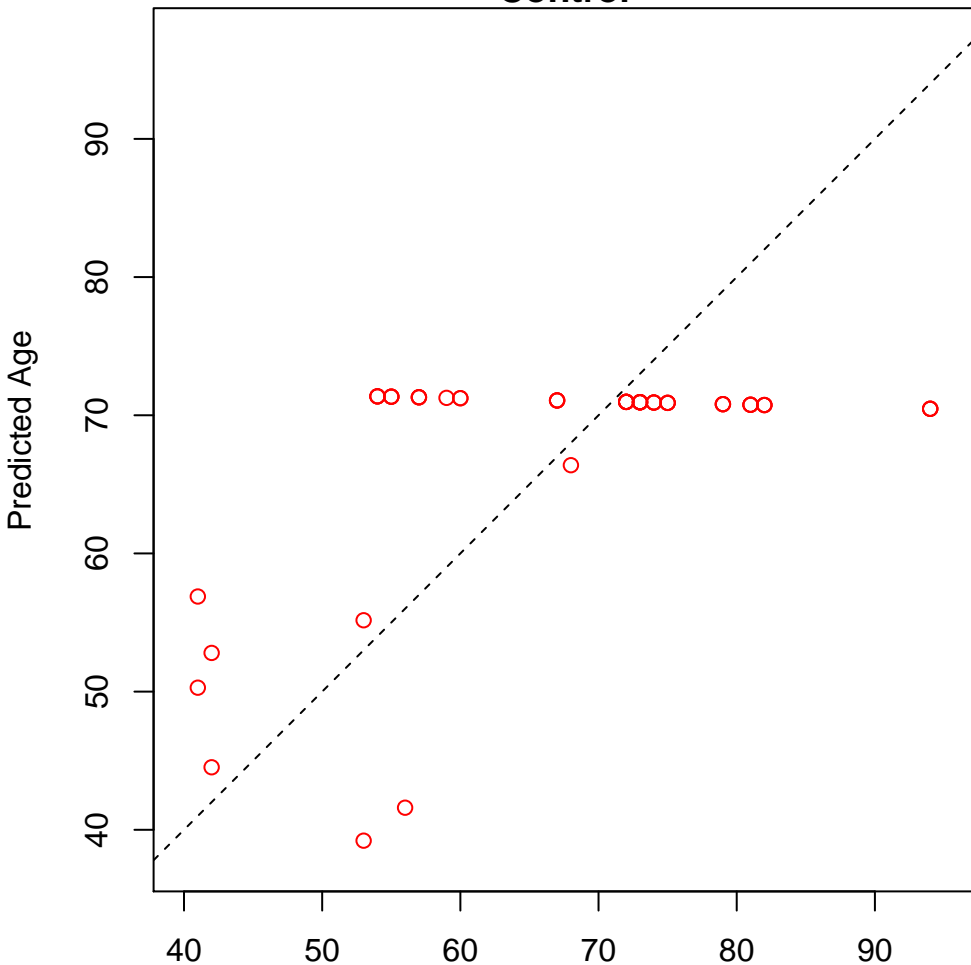
Actual Age

intrinsic apoptotic signaling pathway by p53 class mediator (Score: 0.809335)

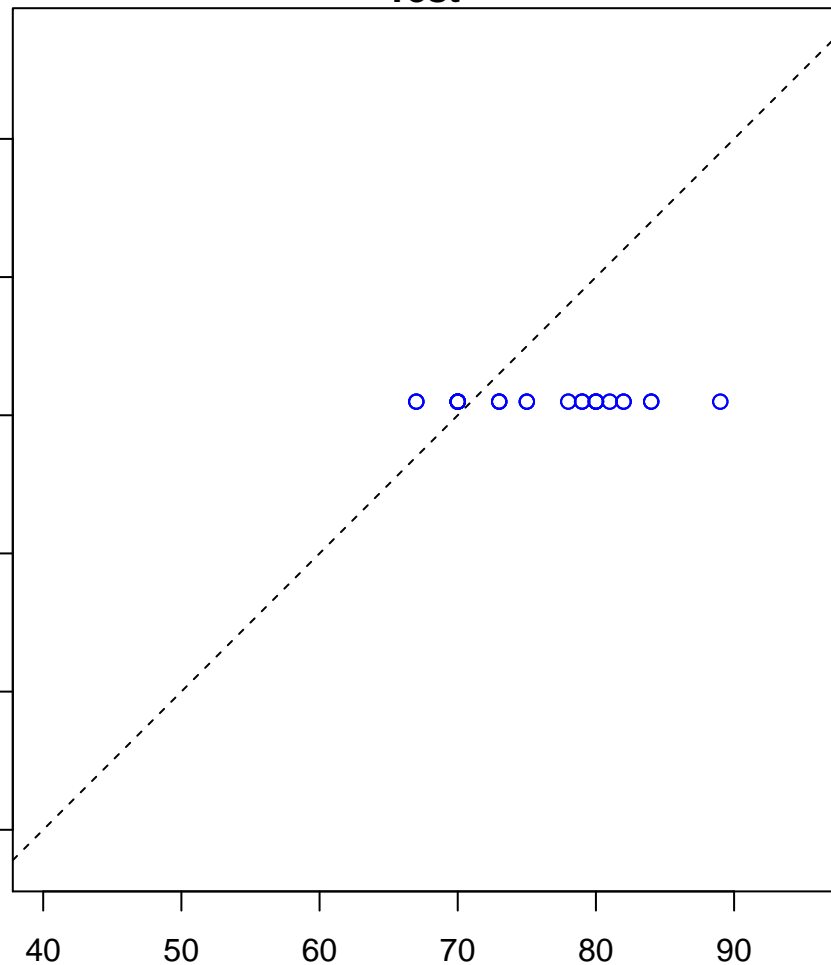


negative regulation of cytokine production (Score: 0.809326)

Control

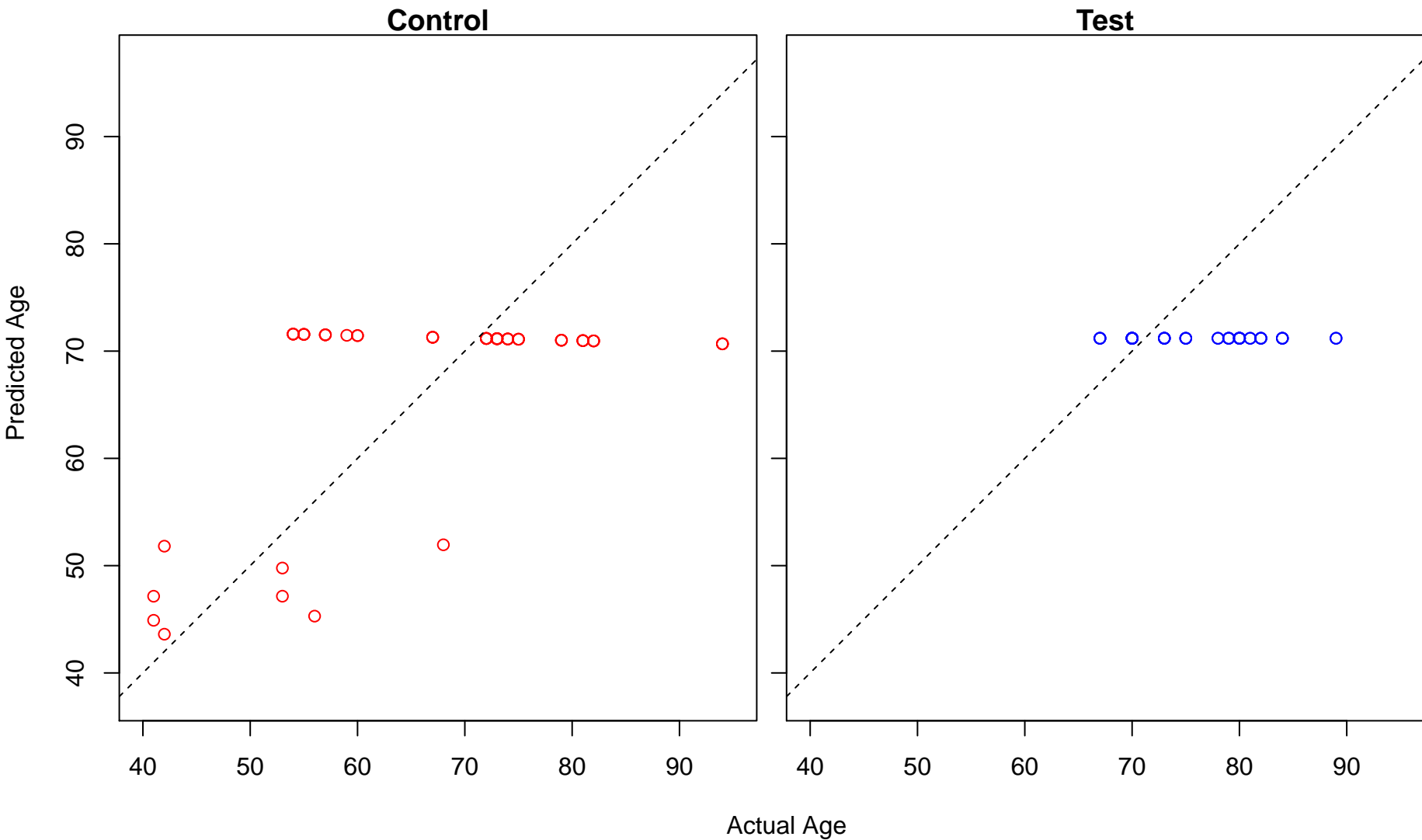


Test

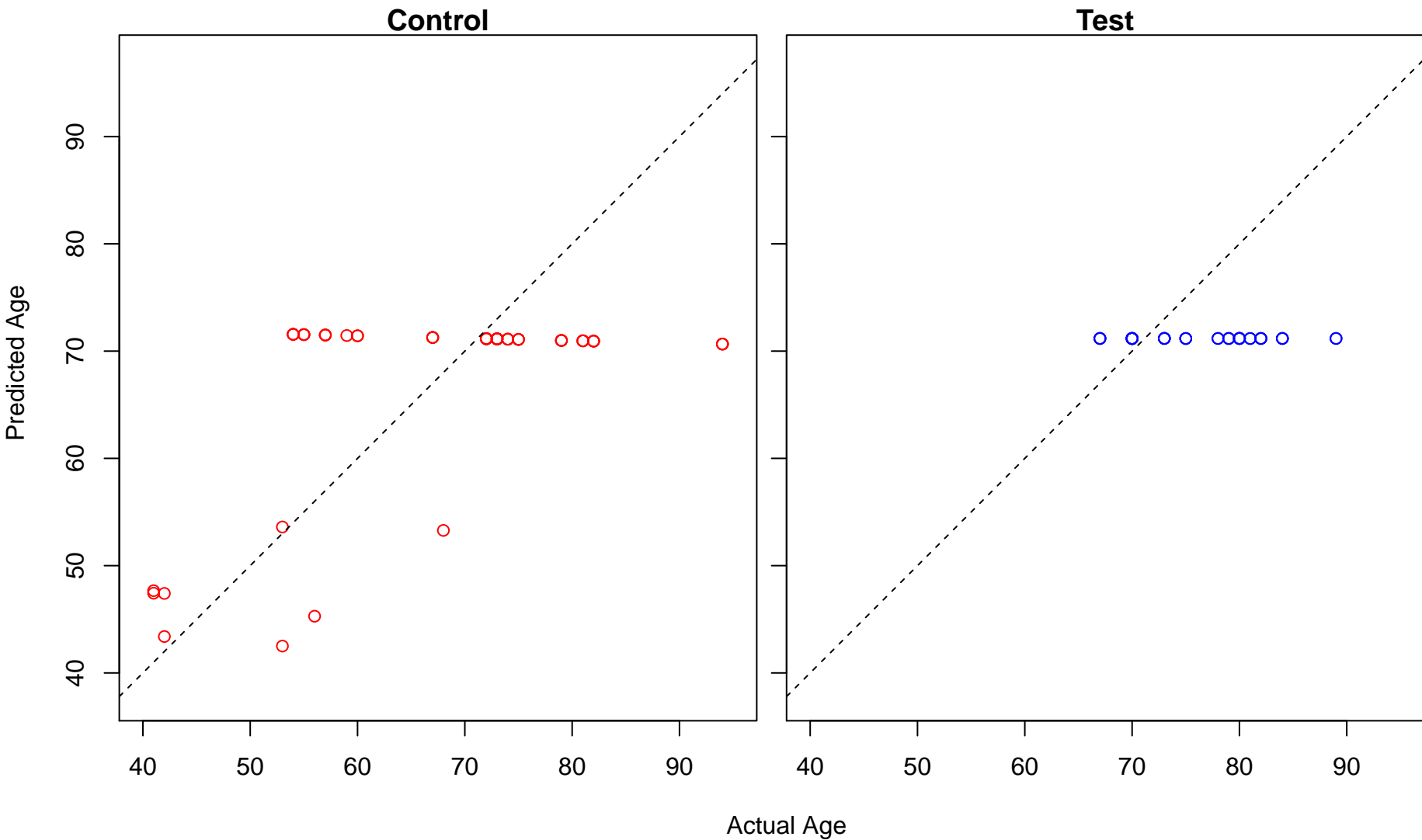


Actual Age

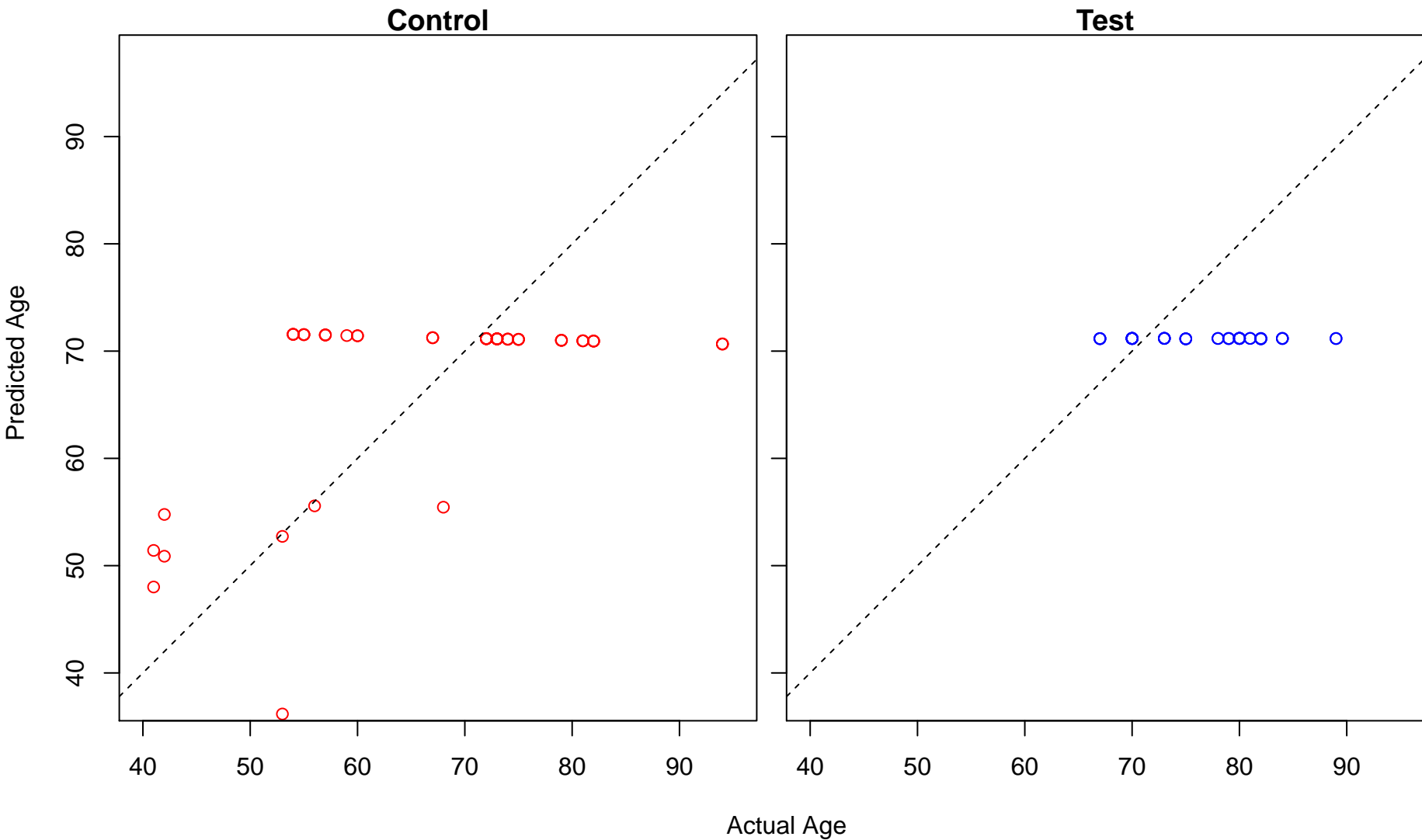
regulation of biological quality (Score: 0.809237)



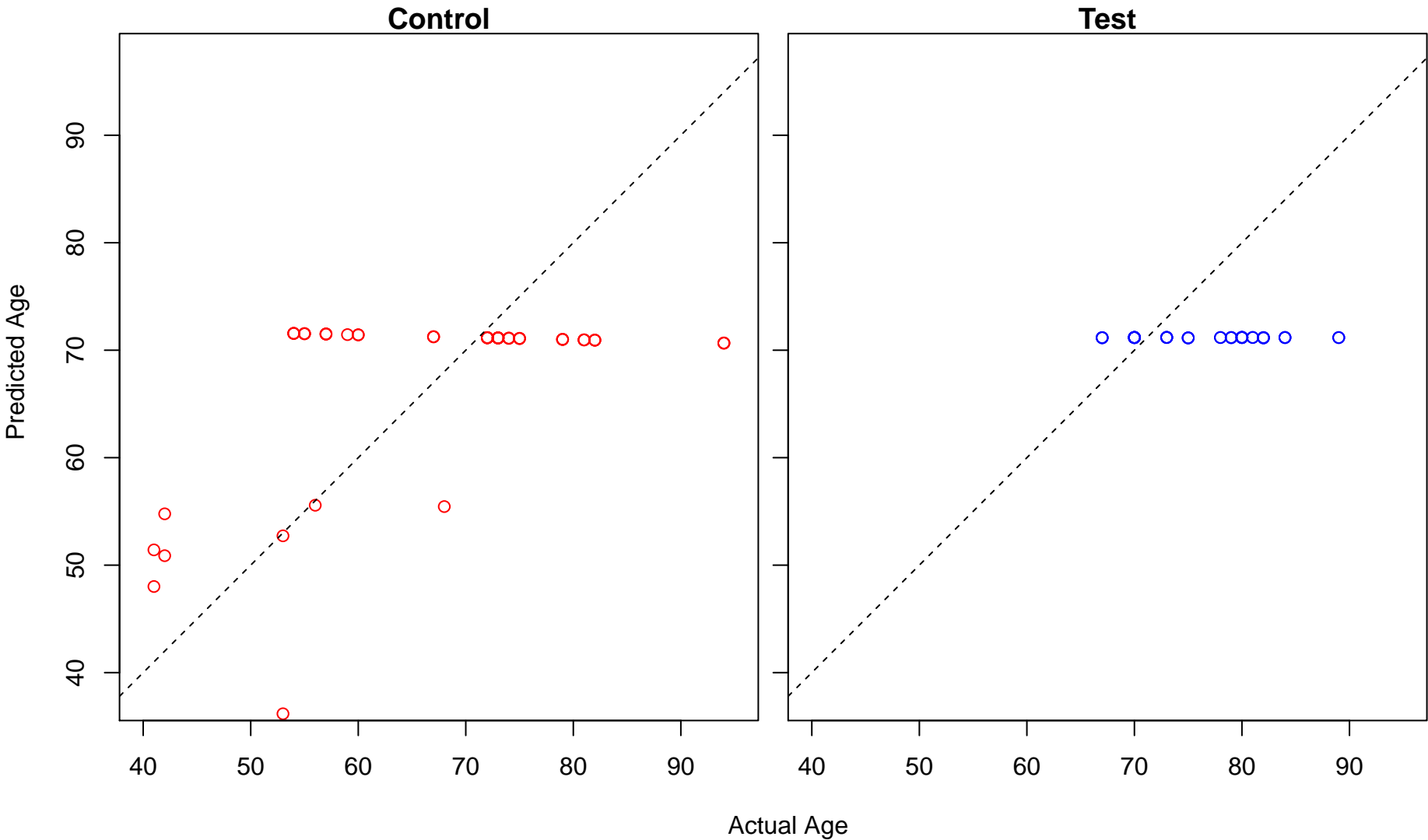
immune response (Score: 0.809223)



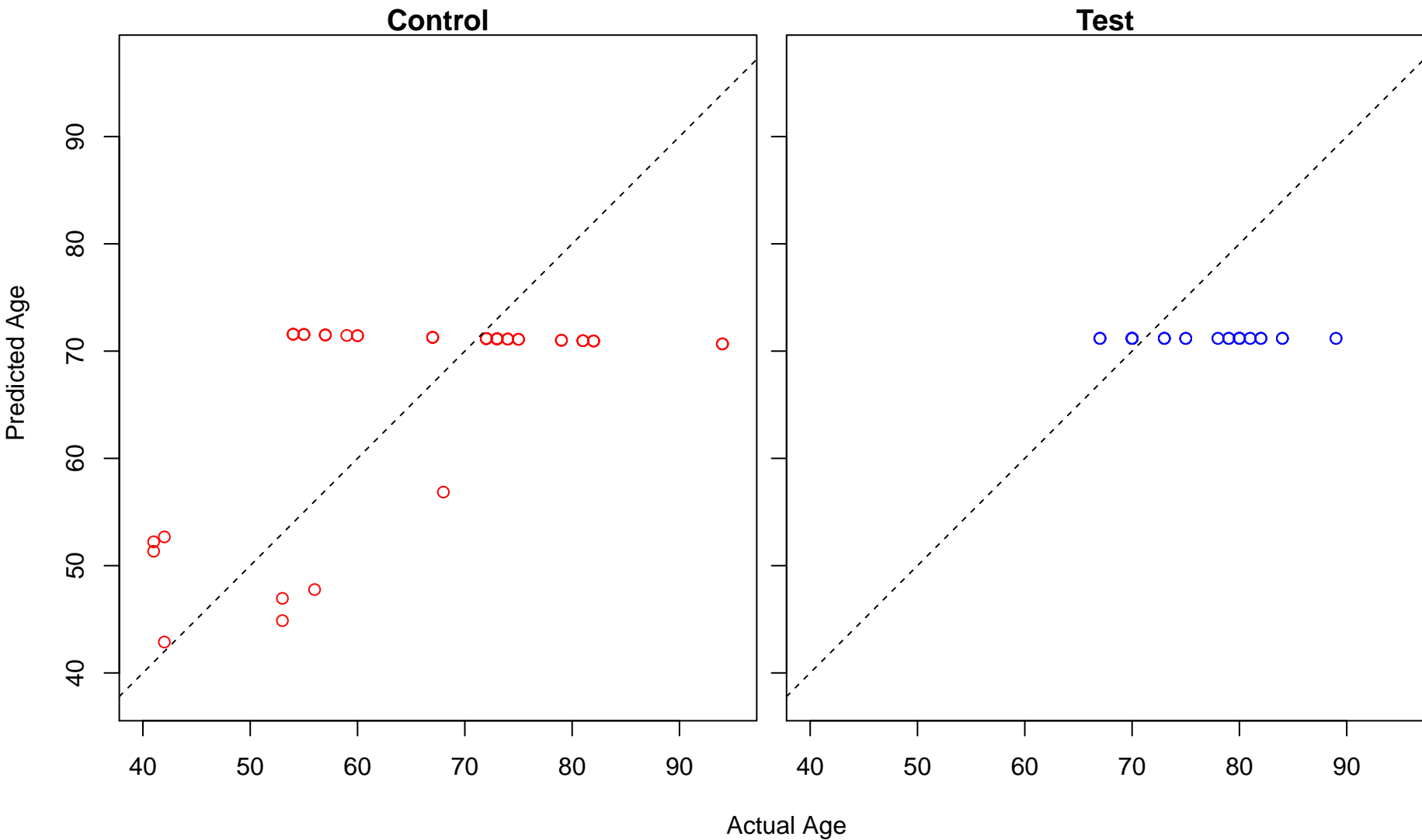
regulation of production of molecular mediator of immune response (Score: 0.809198)



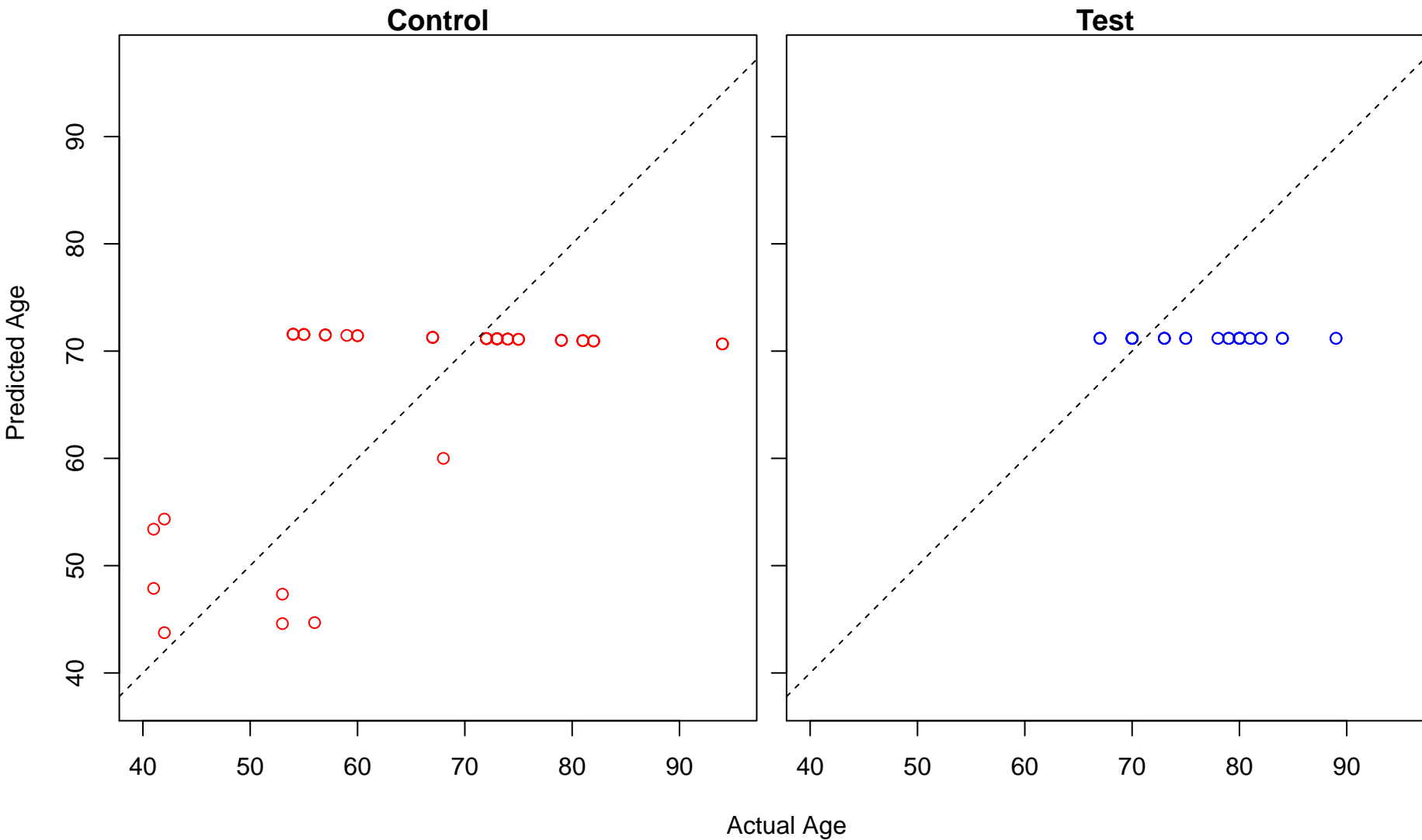
positive regulation of production of molecular mediator of immune response (Score: 0.809198)



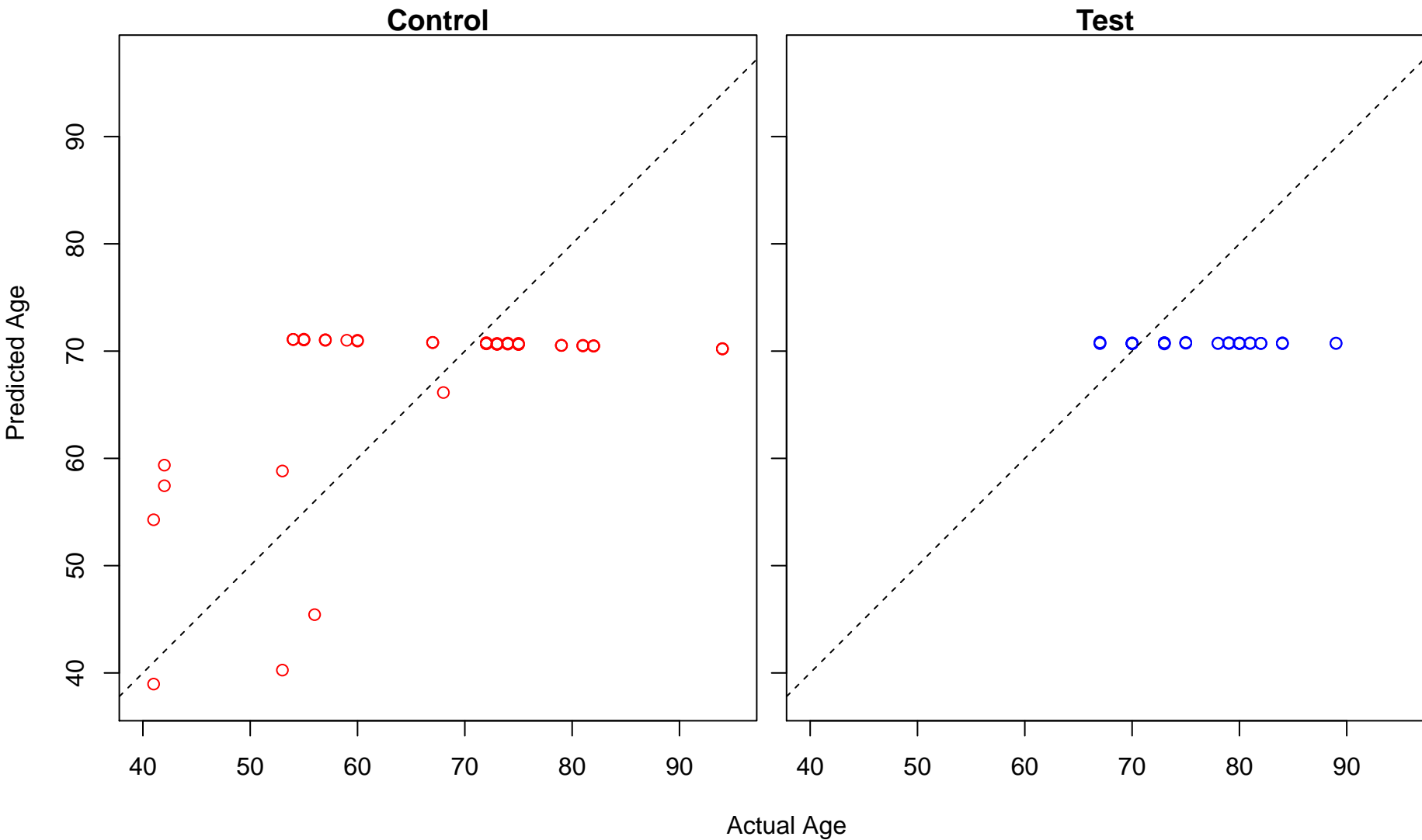
membrane docking (Score: 0.809151)



regulation of protein localization (Score: 0.809077)

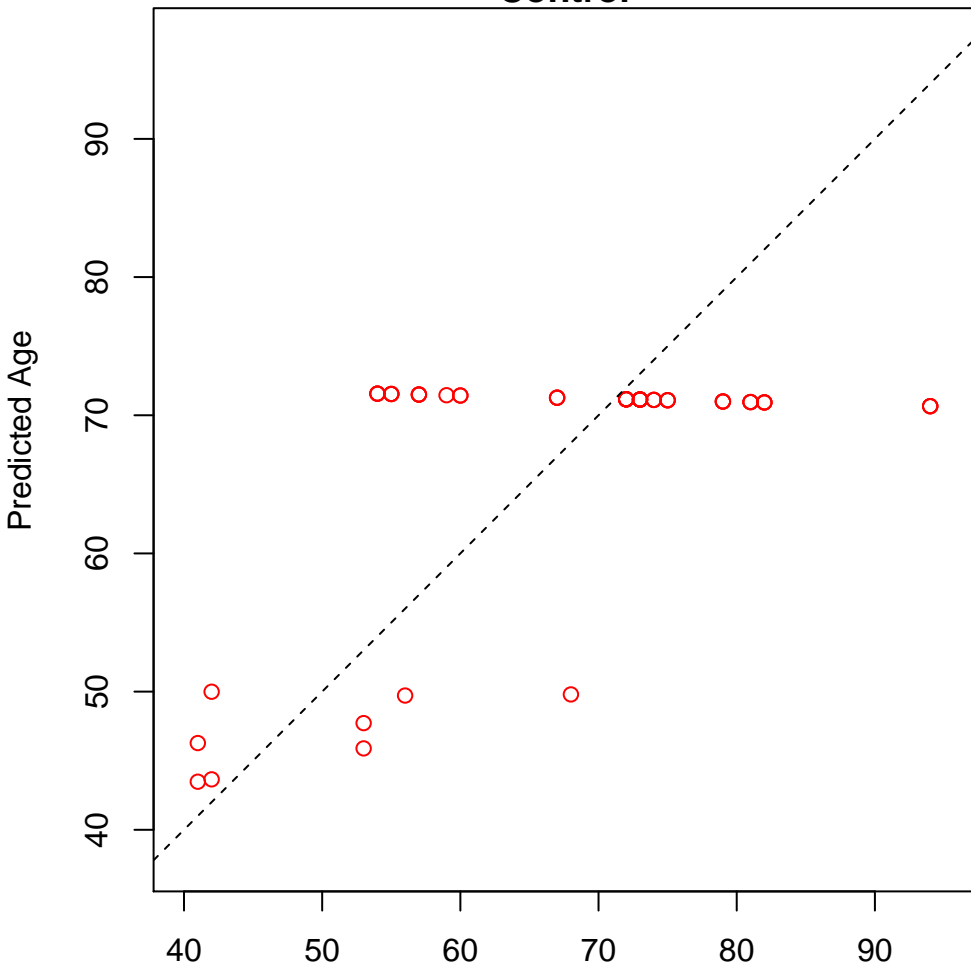


activation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 0.809058)

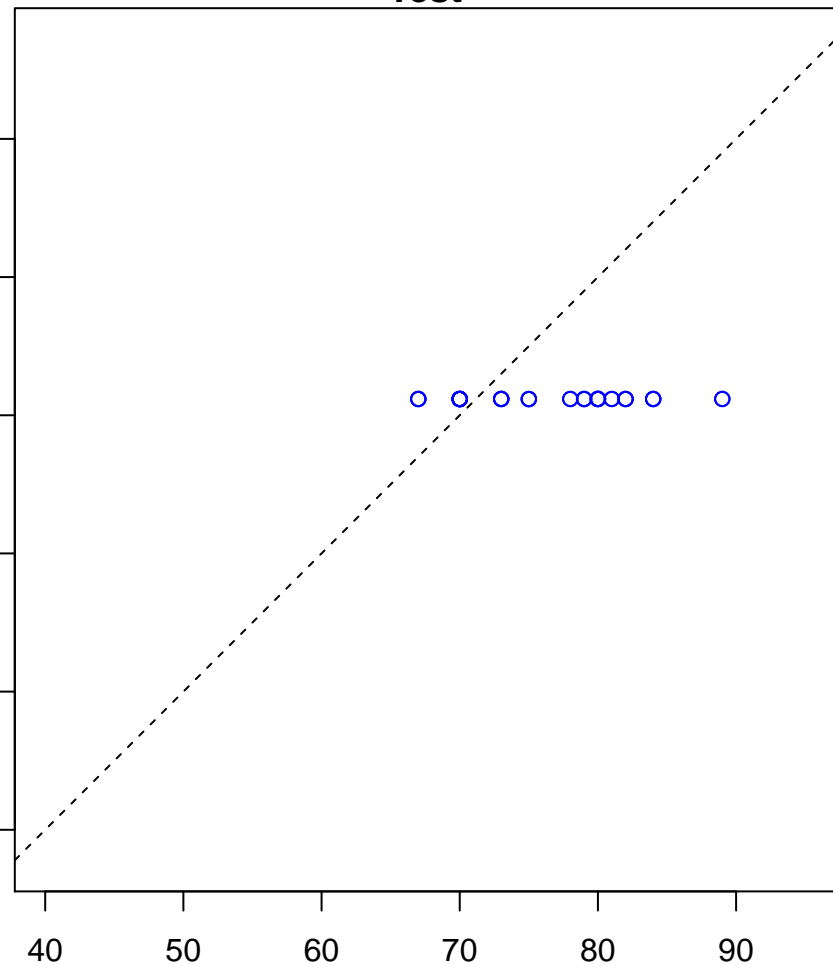


positive regulation of signal transduction (Score: 0.808980)

Control



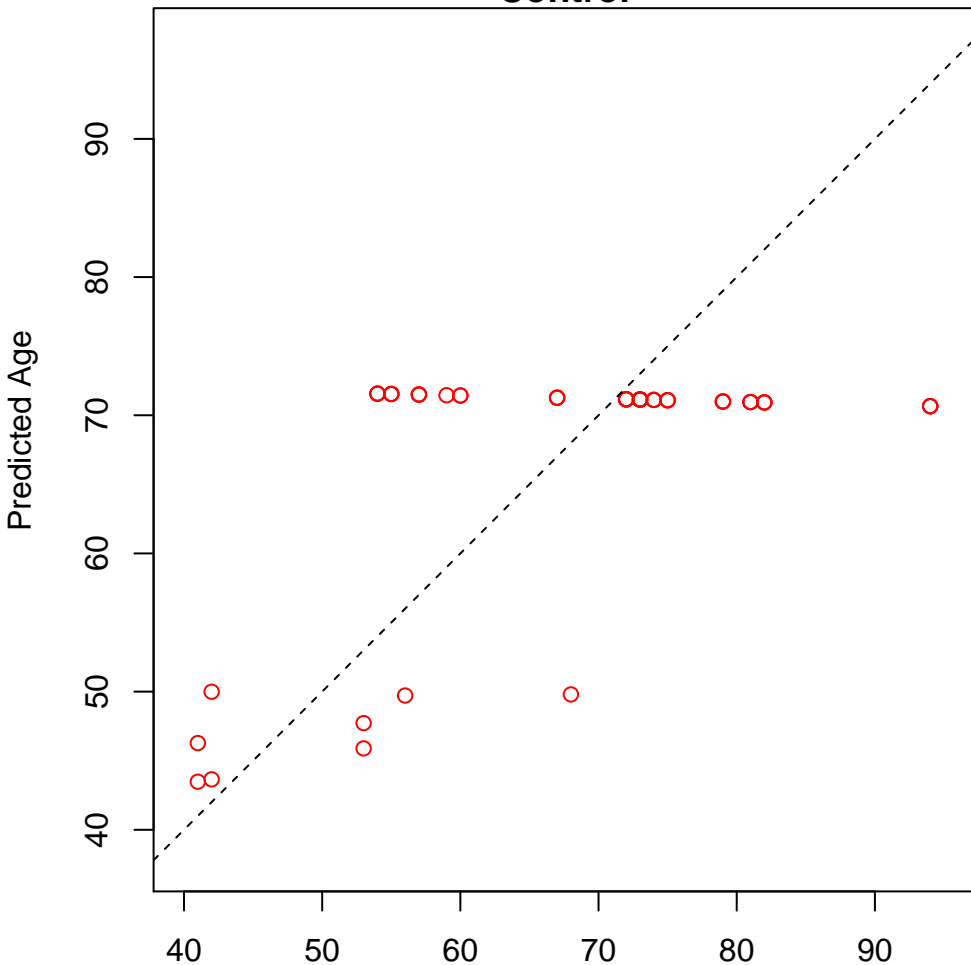
Test



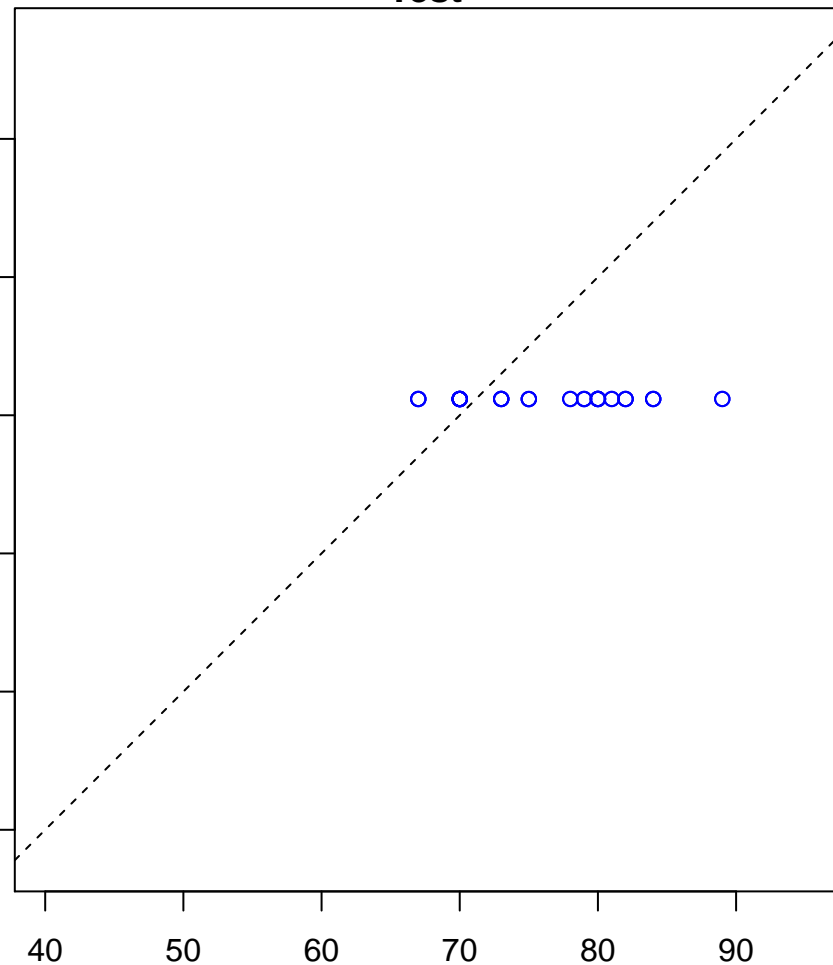
Actual Age

positive regulation of cell communication (Score: 0.808980)

Control

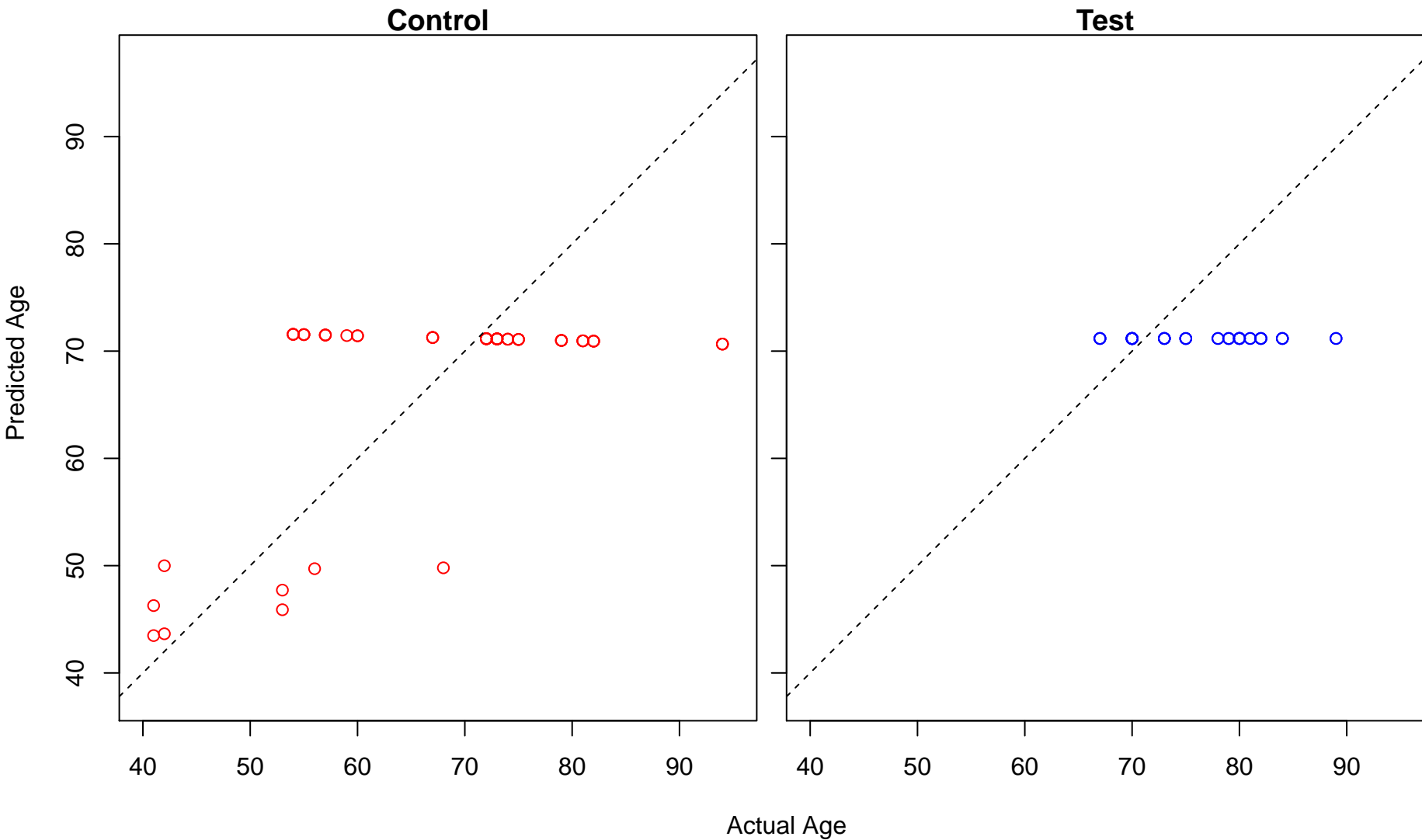


Test

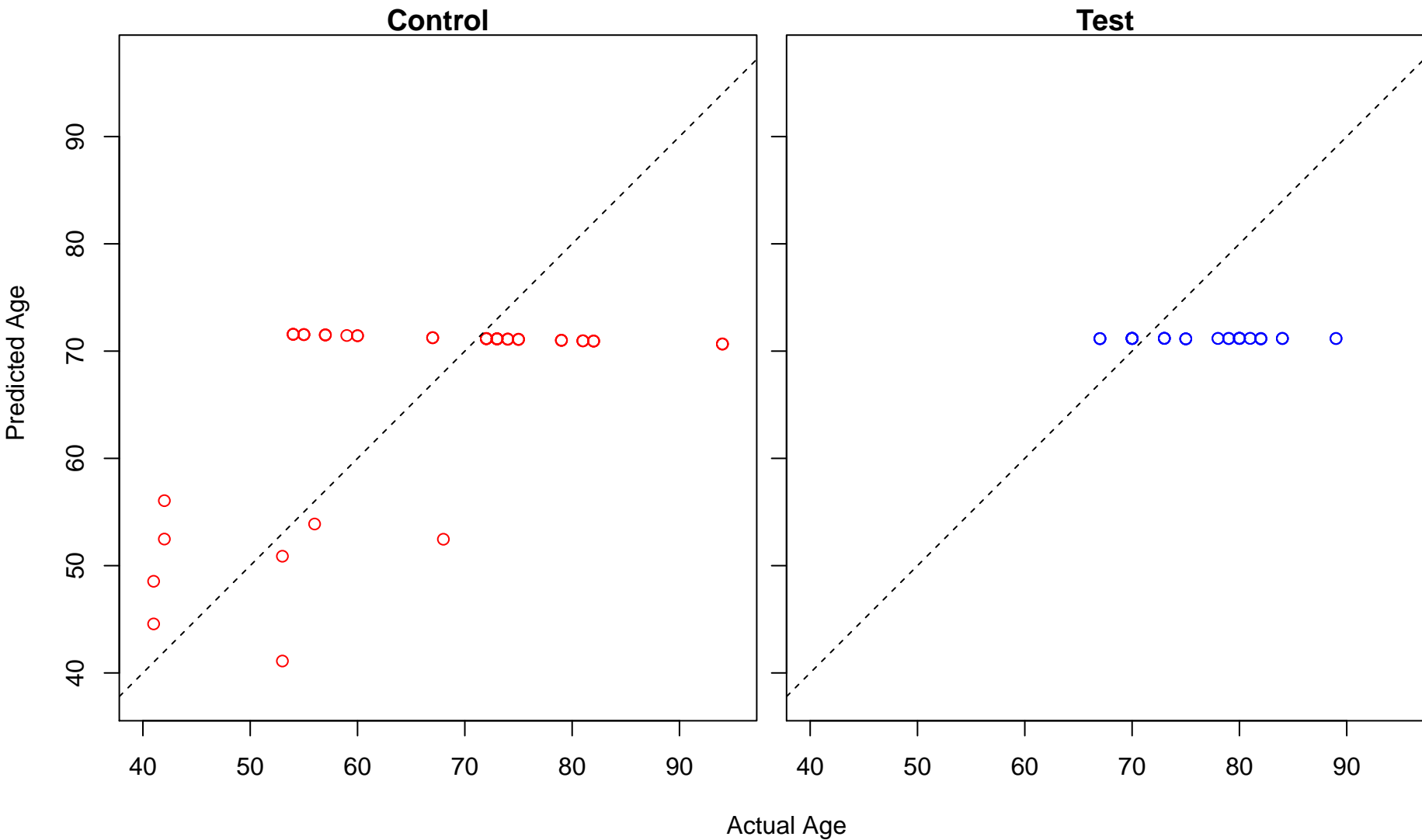


Actual Age

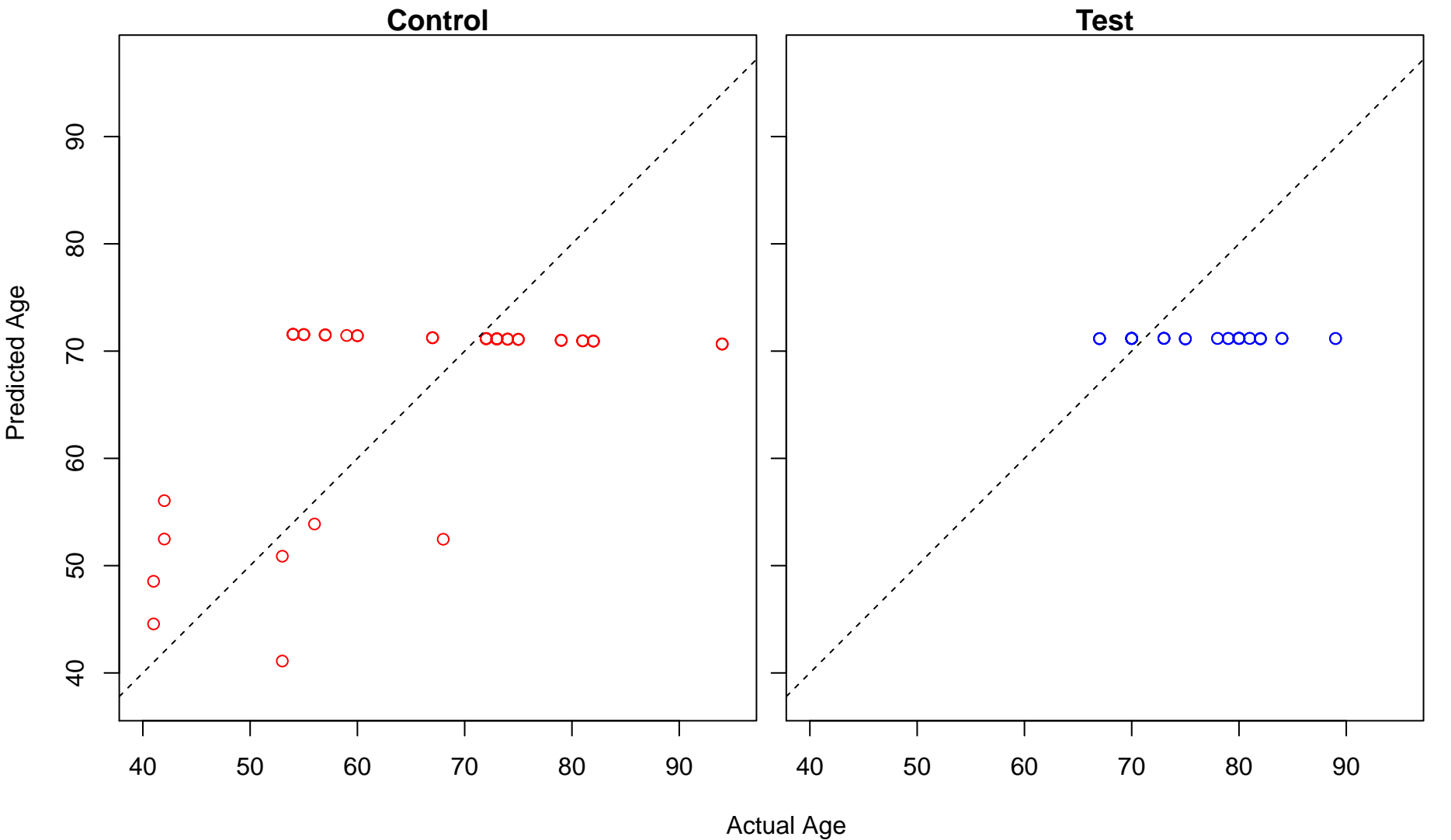
positive regulation of signaling (Score: 0.808980)



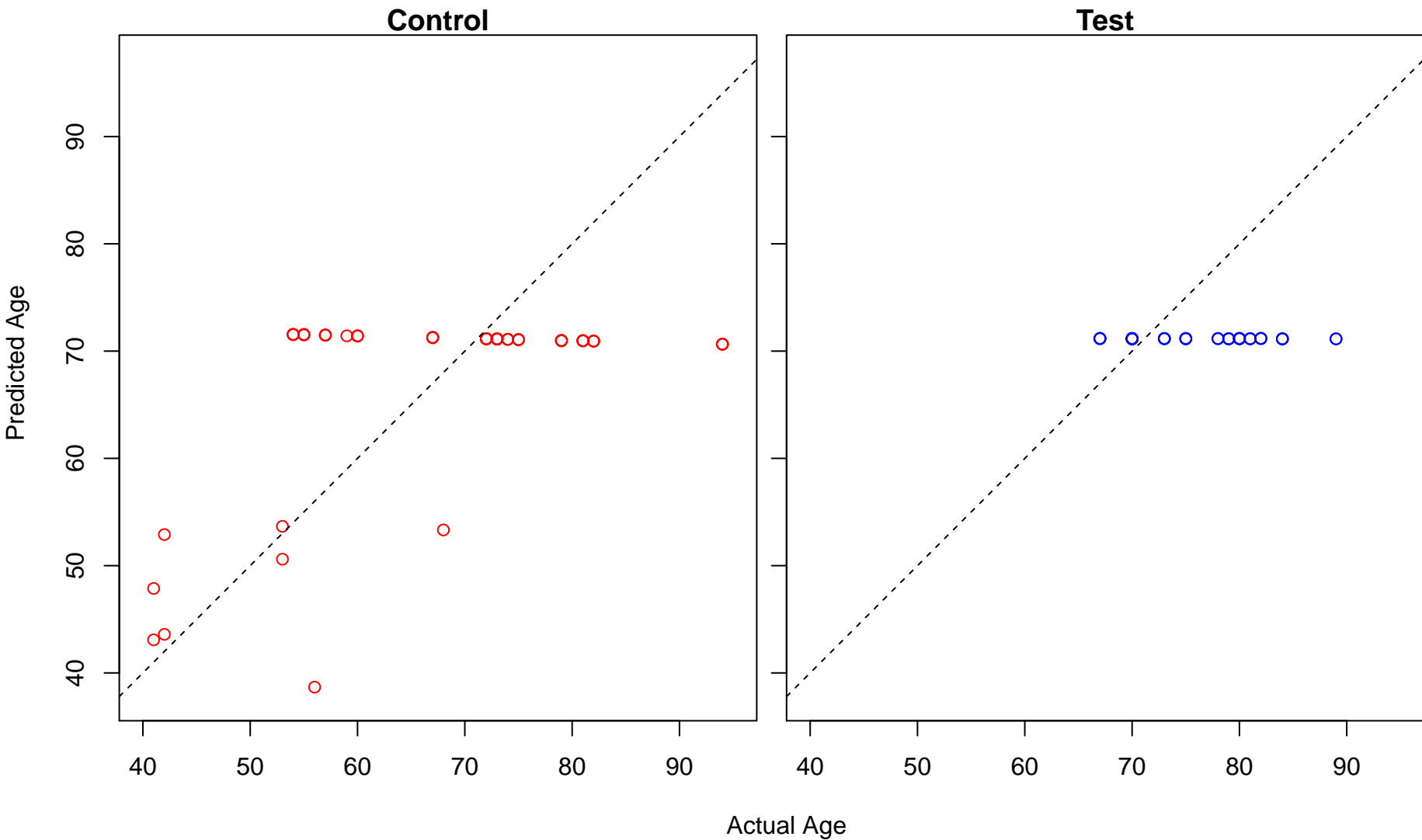
regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway (Score: 0.80)



Negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway (Score: 0.00)

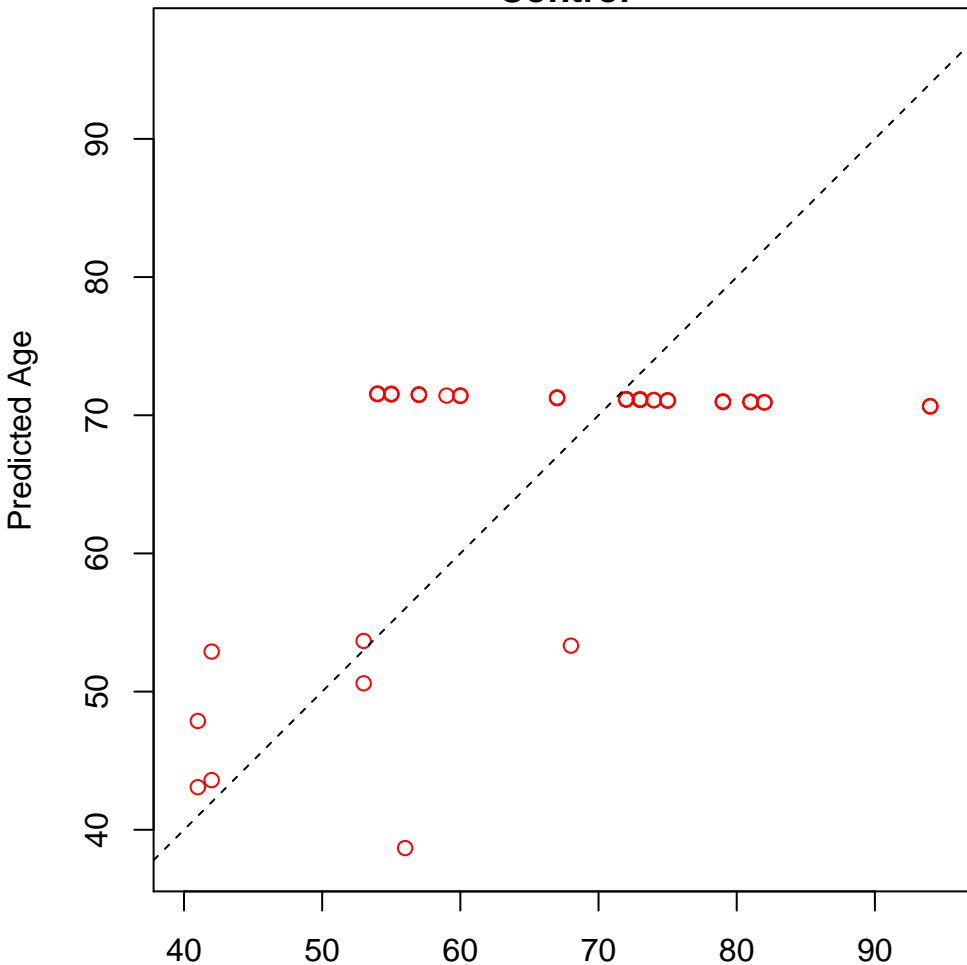


cytoplasmic translation (Score: 0.808842)

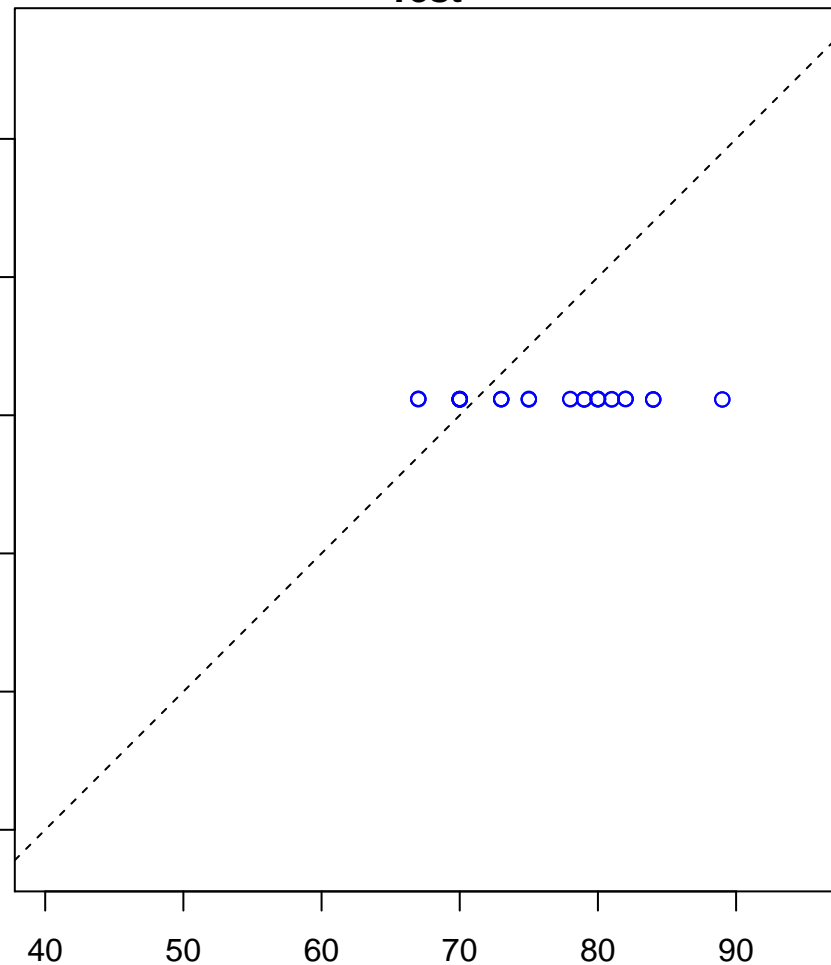


cytoplasmic translational initiation (Score: 0.808842)

Control



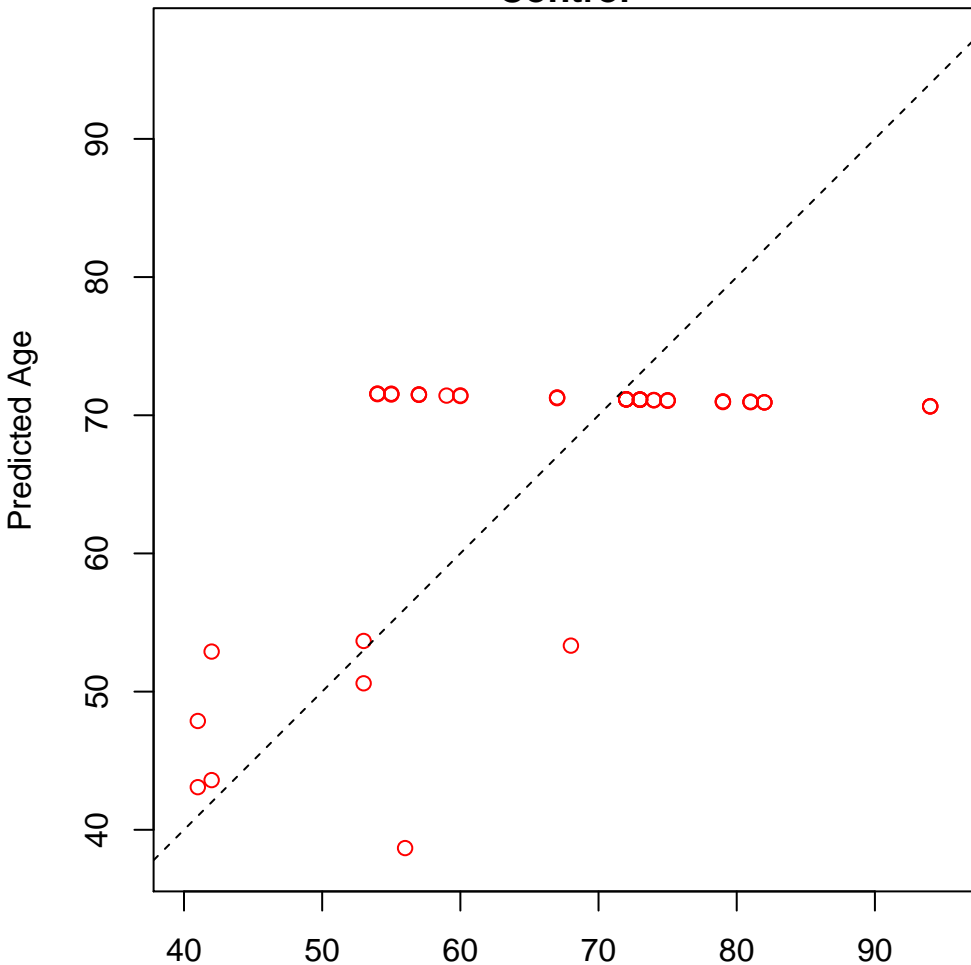
Test



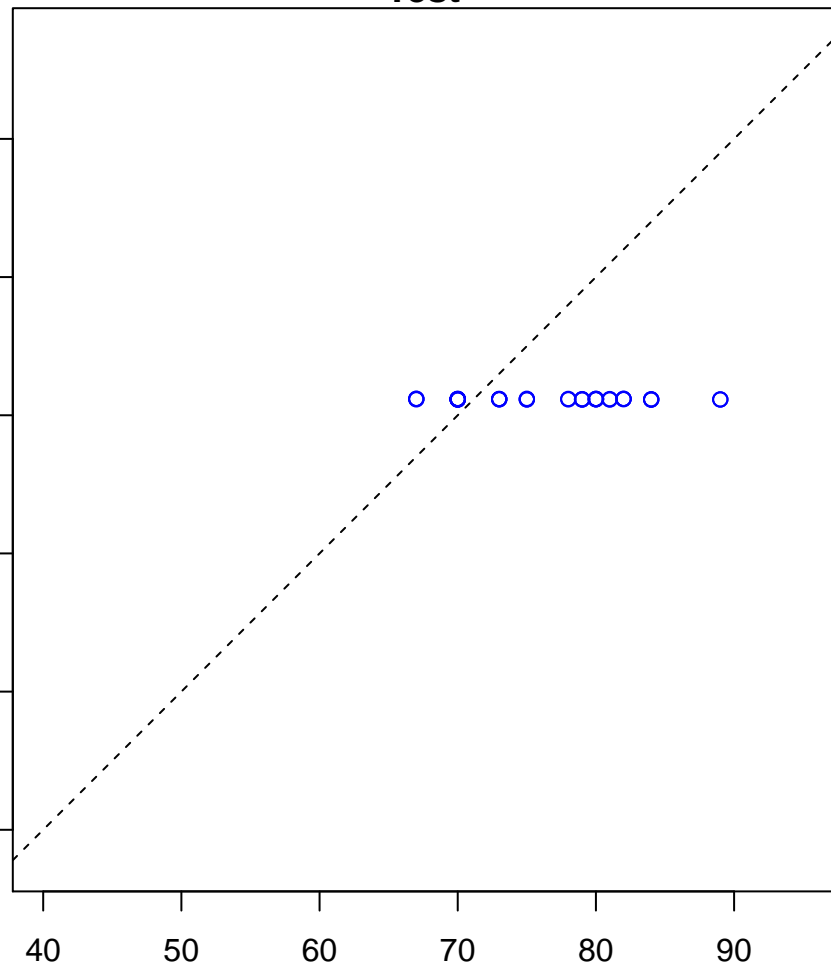
Actual Age

viral translational termination–reinitiation (Score: 0.808842)

Control

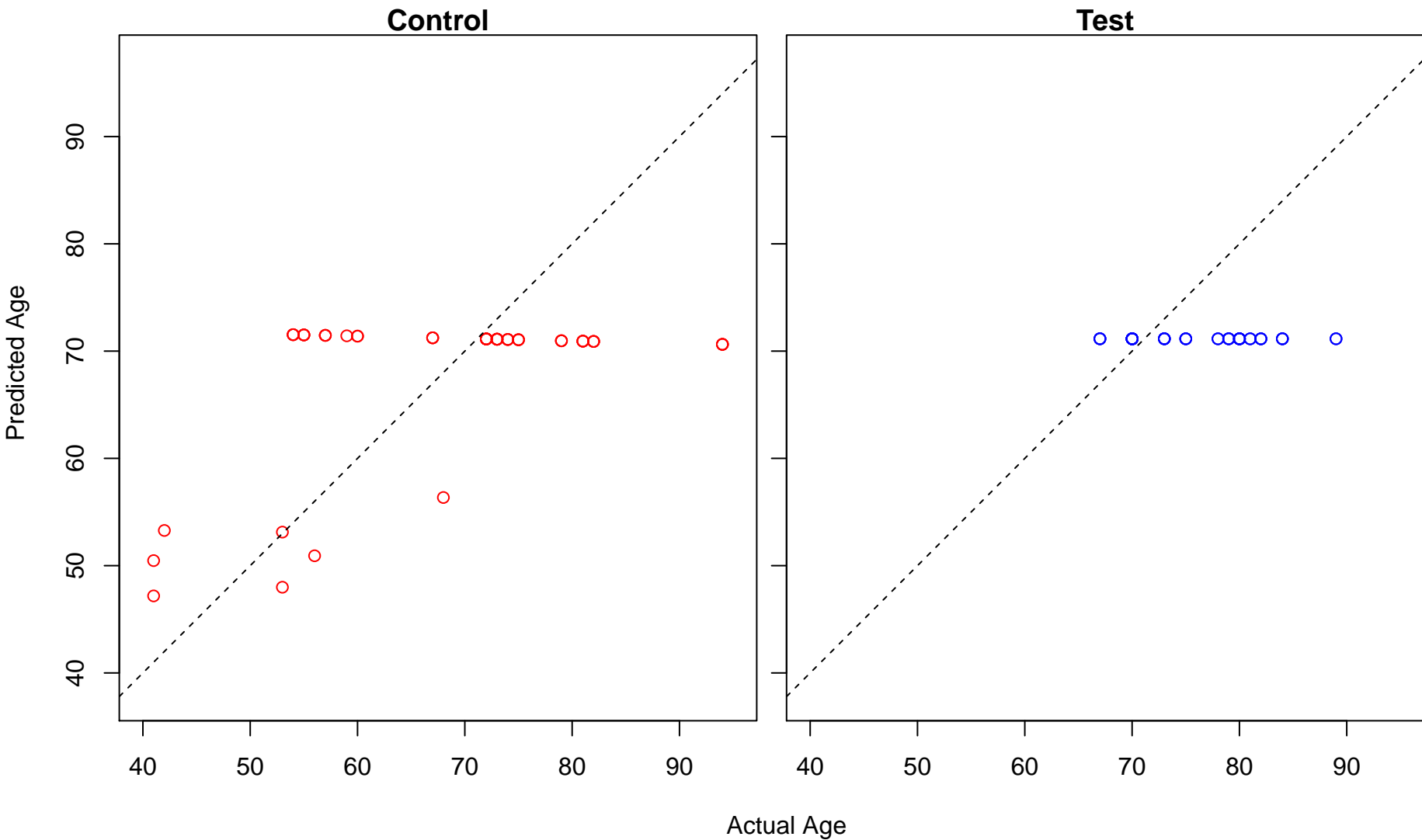


Test

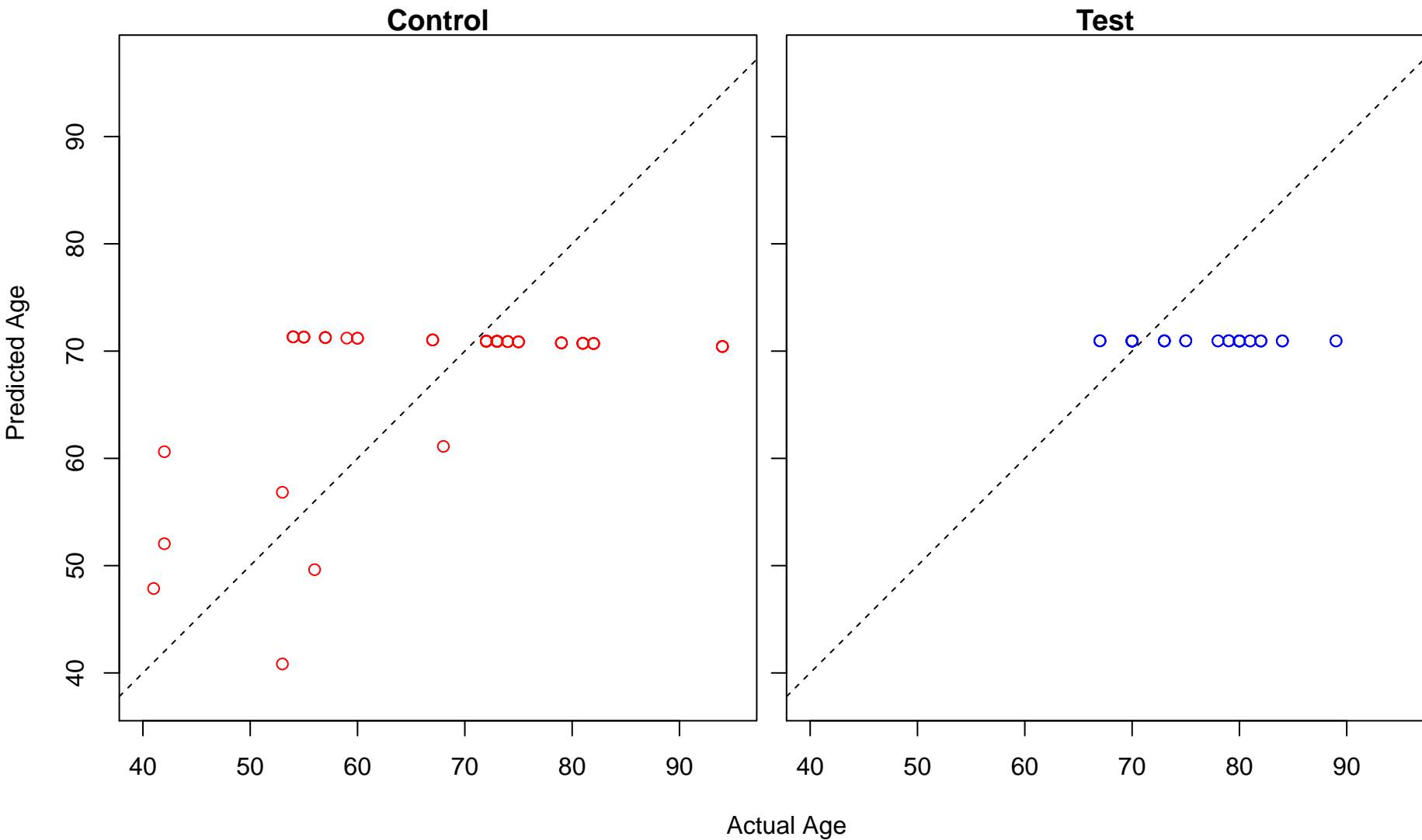


Actual Age

positive regulation of multicellular organismal process (Score: 0.808709)

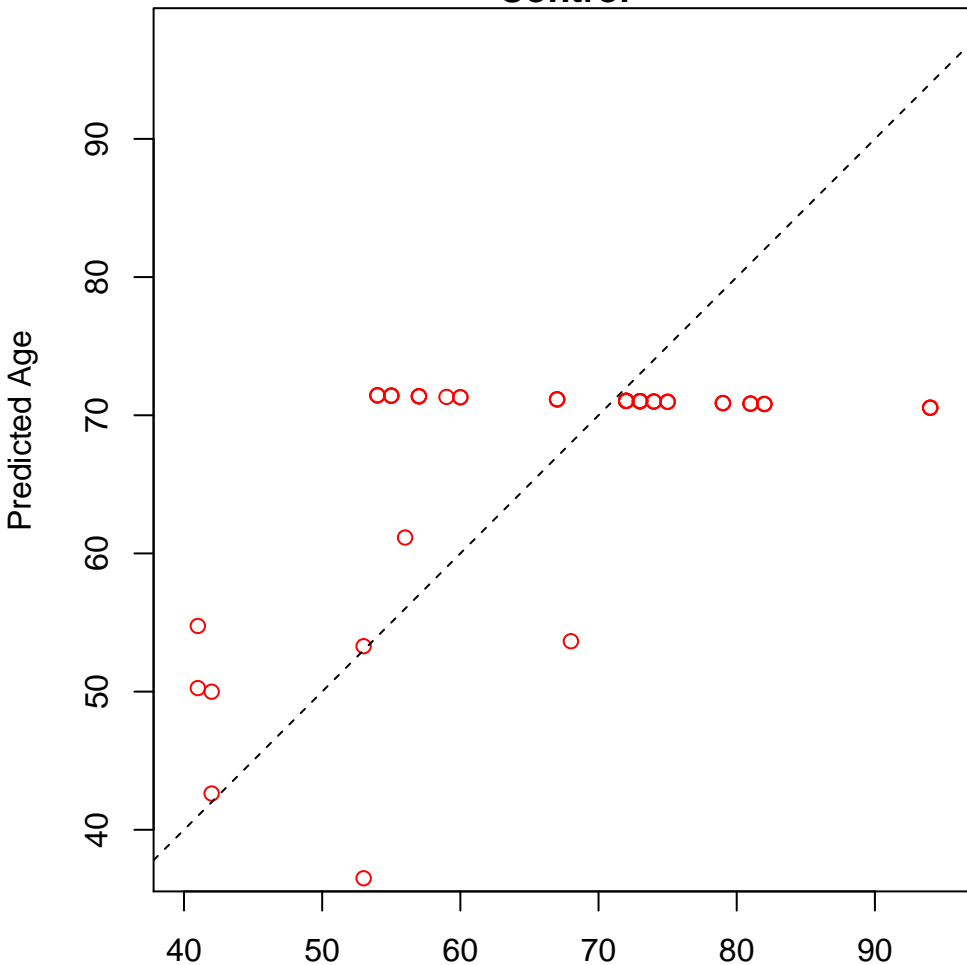


negative regulation of response to DNA damage stimulus (Score: 0.808686)

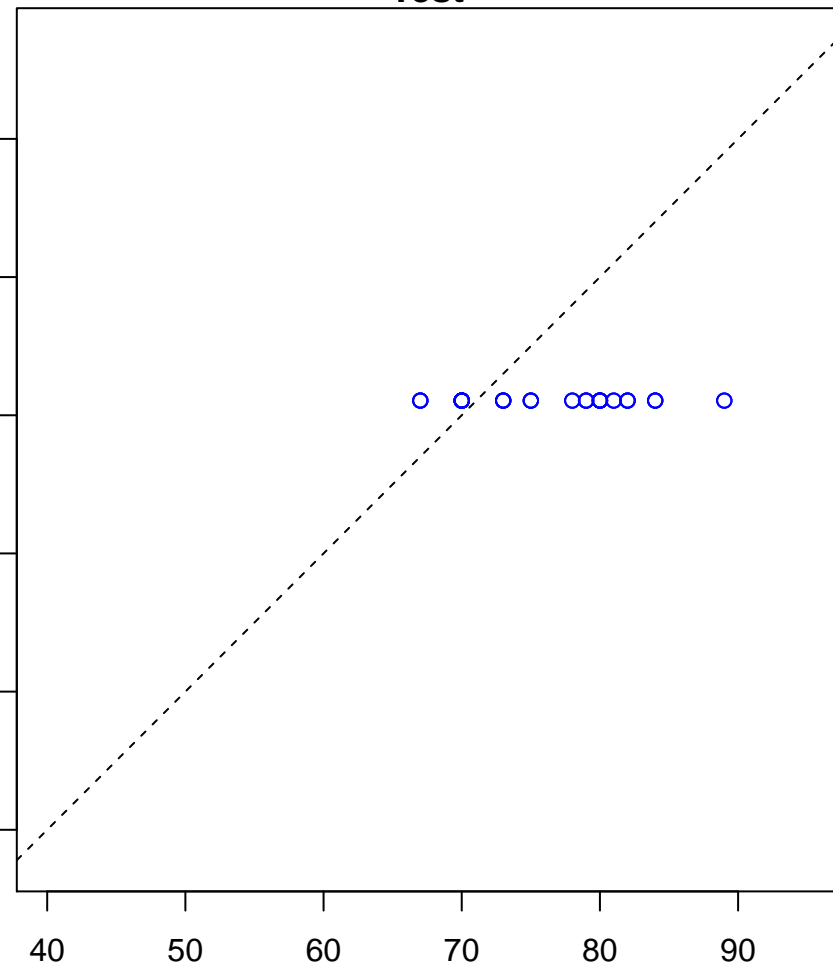


organophosphate biosynthetic process (Score: 0.808680)

Control



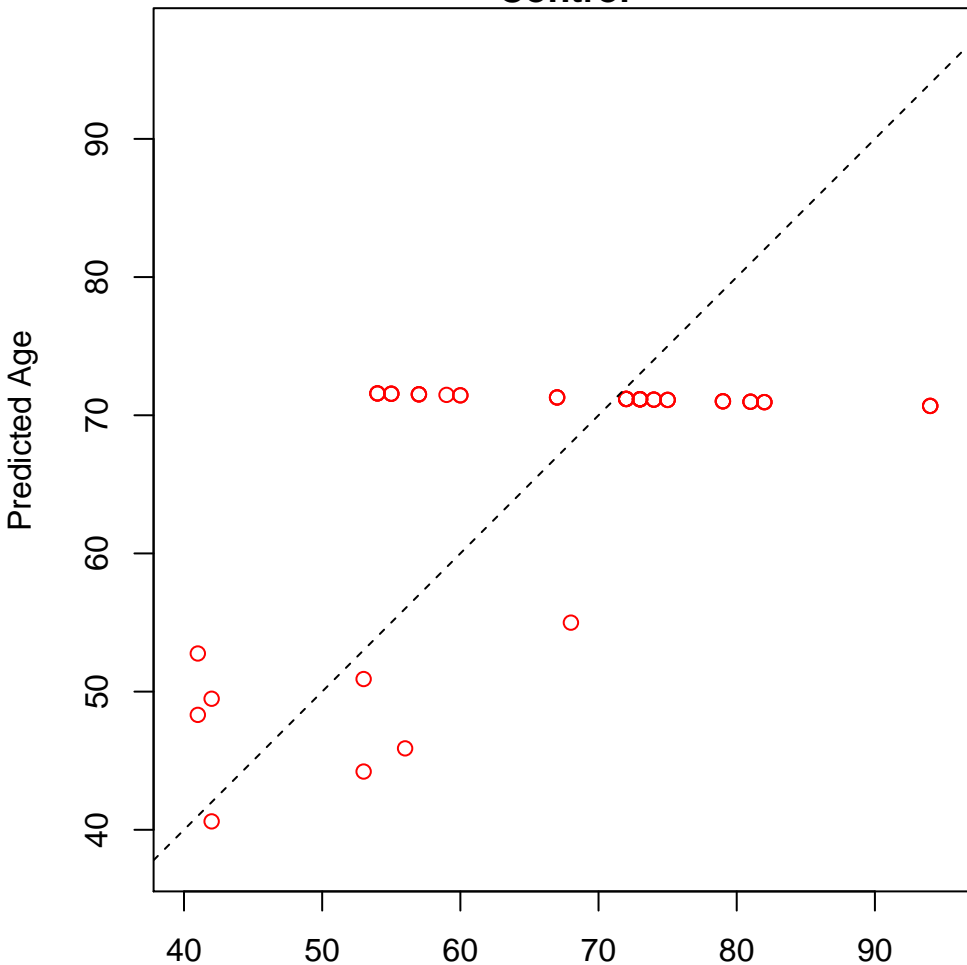
Test



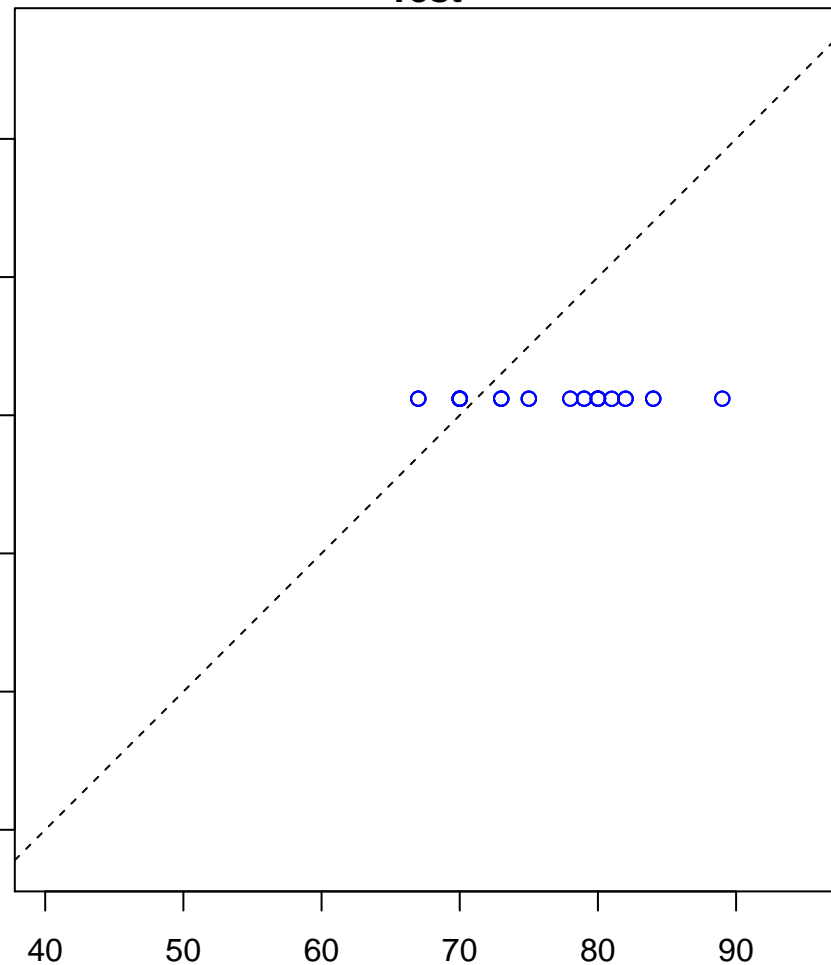
Actual Age

regulation of organelle organization (Score: 0.808666)

Control



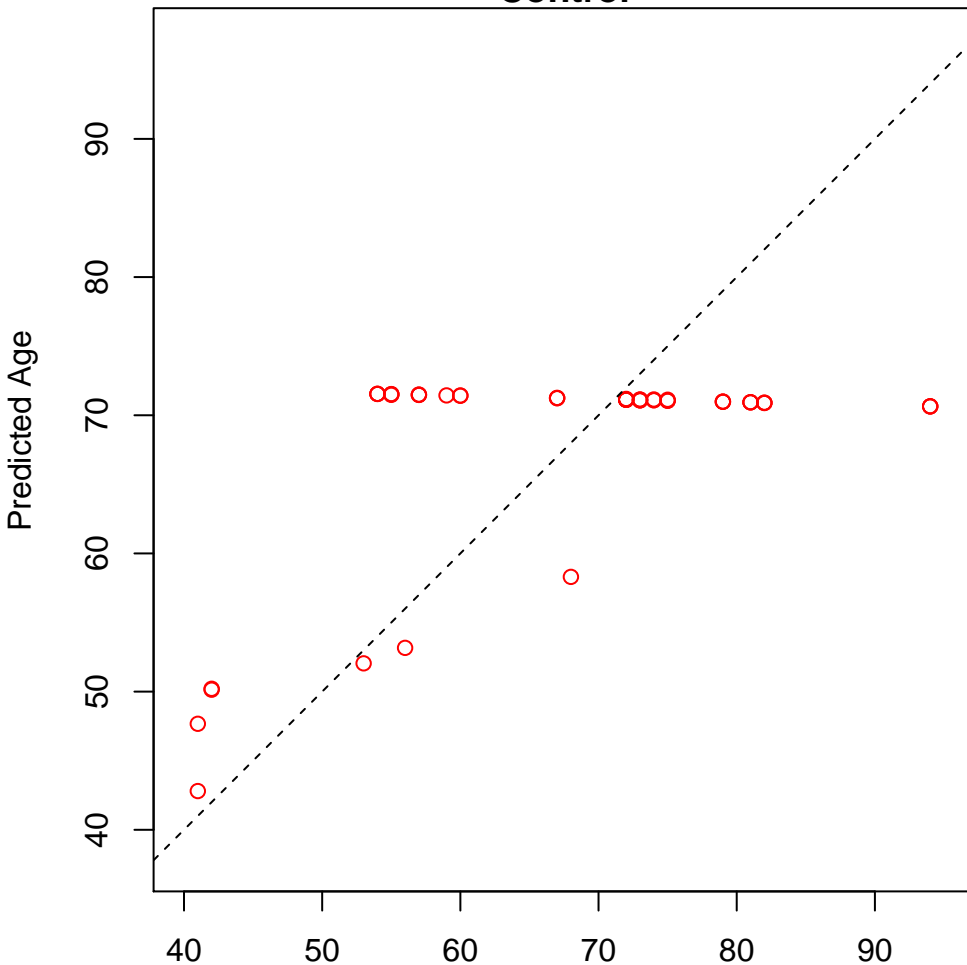
Test



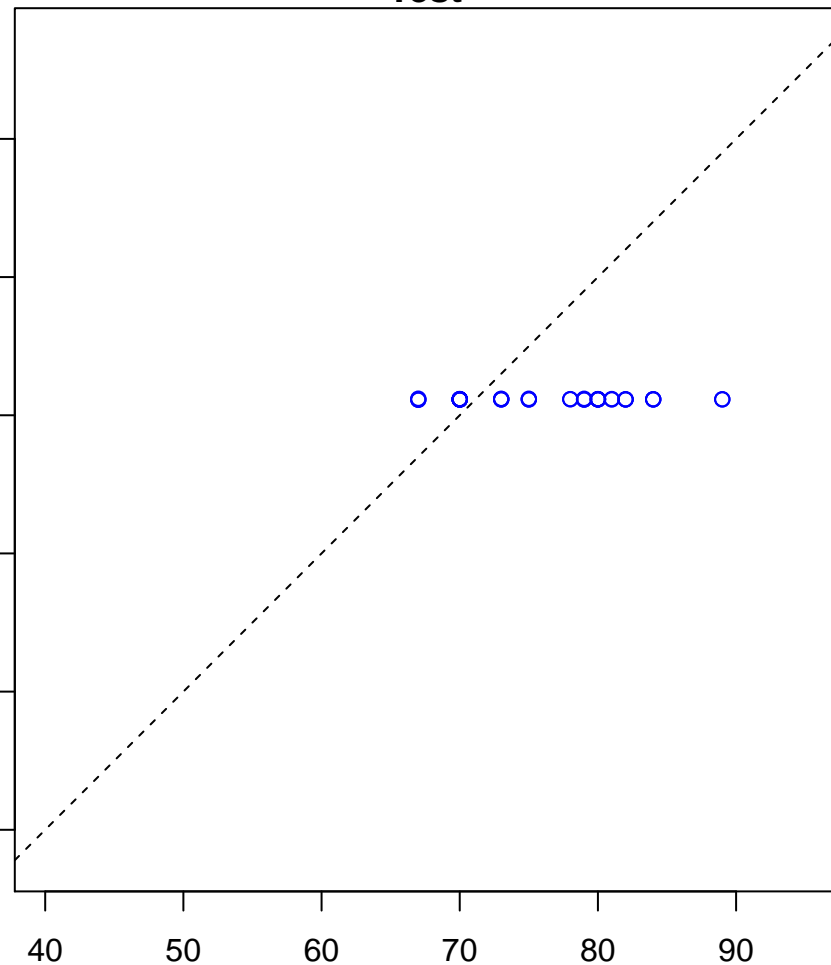
Actual Age

regulation of lymphocyte differentiation (Score: 0.808639)

Control



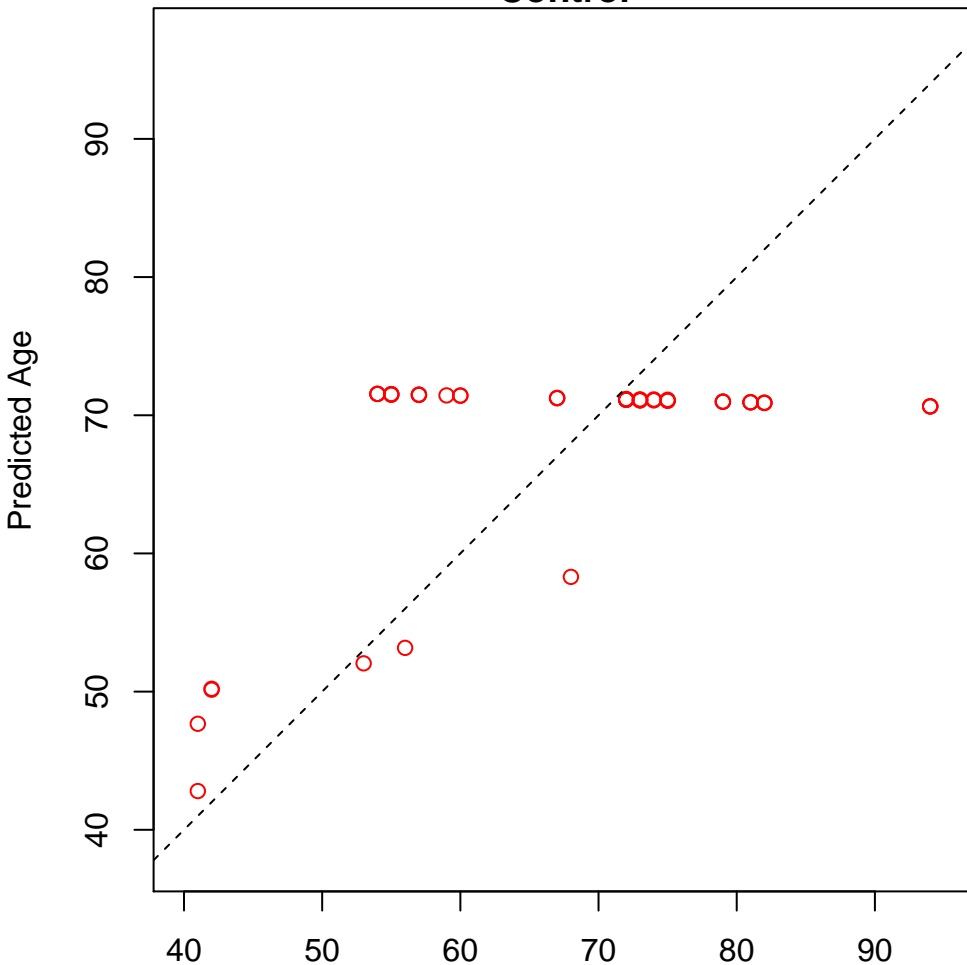
Test



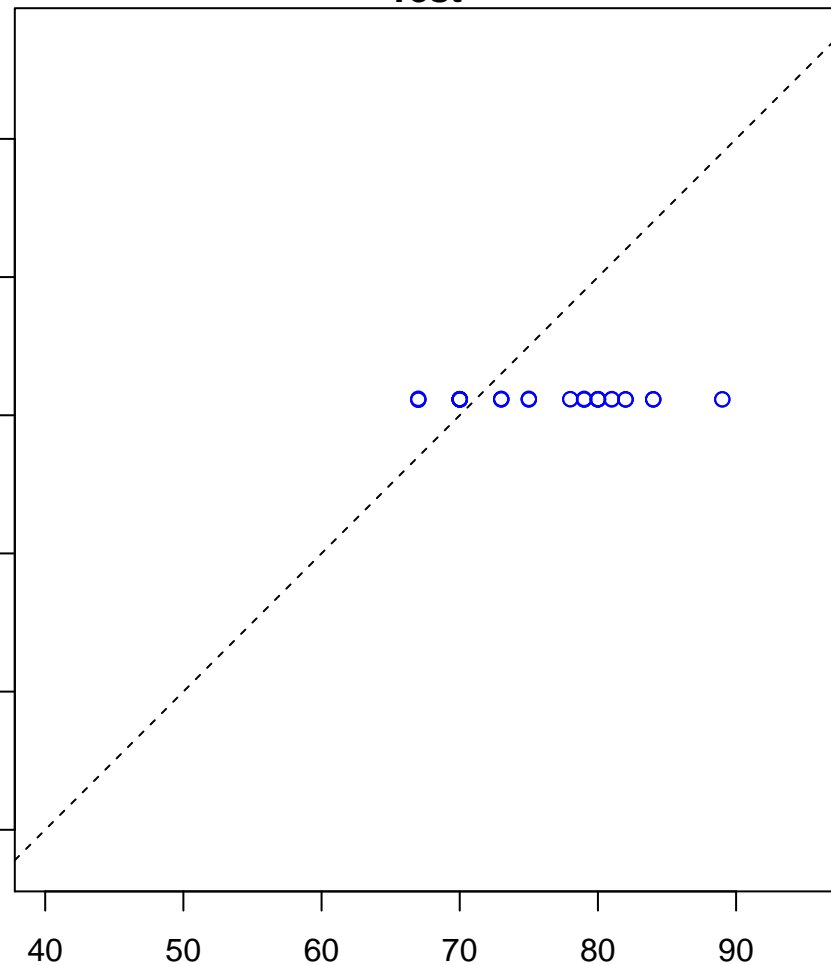
Actual Age

regulation of leukocyte differentiation (Score: 0.808639)

Control

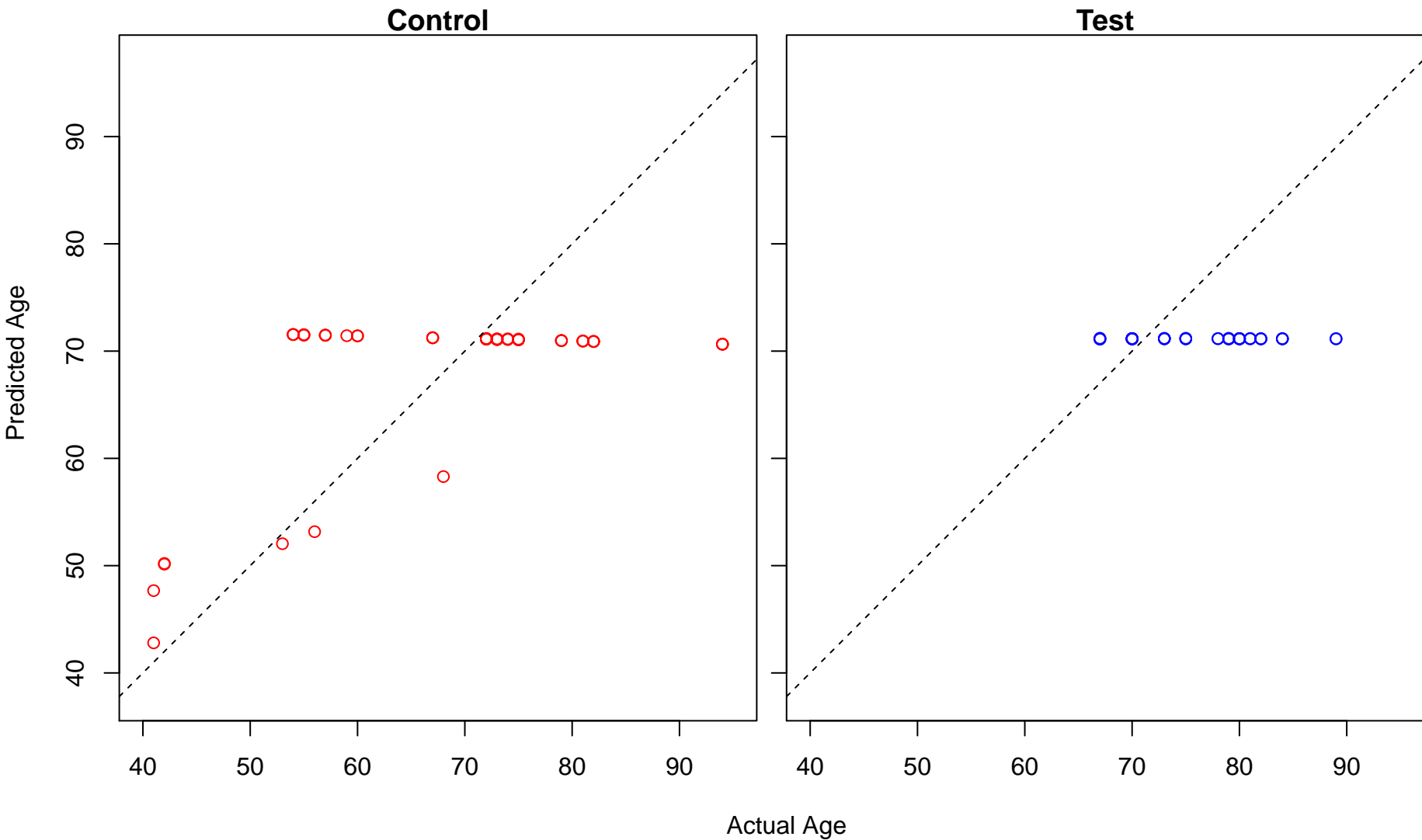


Test



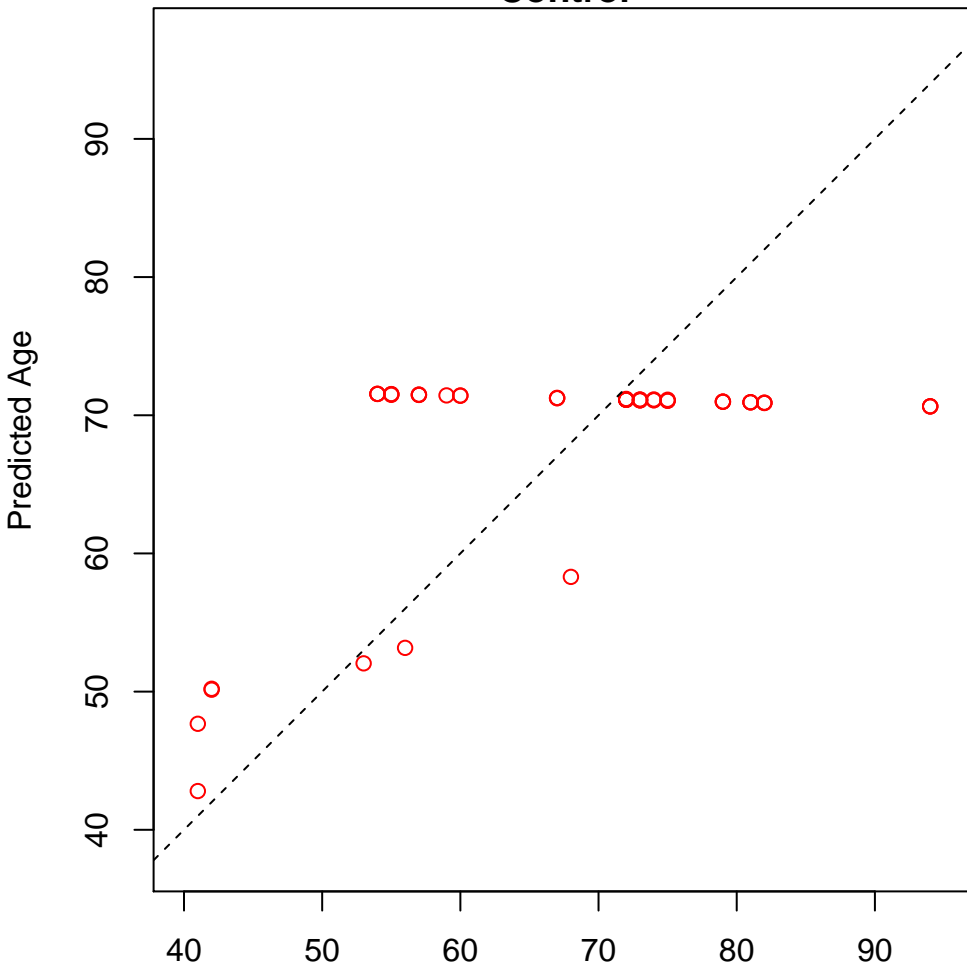
Actual Age

positive regulation of leukocyte differentiation (Score: 0.808639)

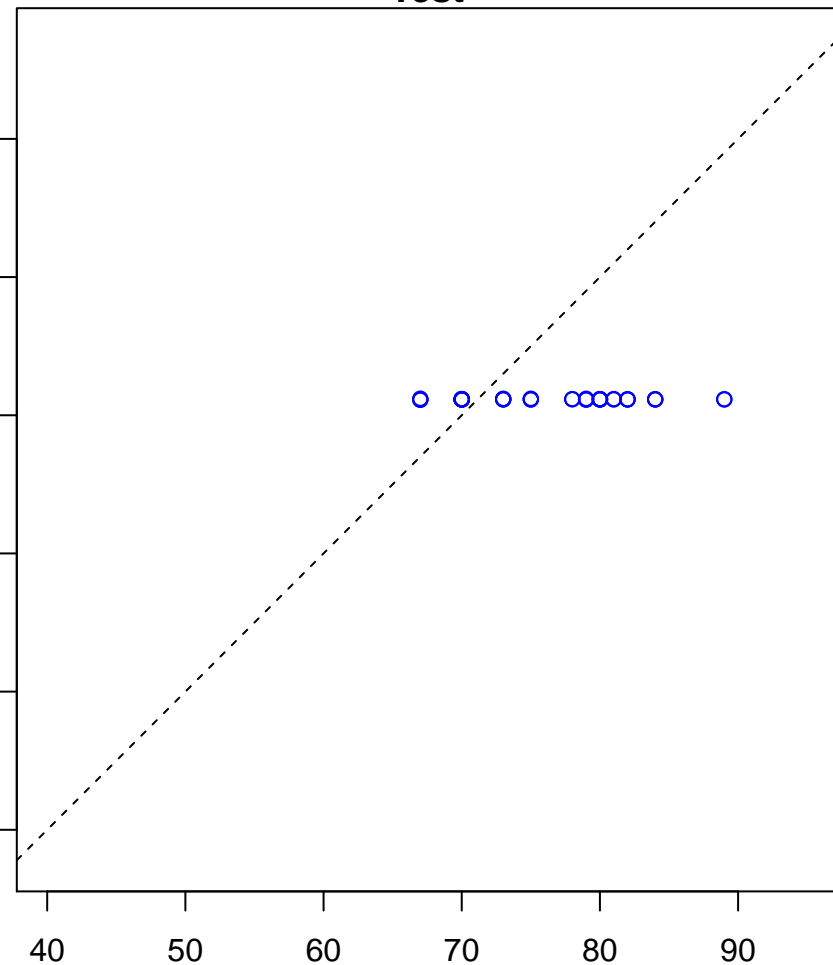


positive regulation of hemopoiesis (Score: 0.808639)

Control

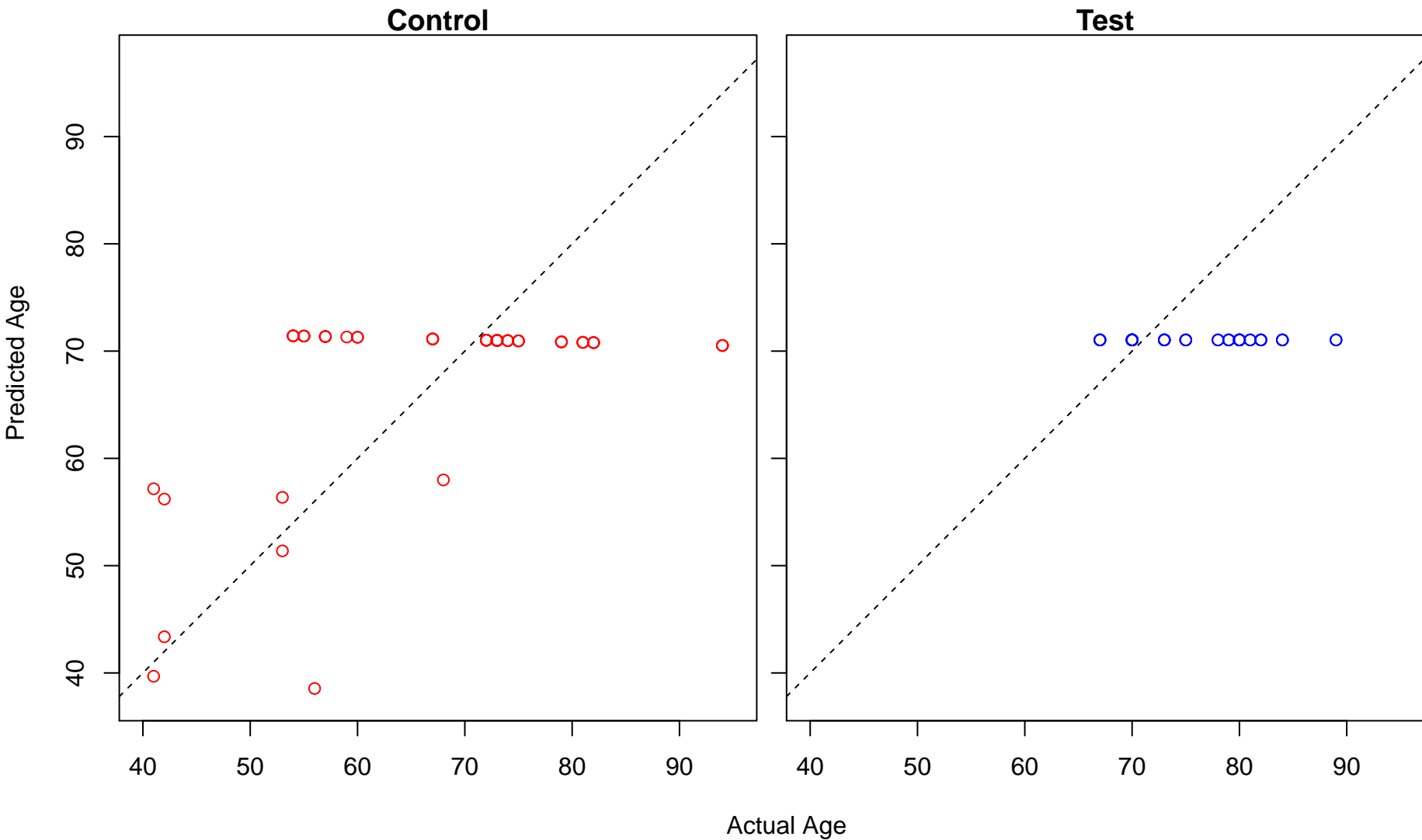


Test



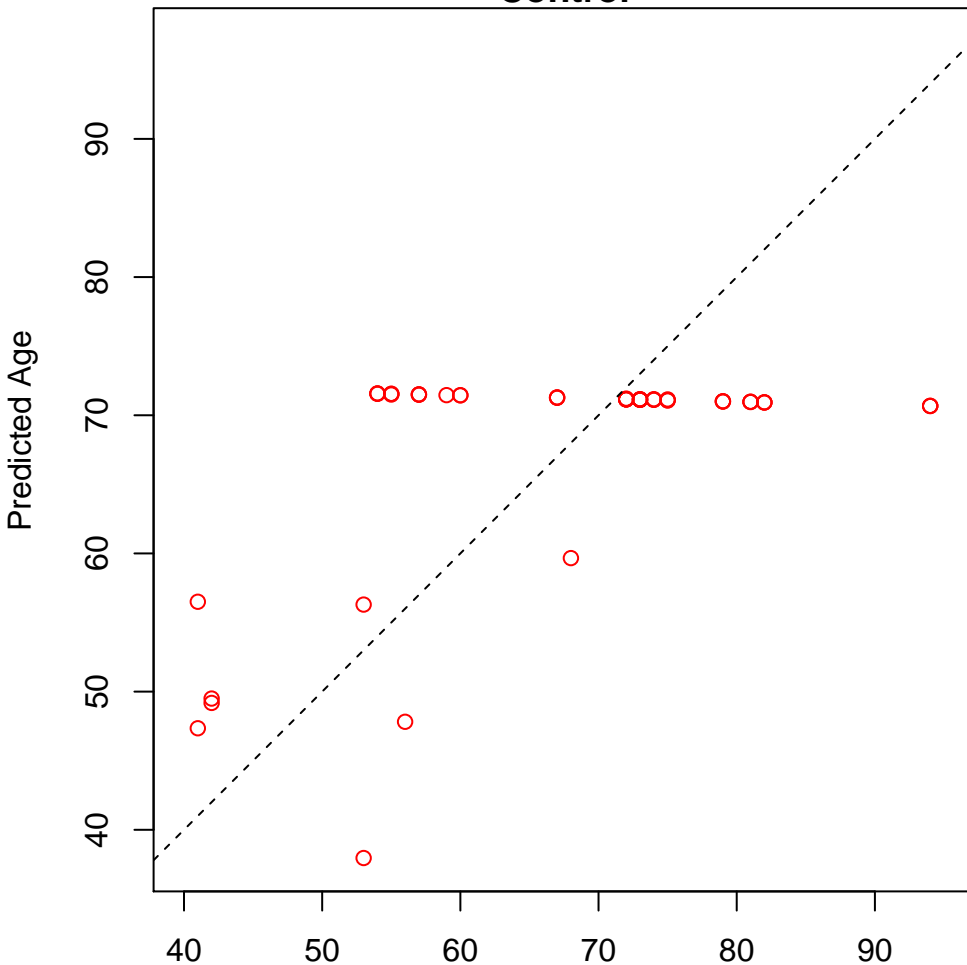
Actual Age

regulation of cellular response to growth factor stimulus (Score: 0.808634)

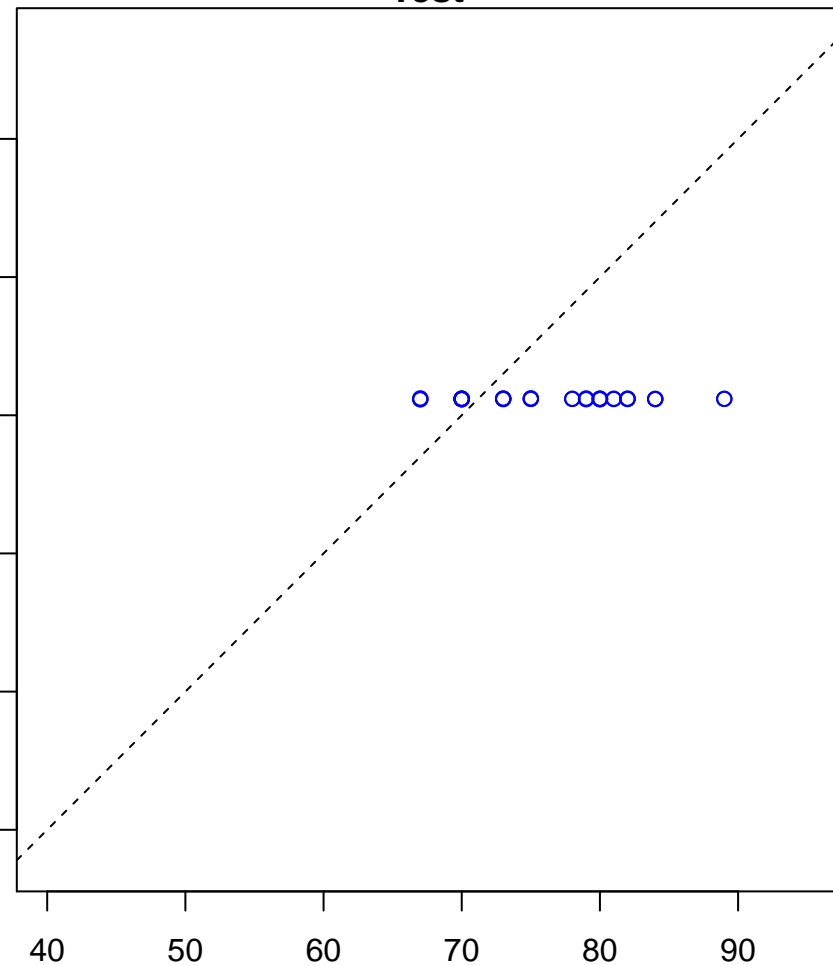


regulation of epithelial cell apoptotic process (Score: 0.808585)

Control

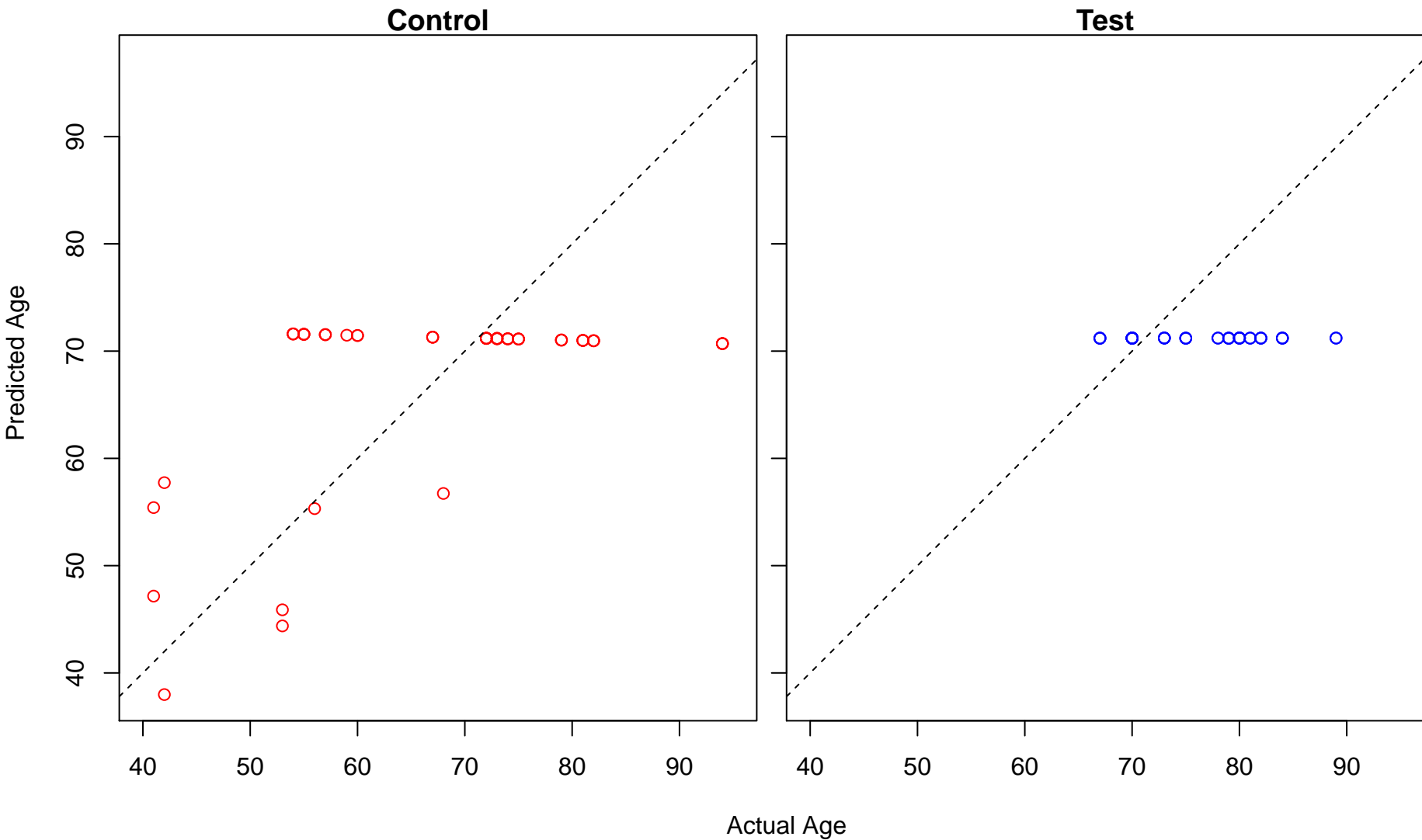


Test

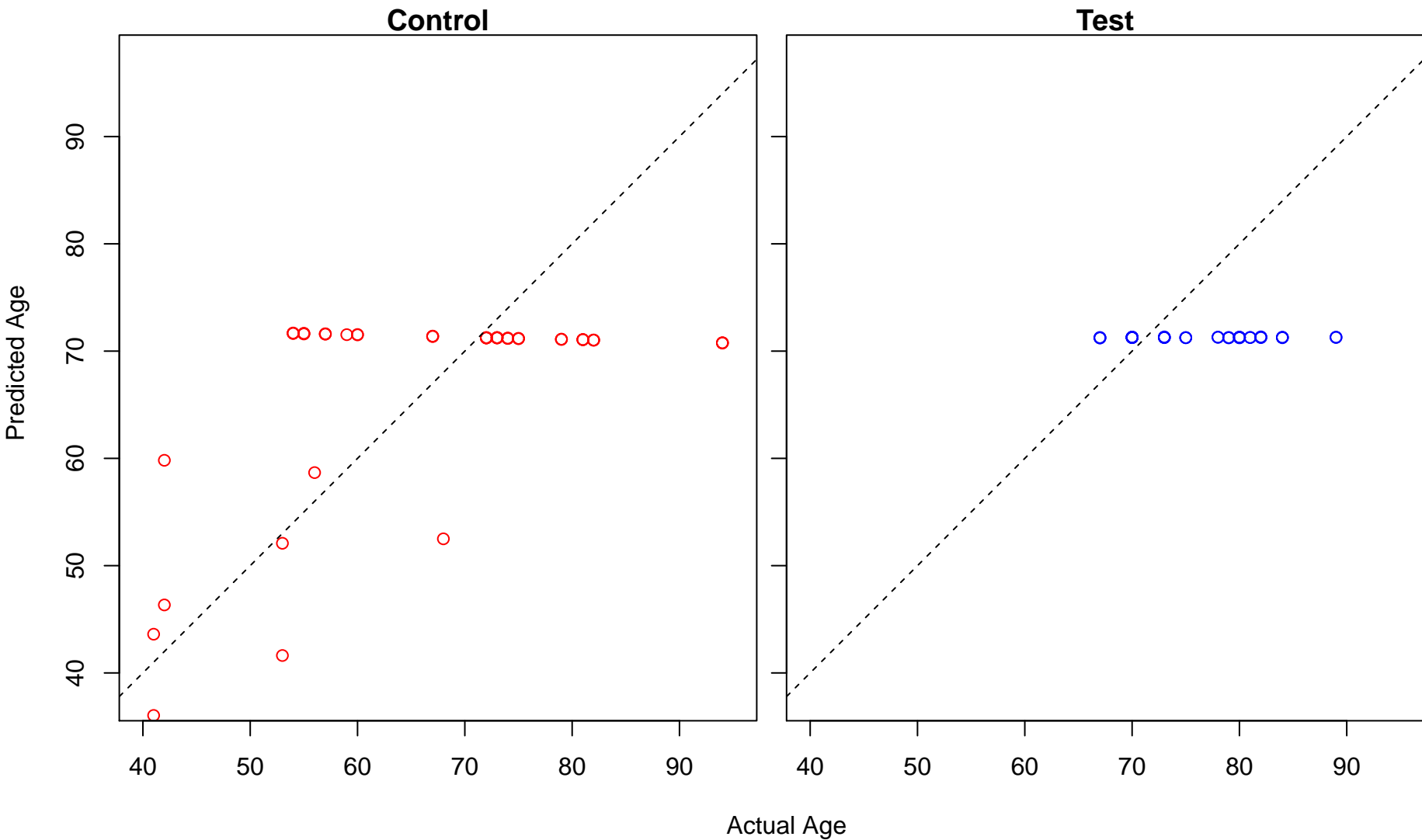


Actual Age

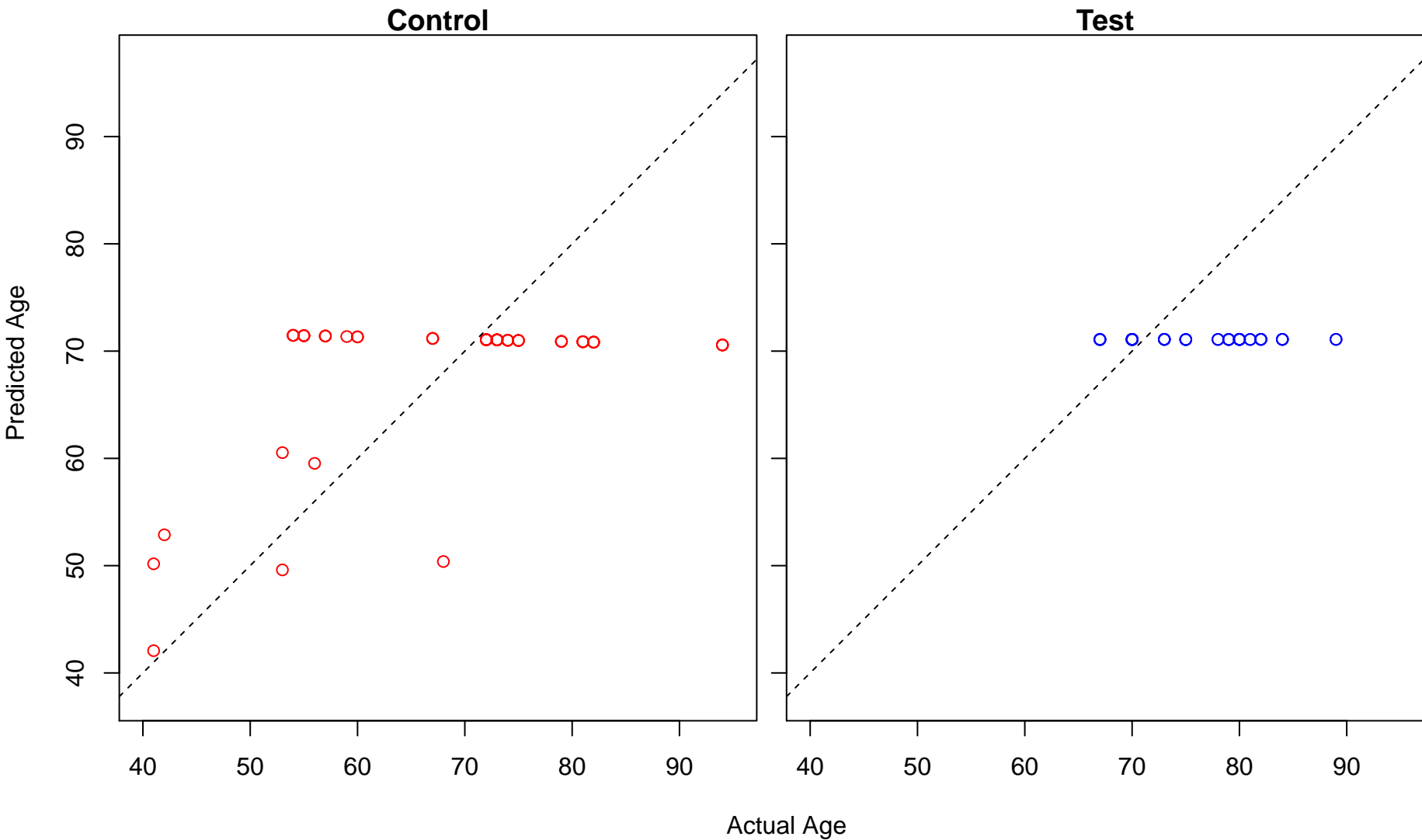
positive regulation of immune effector process (Score: 0.808420)



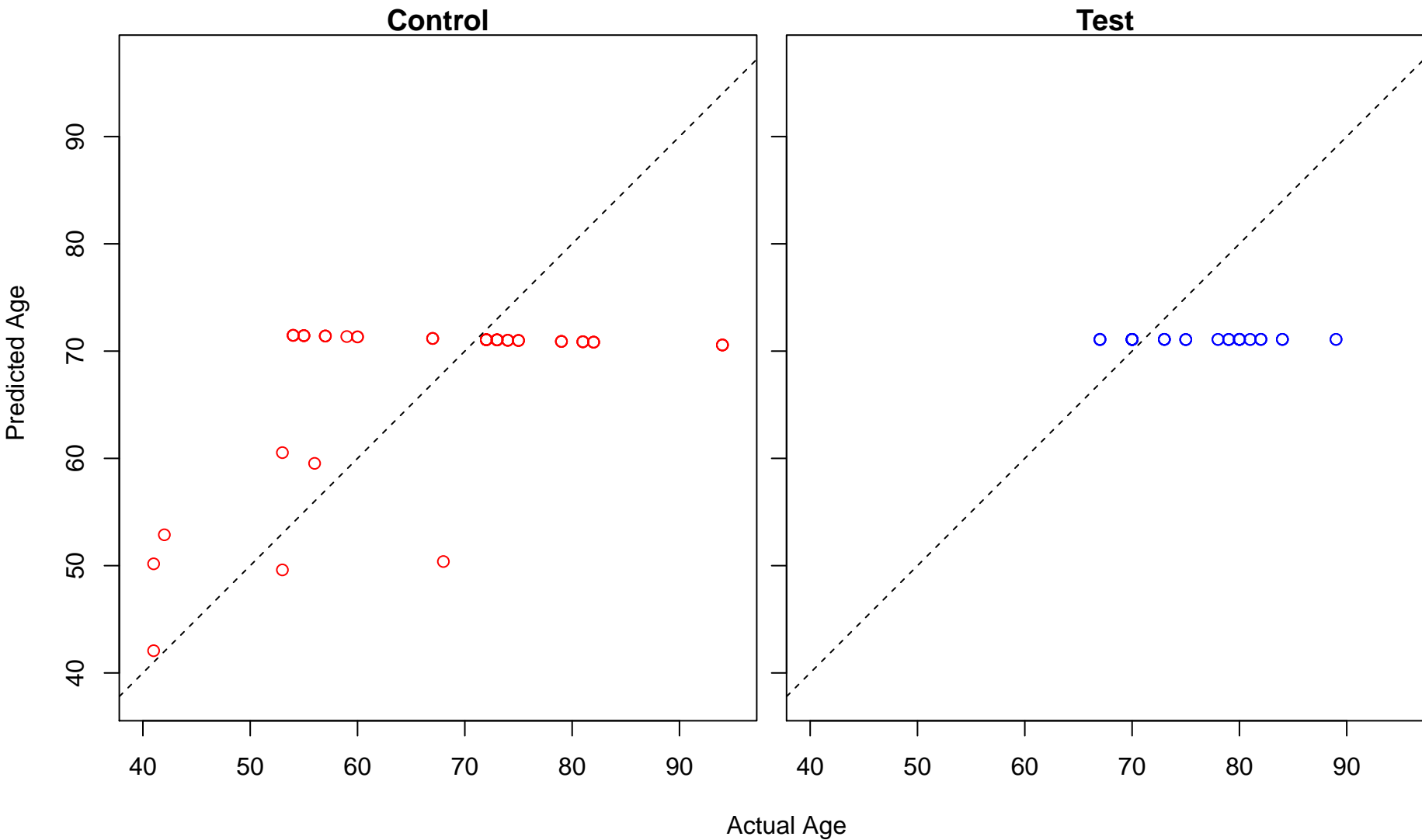
protein maturation (Score: 0.808310)



spindle organization (Score: 0.808235)

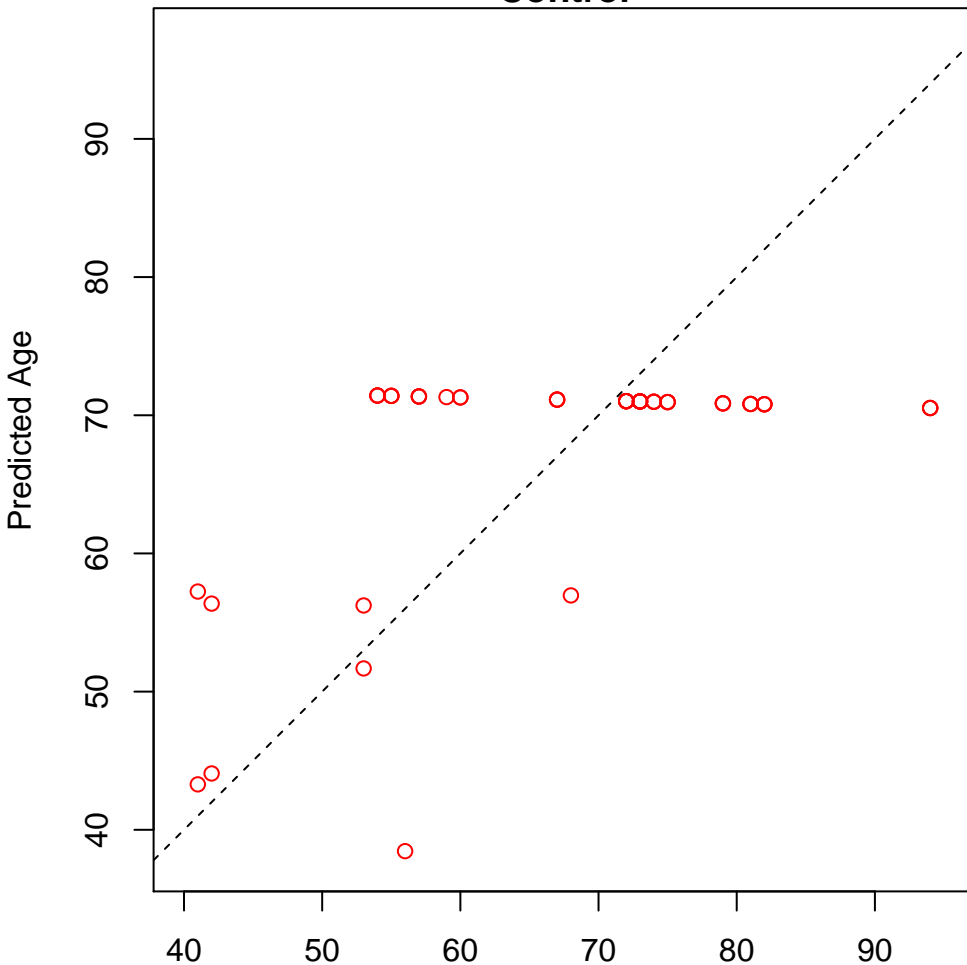


microtubule cytoskeleton organization involved in mitosis (Score: 0.808235)

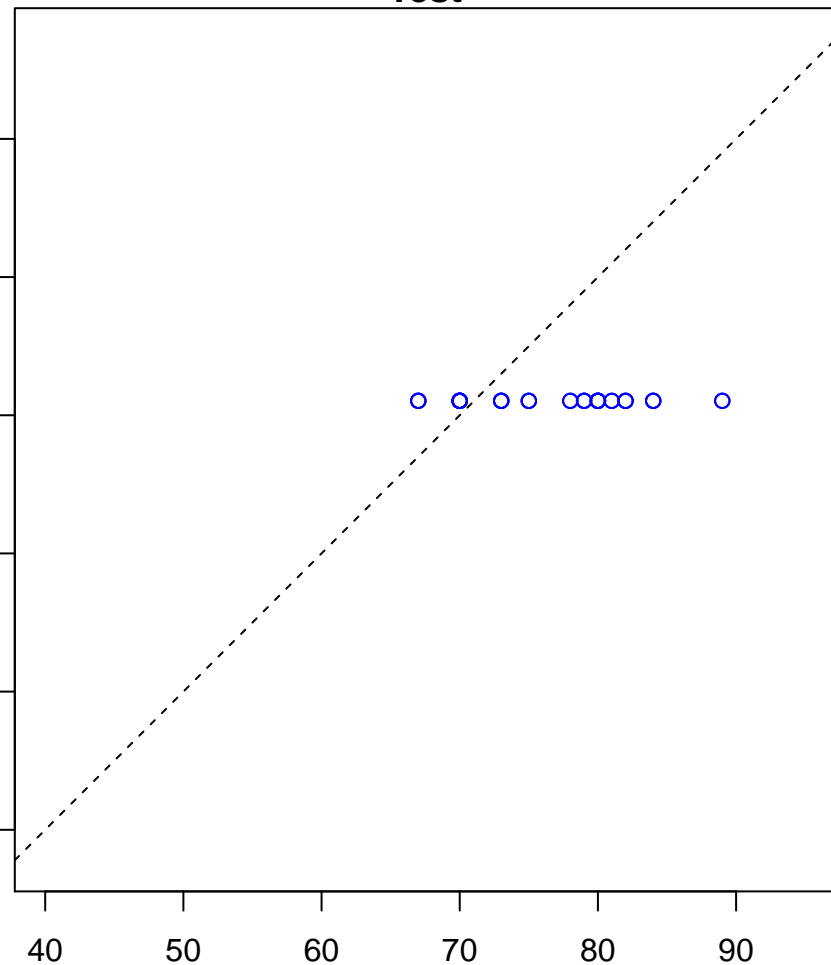


DNA biosynthetic process (Score: 0.808217)

Control

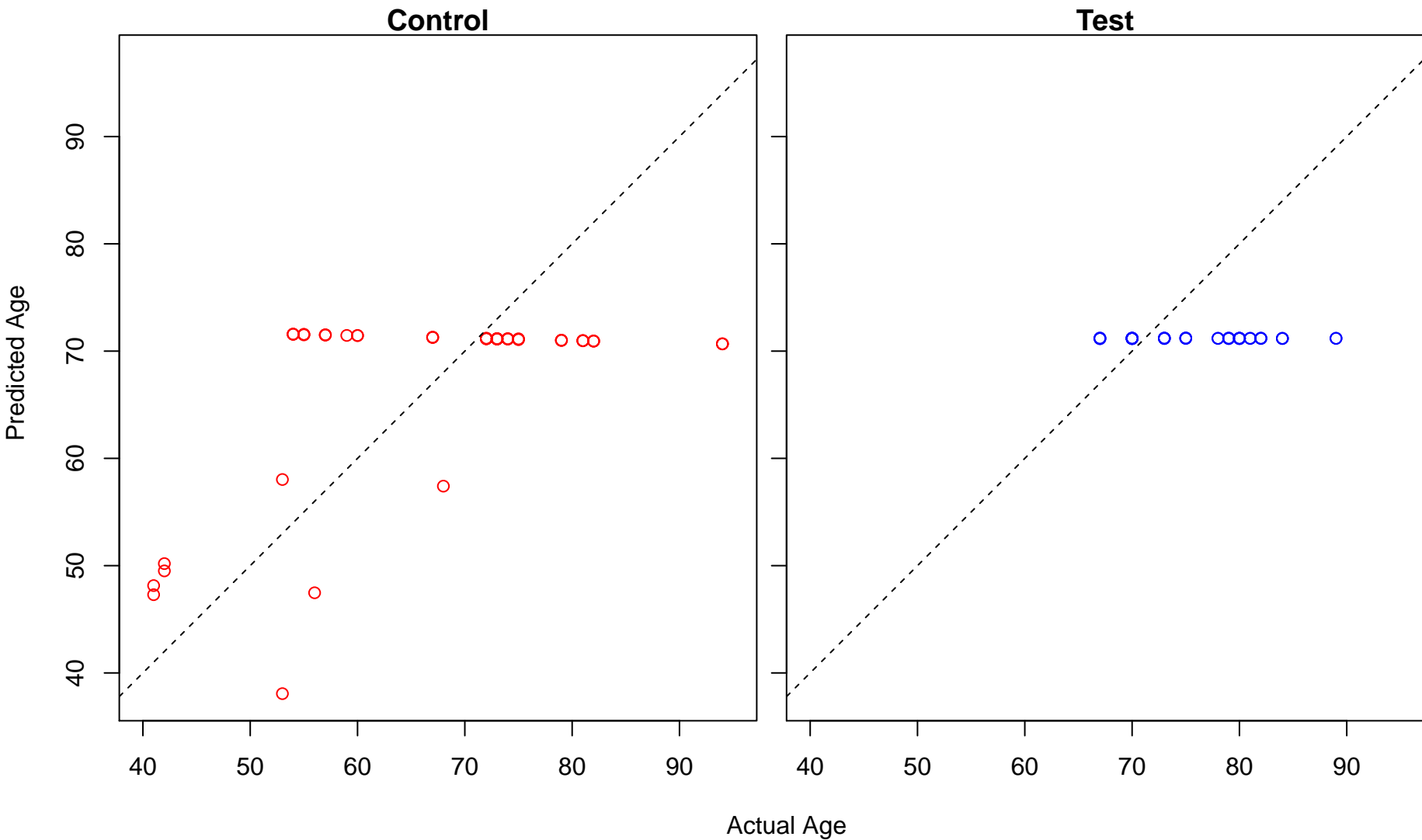


Test



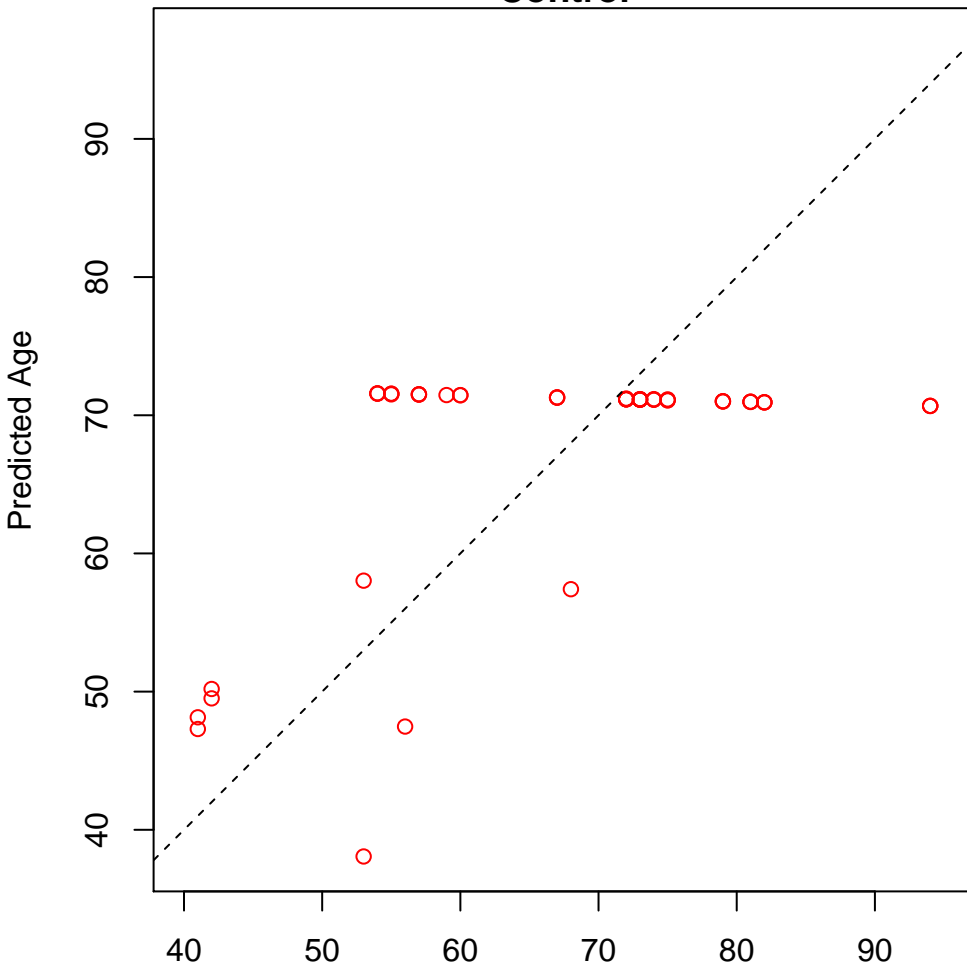
Actual Age

negative regulation of nucleocytoplasmic transport (Score: 0.808197)

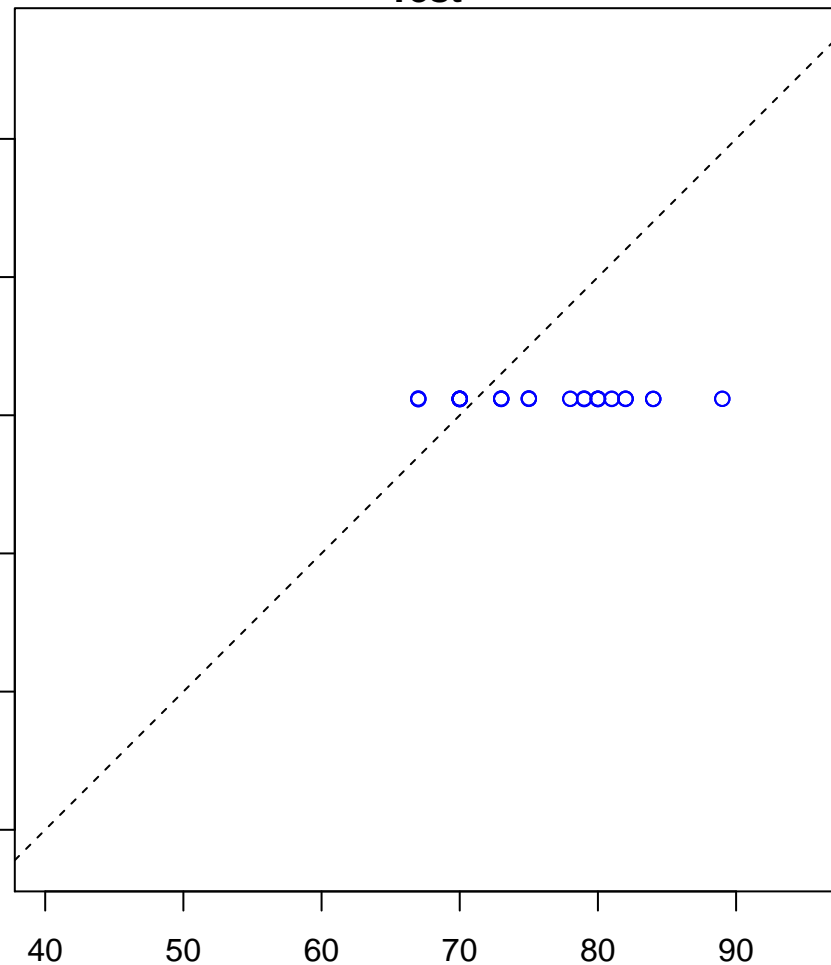


regulation of protein export from nucleus (Score: 0.808197)

Control

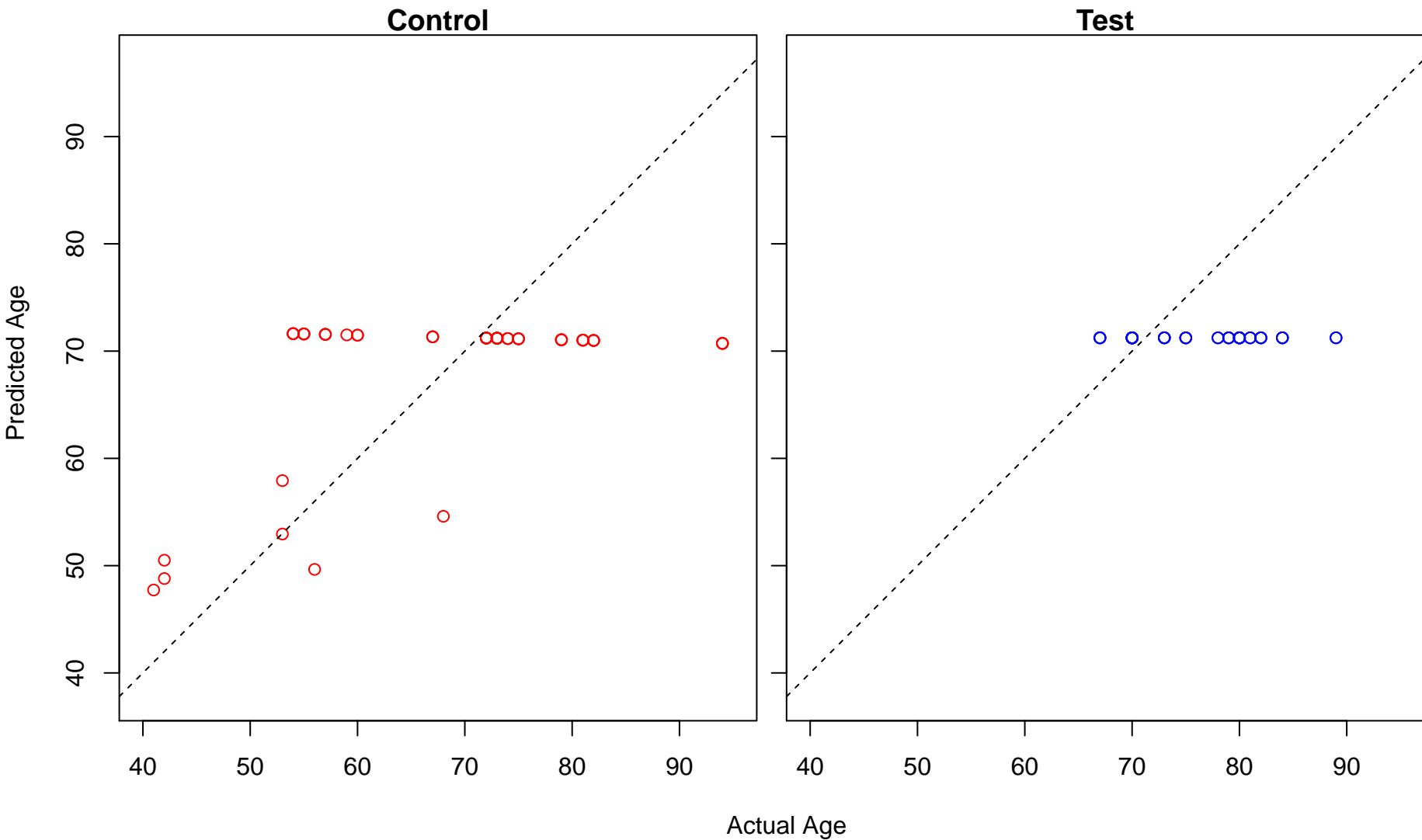


Test

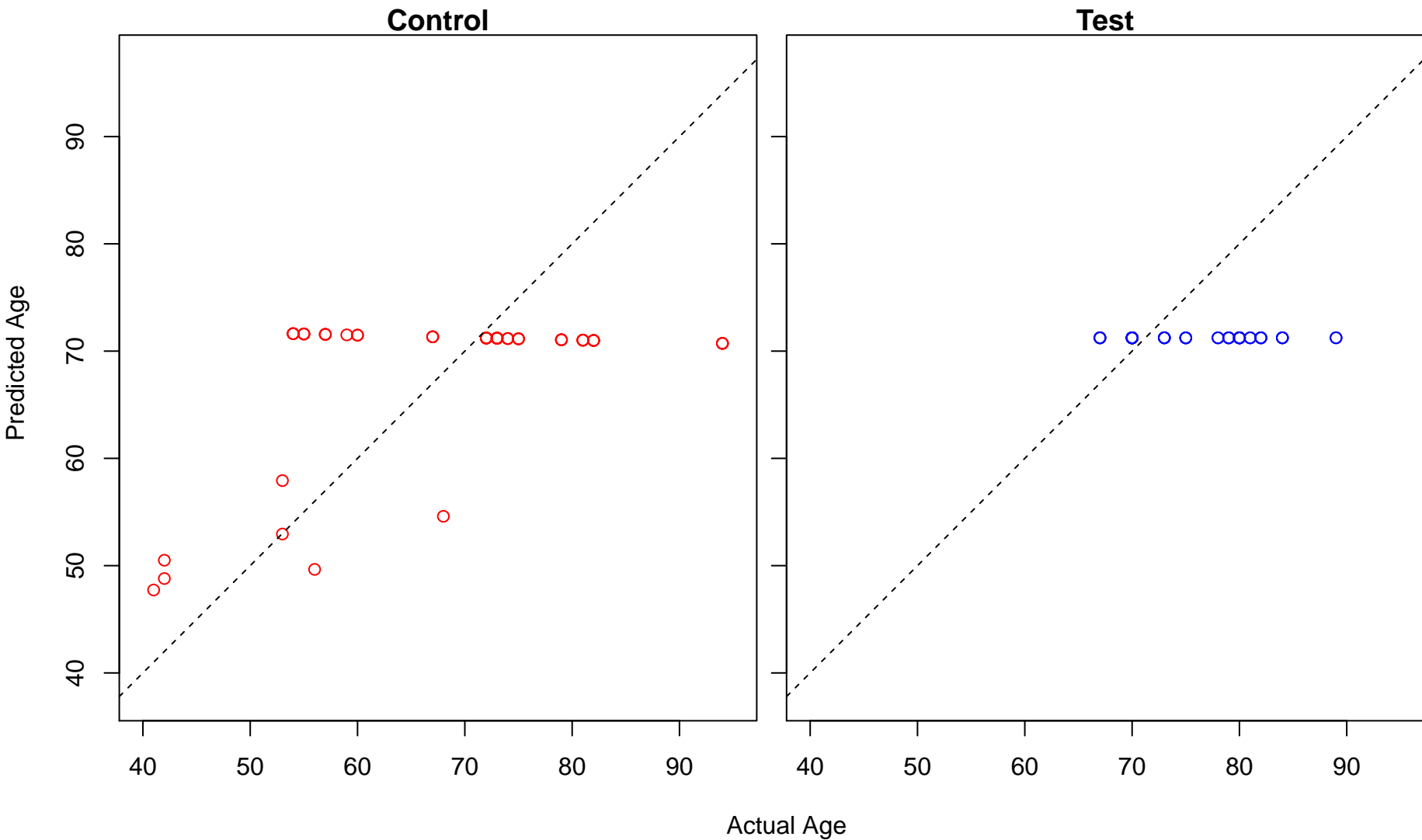


Actual Age

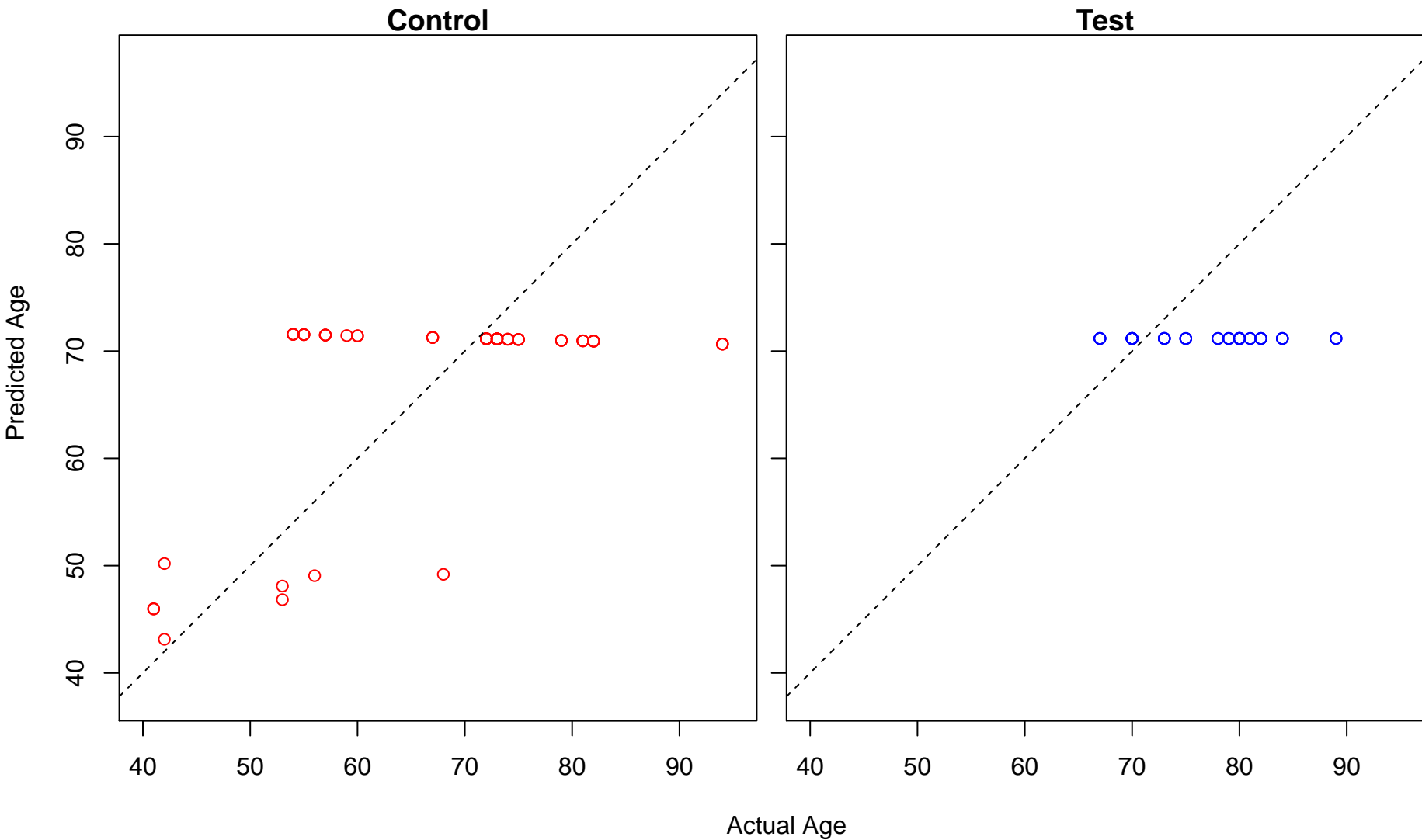
multi-organism transport (Score: 0.808156)



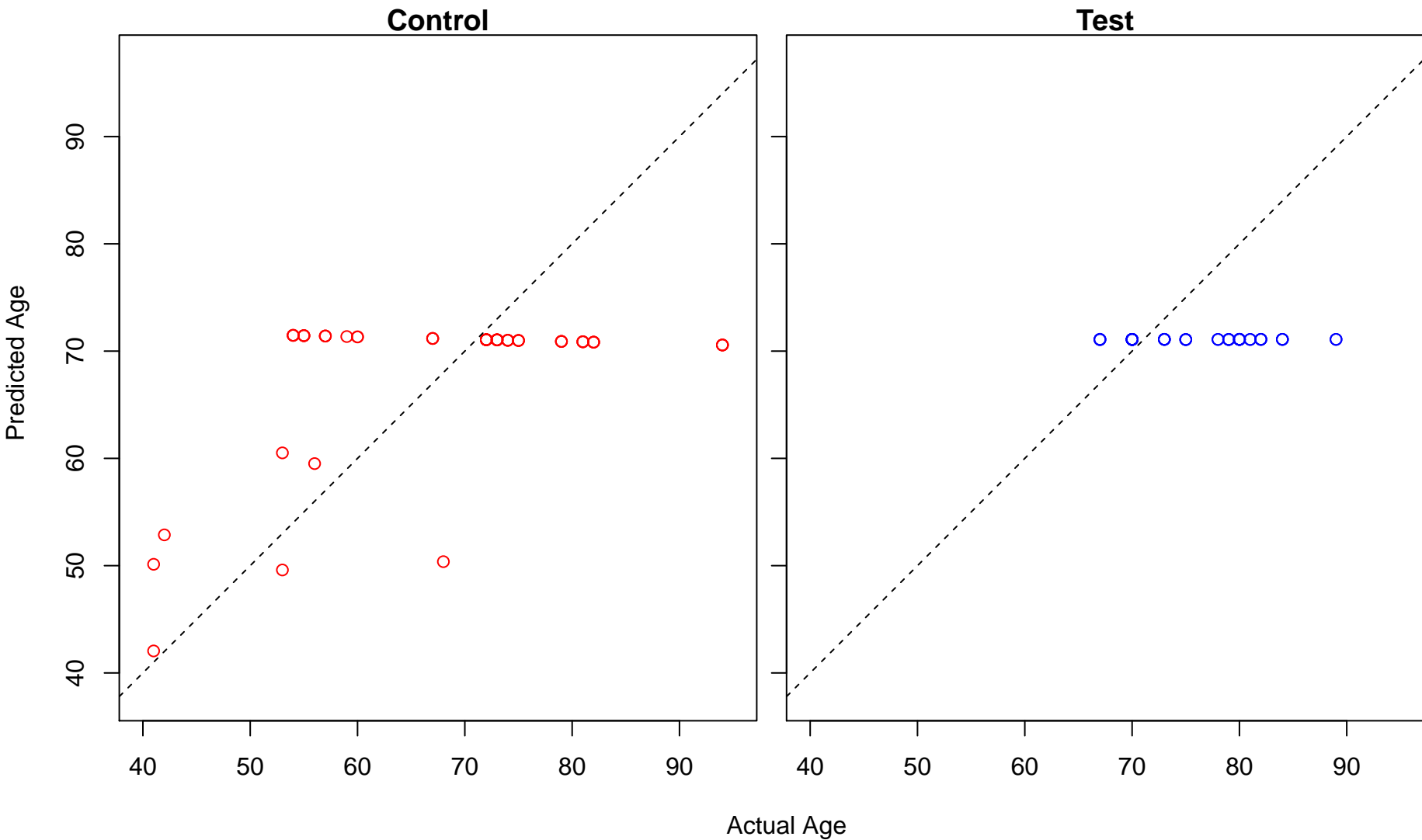
multi-organism localization (Score: 0.808156)



regulation of signal transduction (Score: 0.808155)

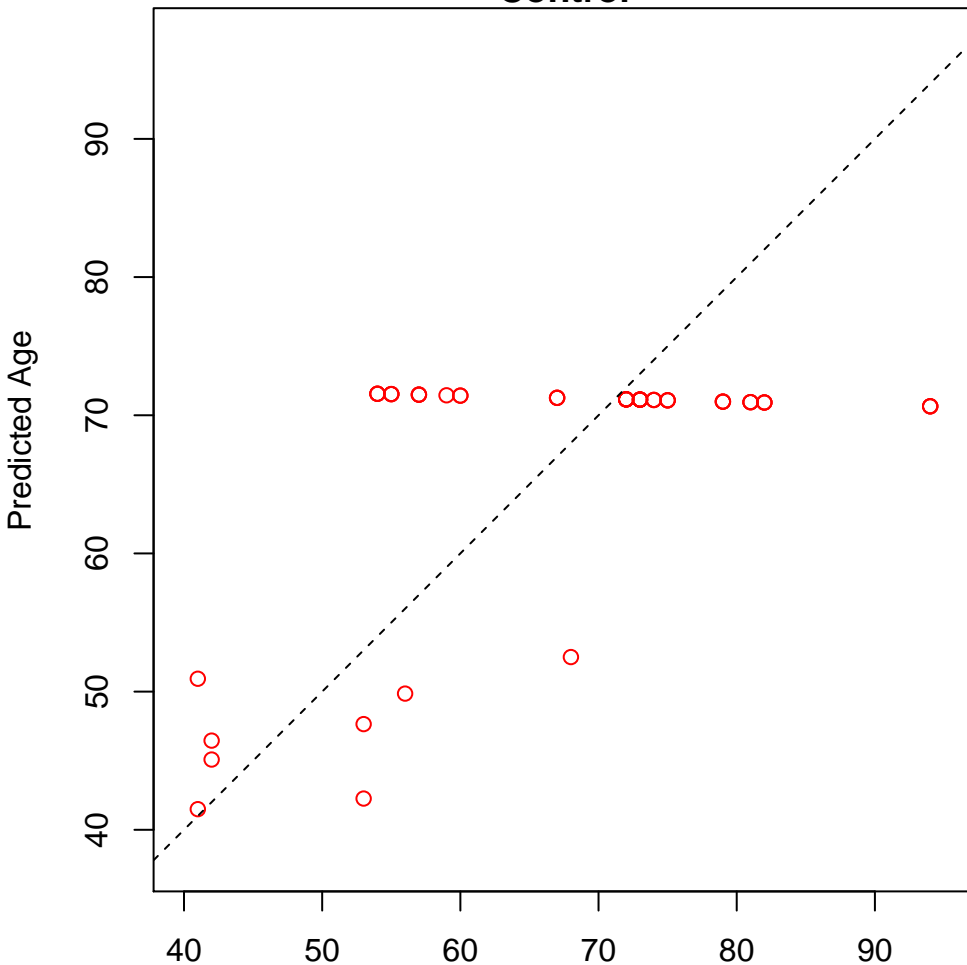


mitotic spindle organization (Score: 0.808154)

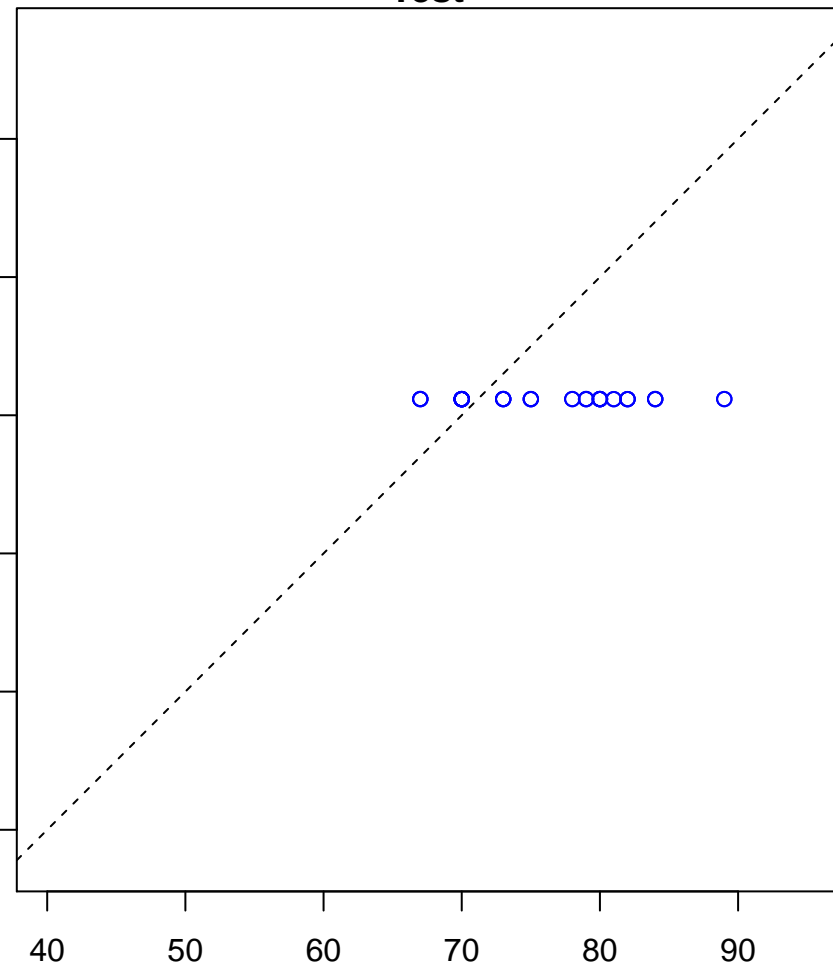


regulation of defense response (Score: 0.808098)

Control

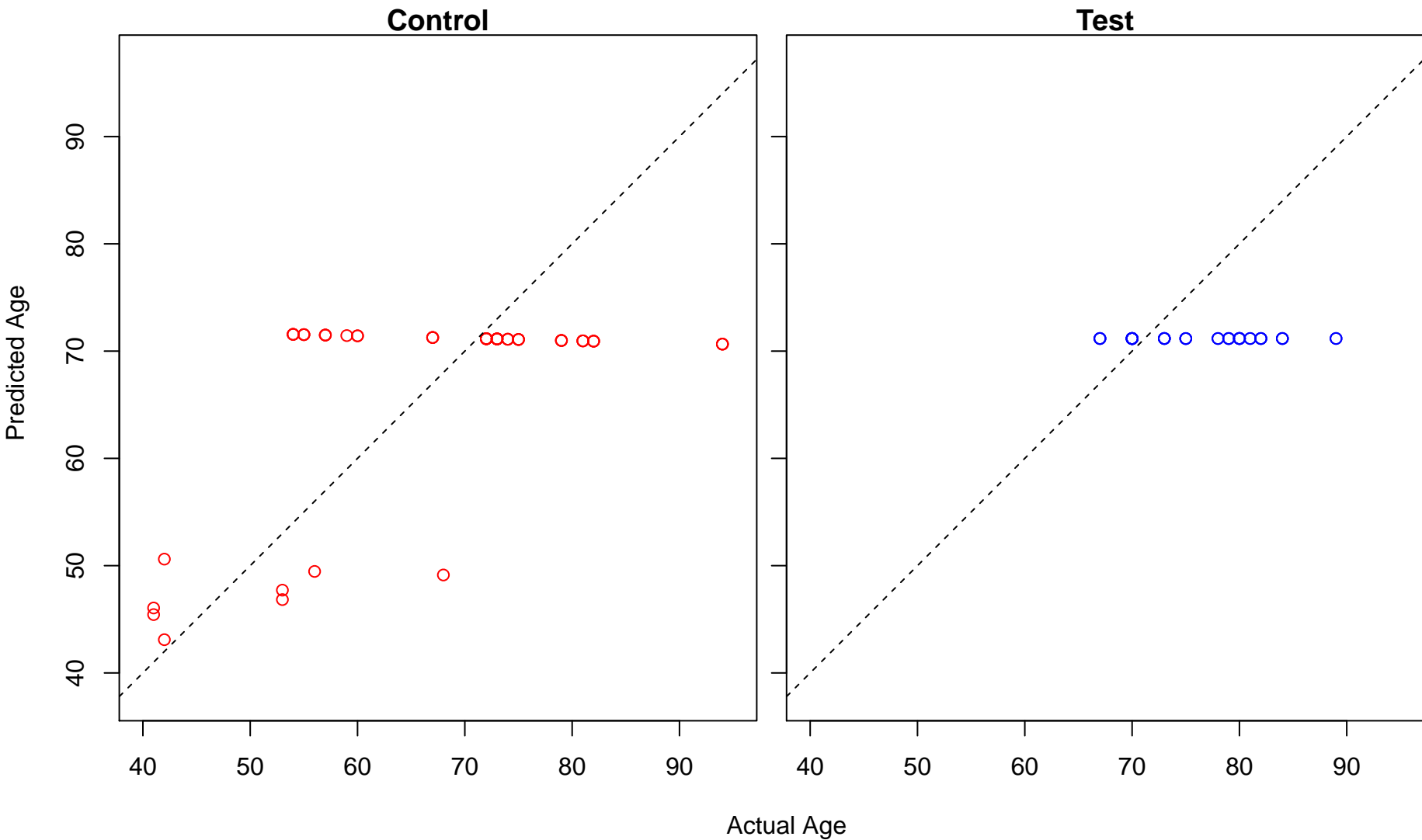


Test

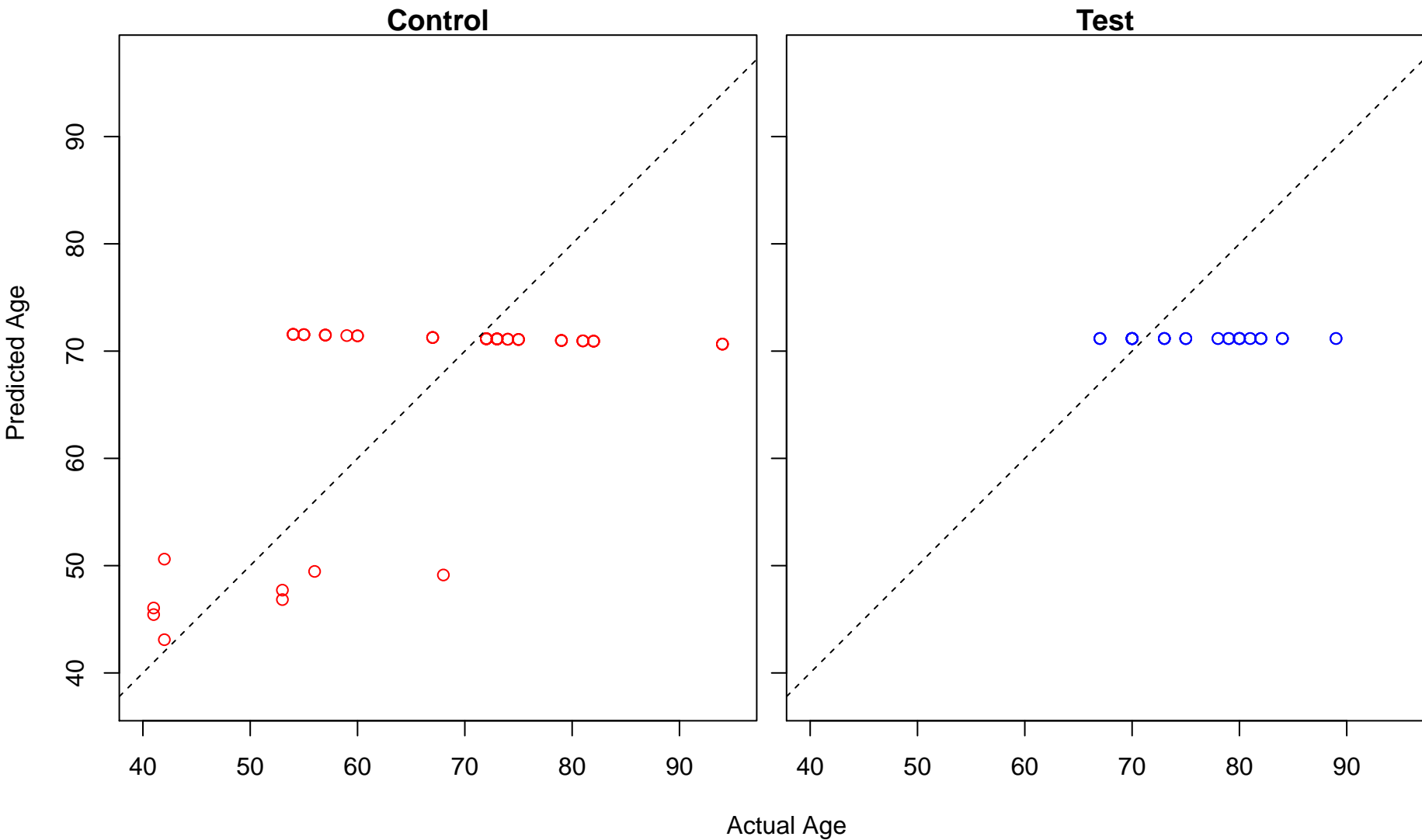


Actual Age

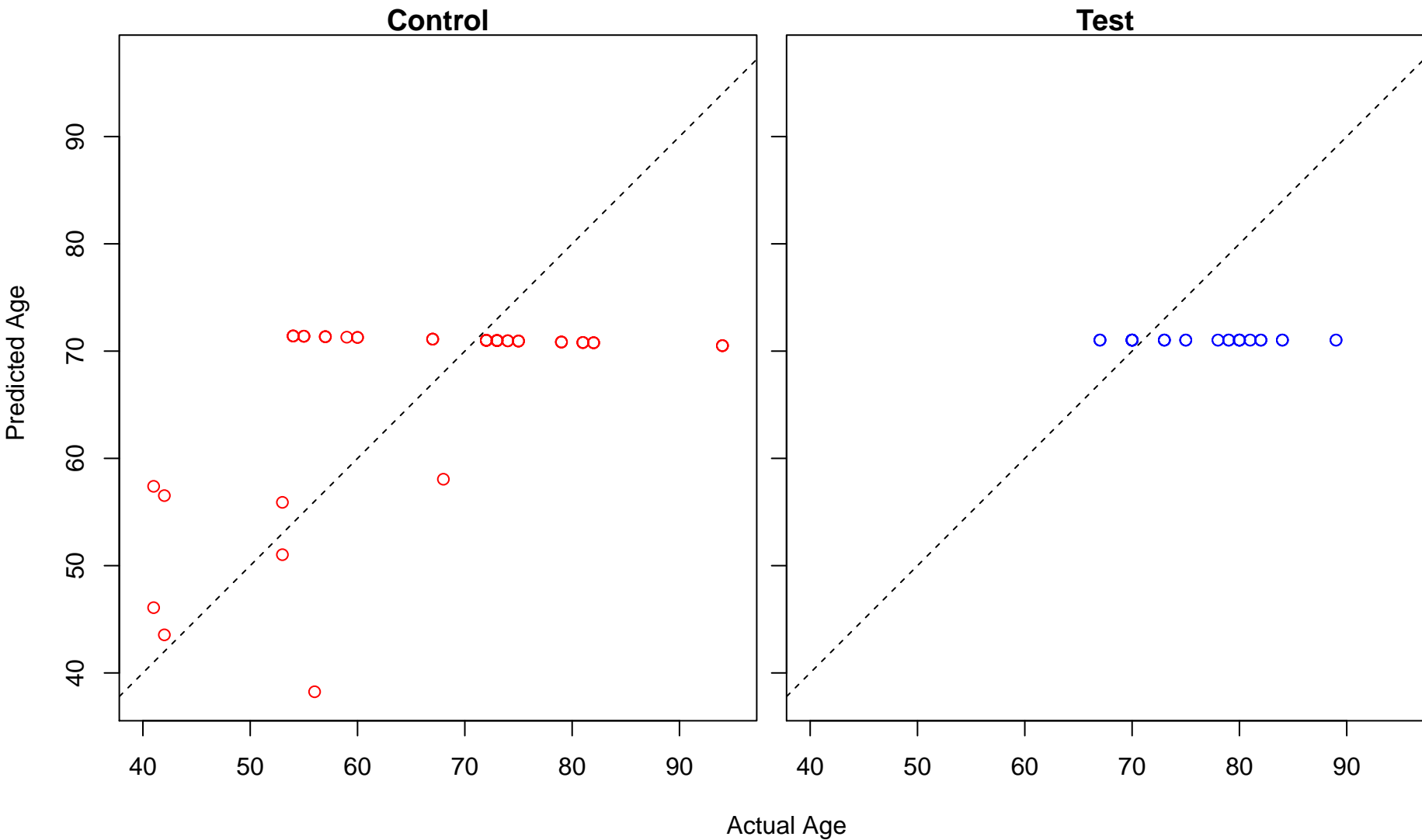
regulation of cell communication (Score: 0.808072)



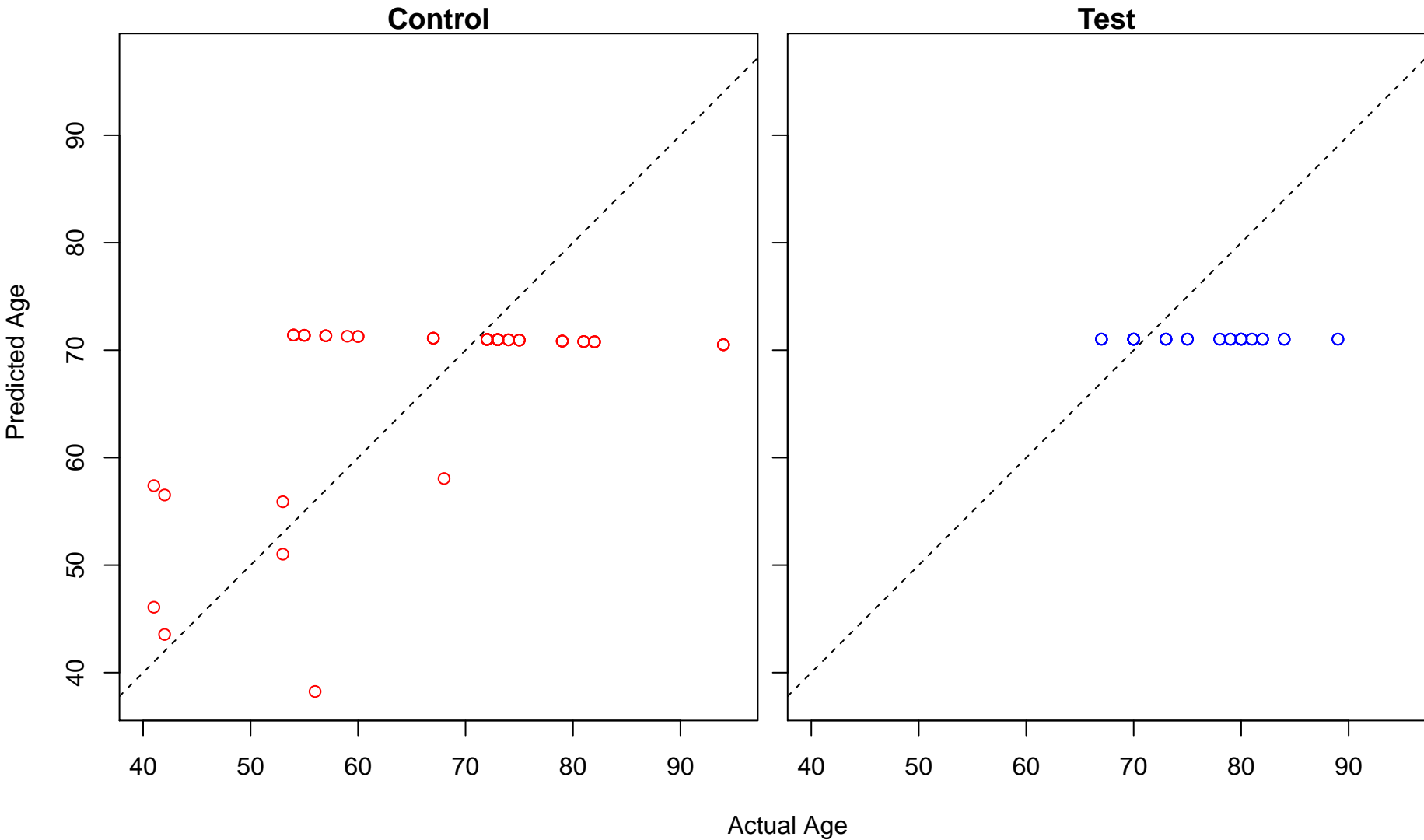
regulation of signaling (Score: 0.808072)



regulation of cytokine-mediated signaling pathway (Score: 0.808069)

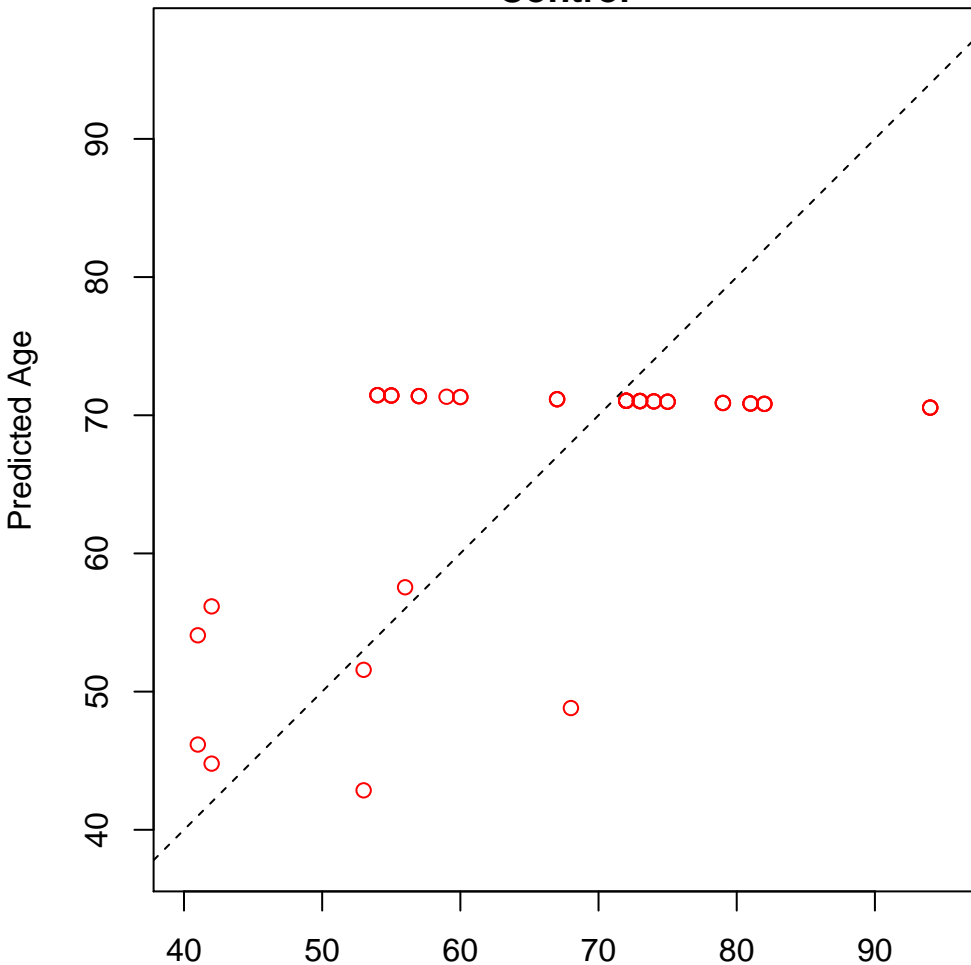


regulation of response to cytokine stimulus (Score: 0.808069)

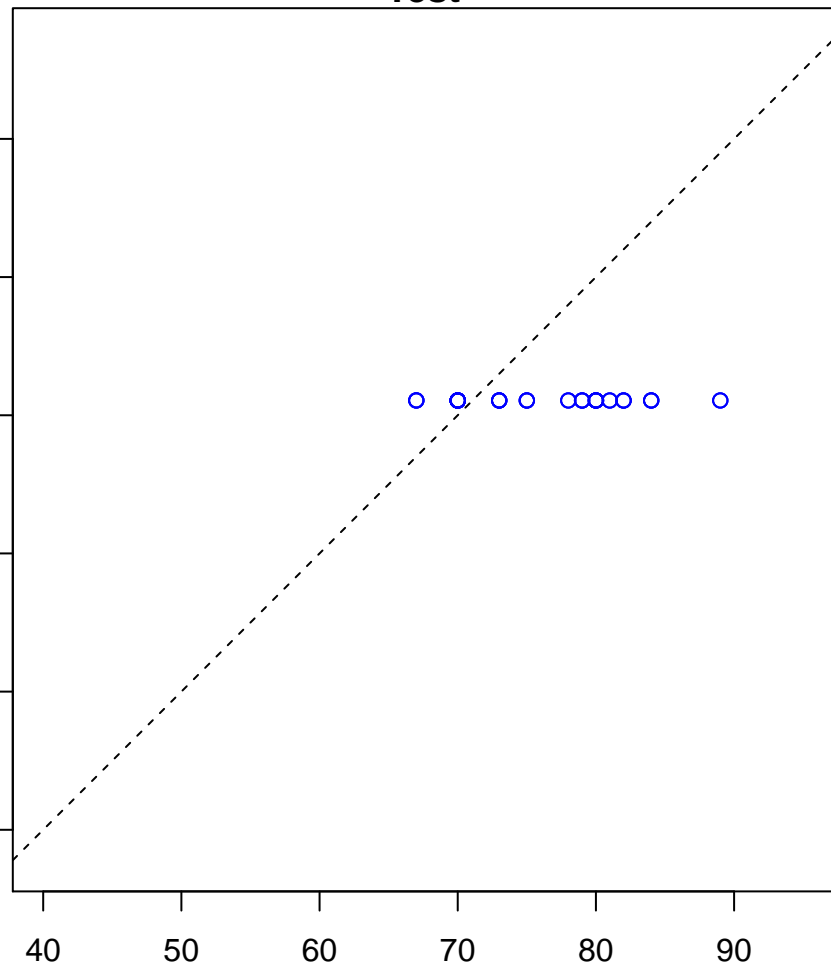


DNA-templated transcription, termination (Score: 0.807997)

Control

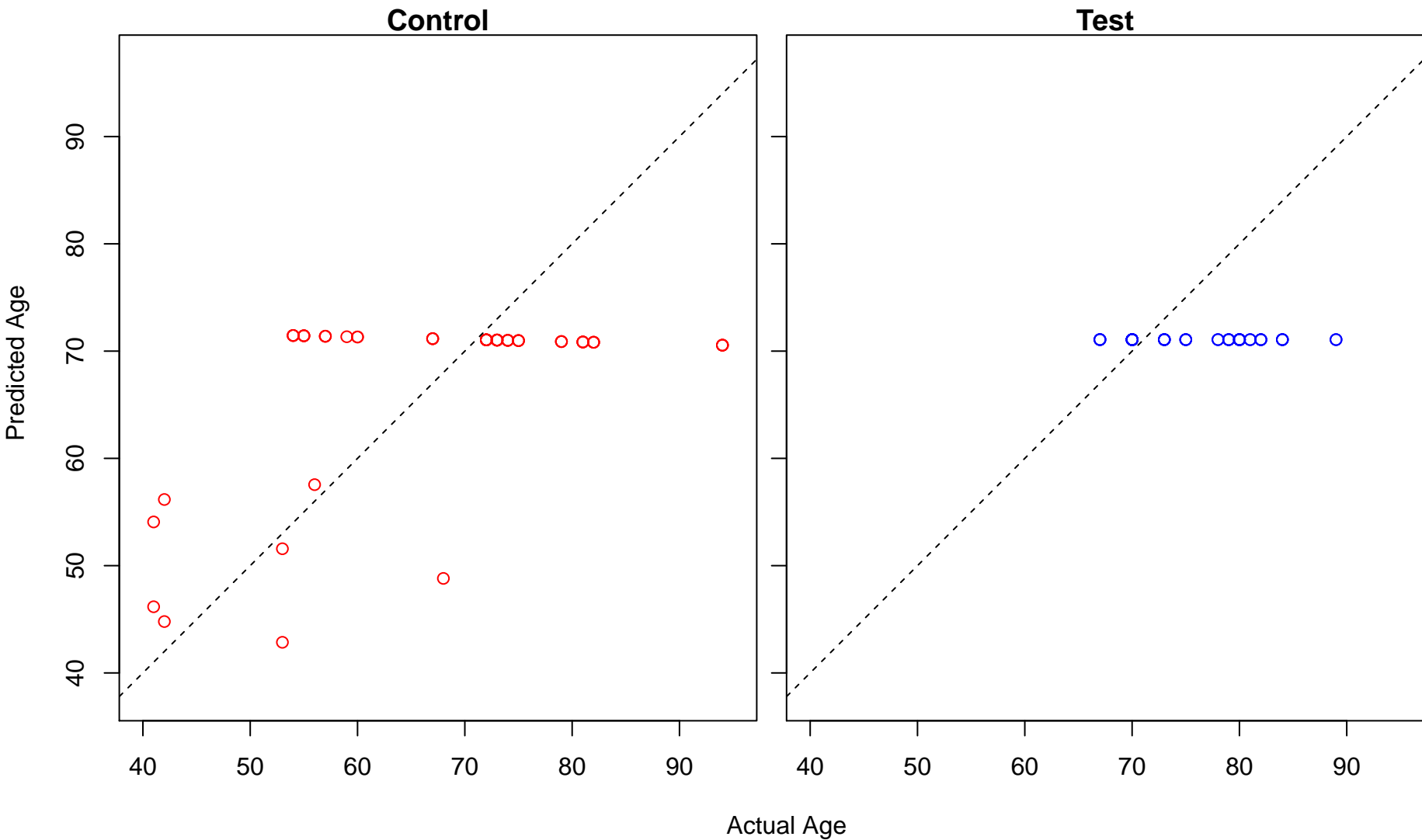


Test

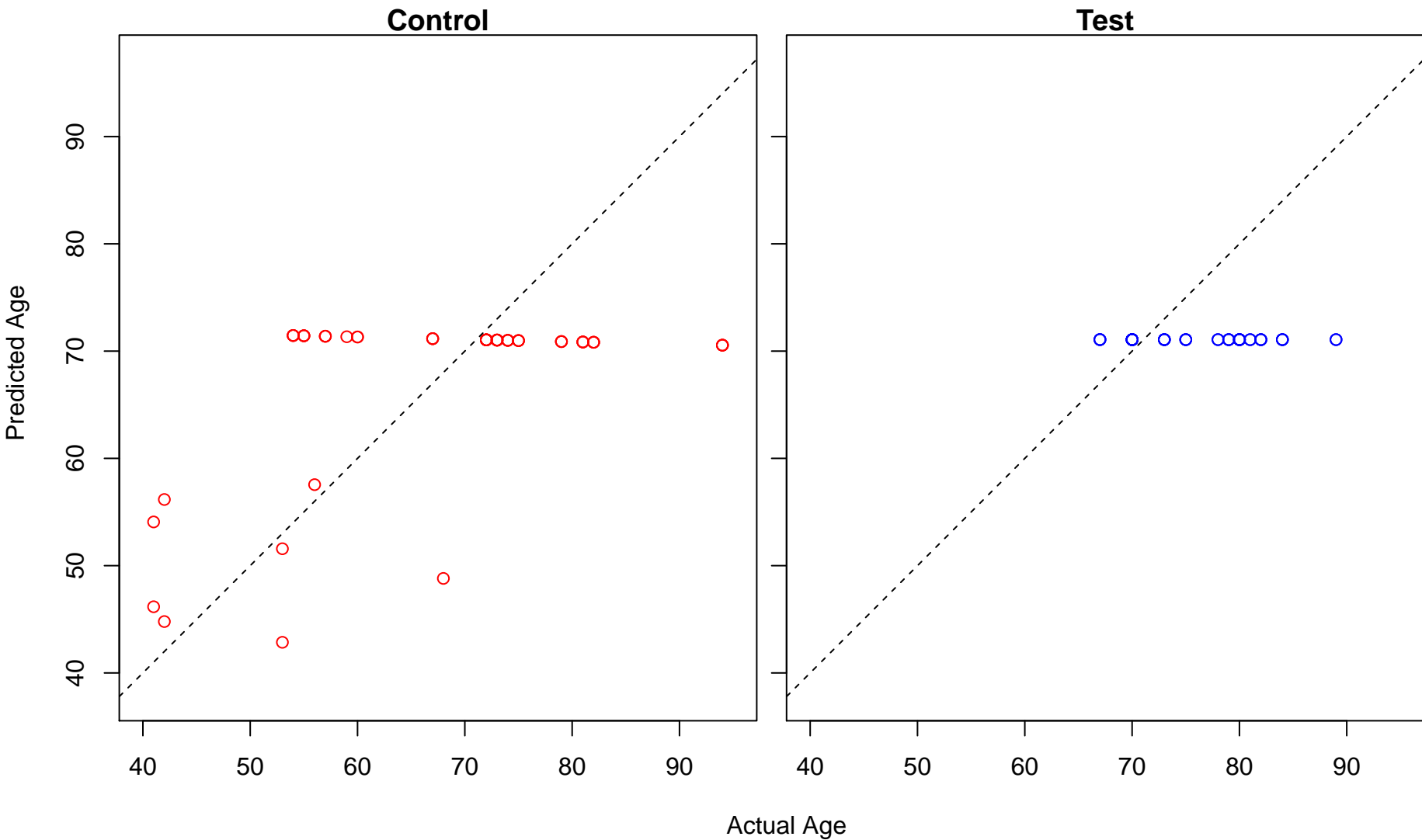


Actual Age

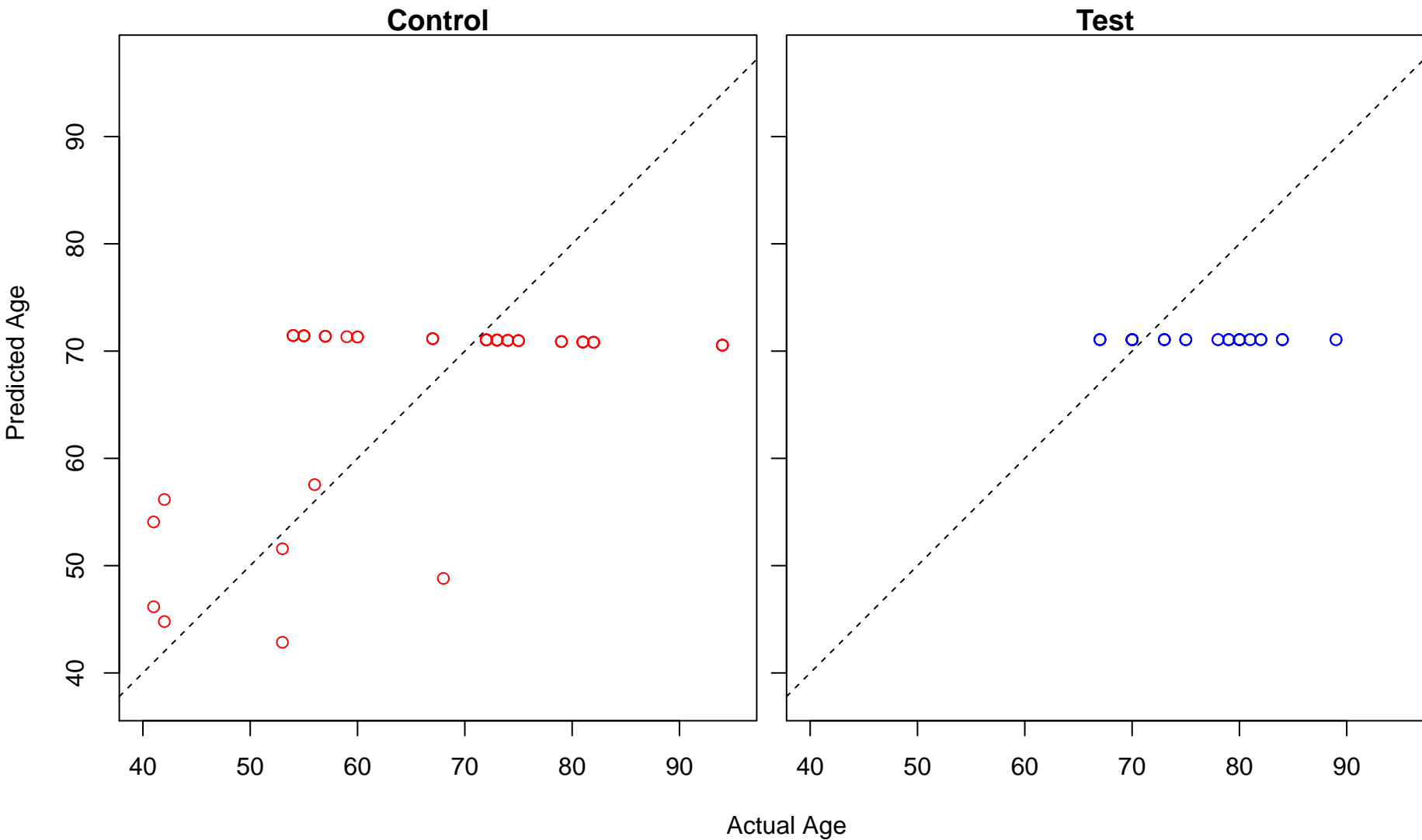
termination of RNA polymerase II transcription (Score: 0.807997)



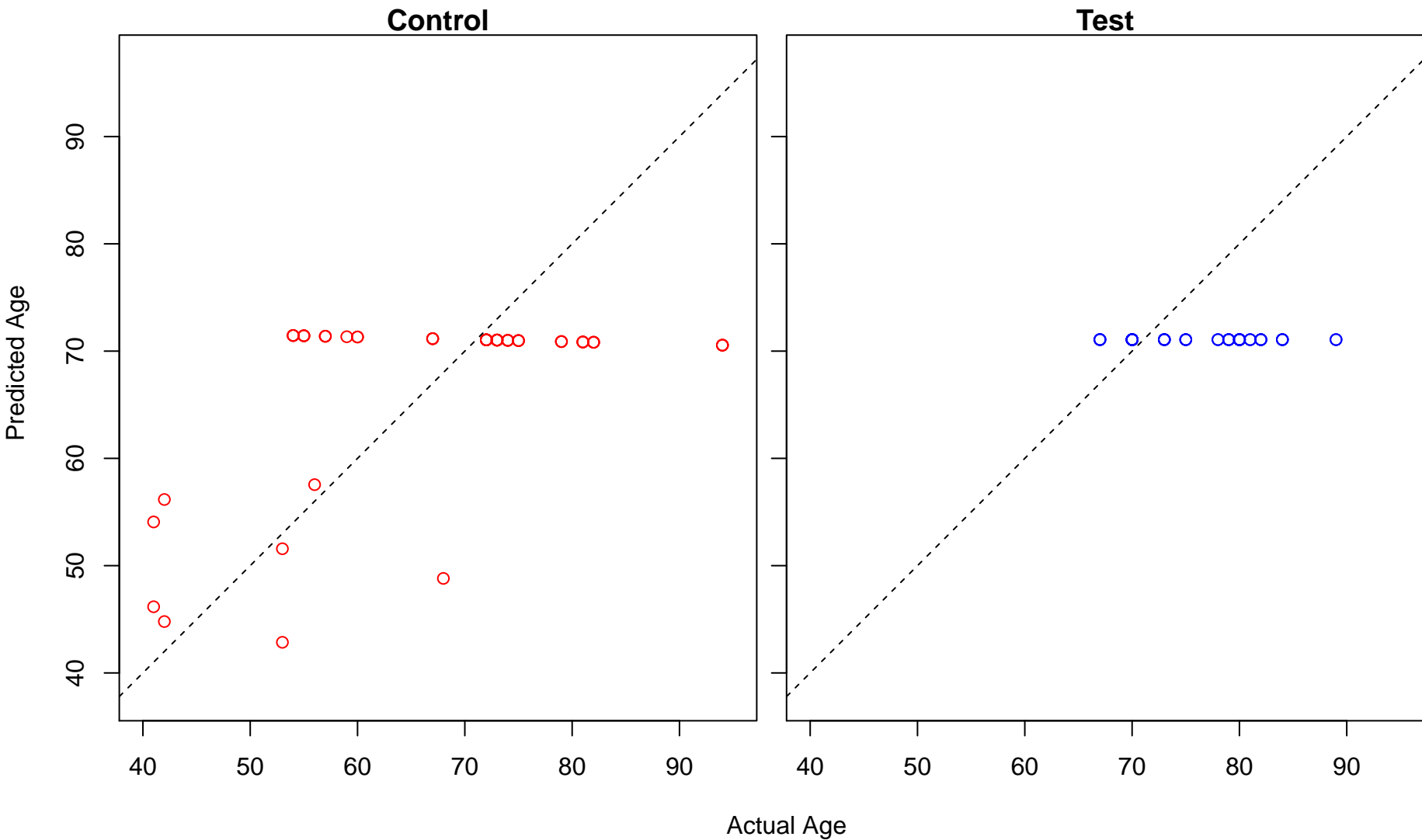
mRNA export from nucleus (Score: 0.807997)



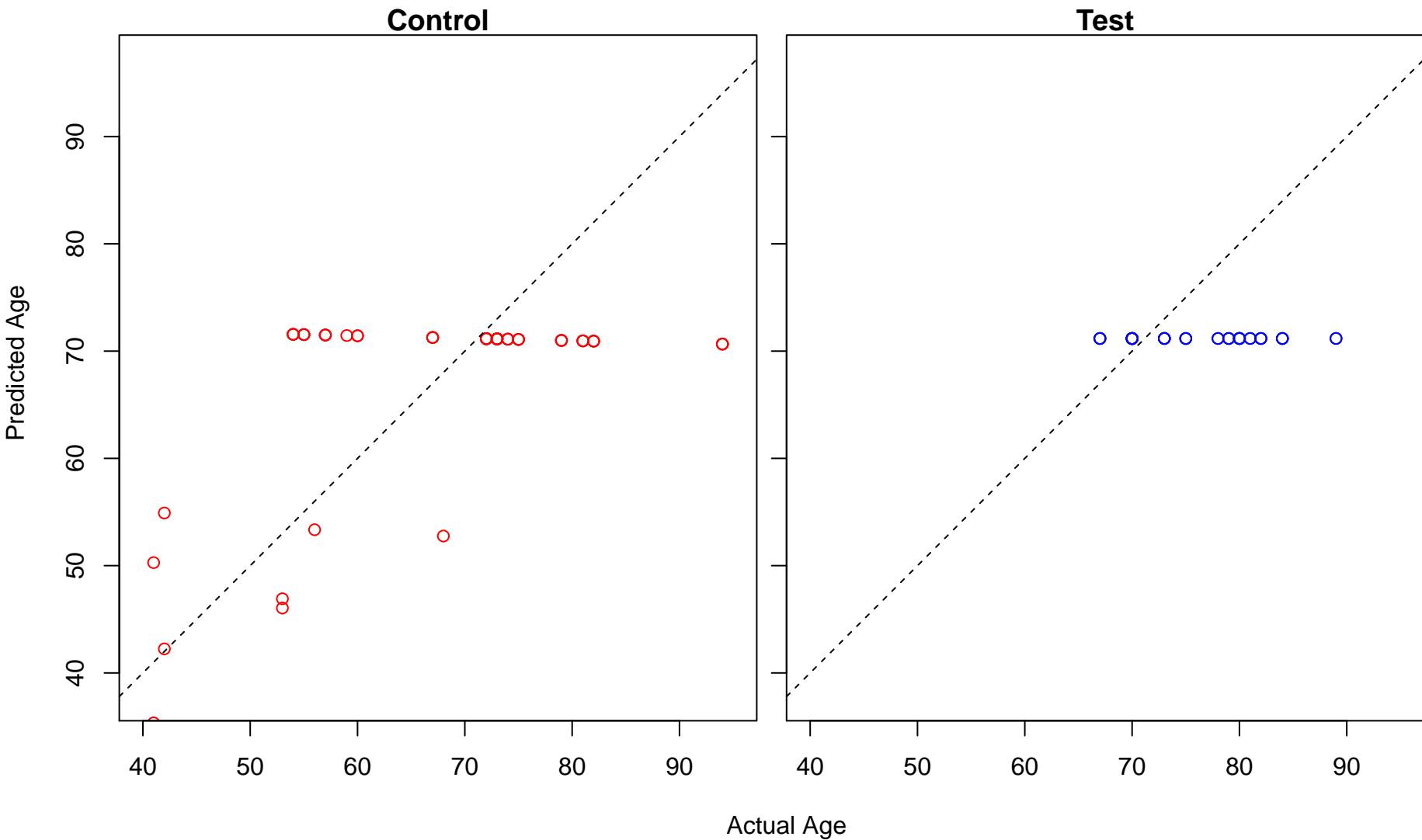
mRNA transport (Score: 0.807997)



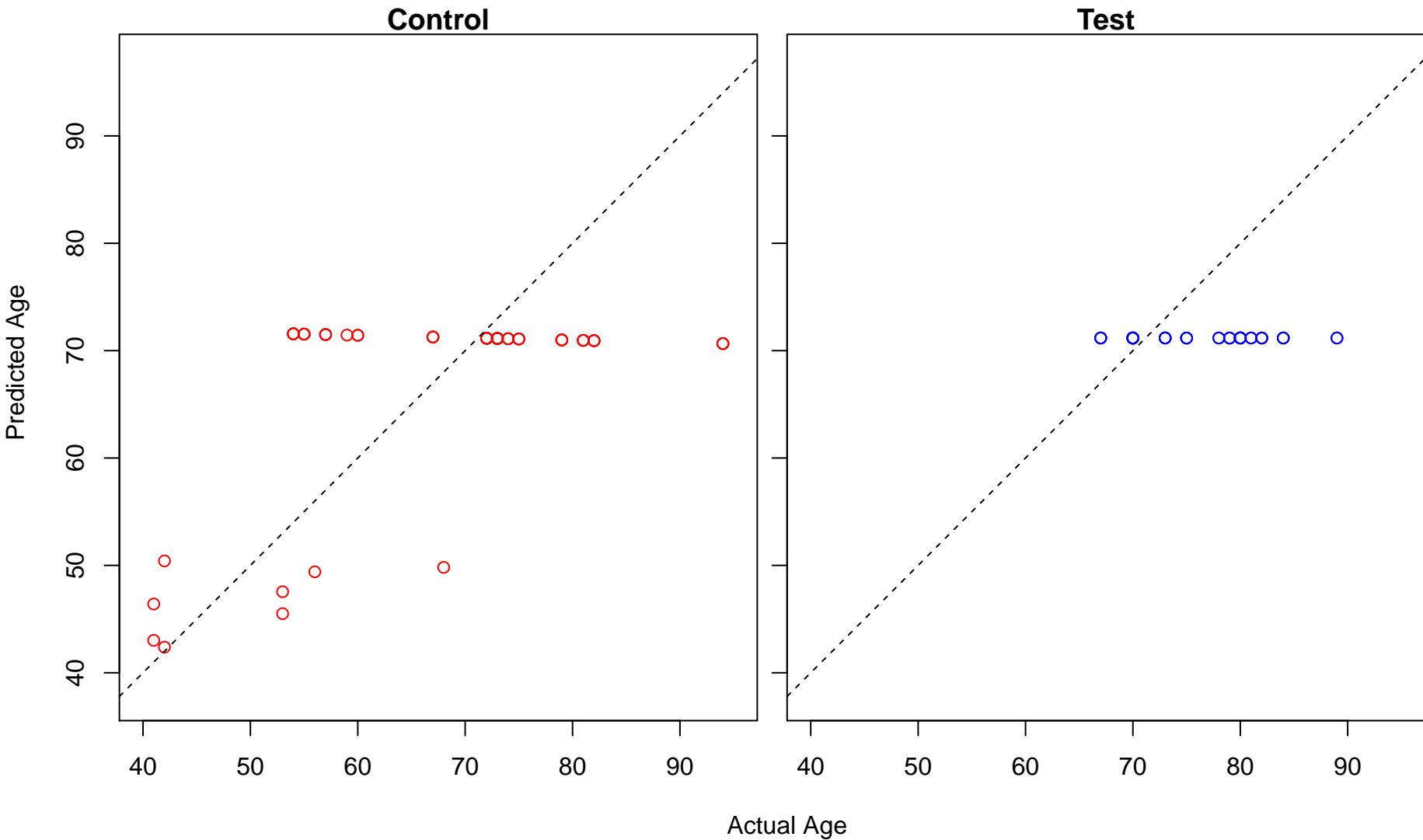
mRNA-containing ribonucleoprotein complex export from nucleus (Score: 0.807997)



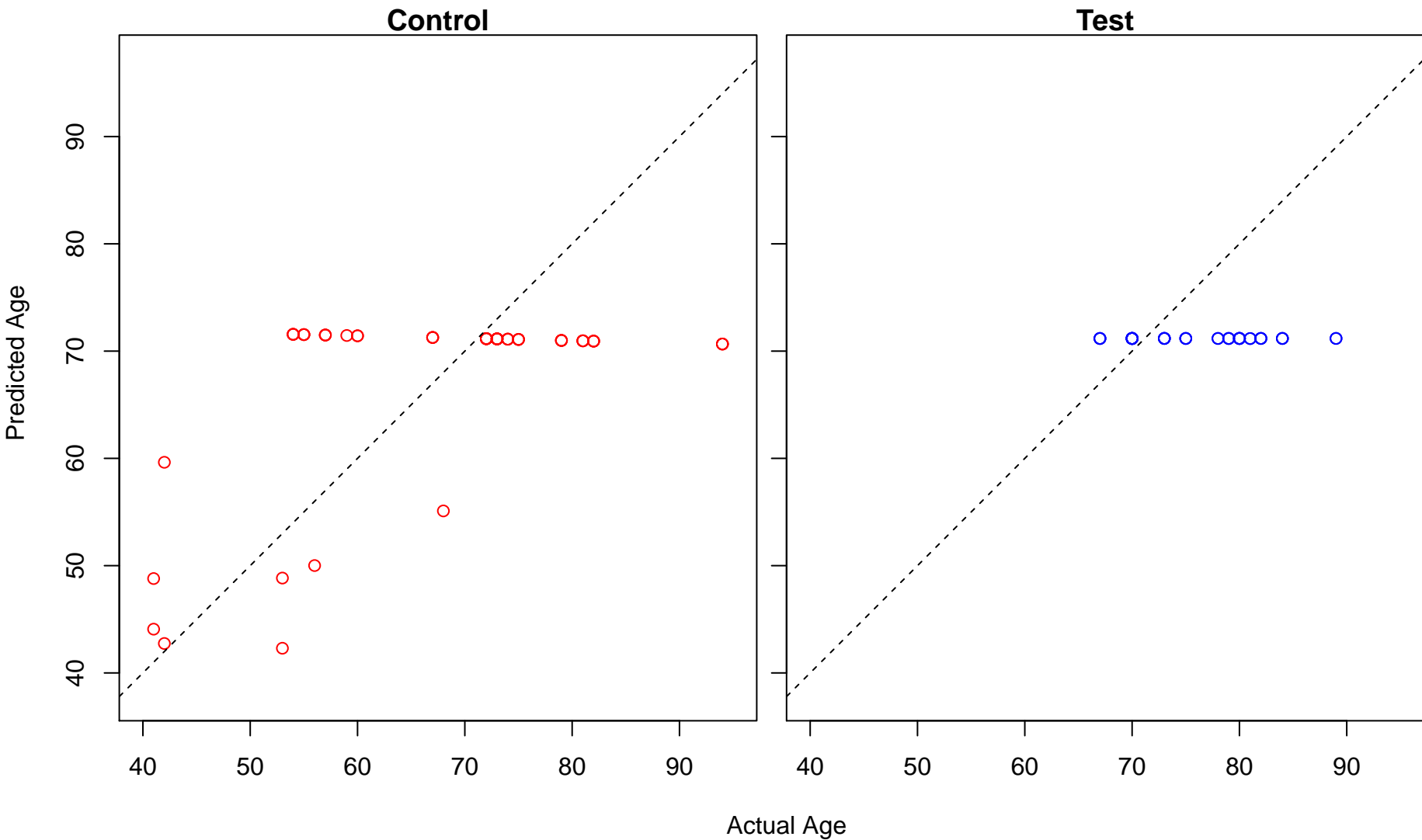
positive regulation of protein metabolic process (Score: 0.807992)



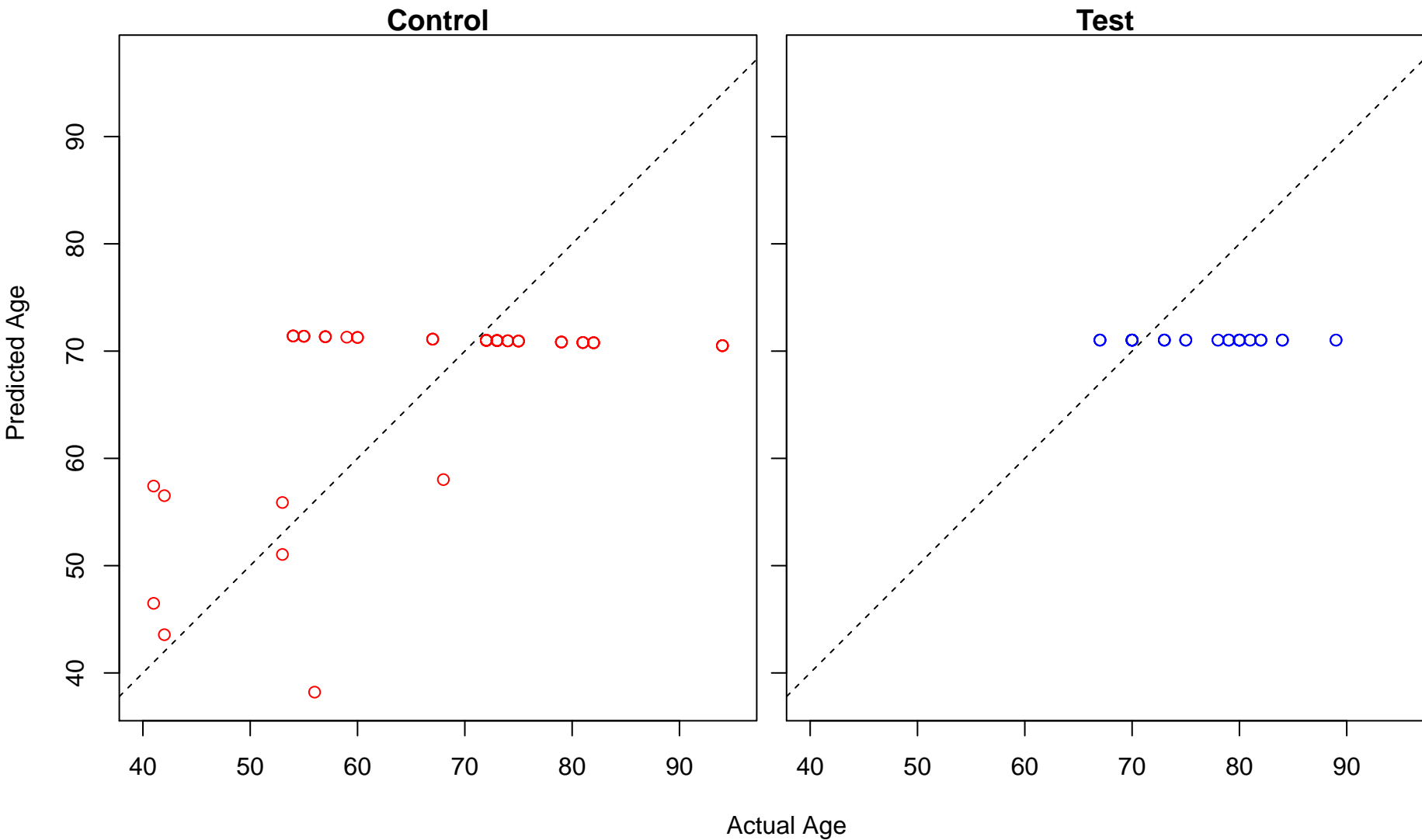
positive regulation of response to stimulus (Score: 0.807986)



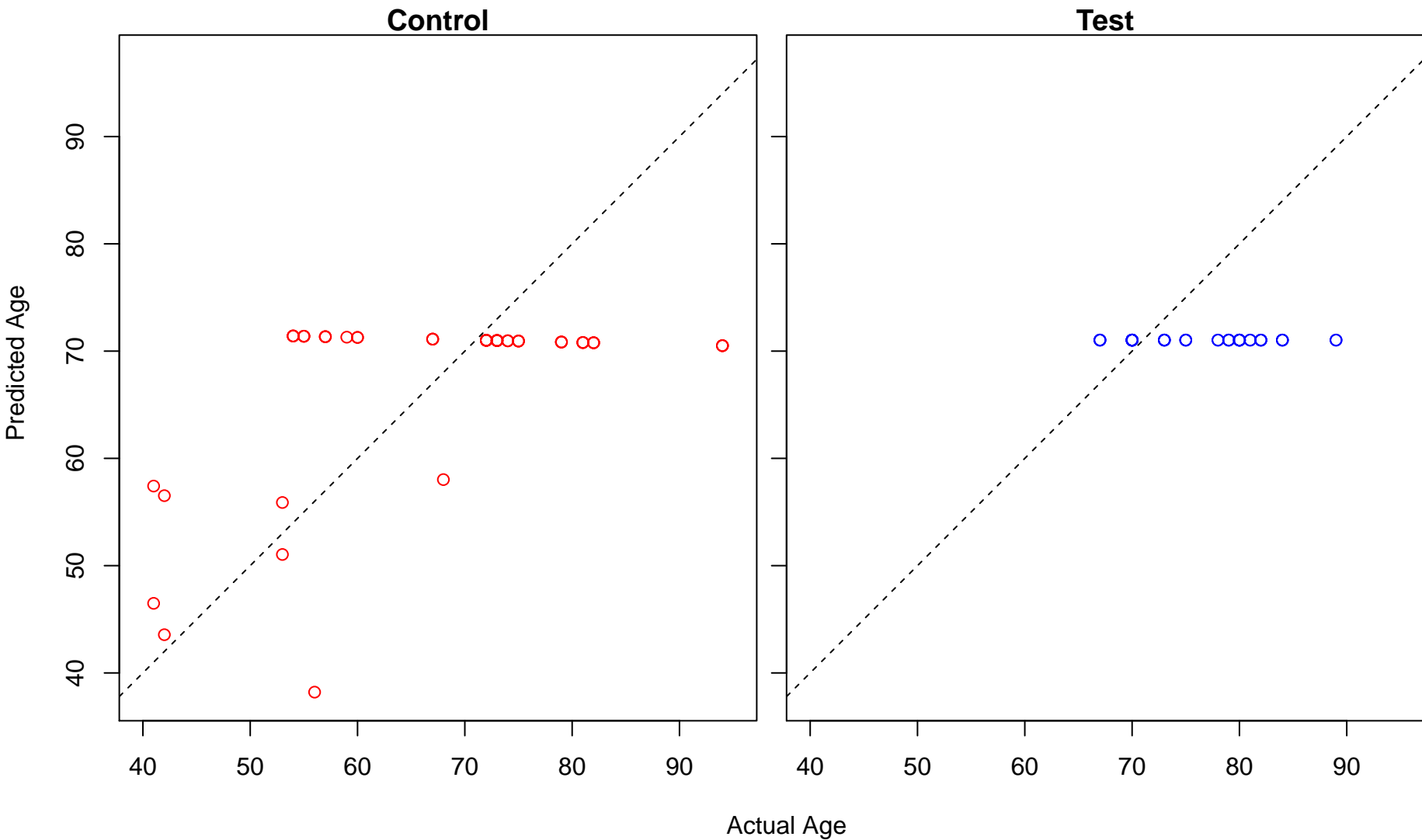
cell activation (Score: 0.807923)



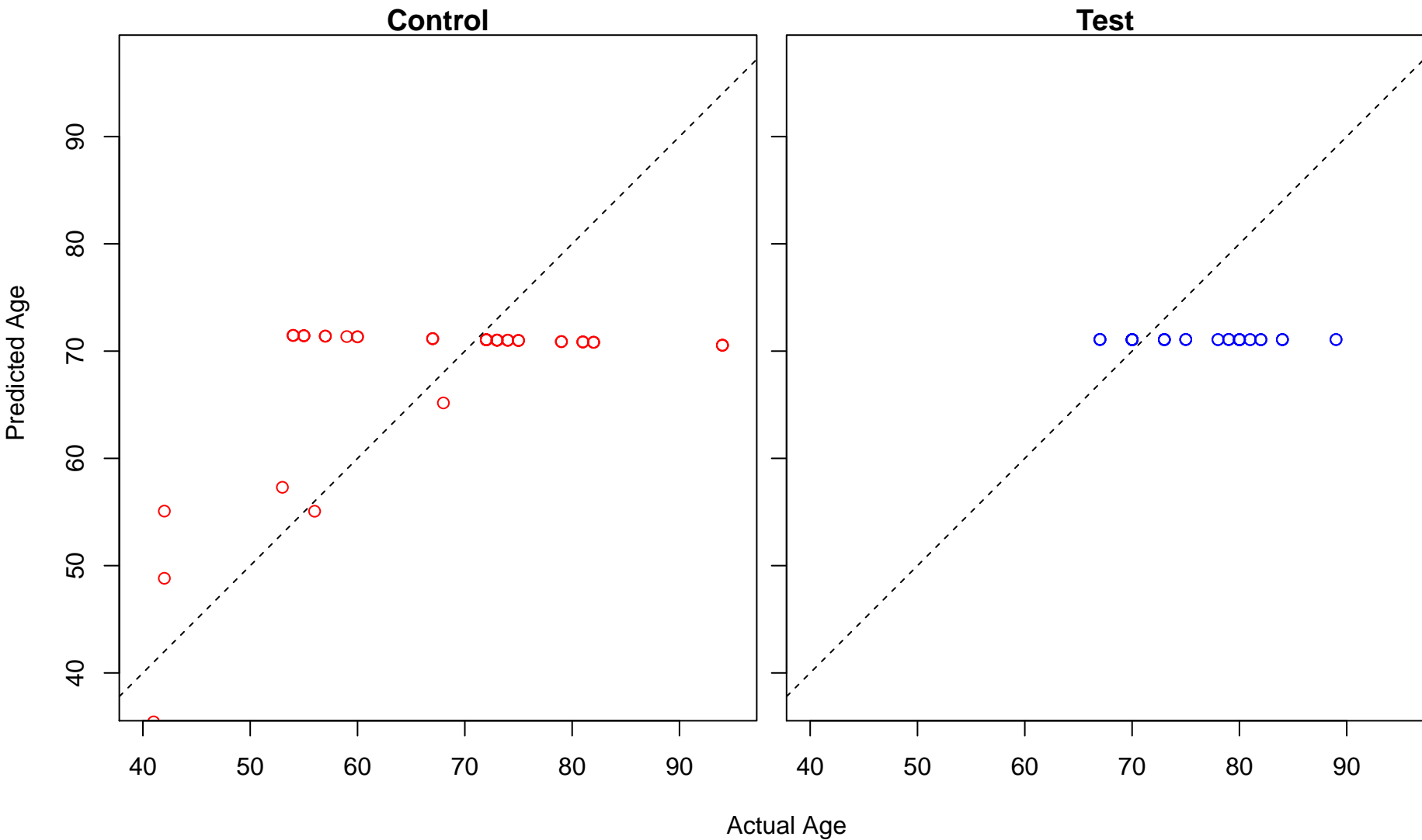
regulation of transforming growth factor beta receptor signaling pathway (Score: 0.807864)



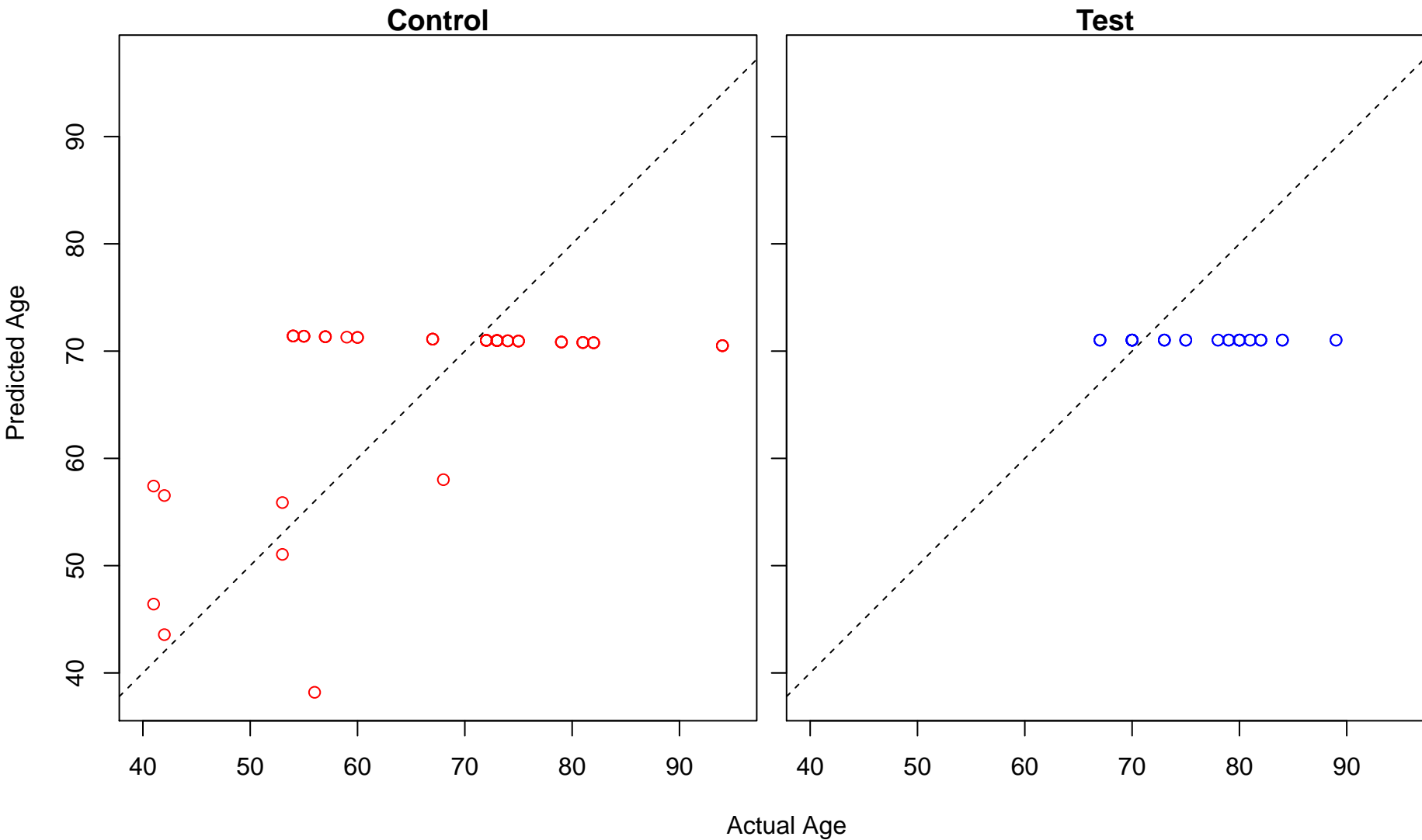
regulation of cellular response to transforming growth factor beta stimulus (Score: 0.807864)



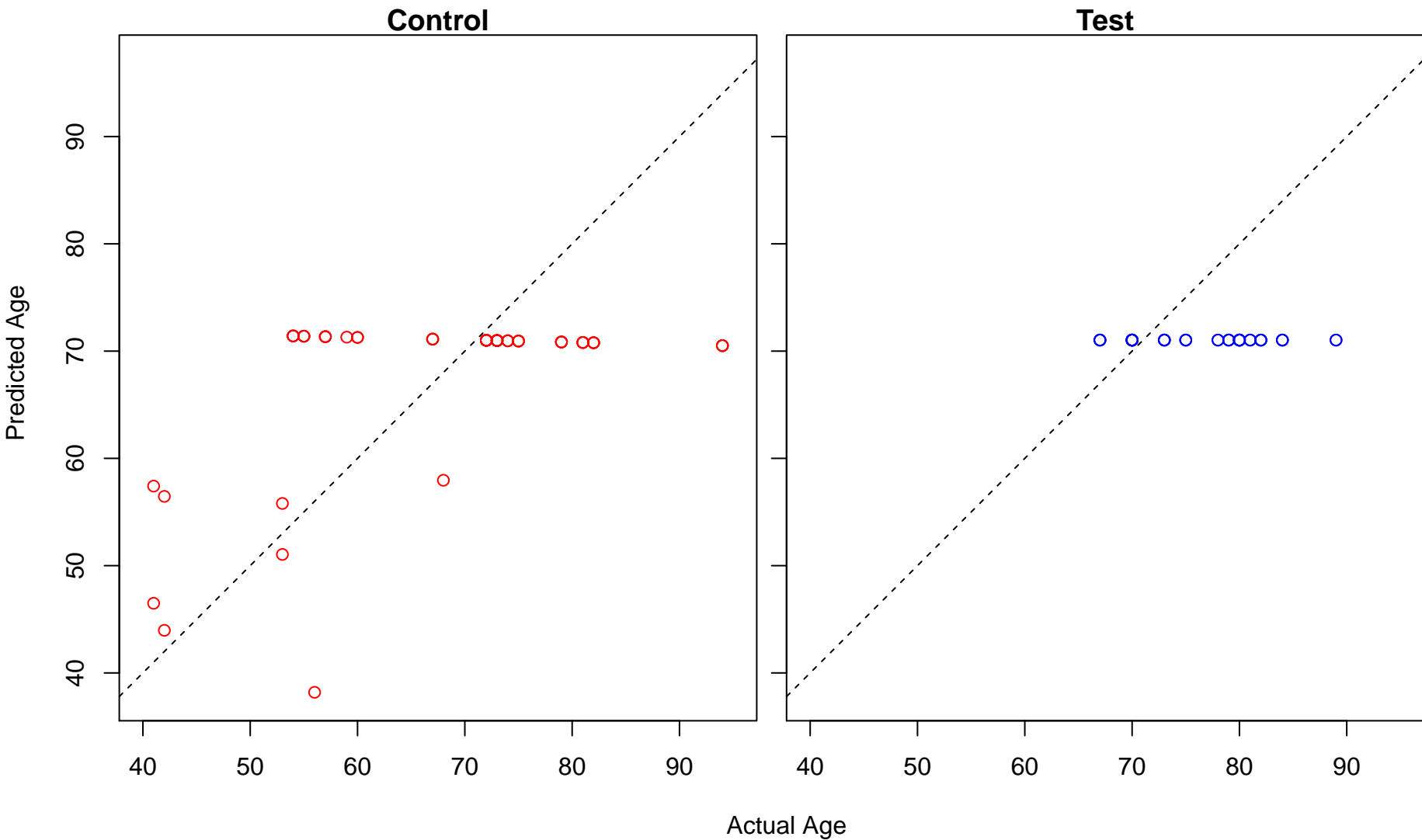
actin filament-based process (Score: 0.807845)



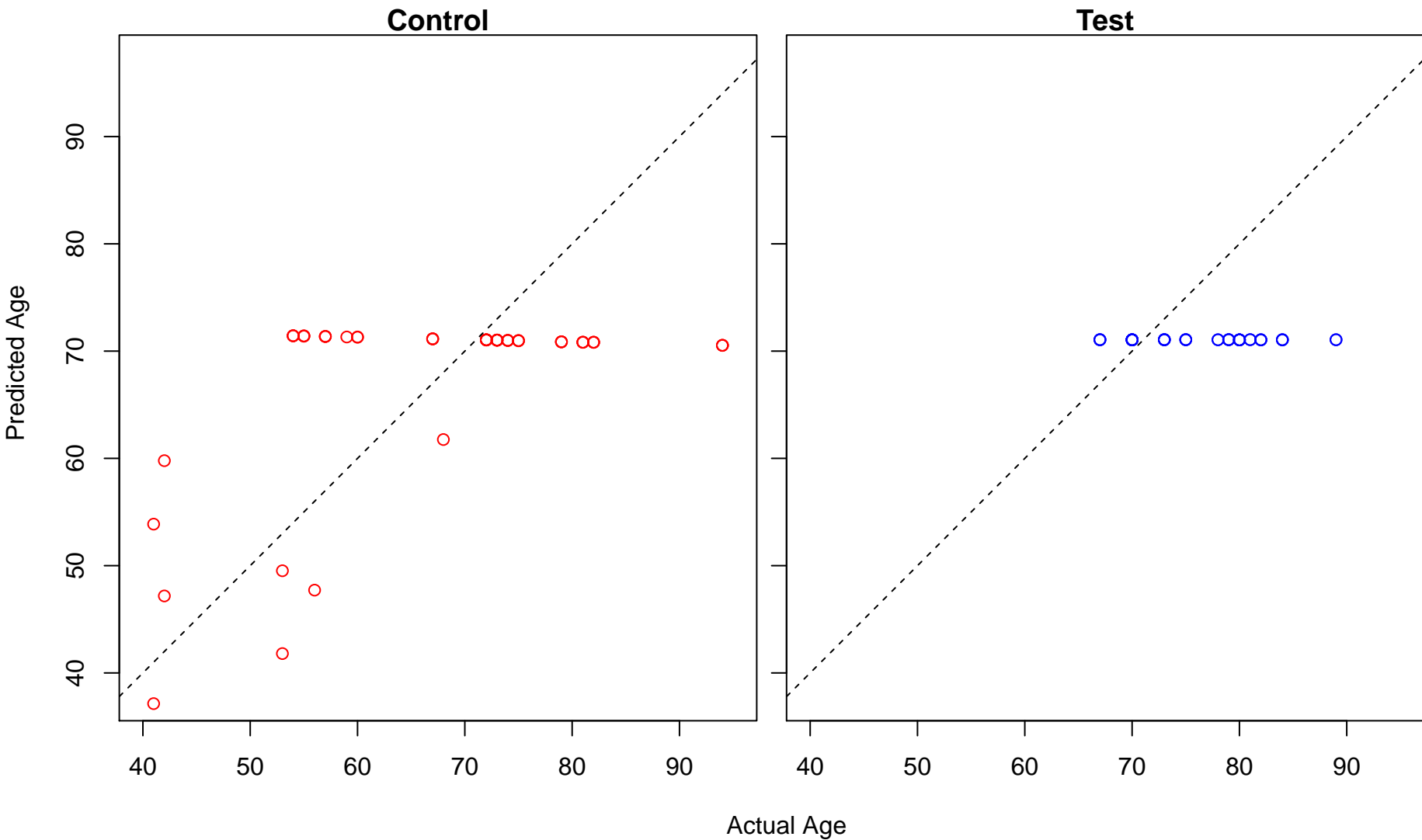
regulation of cell cycle arrest (Score: 0.807840)



regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 0.807)

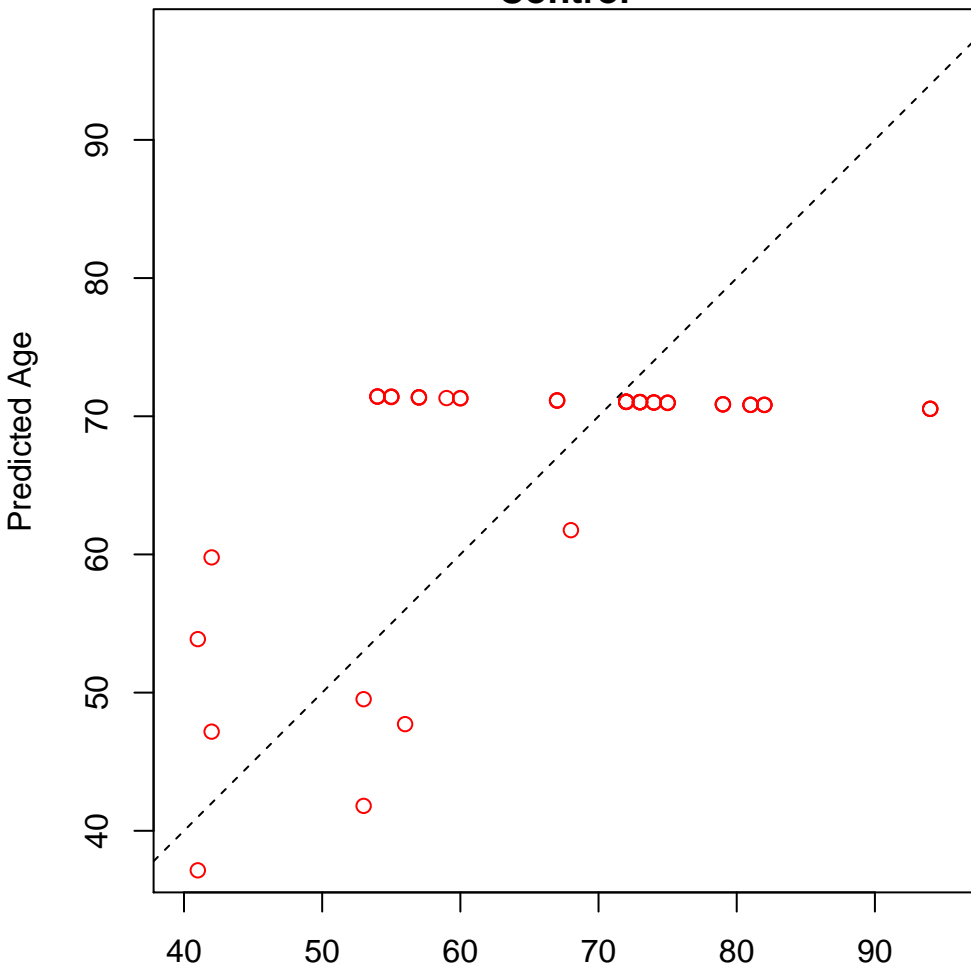


protein acetylation (Score: 0.807717)

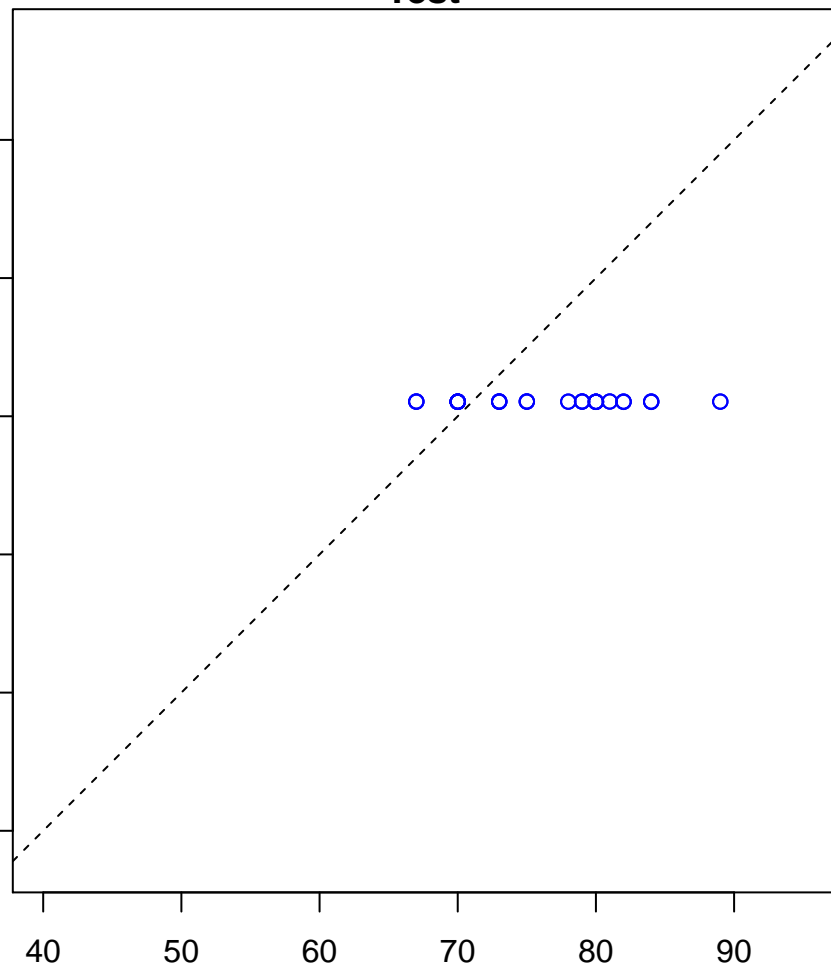


internal protein amino acid acetylation (Score: 0.807717)

Control

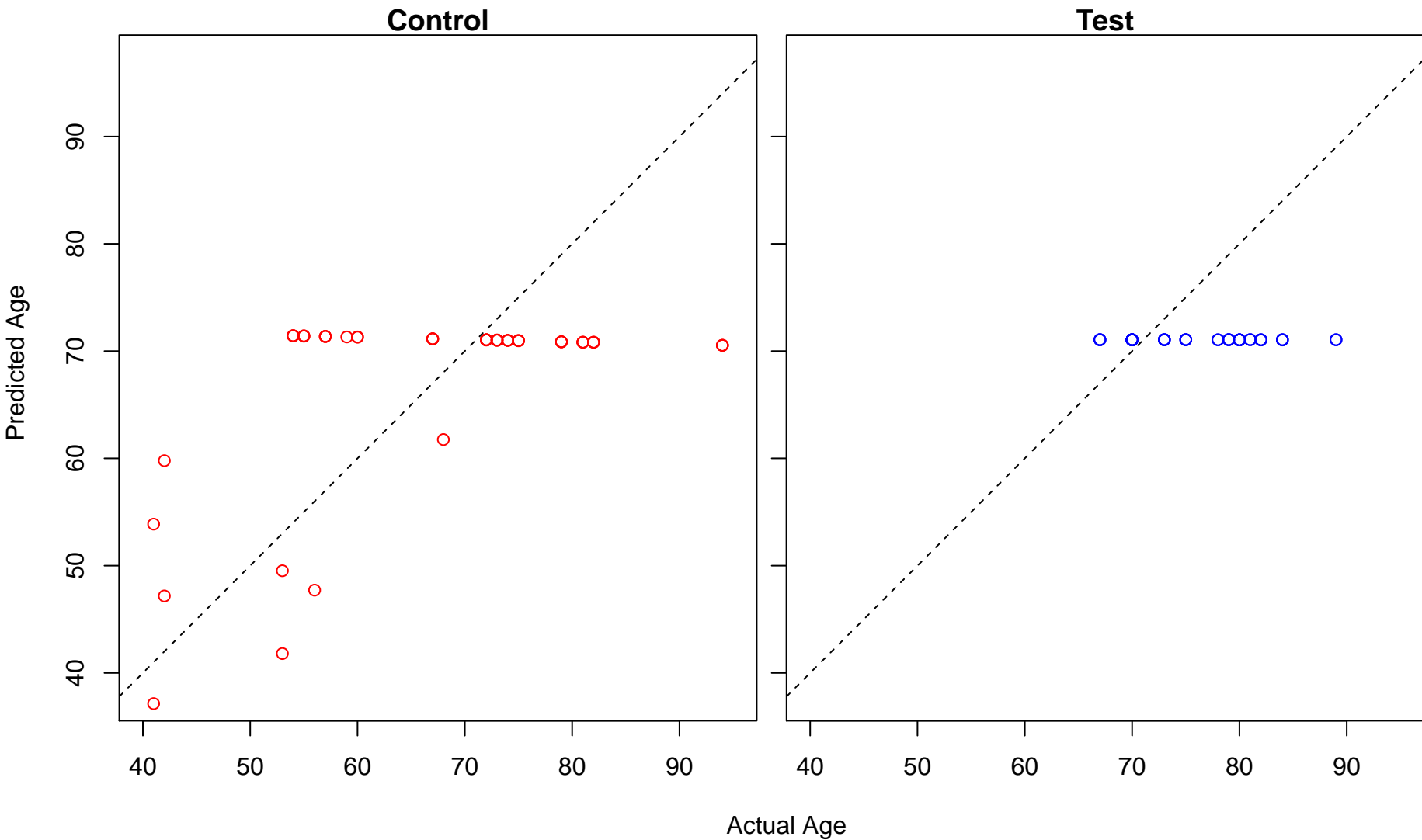


Test



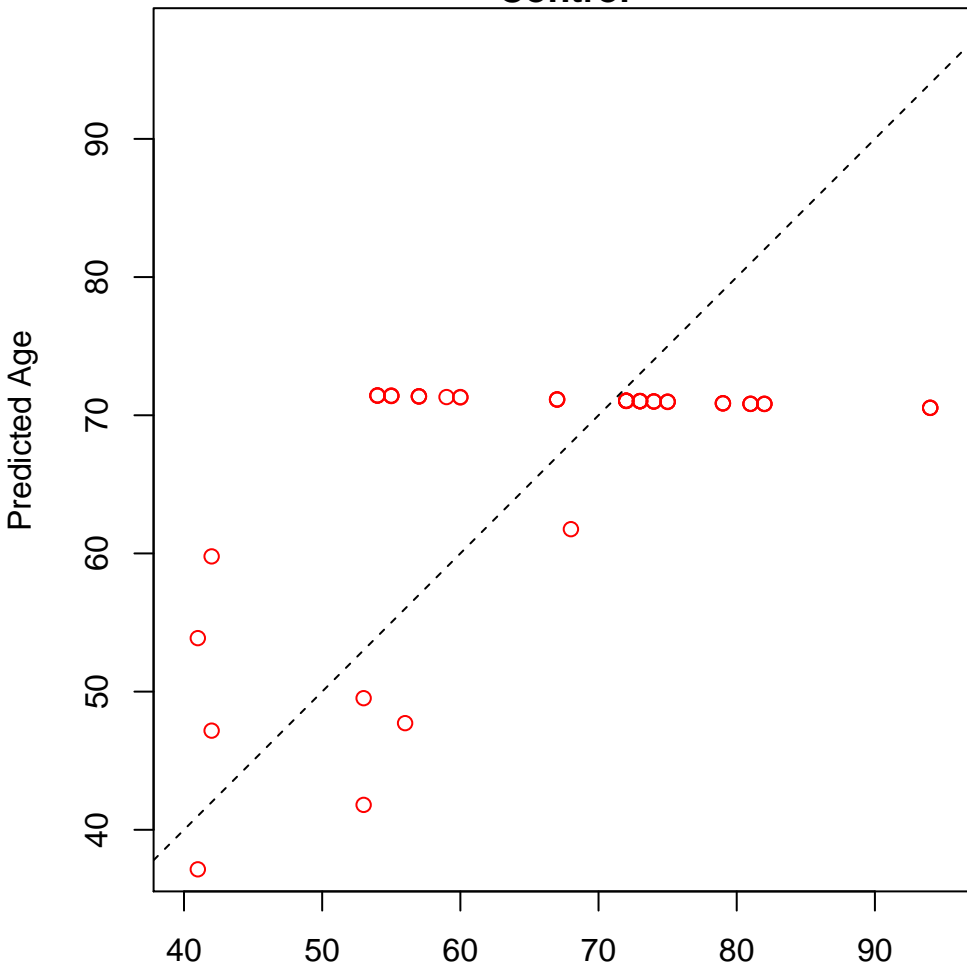
Actual Age

histone acetylation (Score: 0.807717)

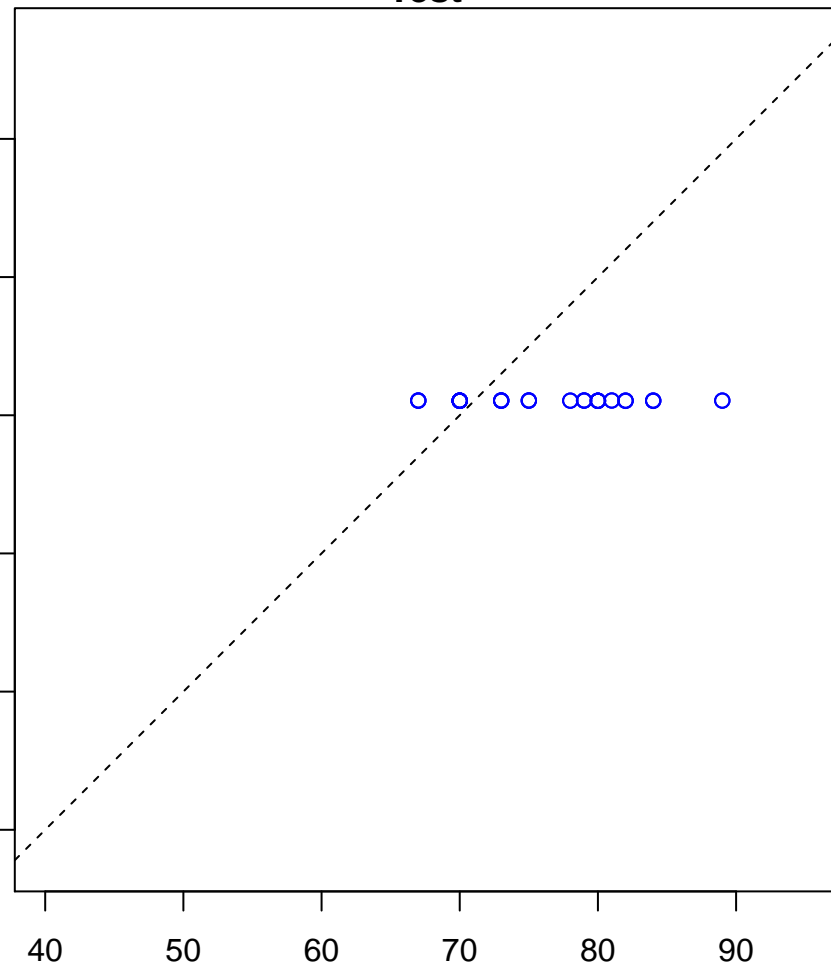


internal peptidyl-lysine acetylation (Score: 0.807717)

Control

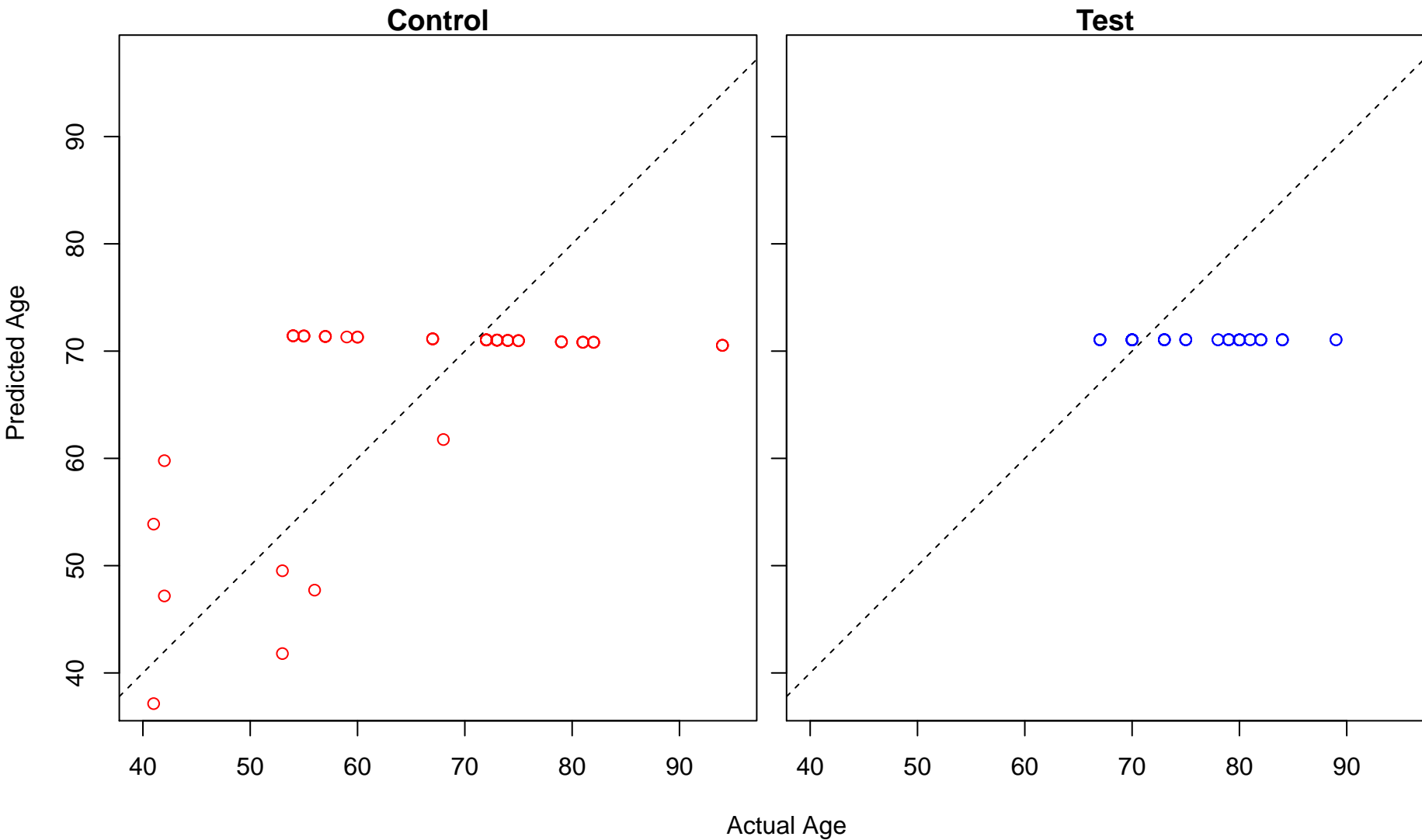


Test

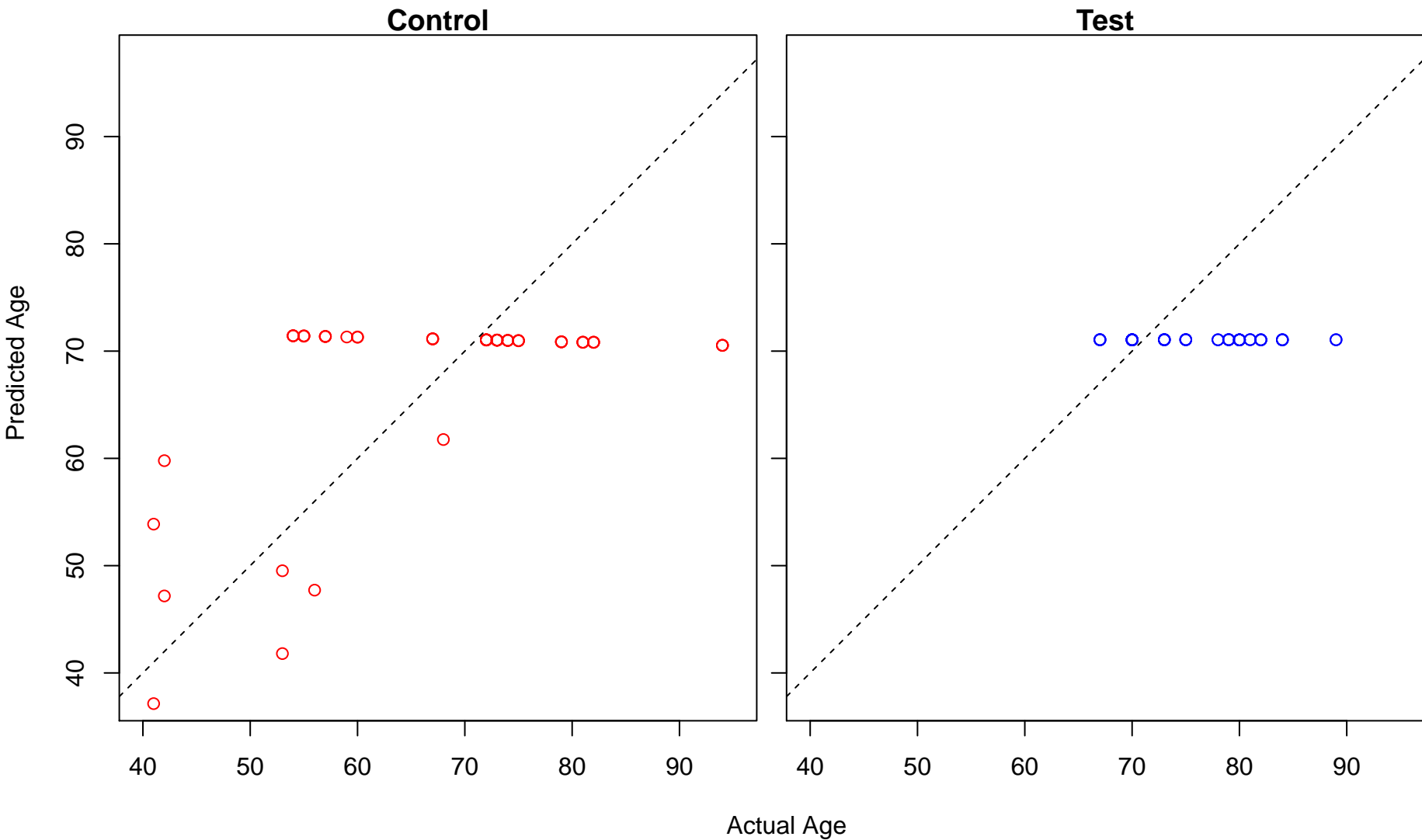


Actual Age

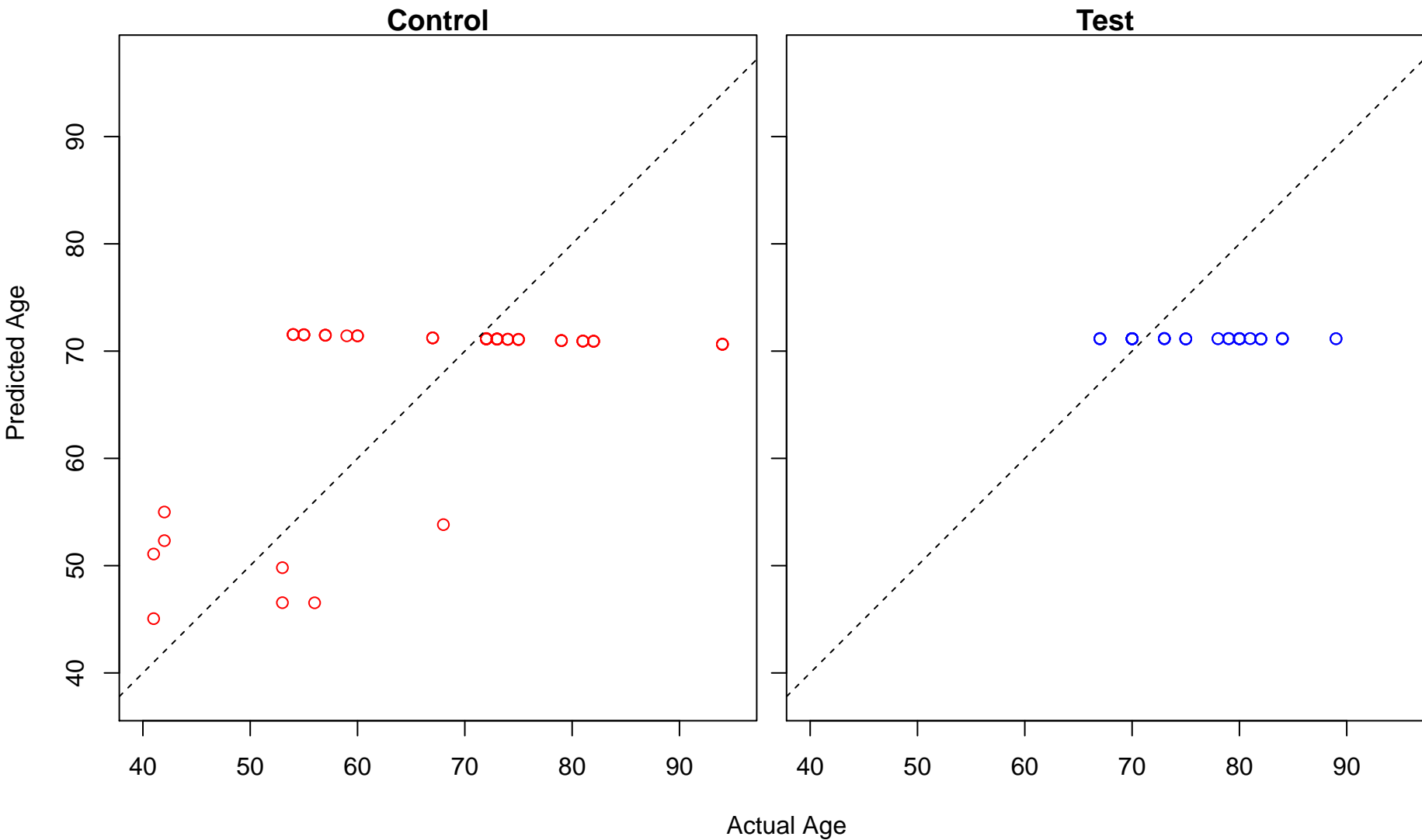
peptidyl-lysine acetylation (Score: 0.807717)



protein acylation (Score: 0.807717)

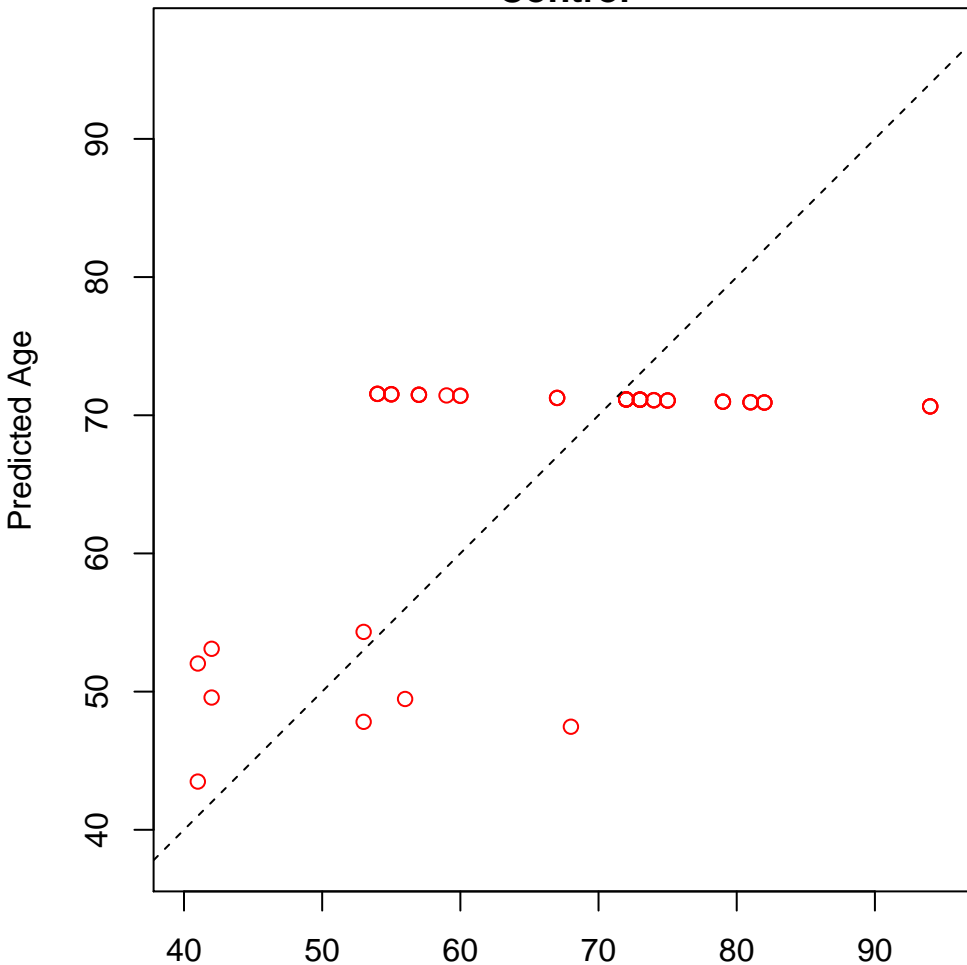


positive regulation of epithelial cell proliferation (Score: 0.807640)

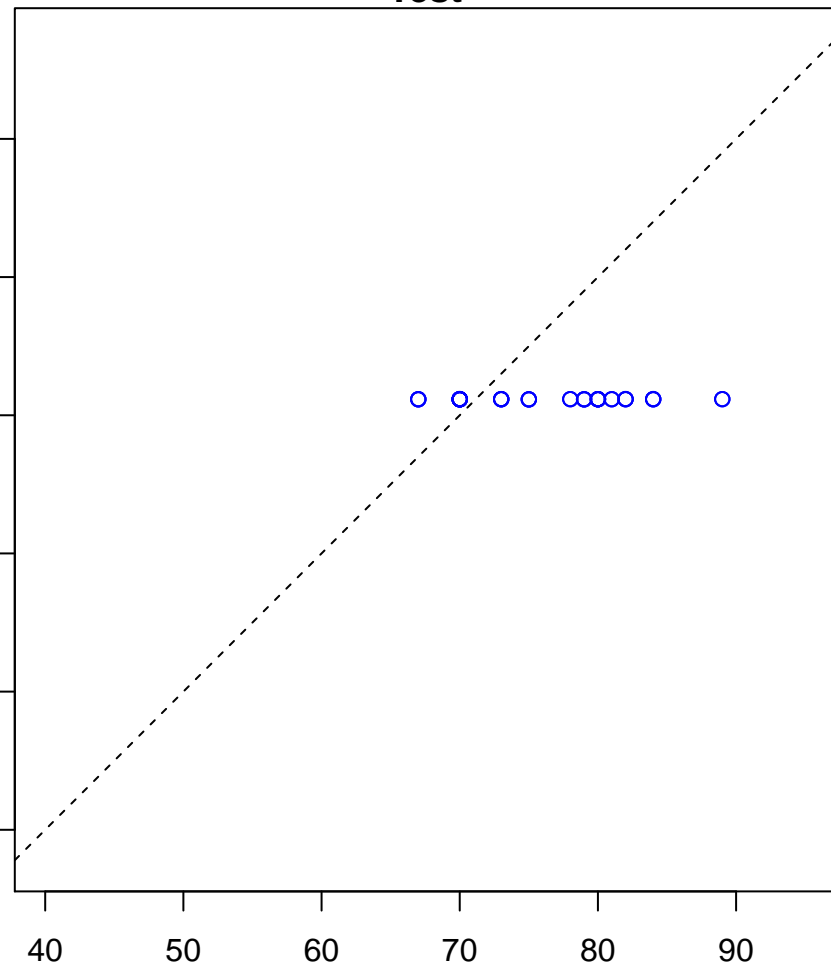


protein K11-linked ubiquitination (Score: 0.807638)

Control

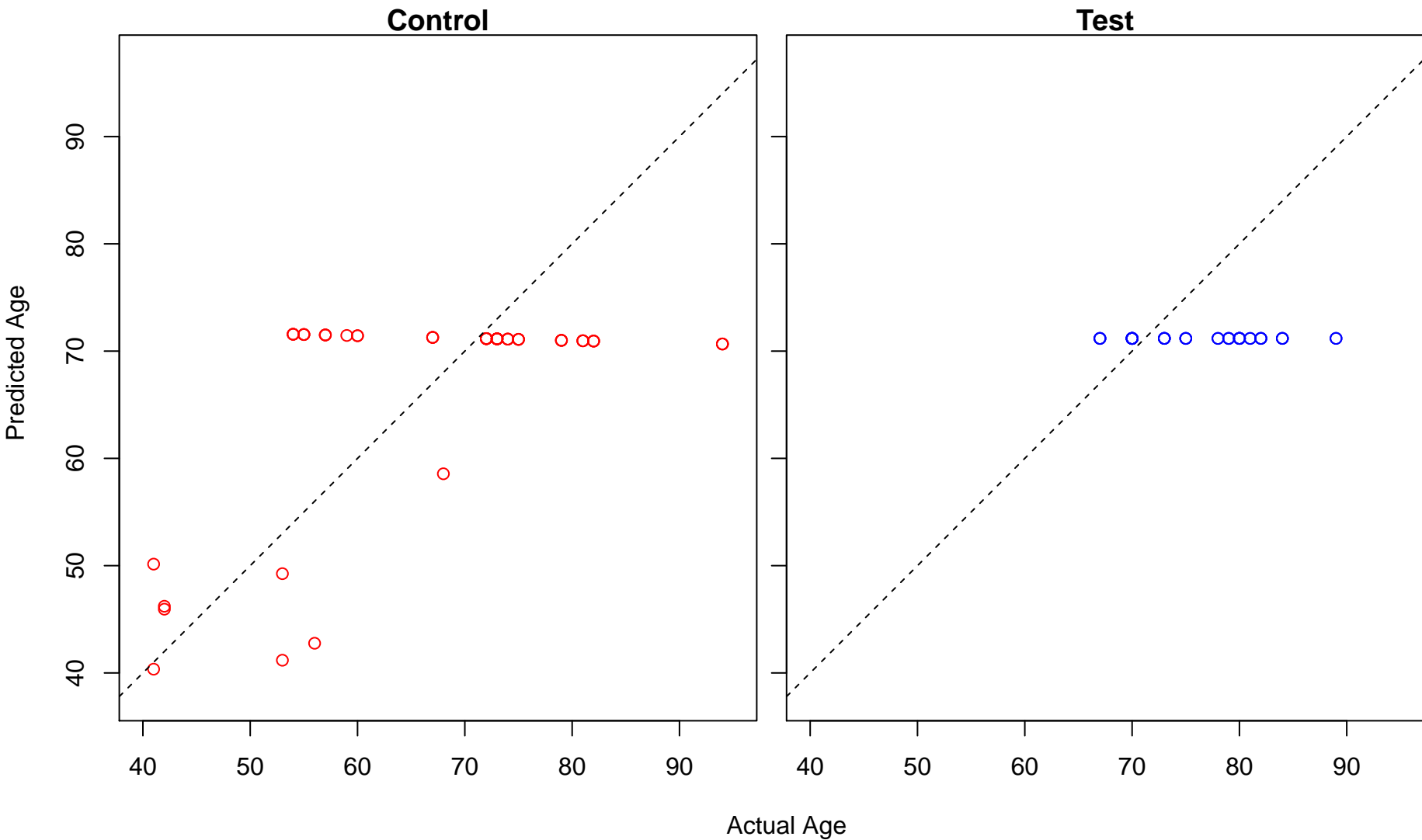


Test

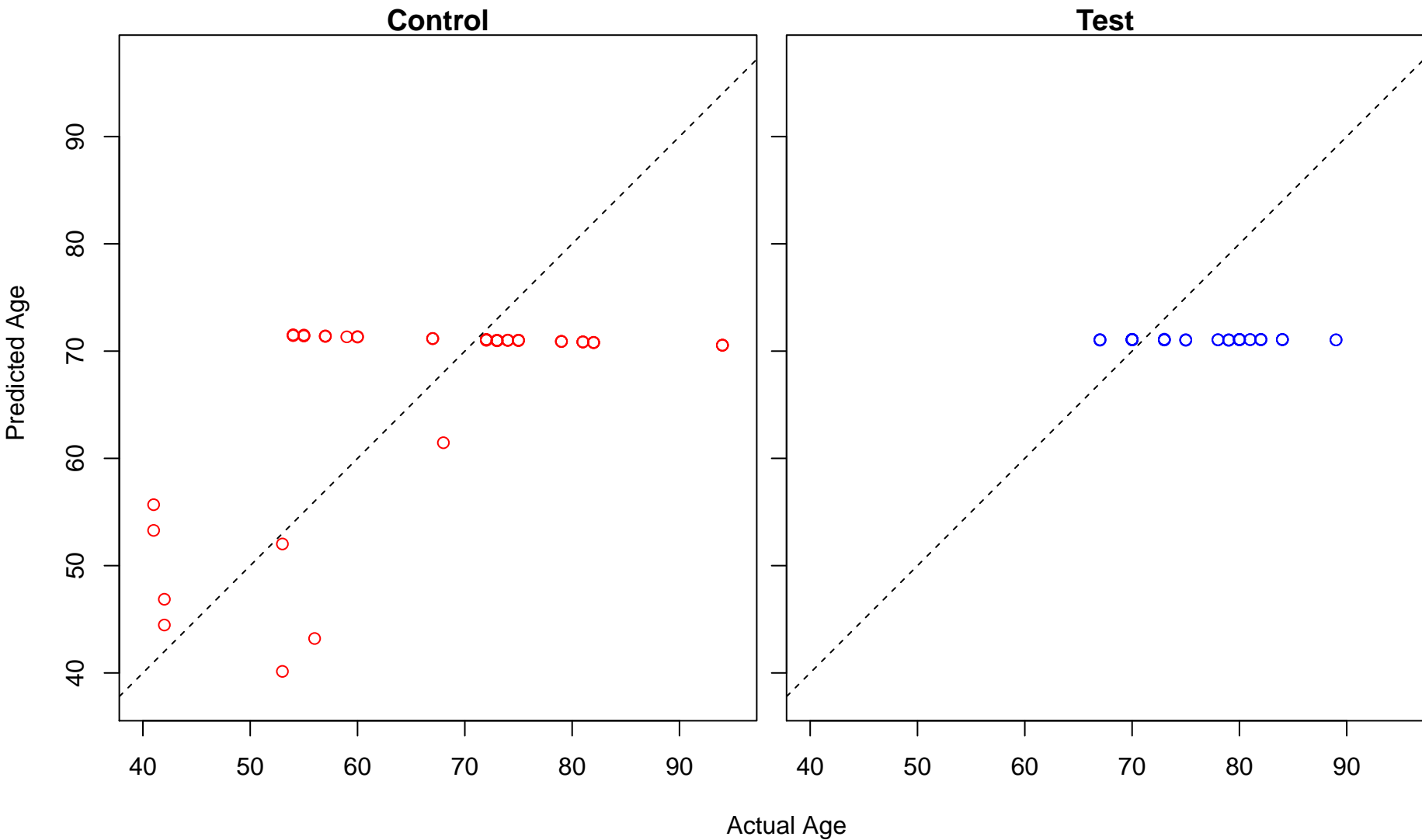


Actual Age

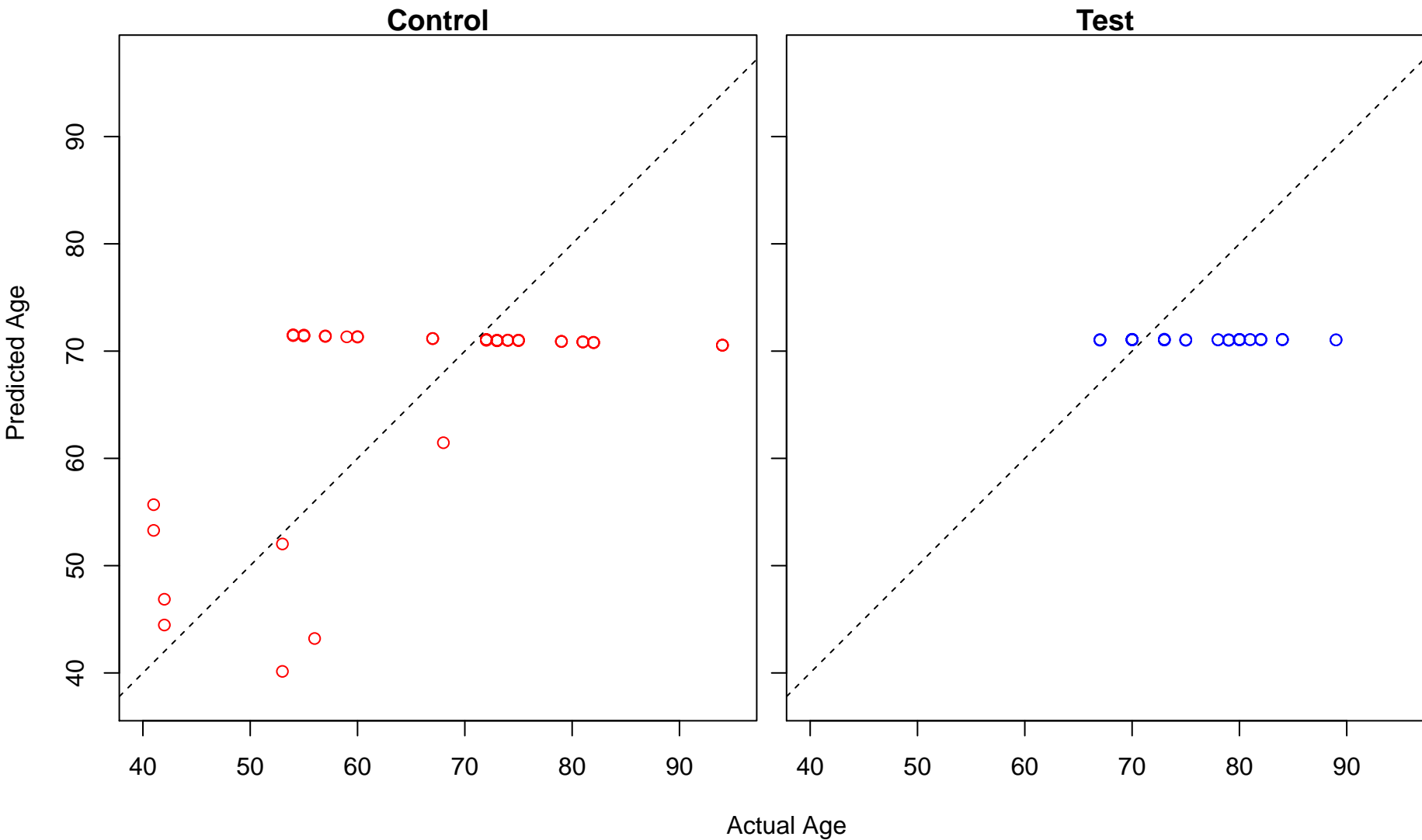
intracellular signal transduction (Score: 0.807629)



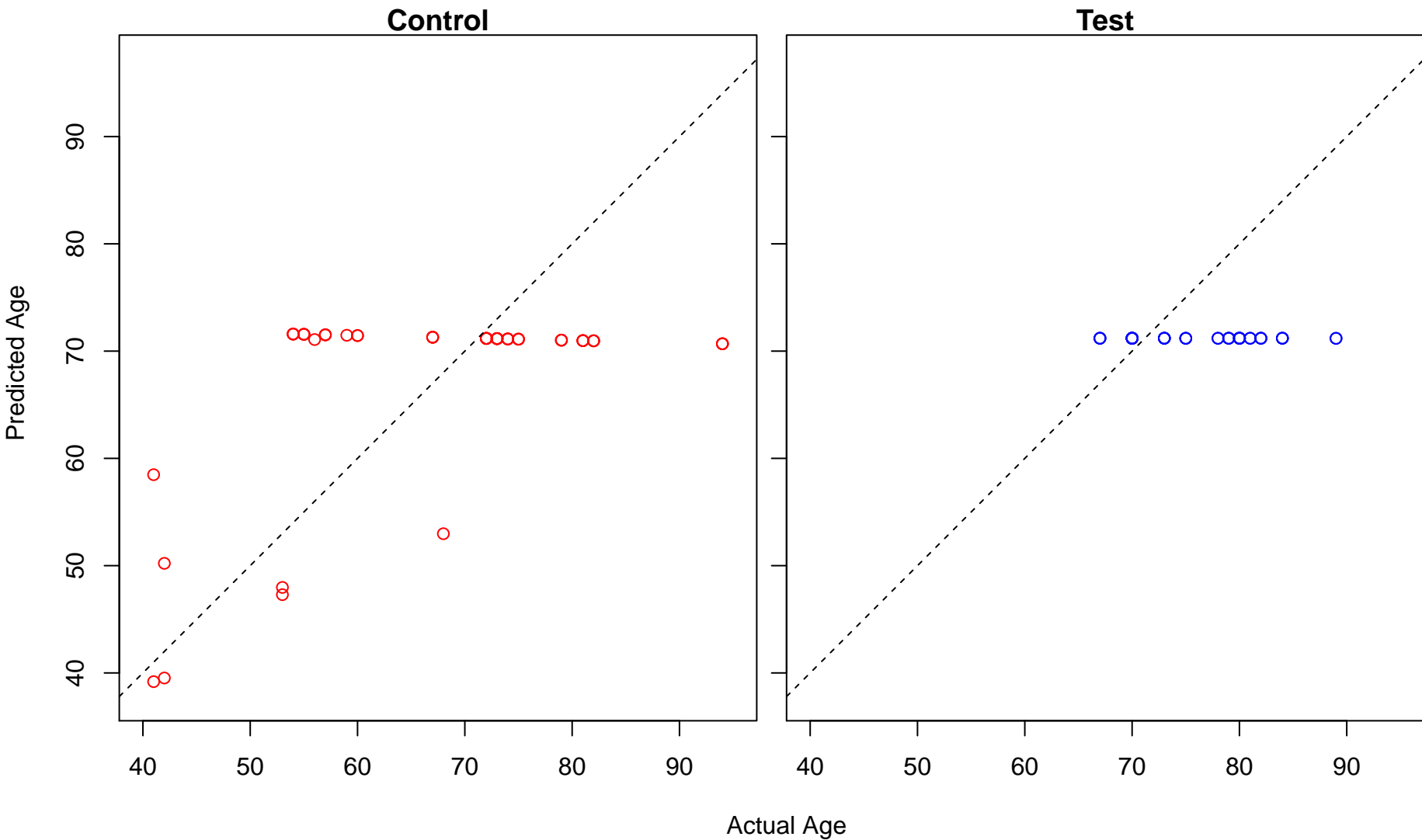
steroid metabolic process (Score: 0.807623)



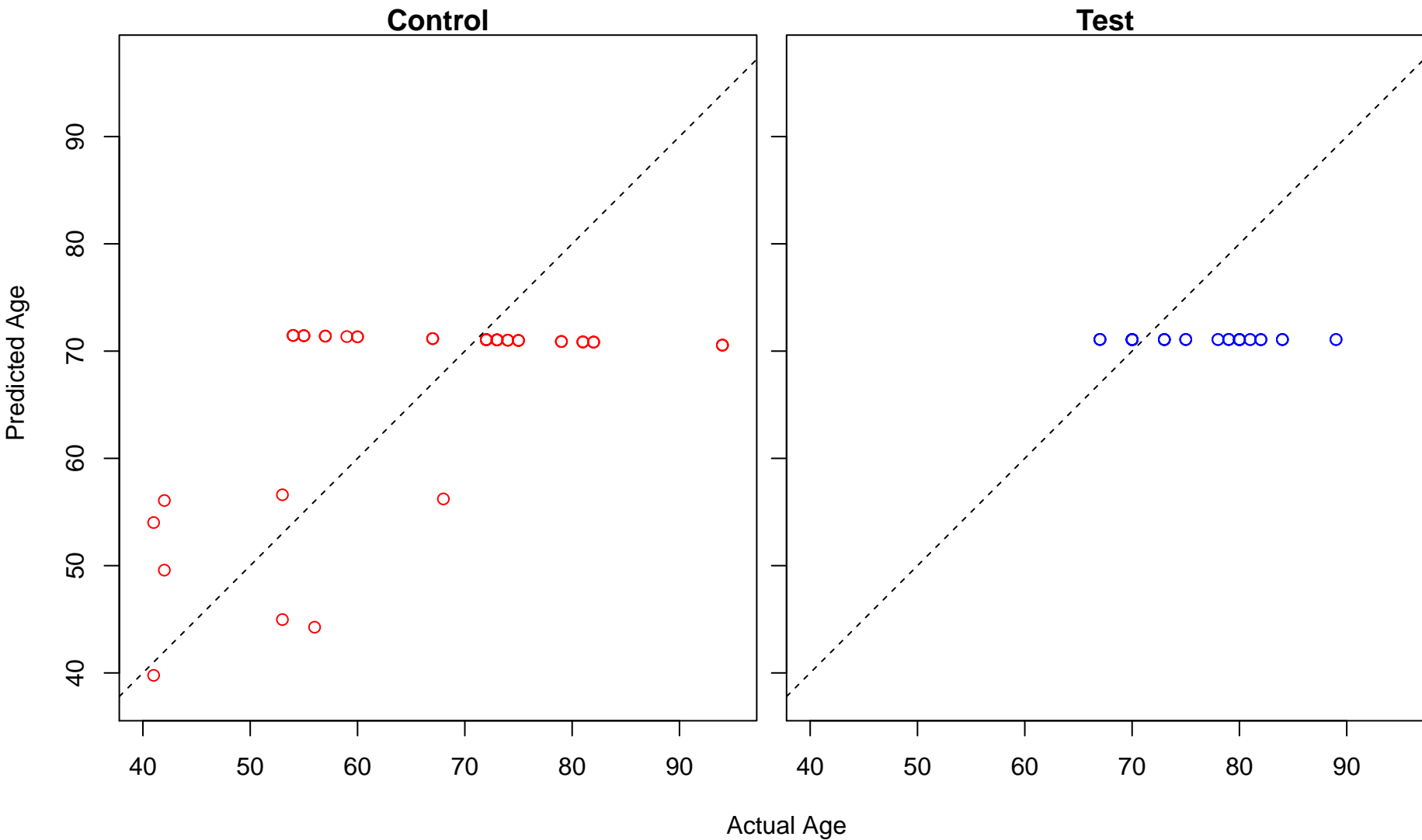
drug metabolic process (Score: 0.807623)



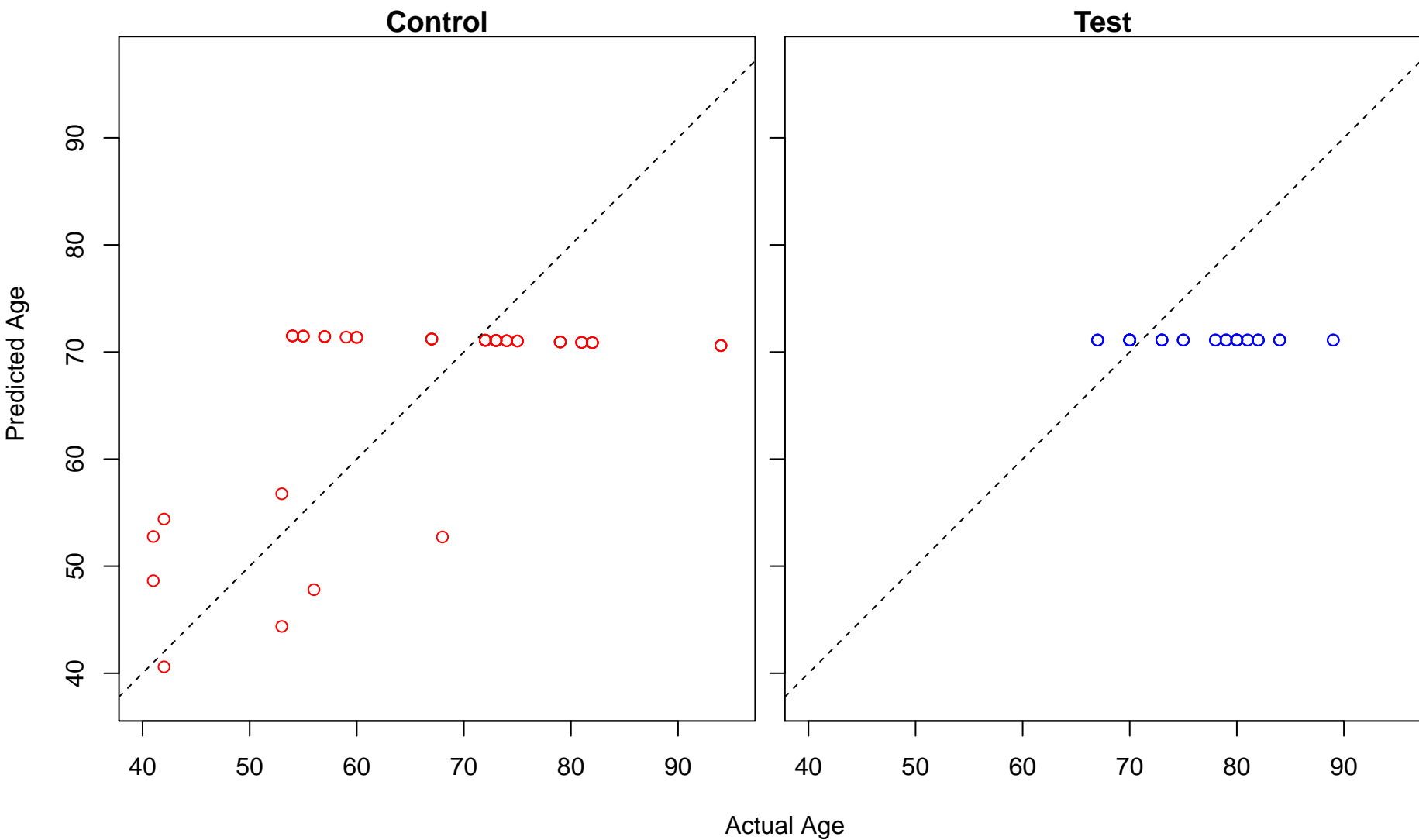
protein-DNA complex subunit organization (Score: 0.807546)



negative regulation of actin filament polymerization (Score: 0.807479)



regulation of cyclase activity (Score: 0.807337)

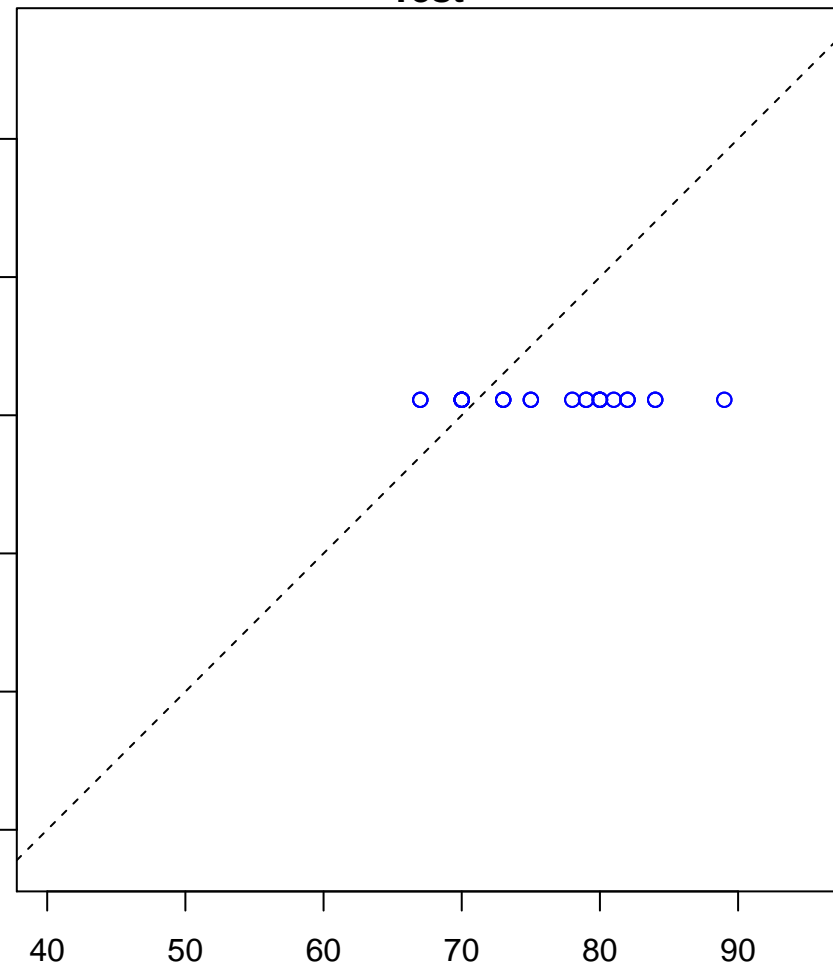
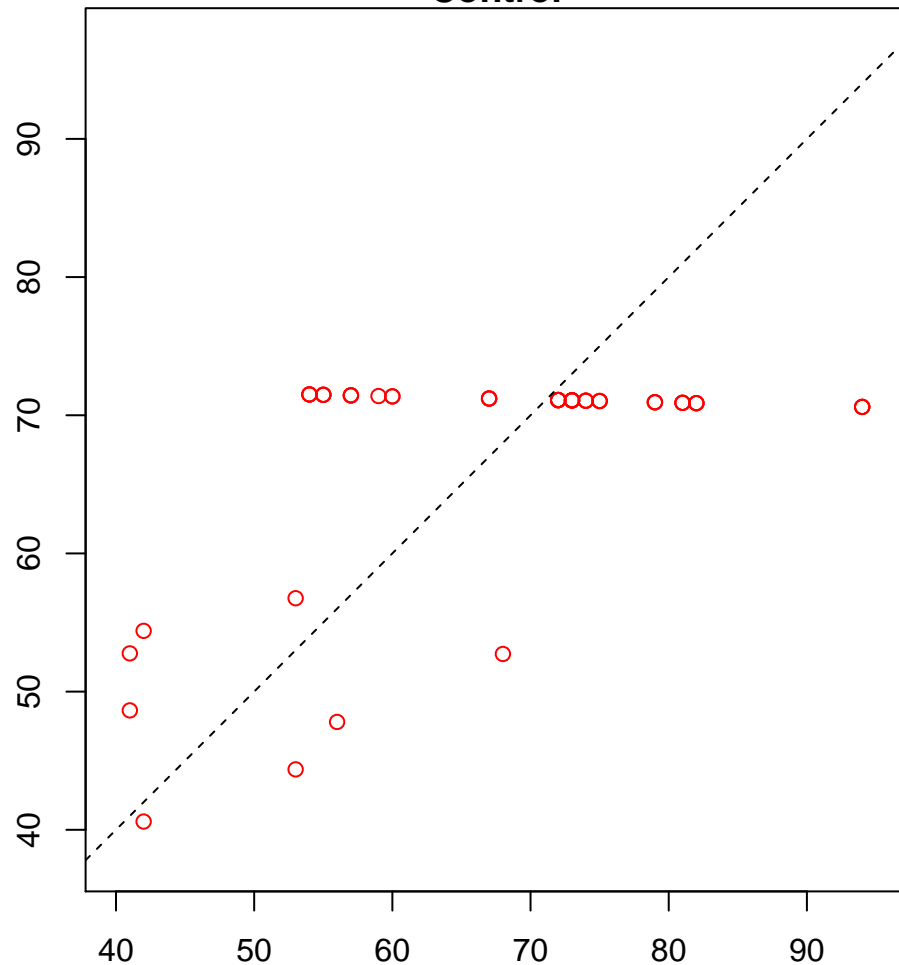


positive regulation of cyclase activity (Score: 0.807337)

Control

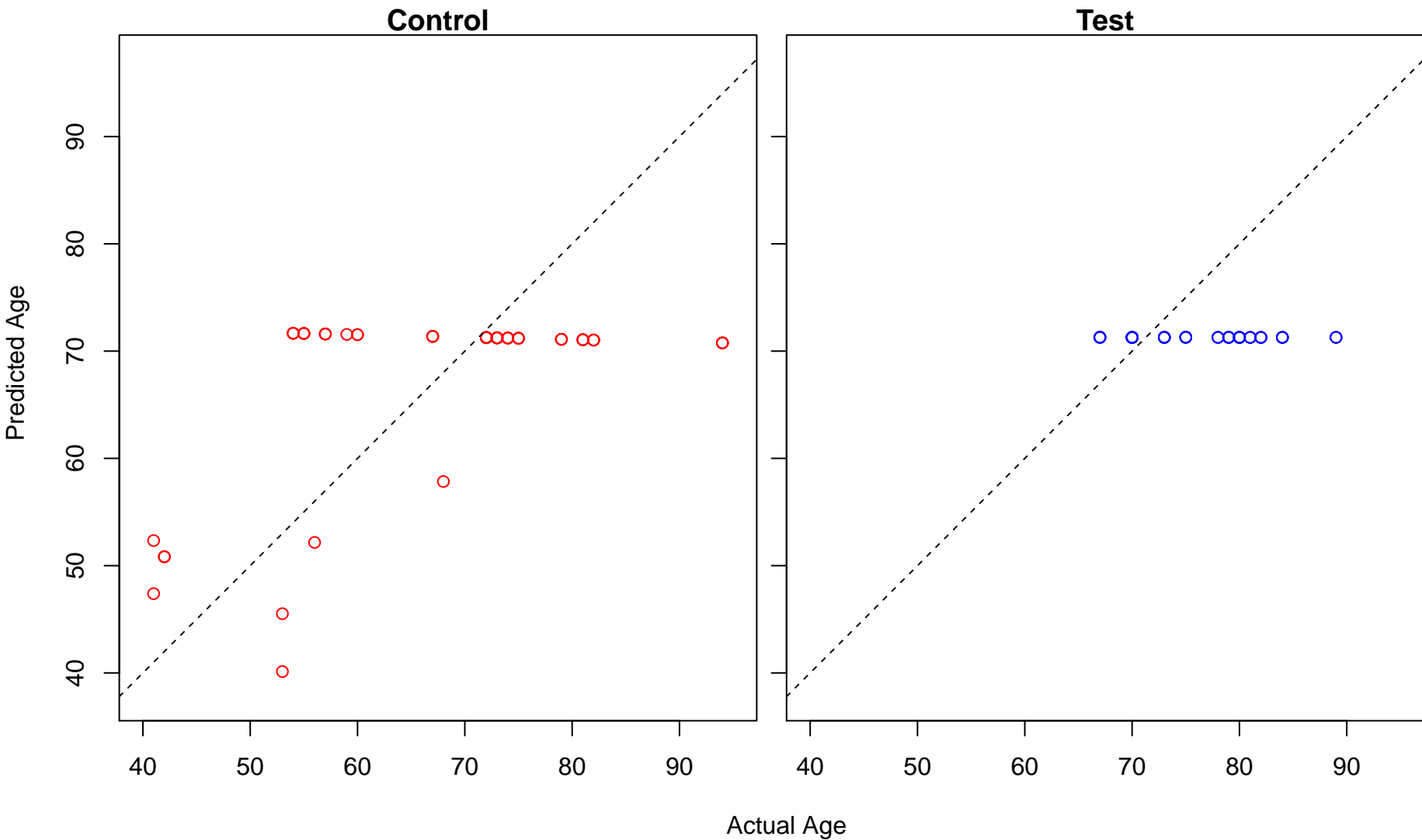
Test

Predicted Age

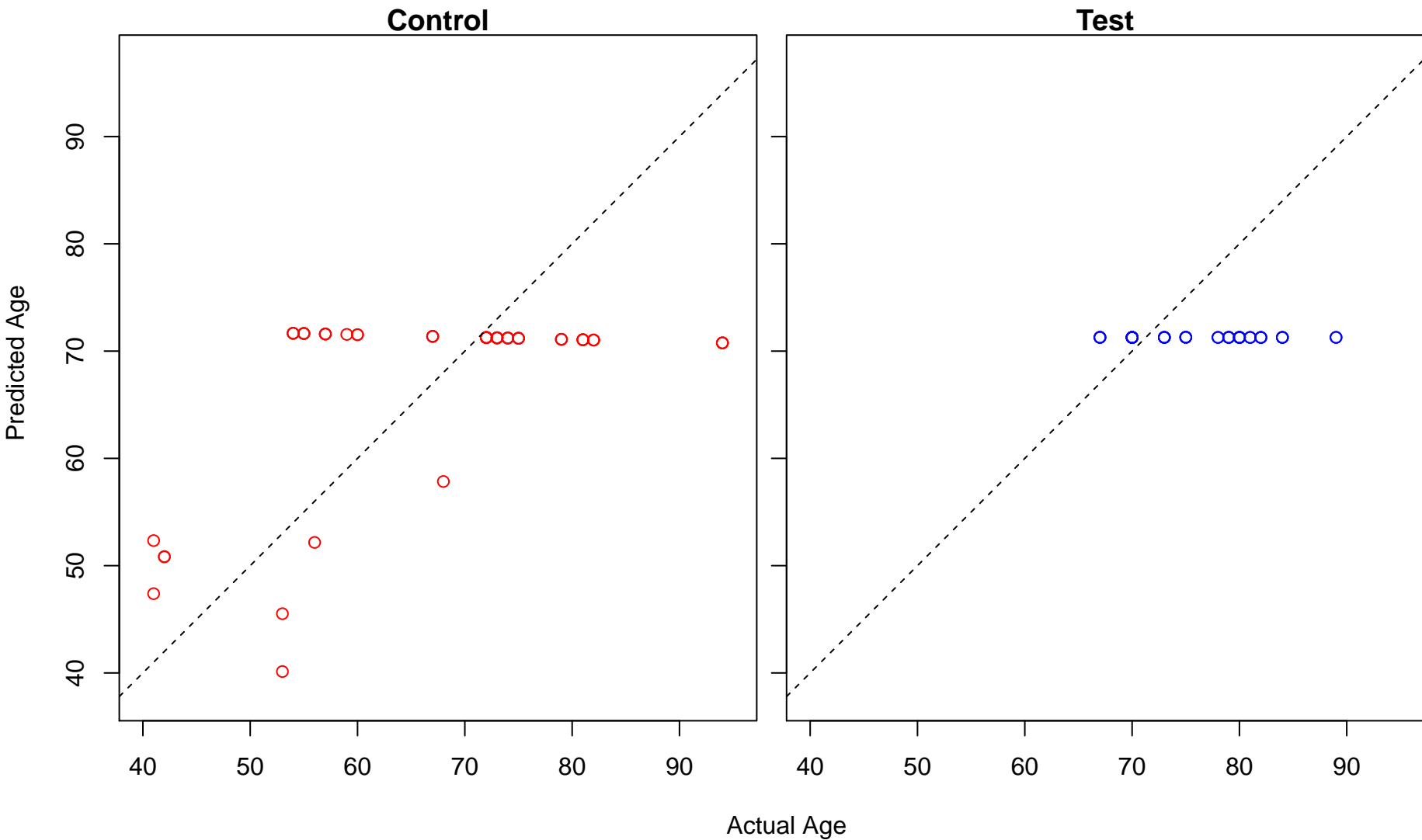


Actual Age

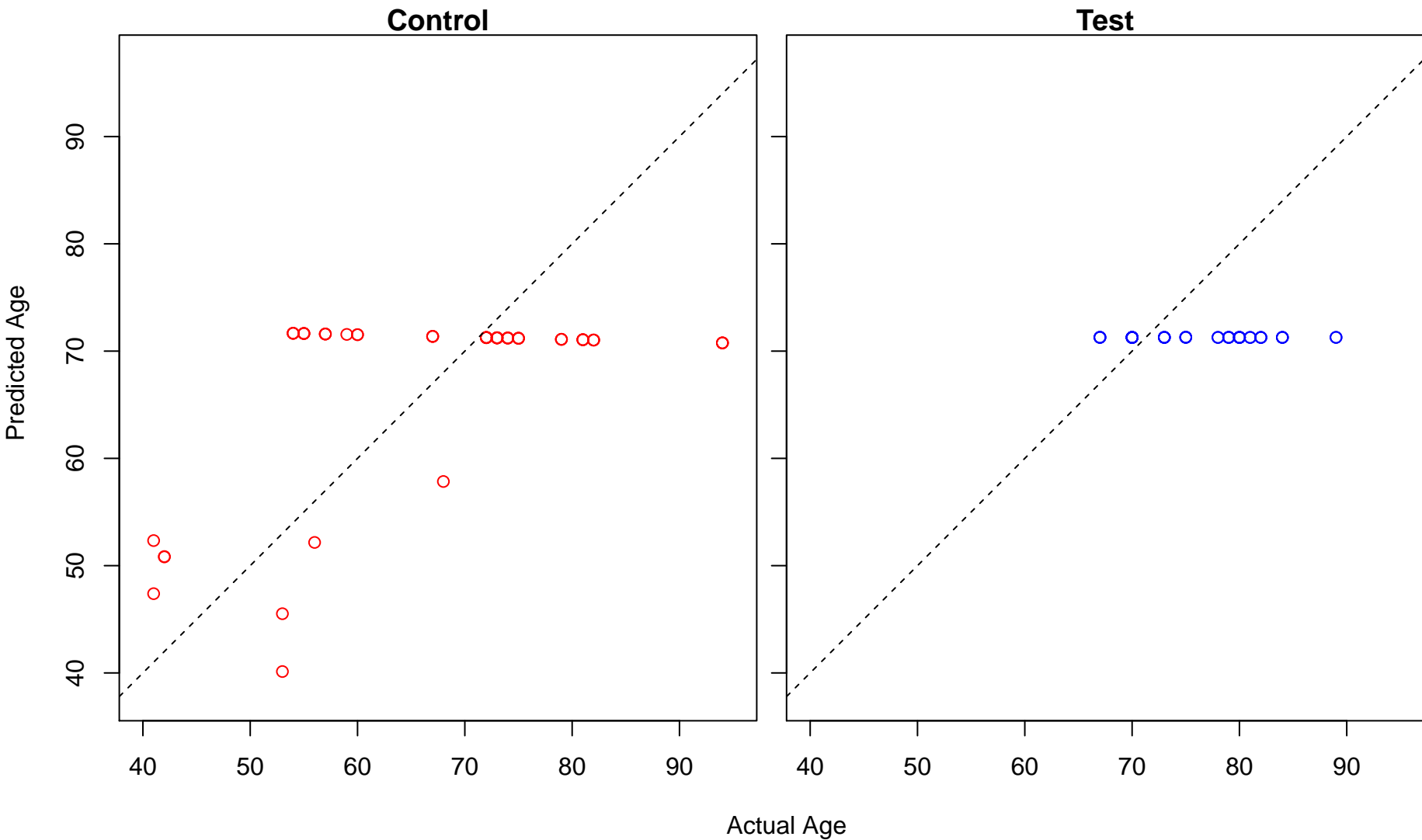
nucleoside diphosphate metabolic process (Score: 0.807217)



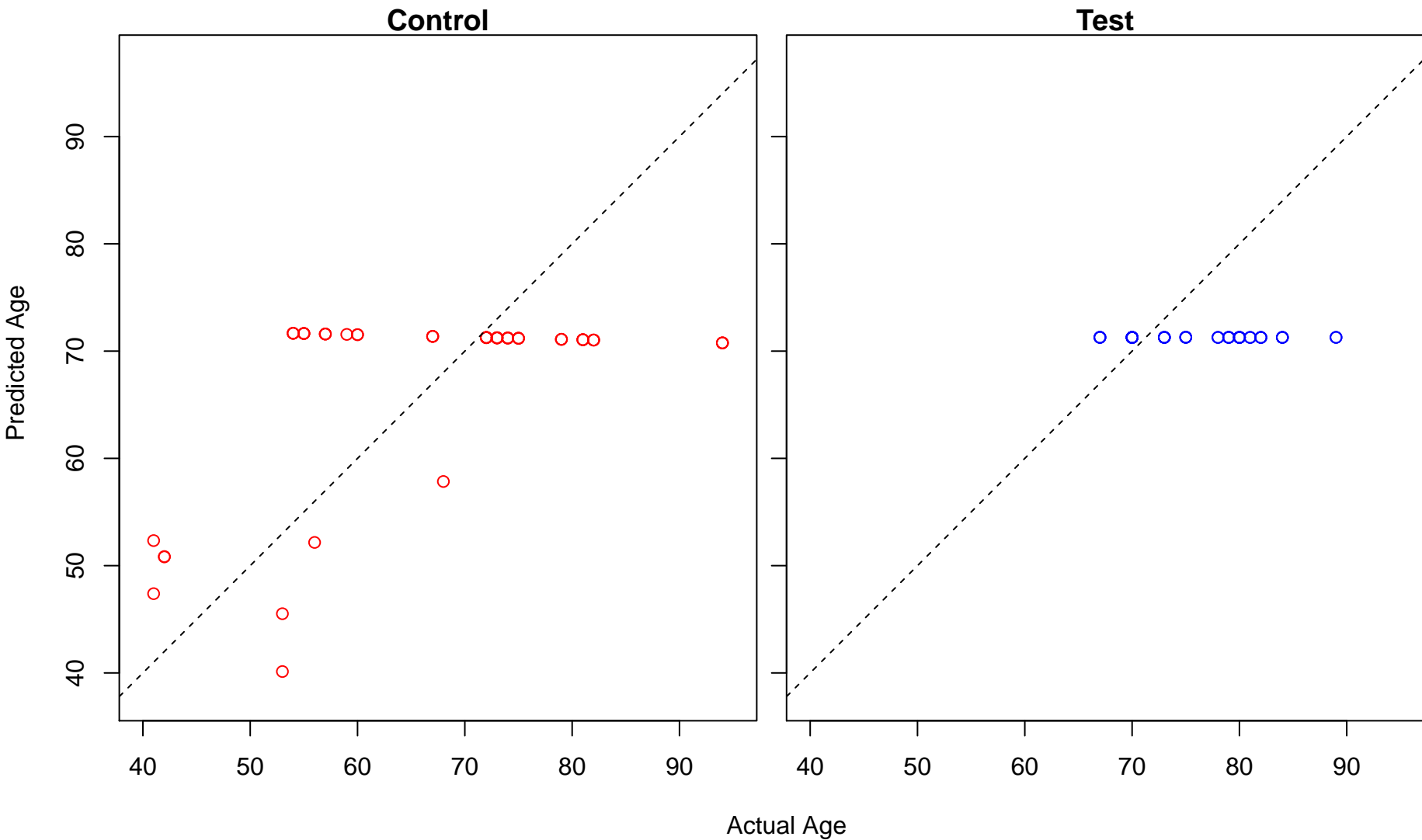
purine nucleoside diphosphate metabolic process (Score: 0.807217)



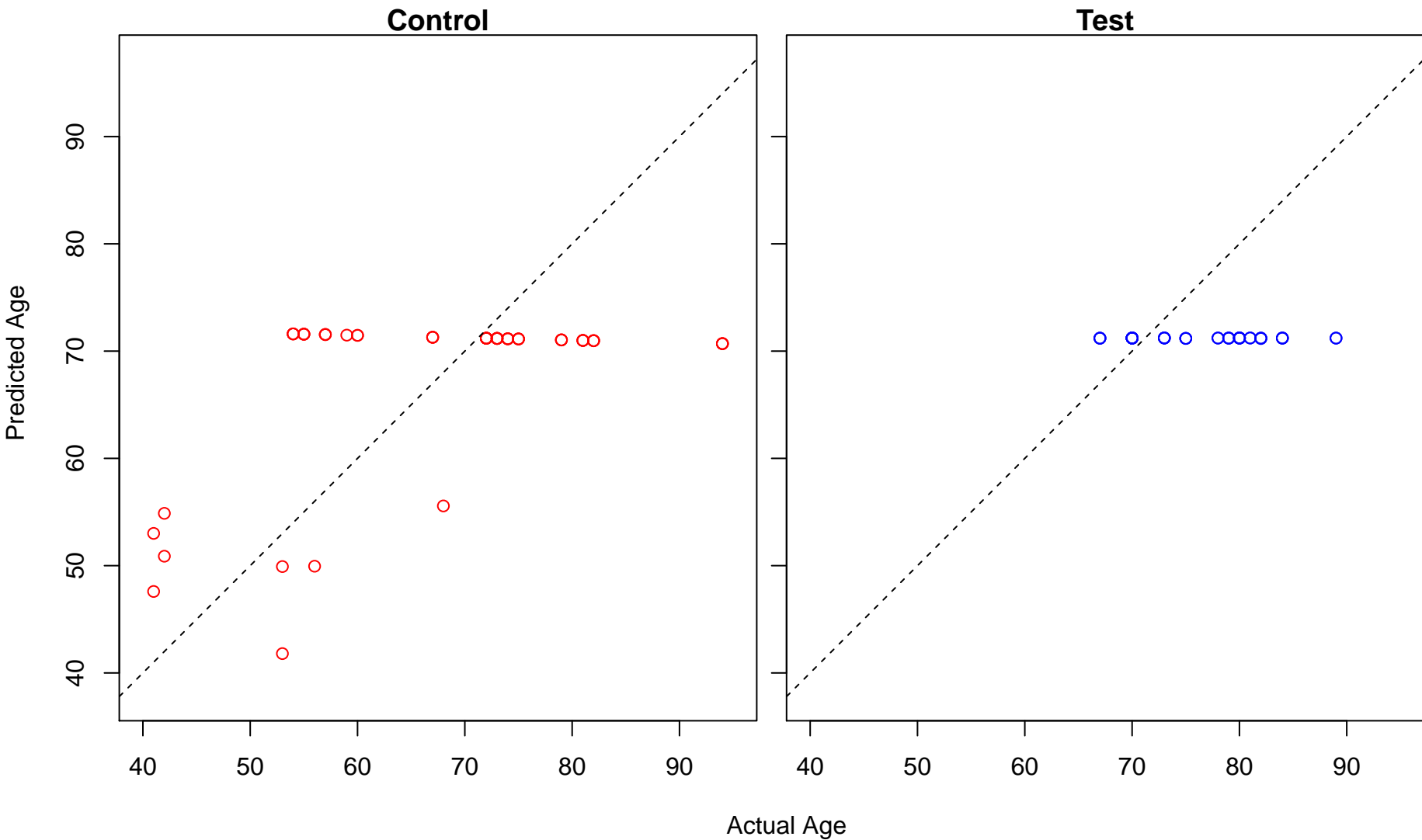
purine ribonucleoside diphosphate metabolic process (Score: 0.807217)



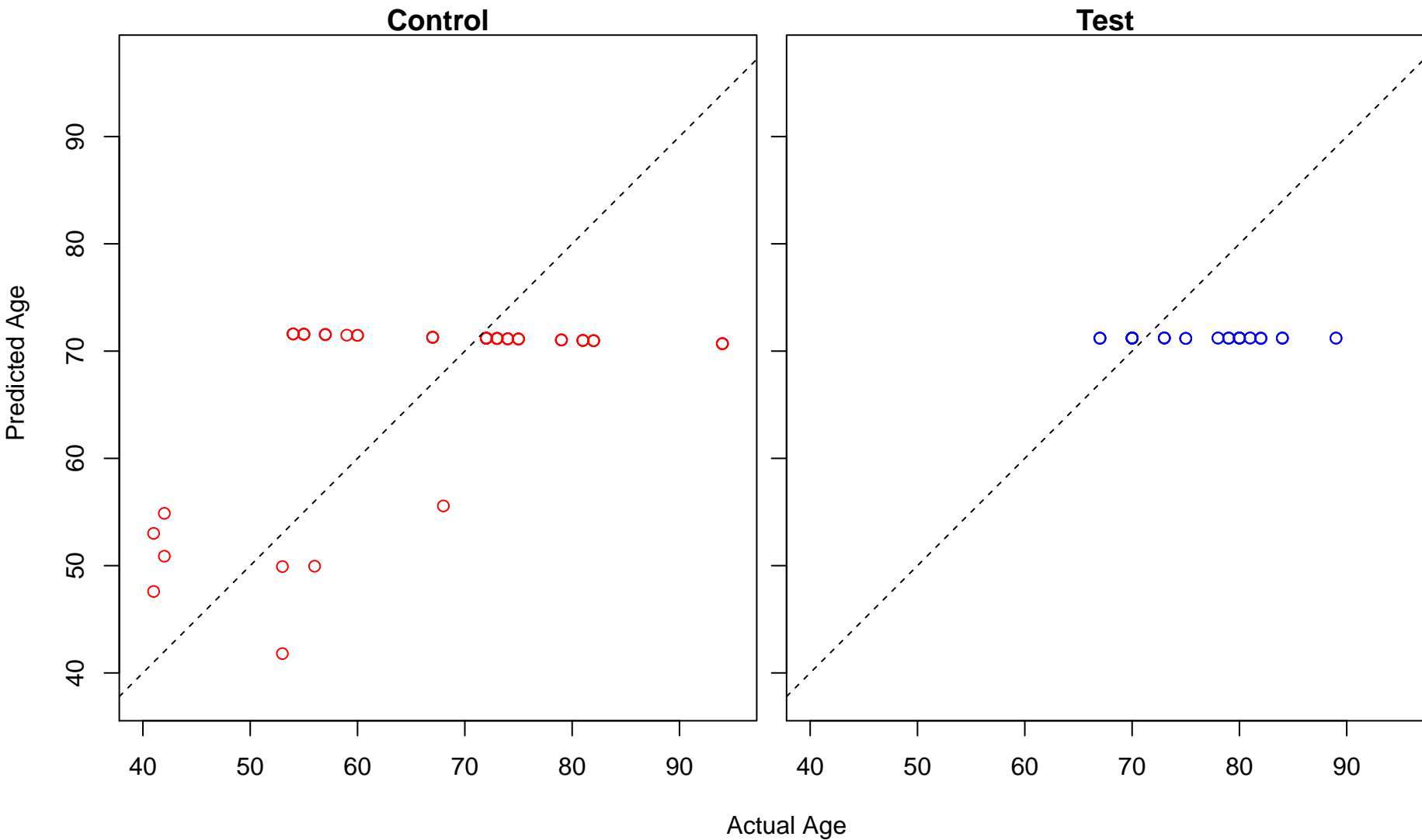
ribonucleoside diphosphate metabolic process (Score: 0.807217)



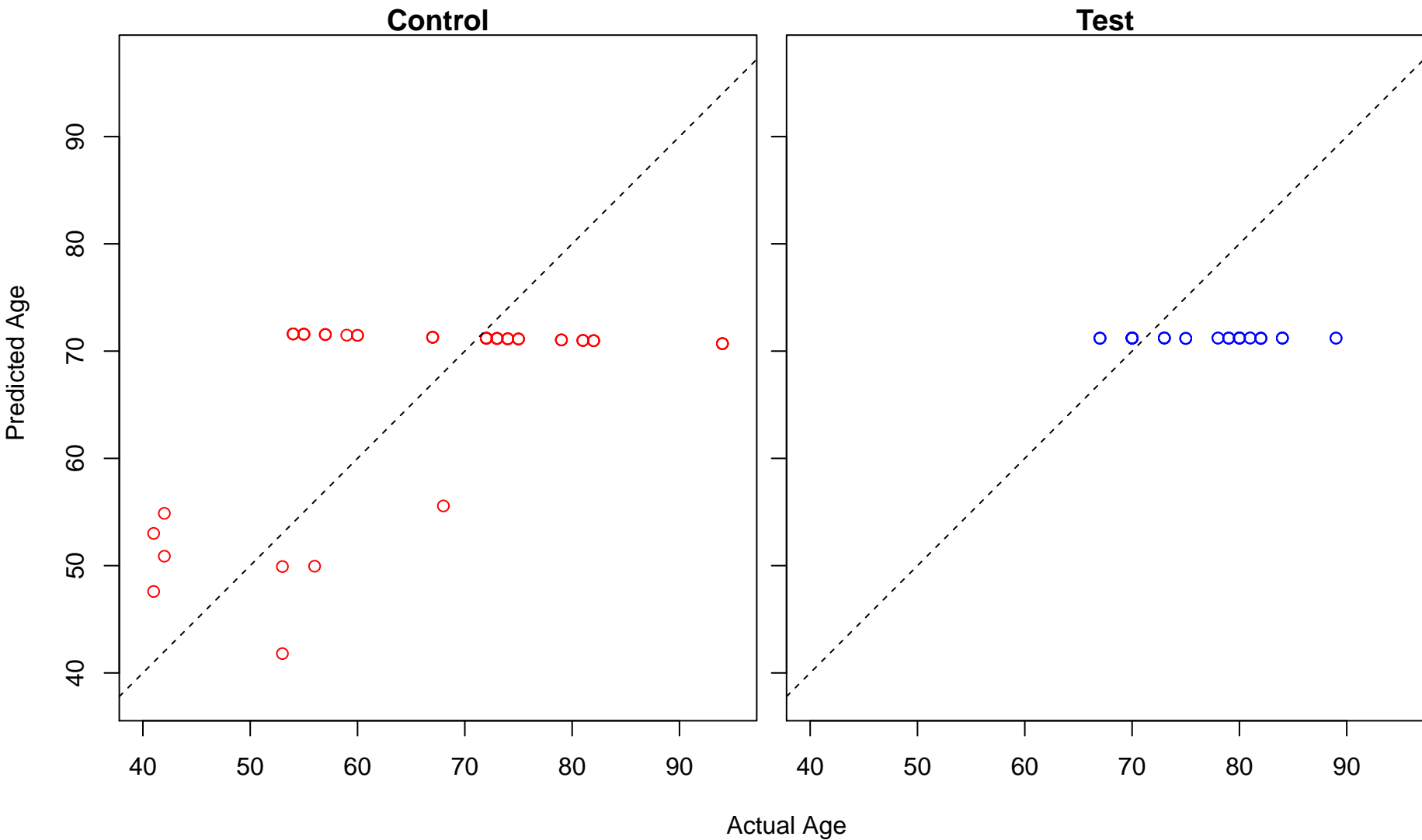
cholesterol homeostasis (Score: 0.807208)



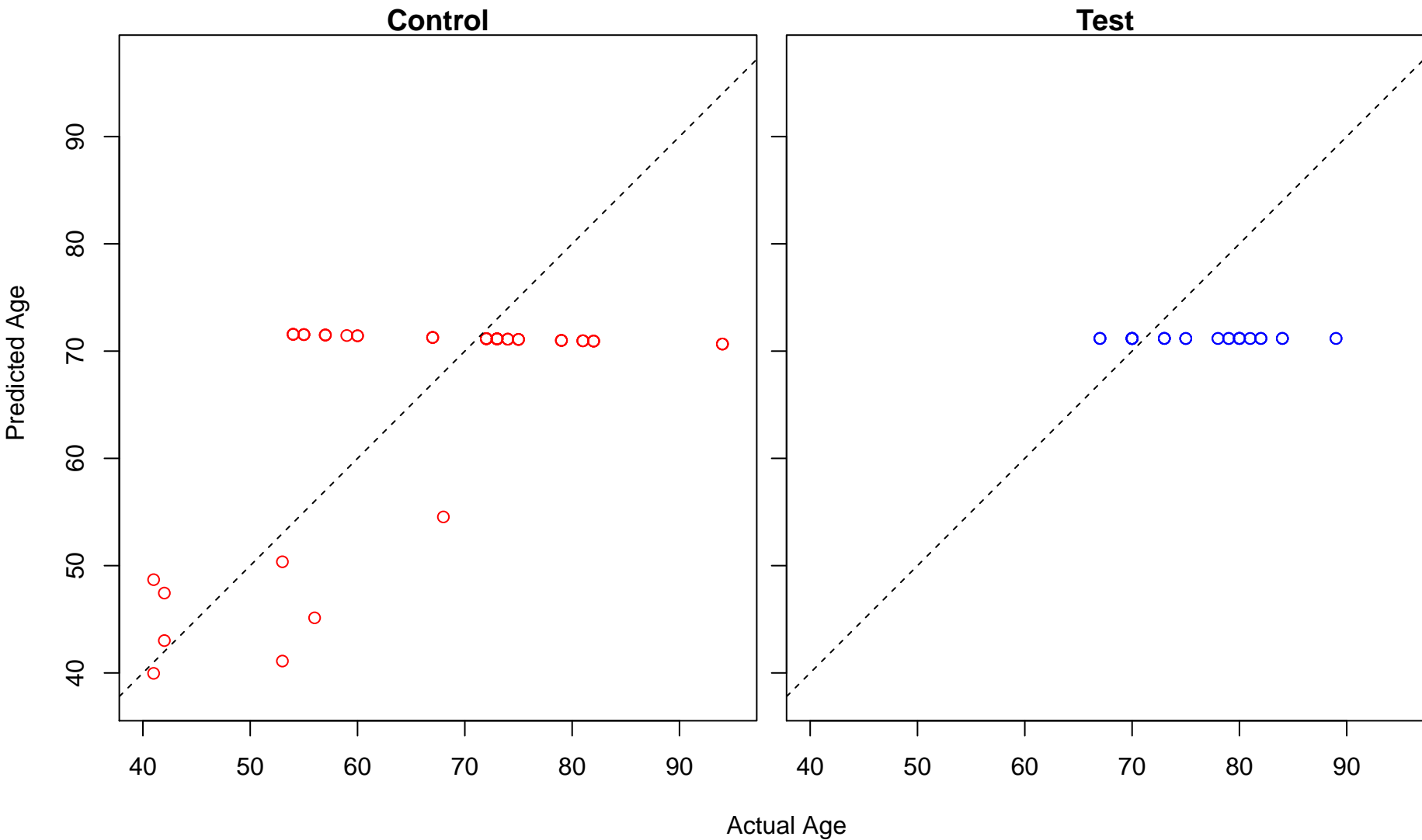
lipid homeostasis (Score: 0.807208)



sterol homeostasis (Score: 0.807208)

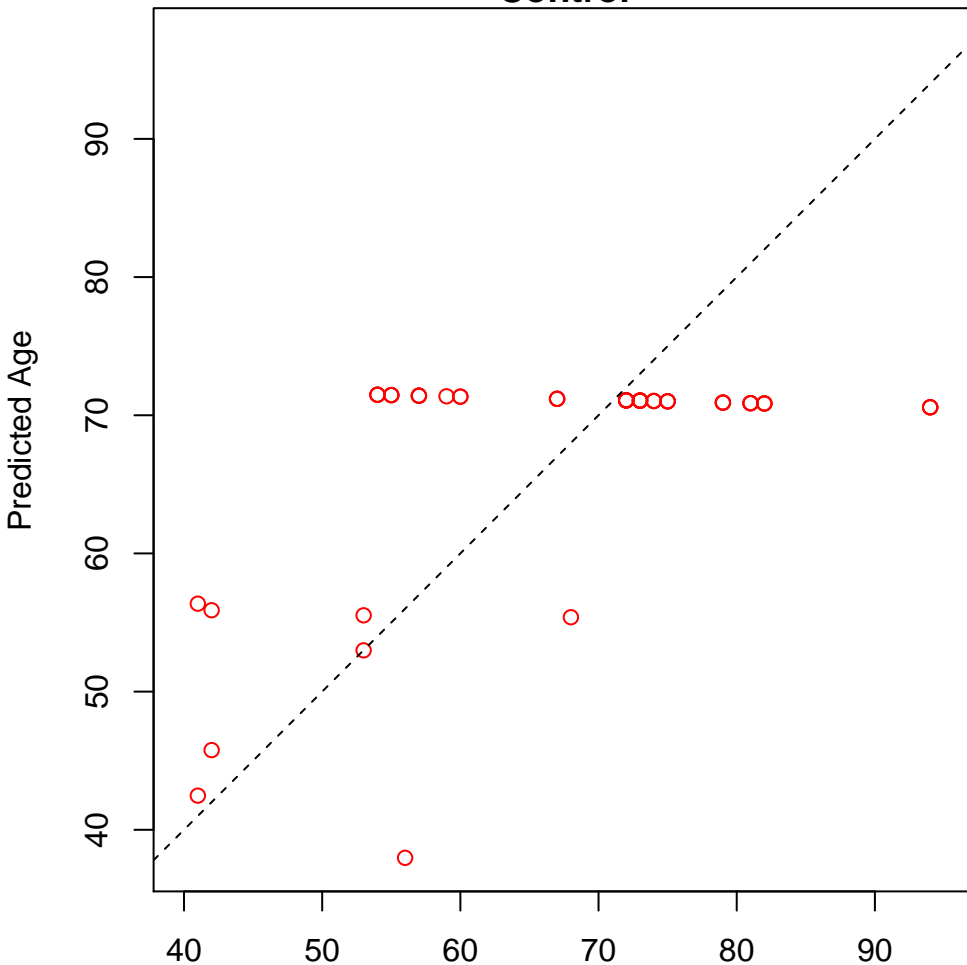


organelle organization (Score: 0.807154)

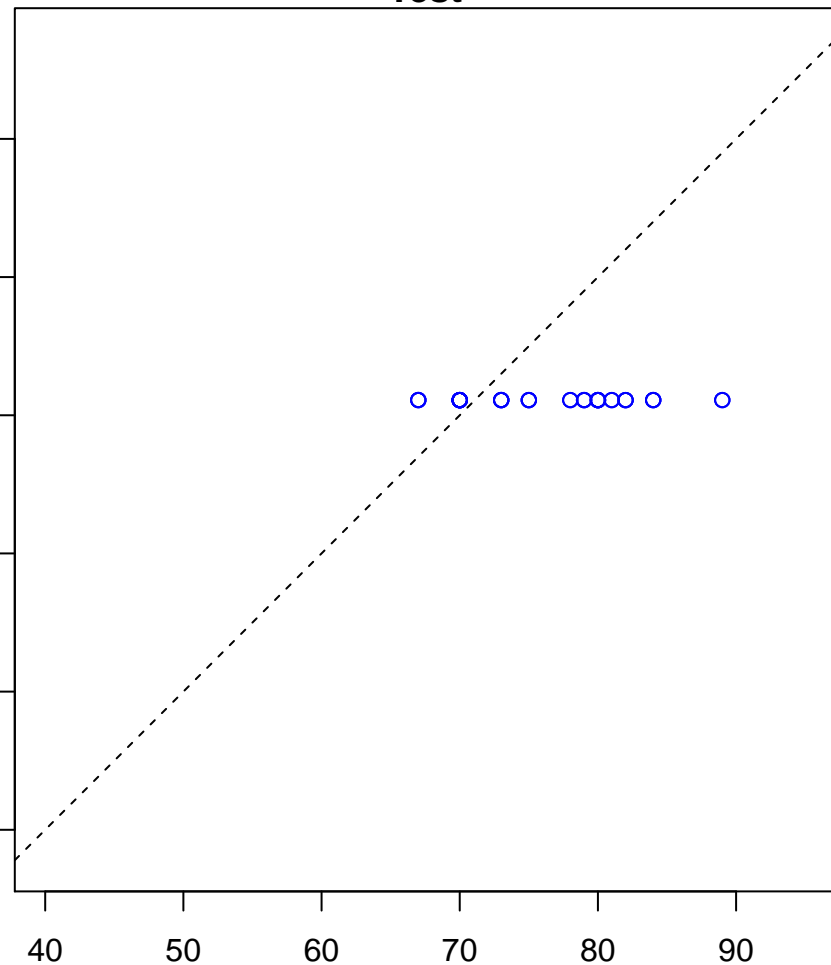


macromolecular complex assembly (Score: 0.807121)

Control



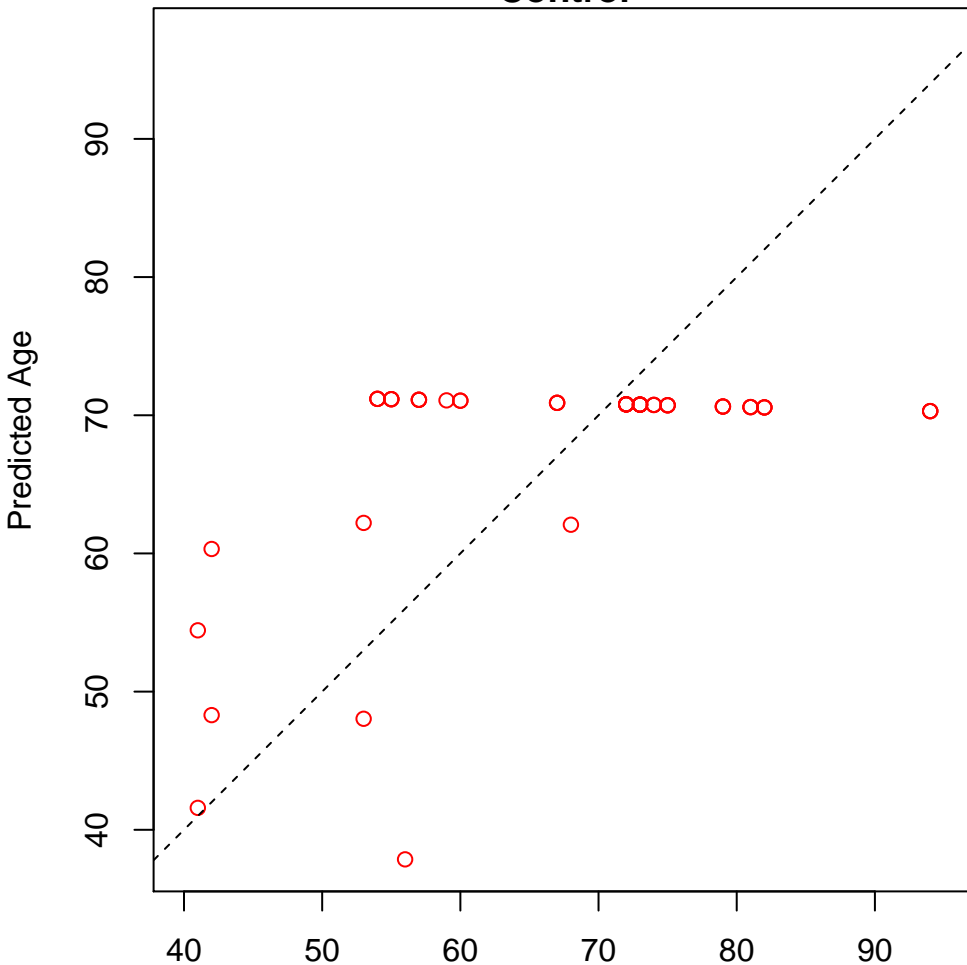
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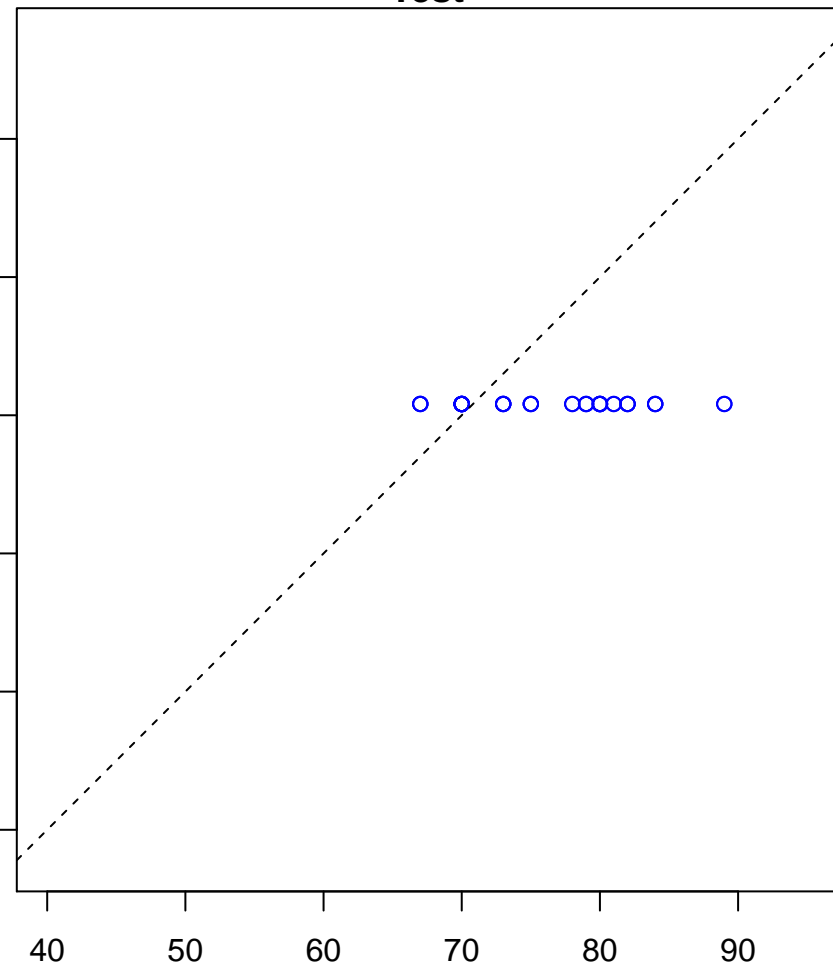
Actual Age

platelet aggregation (Score: 0.807094)

Control



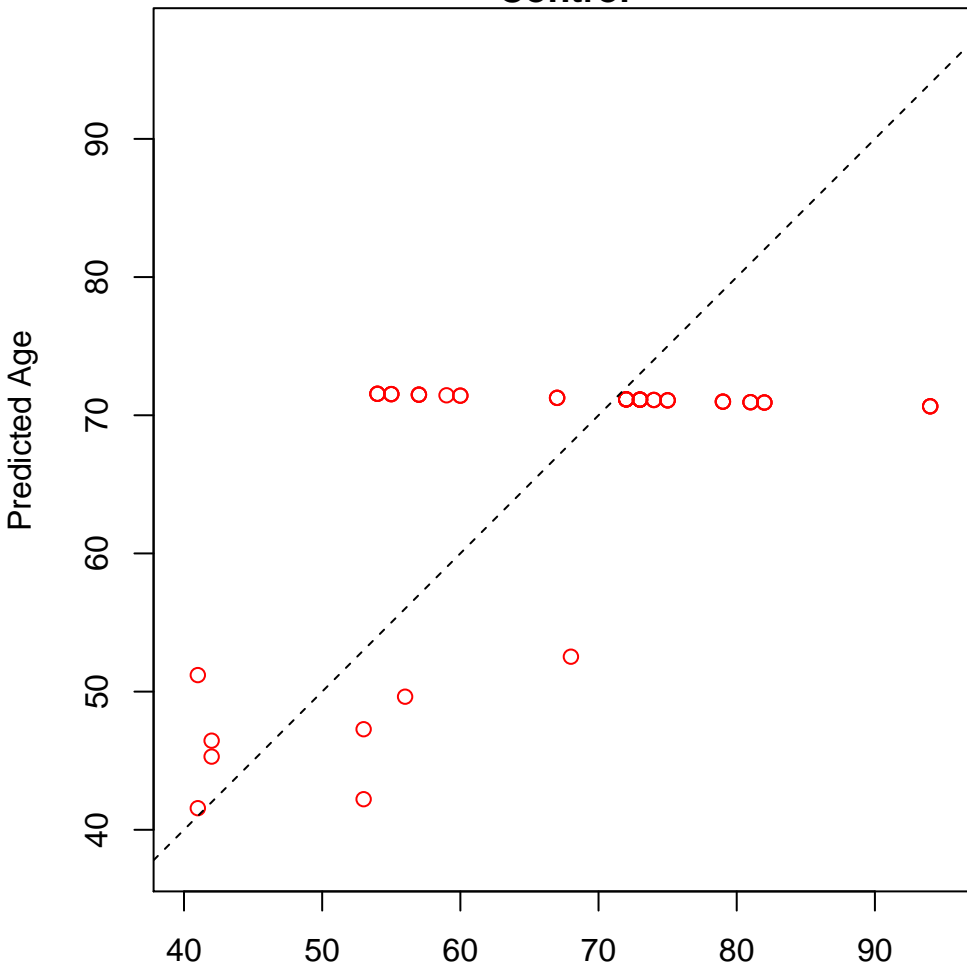
Test



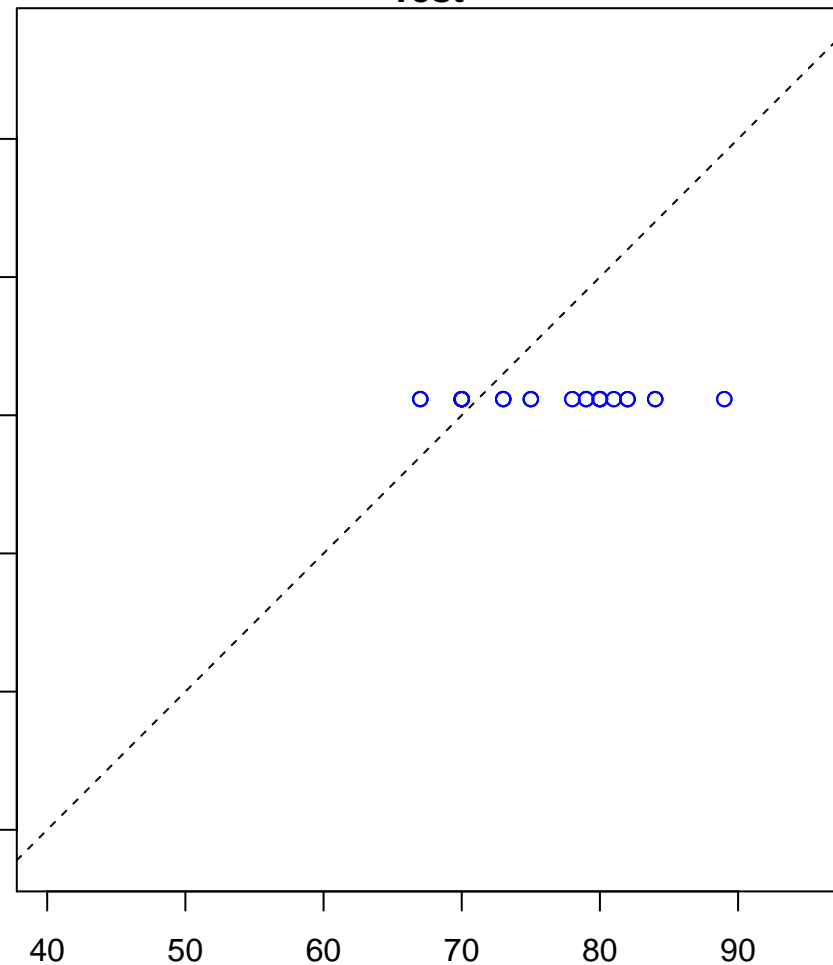
Actual Age

regulation of immune response (Score: 0.807084)

Control



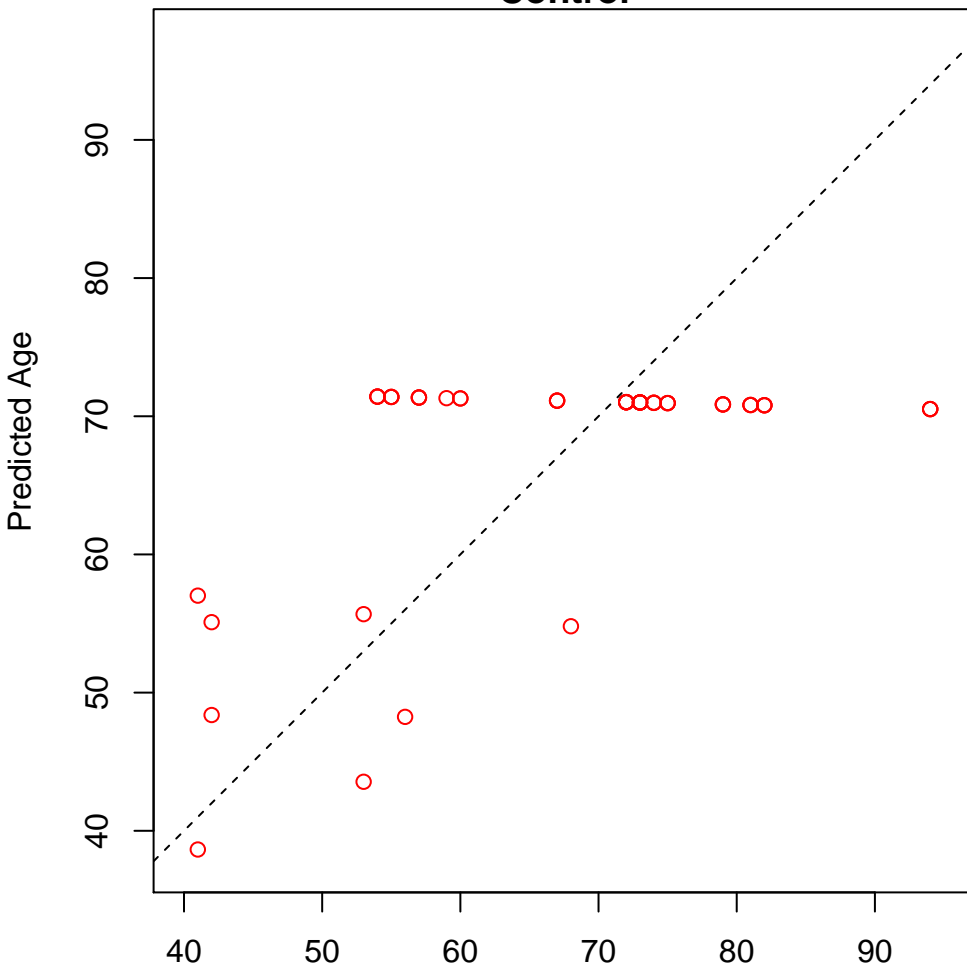
Test



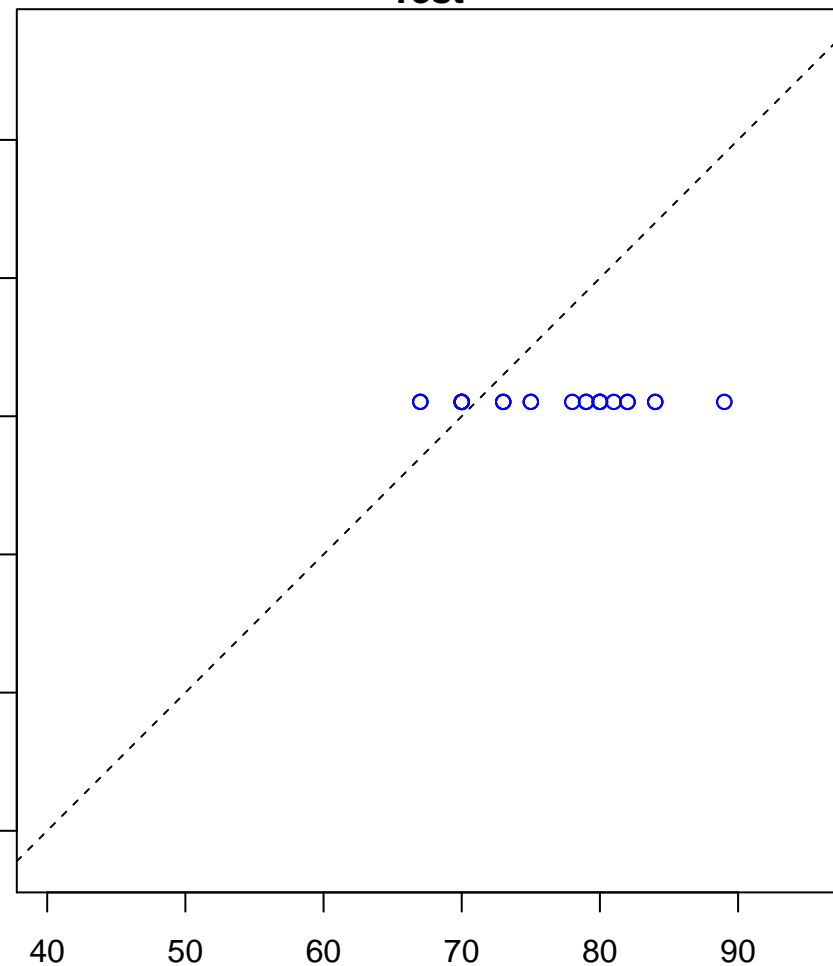
Actual Age

positive regulation of protein processing (Score: 0.807071)

Control



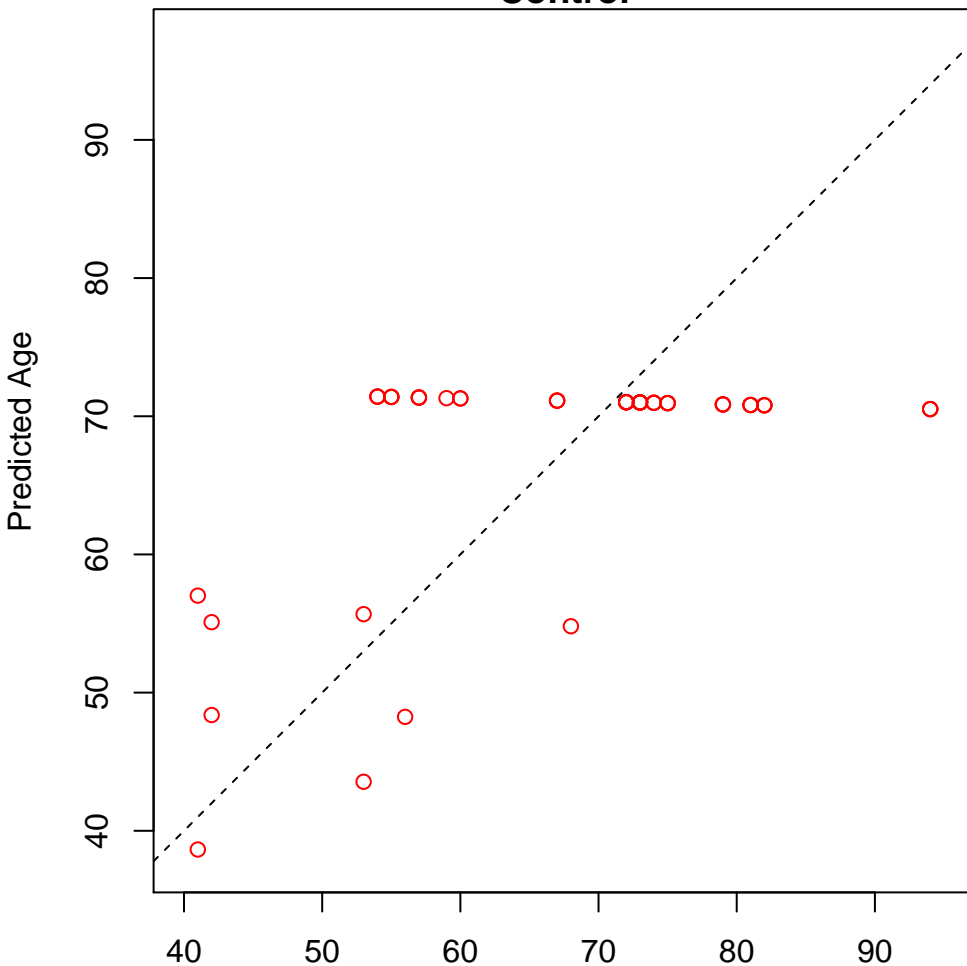
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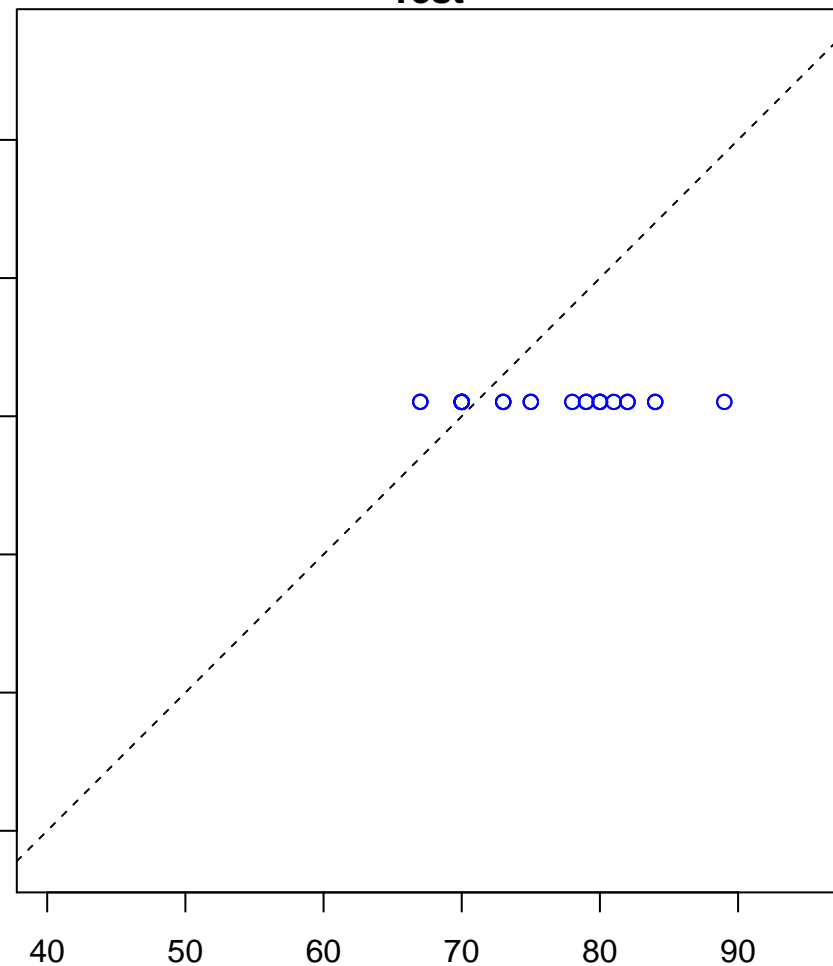
Actual Age

positive regulation of protein maturation (Score: 0.807071)

Control

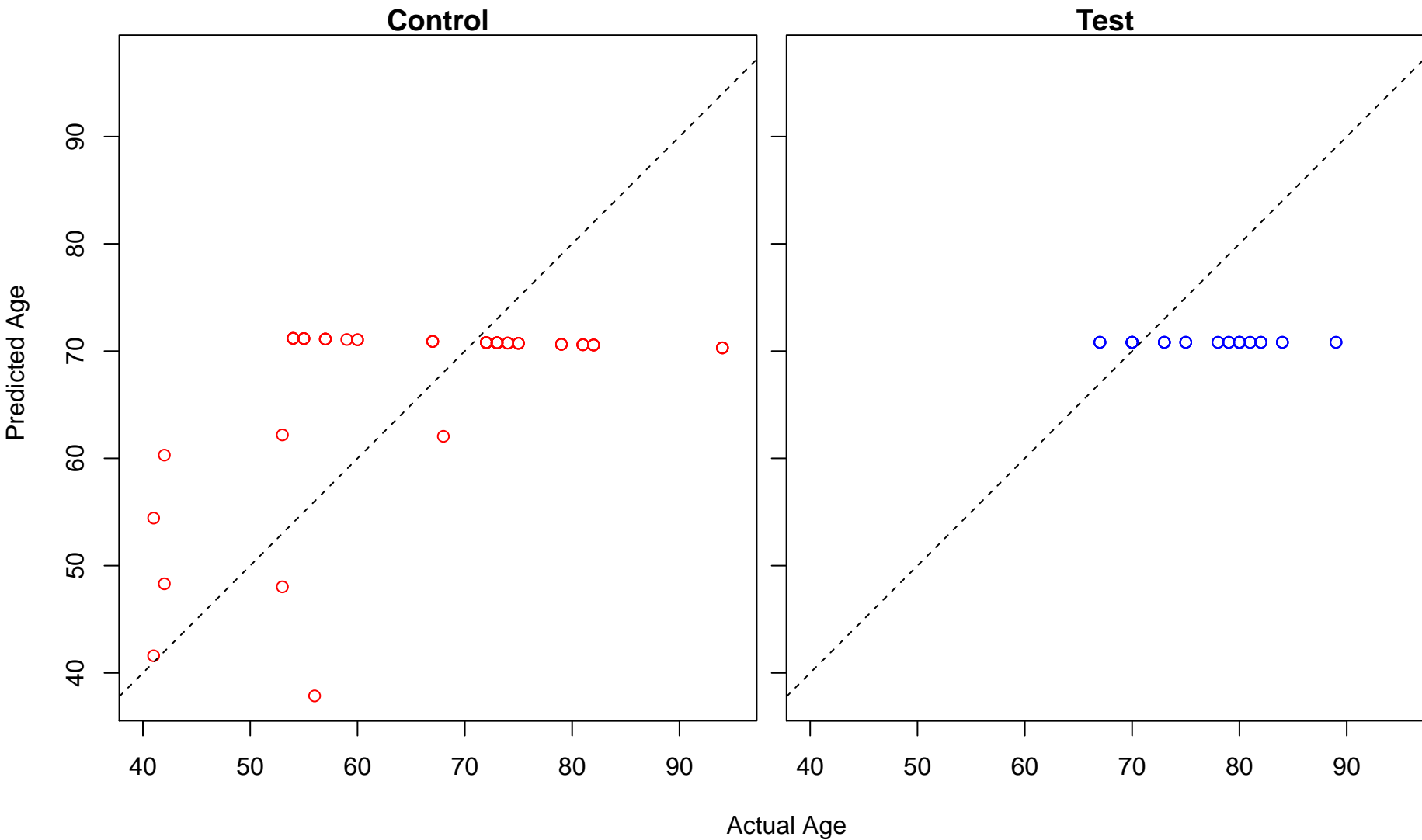


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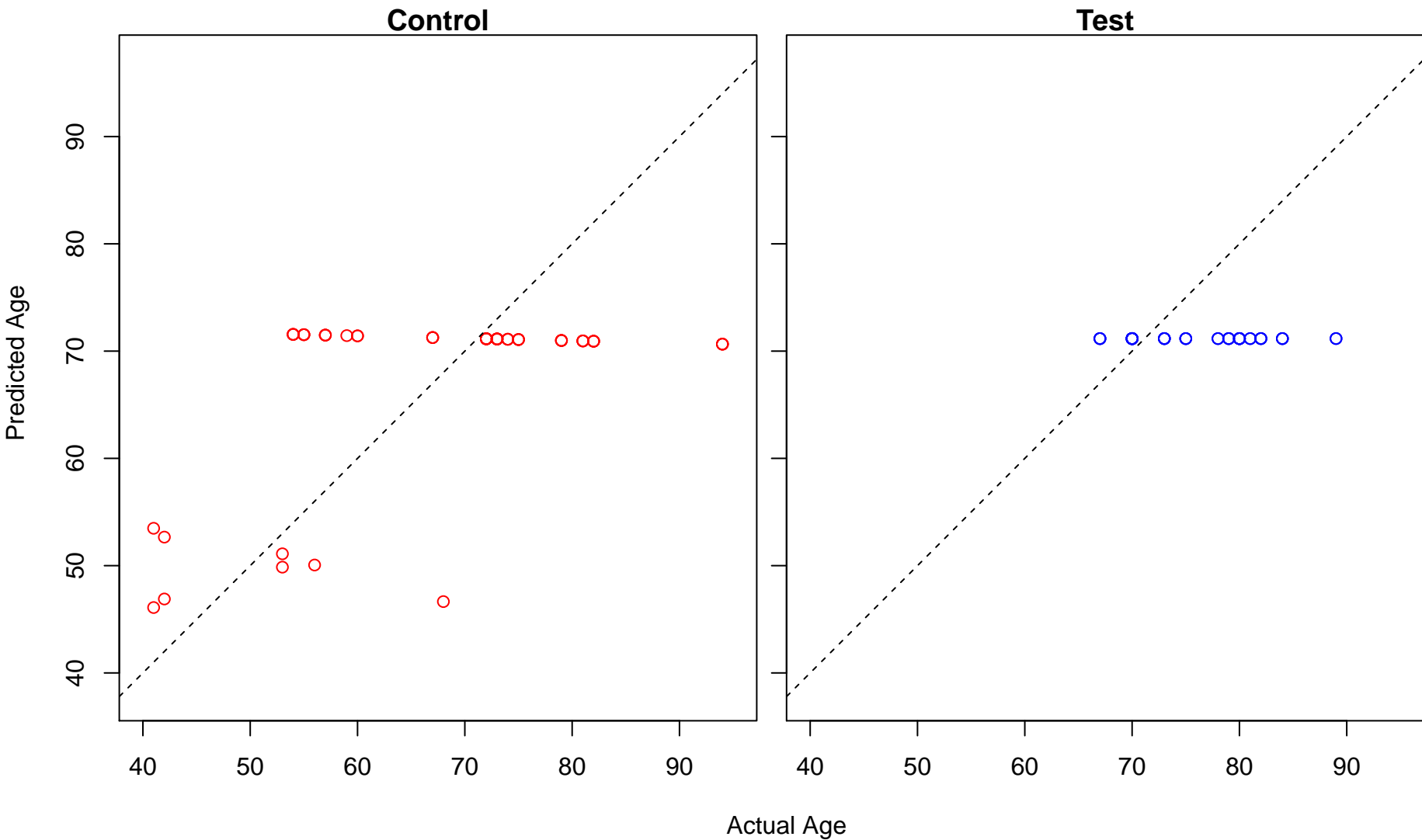


Actual Age

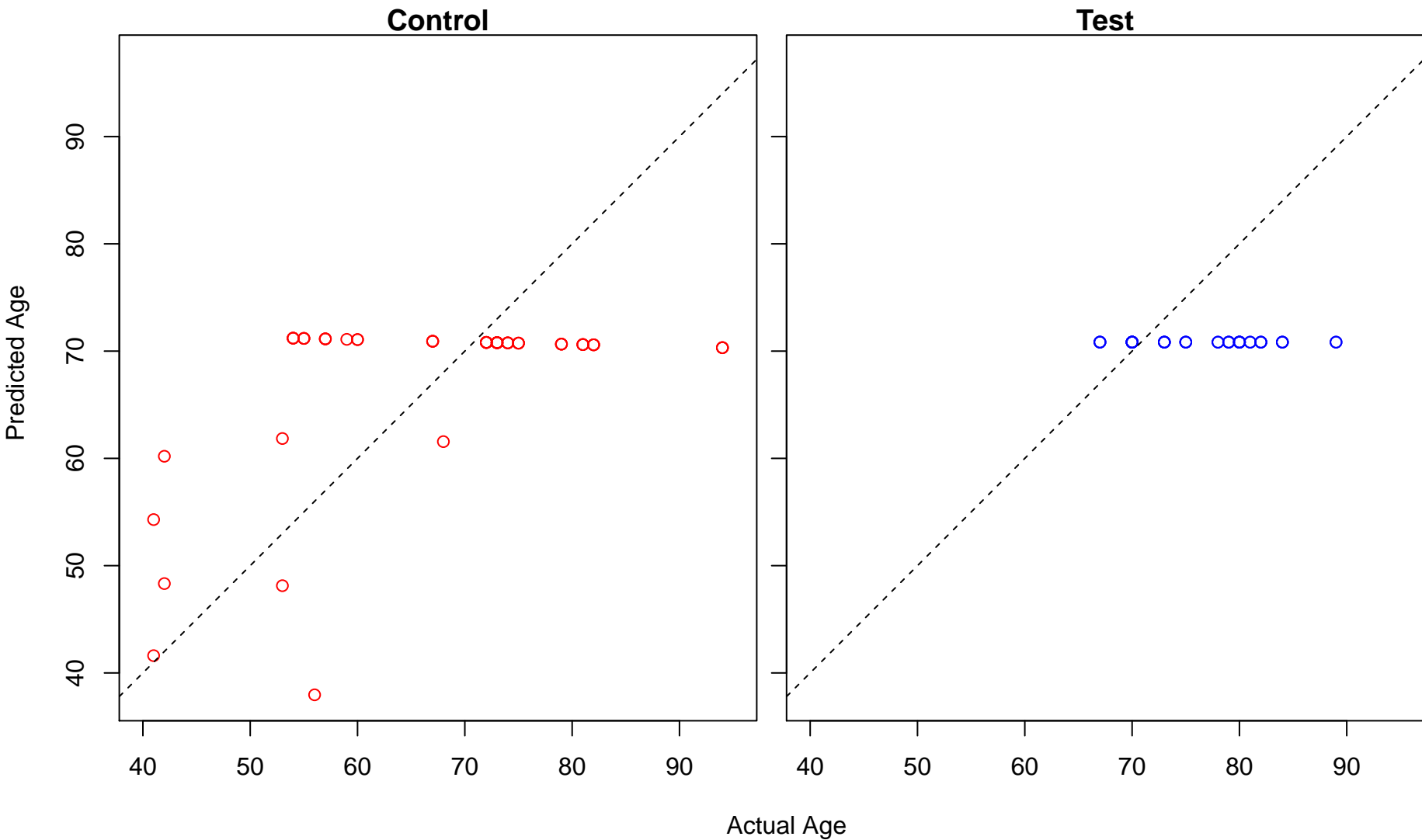
homotypic cell-cell adhesion (Score: 0.807065)



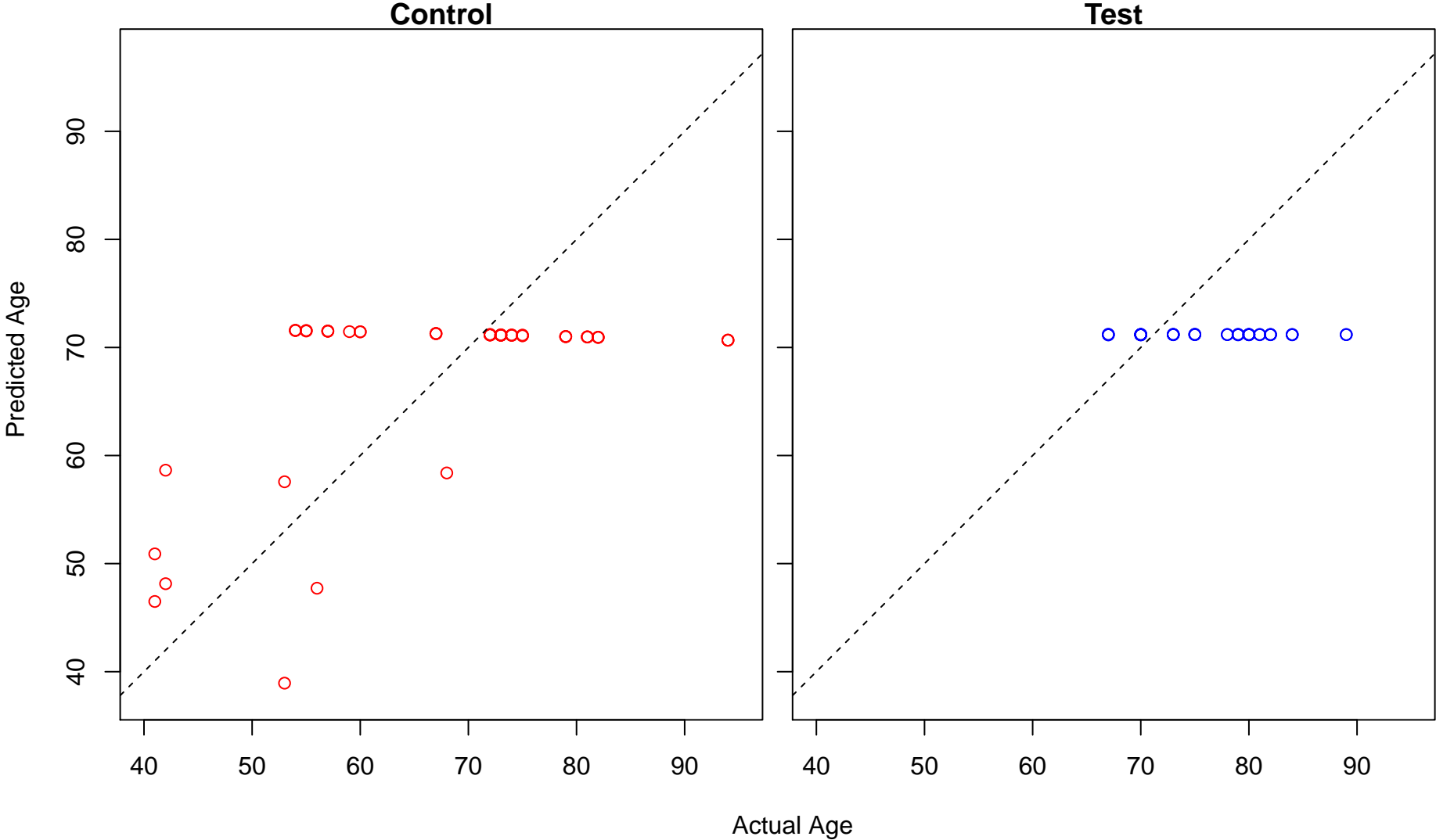
protein heterooligomerization (Score: 0.807060)



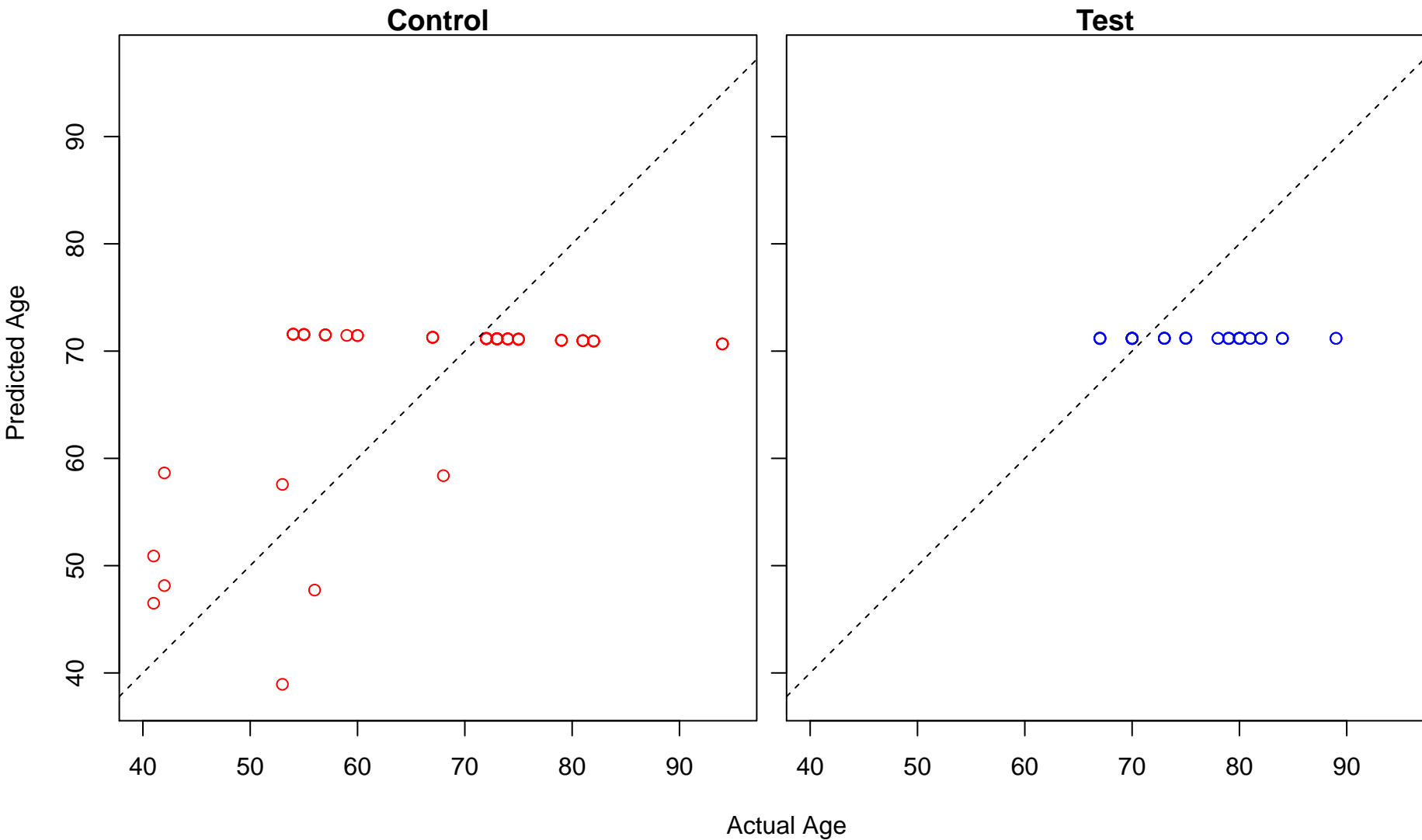
cell-cell adhesion (Score: 0.806955)



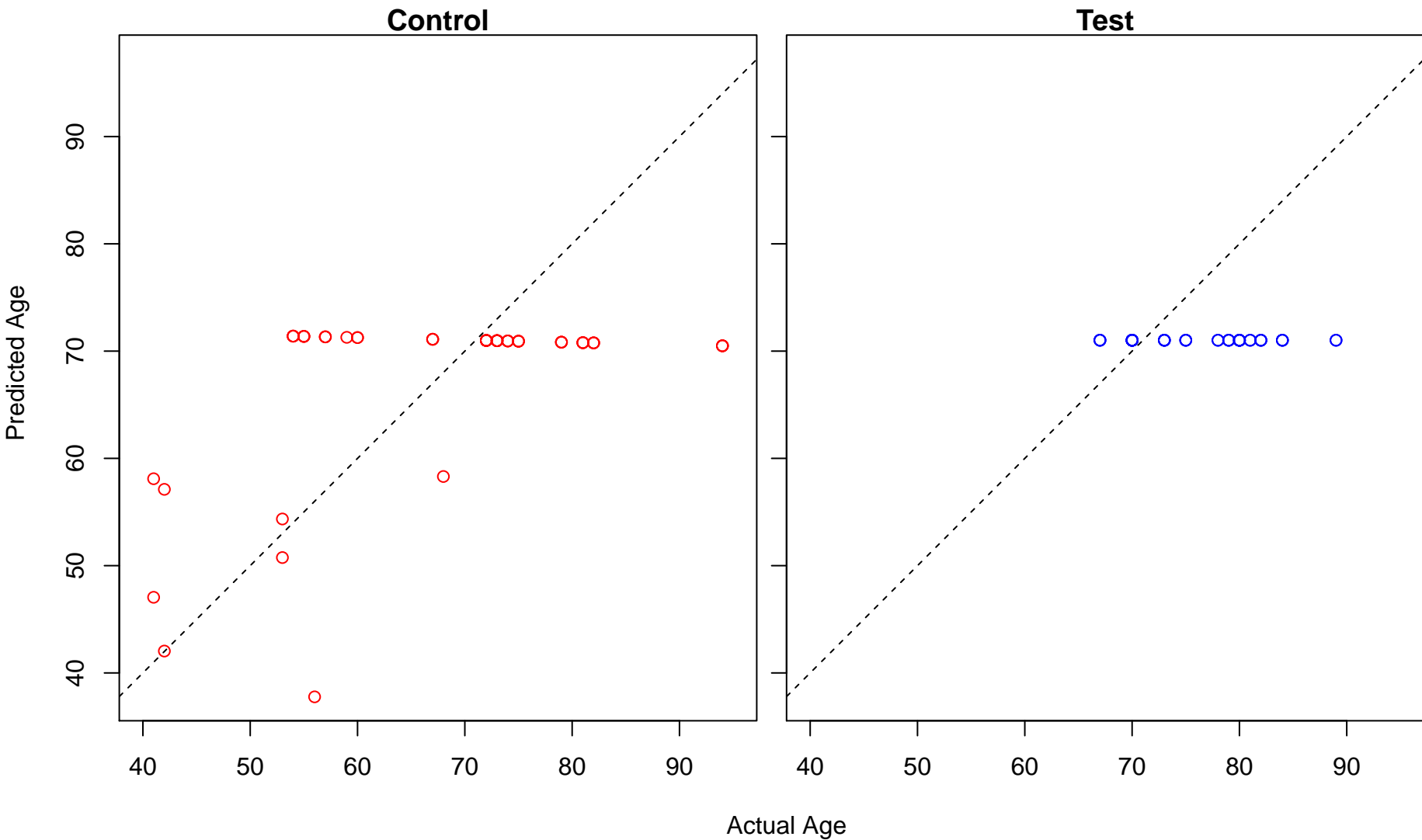
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 0.80)



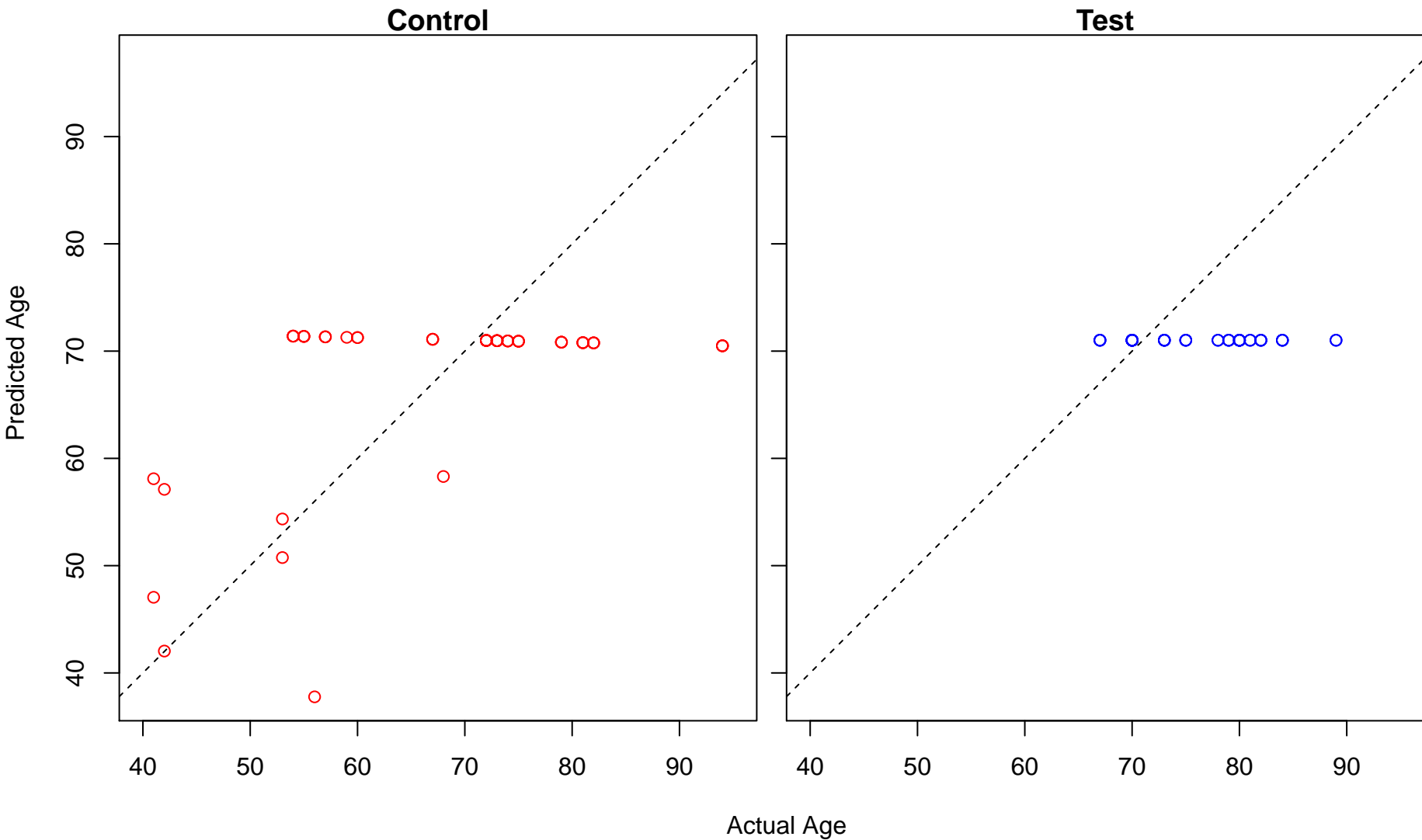
negative regulation of cysteine-type endopeptidase activity (Score: 0.806786)



regulation of epidermal growth factor receptor signaling pathway (Score: 0.806673)

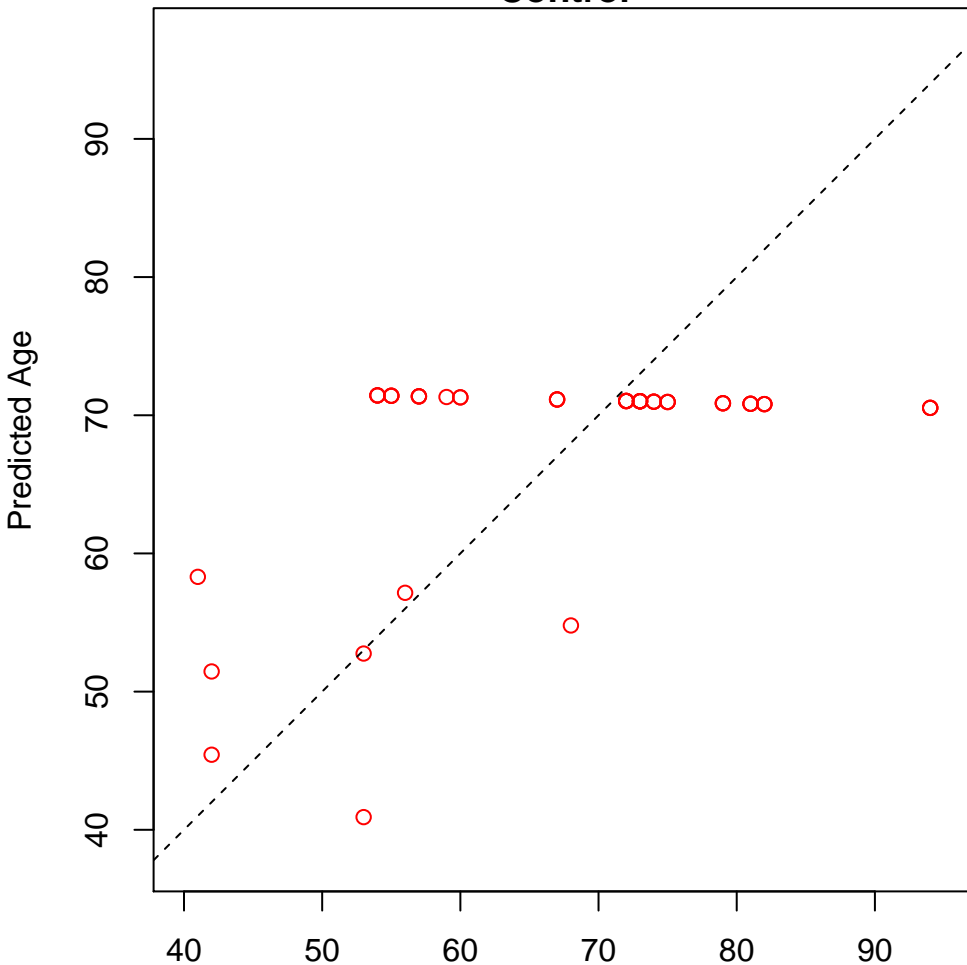


regulation of ERBB signaling pathway (Score: 0.806673)

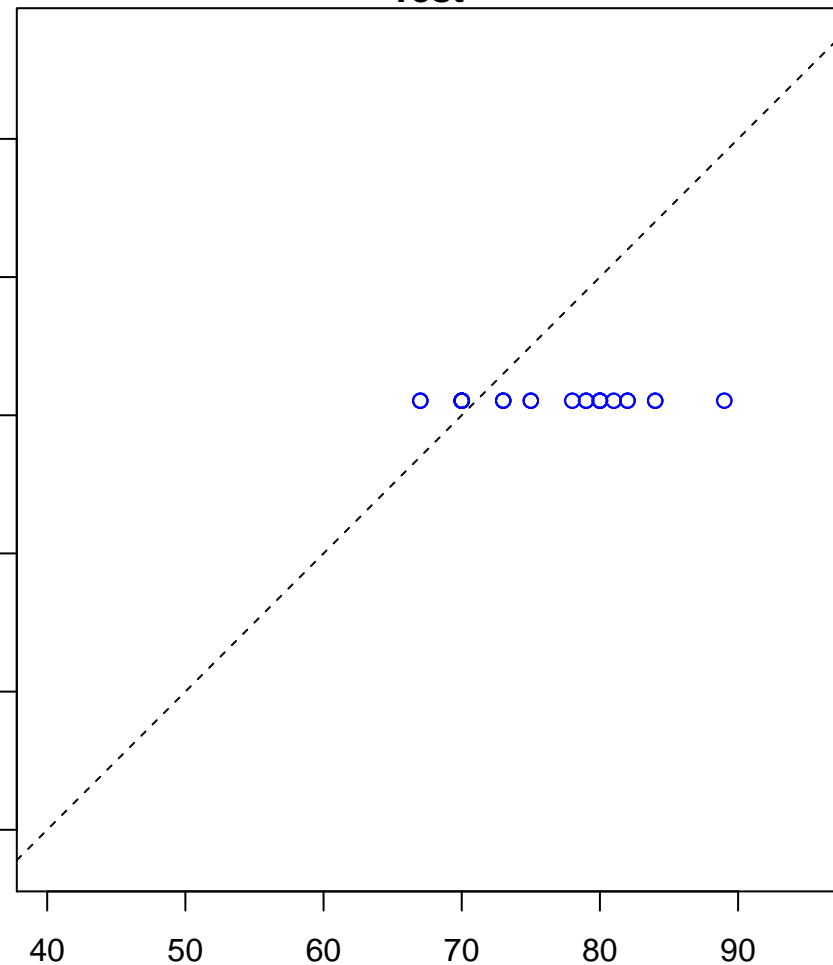


cellular aldehyde metabolic process (Score: 0.806622)

Control

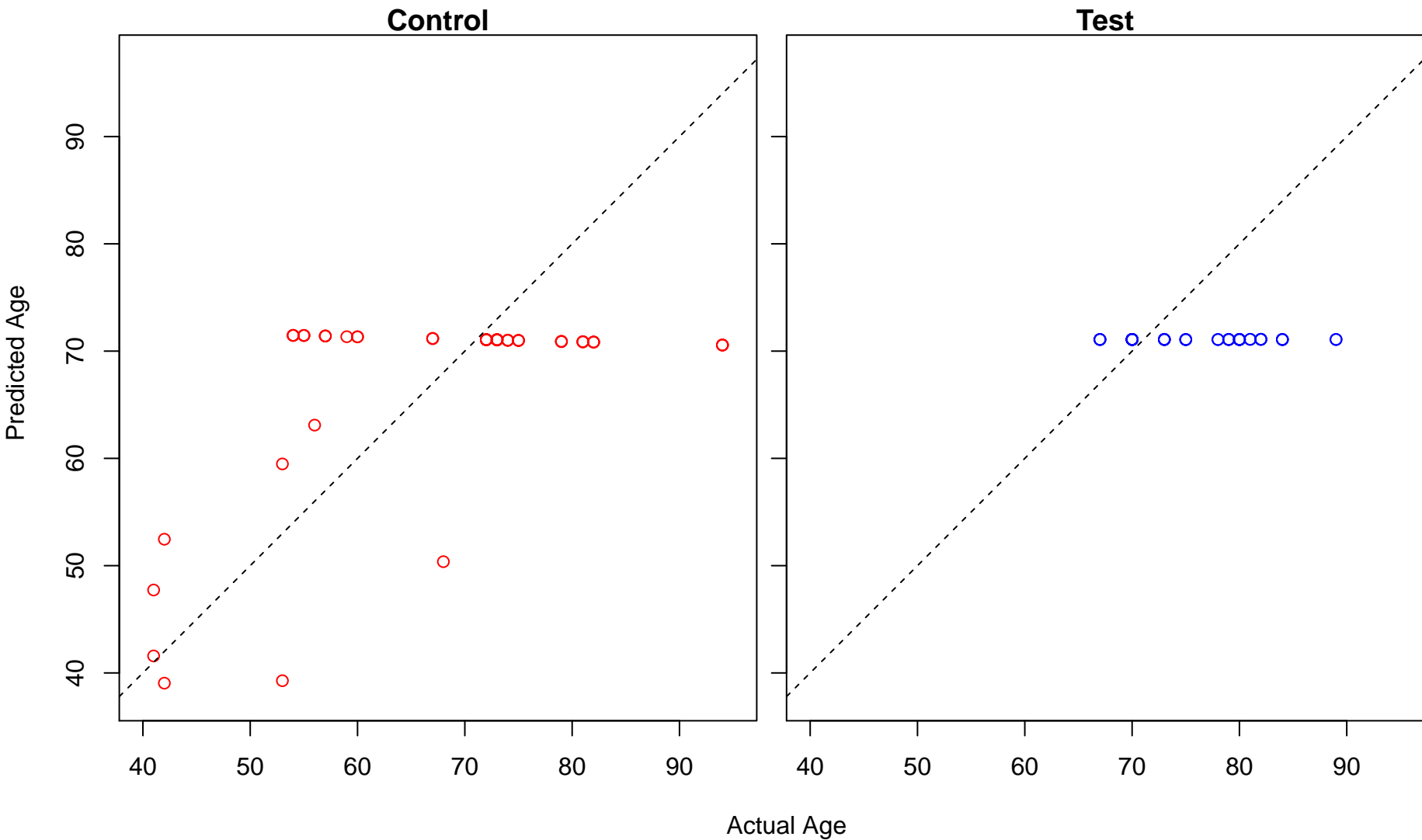


Test

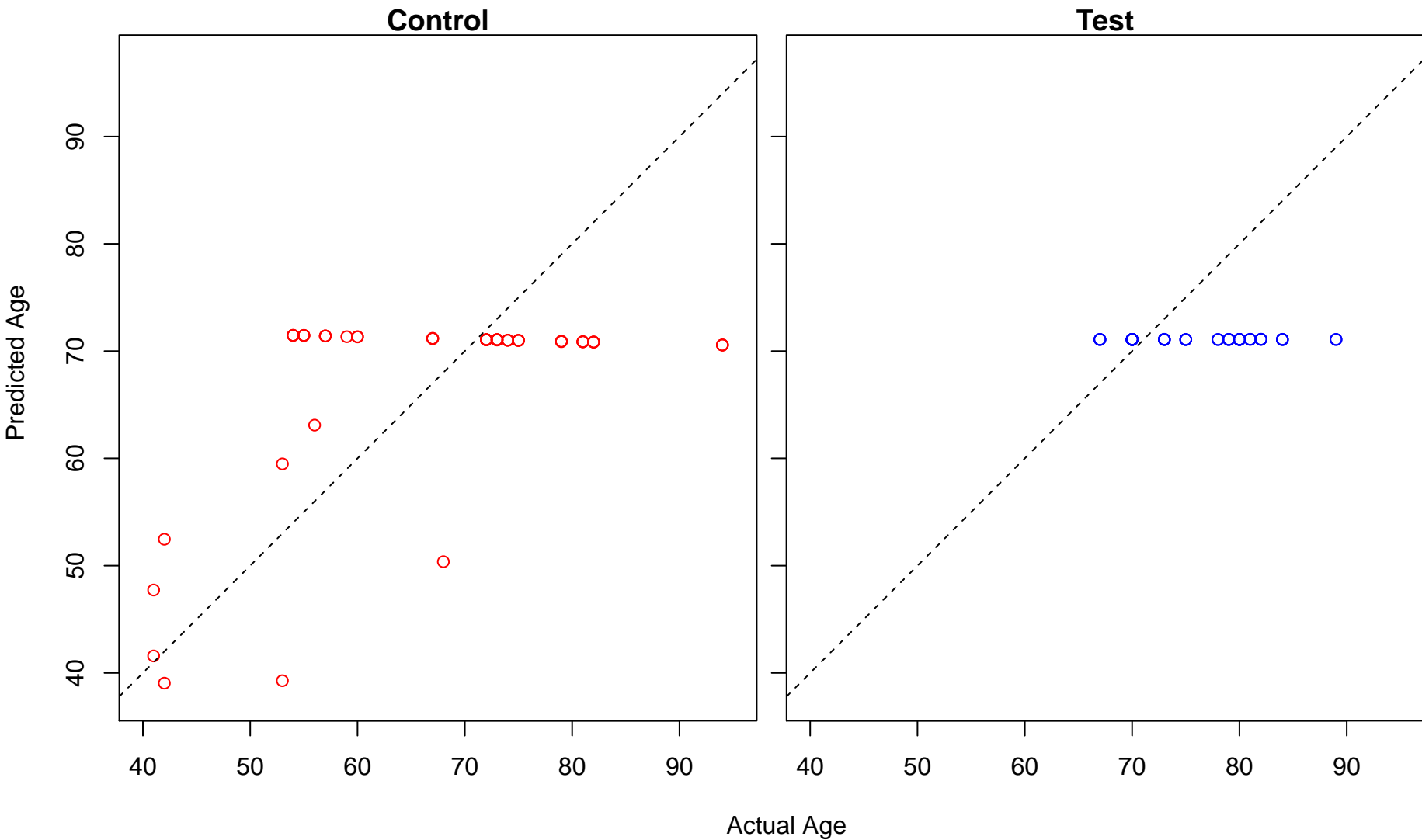


Actual Age

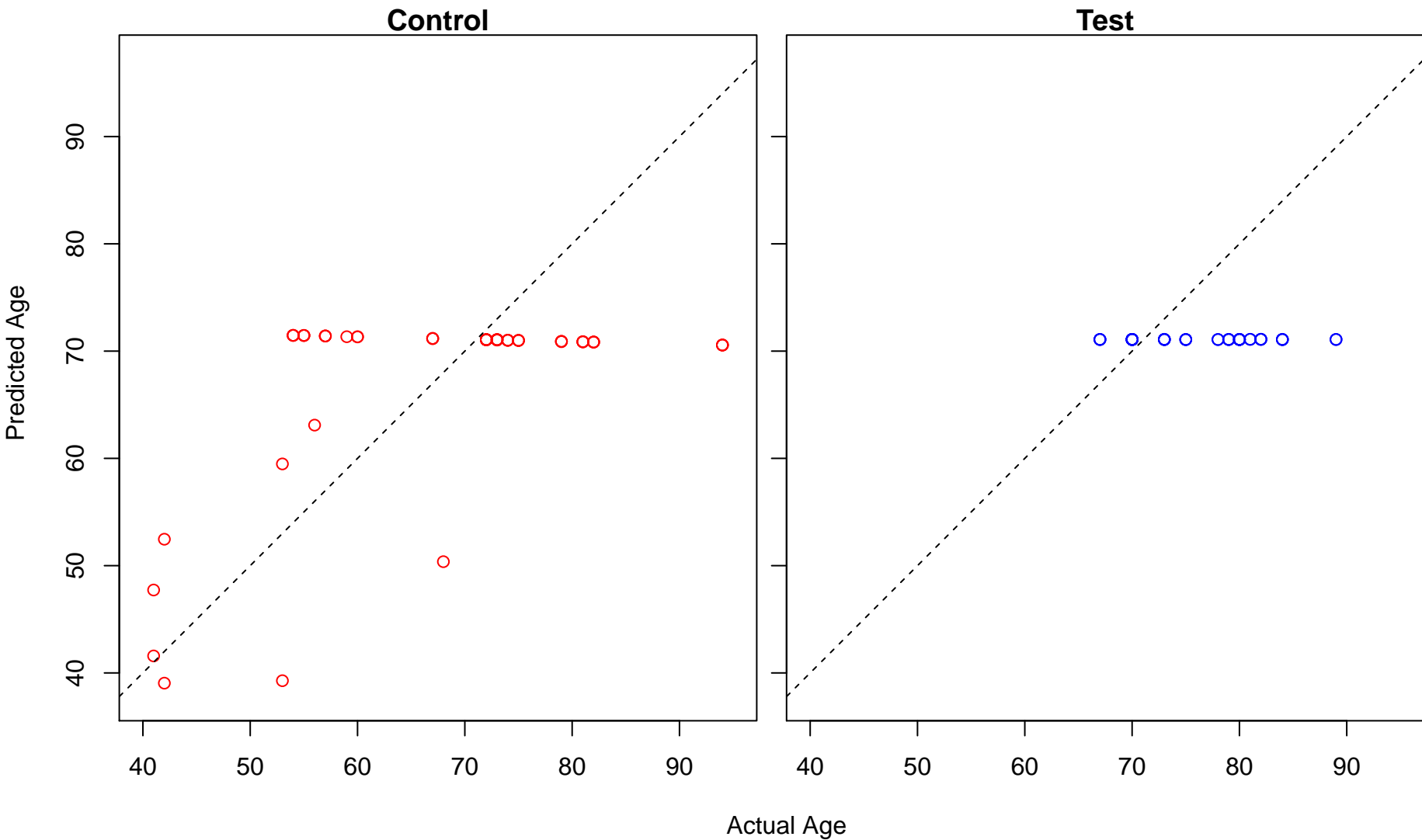
negative regulation of telomere maintenance (Score: 0.806574)



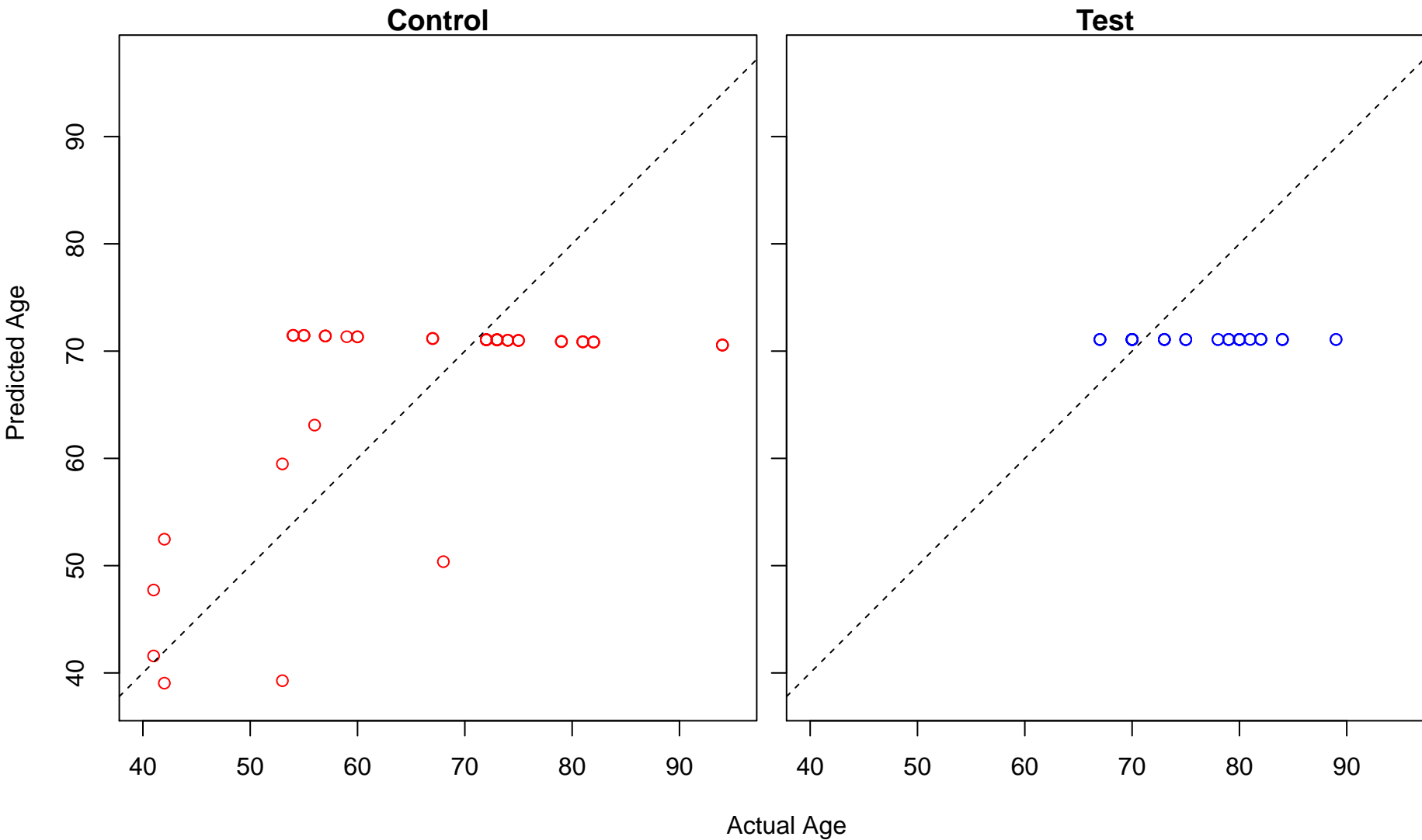
regulation of telomere maintenance via telomerase (Score: 0.806574)



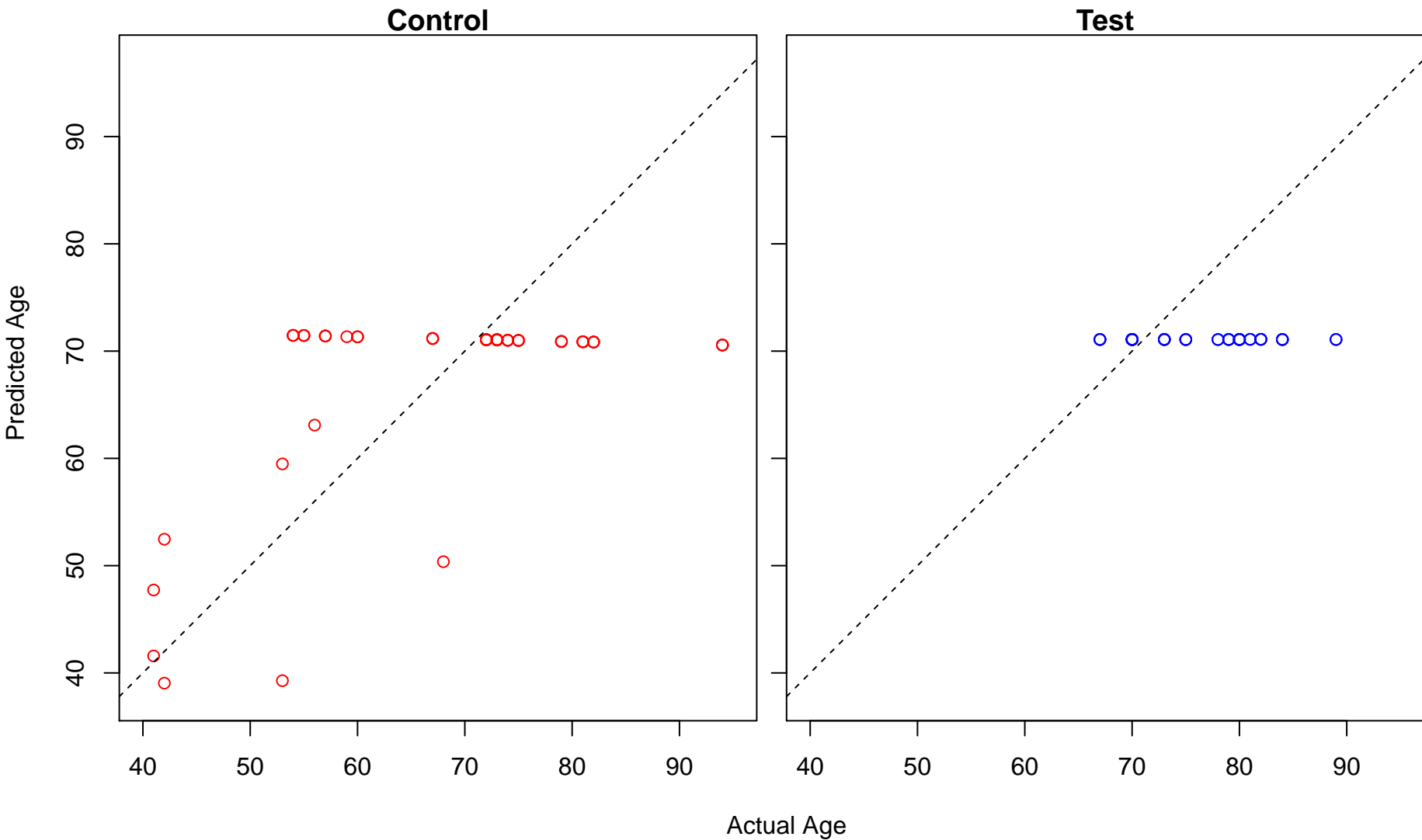
negative regulation of telomere maintenance via telomerase (Score: 0.806574)



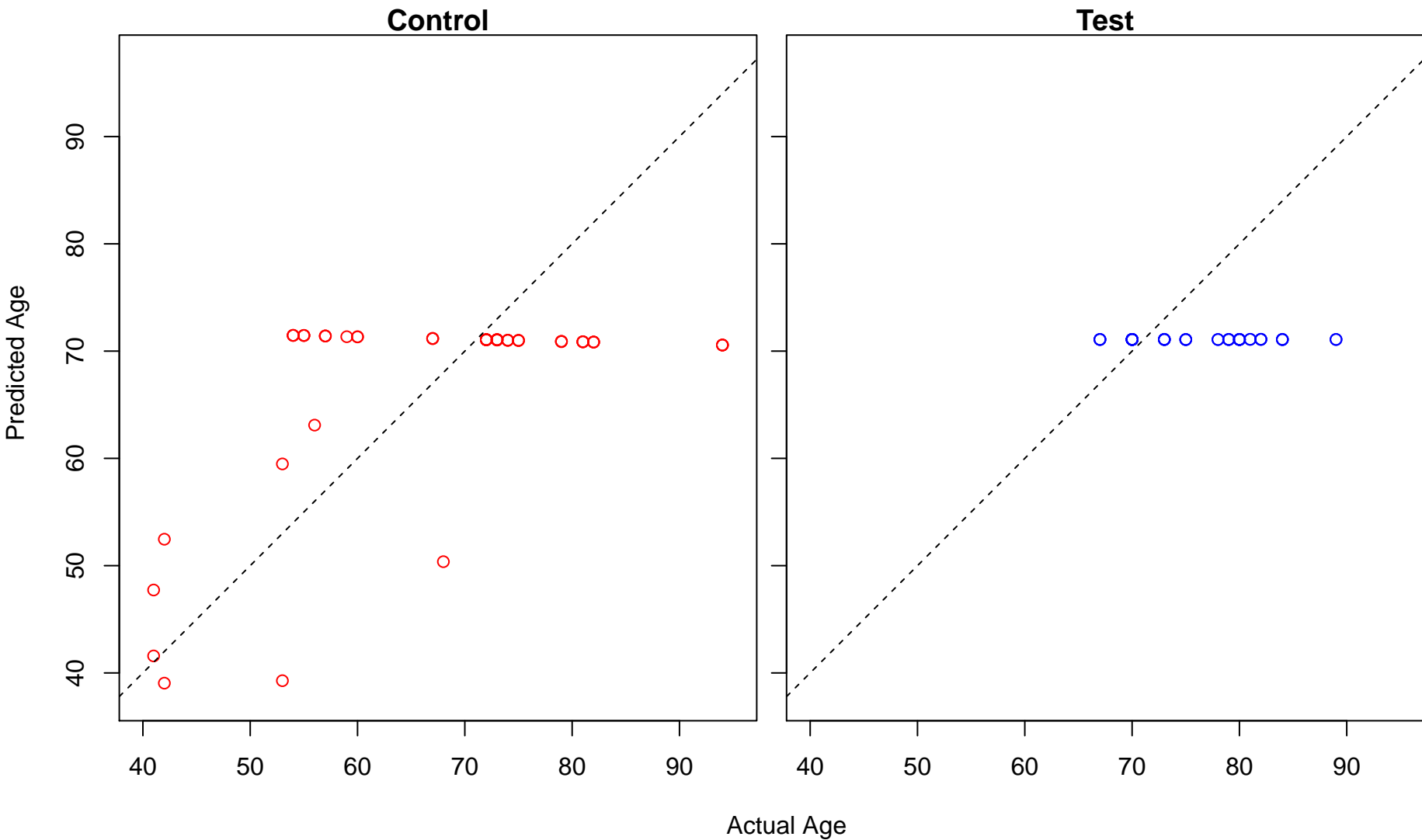
regulation of telomere maintenance via telomere lengthening (Score: 0.806574)



negative regulation of telomere maintenance via telomere lengthening (Score: 0.806574)

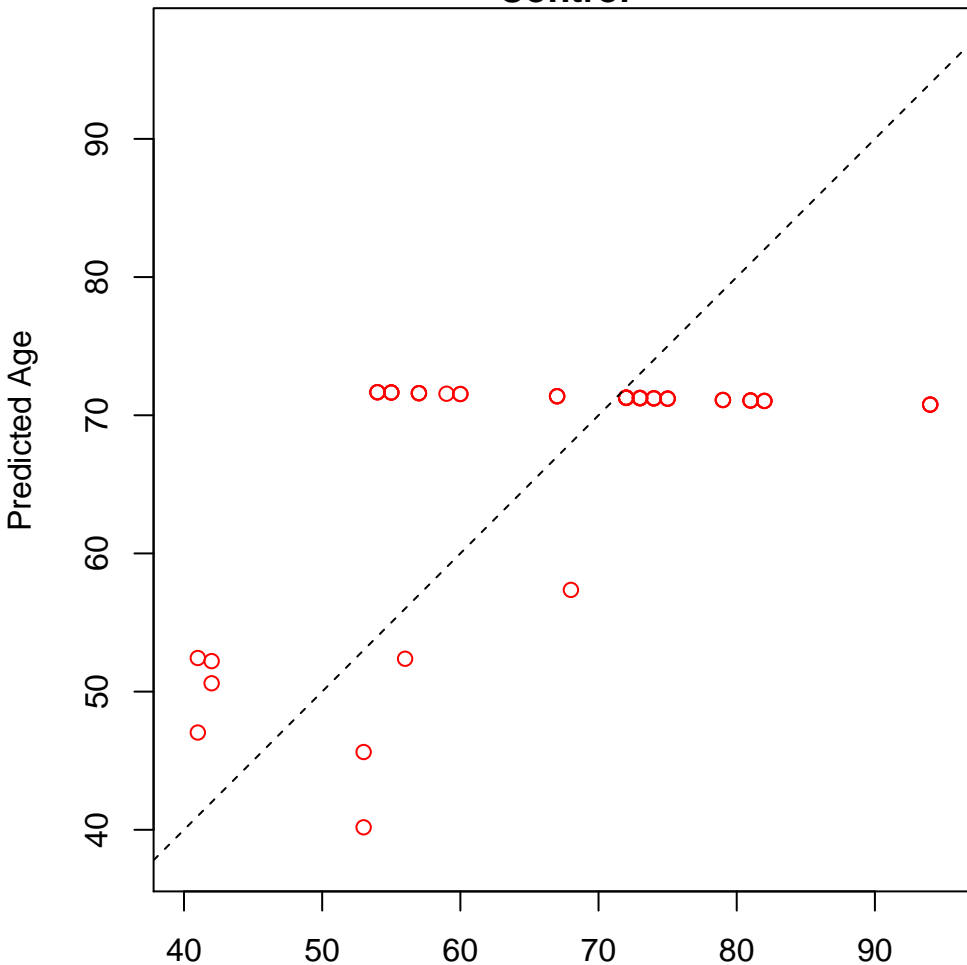


negative regulation of DNA biosynthetic process (Score: 0.806574)

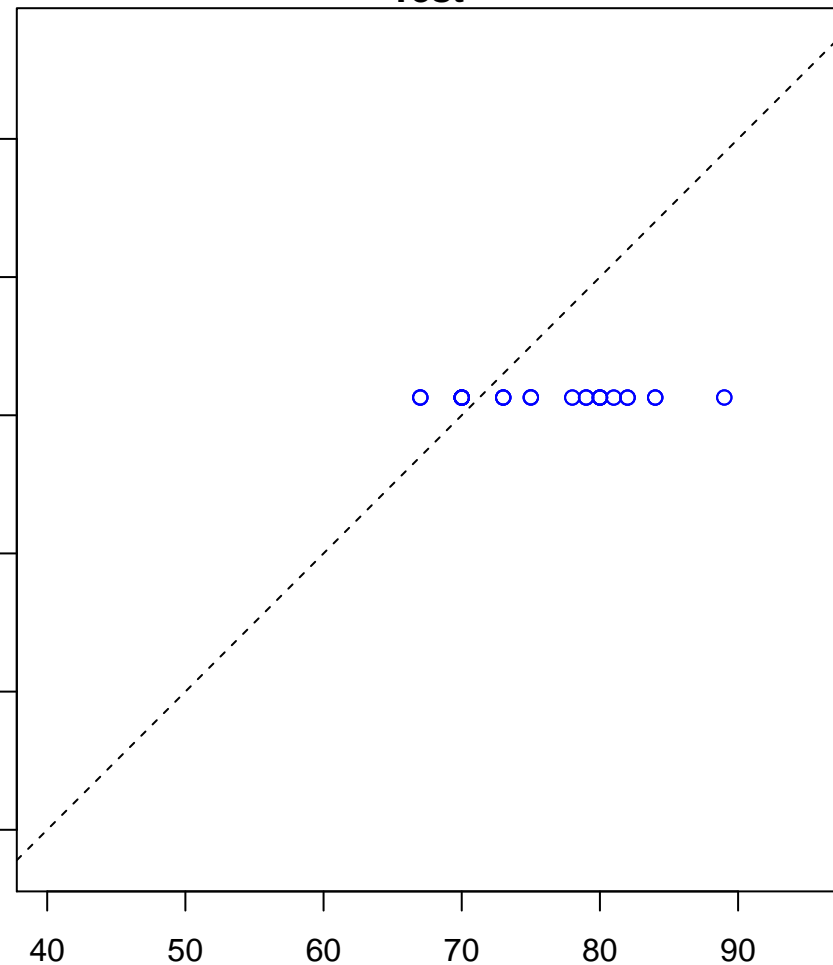


nucleotide phosphorylation (Score: 0.806516)

Control

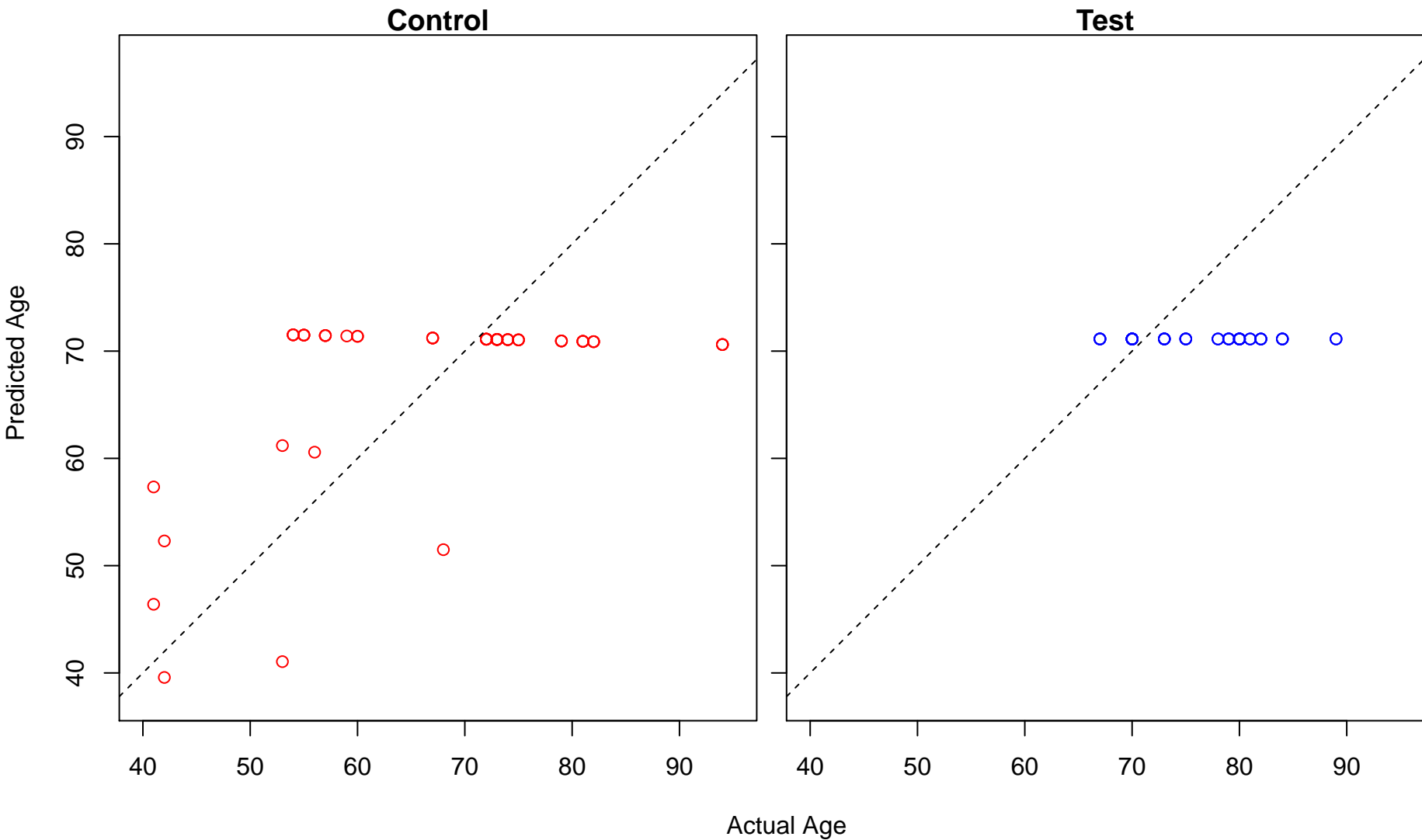


Test

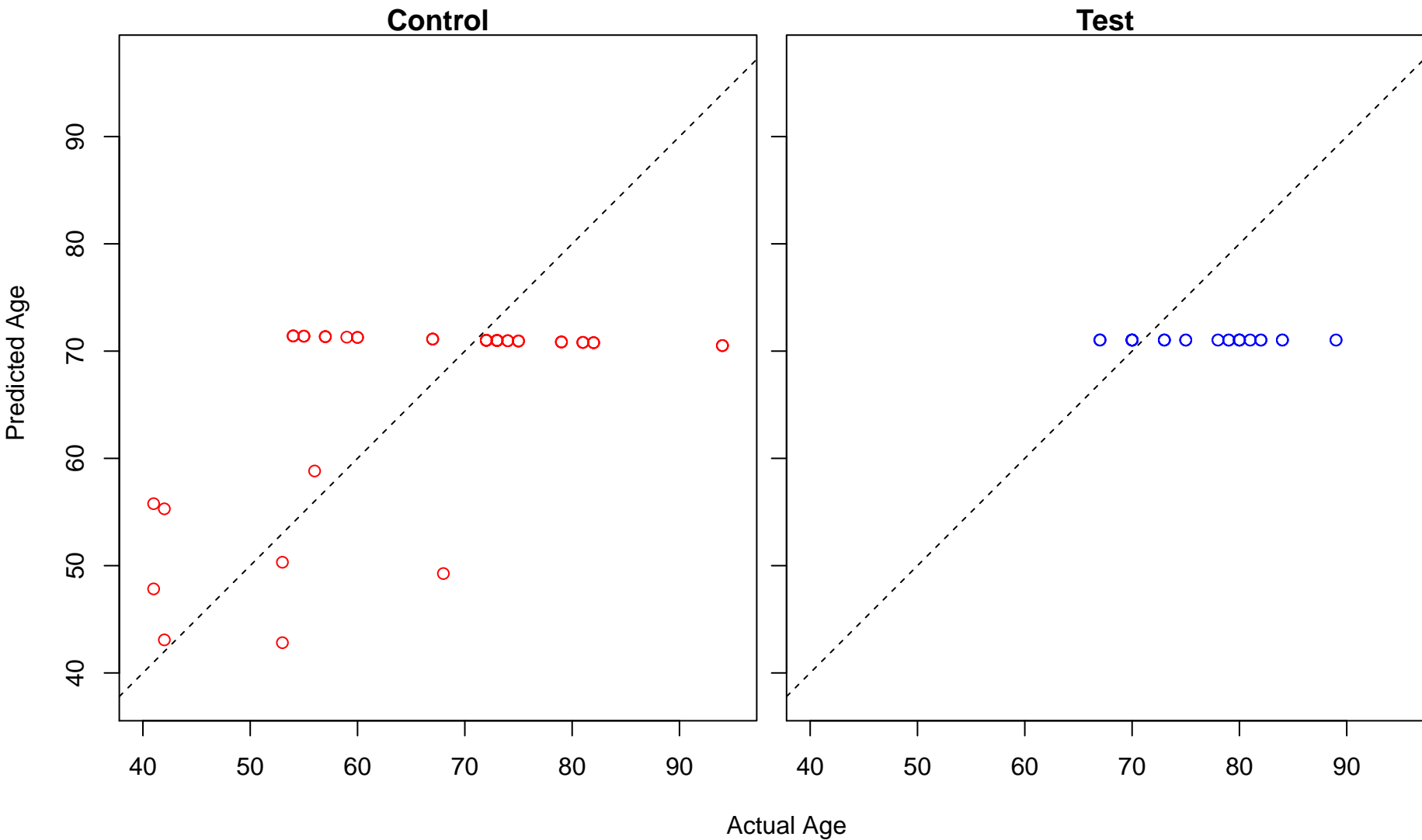


Actual Age

regulation of endocytosis (Score: 0.806435)

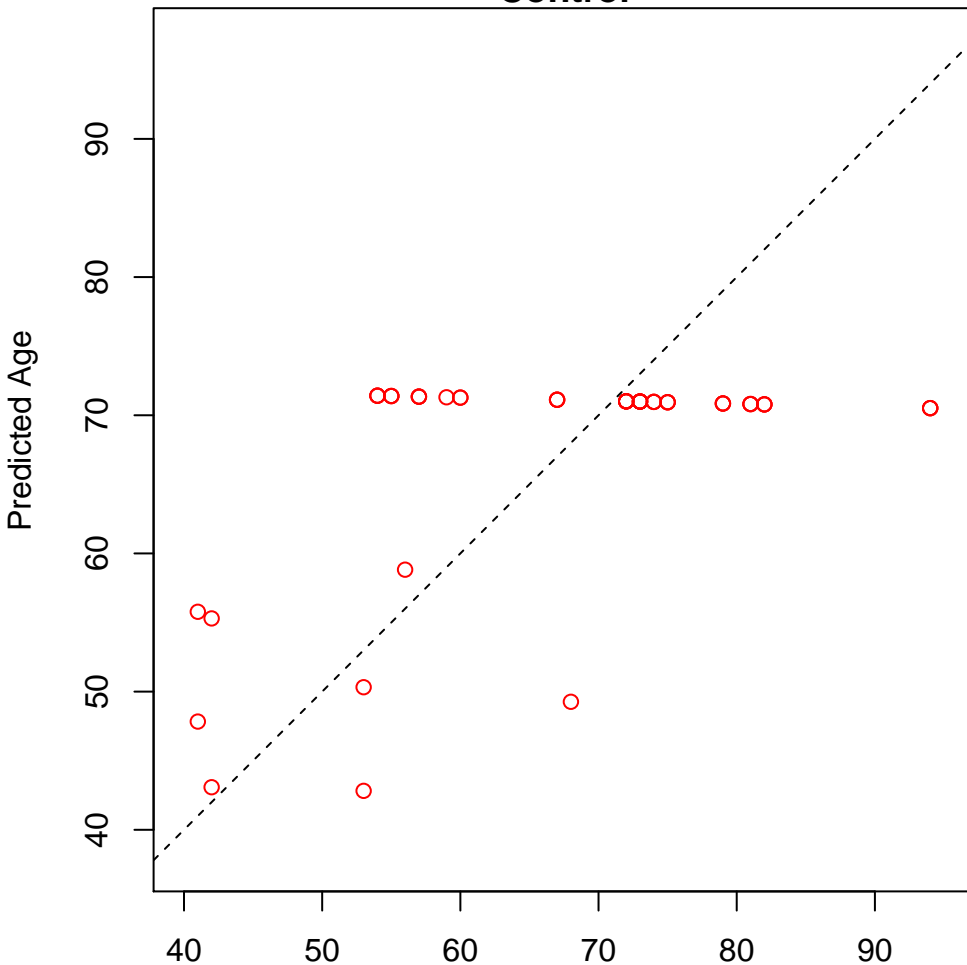


negative regulation of mRNA splicing, via spliceosome (Score: 0.806413)

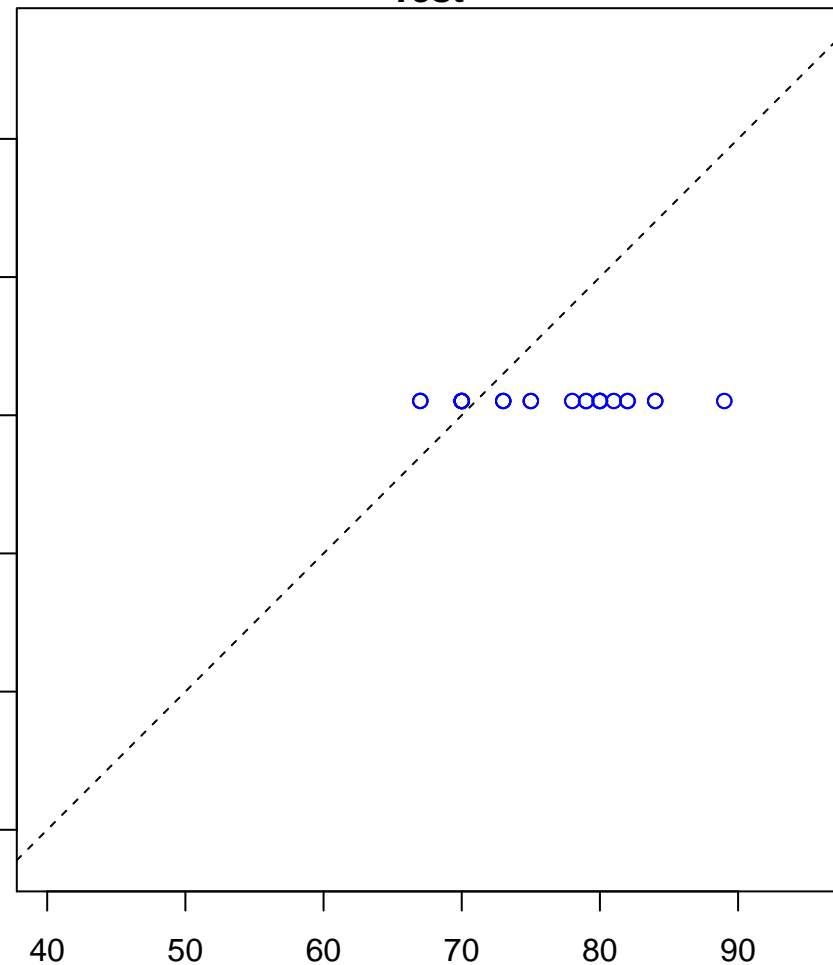


negative regulation of mRNA processing (Score: 0.806413)

Control



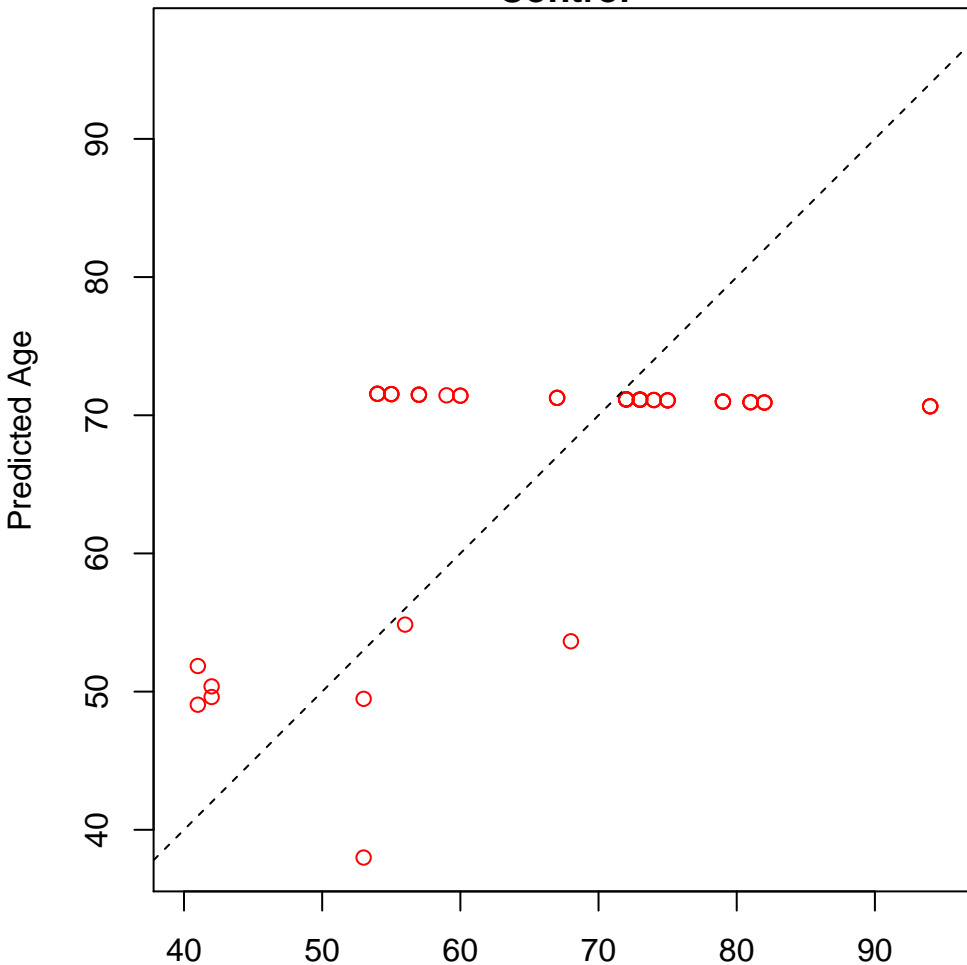
Test



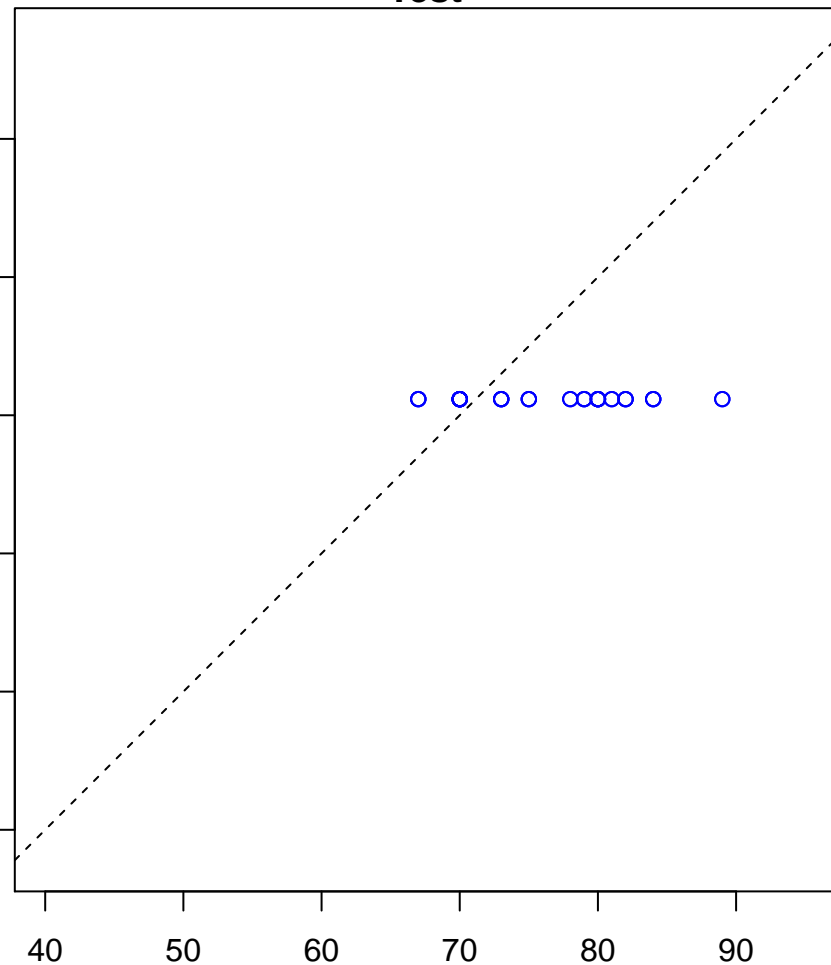
Actual Age

protein complex subunit organization (Score: 0.806387)

Control

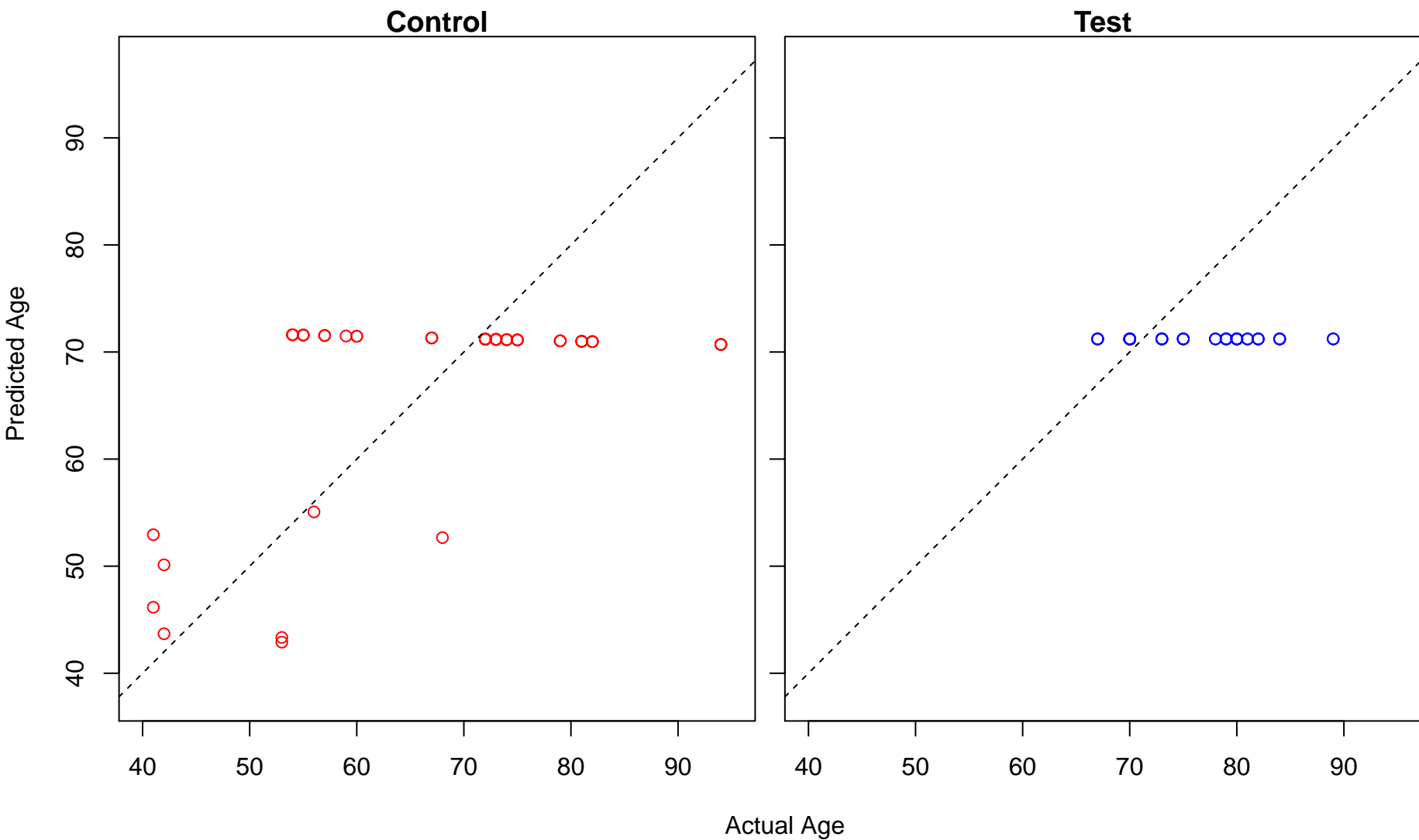


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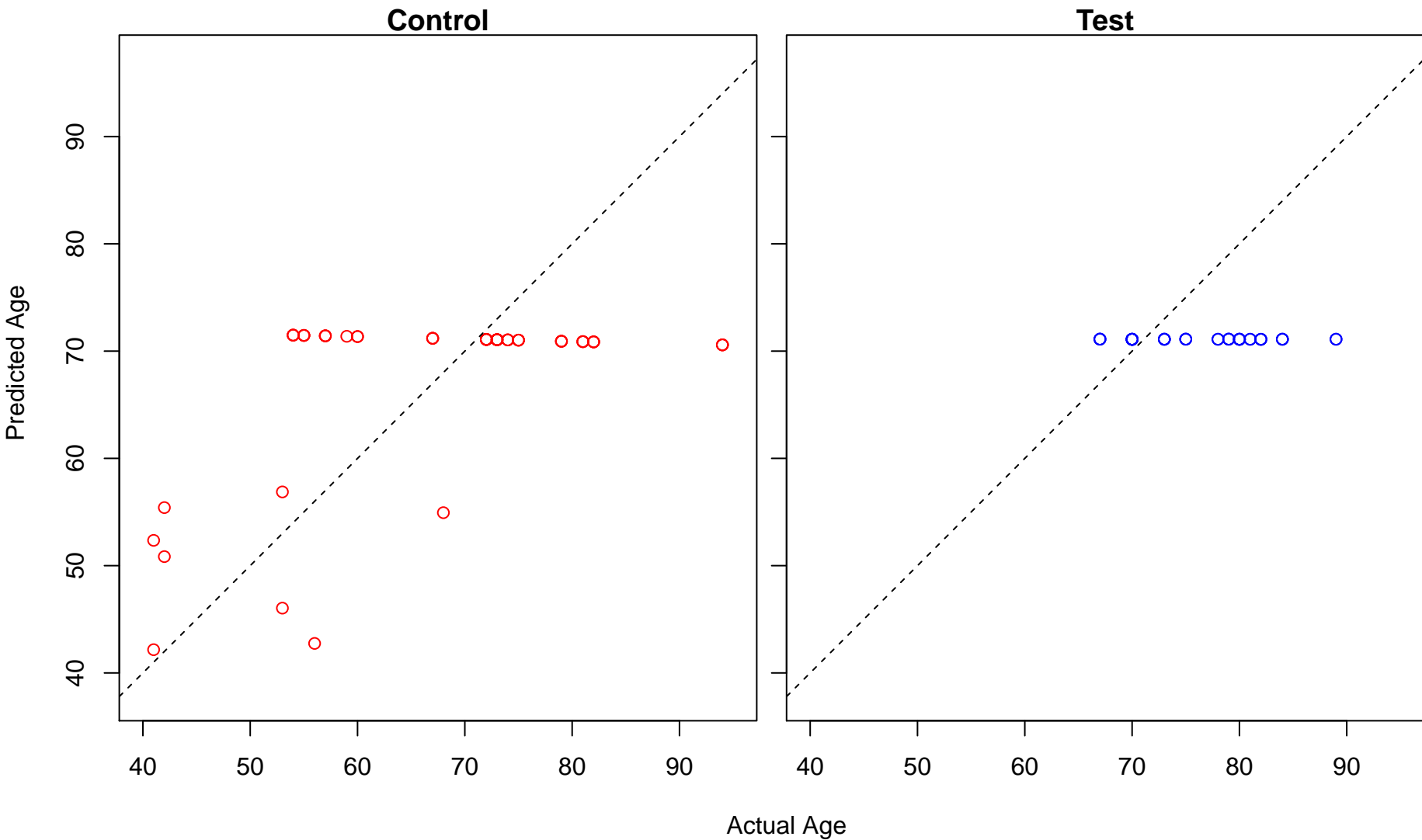


Actual Age

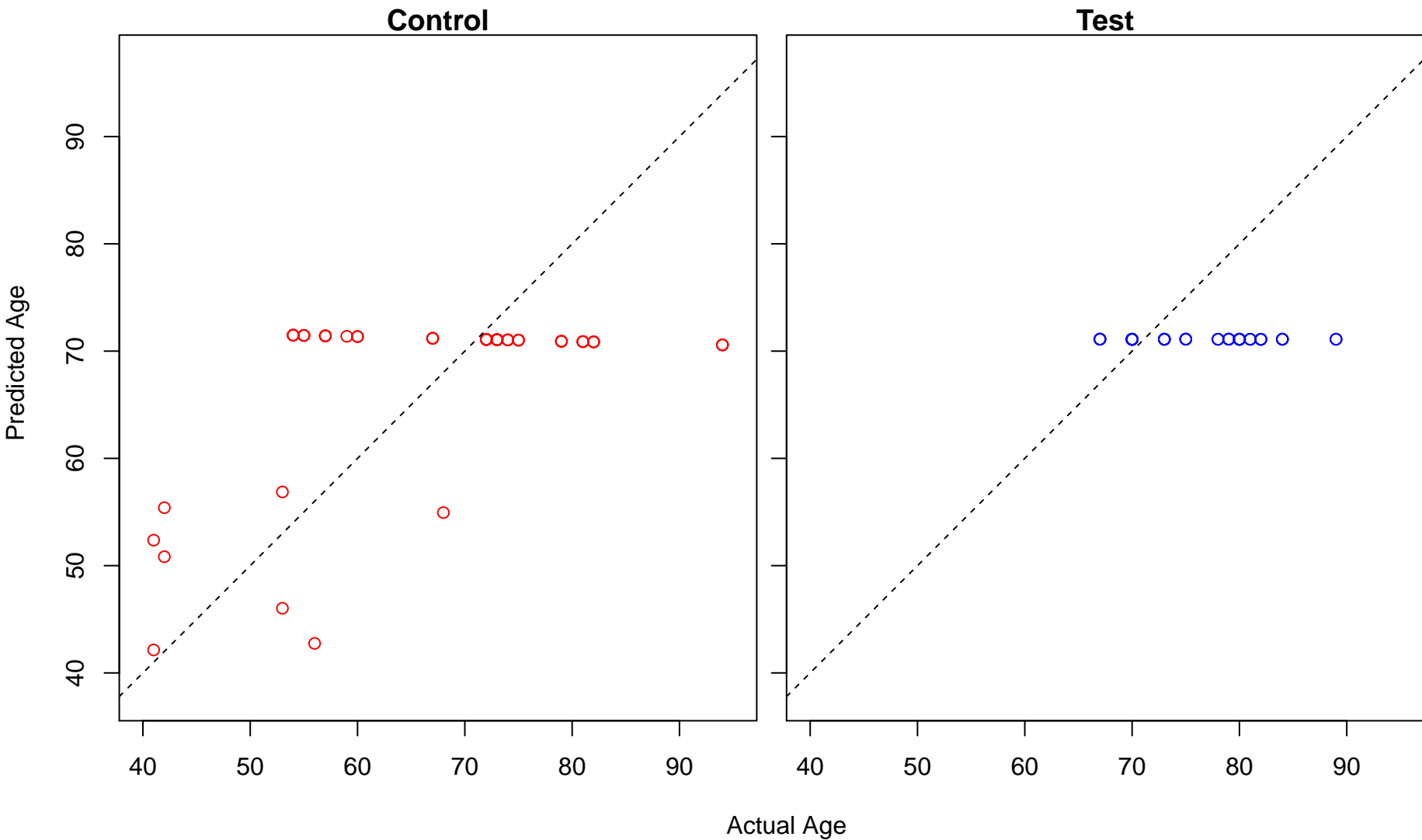
DNA ligation (Score: 0.806381)



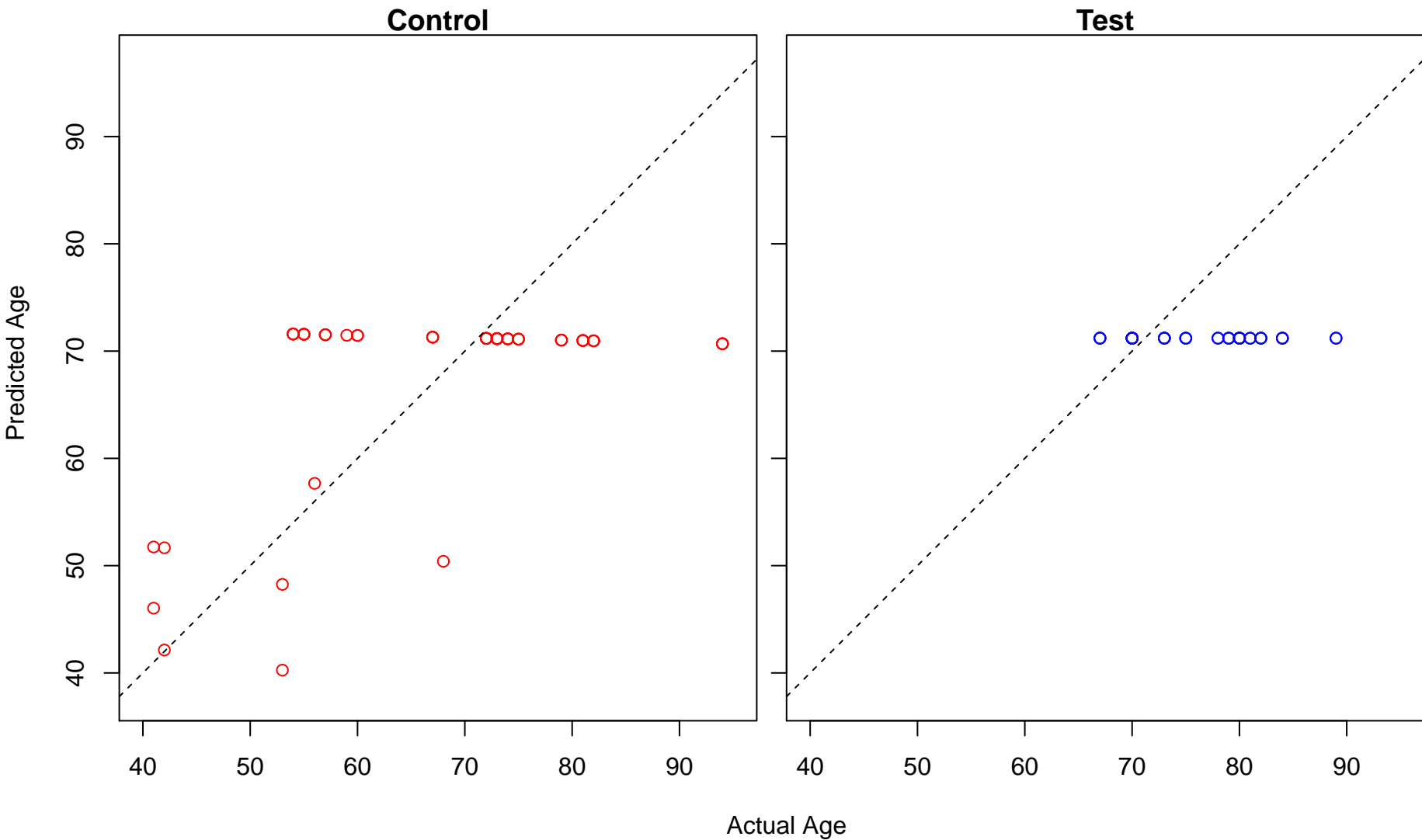
positive regulation of protein polymerization (Score: 0.806377)



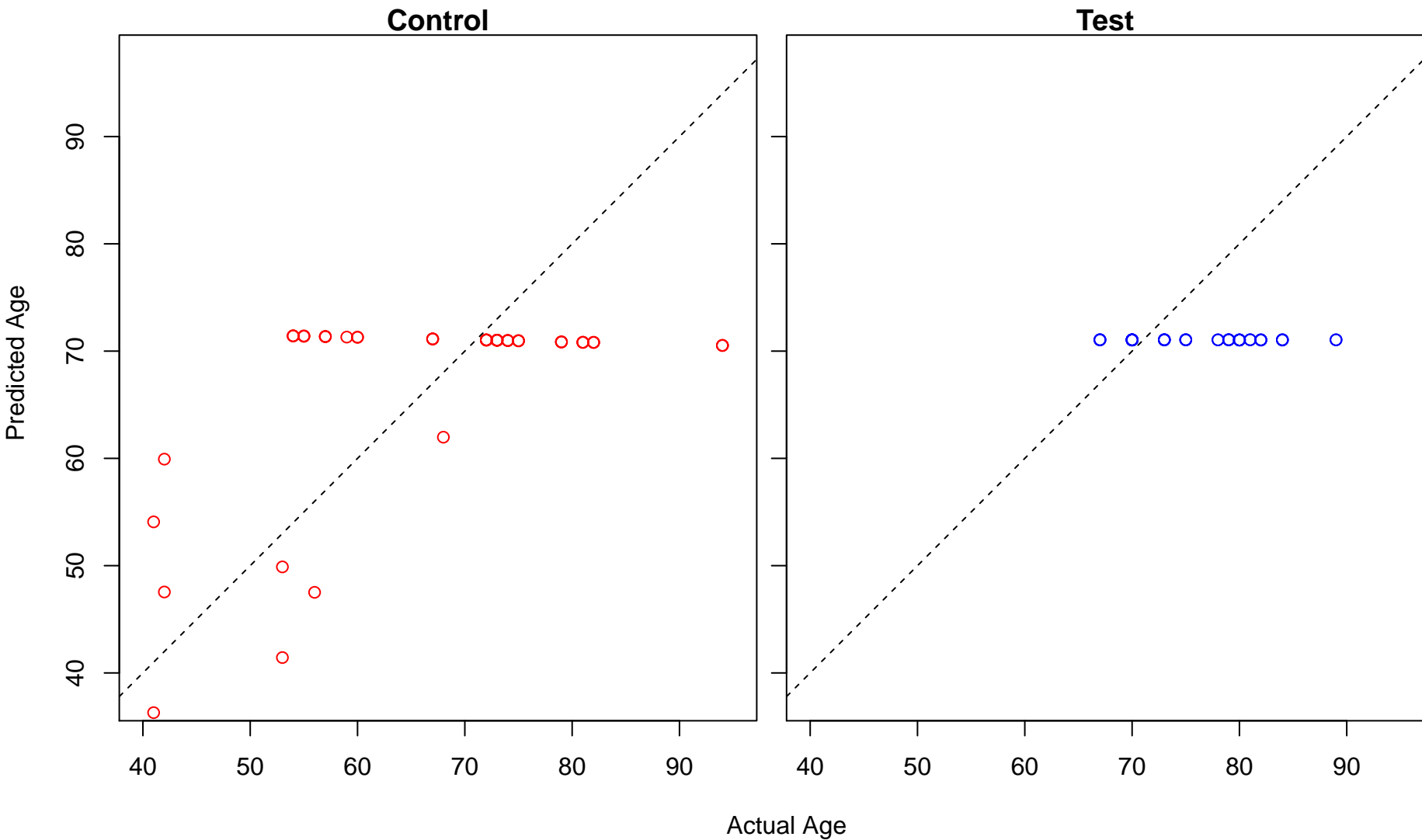
positive regulation of actin filament polymerization (Score: 0.806376)



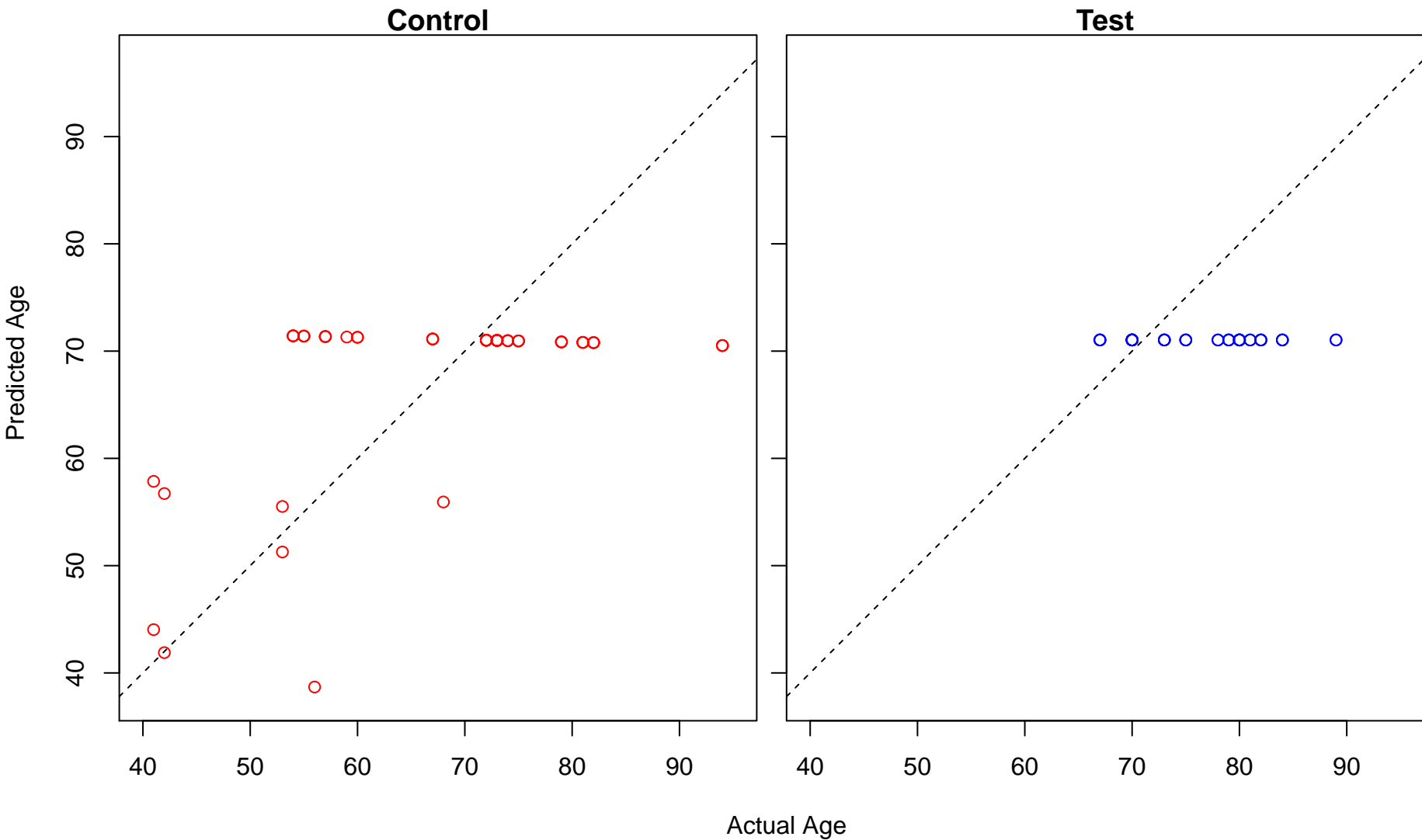
inflammatory response (Score: 0.806208)



histone H3 acetylation (Score: 0.806205)

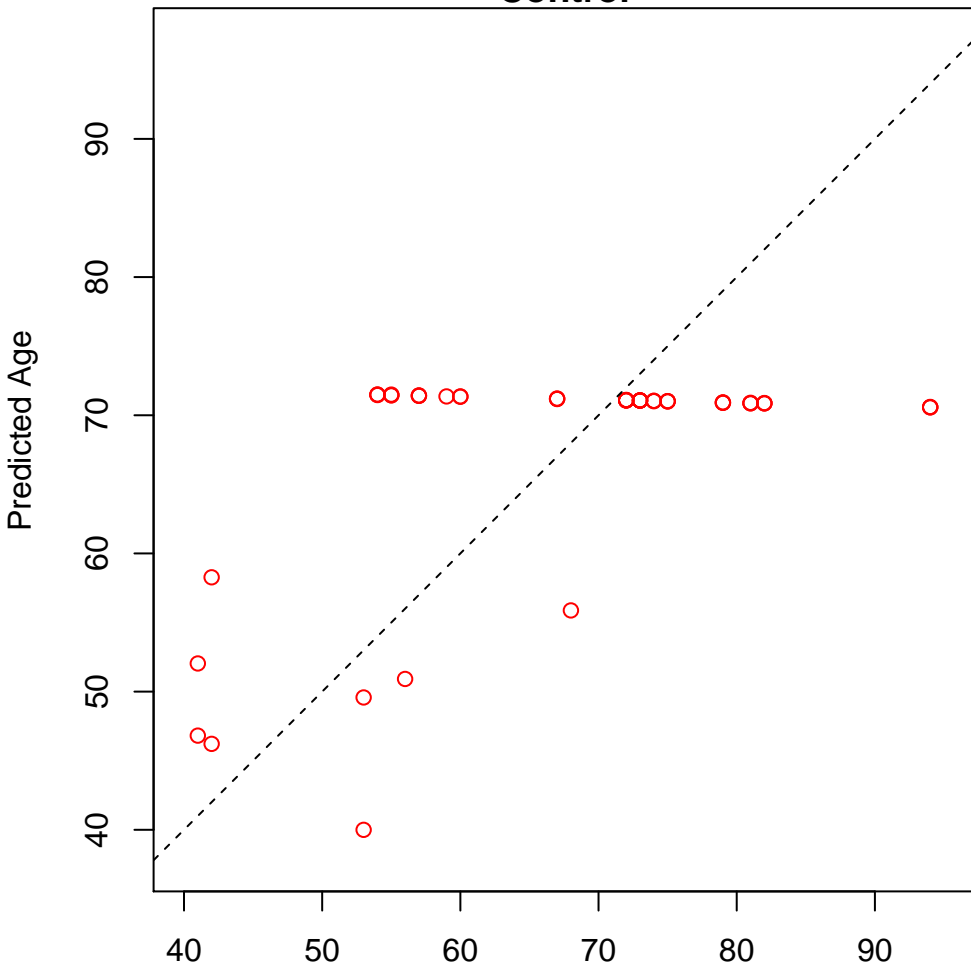


protein folding (Score: 0.806117)

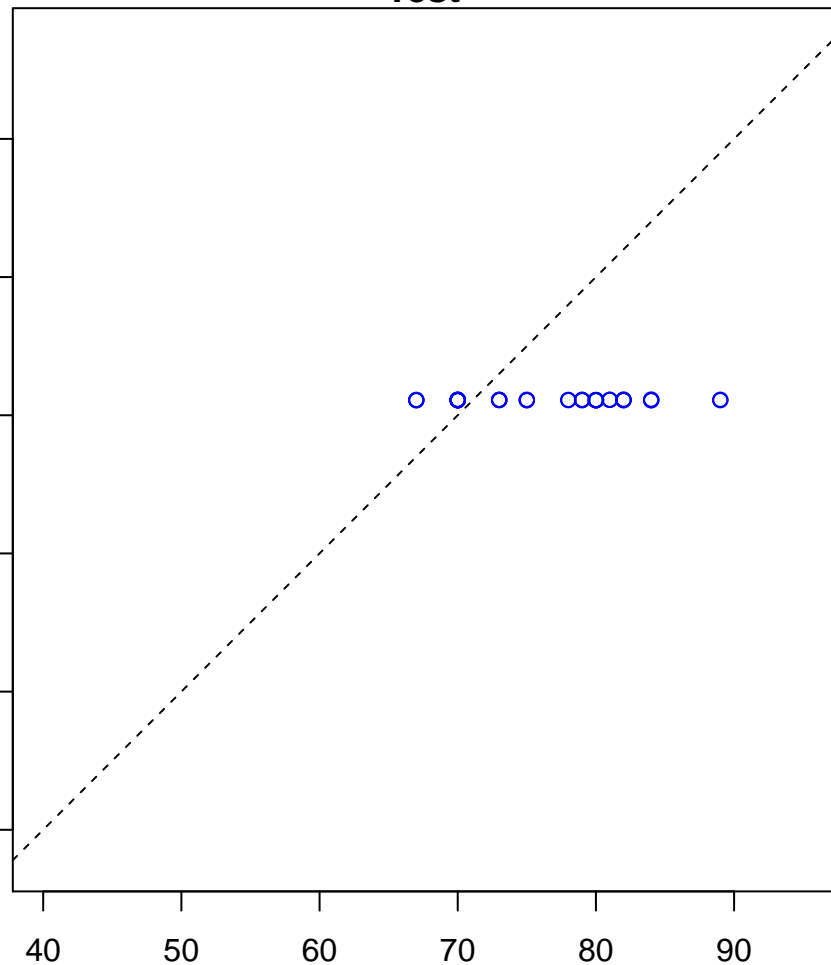


positive regulation of histone modification (Score: 0.806085)

Control

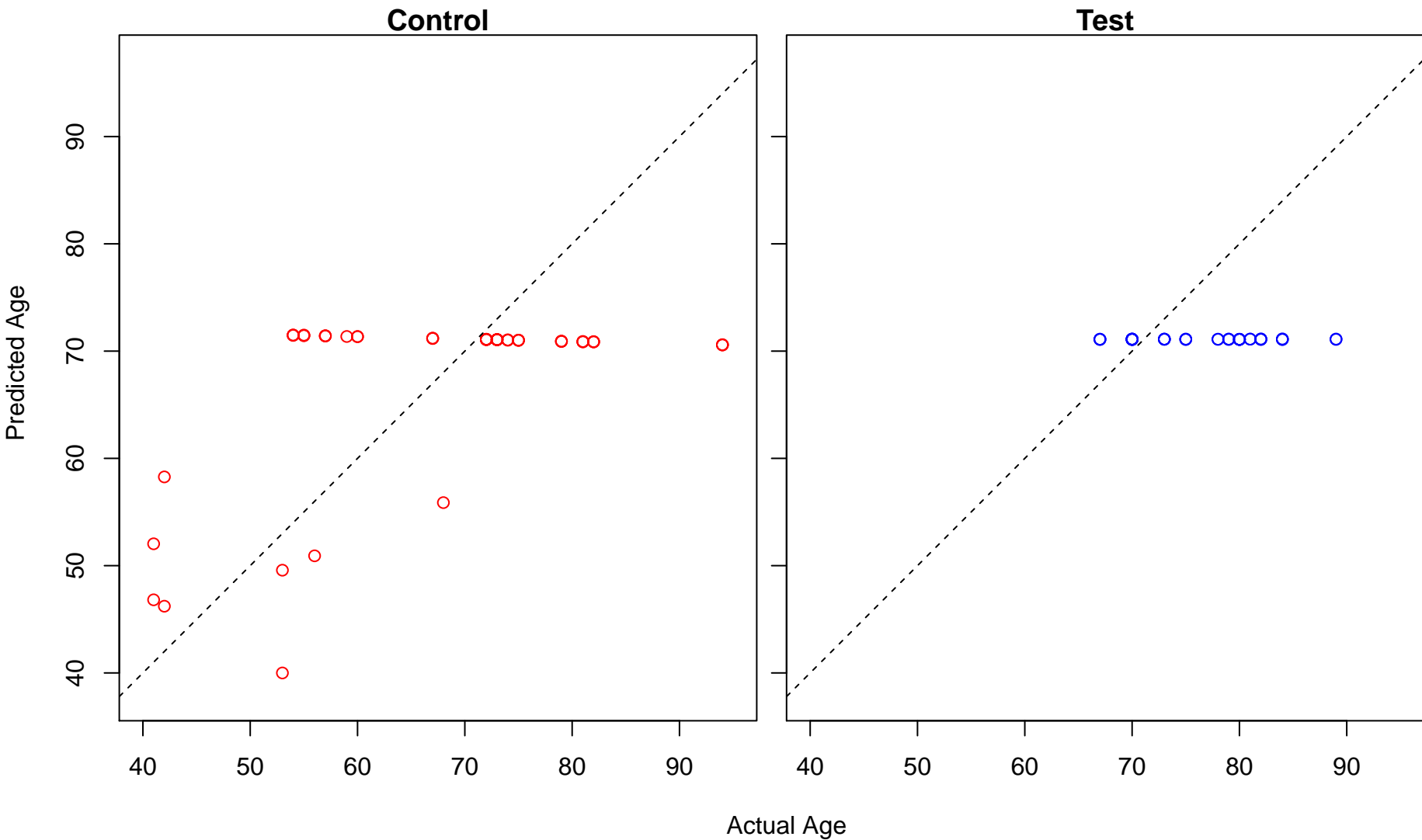


Test

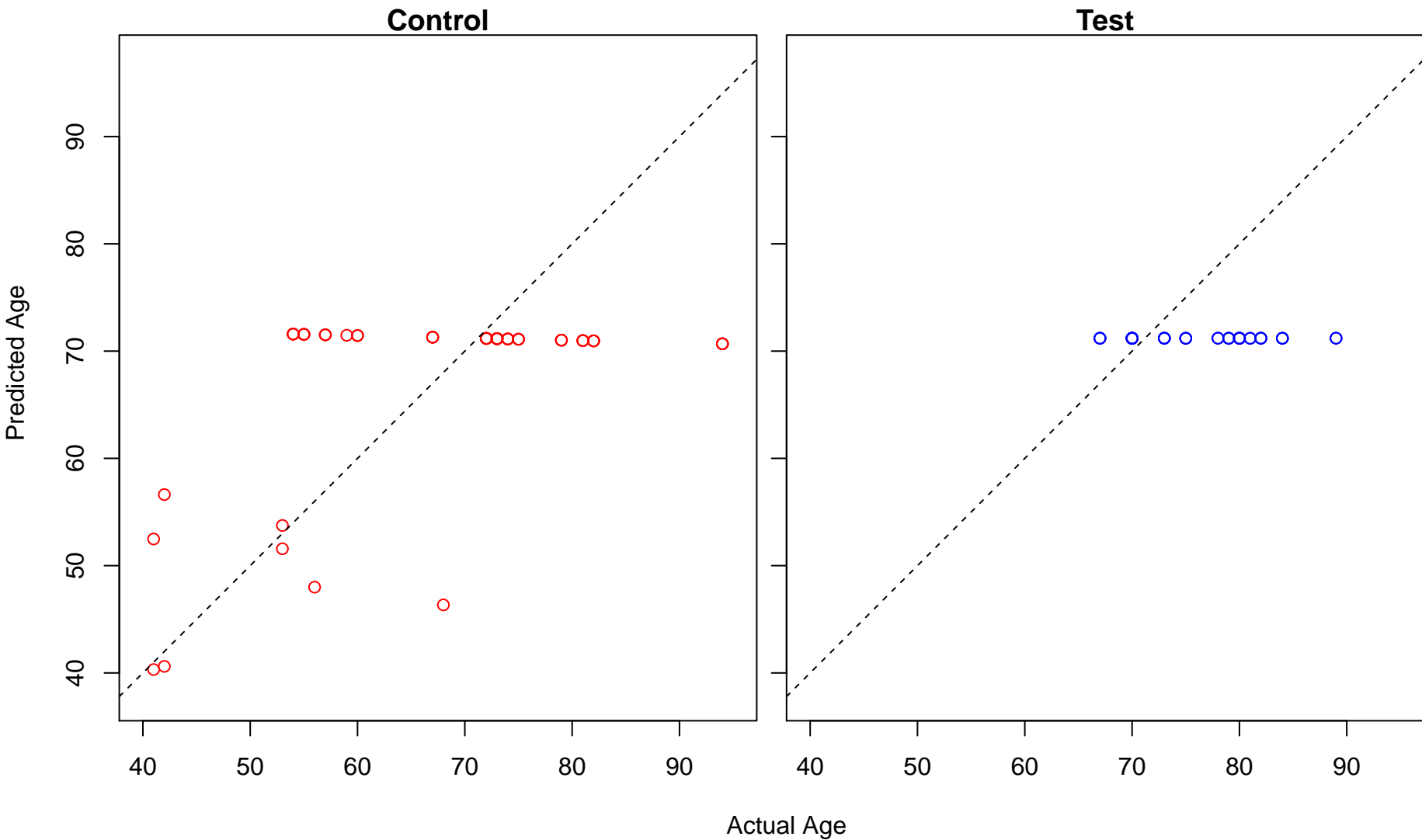


Actual Age

positive regulation of chromatin organization (Score: 0.806085)

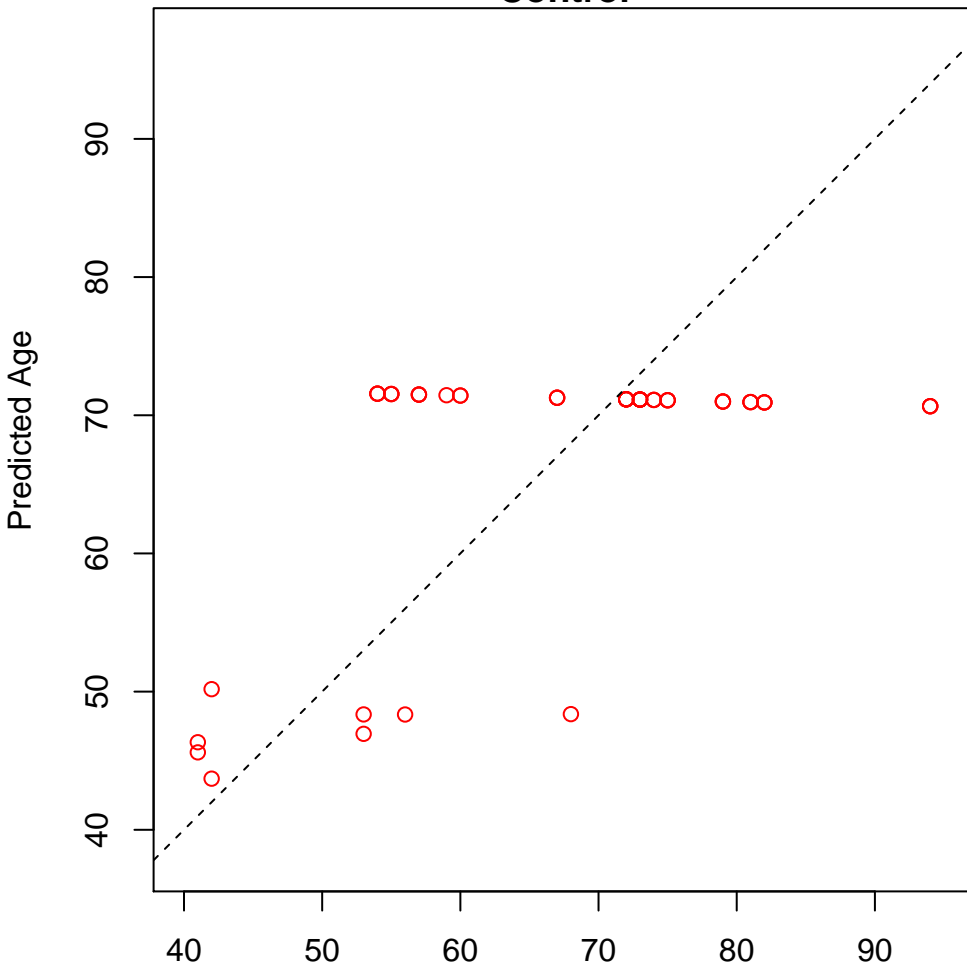


protein ubiquitination involved in ubiquitin-dependent protein catabolic process (Score: 0.806024)

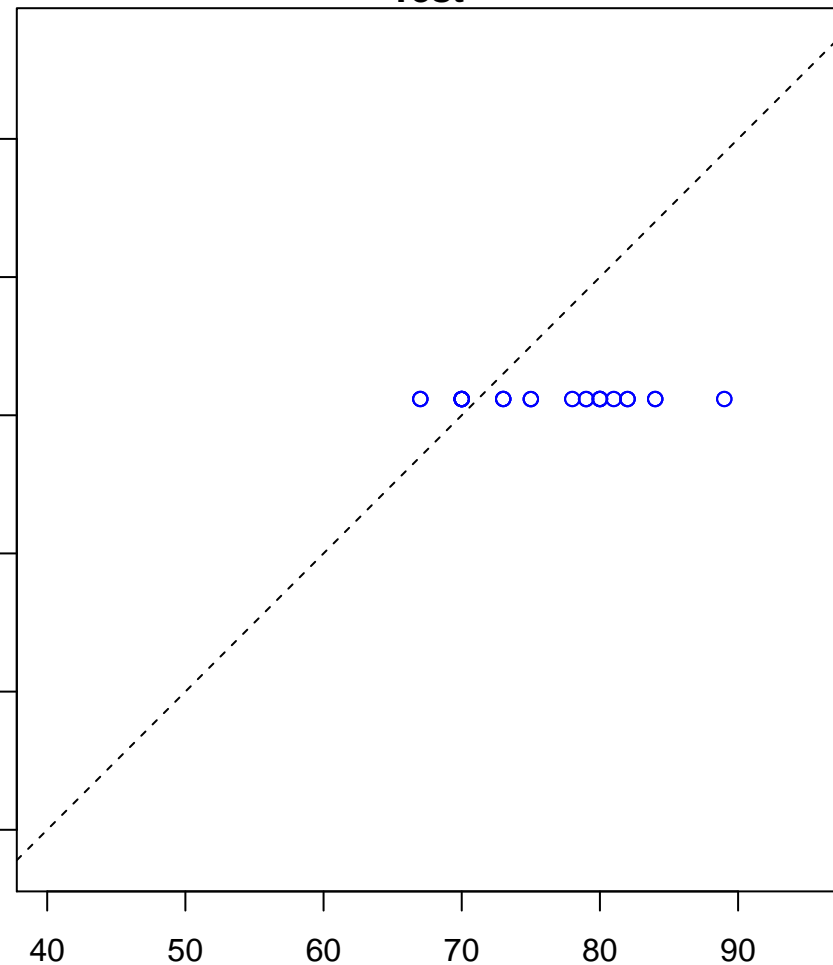


regulation of response to stimulus (Score: 0.806017)

Control

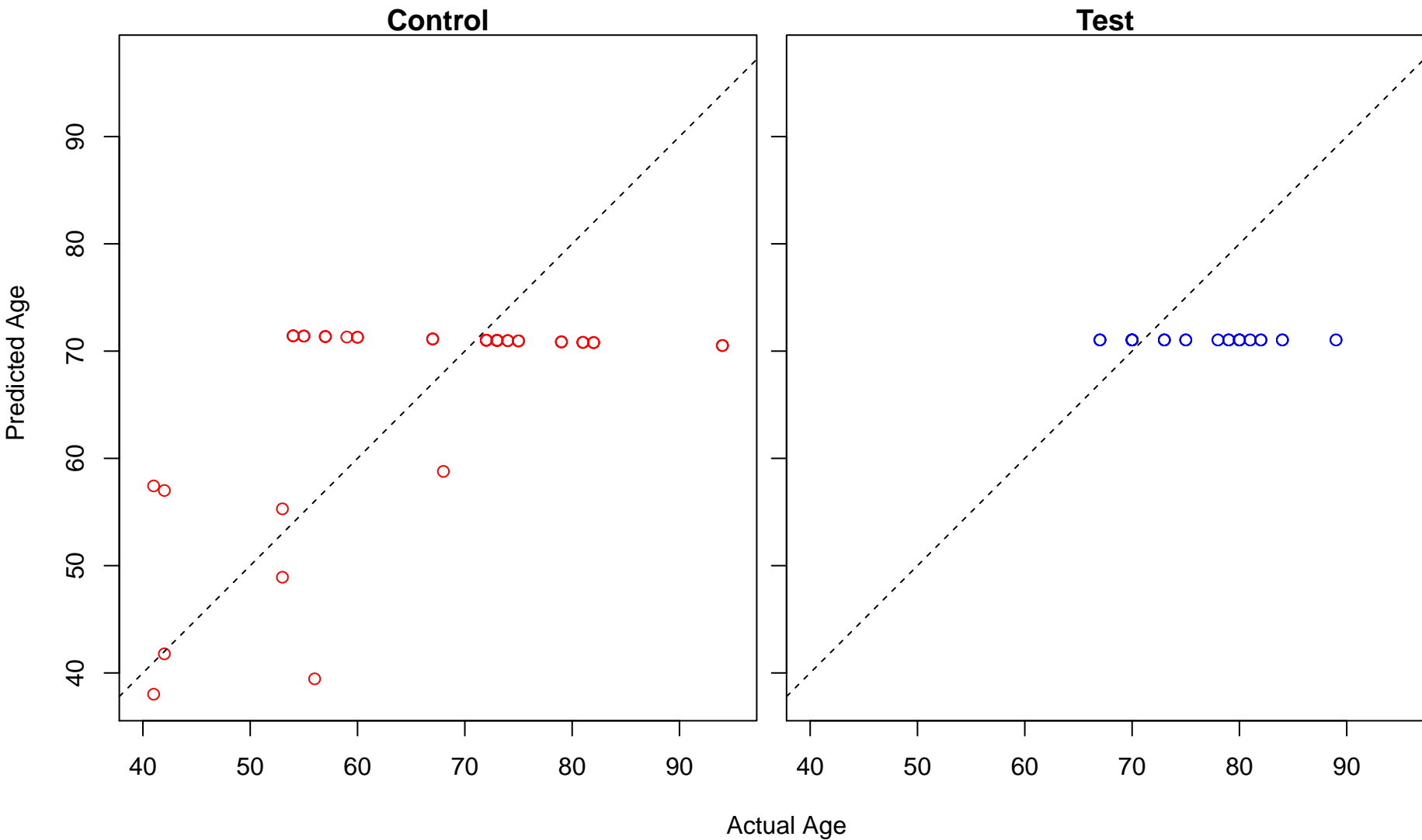


Test



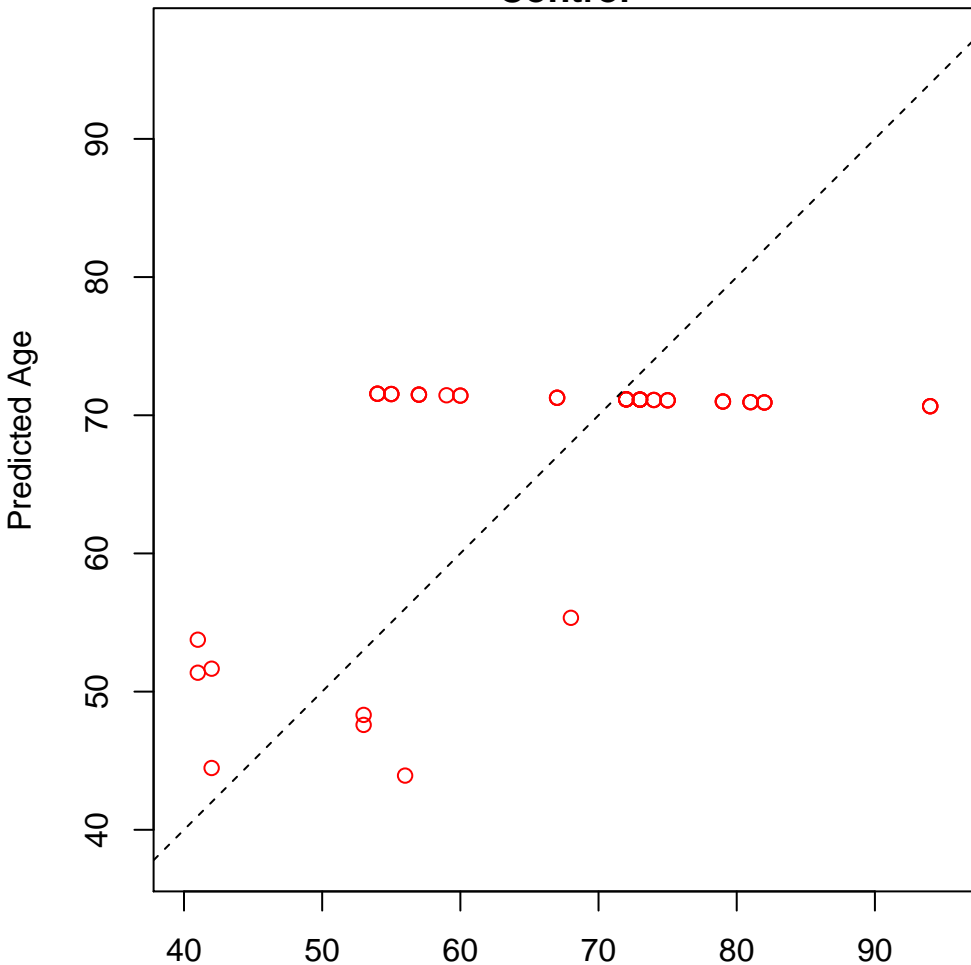
Actual Age

interaction with host (Score: 0.805931)

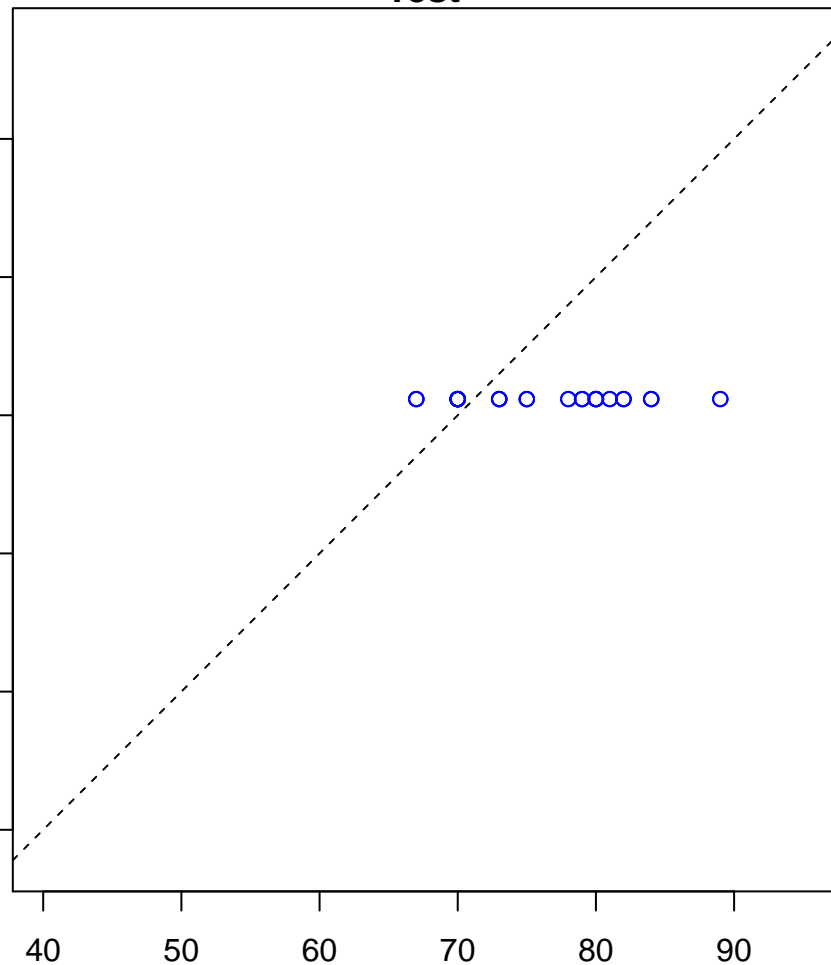


substantia nigra development (Score: 0.805910)

Control

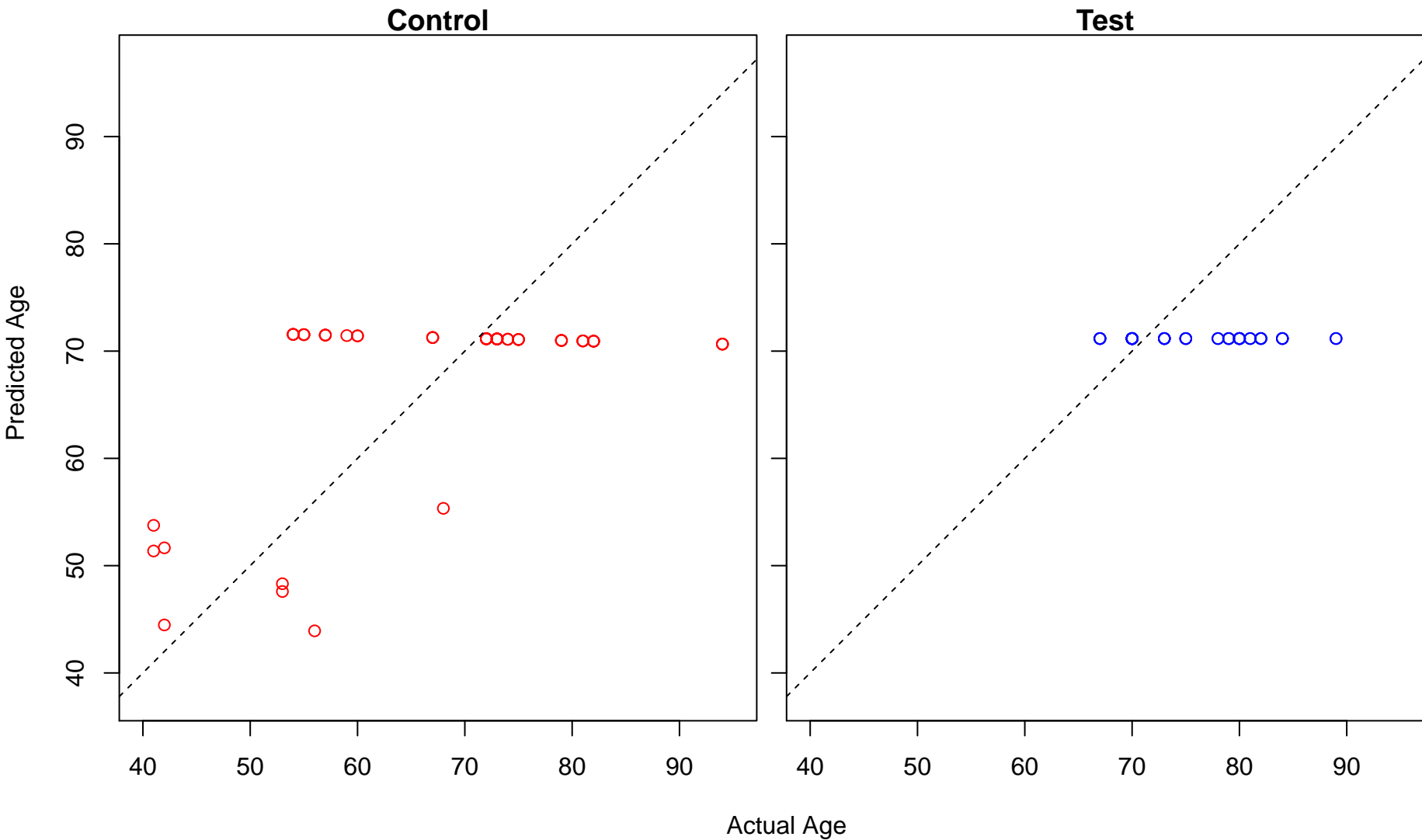


Test

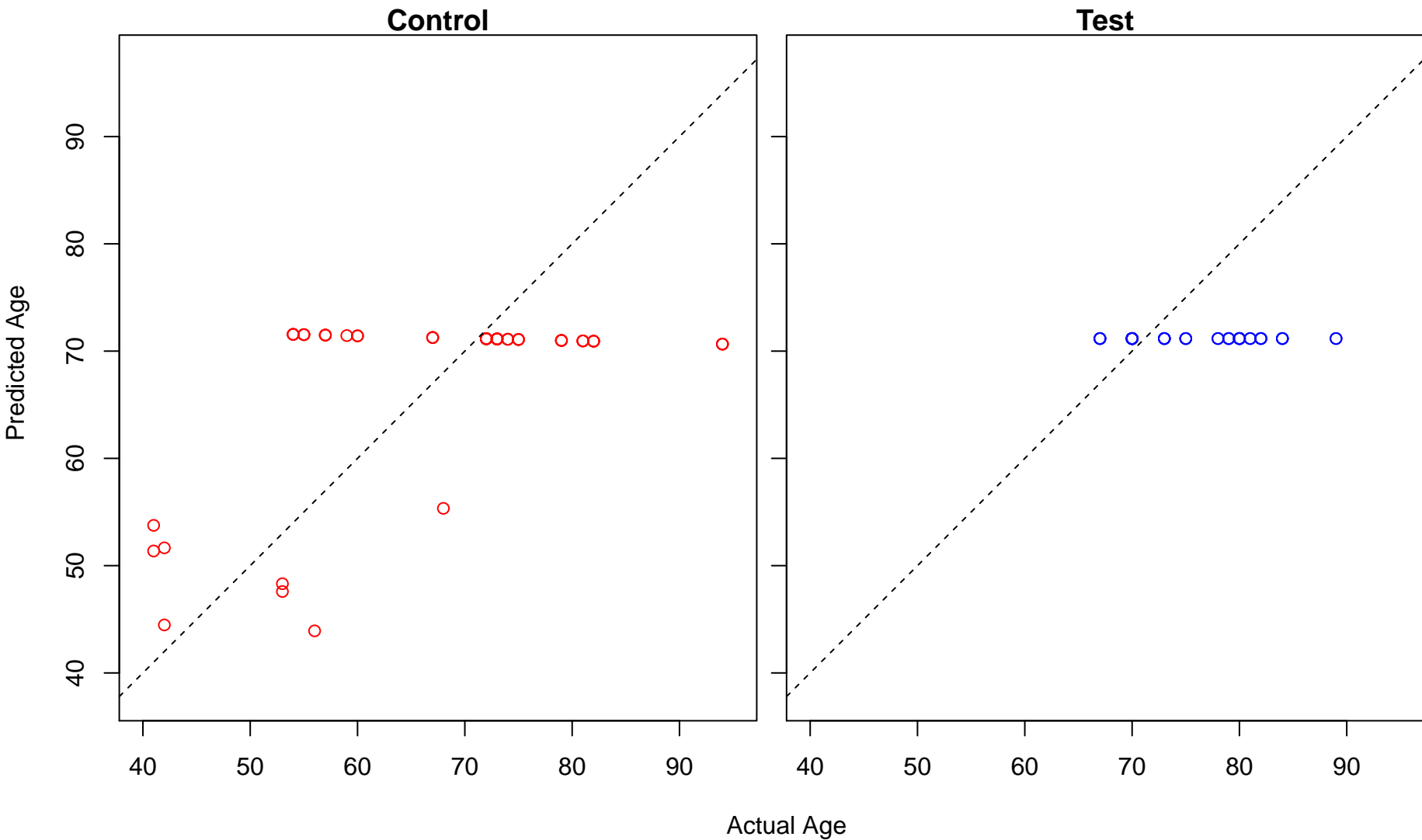


Actual Age

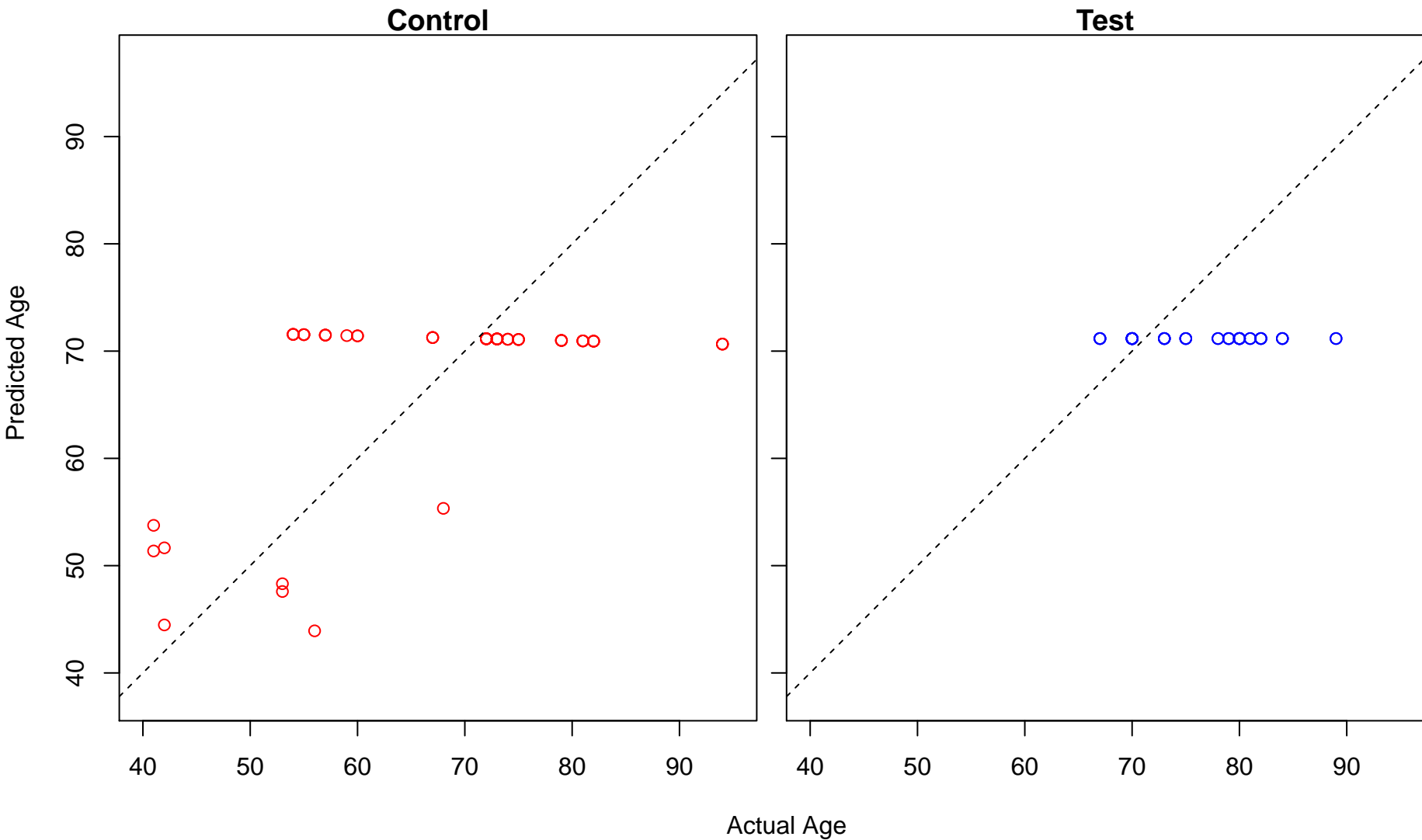
midbrain development (Score: 0.805910)



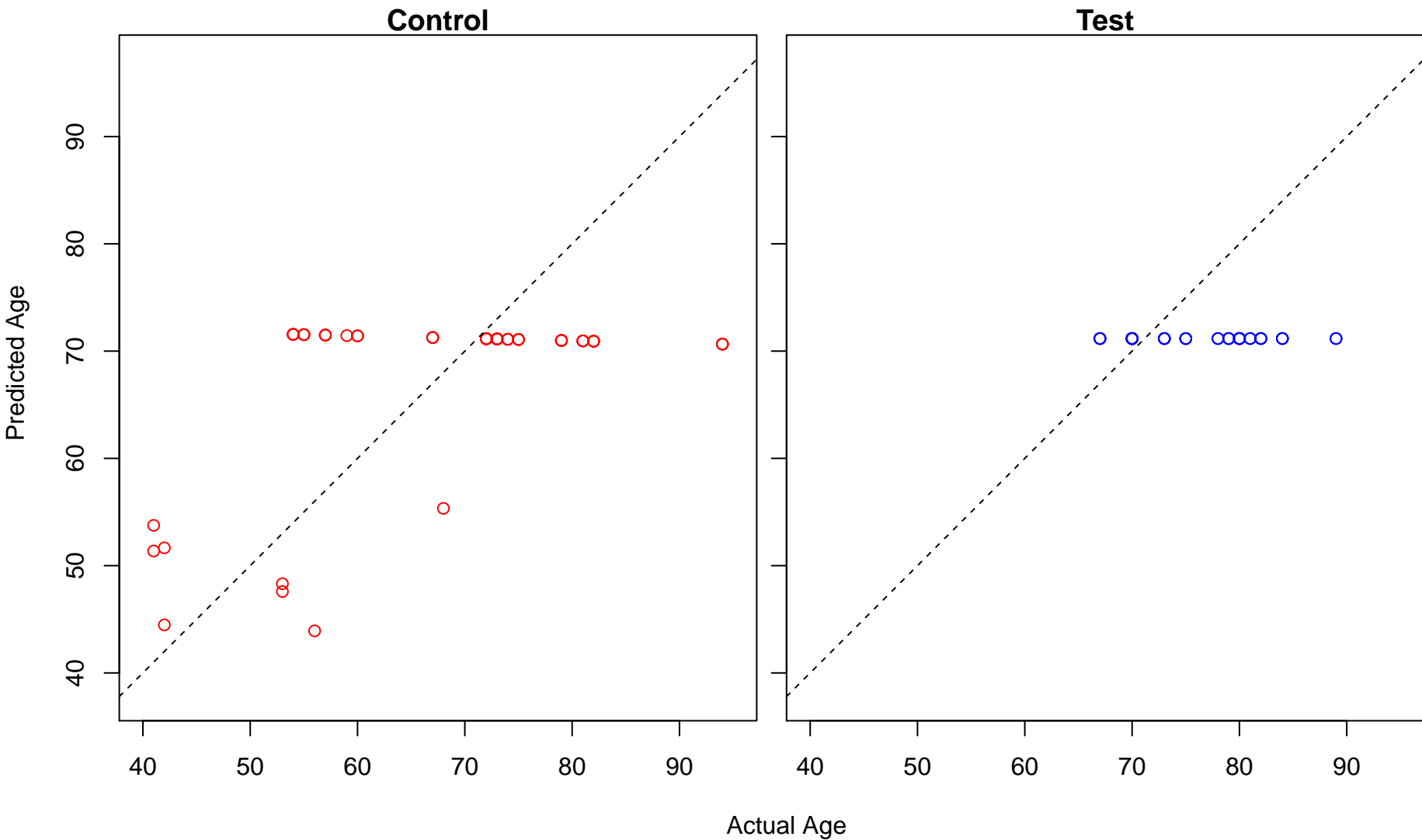
neural nucleus development (Score: 0.805910)



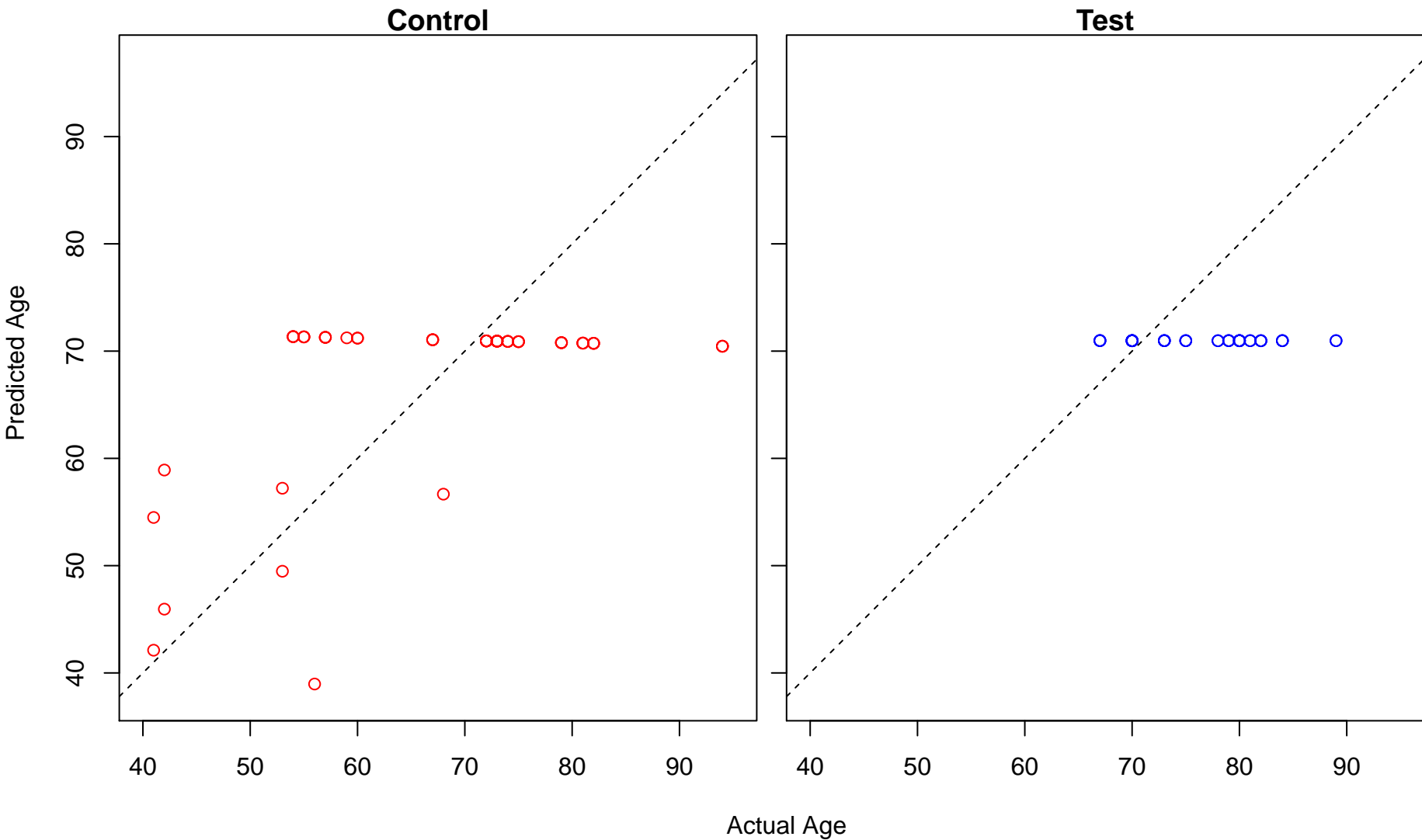
brain development (Score: 0.805908)



head development (Score: 0.805908)

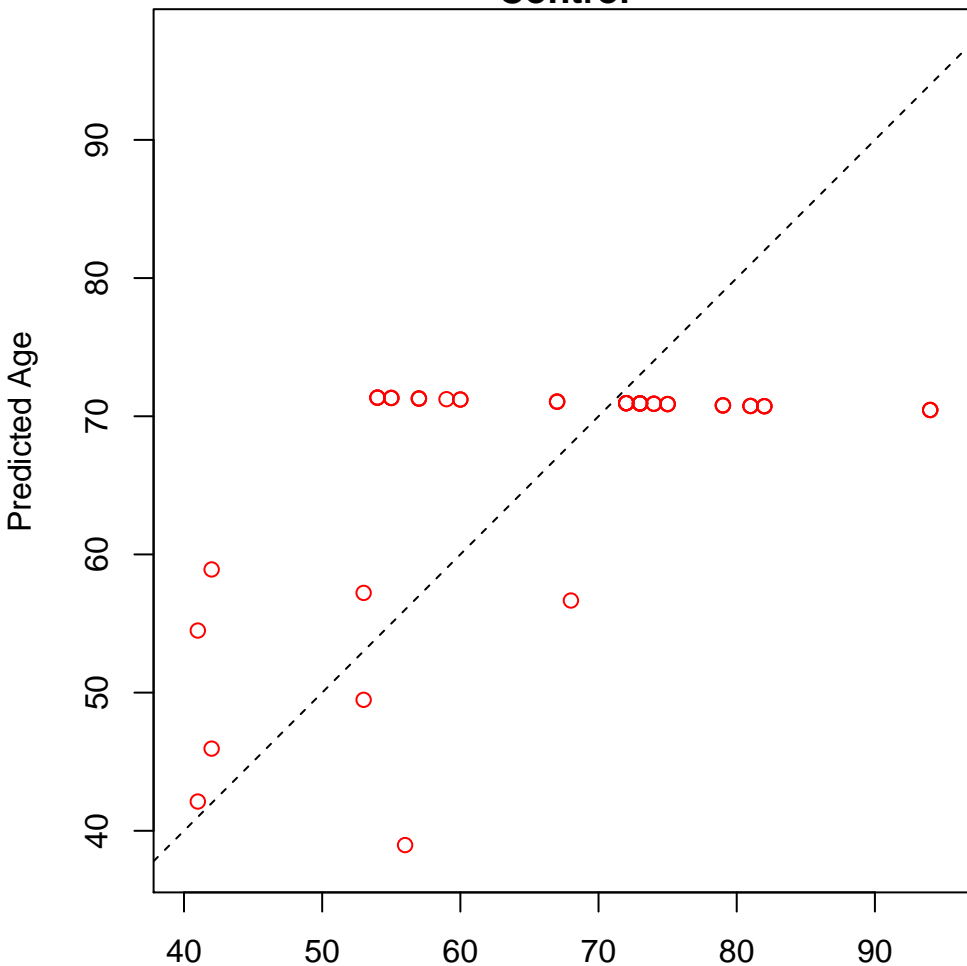


regulation of histone acetylation (Score: 0.805856)

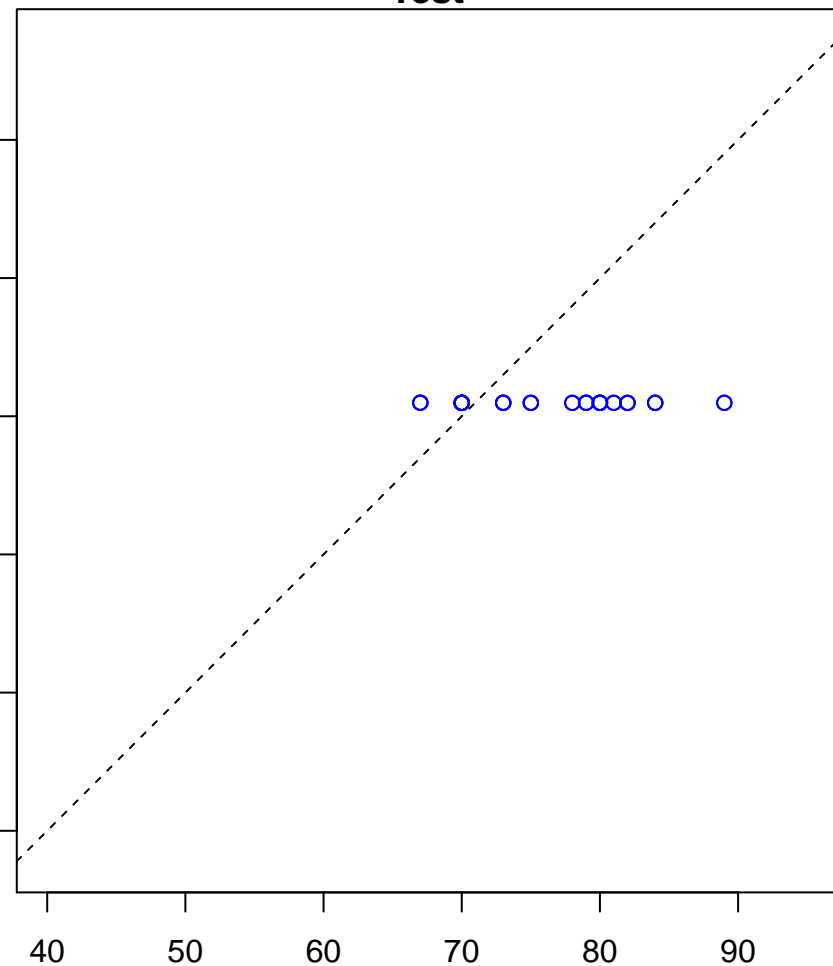


regulation of peptidyl-lysine acetylation (Score: 0.805856)

Control

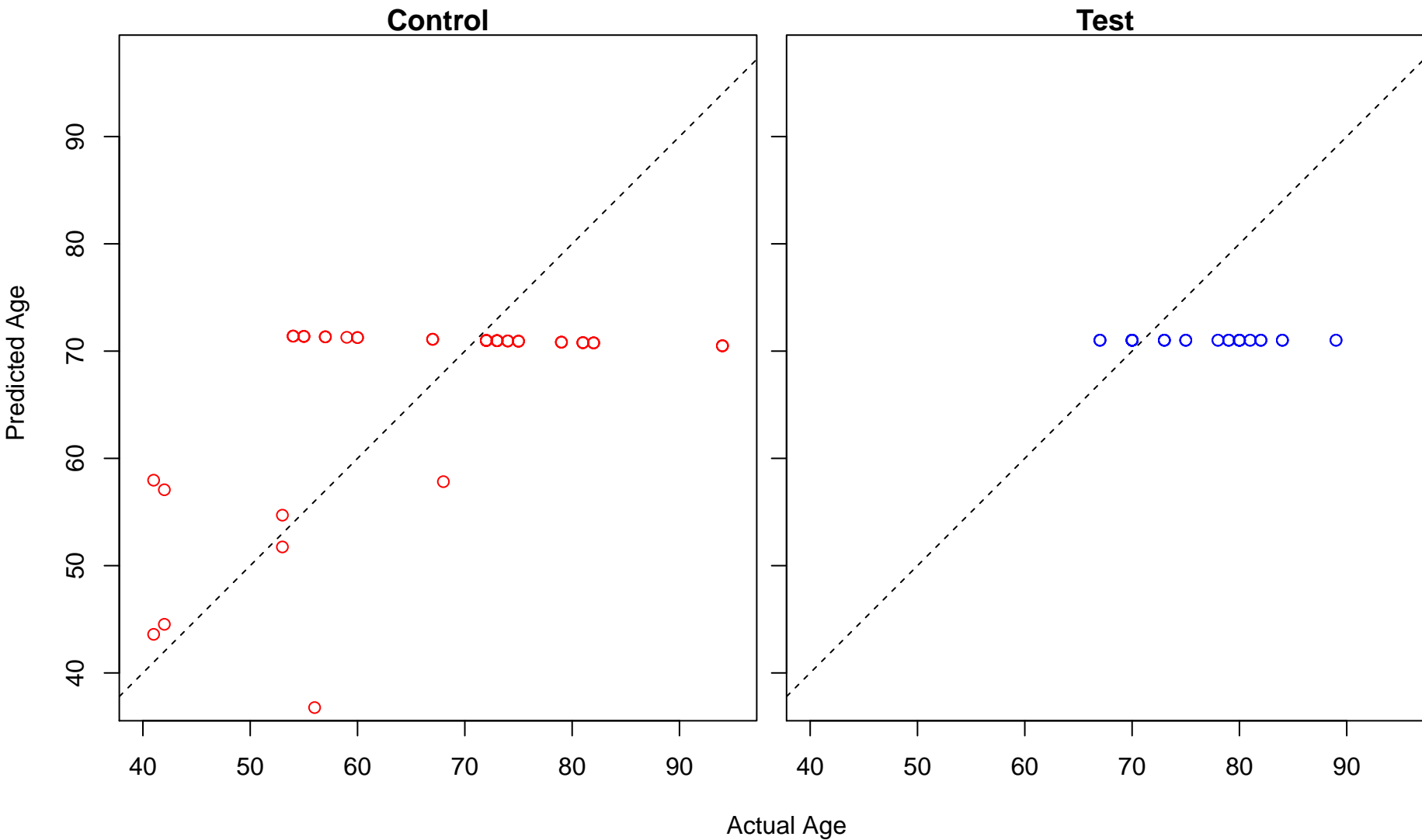


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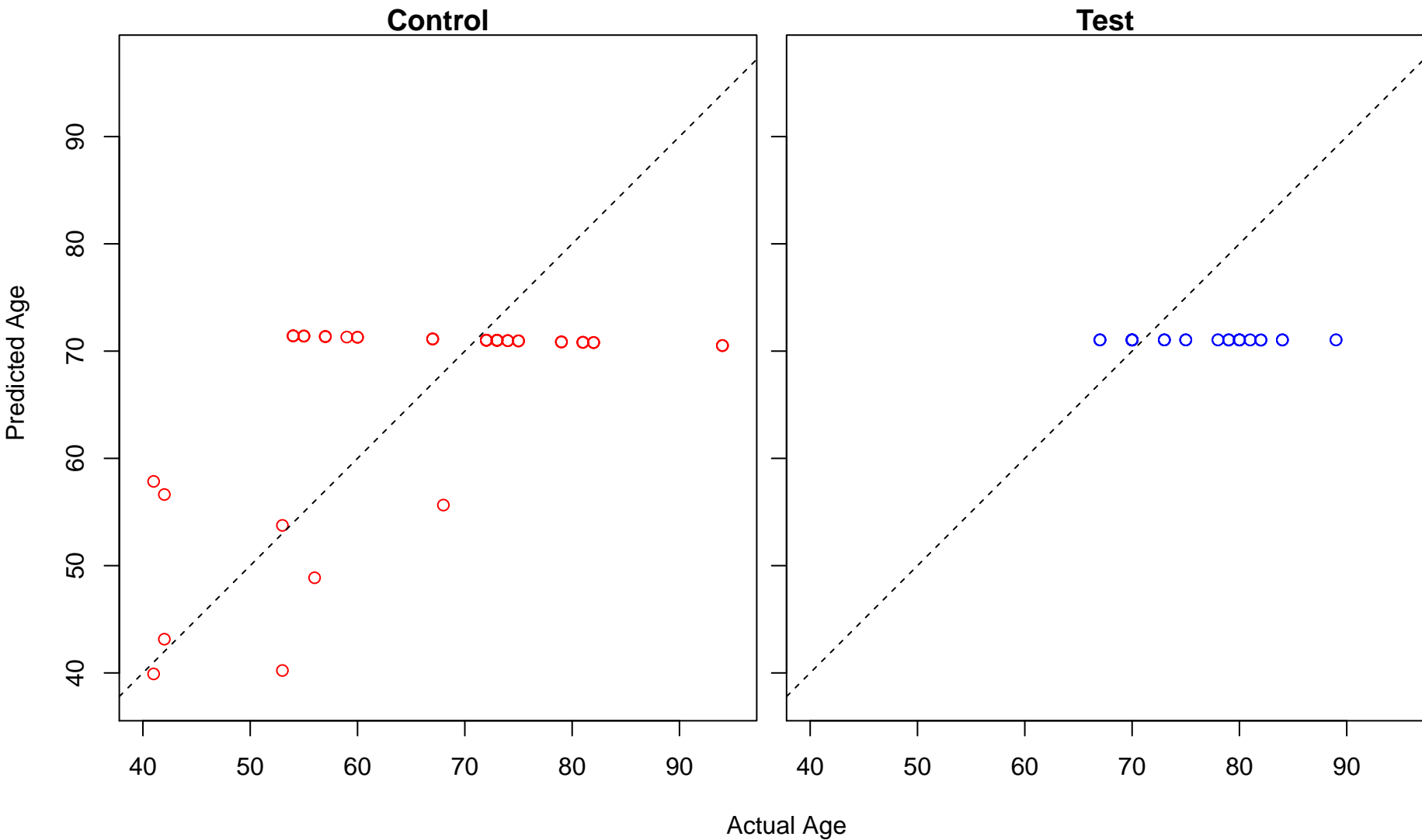


Actual Age

positive regulation of cell cycle (Score: 0.805846)

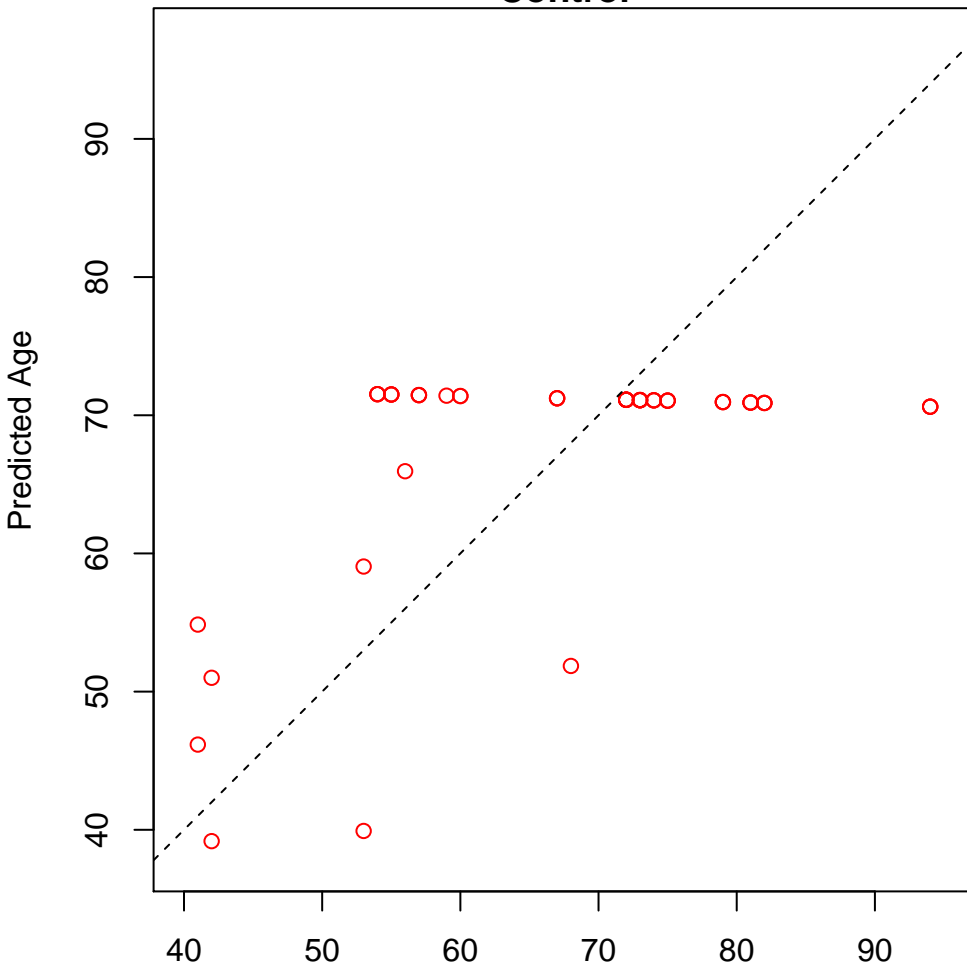


retrograde vesicle-mediated transport, Golgi to ER (Score: 0.805825)

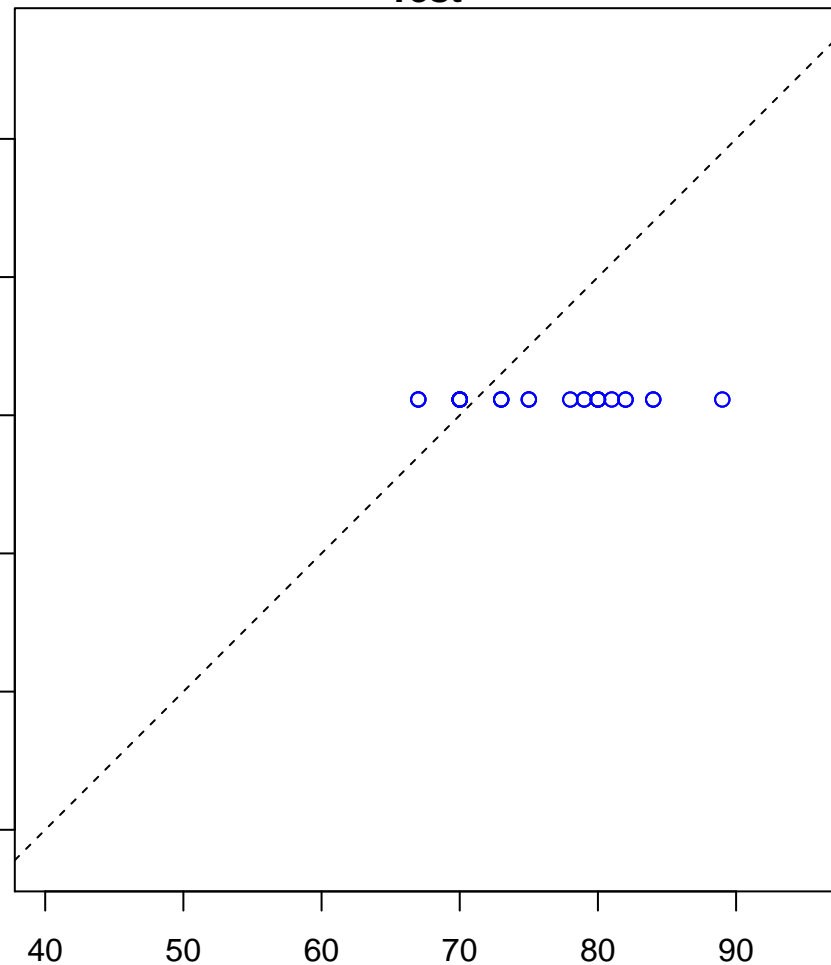


regulation of vesicle-mediated transport (Score: 0.805823)

Control

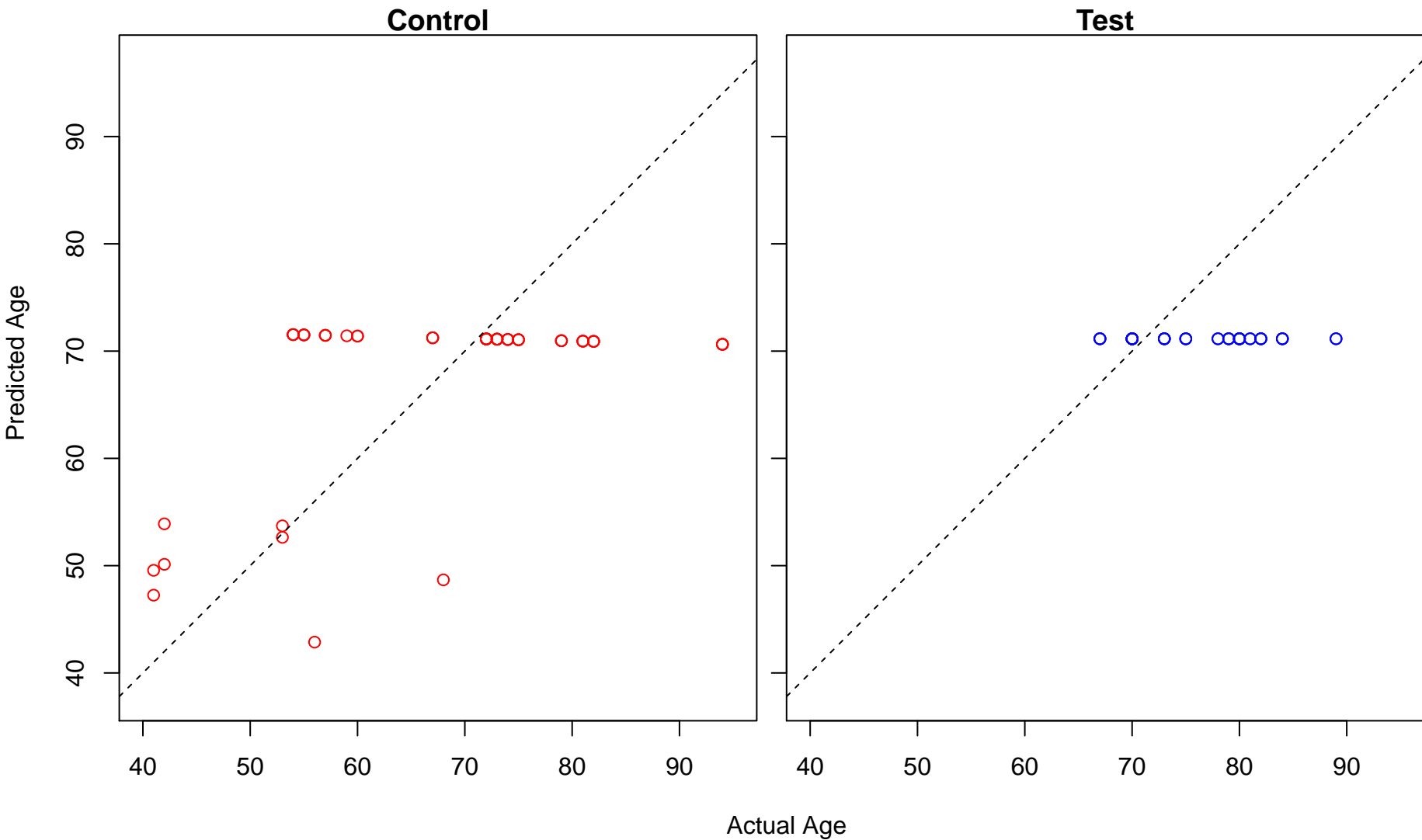


Test

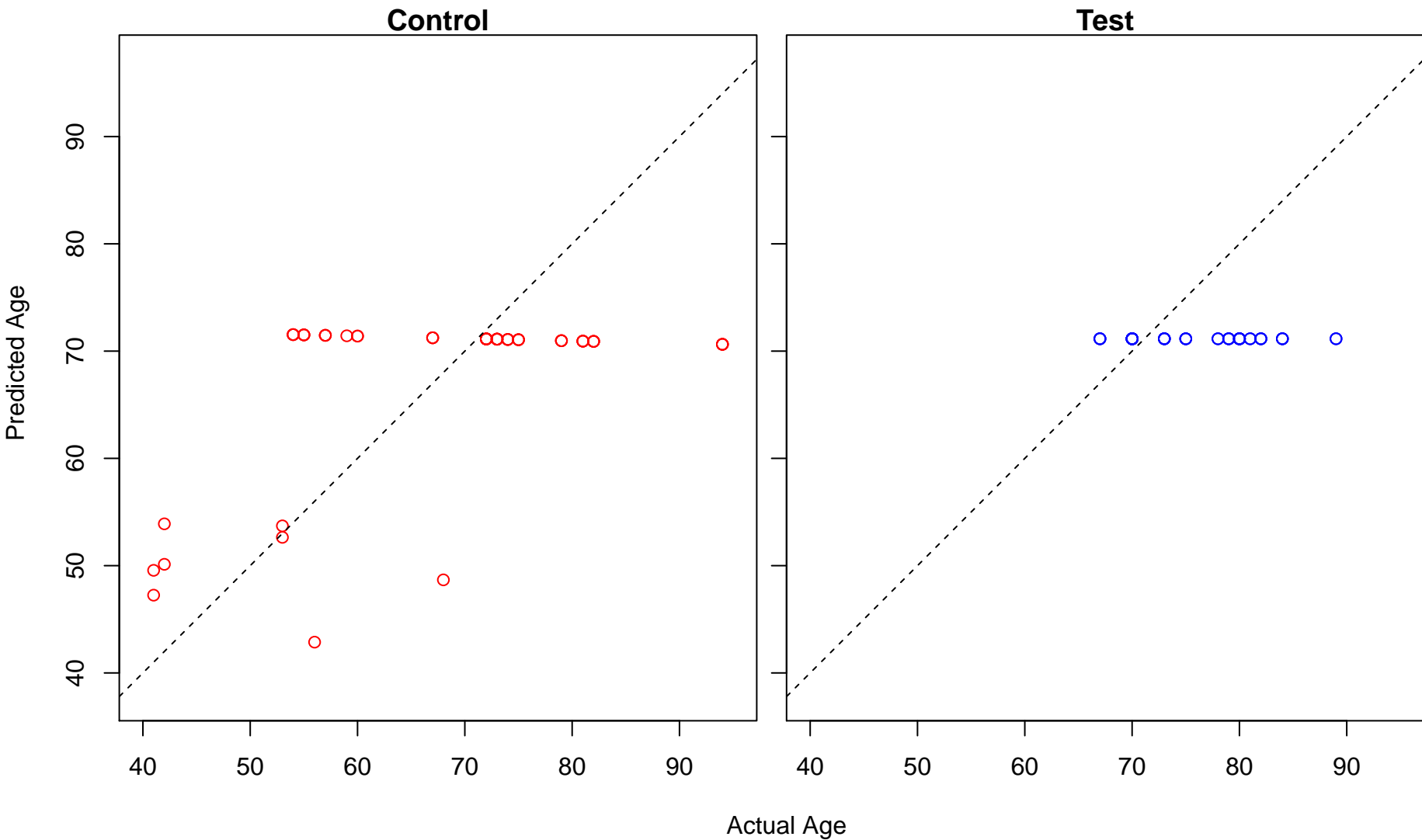


Actual Age

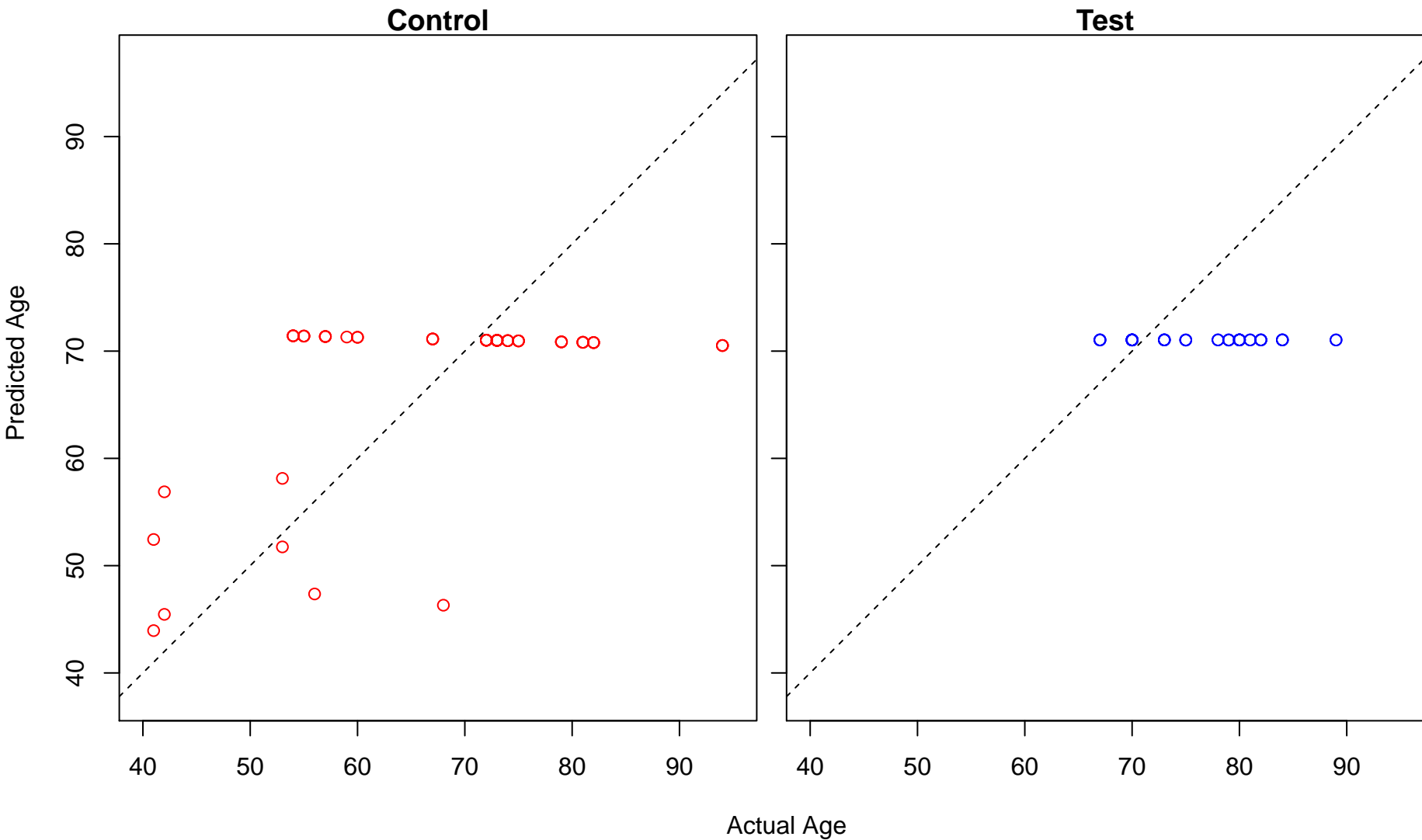
protein complex assembly (Score: 0.805787)



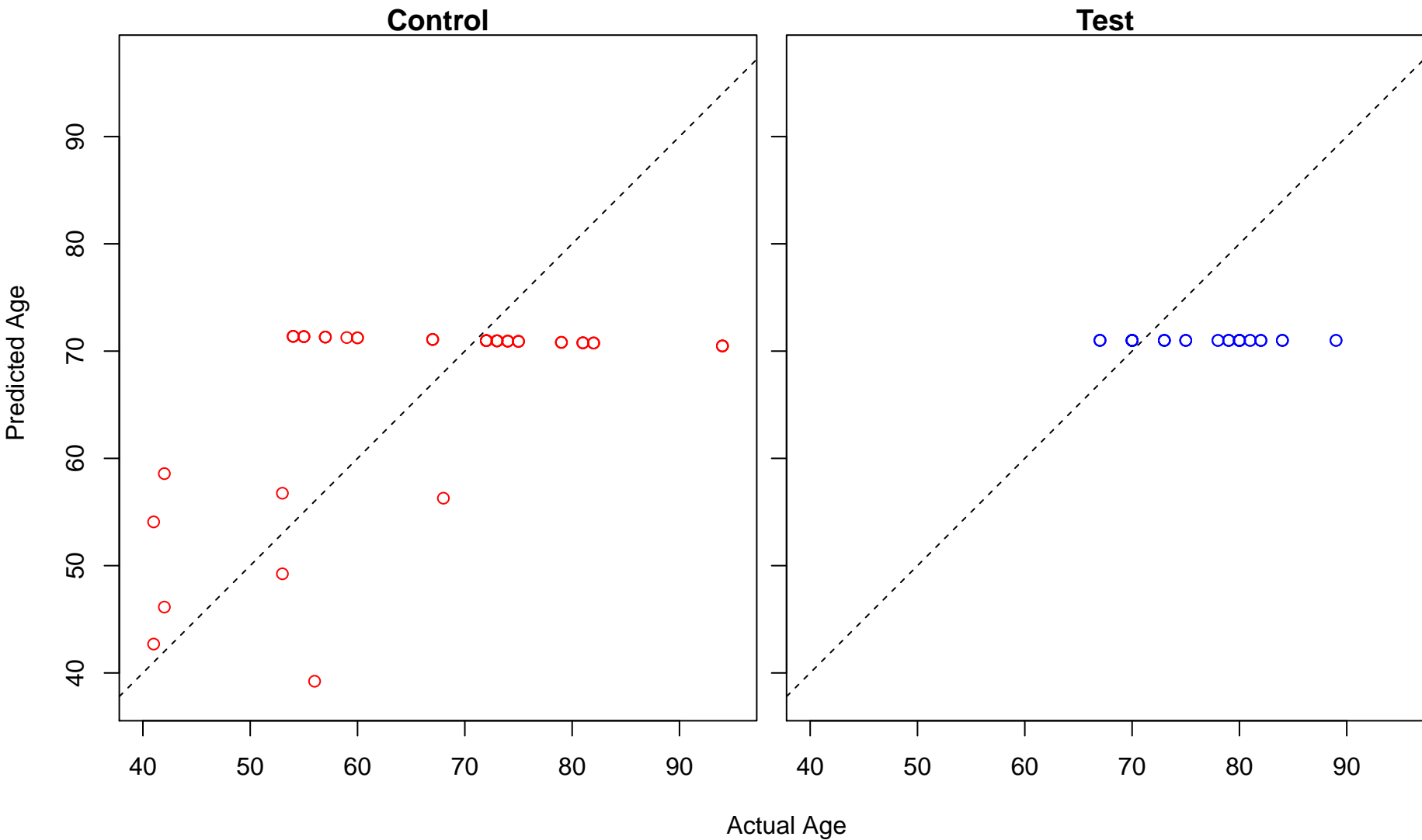
protein complex biogenesis (Score: 0.805787)



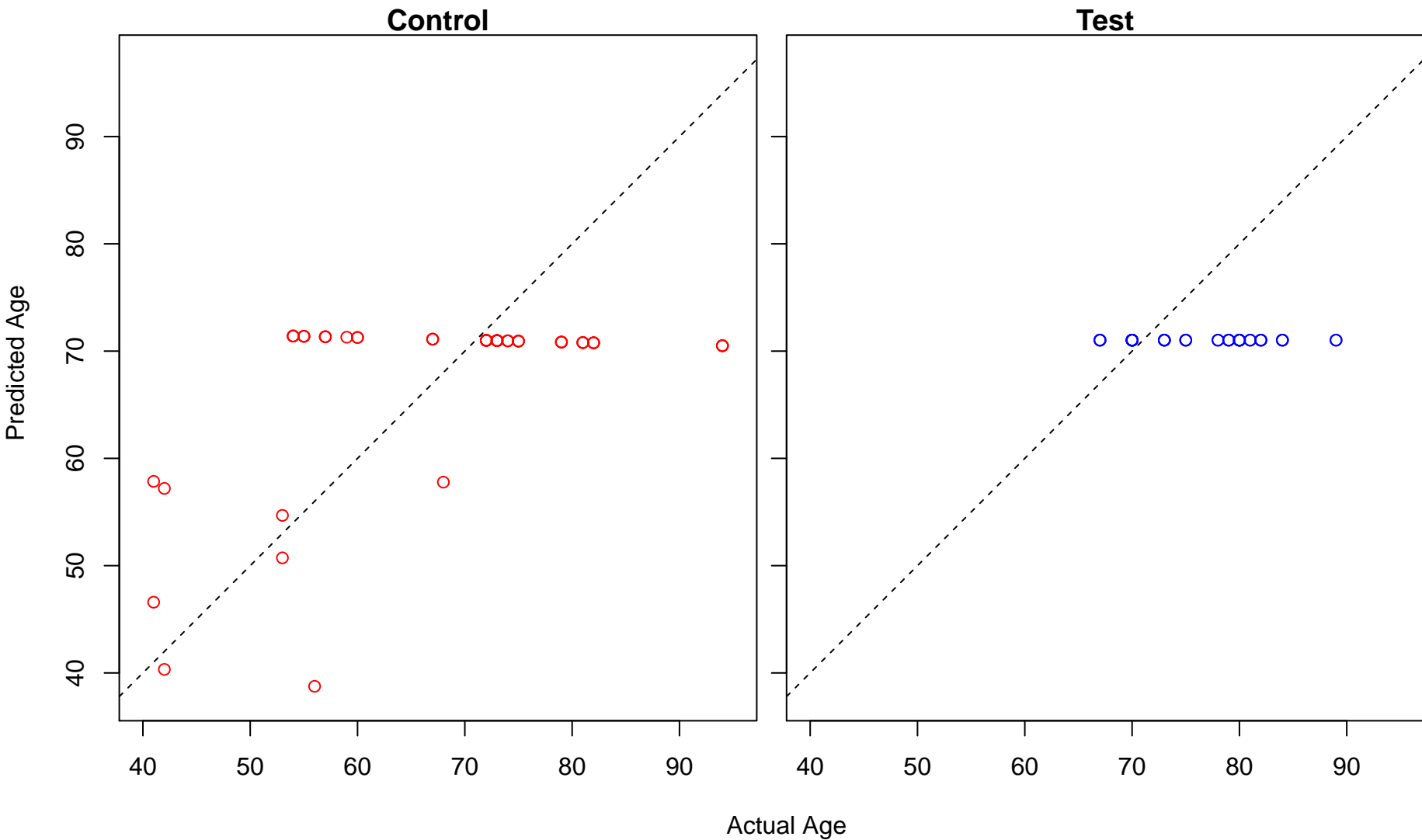
fatty acid metabolic process (Score: 0.805765)



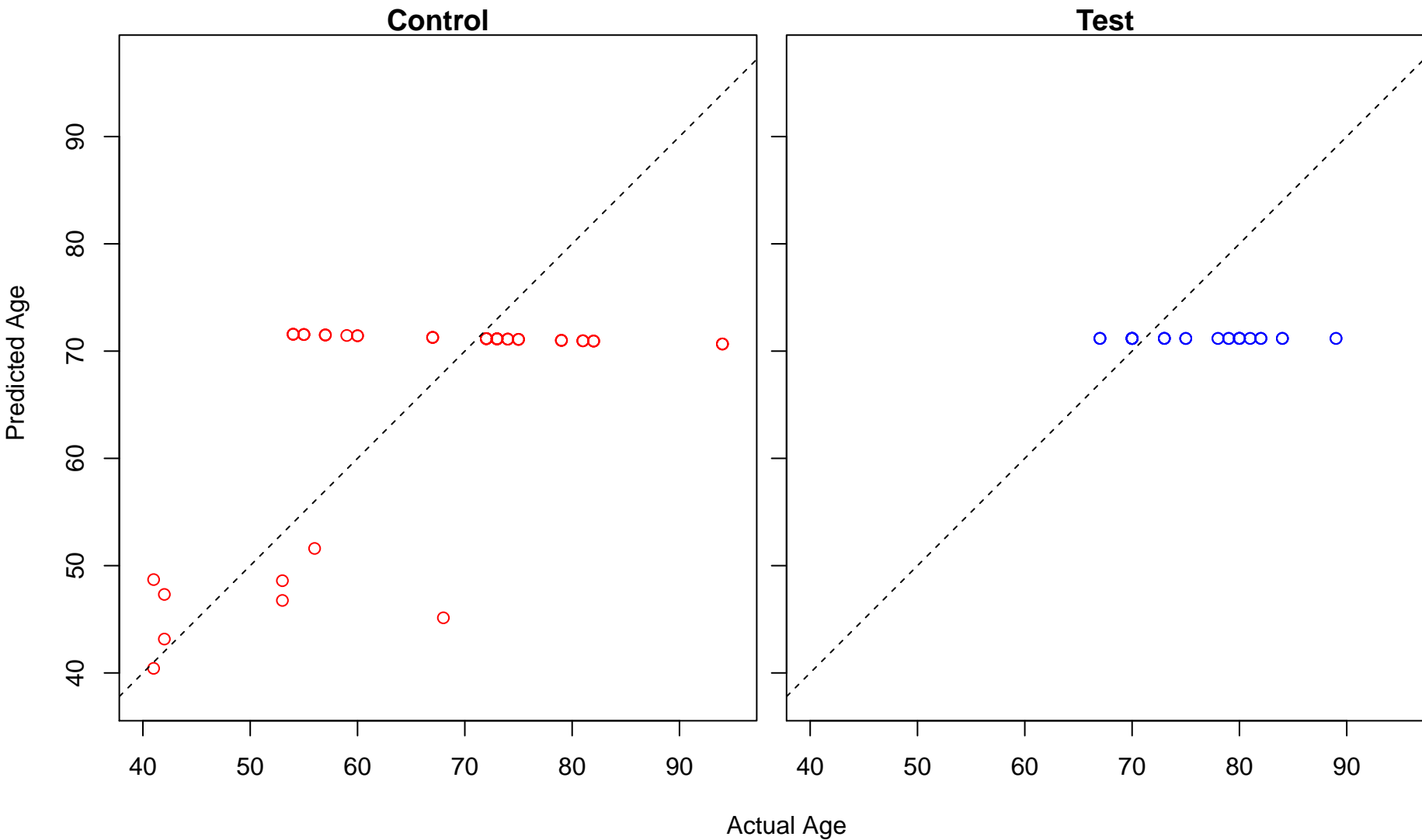
regulation of histone modification (Score: 0.805764)



stress-activated protein kinase signaling cascade (Score: 0.805731)

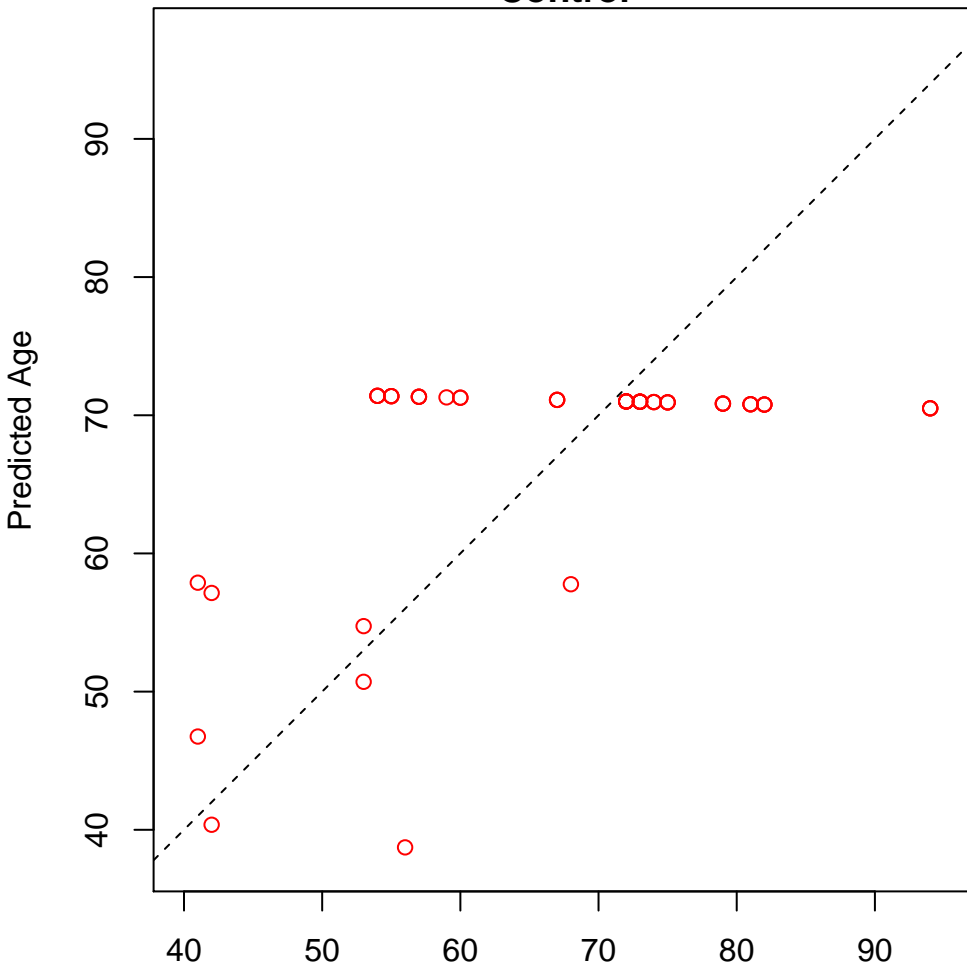


negative regulation of biosynthetic process (Score: 0.805659)

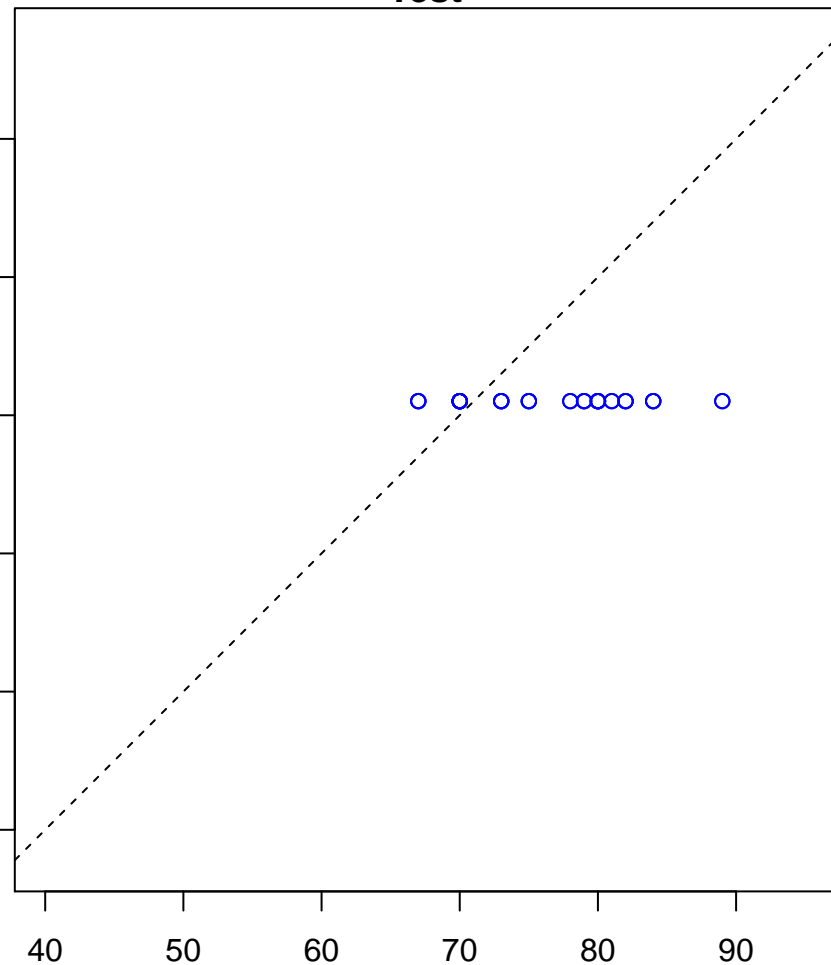


stress-activated MAPK cascade (Score: 0.805659)

Control



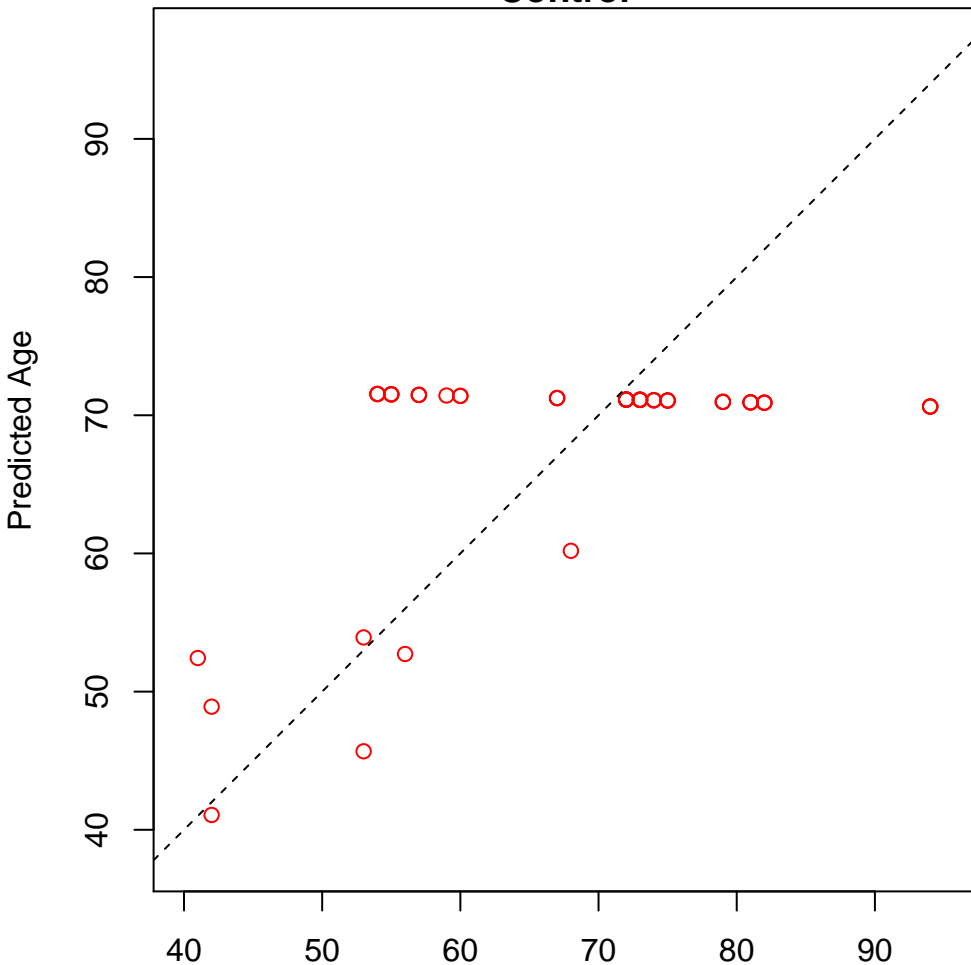
Test



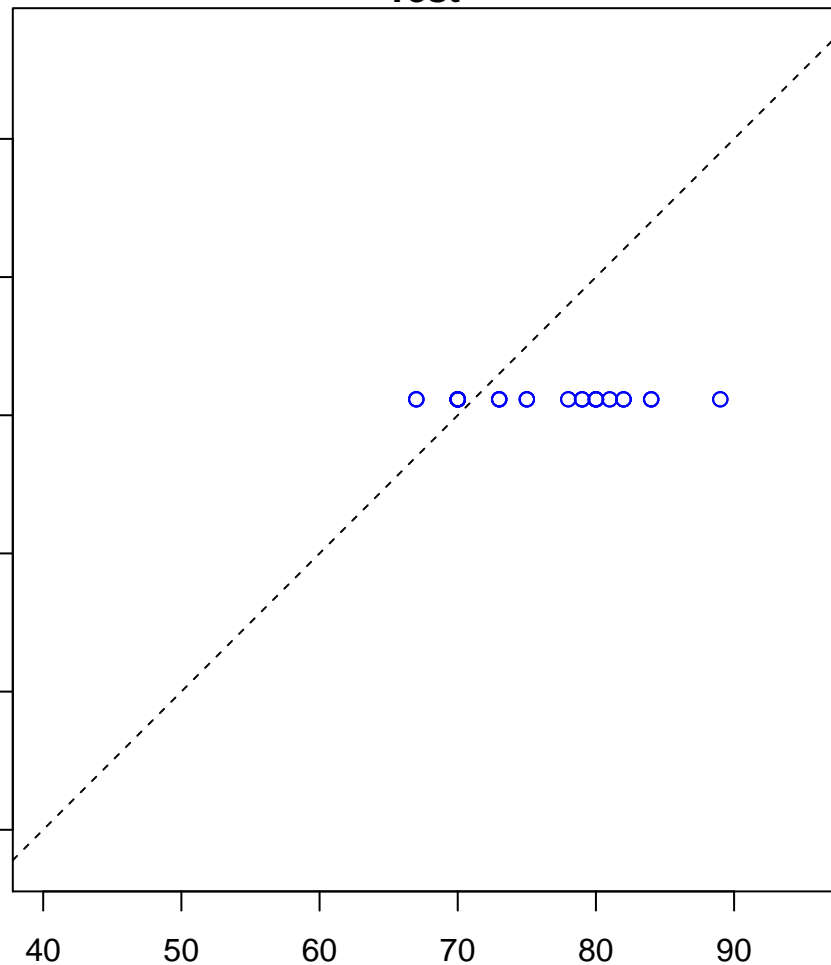
Actual Age

regulation of protein catabolic process (Score: 0.805596)

Control

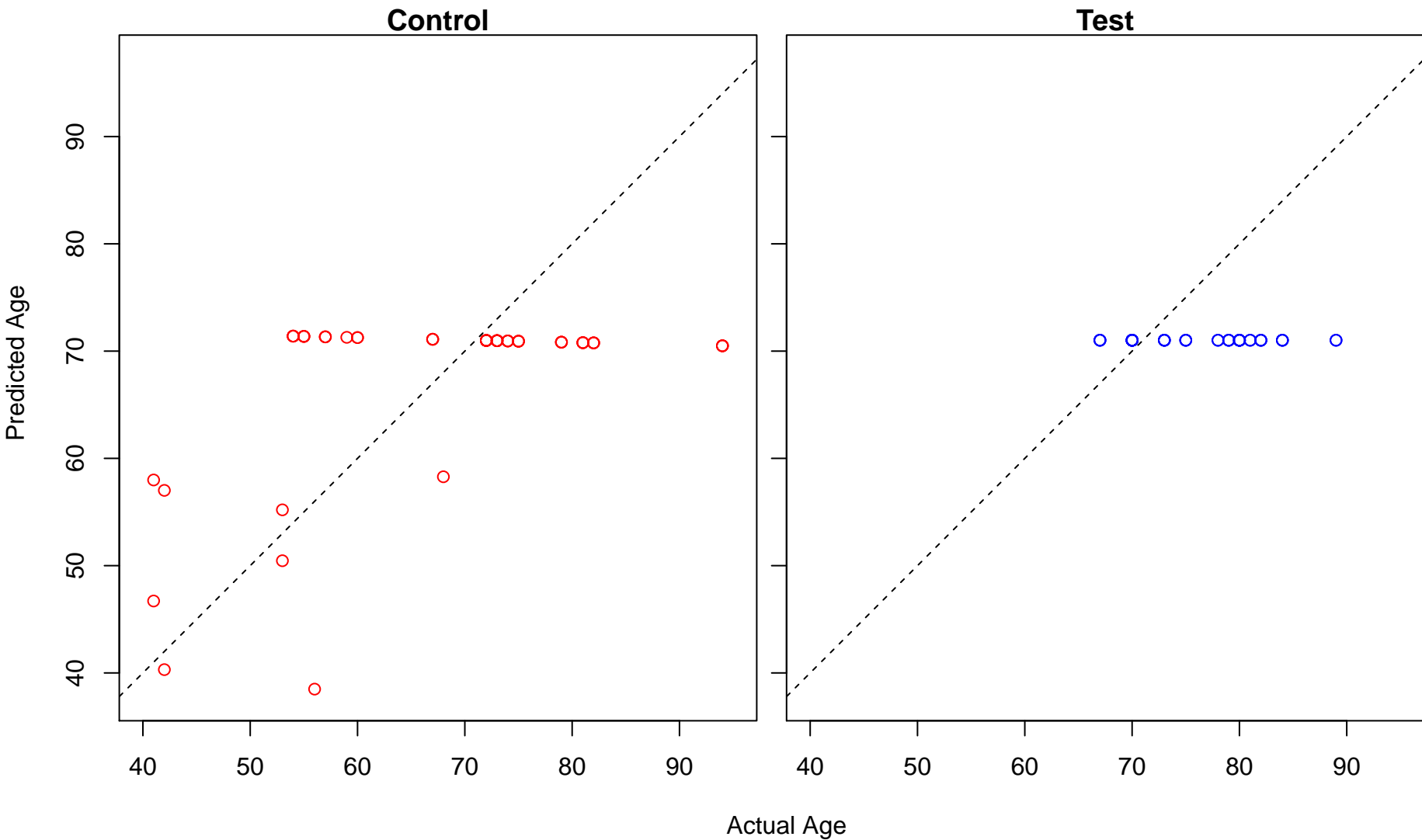


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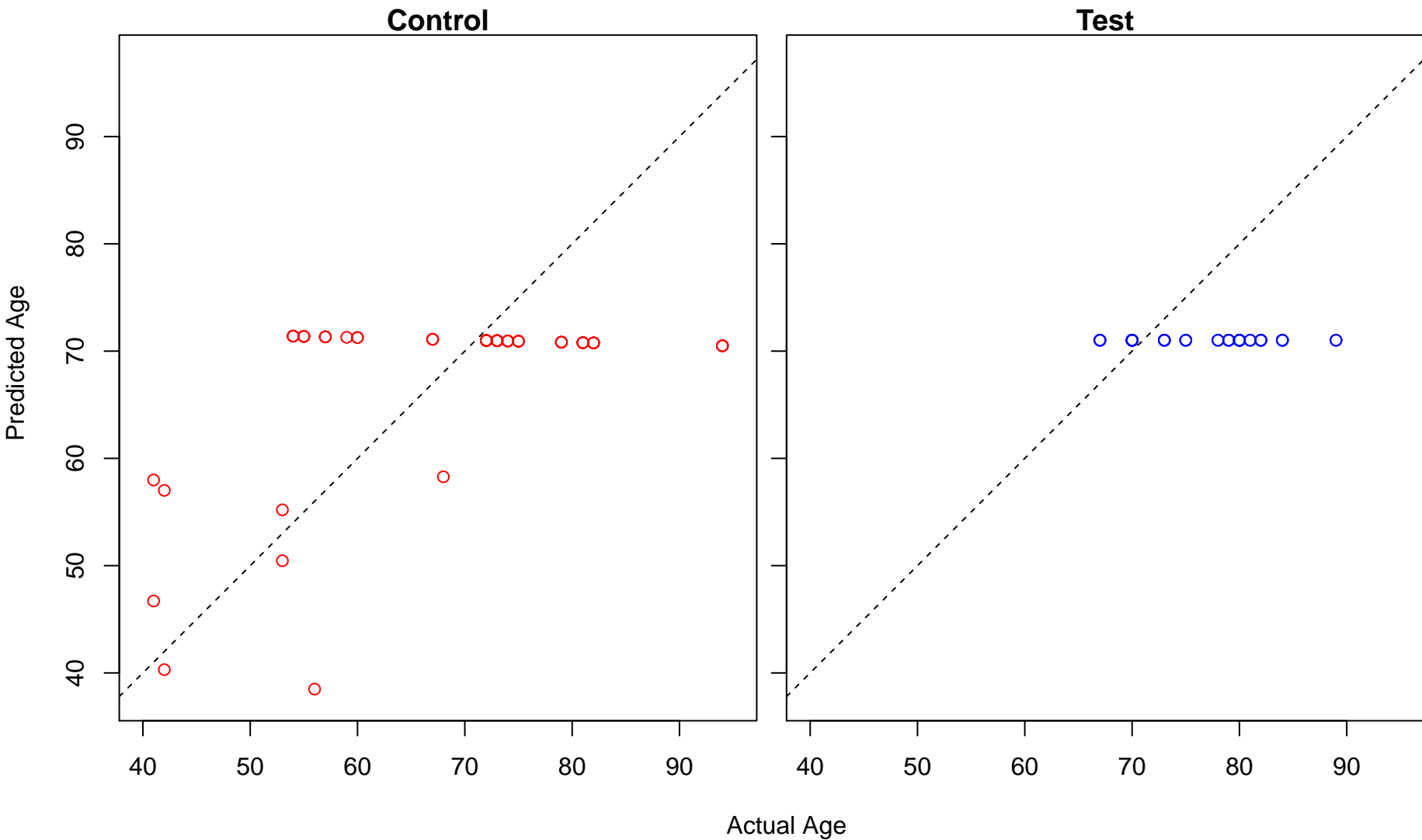


Actual Age

MyD88-independent toll-like receptor signaling pathway (Score: 0.805592)

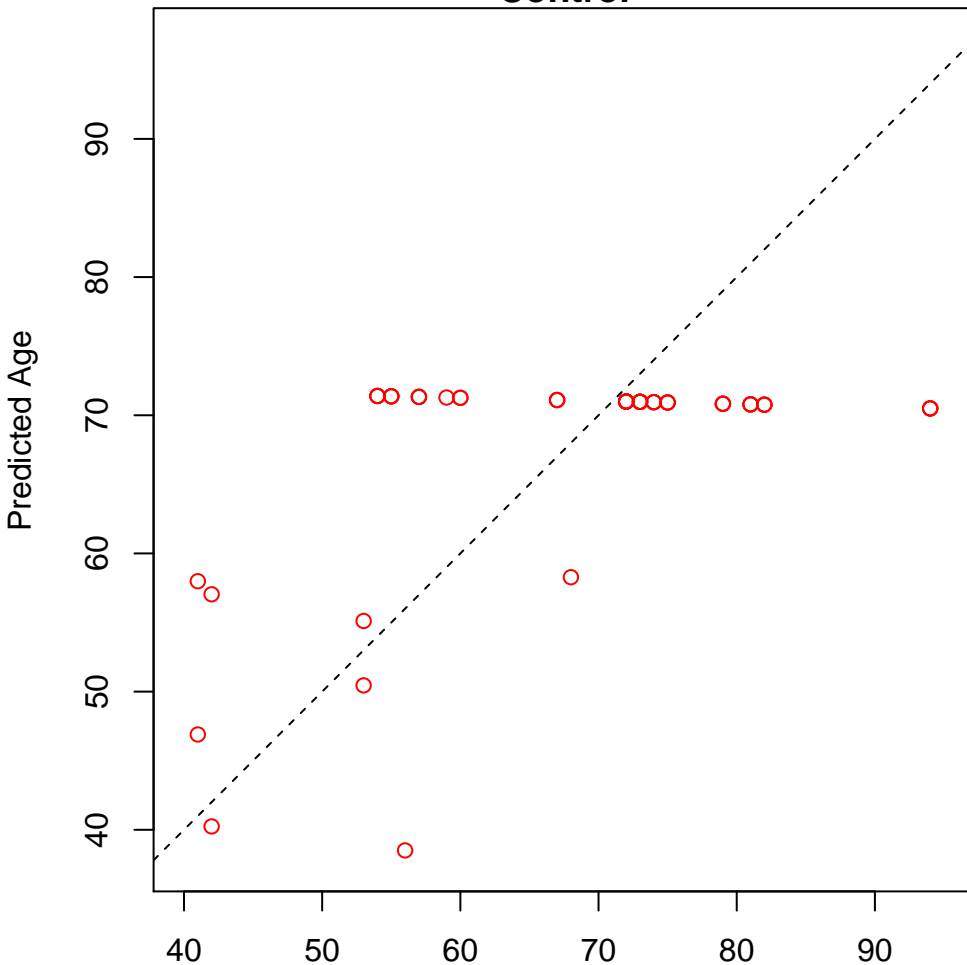


TRIF-dependent toll-like receptor signaling pathway (Score: 0.805592)

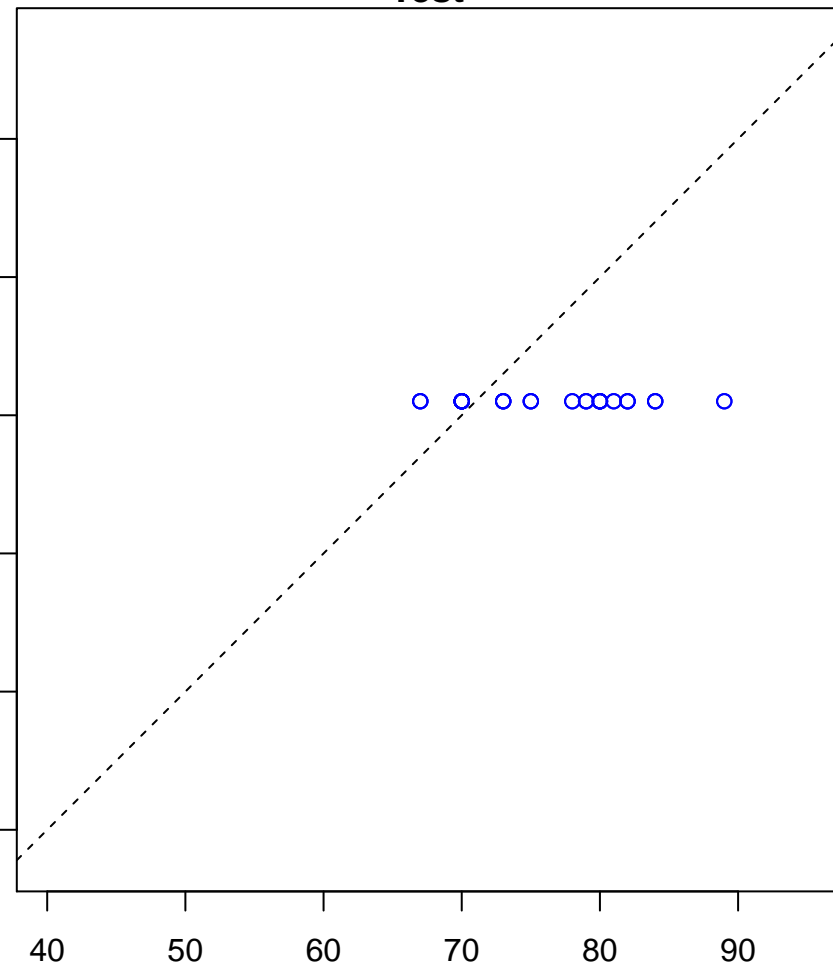


protein demannosylation (Score: 0.805467)

Control



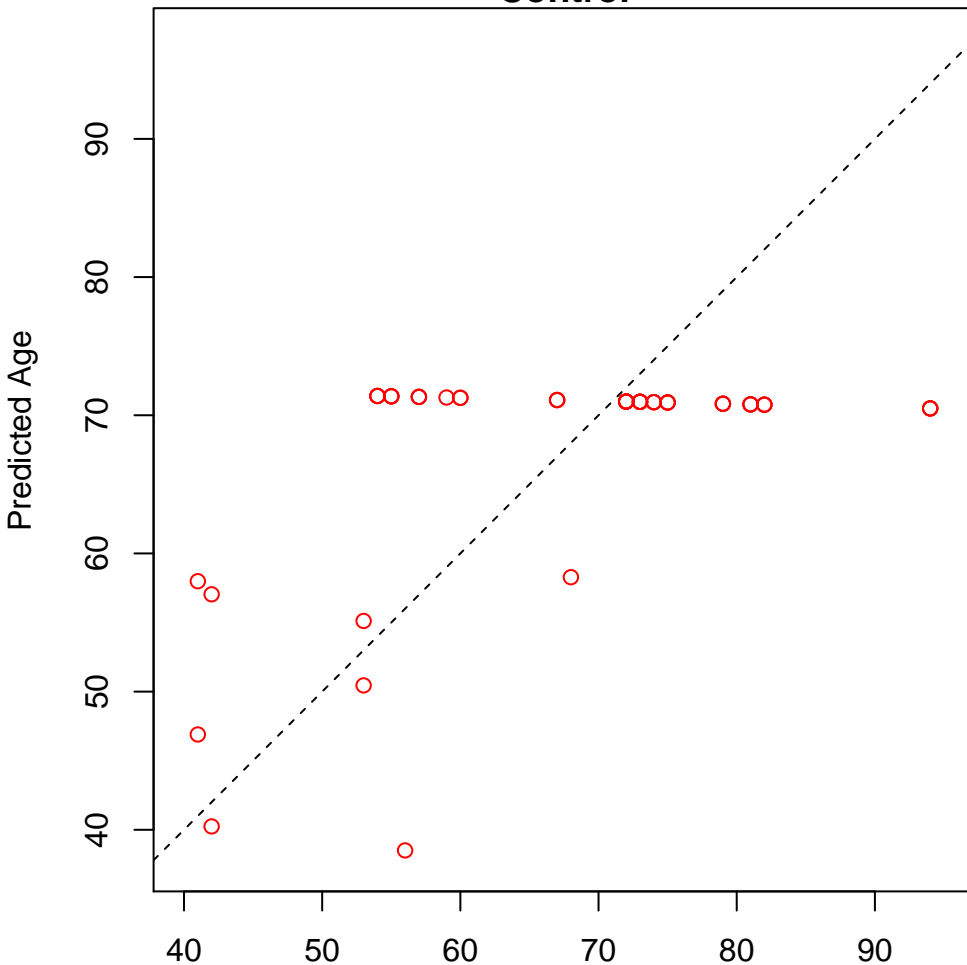
Test



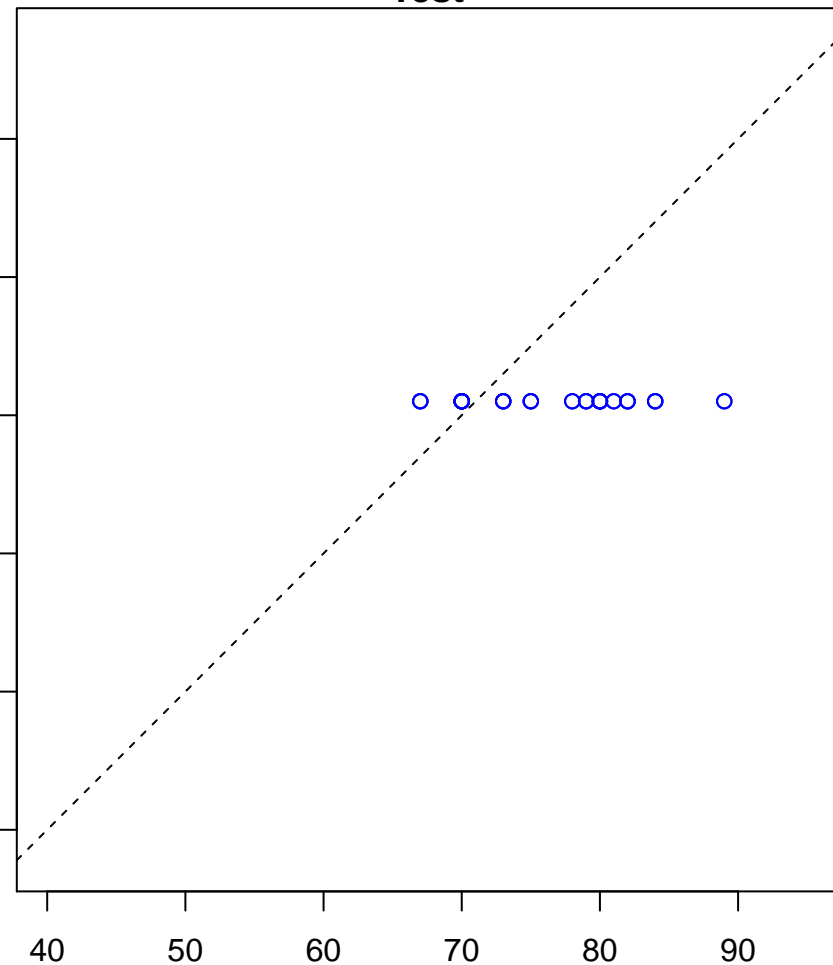
Actual Age

protein alpha-1,2-demannosylation (Score: 0.805467)

Control



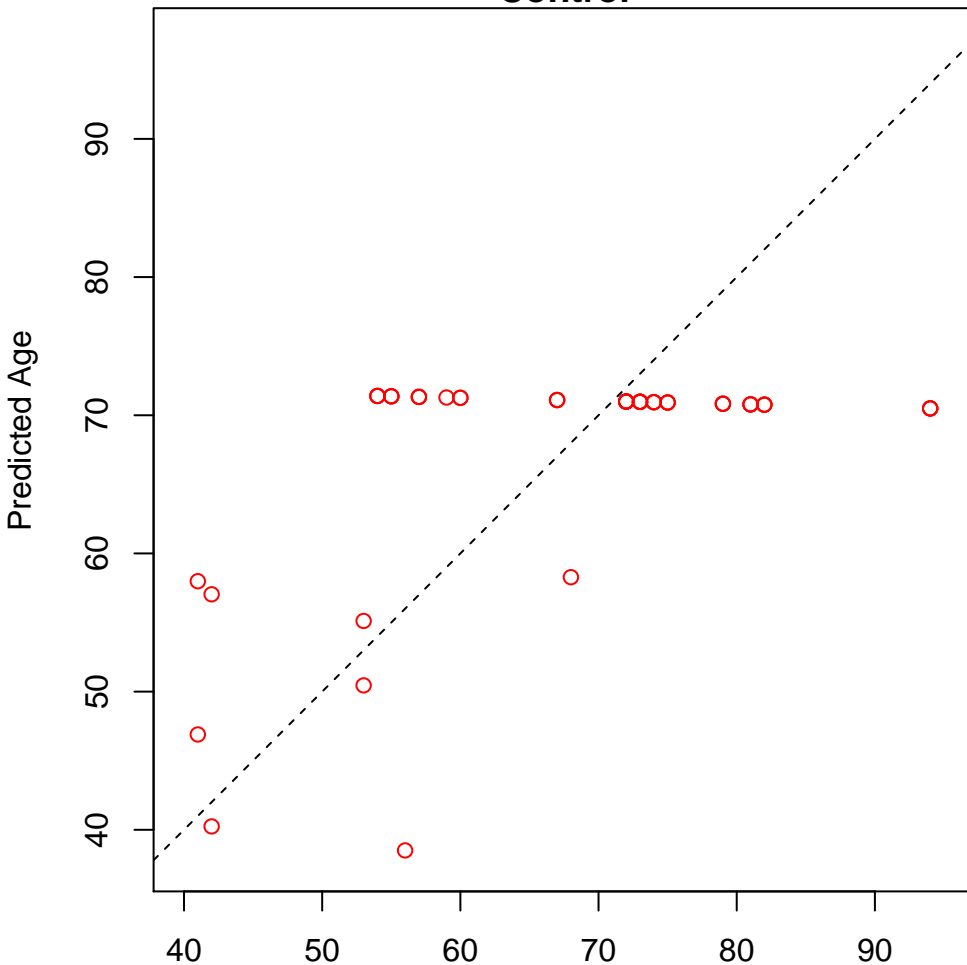
Test



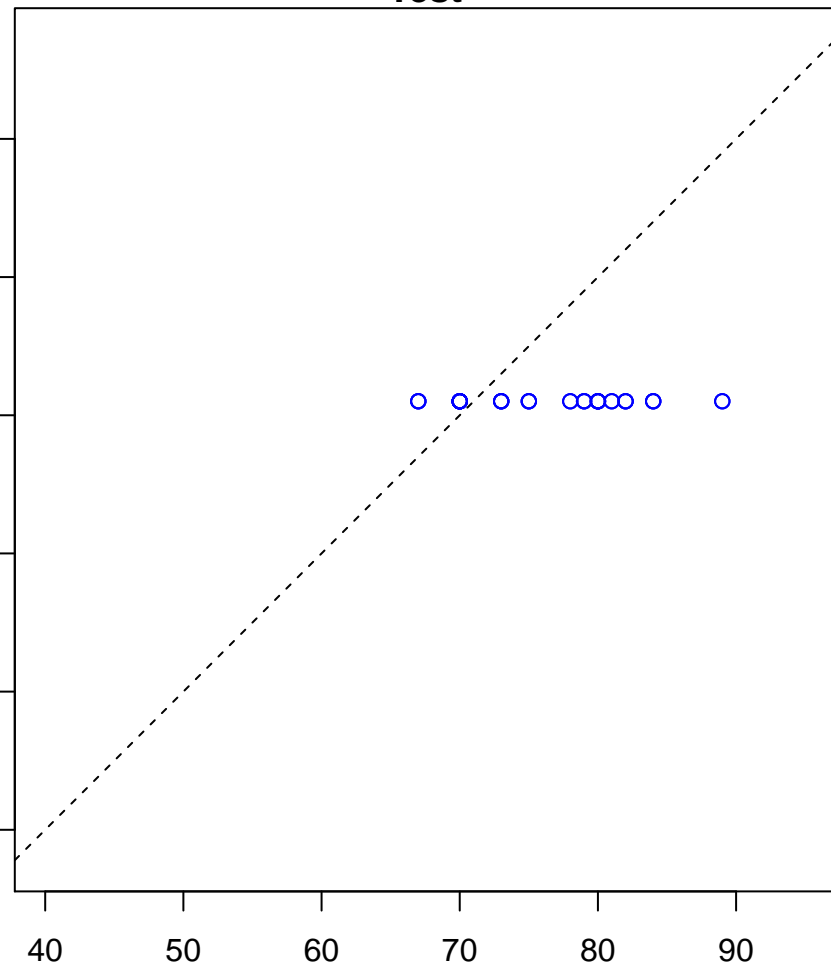
Actual Age

endoplasmic reticulum mannose trimming (Score: 0.805467)

Control

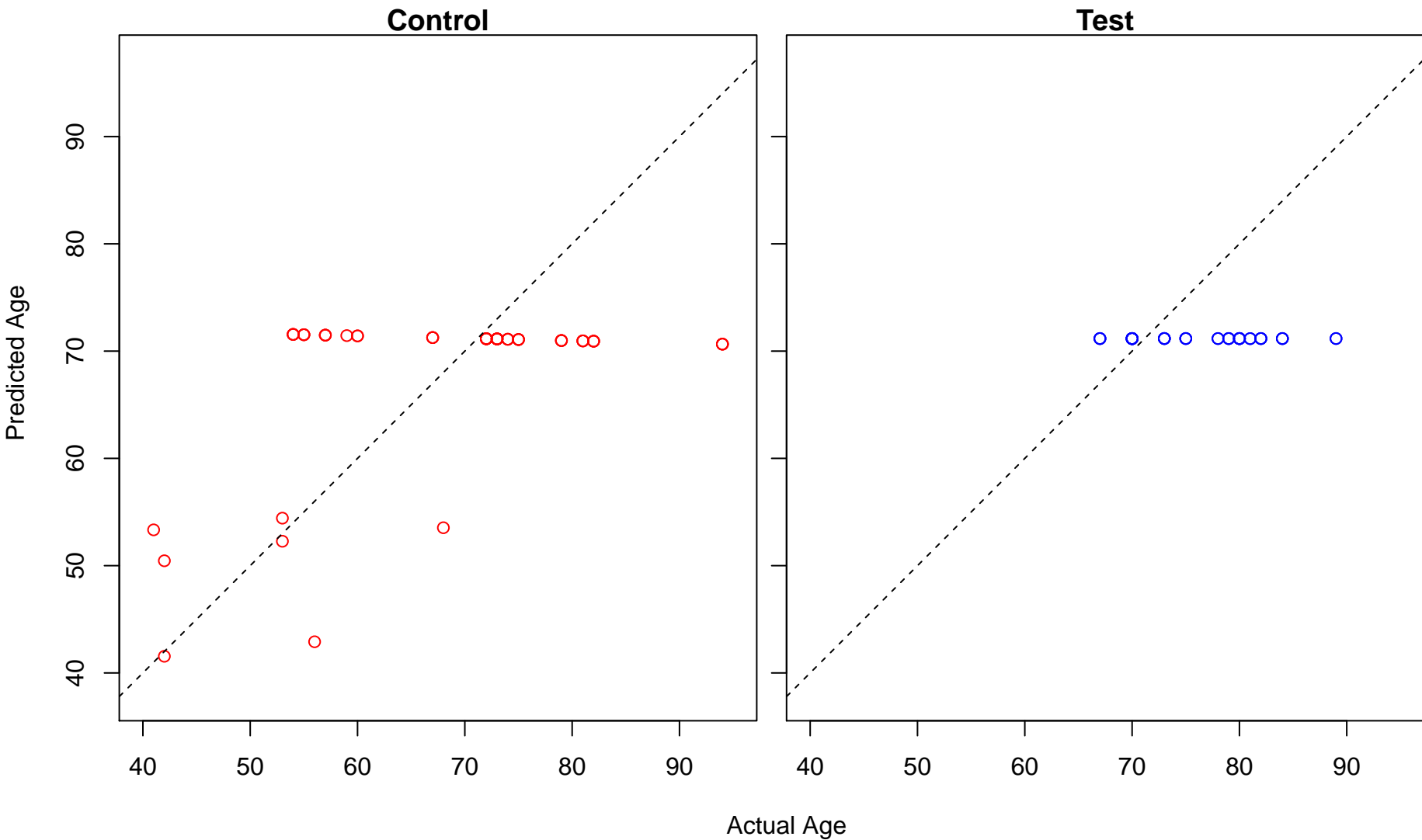


Test



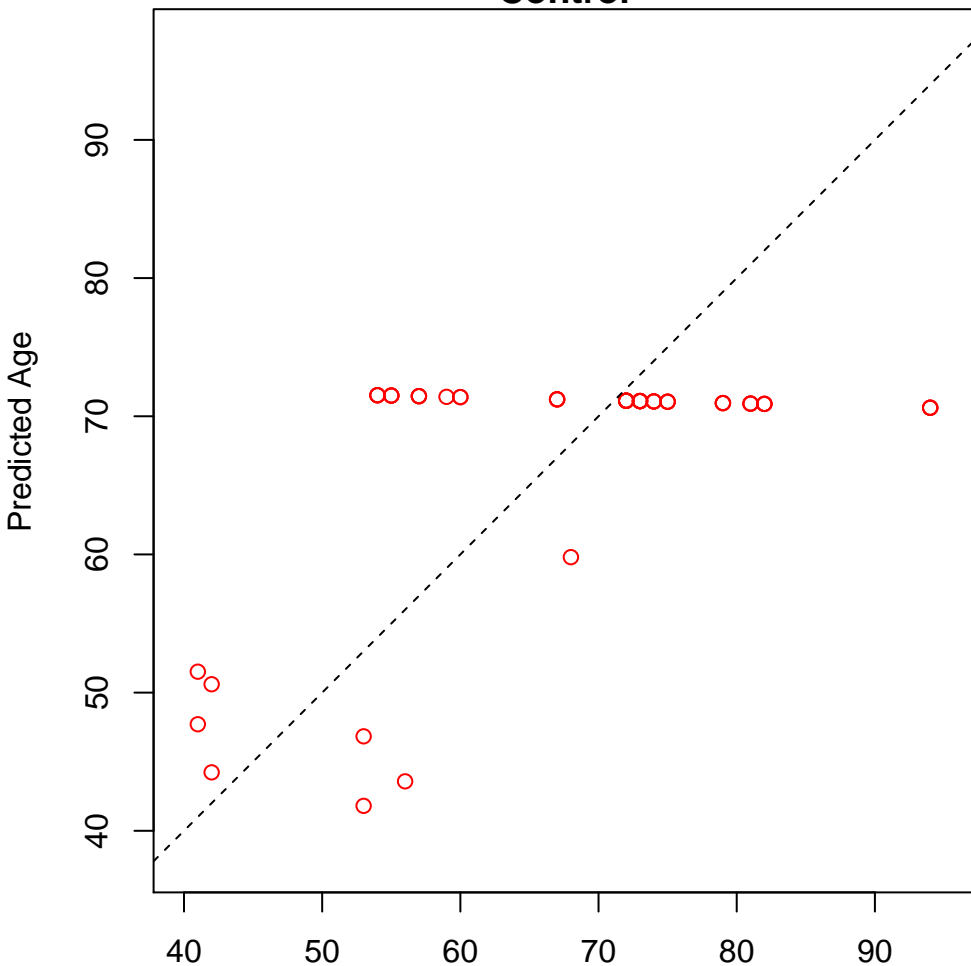
Actual Age

transmembrane receptor protein tyrosine kinase signaling pathway (Score: 0.805467)

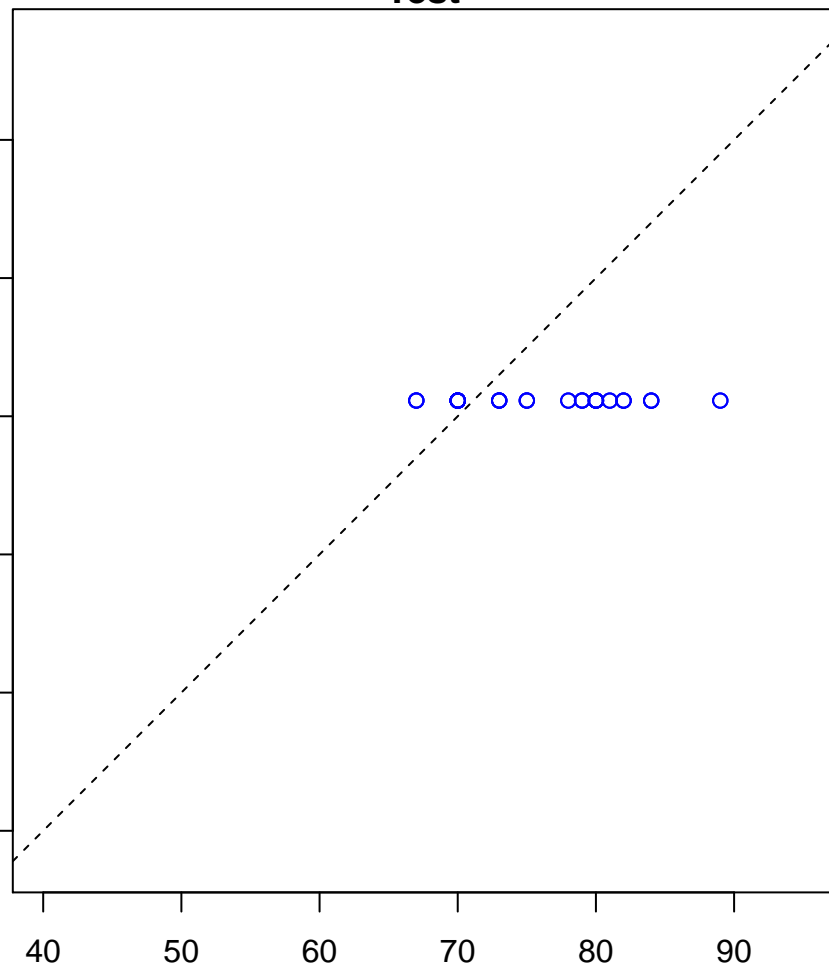


response to organonitrogen compound (Score: 0.805449)

Control

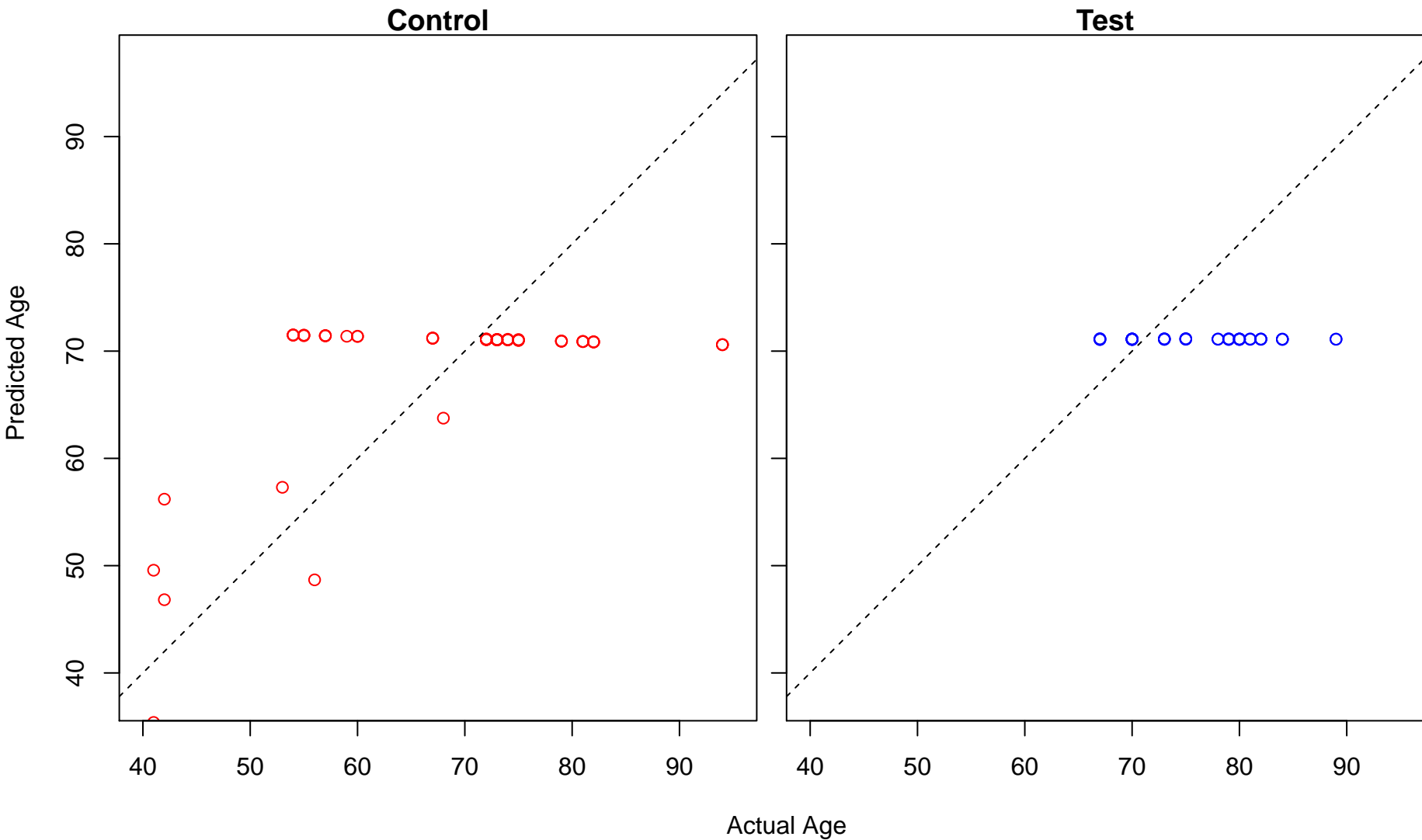


Test

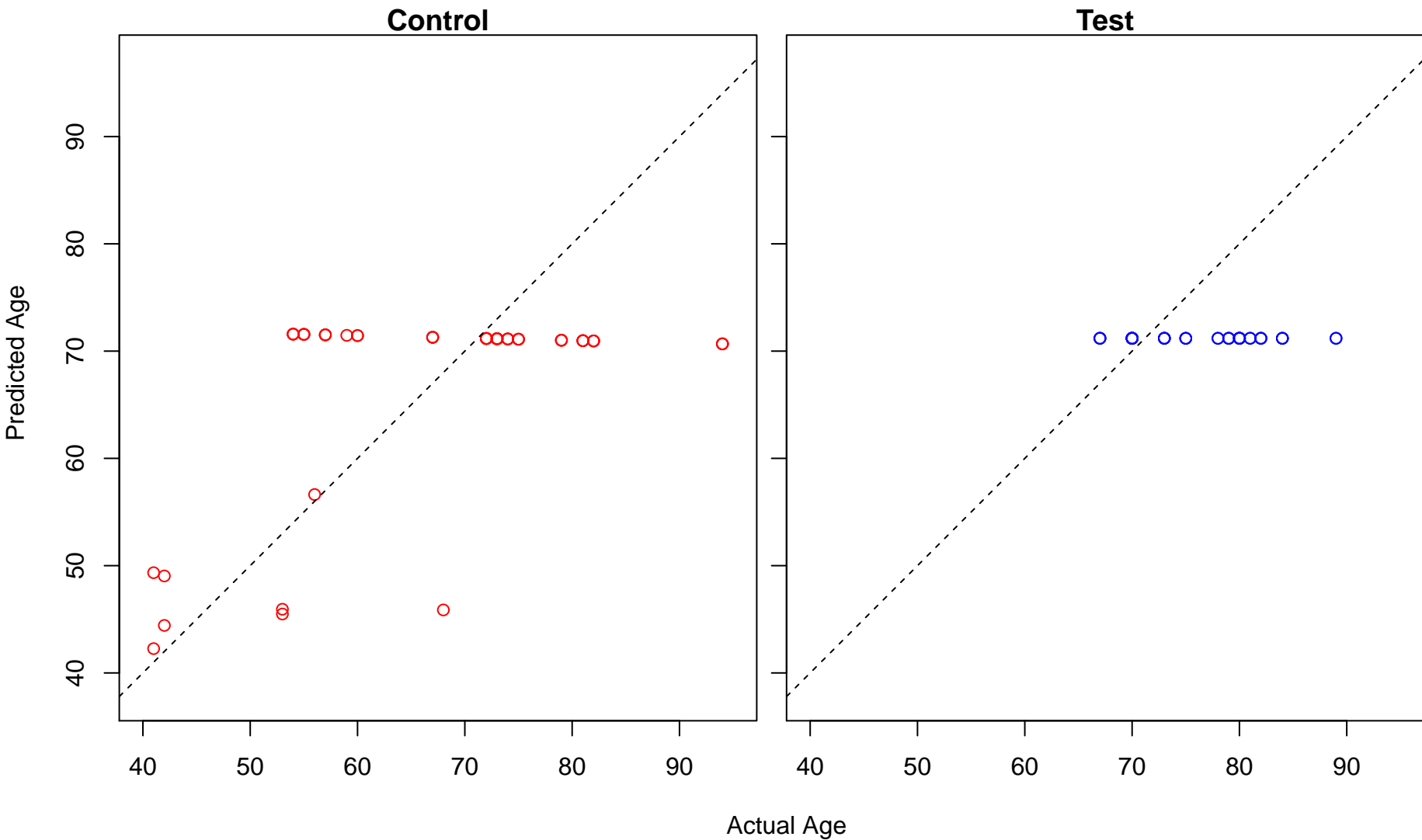


Actual Age

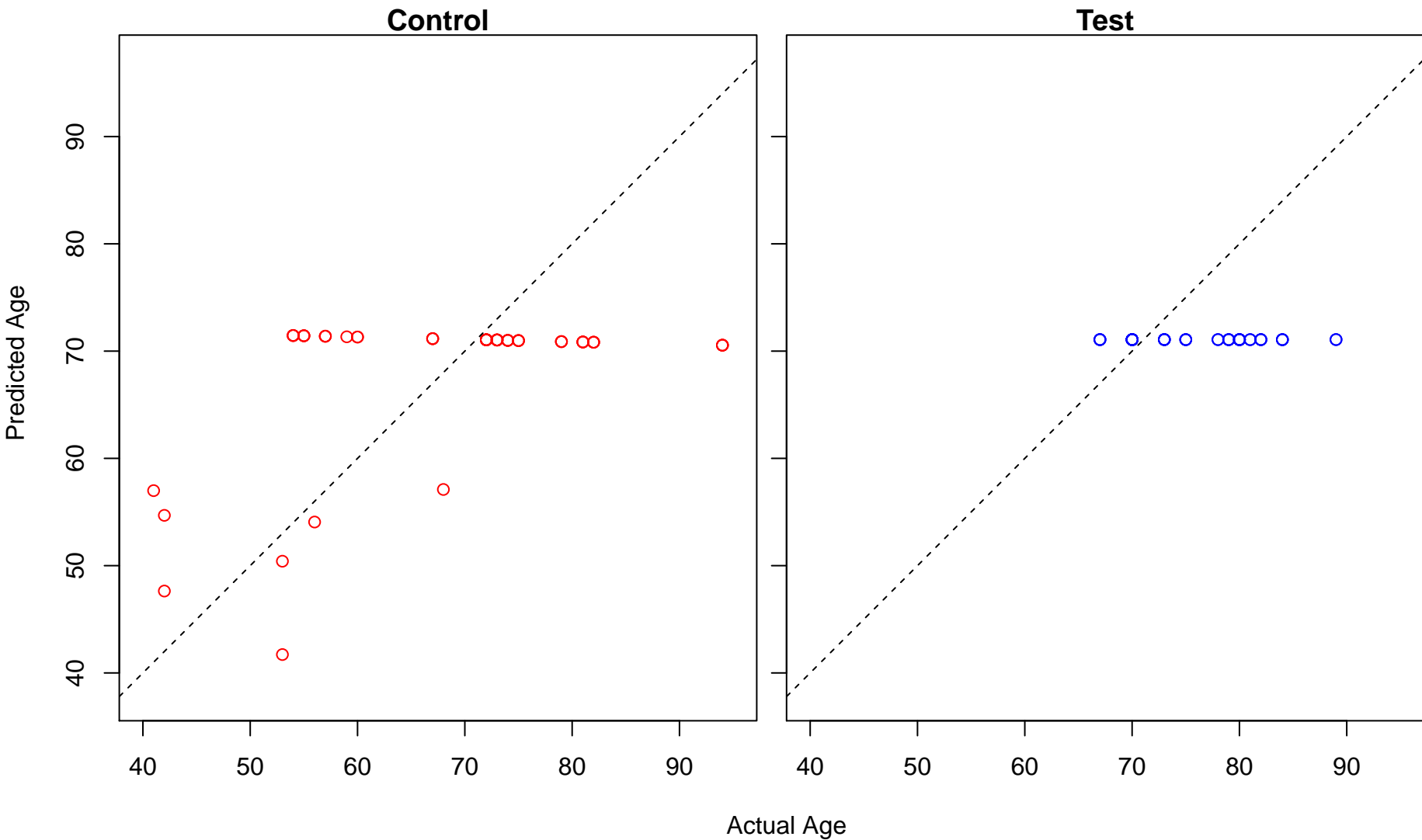
regulation of tumor necrosis factor-mediated signaling pathway (Score: 0.805237)



positive regulation of intracellular signal transduction (Score: 0.805206)

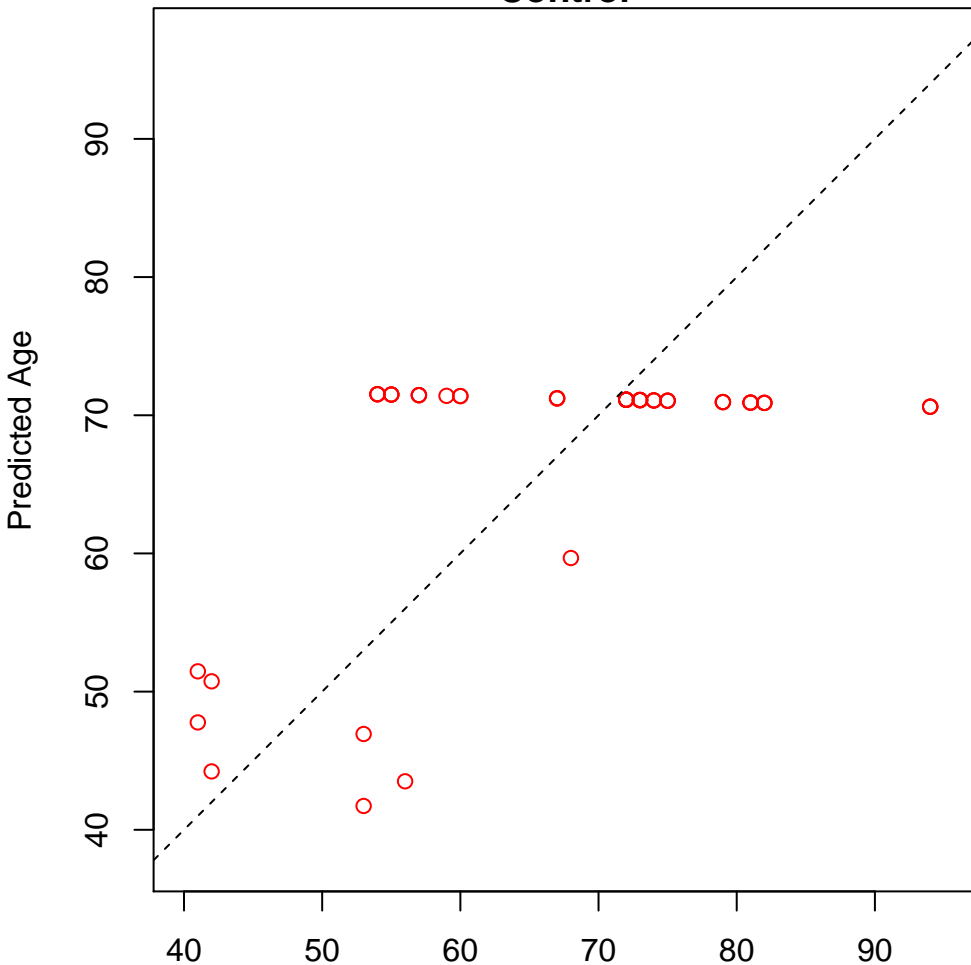


organic anion transport (Score: 0.805096)

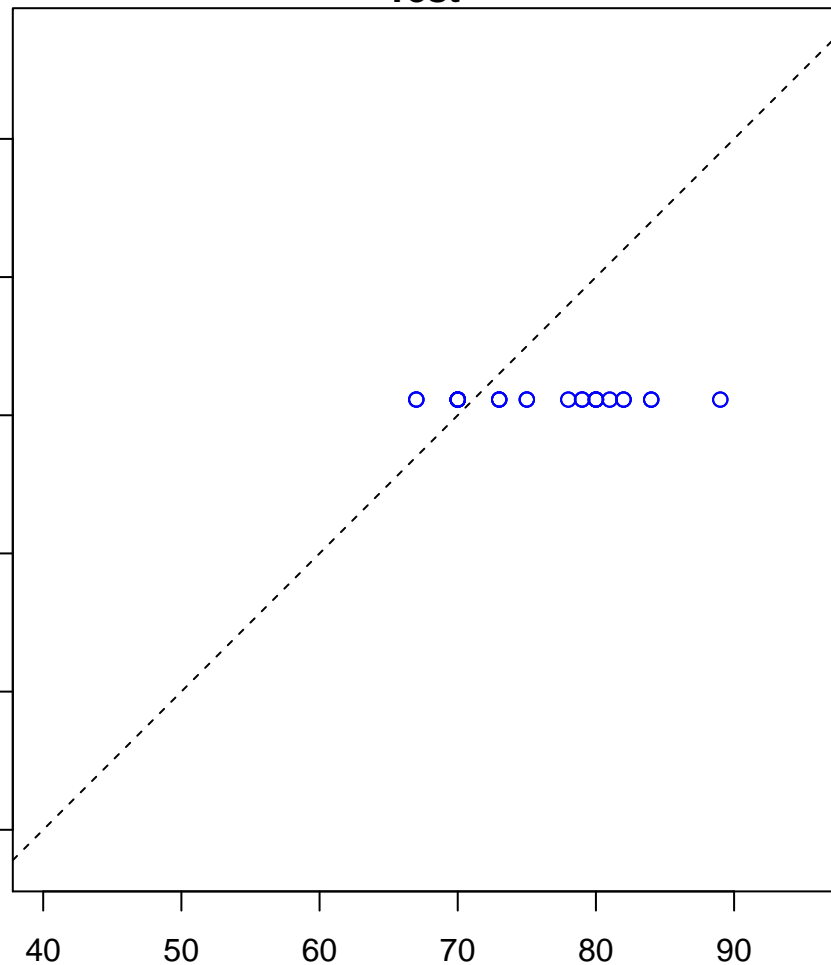


response to nitrogen compound (Score: 0.805092)

Control

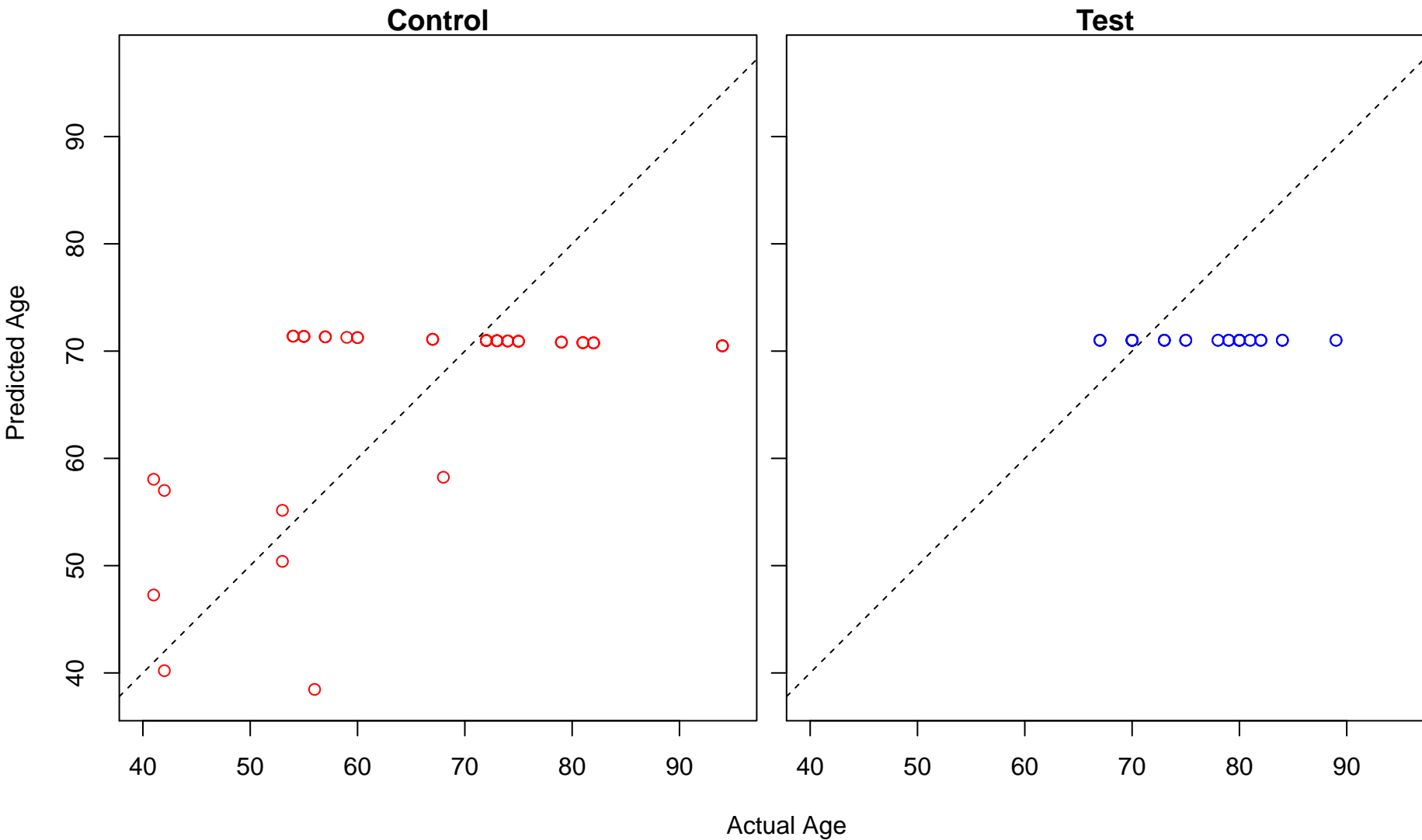


Test



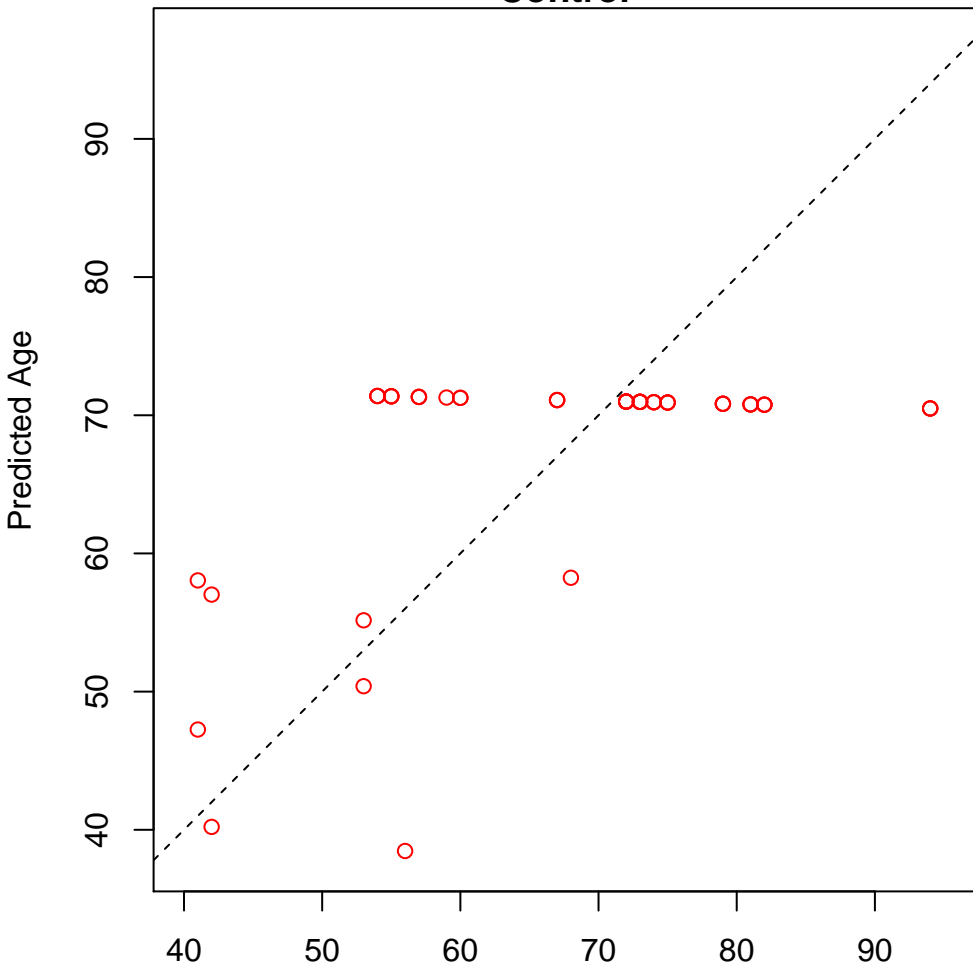
Actual Age

ERBB signaling pathway (Score: 0.805084)

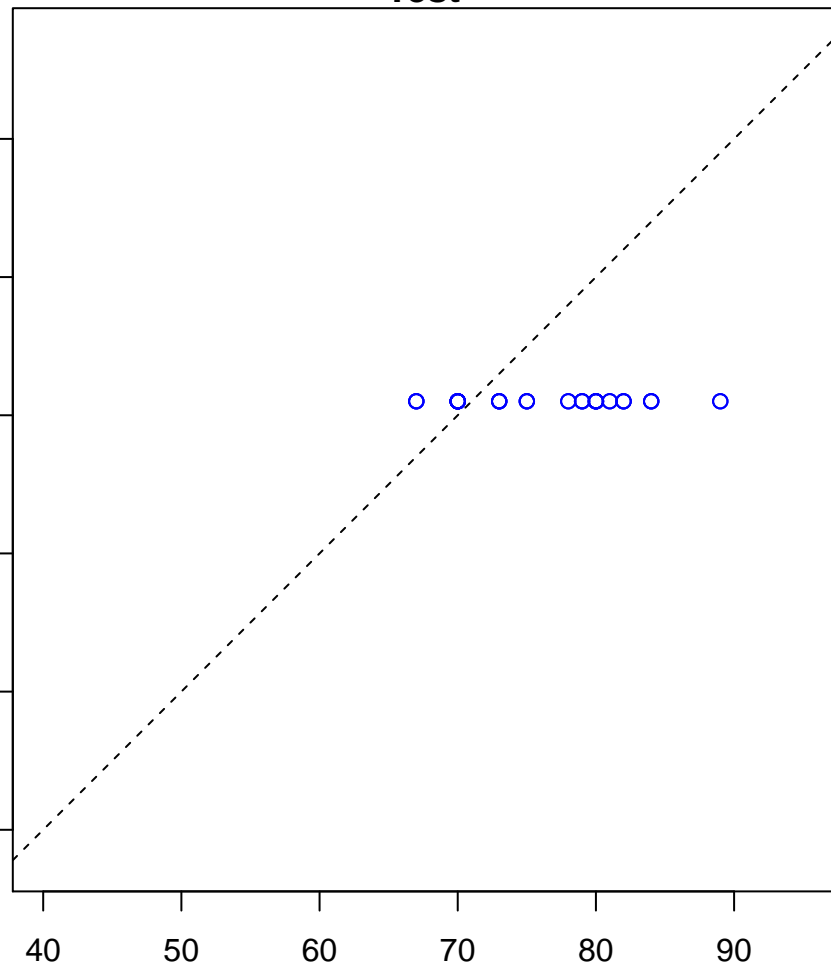


I-kappaB kinase/NF-kappaB signaling (Score: 0.805075)

Control

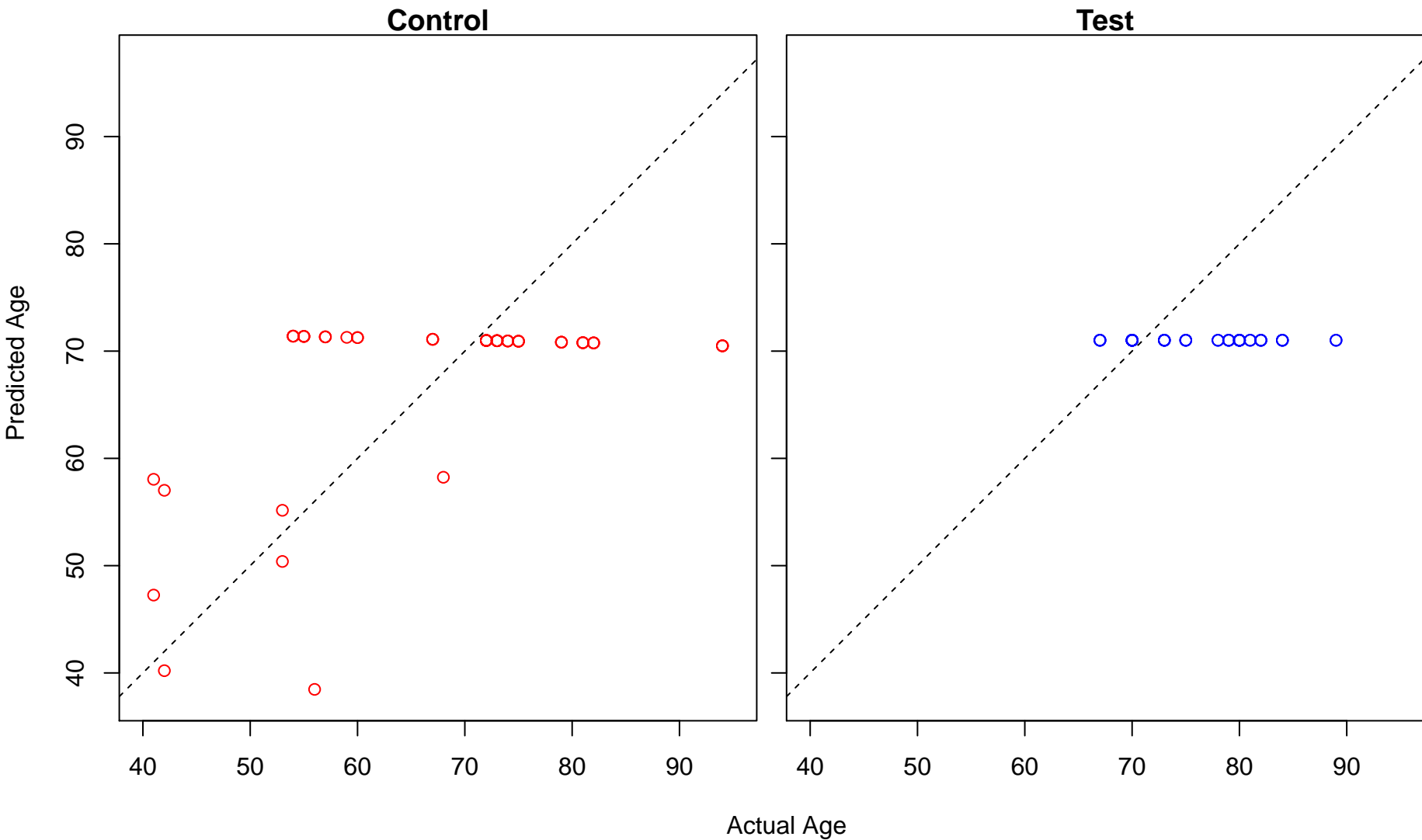


Test



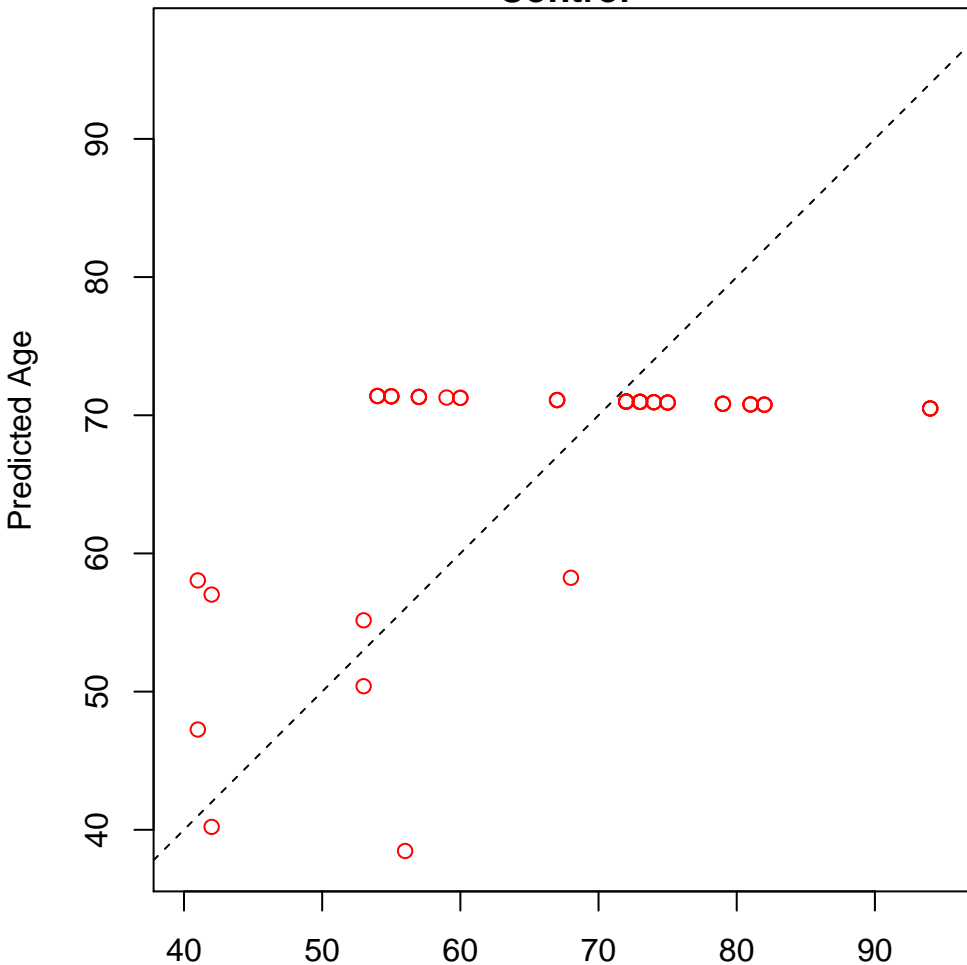
Actual Age

regulation of necrotic cell death (Score: 0.805075)

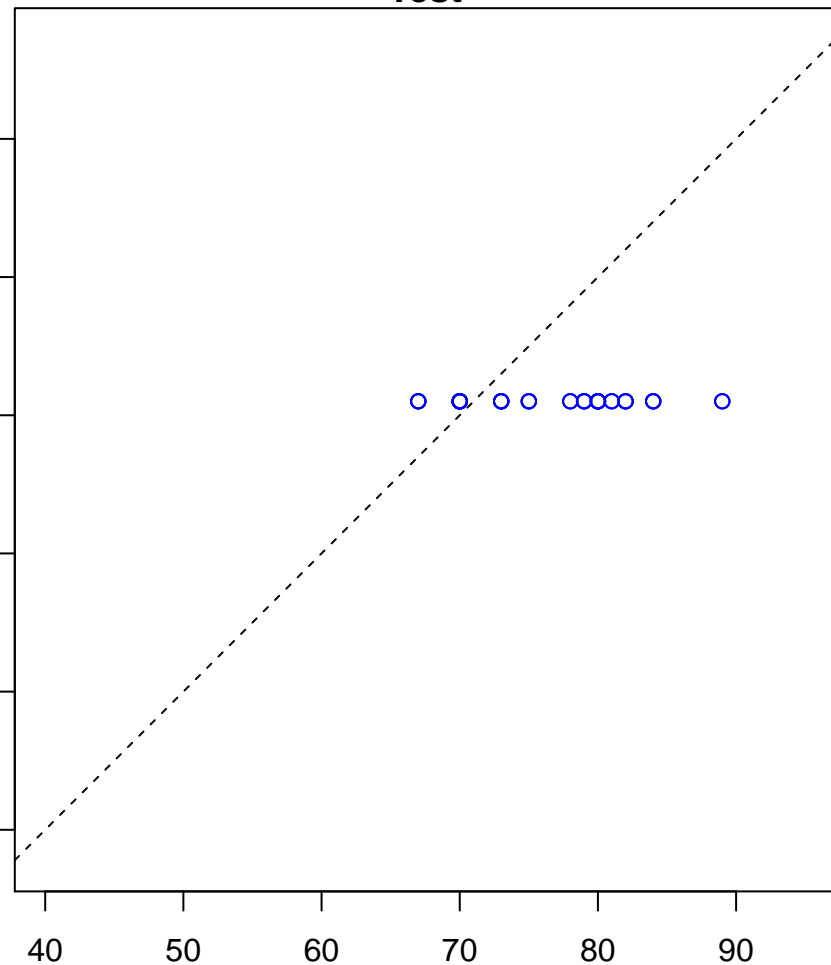


regulation of necroptotic process (Score: 0.805075)

Control

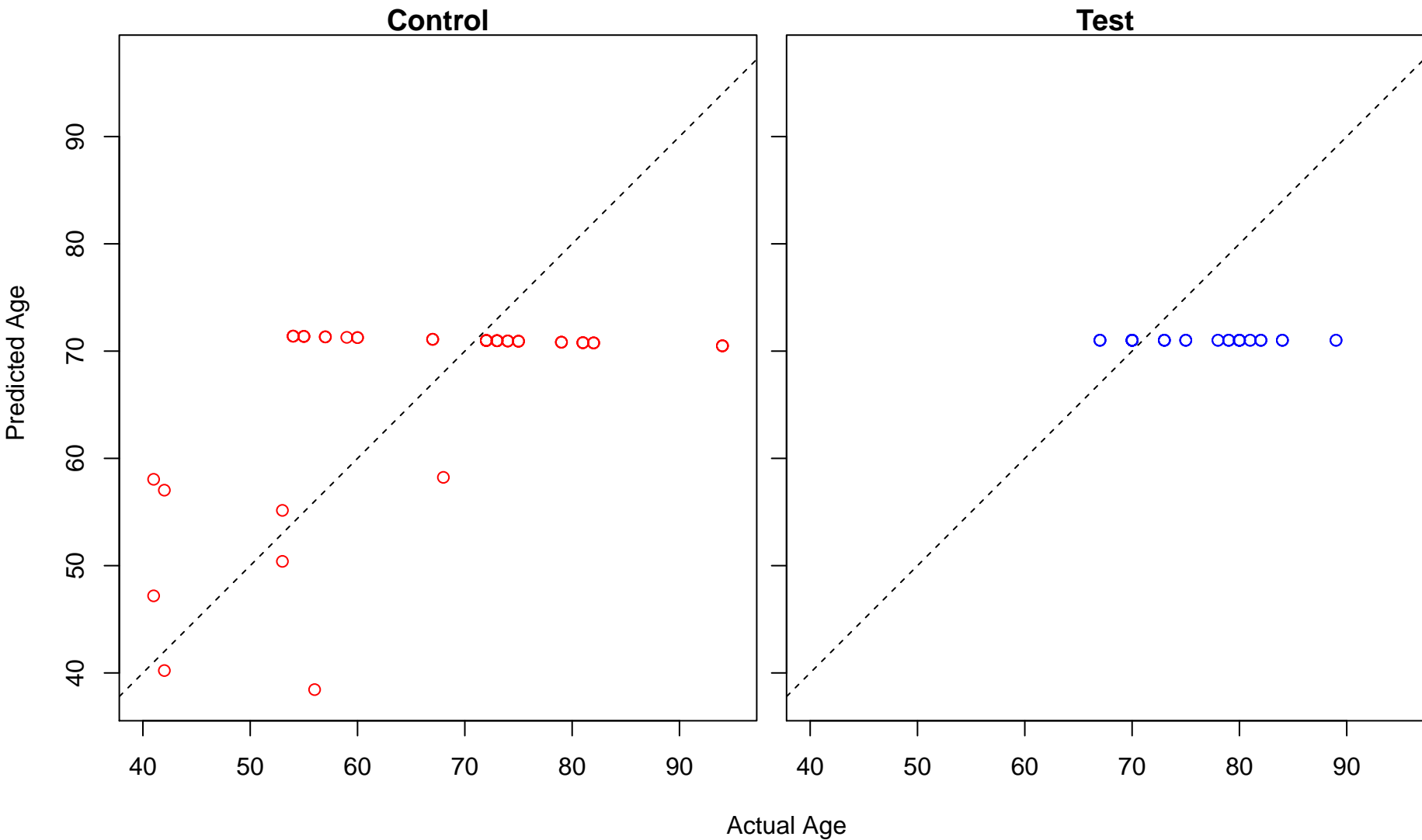


Test

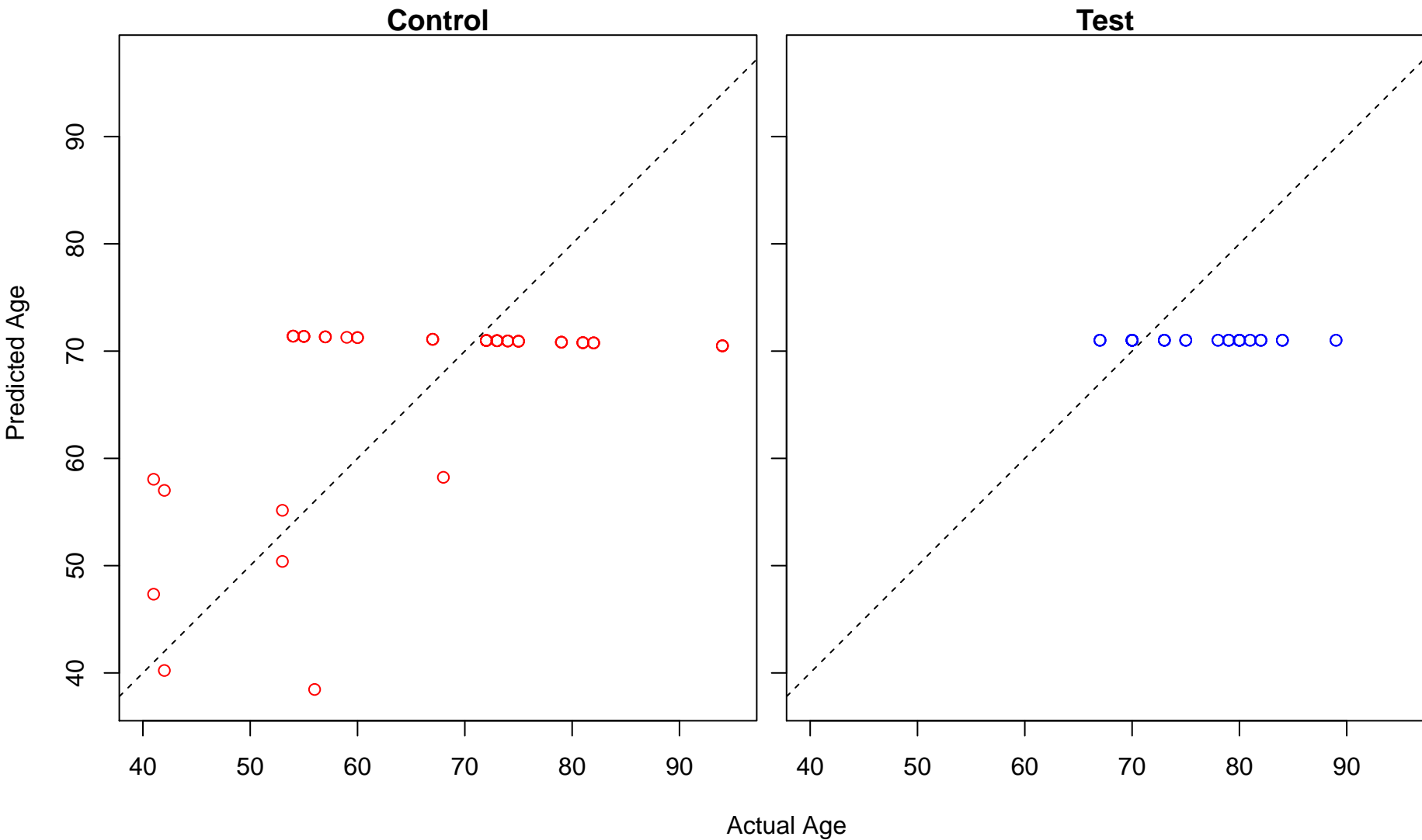


Actual Age

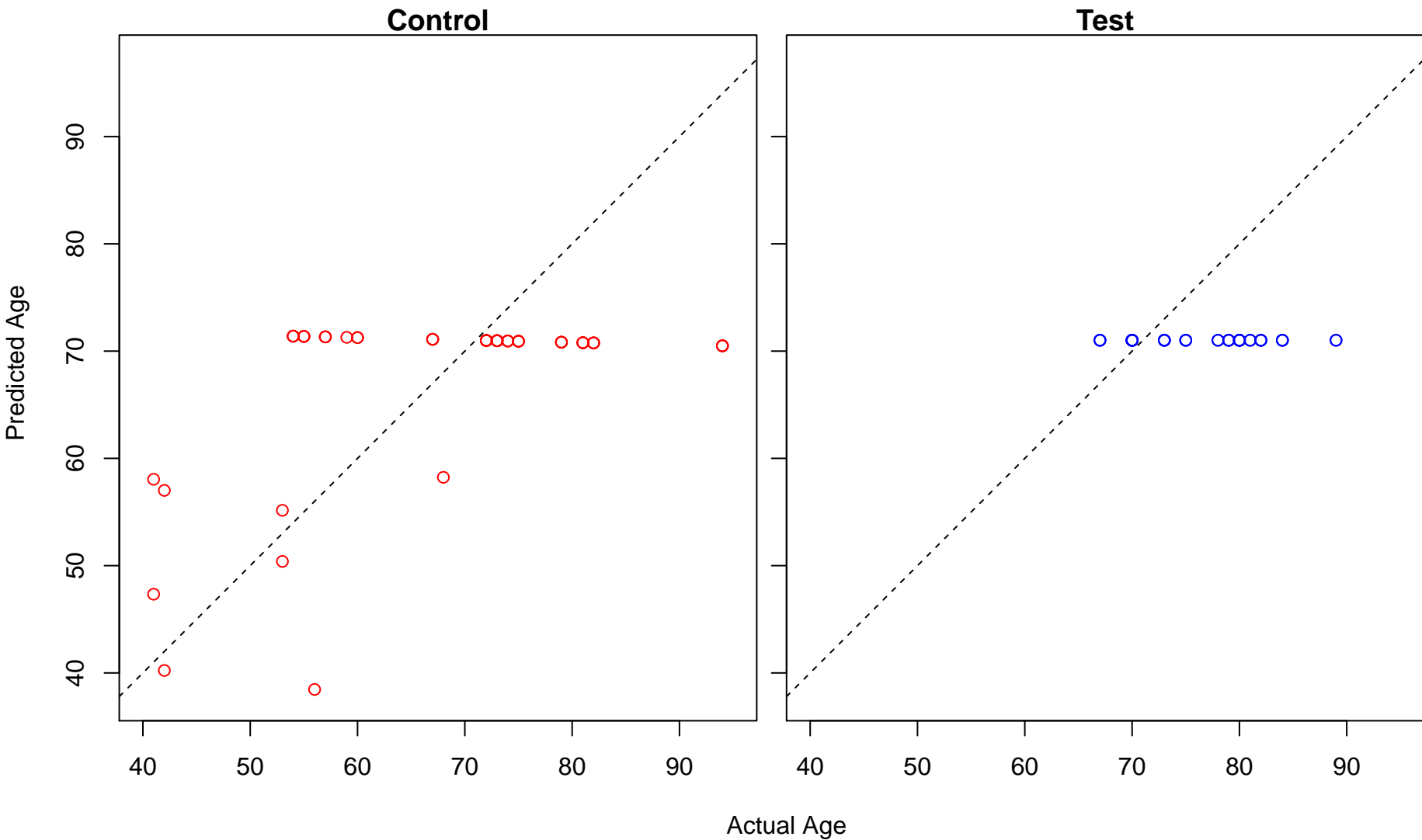
positive regulation of NF-kappaB transcription factor activity (Score: 0.805062)



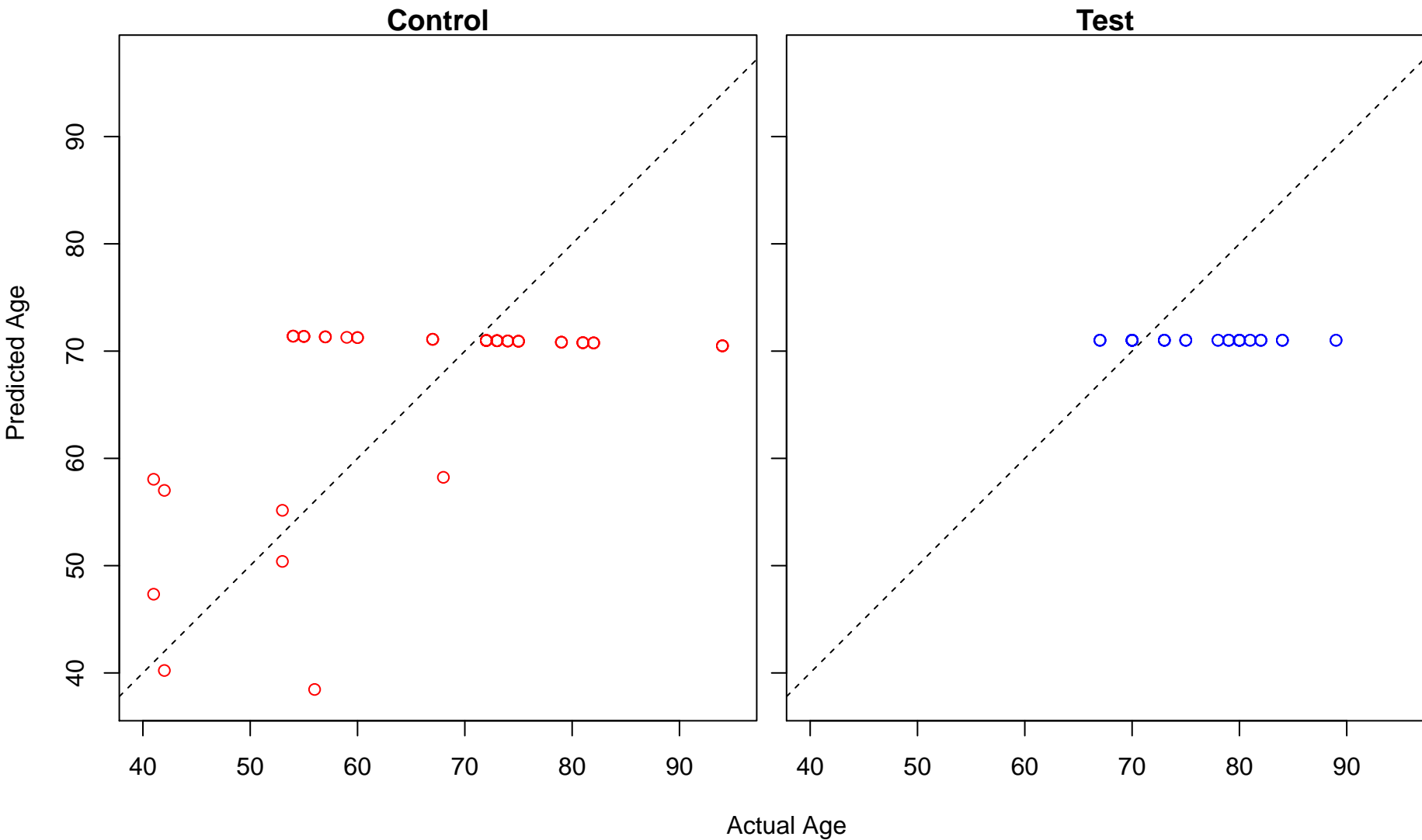
transcription-coupled nucleotide-excision repair (Score: 0.805056)



nucleotide-excision repair, DNA incision, 5'-to lesion (Score: 0.805056)

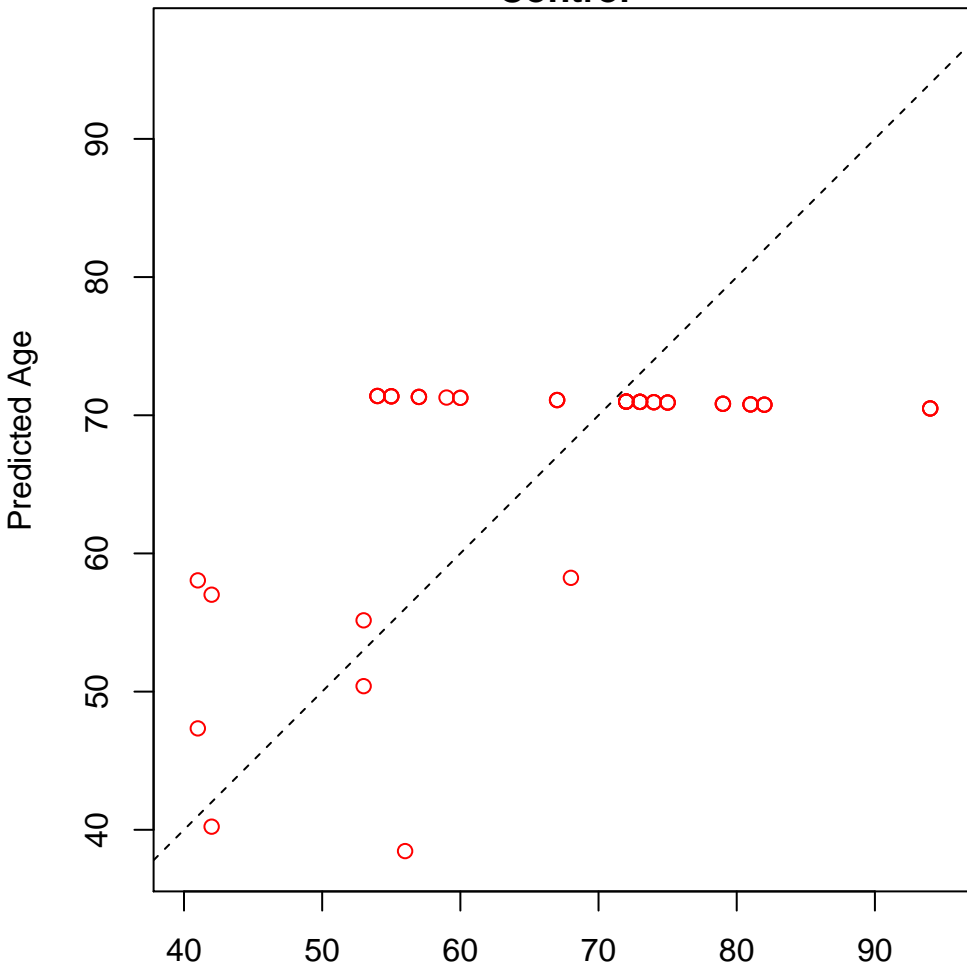


nucleotide-excision repair, DNA gap filling (Score: 0.805056)

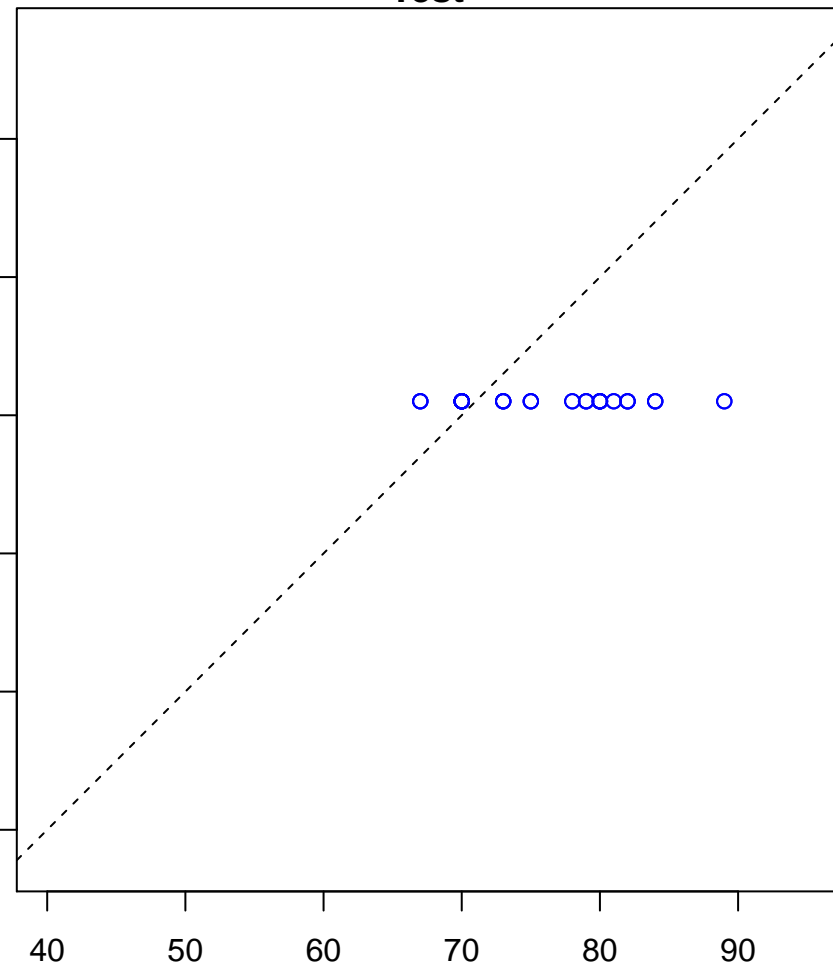


nucleotide–excision repair, DNA incision (Score: 0.805056)

Control



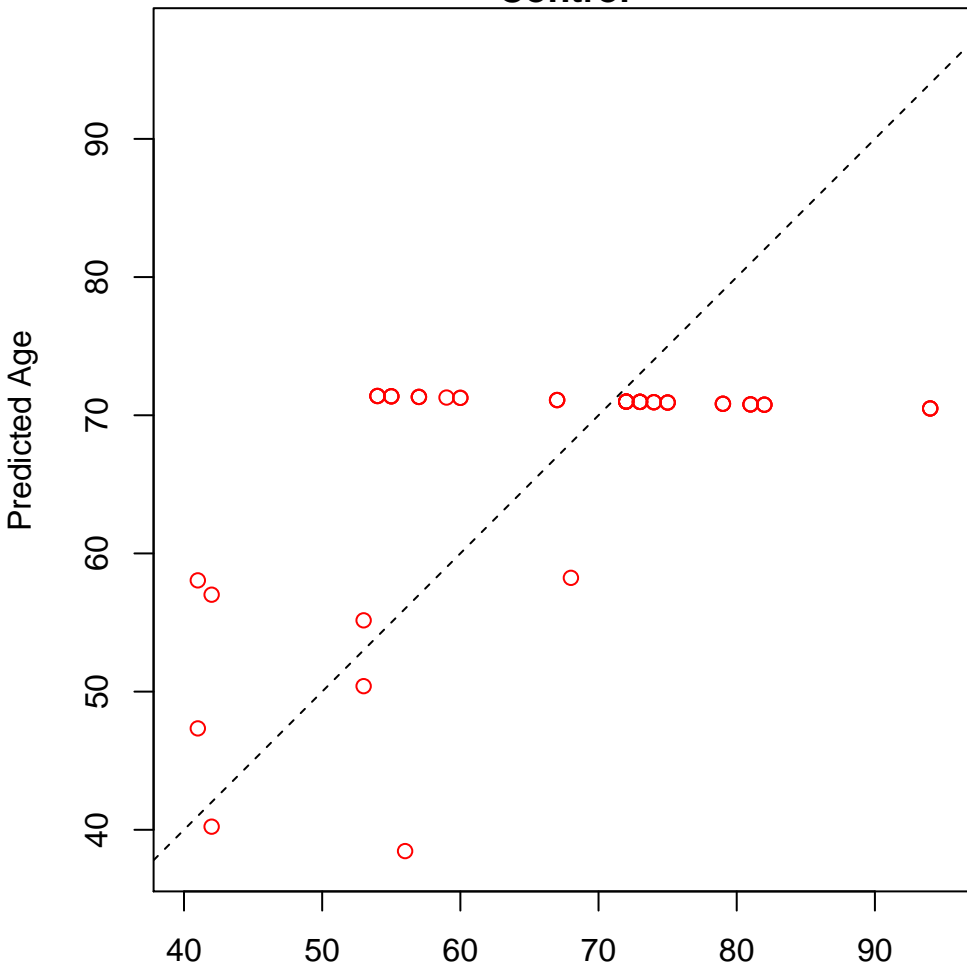
Test



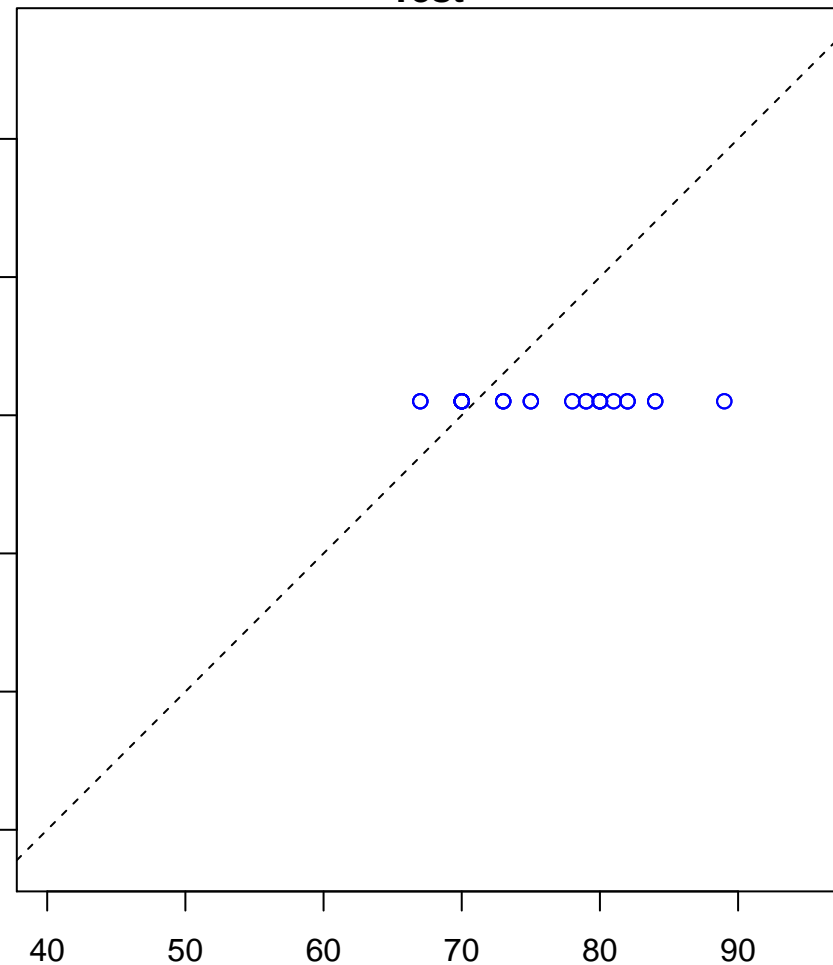
Actual Age

error-prone translesion synthesis (Score: 0.805056)

Control

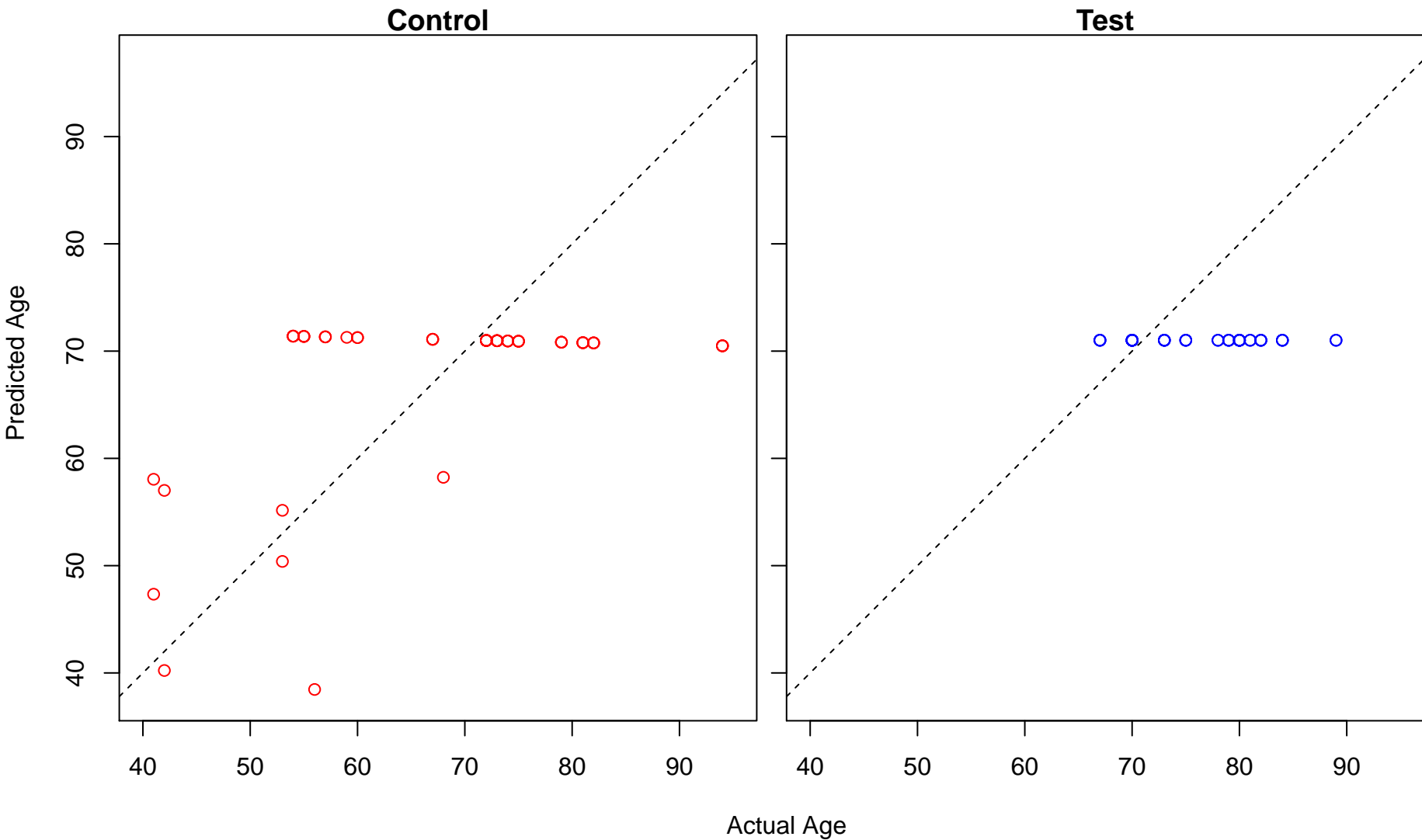


Test

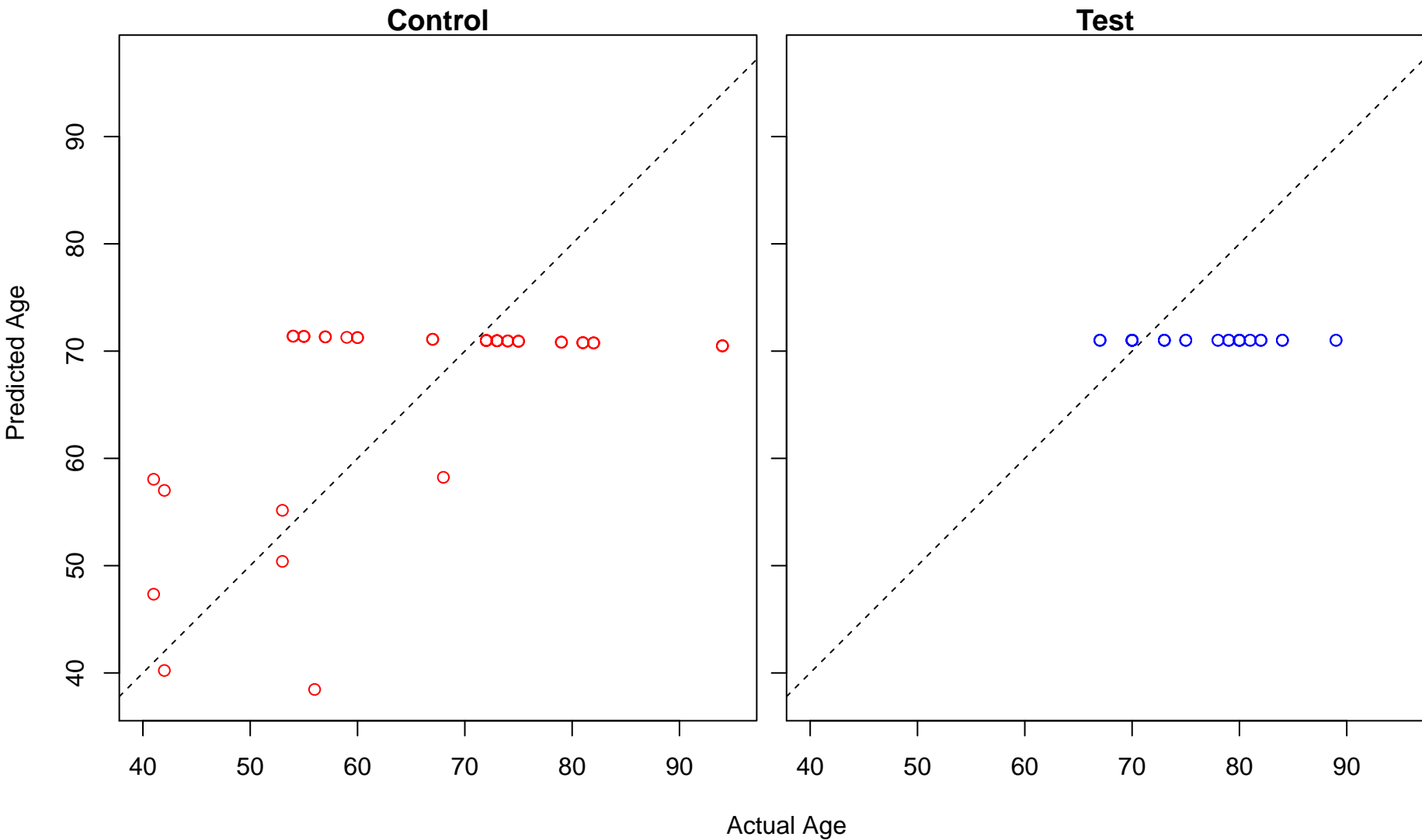


Actual Age

DNA damage response, detection of DNA damage (Score: 0.805056)

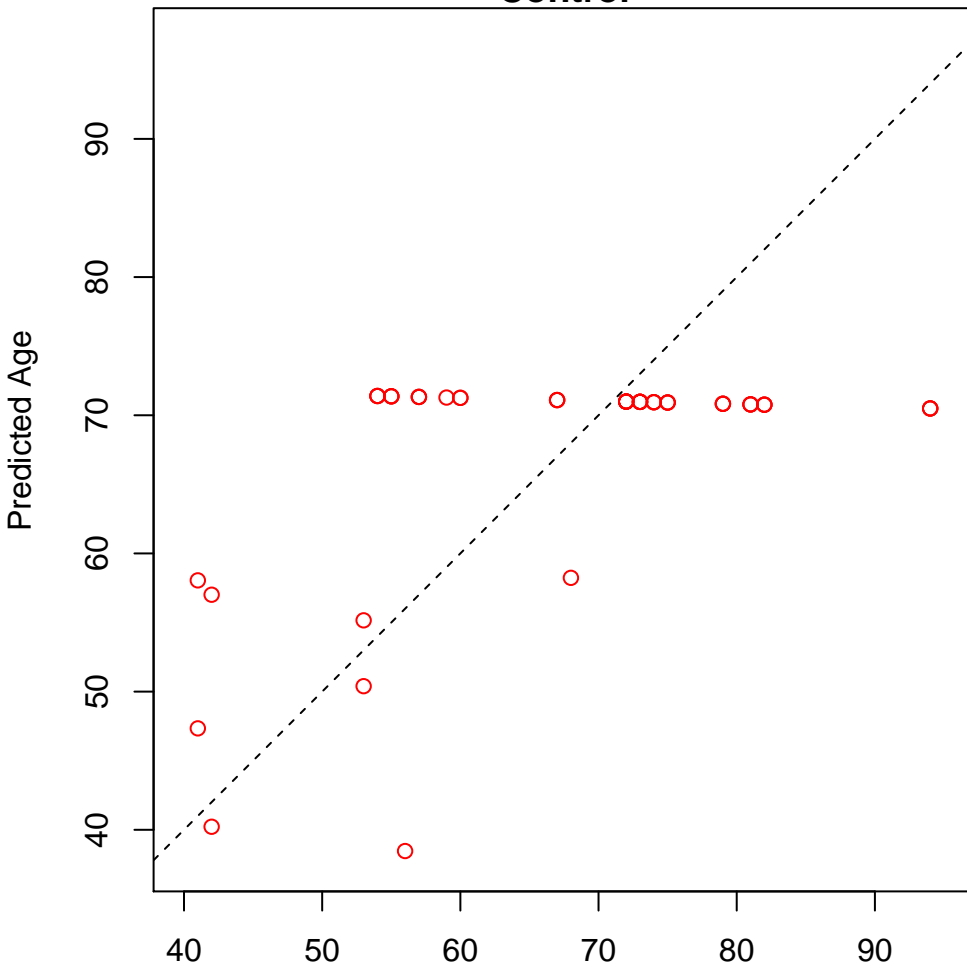


error-free translesion synthesis (Score: 0.805056)

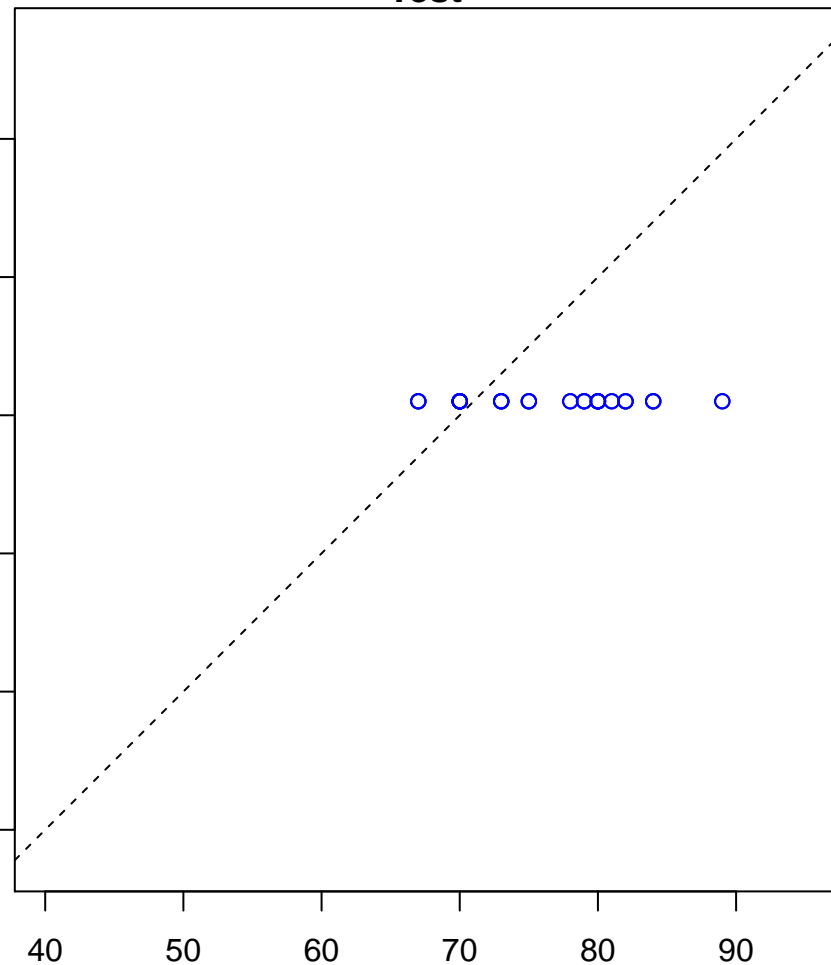


polysaccharide biosynthetic process (Score: 0.805053)

Control

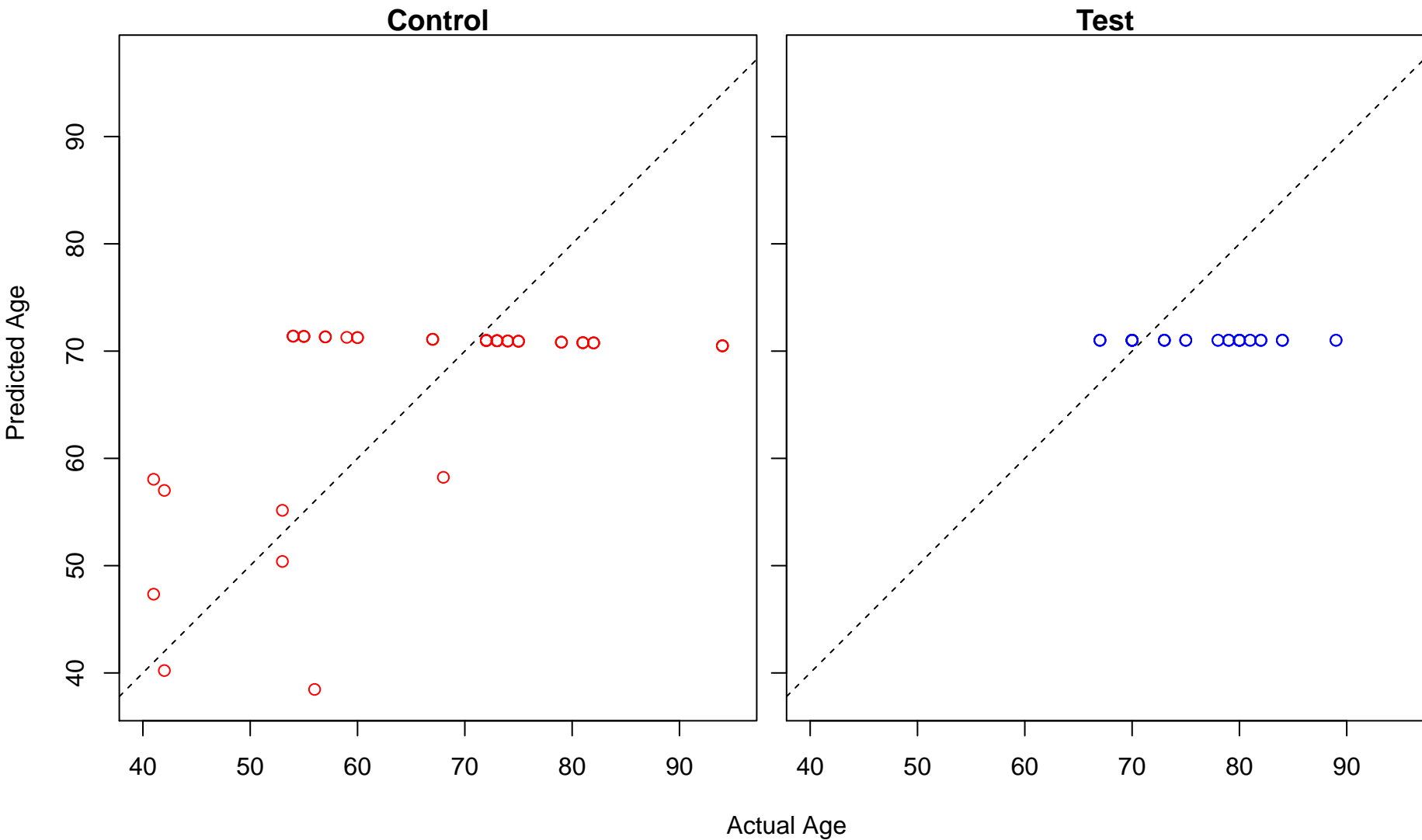


Test

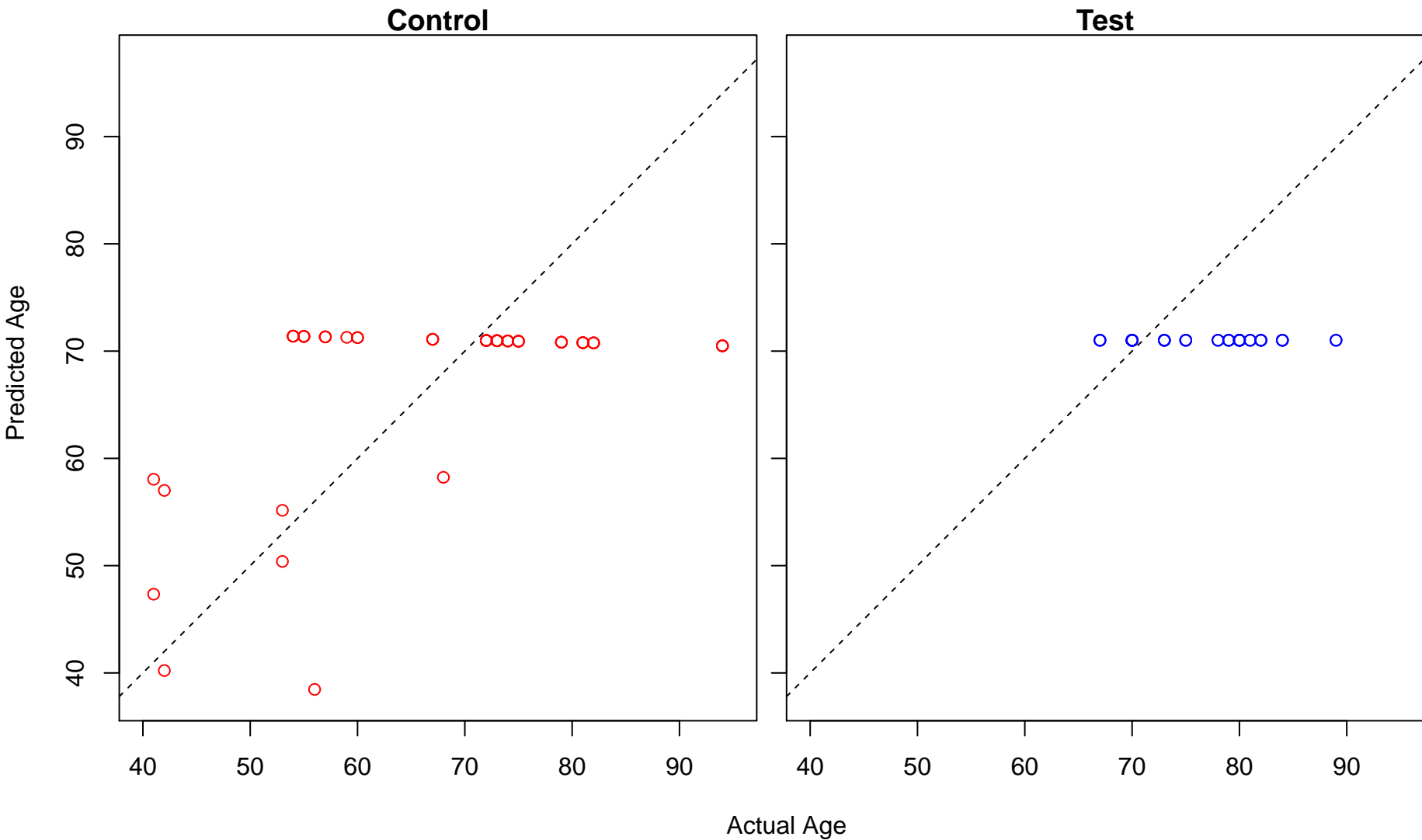


Actual Age

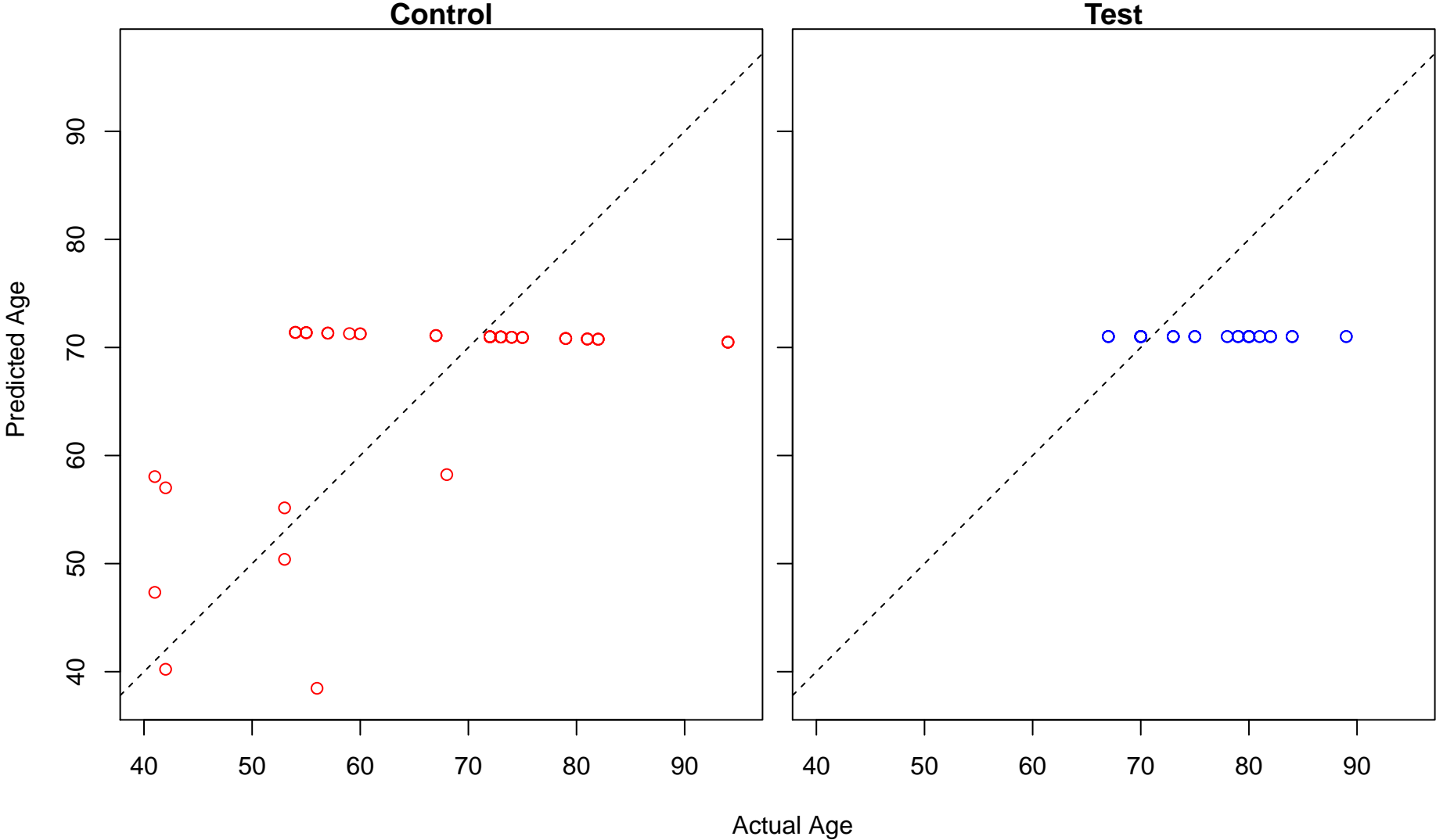
nucleotide-excision repair, DNA damage recognition (Score: 0.805053)



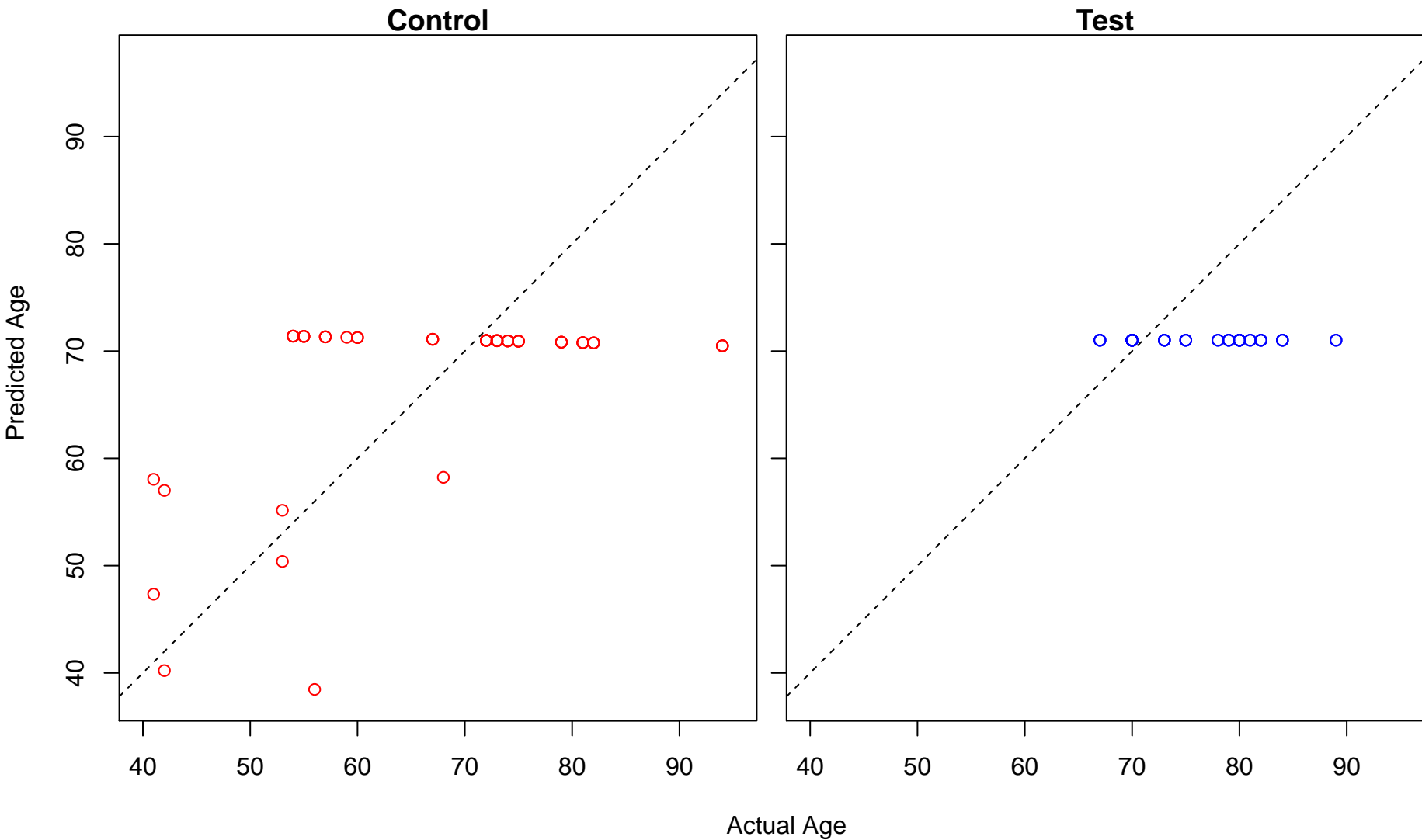
nucleotide-excision repair, DNA duplex unwinding (Score: 0.805053)



cytoplasmic pattern recognition receptor signaling pathway (Score: 0.805053)

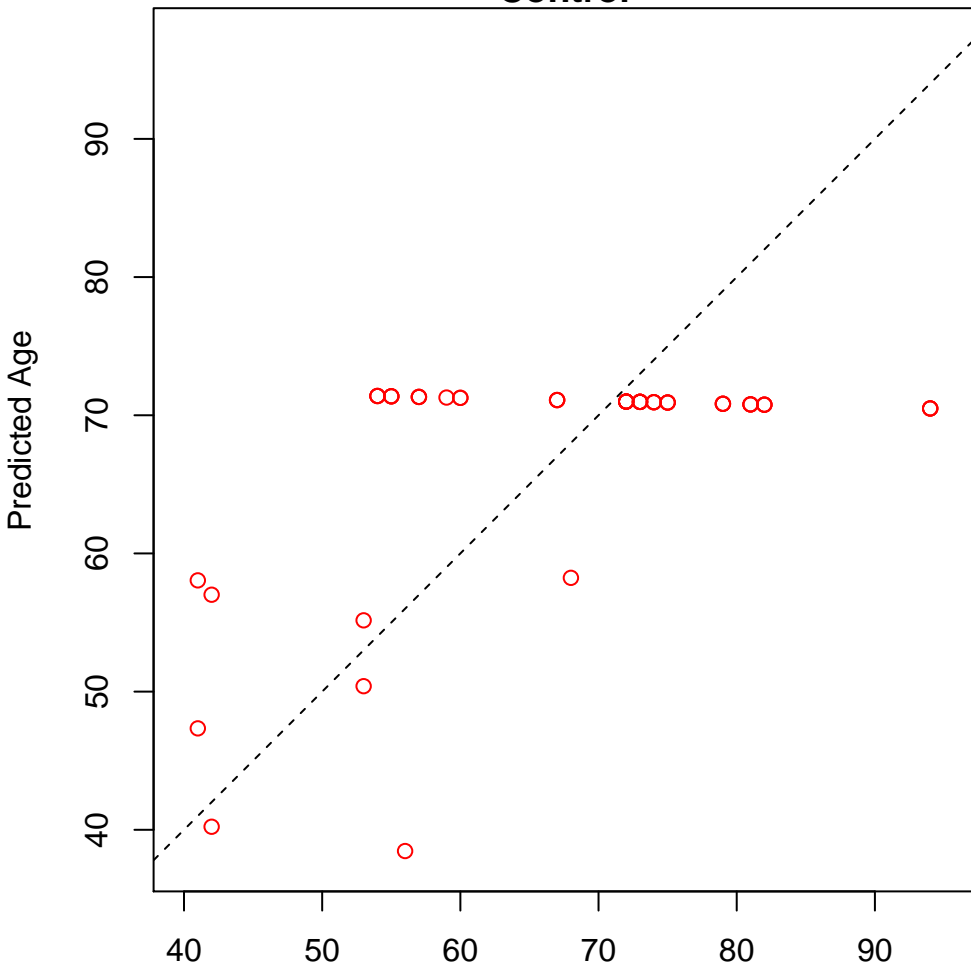


MyD88-dependent toll-like receptor signaling pathway (Score: 0.805053)

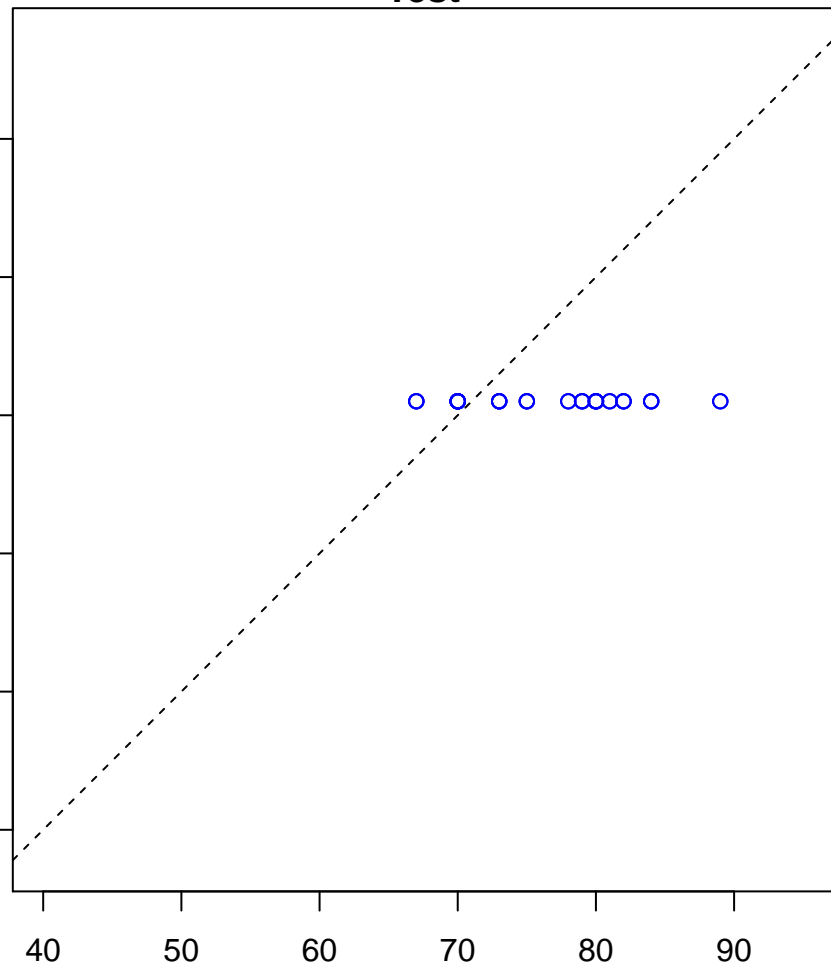


polysaccharide metabolic process (Score: 0.805053)

Control



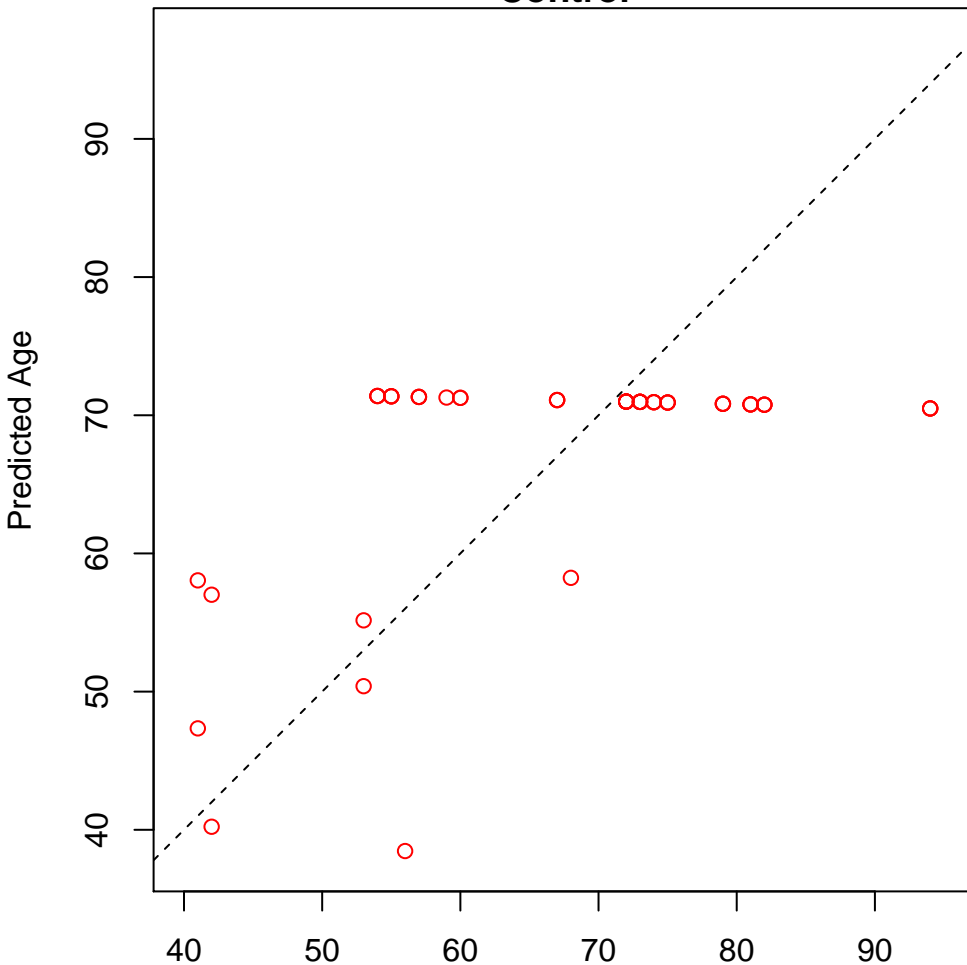
Test



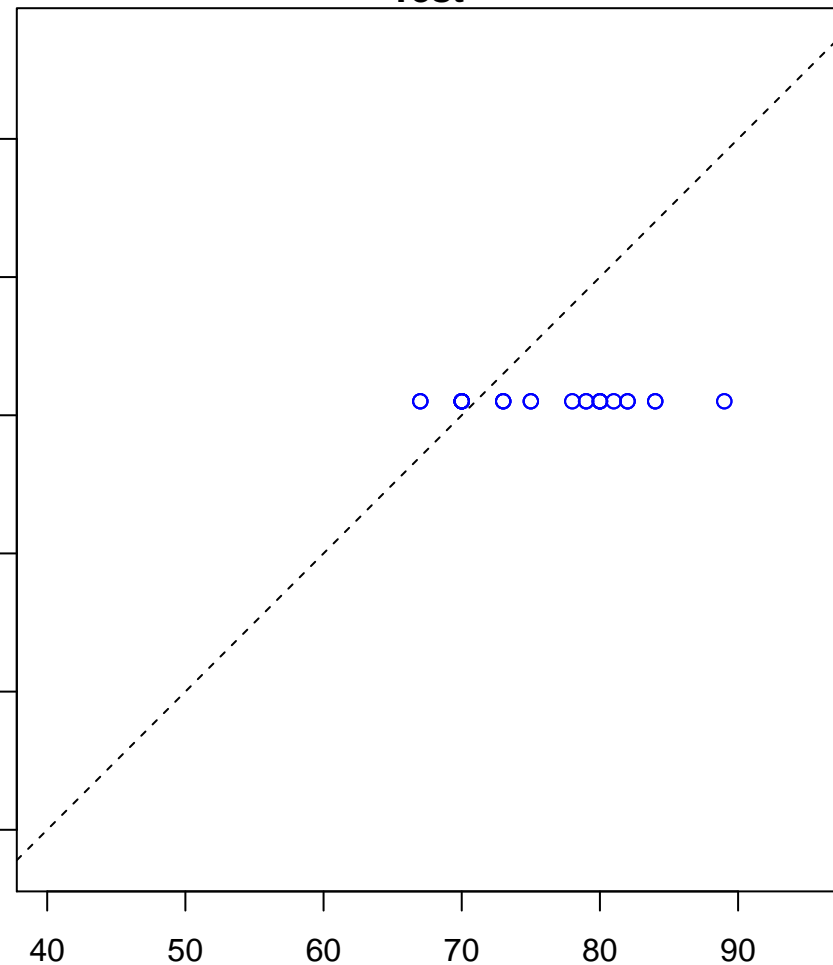
Actual Age

glycogen metabolic process (Score: 0.805053)

Control



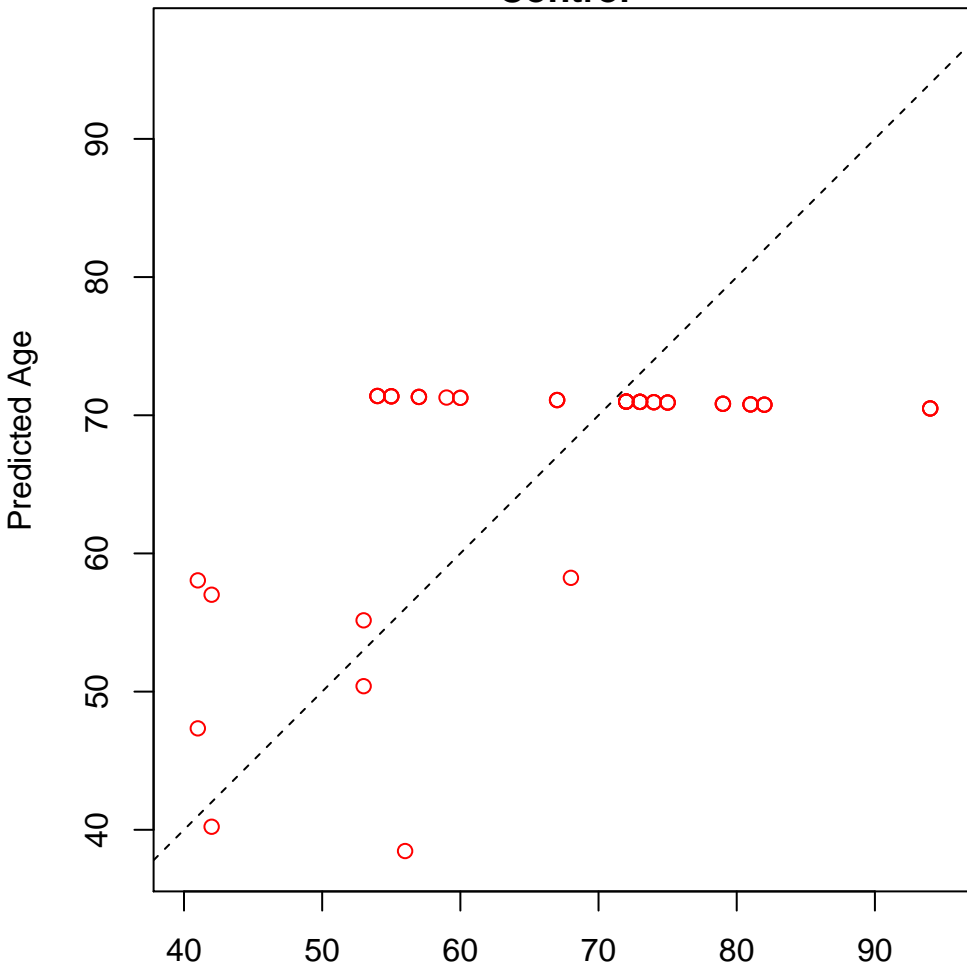
Test



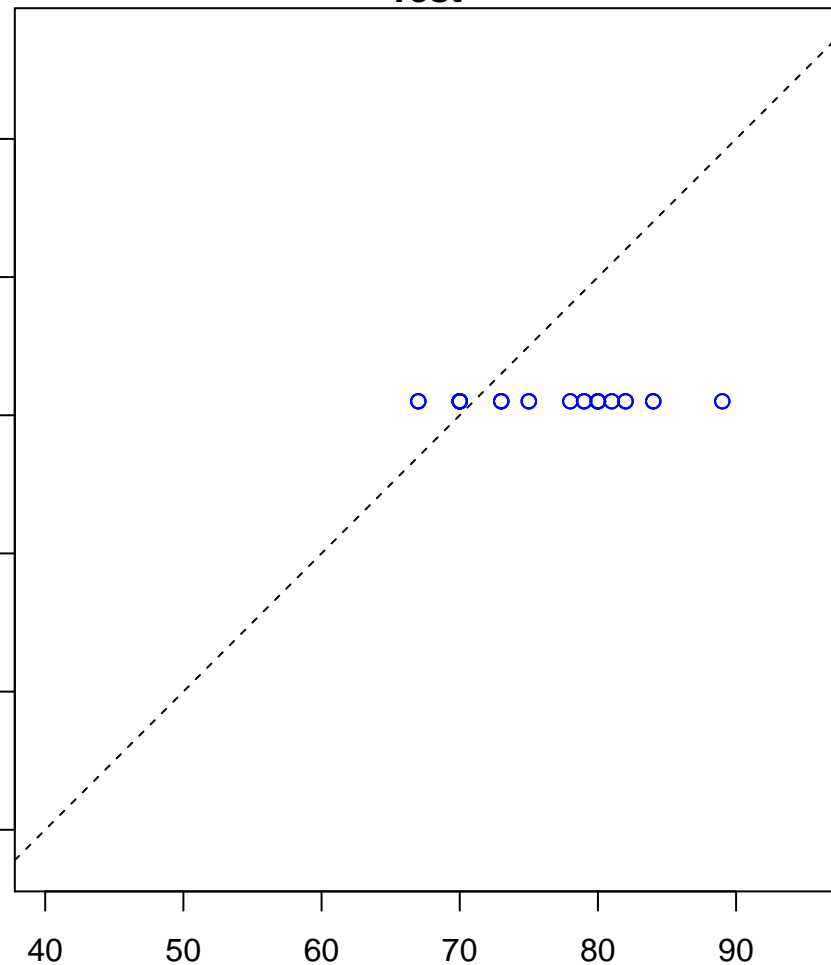
Actual Age

glycogen biosynthetic process (Score: 0.805053)

Control



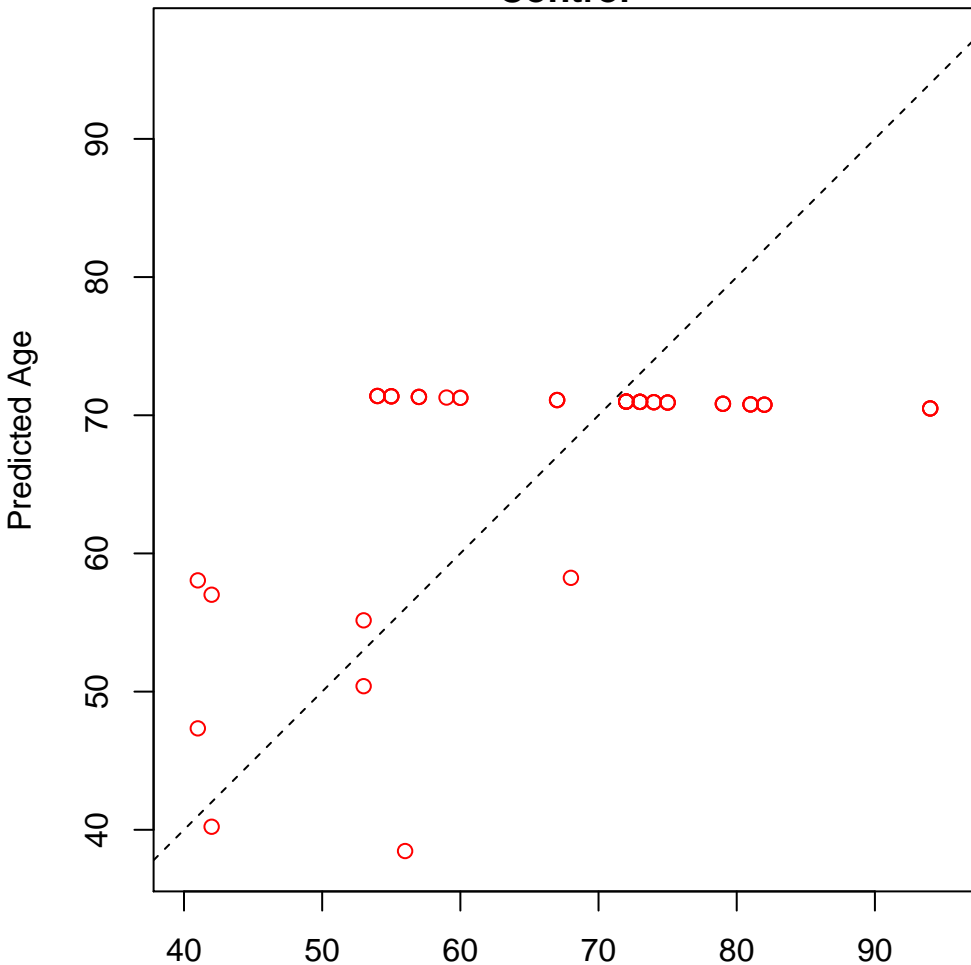
Test



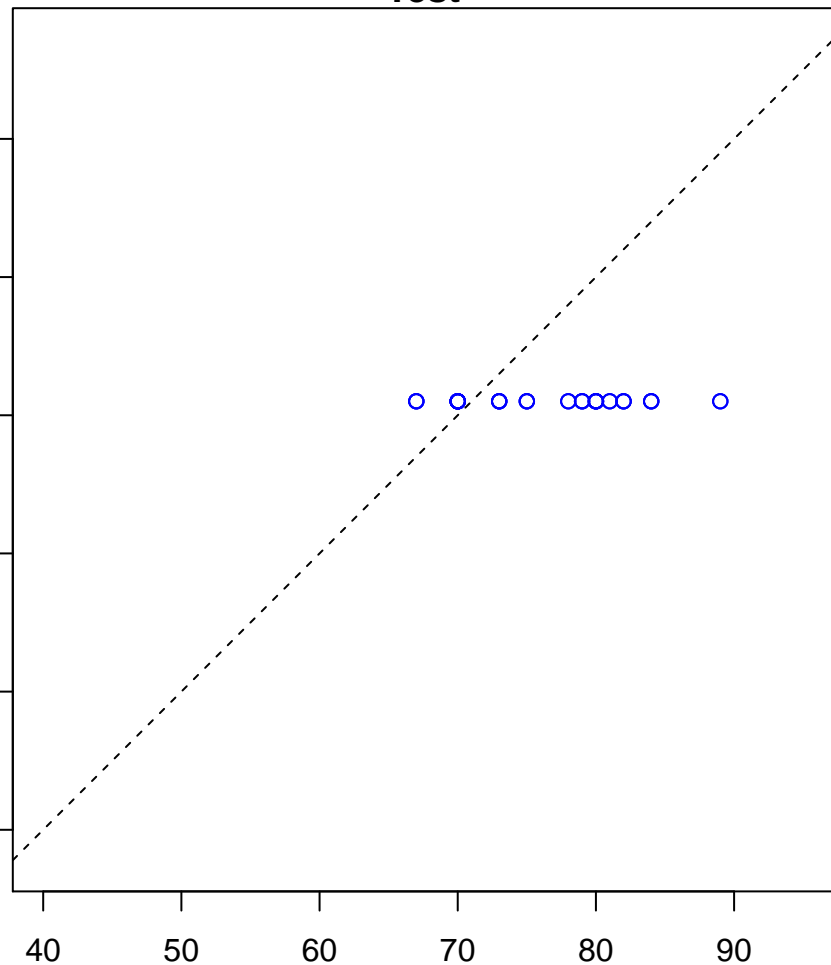
Actual Age

cellular glucan metabolic process (Score: 0.805053)

Control



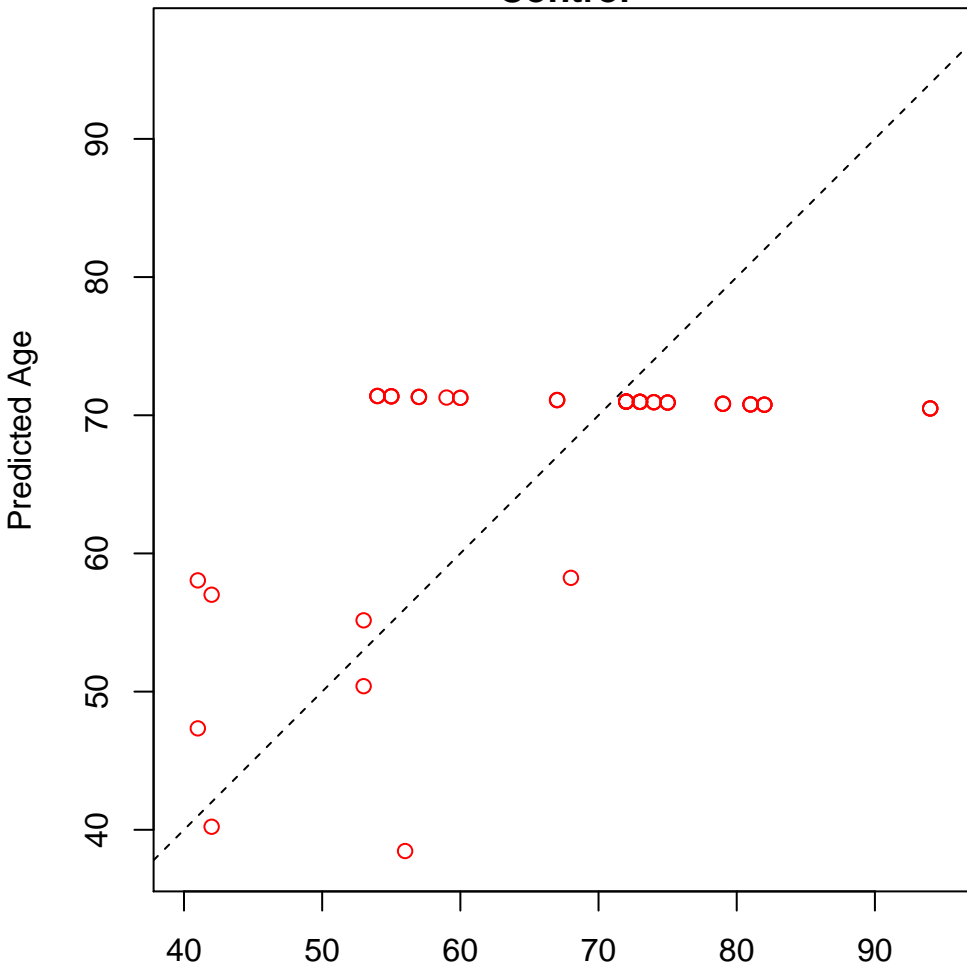
Test



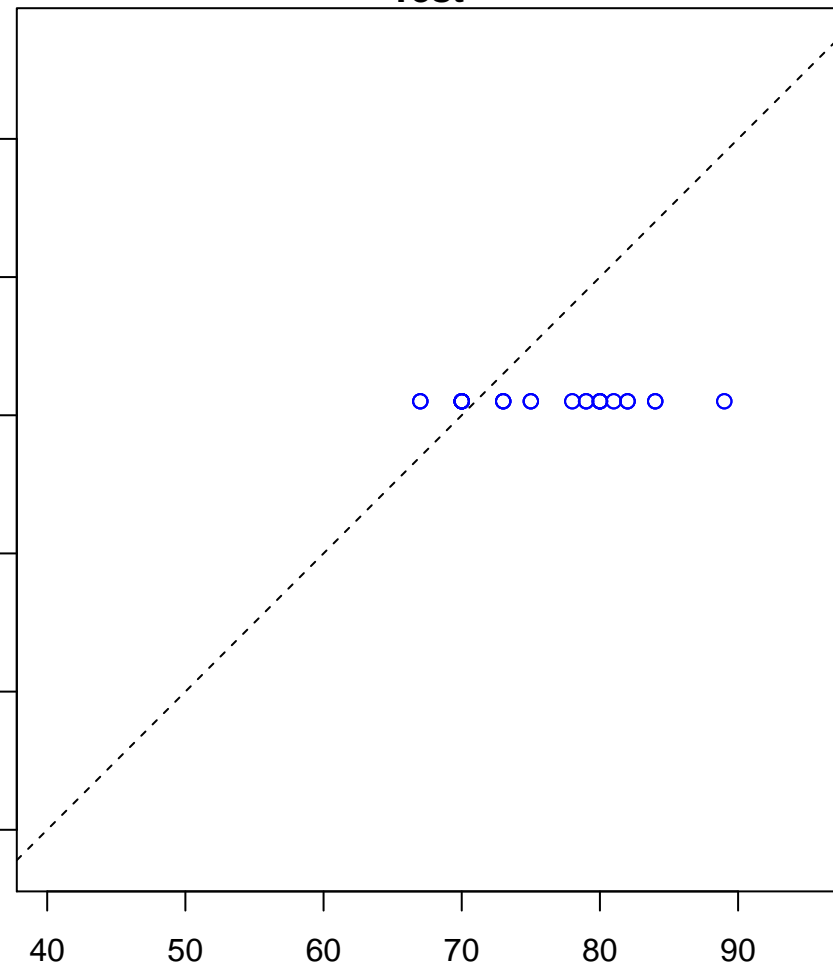
Actual Age

energy reserve metabolic process (Score: 0.805053)

Control

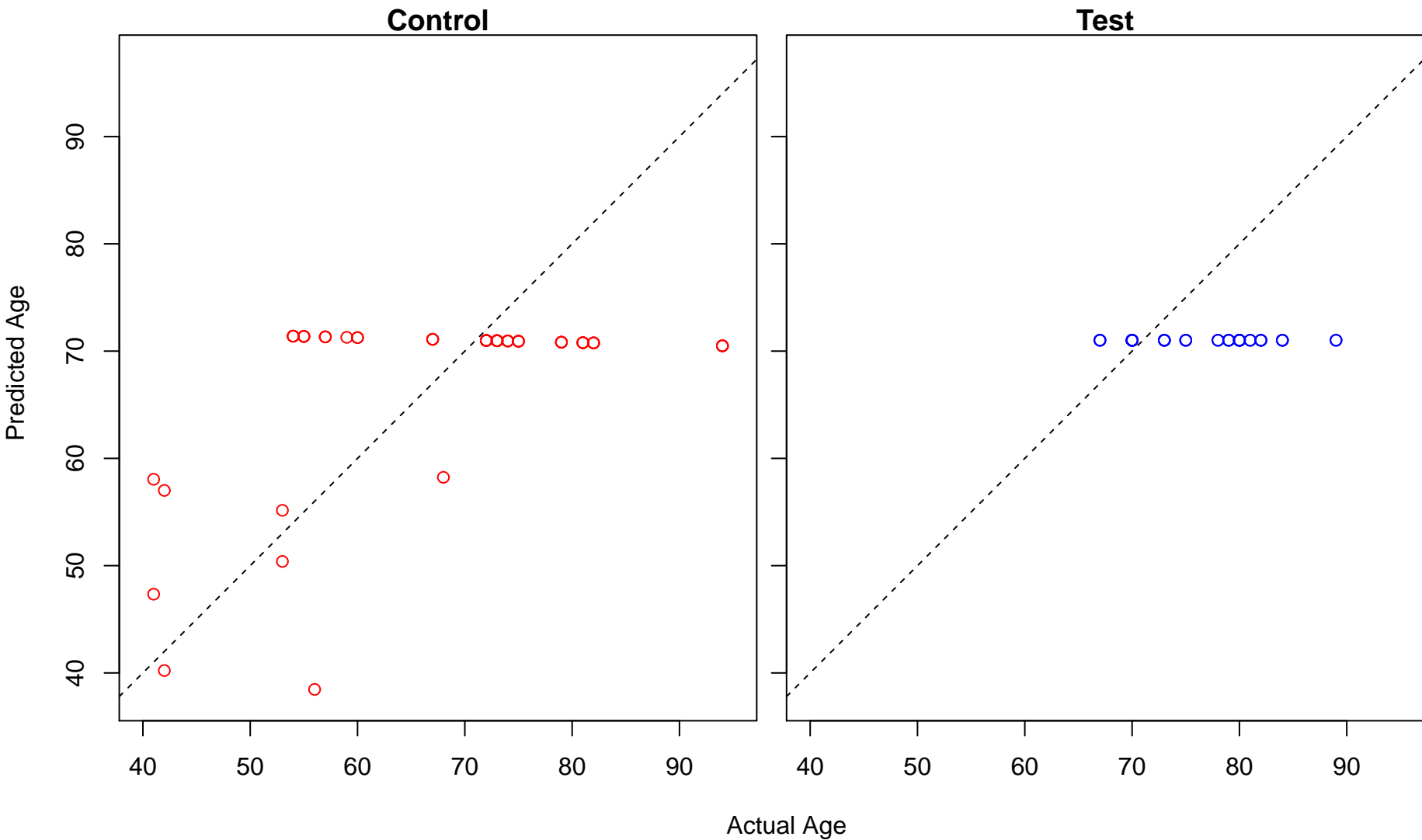


Test

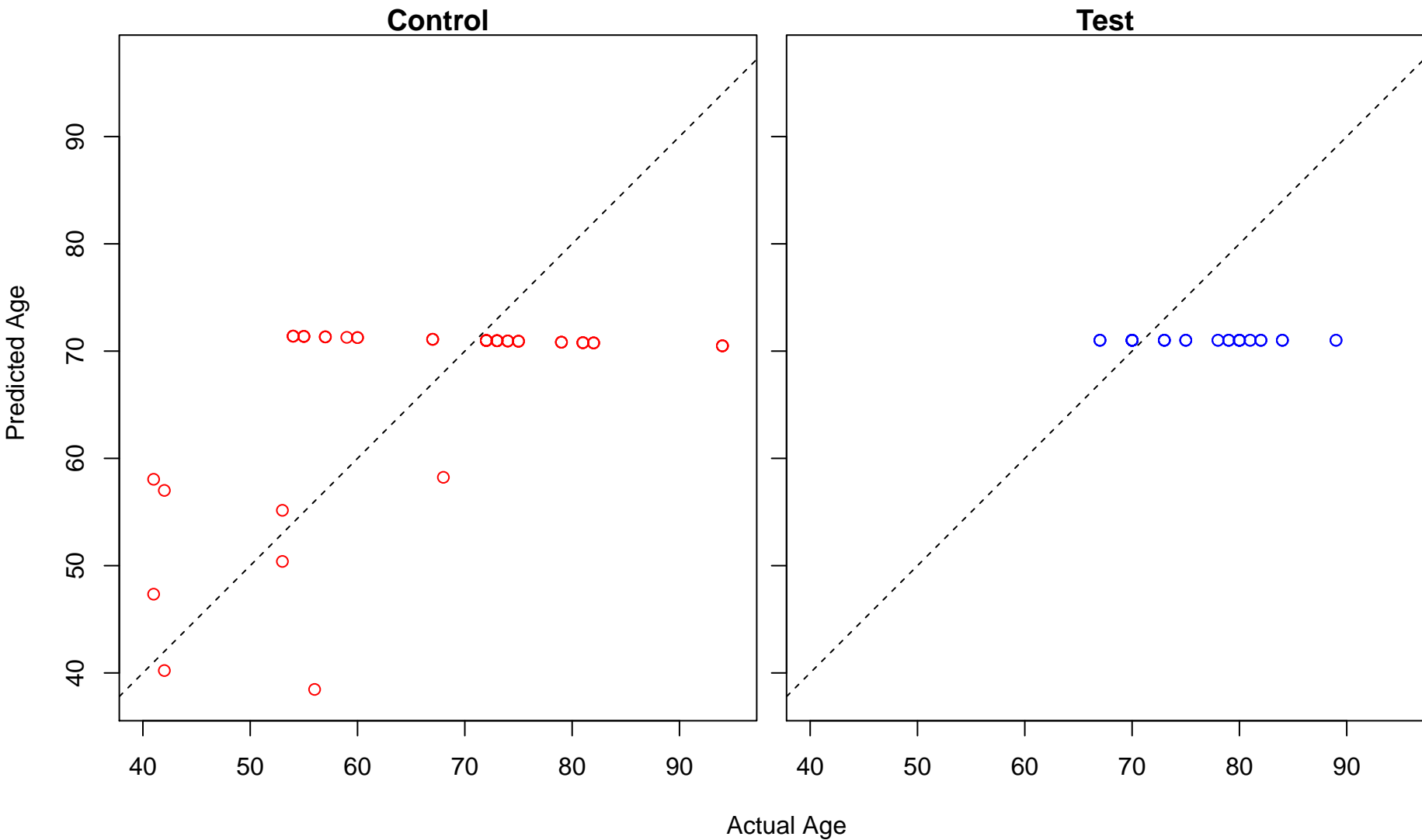


Actual Age

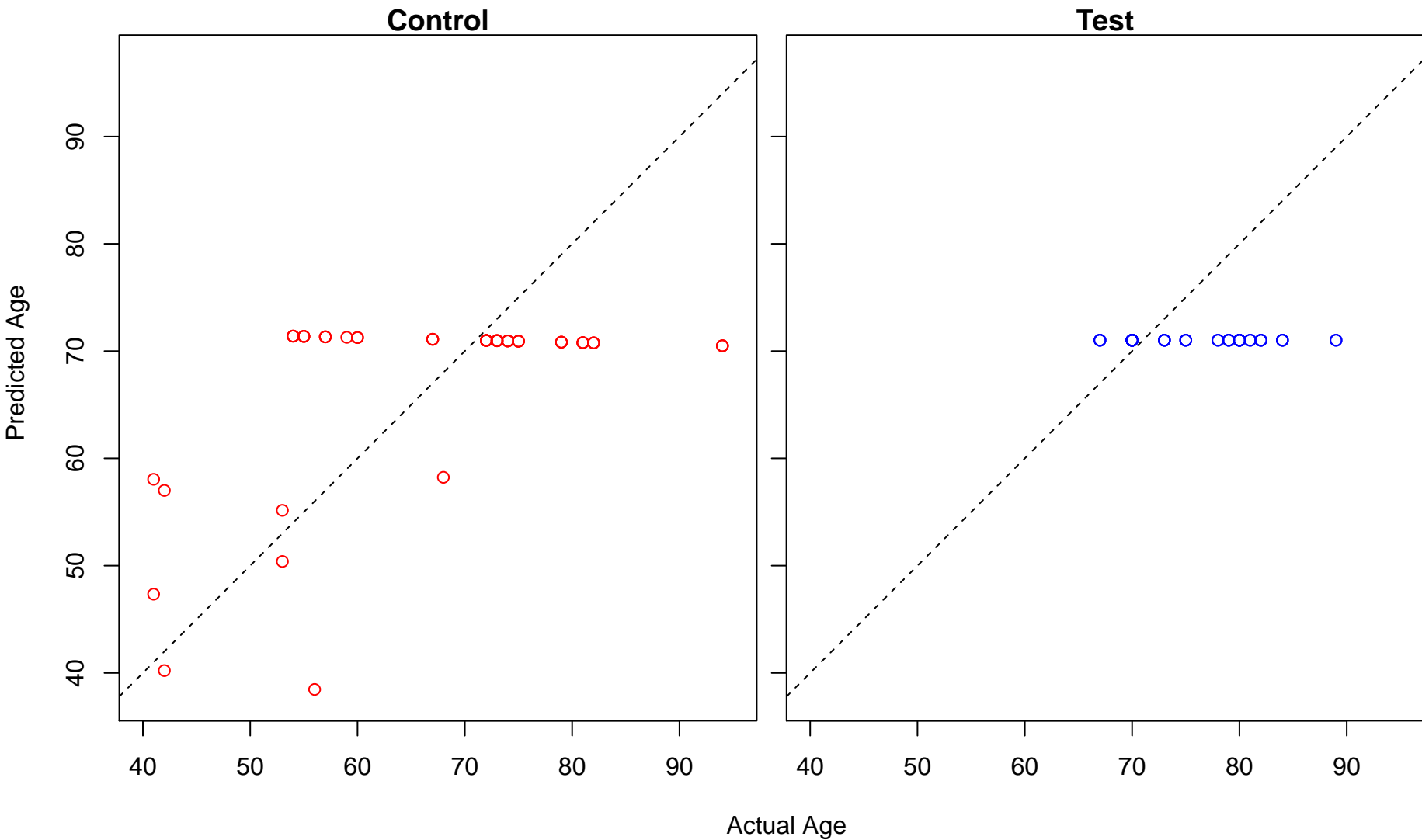
nucleotide-excision repair, preincision complex assembly (Score: 0.805053)



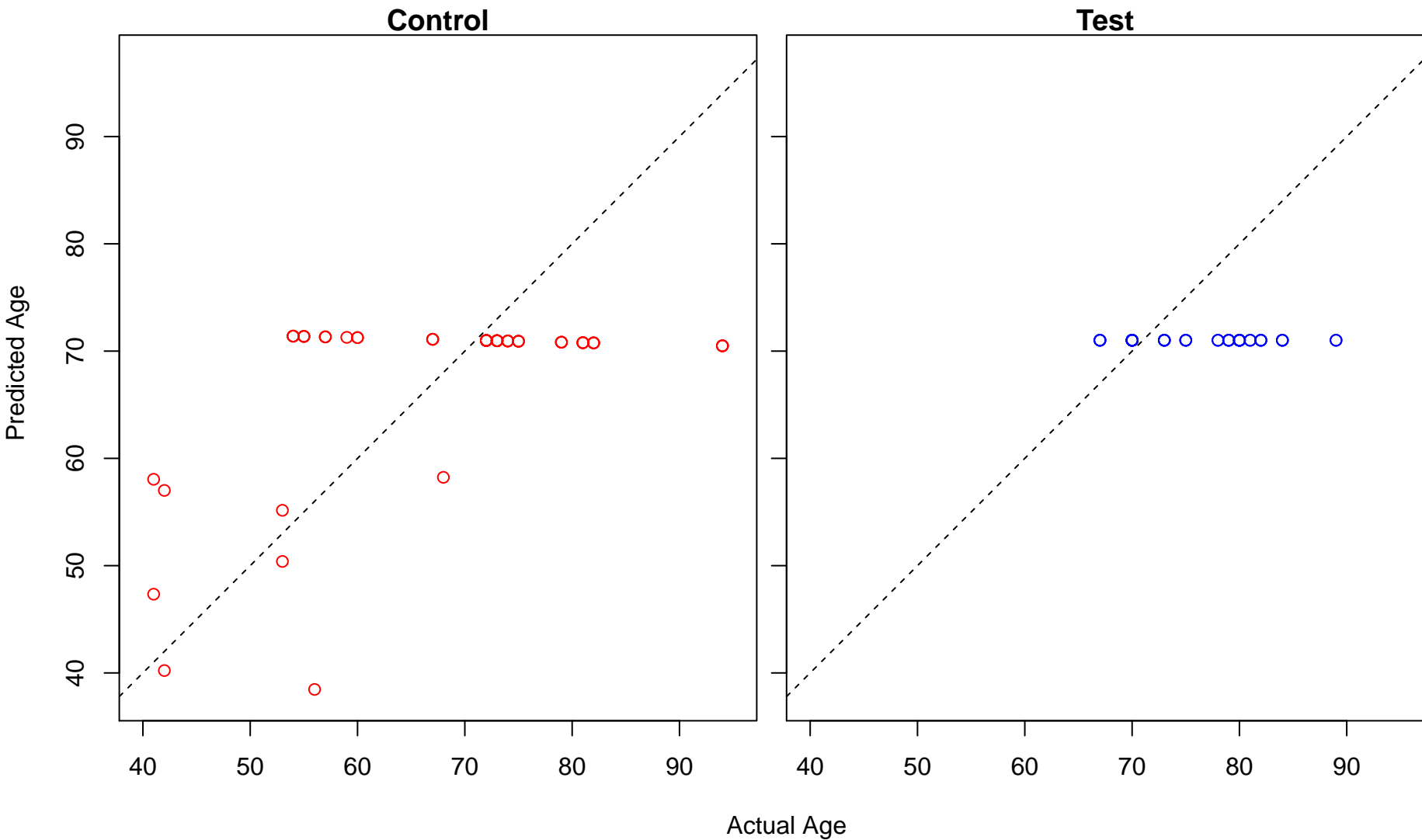
Notch signaling pathway (Score: 0.805053)



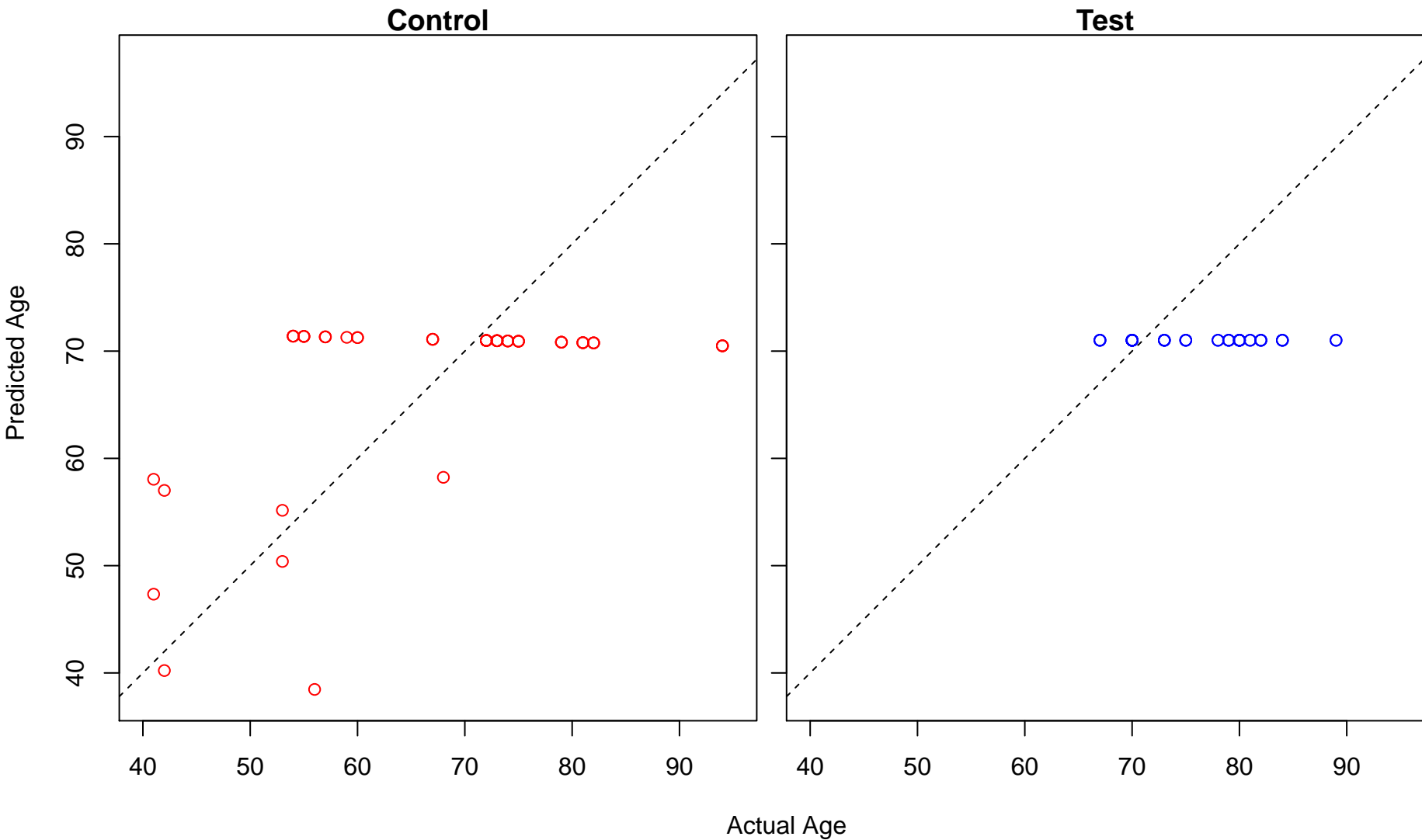
JNK cascade (Score: 0.805053)



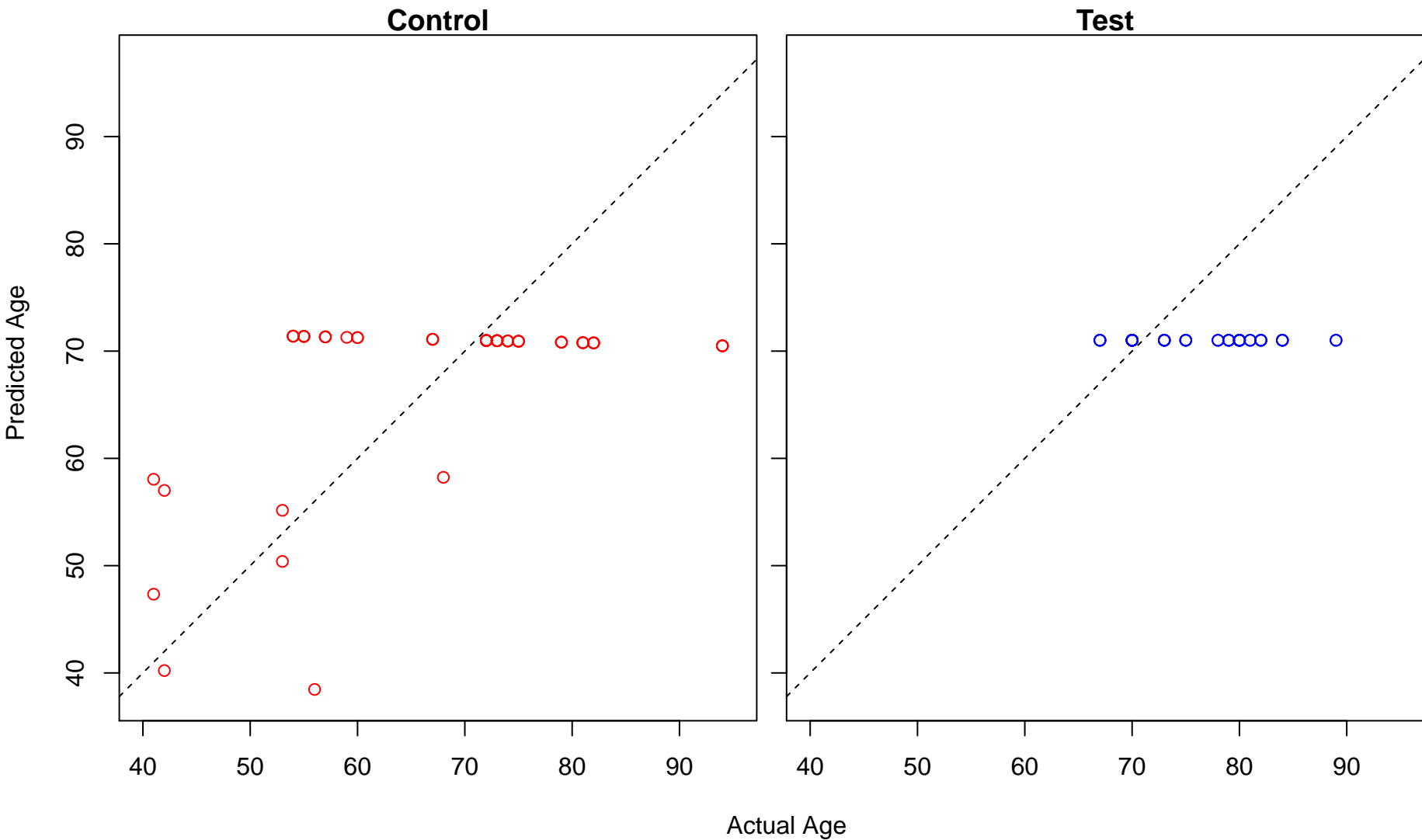
glucan biosynthetic process (Score: 0.805053)



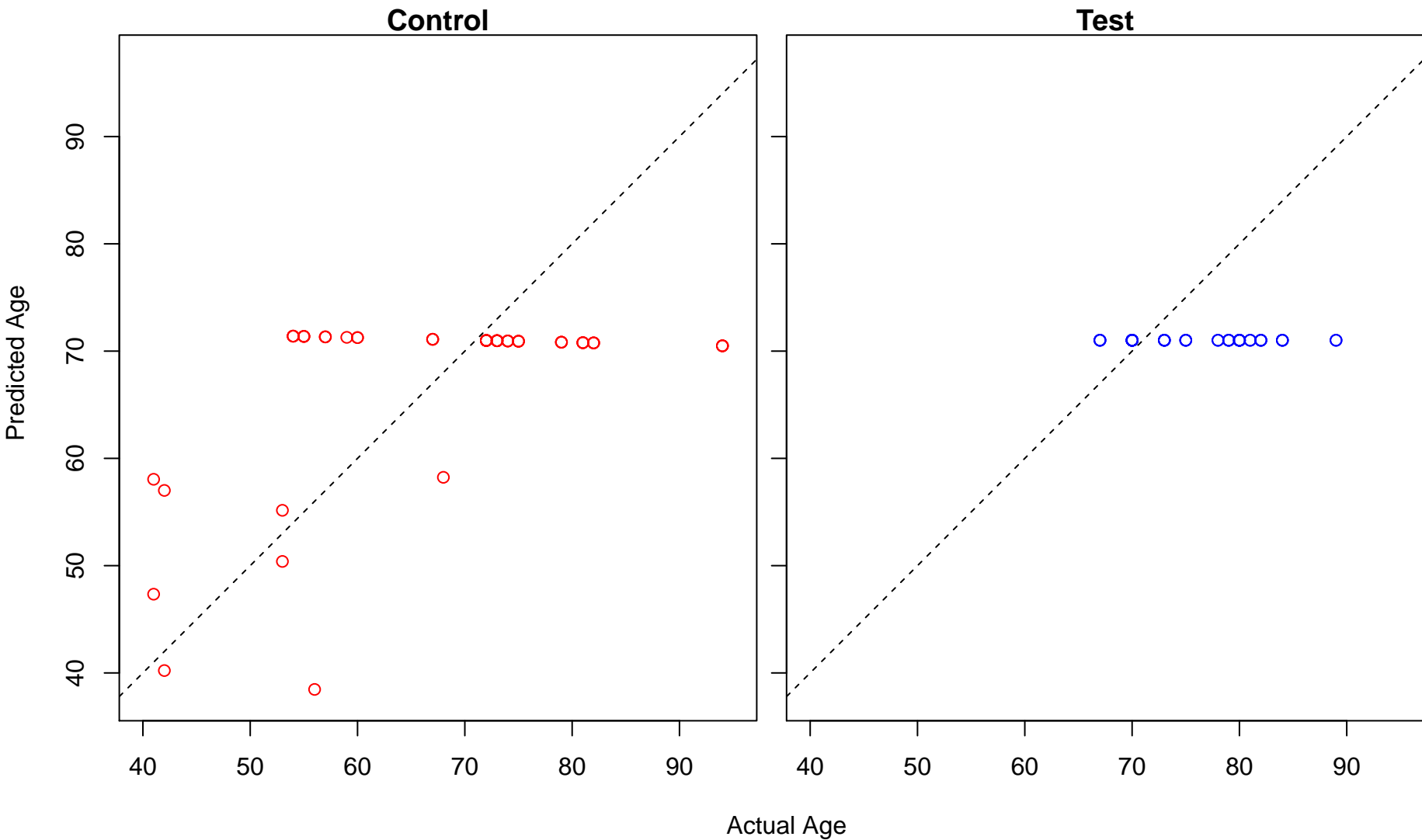
virion assembly (Score: 0.805053)



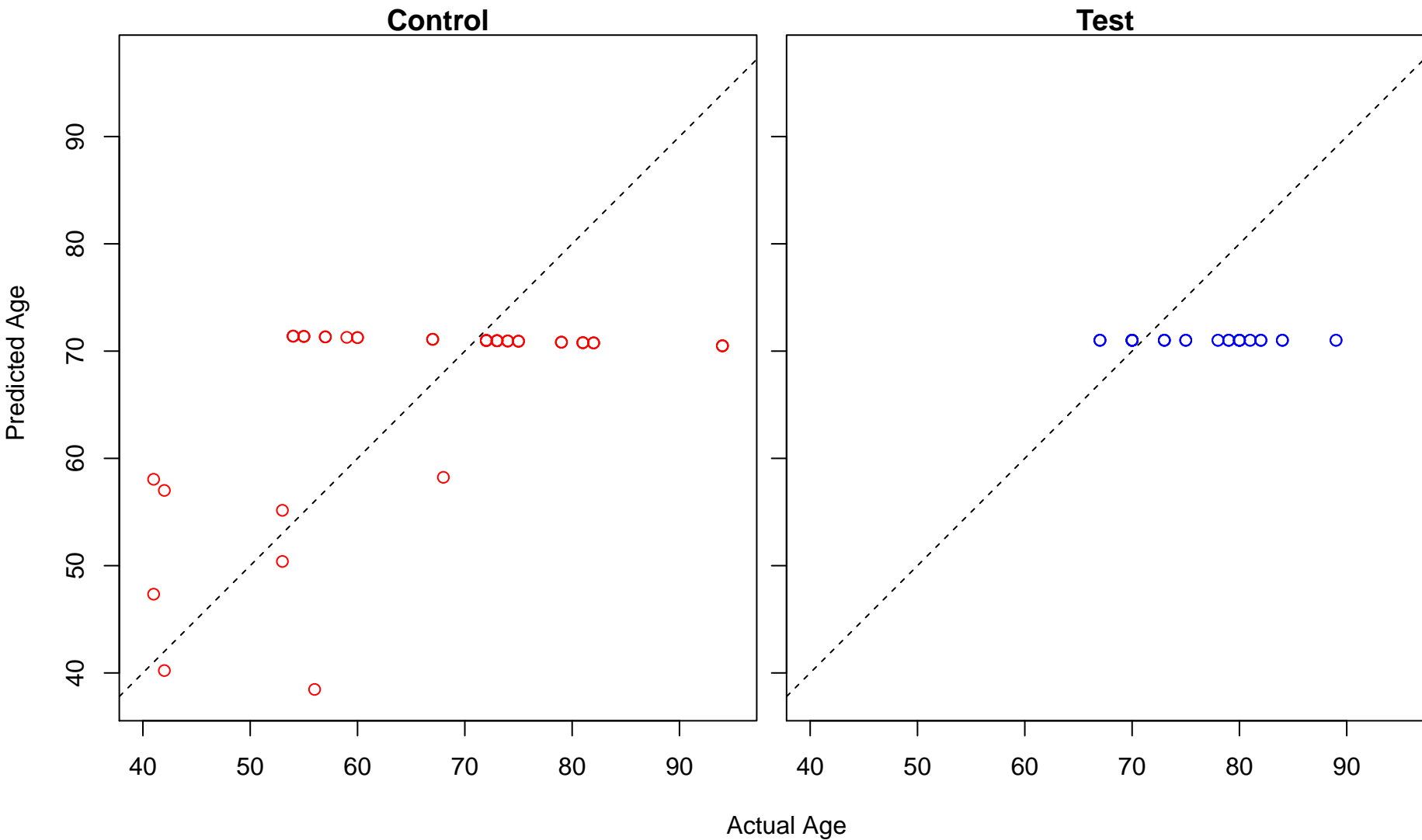
negative regulation of transforming growth factor beta receptor signaling pathway (Score: 0.80505)



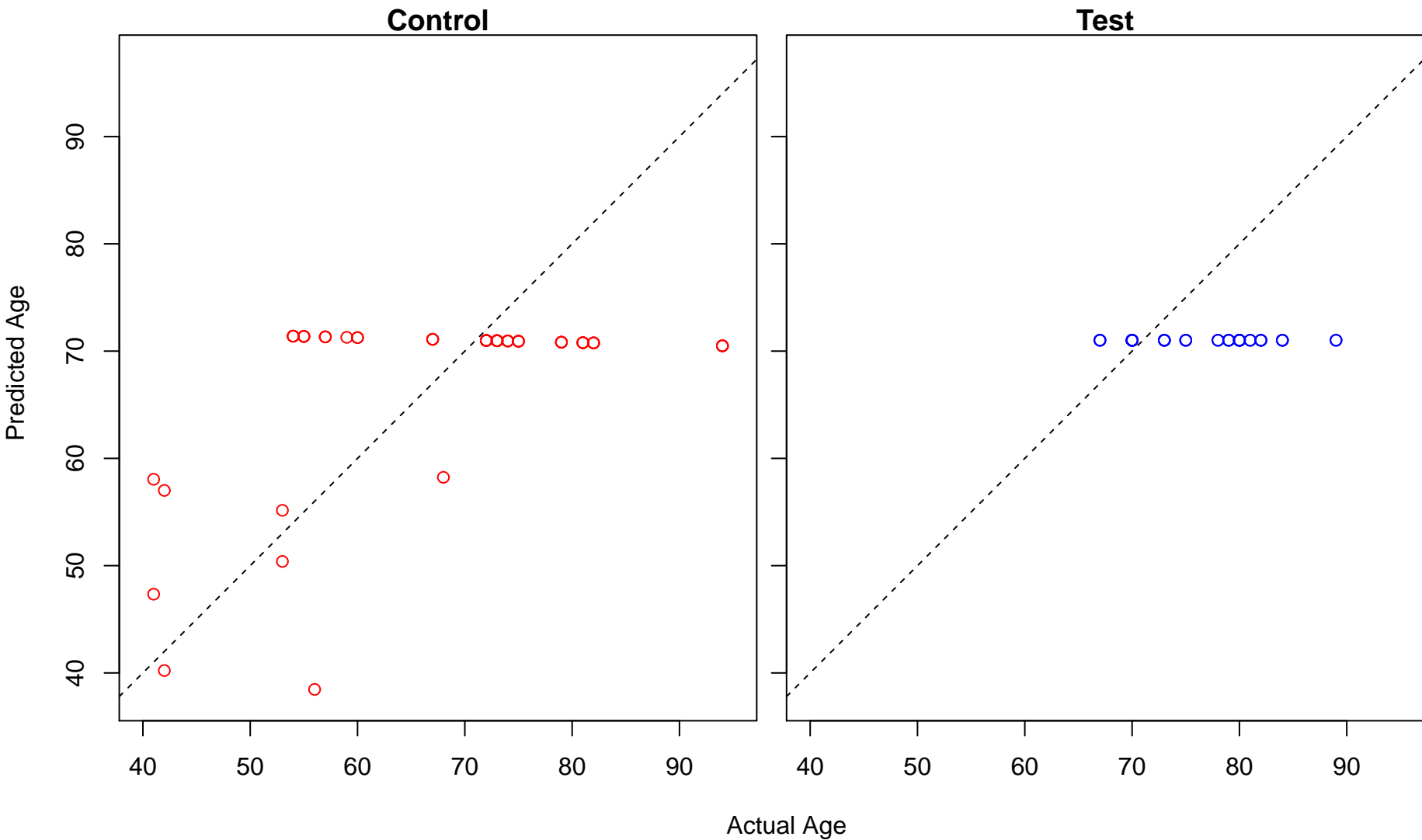
DNA duplex unwinding (Score: 0.805053)



cellular polysaccharide biosynthetic process (Score: 0.805053)

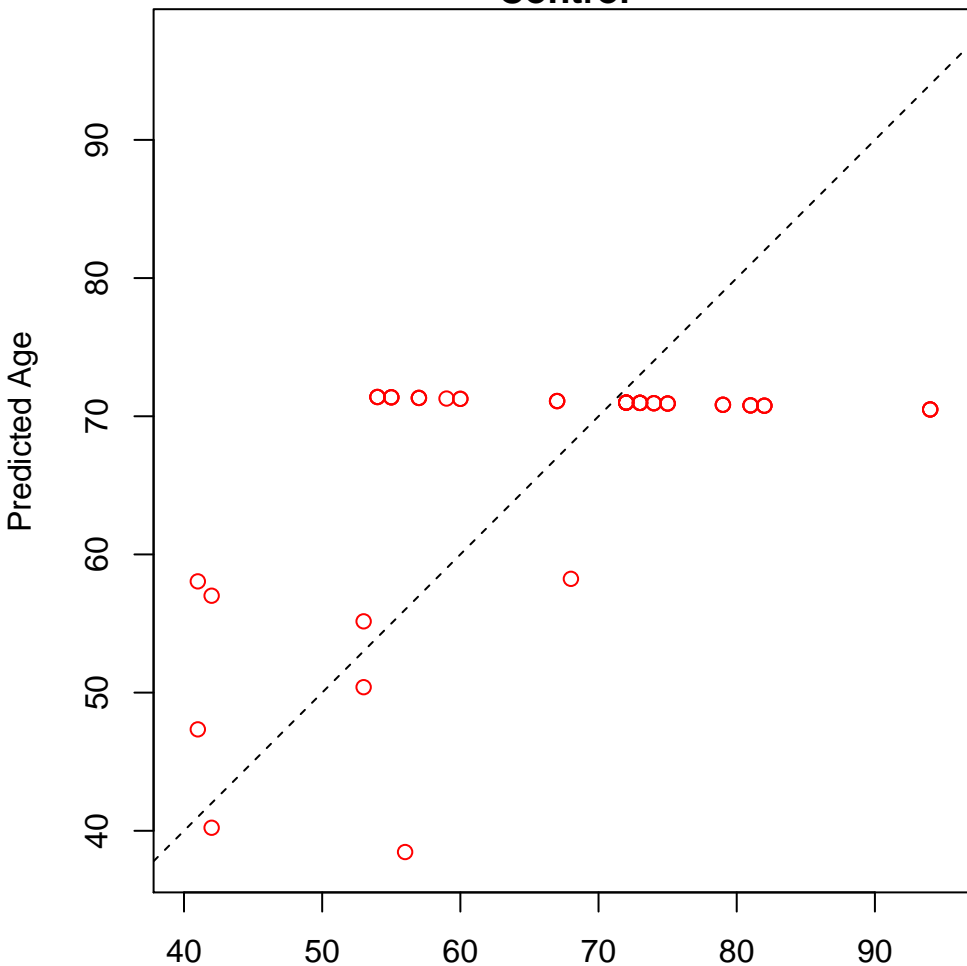


cellular carbohydrate biosynthetic process (Score: 0.805053)

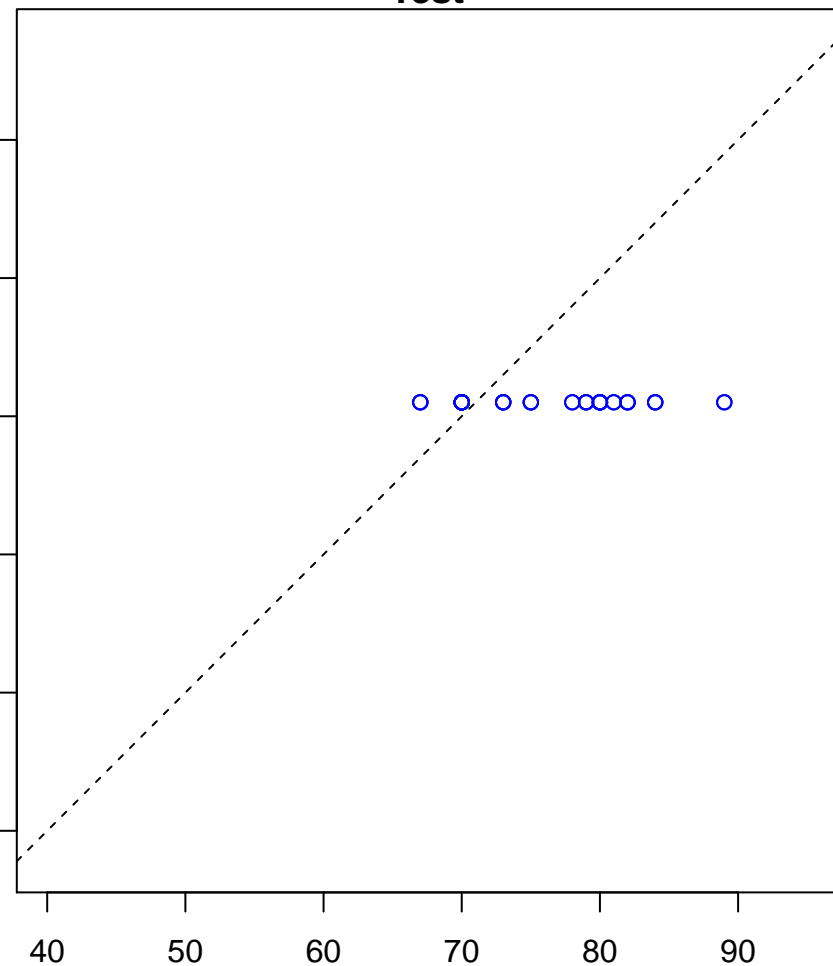


entry of bacterium into host cell (Score: 0.805053)

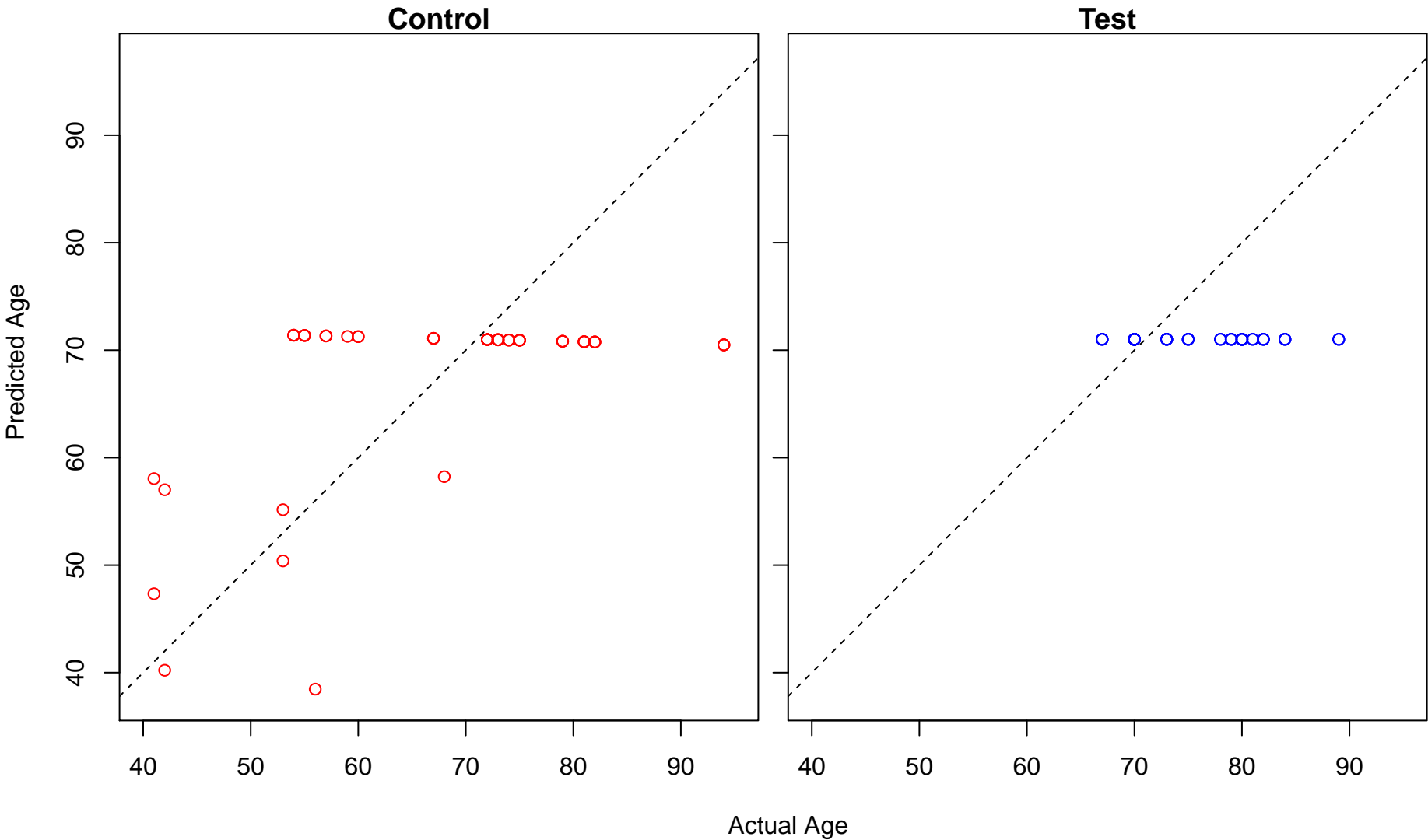
Control



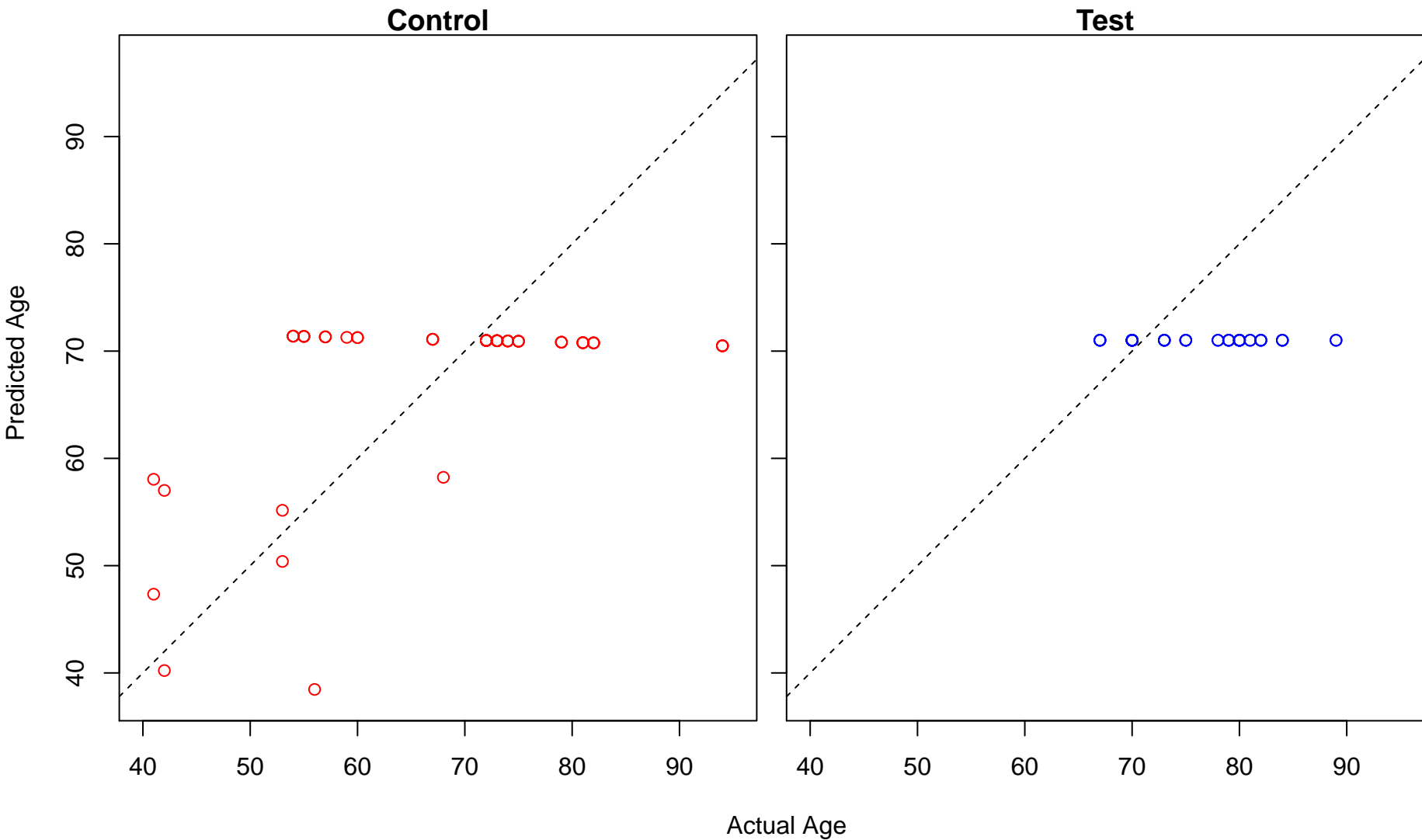
Test



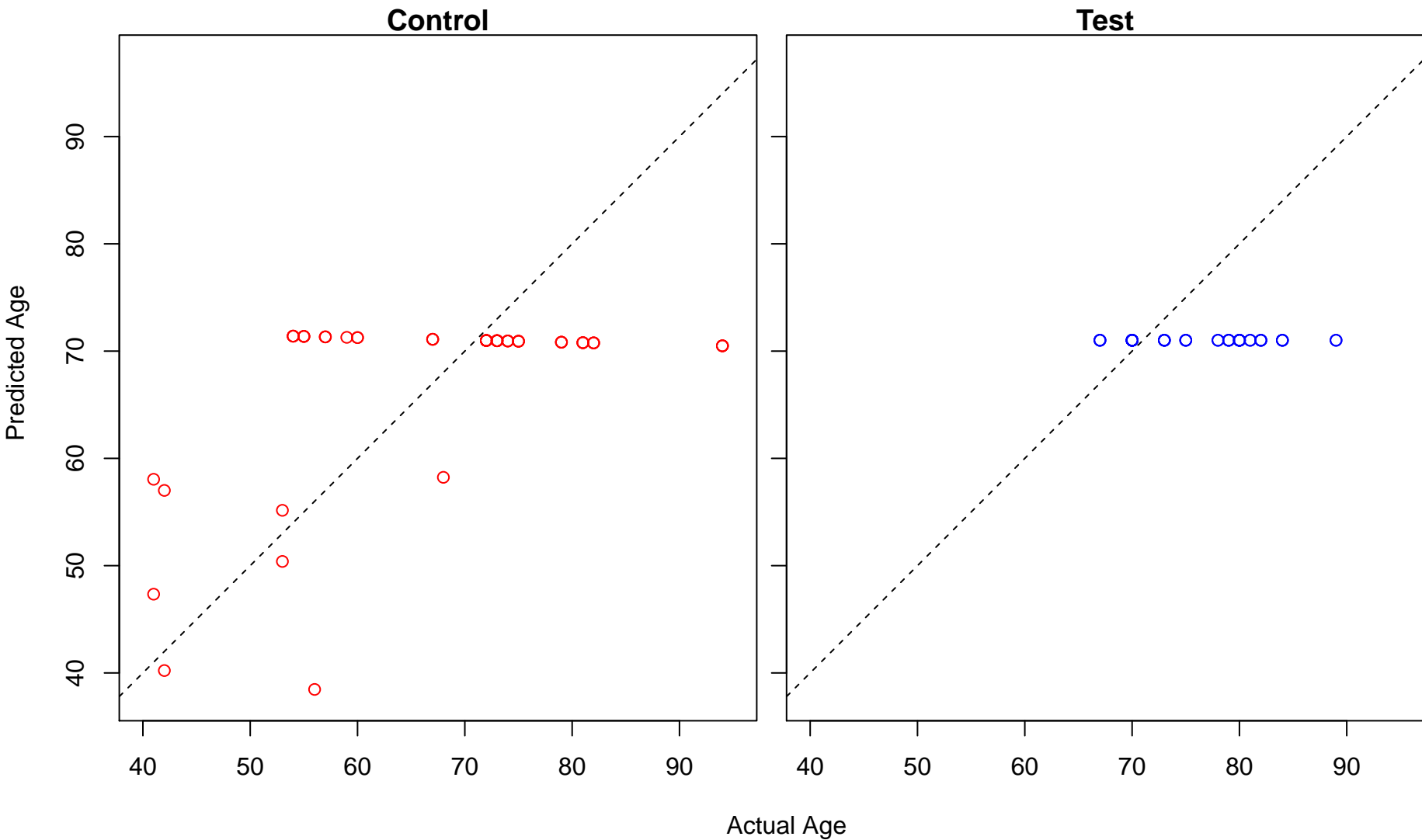
Actual Age



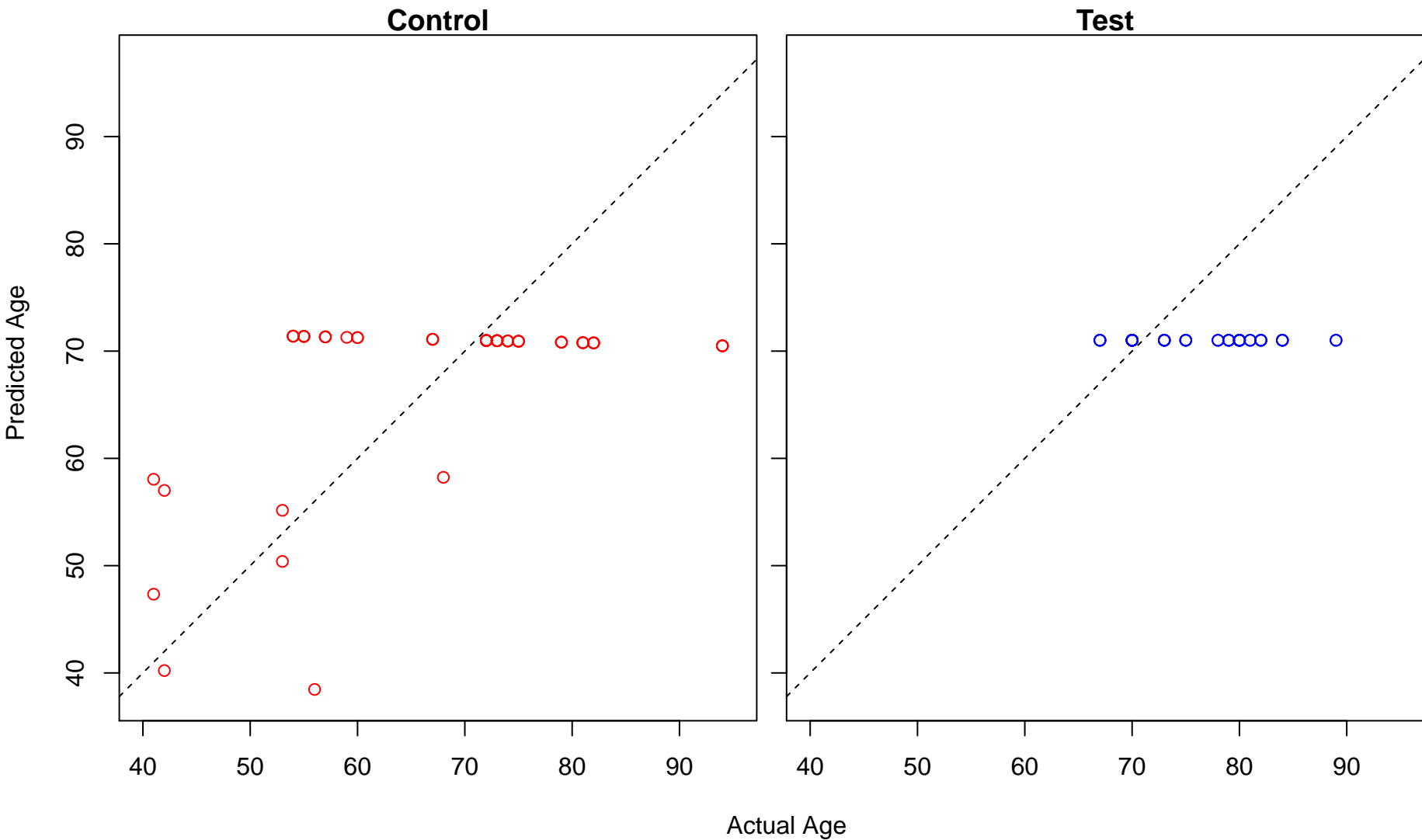
interstrand cross-link repair (Score: 0.805053)



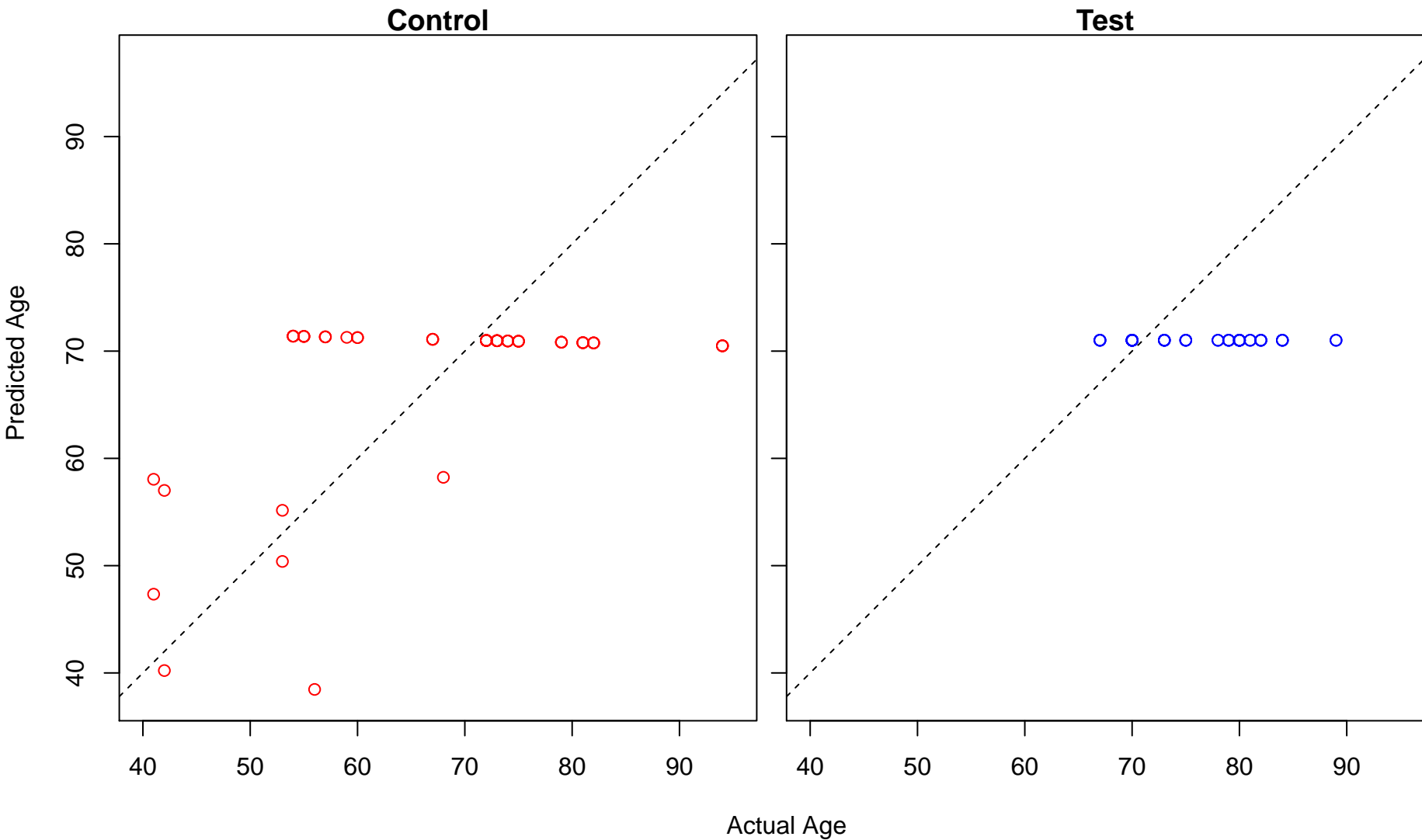
ERBB2 signaling pathway (Score: 0.805053)



negative regulation of epidermal growth factor receptor signaling pathway (Score: 0.805053)

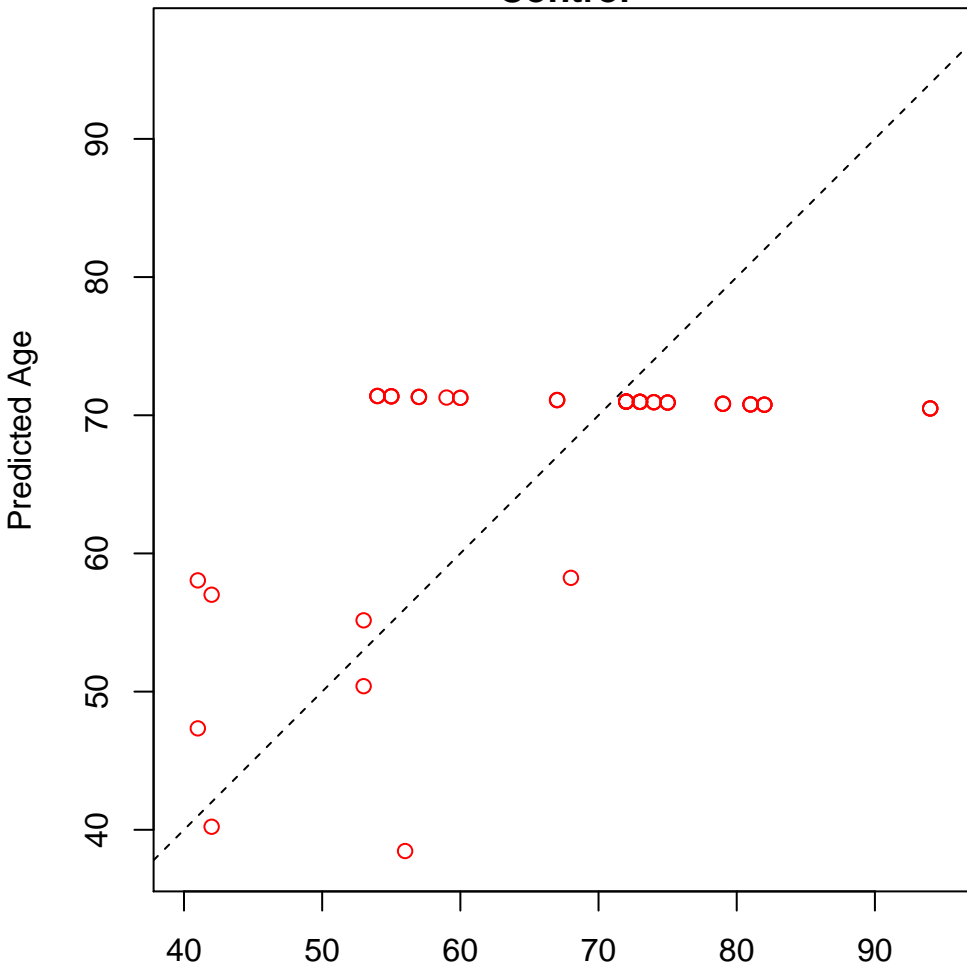


glucan metabolic process (Score: 0.805053)

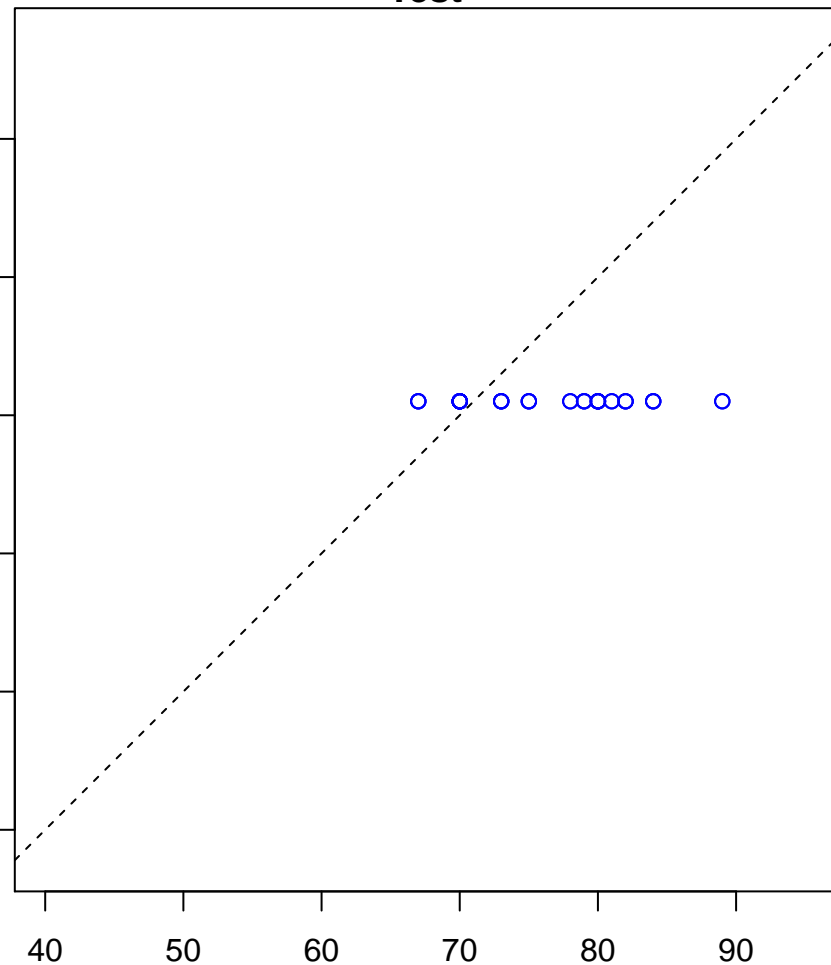


cellular polysaccharide metabolic process (Score: 0.805053)

Control

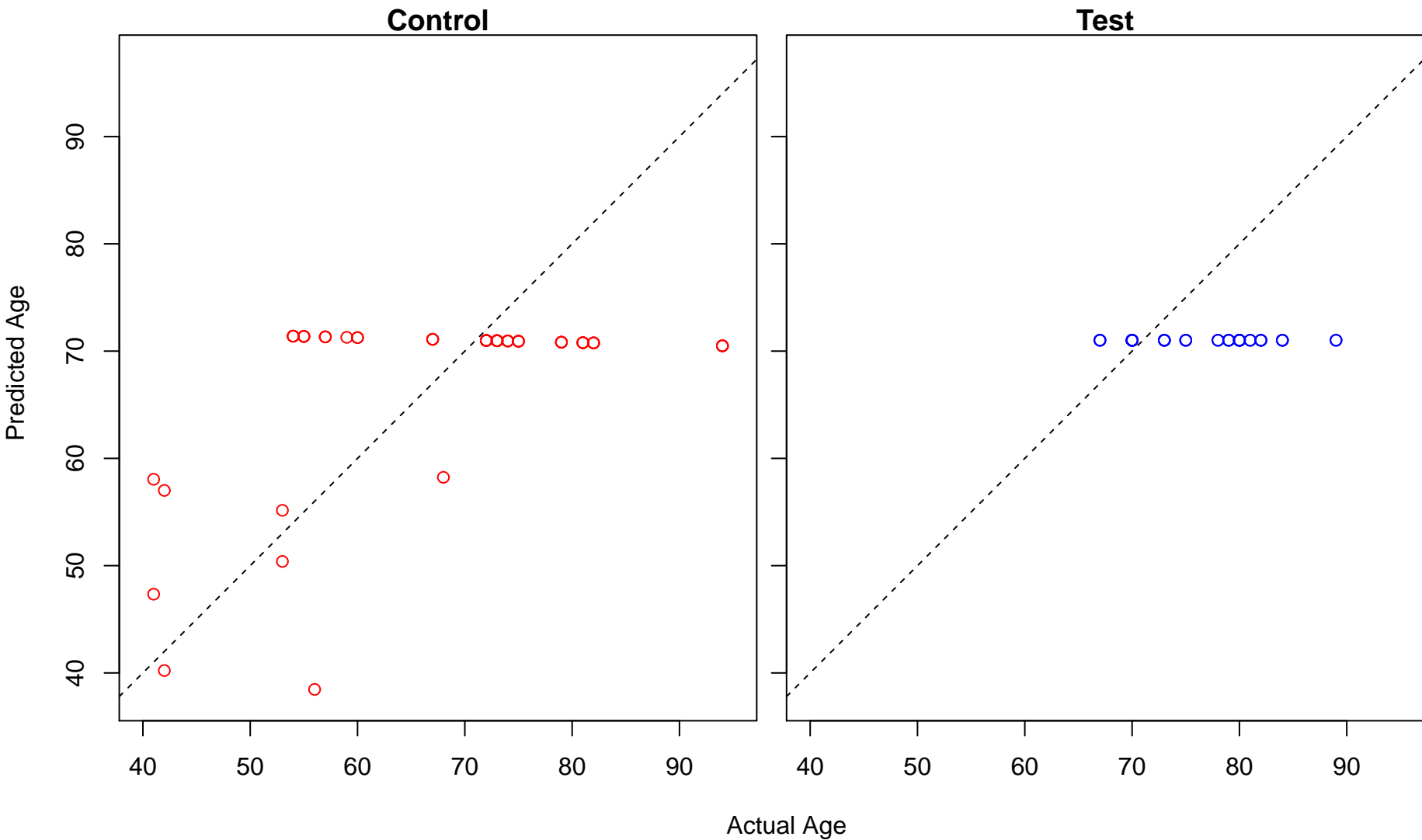


Test

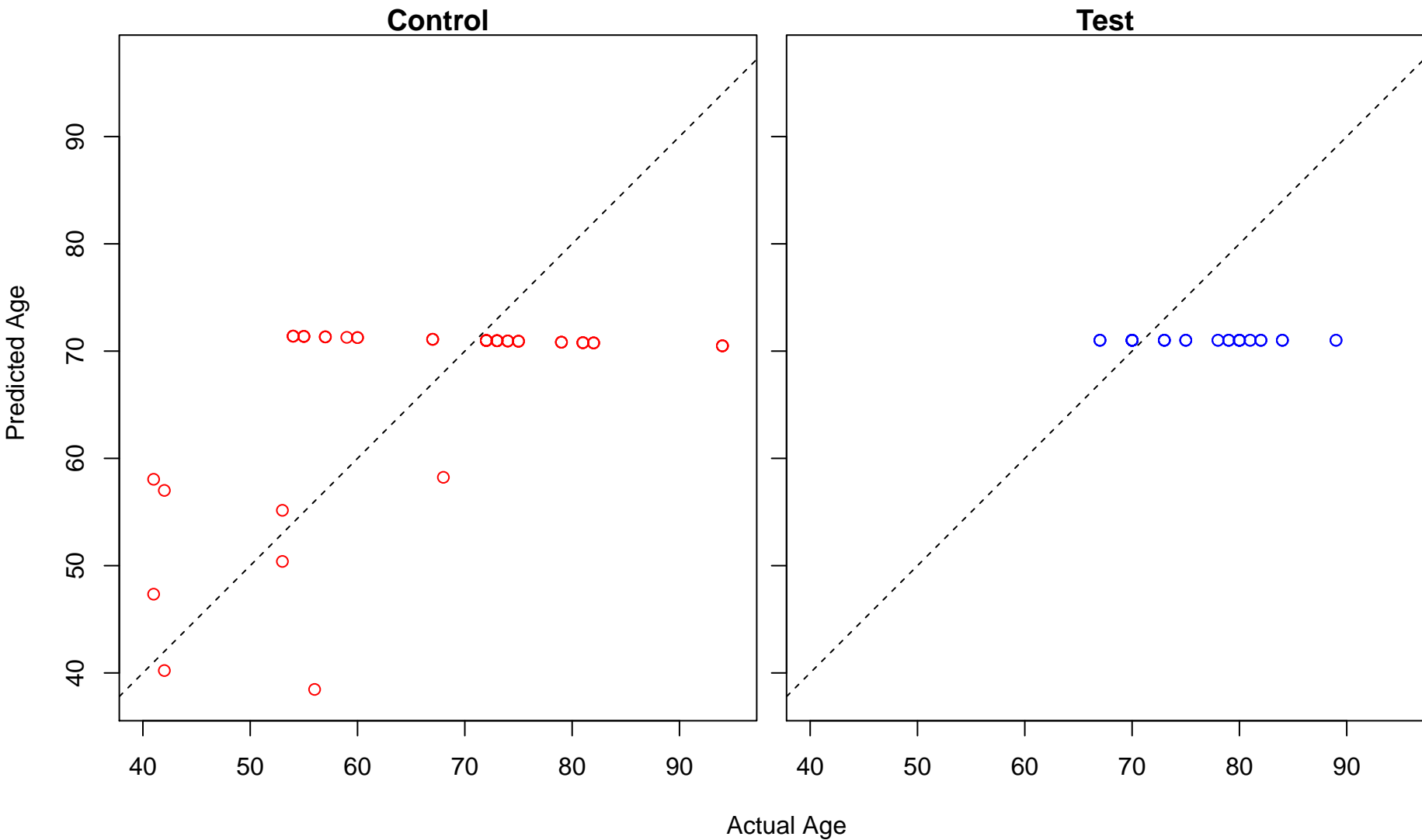


Actual Age

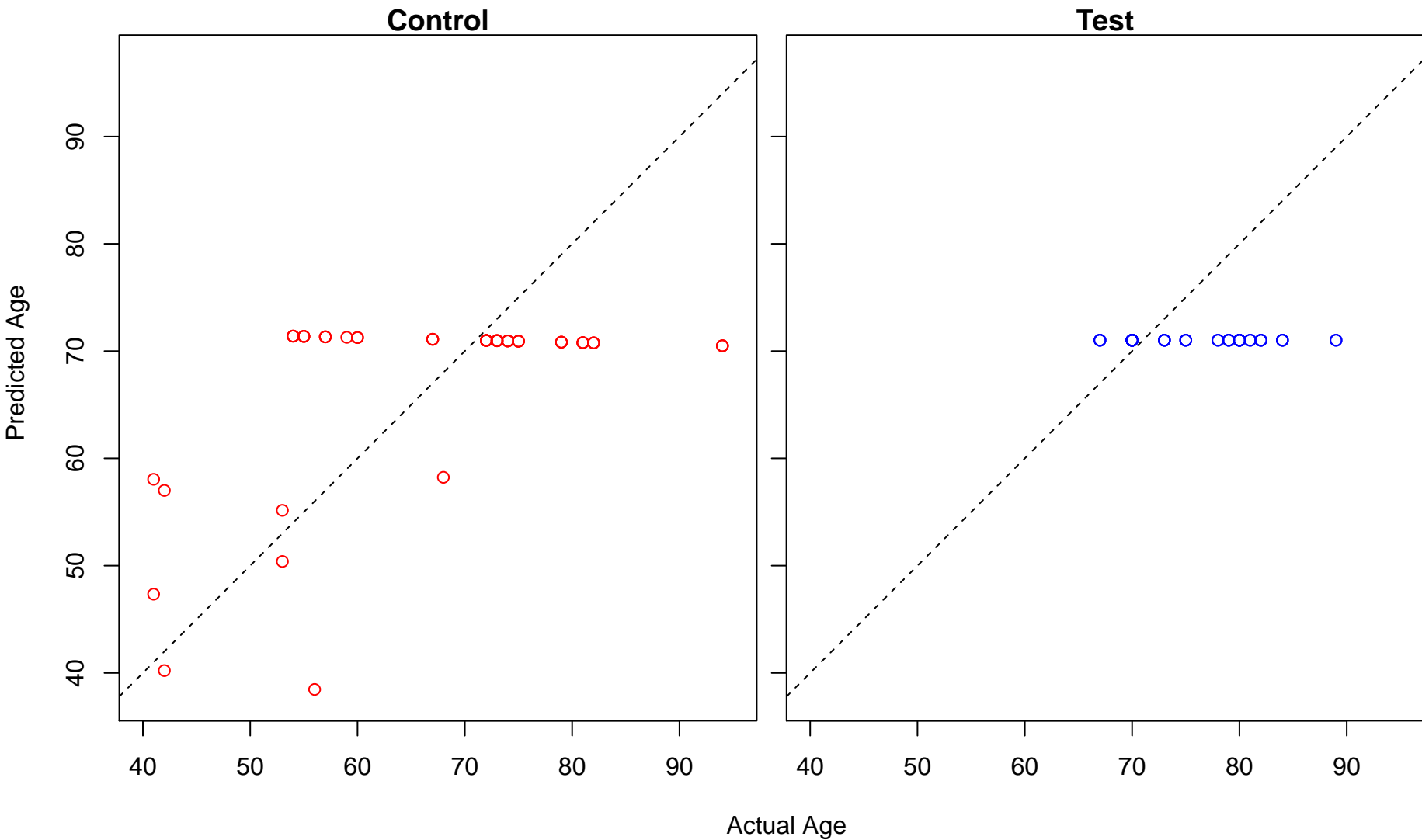
positive regulation of epidermal growth factor receptor signaling pathway (Score: 0.805053)



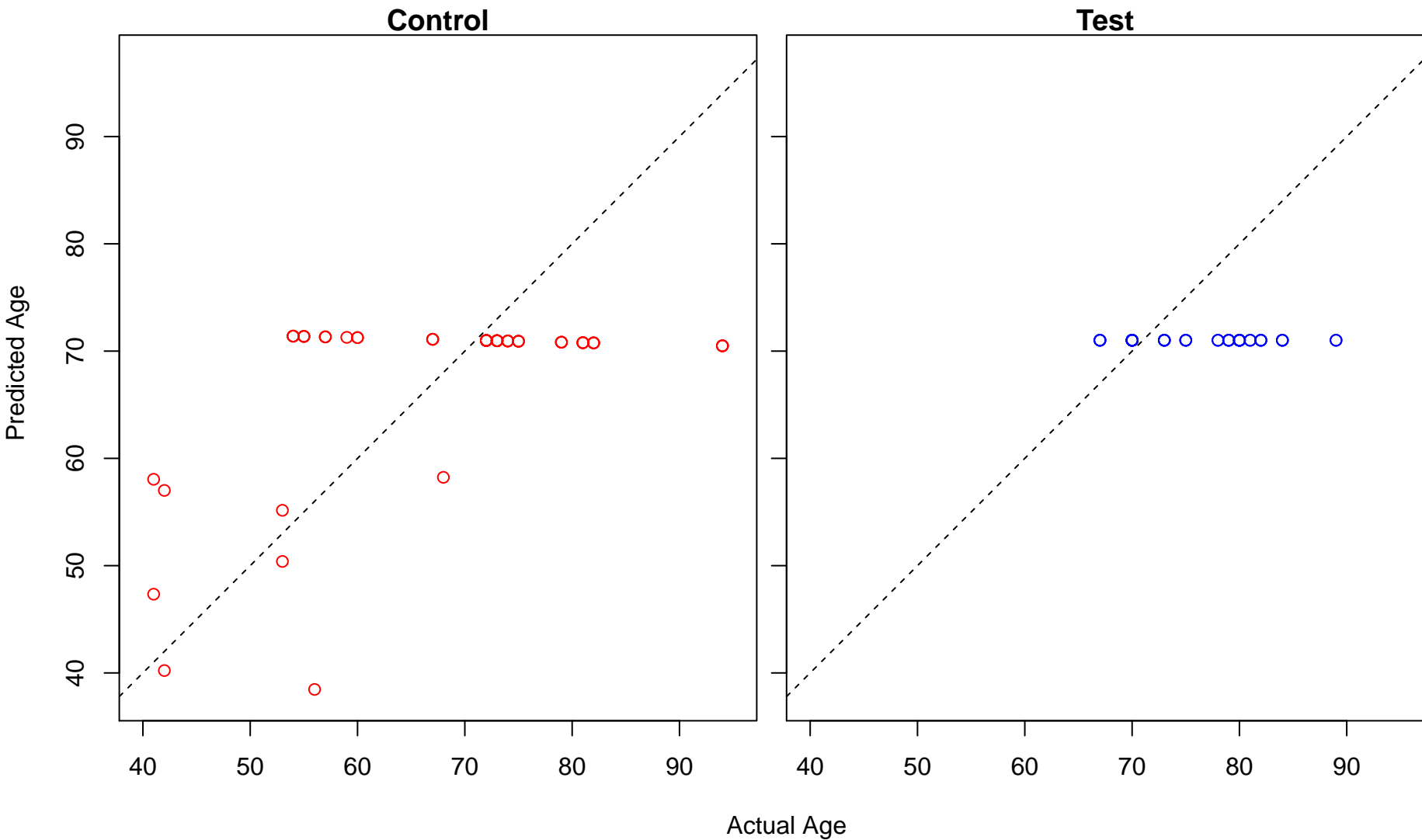
nucleotide-binding oligomerization domain containing signaling pathway (Score: 0.805053)



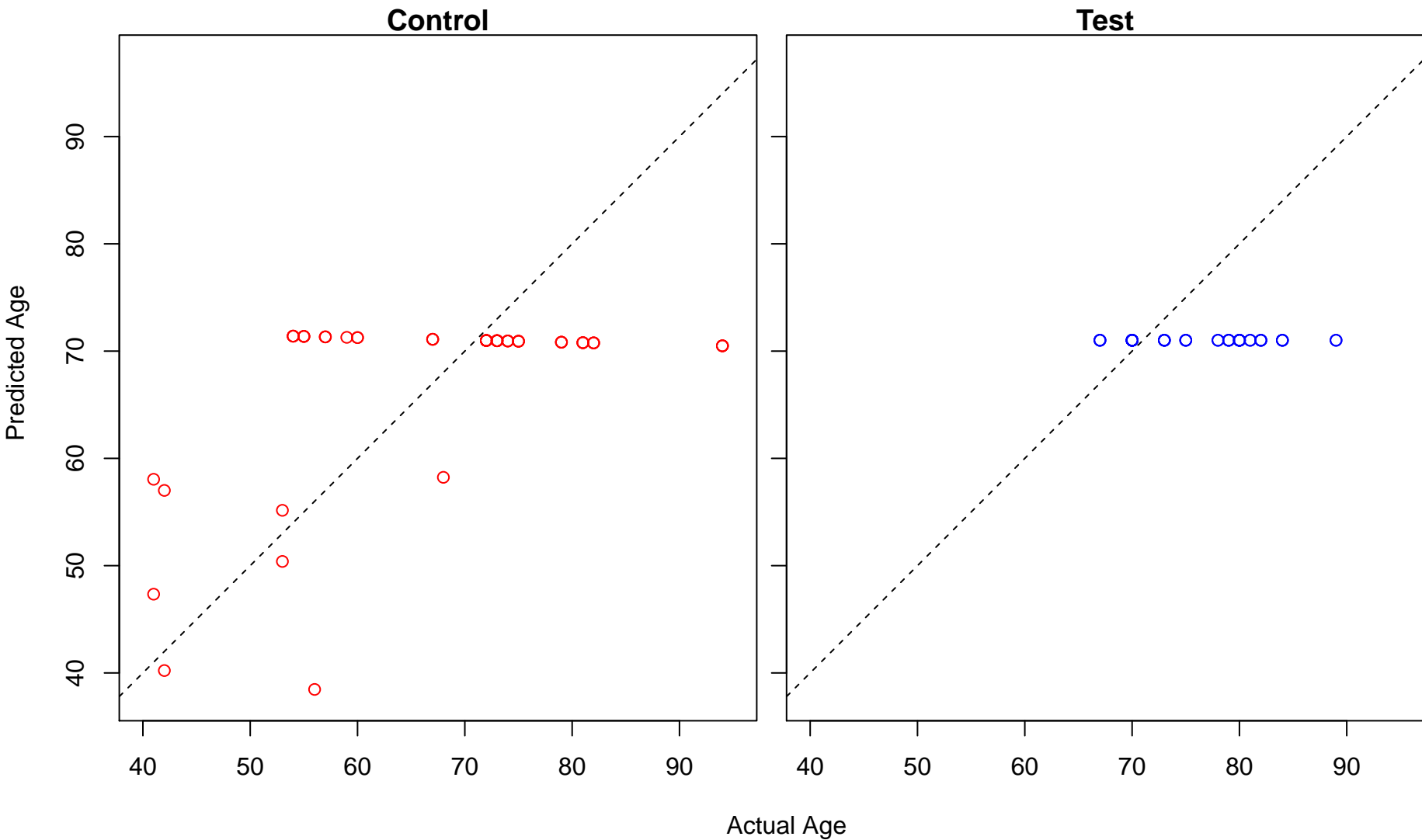
Negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 1)



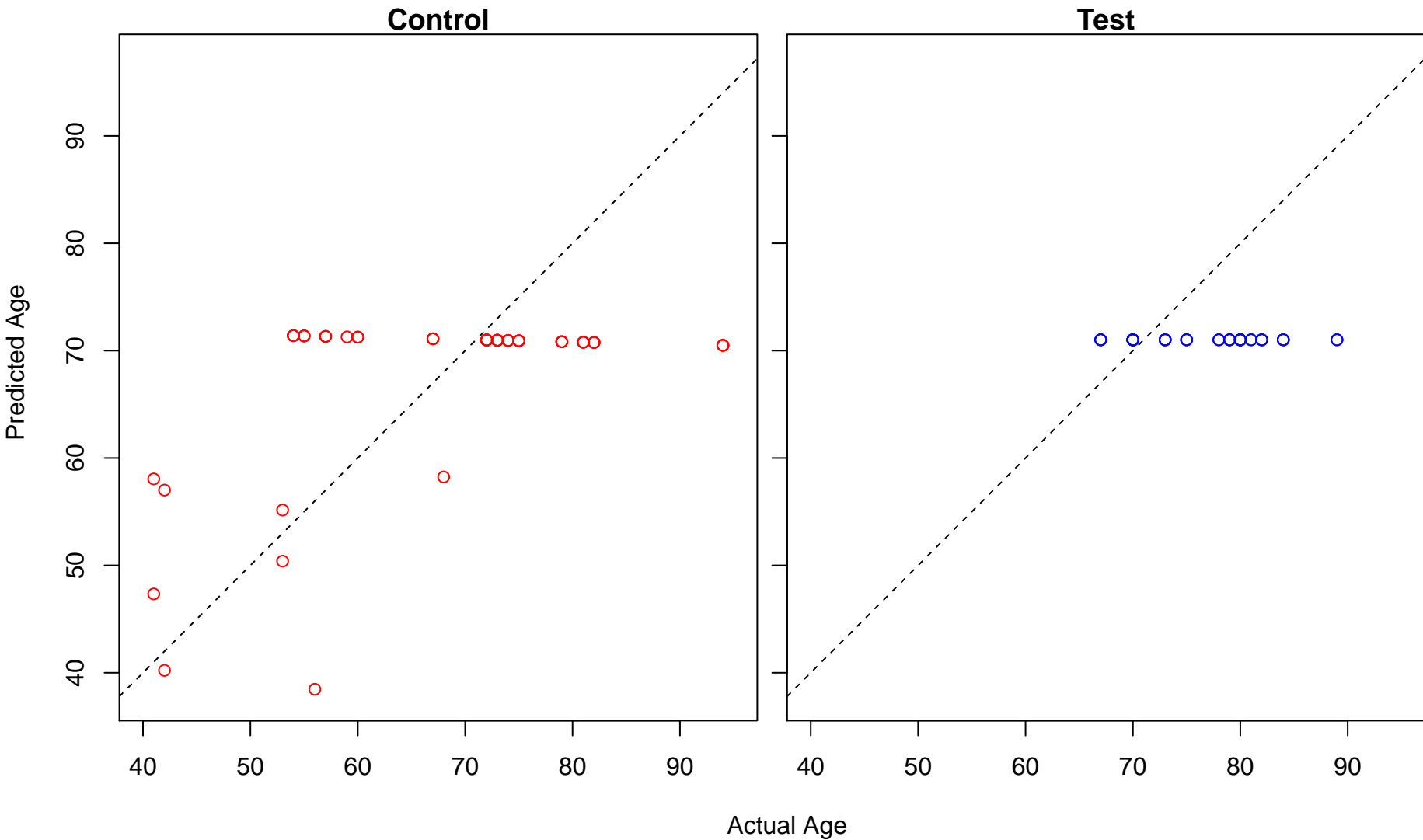
negative regulation of cellular response to growth factor stimulus (Score: 0.805053)



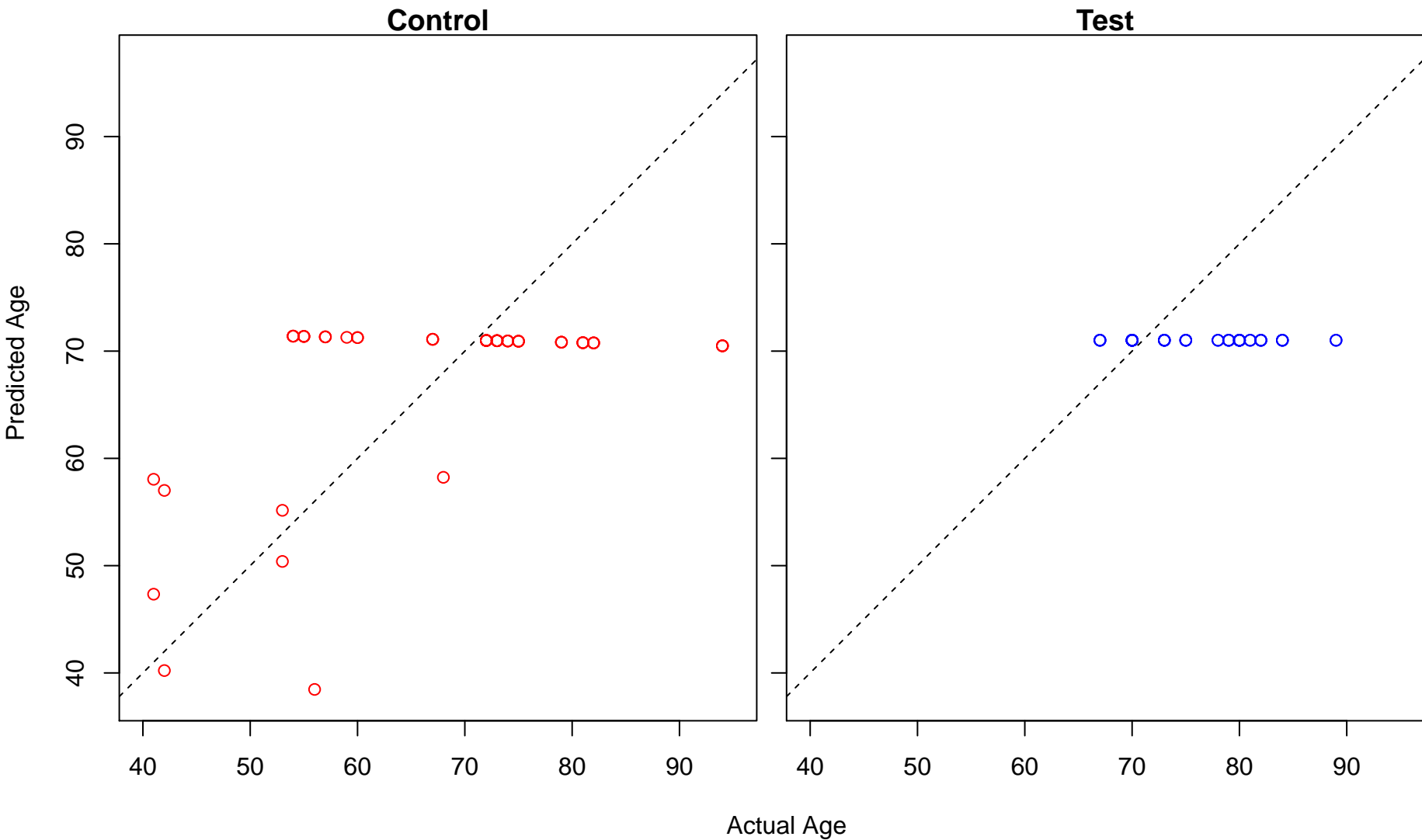
negative regulation of ERBB signaling pathway (Score: 0.805053)



positive regulation of ERBB signaling pathway (Score: 0.805053)

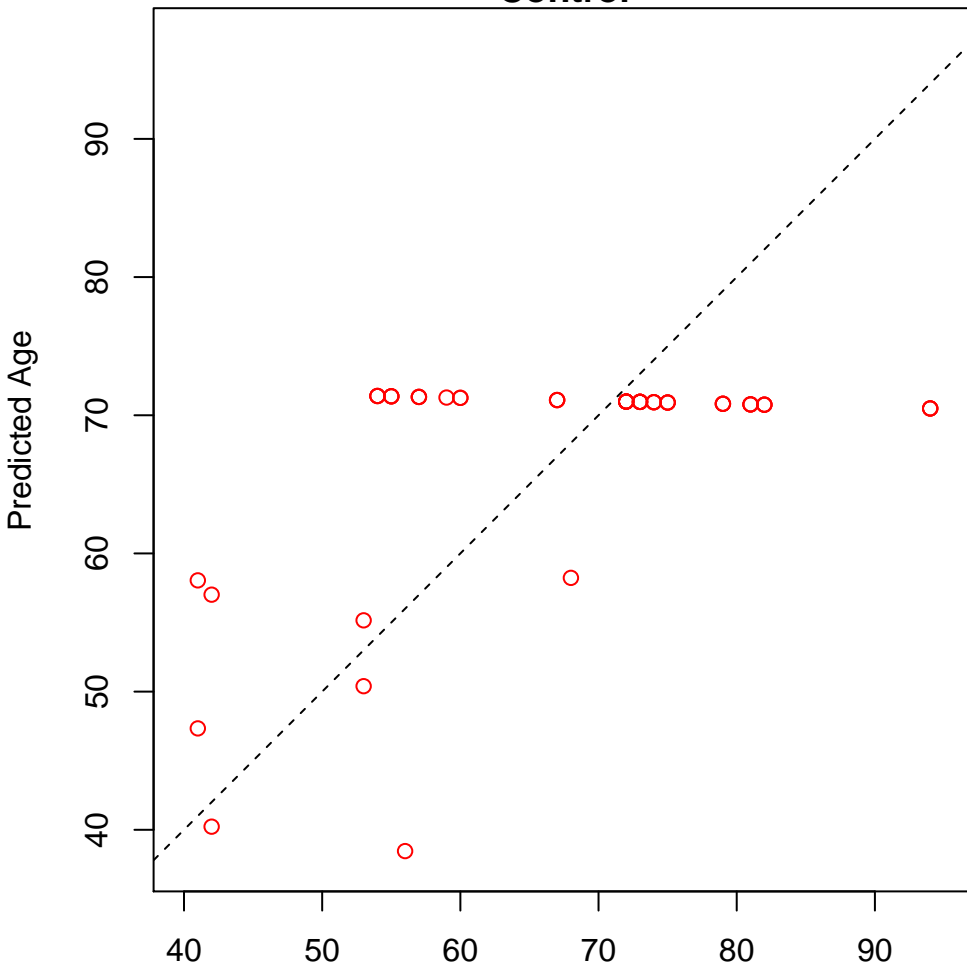


negative regulation of cellular response to transforming growth factor beta stimulus (Score: 0.80505)

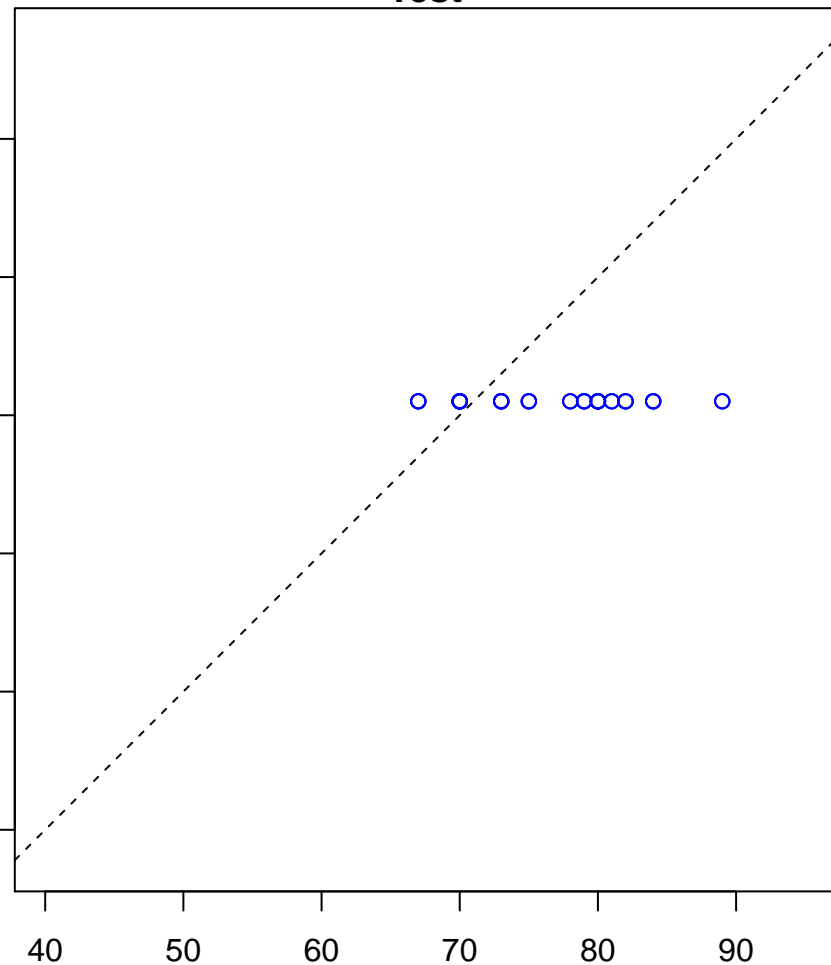


DNA synthesis involved in DNA repair (Score: 0.805053)

Control

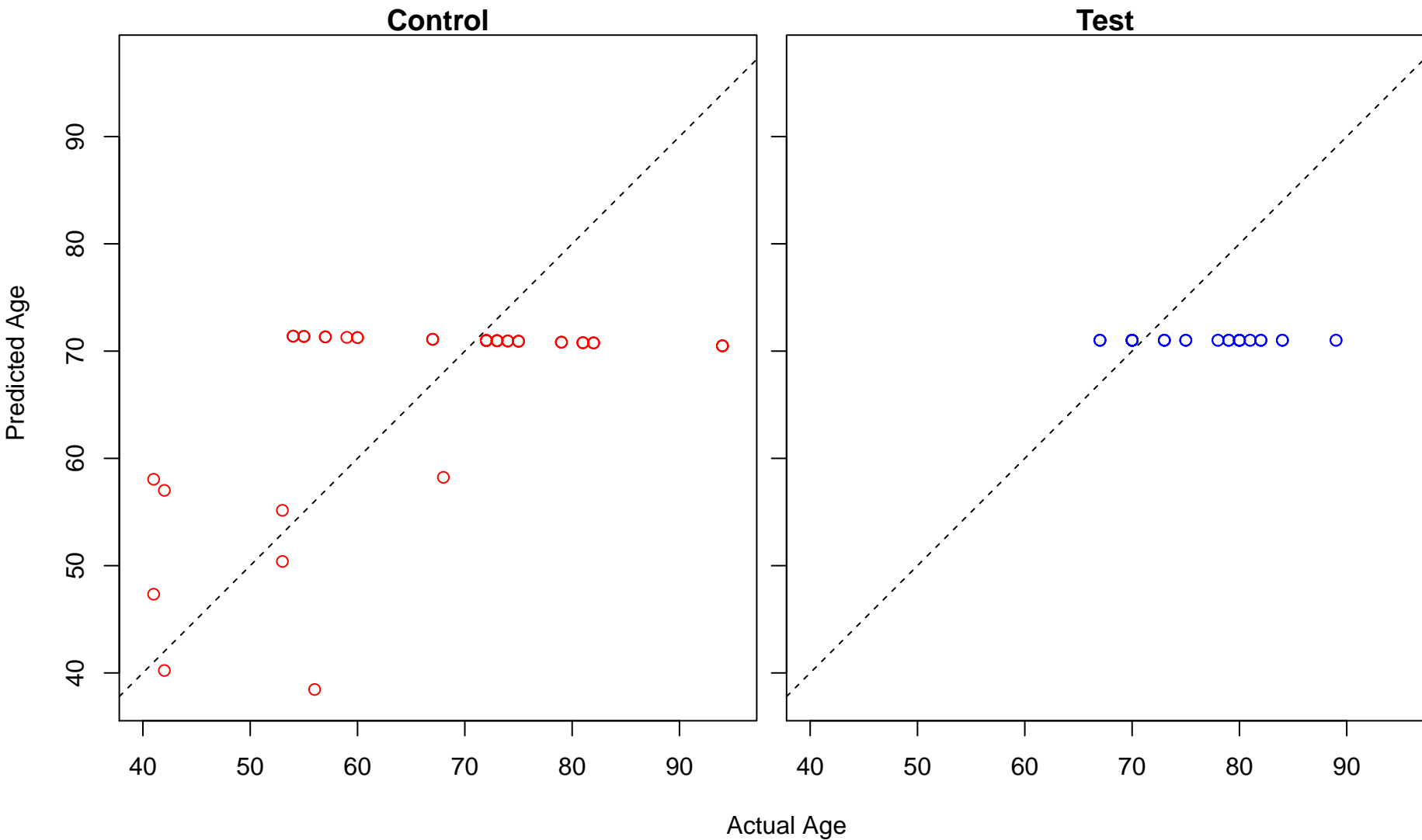


Test

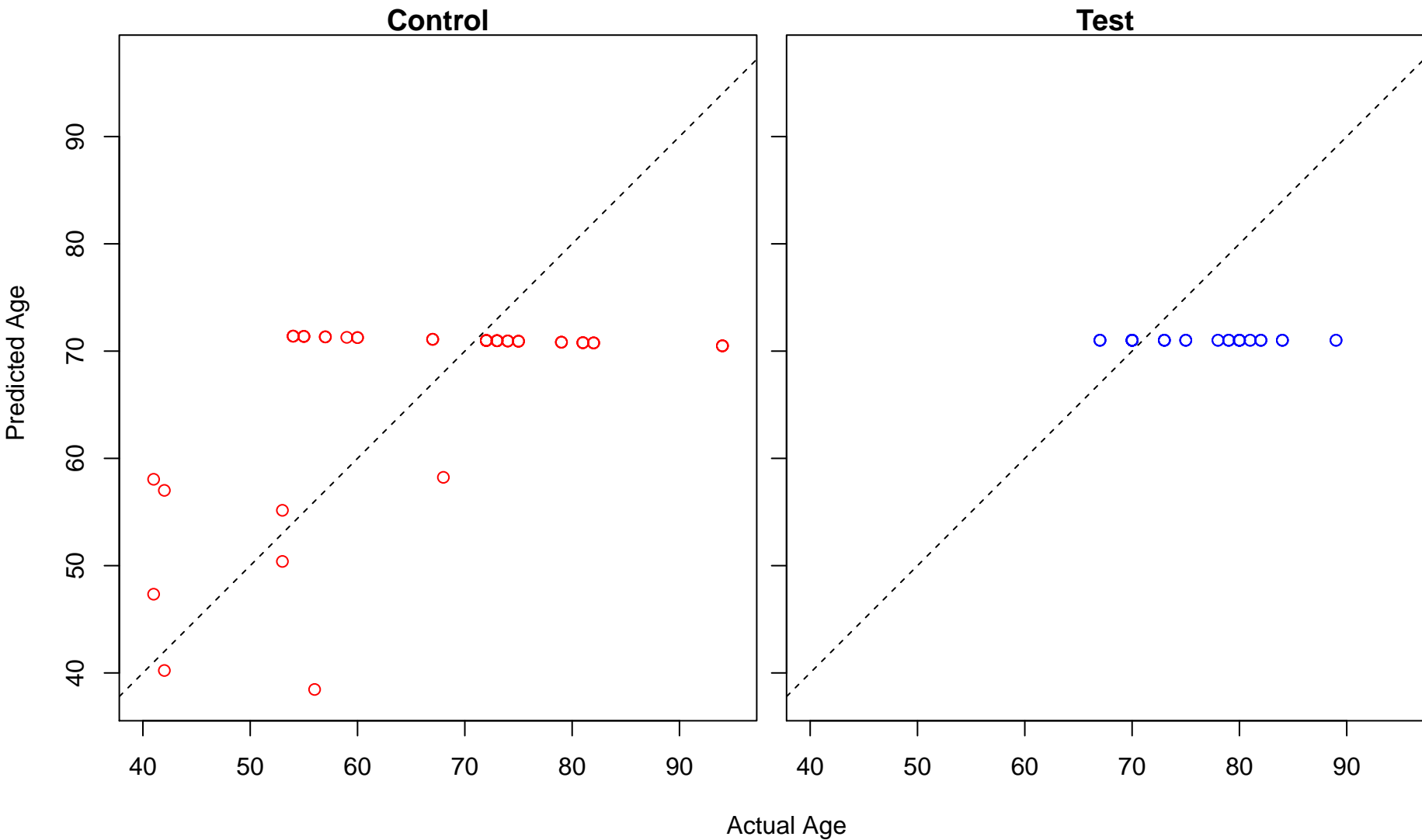


Actual Age

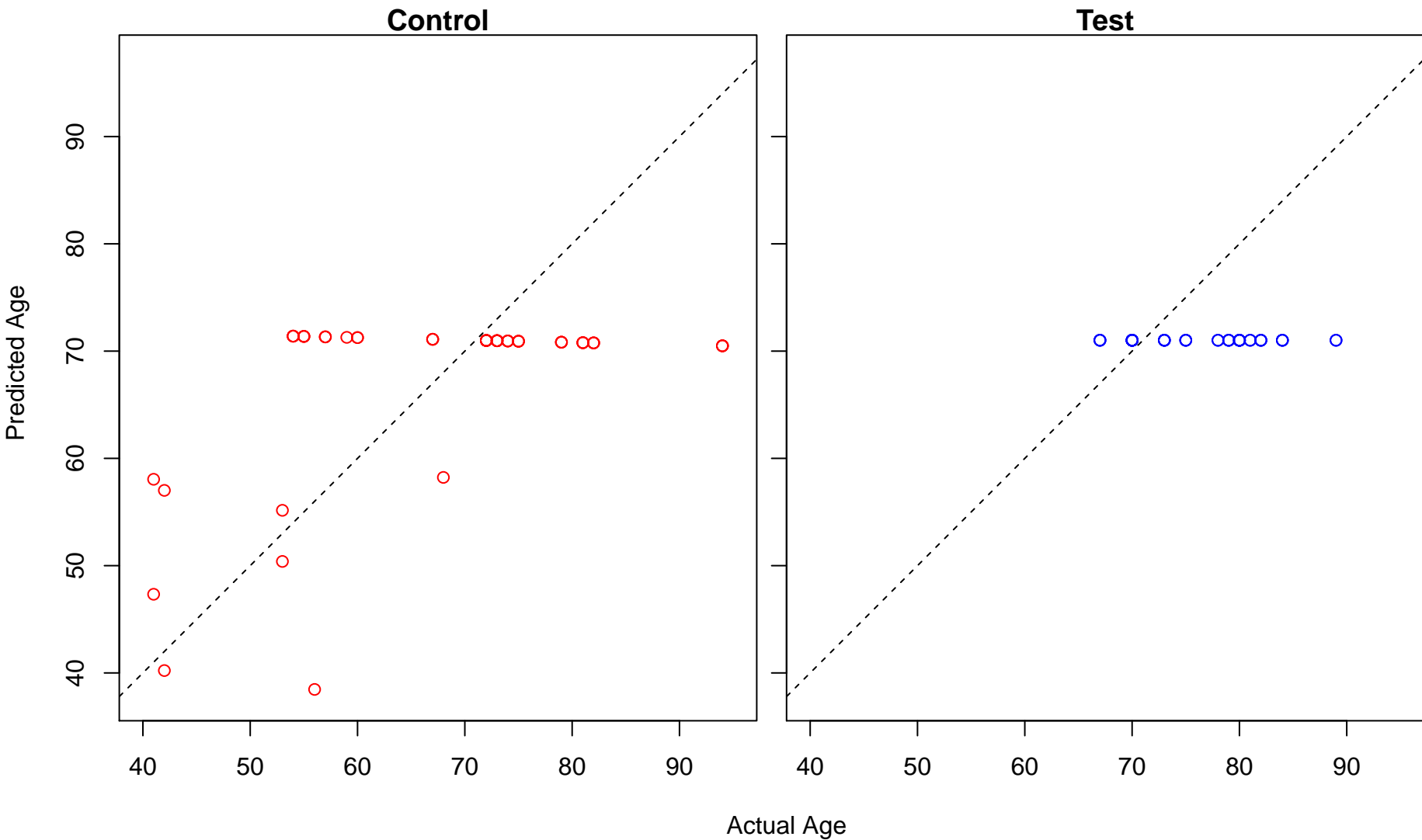
postreplication repair (Score: 0.805053)



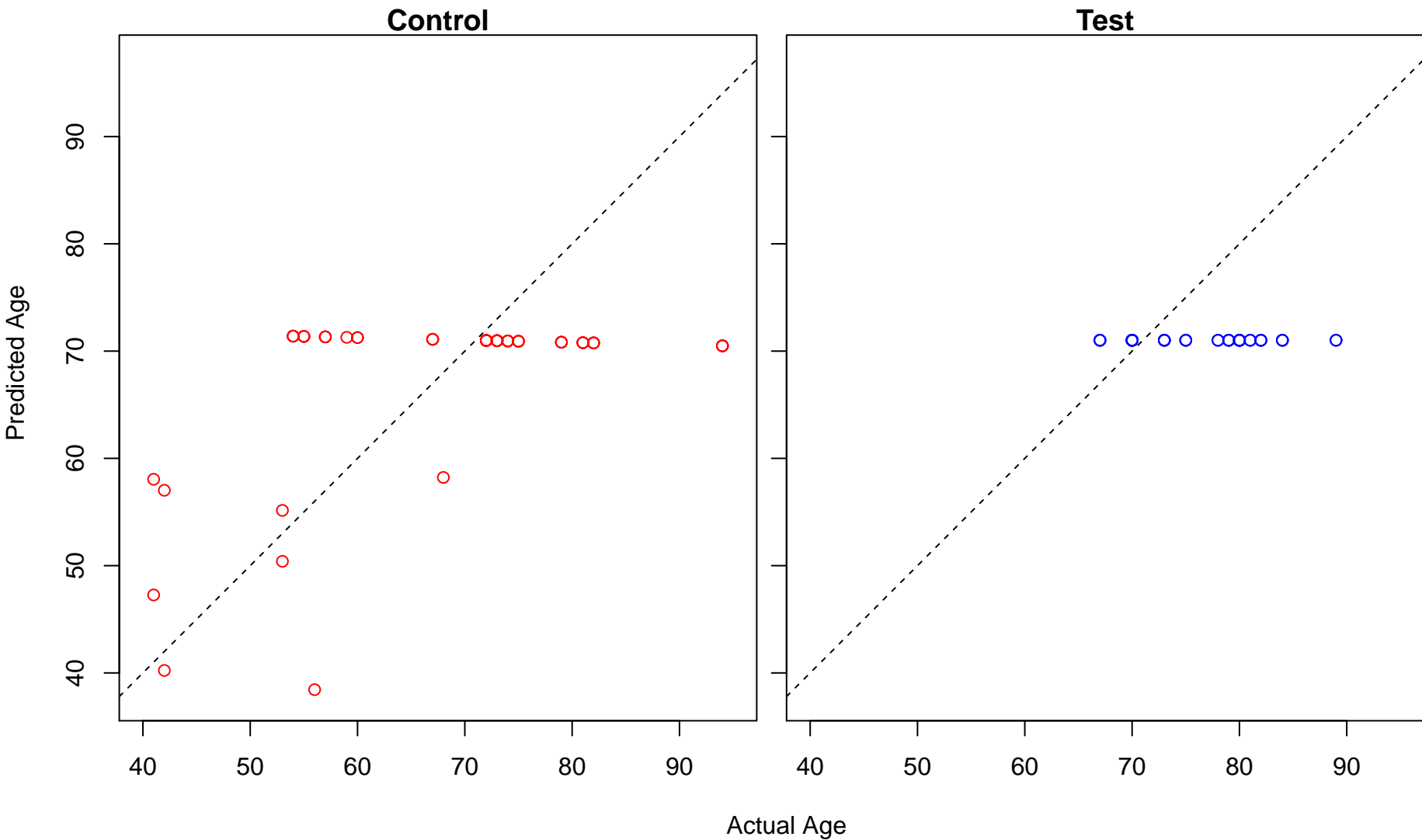
translesion synthesis (Score: 0.805053)



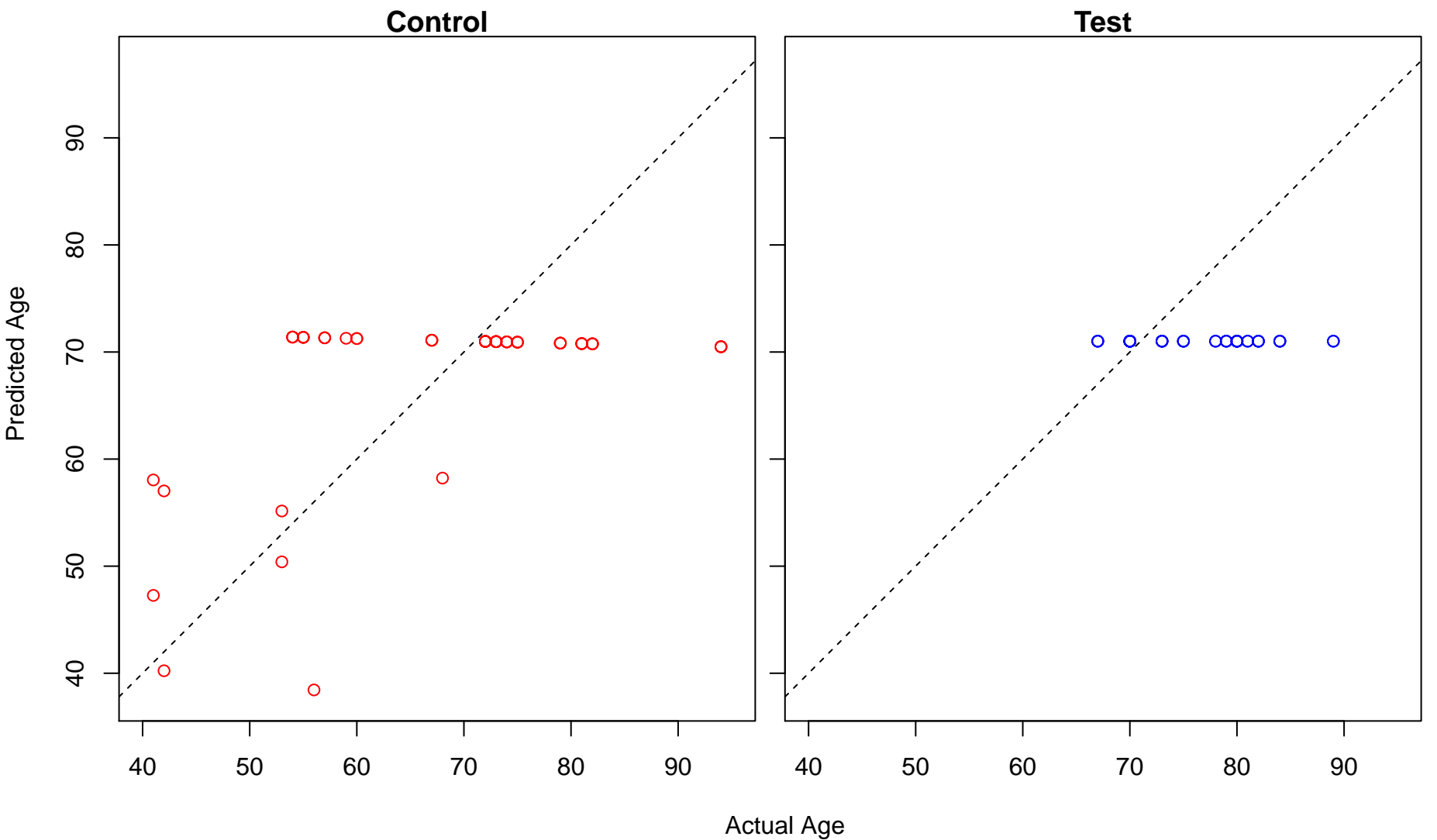
negative regulation of type I interferon production (Score: 0.805044)



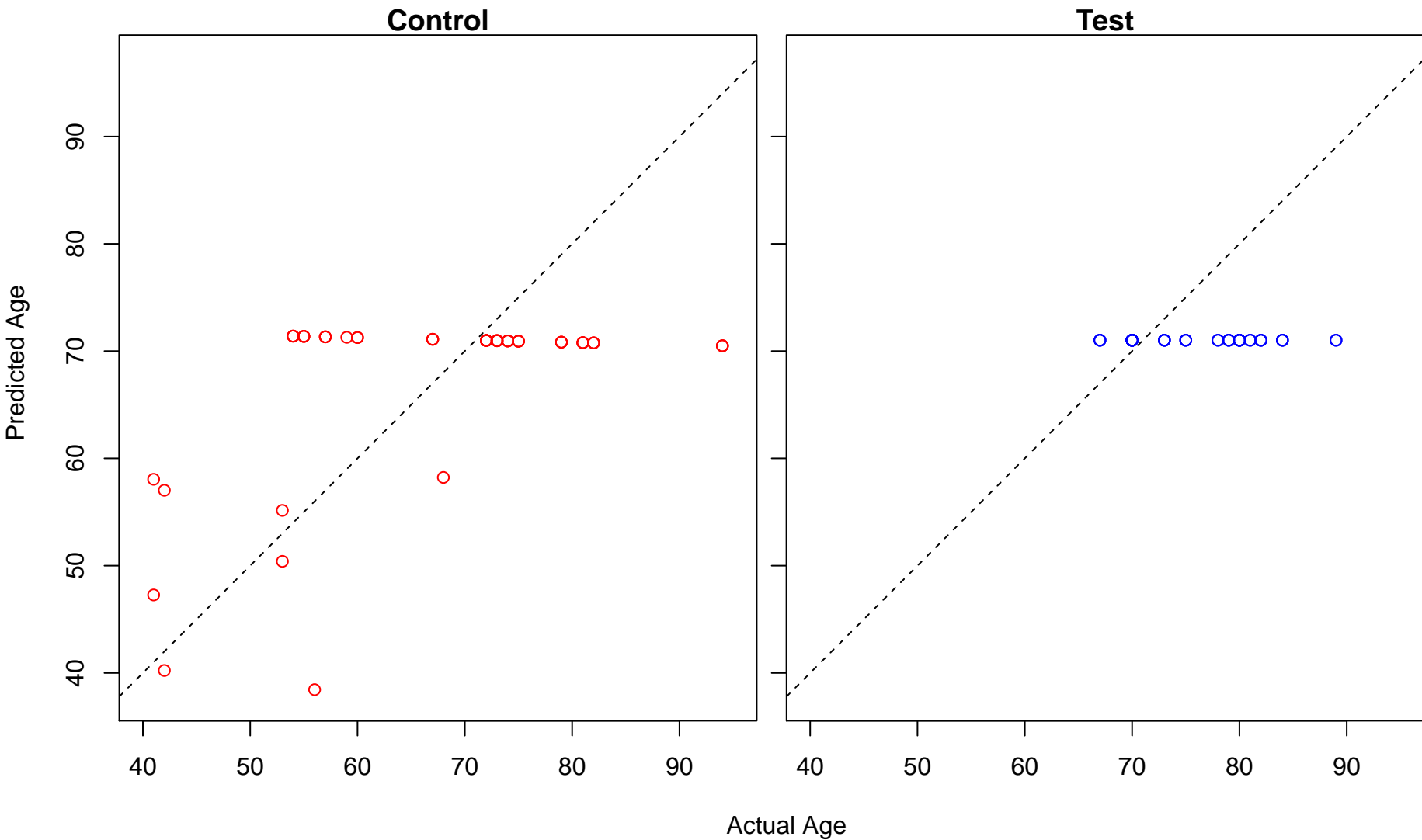
DNA damage checkpoint (Score: 0.805041)



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

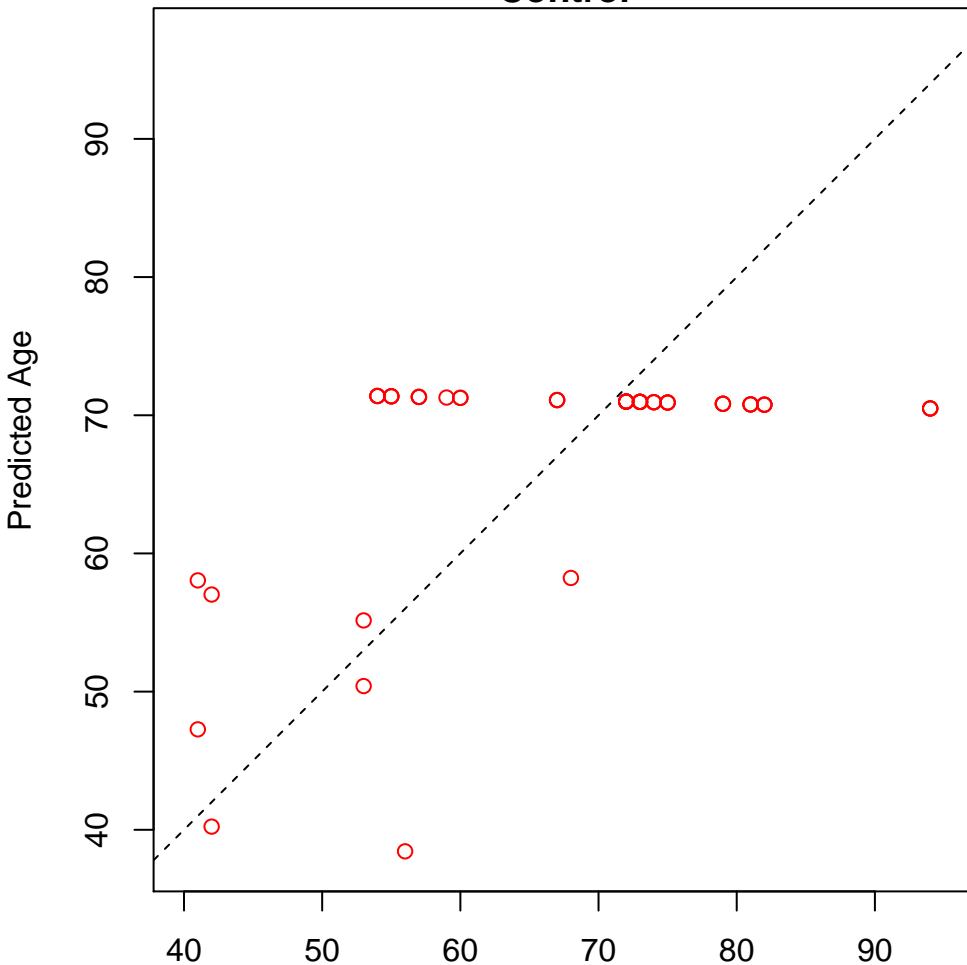


DNA integrity checkpoint (Score: 0.805041)

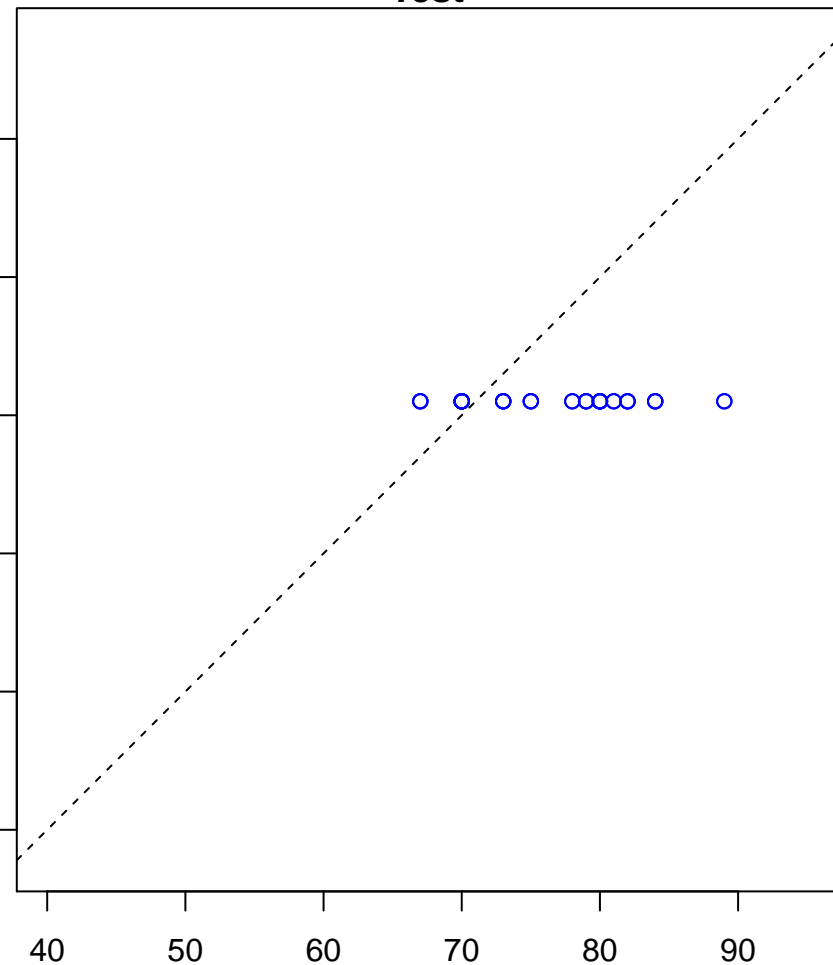


mitotic G1 DNA damage checkpoint (Score: 0.805041)

Control



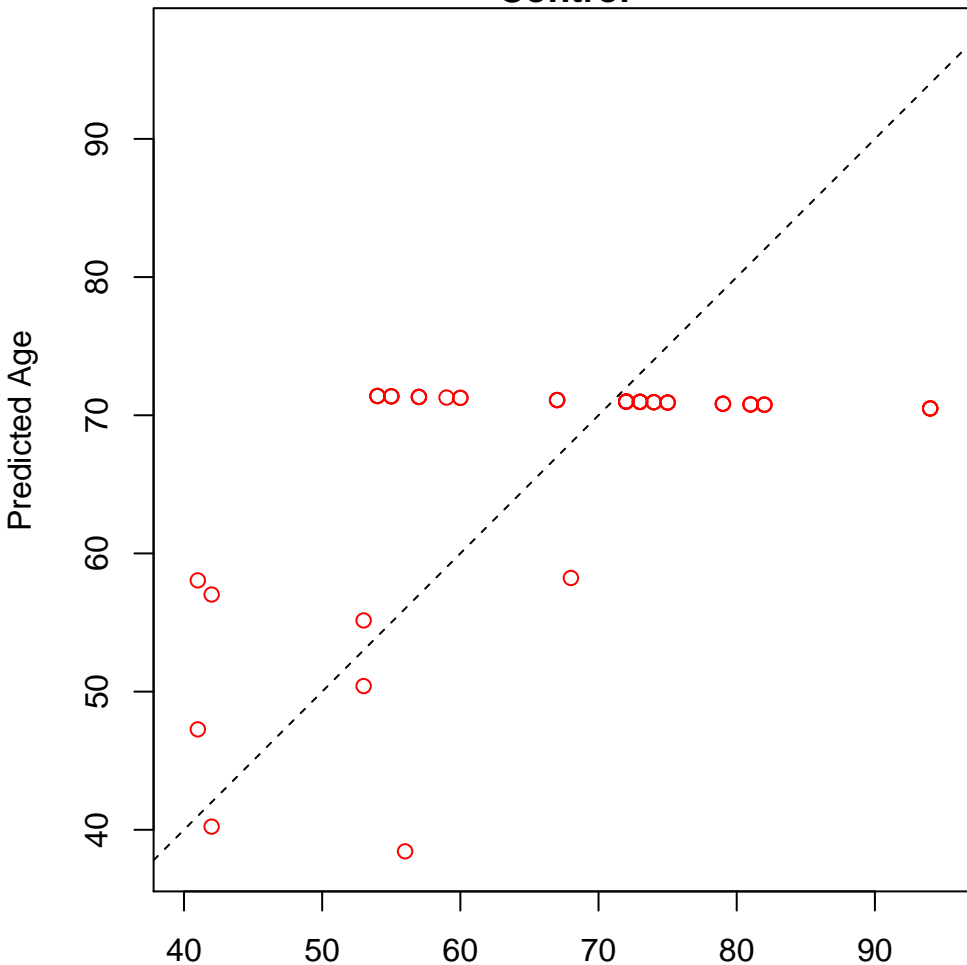
Test



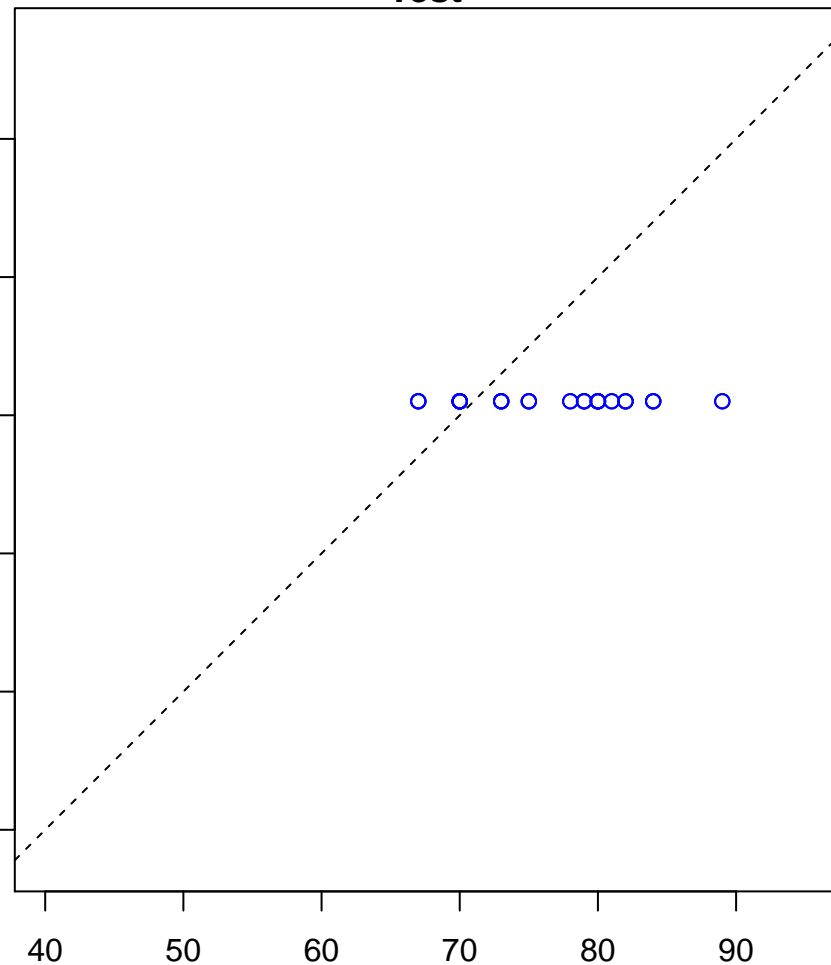
Actual Age

mitotic DNA damage checkpoint (Score: 0.805041)

Control

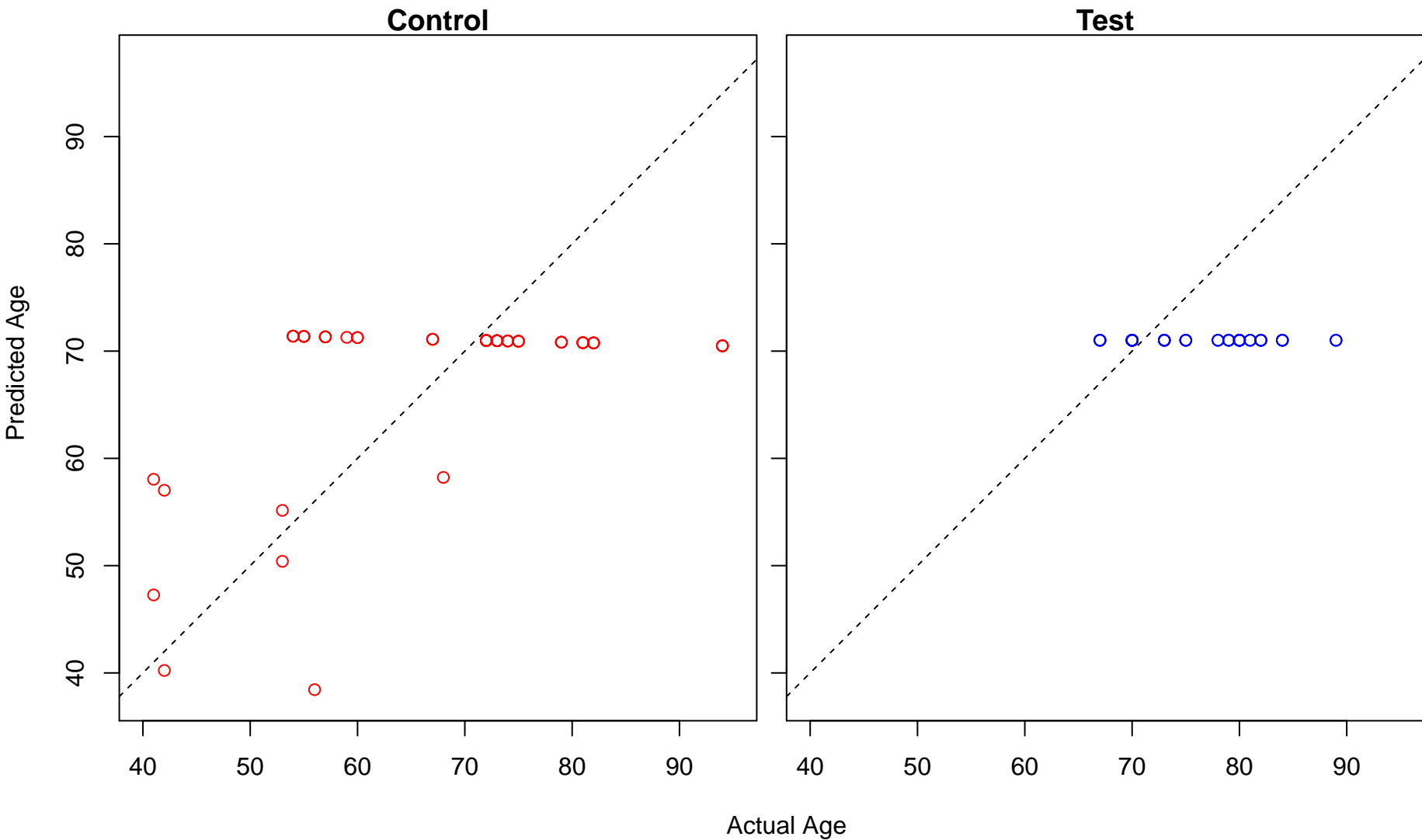


Test

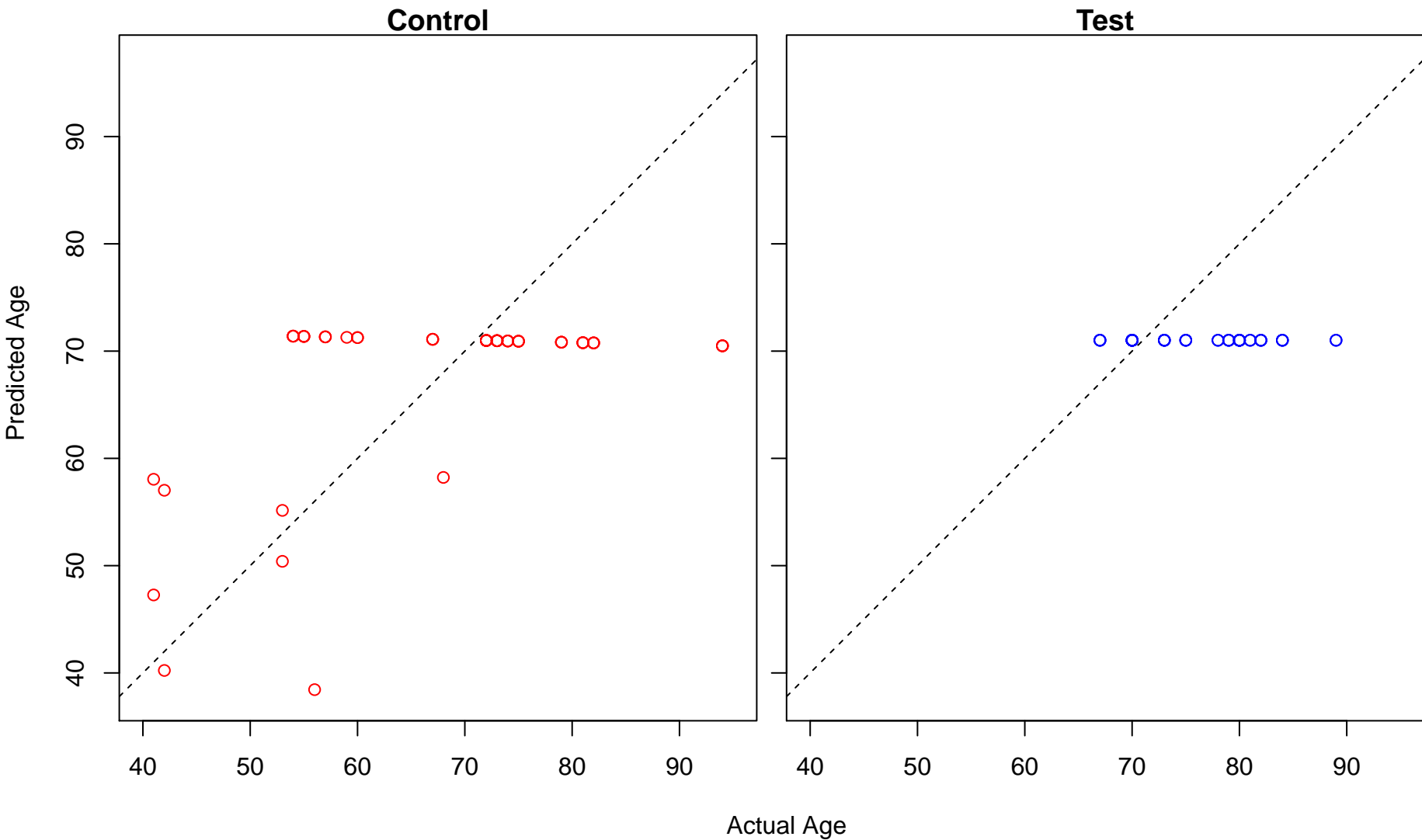


Actual Age

mitotic DNA integrity checkpoint (Score: 0.805041)

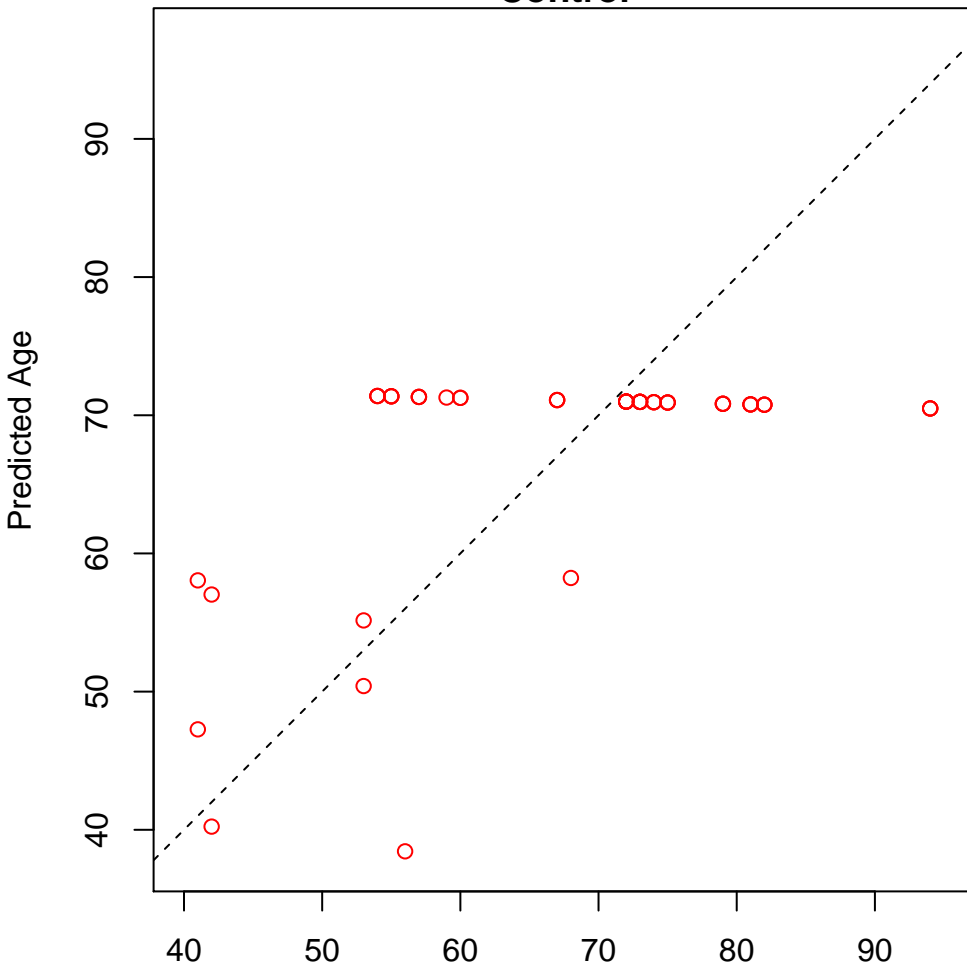


G1 DNA damage checkpoint (Score: 0.805041)

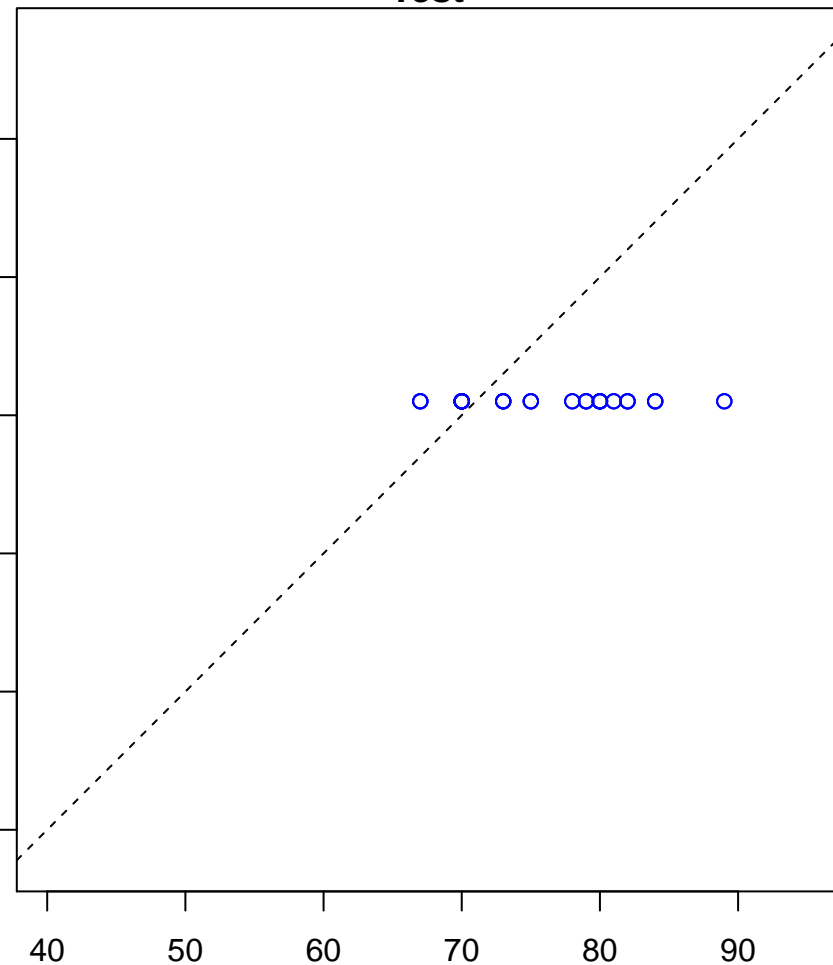


mitotic G1/S transition checkpoint (Score: 0.805041)

Control



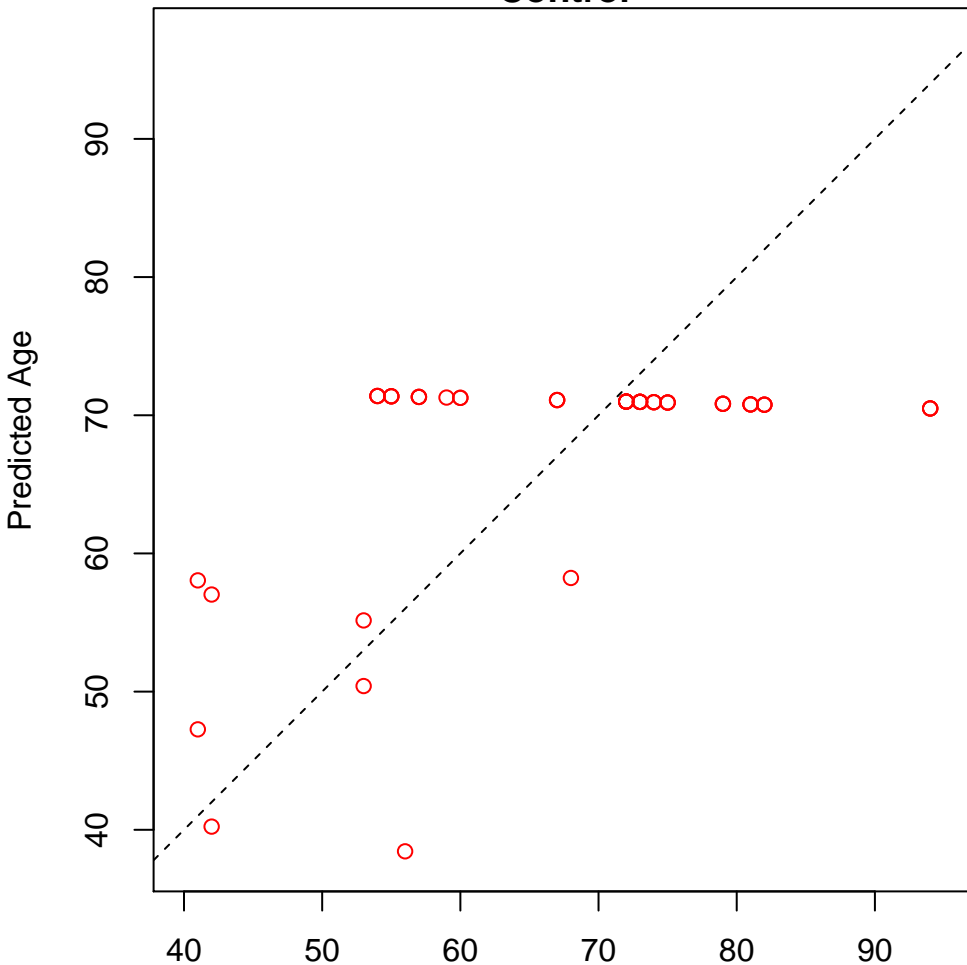
Test



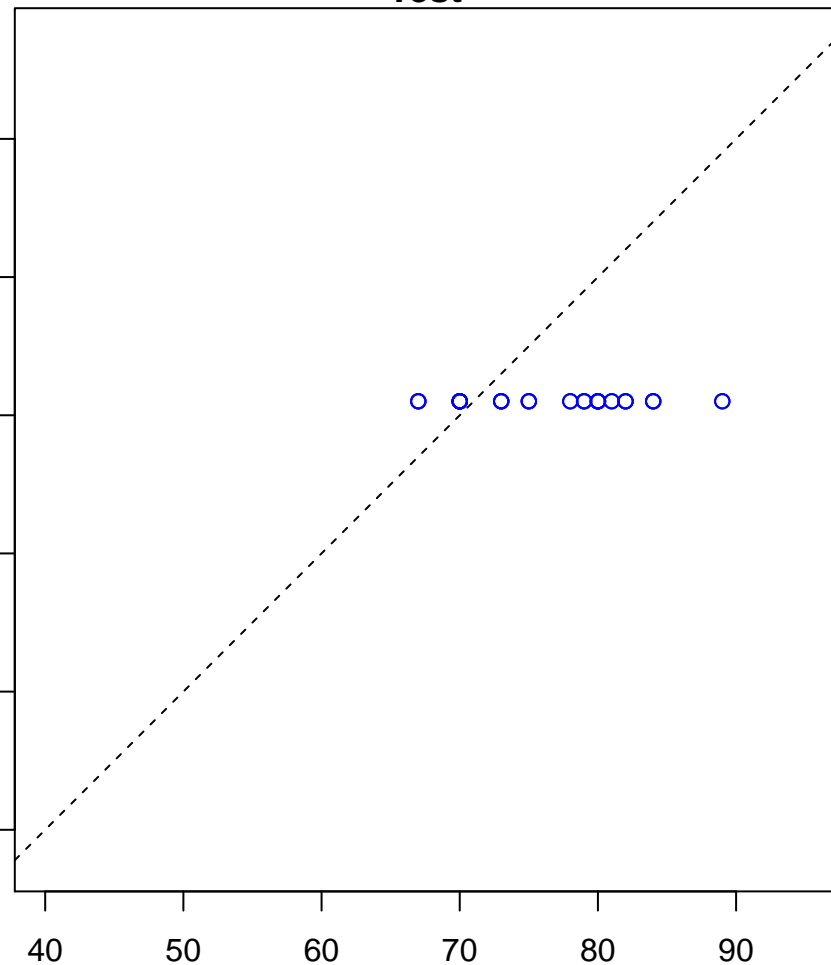
Actual Age

positive regulation of cell cycle arrest (Score: 0.805041)

Control

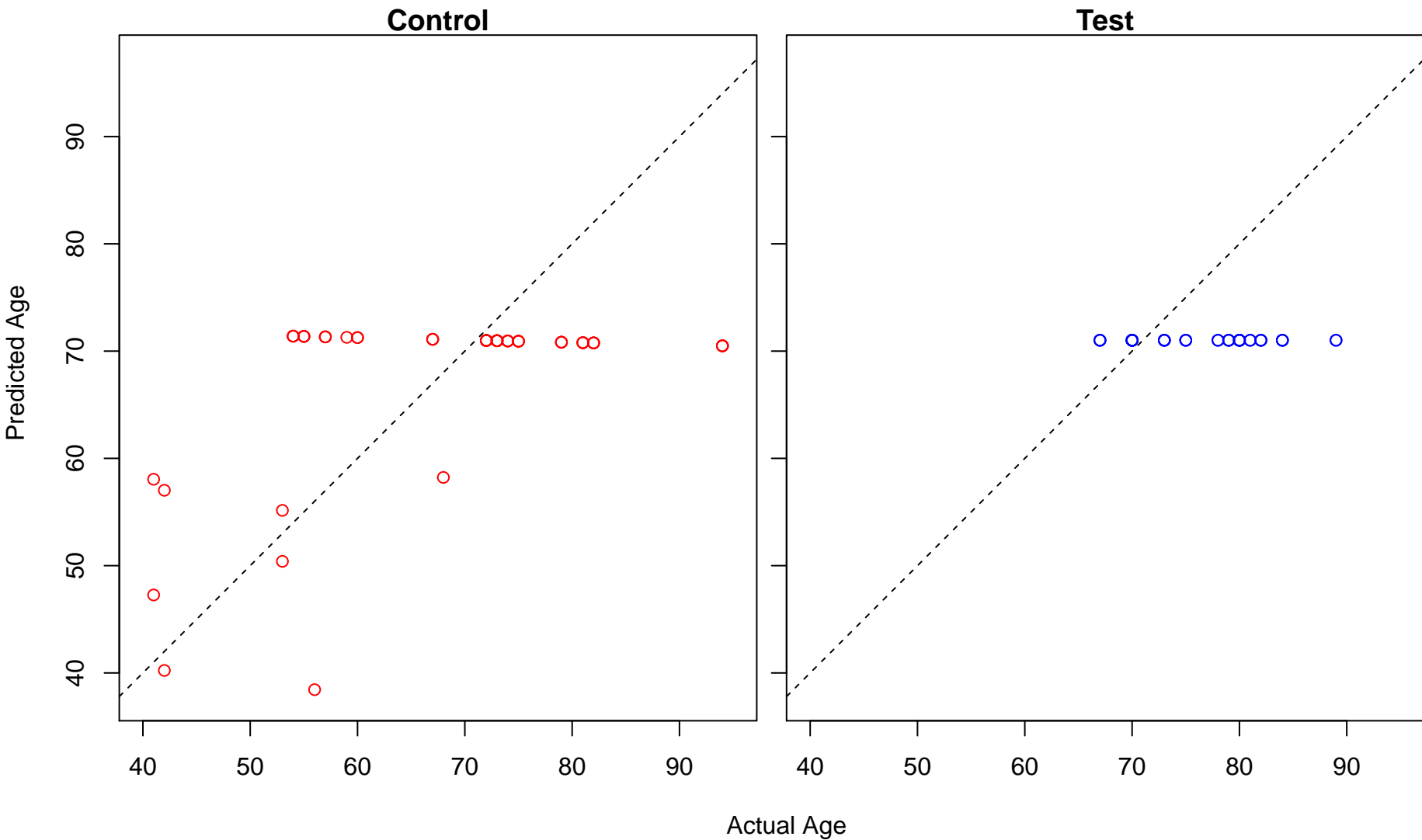


Test

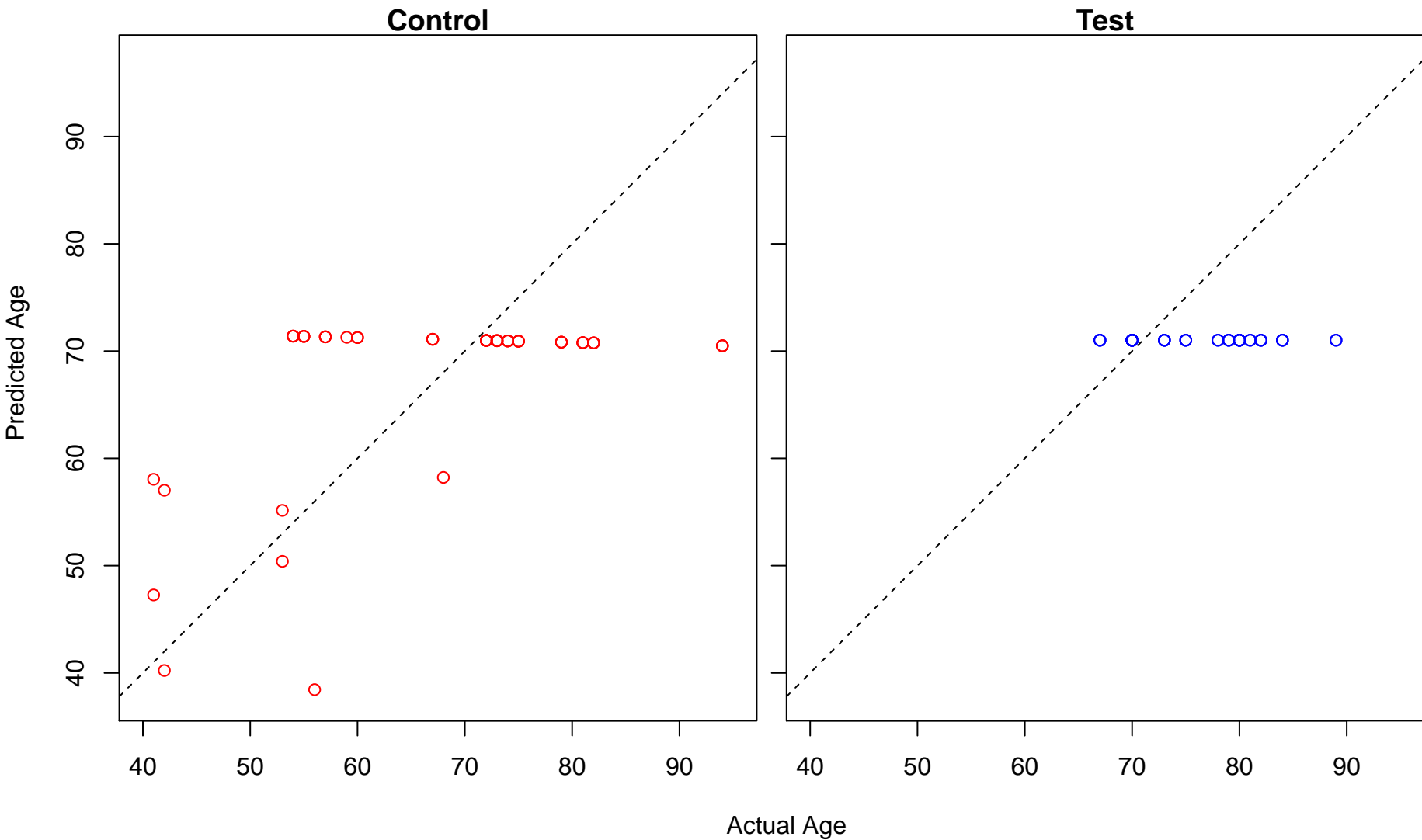


Actual Age

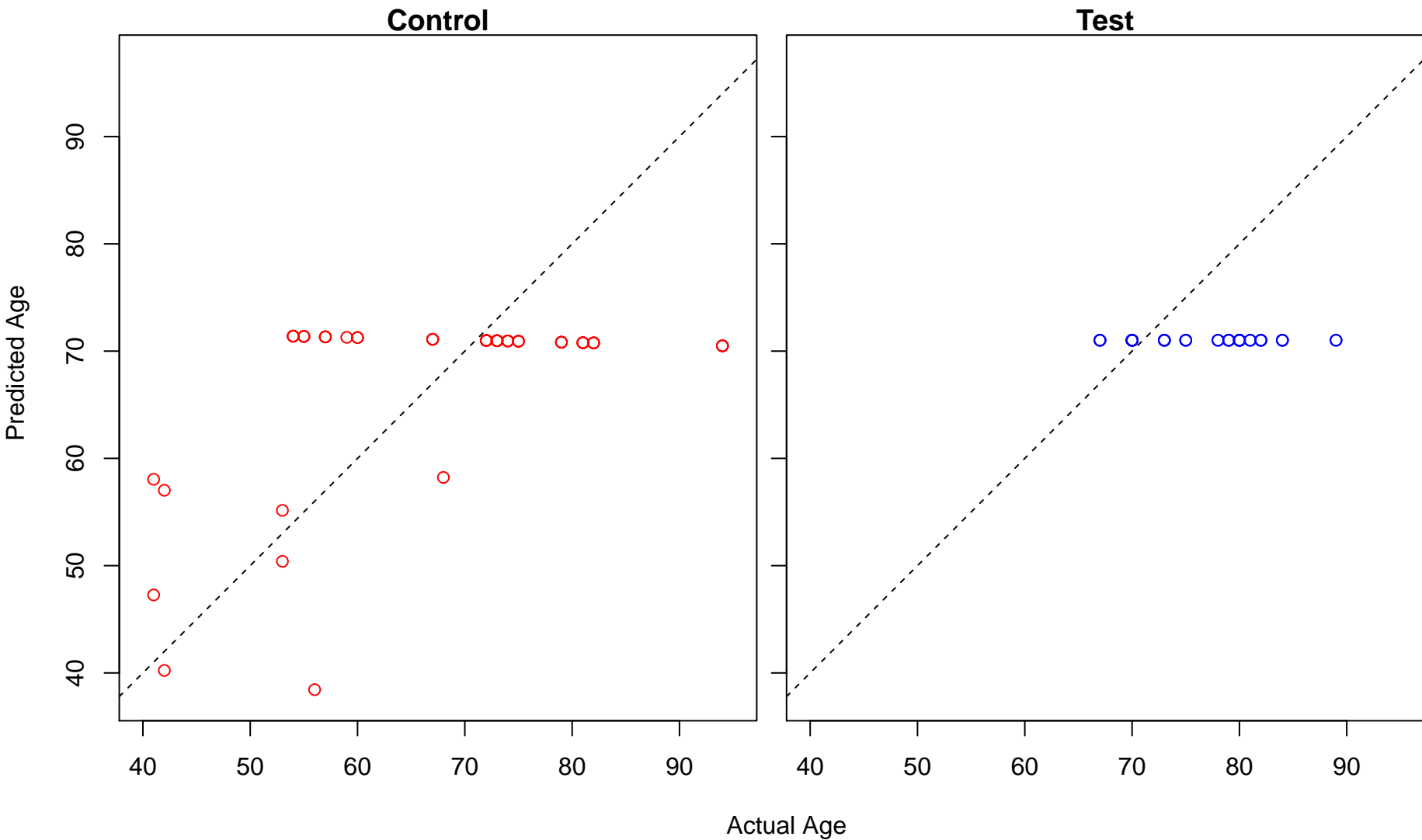
signal transduction involved in cell cycle checkpoint (Score: 0.805041)



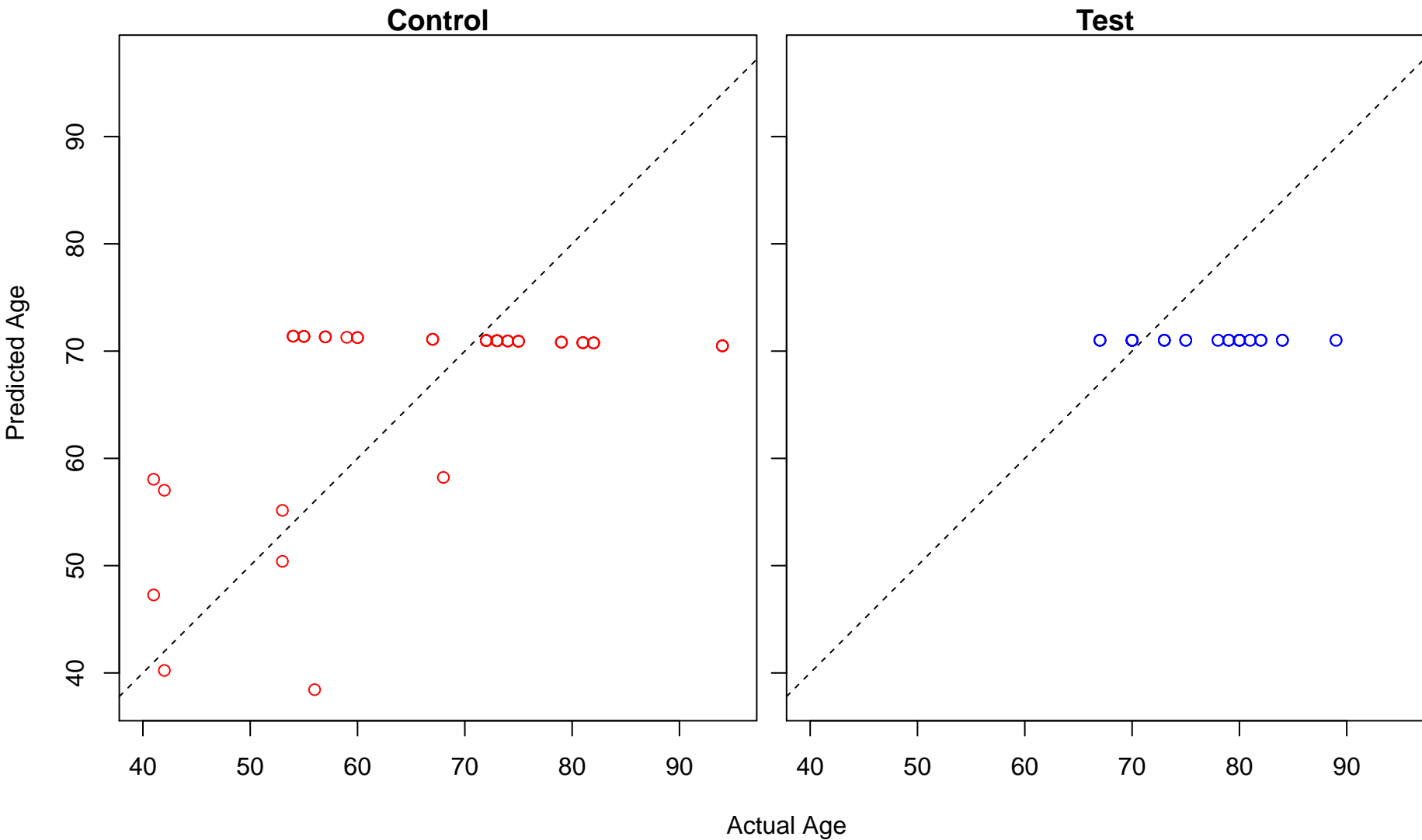
signal transduction involved in DNA integrity checkpoint (Score: 0.805041)



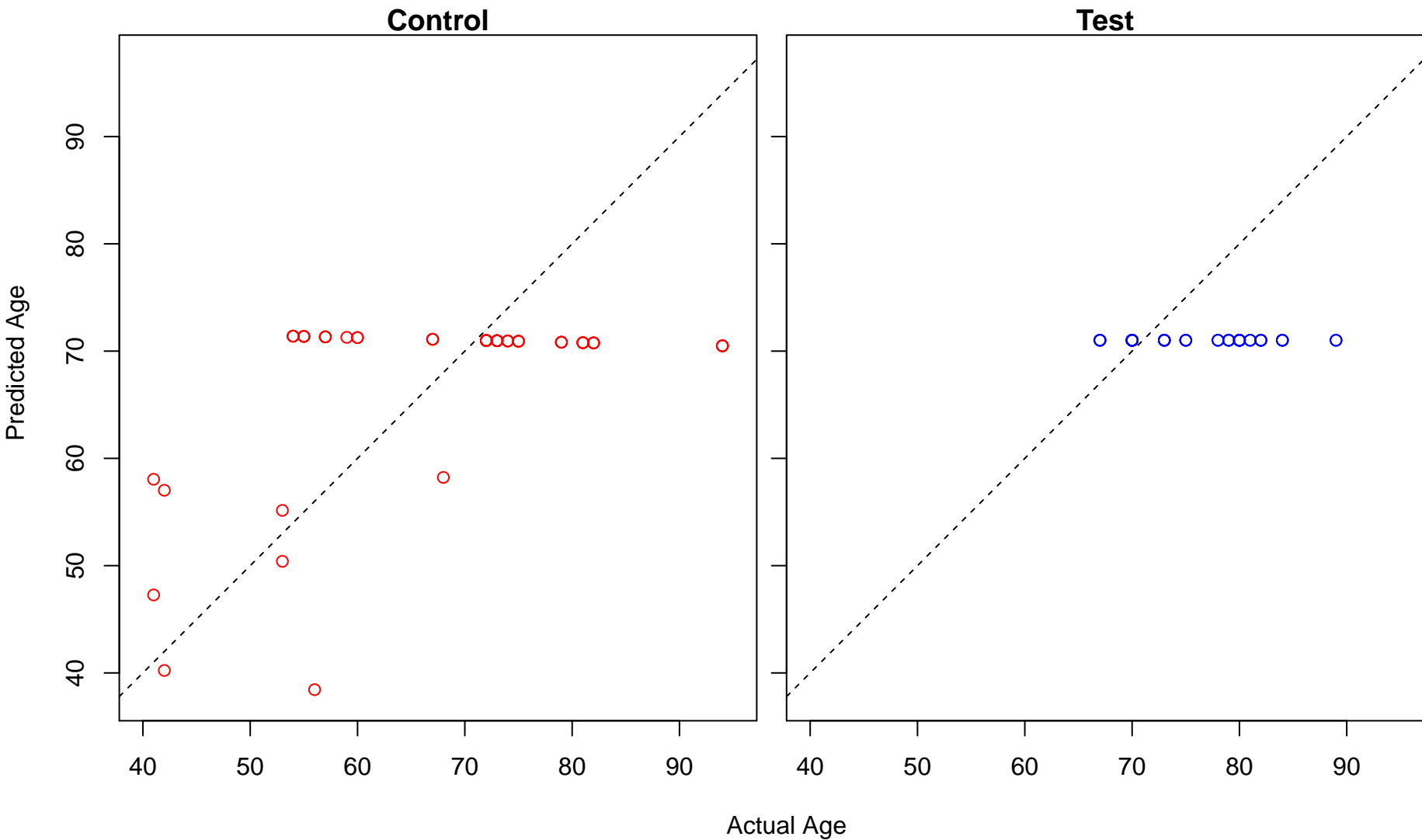
signal transduction involved in mitotic cell cycle checkpoint (Score: 0.805041)



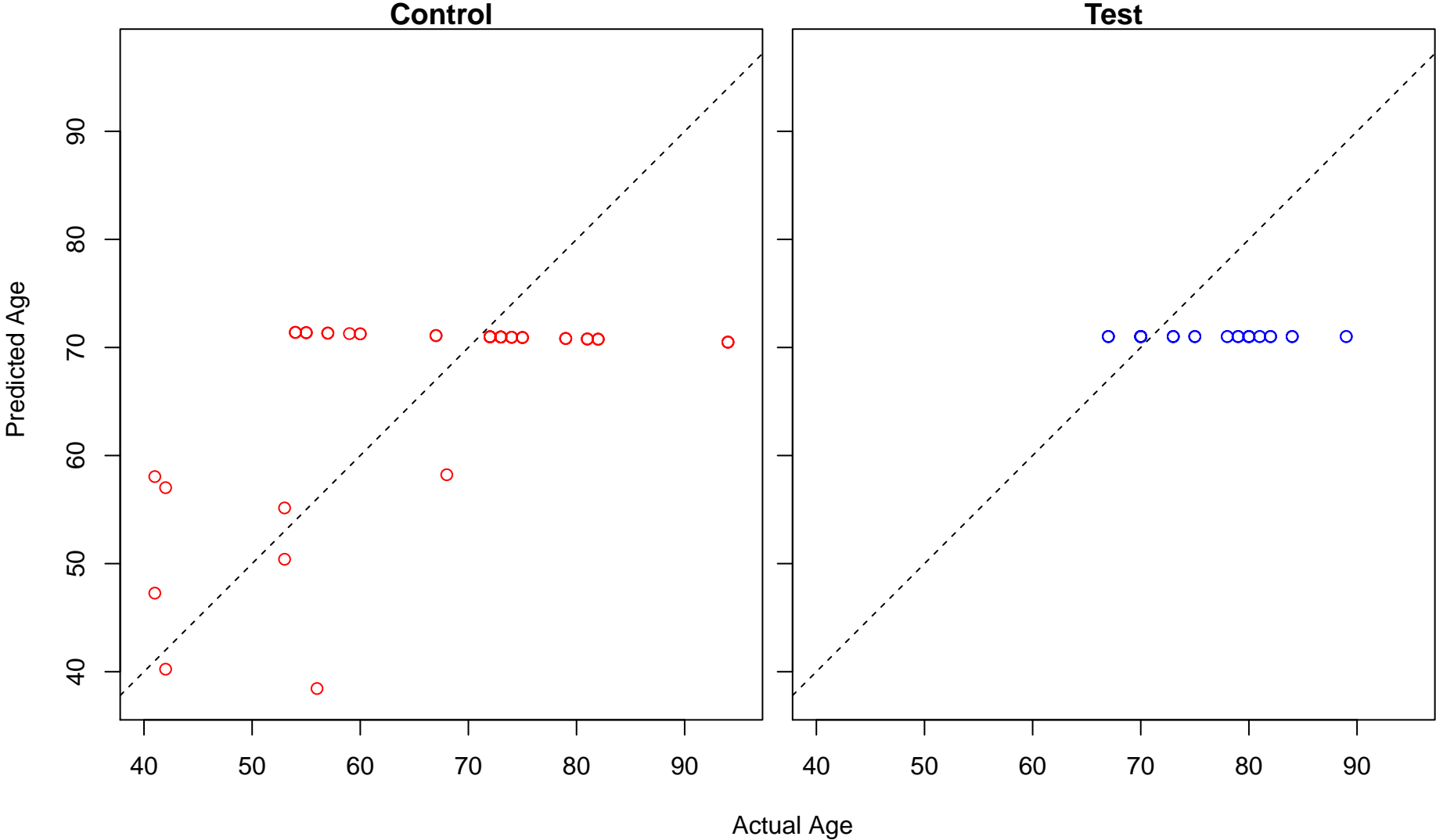
signal transduction involved in DNA damage checkpoint (Score: 0.805041)



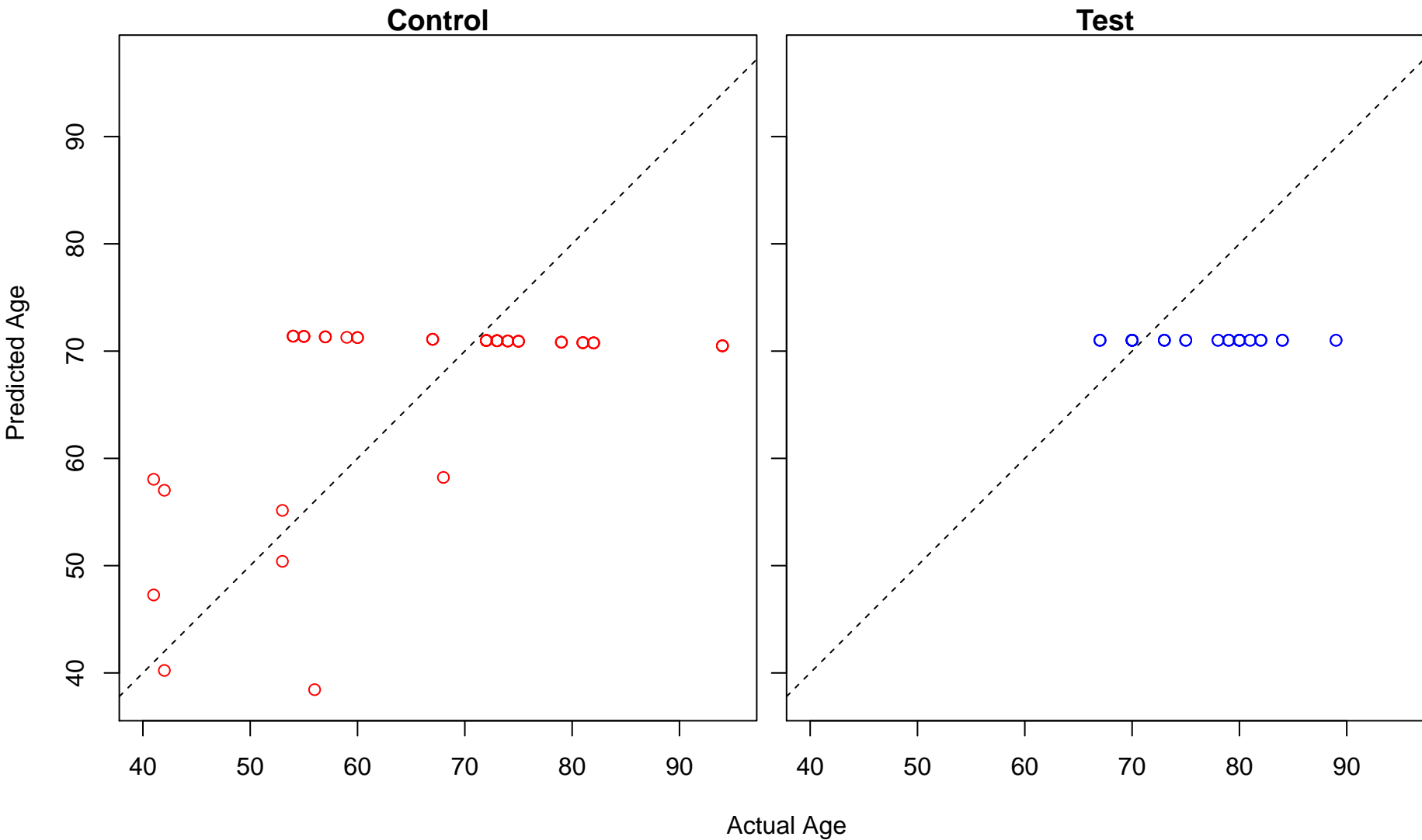
signal transduction involved in mitotic G1 DNA damage checkpoint (Score: 0.805041)



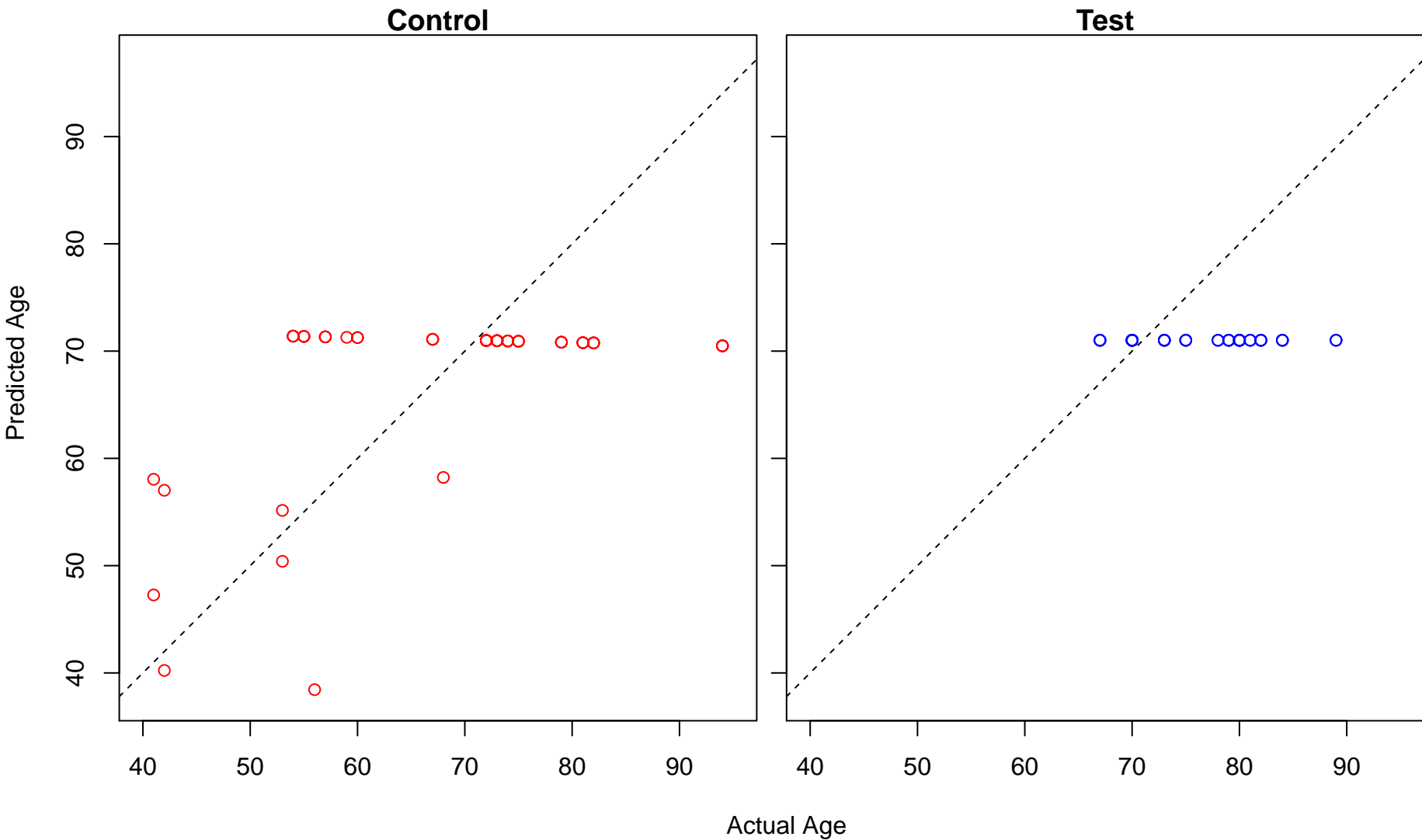
intracellular signal transduction involved in G1 DNA damage checkpoint (Score: 0.805041)



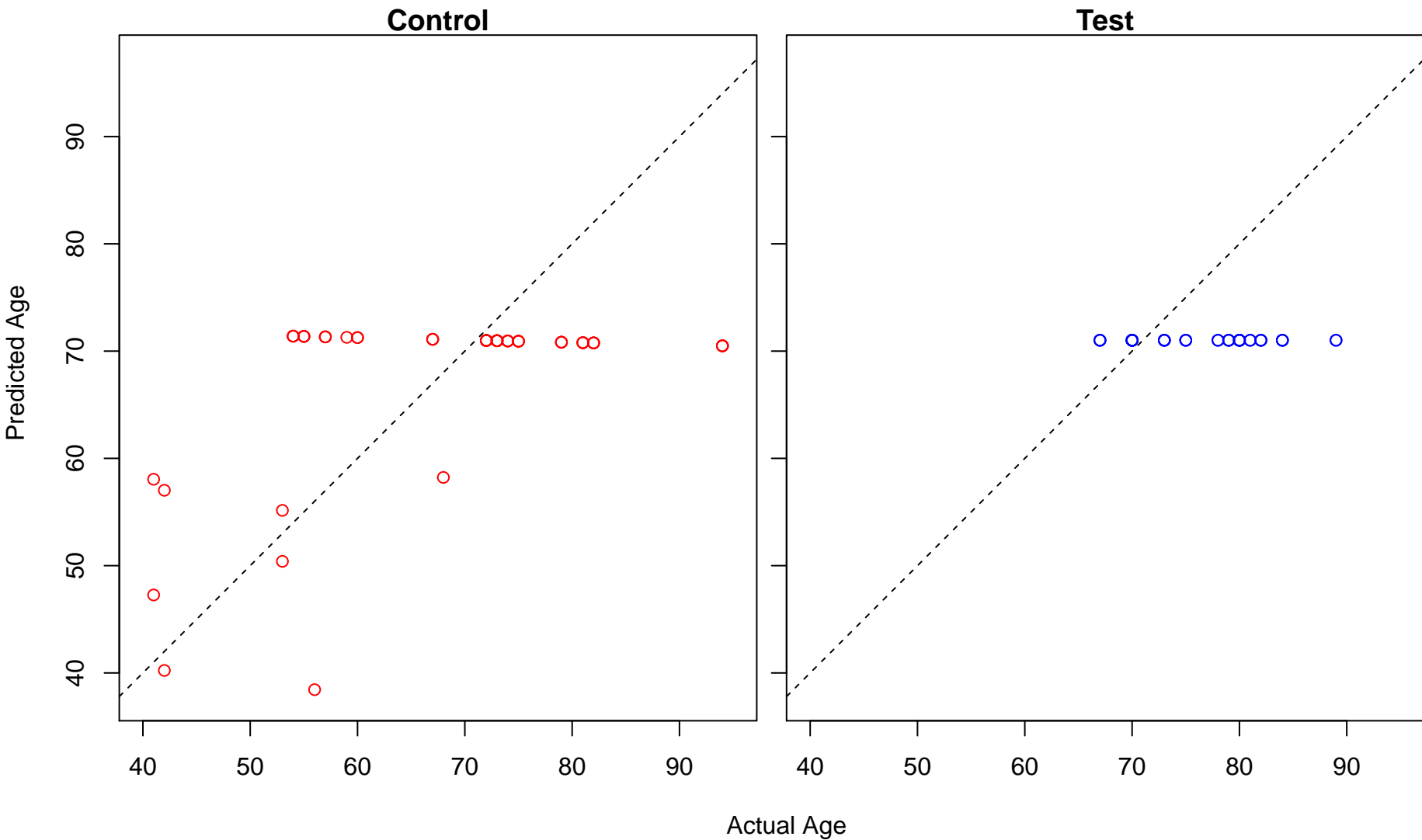
signal transduction involved in mitotic DNA damage checkpoint (Score: 0.805041)



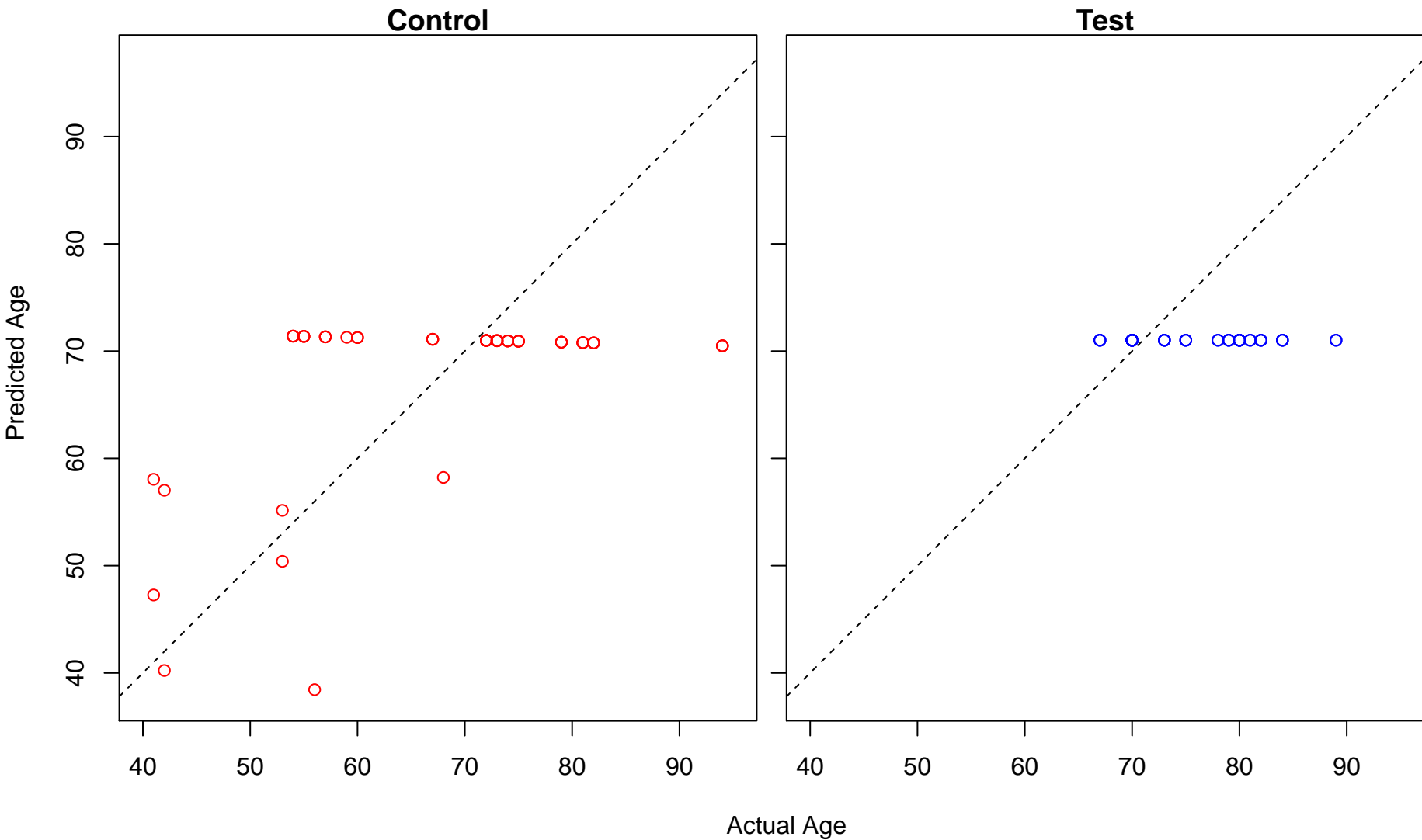
signal transduction involved in mitotic DNA integrity checkpoint (Score: 0.805041)



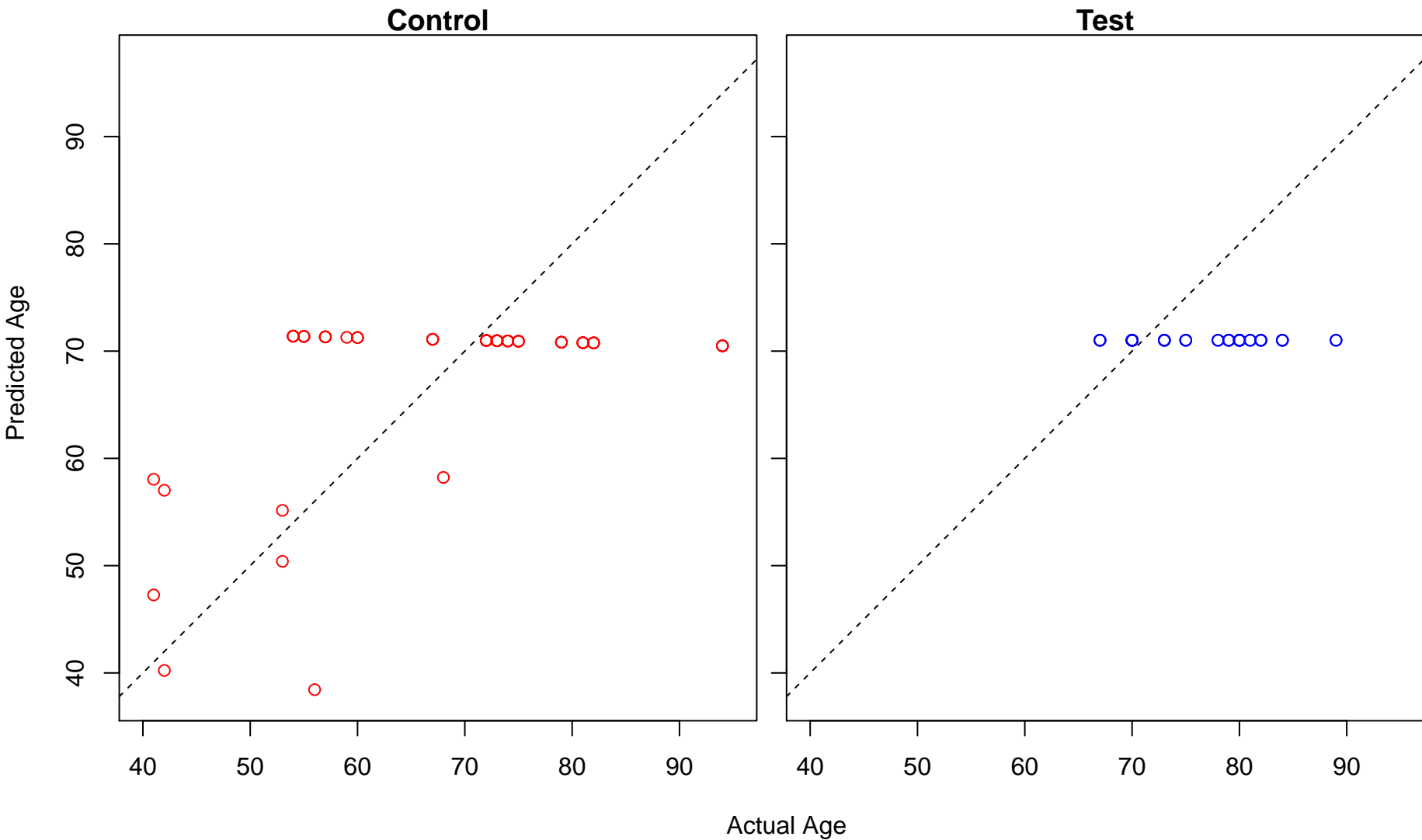
regulation of cell cycle G1/S phase transition (Score: 0.805041)



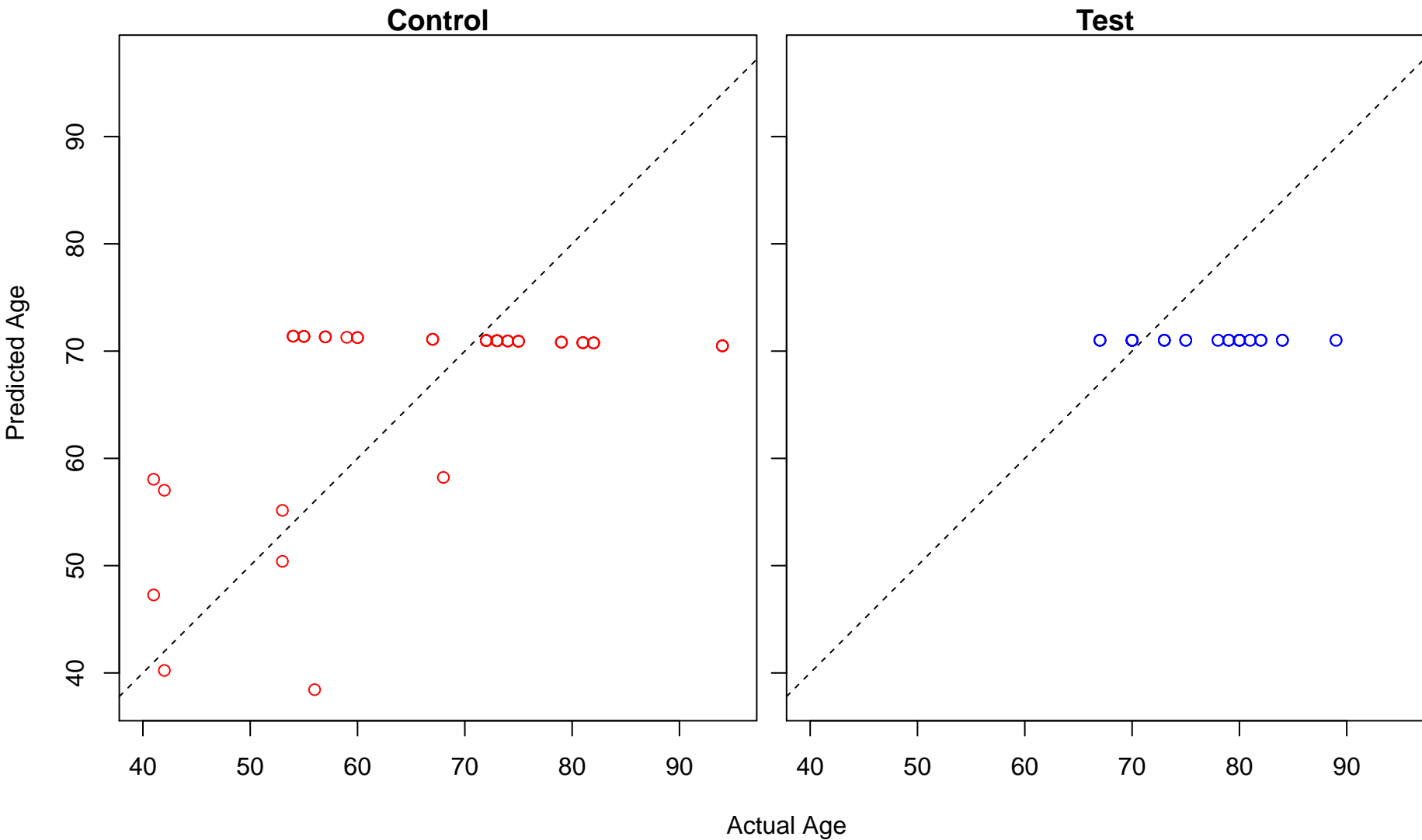
negative regulation of cell cycle G1/S phase transition (Score: 0.805041)



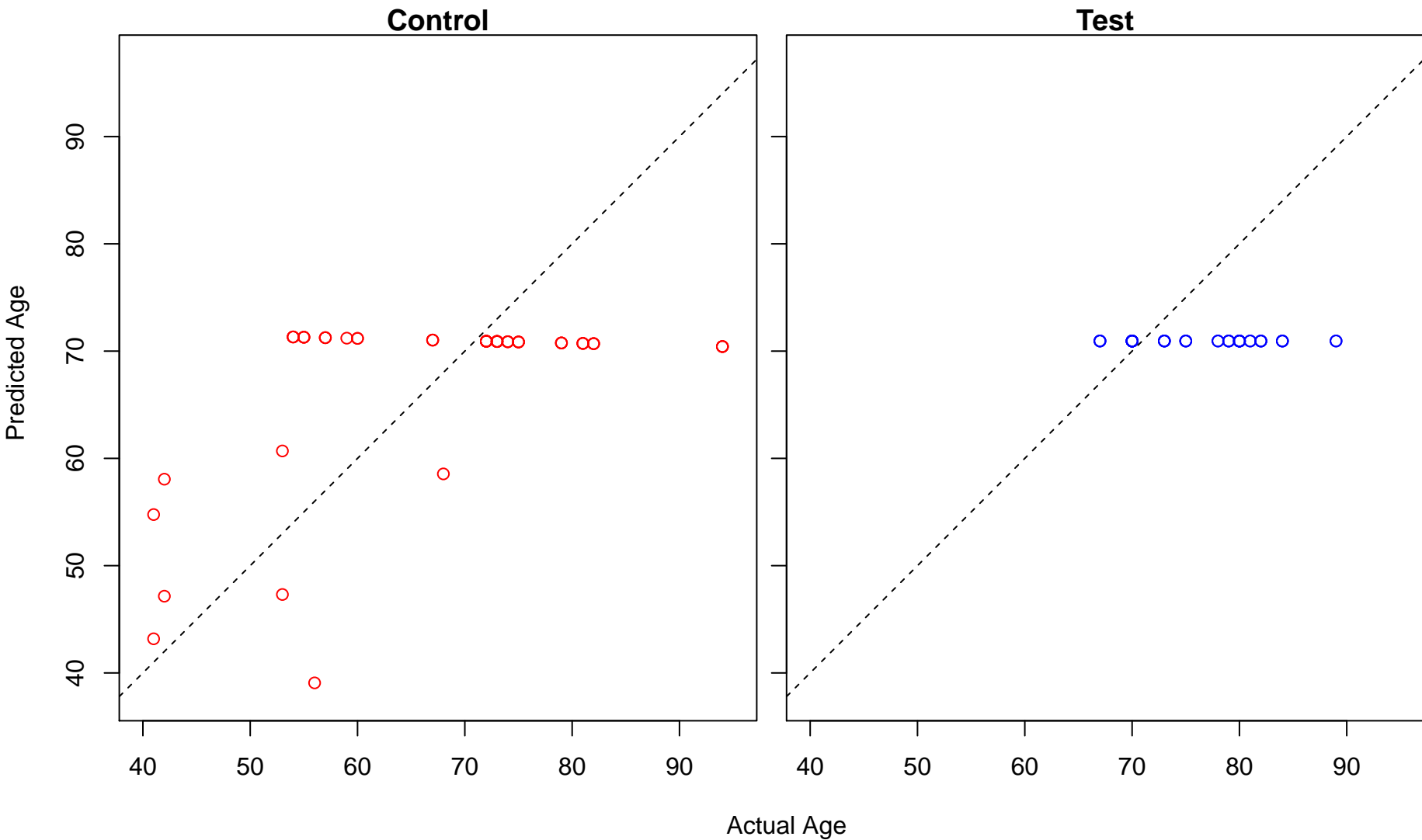
regulation of G1/S transition of mitotic cell cycle (Score: 0.805041)



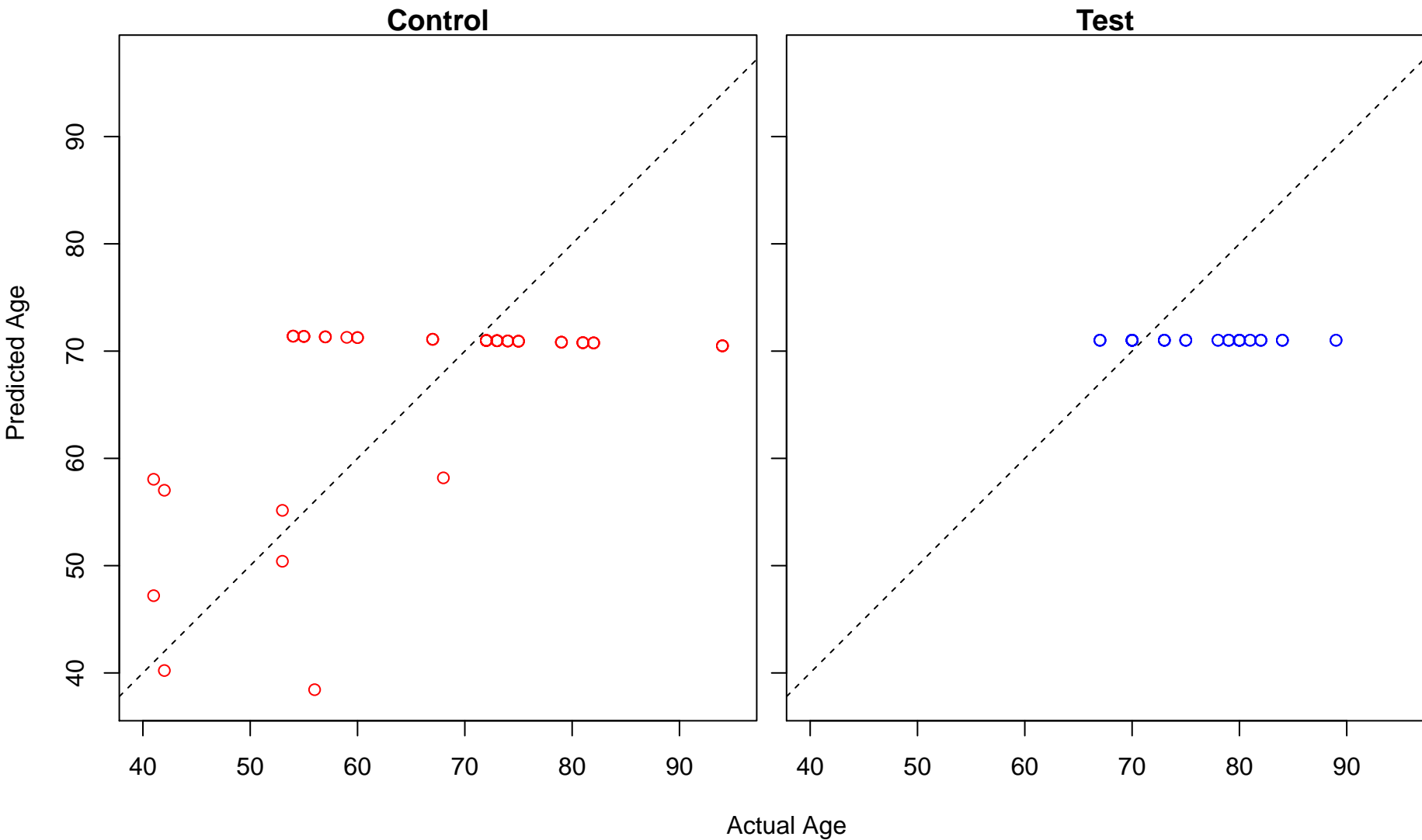
negative regulation of G1/S transition of mitotic cell cycle (Score: 0.805041)



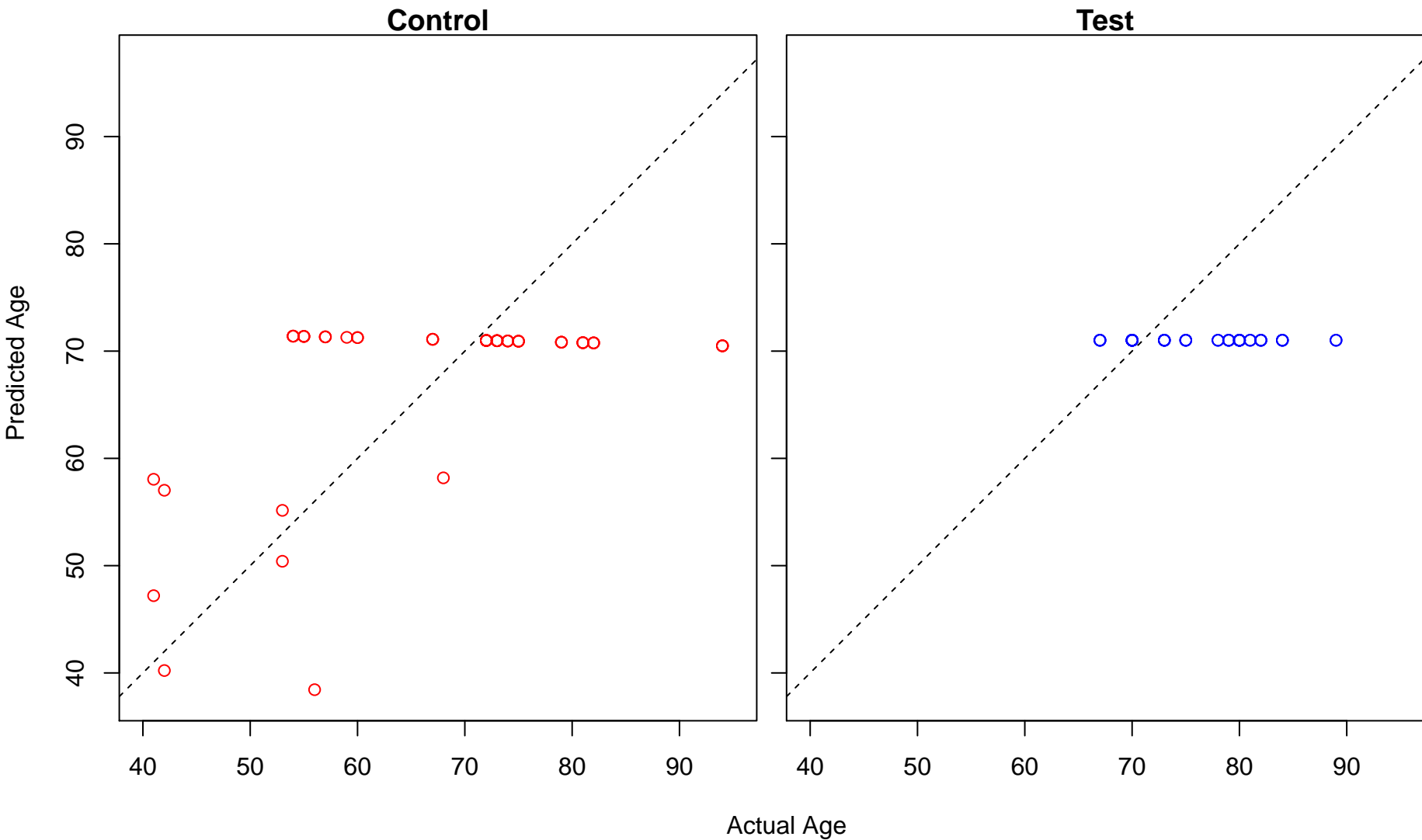
cell adhesion (Score: 0.805012)



cell cycle checkpoint (Score: 0.804996)

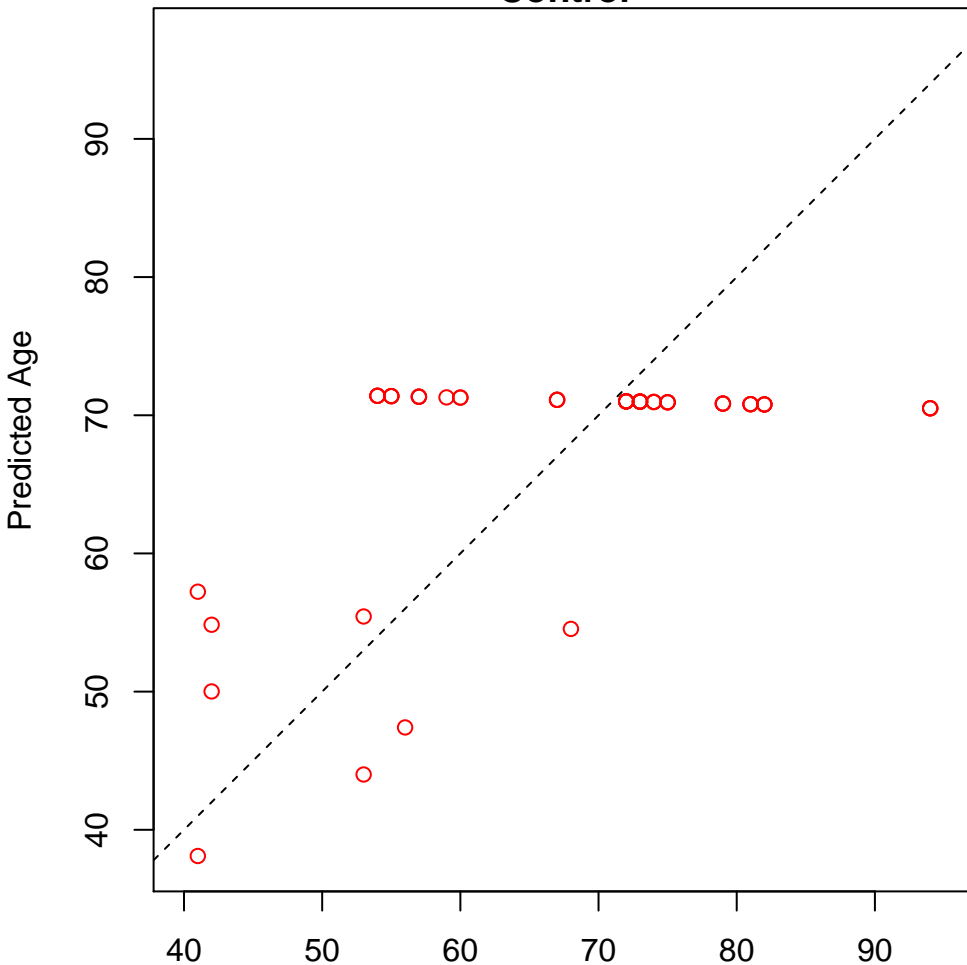


mitotic cell cycle checkpoint (Score: 0.804996)

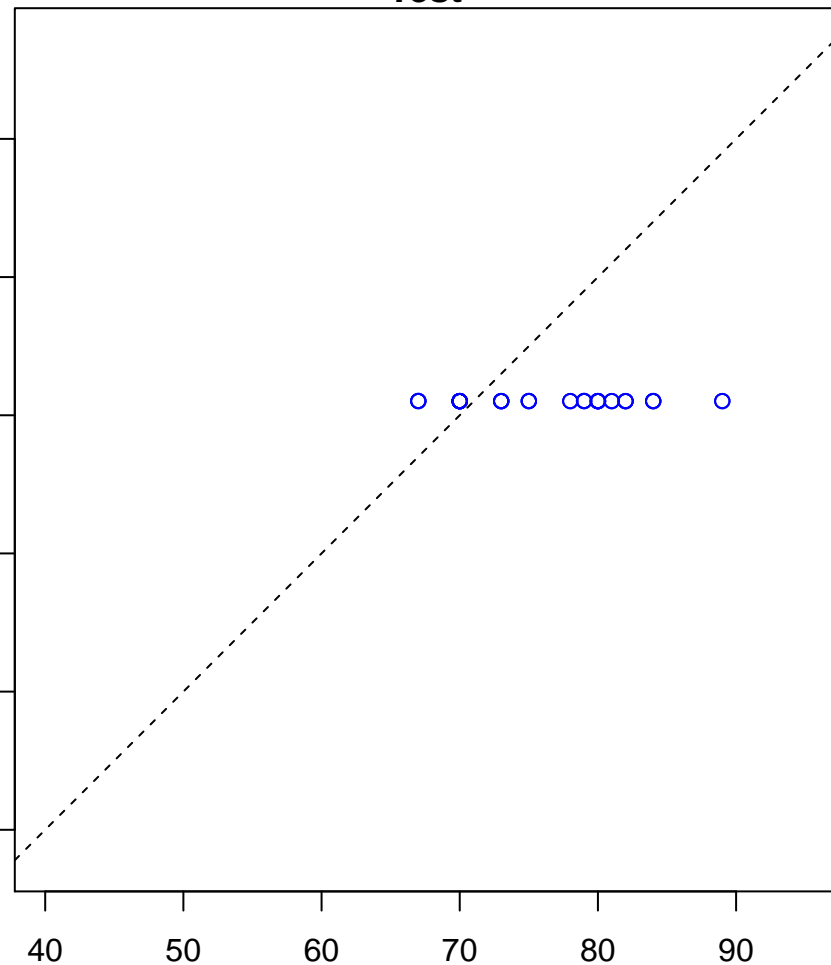


regulation of actin filament depolymerization (Score: 0.804980)

Control

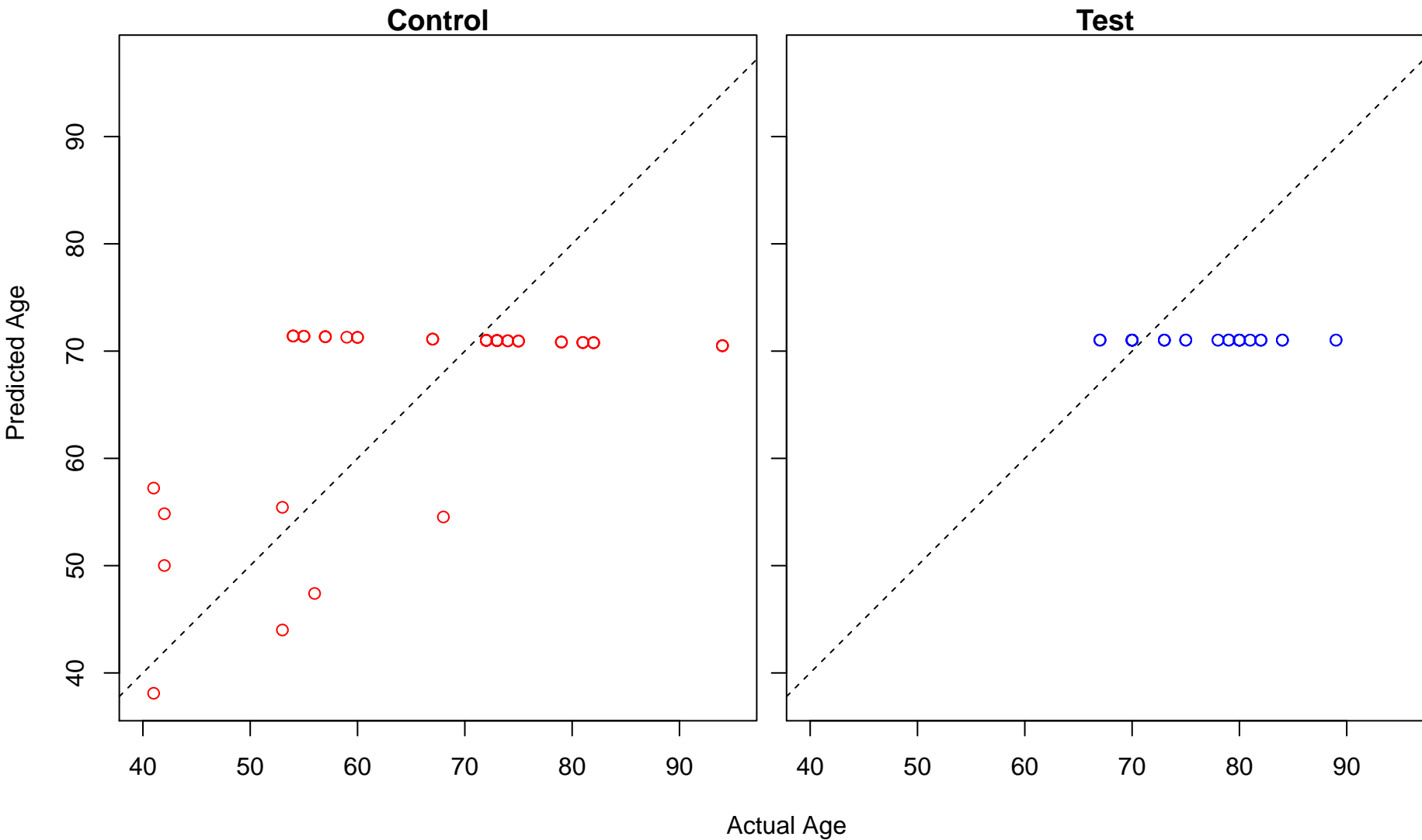


Test



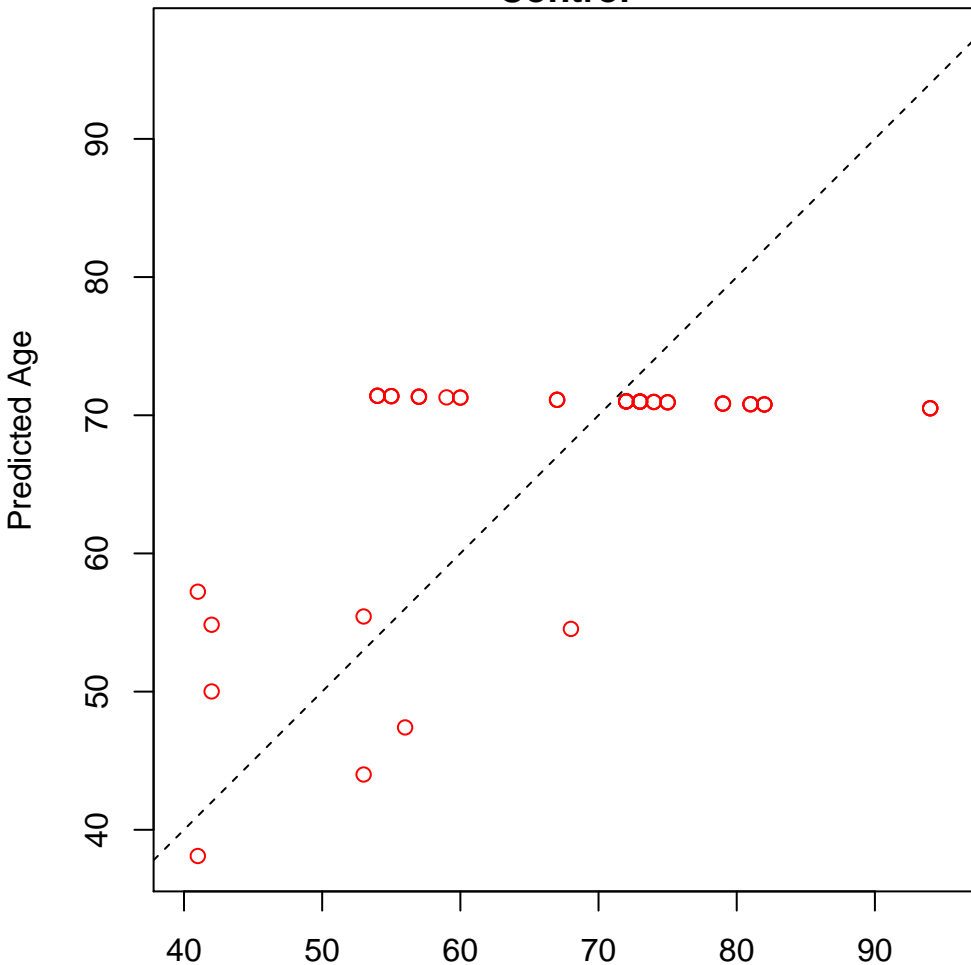
Actual Age

regulation of protein complex disassembly (Score: 0.804980)

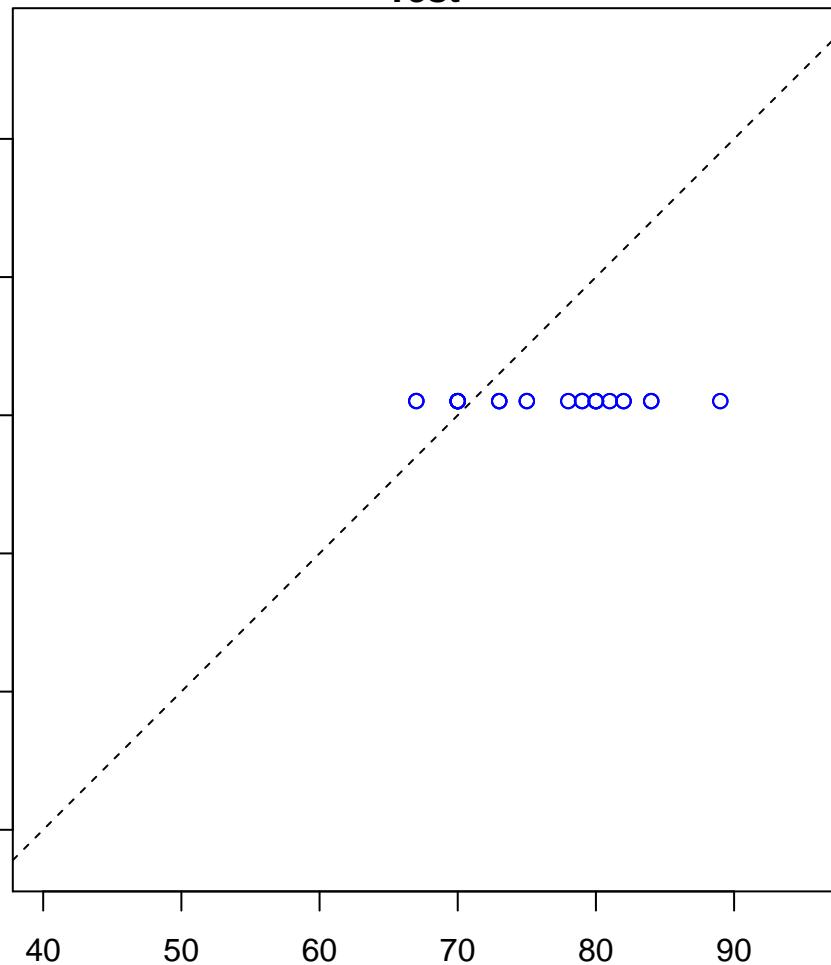


regulation of protein depolymerization (Score: 0.804980)

Control



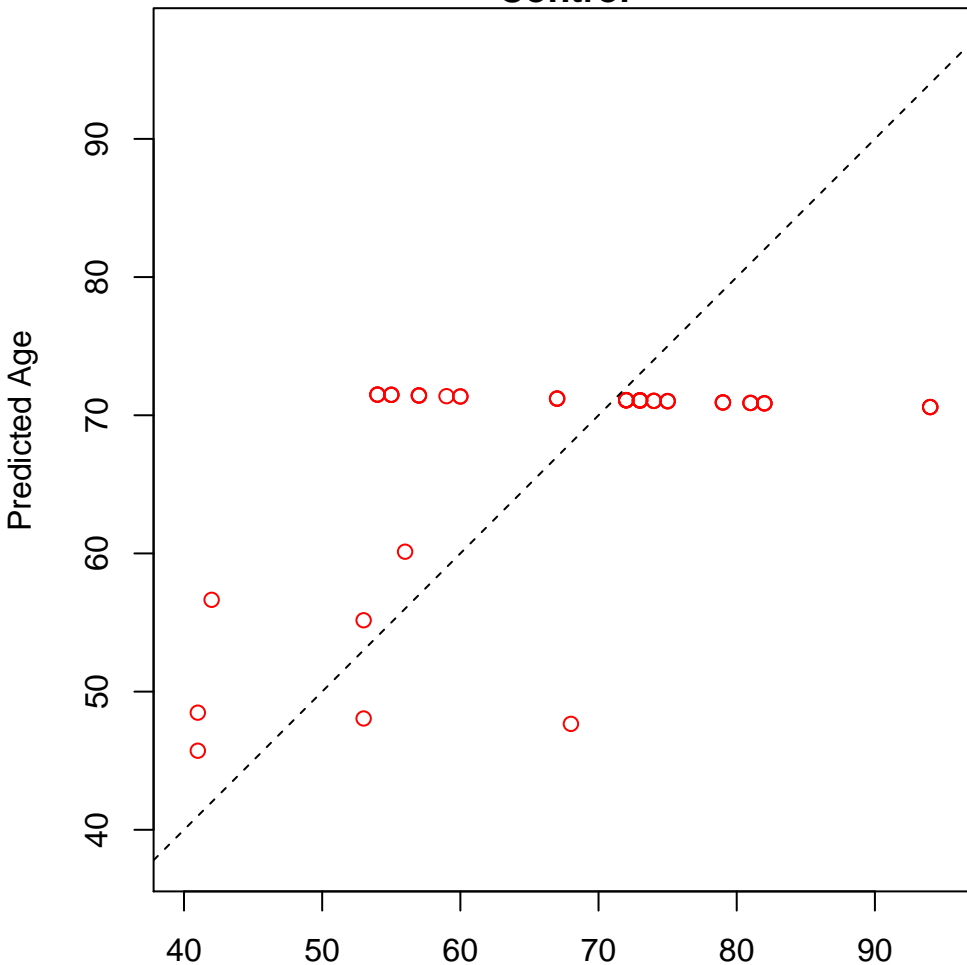
Test



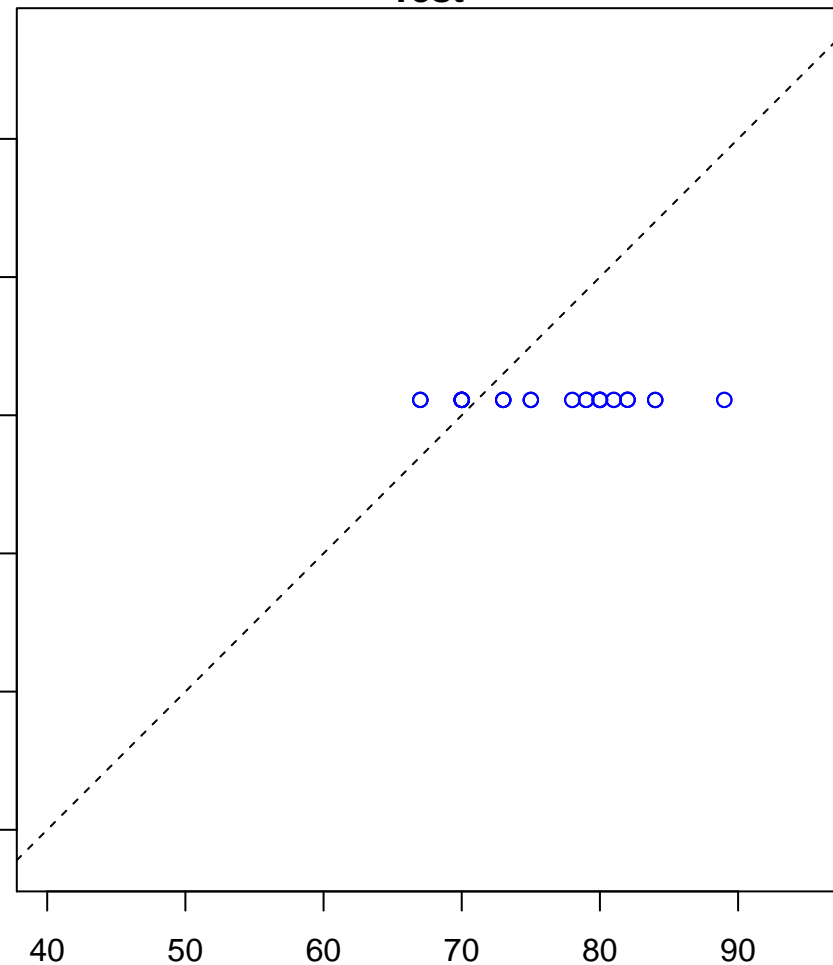
Actual Age

regulation of mitotic spindle organization (Score: 0.804976)

Control



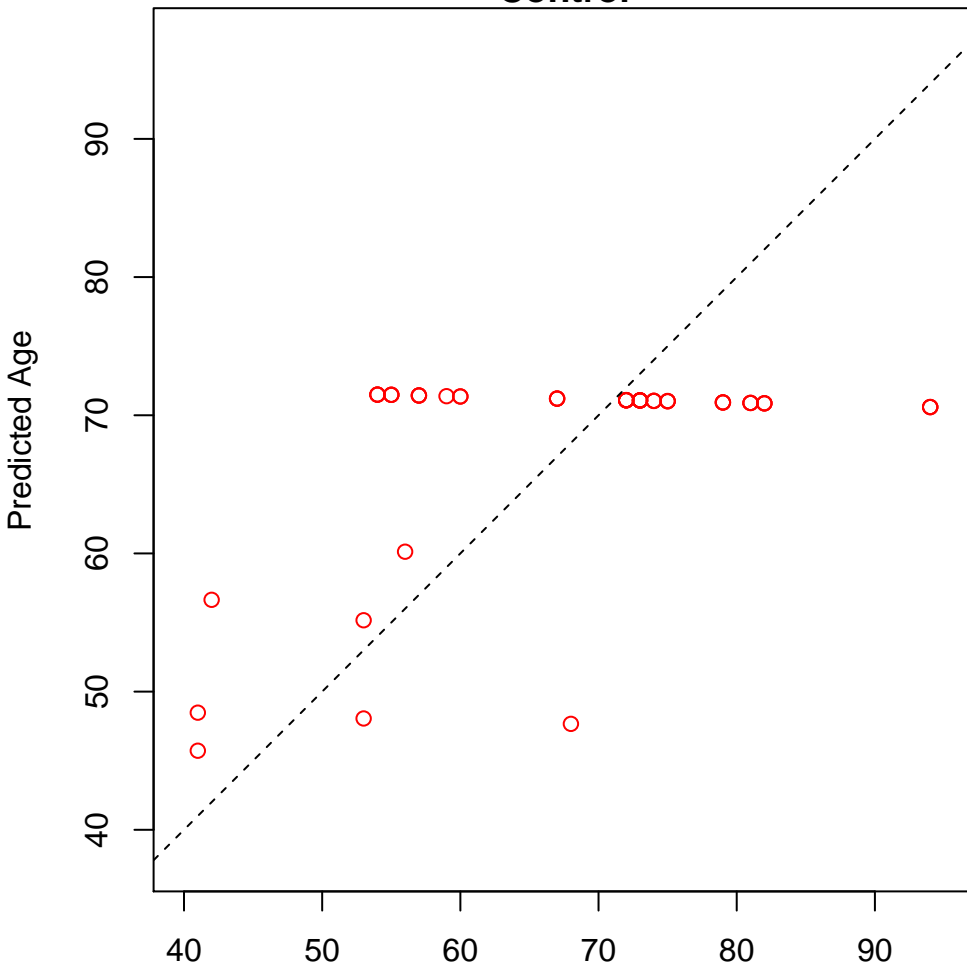
Test



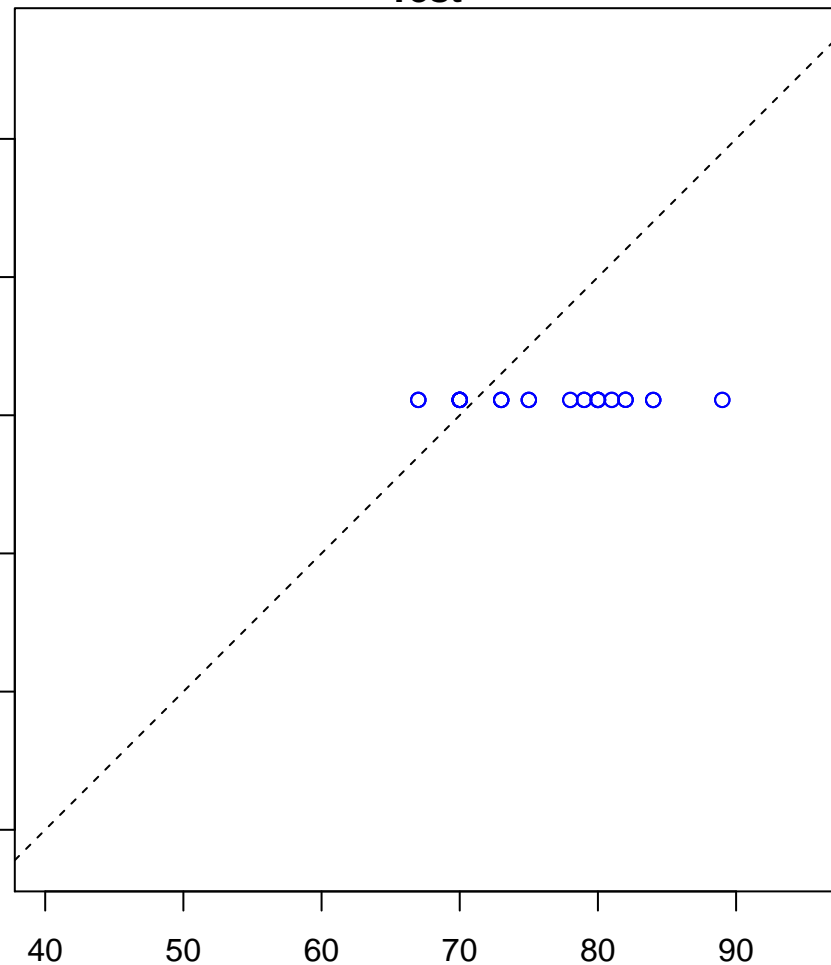
Actual Age

regulation of spindle organization (Score: 0.804976)

Control

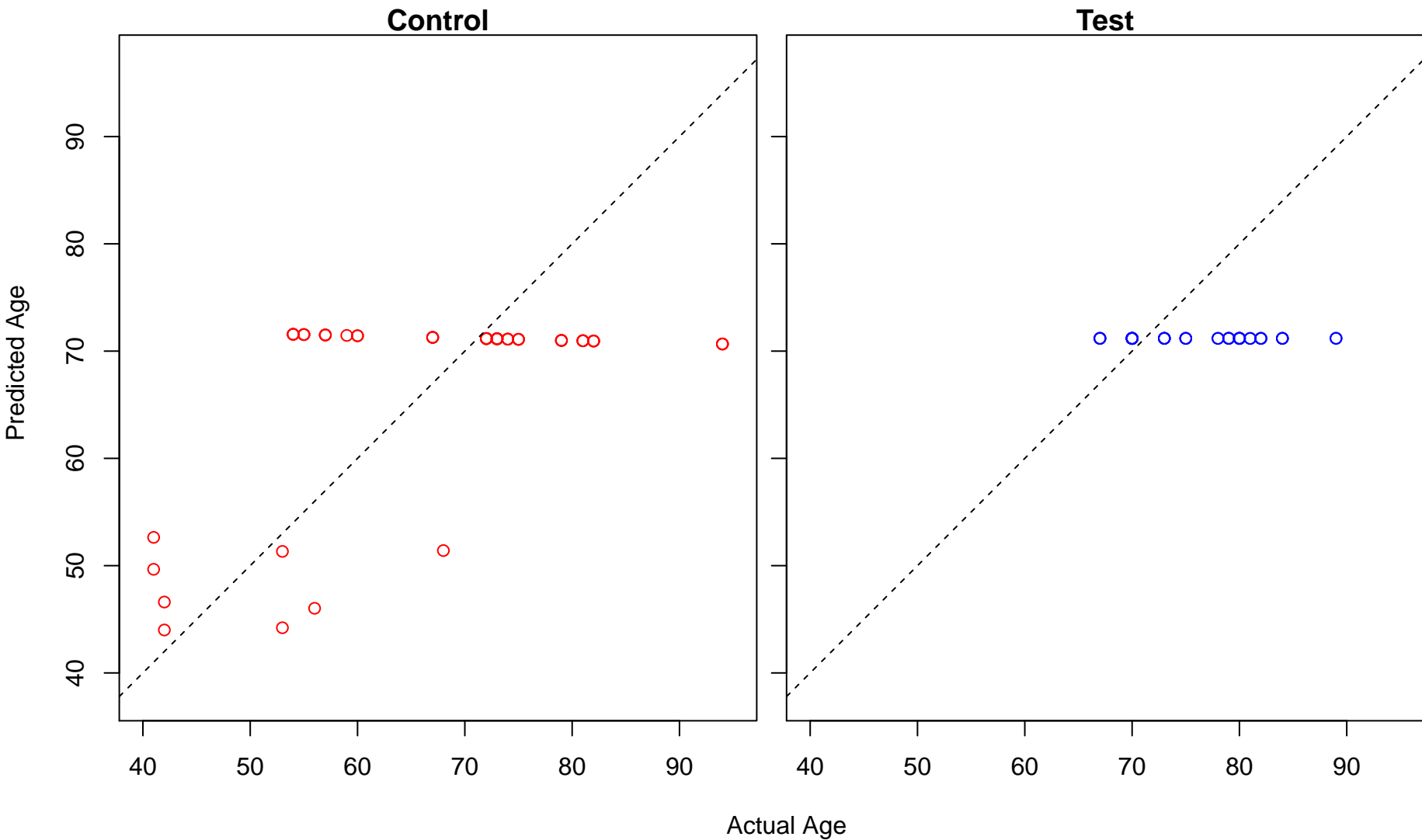


Test

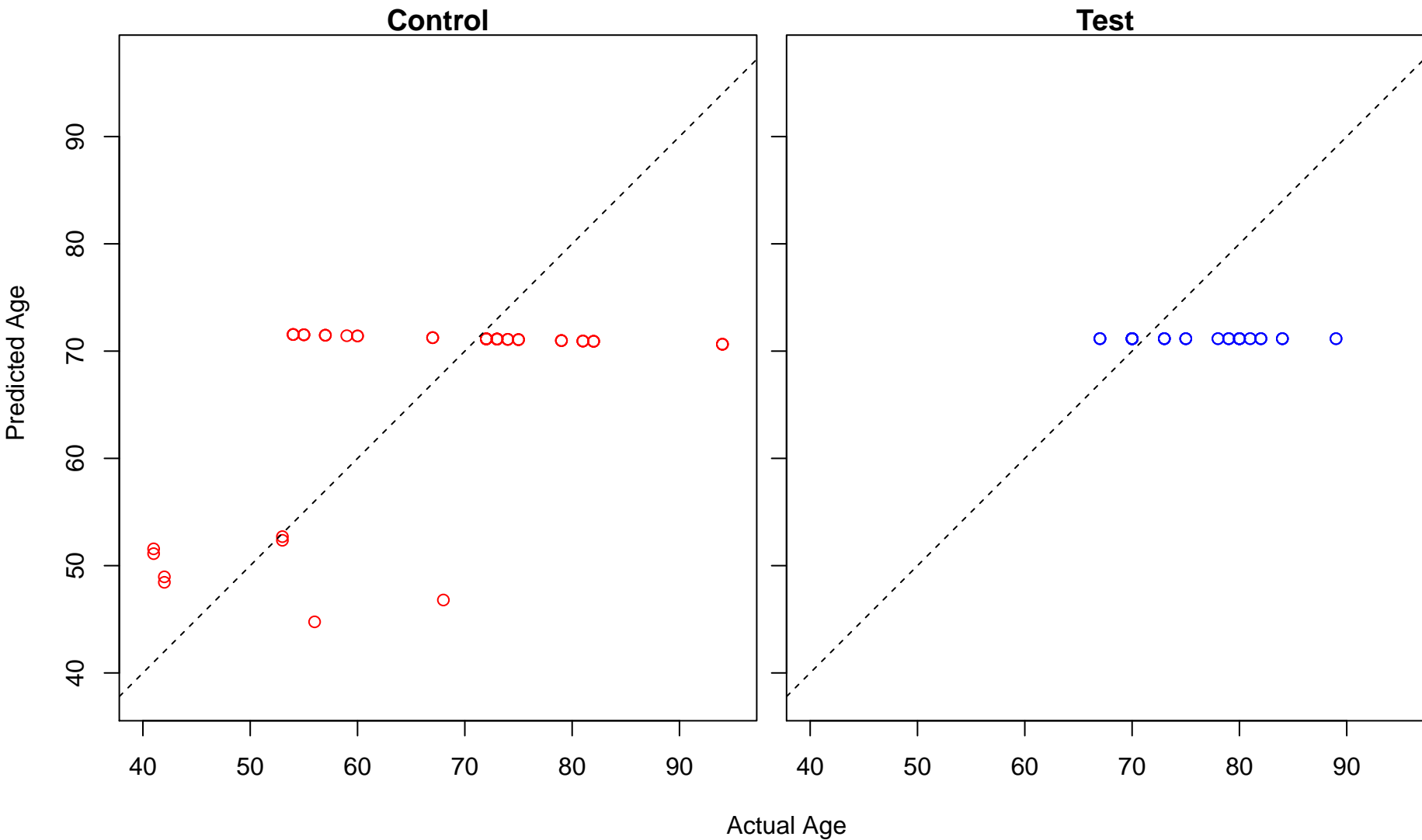


Actual Age

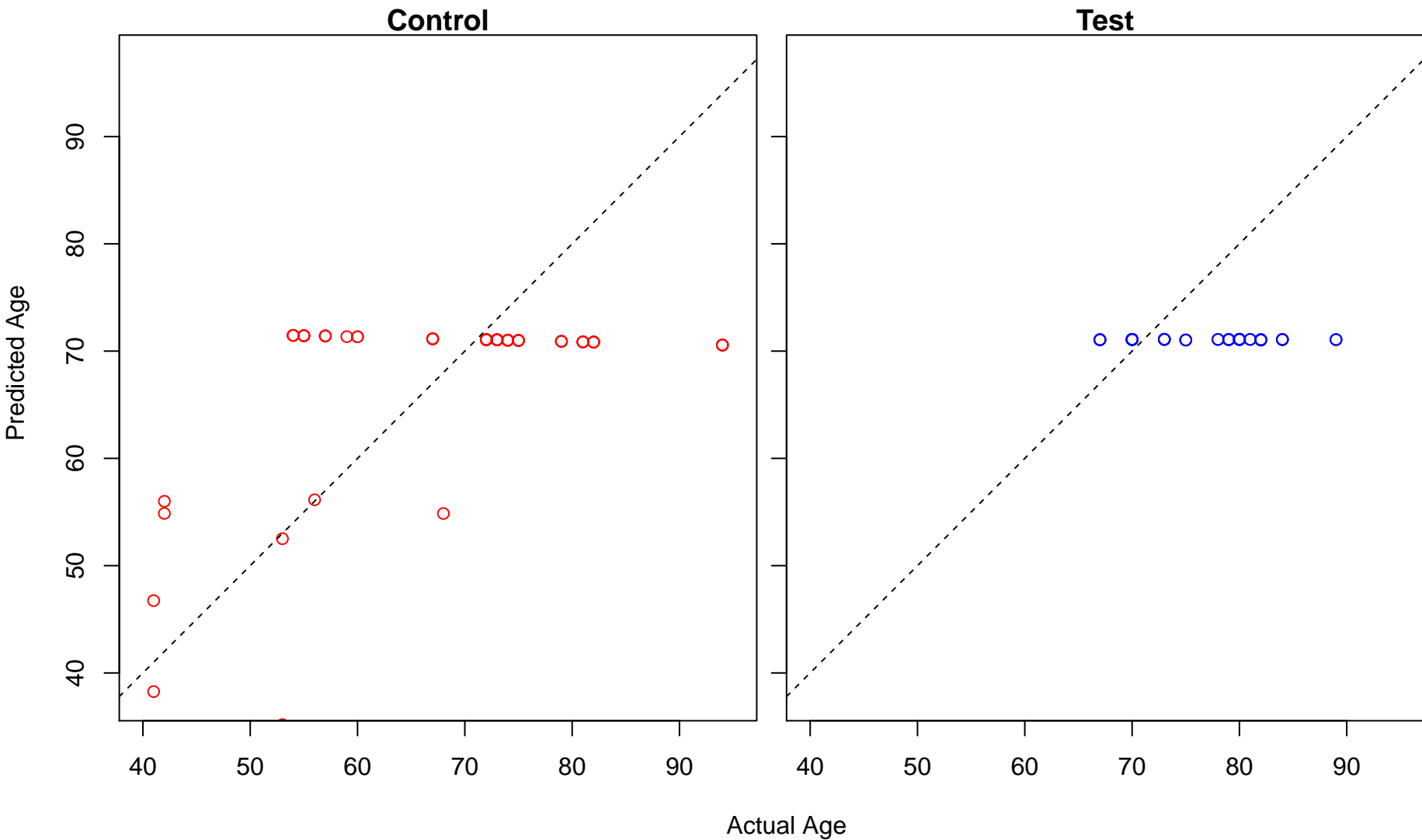
positive regulation of organelle organization (Score: 0.804973)



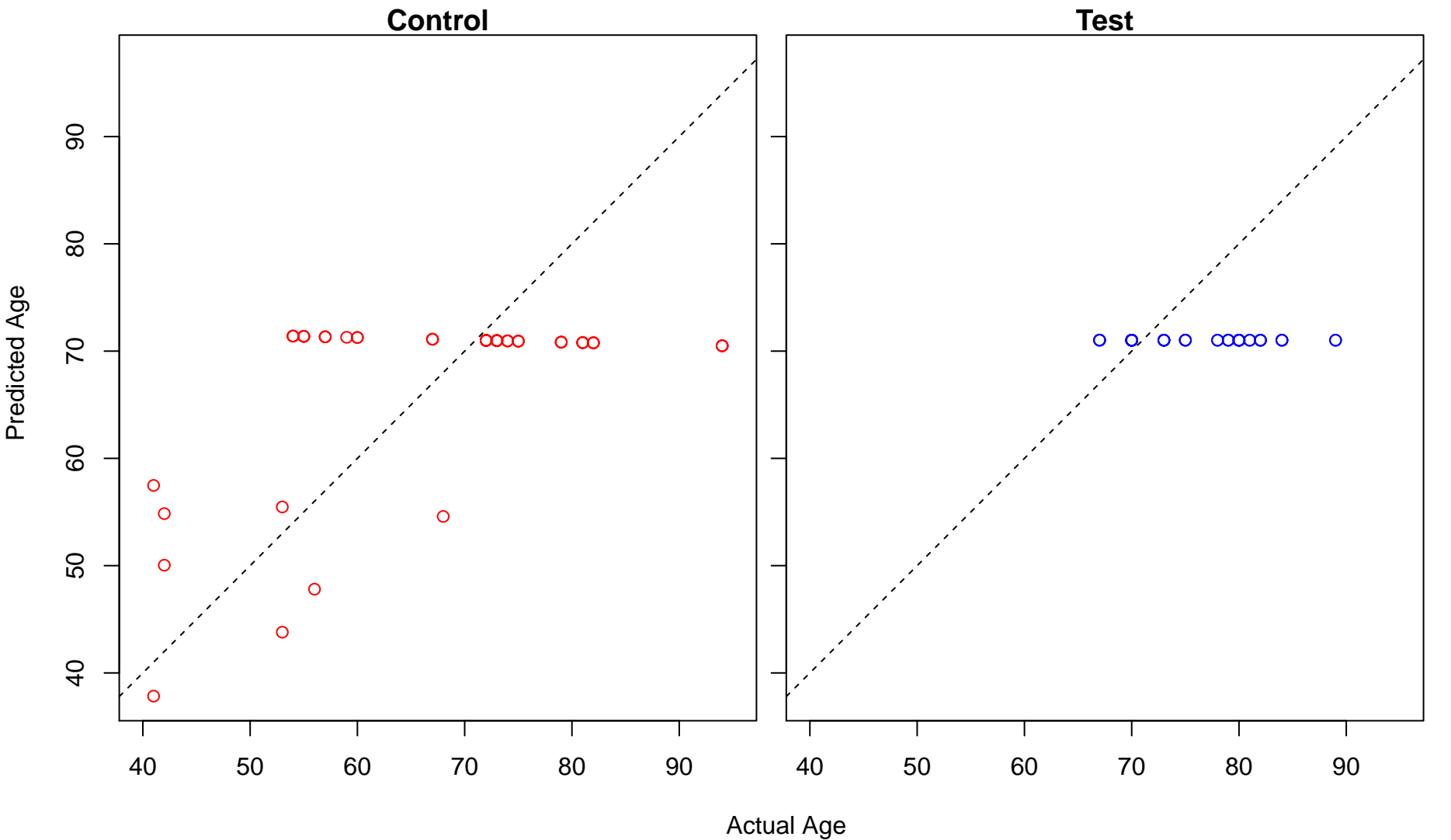
cell cycle arrest (Score: 0.804935)



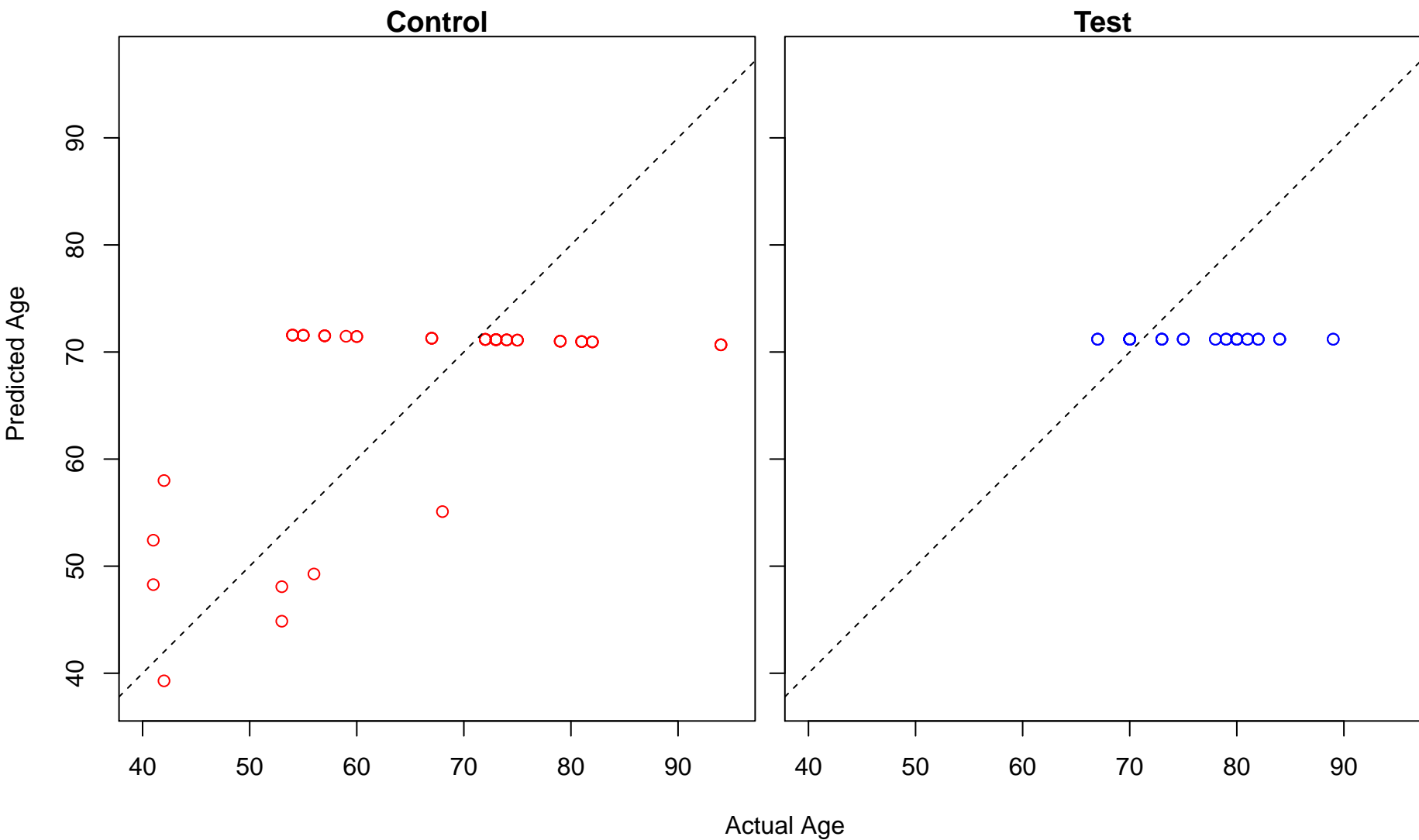
ATF6-mediated unfolded protein response (Score: 0.804857)



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

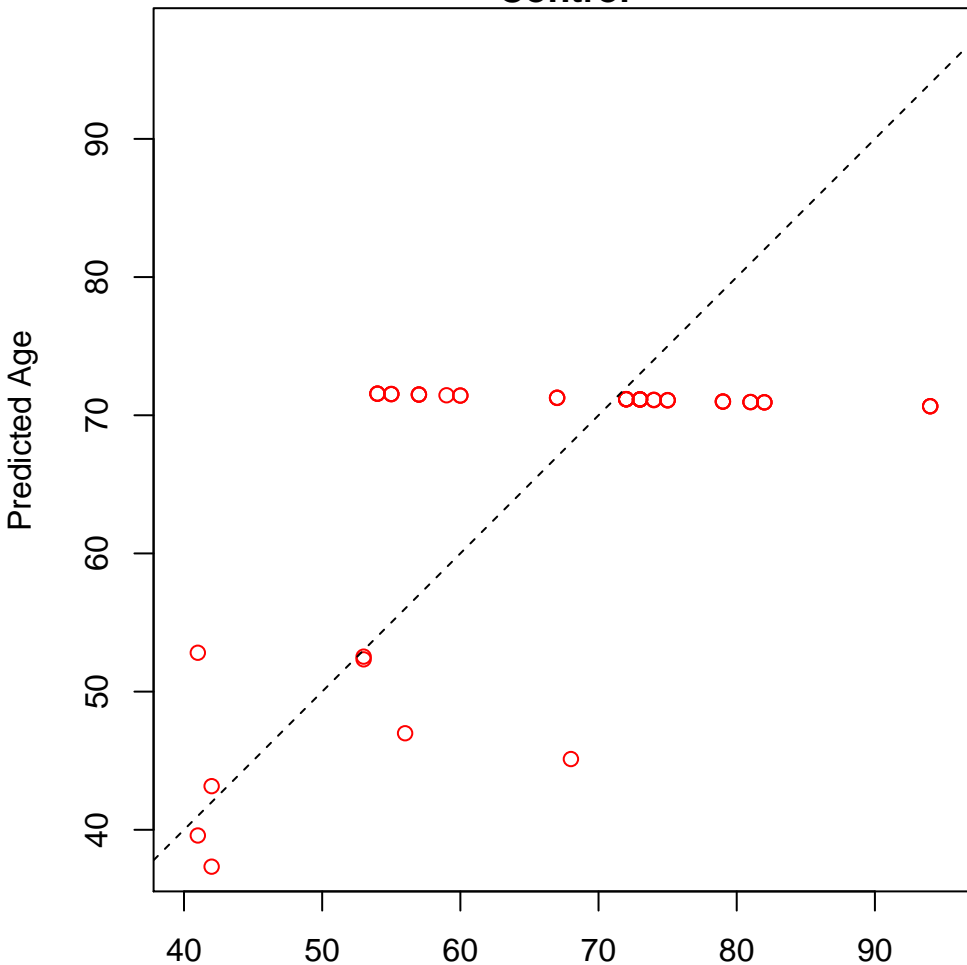


regulation of hydrolase activity (Score: 0.804770)

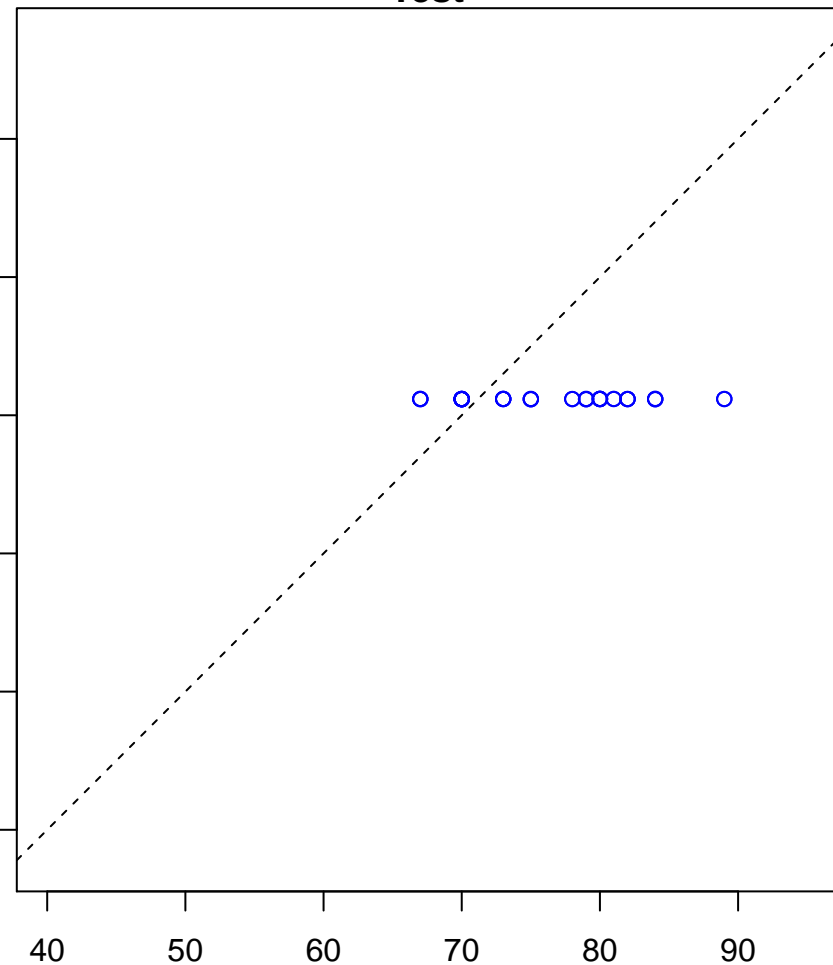


cellular response to endogenous stimulus (Score: 0.804762)

Control

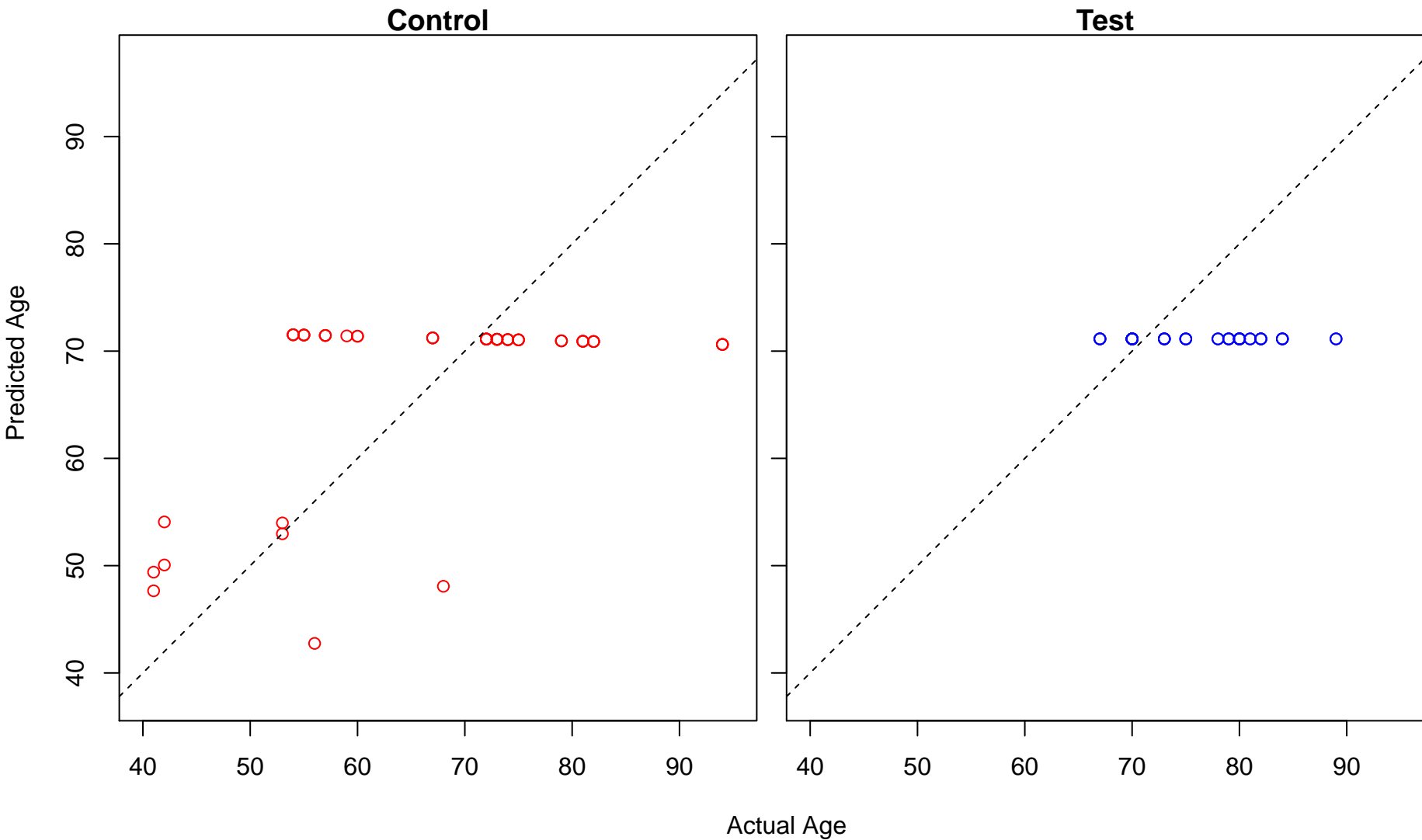


Test



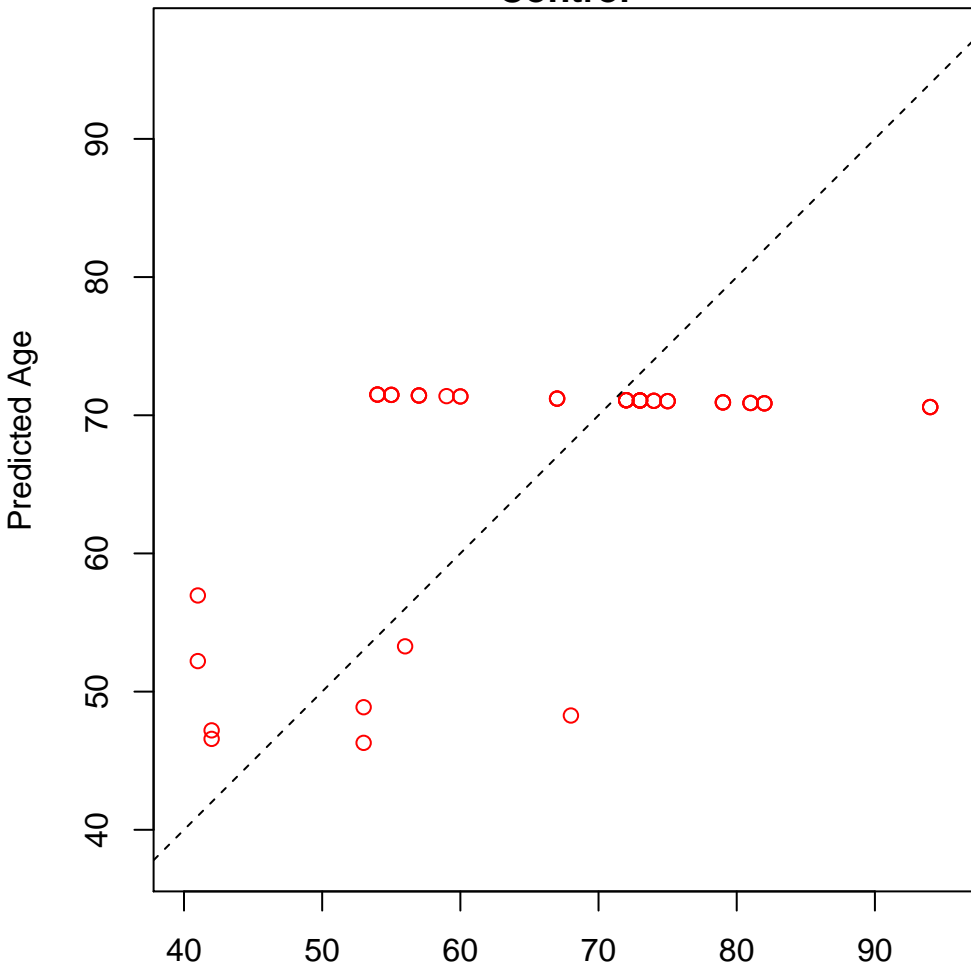
Actual Age

cellular protein complex assembly (Score: 0.804734)

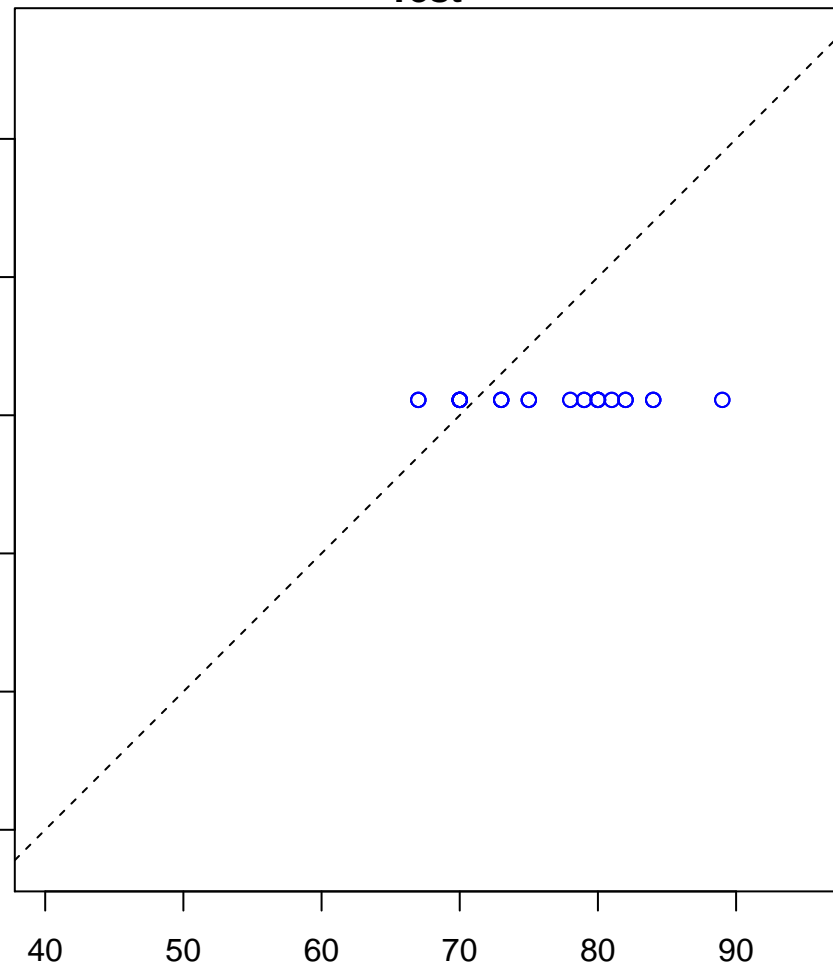


organic acid metabolic process (Score: 0.804649)

Control



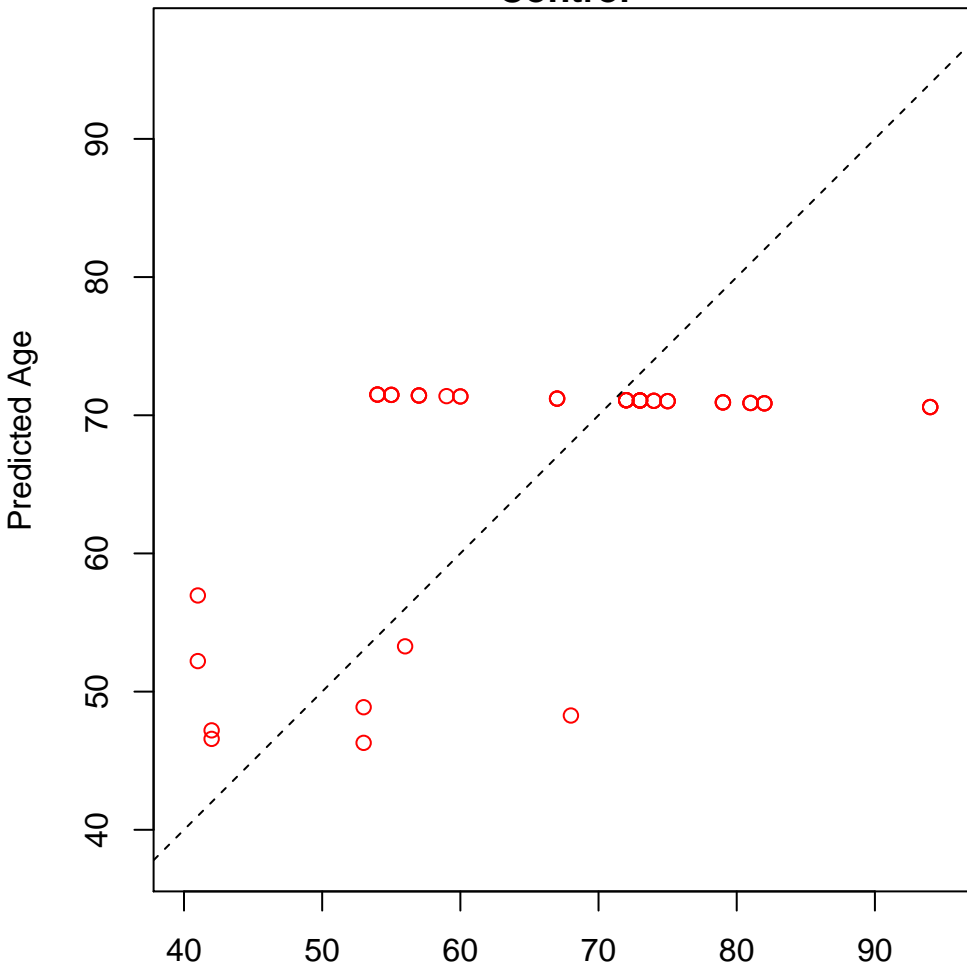
Test



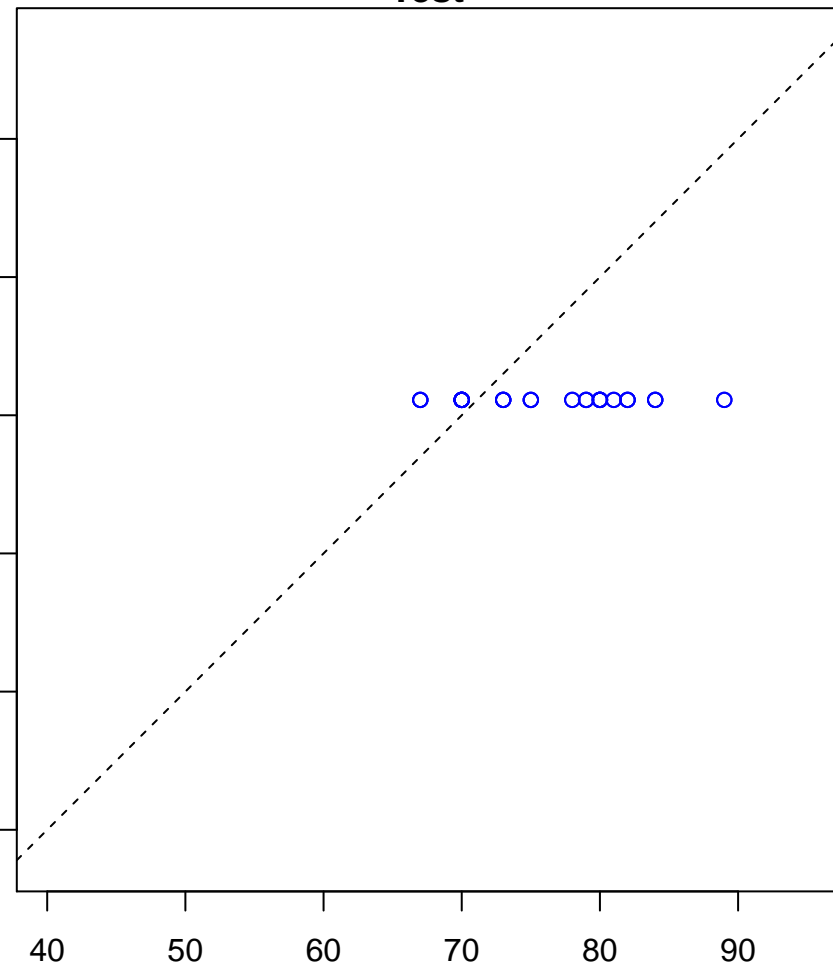
Actual Age

carboxylic acid metabolic process (Score: 0.804649)

Control

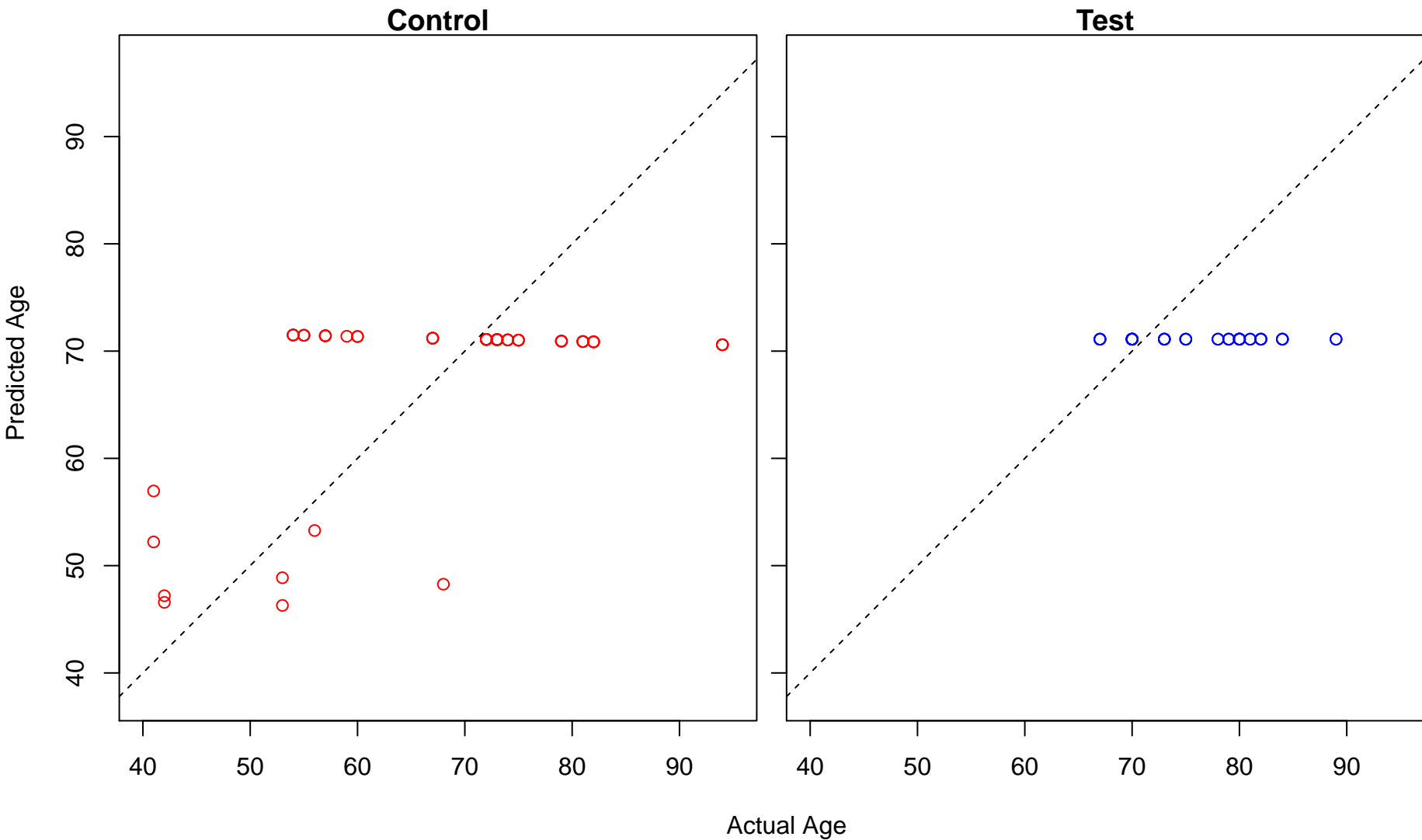


Test

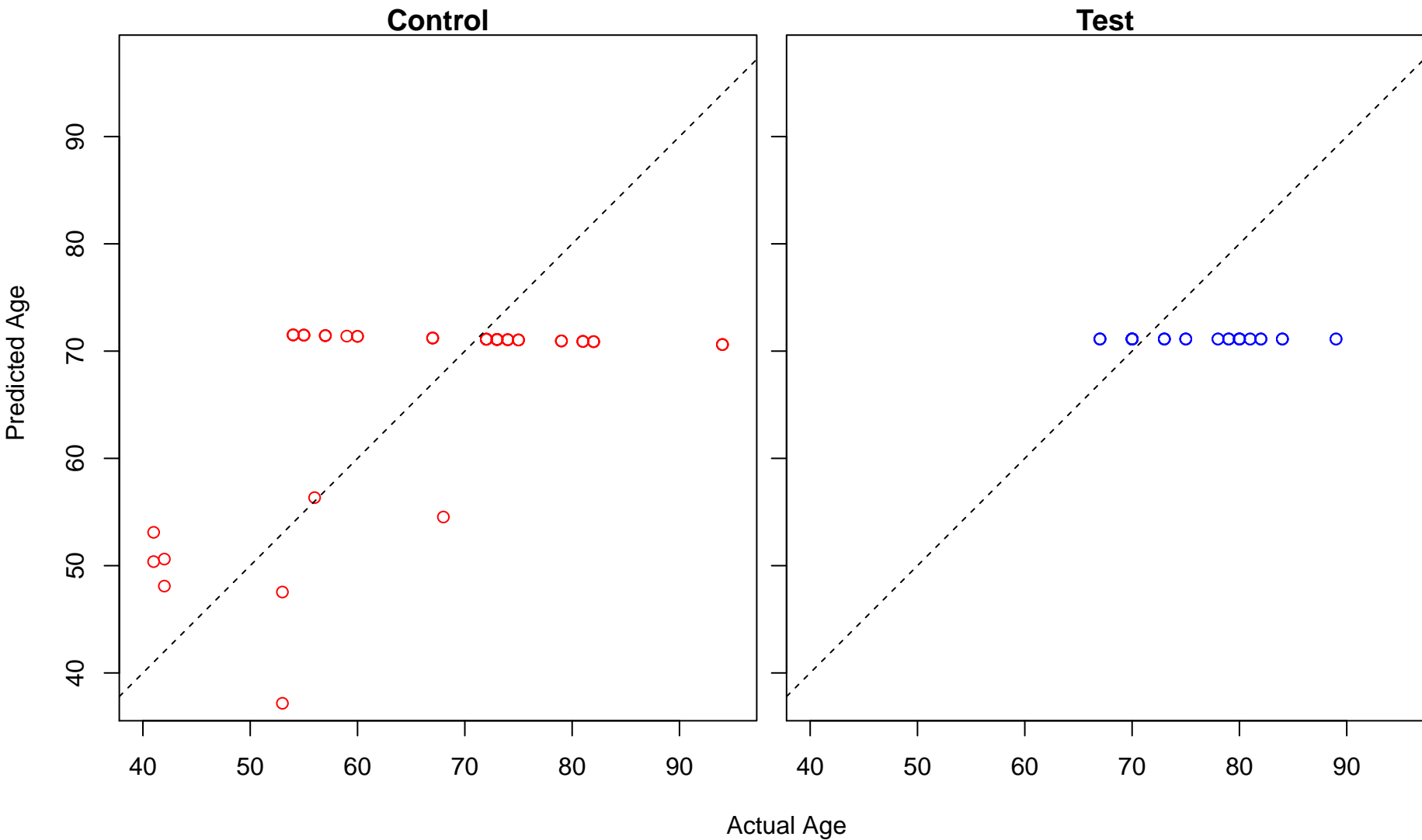


Actual Age

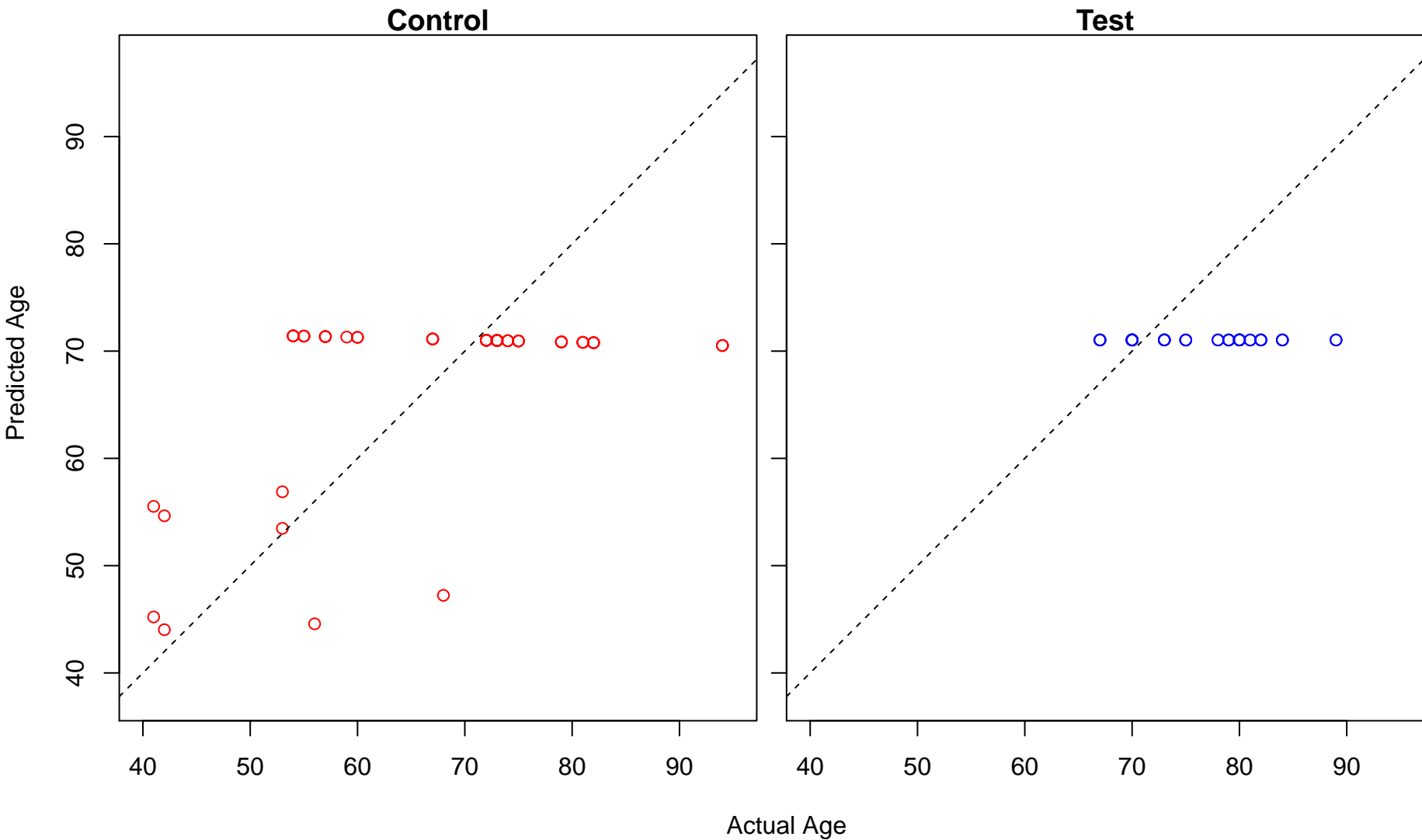
oxoacid metabolic process (Score: 0.804649)



response to virus (Score: 0.804620)

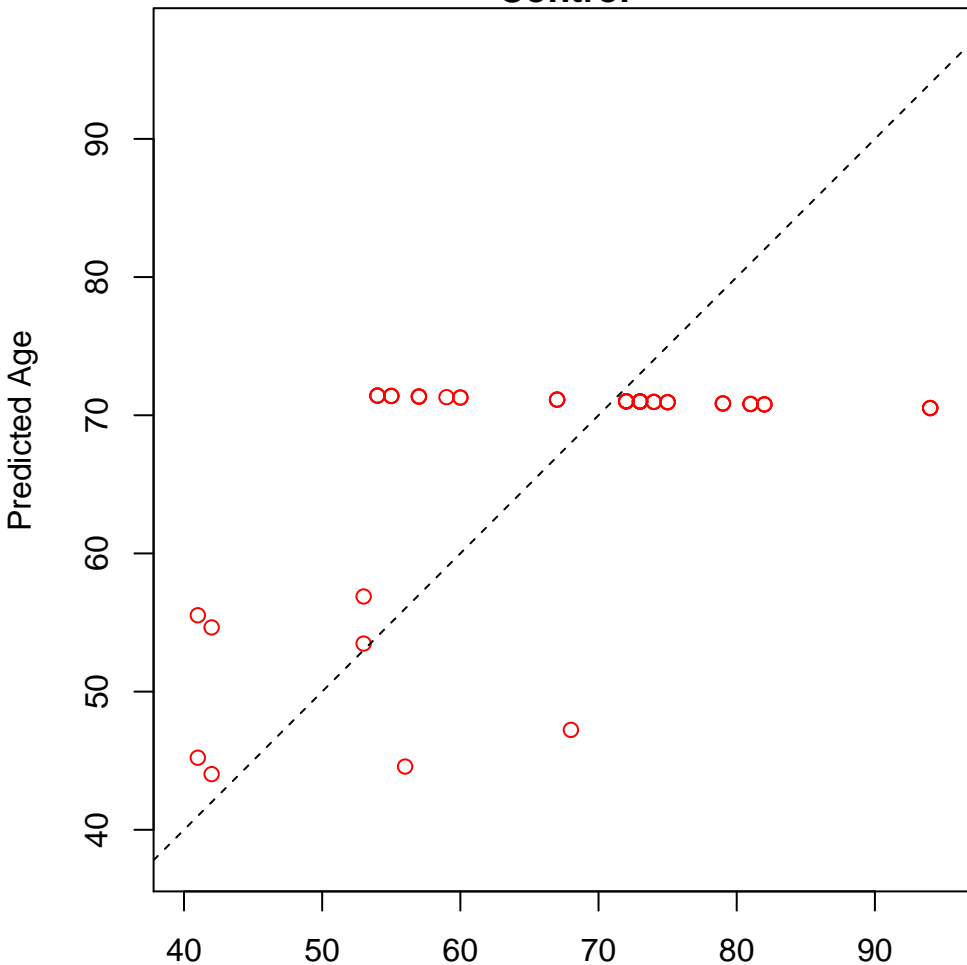


regulation of hormone secretion (Score: 0.804615)

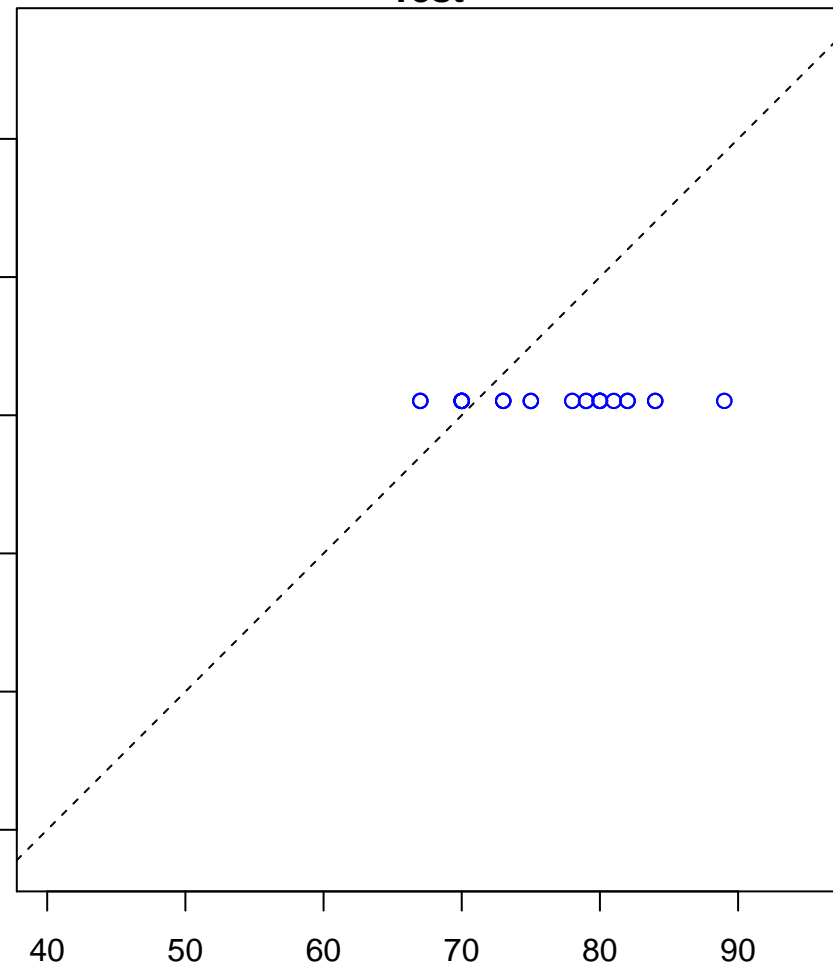


regulation of peptide hormone secretion (Score: 0.804615)

Control

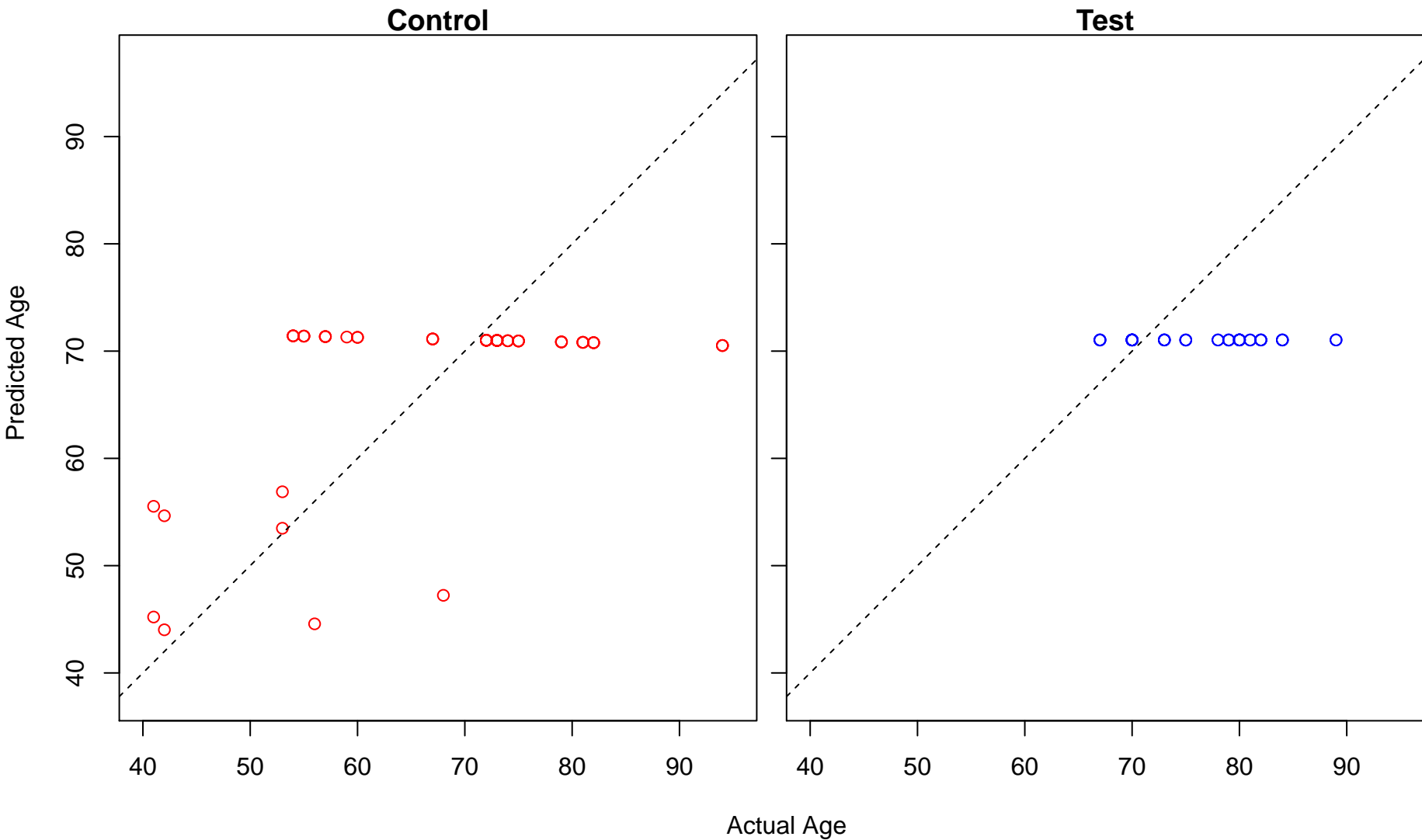


Test



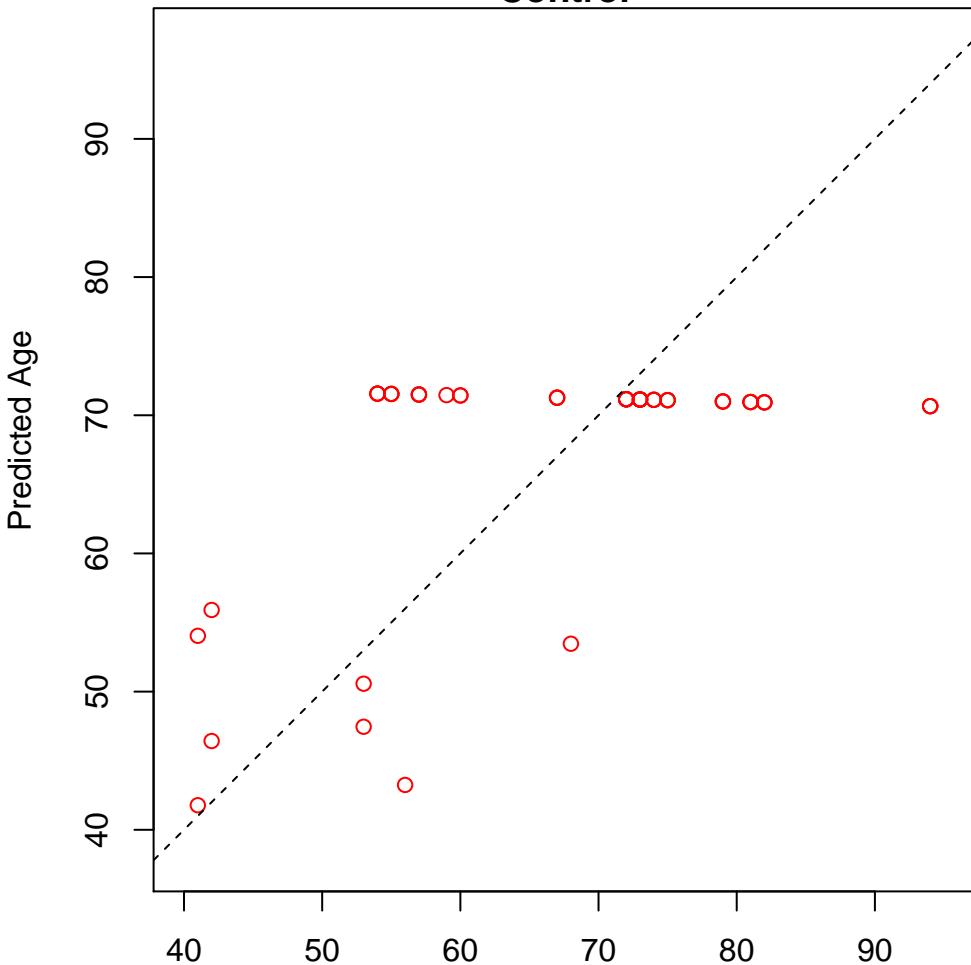
Actual Age

regulation of insulin secretion (Score: 0.804613)

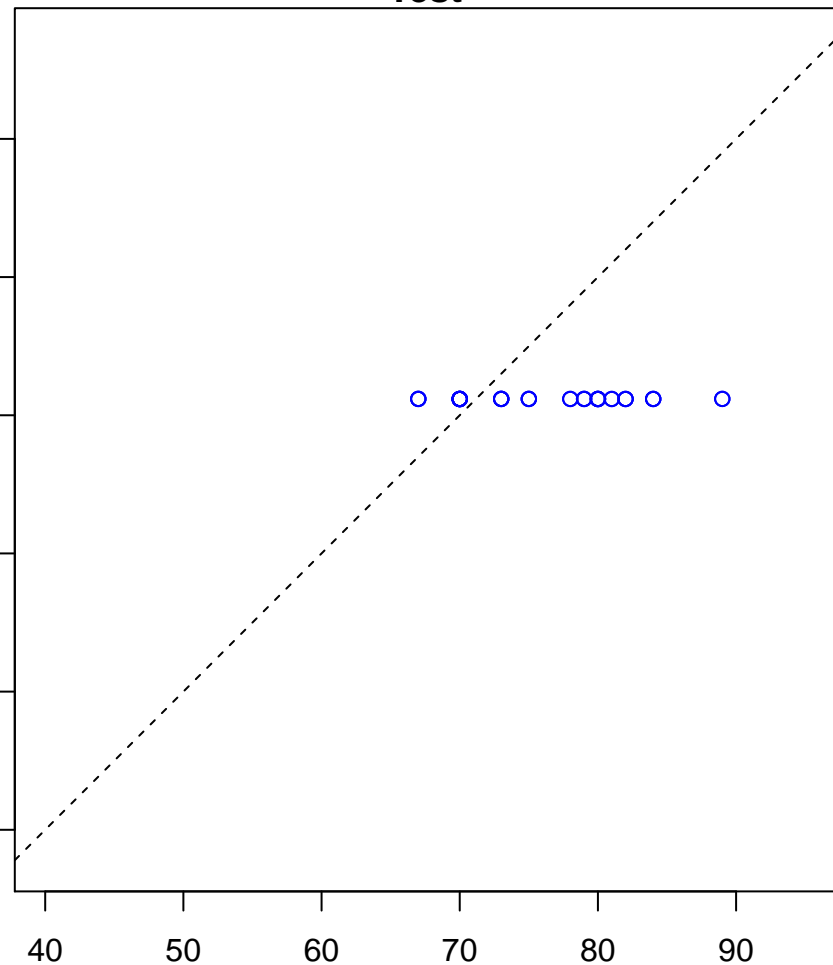


peptidyl-amino acid modification (Score: 0.804607)

Control

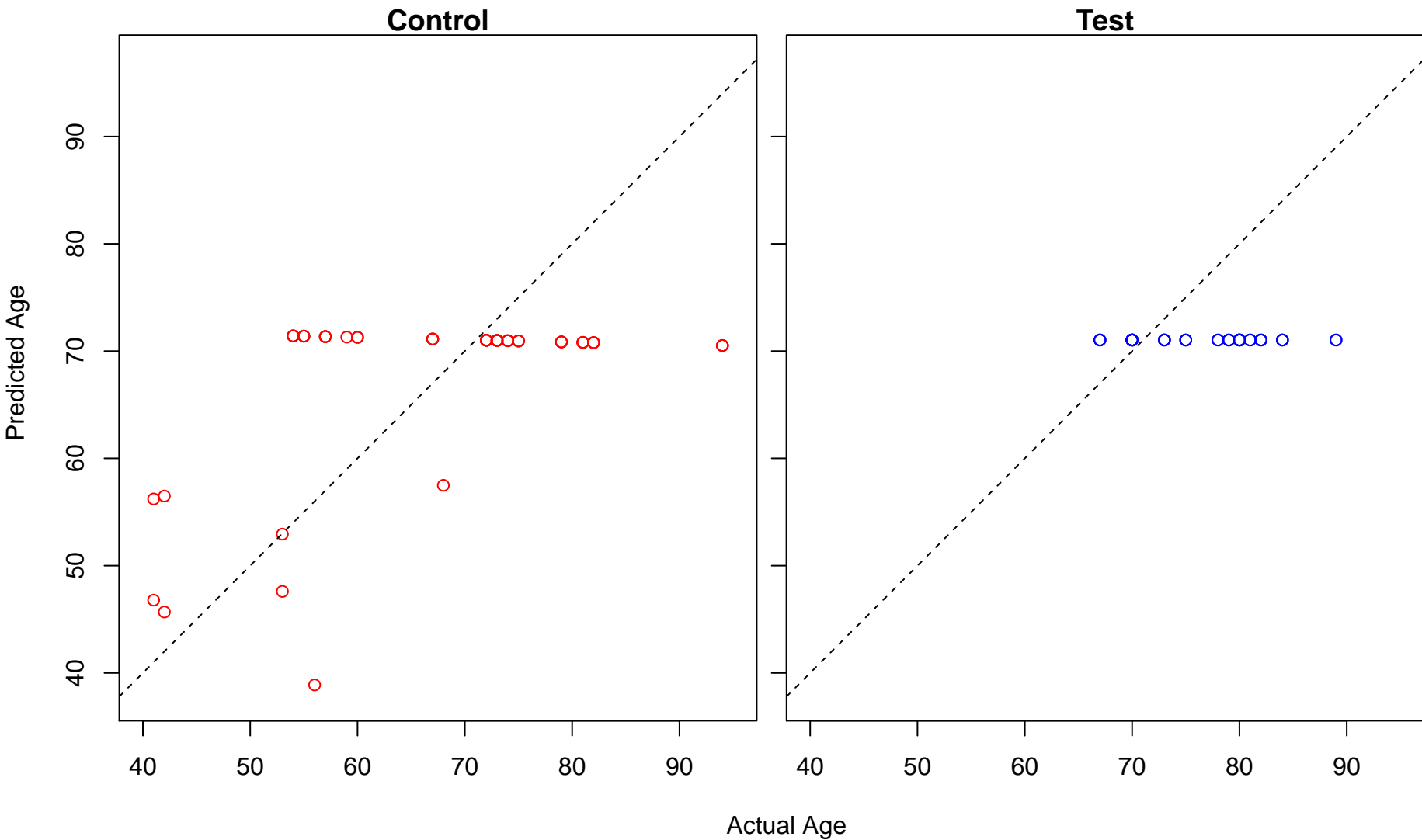


Test

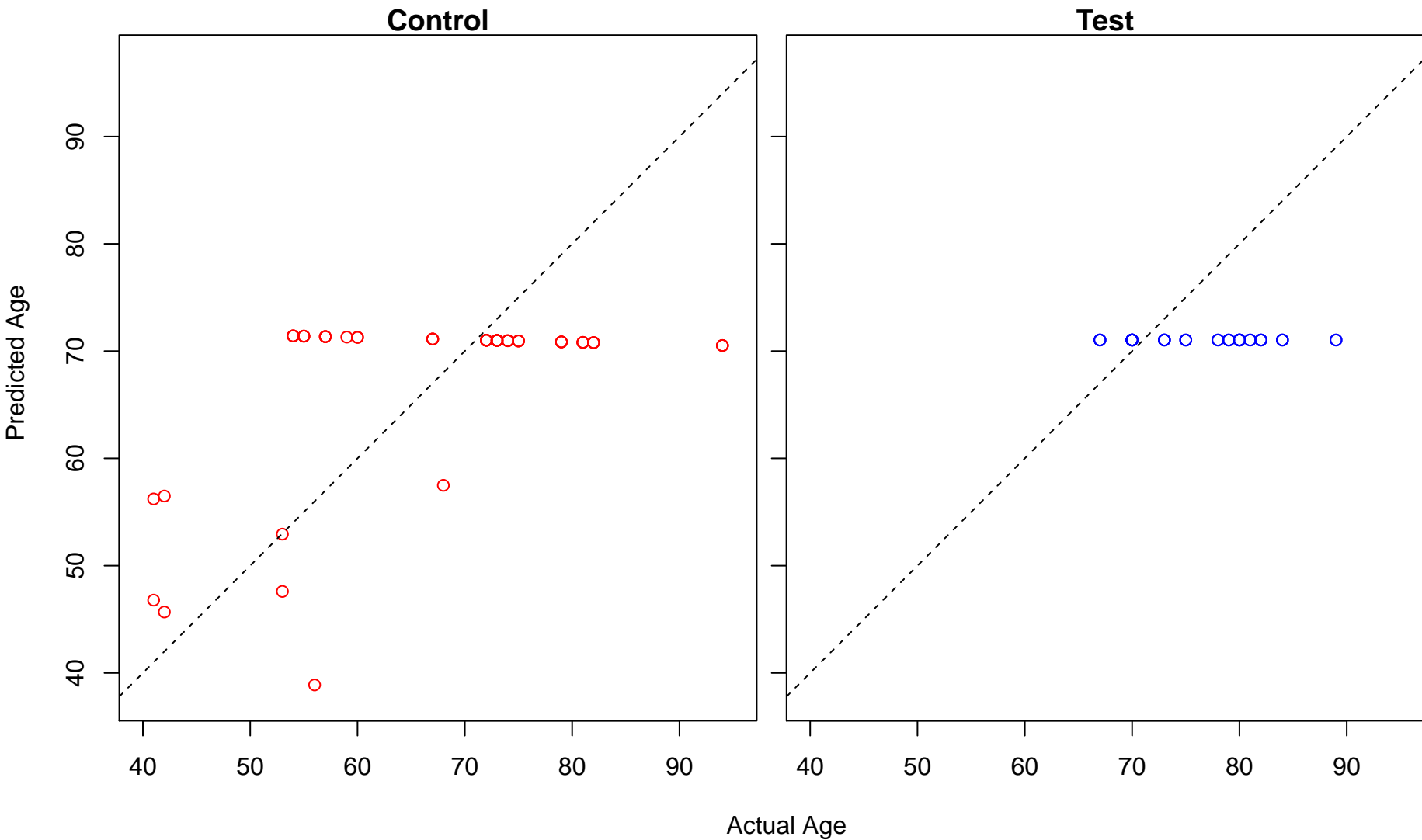


Actual Age

sister chromatid segregation (Score: 0.804520)

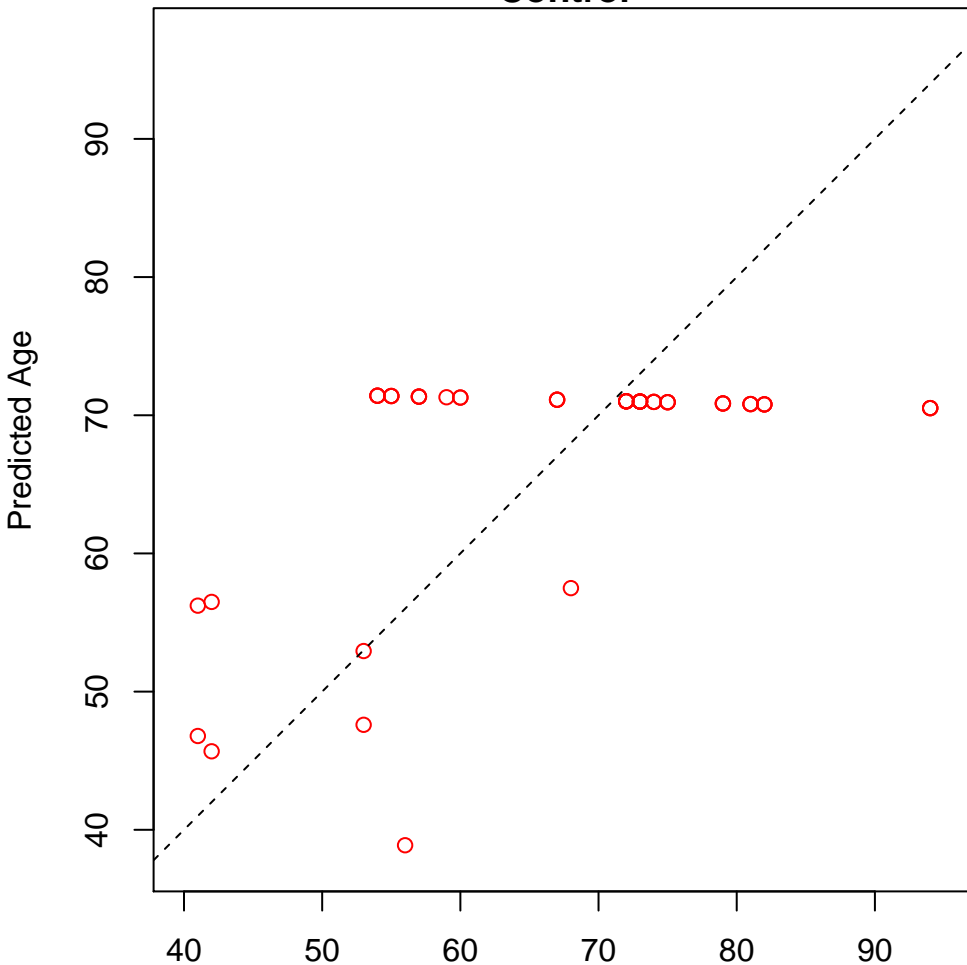


sister chromatid cohesion (Score: 0.804520)

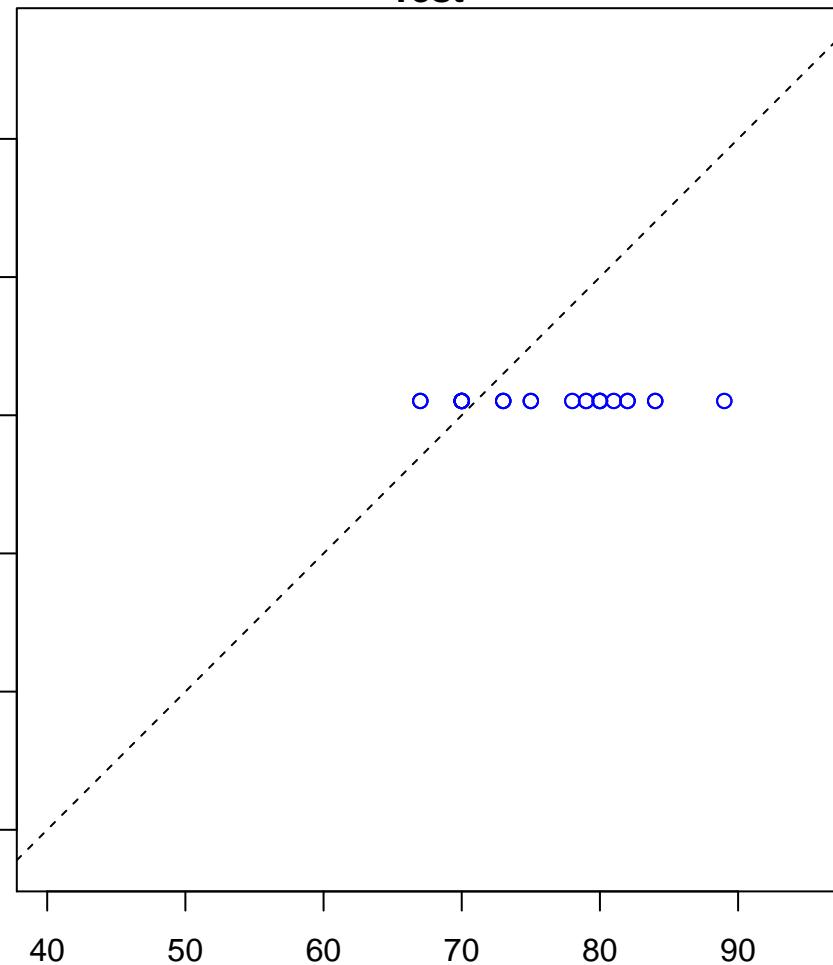


nuclear chromosome segregation (Score: 0.804520)

Control

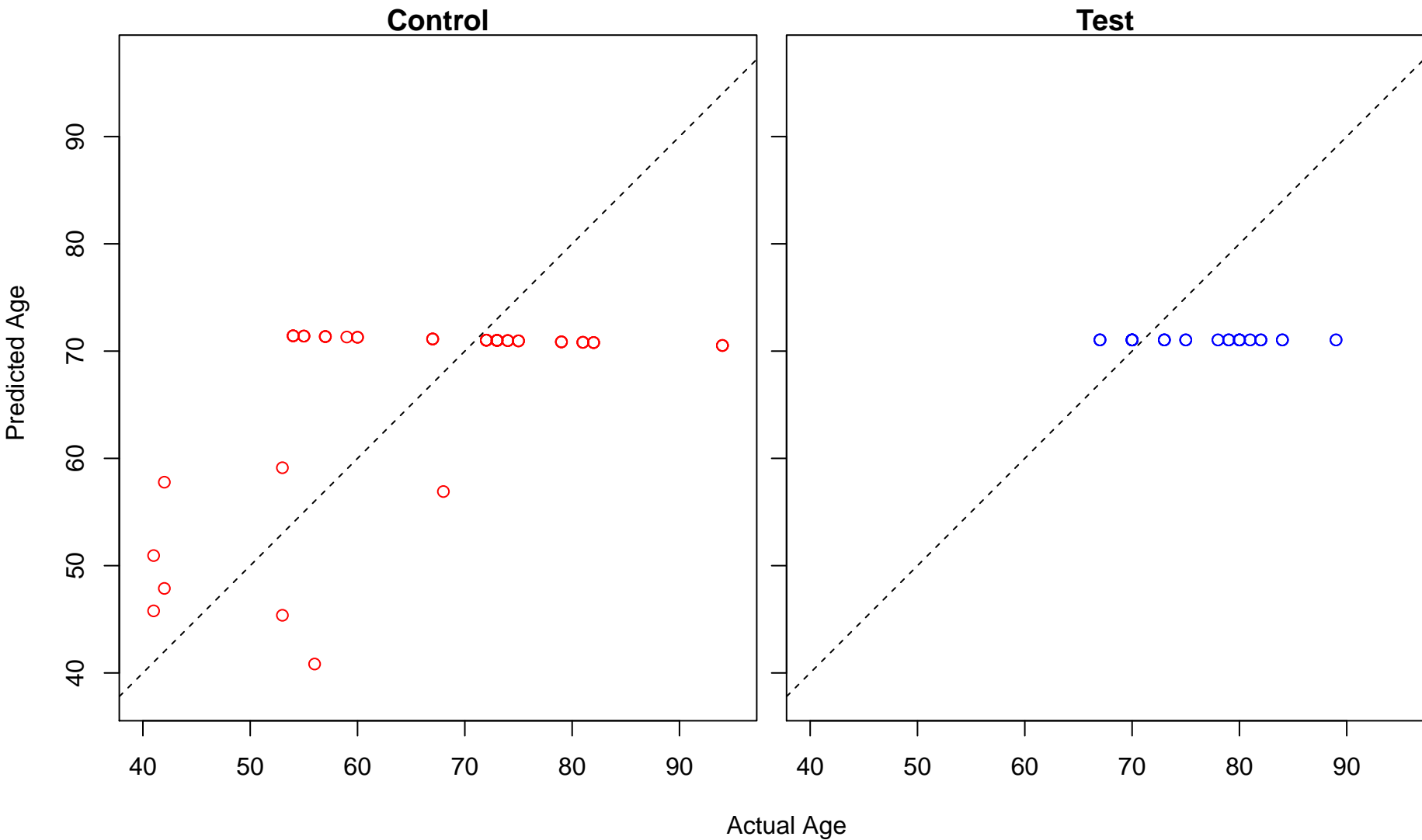


Test

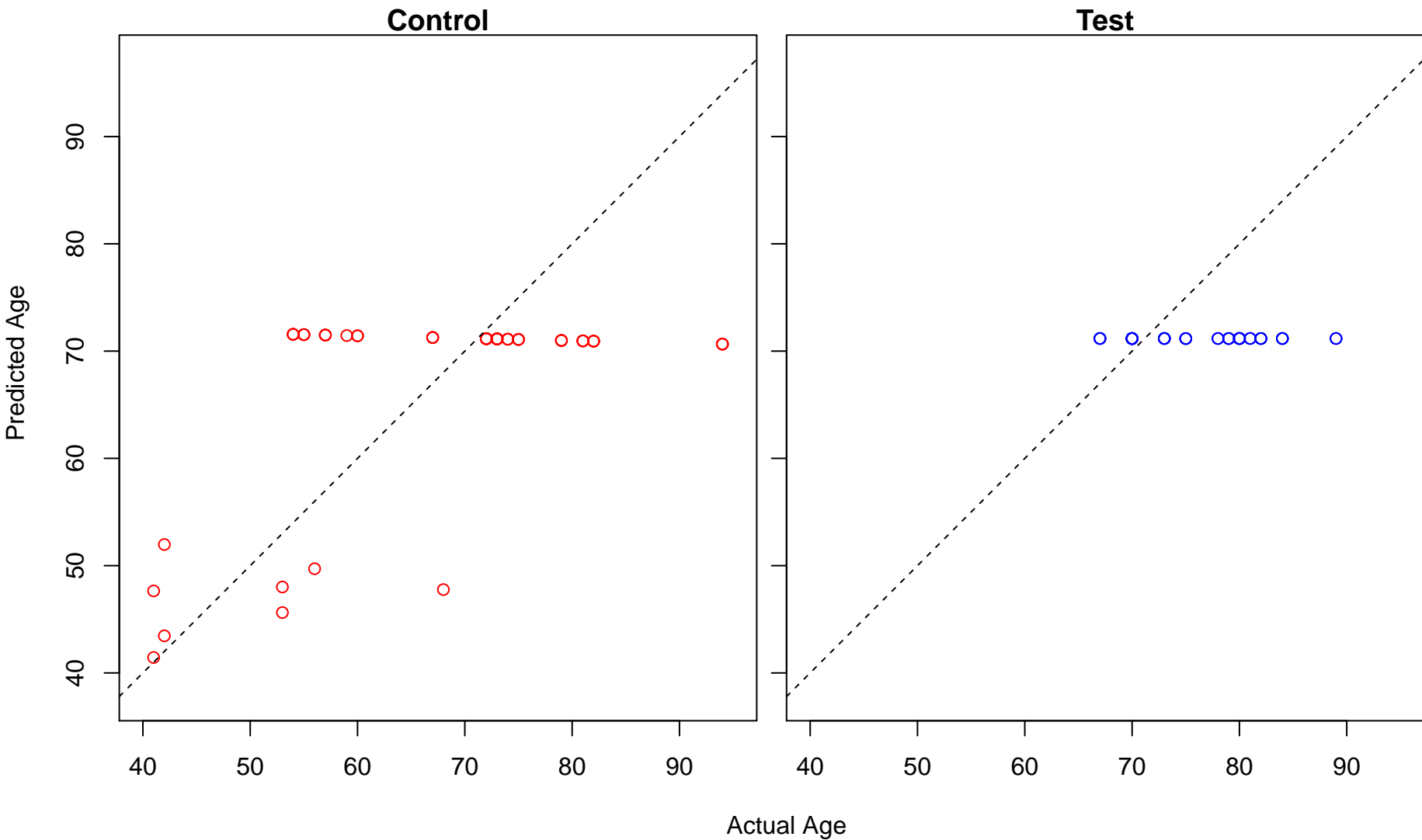


Actual Age

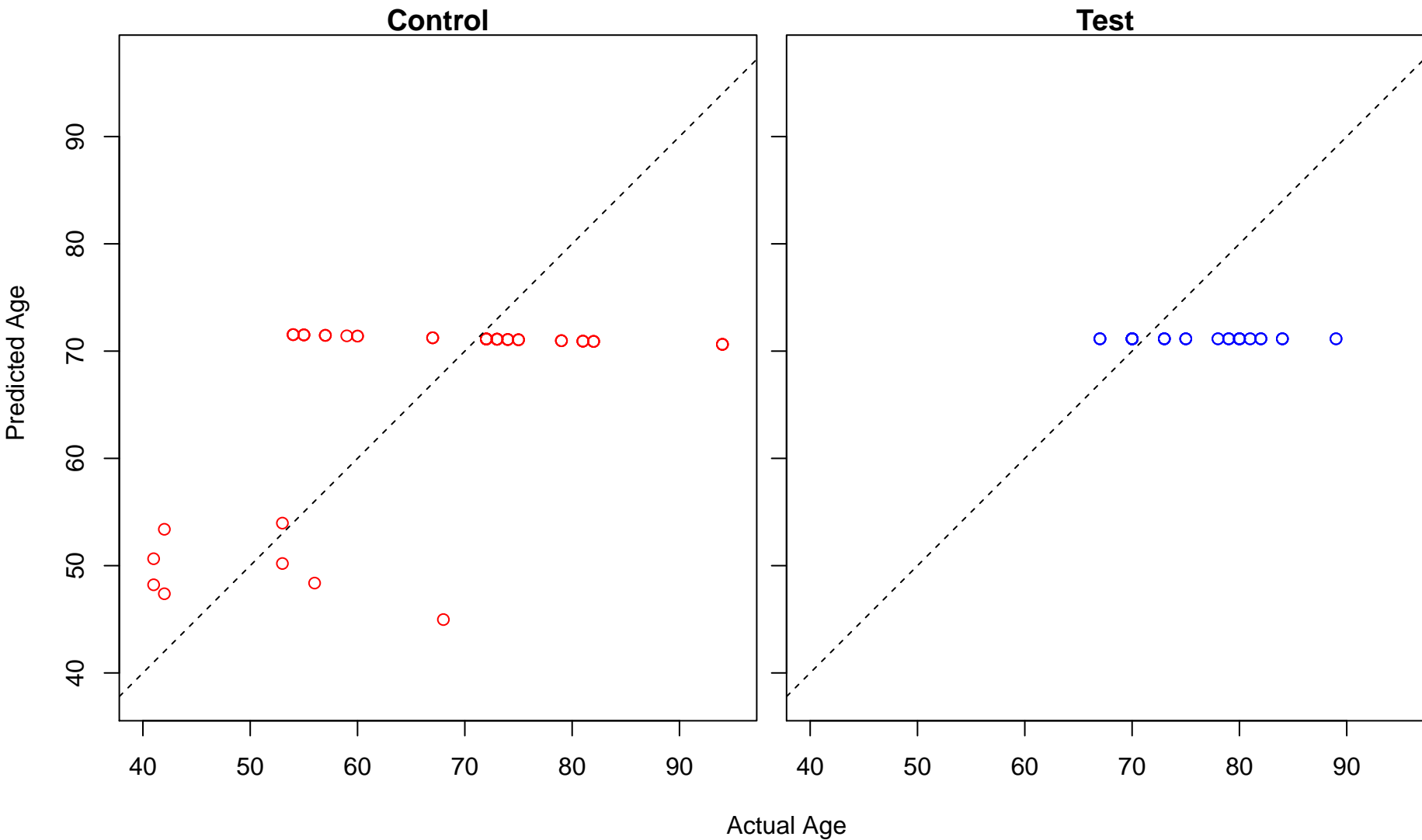
biological adhesion (Score: 0.804465)



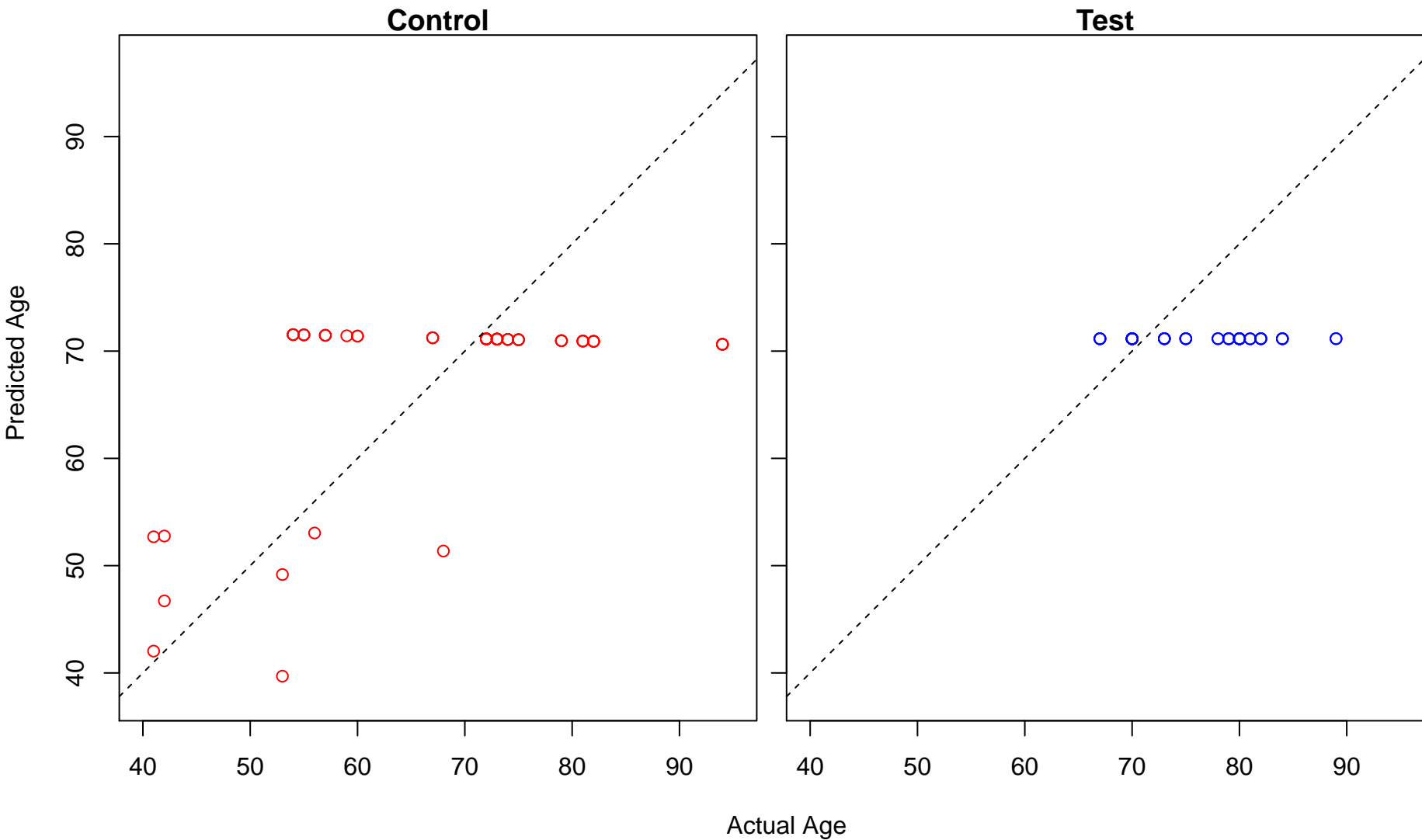
positive regulation of cellular metabolic process (Score: 0.804370)



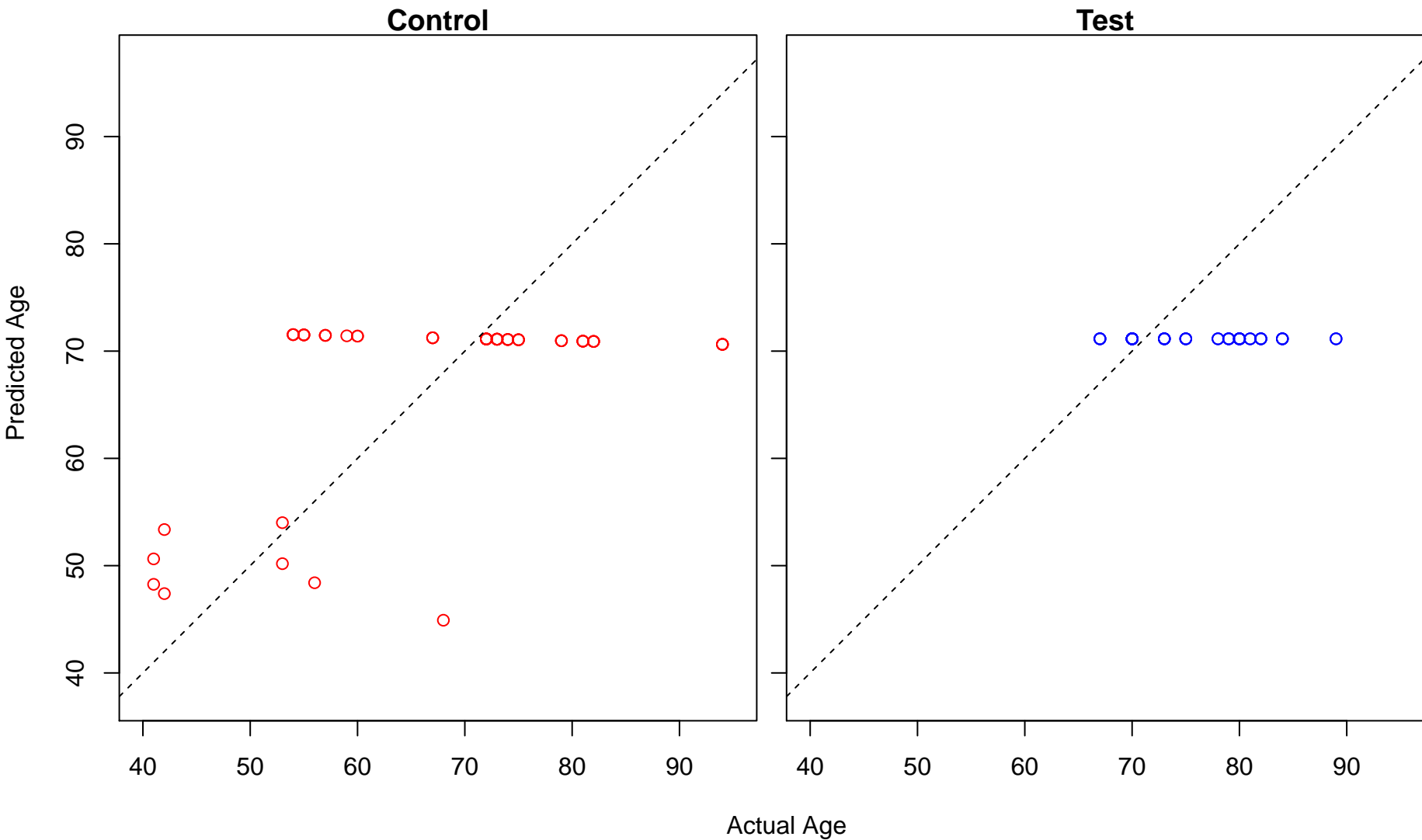
regulation of carbohydrate metabolic process (Score: 0.804274)



regulation of binding (Score: 0.804240)

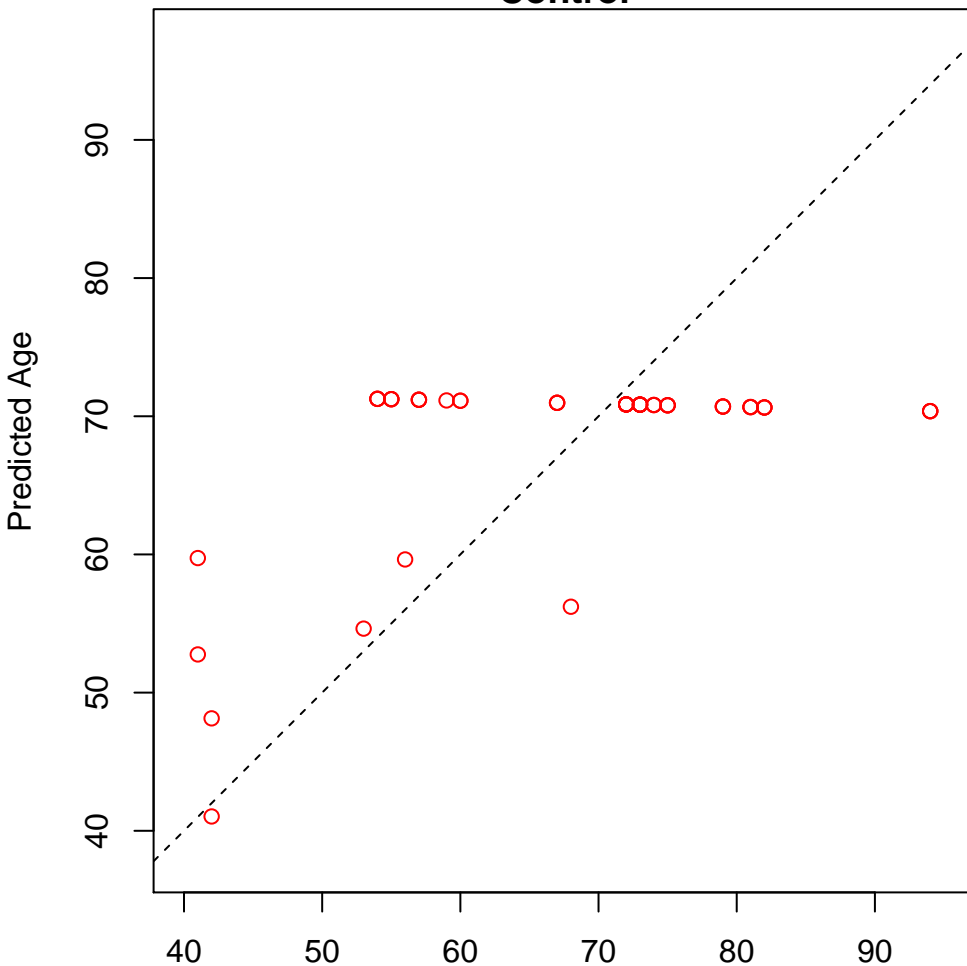


transcytosis (Score: 0.804167)

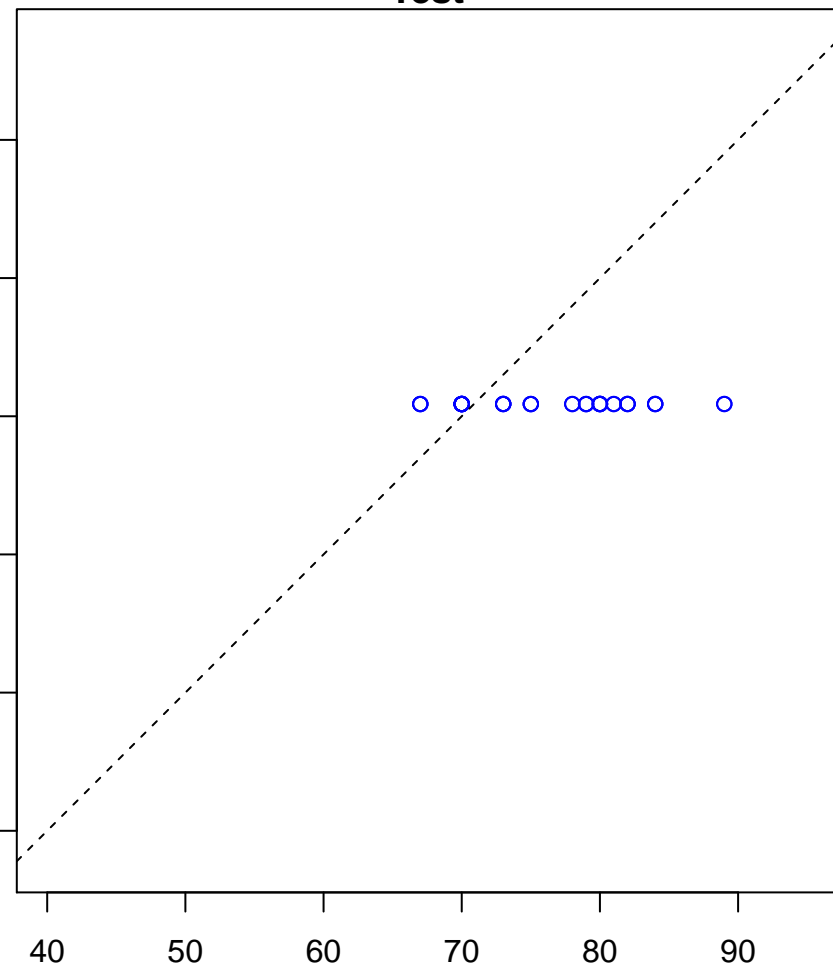


regulation of macrophage chemotaxis (Score: 0.803981)

Control

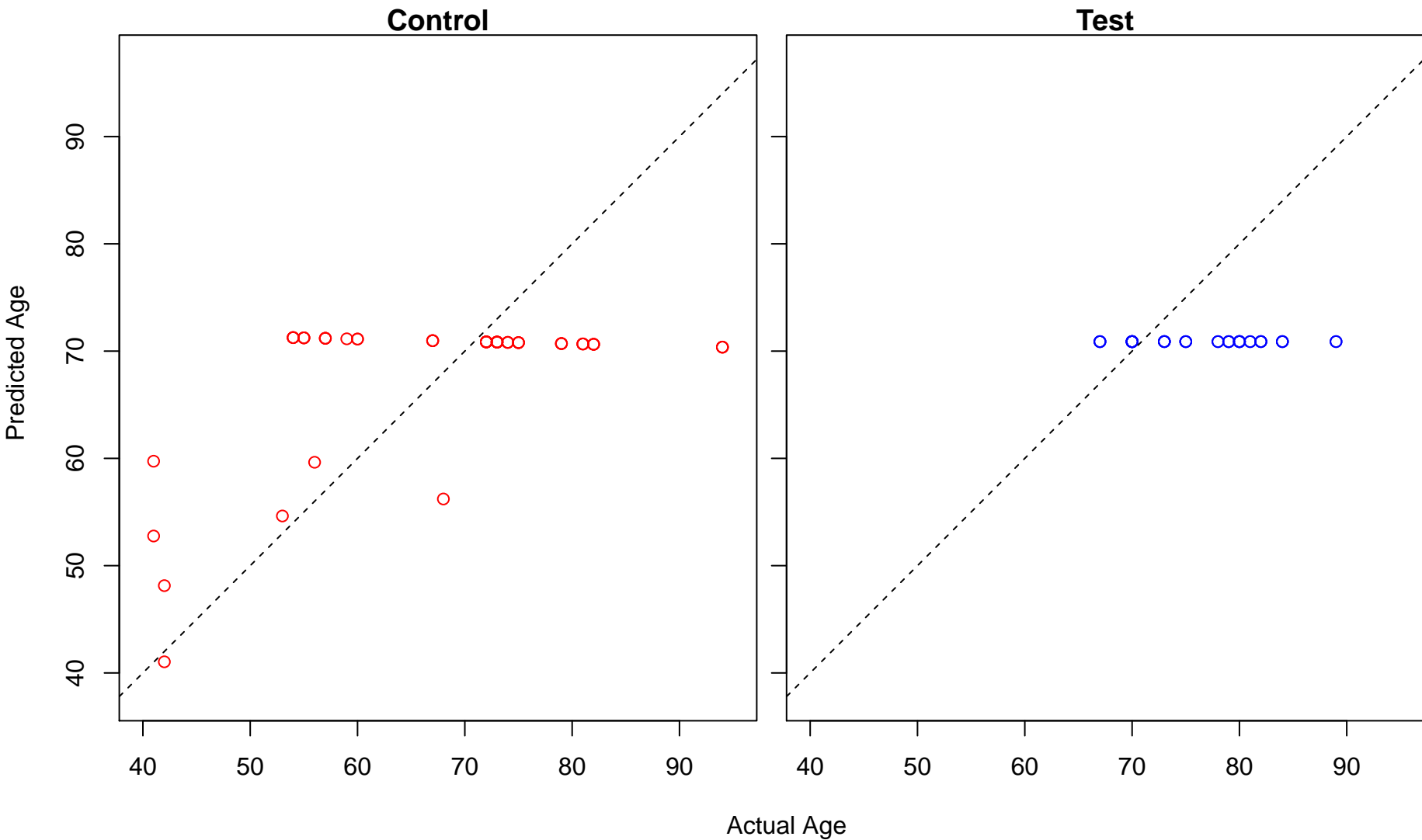


Test



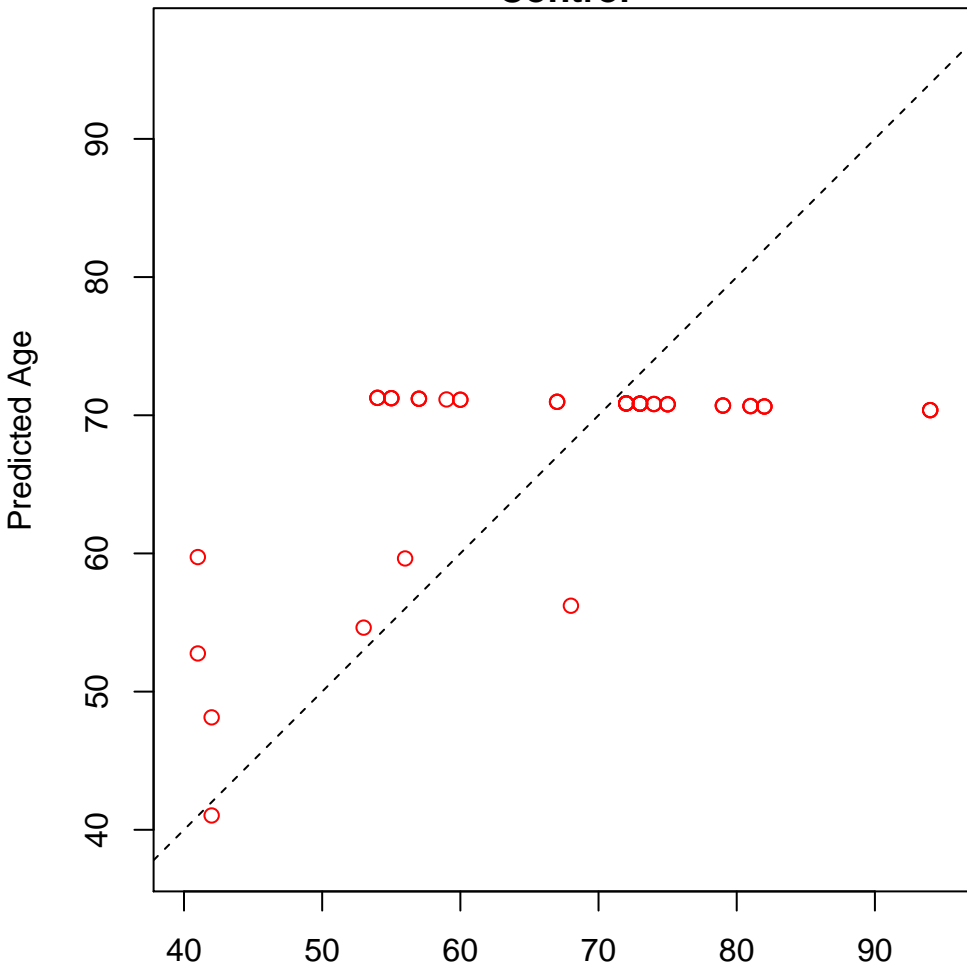
Actual Age

positive regulation of macrophage chemotaxis (Score: 0.803981)

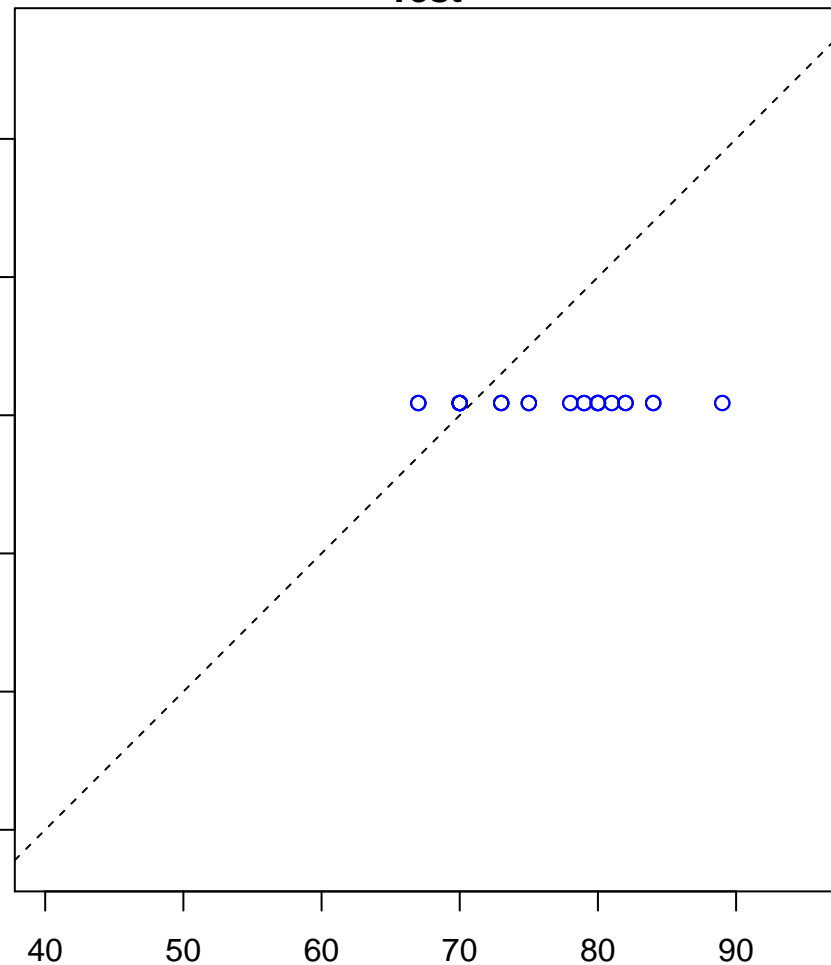


regulation of granulocyte chemotaxis (Score: 0.803981)

Control



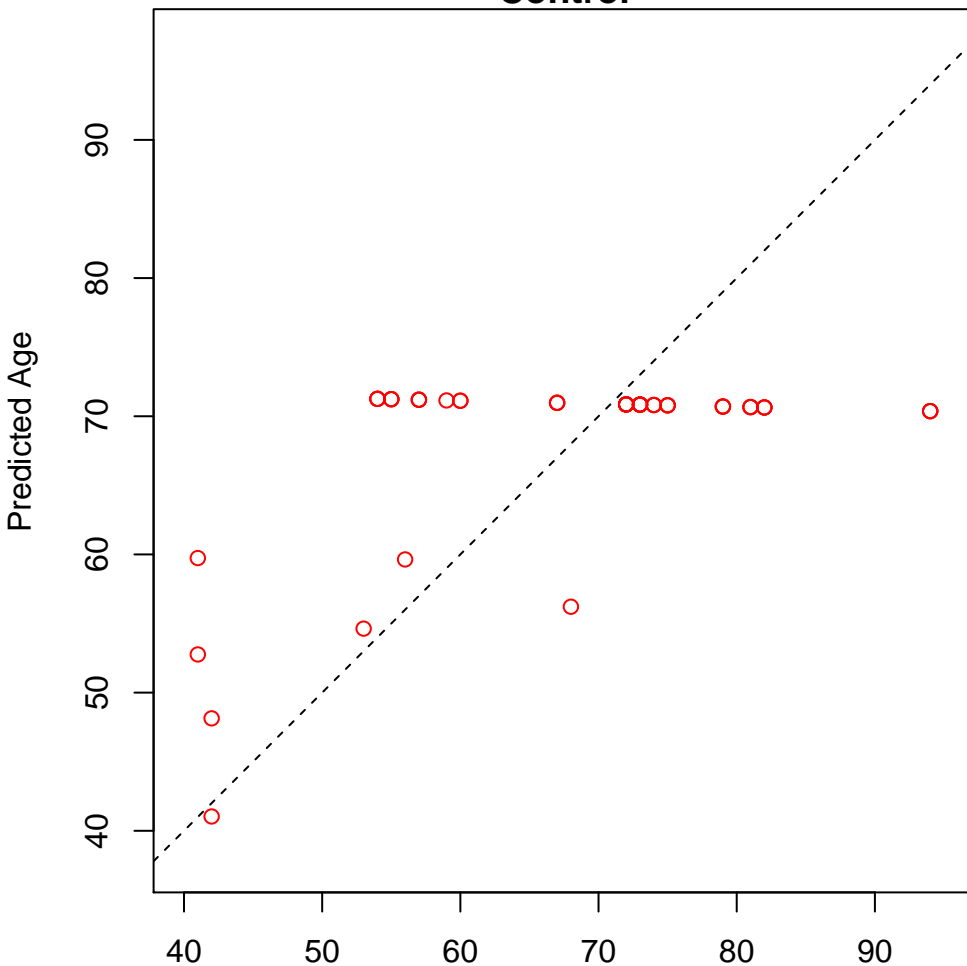
Test



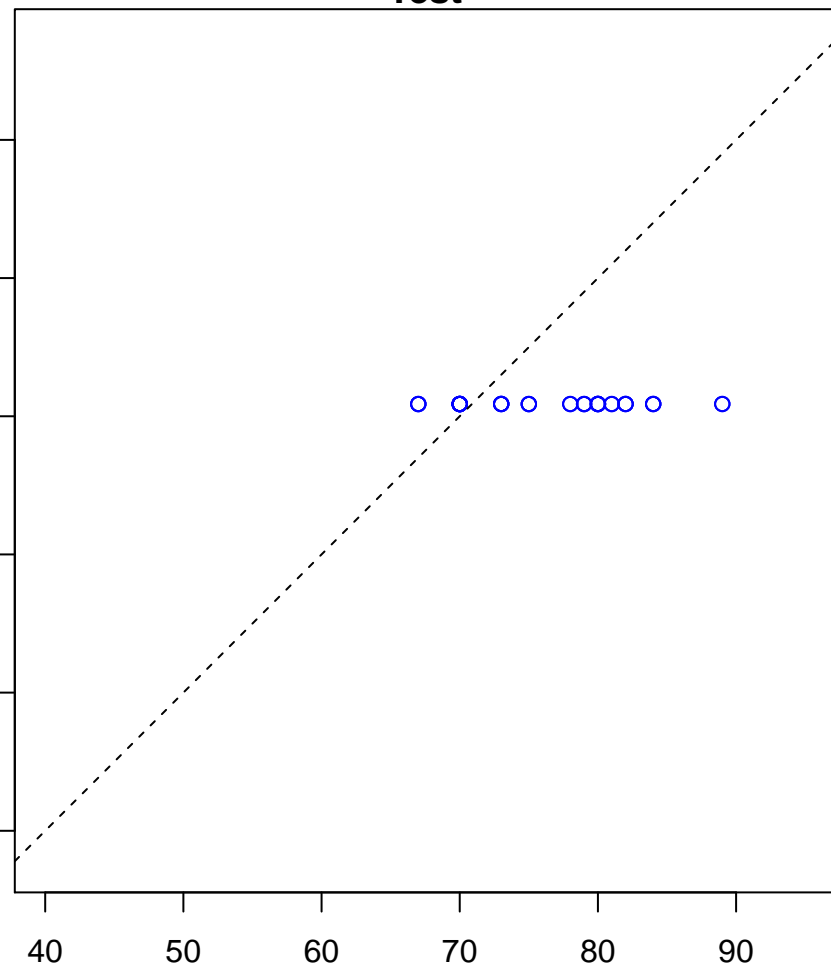
Actual Age

regulation of macrophage migration (Score: 0.803981)

Control

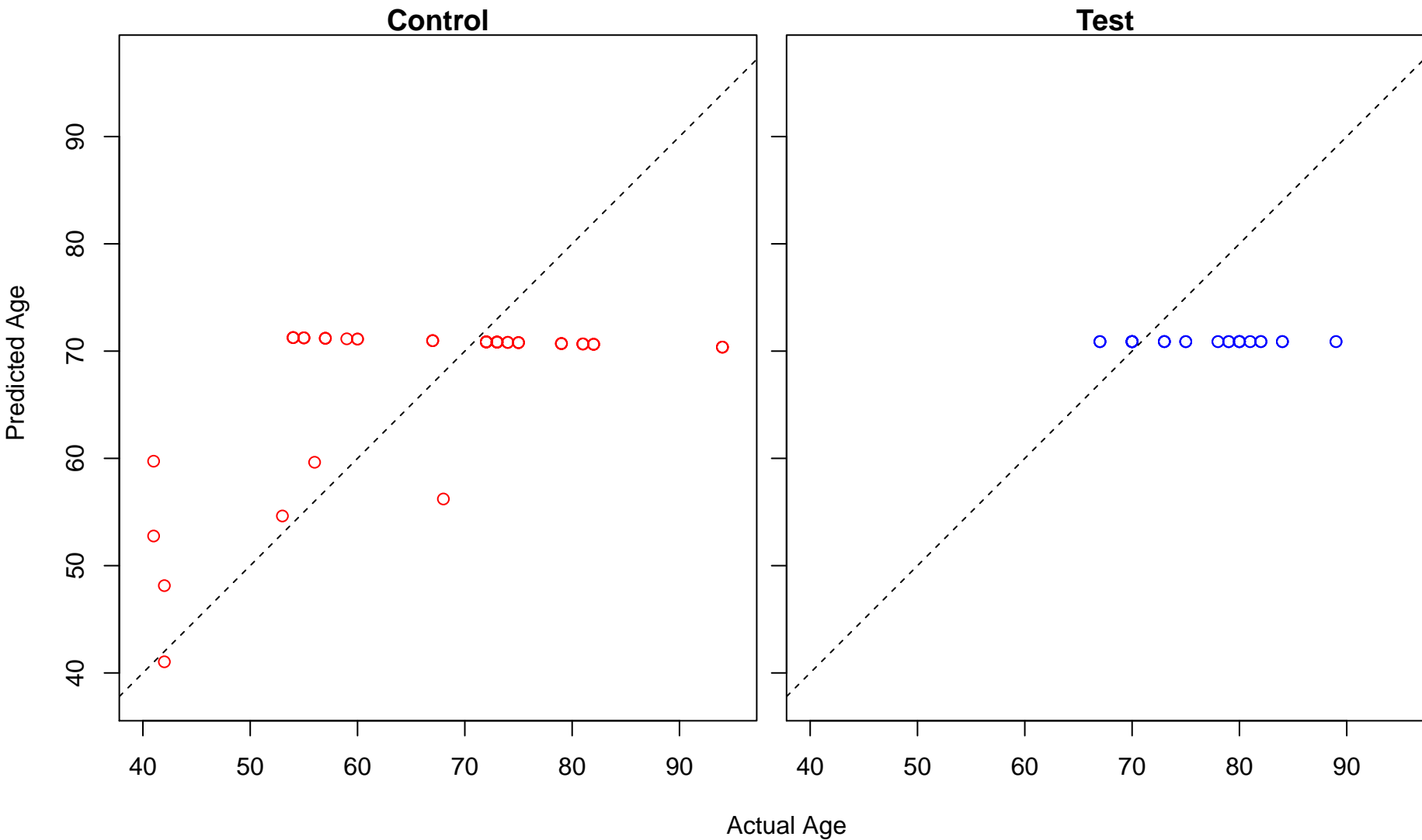


Test



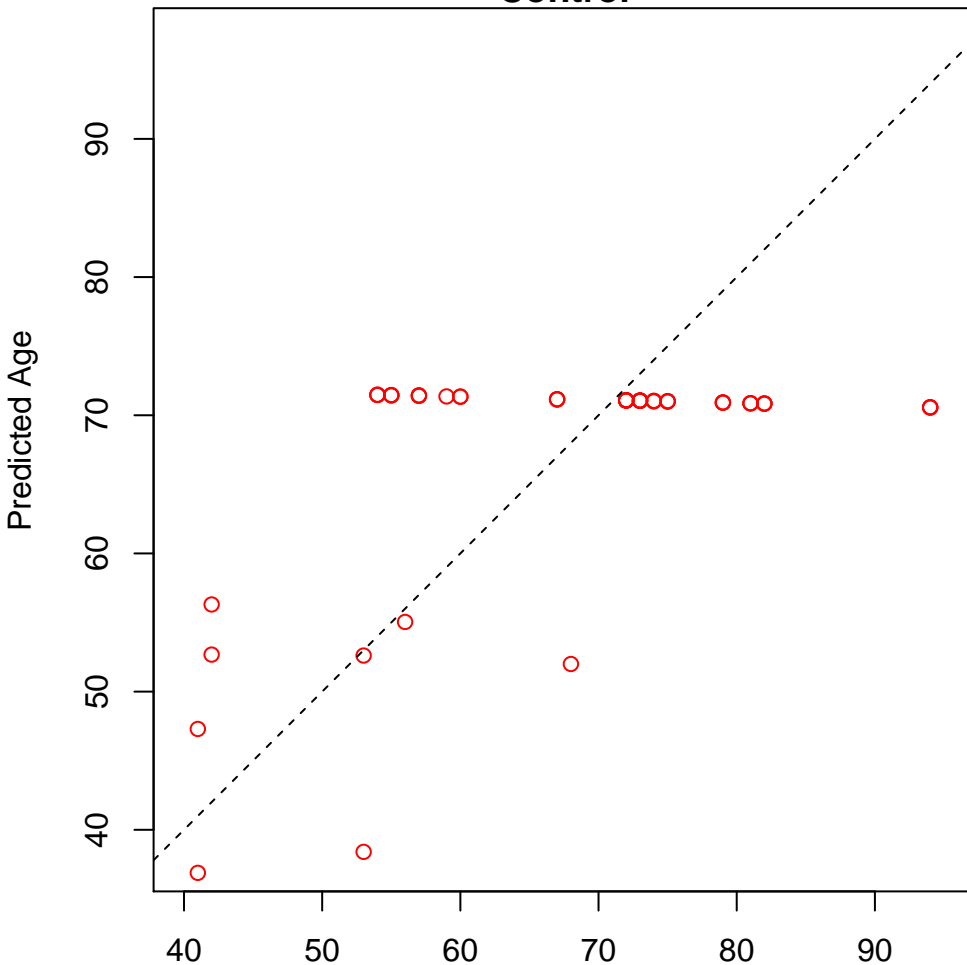
Actual Age

positive regulation of macrophage migration (Score: 0.803981)

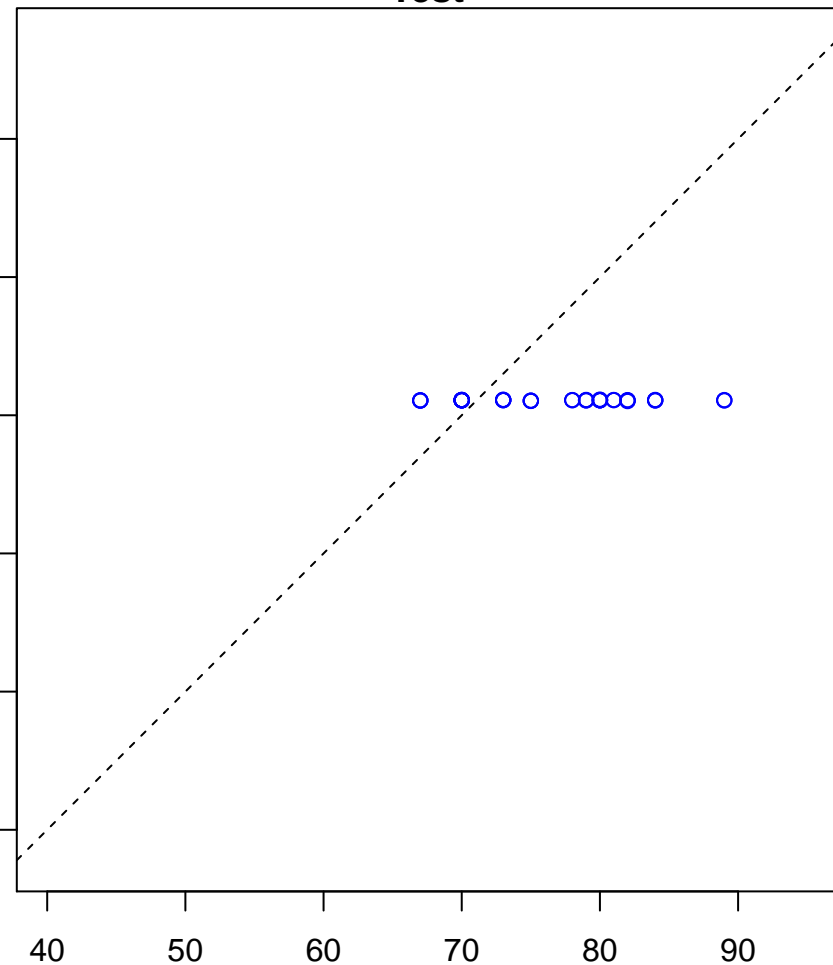


response to molecule of bacterial origin (Score: 0.803787)

Control



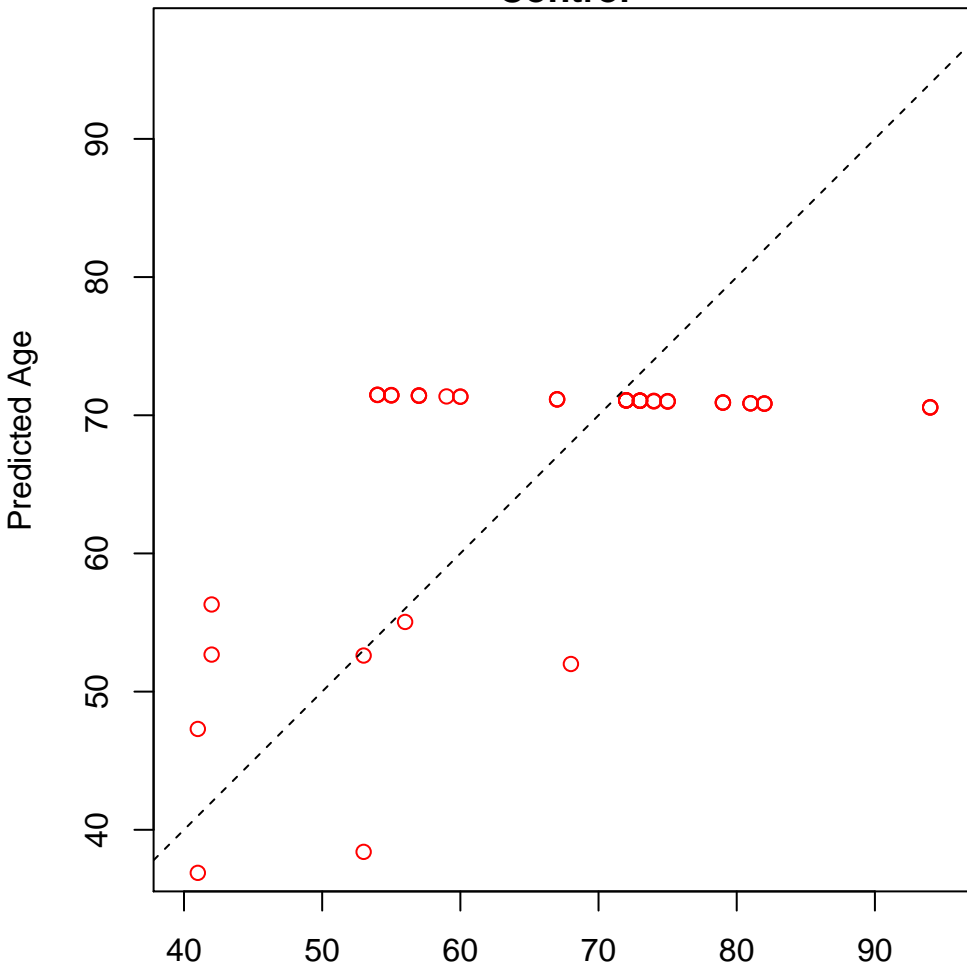
Test



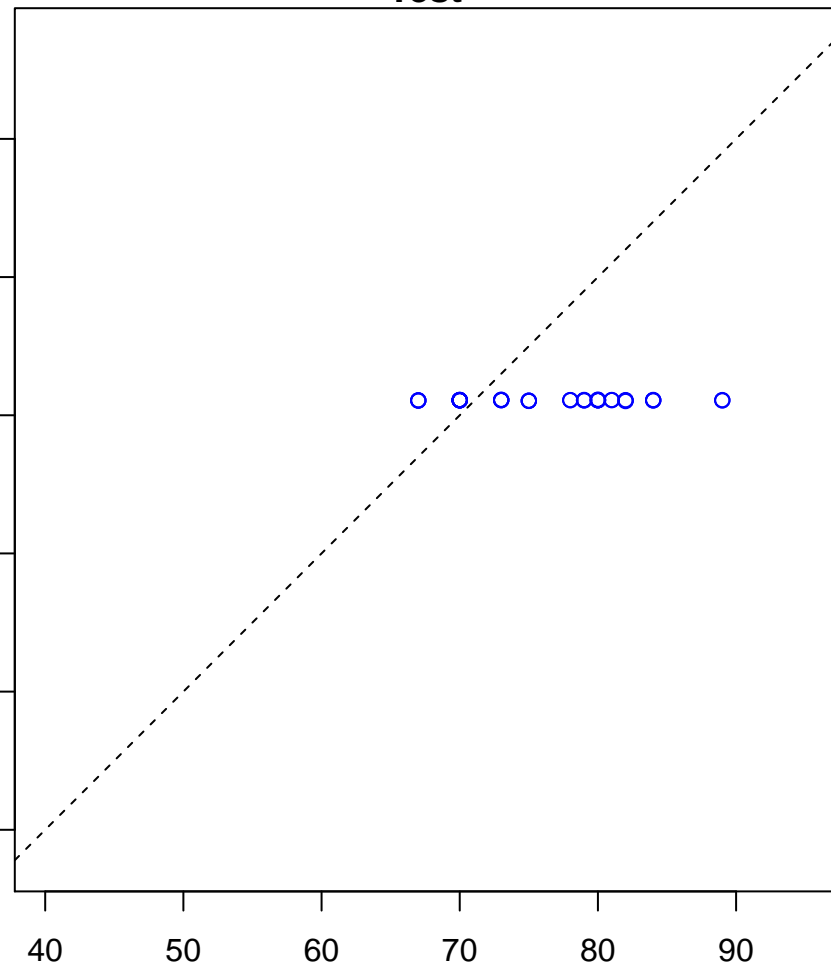
Actual Age

response to lipopolysaccharide (Score: 0.803787)

Control



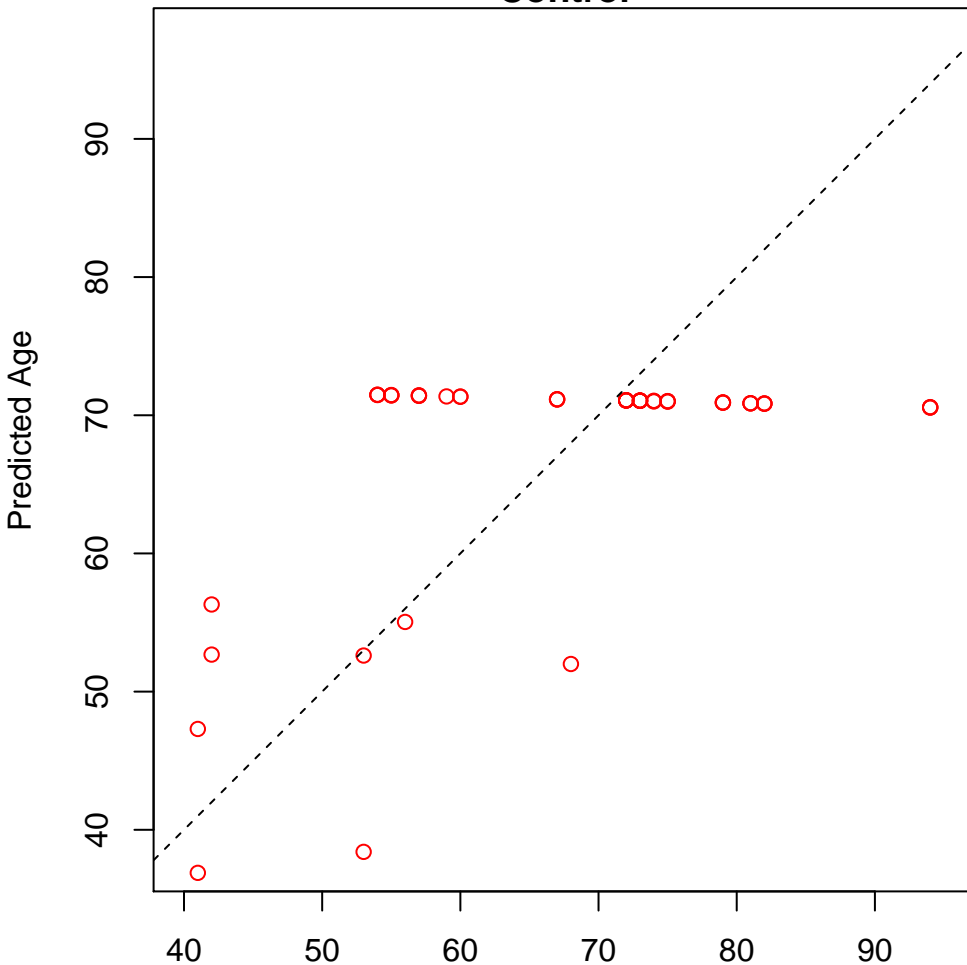
Test



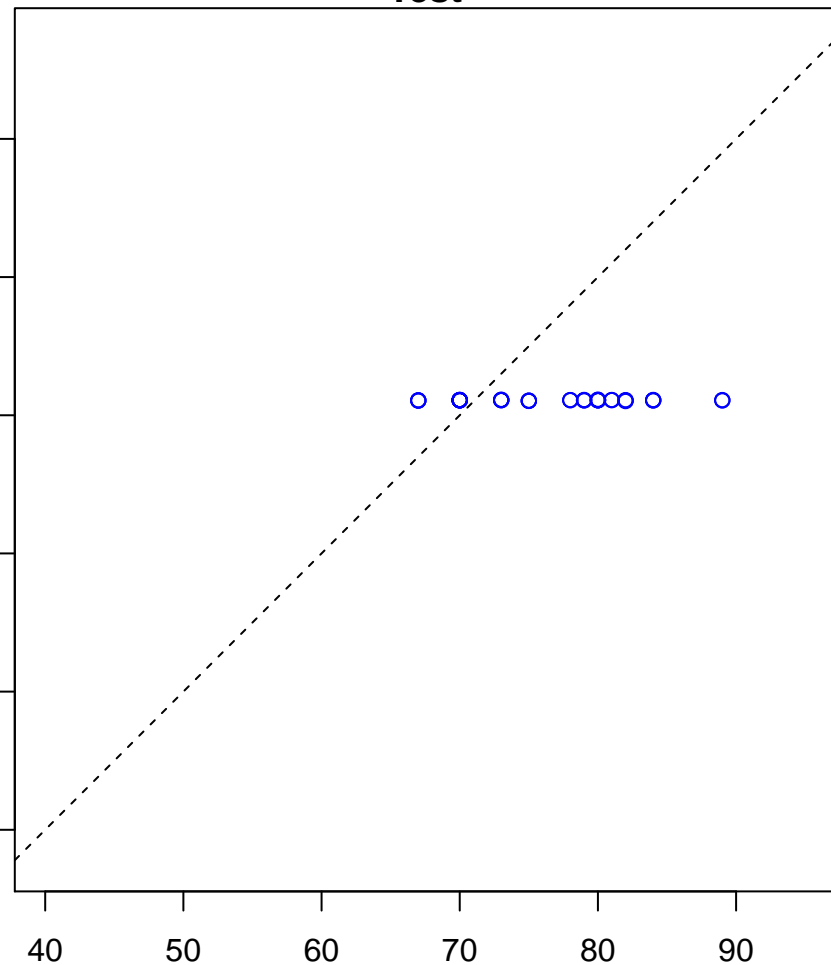
Actual Age

cellular response to biotic stimulus (Score: 0.803787)

Control

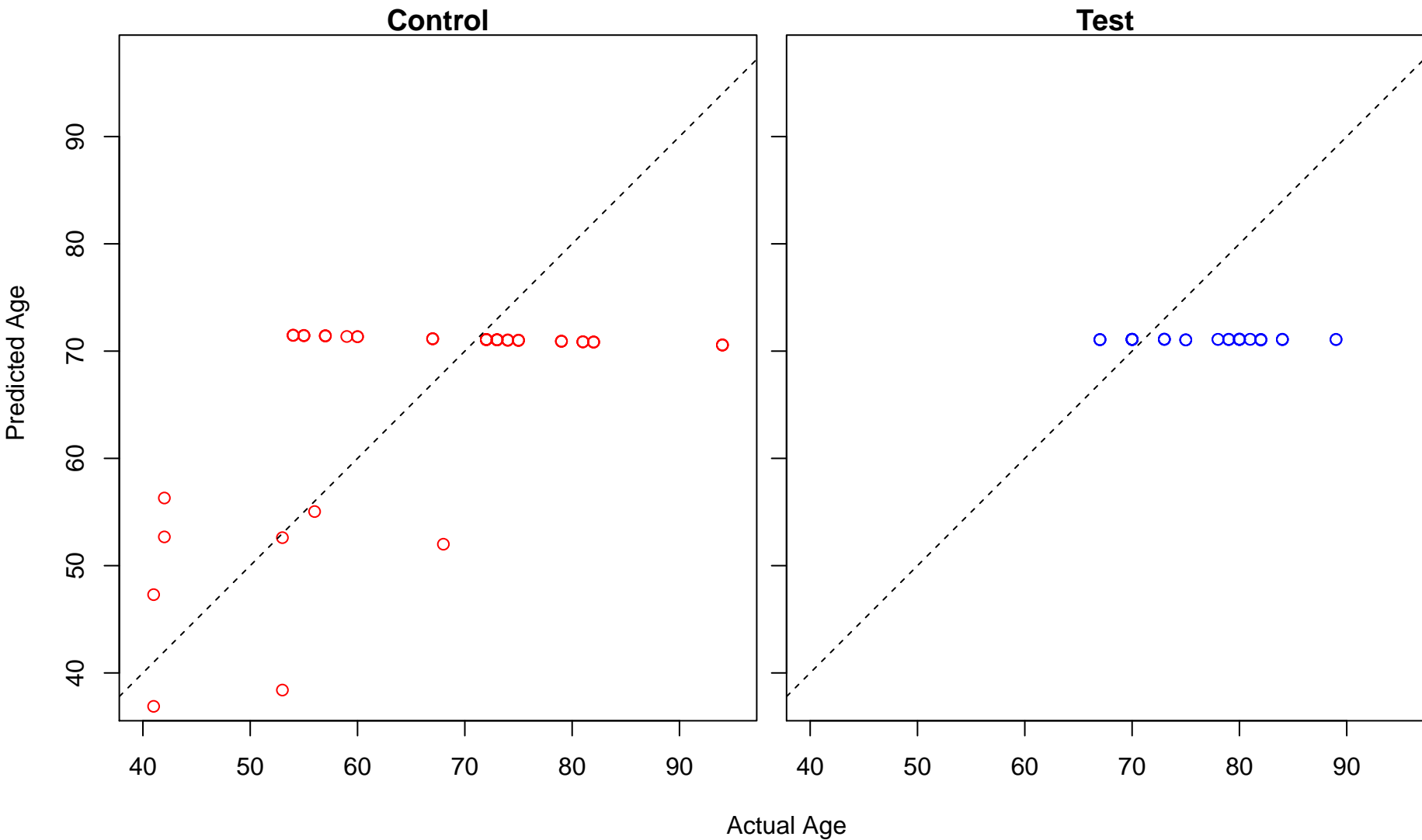


Test



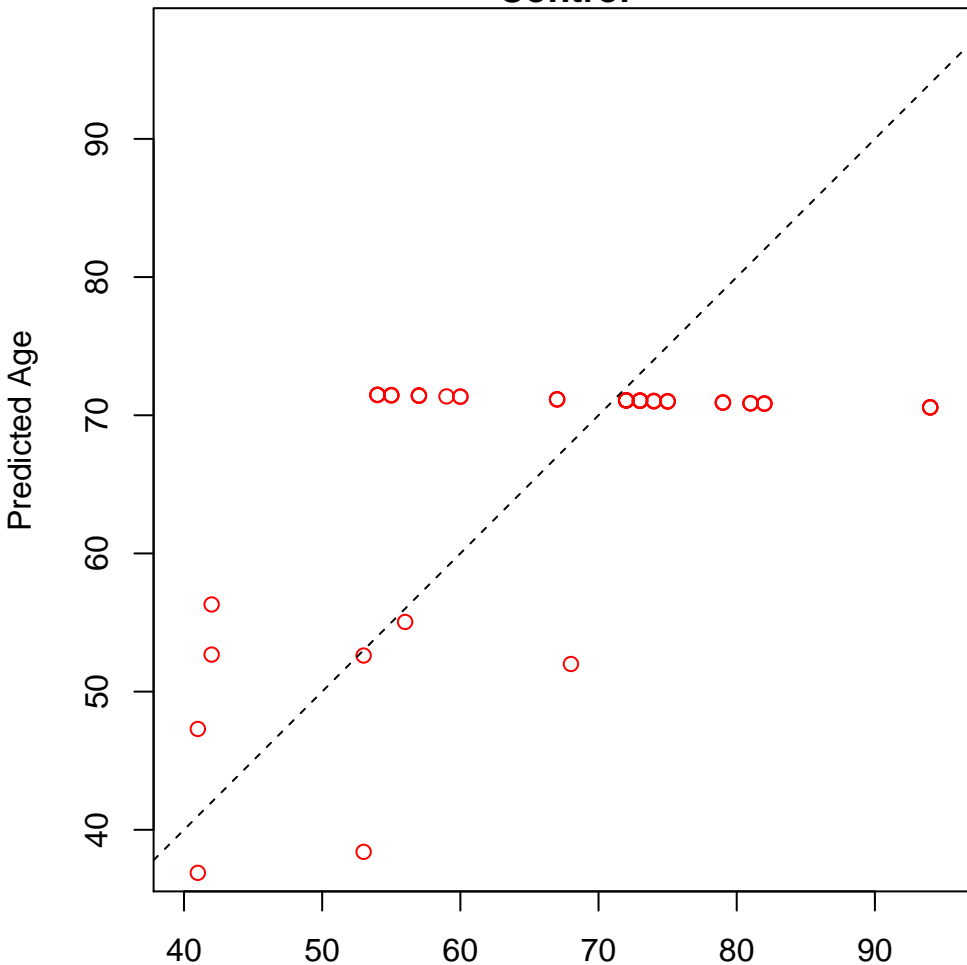
Actual Age

cellular response to molecule of bacterial origin (Score: 0.803787)

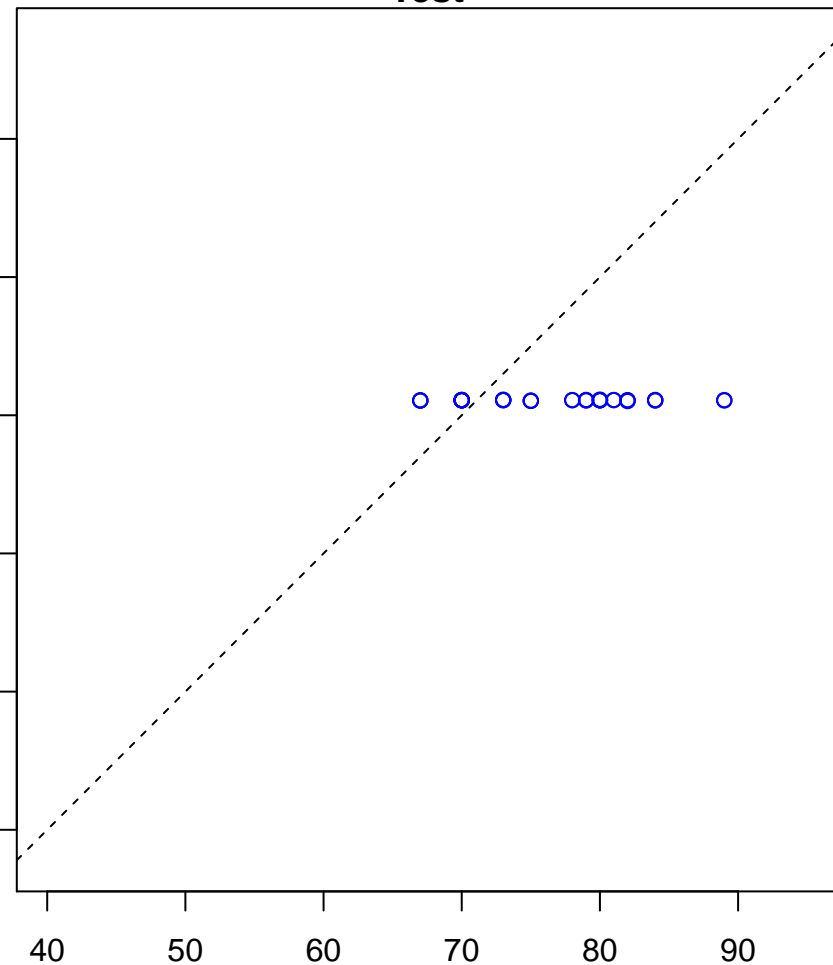


cellular response to lipopolysaccharide (Score: 0.803787)

Control

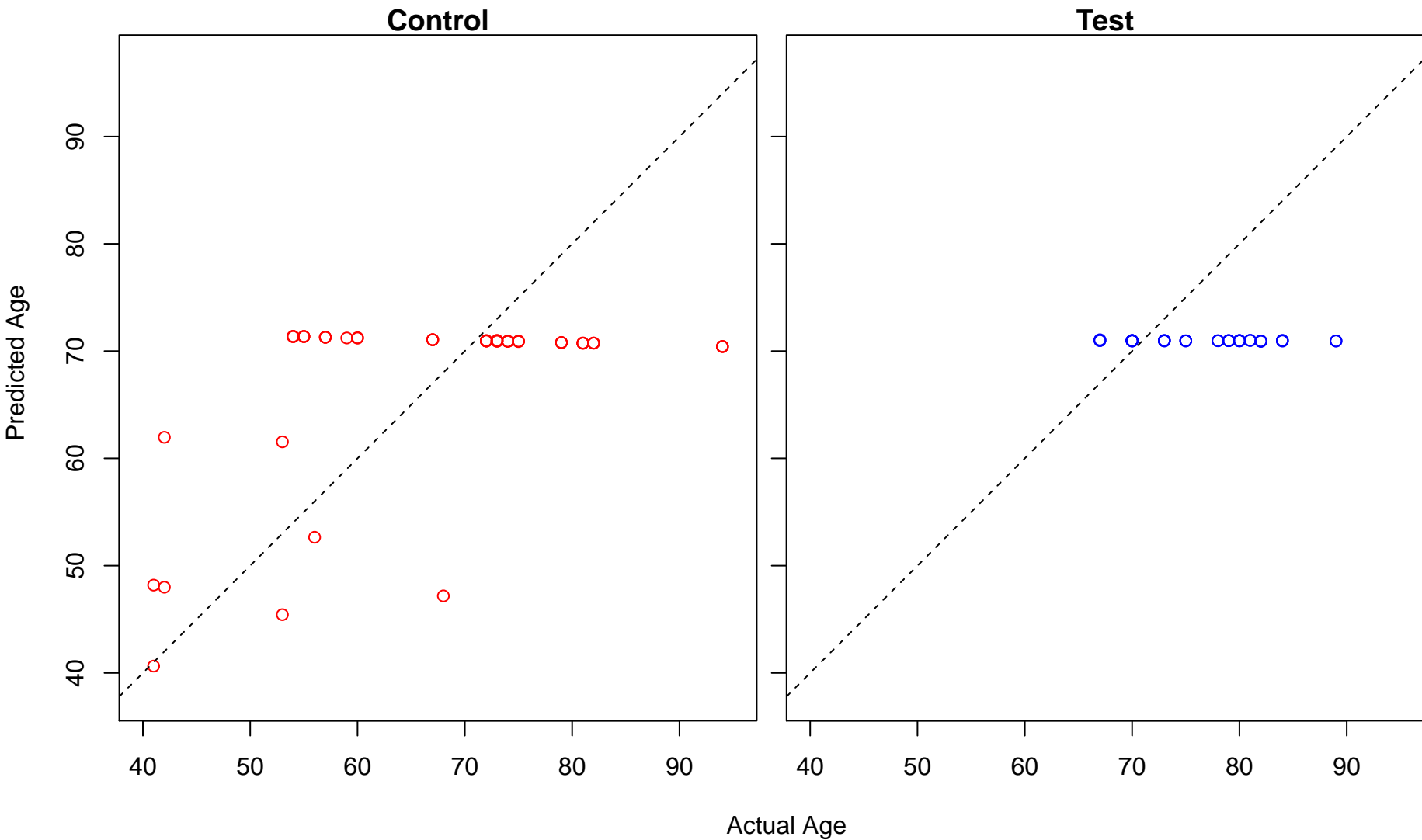


Test

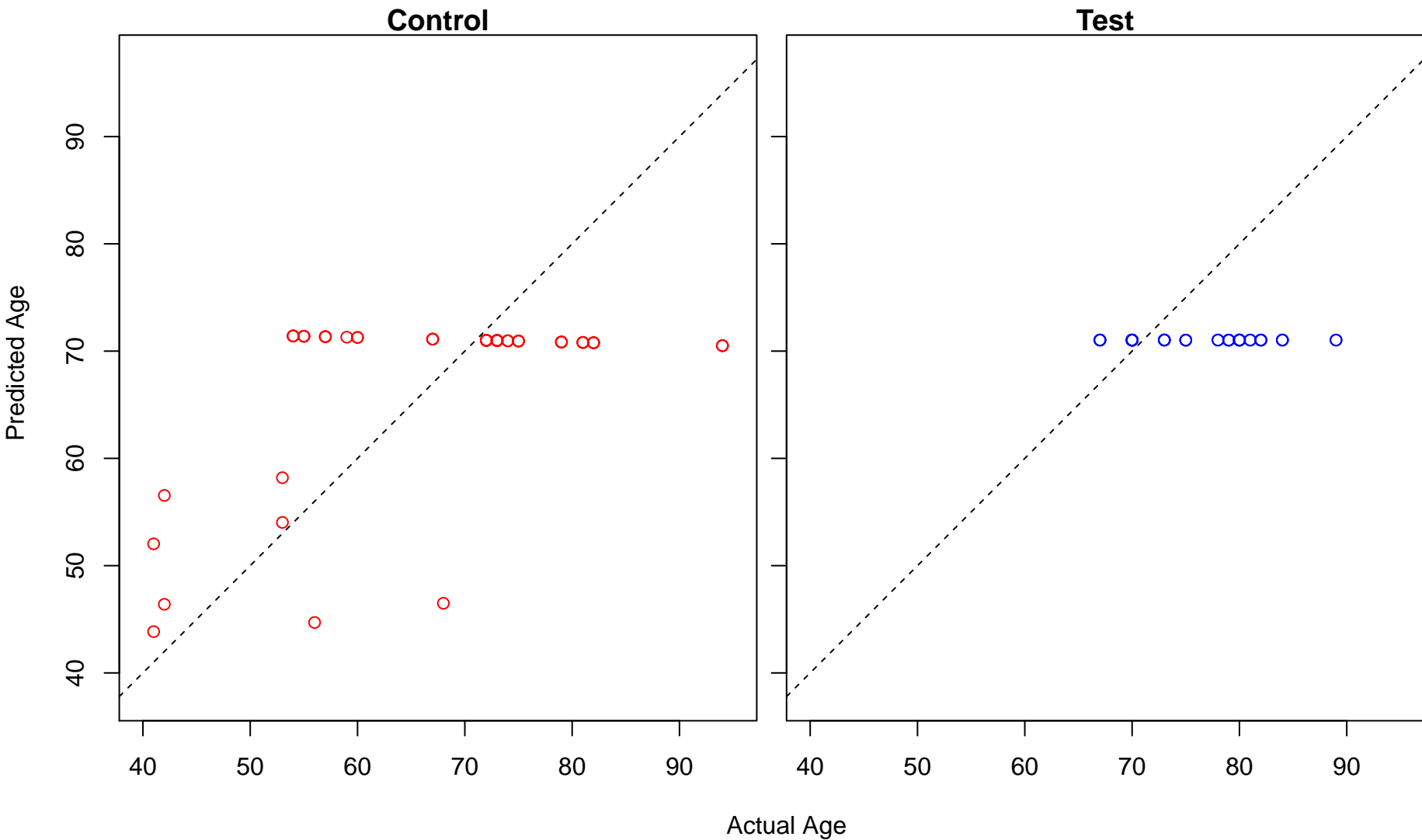


Actual Age

establishment of cell polarity (Score: 0.803770)

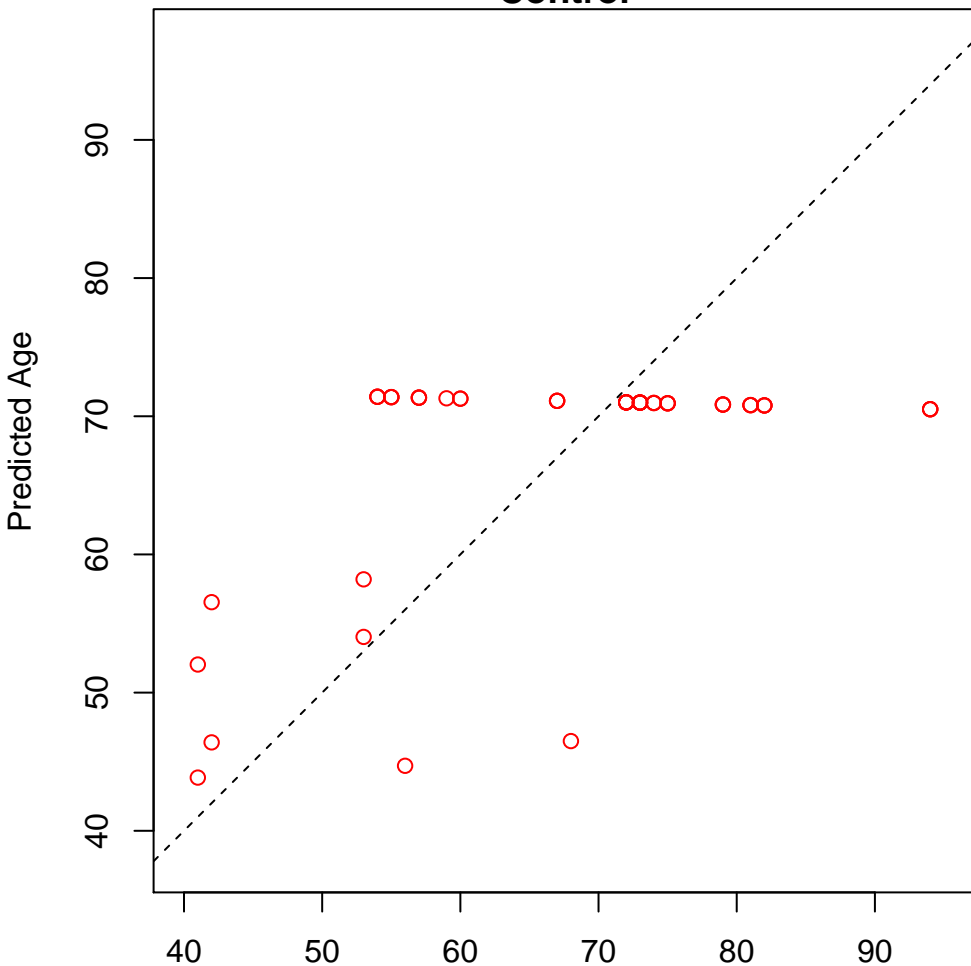


icosanoid metabolic process (Score: 0.803719)

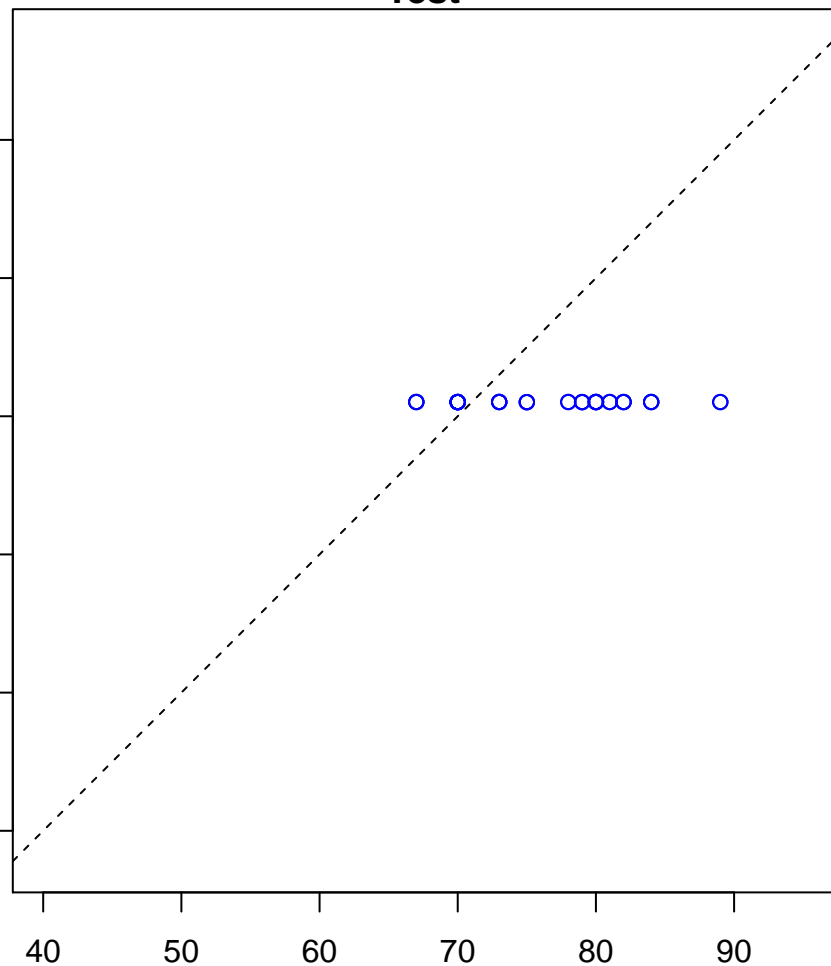


fatty acid derivative metabolic process (Score: 0.803719)

Control



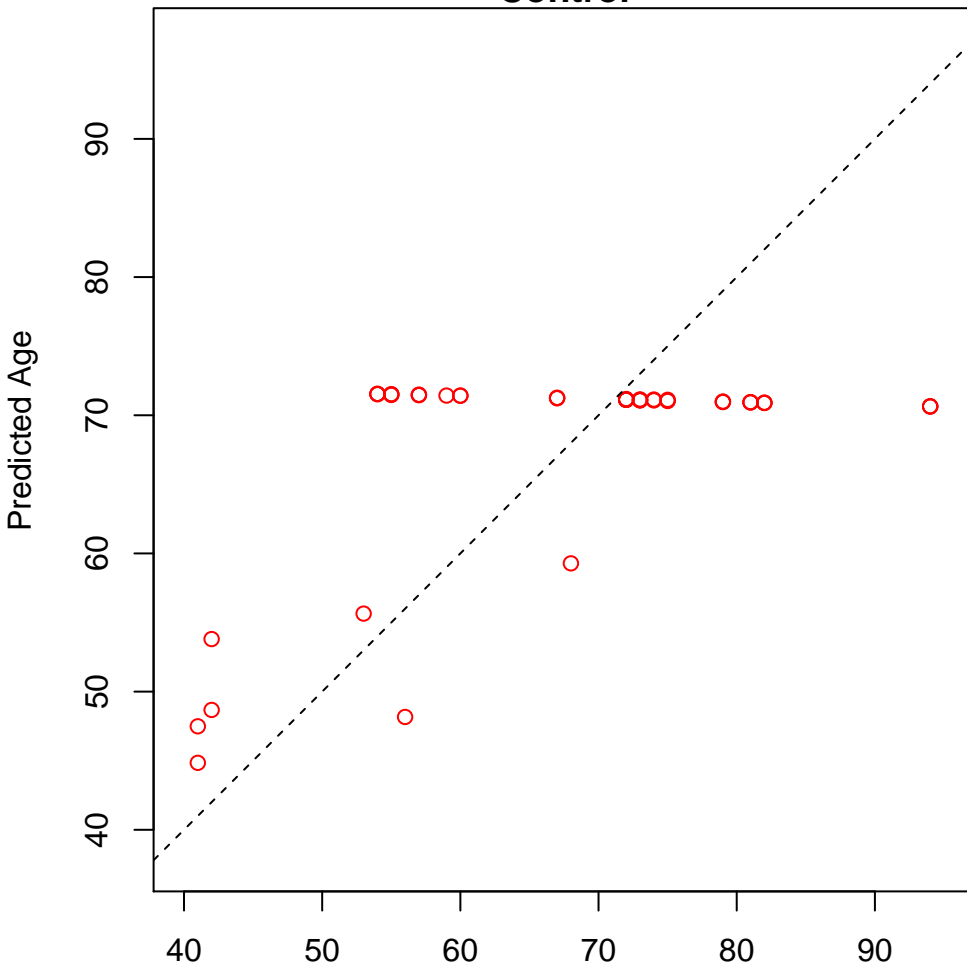
Test



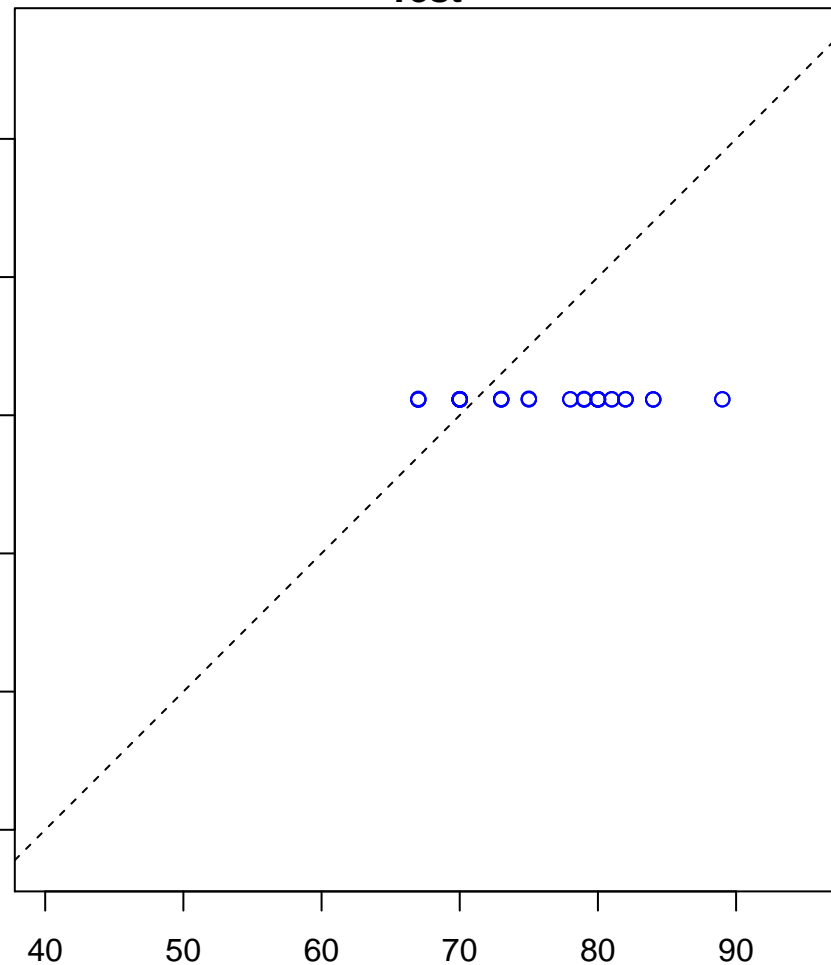
Actual Age

regulation of fibroblast proliferation (Score: 0.803705)

Control



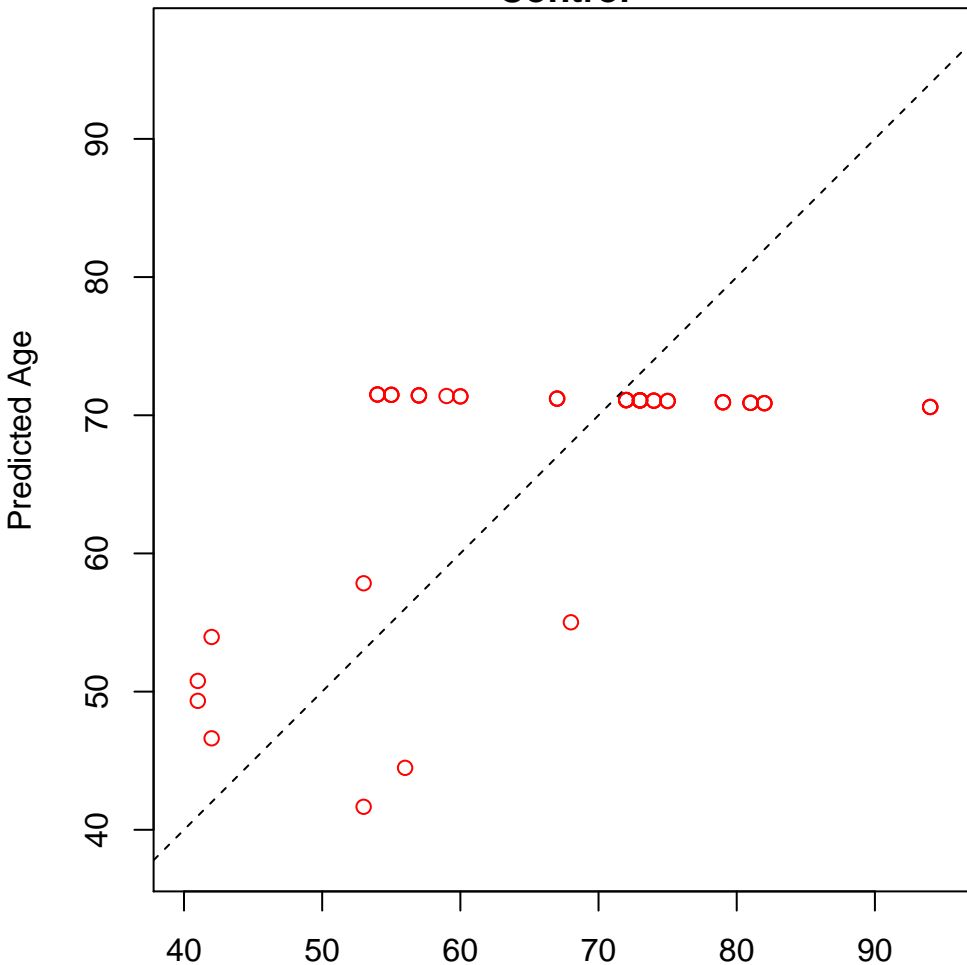
Test



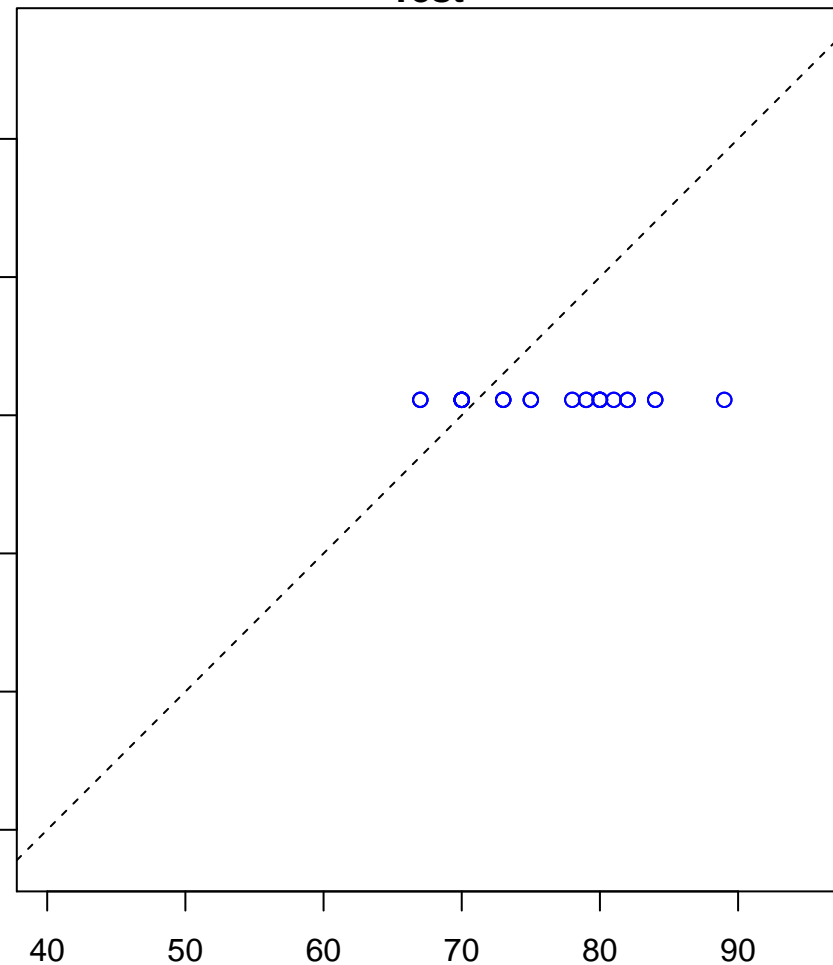
Actual Age

response to endoplasmic reticulum stress (Score: 0.803695)

Control



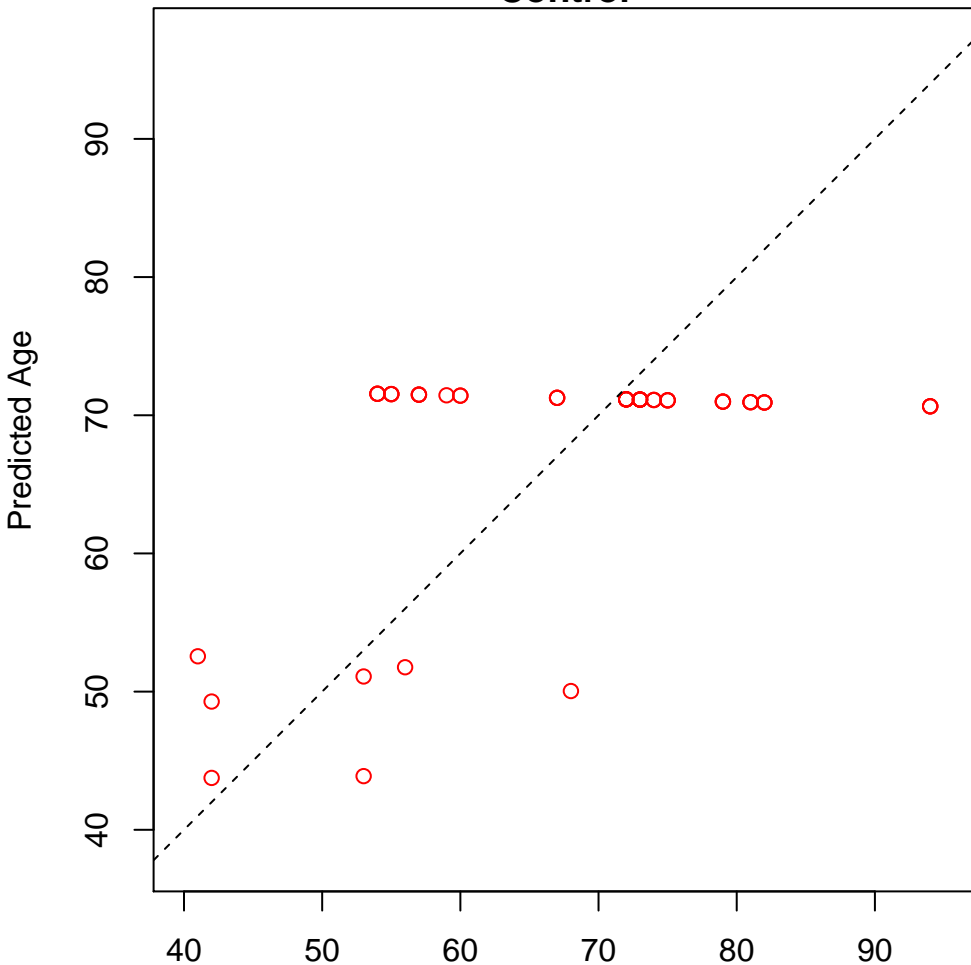
Test



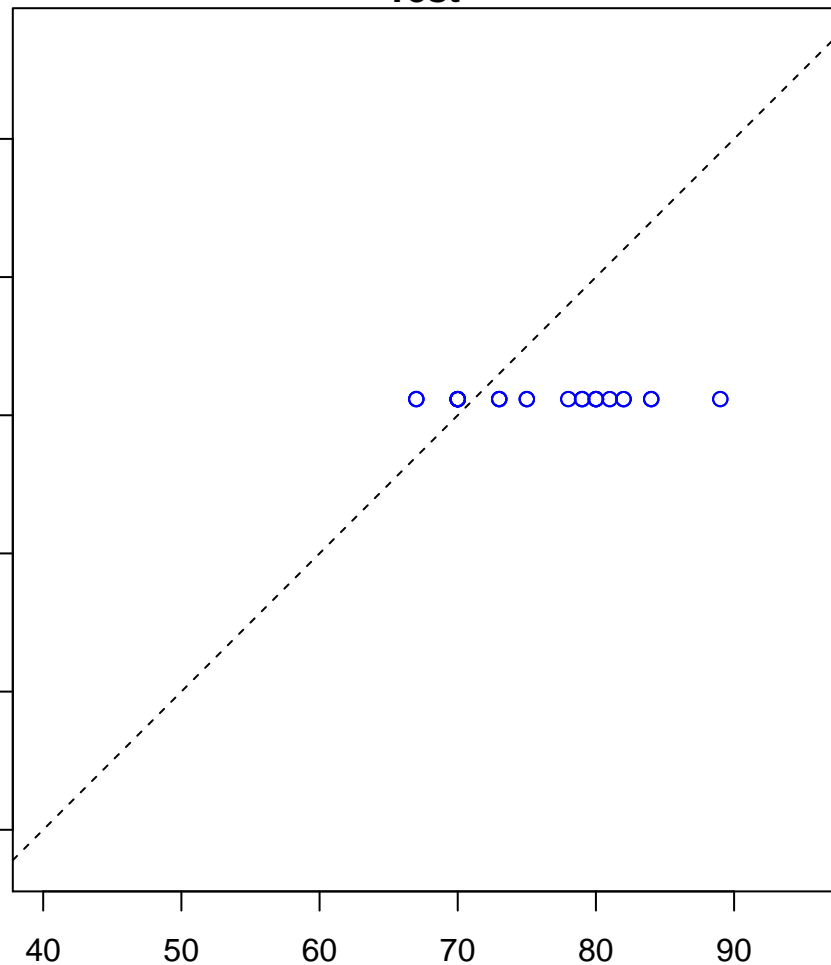
Actual Age

regulation of catabolic process (Score: 0.803628)

Control

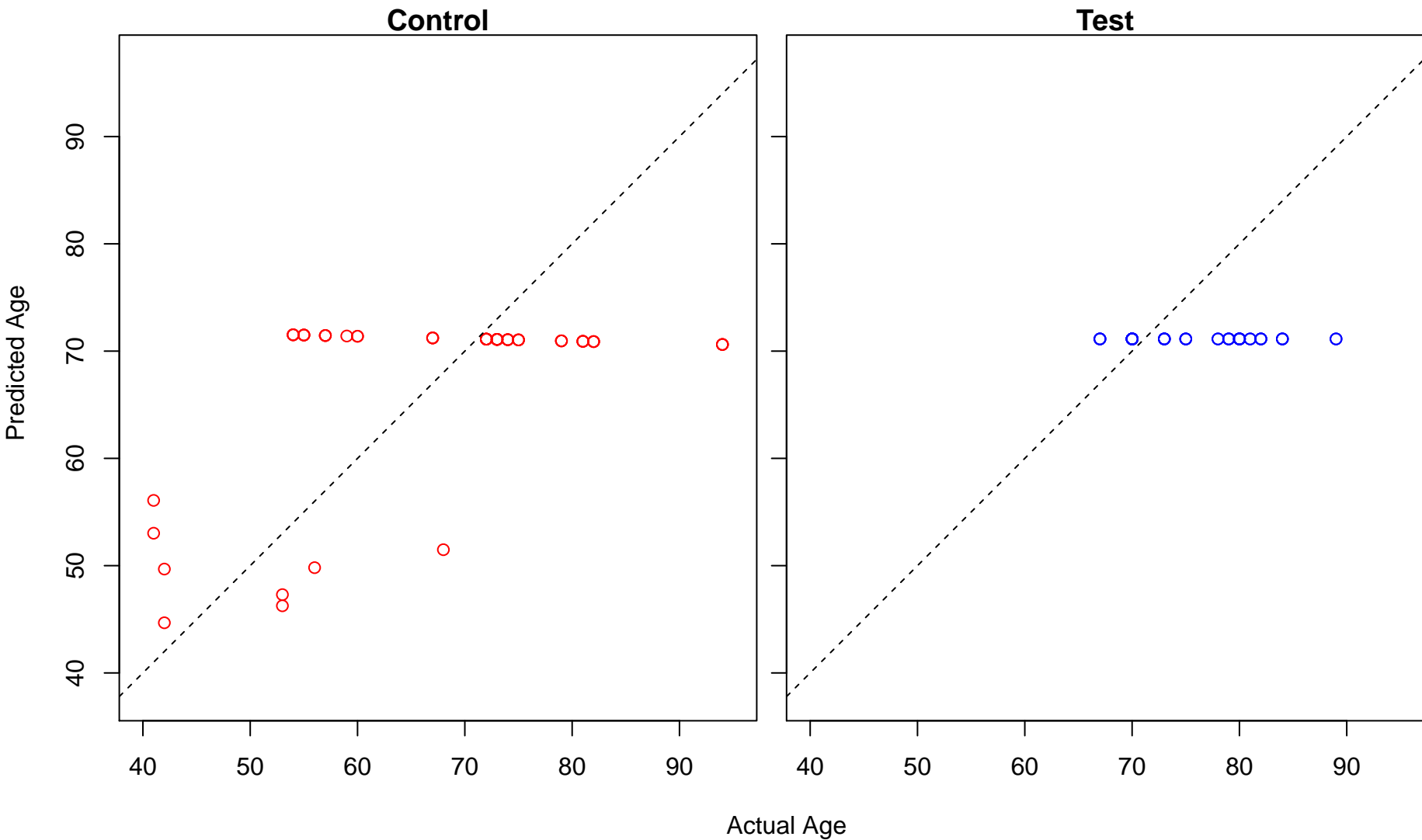


Test

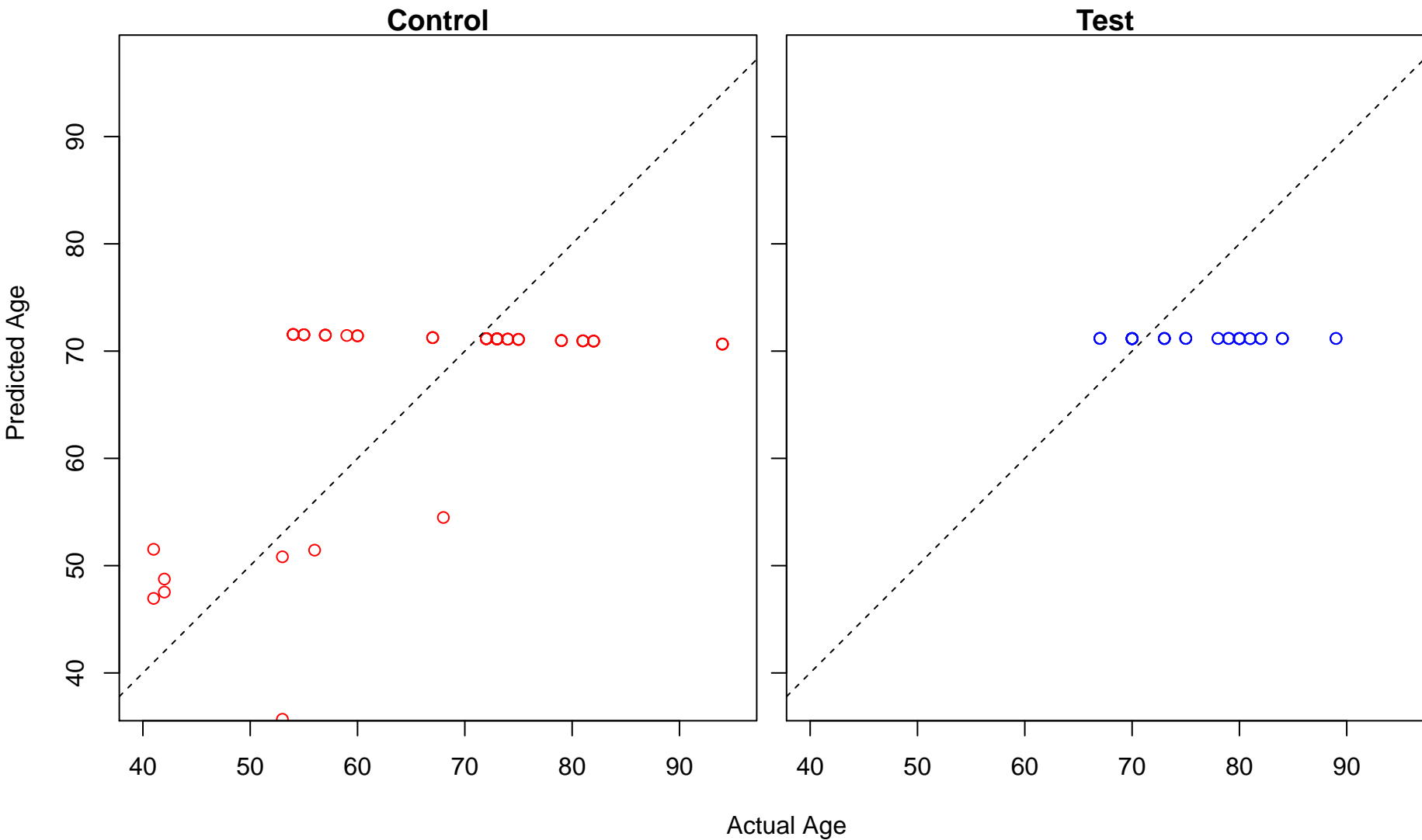


Actual Age

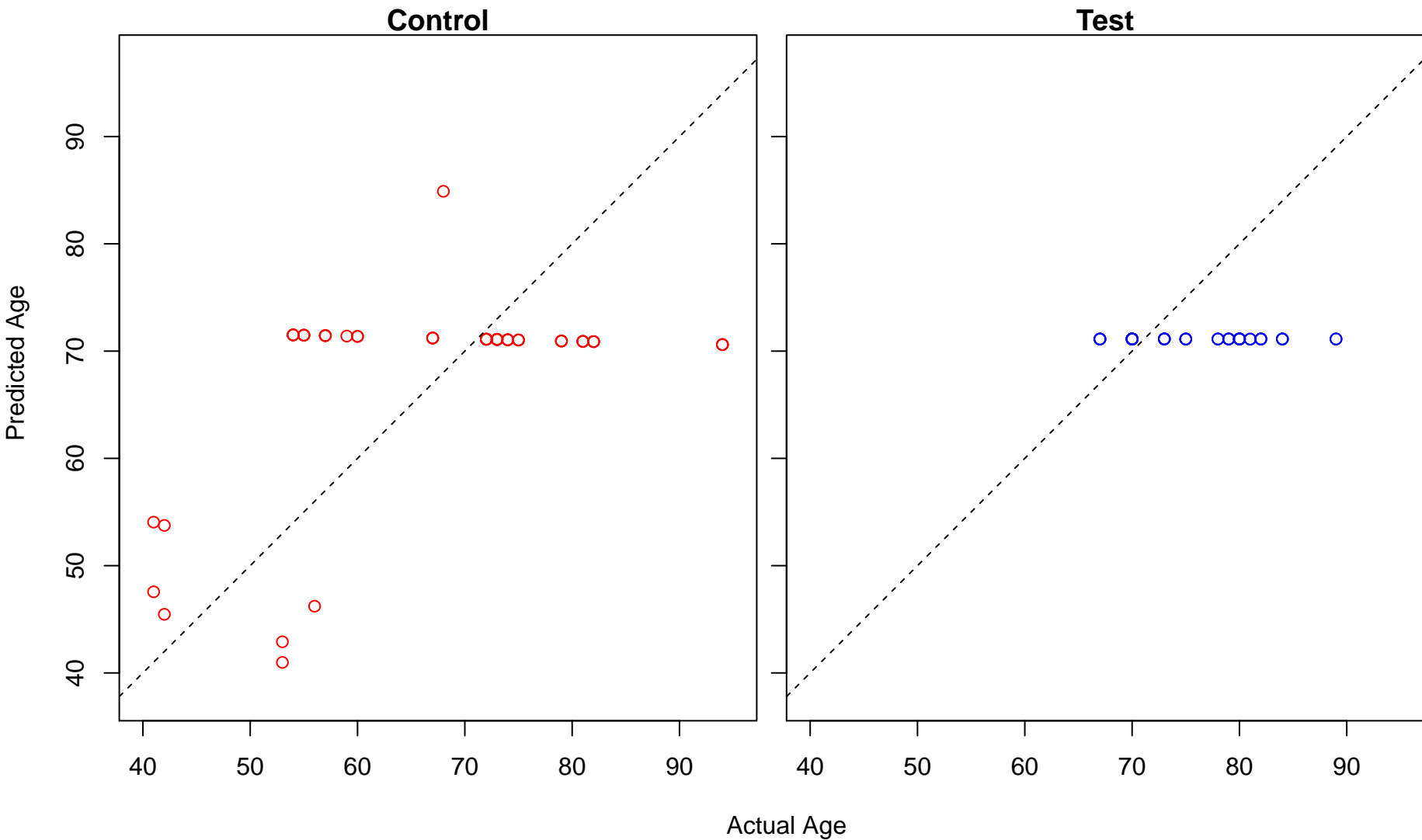
mitochondrion organization (Score: 0.803564)



chromosome segregation (Score: 0.803540)

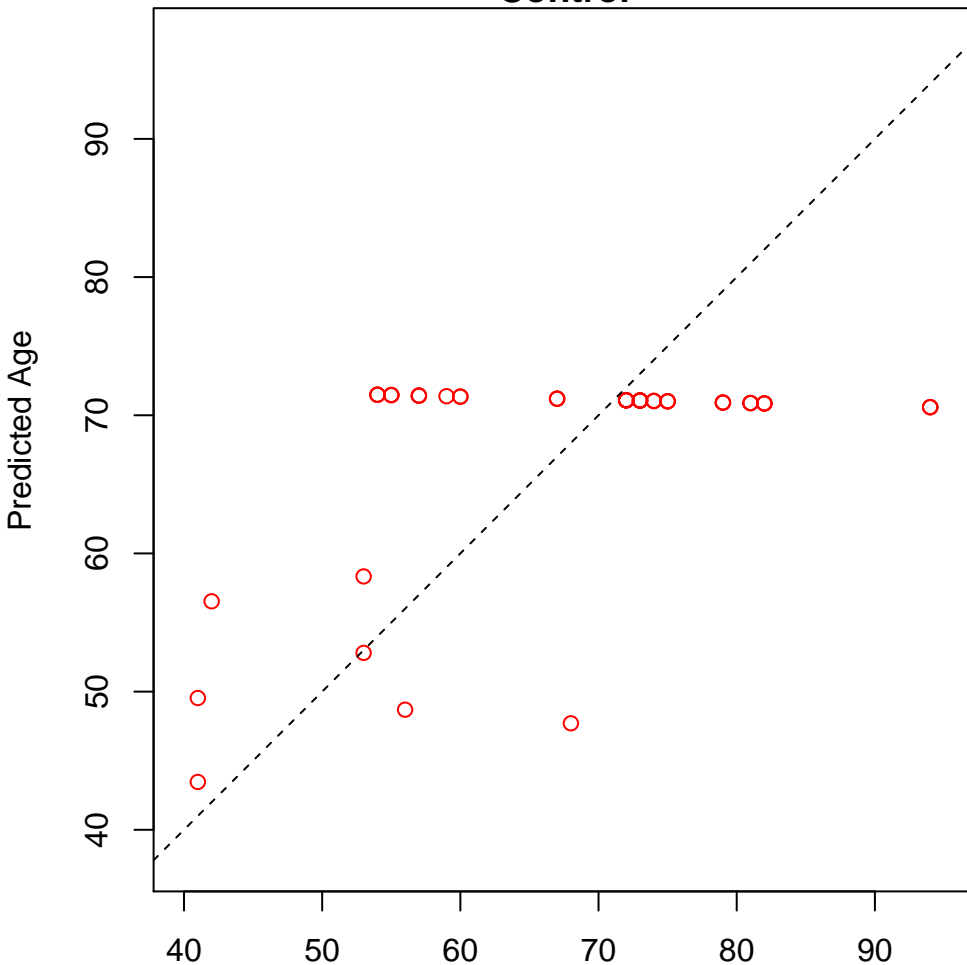


hemopoiesis (Score: 0.803514)

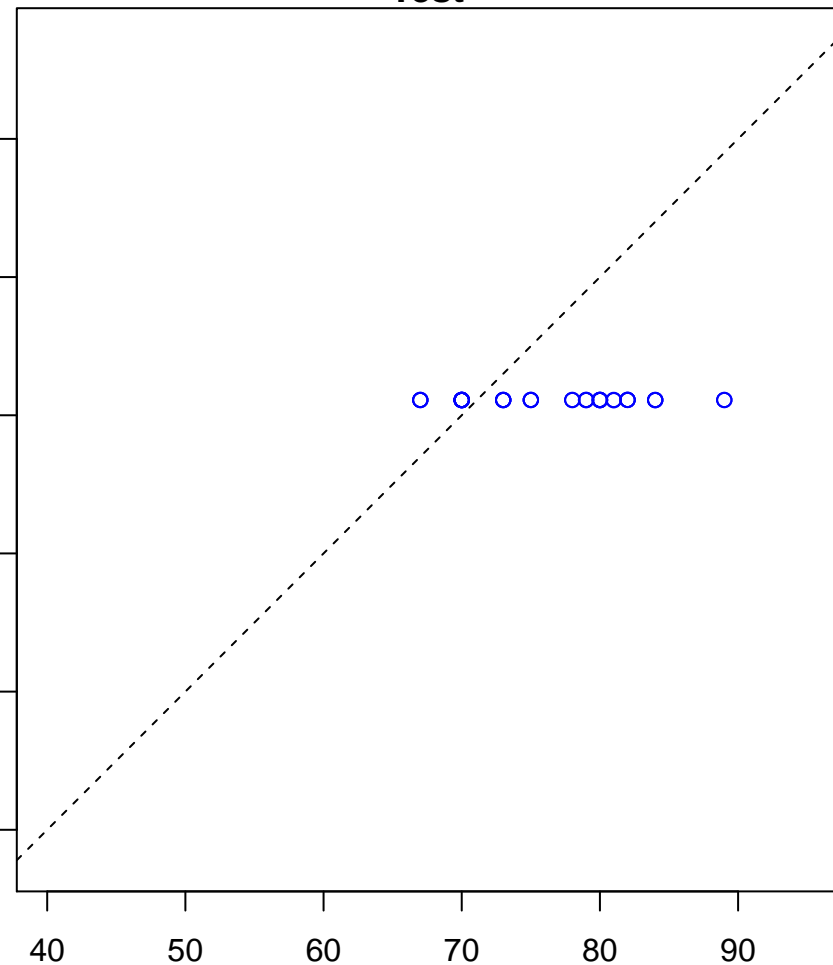


regulation of microtubule-based process (Score: 0.803492)

Control

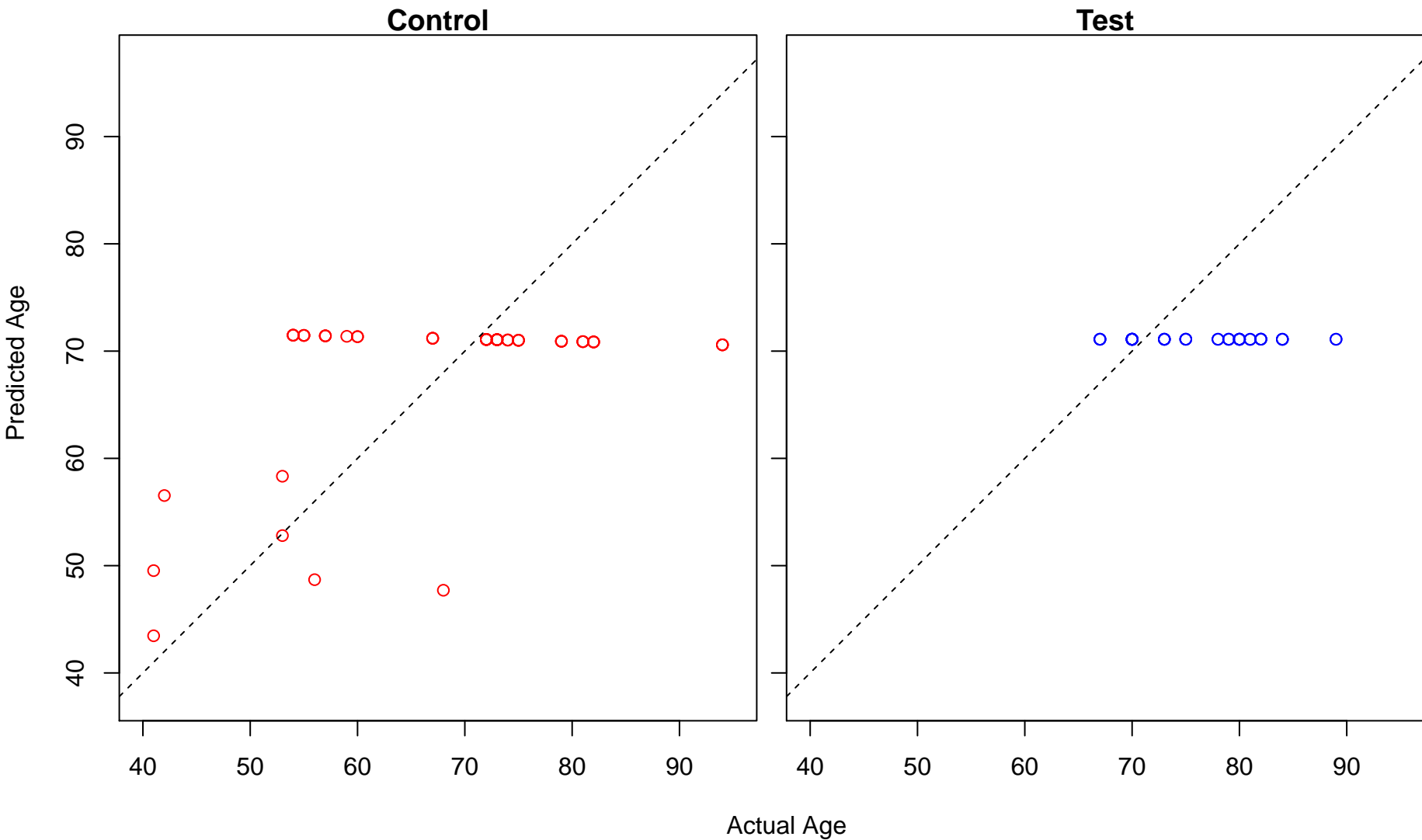


Test



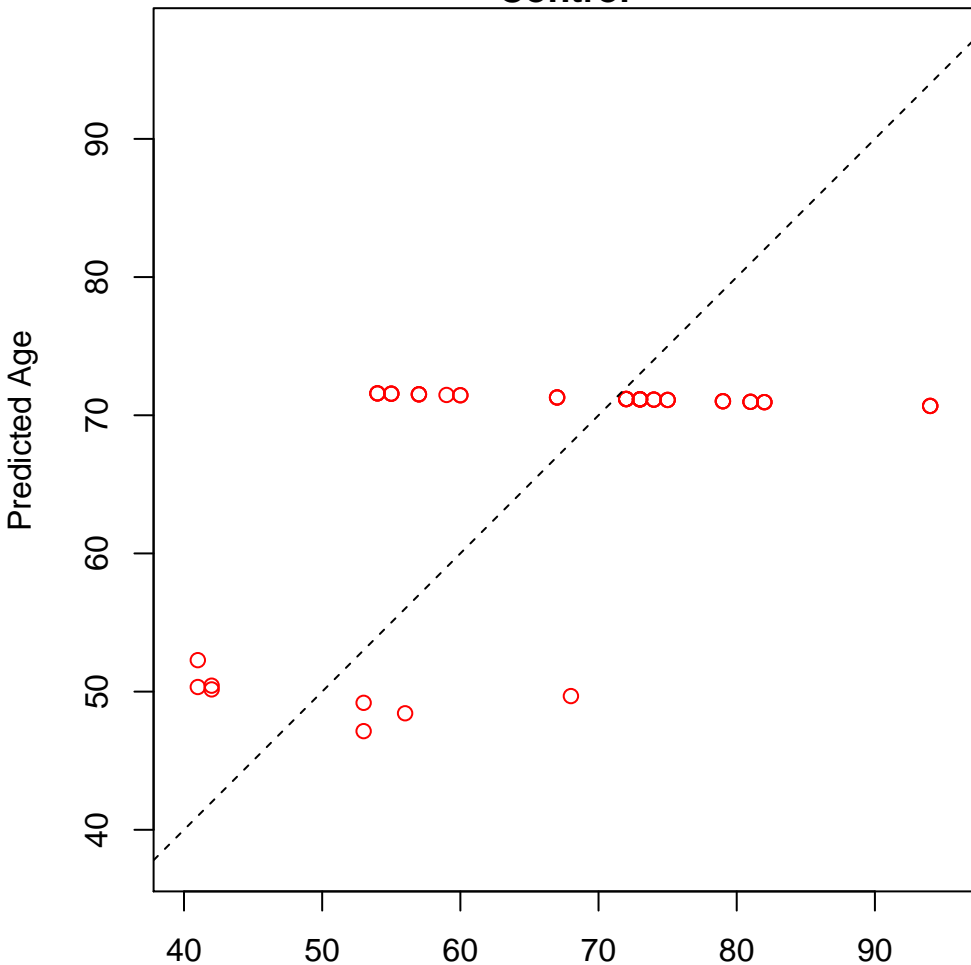
Actual Age

regulation of microtubule cytoskeleton organization (Score: 0.803492)

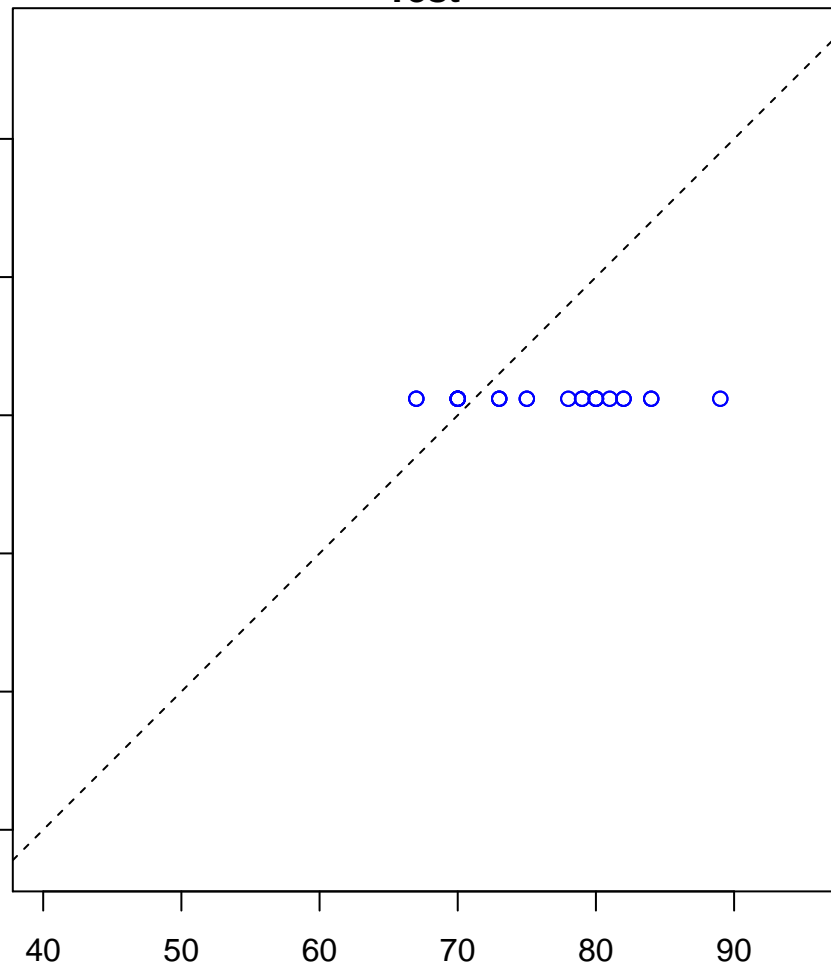


positive regulation of leukocyte activation (Score: 0.803458)

Control



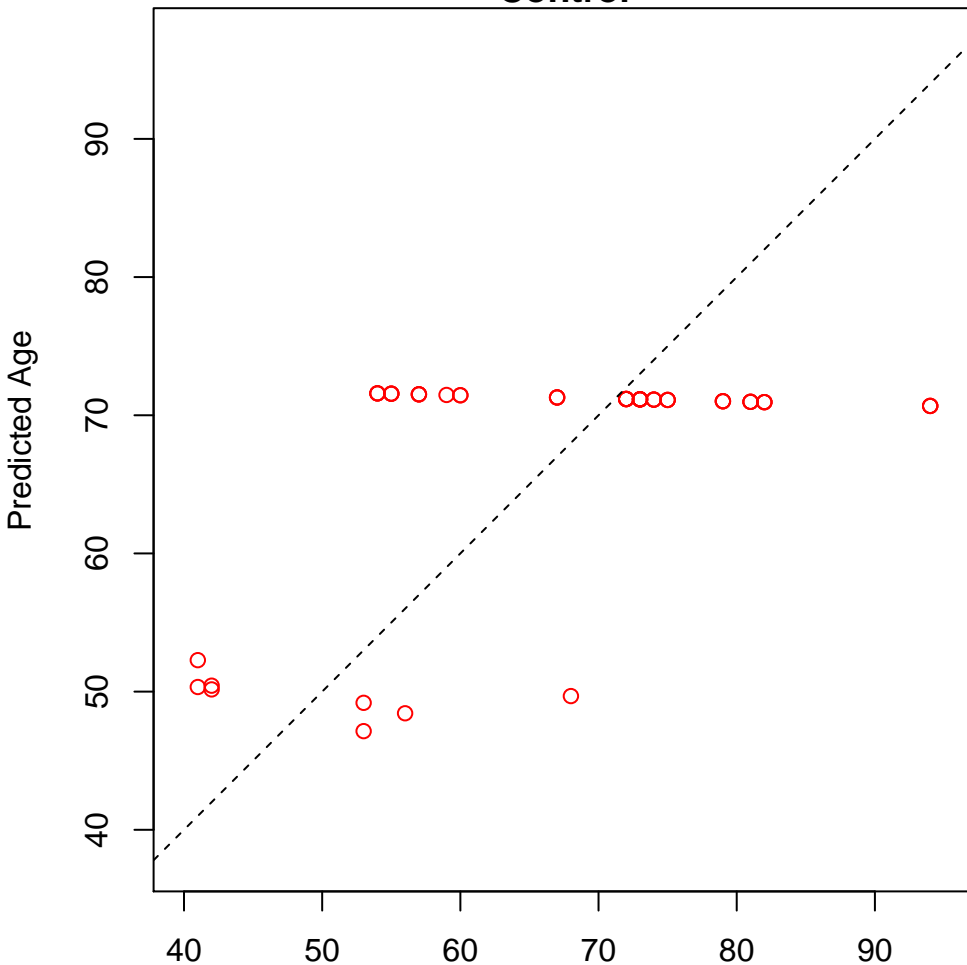
Test



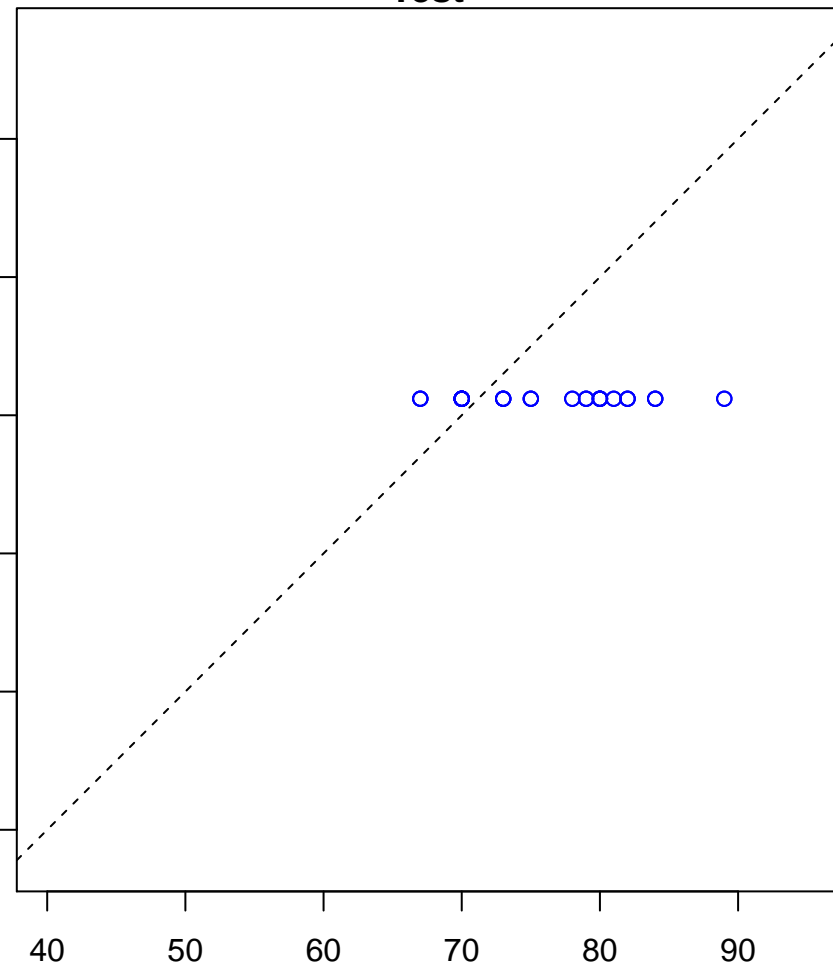
Actual Age

positive regulation of cell activation (Score: 0.803458)

Control



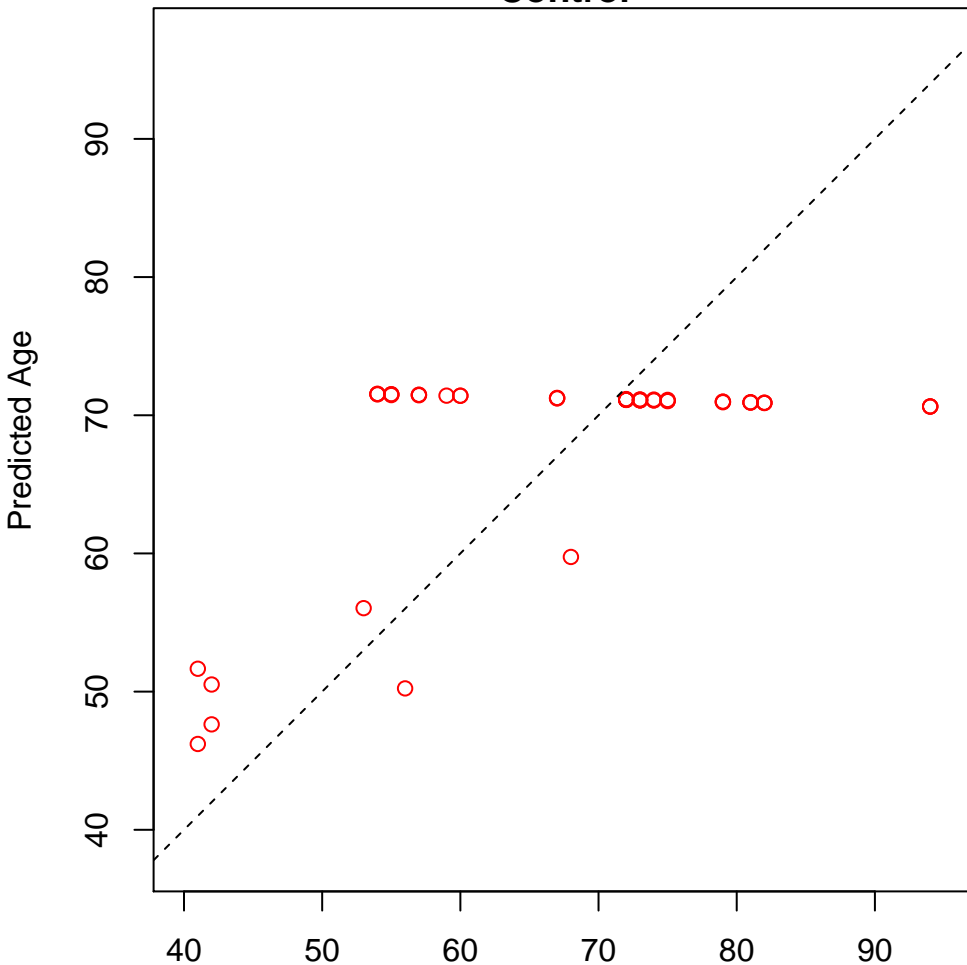
Test



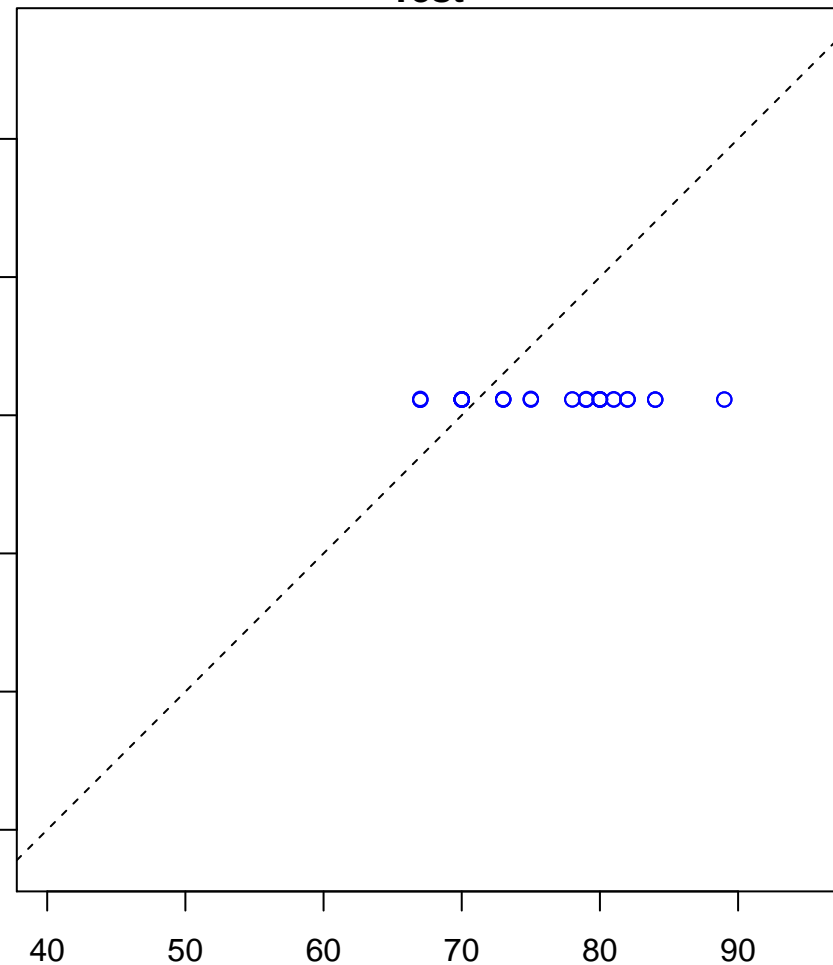
Actual Age

regulation of nucleocytoplasmic transport (Score: 0.803454)

Control

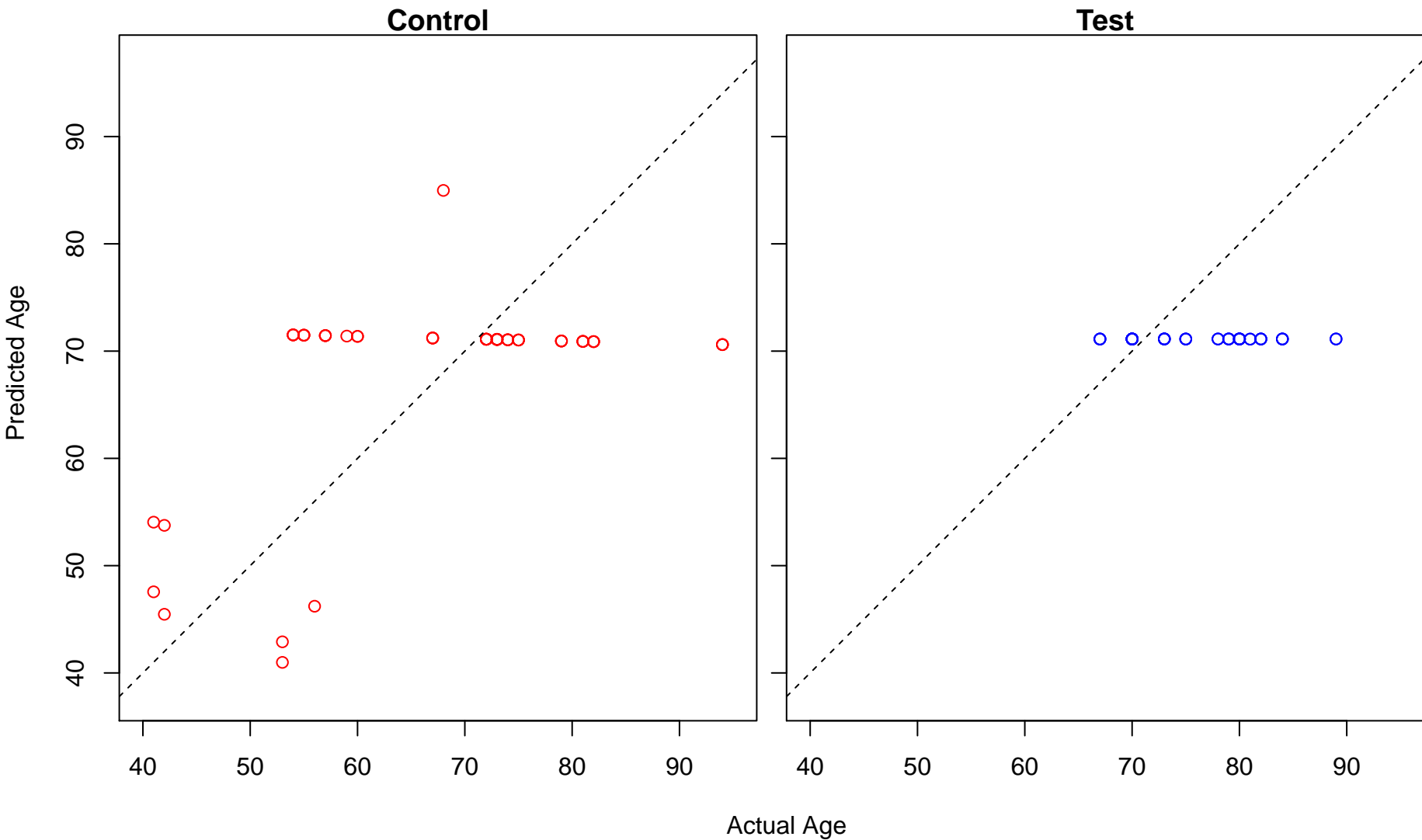


Test

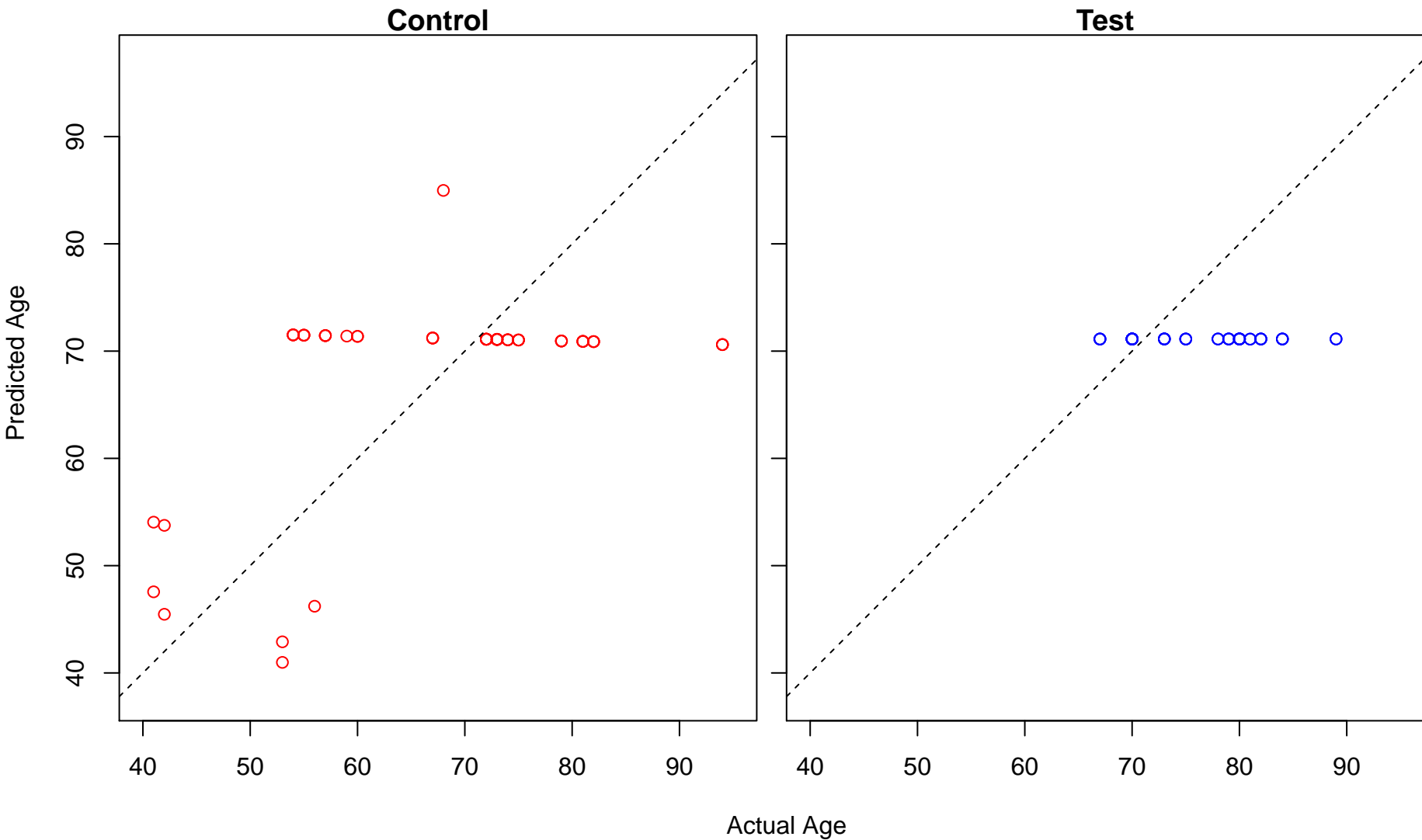


Actual Age

immune system development (Score: 0.803453)

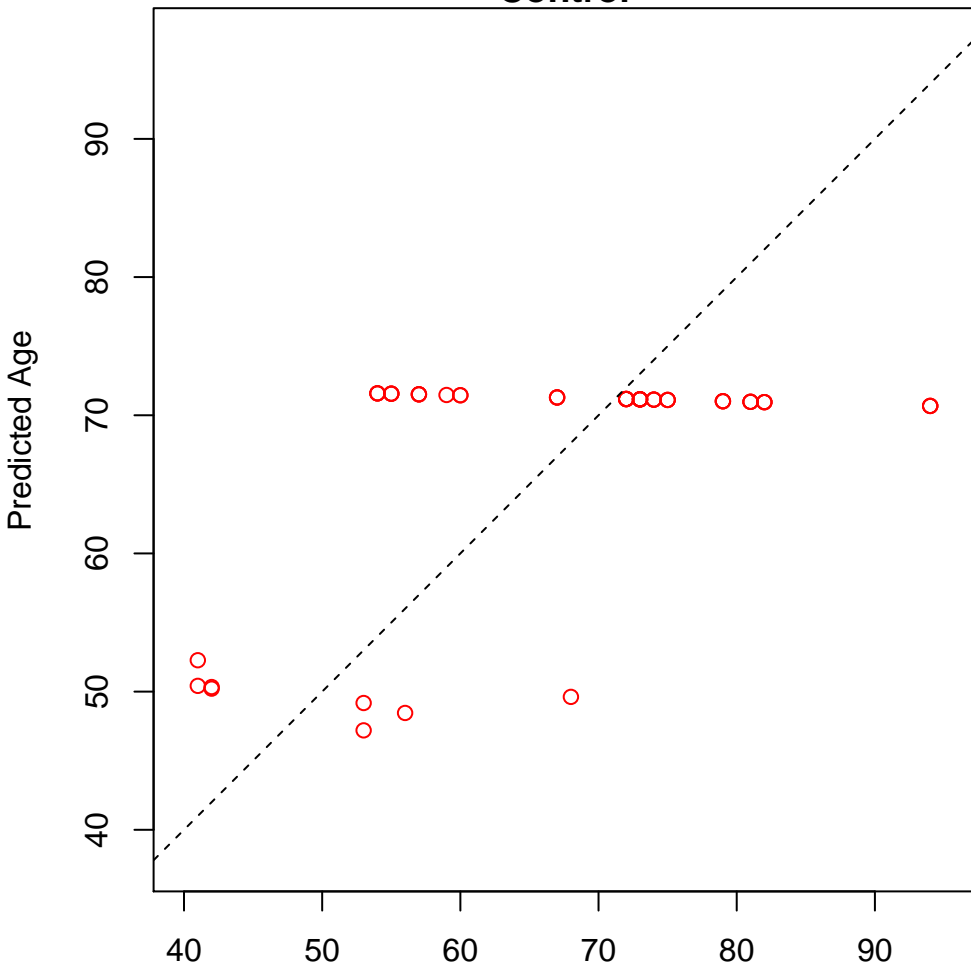


hematopoietic or lymphoid organ development (Score: 0.803453)

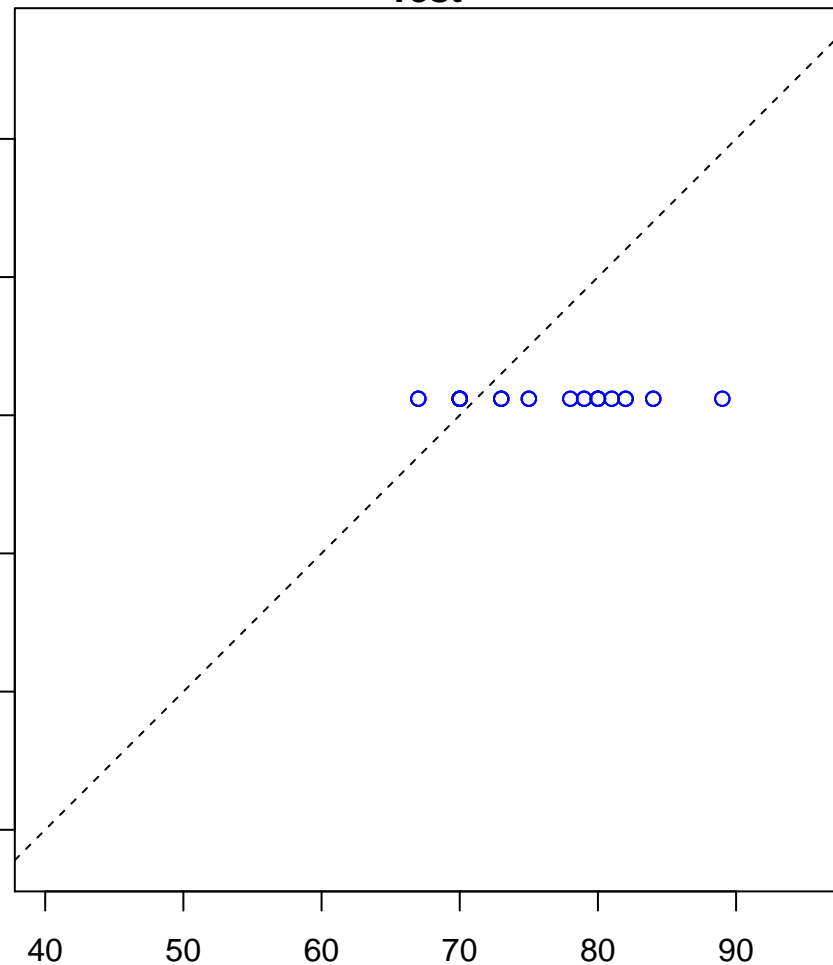


regulation of immune effector process (Score: 0.803428)

Control

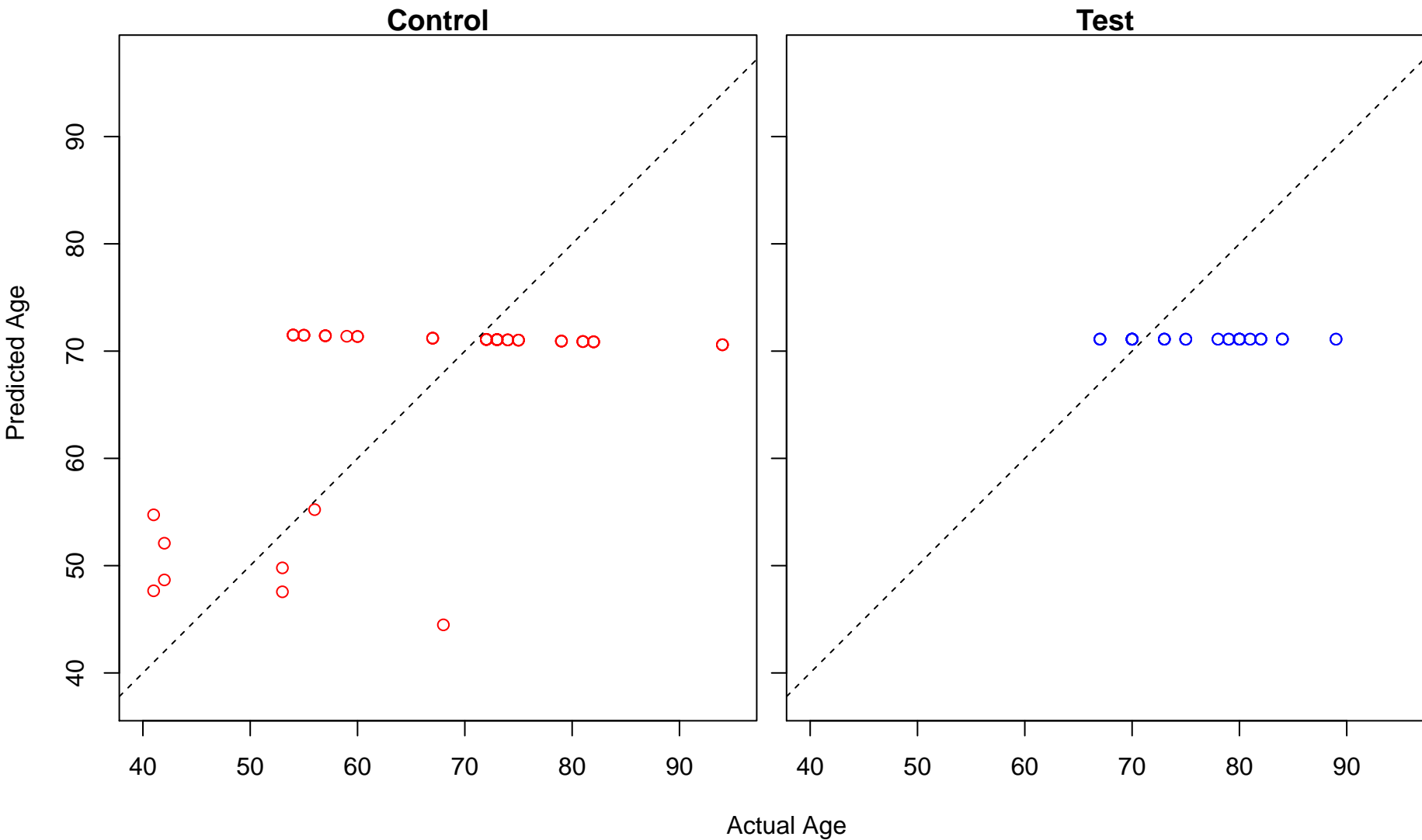


Test

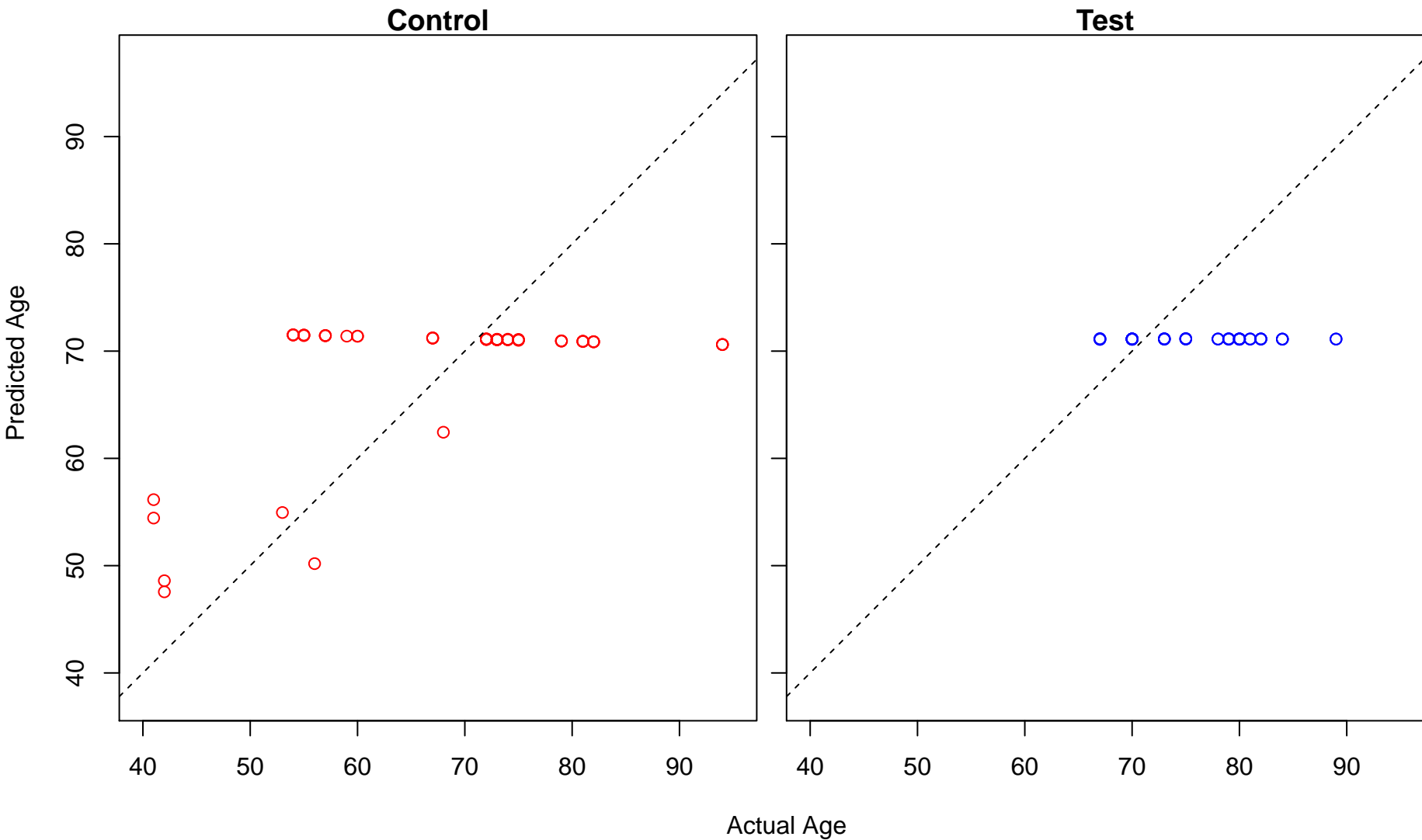


Actual Age

negative regulation of mRNA metabolic process (Score: 0.803420)

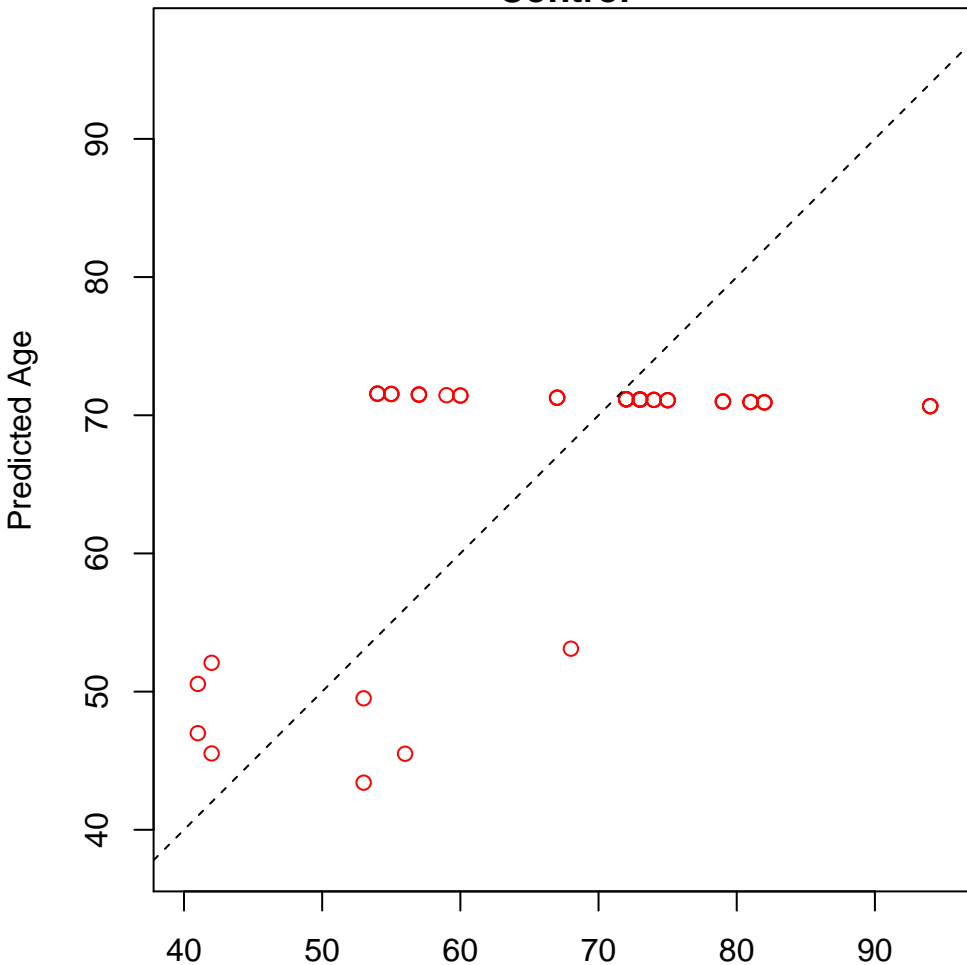


renal system process (Score: 0.803363)

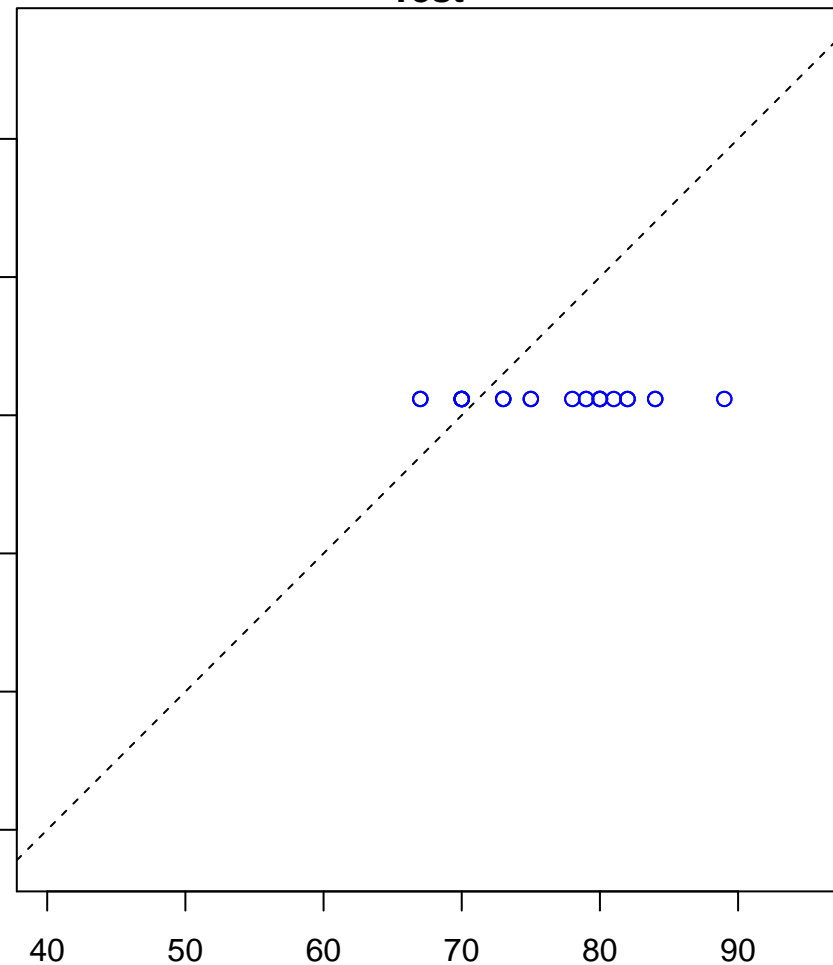


organonitrogen compound metabolic process (Score: 0.803333)

Control

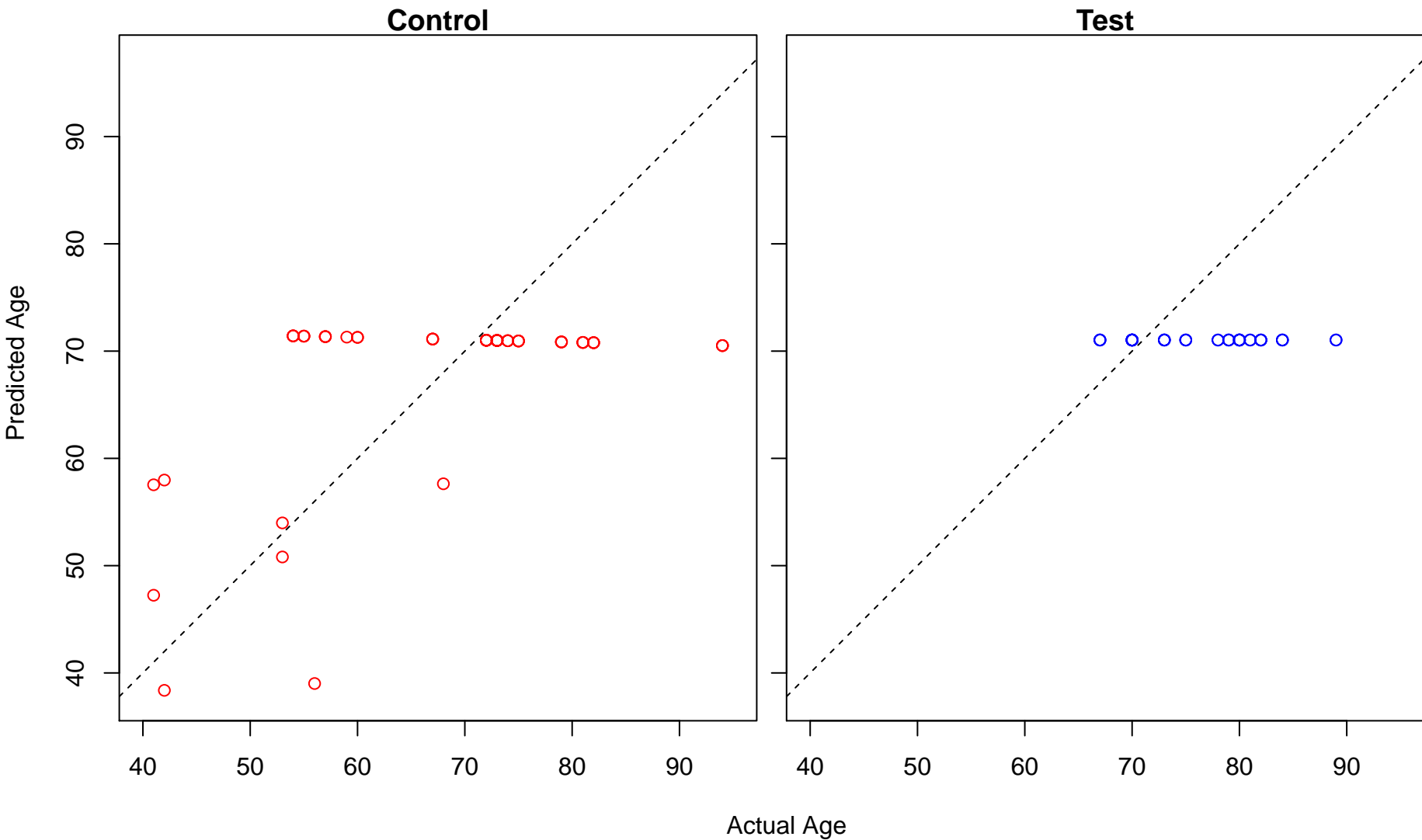


Test



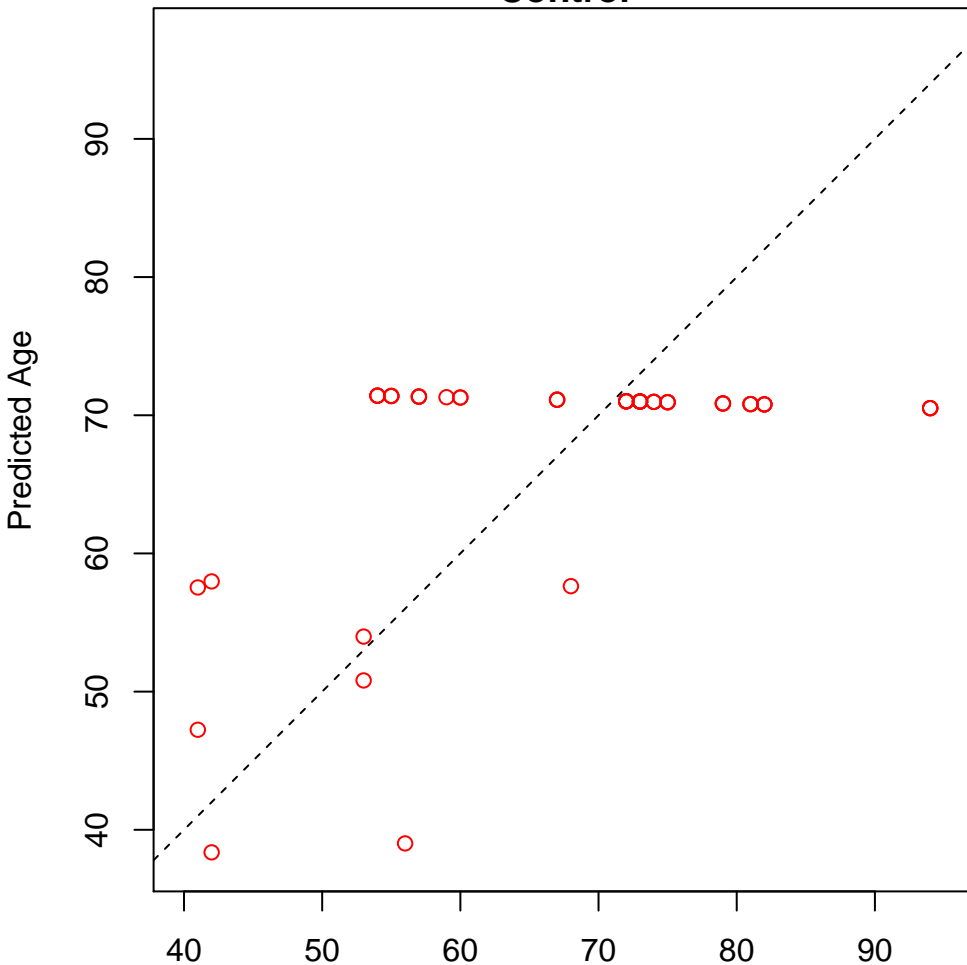
Actual Age

nucleotide-excision repair (Score: 0.803271)

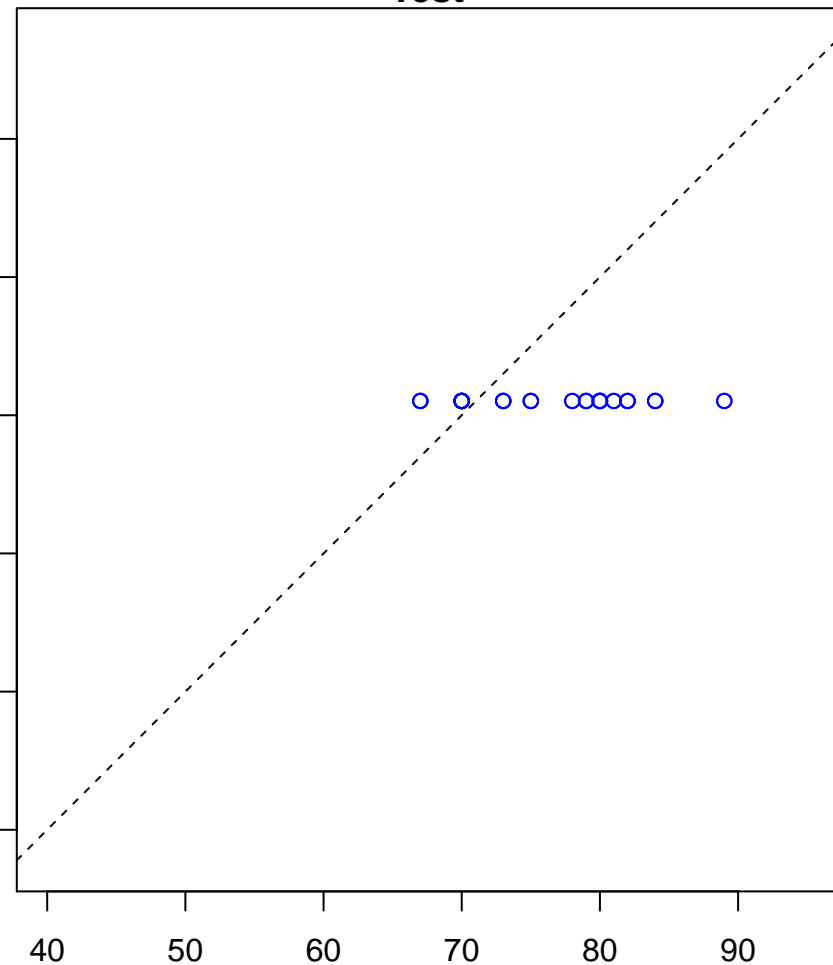


global genome nucleotide–excision repair (Score: 0.803267)

Control



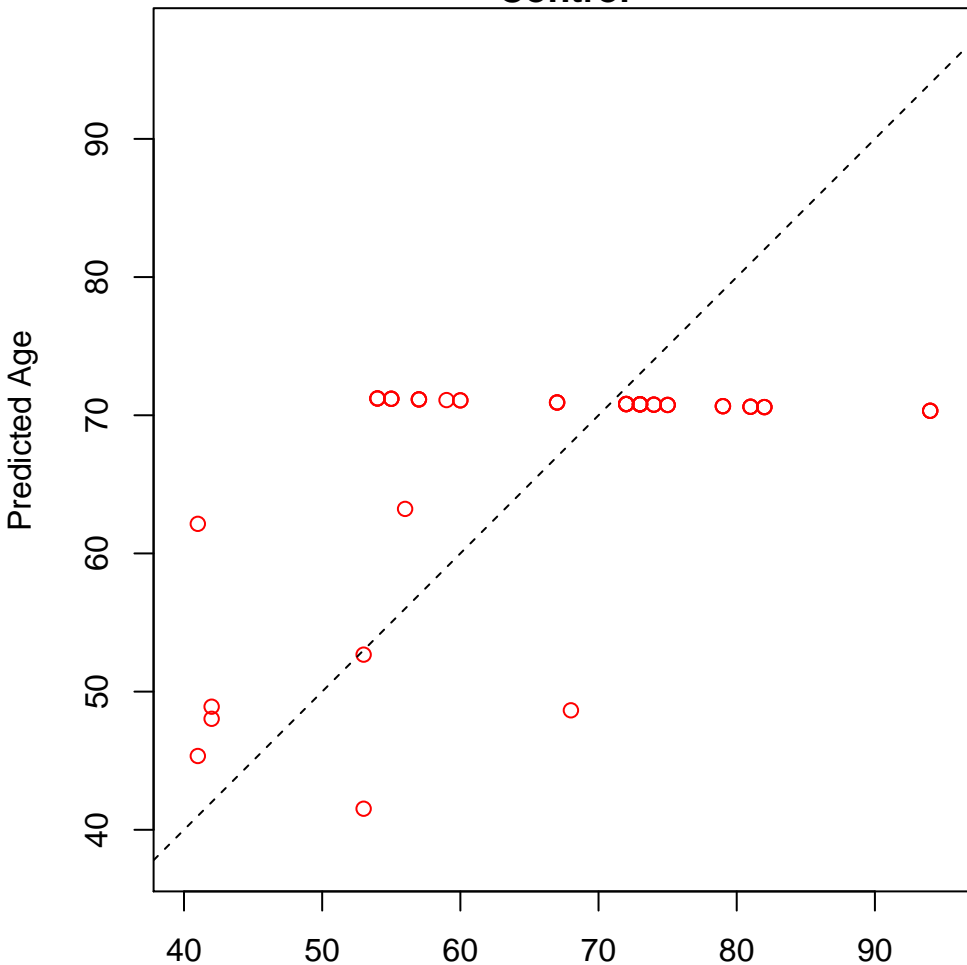
Test



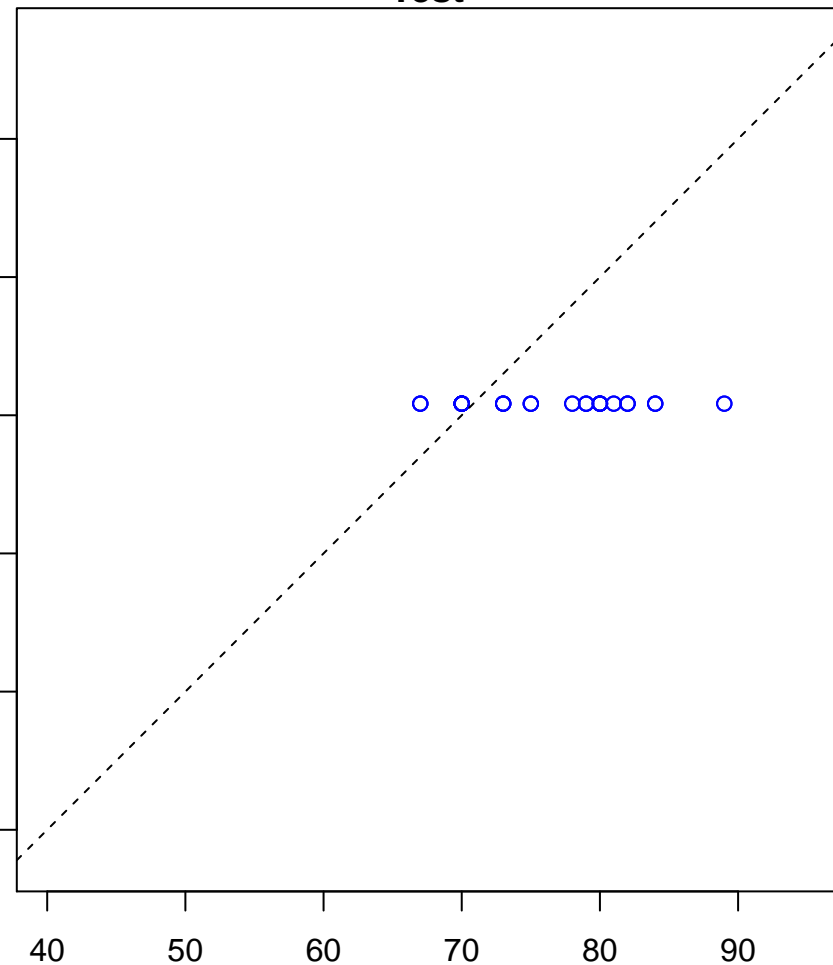
Actual Age

ammonium ion metabolic process (Score: 0.803242)

Control



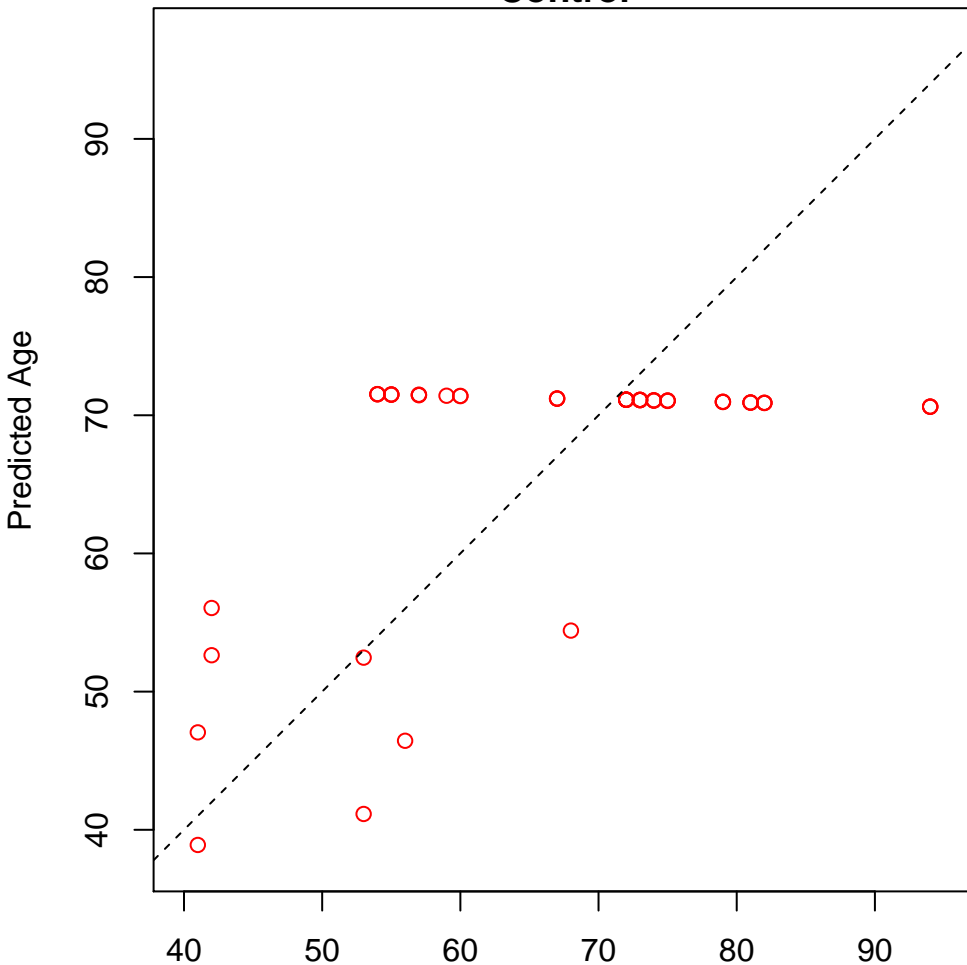
Test



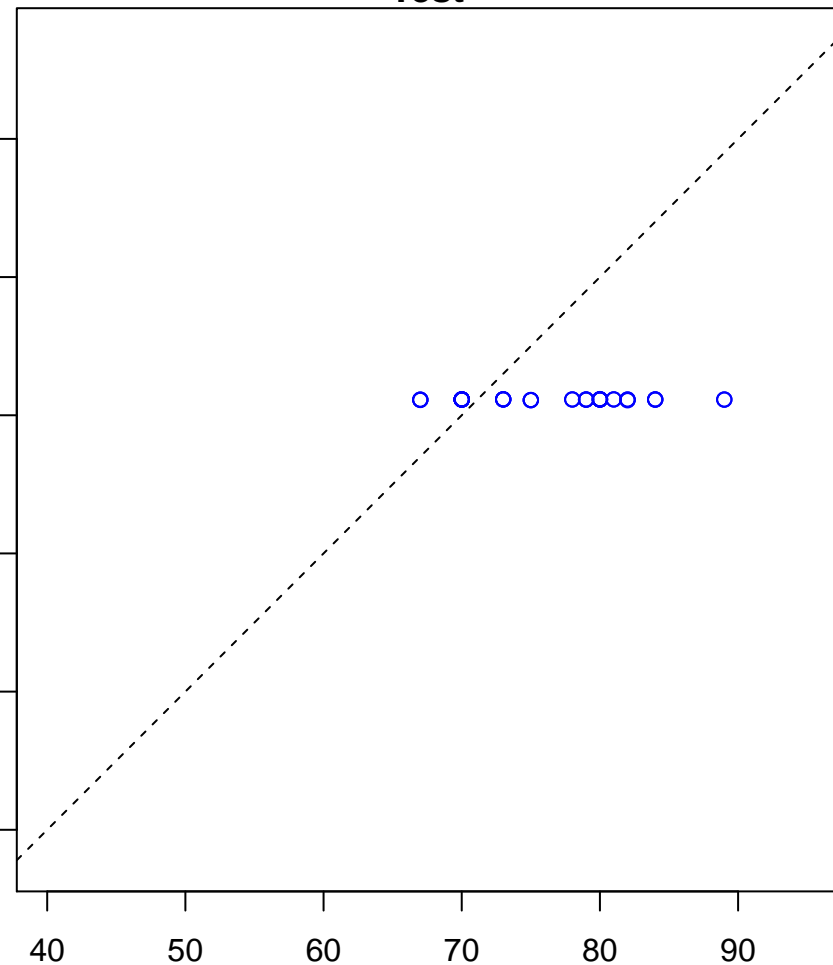
Actual Age

regulation of muscle cell differentiation (Score: 0.803211)

Control



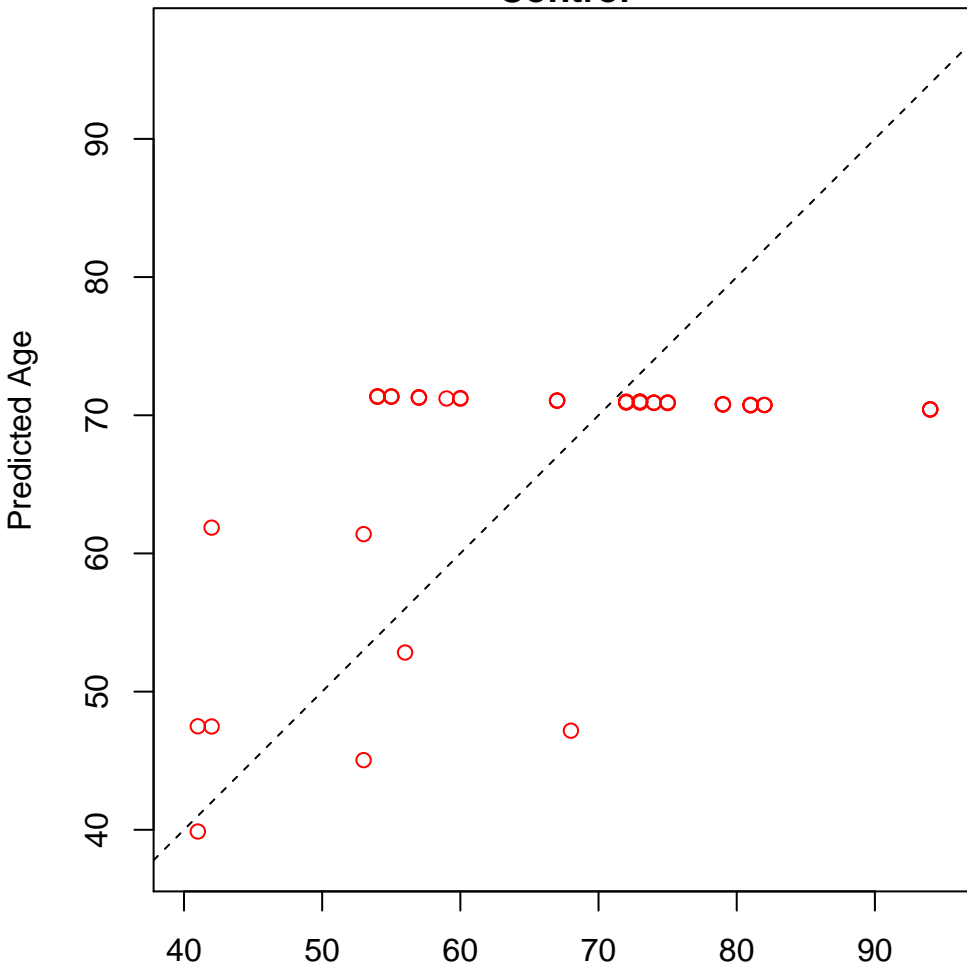
Test



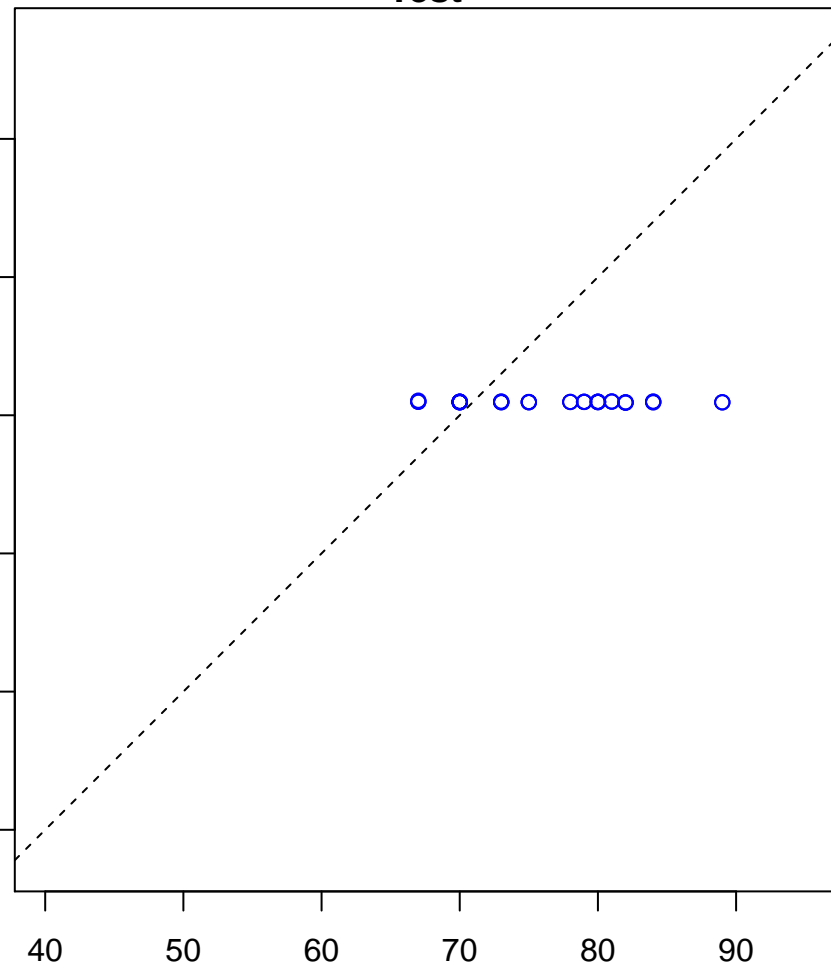
Actual Age

morphogenesis of a polarized epithelium (Score: 0.803180)

Control

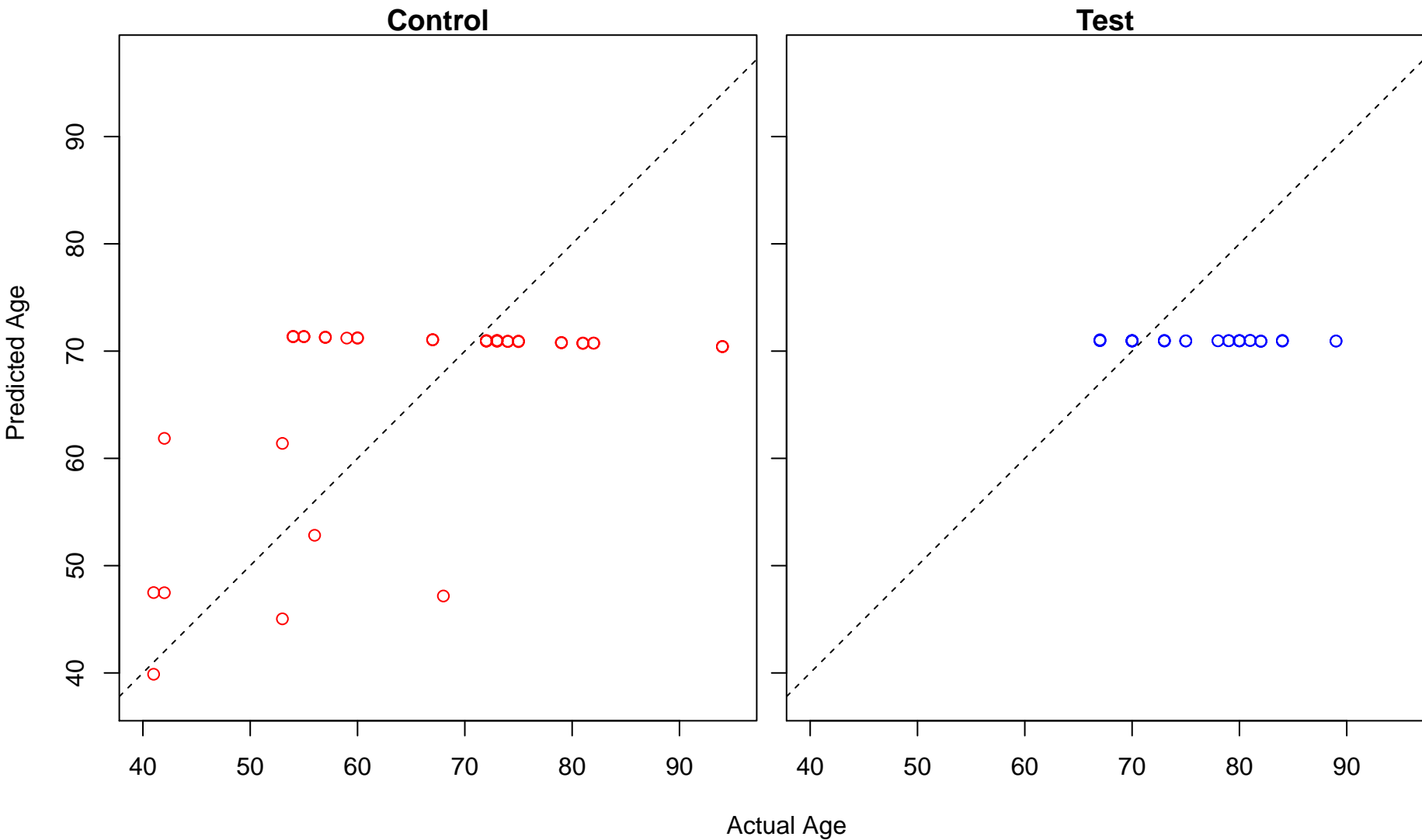


Test



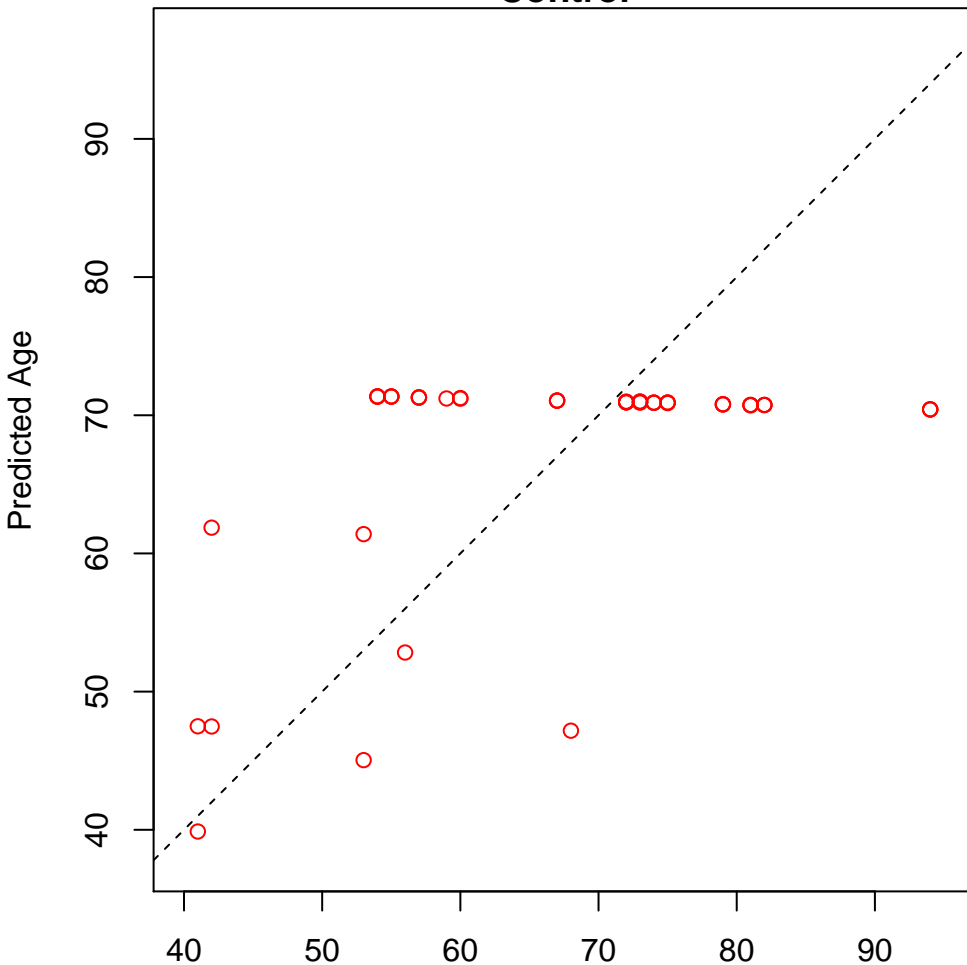
Actual Age

regulation of cell size (Score: 0.803180)

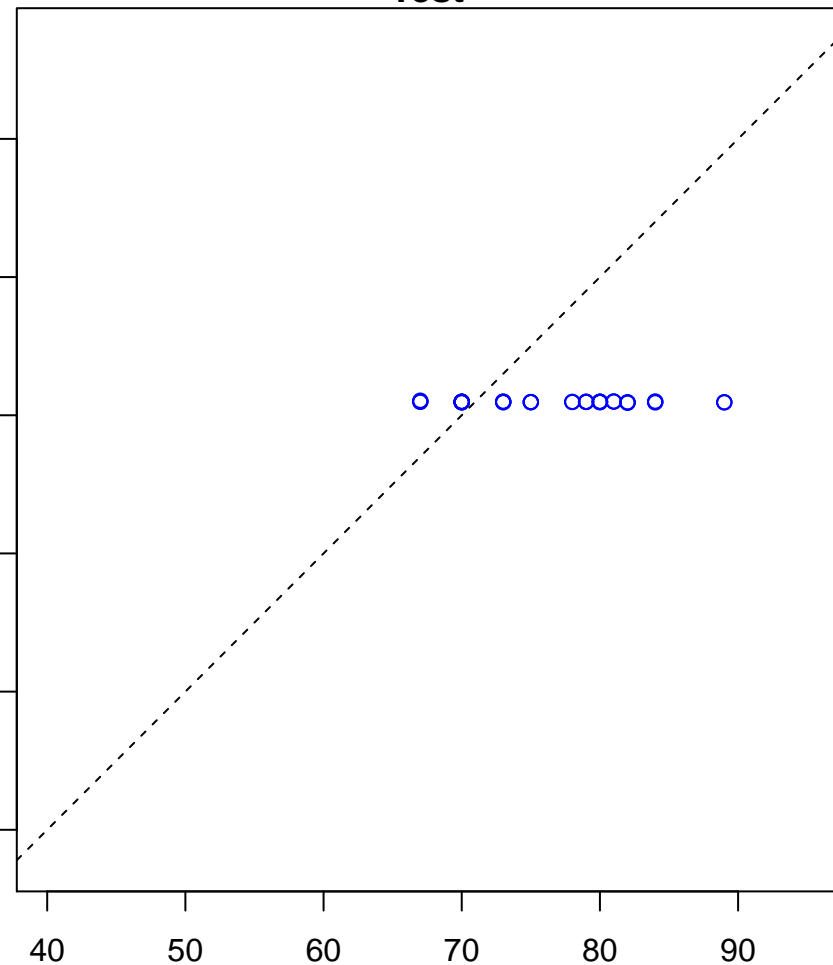


polarized epithelial cell differentiation (Score: 0.803180)

Control



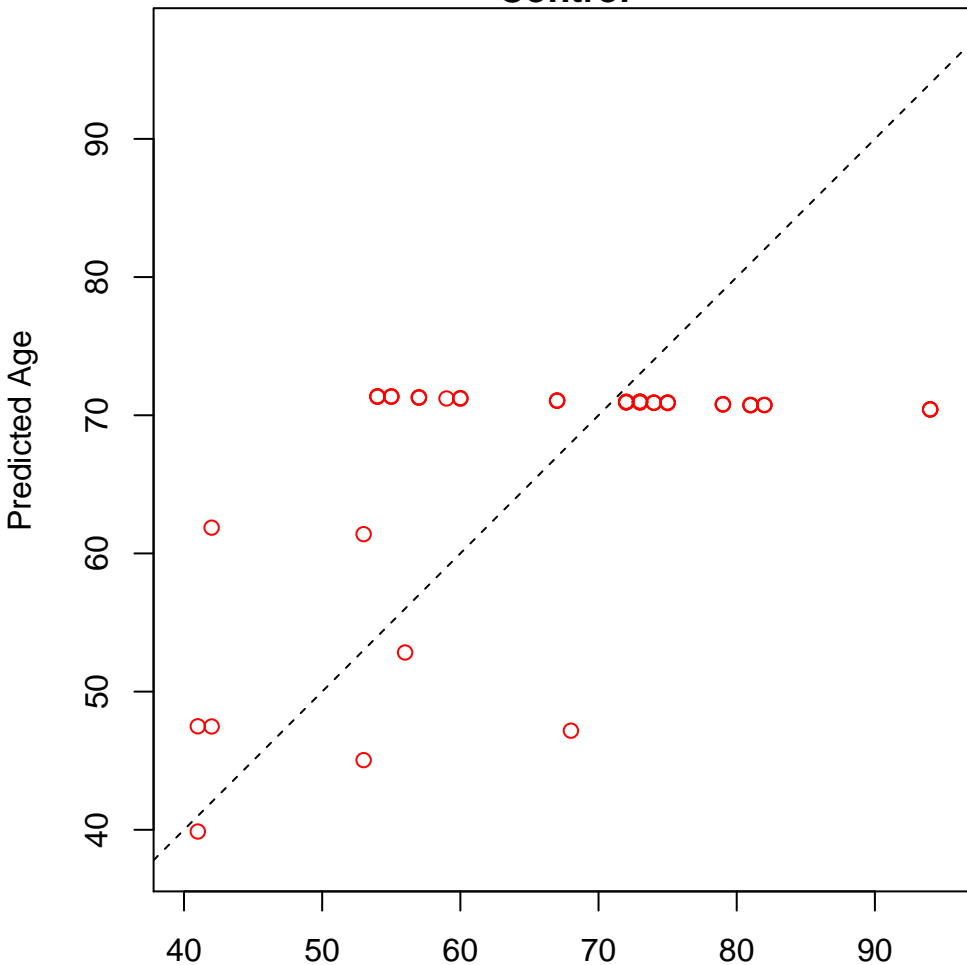
Test



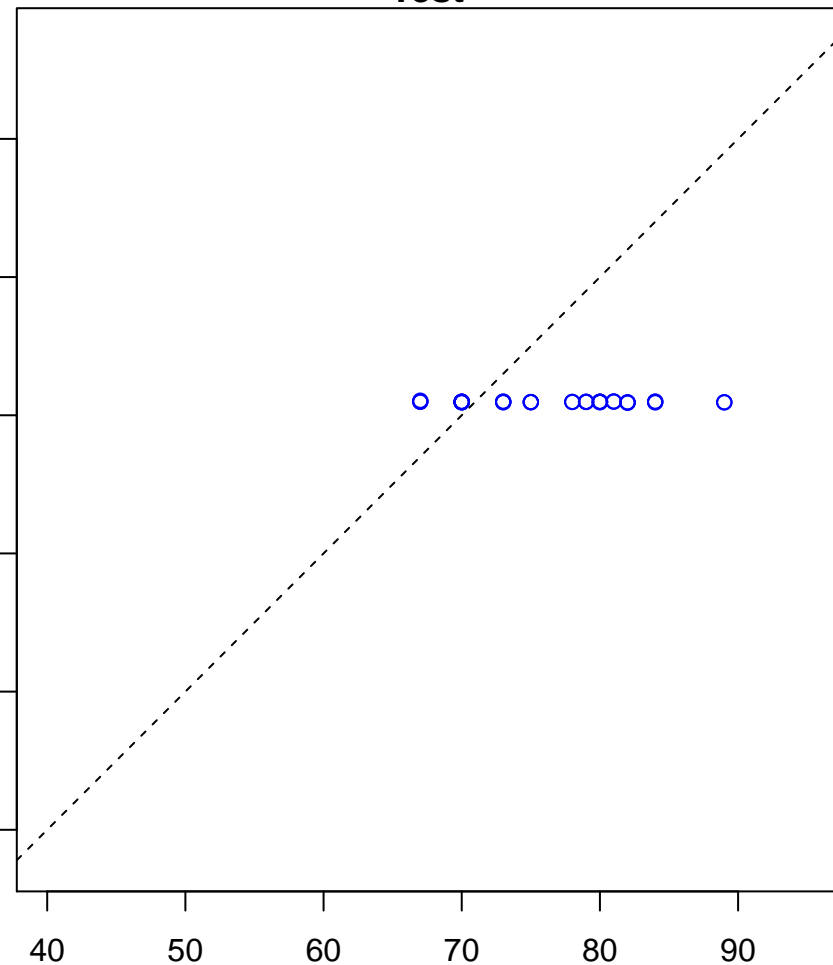
Actual Age

establishment of apical/basal cell polarity (Score: 0.803180)

Control

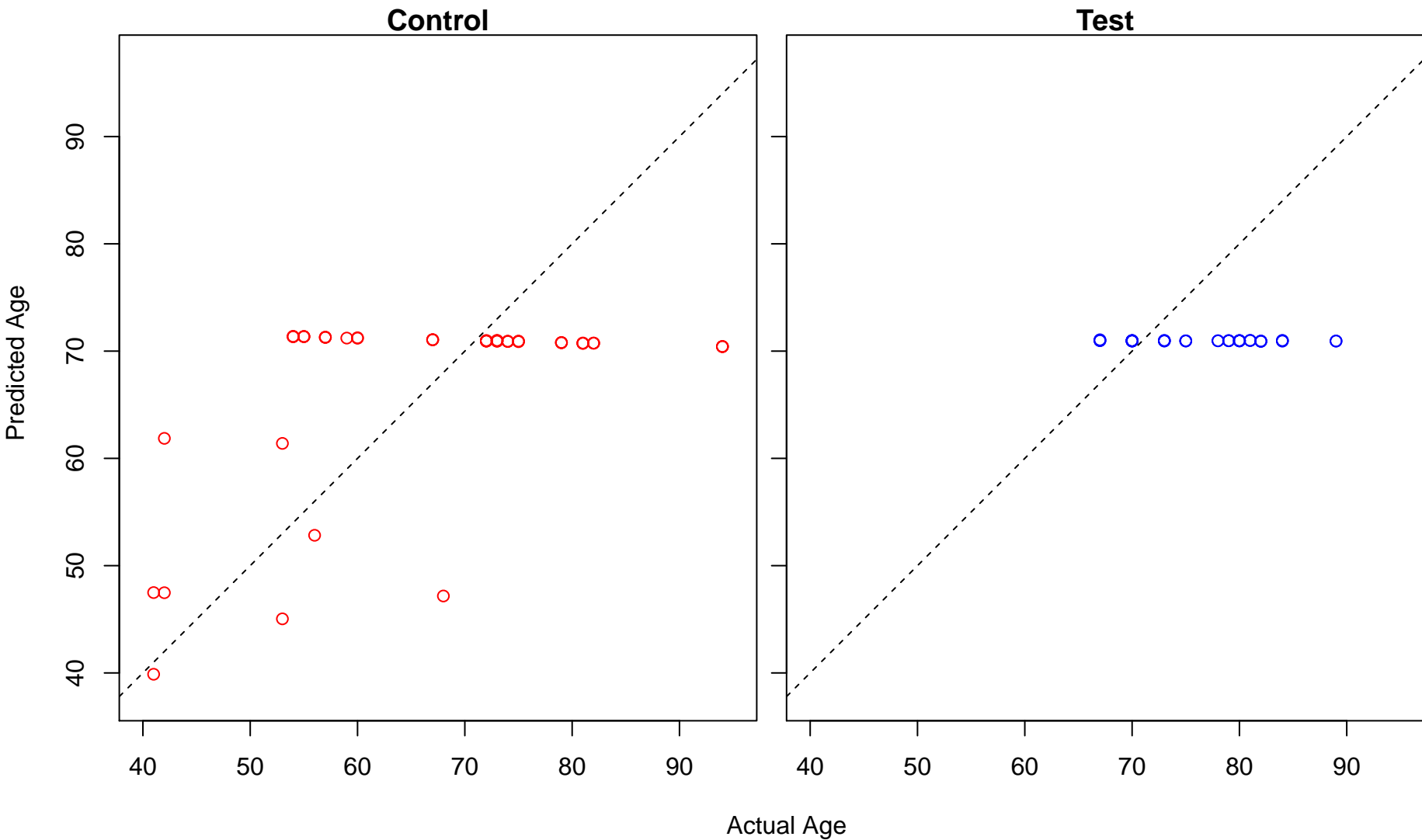


Test



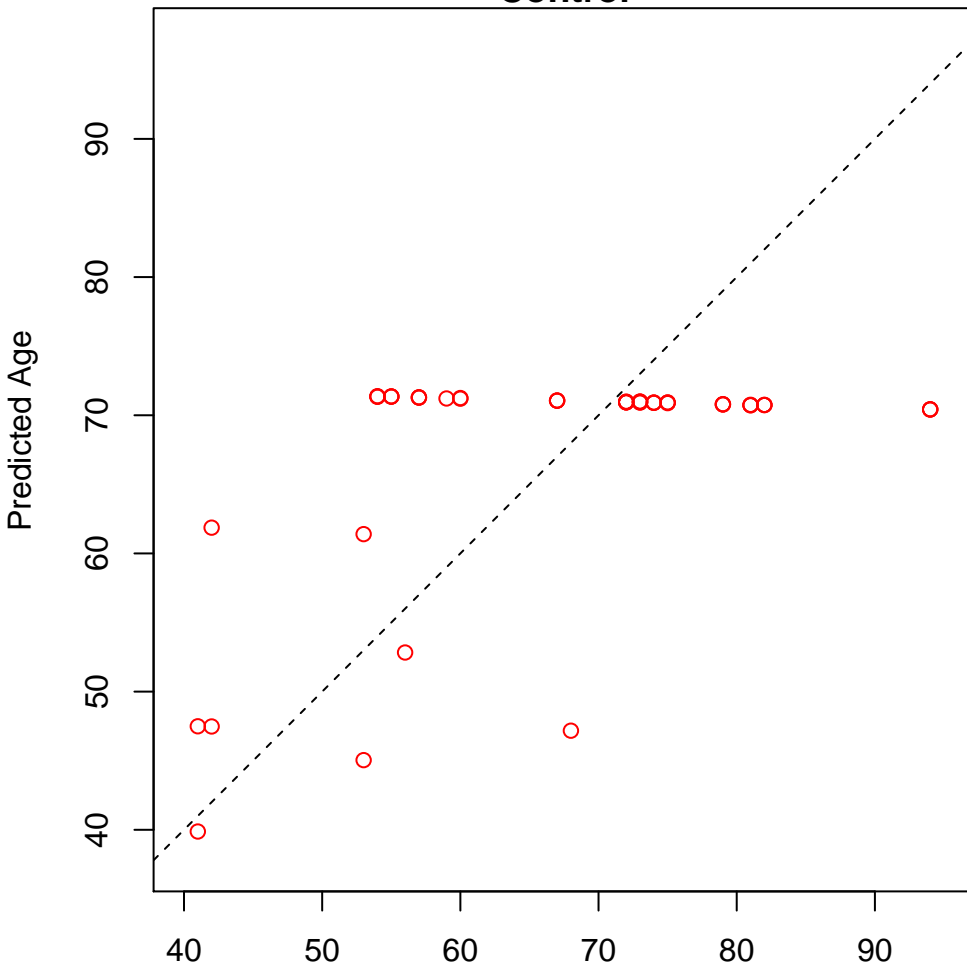
Actual Age

establishment of epithelial cell apical/basal polarity (Score: 0.803180)

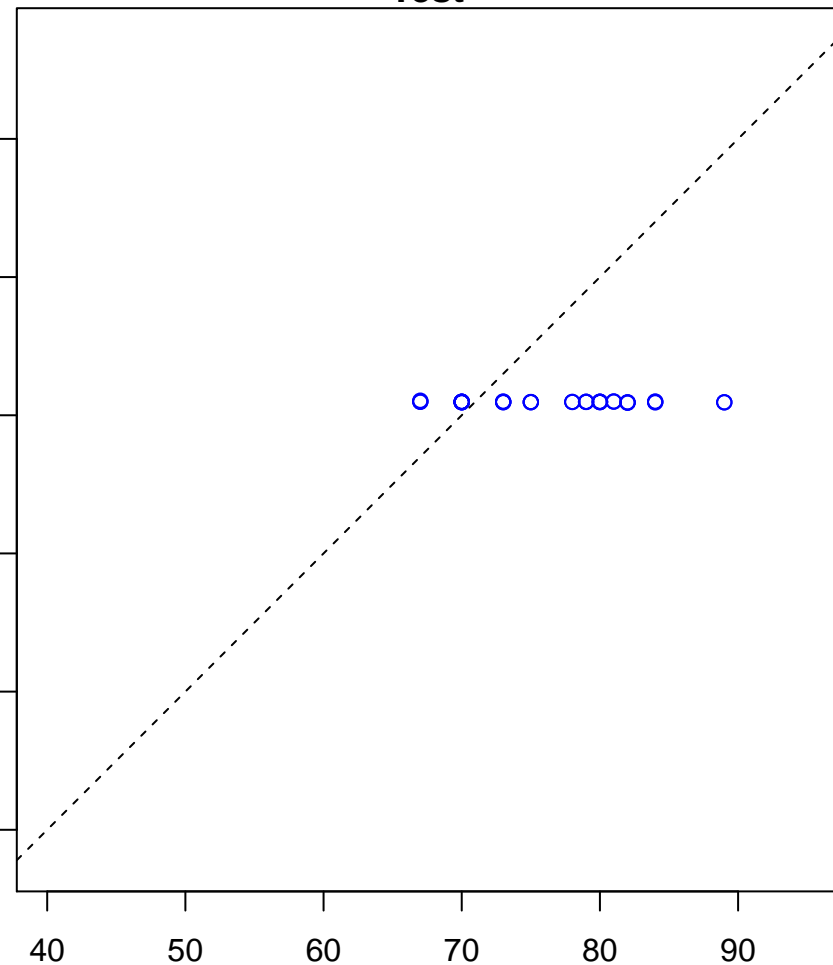


establishment of monopolar cell polarity (Score: 0.803180)

Control

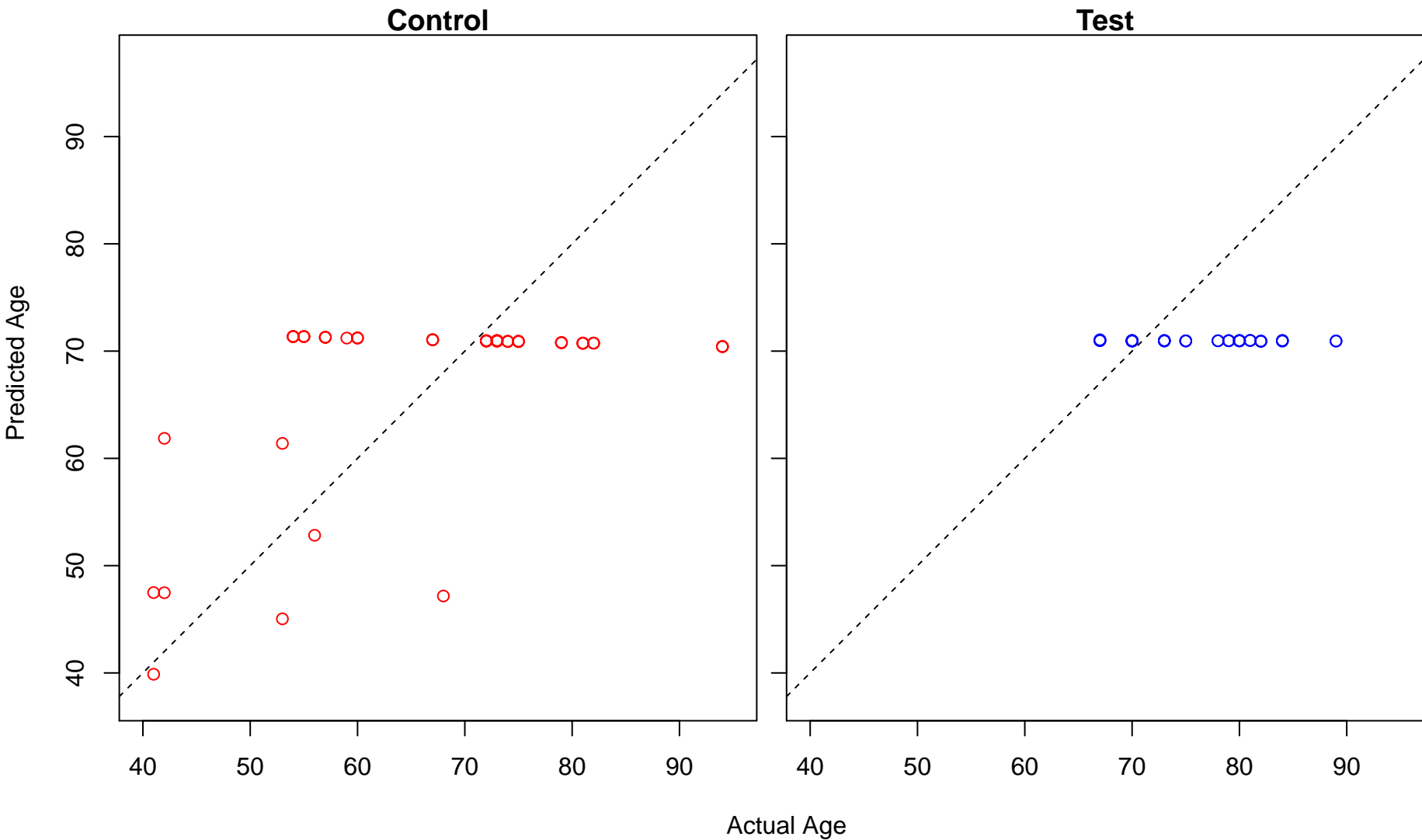


Test



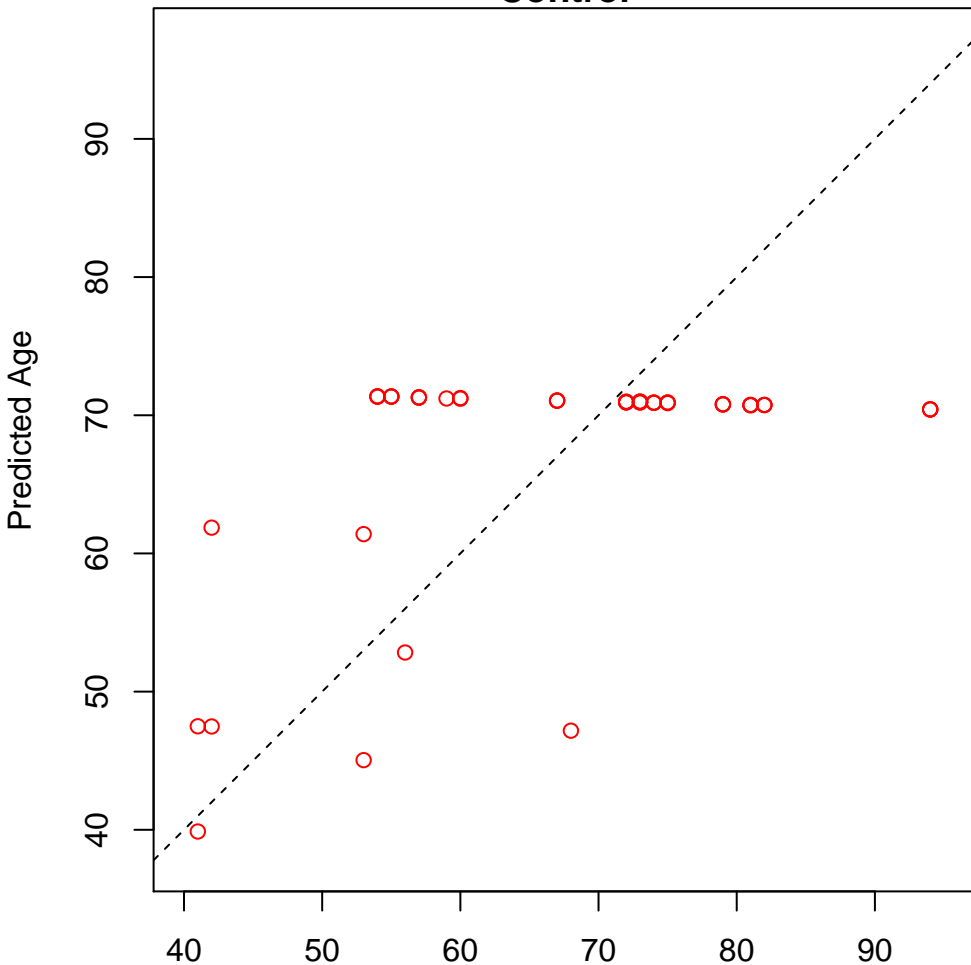
Actual Age

establishment or maintenance of monopolar cell polarity (Score: 0.803180)

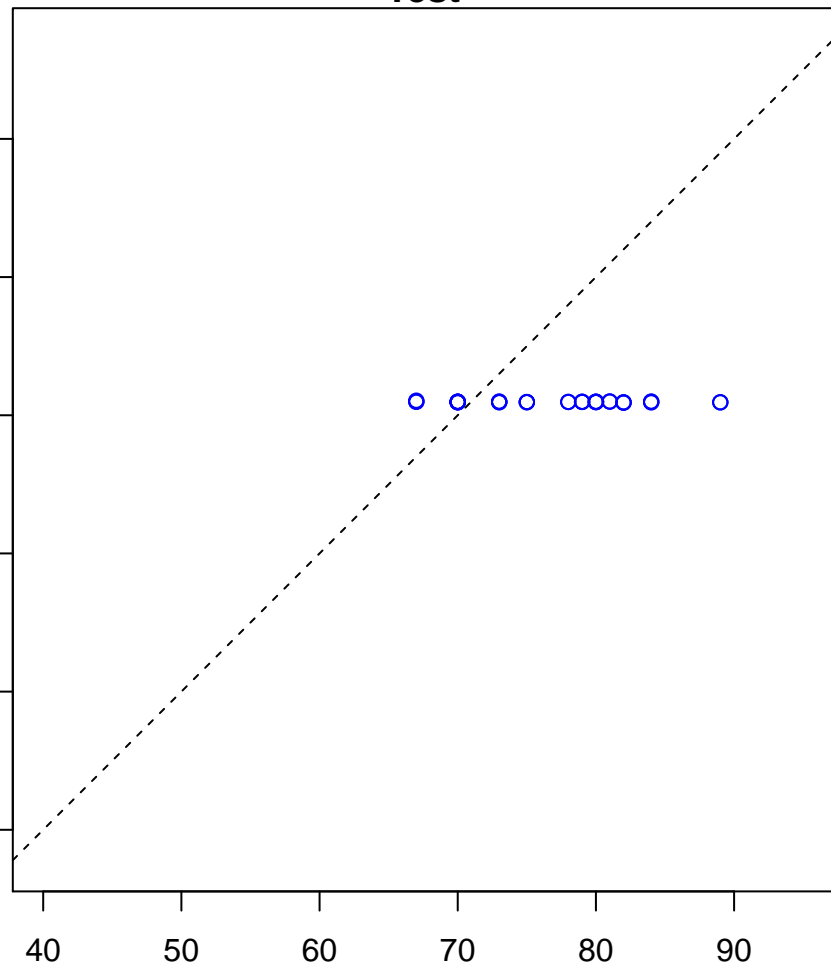


establishment of epithelial cell polarity (Score: 0.803180)

Control

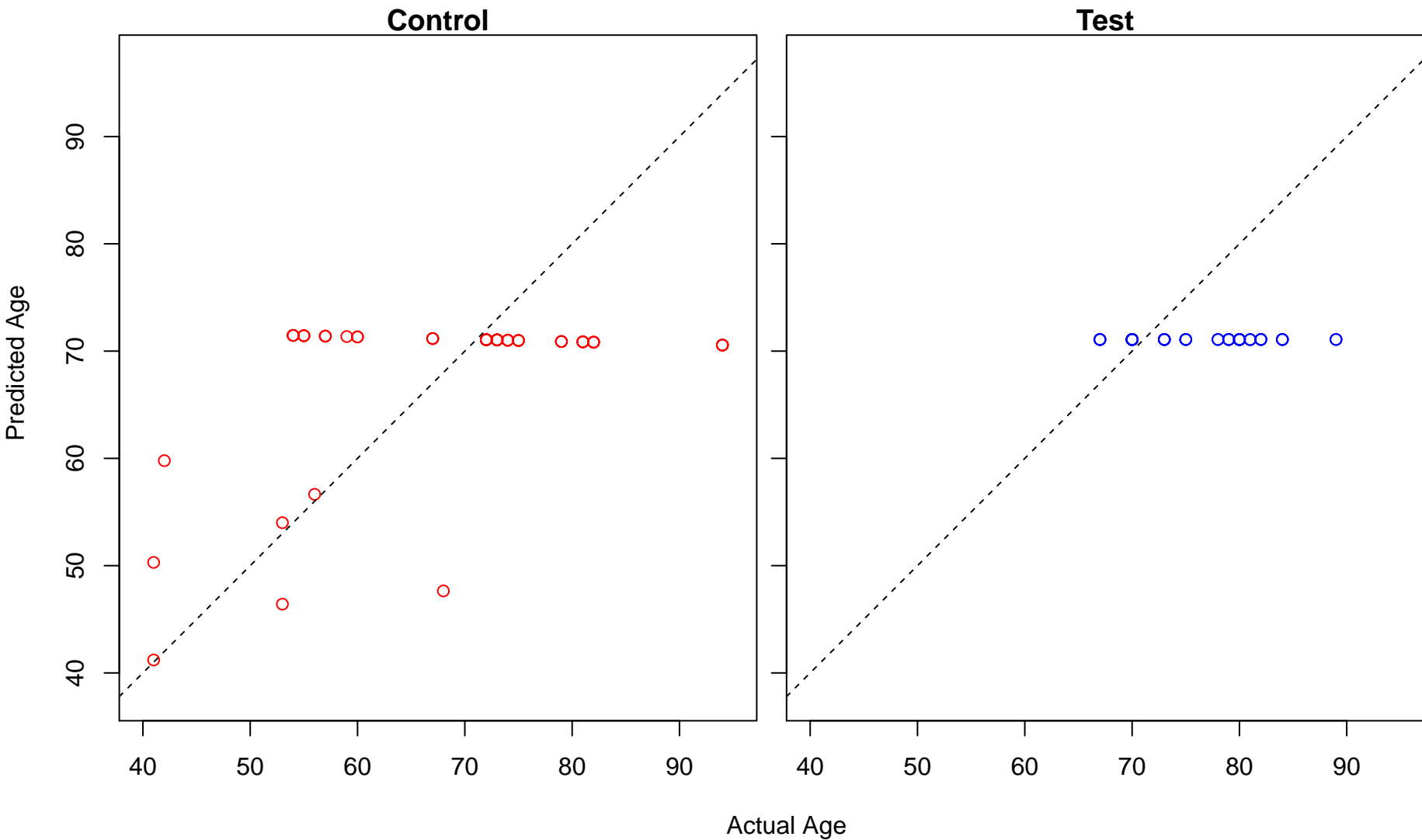


Test



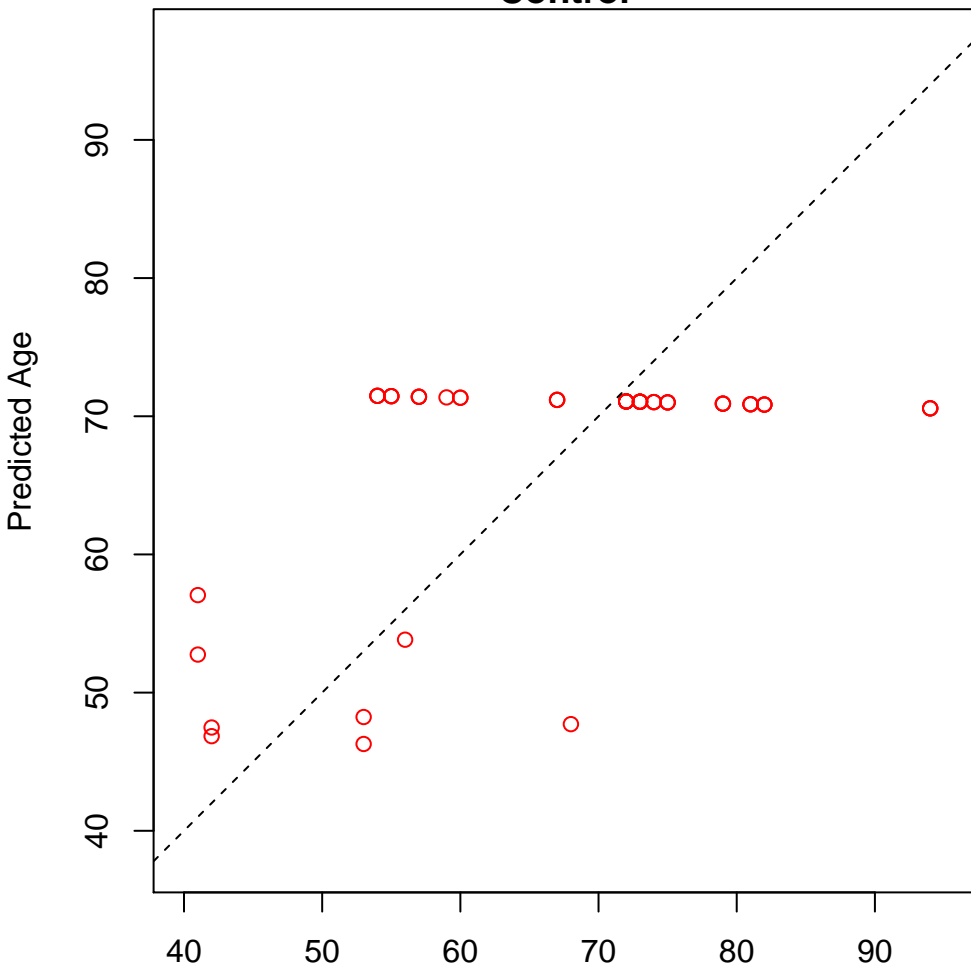
Actual Age

vesicle organization (Score: 0.803055)

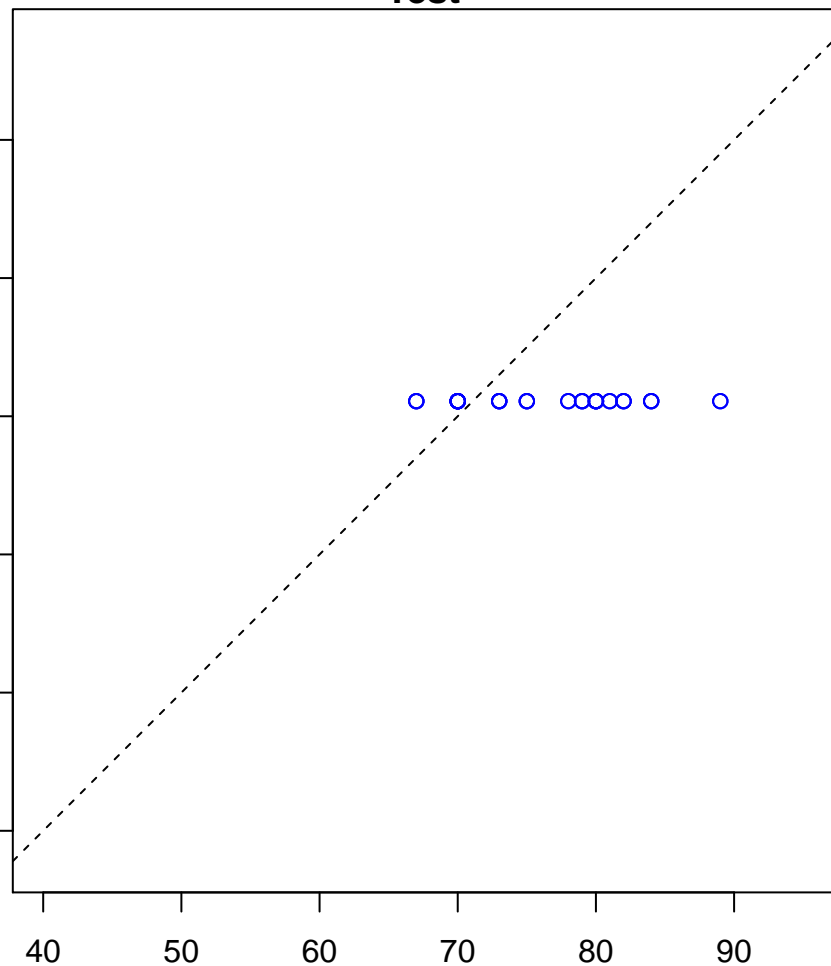


monocarboxylic acid metabolic process (Score: 0.803051)

Control

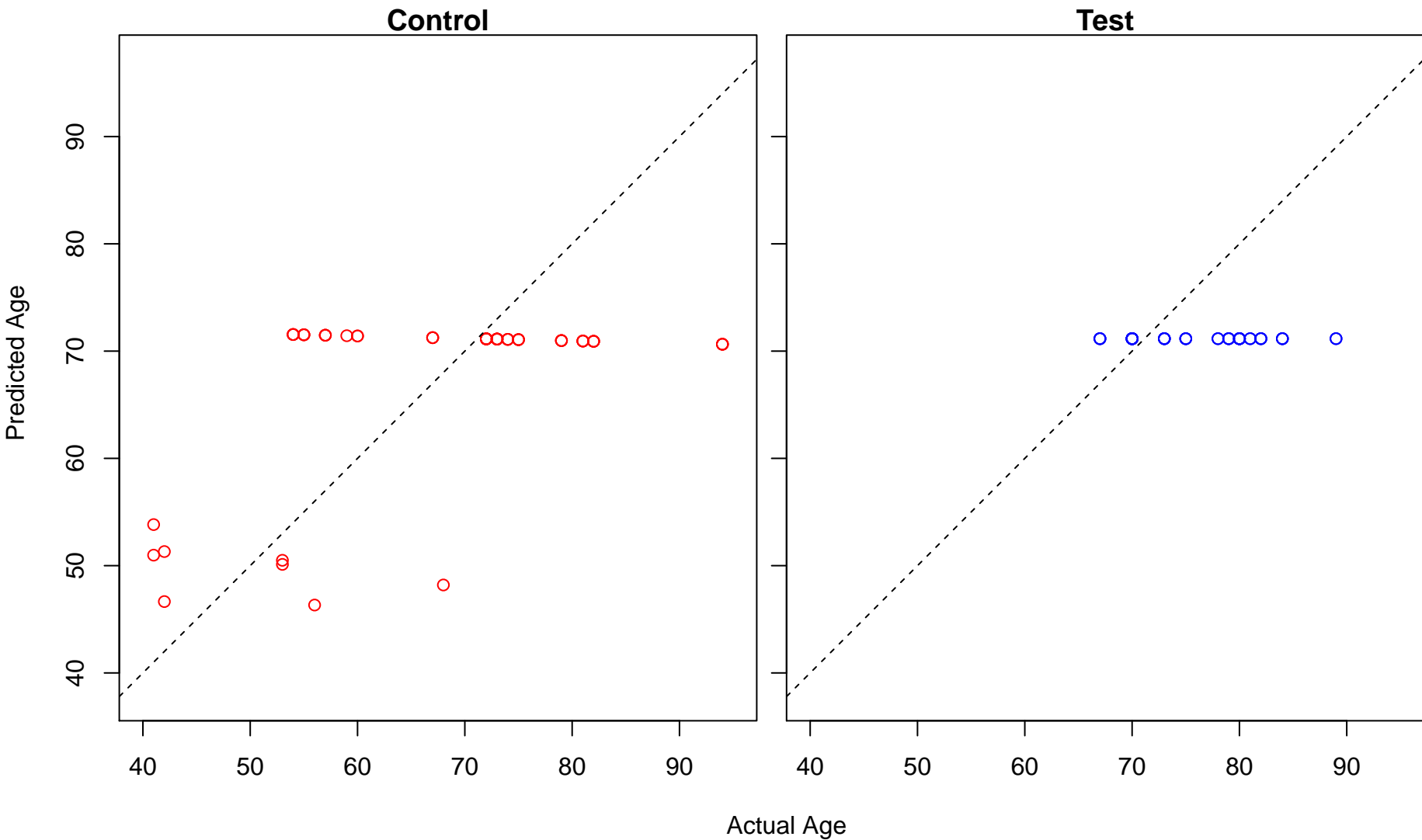


Test

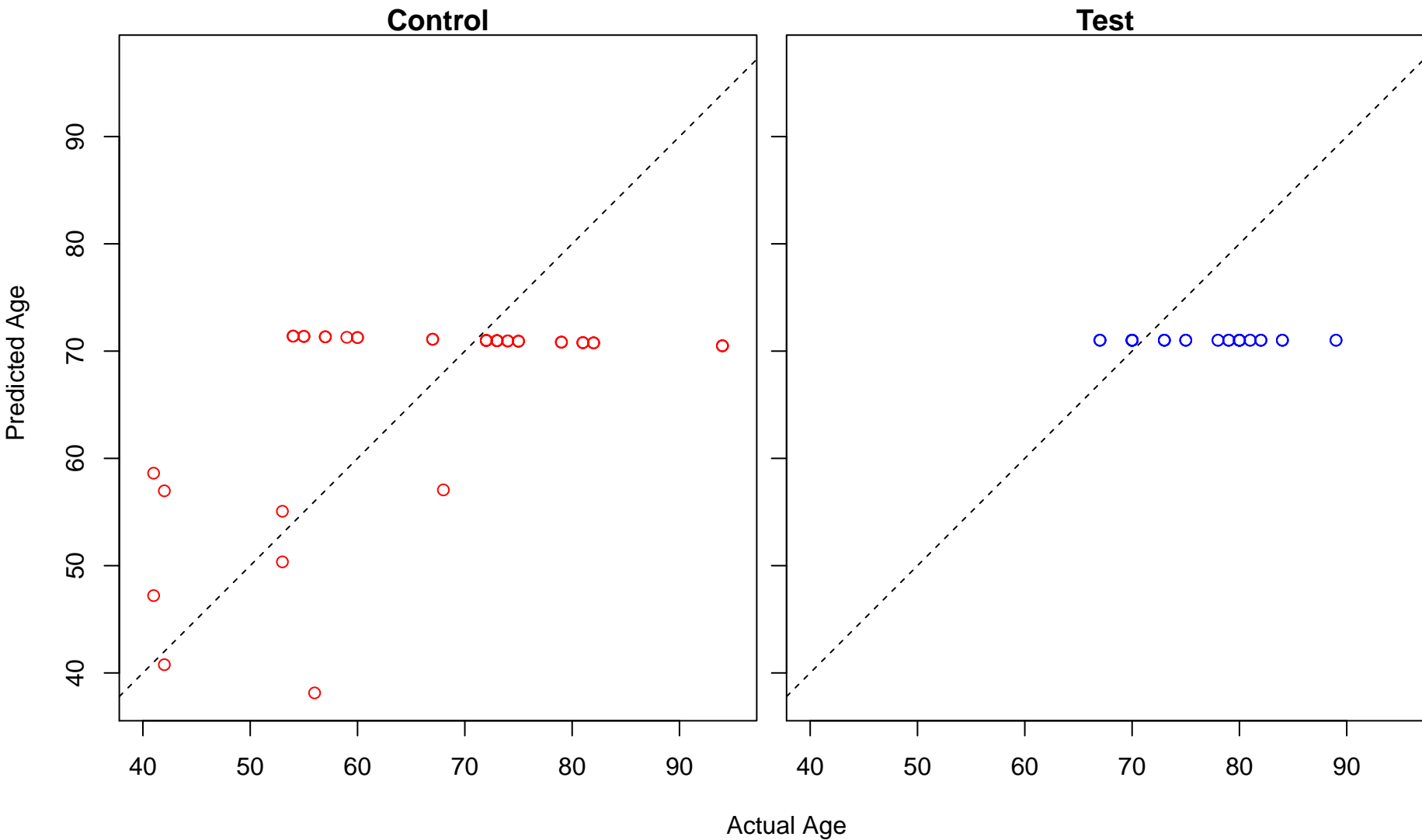


Actual Age

positive regulation of transport (Score: 0.803039)

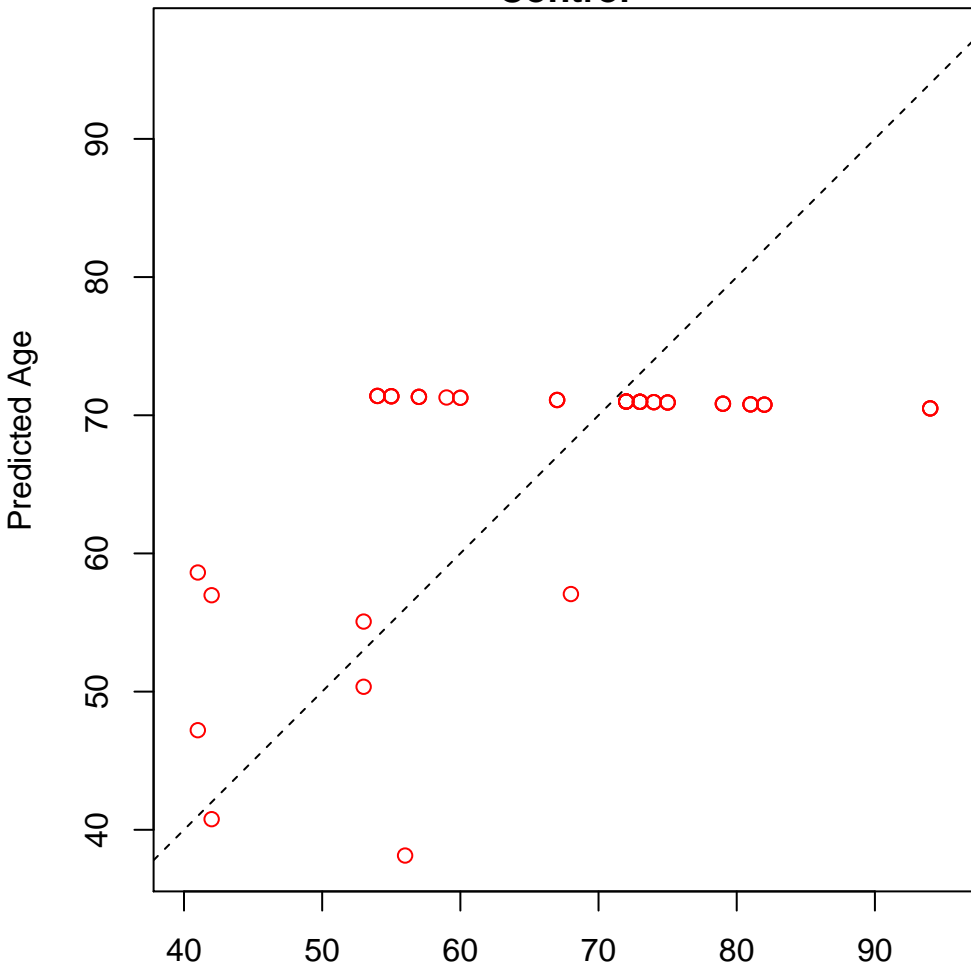


transforming growth factor beta receptor signaling pathway (Score: 0.803022)

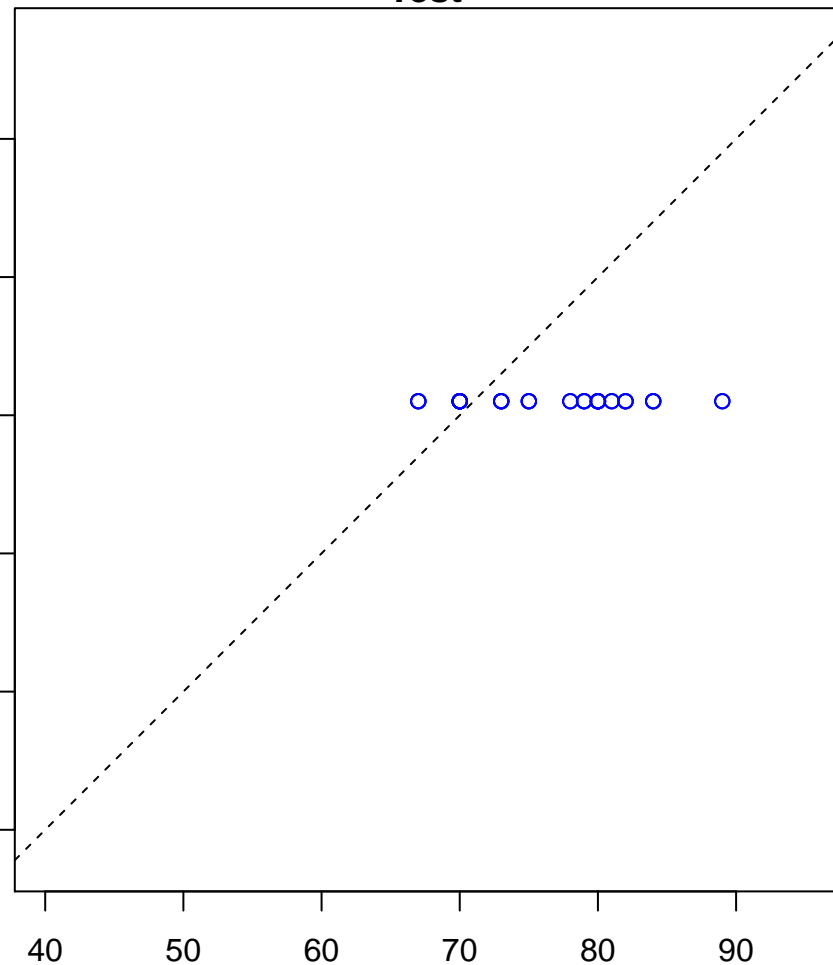


response to transforming growth factor beta (Score: 0.803022)

Control

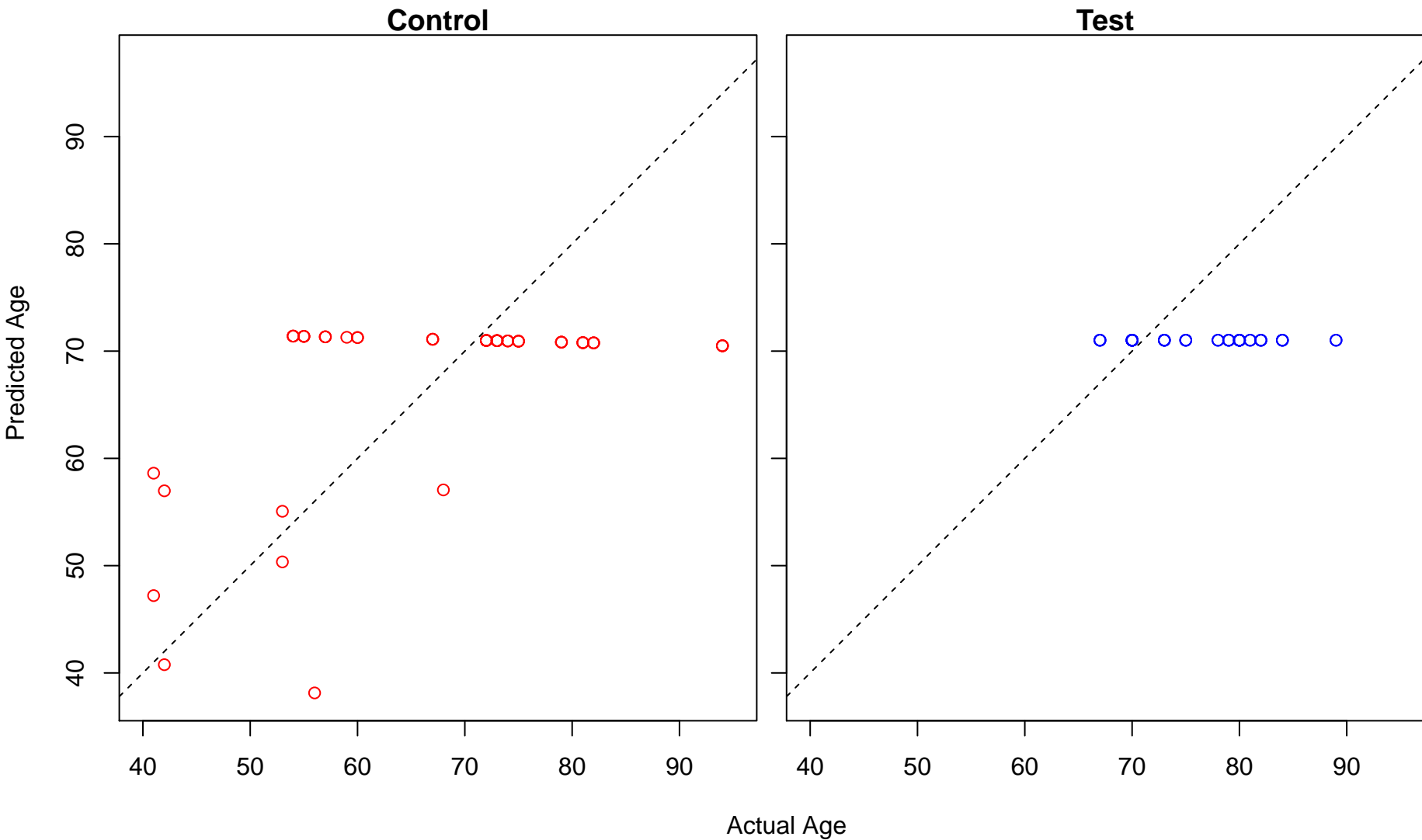


Test

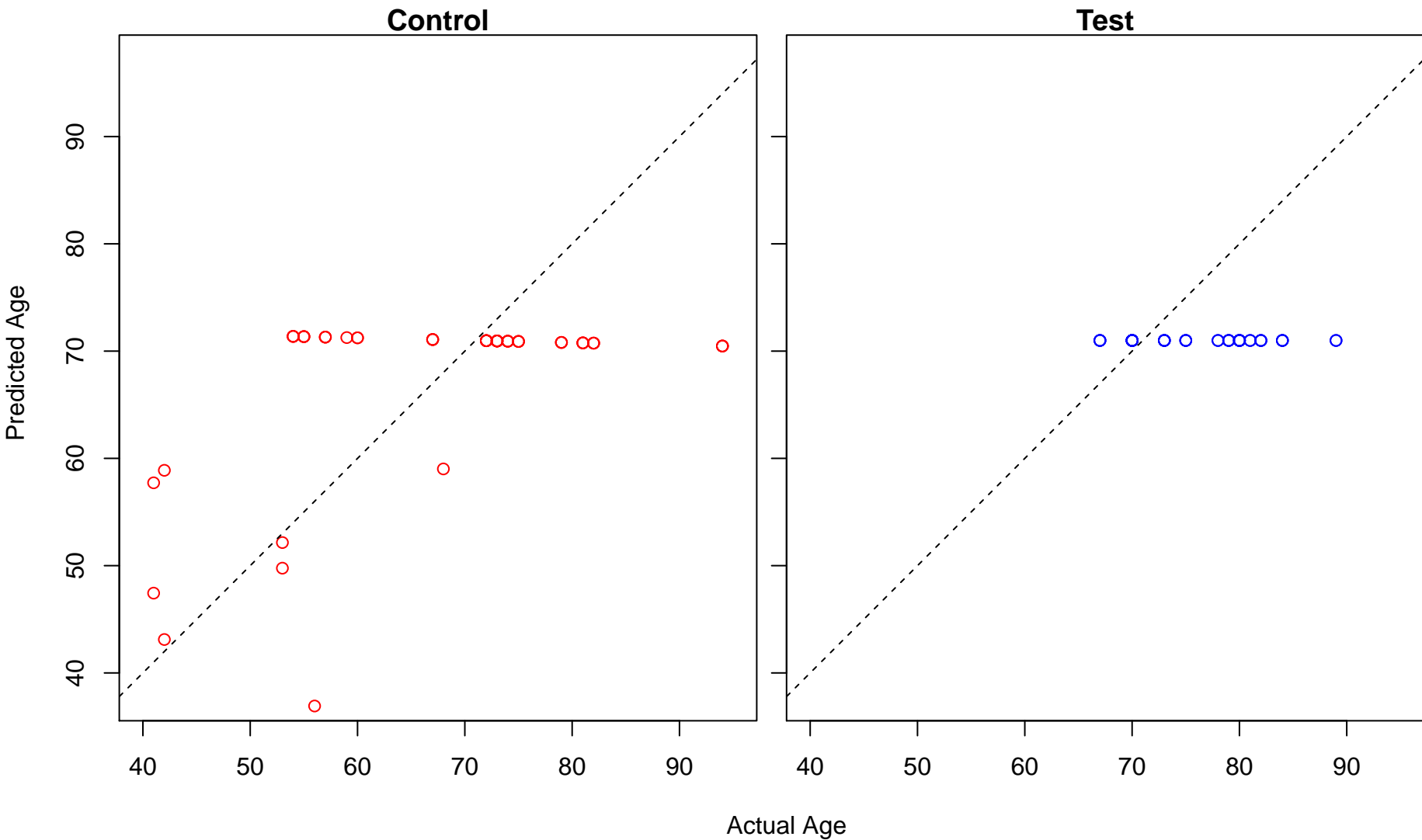


Actual Age

cellular response to transforming growth factor beta stimulus (Score: 0.803022)

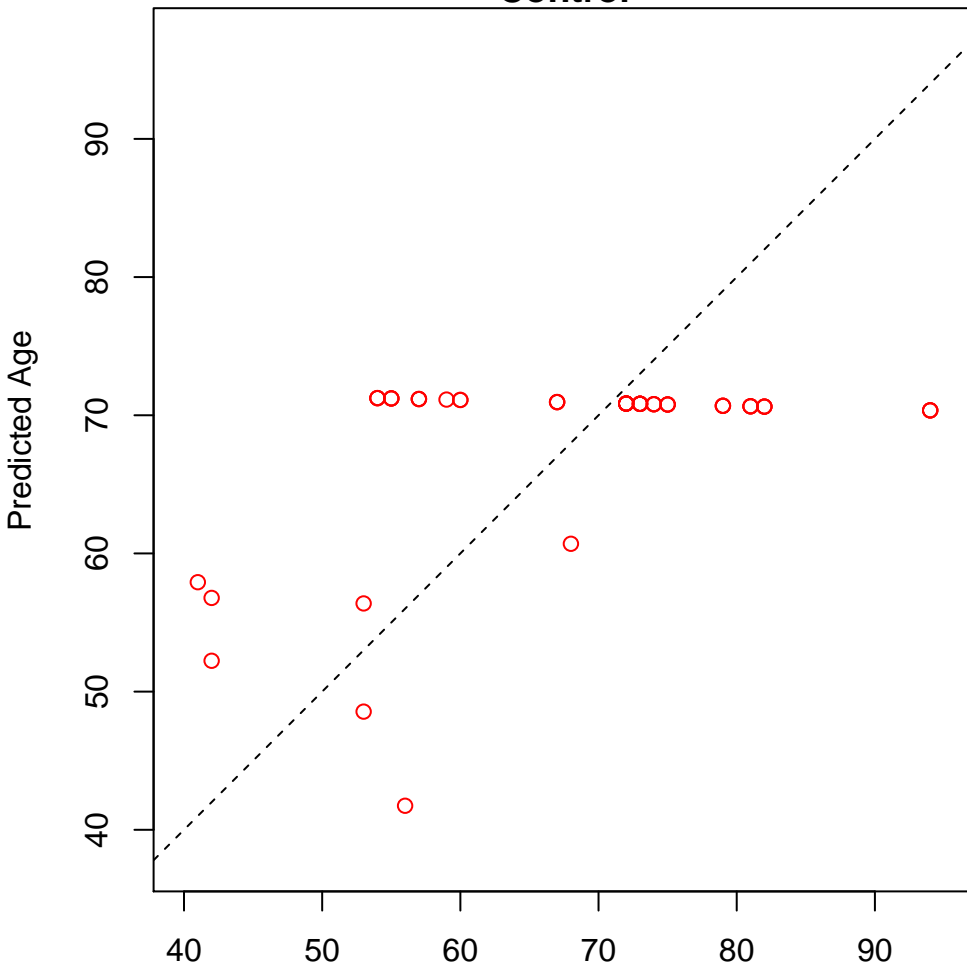


innate immune response (Score: 0.803010)

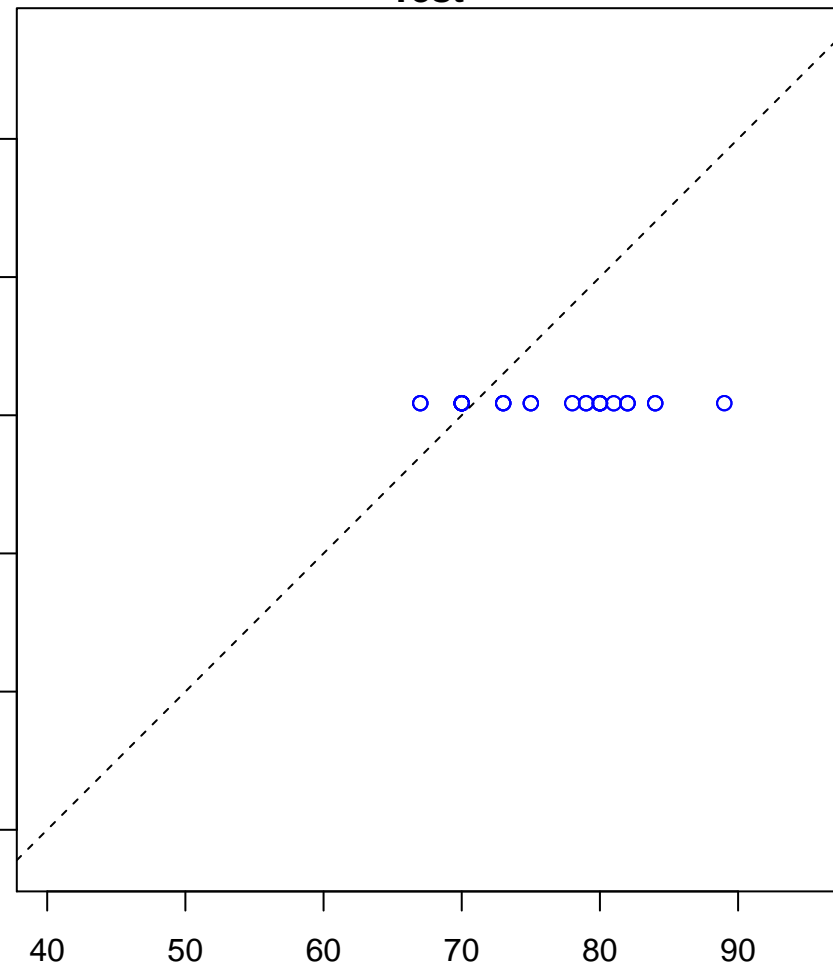


cellular copper ion homeostasis (Score: 0.802966)

Control

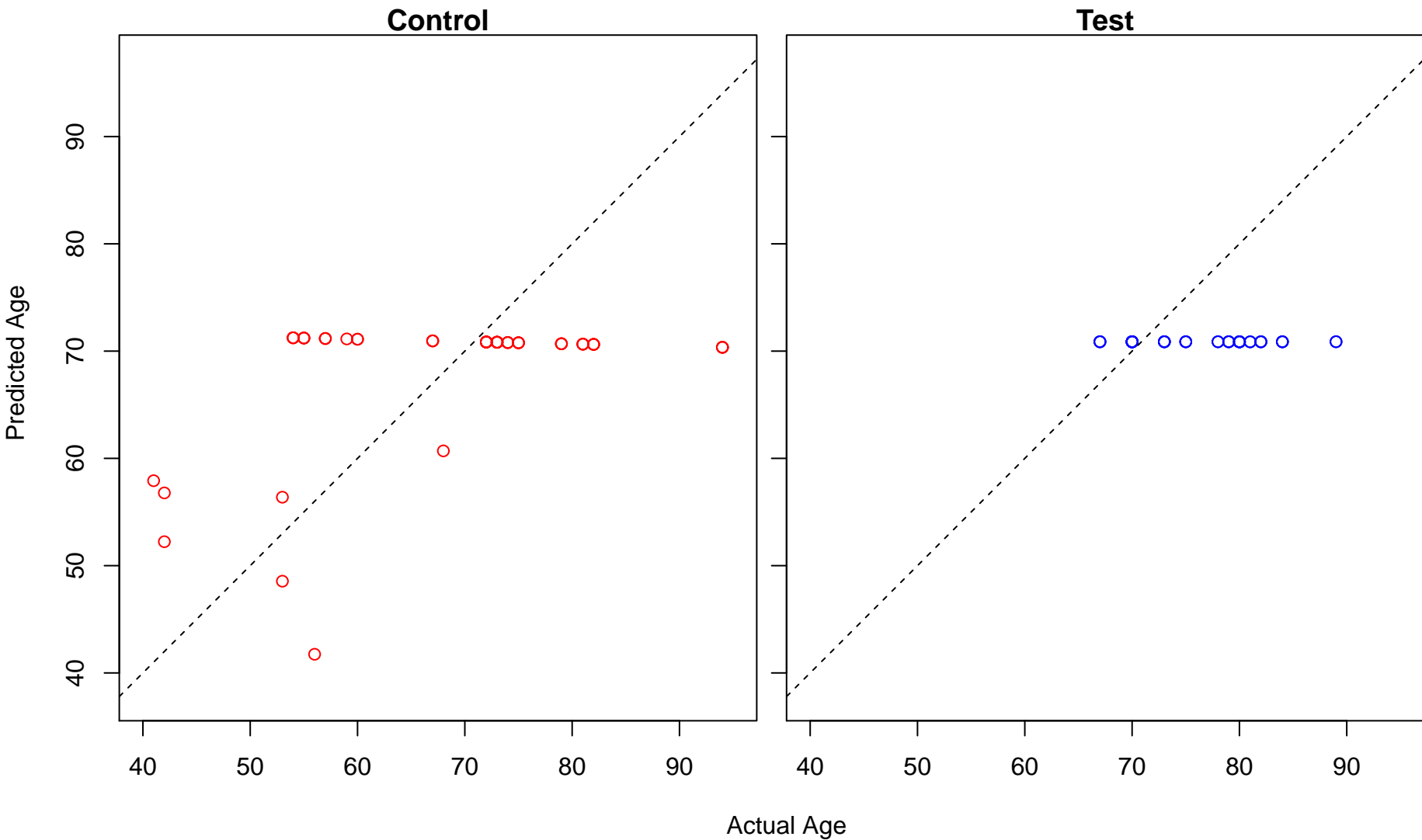


Test

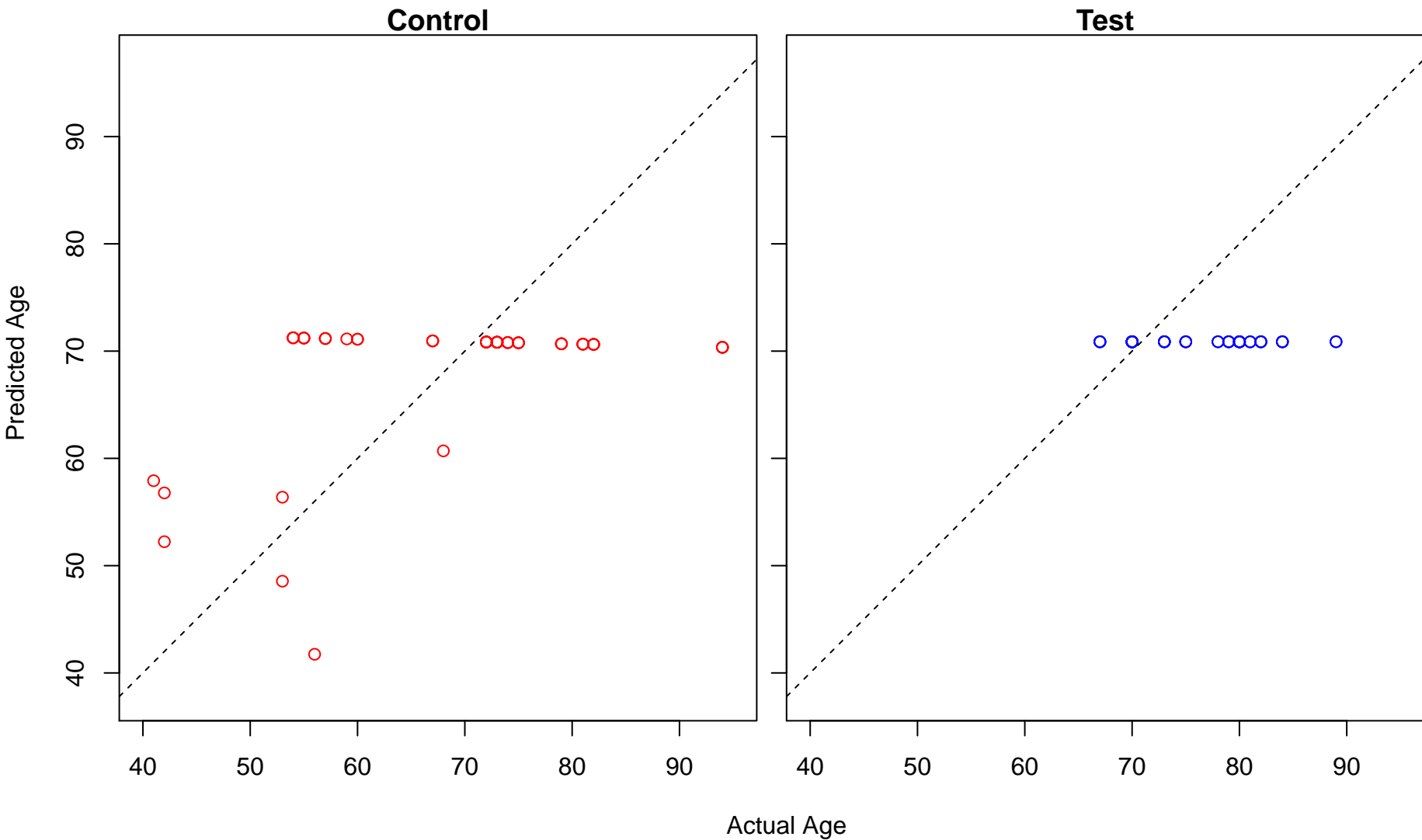


Actual Age

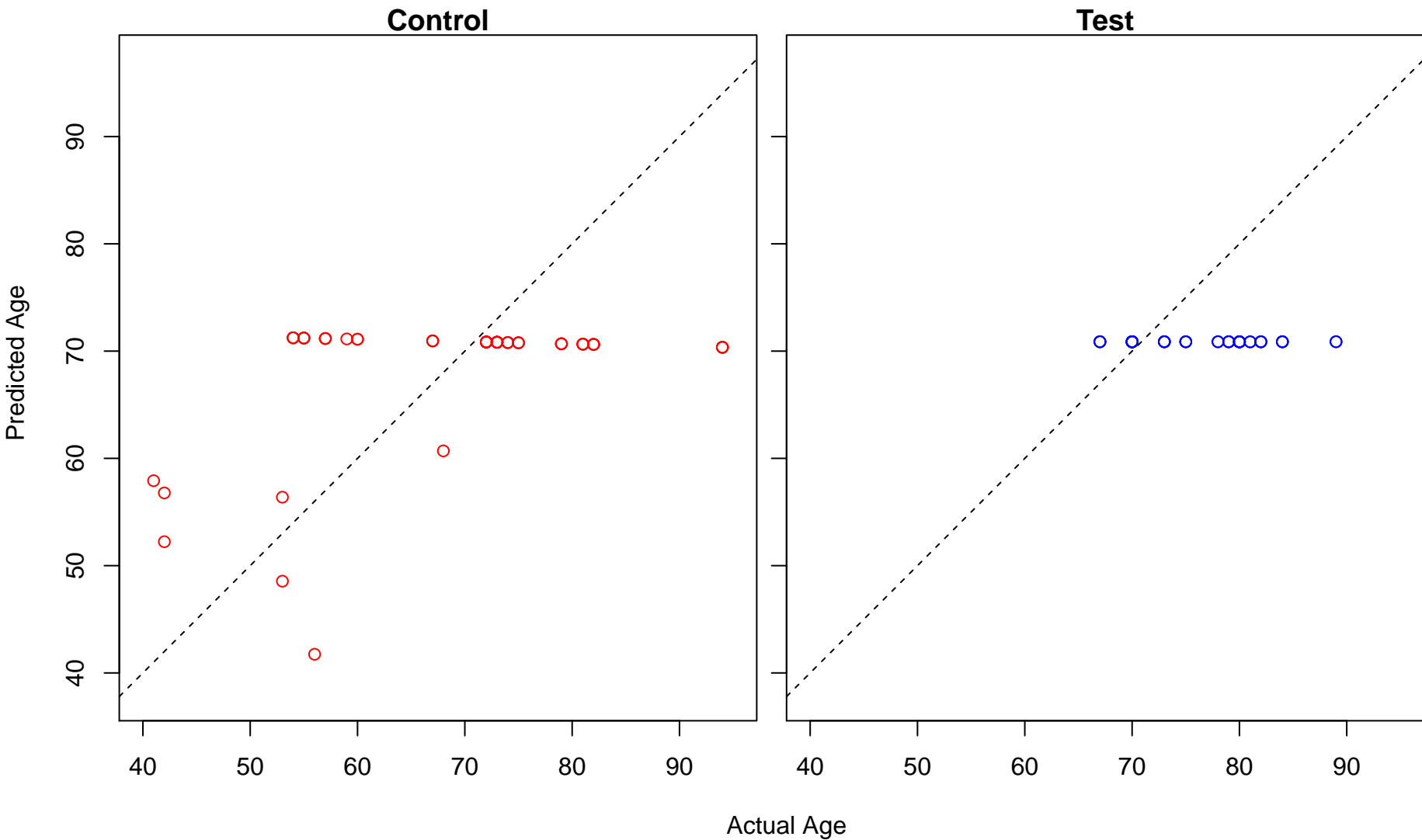
regulation of synaptic plasticity (Score: 0.802966)



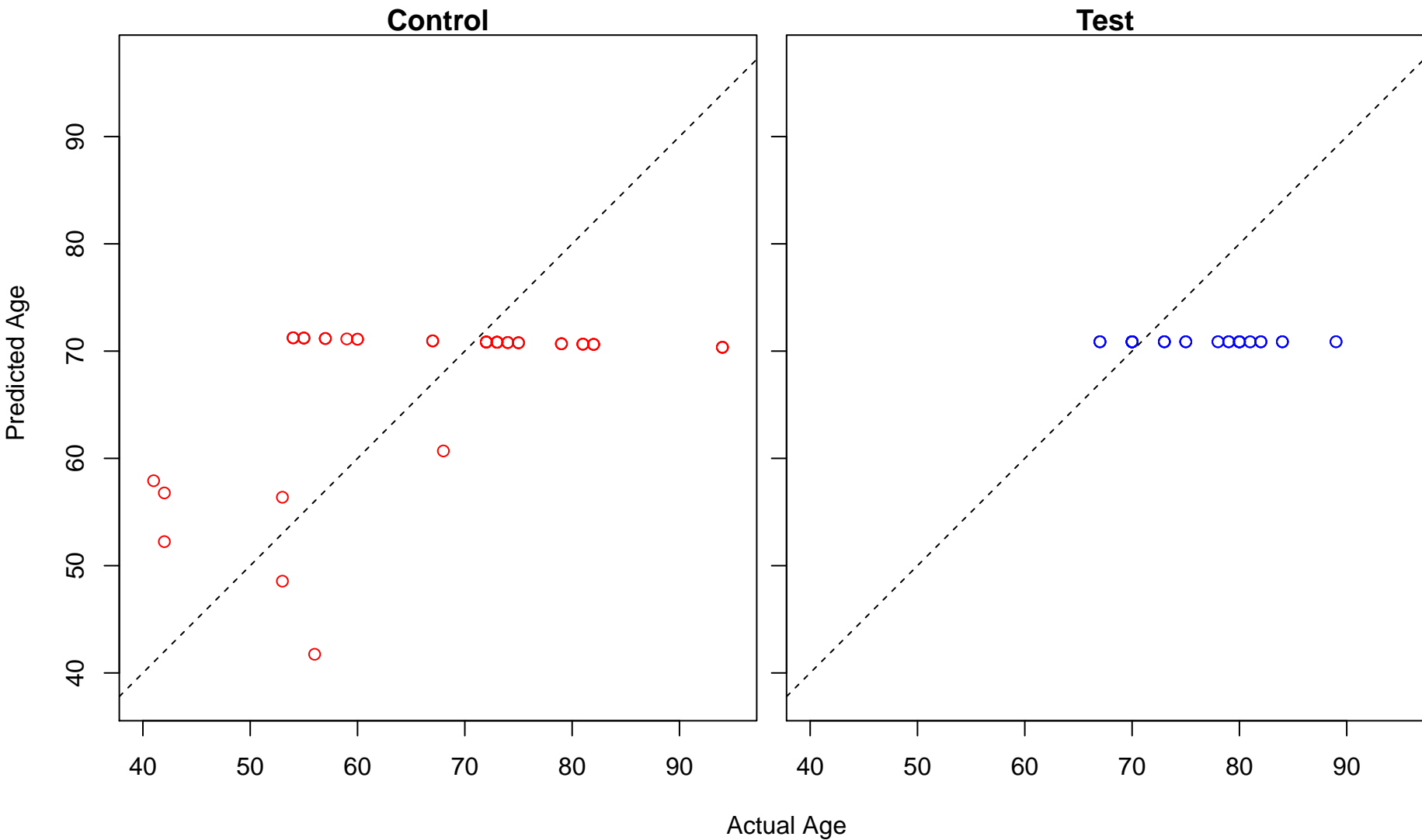
modulation of chemical synaptic transmission (Score: 0.802966)



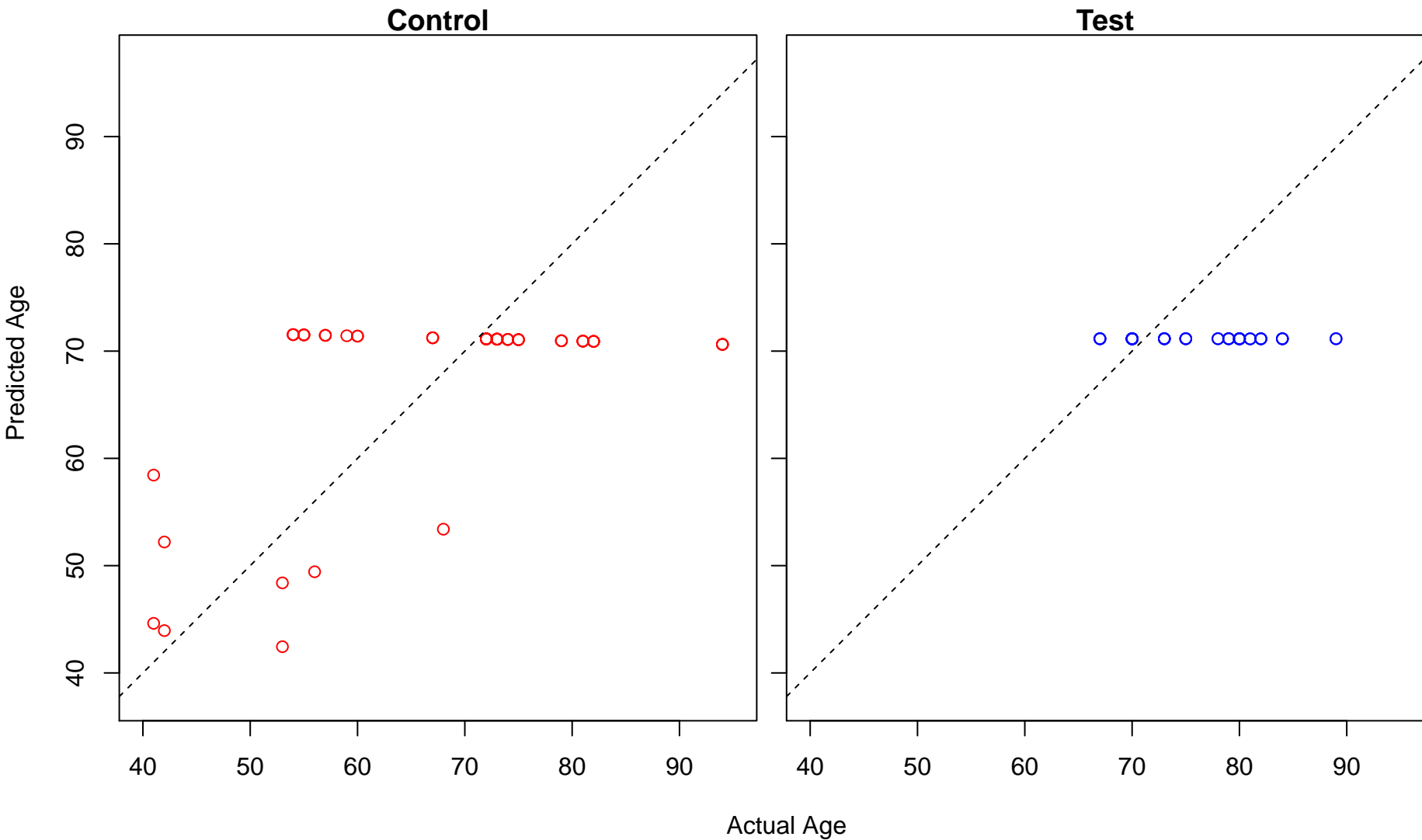
copper ion homeostasis (Score: 0.802966)



neuron projection organization (Score: 0.802964)

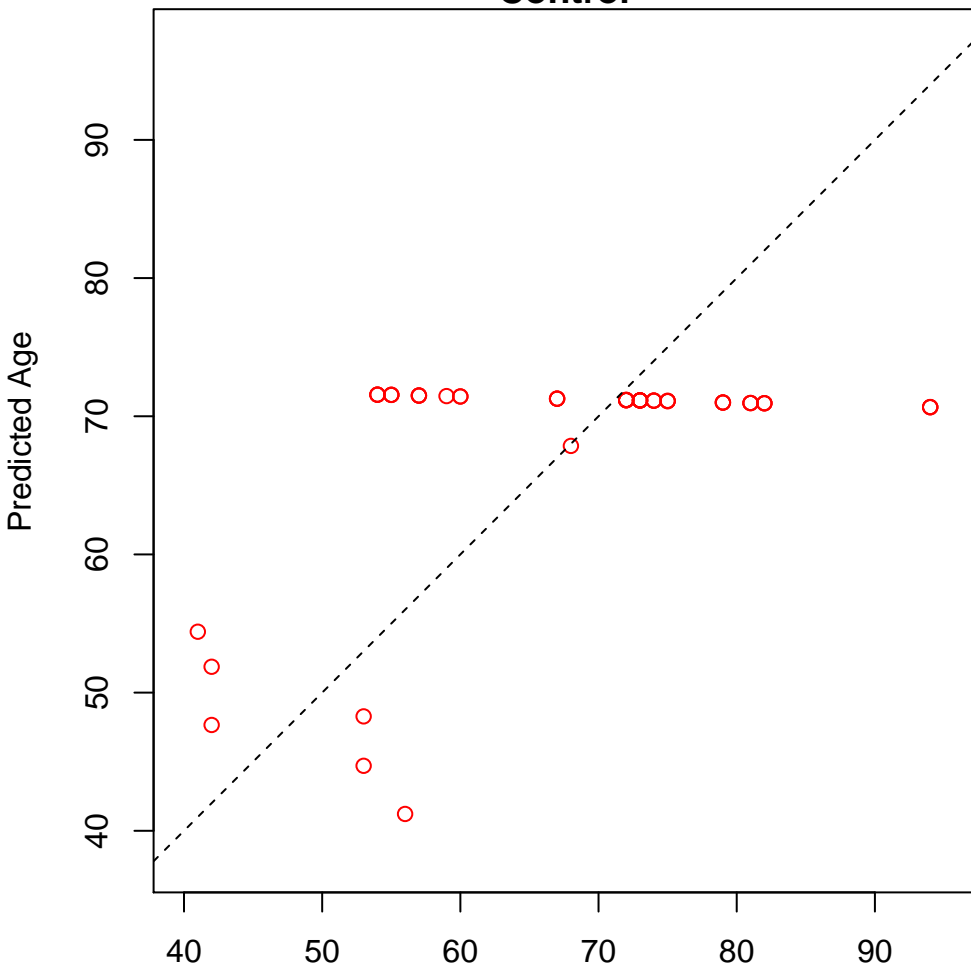


regulation of supramolecular fiber organization (Score: 0.802890)

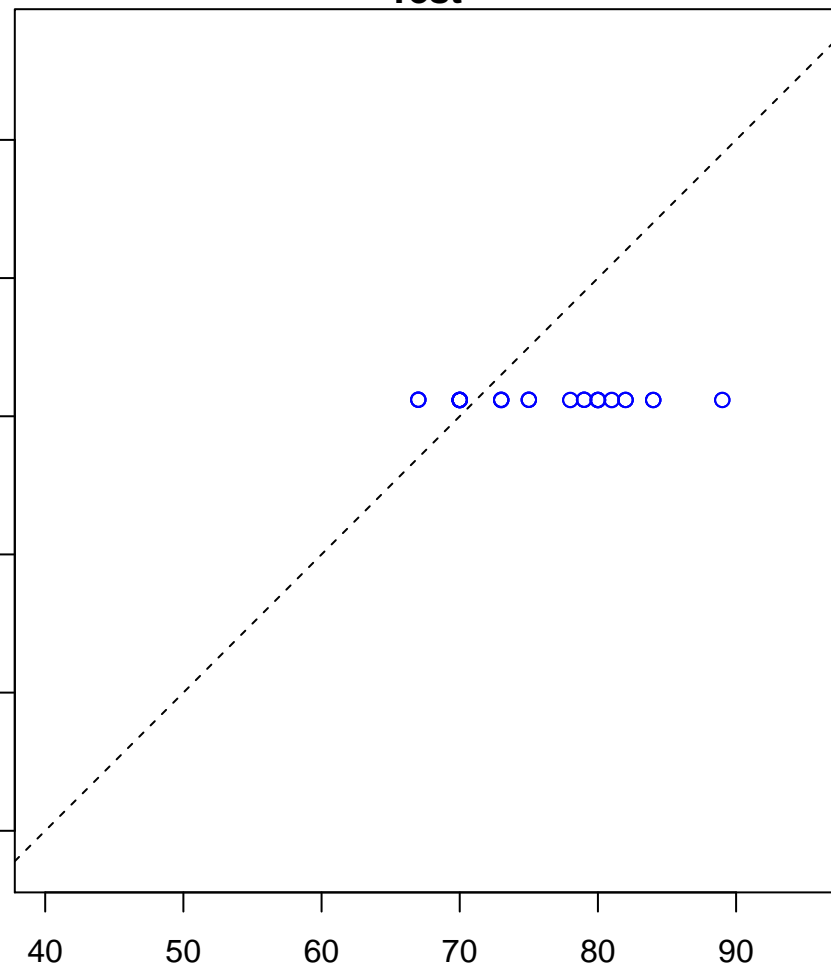


negative regulation of catabolic process (Score: 0.802809)

Control



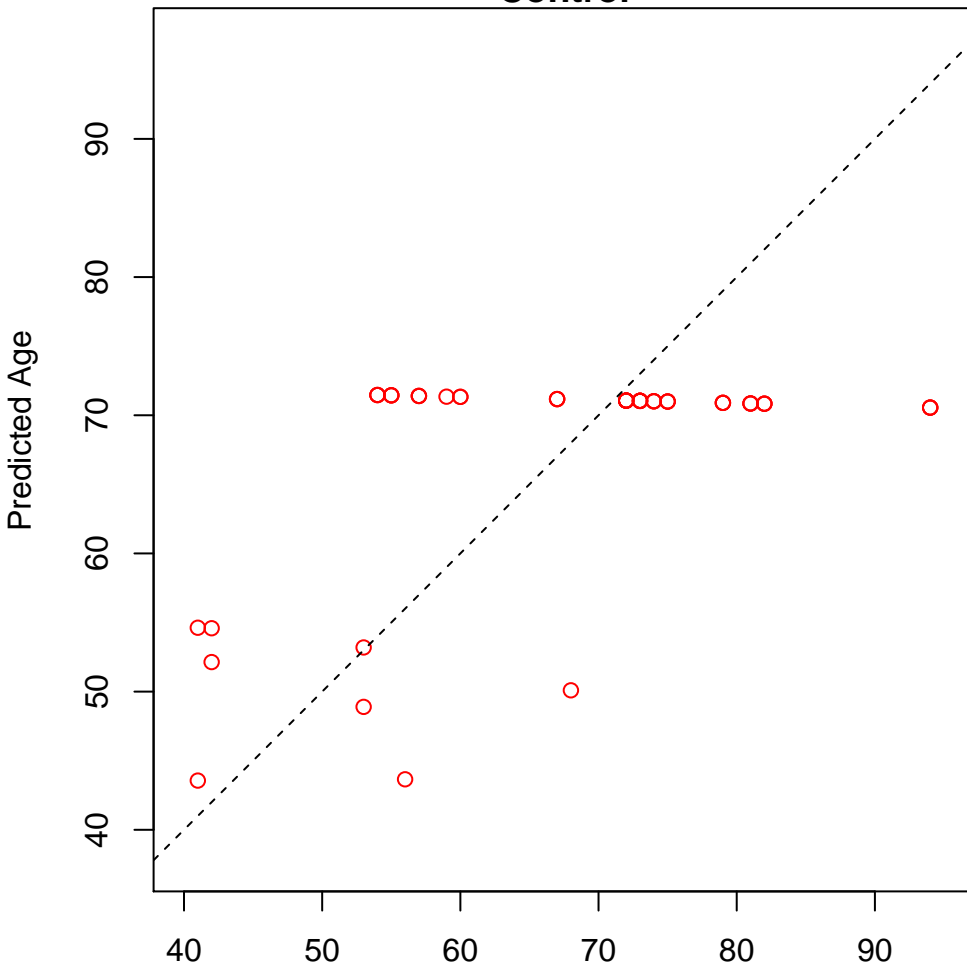
Test



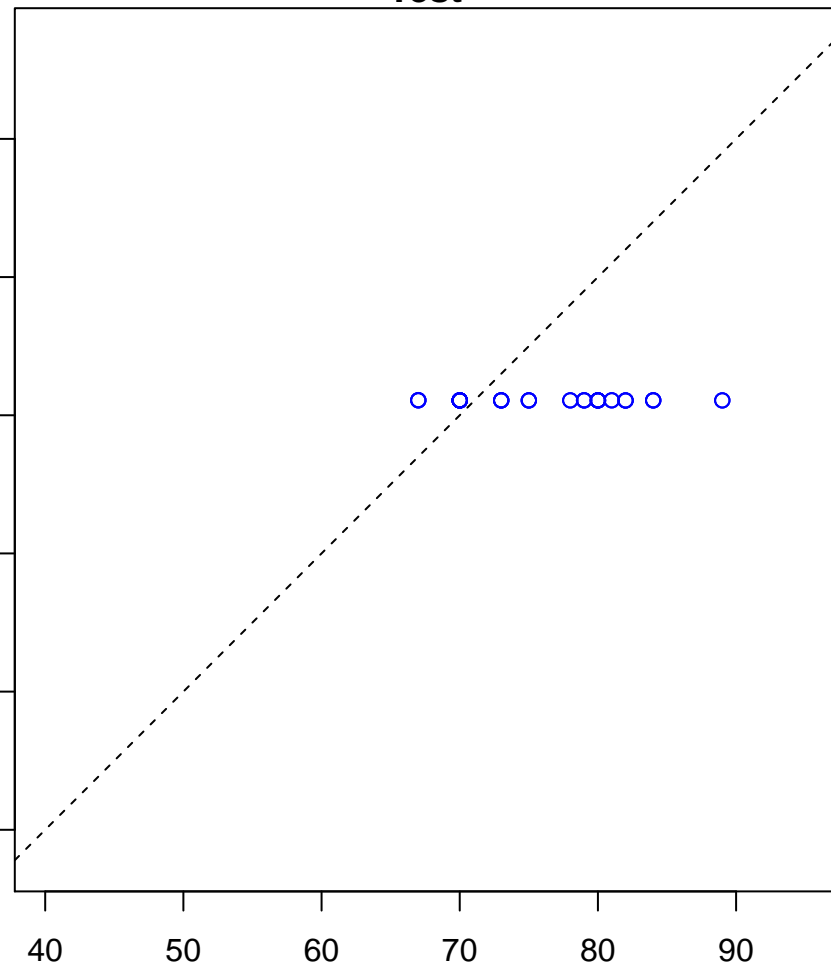
Actual Age

regulation of organelle assembly (Score: 0.802717)

Control

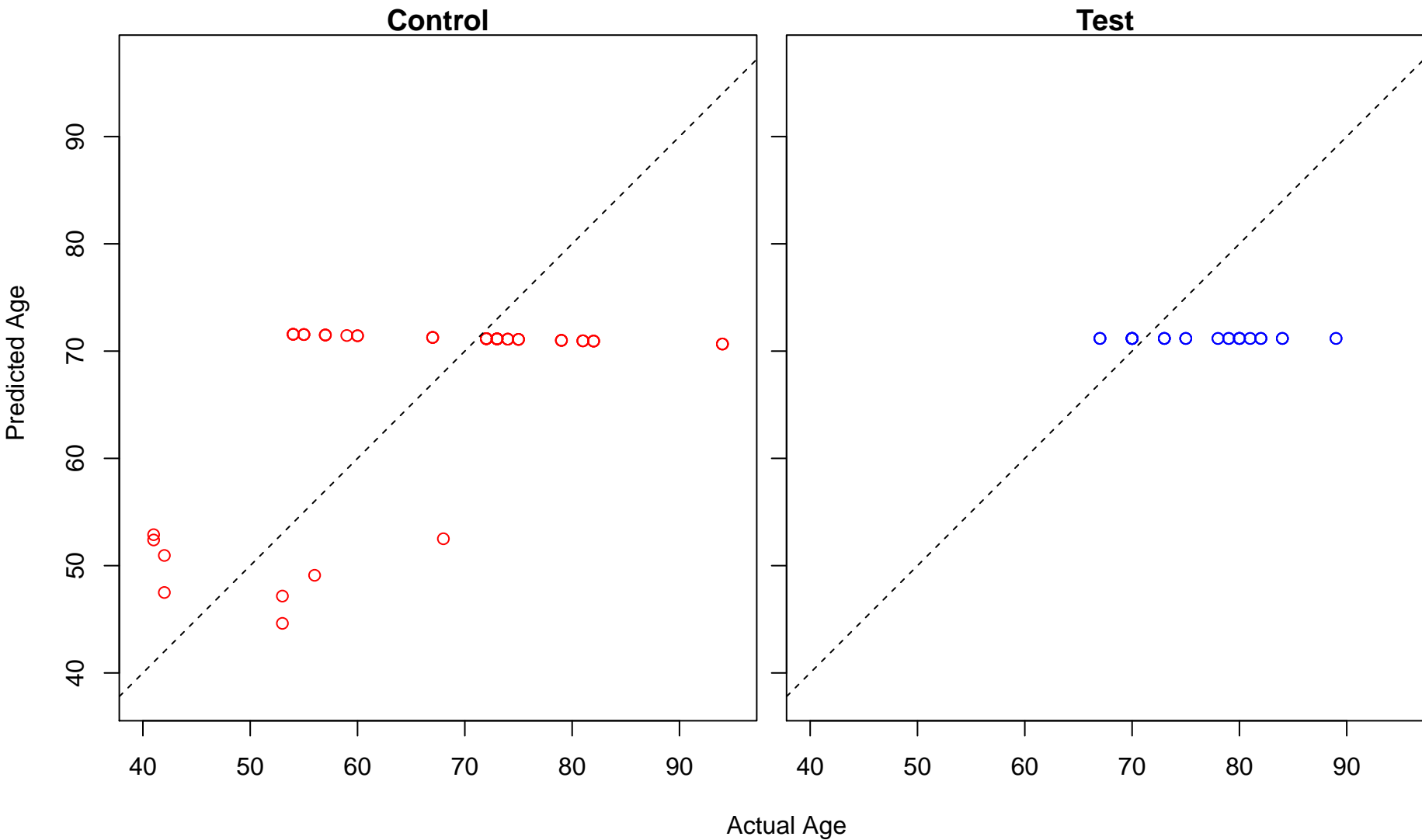


Test



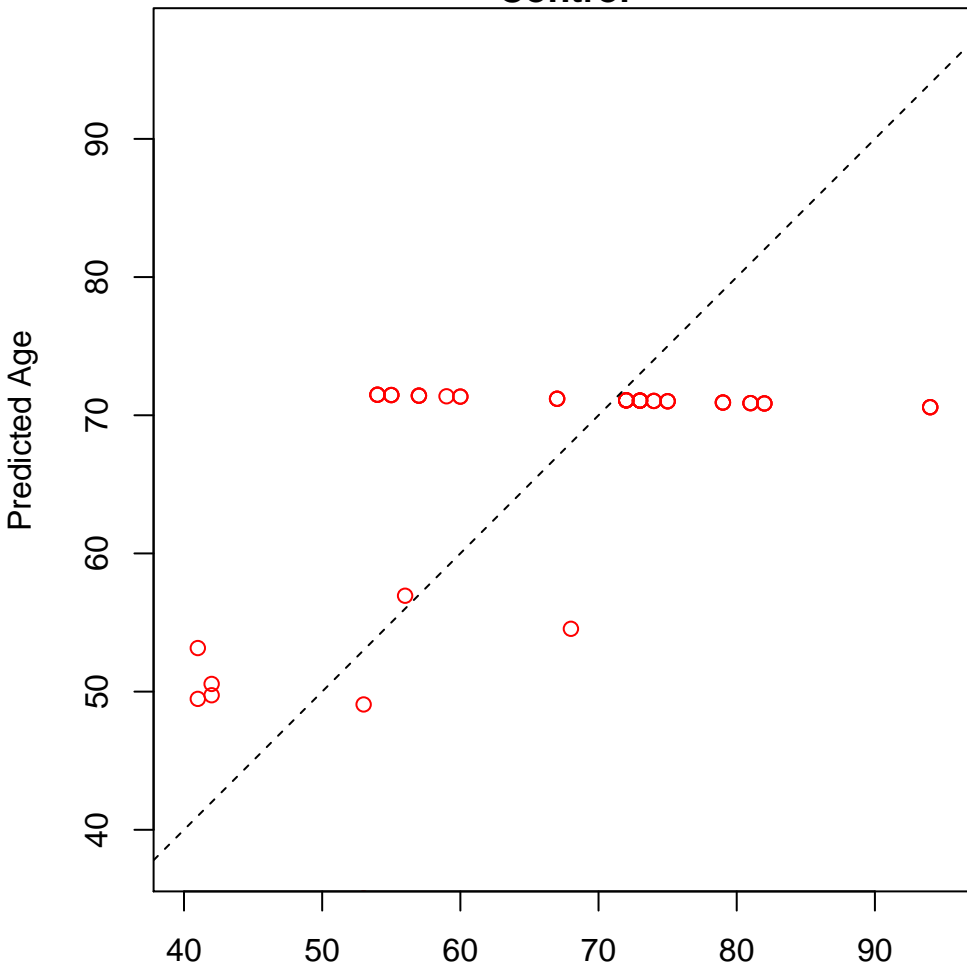
Actual Age

regulation of cellular component organization (Score: 0.802697)

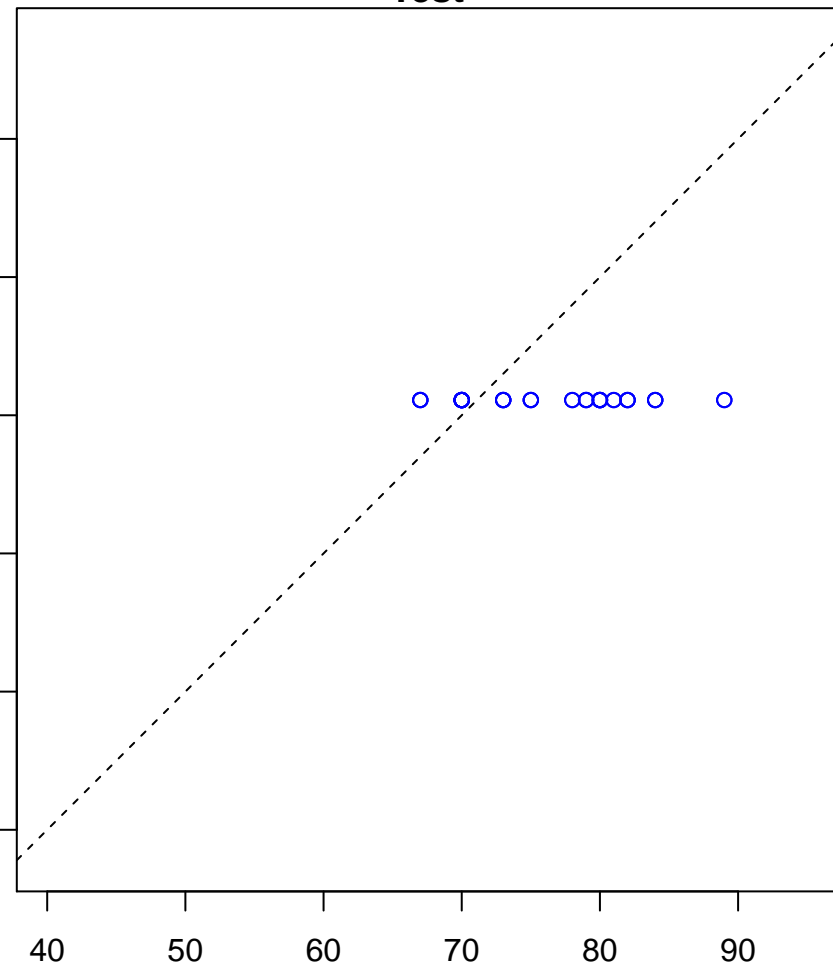


cellular component disassembly (Score: 0.802686)

Control

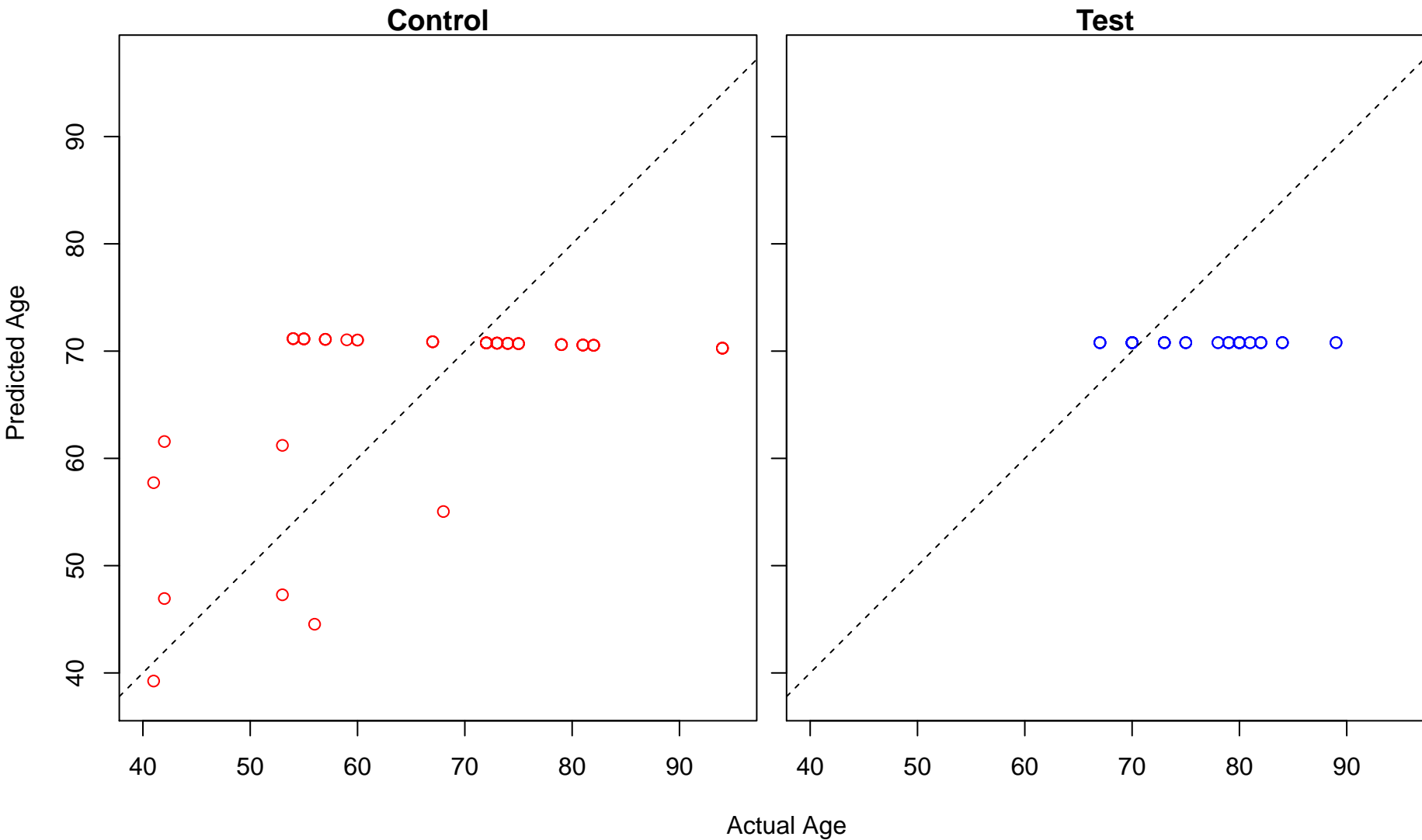


Test

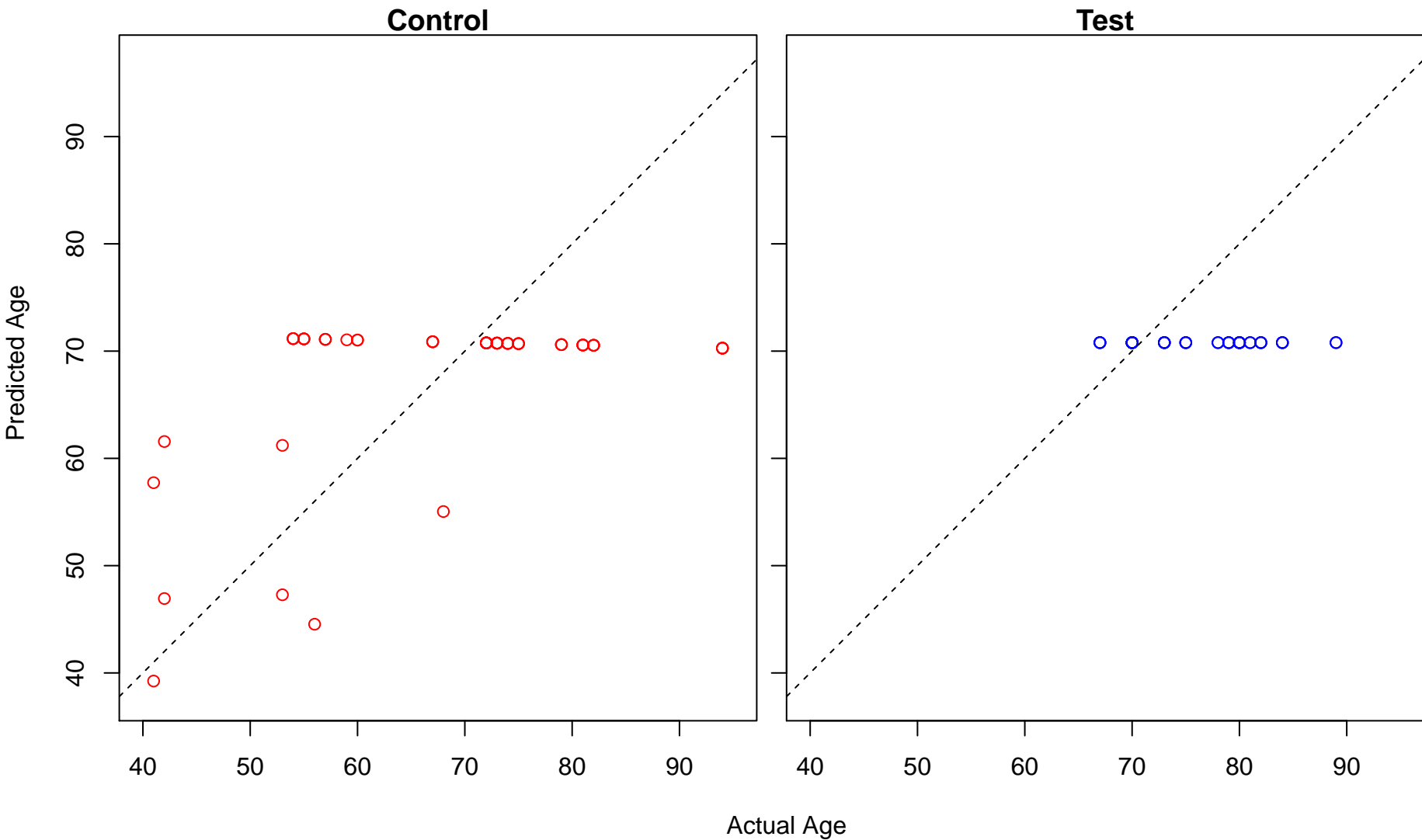


Actual Age

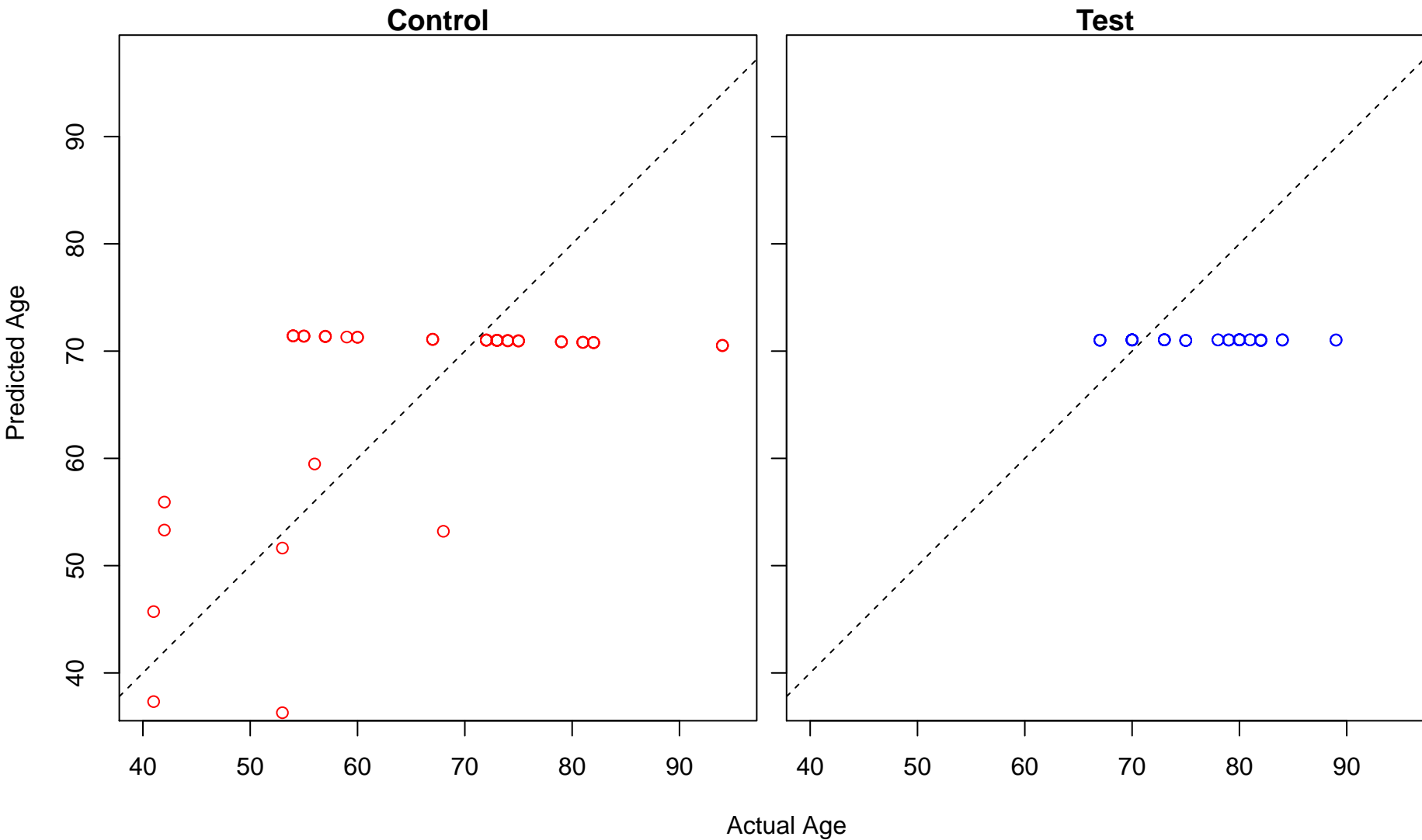
skeletal system development (Score: 0.802681)



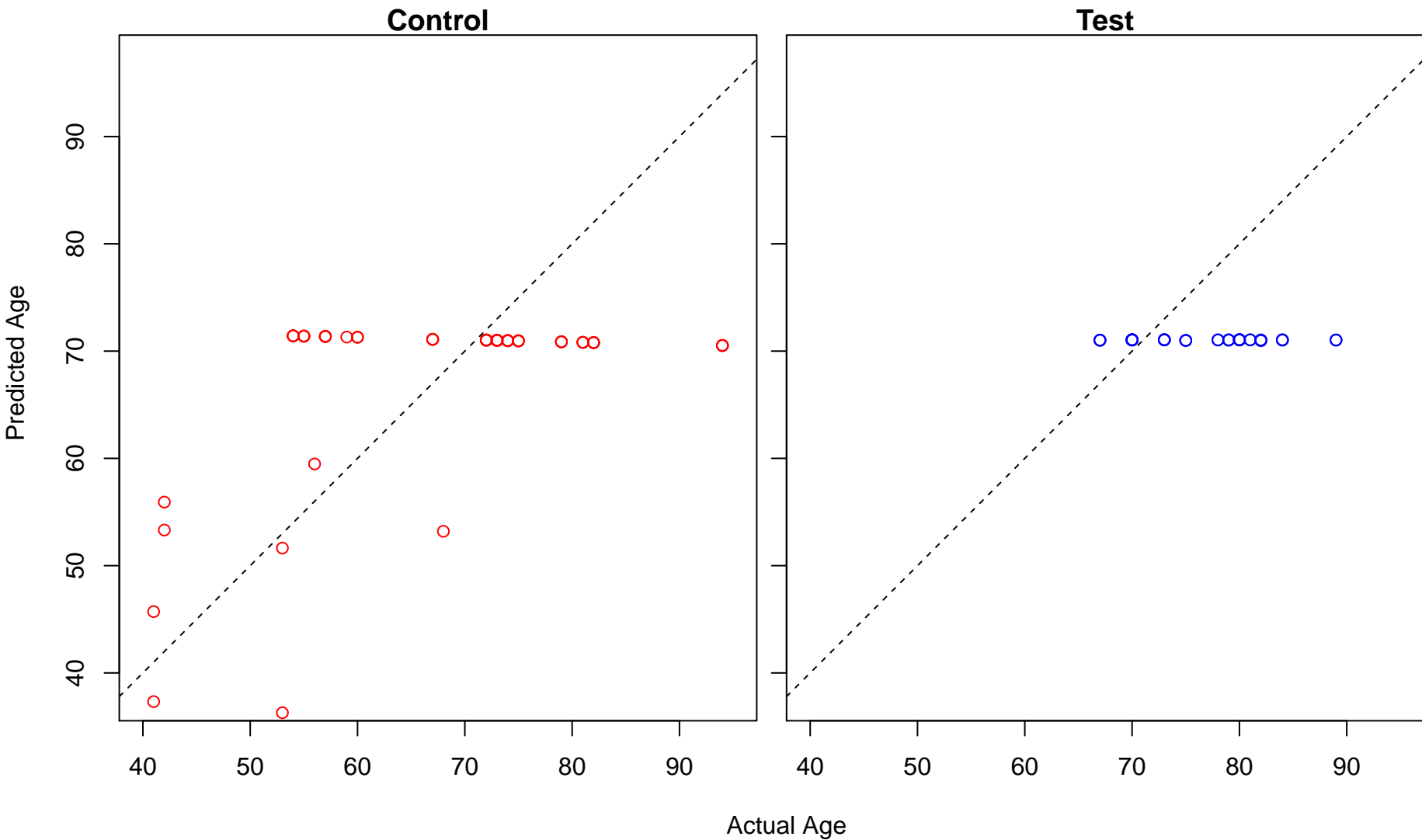
bone development (Score: 0.802681)



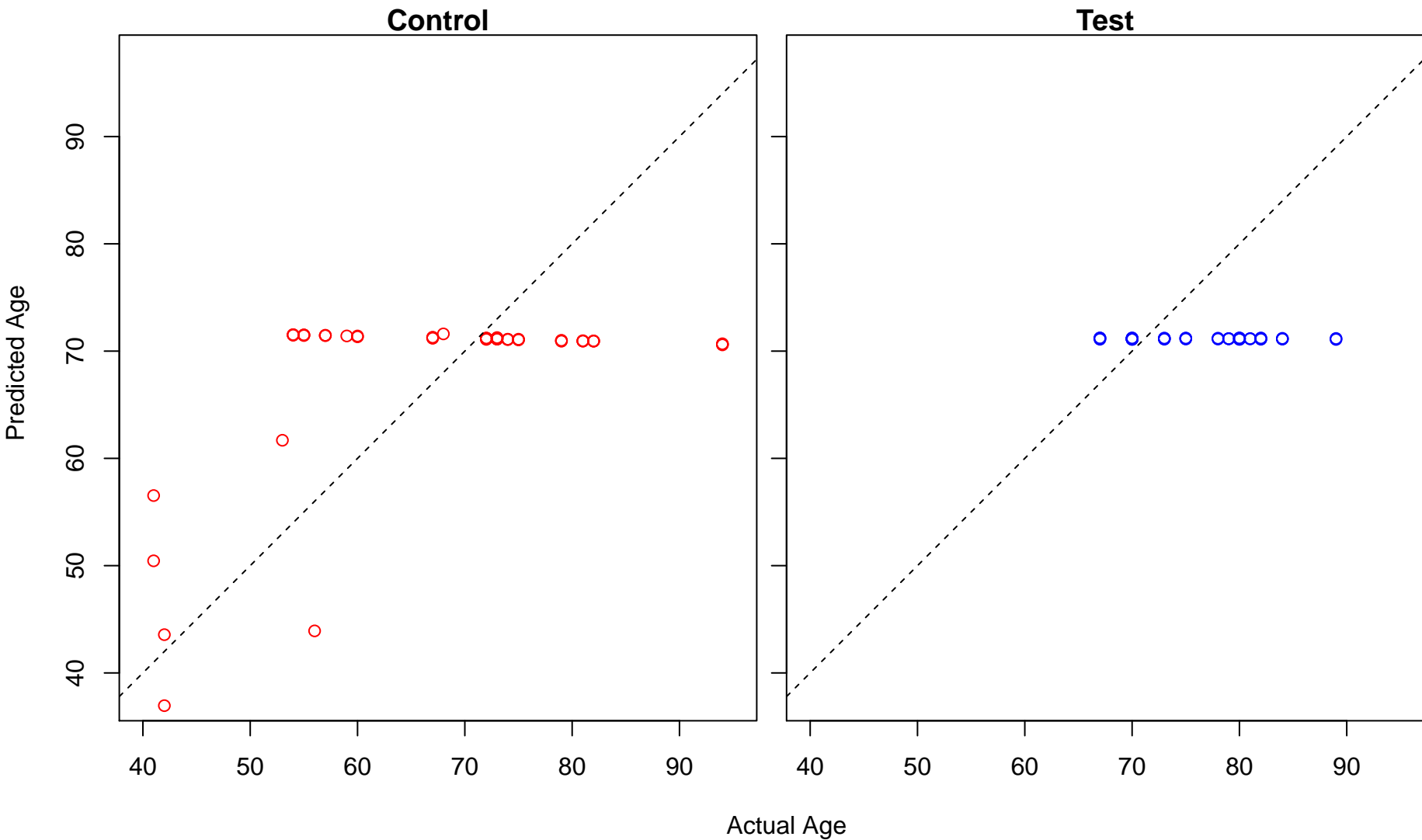
positive regulation of interleukin-6 production (Score: 0.802546)



positive regulation of interleukin-6 secretion (Score: 0.802546)

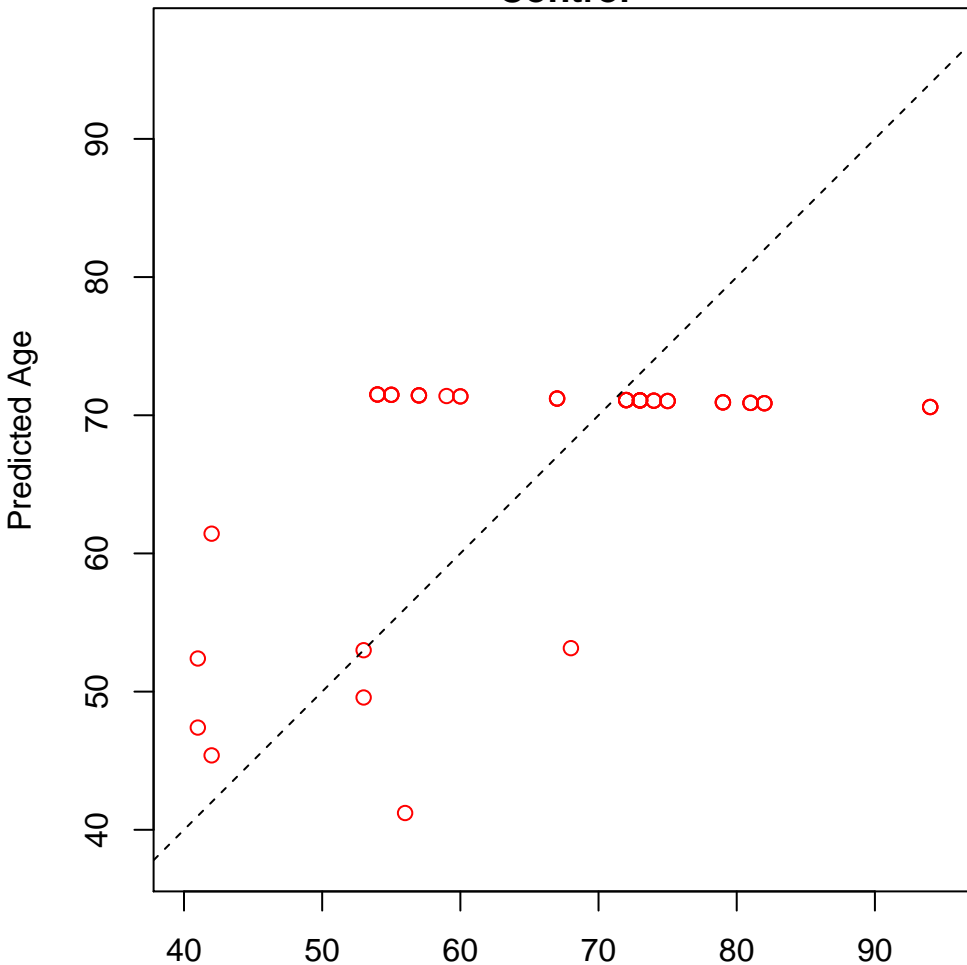


response to metal ion (Score: 0.802530)

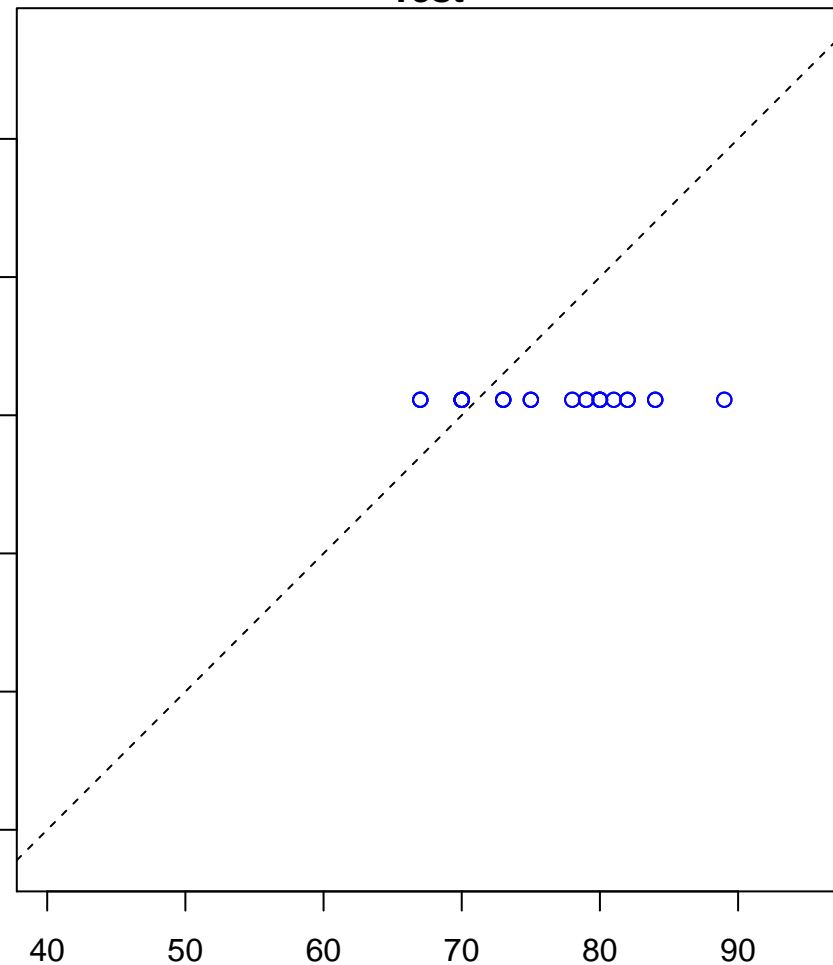


regulation of metal ion transport (Score: 0.802476)

Control

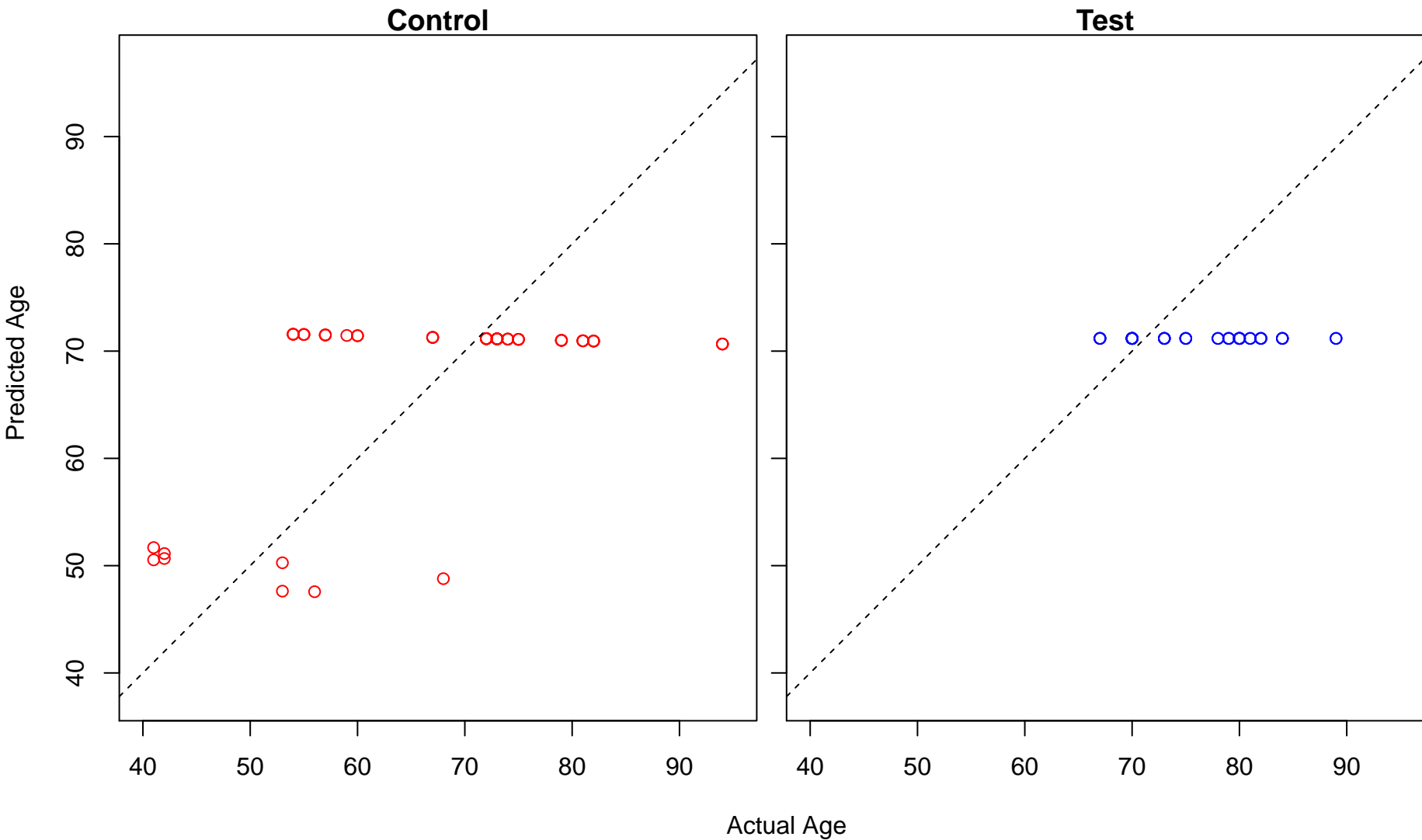


Test

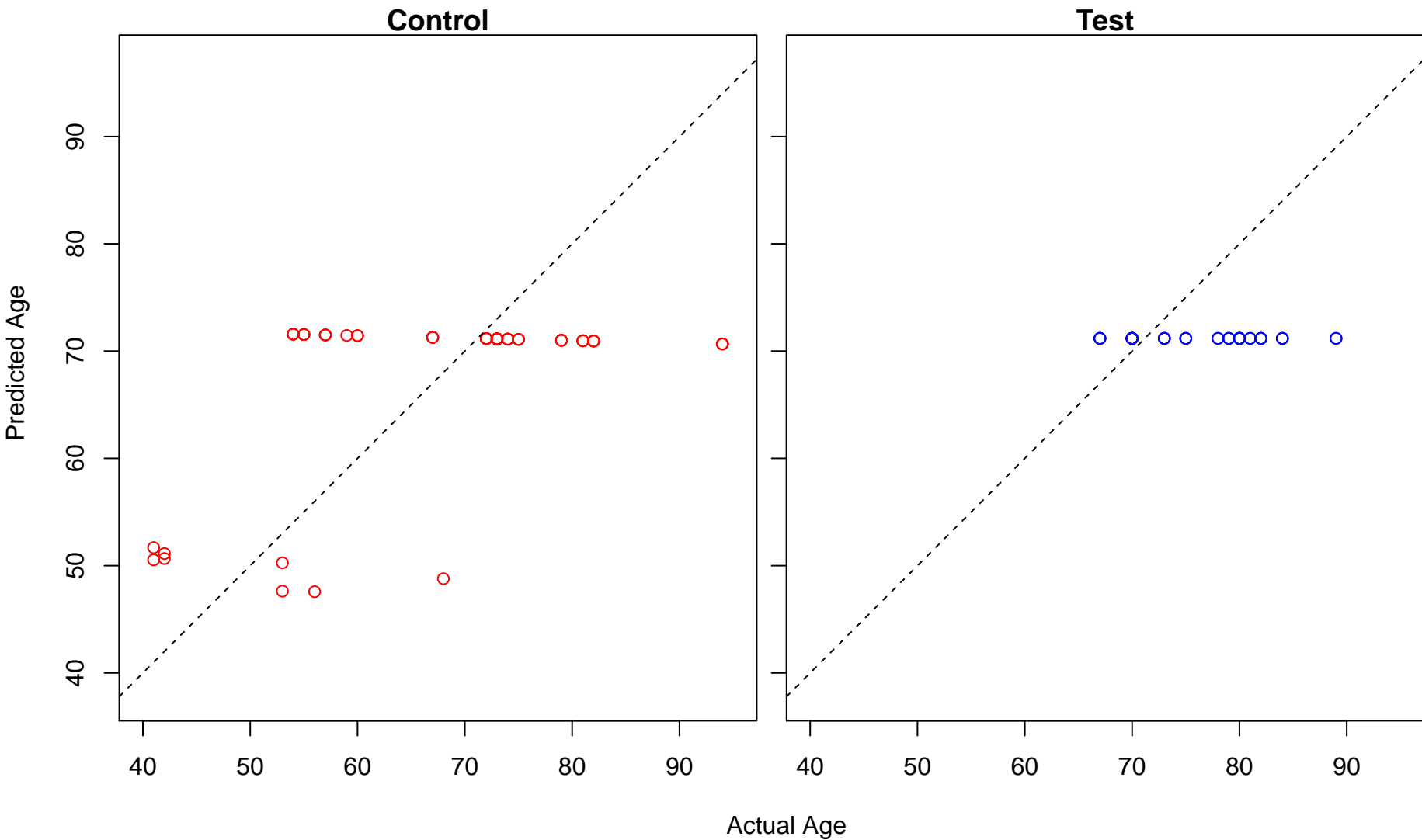


Actual Age

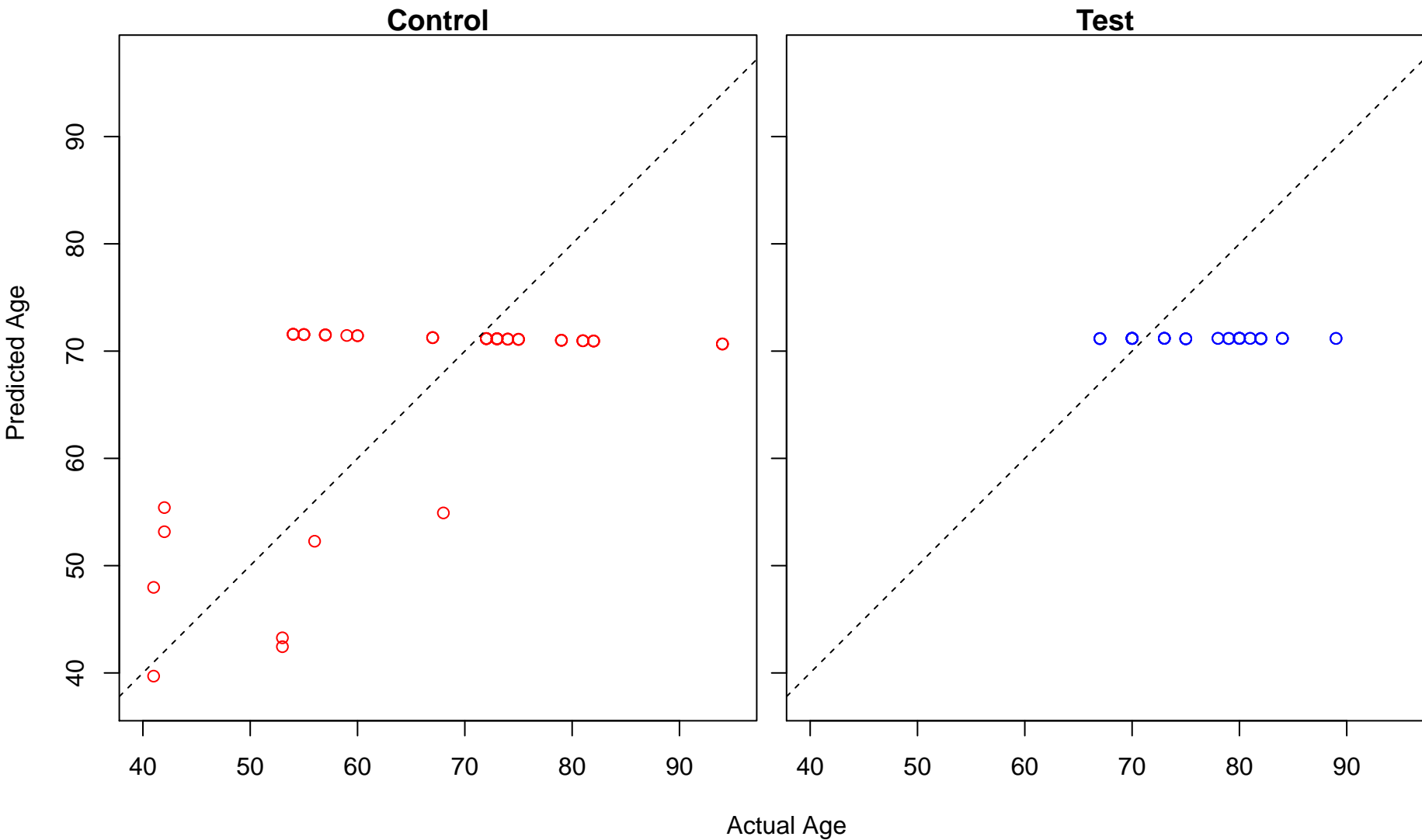
regulation of leukocyte activation (Score: 0.802370)



regulation of cell activation (Score: 0.802370)

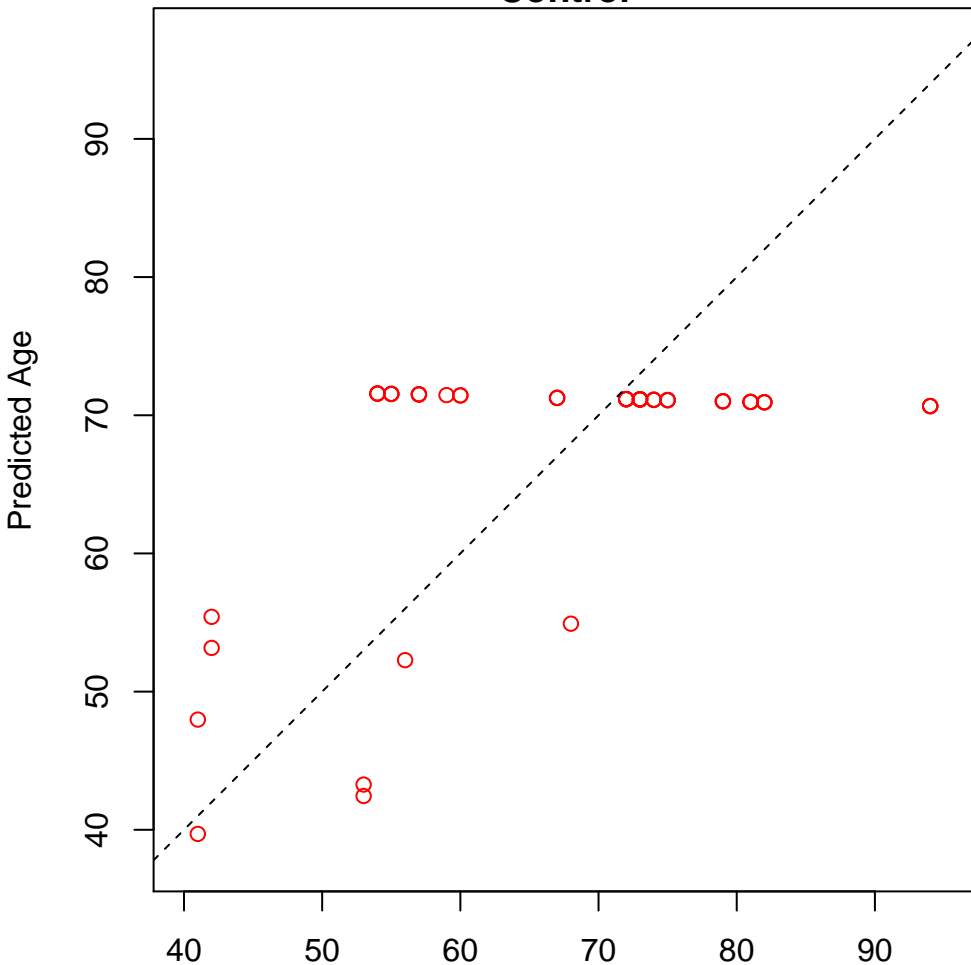


regulation of B cell activation (Score: 0.802362)

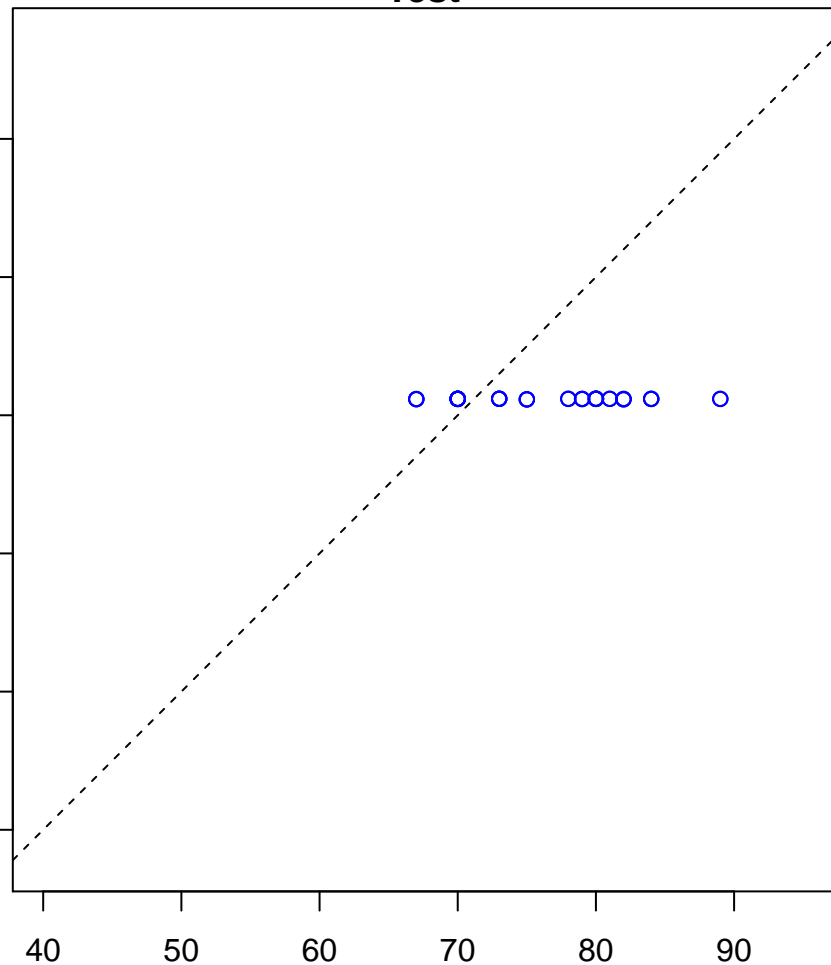


positive regulation of B cell activation (Score: 0.802362)

Control

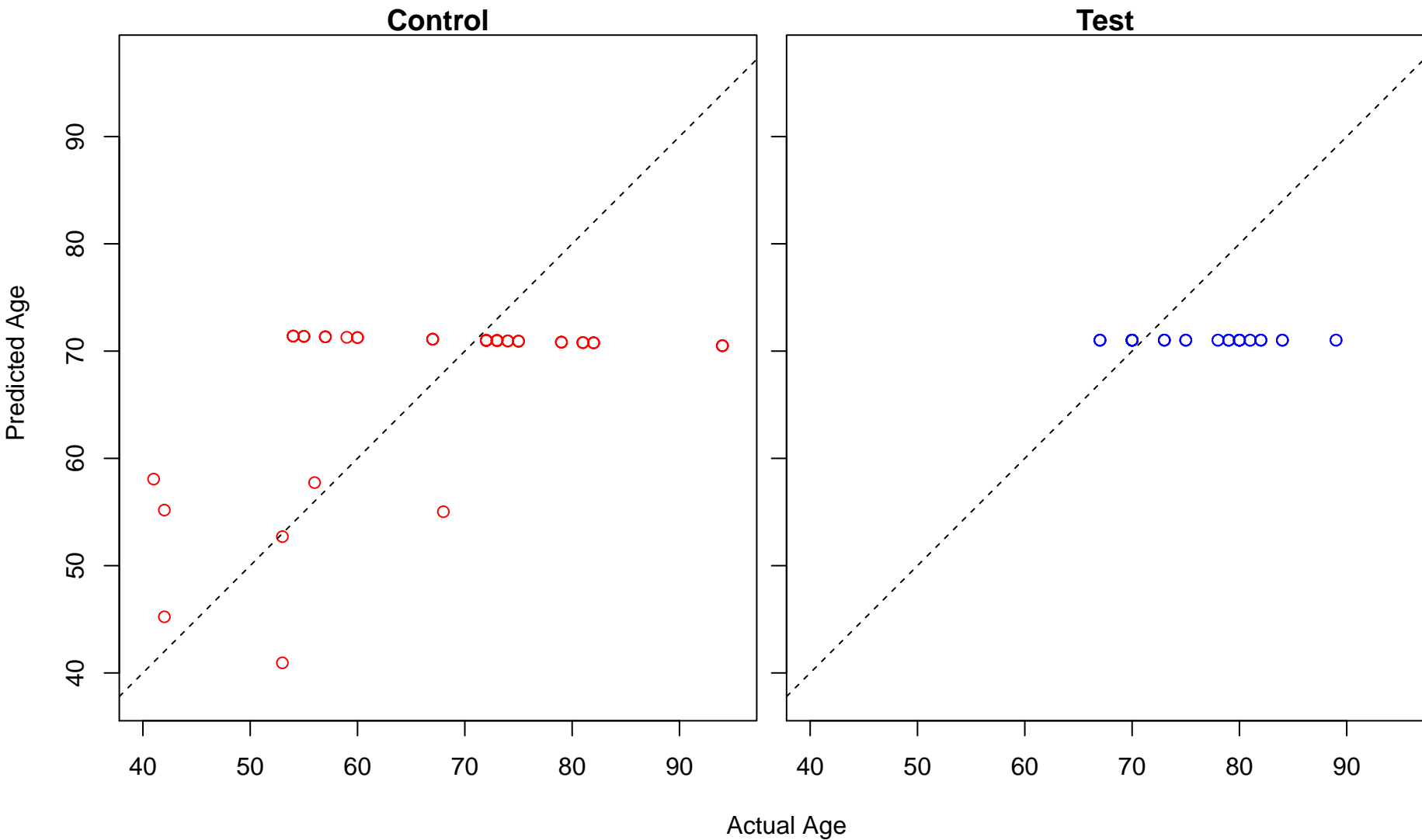


Test

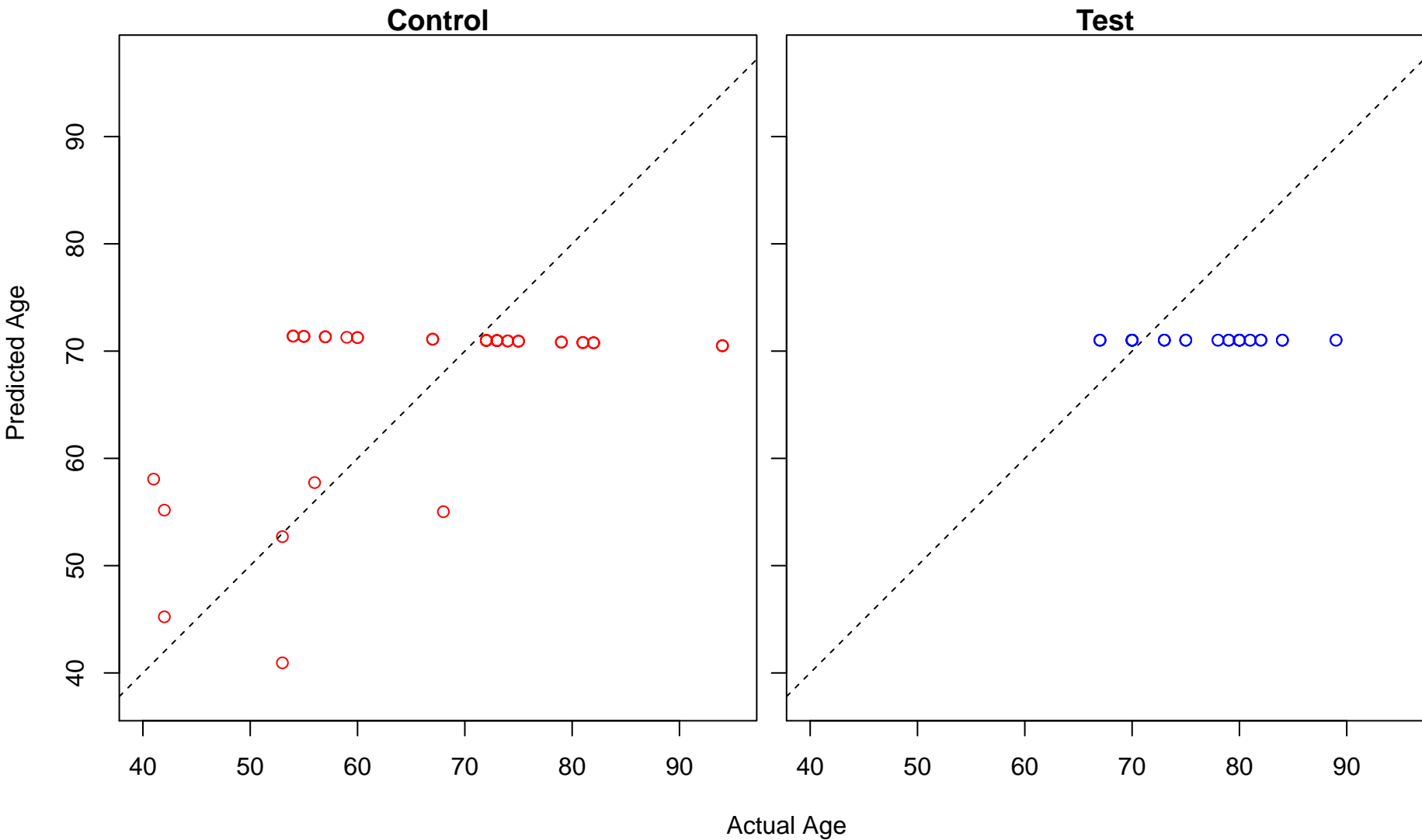


Actual Age

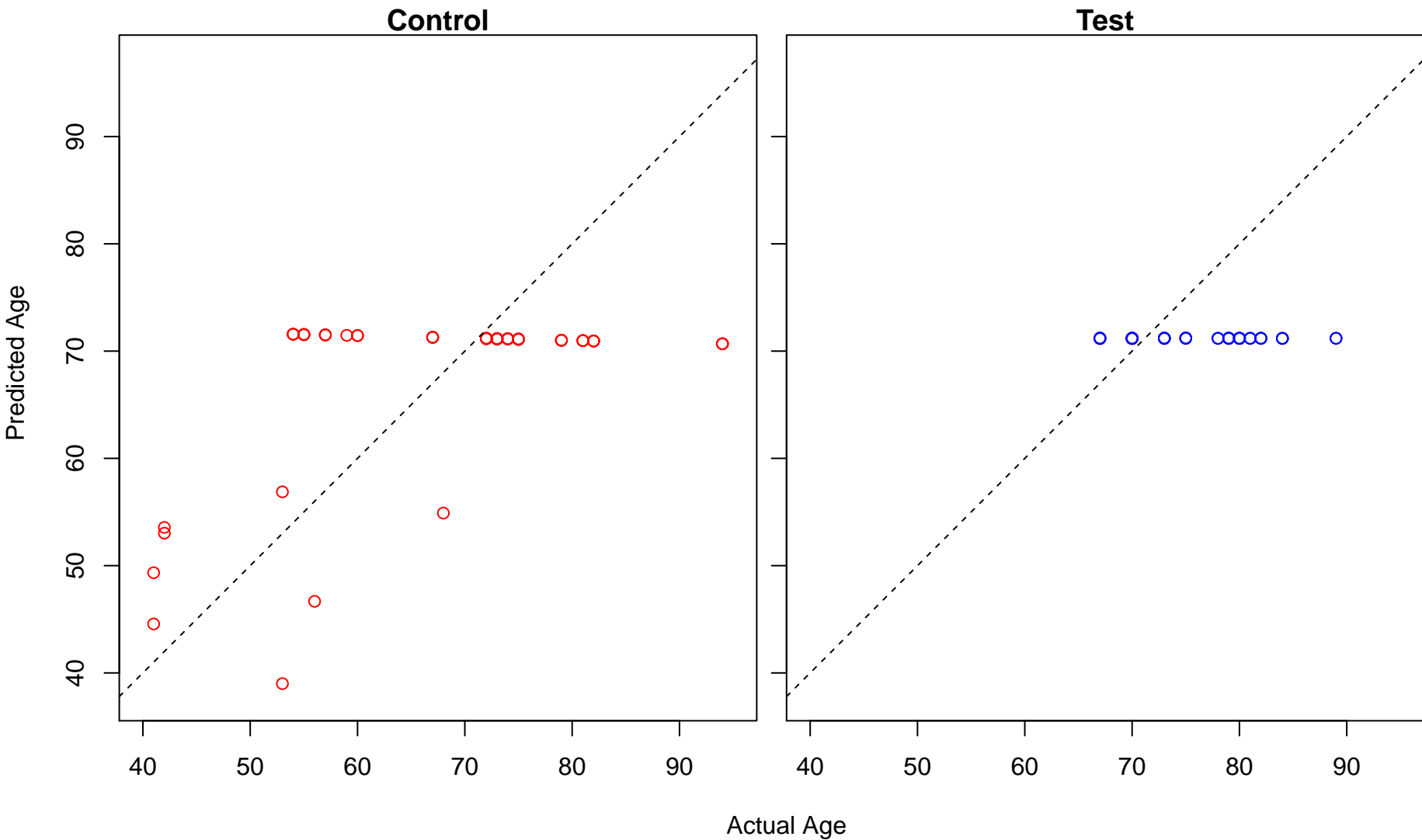
organic acid transport (Score: 0.802359)



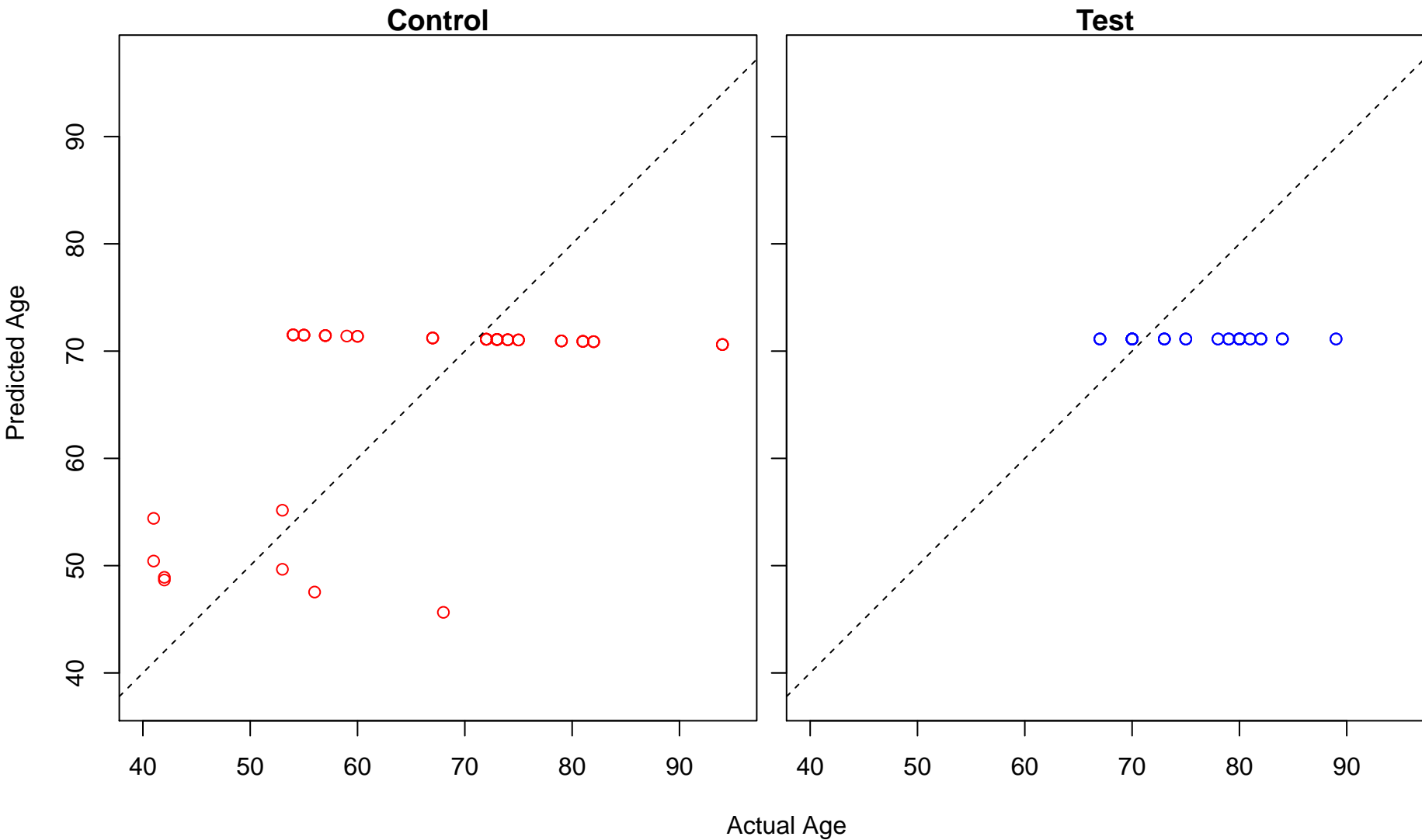
carboxylic acid transport (Score: 0.802359)



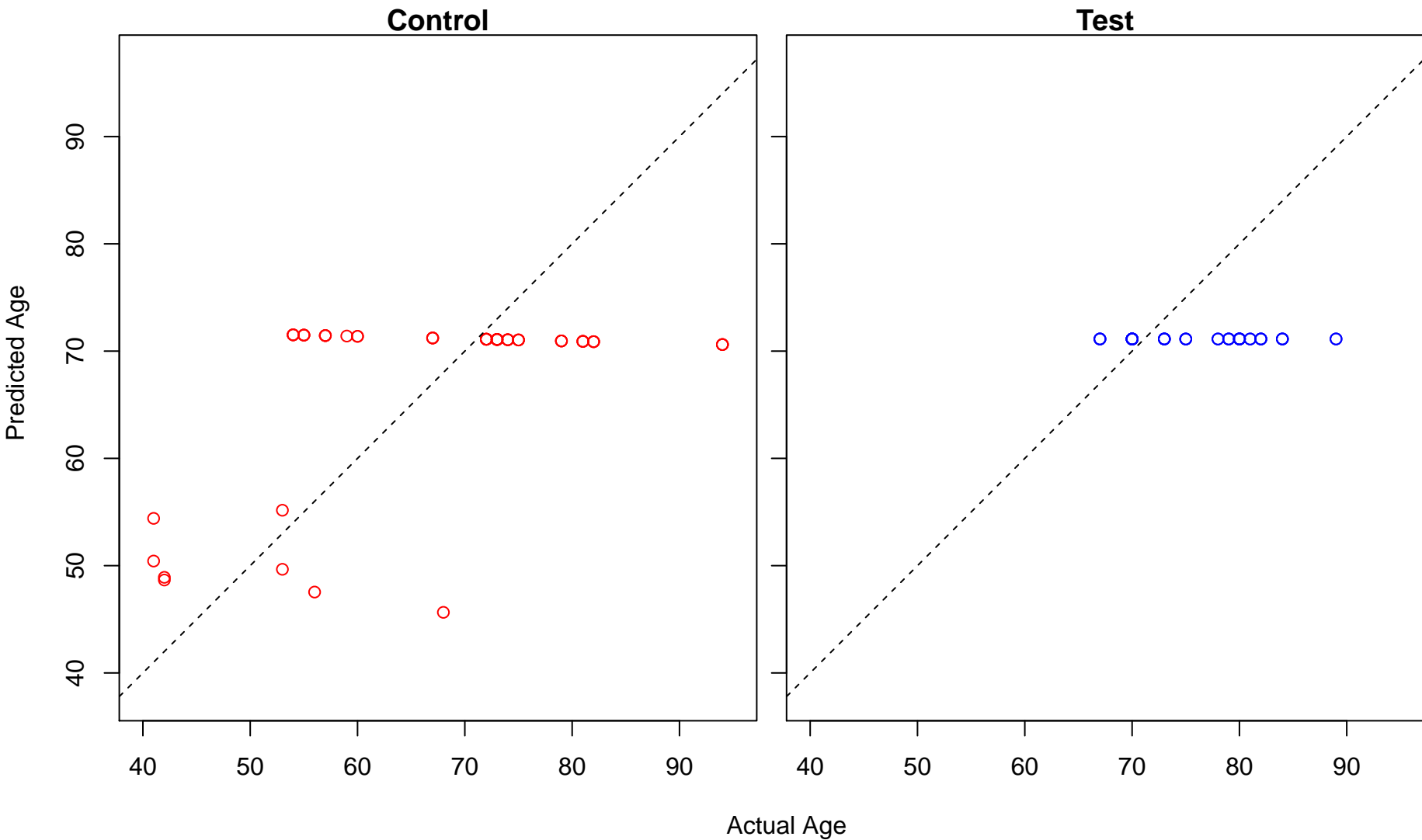
protein processing (Score: 0.802326)



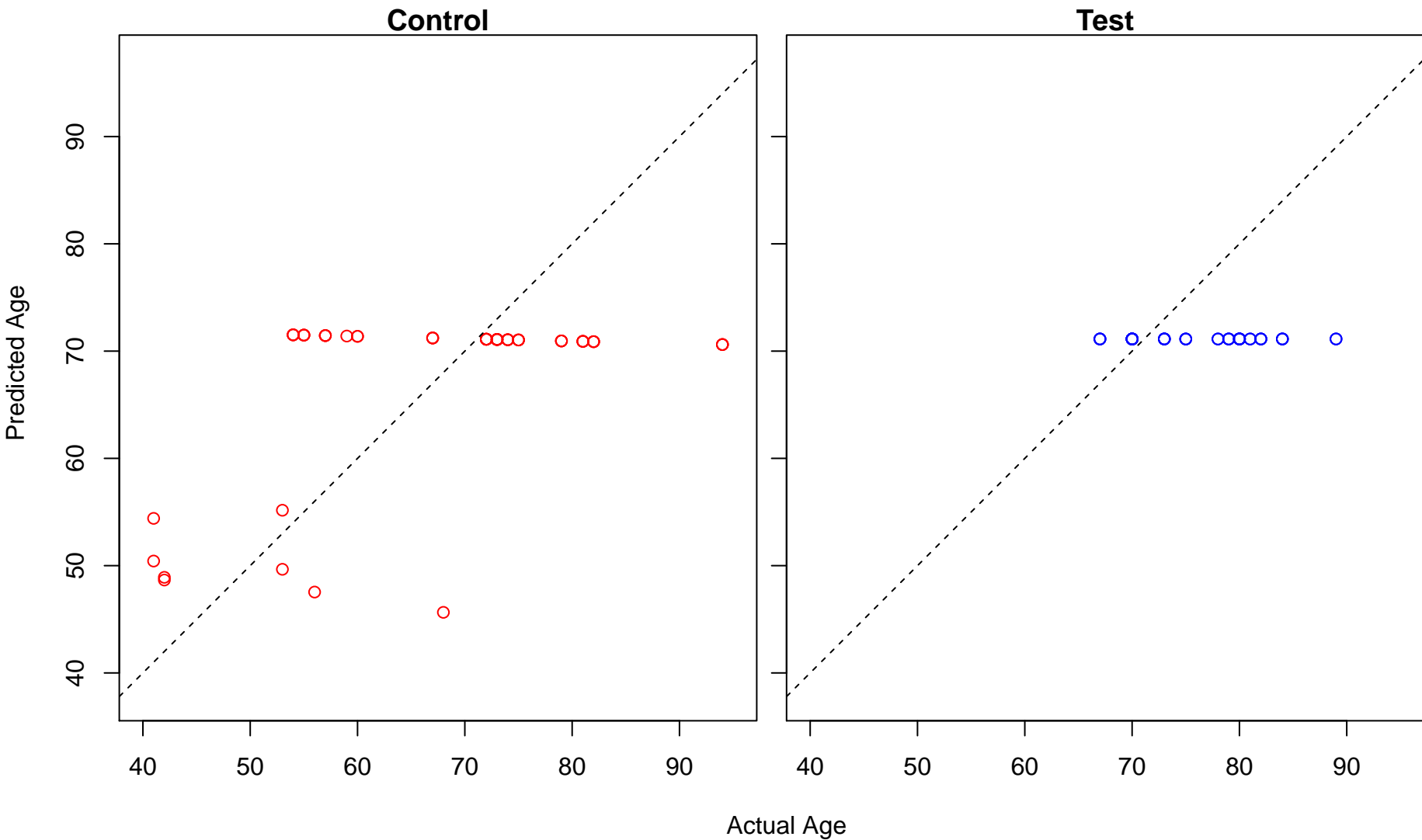
regulation of peptide secretion (Score: 0.802316)



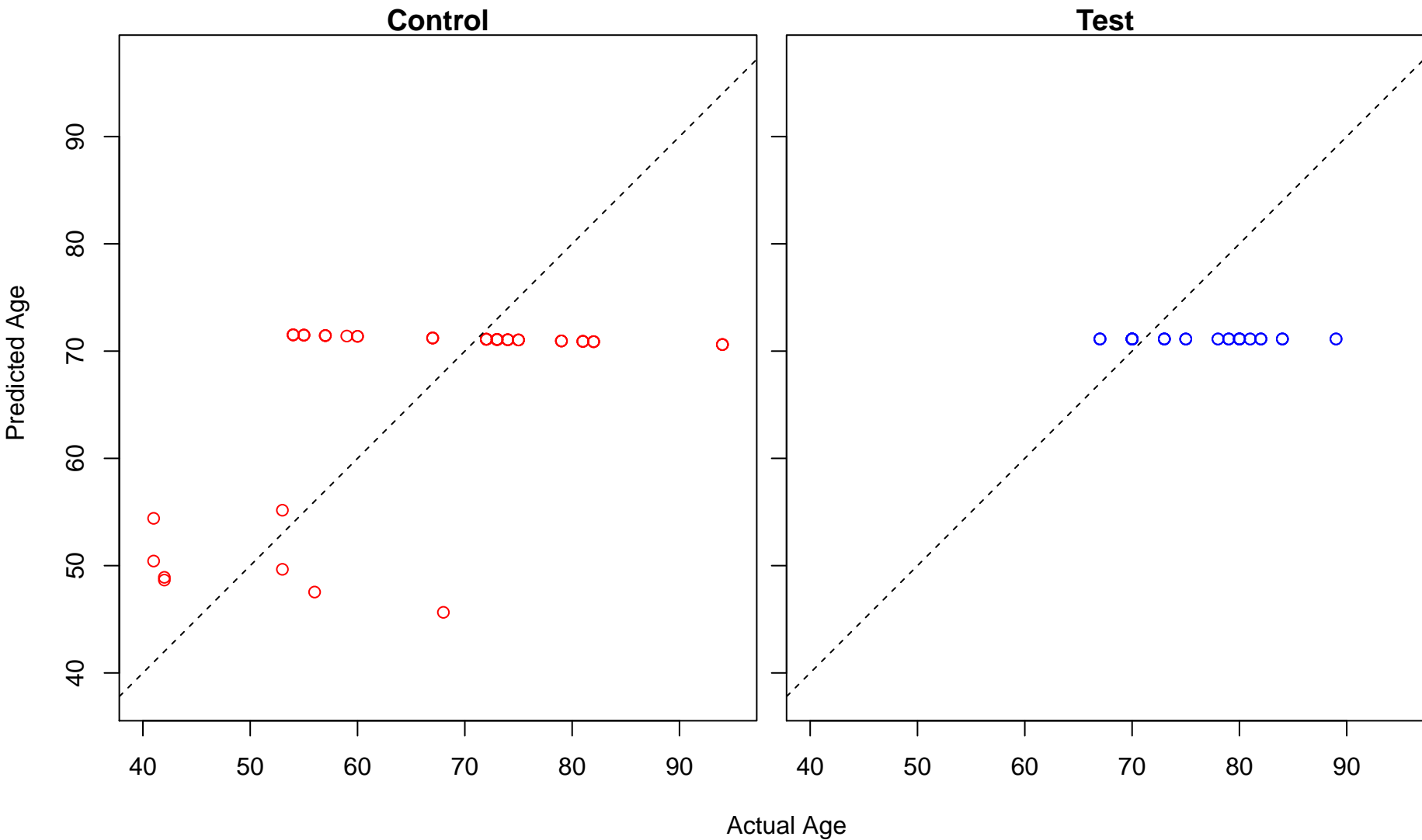
regulation of secretion (Score: 0.802316)



regulation of secretion by cell (Score: 0.802316)

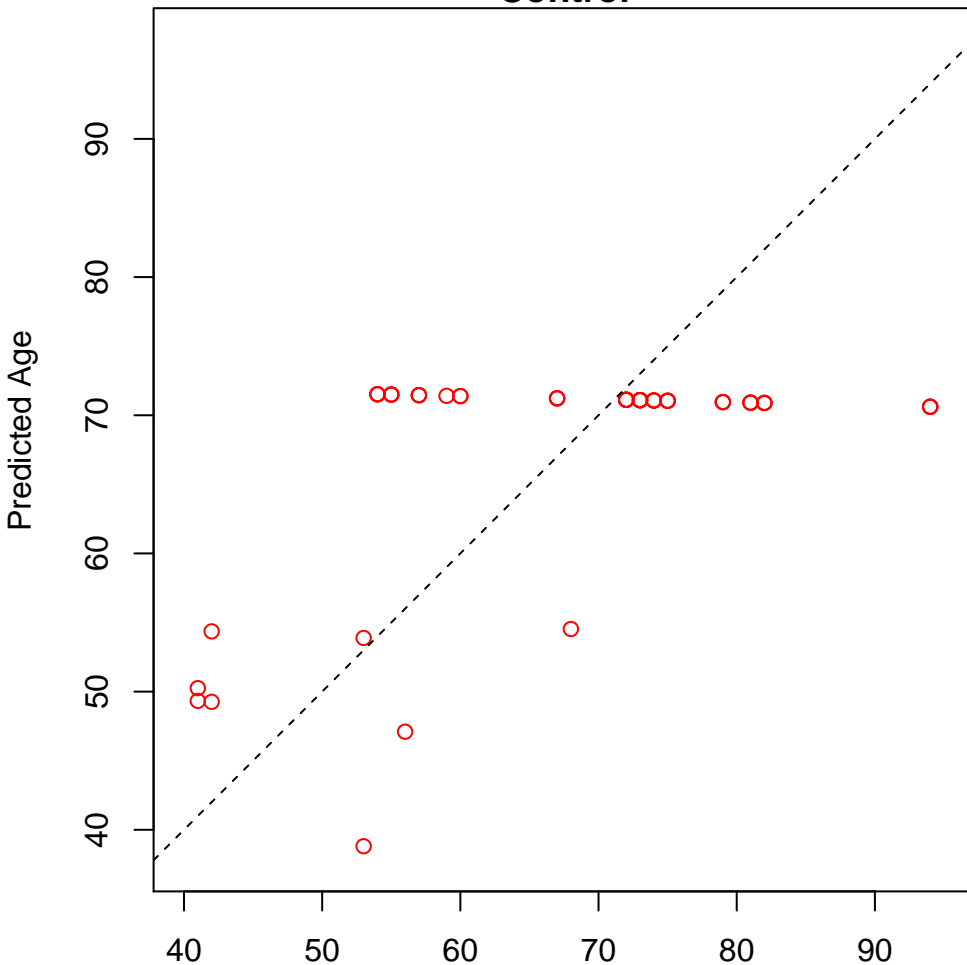


regulation of protein secretion (Score: 0.802314)

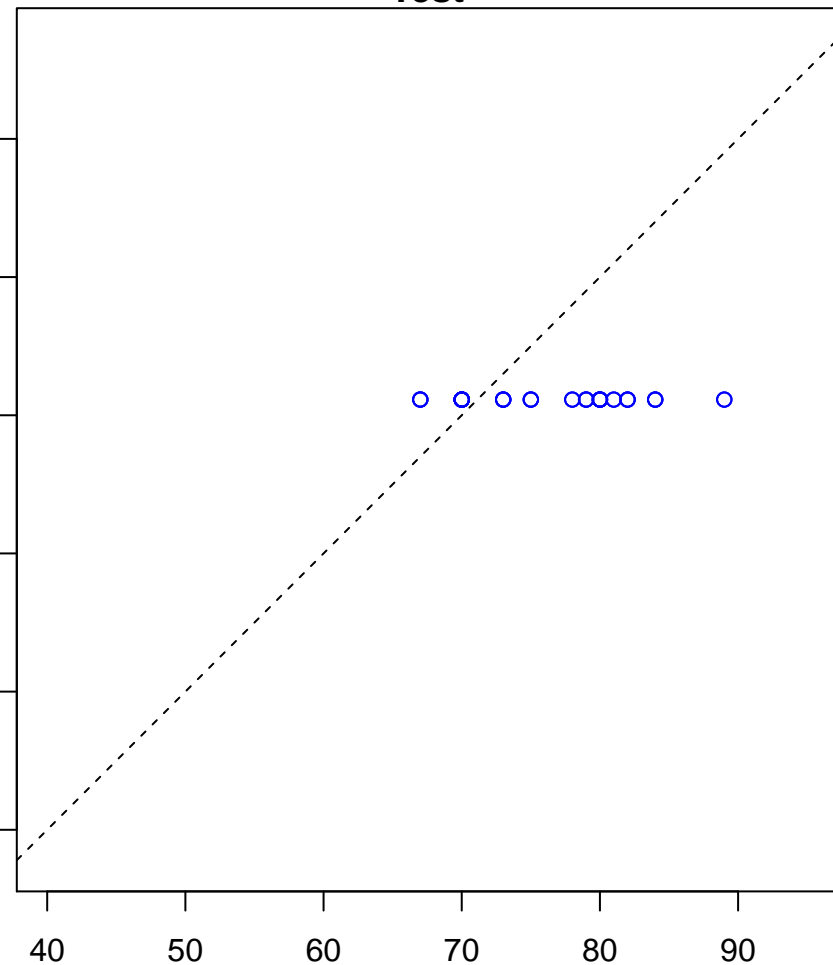


regulation of protein processing (Score: 0.802152)

Control



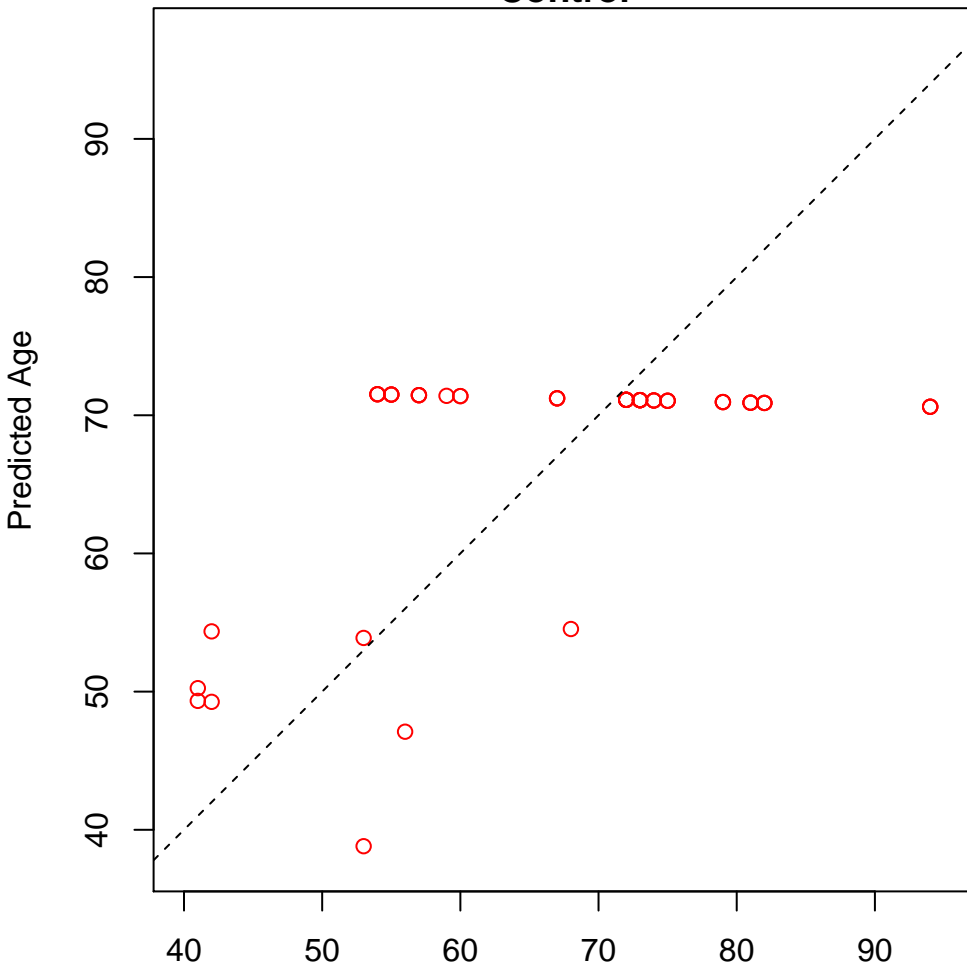
Test



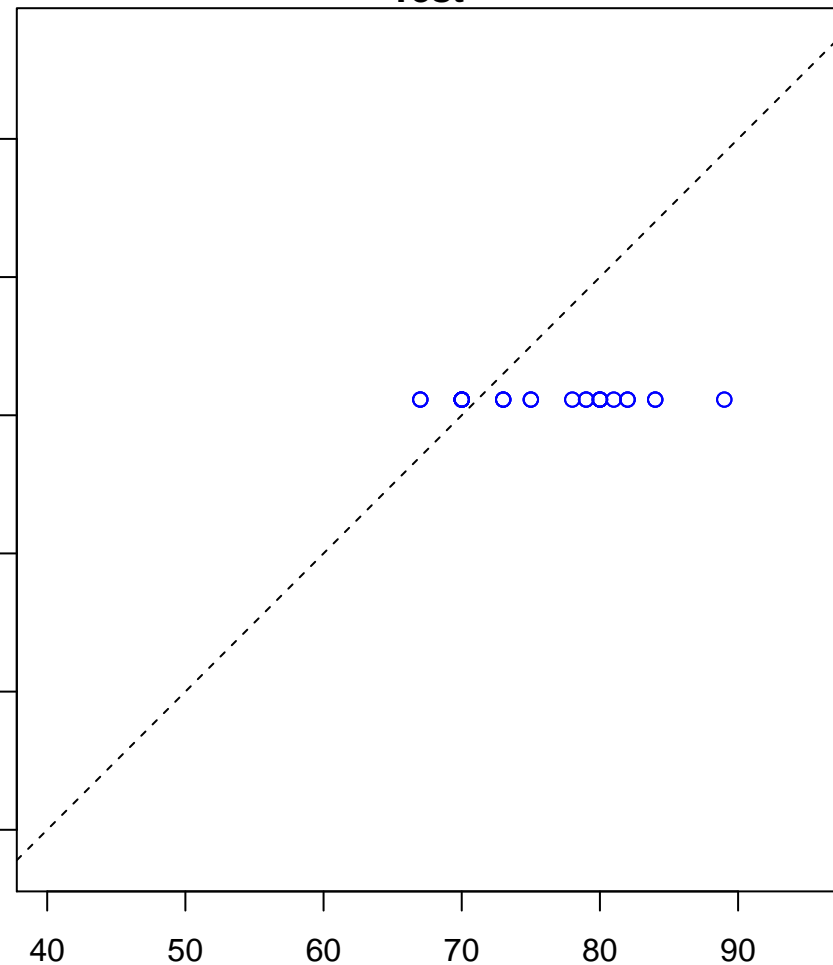
Actual Age

regulation of protein maturation (Score: 0.802152)

Control

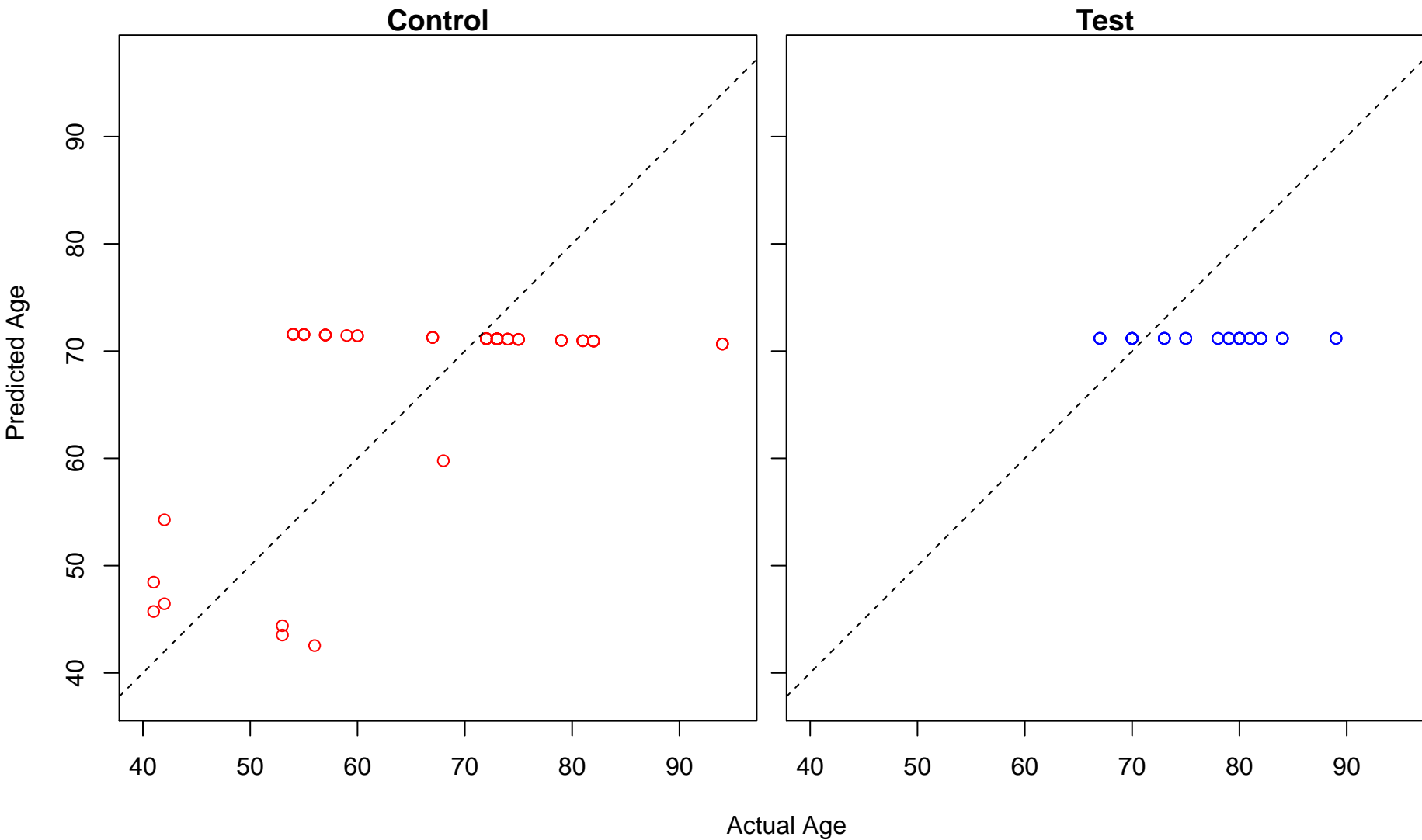


Test



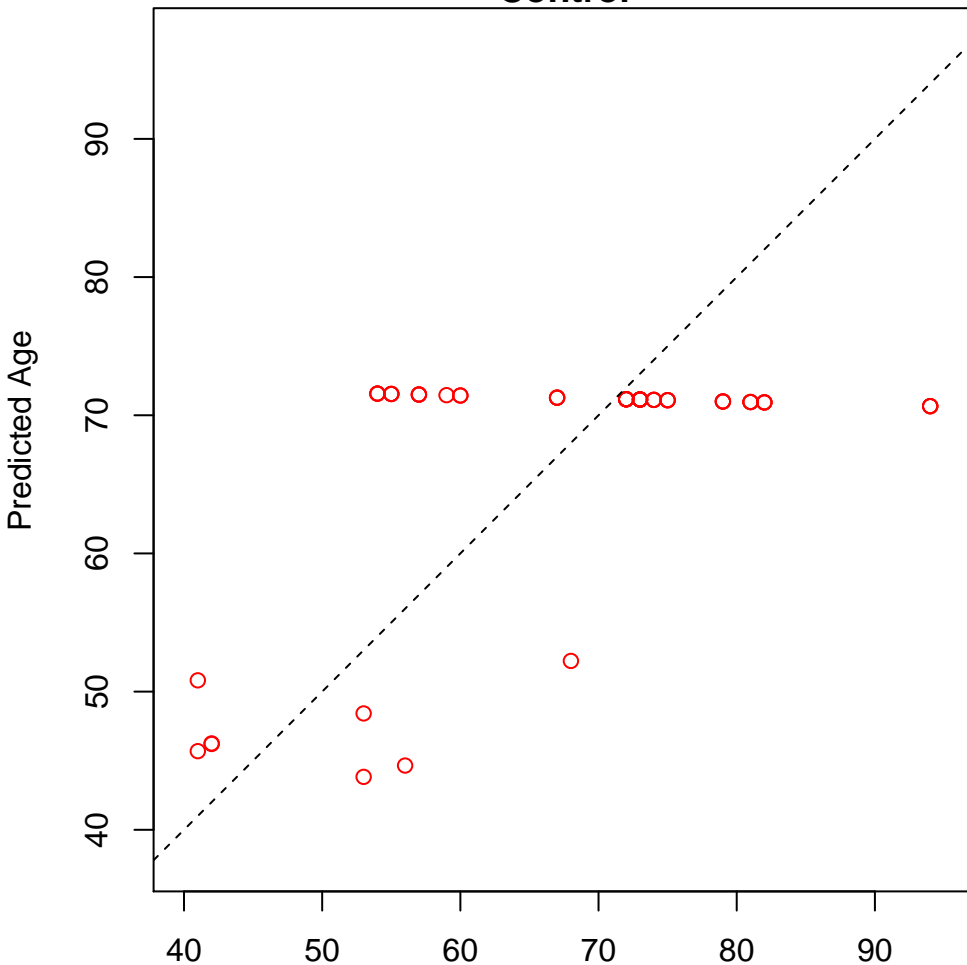
Actual Age

RNA splicing (Score: 0.802146)

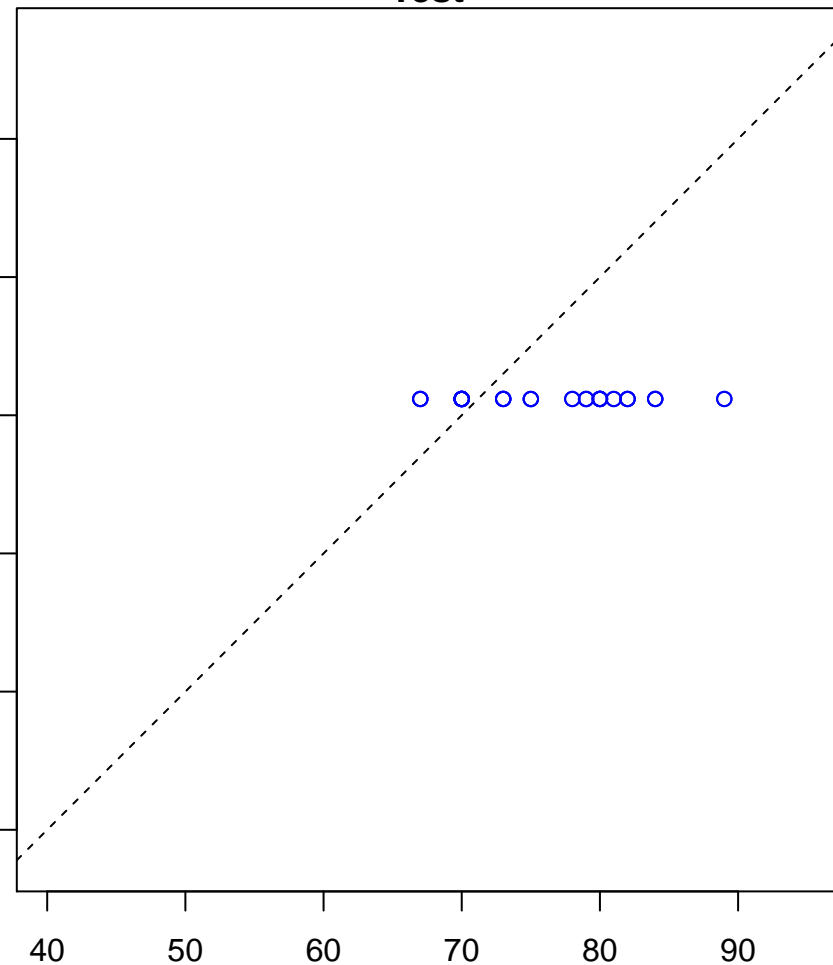


regulation of apoptotic process (Score: 0.802143)

Control

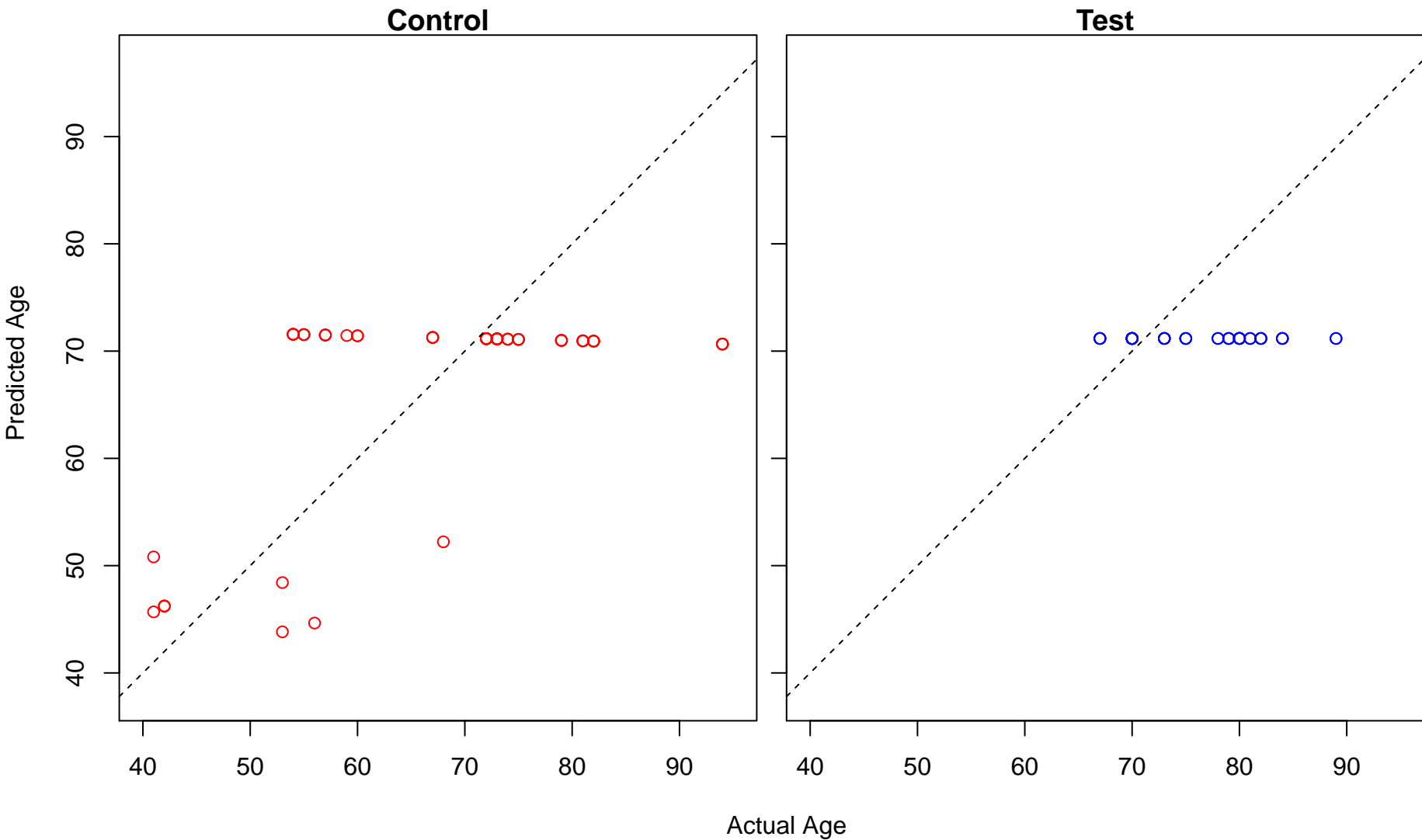


Test

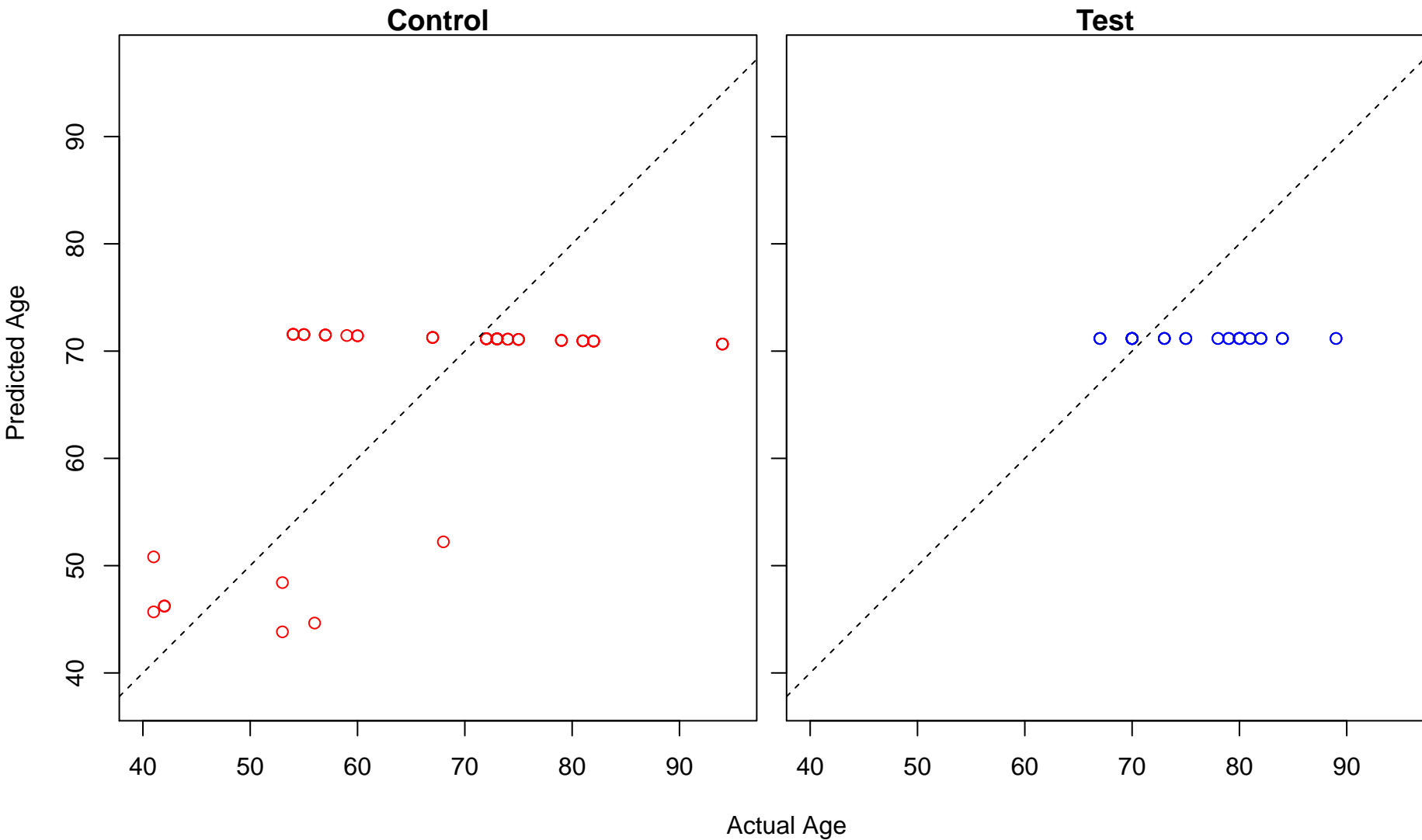


Actual Age

regulation of programmed cell death (Score: 0.802143)

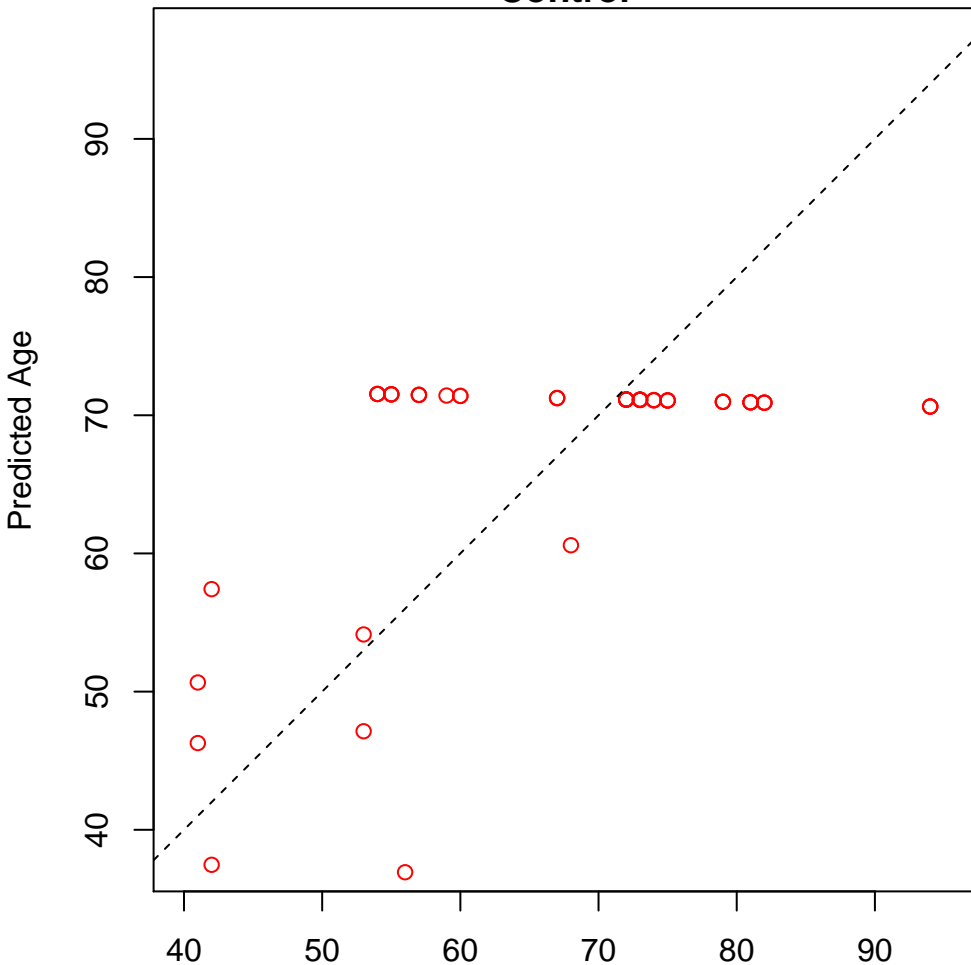


regulation of cell death (Score: 0.802139)

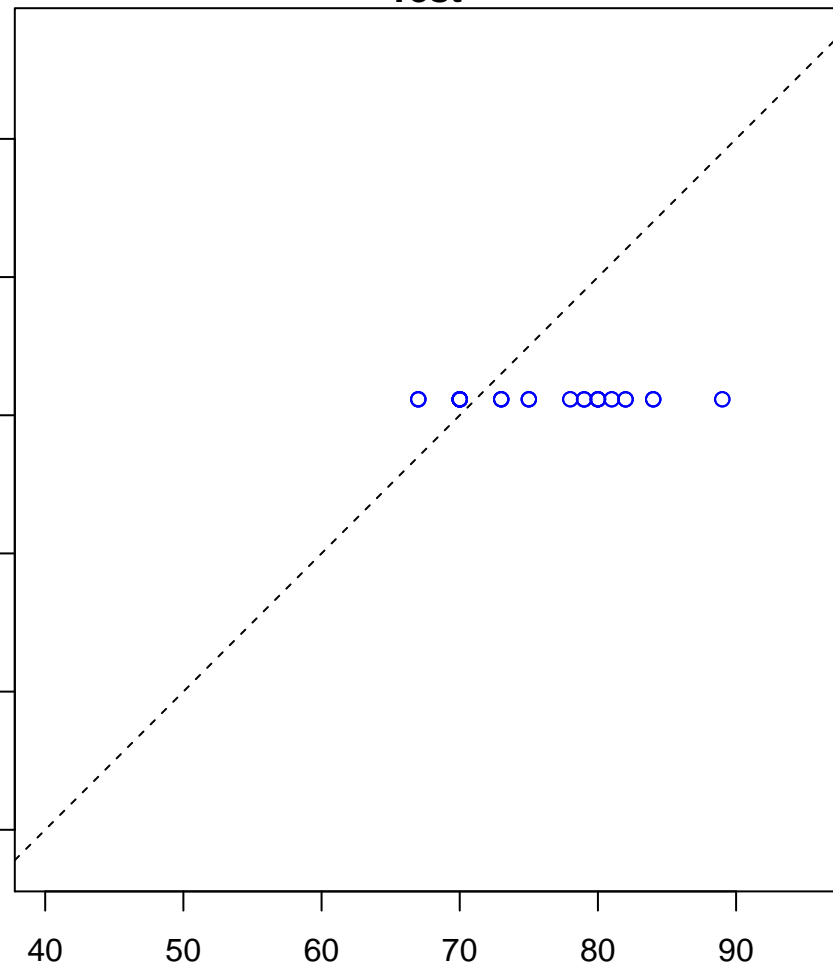


regulation of gene expression, epigenetic (Score: 0.802124)

Control

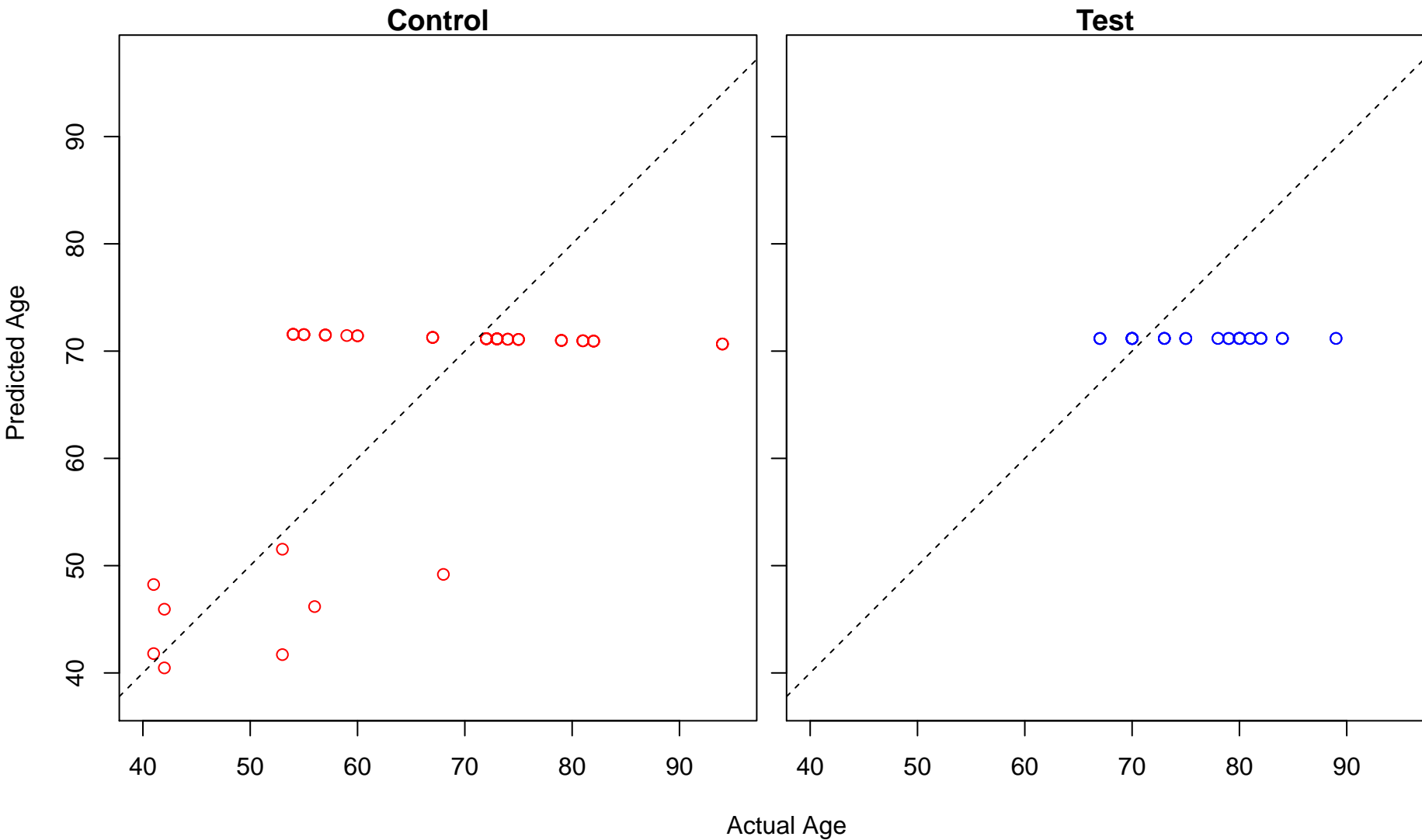


Test



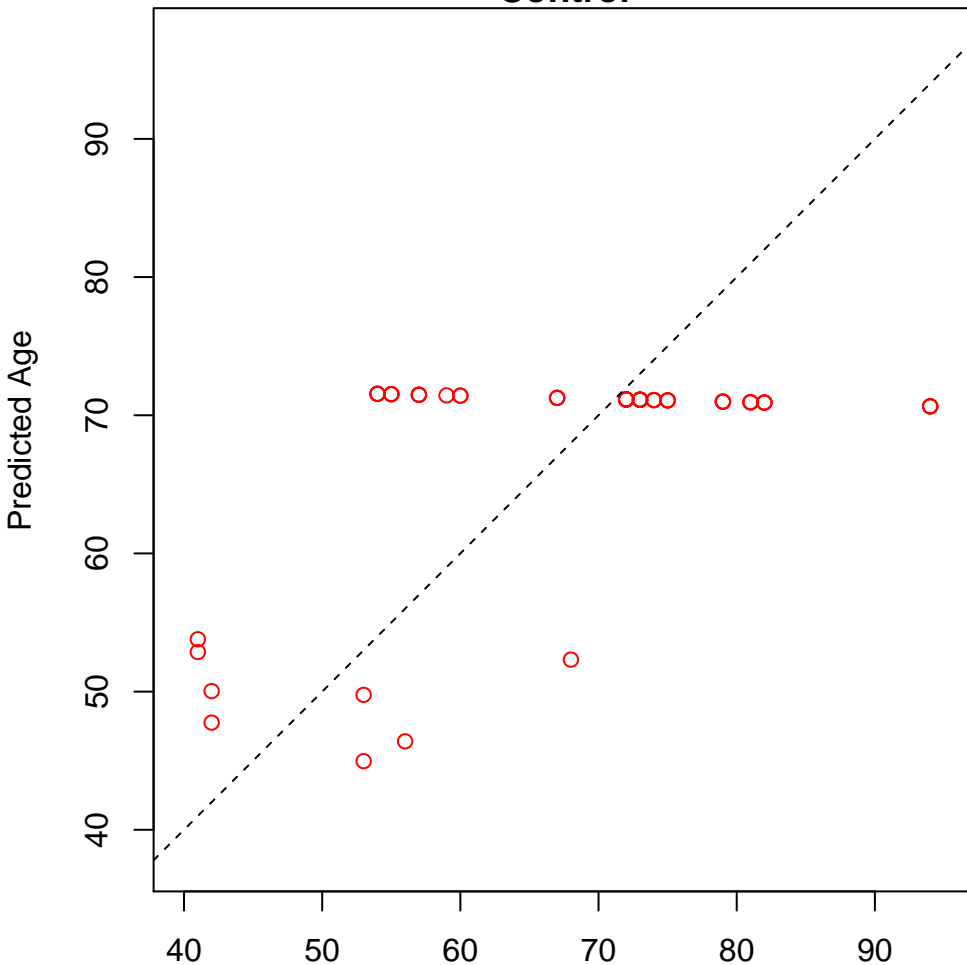
Actual Age

negative regulation of protein modification process (Score: 0.802120)

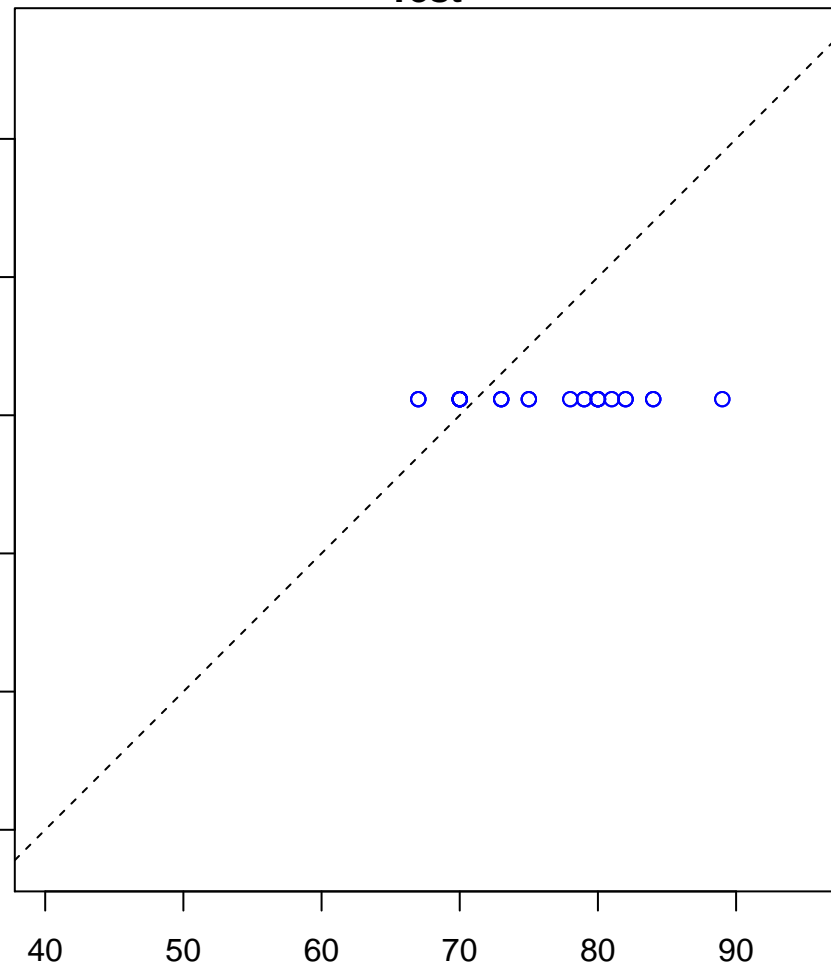


cellular response to chemical stimulus (Score: 0.802034)

Control

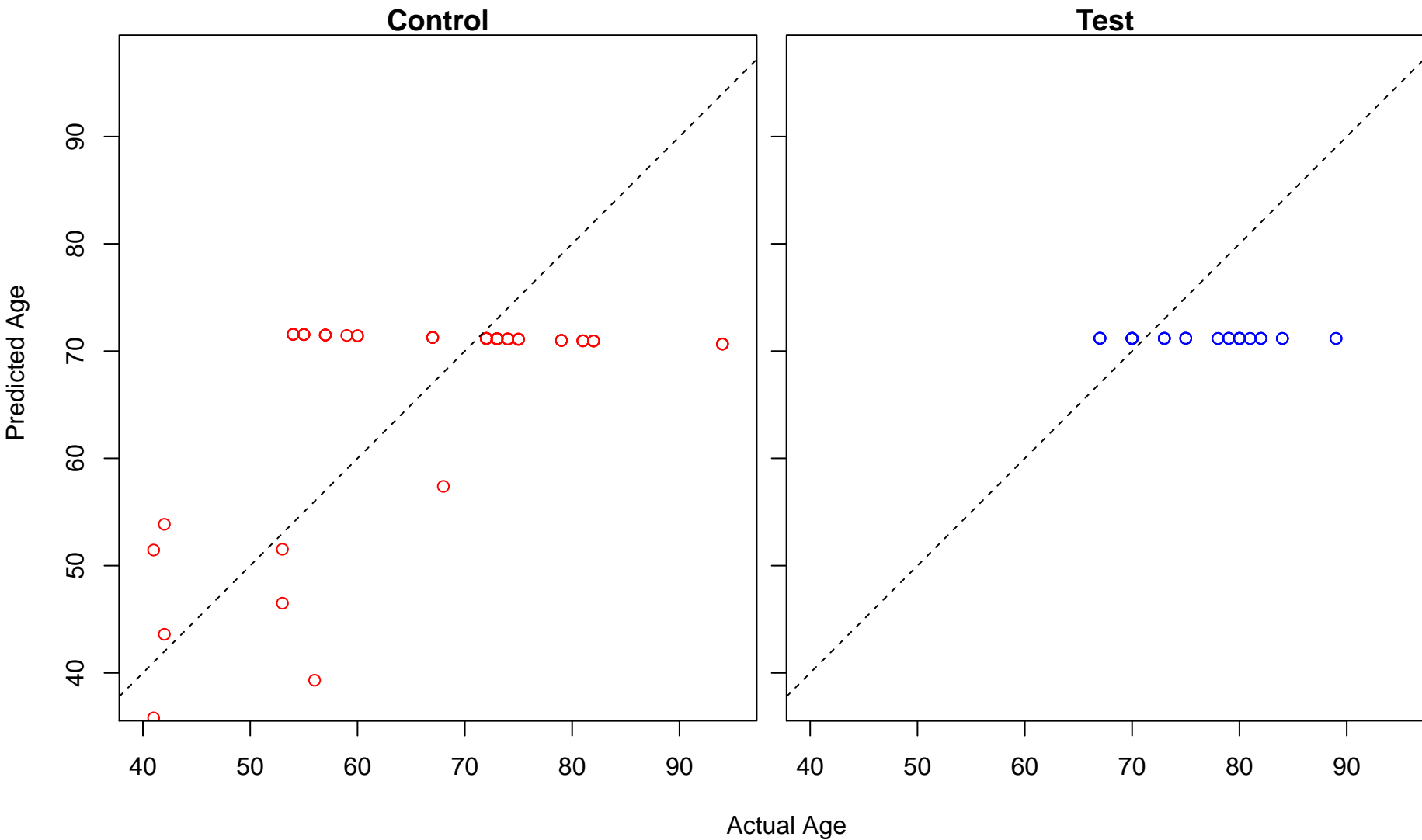


Test

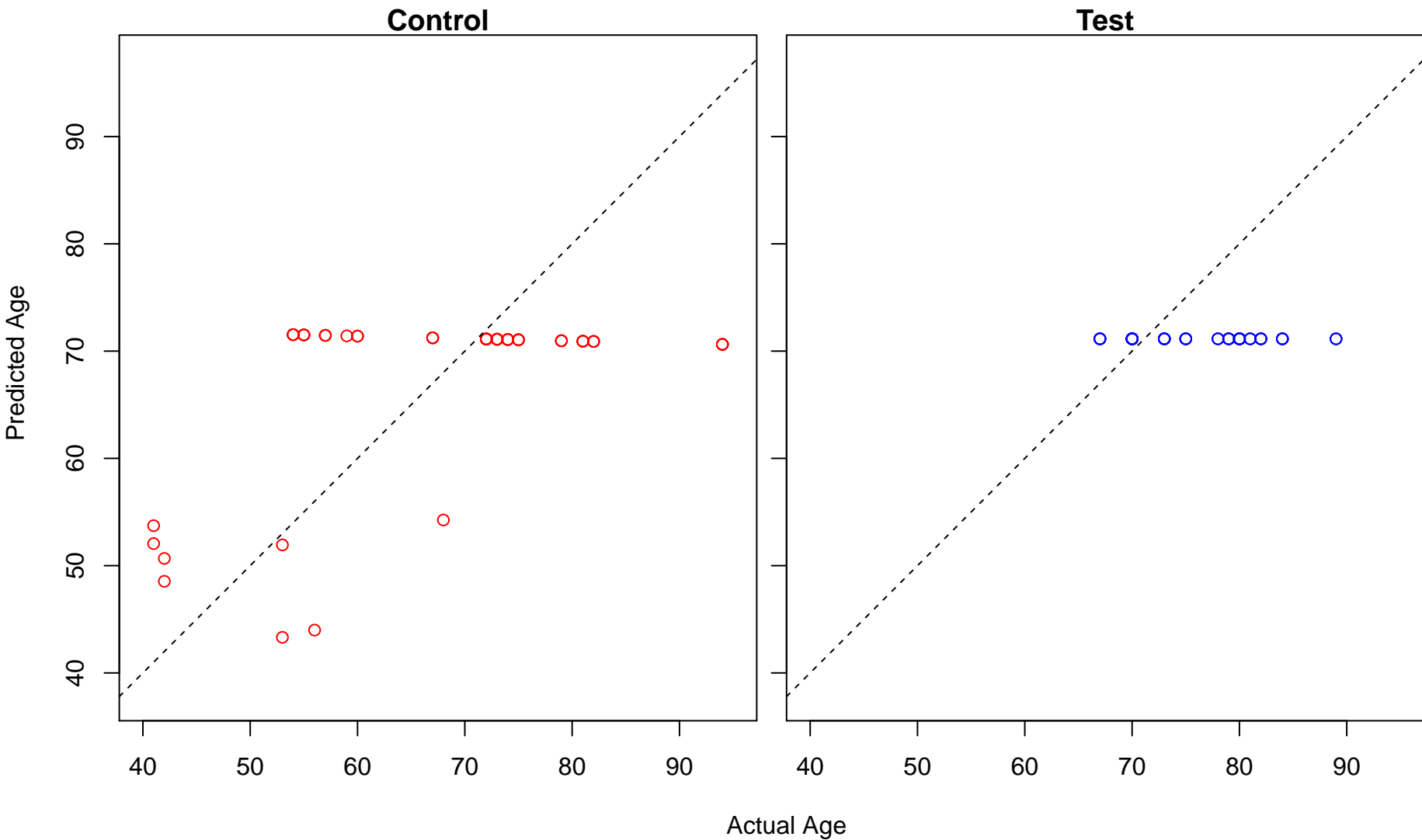


Actual Age

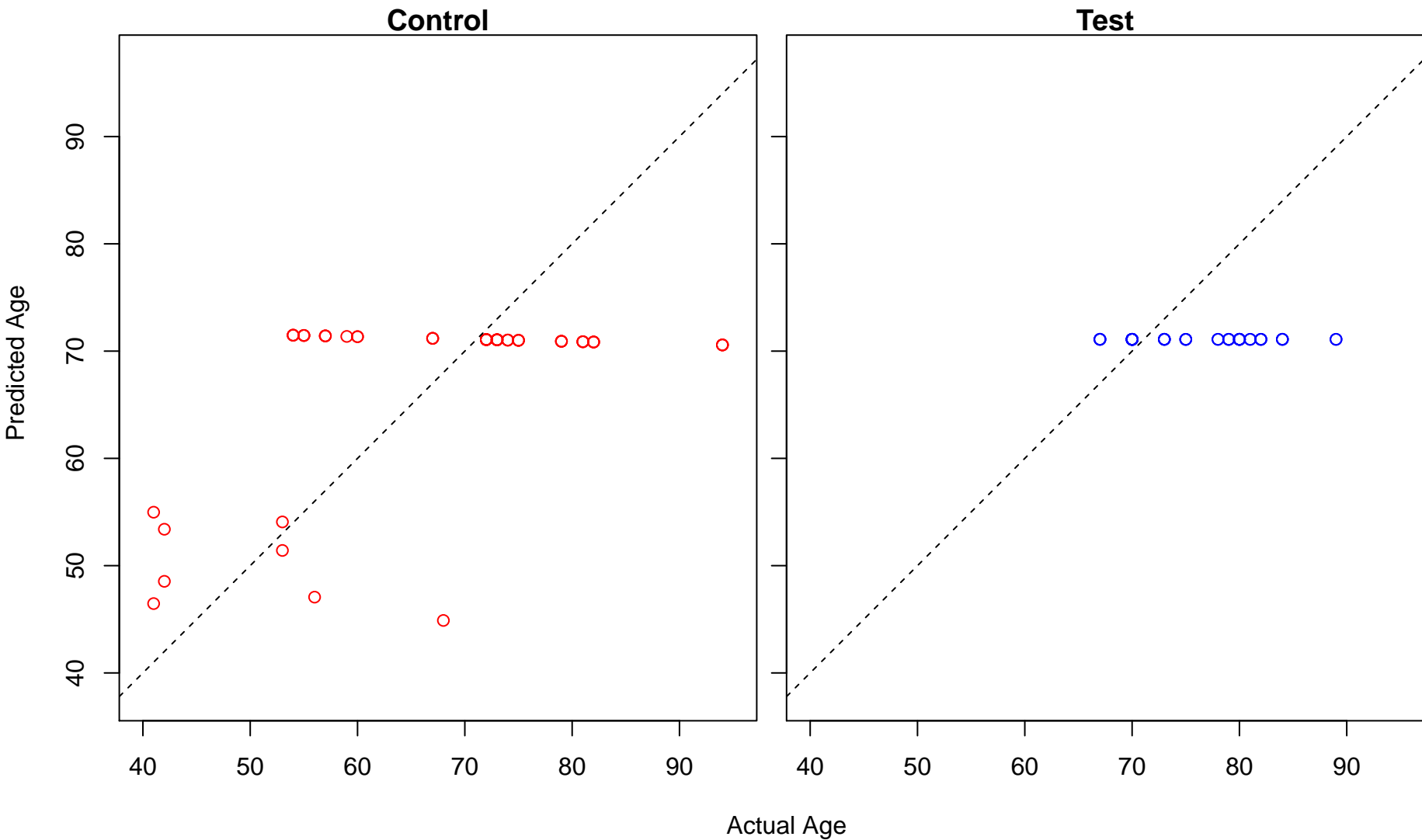
negative regulation of cellular catabolic process (Score: 0.801980)



macromolecular complex subunit organization (Score: 0.801937)

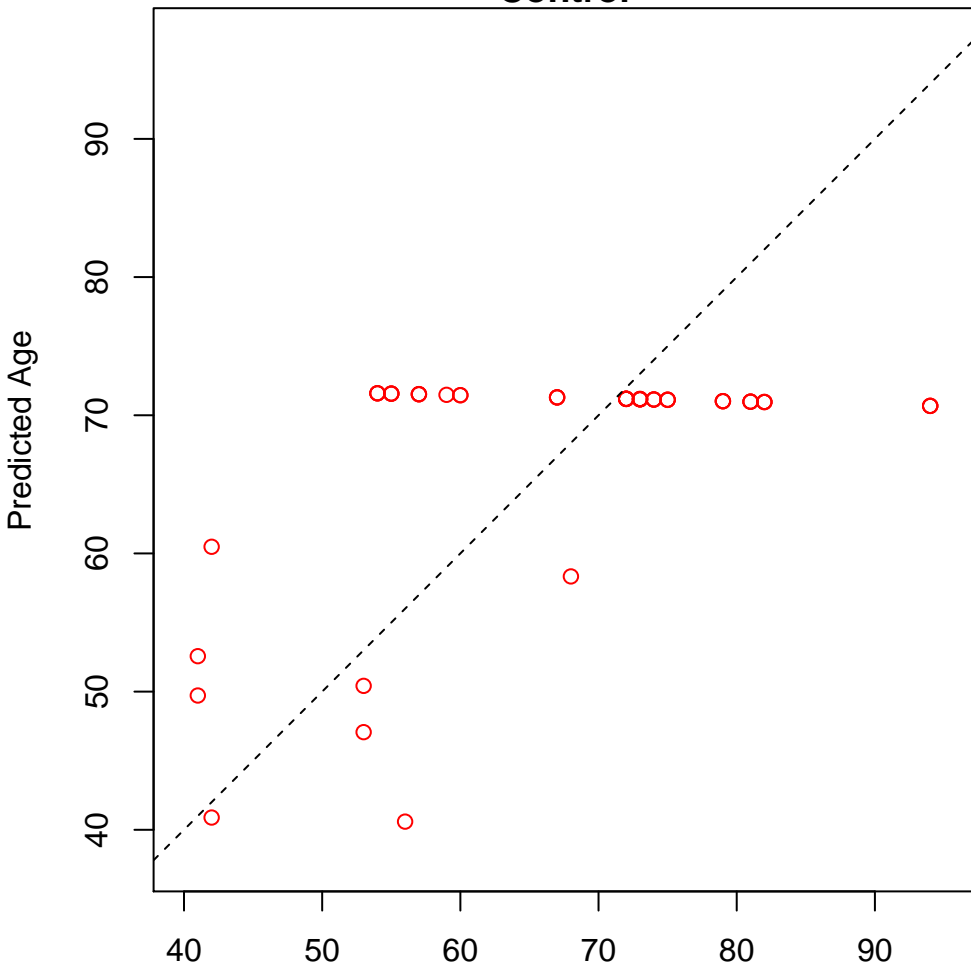


negative regulation of organelle organization (Score: 0.801927)

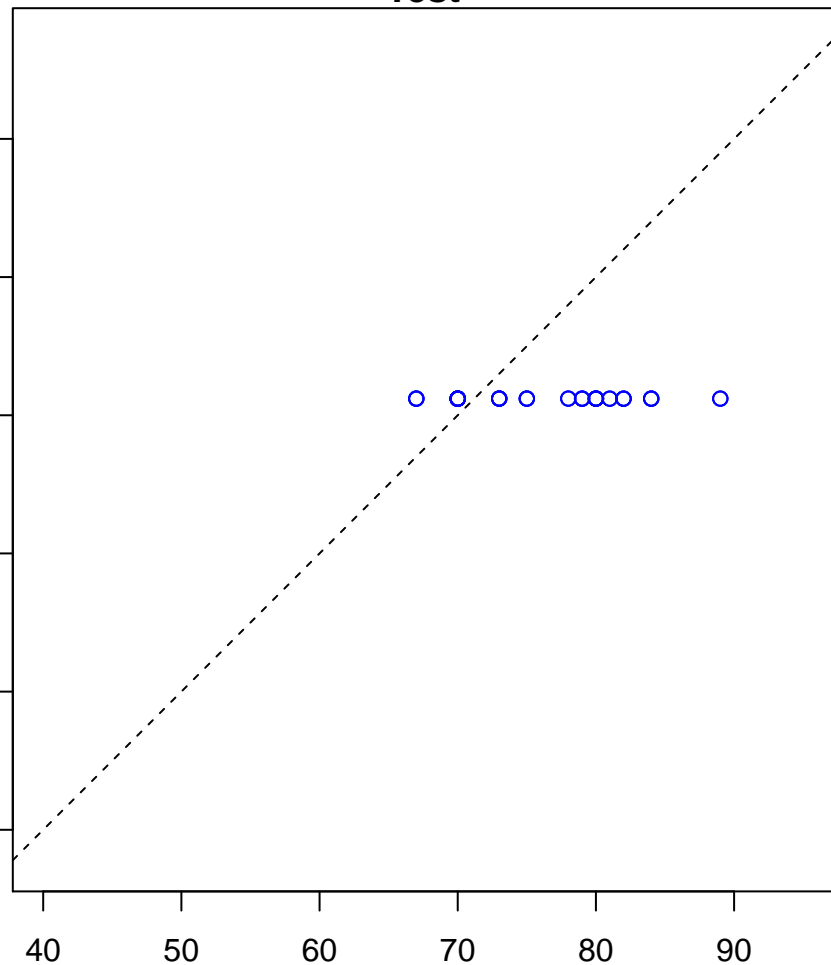


negative regulation of peptidase activity (Score: 0.801910)

Control

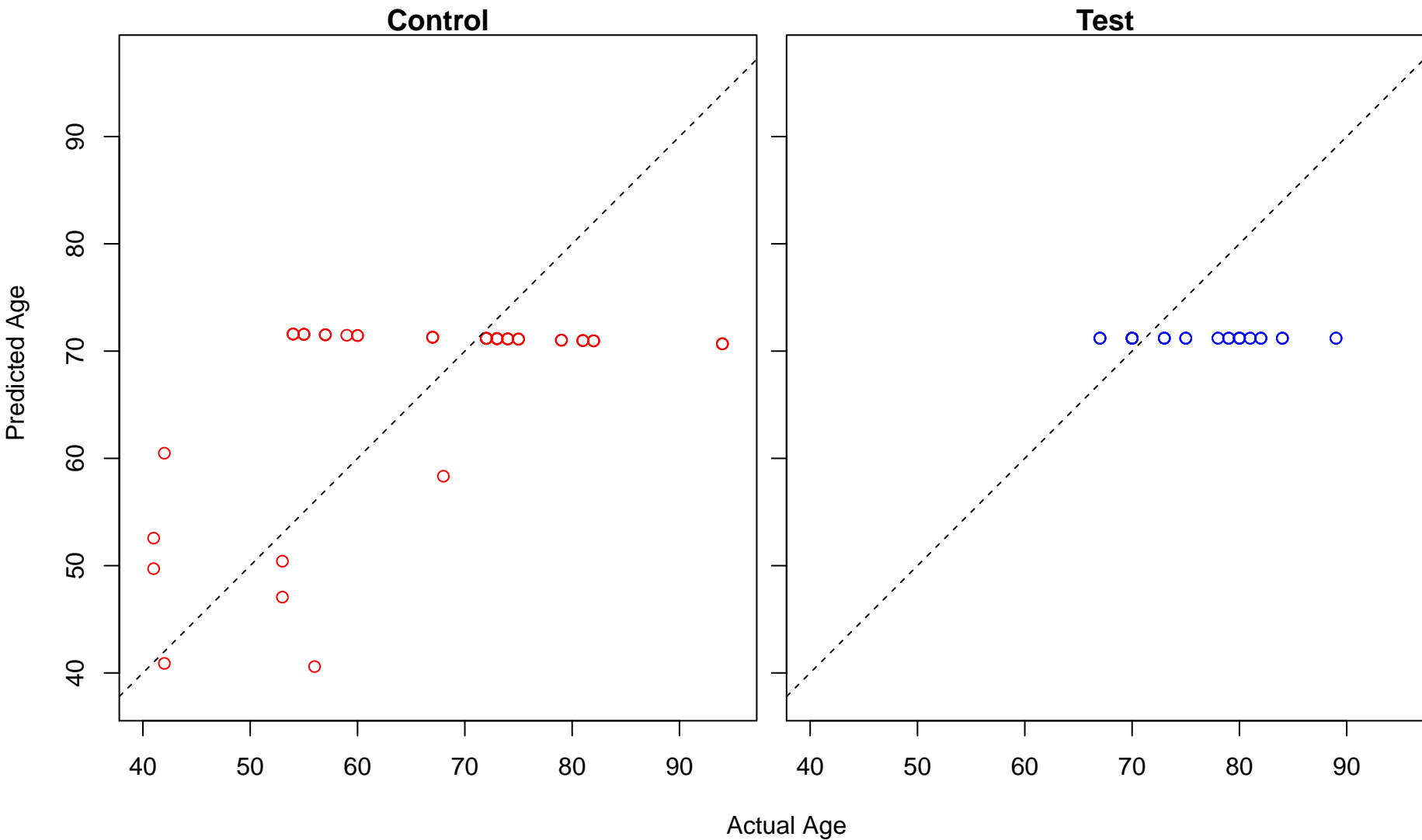


Test



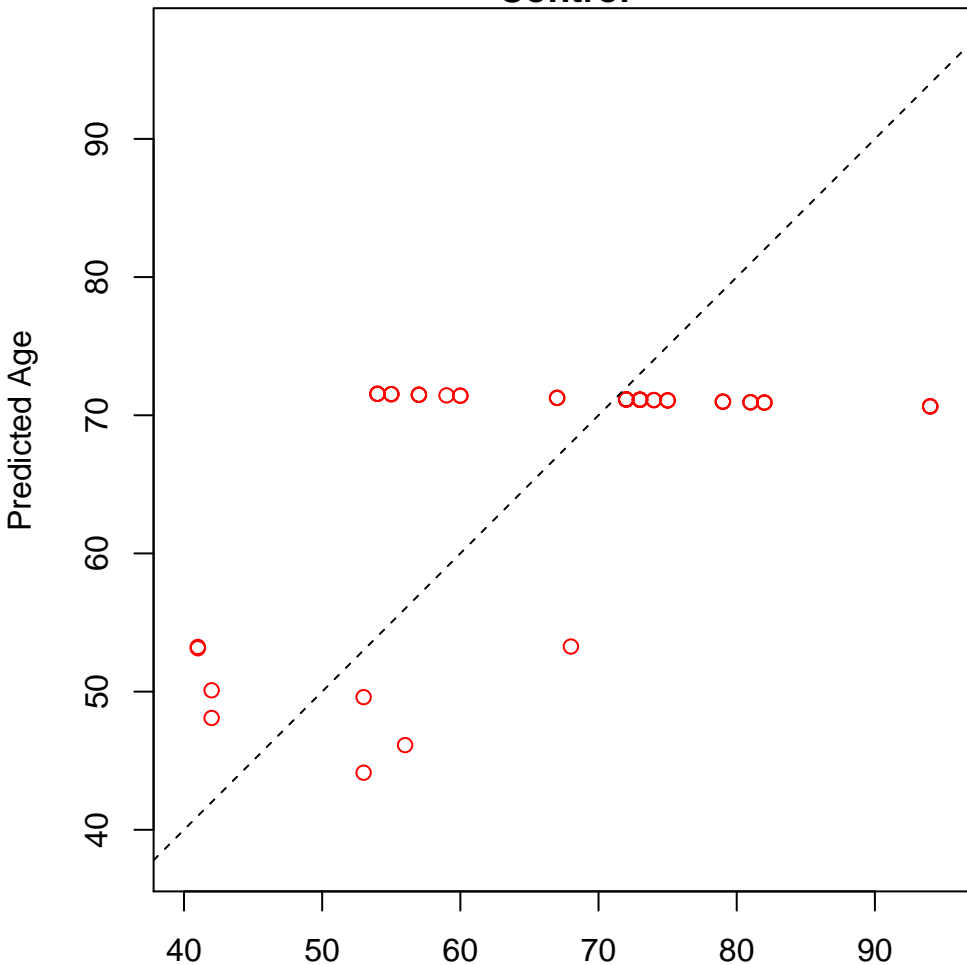
Actual Age

negative regulation of endopeptidase activity (Score: 0.801910)

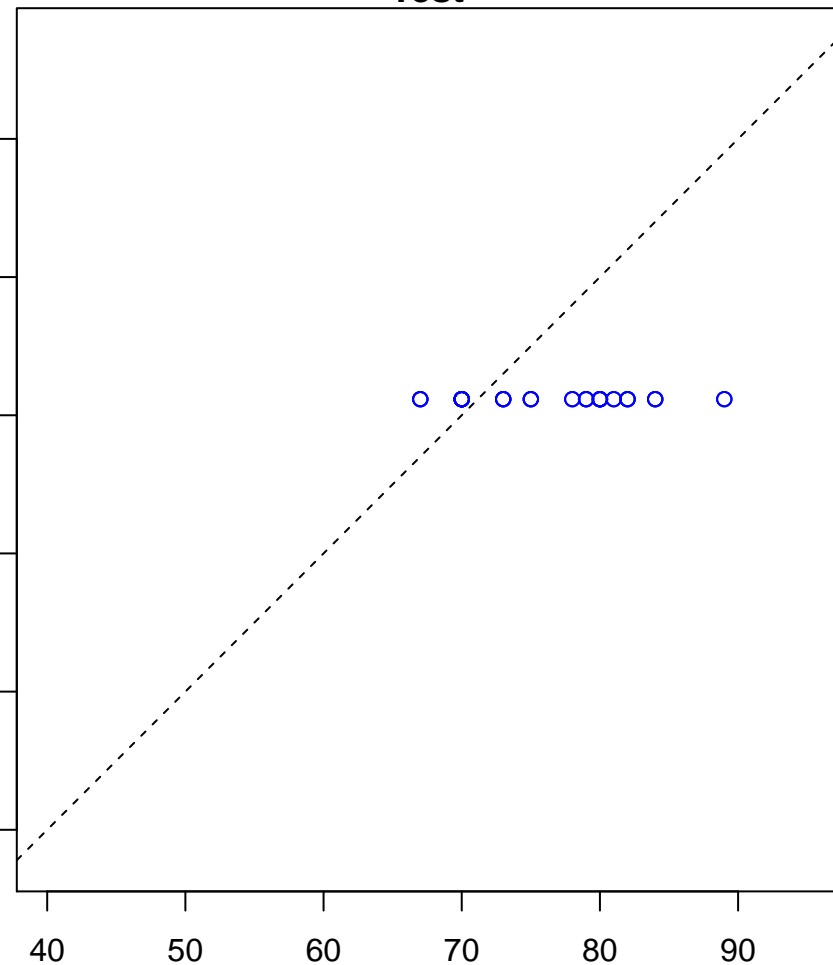


response to organic substance (Score: 0.801865)

Control



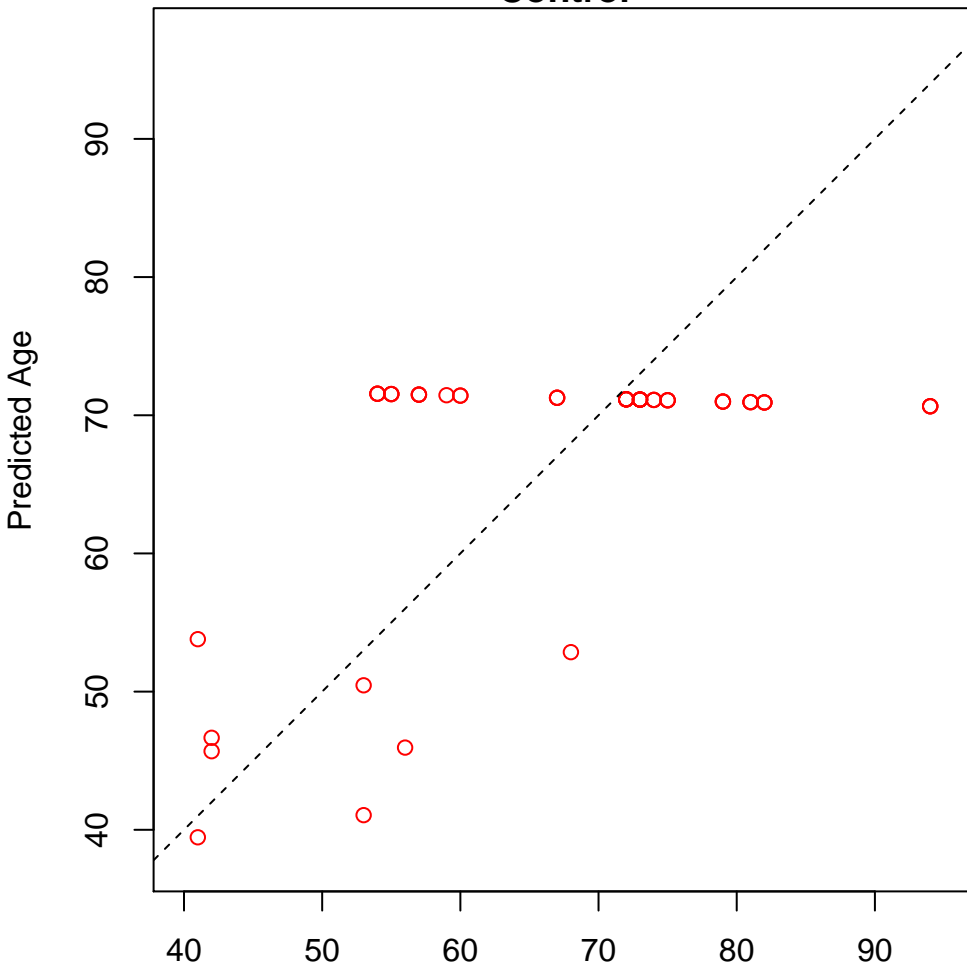
Test



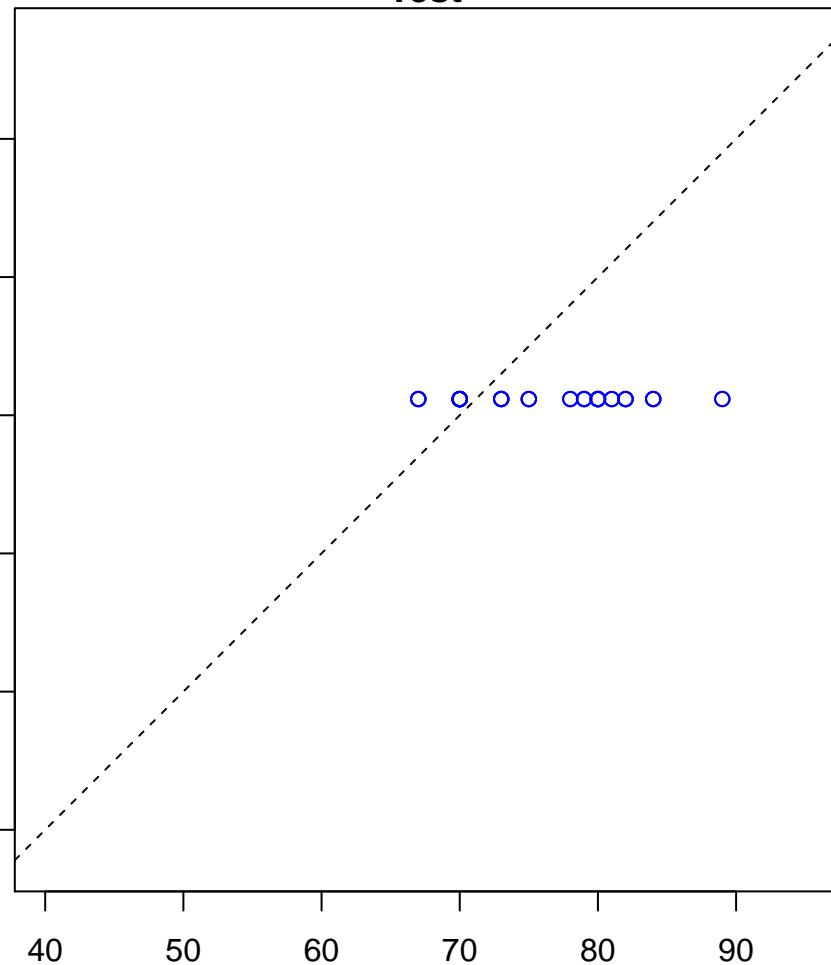
Actual Age

regulation of developmental process (Score: 0.801863)

Control



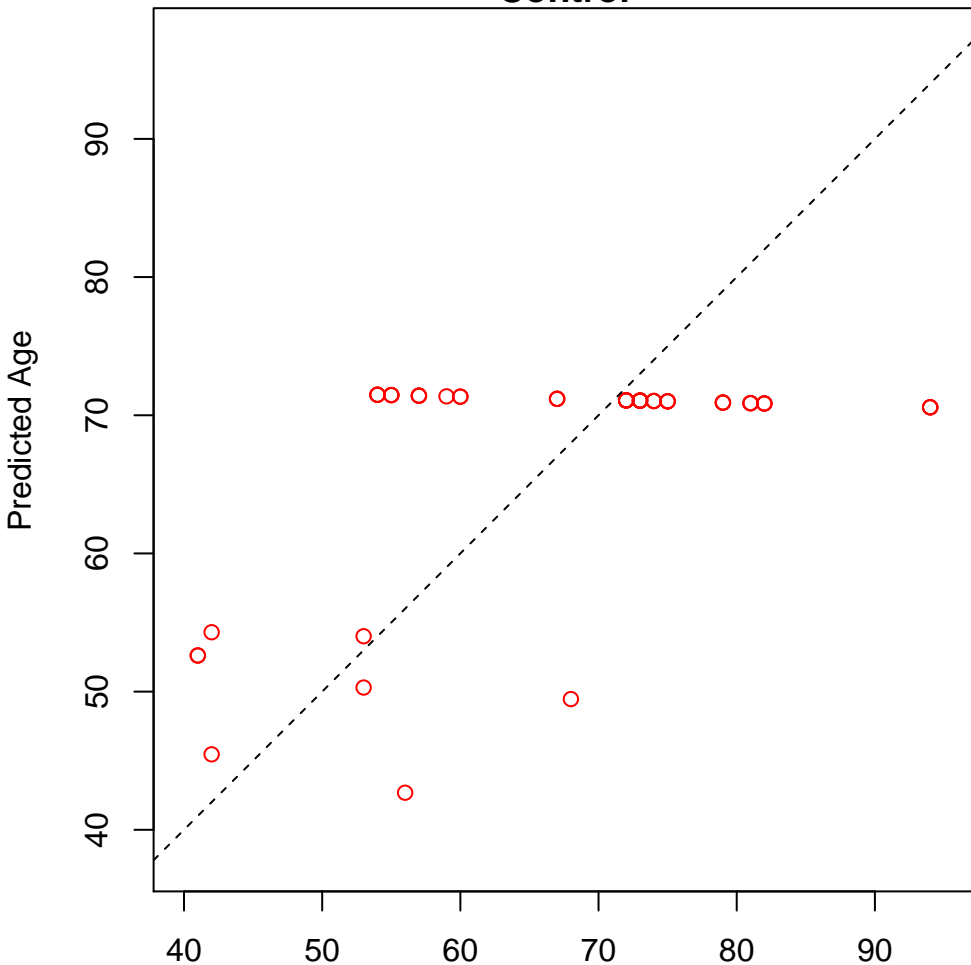
Test



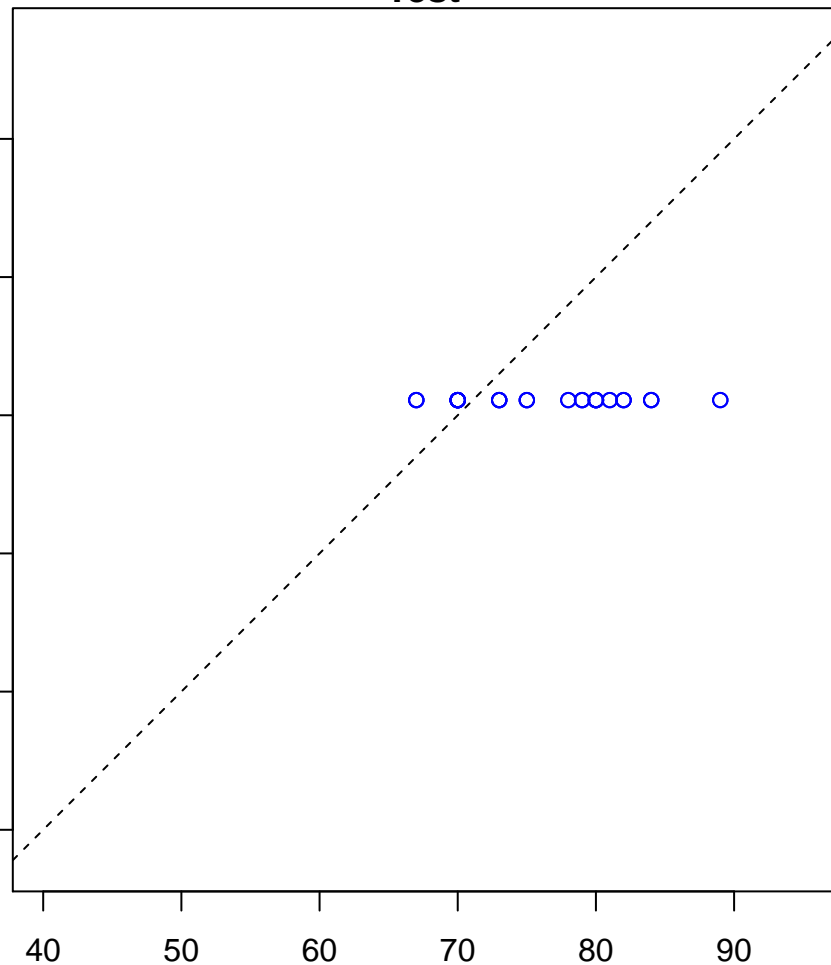
Actual Age

negative regulation of cell proliferation (Score: 0.801860)

Control

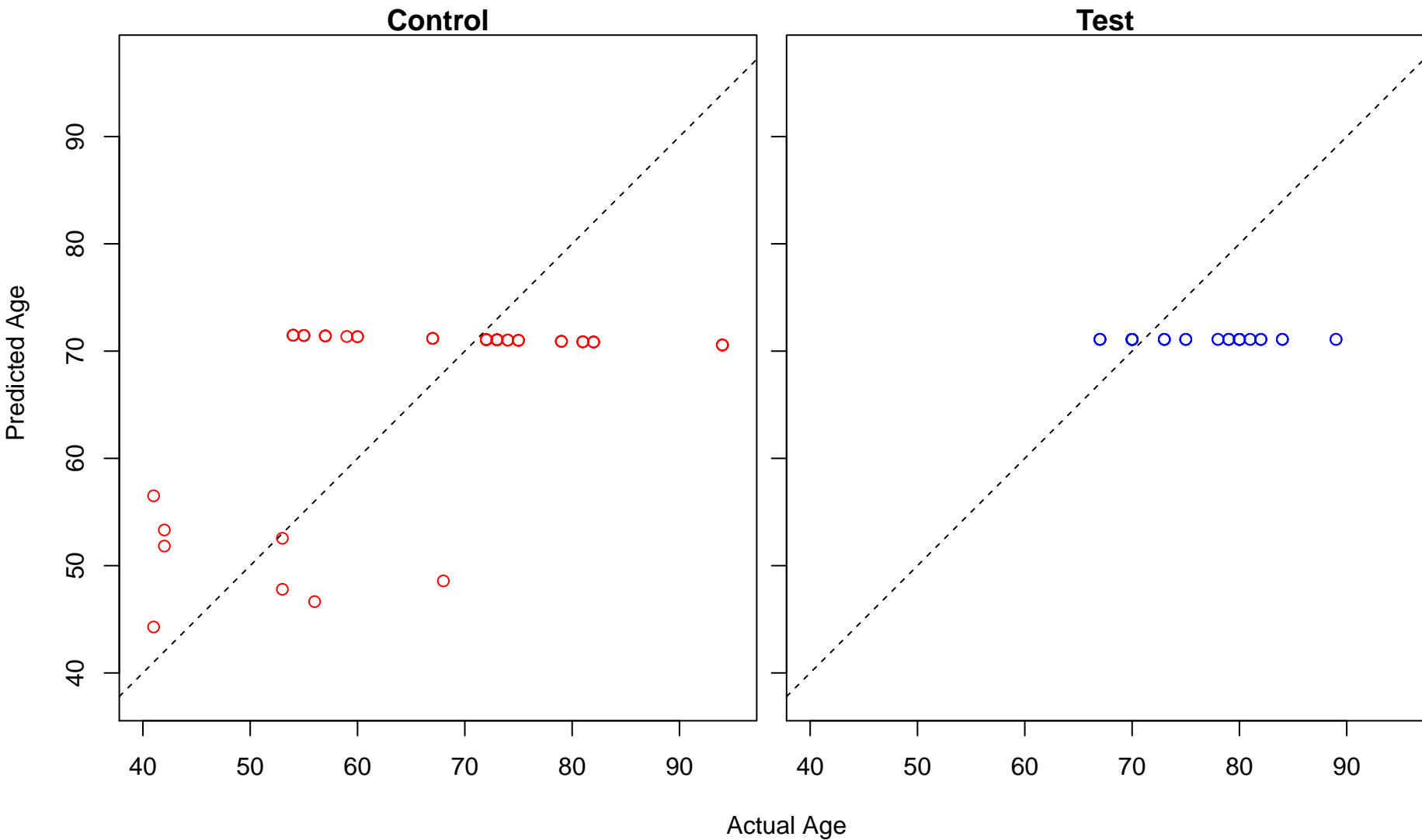


Test

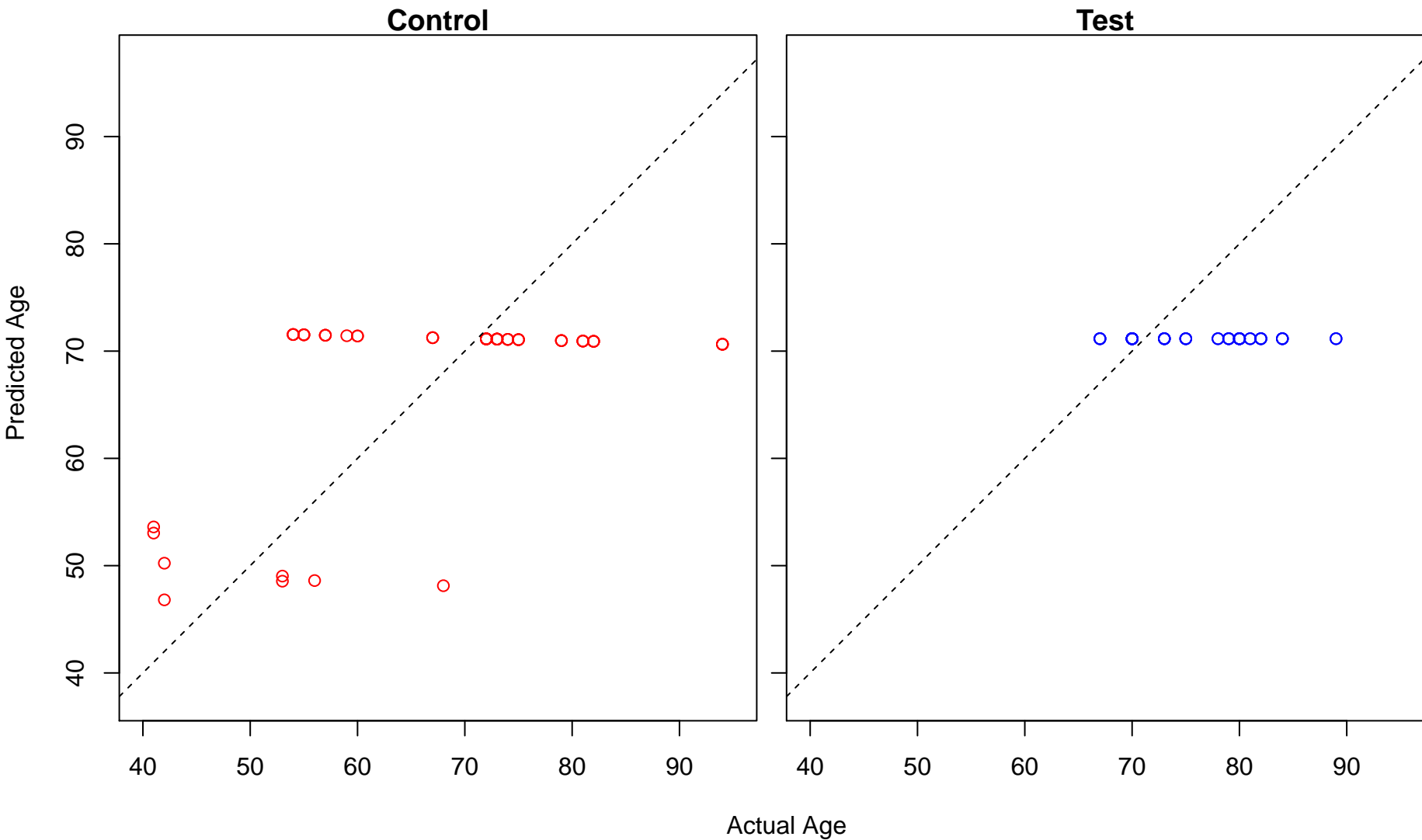


Actual Age

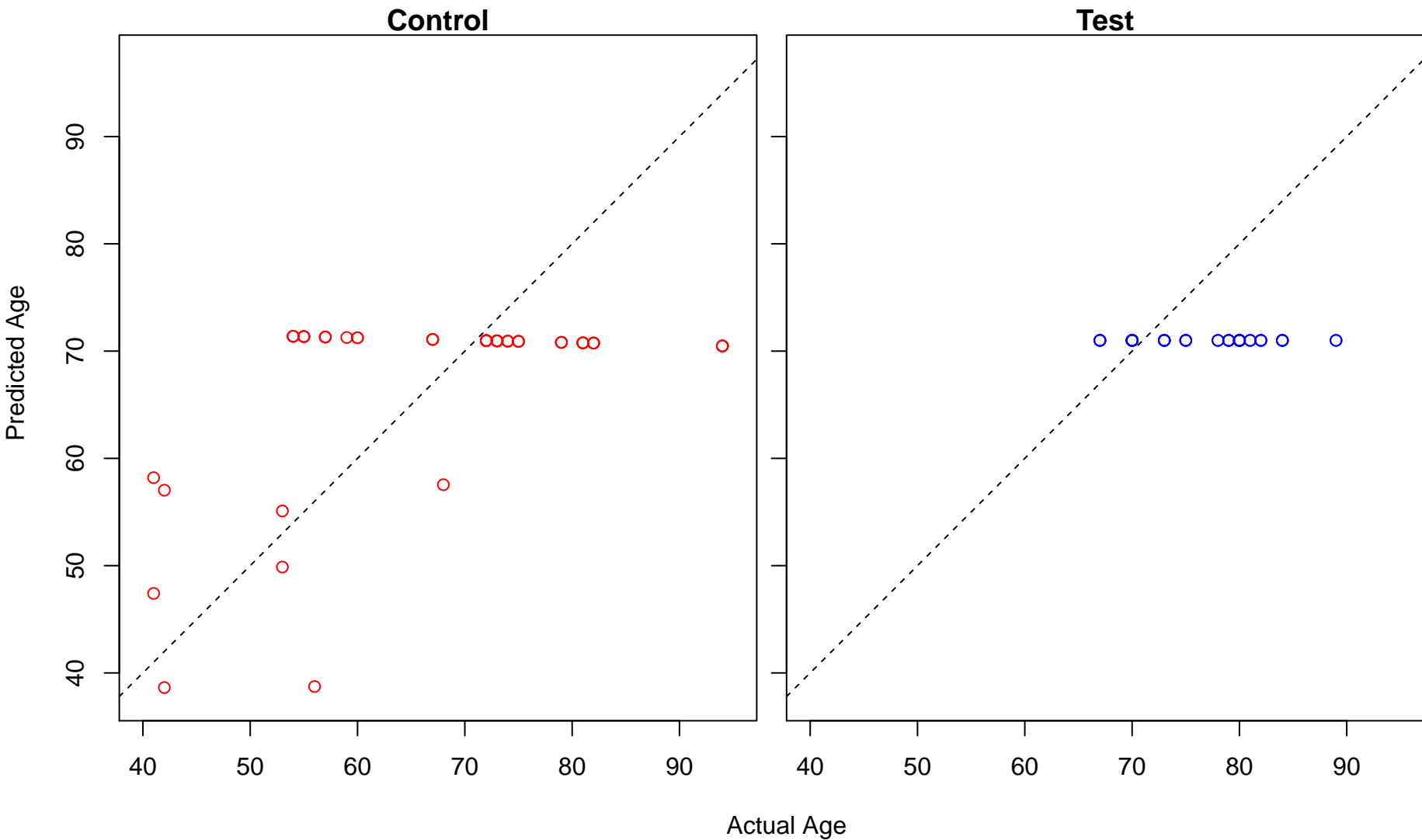
negative regulation of cytoskeleton organization (Score: 0.801858)



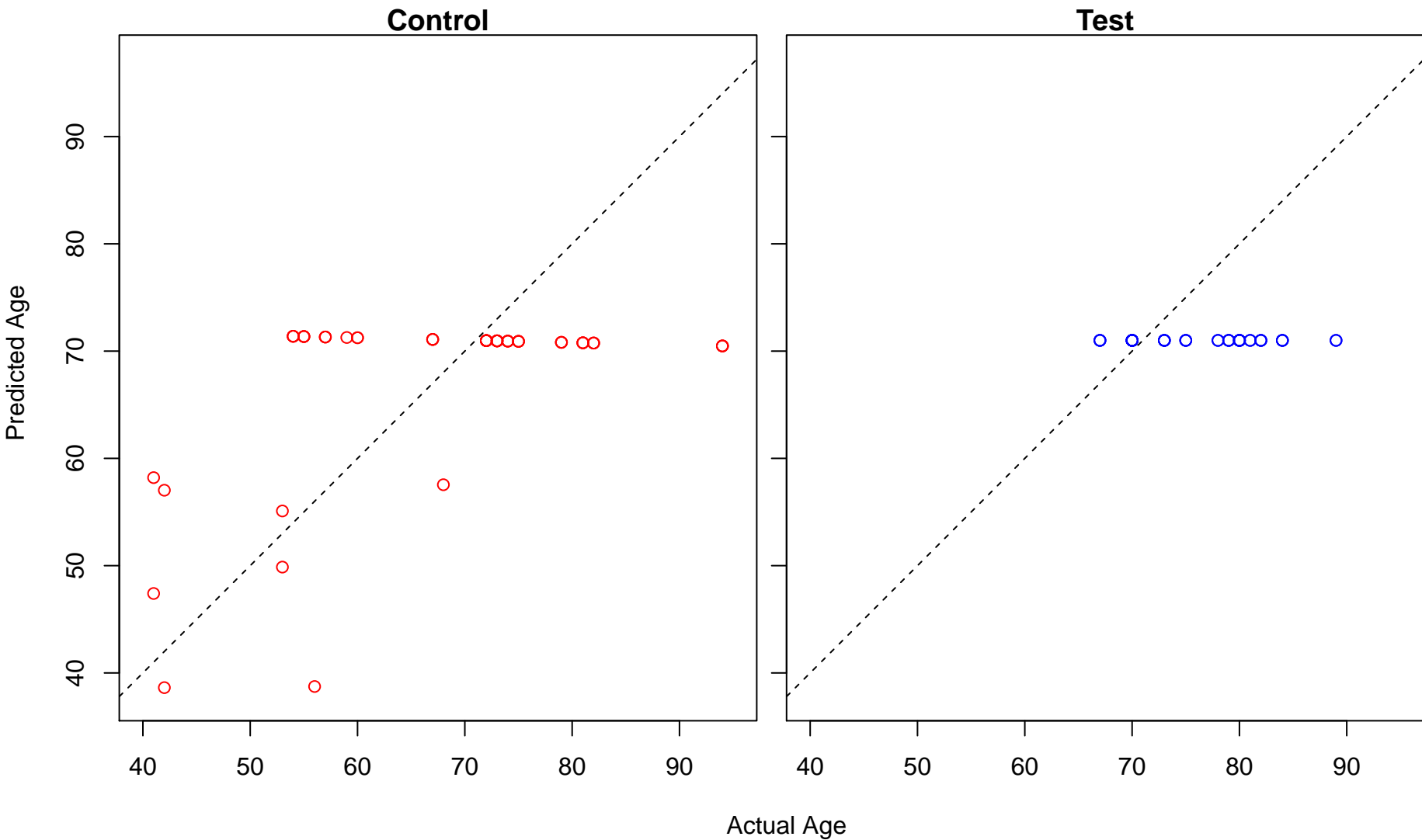
regulation of cellular localization (Score: 0.801851)



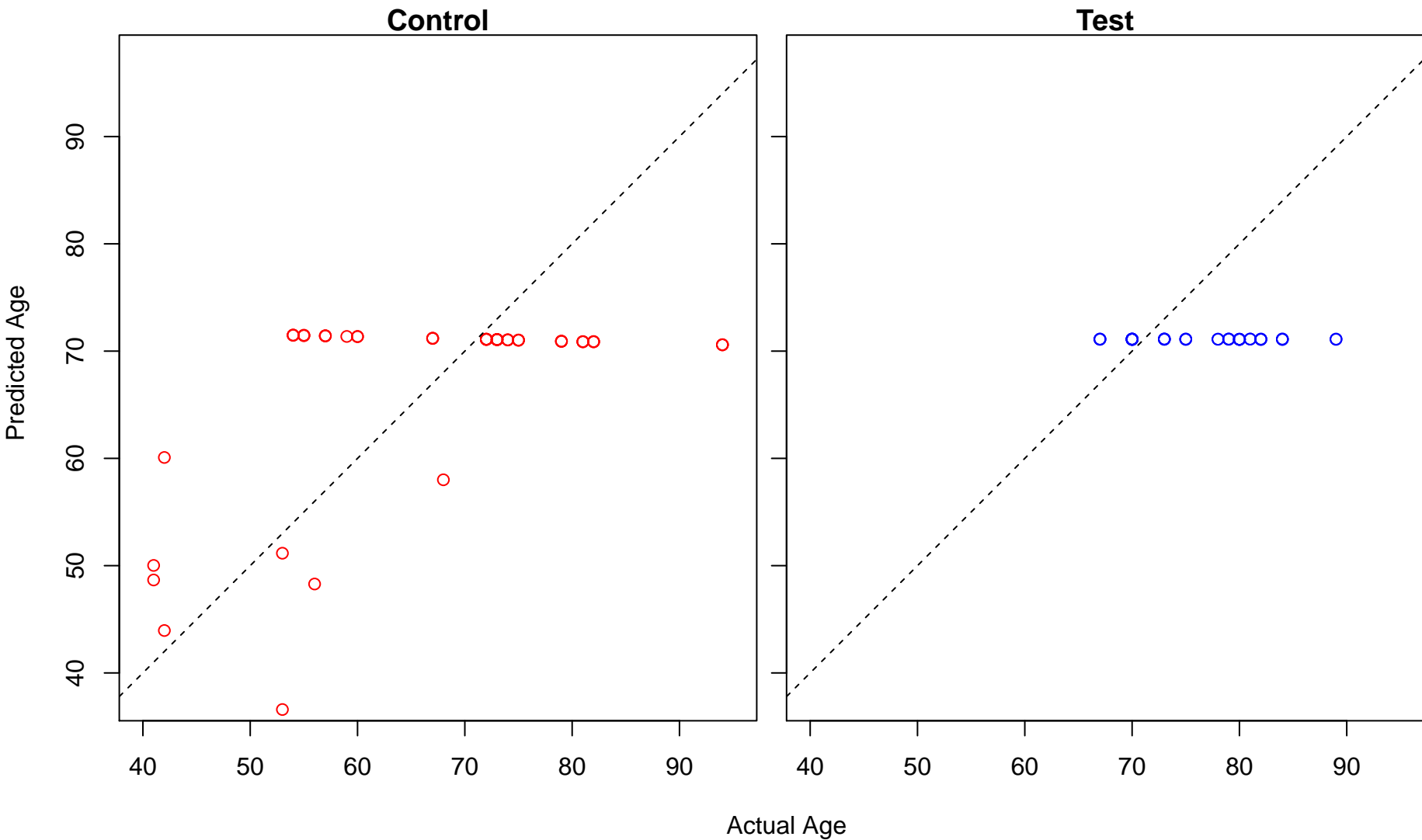
nucleic acid phosphodiester bond hydrolysis (Score: 0.801840)



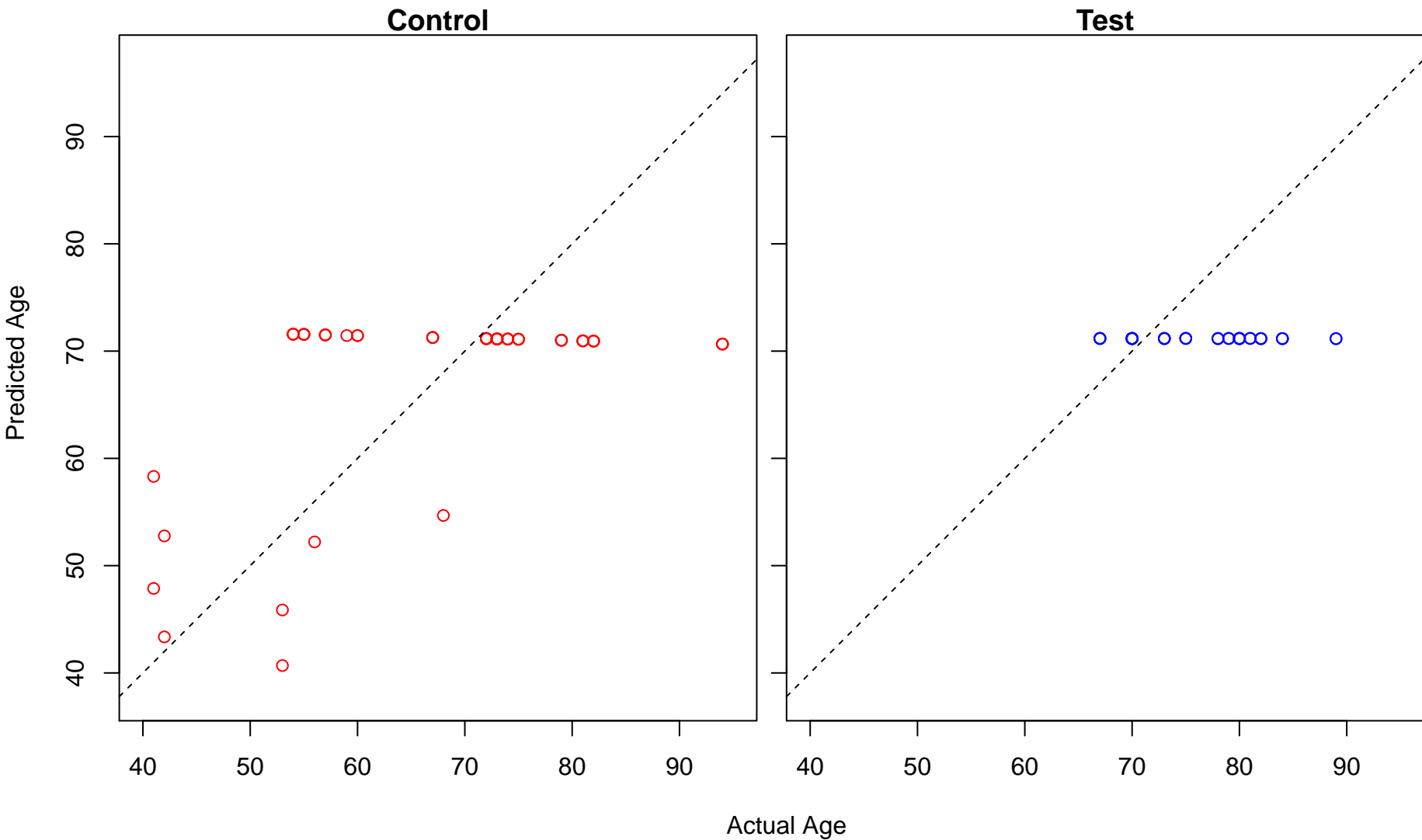
DNA geometric change (Score: 0.801837)



DNA replication (Score: 0.801808)

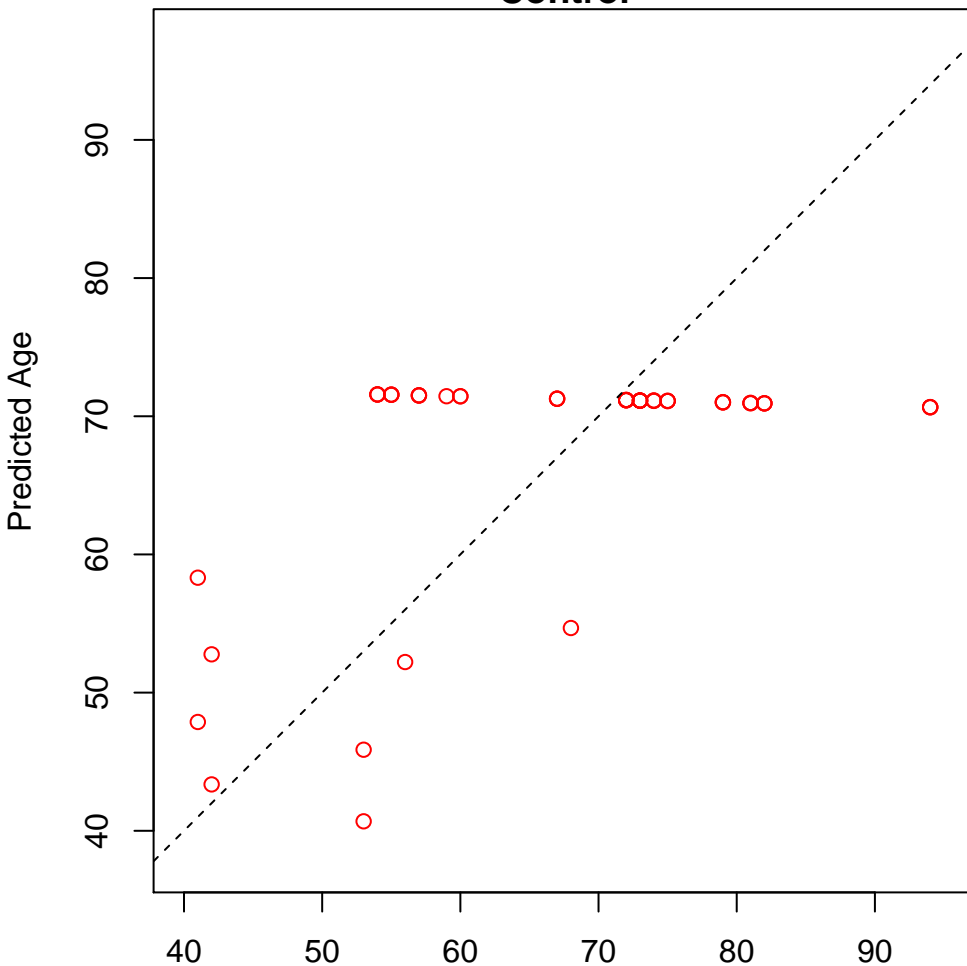


regulation of T cell activation (Score: 0.801795)

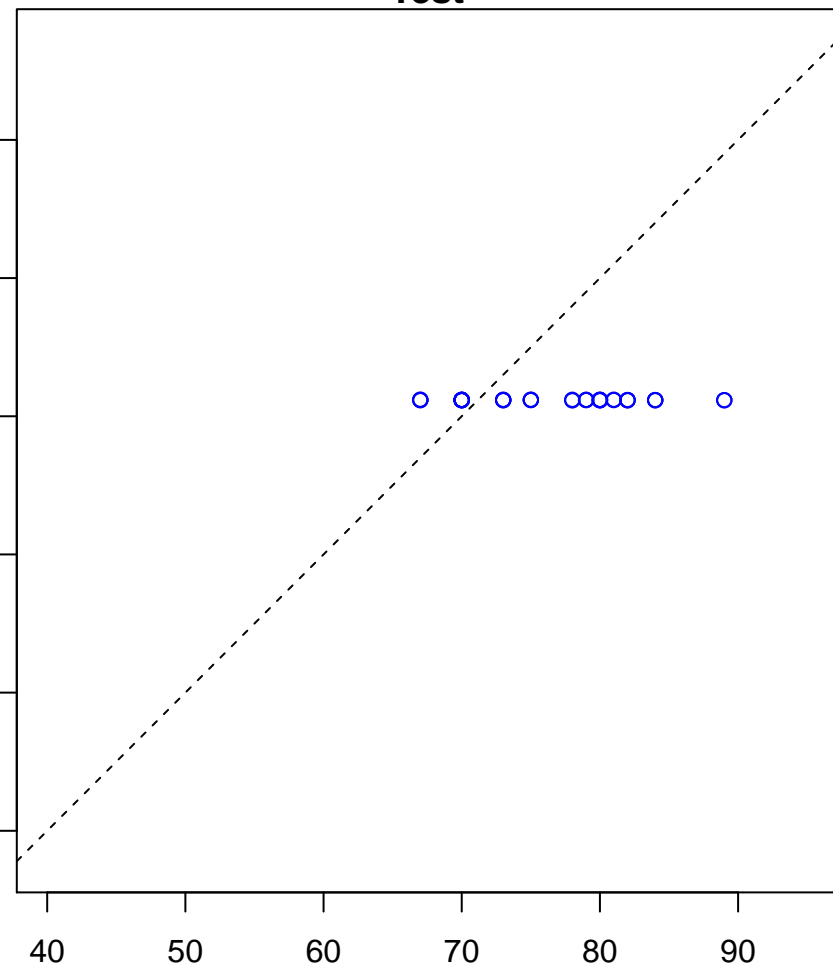


regulation of leukocyte cell-cell adhesion (Score: 0.801795)

Control



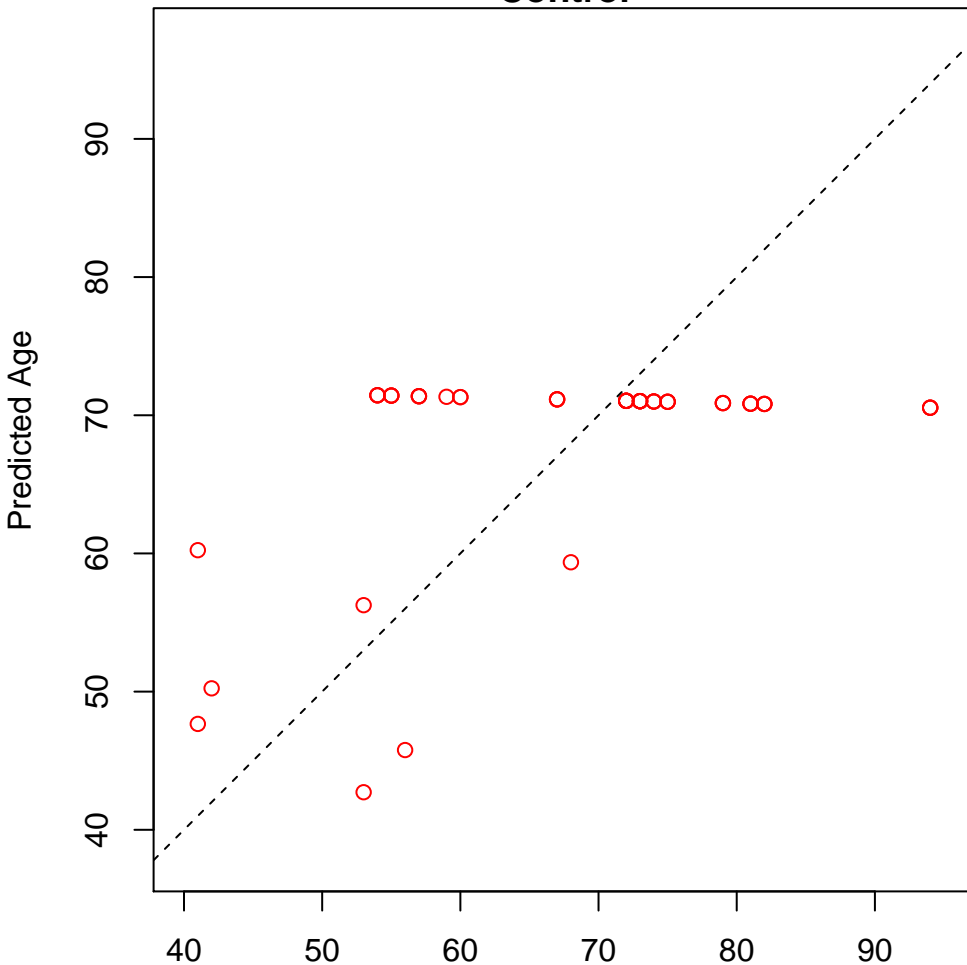
Test



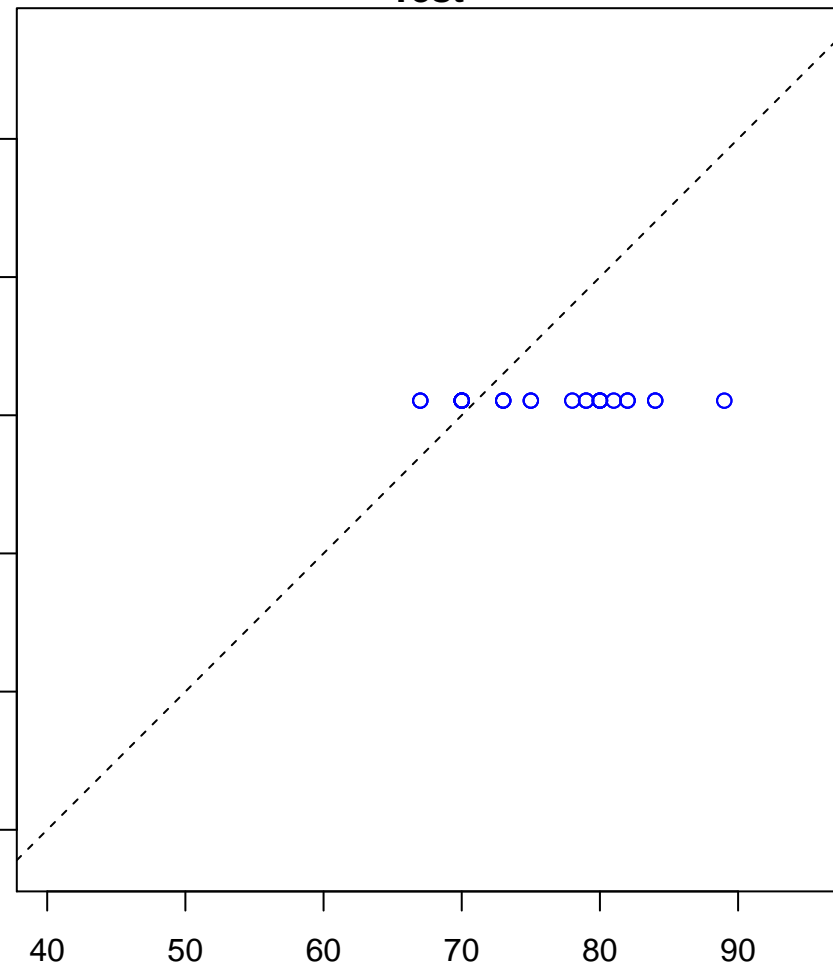
Actual Age

protein-DNA complex assembly (Score: 0.801778)

Control



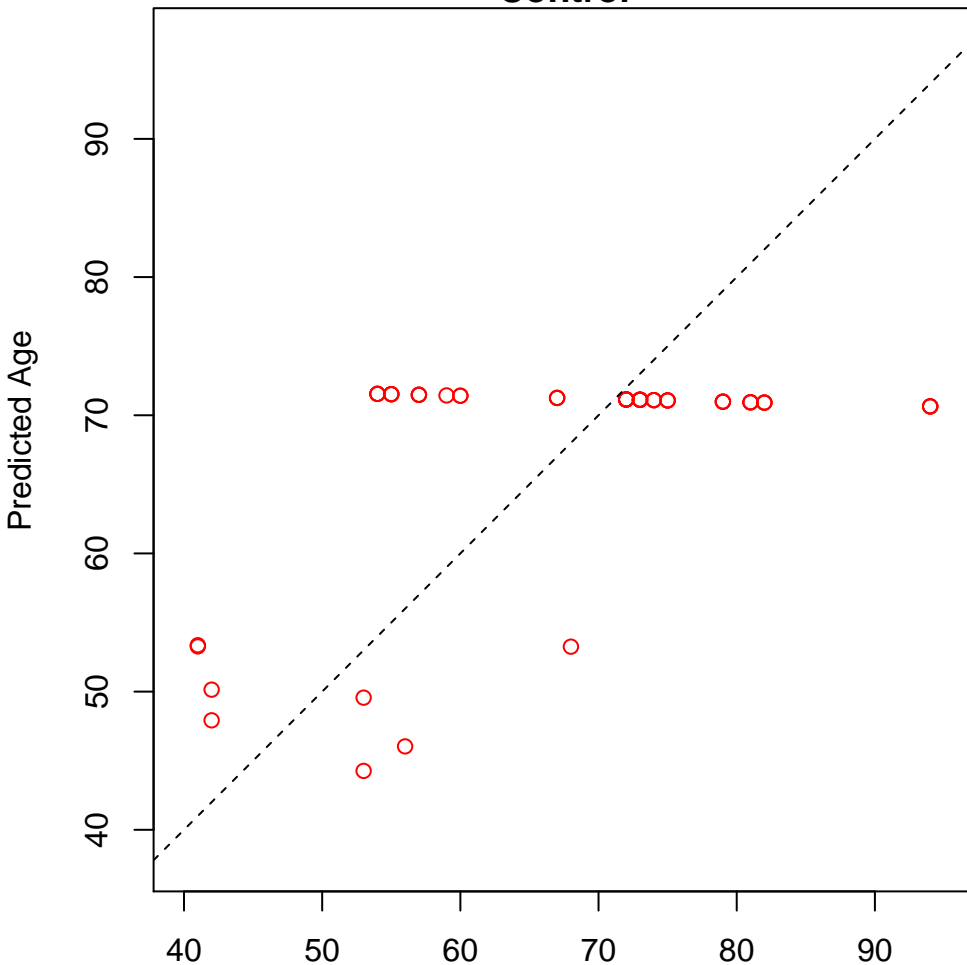
Test



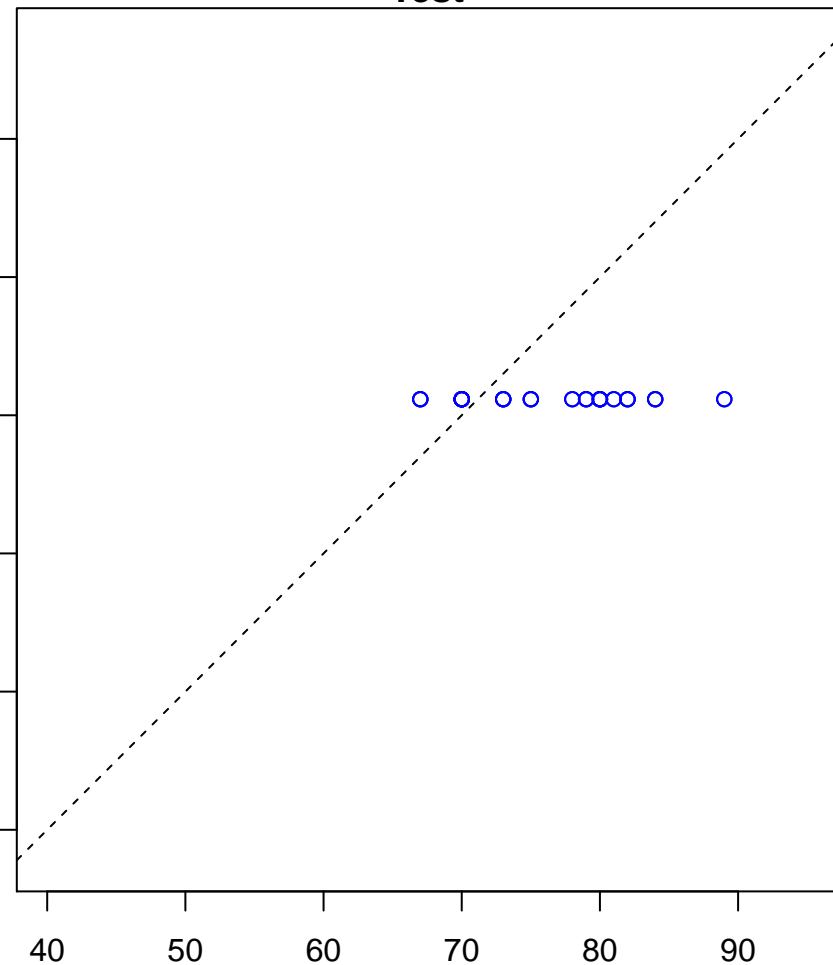
Actual Age

cellular response to organic substance (Score: 0.801761)

Control



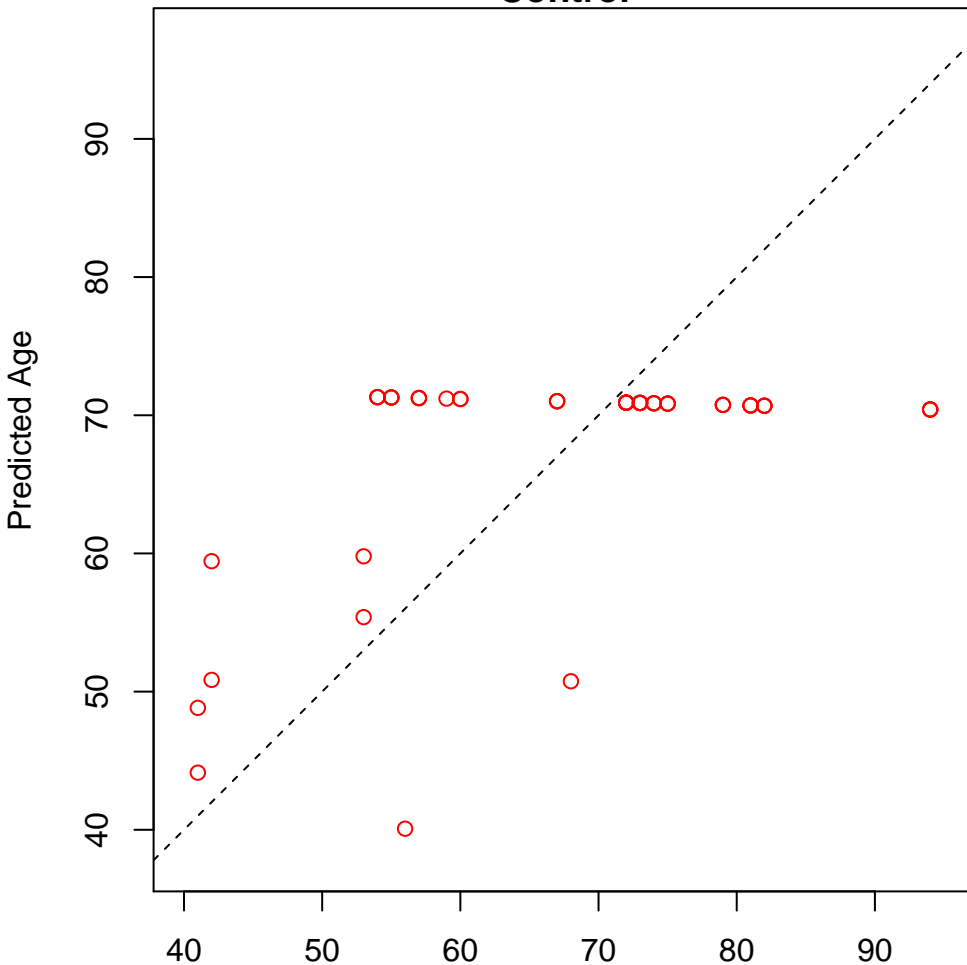
Test



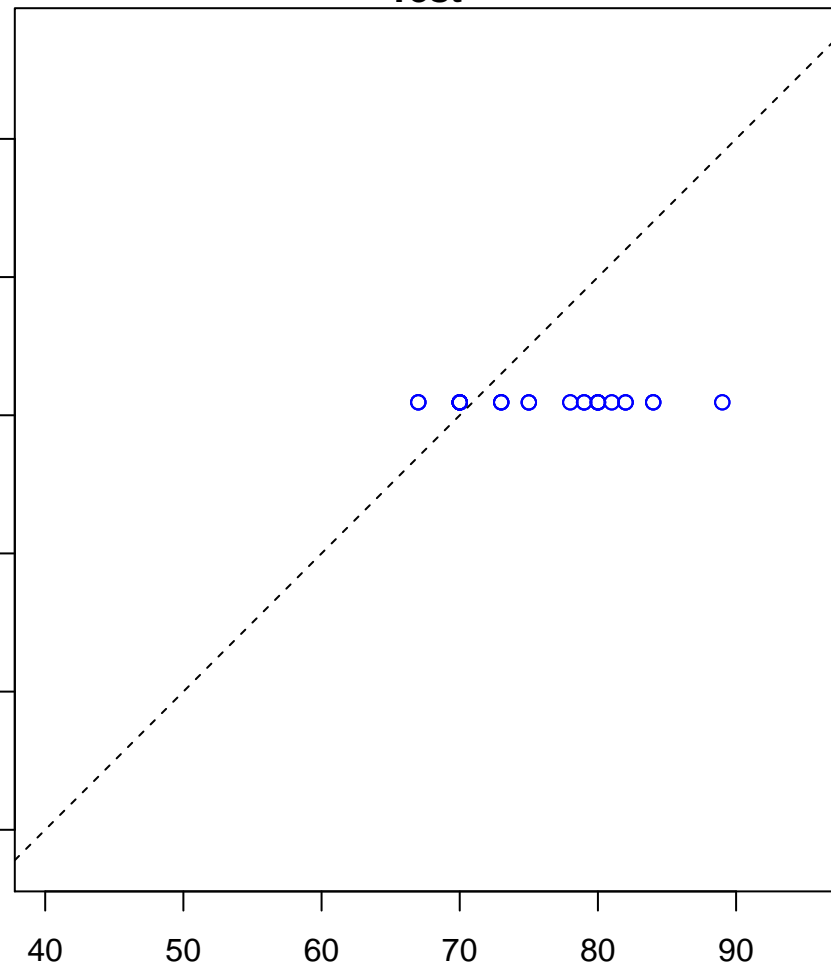
Actual Age

ribonucleoprotein complex assembly (Score: 0.801750)

Control

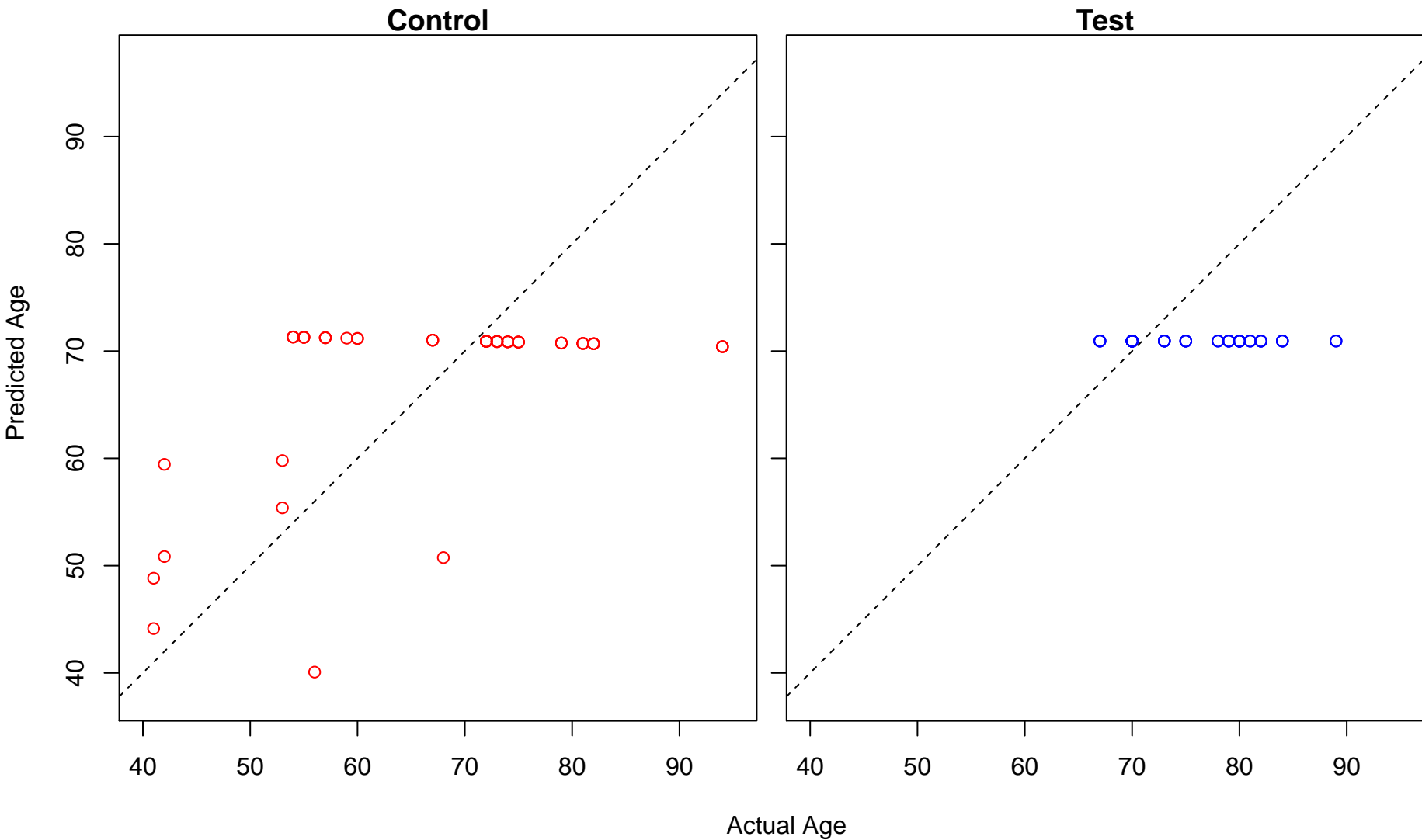


Test

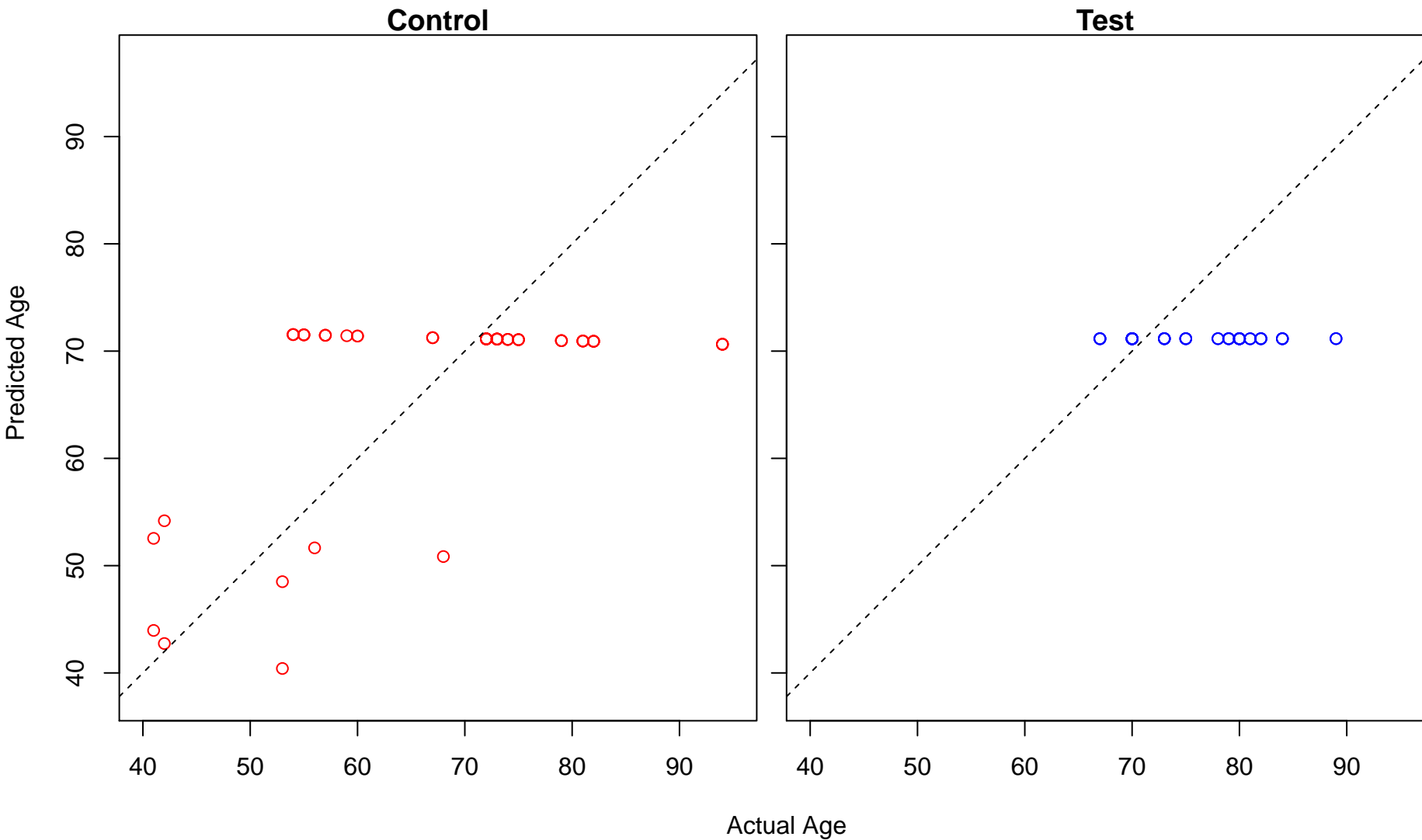


Actual Age

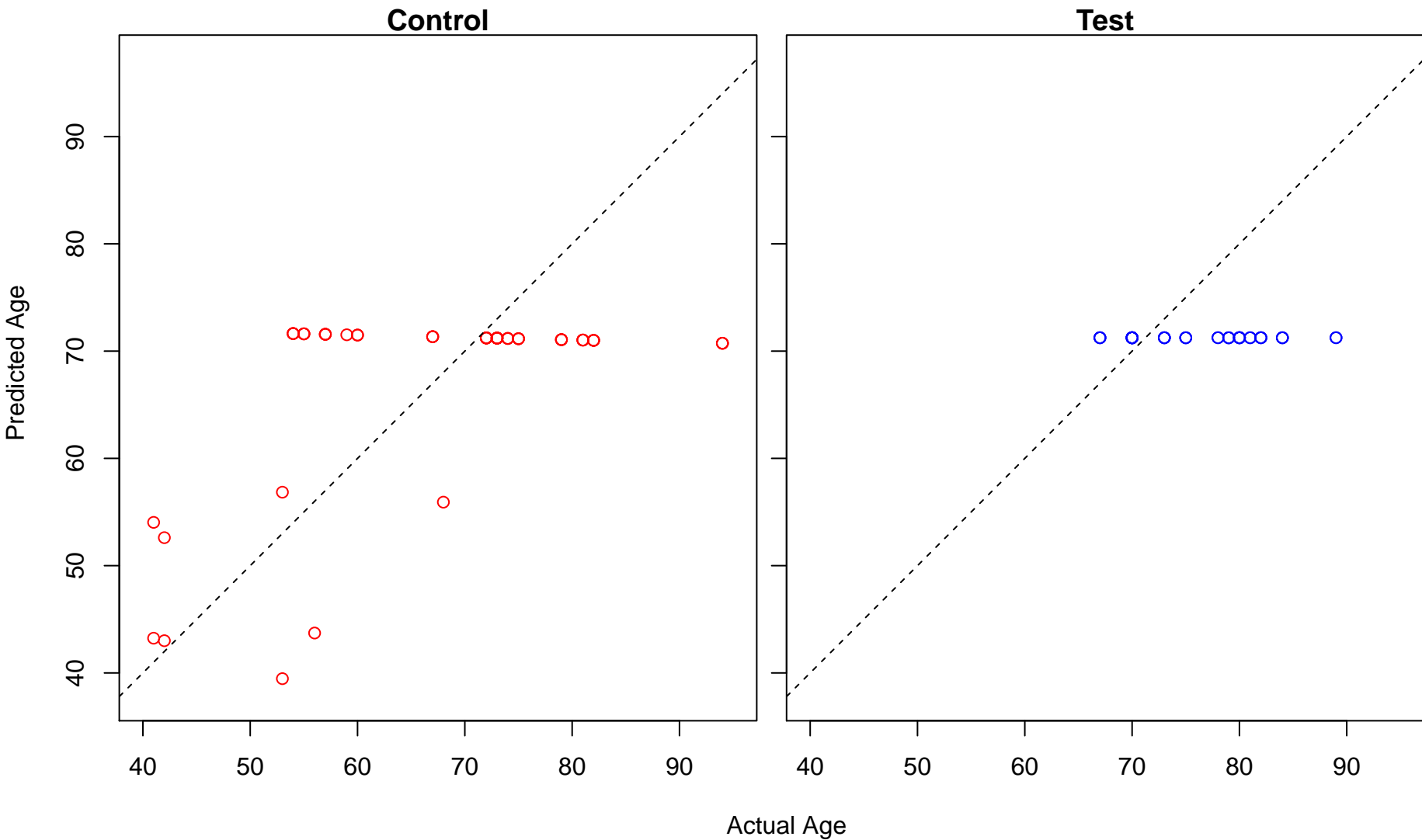
ribonucleoprotein complex subunit organization (Score: 0.801750)



positive regulation of binding (Score: 0.801735)

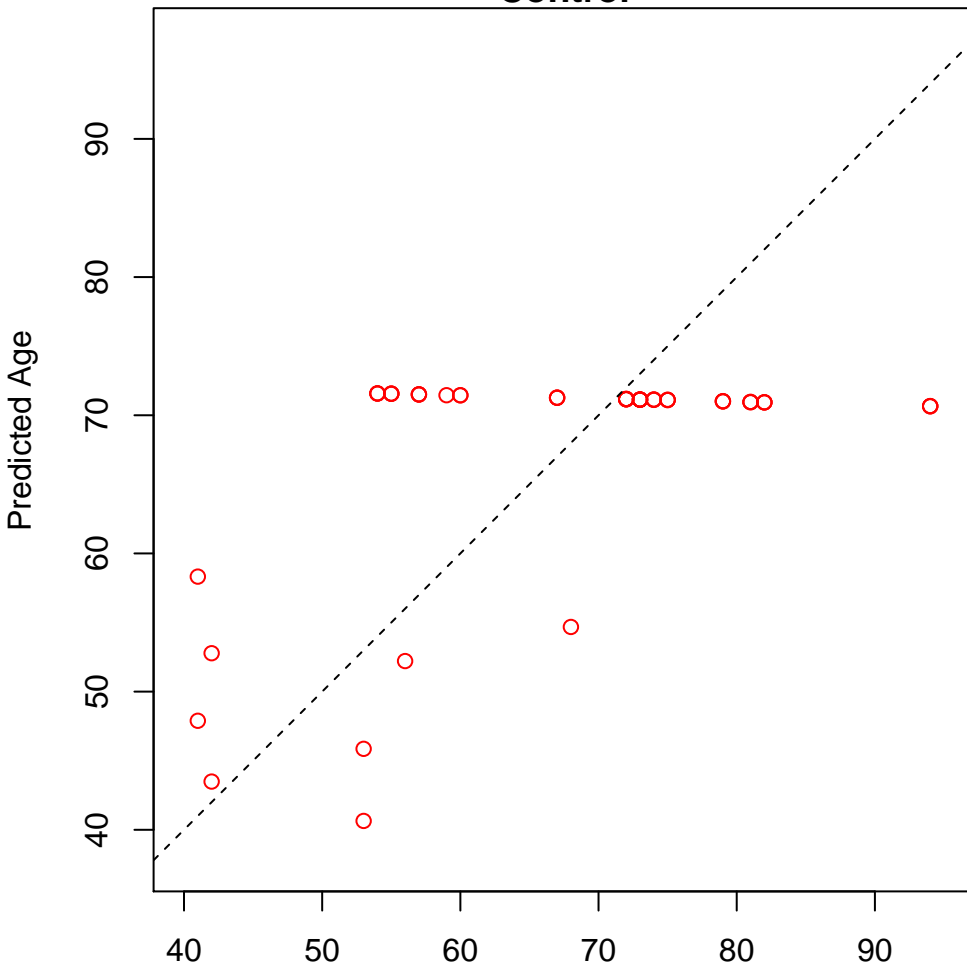


protein complex disassembly (Score: 0.801701)

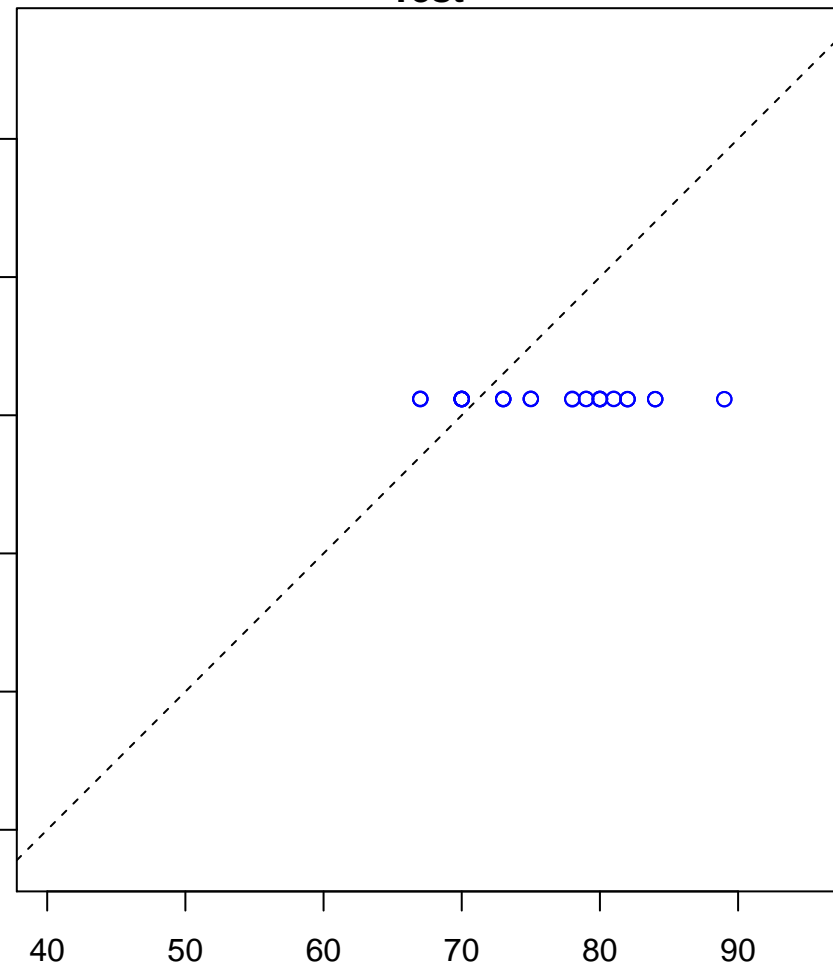


regulation of cell-cell adhesion (Score: 0.801680)

Control

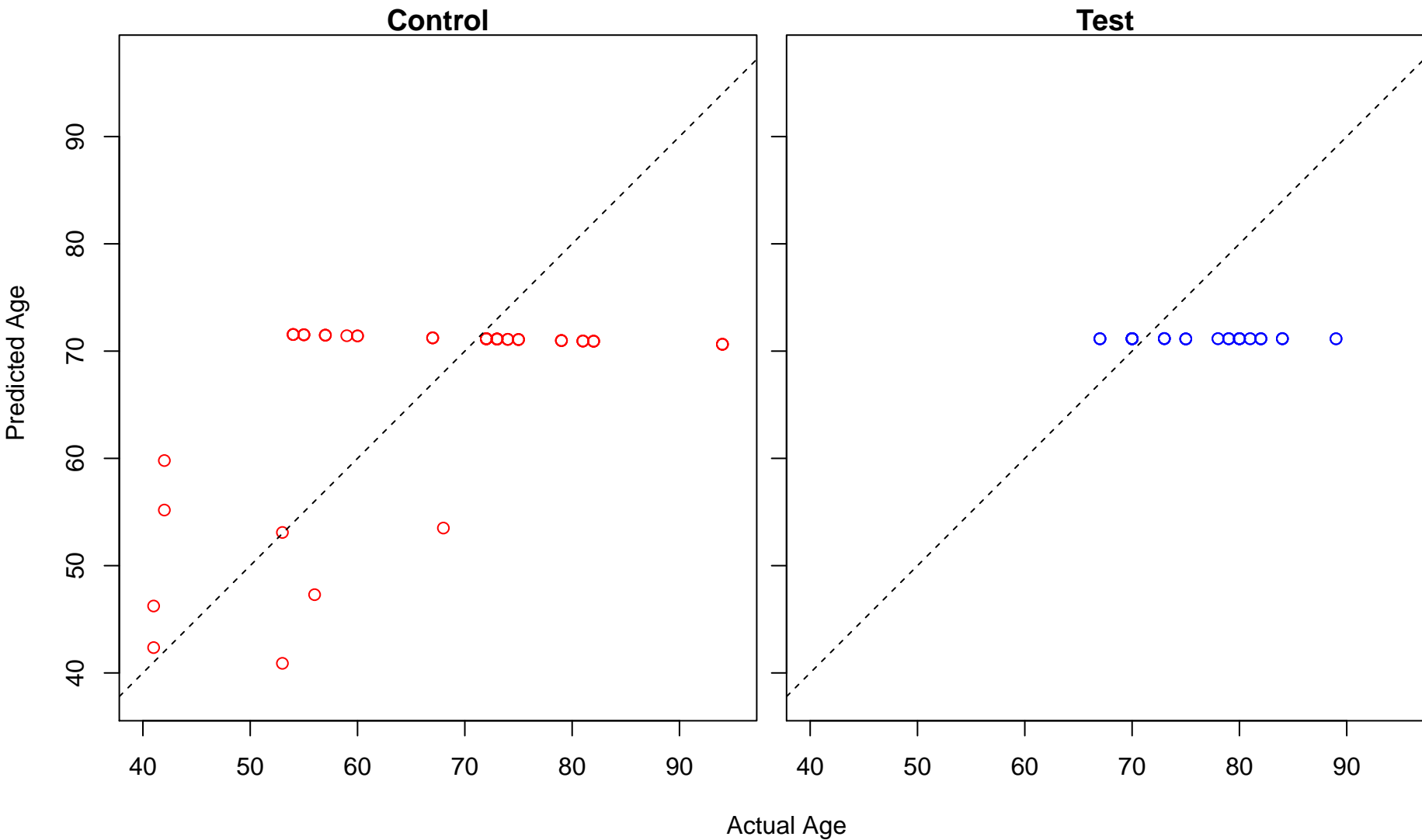


Test



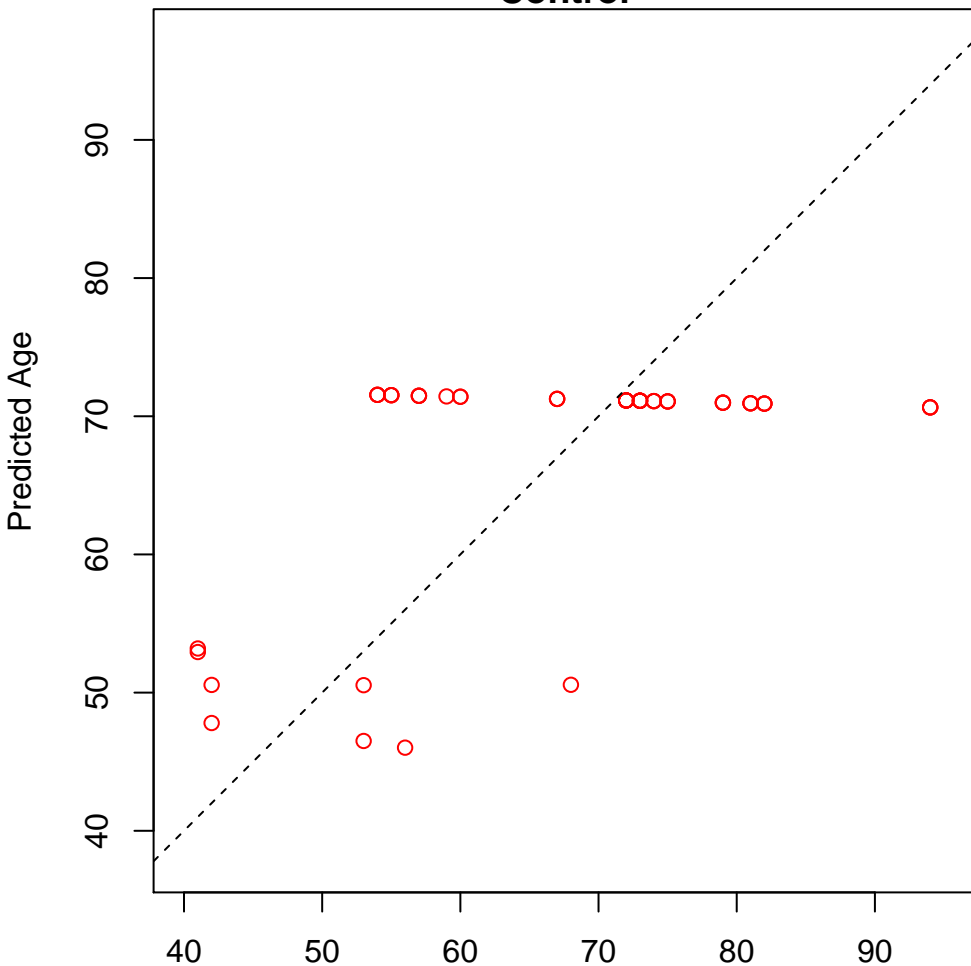
Actual Age

IRE1-mediated unfolded protein response (Score: 0.801623)

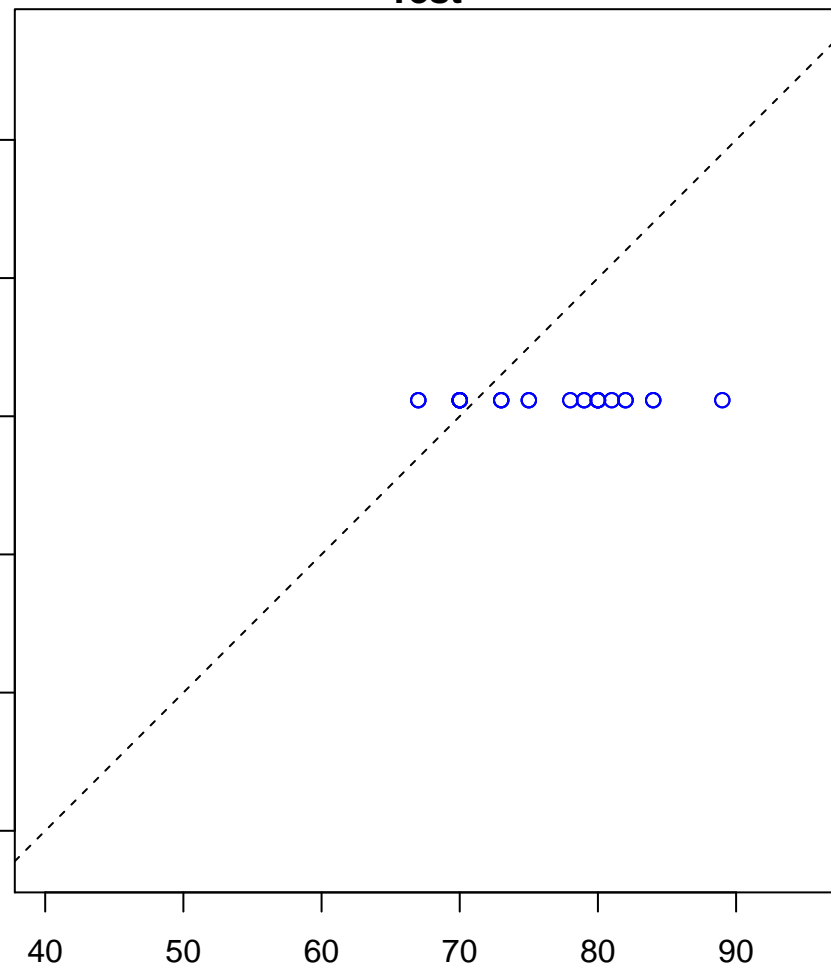


positive regulation of biological process (Score: 0.801600)

Control

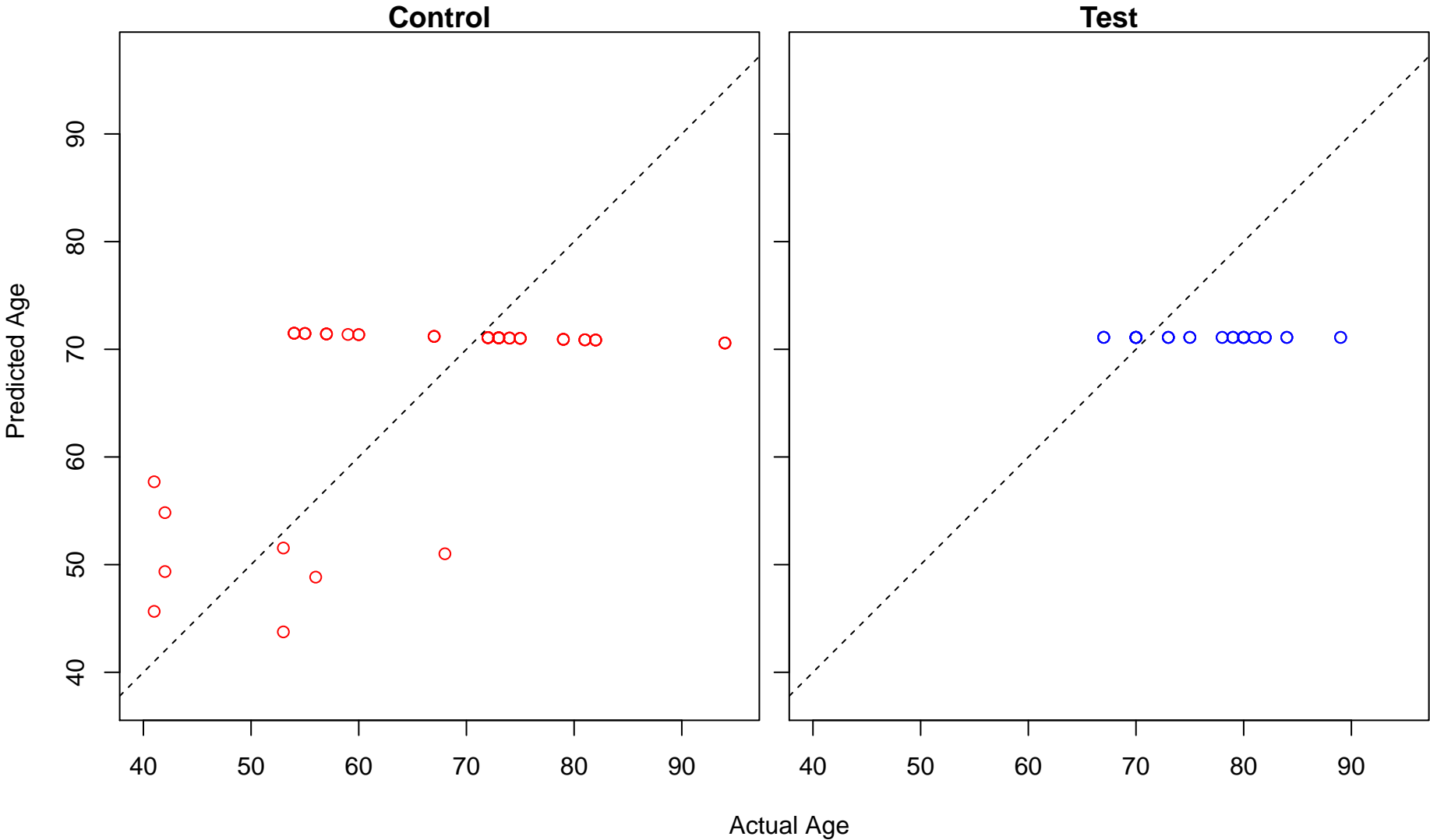


Test

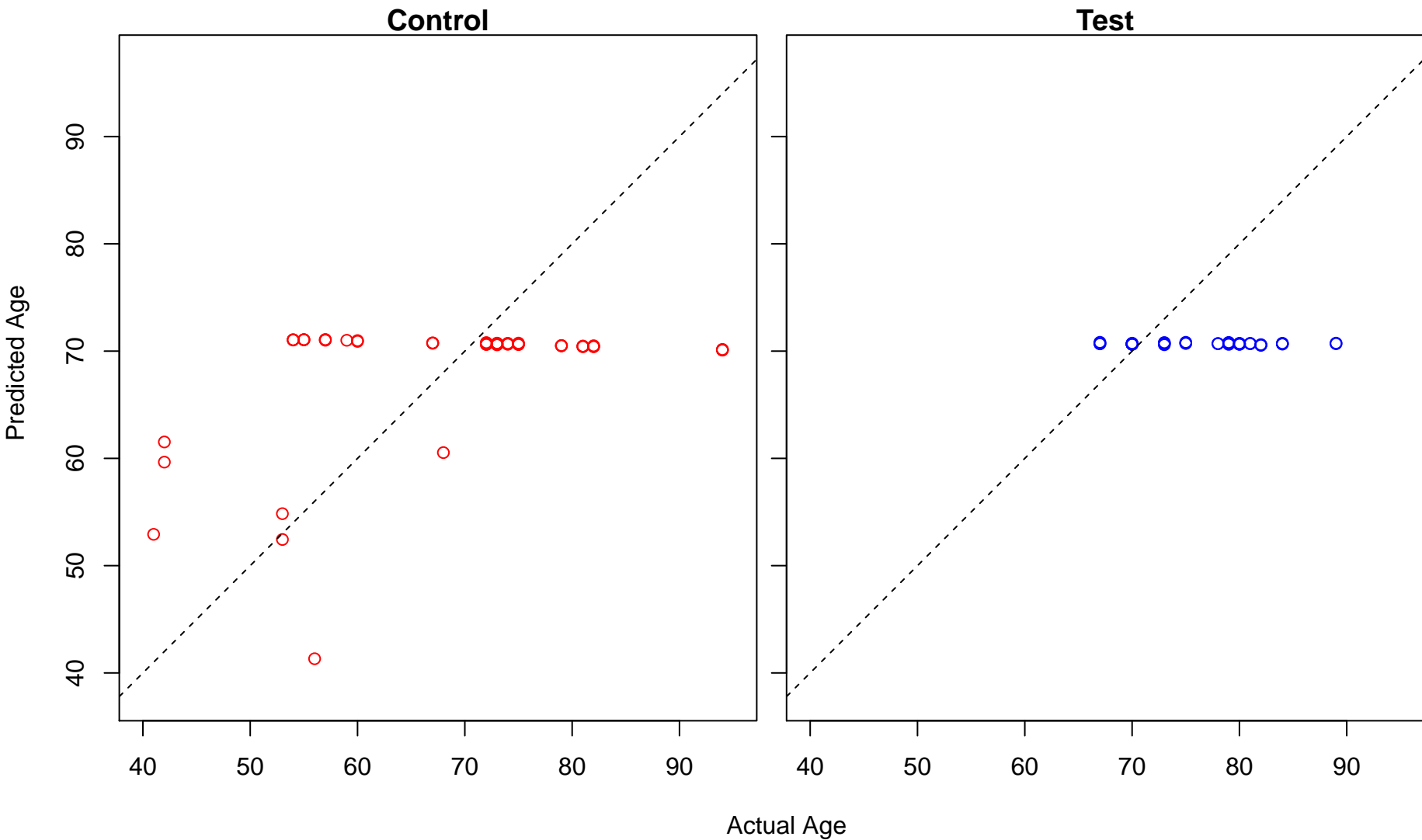


Actual Age

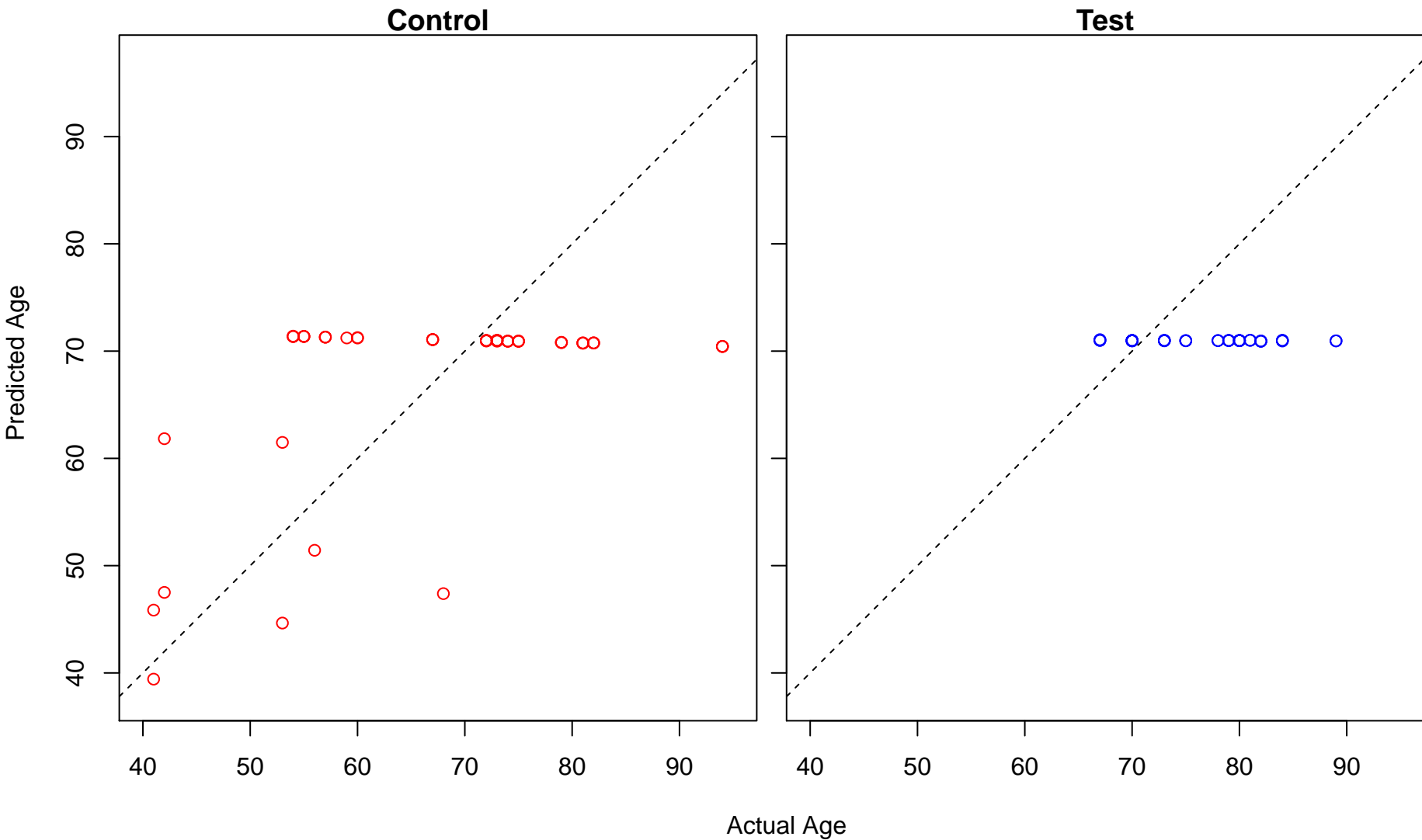
regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 0.80)



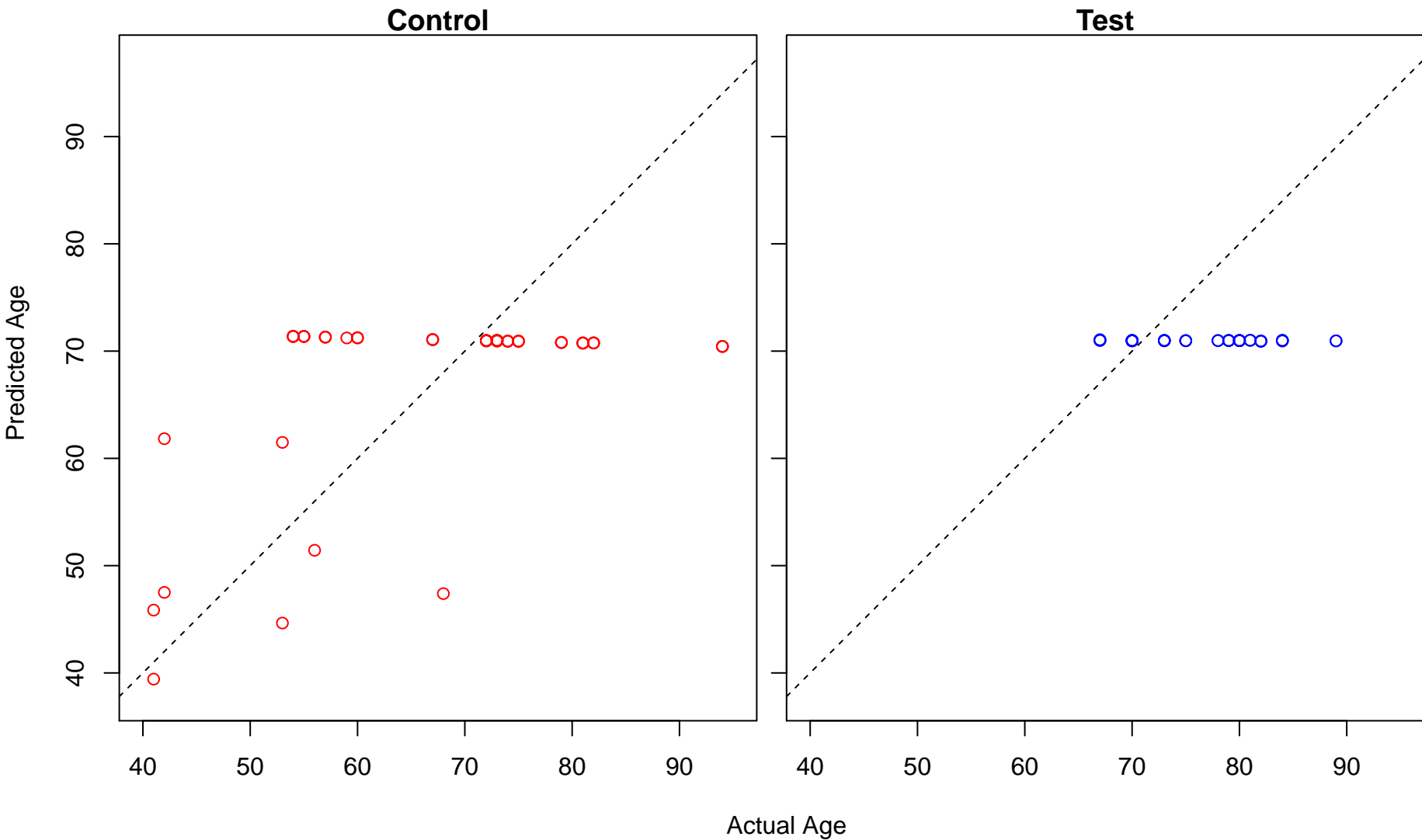
regulation of DNA replication (Score: 0.801438)



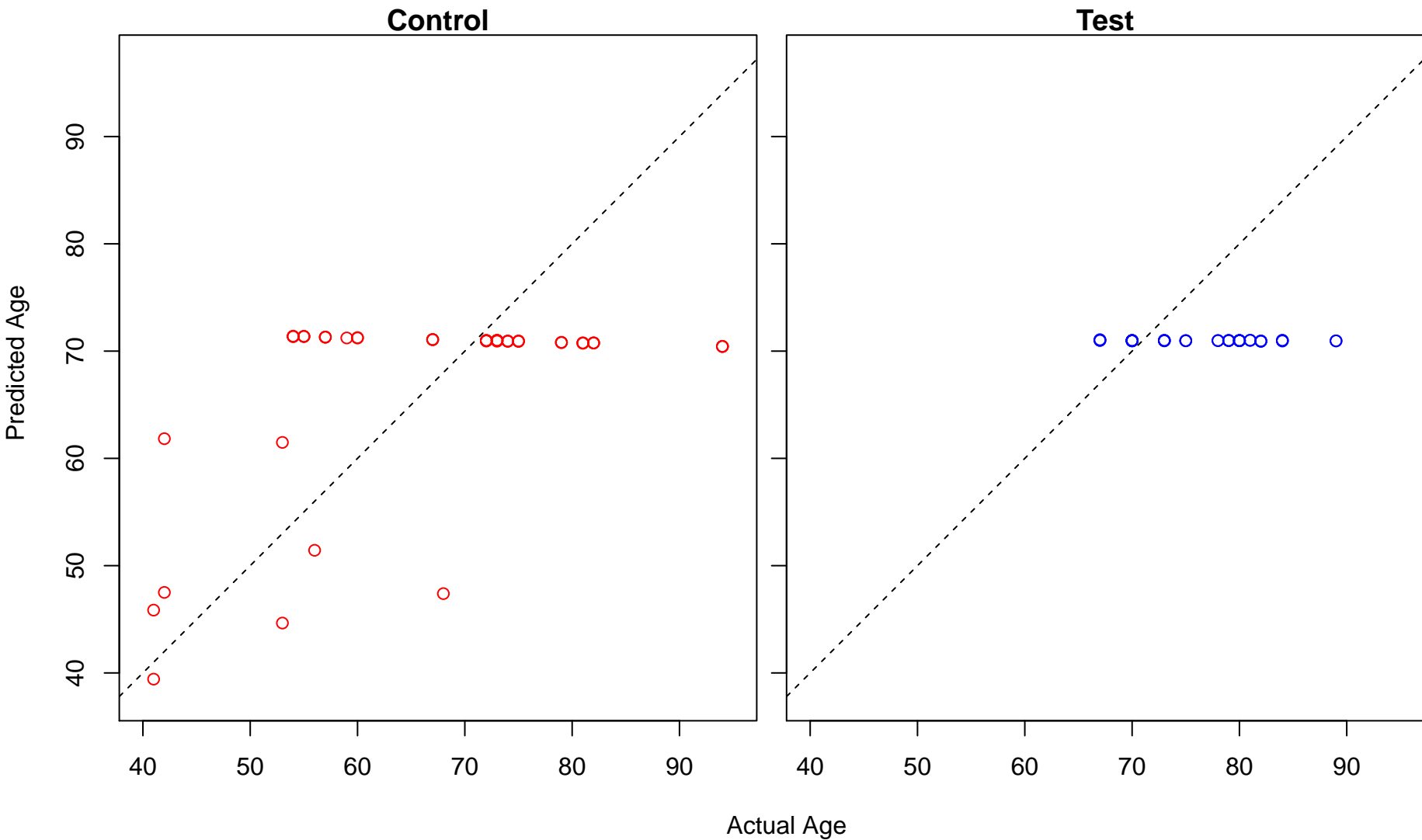
establishment or maintenance of apical/basal cell polarity (Score: 0.801241)



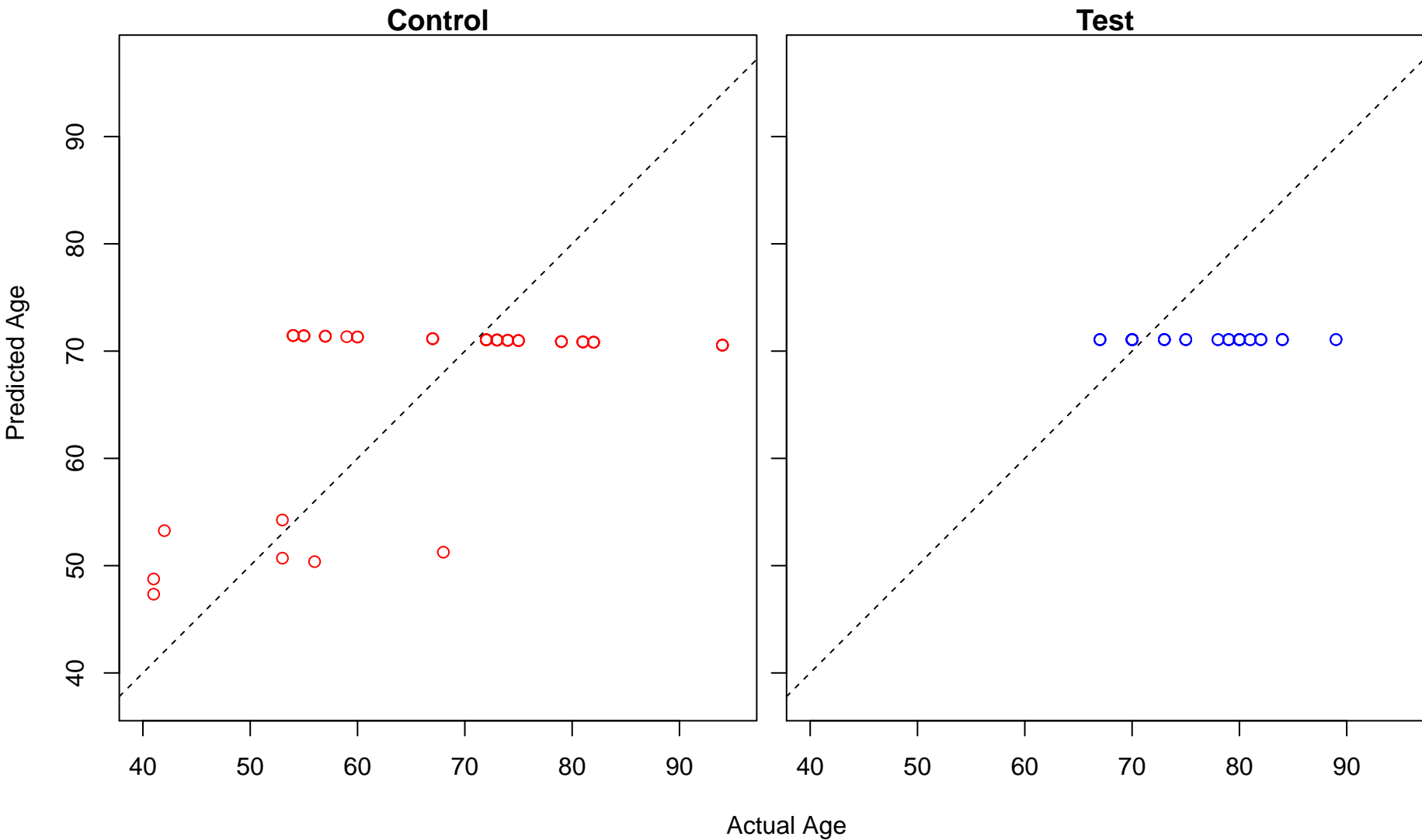
establishment or maintenance of epithelial cell apical/basal polarity (Score: 0.801241)



establishment or maintenance of bipolar cell polarity (Score: 0.801241)

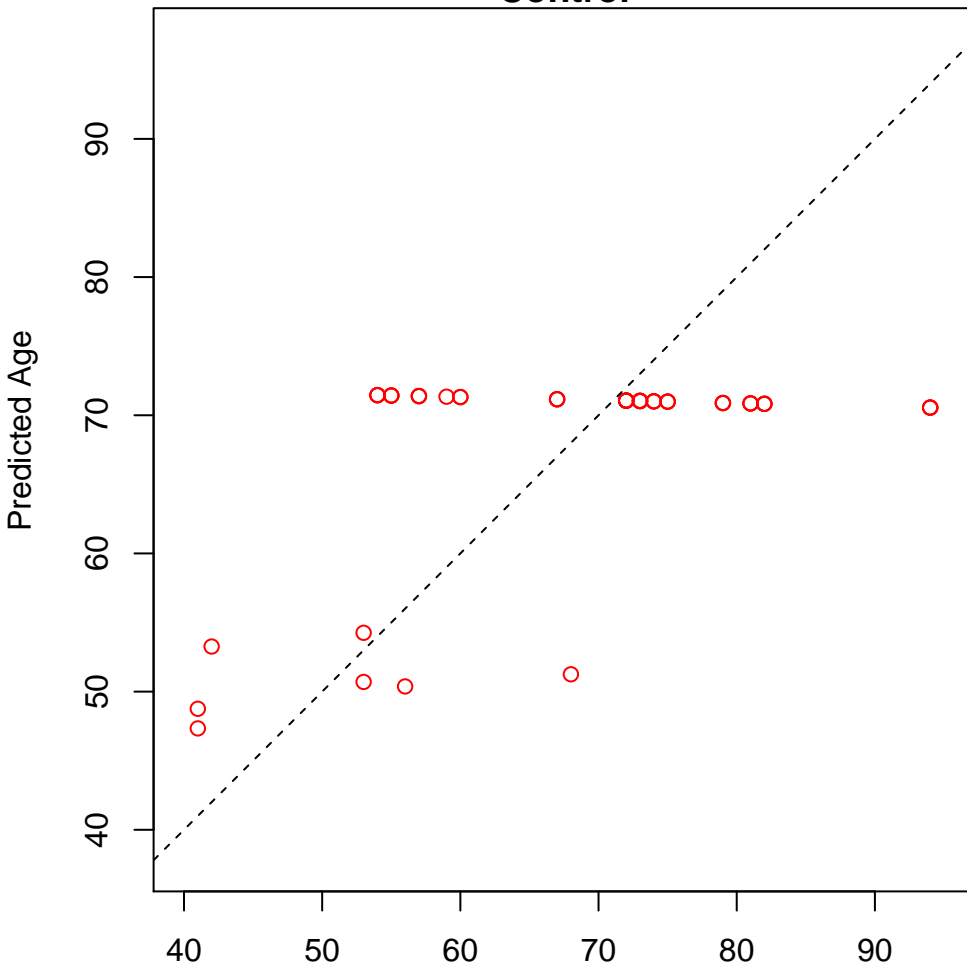


response to hormone (Score: 0.801220)

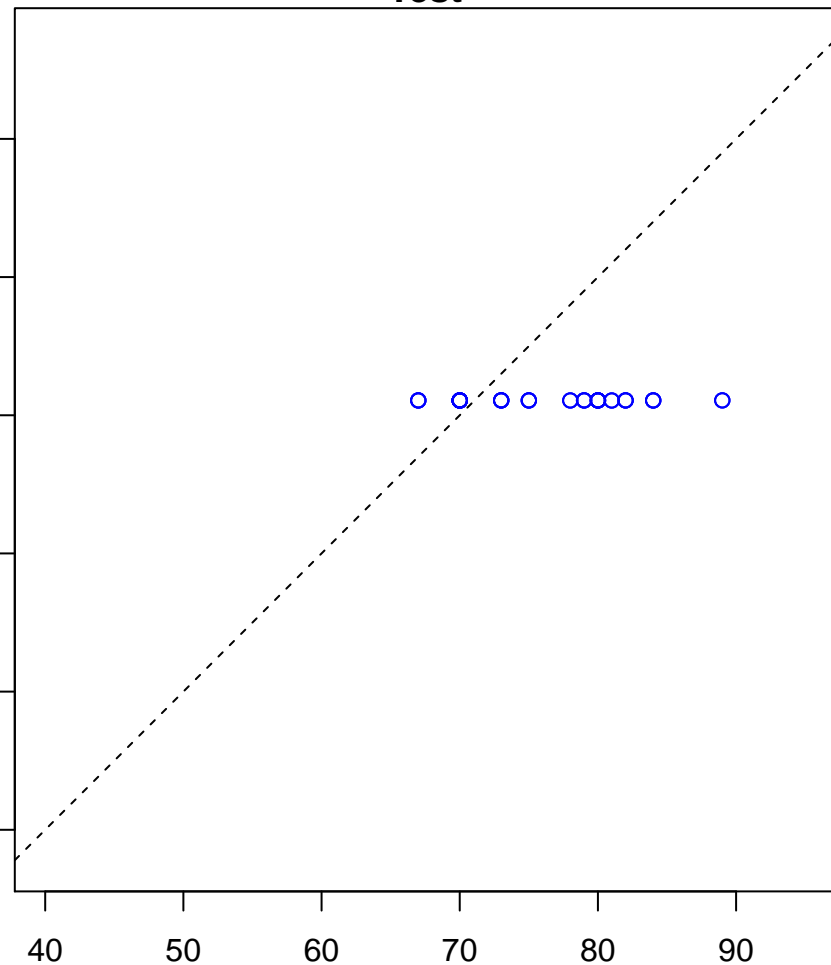


cellular response to hormone stimulus (Score: 0.801220)

Control

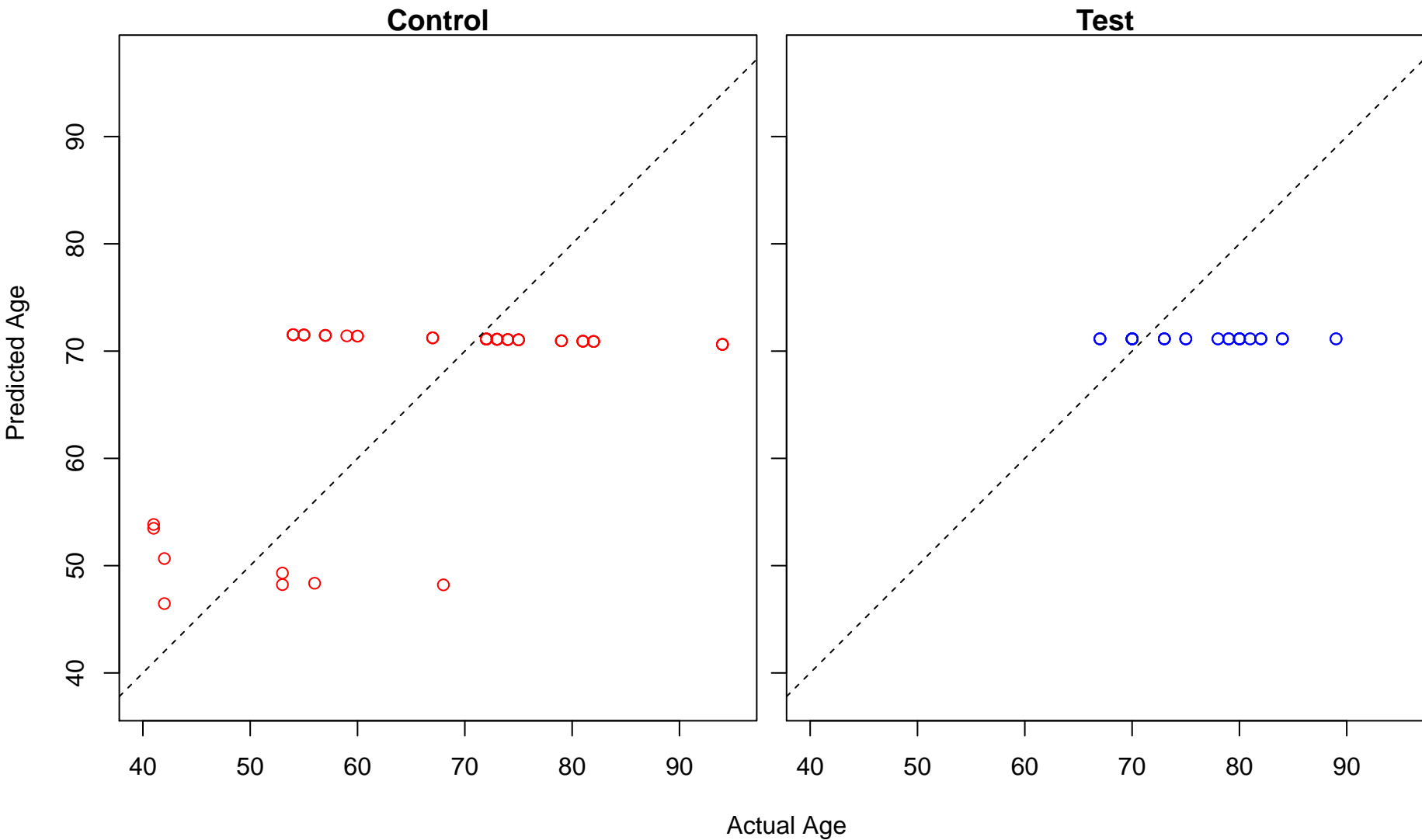


Test



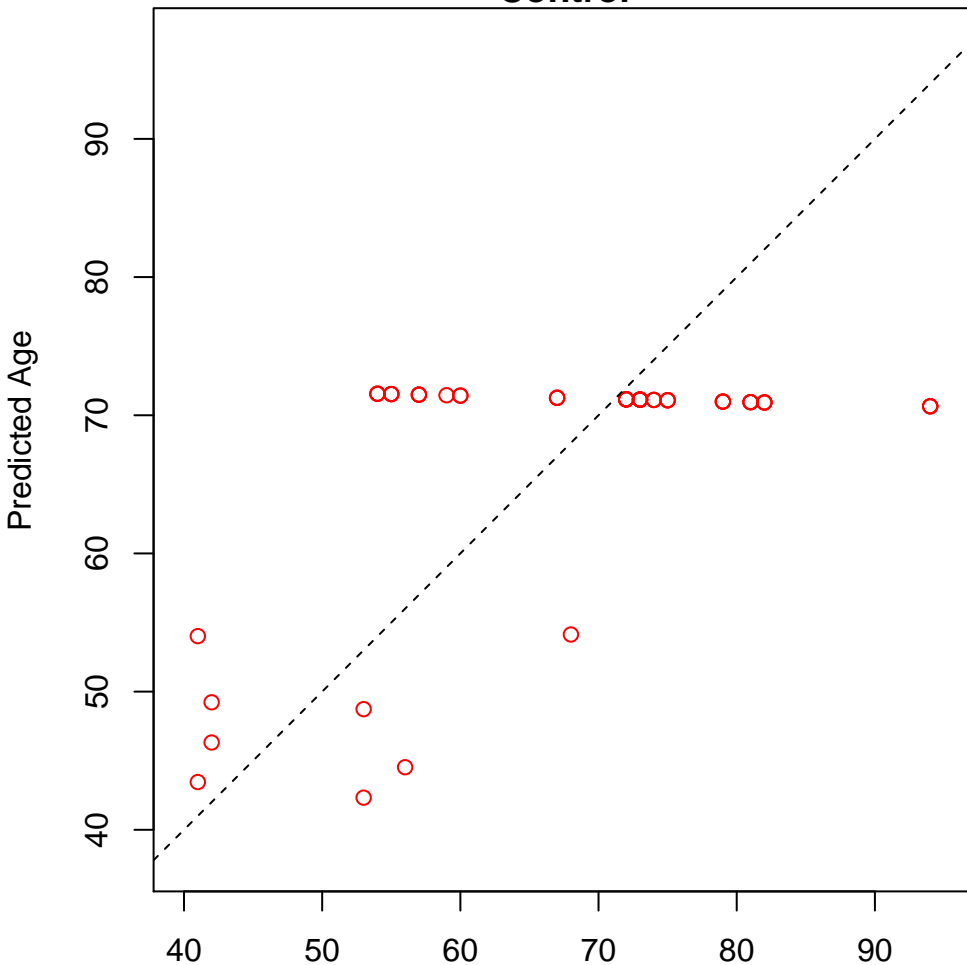
Actual Age

regulation of transport (Score: 0.801209)

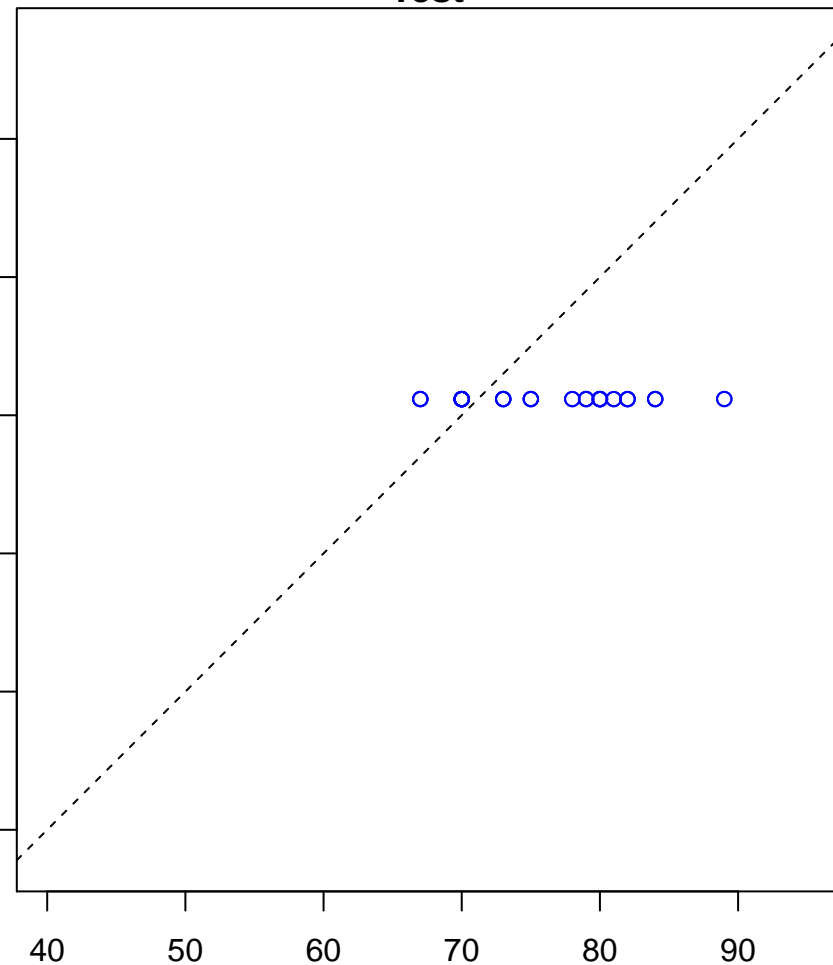


cell surface receptor signaling pathway (Score: 0.801199)

Control

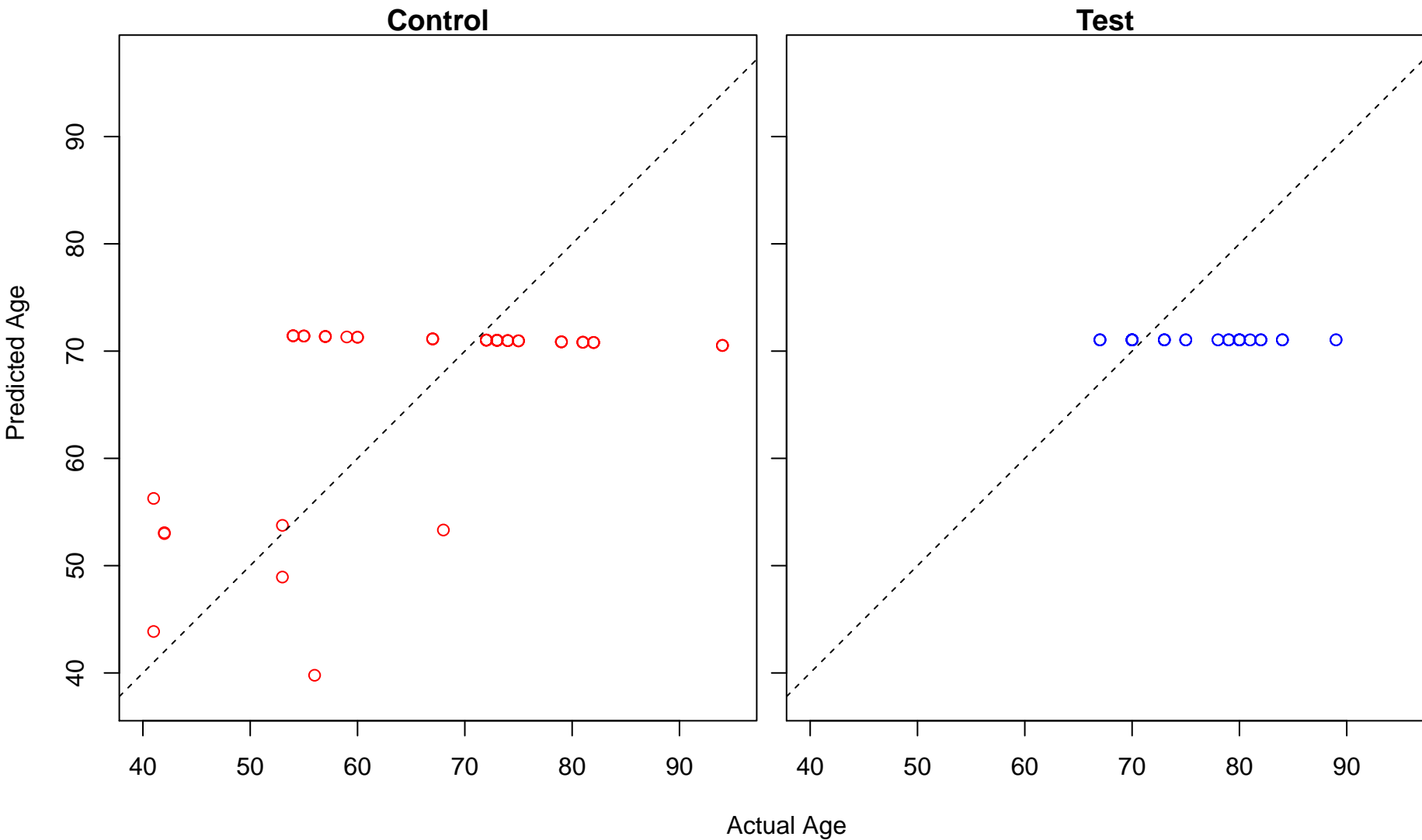


Test

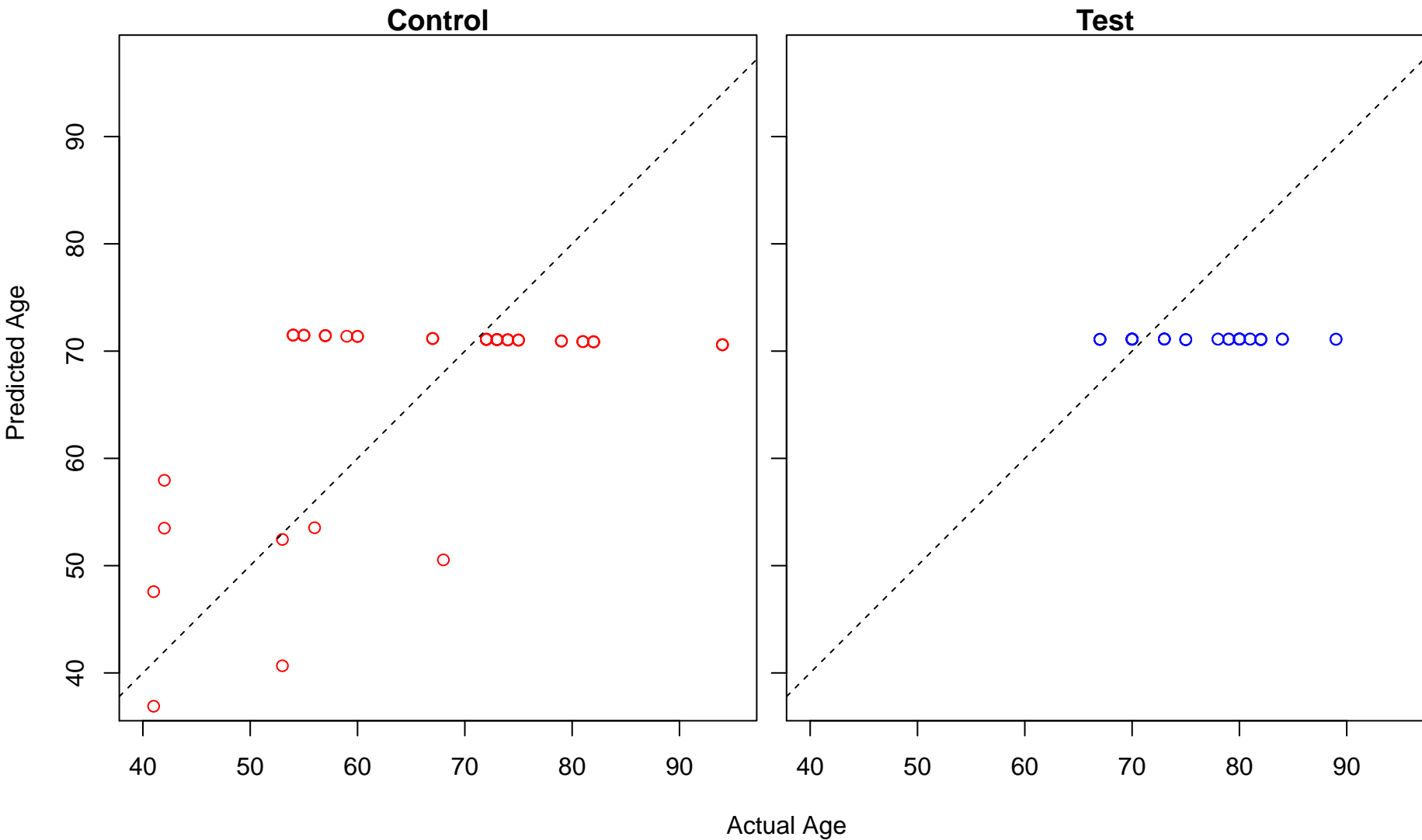


Actual Age

myeloid cell differentiation (Score: 0.801182)

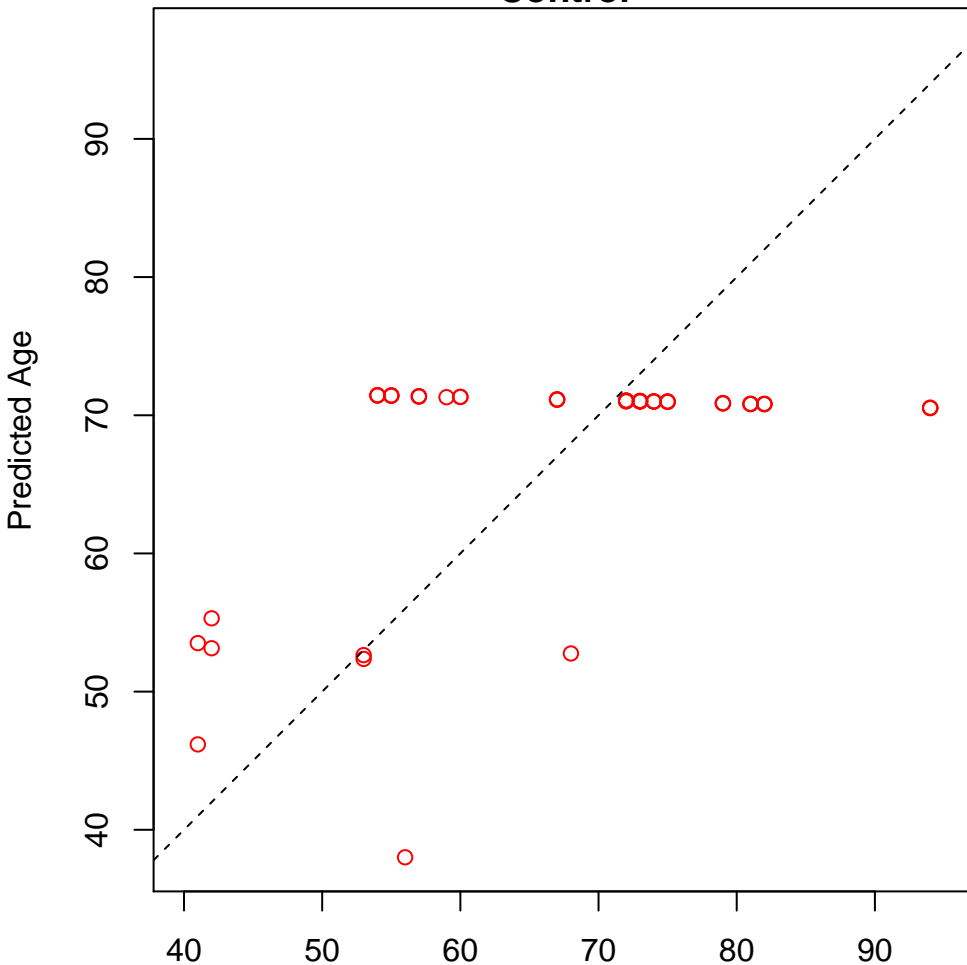


gland development (Score: 0.801175)

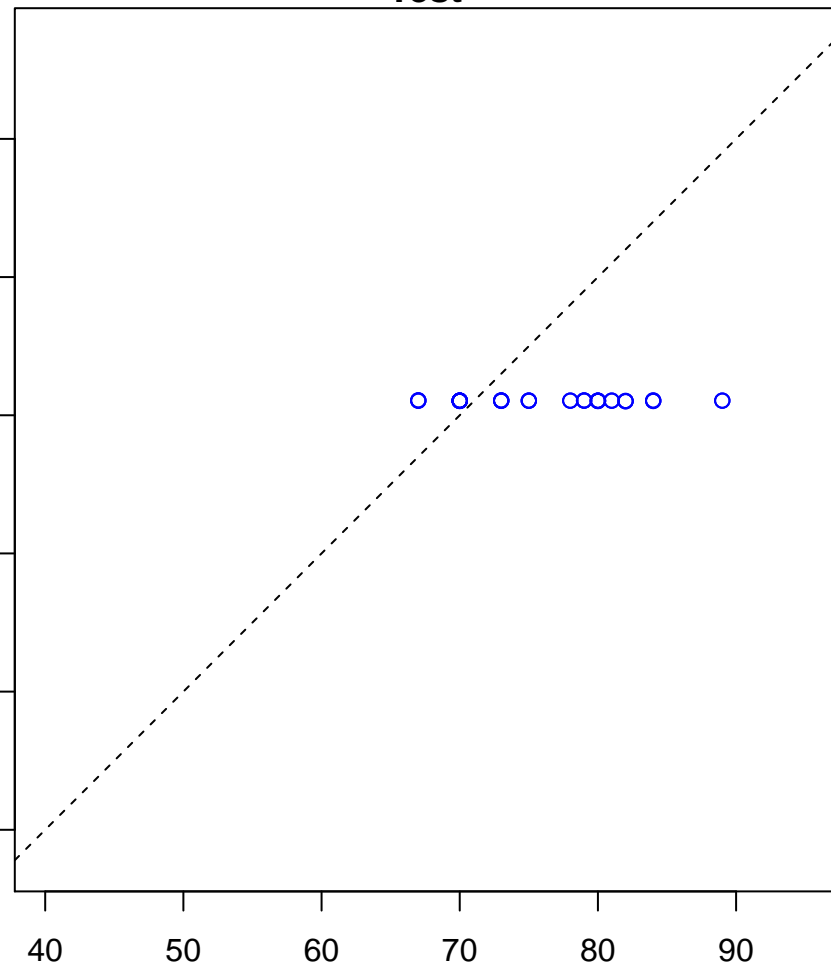


extracellular matrix disassembly (Score: 0.801165)

Control

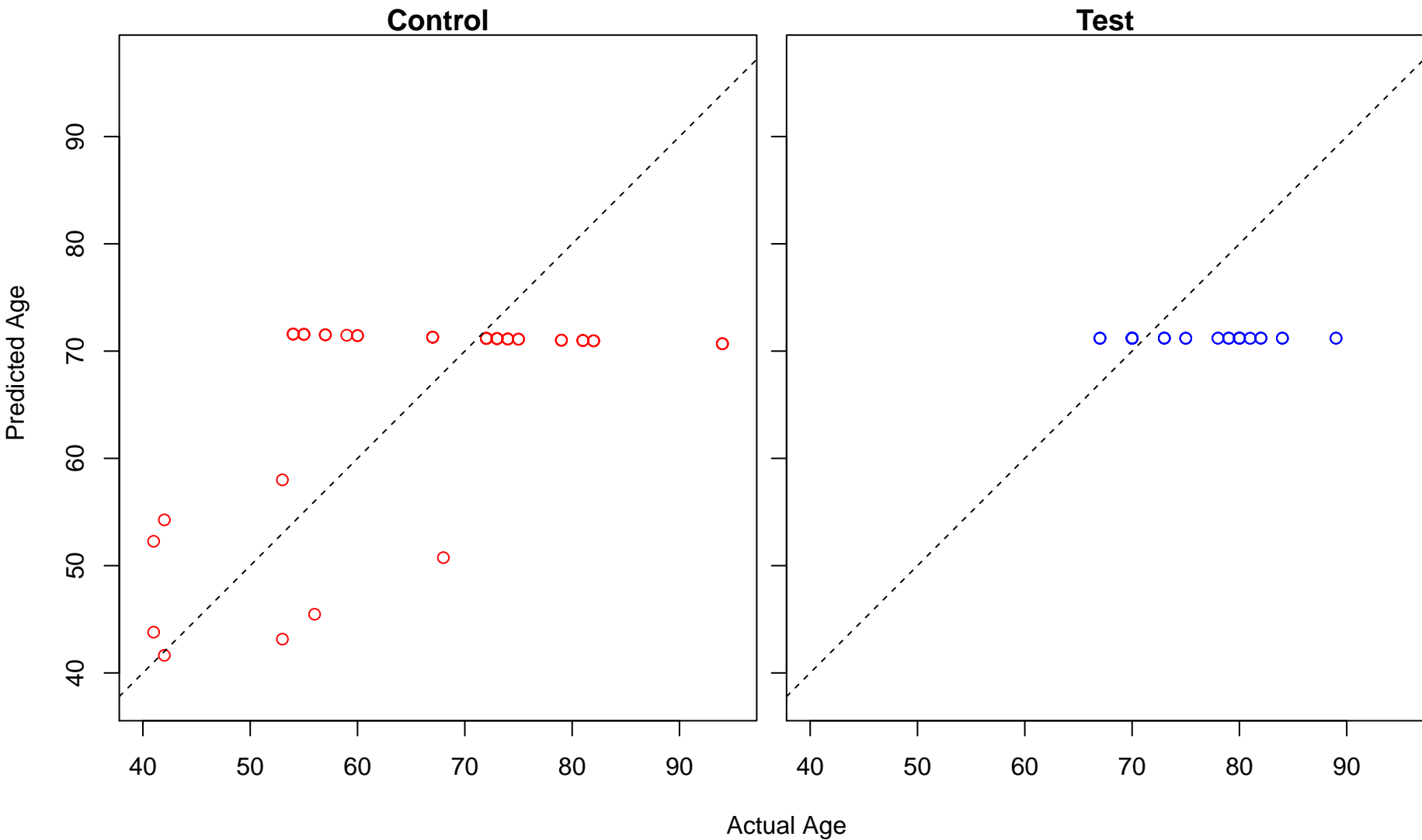


Test

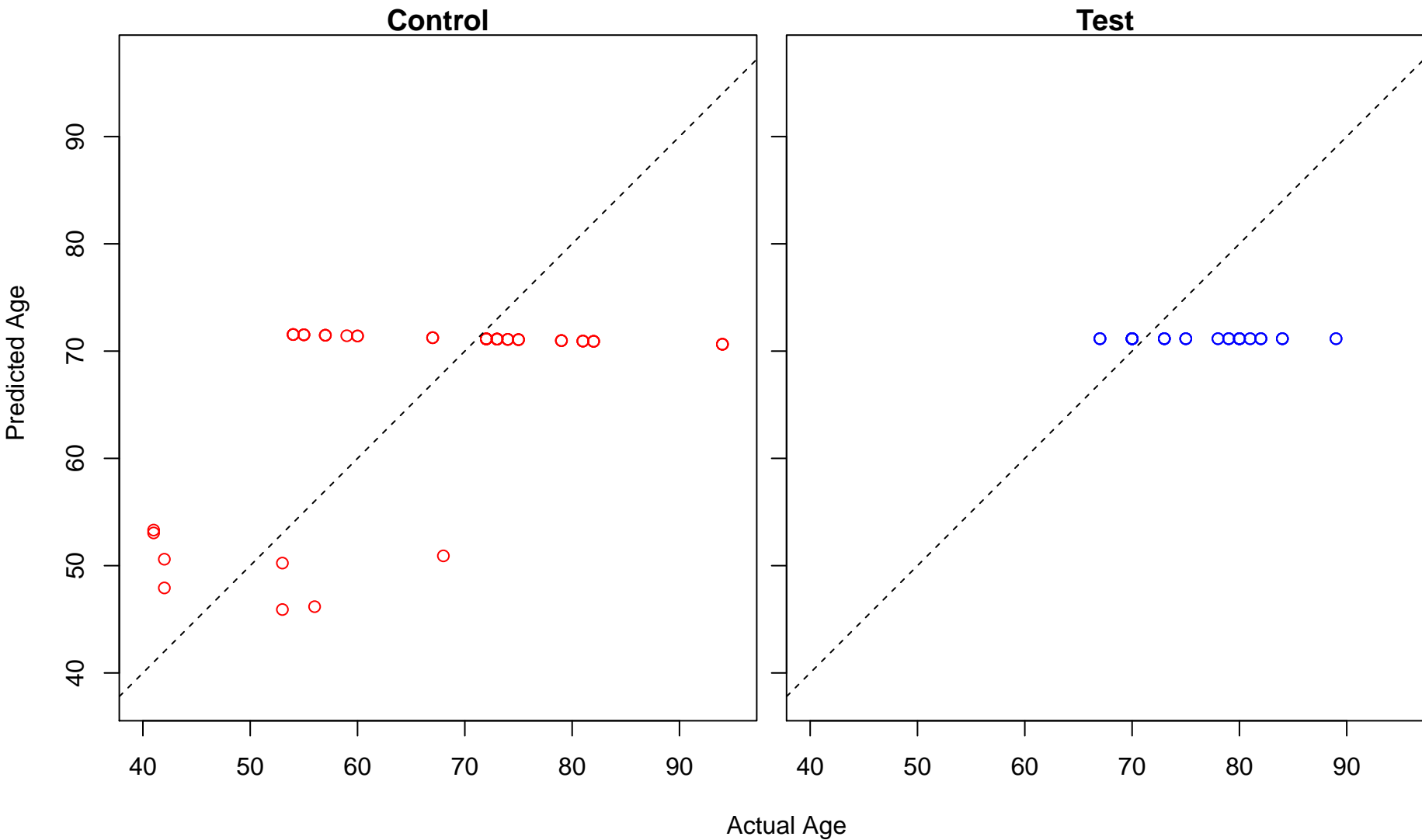


Actual Age

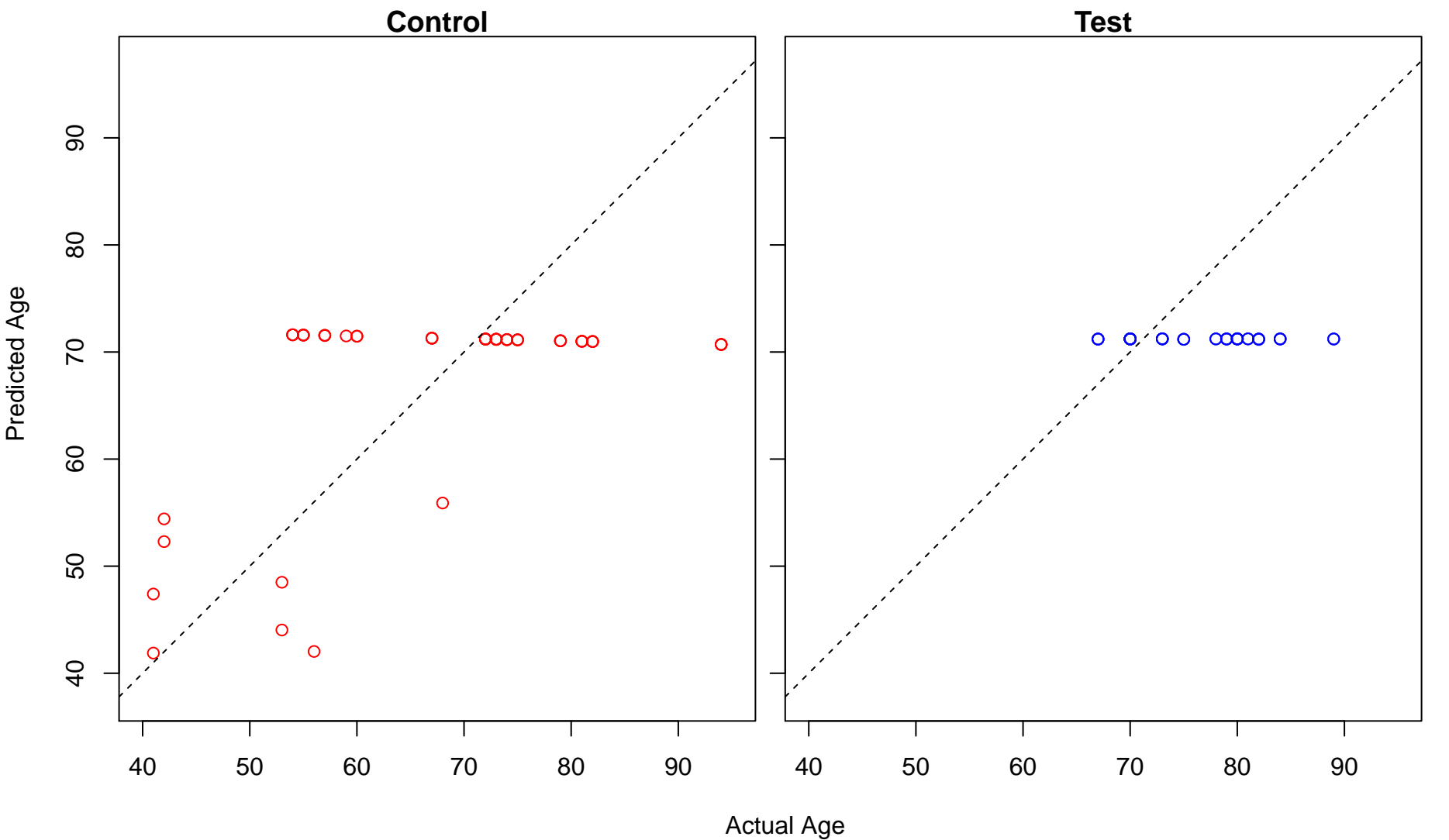
regulation of protein binding (Score: 0.801143)



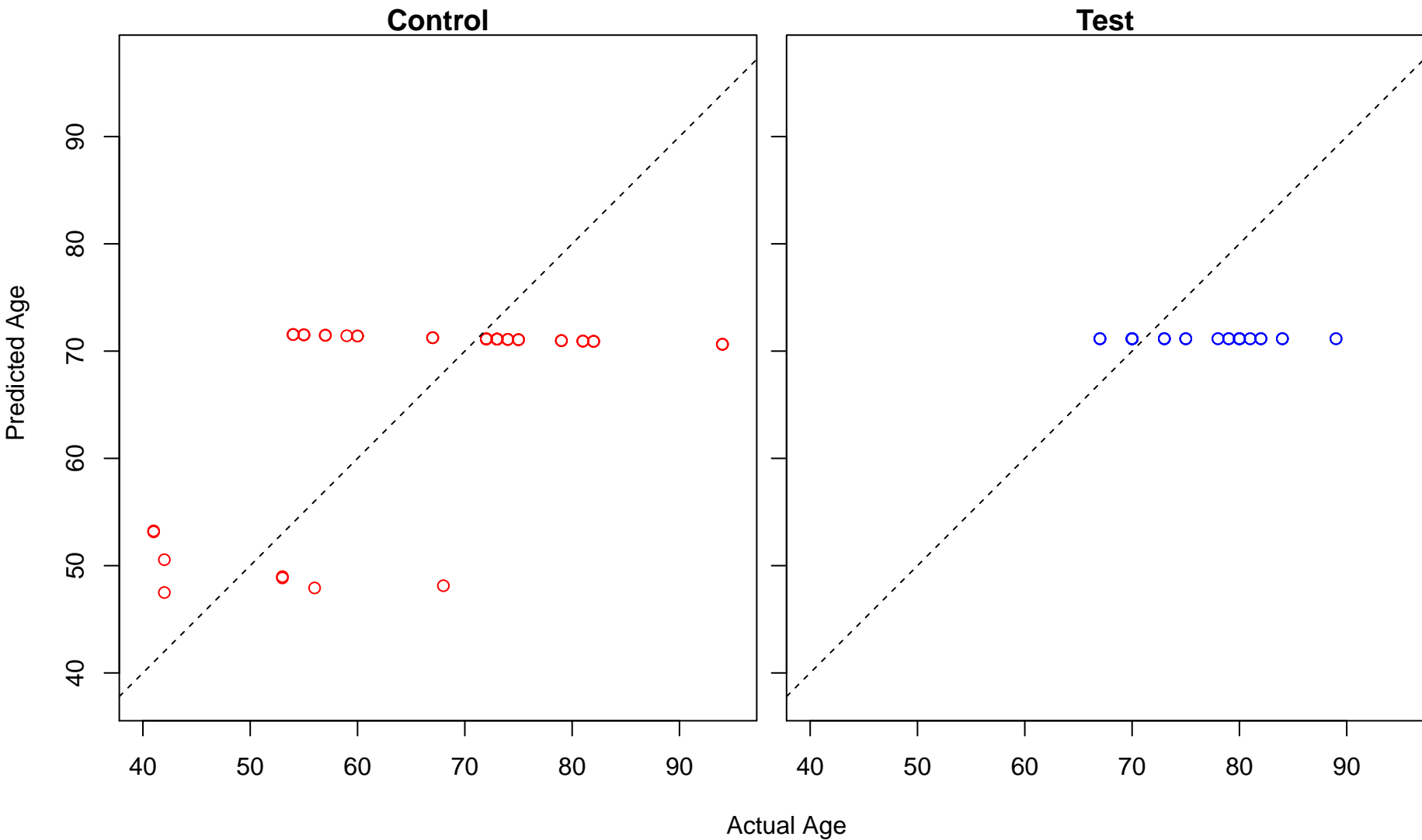
response to chemical (Score: 0.801107)



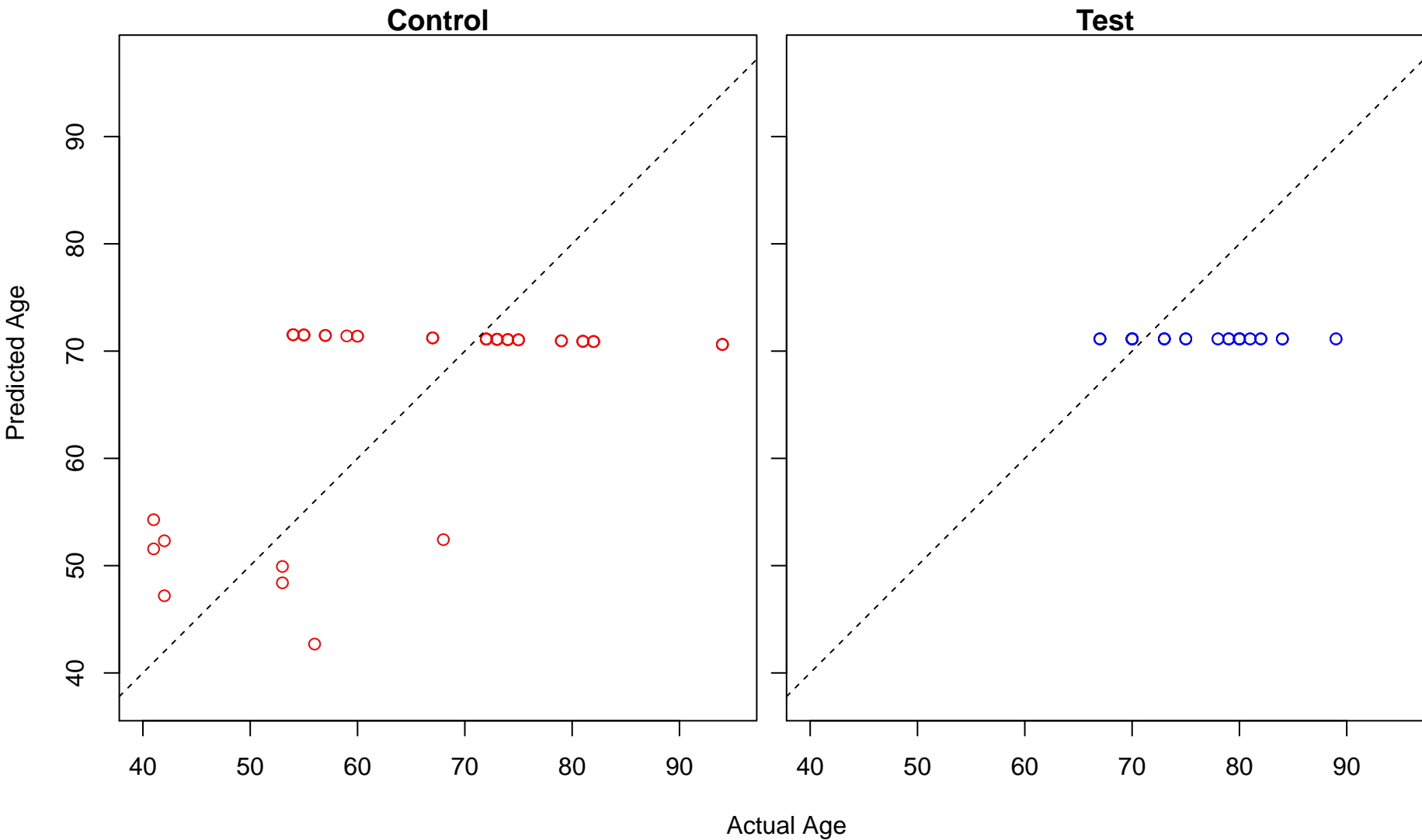
ulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimul



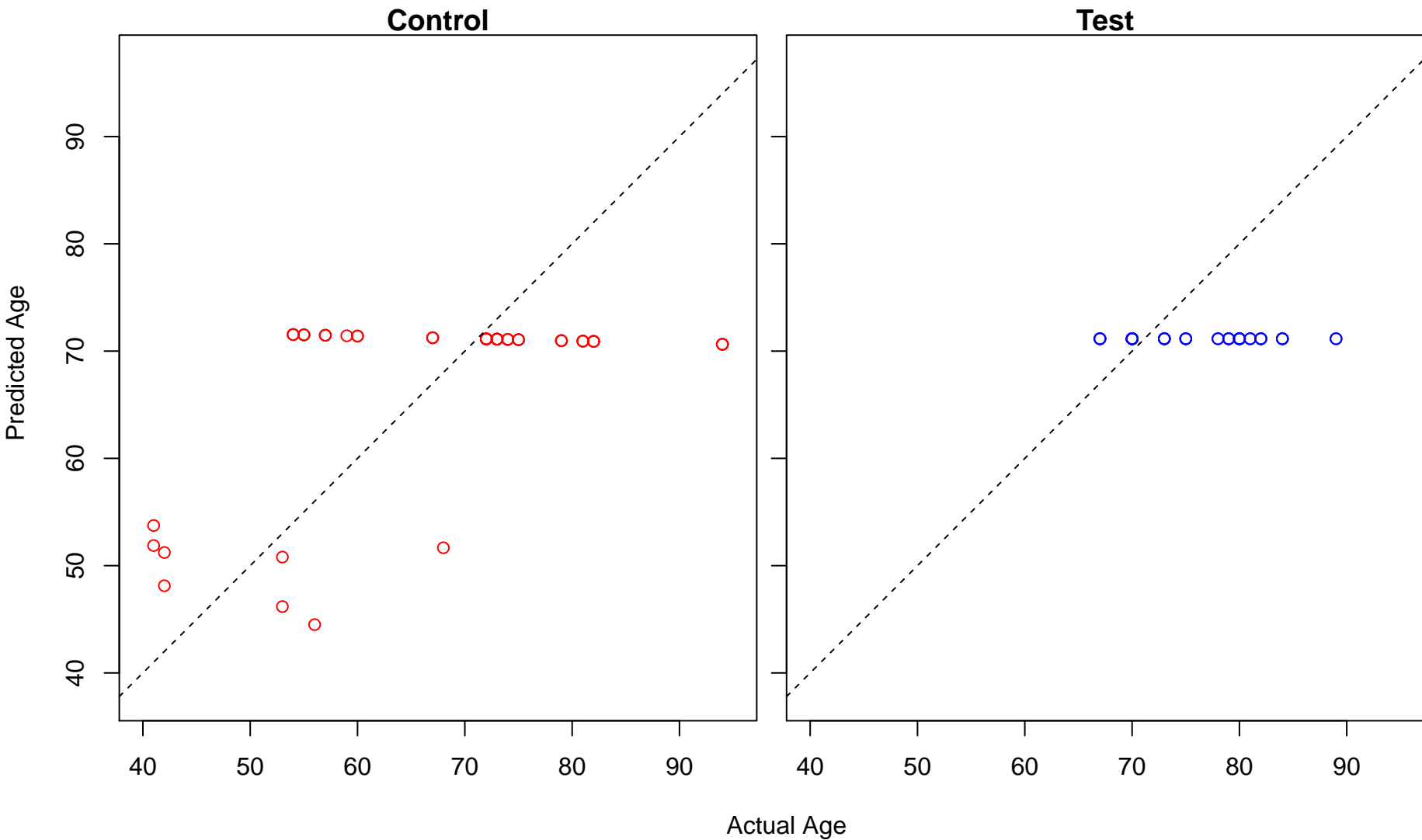
regulation of localization (Score: 0.801049)



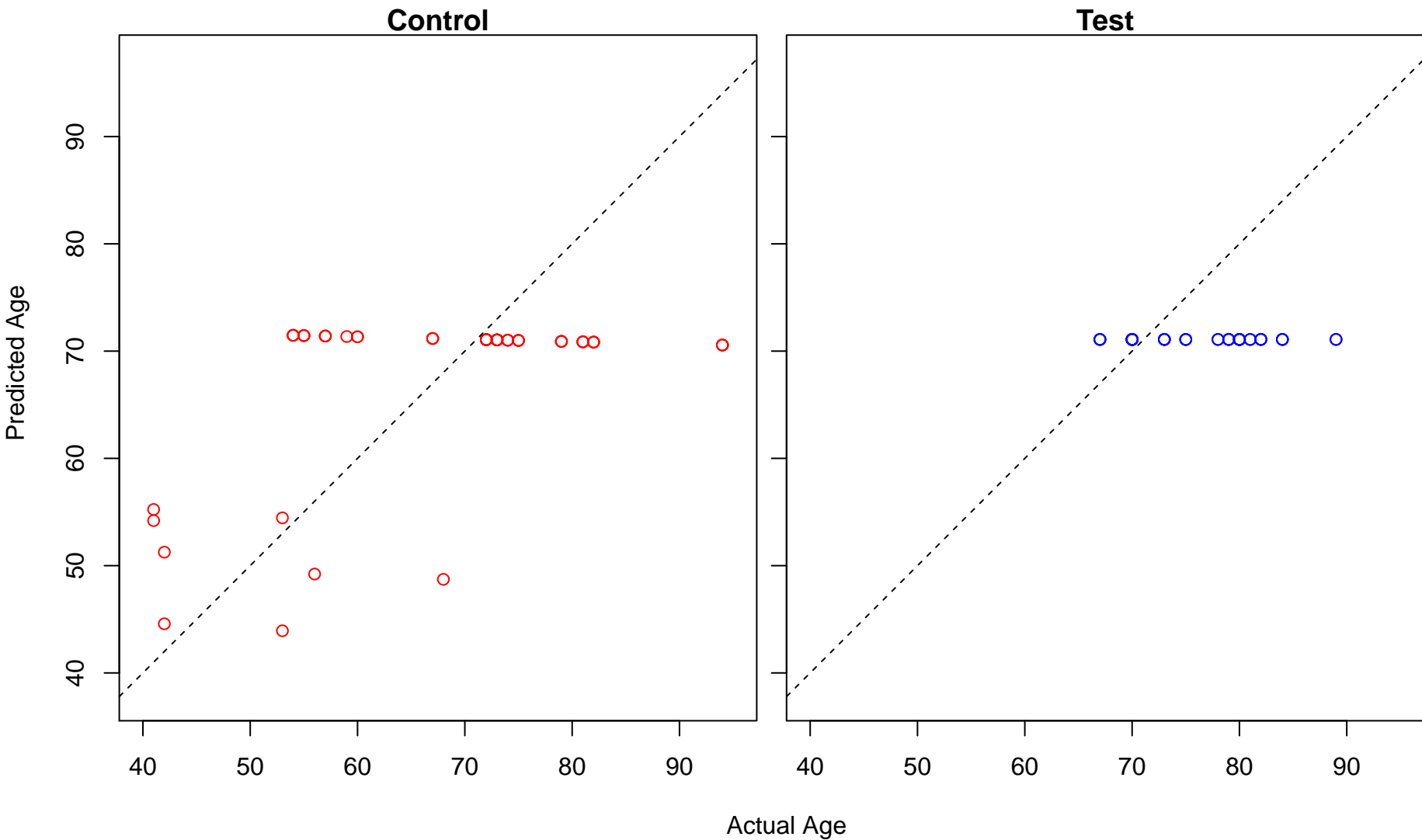
cellular process (Score: 0.801044)



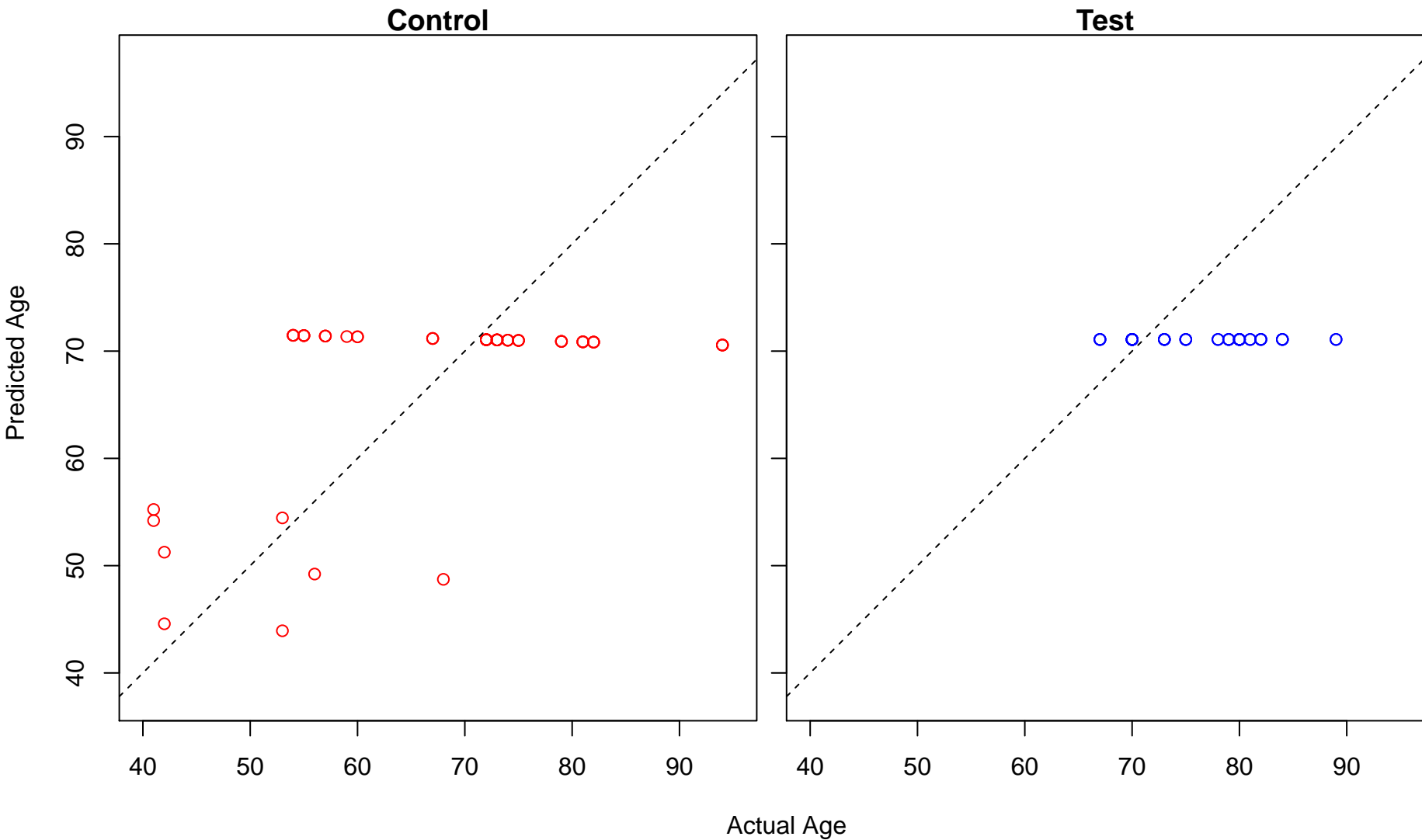
negative regulation of cellular process (Score: 0.801027)



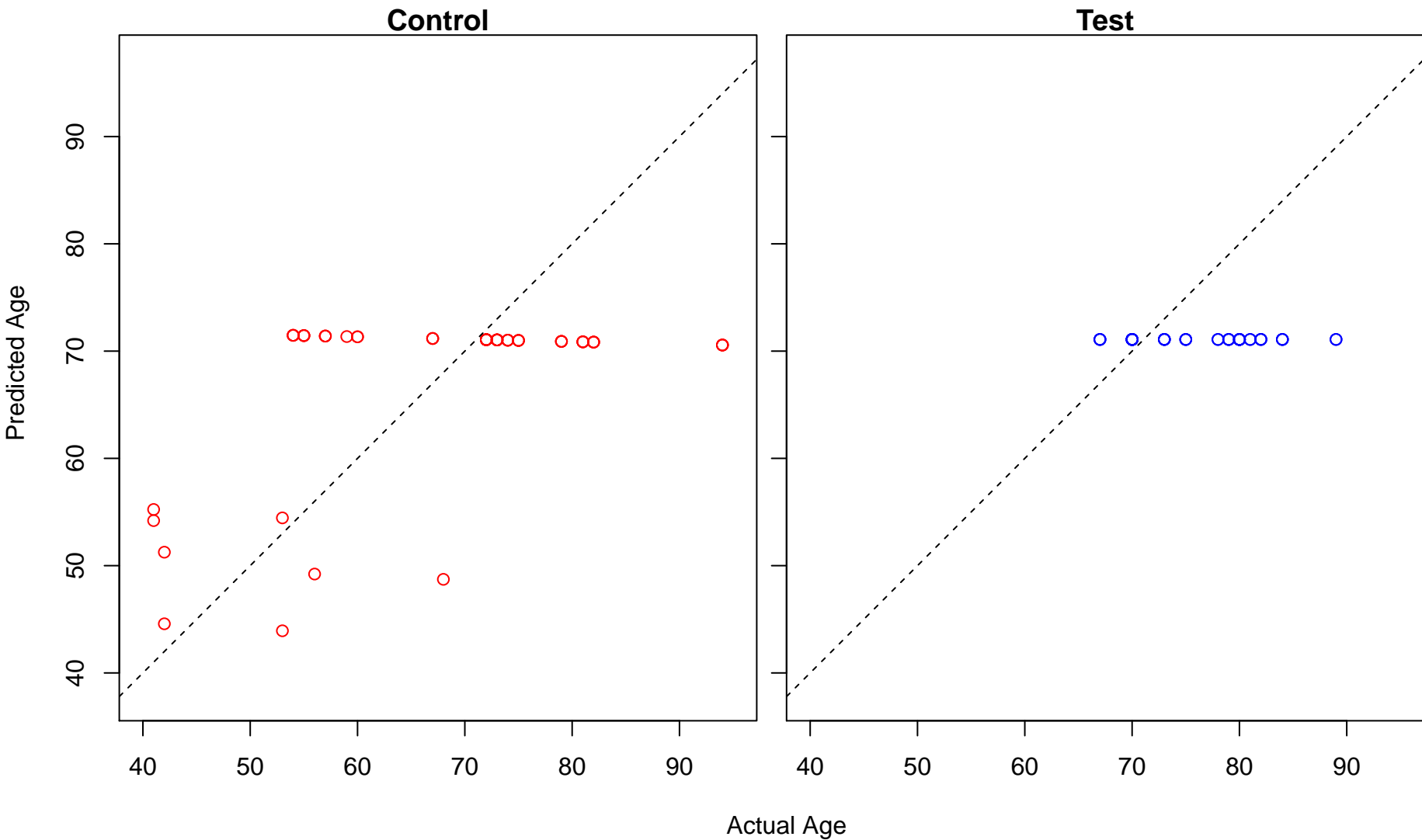
regulation of stress-activated MAPK cascade (Score: 0.800934)



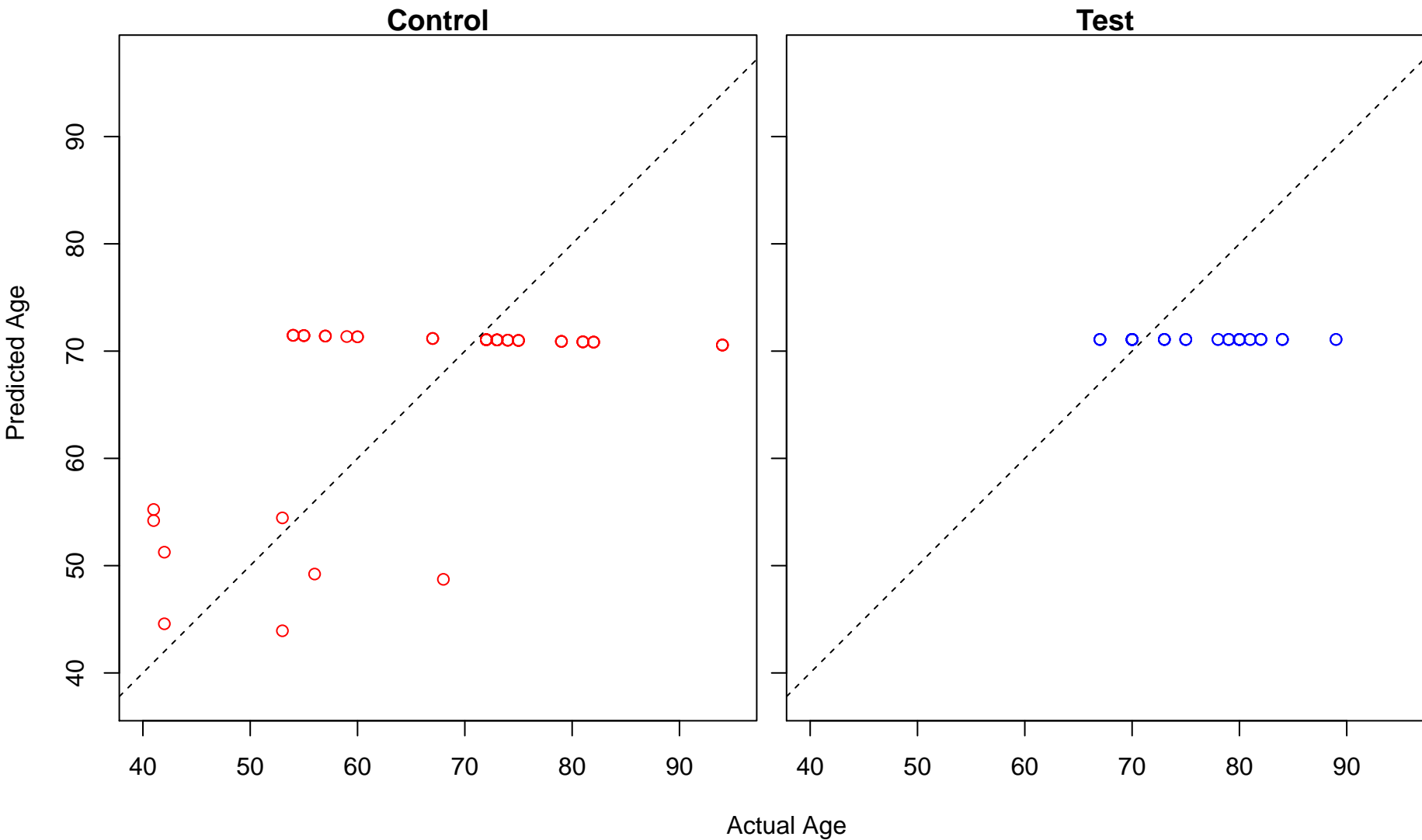
positive regulation of stress-activated MAPK cascade (Score: 0.800934)



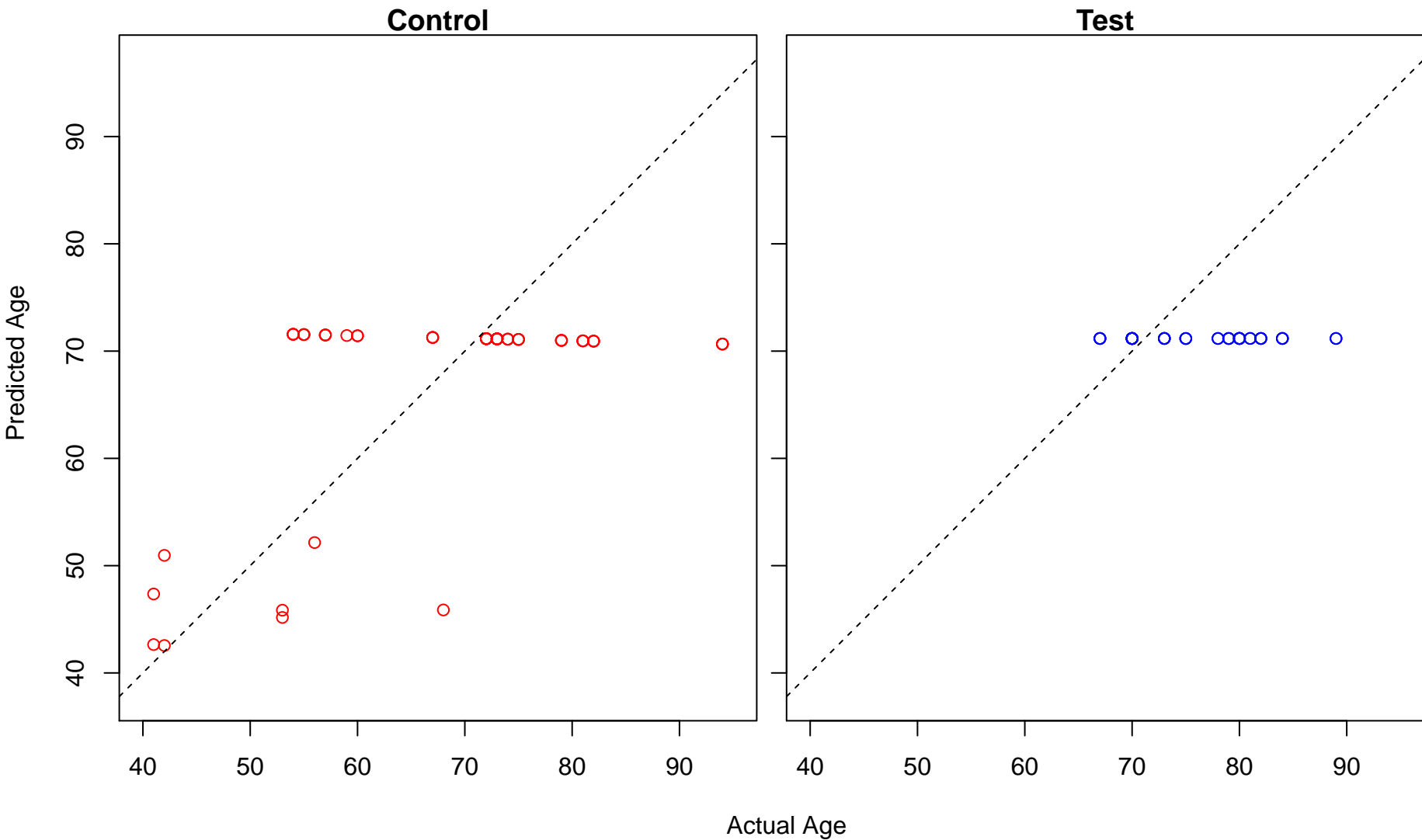
regulation of stress-activated protein kinase signaling cascade (Score: 0.800934)



positive regulation of stress-activated protein kinase signaling cascade (Score: 0.800934)

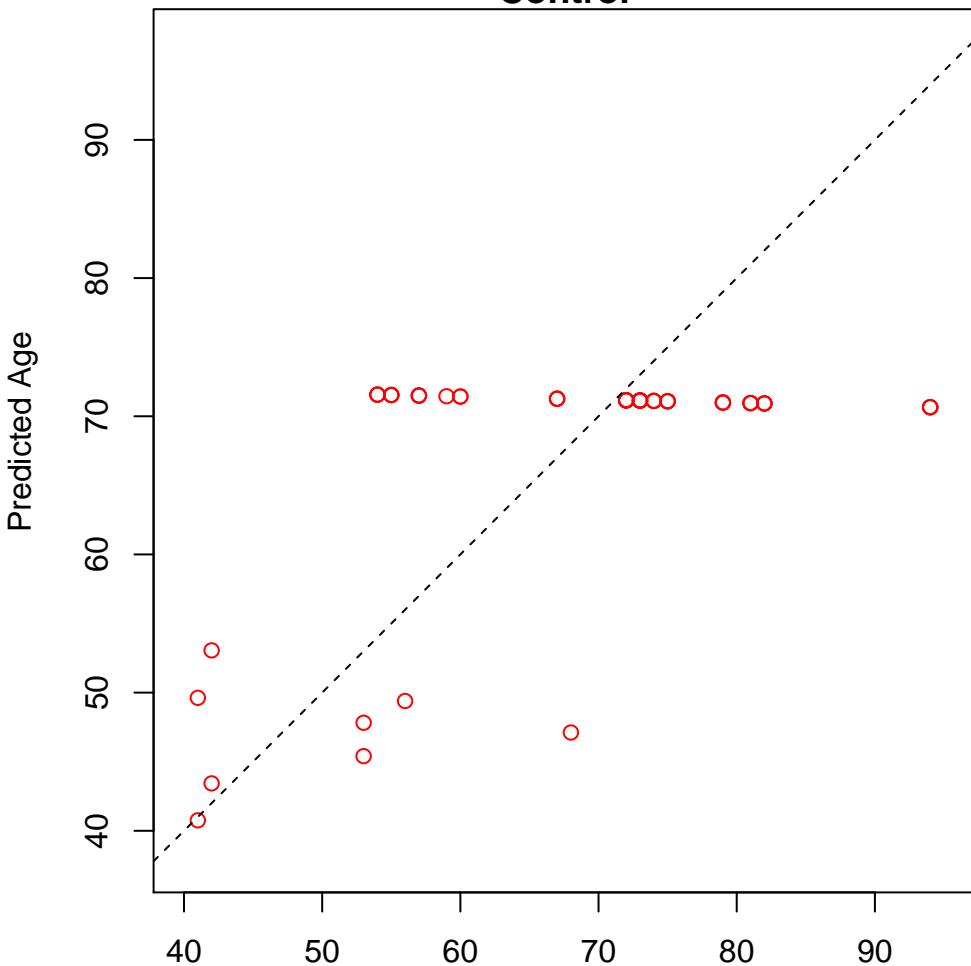


regulation of intracellular signal transduction (Score: 0.800932)

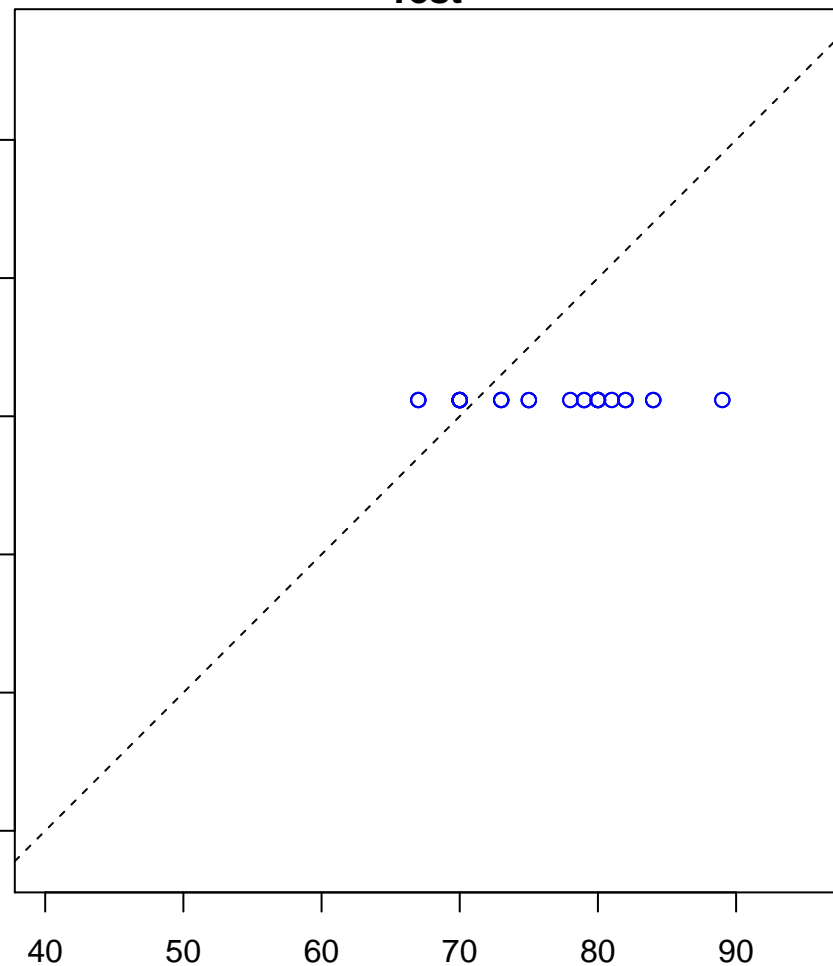


positive regulation of metabolic process (Score: 0.800927)

Control



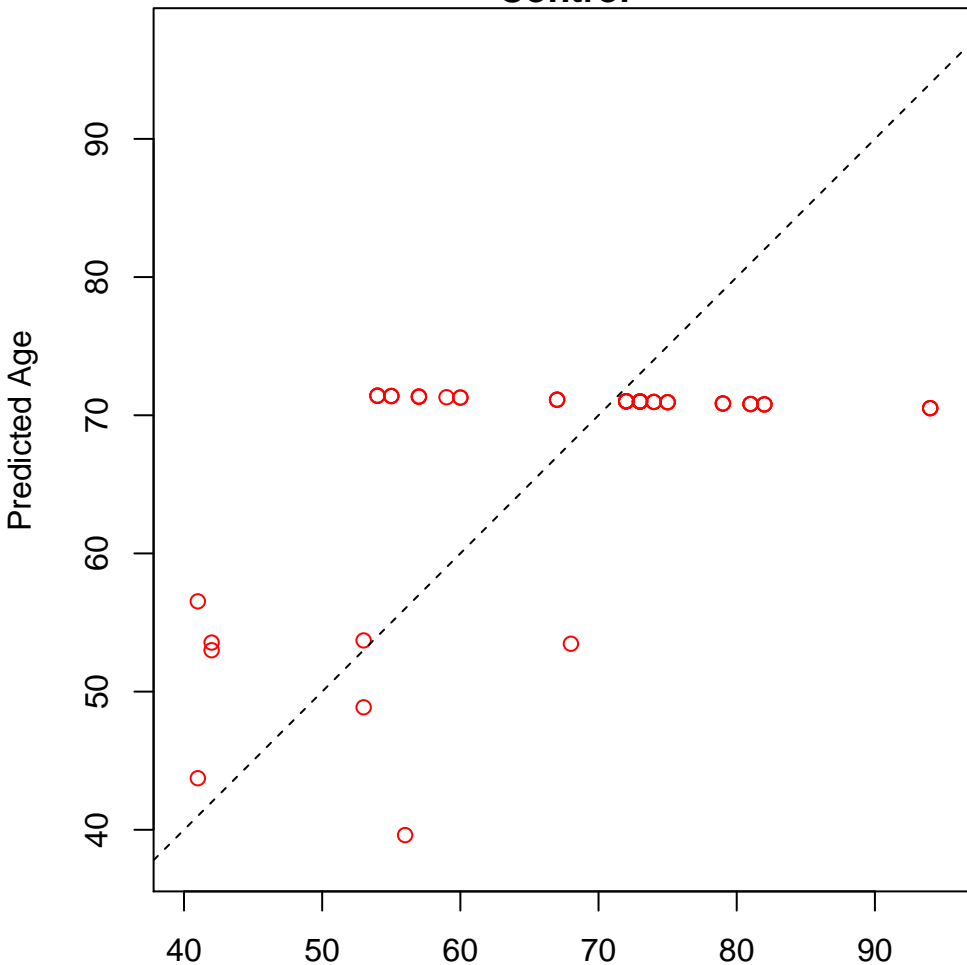
Test



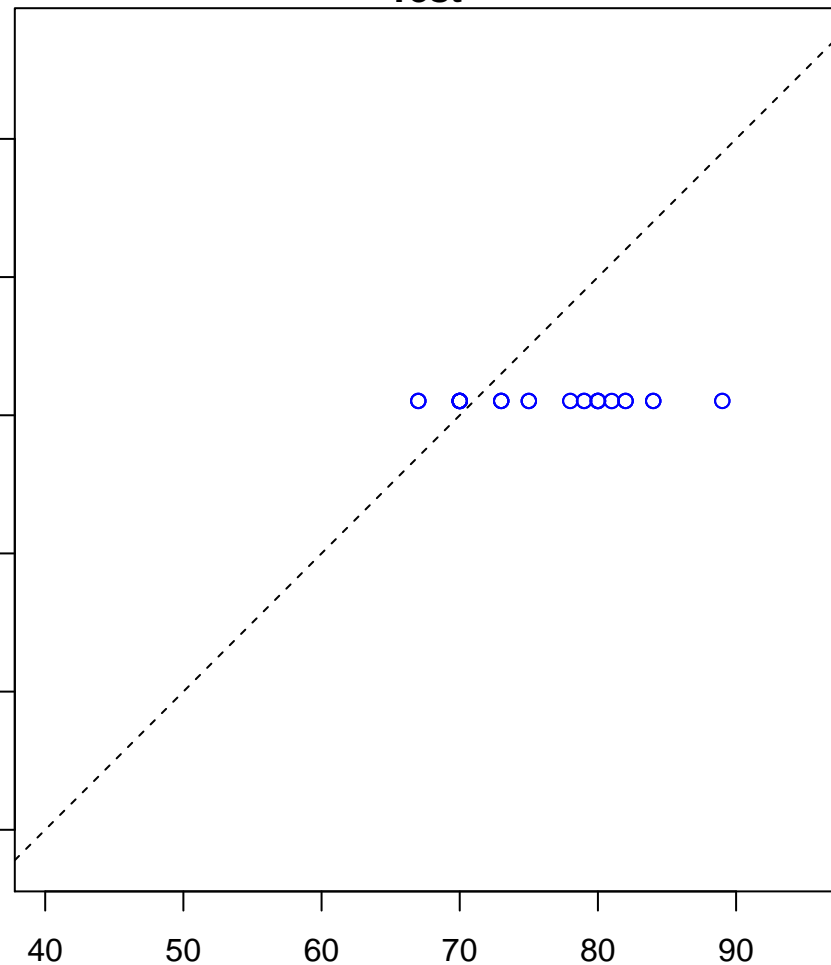
Actual Age

myeloid leukocyte differentiation (Score: 0.800725)

Control

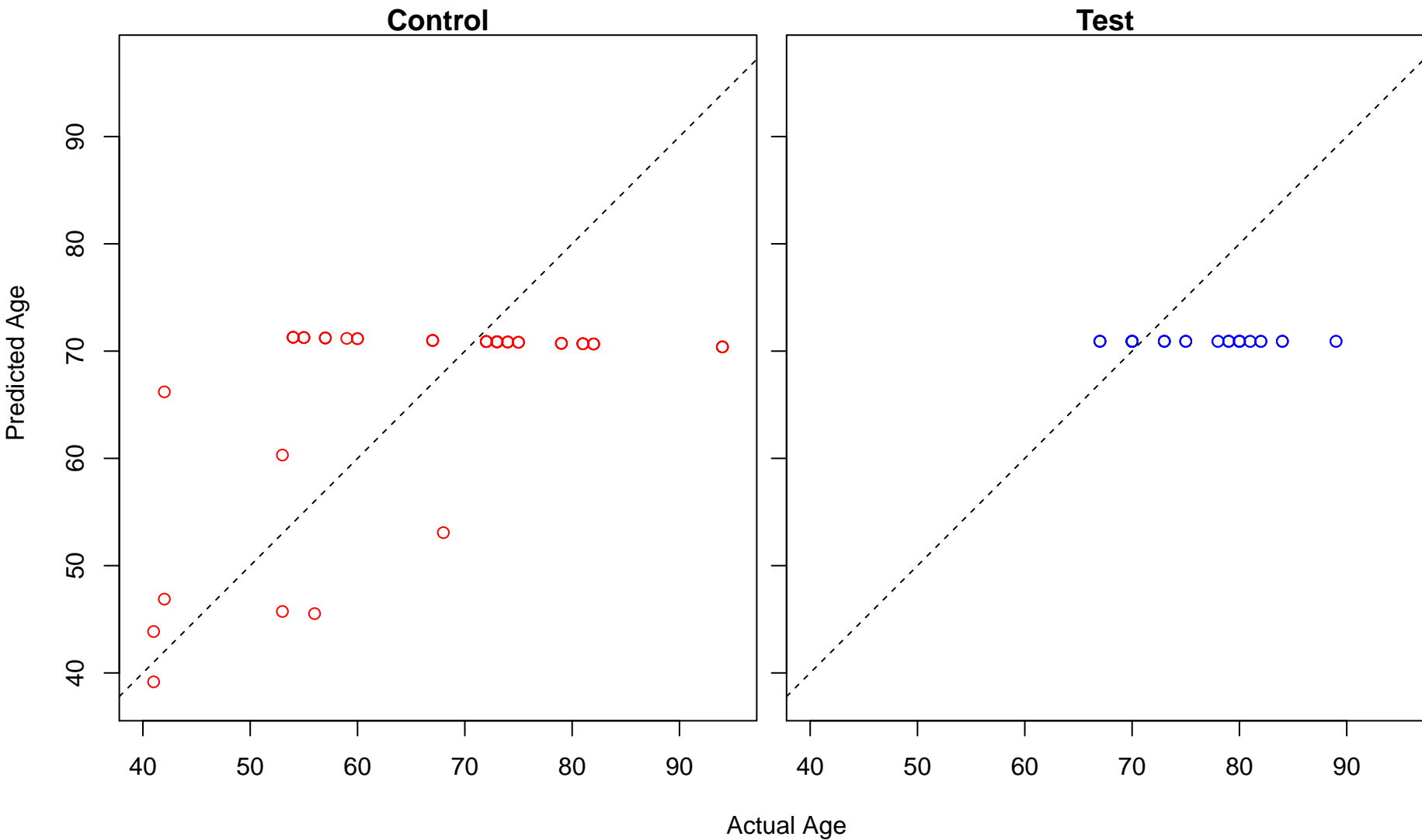


Test

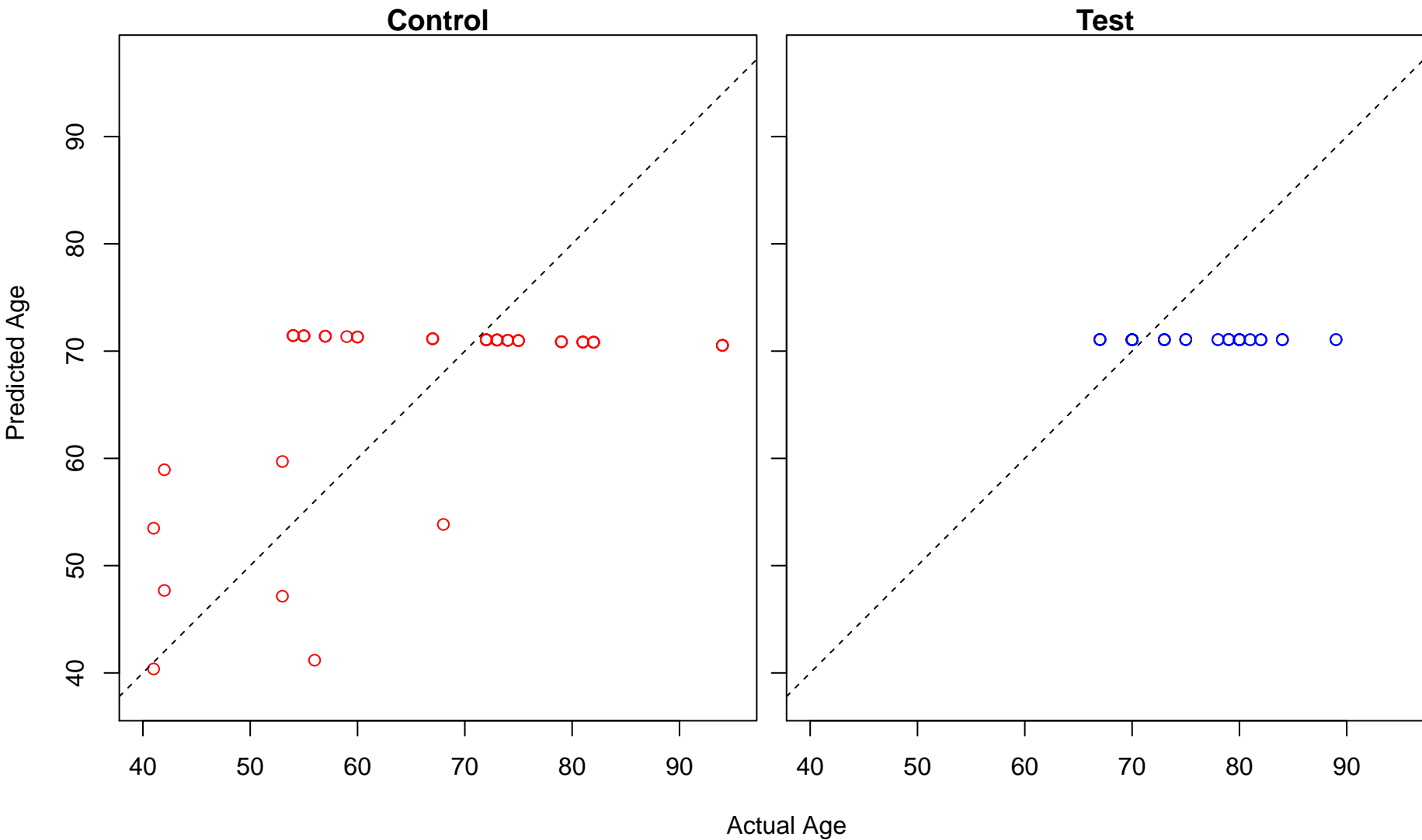


Actual Age

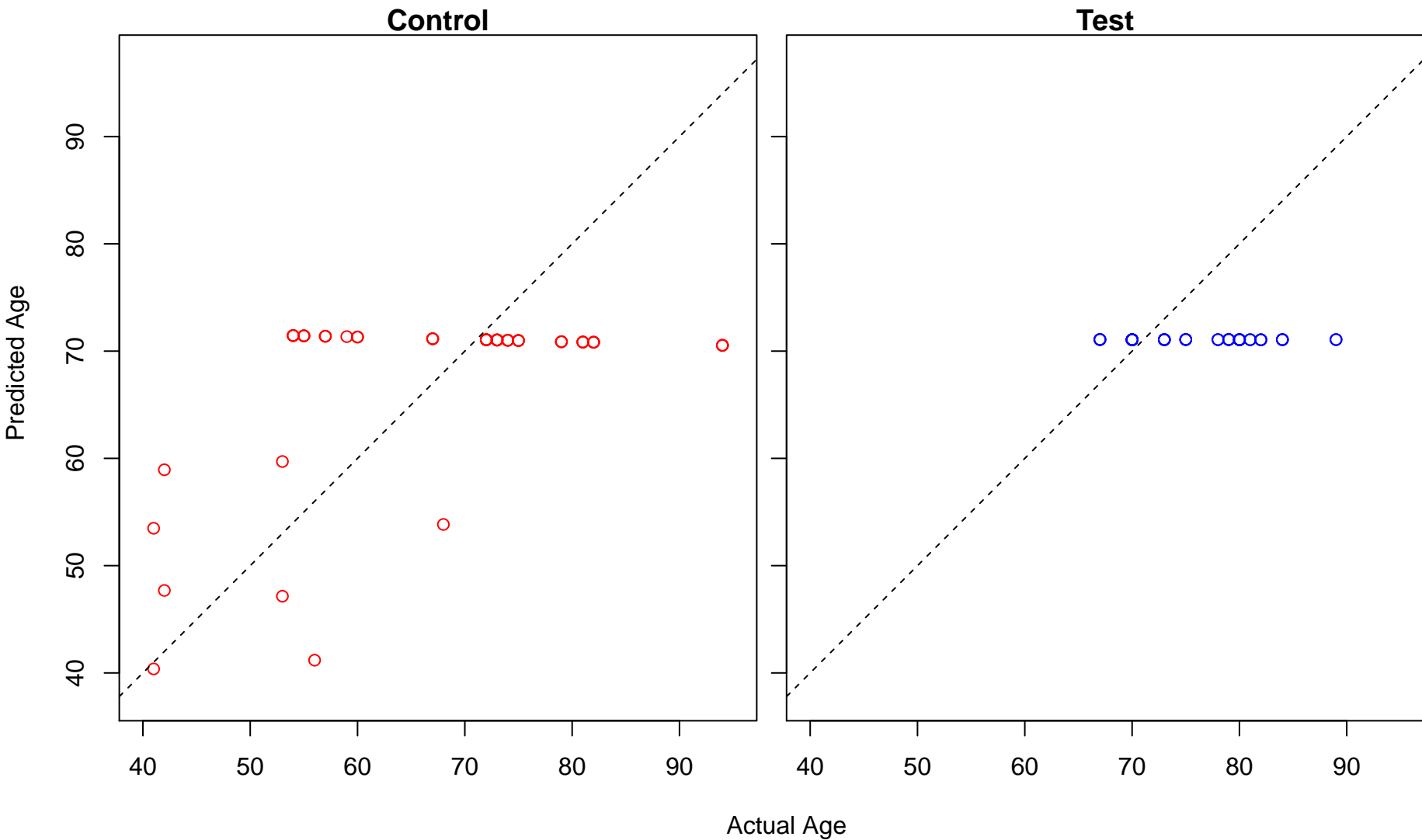
phagocytosis (Score: 0.800705)



negative regulation of protein polymerization (Score: 0.800699)

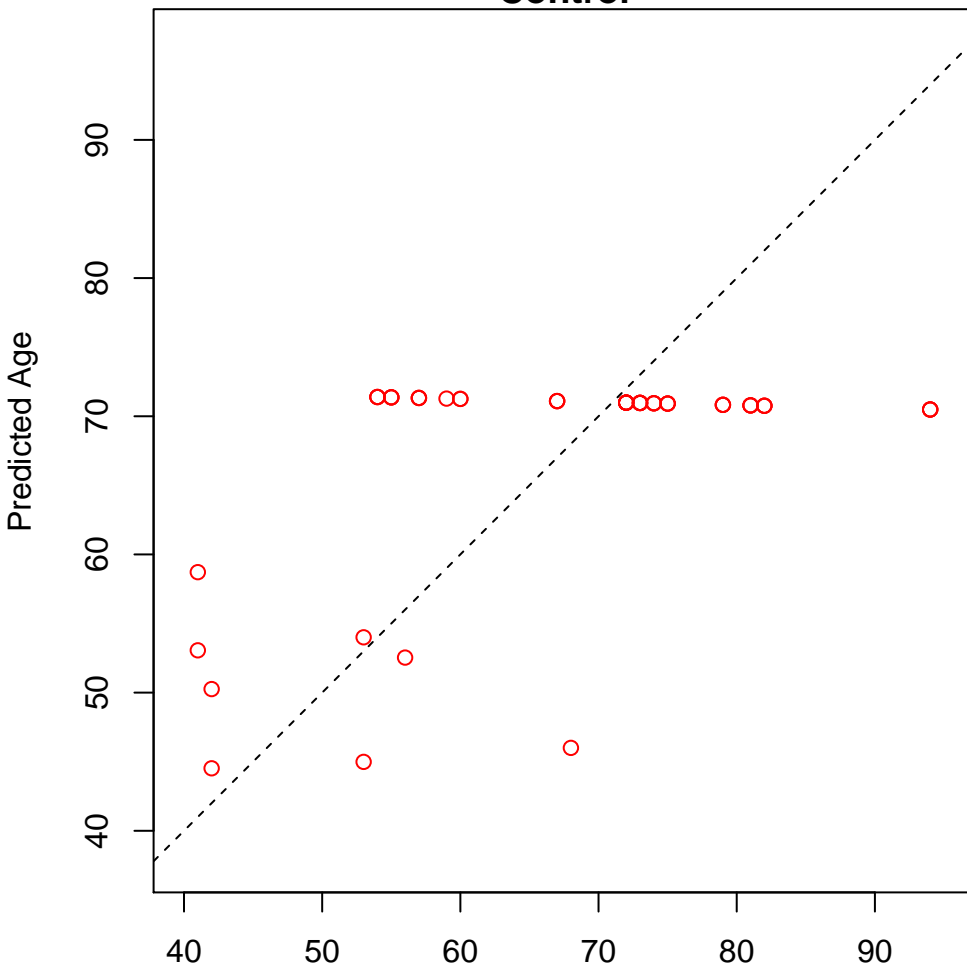


negative regulation of supramolecular fiber organization (Score: 0.800699)

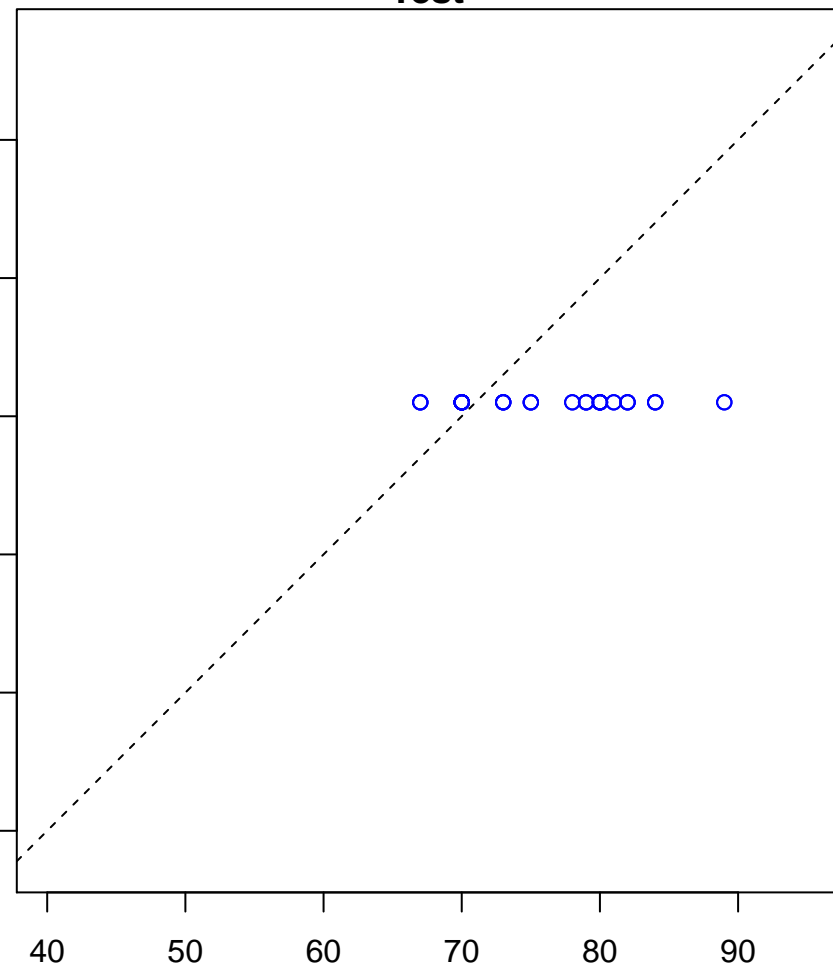


positive regulation of peptidase activity (Score: 0.800697)

Control

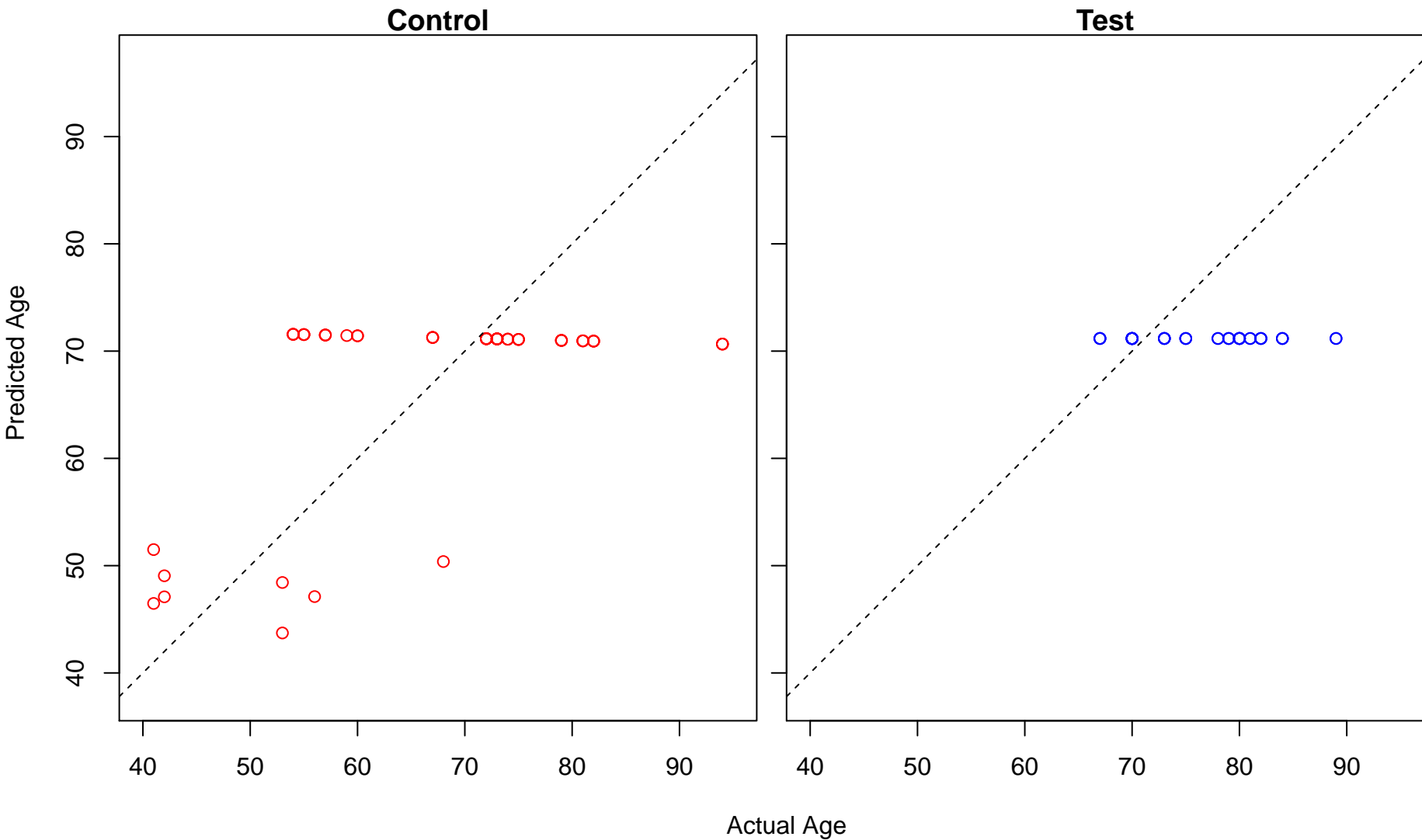


Test

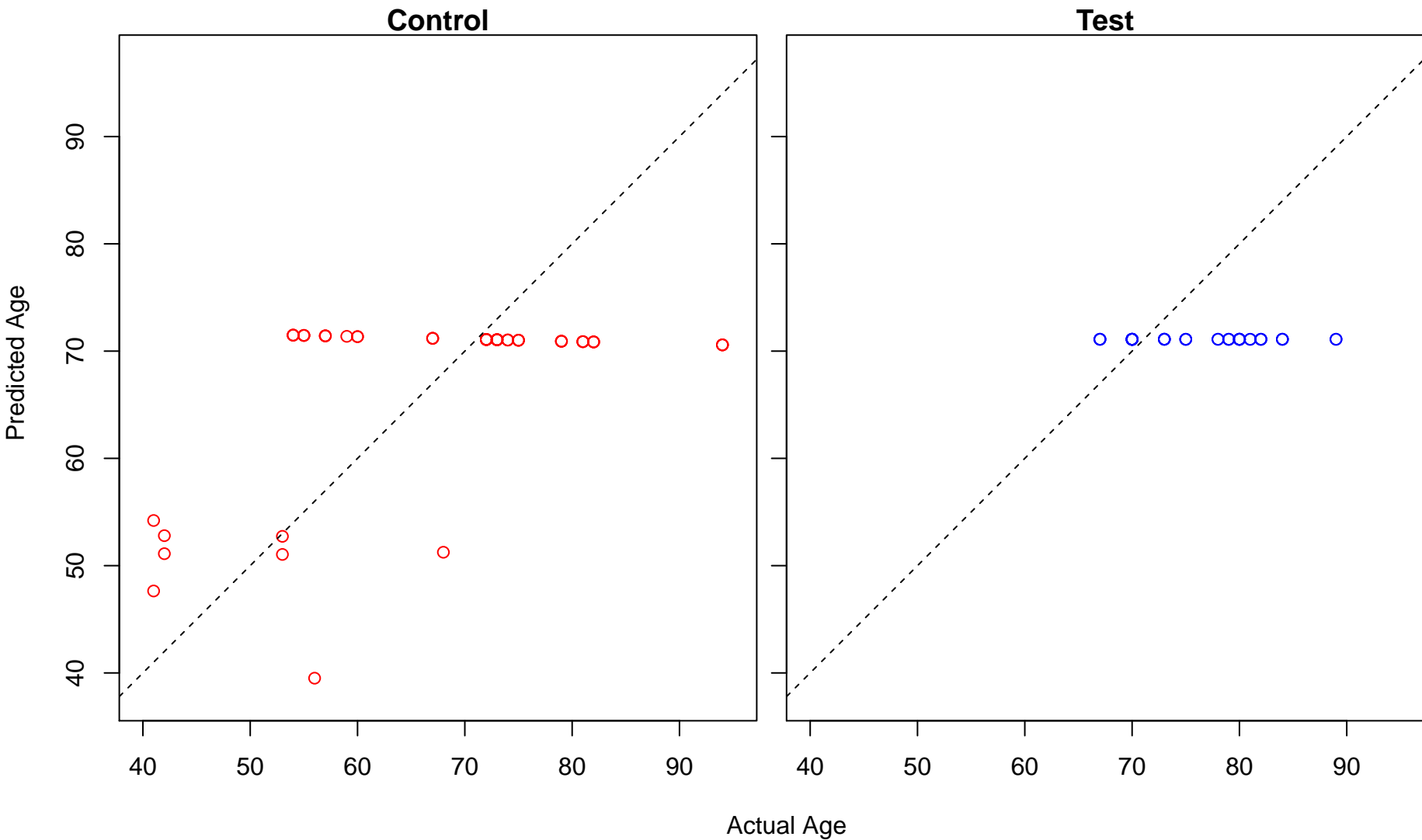


Actual Age

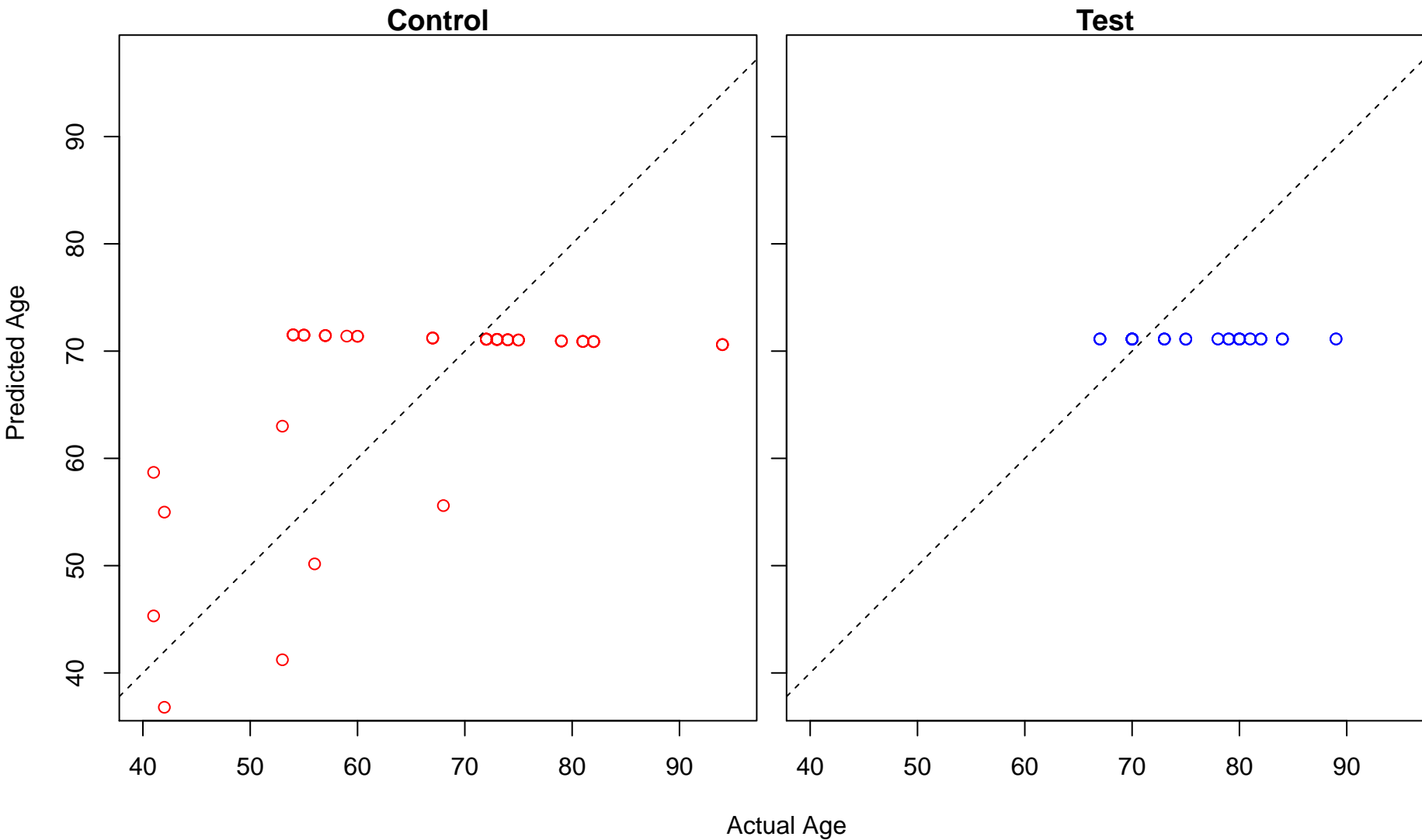
organonitrogen compound biosynthetic process (Score: 0.800675)



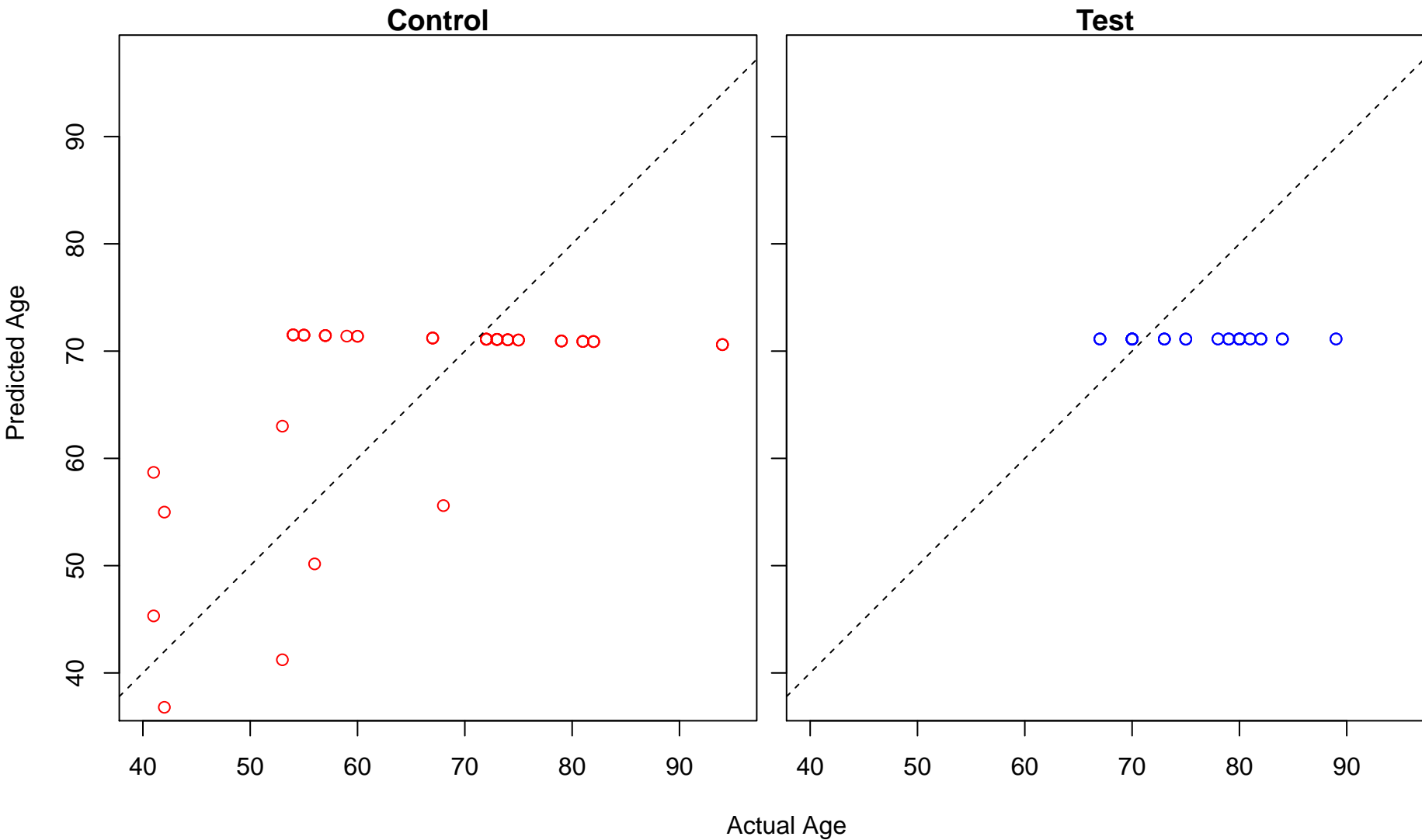
response to radiation (Score: 0.800669)



regulation of I-kappaB kinase/NF-kappaB signaling (Score: 0.800661)

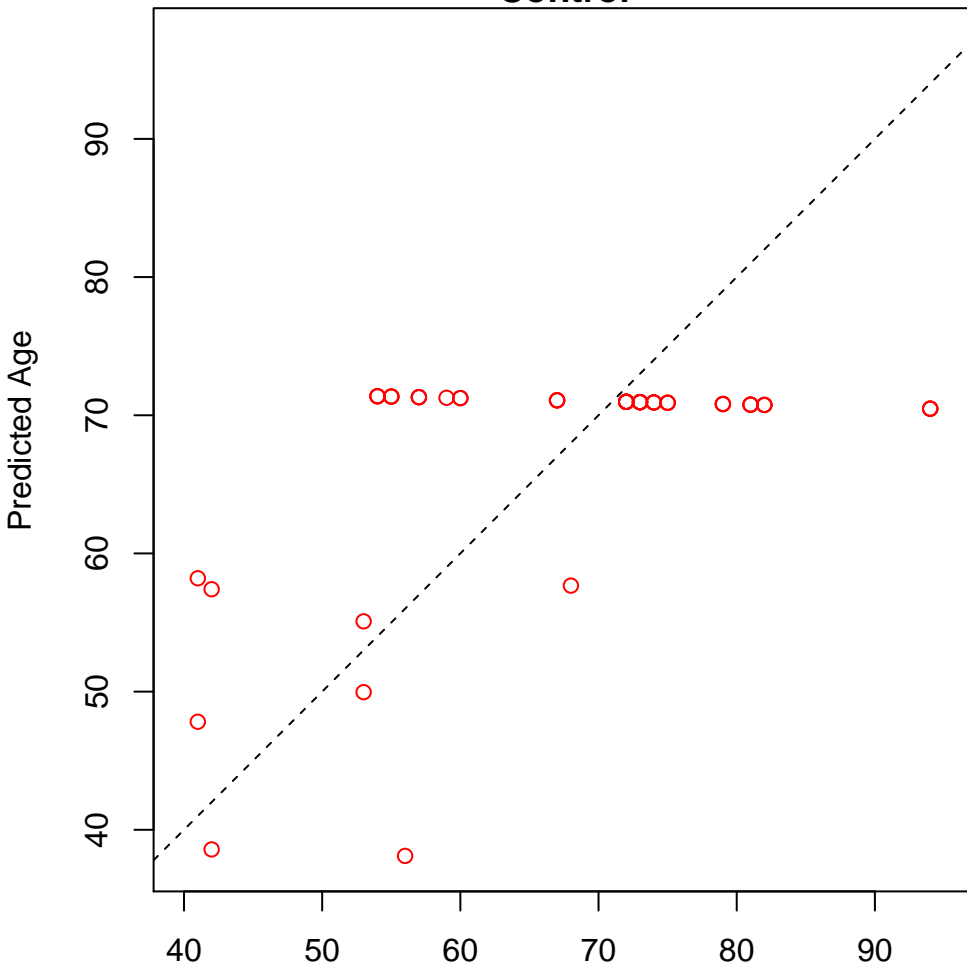


positive regulation of I-kappaB kinase/NF-kappaB signaling (Score: 0.800661)

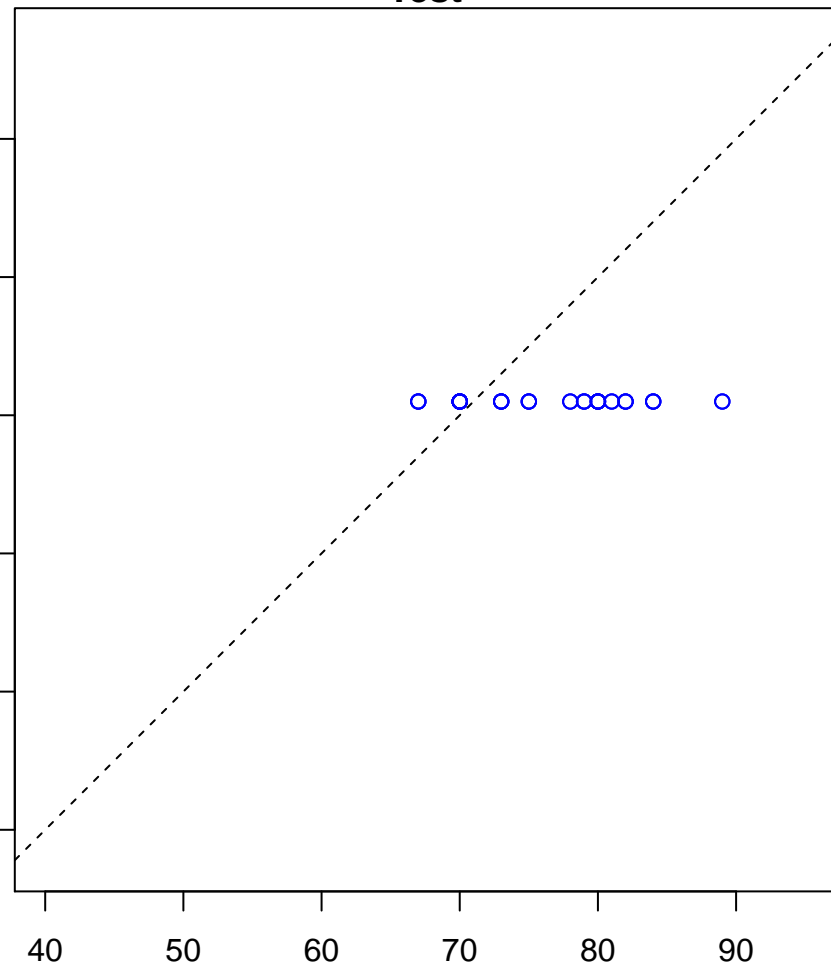


DNA conformation change (Score: 0.800653)

Control

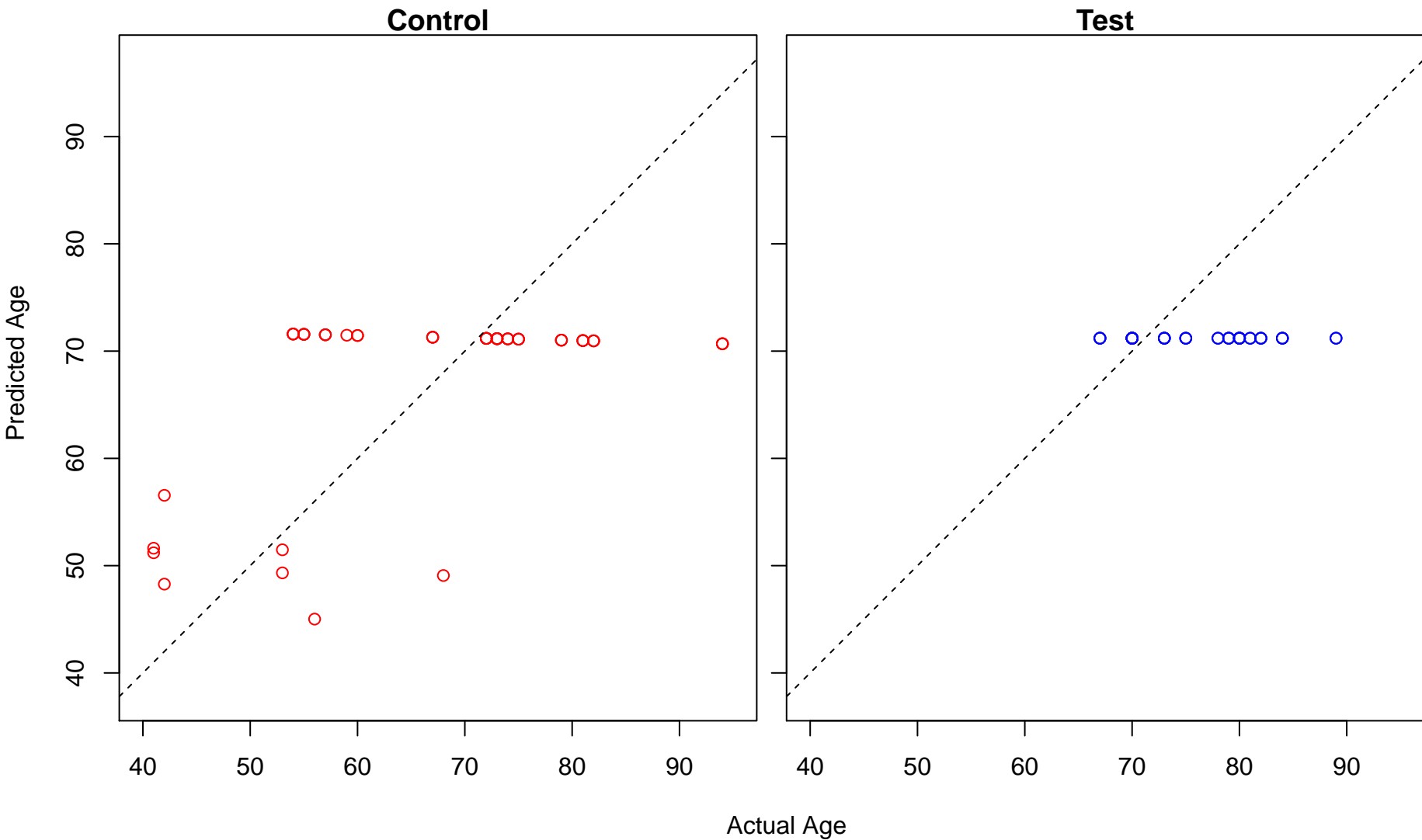


Test

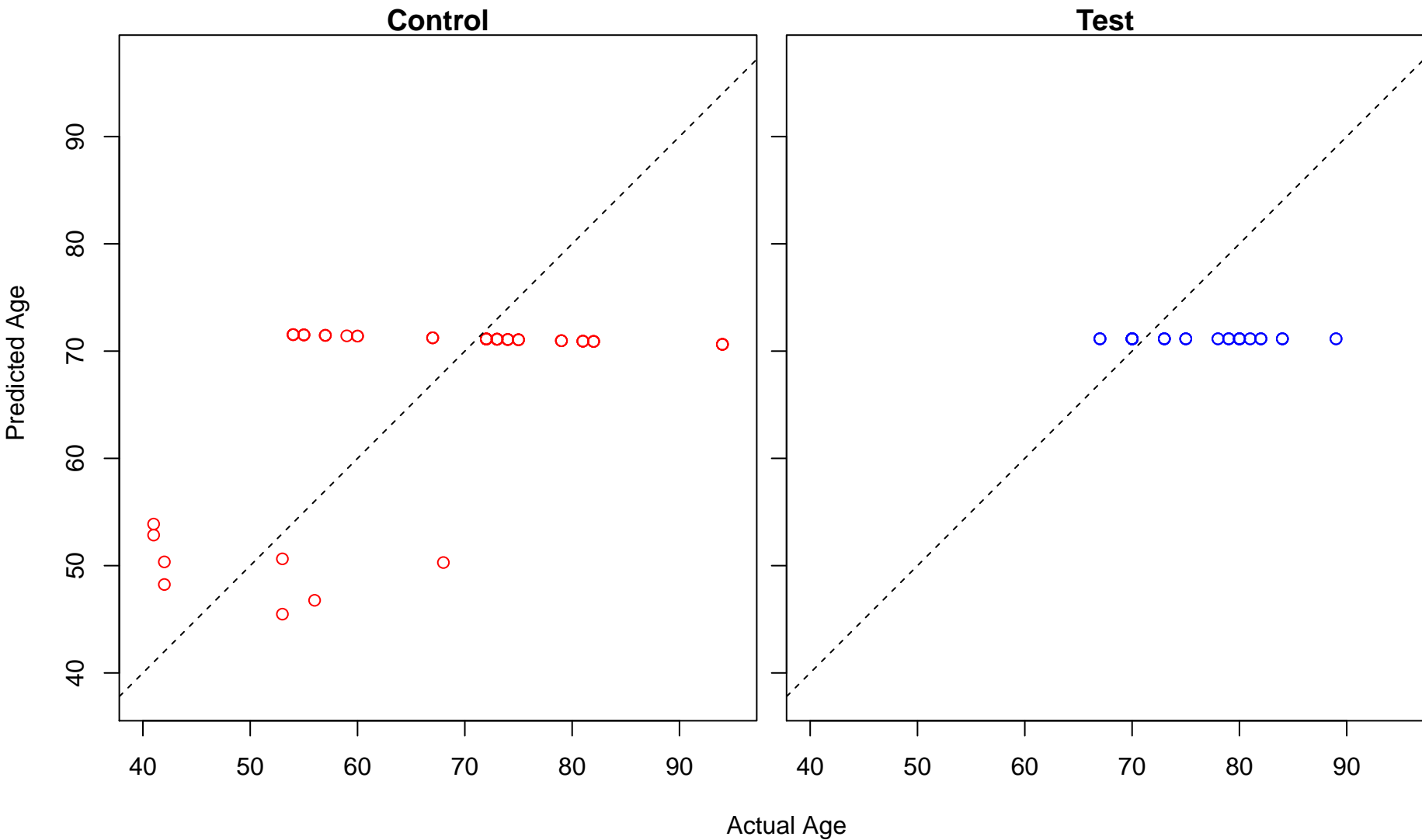


Actual Age

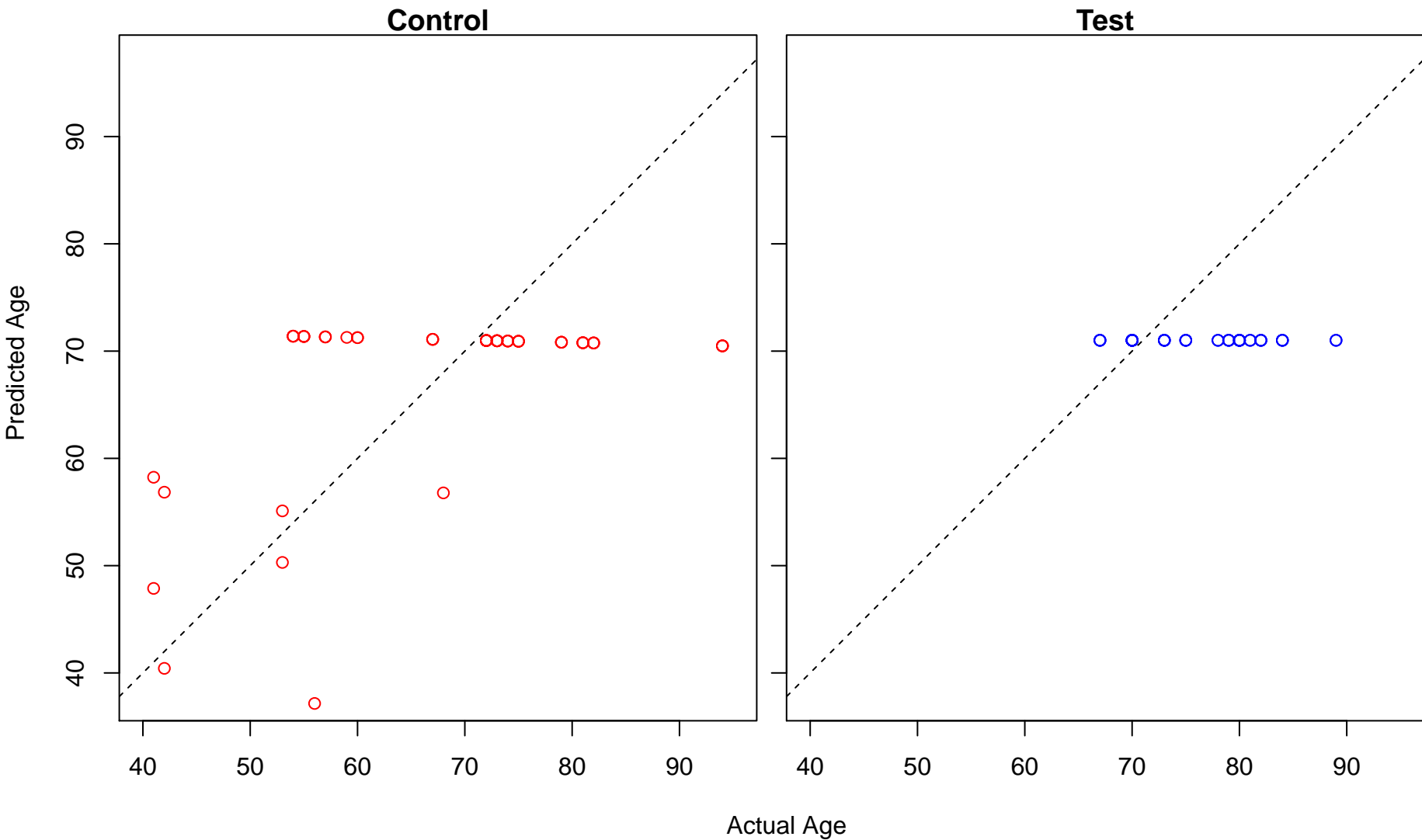
regulation of reactive oxygen species biosynthetic process (Score: 0.800643)



regulation of multicellular organismal process (Score: 0.800602)

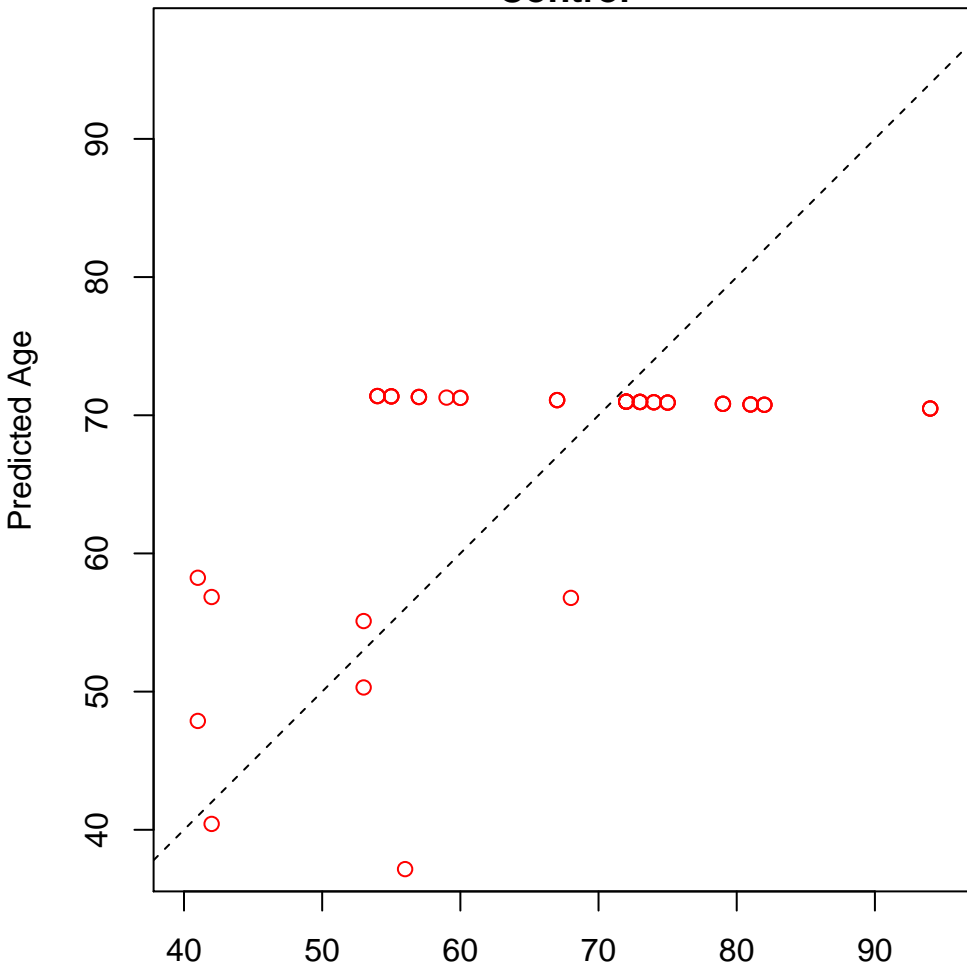


cellular response to fibroblast growth factor stimulus (Score: 0.800581)

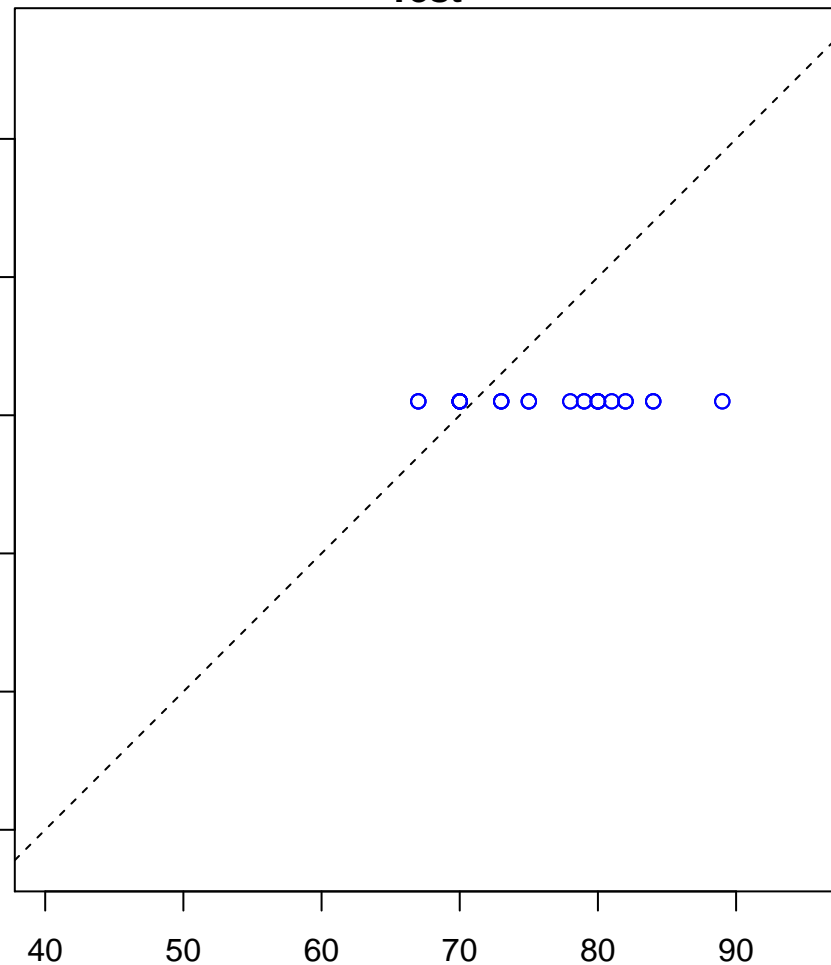


response to fibroblast growth factor (Score: 0.800581)

Control

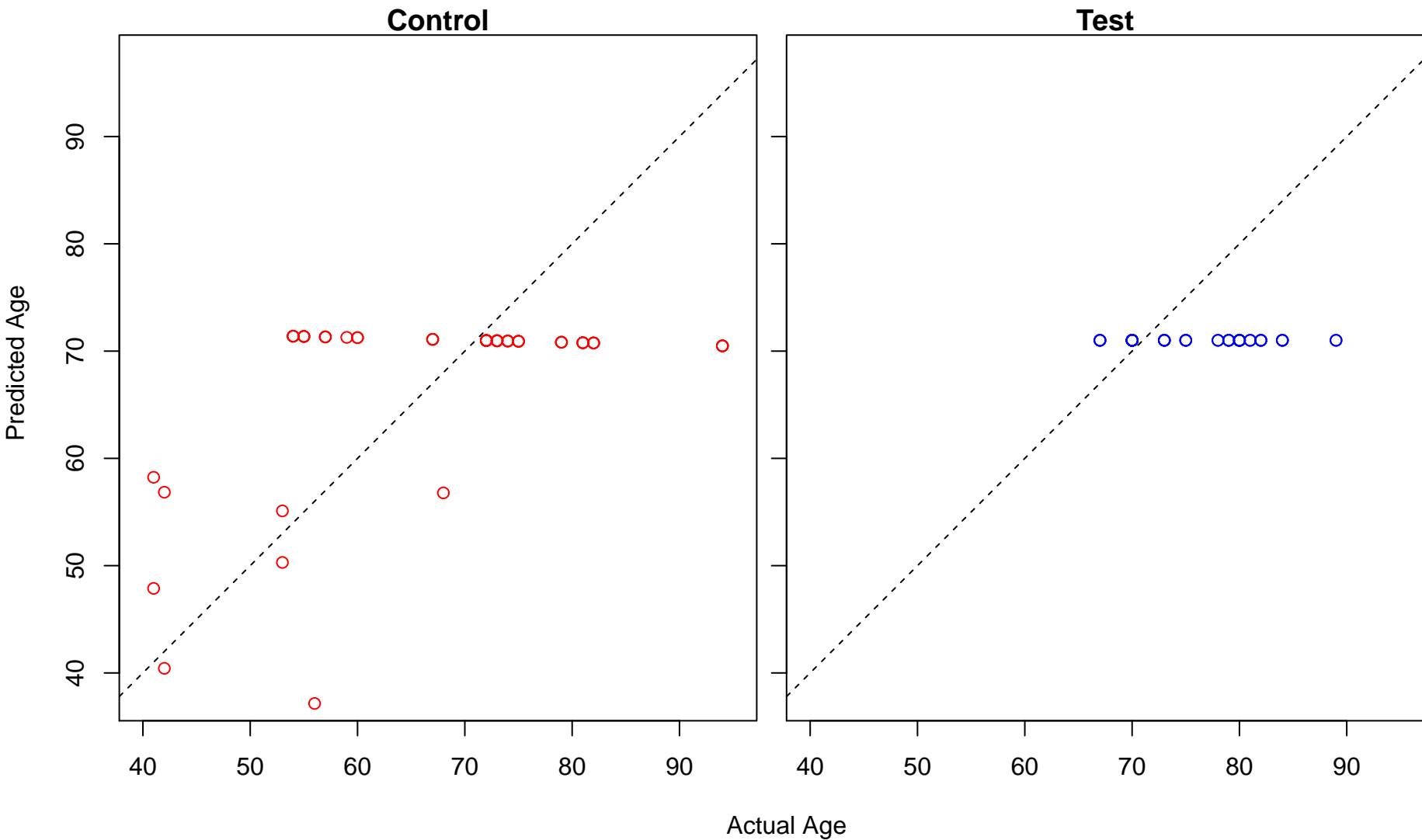


Test

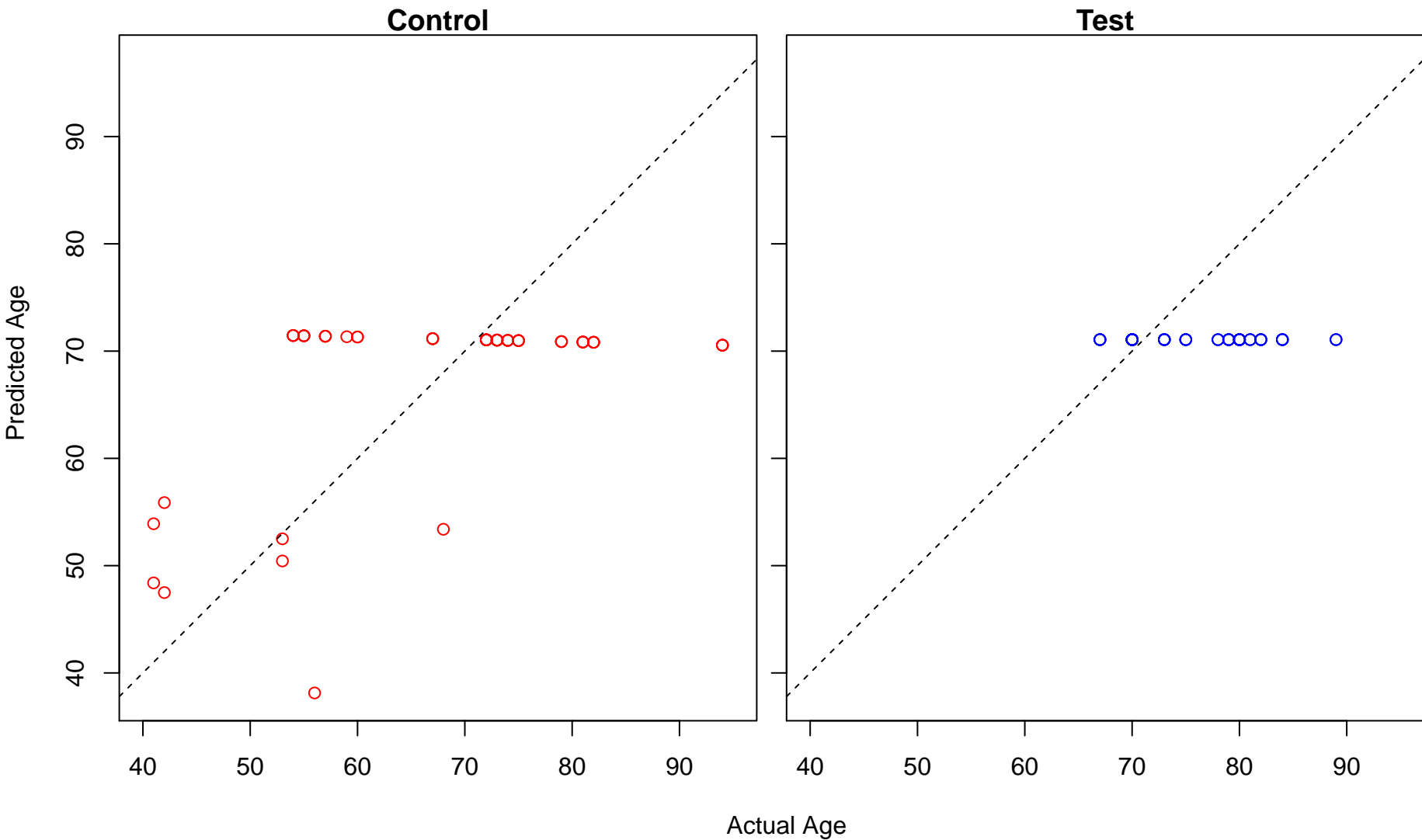


Actual Age

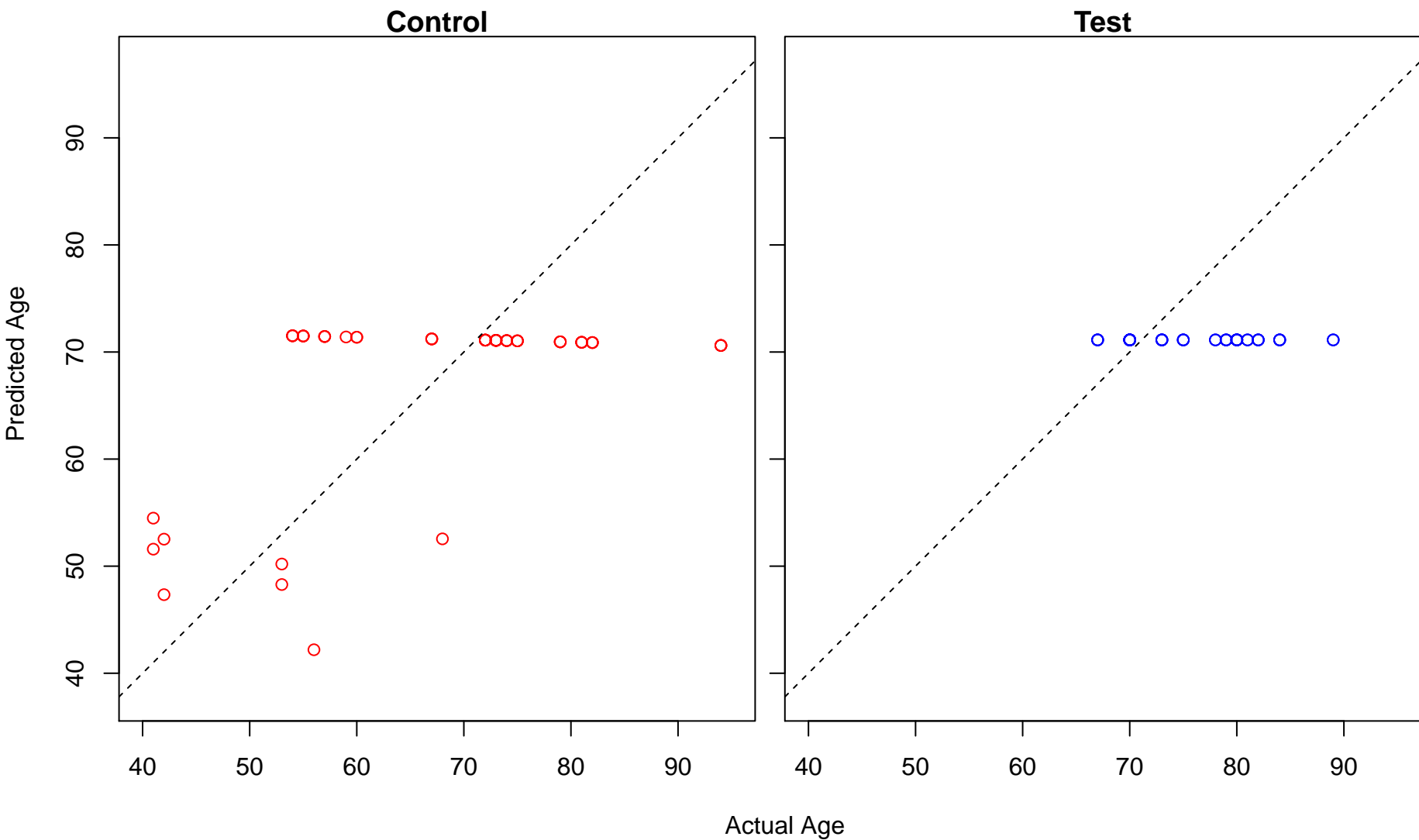
fibroblast growth factor receptor signaling pathway (Score: 0.800581)



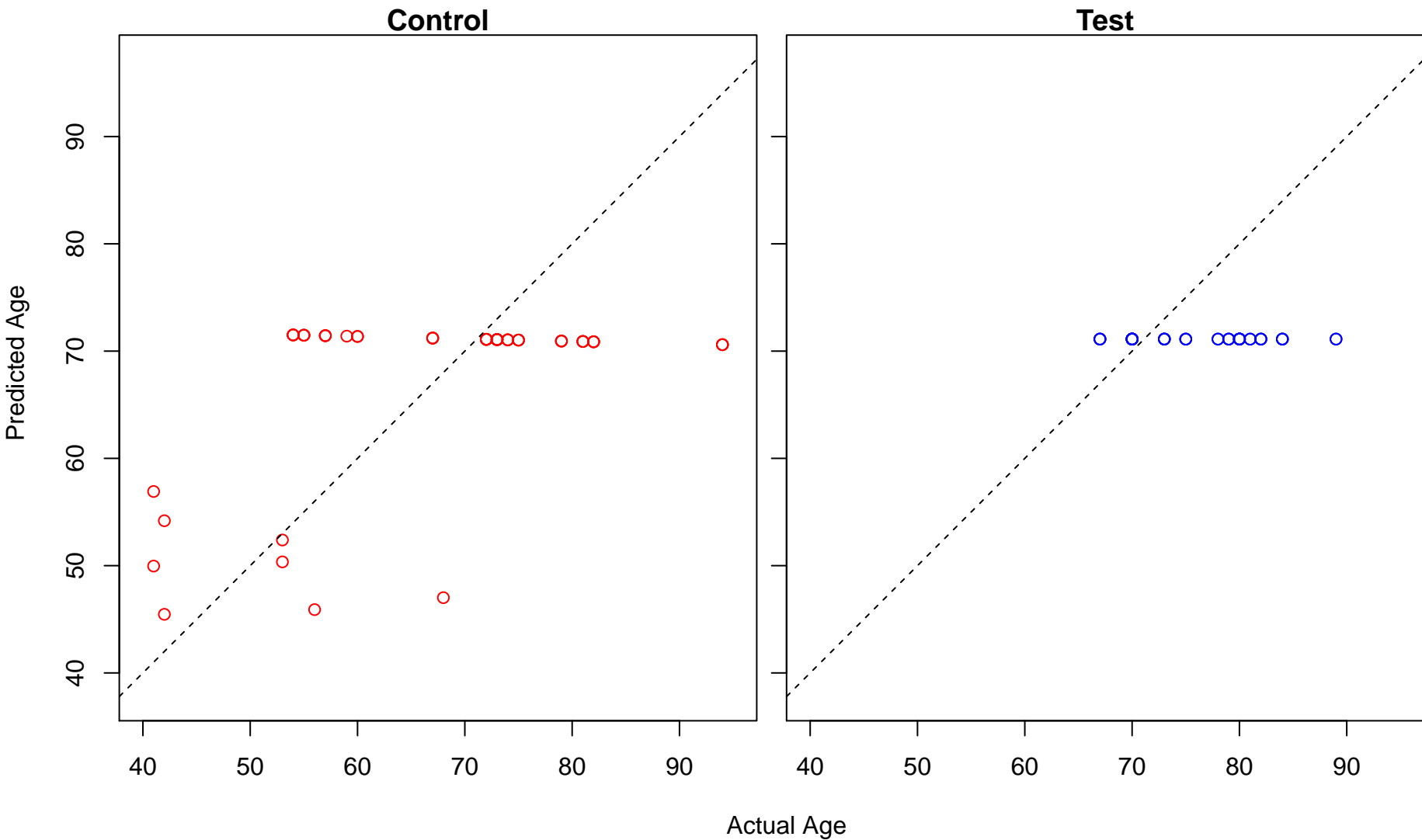
chromatin organization (Score: 0.800509)



biological regulation (Score: 0.800424)

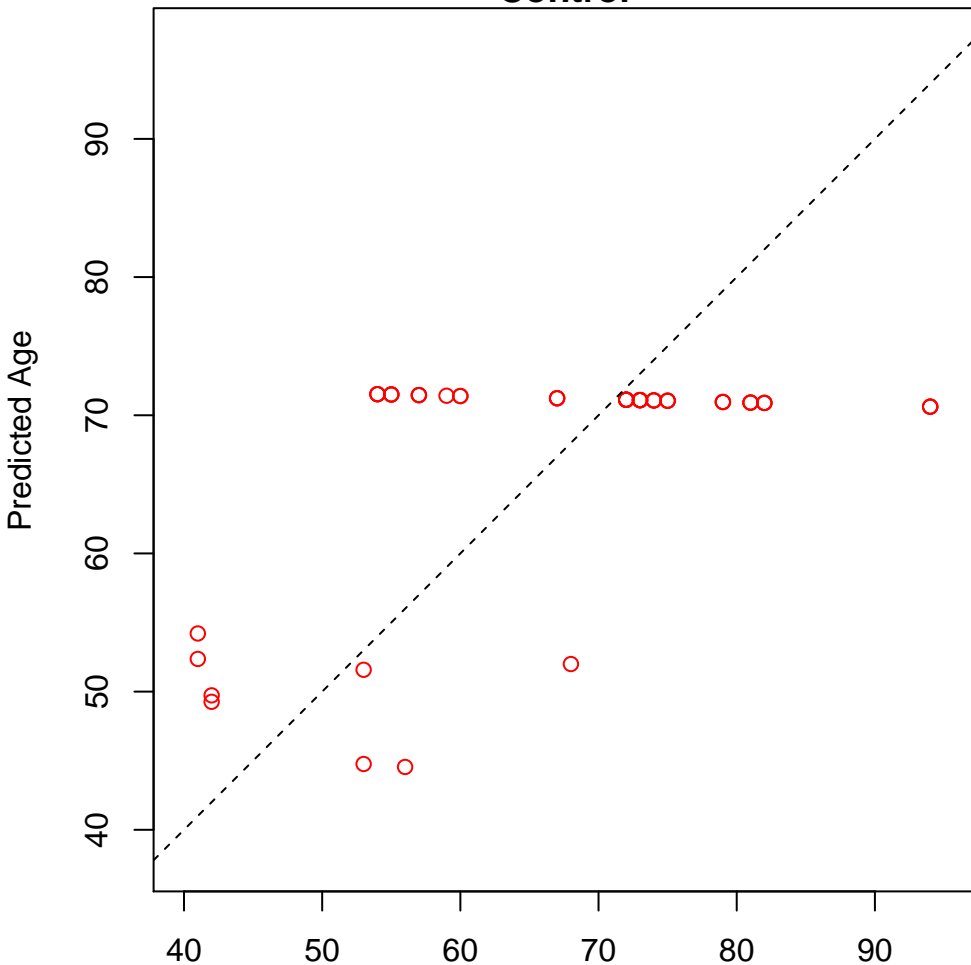


regulation of hormone levels (Score: 0.800409)

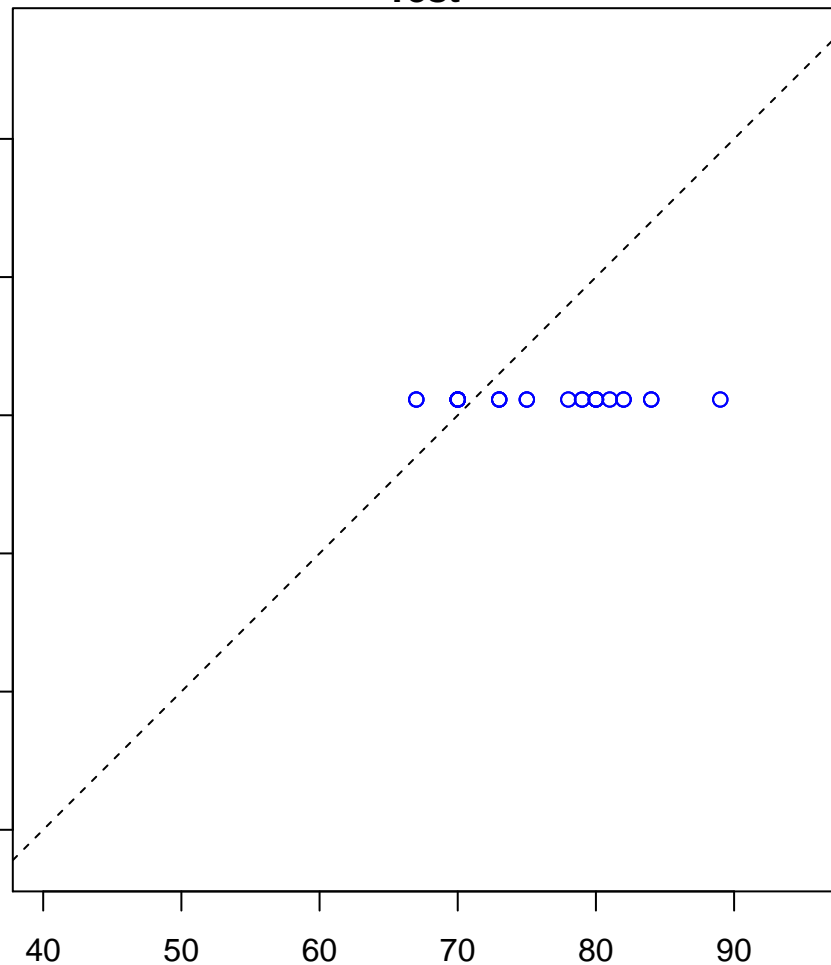


developmental process (Score: 0.800402)

Control



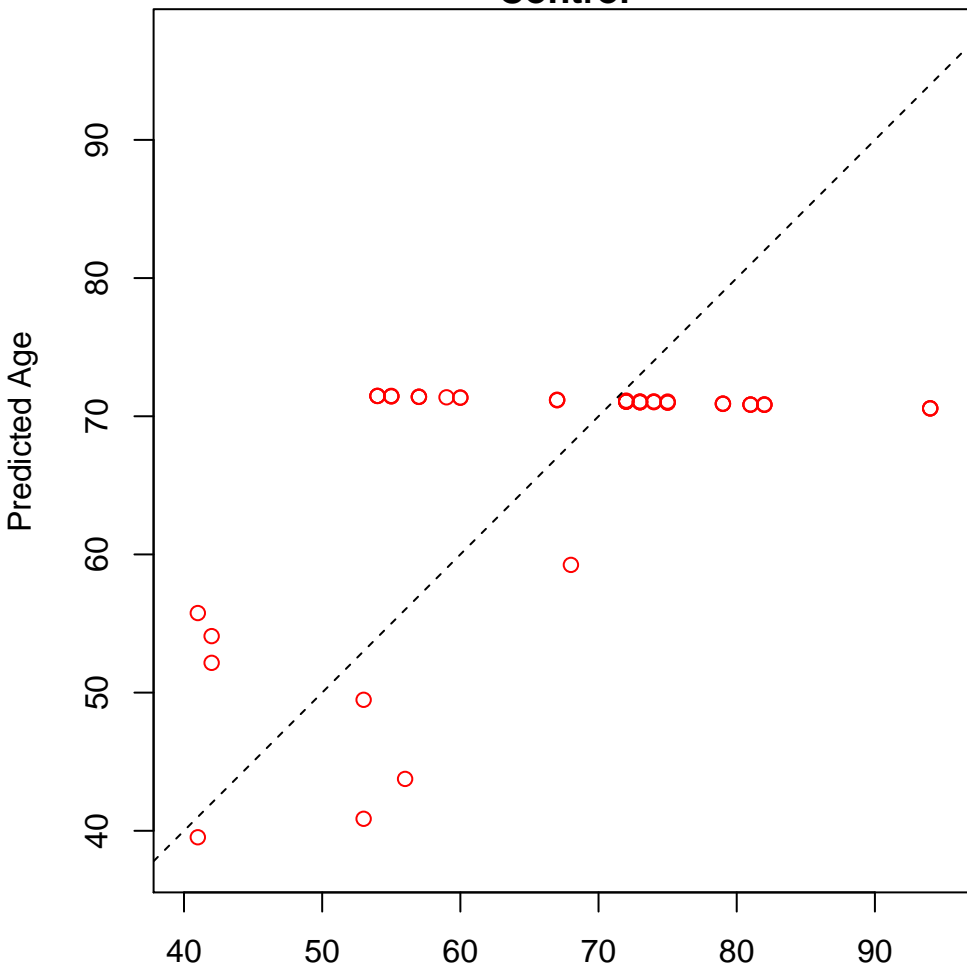
Test



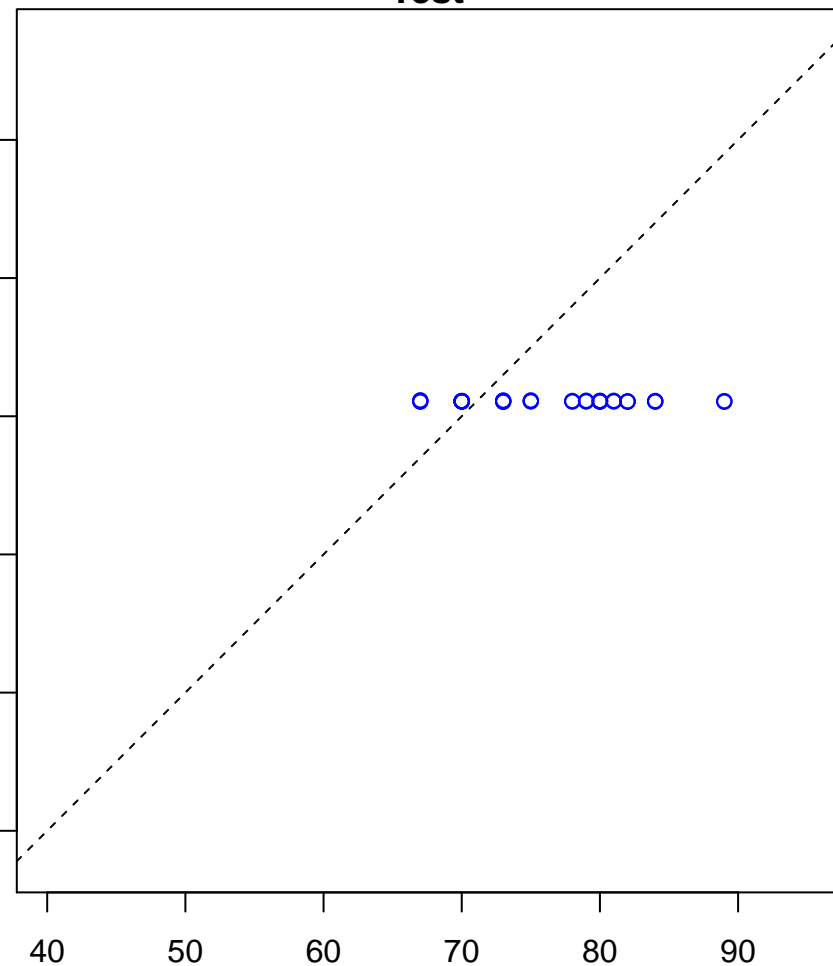
Actual Age

DNA-templated transcription, initiation (Score: 0.800386)

Control

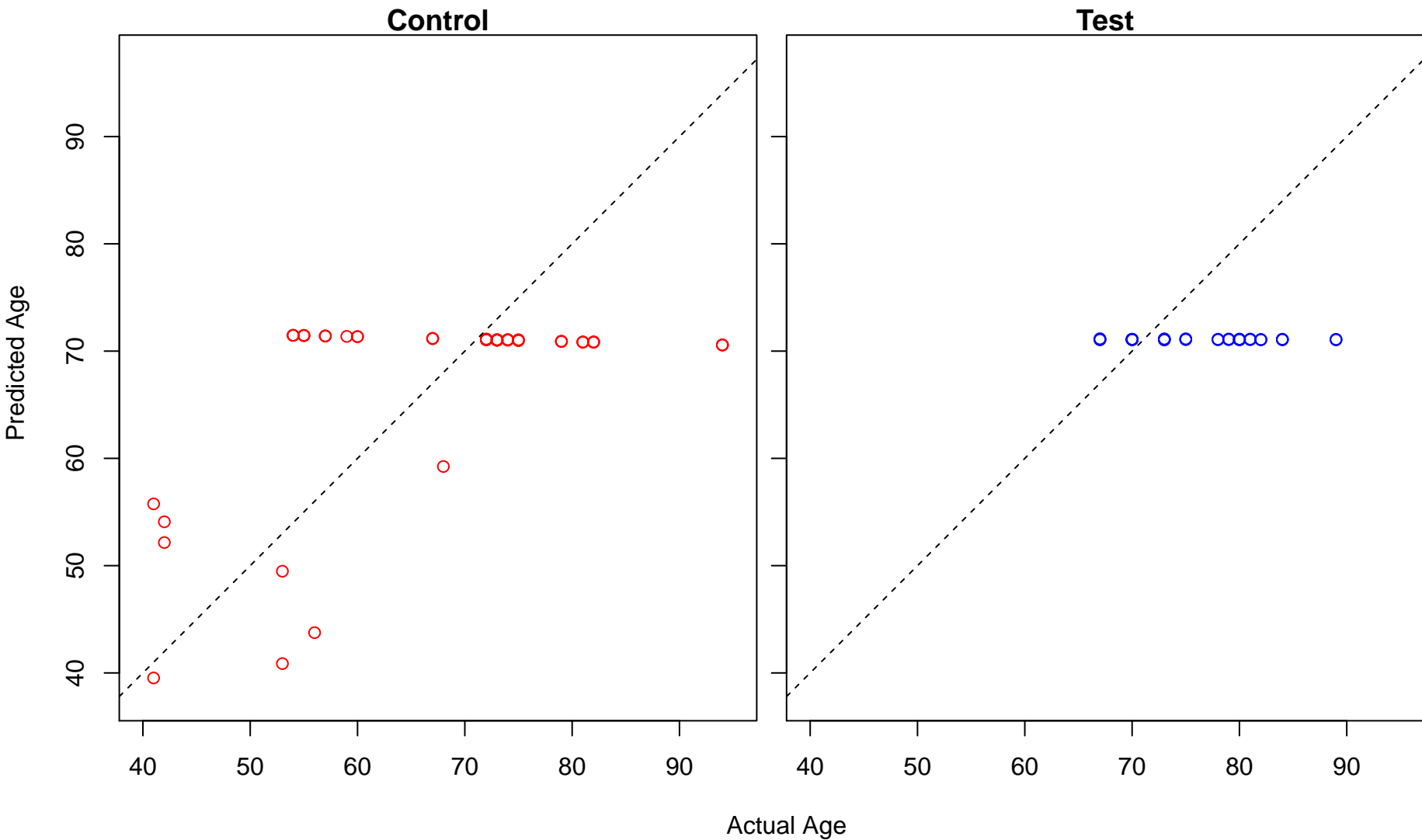


Test



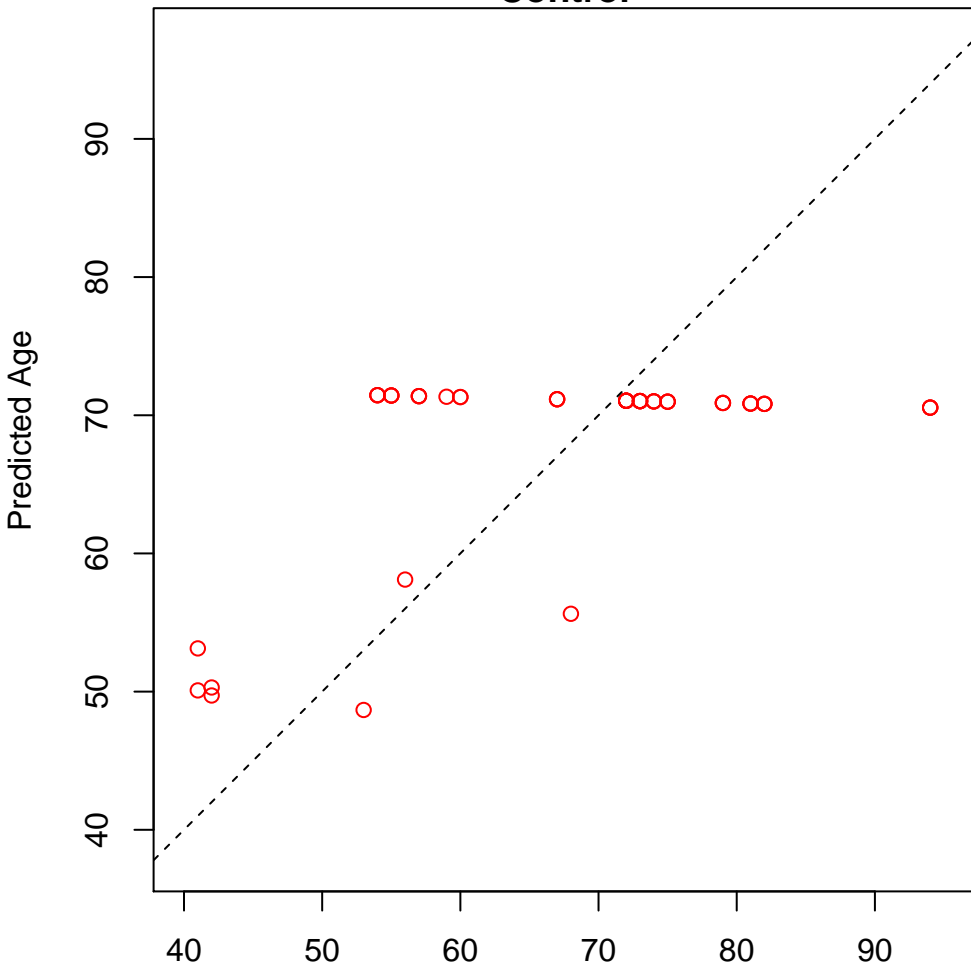
Actual Age

transcription initiation from RNA polymerase II promoter (Score: 0.800386)

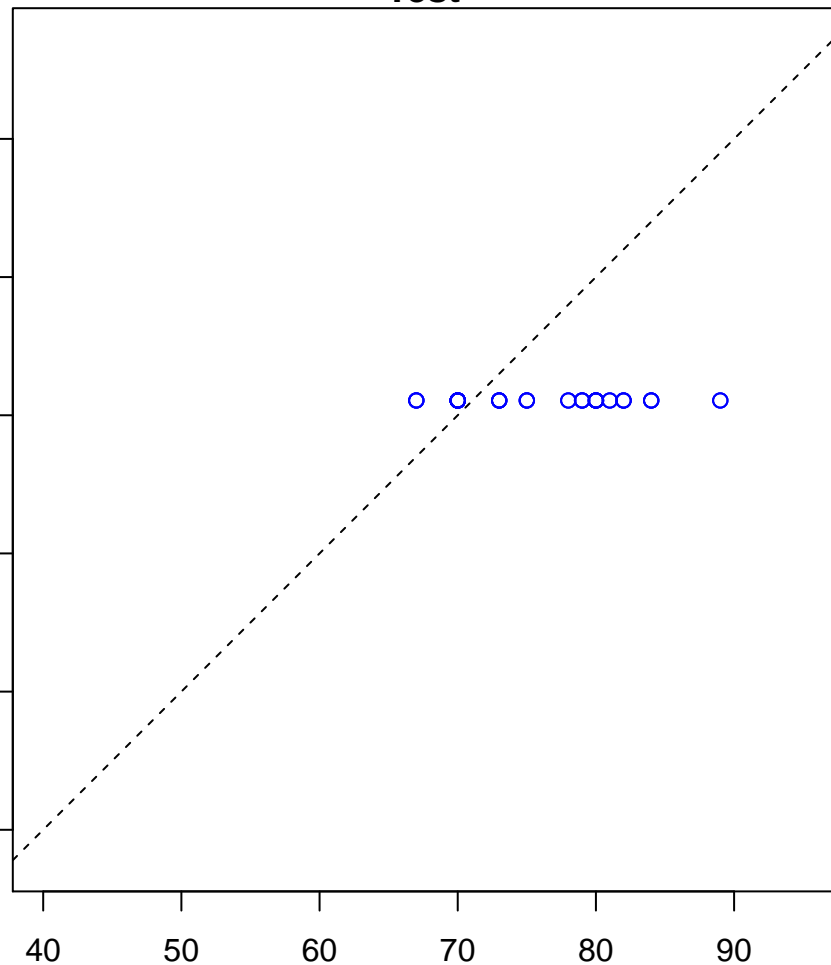


macromolecular complex disassembly (Score: 0.800382)

Control



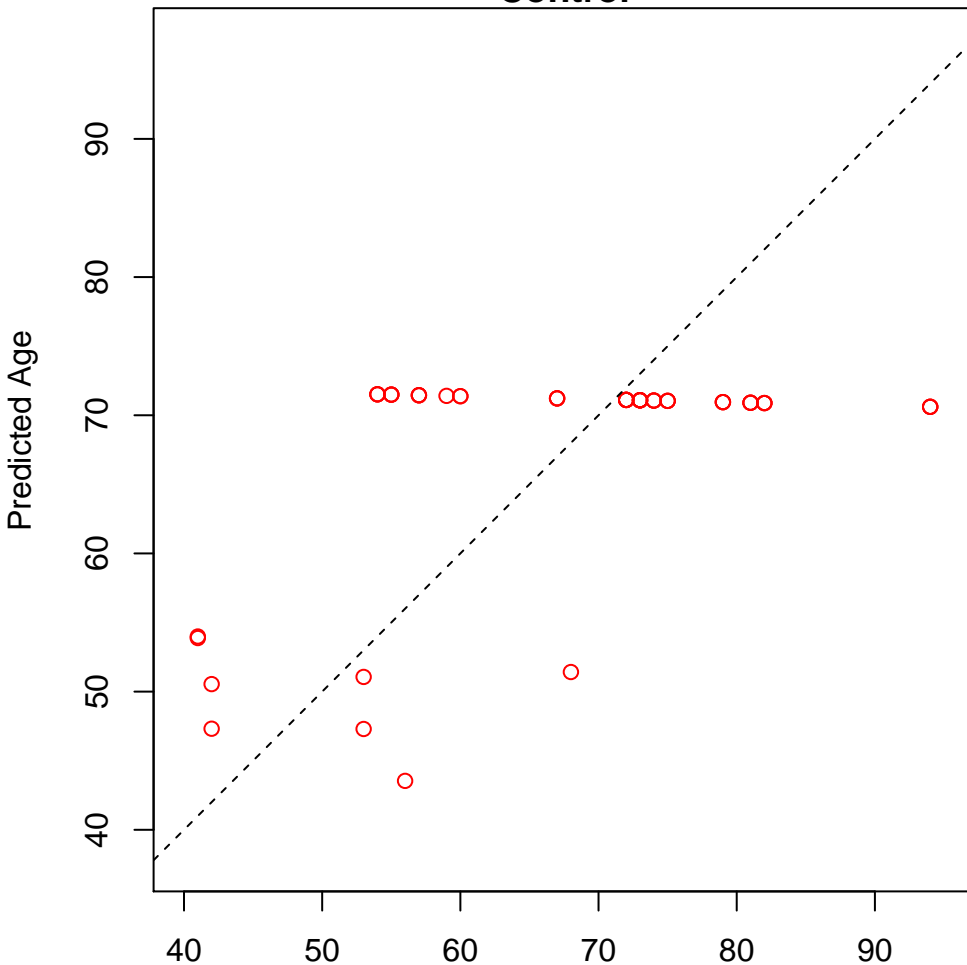
Test



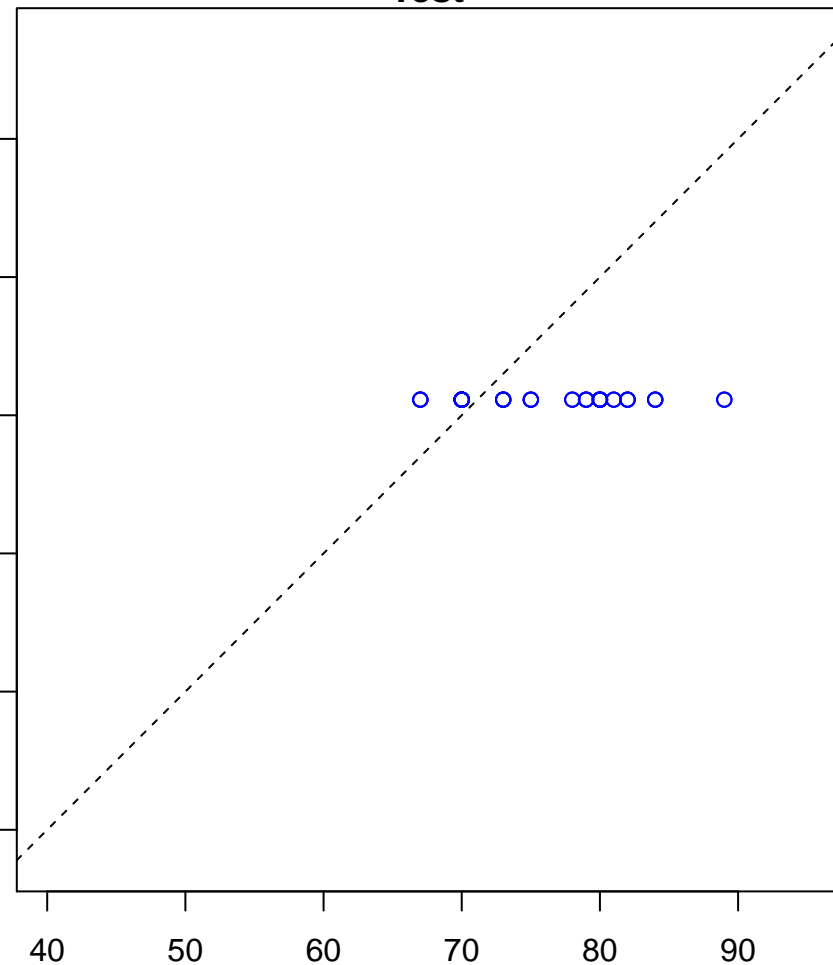
Actual Age

regulation of RNA metabolic process (Score: 0.800378)

Control

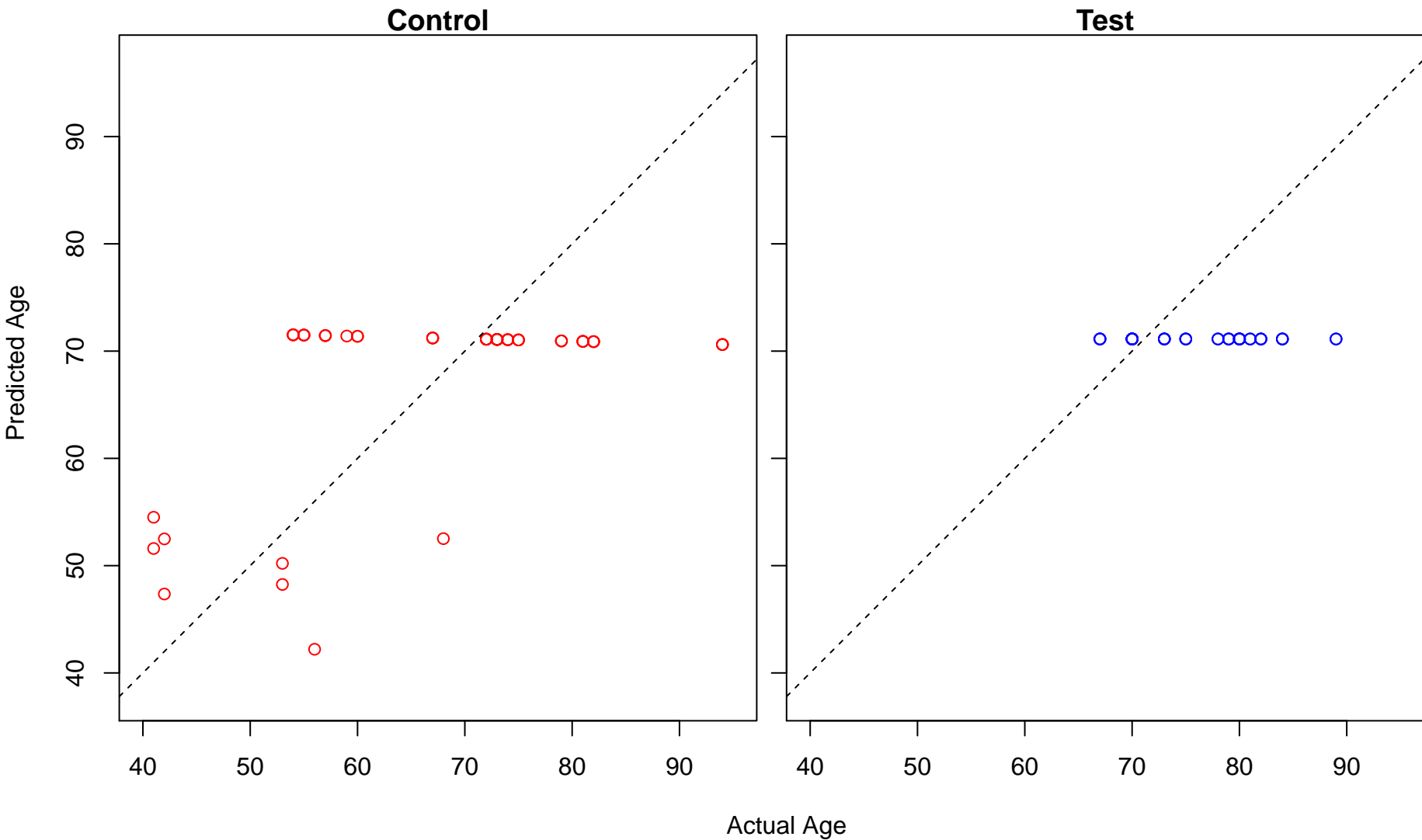


Test

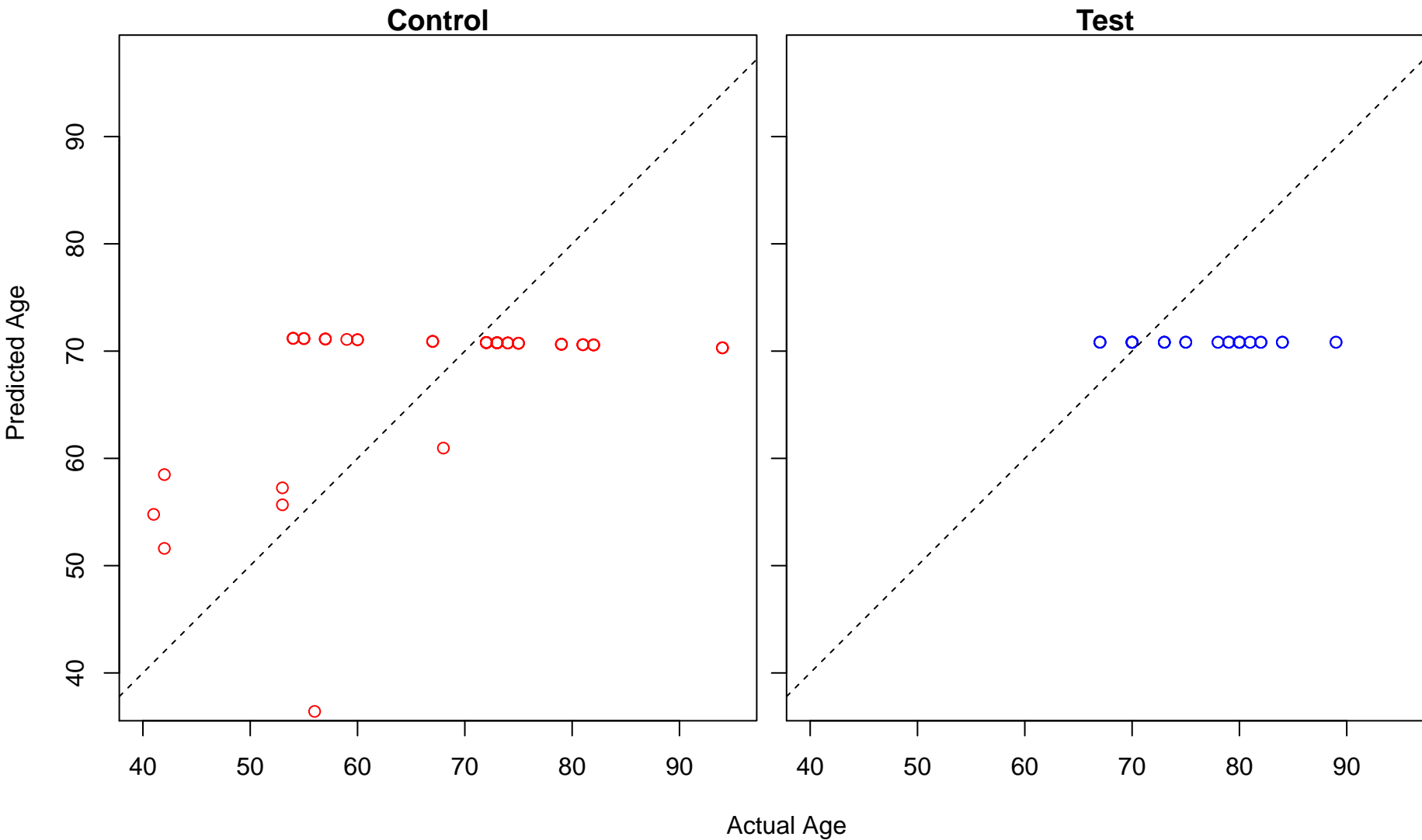


Actual Age

regulation of biological process (Score: 0.800355)

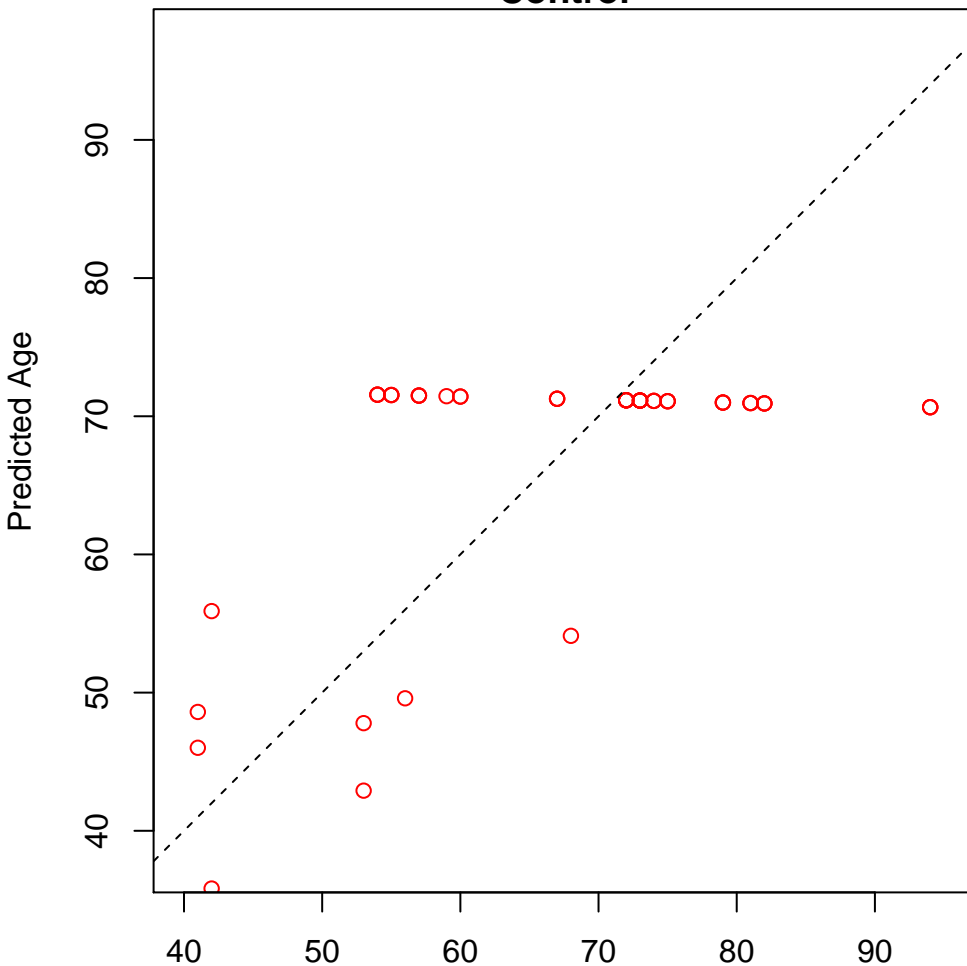


methylation (Score: 0.800348)

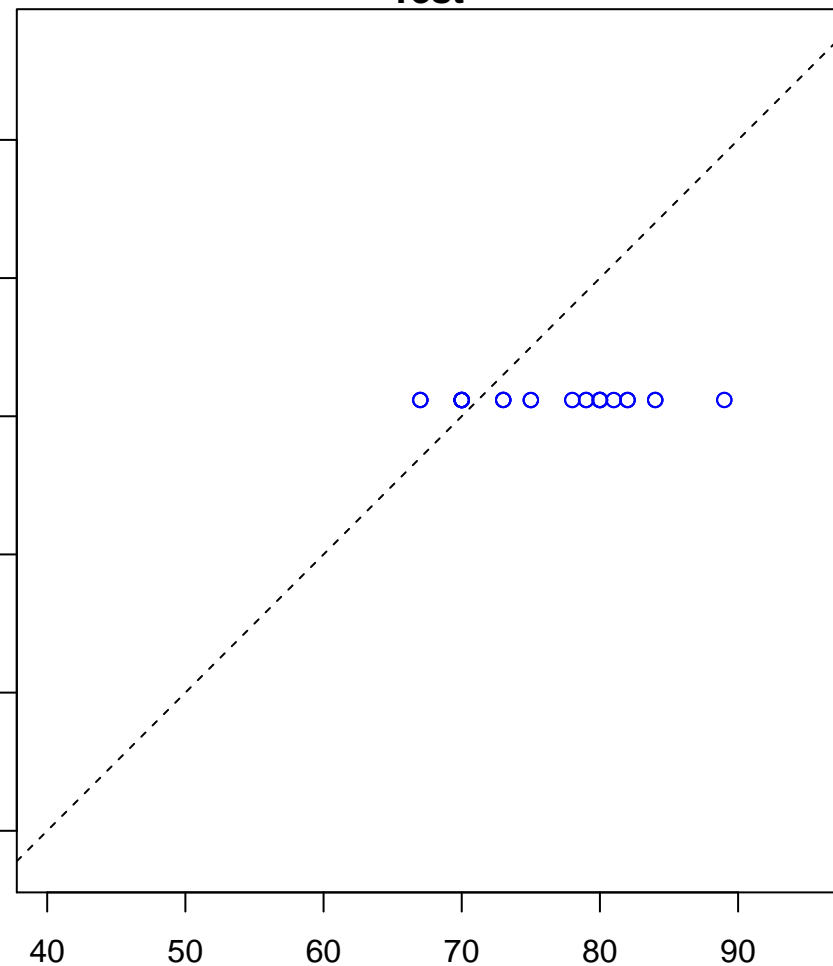


regulation of cellular response to stress (Score: 0.800290)

Control

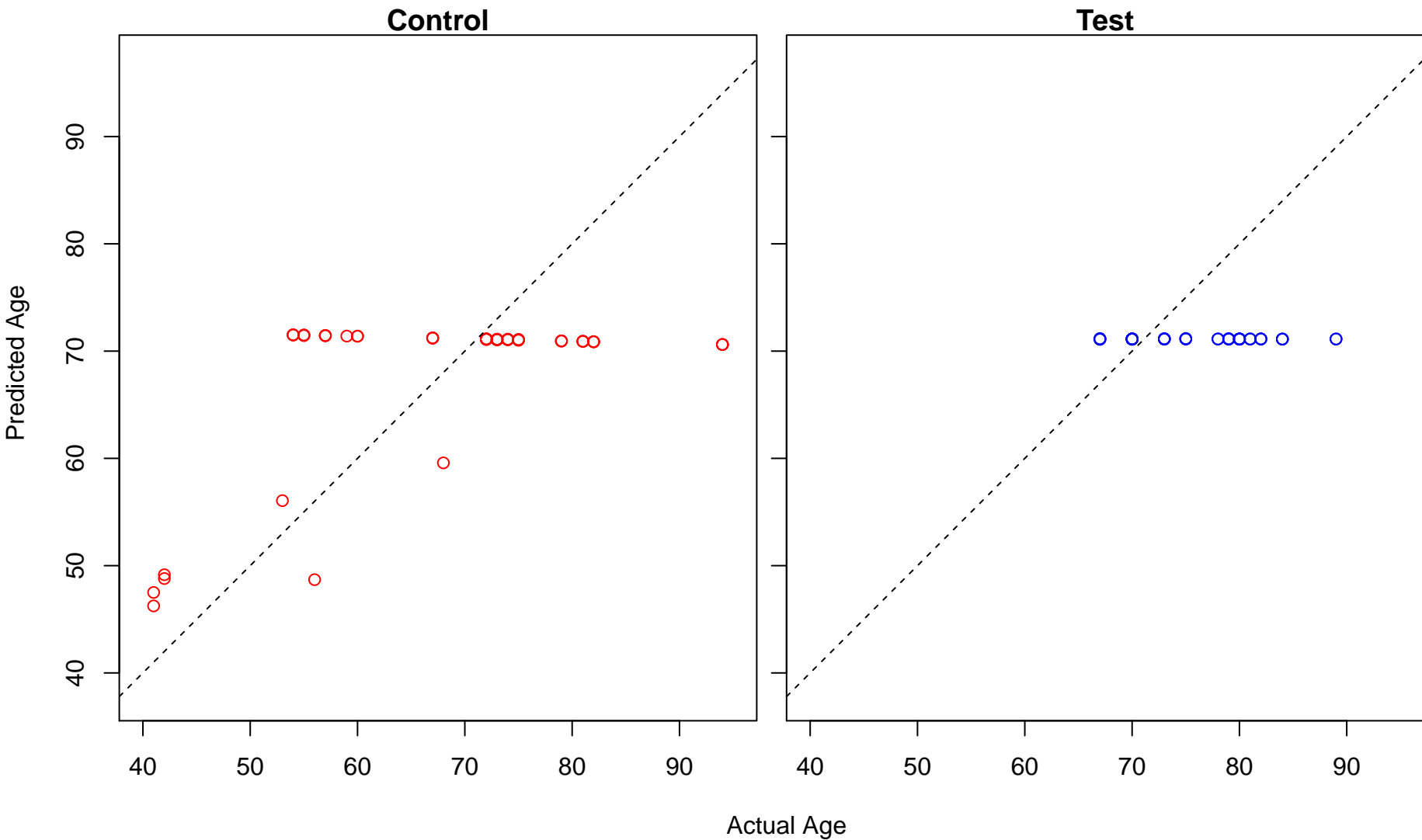


Test

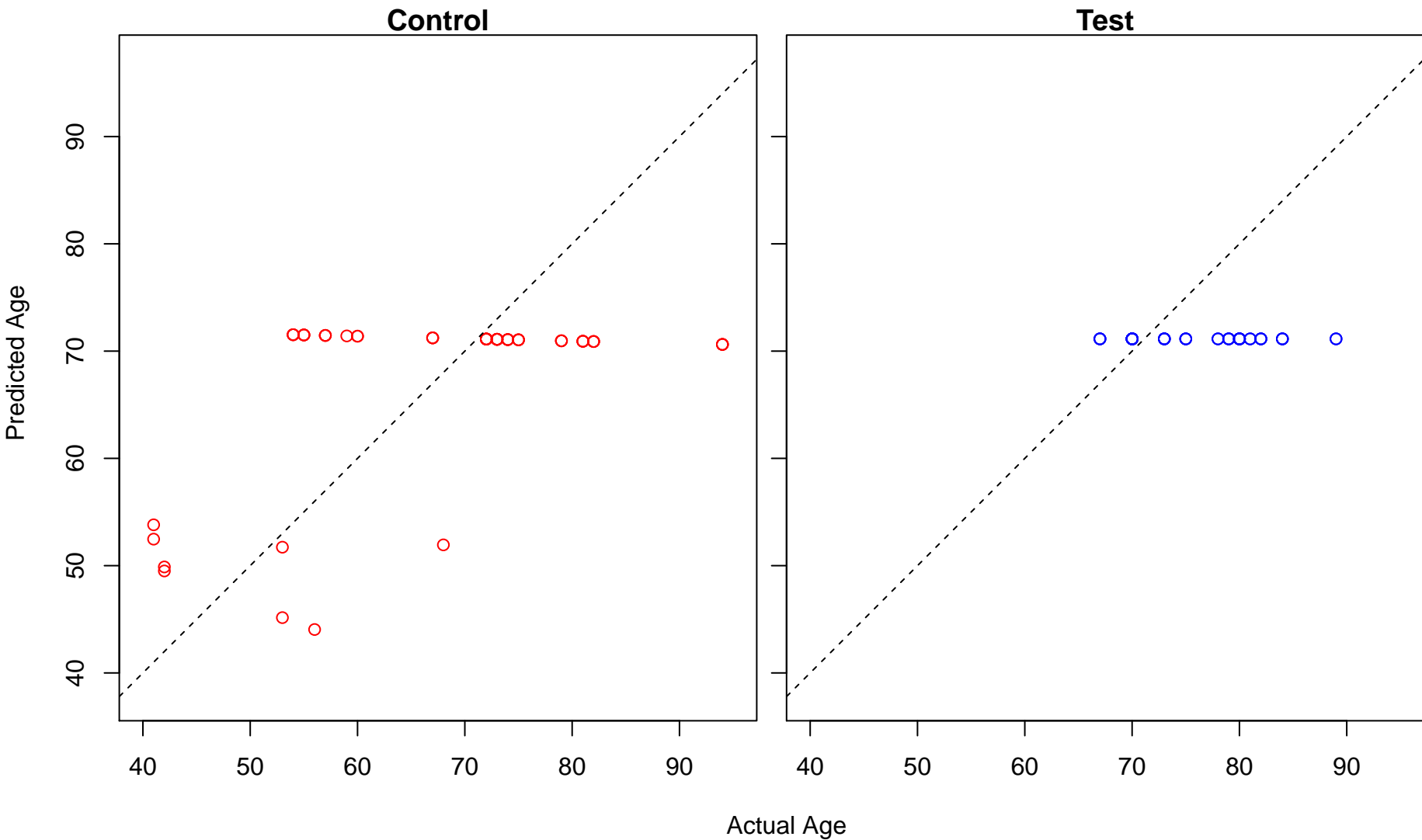


Actual Age

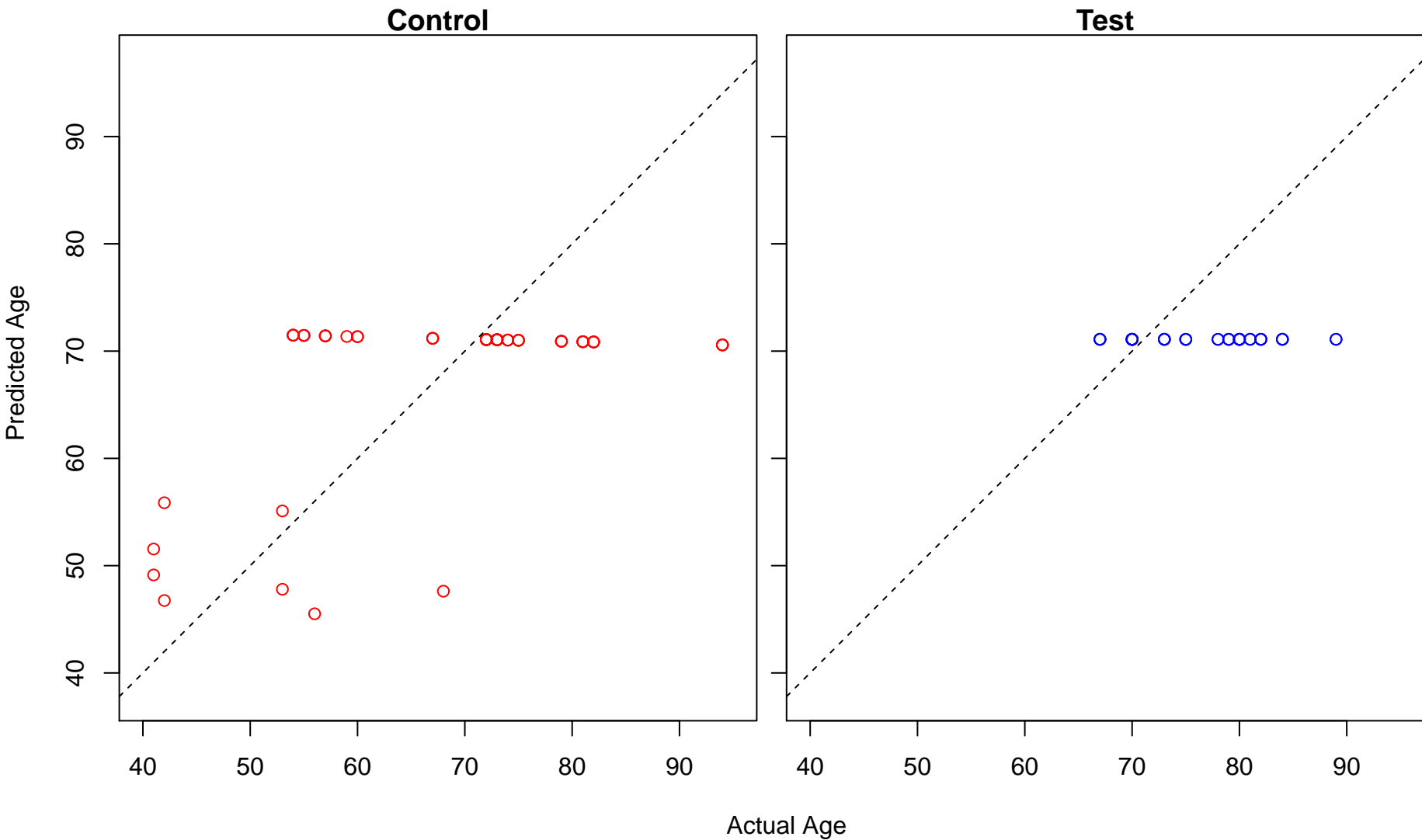
apoptotic cell clearance (Score: 0.800289)



multicellular organismal process (Score: 0.800279)

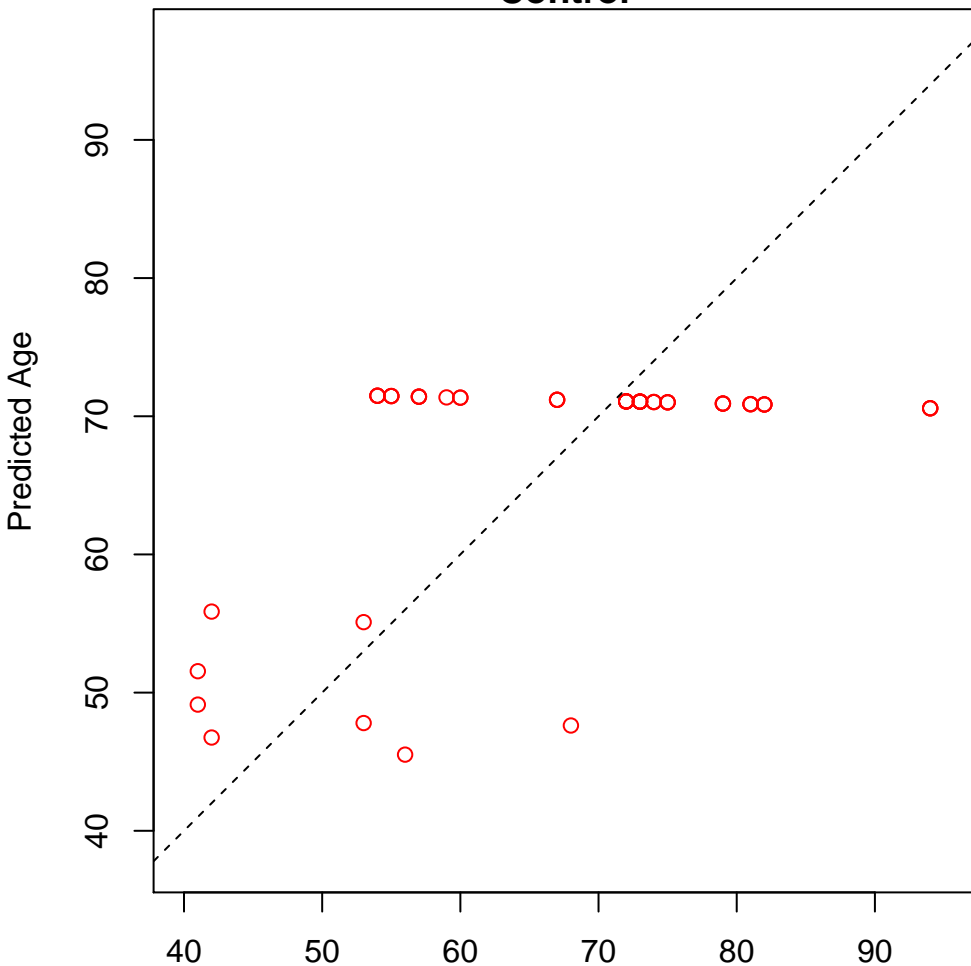


chromatin remodeling (Score: 0.800249)

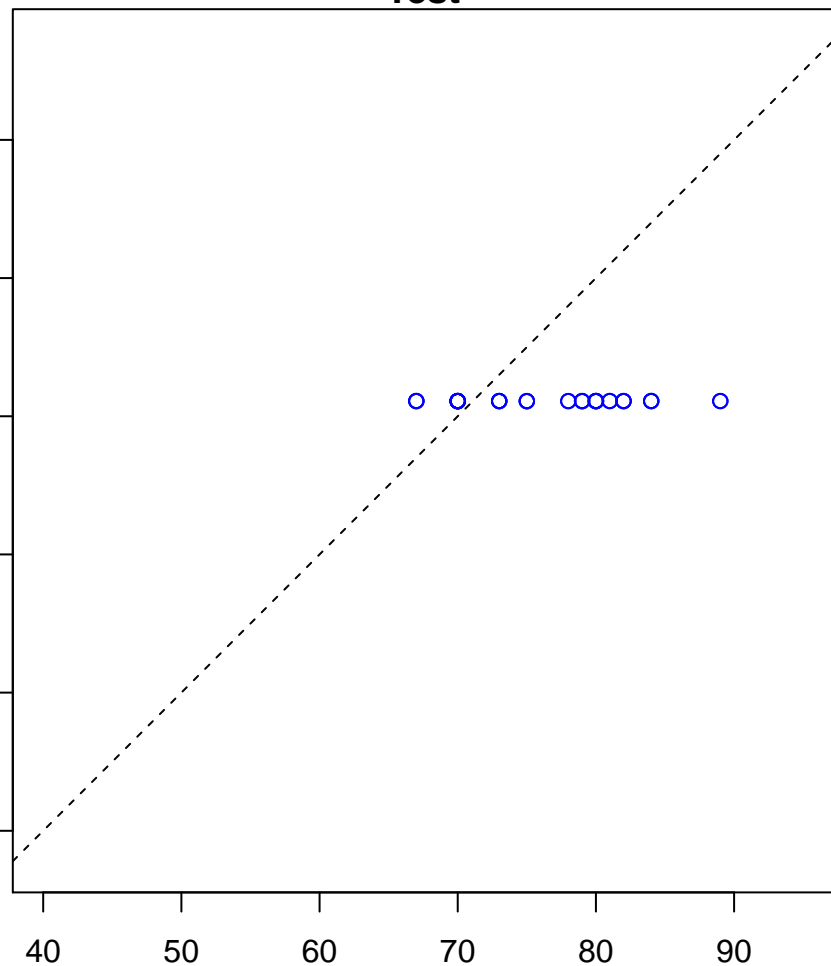


ATP-dependent chromatin remodeling (Score: 0.800249)

Control

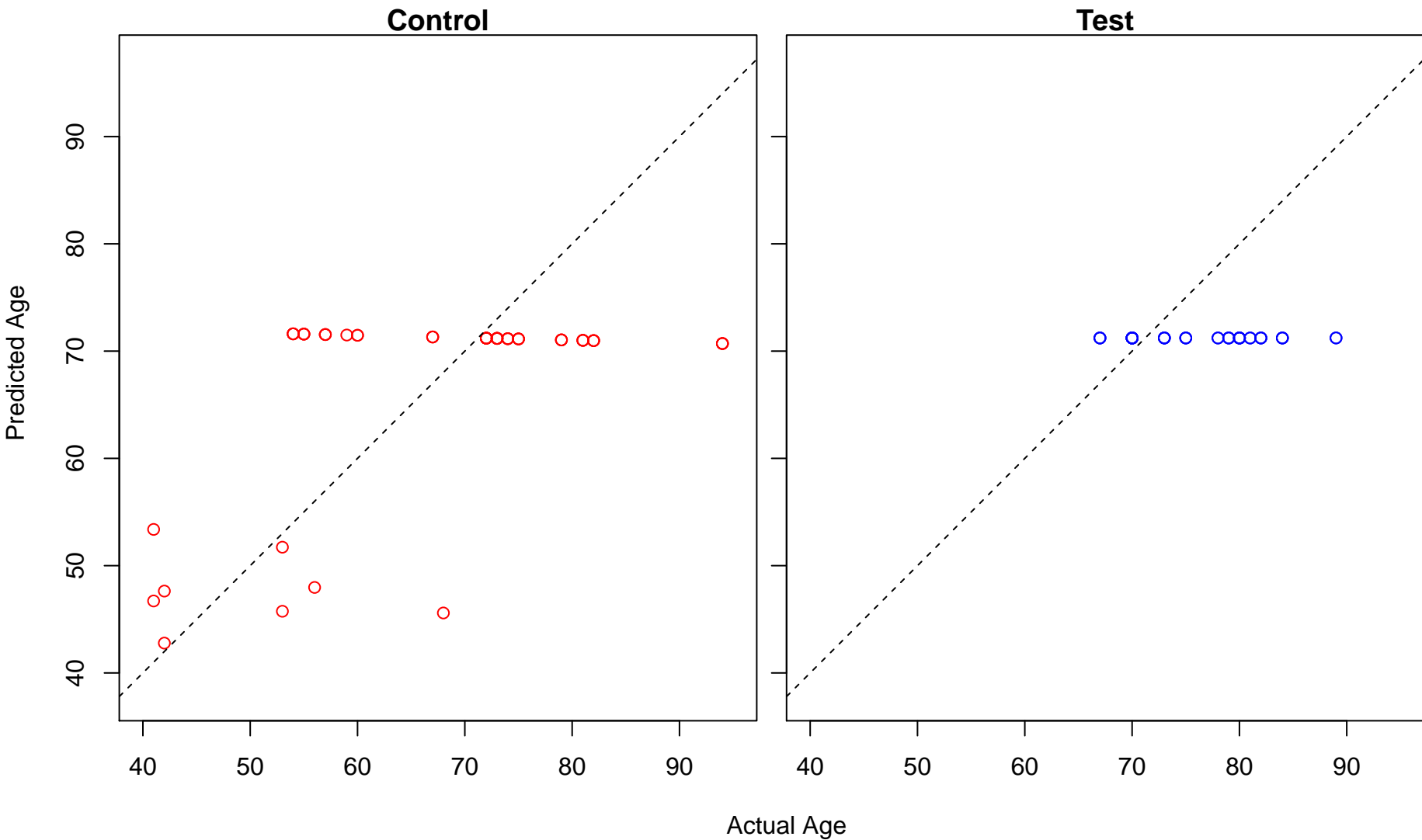


Test



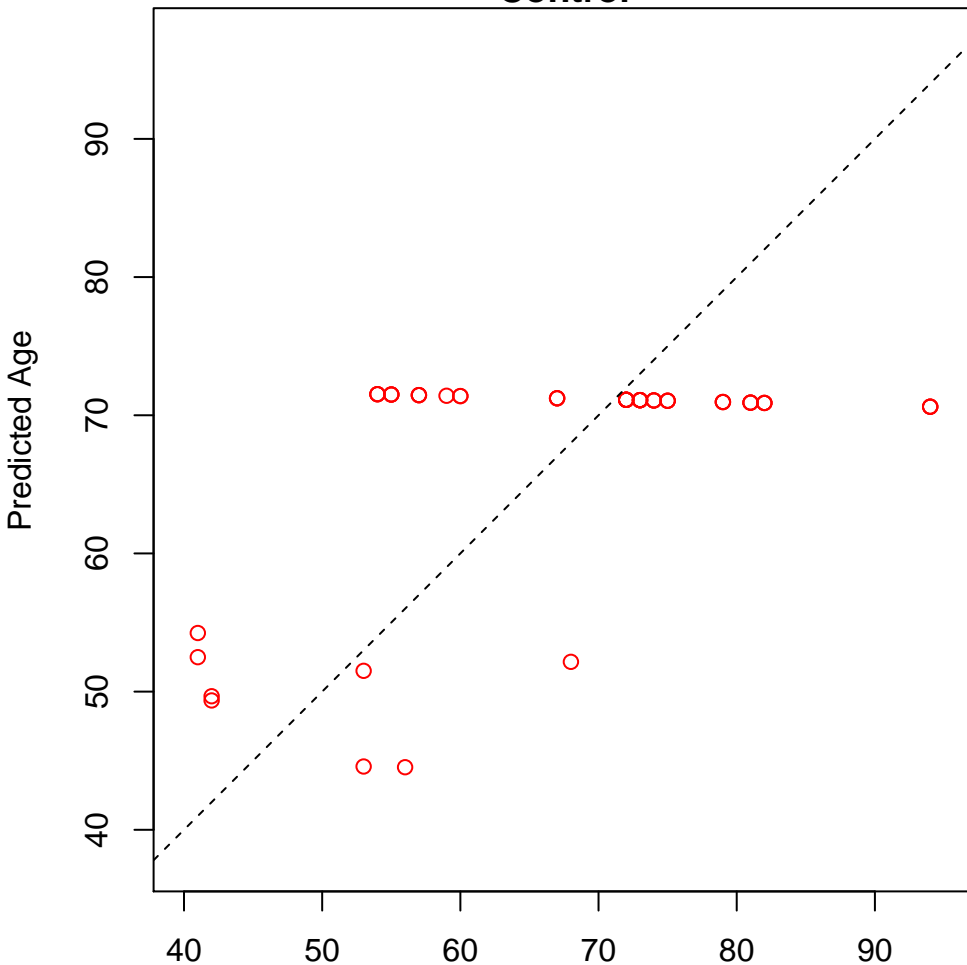
Actual Age

posttranscriptional regulation of gene expression (Score: 0.800235)

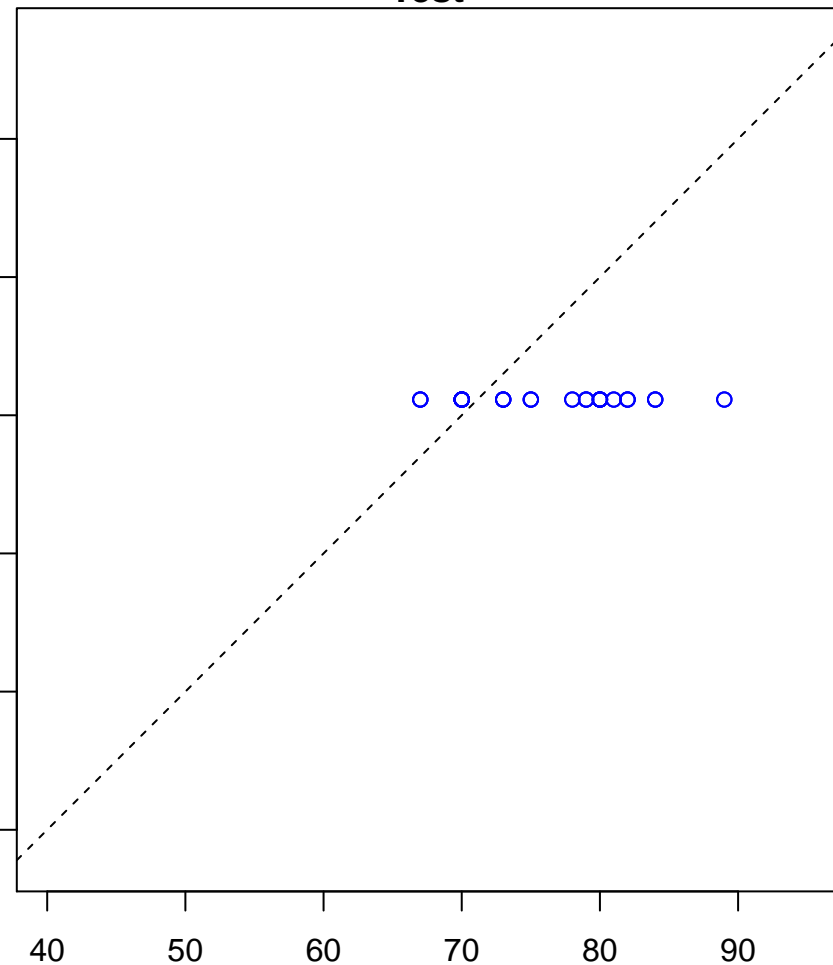


anatomical structure development (Score: 0.800217)

Control

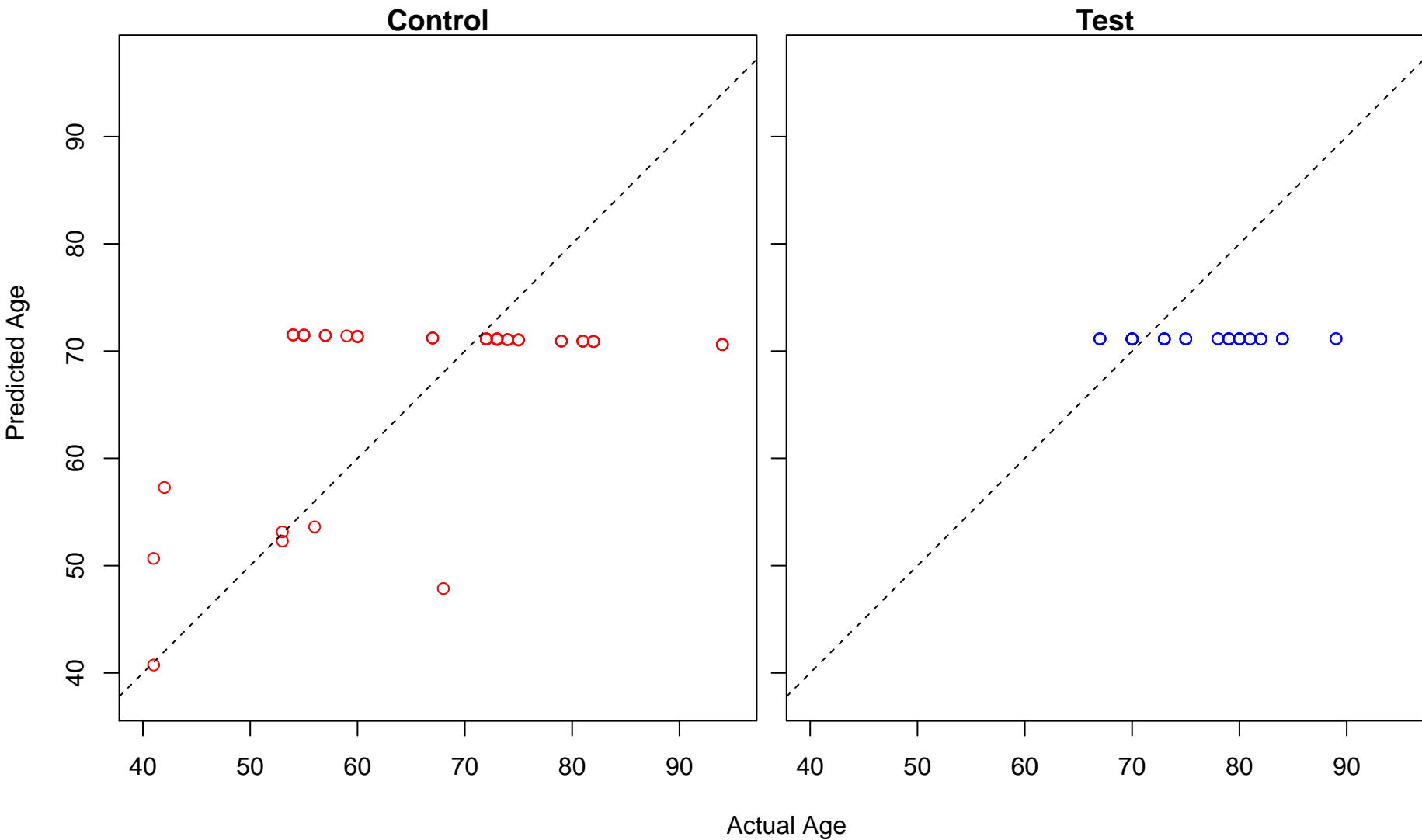


Test

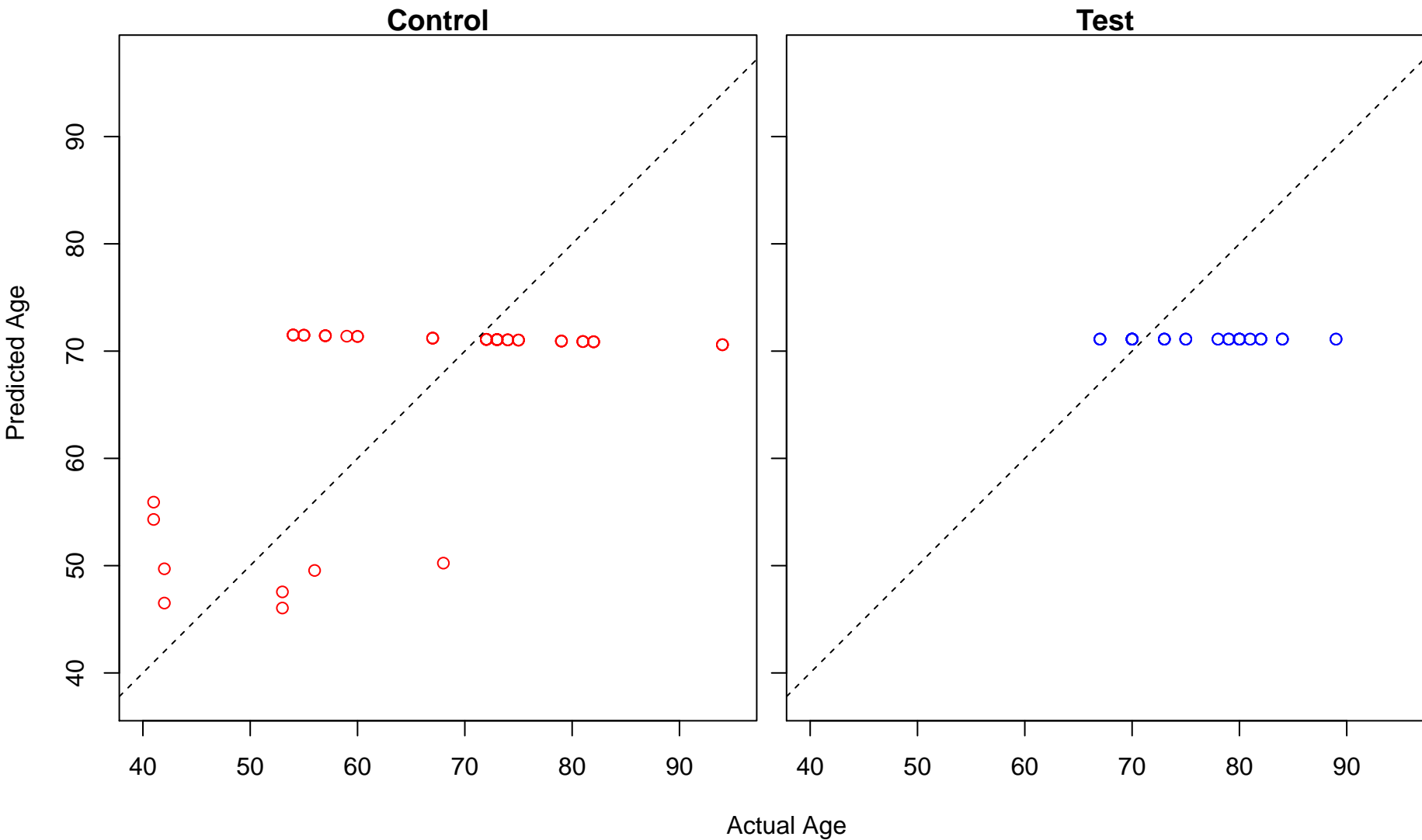


Actual Age

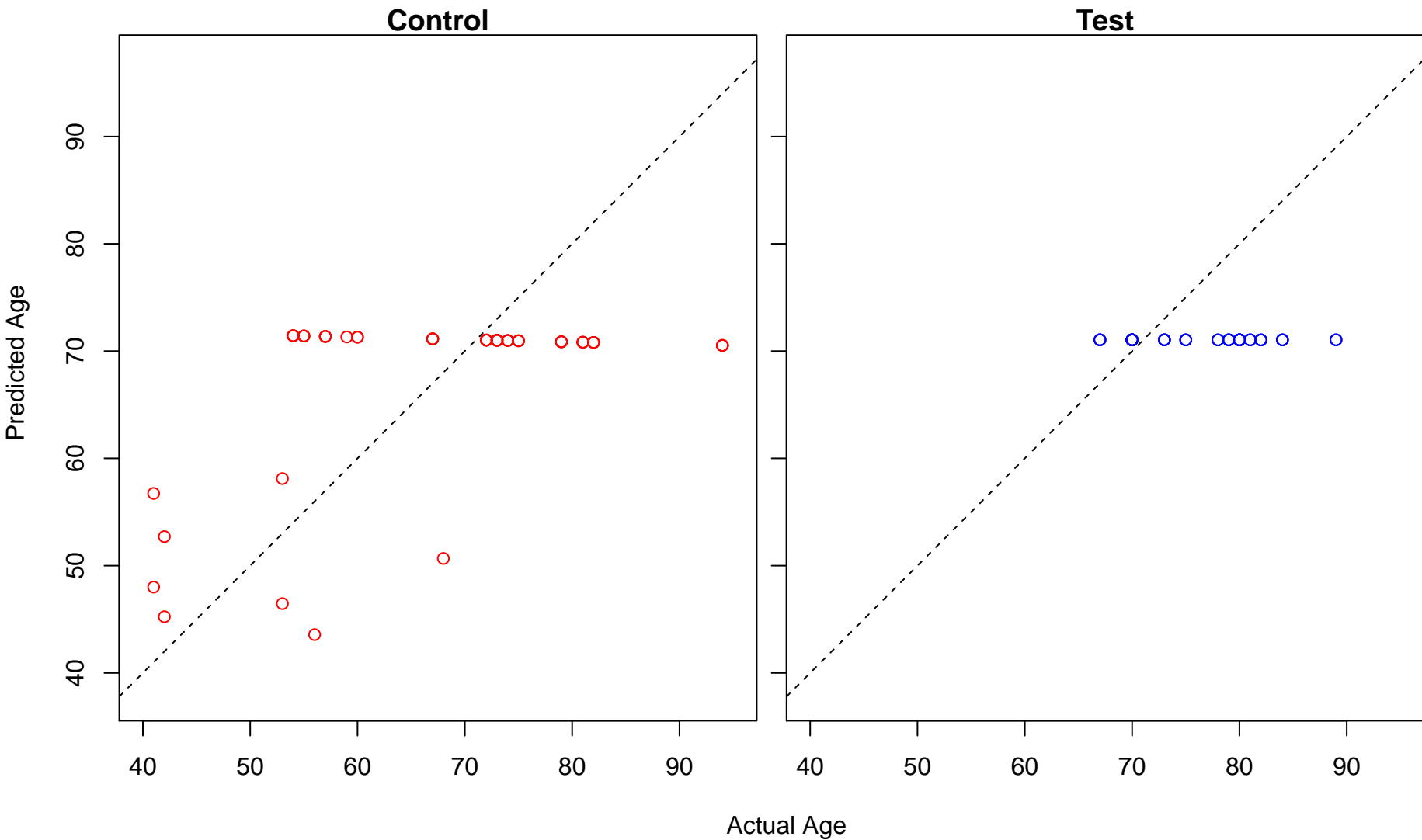
negative regulation of protein complex assembly (Score: 0.800165)



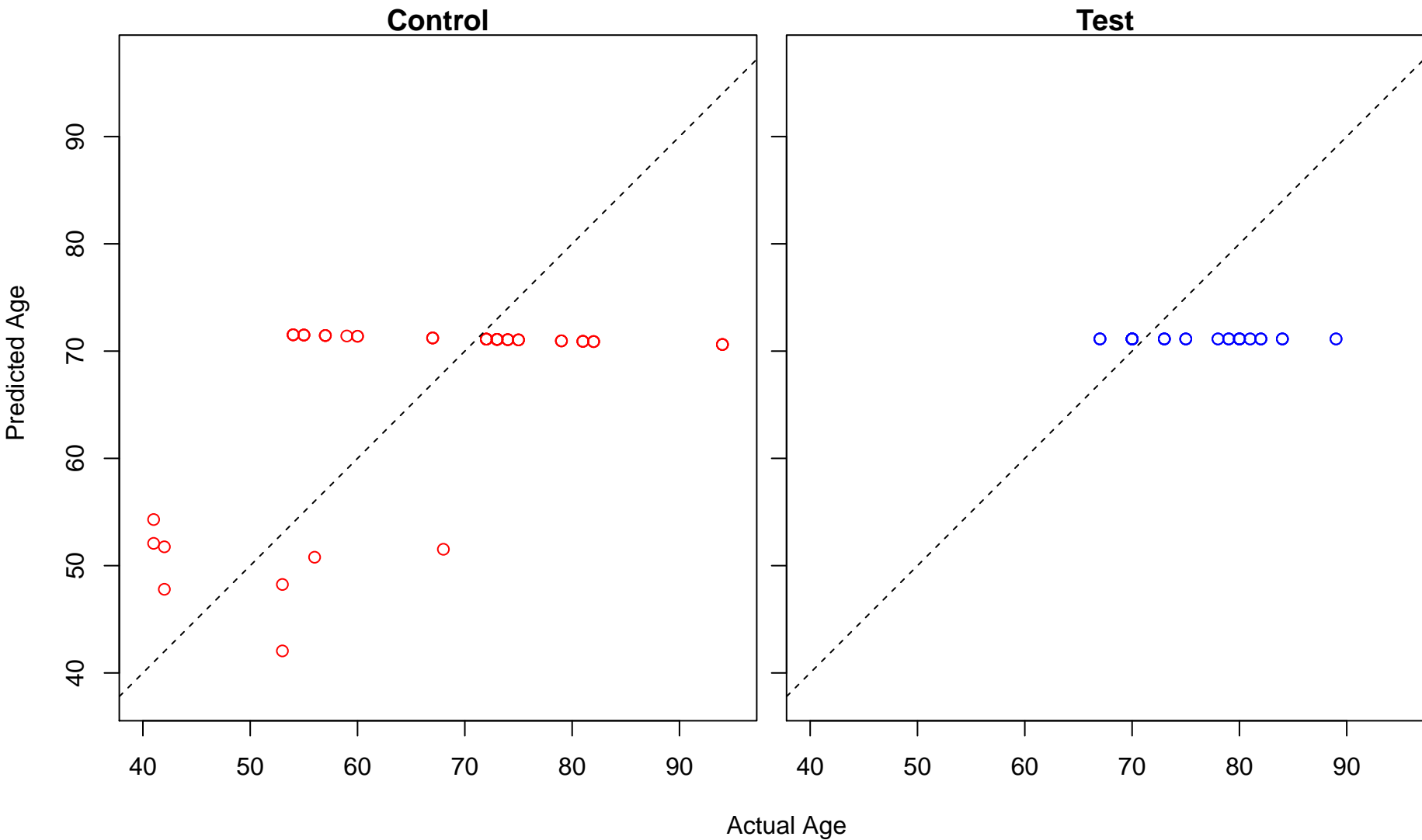
negative regulation of proteolysis (Score: 0.800129)



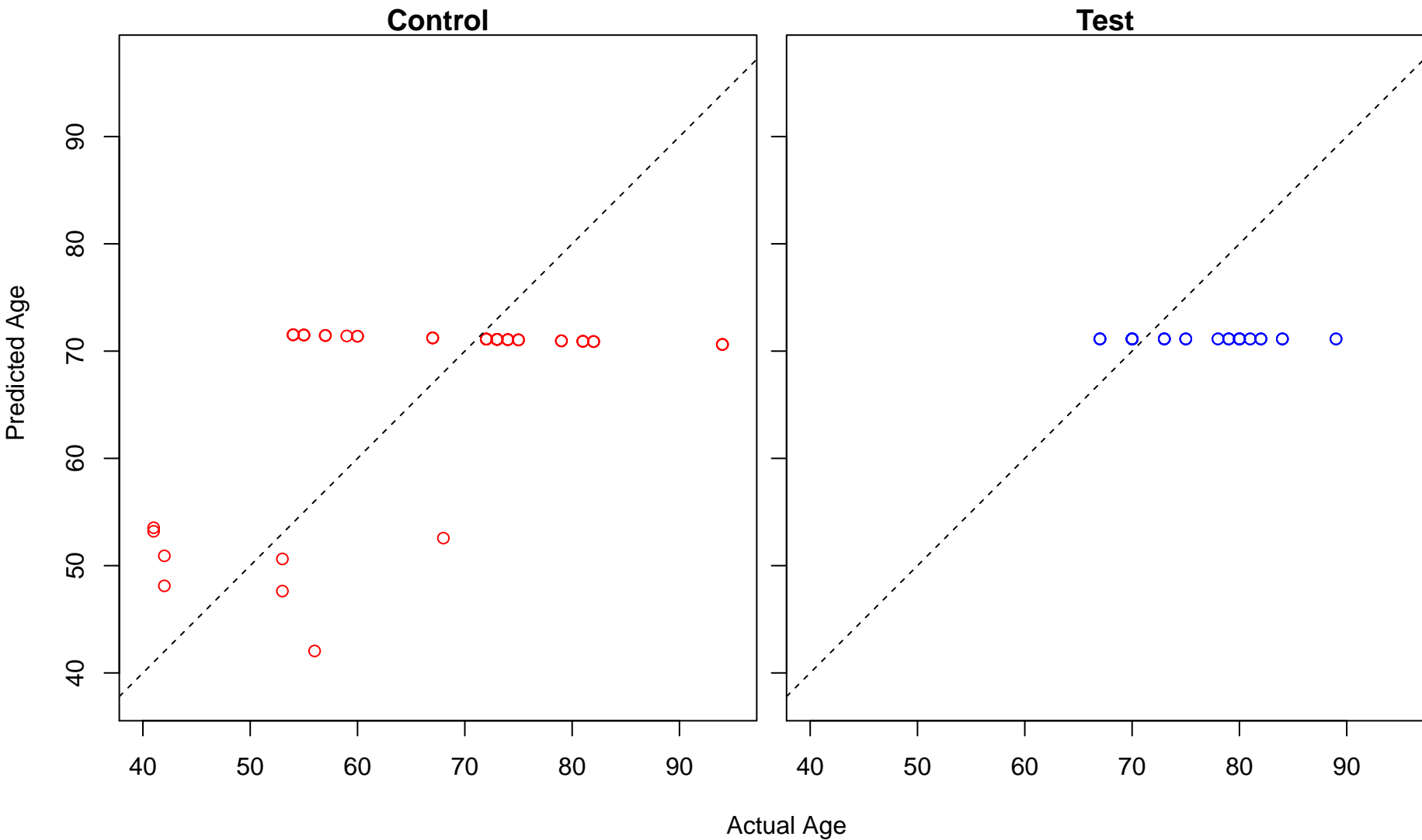
cell-matrix adhesion (Score: 0.800097)



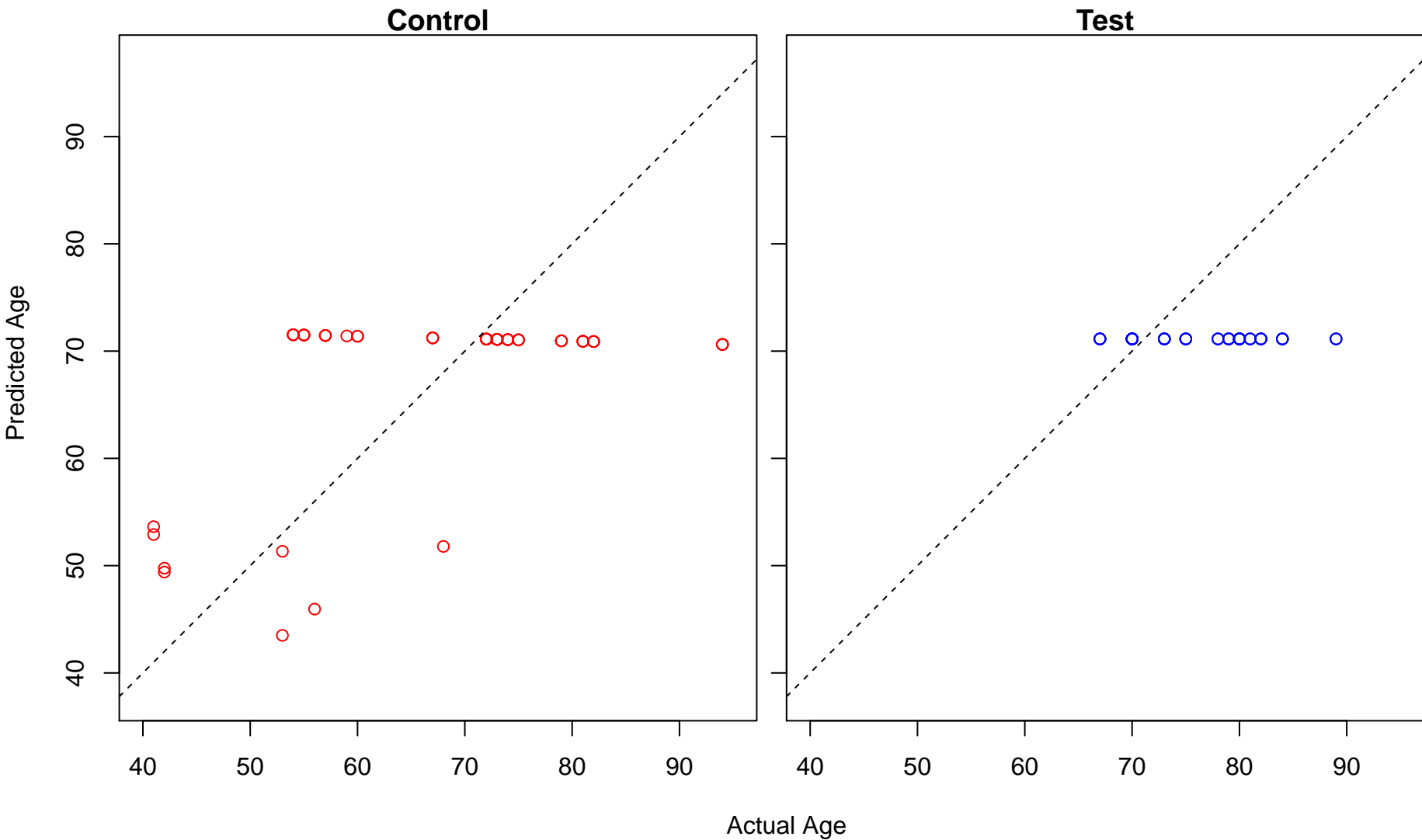
response to external stimulus (Score: 0.800088)



regulation of macromolecule biosynthetic process (Score: 0.800071)

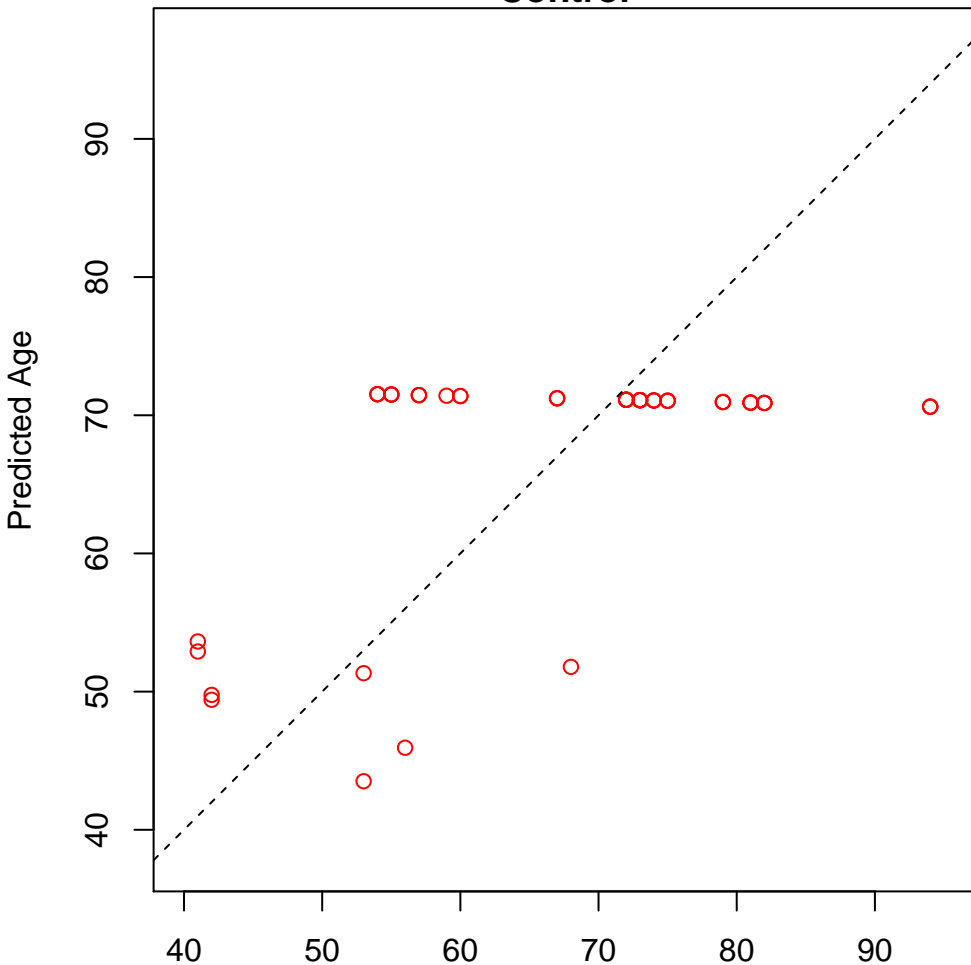


cell differentiation (Score: 0.800061)

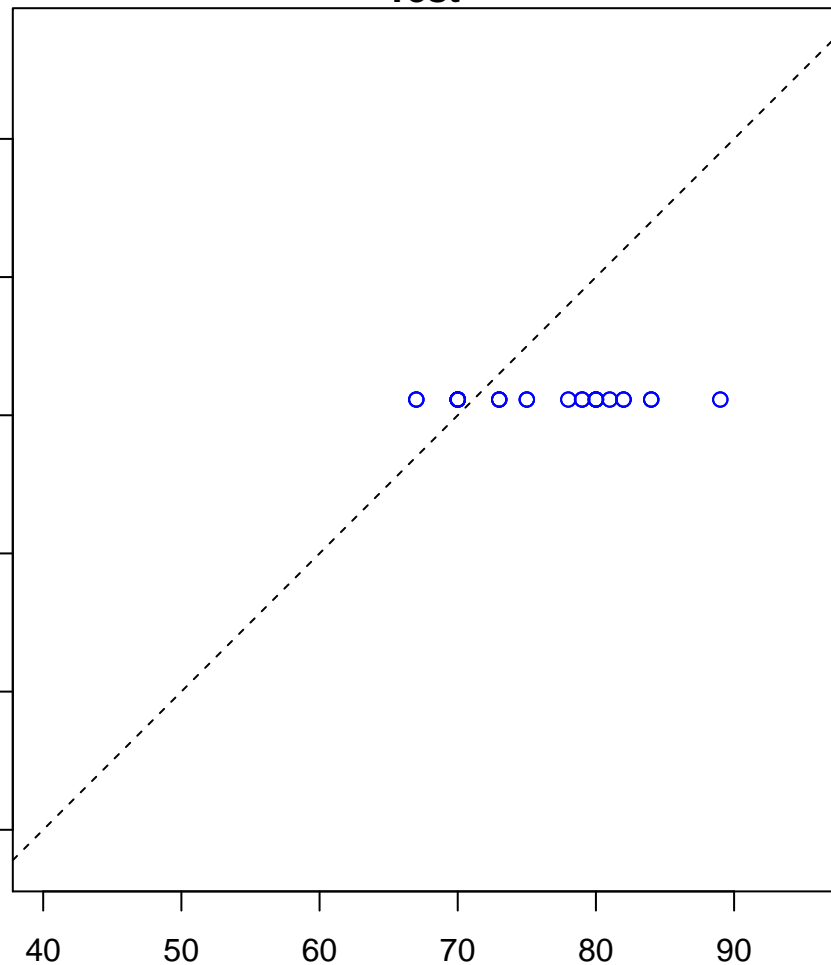


cellular developmental process (Score: 0.800056)

Control



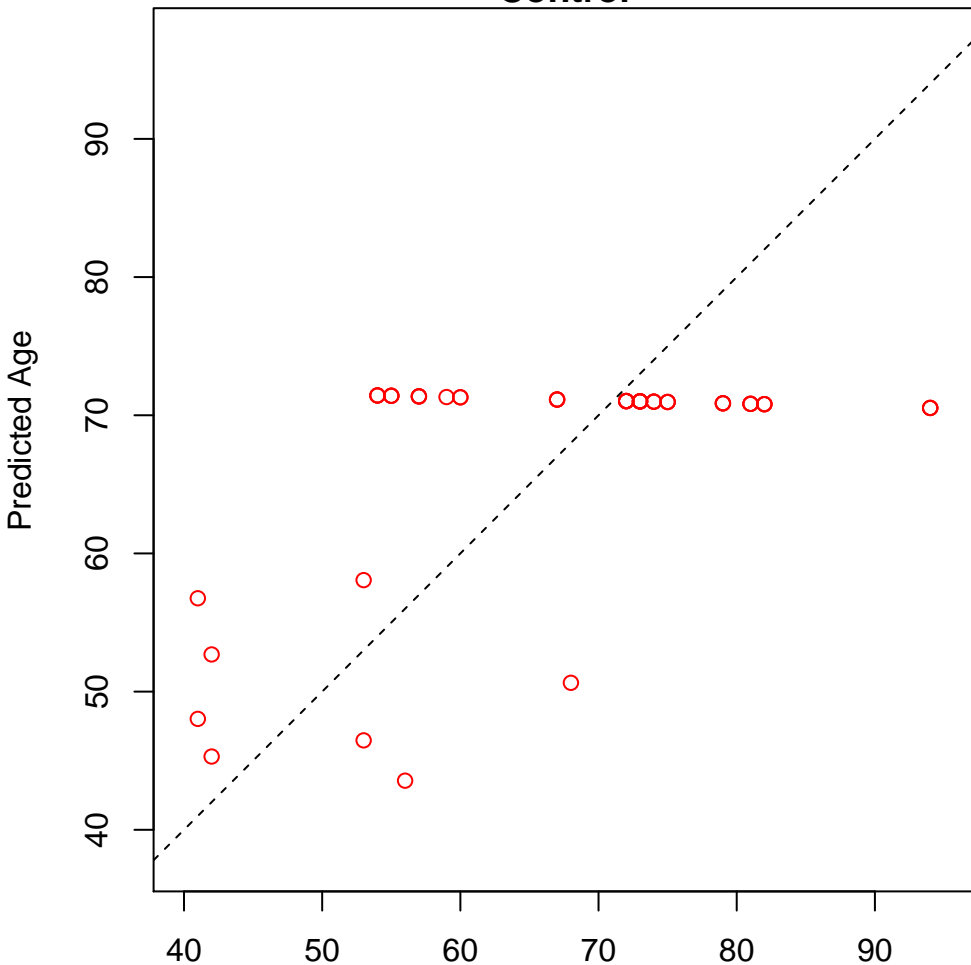
Test



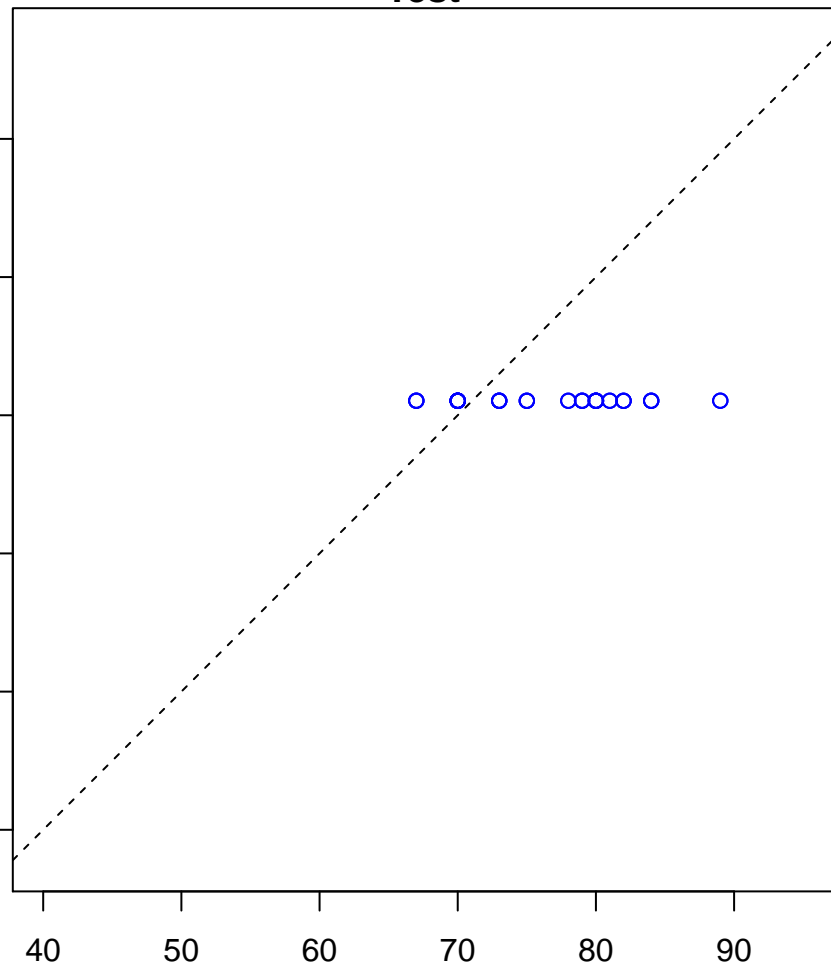
Actual Age

cell-substrate adhesion (Score: 0.800021)

Control

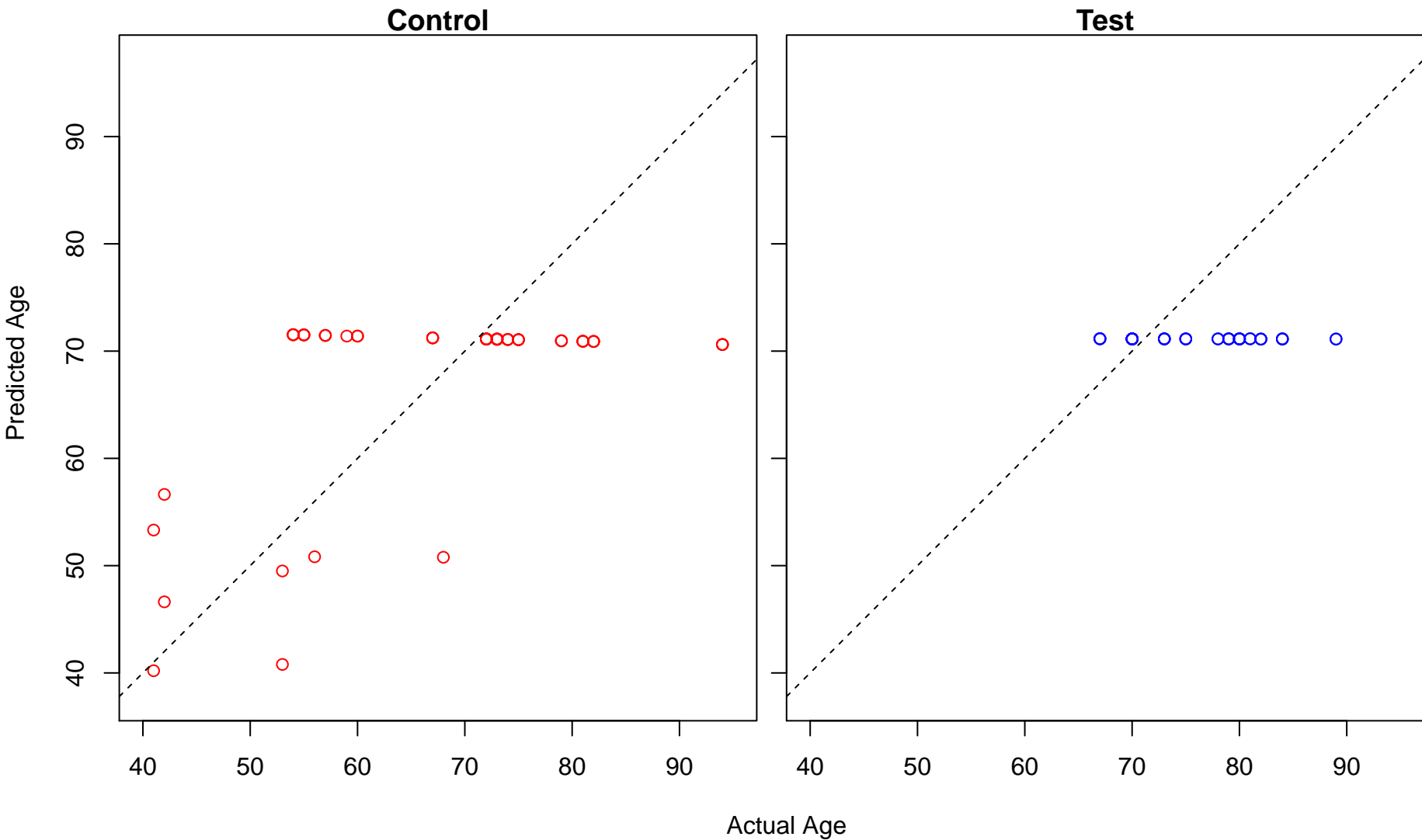


Test

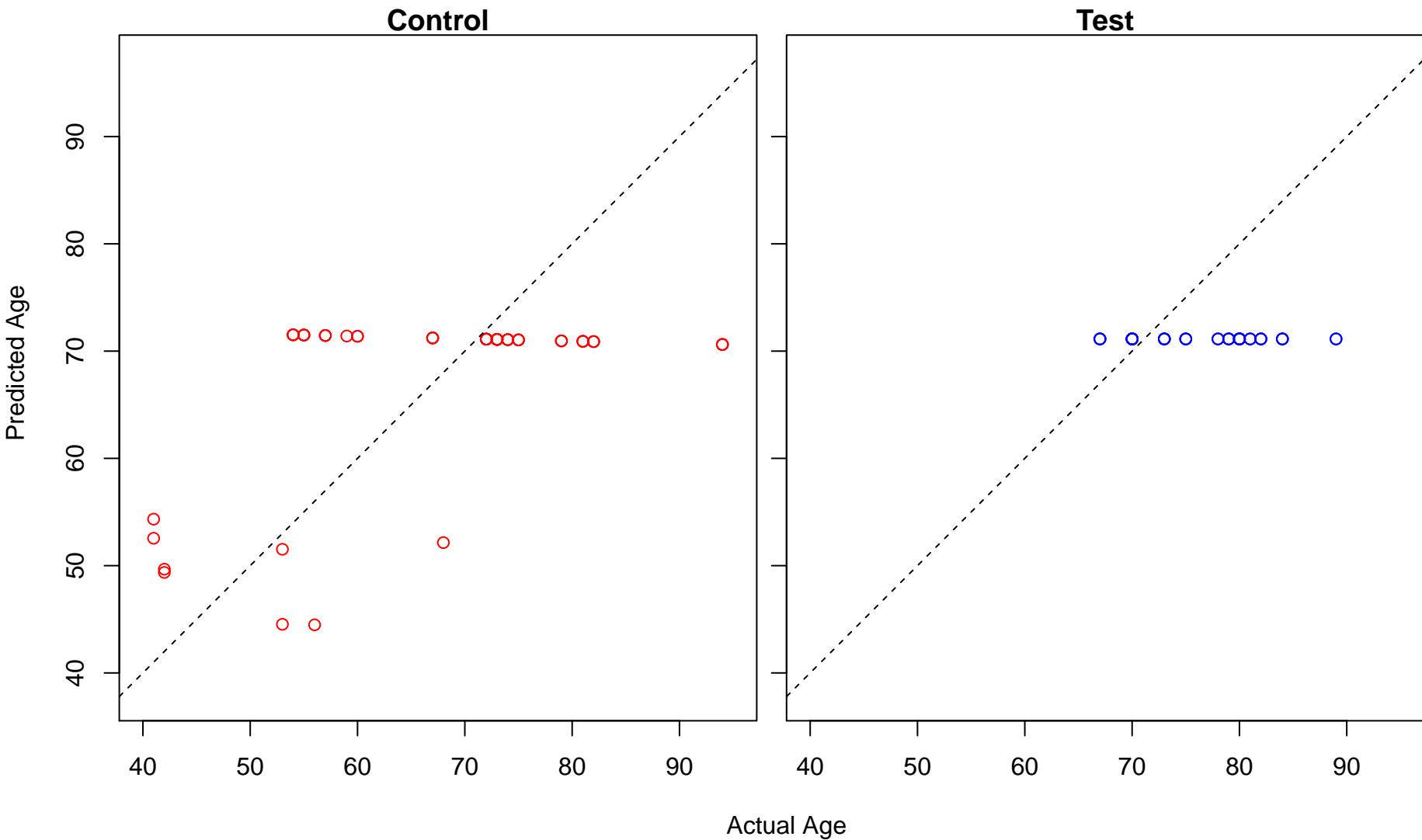


Actual Age

leukocyte migration (Score: 0.800019)

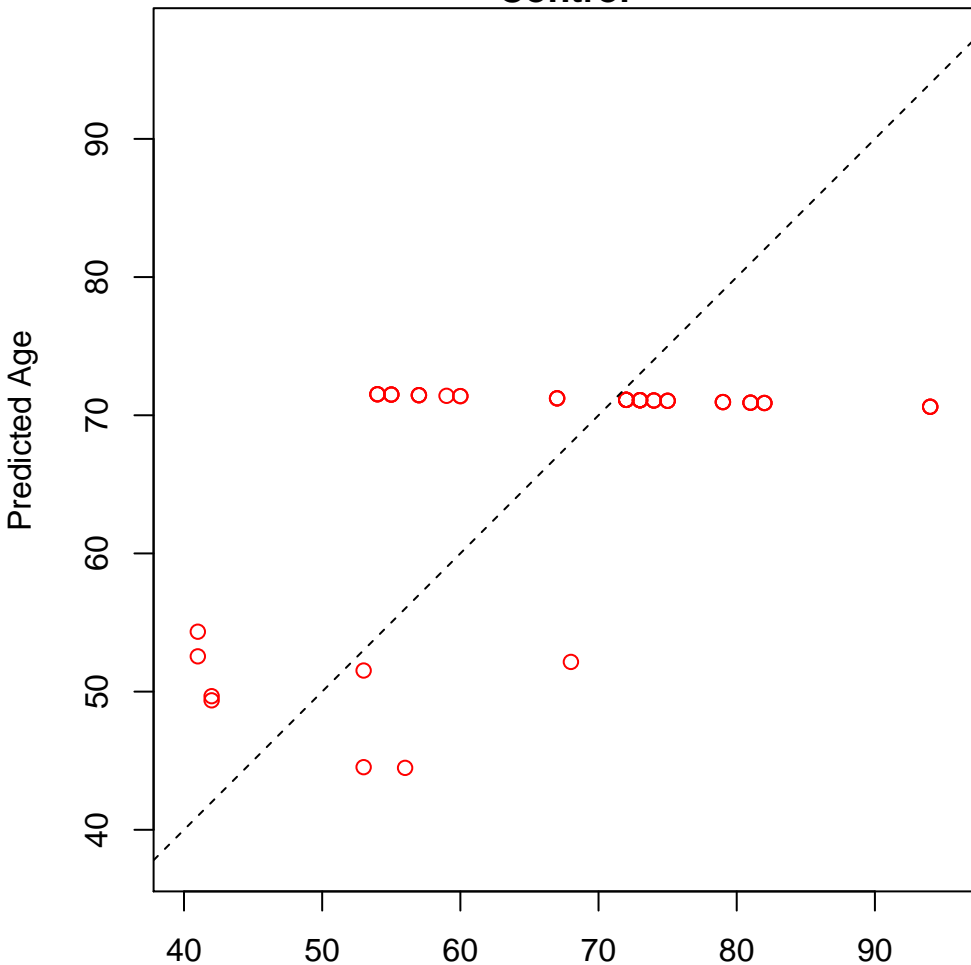


system development (Score: 0.800017)

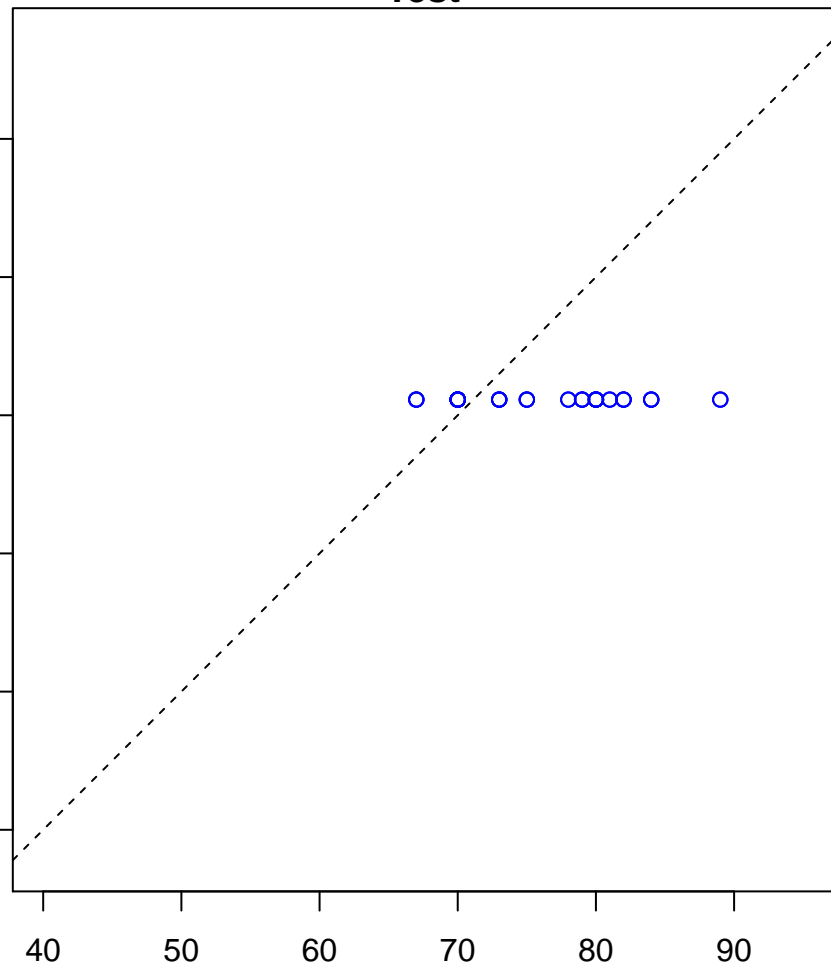


multicellular organism development (Score: 0.800017)

Control



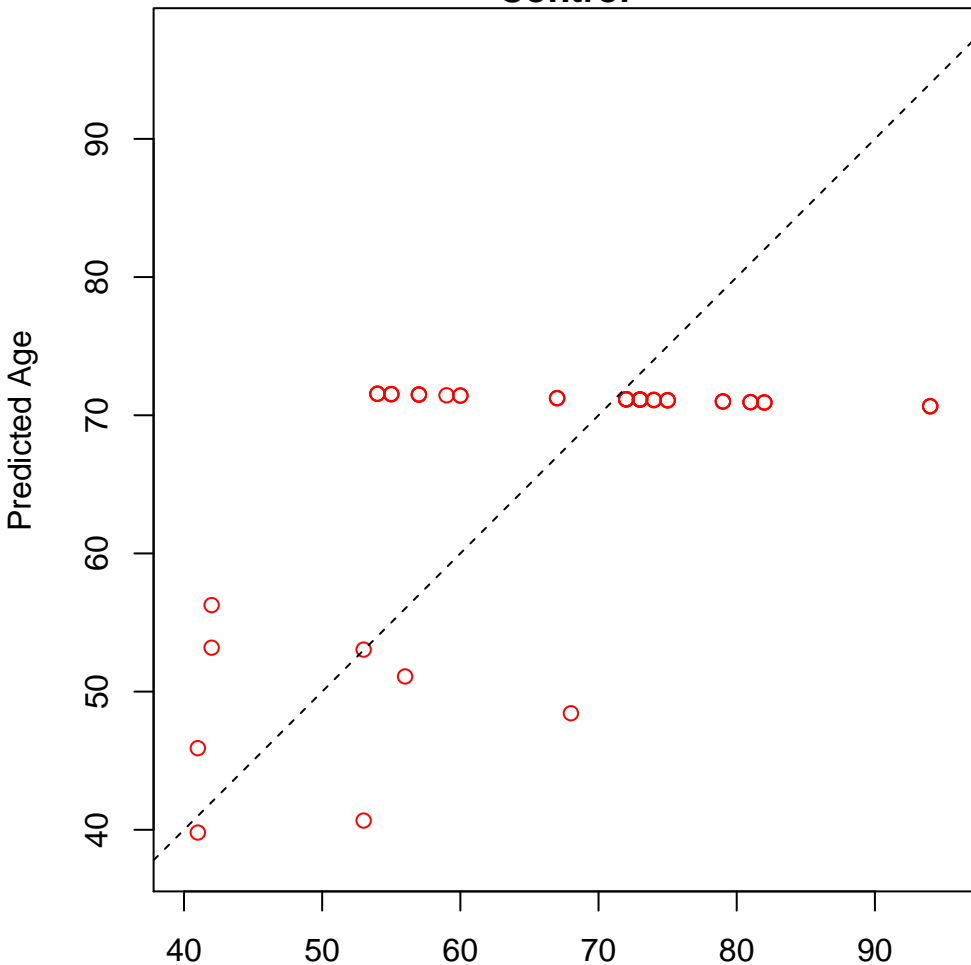
Test



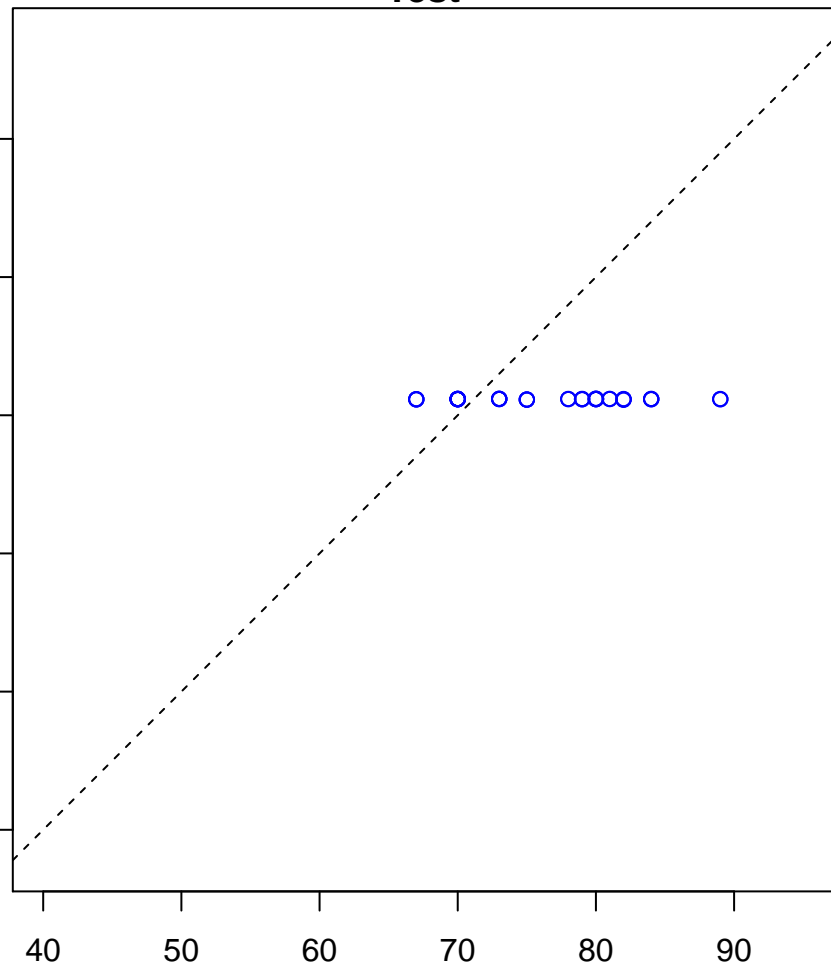
Actual Age

fatty acid biosynthetic process (Score: 0.799997)

Control



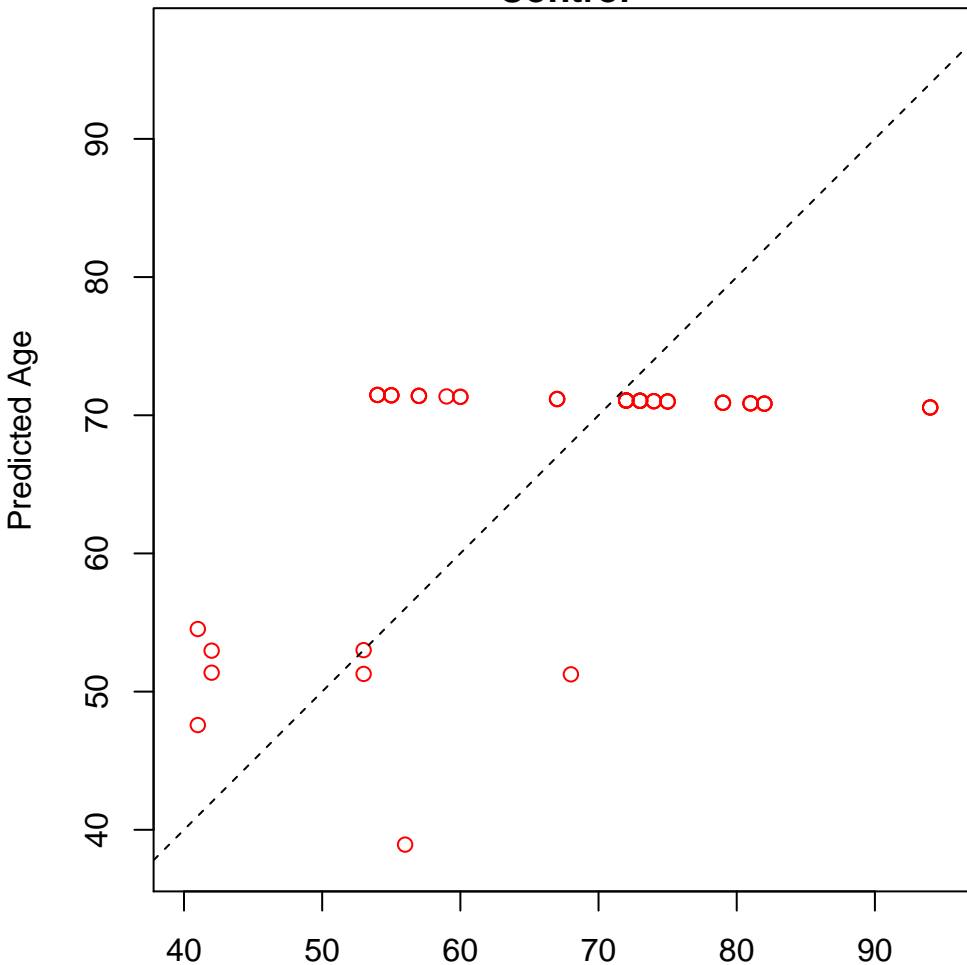
Test



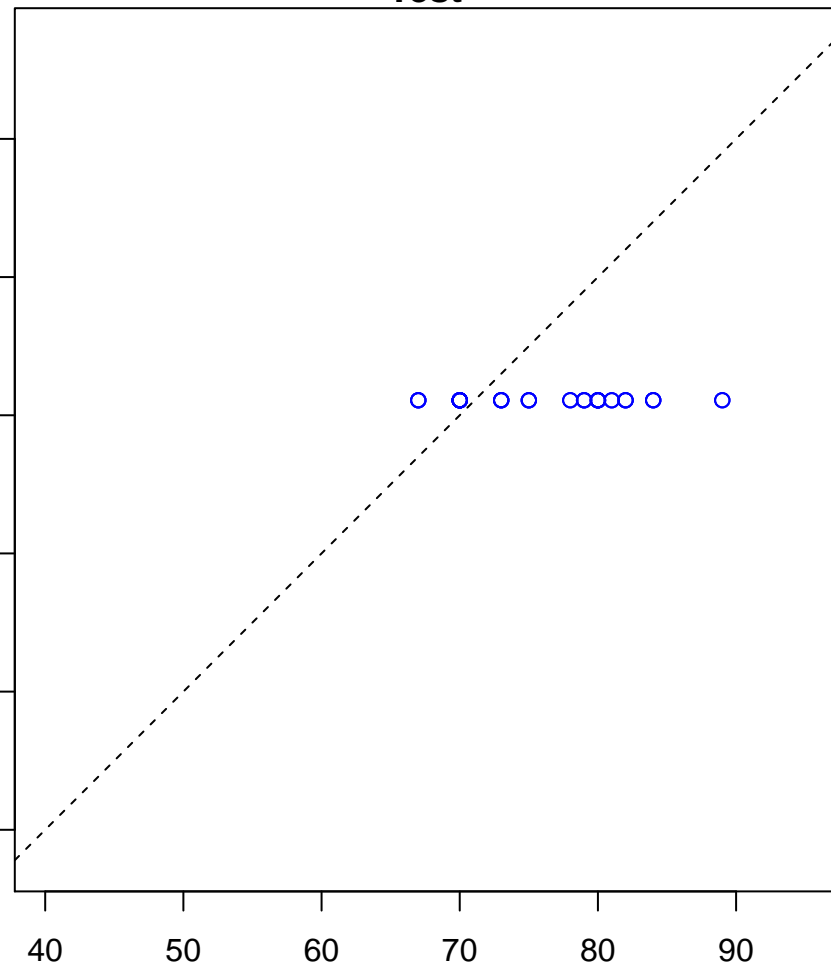
Actual Age

response to light stimulus (Score: 0.799996)

Control

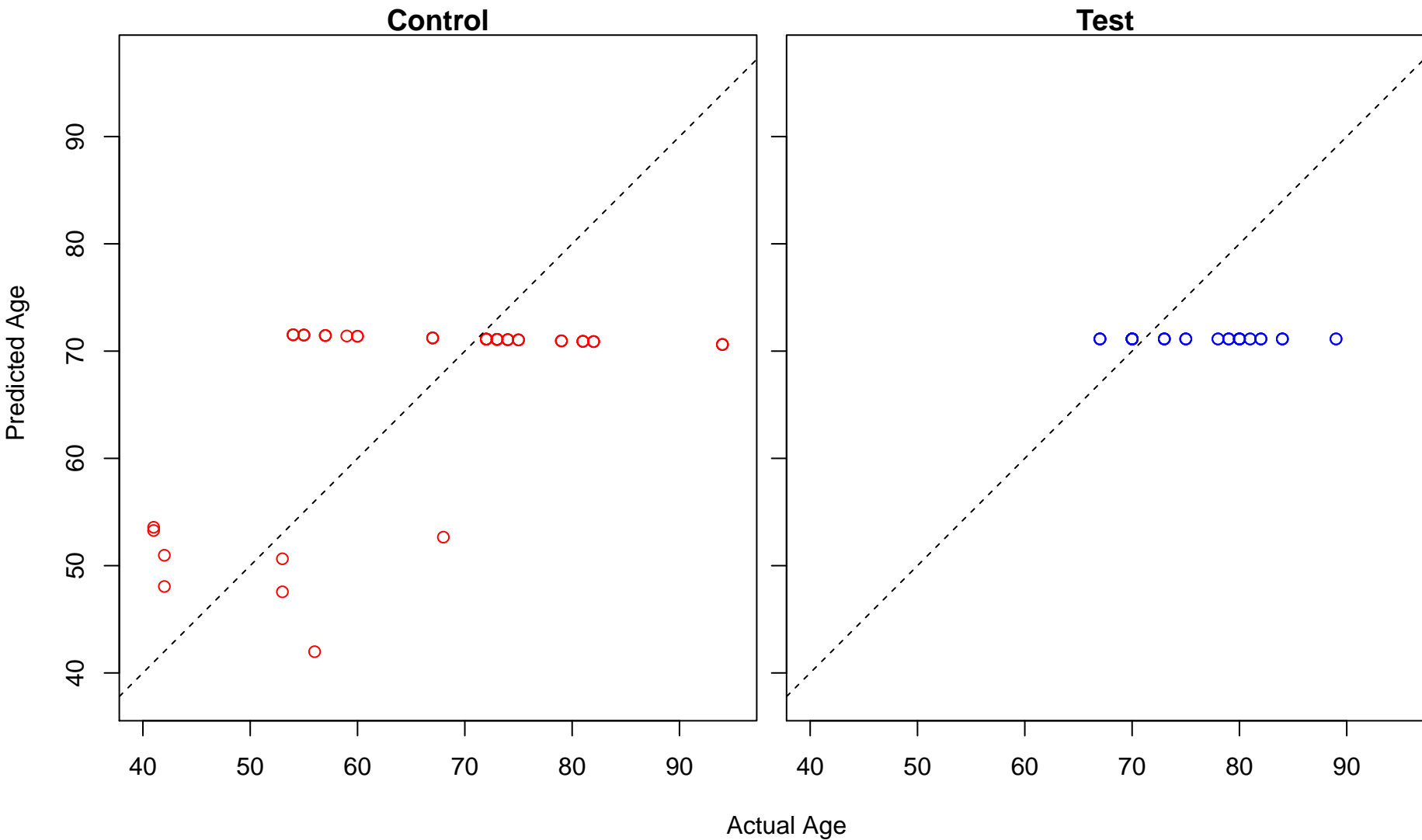


Test

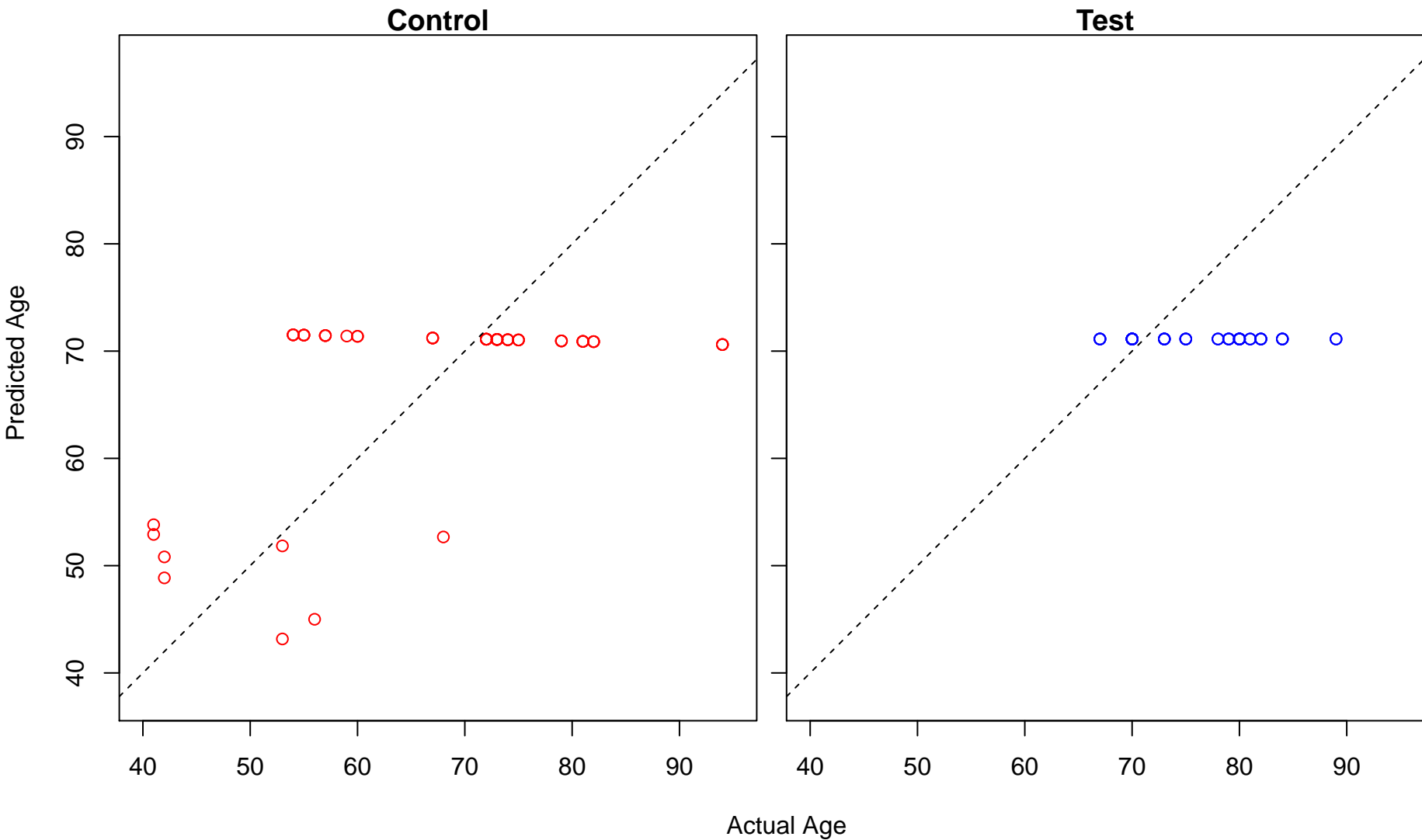


Actual Age

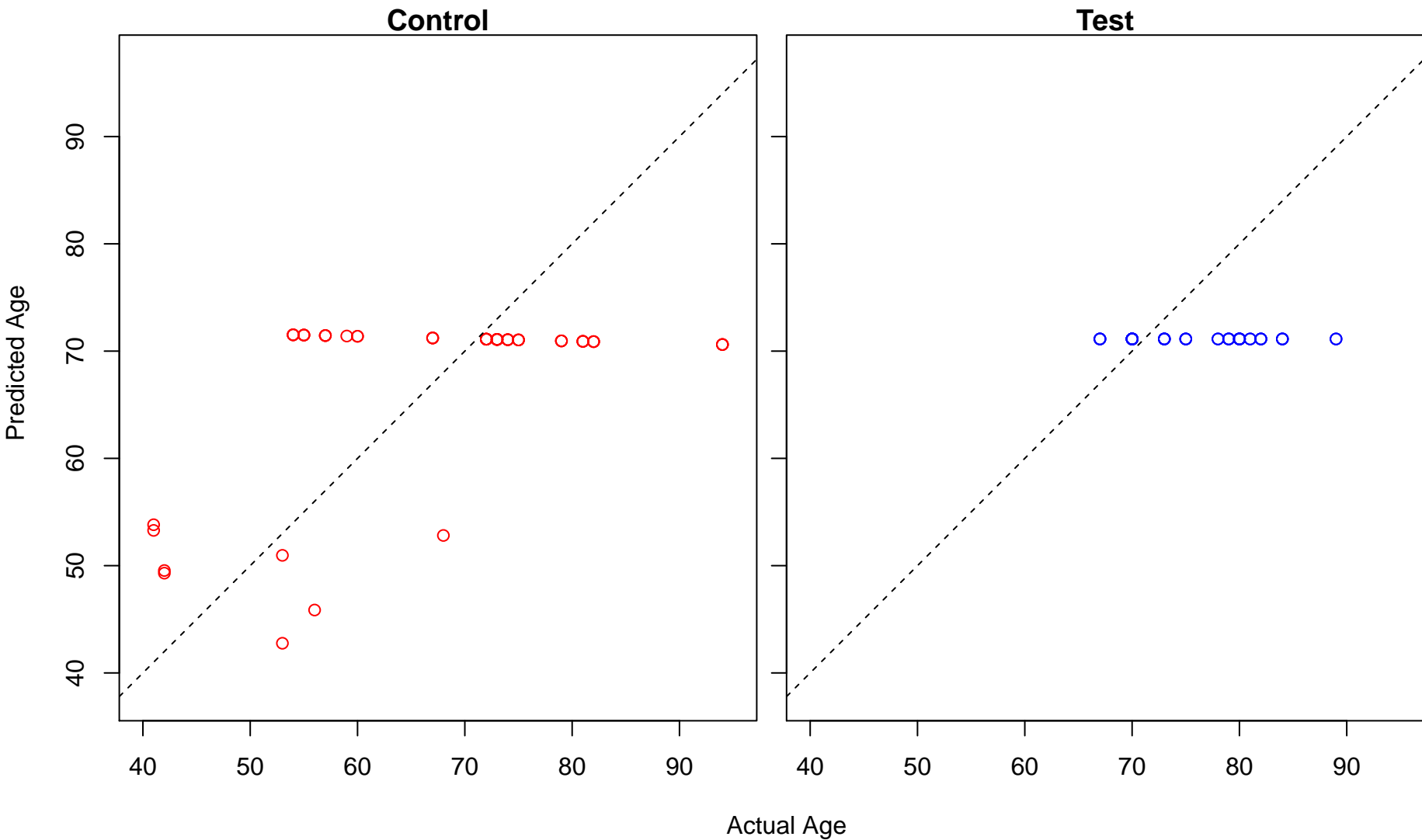
regulation of cellular macromolecule biosynthetic process (Score: 0.799984)



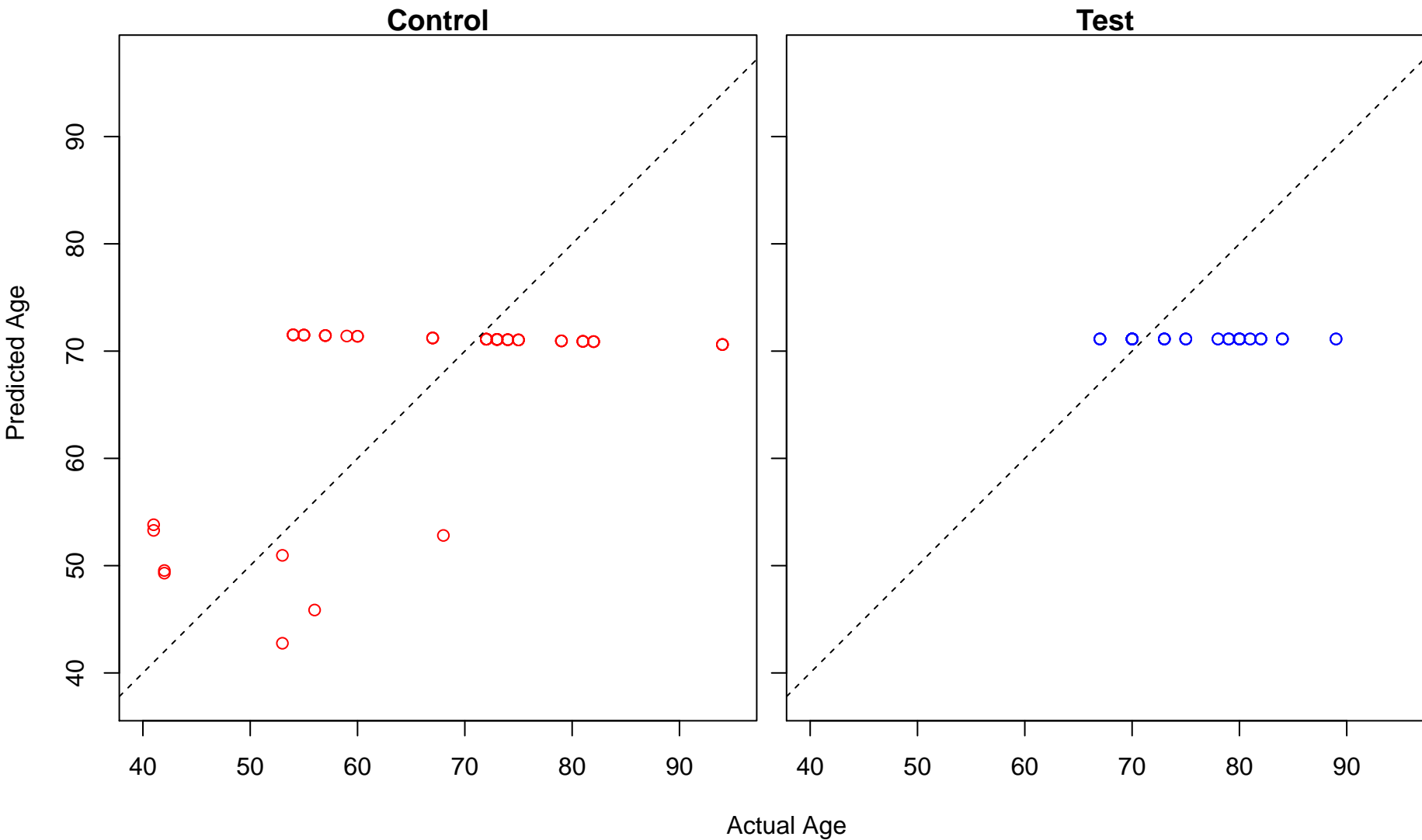
regulation of multicellular organismal development (Score: 0.799967)



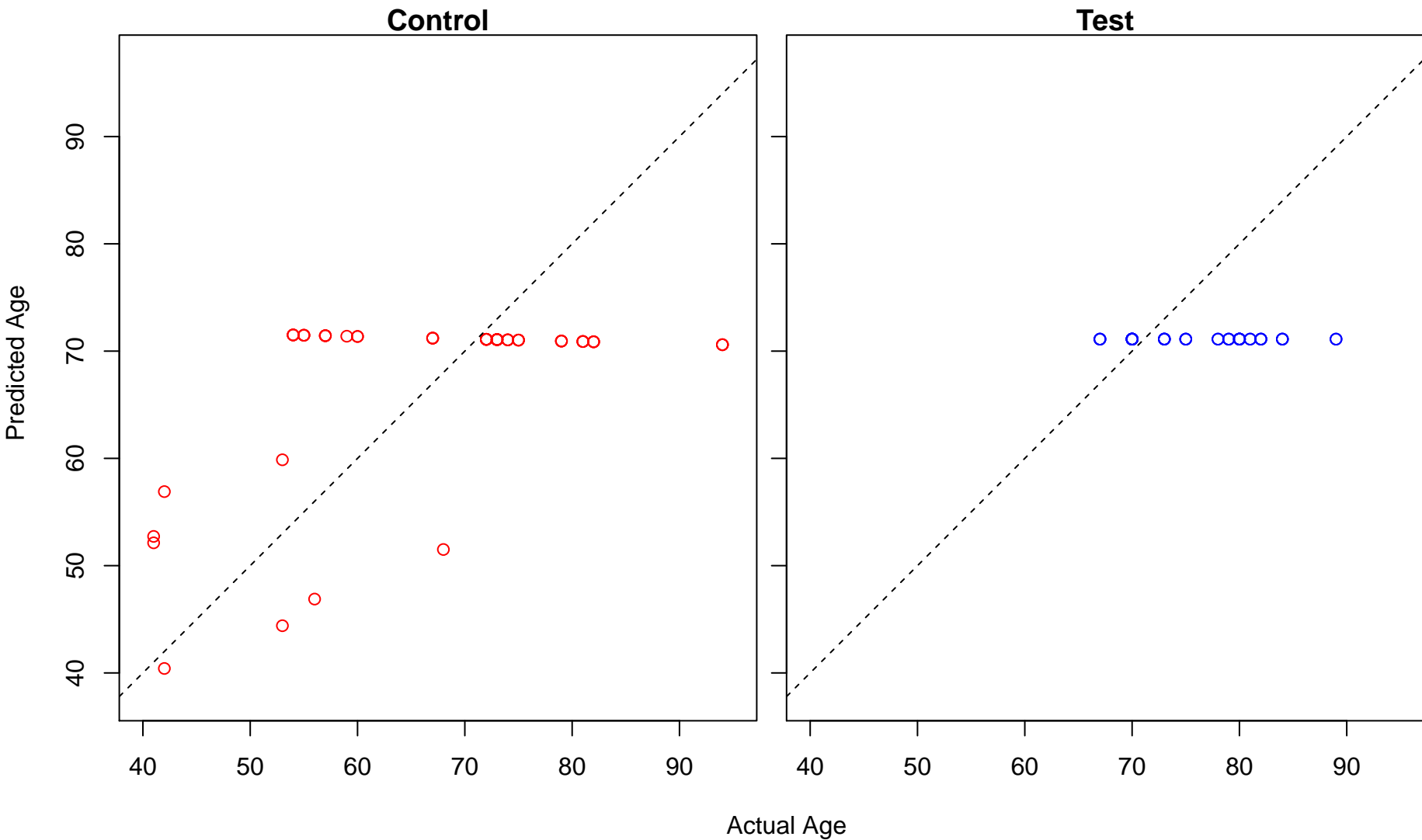
neurogenesis (Score: 0.799956)



generation of neurons (Score: 0.799956)

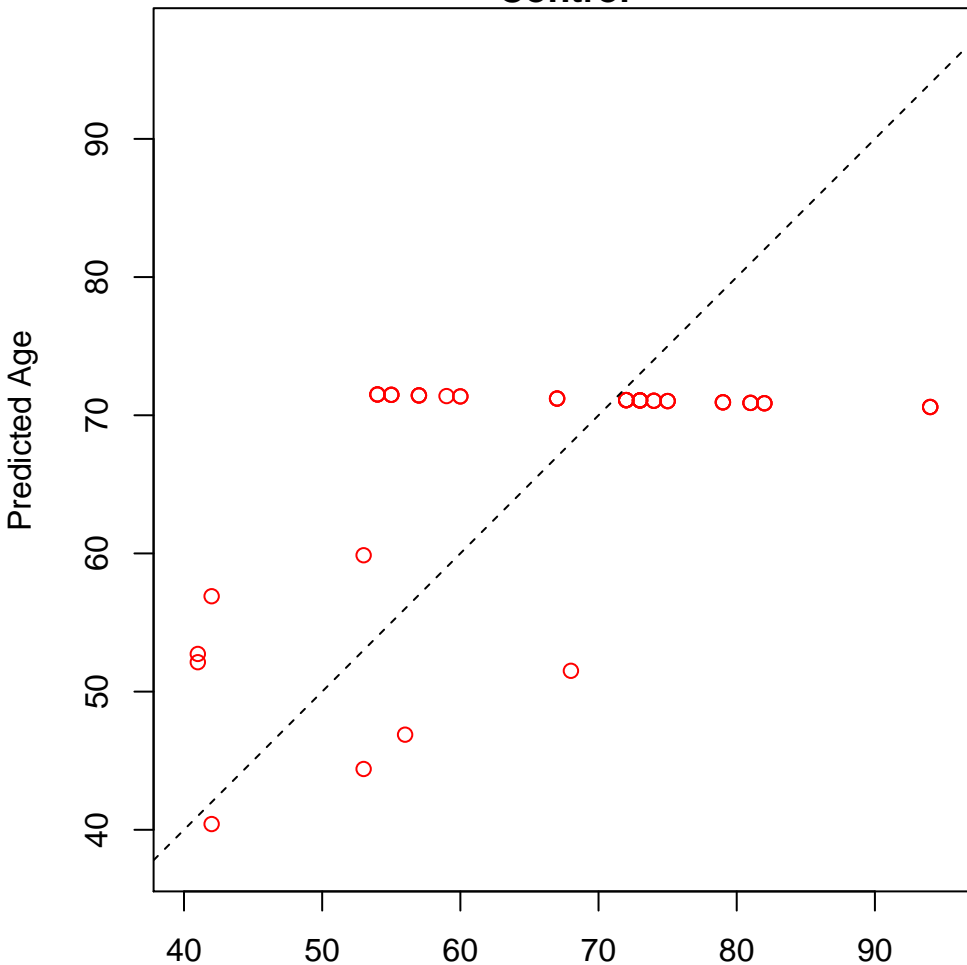


regulation of lyase activity (Score: 0.799926)

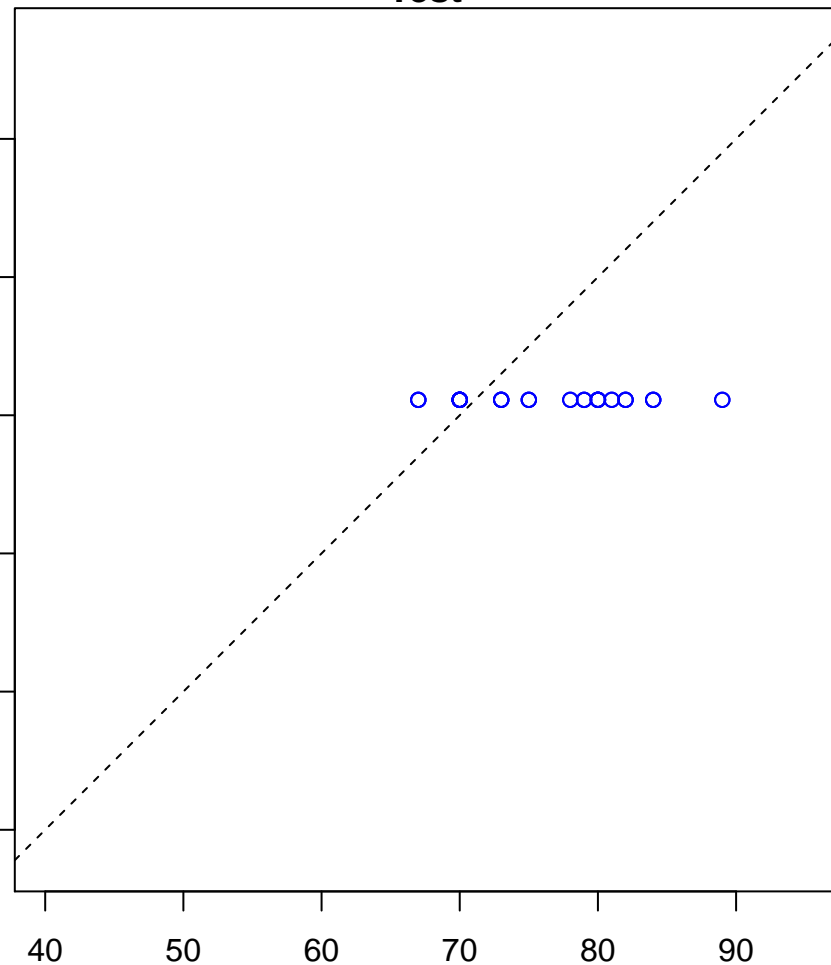


positive regulation of lyase activity (Score: 0.799926)

Control



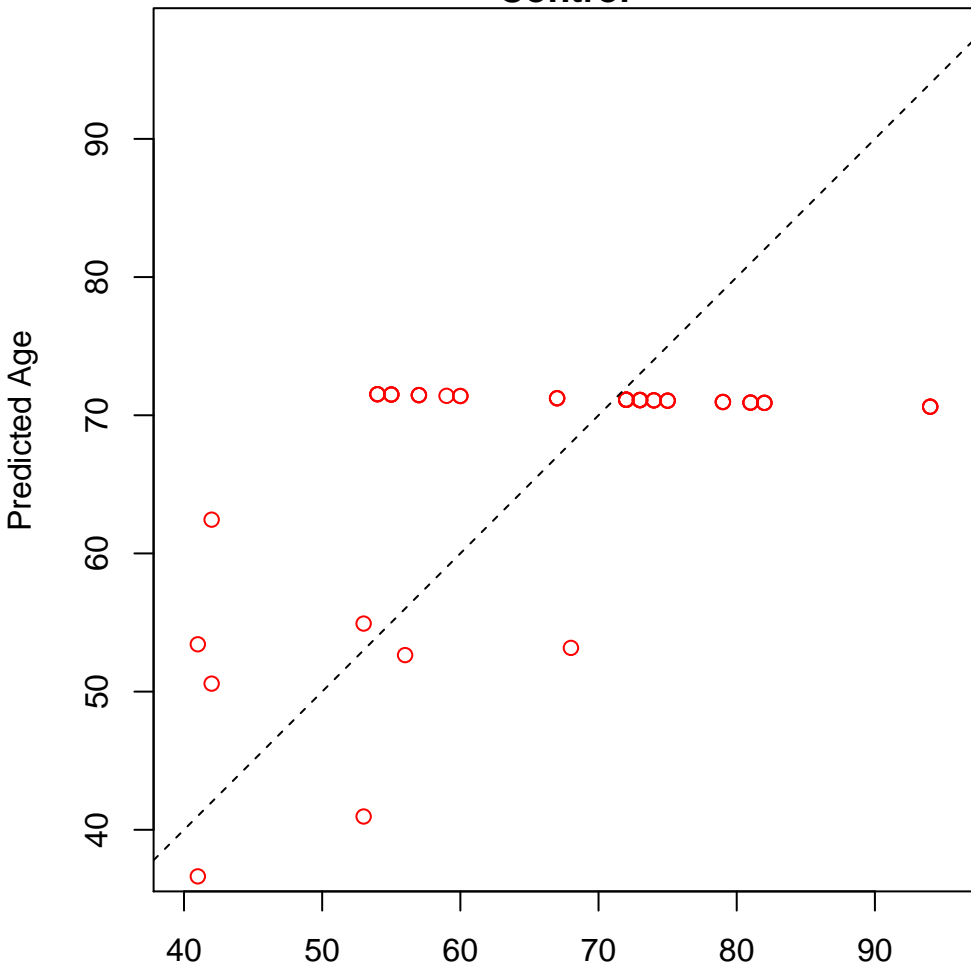
Test



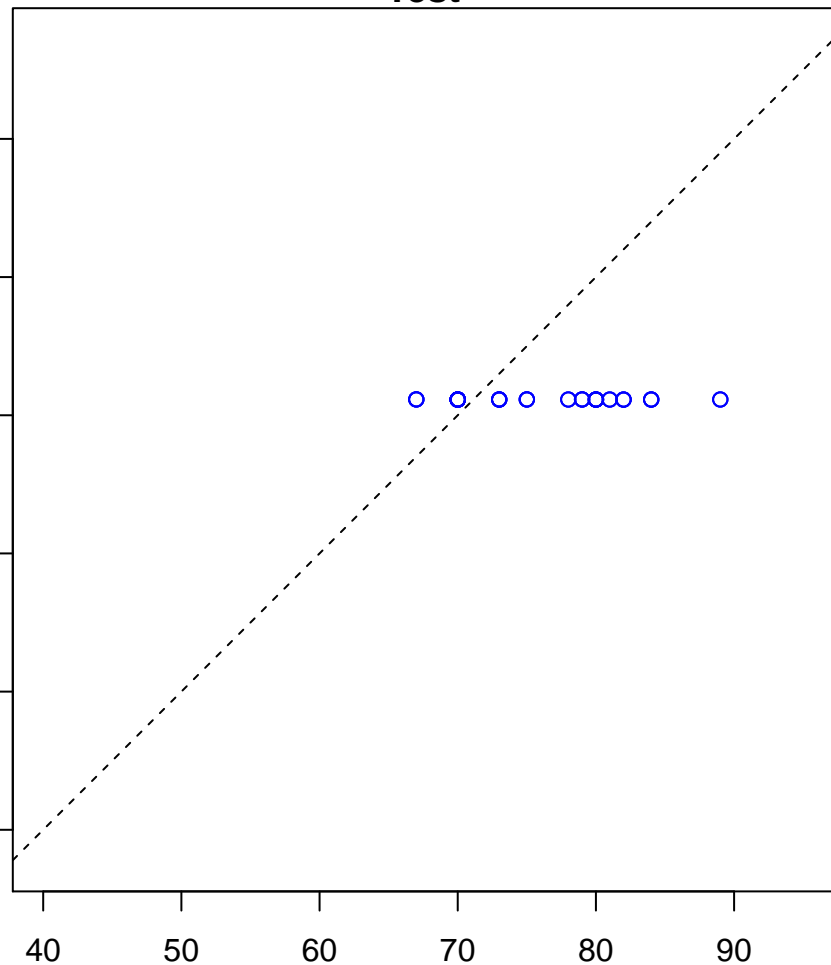
Actual Age

regulation of cell cycle checkpoint (Score: 0.799917)

Control

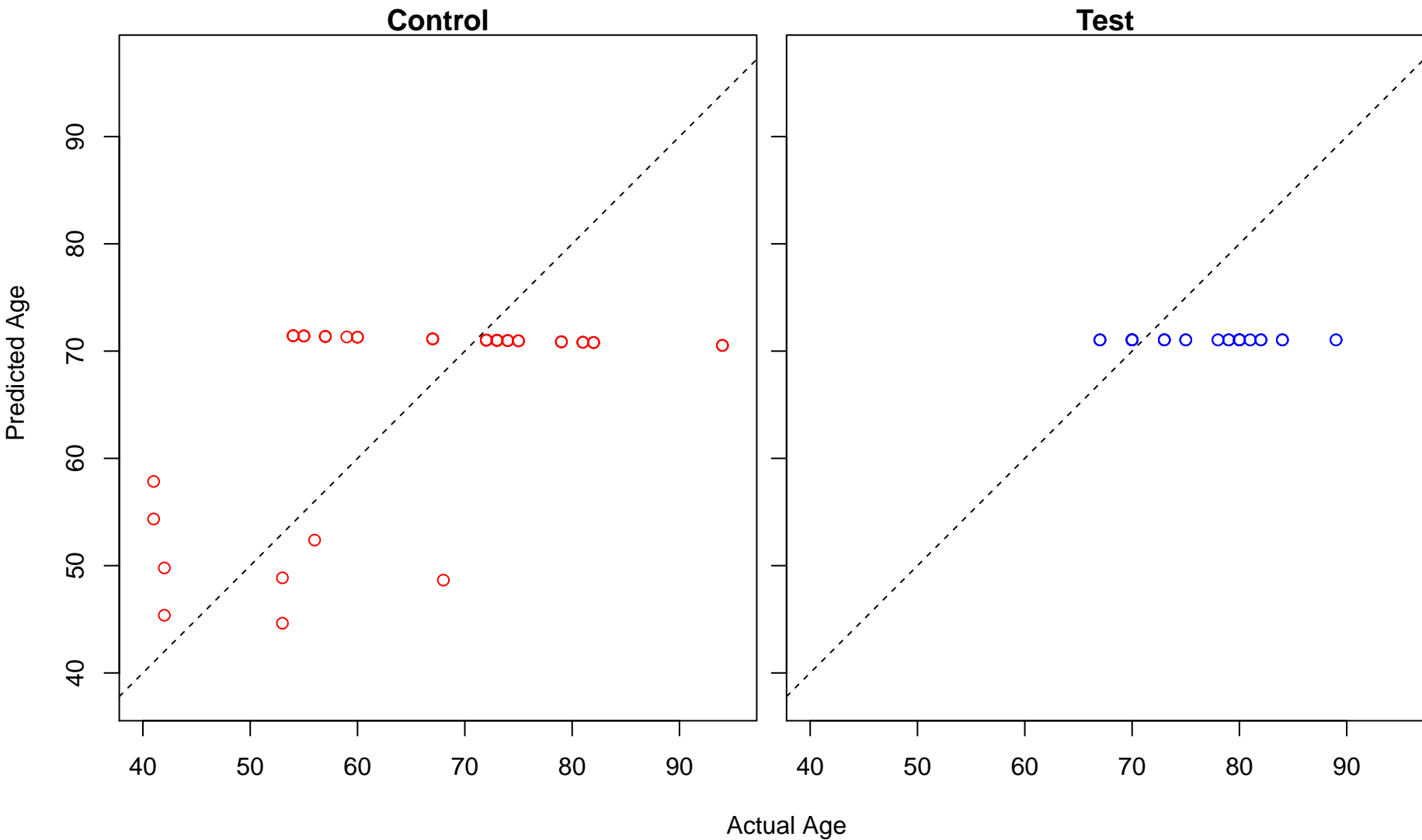


Test



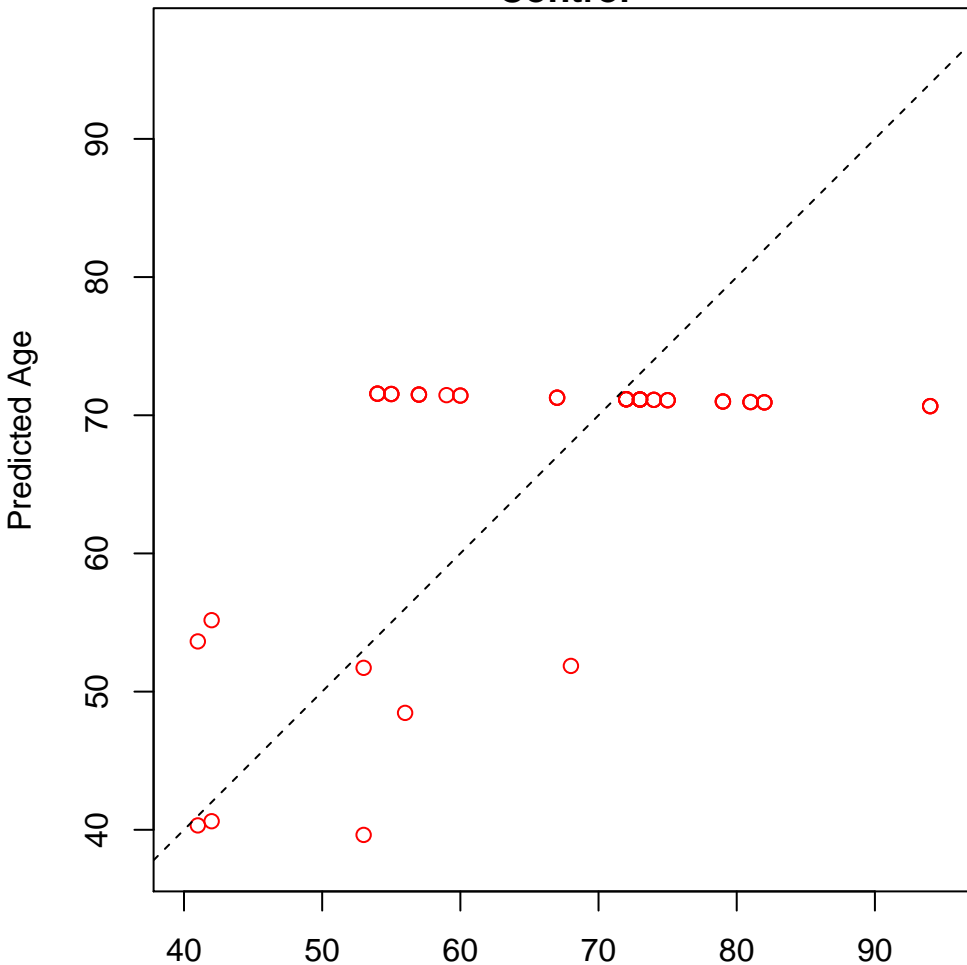
Actual Age

regulation of peptidase activity (Score: 0.799893)

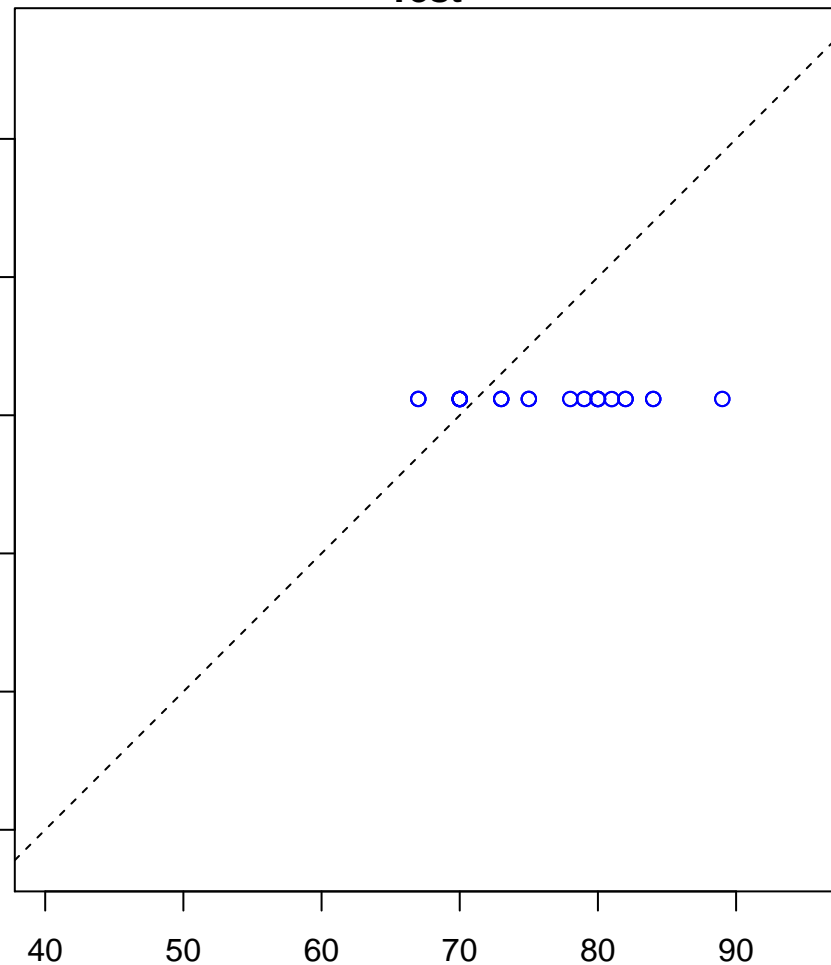


receptor-mediated endocytosis (Score: 0.799872)

Control

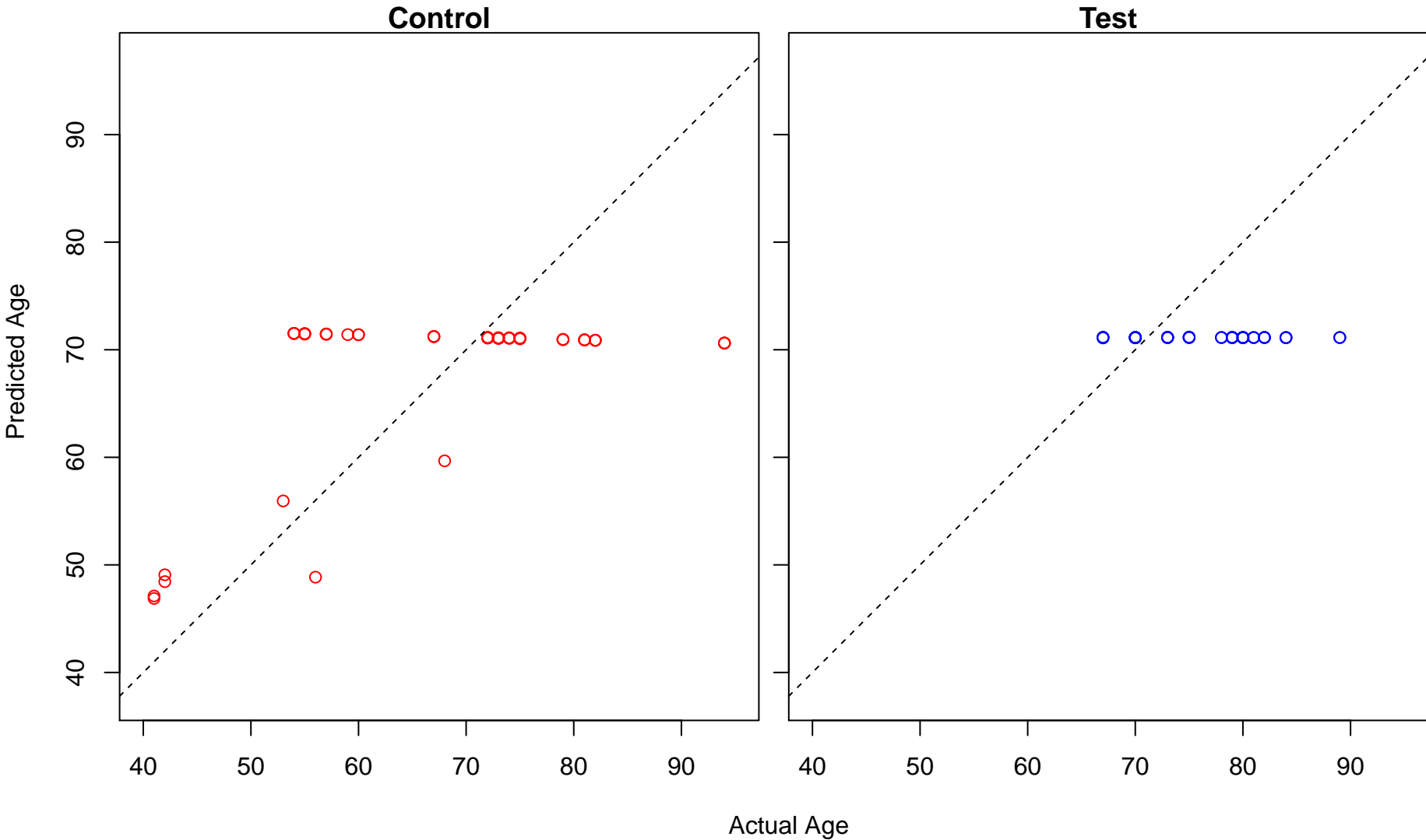


Test



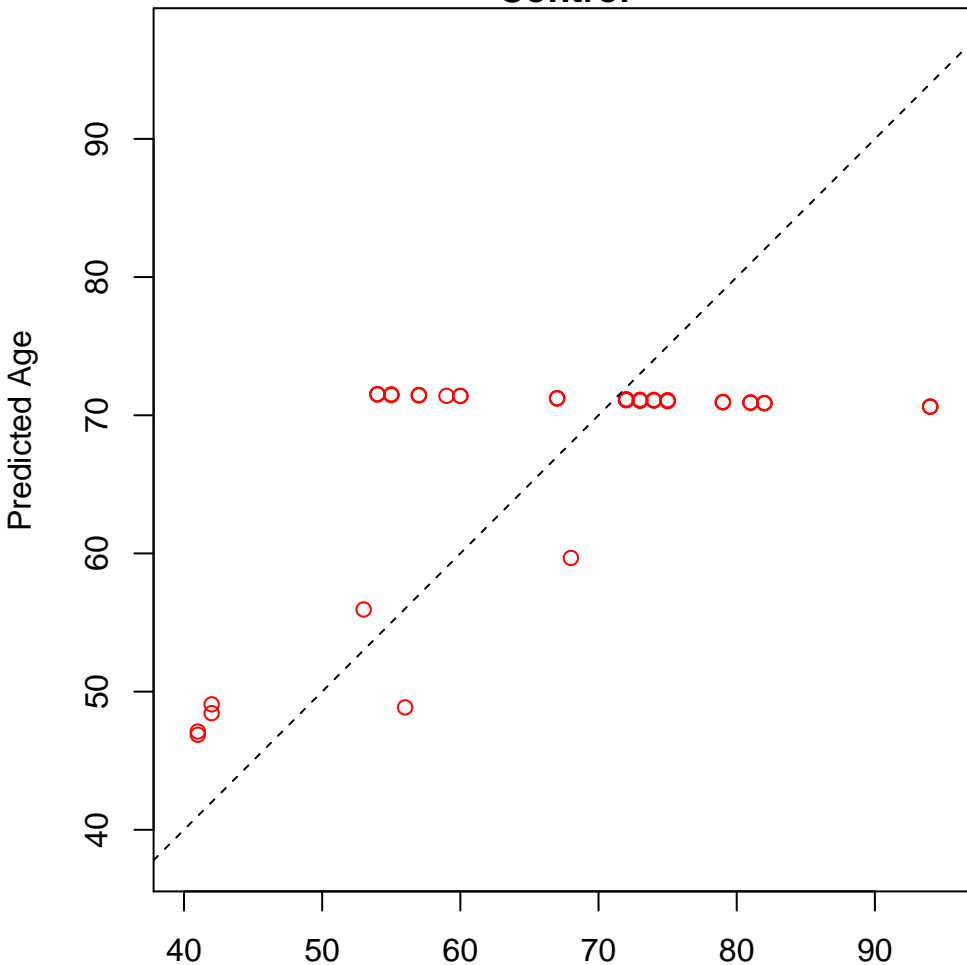
Actual Age

regulation of interferon- γ production (Score: 0.799847)

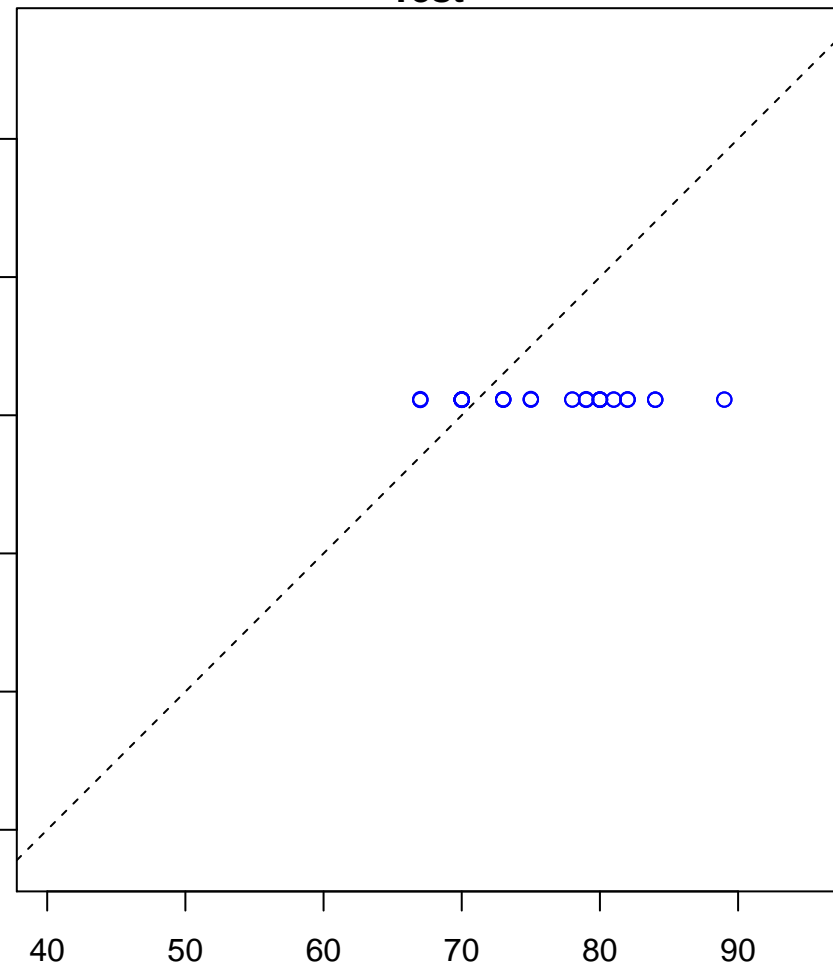


regulation of interleukin-1 production (Score: 0.799847)

Control

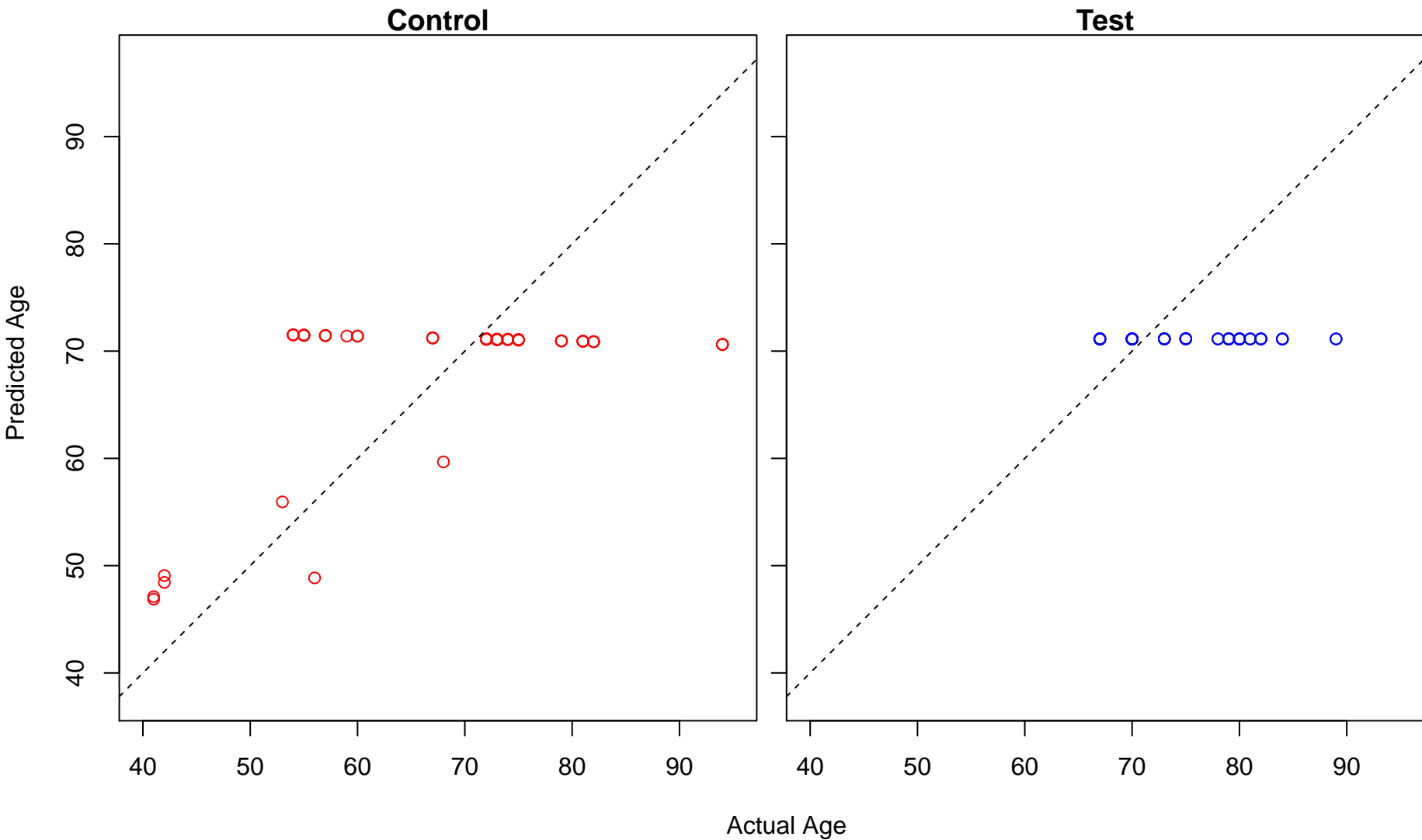


Test



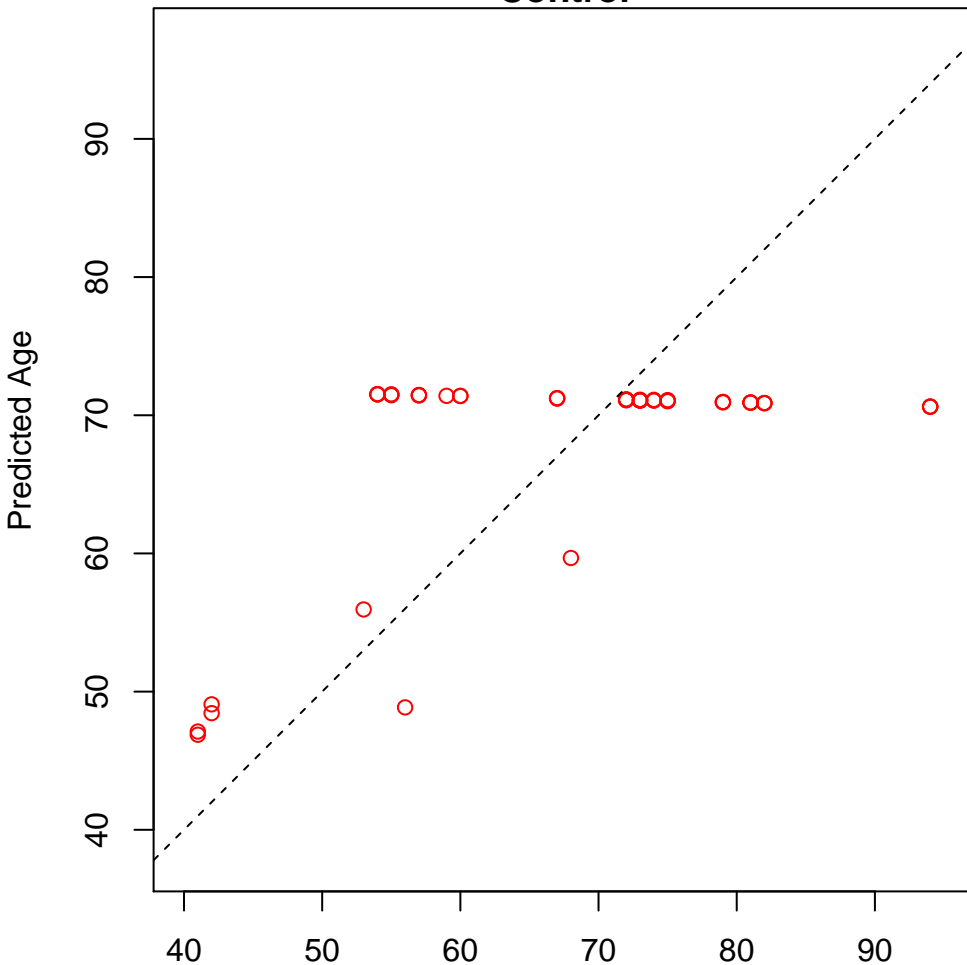
Actual Age

negative regulation of interferon-gamma production (Score: 0.799847)

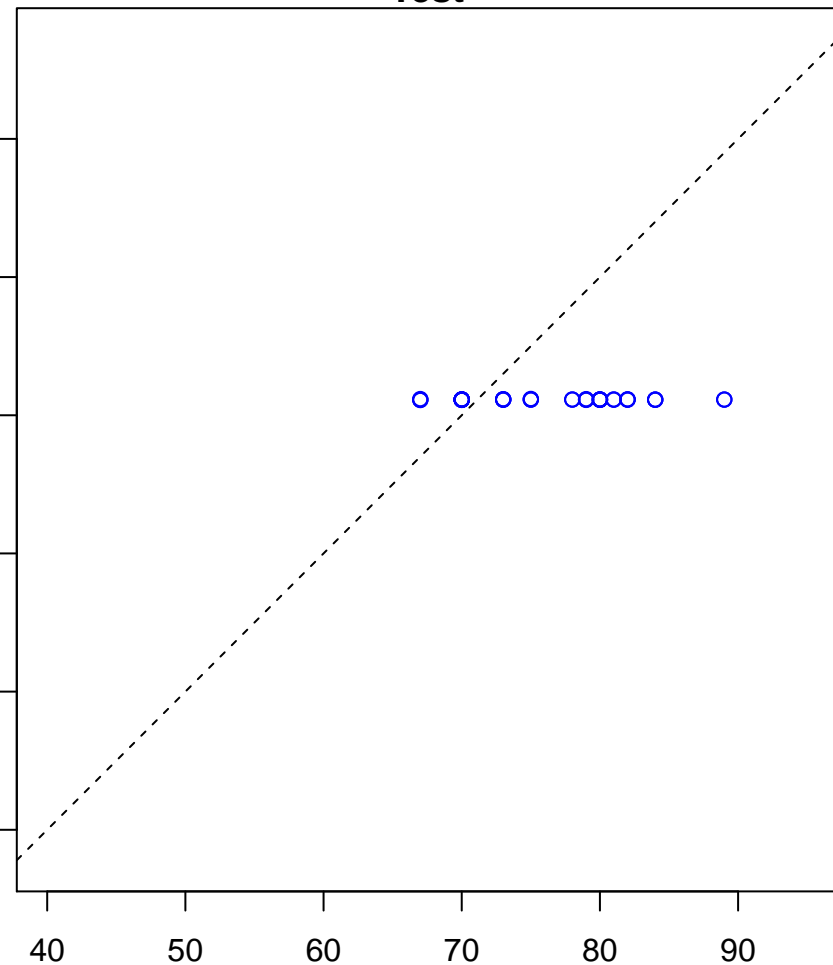


regulation of interleukin-1 secretion (Score: 0.799847)

Control

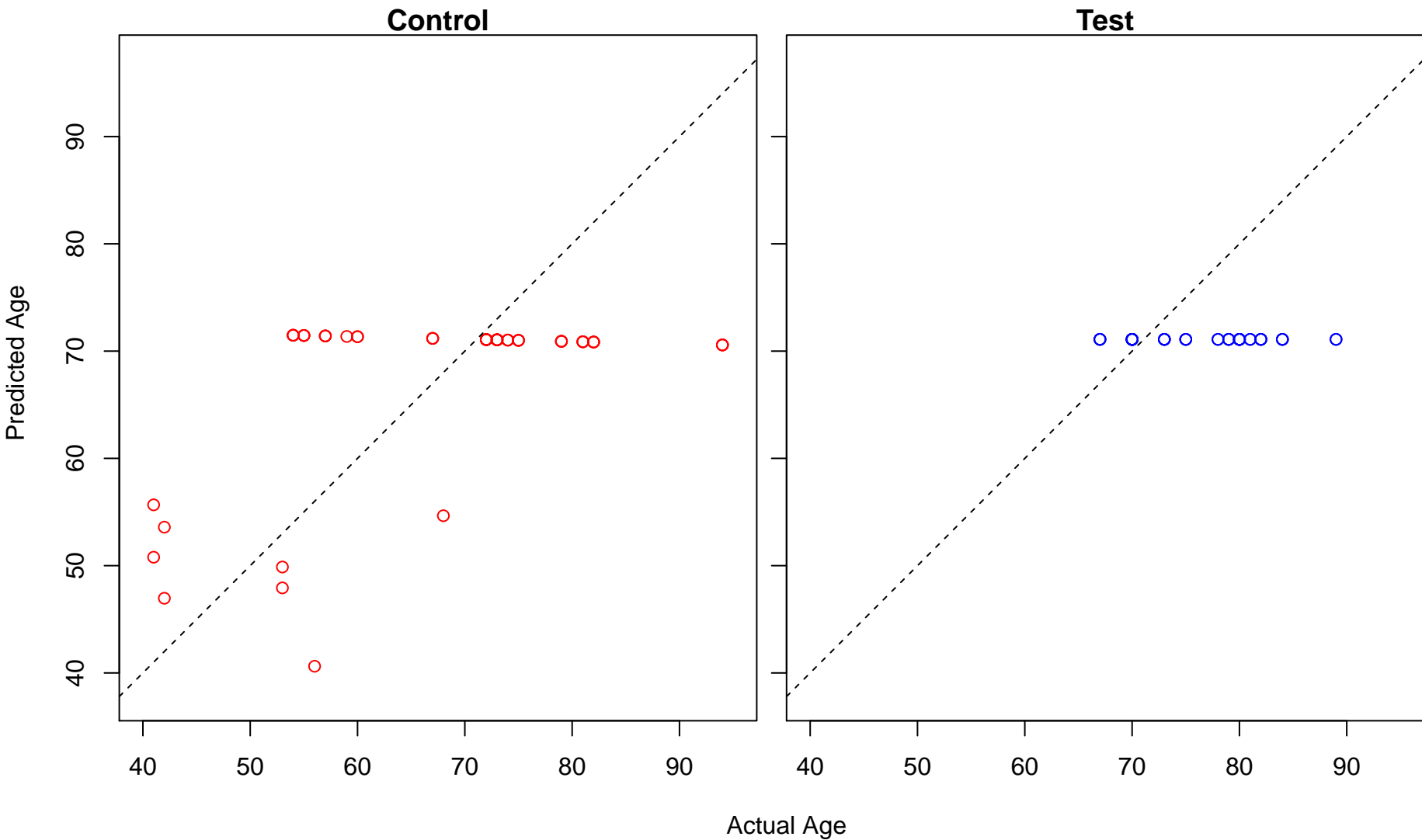


Test

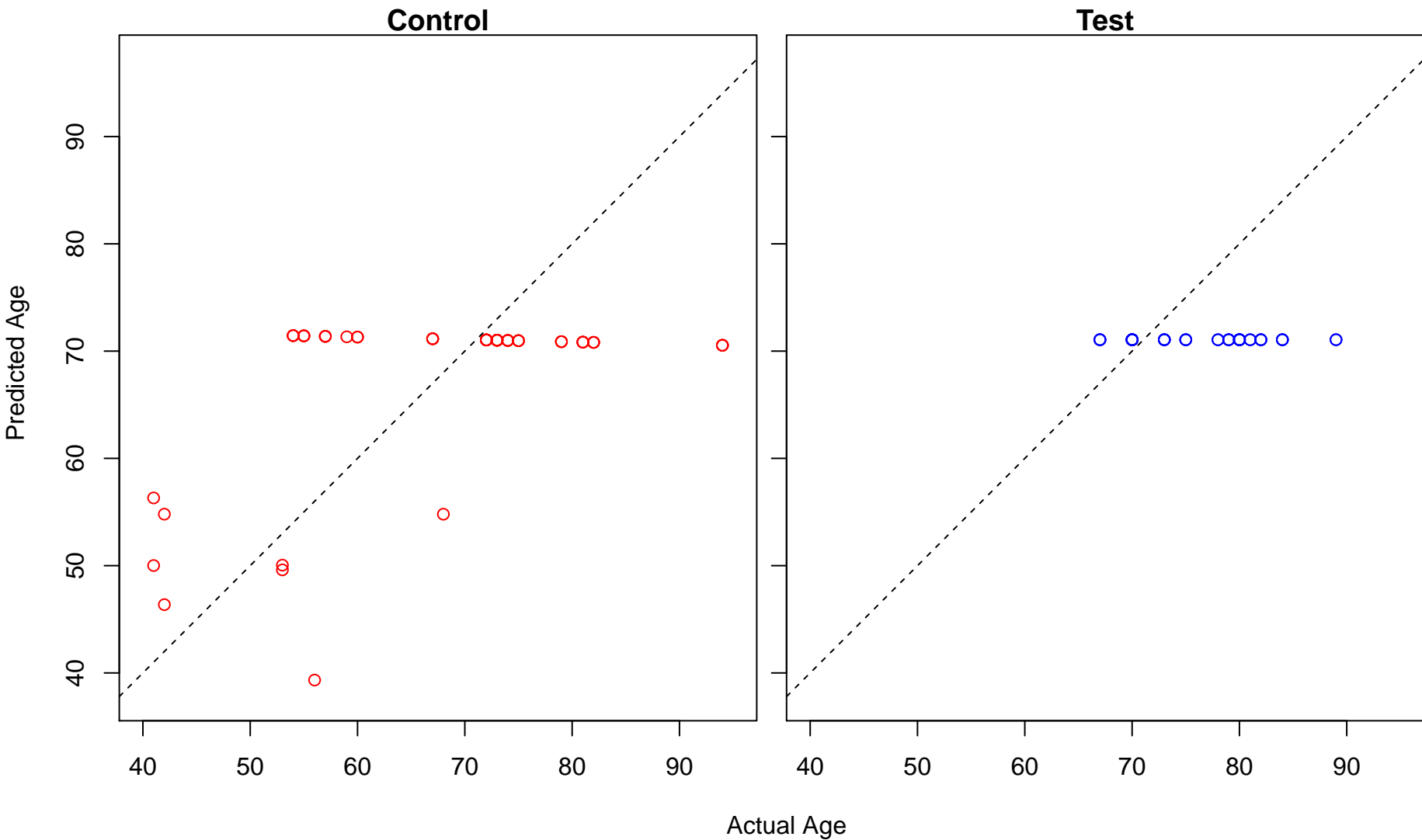


Actual Age

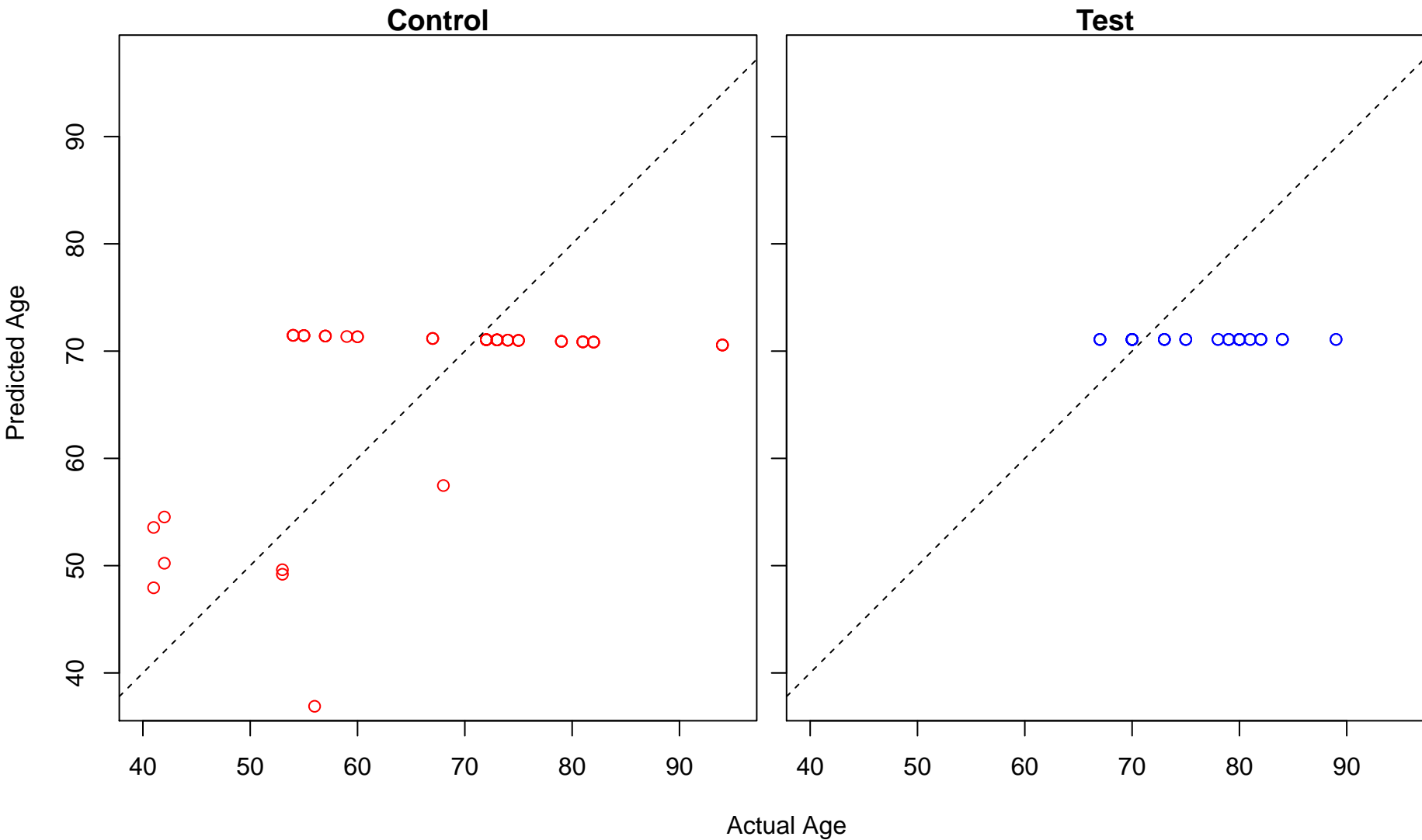
multi-organism process (Score: 0.799814)



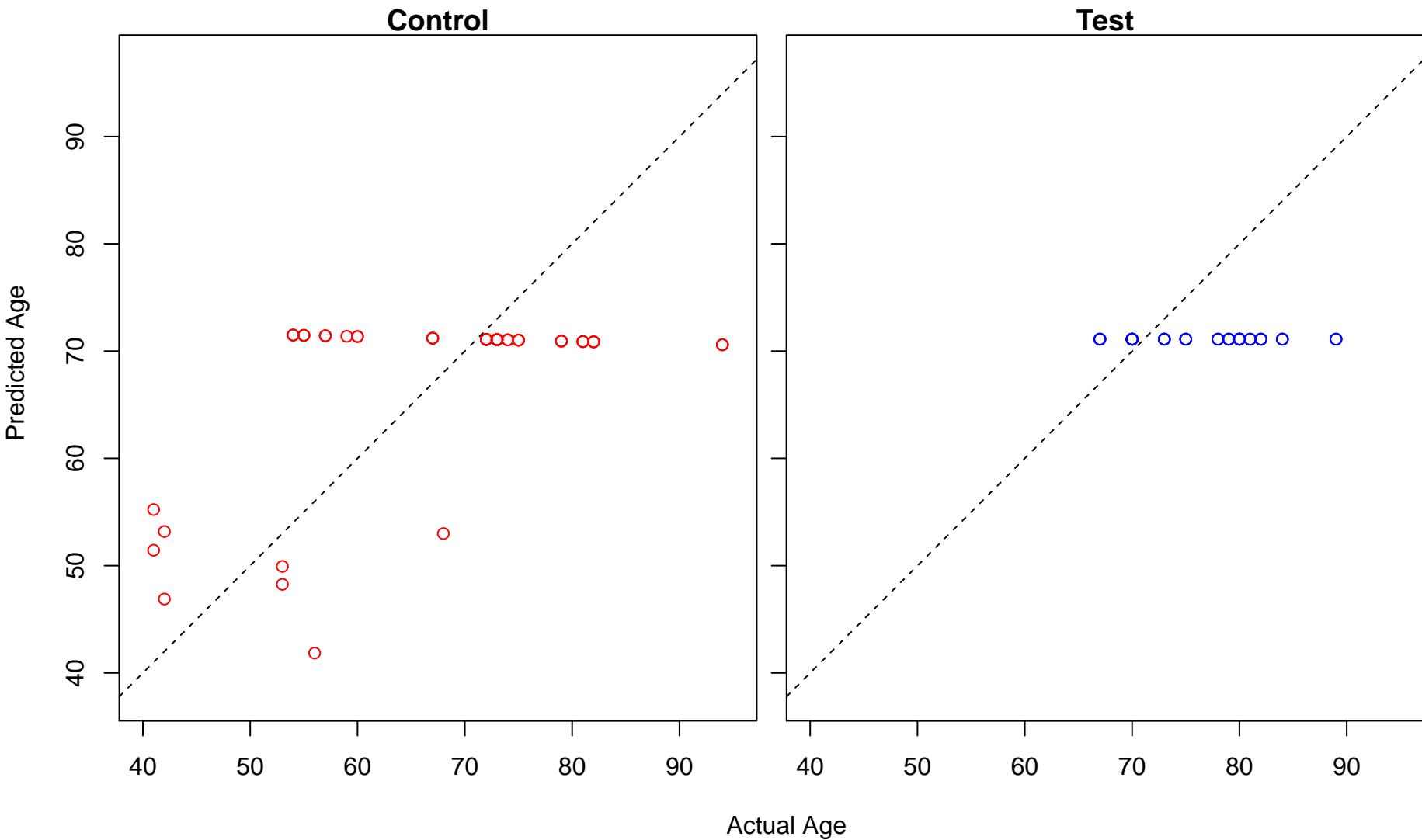
gene expression (Score: 0.799803)



regulation of cellular amide metabolic process (Score: 0.799774)

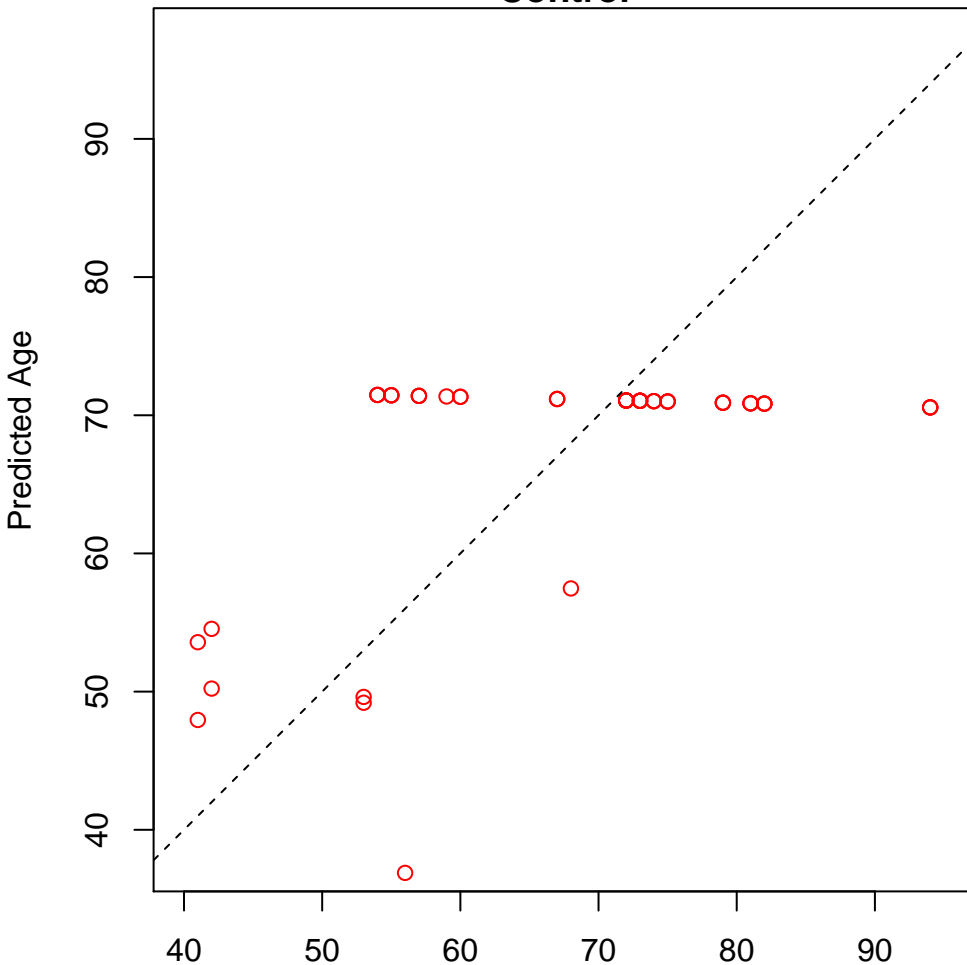


negative regulation of biological process (Score: 0.799768)

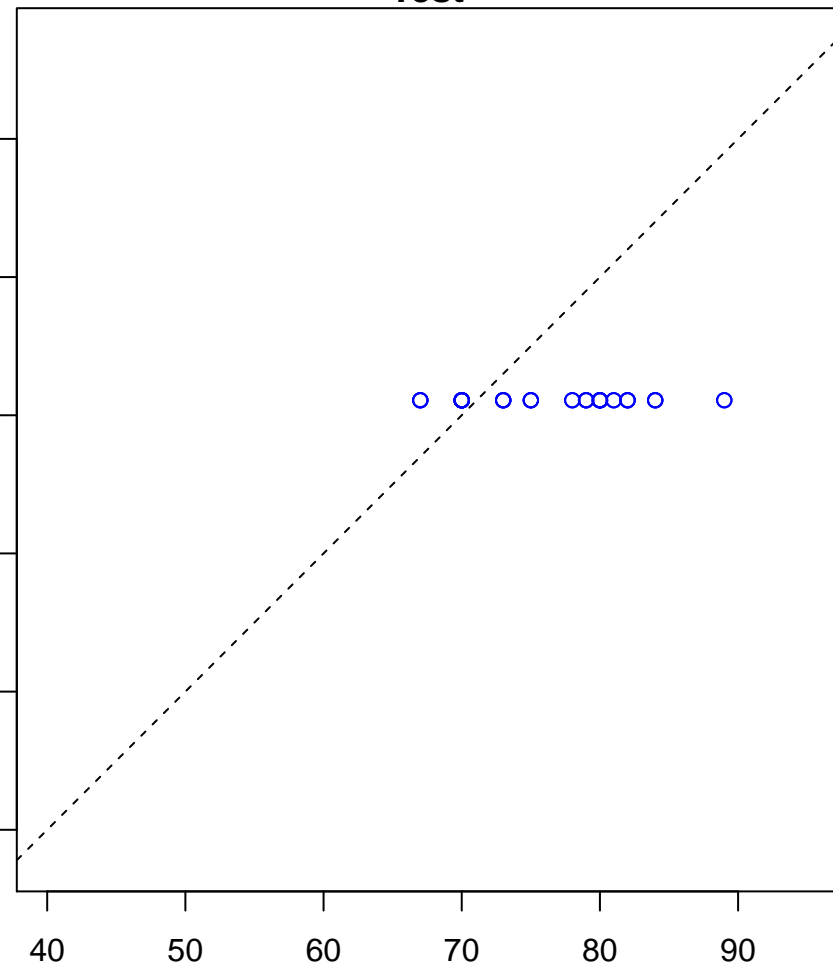


regulation of translation (Score: 0.799735)

Control

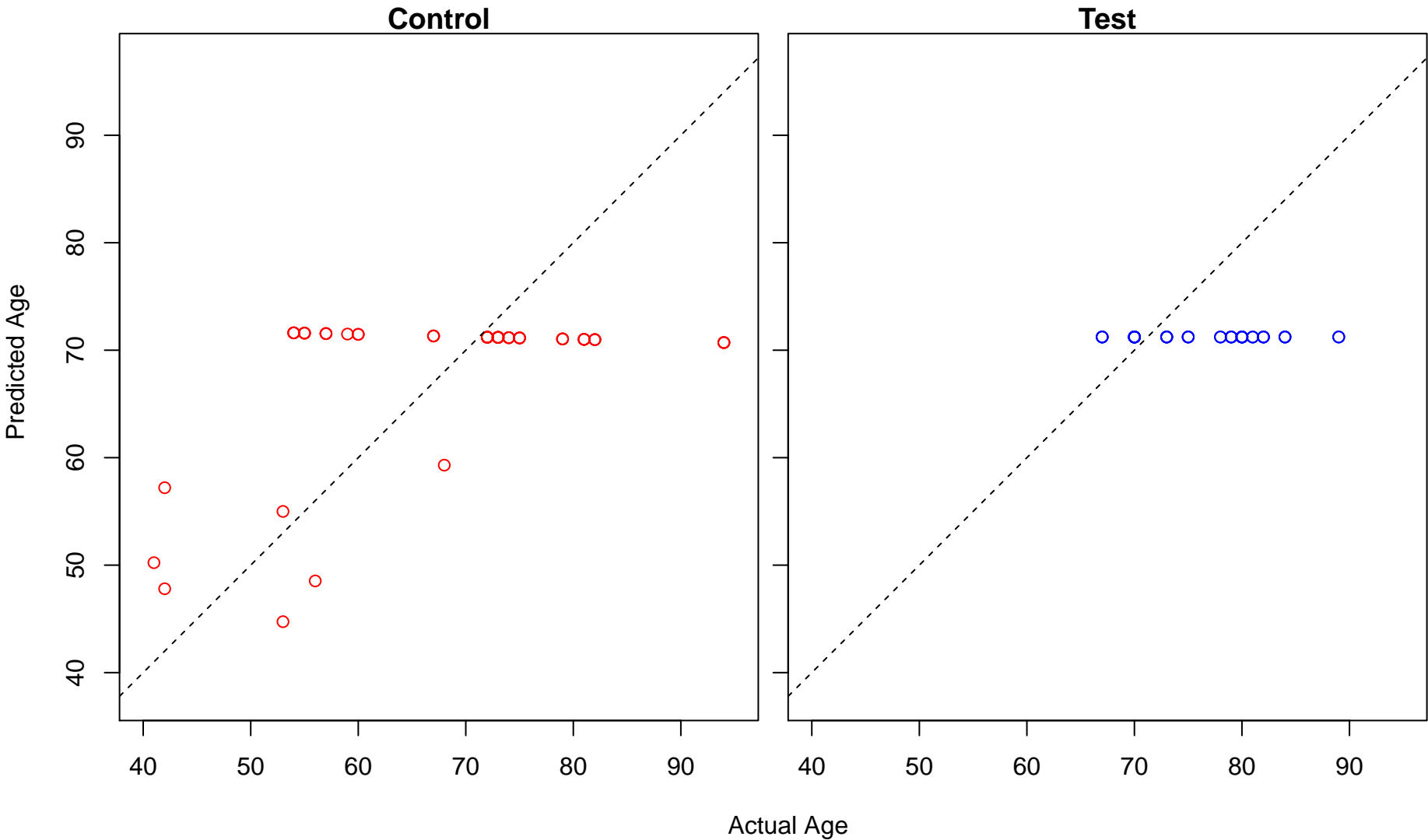


Test



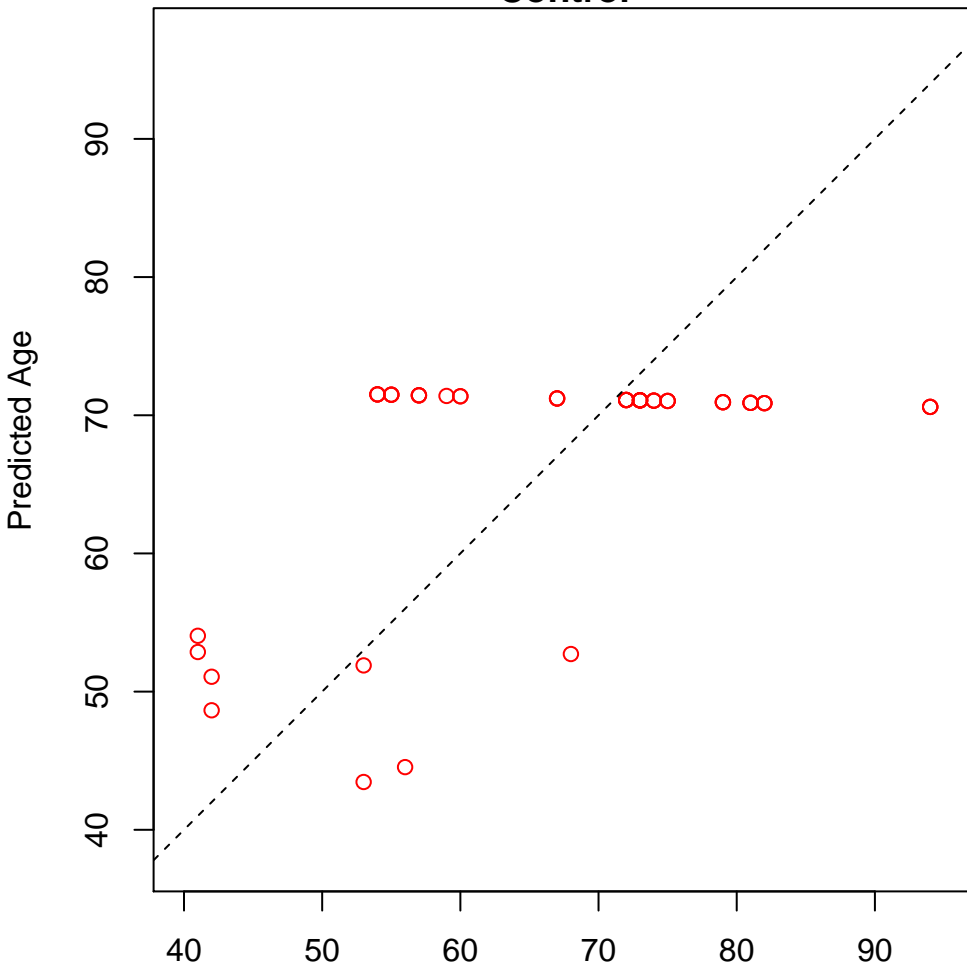
Actual Age

carbohydrate derivative metabolic process (Score: 0.799721)

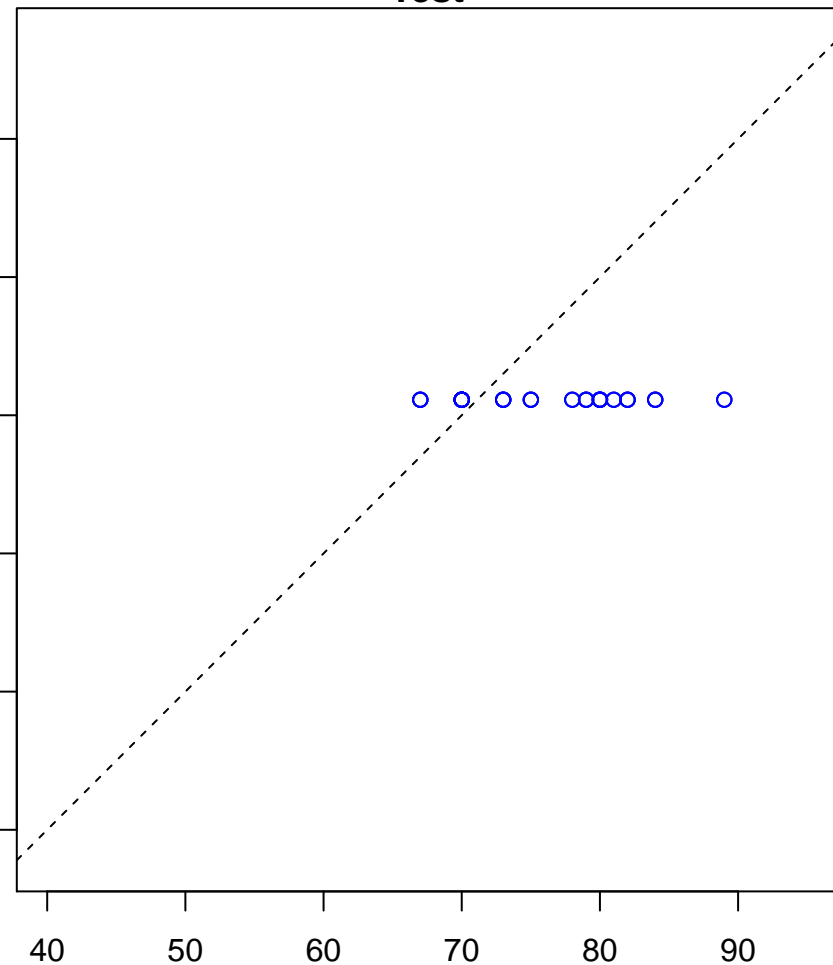


regulation of cell differentiation (Score: 0.799718)

Control



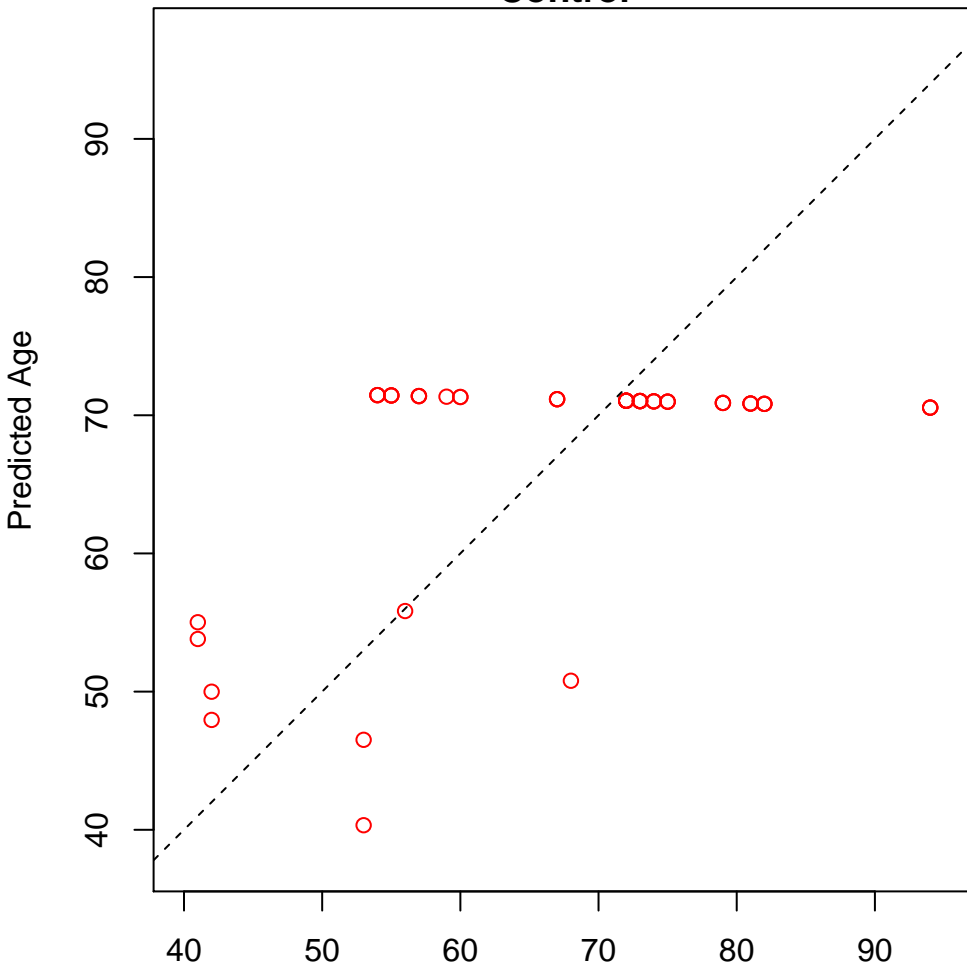
Test



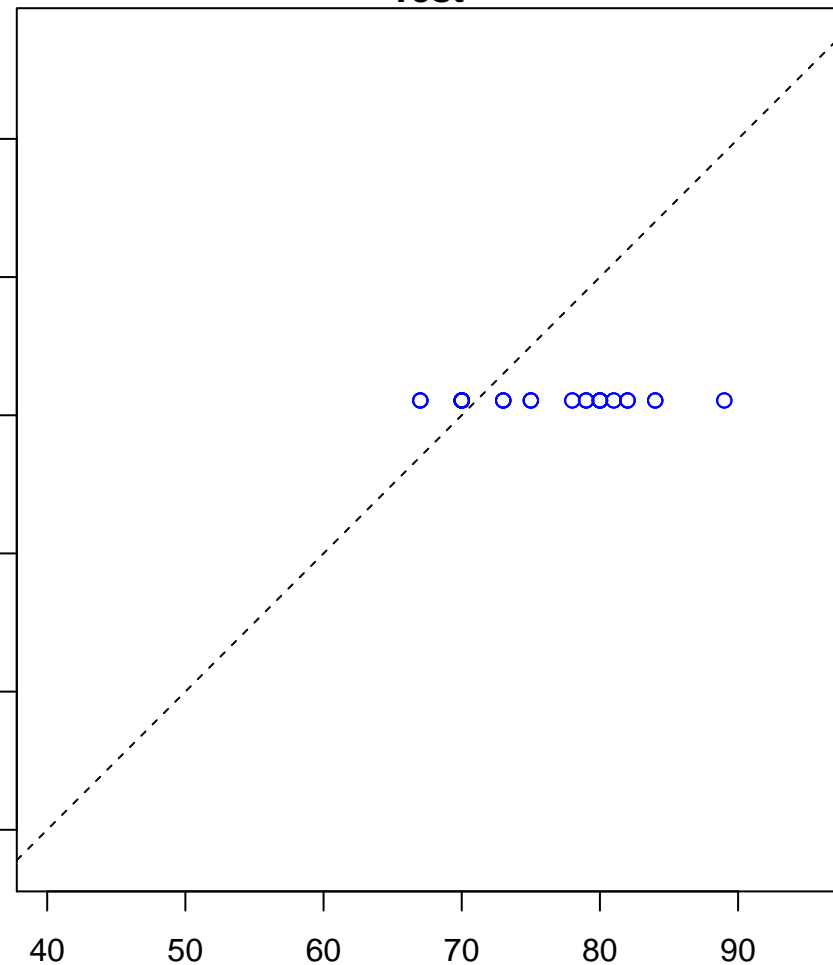
Actual Age

small GTPase mediated signal transduction (Score: 0.799718)

Control



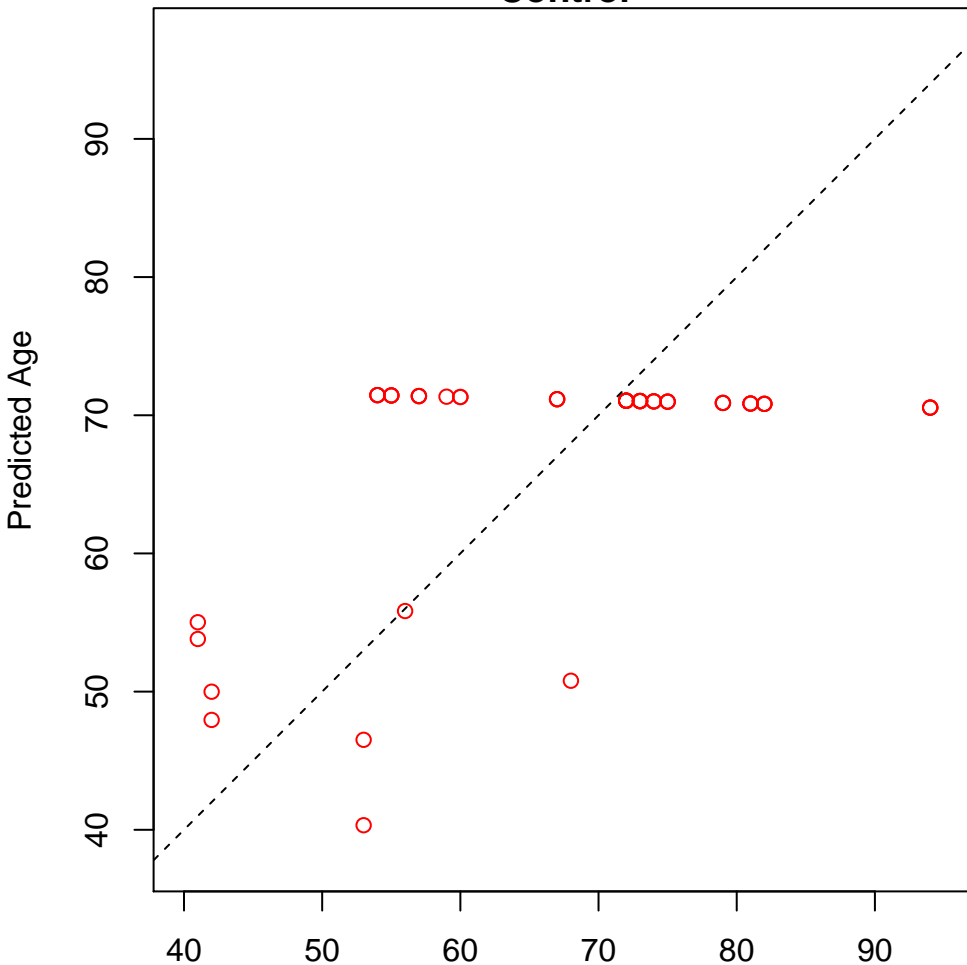
Test



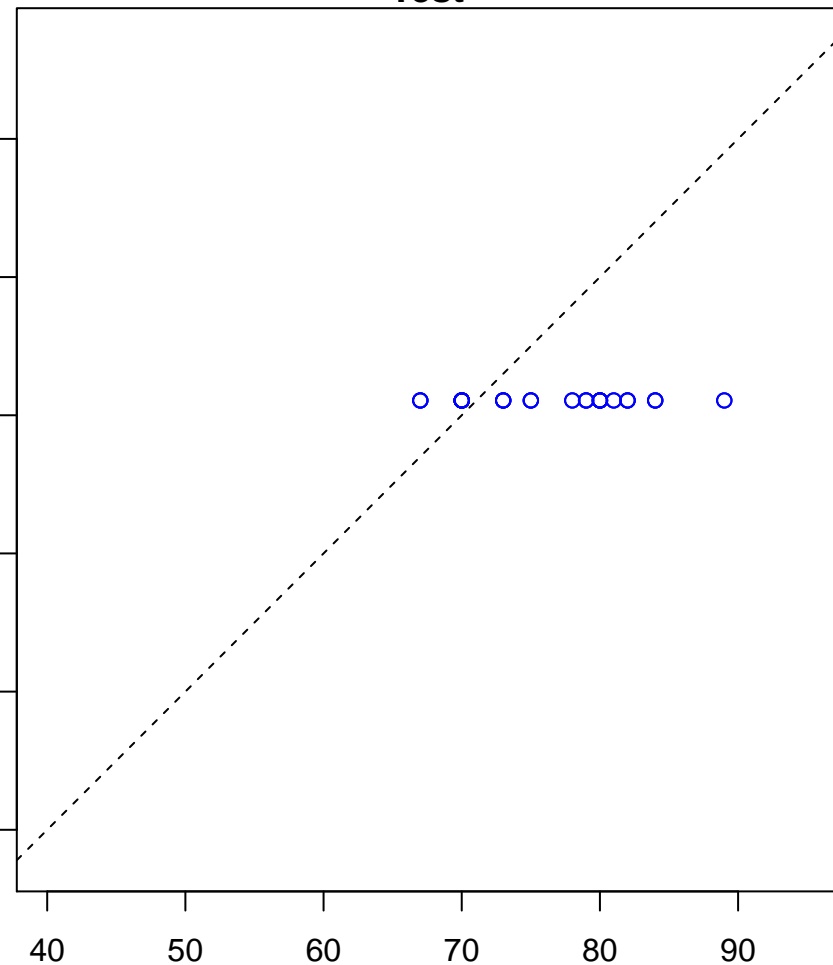
Actual Age

Ras protein signal transduction (Score: 0.799718)

Control



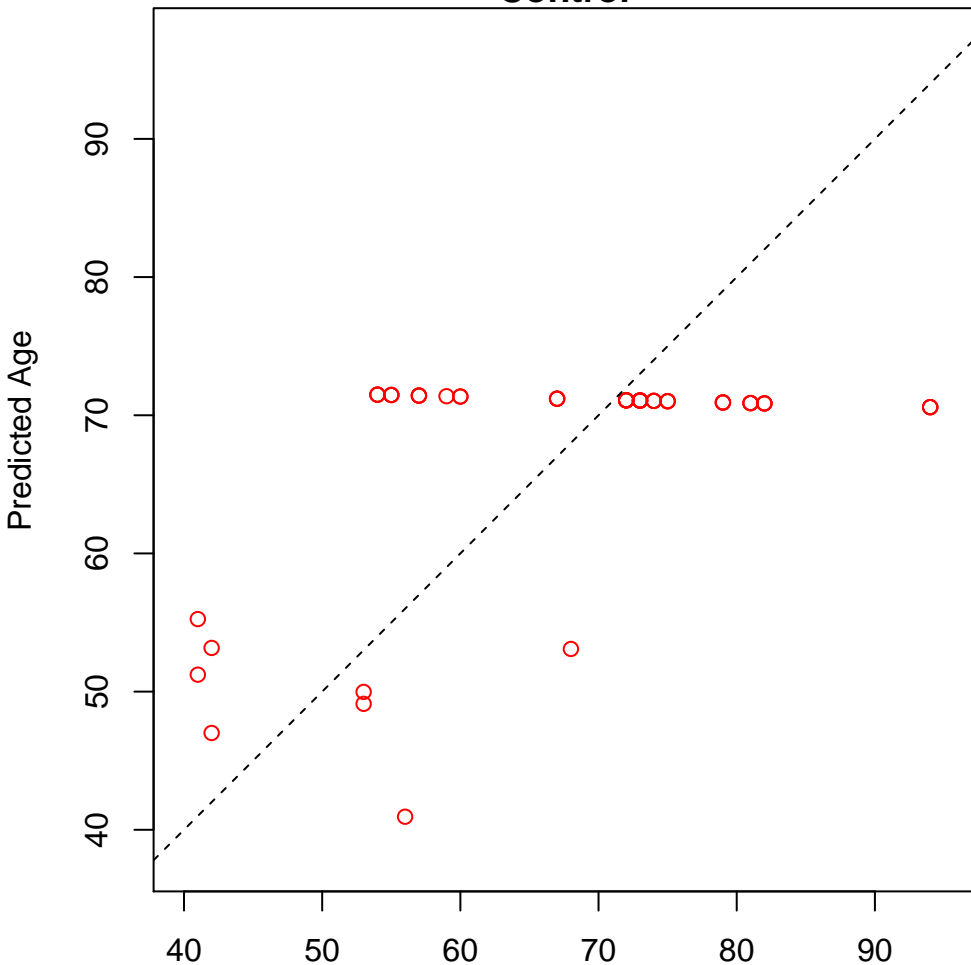
Test



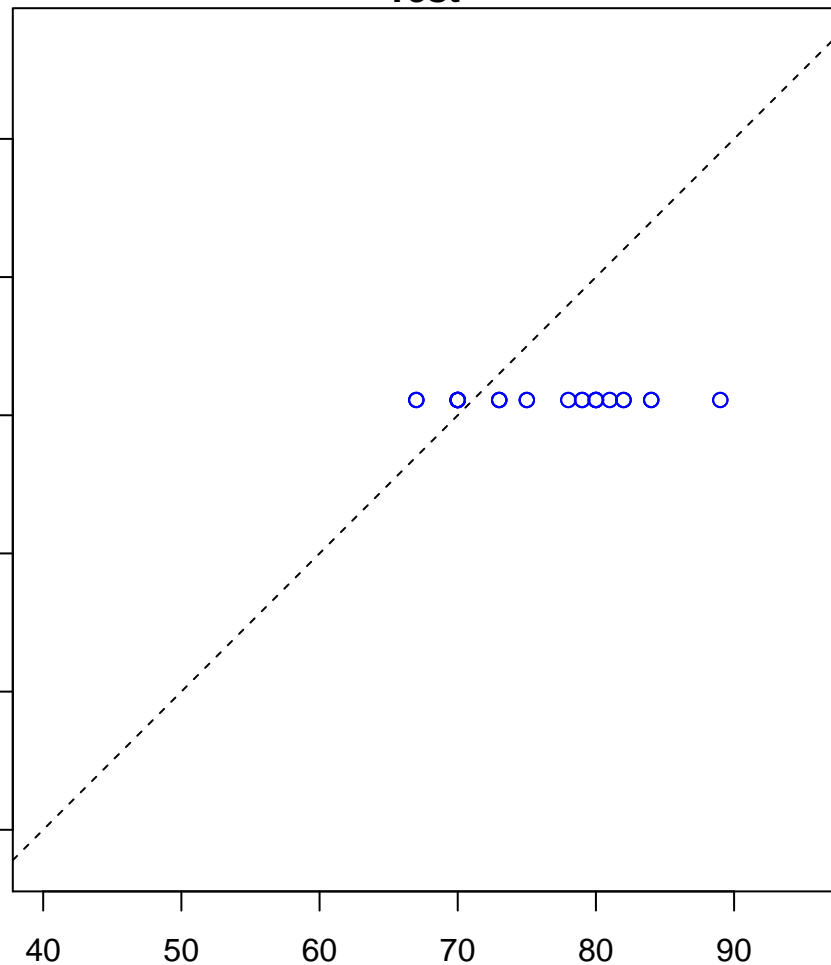
Actual Age

regulation of metabolic process (Score: 0.799688)

Control

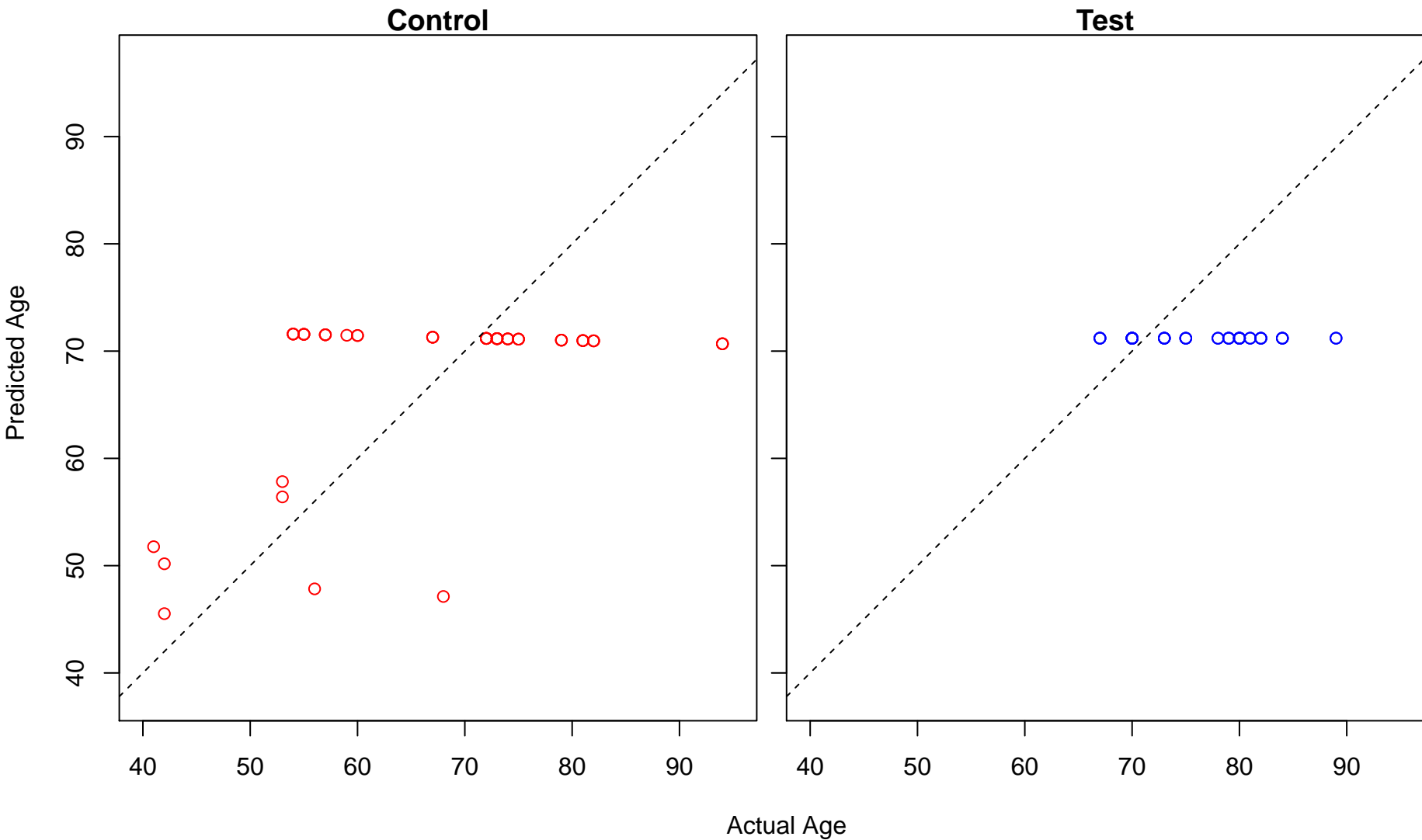


Test

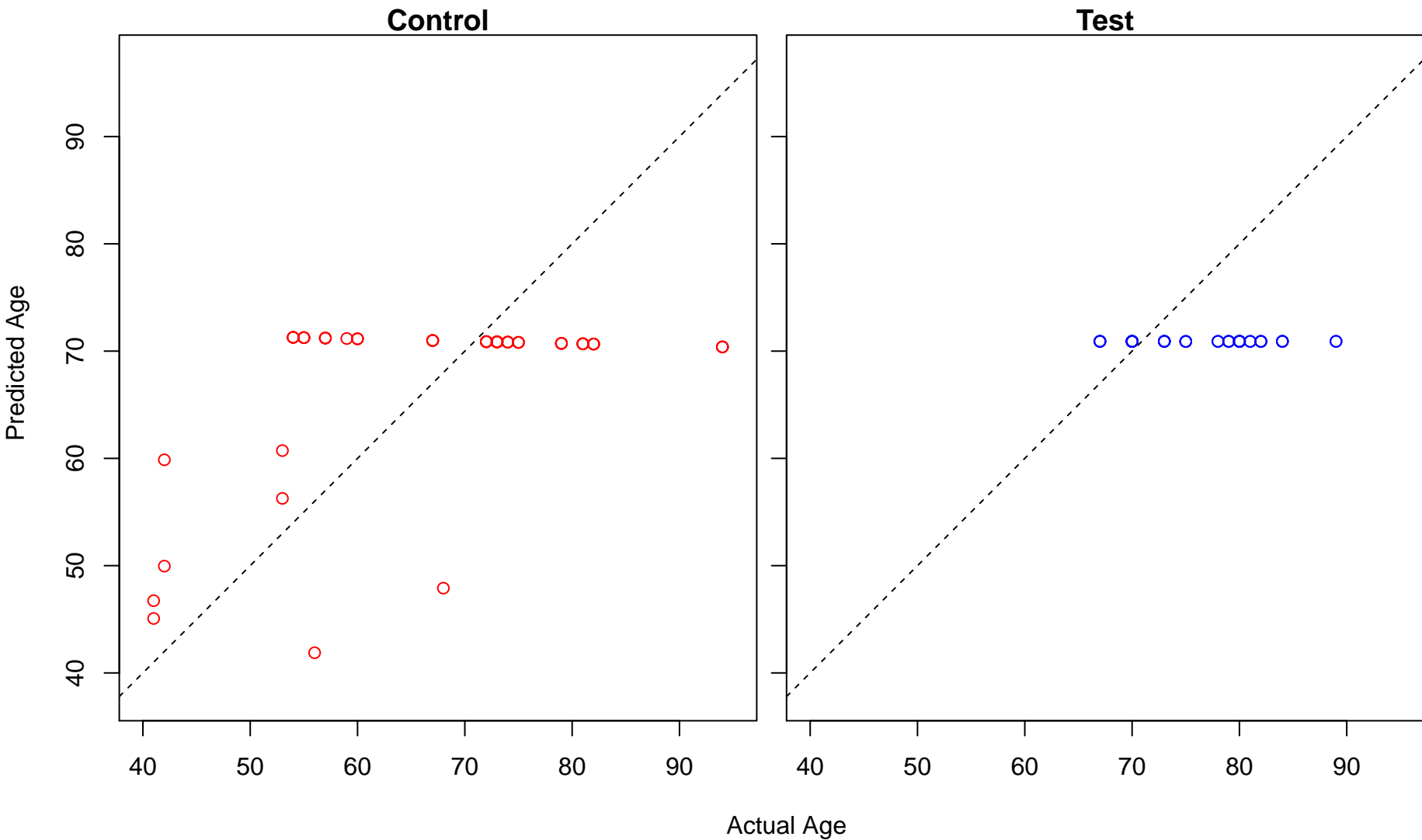


Actual Age

endosomal transport (Score: 0.799675)

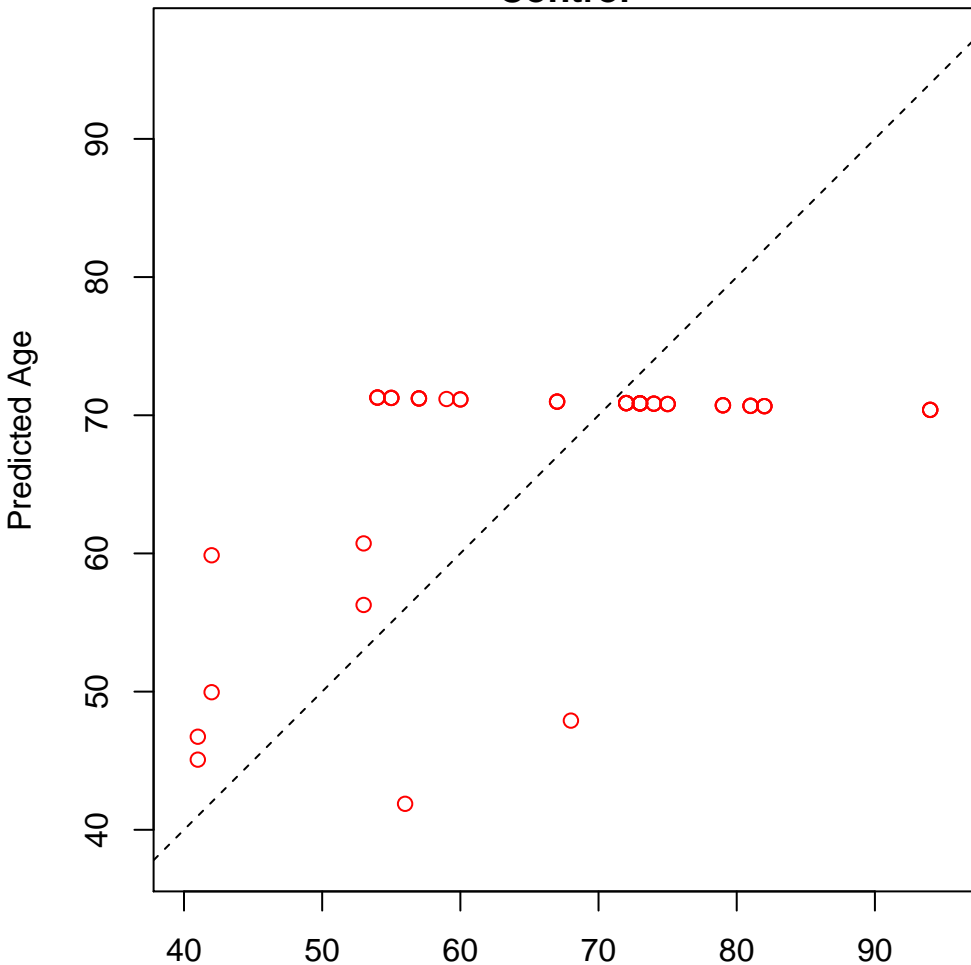


xenobiotic metabolic process (Score: 0.799665)

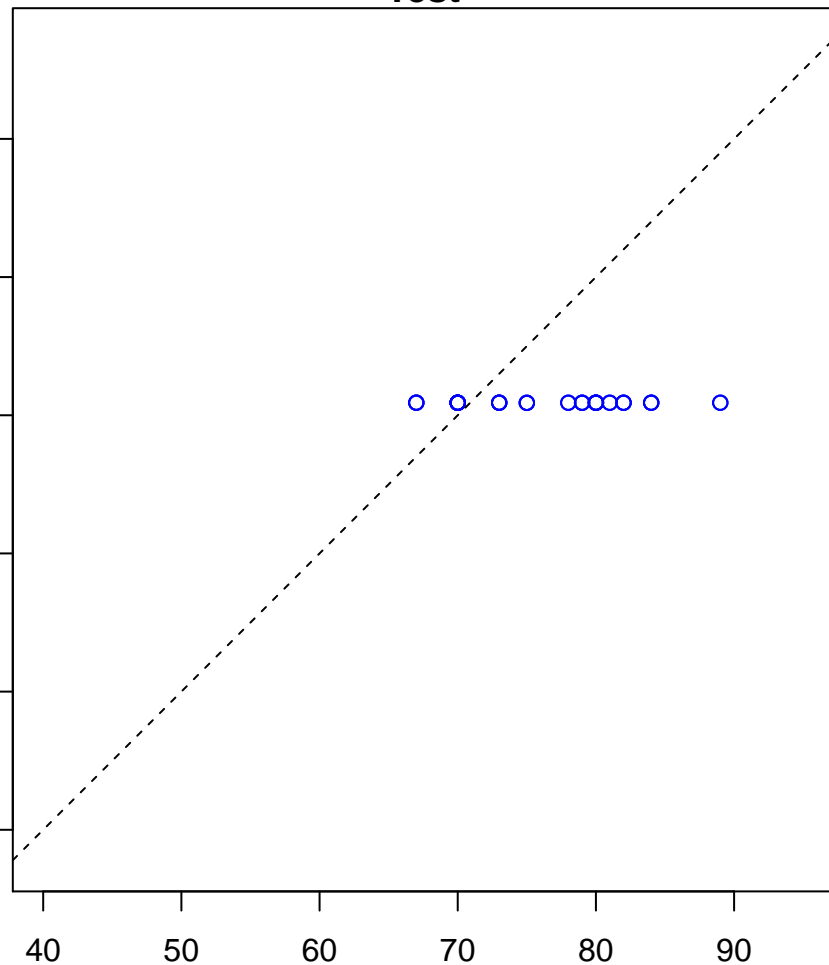


response to xenobiotic stimulus (Score: 0.799665)

Control



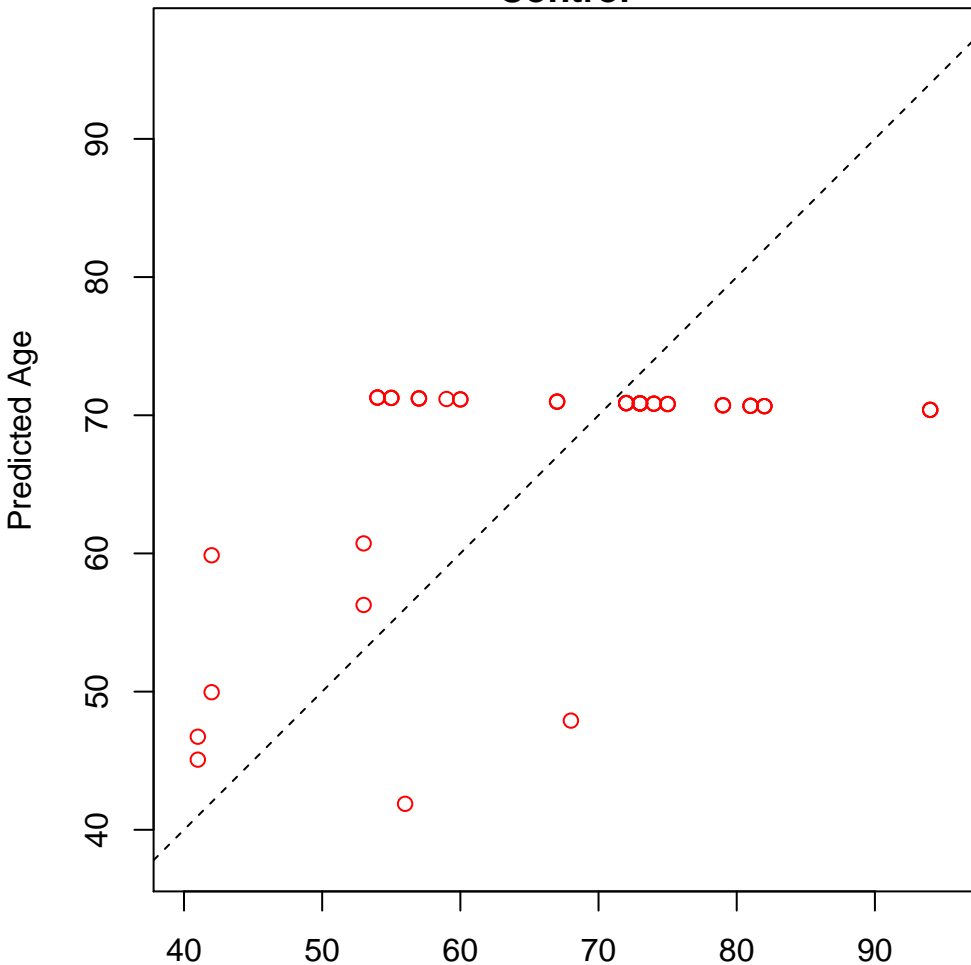
Test



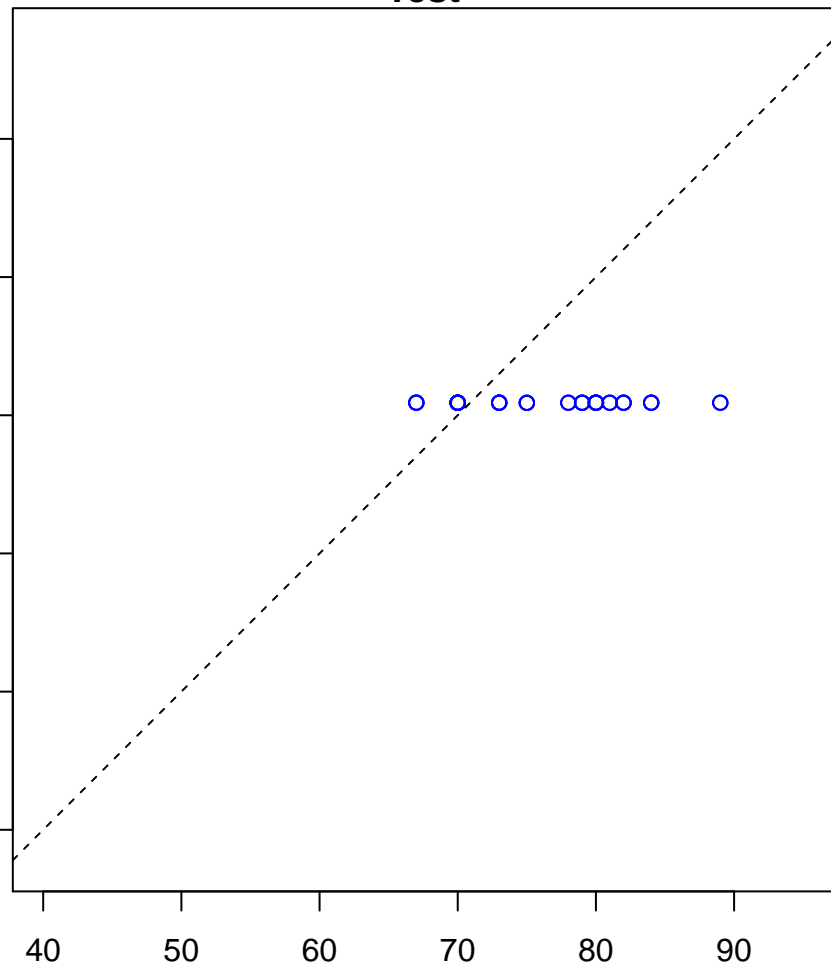
Actual Age

cellular response to xenobiotic stimulus (Score: 0.799665)

Control

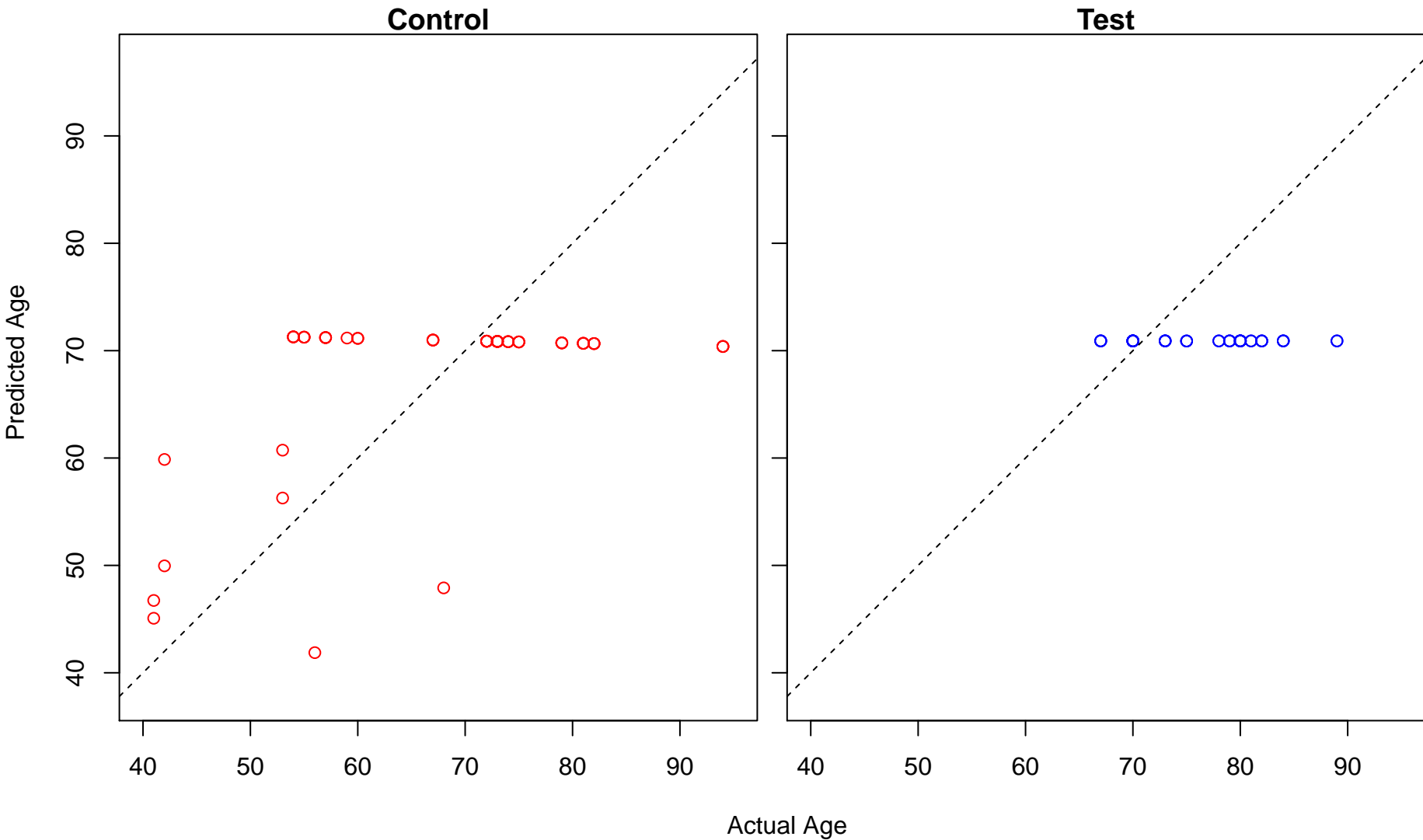


Test



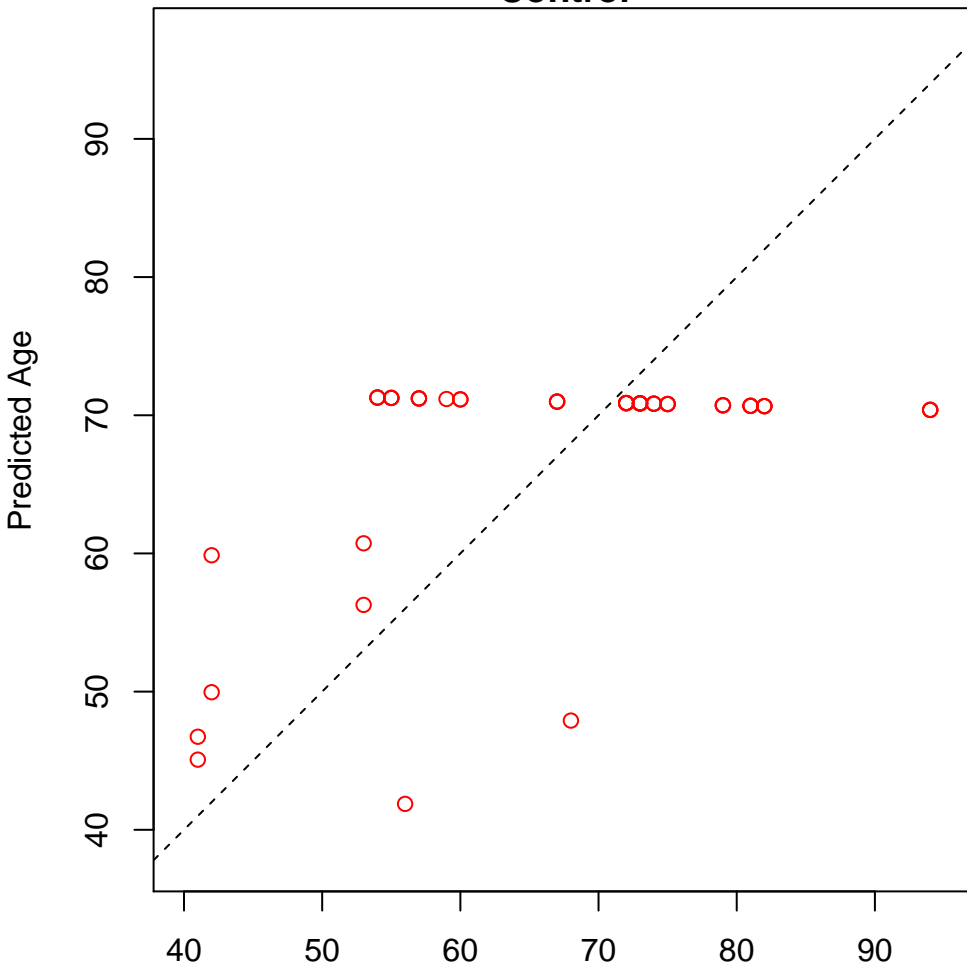
Actual Age

RNA-dependent DNA biosynthetic process (Score: 0.799660)

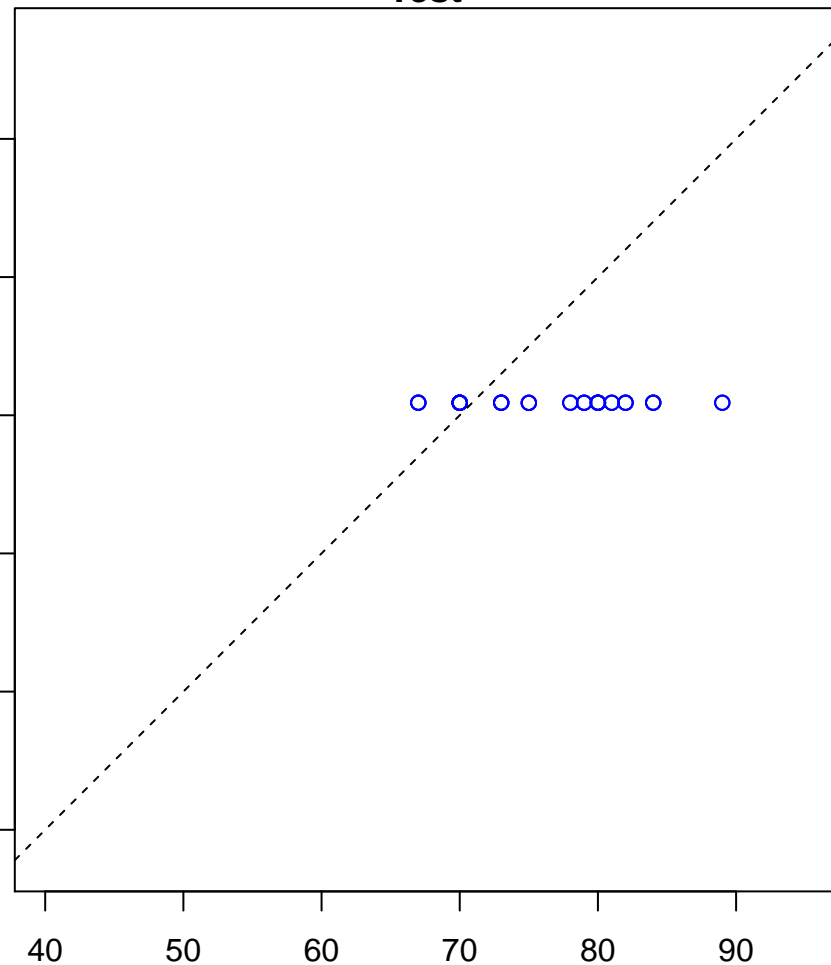


telomere maintenance via telomerase (Score: 0.799660)

Control

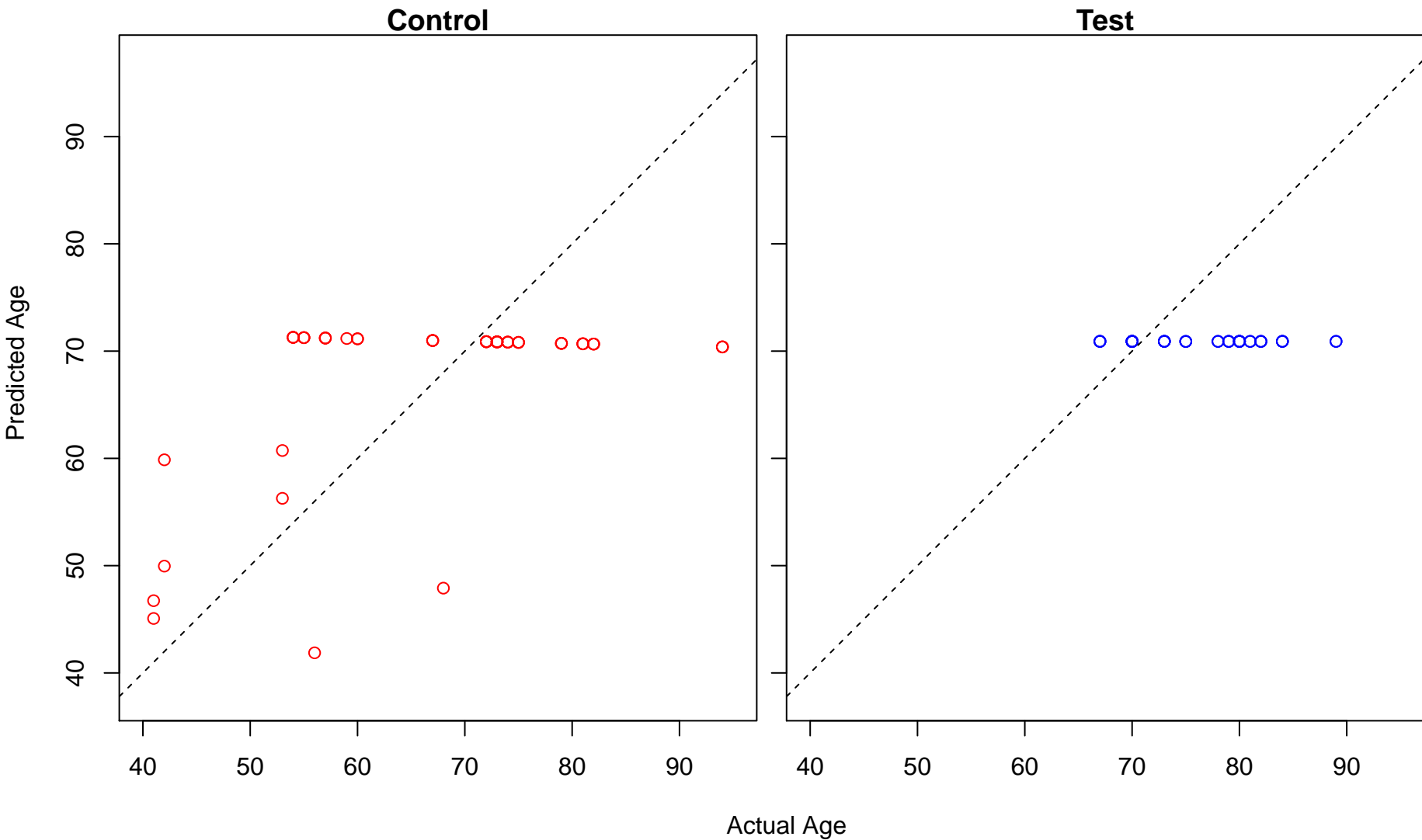


Test

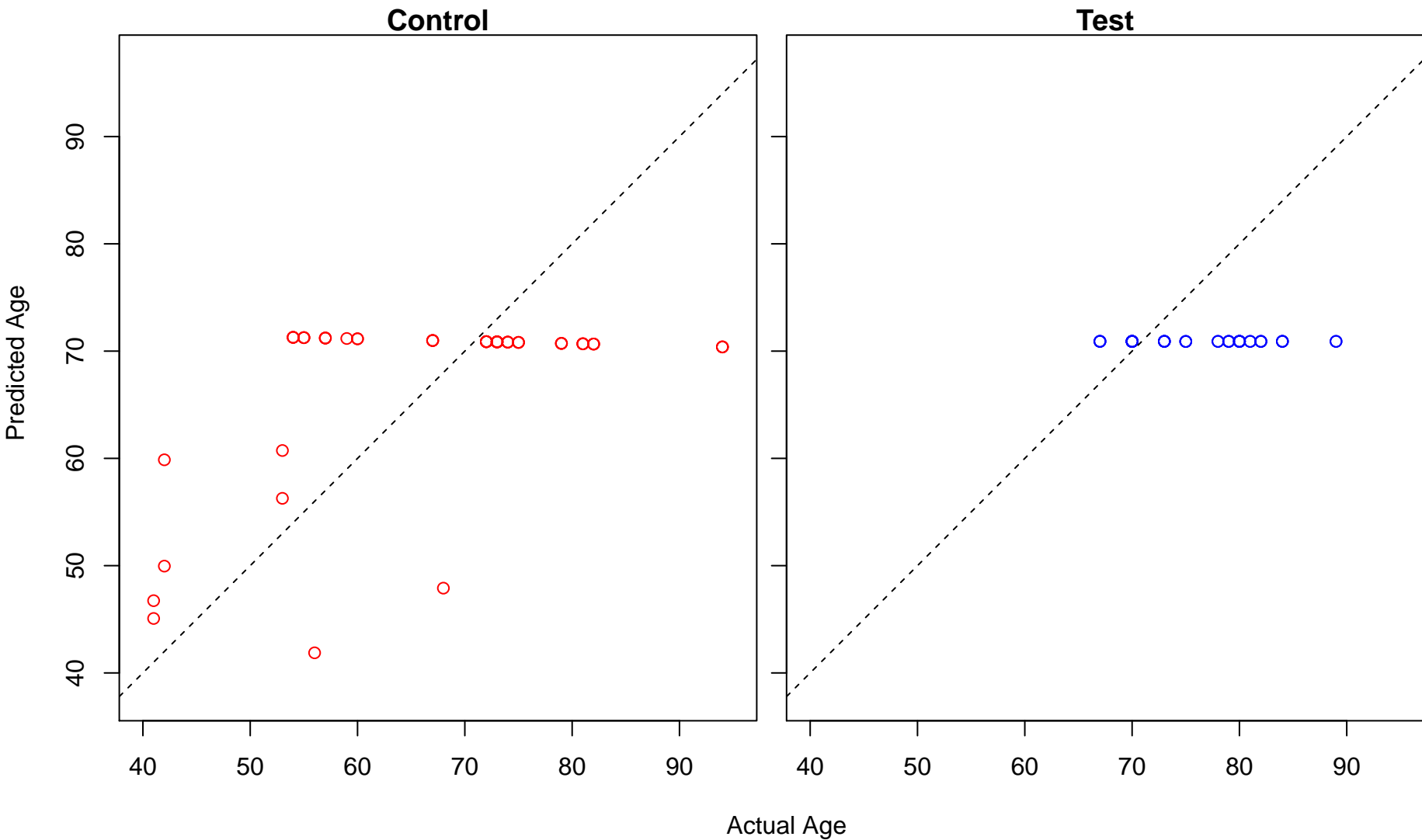


Actual Age

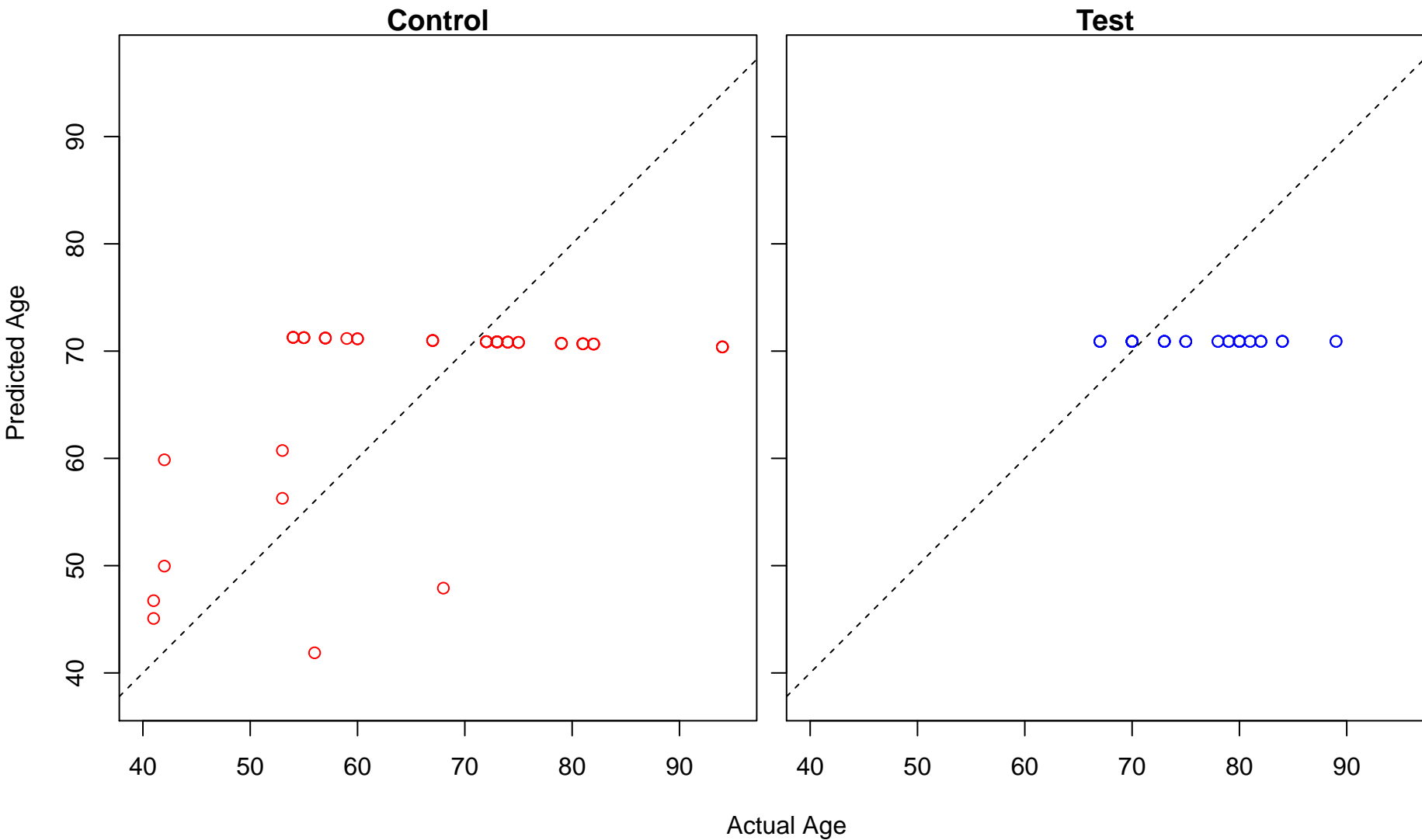
telomere maintenance via telomere lengthening (Score: 0.799660)



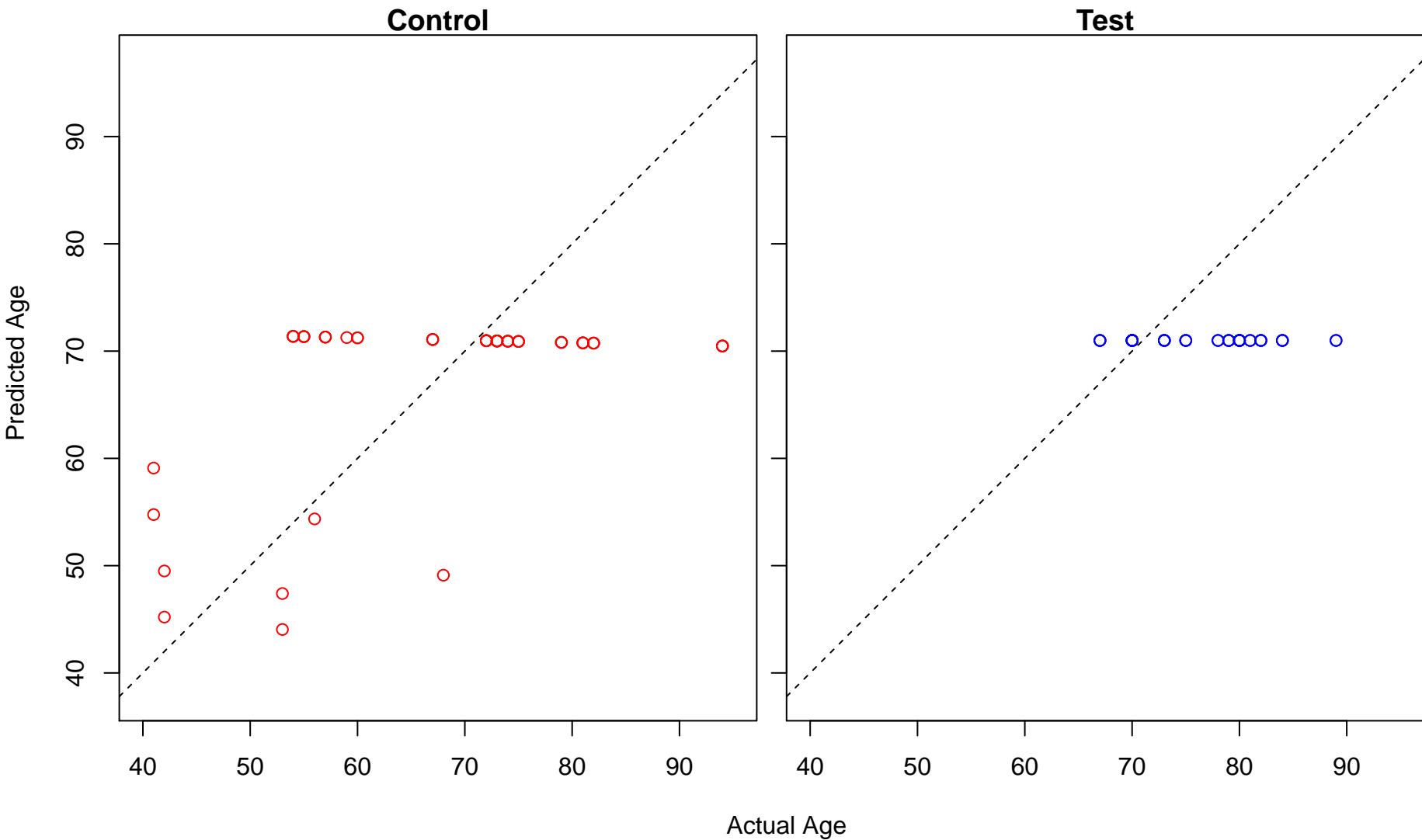
chaperone-mediated protein complex assembly (Score: 0.799660)



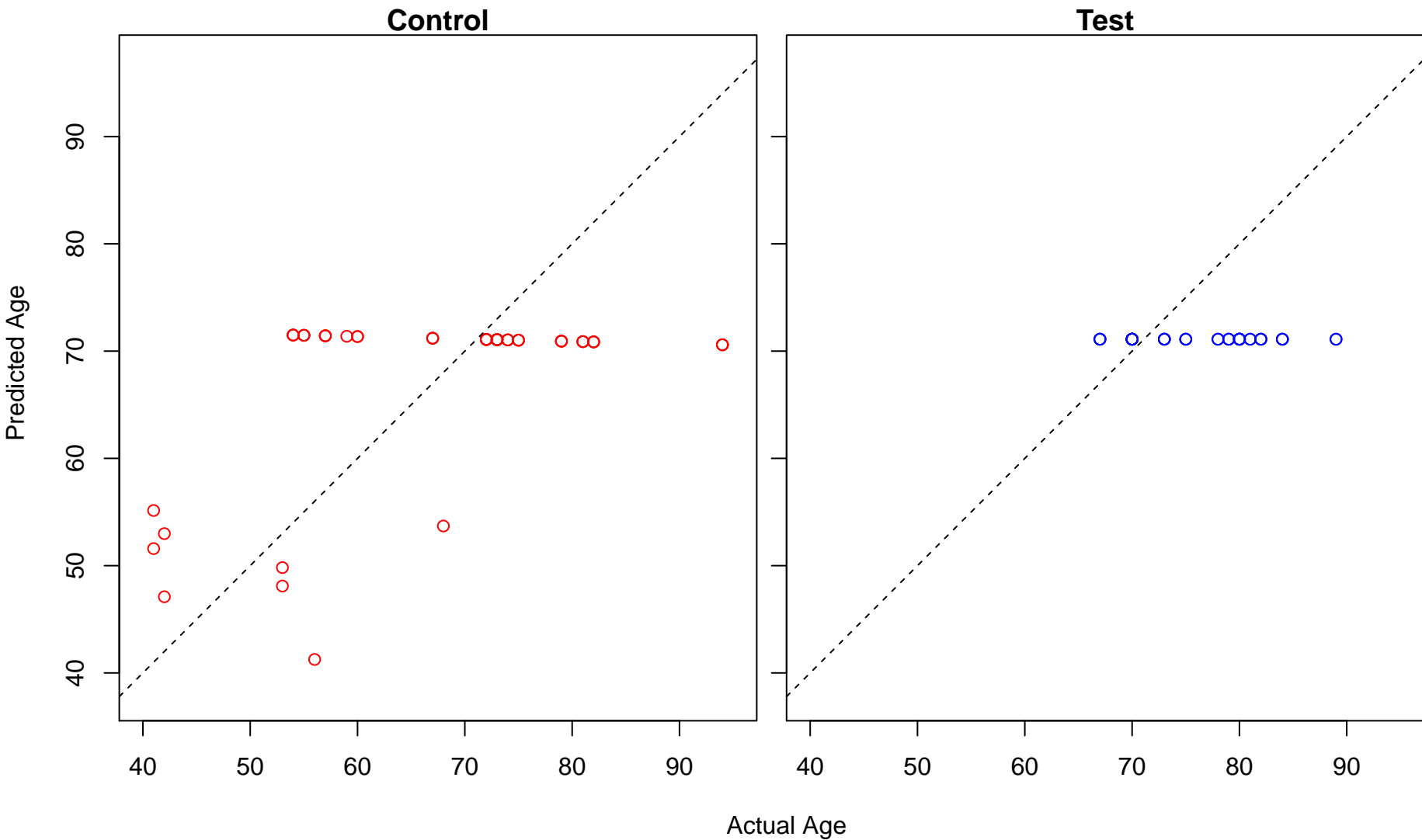
telomerase holoenzyme complex assembly (Score: 0.799660)



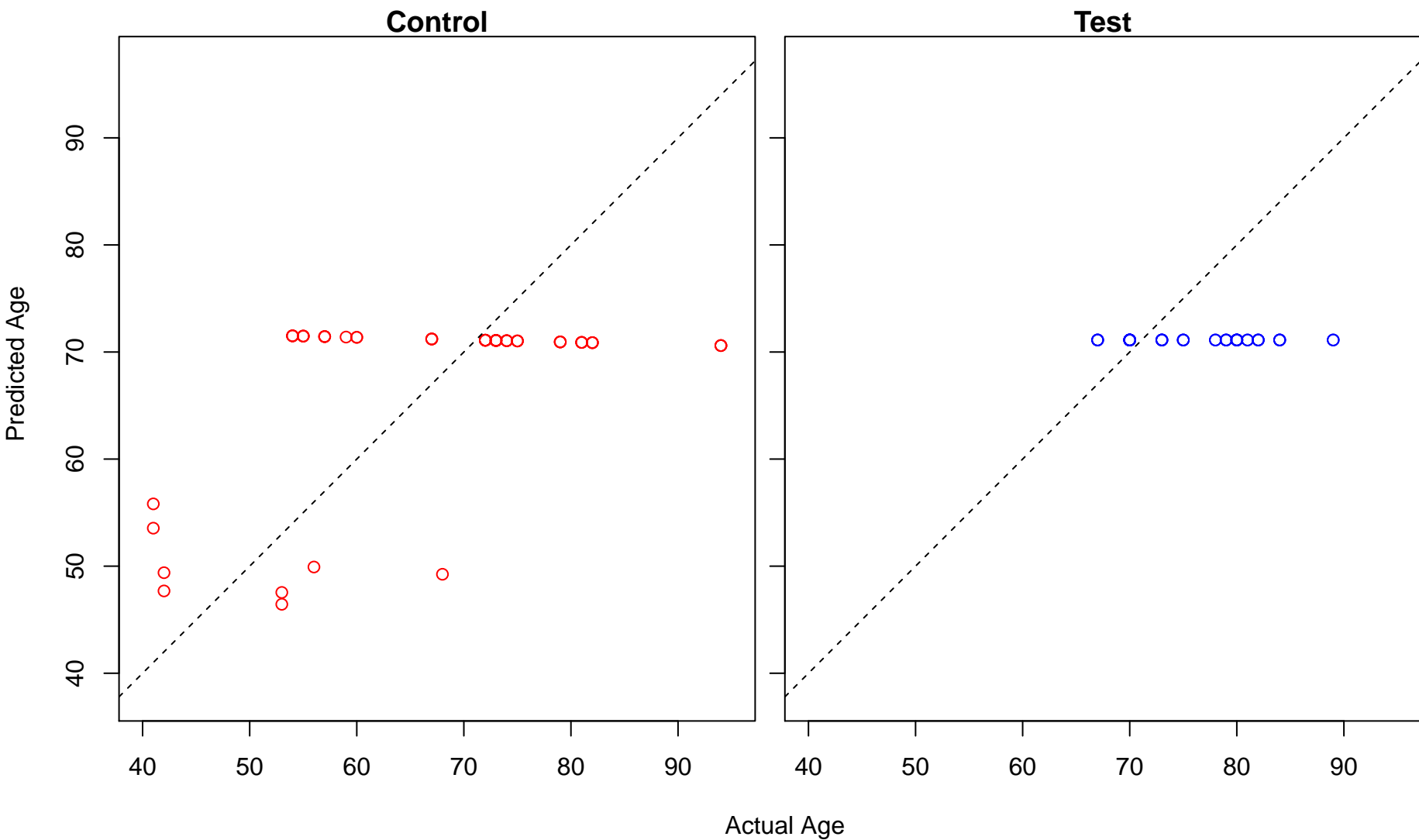
positive regulation of inflammatory response (Score: 0.799656)



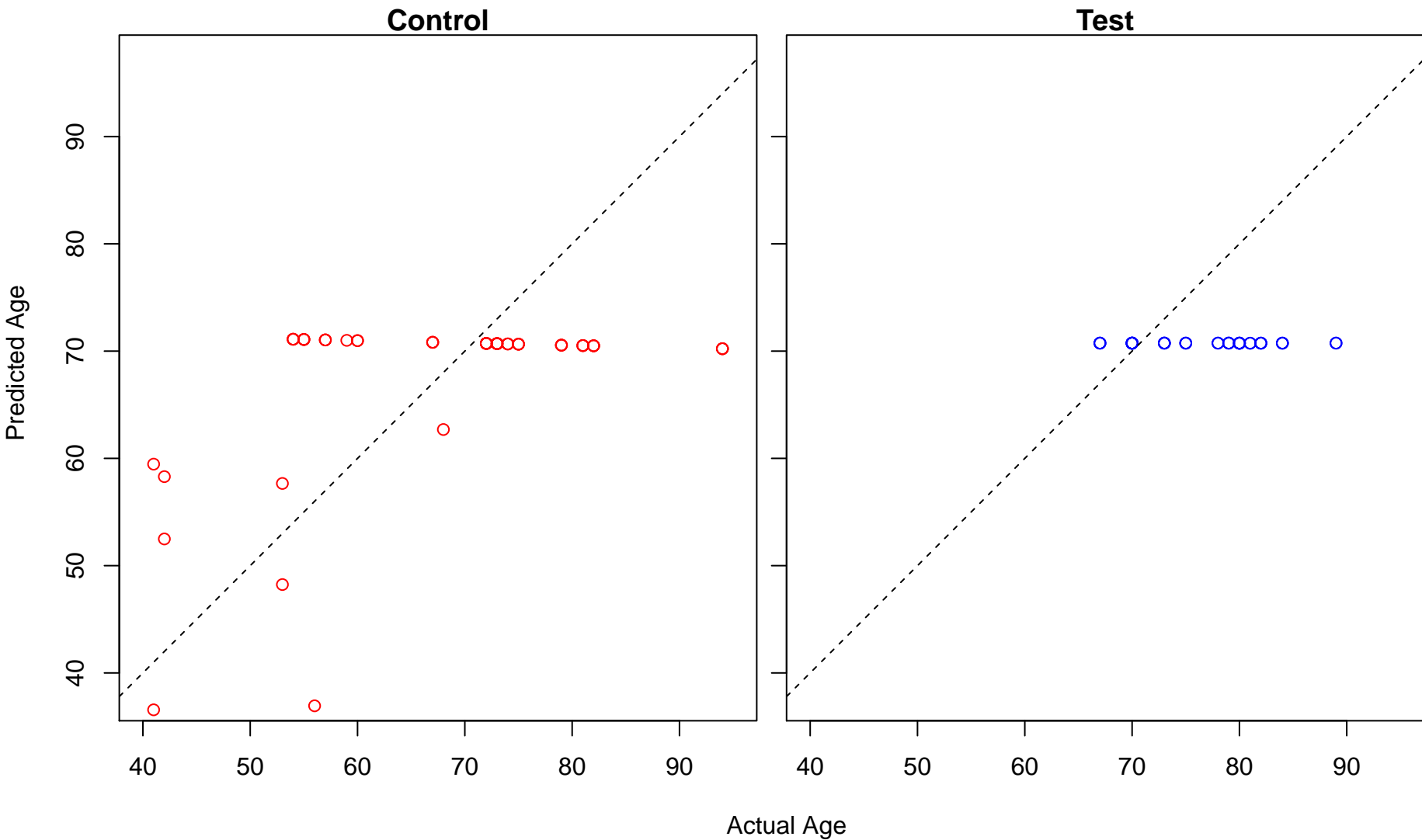
cellular component organization or biogenesis (Score: 0.799637)



regulation of protein stability (Score: 0.799622)

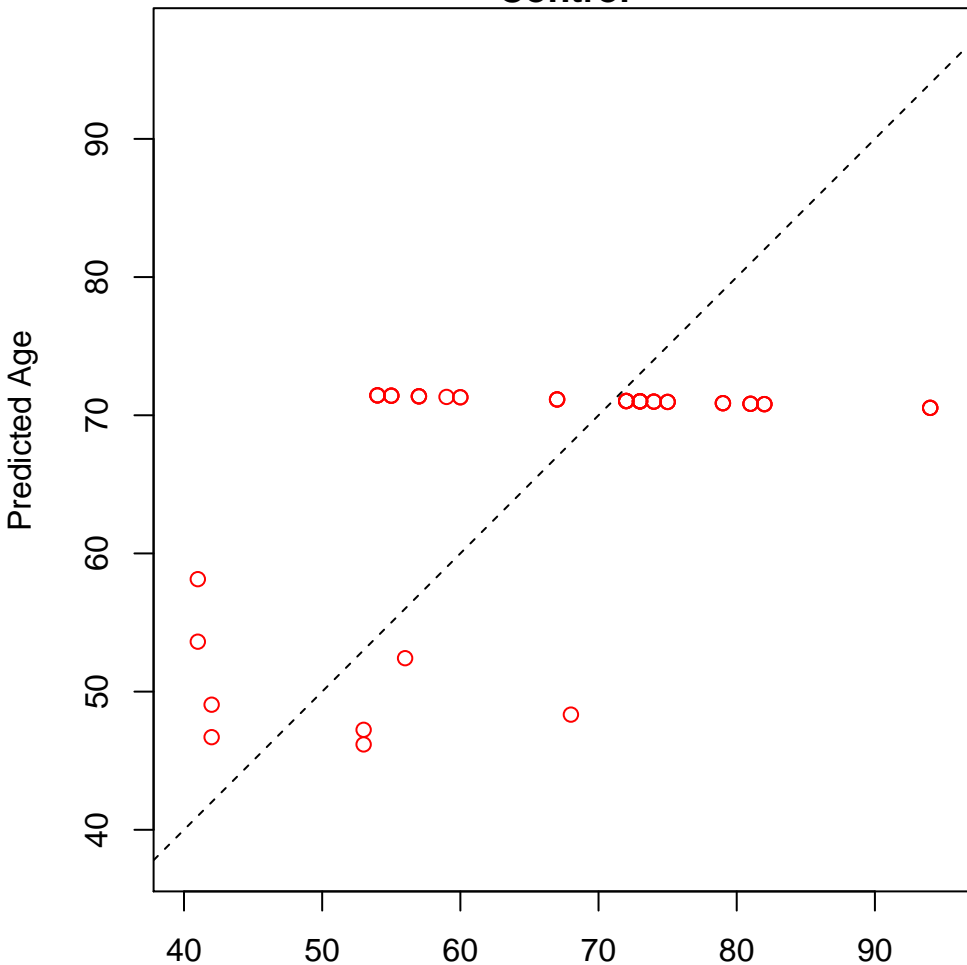


regulation of amyloid precursor protein catabolic process (Score: 0.799543)

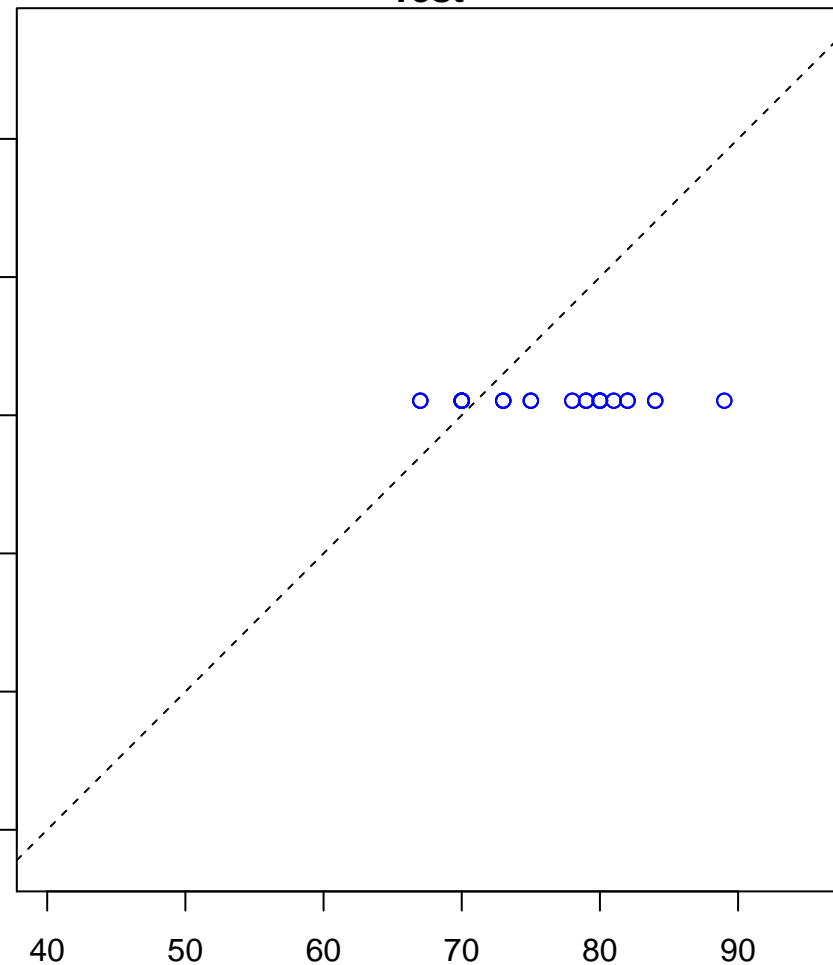


small molecule biosynthetic process (Score: 0.799512)

Control

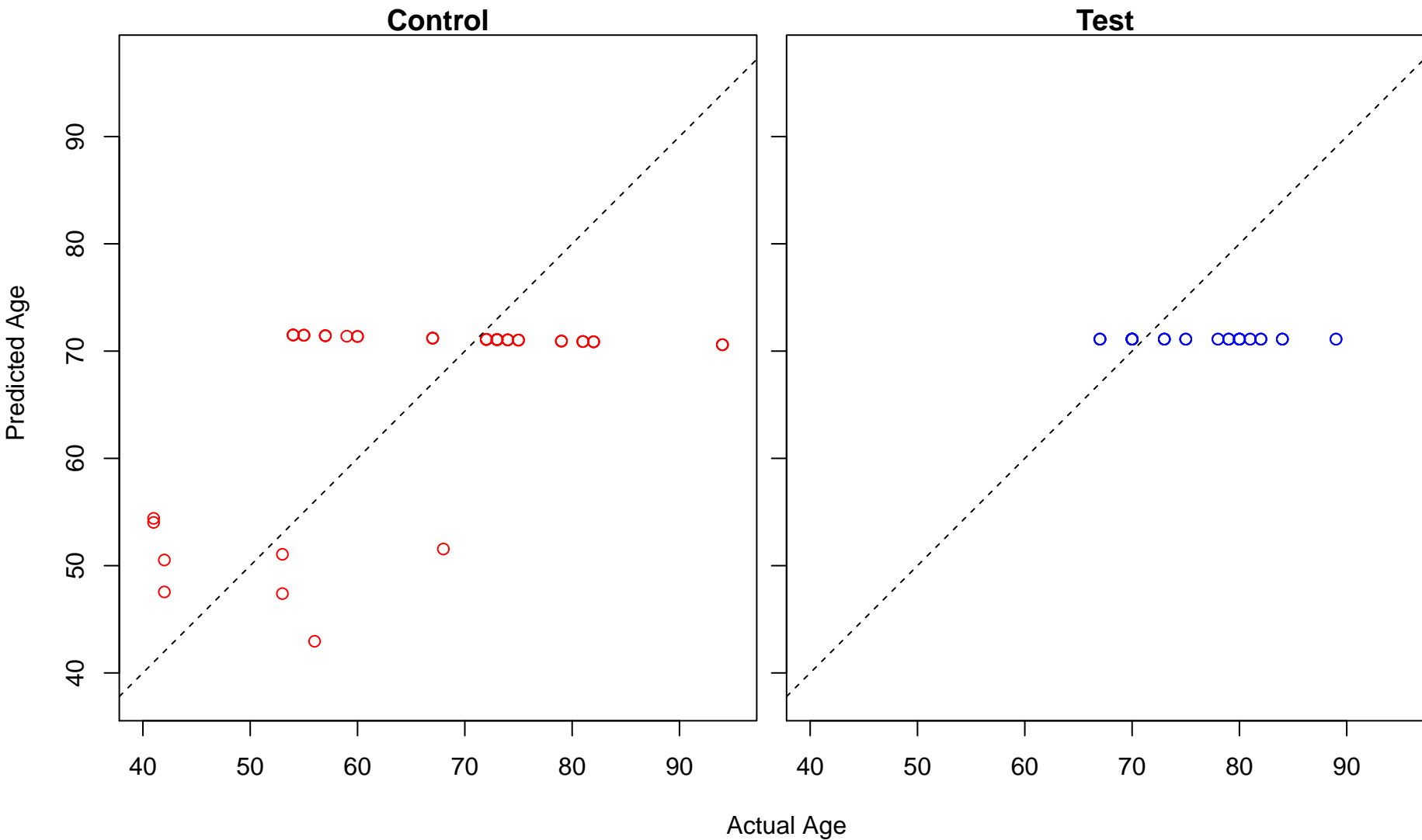


Test



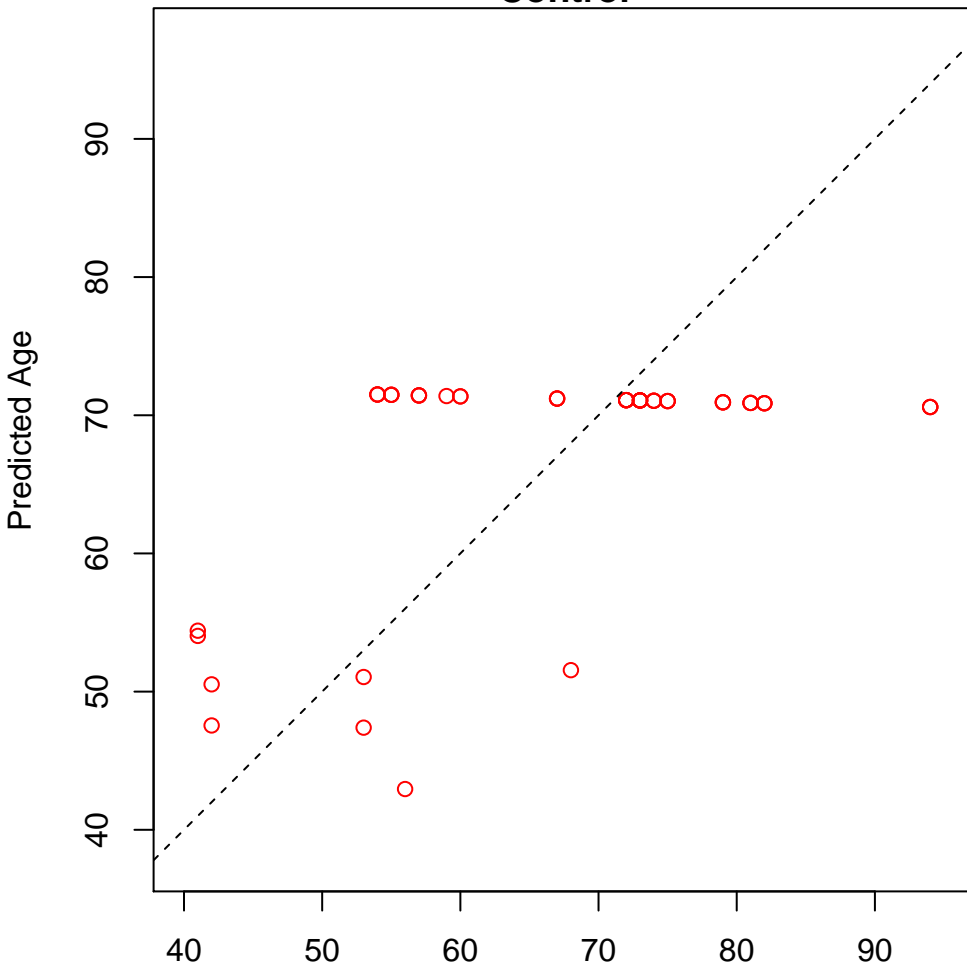
Actual Age

regulation of nucleic acid-templated transcription (Score: 0.799483)

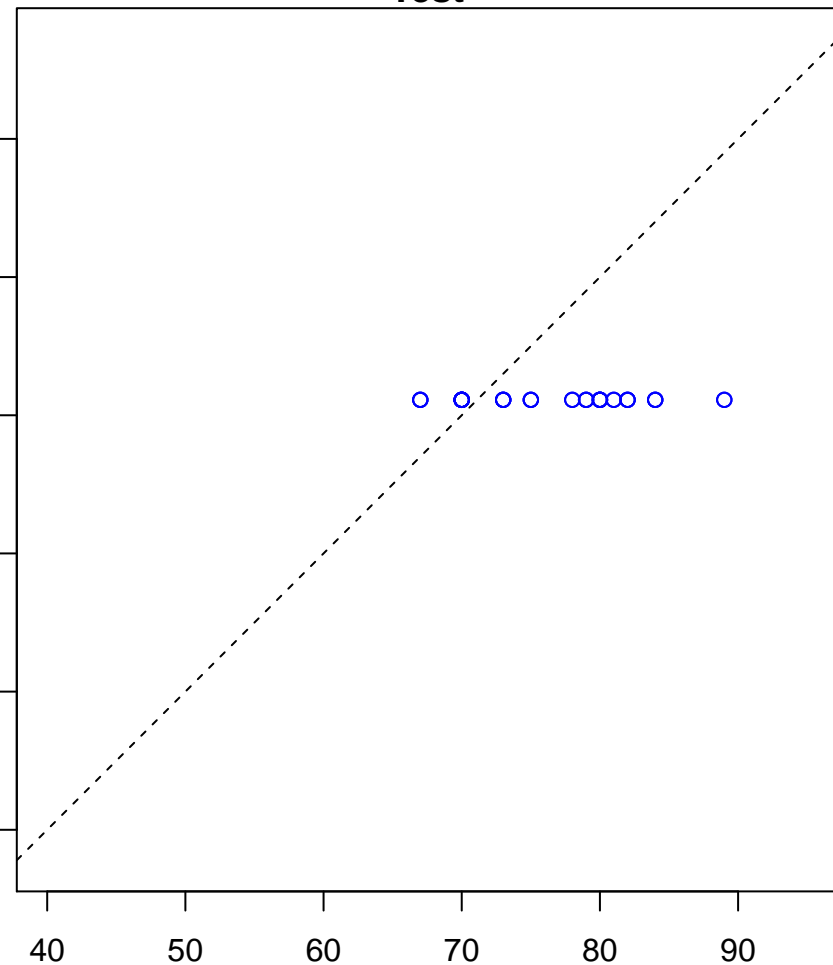


regulation of RNA biosynthetic process (Score: 0.799483)

Control

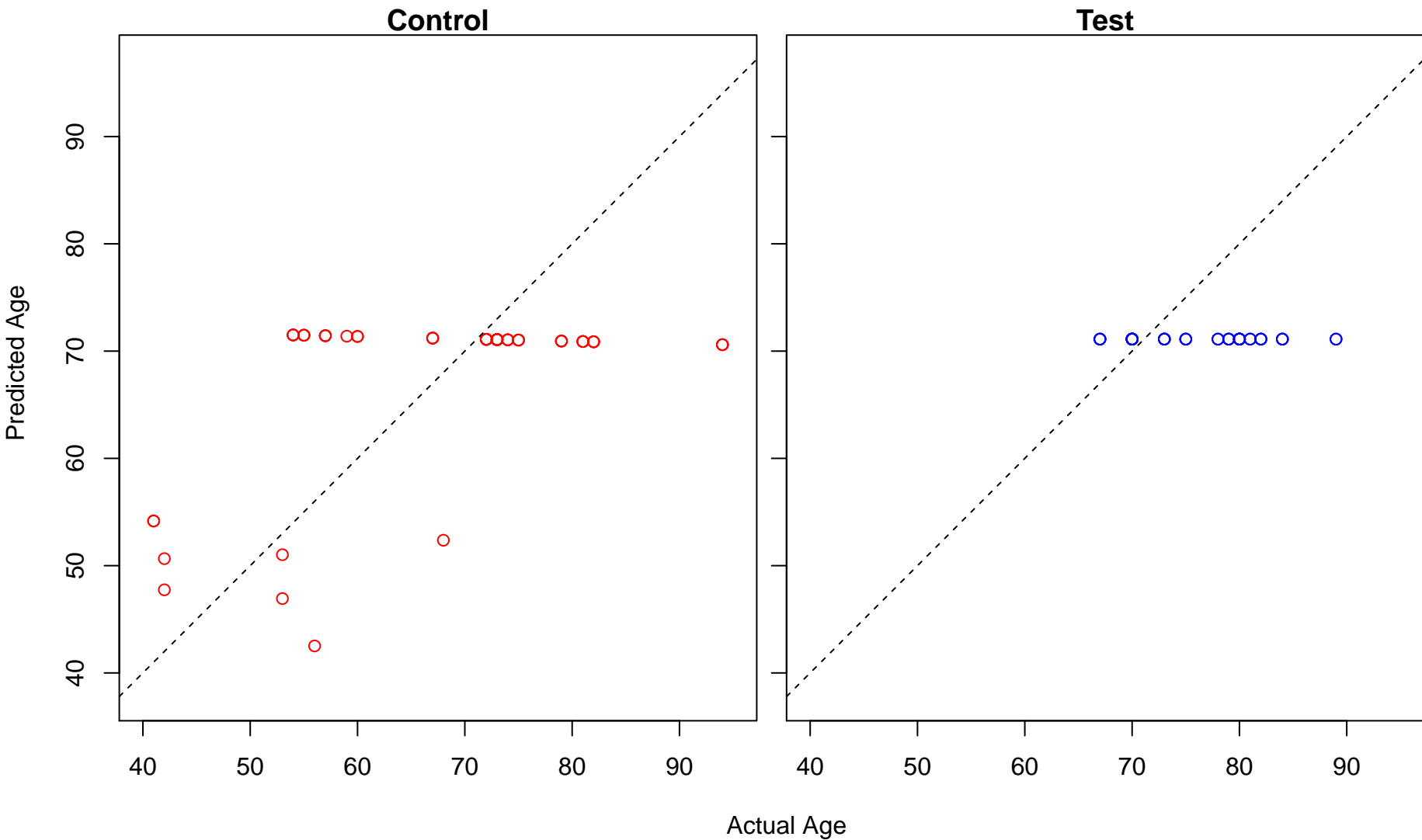


Test

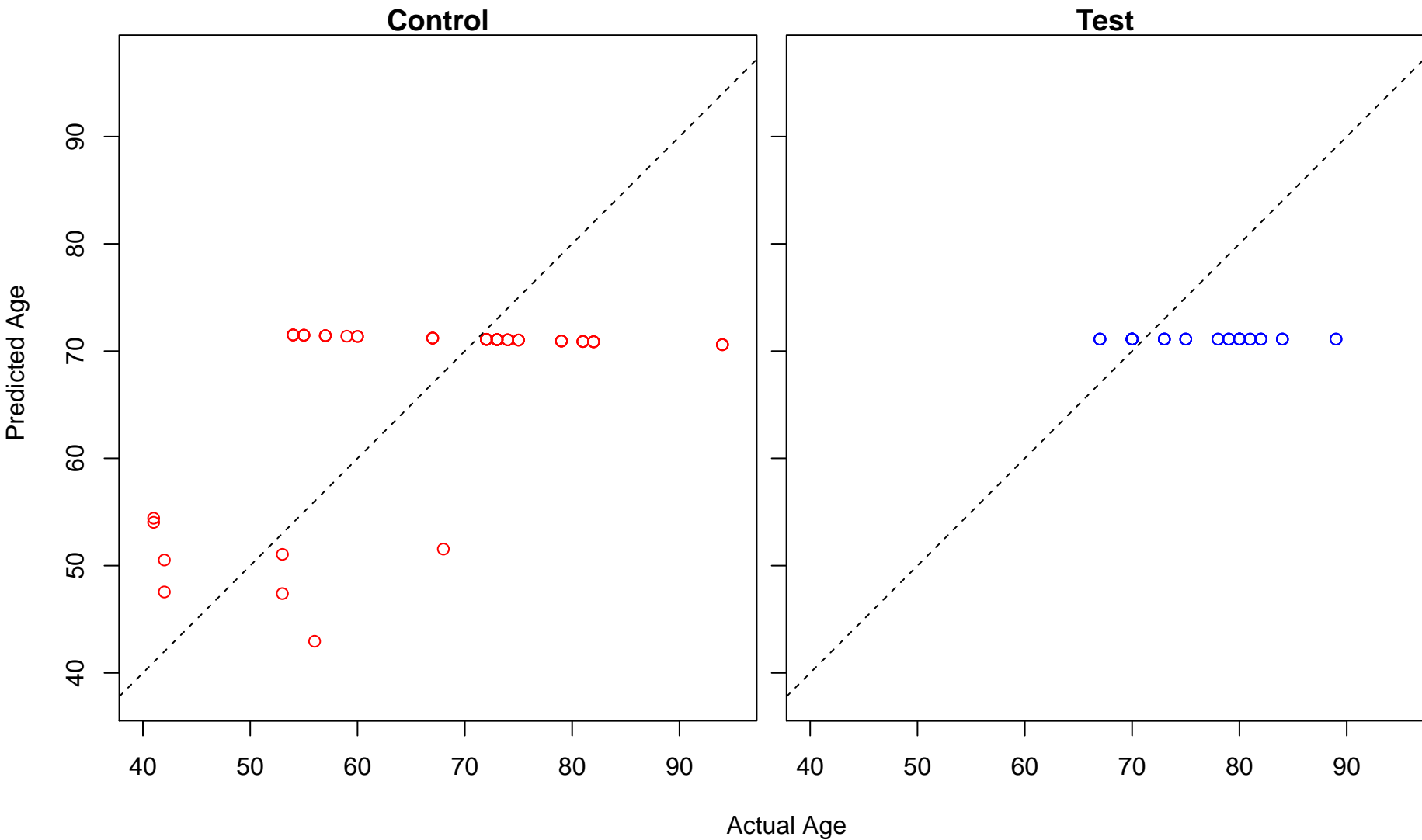


Actual Age

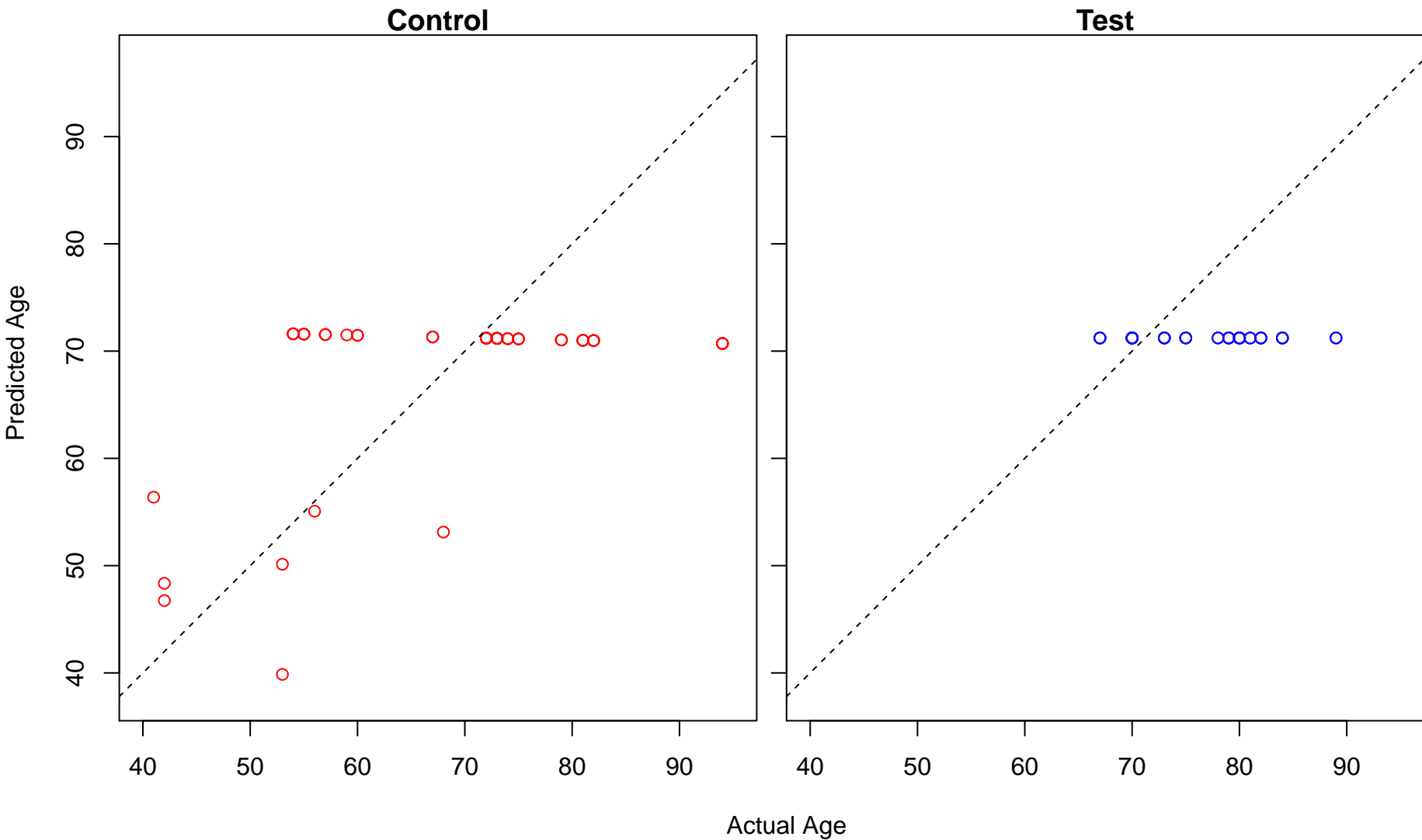
positive regulation of macromolecule biosynthetic process (Score: 0.799472)



regulation of transcription, DNA-templated (Score: 0.799471)

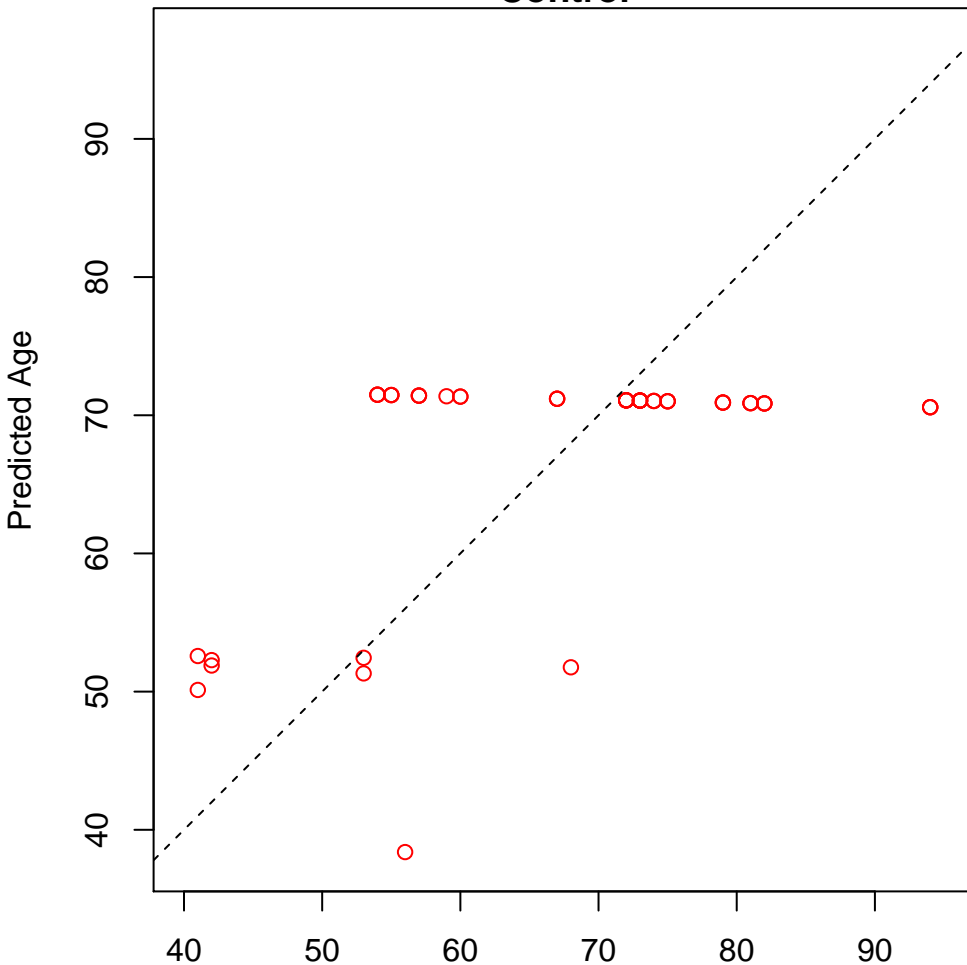


regulation of anatomical structure morphogenesis (Score: 0.799451)

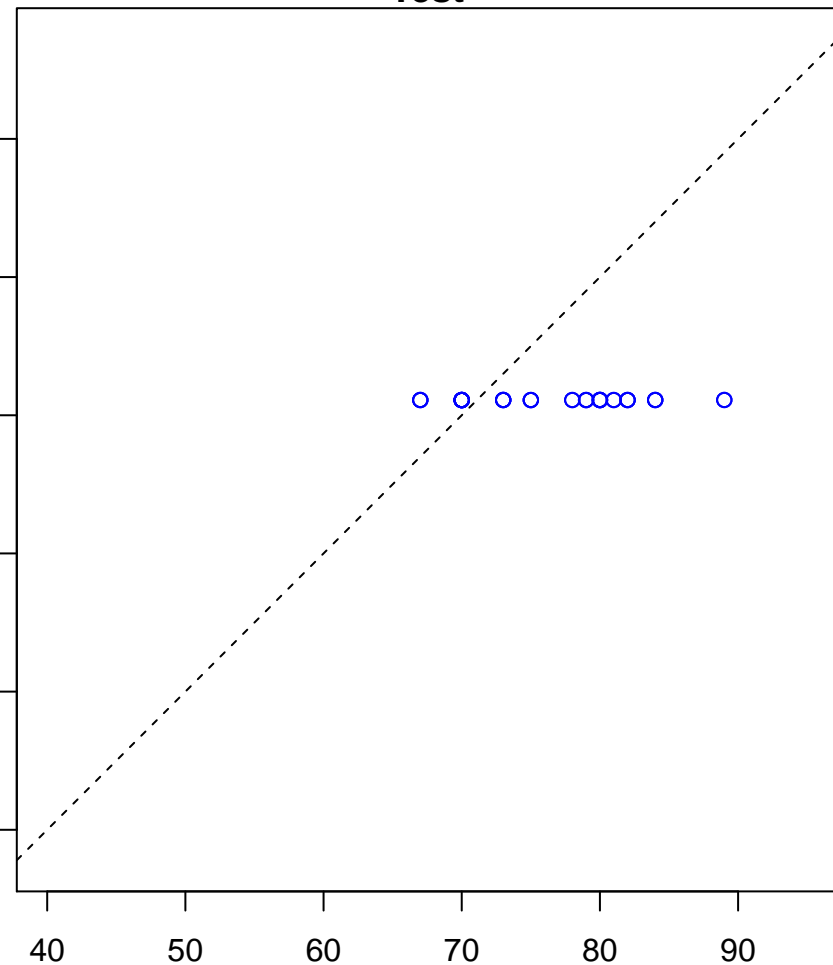


protein localization to nucleus (Score: 0.799410)

Control

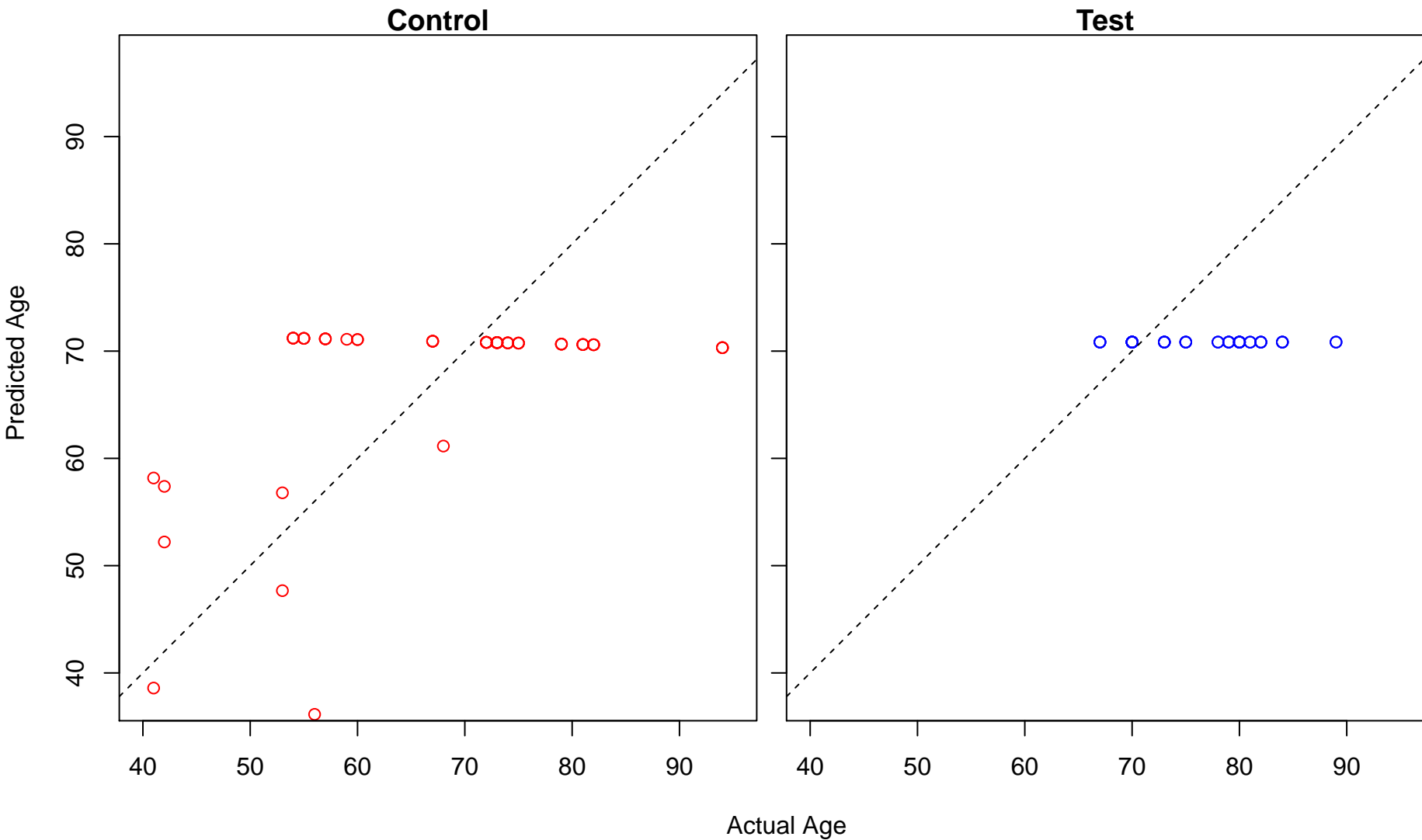


Test

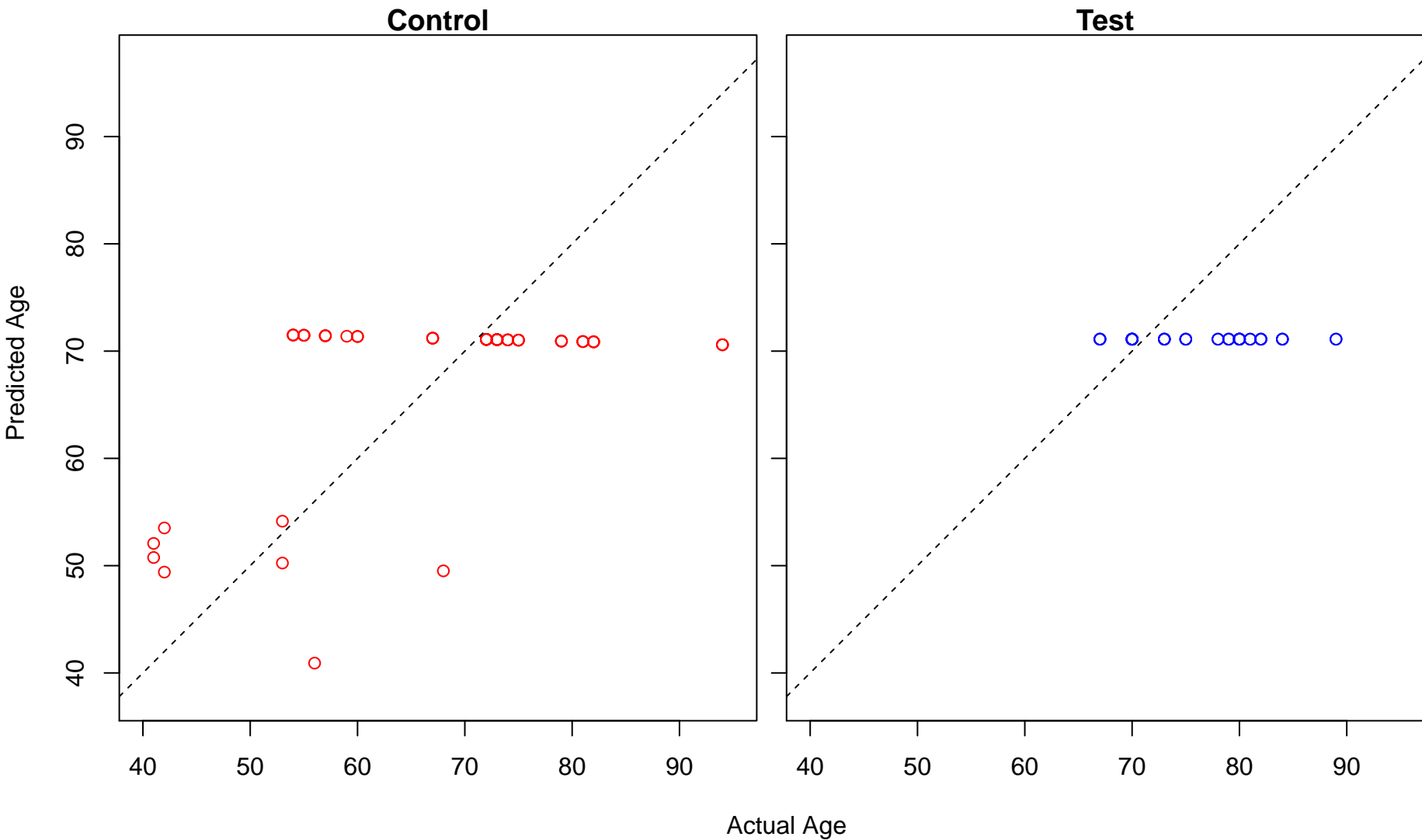


Actual Age

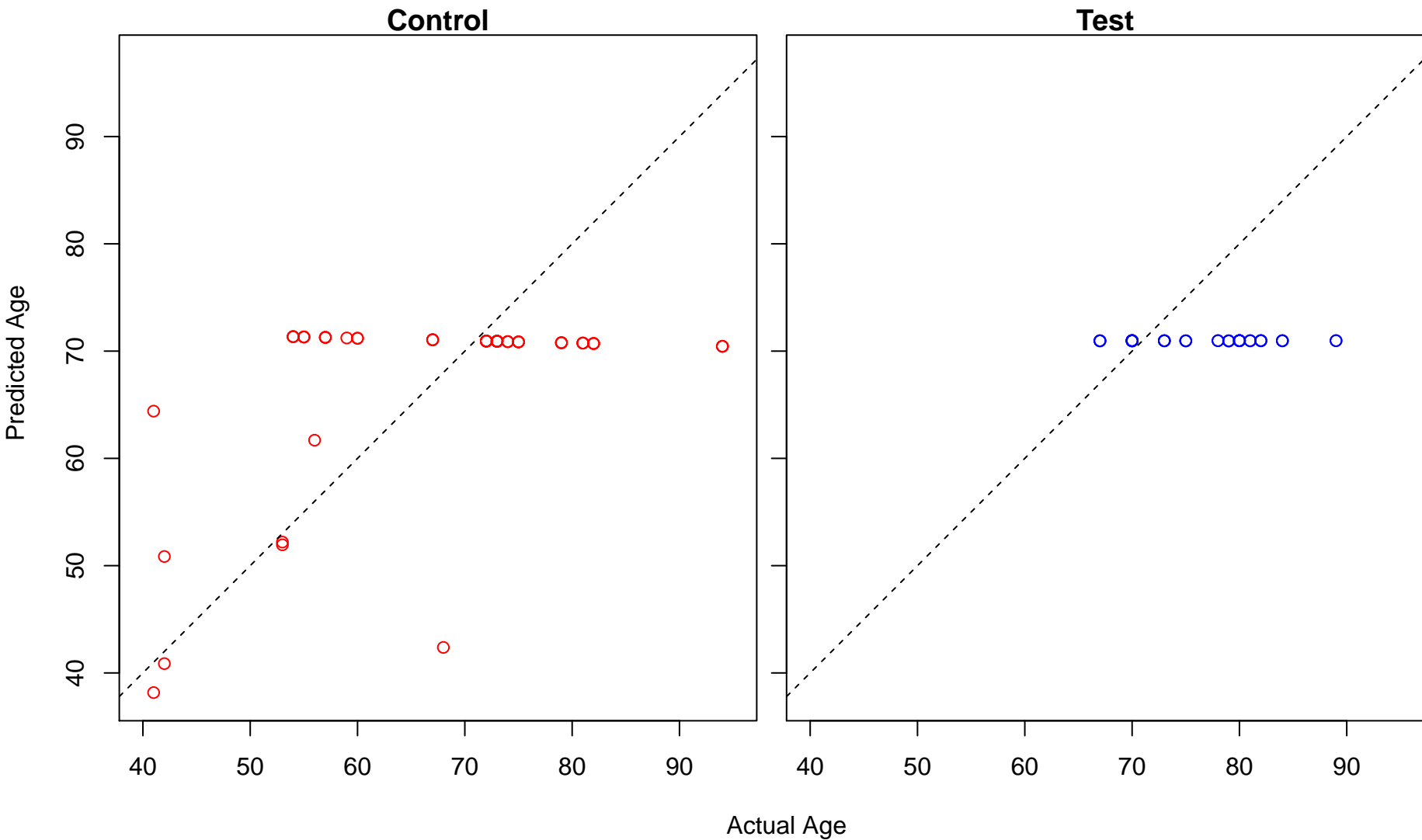
cell recognition (Score: 0.799406)



regulation of cell proliferation (Score: 0.799367)

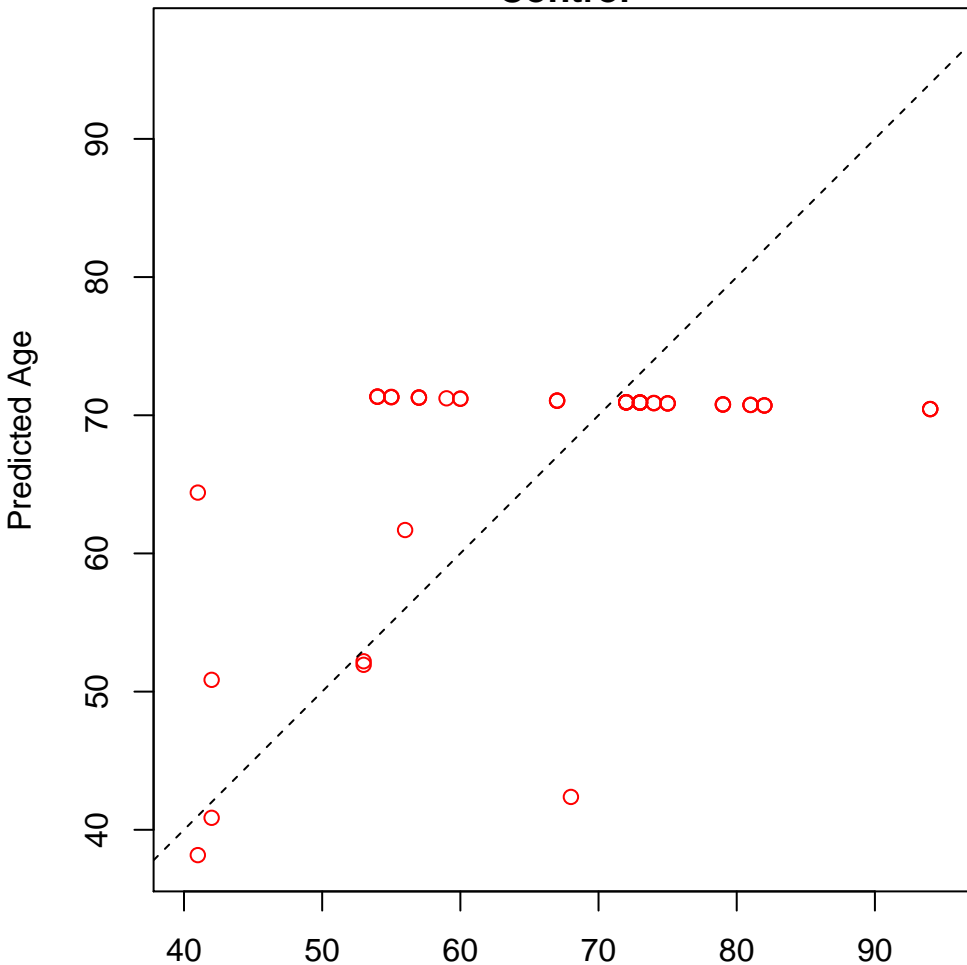


water homeostasis (Score: 0.799364)

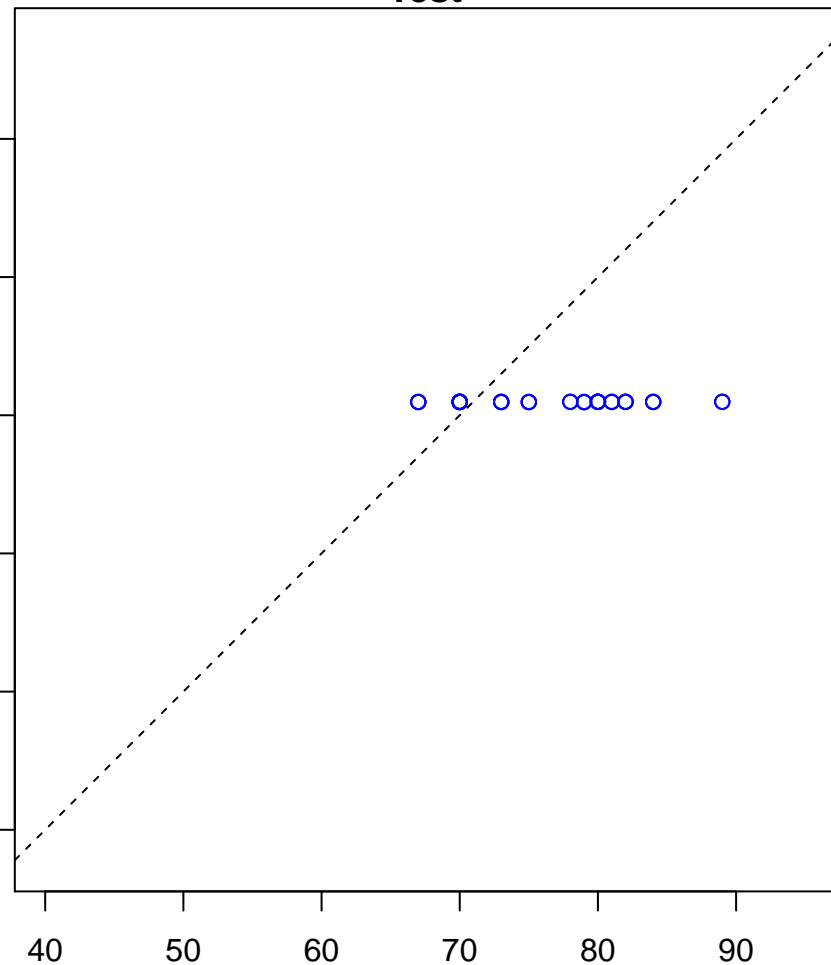


multicellular organismal water homeostasis (Score: 0.799364)

Control

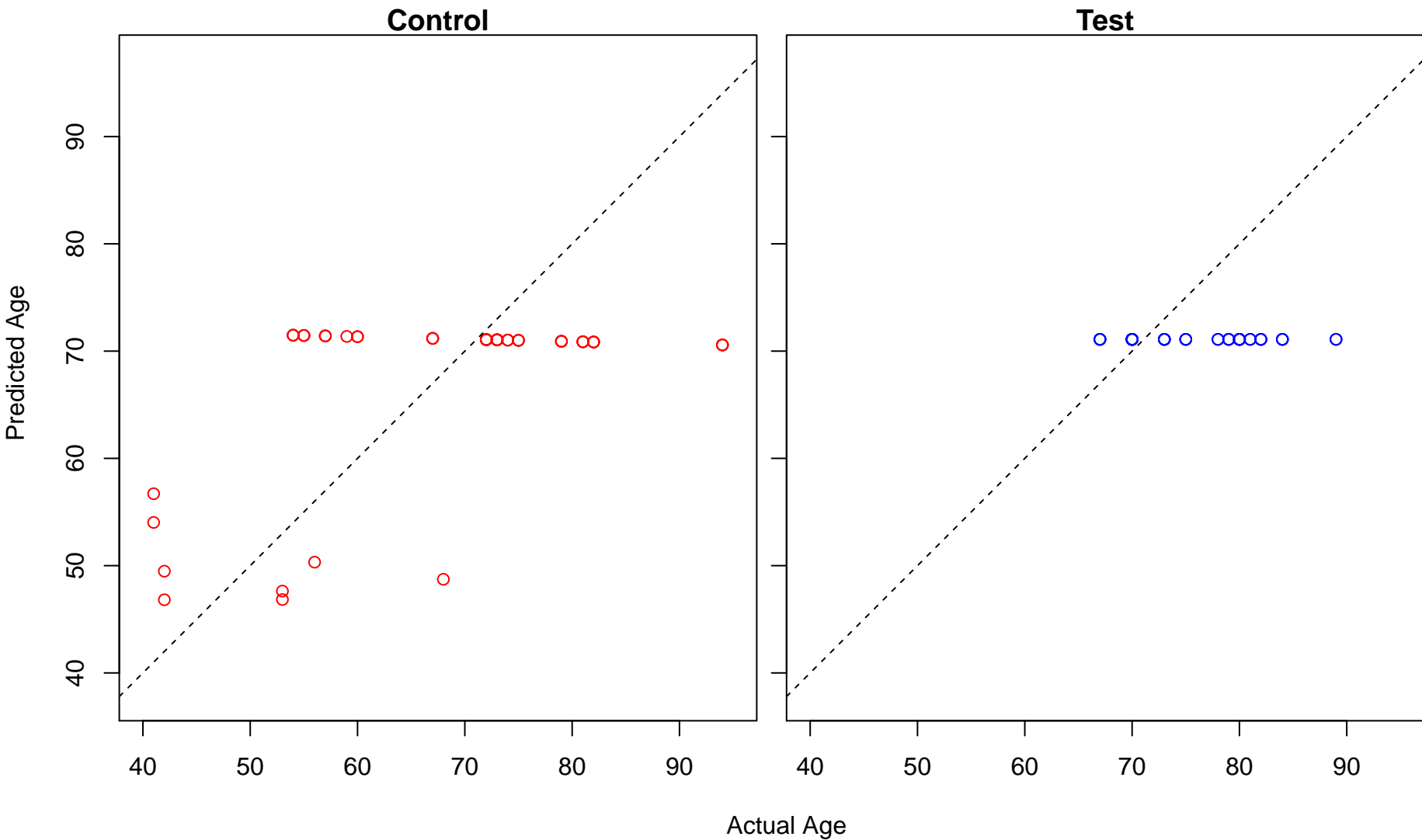


Test

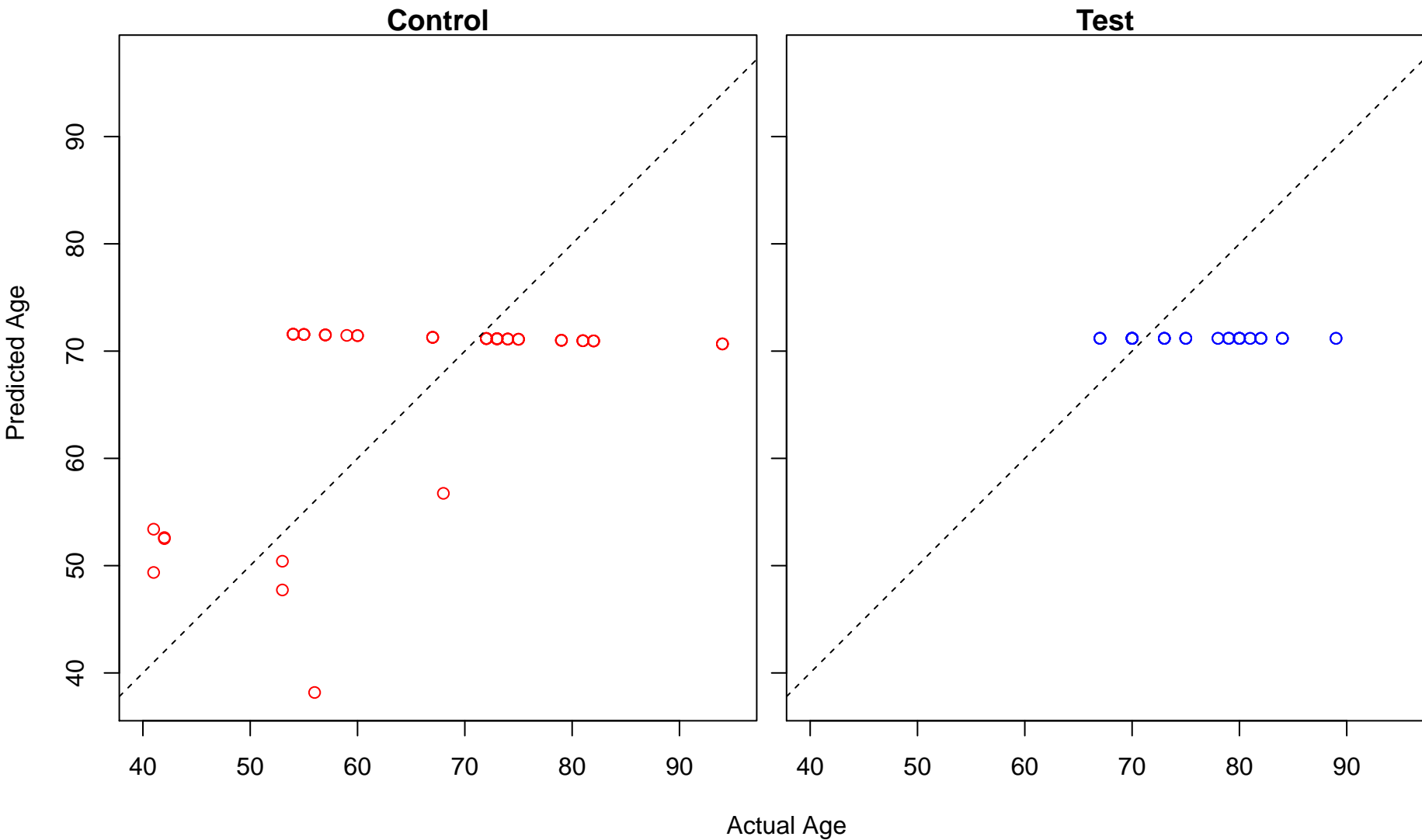


Actual Age

protein stabilization (Score: 0.799362)

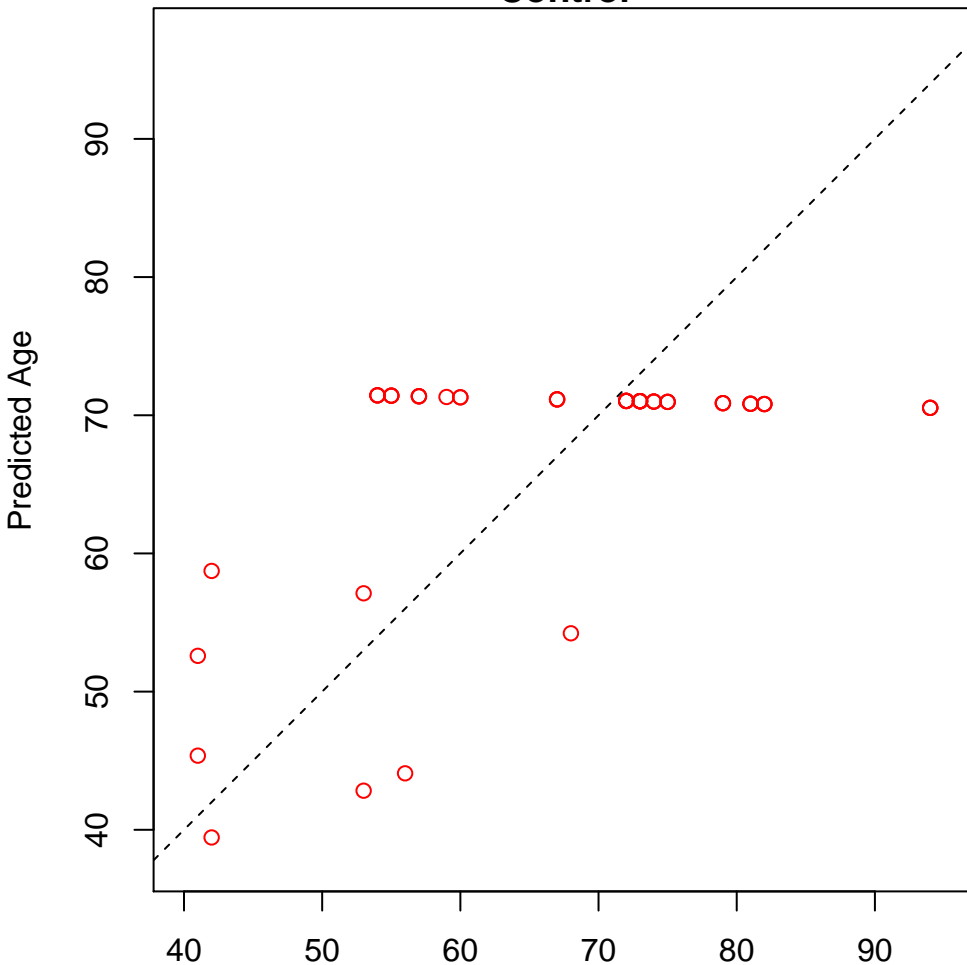


amyloid fibril formation (Score: 0.799332)

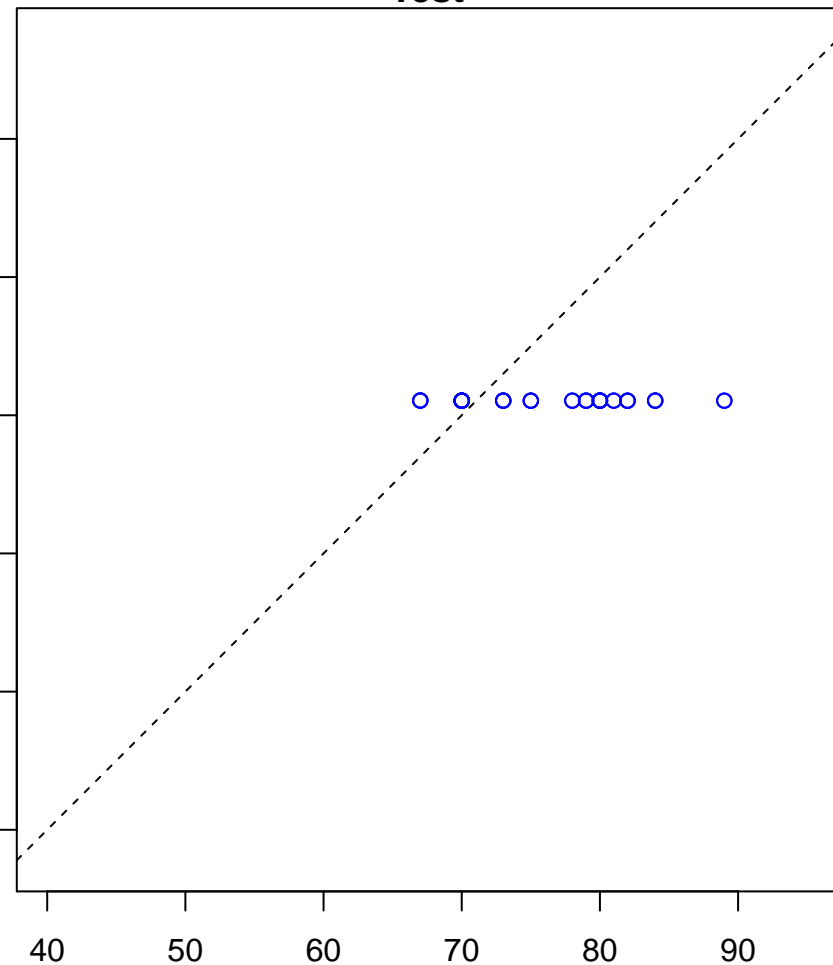


endothelium development (Score: 0.799315)

Control

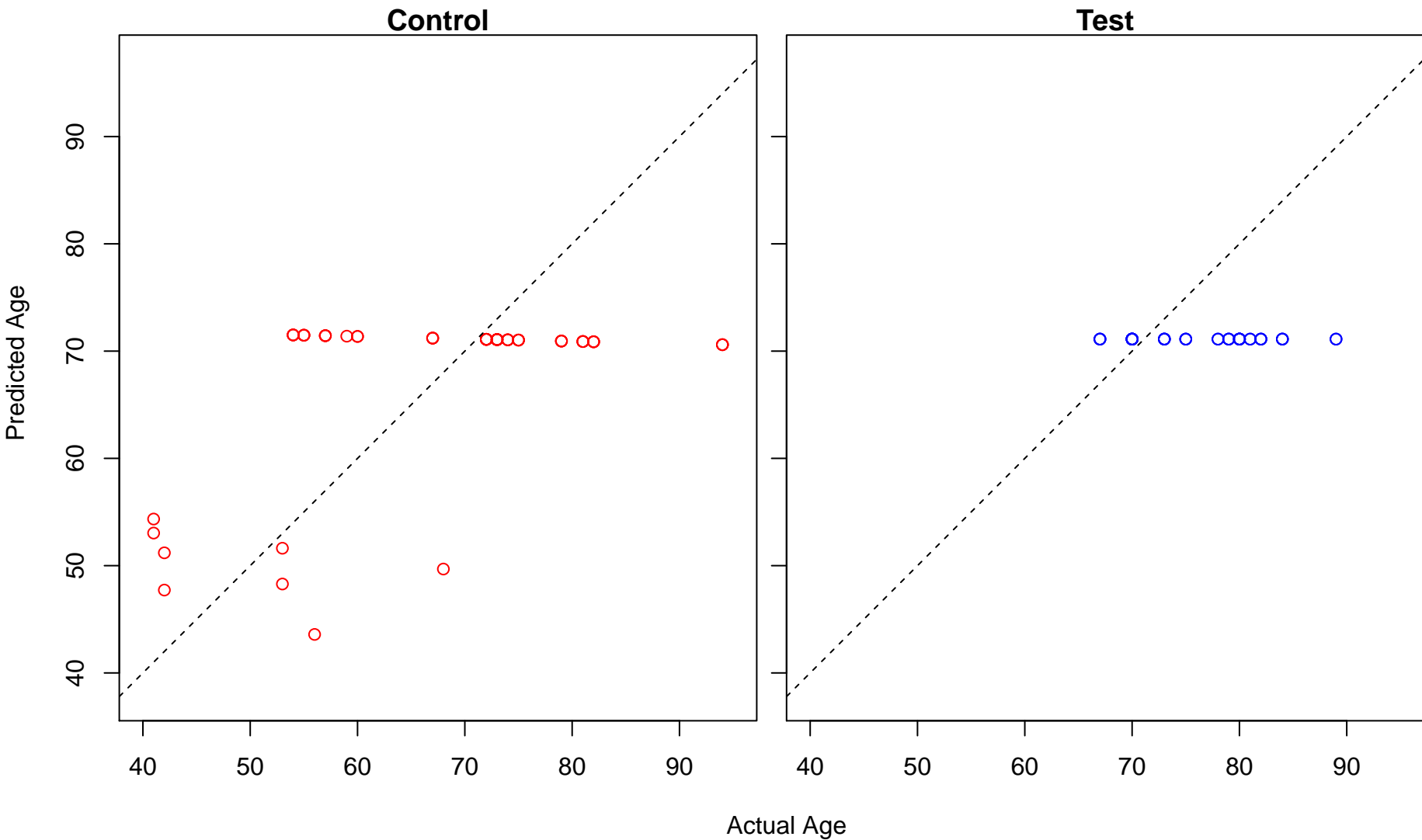


Test

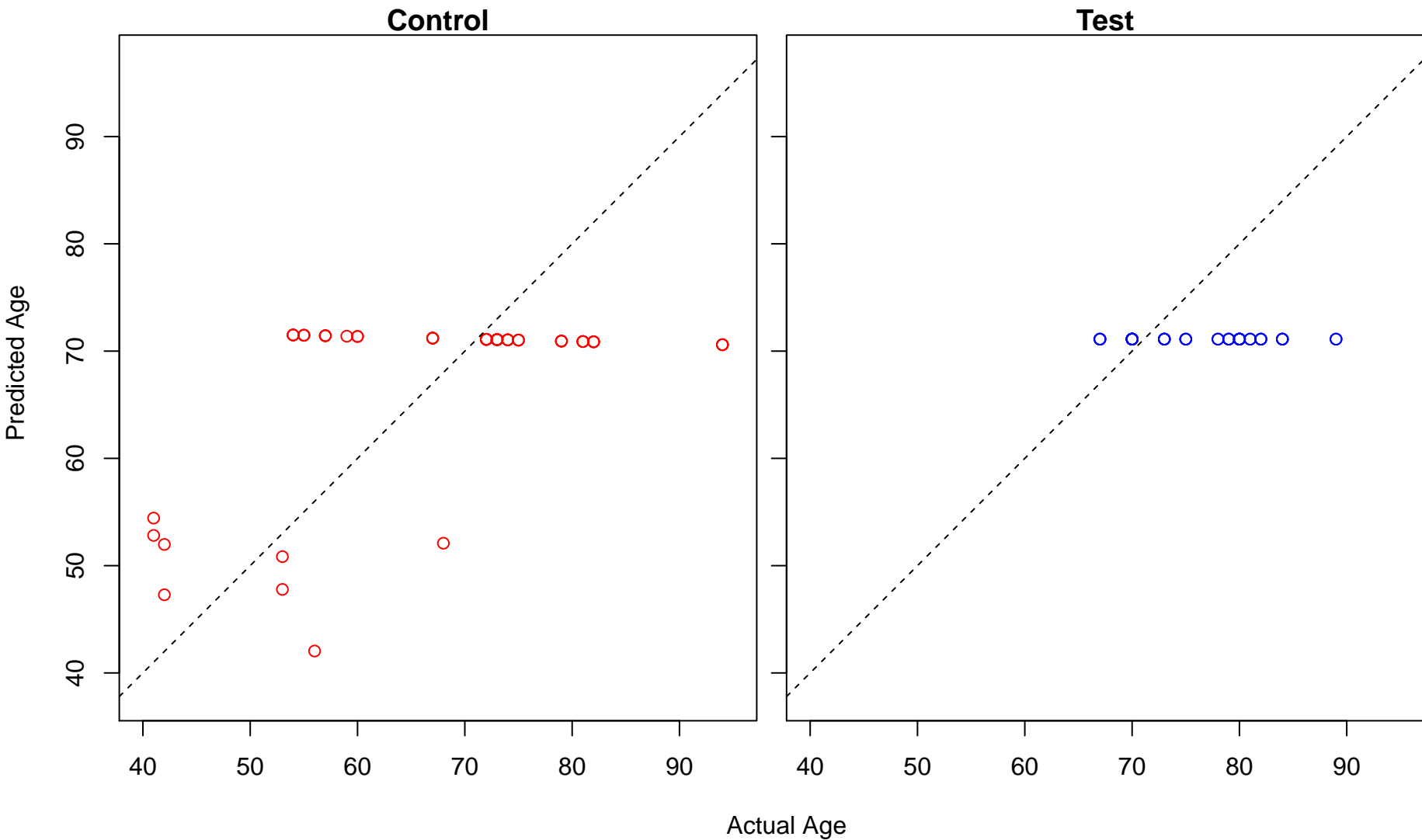


Actual Age

regulation of nucleobase-containing compound metabolic process (Score: 0.799313)

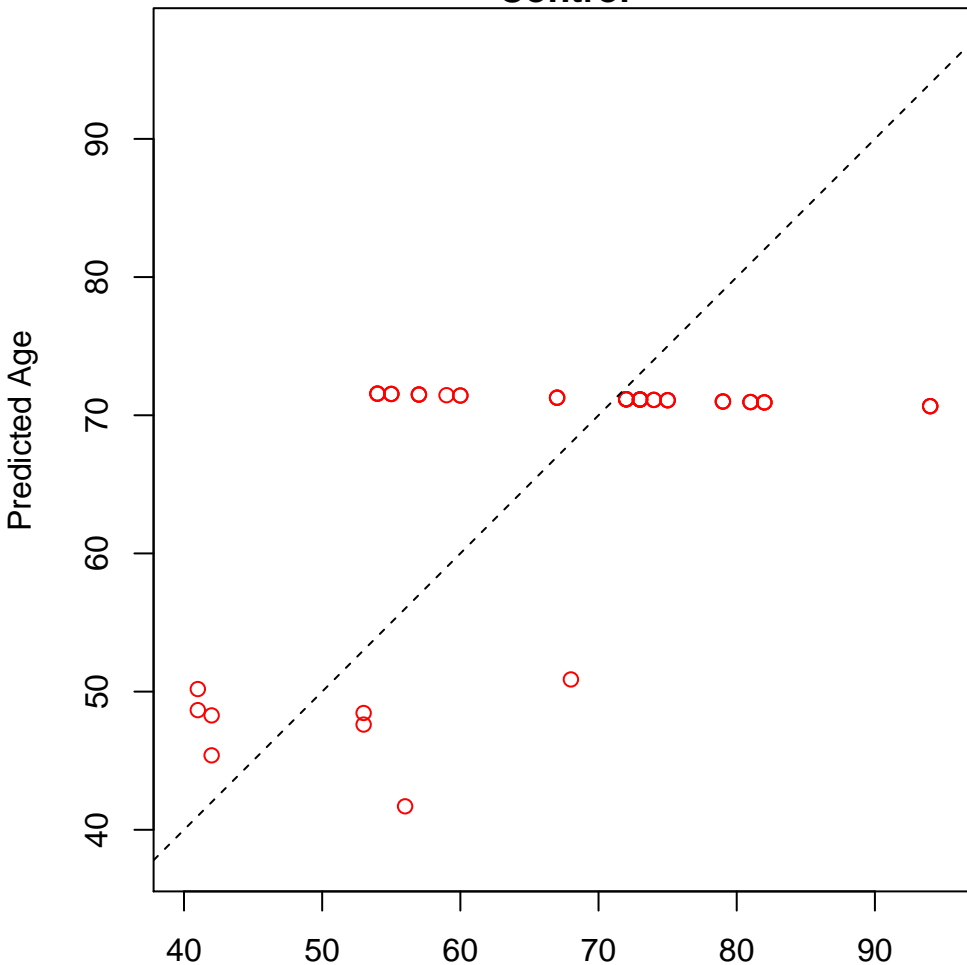


negative regulation of cellular metabolic process (Score: 0.799309)

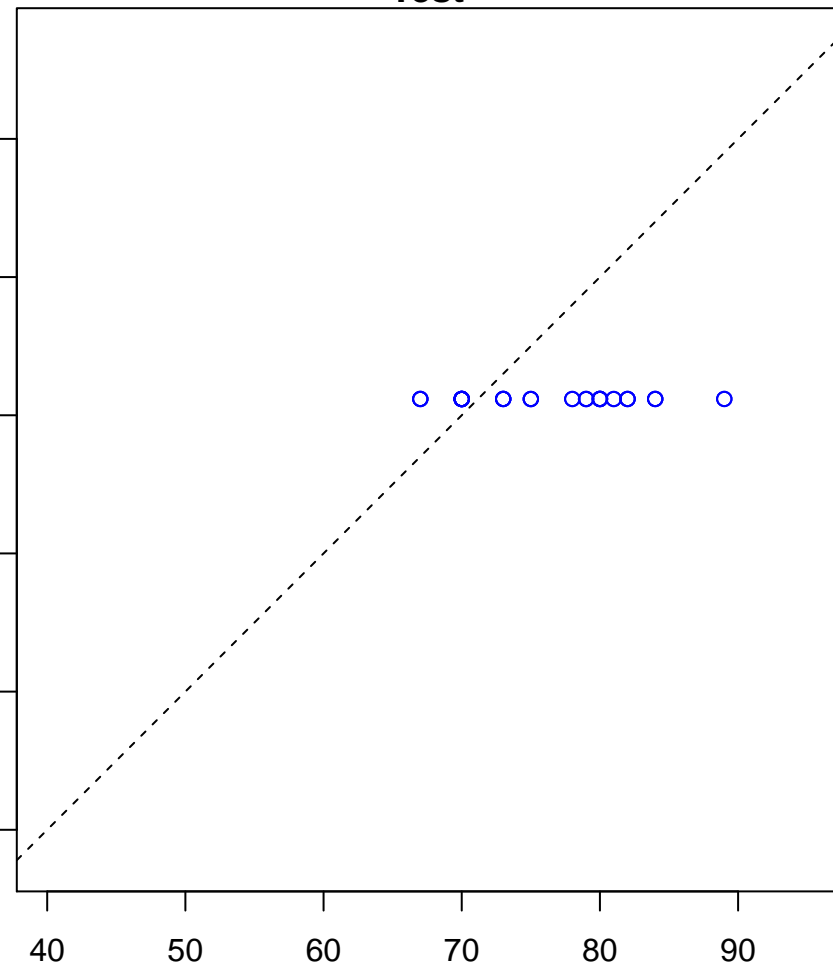


establishment of localization in cell (Score: 0.799277)

Control

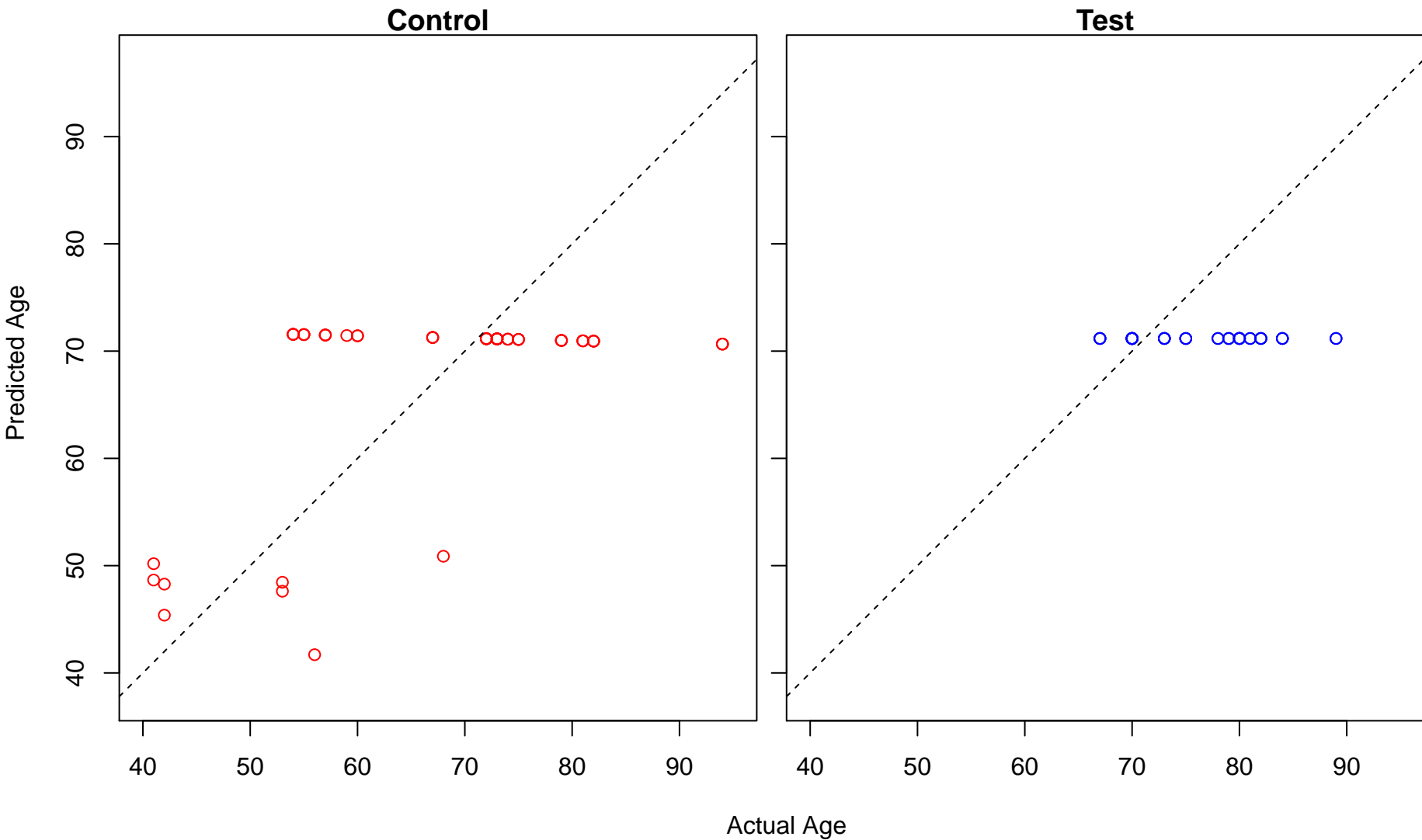


Test



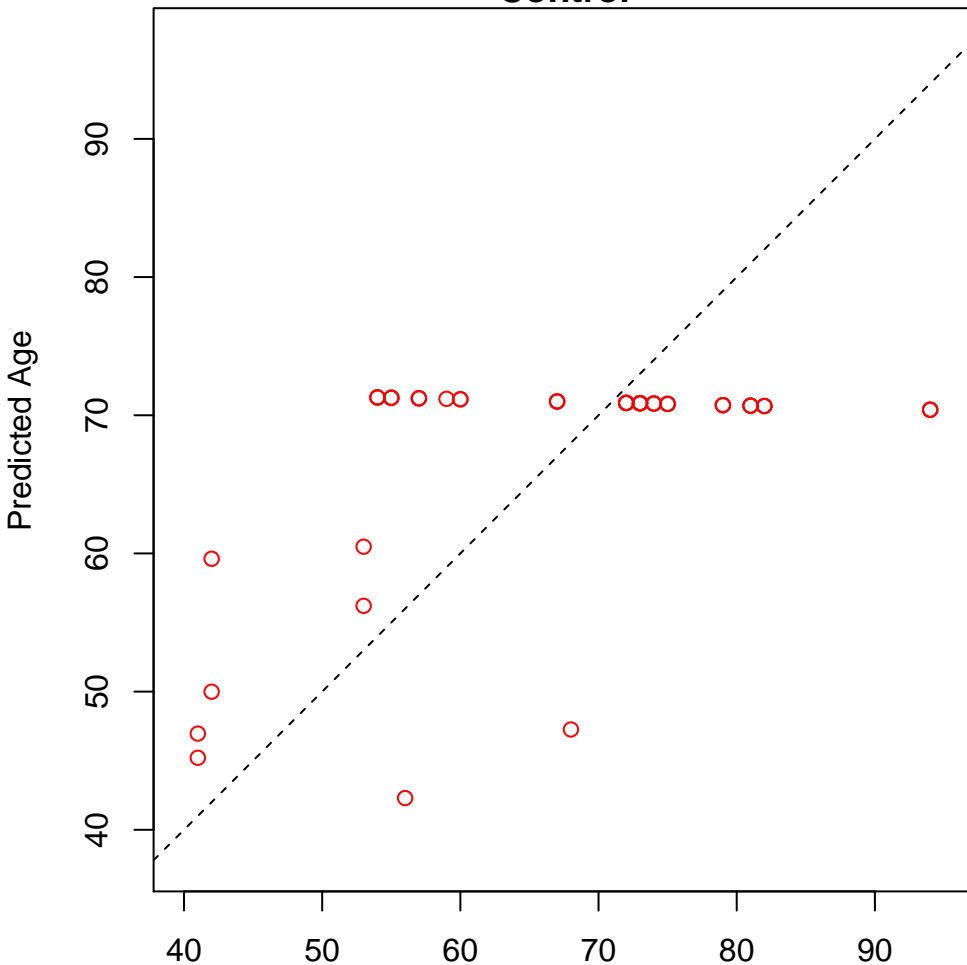
Actual Age

intracellular transport (Score: 0.799274)

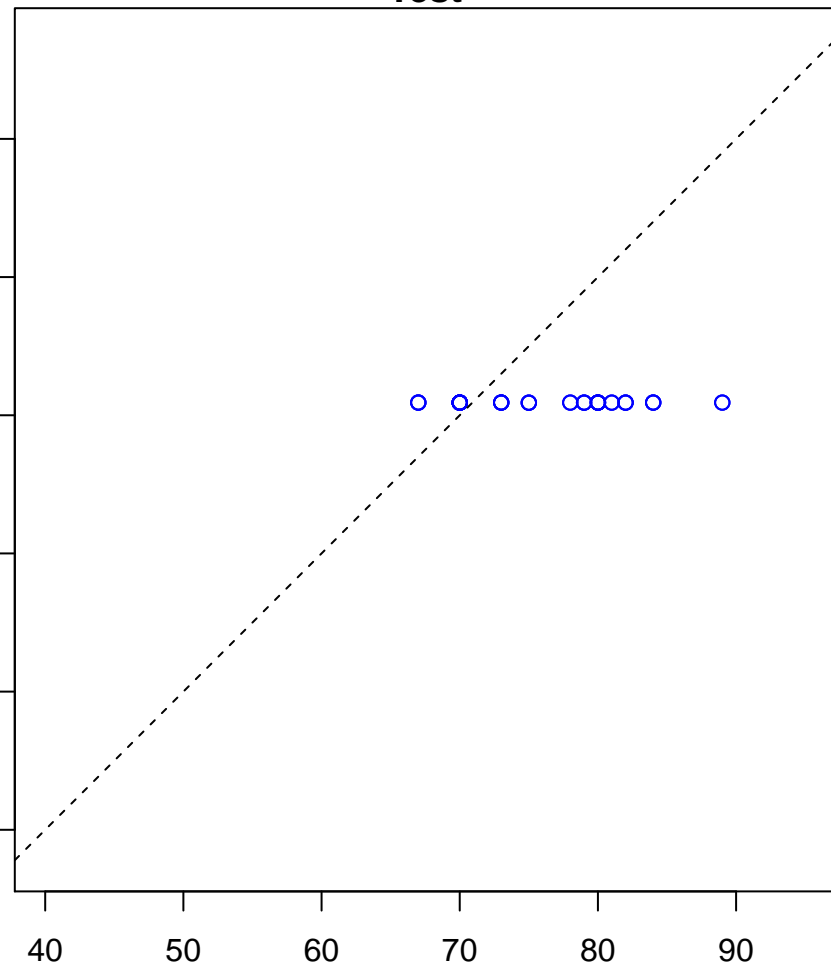


regulation of telomerase activity (Score: 0.799258)

Control



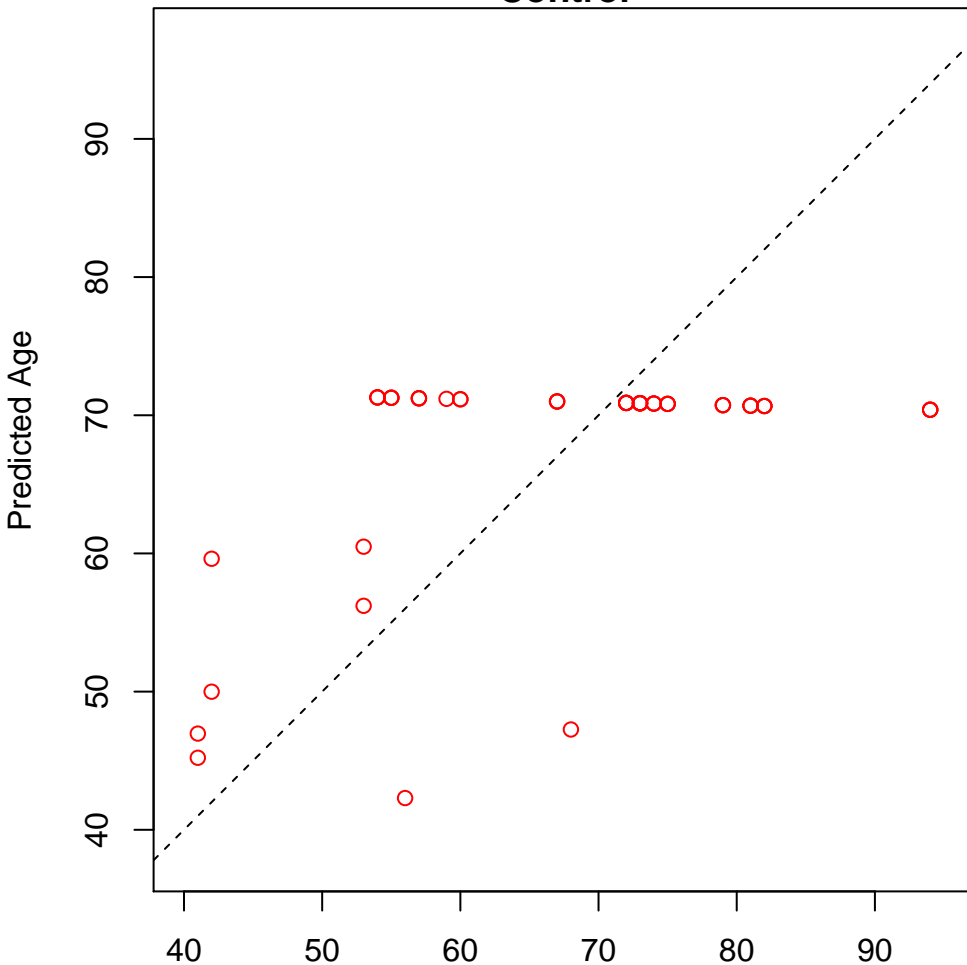
Test



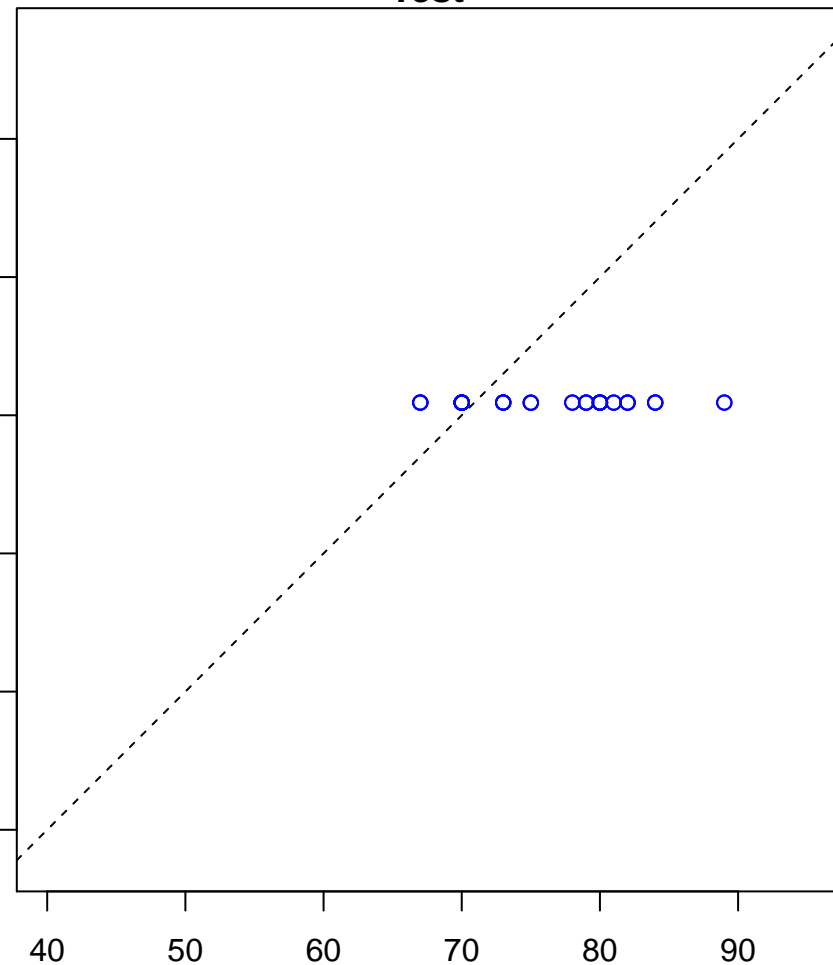
Actual Age

positive regulation of telomerase activity (Score: 0.799258)

Control

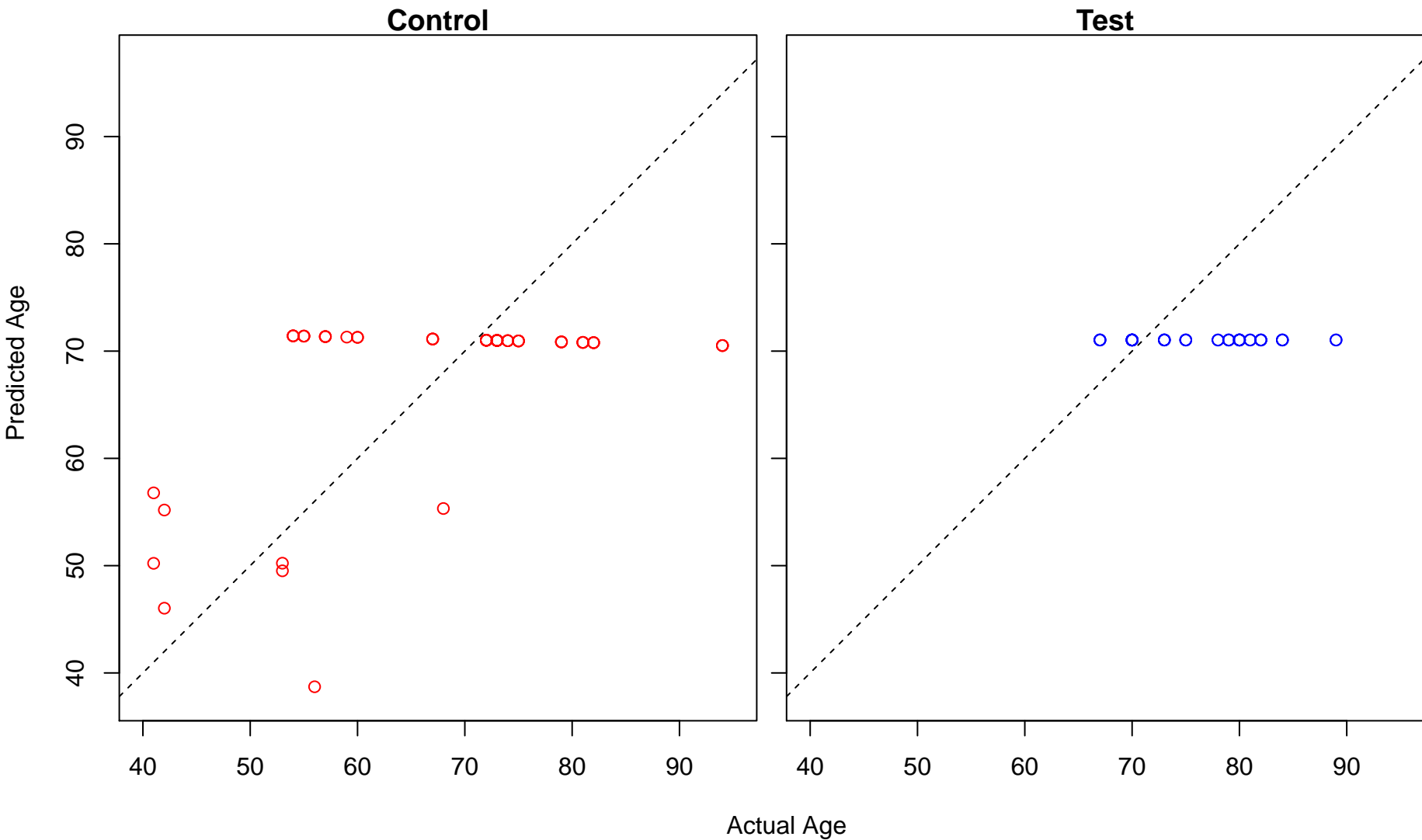


Test

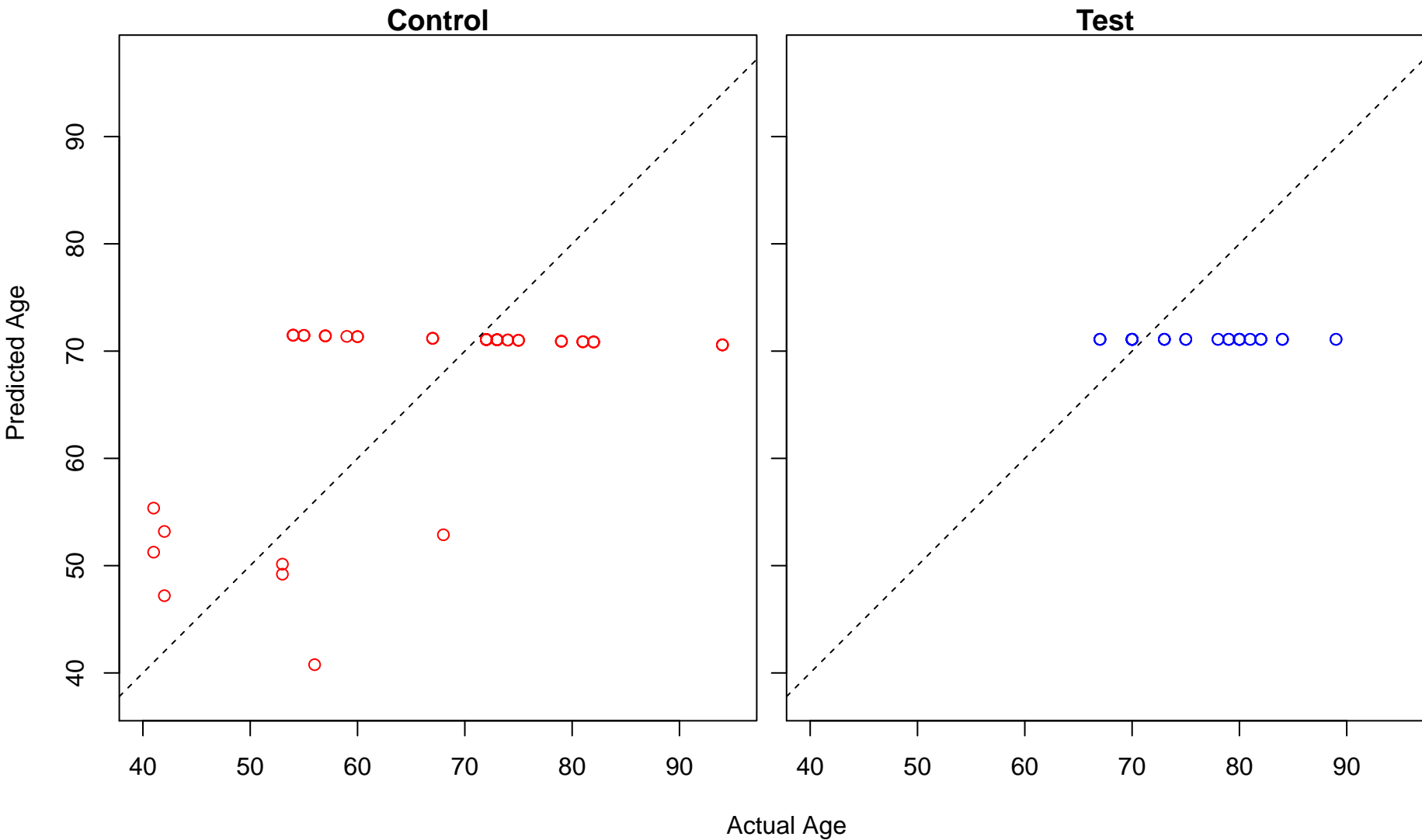


Actual Age

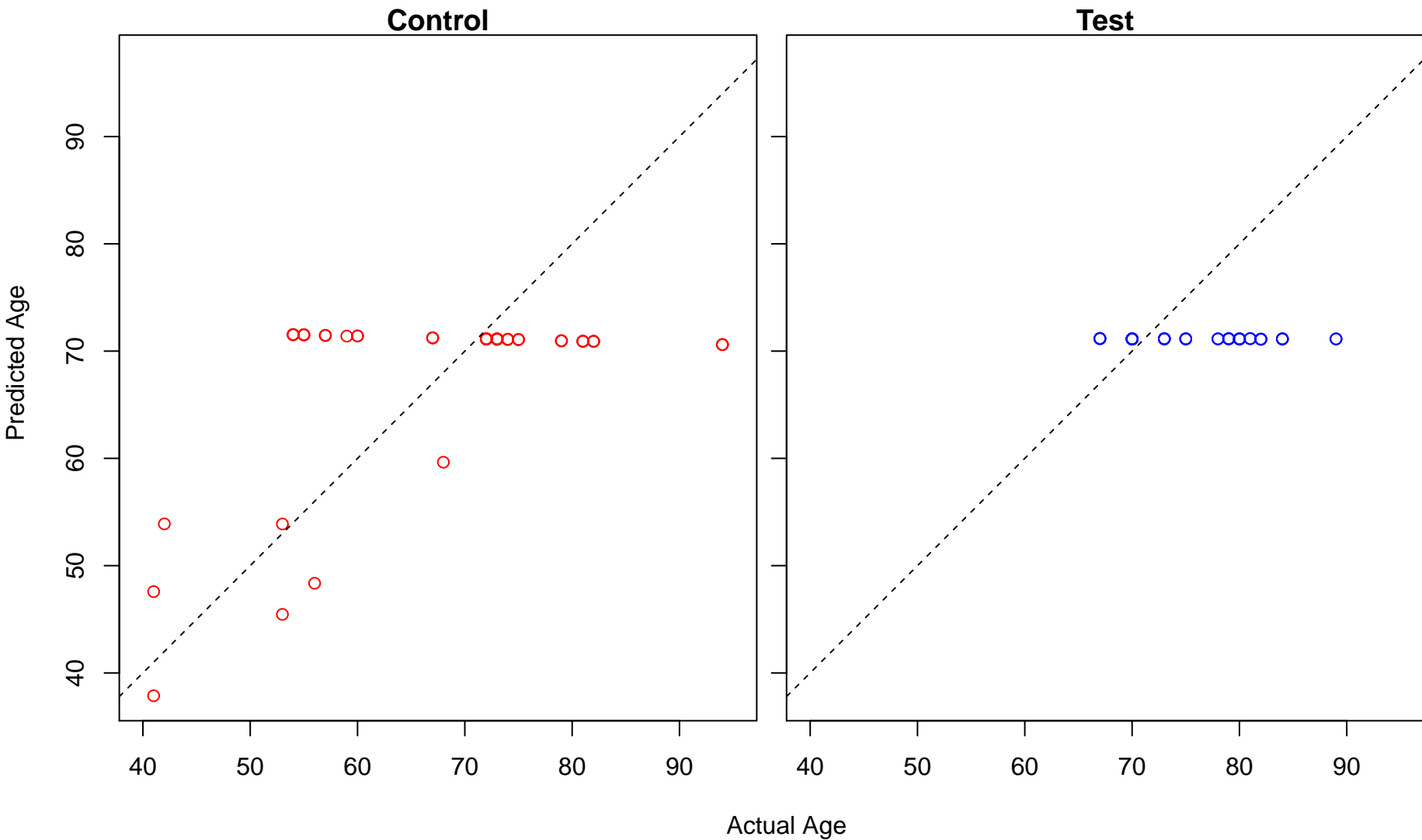
ncRNA metabolic process (Score: 0.799249)



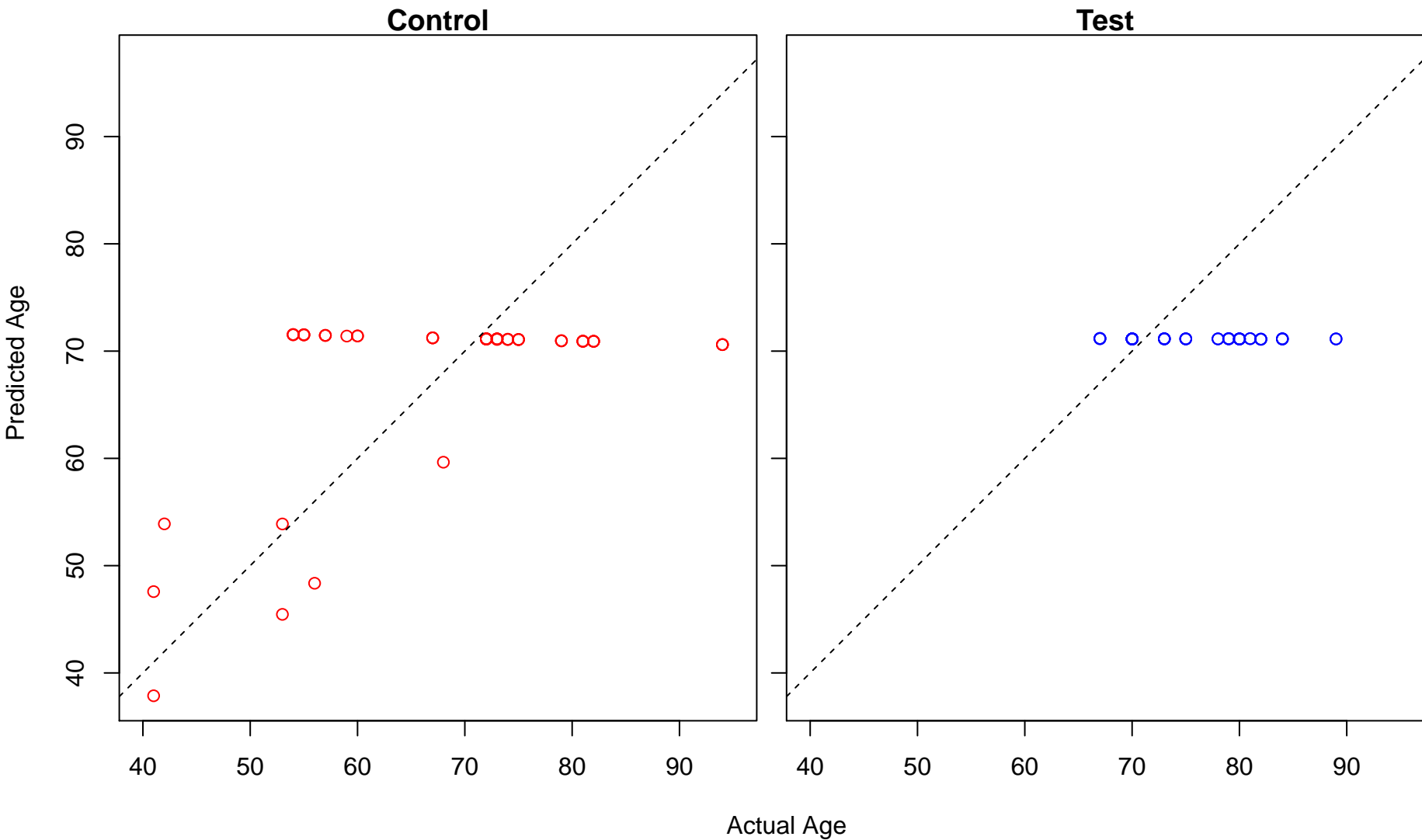
regulation of macromolecule metabolic process (Score: 0.799229)



cell motility (Score: 0.799217)

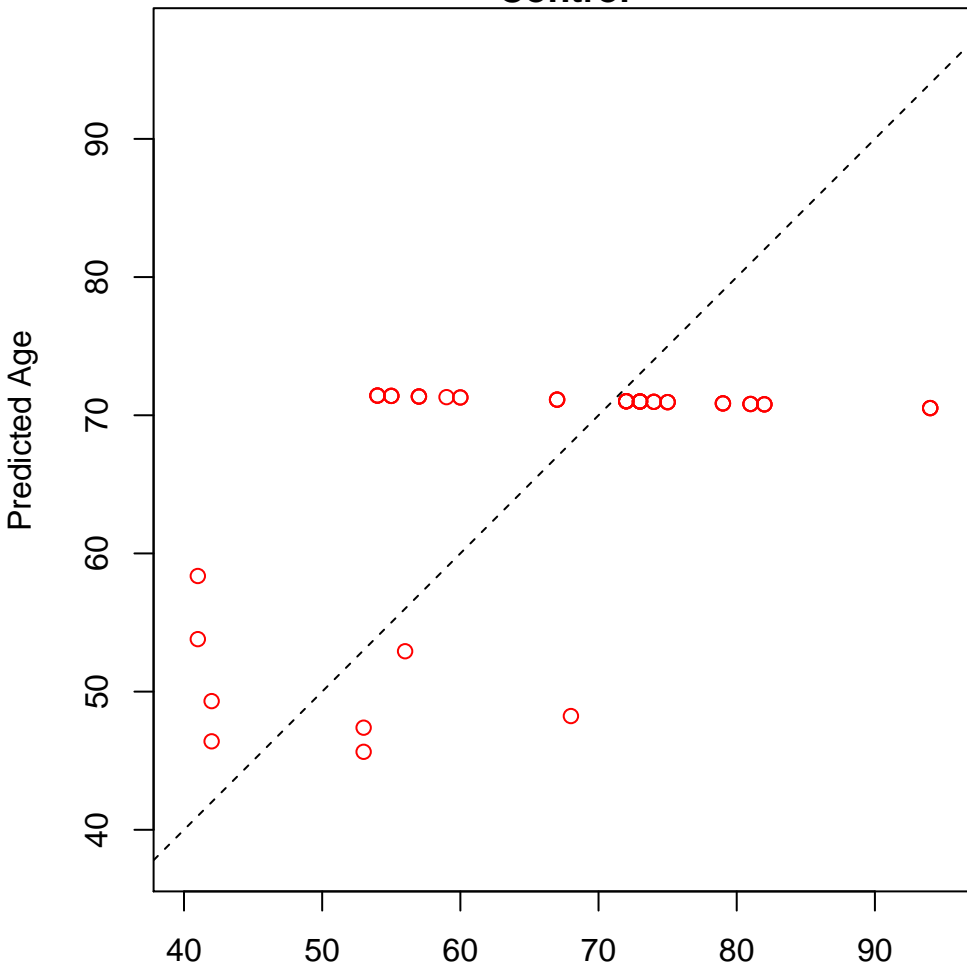


localization of cell (Score: 0.799217)

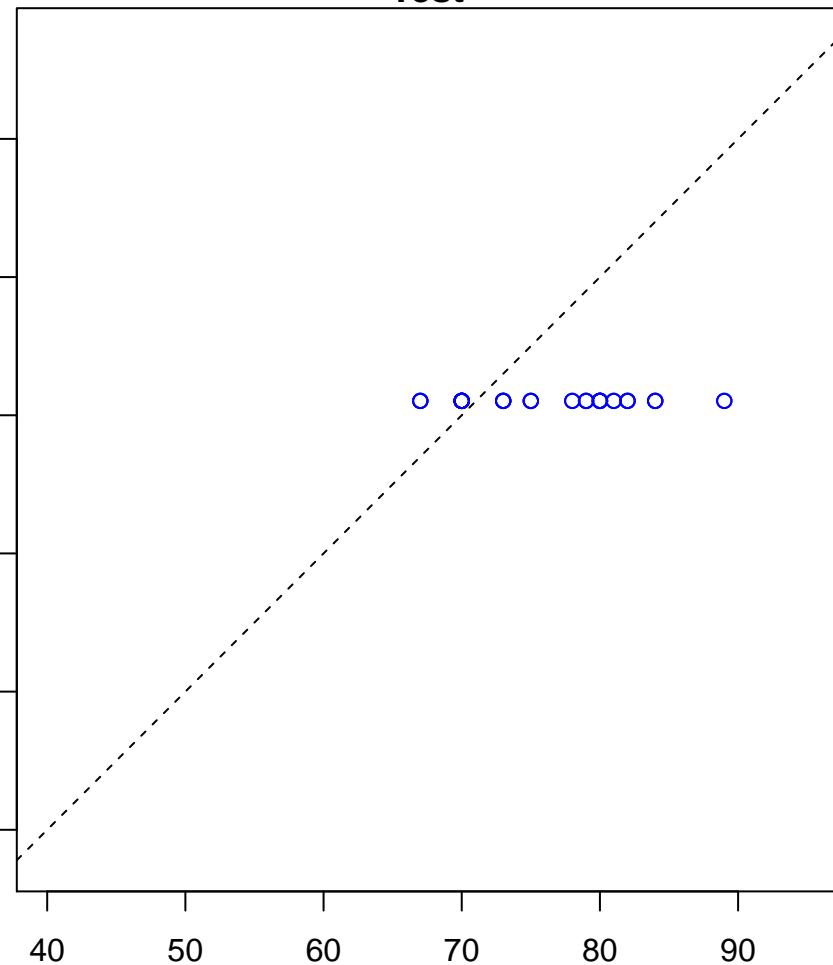


organic acid biosynthetic process (Score: 0.799205)

Control



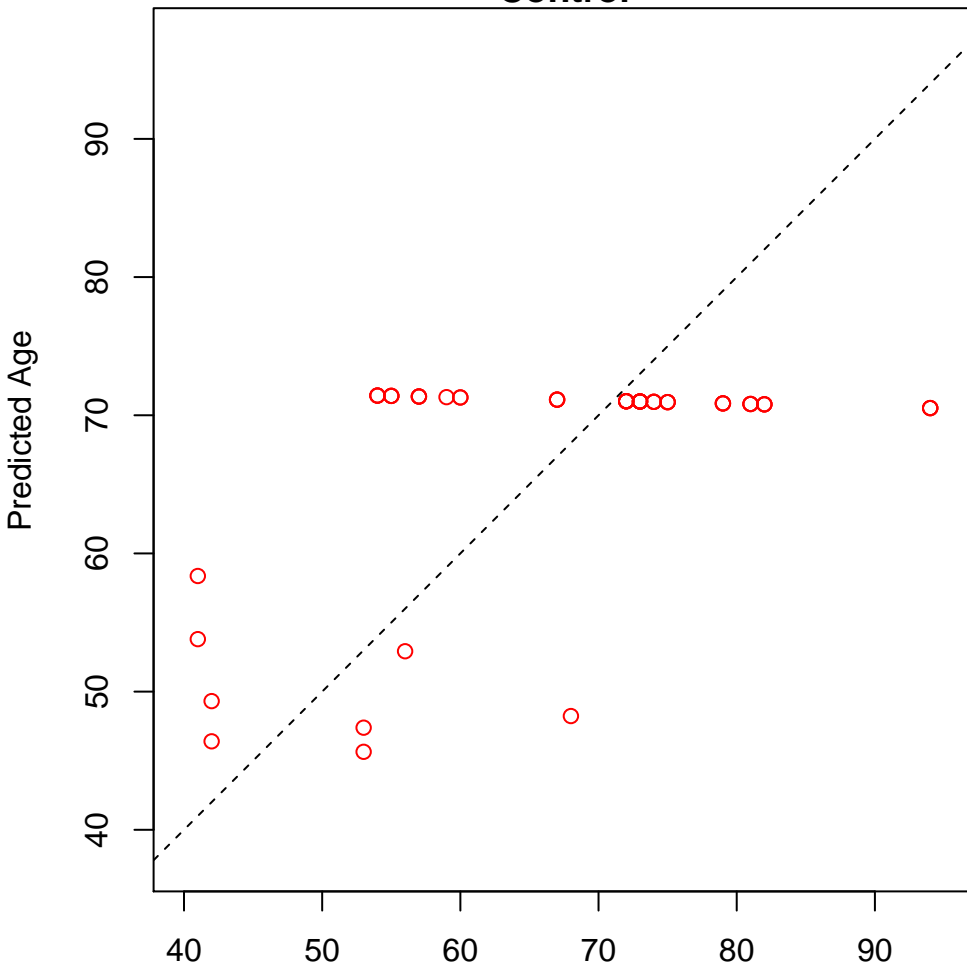
Test



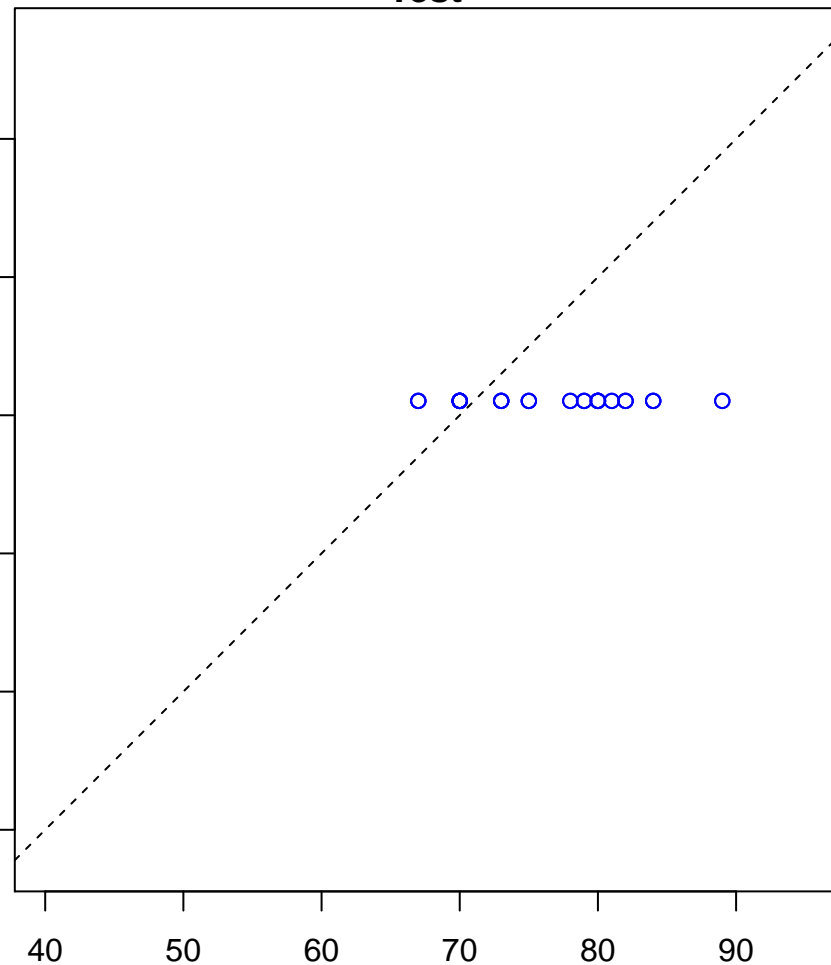
Actual Age

carboxylic acid biosynthetic process (Score: 0.799205)

Control

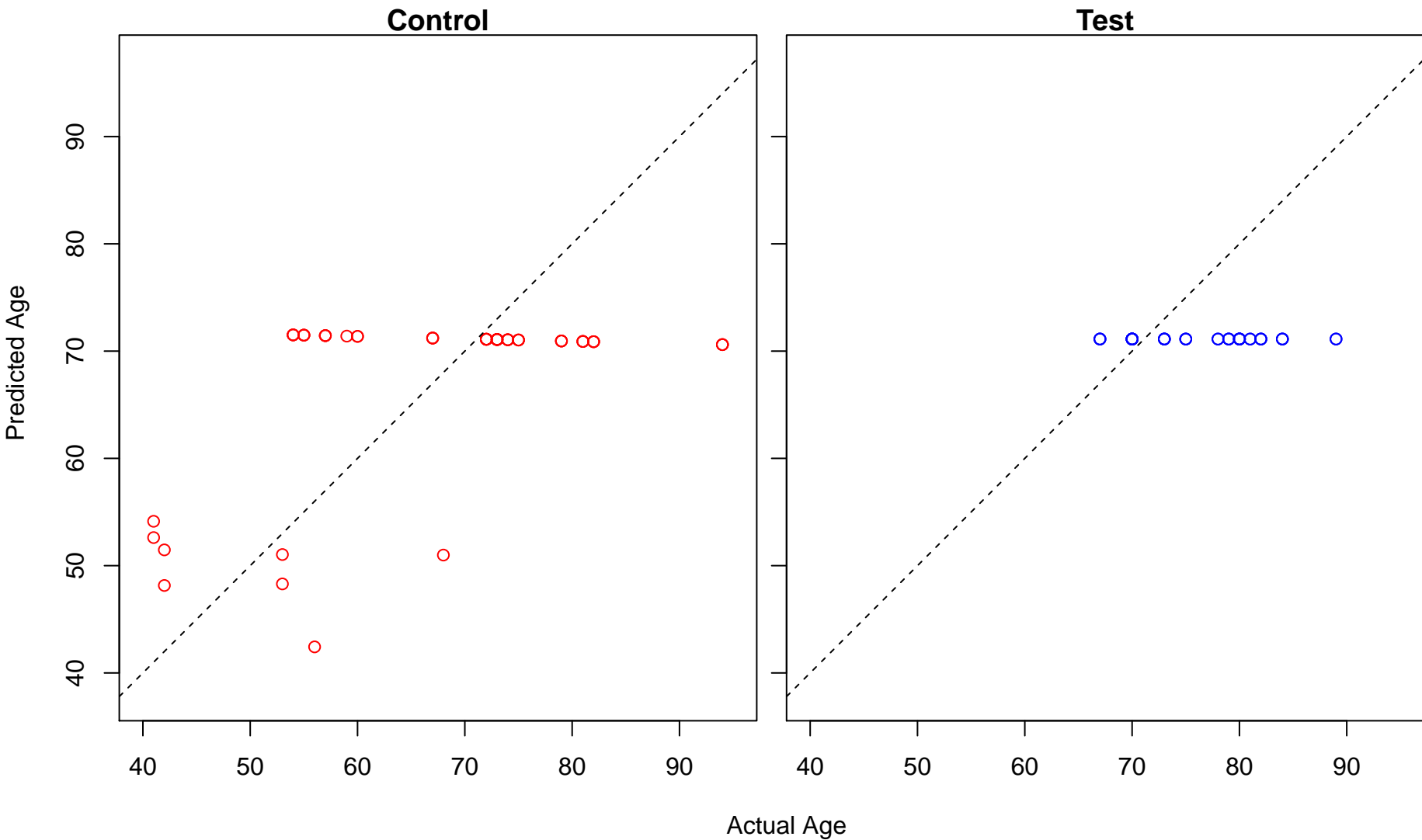


Test

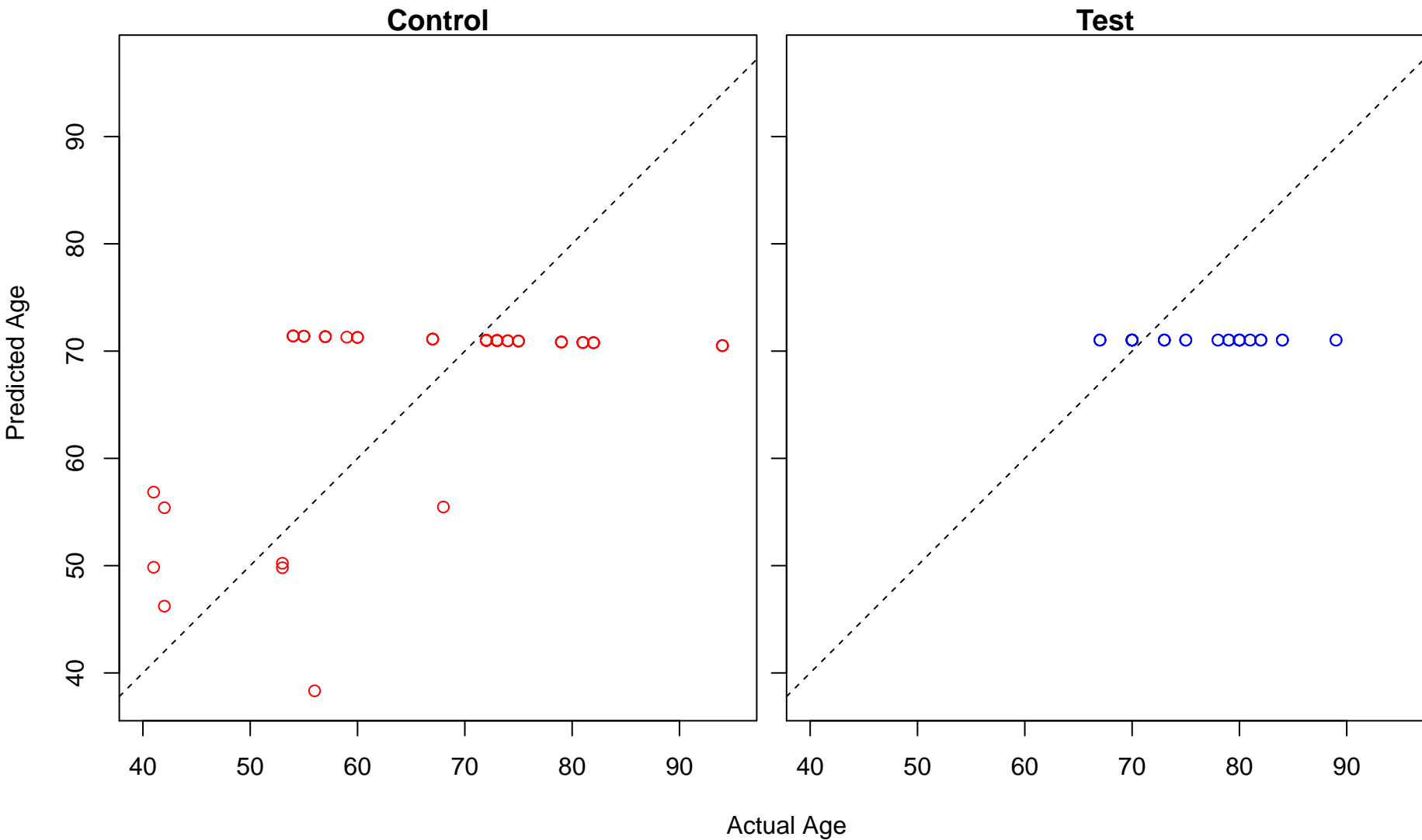


Actual Age

regulation of cellular biosynthetic process (Score: 0.799147)

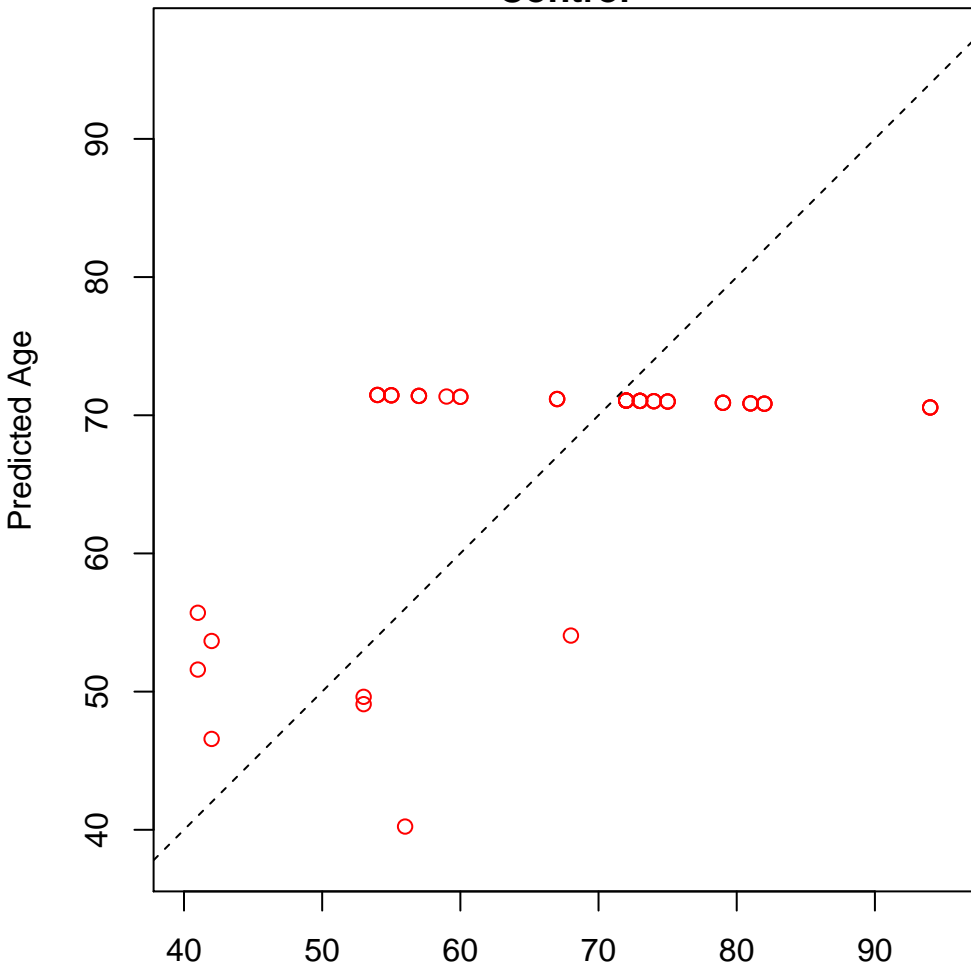


protein targeting (Score: 0.799140)

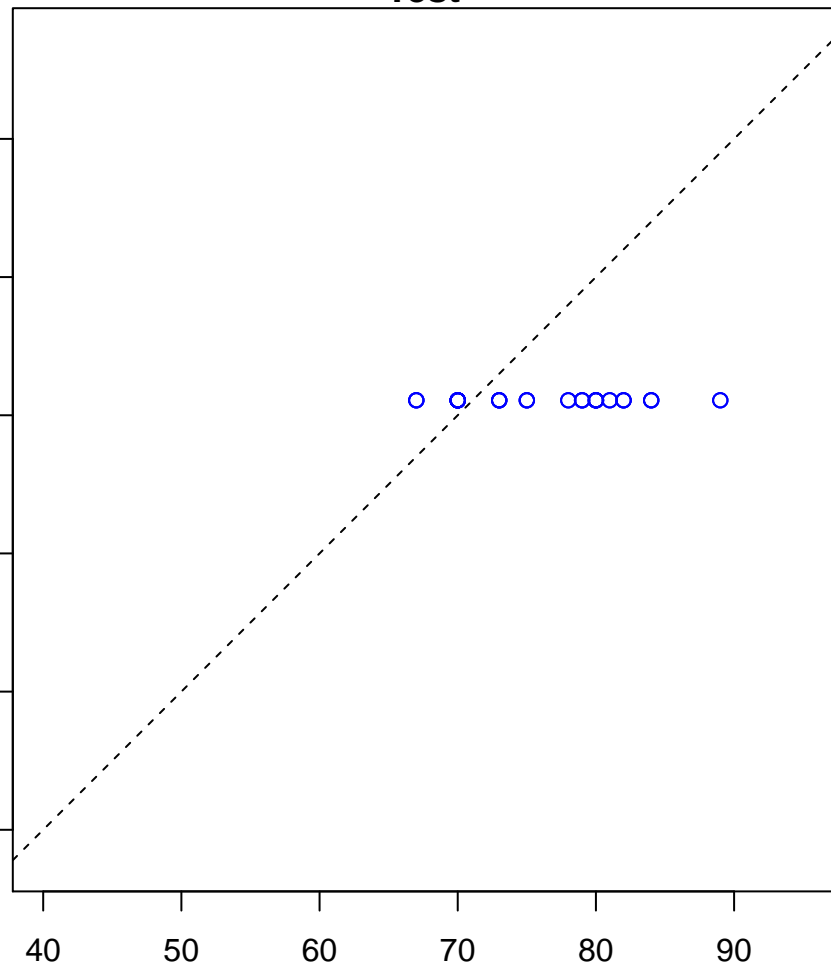


organic substance biosynthetic process (Score: 0.799118)

Control



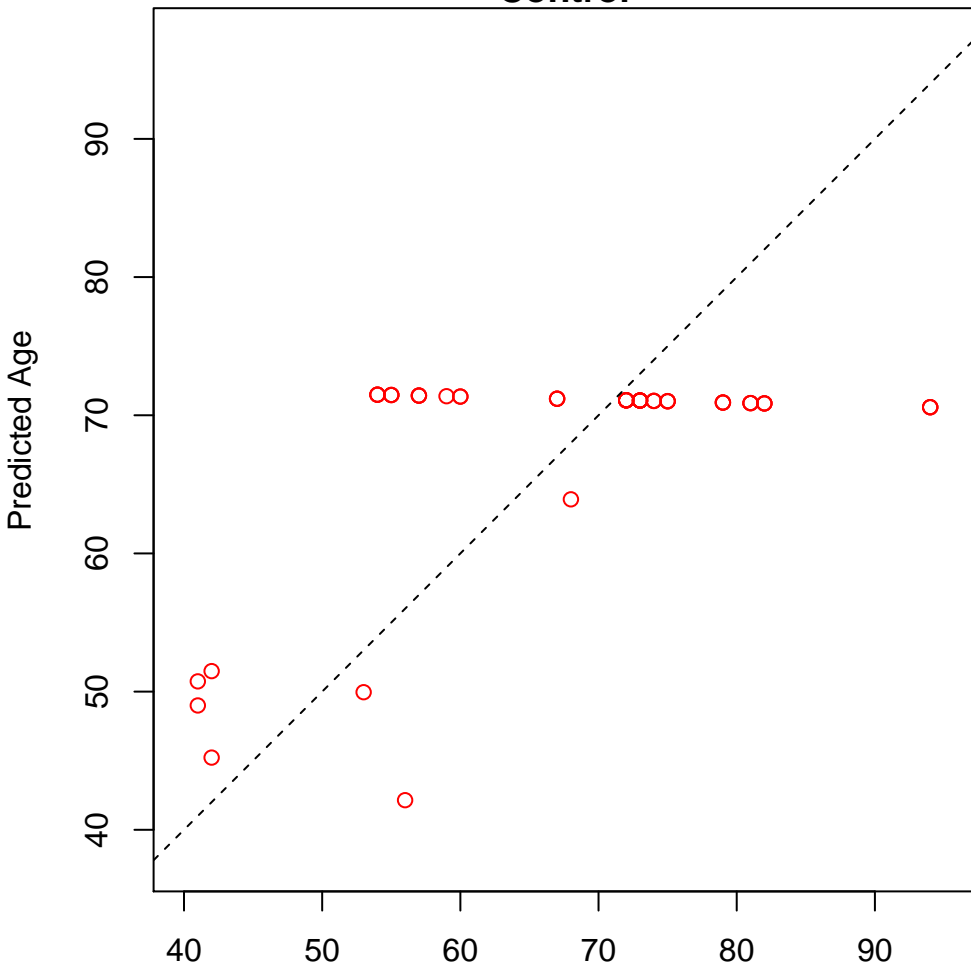
Test



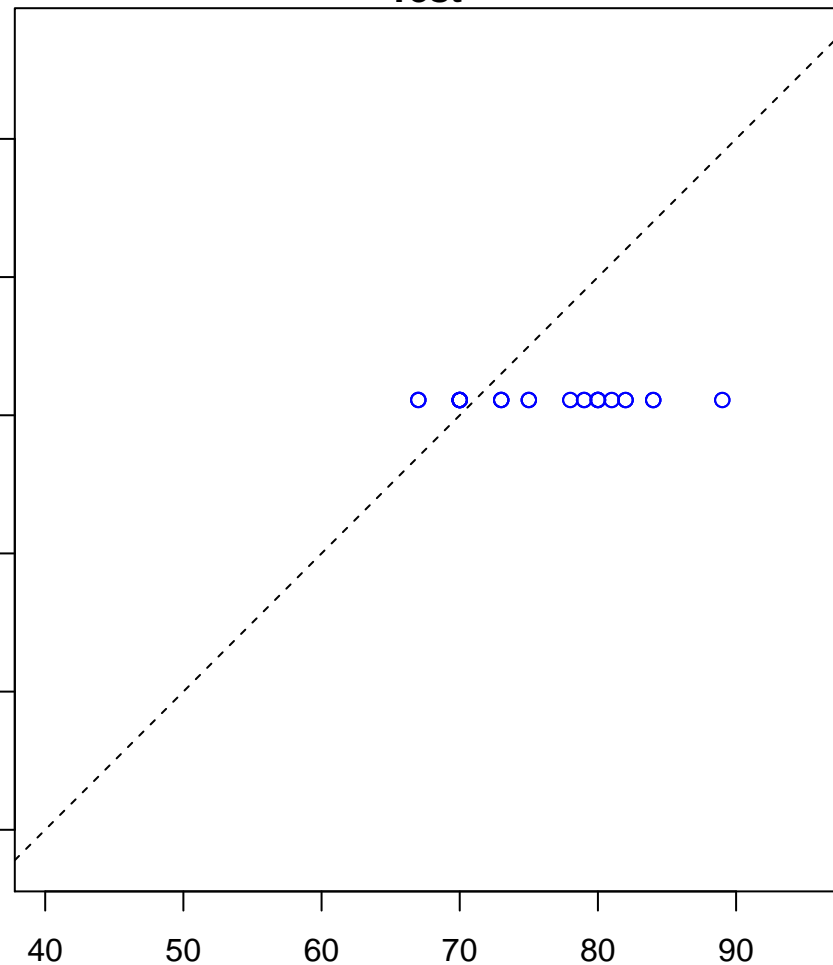
Actual Age

positive regulation of cell proliferation (Score: 0.799116)

Control

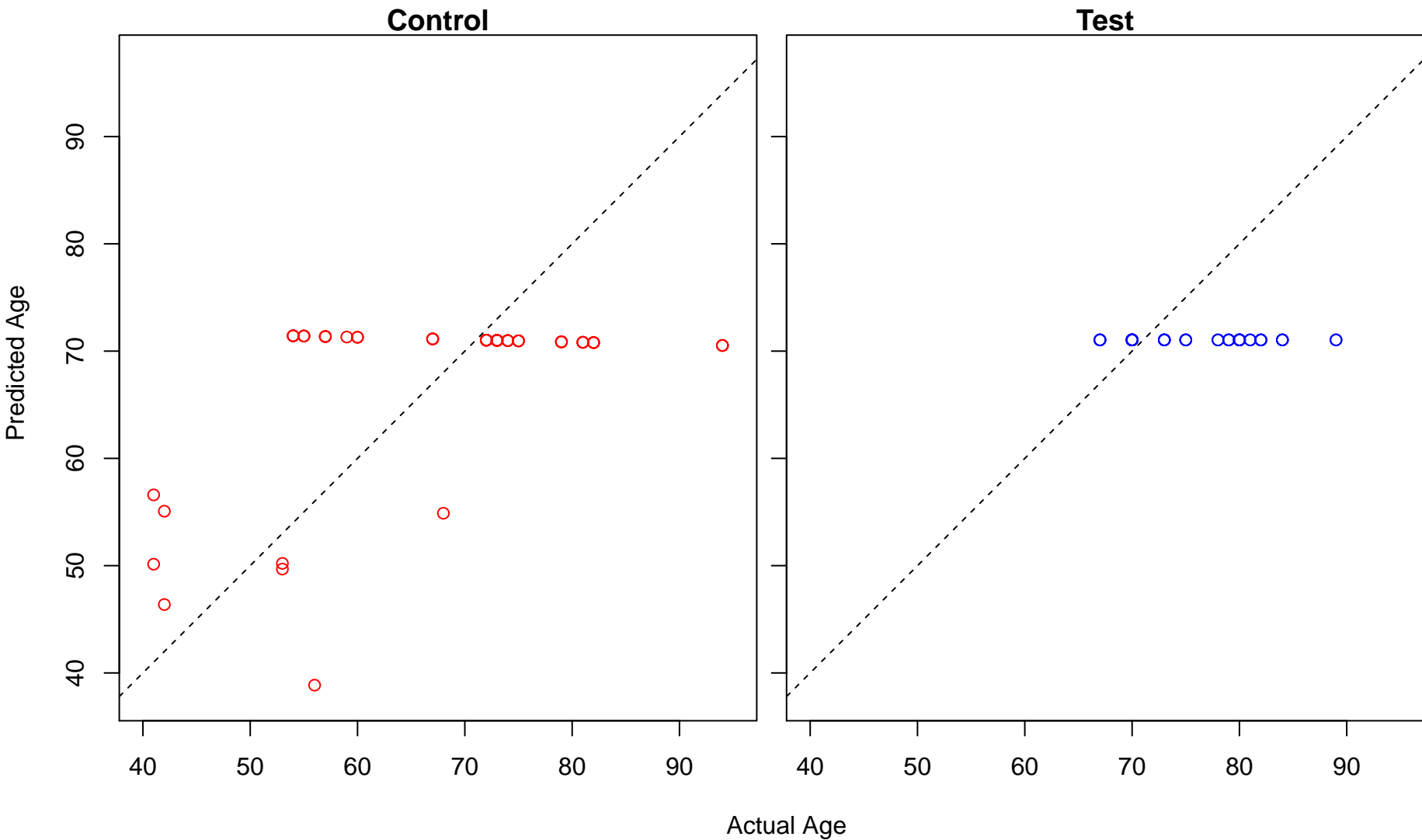


Test



Actual Age

RNA metabolic process (Score: 0.799107)

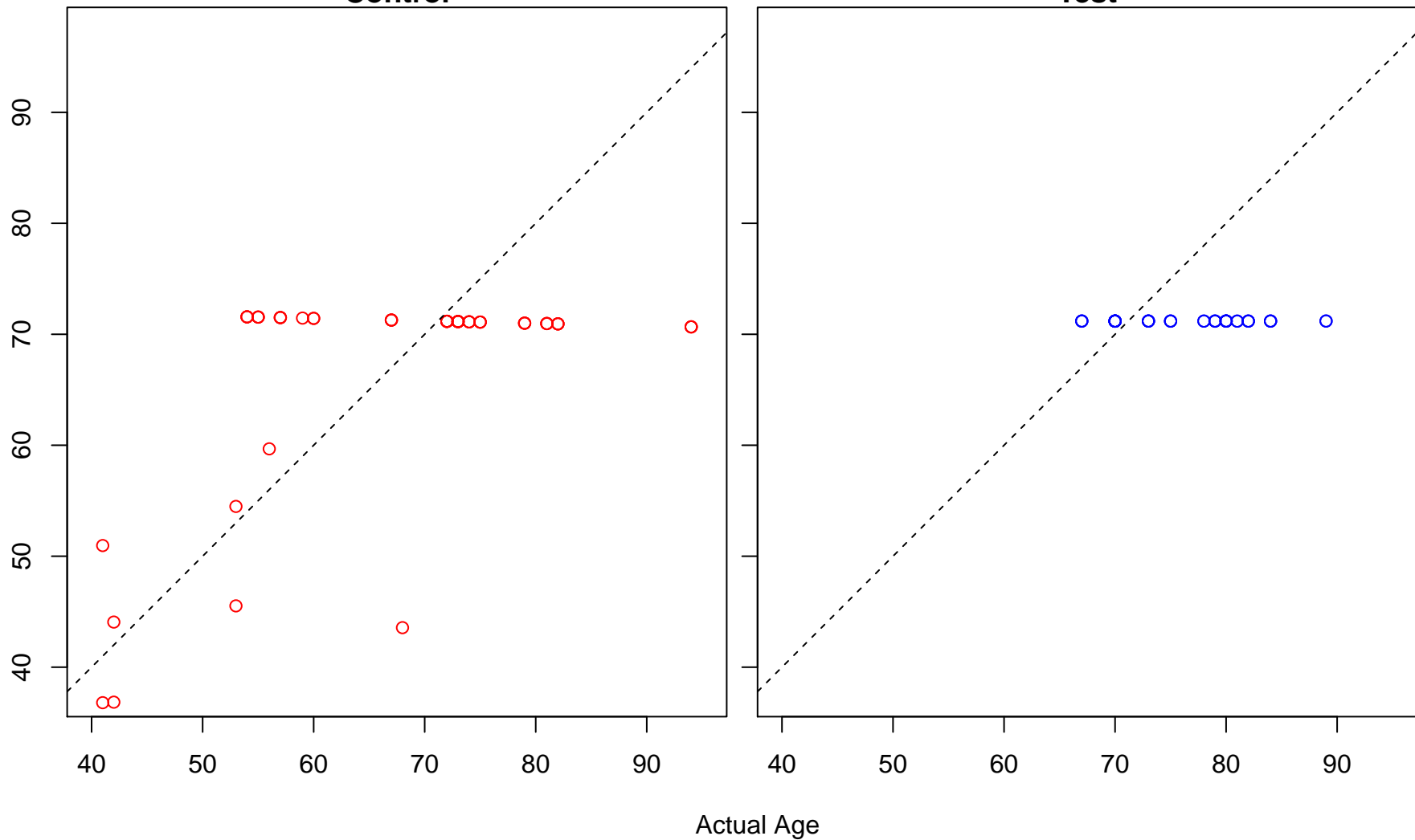


regulation of mRNA metabolic process (Score: 0.799102)

Control

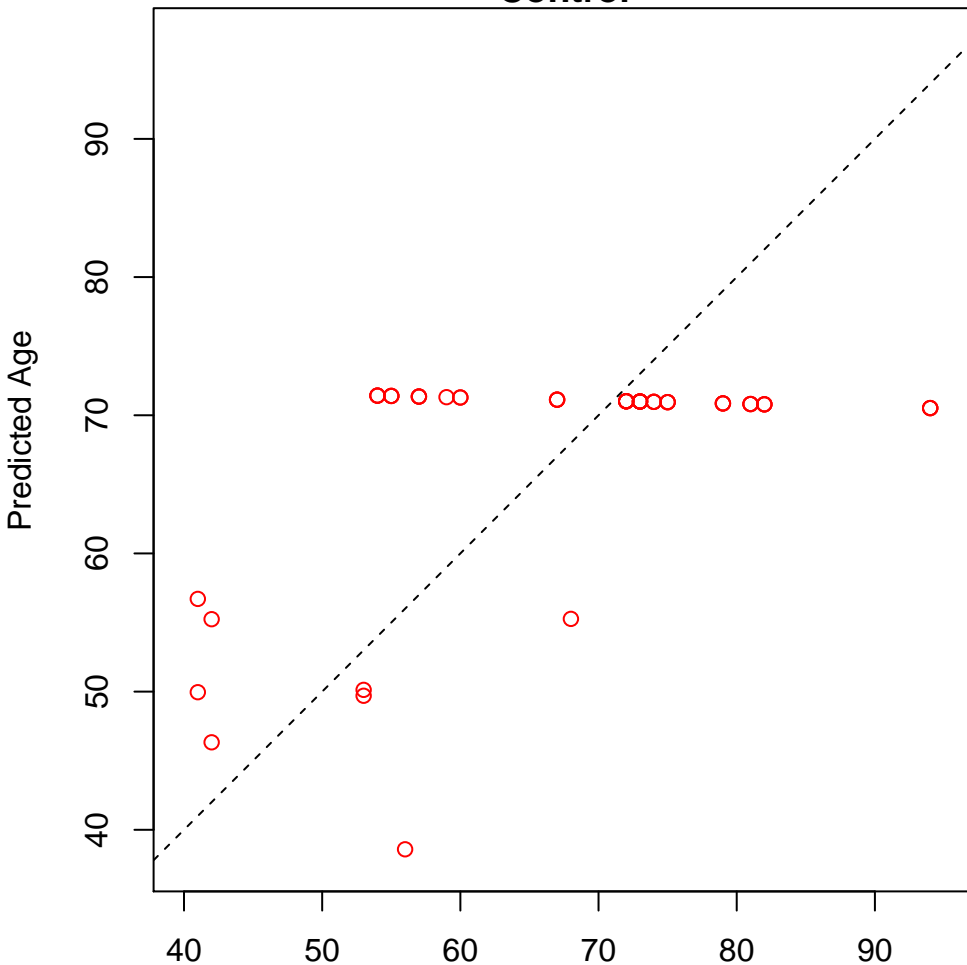
Test

Predicted Age

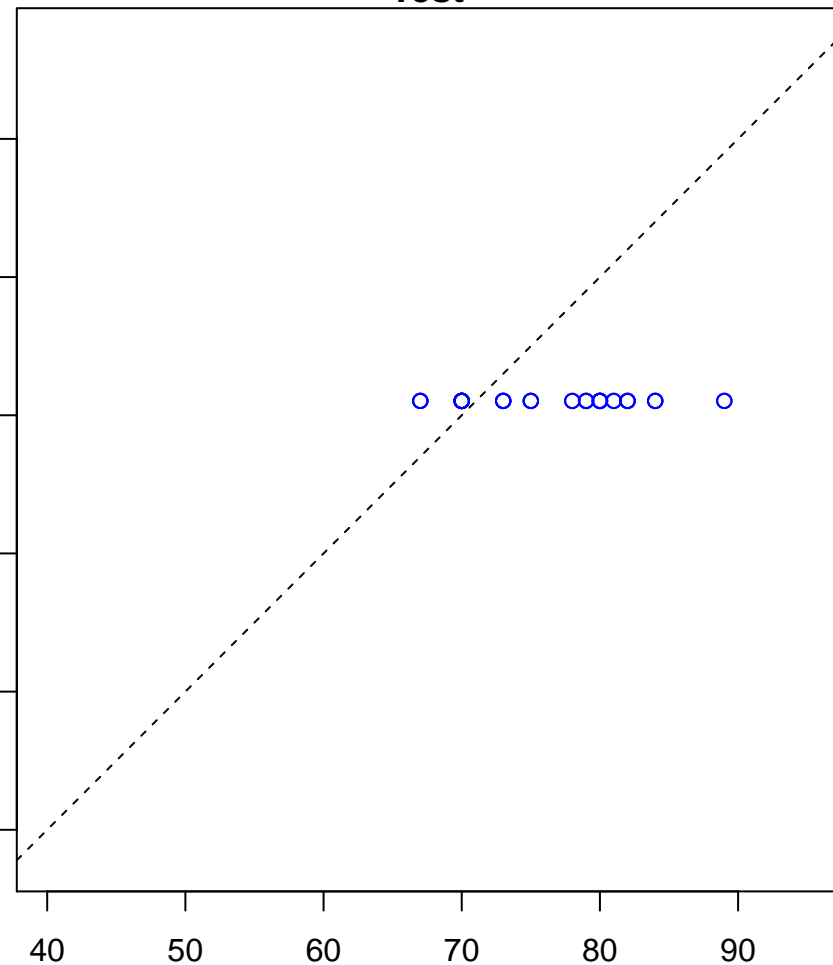


protein localization to organelle (Score: 0.799093)

Control

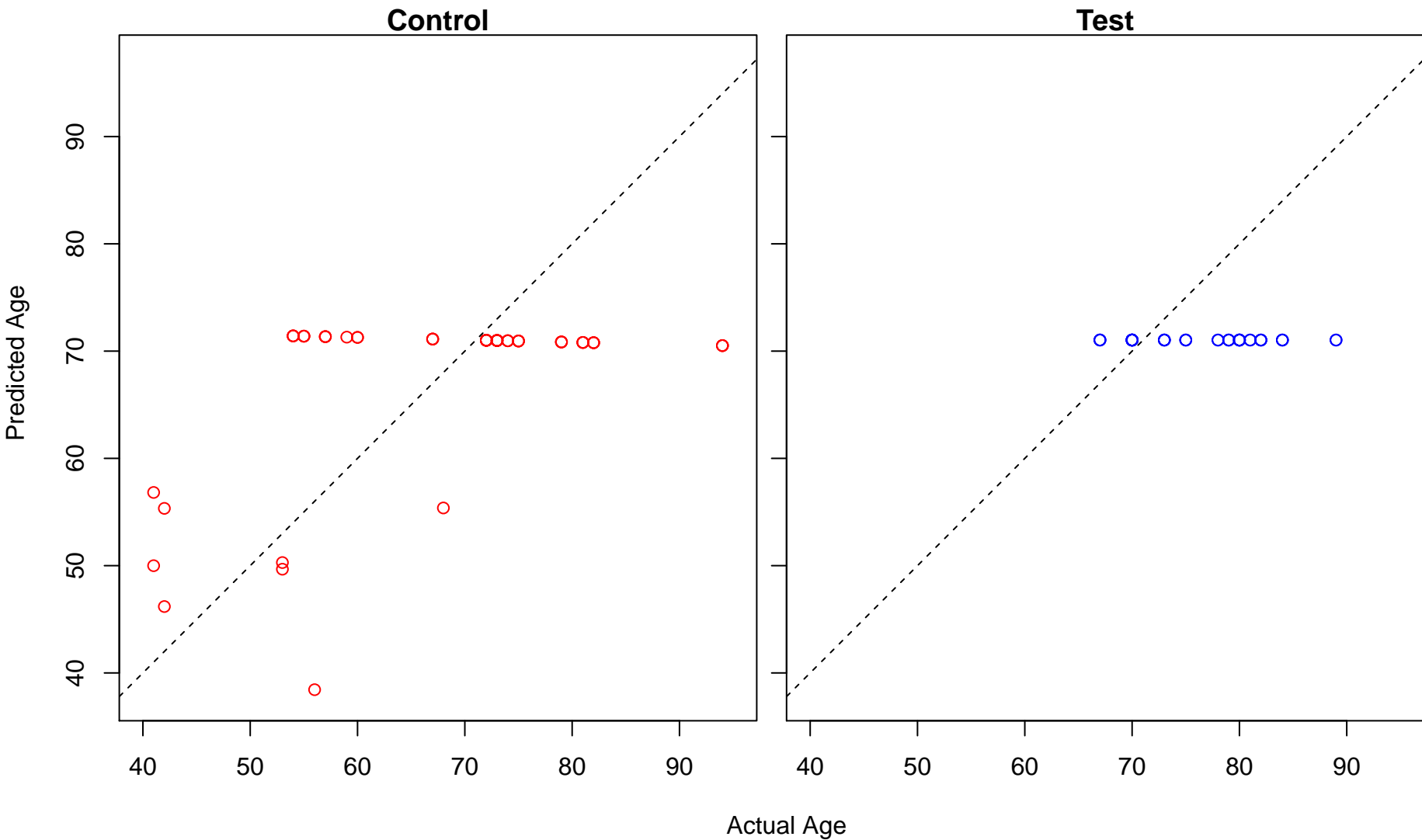


Test

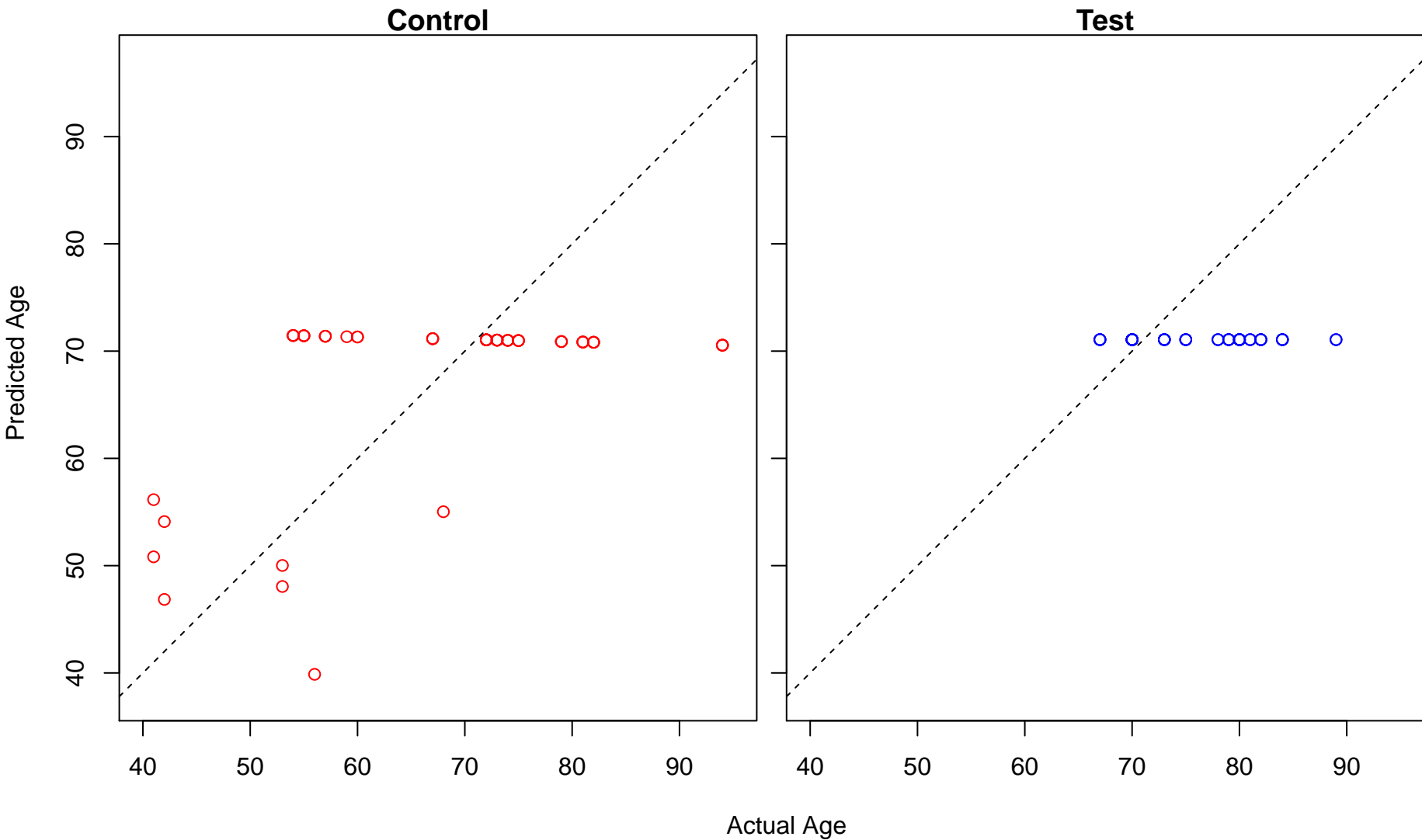


Actual Age

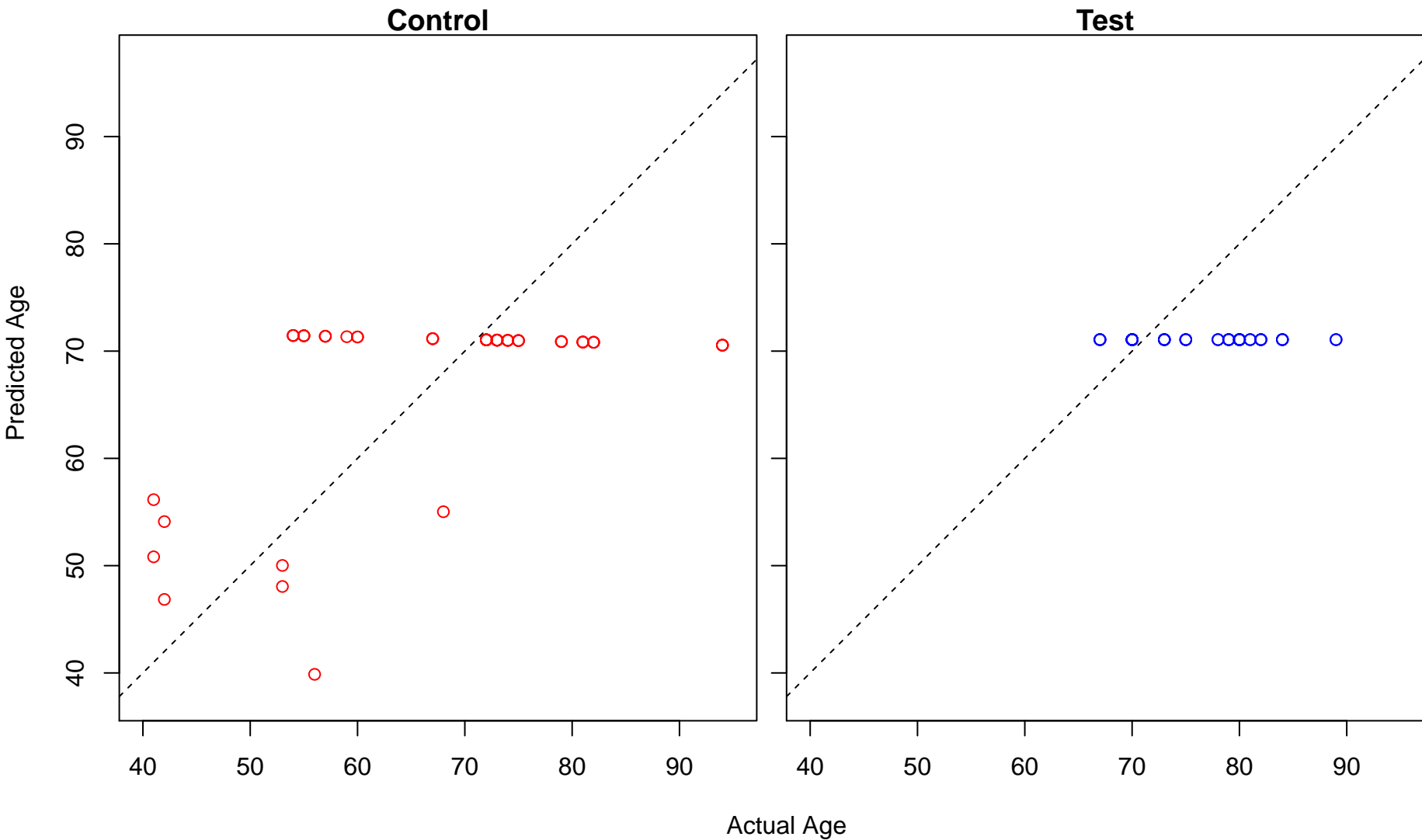
establishment of protein localization to organelle (Score: 0.799082)



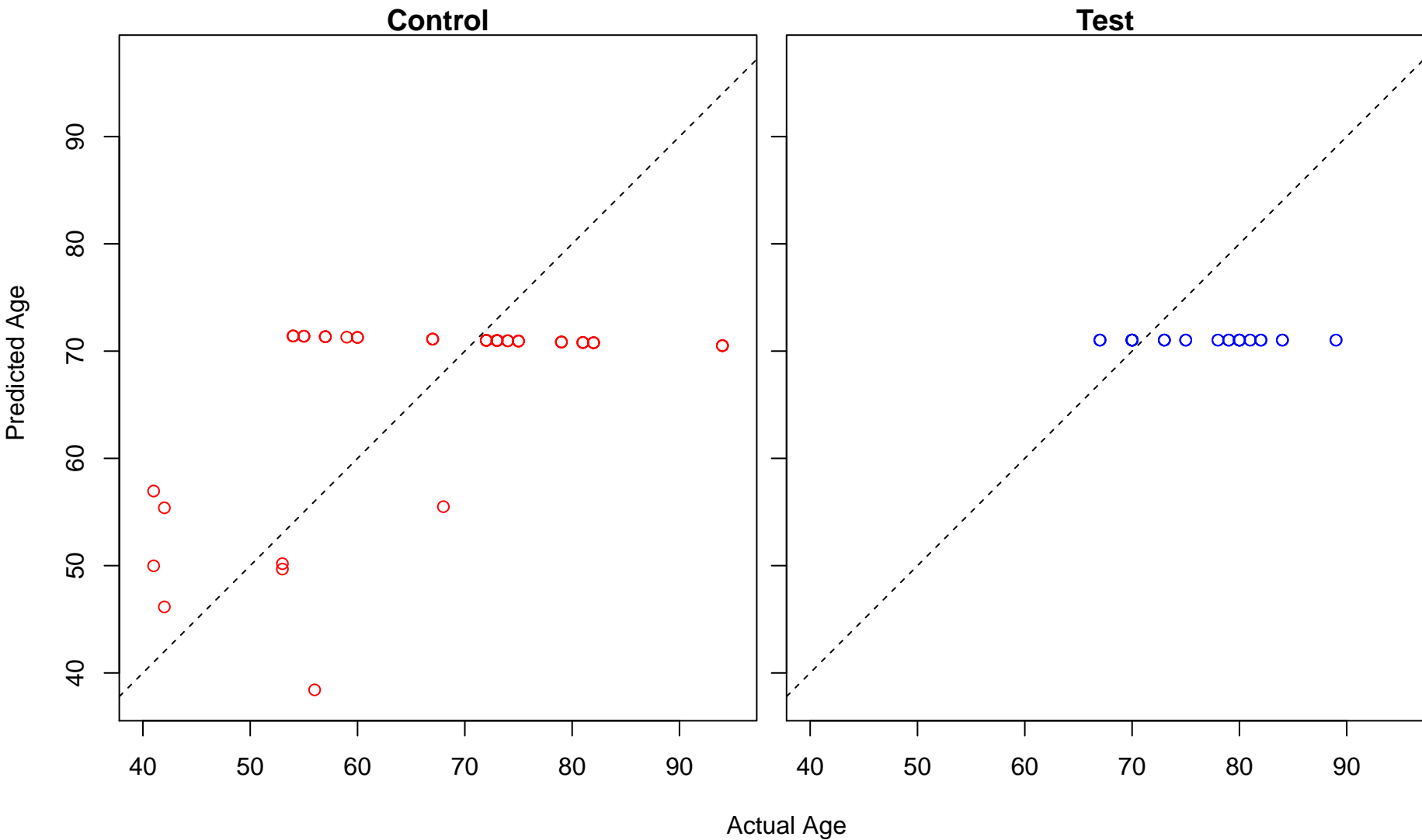
symbiosis, encompassing mutualism through parasitism (Score: 0.799041)



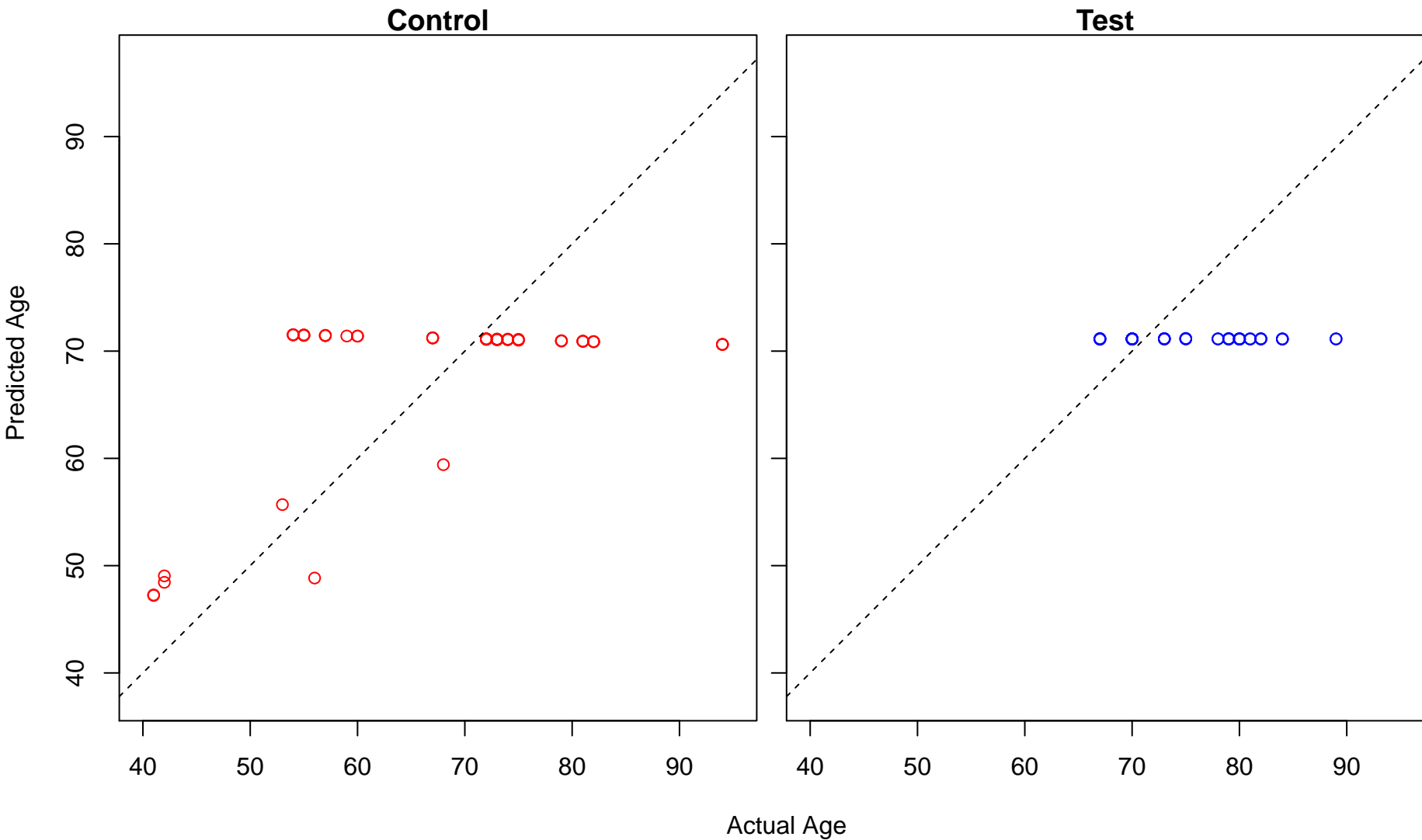
interspecies interaction between organisms (Score: 0.799041)



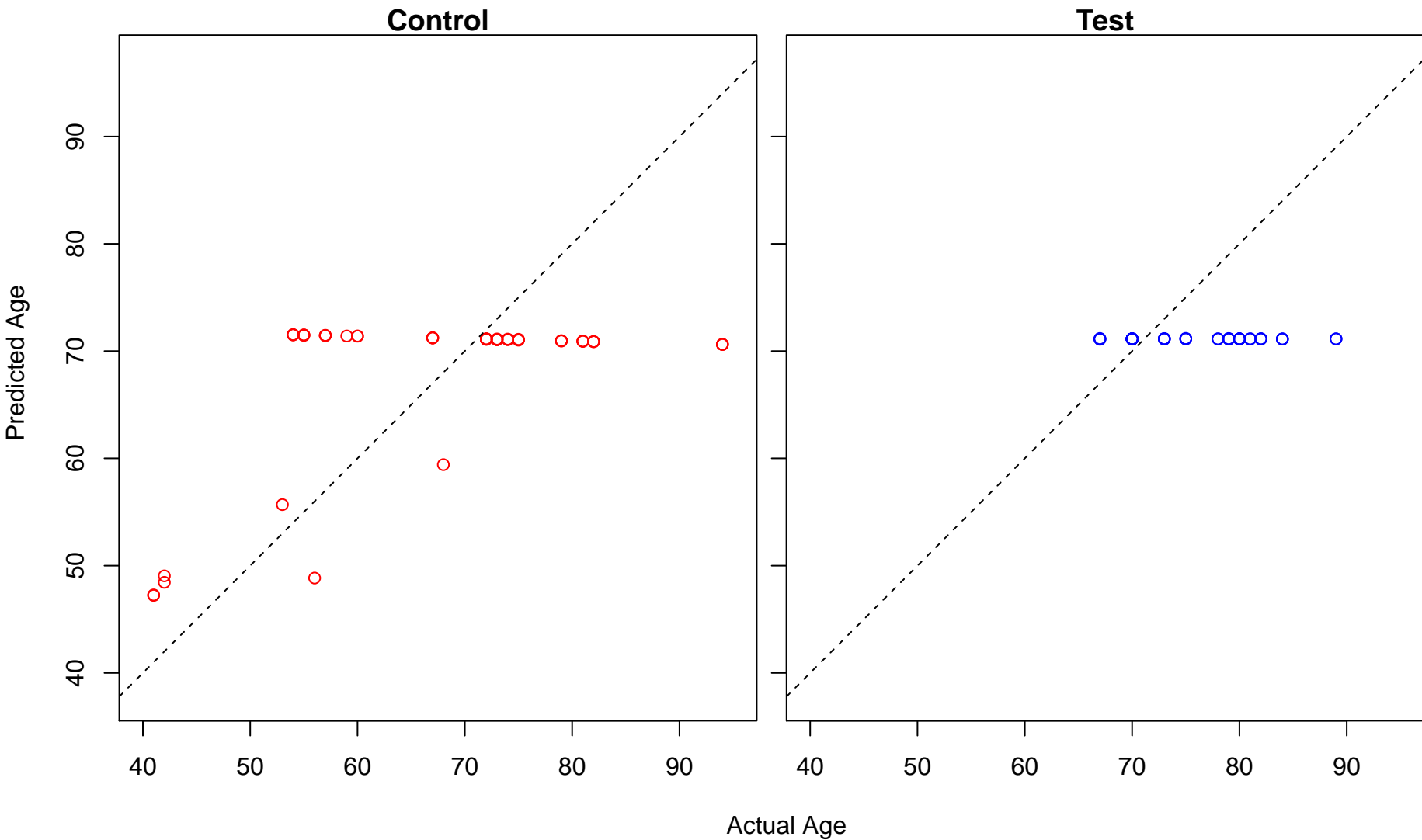
translational initiation (Score: 0.799037)



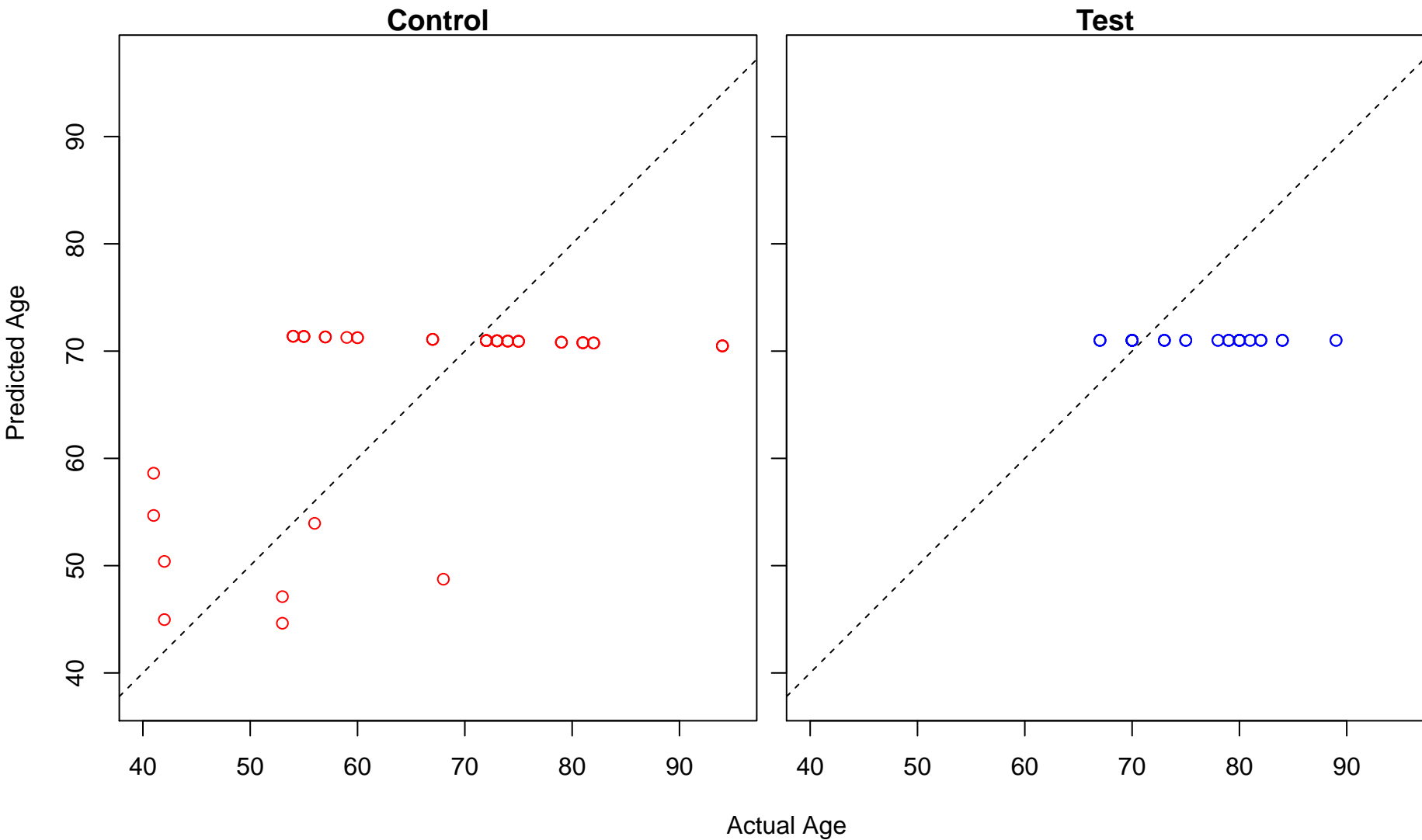
leukocyte chemotaxis (Score: 0.799024)



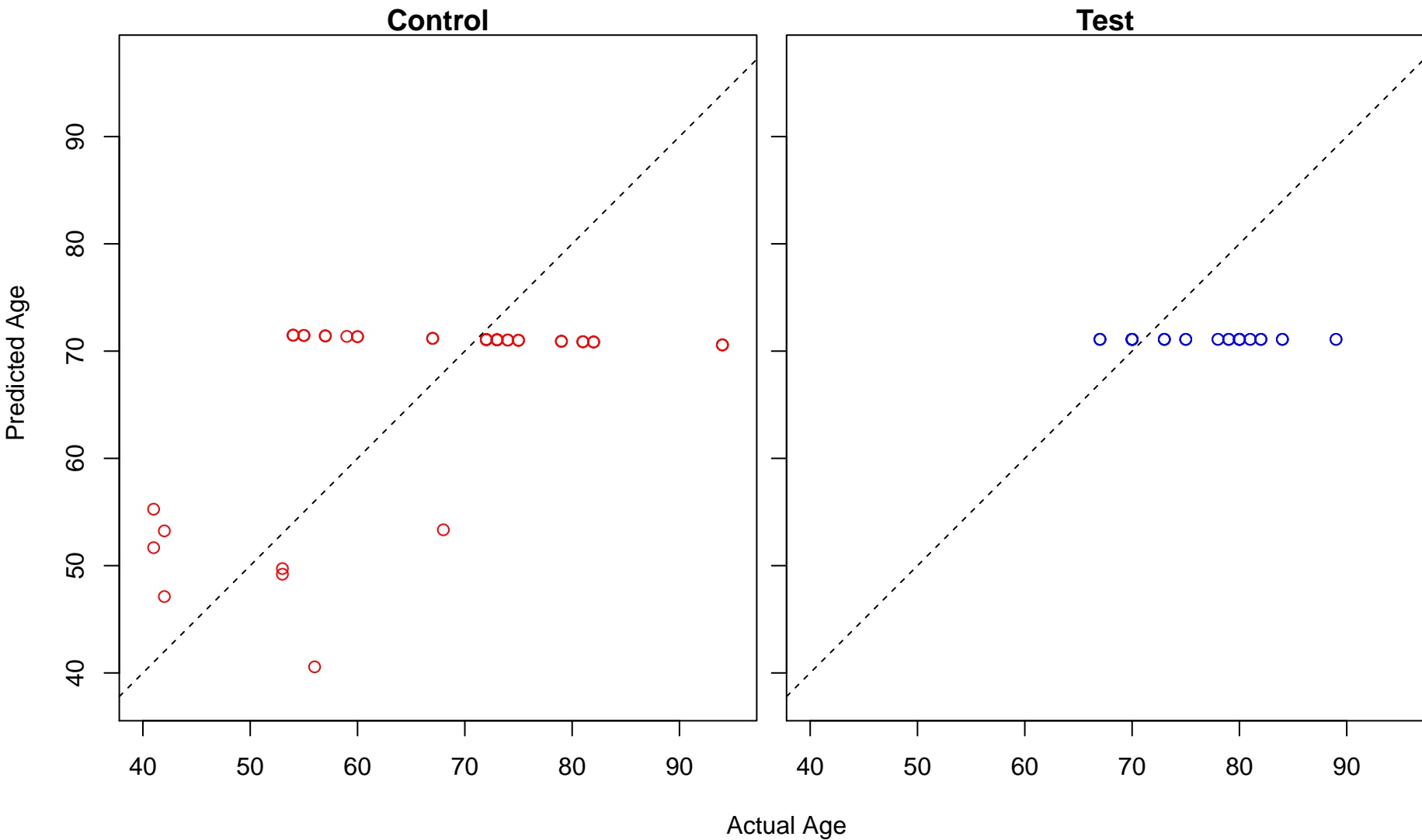
cell chemotaxis (Score: 0.799024)



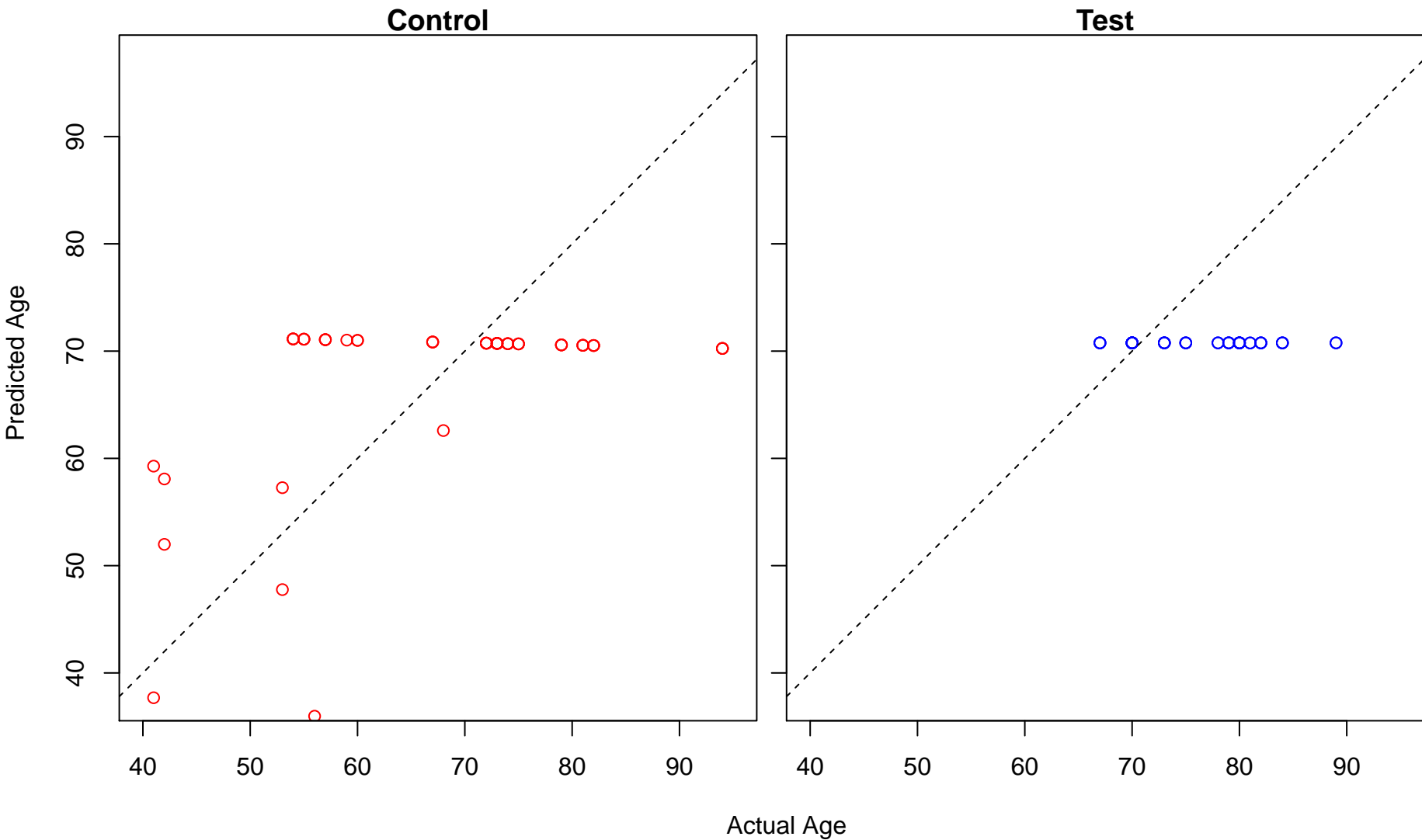
peptidyl-lysine modification (Score: 0.799019)



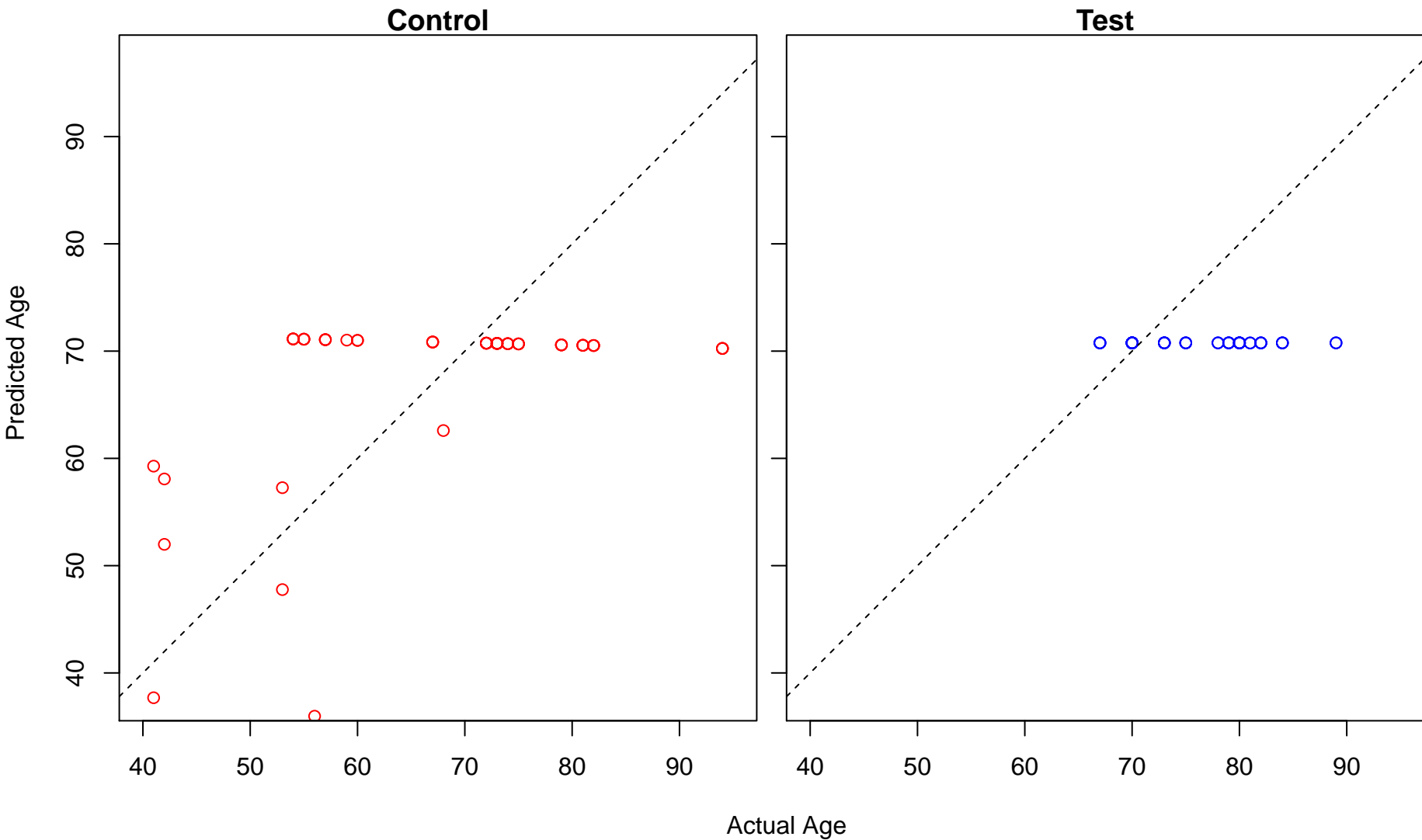
primary metabolic process (Score: 0.799009)



neuron recognition (Score: 0.799005)

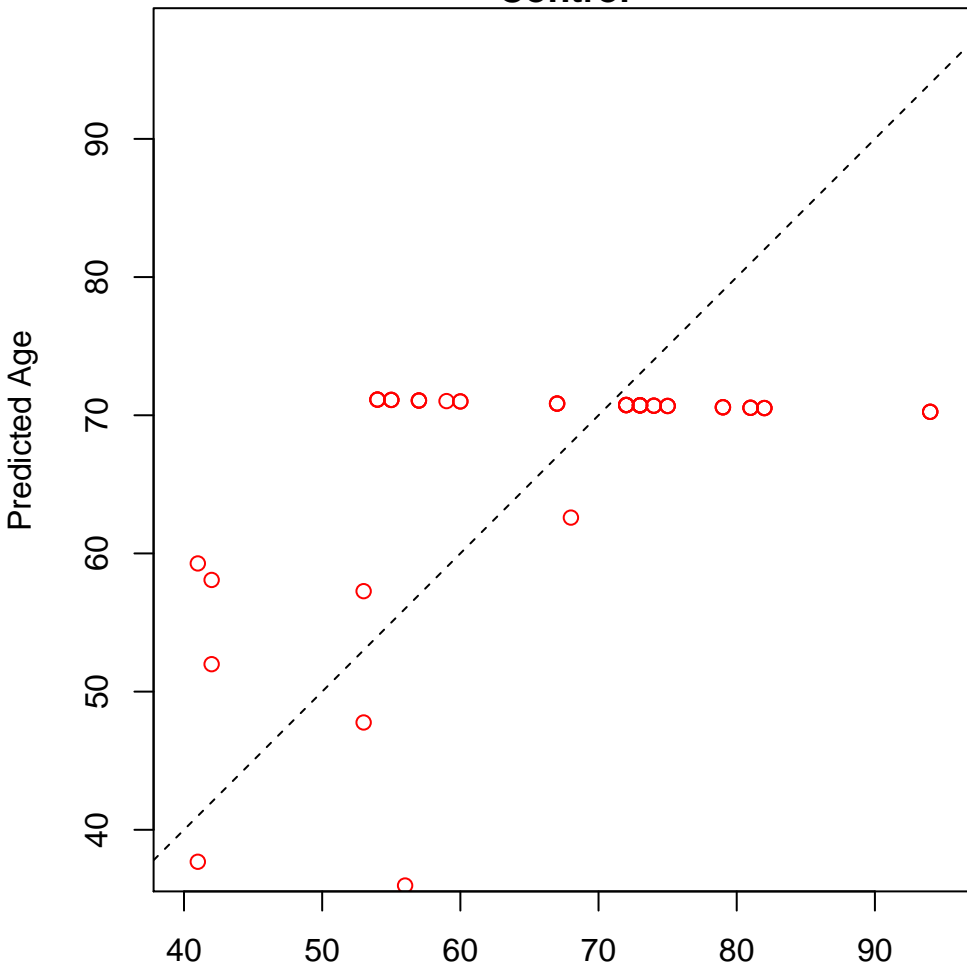


dendrite development (Score: 0.799005)

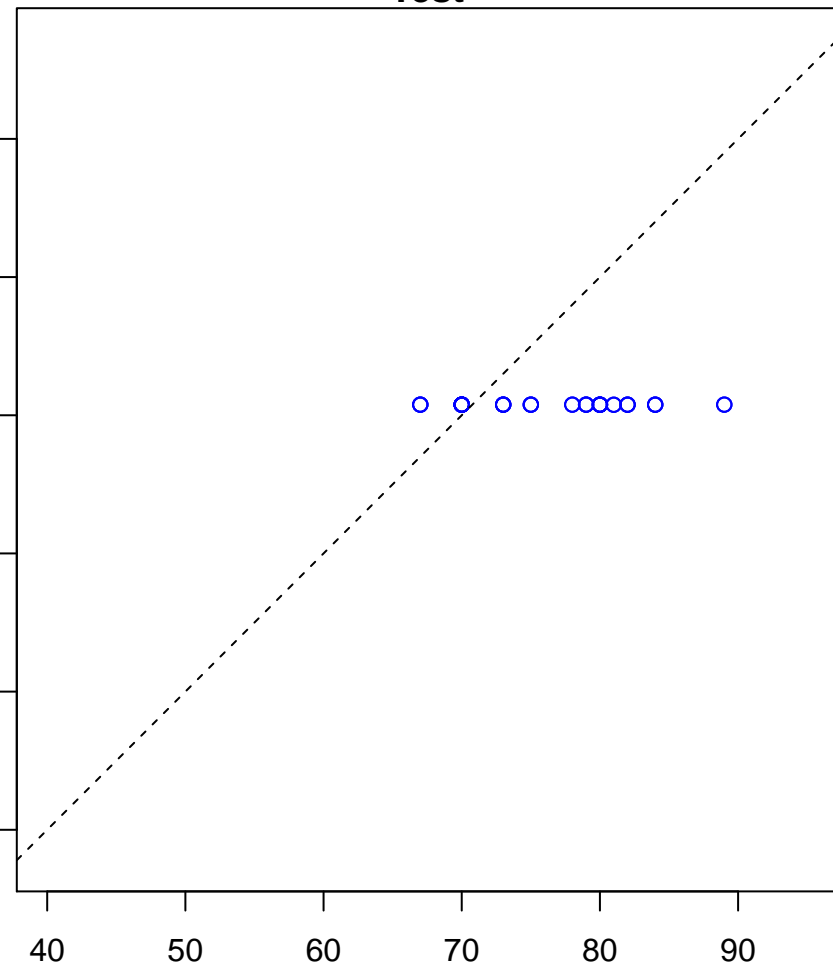


regulation of synapse structure or activity (Score: 0.799005)

Control

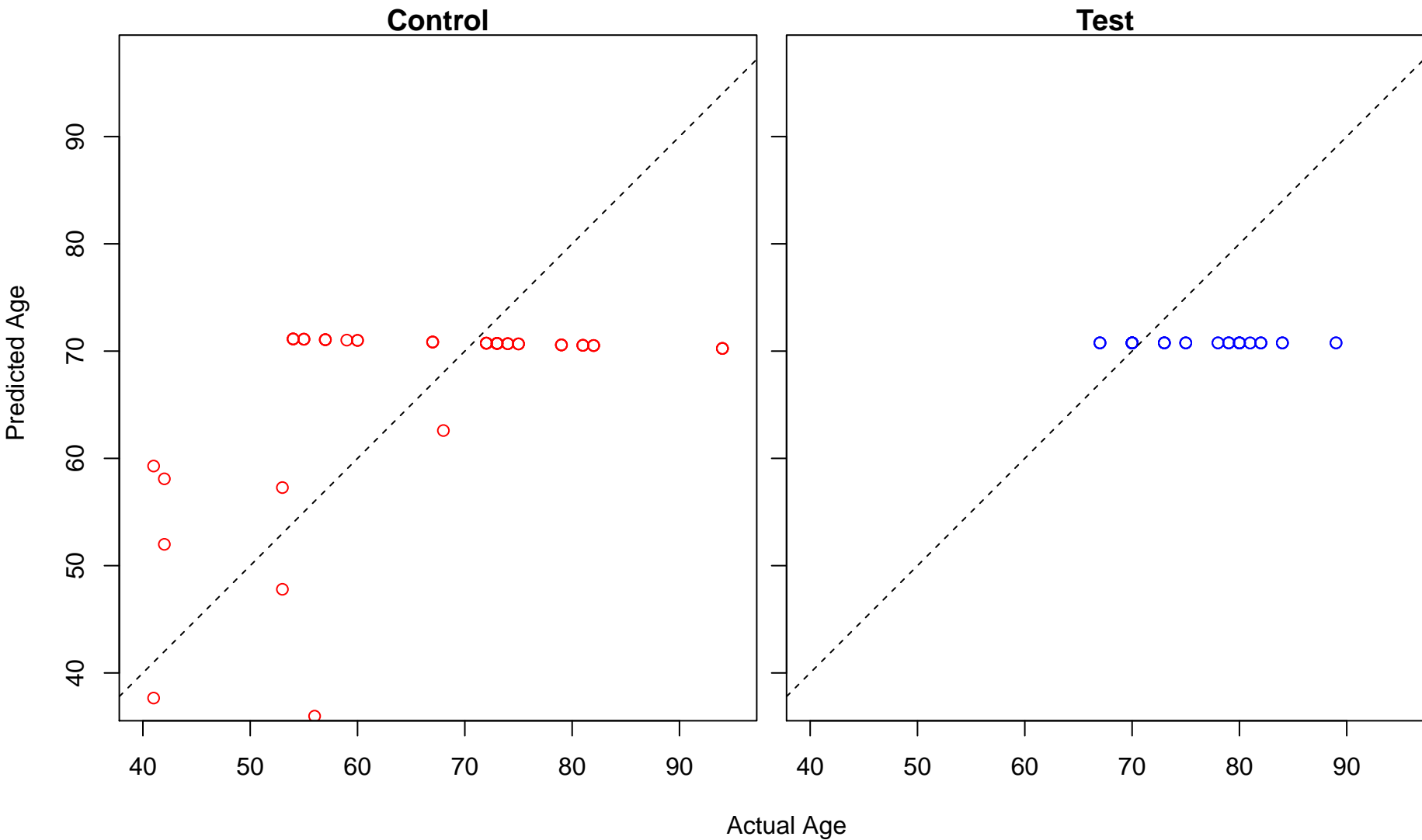


Test

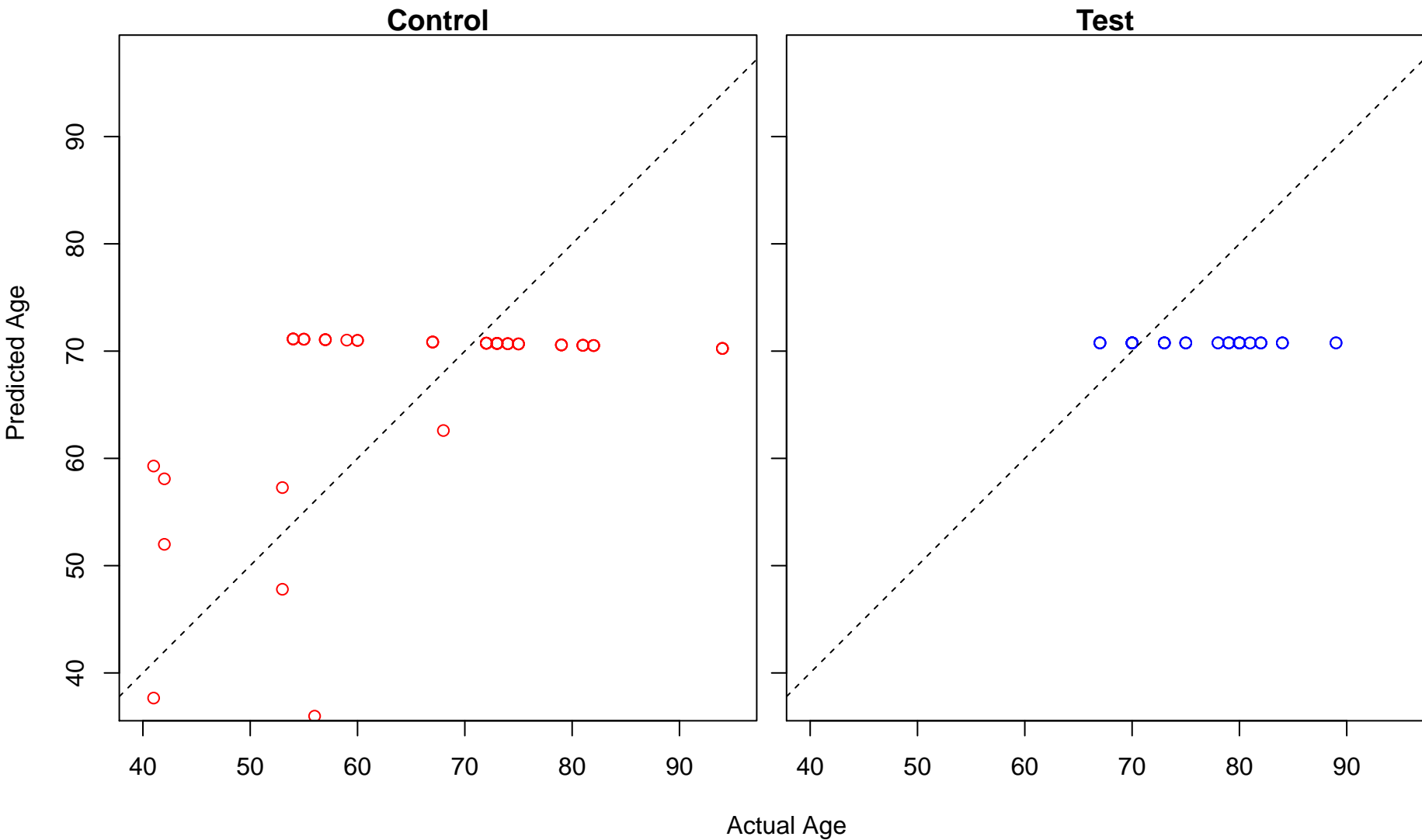


Actual Age

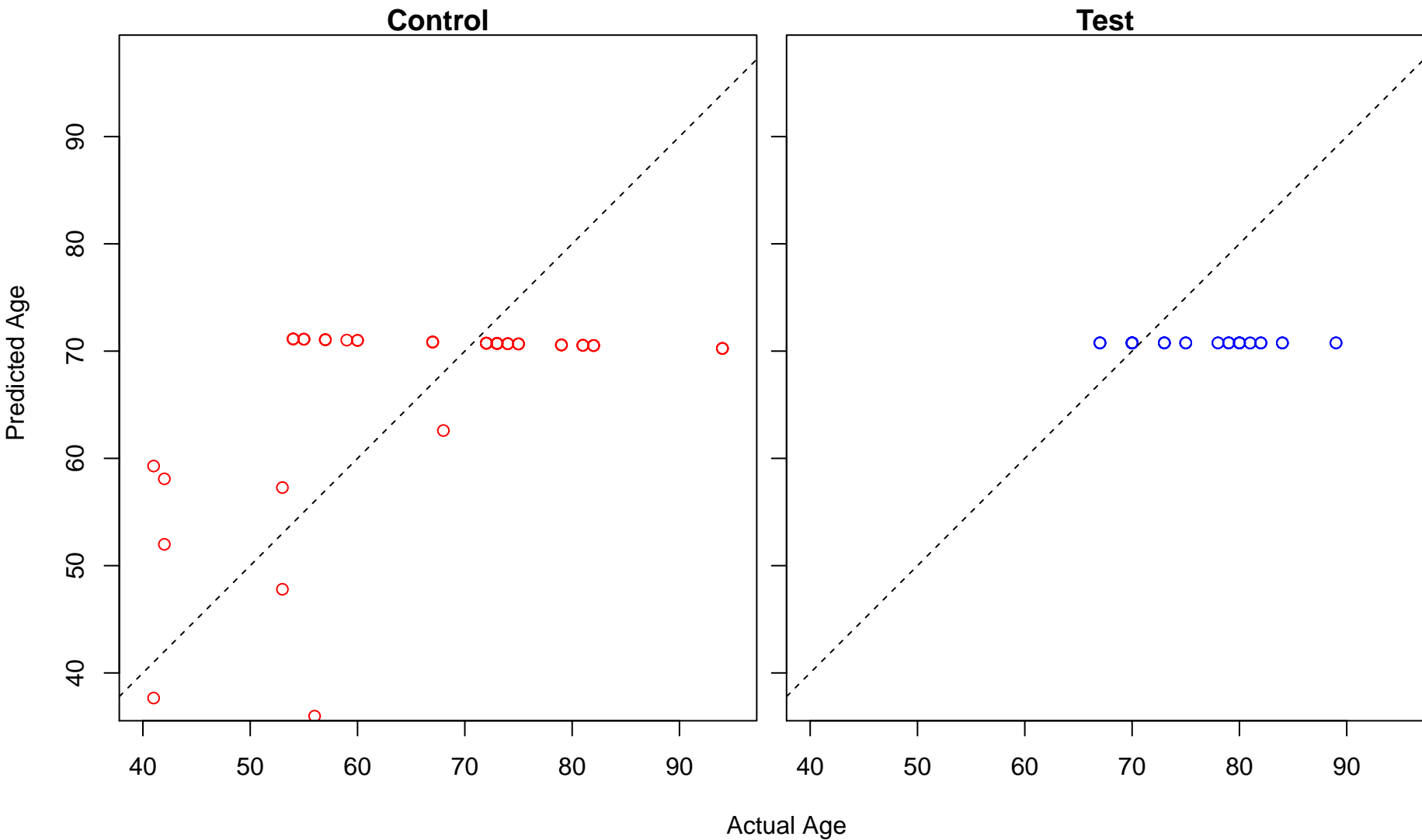
astrocyte activation involved in immune response (Score: 0.799004)



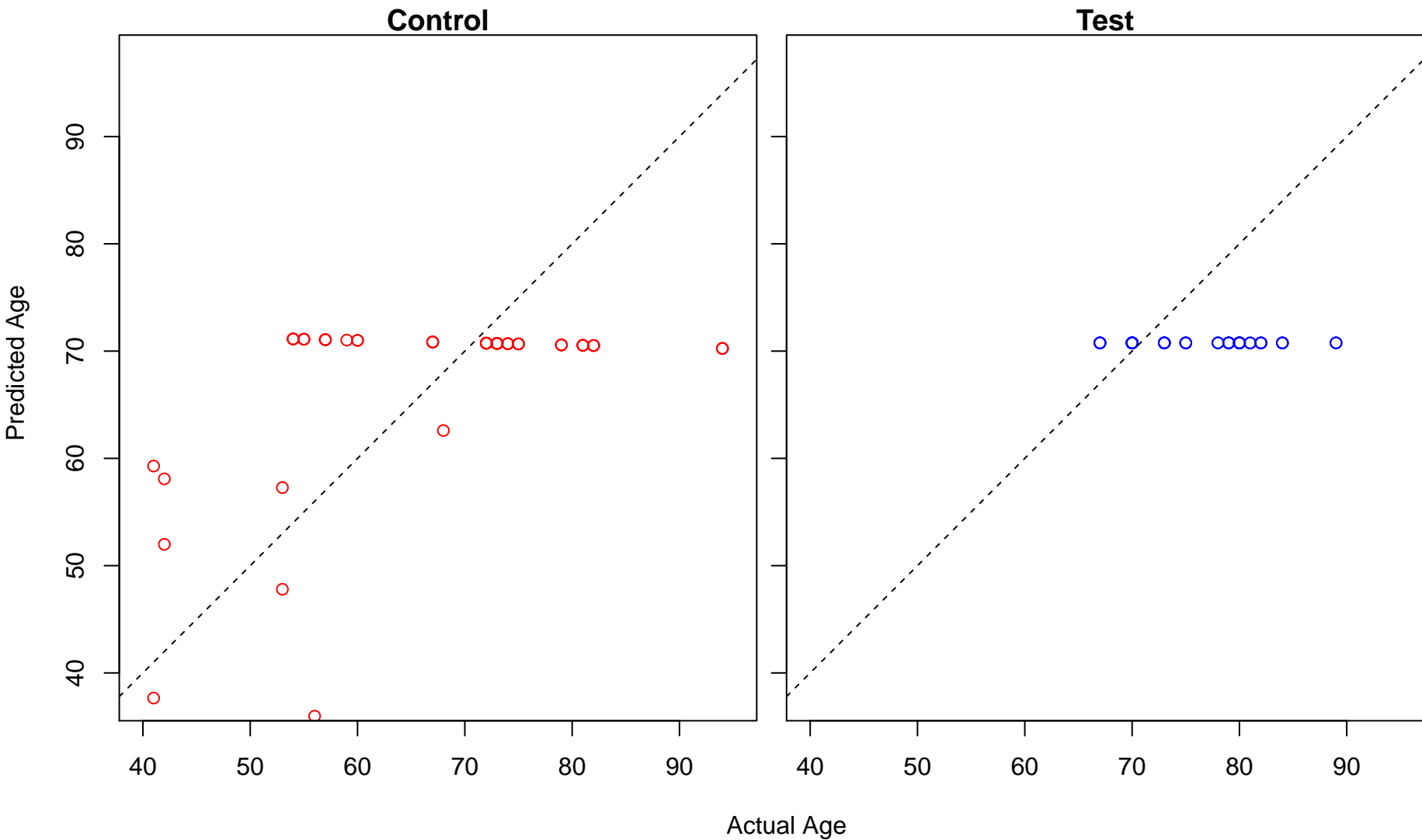
astrocyte development (Score: 0.799004)



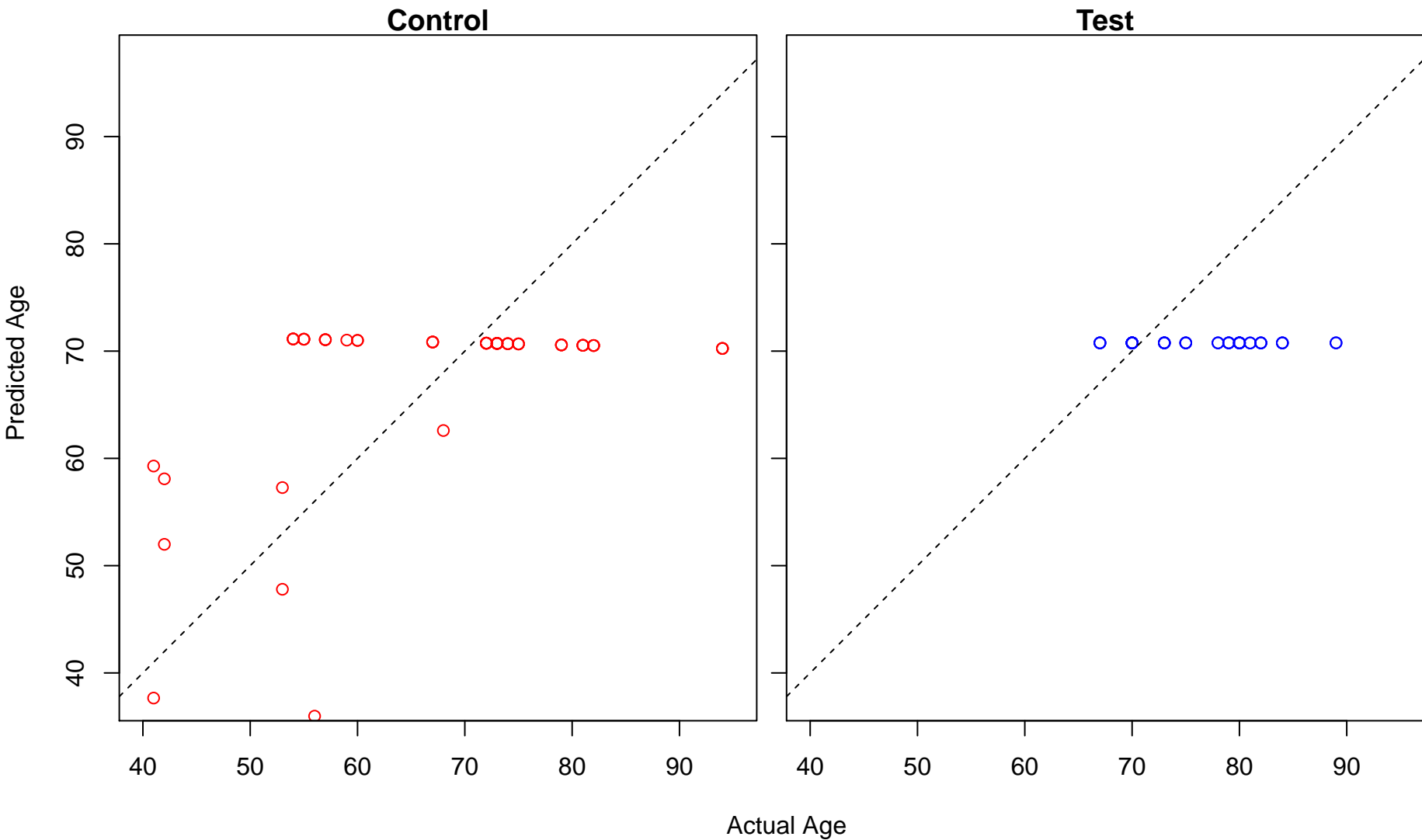
astrocyte activation (Score: 0.799004)



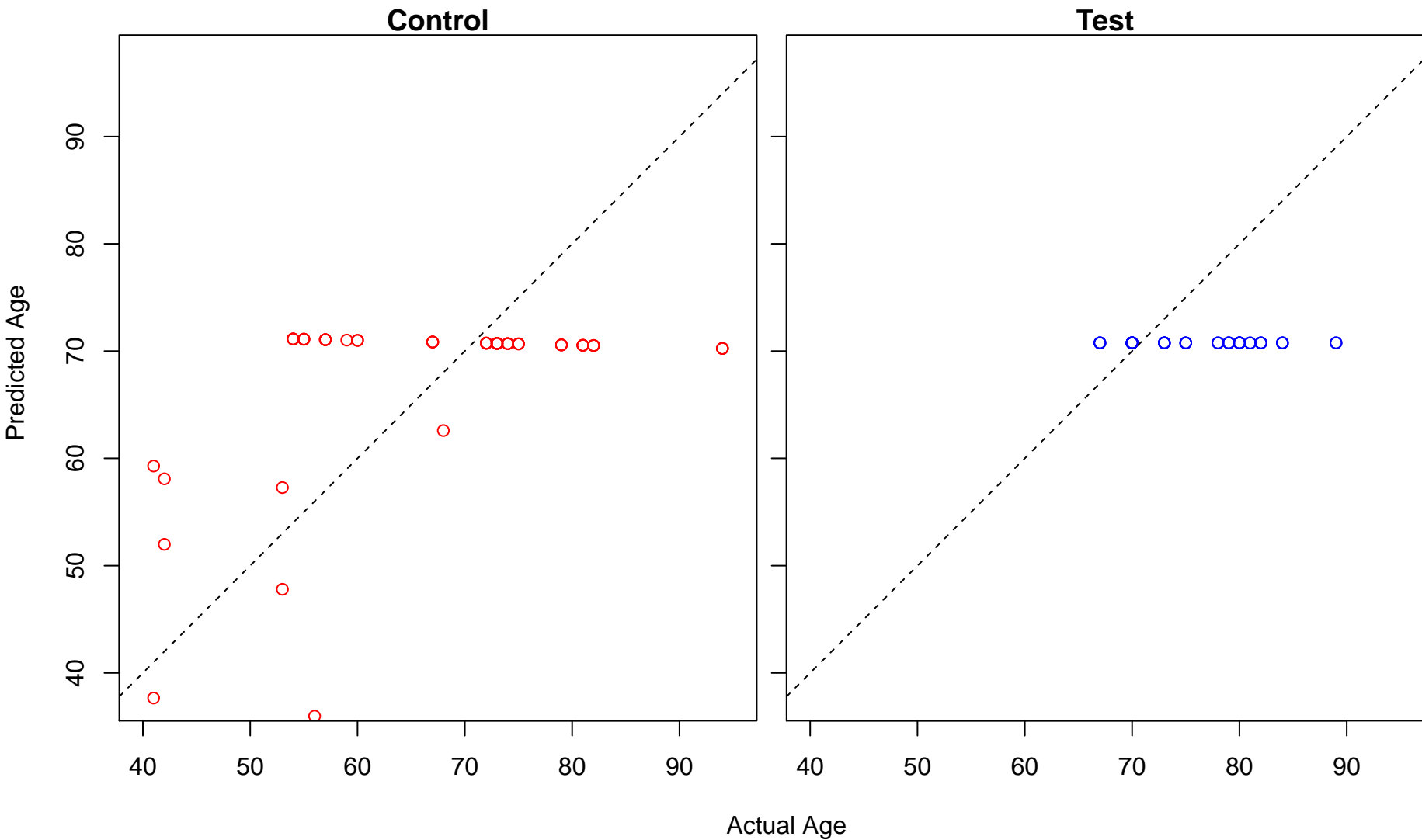
astrocyte differentiation (Score: 0.799004)



glial cell activation (Score: 0.799004)

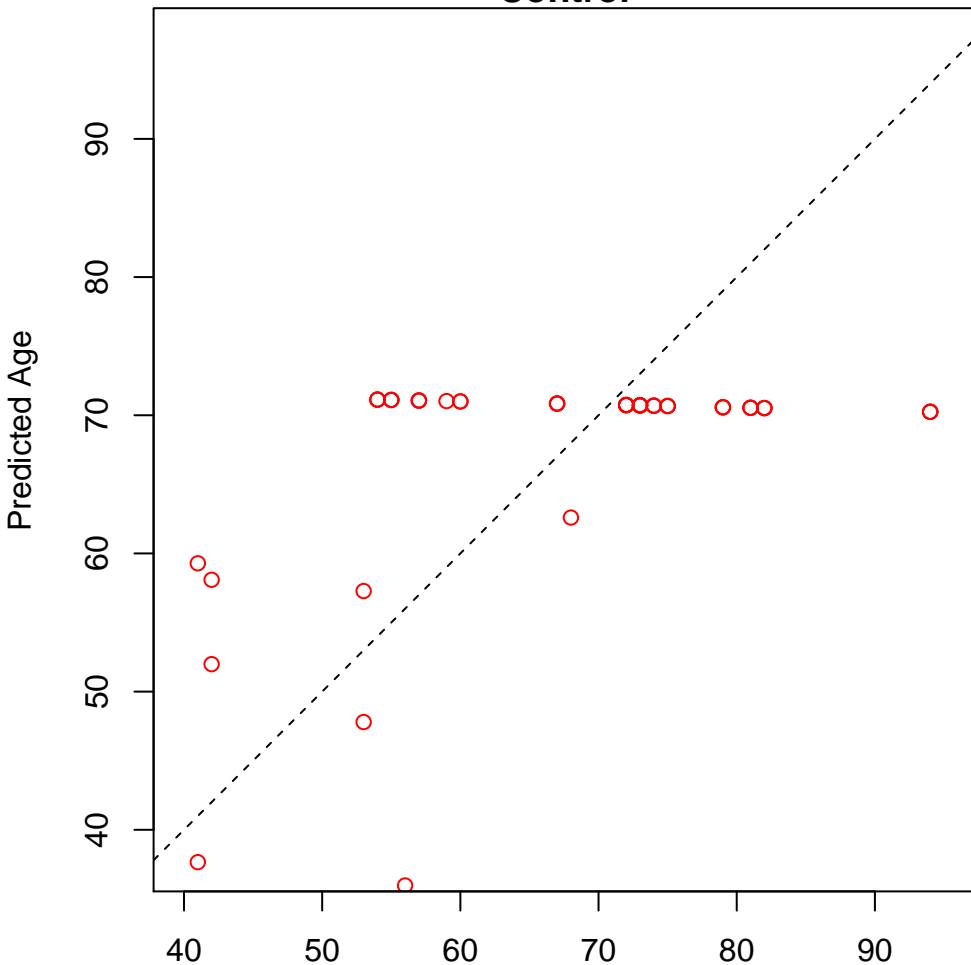


response to amyloid-beta (Score: 0.799004)

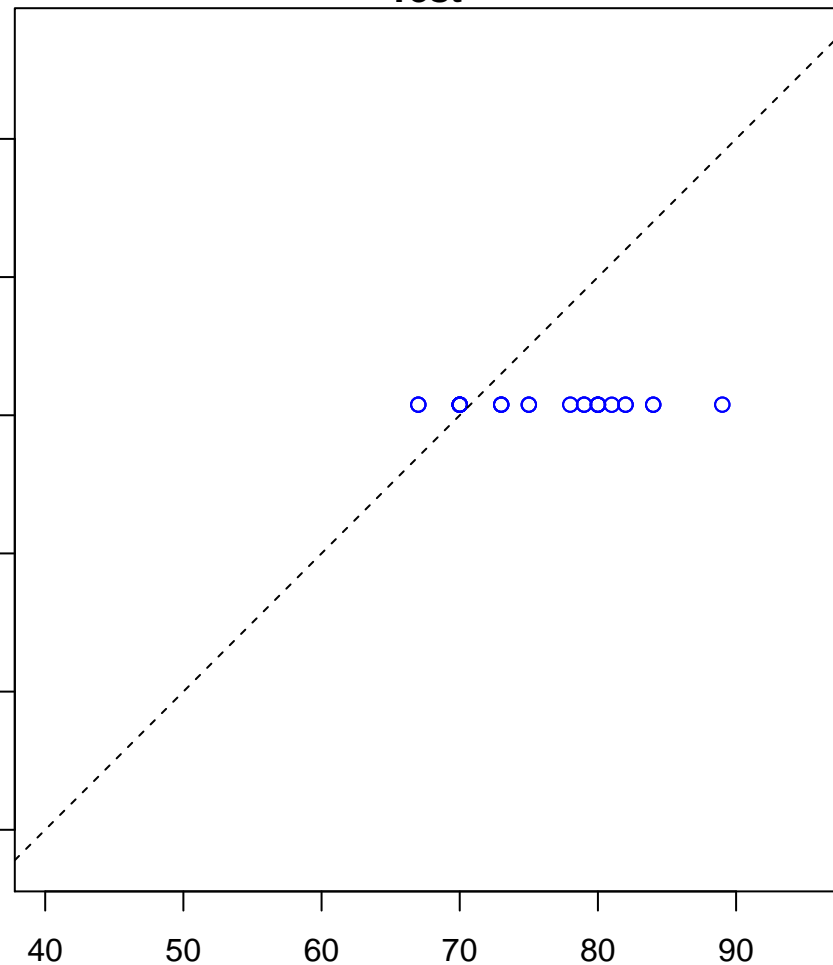


cellular response to amyloid-beta (Score: 0.799004)

Control



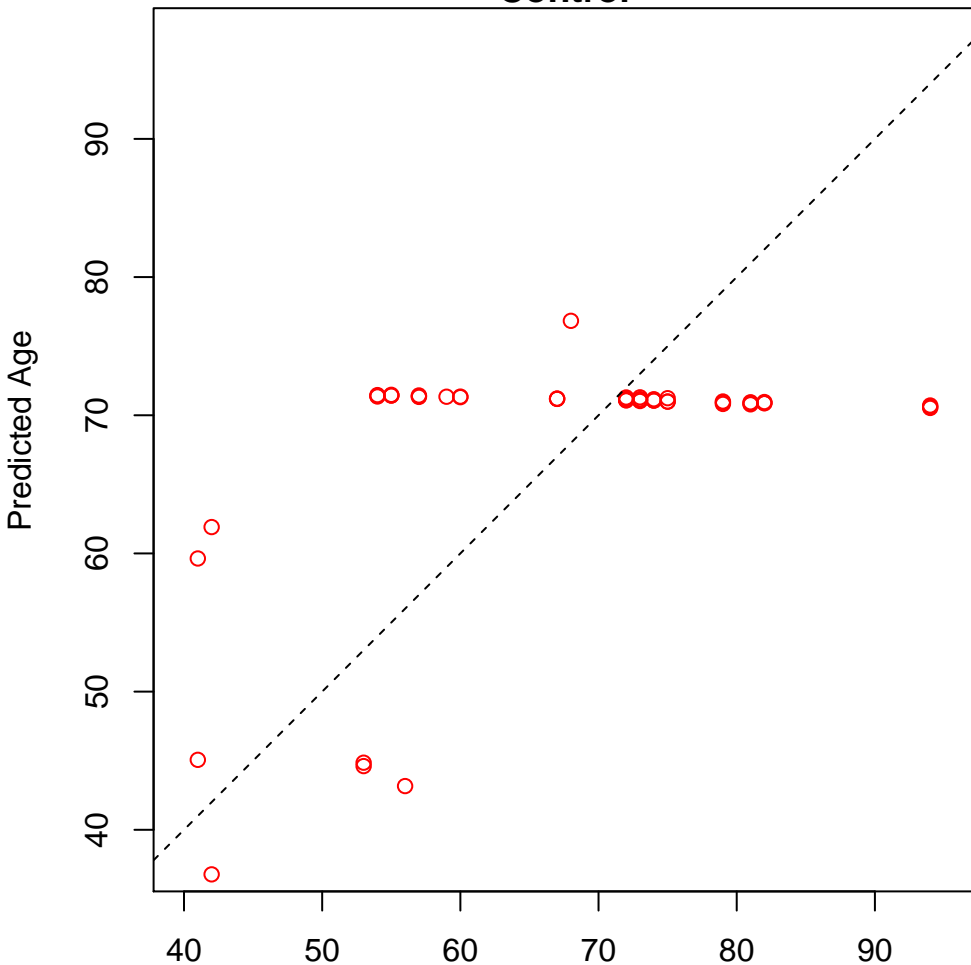
Test



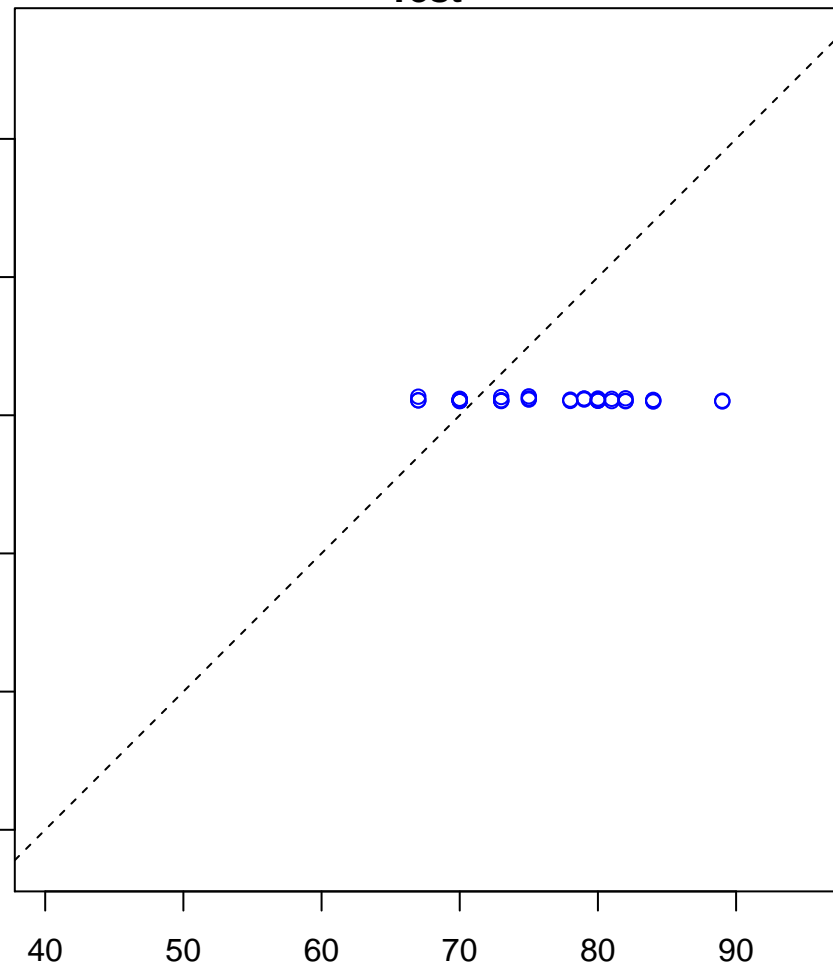
Actual Age

cell part morphogenesis (Score: 0.799000)

Control



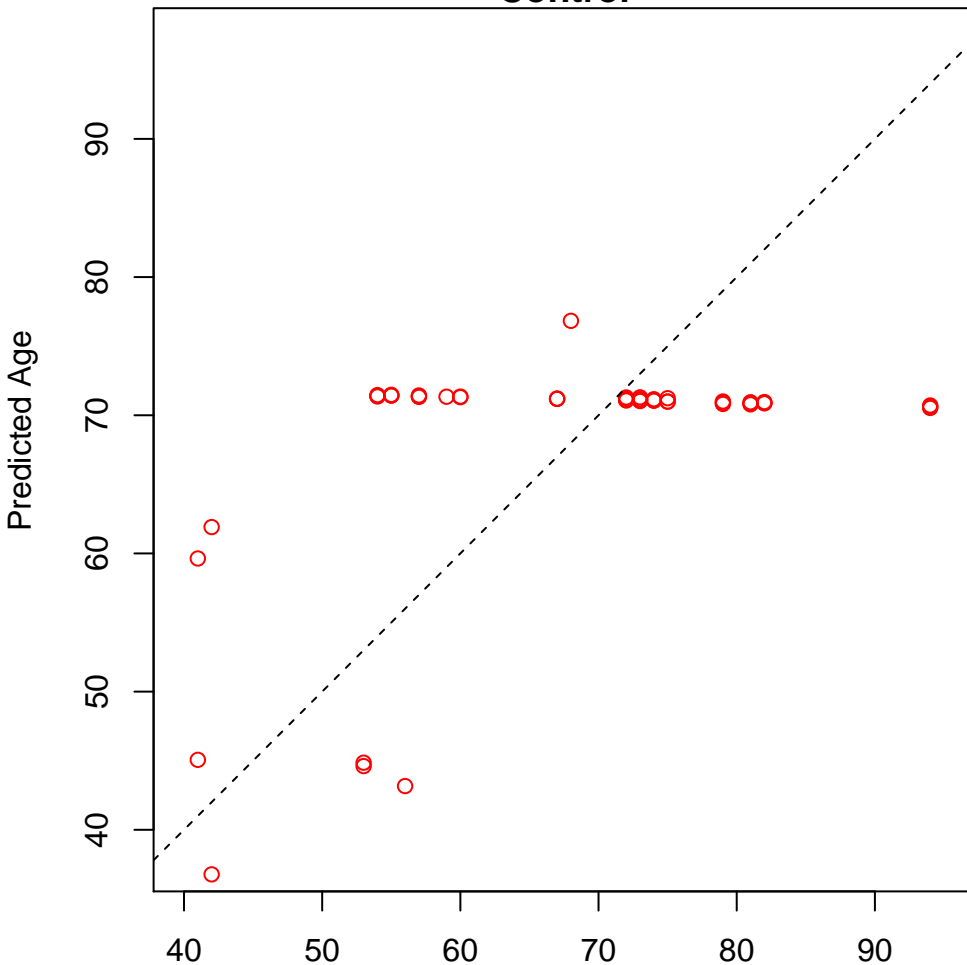
Test



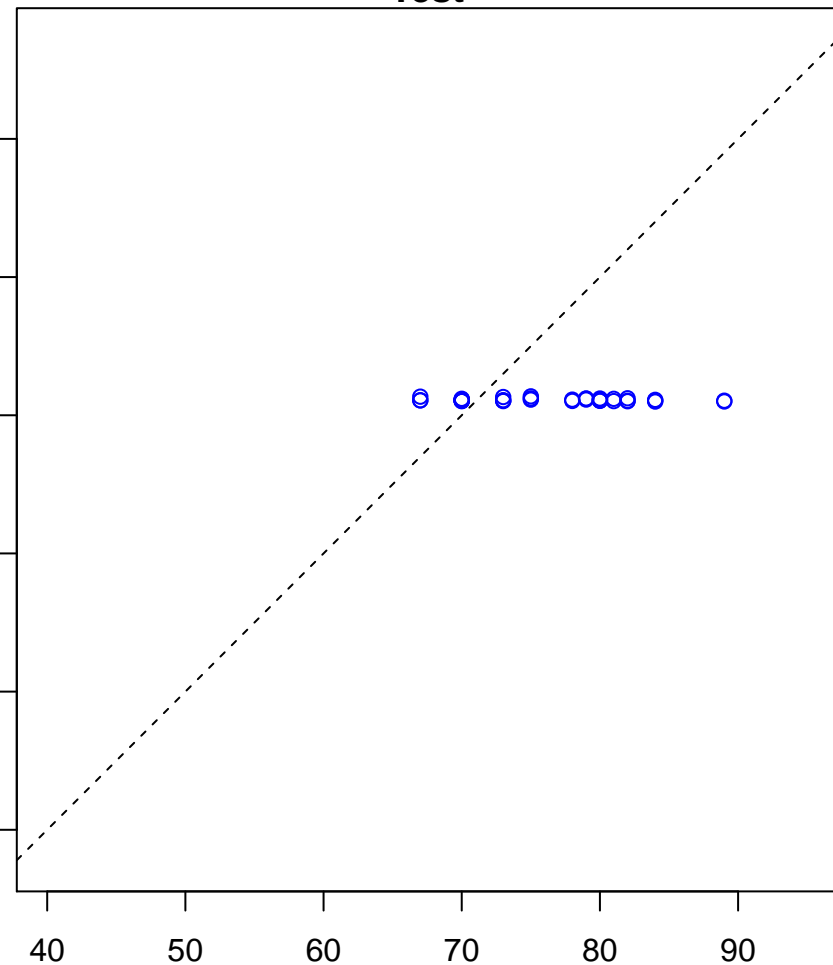
Actual Age

neuron projection morphogenesis (Score: 0.799000)

Control



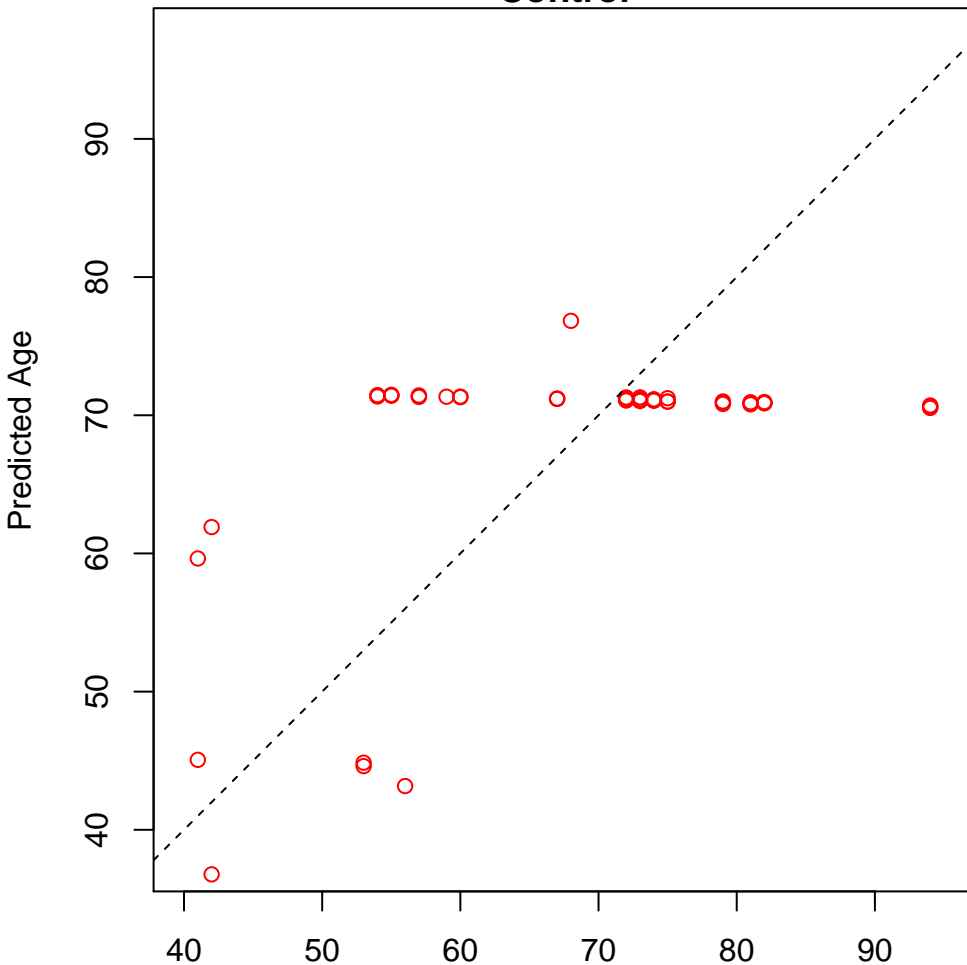
Test



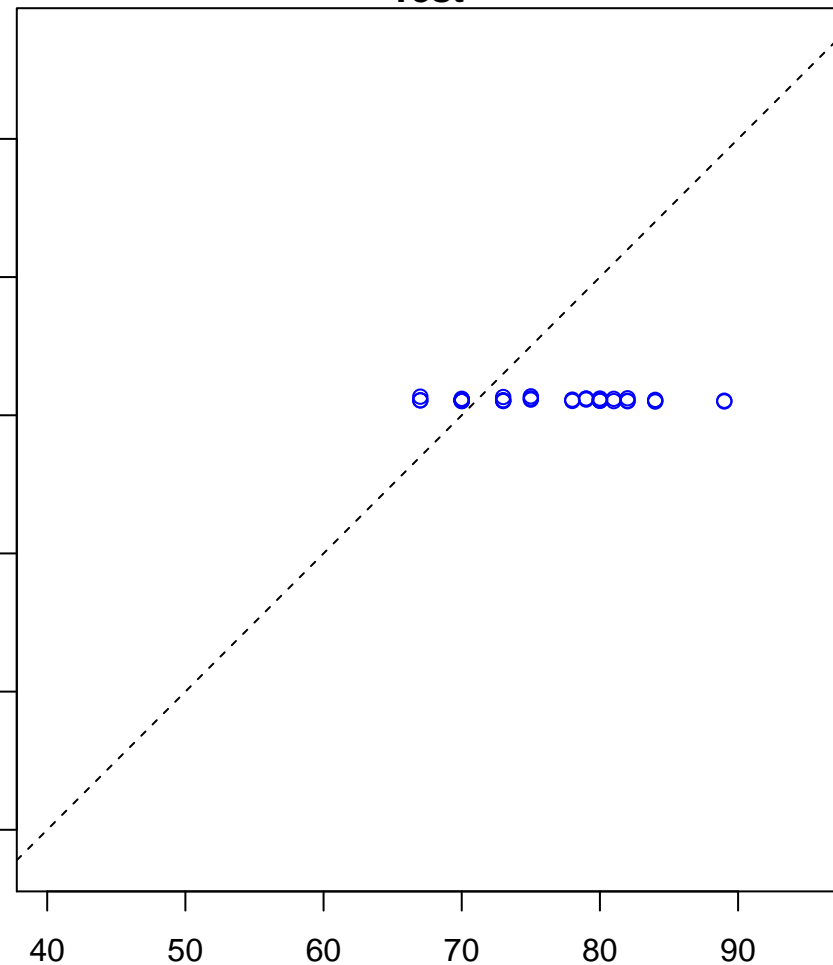
Actual Age

cell projection morphogenesis (Score: 0.799000)

Control

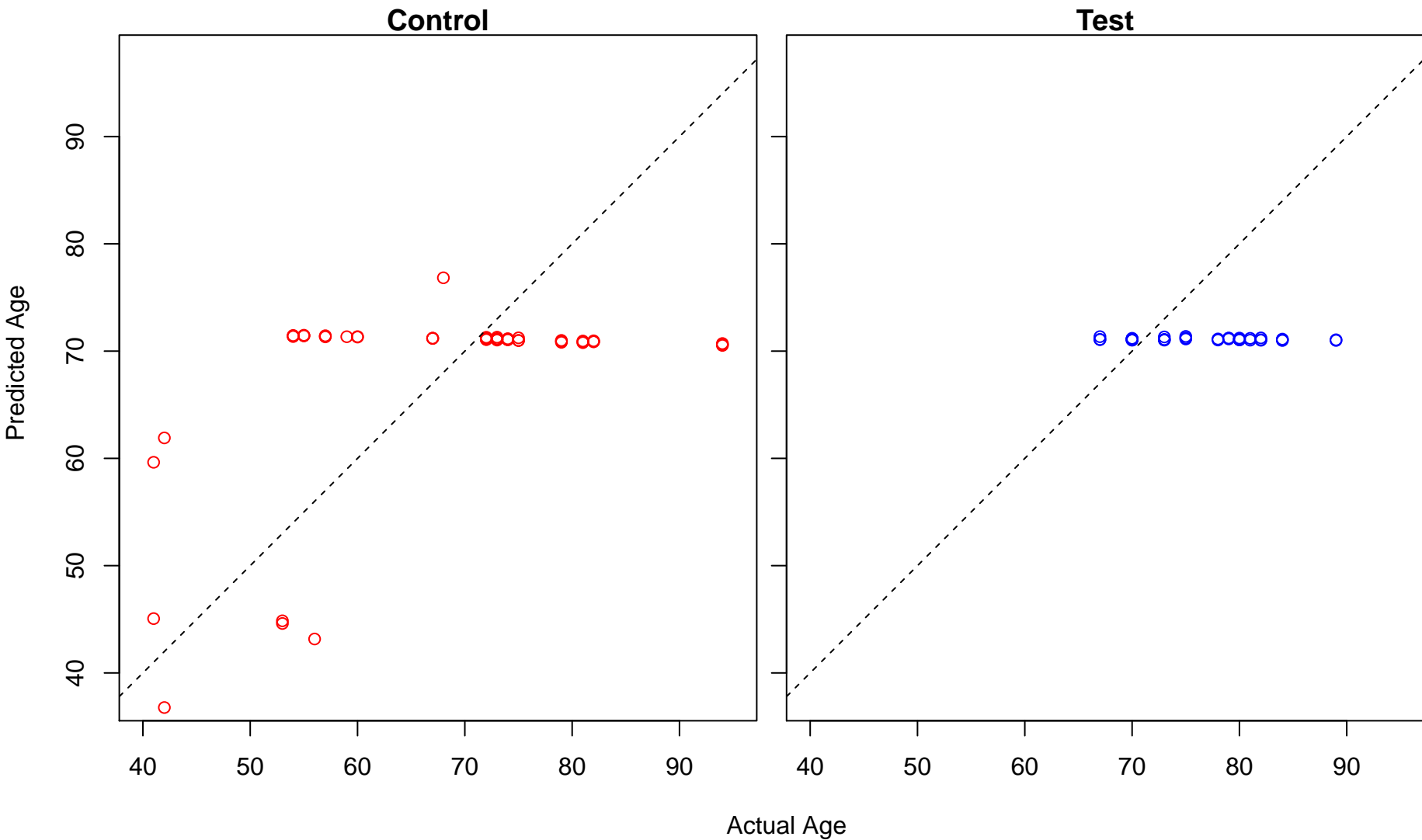


Test



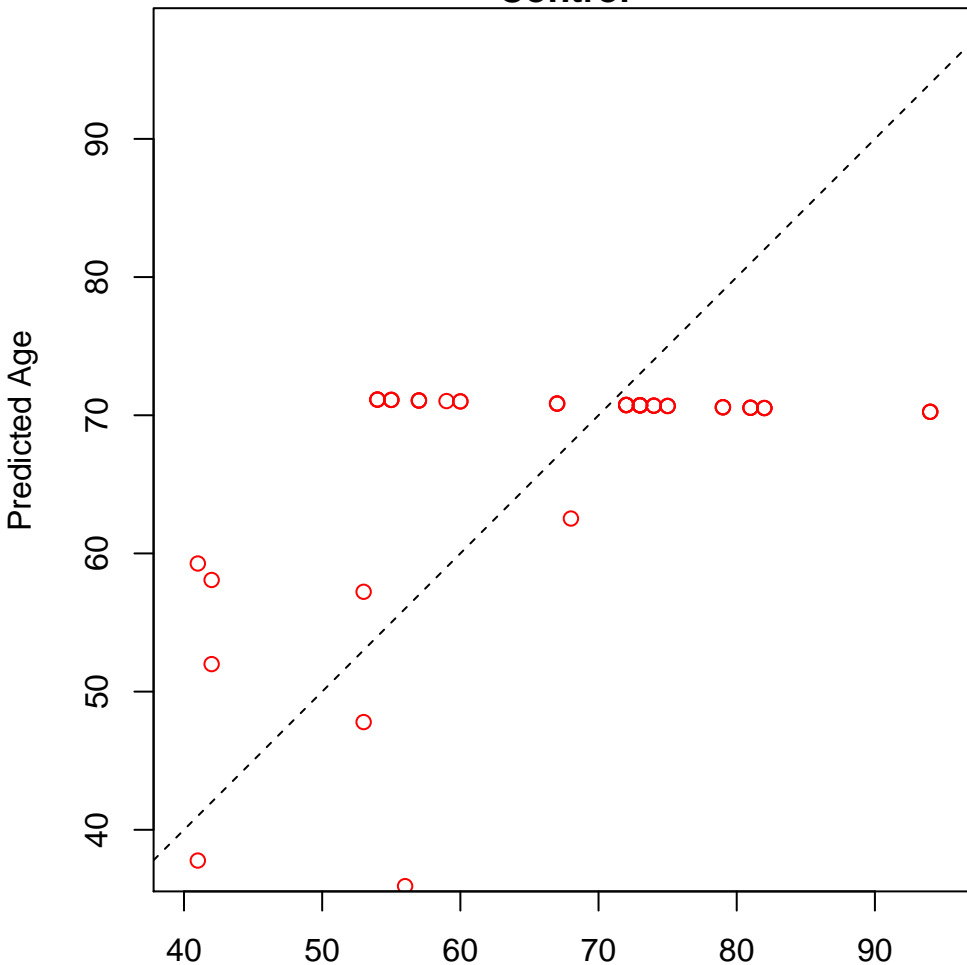
Actual Age

plasma membrane bounded cell projection morphogenesis (Score: 0.799000)

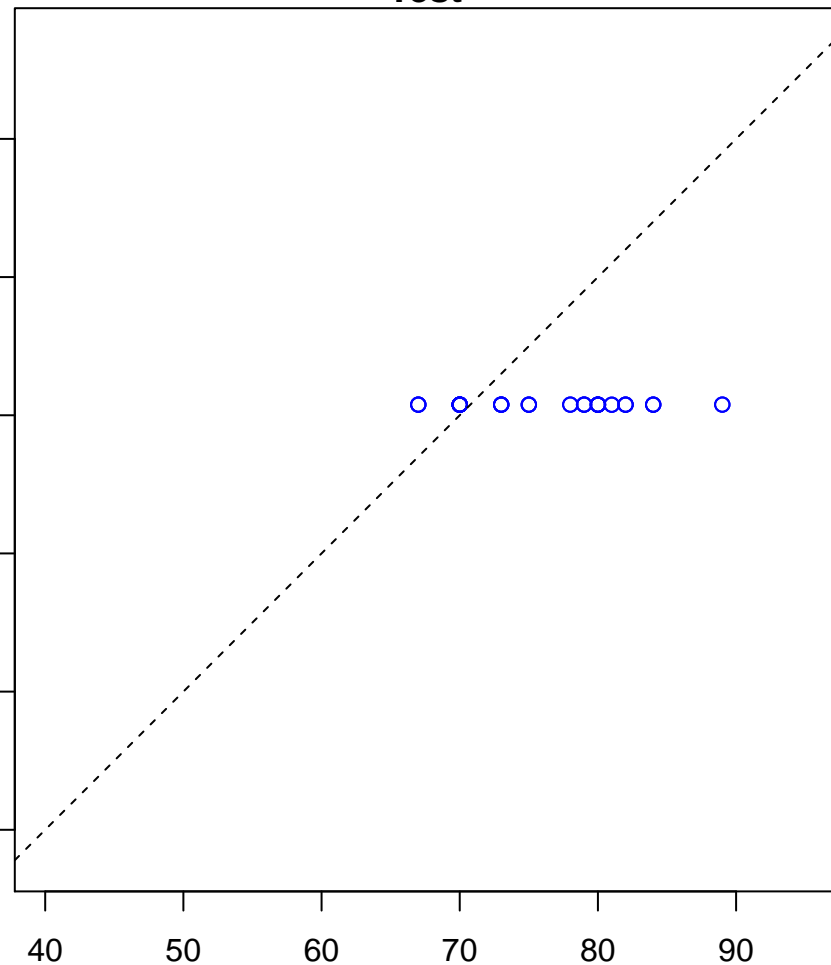


developmental cell growth (Score: 0.798991)

Control

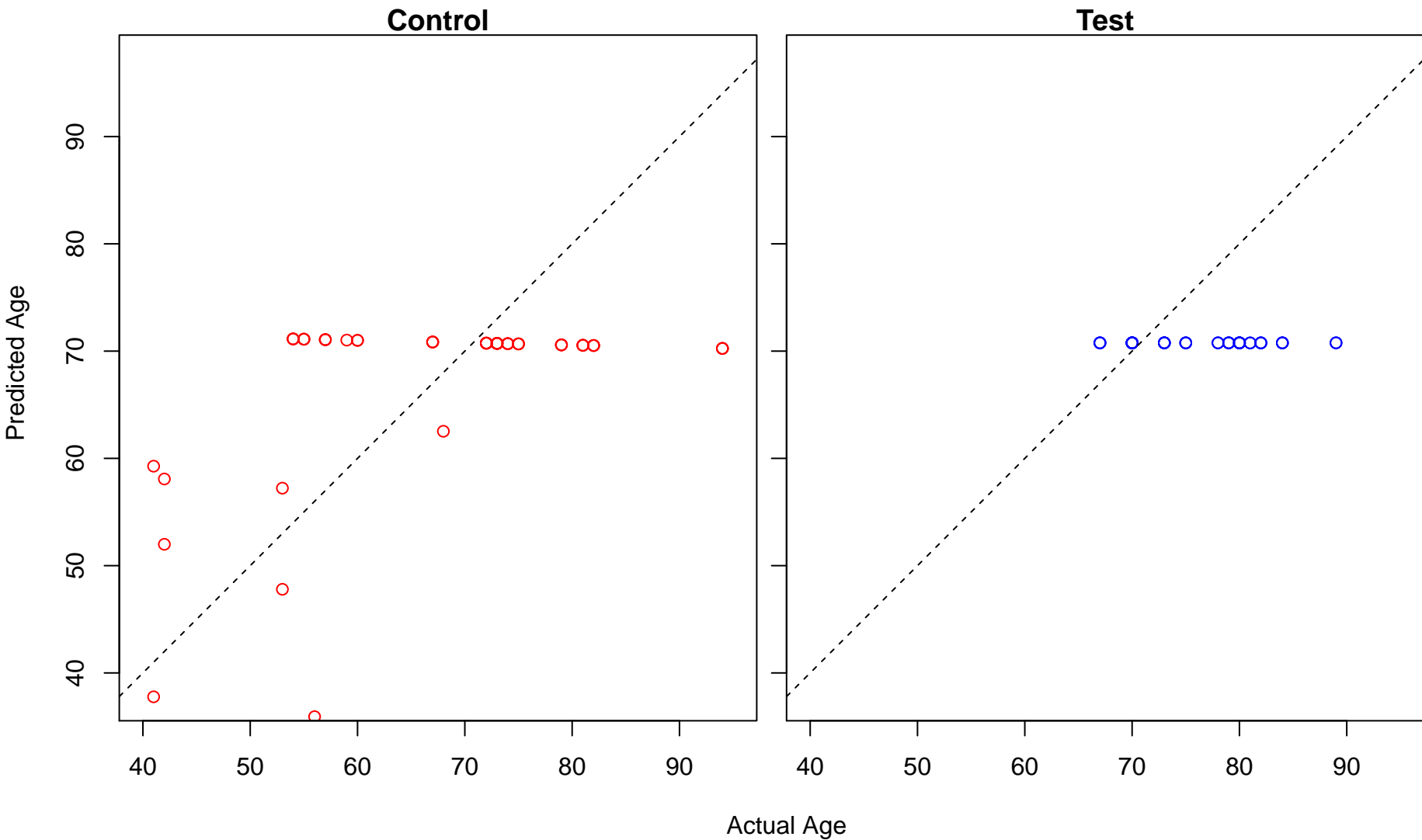


Test



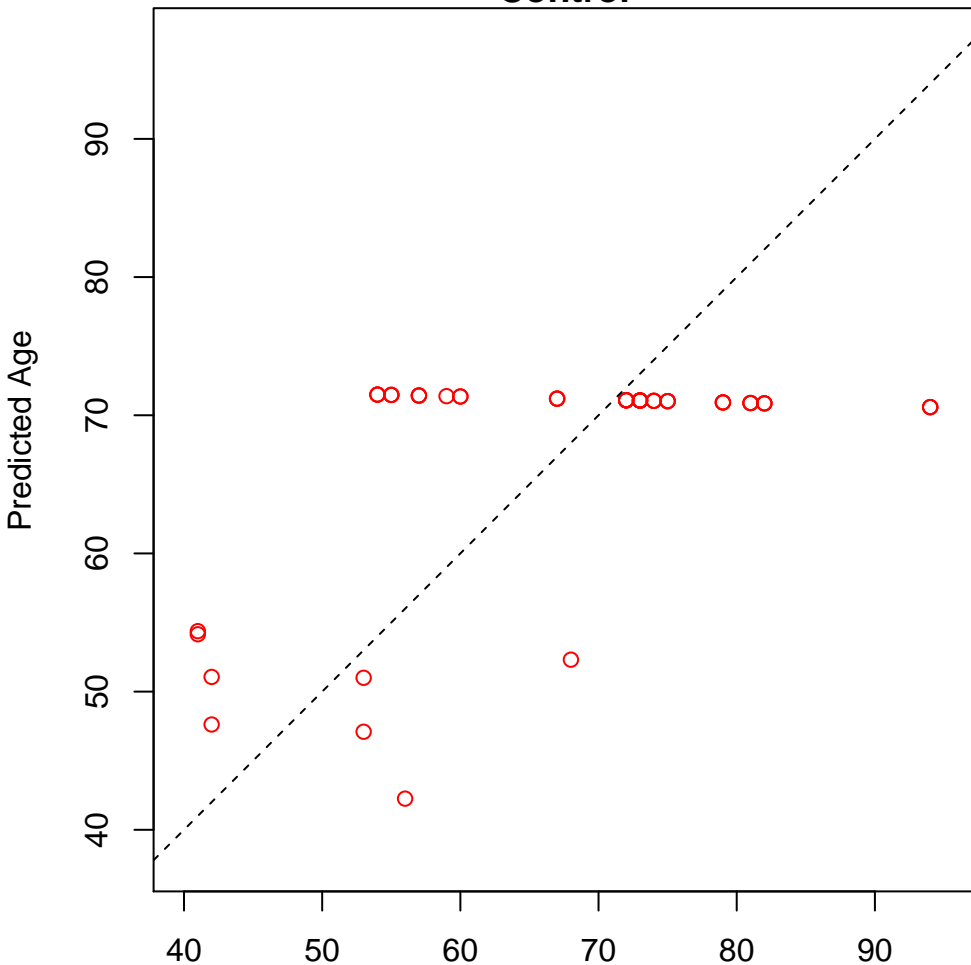
Actual Age

developmental growth involved in morphogenesis (Score: 0.798991)

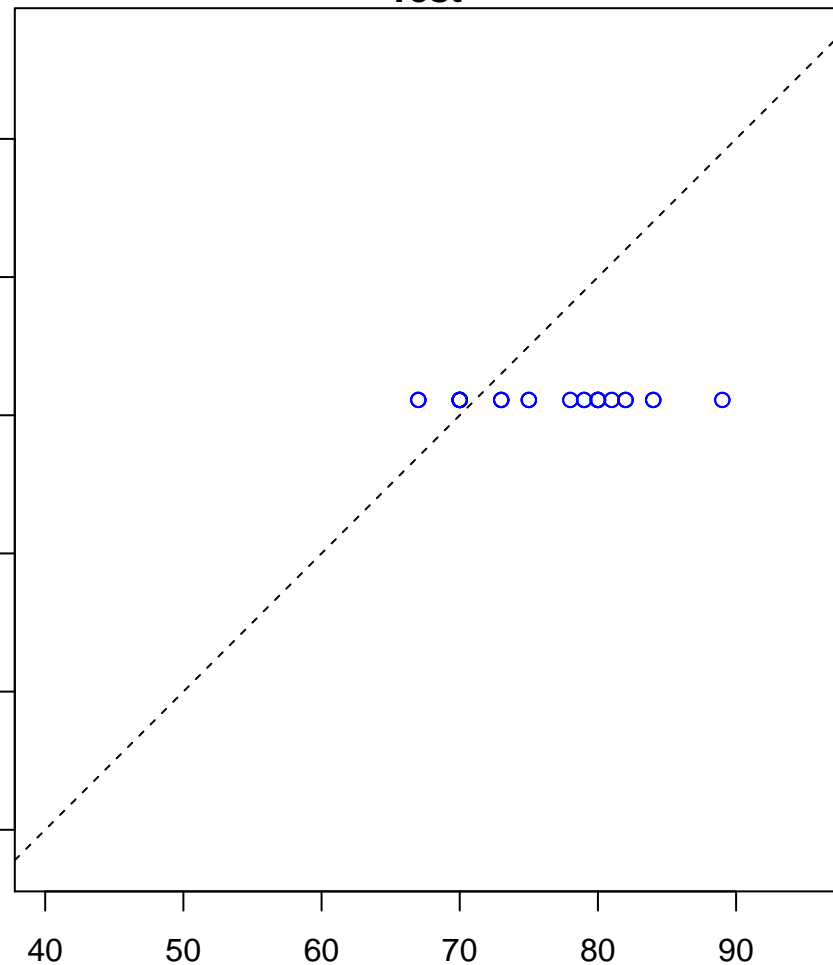


positive regulation of gene expression (Score: 0.798958)

Control



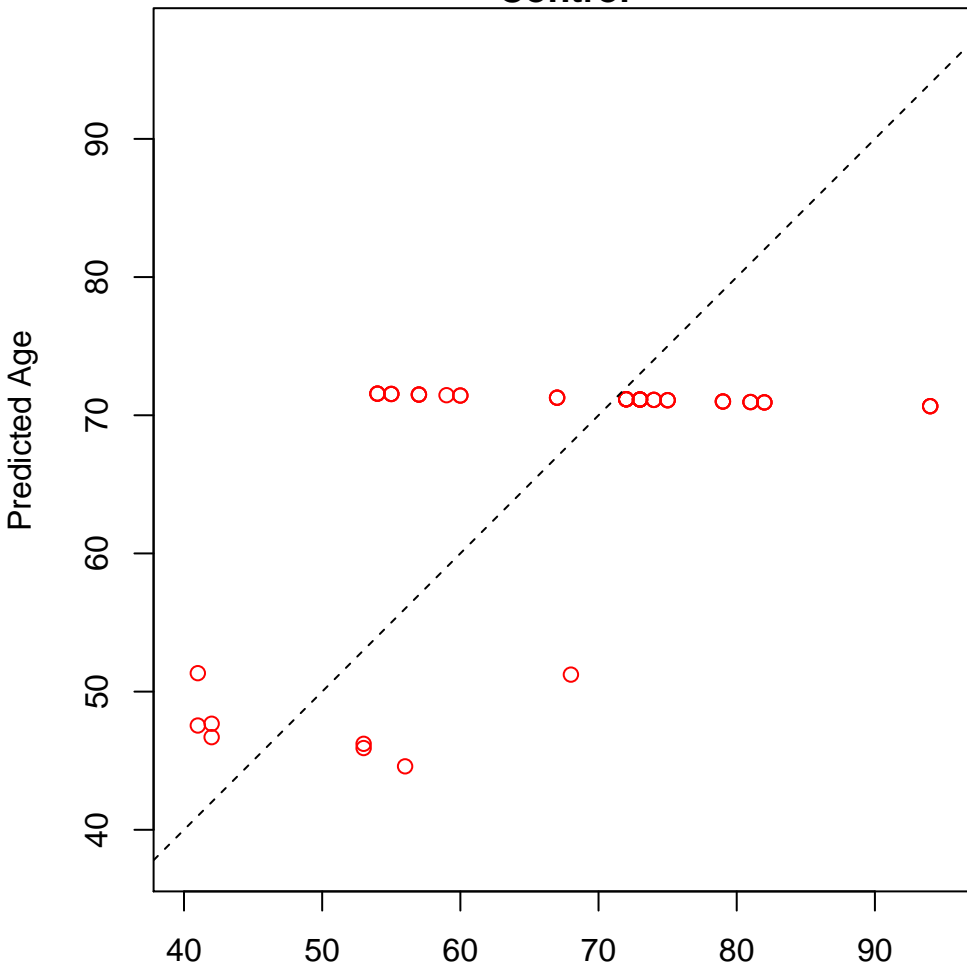
Test



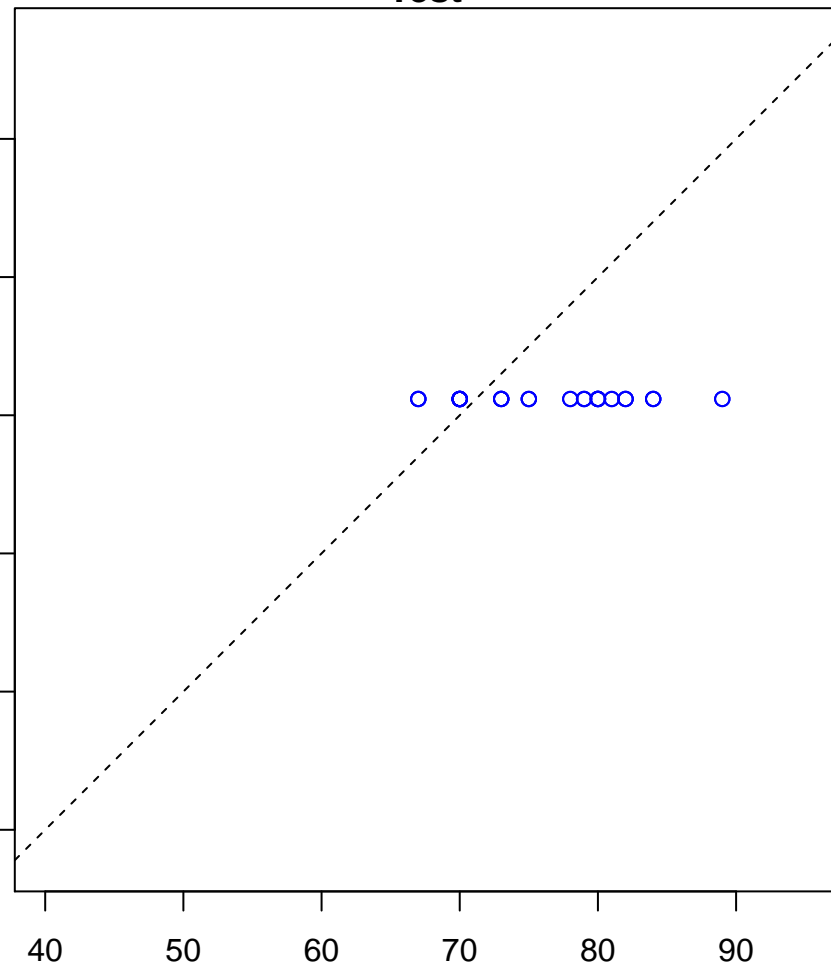
Actual Age

establishment of protein localization (Score: 0.798958)

Control



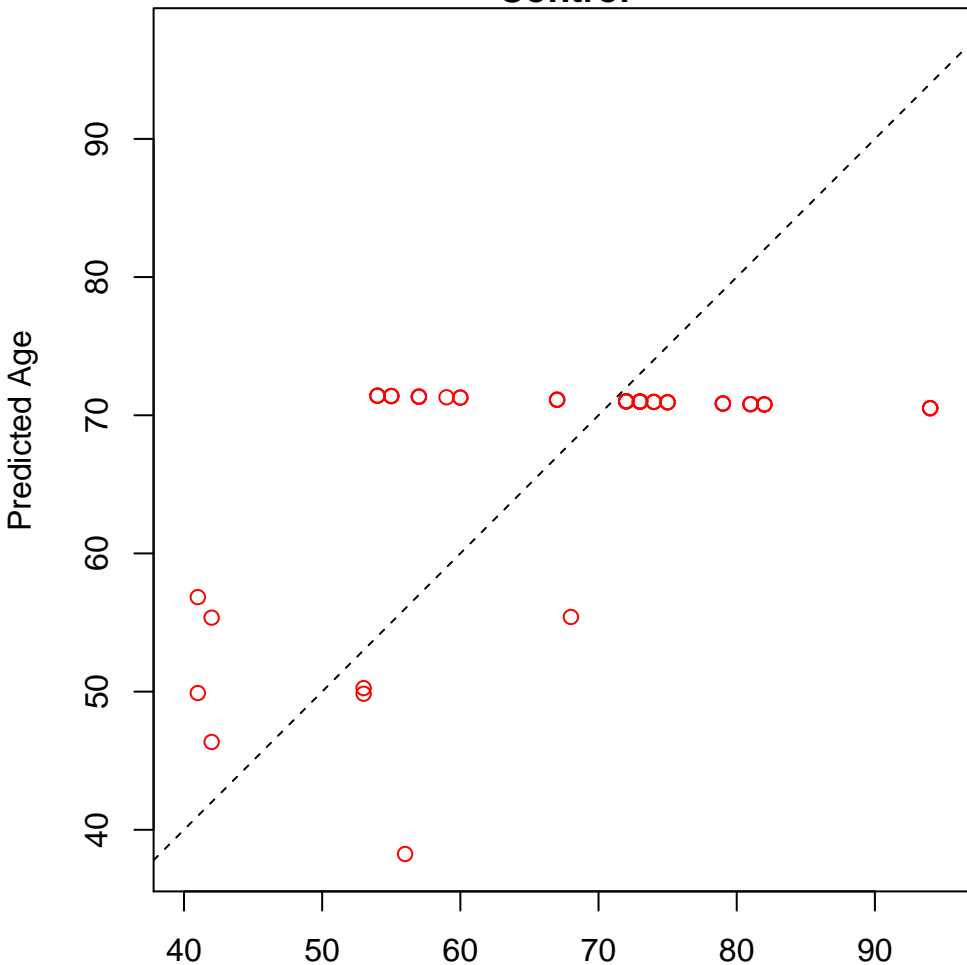
Test



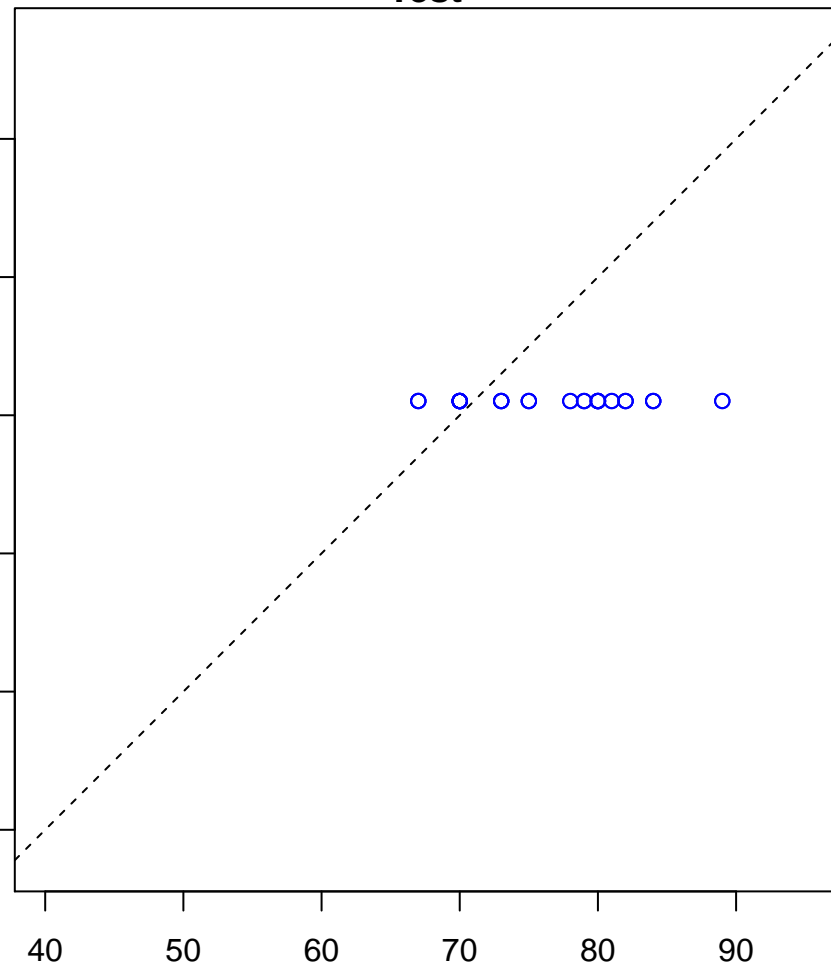
Actual Age

ribonucleoprotein complex biogenesis (Score: 0.798957)

Control



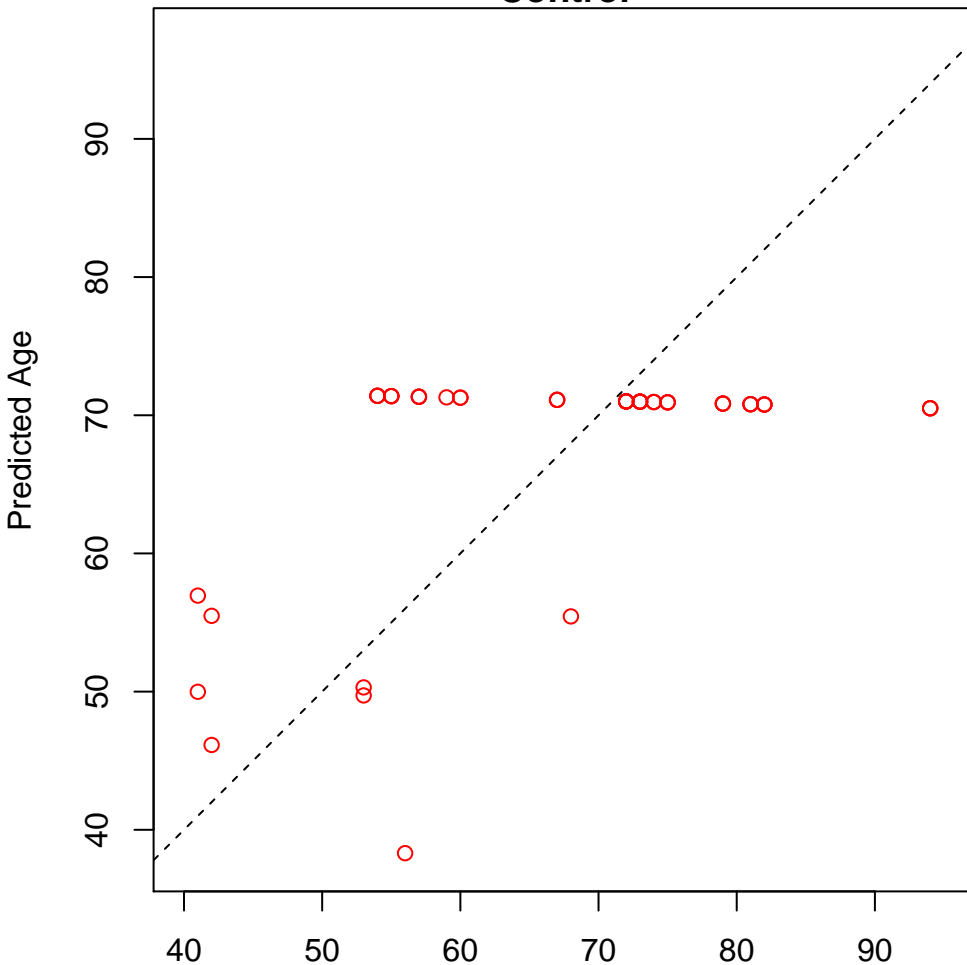
Test



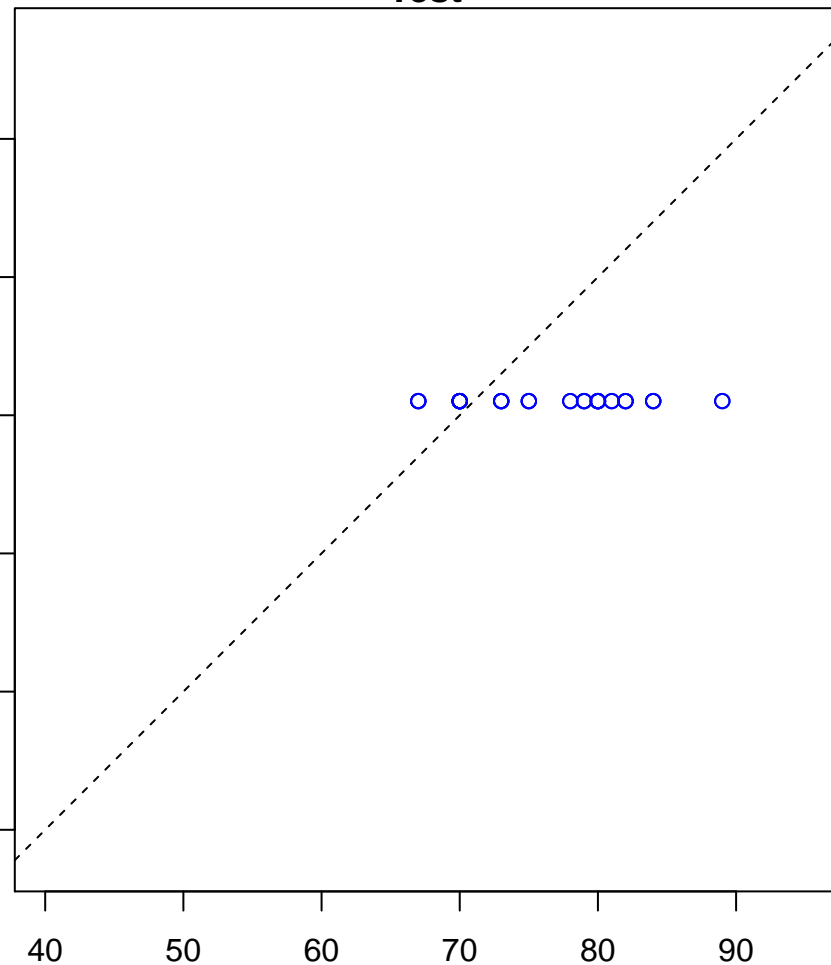
Actual Age

protein localization to membrane (Score: 0.798925)

Control

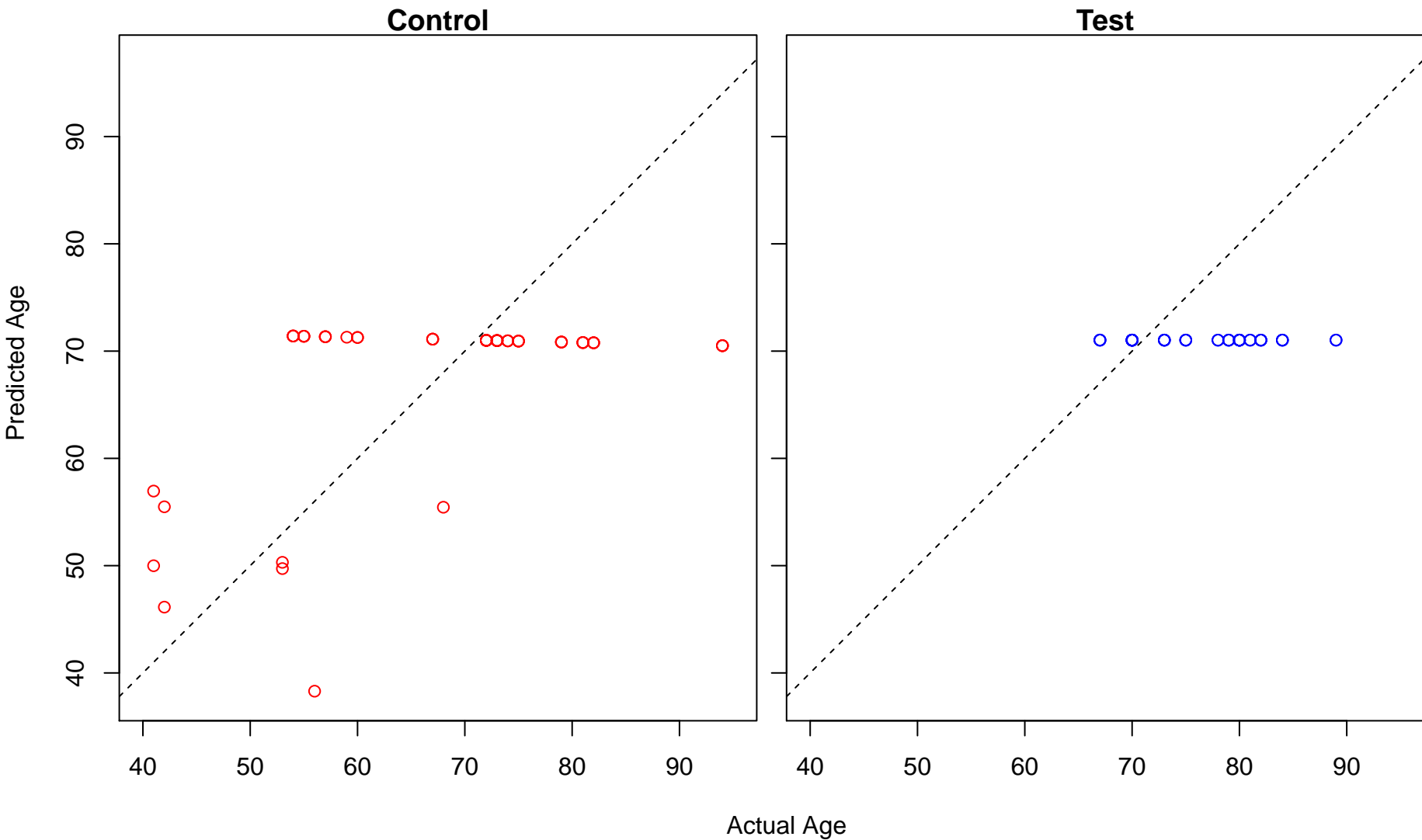


Test



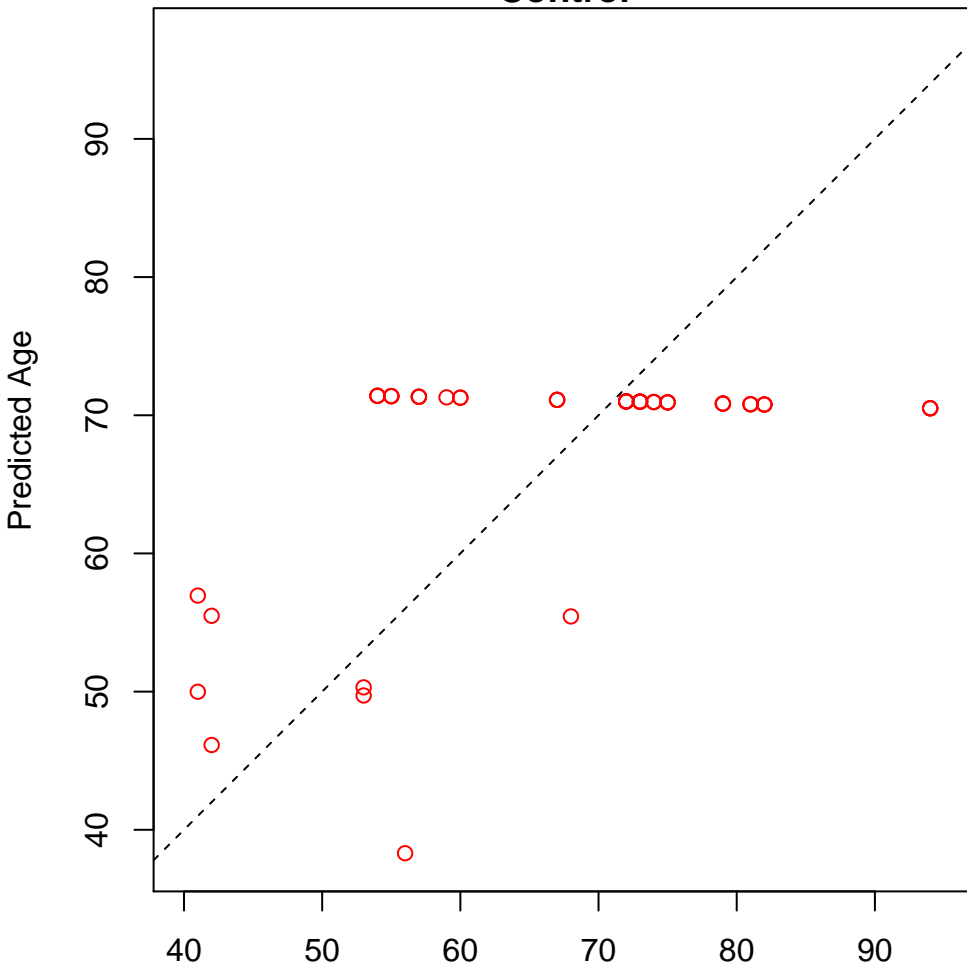
Actual Age

protein localization to endoplasmic reticulum (Score: 0.798921)

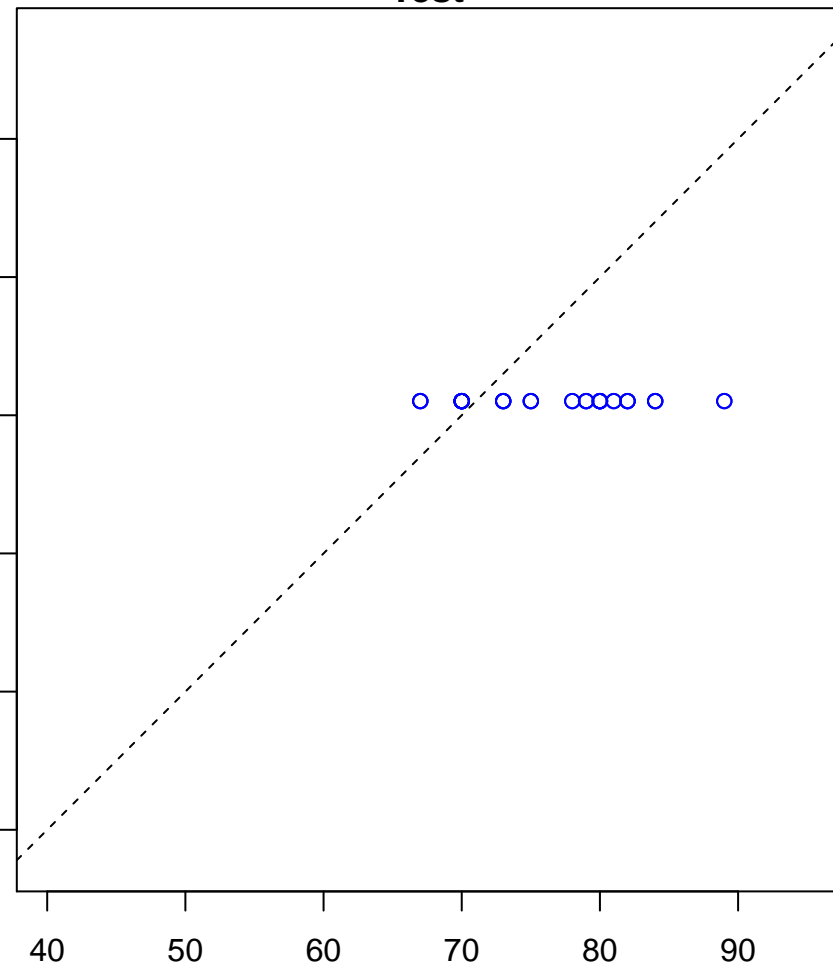


protein targeting to membrane (Score: 0.798921)

Control

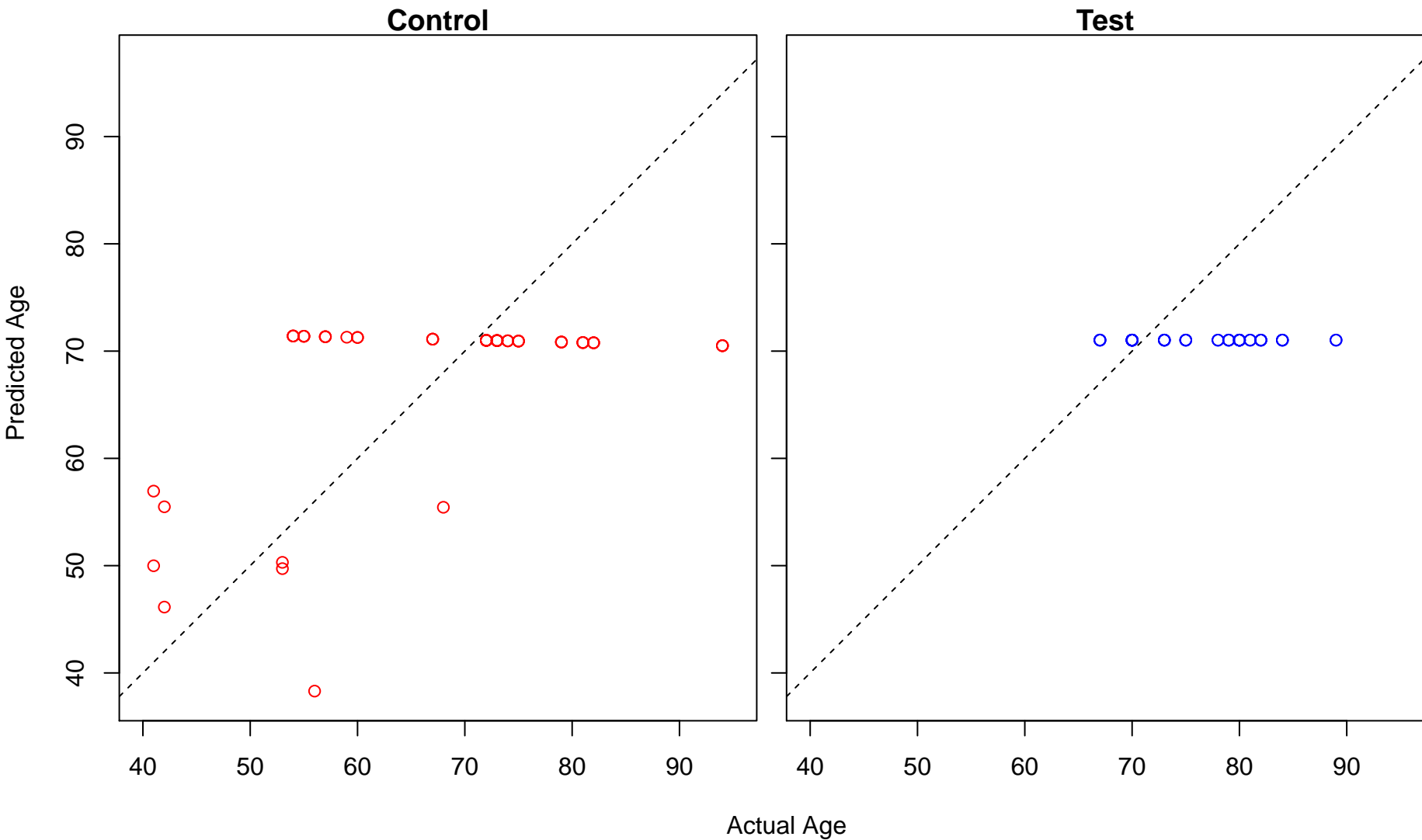


Test

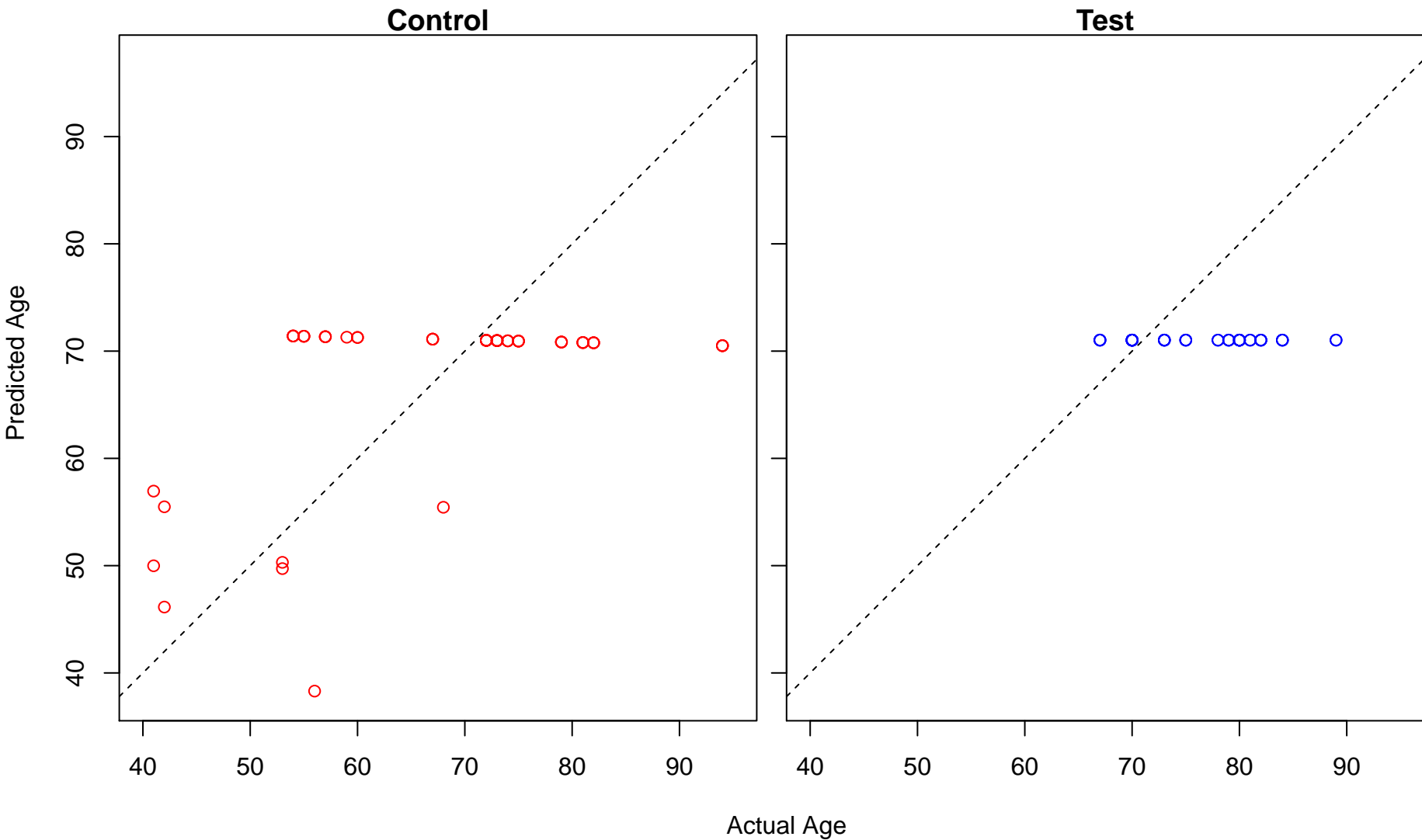


Actual Age

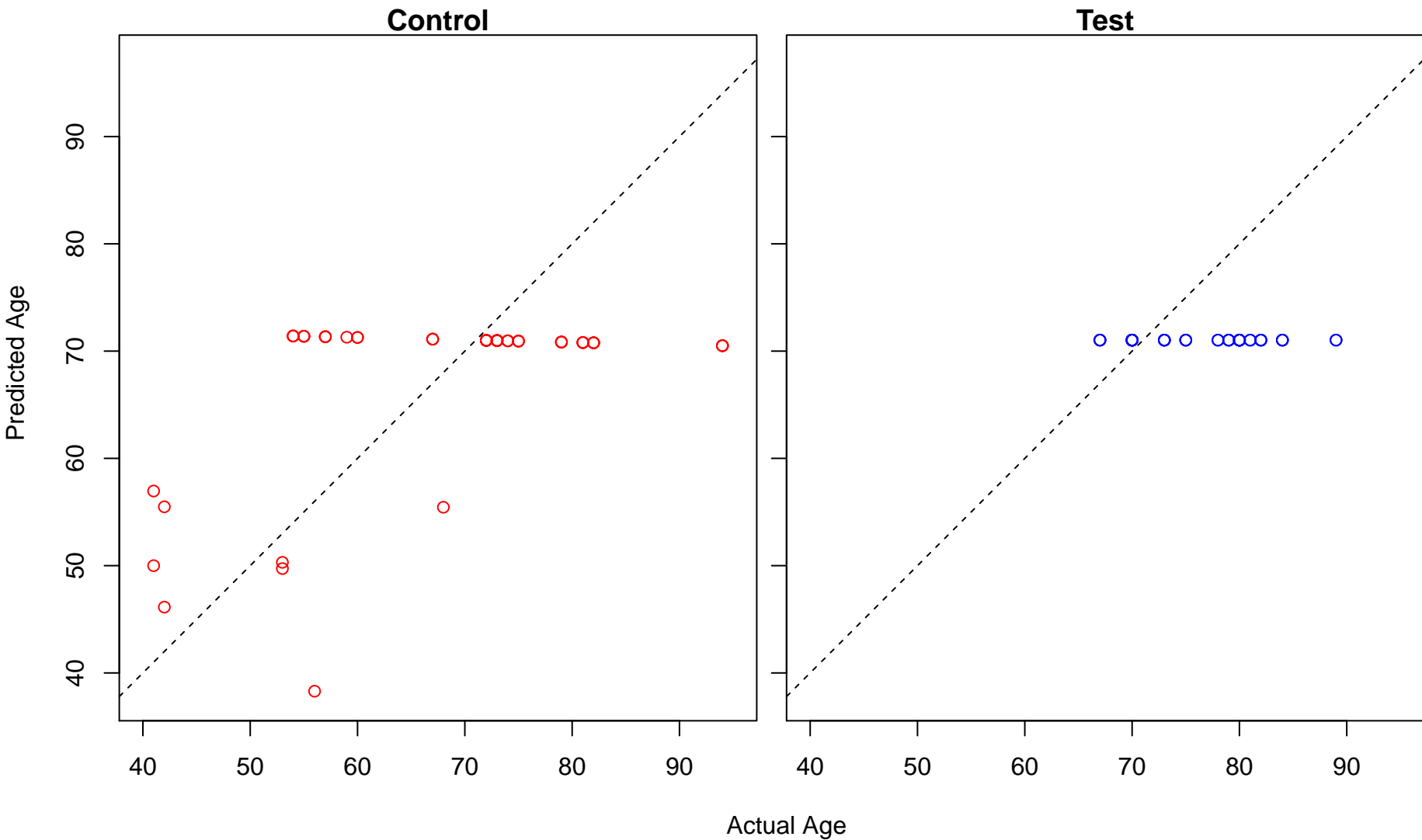
cotranslational protein targeting to membrane (Score: 0.798921)



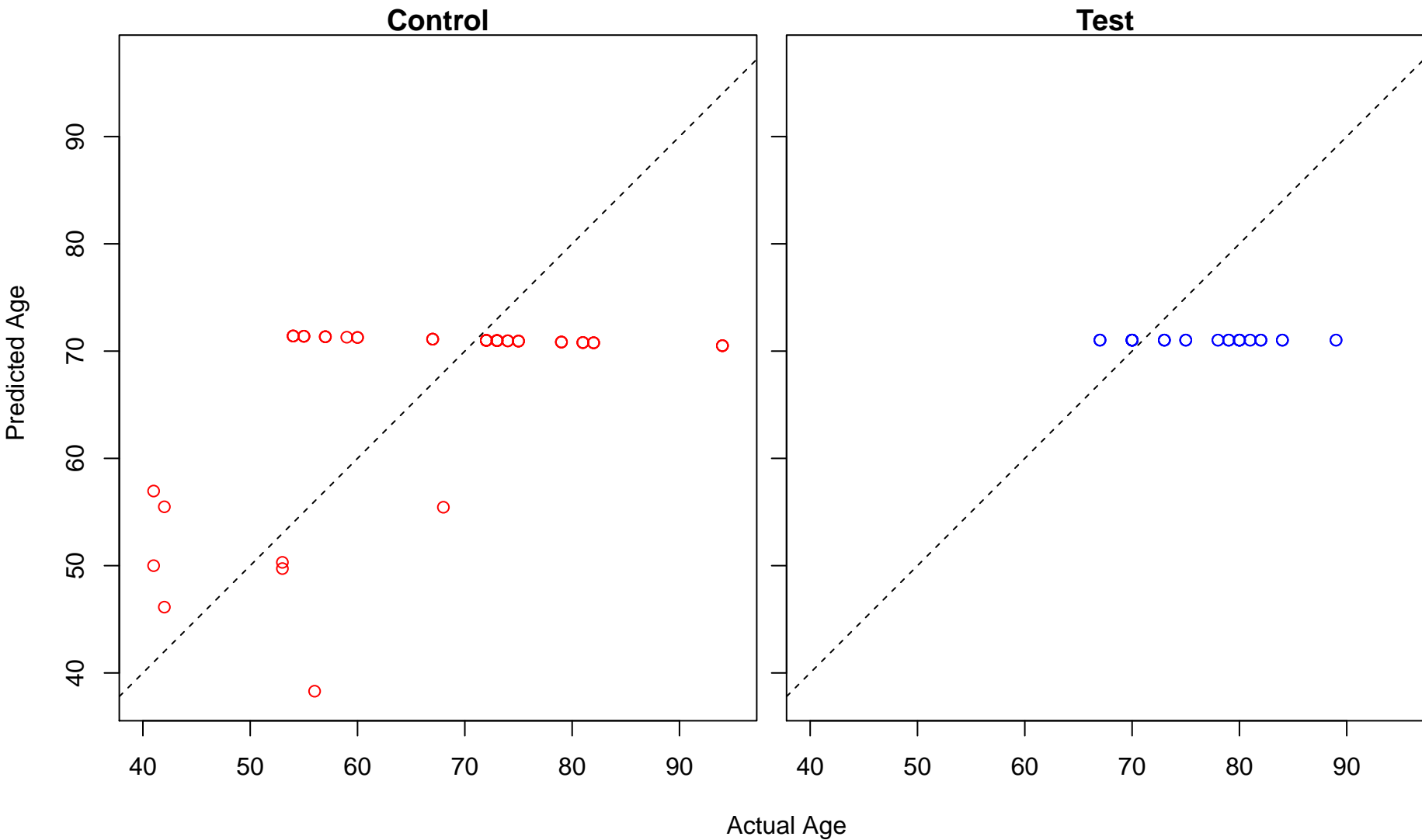
establishment of protein localization to membrane (Score: 0.798921)



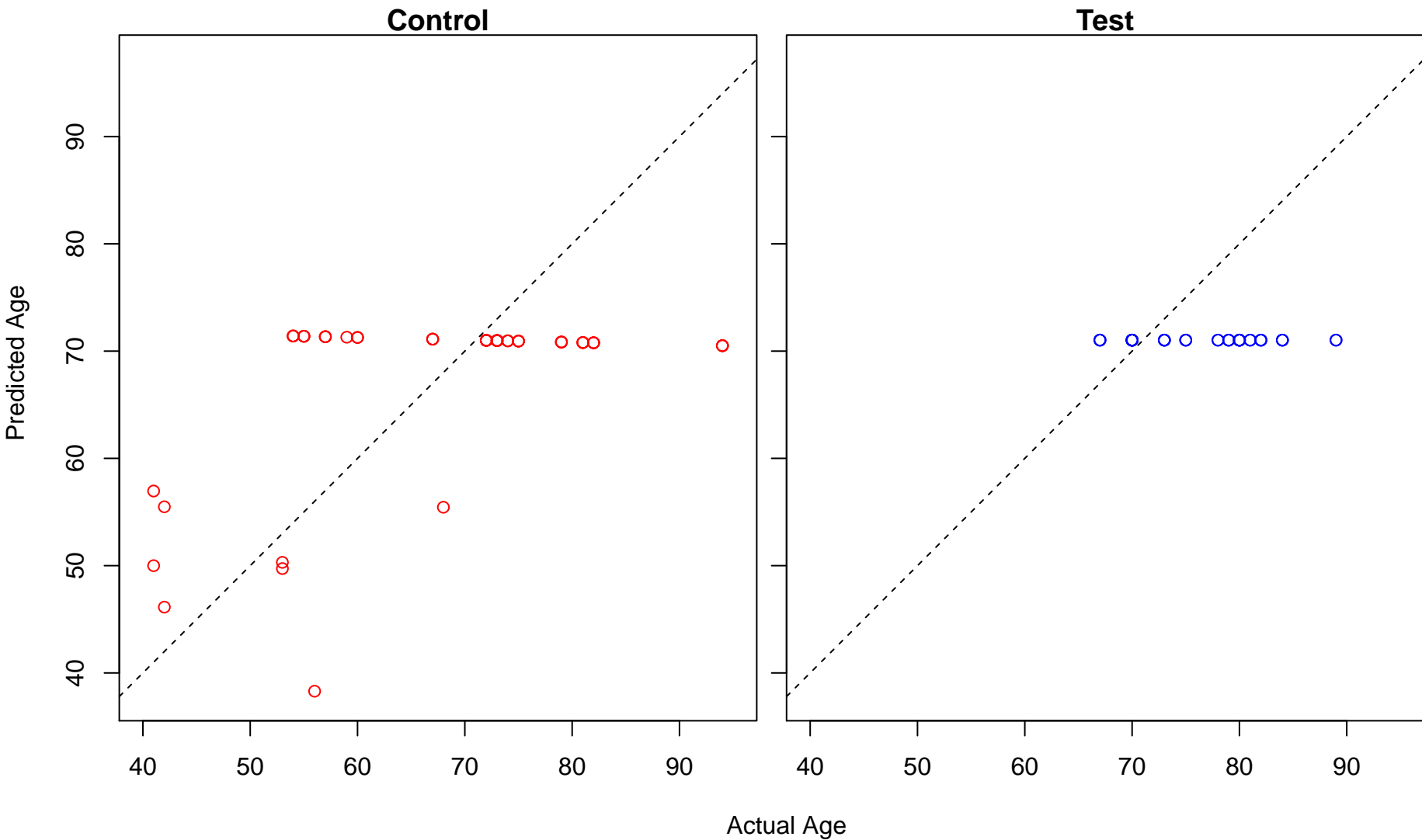
SRP-dependent cotranslational protein targeting to membrane (Score: 0.798912)



protein targeting to ER (Score: 0.798912)

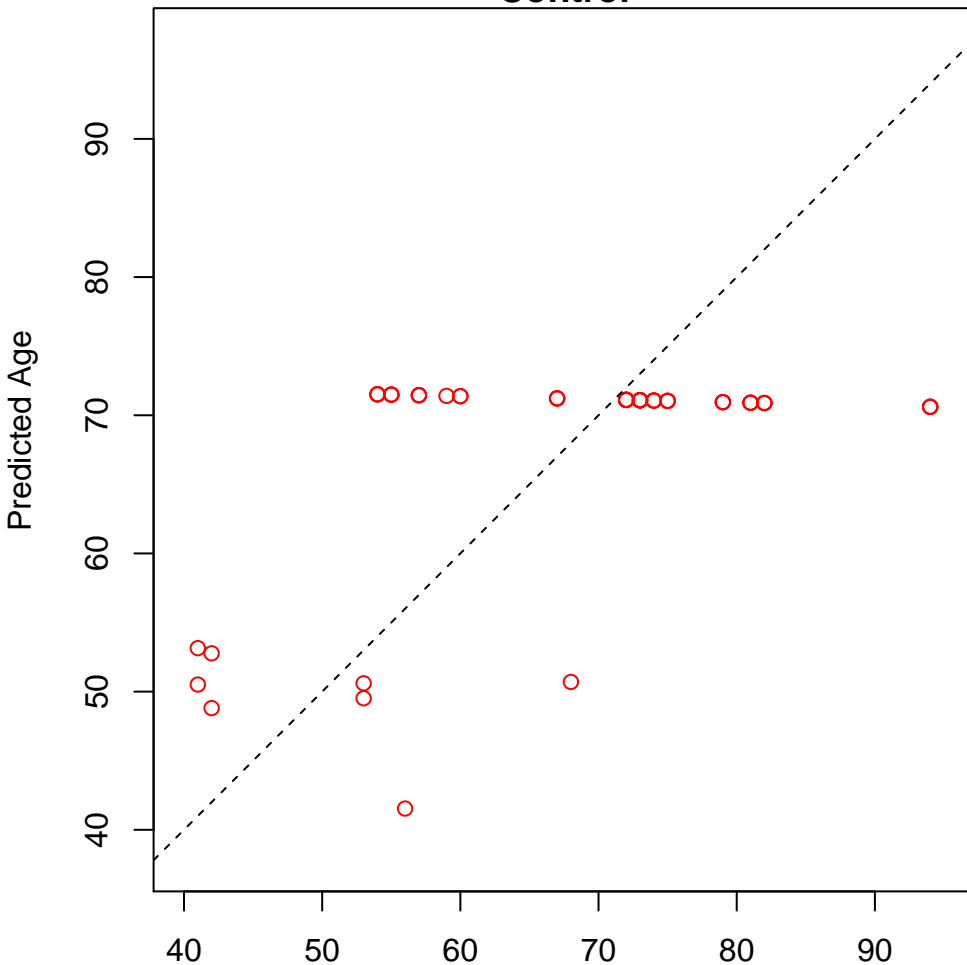


establishment of protein localization to endoplasmic reticulum (Score: 0.798912)

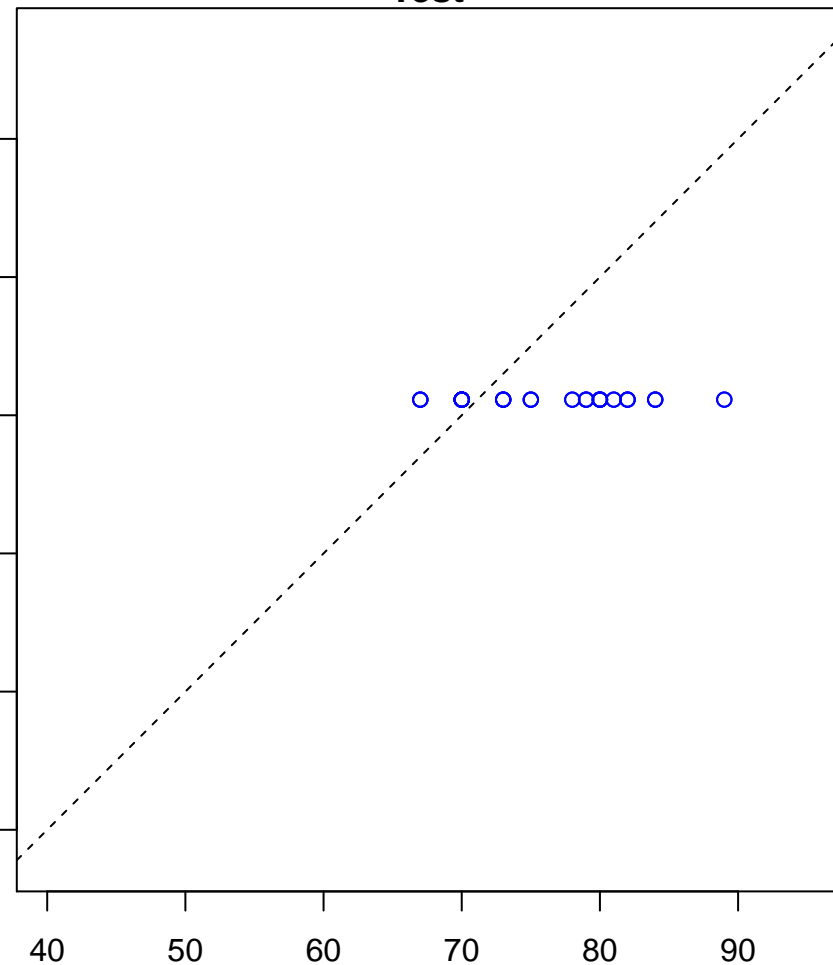


protein monoubiquitination (Score: 0.798909)

Control

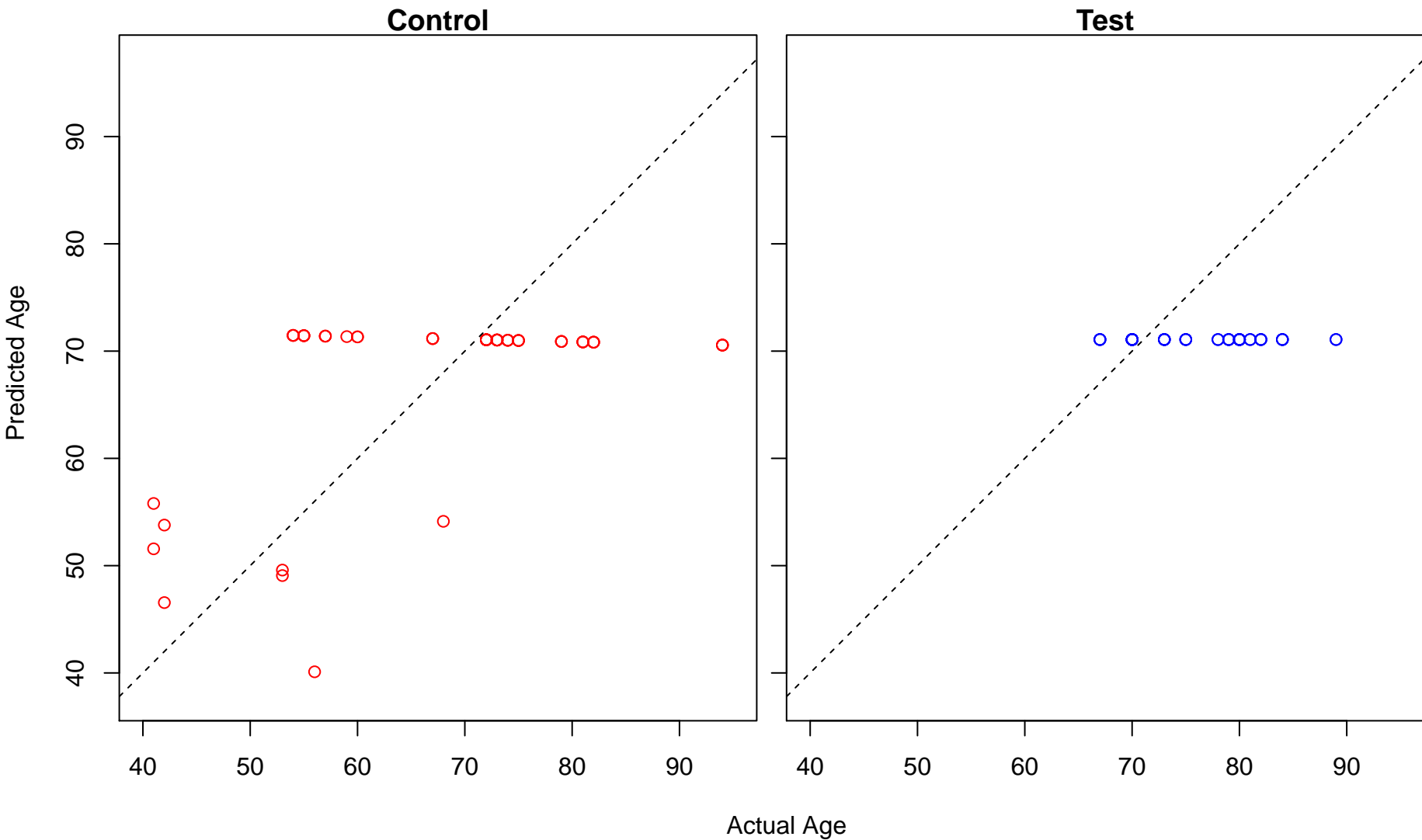


Test

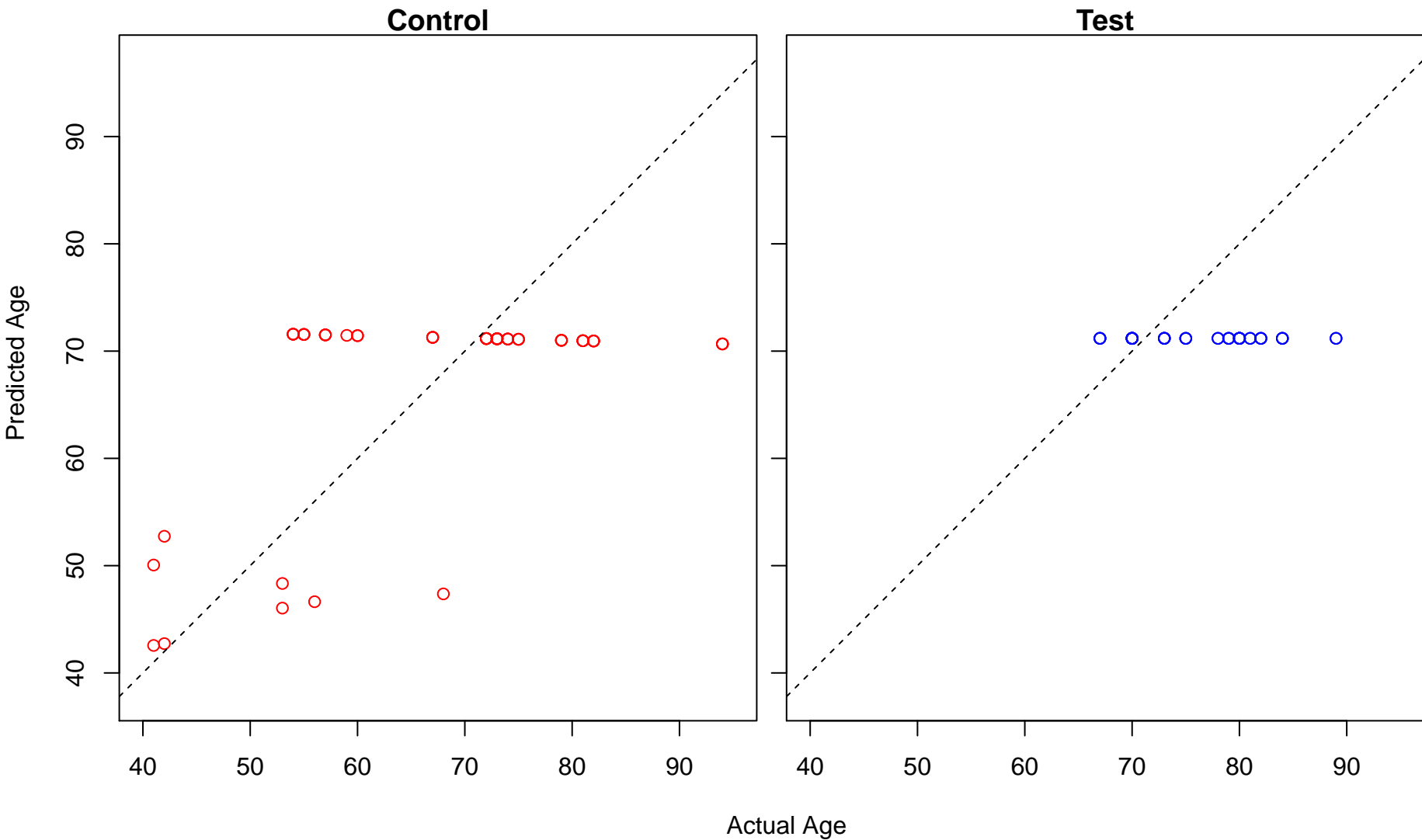


Actual Age

protein metabolic process (Score: 0.798880)

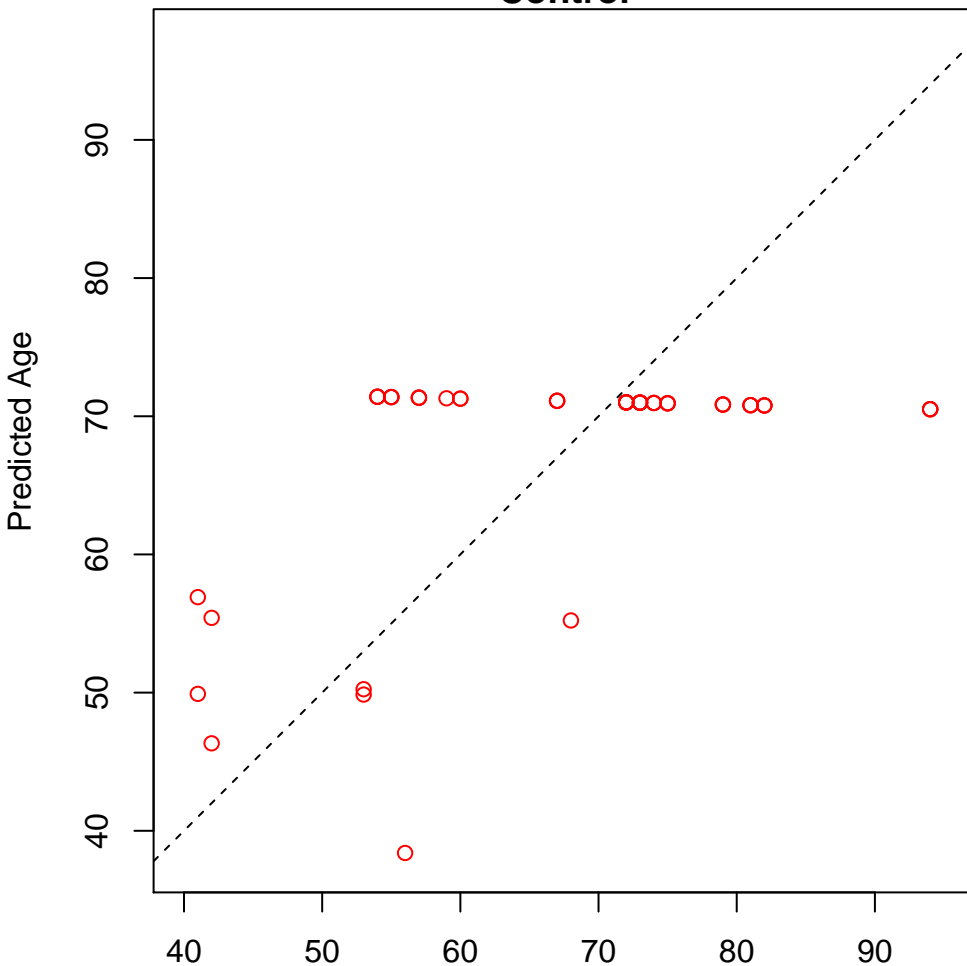


positive regulation of macromolecule metabolic process (Score: 0.798871)

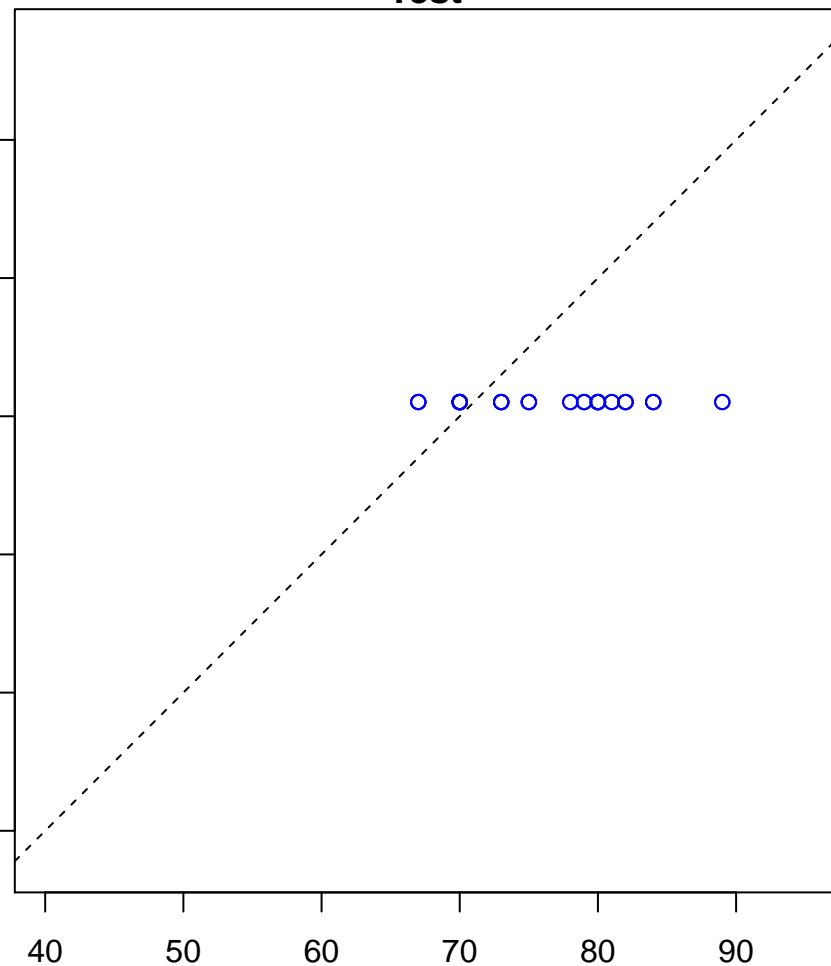


aromatic compound catabolic process (Score: 0.798866)

Control

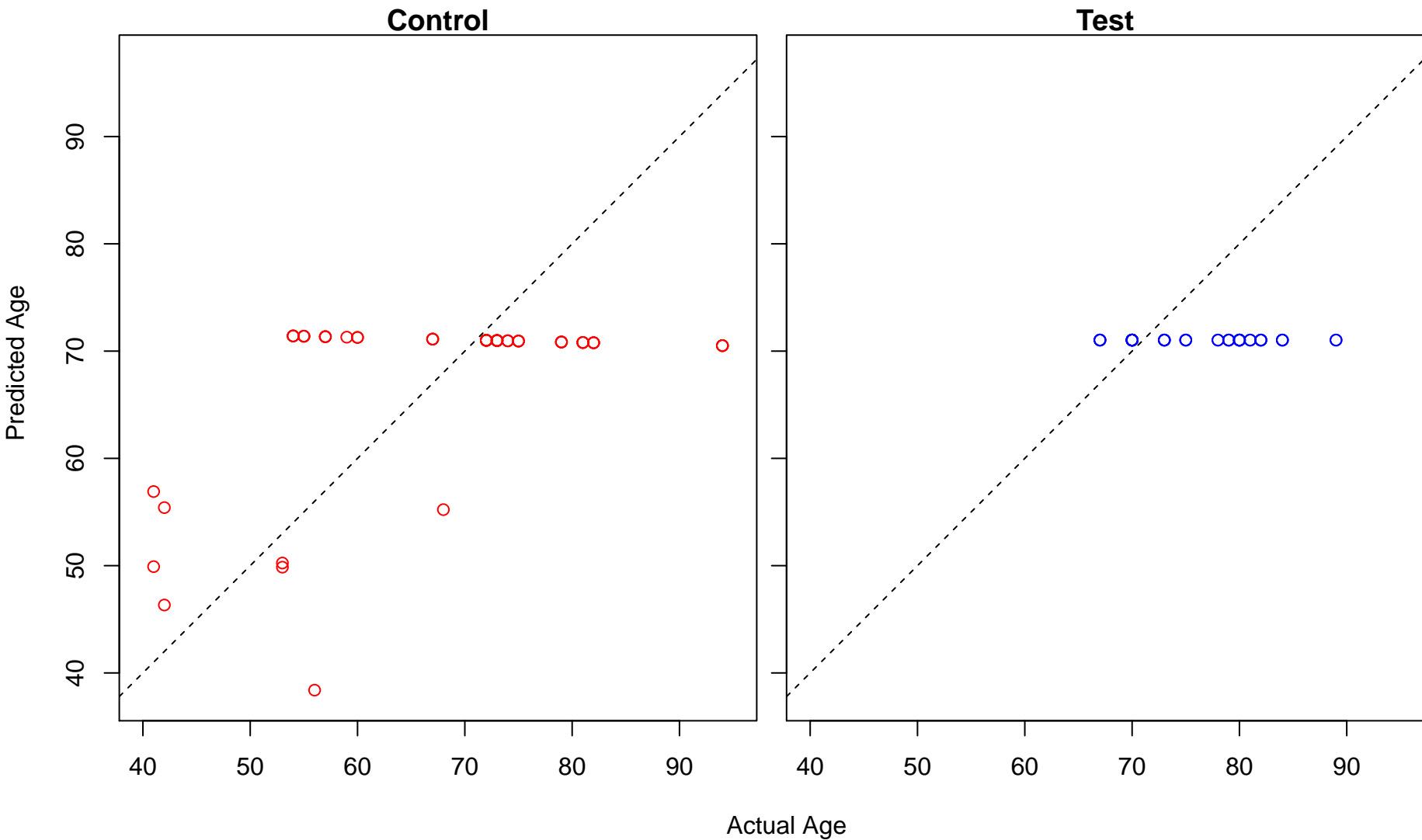


Test



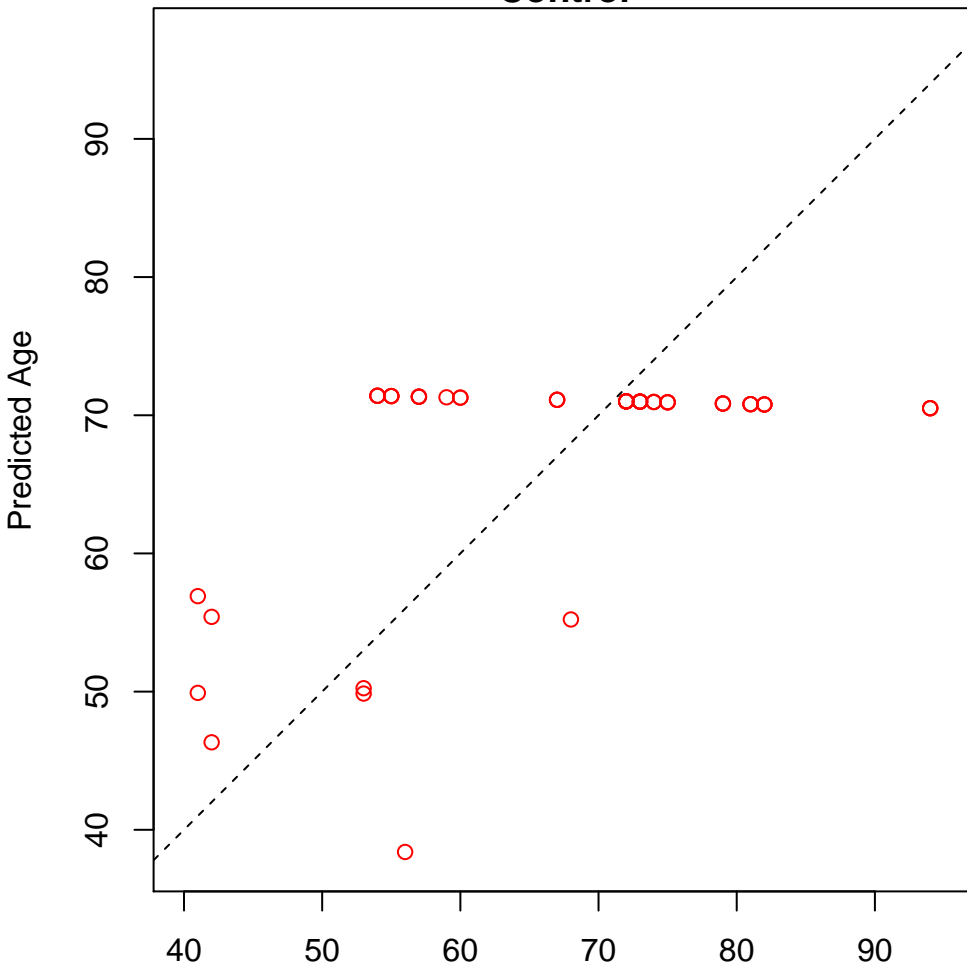
Actual Age

heterocycle catabolic process (Score: 0.798866)

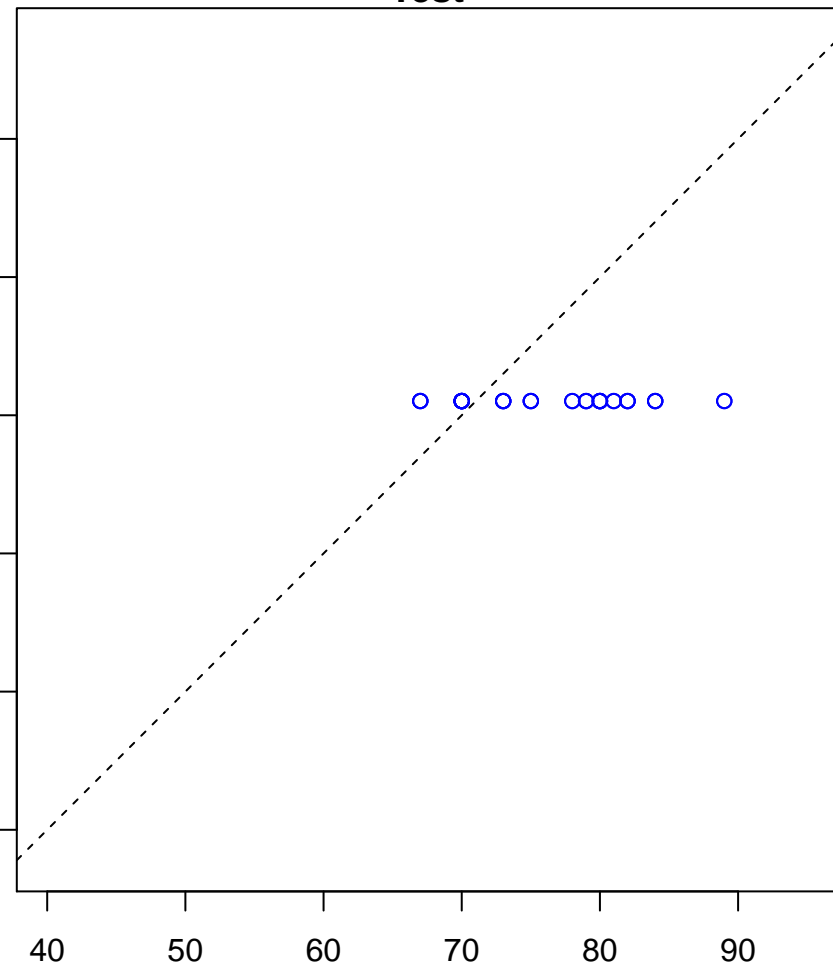


organic cyclic compound catabolic process (Score: 0.798866)

Control

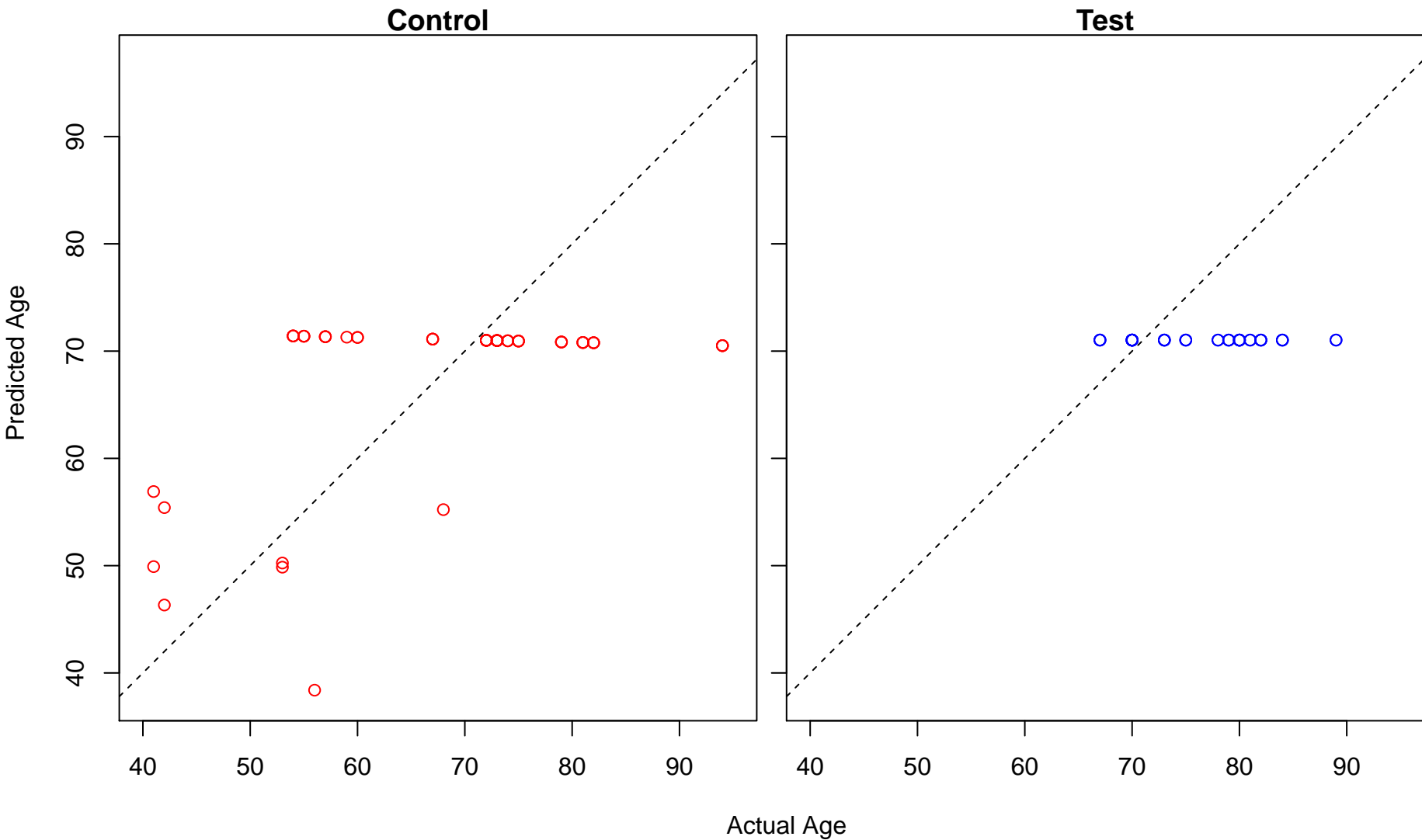


Test

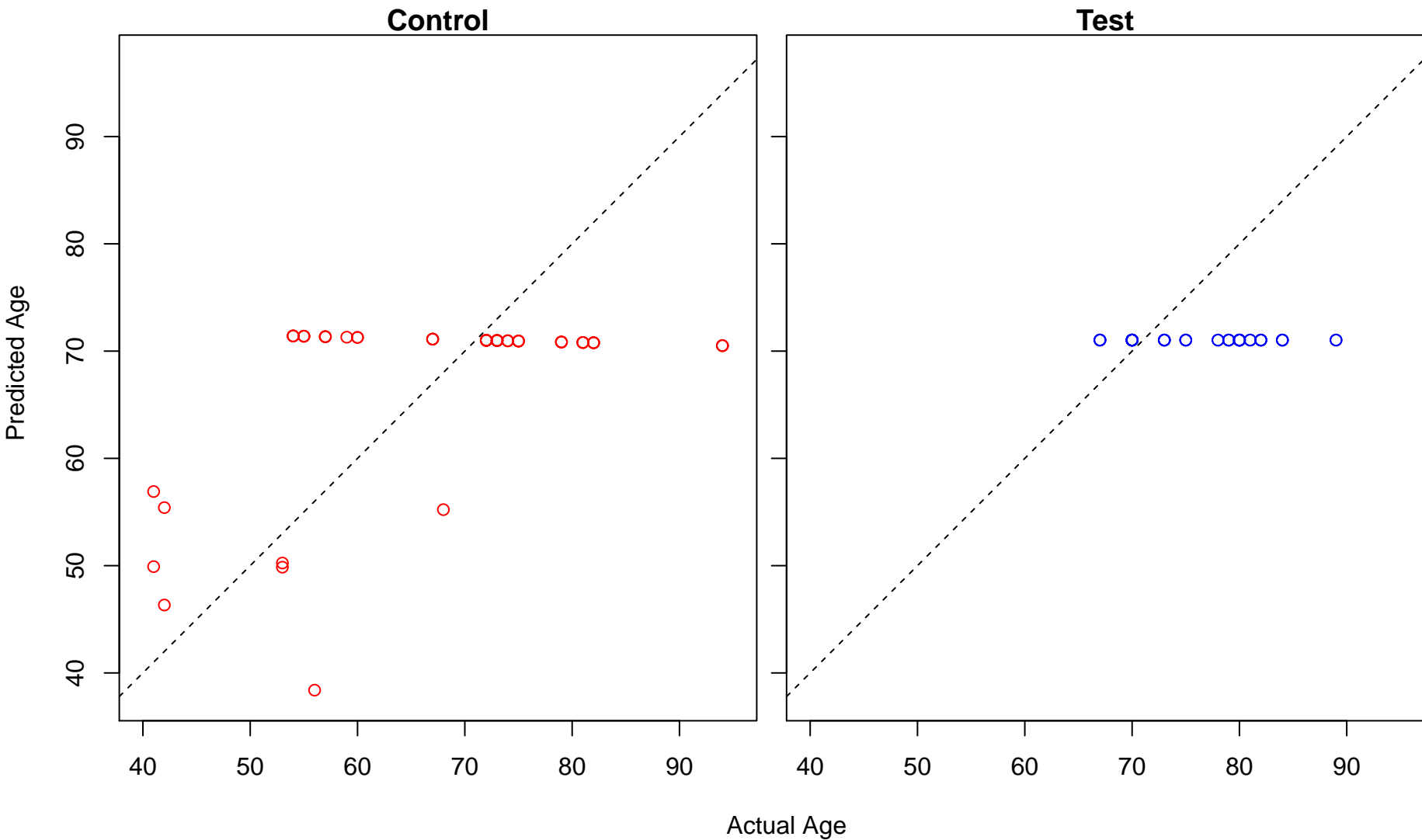


Actual Age

nucleobase-containing compound catabolic process (Score: 0.798866)

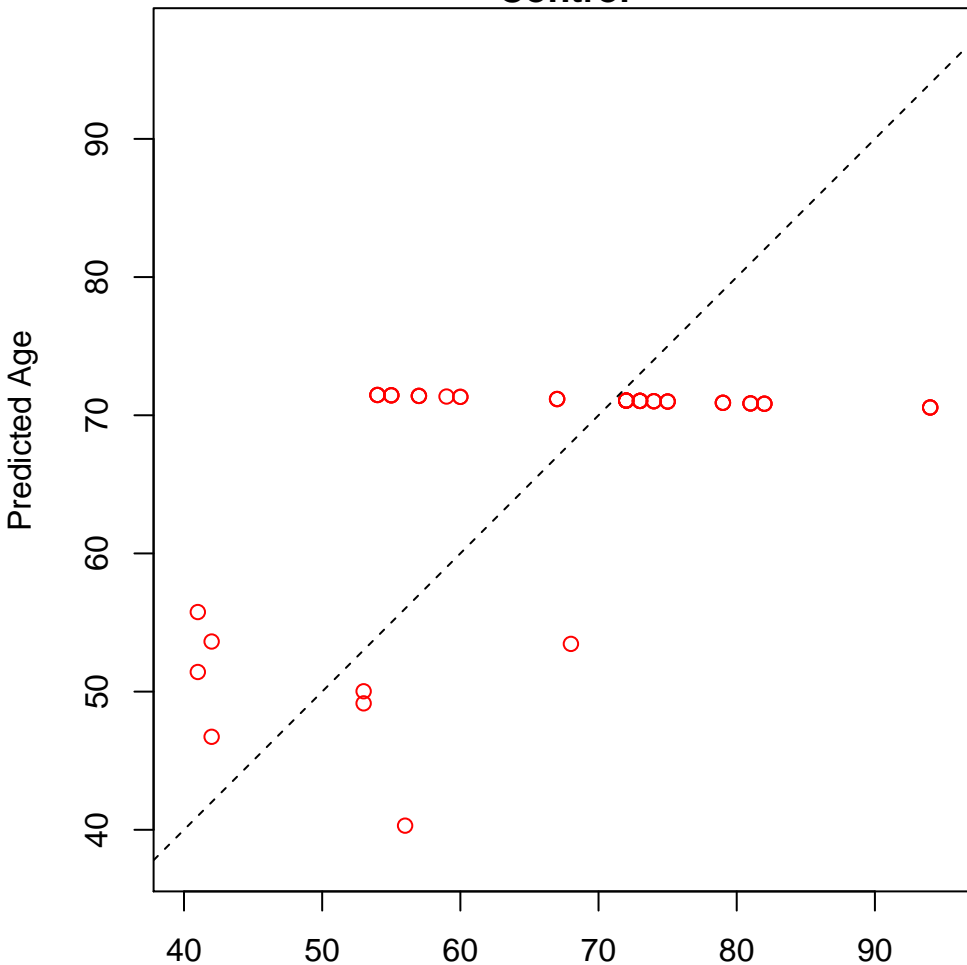


cellular nitrogen compound catabolic process (Score: 0.798866)

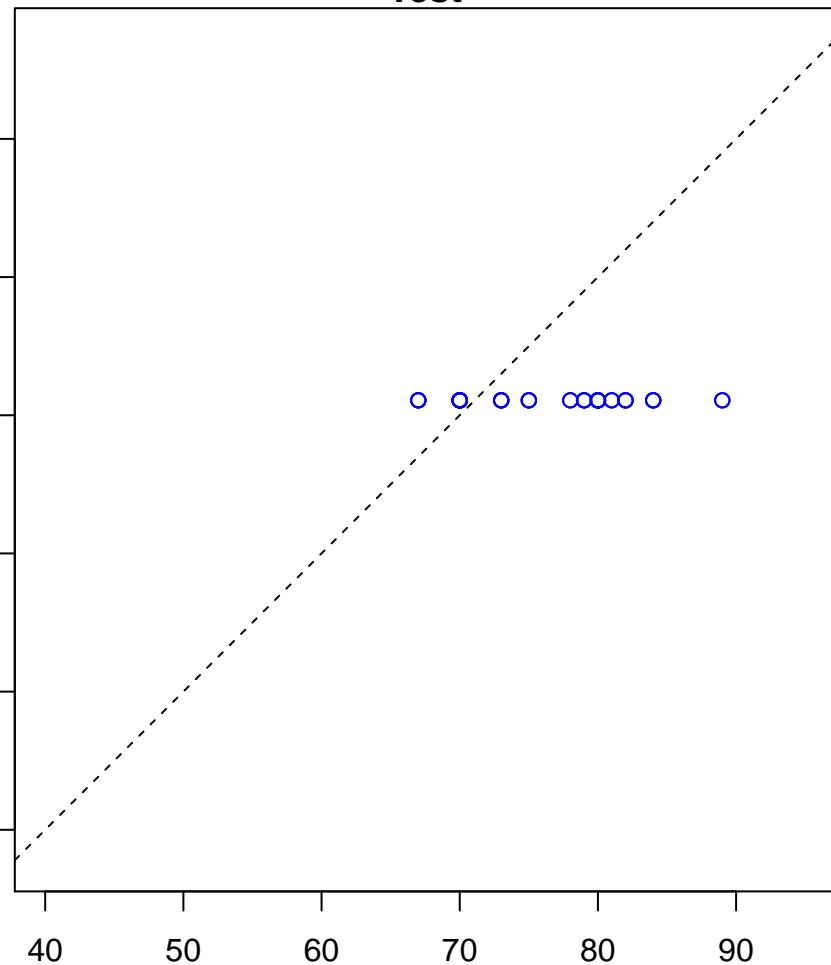


negative regulation of metabolic process (Score: 0.798860)

Control



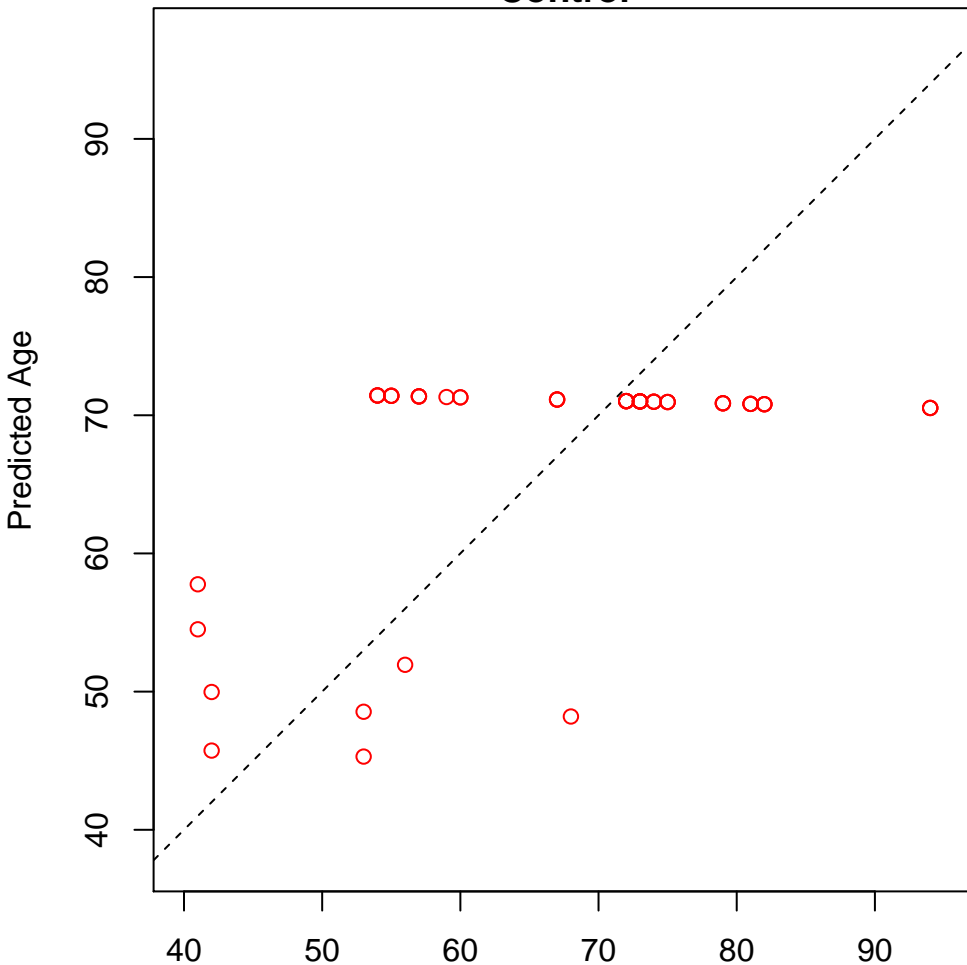
Test



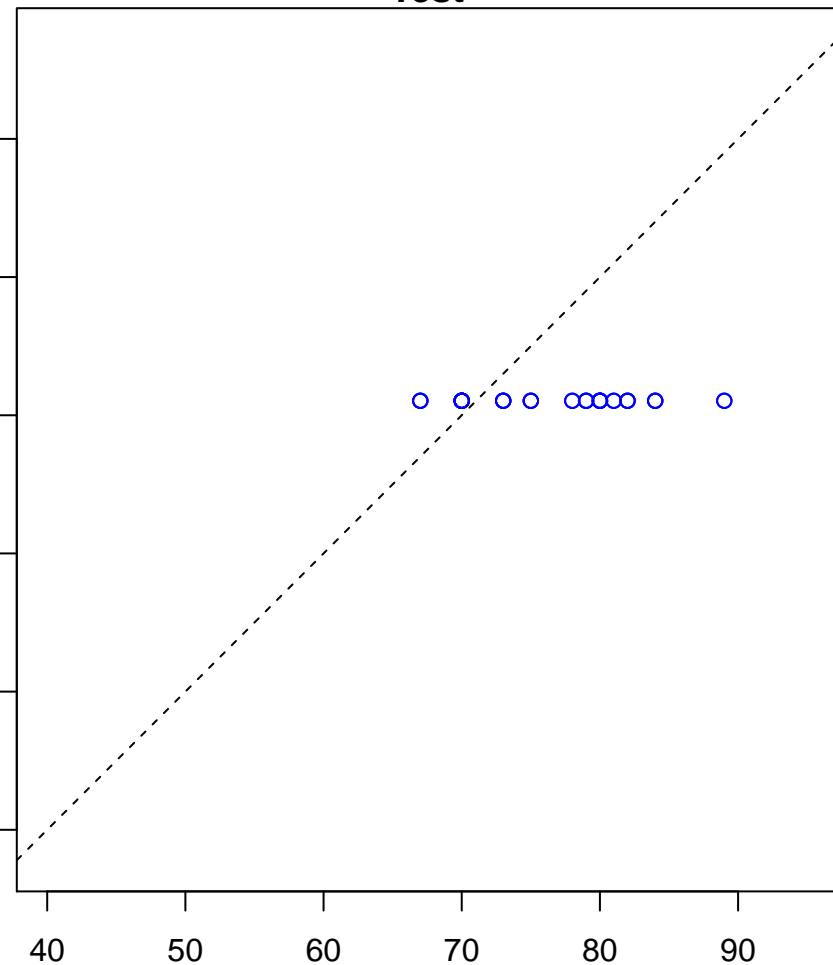
Actual Age

regulation of endopeptidase activity (Score: 0.798859)

Control

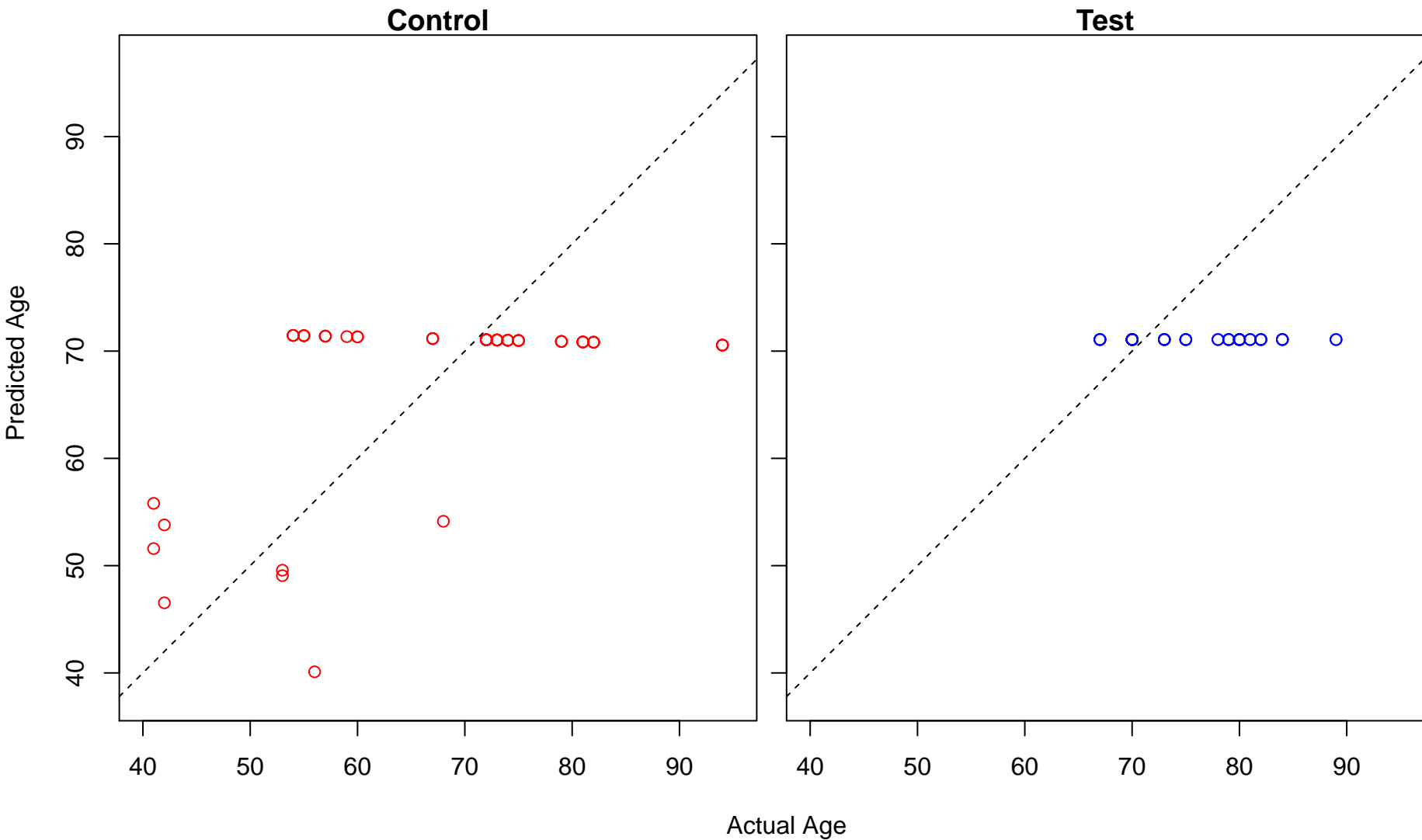


Test

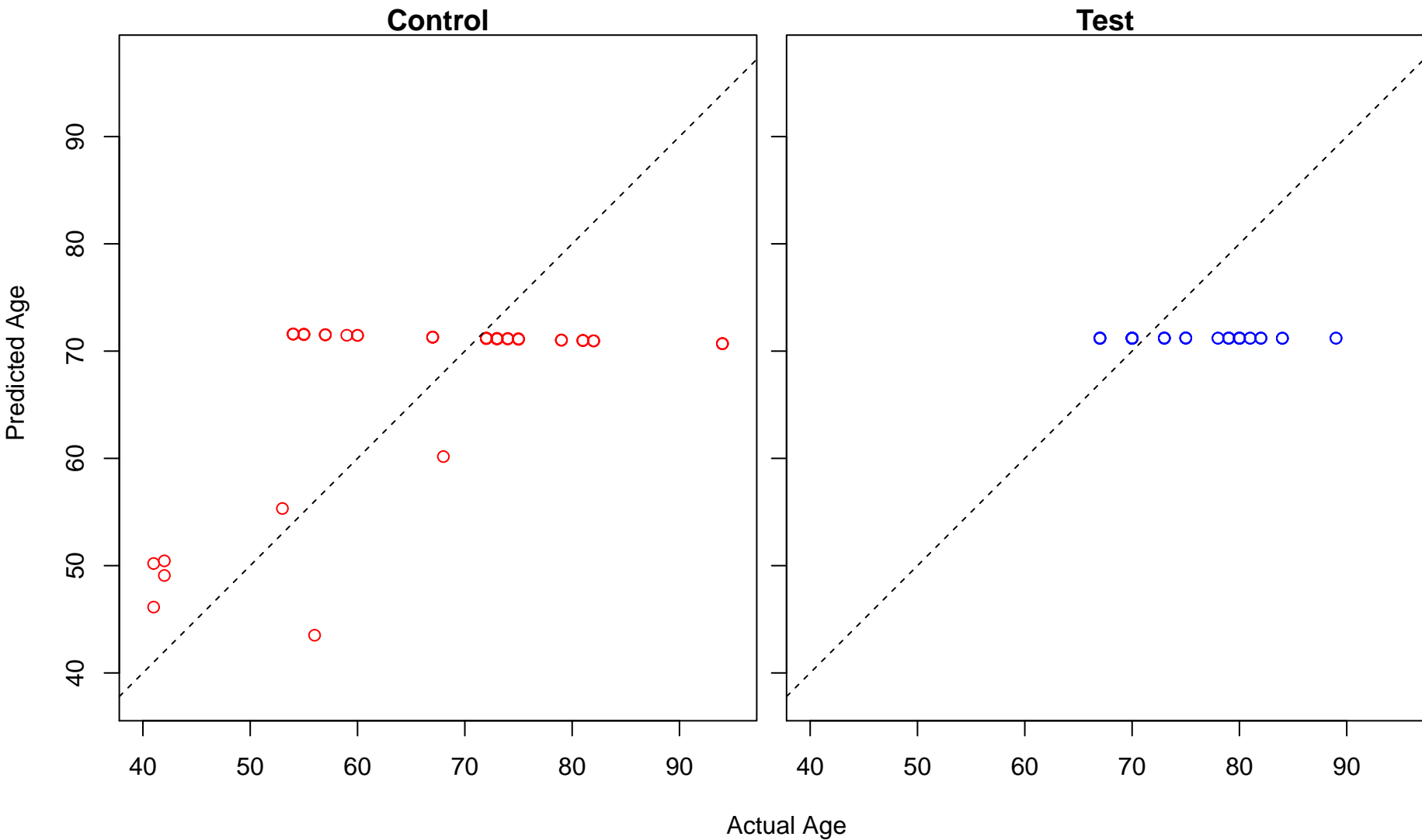


Actual Age

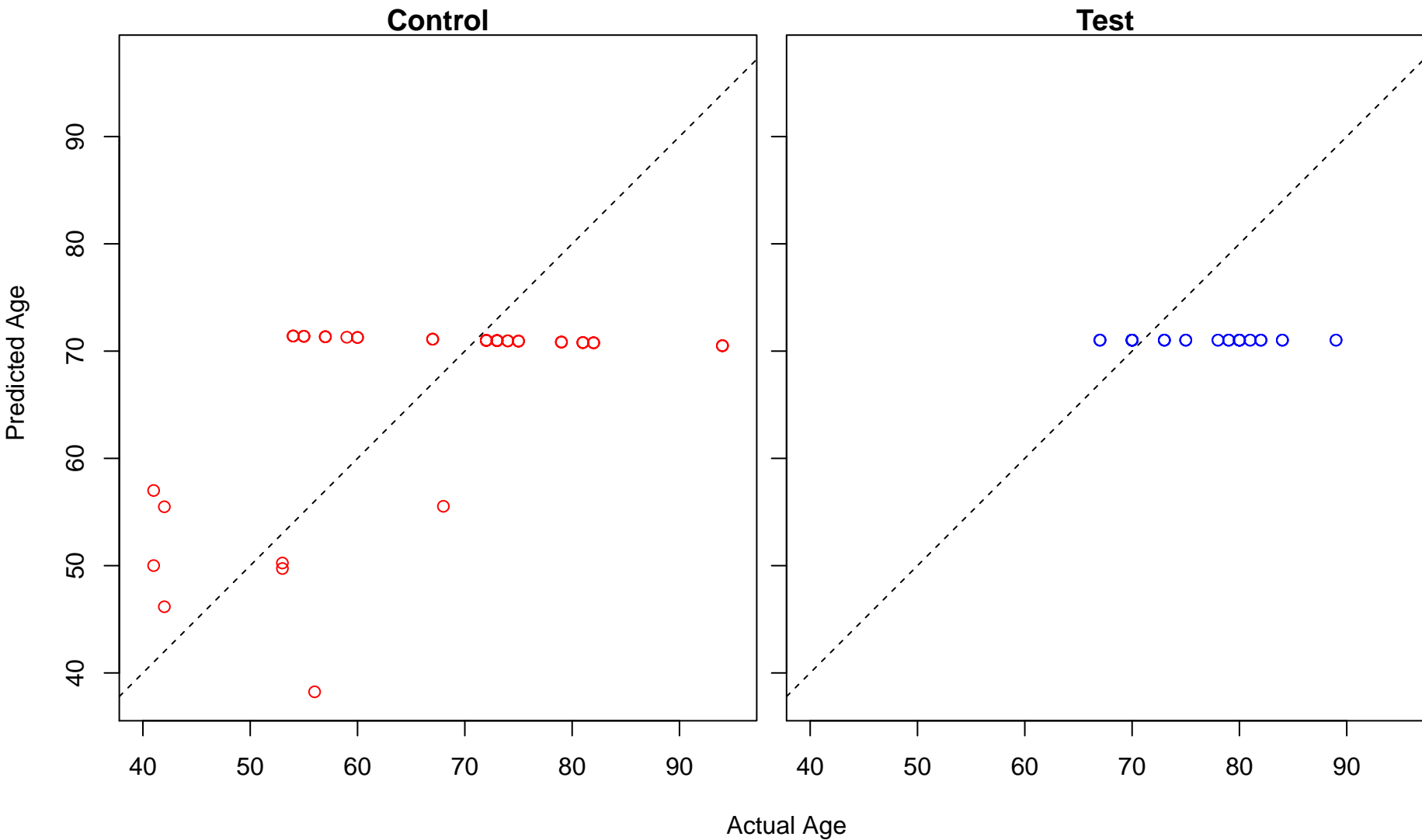
cellular protein metabolic process (Score: 0.798846)



regulation of protein tyrosine kinase activity (Score: 0.798839)

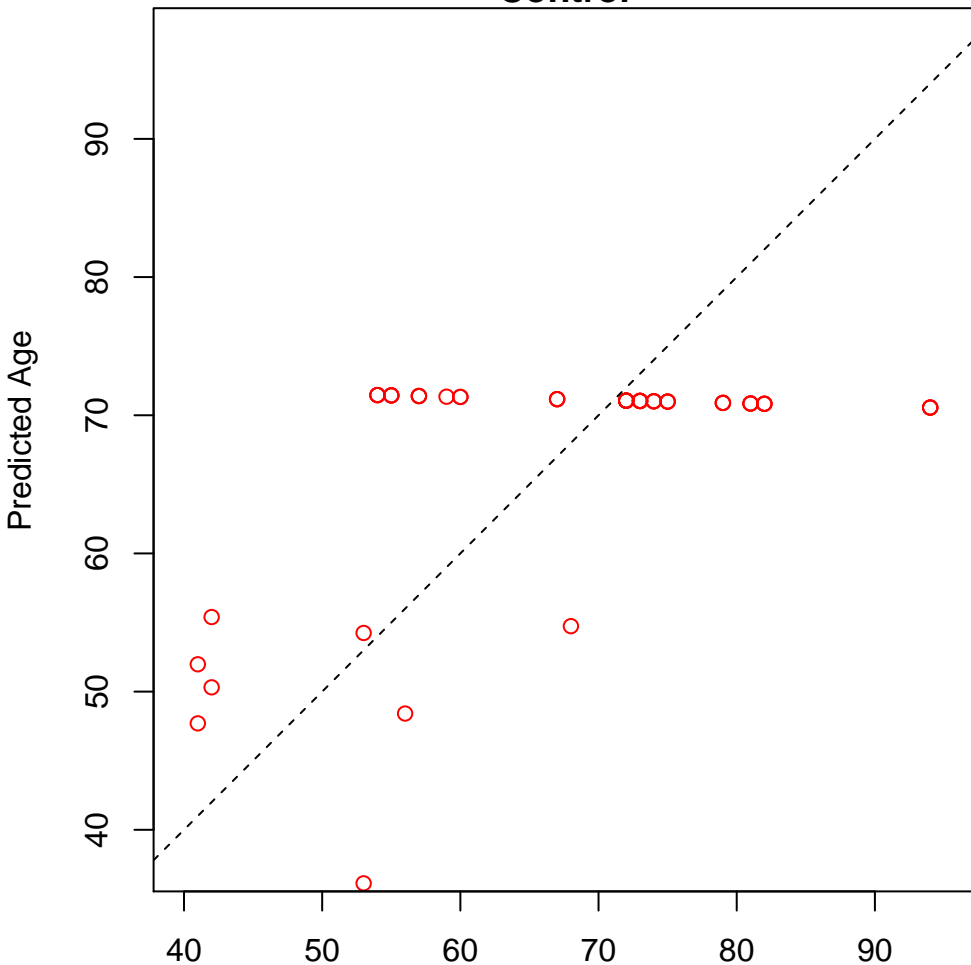


ribosome biogenesis (Score: 0.798833)

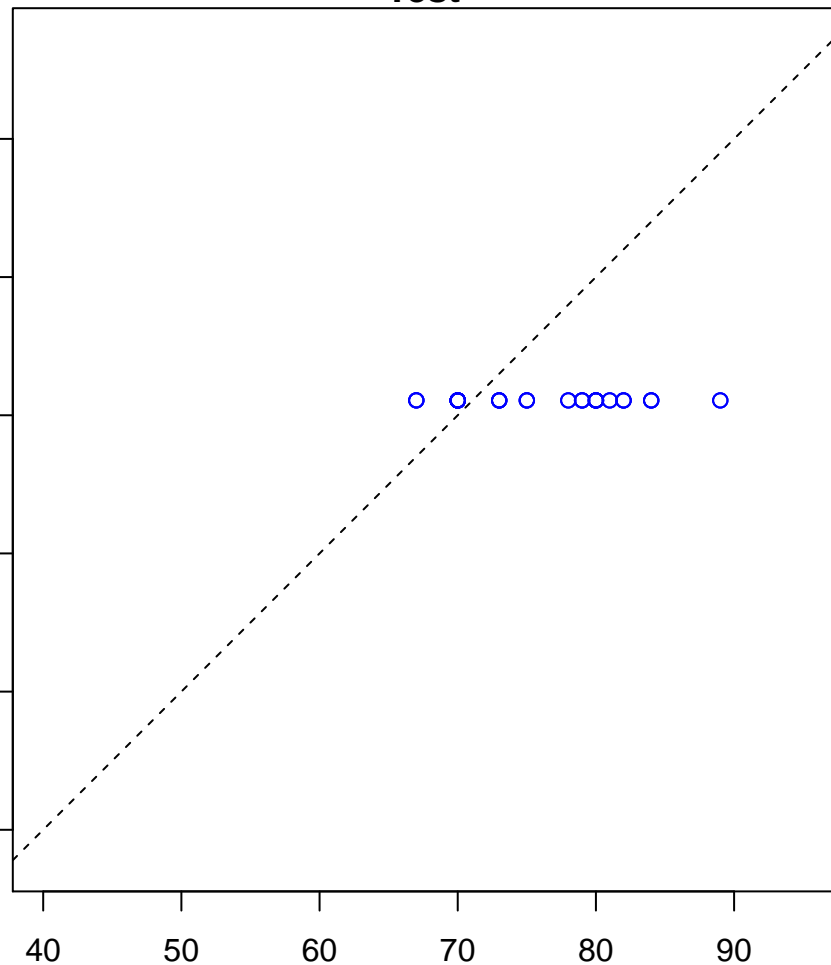


regulation of humoral immune response (Score: 0.798831)

Control



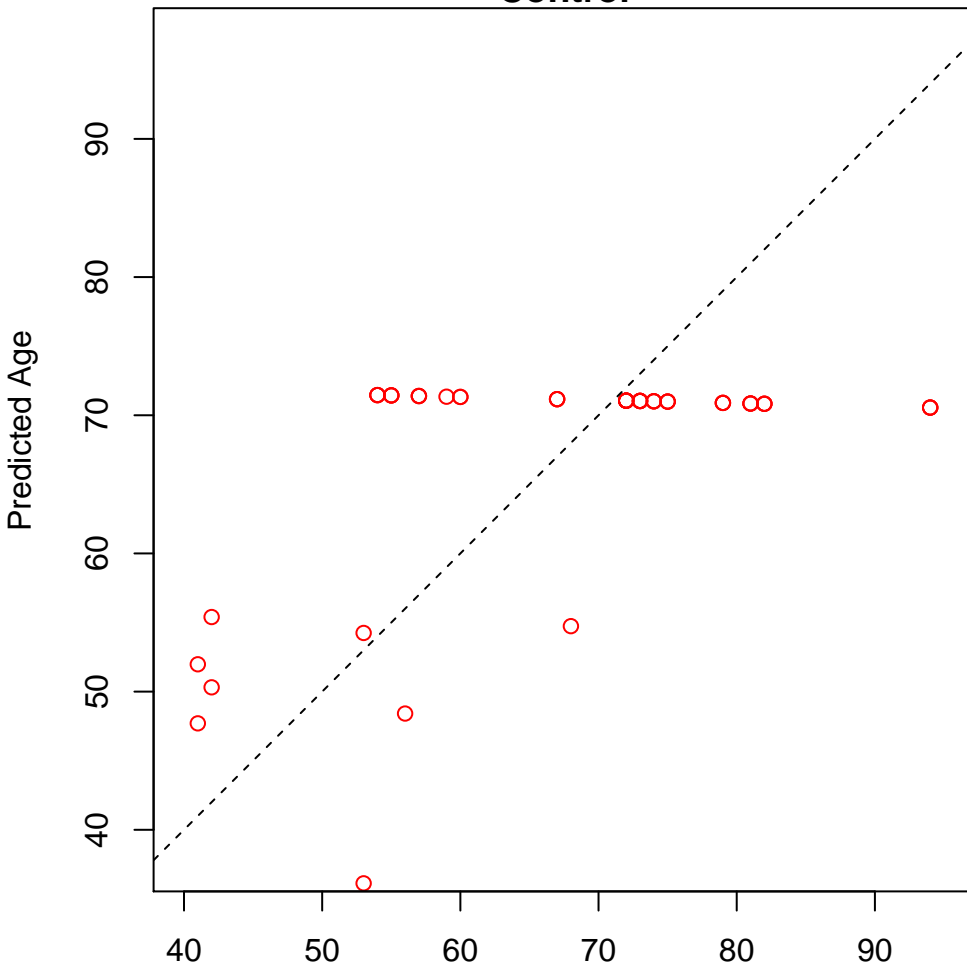
Test



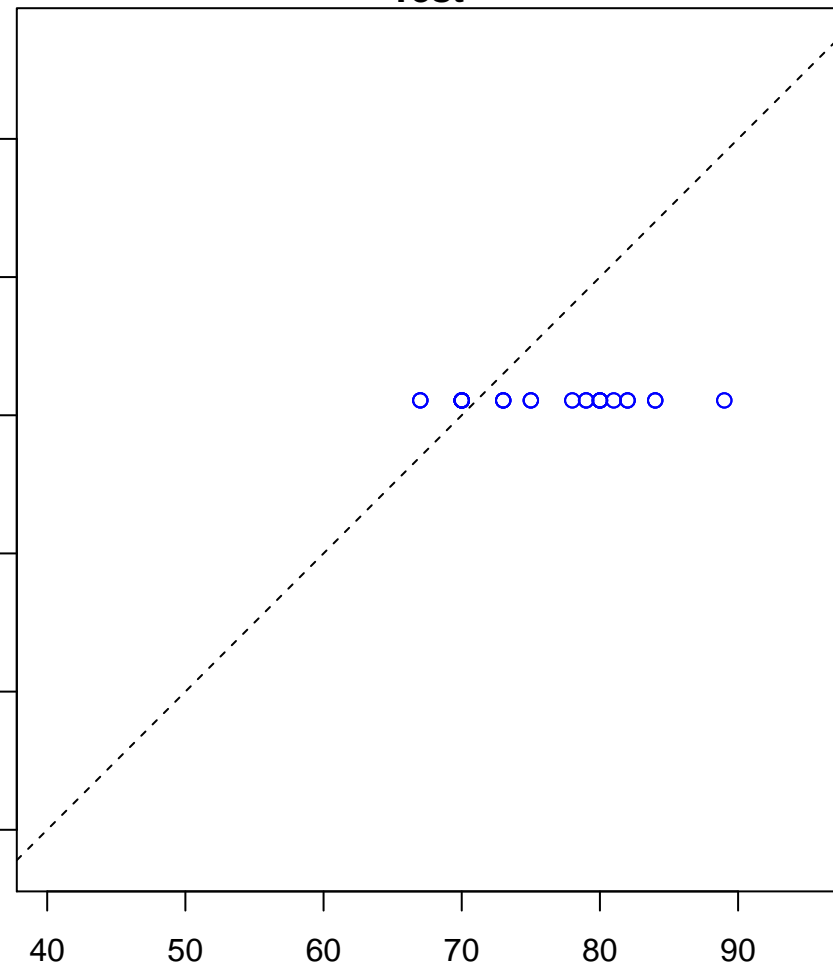
Actual Age

regulation of complement activation (Score: 0.798831)

Control



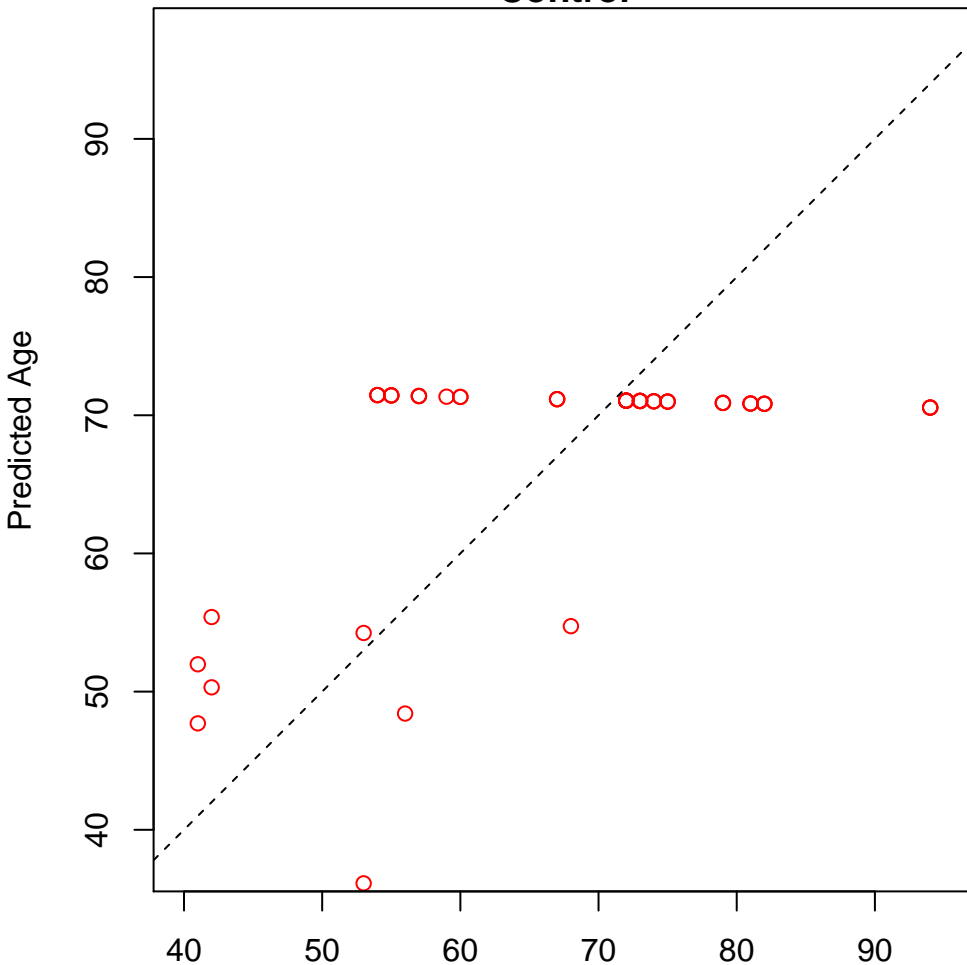
Test



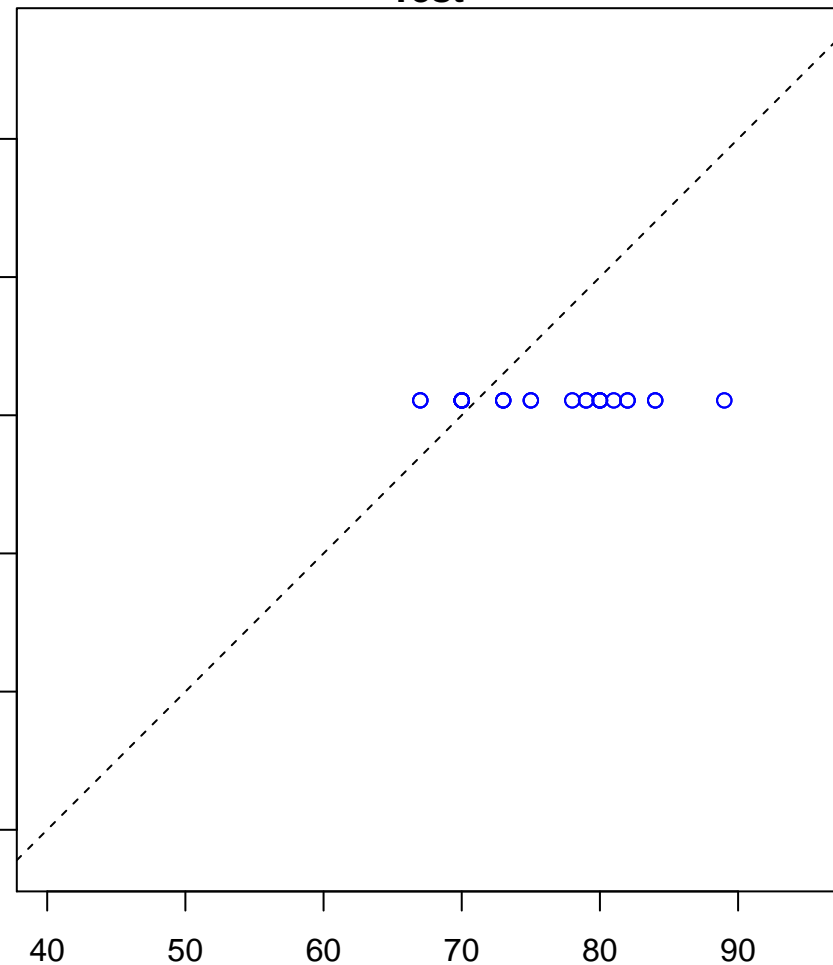
Actual Age

regulation of protein activation cascade (Score: 0.798831)

Control



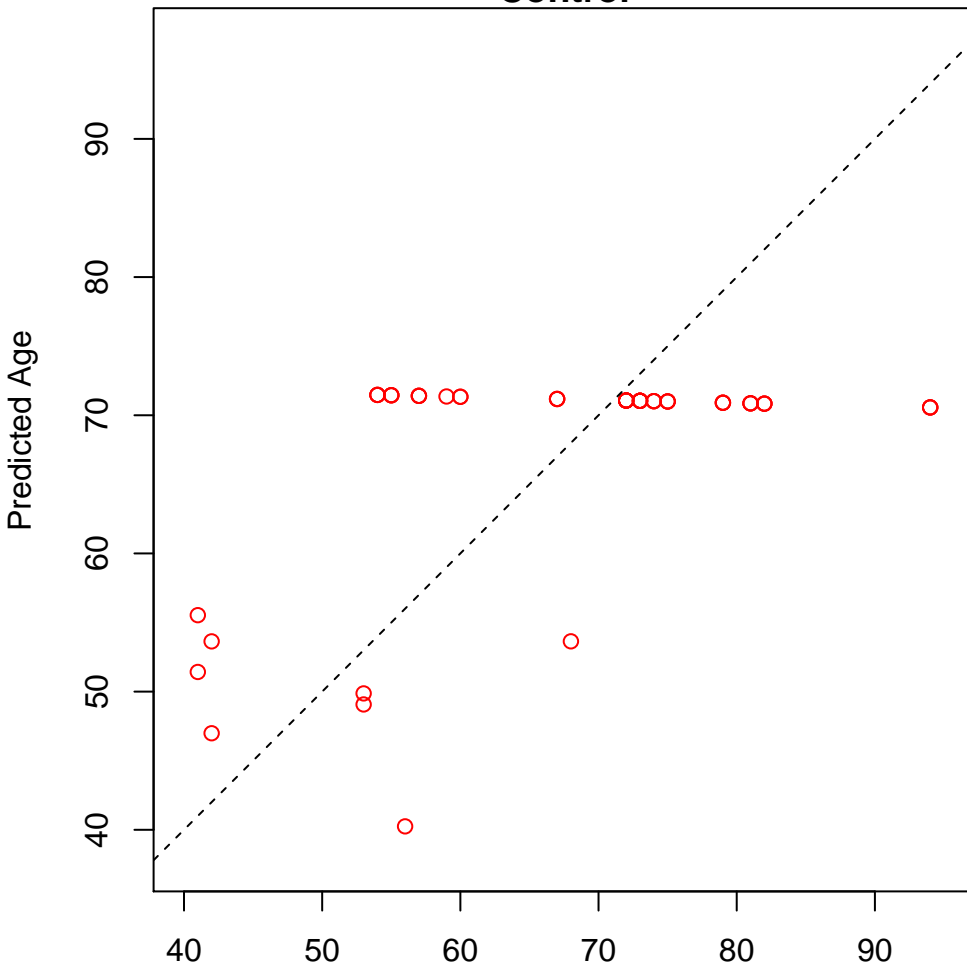
Test



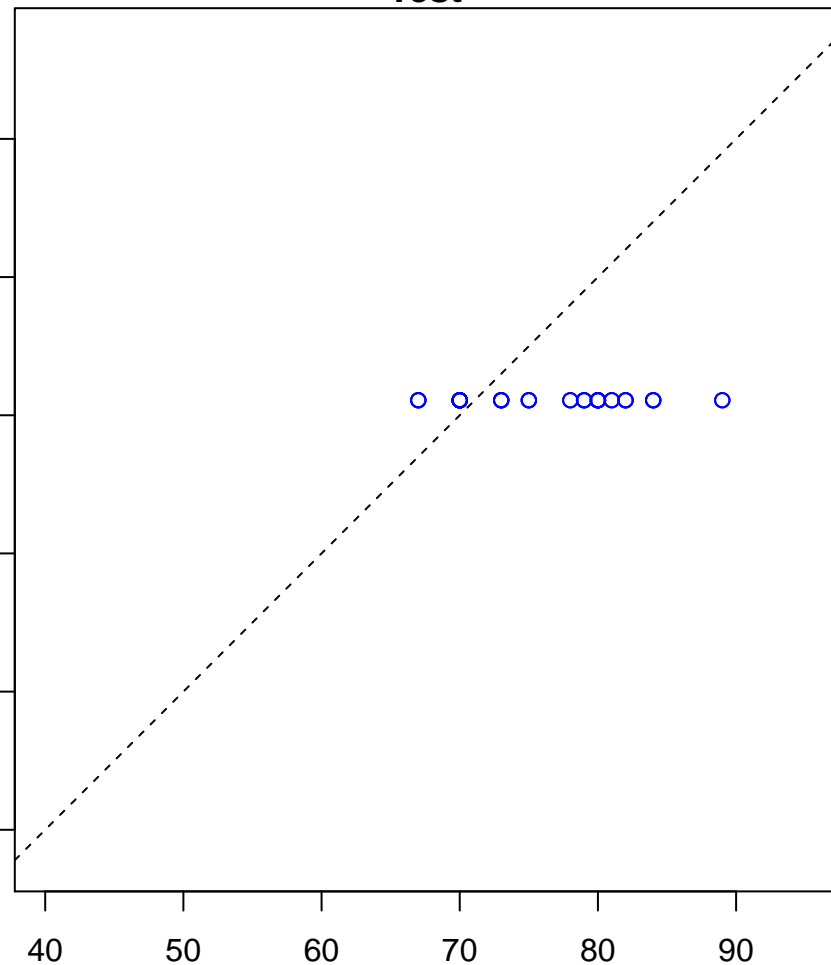
Actual Age

macromolecule metabolic process (Score: 0.798829)

Control



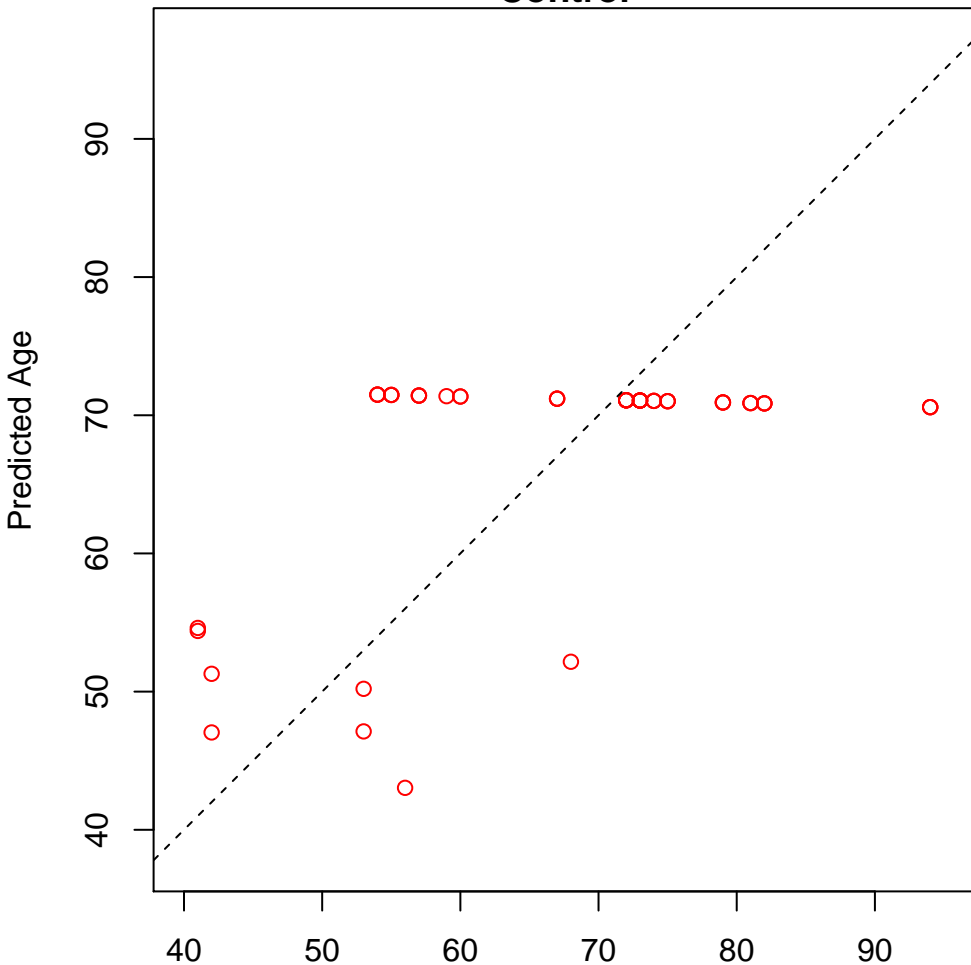
Test



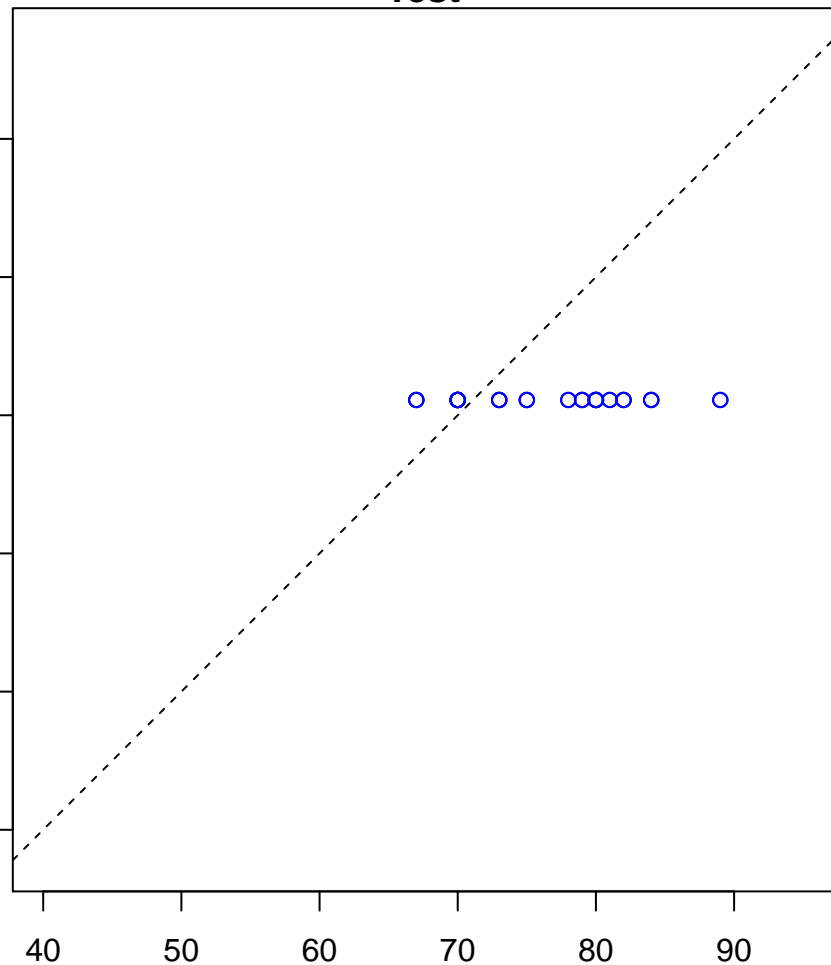
Actual Age

cellular protein modification process (Score: 0.798804)

Control

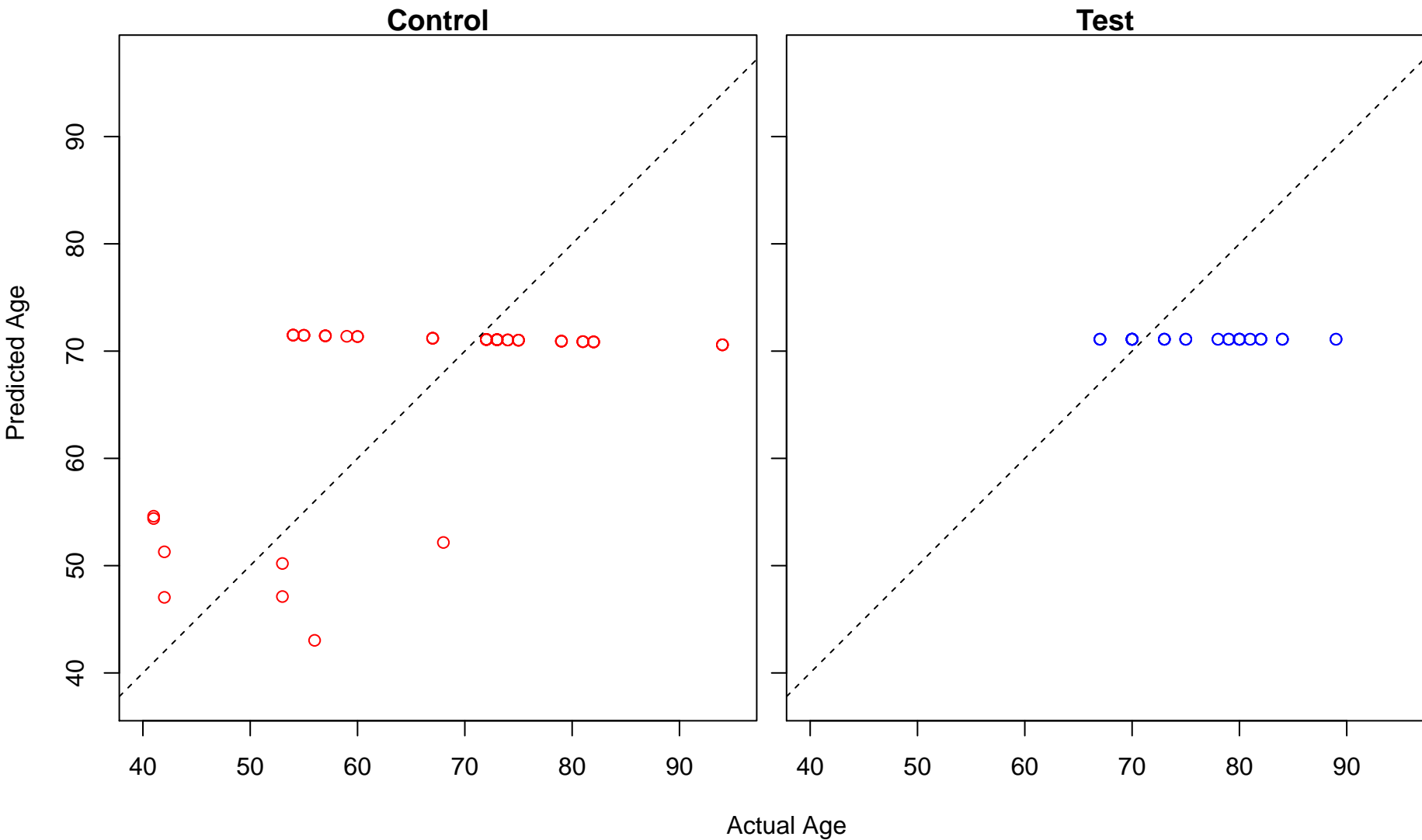


Test

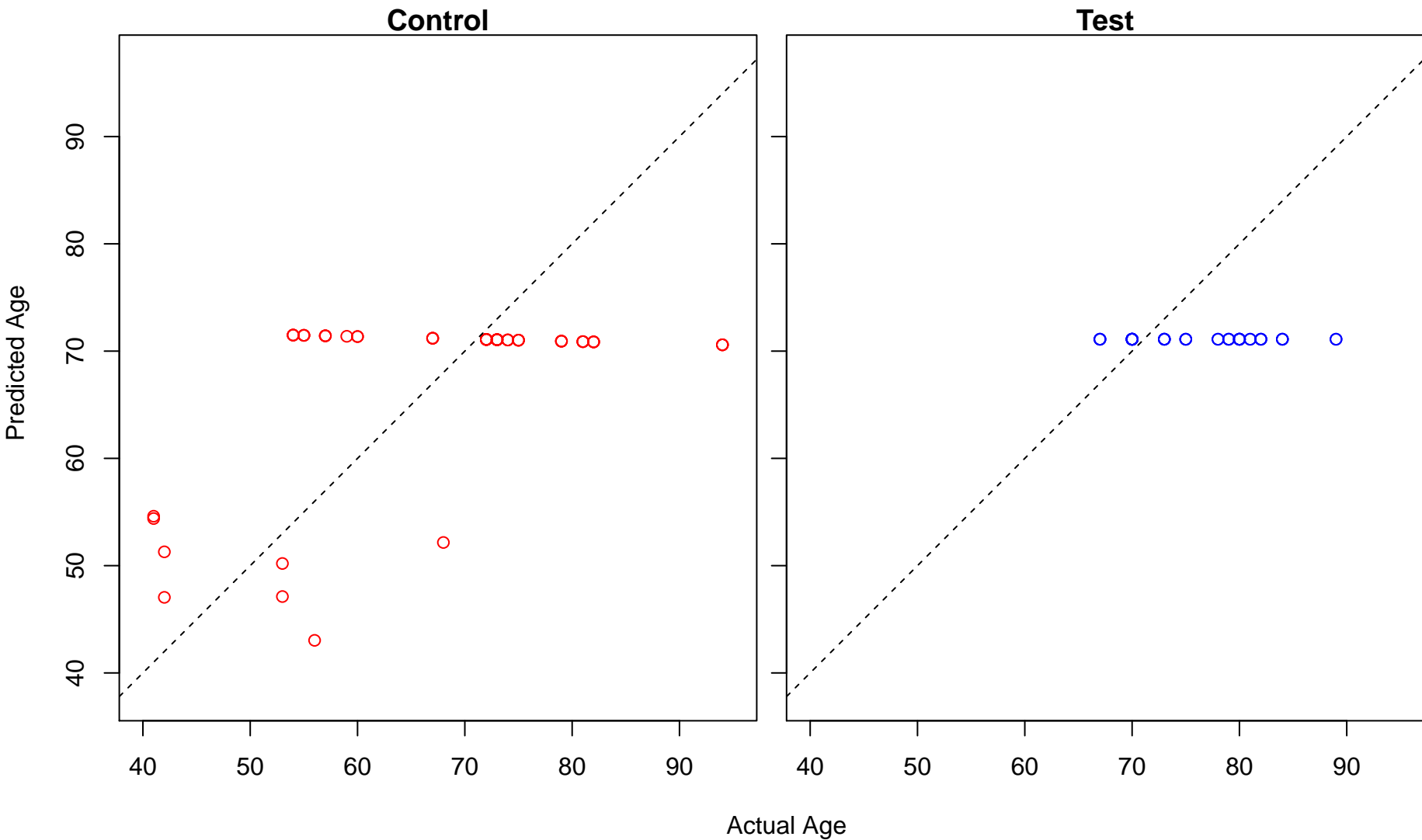


Actual Age

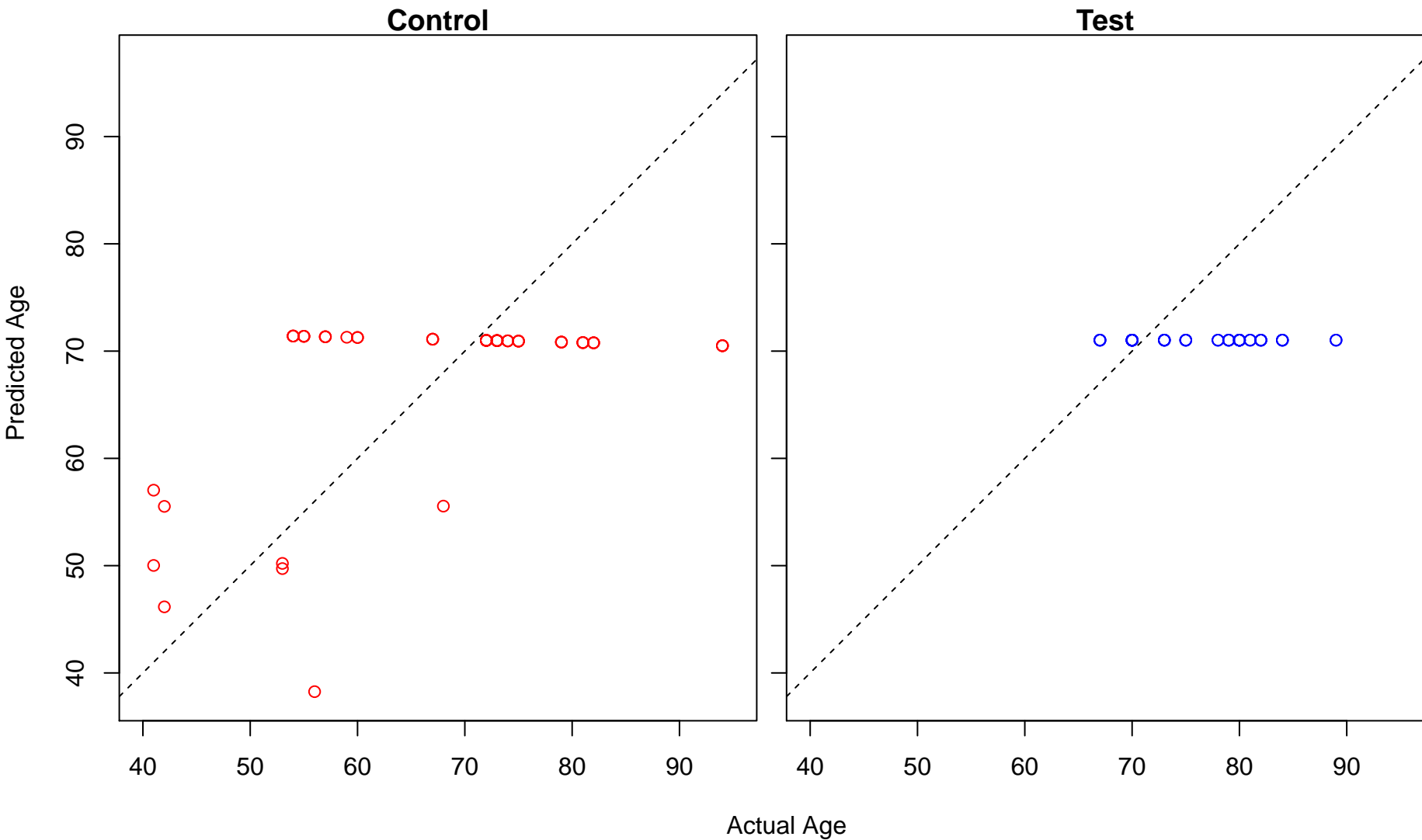
protein modification process (Score: 0.798804)



macromolecule modification (Score: 0.798804)

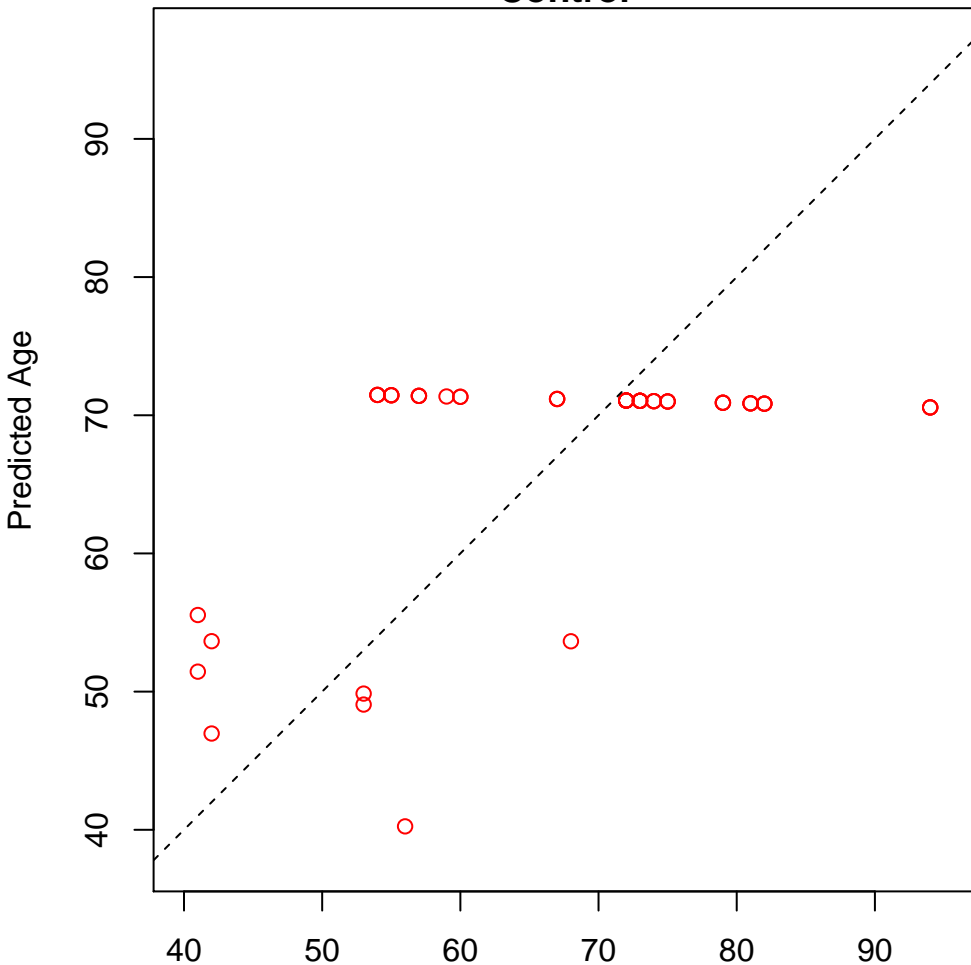


nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (Score: 0.798798)

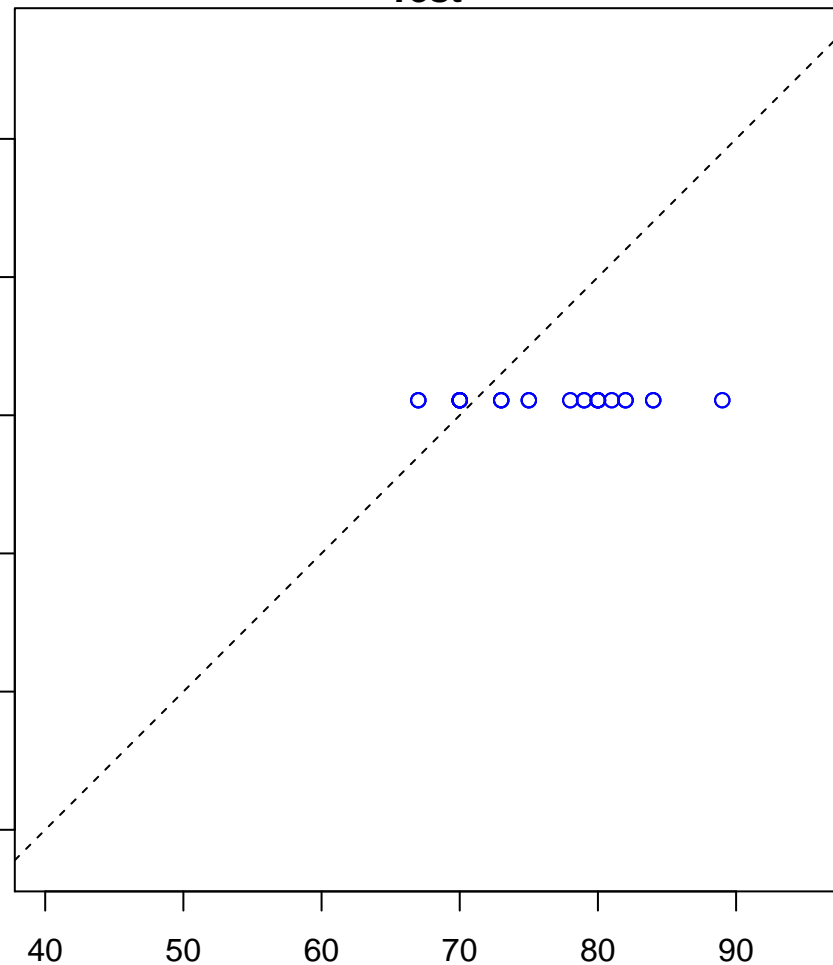


cellular macromolecule metabolic process (Score: 0.798795)

Control

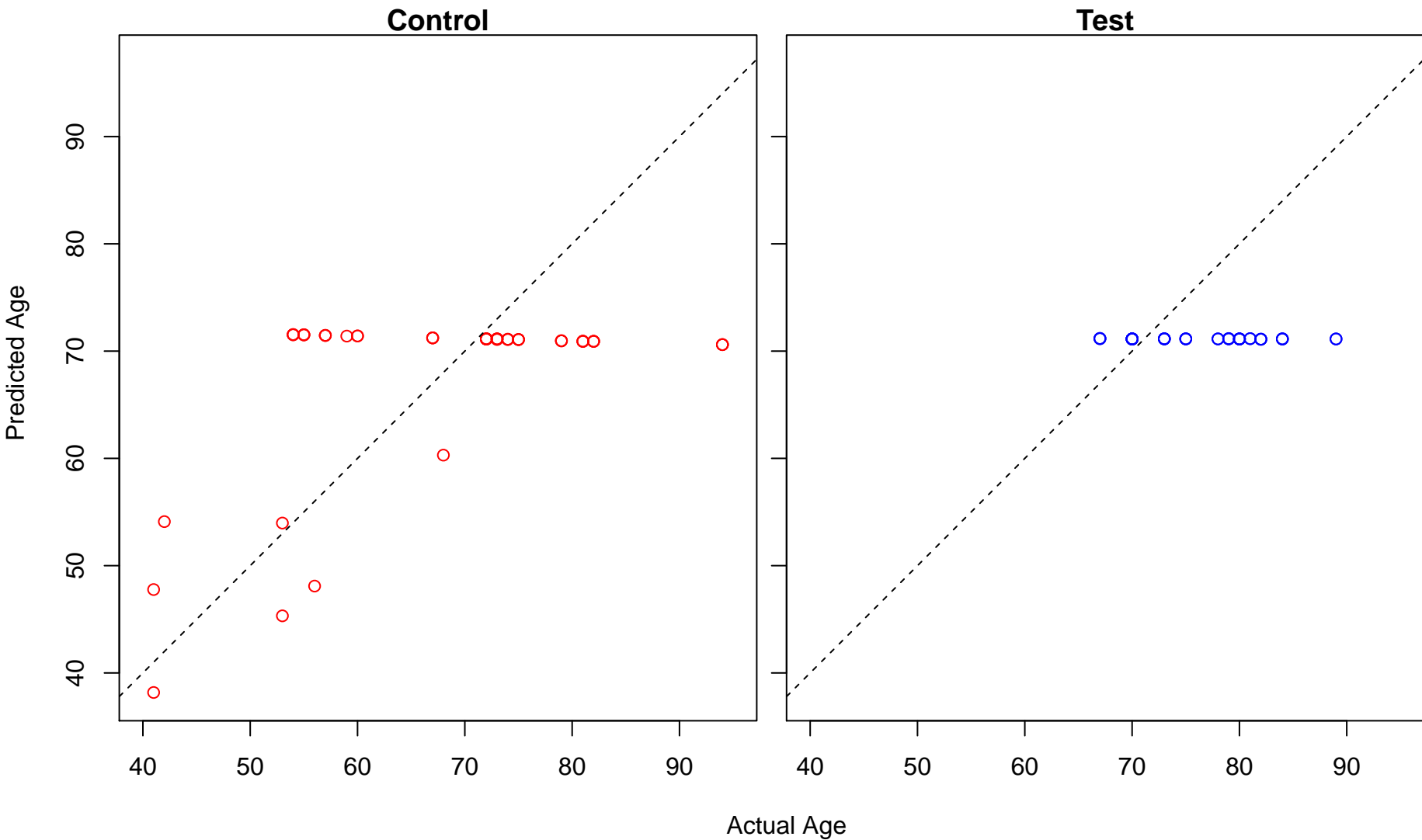


Test

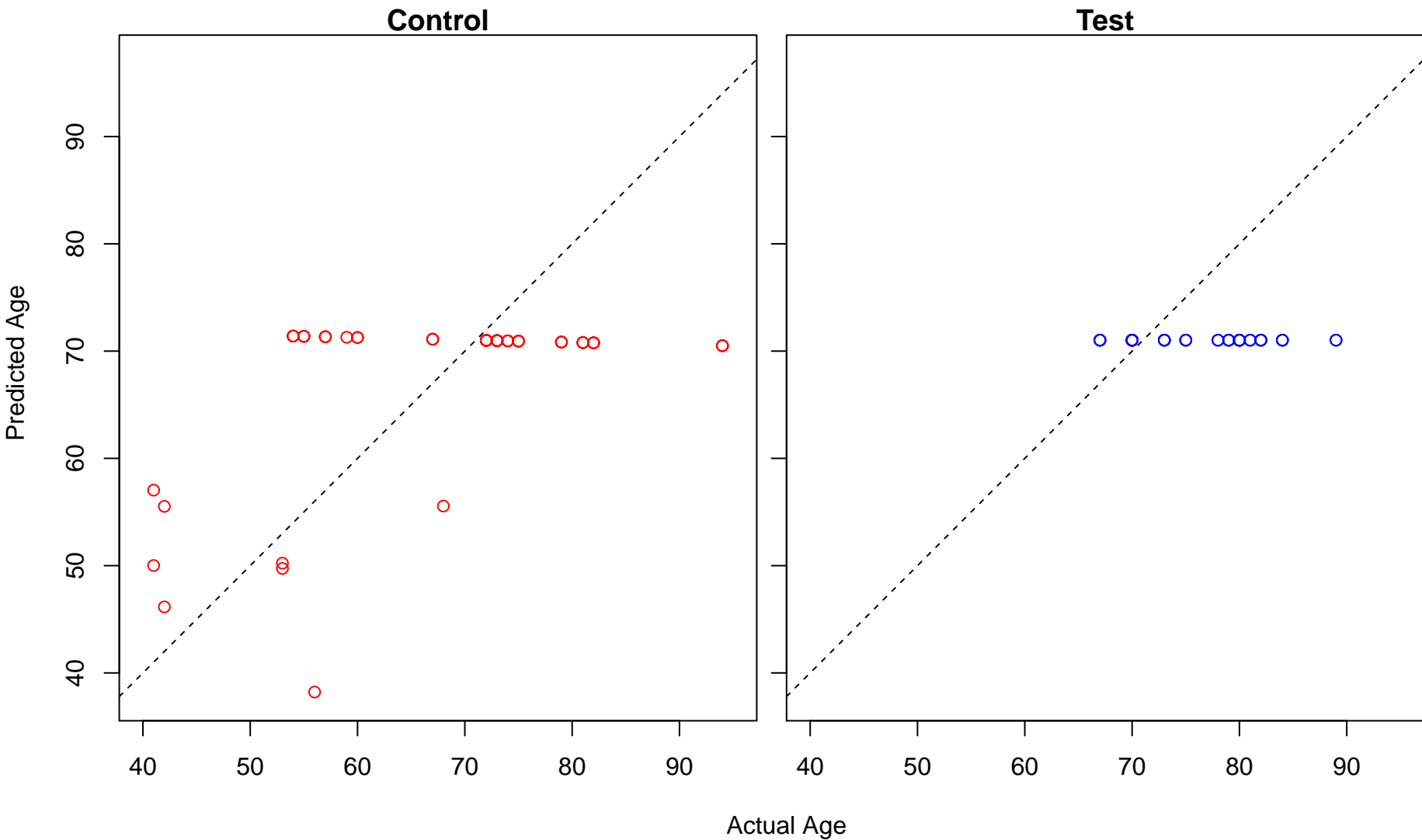


Actual Age

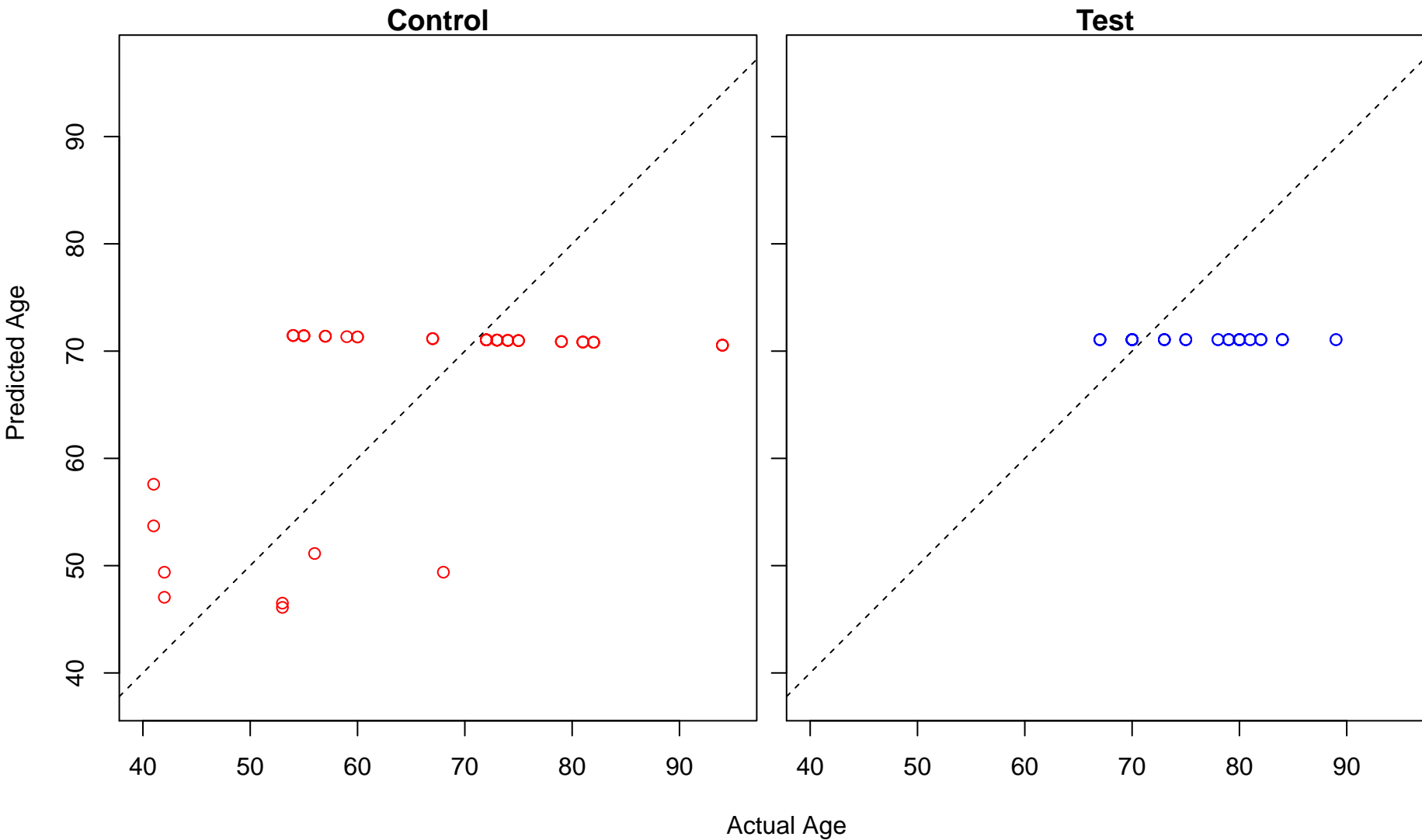
cell migration (Score: 0.798790)



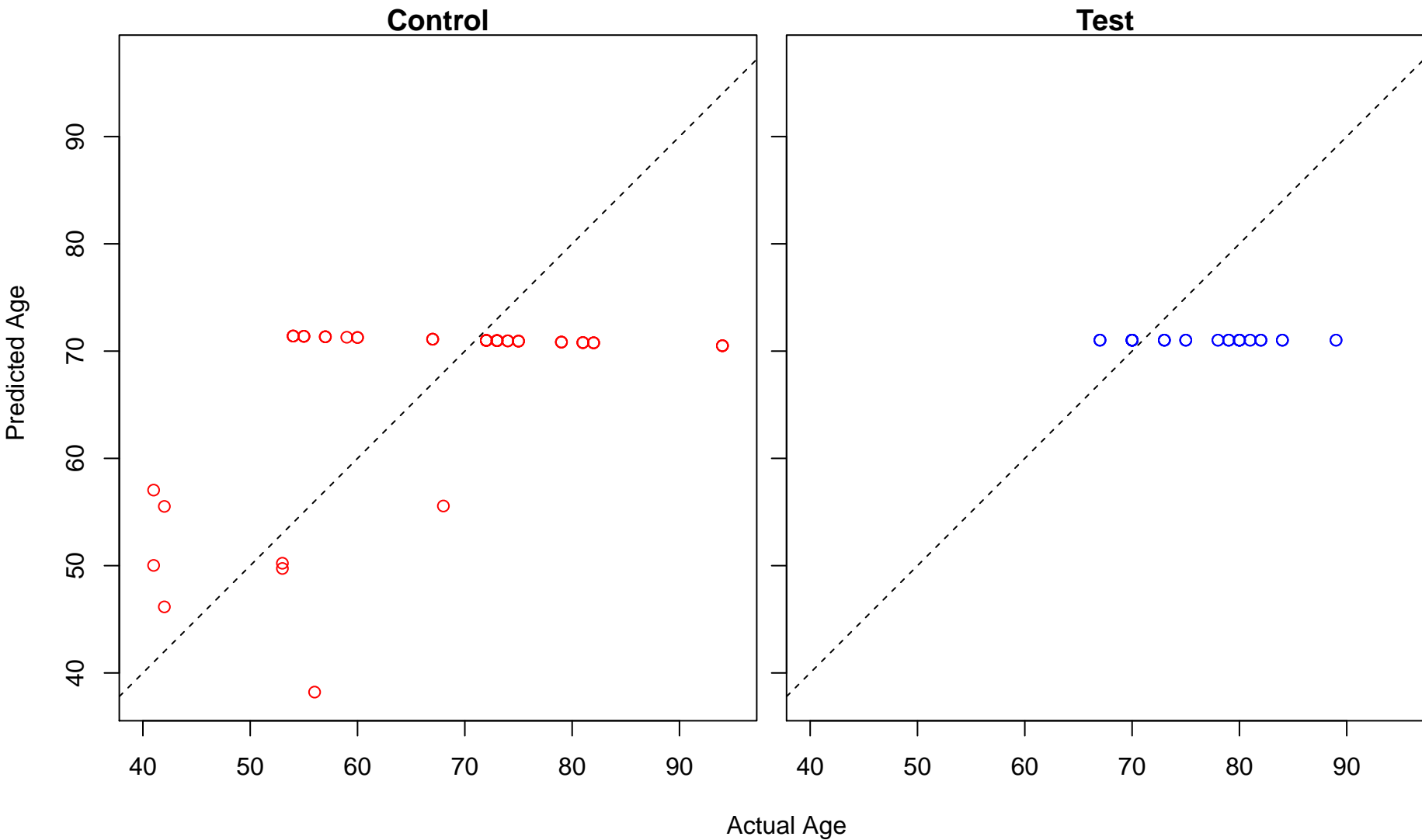
viral gene expression (Score: 0.798789)



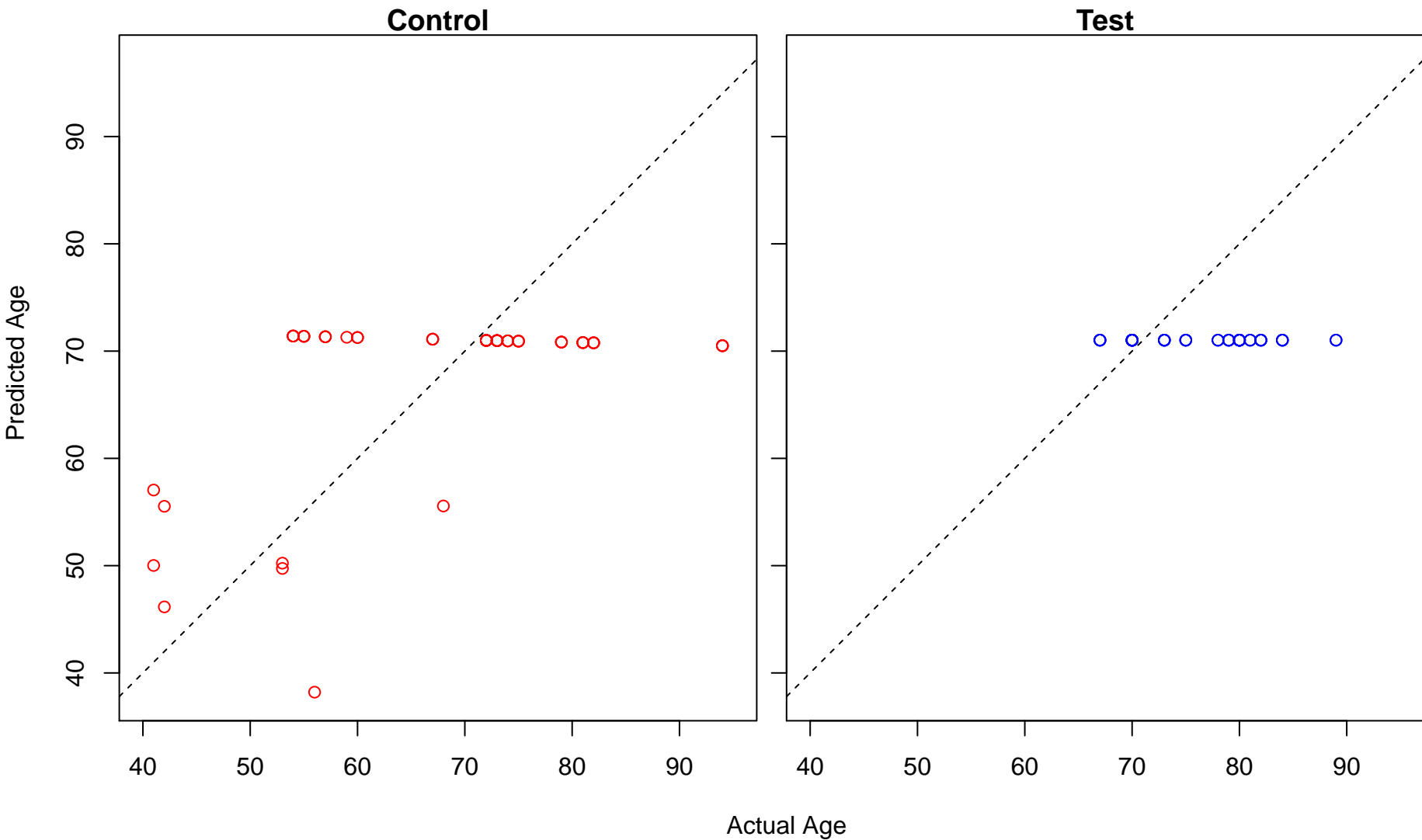
negative regulation of apoptotic signaling pathway (Score: 0.798778)



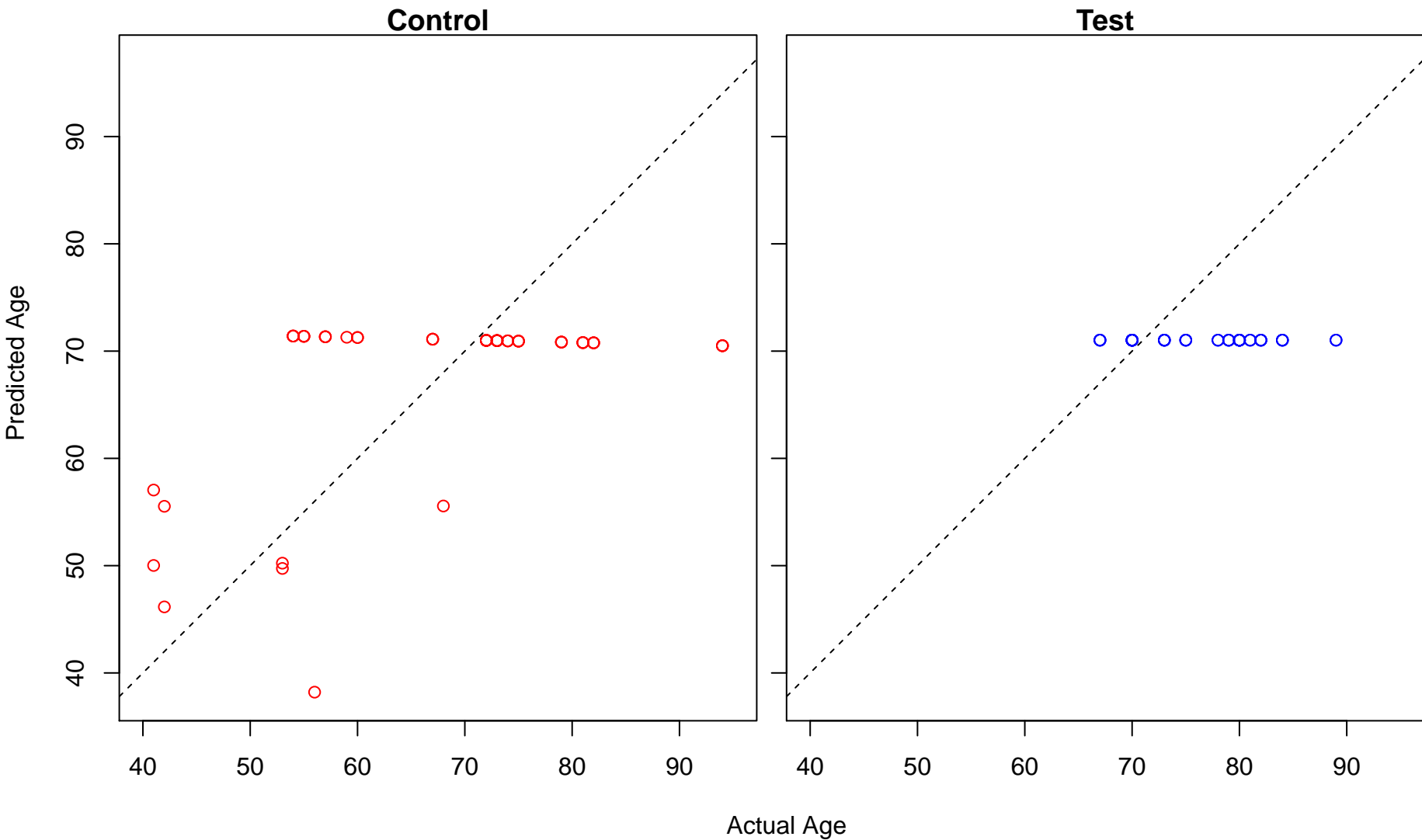
ncRNA processing (Score: 0.798777)



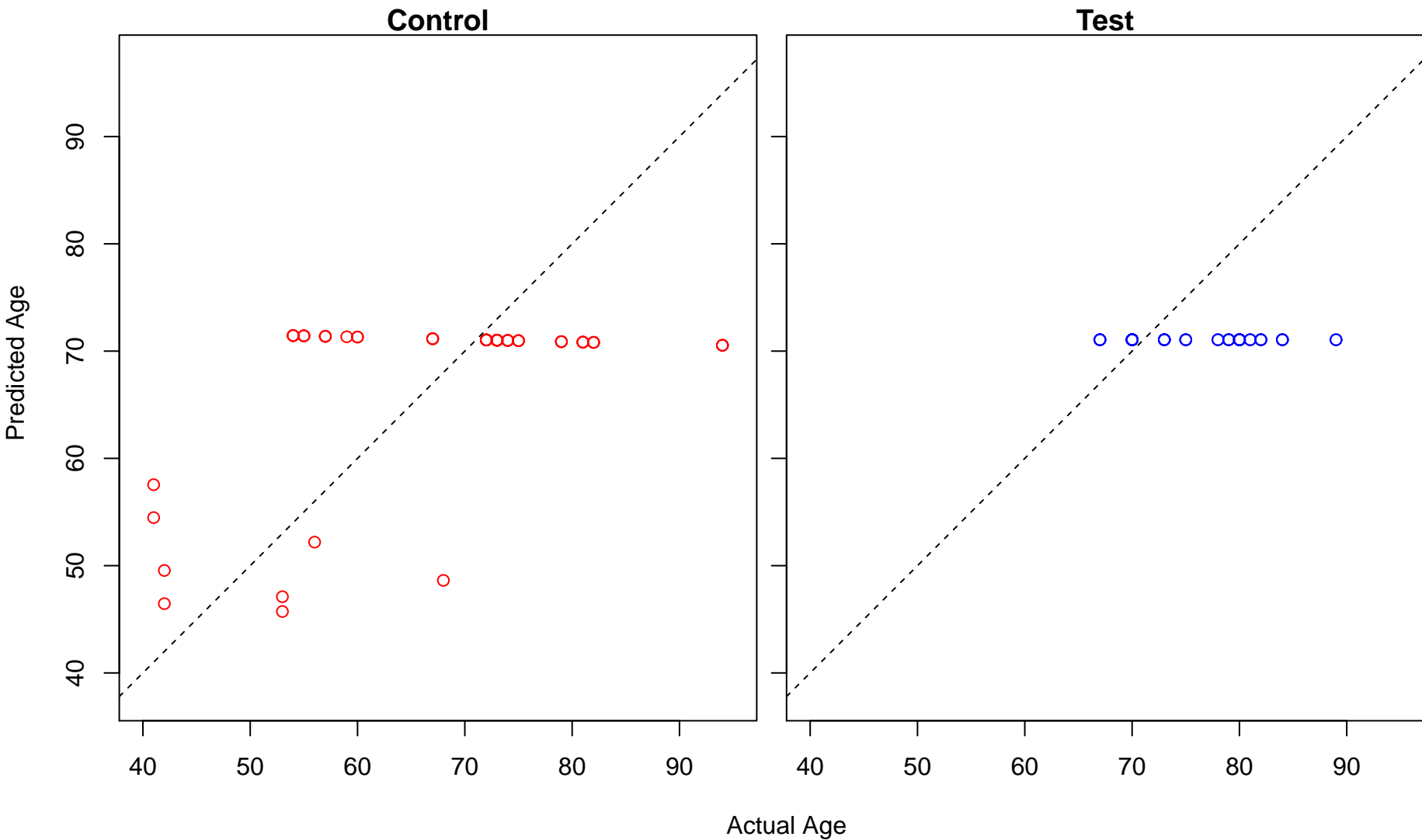
rRNA processing (Score: 0.798773)



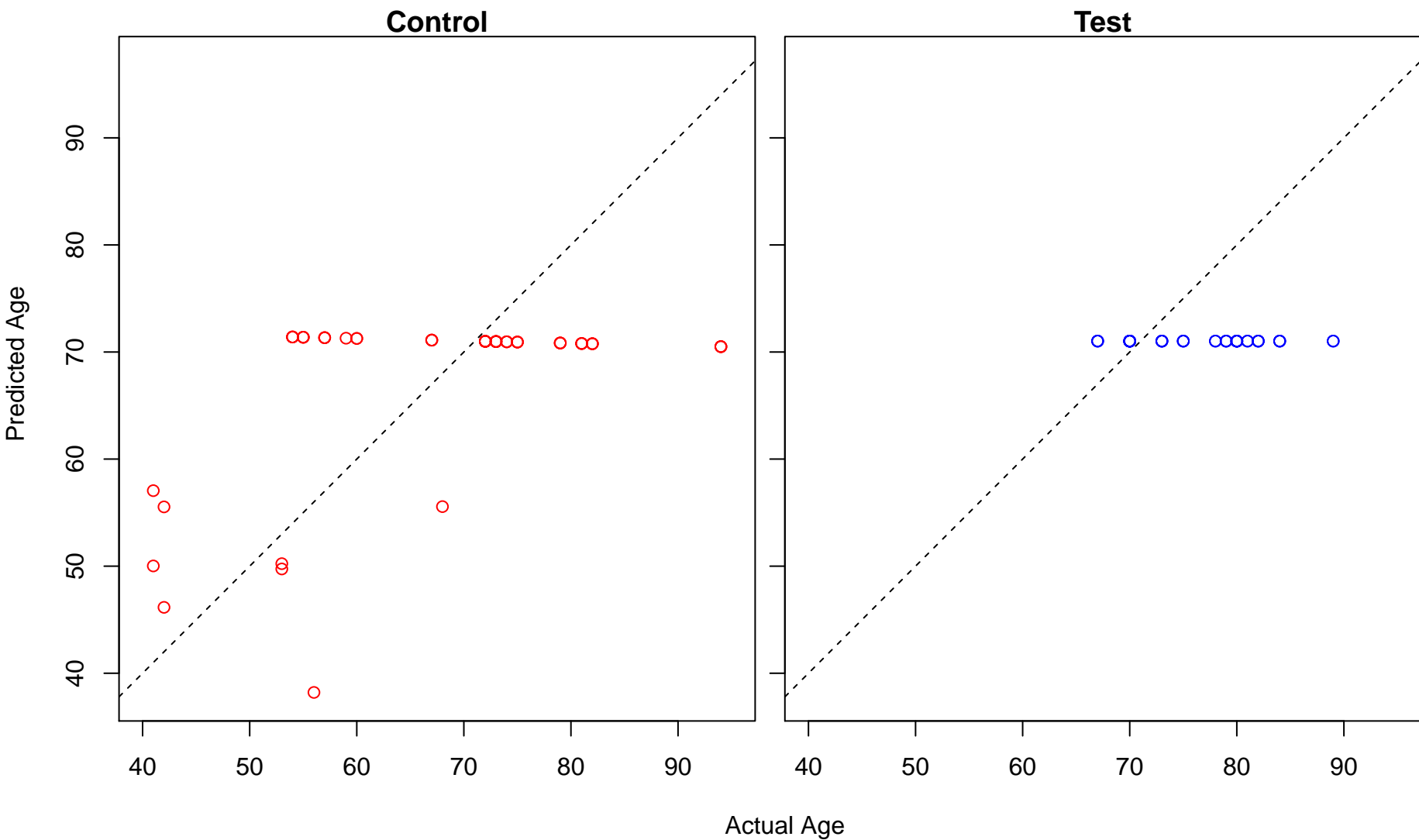
rRNA metabolic process (Score: 0.798773)



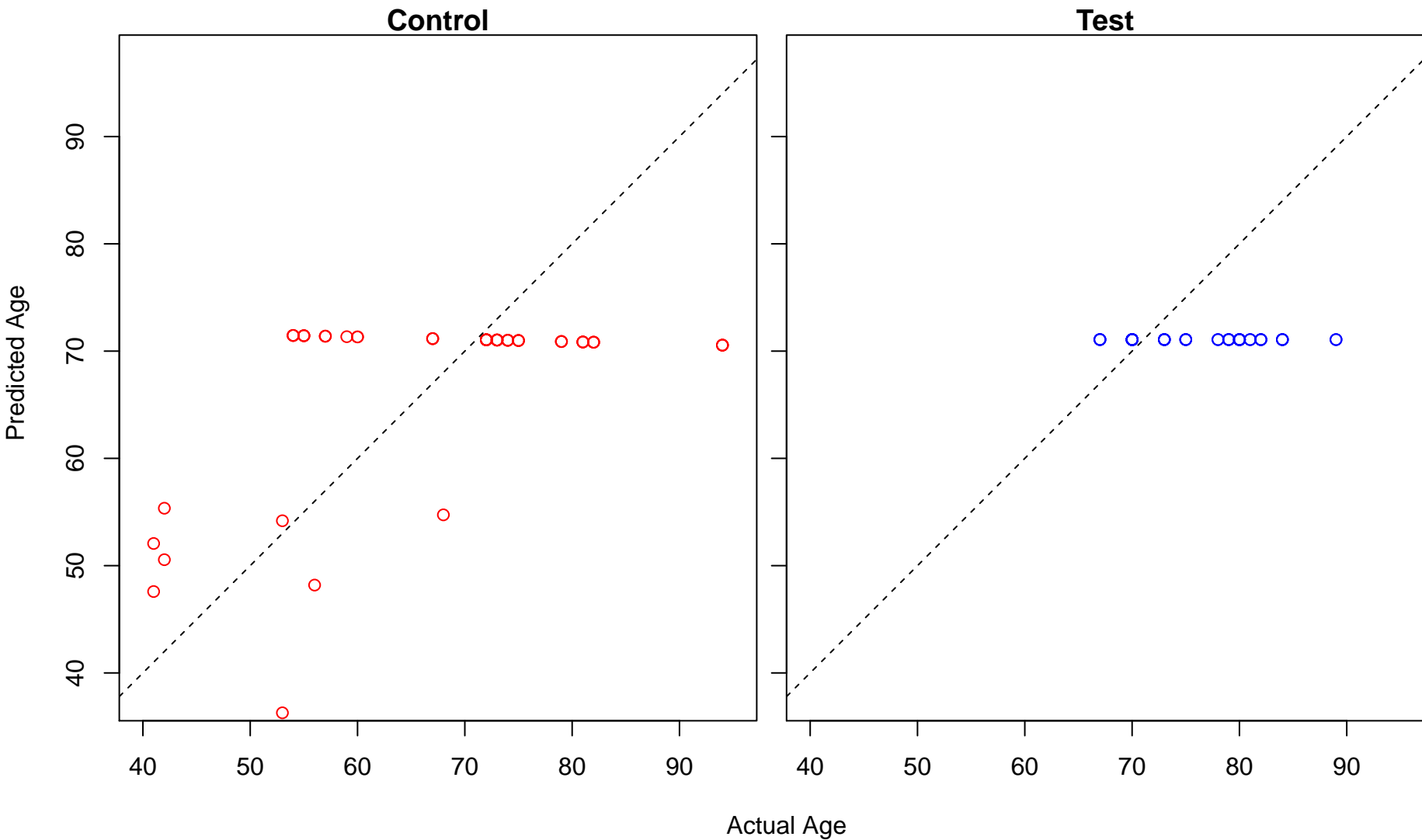
negative regulation of proteasomal protein catabolic process (Score: 0.798768)



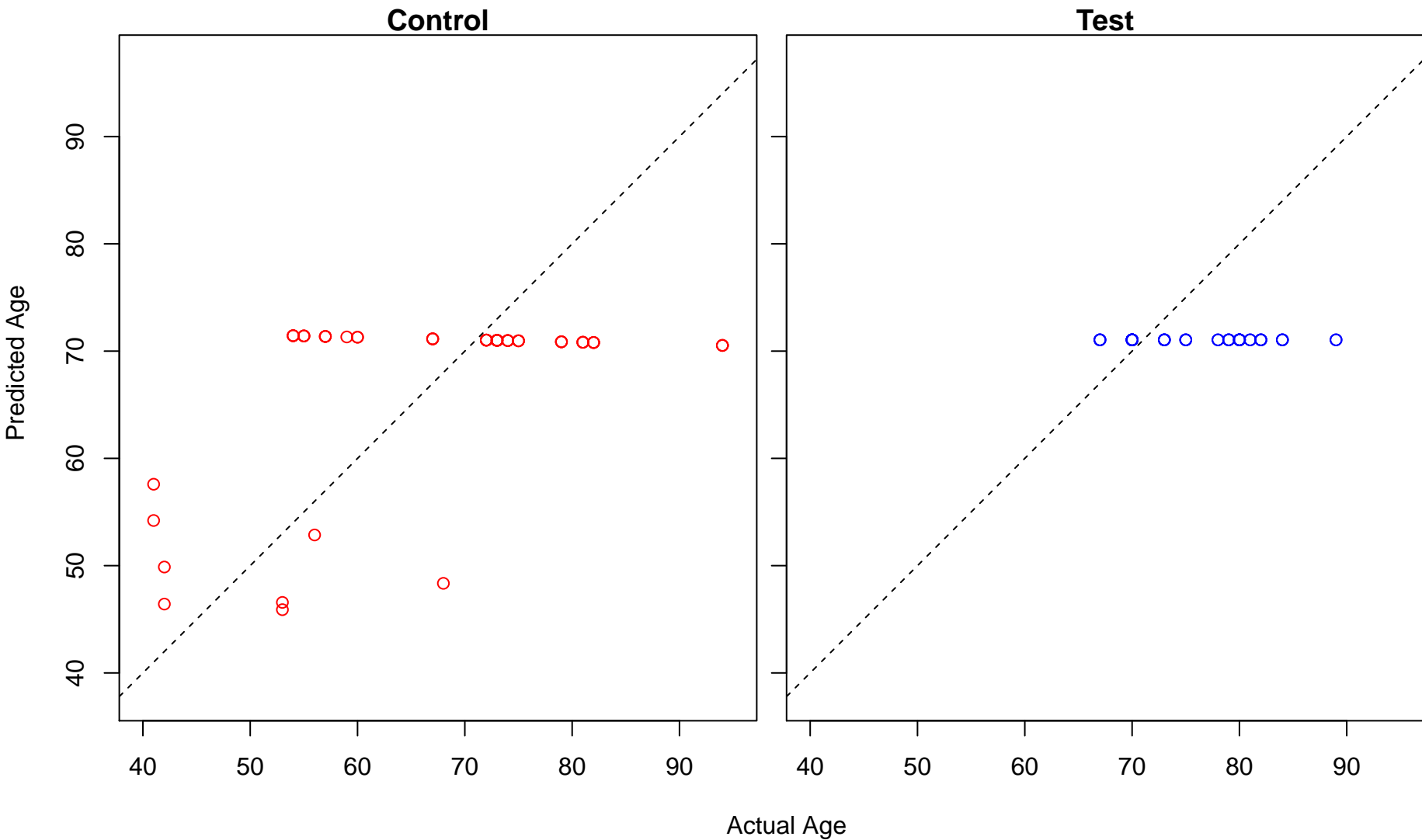
viral transcription (Score: 0.798768)



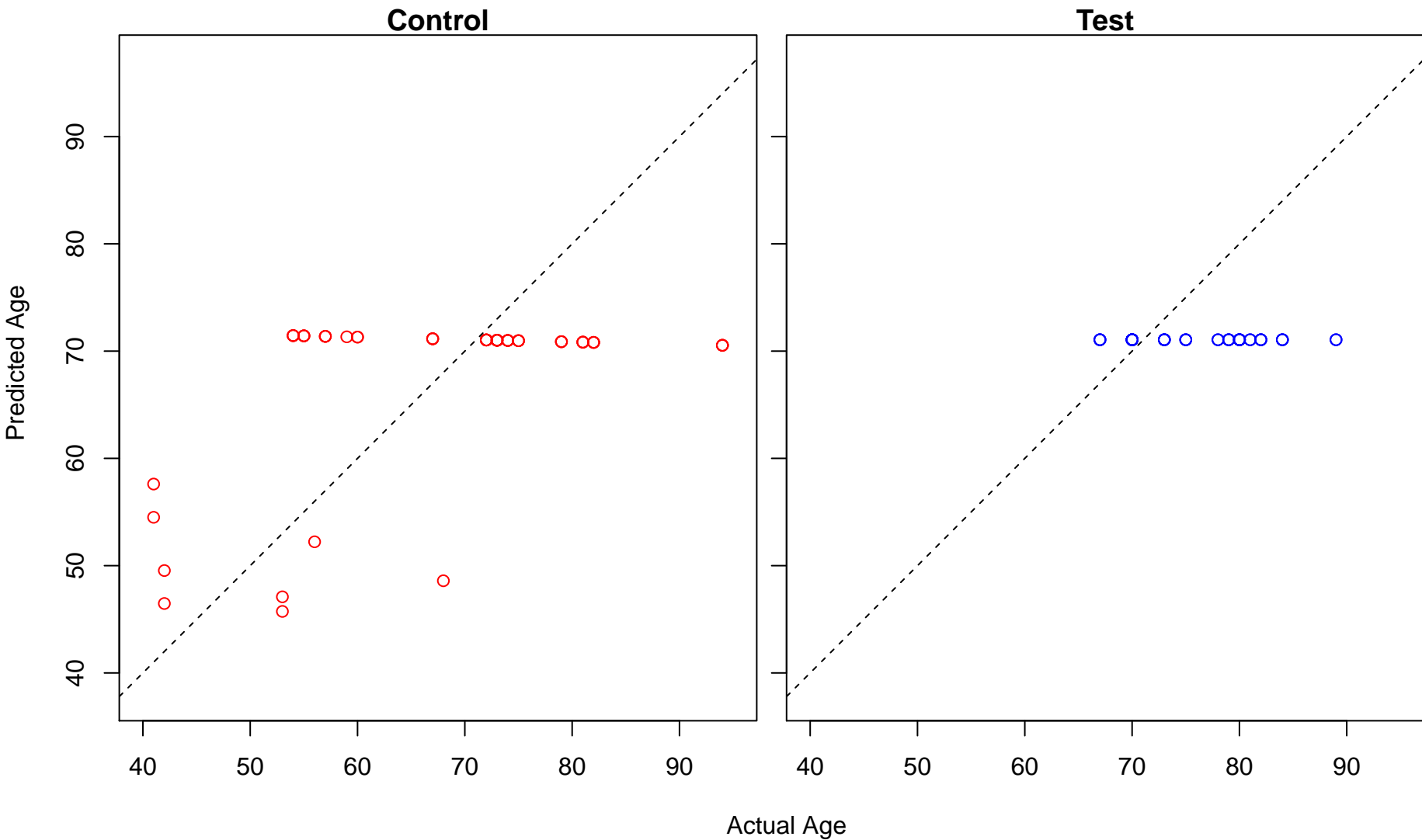
positive regulation of lipid metabolic process (Score: 0.798735)



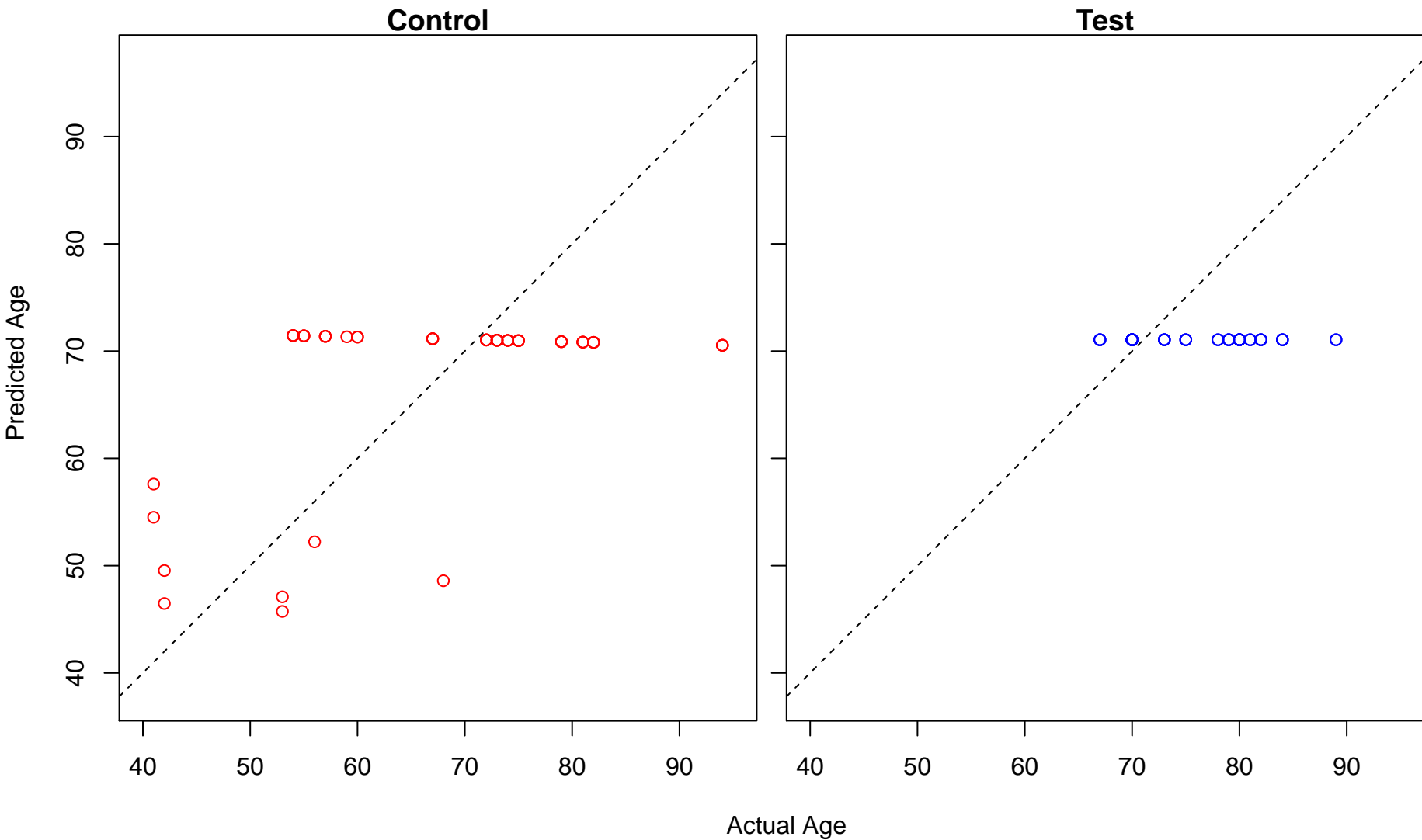
regulation of response to external stimulus (Score: 0.798696)



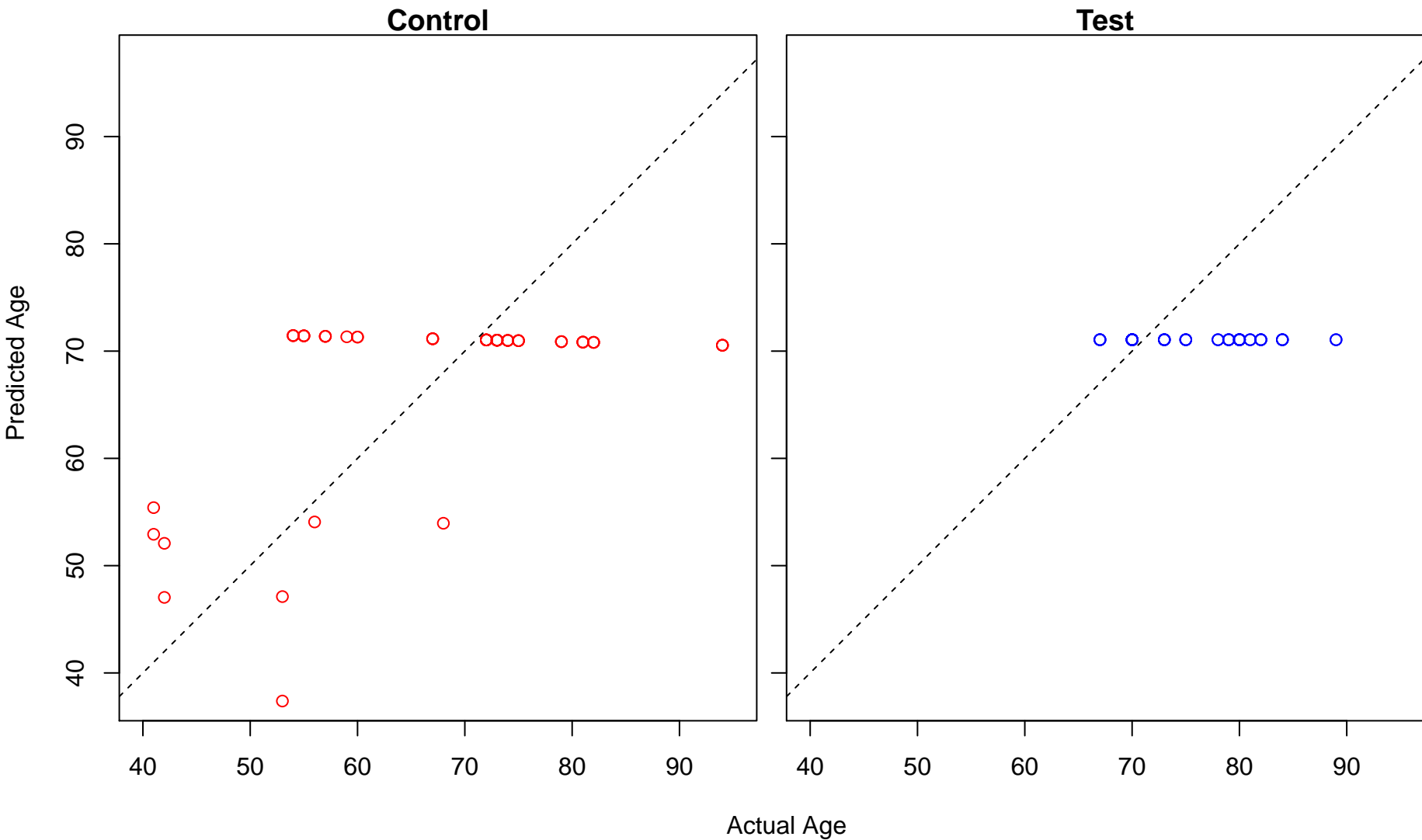
regulation of proteasomal ubiquitin-dependent protein catabolic process (Score: 0.798693)



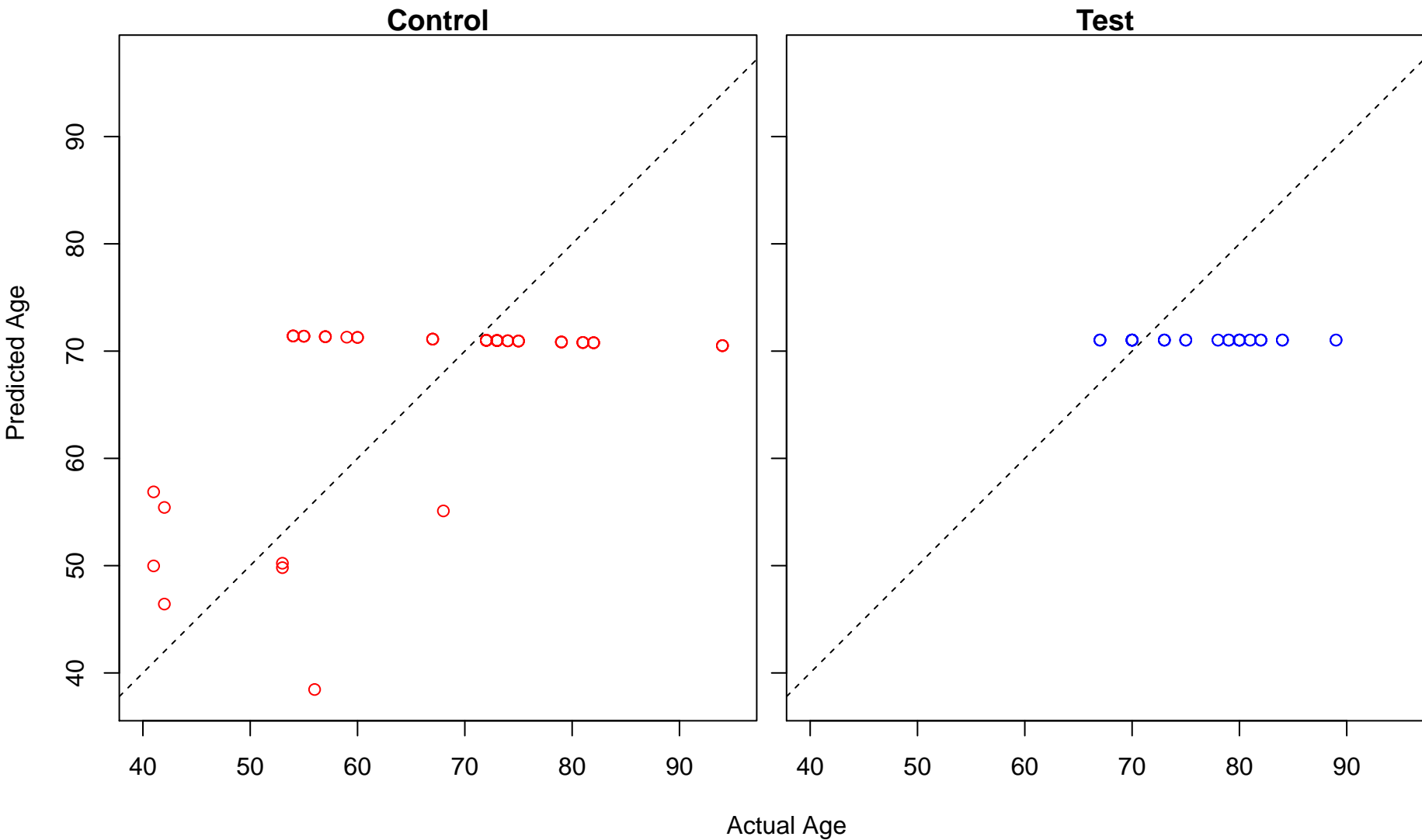
negative regulation of proteasomal ubiquitin-dependent protein catabolic process (Score: 0.79869)



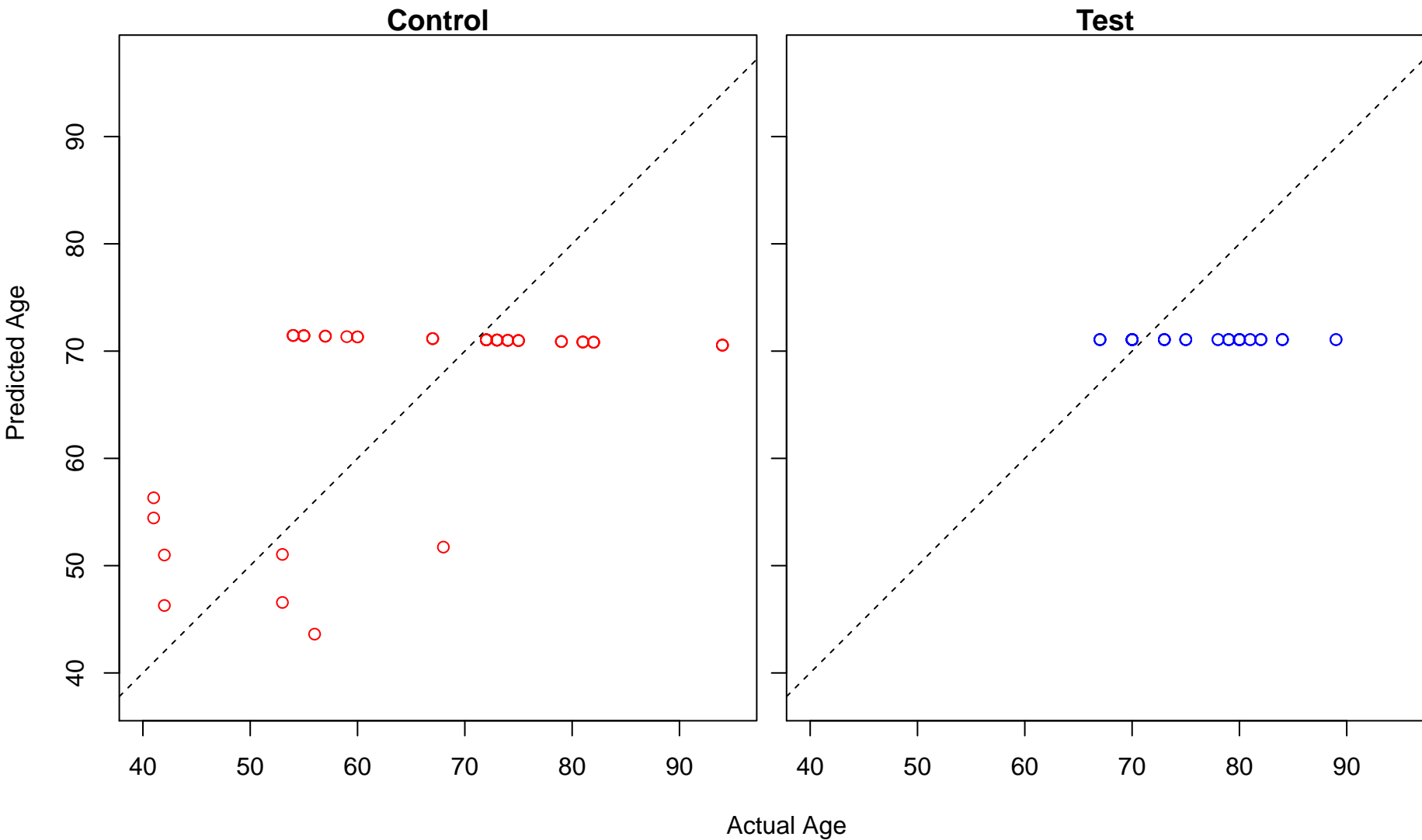
modification of morphology or physiology of other organism (Score: 0.798684)



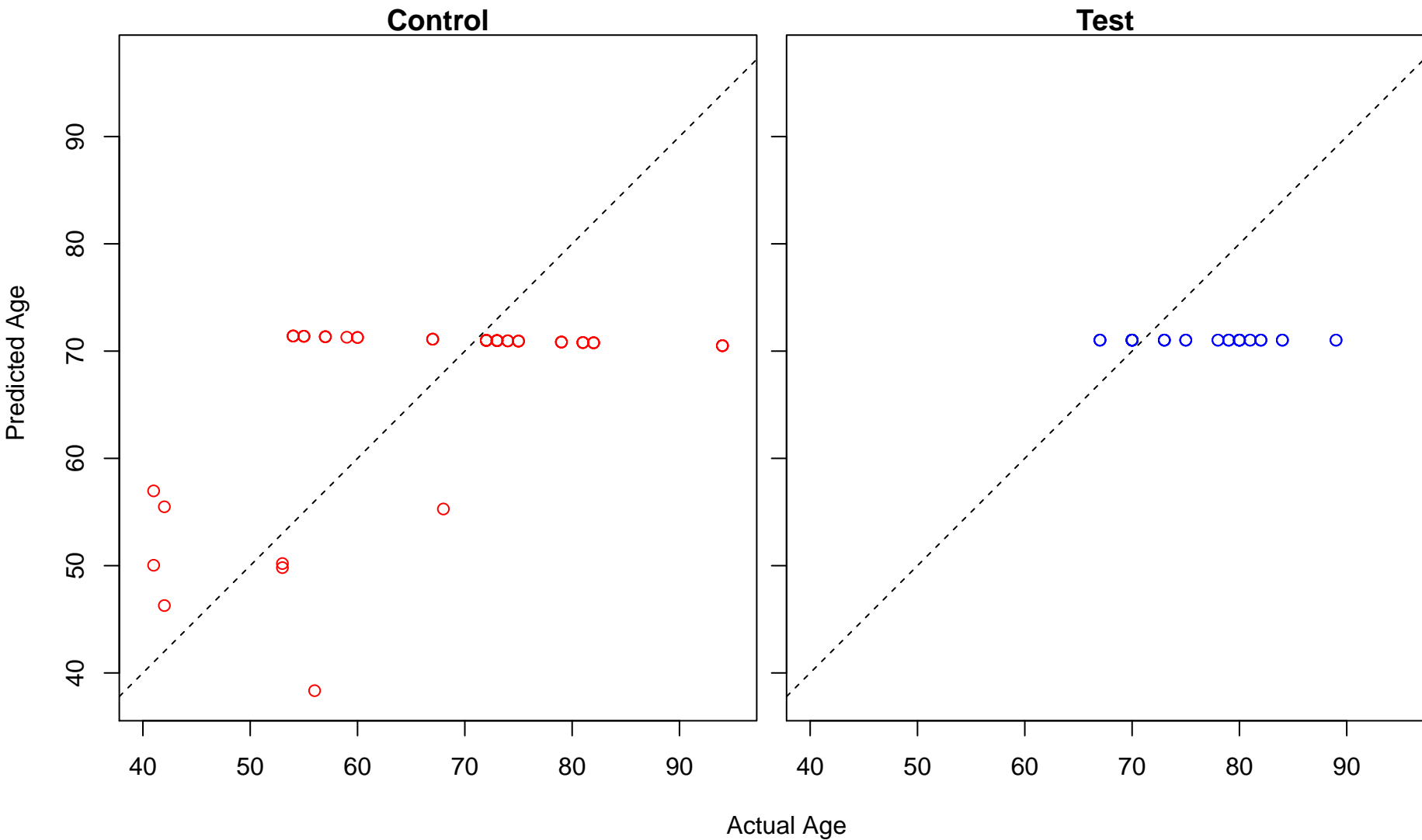
RNA processing (Score: 0.798667)



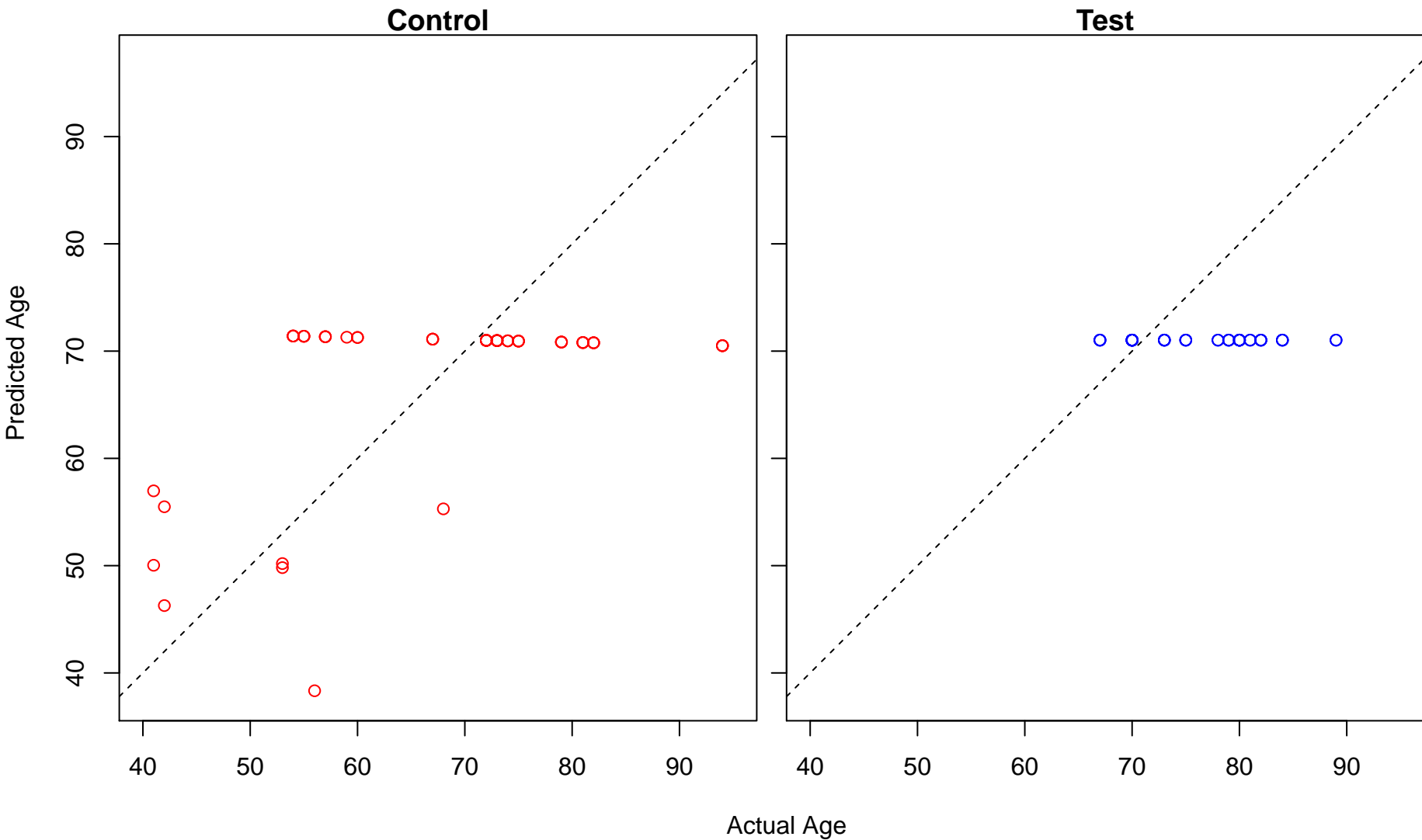
cellular response to DNA damage stimulus (Score: 0.798658)



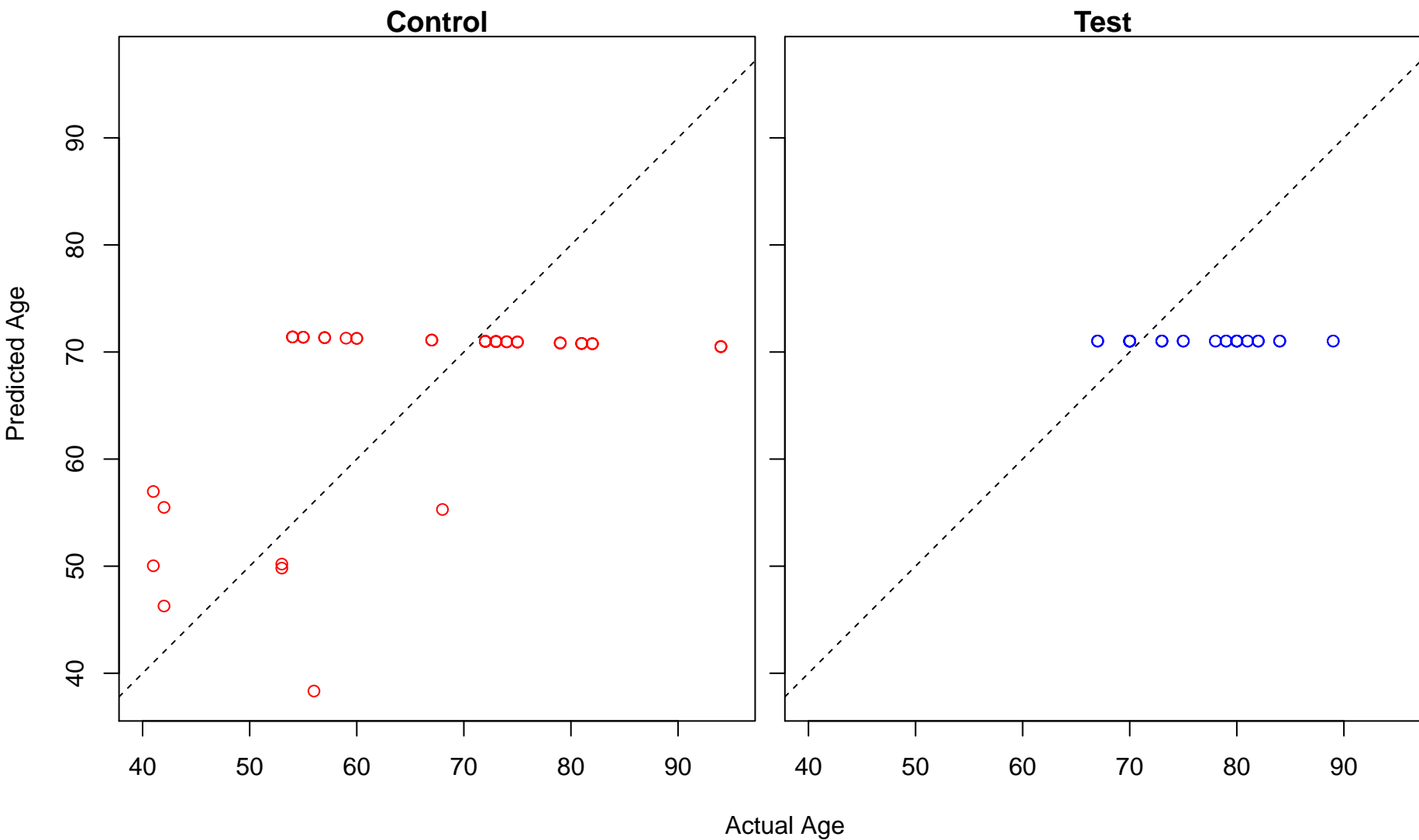
RNA catabolic process (Score: 0.798658)



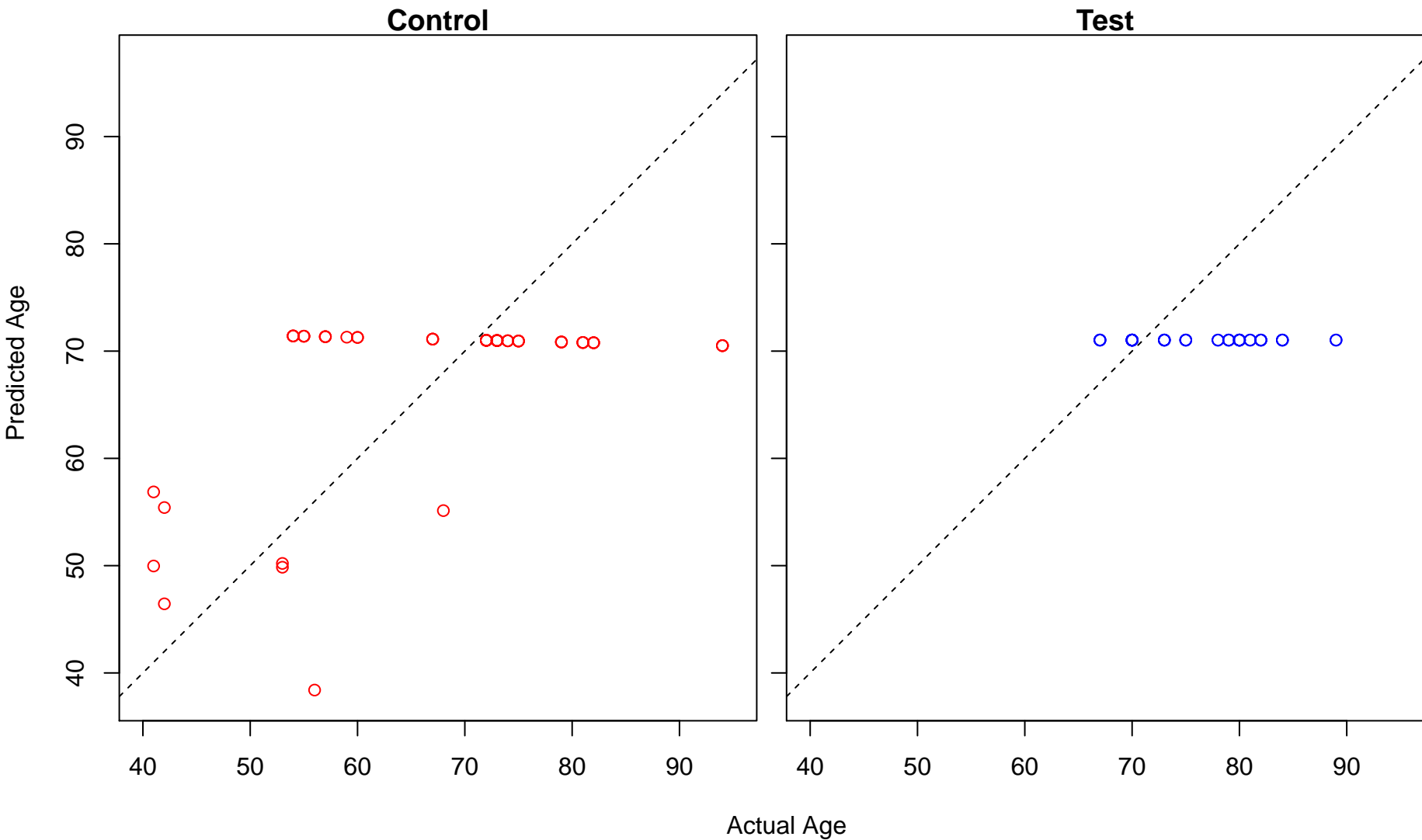
nuclear-transcribed mRNA catabolic process (Score: 0.798657)



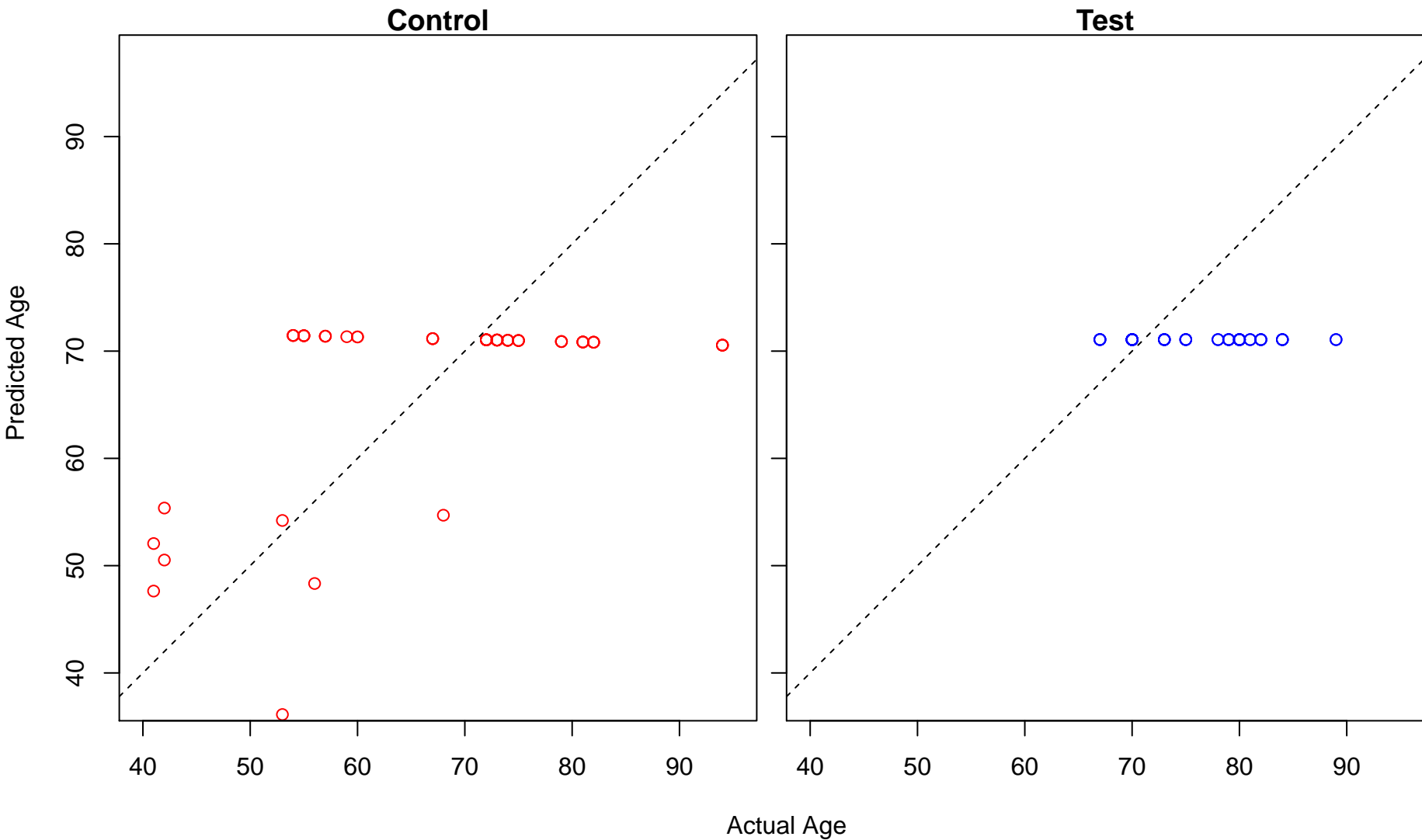
mRNA catabolic process (Score: 0.798657)



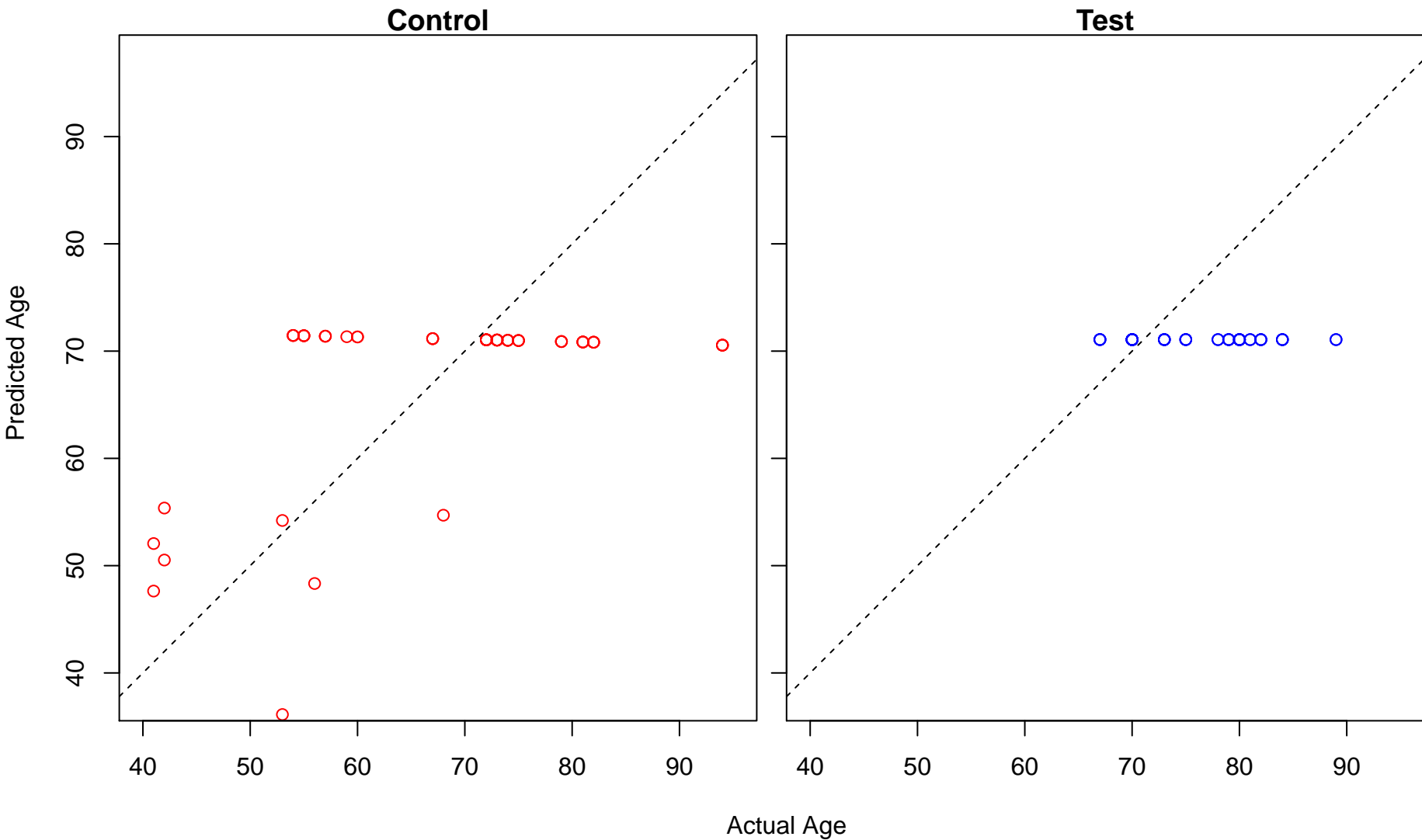
mRNA metabolic process (Score: 0.798655)



regulation of protein catabolic process in the vacuole (Score: 0.798602)

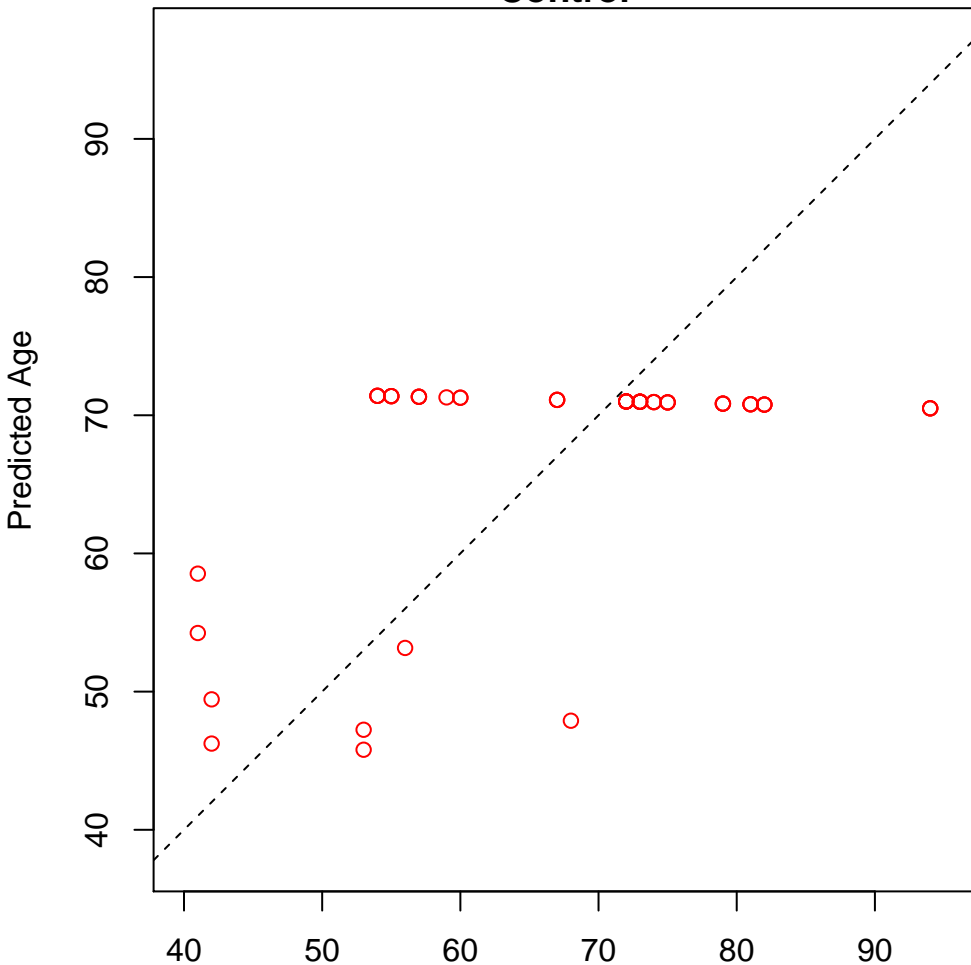


positive regulation of protein catabolic process in the vacuole (Score: 0.798602)

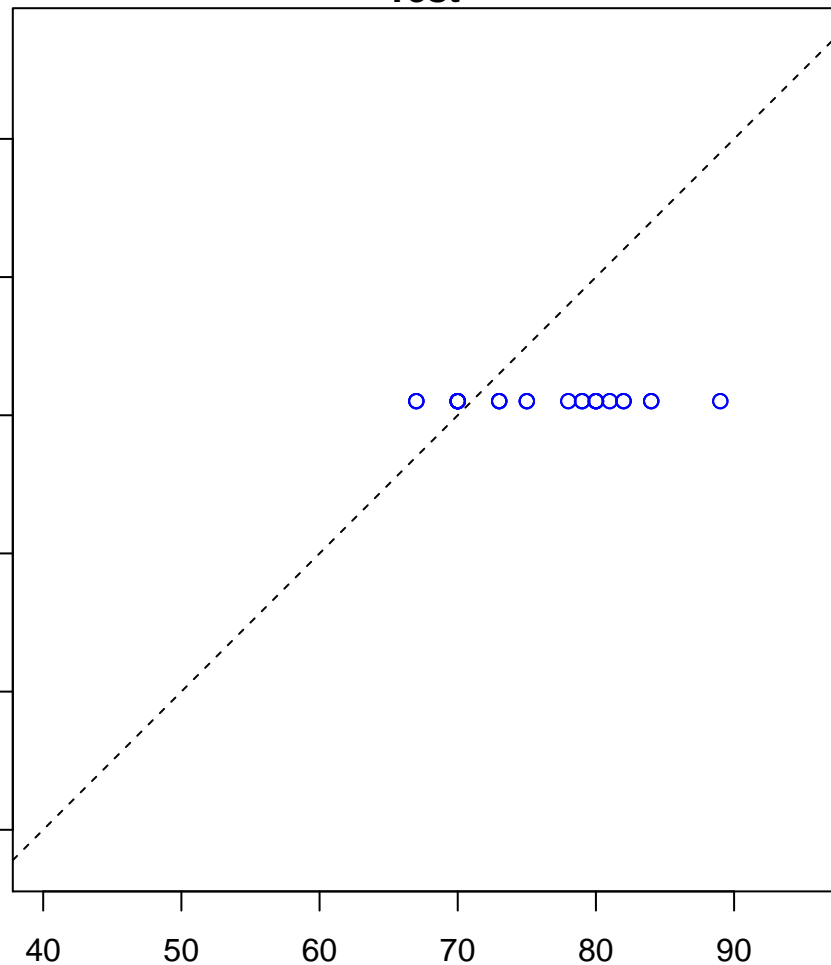


monocarboxylic acid biosynthetic process (Score: 0.798599)

Control

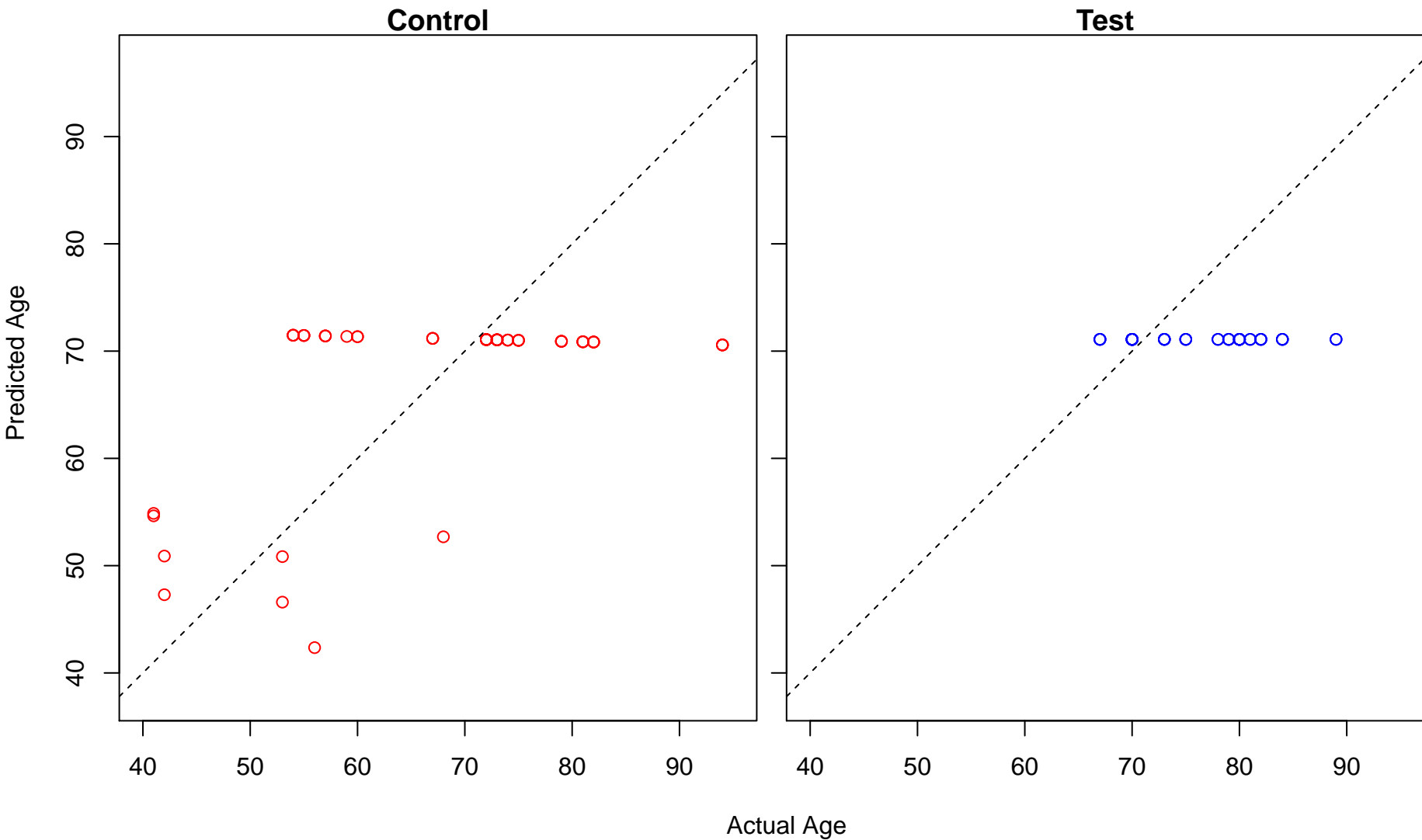


Test

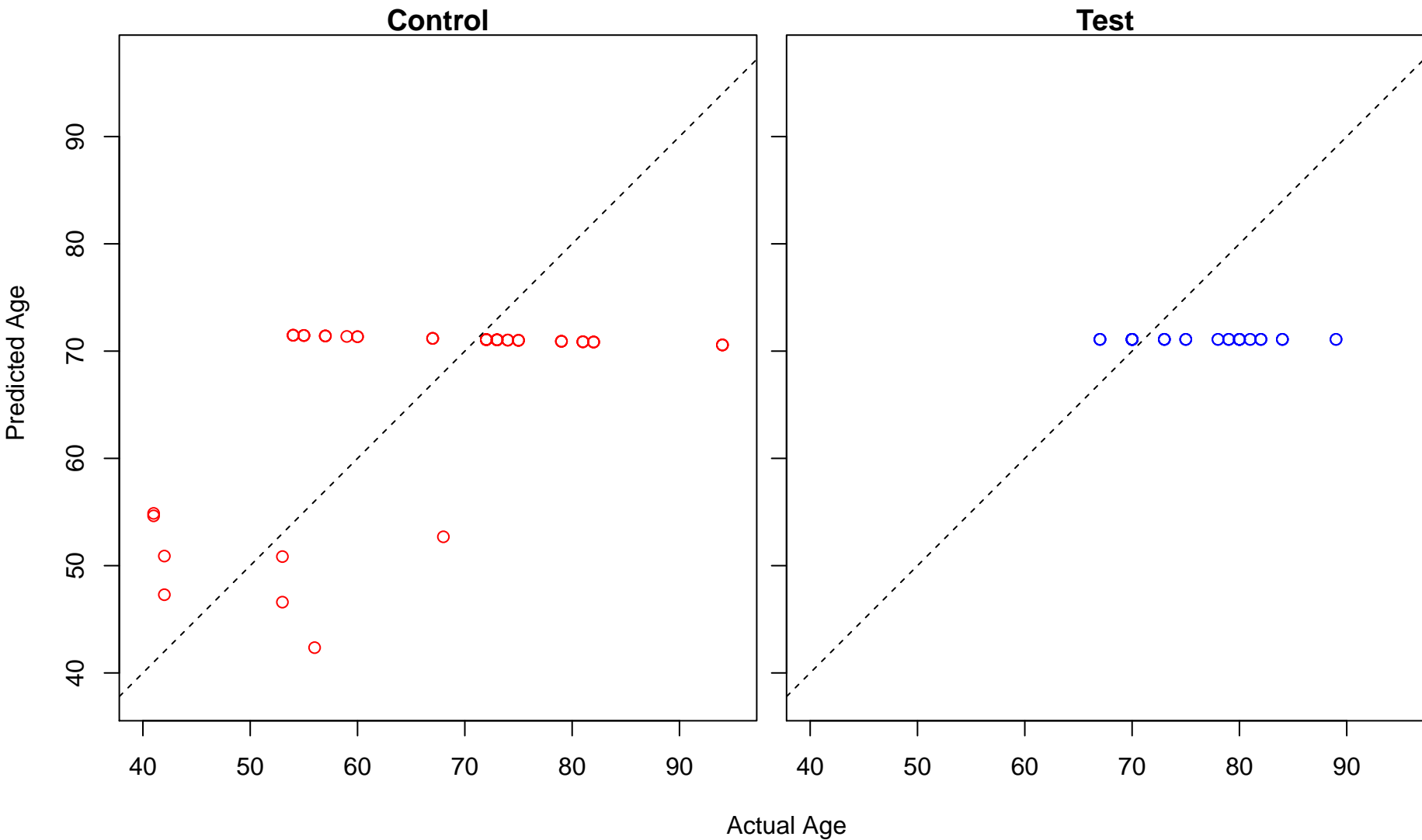


Actual Age

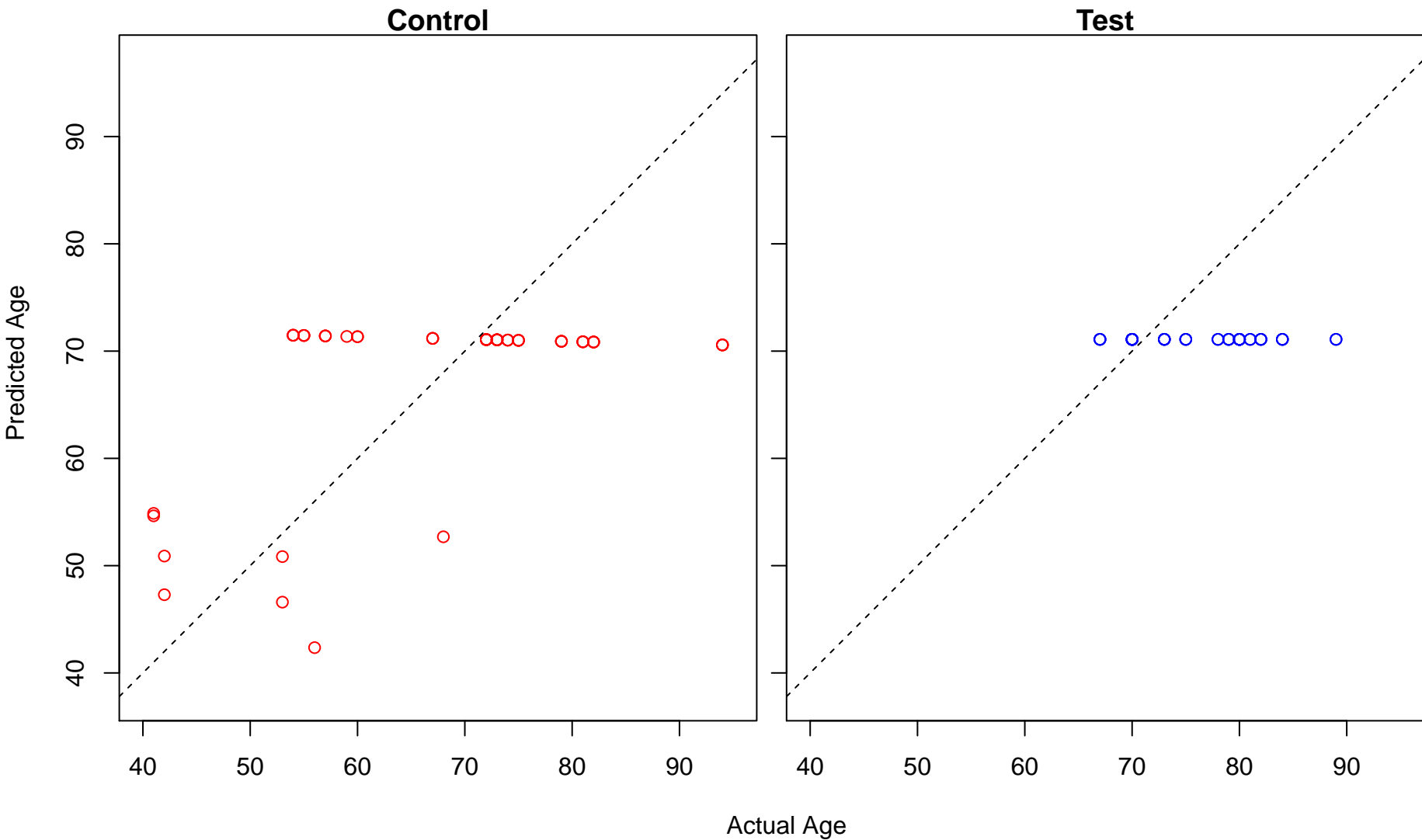
positive regulation of transcription, DNA-templated (Score: 0.798558)



positive regulation of RNA biosynthetic process (Score: 0.798558)

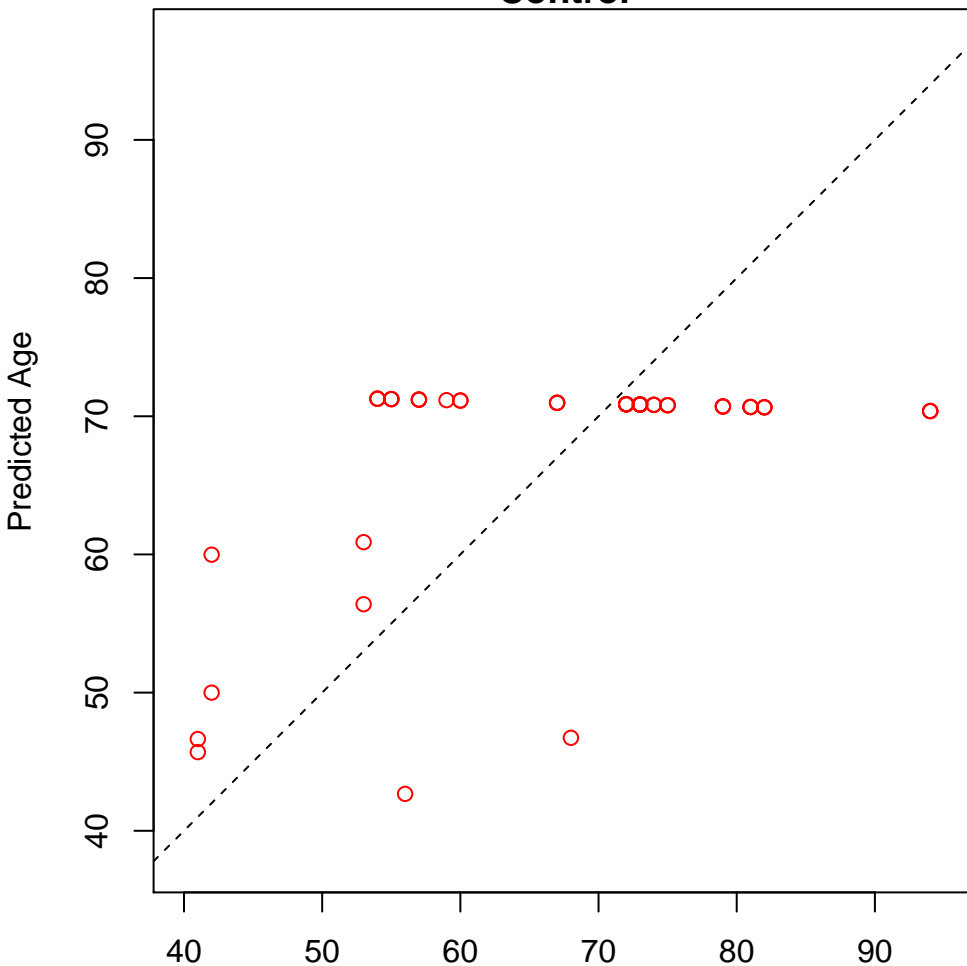


positive regulation of nucleic acid-templated transcription (Score: 0.798558)

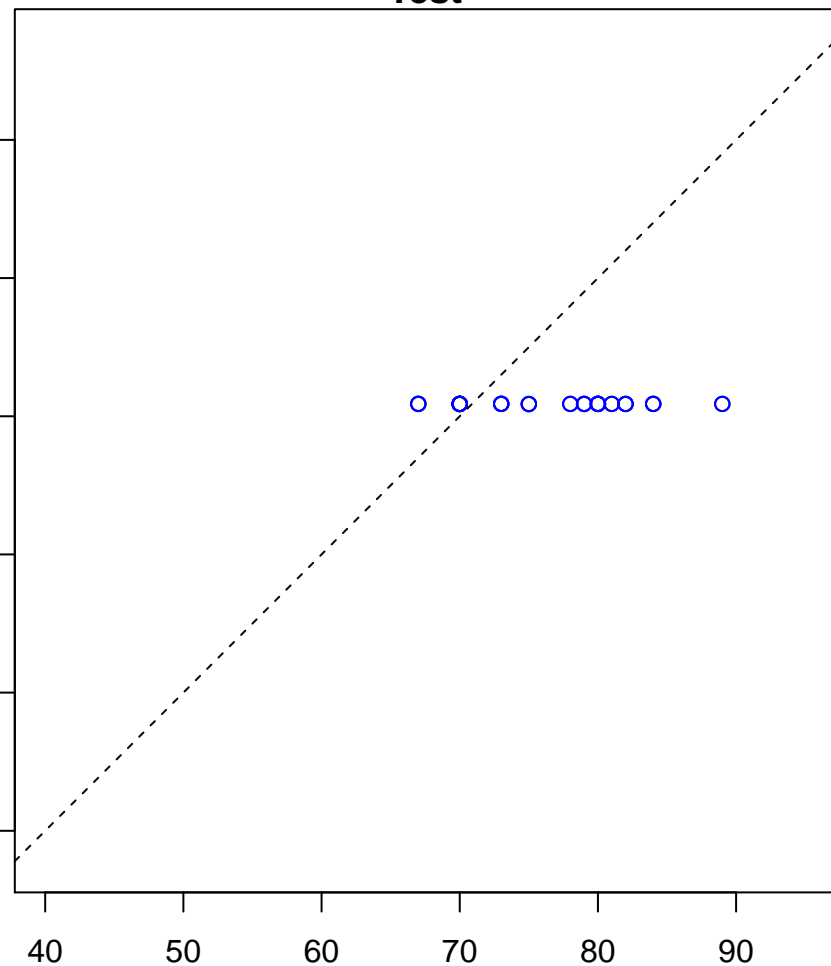


regulation of cellular response to heat (Score: 0.798534)

Control

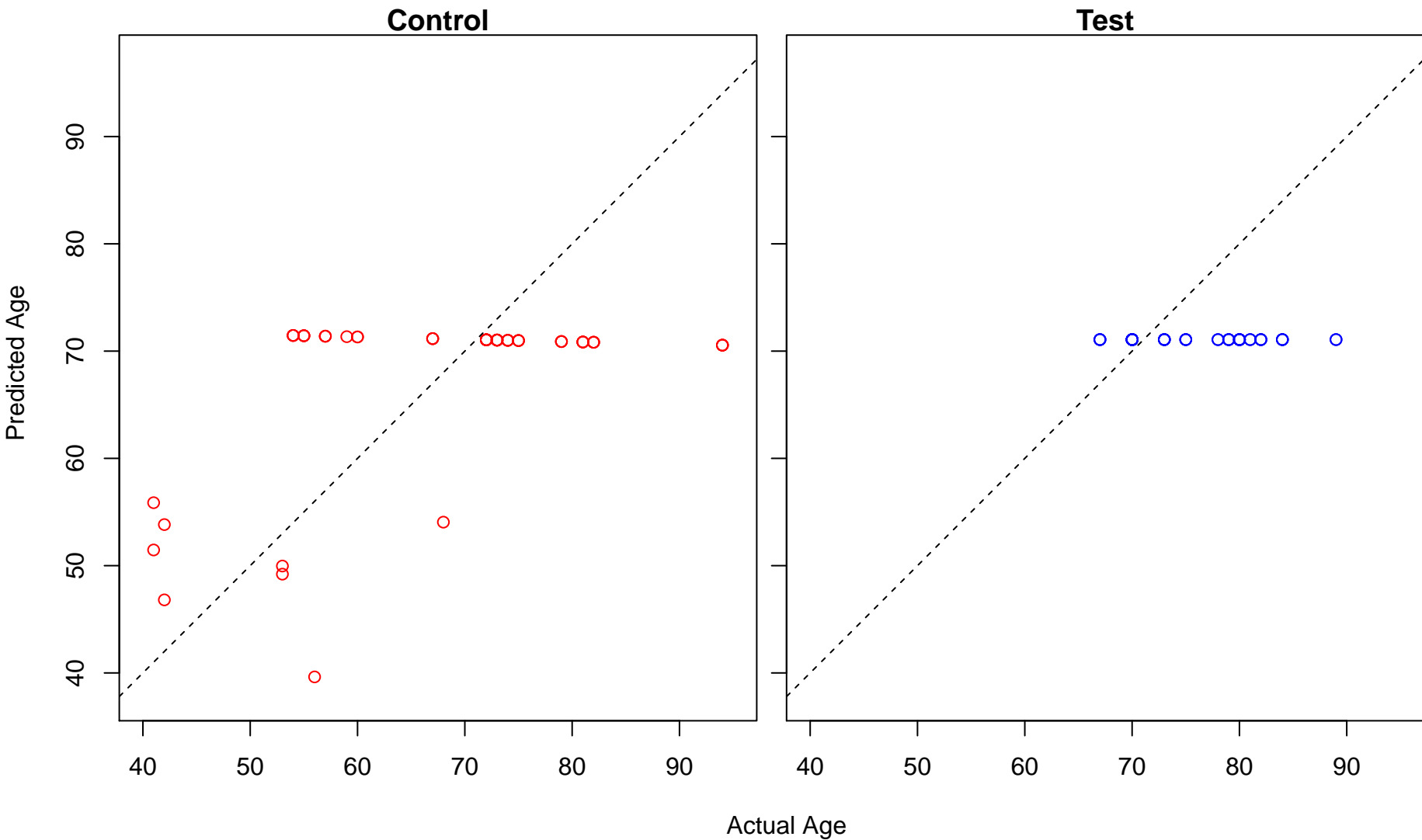


Test

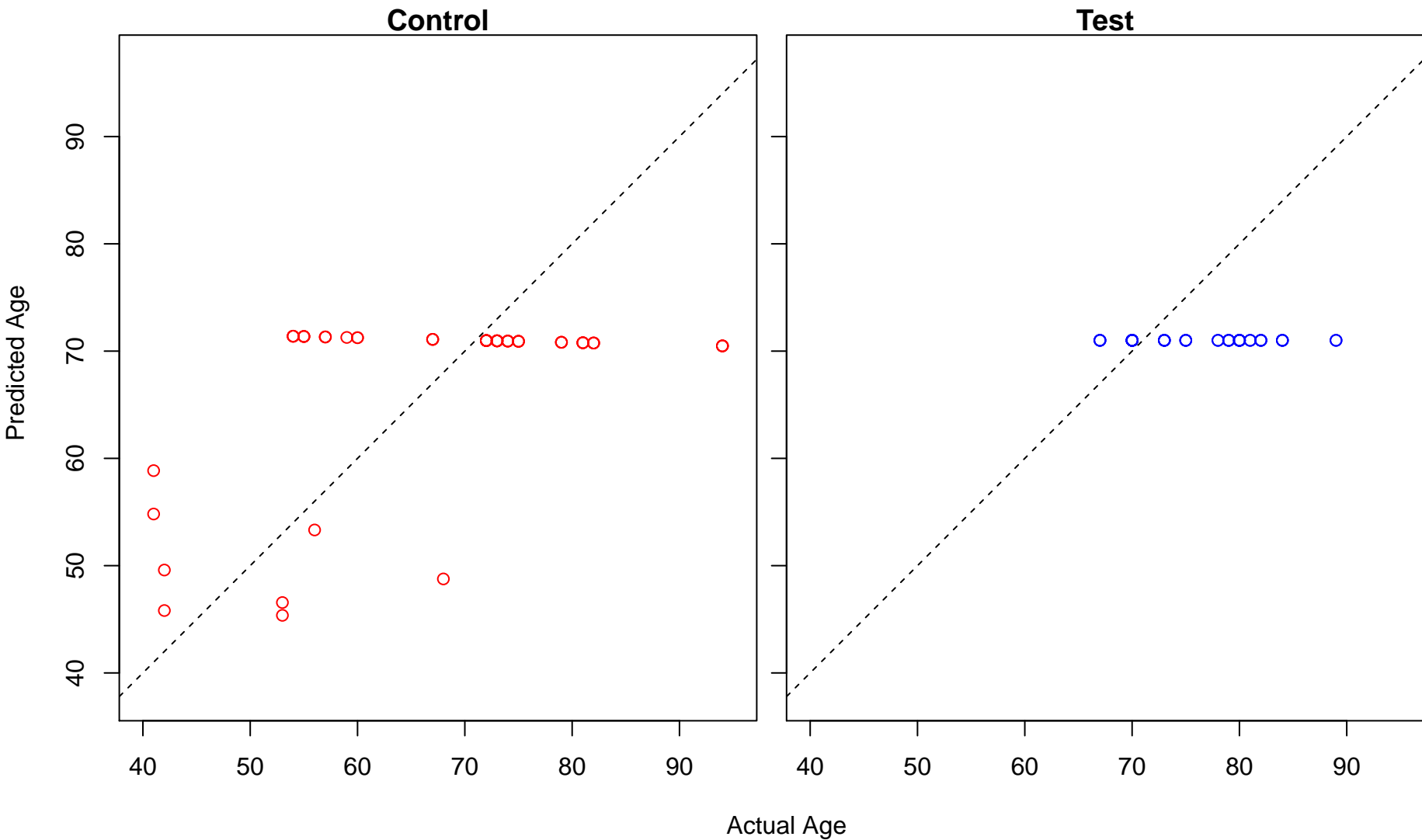


Actual Age

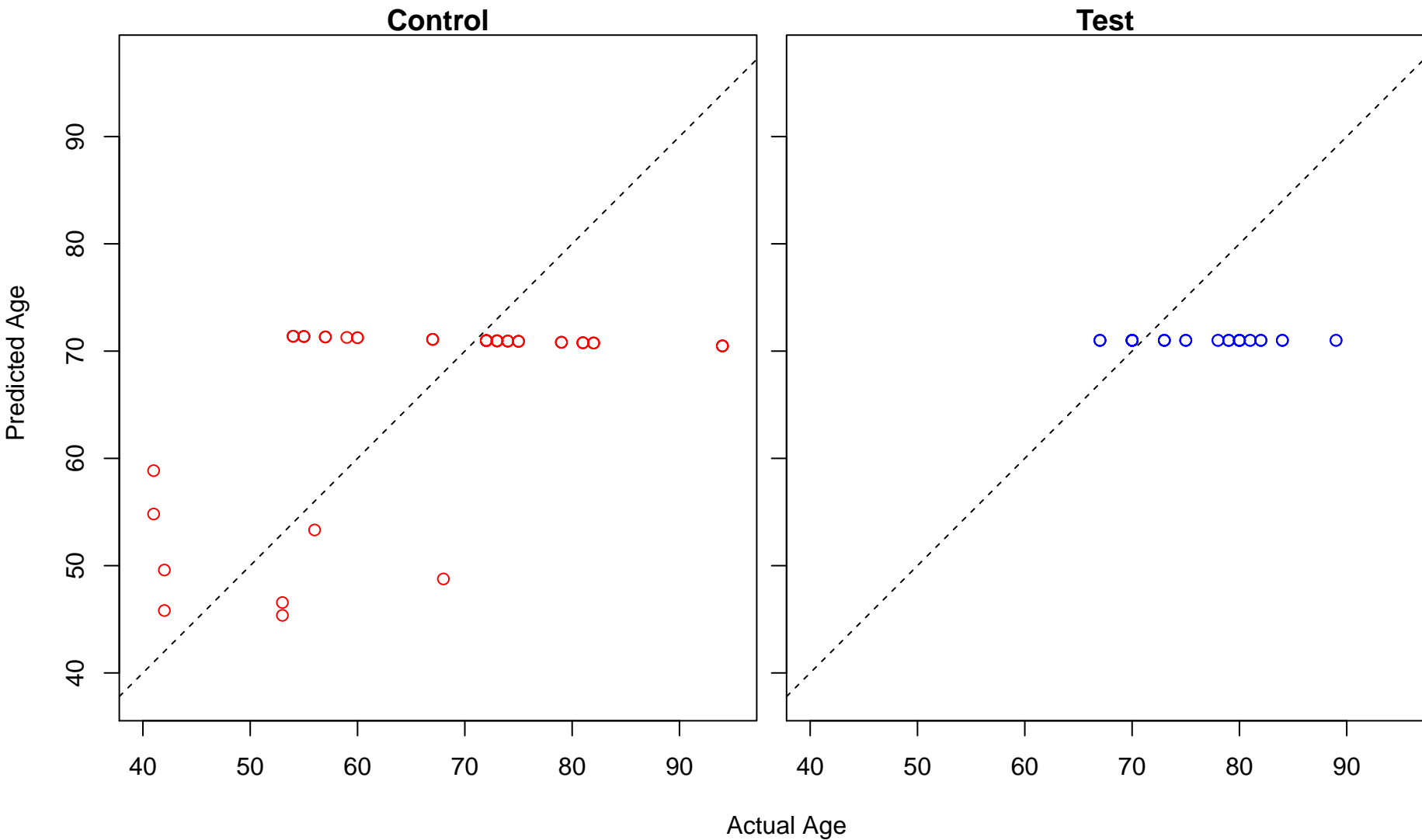
regulation of gene expression (Score: 0.798533)



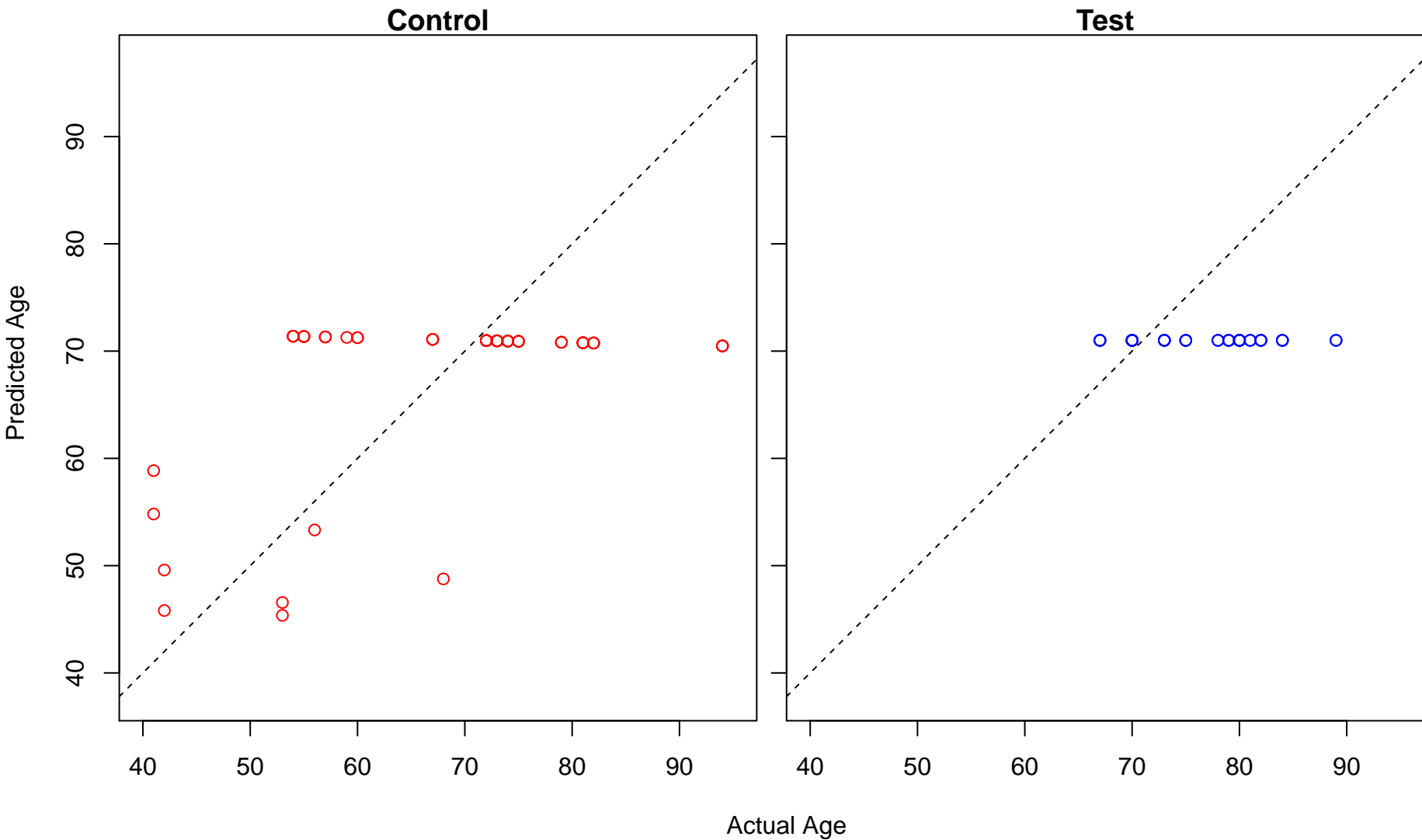
negative regulation of cellular response to oxidative stress (Score: 0.798465)



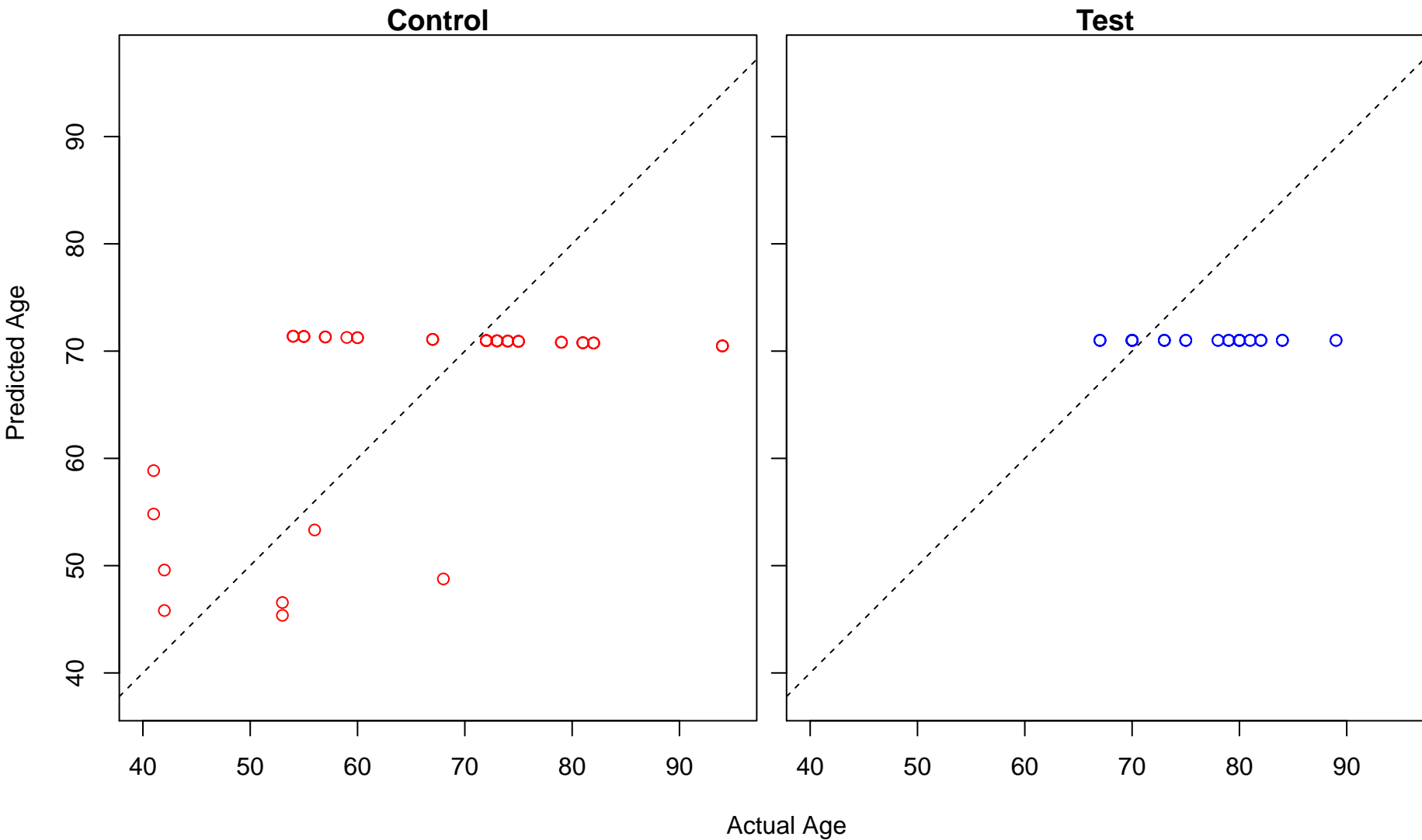
negative regulation of response to oxidative stress (Score: 0.798465)



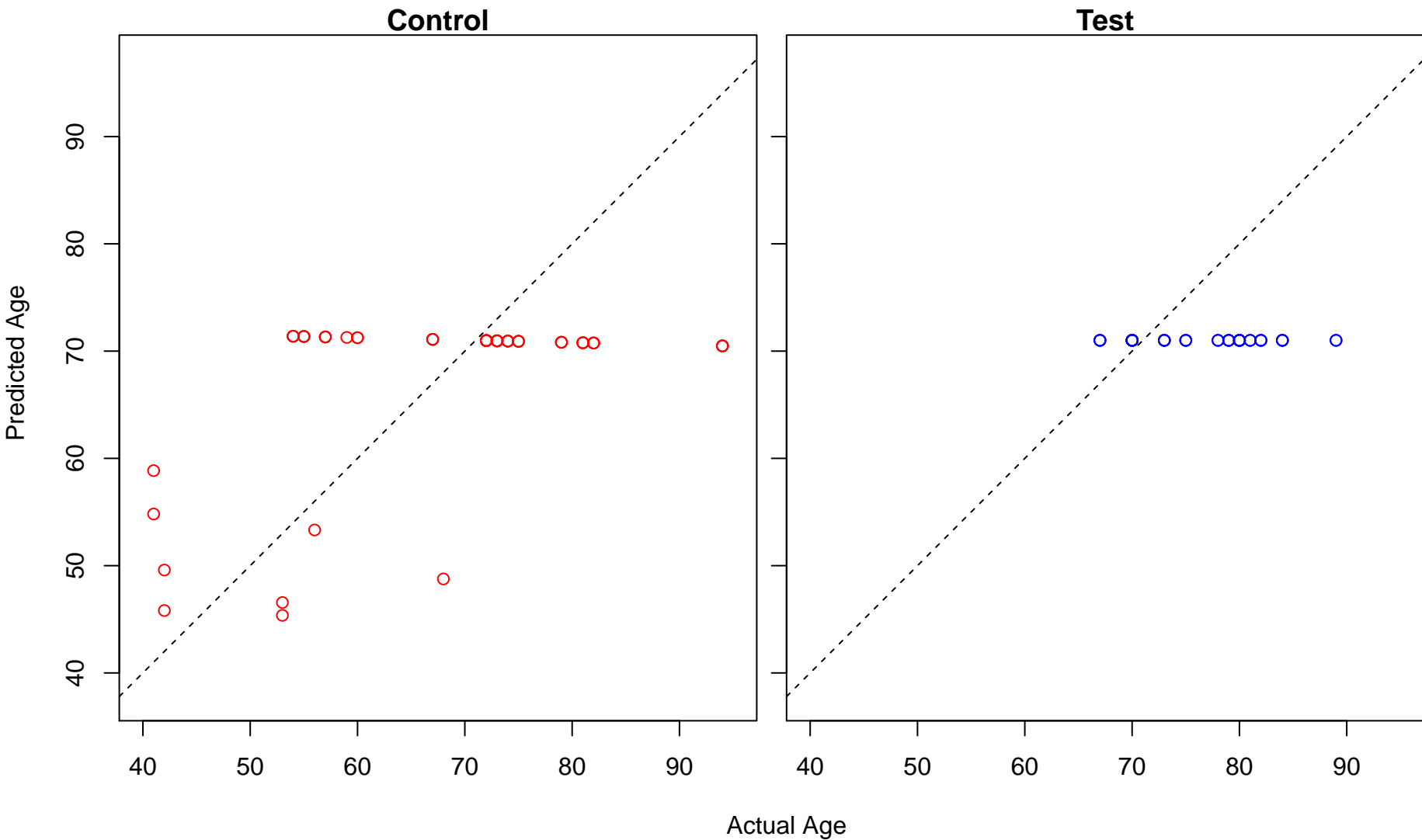
negative regulation of oxidative stress-induced cell death (Score: 0.798465)



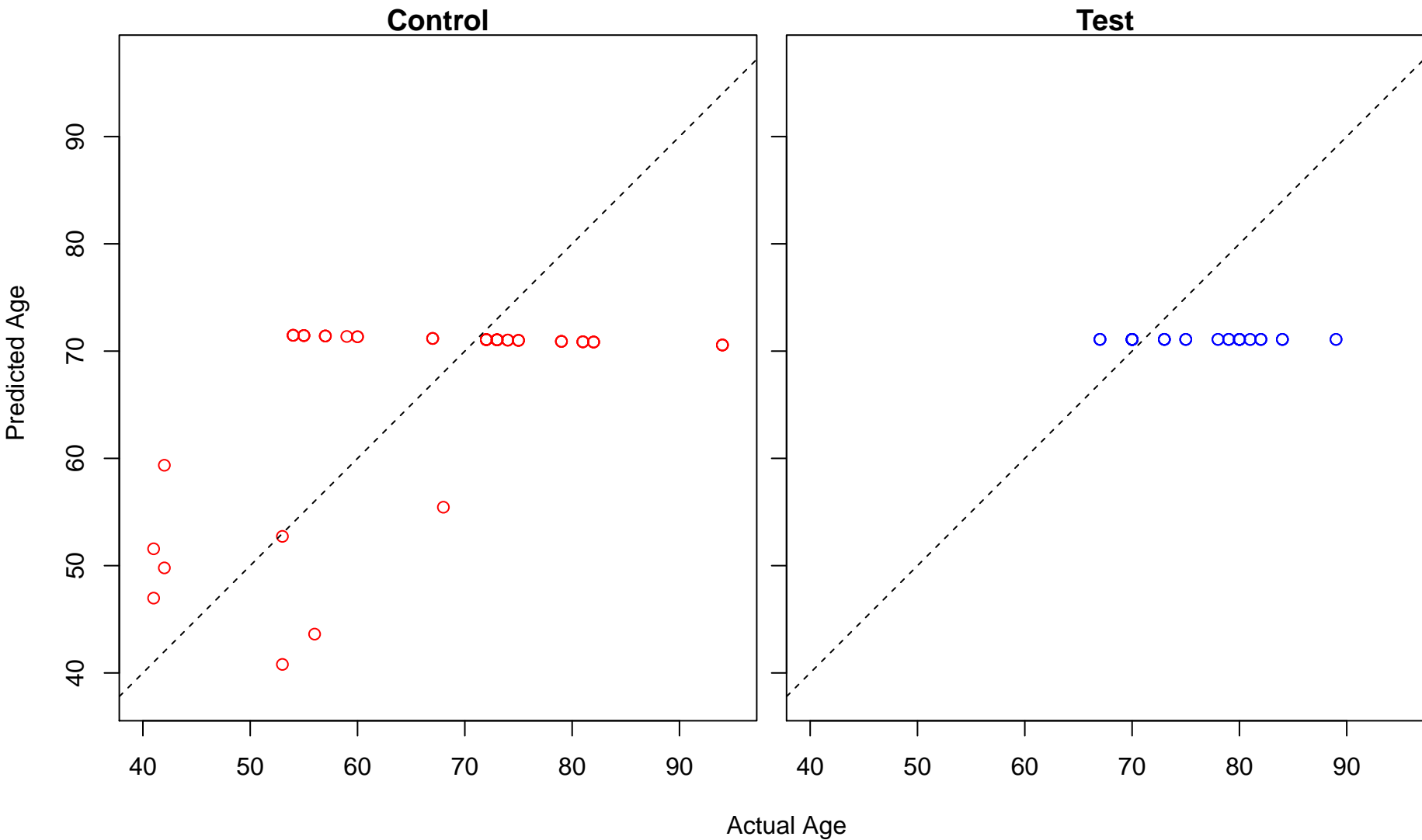
regulation of oxidative stress-induced neuron death (Score: 0.798465)



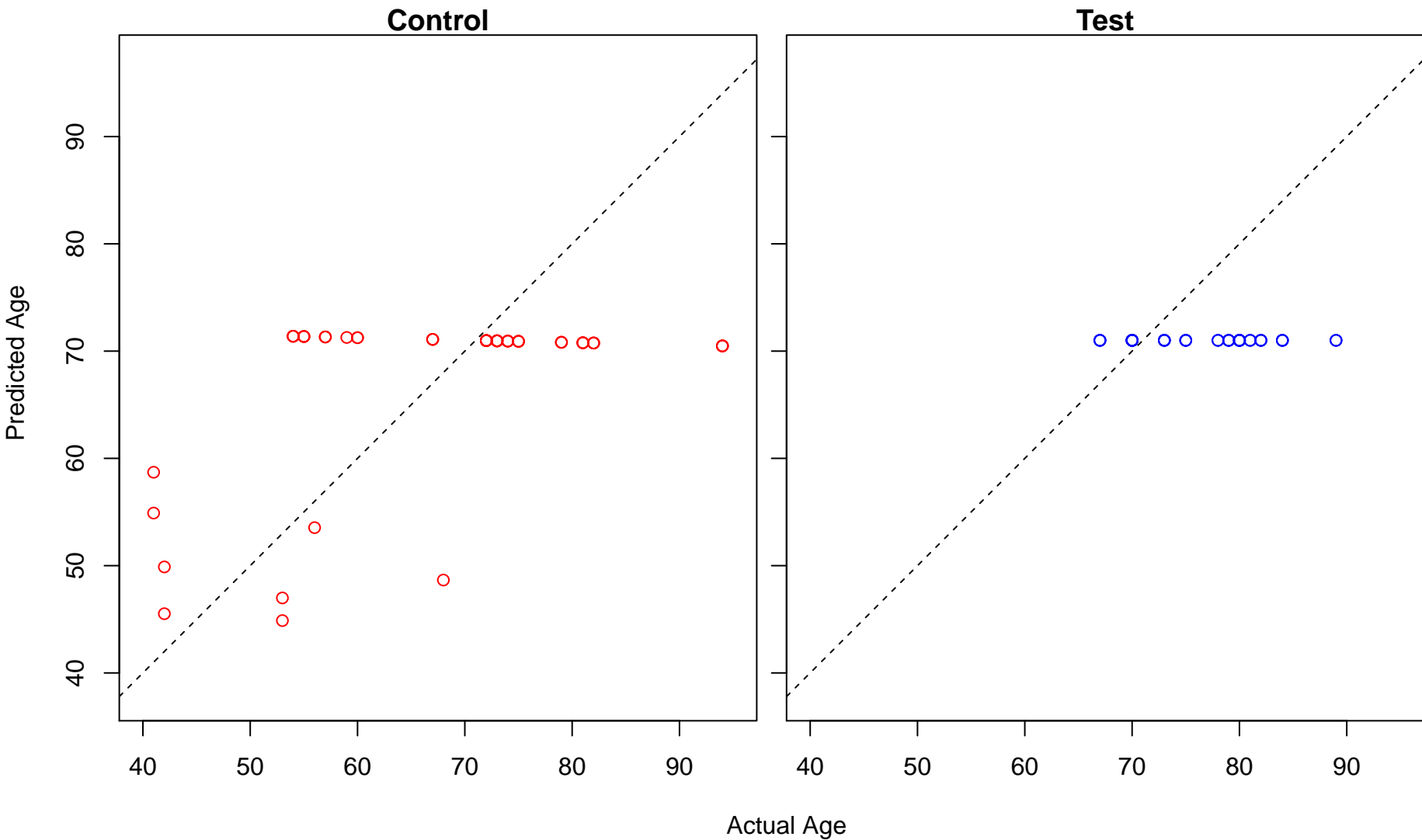
negative regulation of oxidative stress-induced neuron death (Score: 0.798465)



endocytosis (Score: 0.798464)

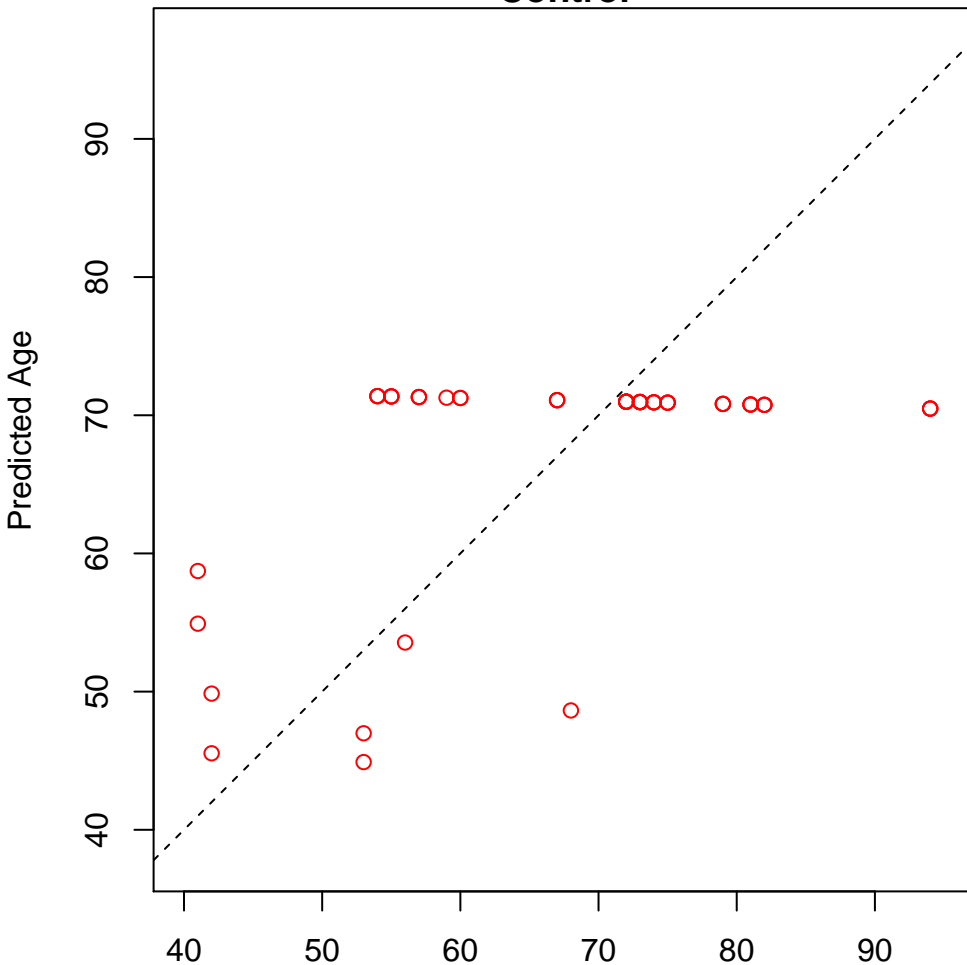


regulation of protein acetylation (Score: 0.798462)

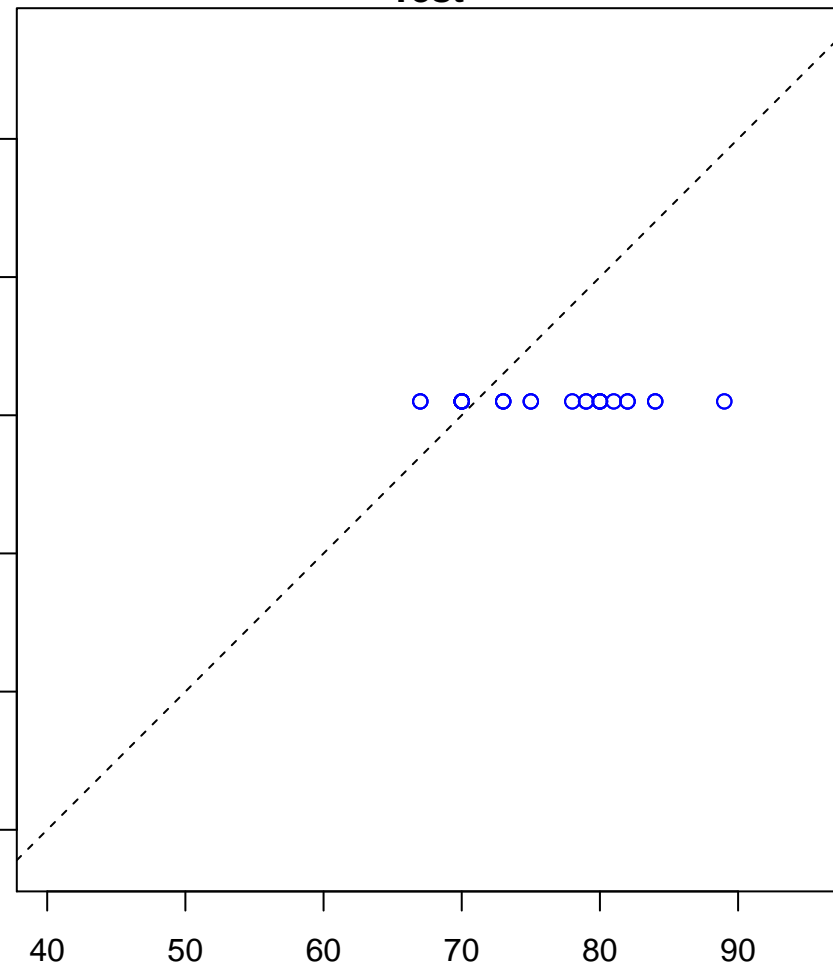


negative regulation of protein acetylation (Score: 0.798443)

Control



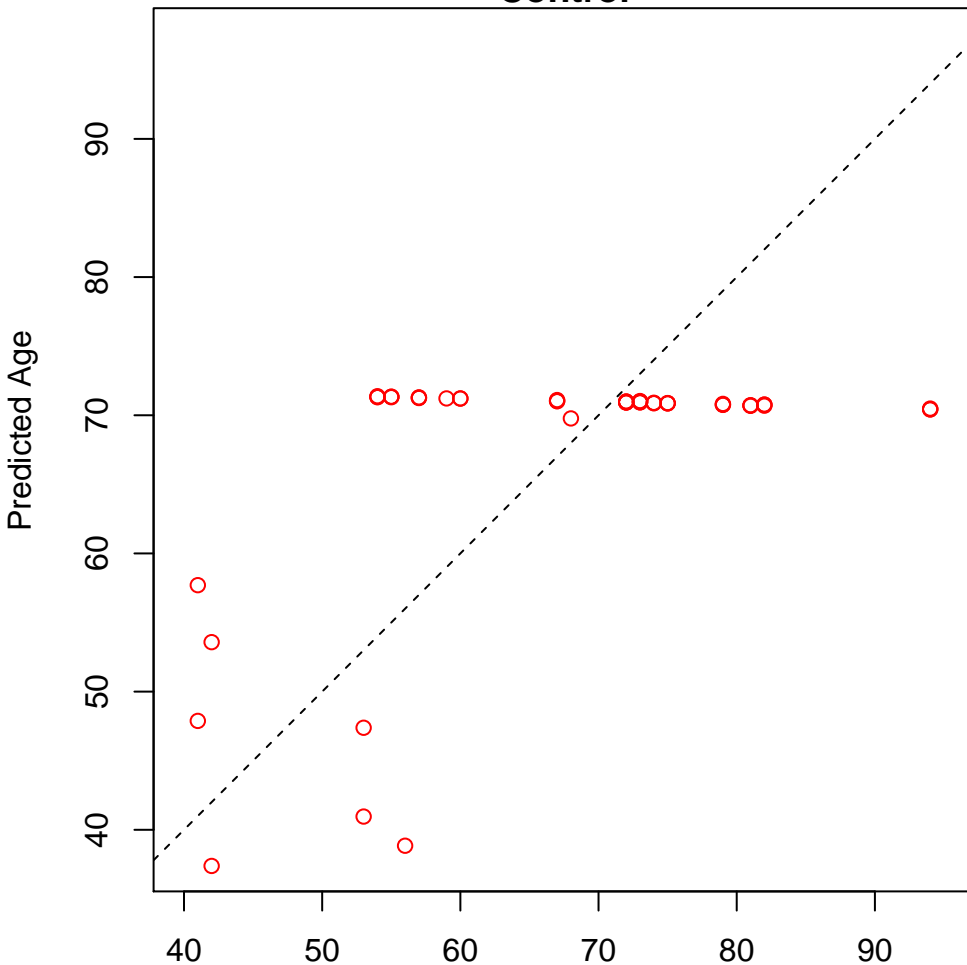
Test



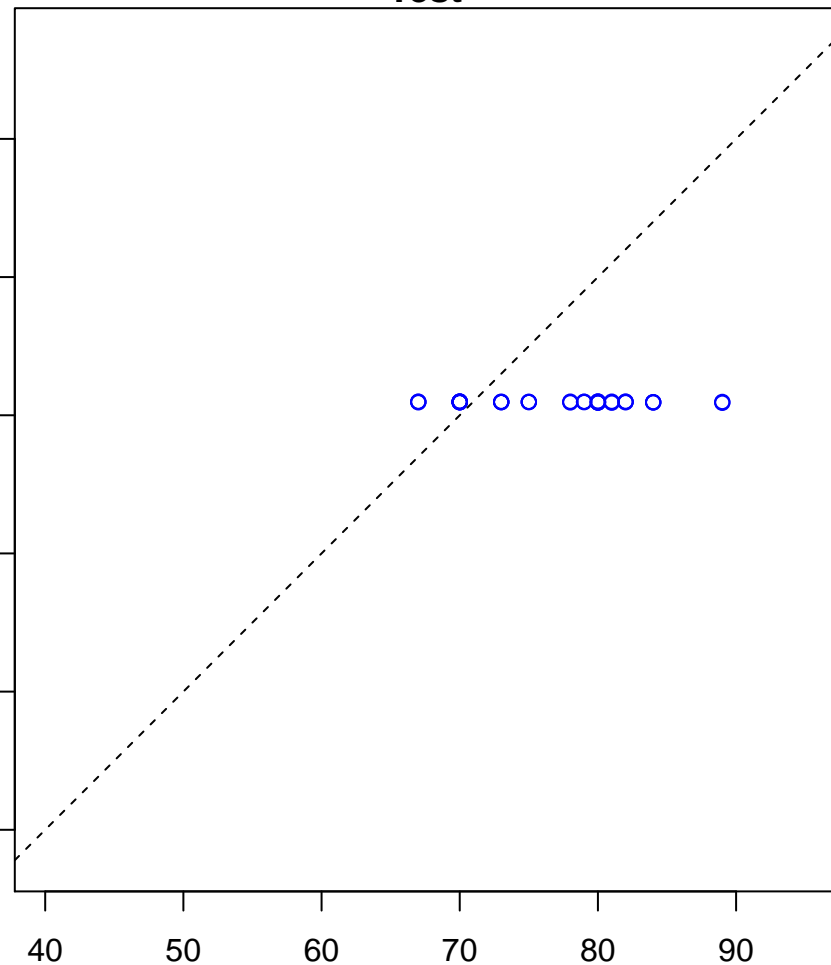
Actual Age

positive regulation of mitotic cell cycle (Score: 0.798395)

Control



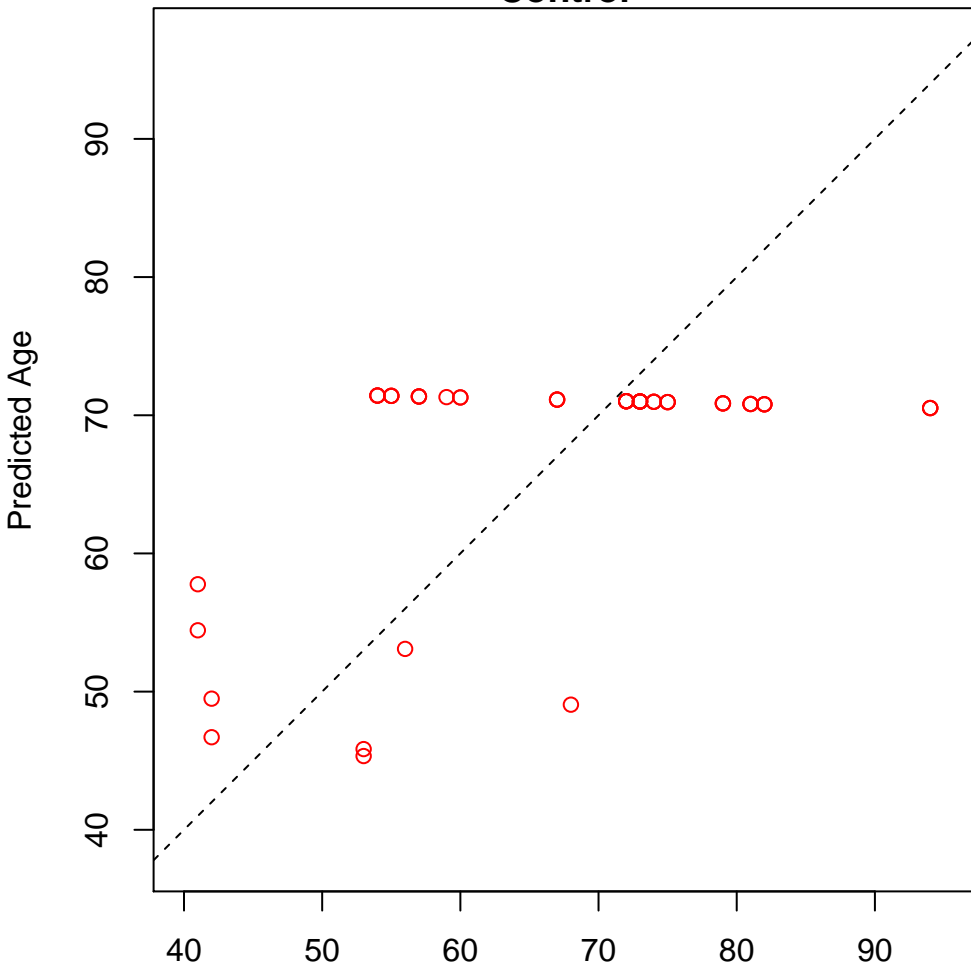
Test



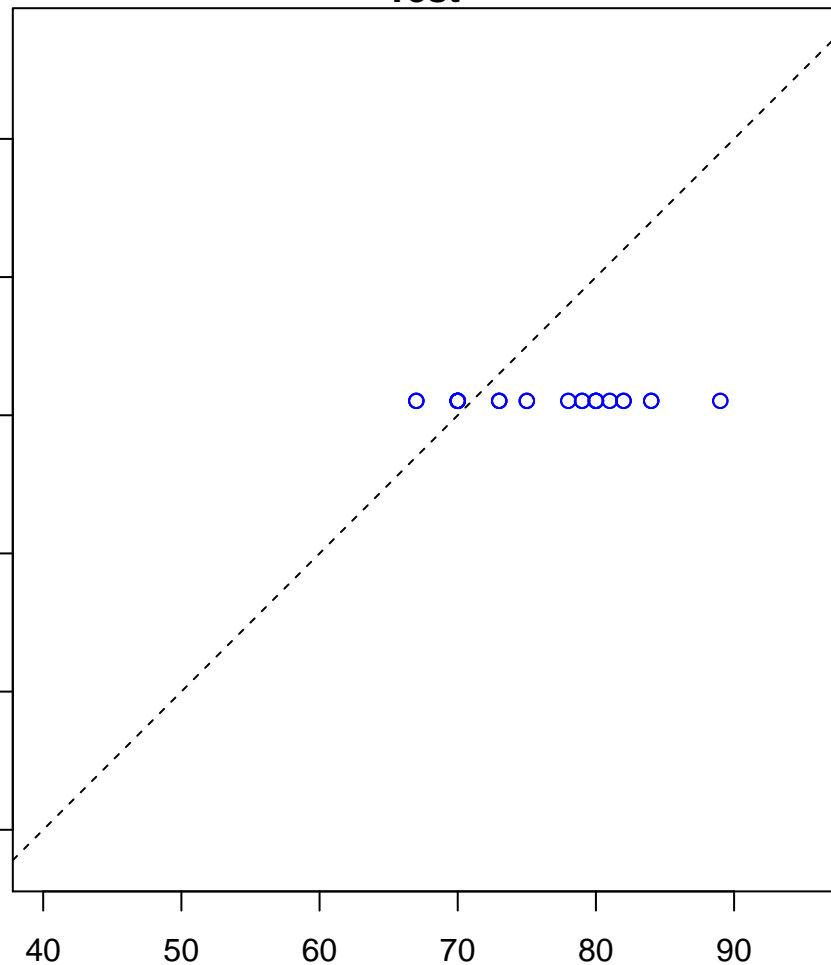
Actual Age

regulation of acute inflammatory response (Score: 0.798351)

Control



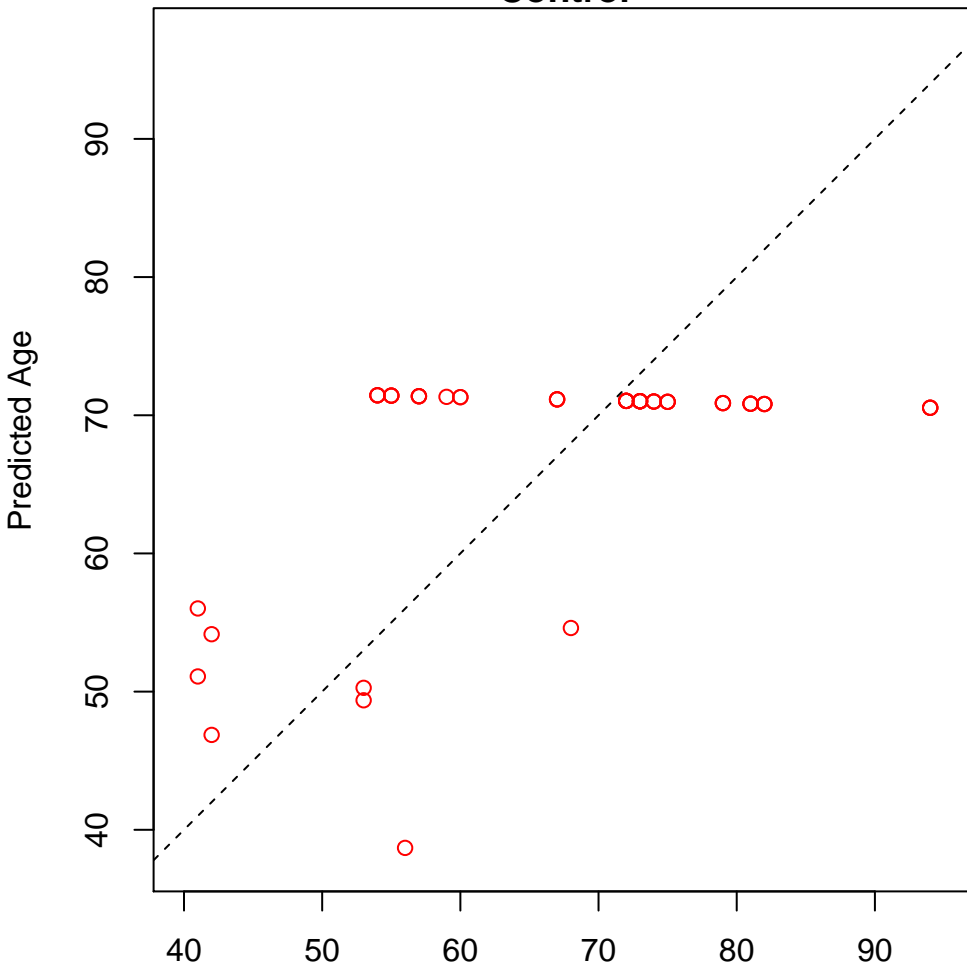
Test



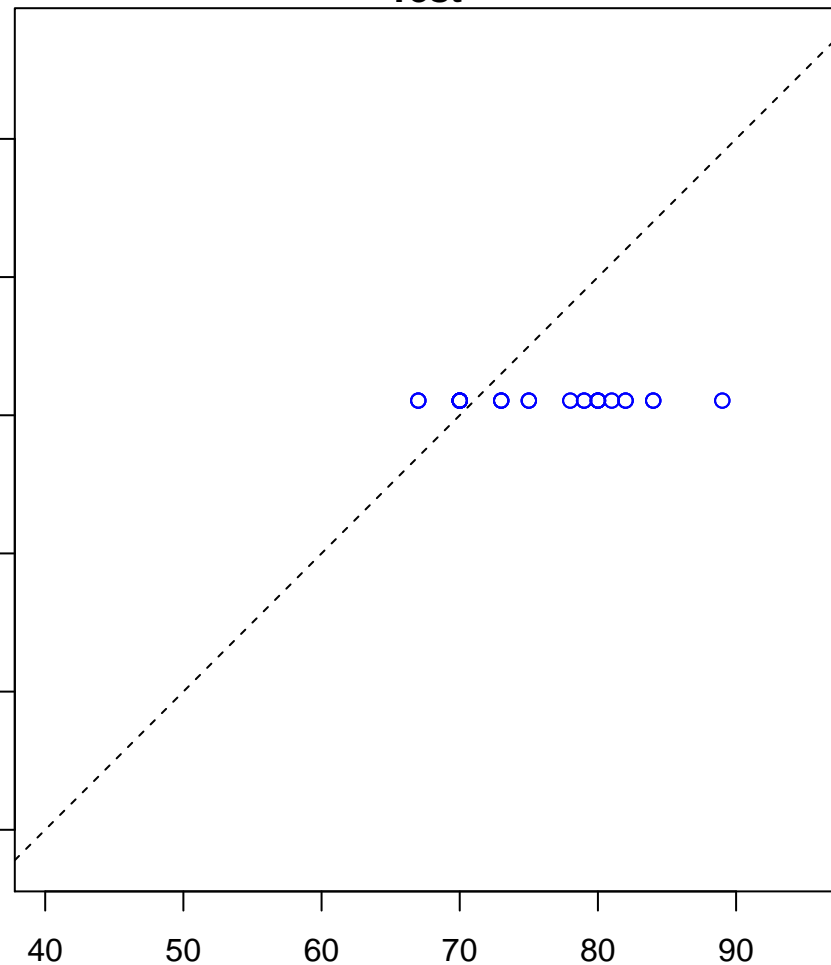
Actual Age

macromolecule biosynthetic process (Score: 0.798329)

Control

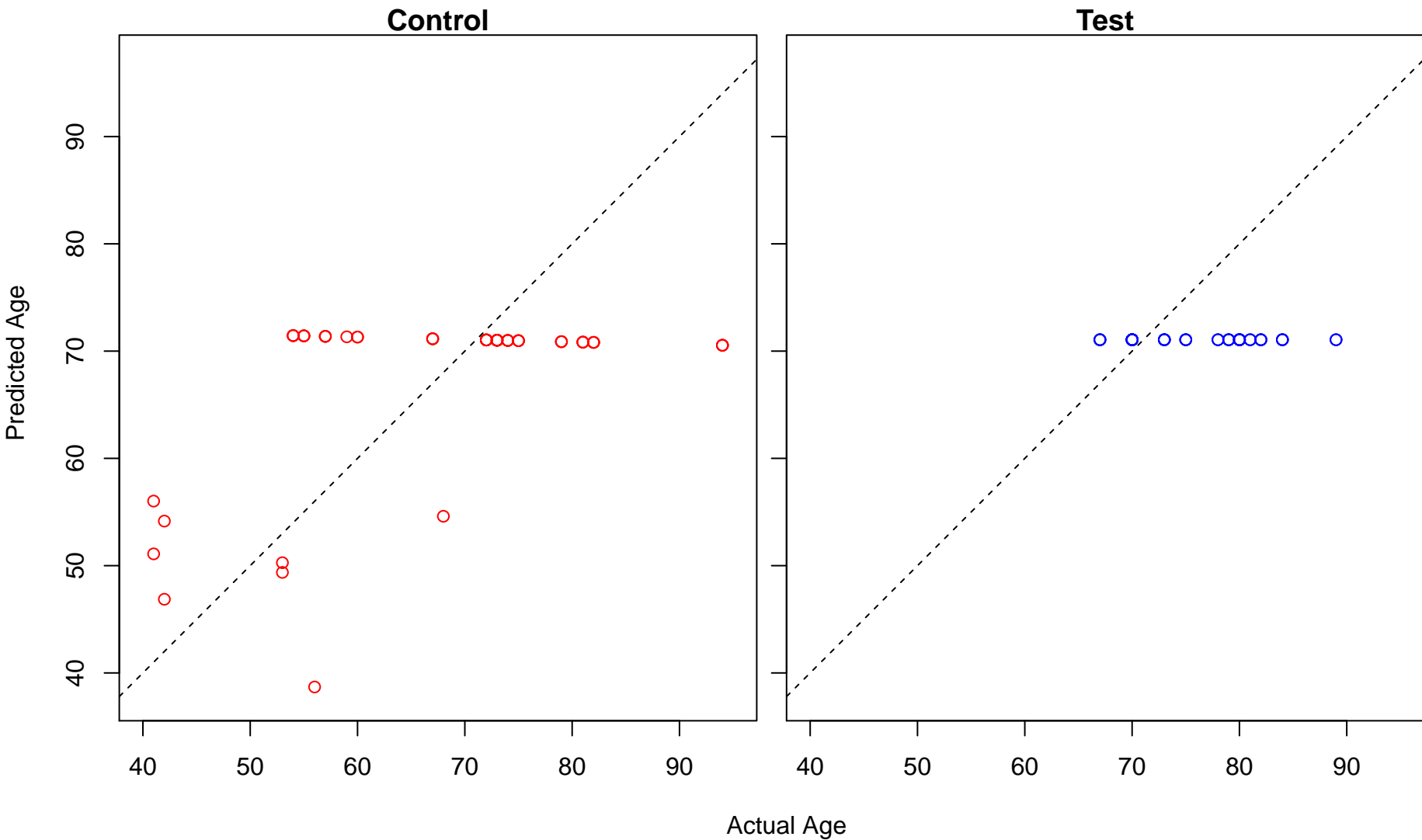


Test

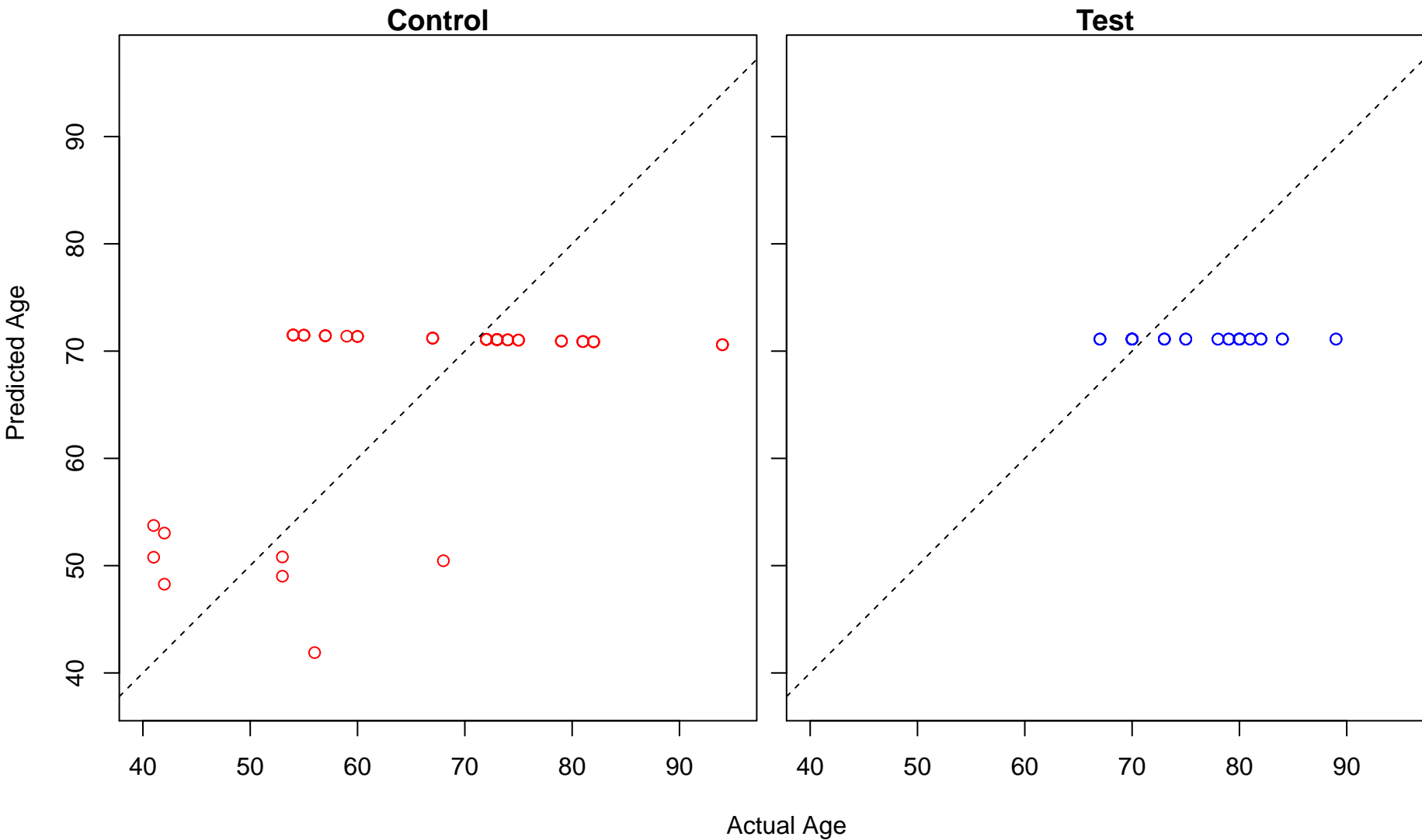


Actual Age

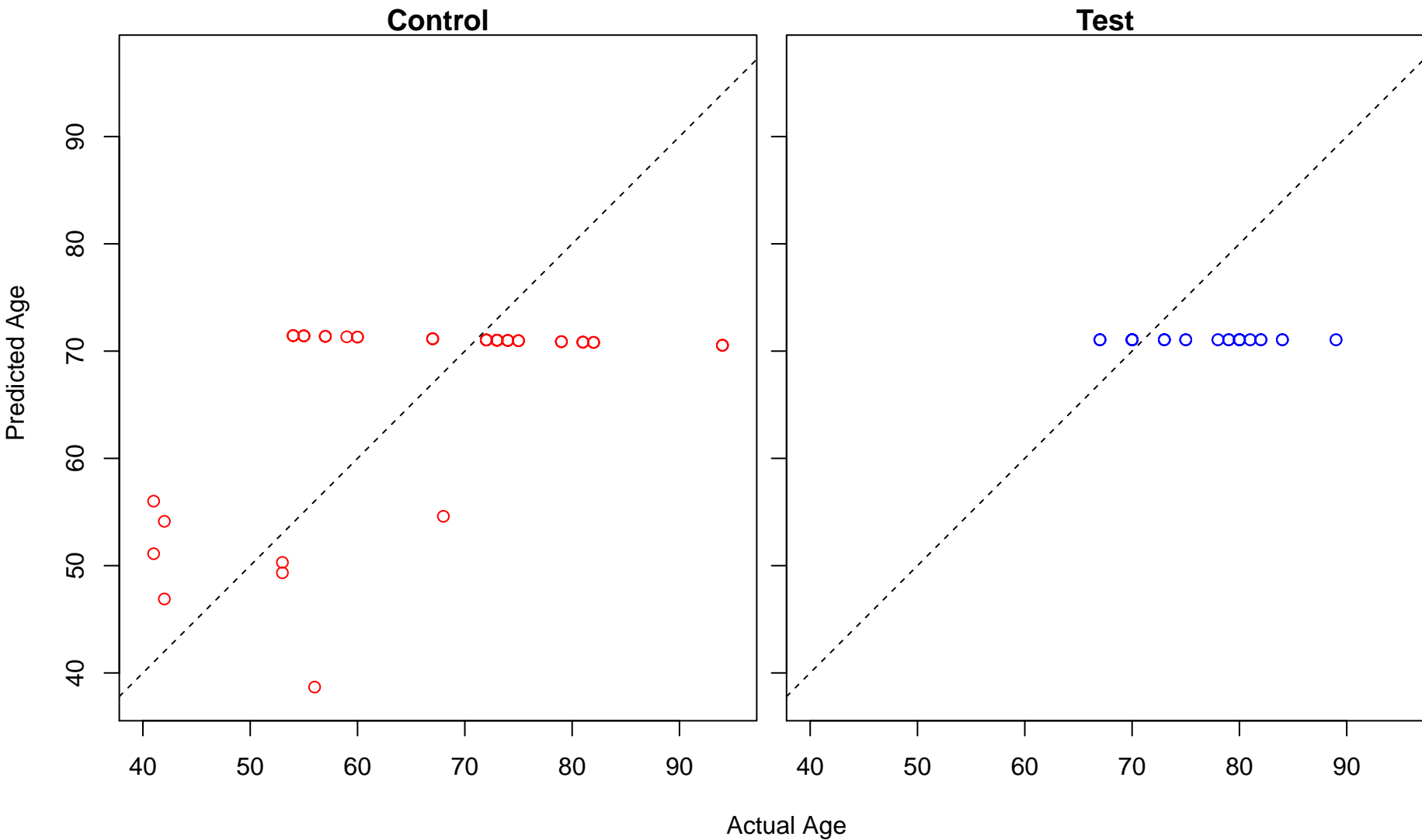
cellular macromolecule biosynthetic process (Score: 0.798329)



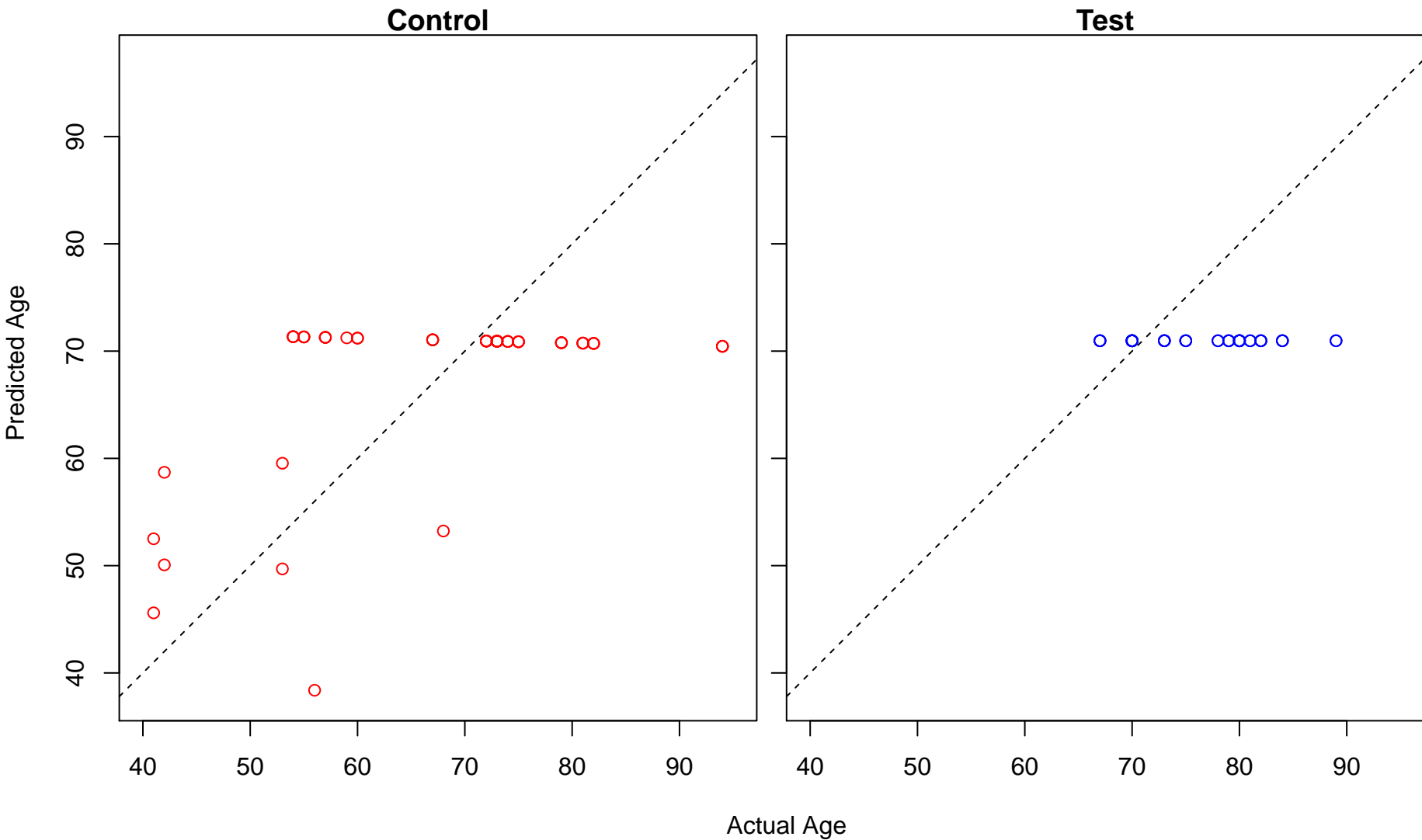
histone ubiquitination (Score: 0.798326)



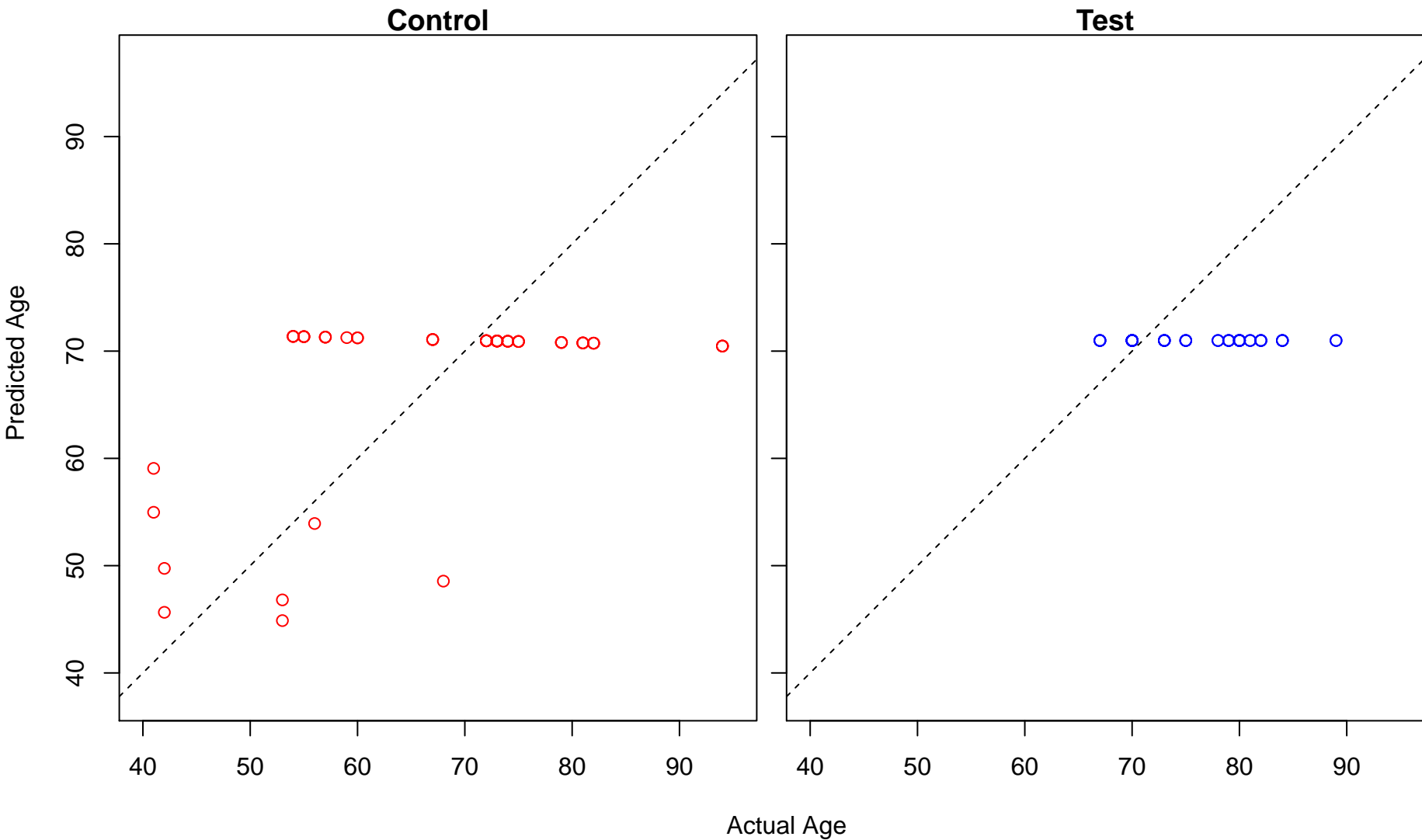
cellular nitrogen compound biosynthetic process (Score: 0.798301)



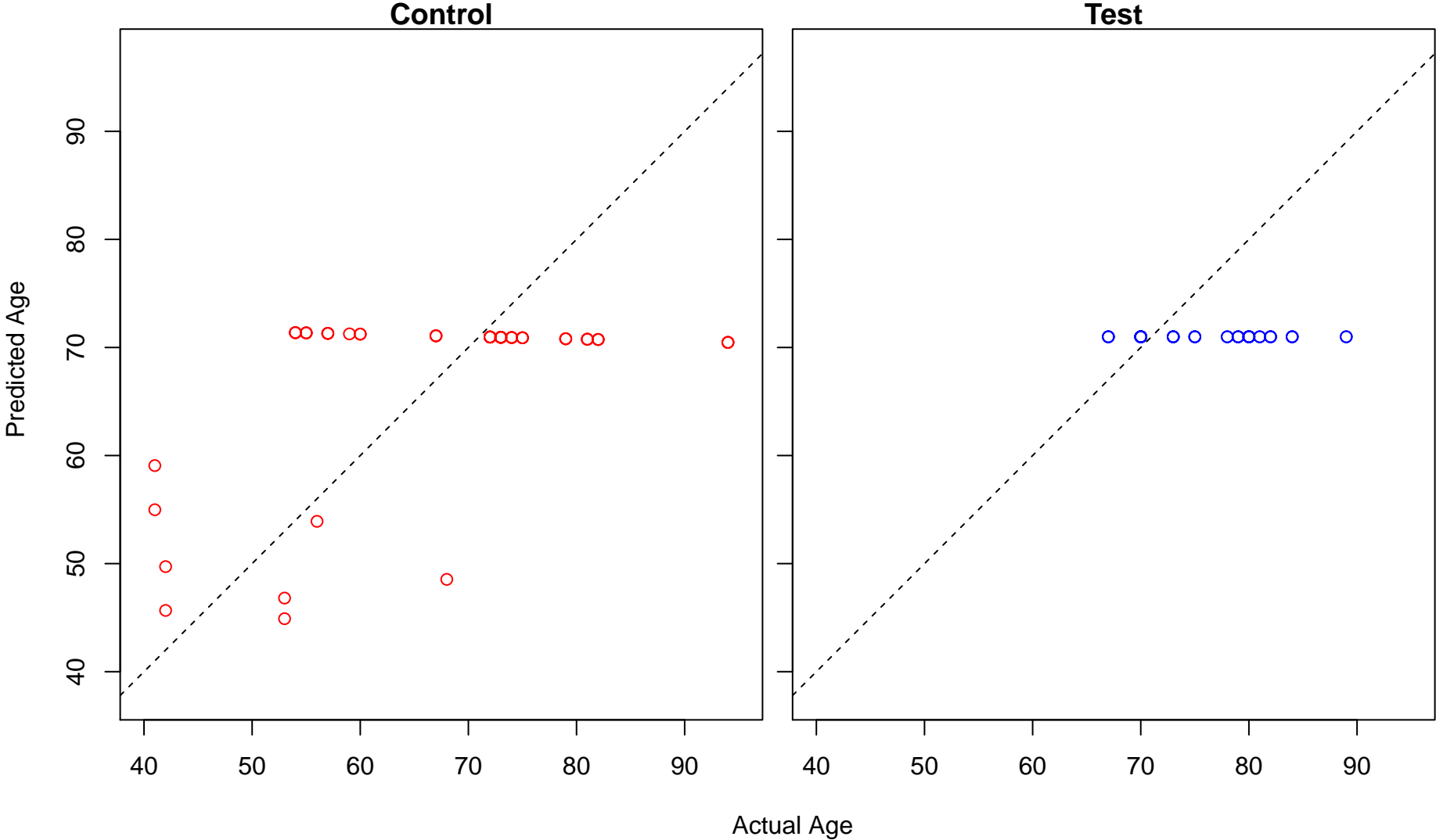
platelet activation (Score: 0.798281)



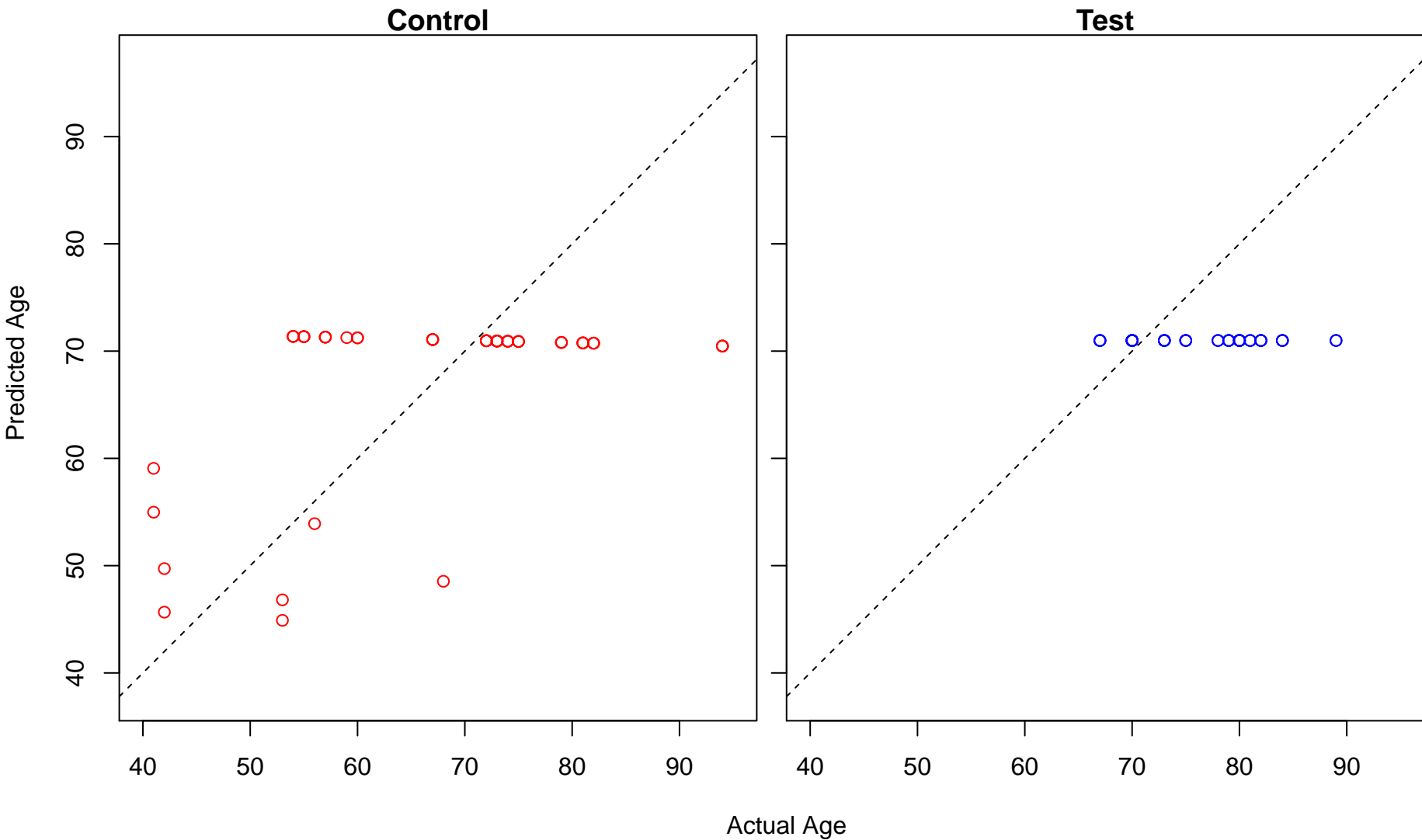
positive regulation of protein localization to nucleus (Score: 0.798277)



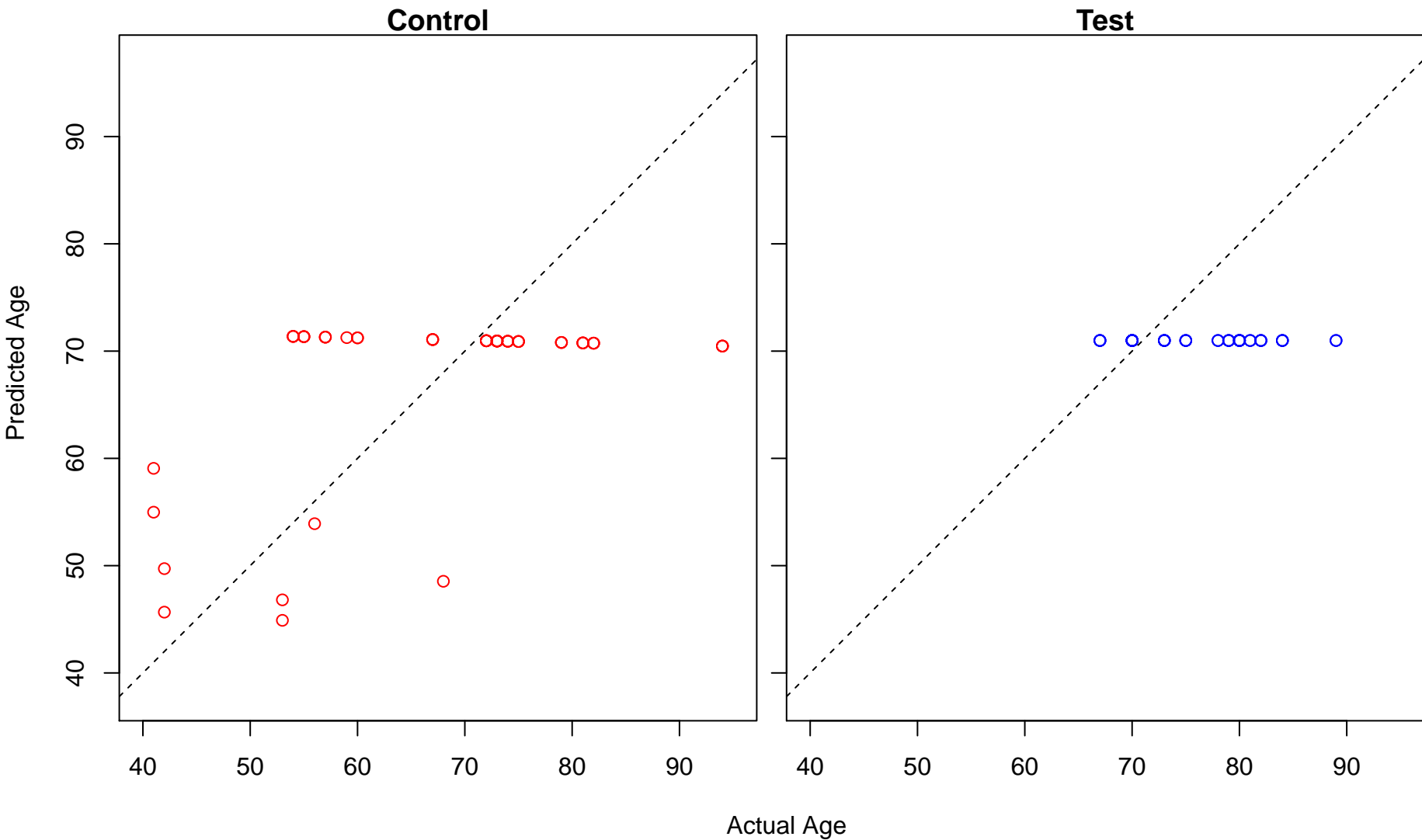
negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway (Score: 0.7982)



regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway (Score: 0.79826)

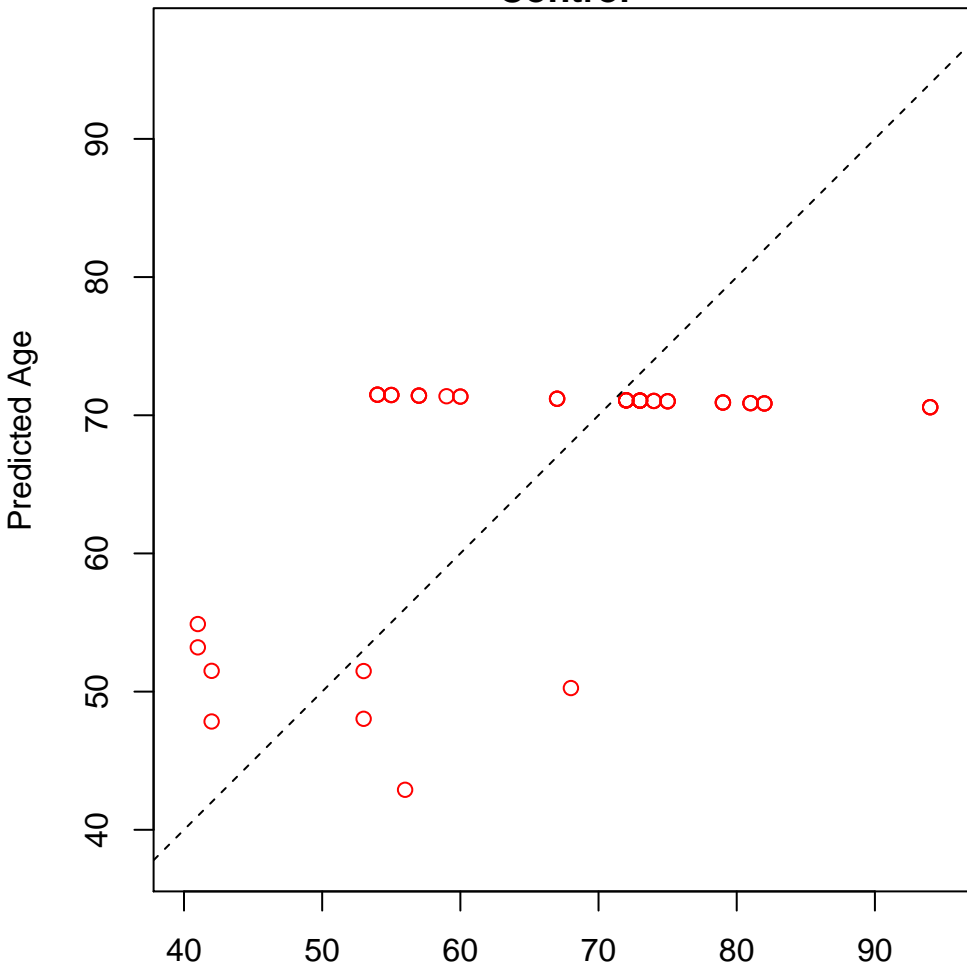


negative regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway (Score: 0.7)

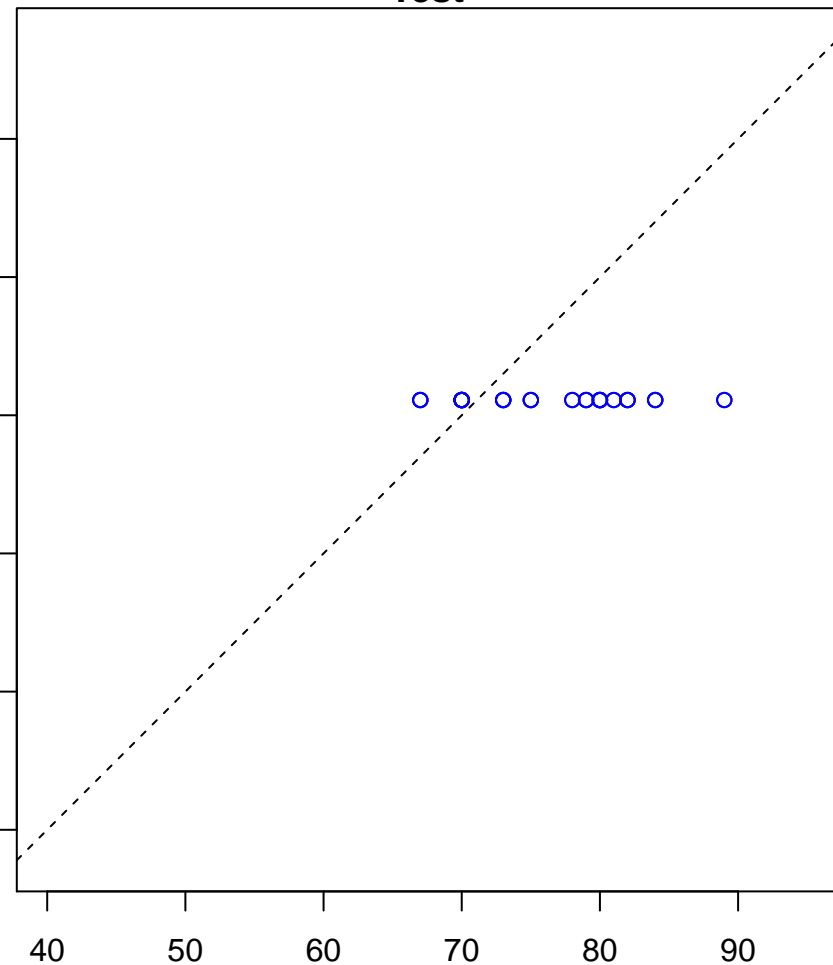


positive regulation of biosynthetic process (Score: 0.798263)

Control

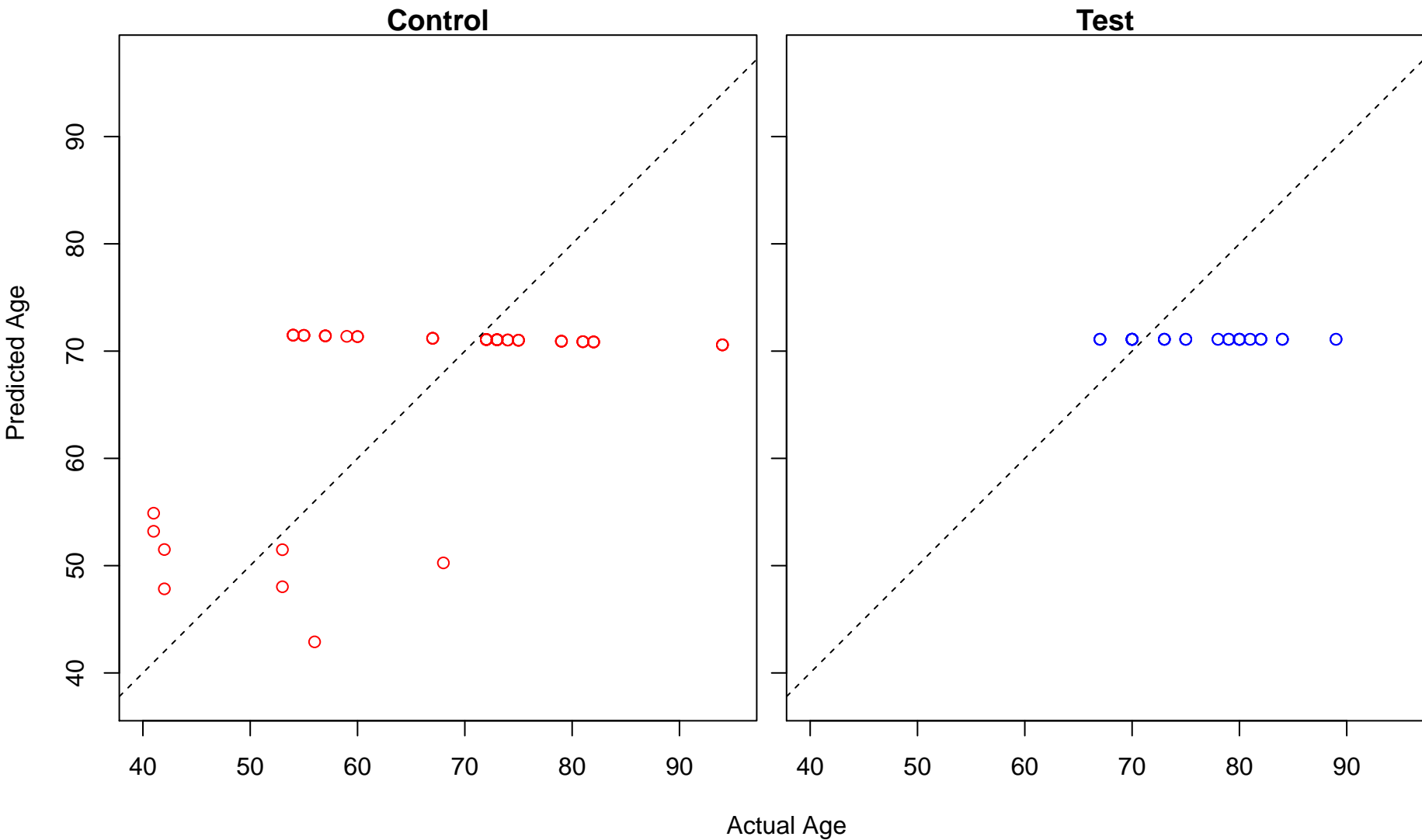


Test



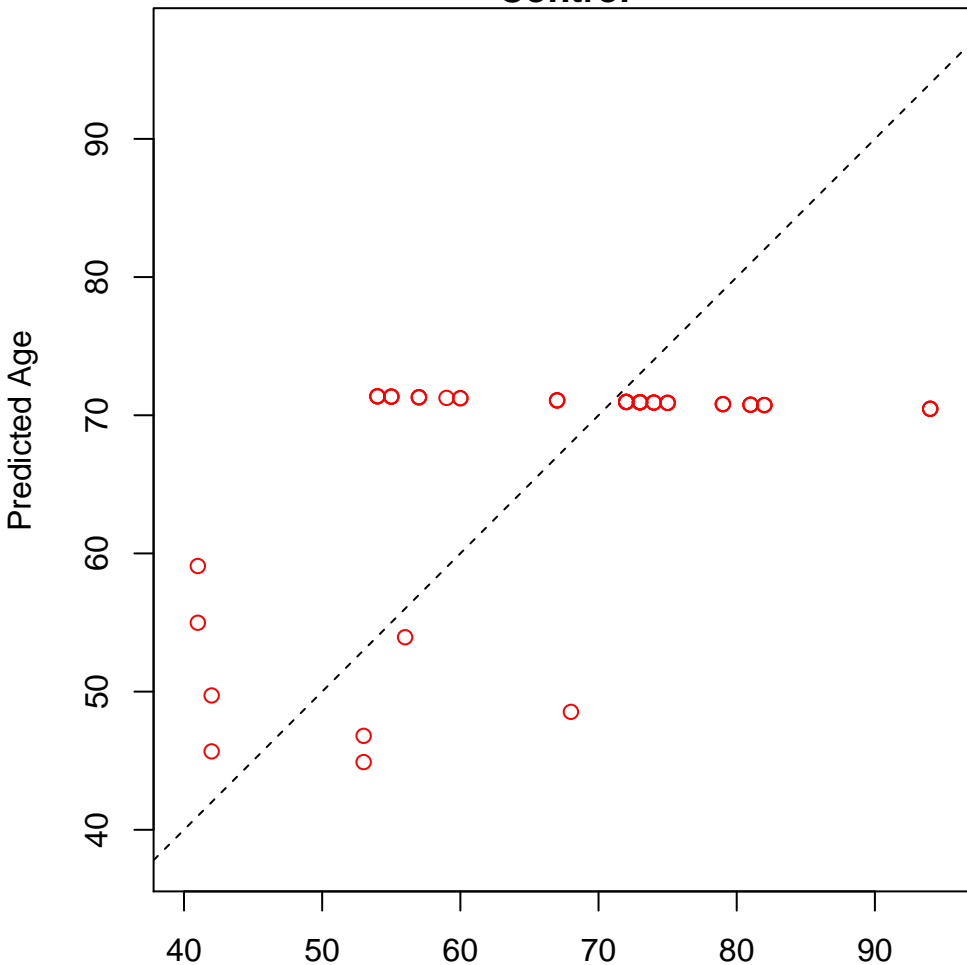
Actual Age

positive regulation of cellular biosynthetic process (Score: 0.798263)

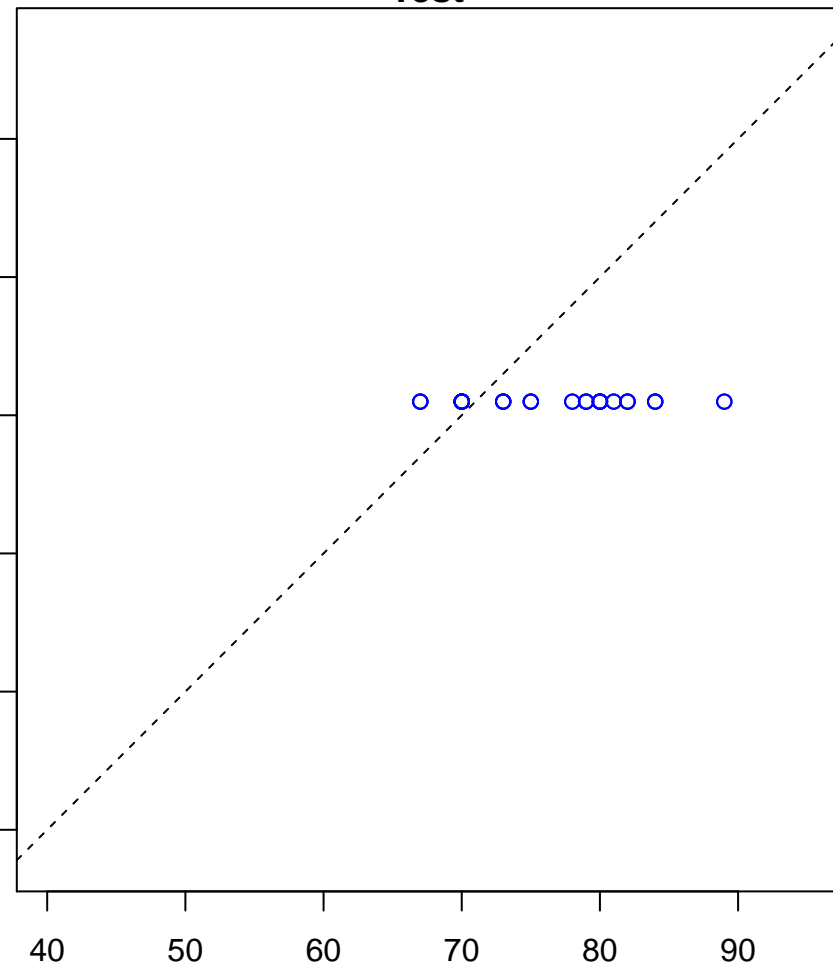


regulation of protein deubiquitination (Score: 0.798248)

Control

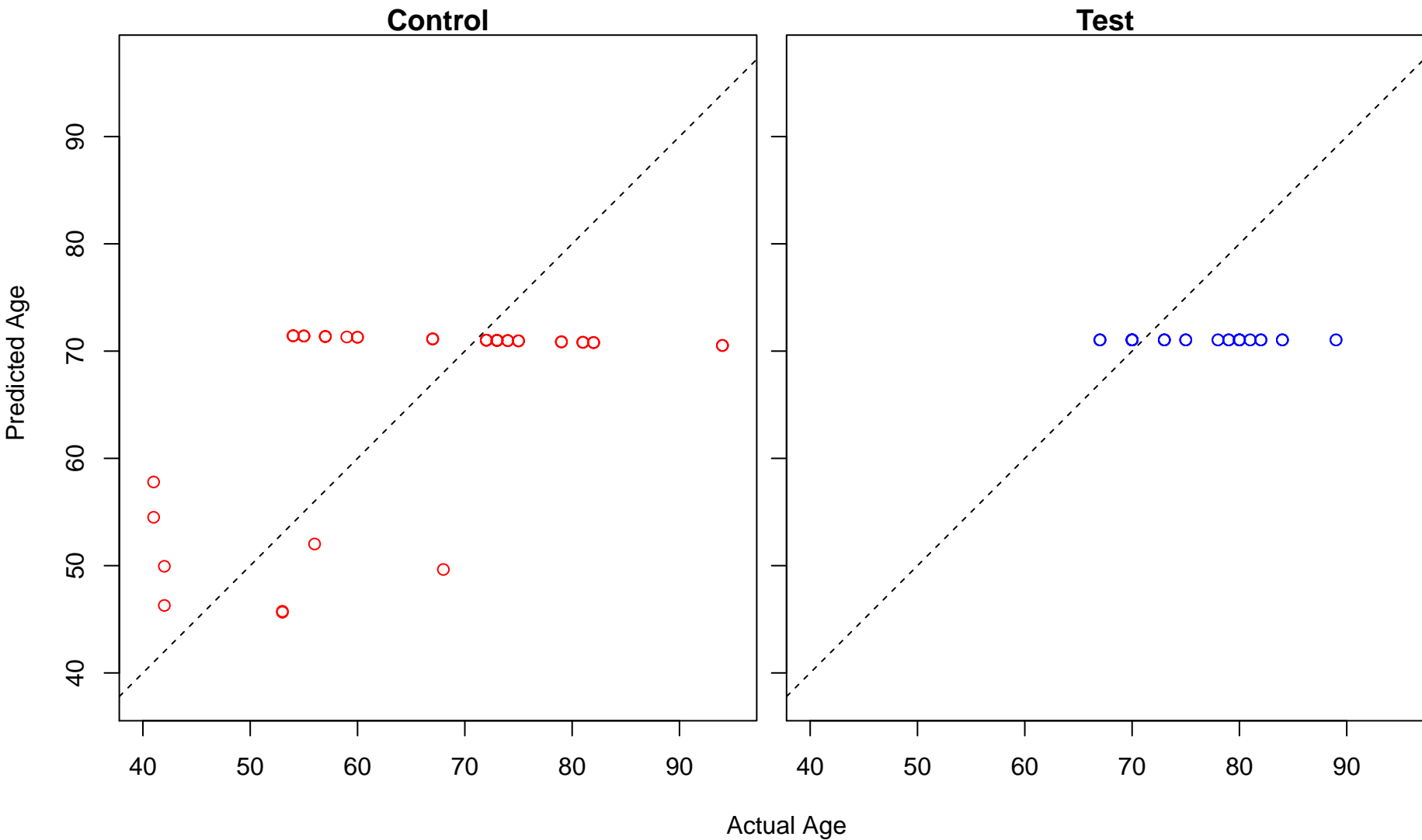


Test

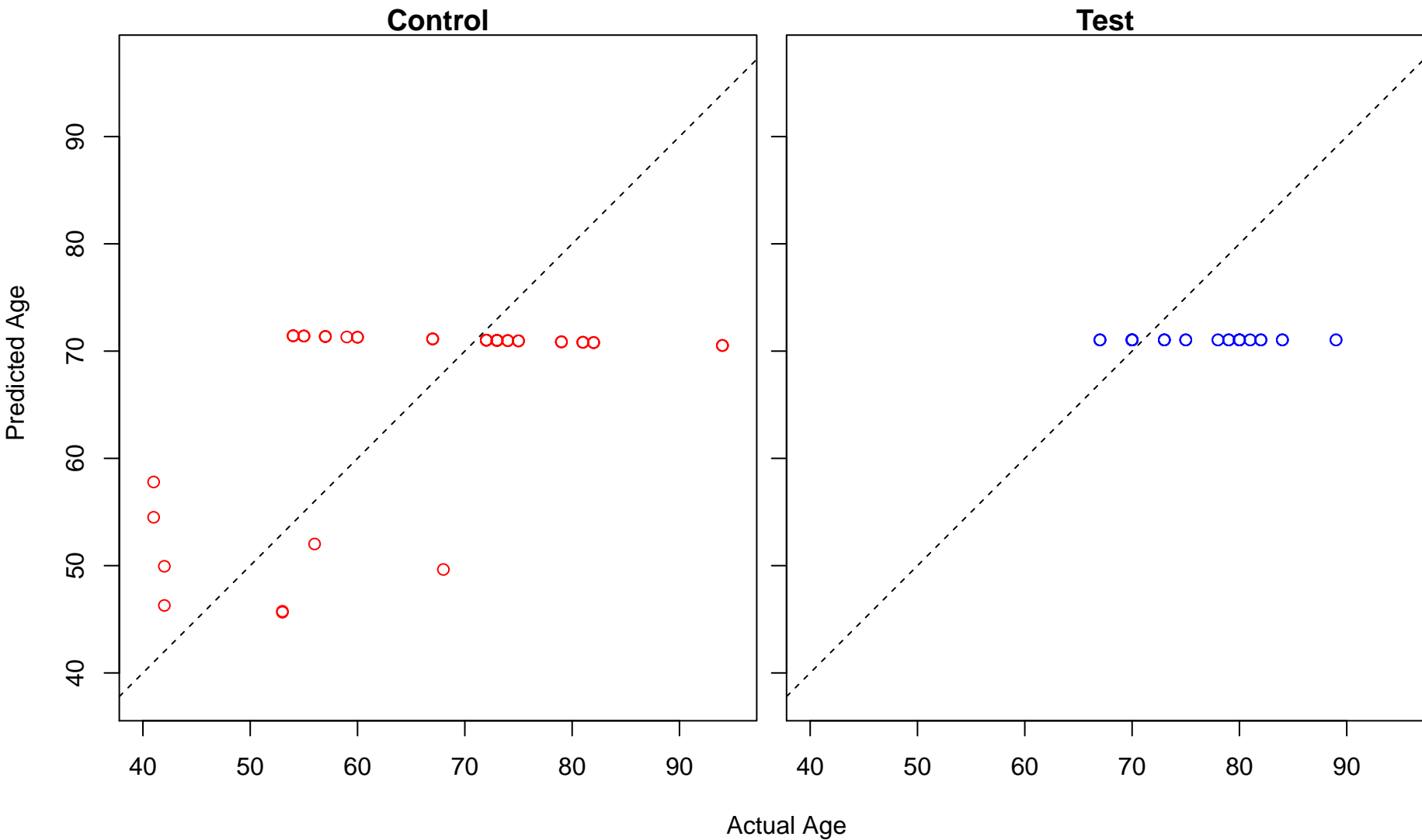


Actual Age

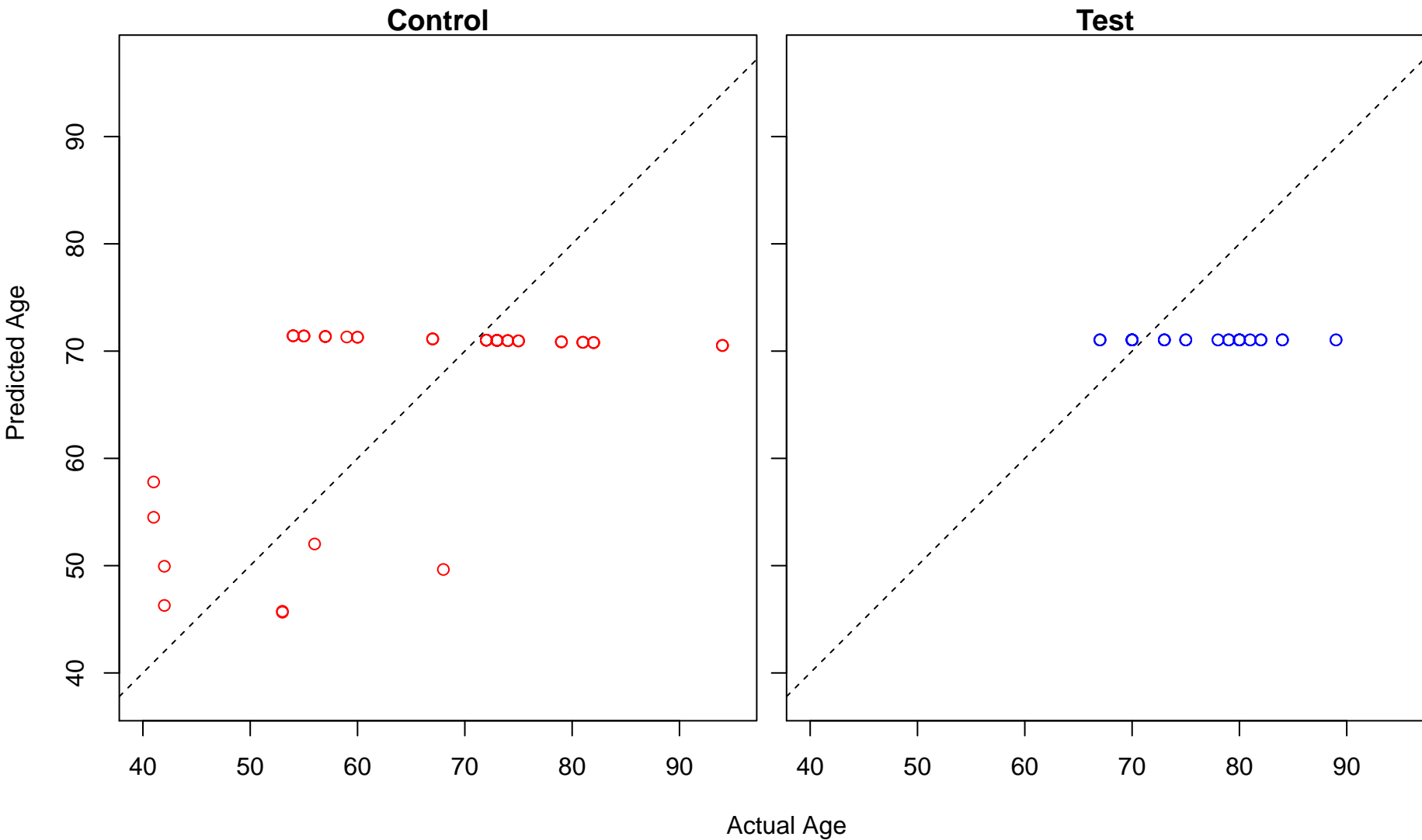
regulation of extrinsic apoptotic signaling pathway via death domain receptors (Score: 0.798246)



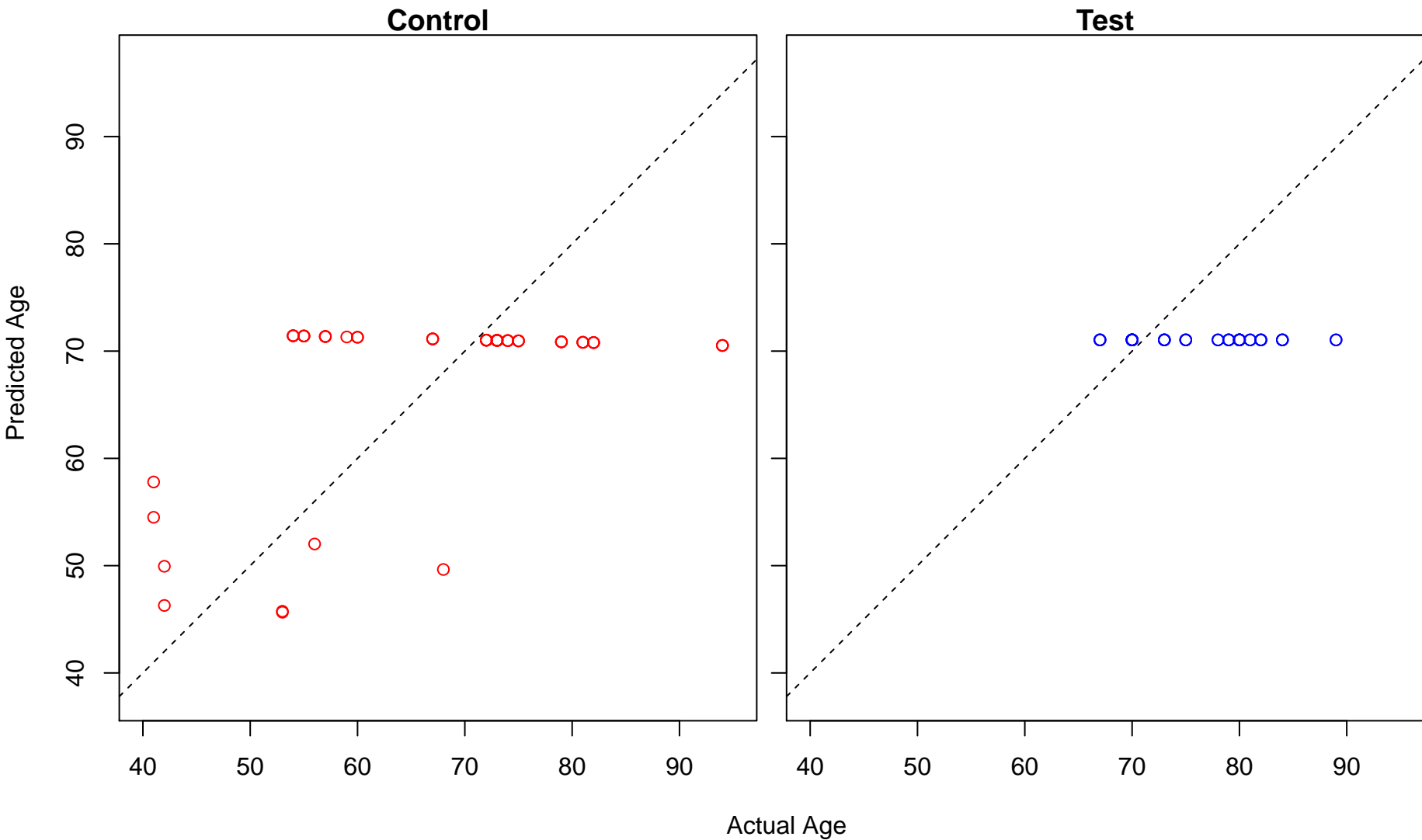
negative regulation of extrinsic apoptotic signaling pathway via death domain receptors (Score: 0.798)



regulation of extrinsic apoptotic signaling pathway (Score: 0.798246)

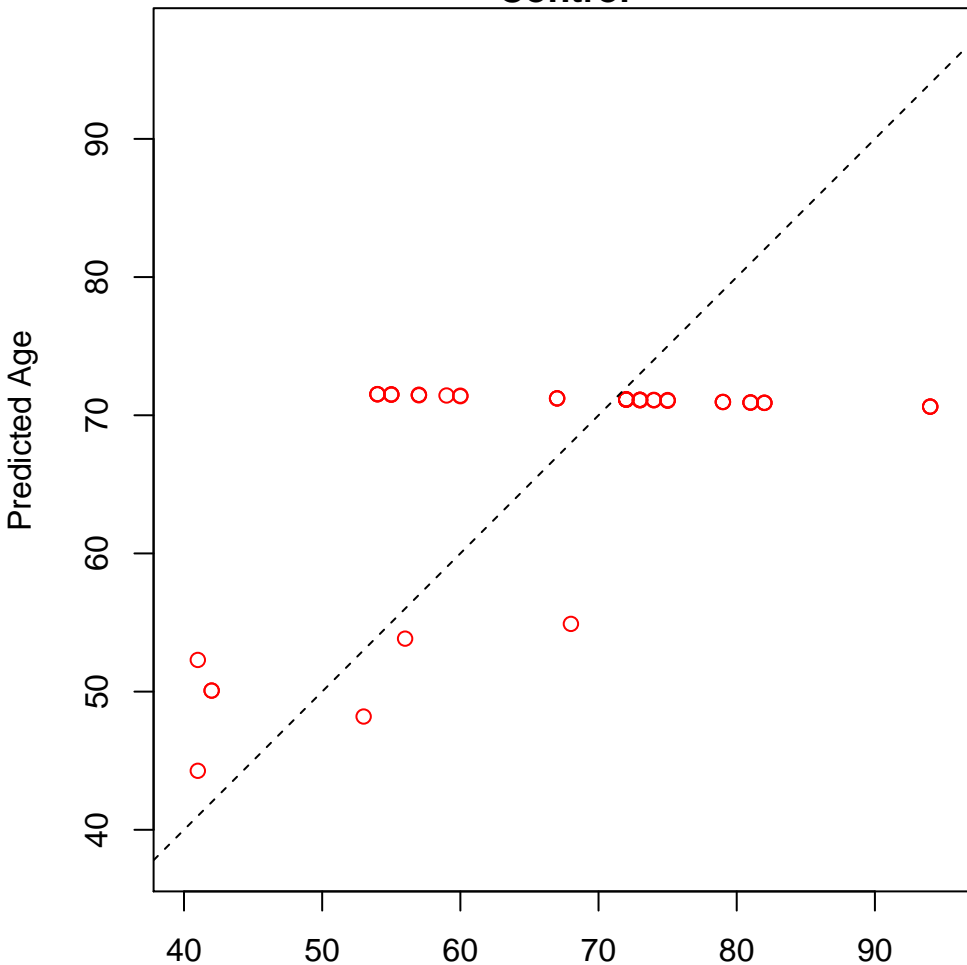


negative regulation of extrinsic apoptotic signaling pathway (Score: 0.798246)

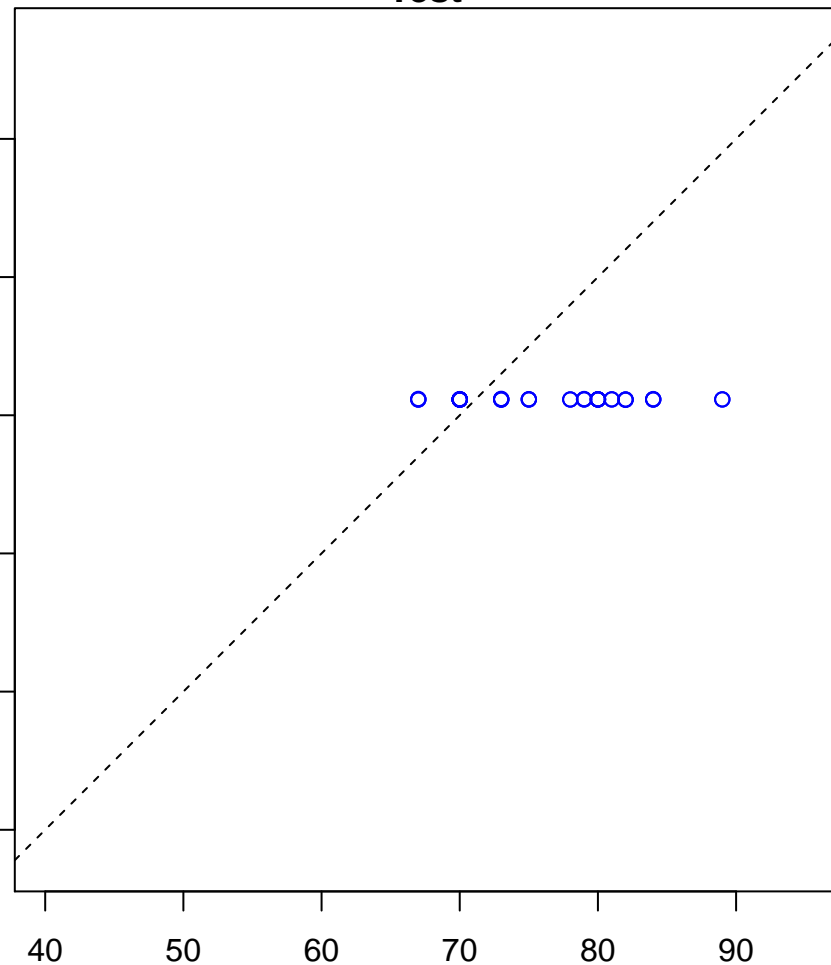


positive regulation of peptide secretion (Score: 0.798206)

Control



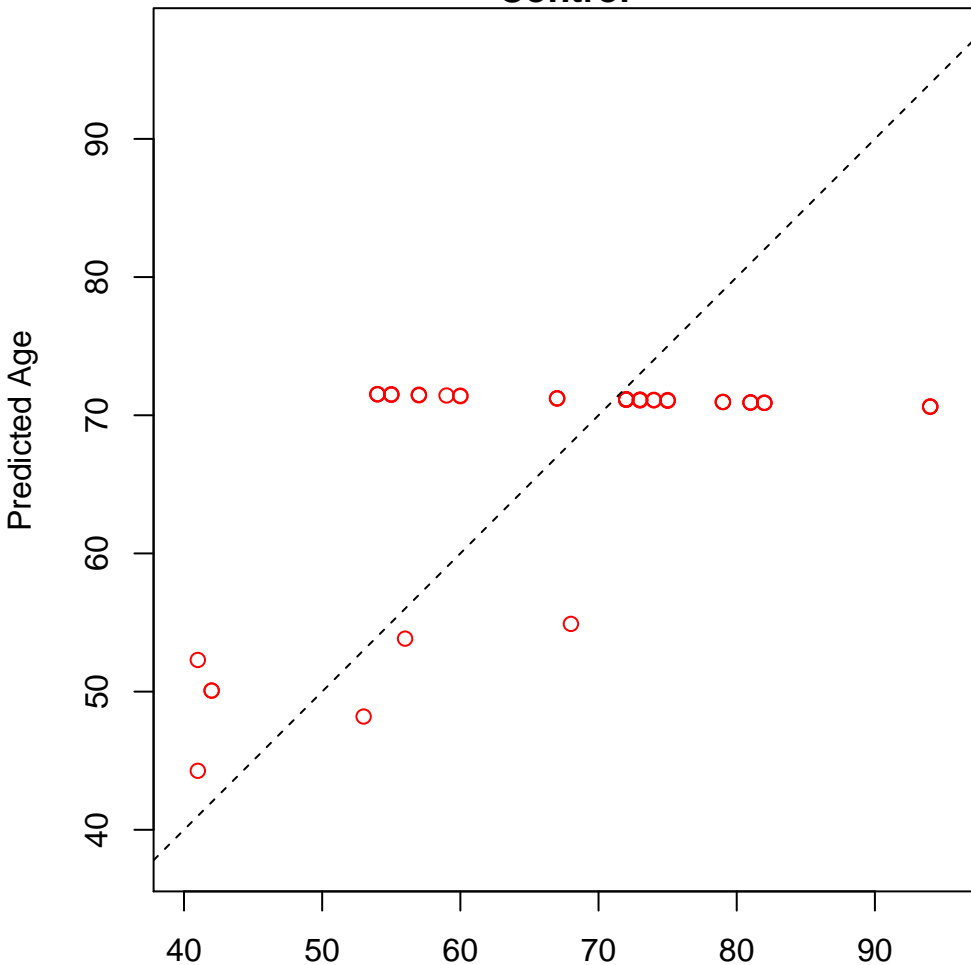
Test



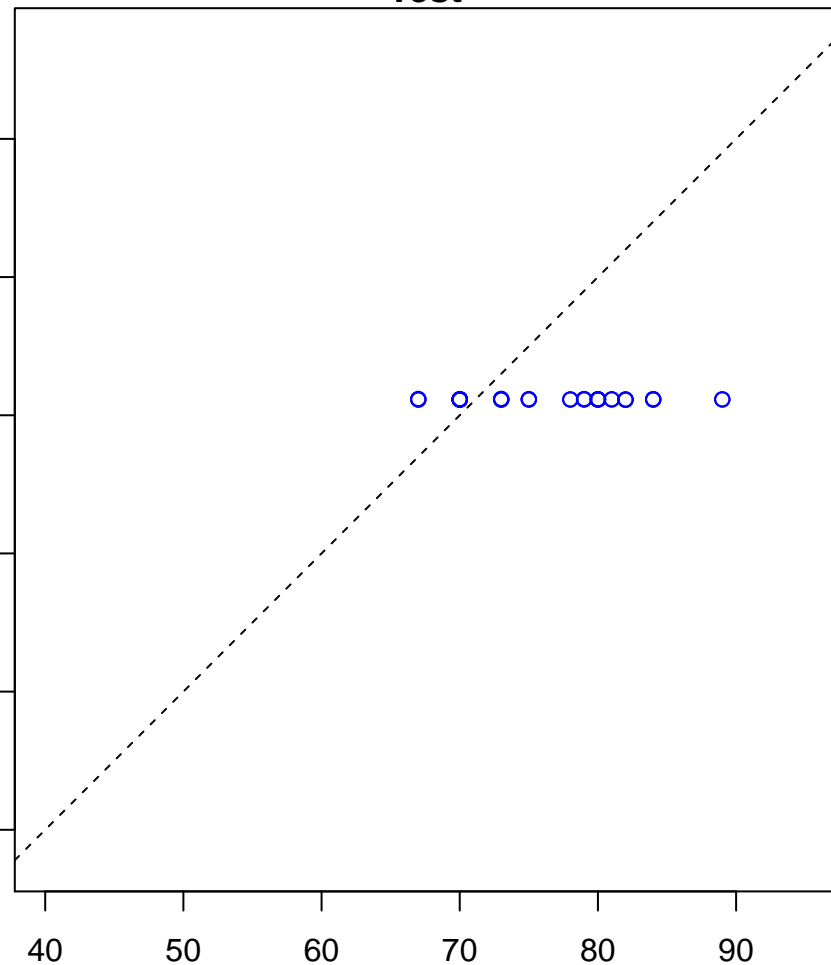
Actual Age

positive regulation of protein secretion (Score: 0.798206)

Control

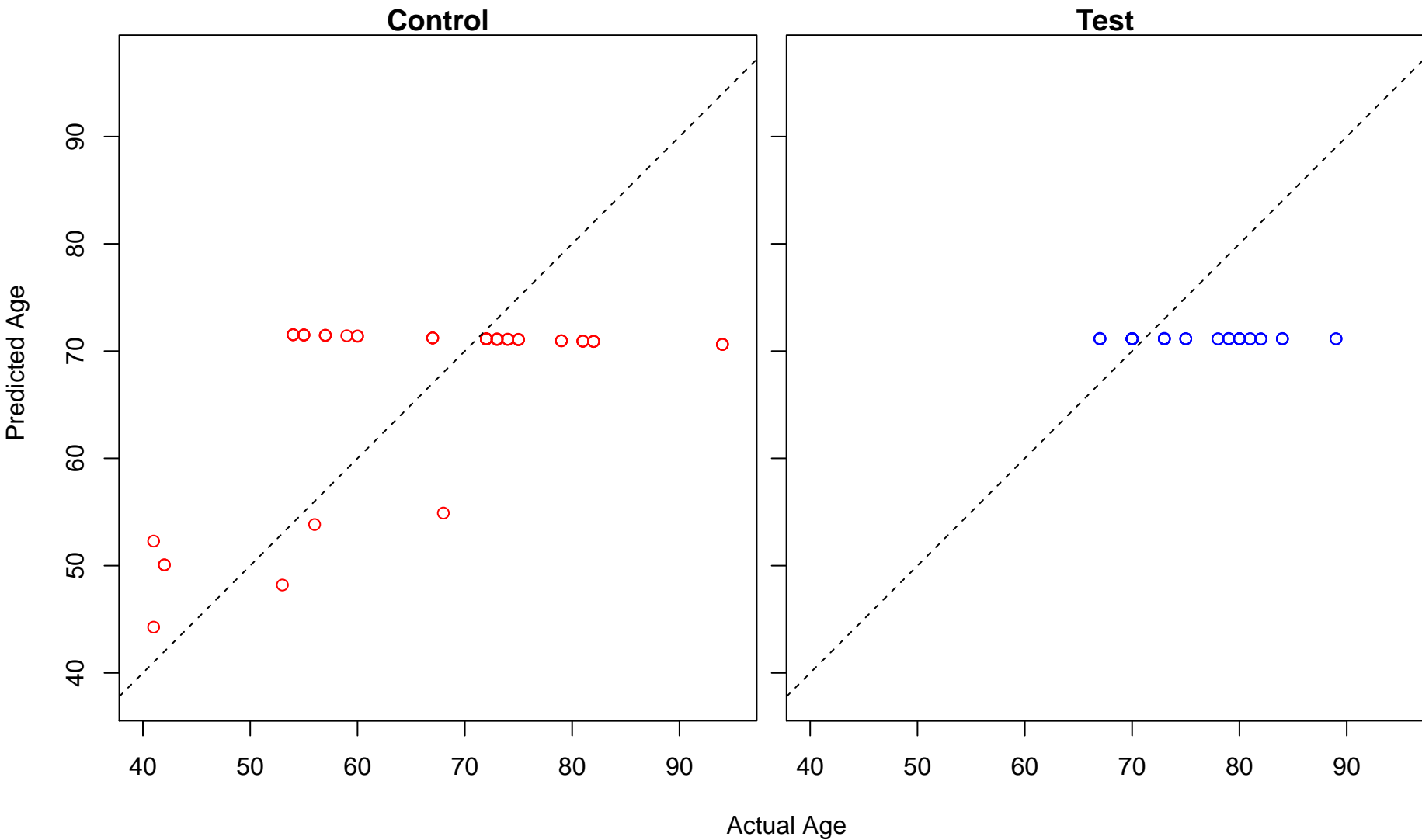


Test



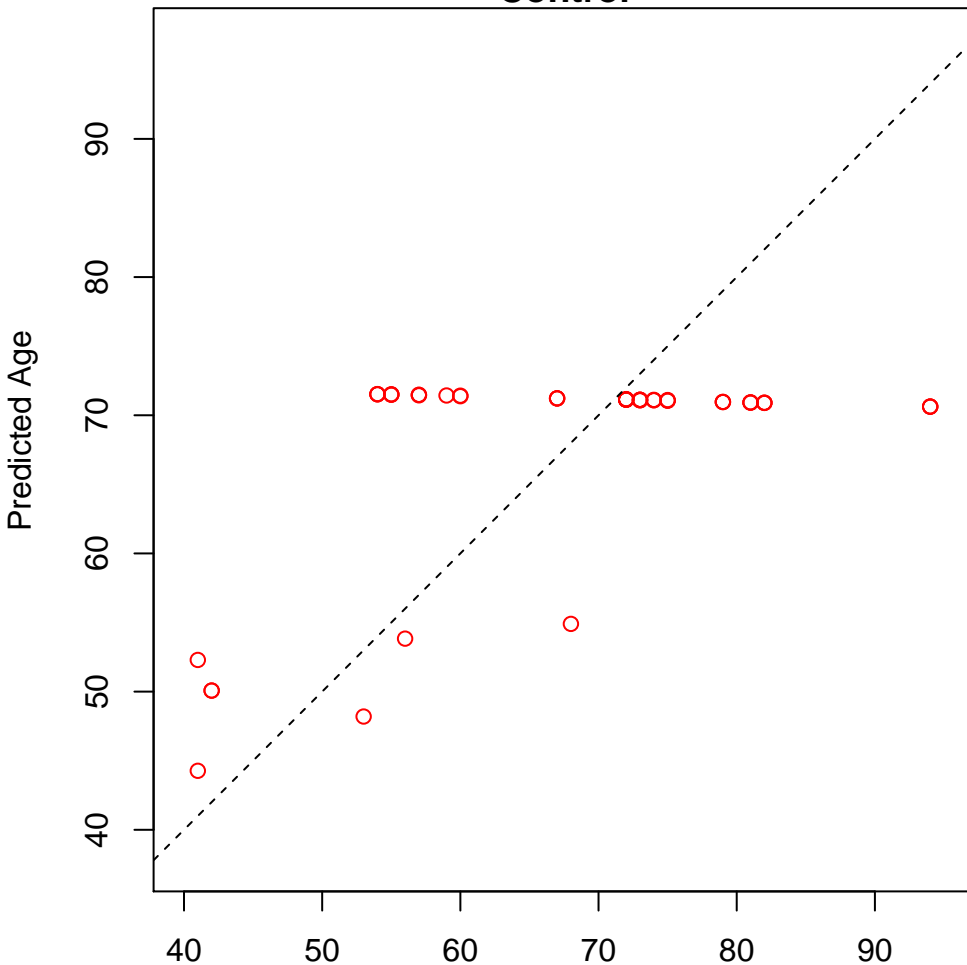
Actual Age

positive regulation of secretion (Score: 0.798206)

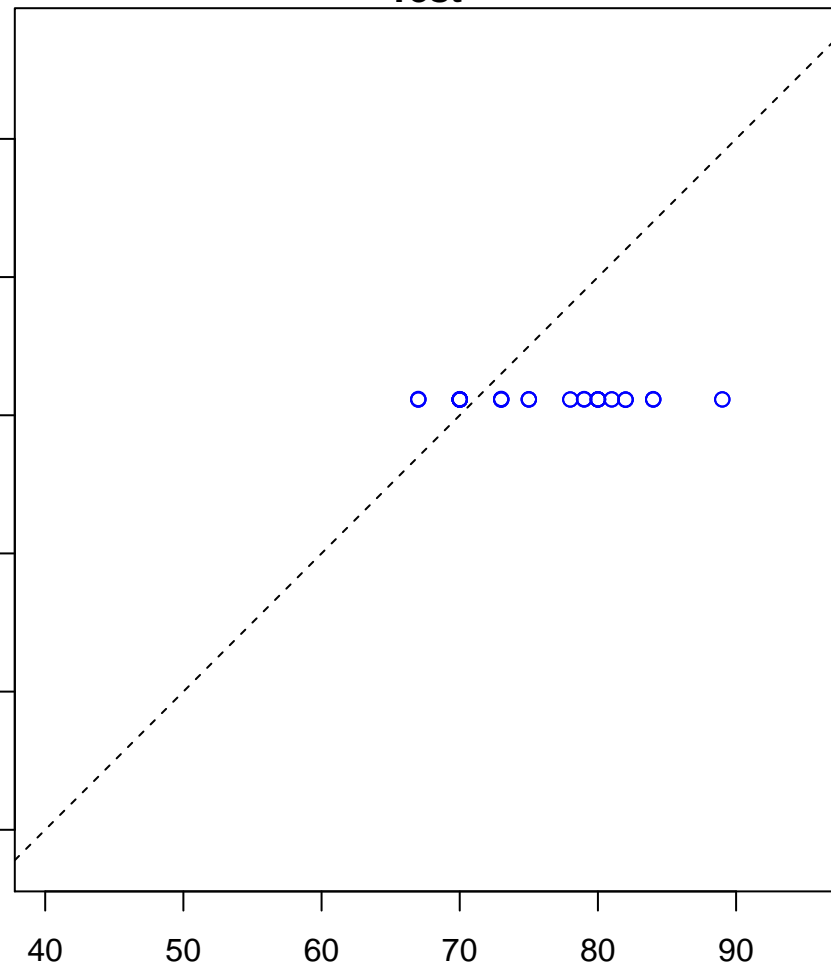


positive regulation of secretion by cell (Score: 0.798206)

Control



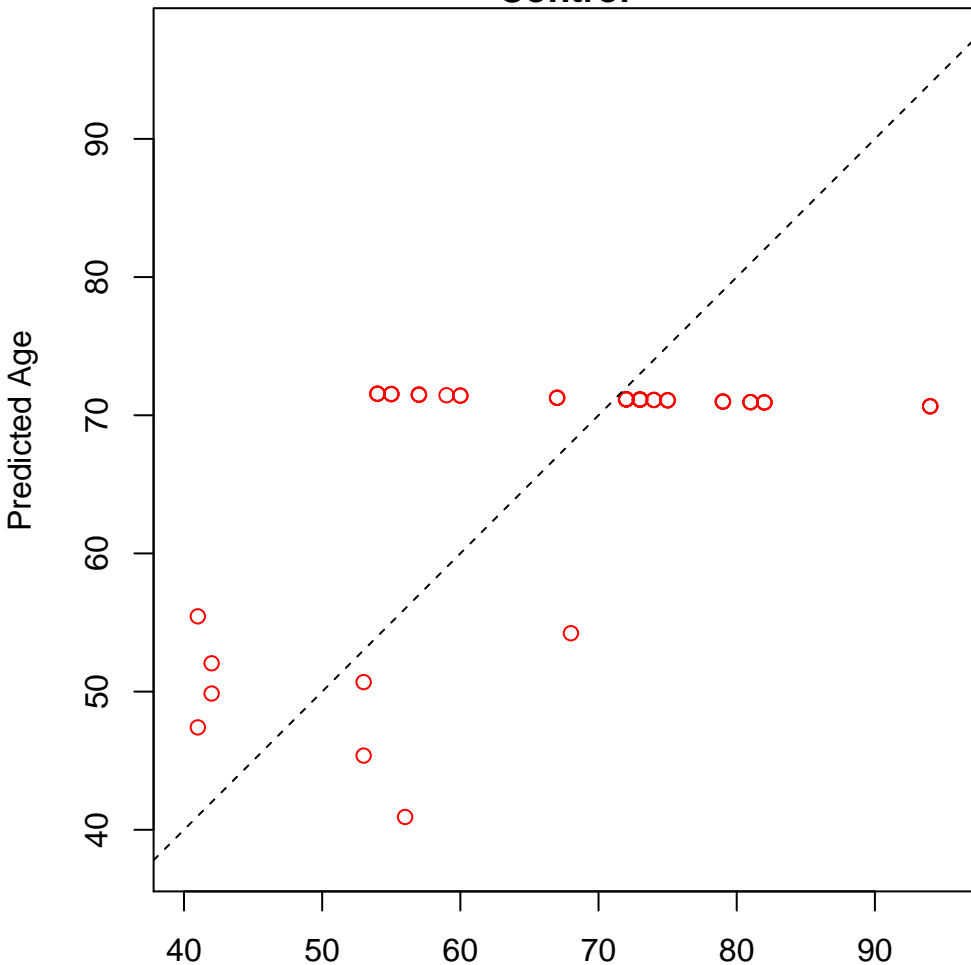
Test



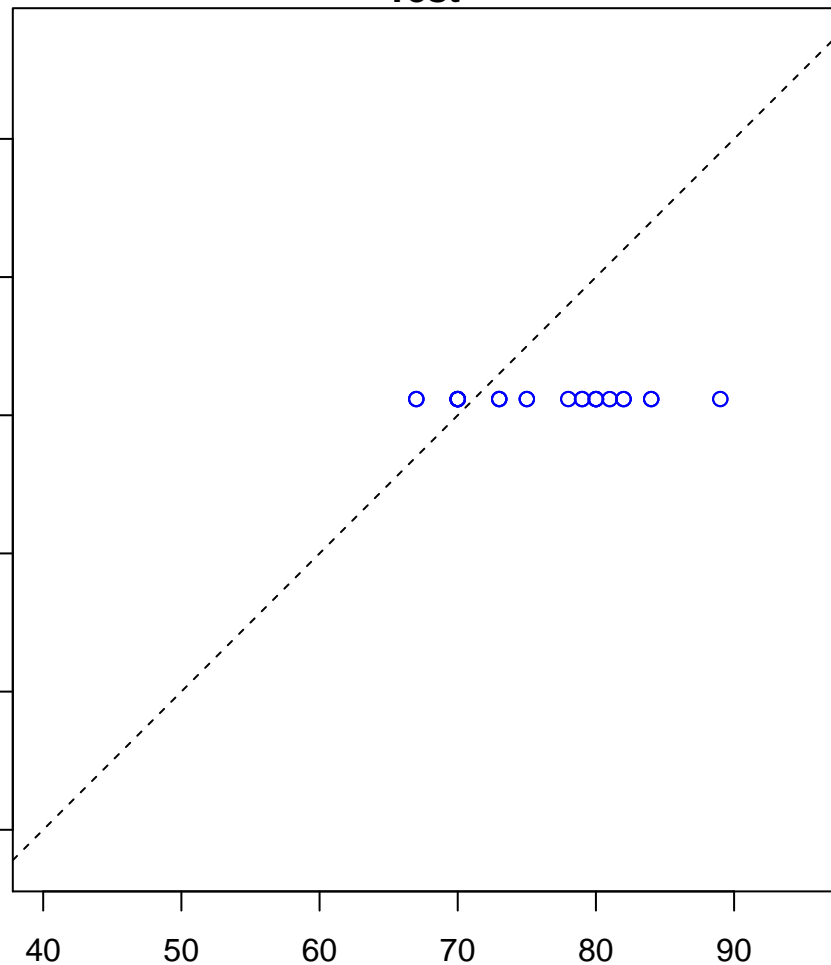
Actual Age

negative regulation of hydrolase activity (Score: 0.798173)

Control

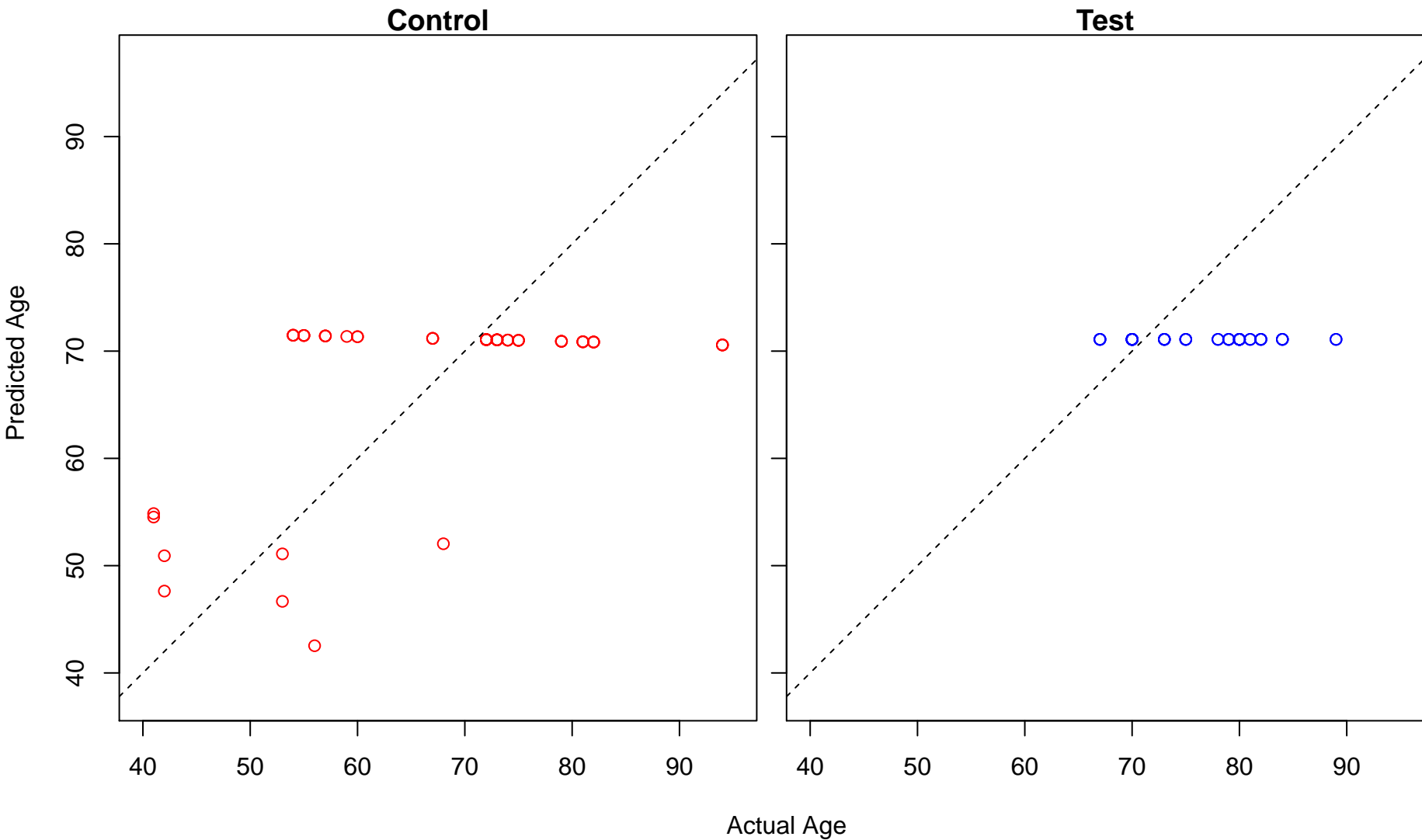


Test



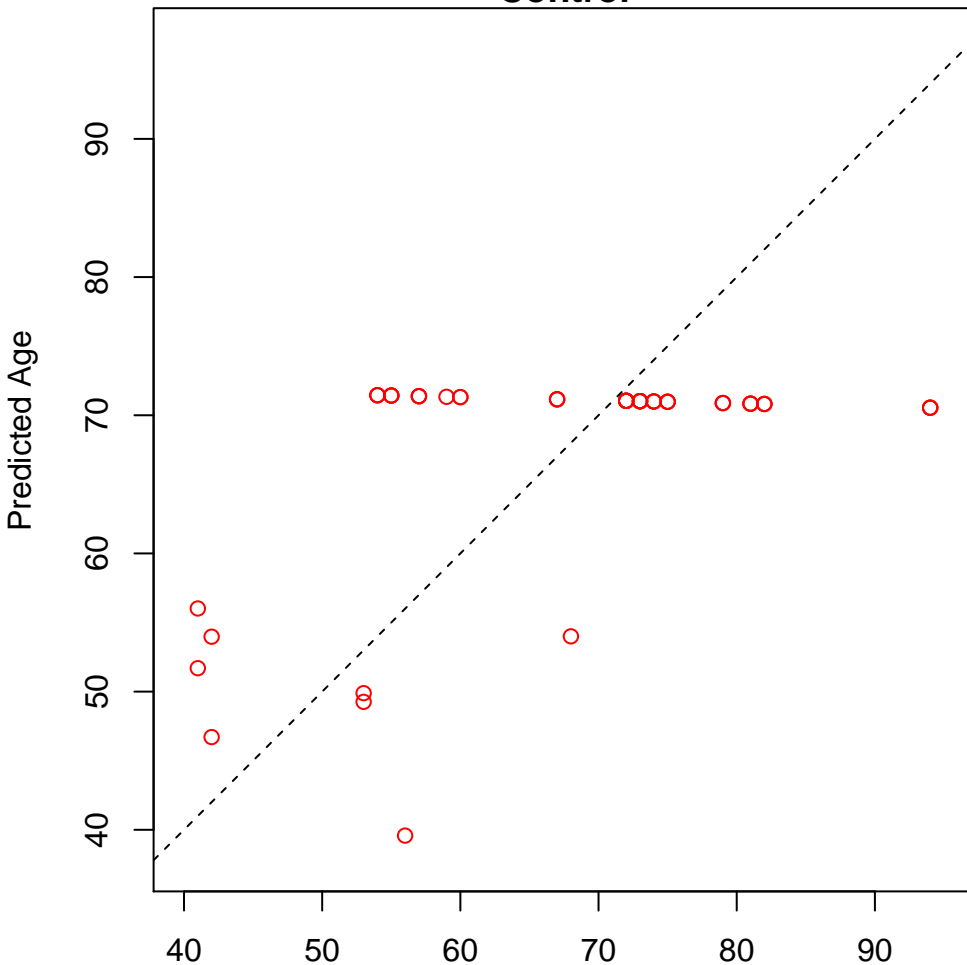
Actual Age

positive regulation of RNA metabolic process (Score: 0.798137)

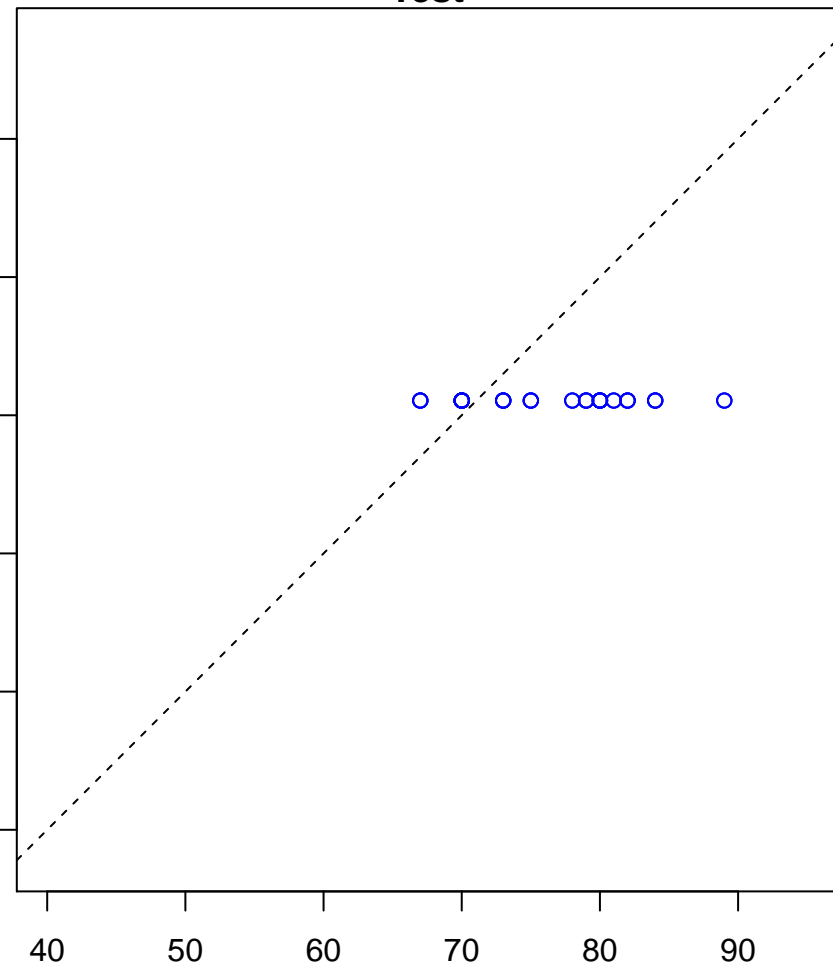


nucleic acid metabolic process (Score: 0.798123)

Control

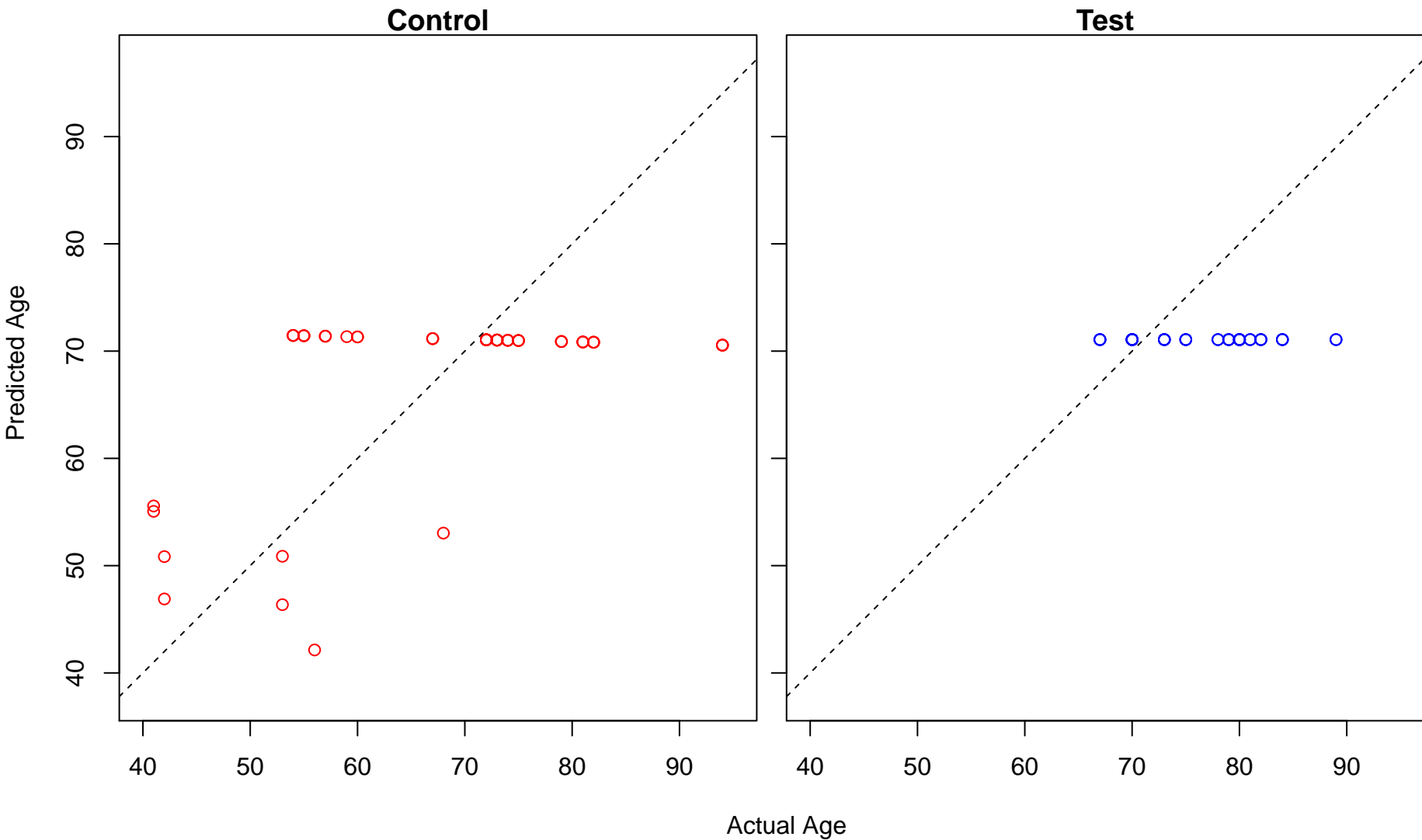


Test

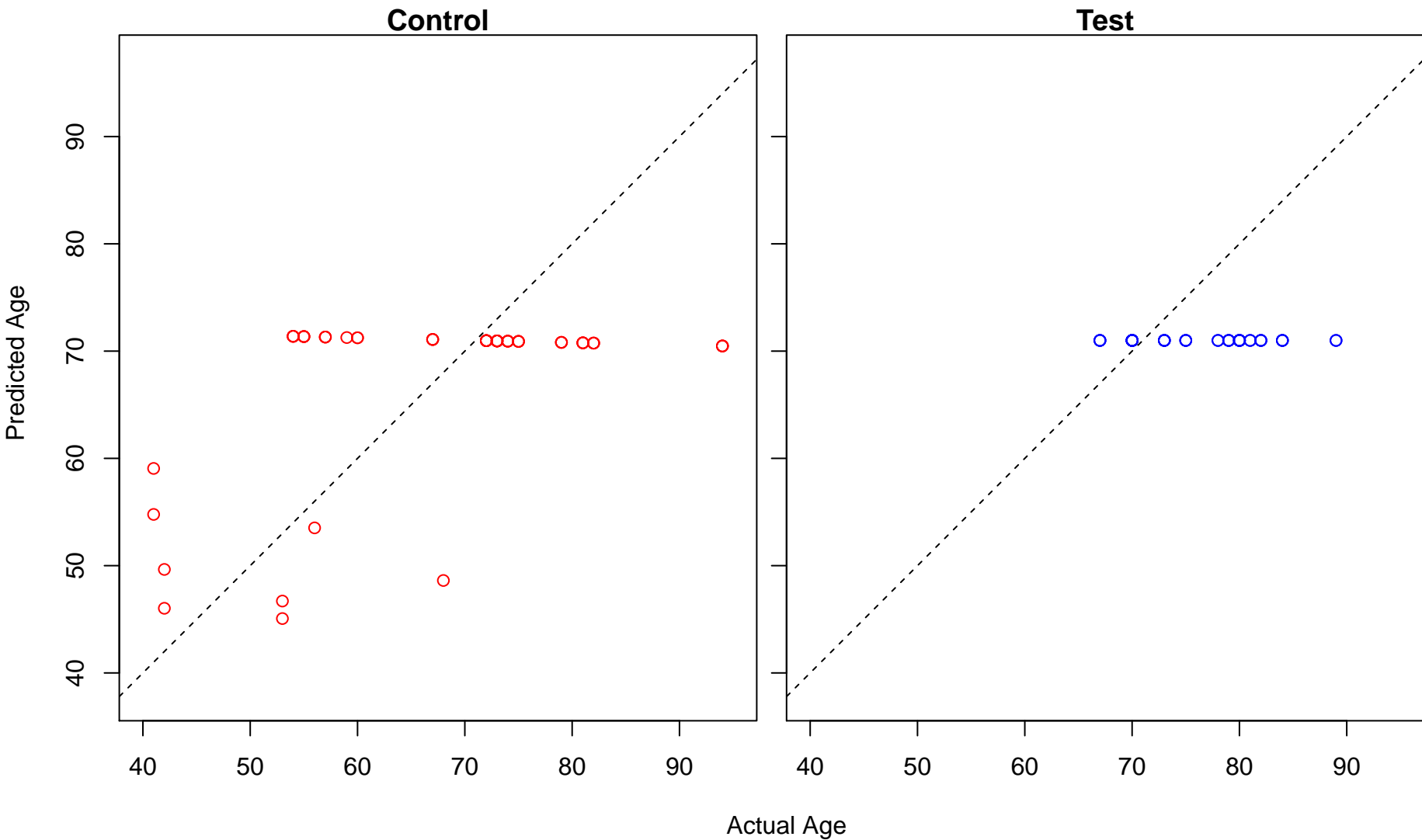


Actual Age

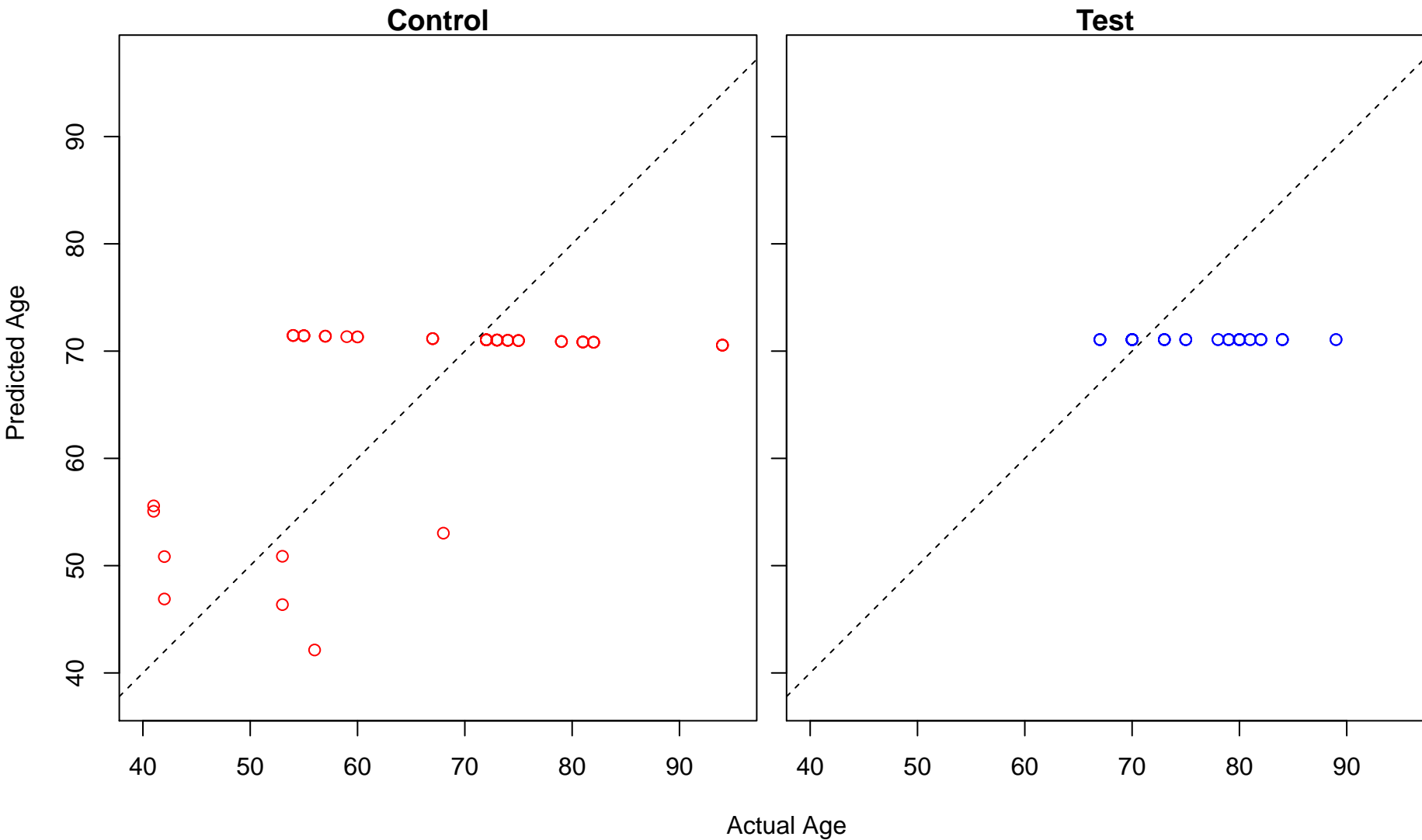
regulation of sequence-specific DNA binding transcription factor activity (Score: 0.798056)



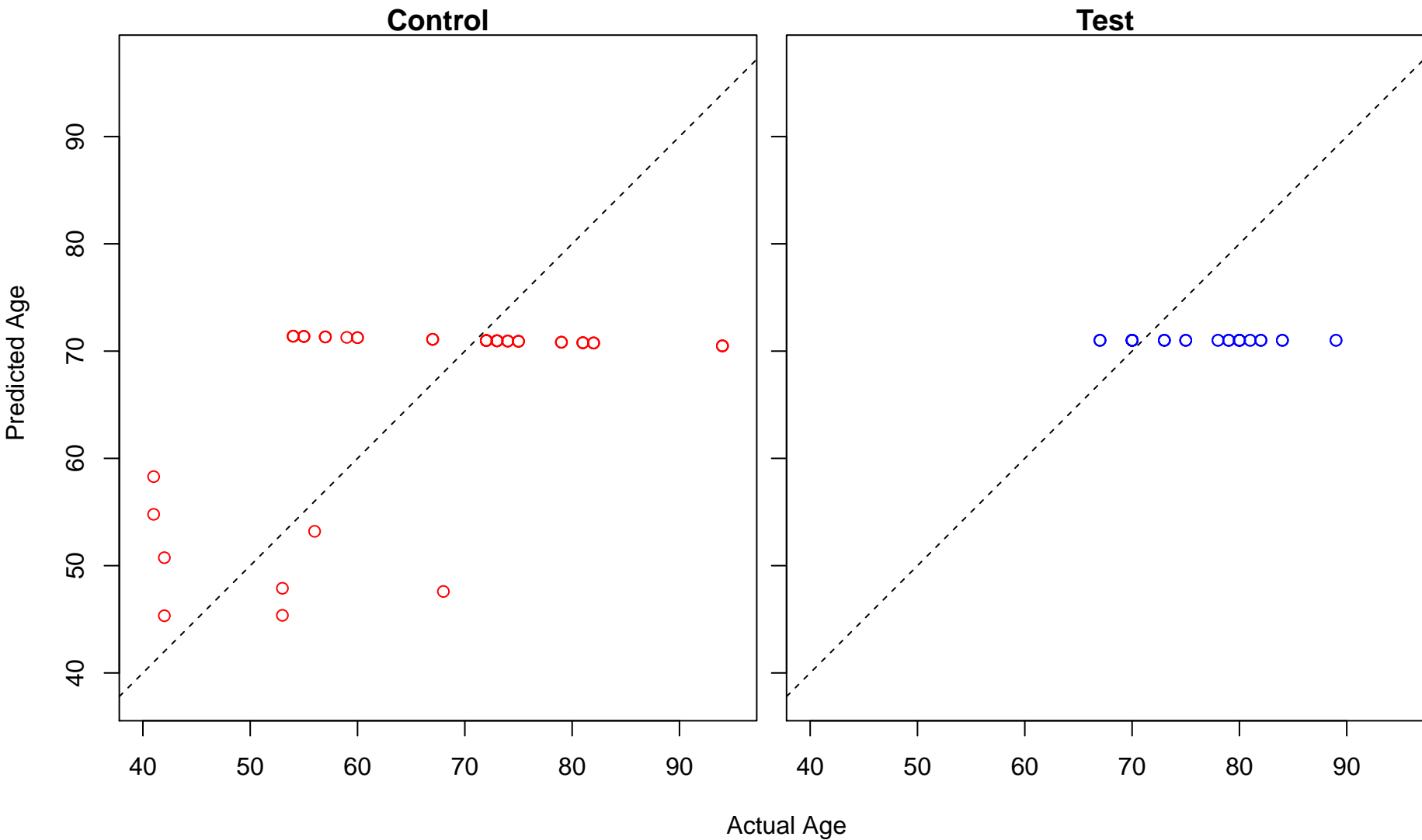
negative regulation of intrinsic apoptotic signaling pathway (Score: 0.798051)



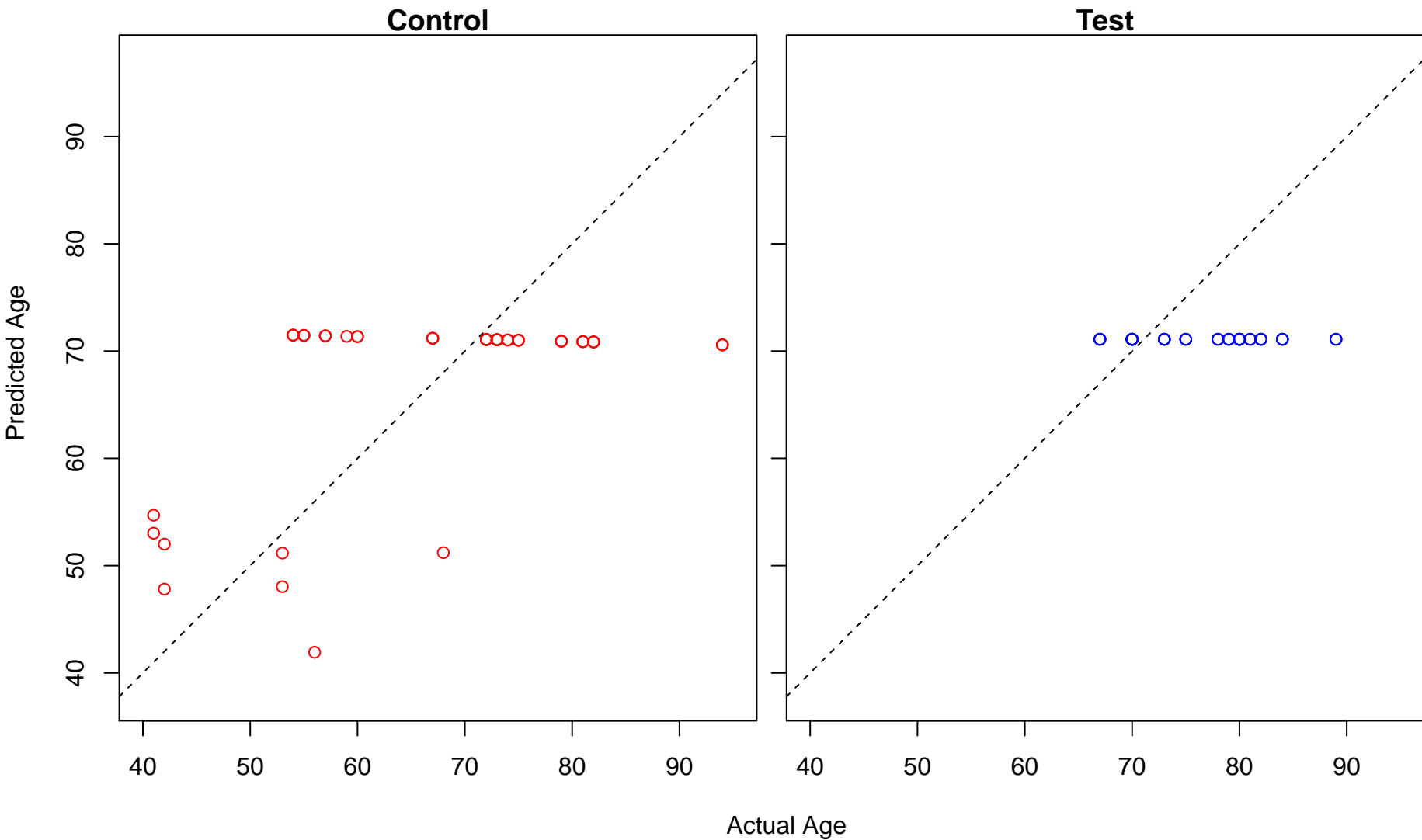
positive regulation of sequence-specific DNA binding transcription factor activity (Score: 0.798043)



regulation of DNA binding (Score: 0.798015)

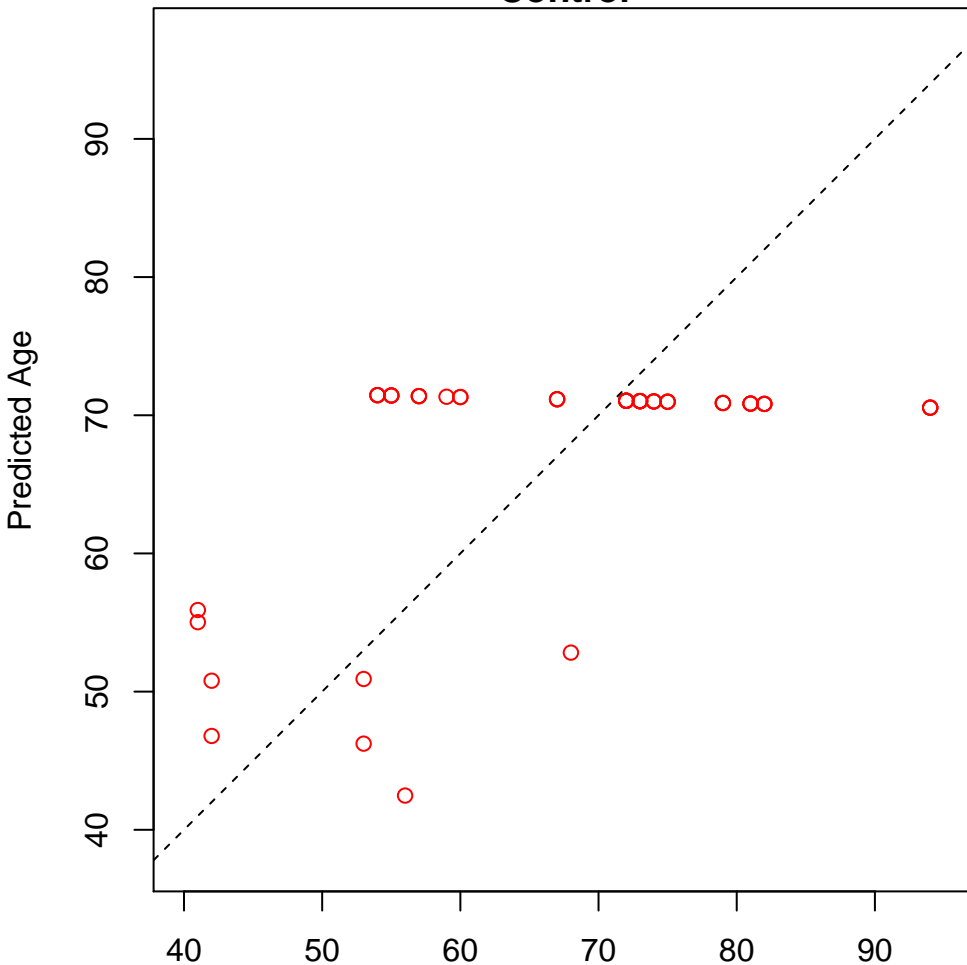


negative regulation of nitrogen compound metabolic process (Score: 0.797999)

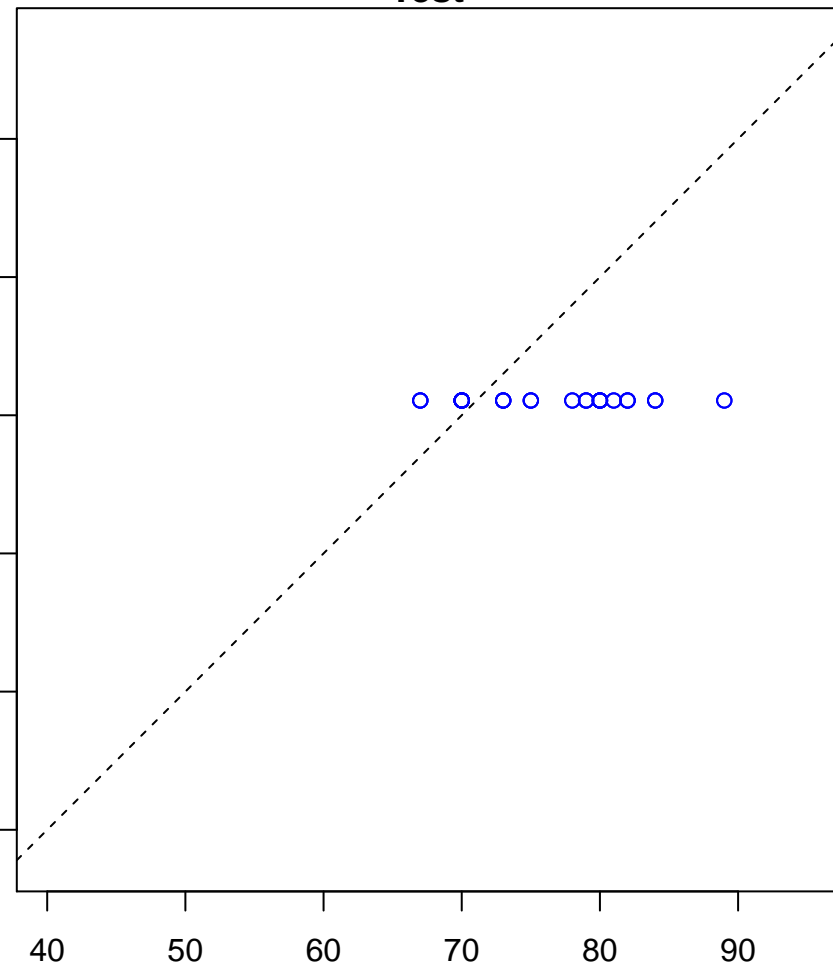


glycoprotein metabolic process (Score: 0.797998)

Control

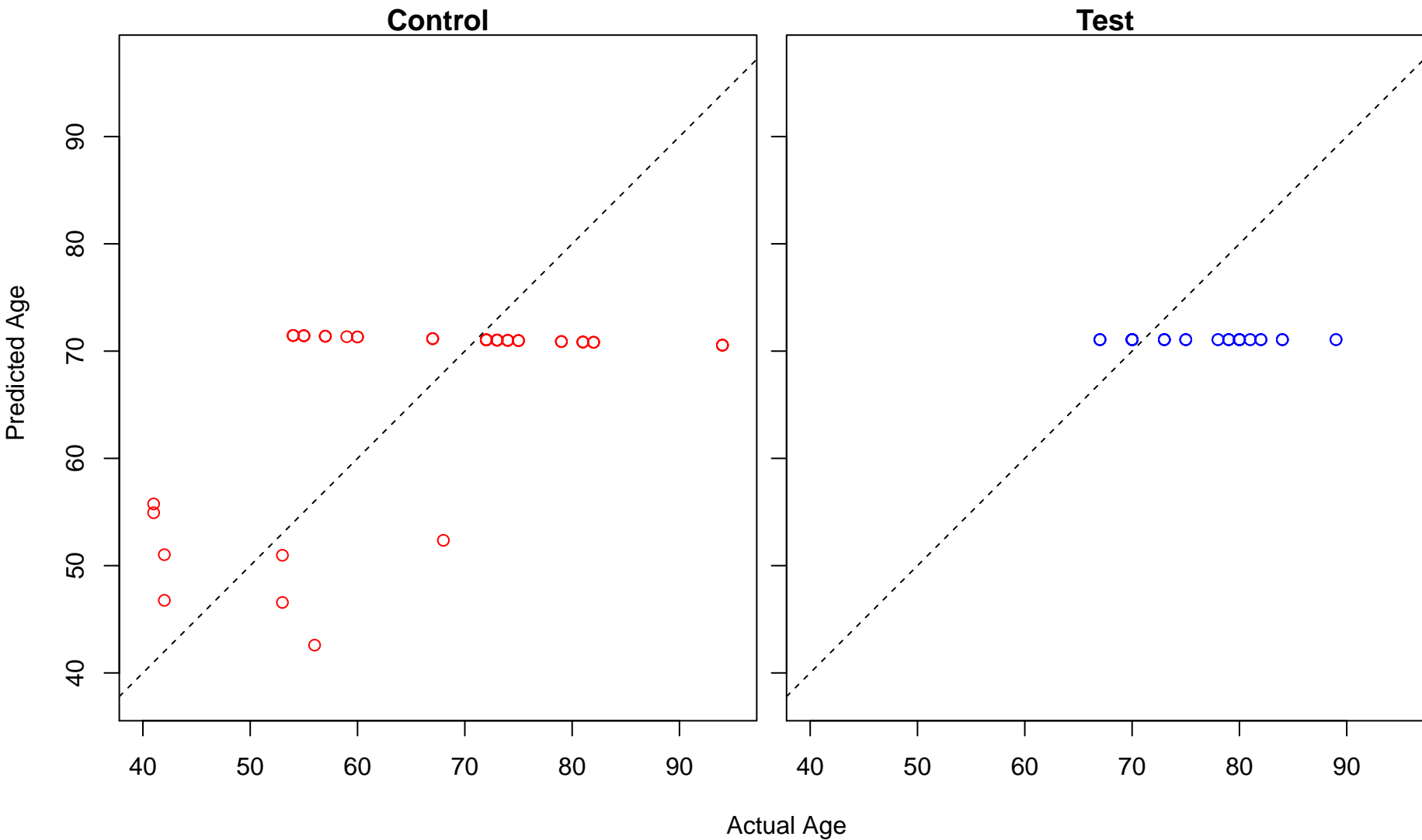


Test



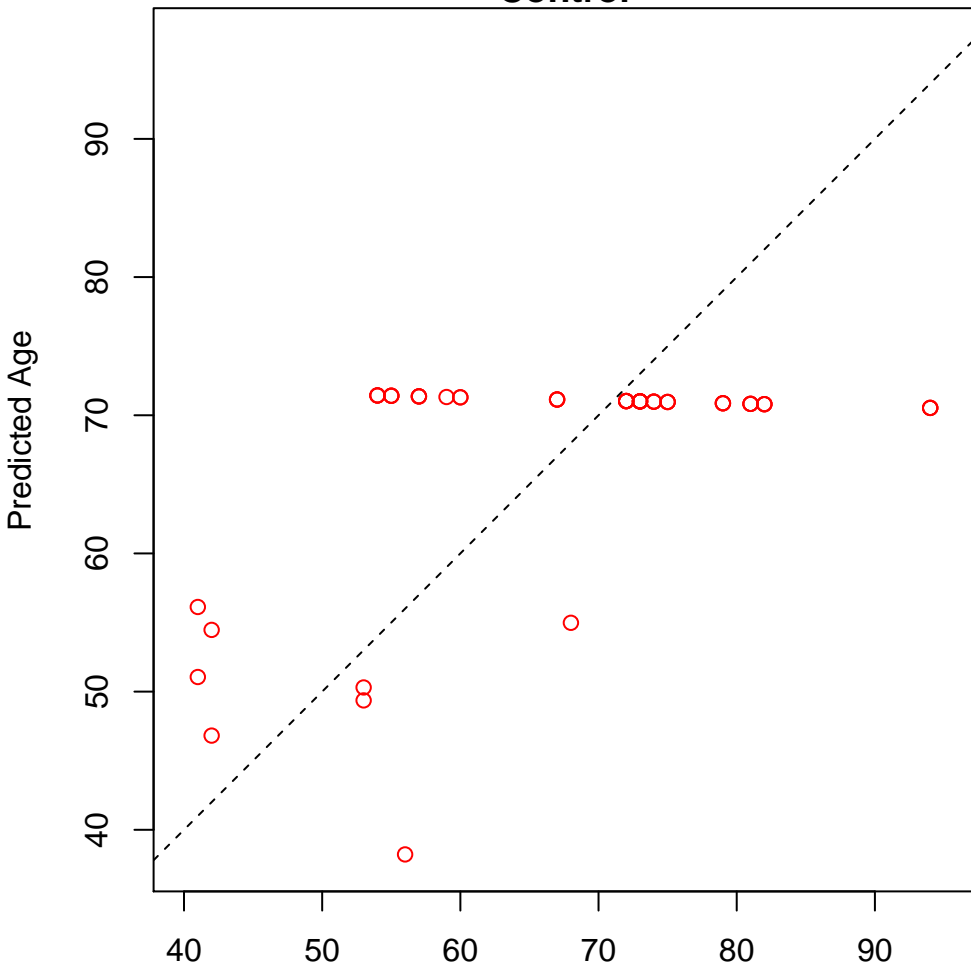
Actual Age

DNA repair (Score: 0.797975)

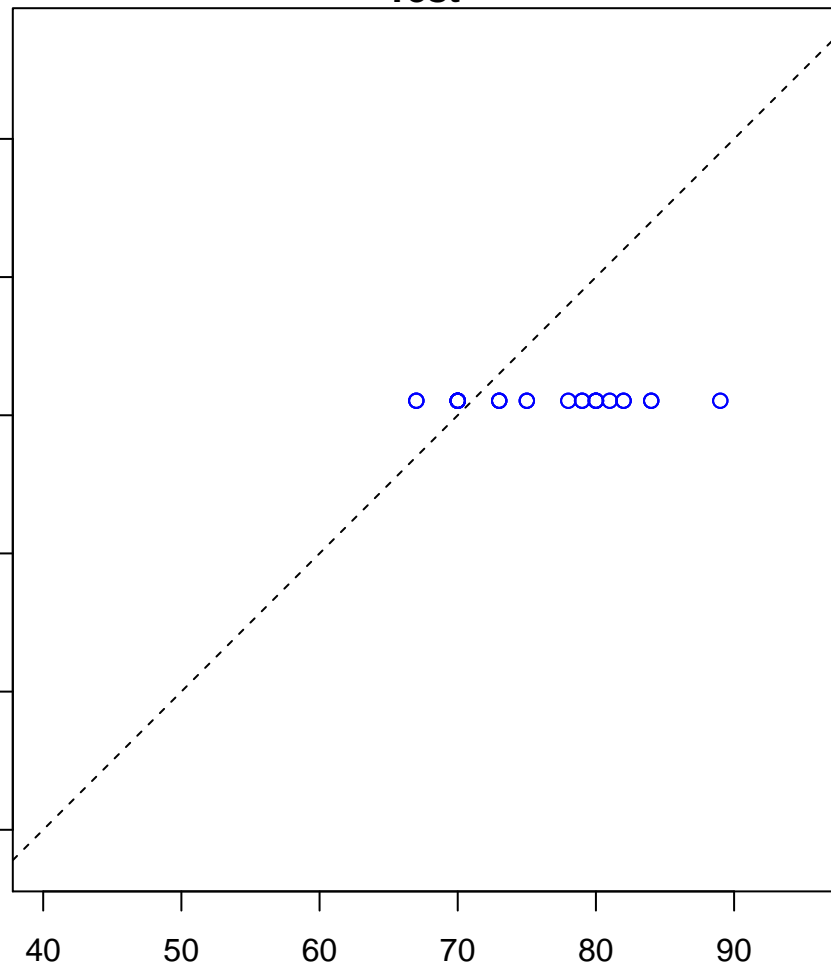


cellular component biogenesis (Score: 0.797969)

Control



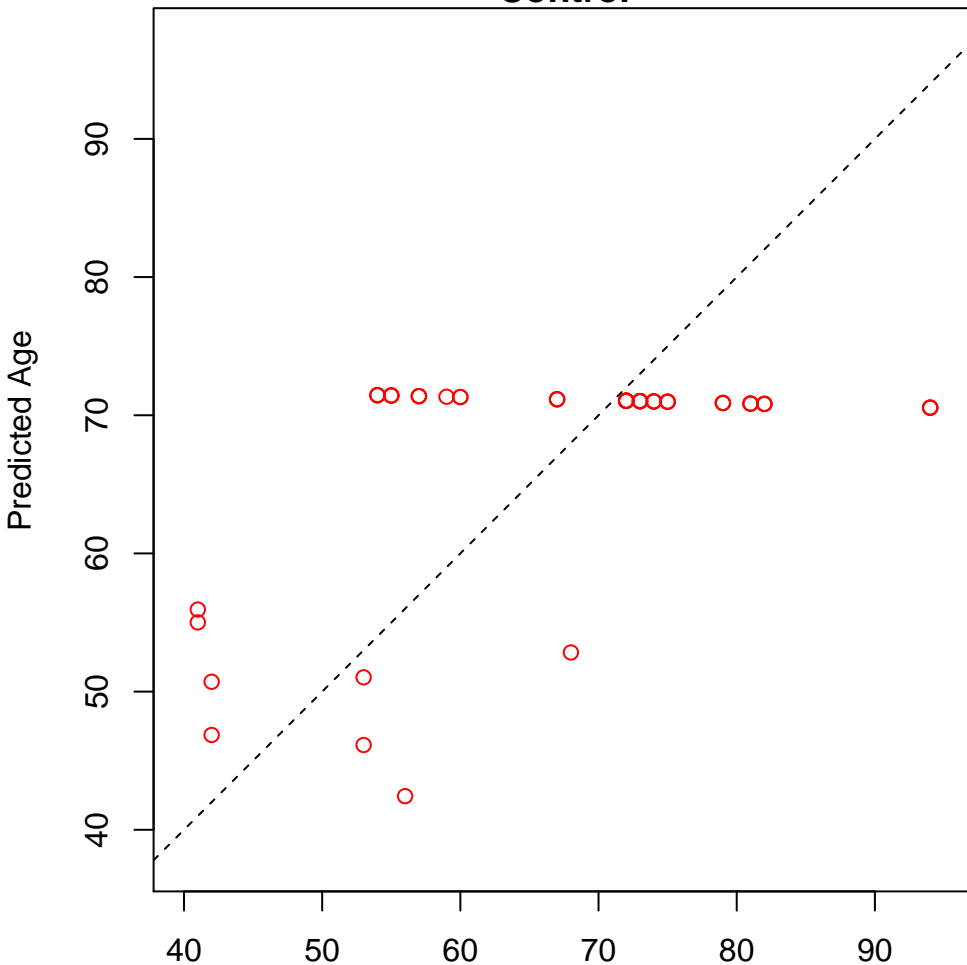
Test



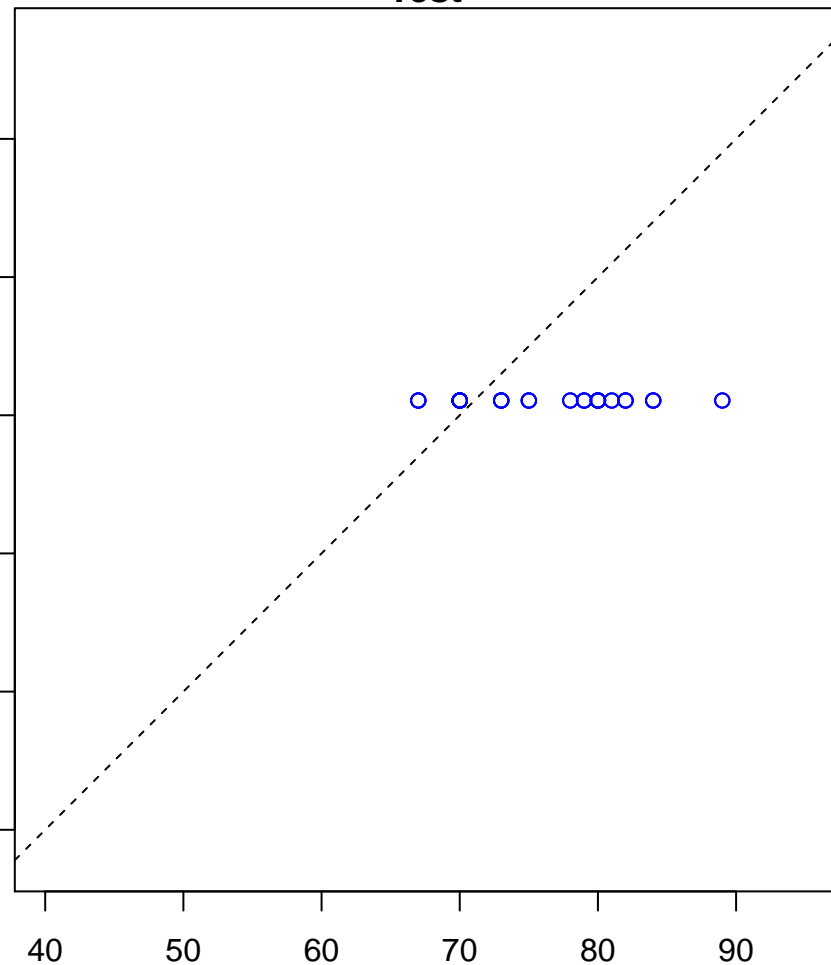
Actual Age

protein deglycosylation (Score: 0.797962)

Control

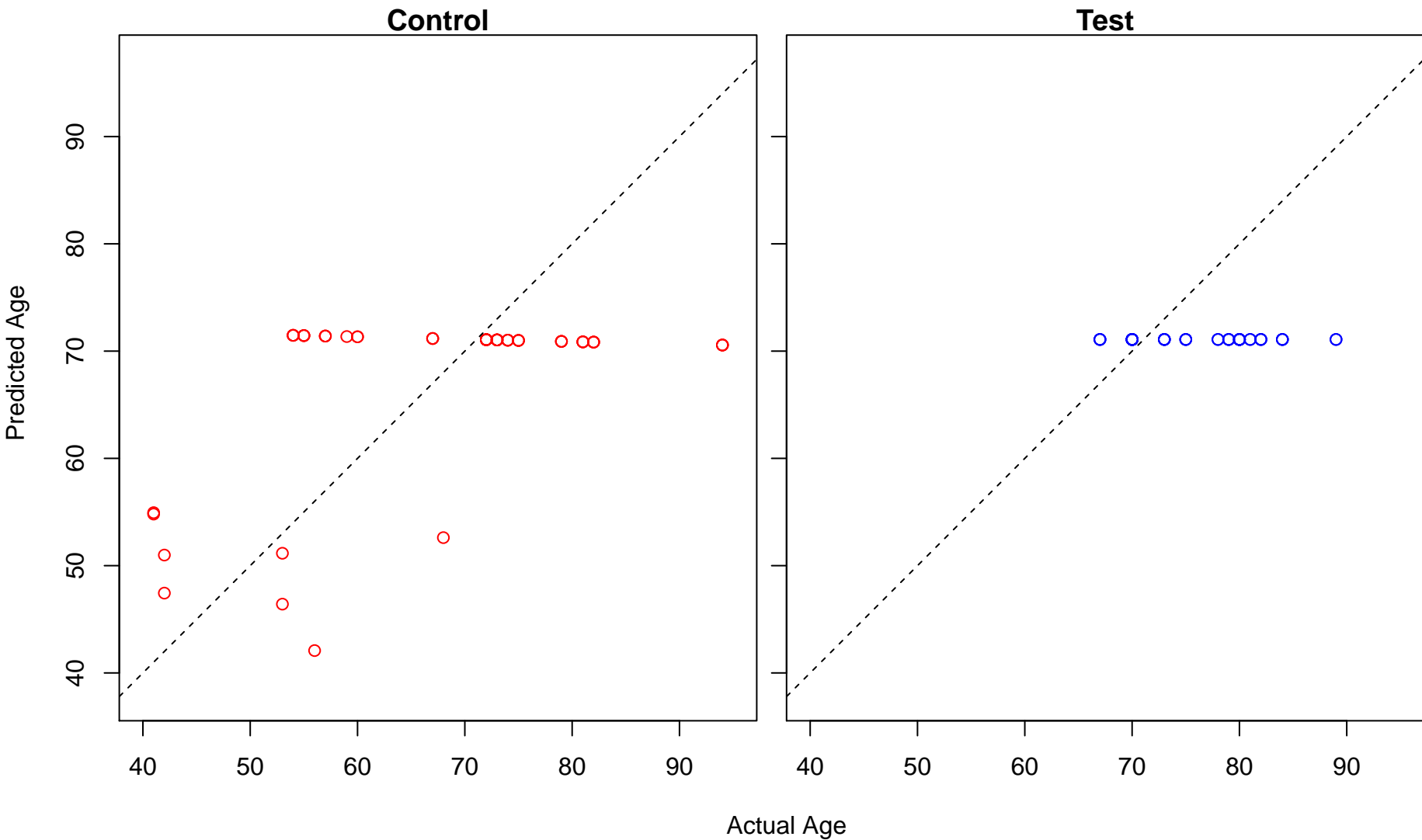


Test

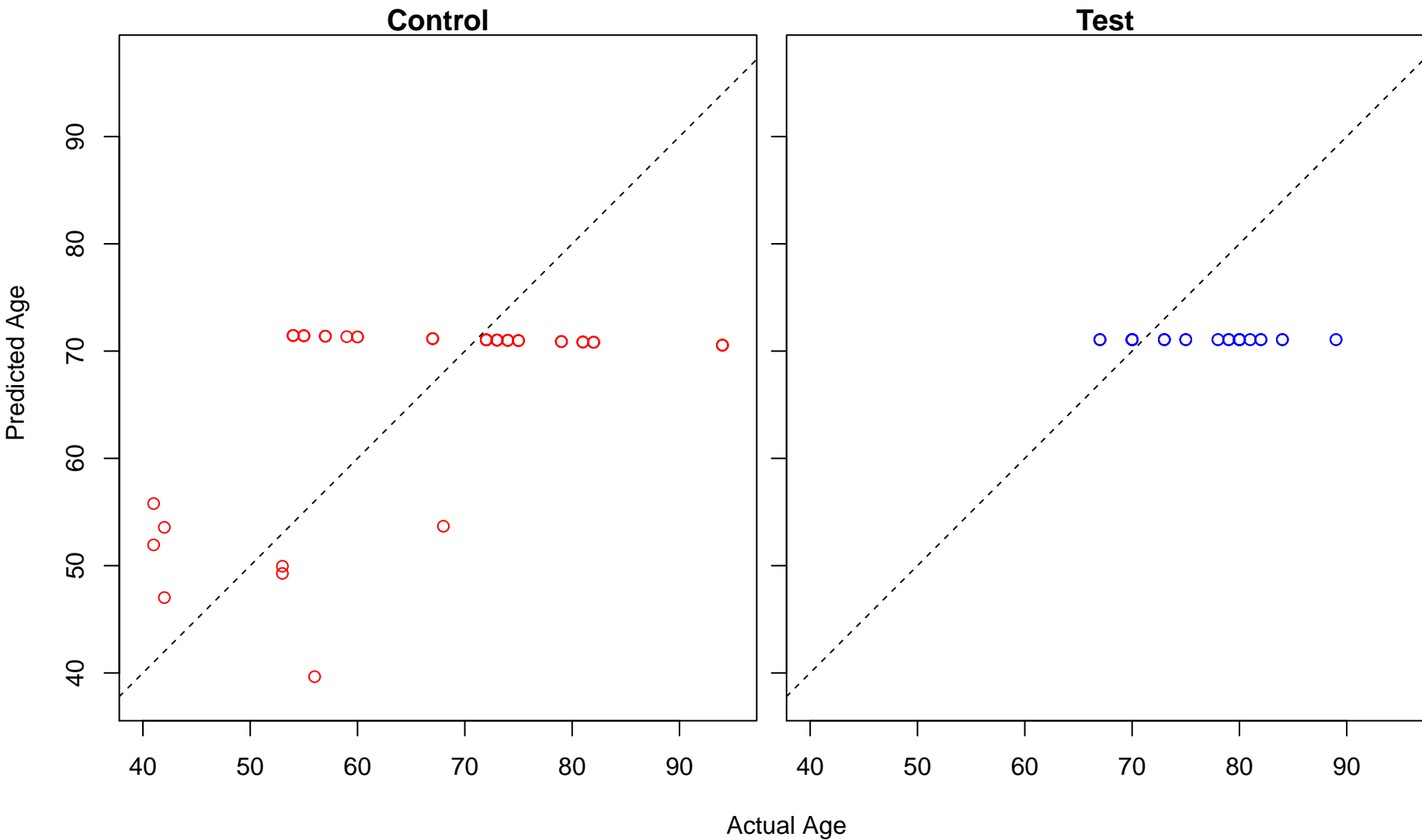


Actual Age

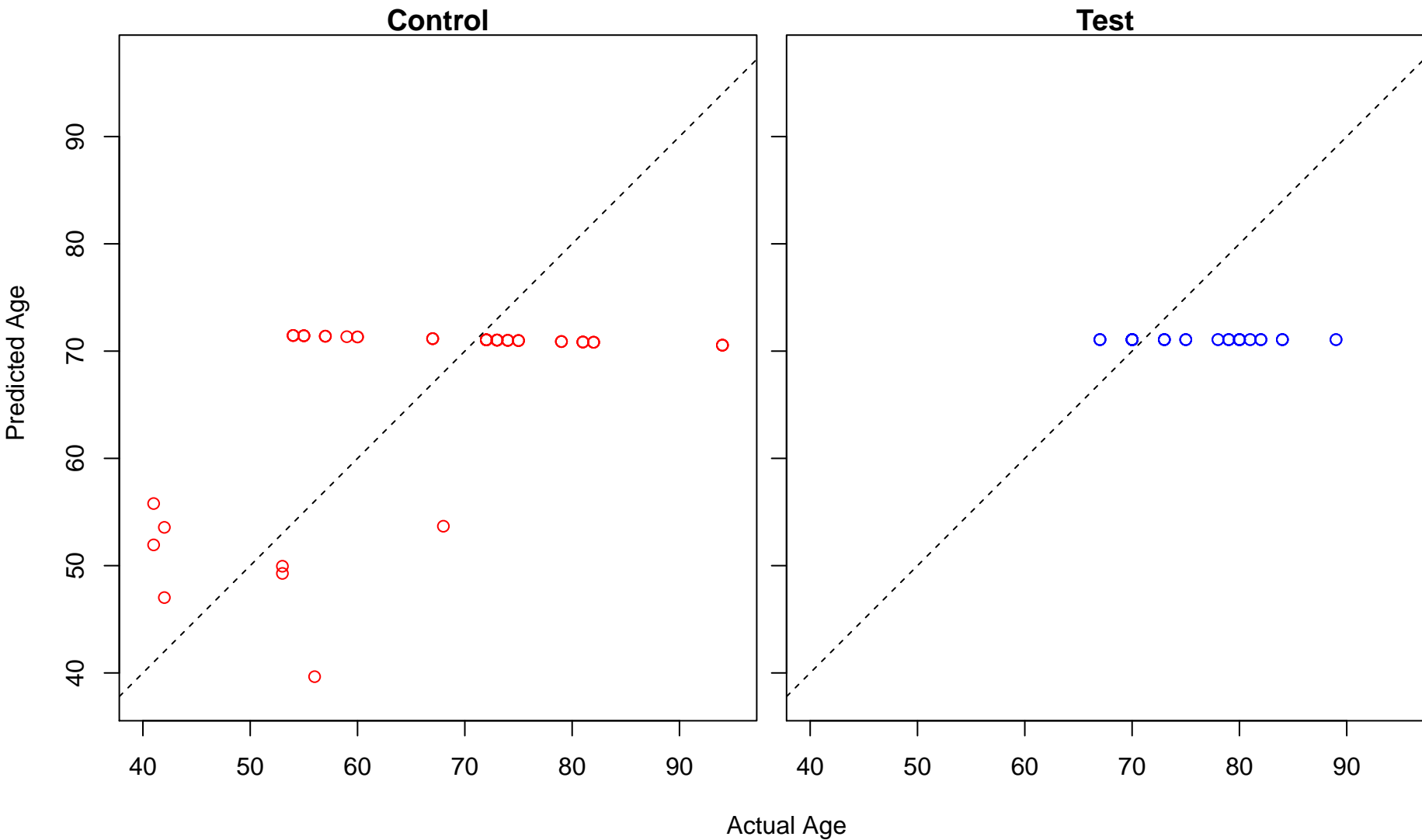
positive regulation of transcription from RNA polymerase II promoter (Score: 0.797949)



cellular aromatic compound metabolic process (Score: 0.797932)

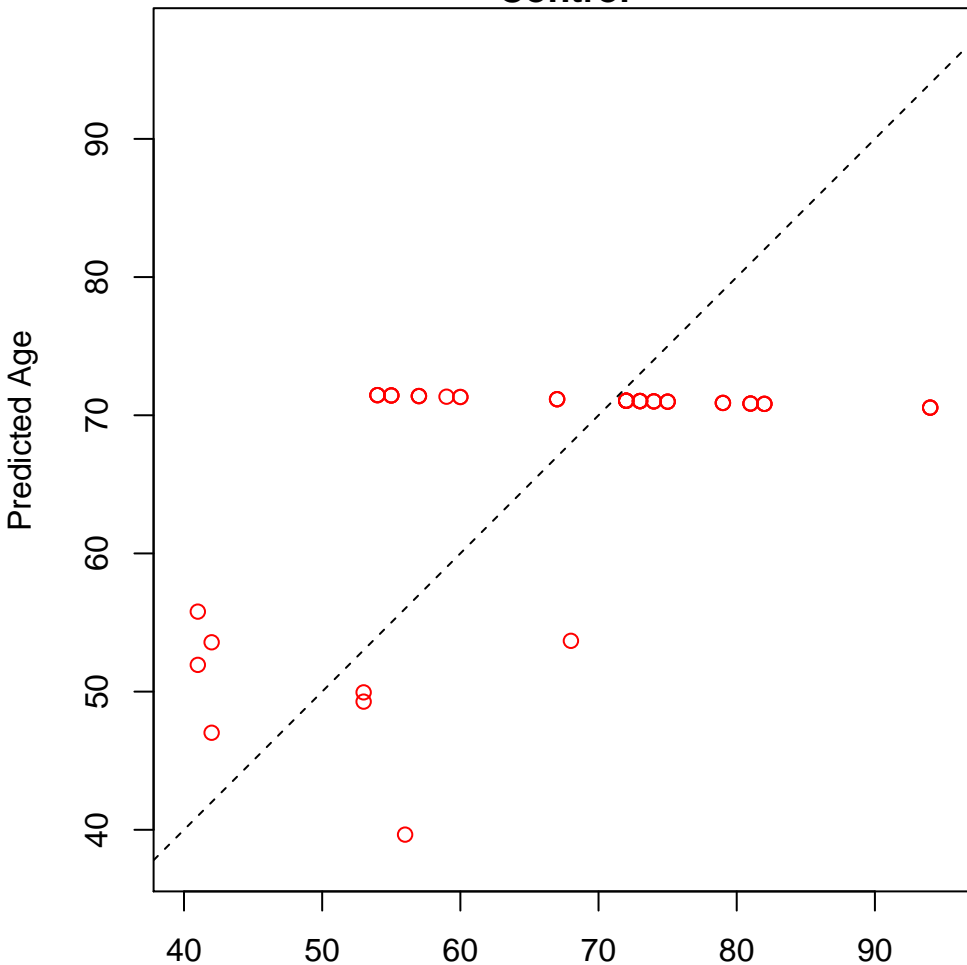


heterocycle metabolic process (Score: 0.797932)

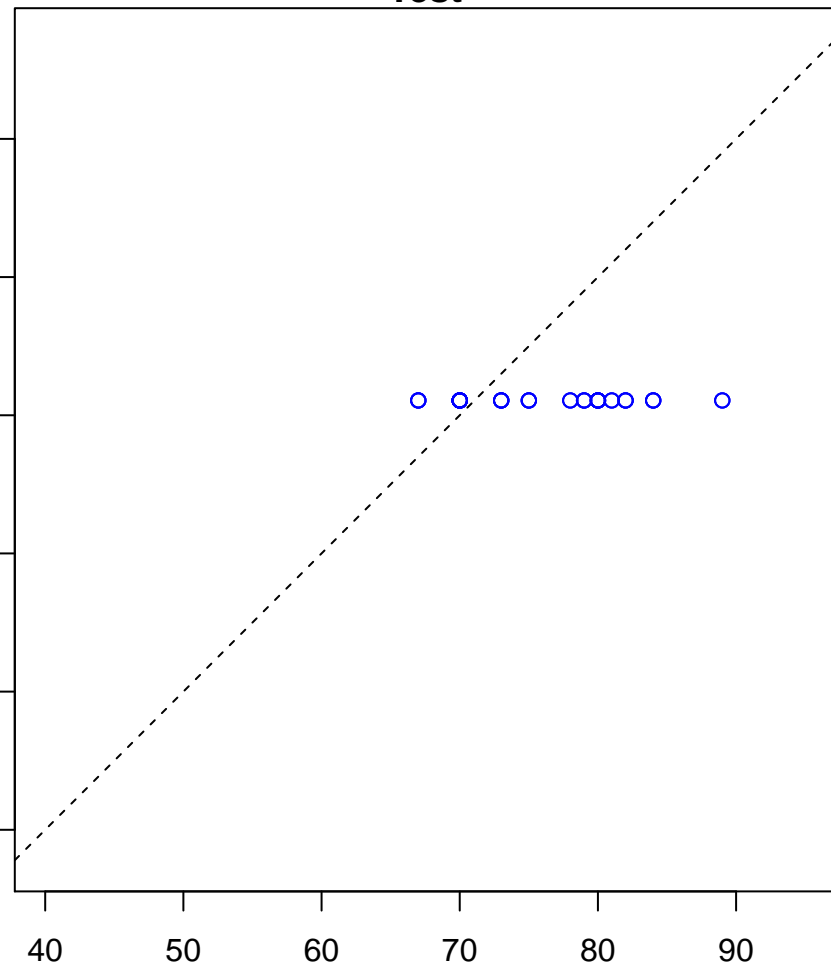


organic cyclic compound metabolic process (Score: 0.797932)

Control

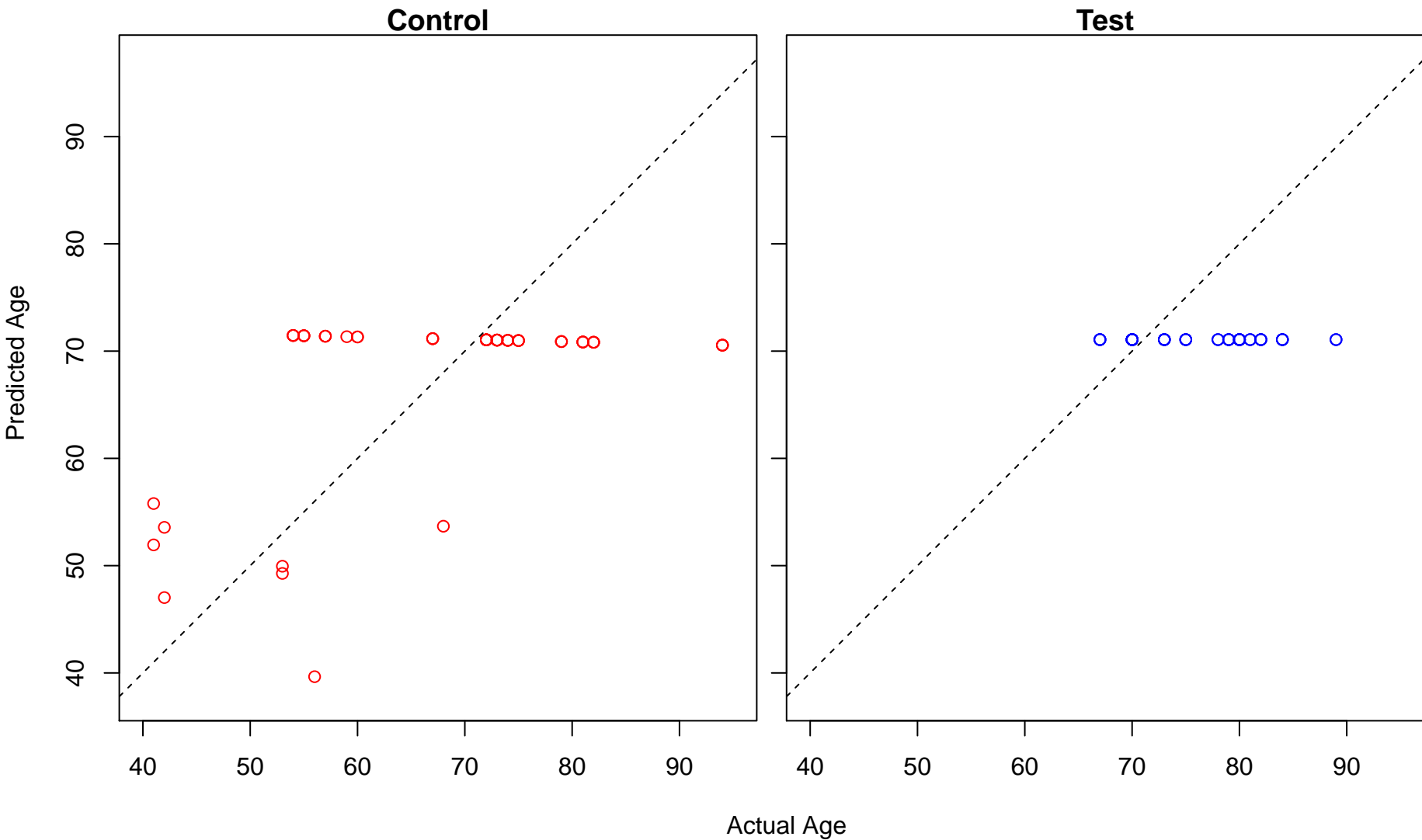


Test



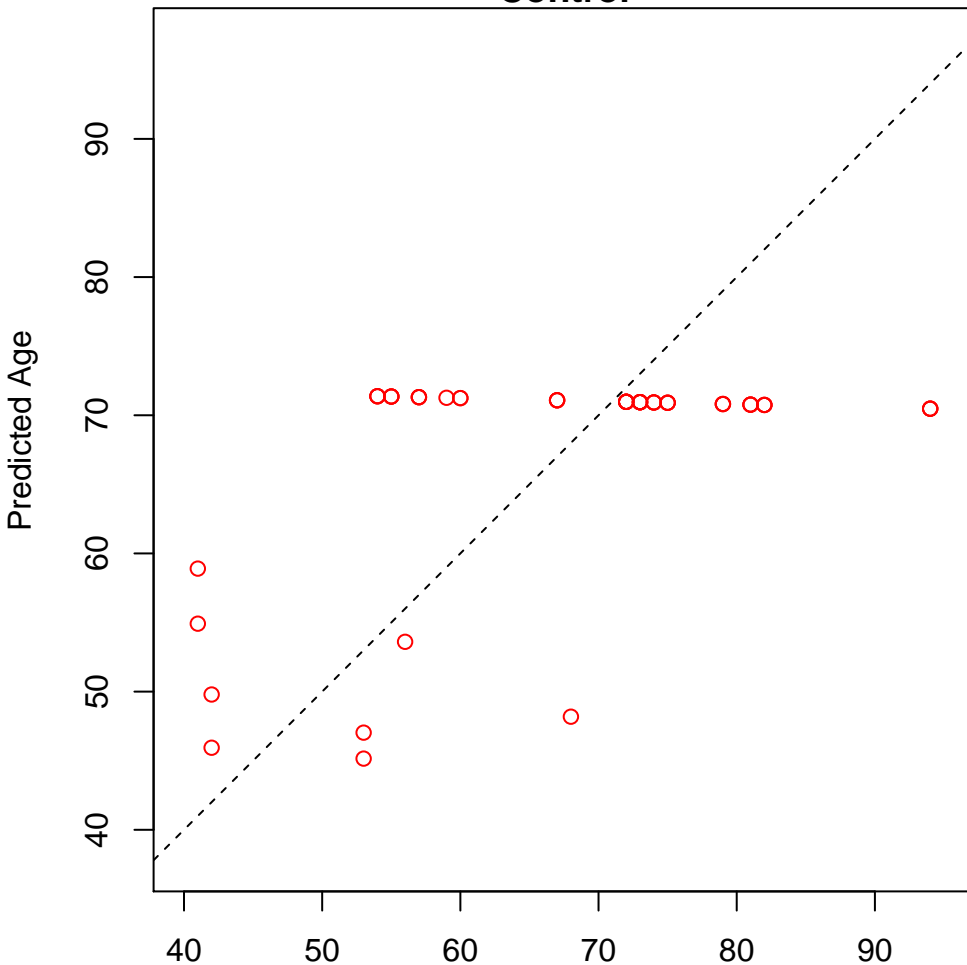
Actual Age

nucleobase-containing compound metabolic process (Score: 0.797932)

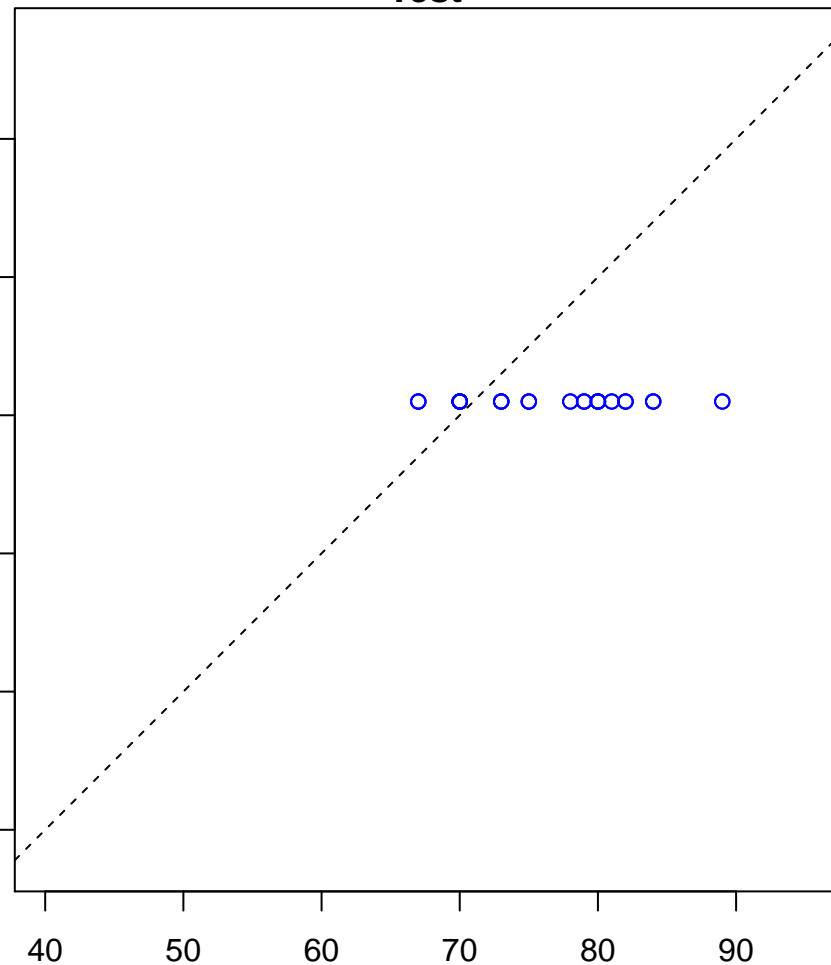


negative regulation of kinase activity (Score: 0.797929)

Control

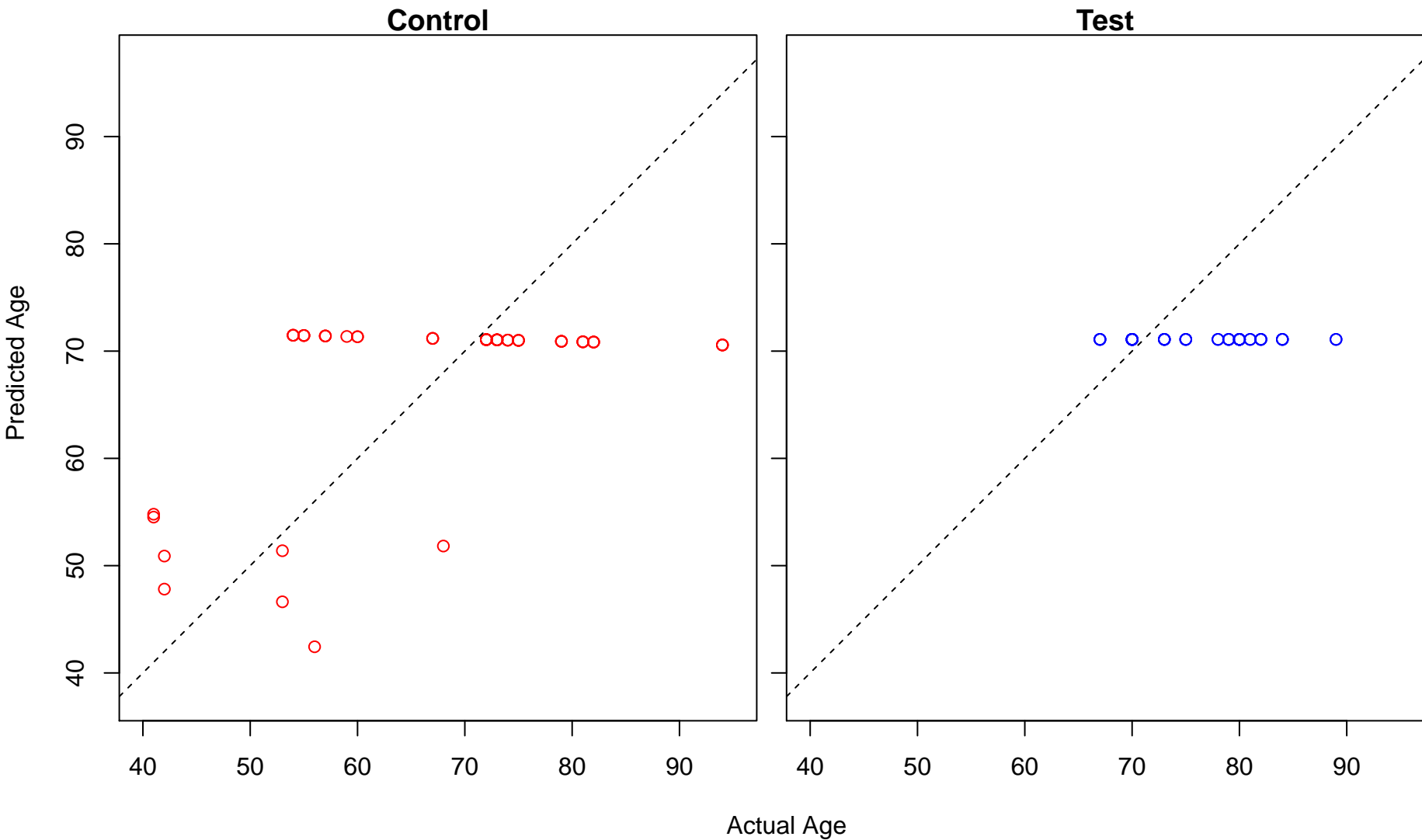


Test



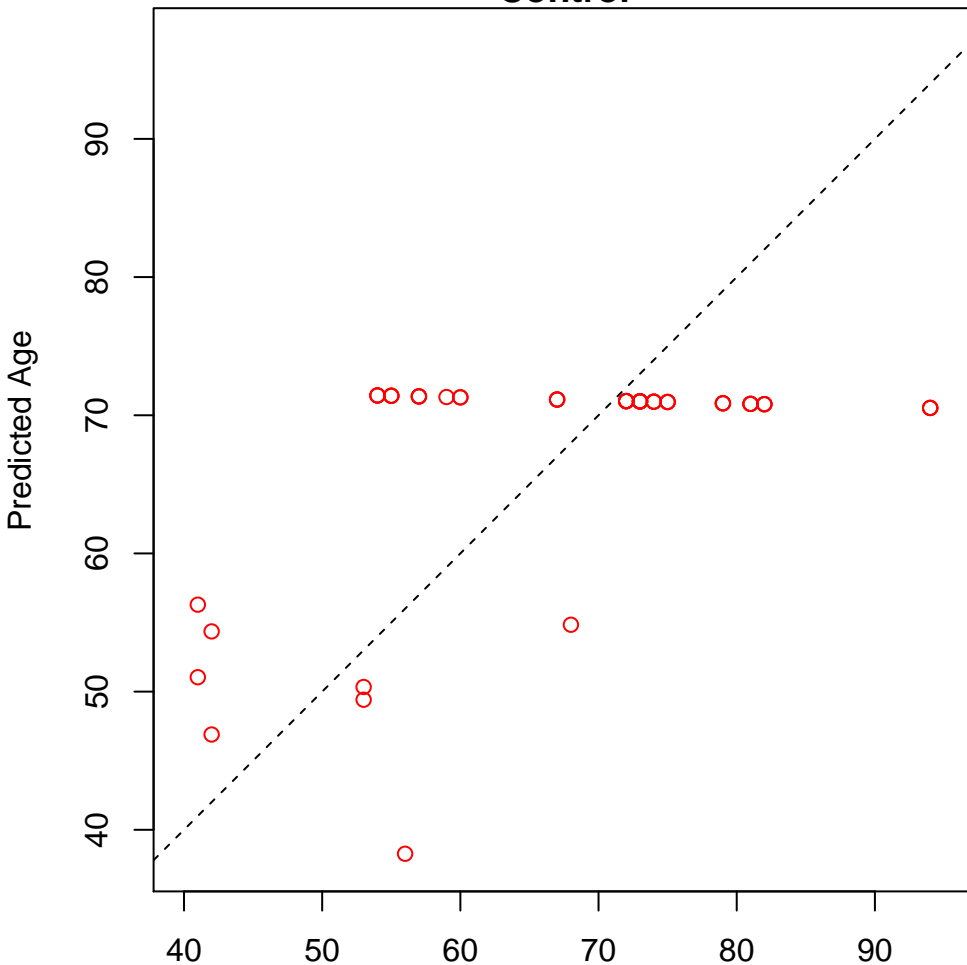
Actual Age

regulation of transcription from RNA polymerase II promoter (Score: 0.797927)

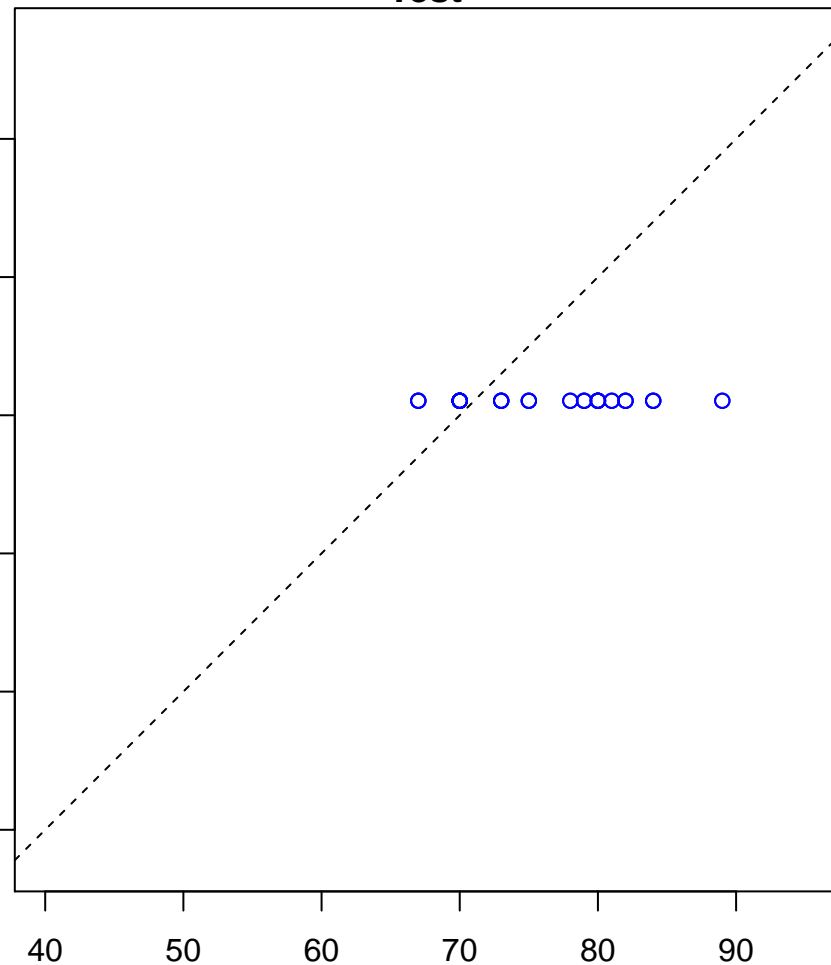


organic substance catabolic process (Score: 0.797885)

Control

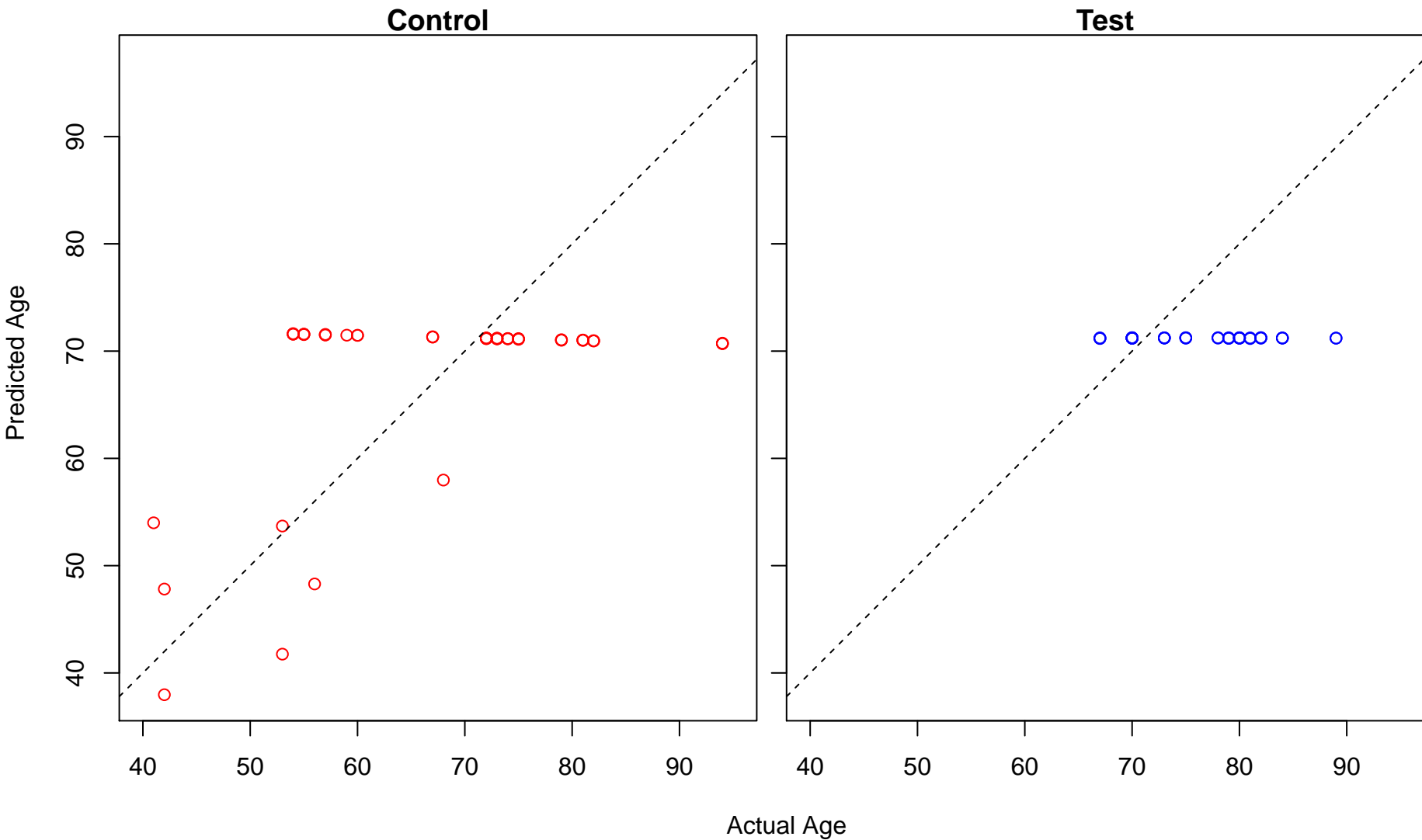


Test



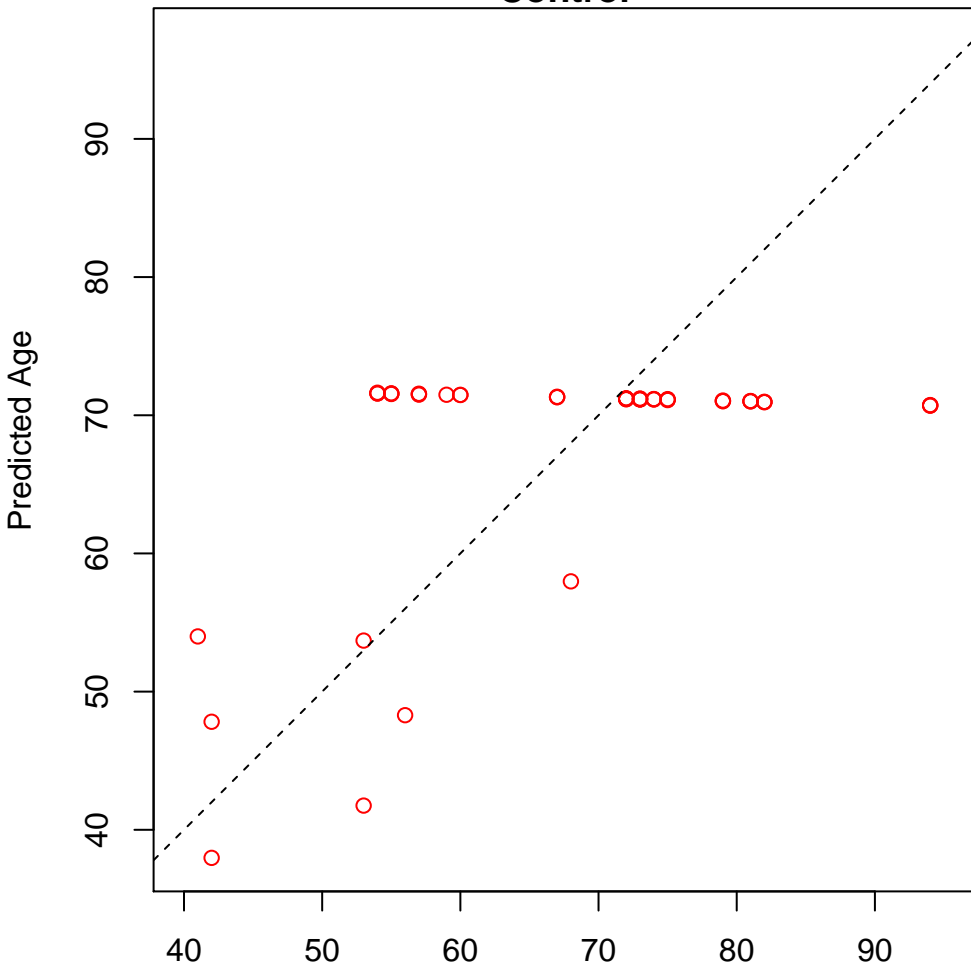
Actual Age

extracellular matrix organization (Score: 0.797870)

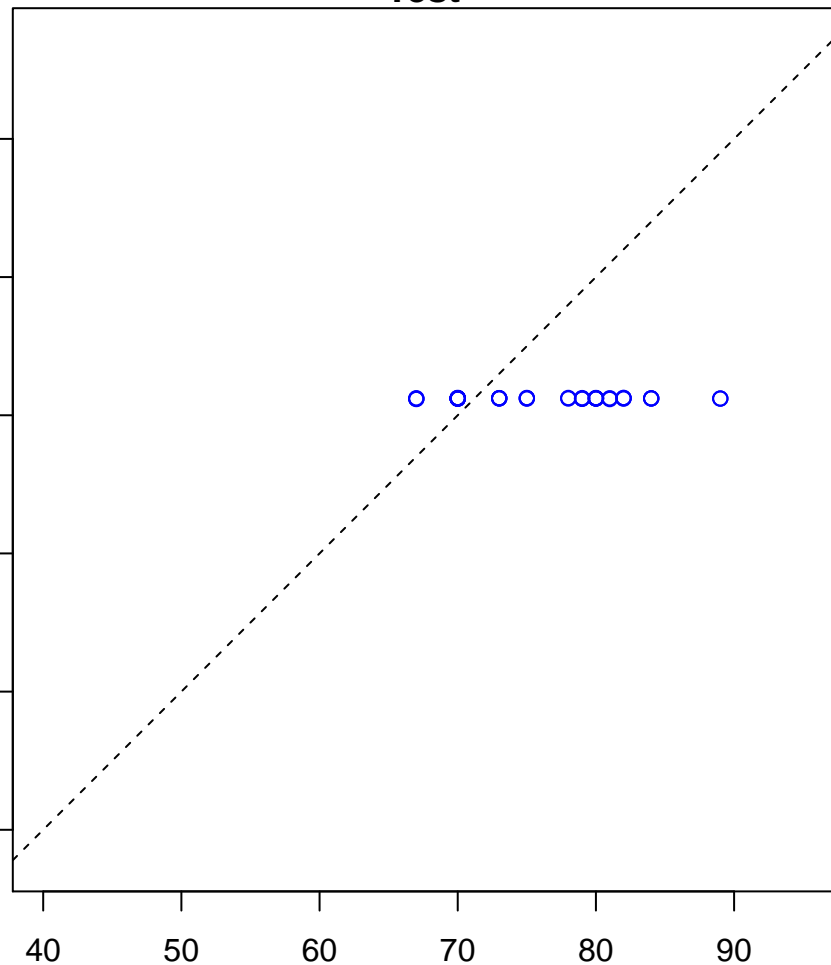


extracellular structure organization (Score: 0.797870)

Control



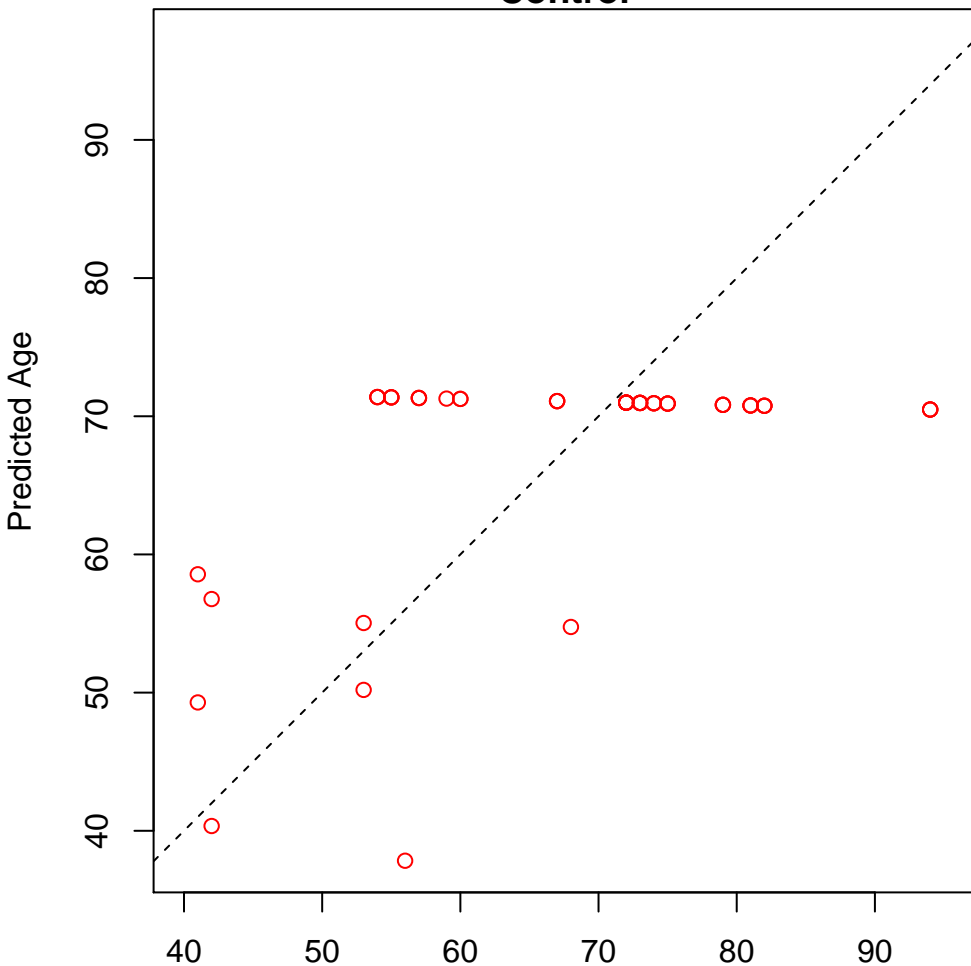
Test



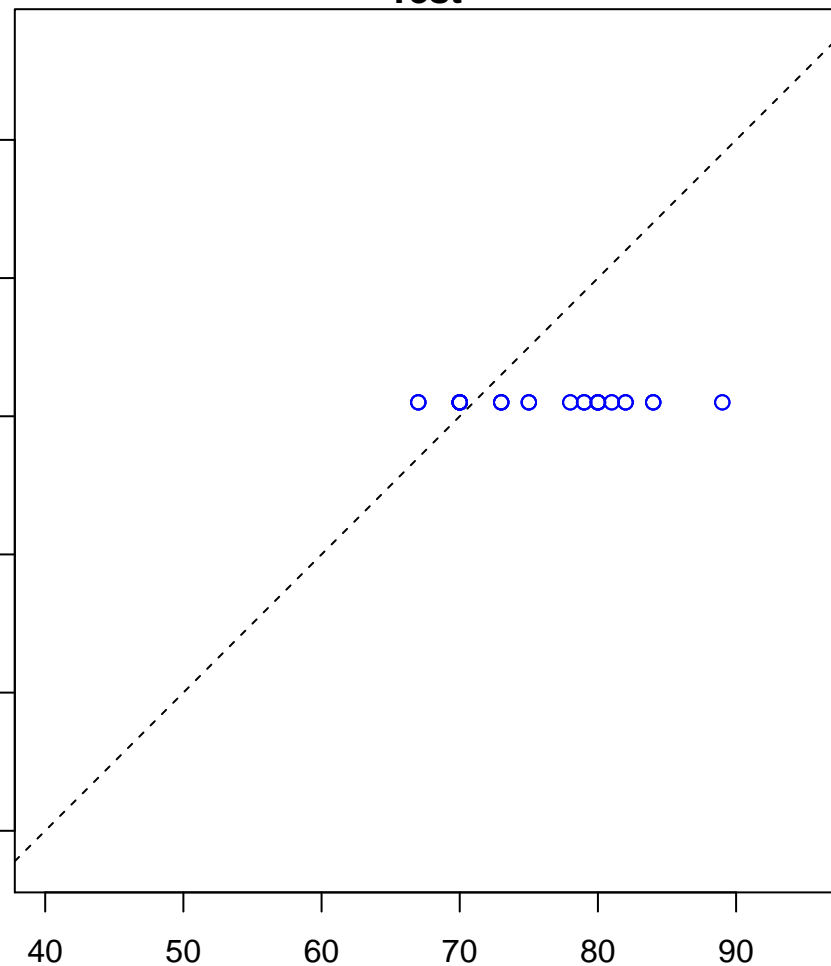
Actual Age

intracellular receptor signaling pathway (Score: 0.797818)

Control

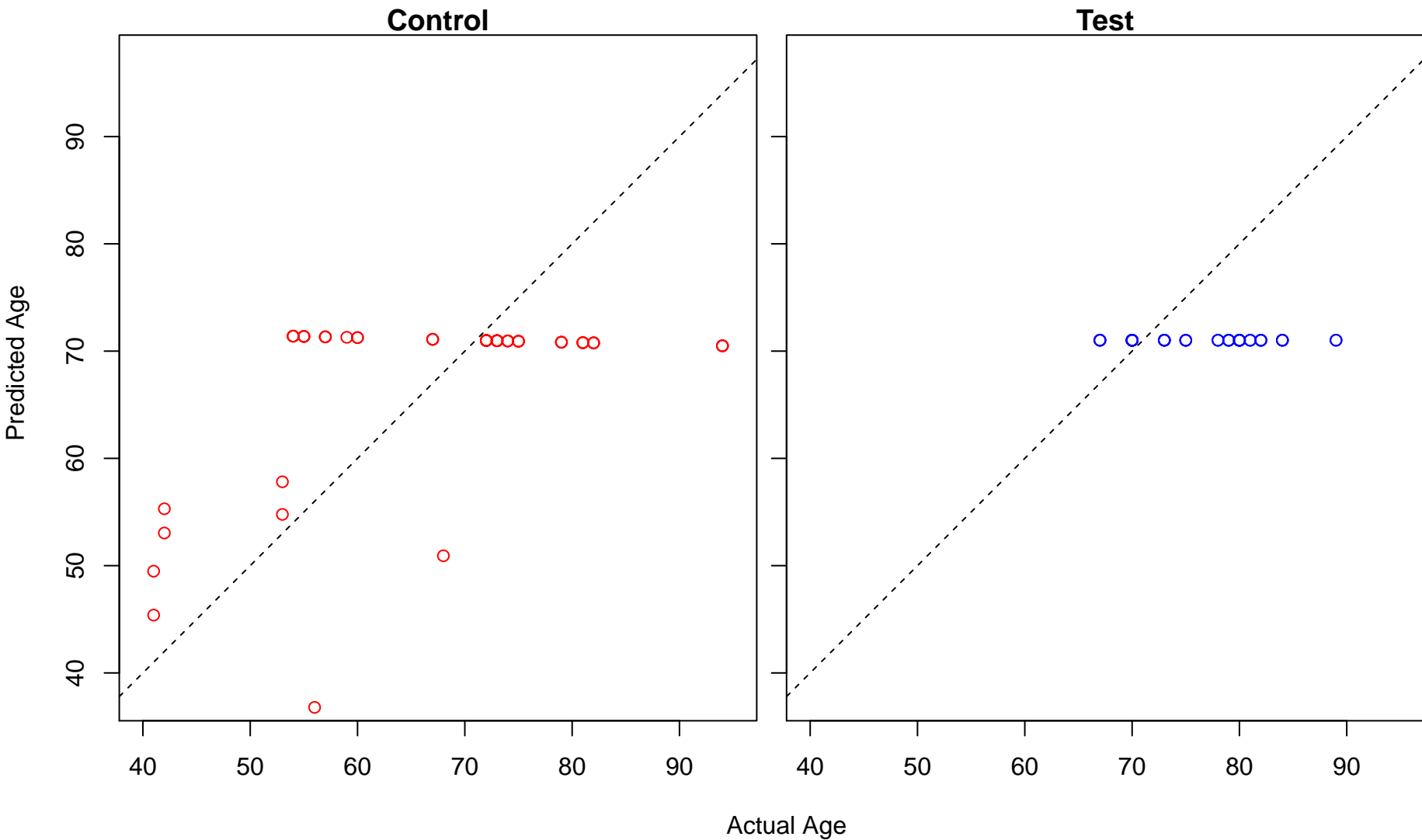


Test



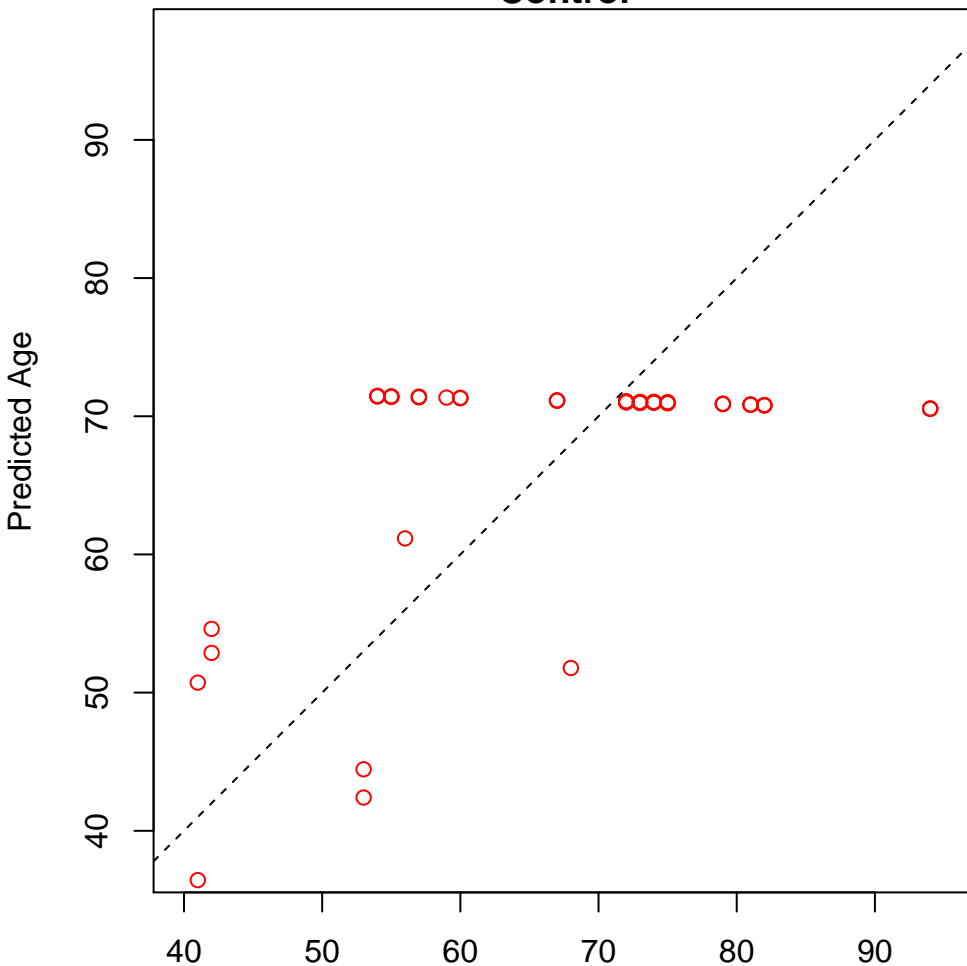
Actual Age

telomere organization (Score: 0.797812)

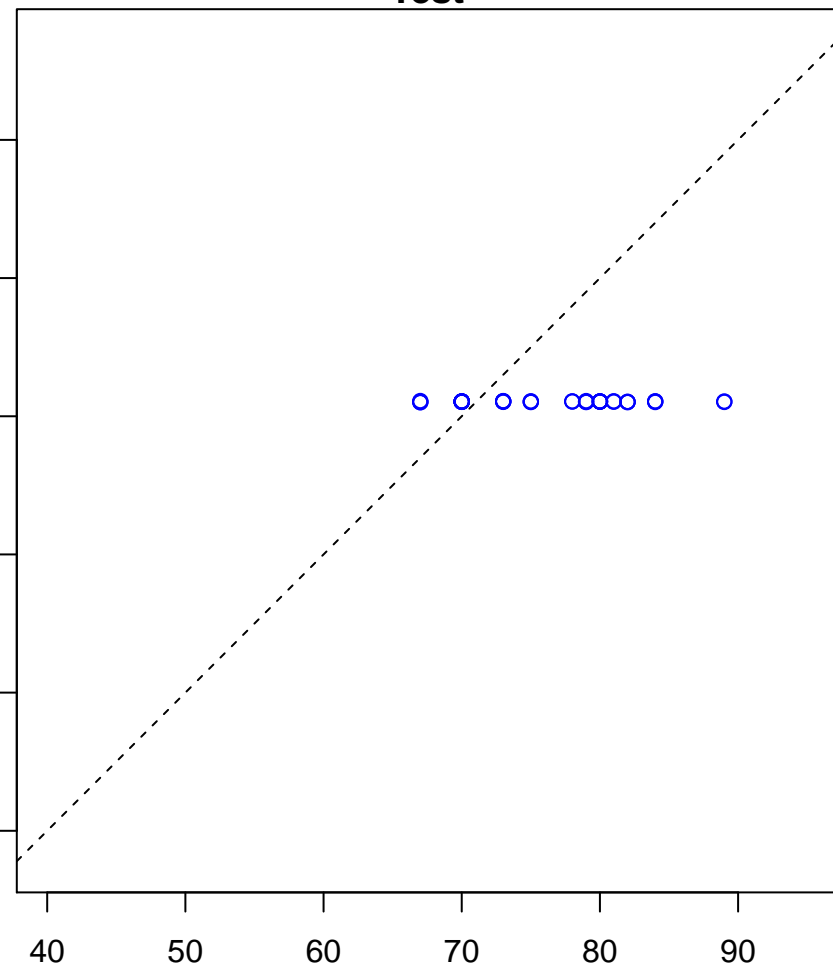


positive regulation of cell-cell adhesion (Score: 0.797740)

Control



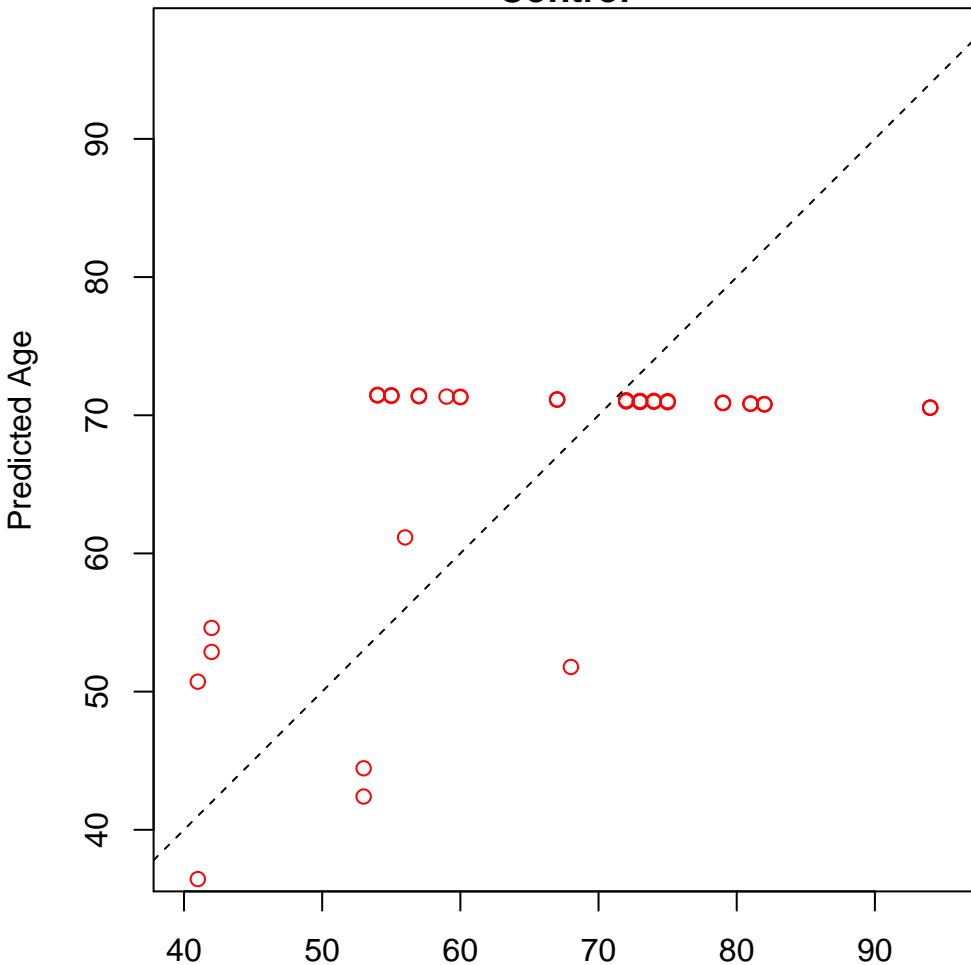
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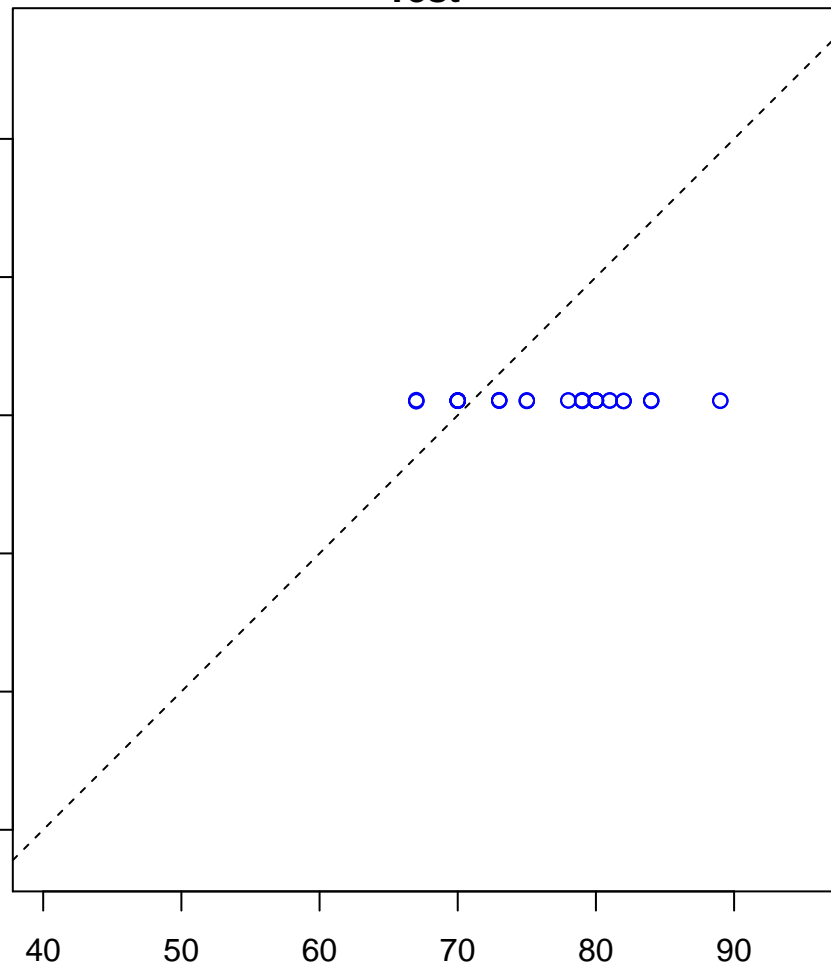
Actual Age

positive regulation of cell adhesion (Score: 0.797740)

Control



Test



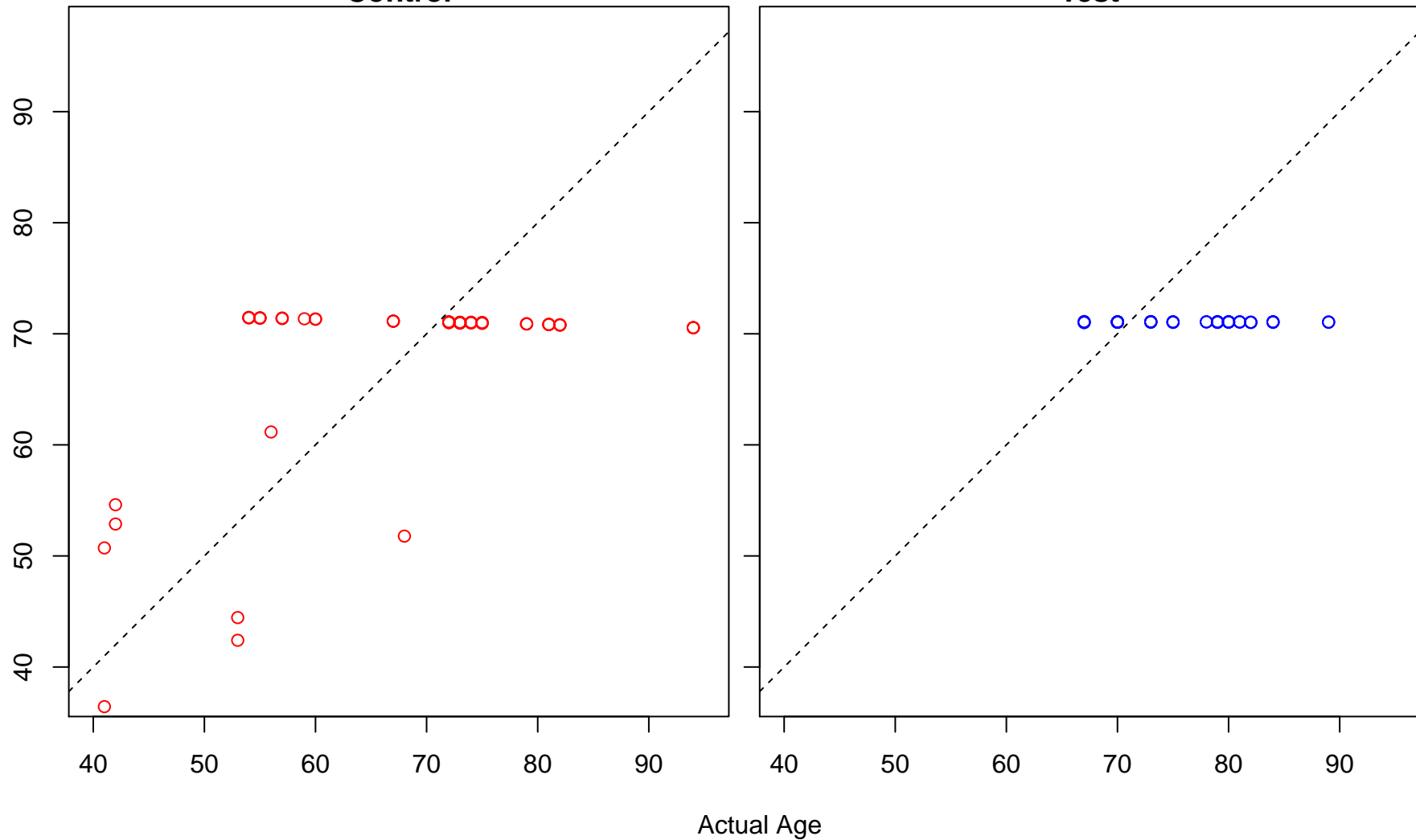
Actual Age

positive regulation of T cell activation (Score: 0.797740)

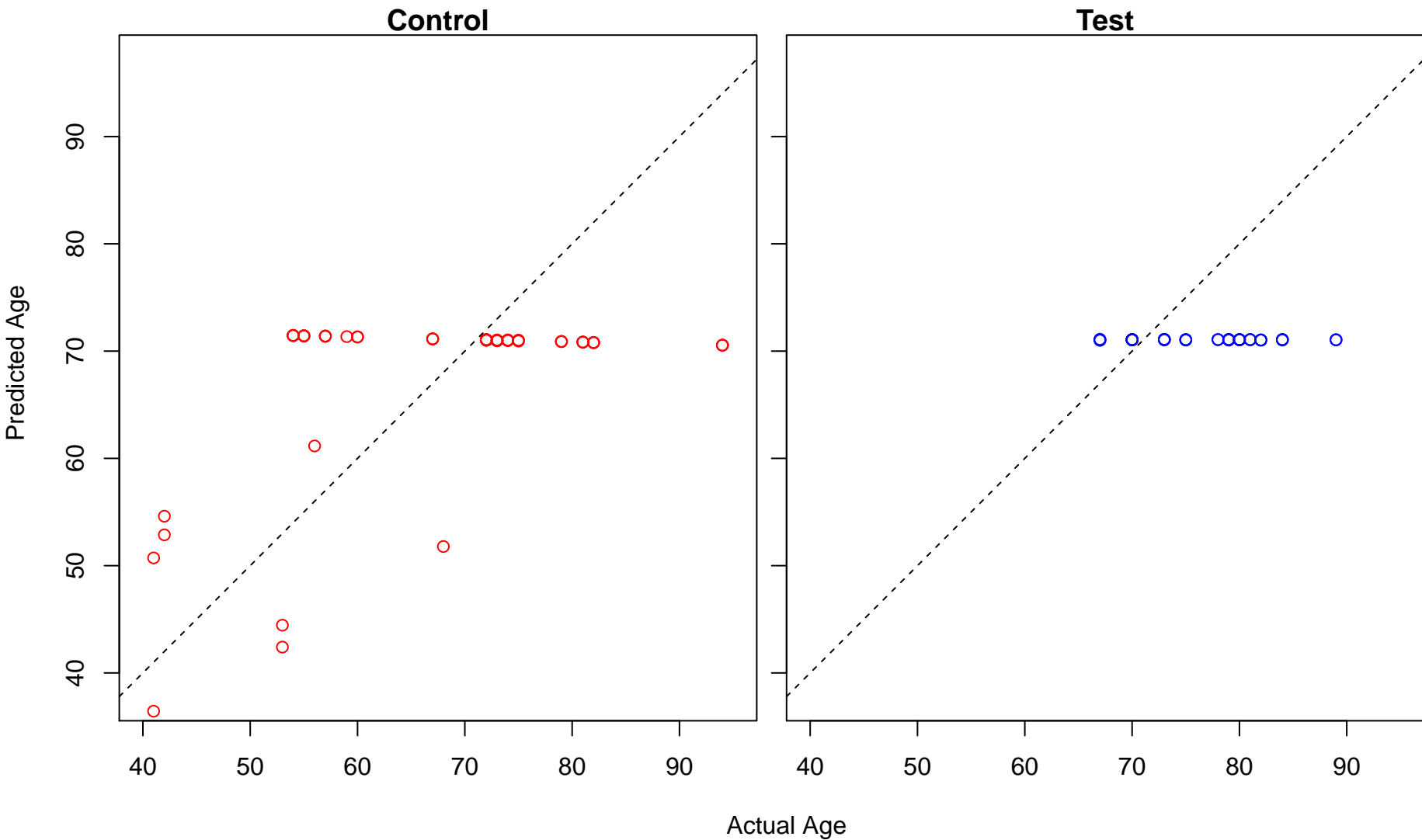
Control

Test

Predicted Age

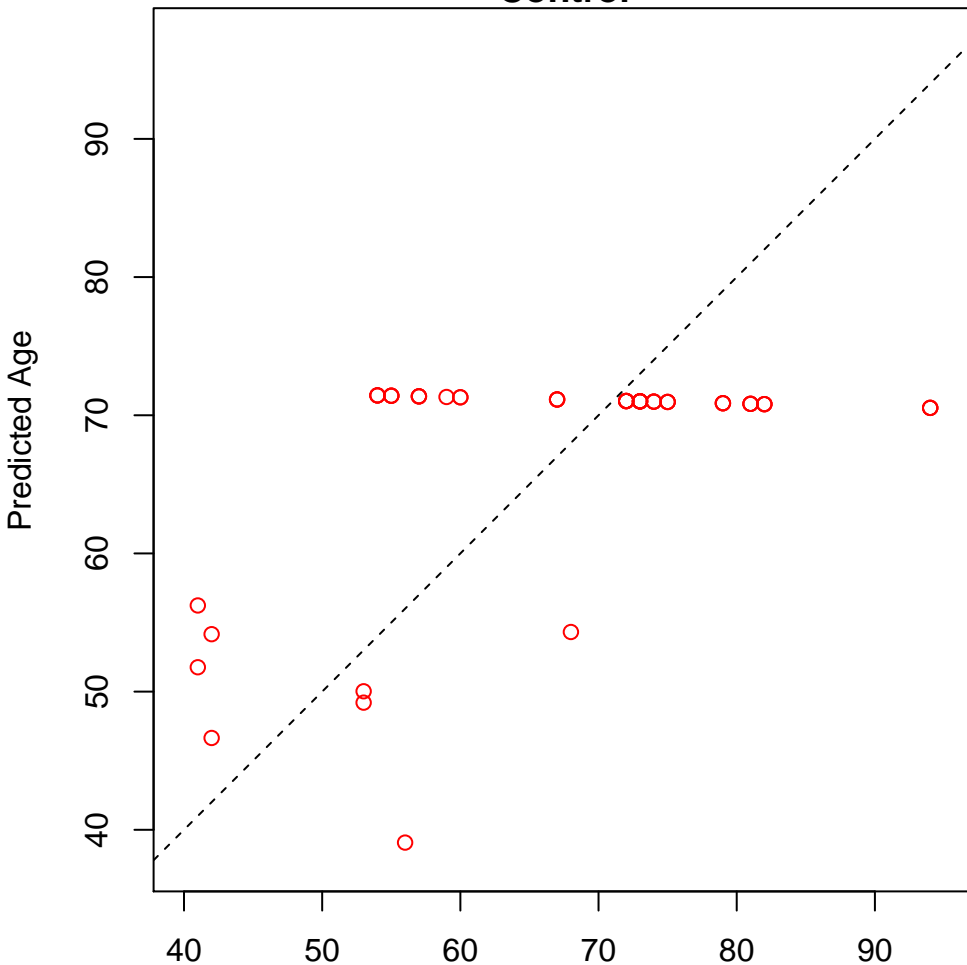


positive regulation of leukocyte cell–cell adhesion (Score: 0.797740)

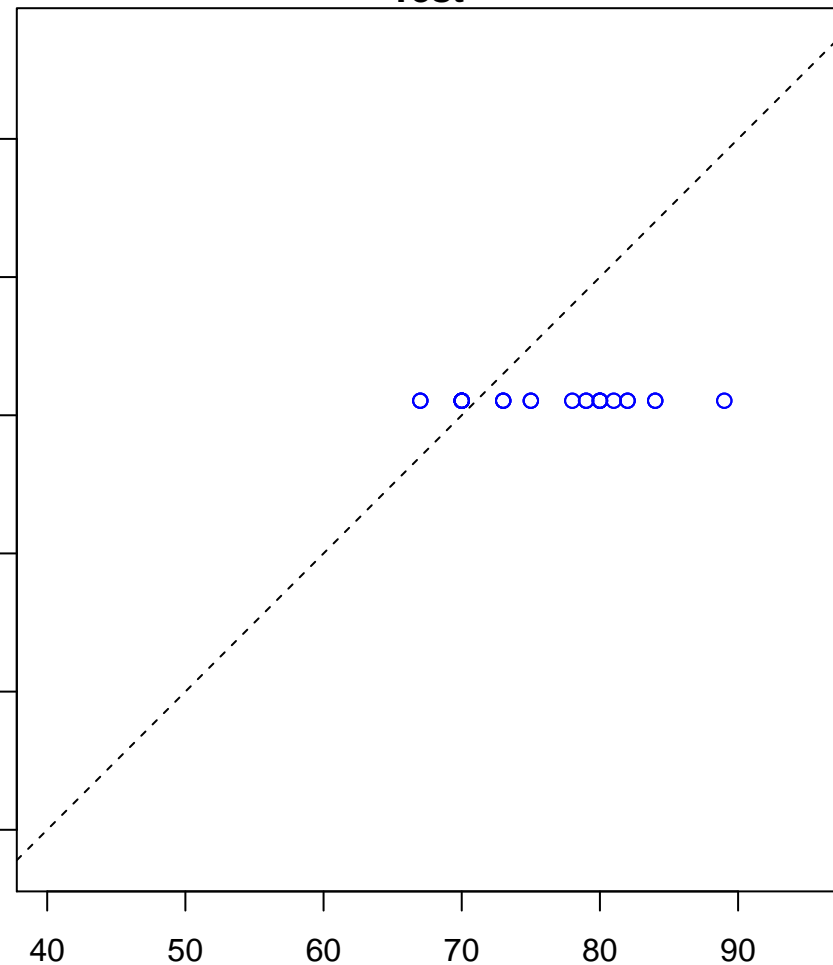


negative regulation of gene expression (Score: 0.797673)

Control

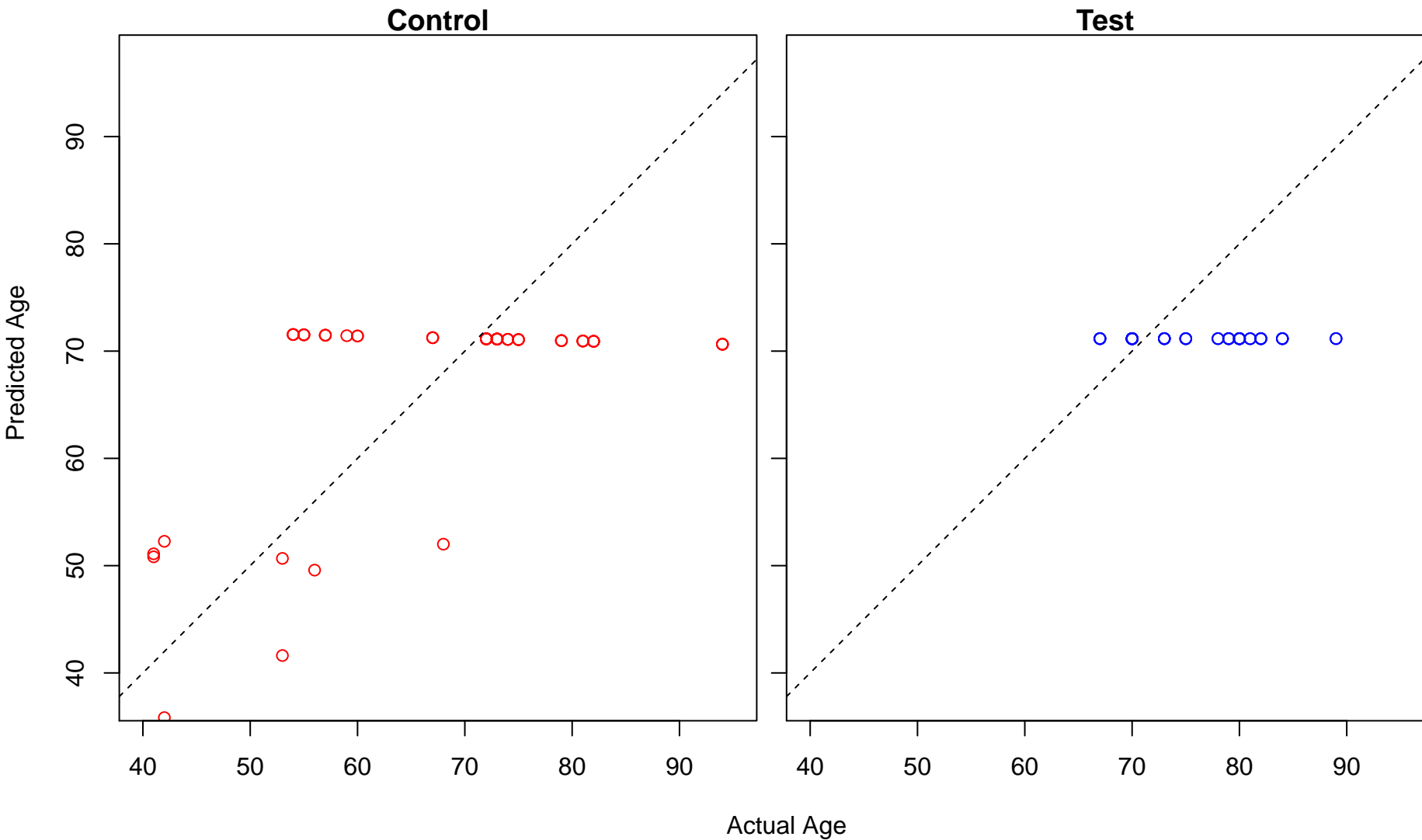


Test

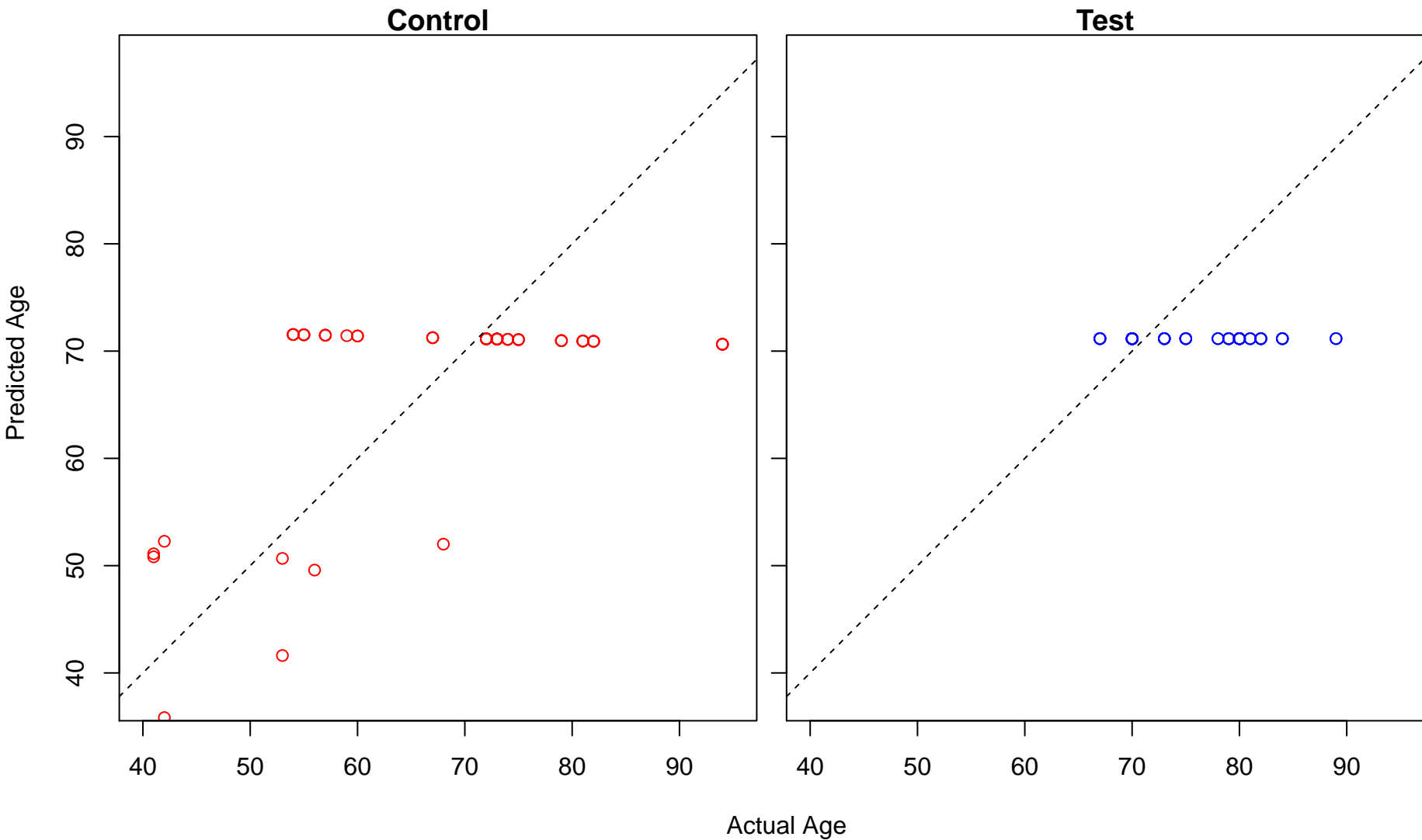


Actual Age

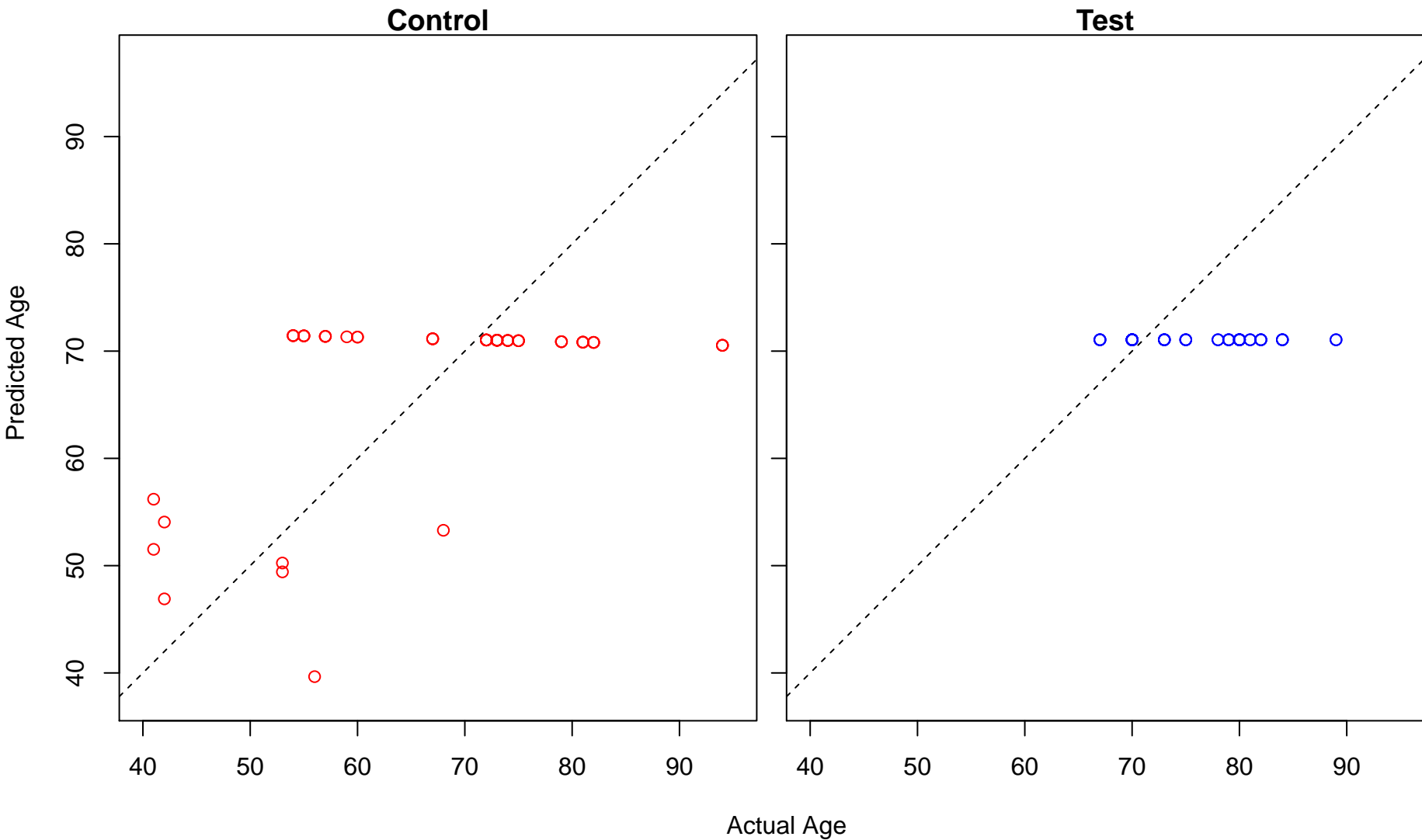
regulation of protein transport (Score: 0.797655)



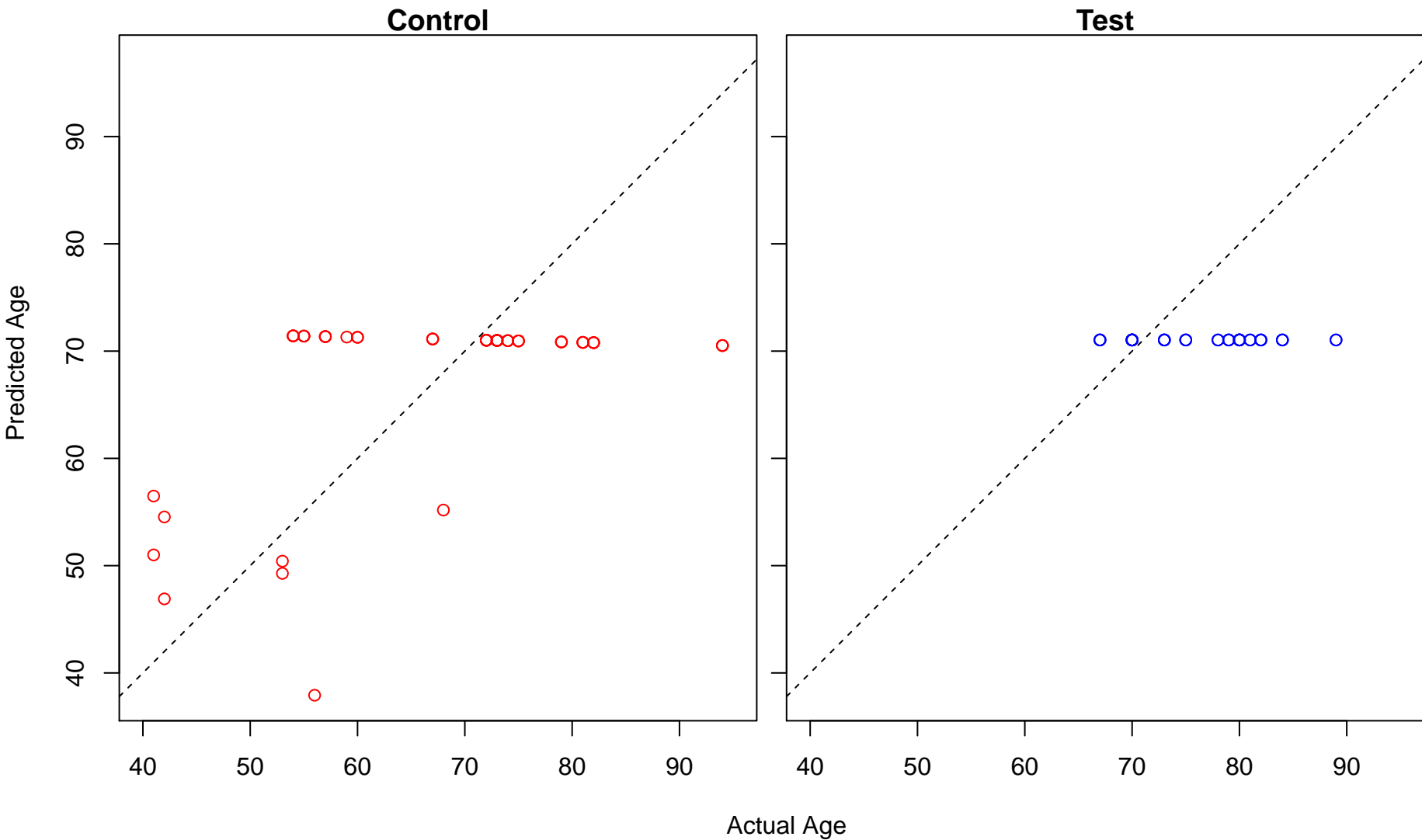
regulation of peptide transport (Score: 0.797654)



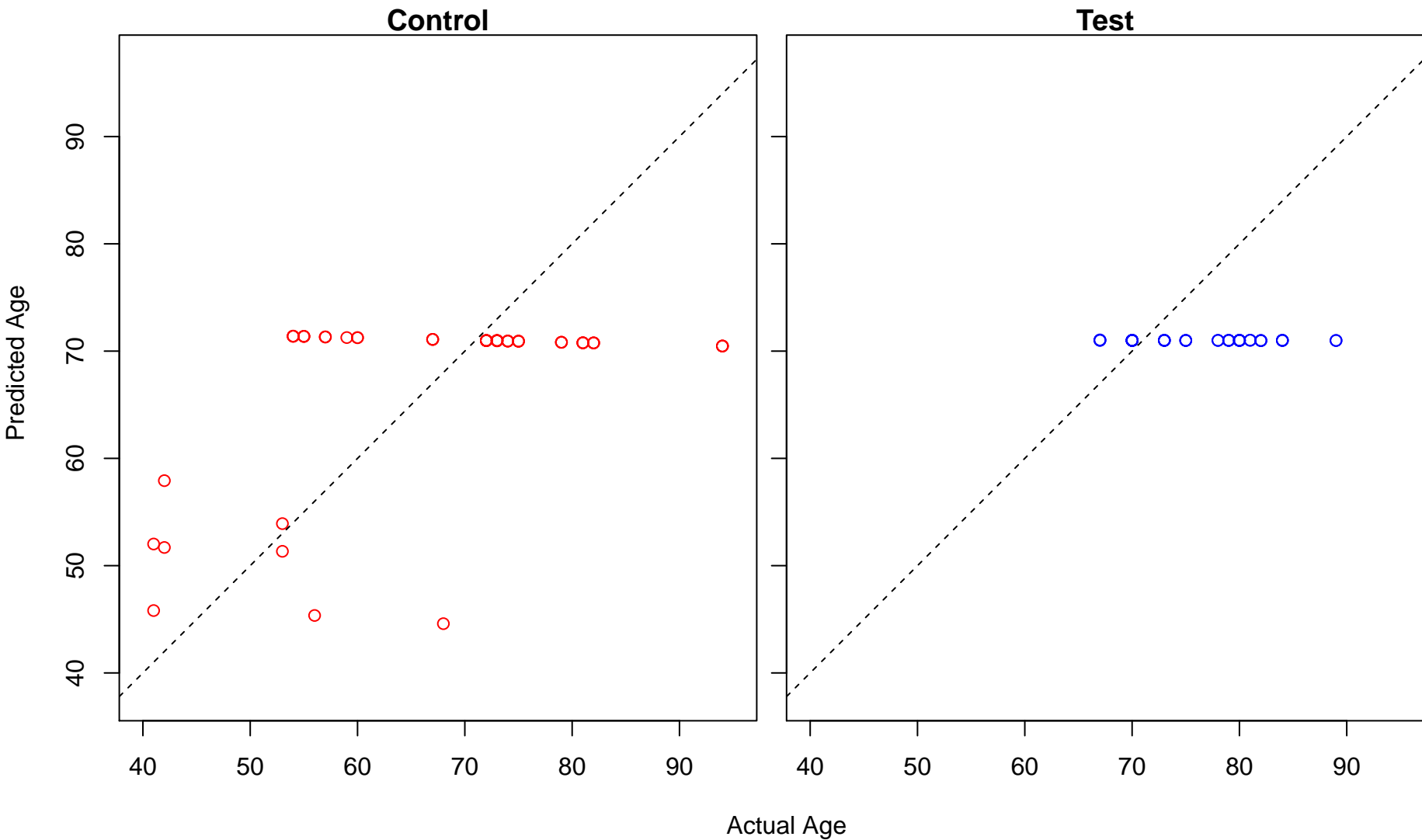
negative regulation of macromolecule metabolic process (Score: 0.797652)



viral process (Score: 0.797589)

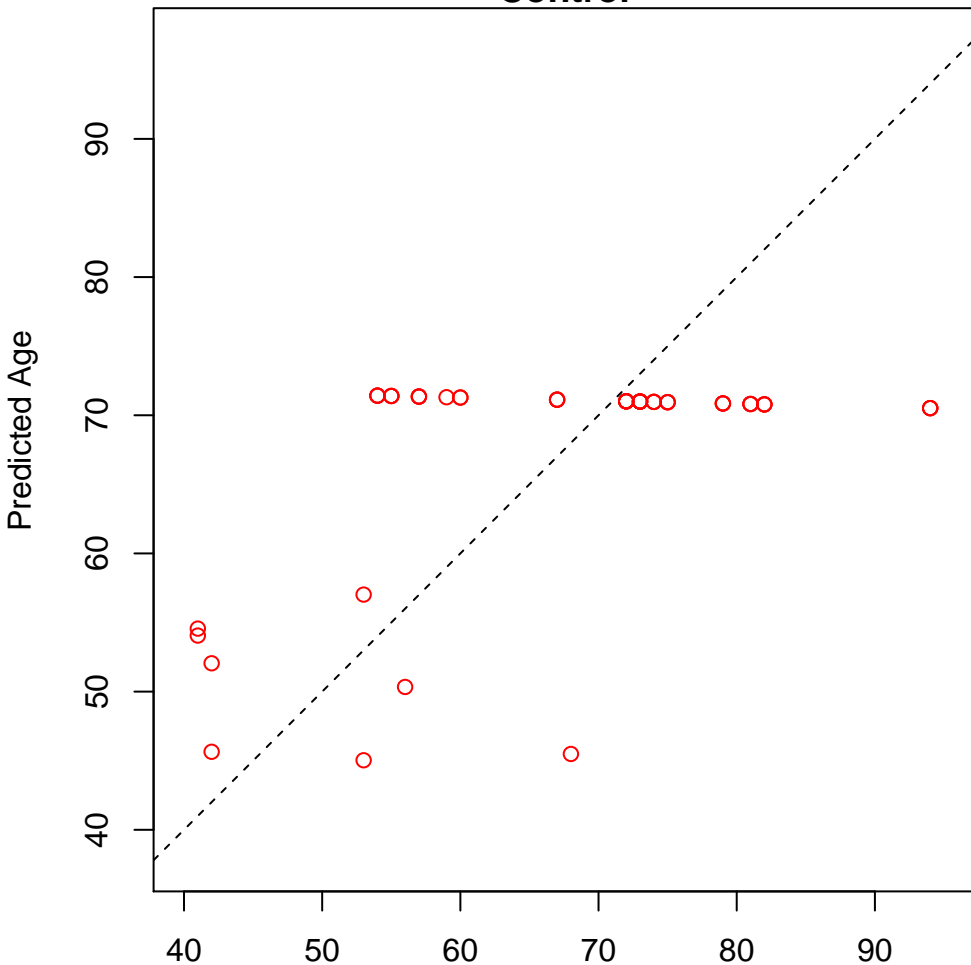


leukocyte cell-cell adhesion (Score: 0.797577)

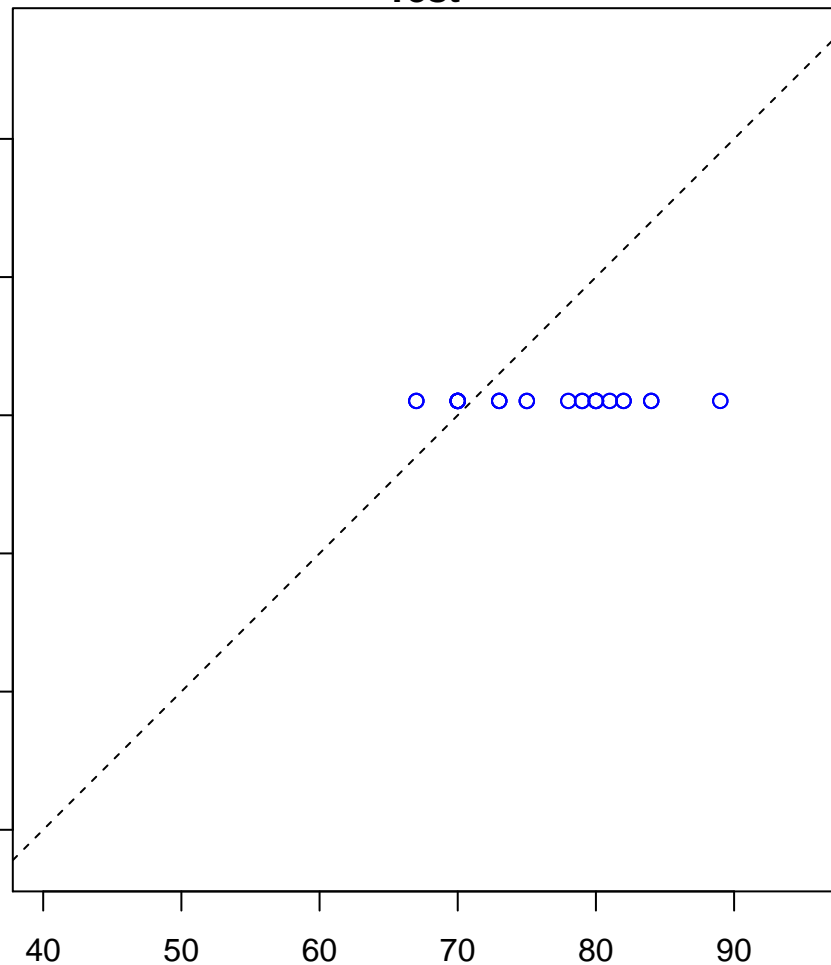


positive regulation of cytokine secretion (Score: 0.797503)

Control

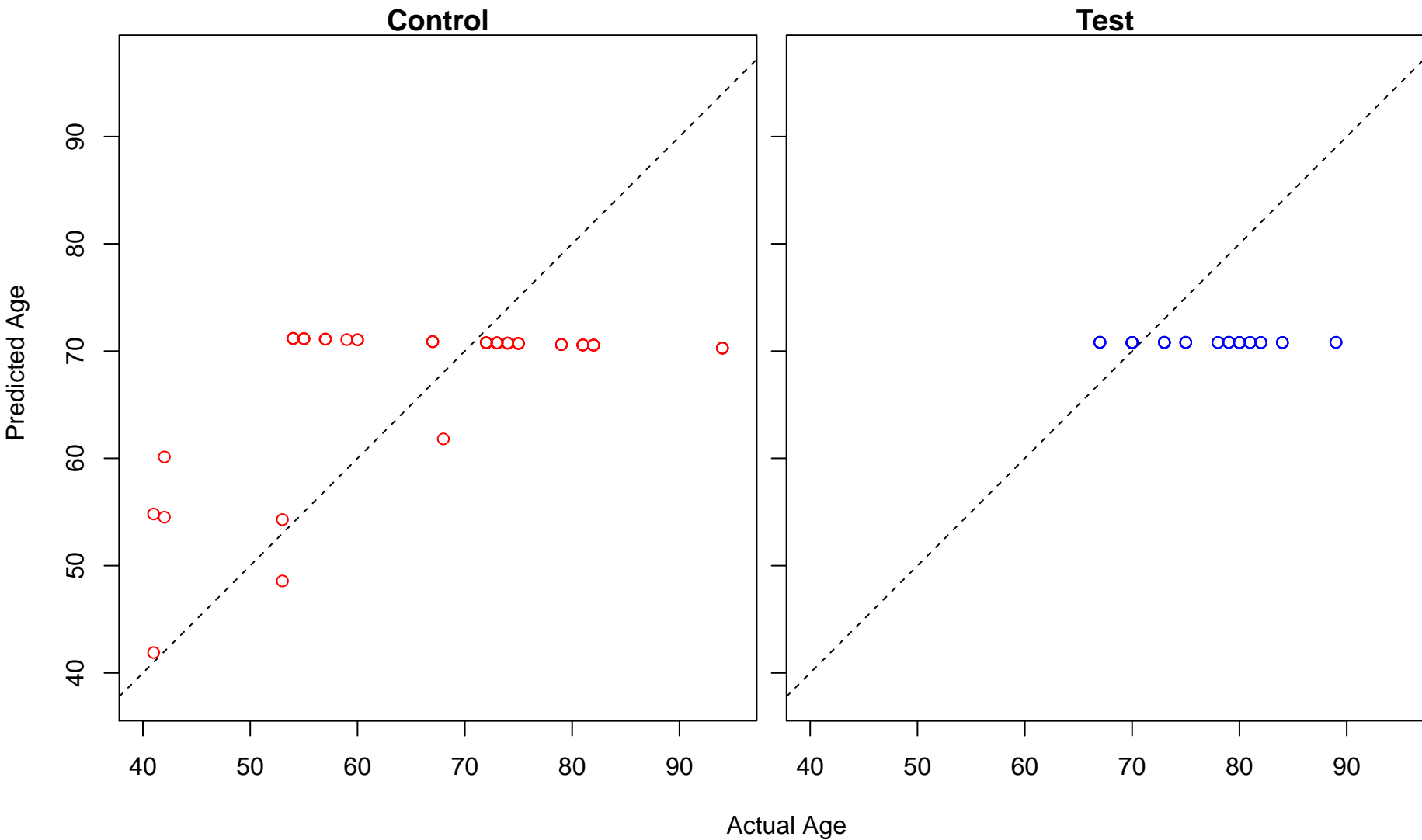


Test

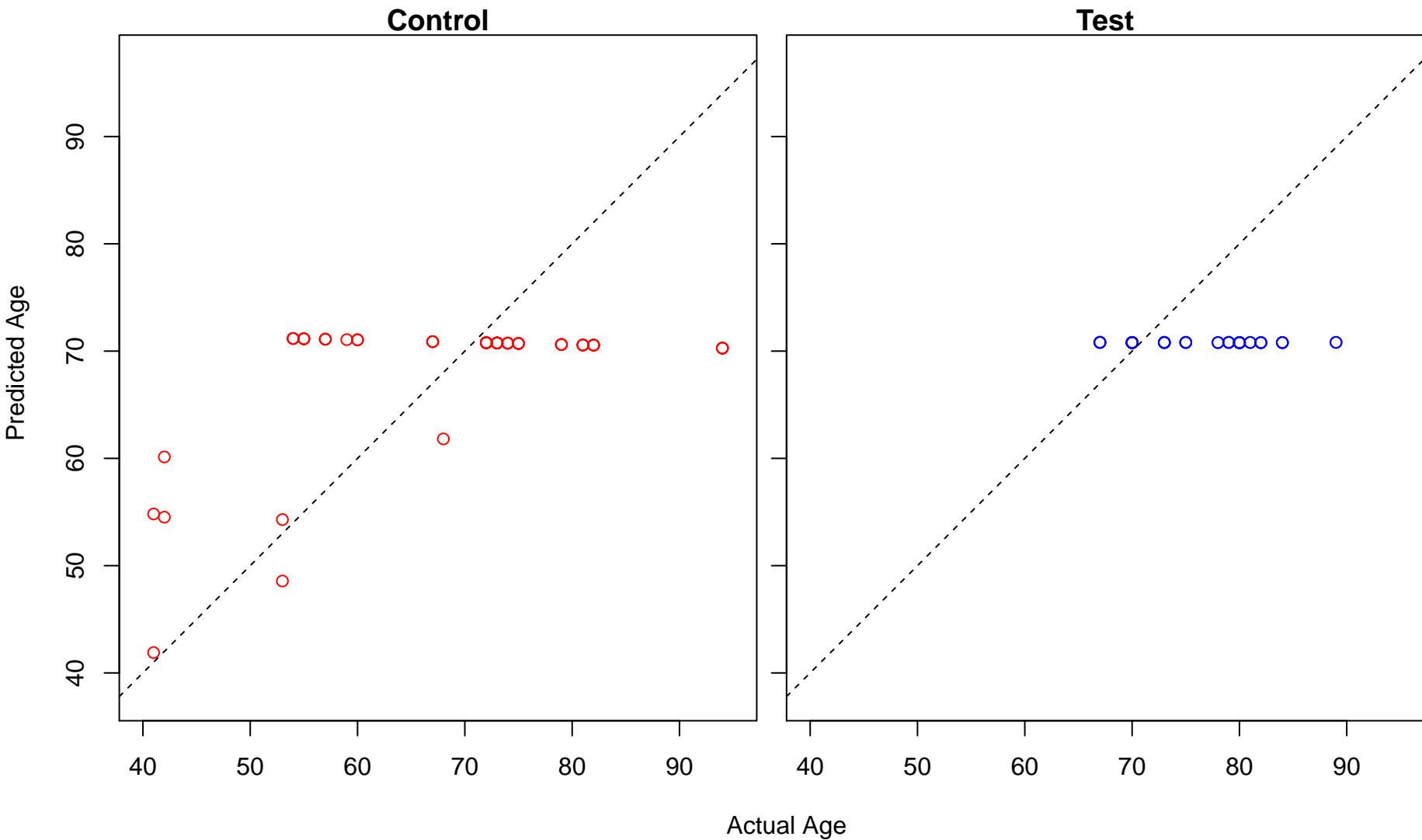


Actual Age

regulation of extracellular matrix disassembly (Score: 0.797485)

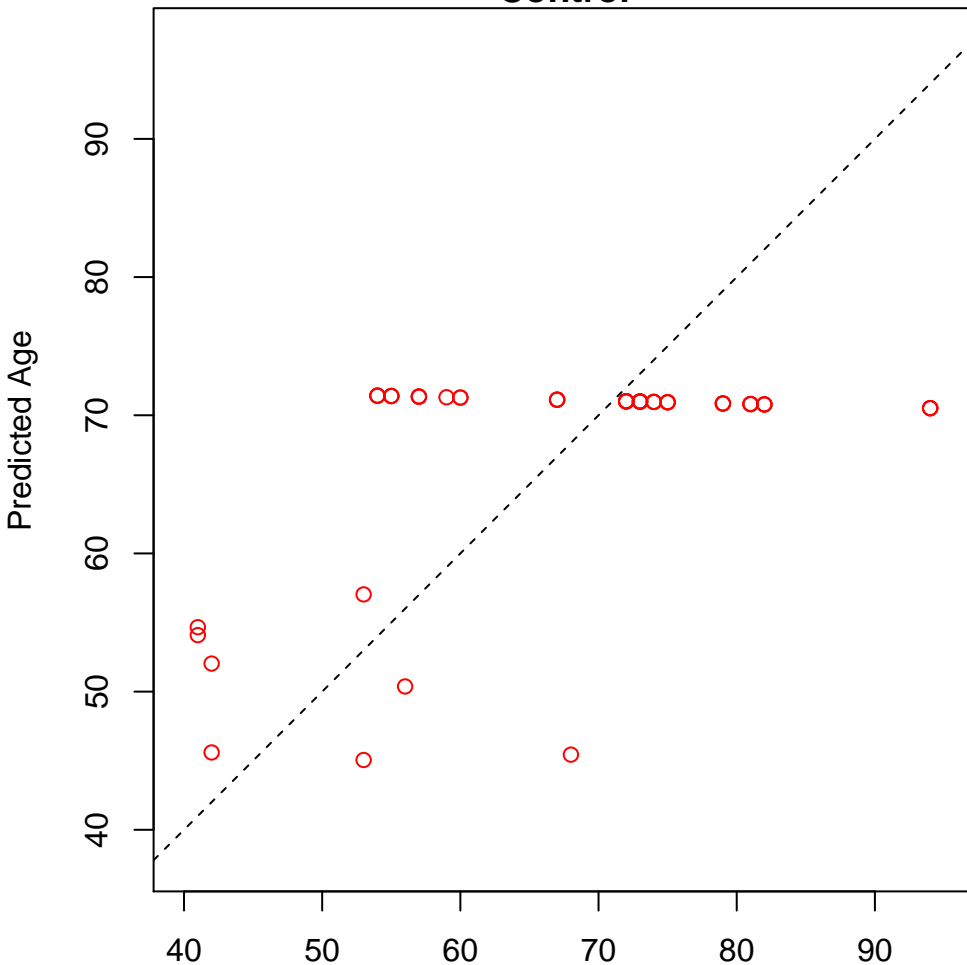


regulation of extracellular matrix organization (Score: 0.797485)

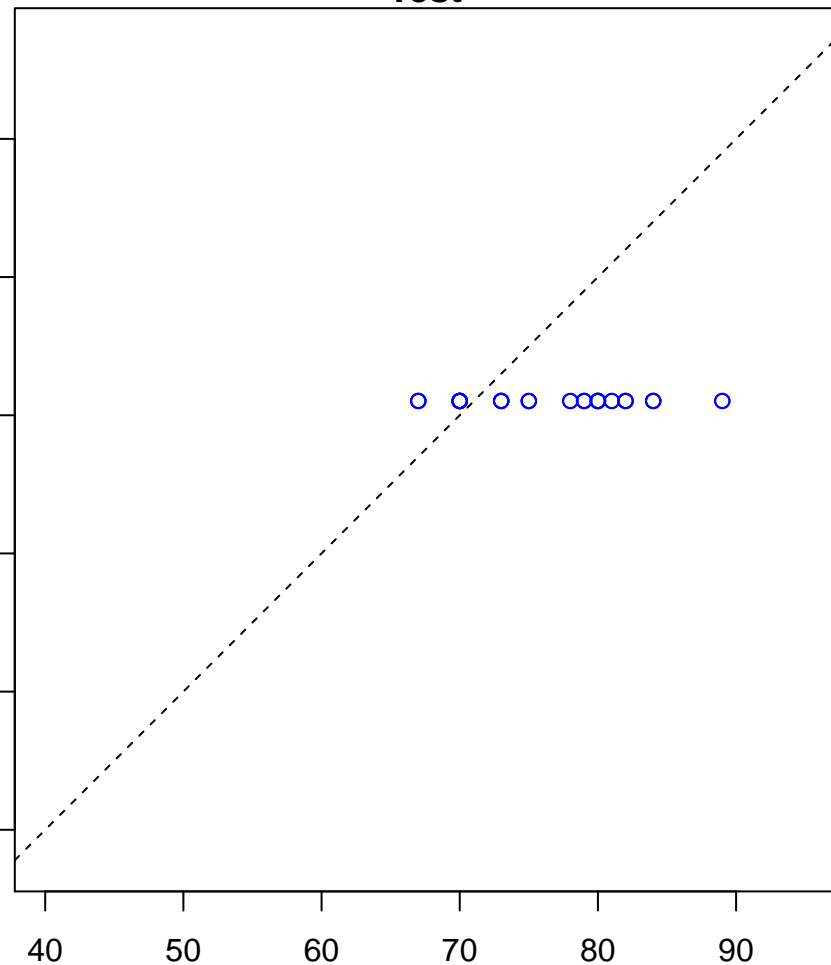


regulation of mononuclear cell migration (Score: 0.797437)

Control

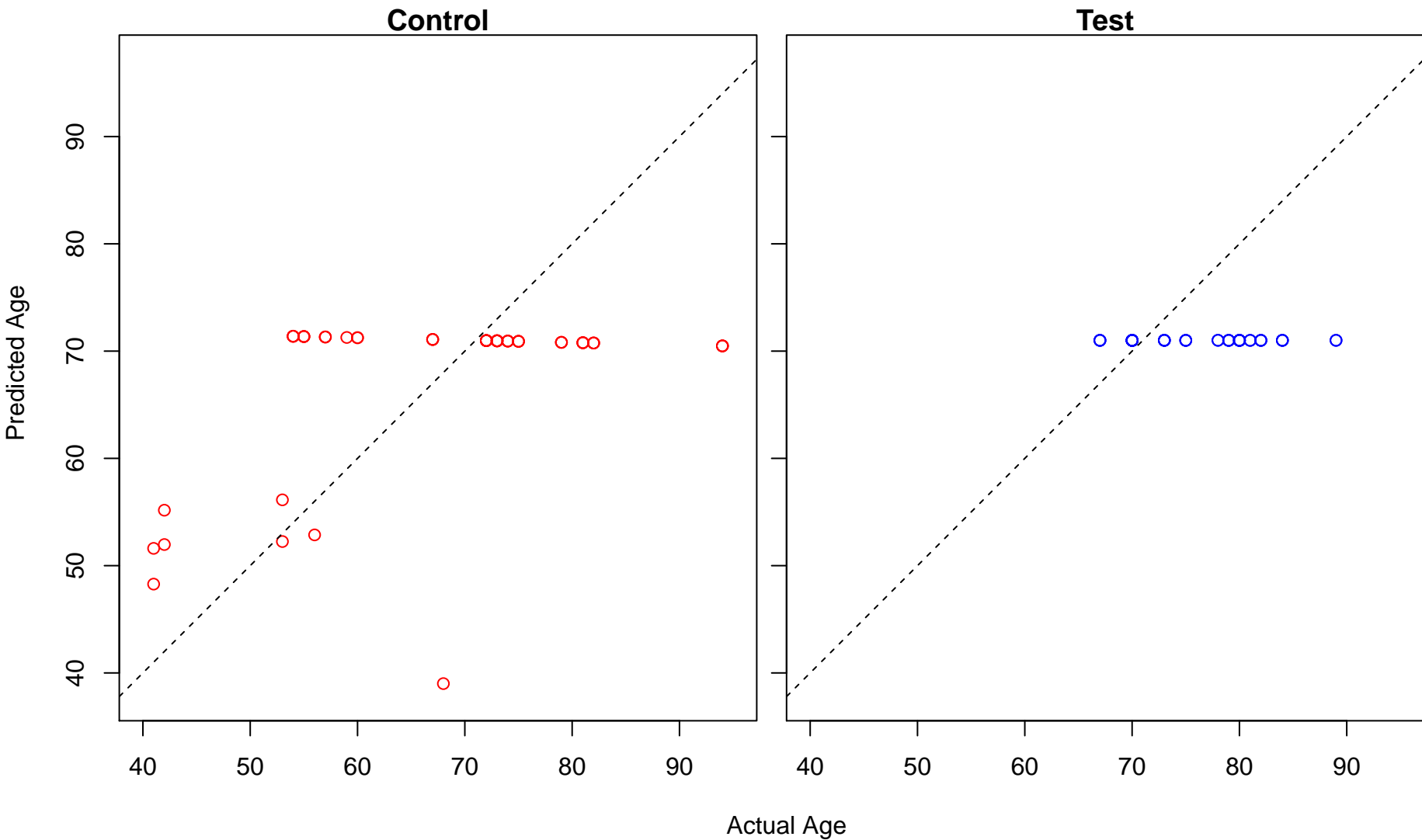


Test



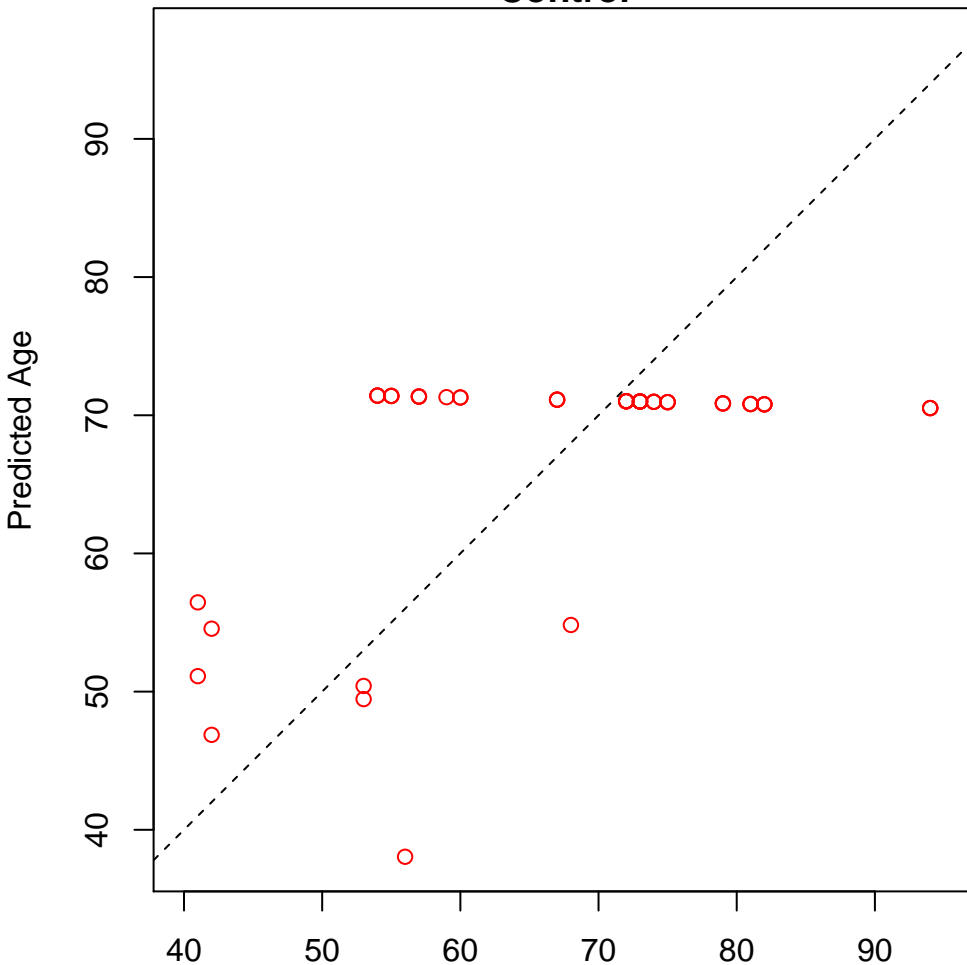
Actual Age

nucleus organization (Score: 0.797435)

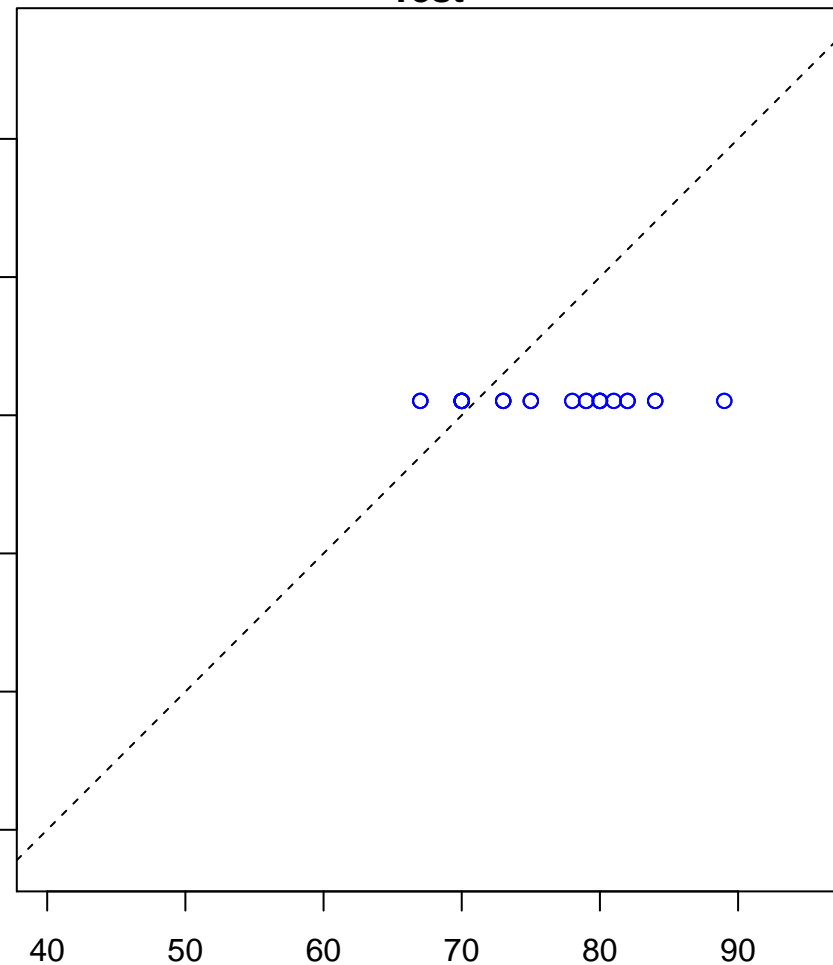


macromolecule catabolic process (Score: 0.797431)

Control



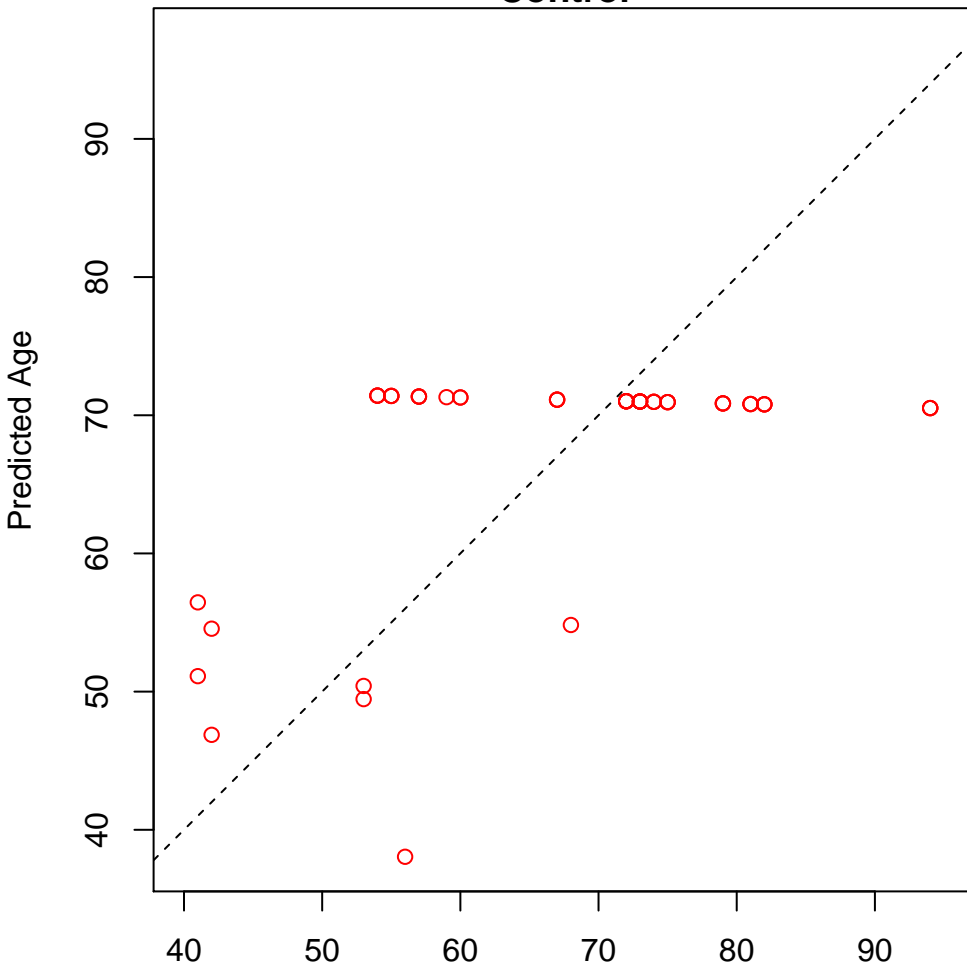
Test



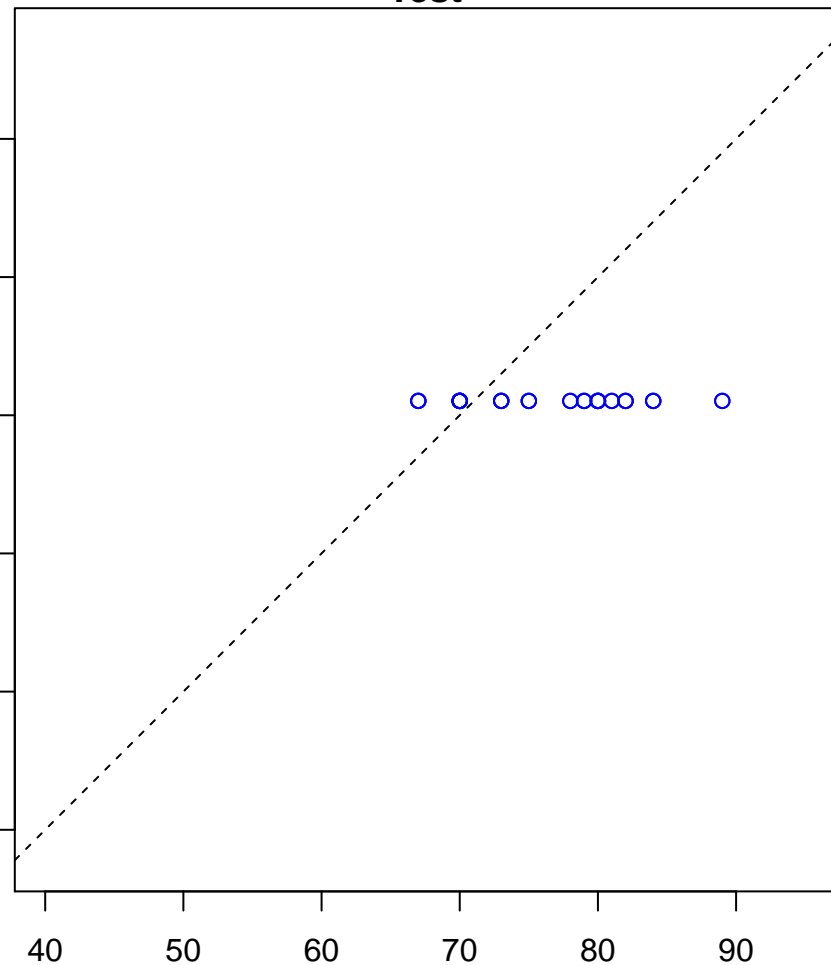
Actual Age

cellular macromolecule catabolic process (Score: 0.797431)

Control



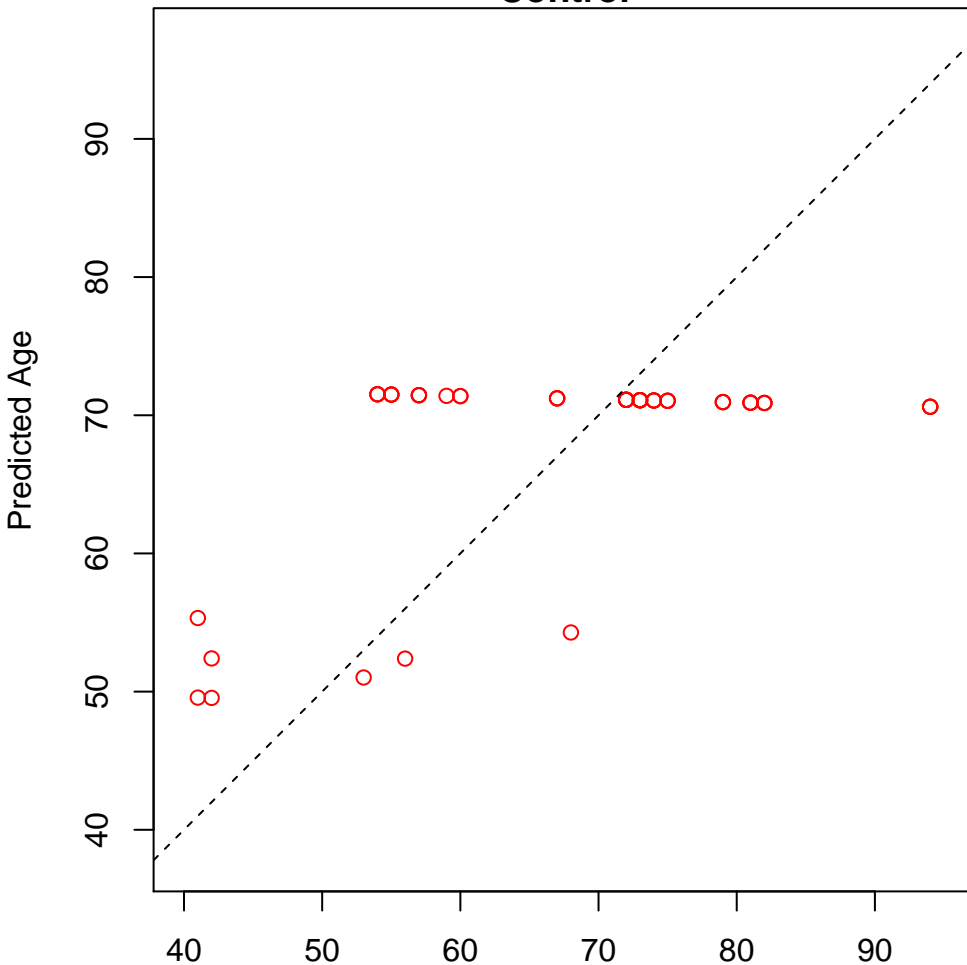
Test



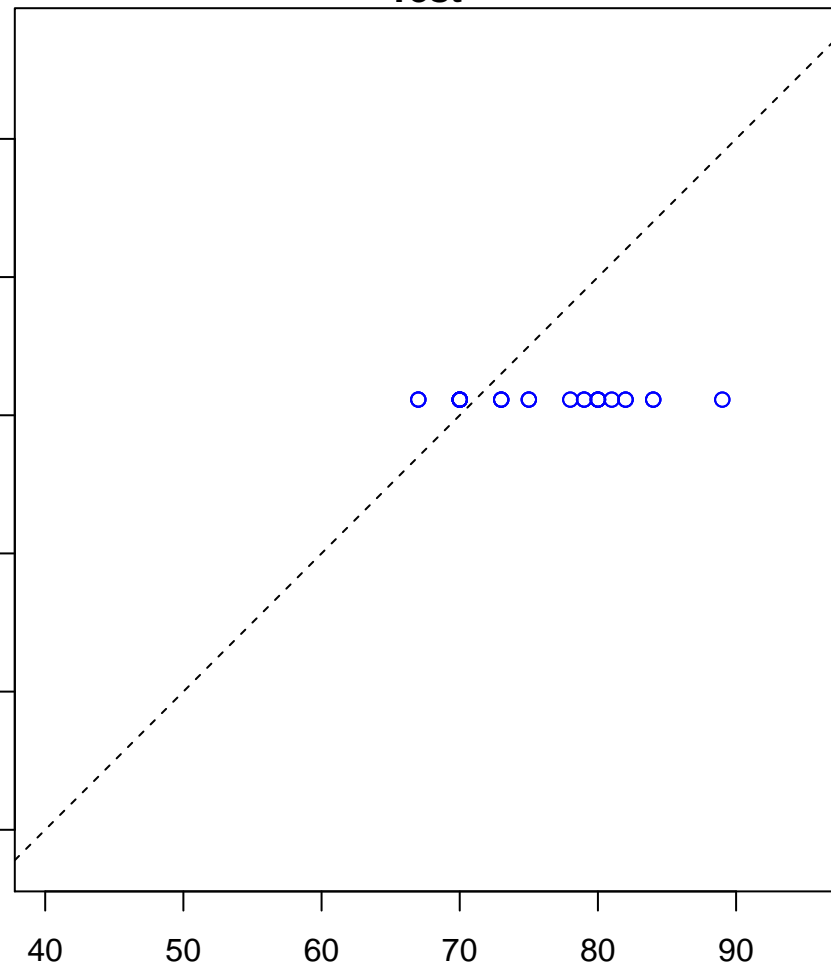
Actual Age

actin polymerization or depolymerization (Score: 0.797395)

Control



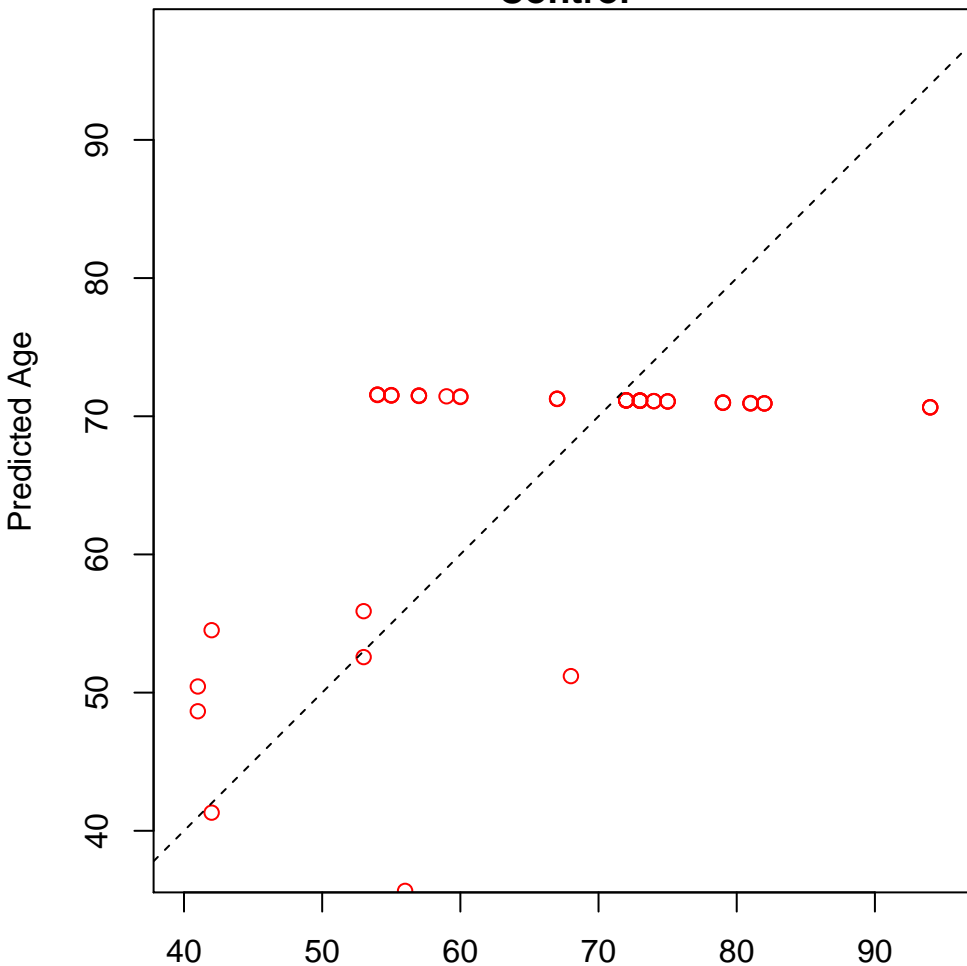
Test



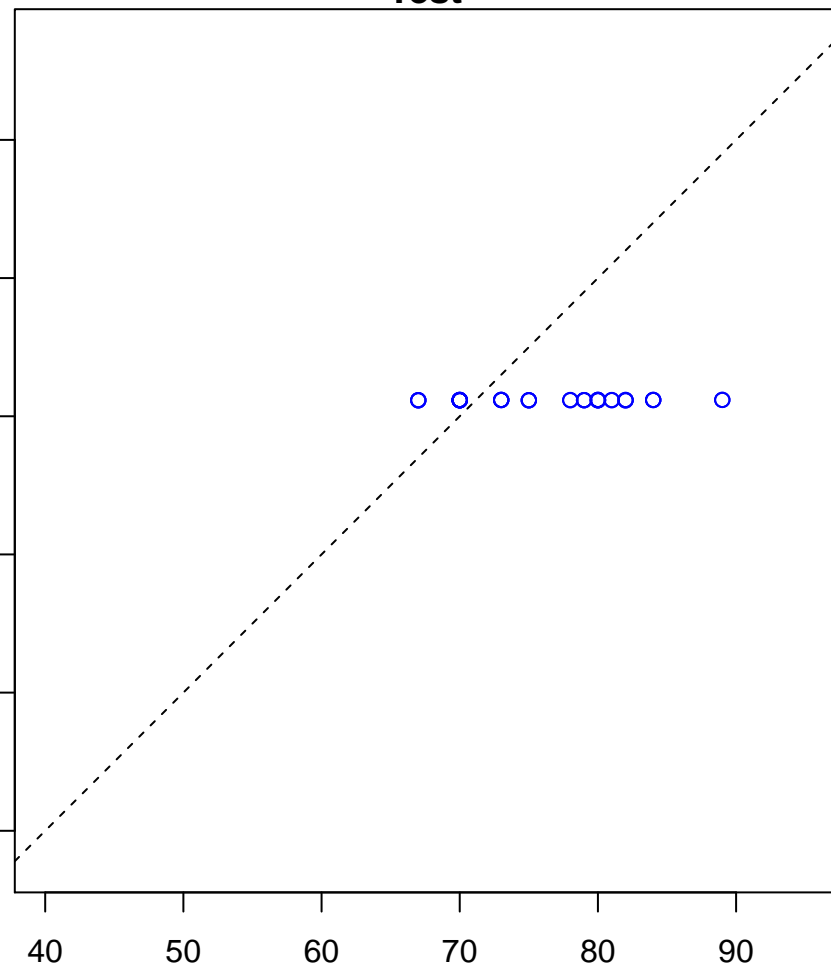
Actual Age

regulation of myeloid cell differentiation (Score: 0.797385)

Control



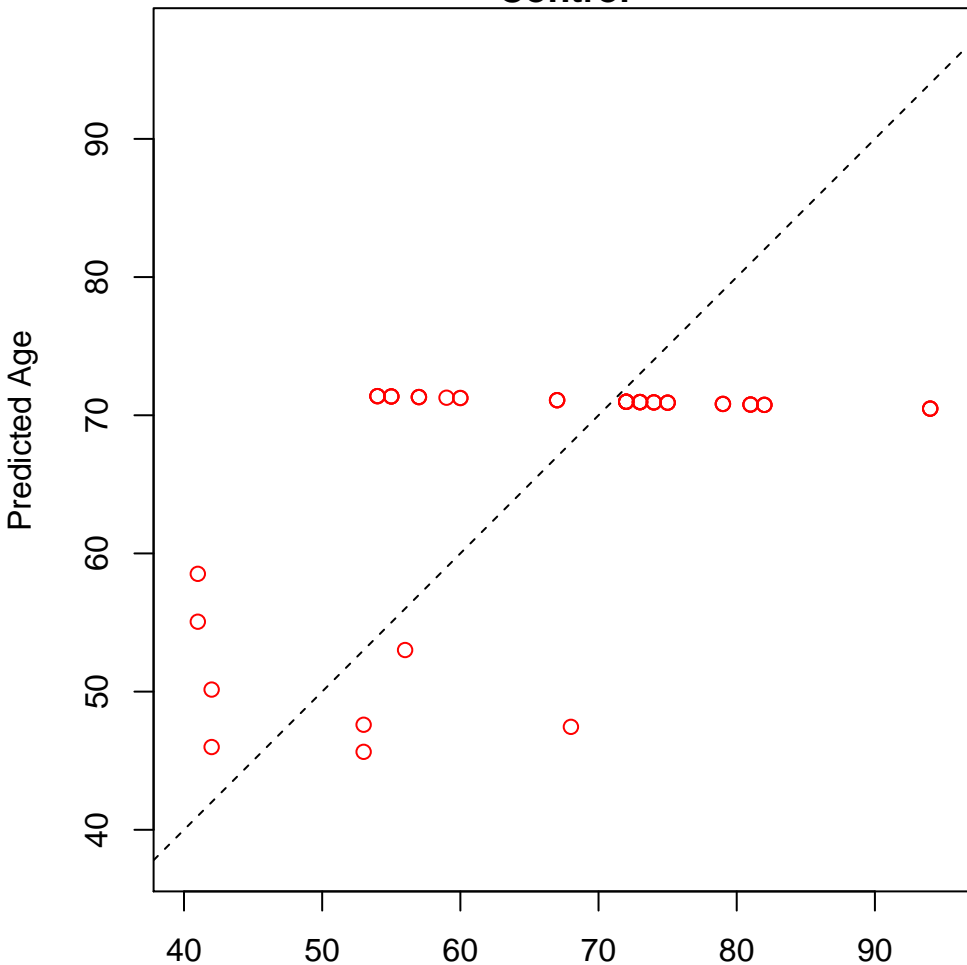
Test



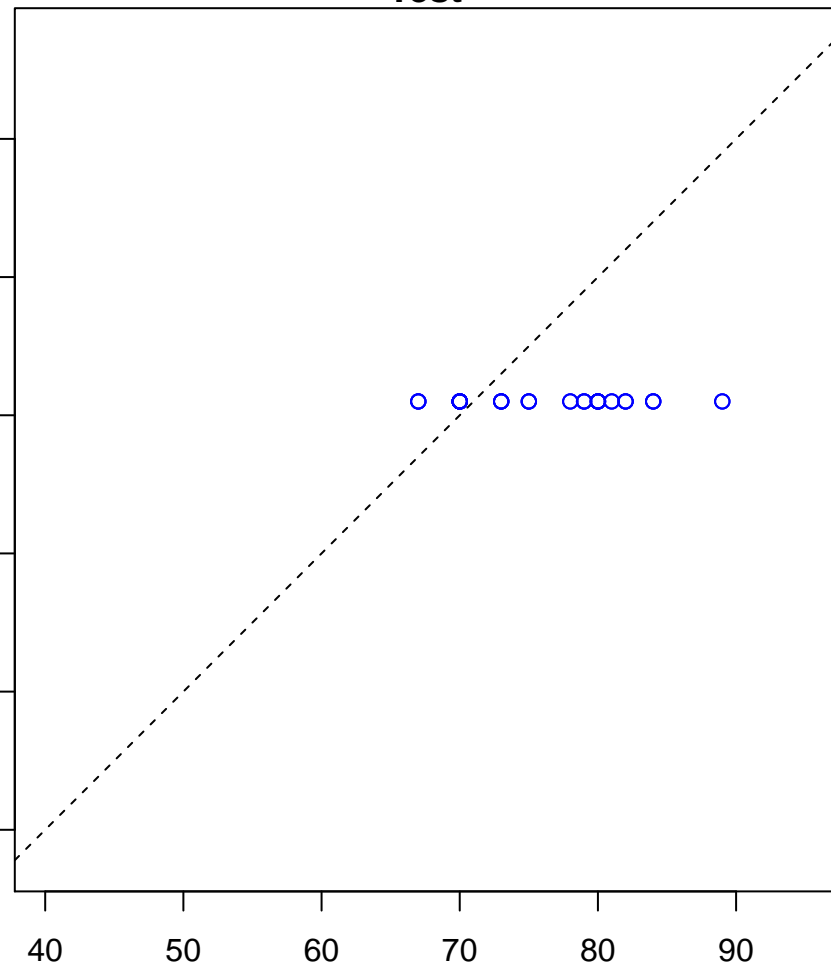
Actual Age

positive regulation of DNA binding (Score: 0.797310)

Control



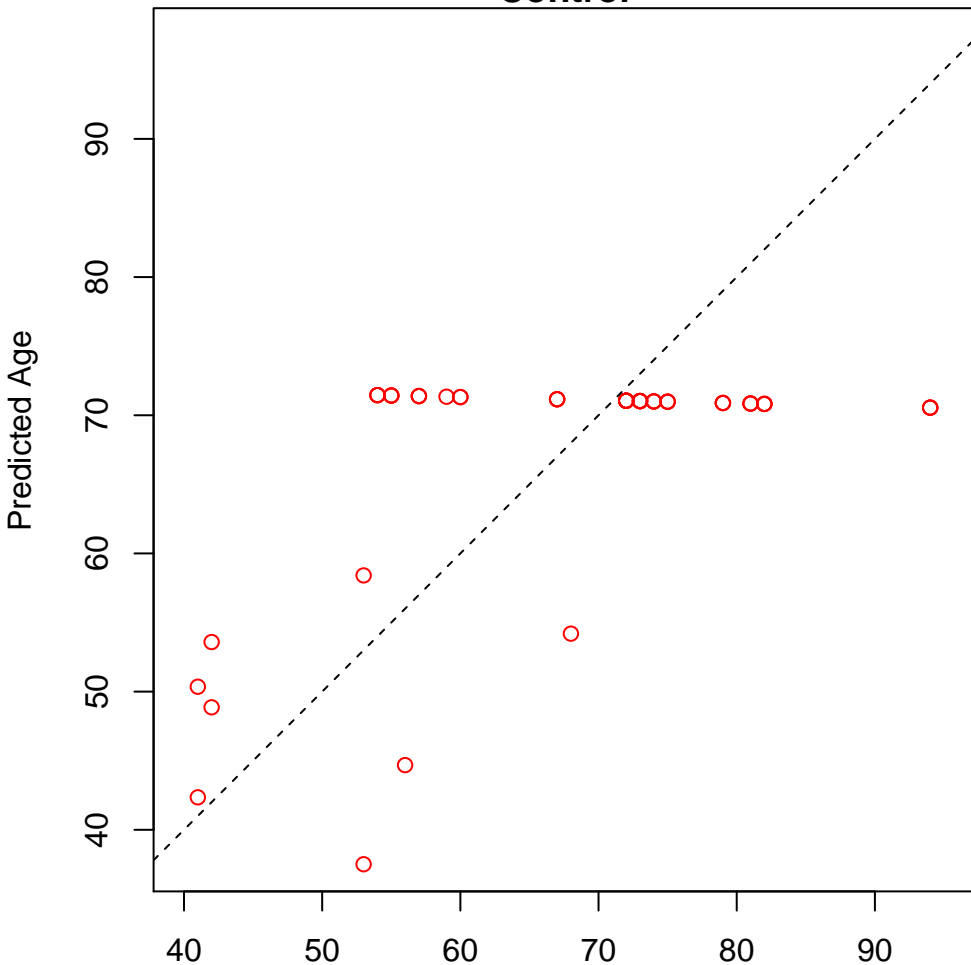
Test



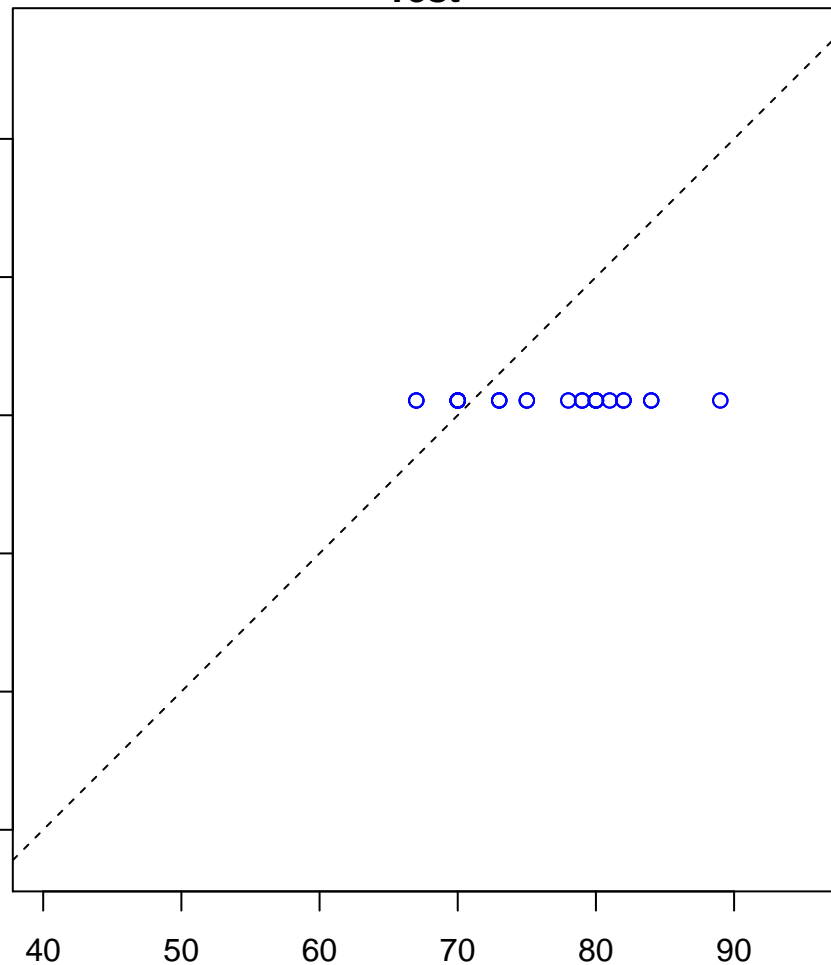
Actual Age

regulation of cAMP metabolic process (Score: 0.797298)

Control

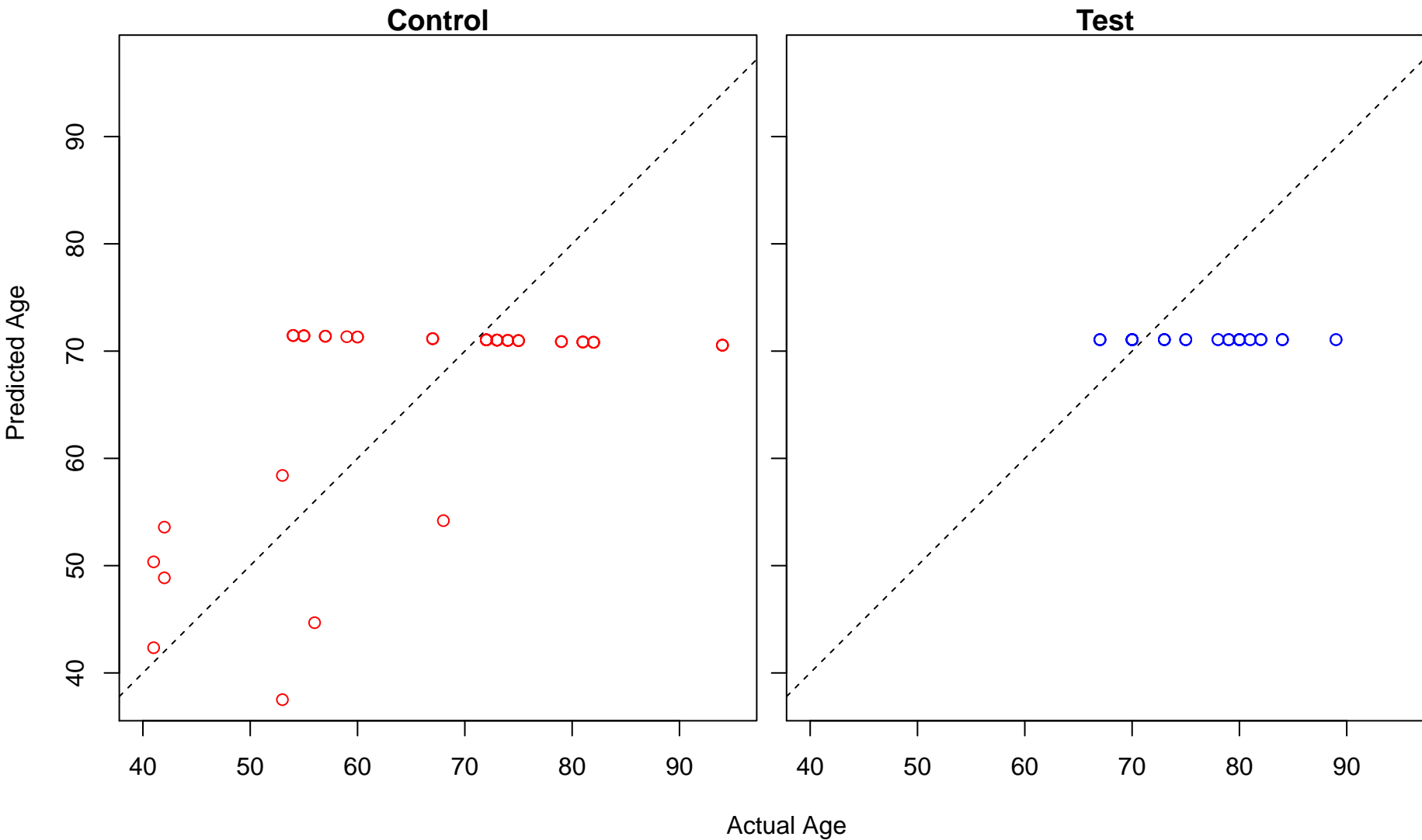


Test



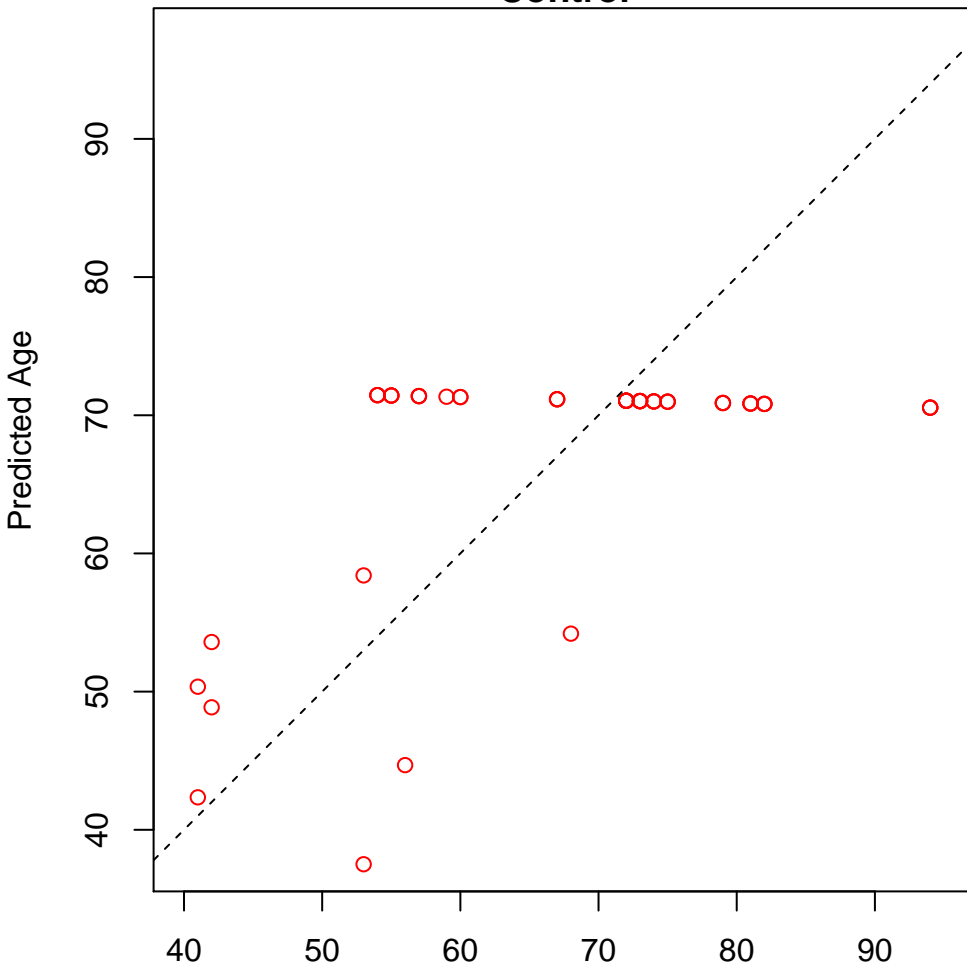
Actual Age

positive regulation of cAMP metabolic process (Score: 0.797298)

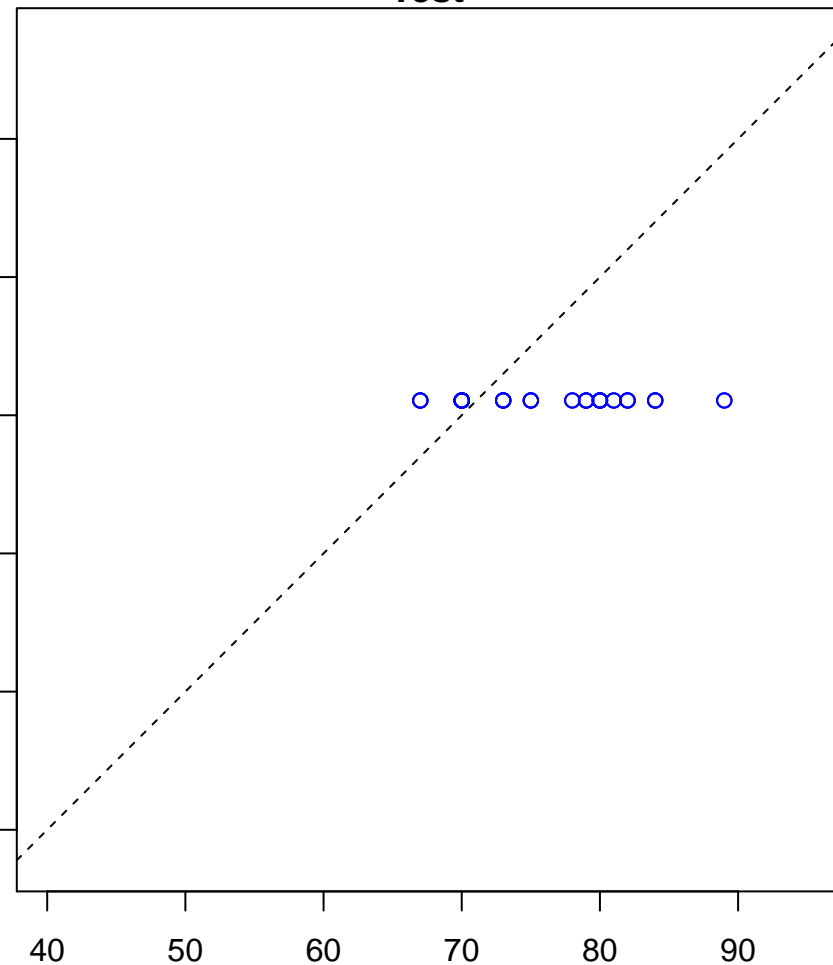


regulation of cAMP biosynthetic process (Score: 0.797298)

Control

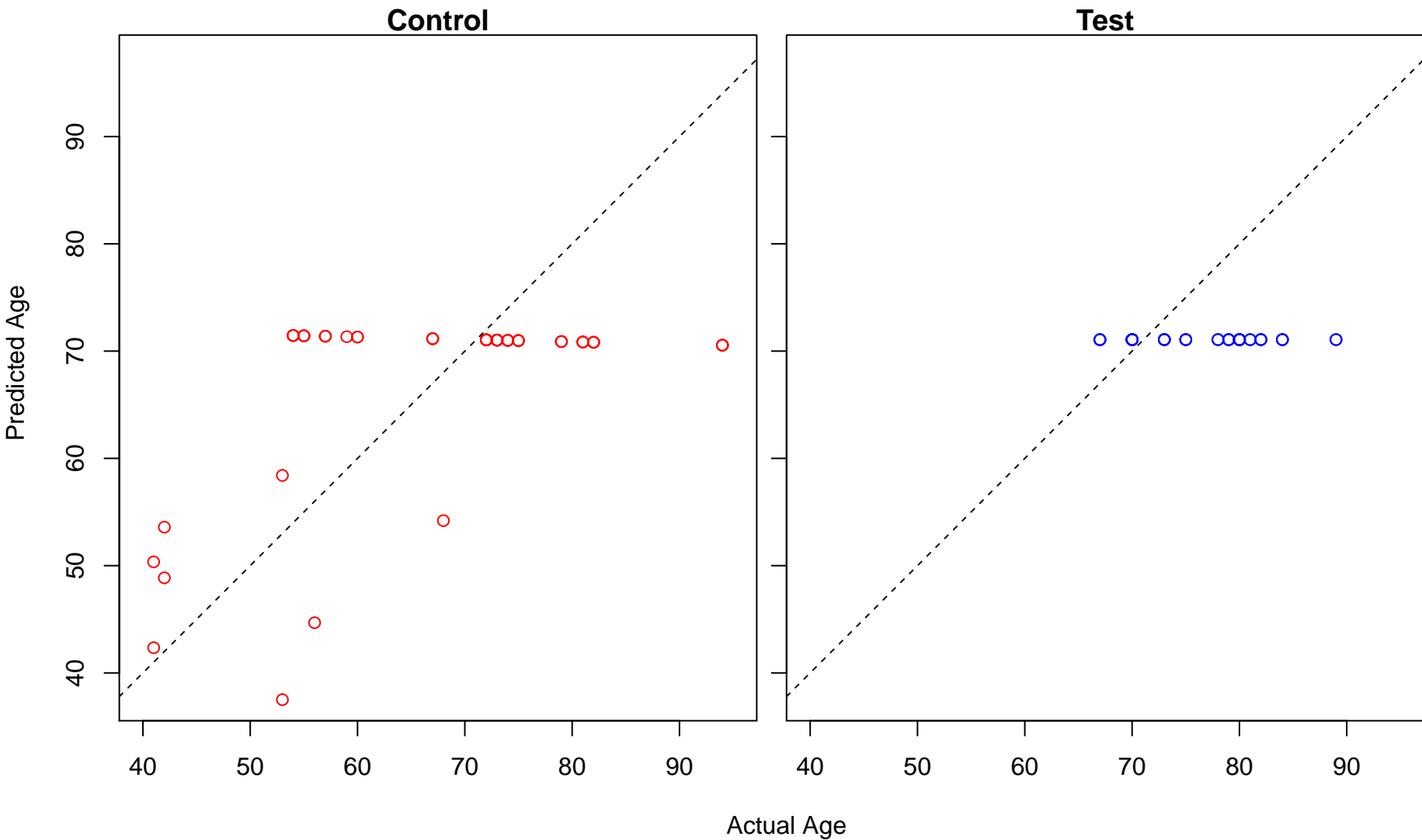


Test



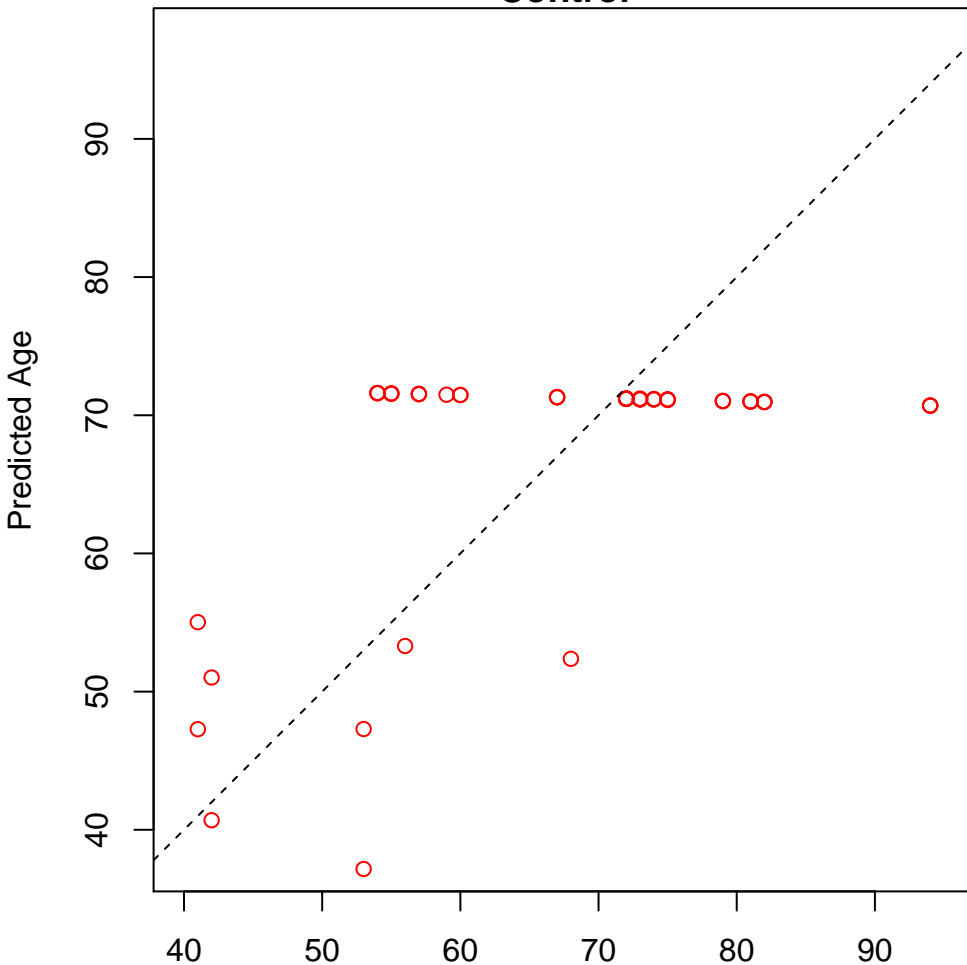
Actual Age

positive regulation of cAMP biosynthetic process (Score: 0.797298)

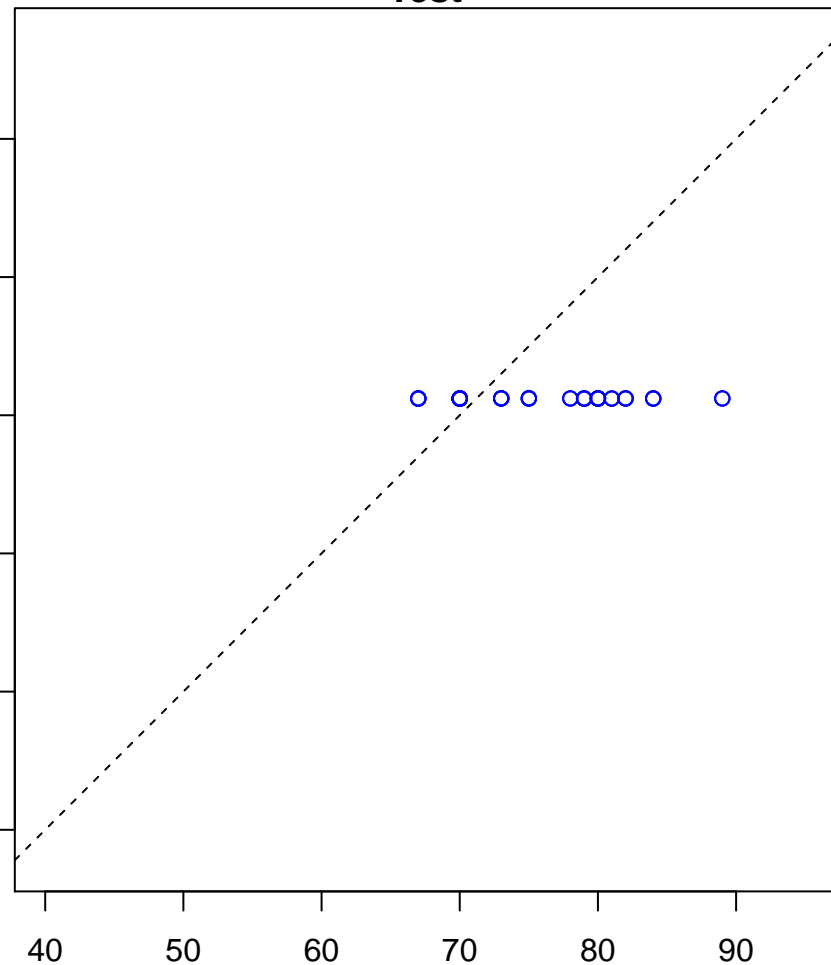


regulation of ERK1 and ERK2 cascade (Score: 0.797285)

Control

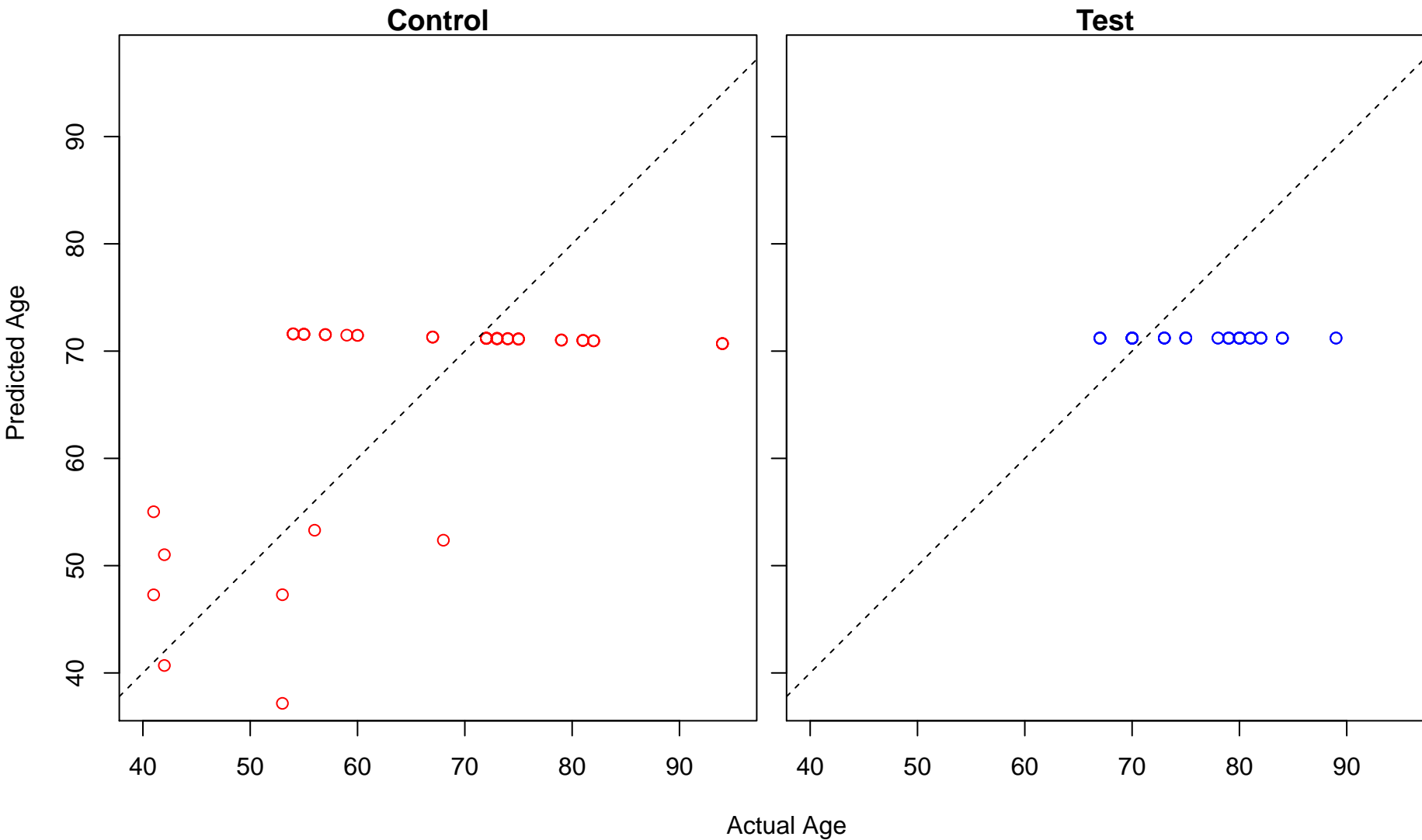


Test

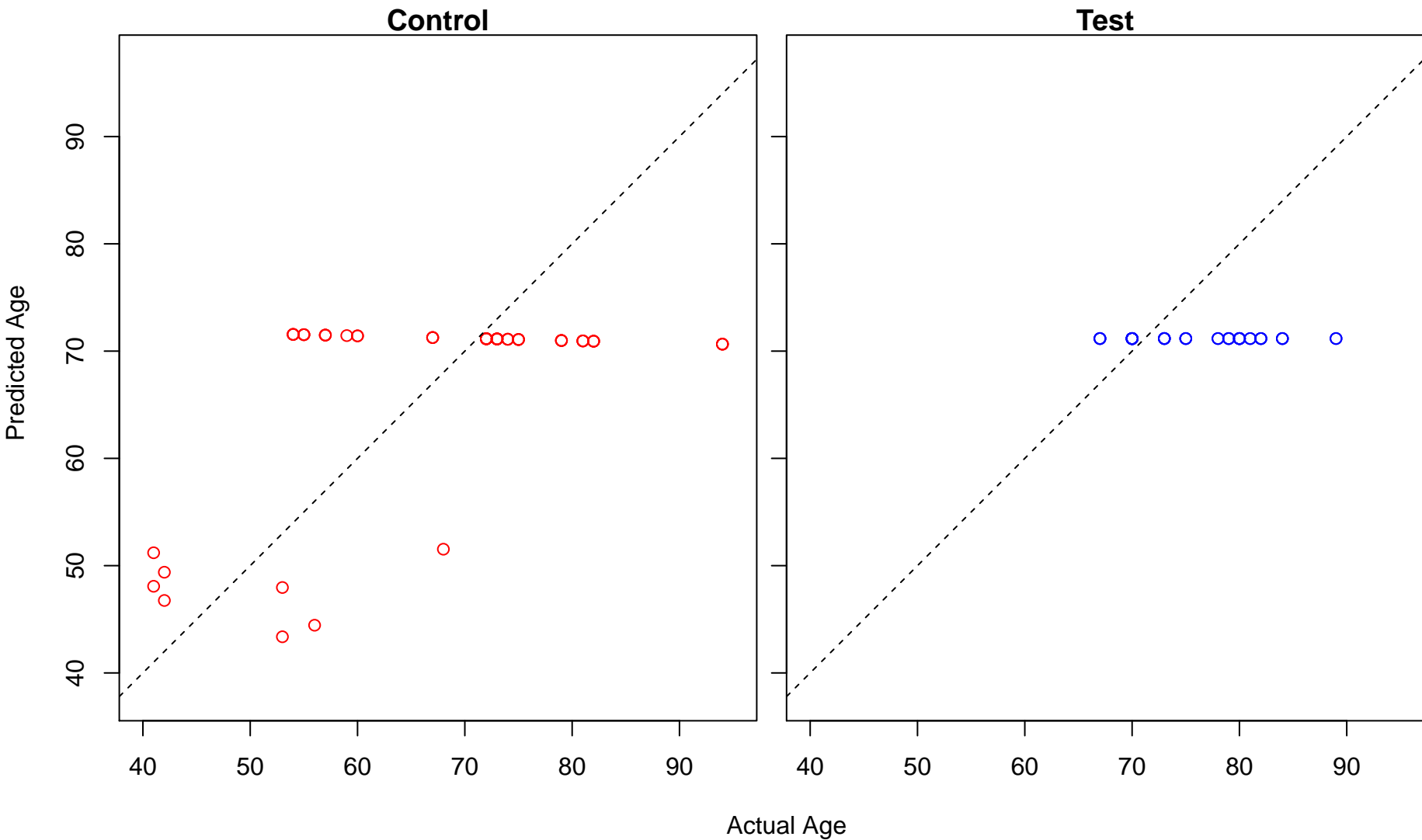


Actual Age

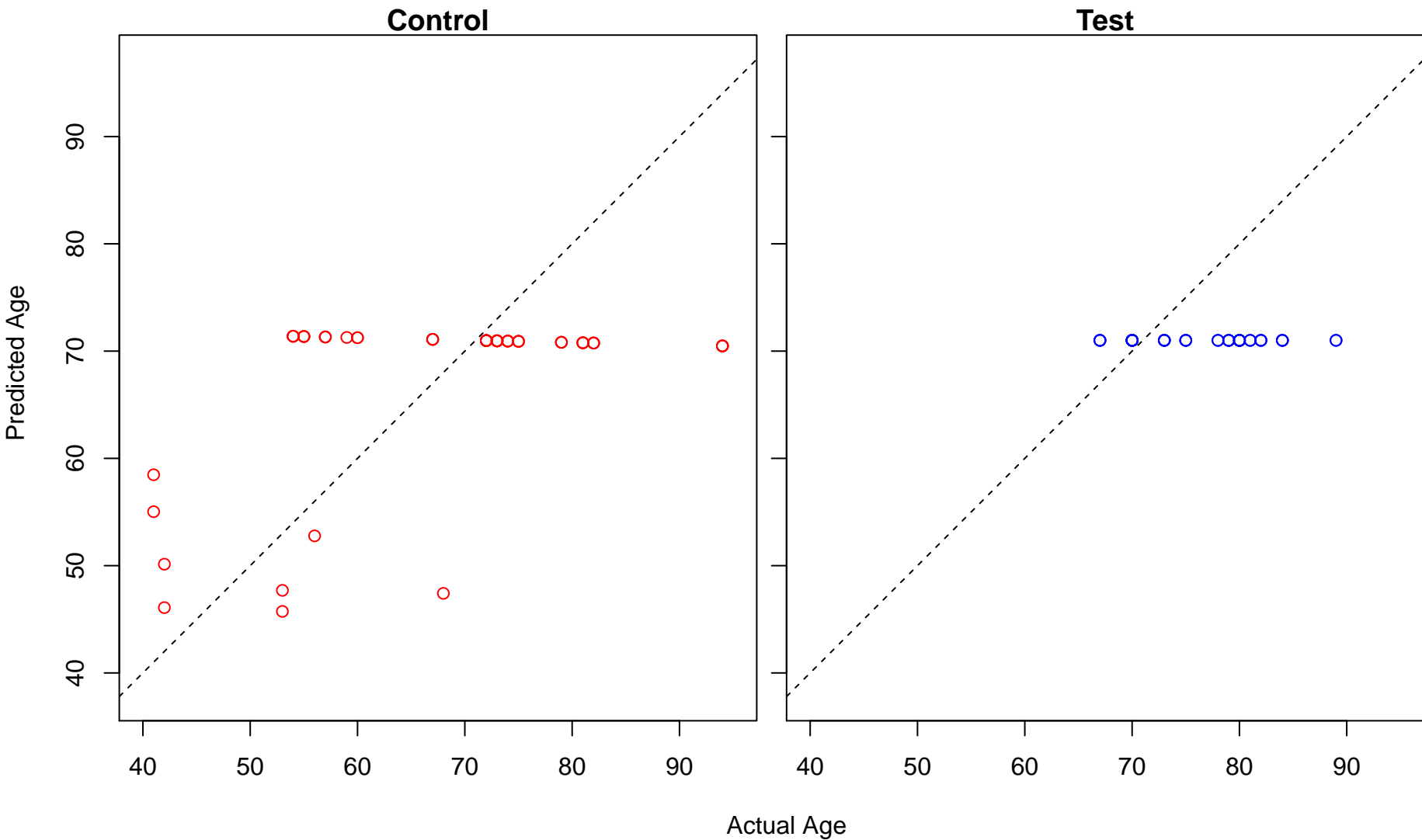
positive regulation of ERK1 and ERK2 cascade (Score: 0.797285)



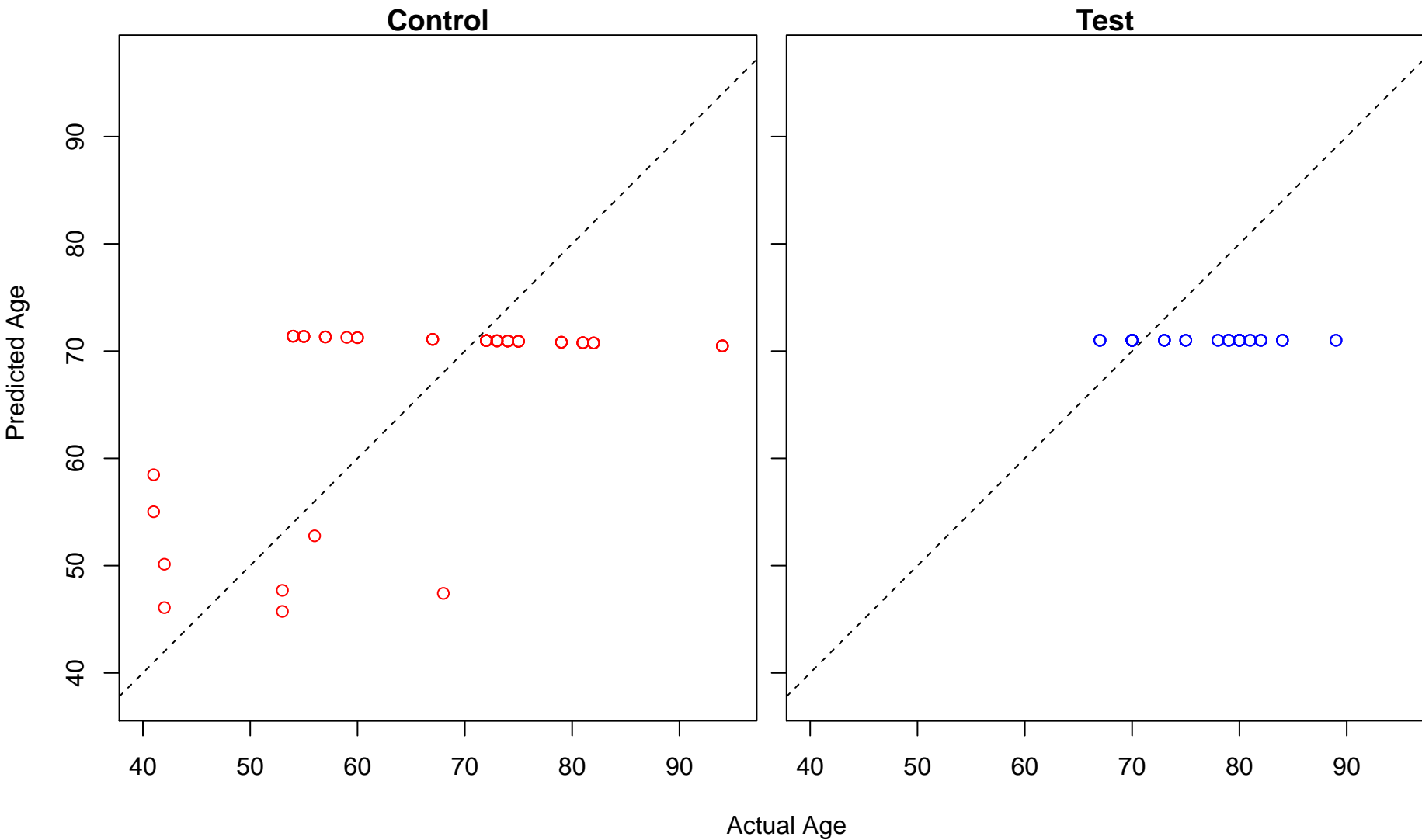
metabolic process (Score: 0.797258)



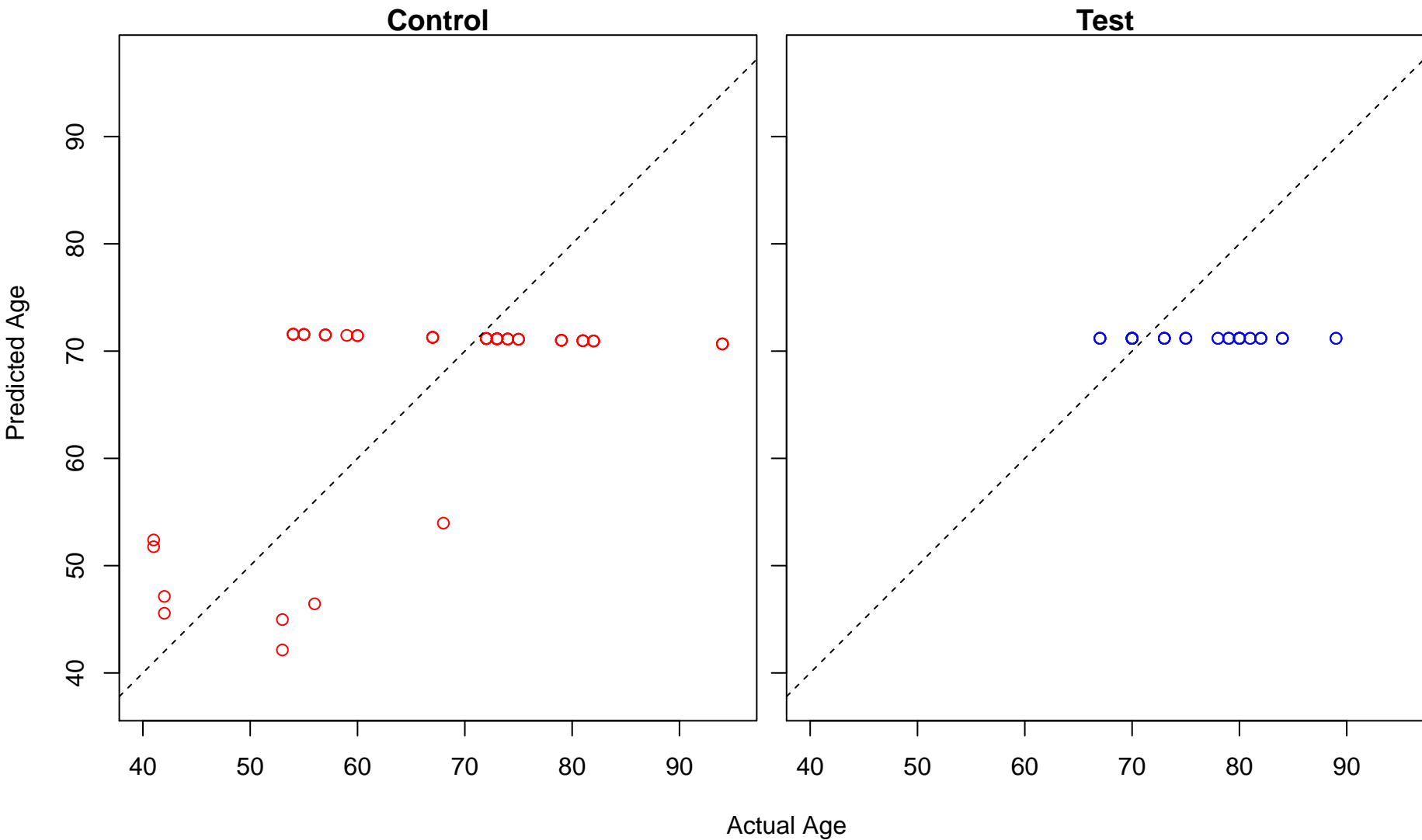
peptide secretion (Score: 0.797231)



protein secretion (Score: 0.797231)

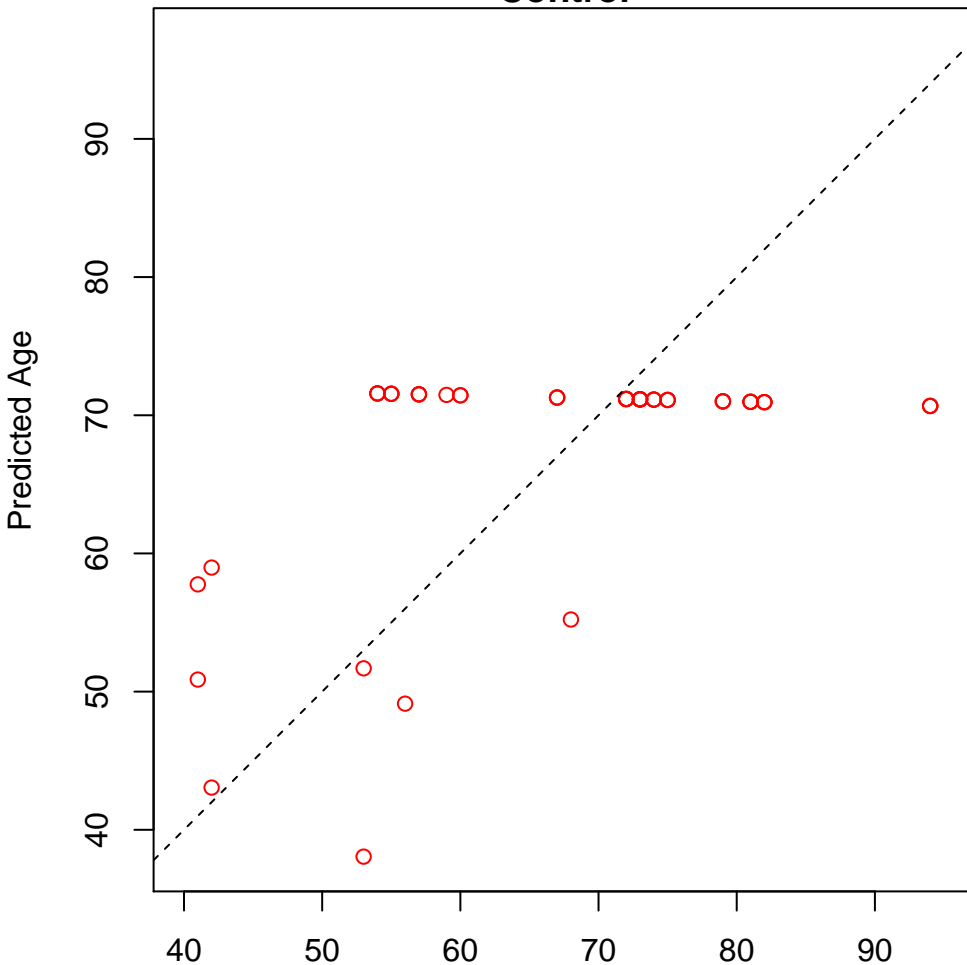


programmed cell death (Score: 0.797229)

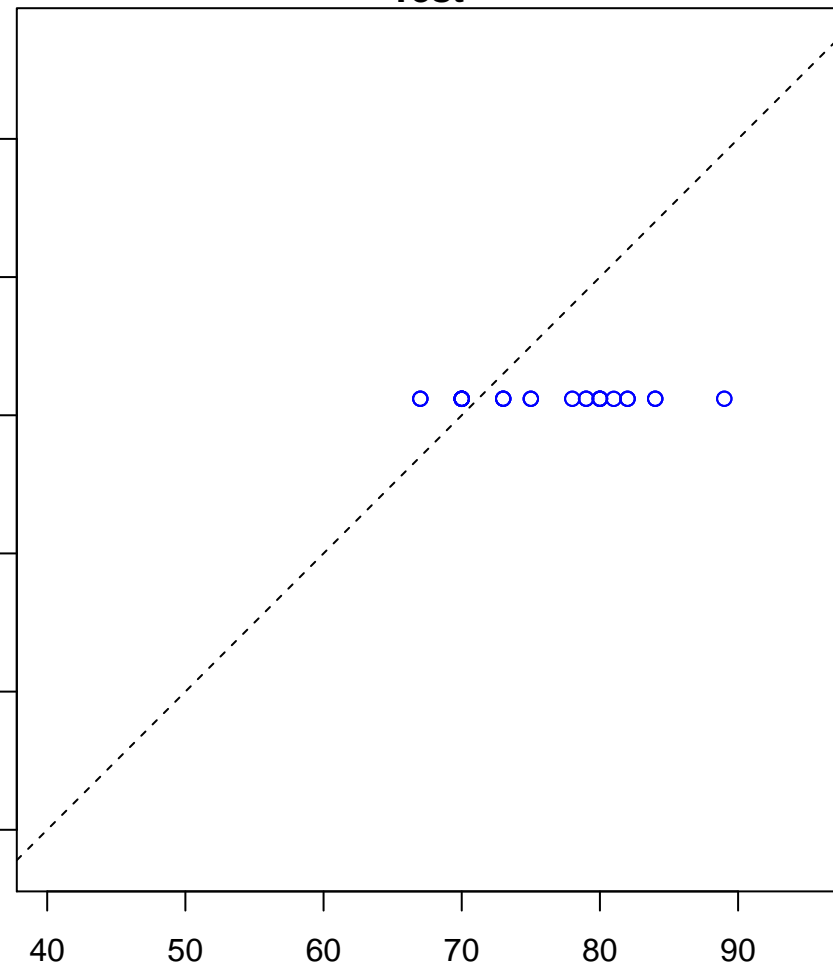


positive regulation of hydrolase activity (Score: 0.797221)

Control



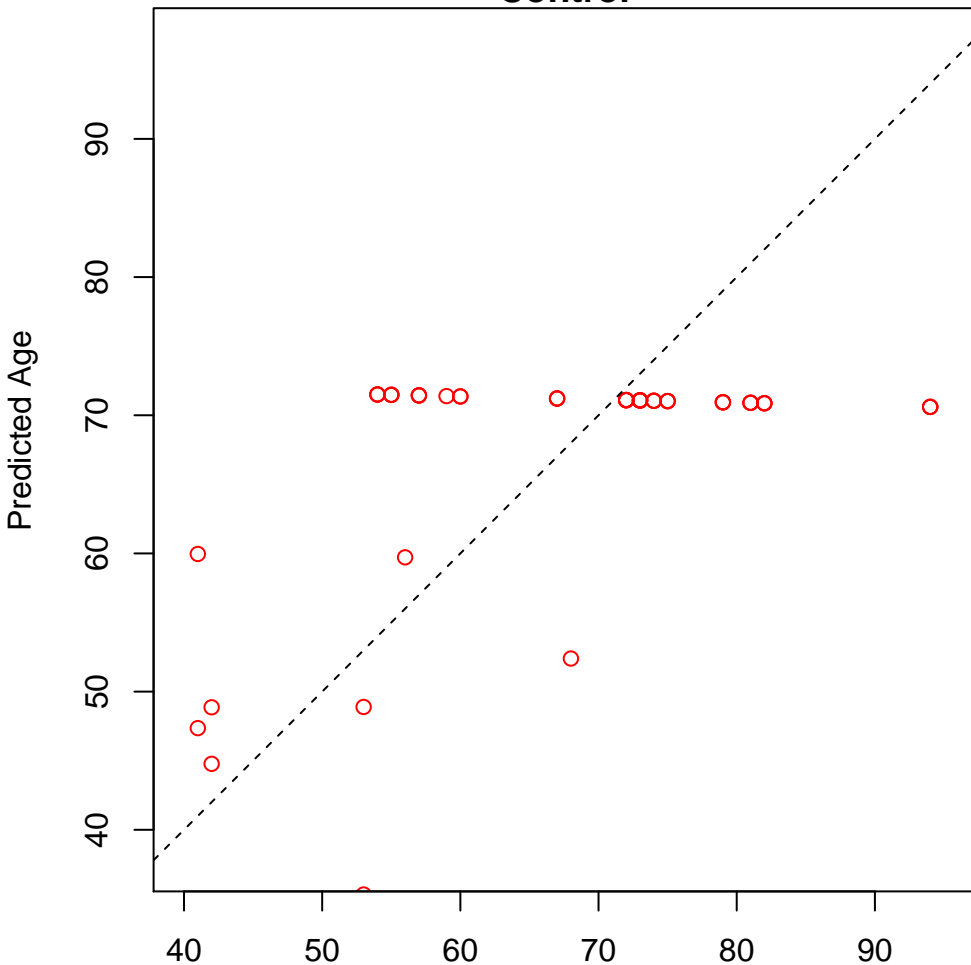
Test



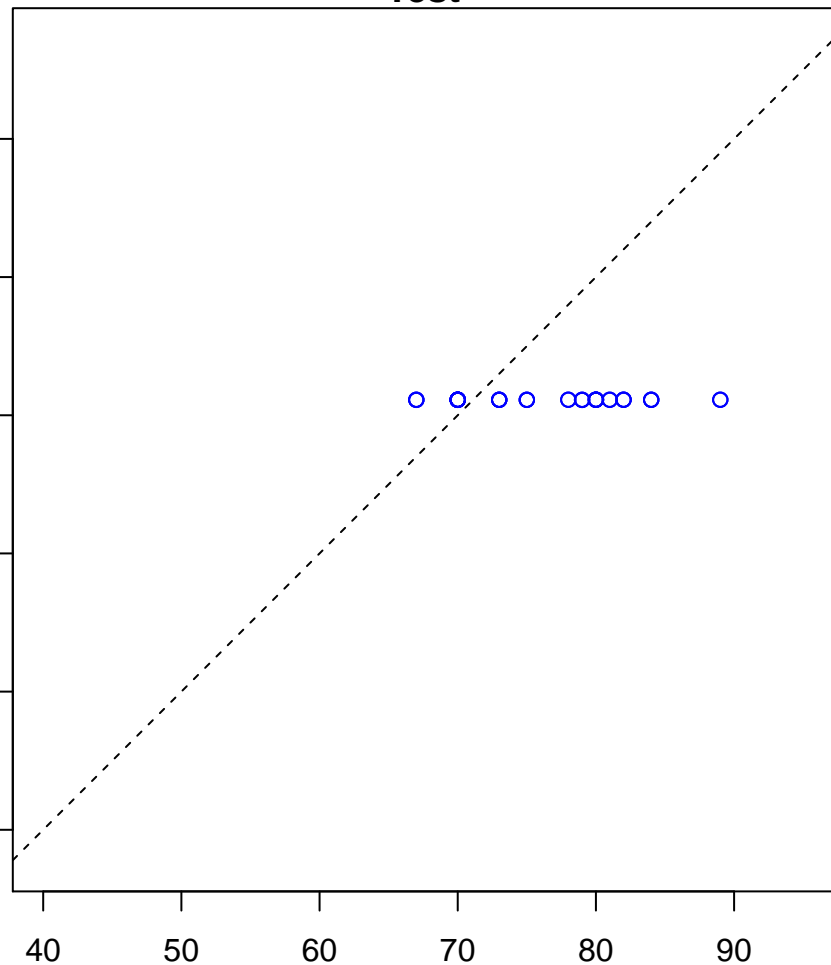
Actual Age

cellular protein complex disassembly (Score: 0.797207)

Control

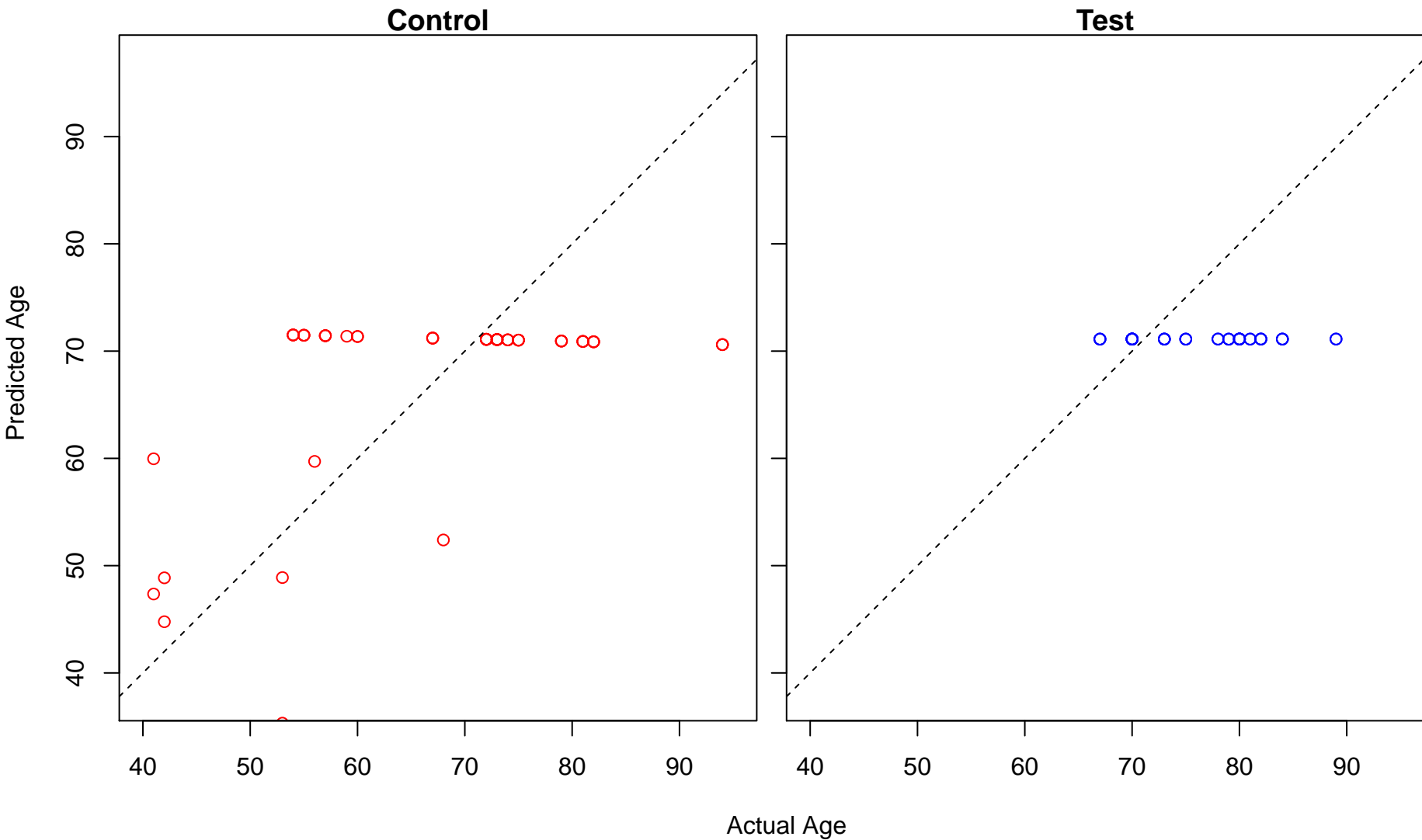


Test

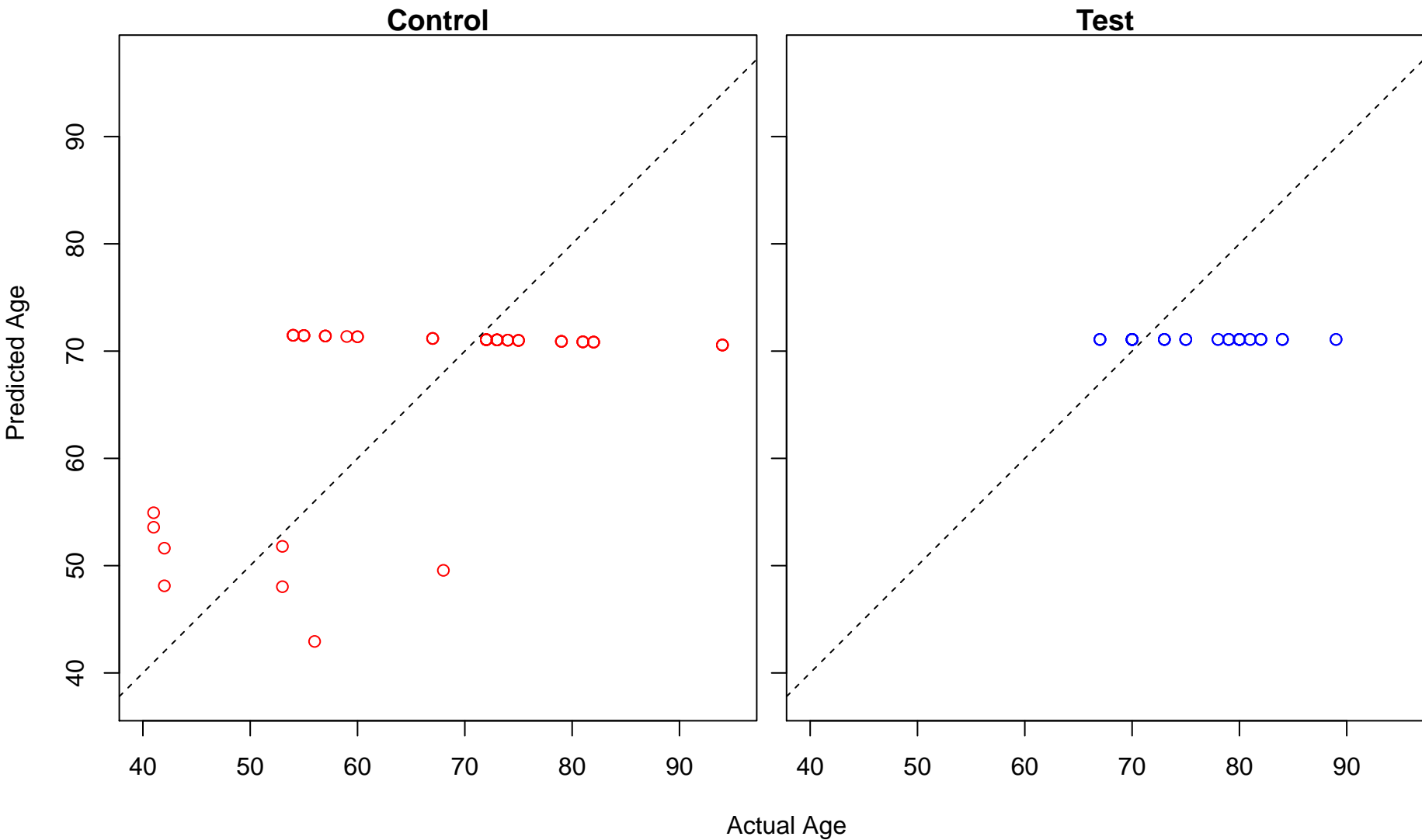


Actual Age

protein depolymerization (Score: 0.797207)

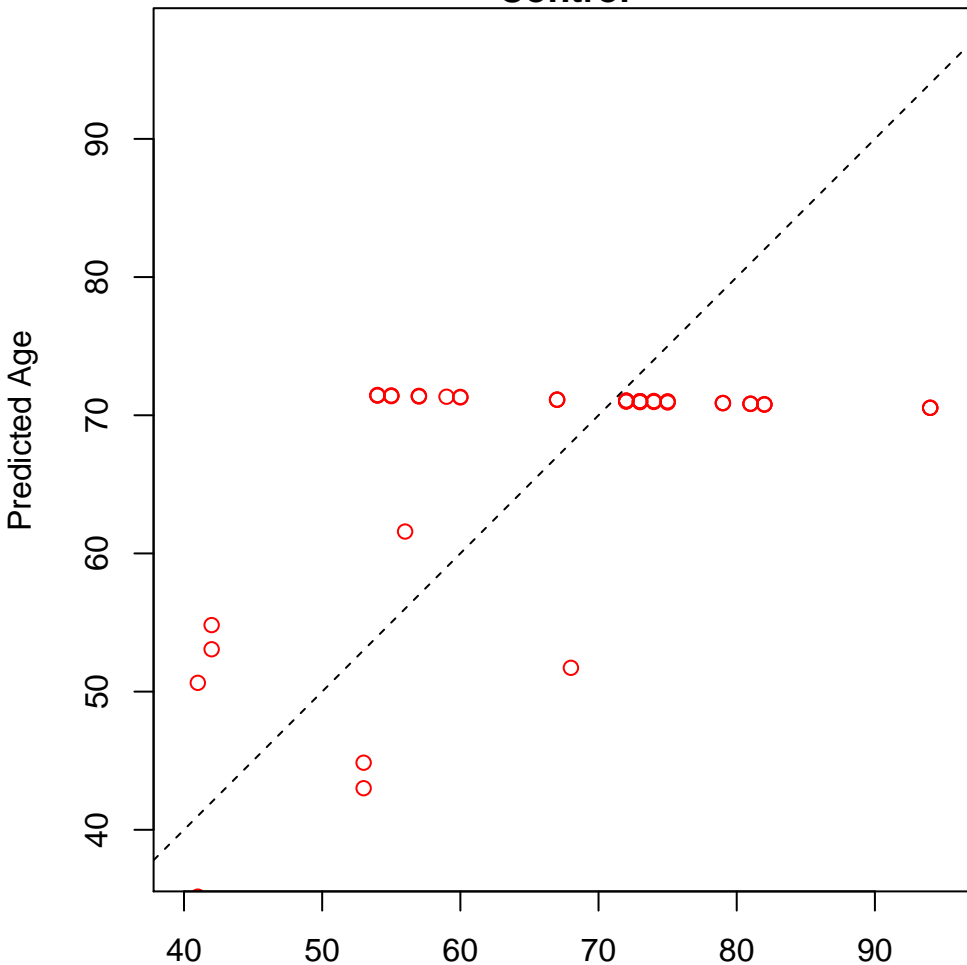


positive regulation of nucleobase-containing compound metabolic process (Score: 0.797187)

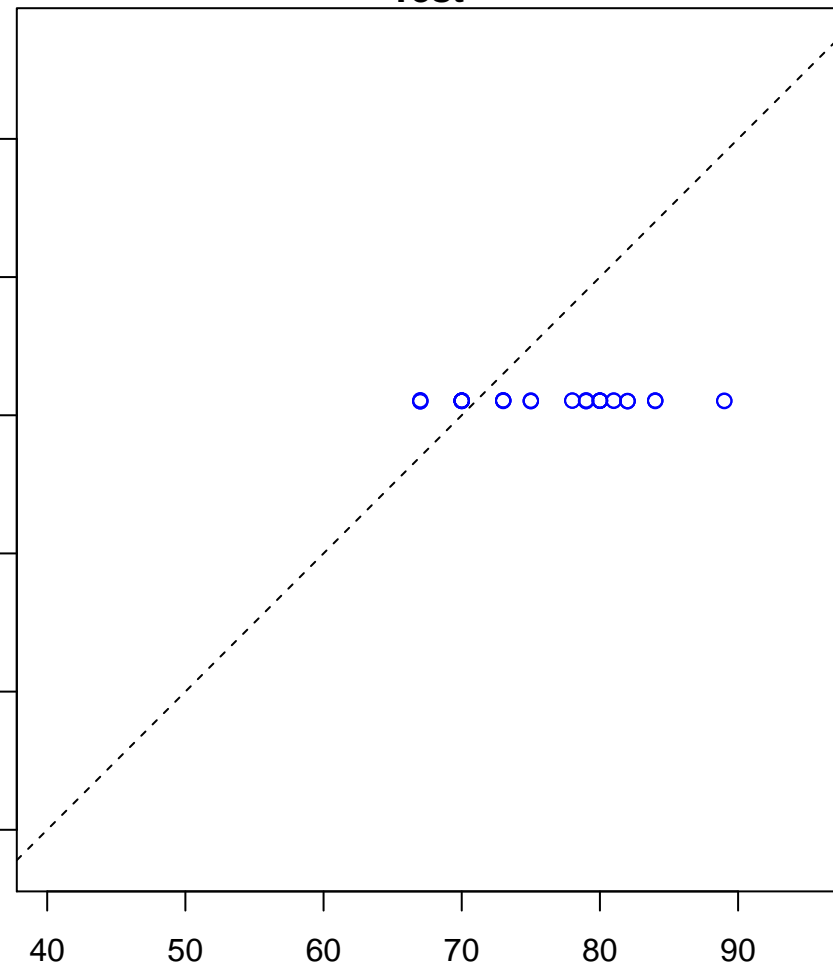


regulation of T cell differentiation (Score: 0.797186)

Control



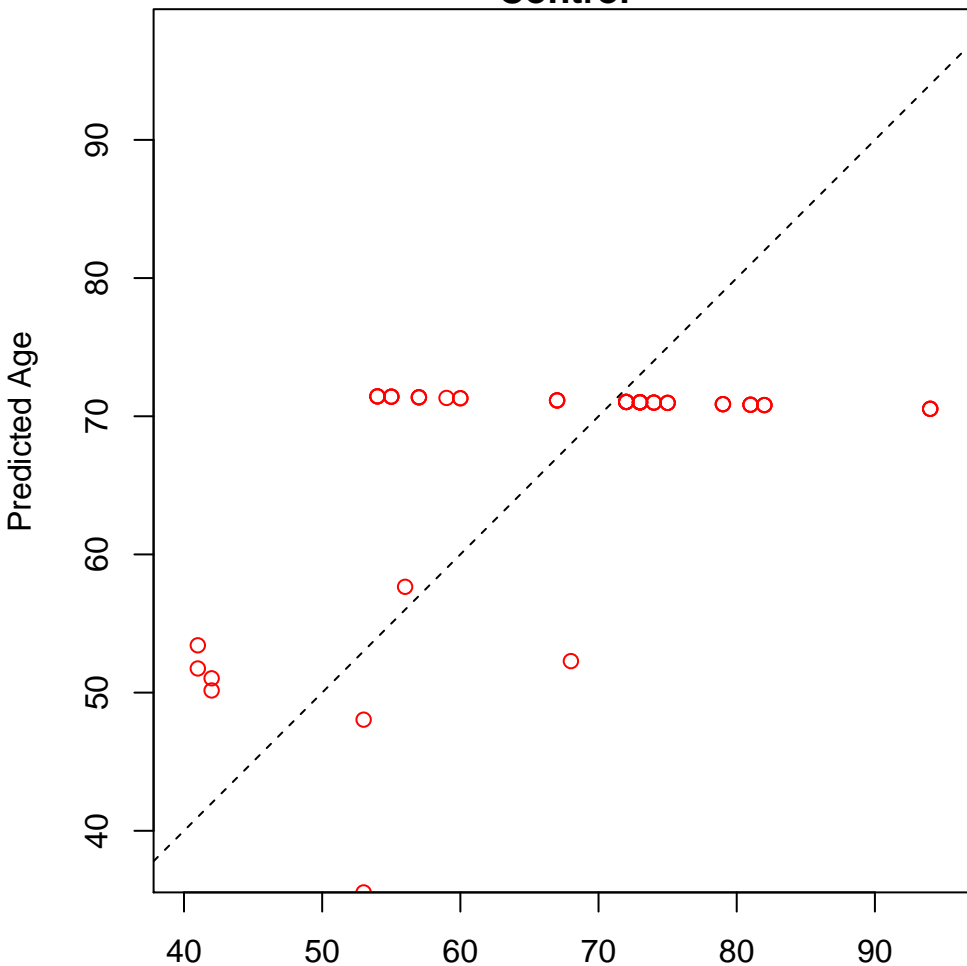
Test



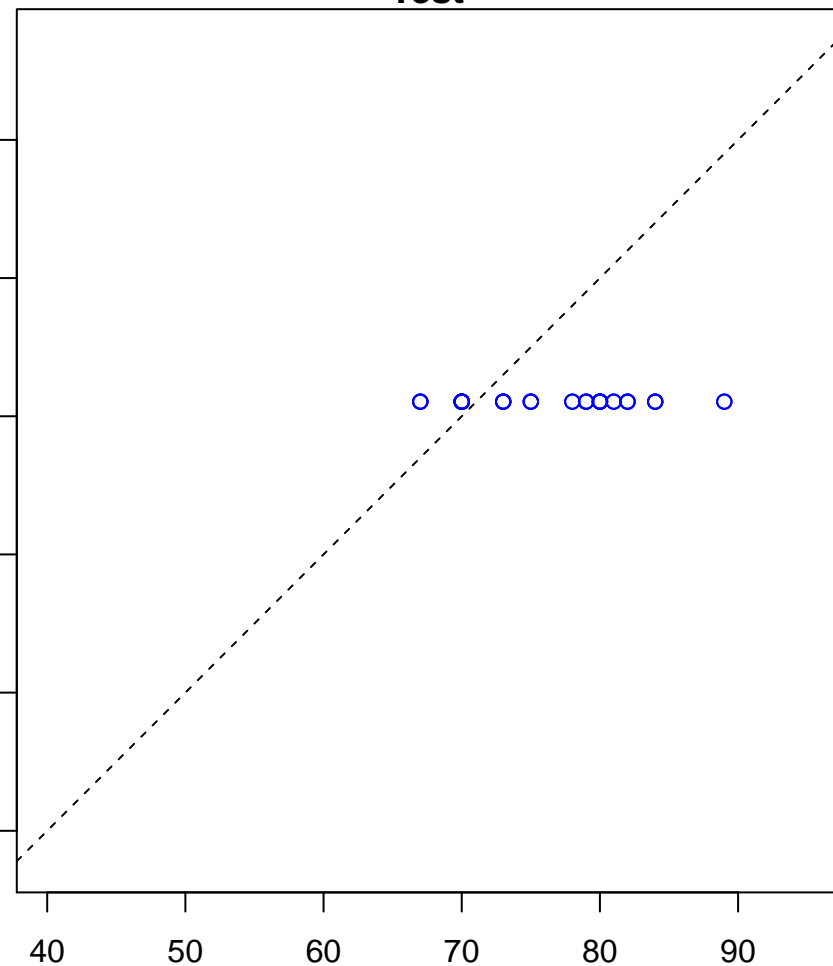
Actual Age

regulation of cell projection organization (Score: 0.797171)

Control

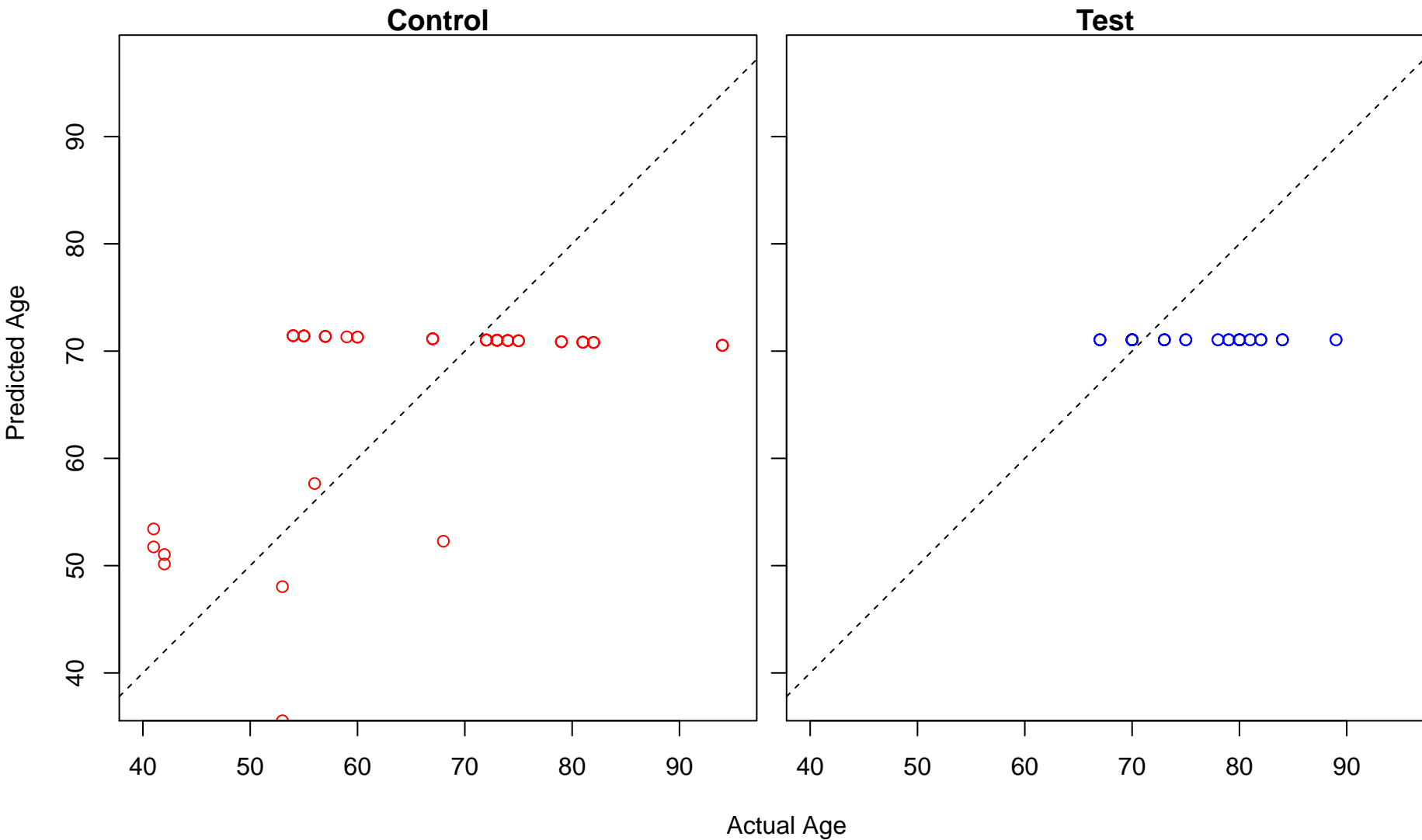


Test



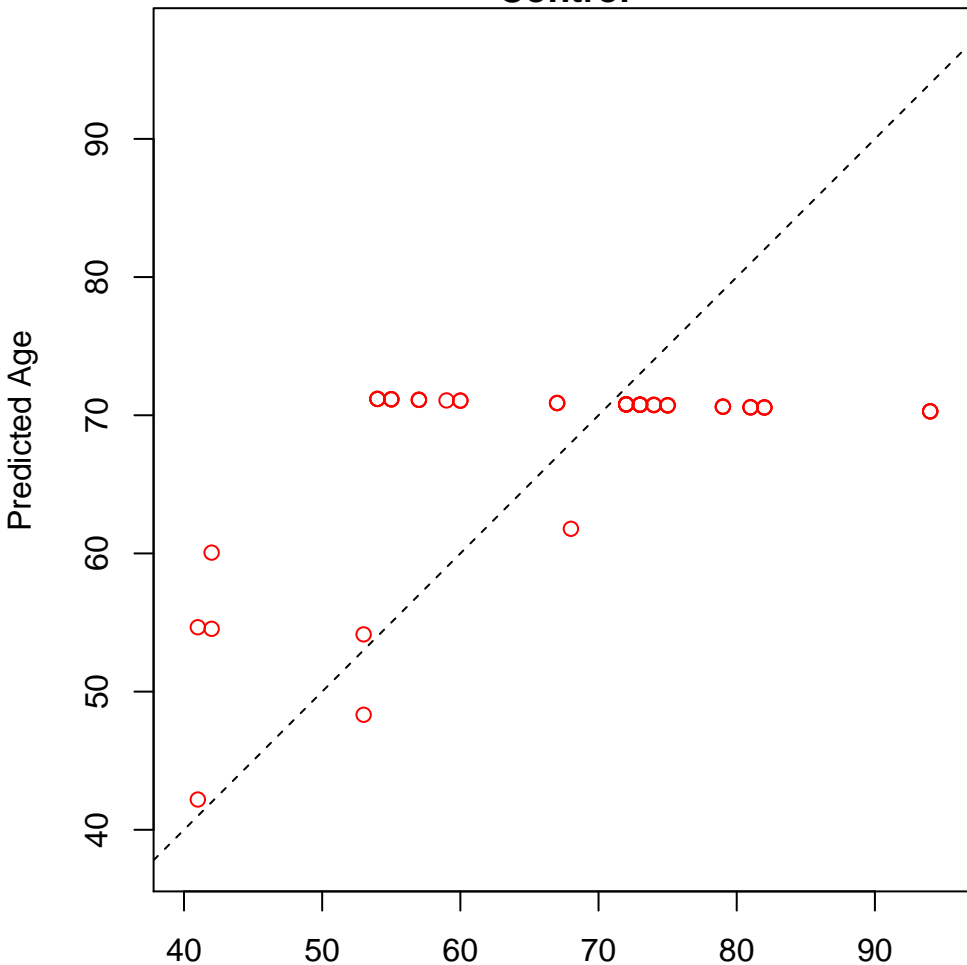
Actual Age

regulation of plasma membrane bounded cell projection organization (Score: 0.797171)

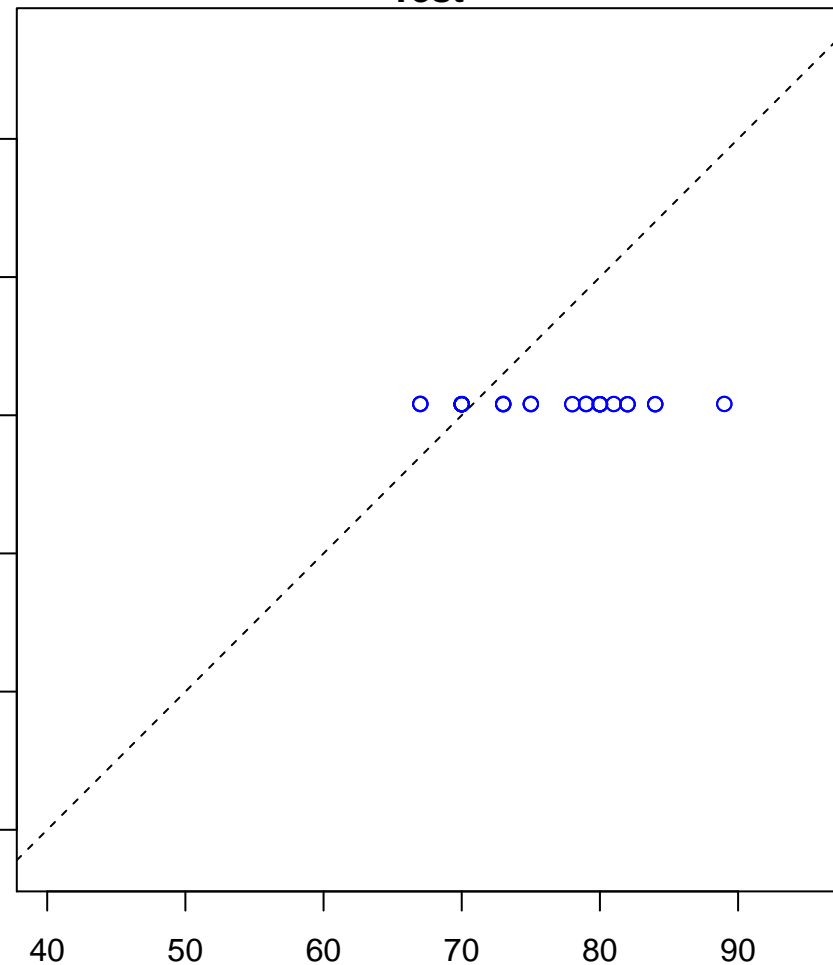


peptidyl-tyrosine phosphorylation (Score: 0.797157)

Control

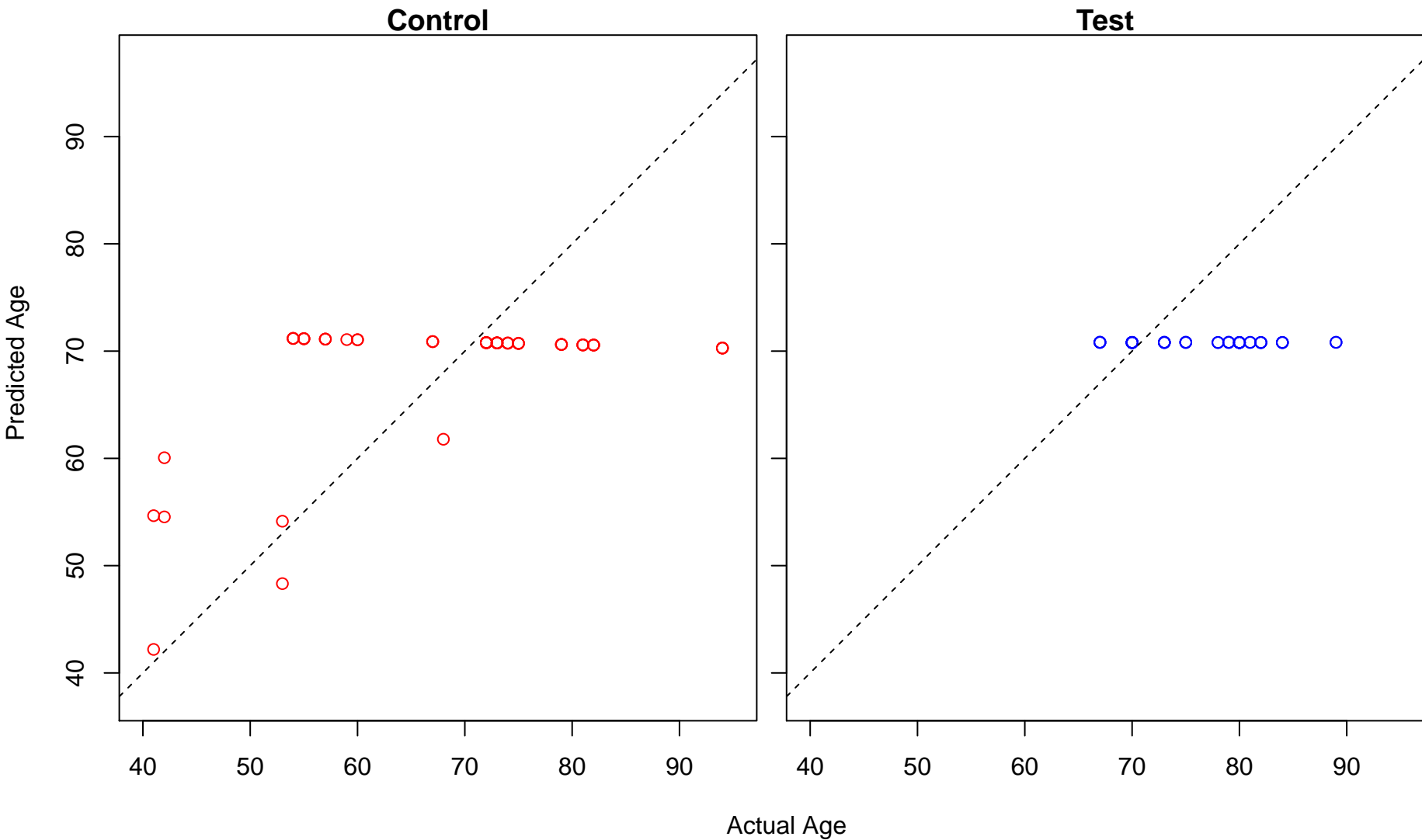


Test

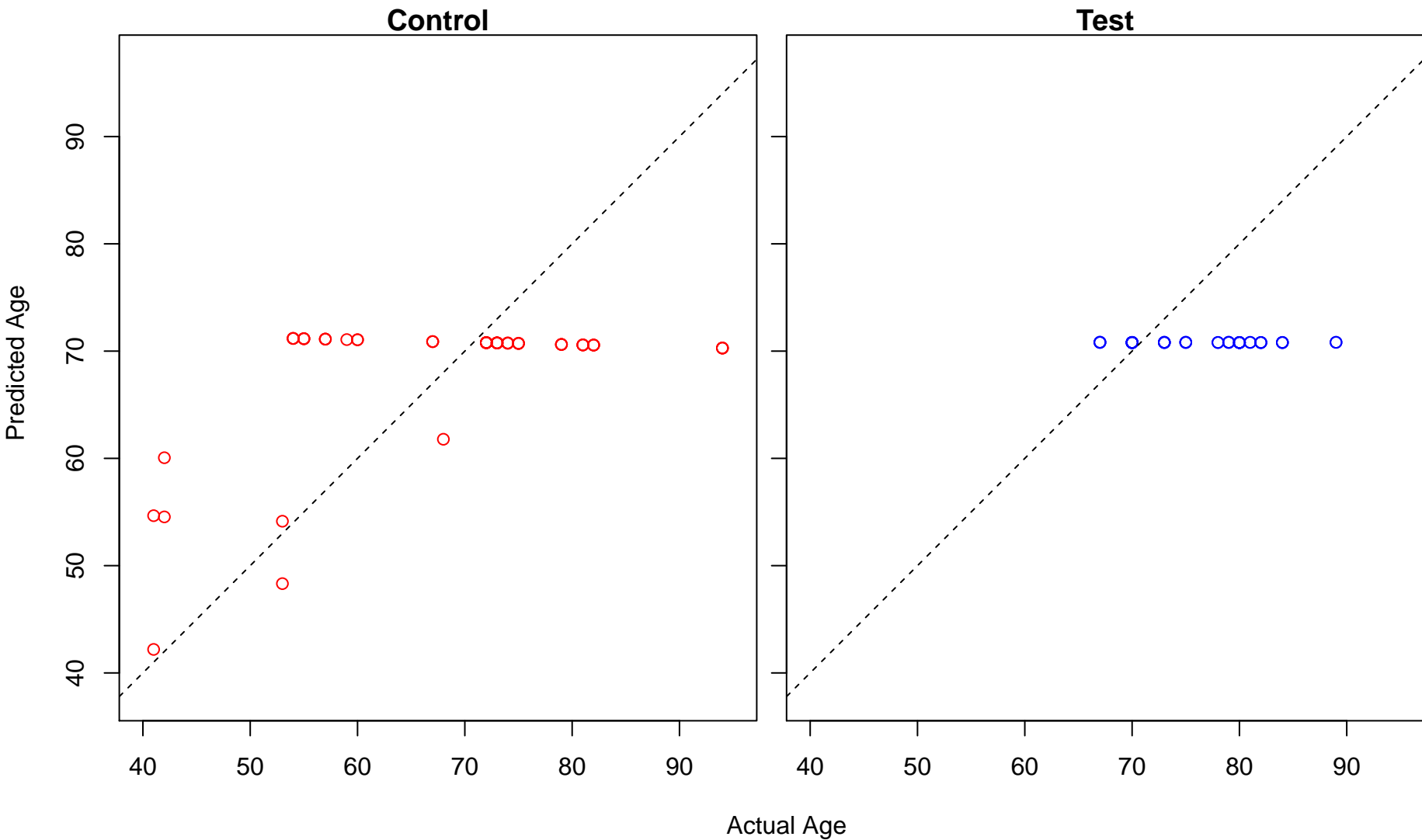


Actual Age

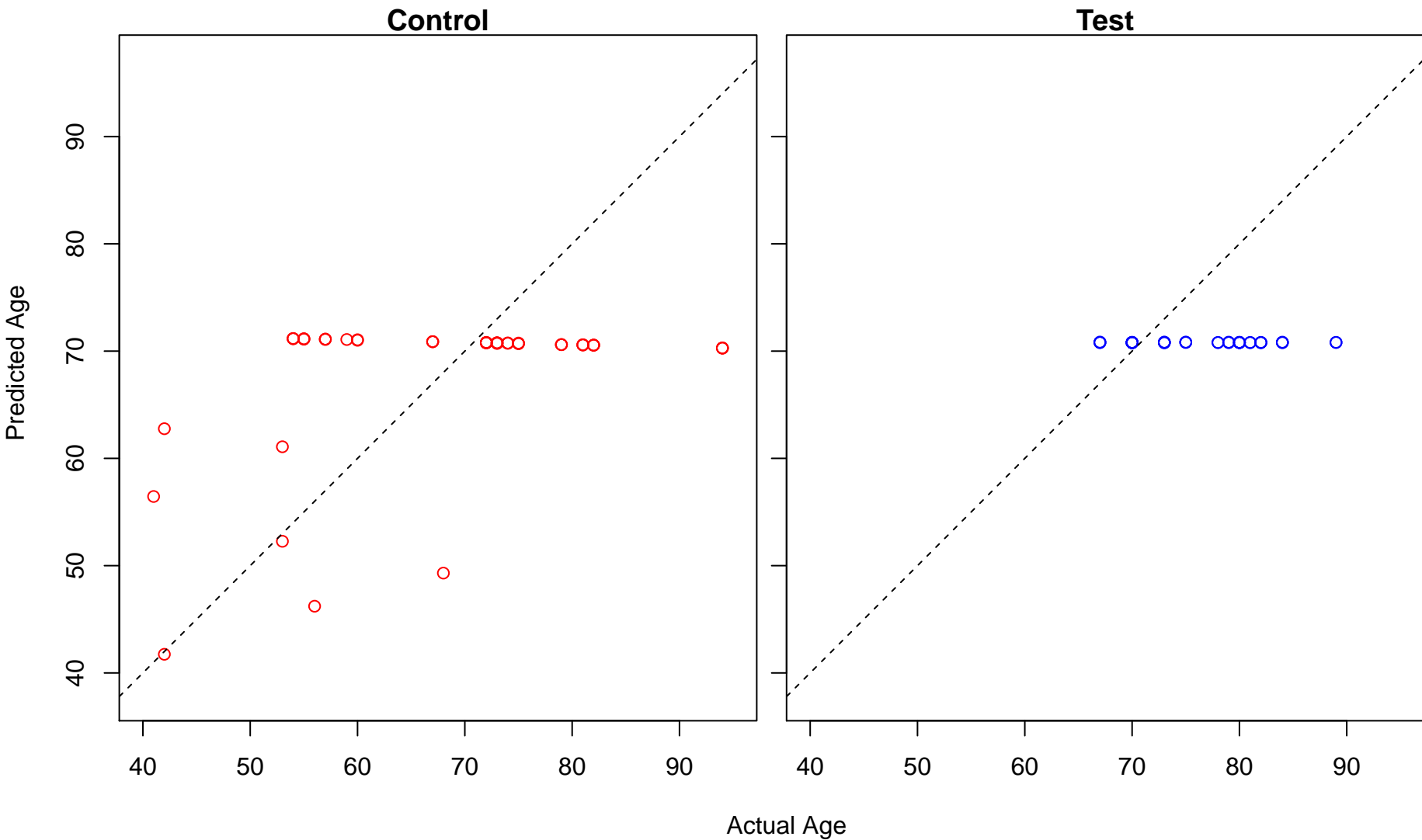
peptidyl-tyrosine modification (Score: 0.797157)



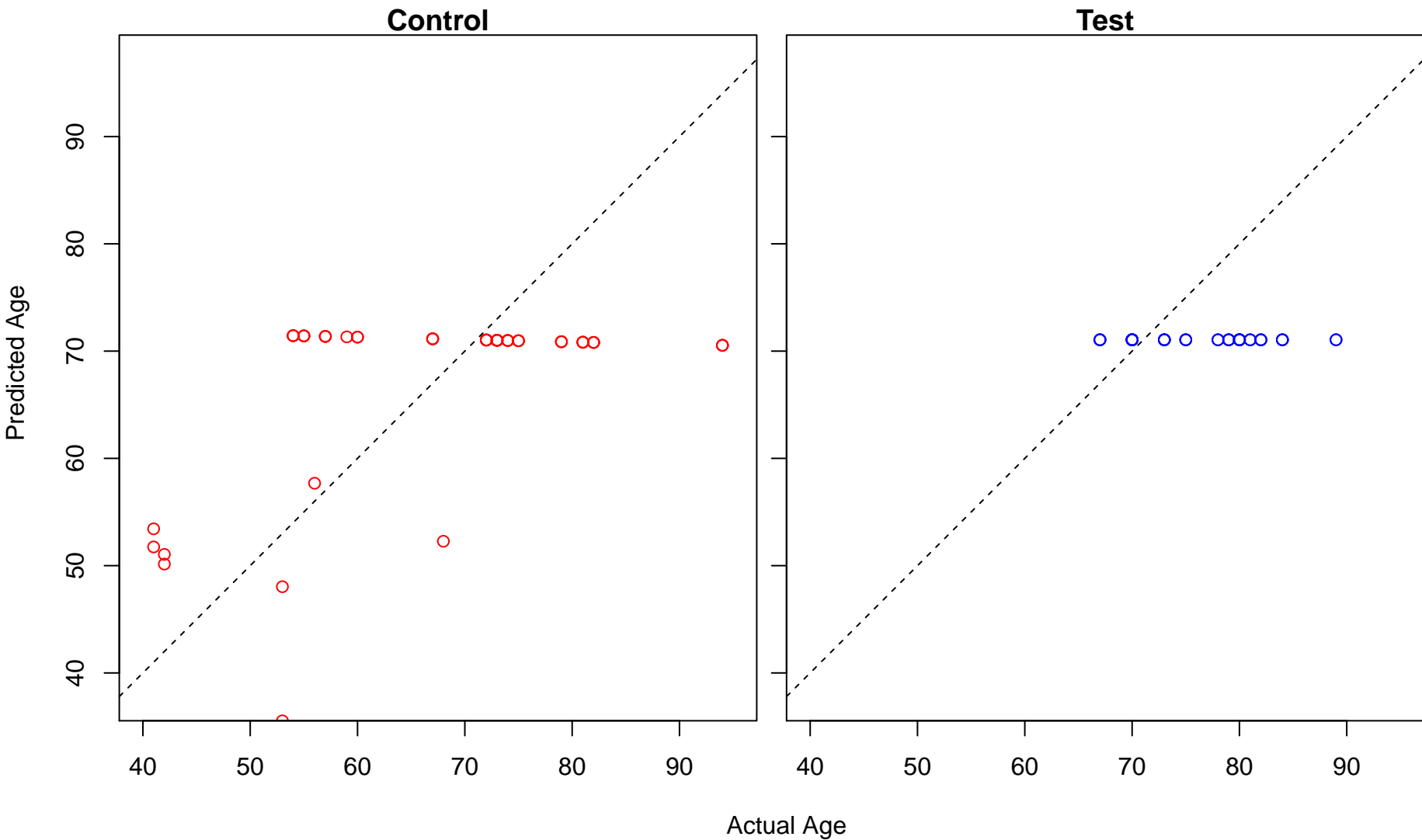
protein autophosphorylation (Score: 0.797157)



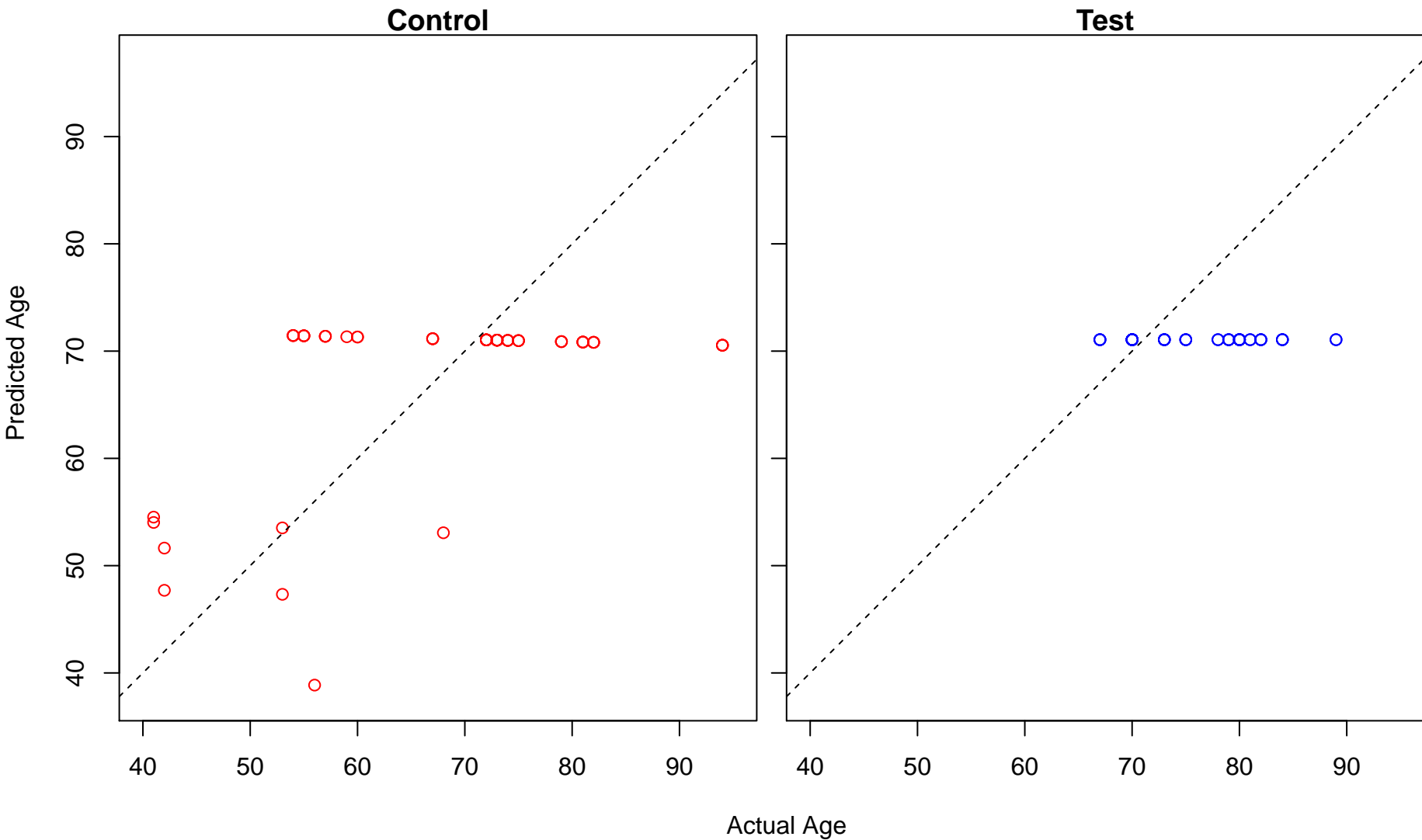
zymogen activation (Score: 0.797145)



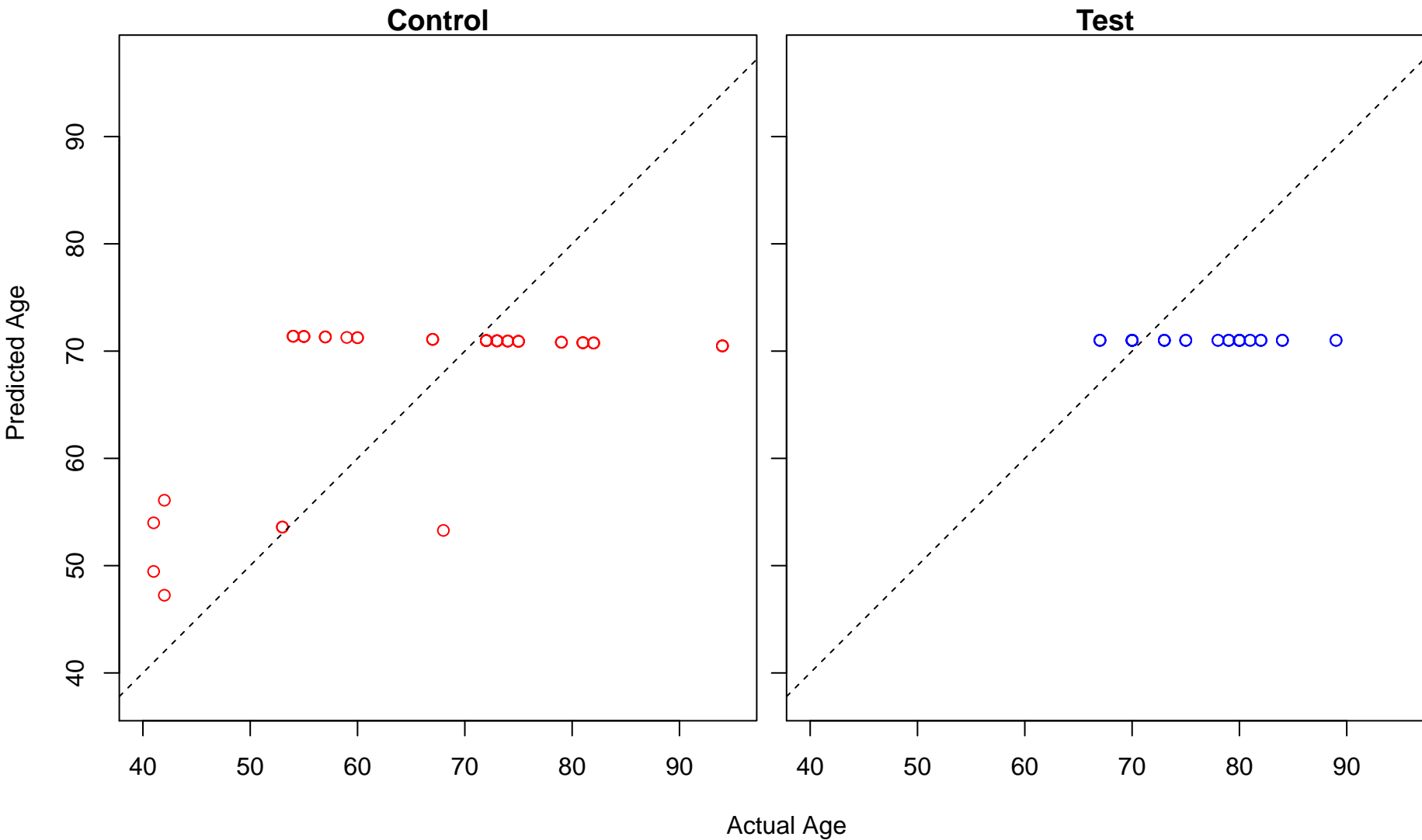
regulation of cell development (Score: 0.797132)



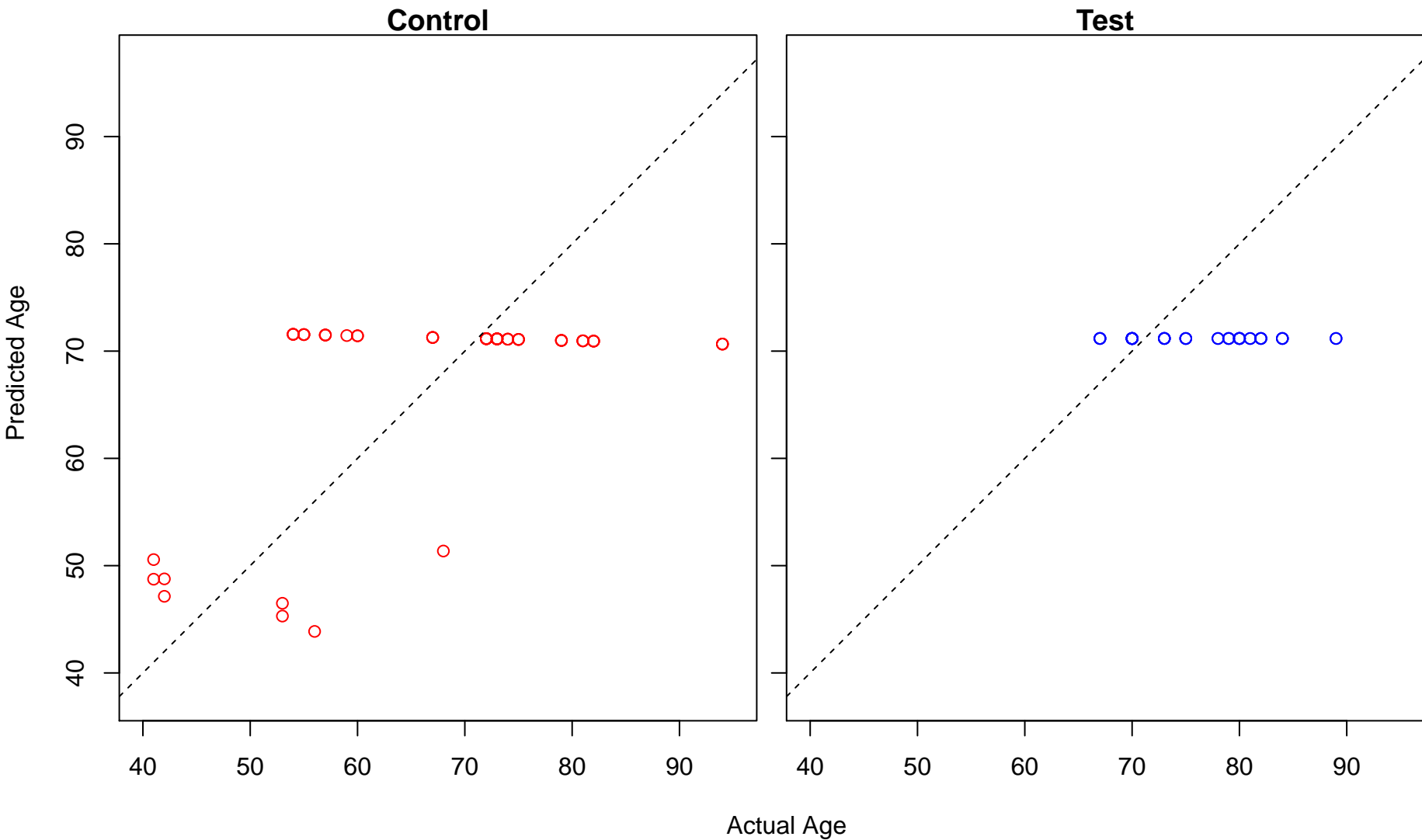
negative regulation of RNA metabolic process (Score: 0.797085)



positive regulation of cell growth (Score: 0.797044)

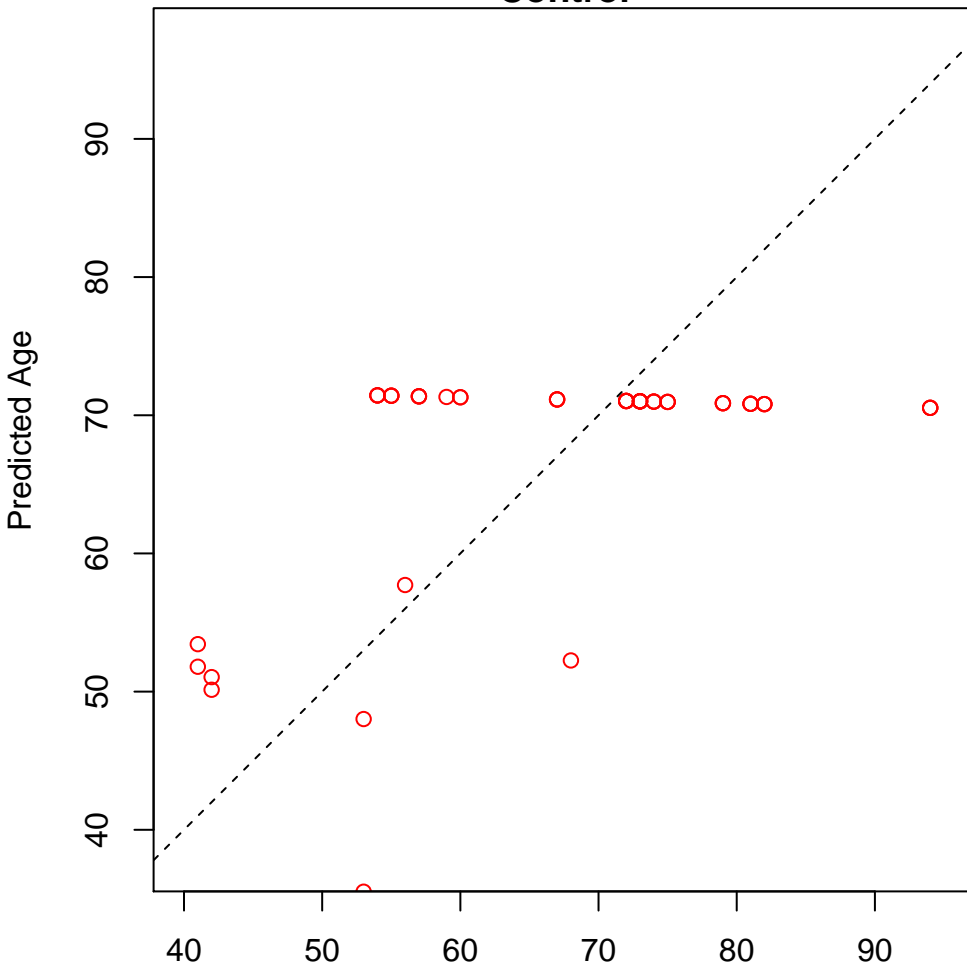


macromolecule localization (Score: 0.797029)

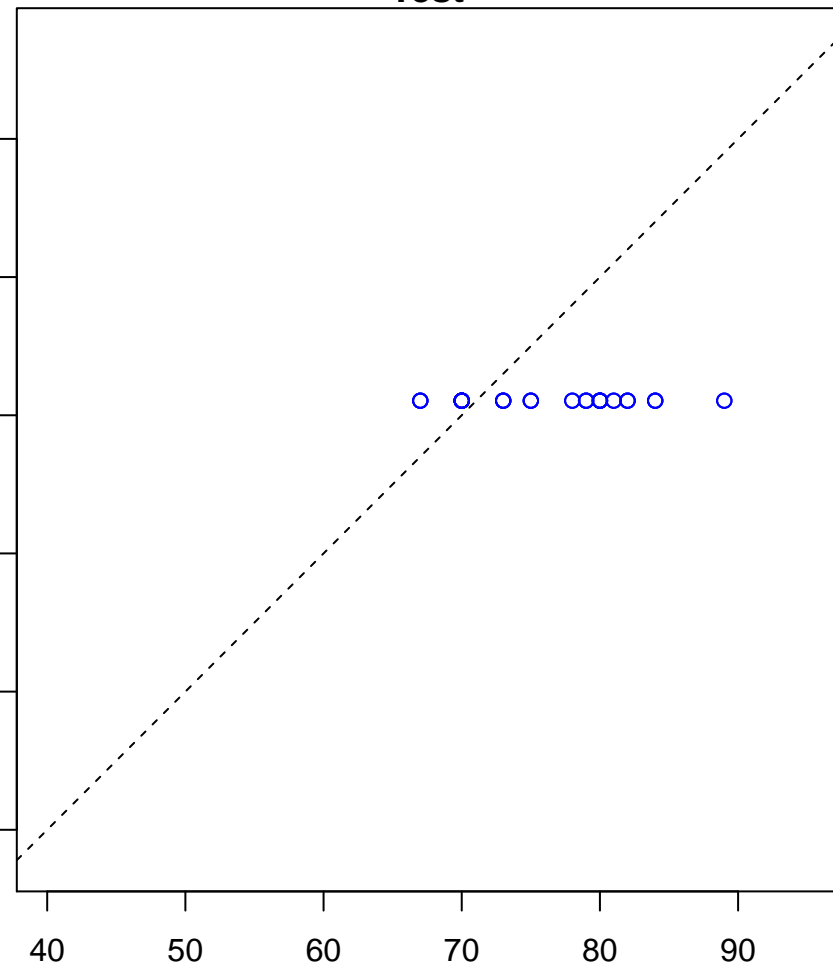


regulation of nervous system development (Score: 0.797026)

Control

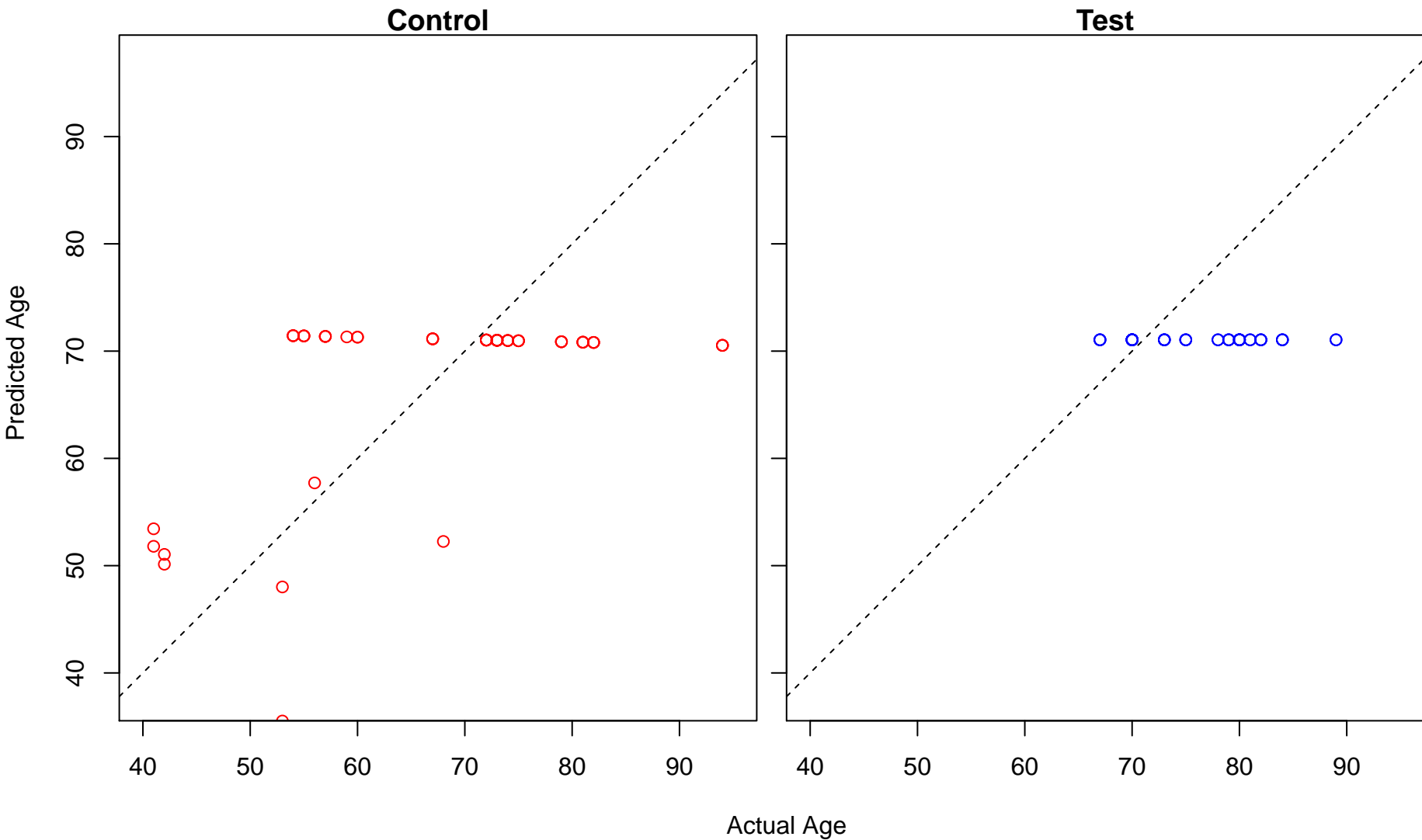


Test



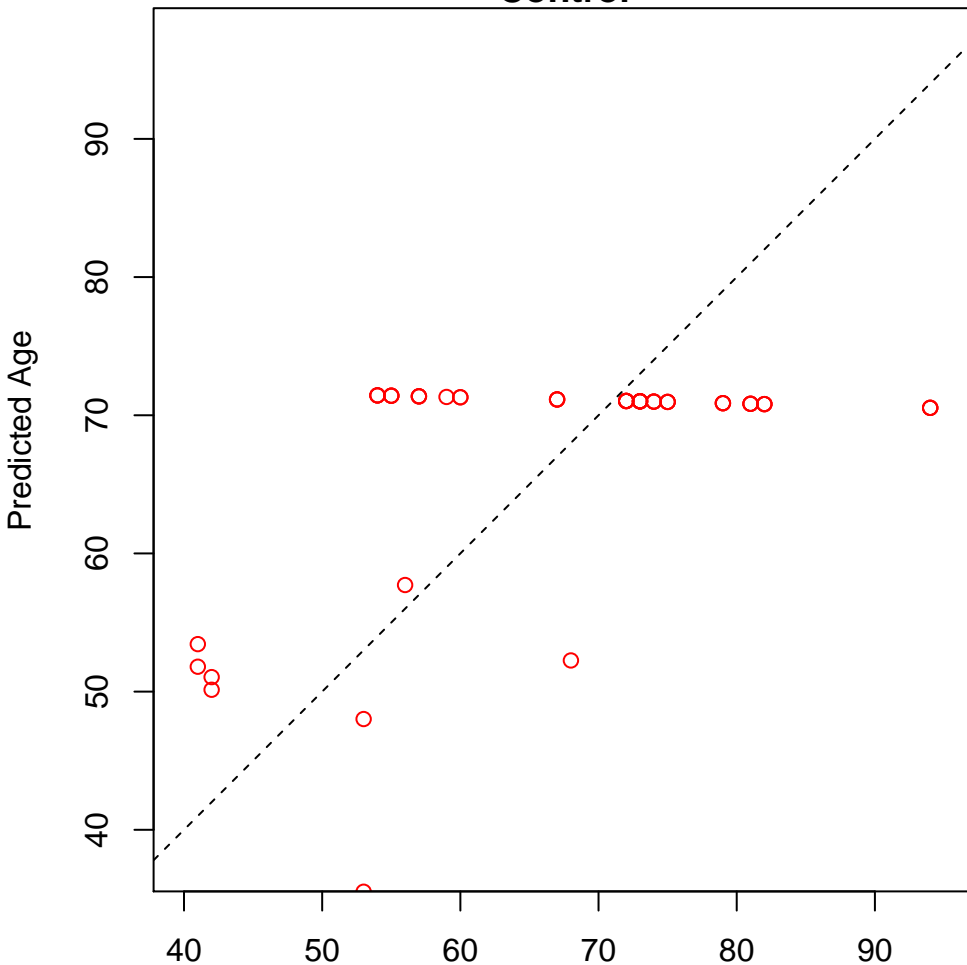
Actual Age

regulation of neuron projection development (Score: 0.797021)

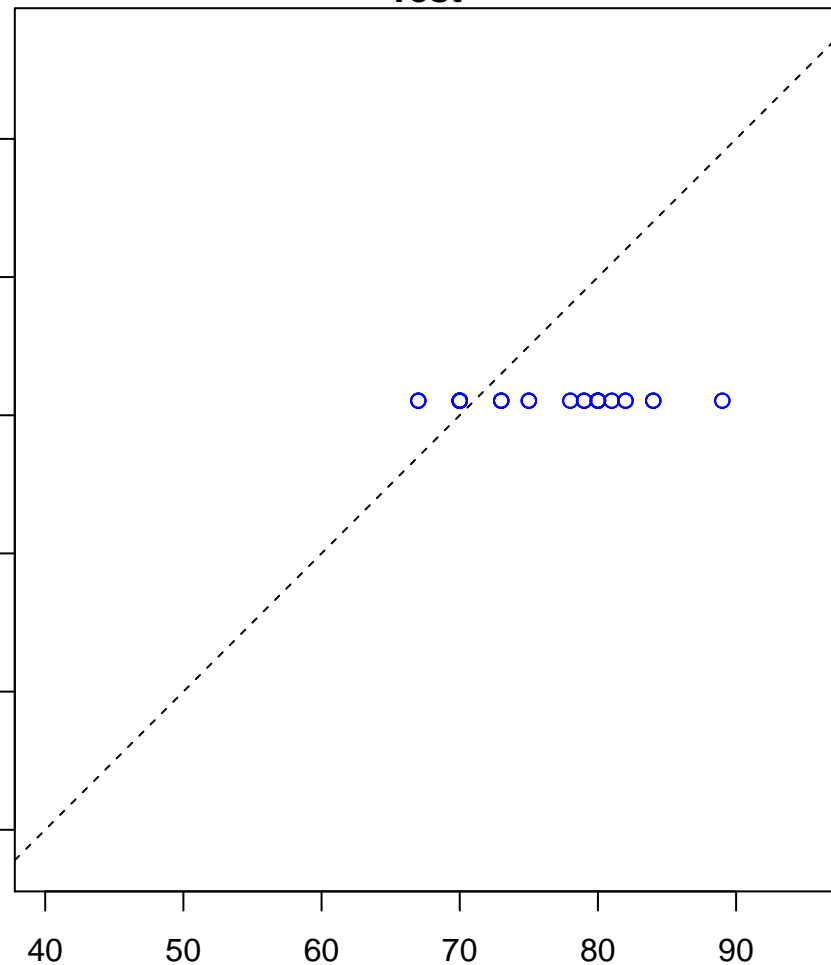


regulation of neuron differentiation (Score: 0.797021)

Control

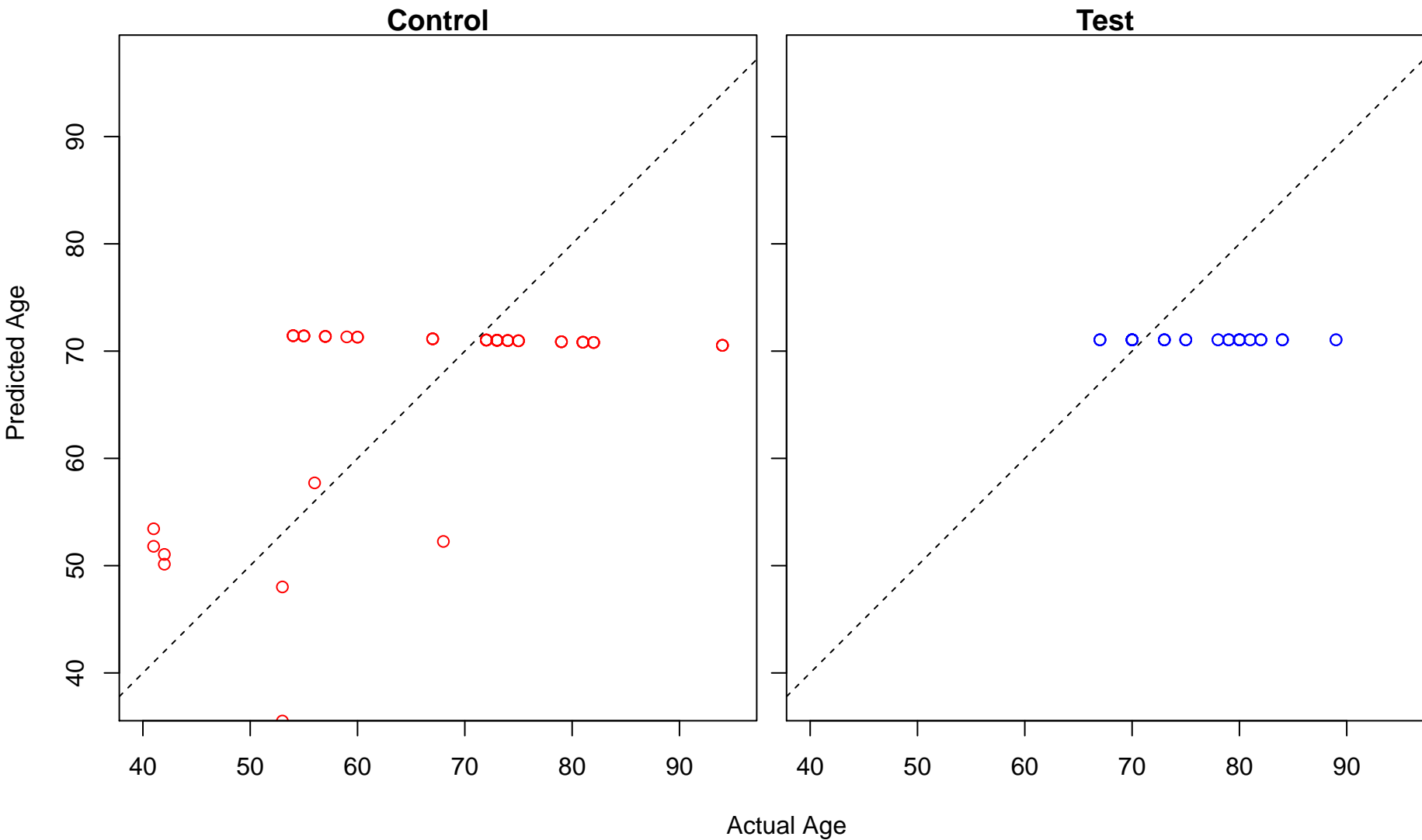


Test

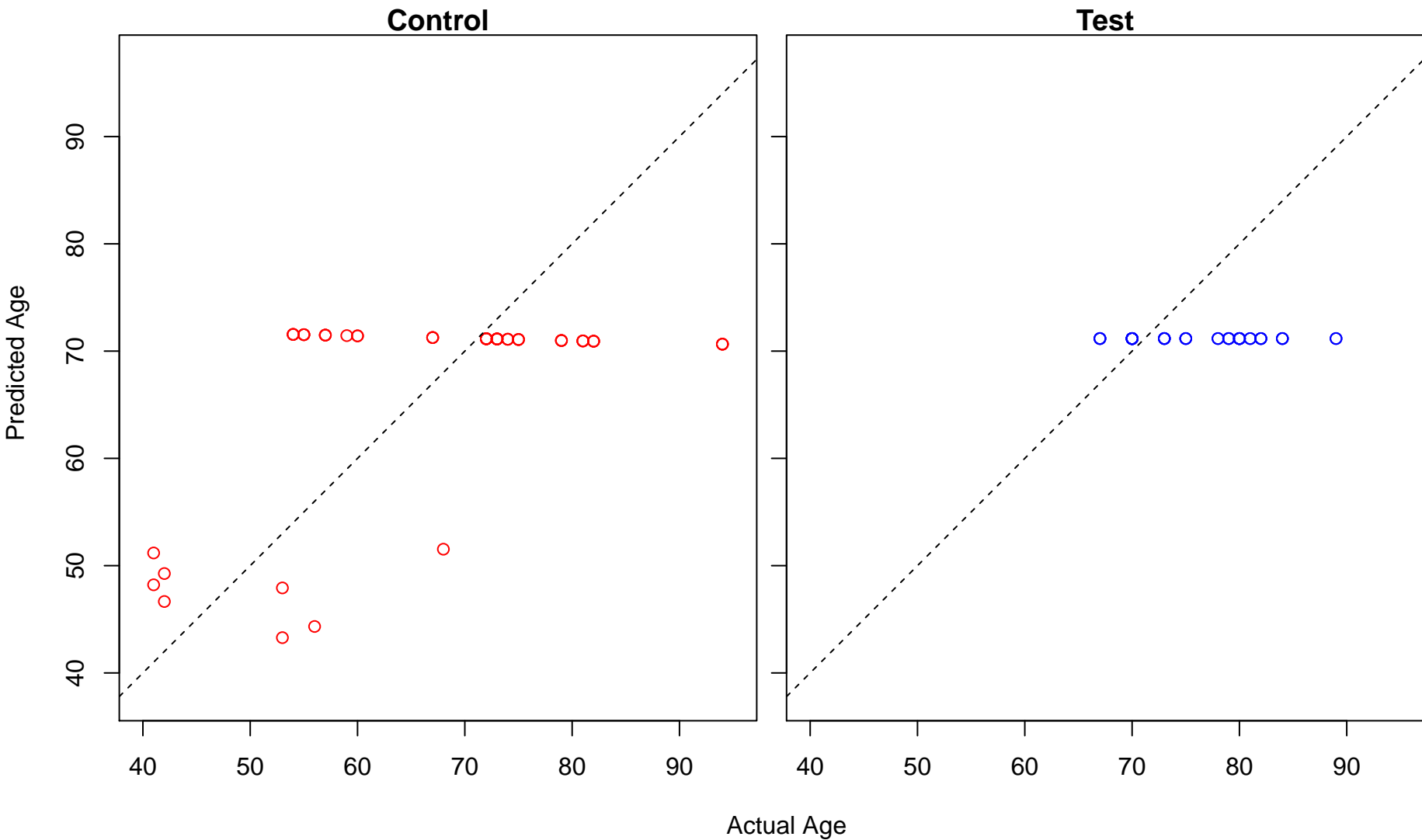


Actual Age

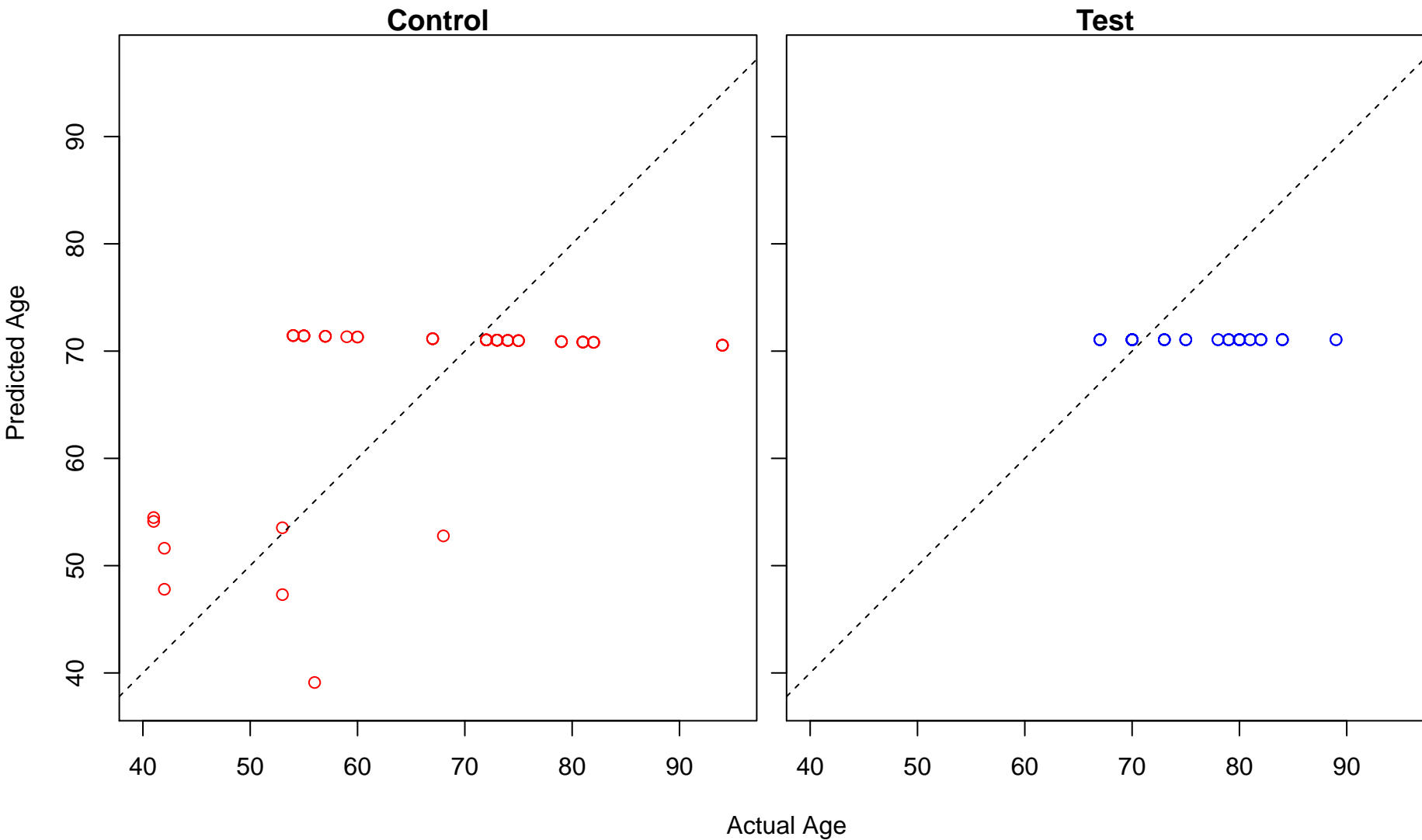
regulation of neurogenesis (Score: 0.797021)



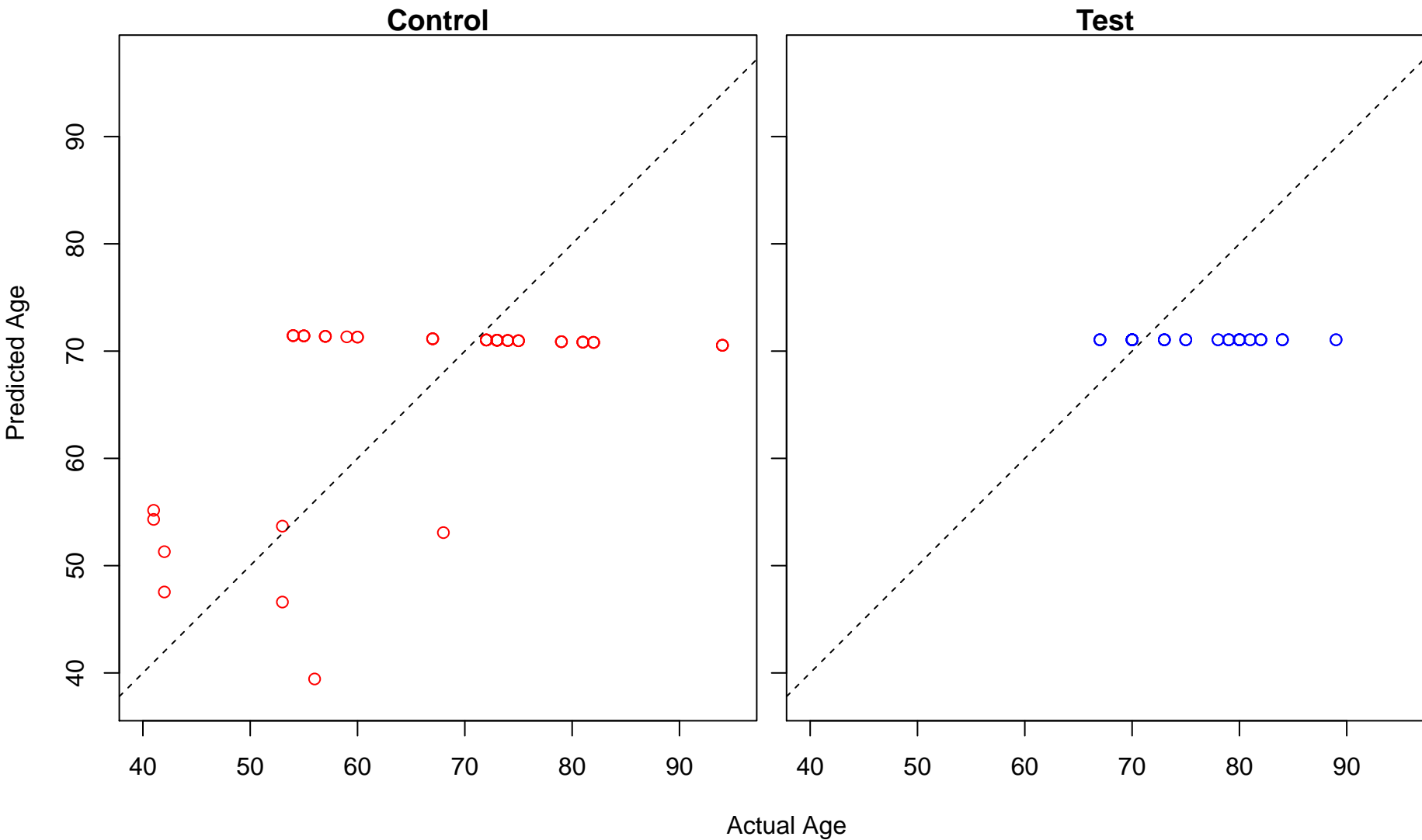
cellular metabolic process (Score: 0.796948)



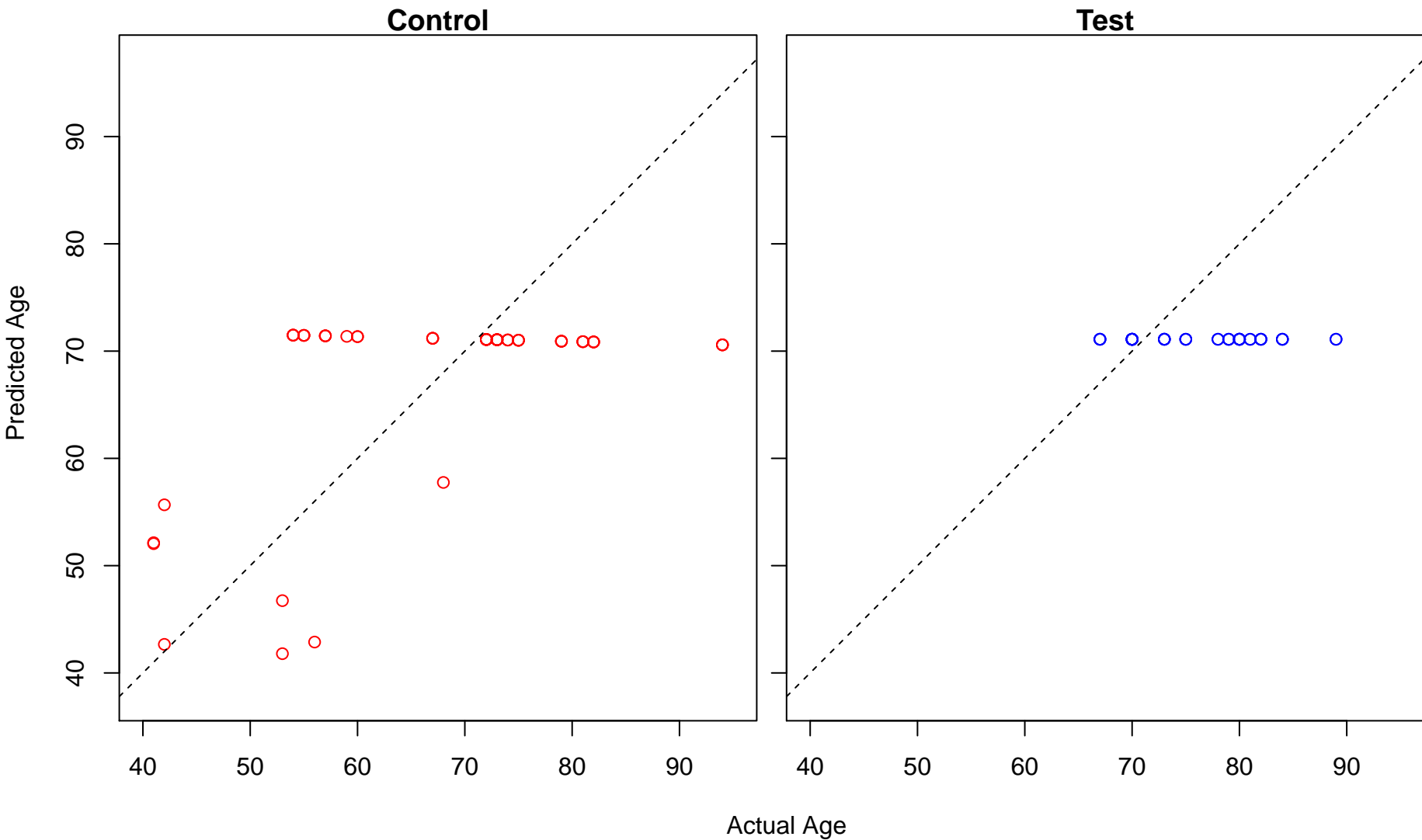
negative regulation of nucleobase-containing compound metabolic process (Score: 0.796939)



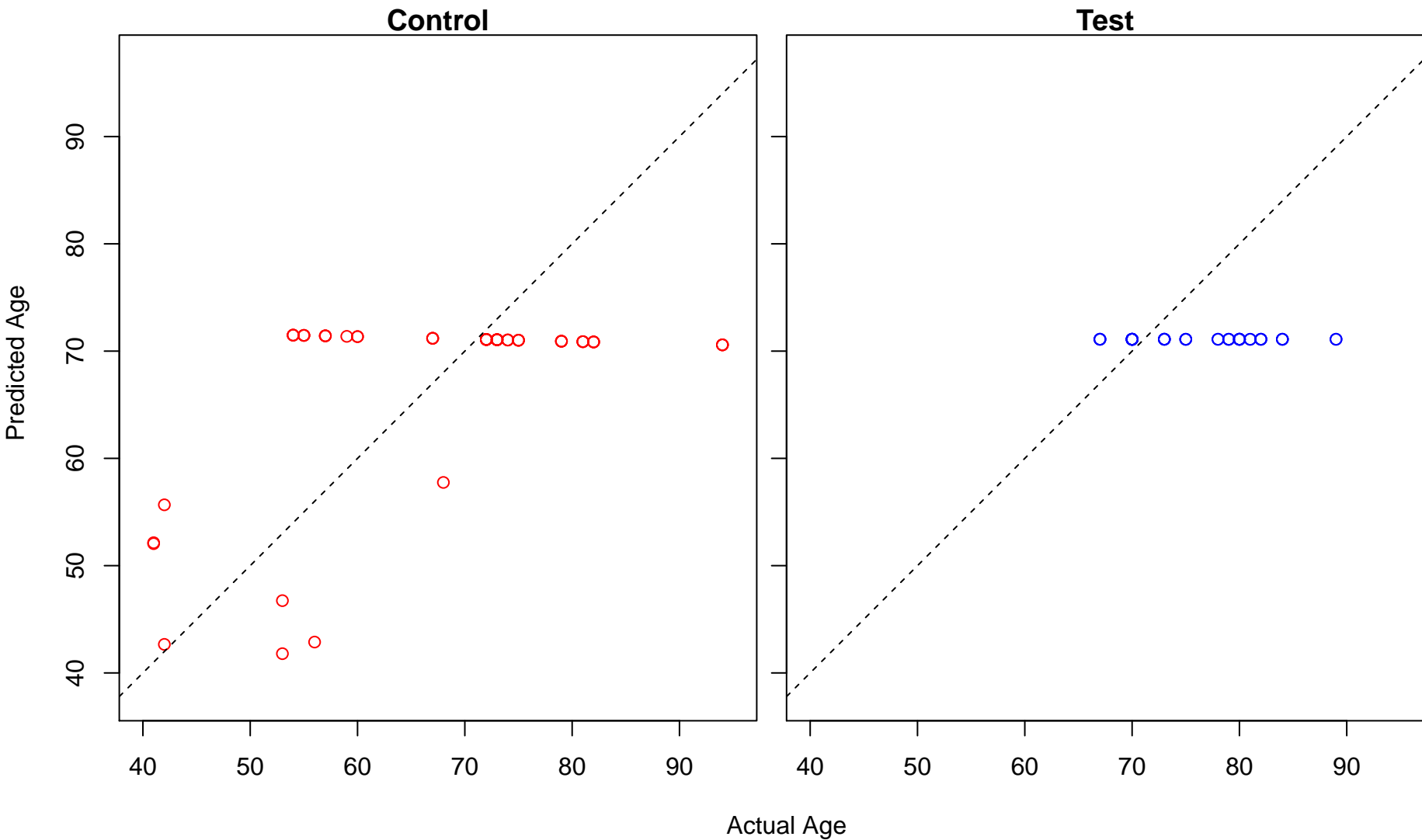
signal transduction by p53 class mediator (Score: 0.796808)



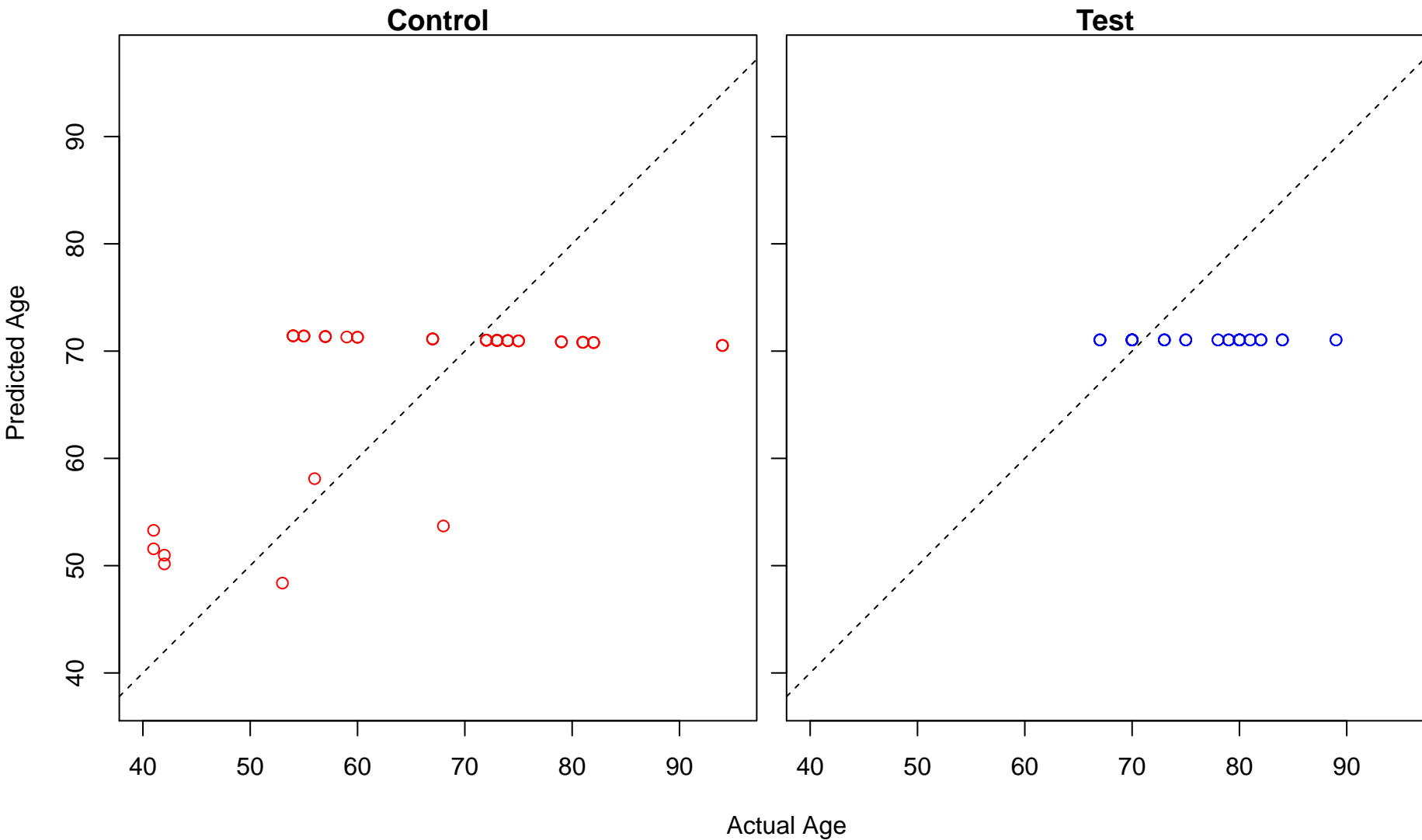
negative regulation of phosphorus metabolic process (Score: 0.796766)



negative regulation of phosphate metabolic process (Score: 0.796766)

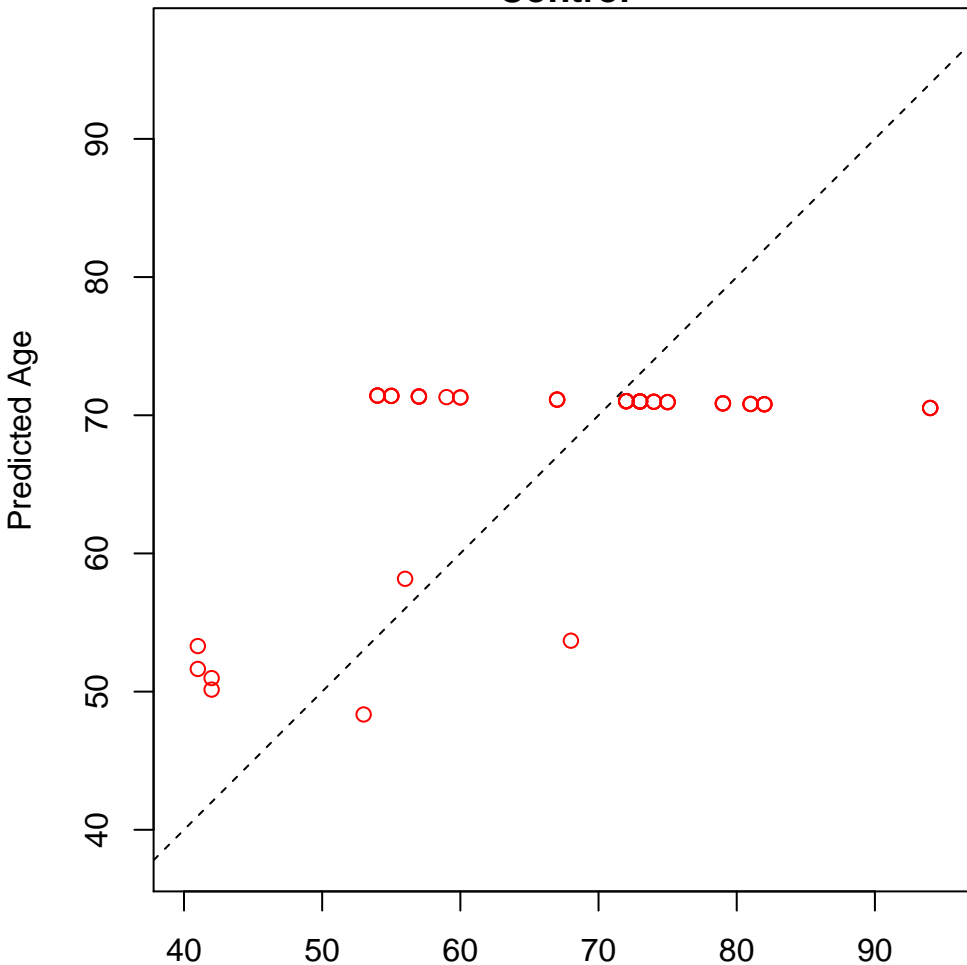


regulation of cell morphogenesis involved in differentiation (Score: 0.796749)

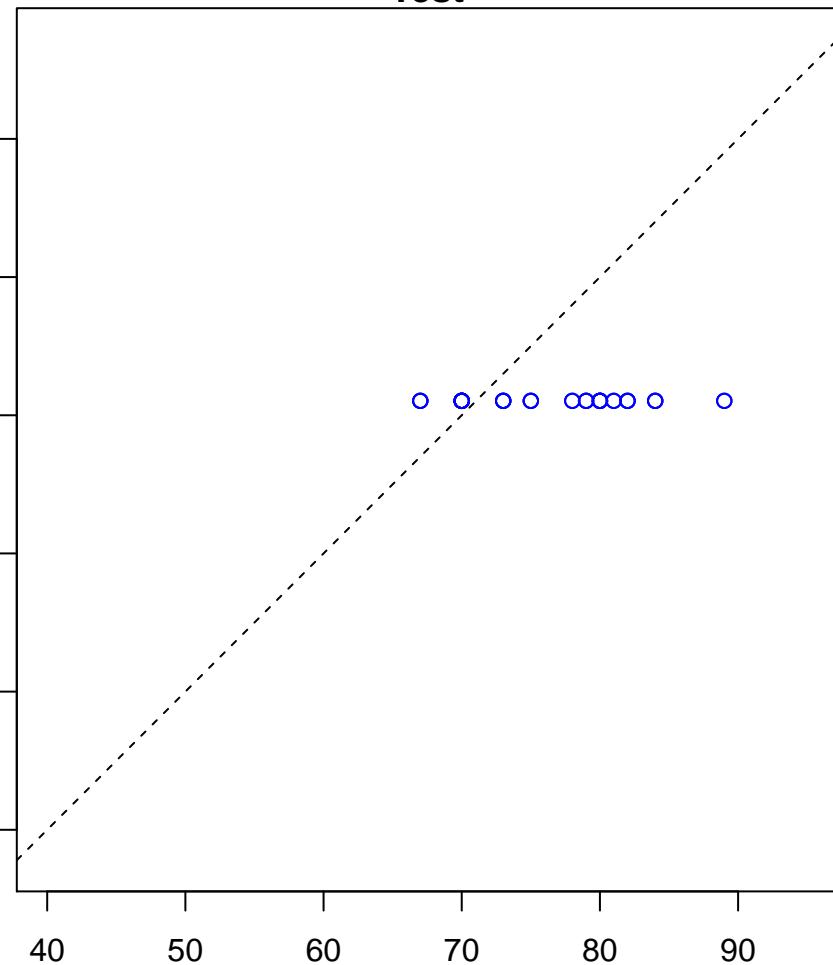


Rho protein signal transduction (Score: 0.796604)

Control

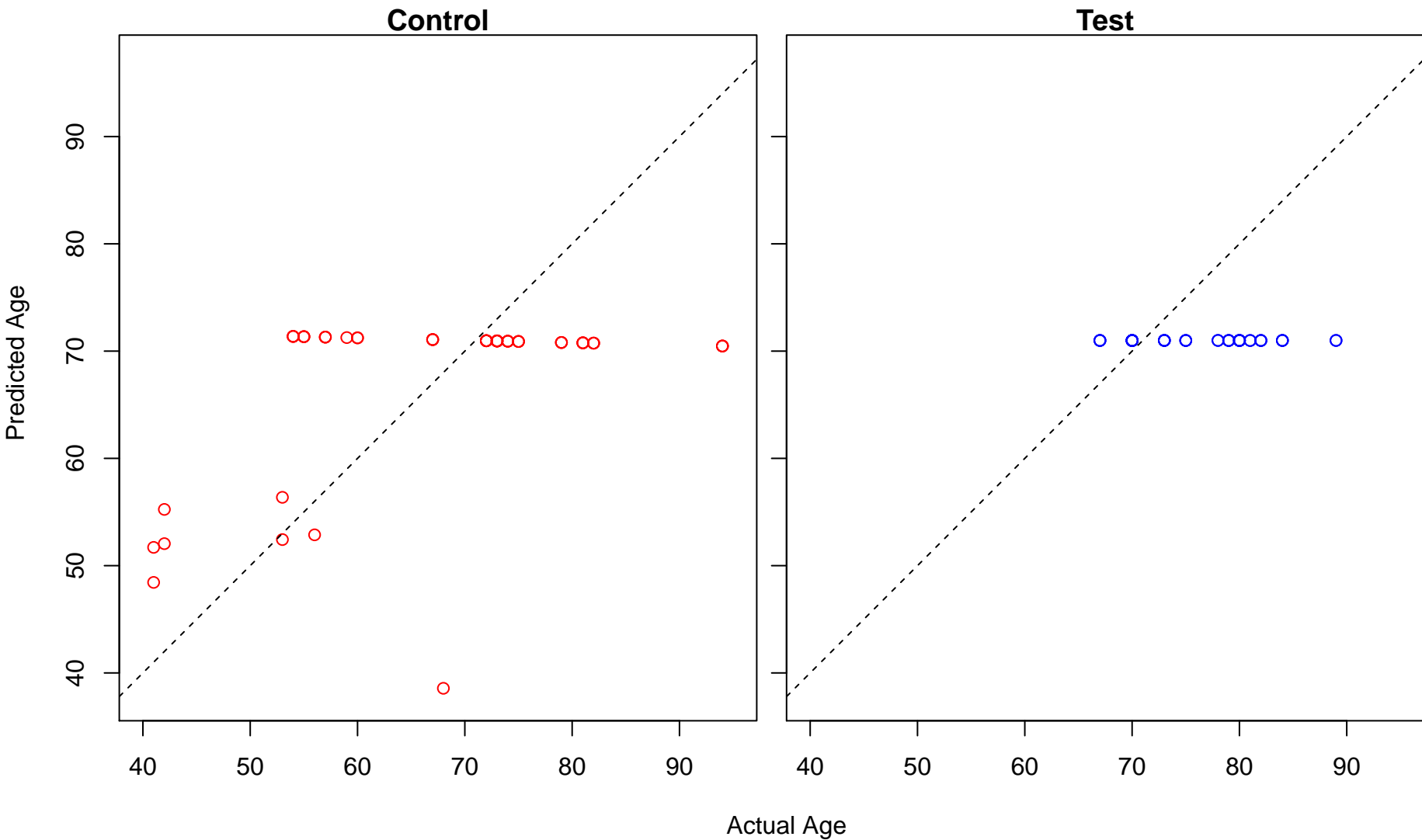


Test

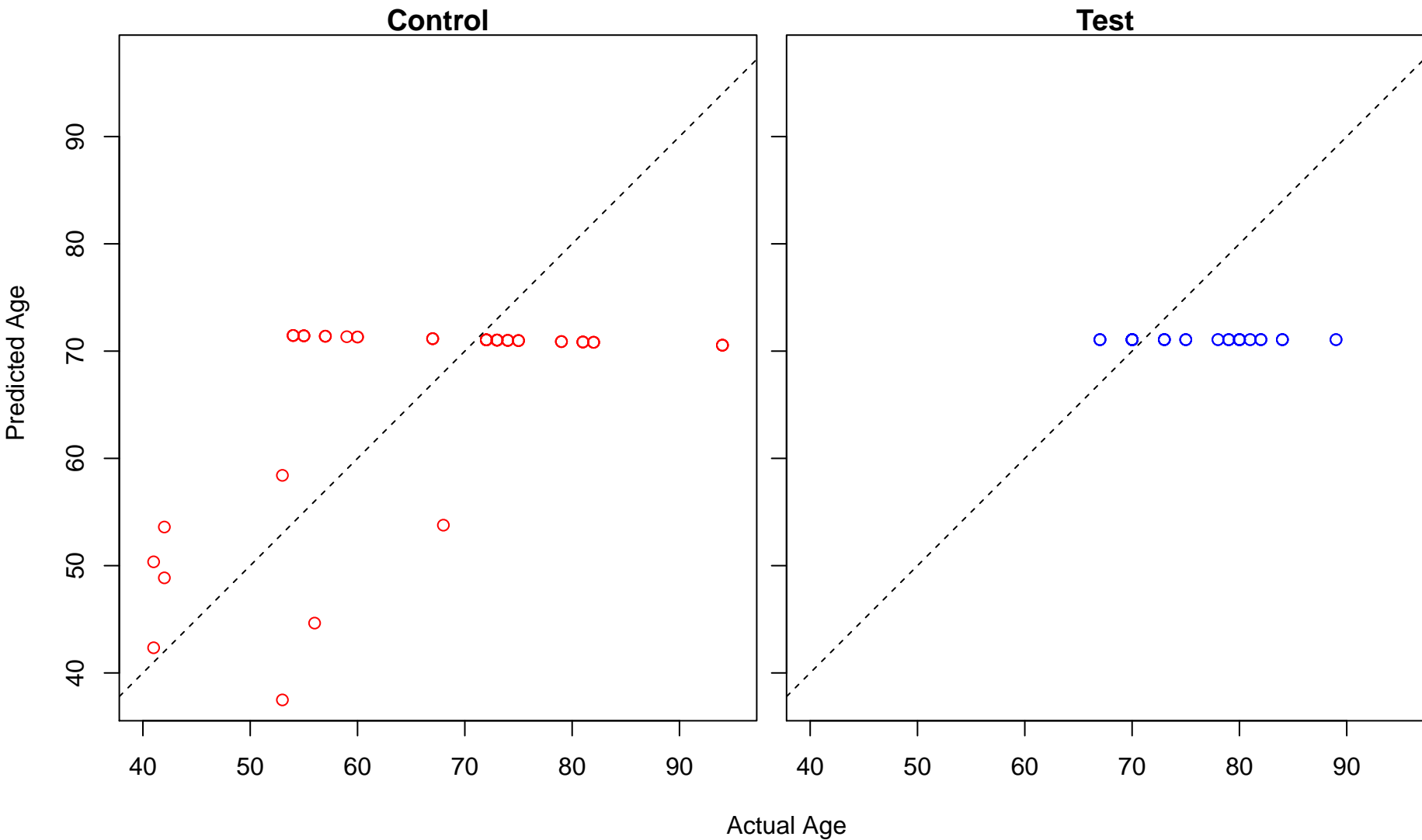


Actual Age

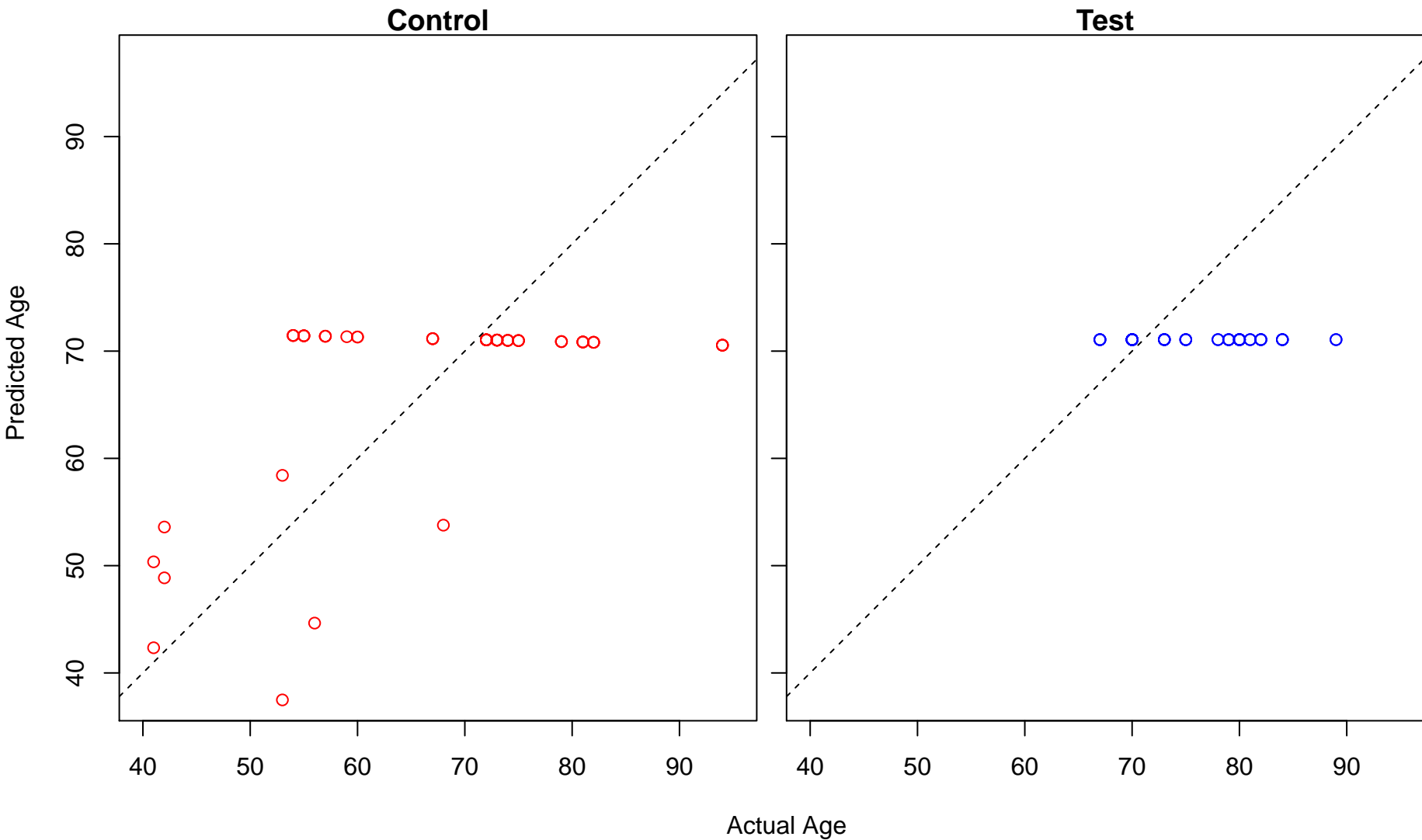
nuclear envelope organization (Score: 0.796545)



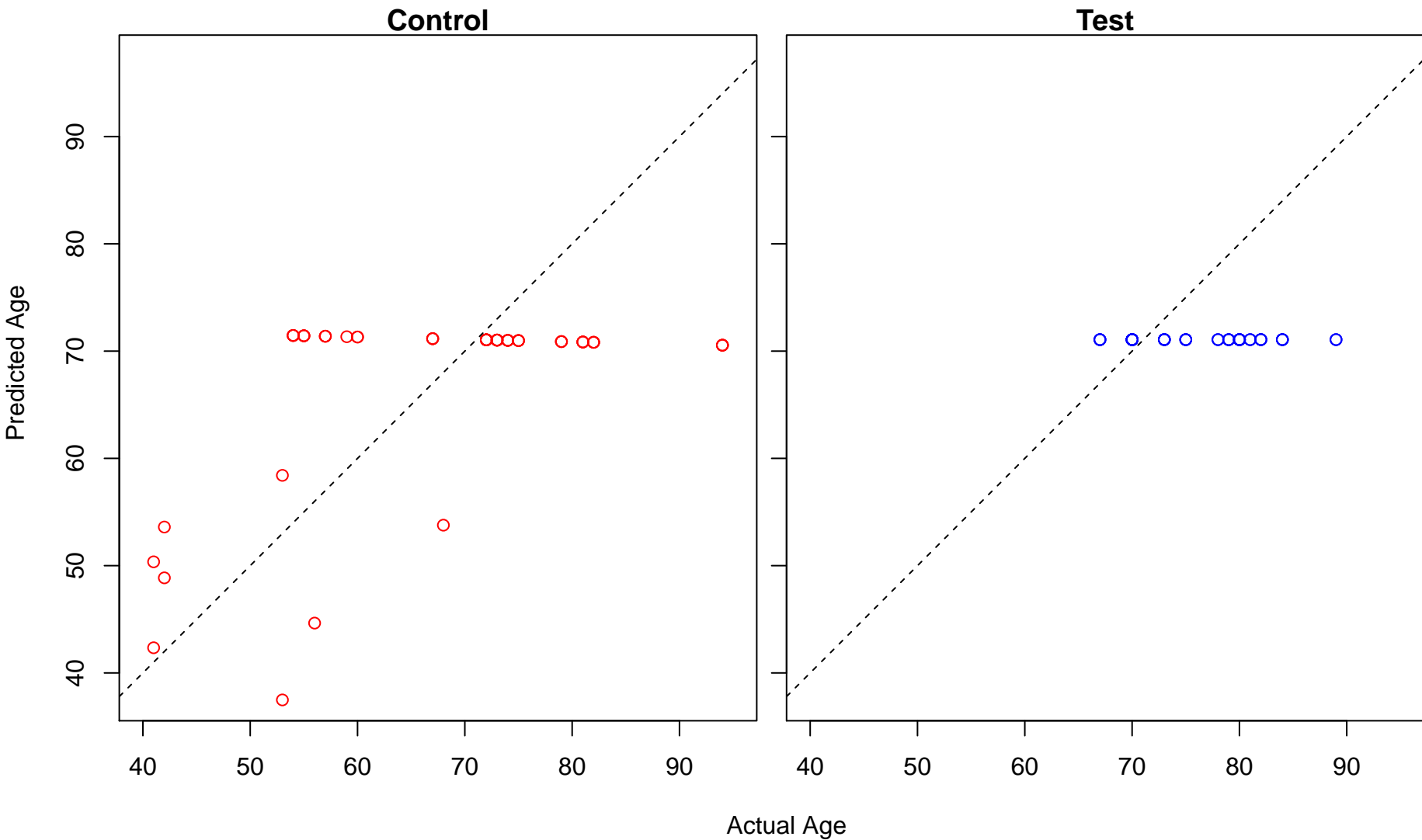
regulation of cyclic nucleotide metabolic process (Score: 0.796527)



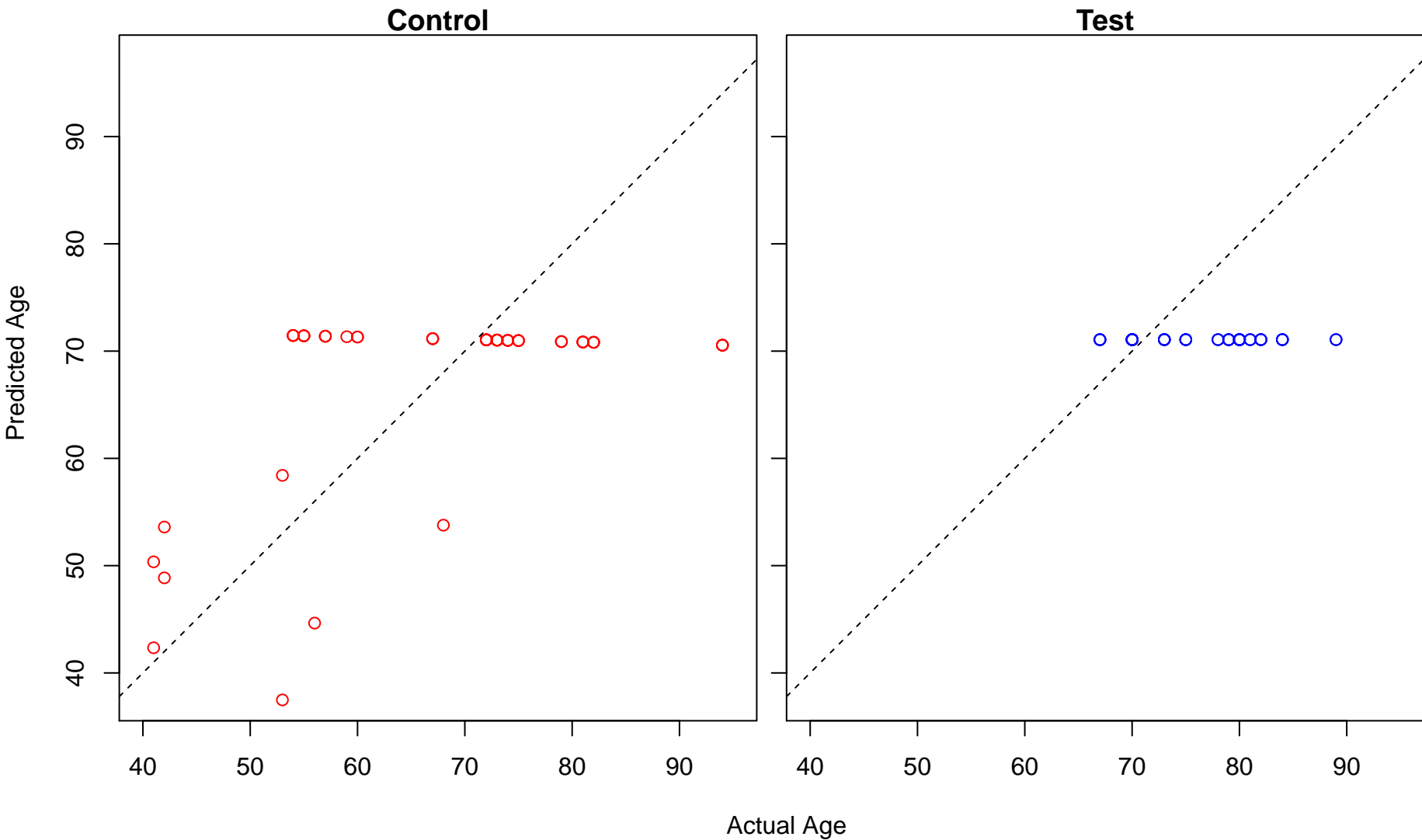
positive regulation of cyclic nucleotide metabolic process (Score: 0.796527)



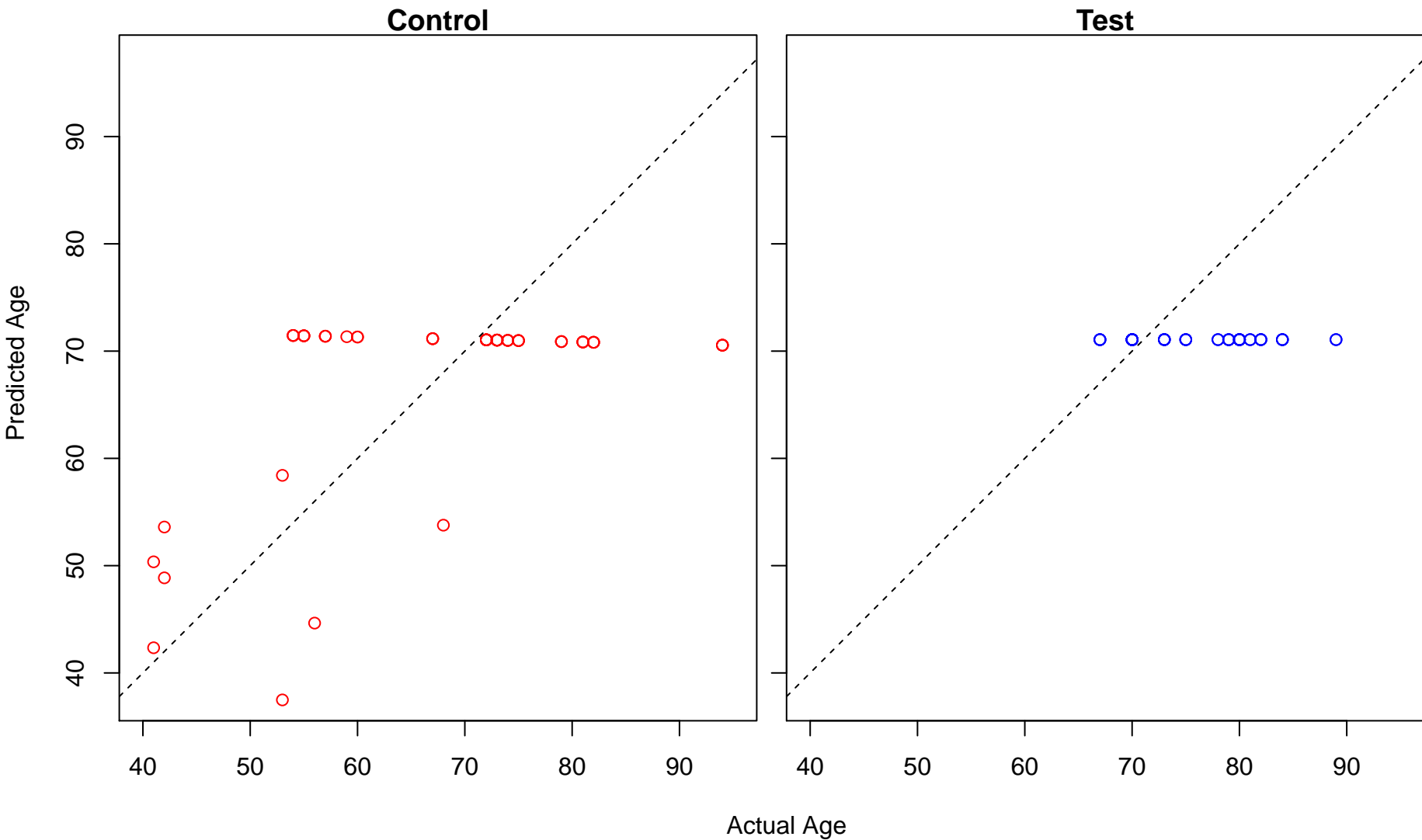
regulation of cyclic nucleotide biosynthetic process (Score: 0.796527)



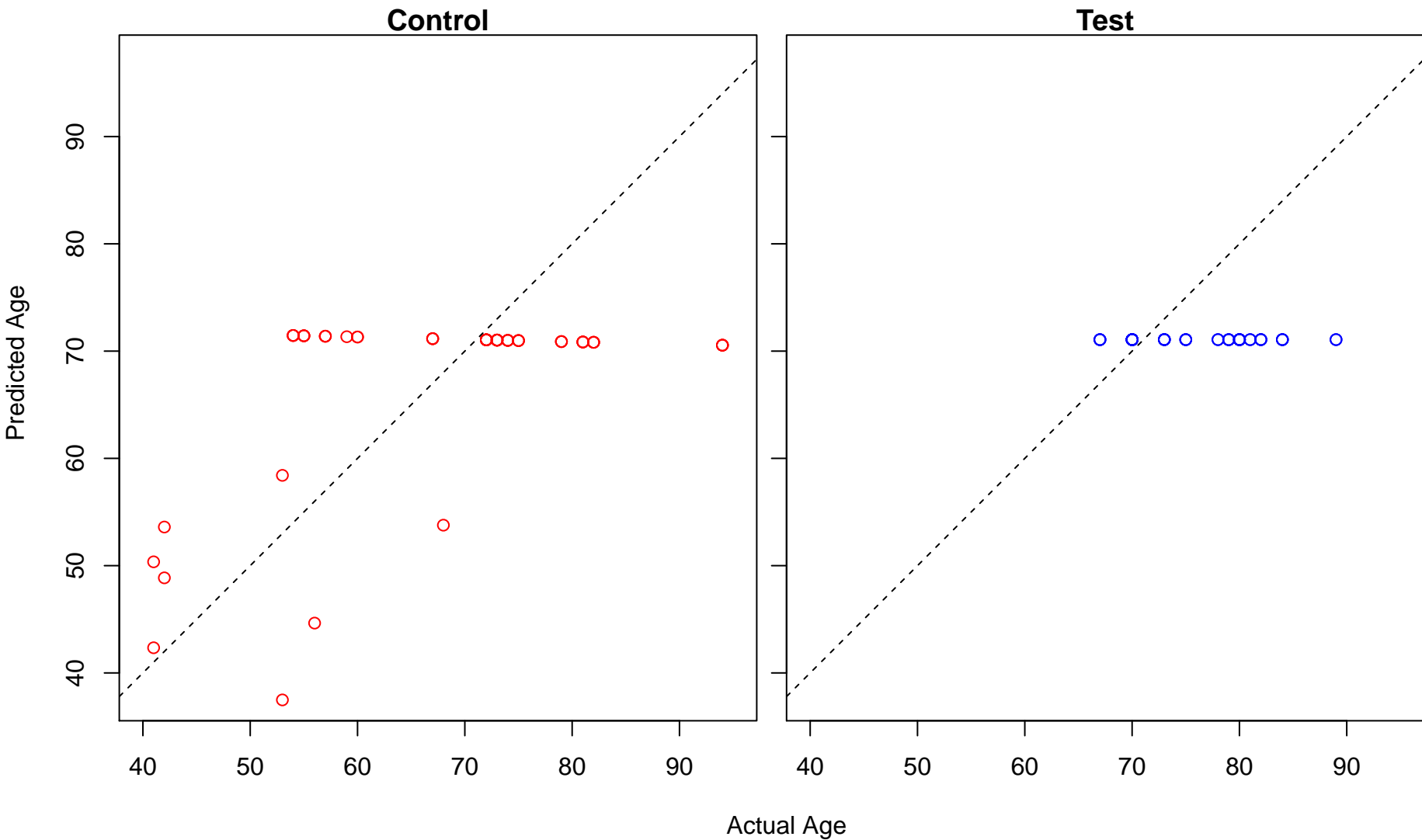
positive regulation of cyclic nucleotide biosynthetic process (Score: 0.796527)



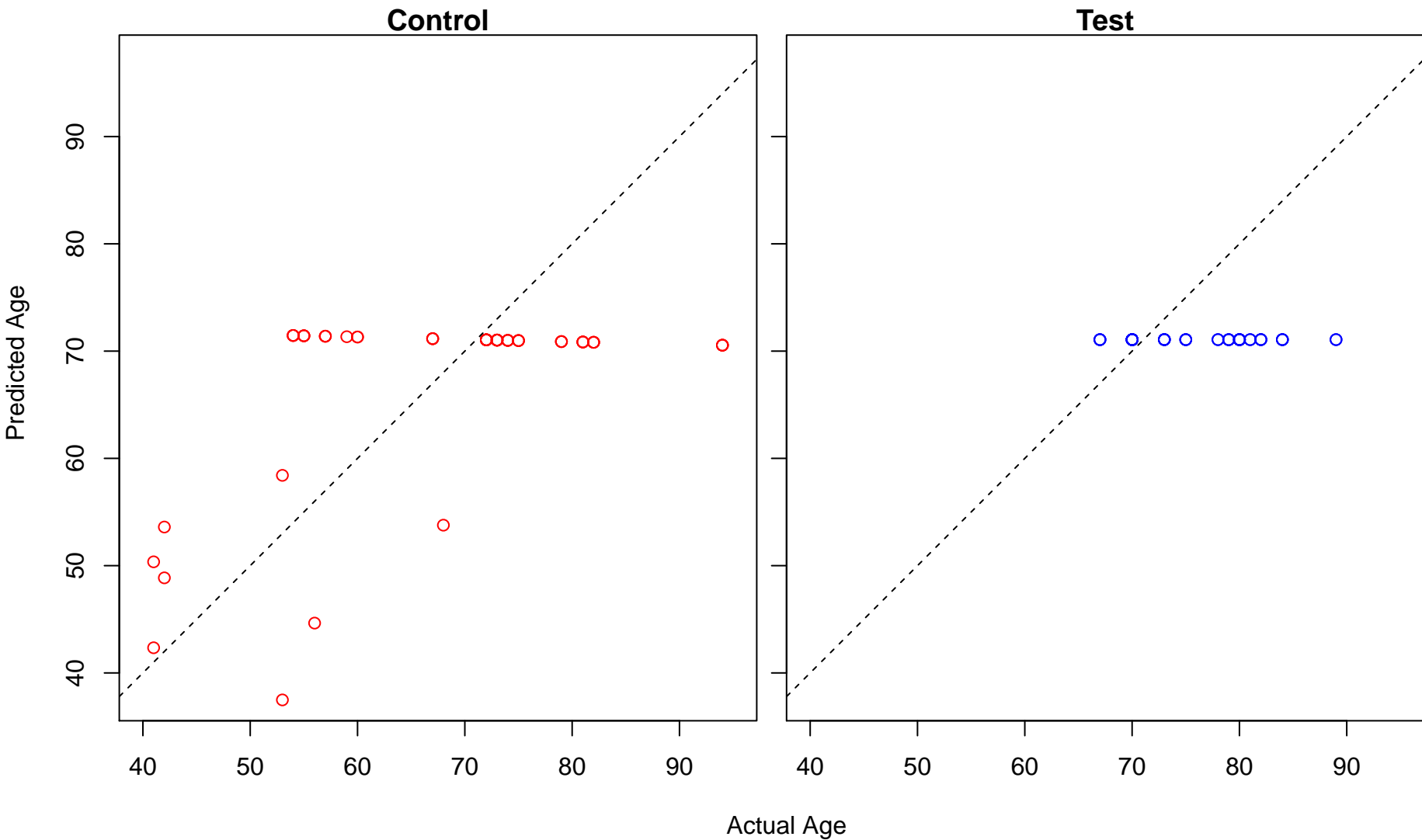
regulation of nucleotide biosynthetic process (Score: 0.796527)



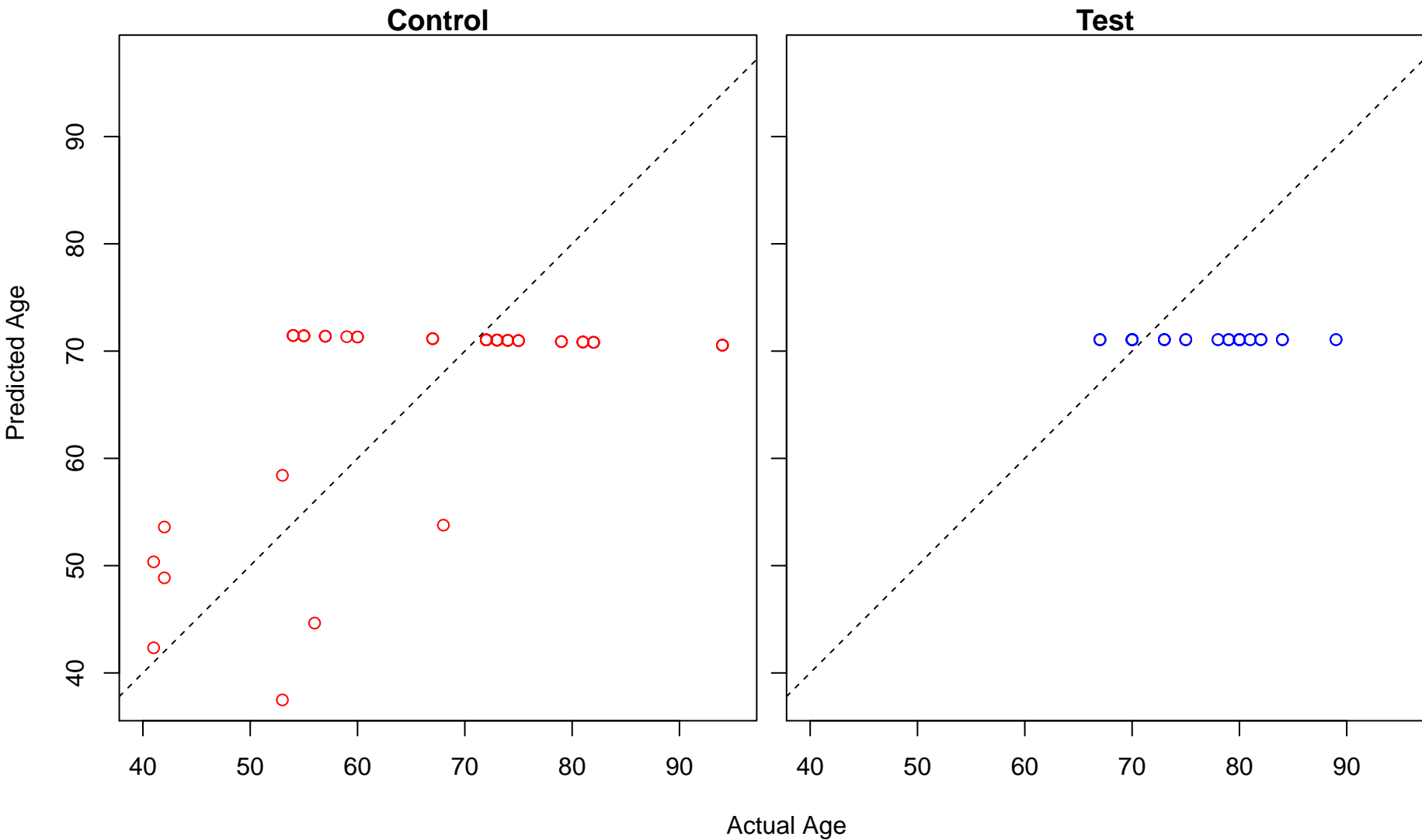
positive regulation of nucleotide biosynthetic process (Score: 0.796527)



regulation of purine nucleotide biosynthetic process (Score: 0.796527)

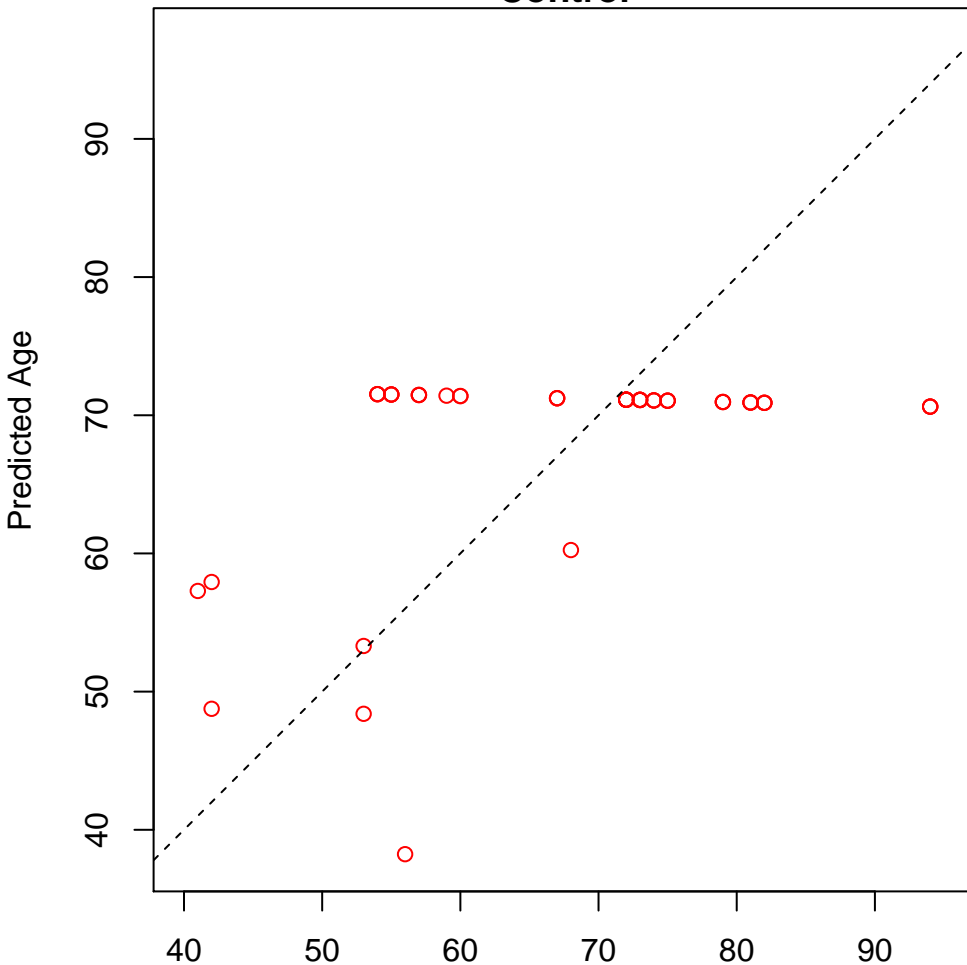


positive regulation of purine nucleotide biosynthetic process (Score: 0.796527)

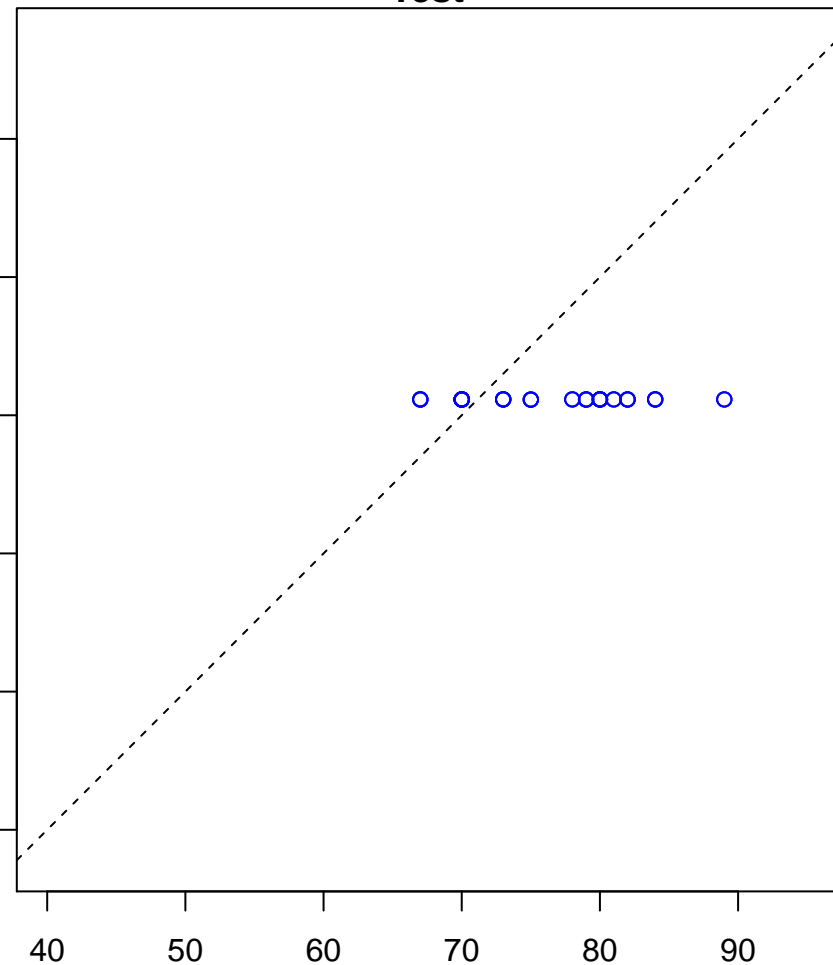


regulation of DNA metabolic process (Score: 0.796485)

Control



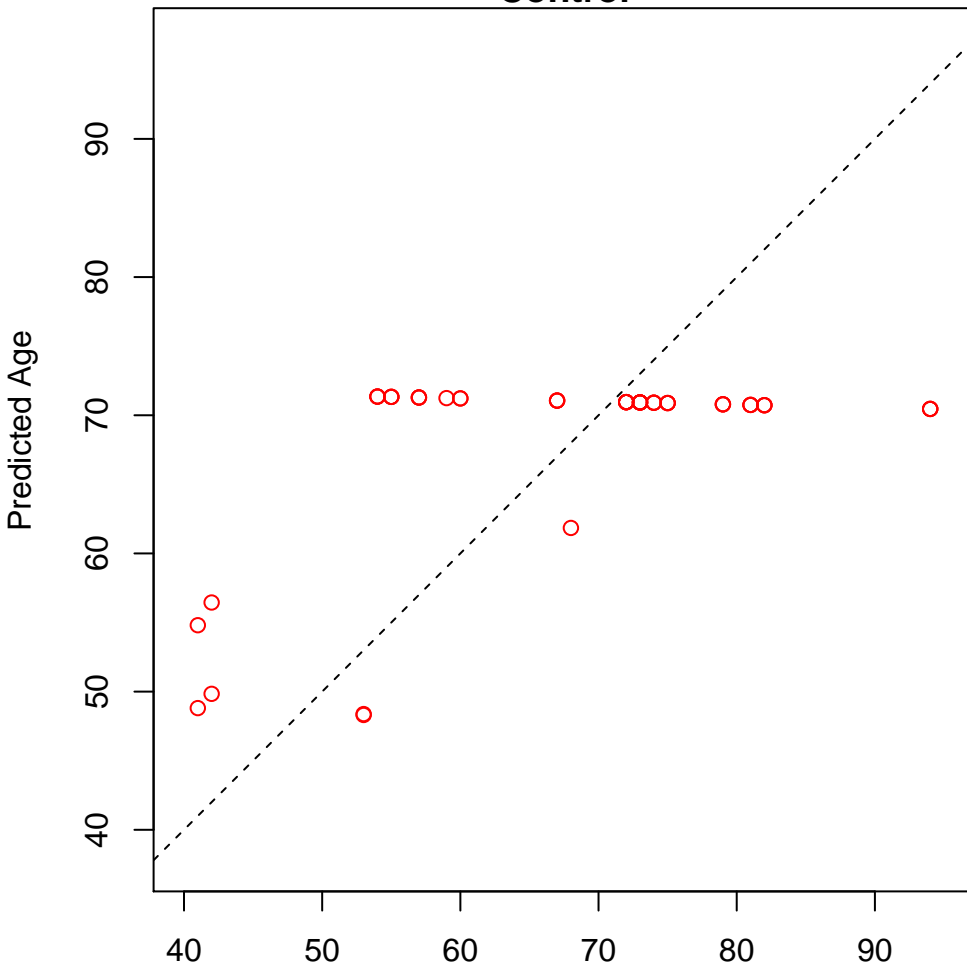
Test



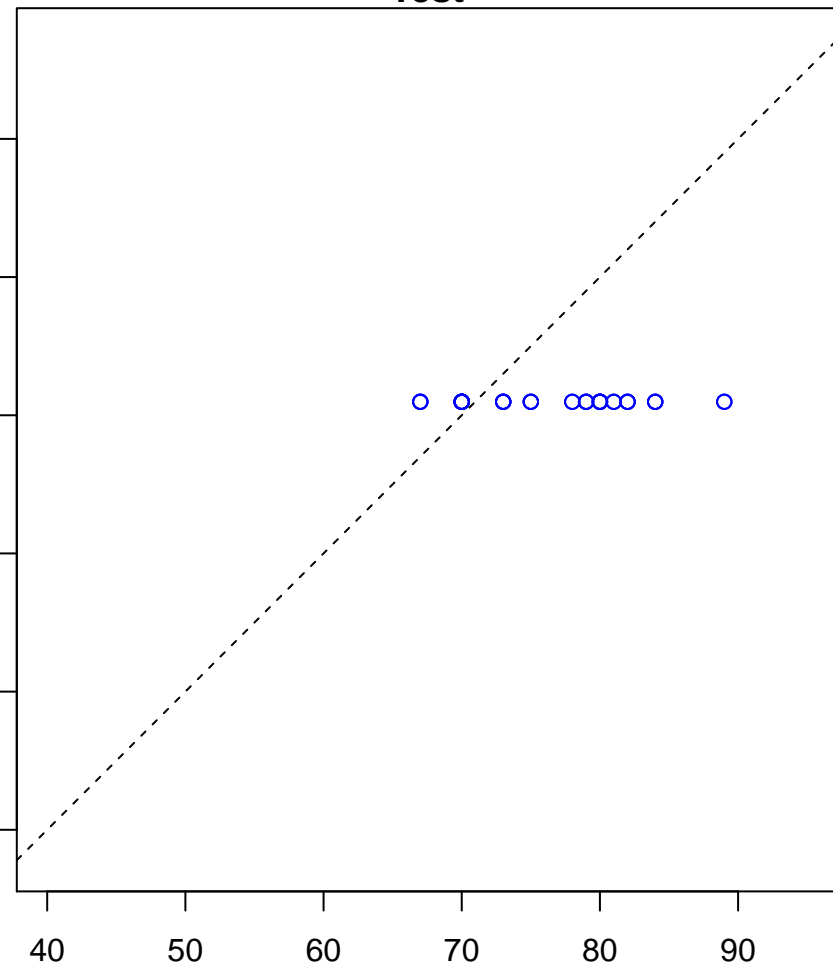
Actual Age

regulation of cytoplasmic translation (Score: 0.796473)

Control

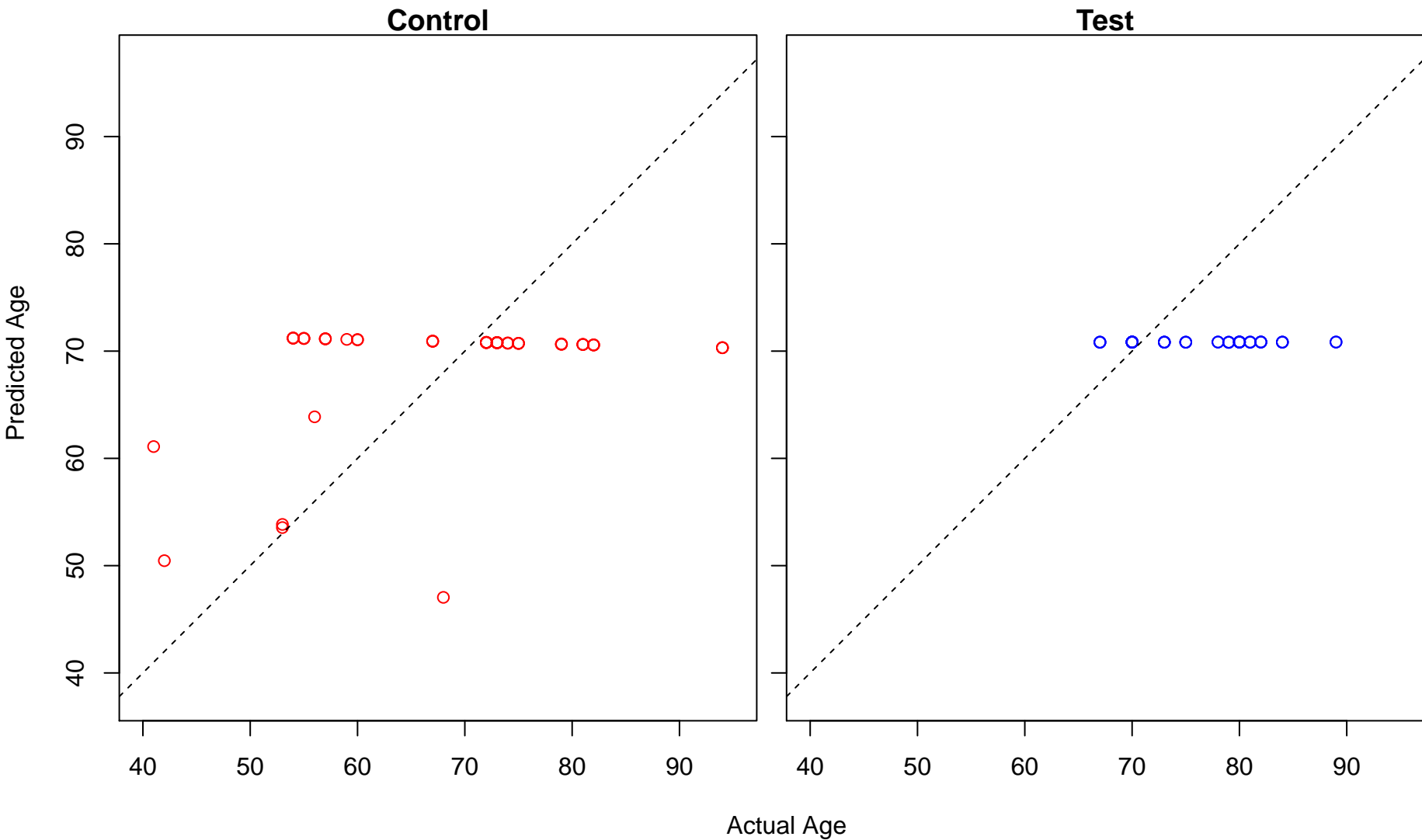


Test

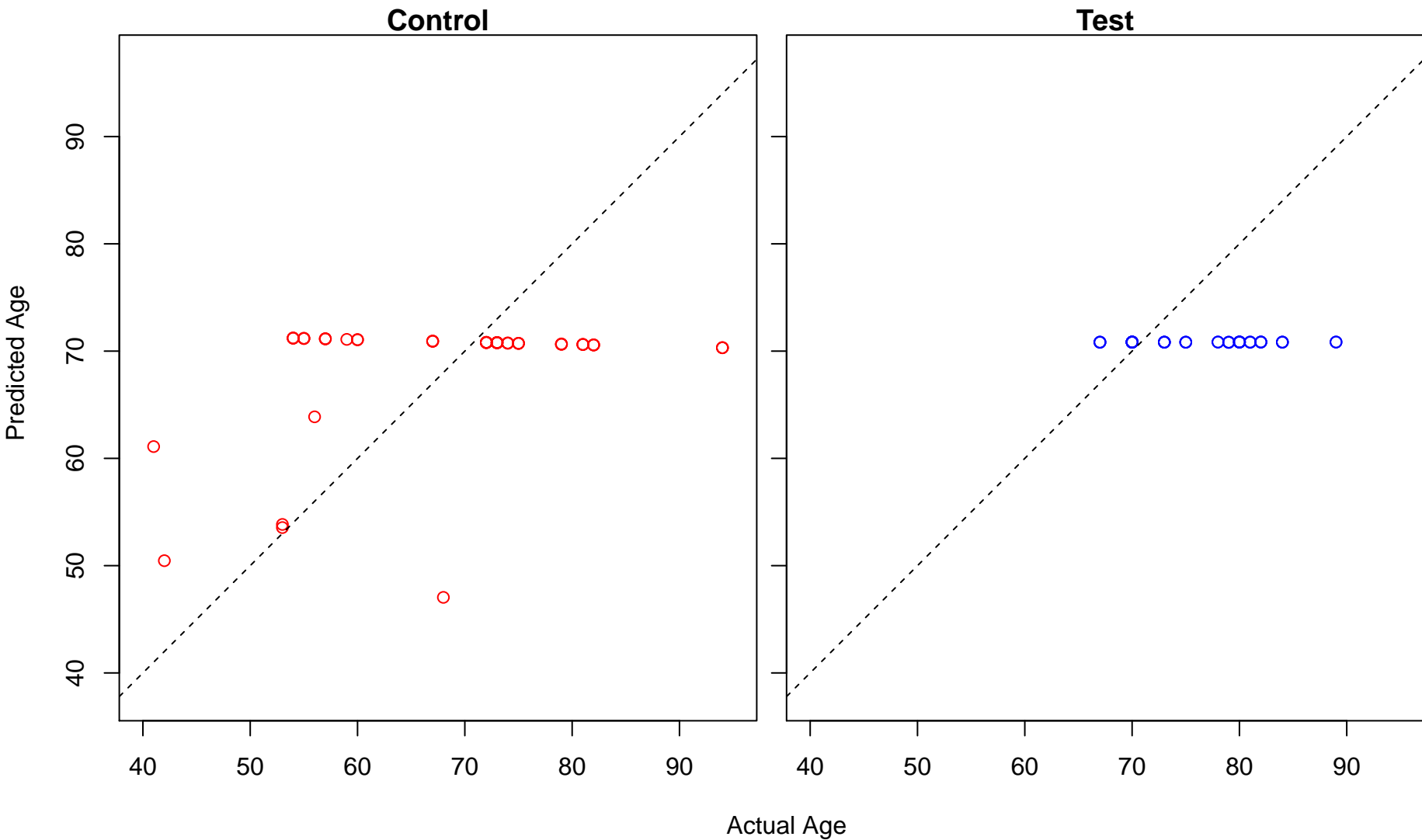


Actual Age

negative regulation of microtubule polymerization or depolymerization (Score: 0.796435)

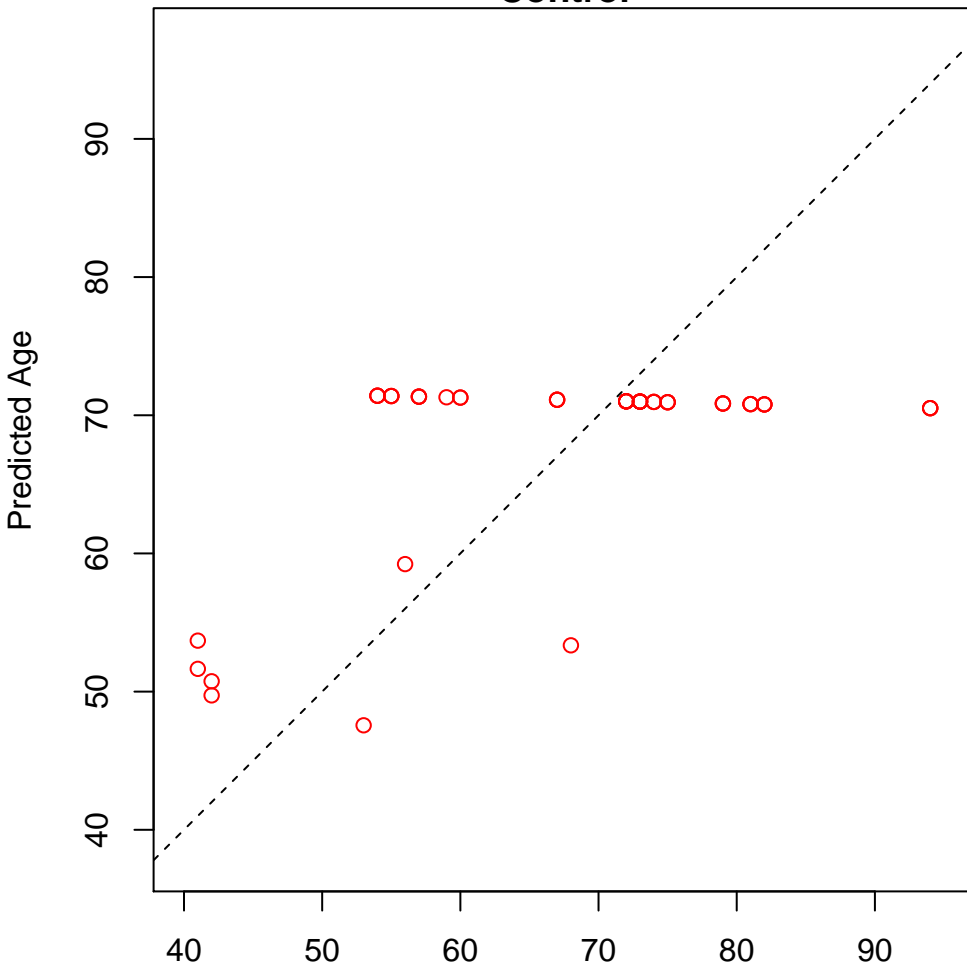


negative regulation of microtubule polymerization (Score: 0.796435)

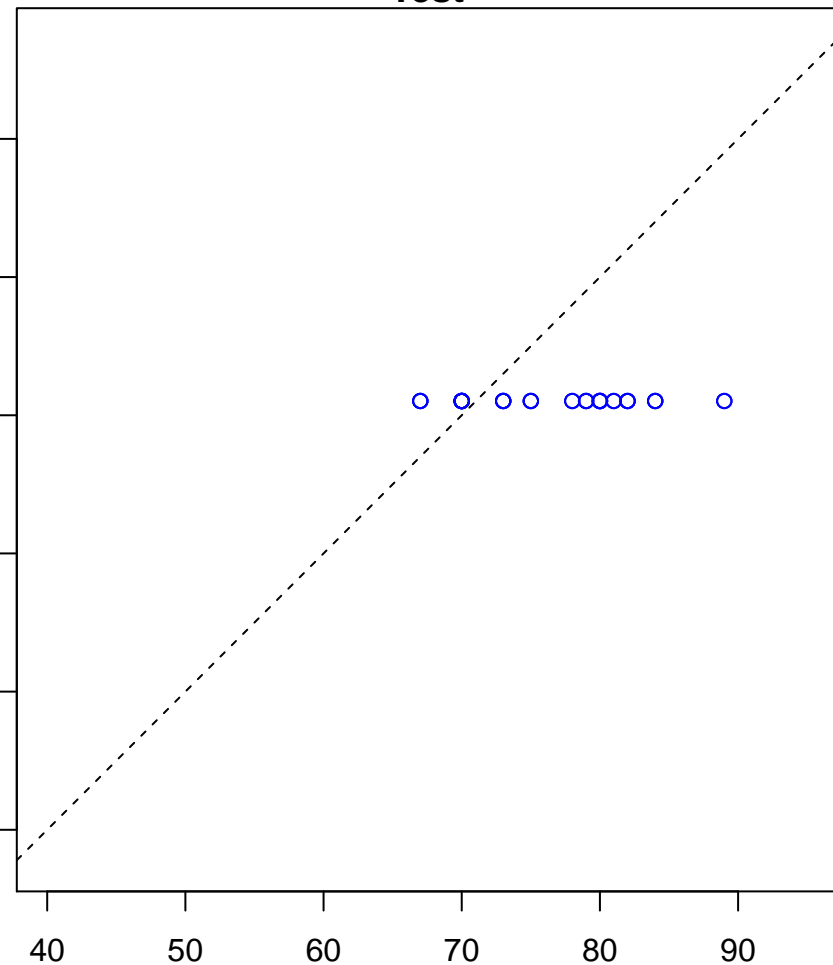


regulation of multi-organism process (Score: 0.796410)

Control

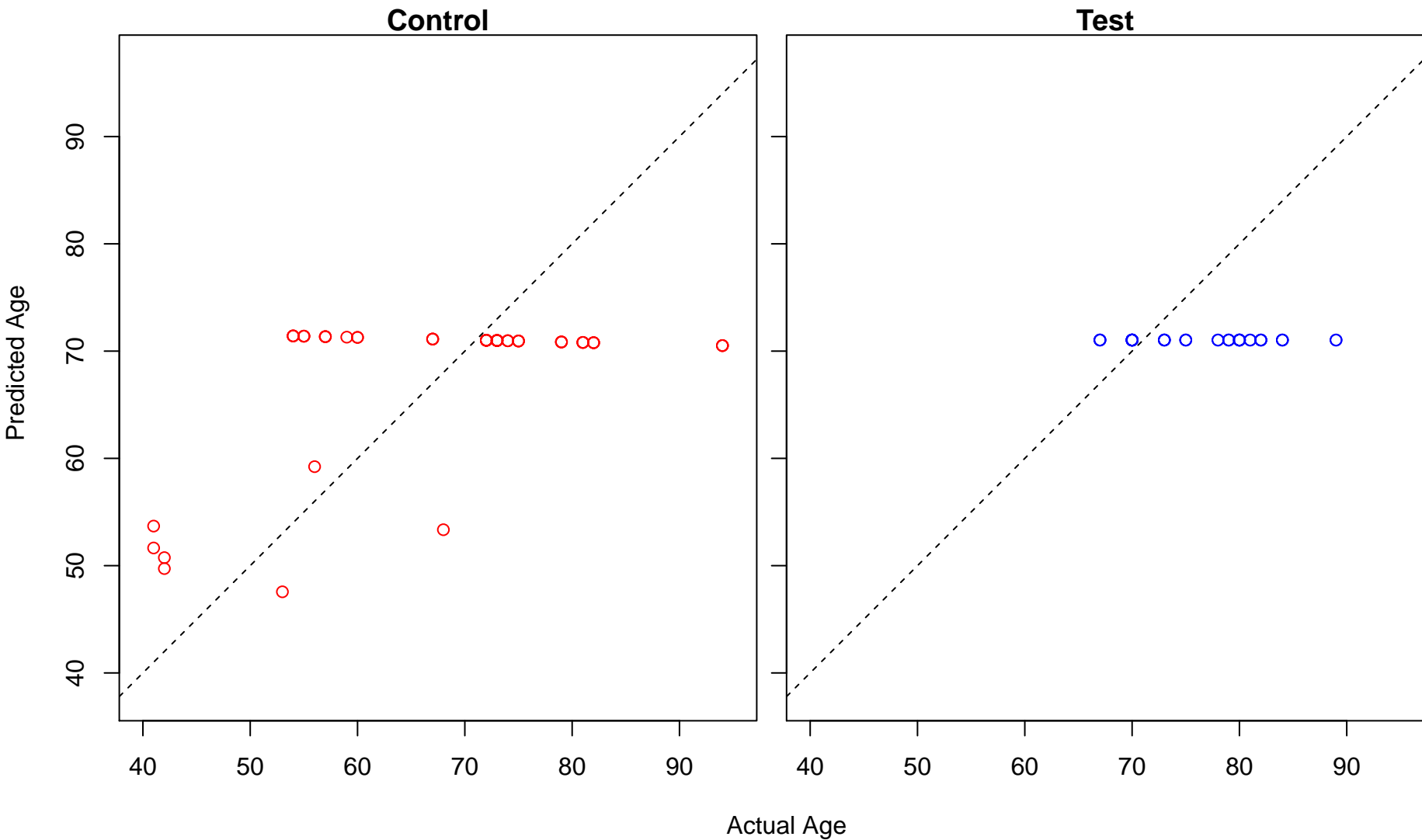


Test

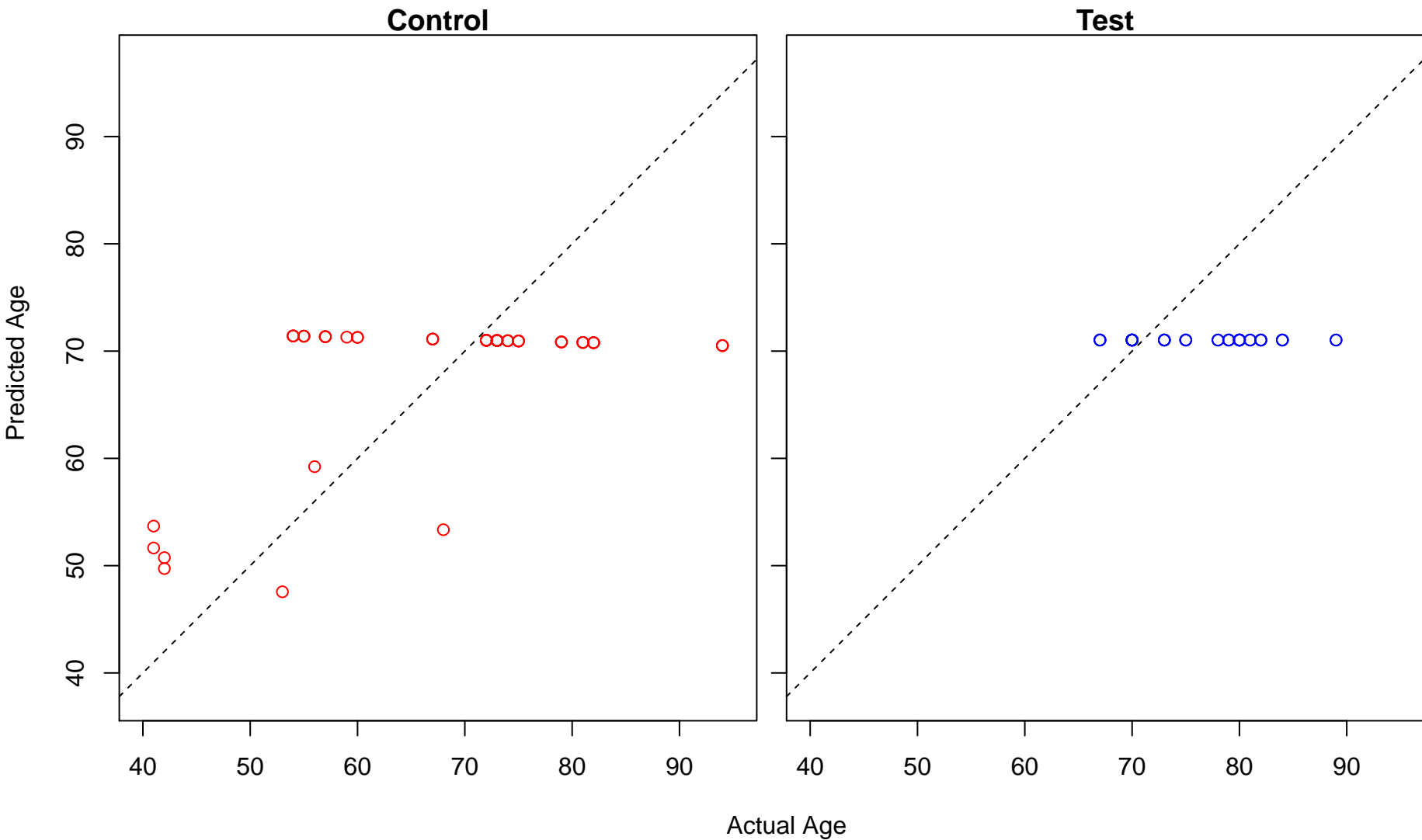


Actual Age

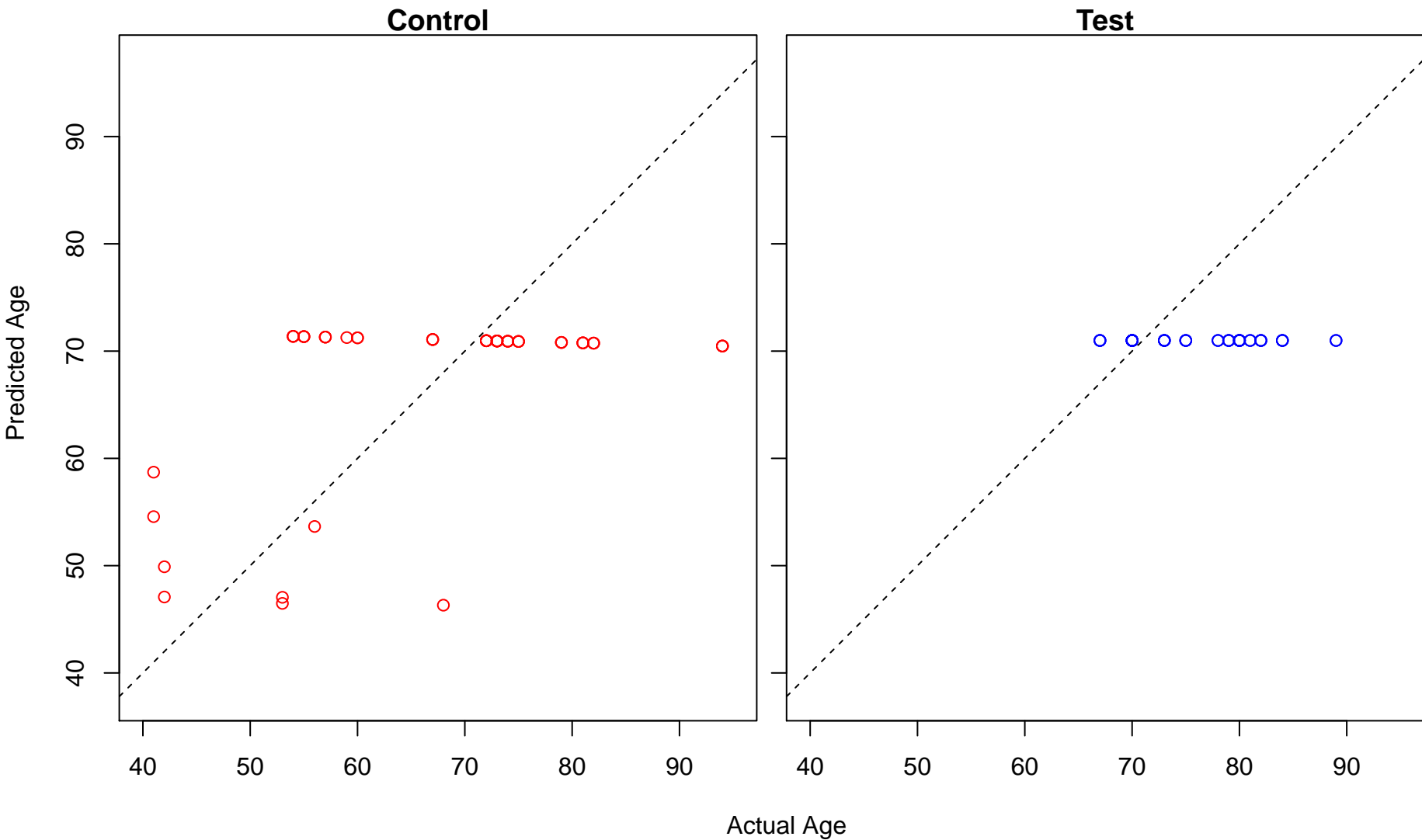
regulation of symbiosis, encompassing mutualism through parasitism (Score: 0.796410)



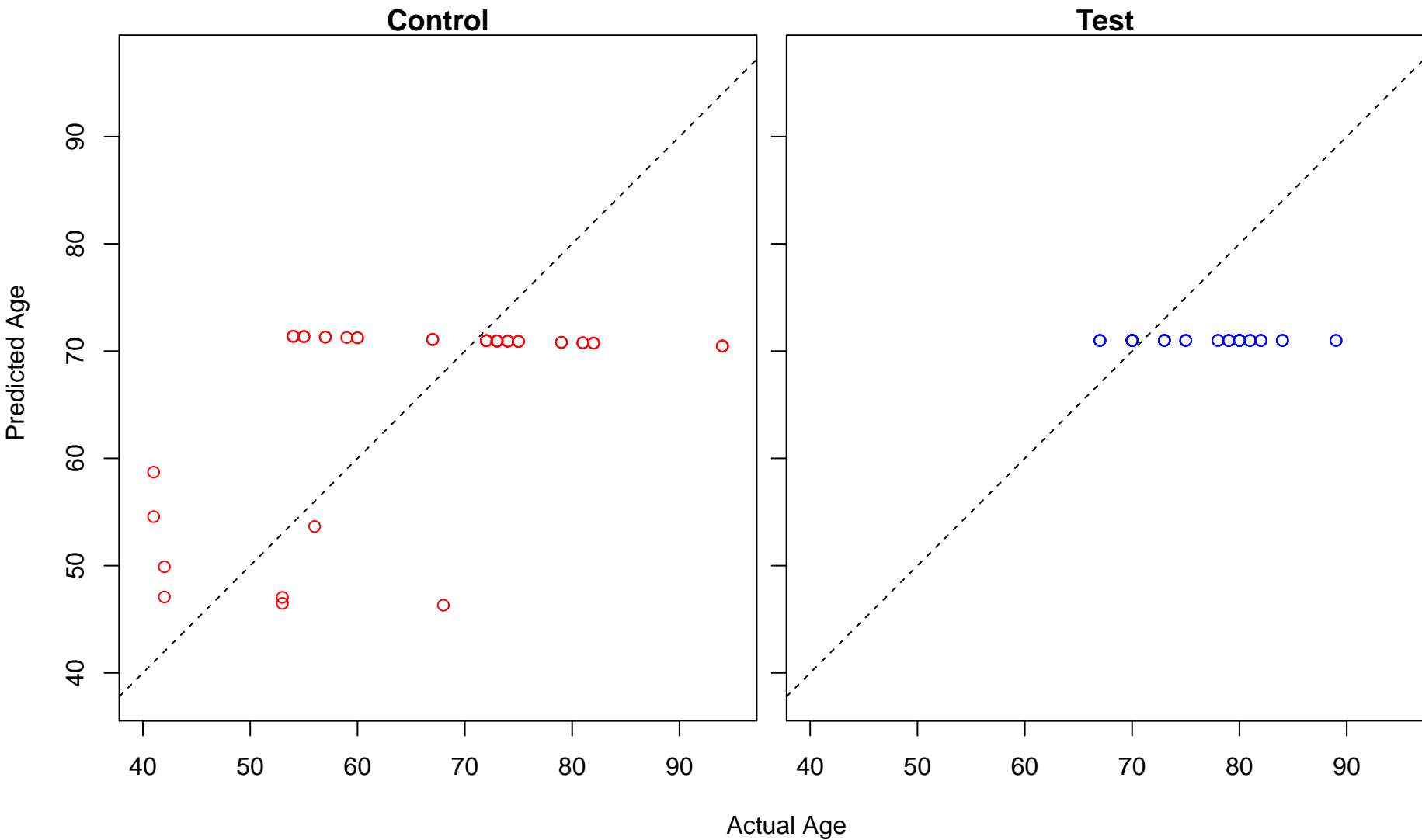
regulation of viral process (Score: 0.796410)



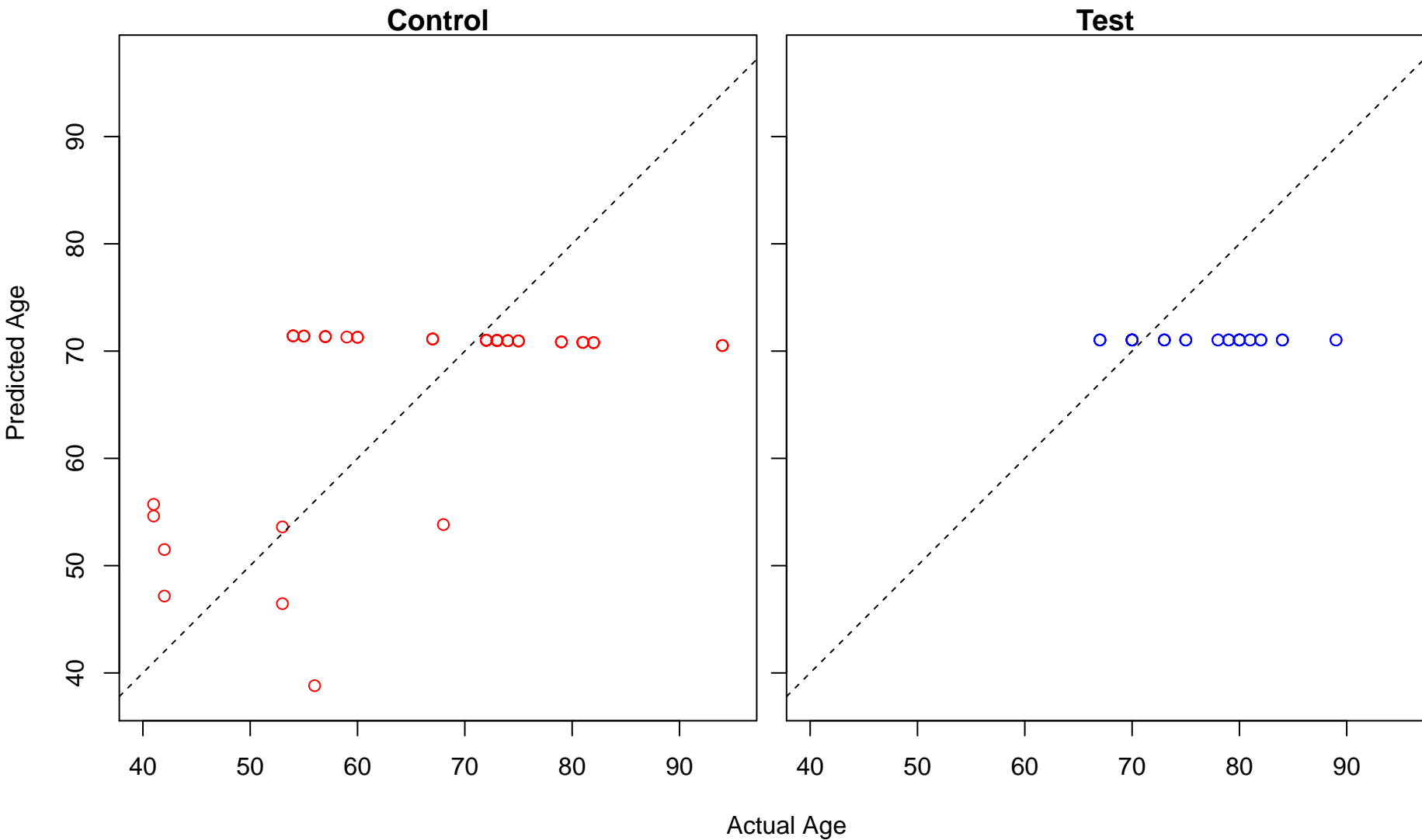
regulation of intracellular steroid hormone receptor signaling pathway (Score: 0.796406)



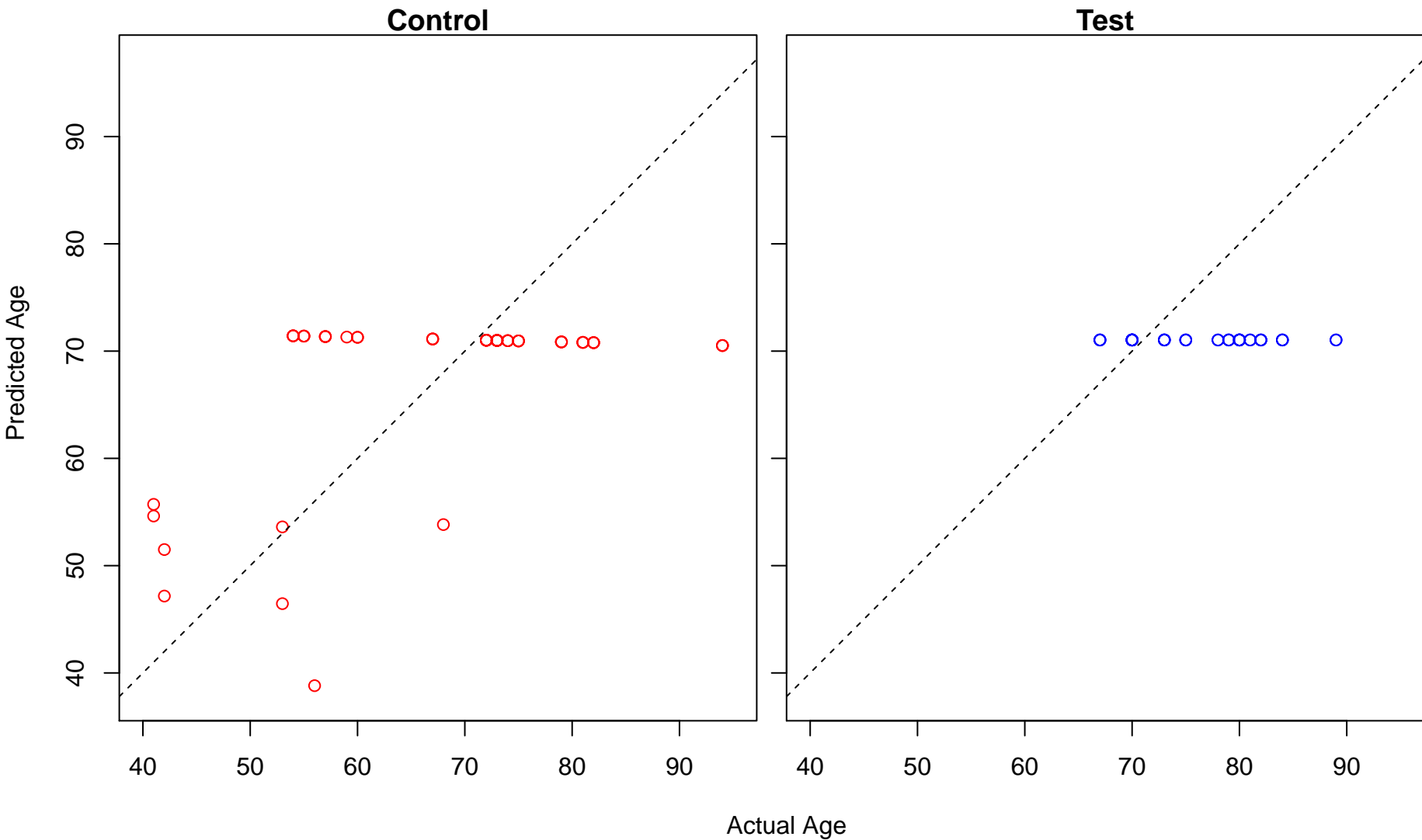
regulation of androgen receptor signaling pathway (Score: 0.796406)



DNA damage response, signal transduction by p53 class mediator (Score: 0.796360)

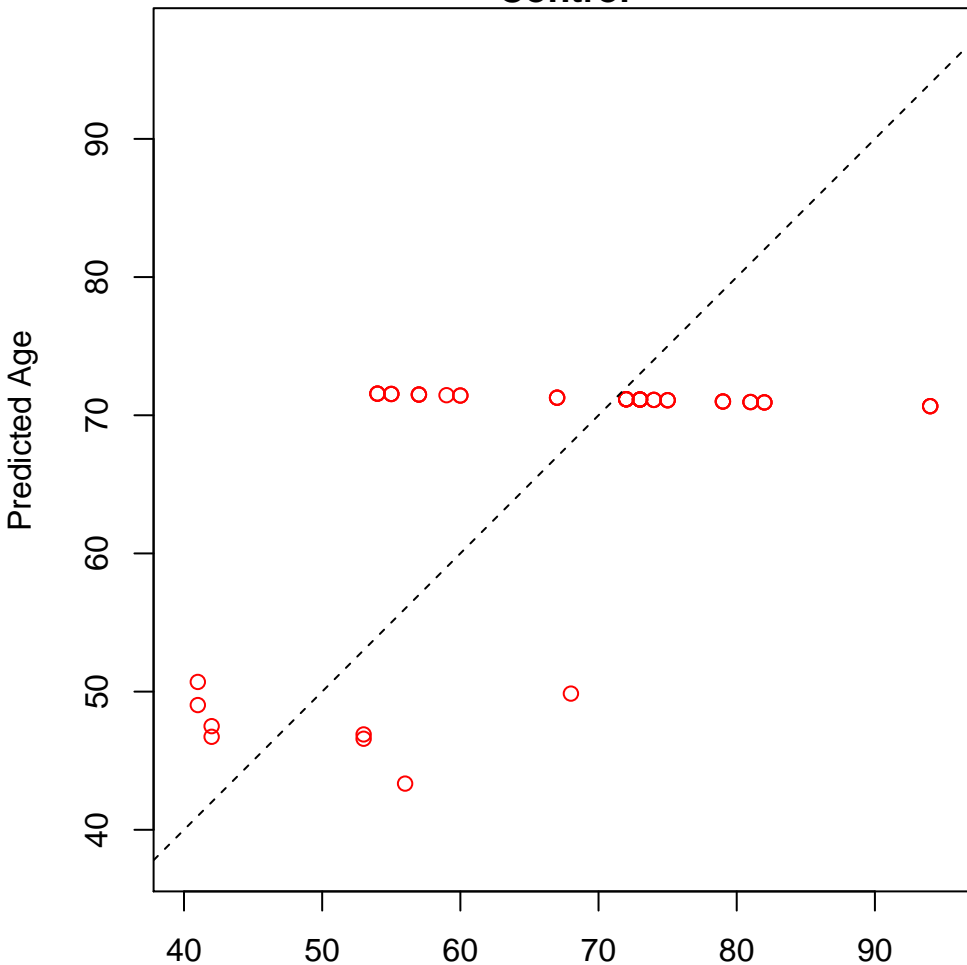


signal transduction in response to DNA damage (Score: 0.796360)

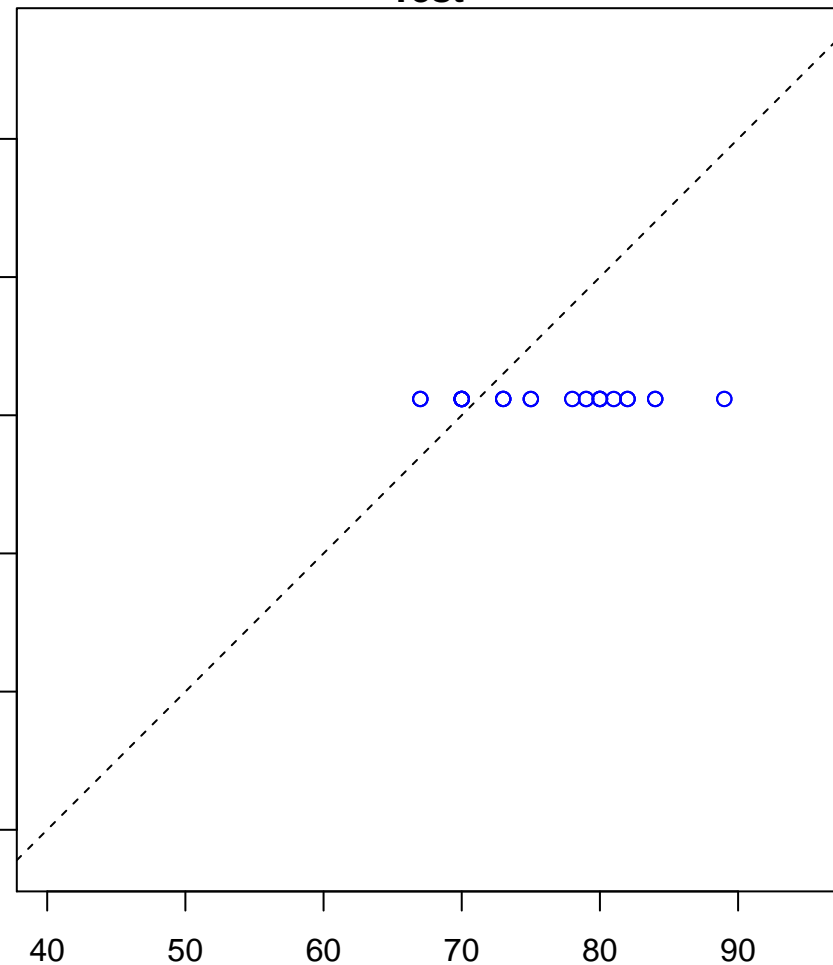


organic substance transport (Score: 0.796273)

Control



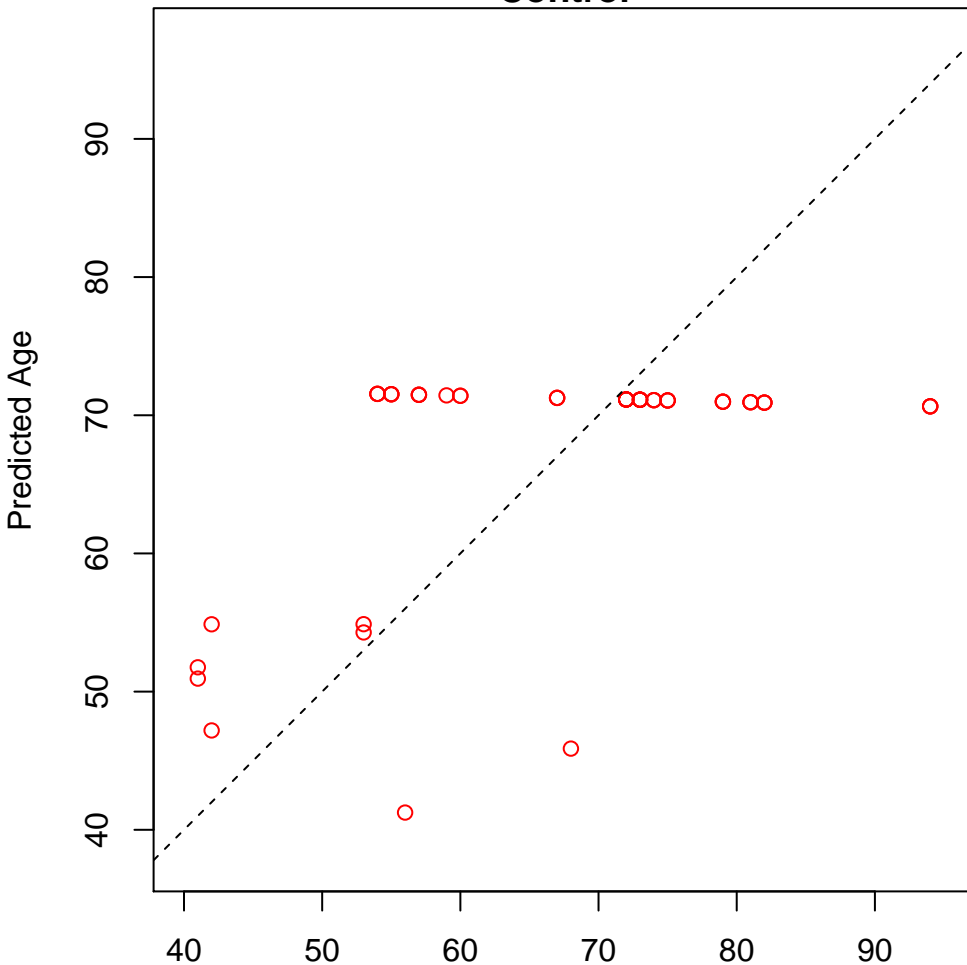
Test



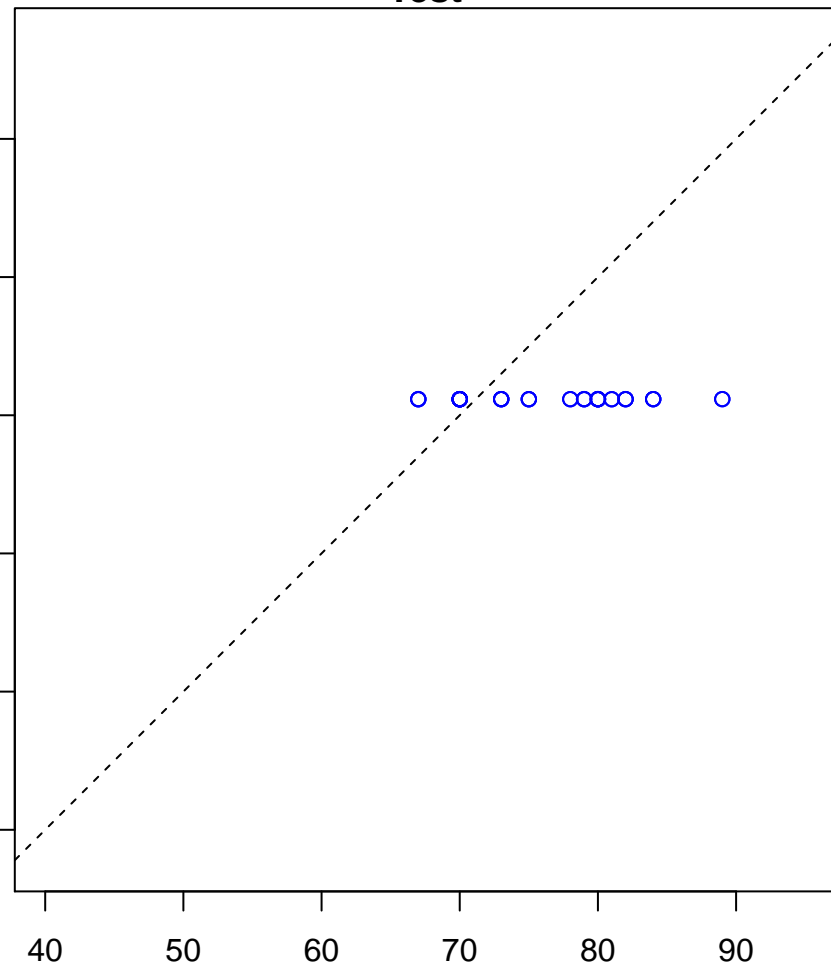
Actual Age

establishment of organelle localization (Score: 0.796233)

Control



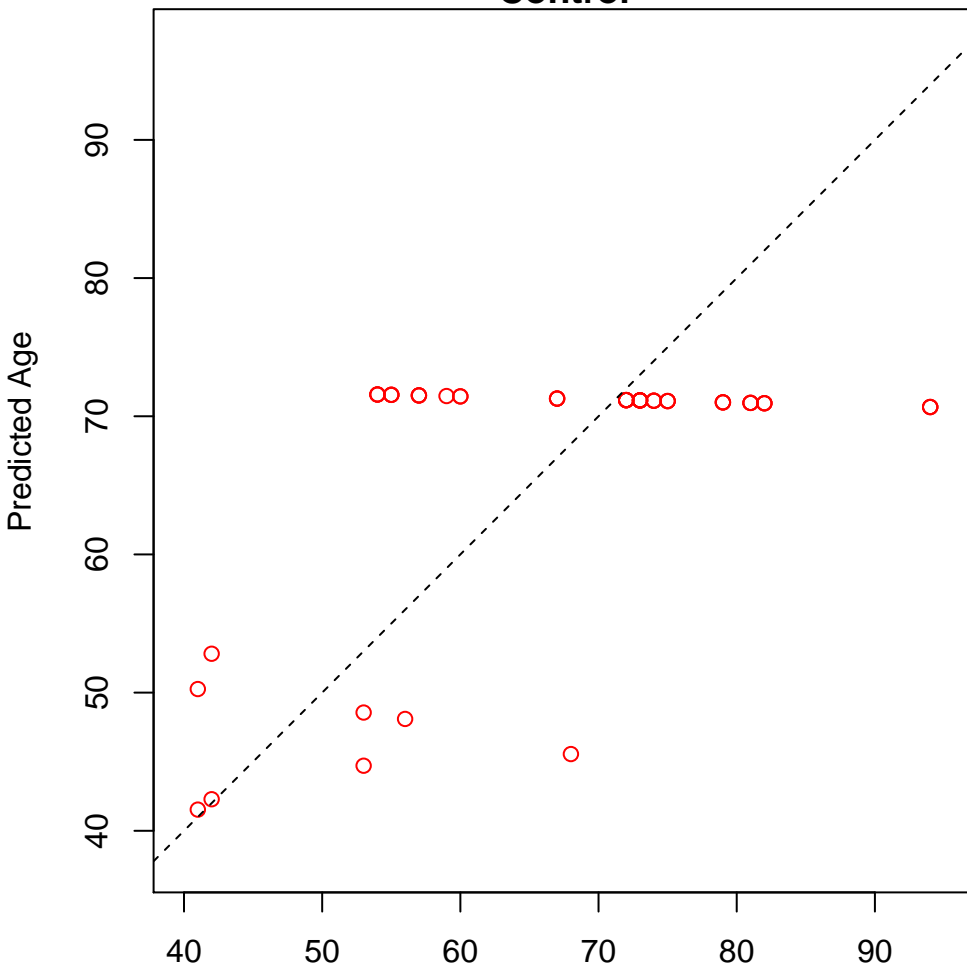
Test



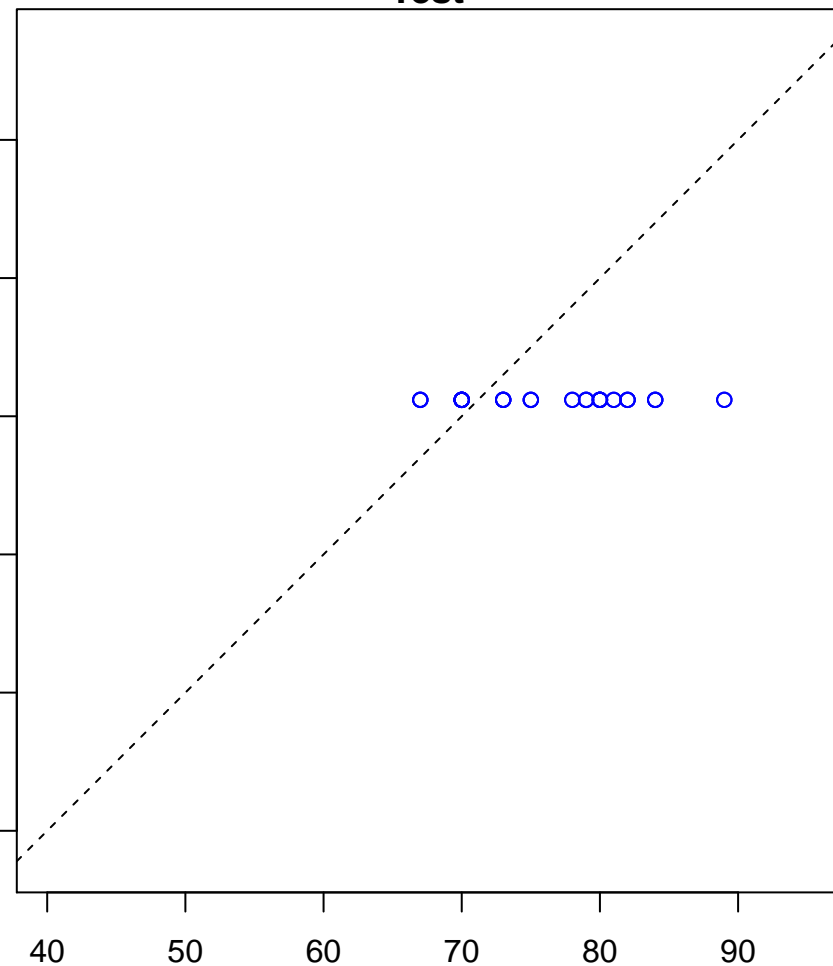
Actual Age

regulation of protein metabolic process (Score: 0.796168)

Control

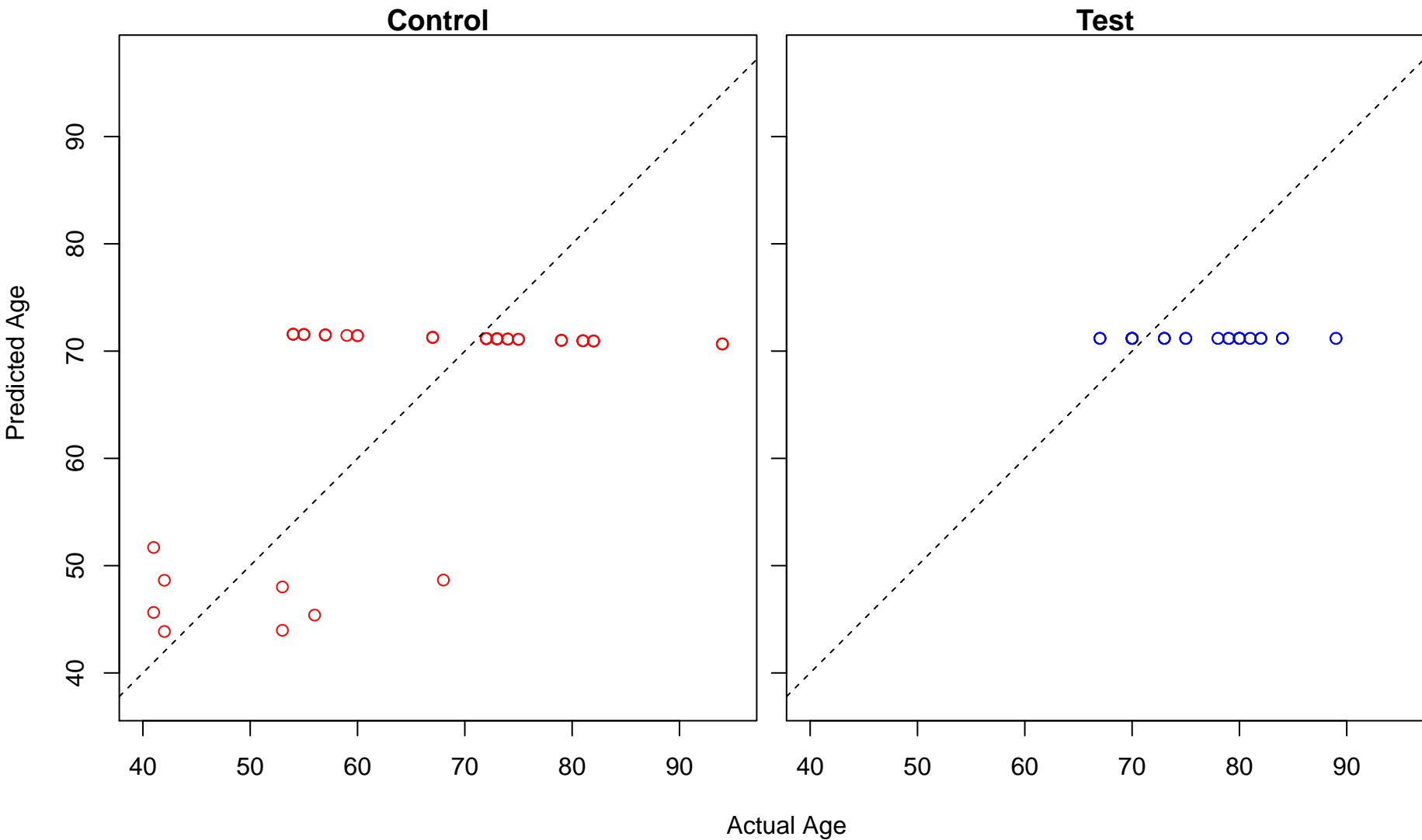


Test

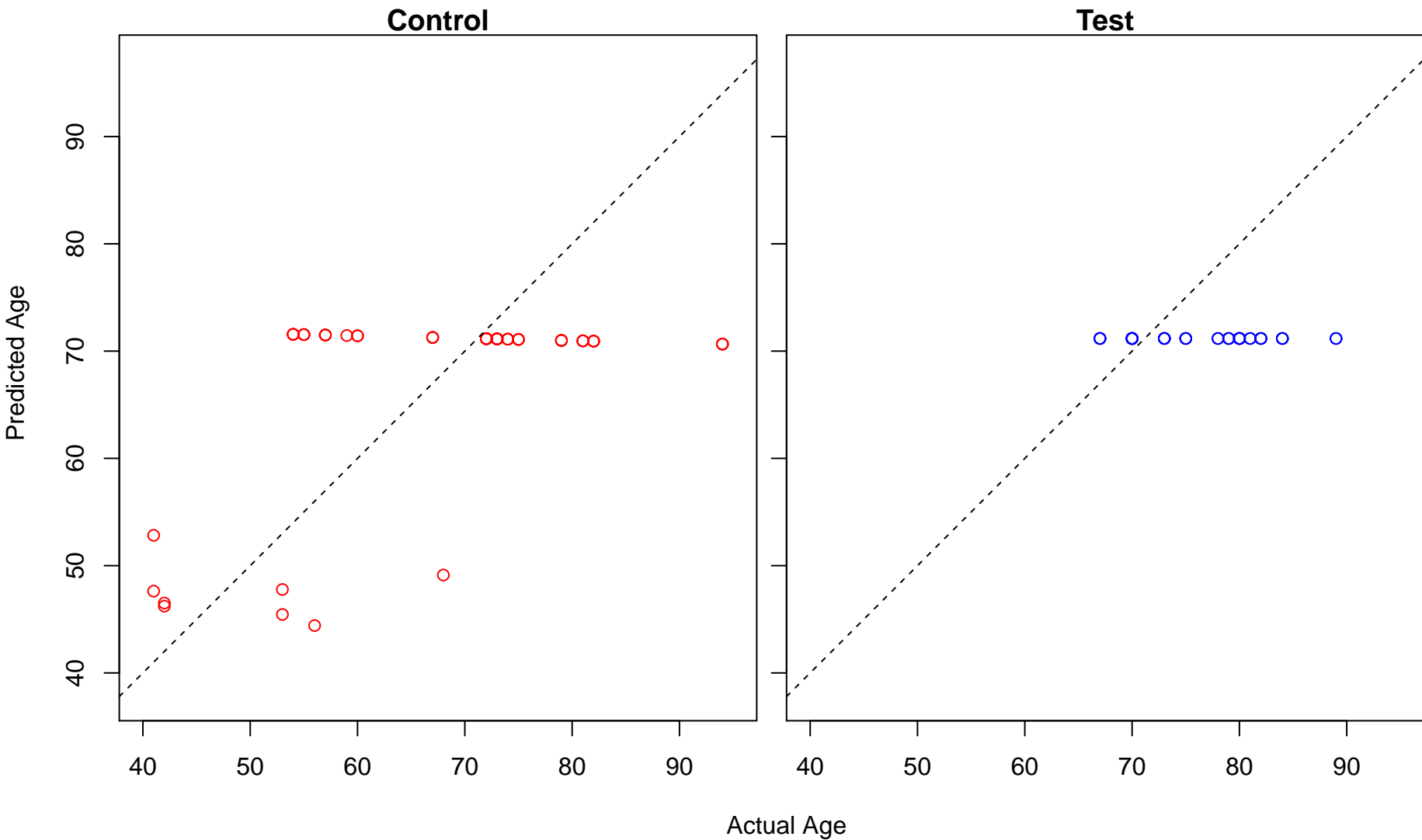


Actual Age

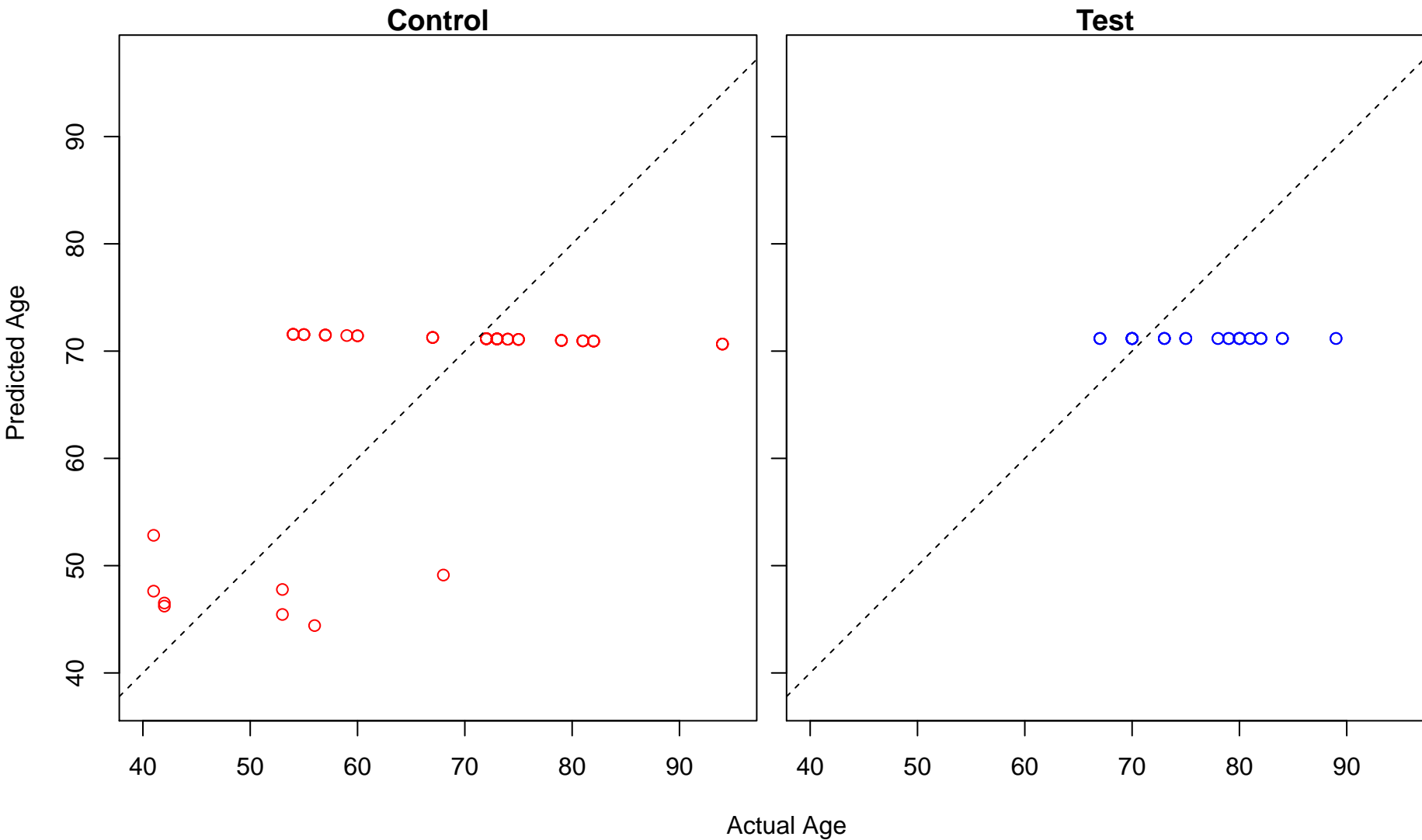
positive regulation of nitrogen compound metabolic process (Score: 0.796152)



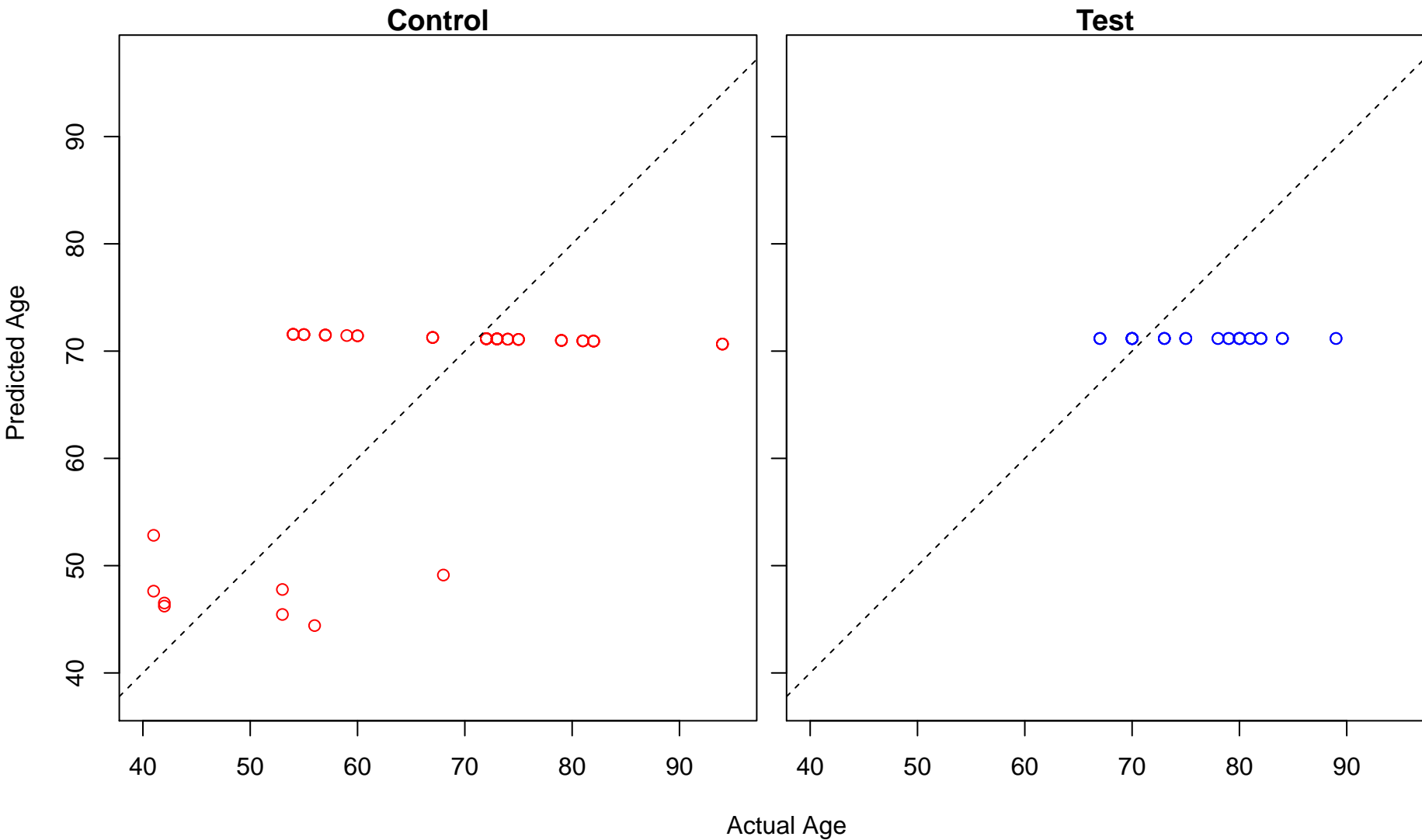
translation (Score: 0.796149)



peptide biosynthetic process (Score: 0.796149)

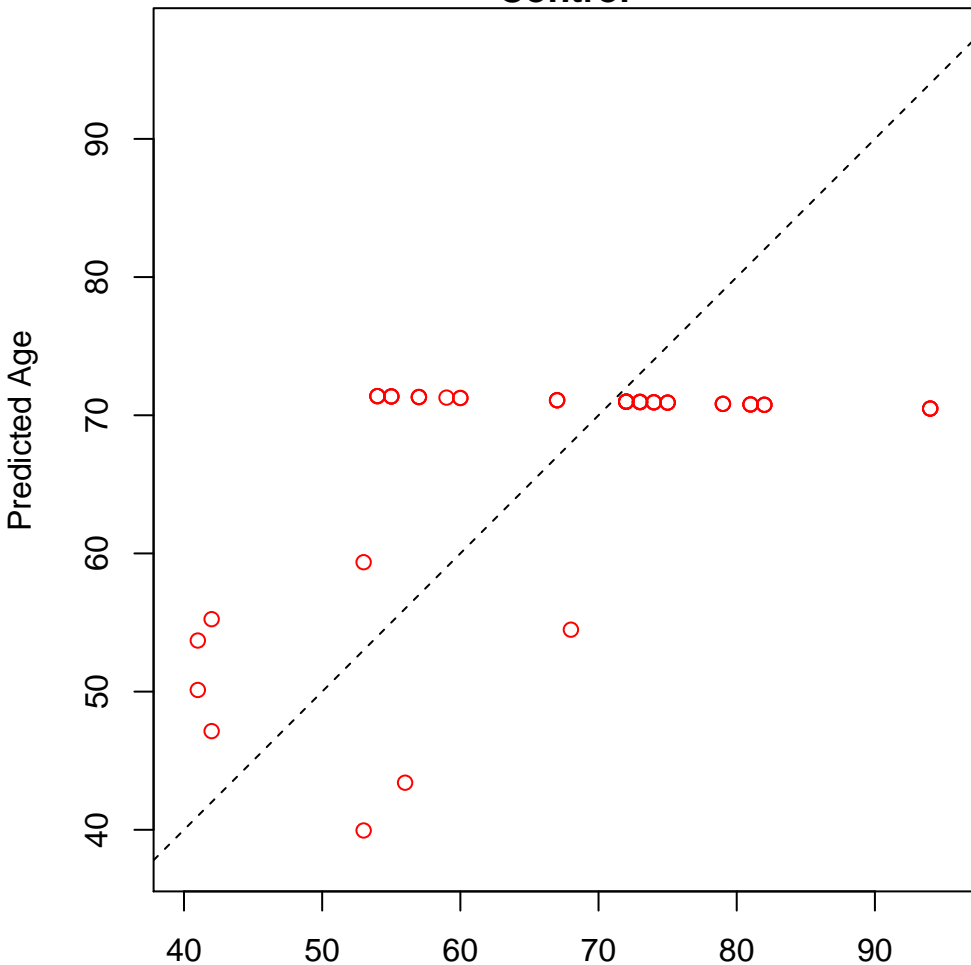


amide biosynthetic process (Score: 0.796149)

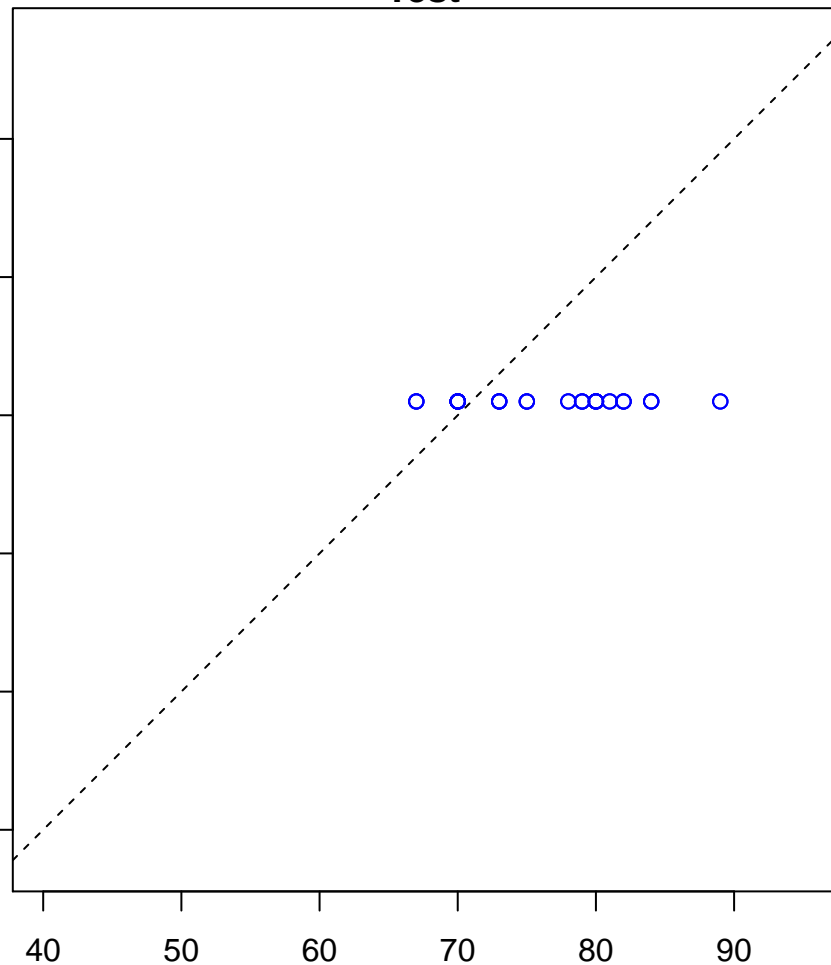


endoplasmic reticulum unfolded protein response (Score: 0.795943)

Control



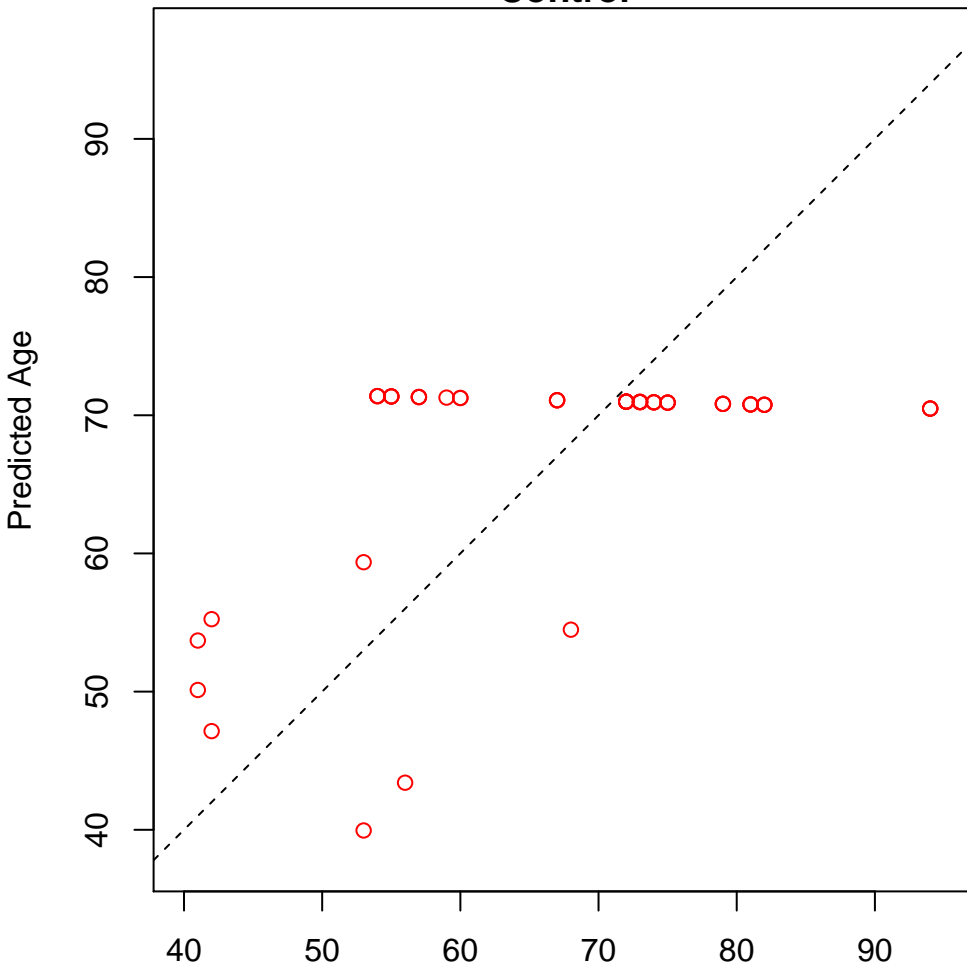
Test



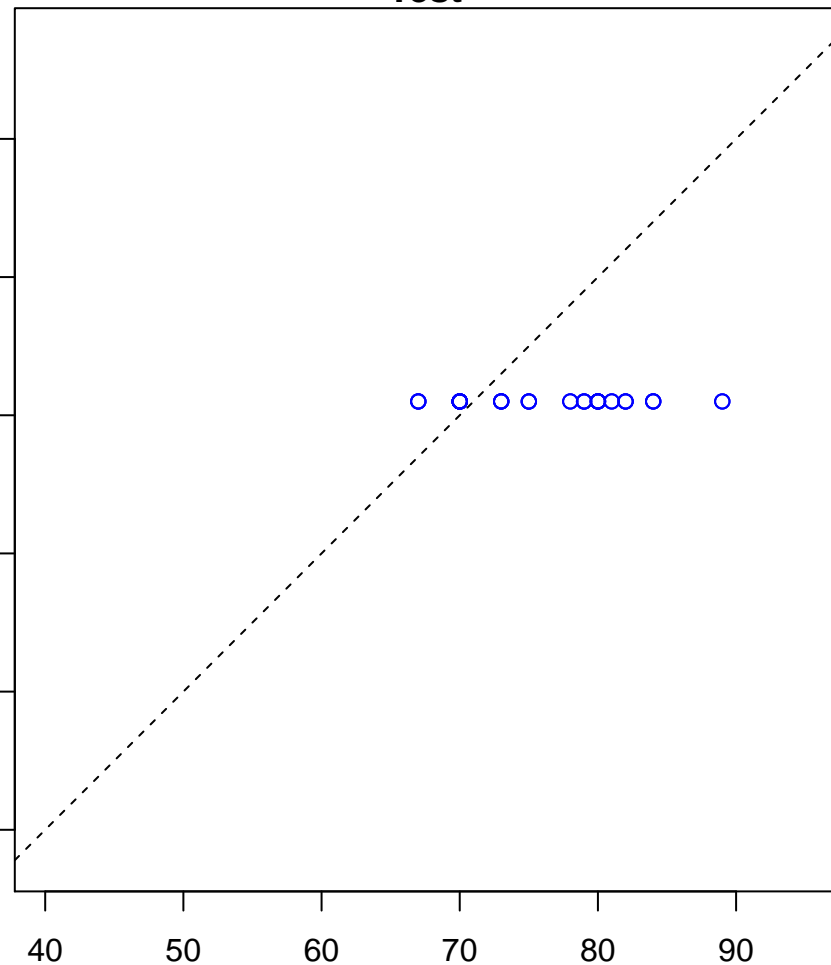
Actual Age

cellular response to unfolded protein (Score: 0.795943)

Control

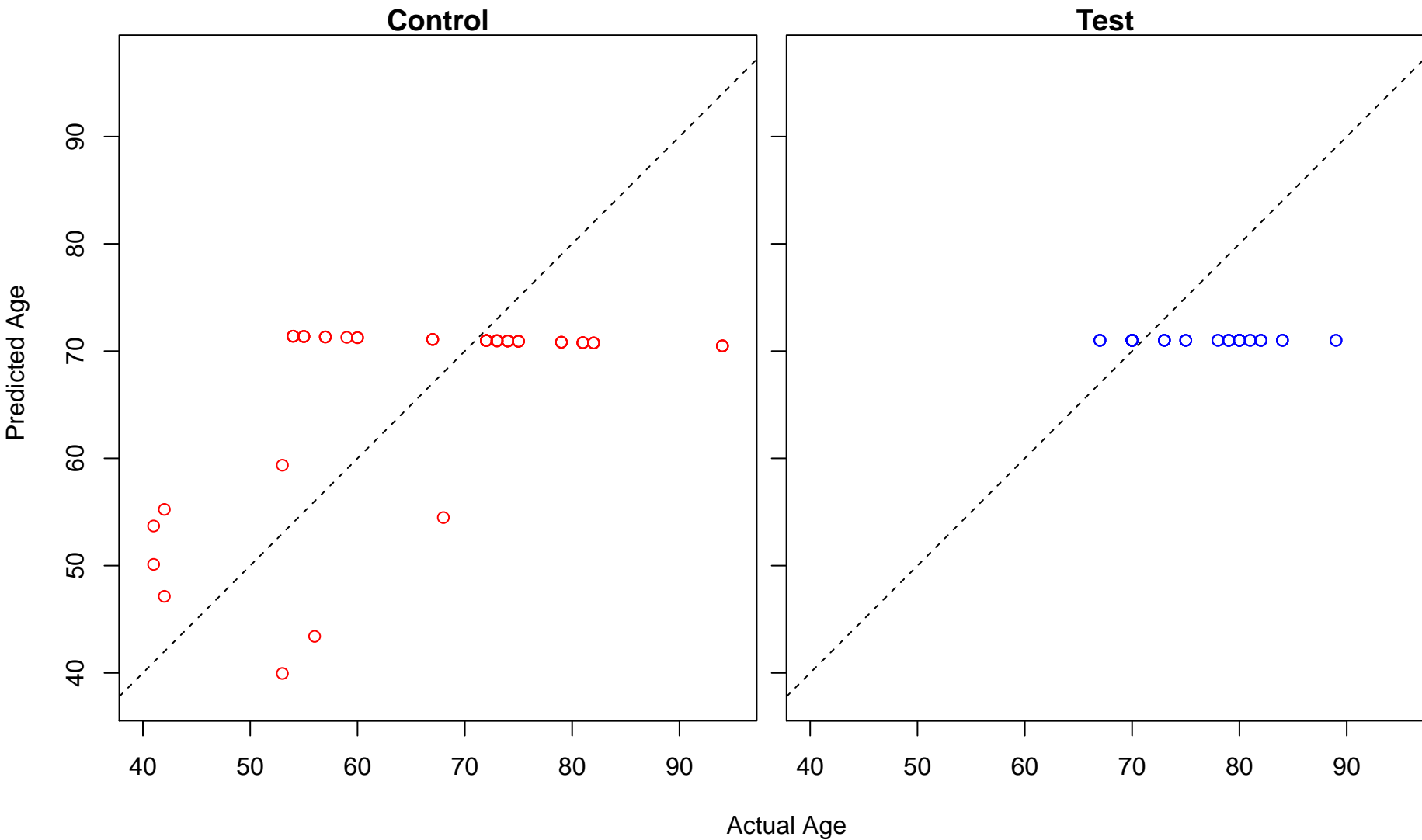


Test

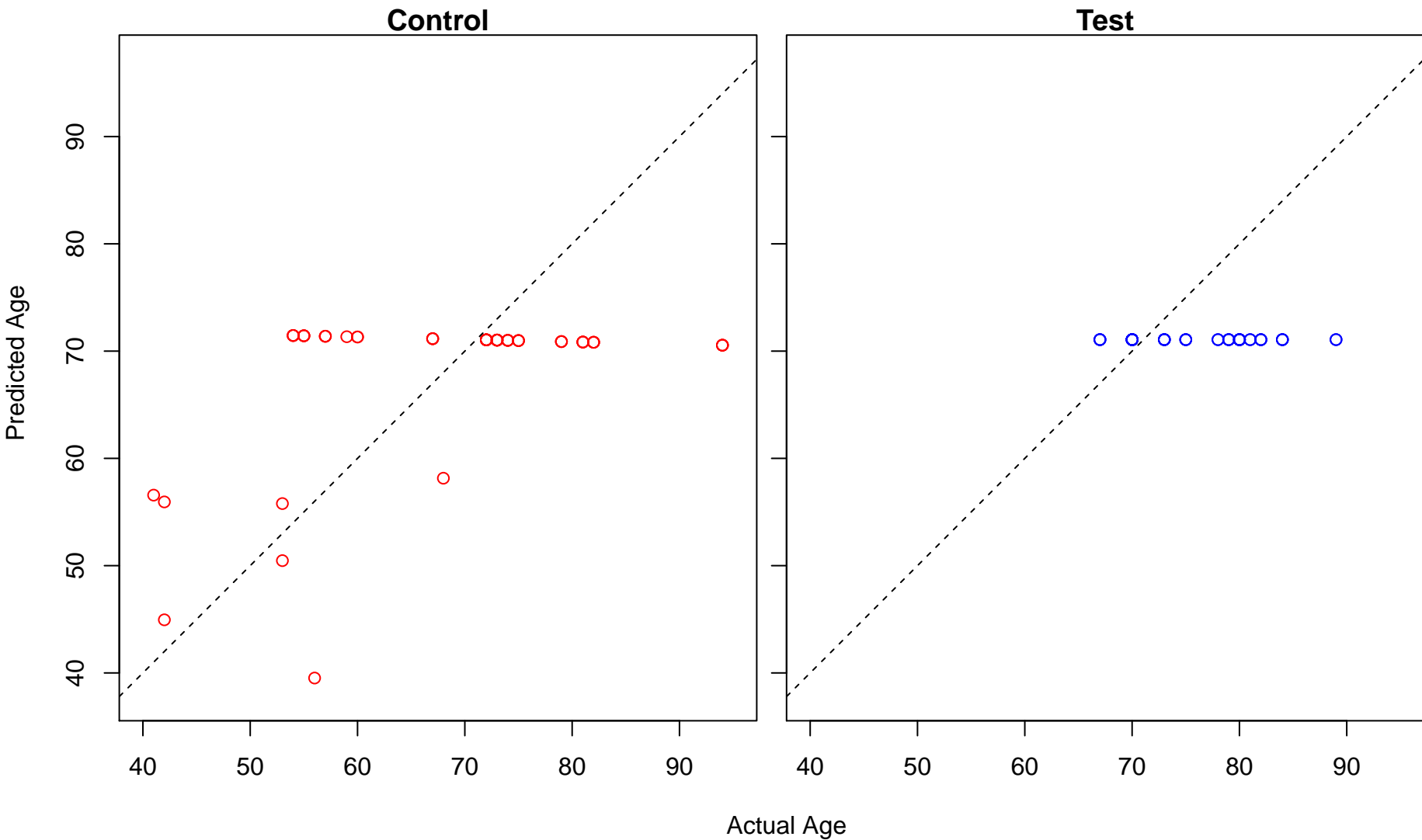


Actual Age

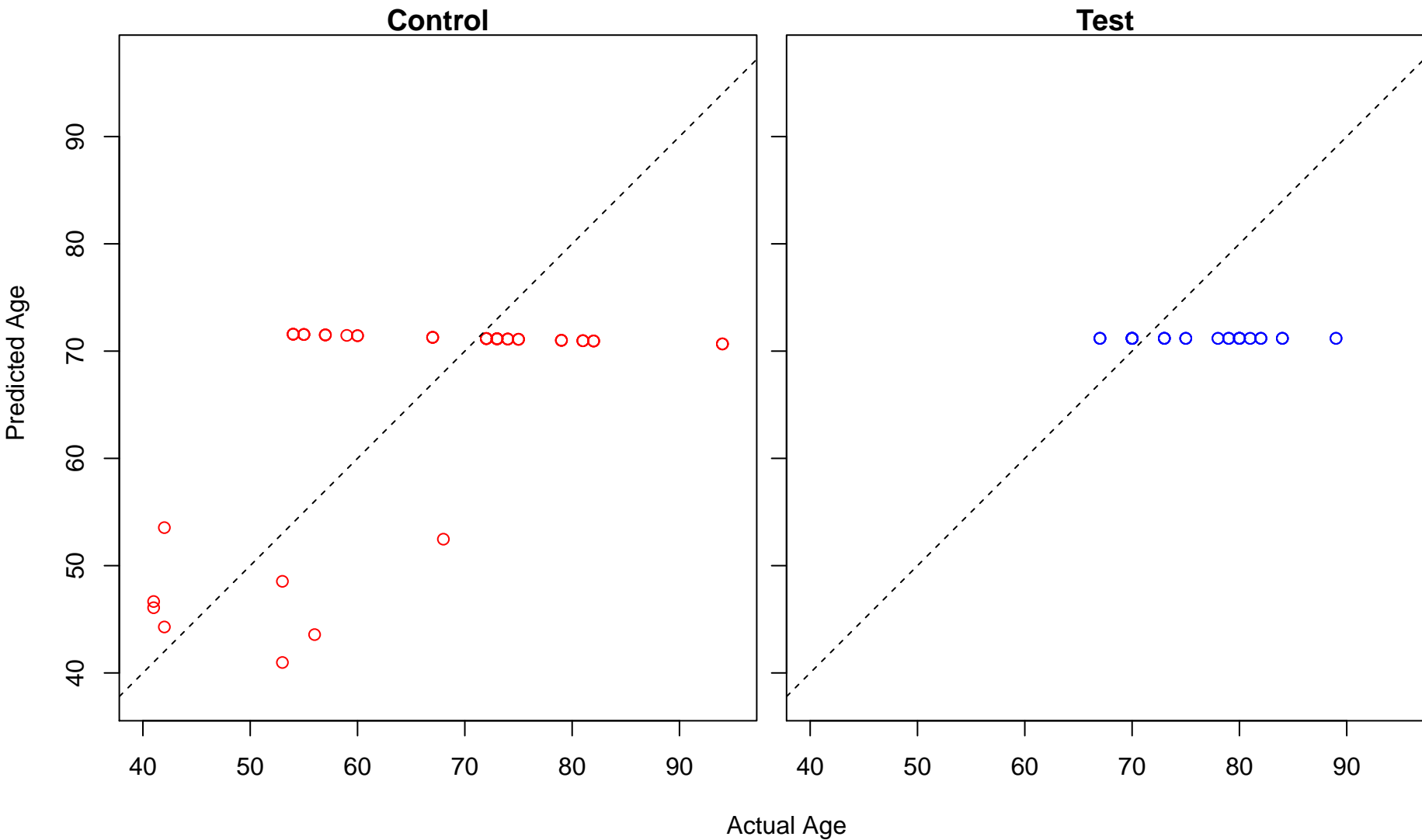
cellular response to topologically incorrect protein (Score: 0.795943)



viral life cycle (Score: 0.795932)

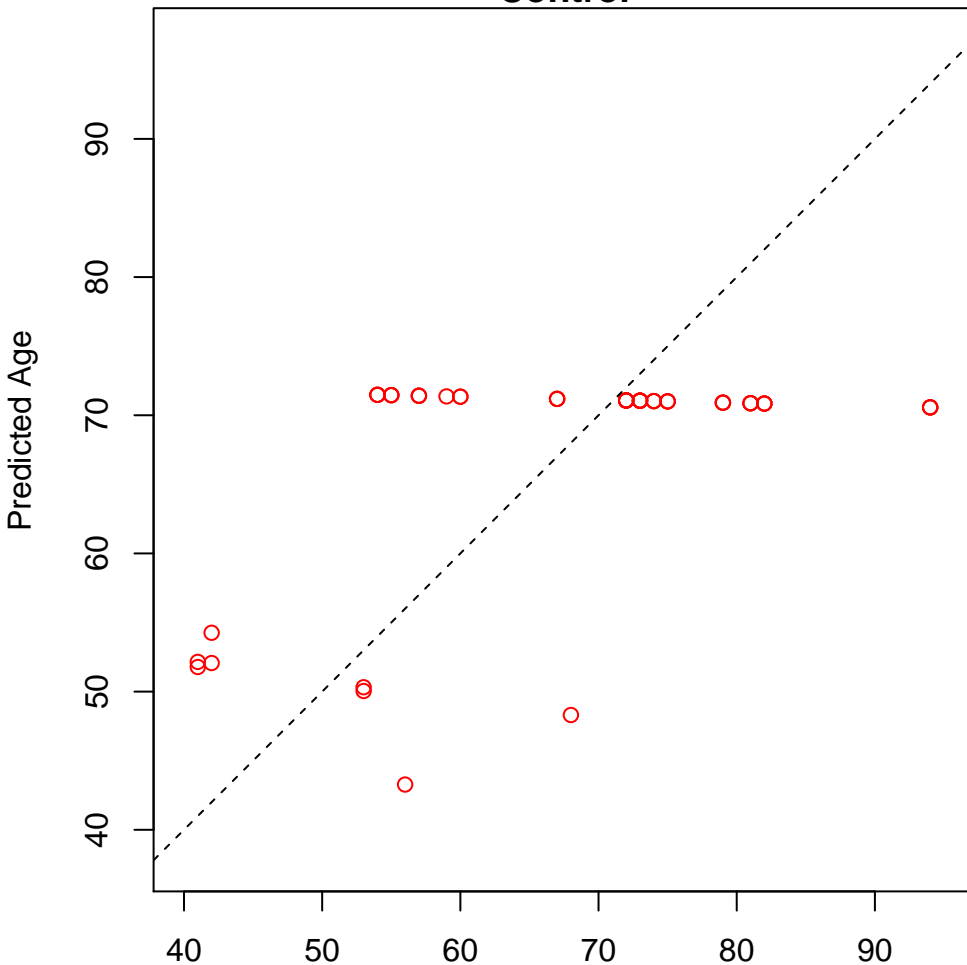


cellular response to stimulus (Score: 0.795927)

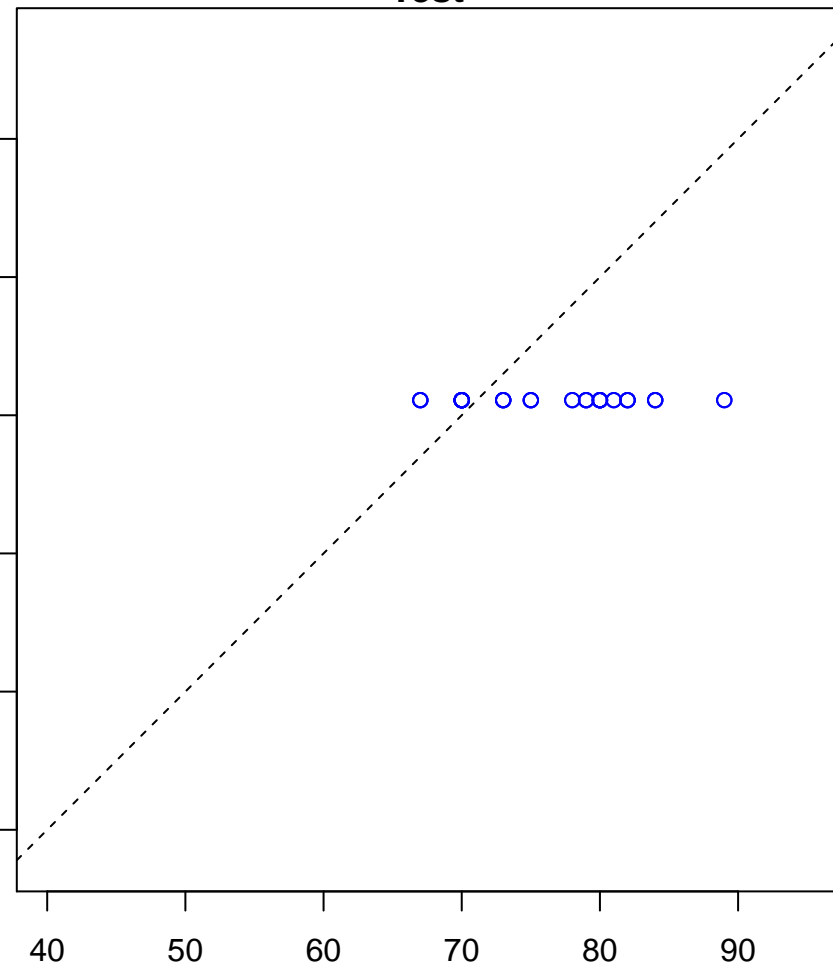


positive regulation of cell migration (Score: 0.795853)

Control



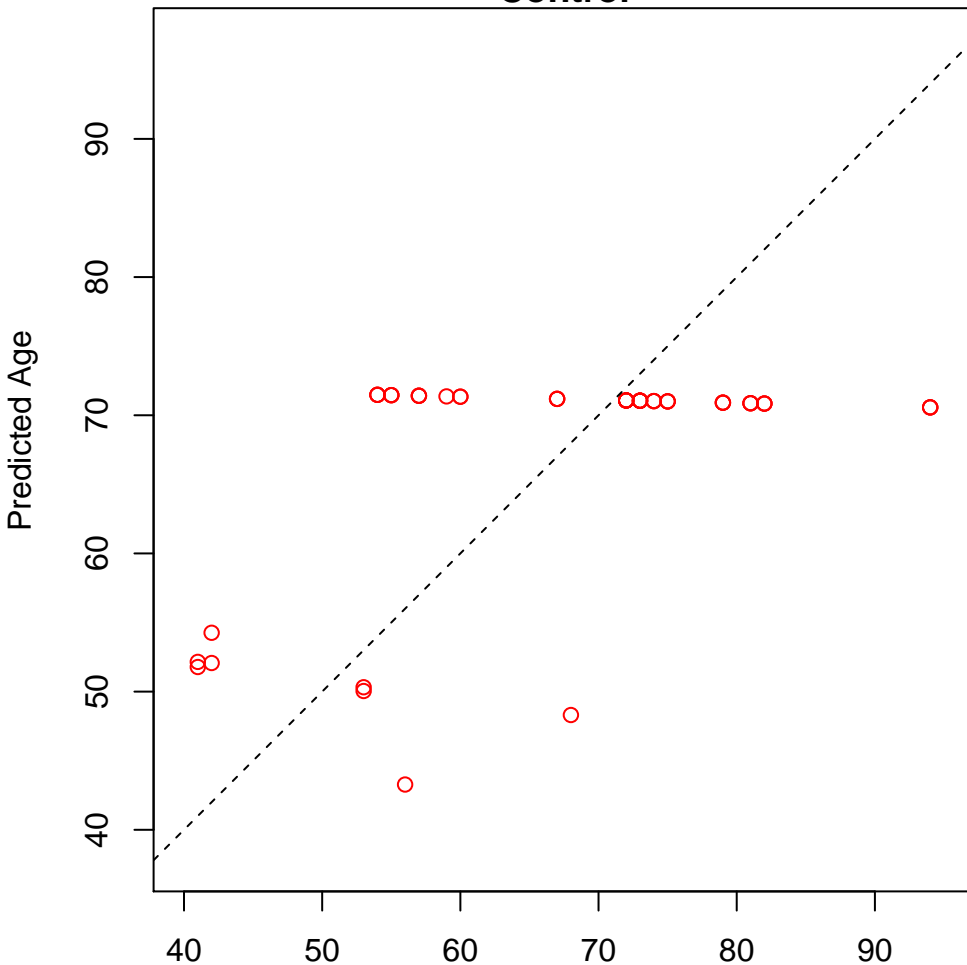
Test



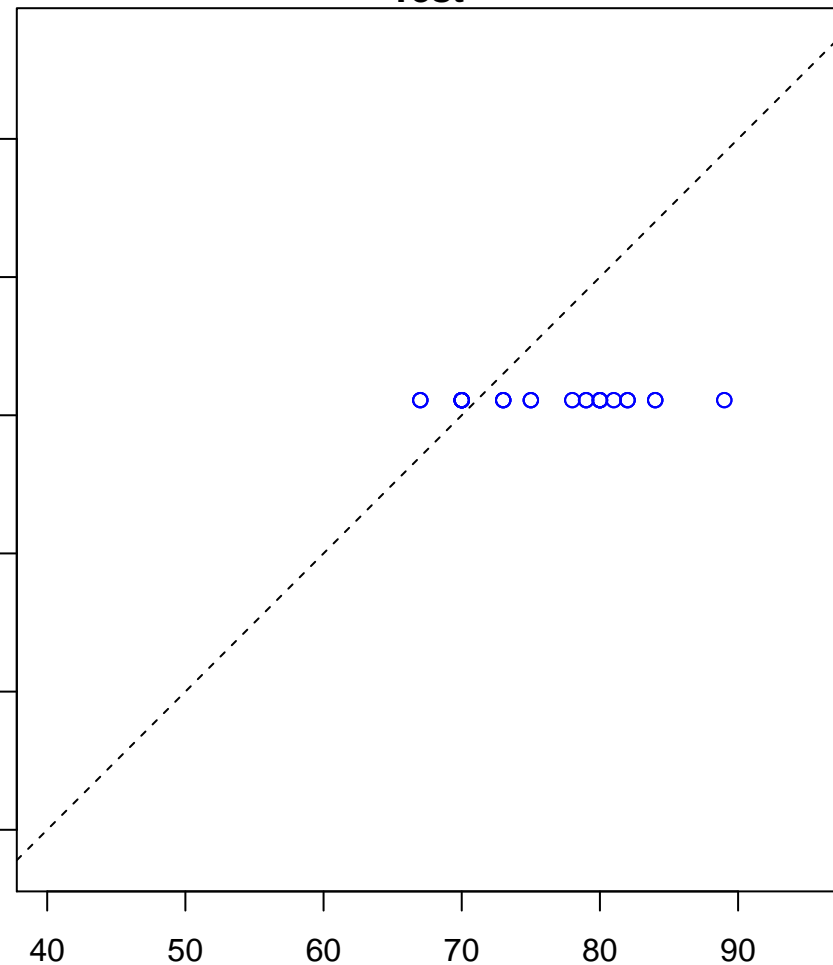
Actual Age

positive regulation of locomotion (Score: 0.795853)

Control

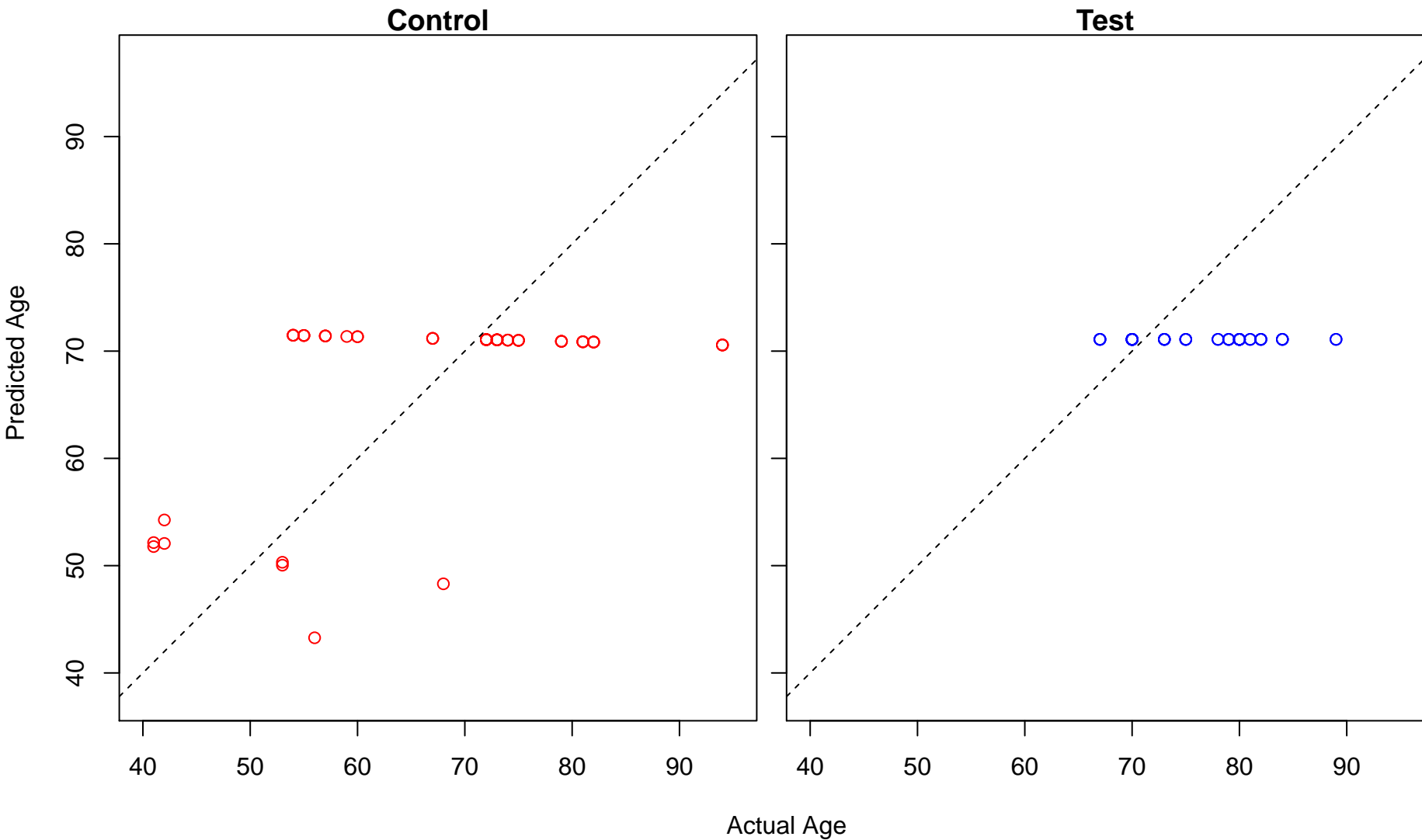


Test



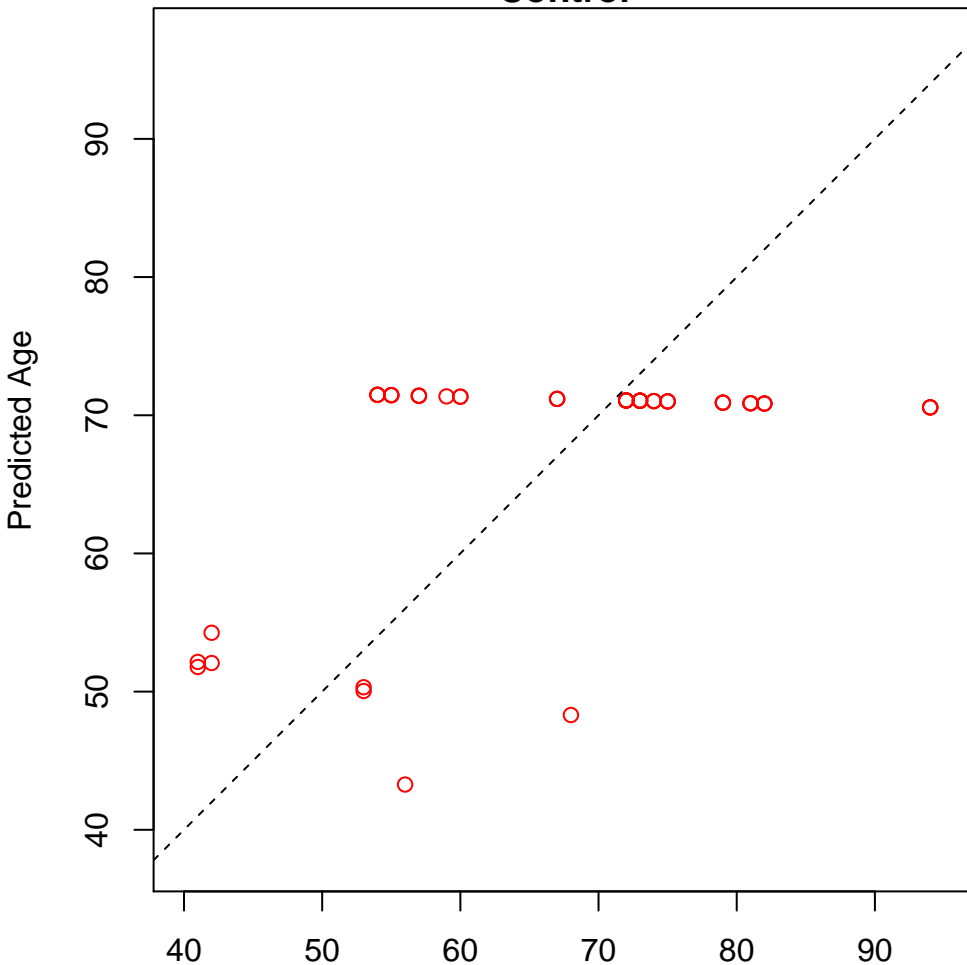
Actual Age

positive regulation of cellular component movement (Score: 0.795853)

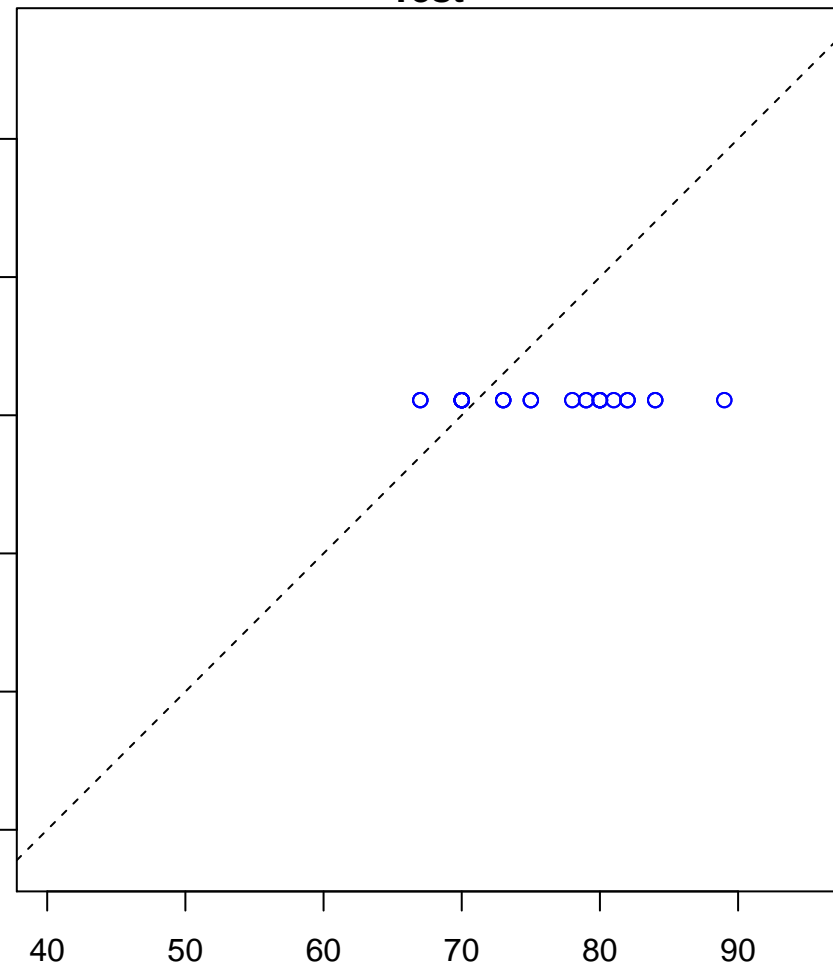


positive regulation of cell motility (Score: 0.795853)

Control



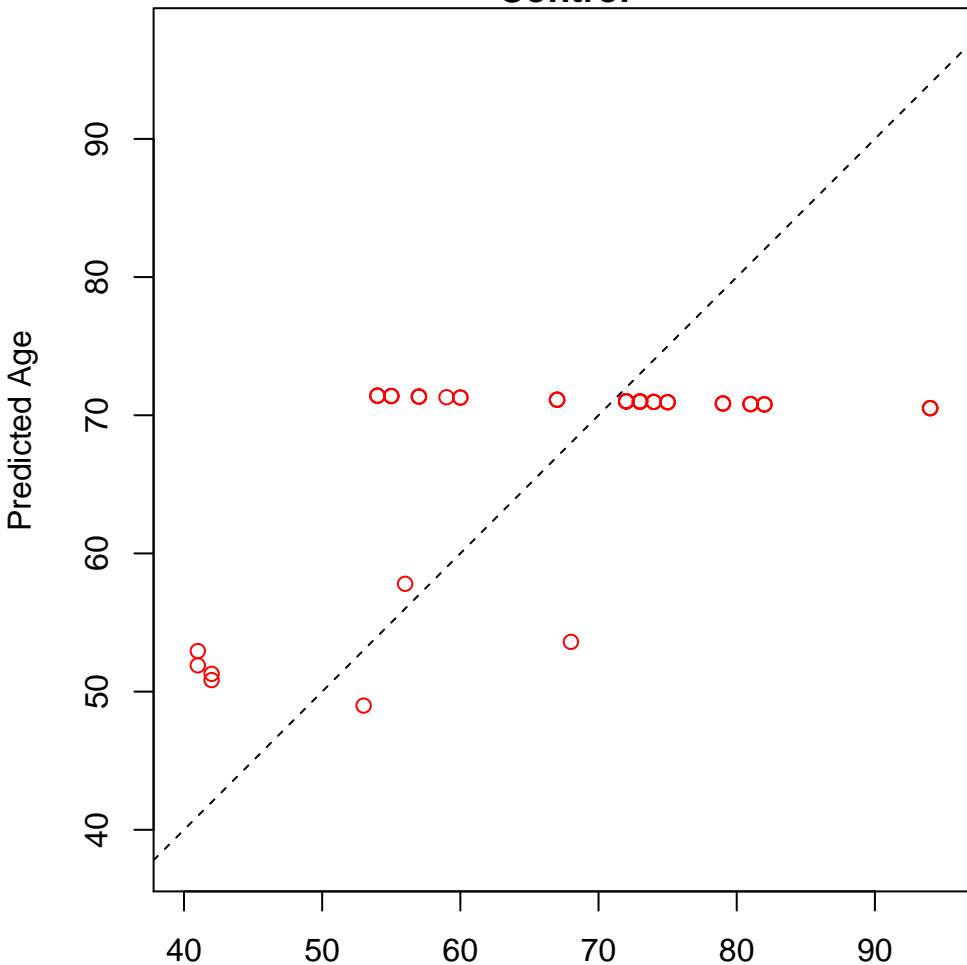
Test



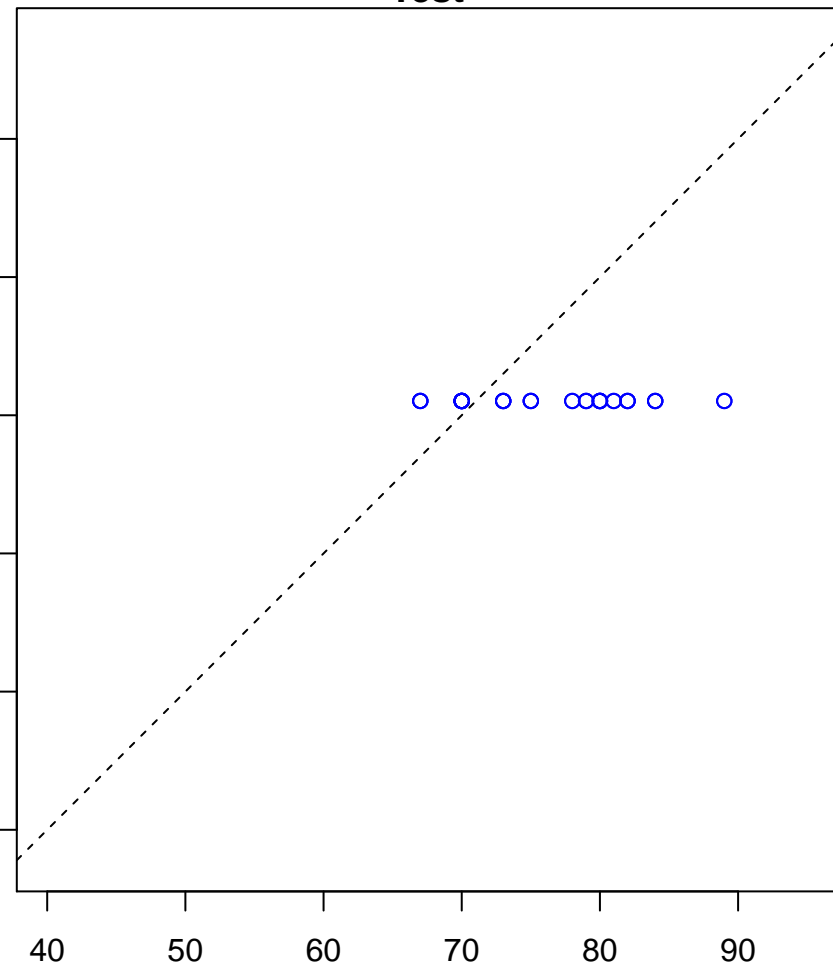
Actual Age

regulation of cell morphogenesis (Score: 0.795796)

Control



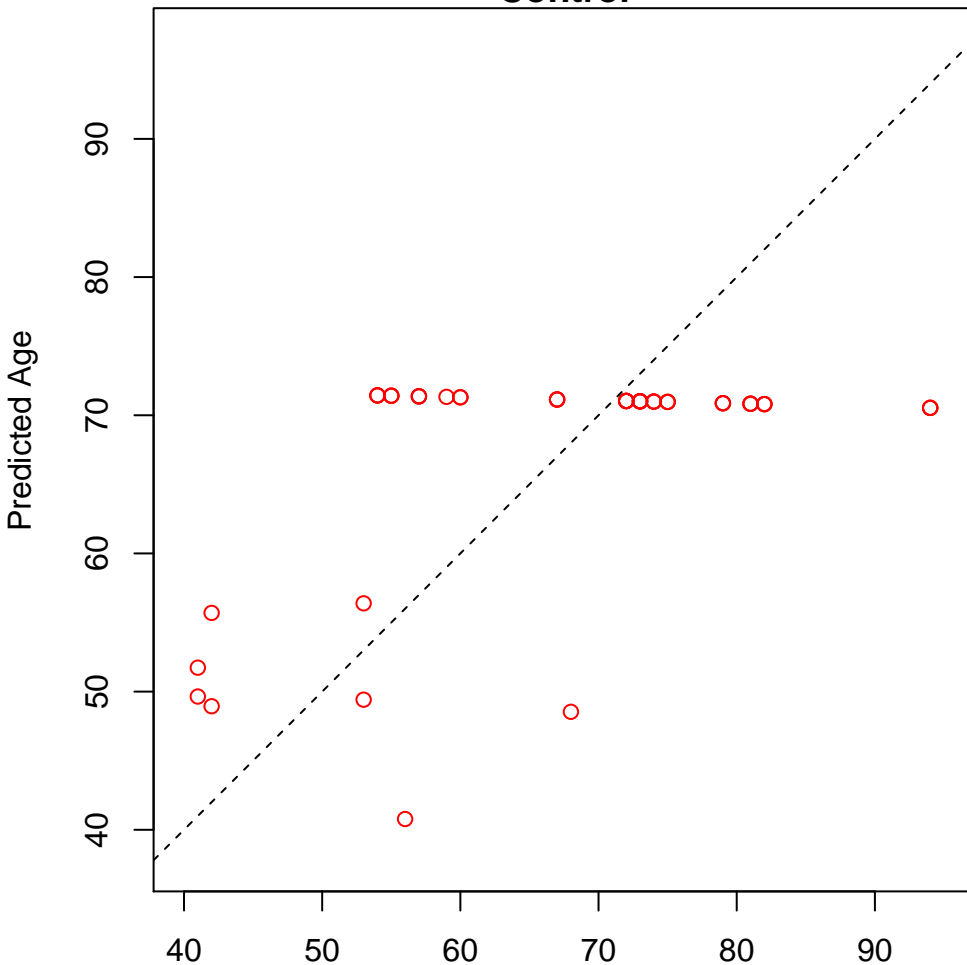
Test



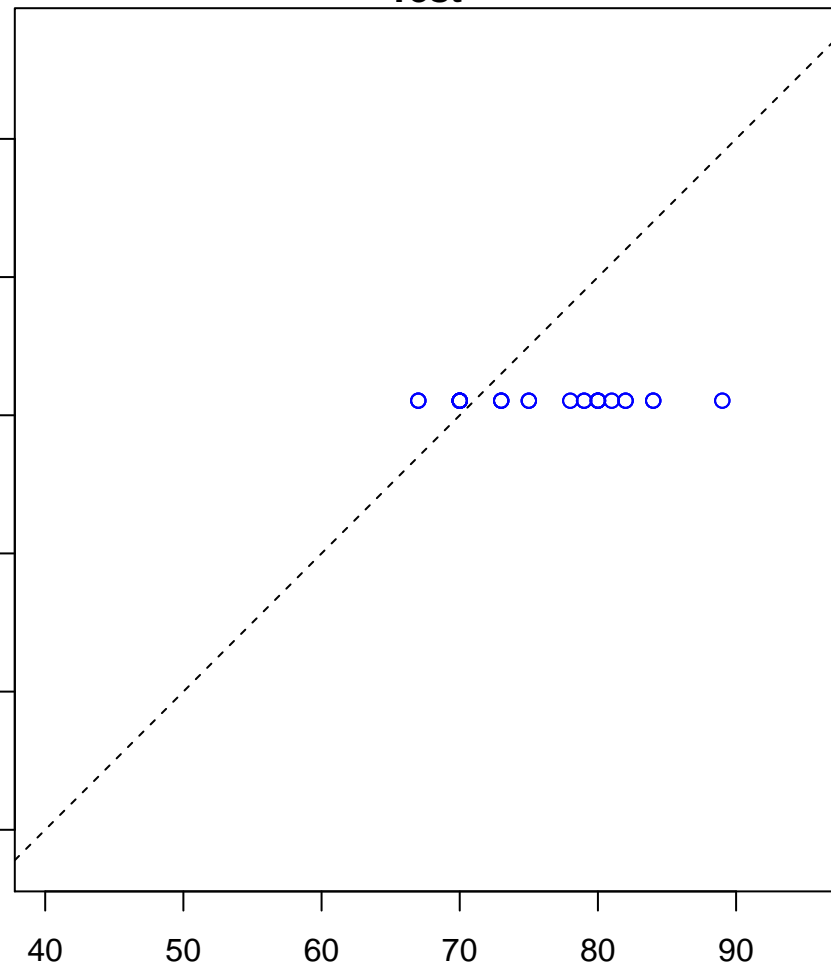
Actual Age

cellular response to abiotic stimulus (Score: 0.795780)

Control

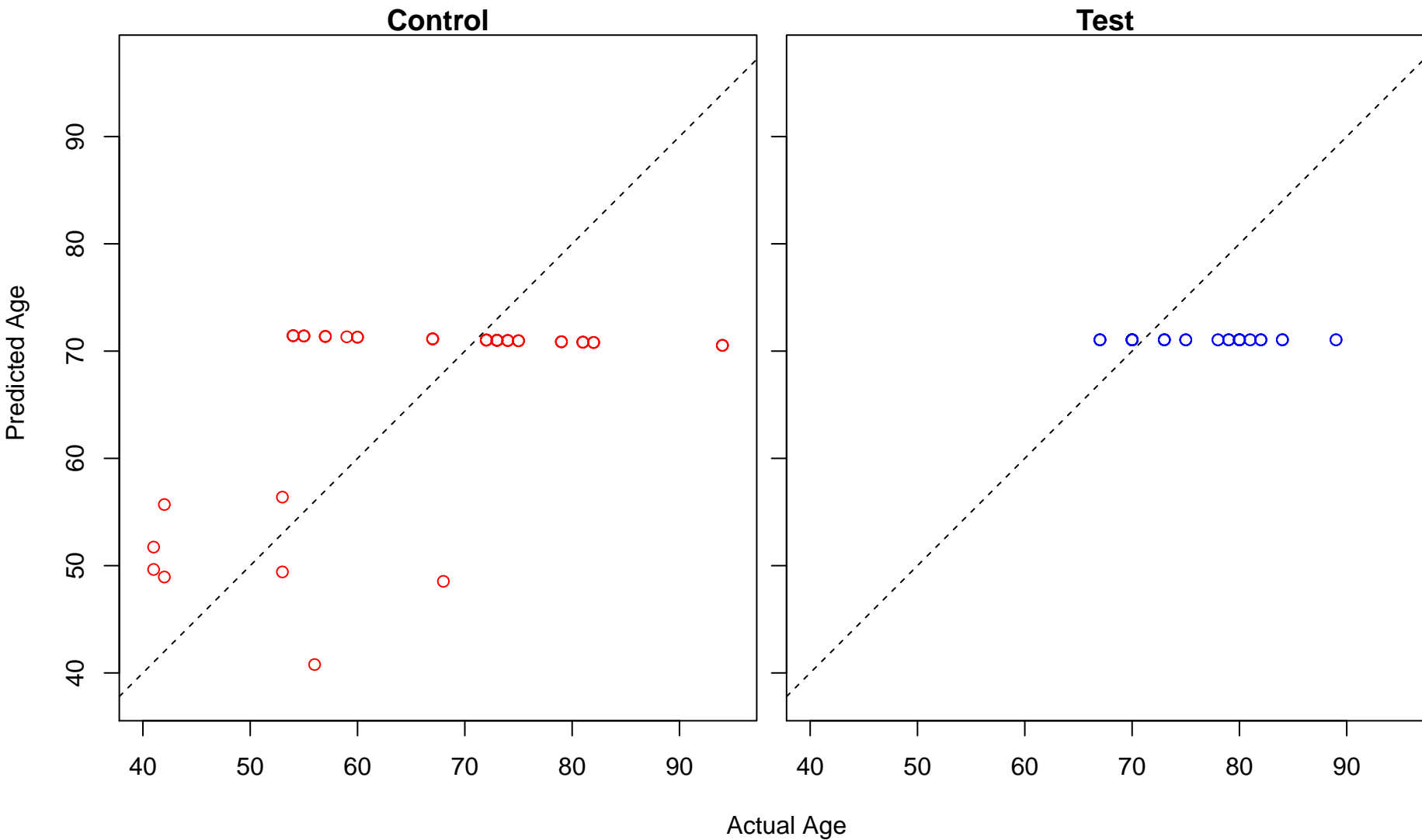


Test



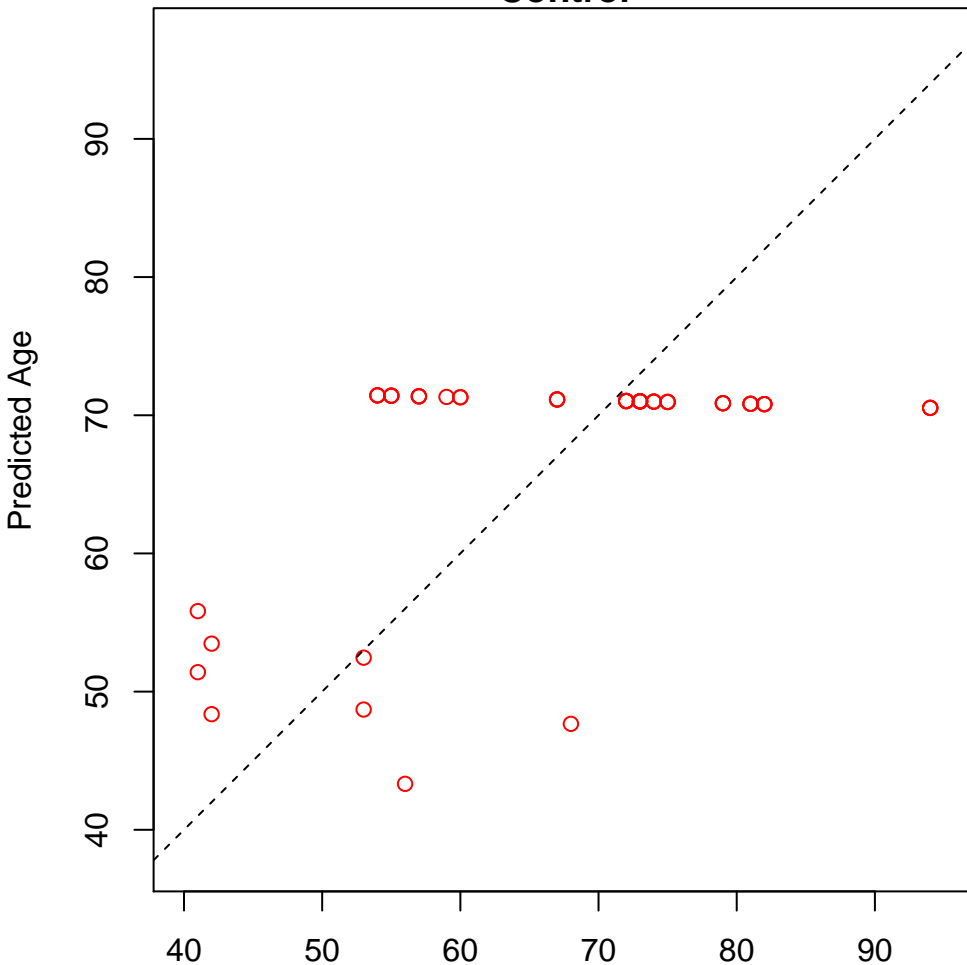
Actual Age

cellular response to environmental stimulus (Score: 0.795780)

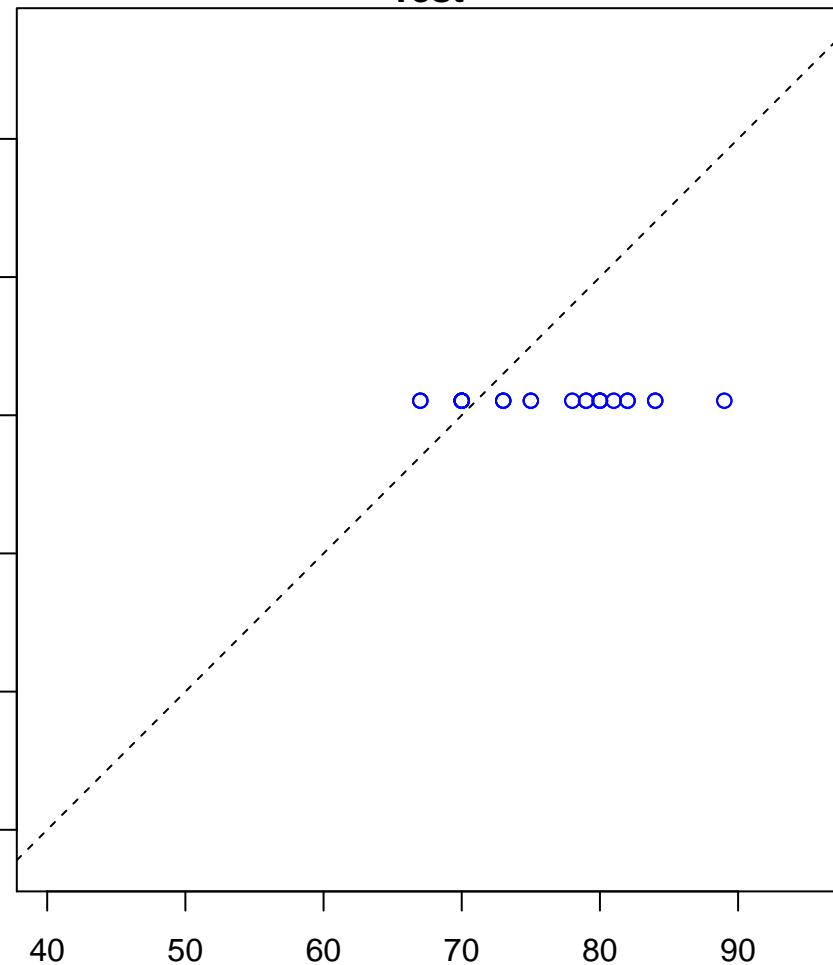


ribosomal large subunit biogenesis (Score: 0.795763)

Control

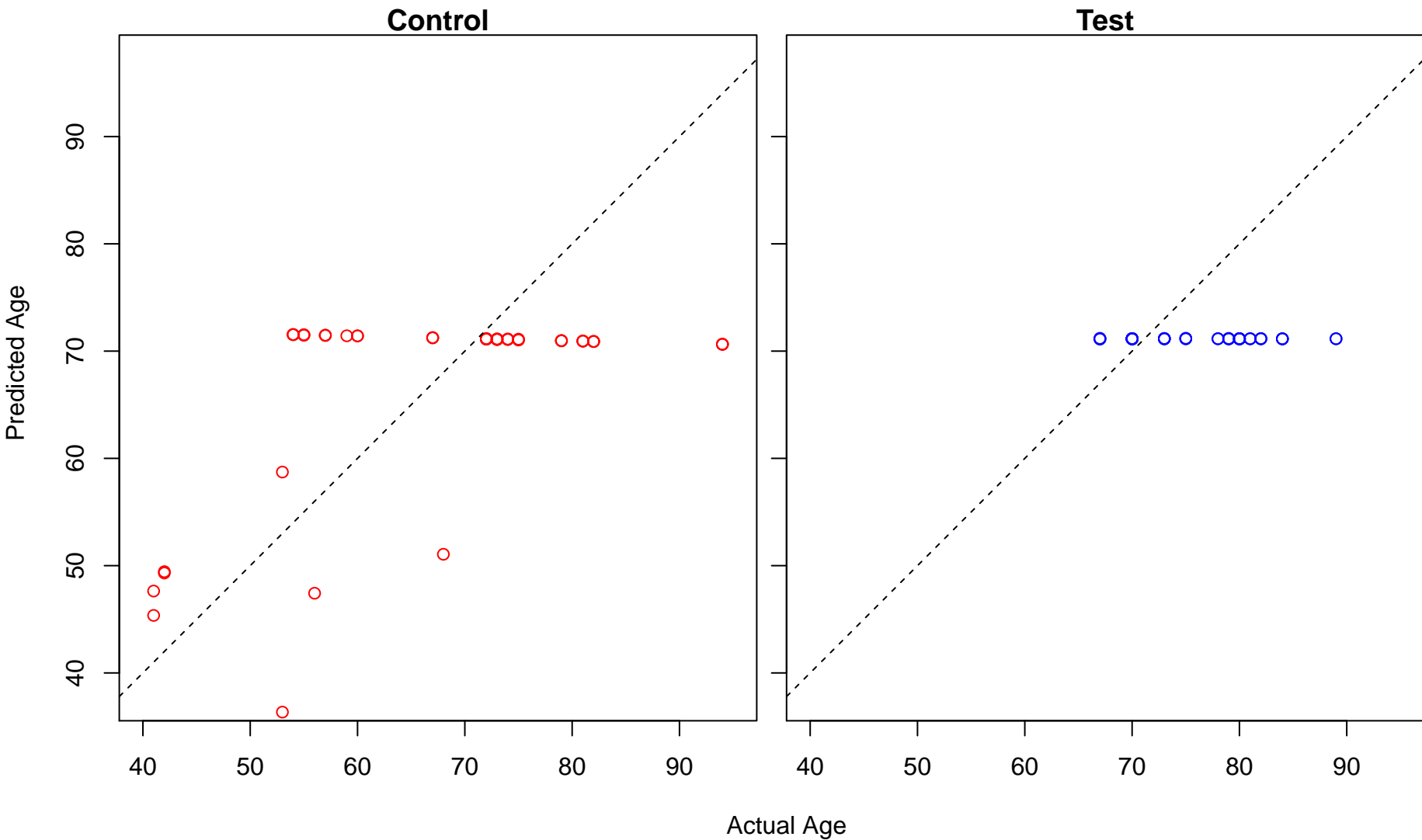


Test

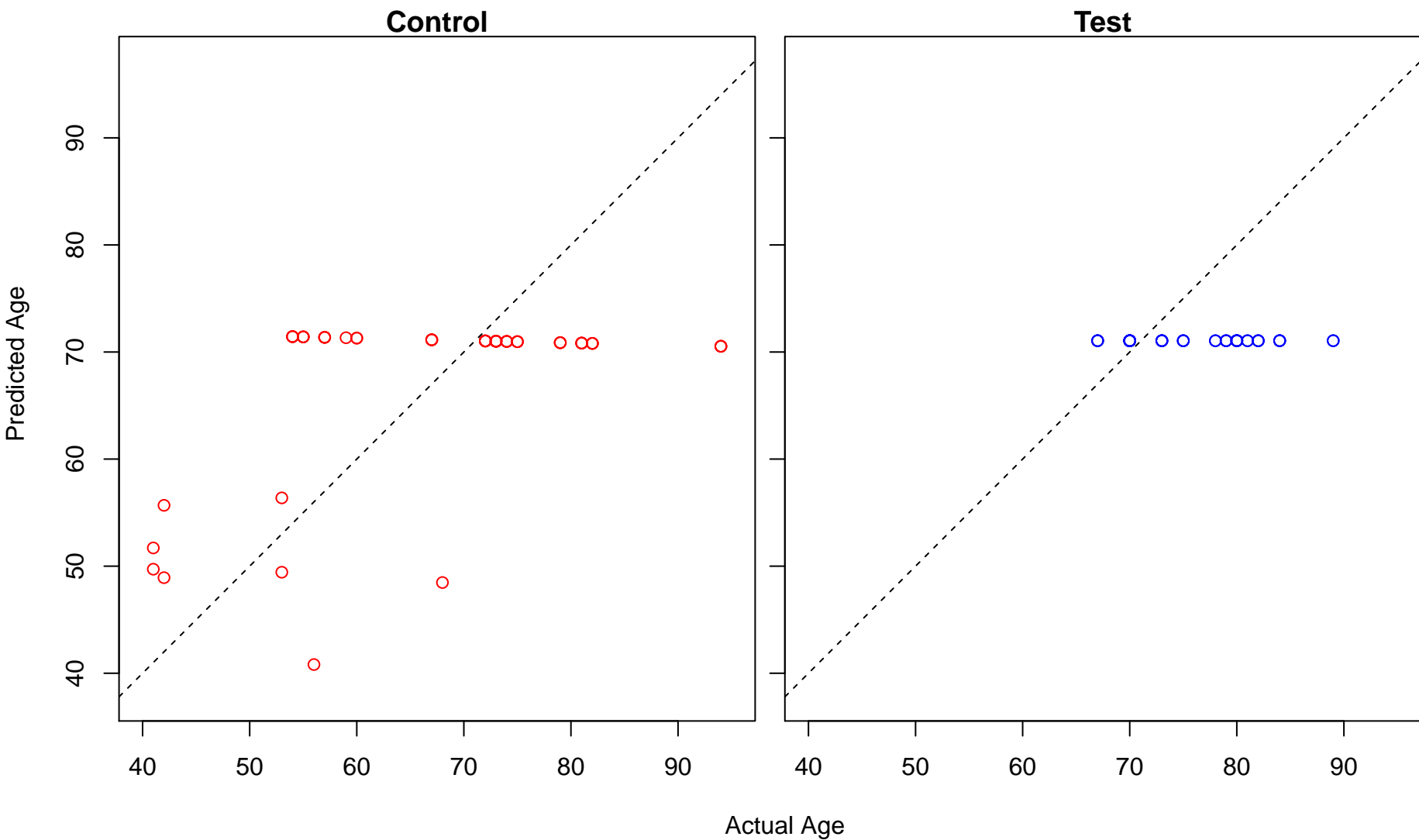


Actual Age

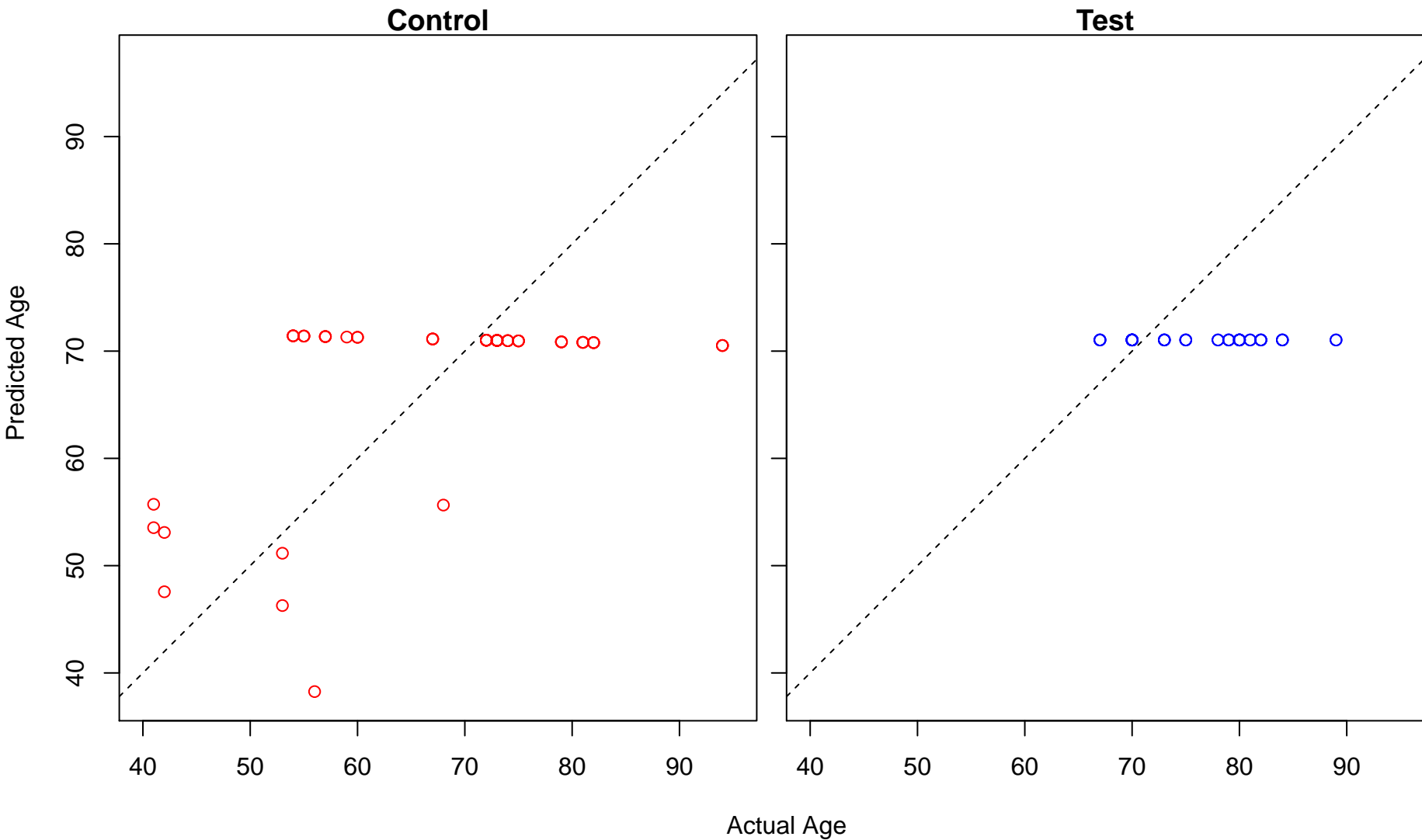
regulation of phagocytosis (Score: 0.795758)



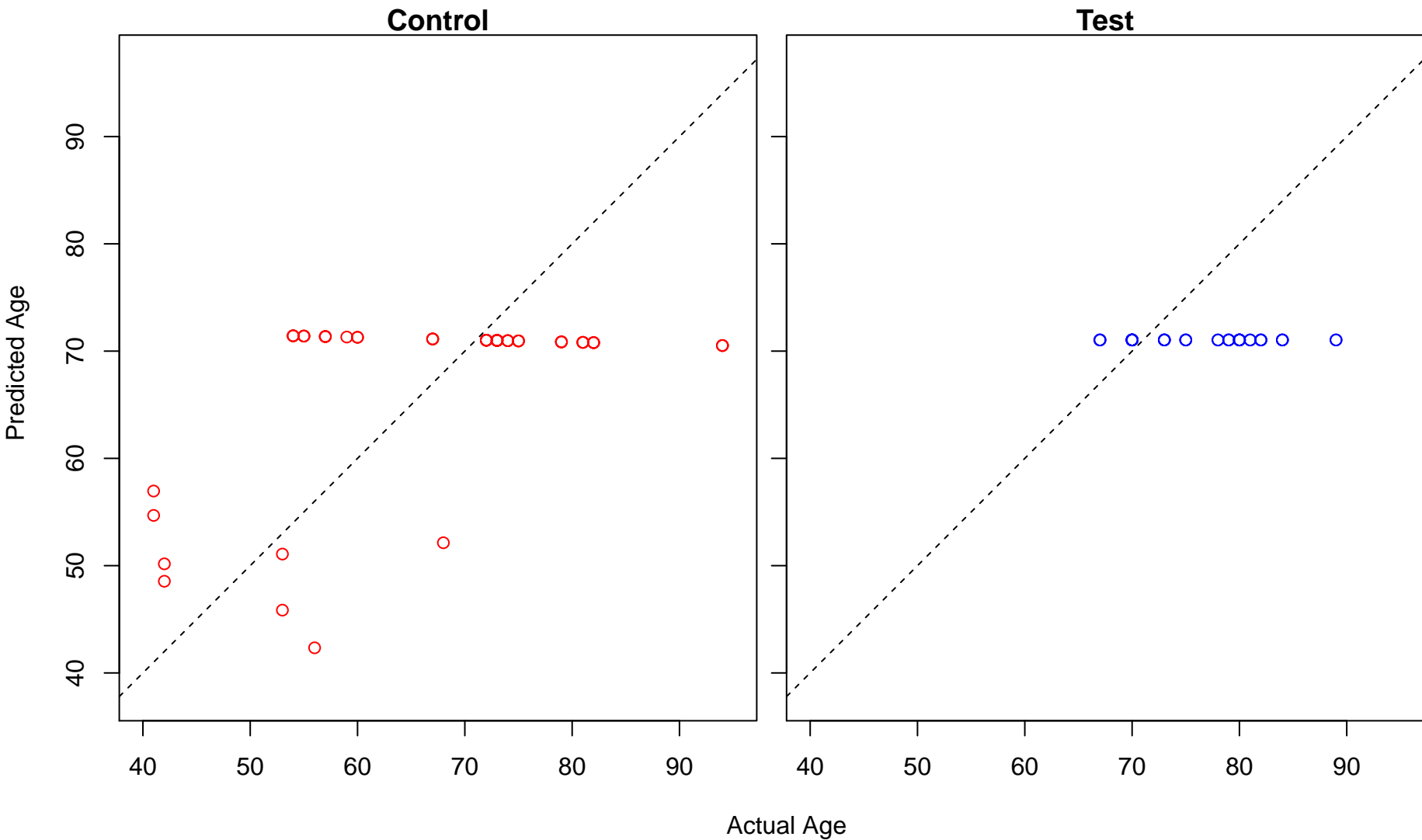
cellular response to radiation (Score: 0.795739)



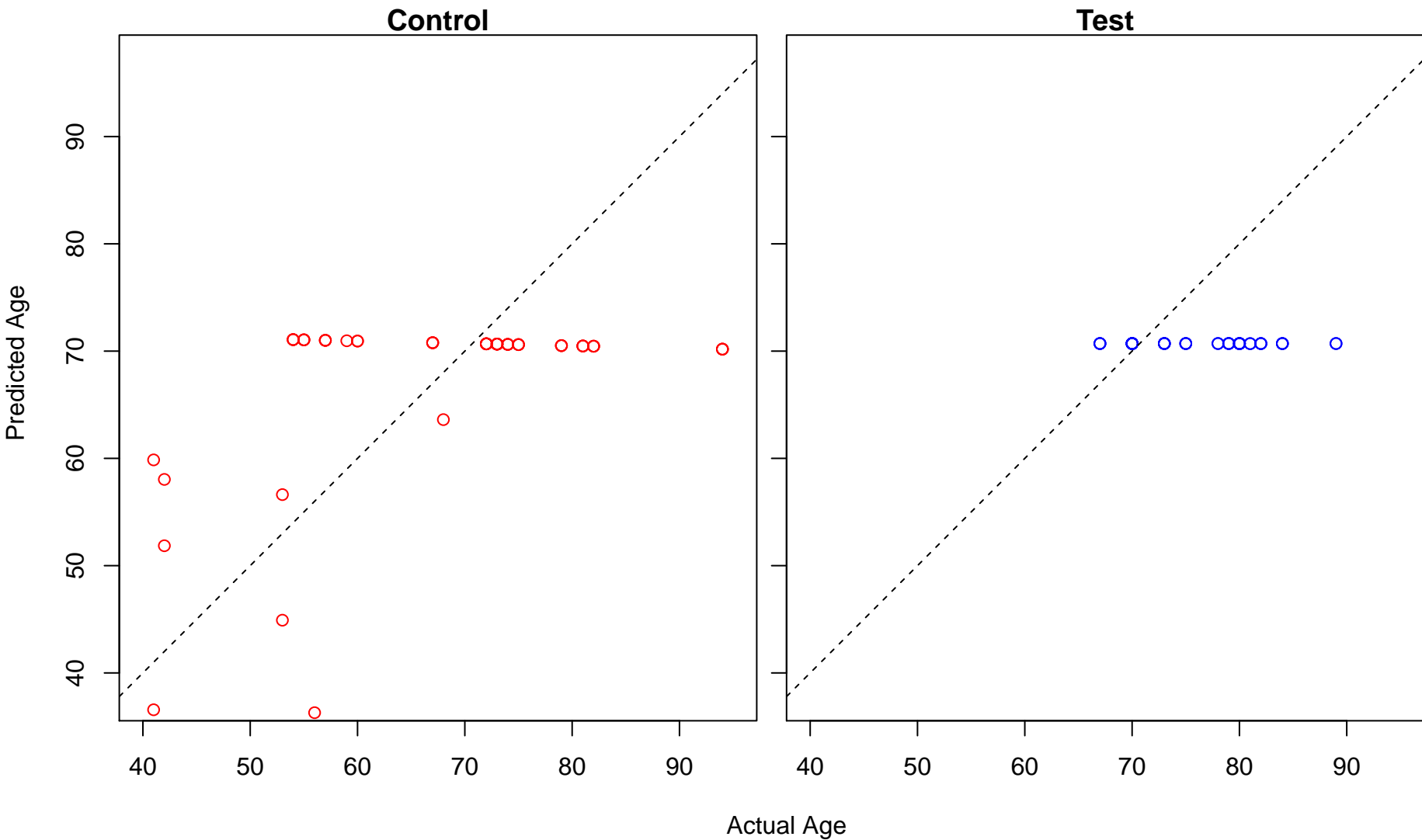
defense response (Score: 0.795733)



regulation of proteasomal protein catabolic process (Score: 0.795721)

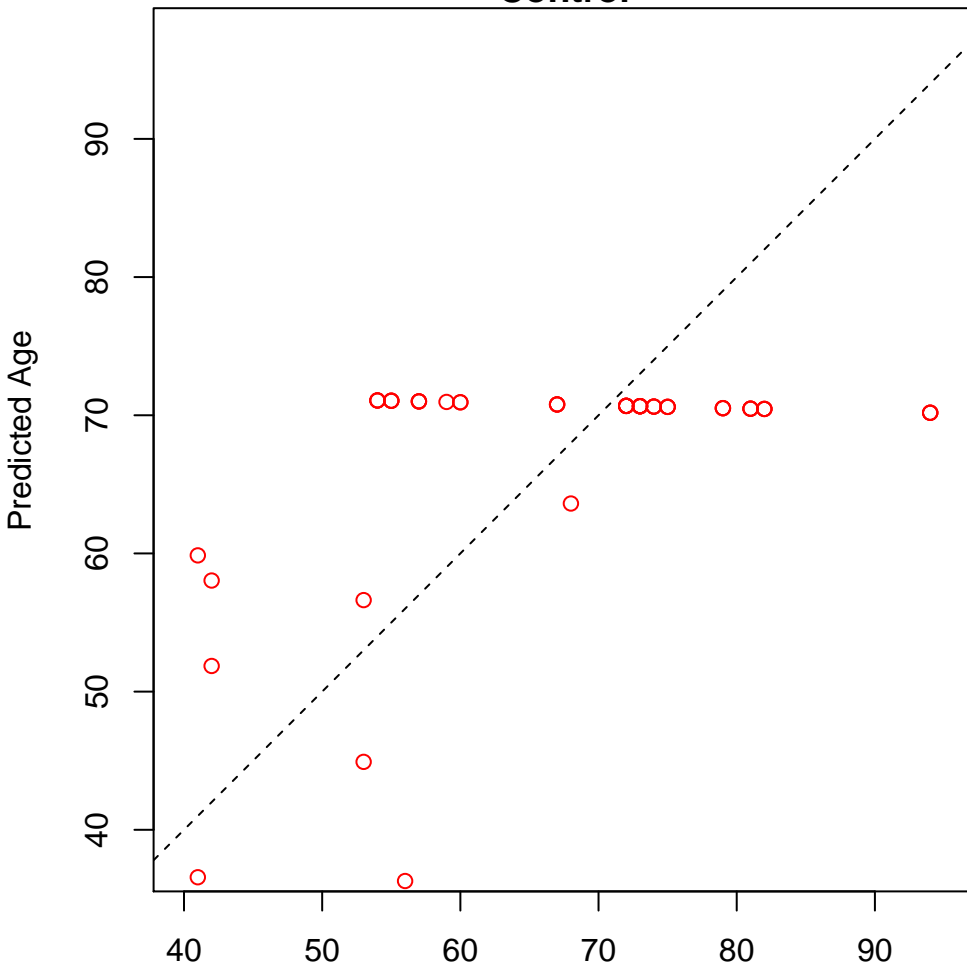


cytokine production (Score: 0.795714)

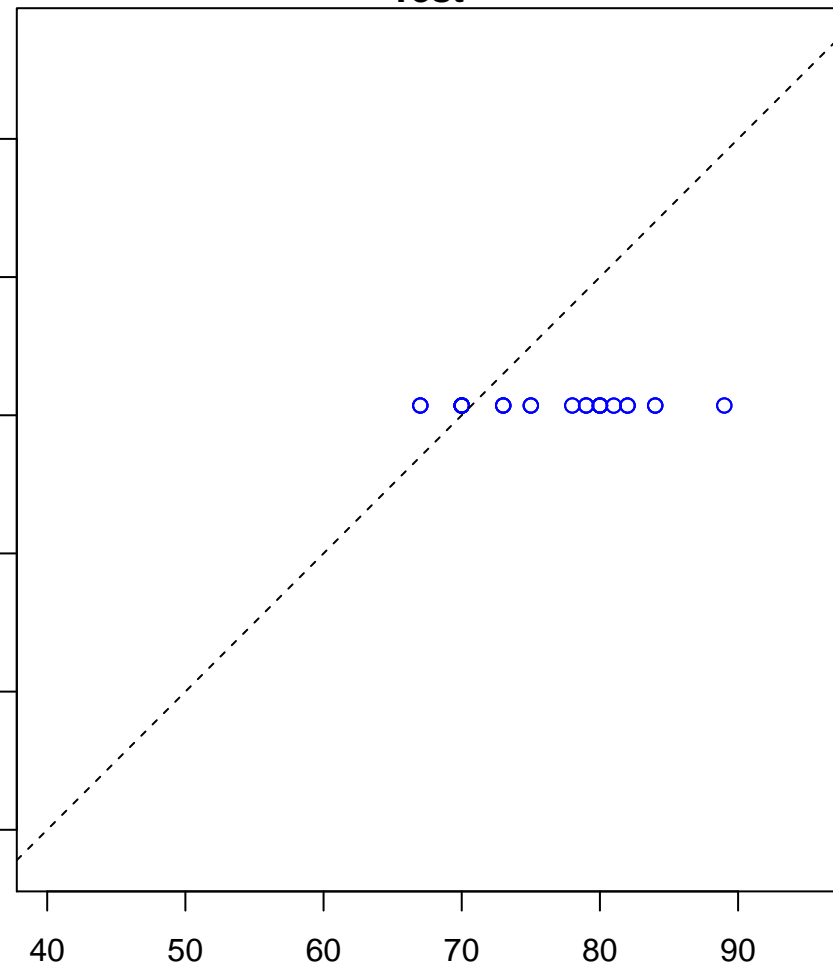


tumor necrosis factor production (Score: 0.795714)

Control

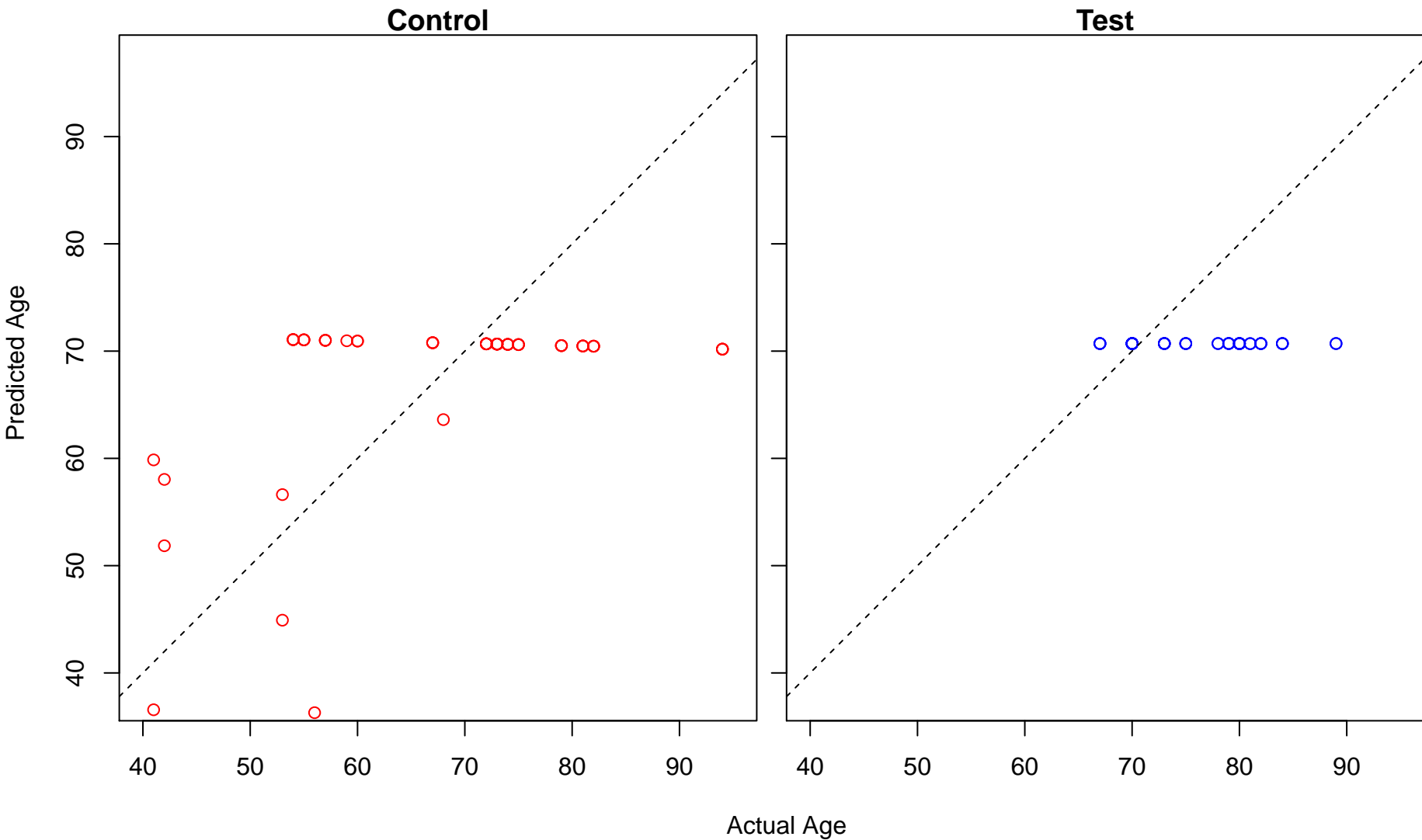


Test

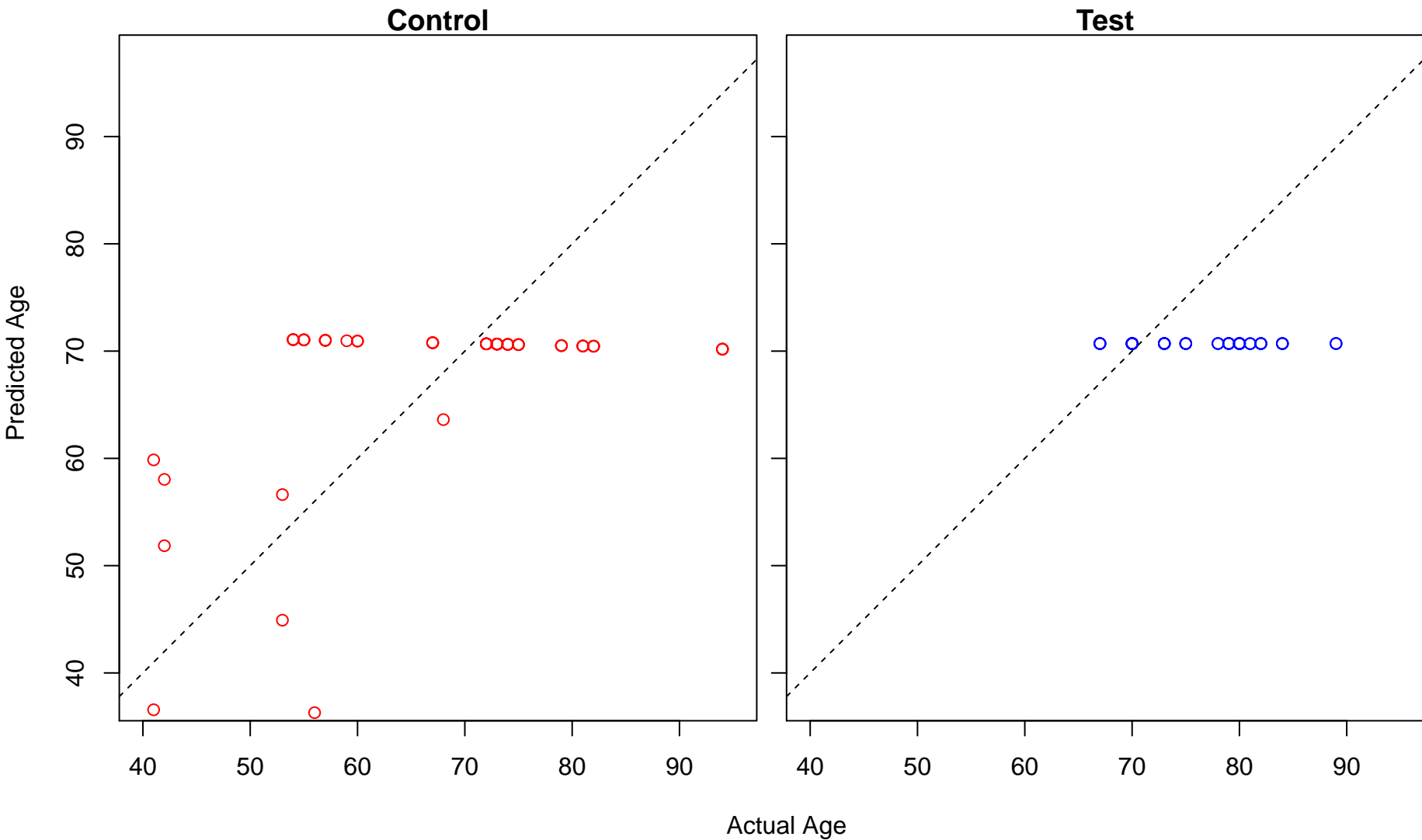


Actual Age

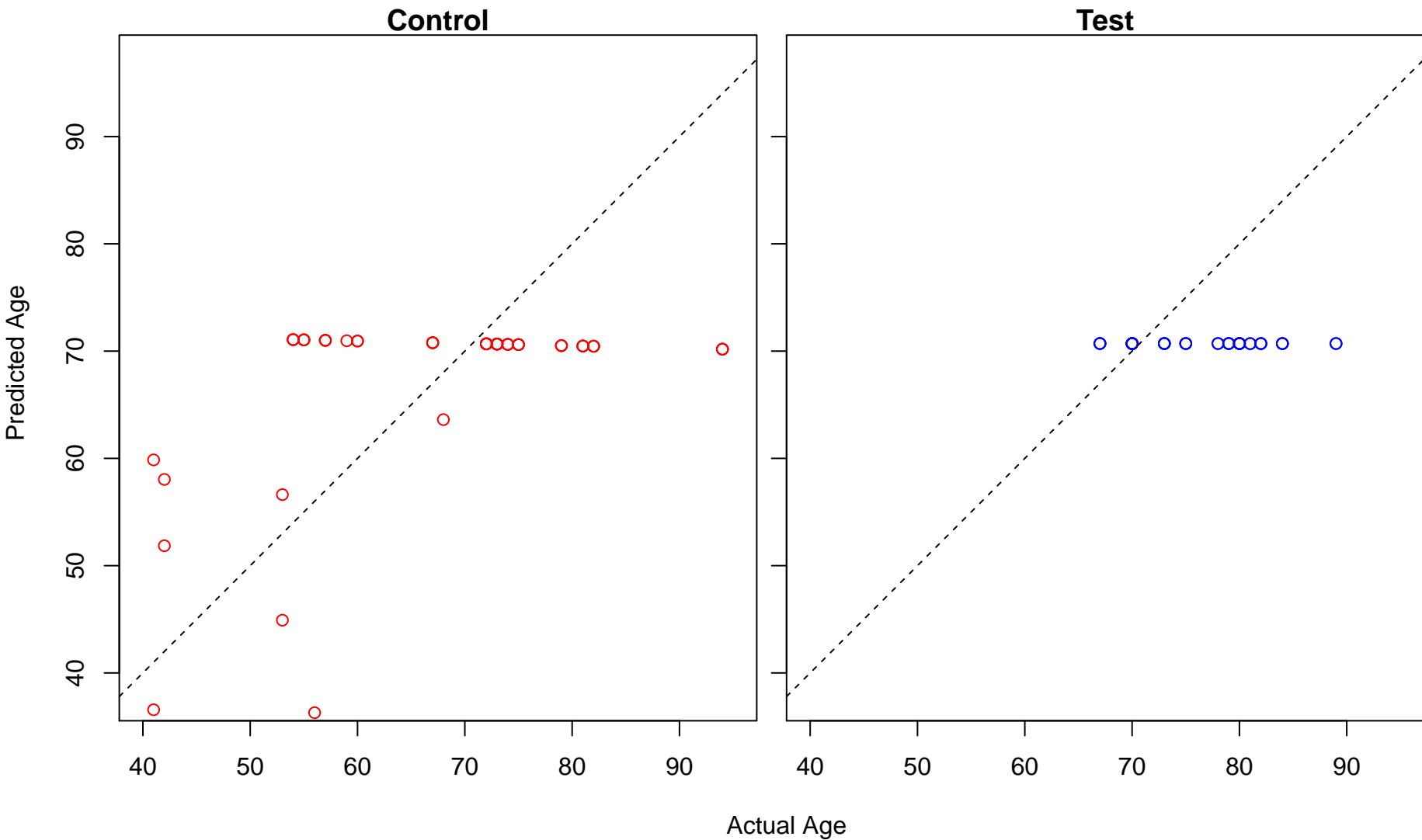
regulation of JNK cascade (Score: 0.795714)



positive regulation of JNK cascade (Score: 0.795714)

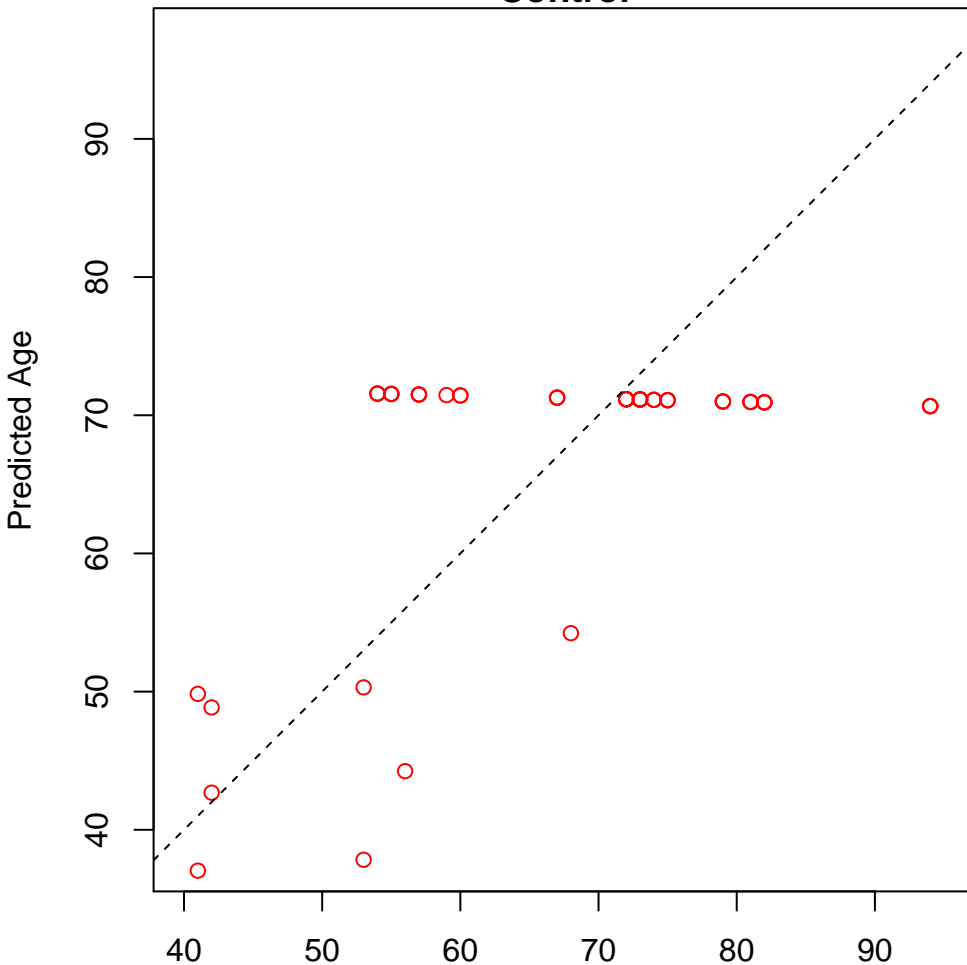


tumor necrosis factor superfamily cytokine production (Score: 0.795714)

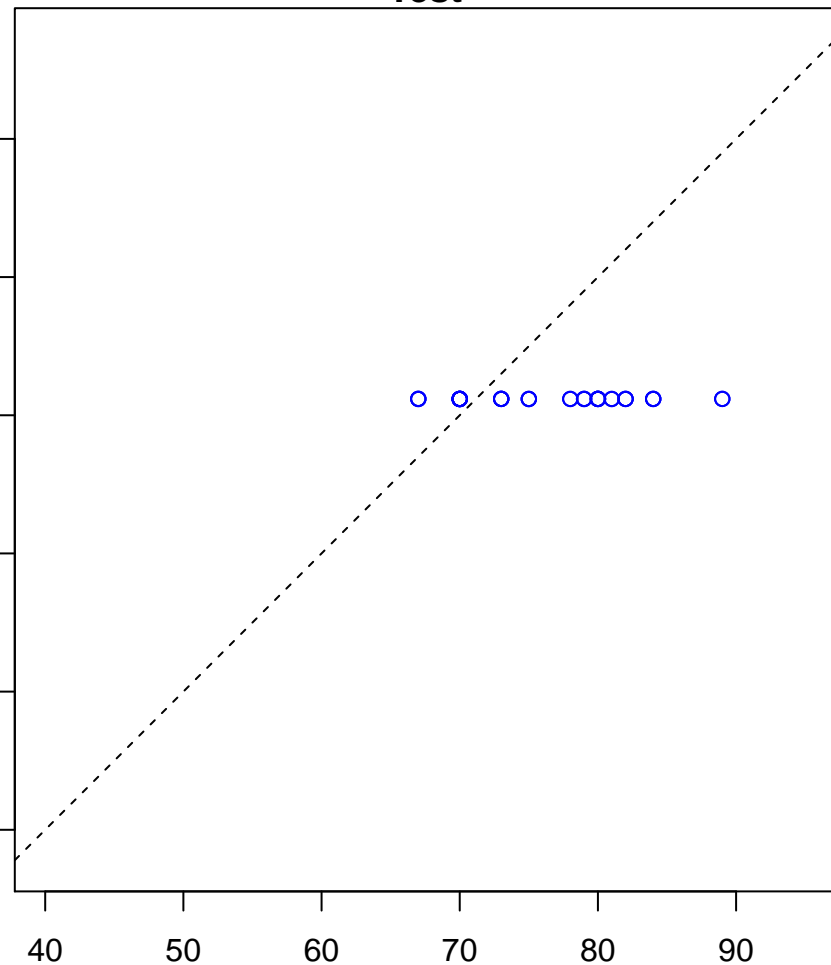


cellular component organization (Score: 0.795710)

Control

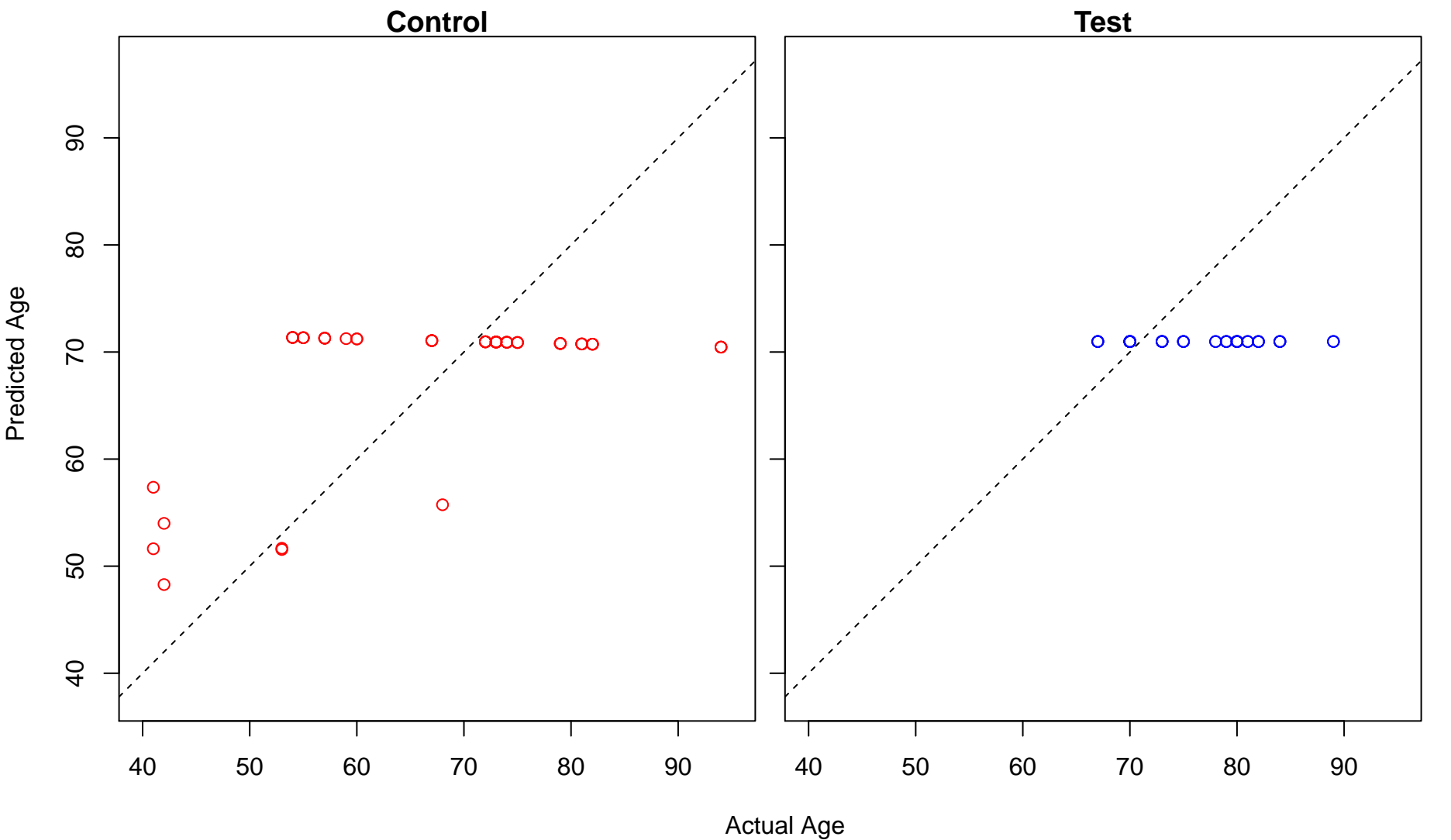


Test



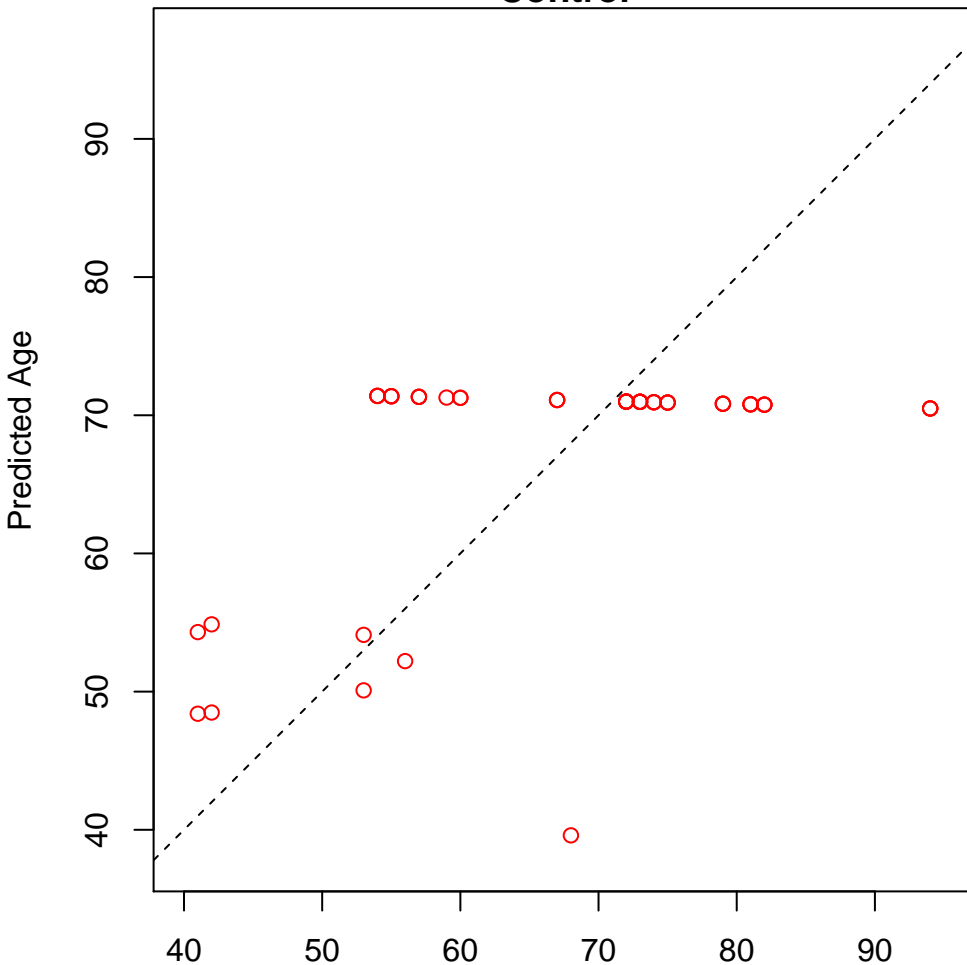
Actual Age

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

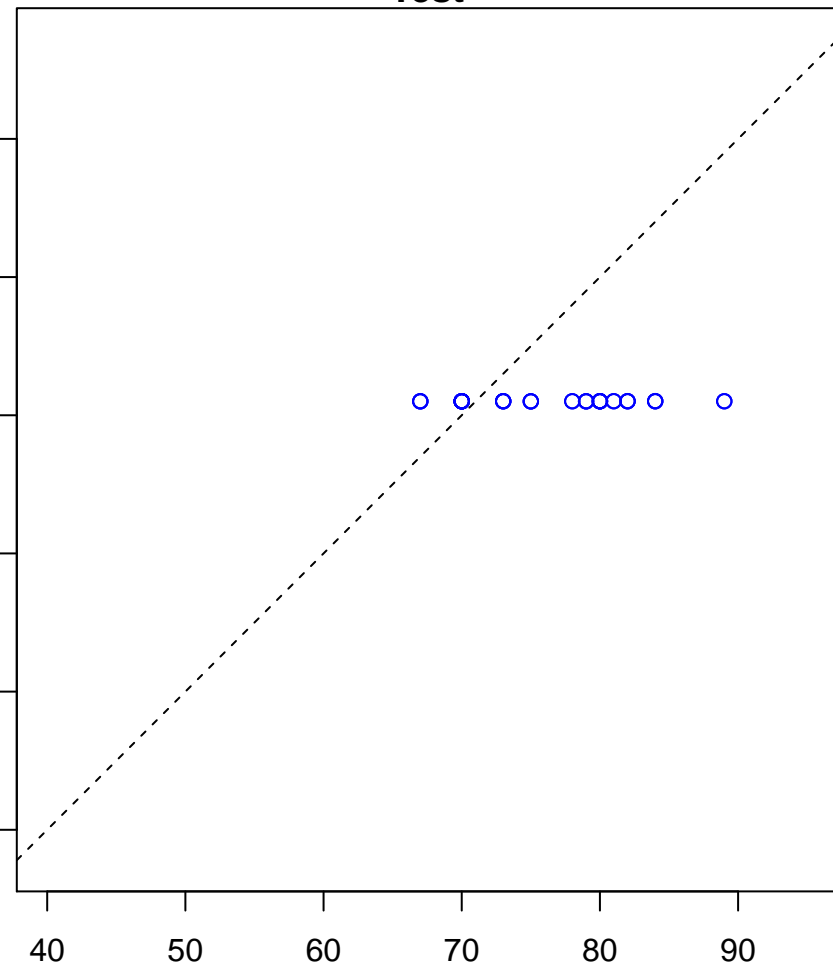


3'-UTR-mediated mRNA stabilization (Score: 0.795640)

Control

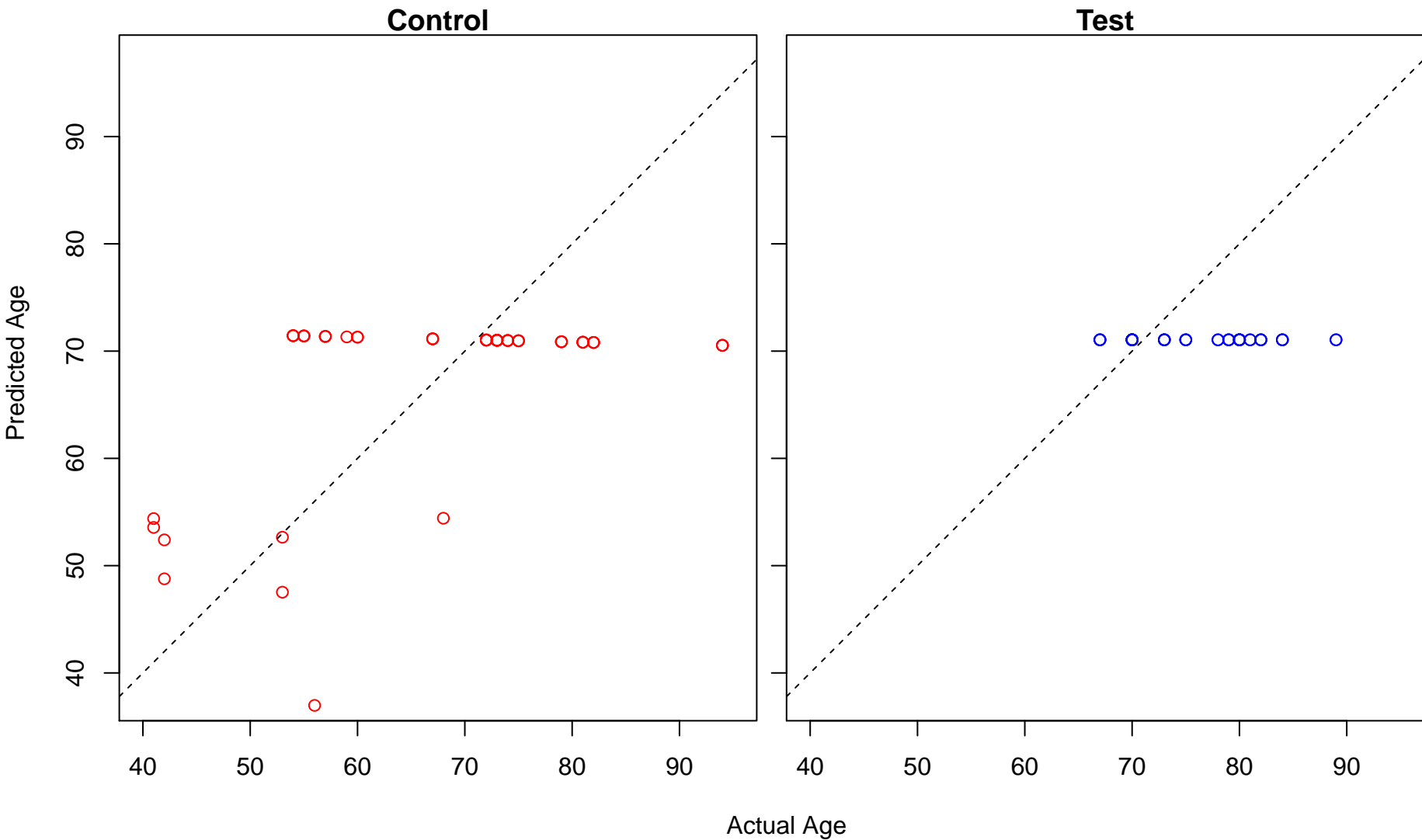


Test

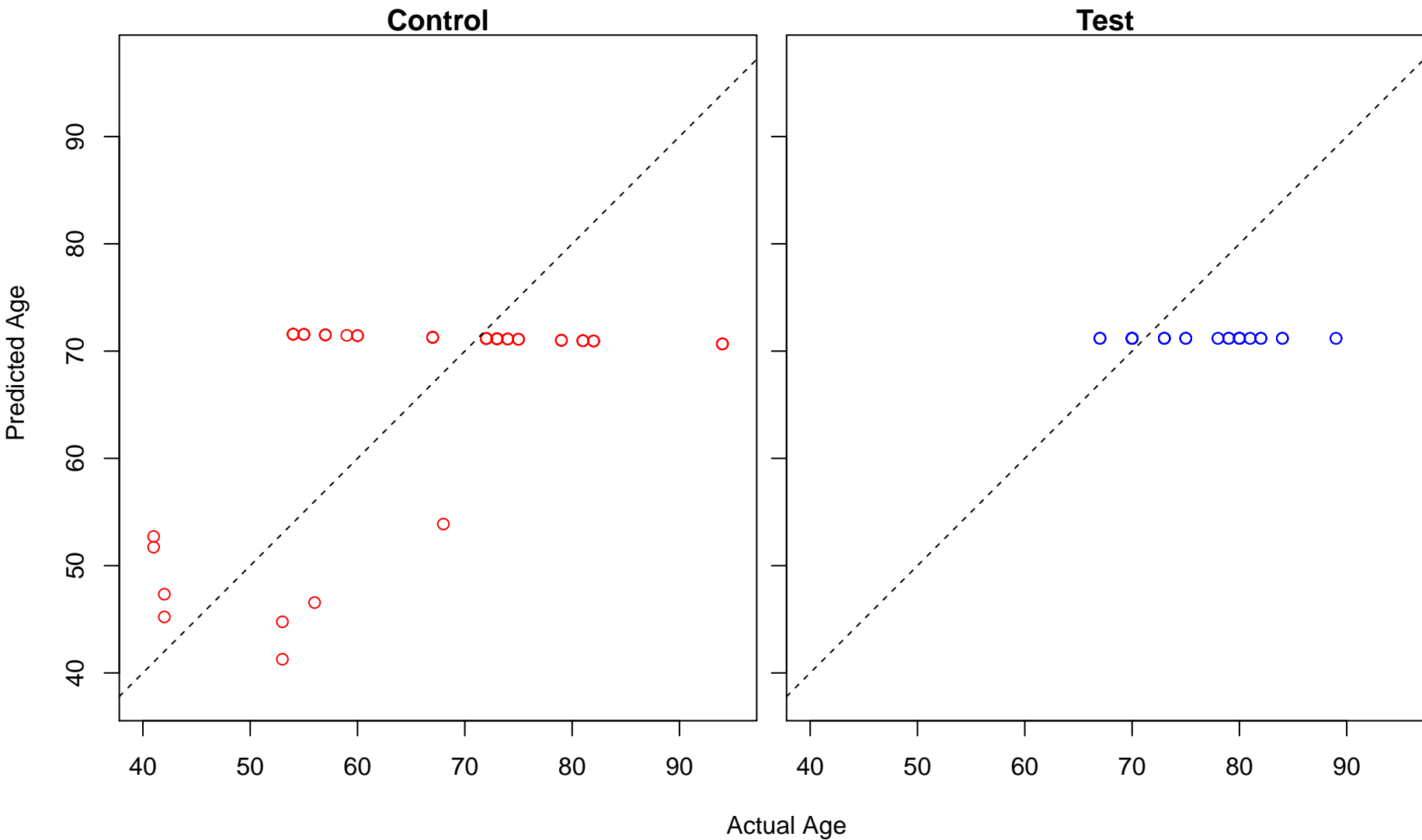


Actual Age

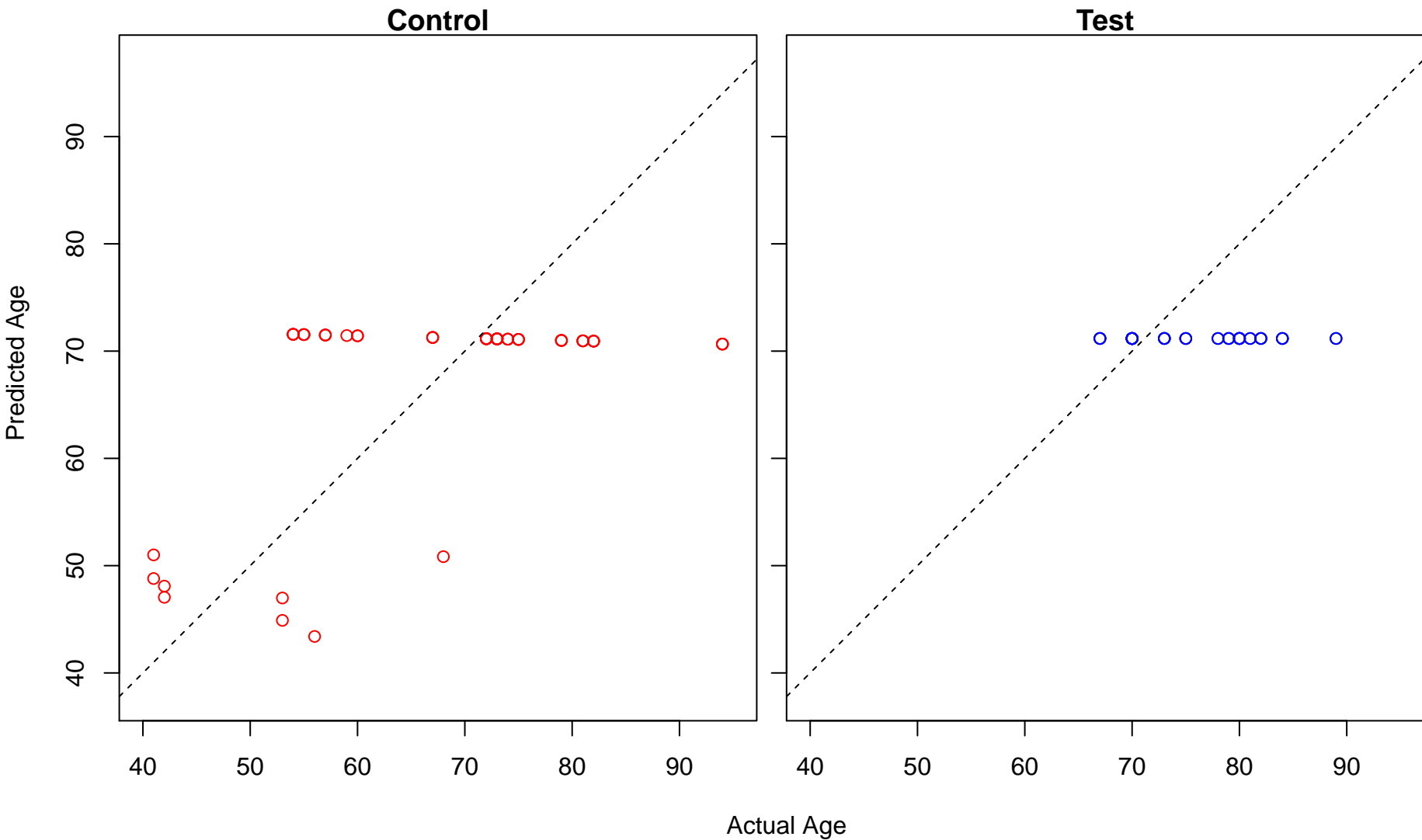
negative regulation of cellular biosynthetic process (Score: 0.795636)



apoptotic process (Score: 0.795583)

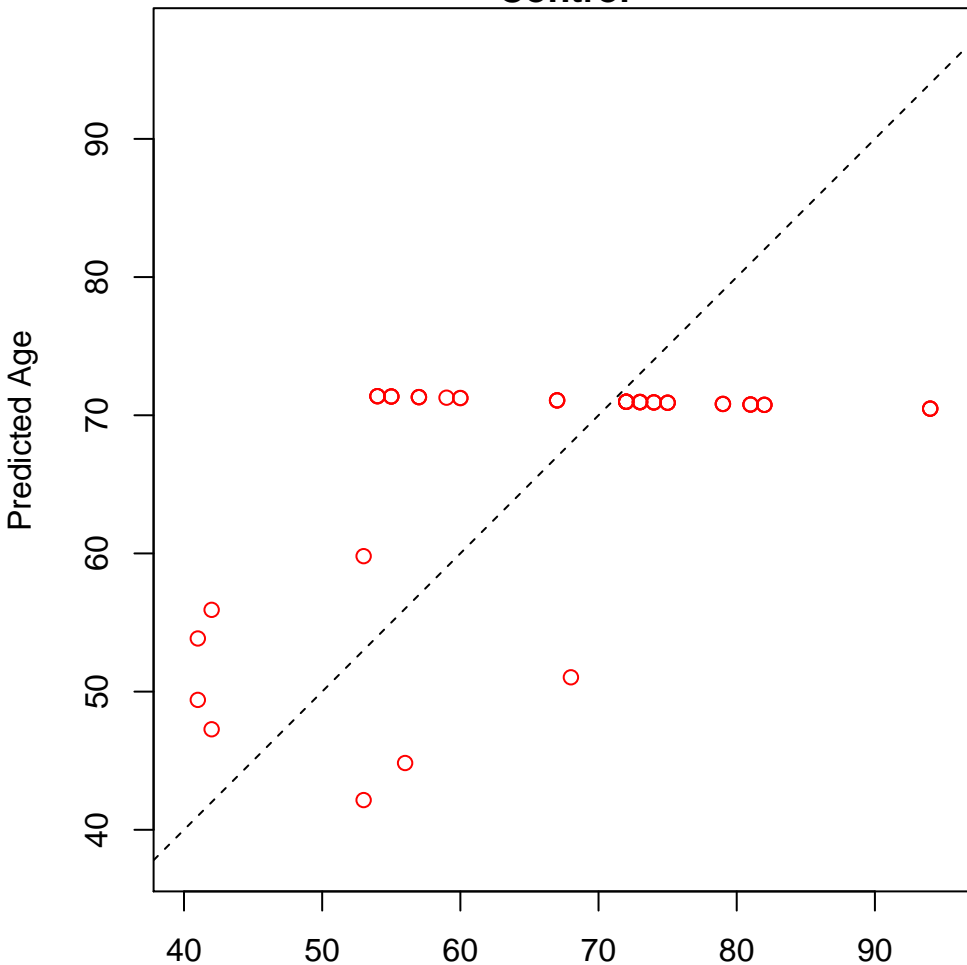


protein localization (Score: 0.795570)

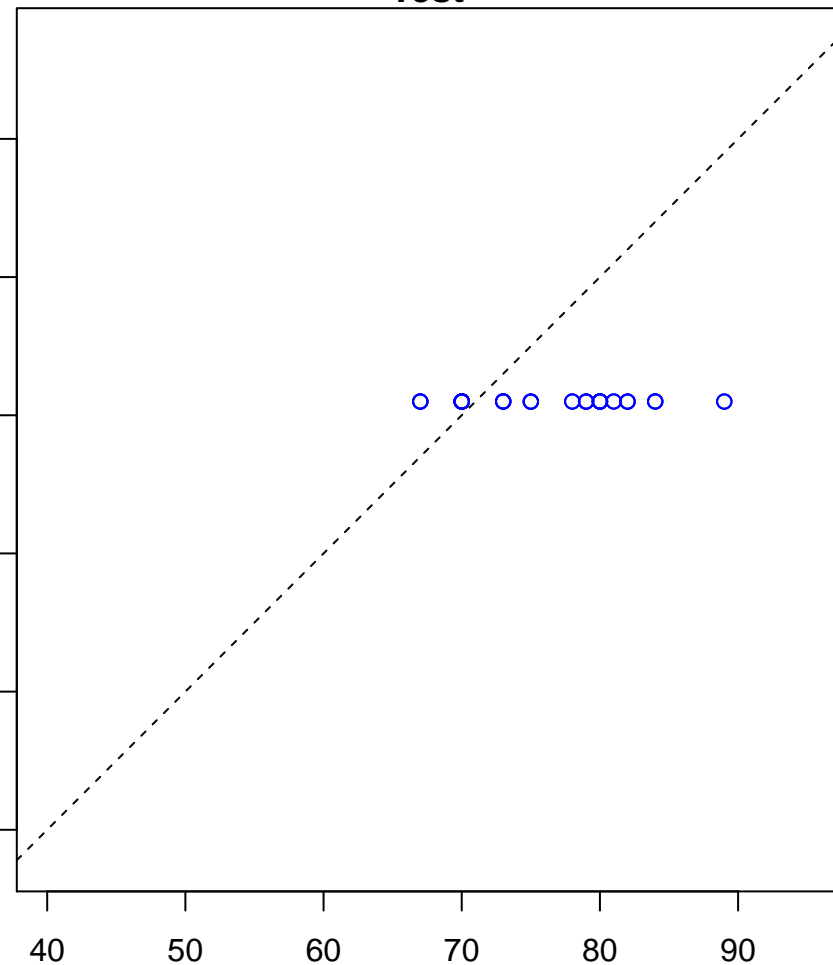


response to unfolded protein (Score: 0.795553)

Control



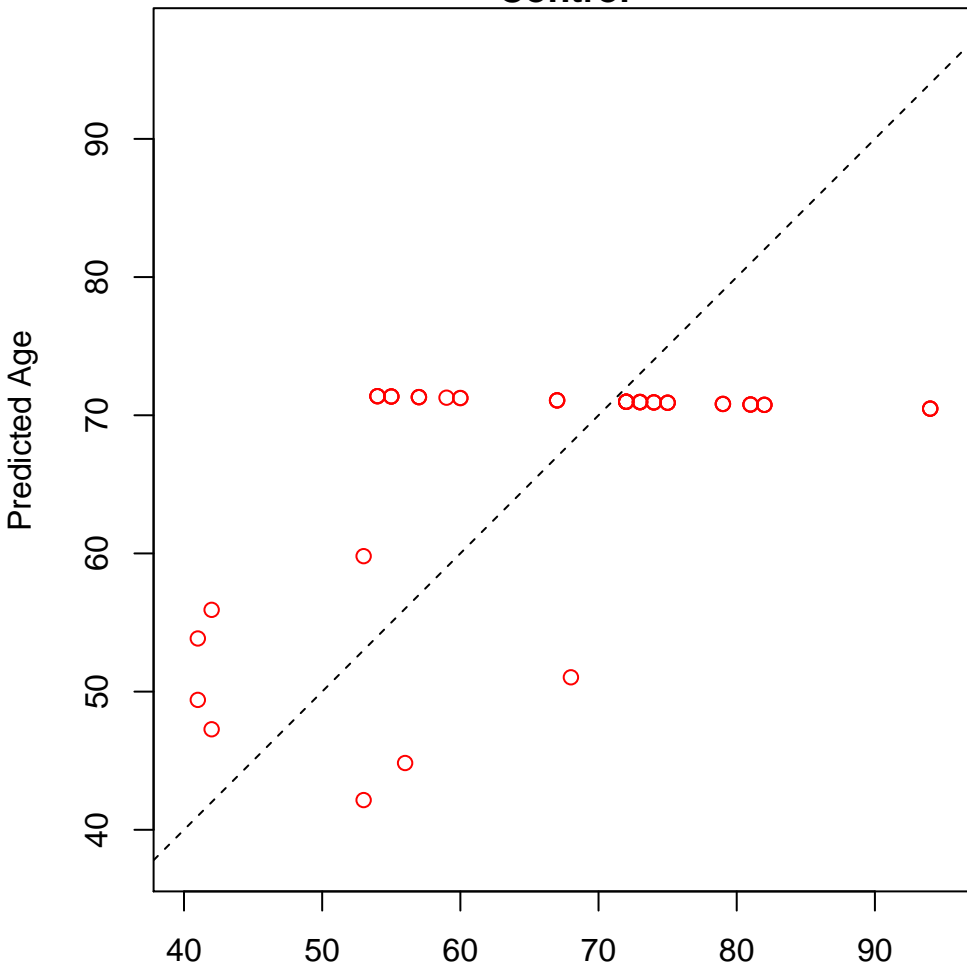
Test



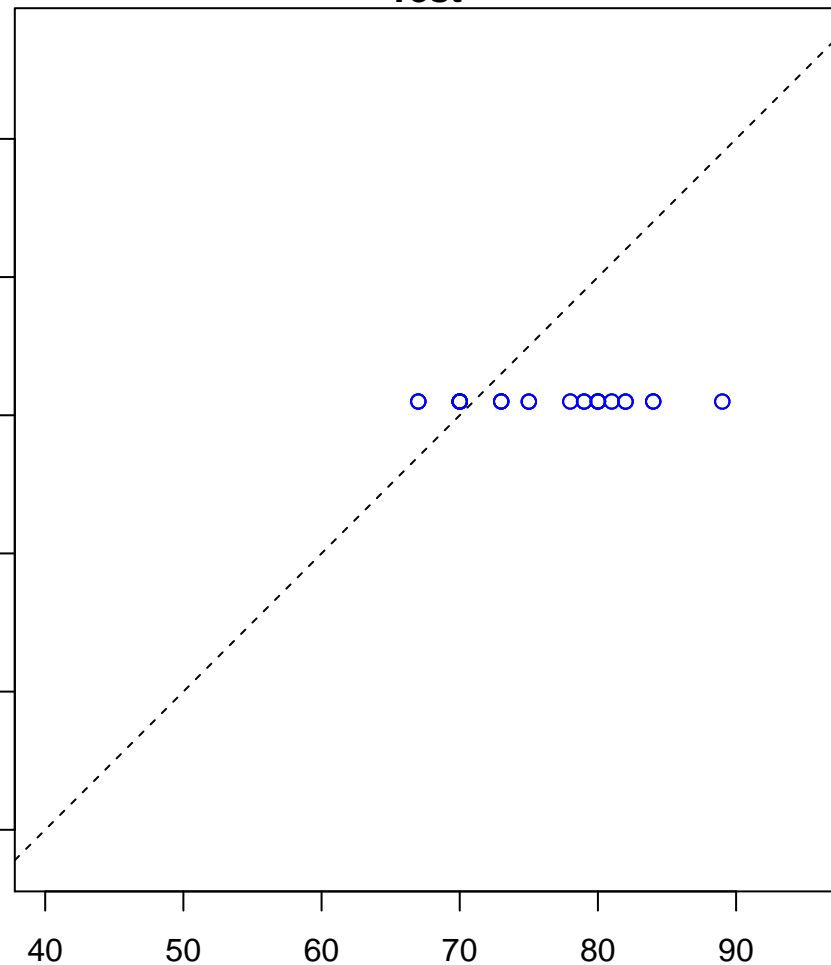
Actual Age

response to topologically incorrect protein (Score: 0.795553)

Control

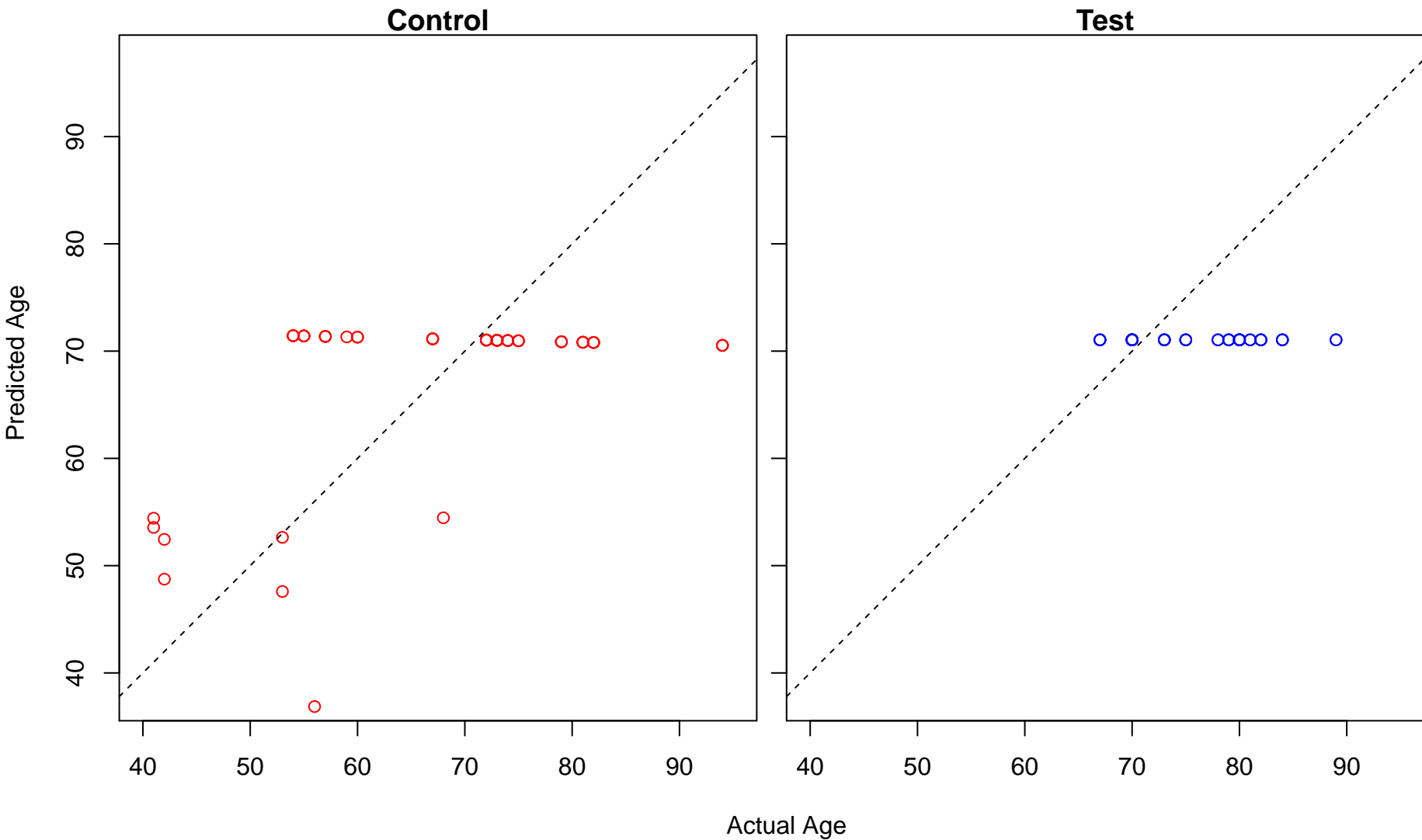


Test



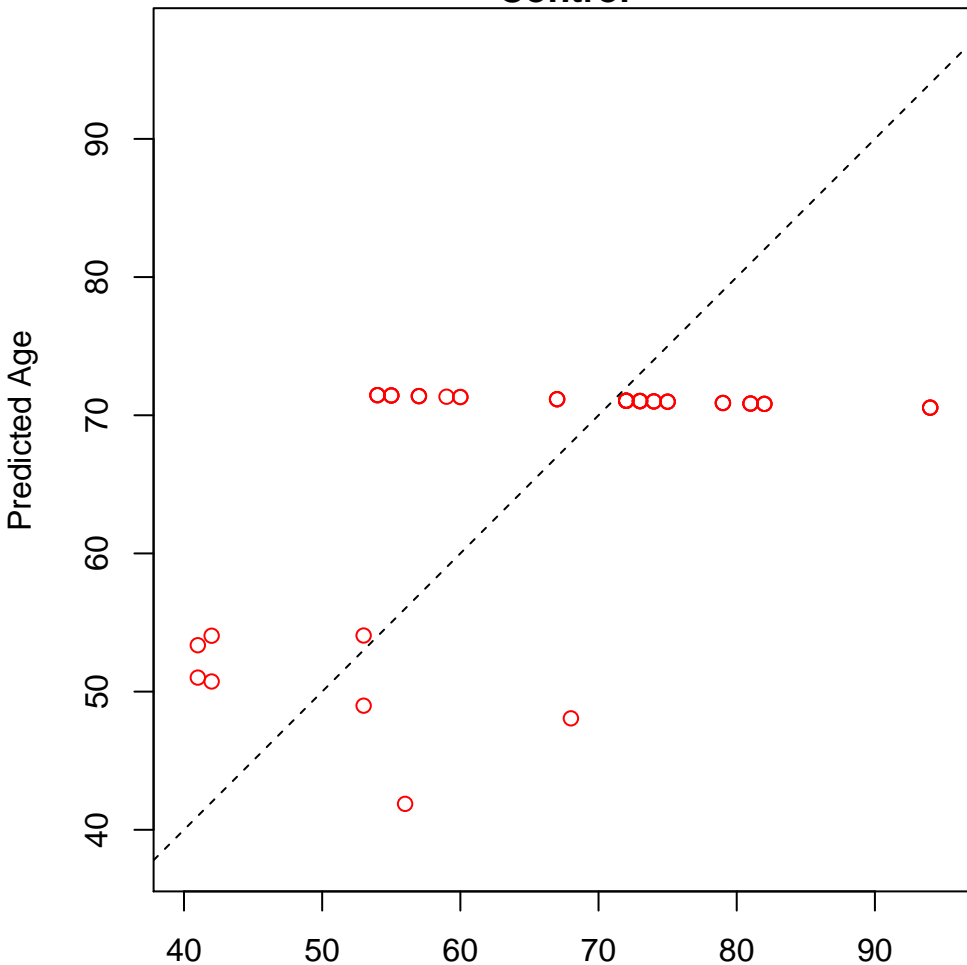
Actual Age

negative regulation of macromolecule biosynthetic process (Score: 0.795545)

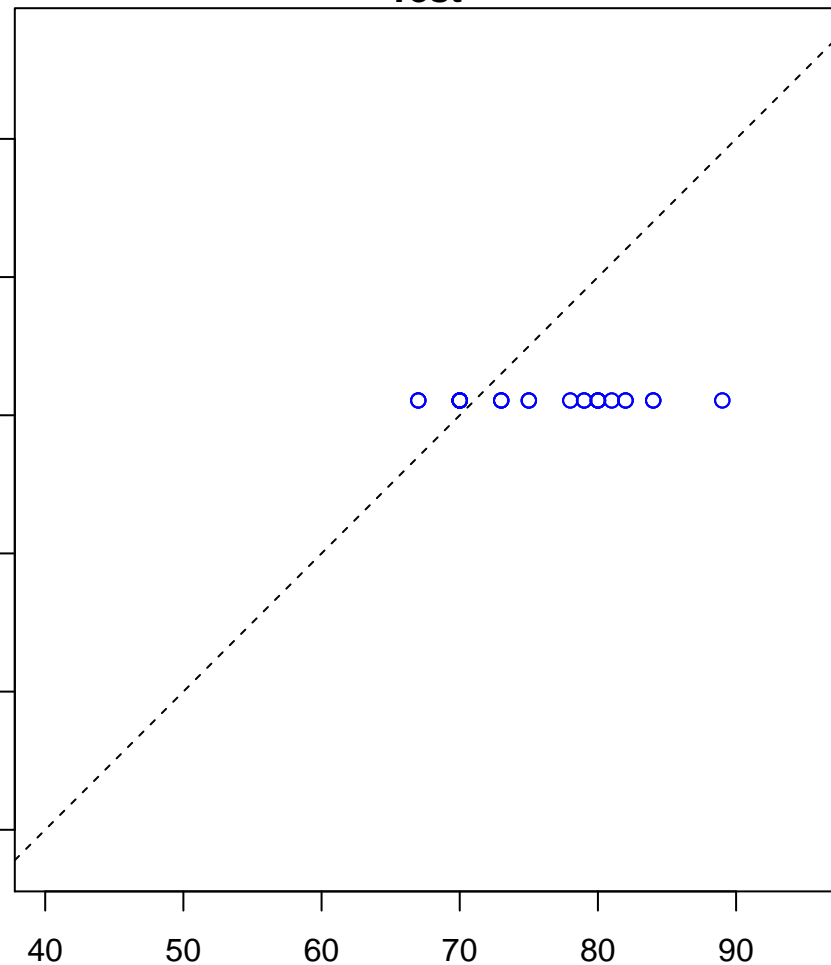


regulation of leukocyte migration (Score: 0.795473)

Control

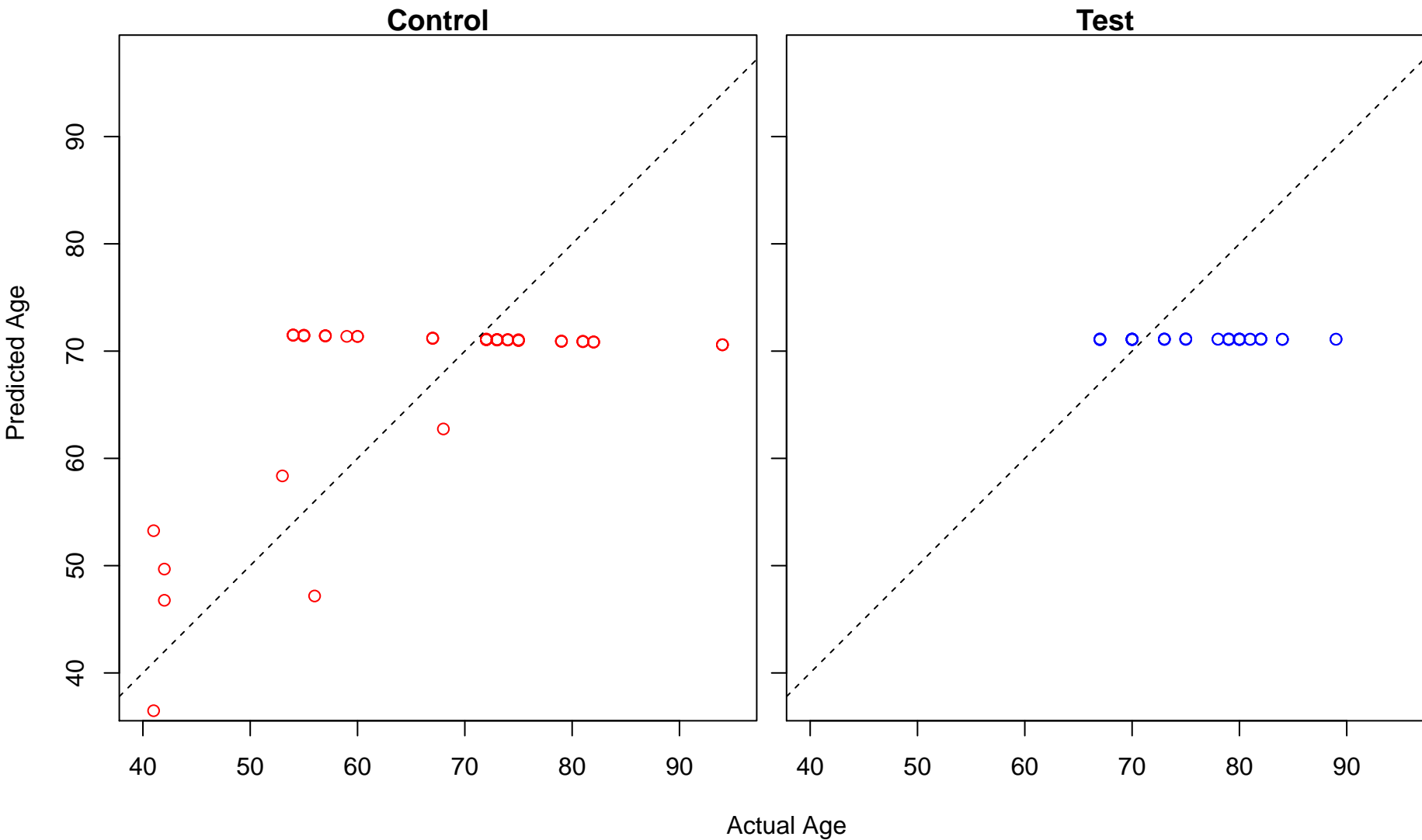


Test

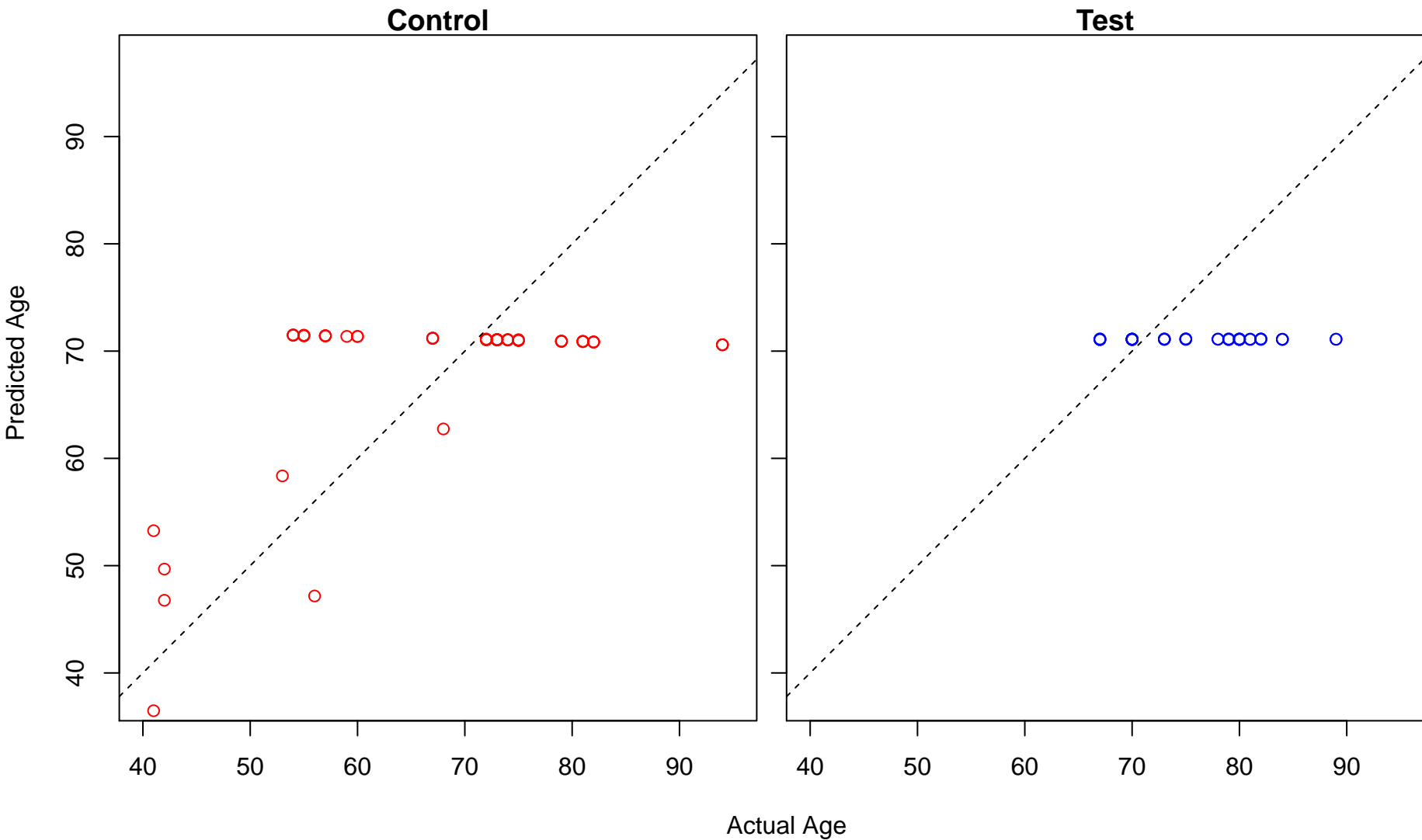


Actual Age

chemotaxis (Score: 0.795439)

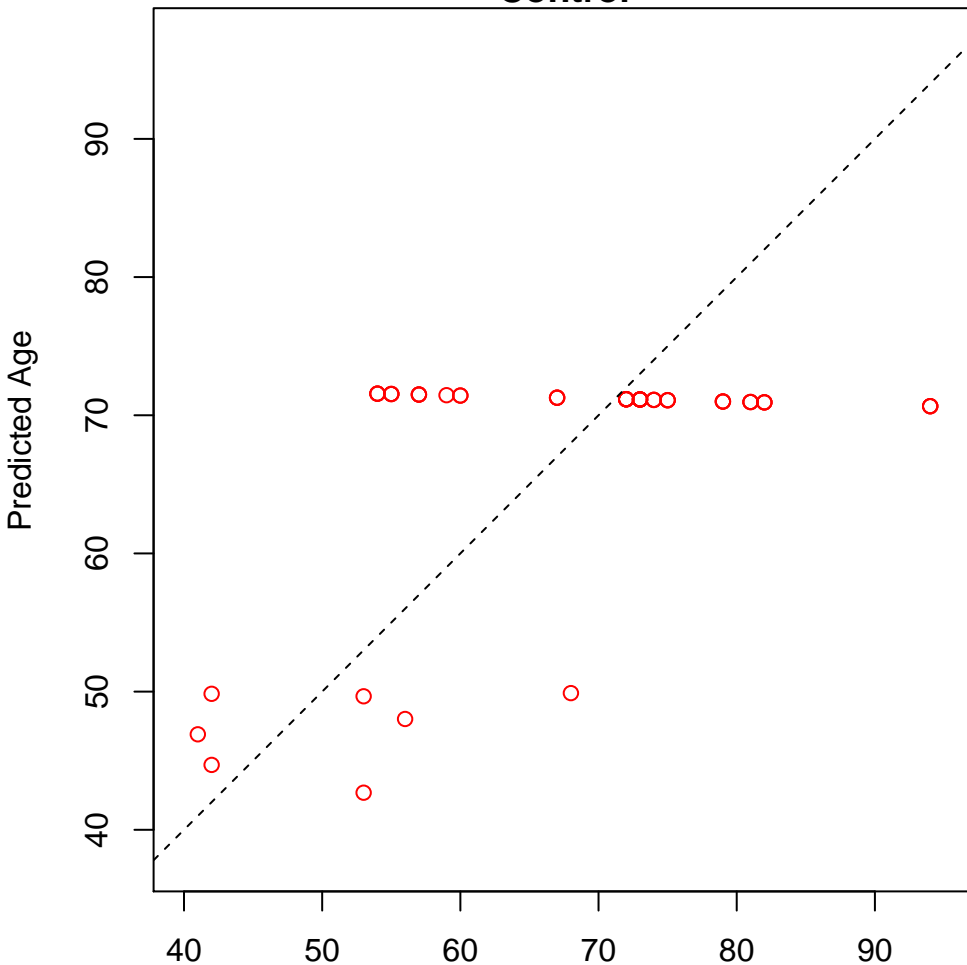


taxi (Score: 0.795439)

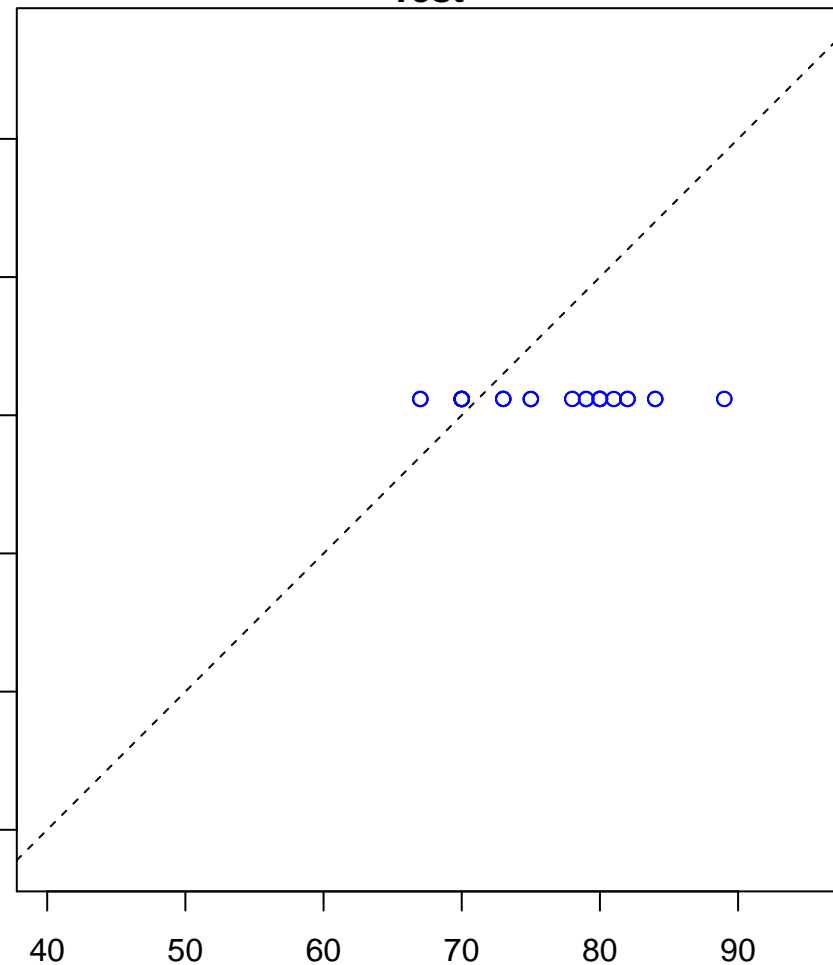


regulation of cellular catabolic process (Score: 0.795432)

Control

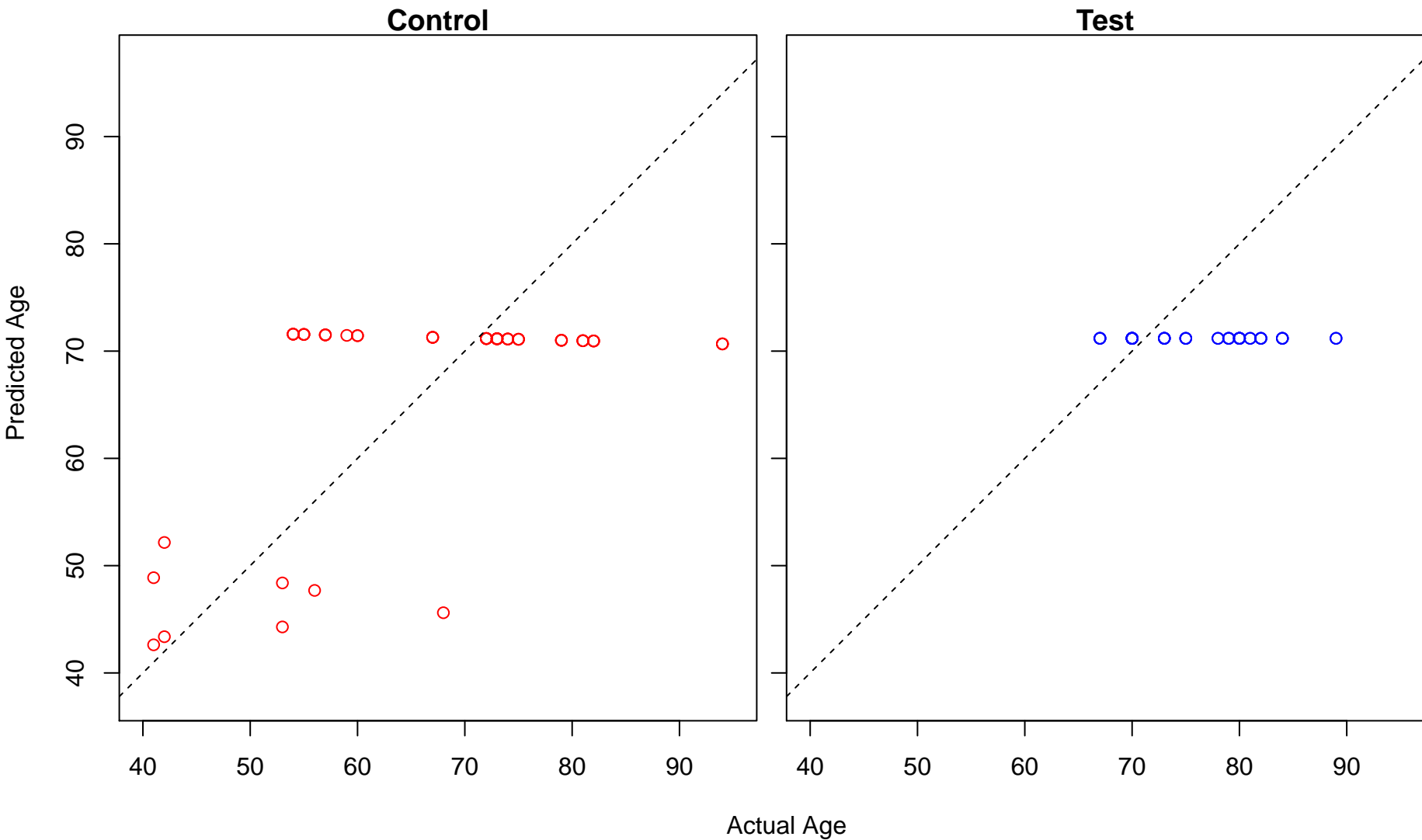


Test

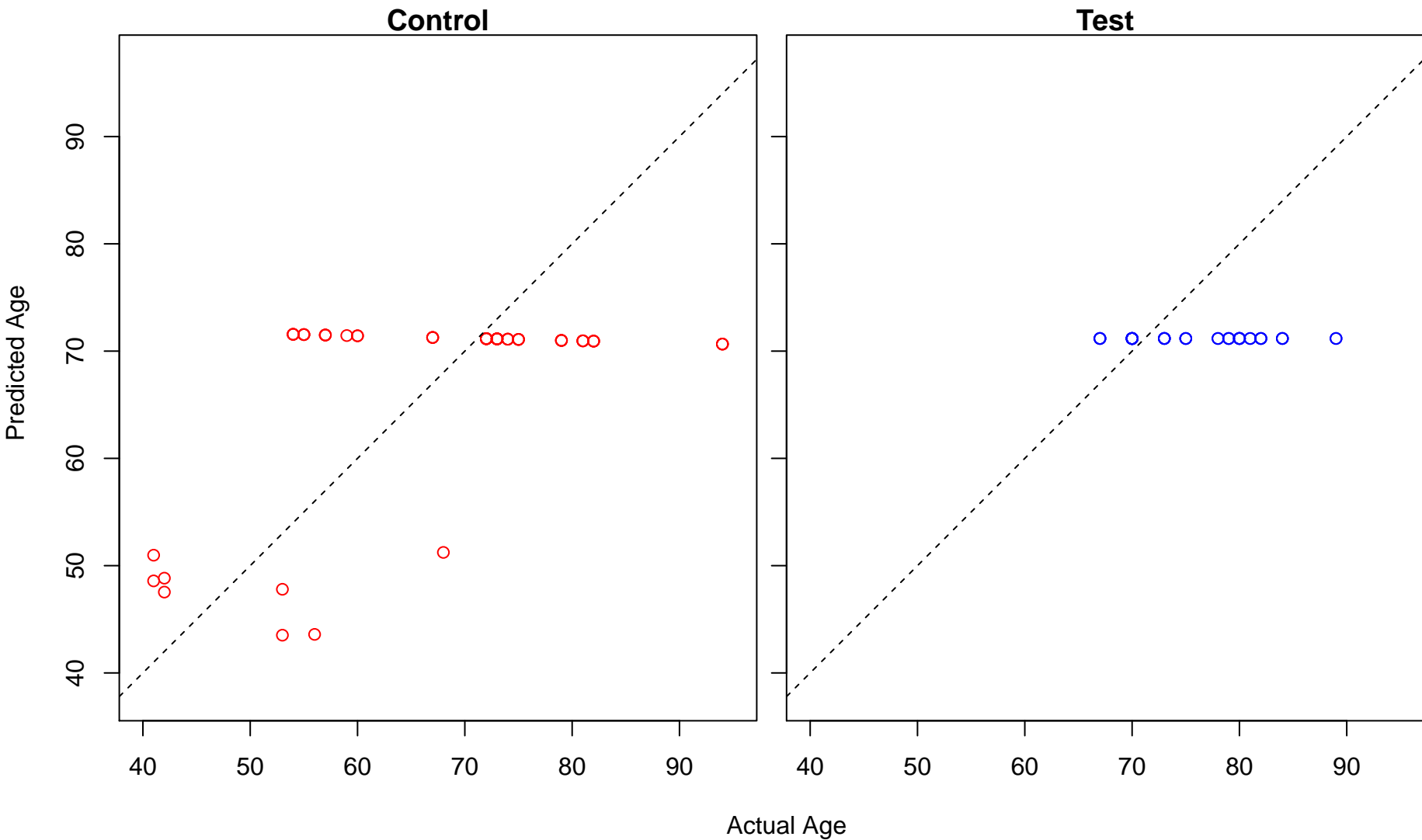


Actual Age

regulation of cellular protein metabolic process (Score: 0.795390)

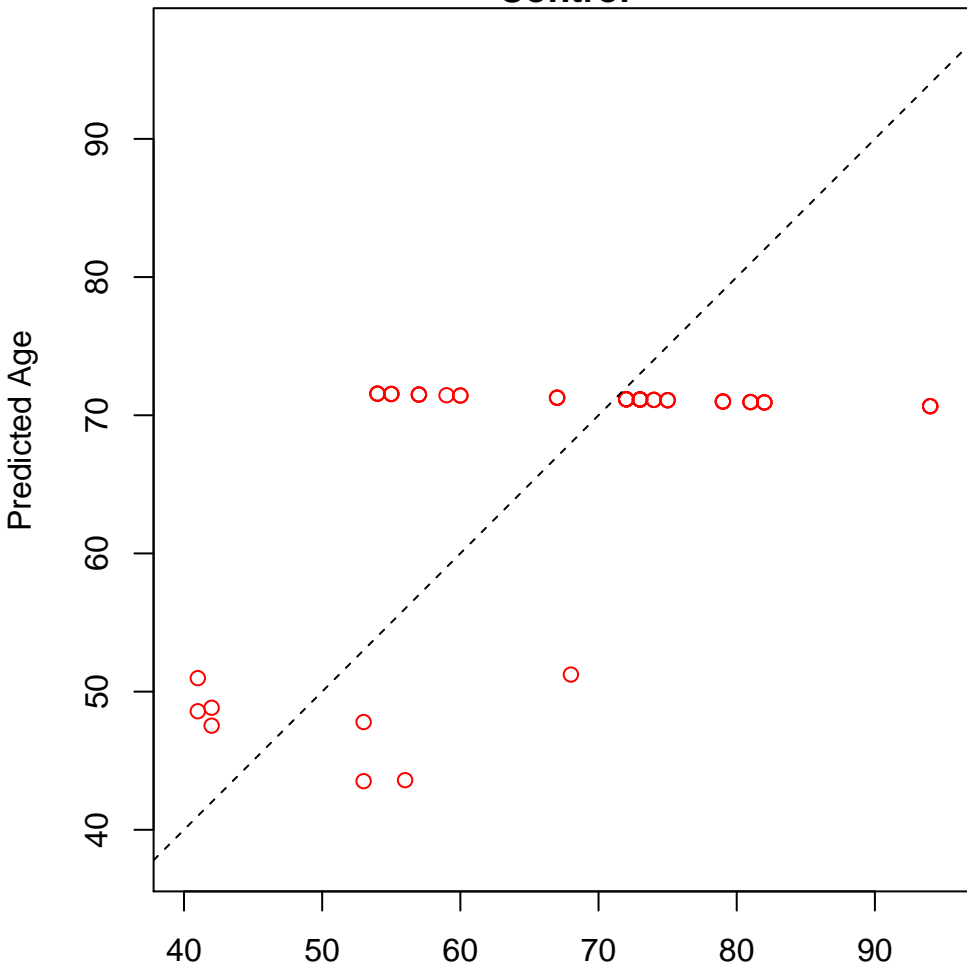


cellular protein localization (Score: 0.795341)

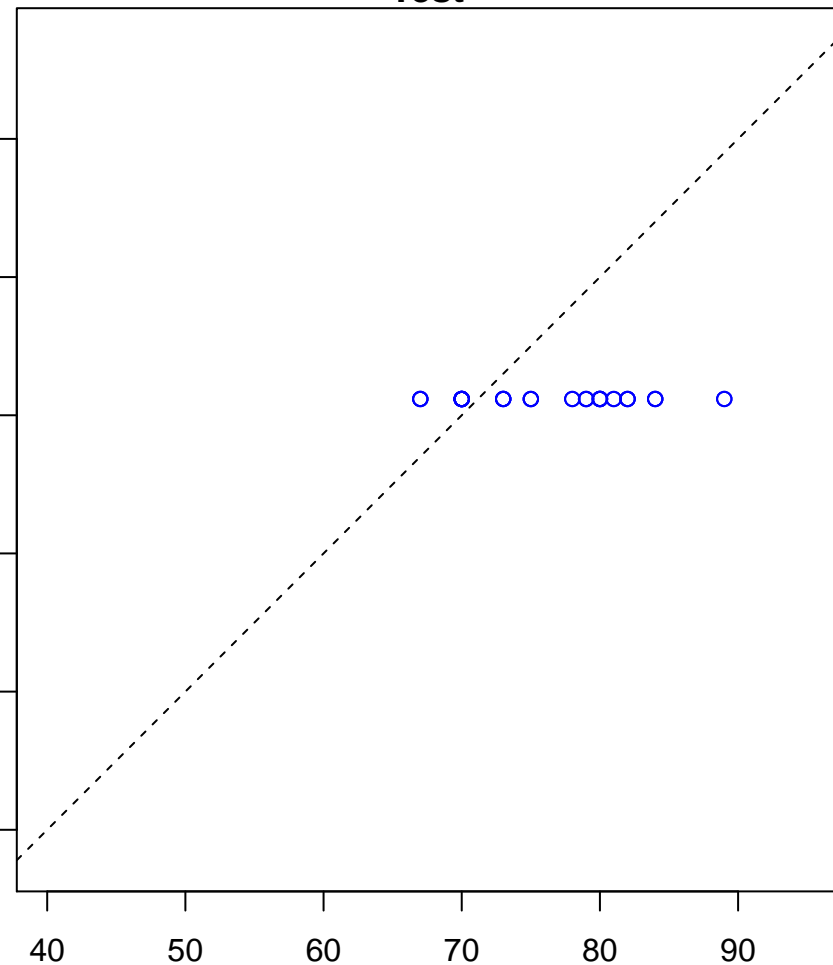


cellular macromolecule localization (Score: 0.795341)

Control

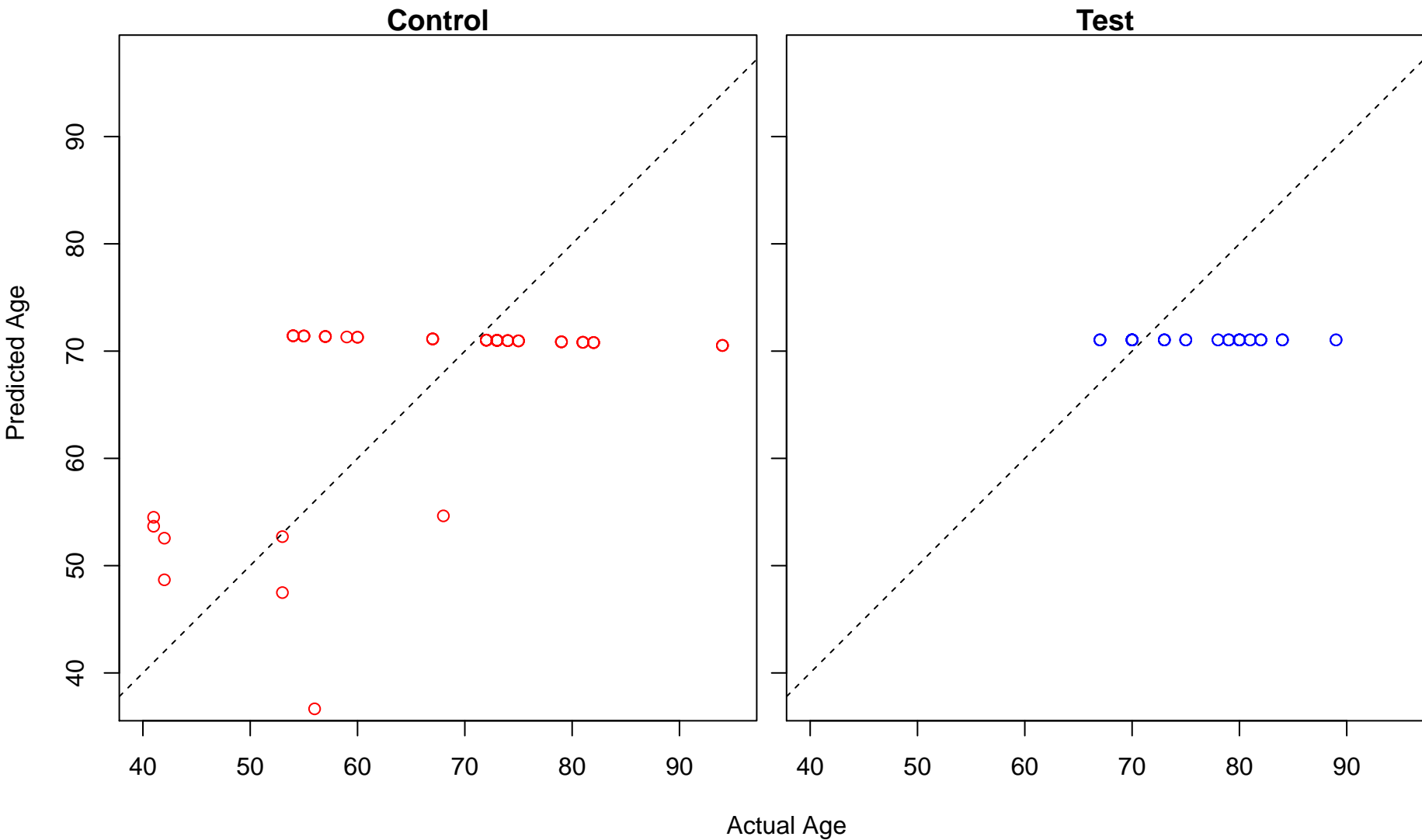


Test



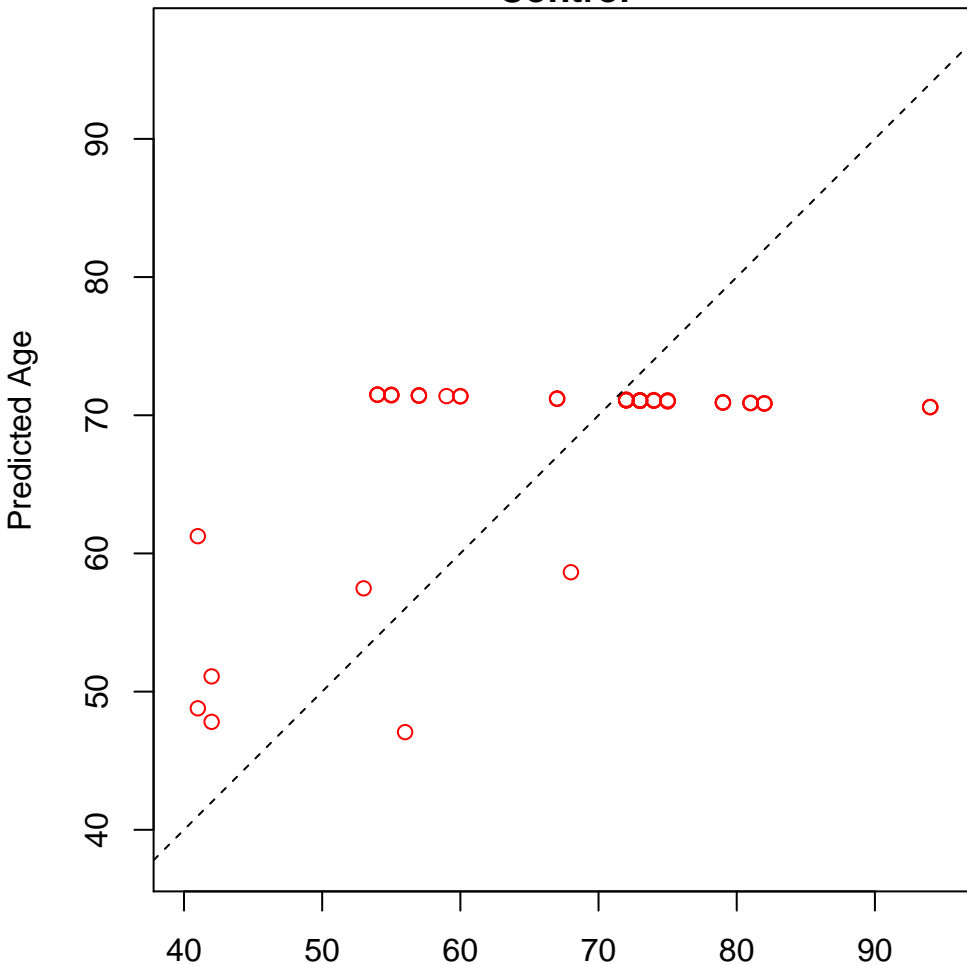
Actual Age

negative regulation of cellular macromolecule biosynthetic process (Score: 0.795293)

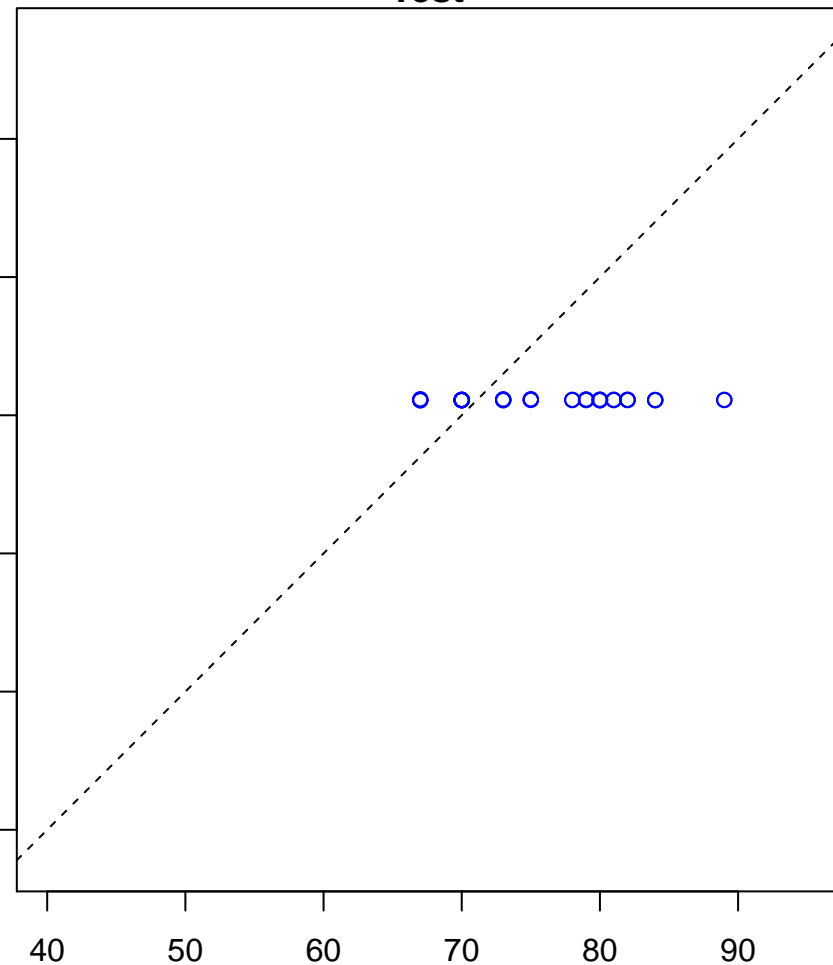


positive regulation of endocytosis (Score: 0.795232)

Control

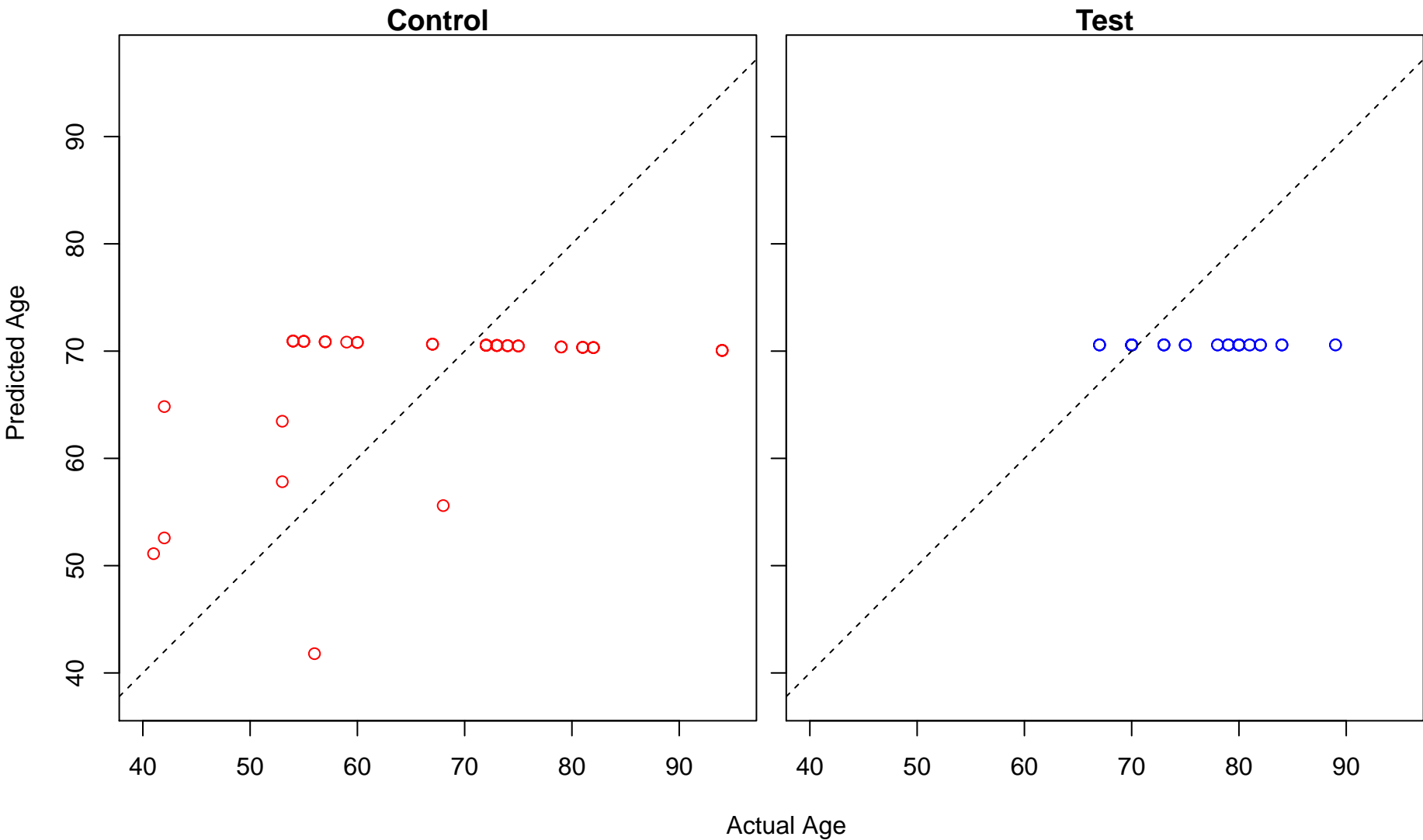


Test



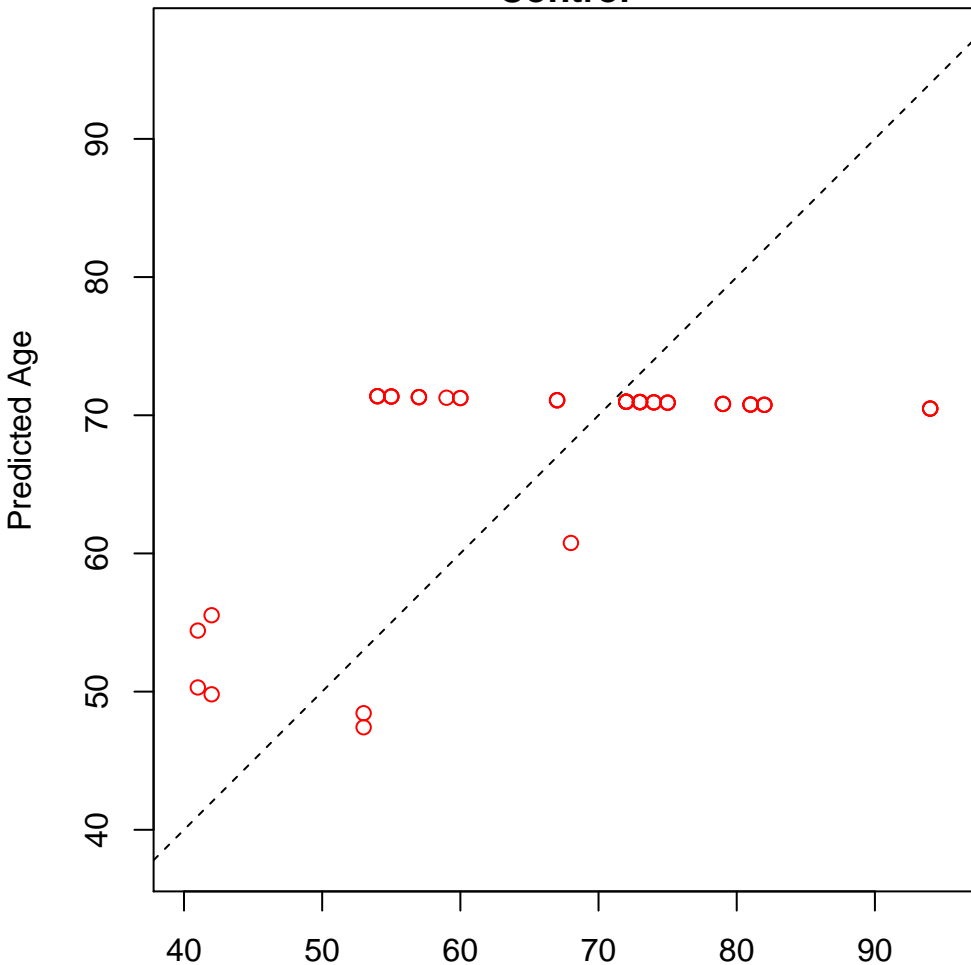
Actual Age

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

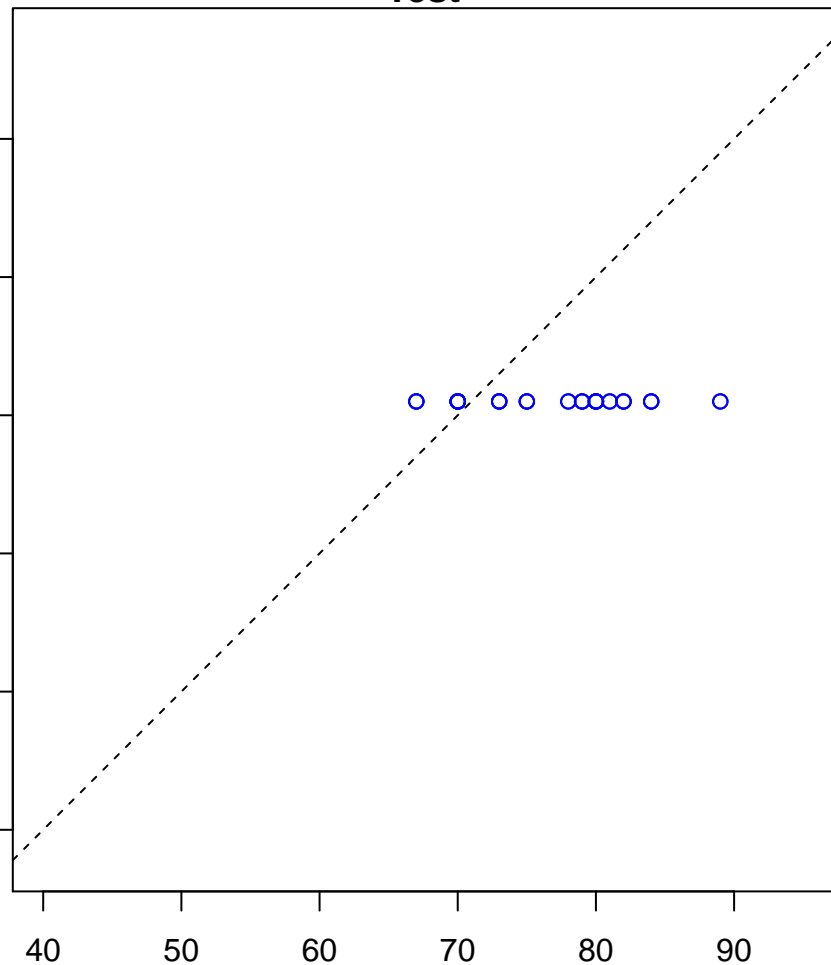


regulation of translational initiation (Score: 0.795144)

Control



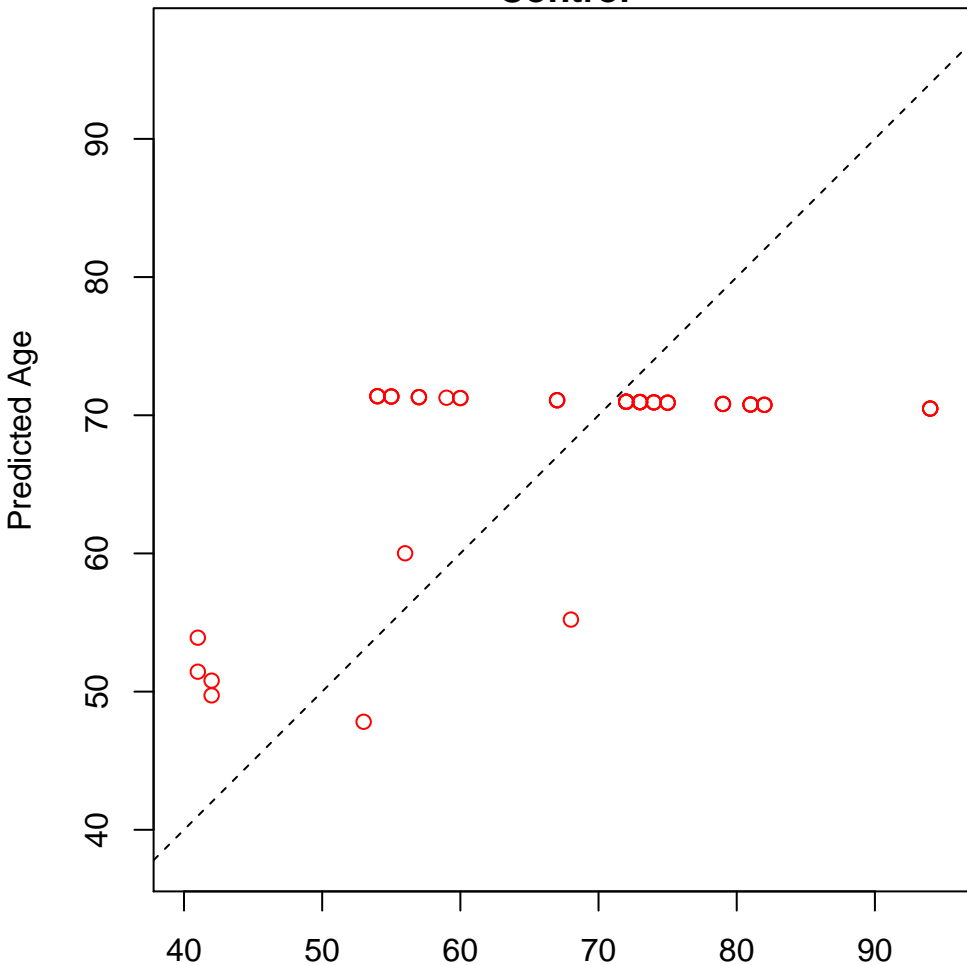
Test



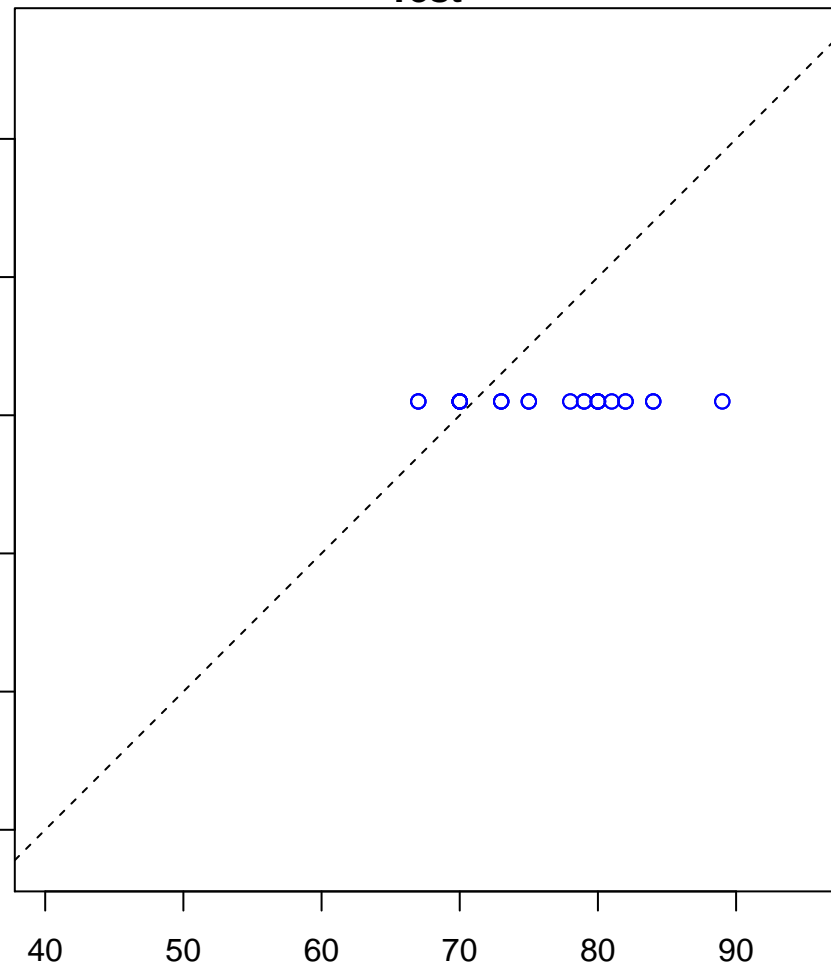
Actual Age

regulation of dendrite morphogenesis (Score: 0.795079)

Control



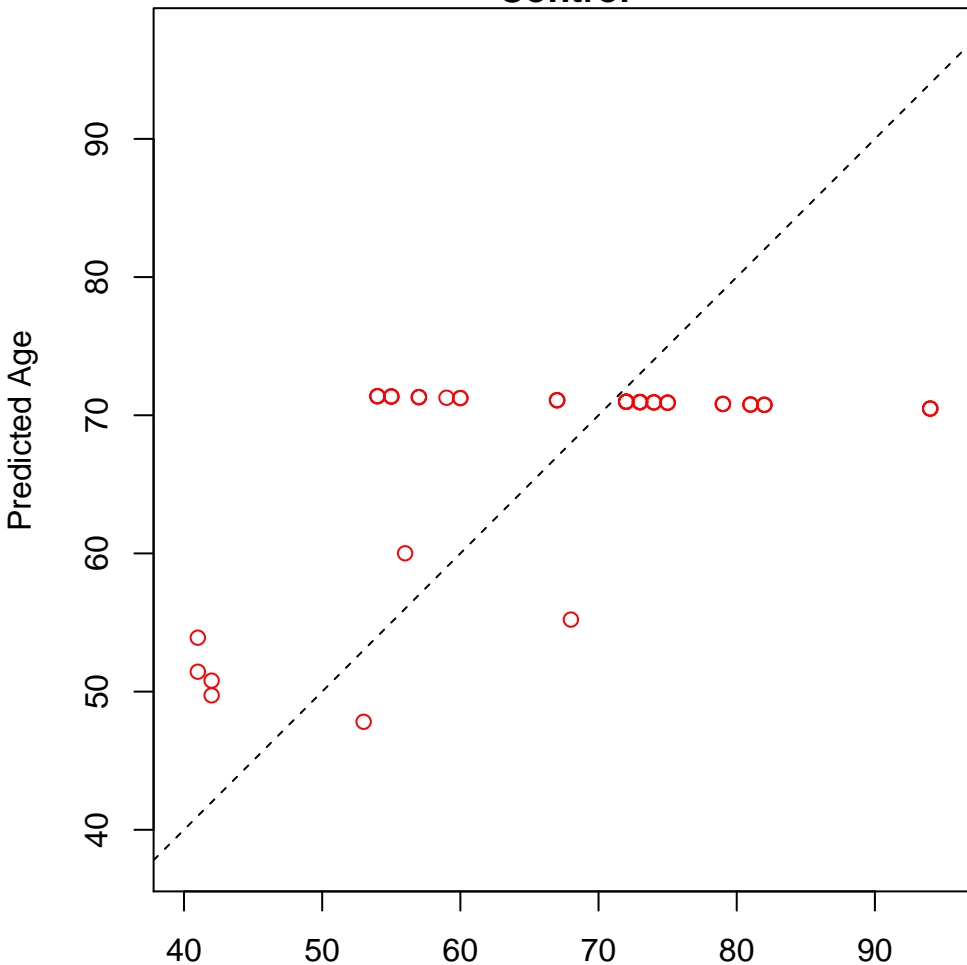
Test



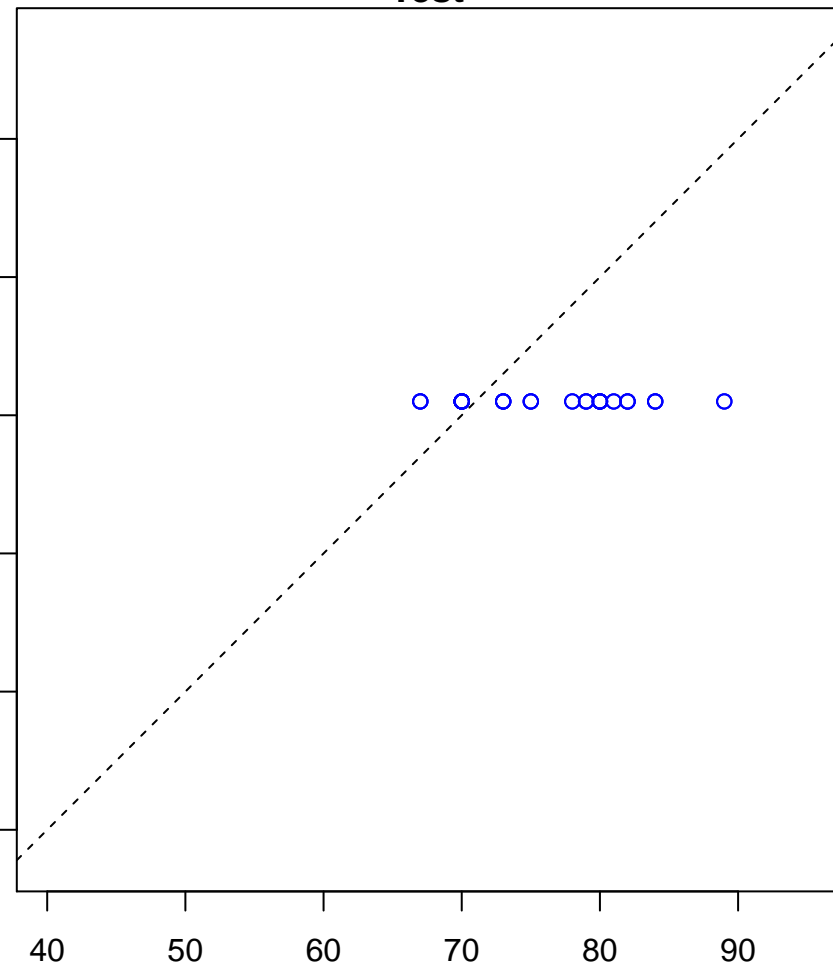
Actual Age

regulation of dendrite development (Score: 0.795079)

Control



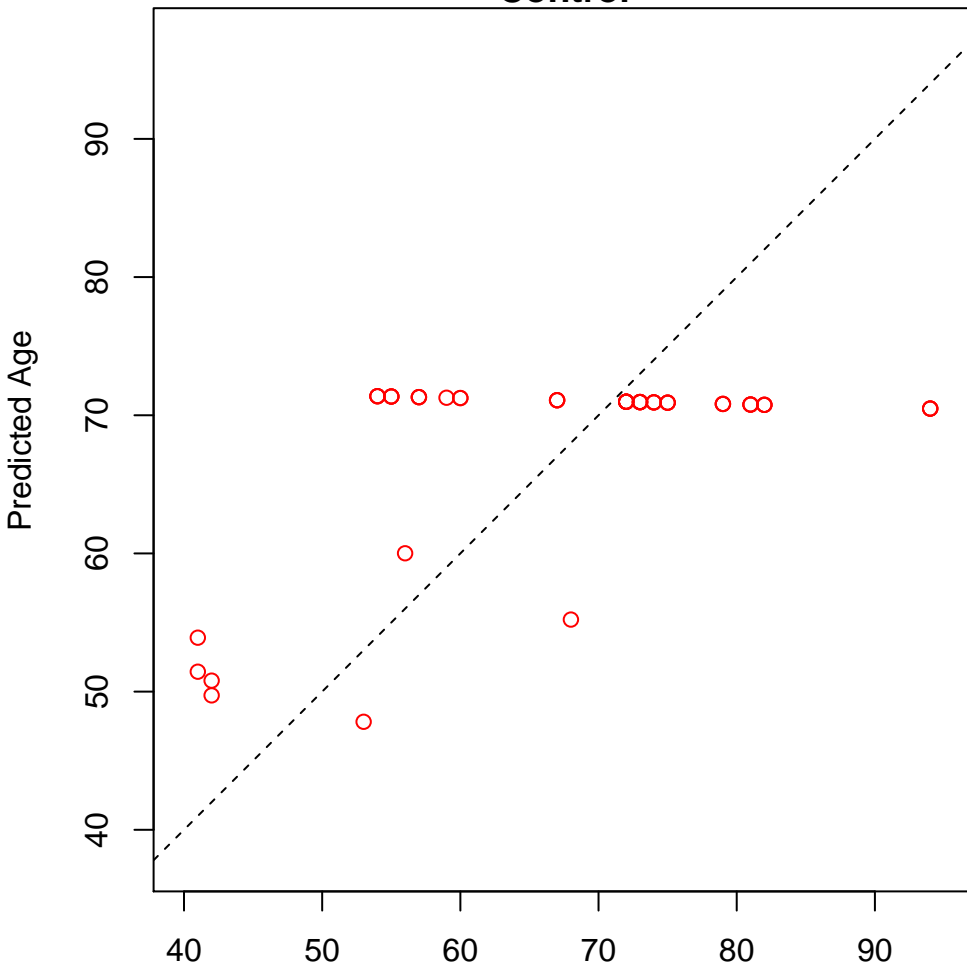
Test



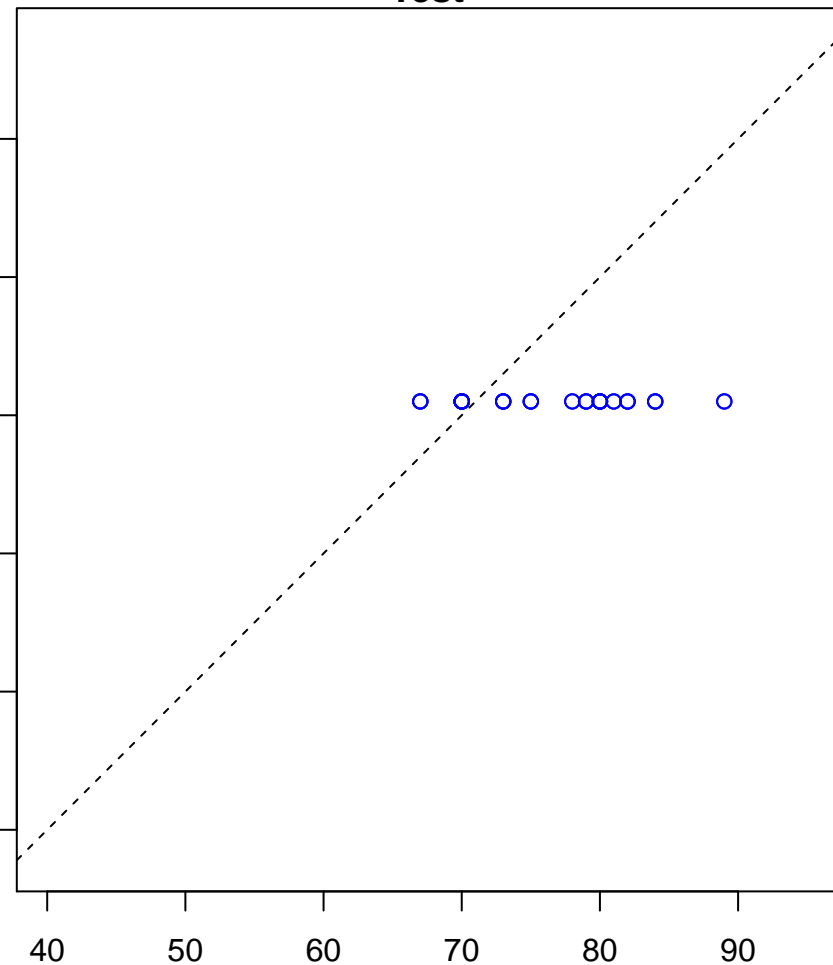
Actual Age

regulation of dendritic spine development (Score: 0.795079)

Control

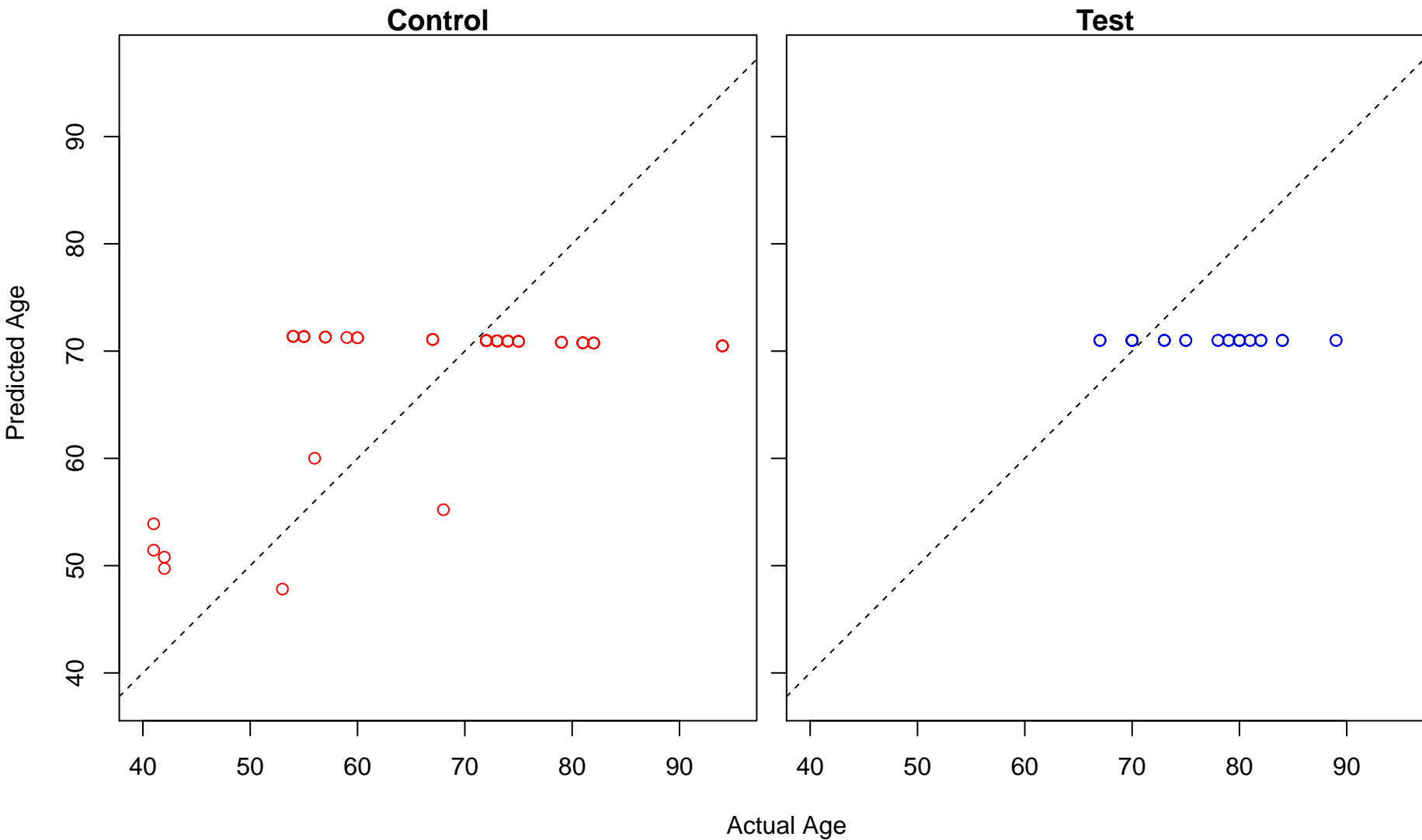


Test

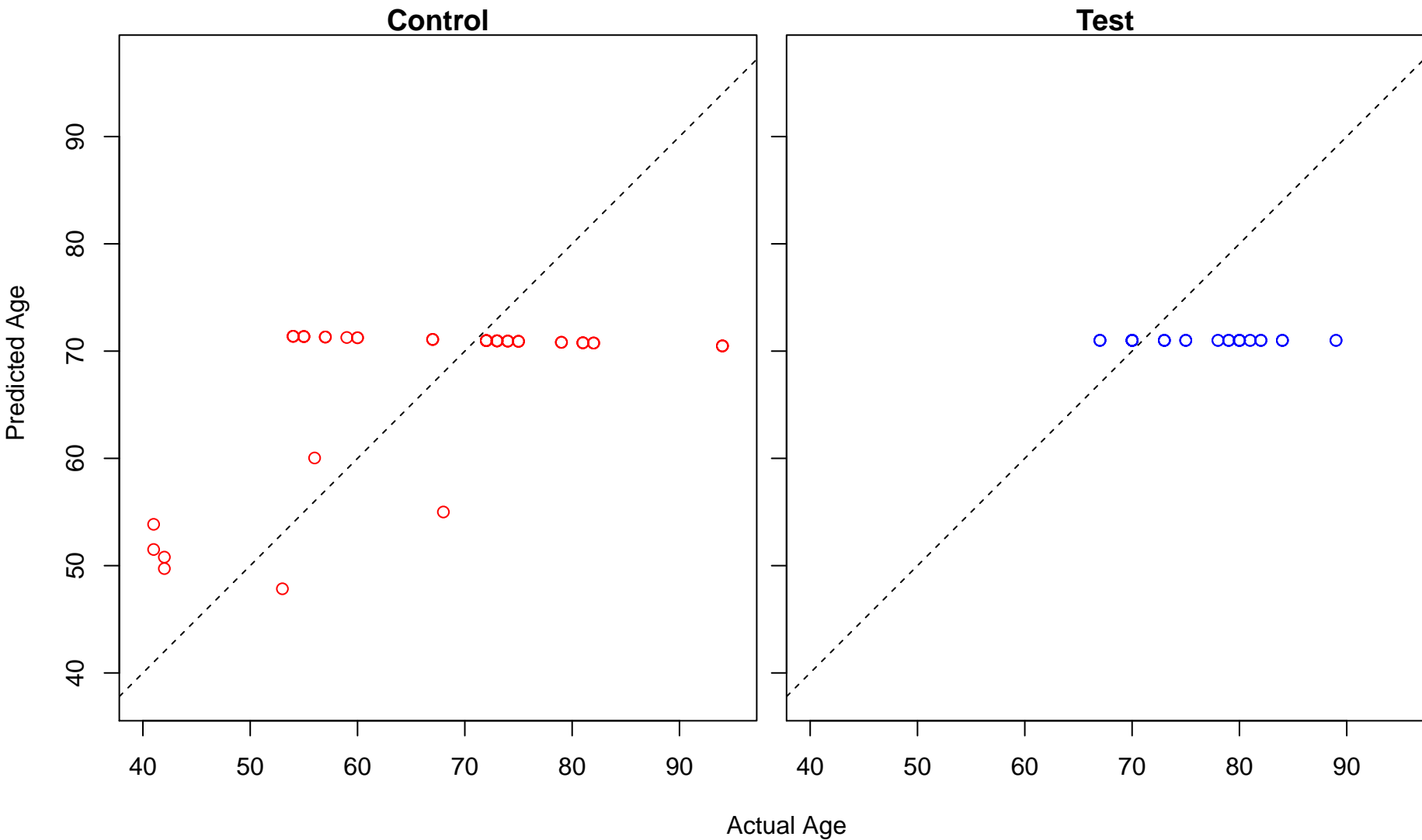


Actual Age

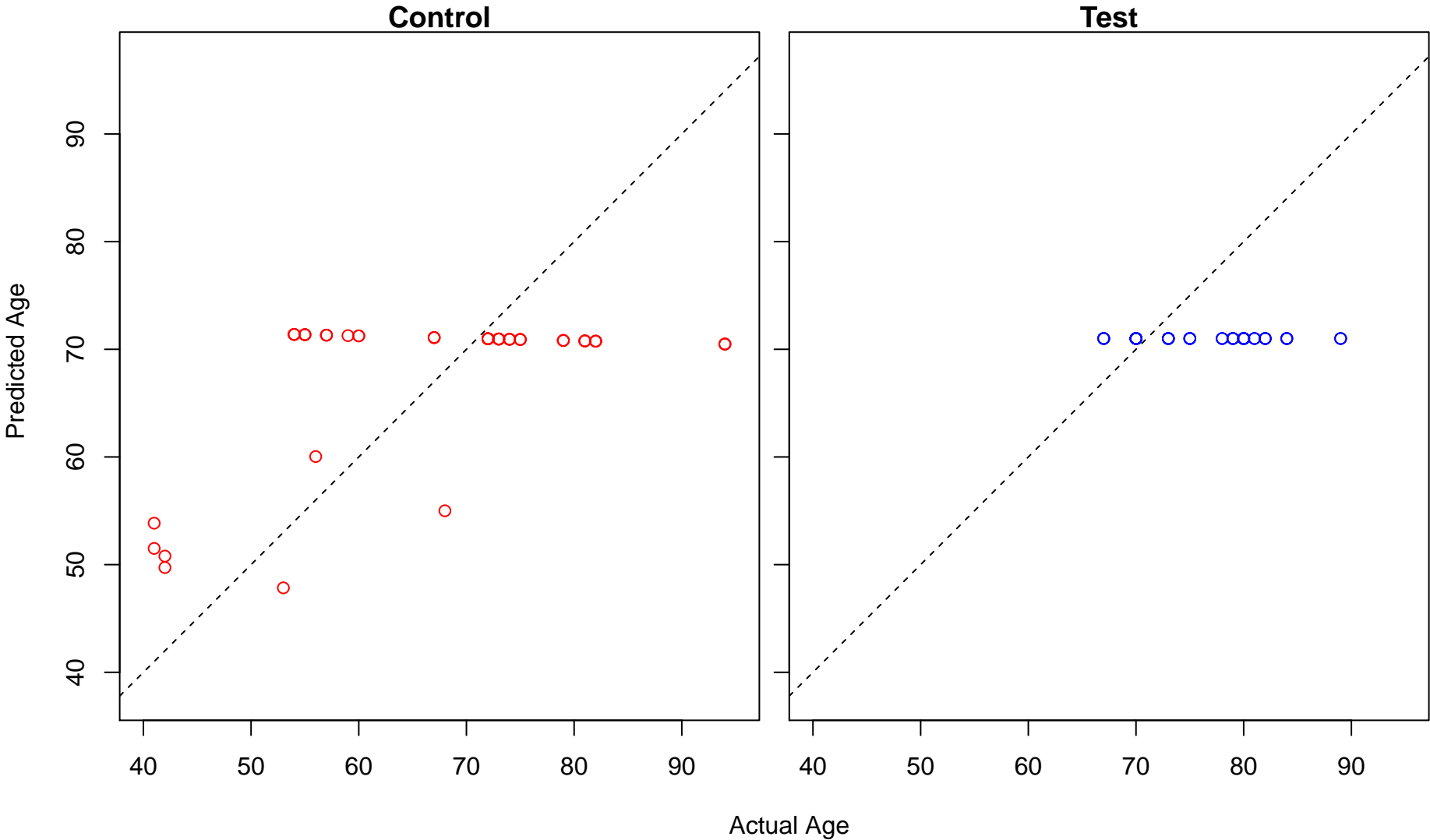
regulation of dendritic spine morphogenesis (Score: 0.795079)



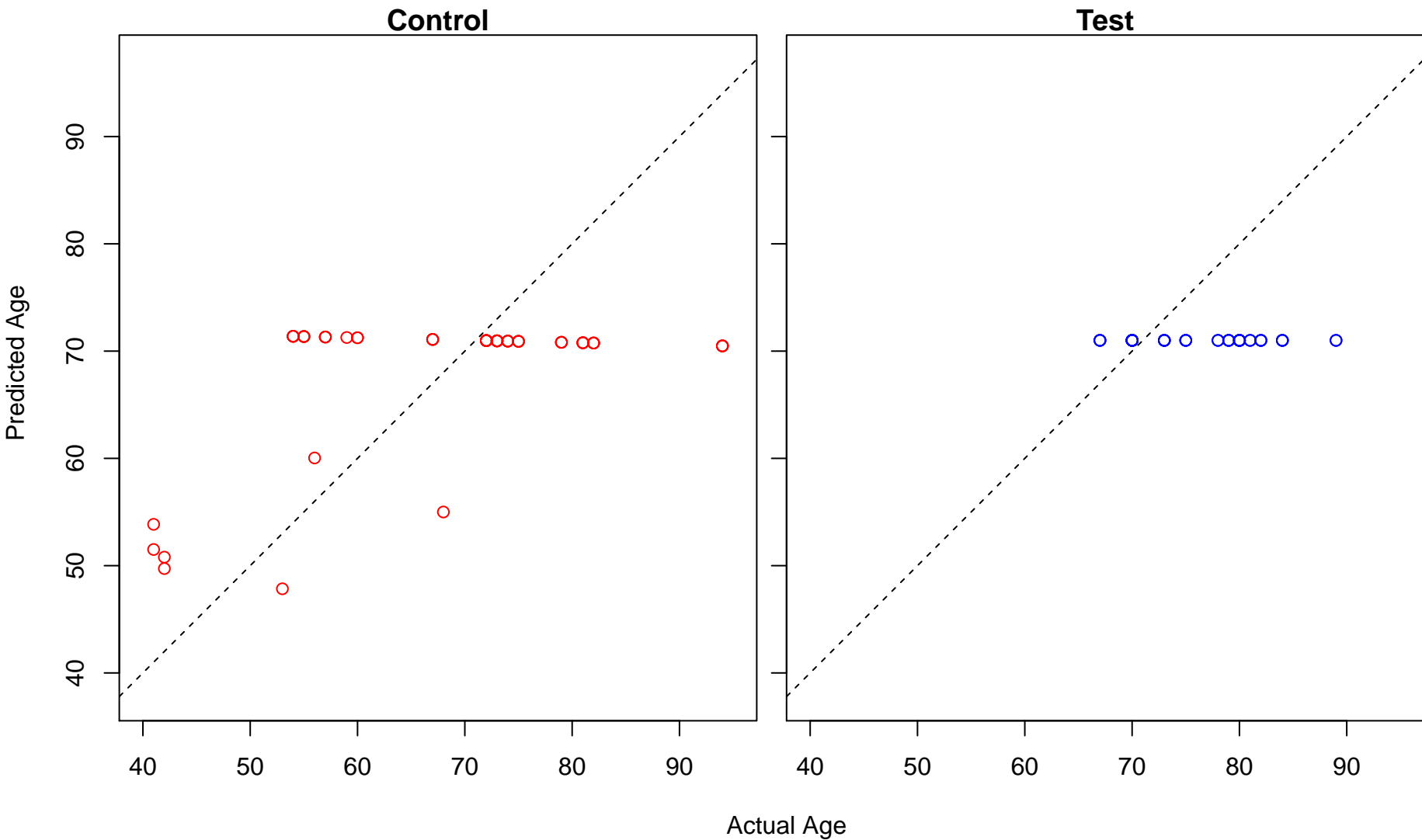
interaction with symbiont (Score: 0.795072)



modification of morphology or physiology of other organism involved in symbiotic interaction (Score: 0.7)

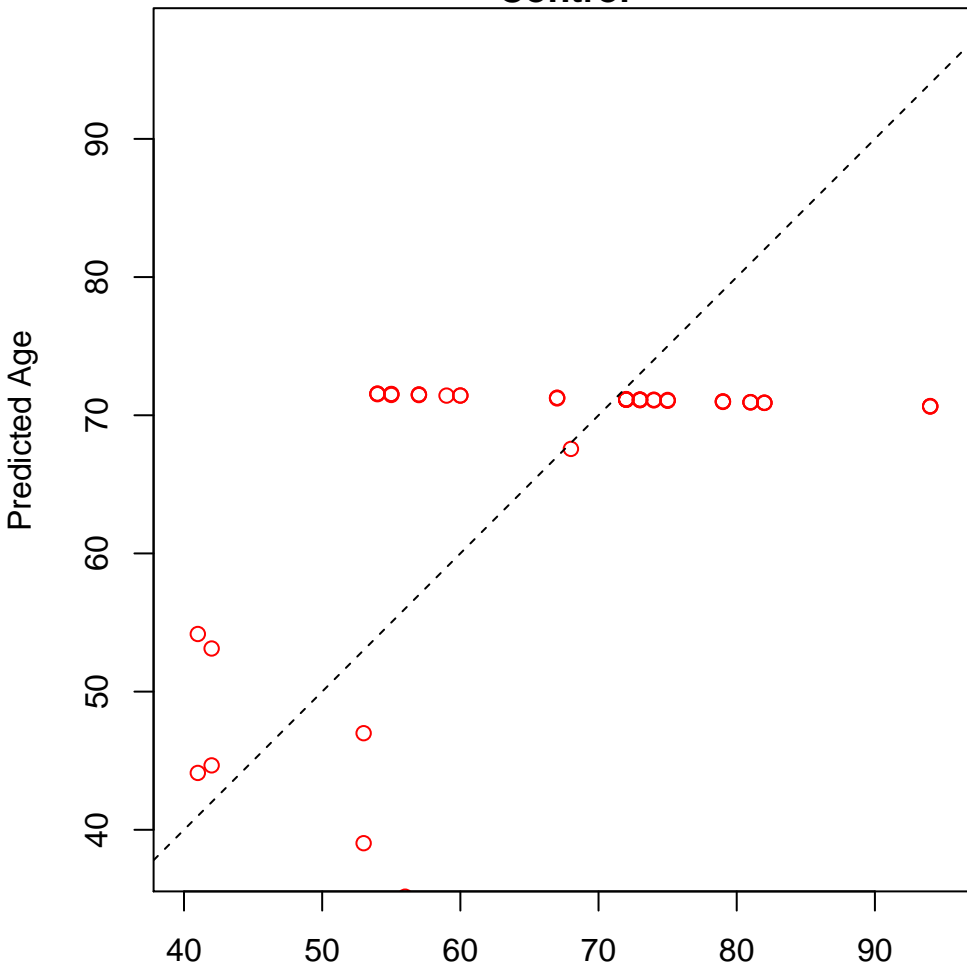


modification by host of symbiont morphology or physiology (Score: 0.795072)

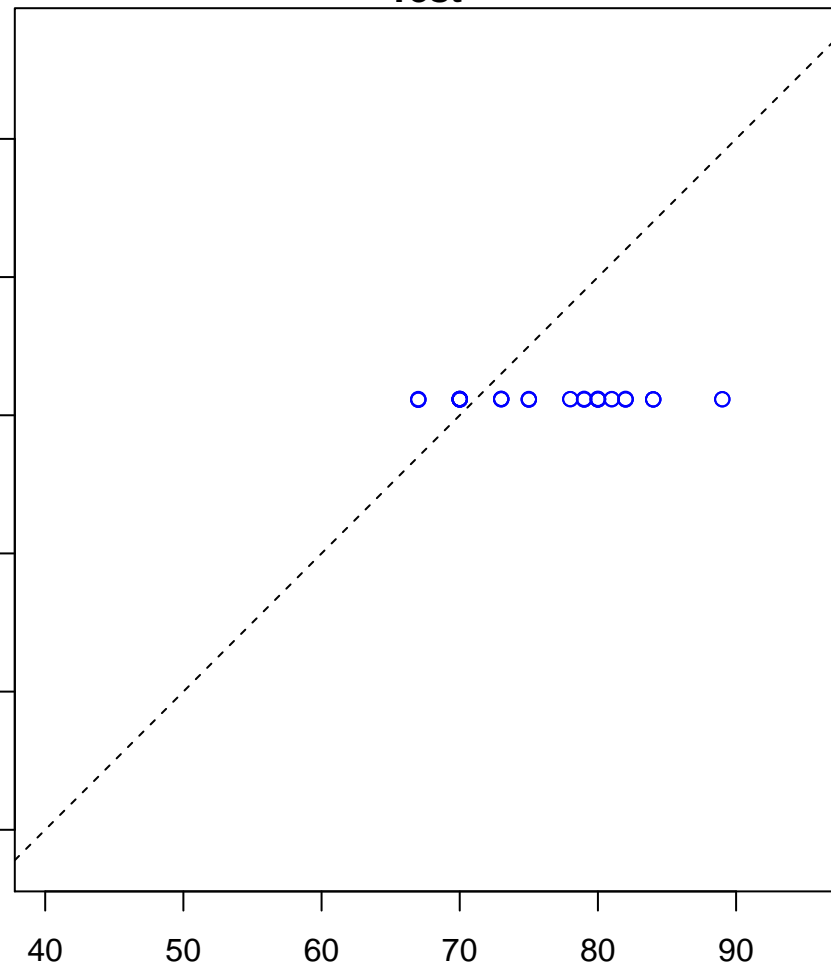


cellular response to external stimulus (Score: 0.795068)

Control

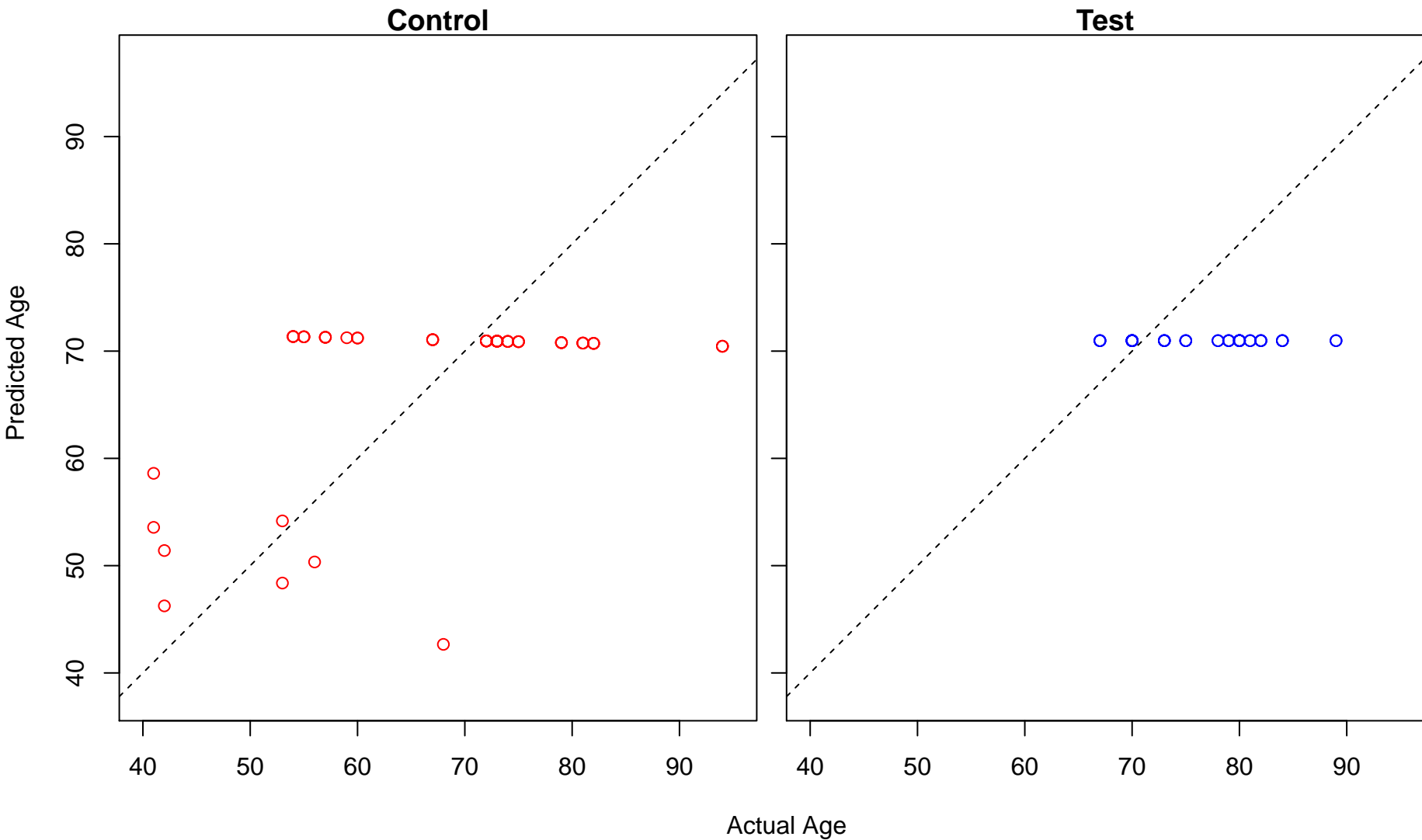


Test

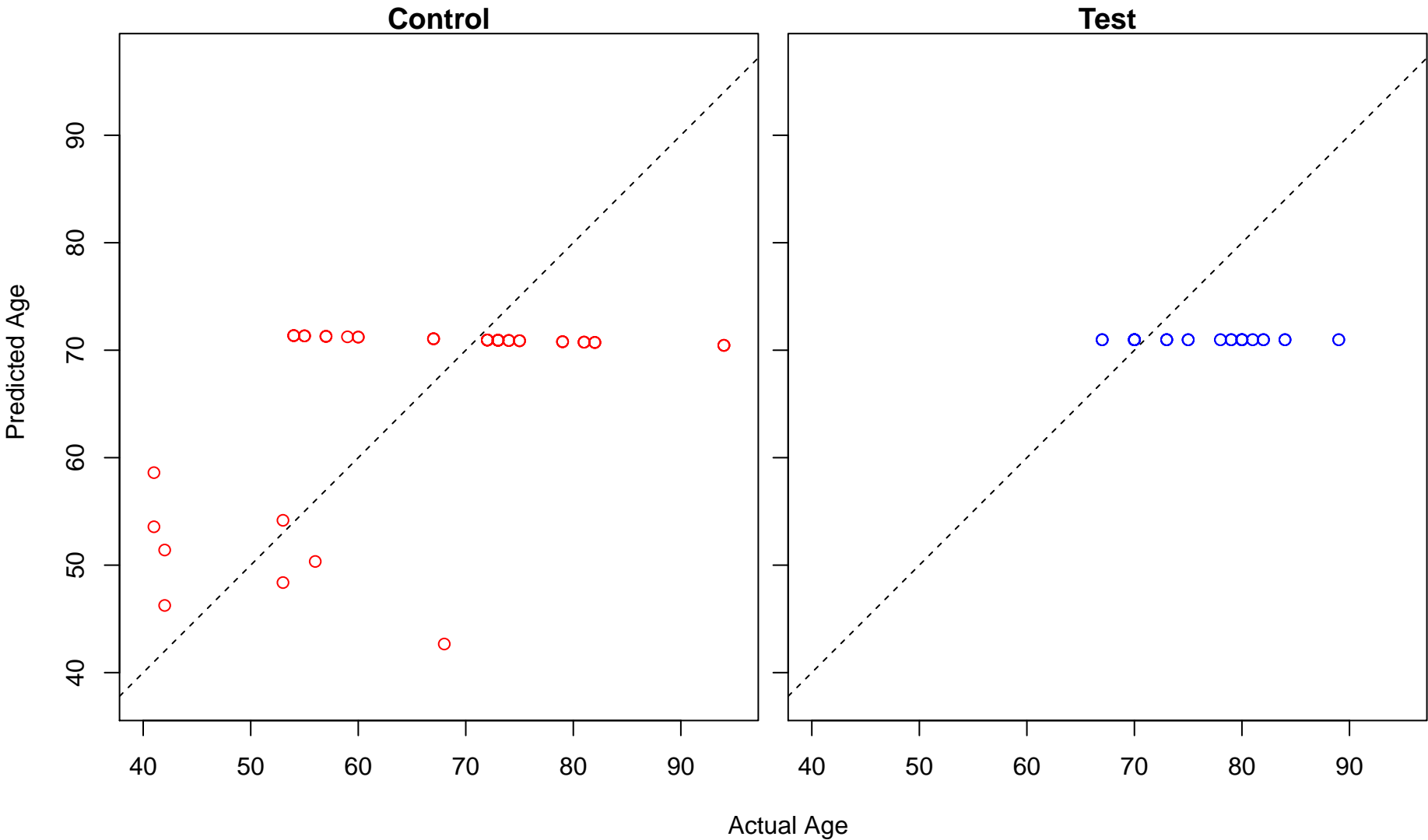


Actual Age

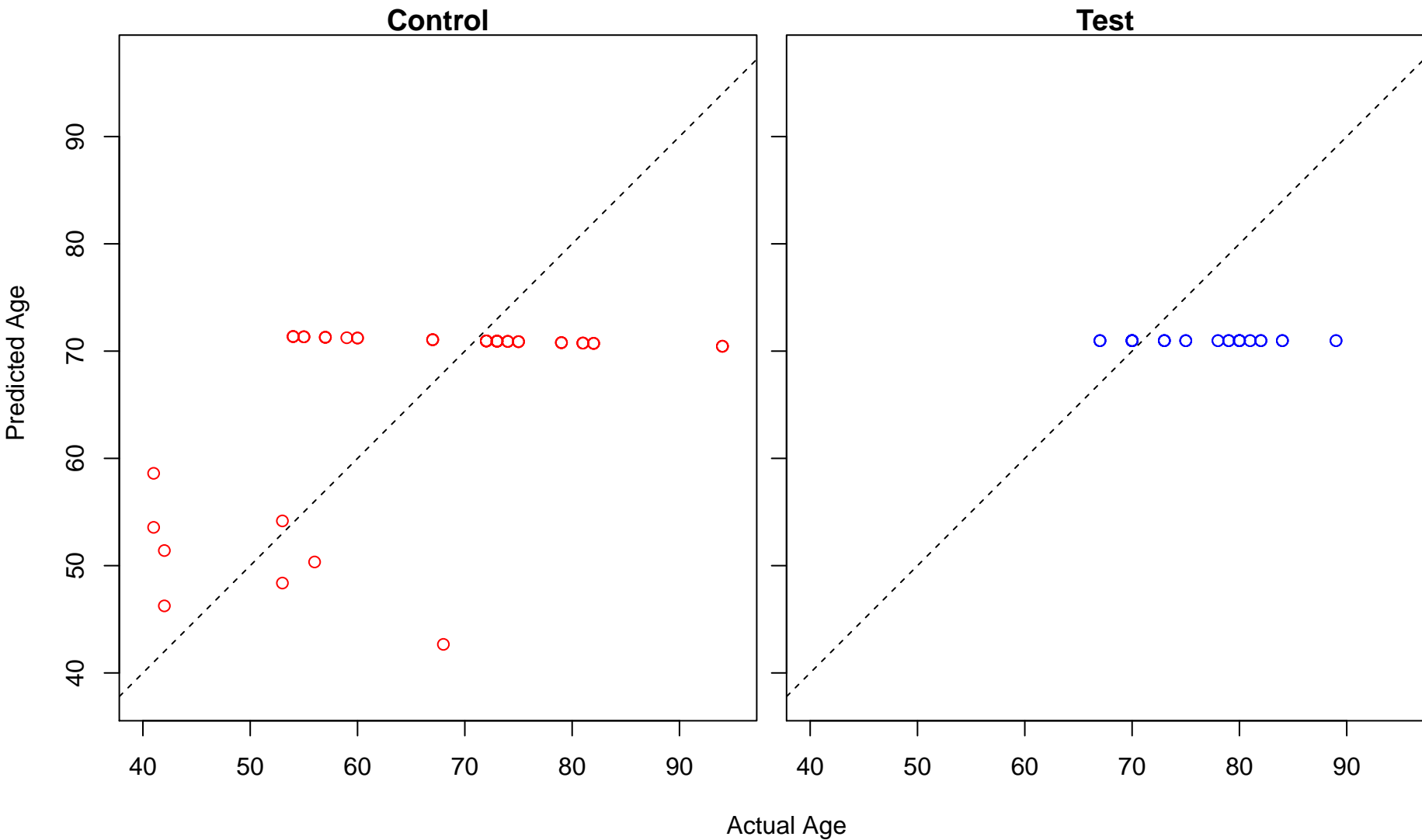
positive regulation of endopeptidase activity (Score: 0.795037)



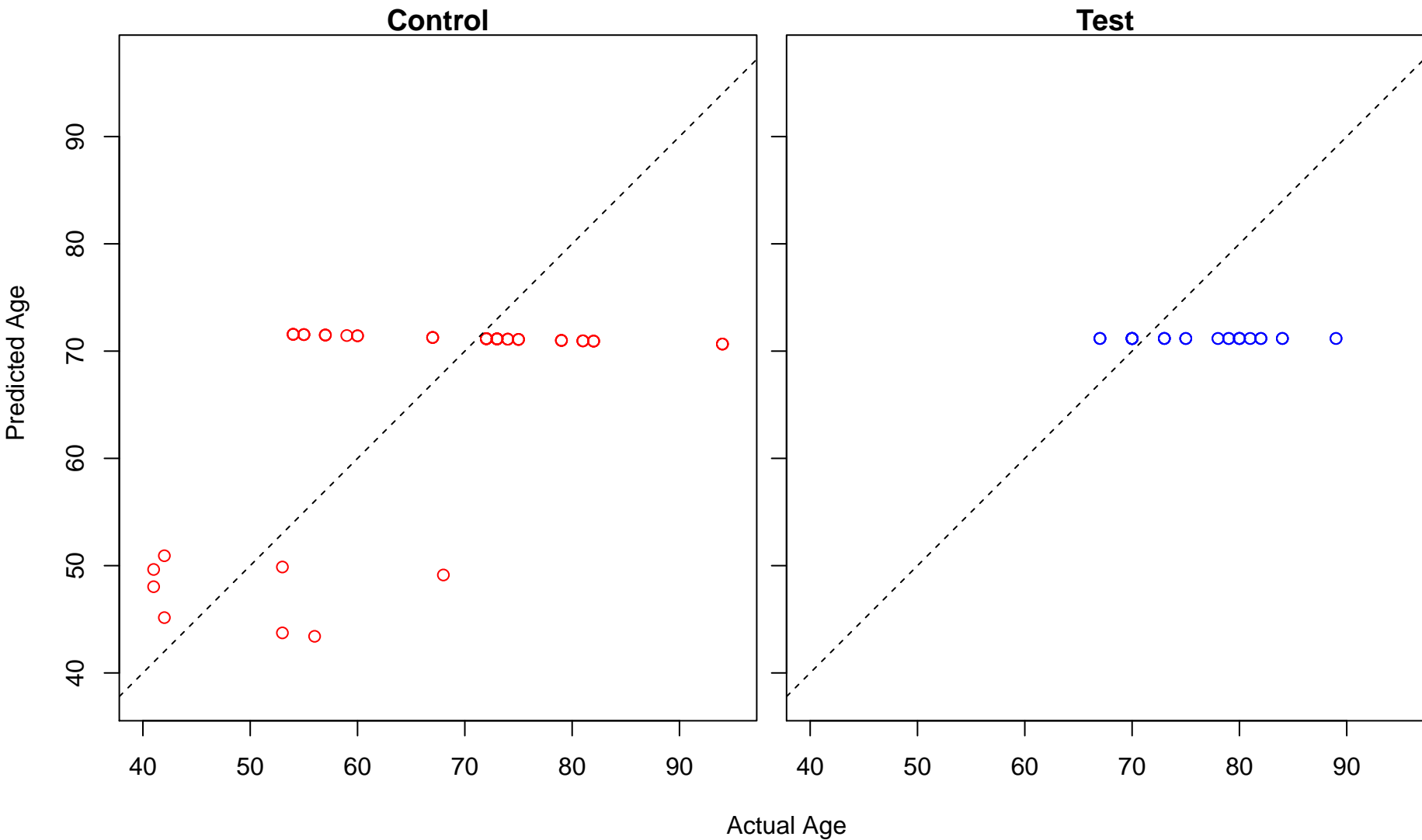
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 0.79)



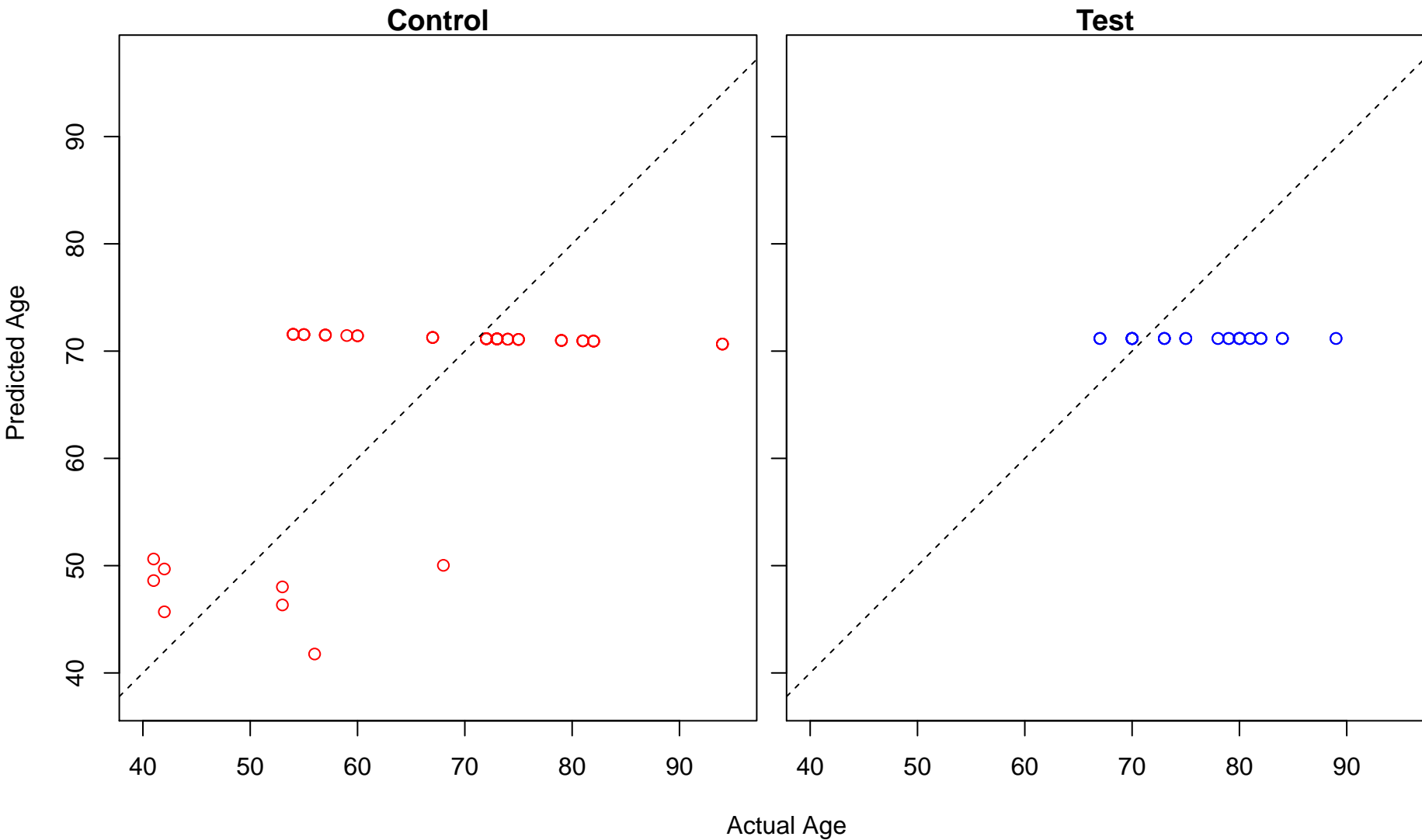
positive regulation of cysteine-type endopeptidase activity (Score: 0.795037)



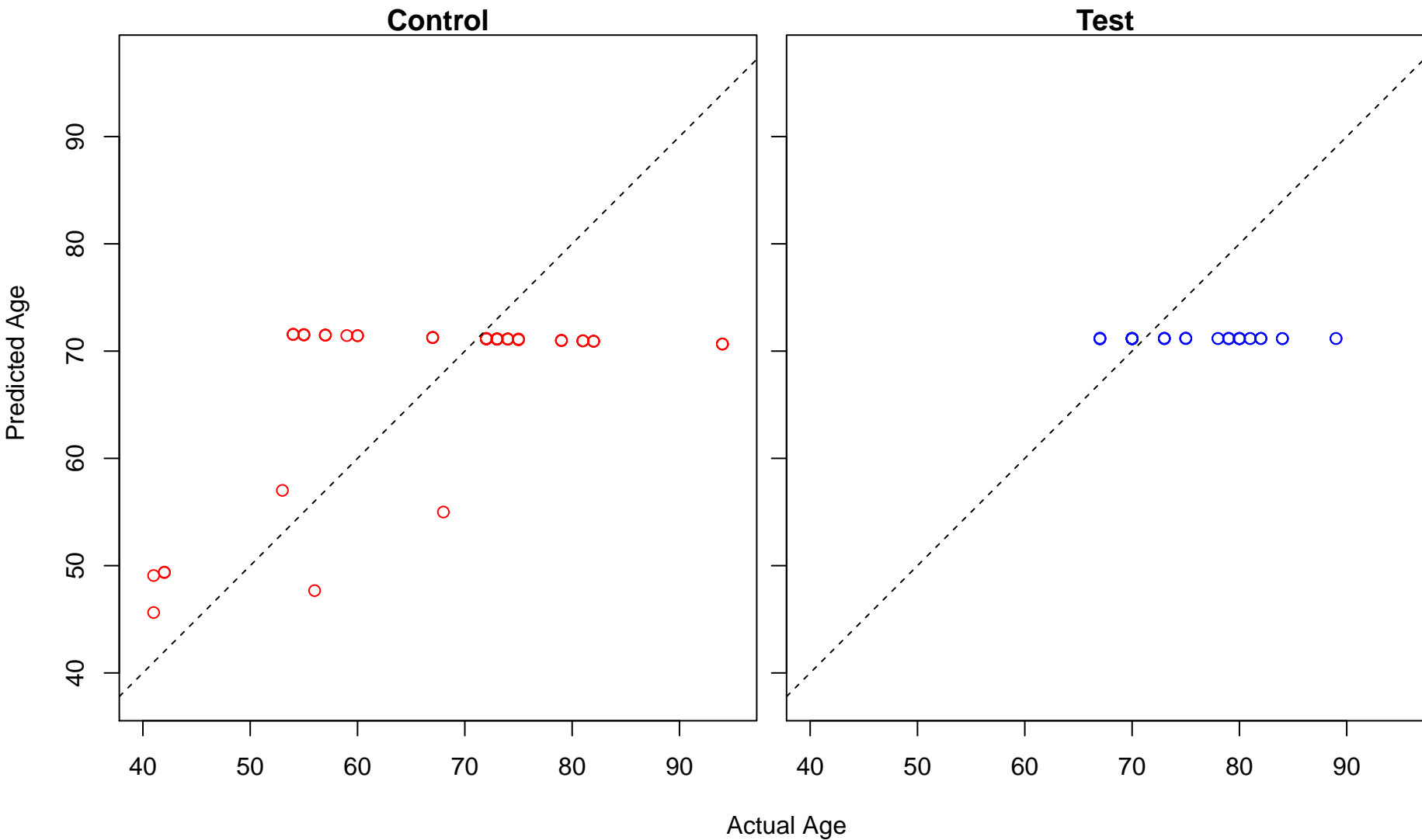
cellular biosynthetic process (Score: 0.794989)



cellular localization (Score: 0.794948)

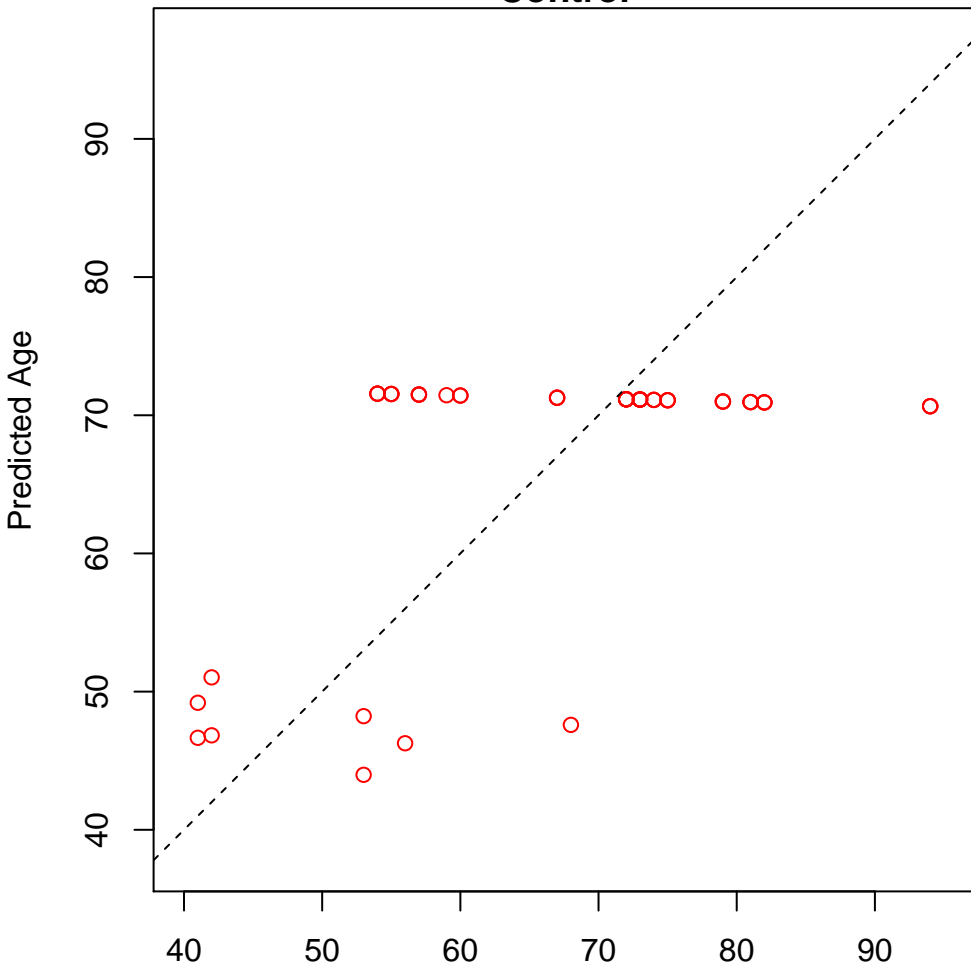


lymphocyte migration (Score: 0.794914)

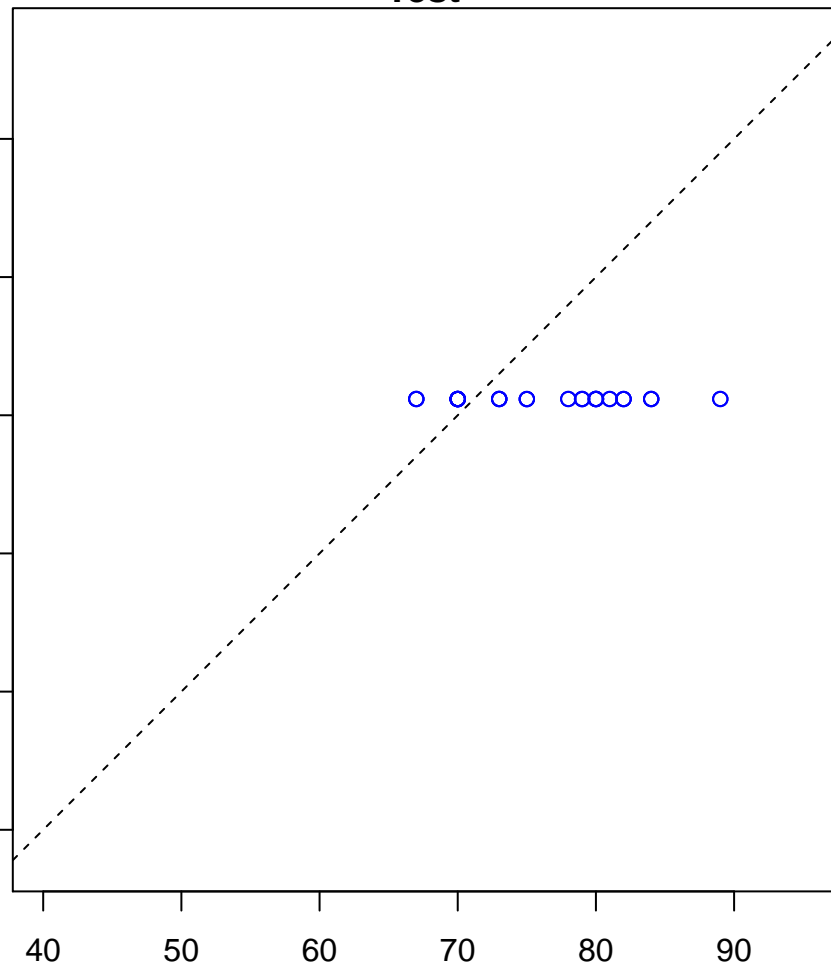


positive regulation of cellular process (Score: 0.794890)

Control



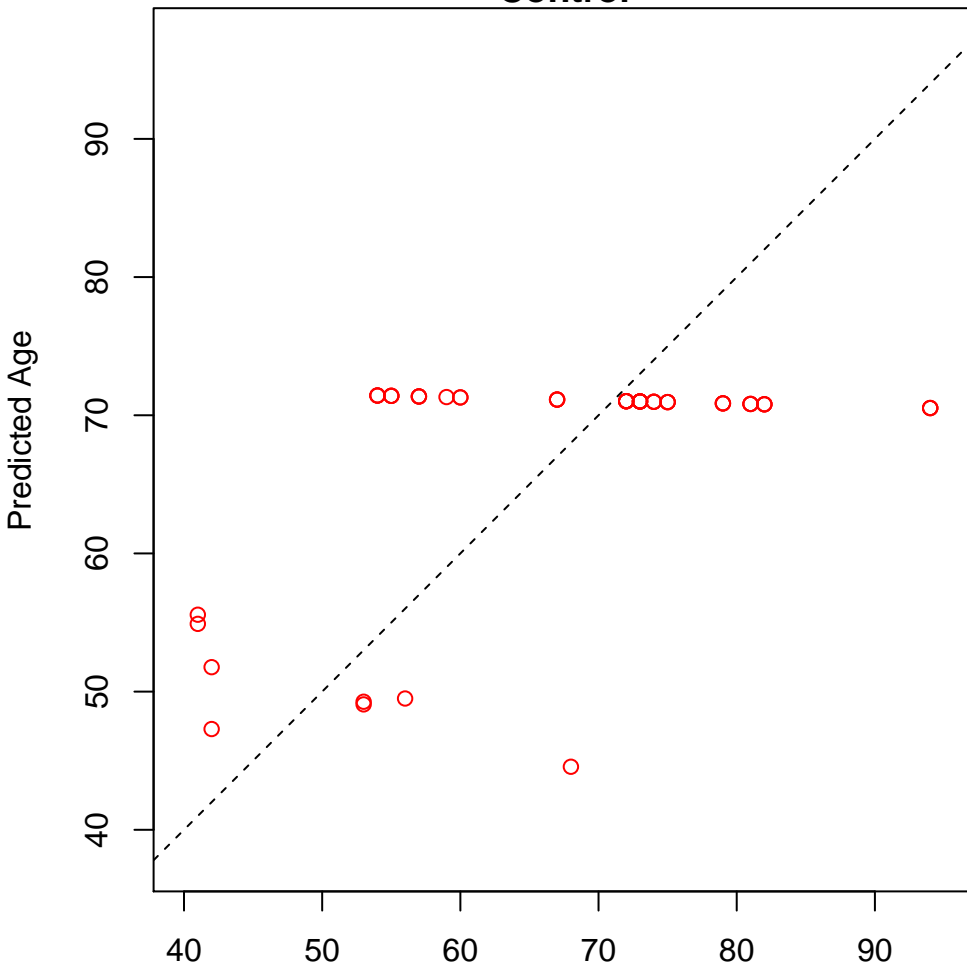
Test



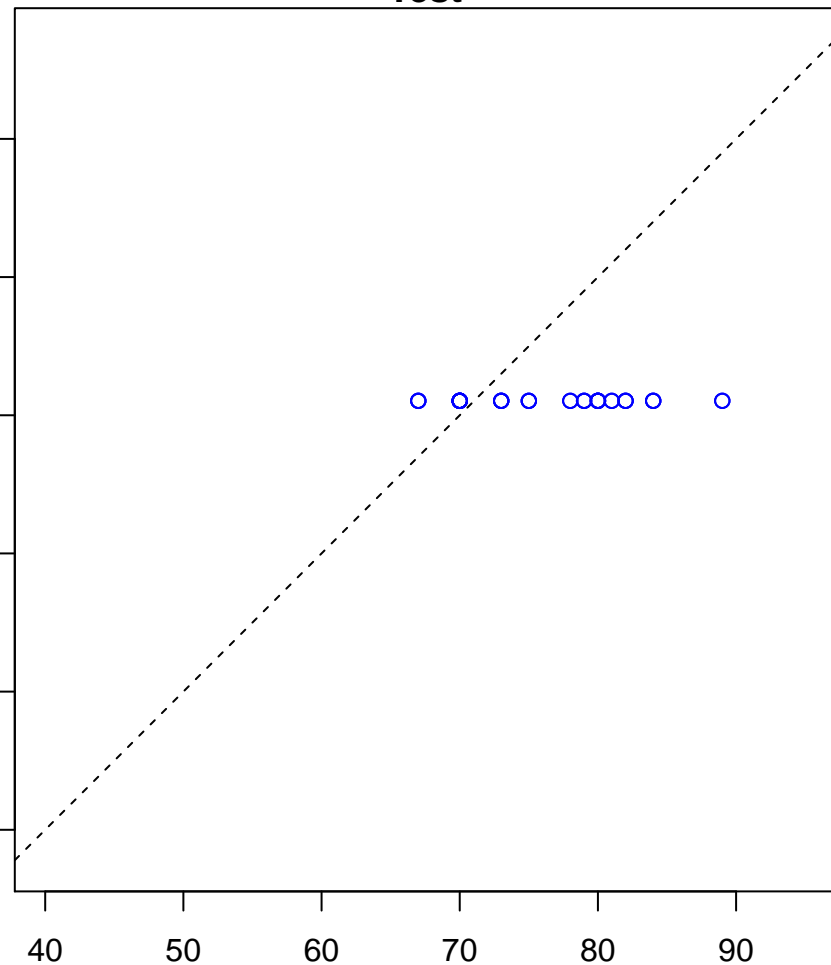
Actual Age

negative regulation of transport (Score: 0.794874)

Control

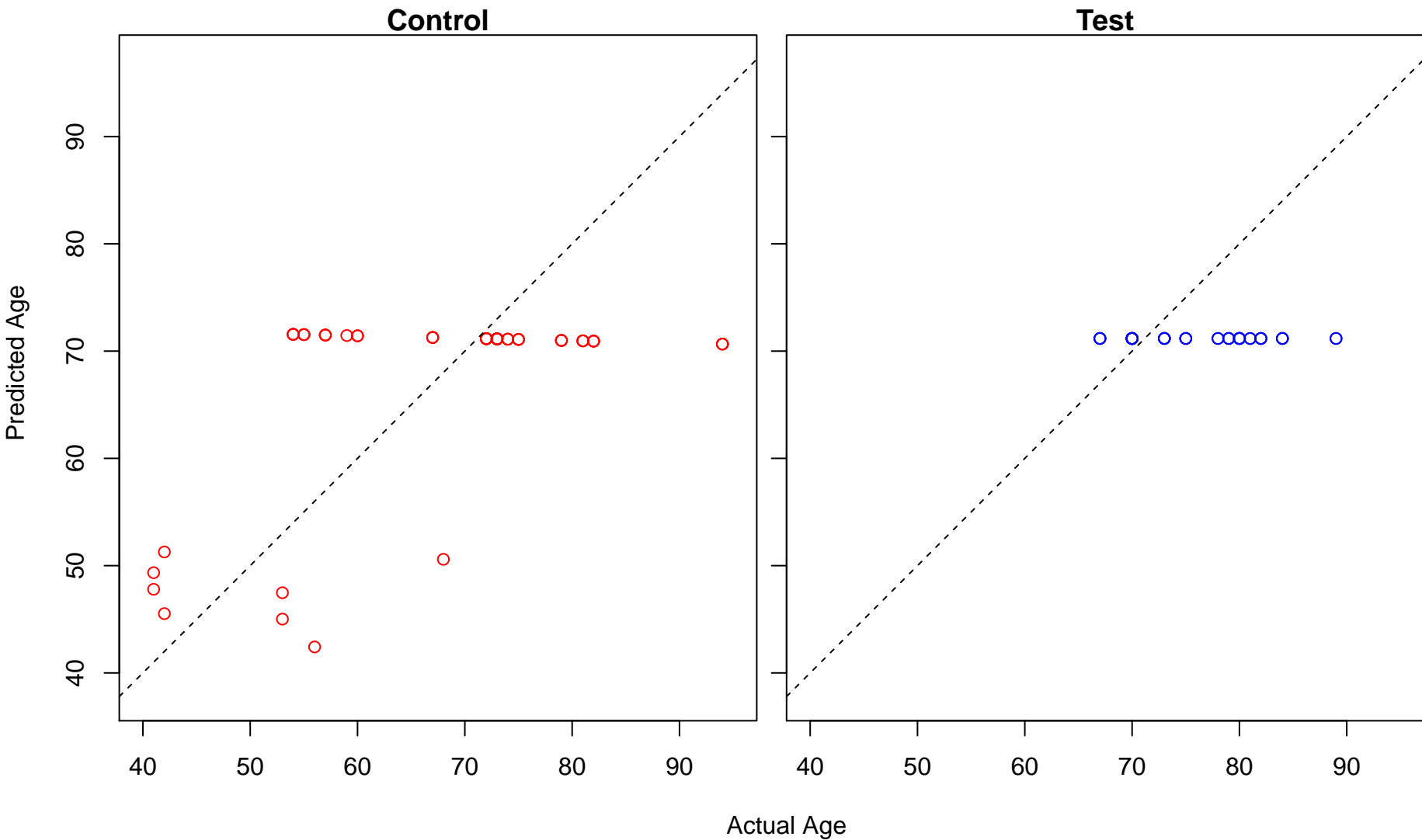


Test

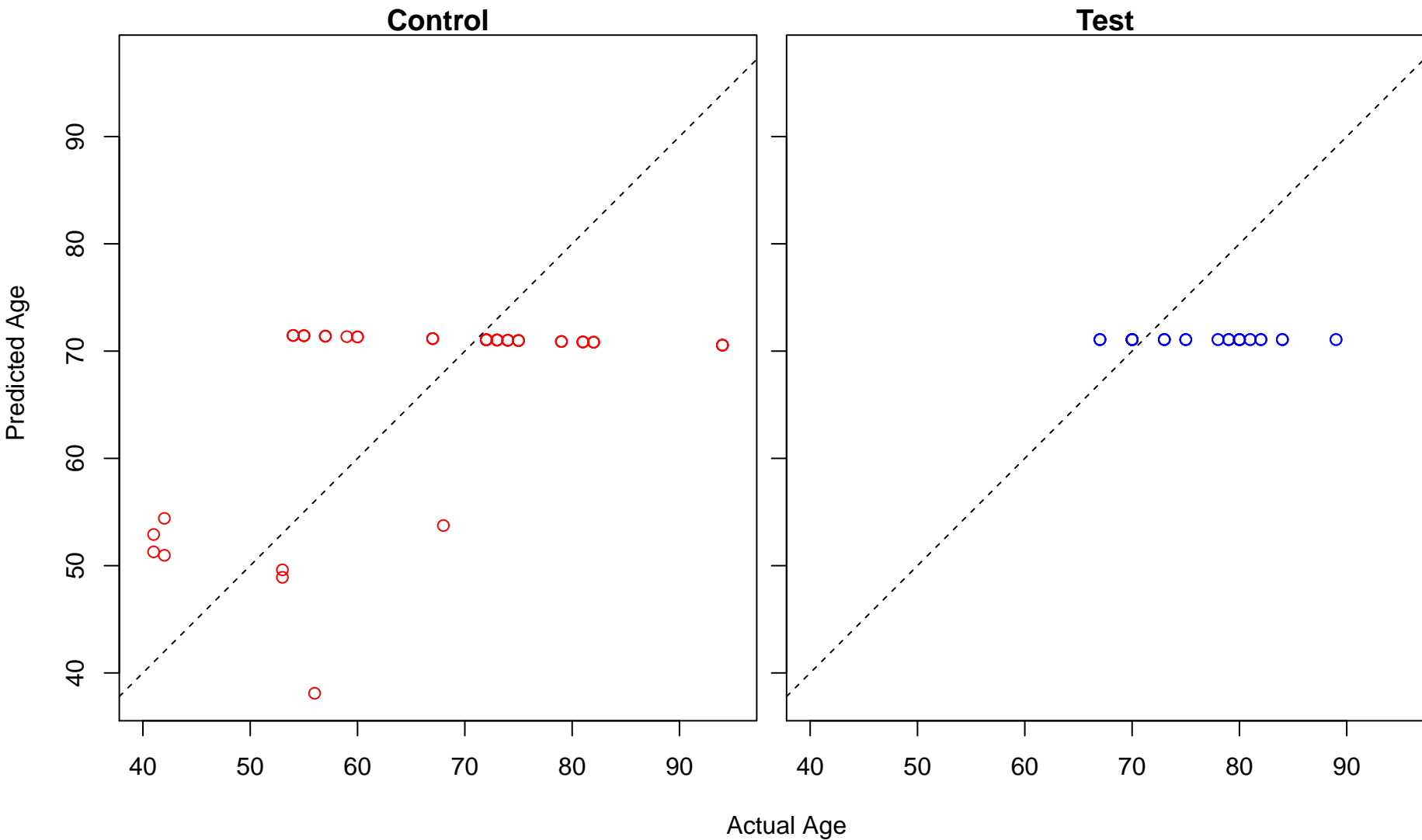


Actual Age

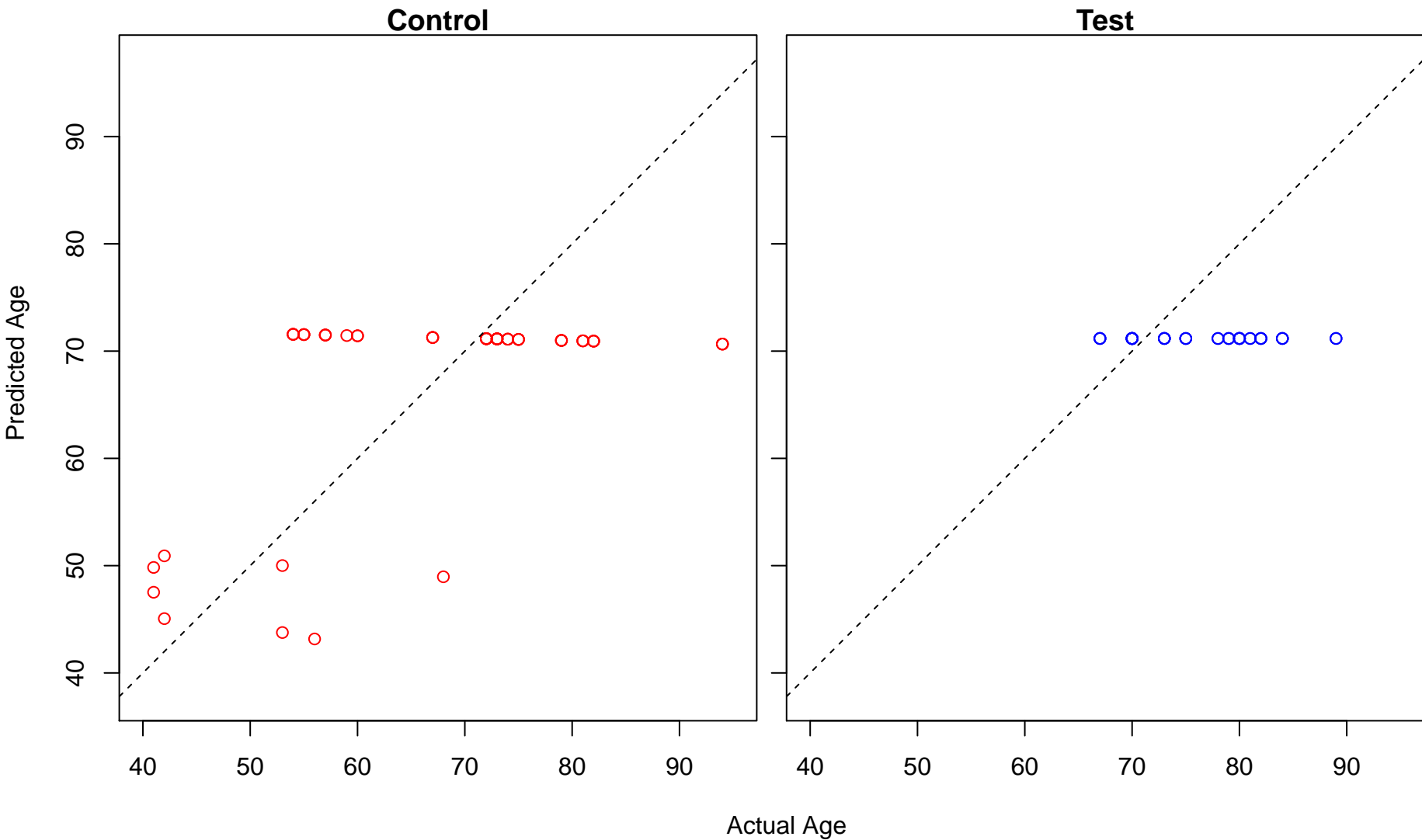
establishment of localization (Score: 0.794722)



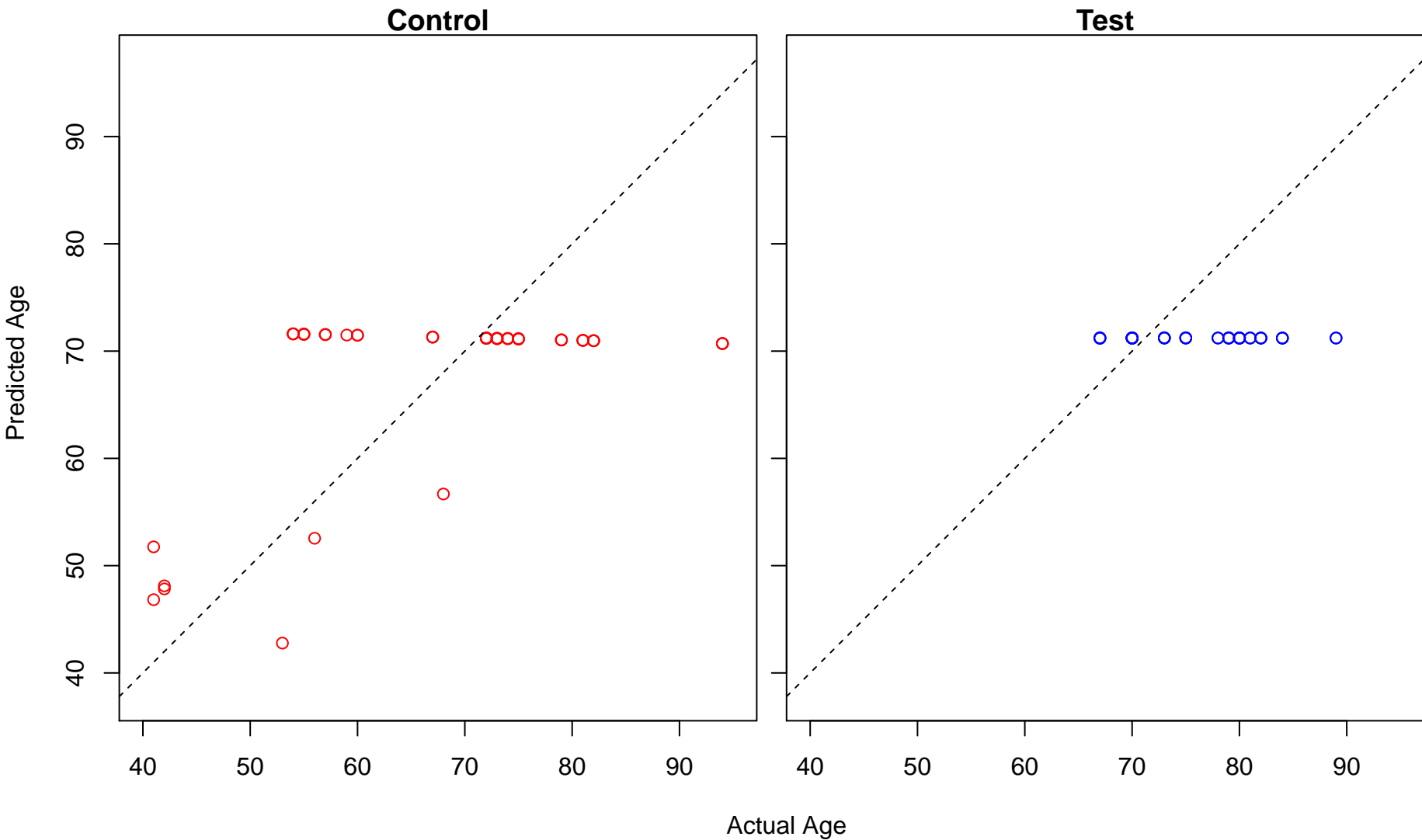
negative regulation of cellular component organization (Score: 0.794700)



biosynthetic process (Score: 0.794664)

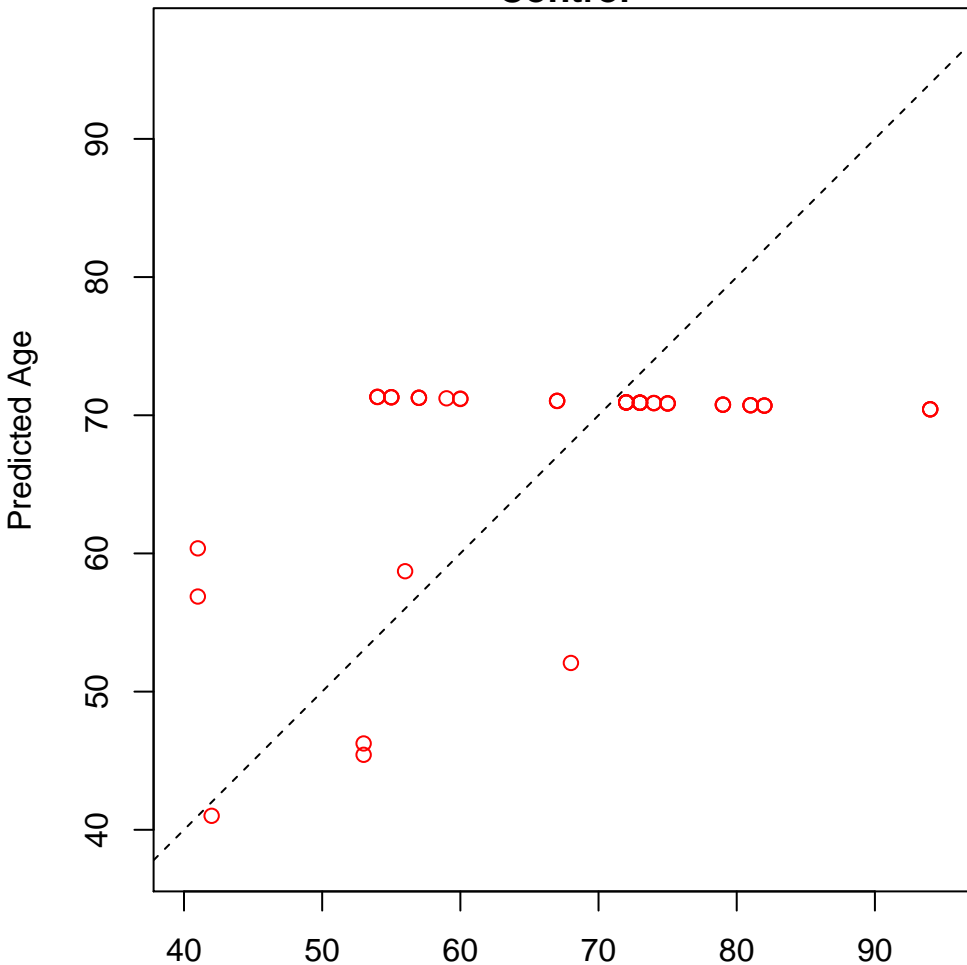


regulation of cytokine secretion (Score: 0.794637)

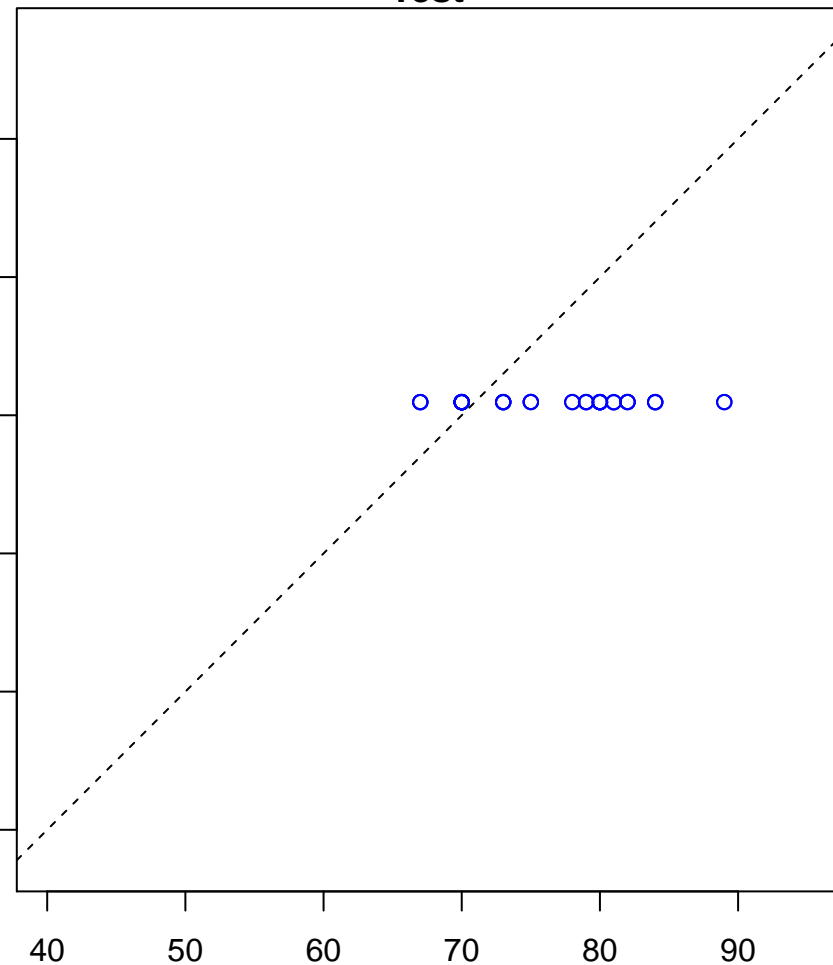


negative regulation of protein binding (Score: 0.794597)

Control



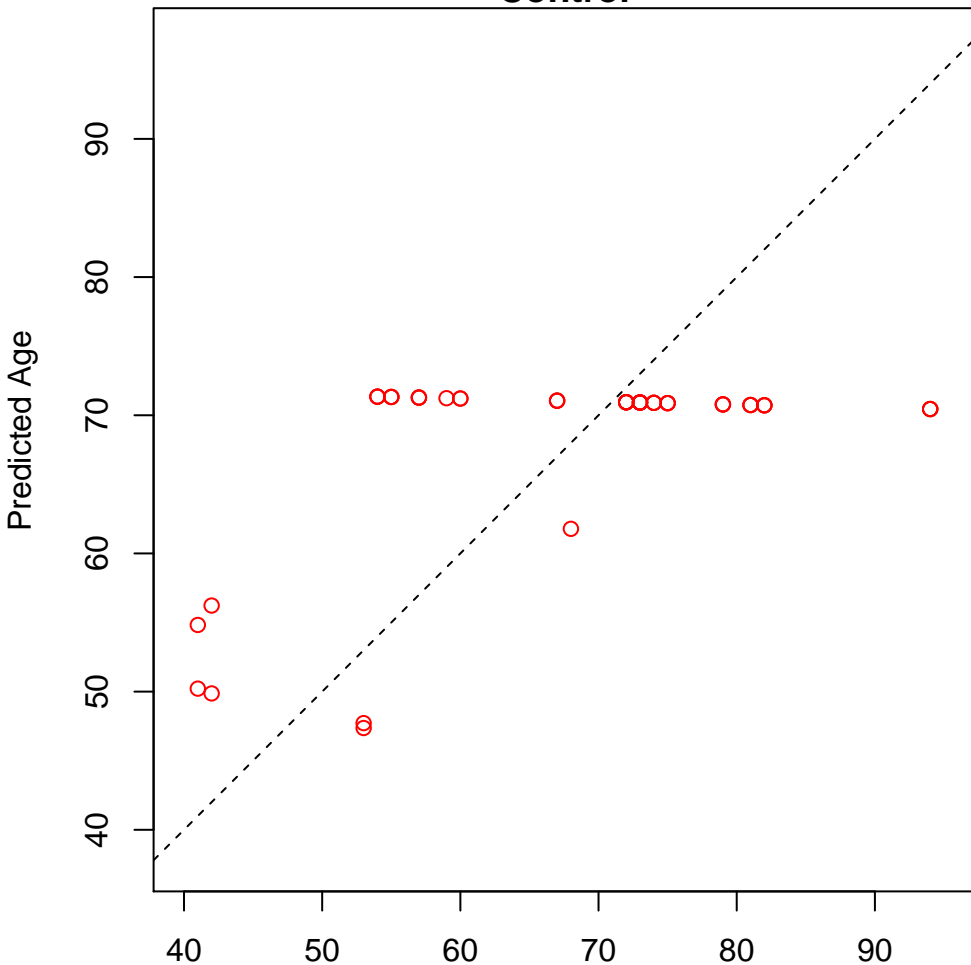
Test



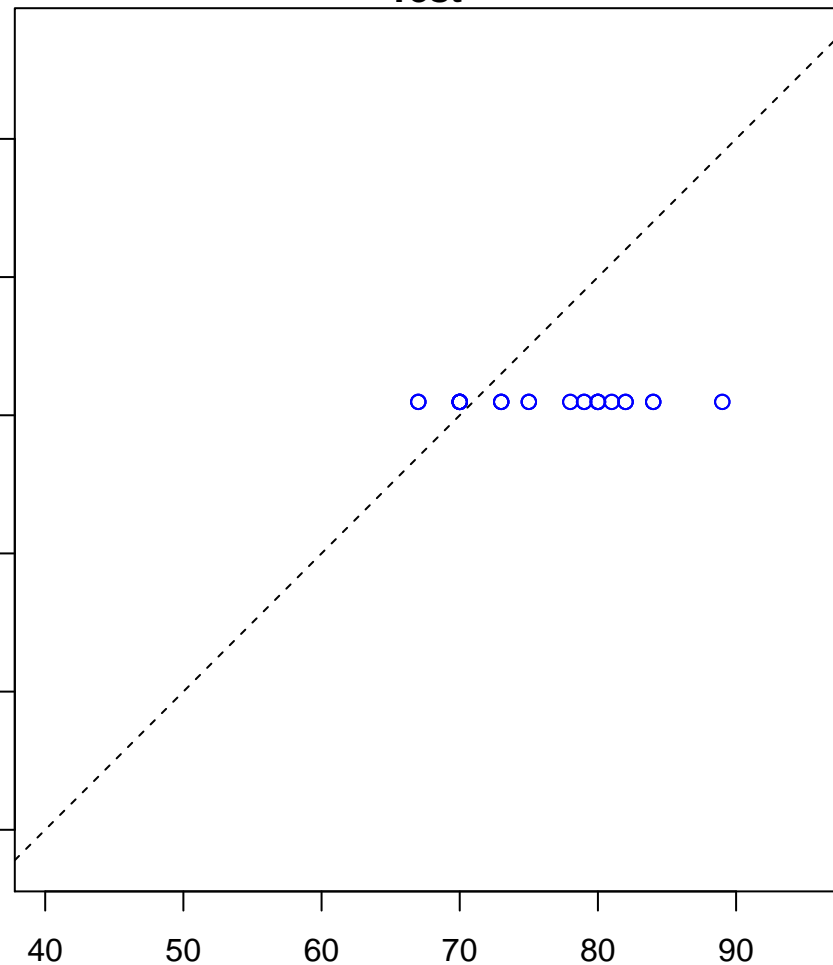
Actual Age

response to interferon-gamma (Score: 0.794574)

Control



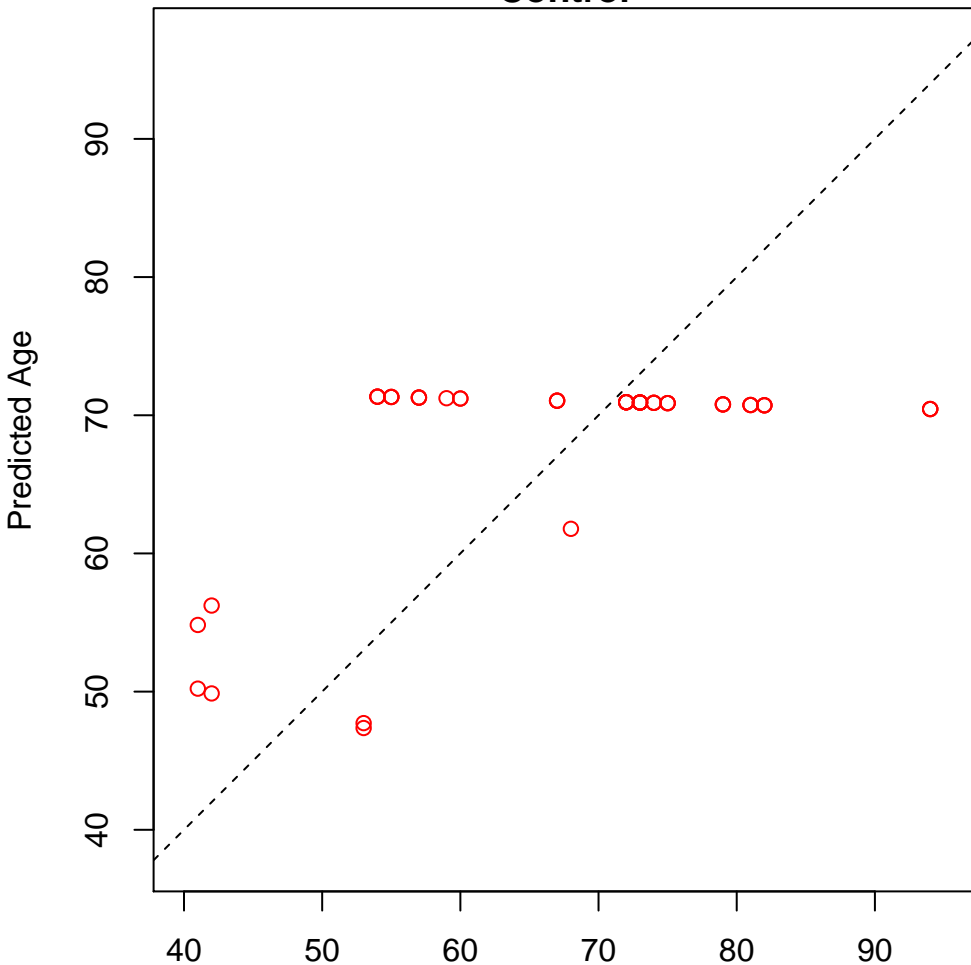
Test



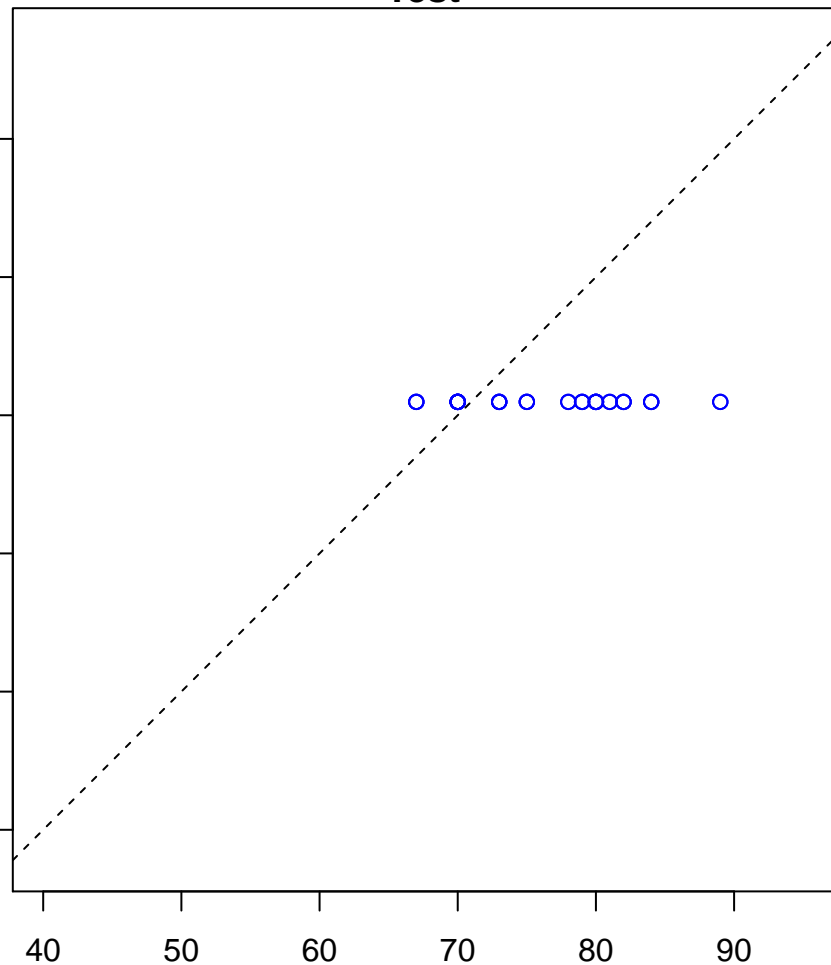
Actual Age

cellular response to interferon-gamma (Score: 0.794574)

Control



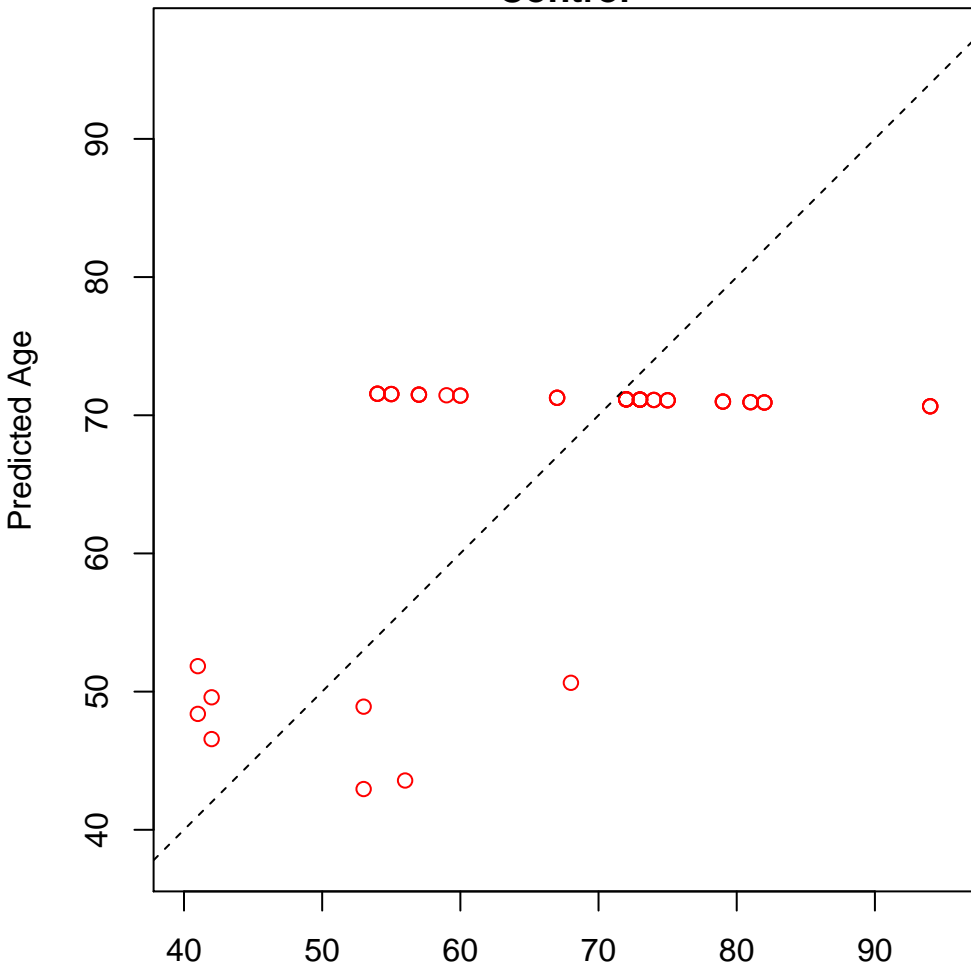
Test



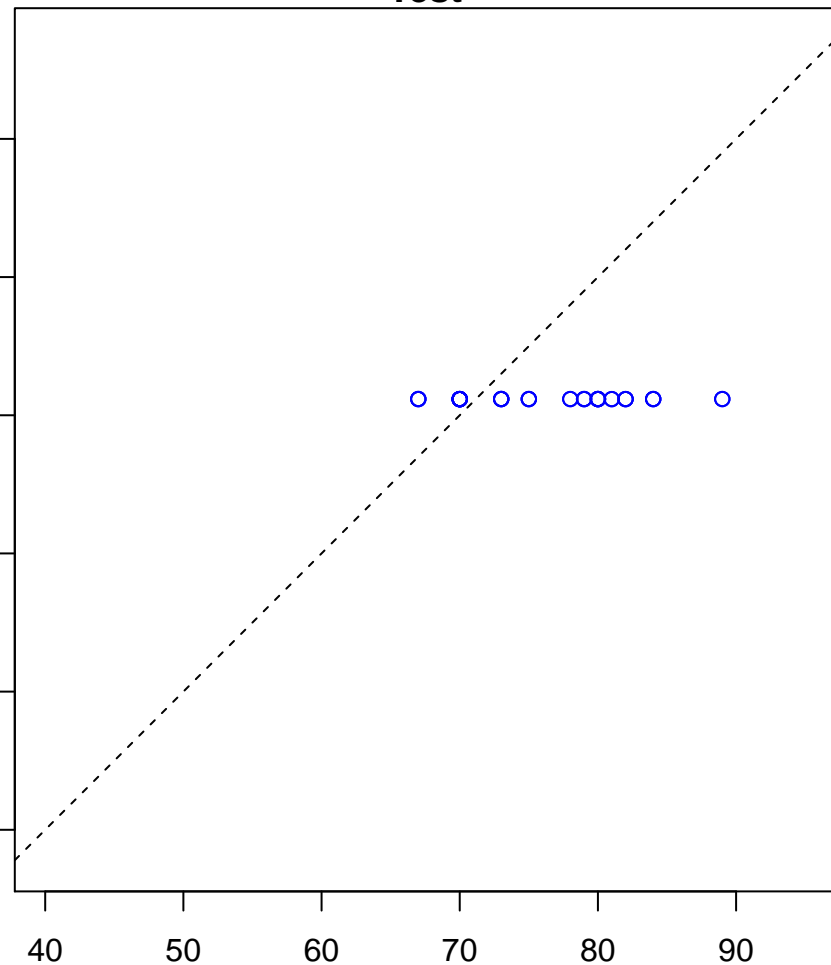
Actual Age

organic substance metabolic process (Score: 0.794564)

Control

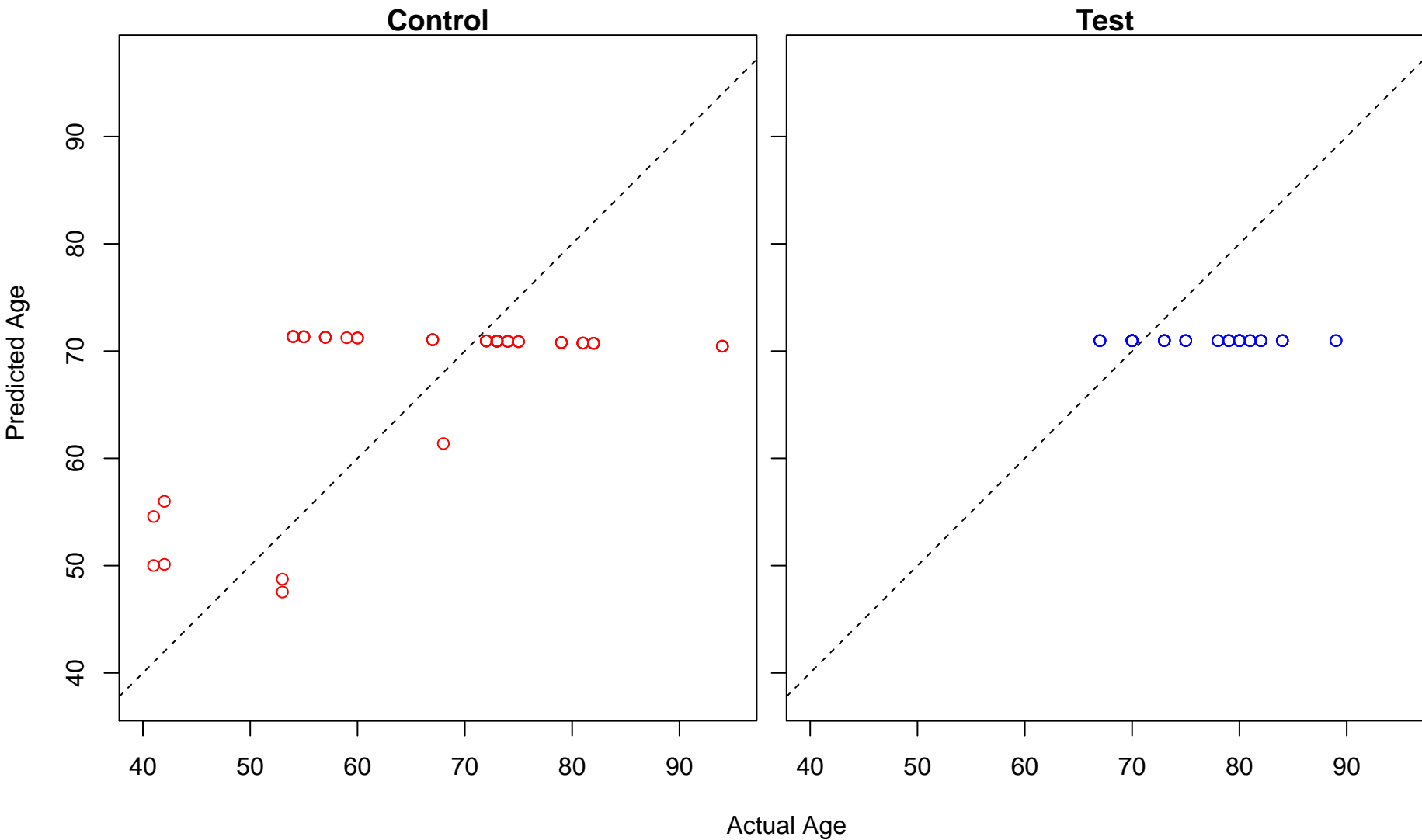


Test

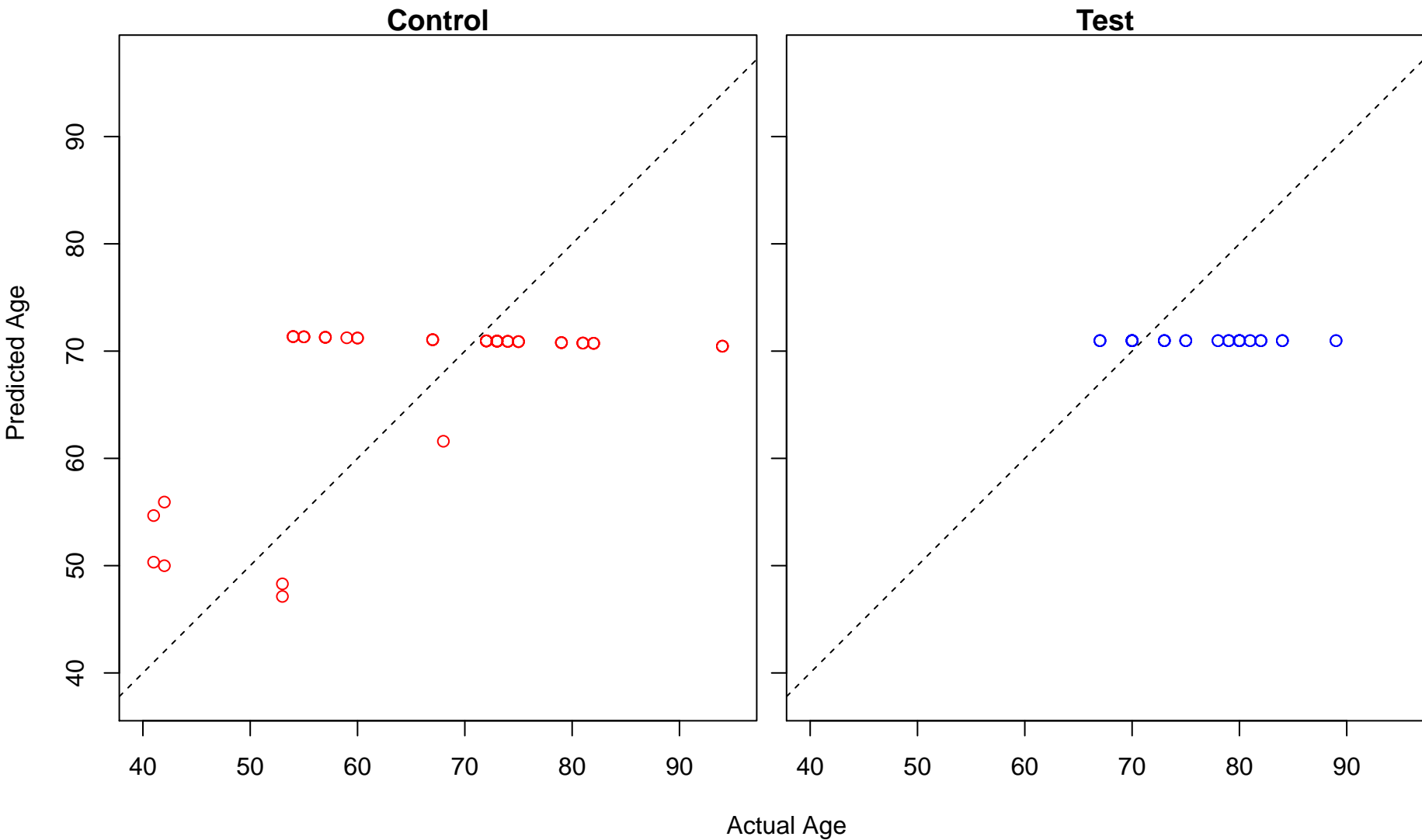


Actual Age

negative regulation of cellular amide metabolic process (Score: 0.794558)

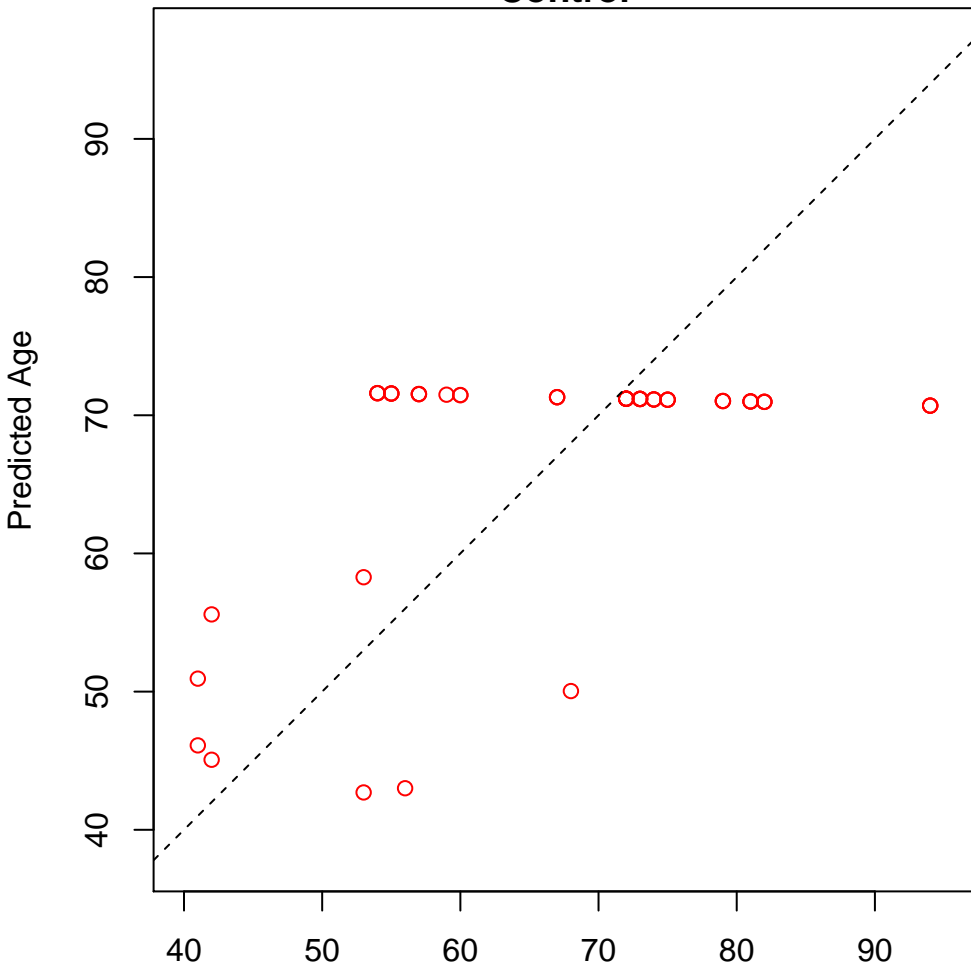


negative regulation of translational initiation (Score: 0.794536)

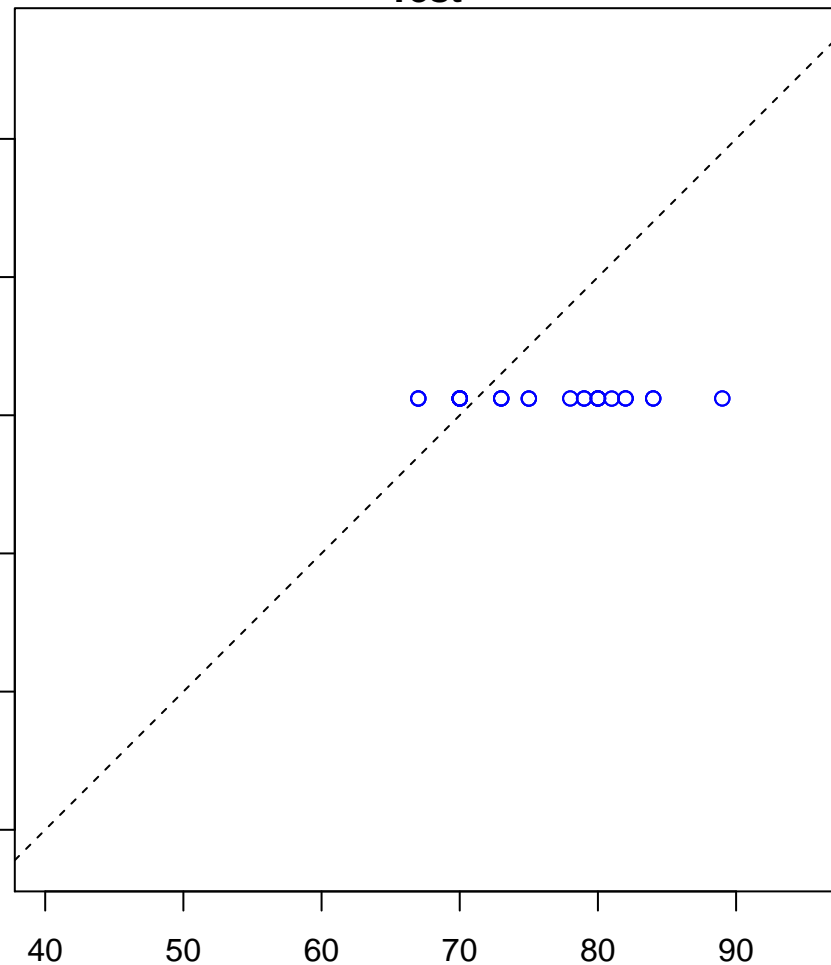


positive regulation of protein binding (Score: 0.794531)

Control

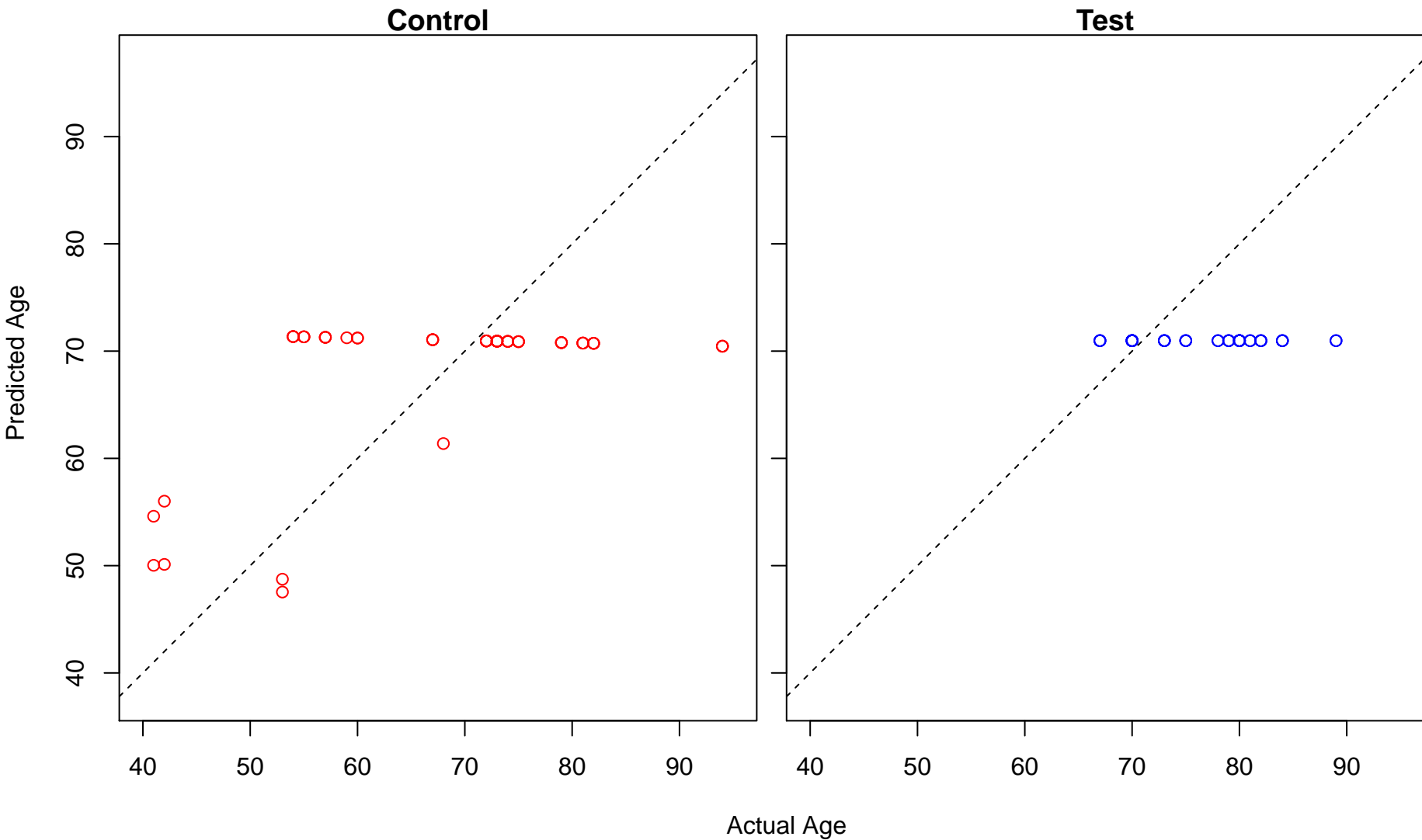


Test

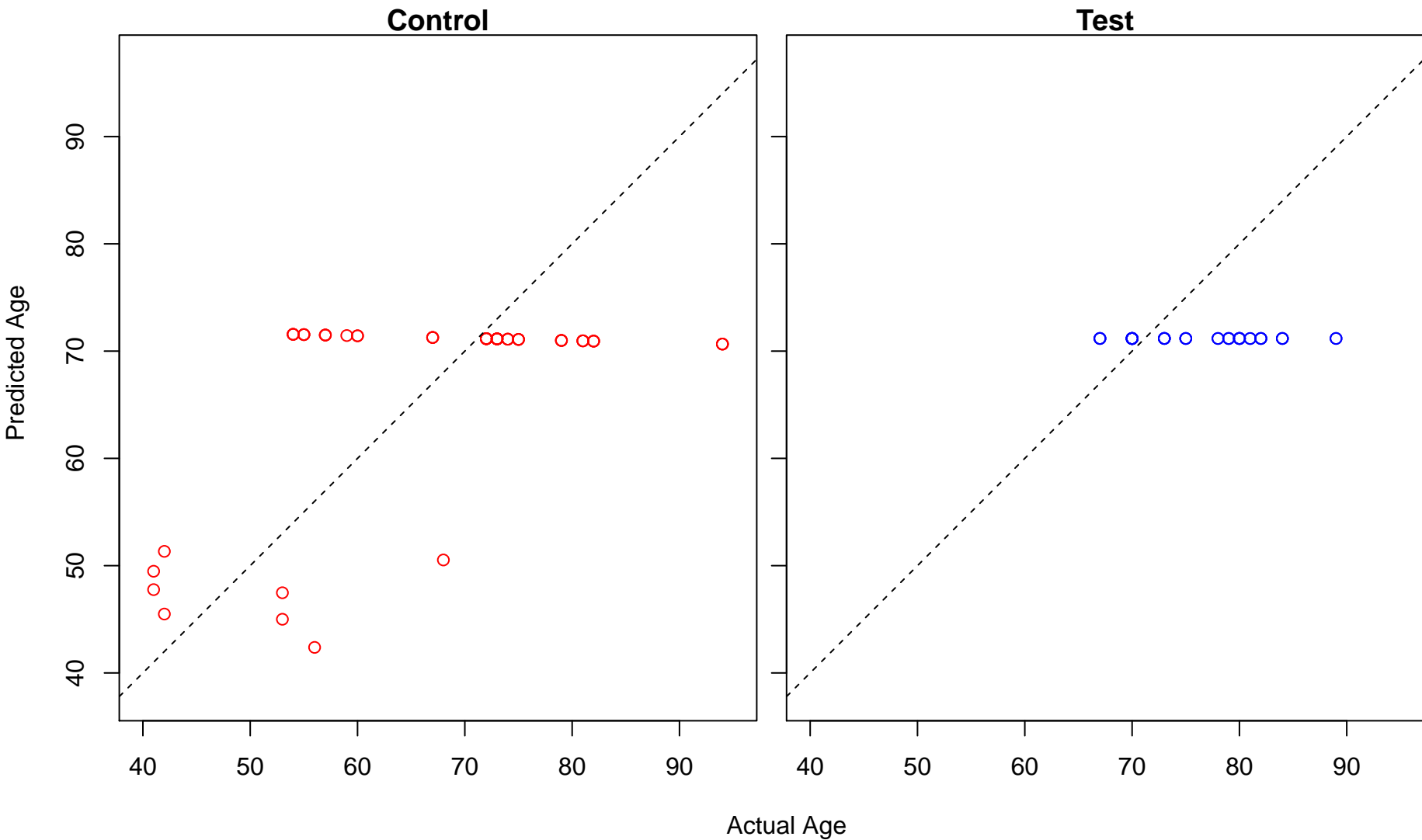


Actual Age

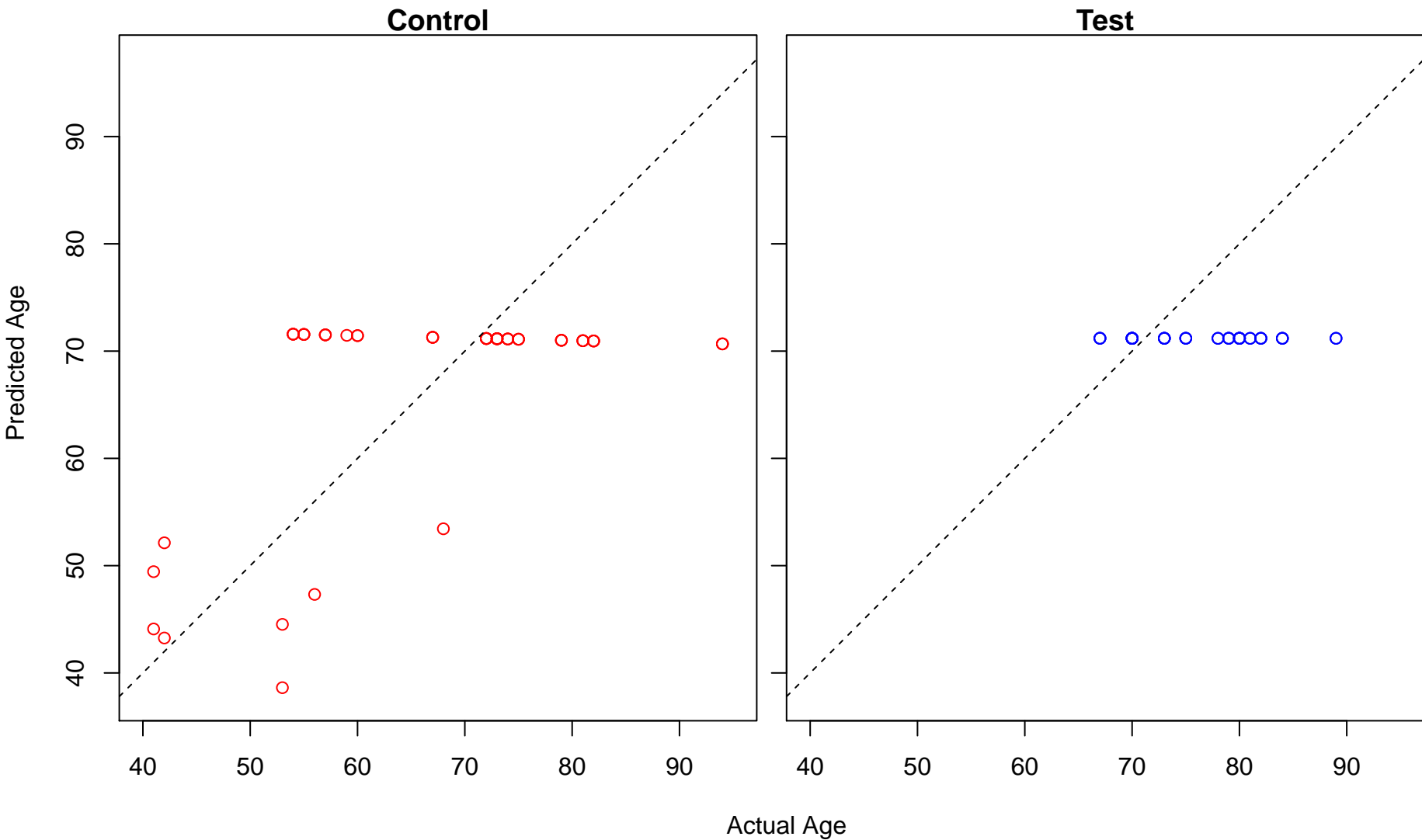
negative regulation of translation (Score: 0.794496)



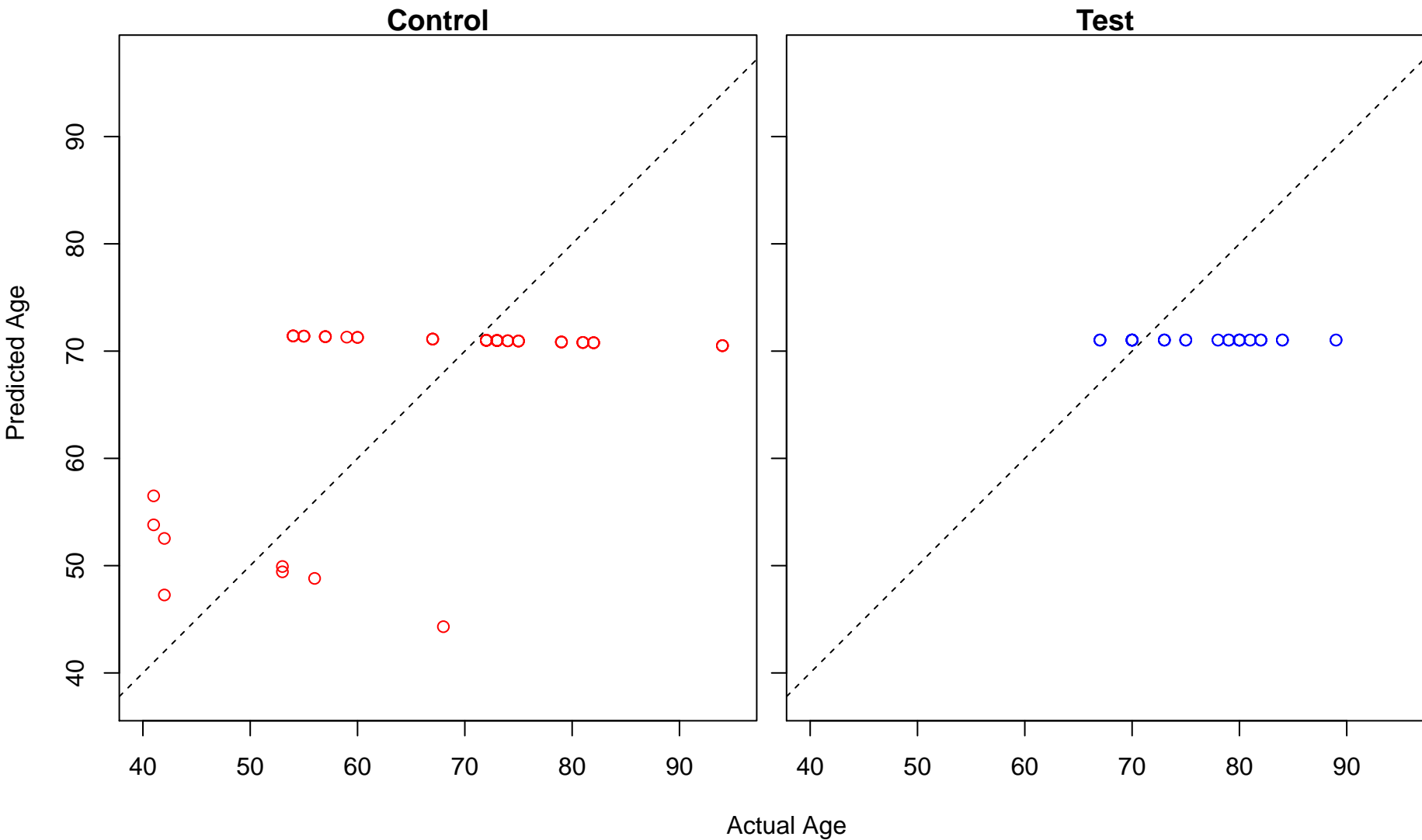
localization (Score: 0.794478)



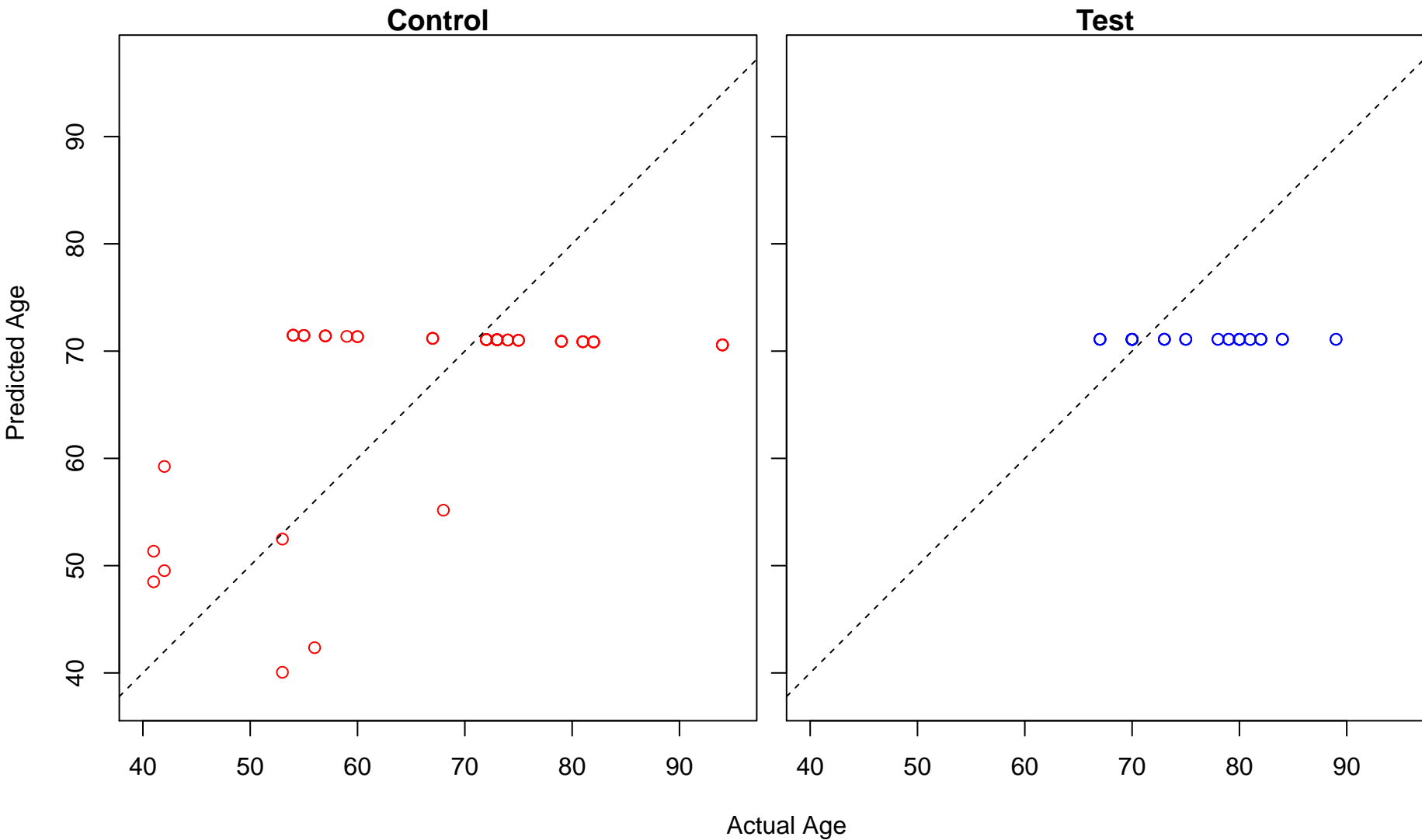
cell death (Score: 0.794475)



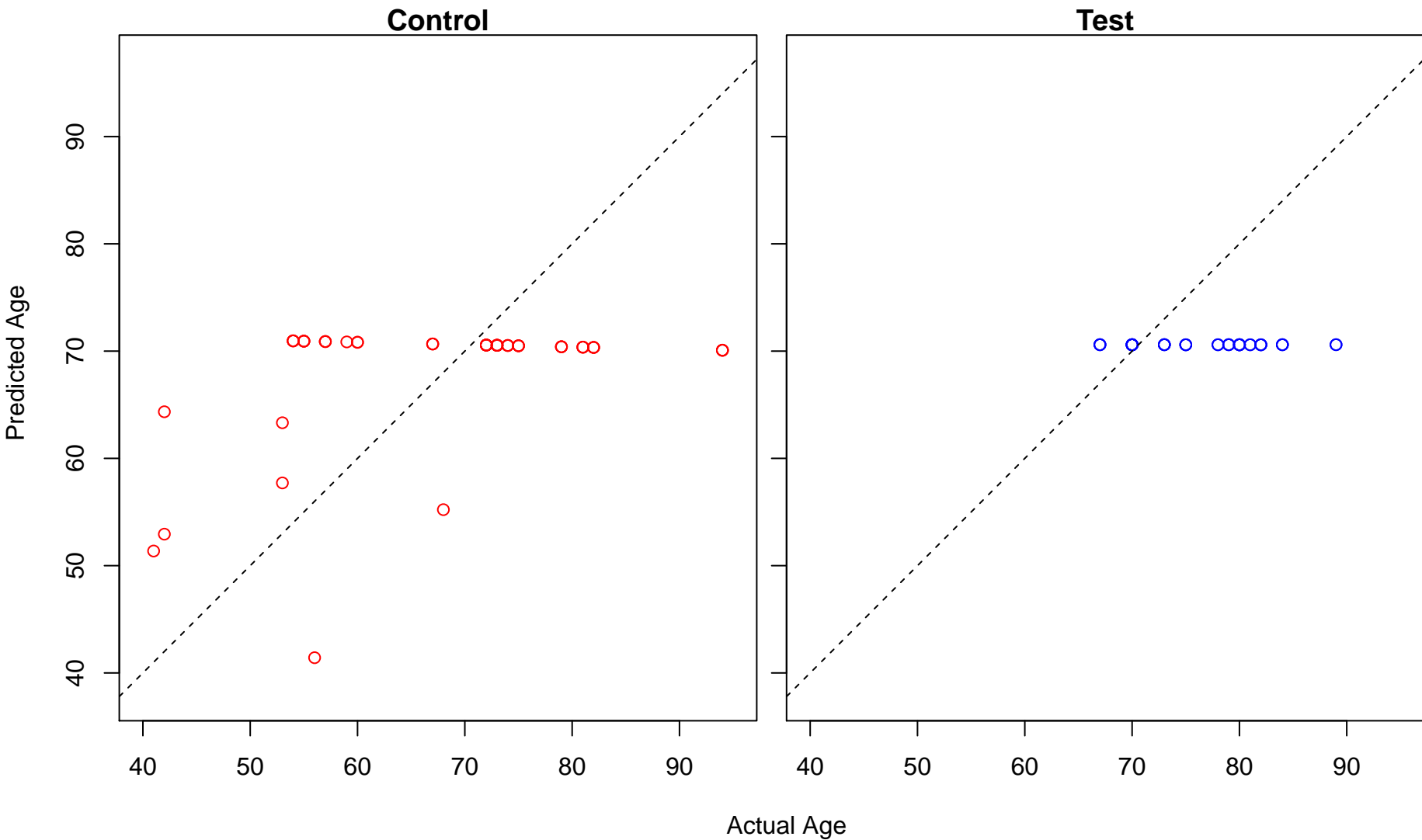
regulation of receptor activity (Score: 0.794468)

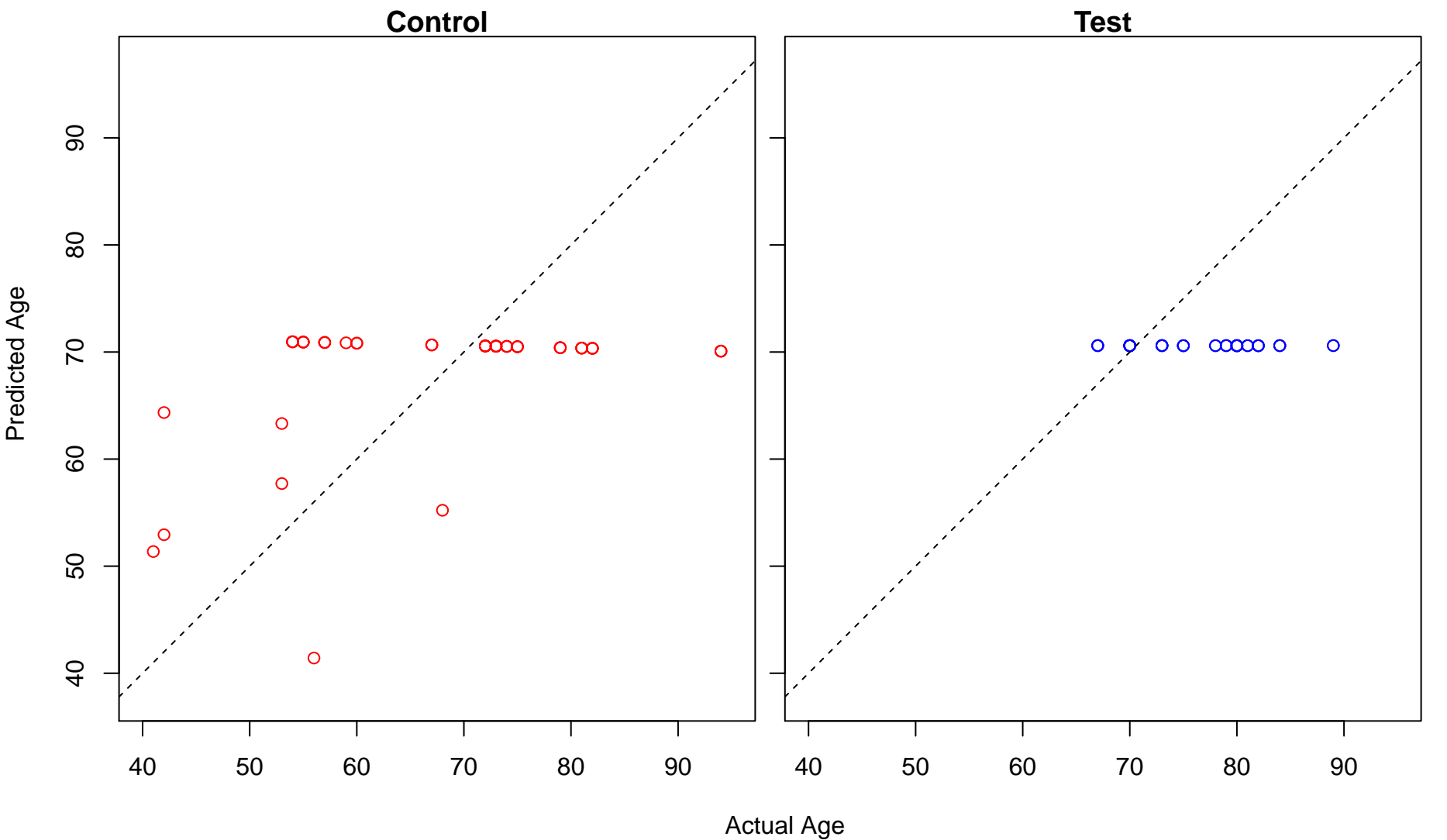


import into cell (Score: 0.794460)



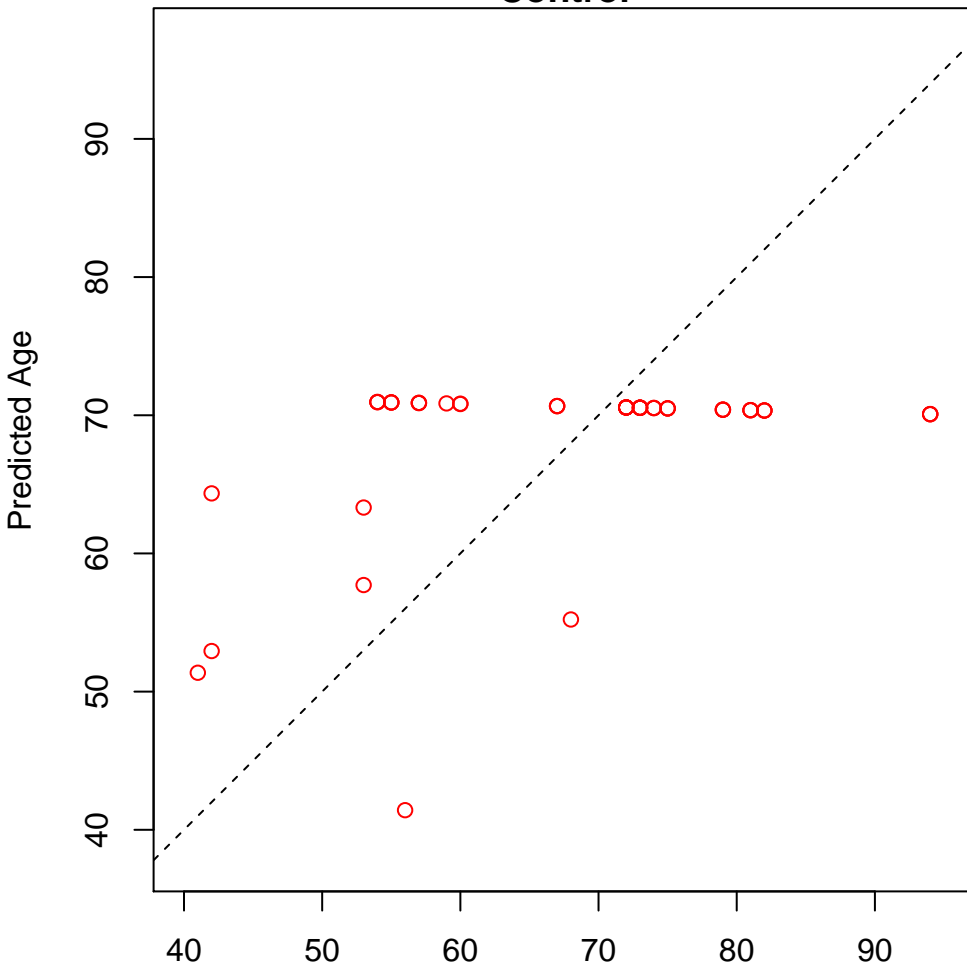
Fc receptor mediated stimulatory signaling pathway (Score: 0.794433)



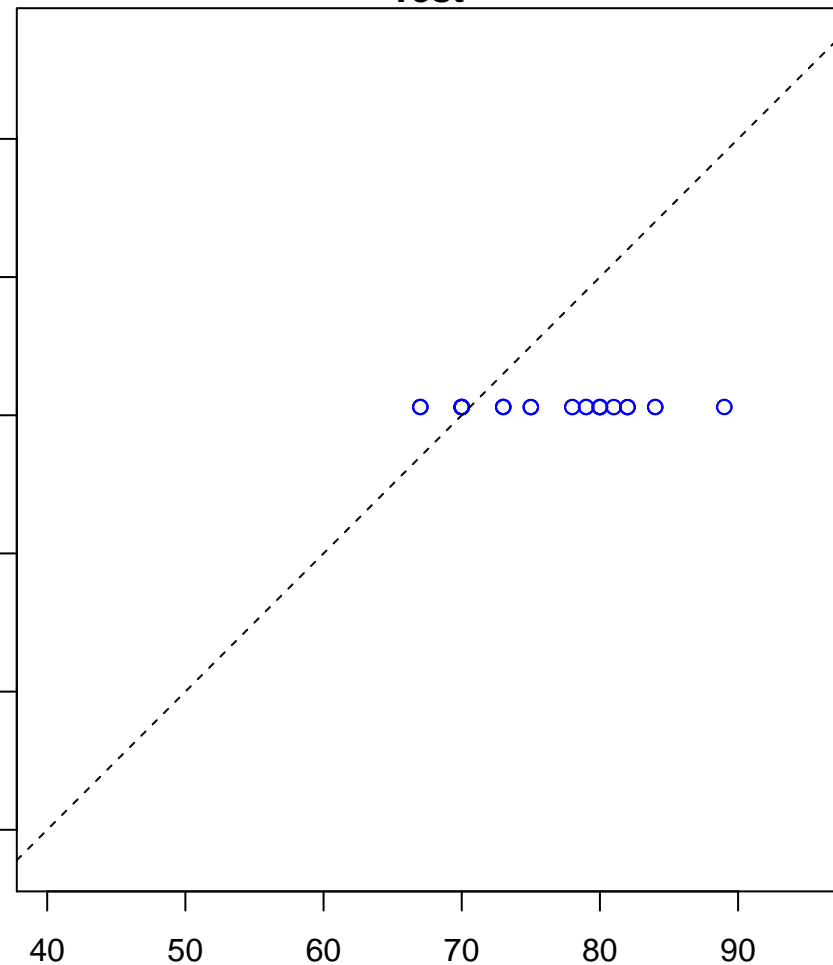


Fc-gamma receptor signaling pathway (Score: 0.794433)

Control

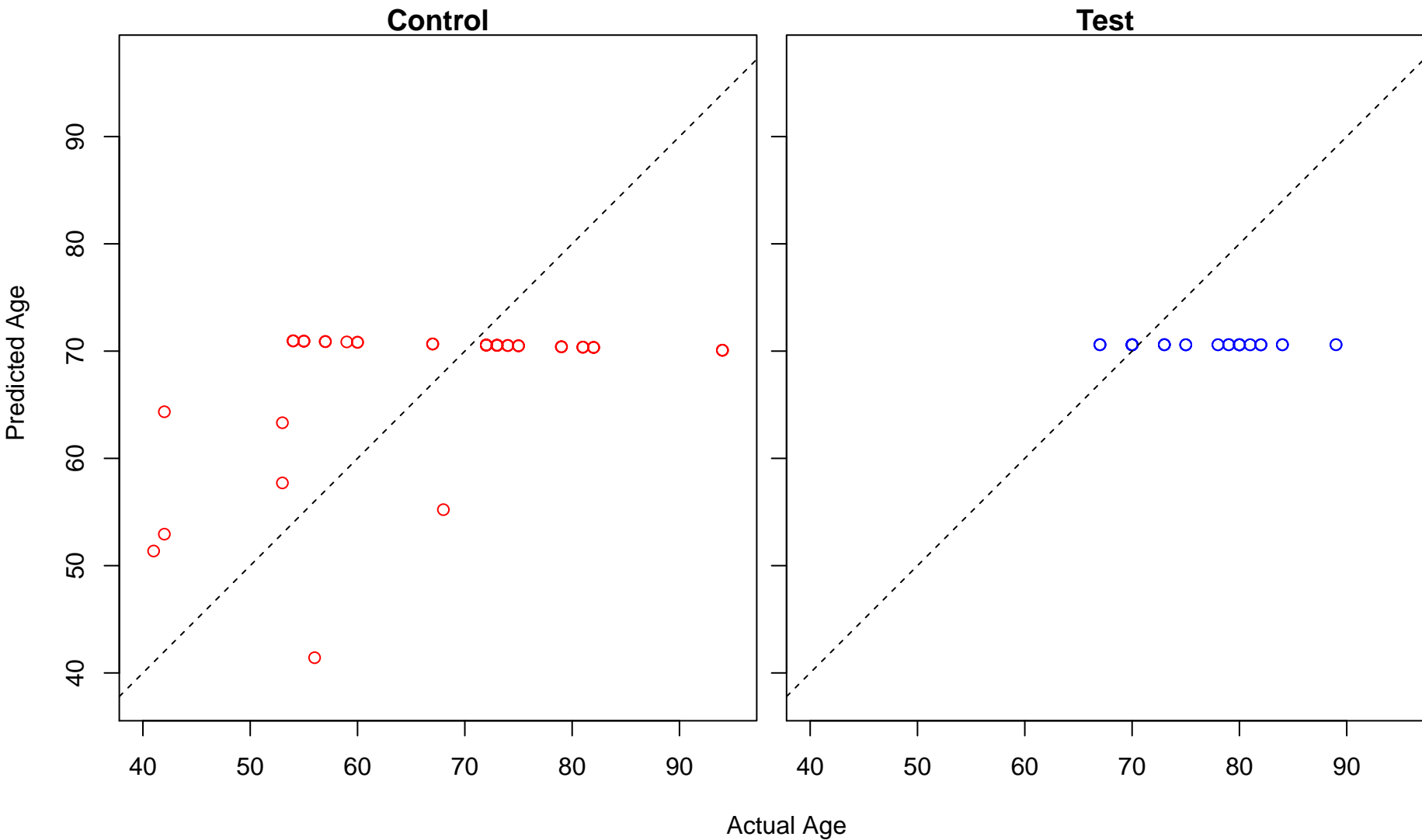


Test



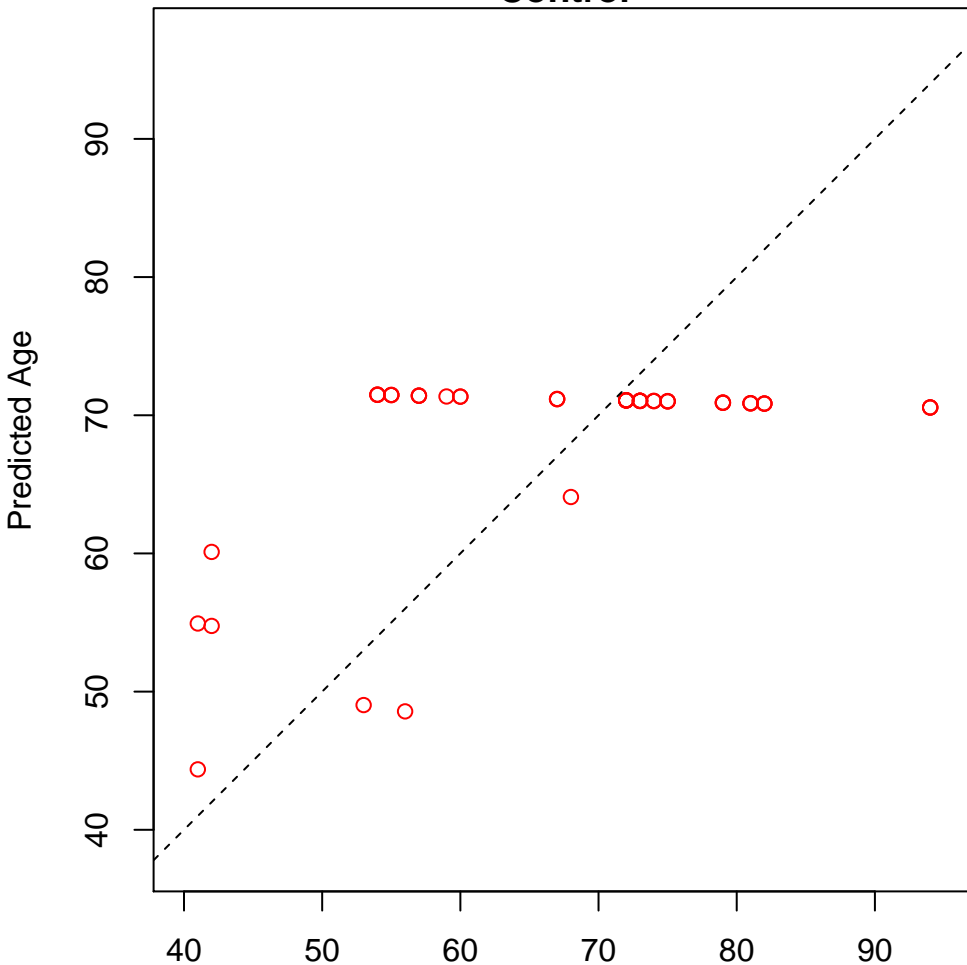
Actual Age

Fc-gamma receptor signaling pathway involved in phagocytosis (Score: 0.794433)

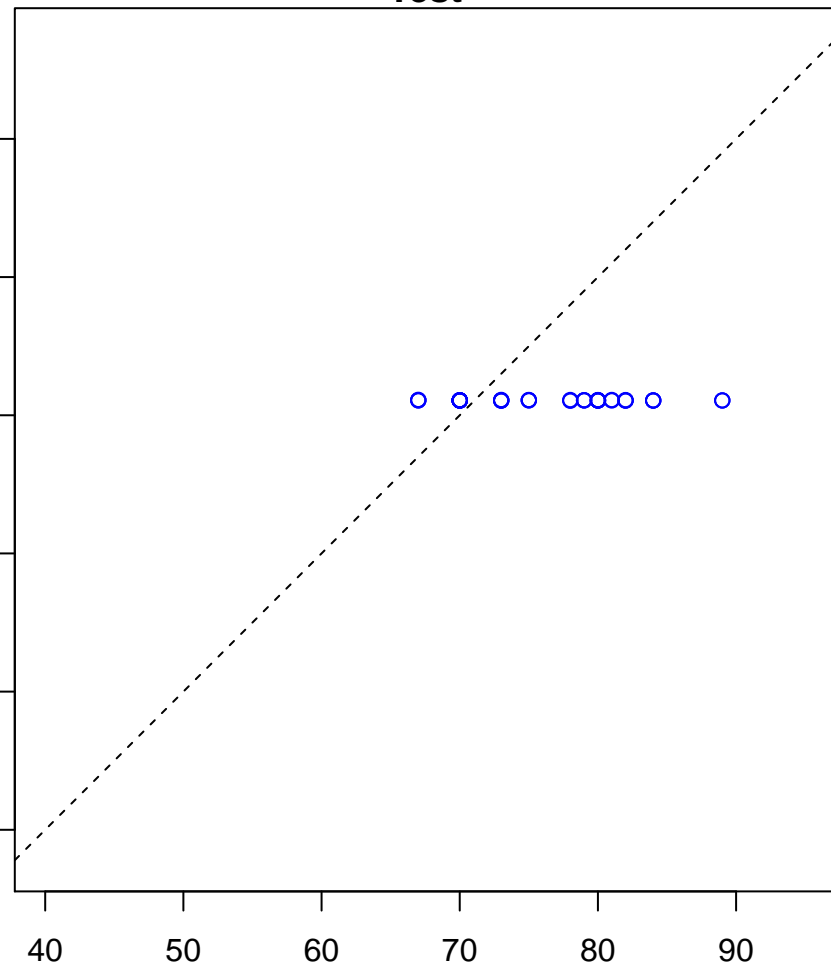


negative regulation of cell adhesion (Score: 0.794419)

Control

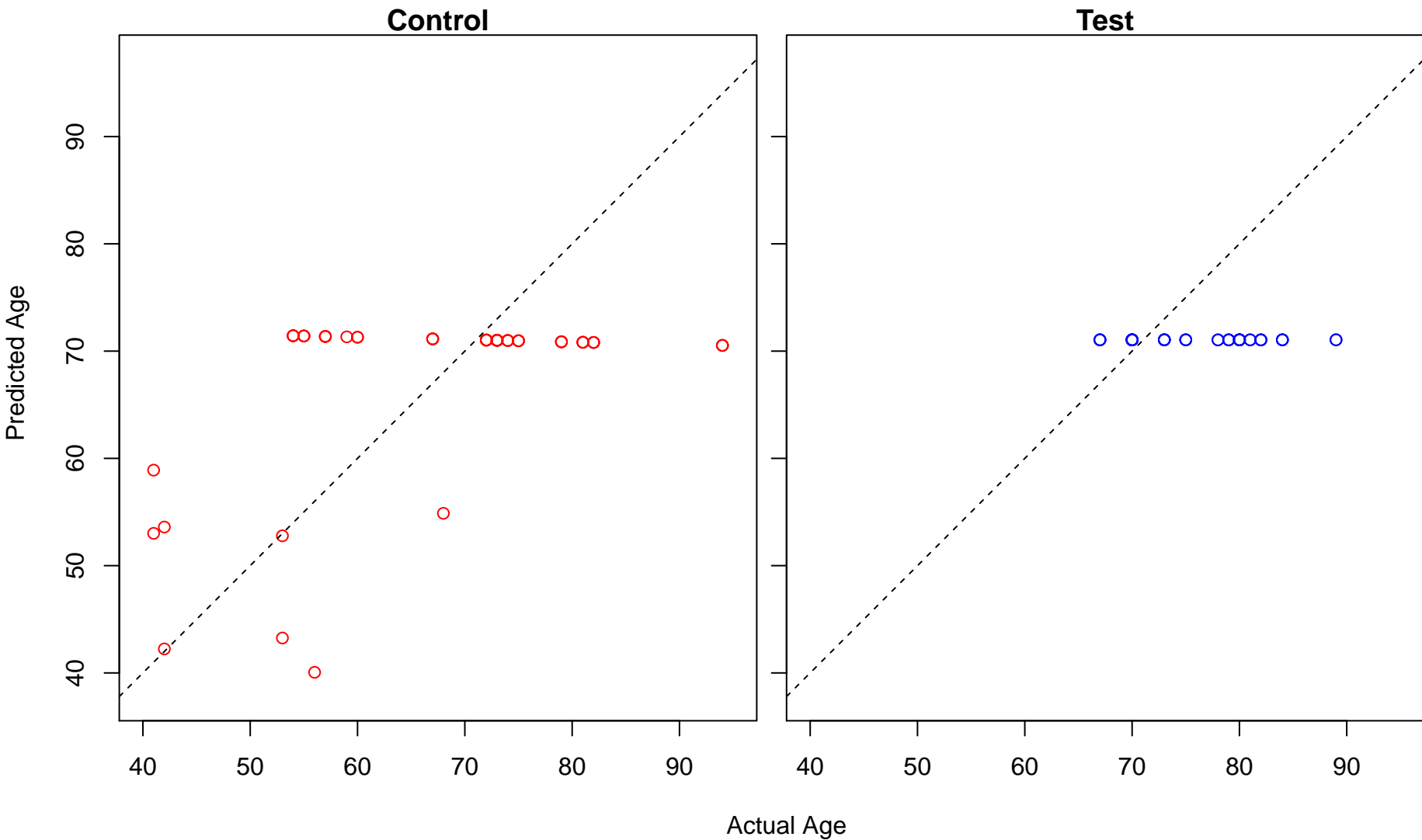


Test



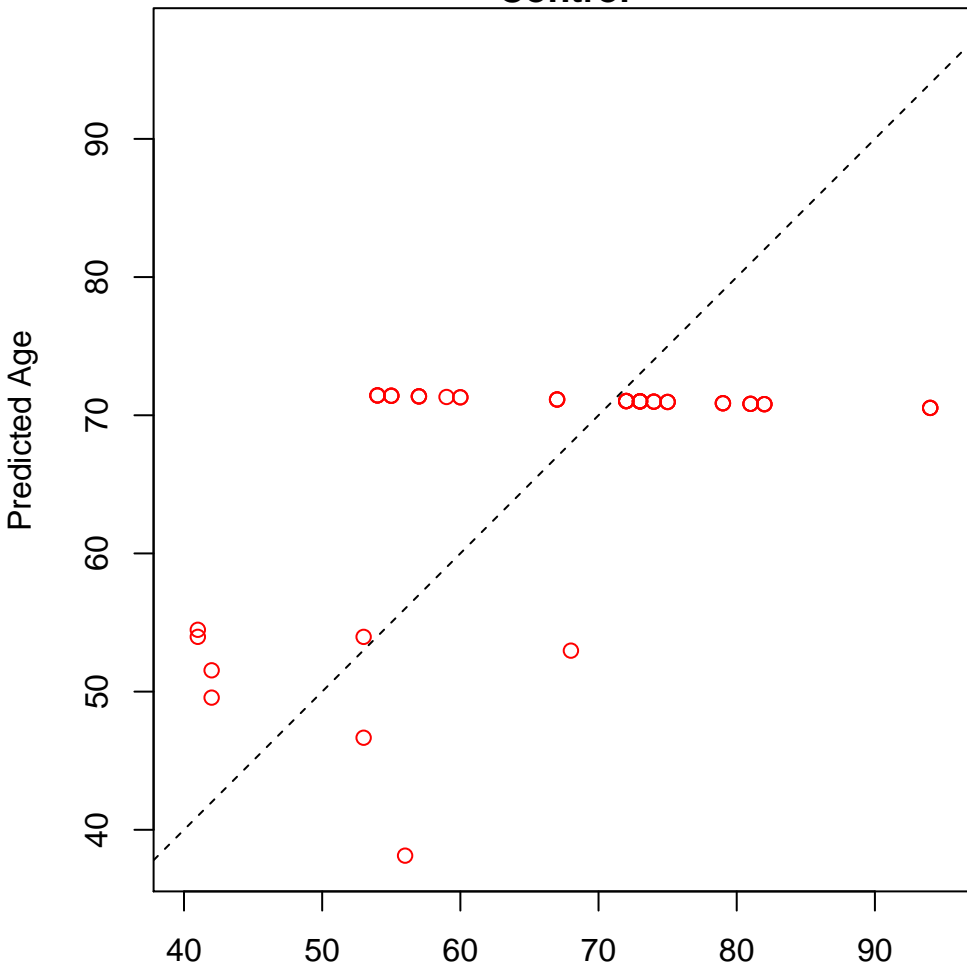
Actual Age

positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator (Score: 0.794406)

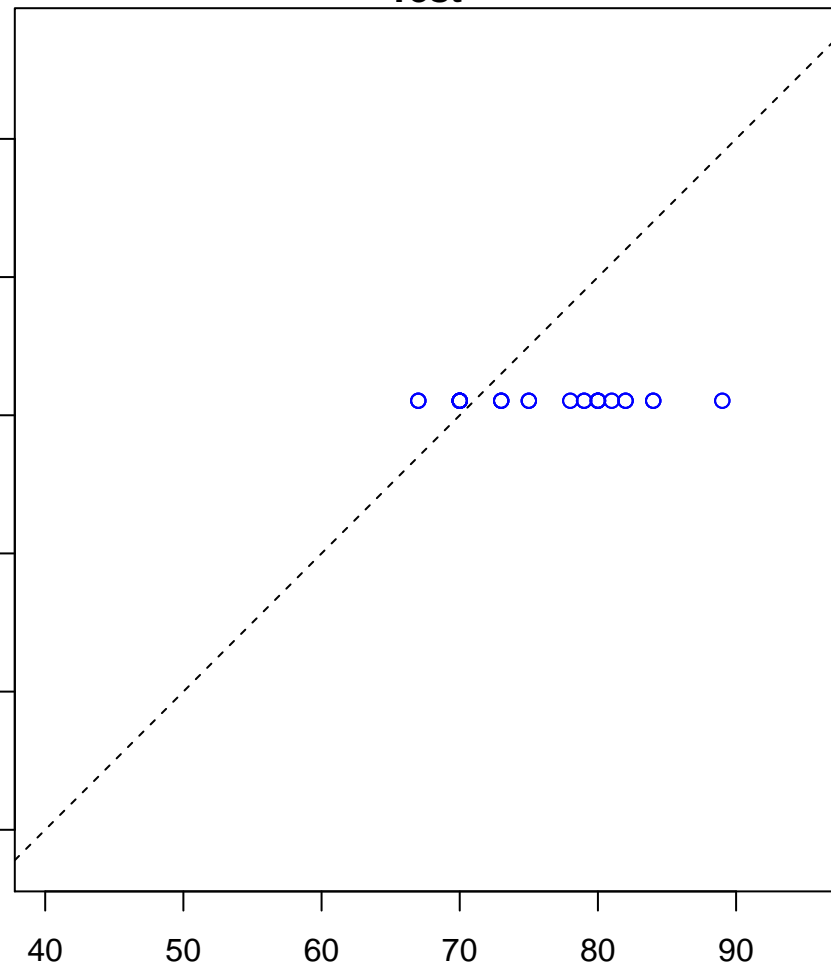


response to endogenous stimulus (Score: 0.794329)

Control

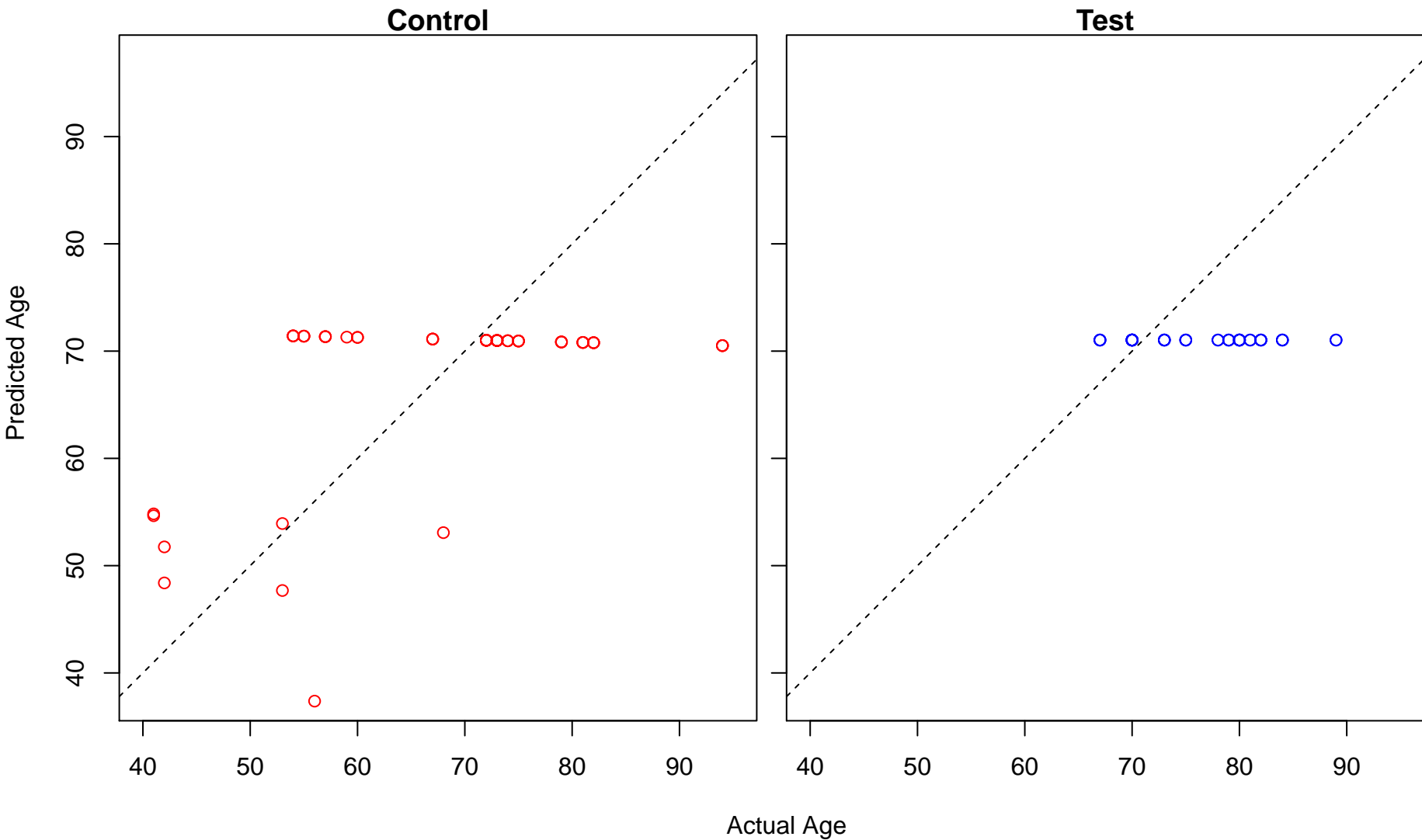


Test

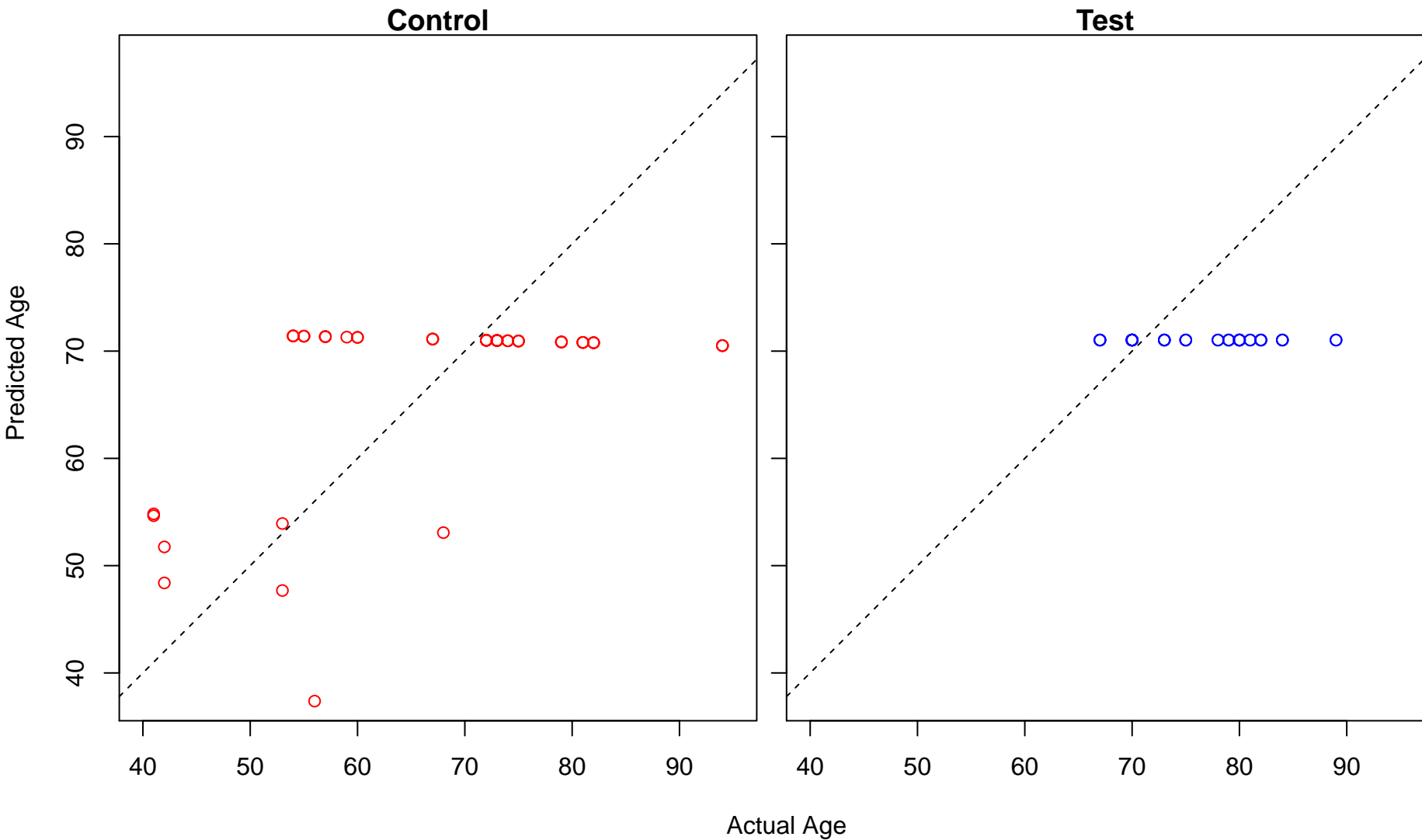


Actual Age

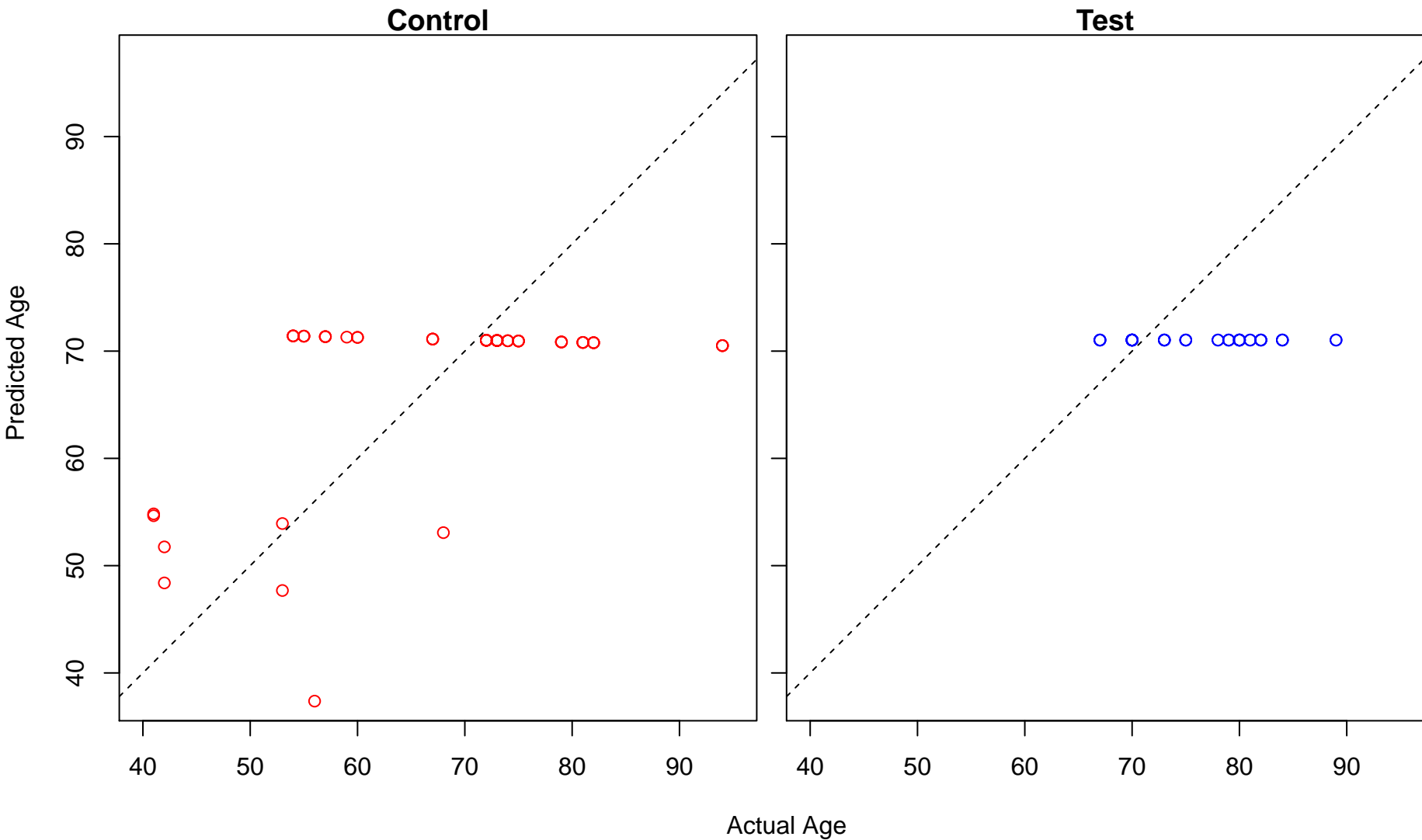
negative regulation of transcription, DNA-templated (Score: 0.794315)



negative regulation of RNA biosynthetic process (Score: 0.794315)

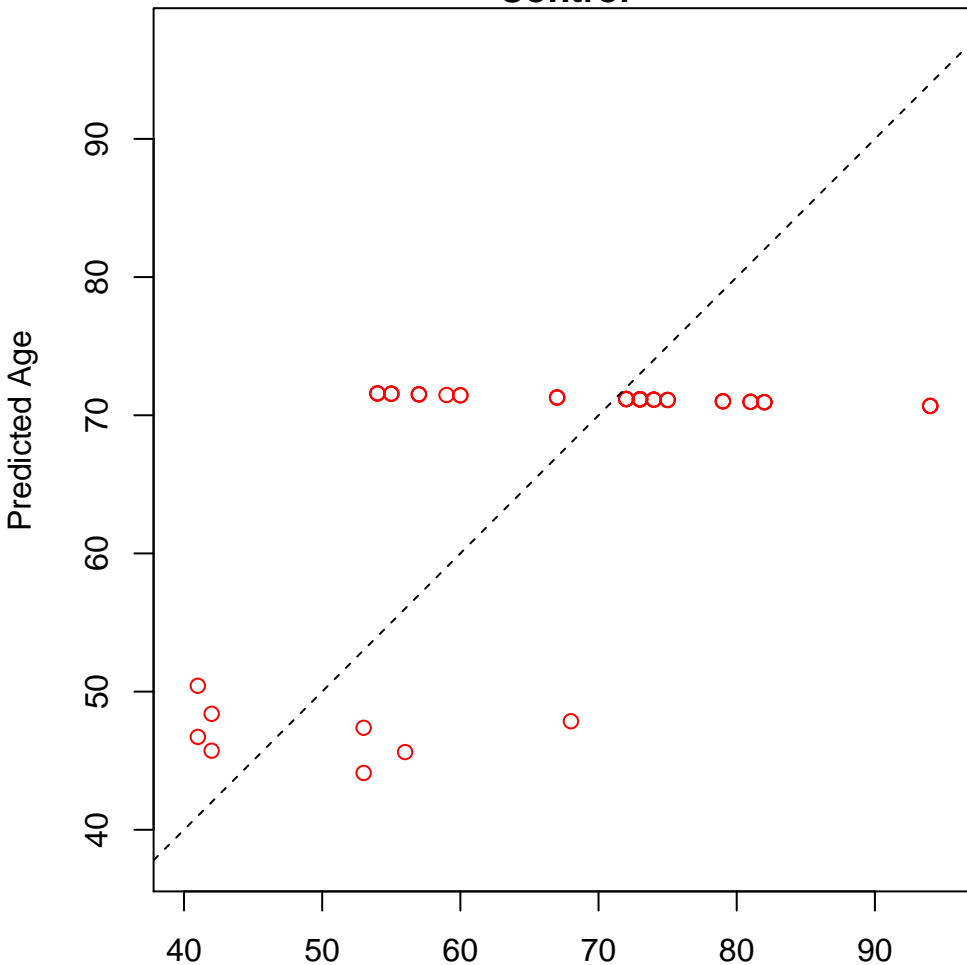


negative regulation of nucleic acid-templated transcription (Score: 0.794315)

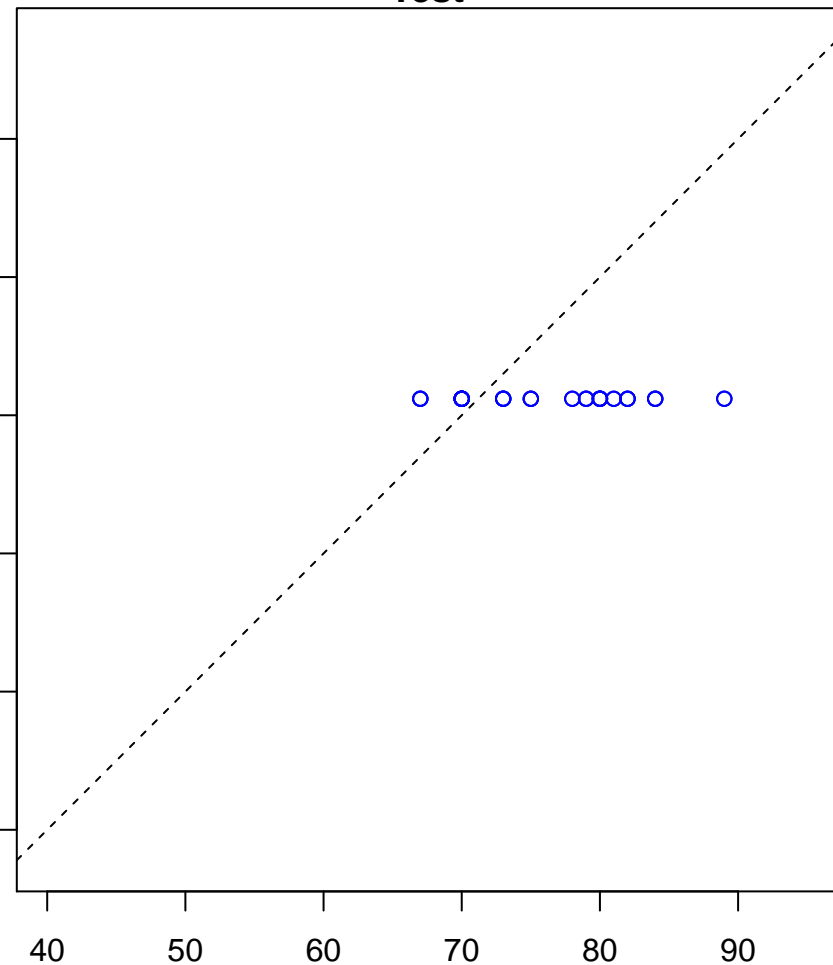


regulation of cellular metabolic process (Score: 0.794311)

Control

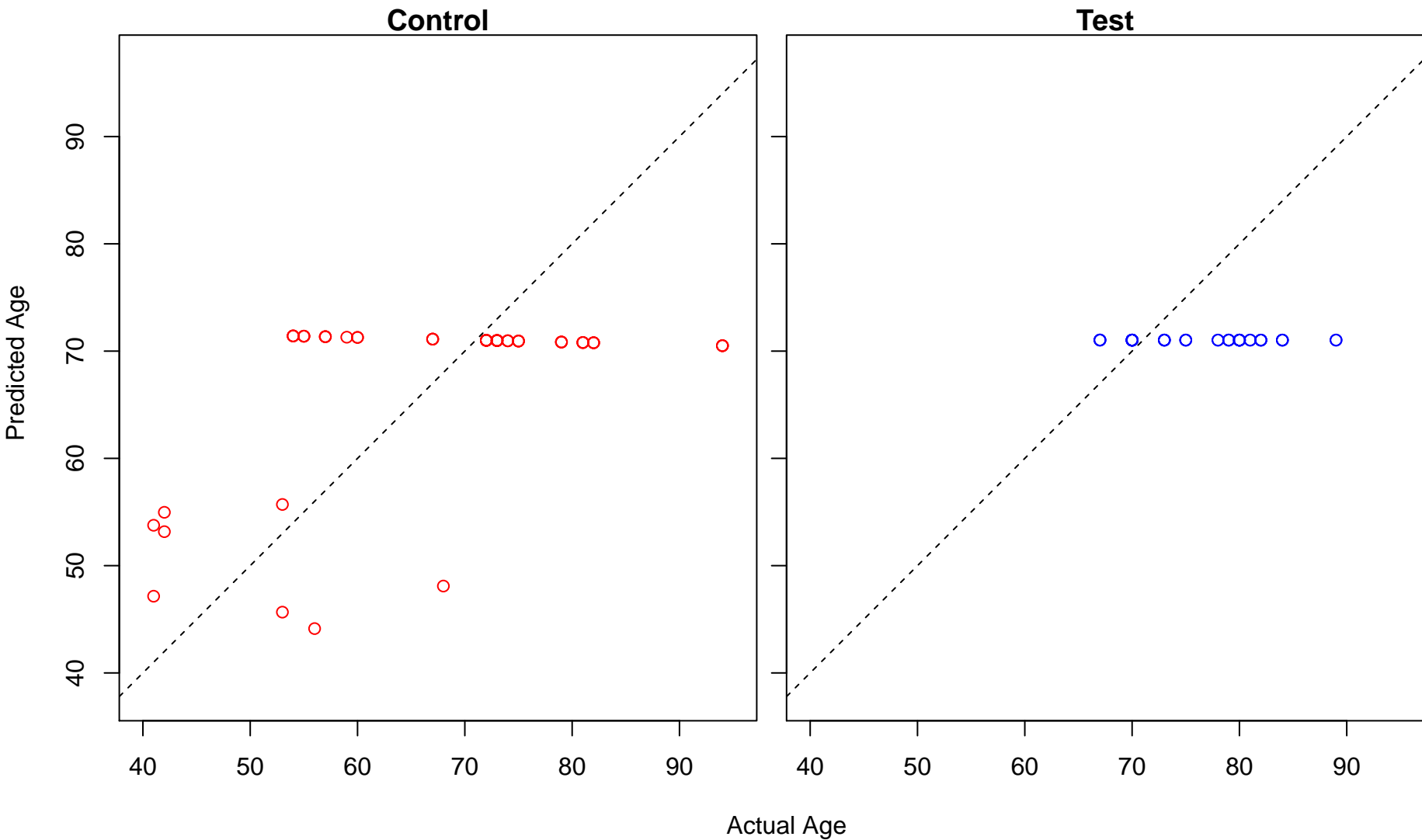


Test

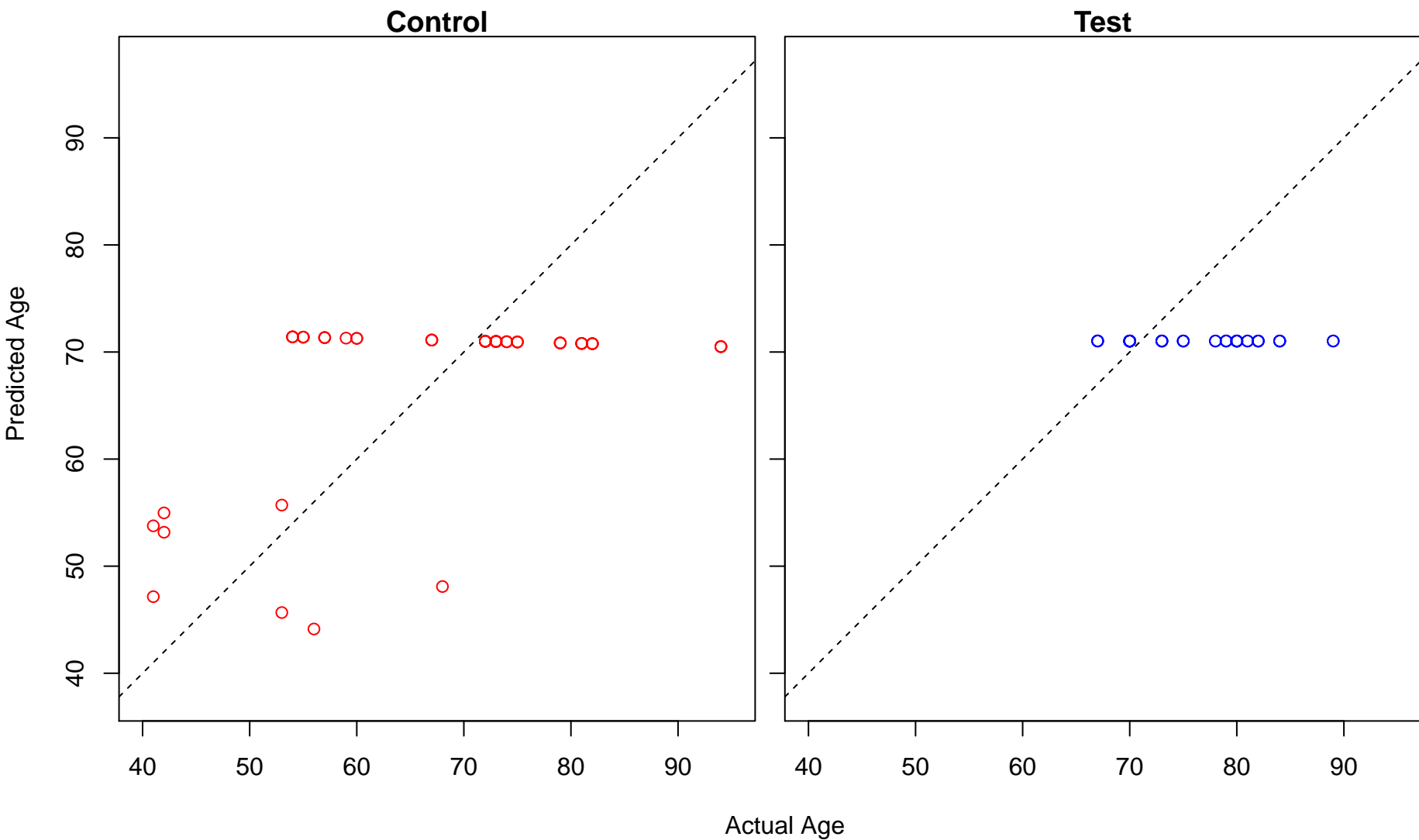


Actual Age

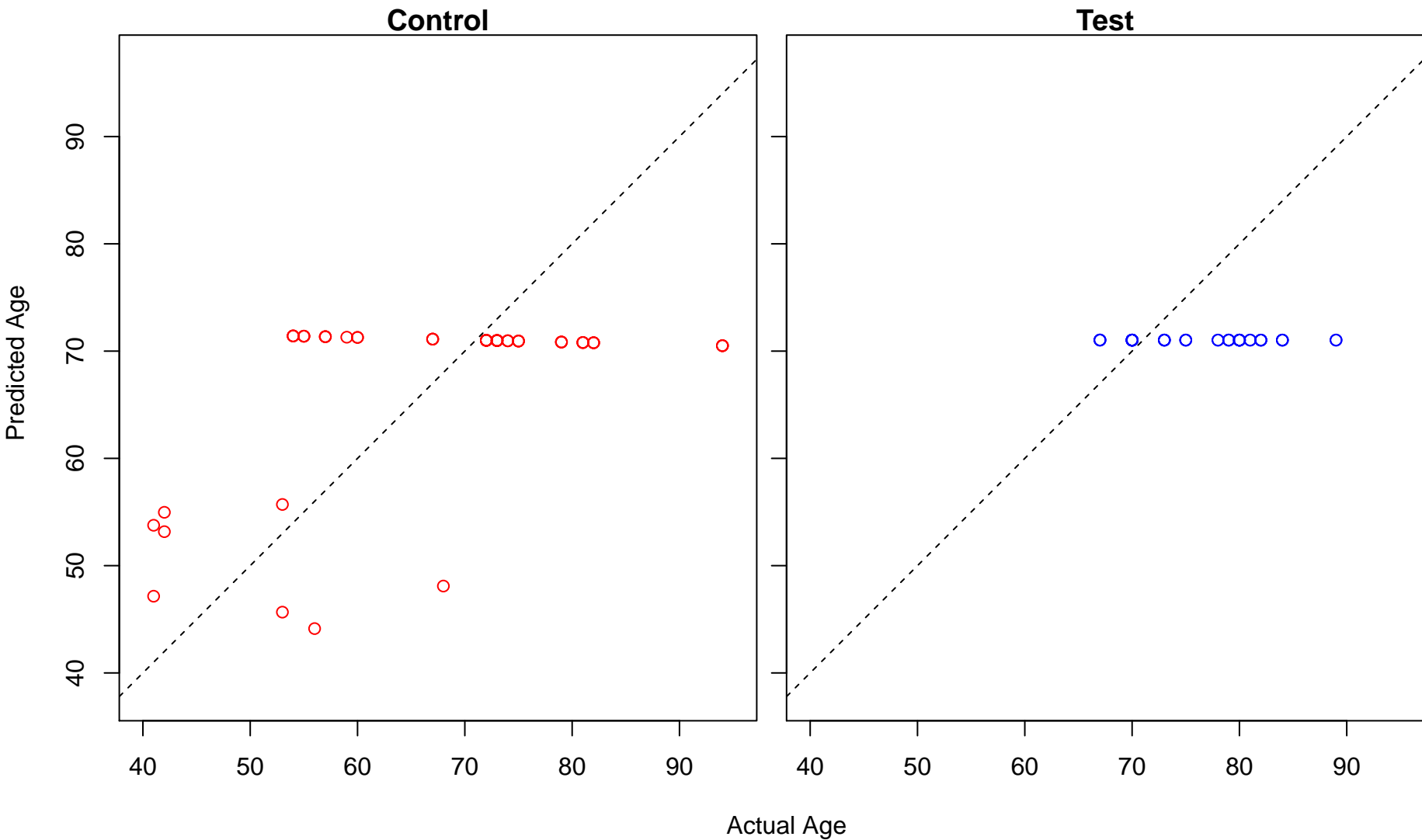
positive regulation of mononuclear cell proliferation (Score: 0.794231)



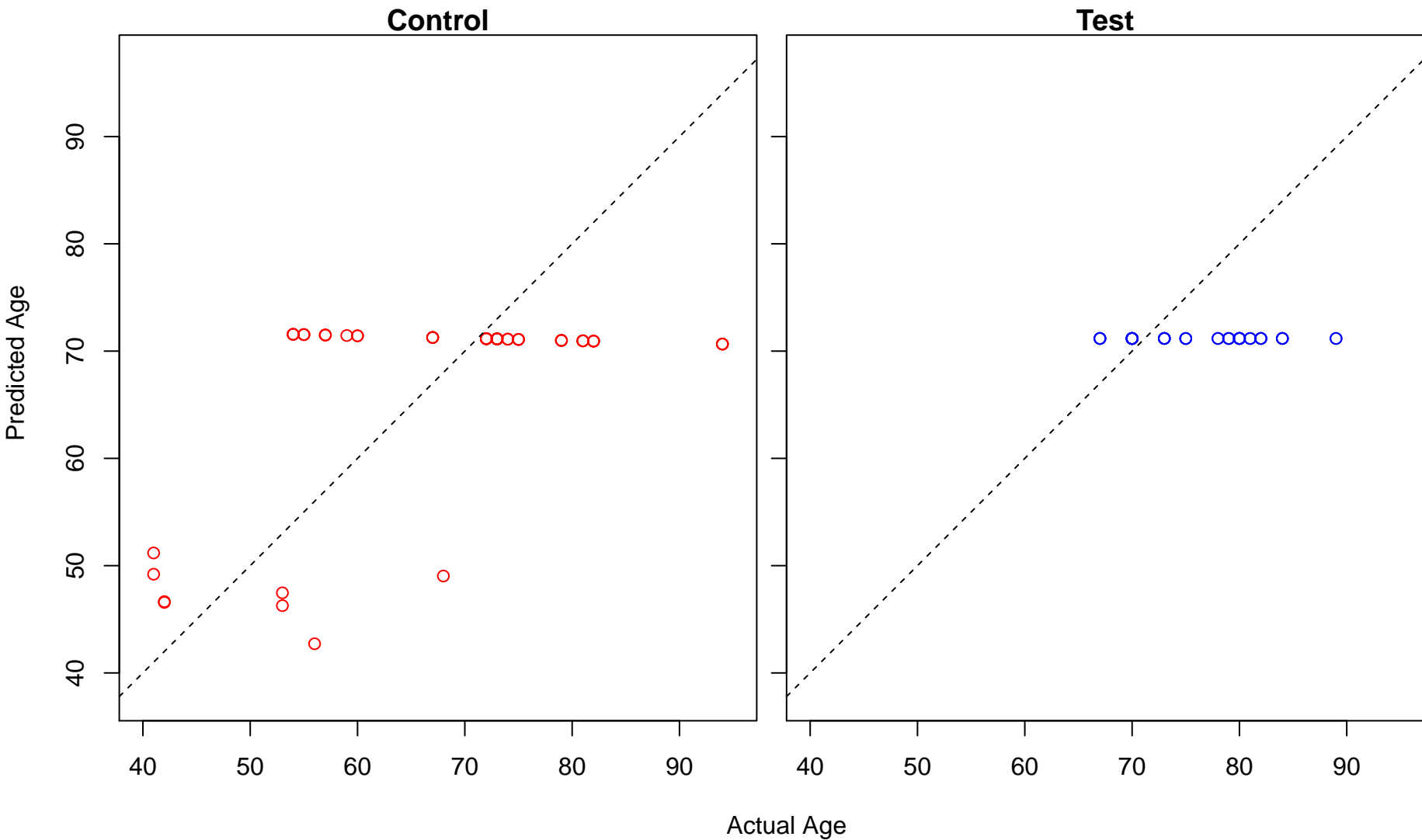
positive regulation of lymphocyte proliferation (Score: 0.794231)



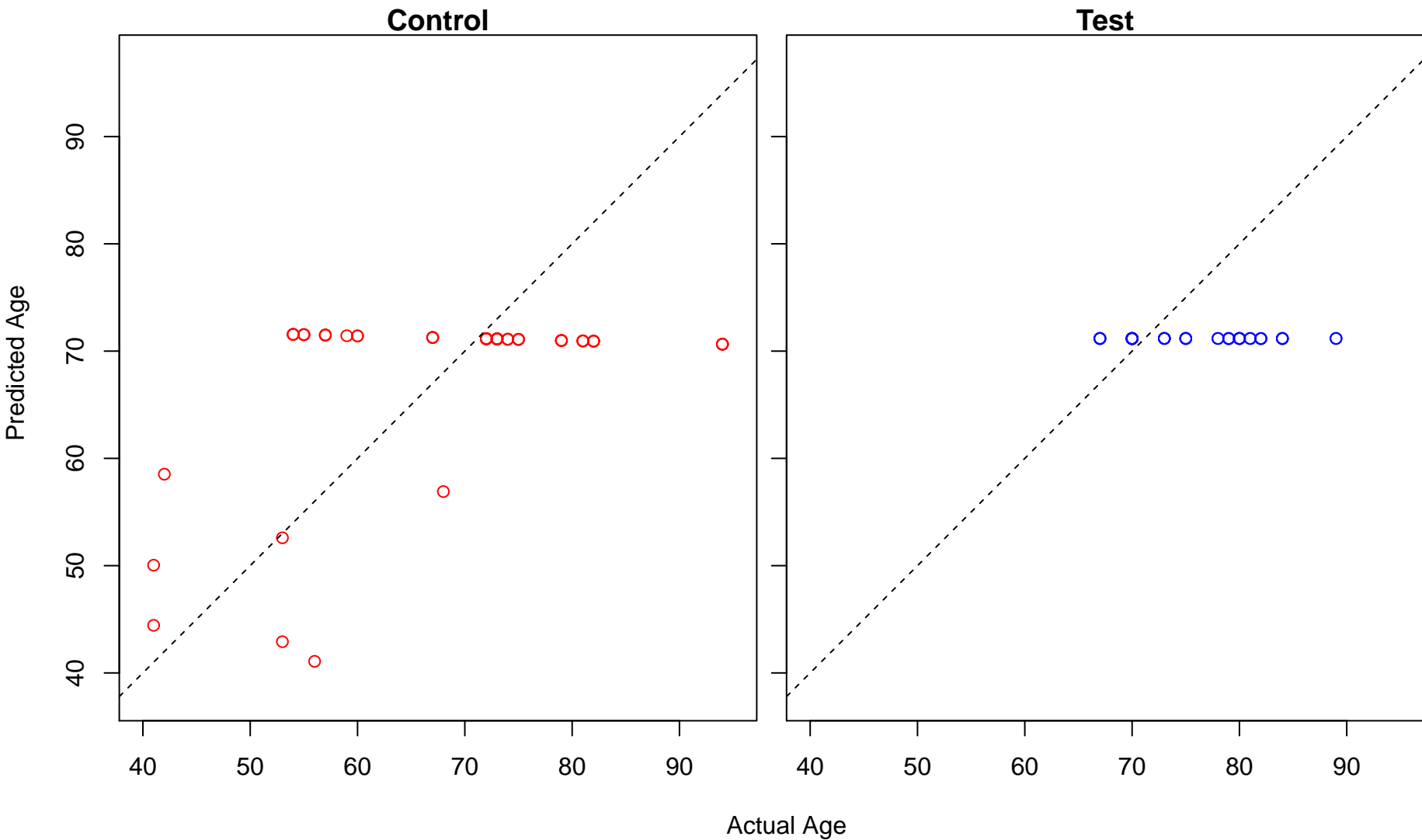
positive regulation of leukocyte proliferation (Score: 0.794231)



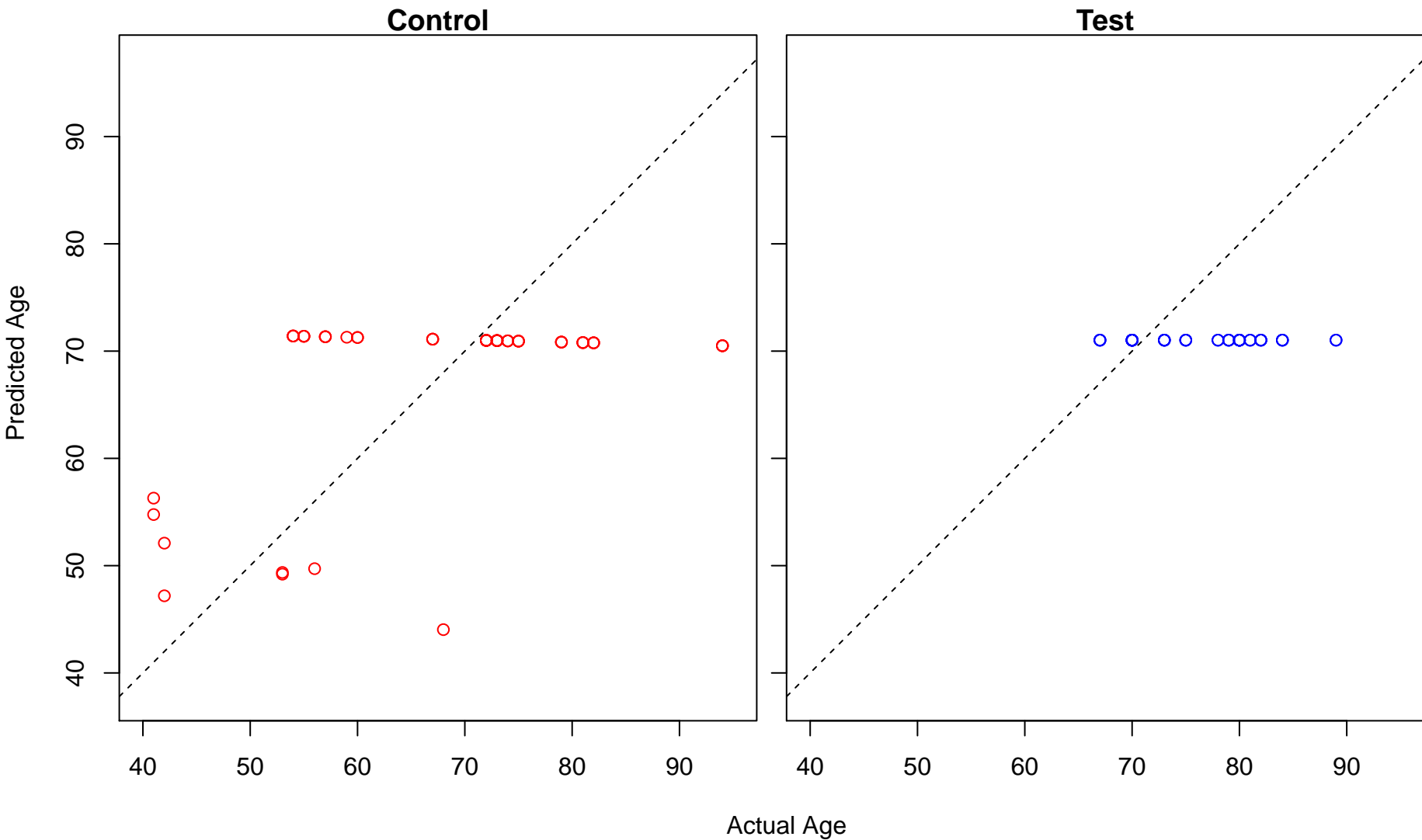
nitrogen compound transport (Score: 0.794220)



response to UV (Score: 0.794193)

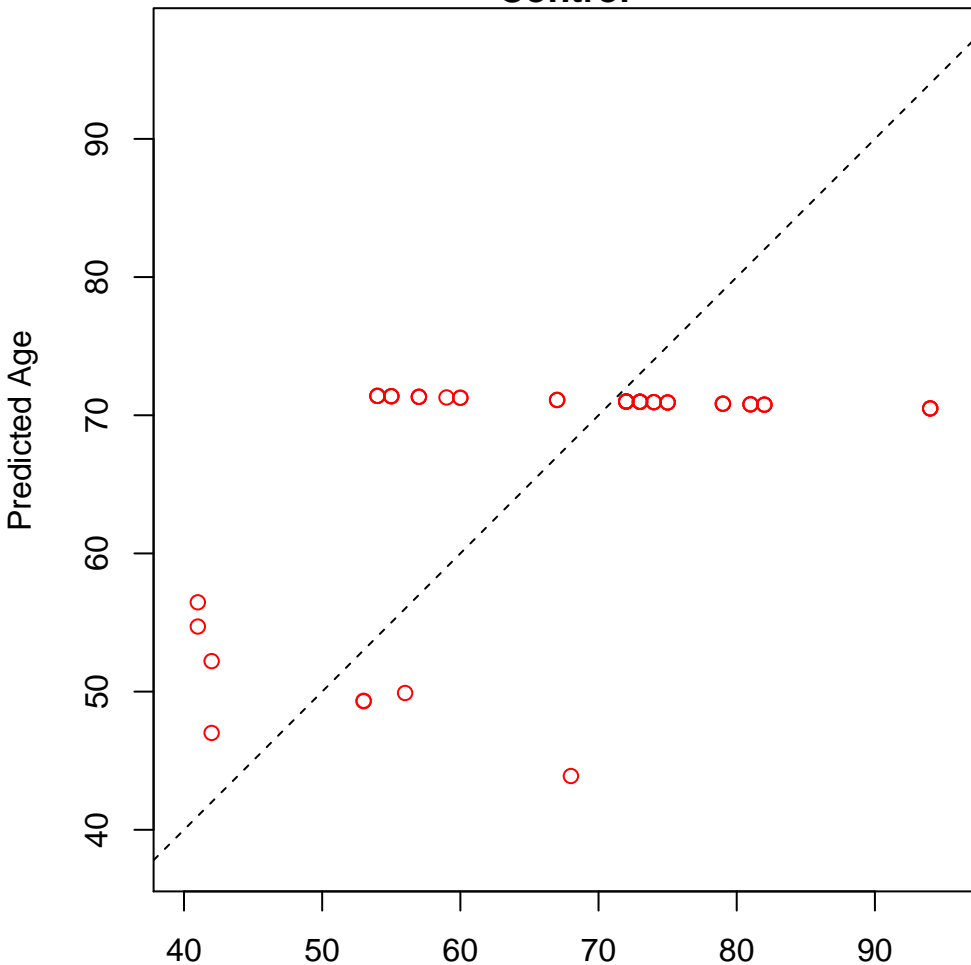


negative regulation of intracellular signal transduction (Score: 0.794053)

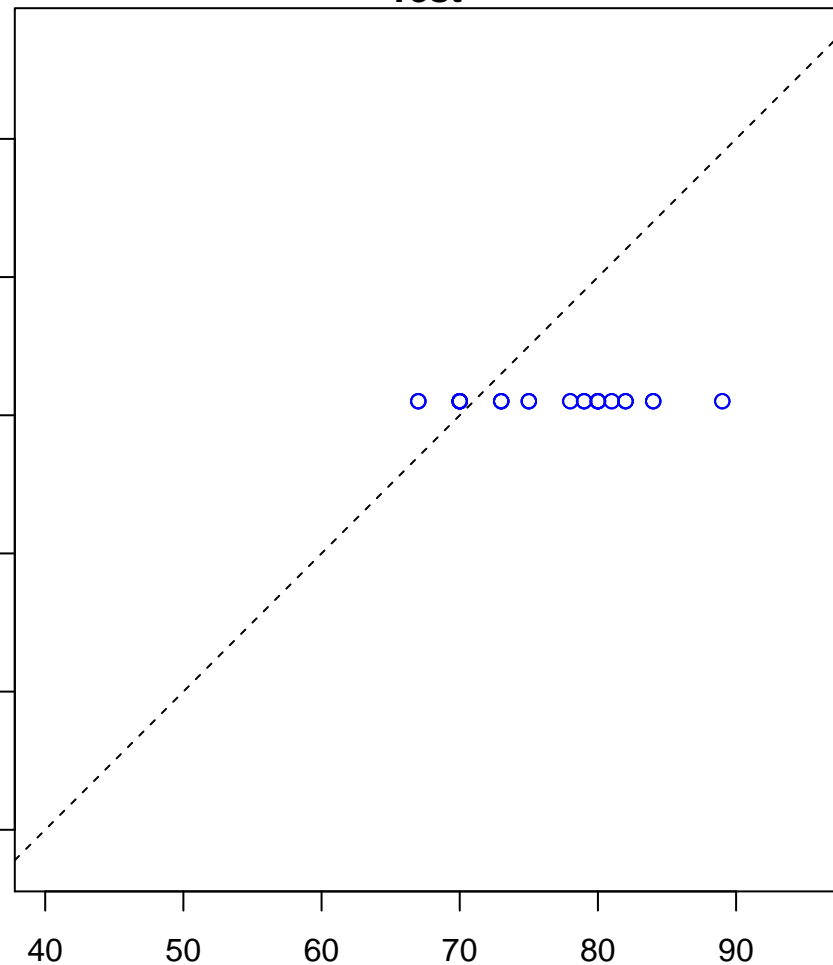


positive regulation of receptor activity (Score: 0.794043)

Control



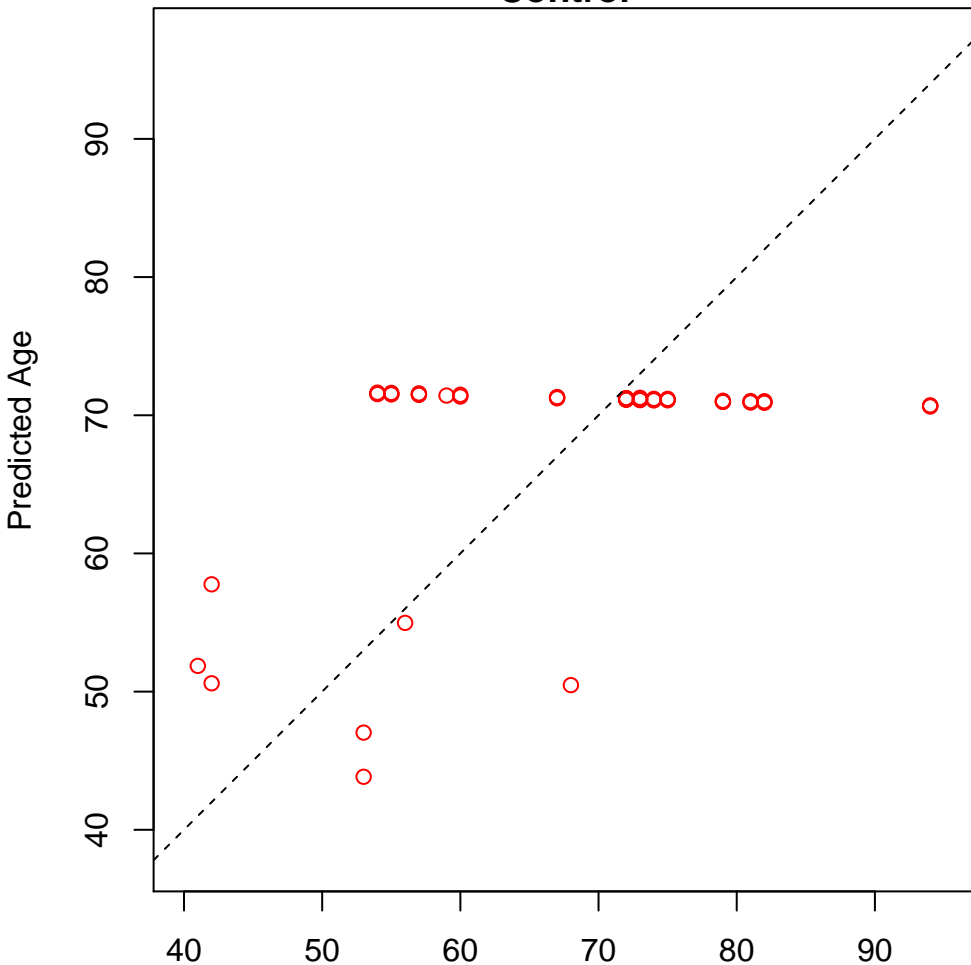
Test



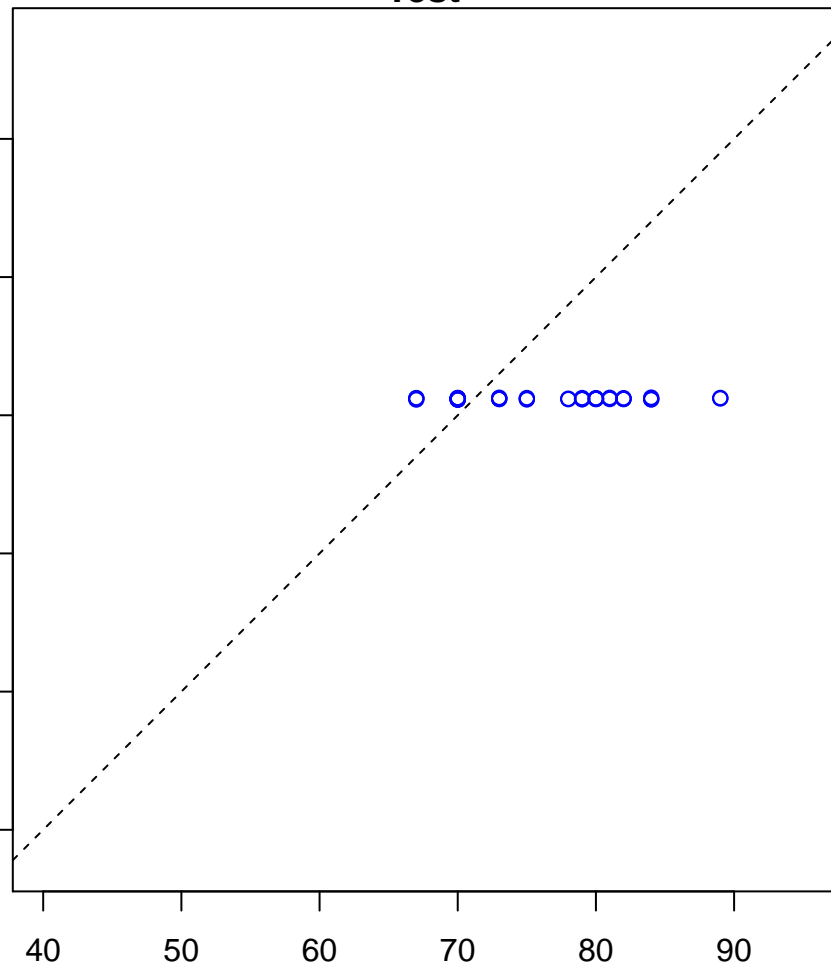
Actual Age

response to organic cyclic compound (Score: 0.794011)

Control

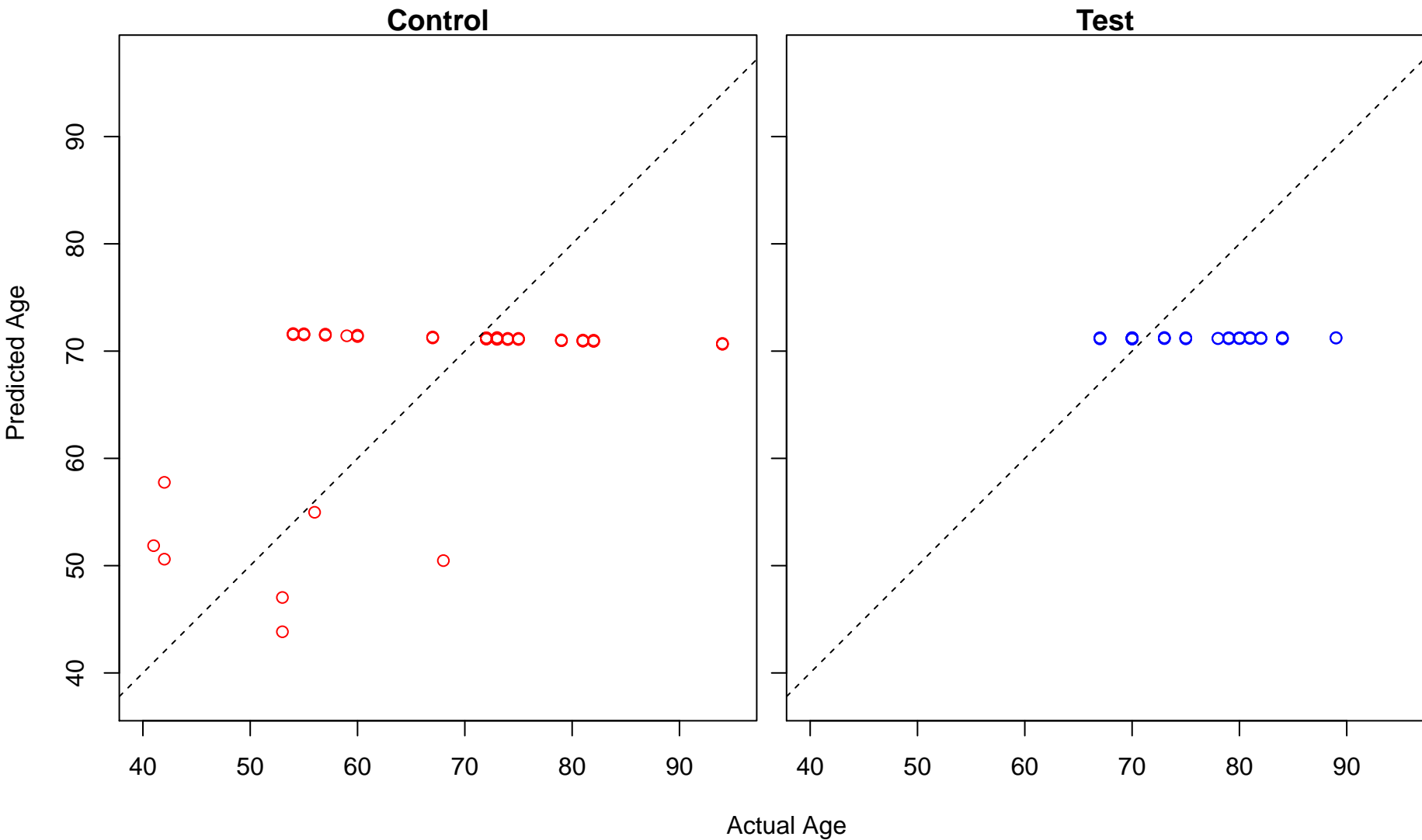


Test

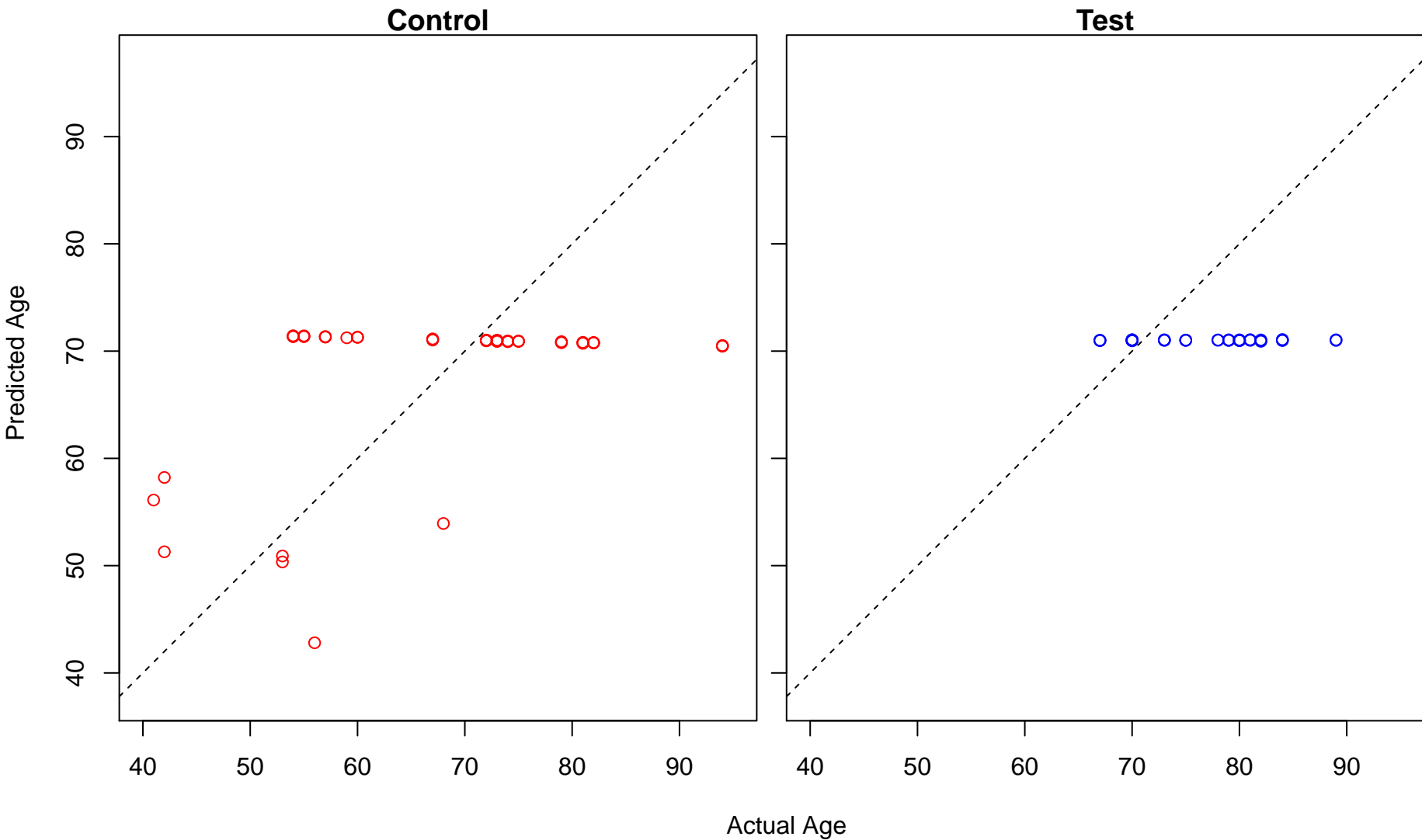


Actual Age

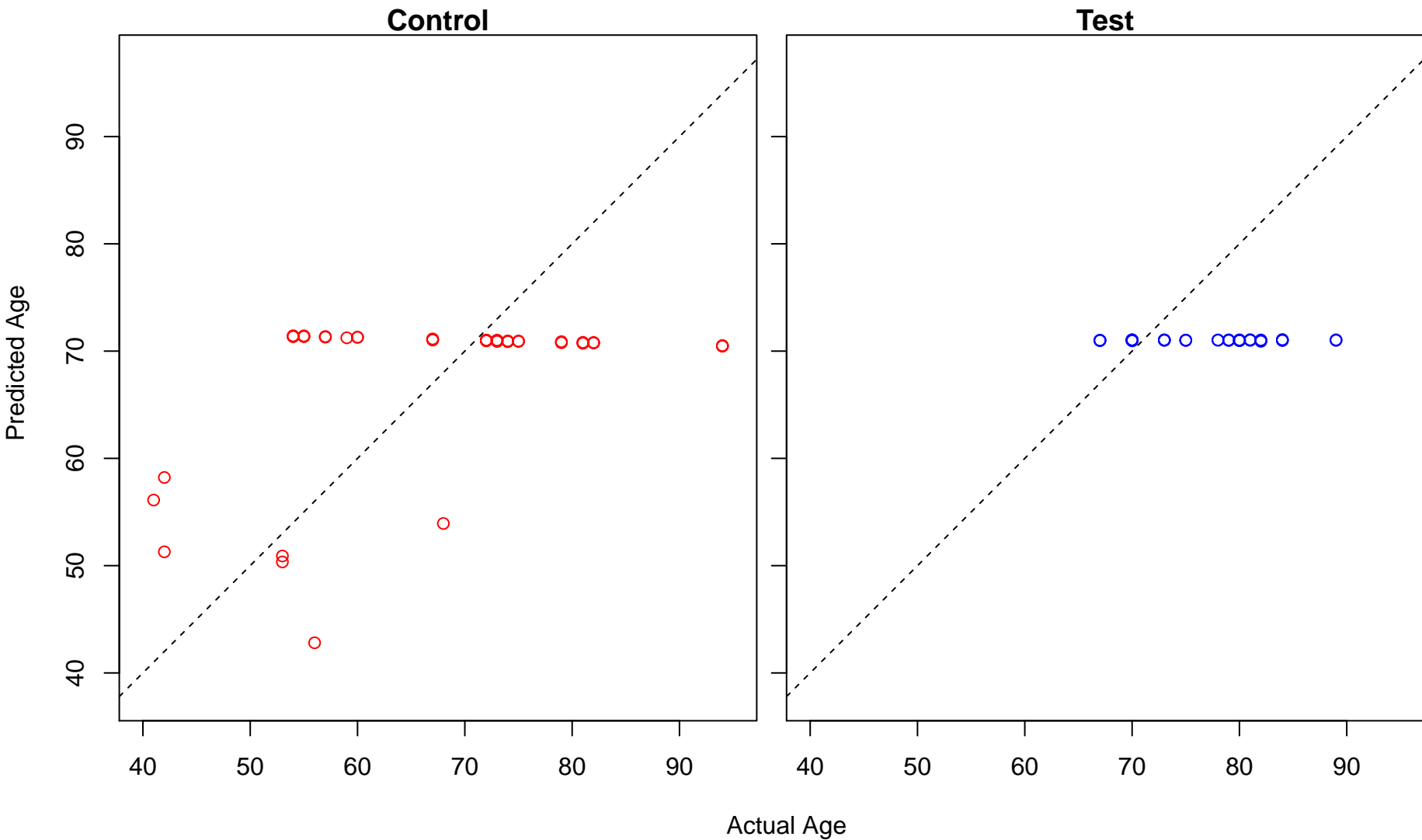
cellular response to organic cyclic compound (Score: 0.794011)



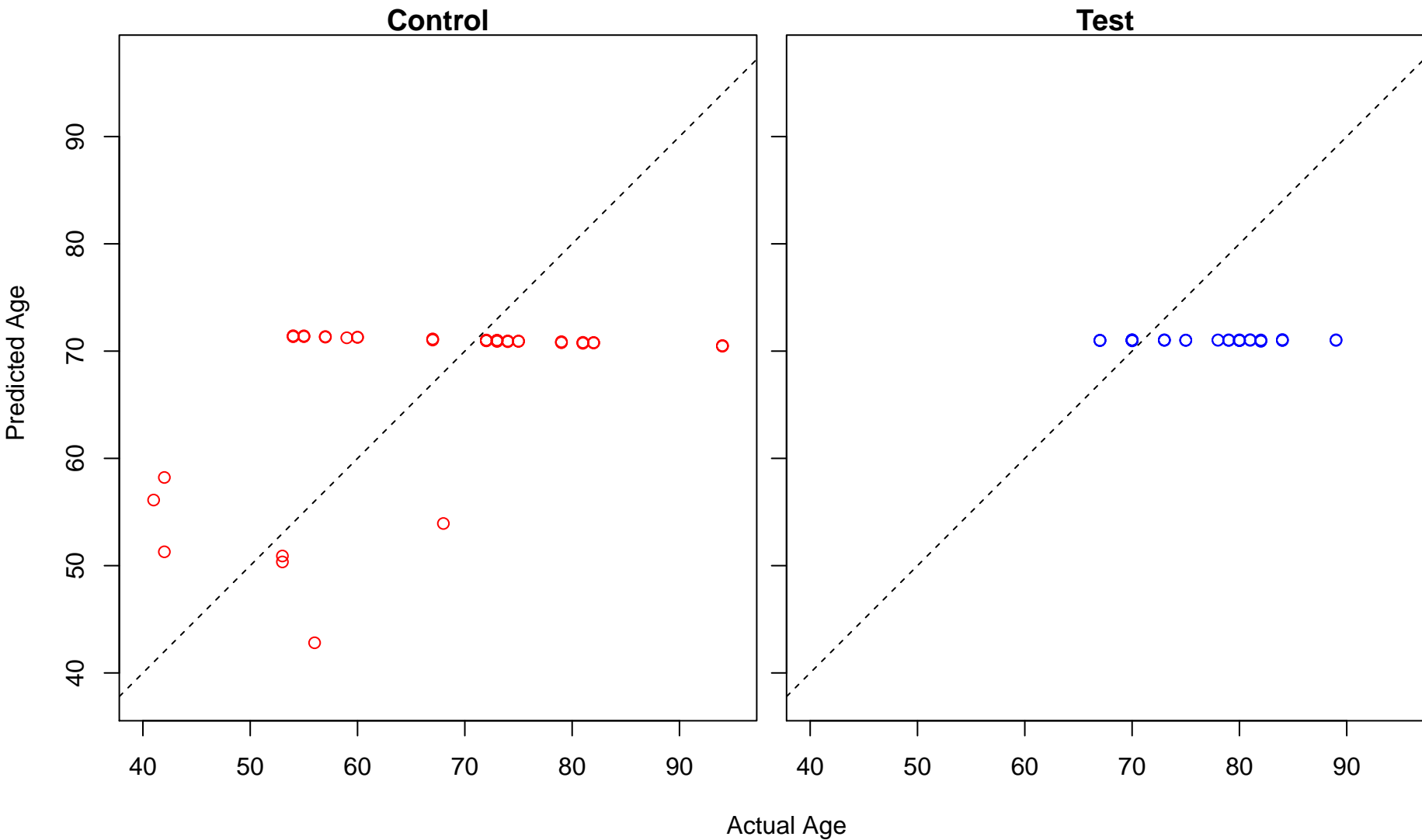
keratinocyte differentiation (Score: 0.793999)



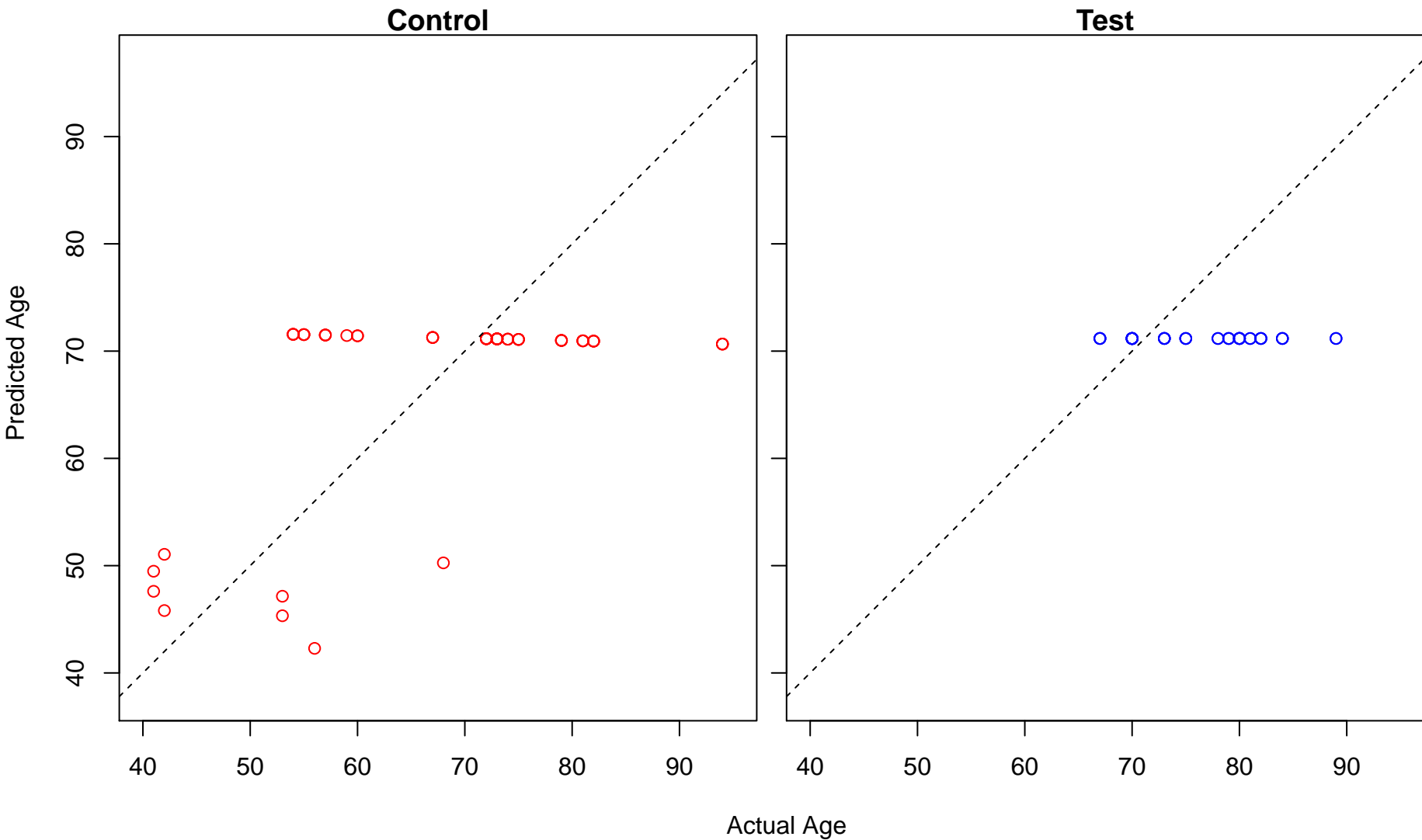
keratinization (Score: 0.793999)



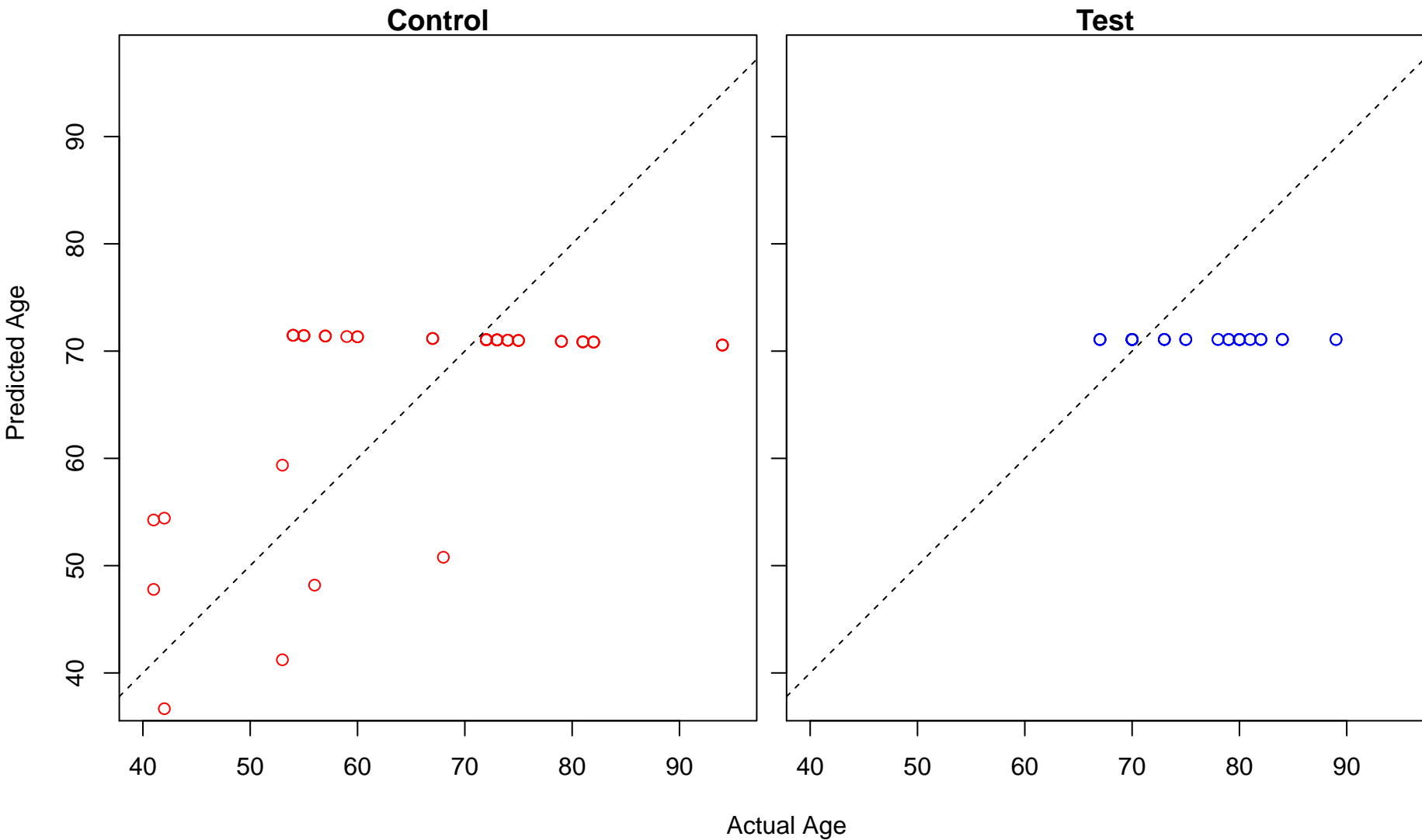
cornification (Score: 0.793999)



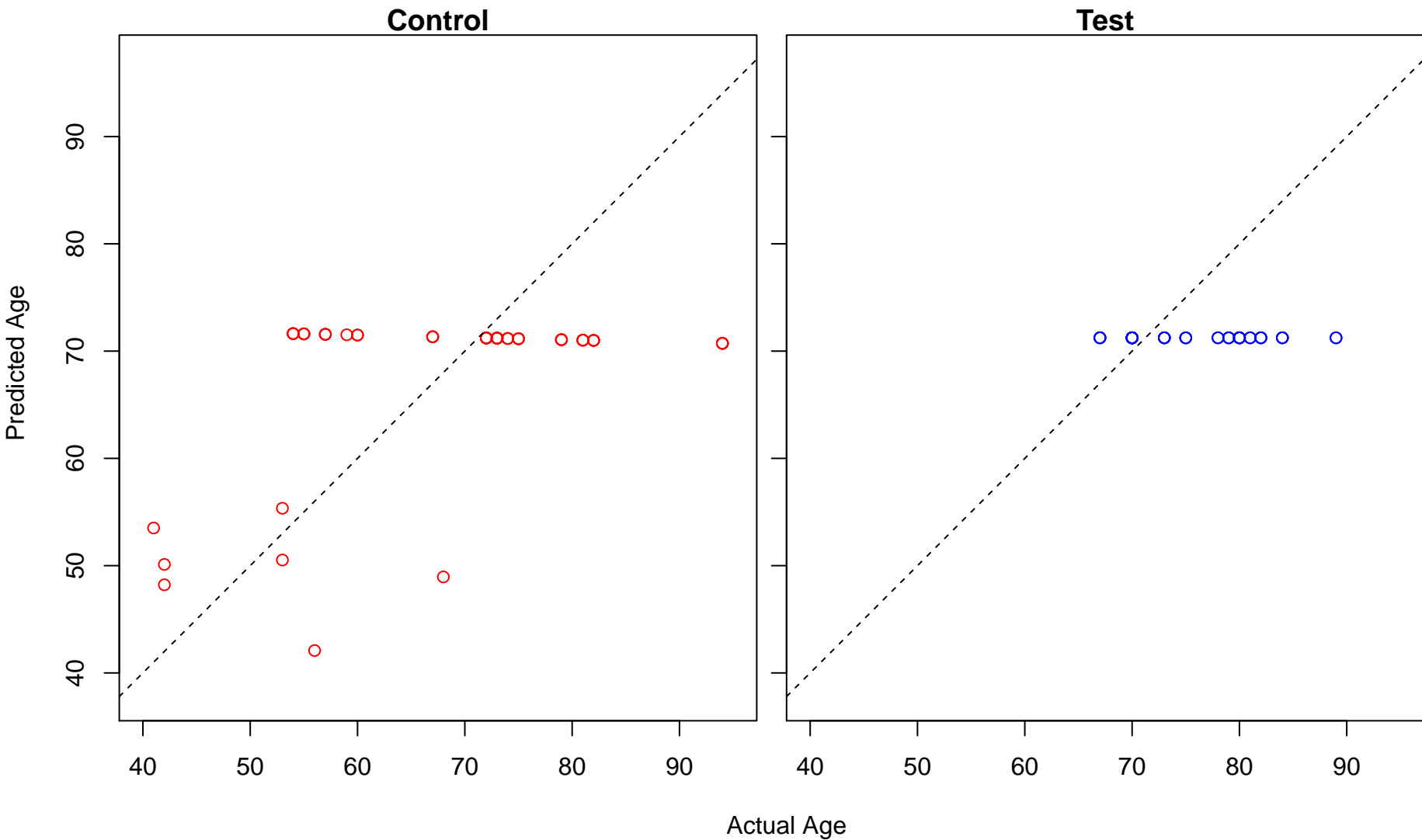
transport (Score: 0.793989)



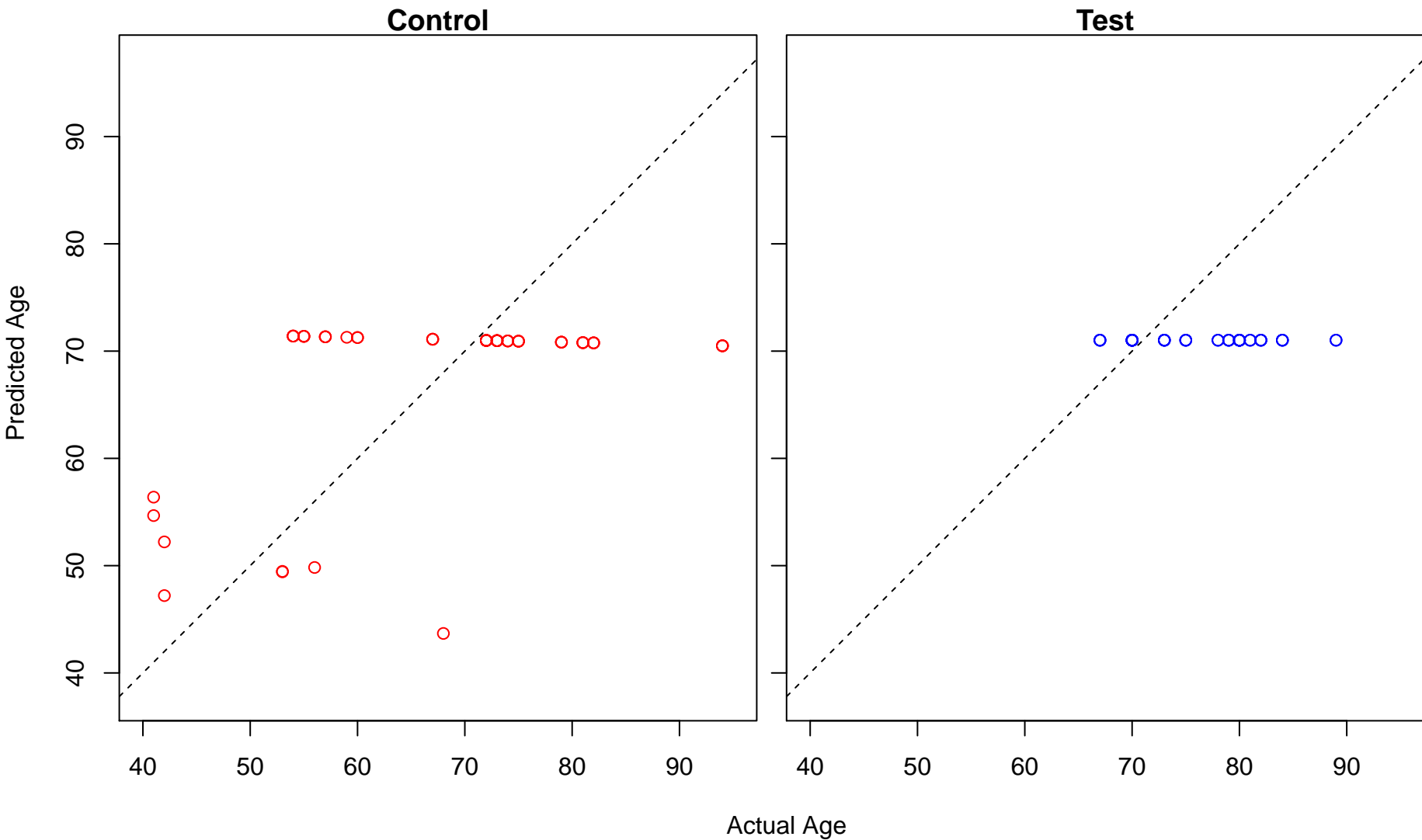
establishment or maintenance of cell polarity (Score: 0.793923)



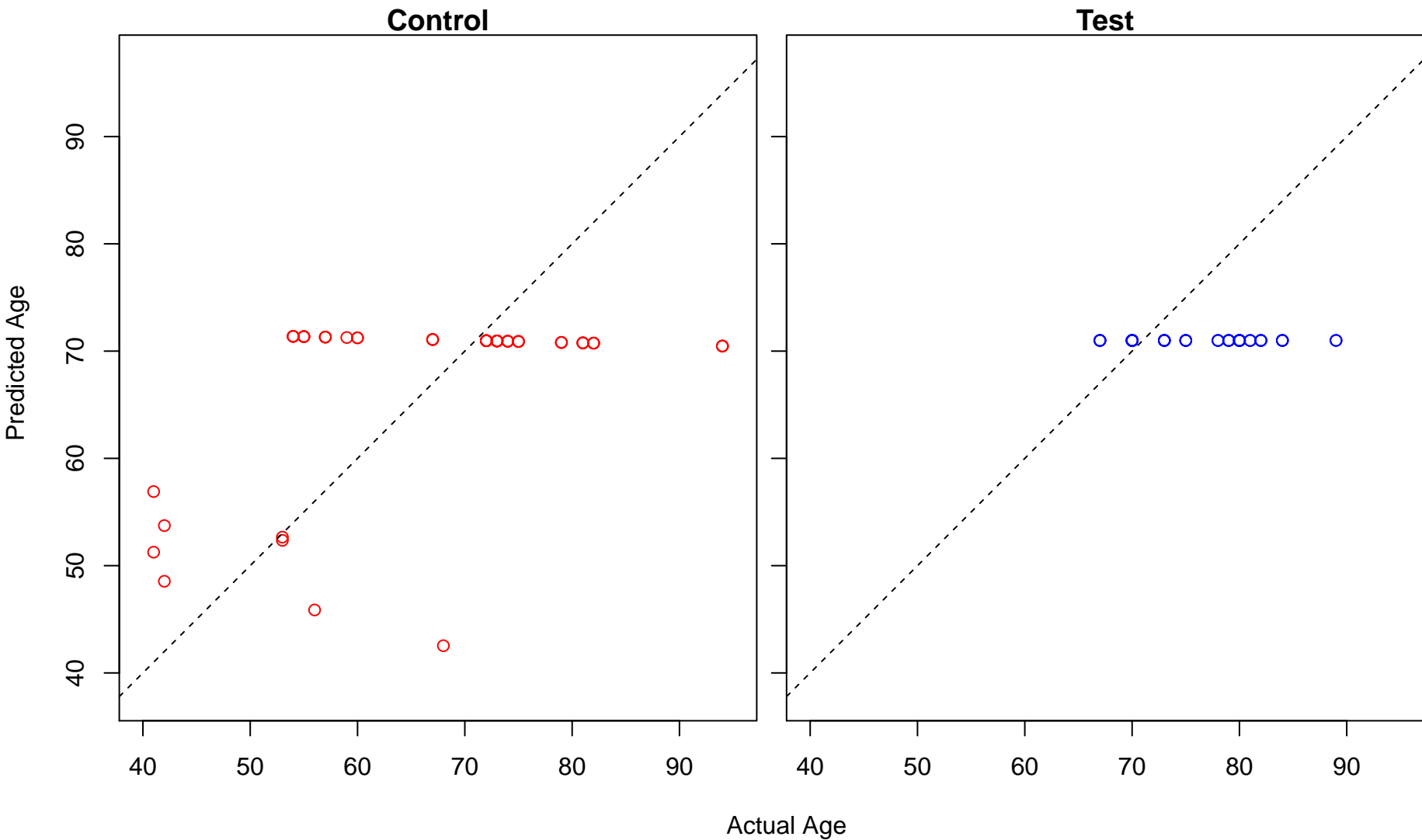
cellular macromolecular complex assembly (Score: 0.793883)



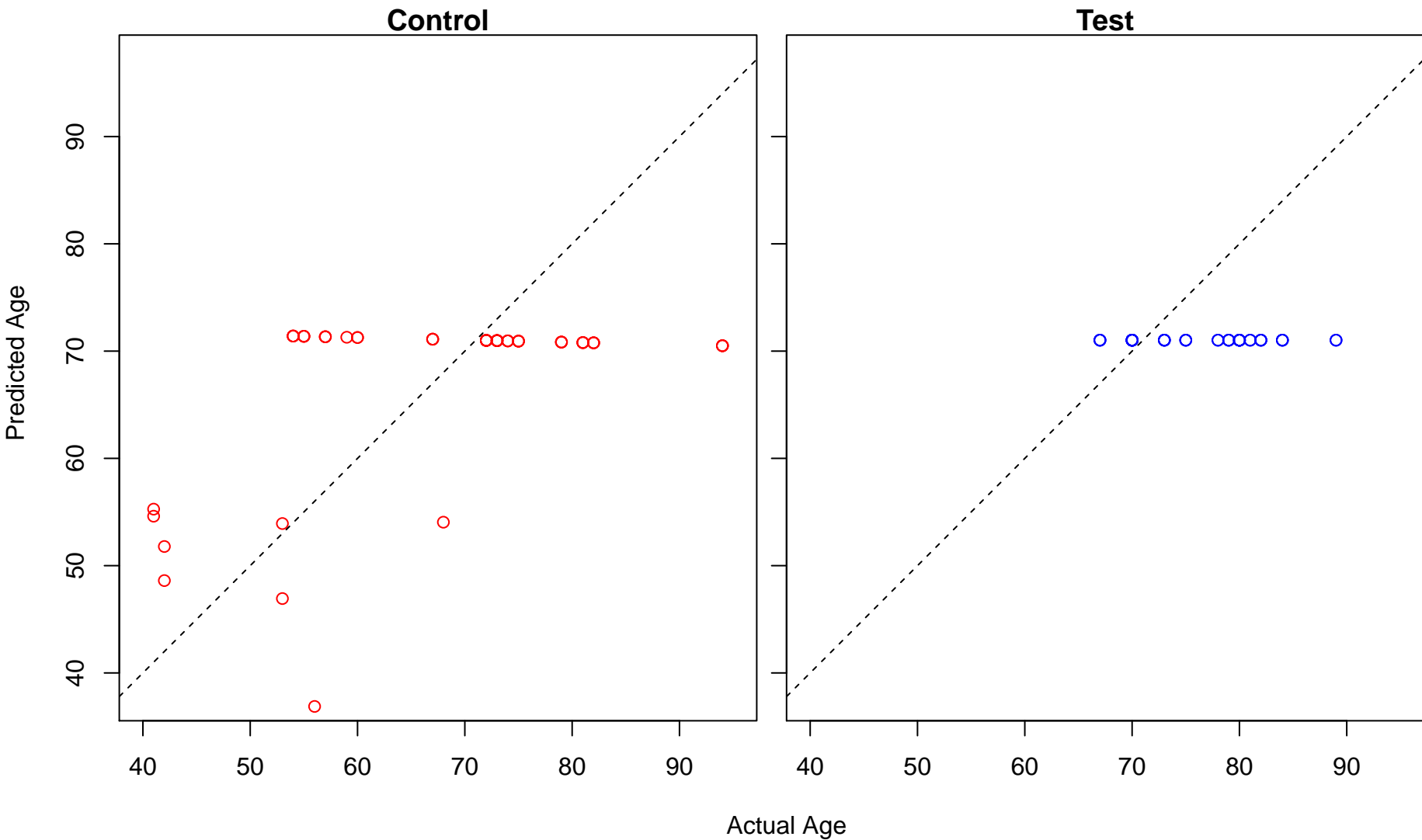
negative regulation of protein phosphorylation (Score: 0.793864)



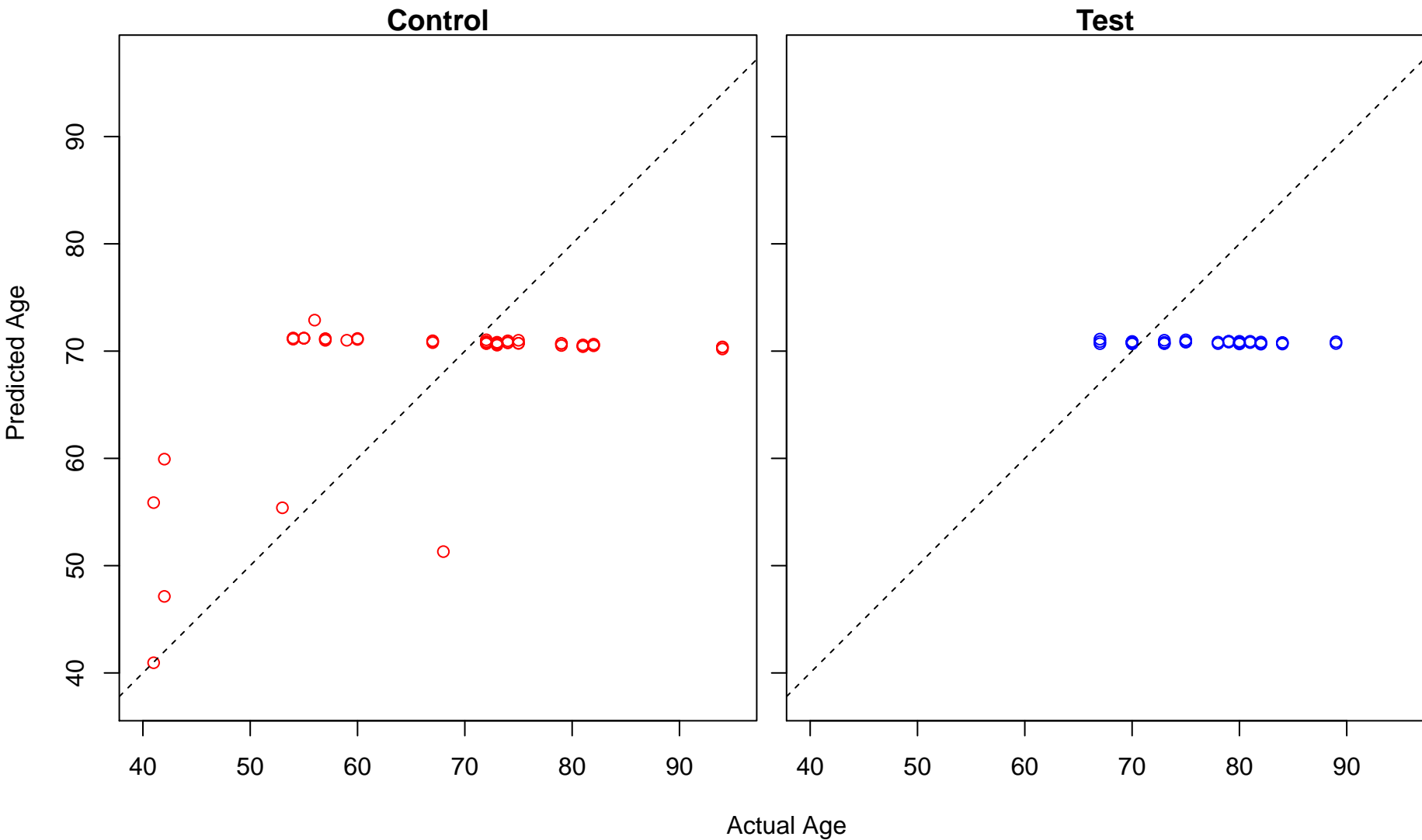
regulation of ion transport (Score: 0.793857)



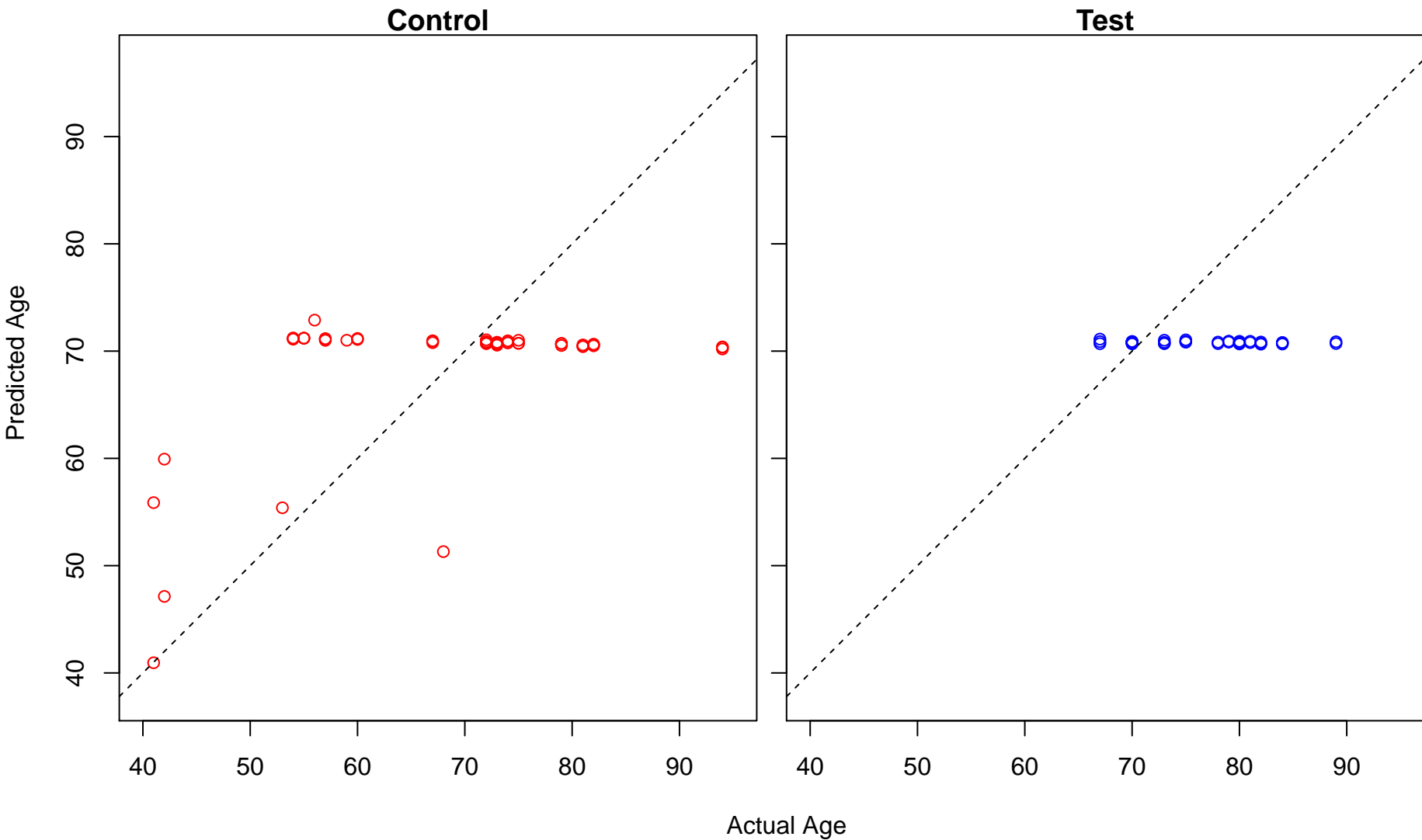
regulation of signal transduction by p53 class mediator (Score: 0.793763)



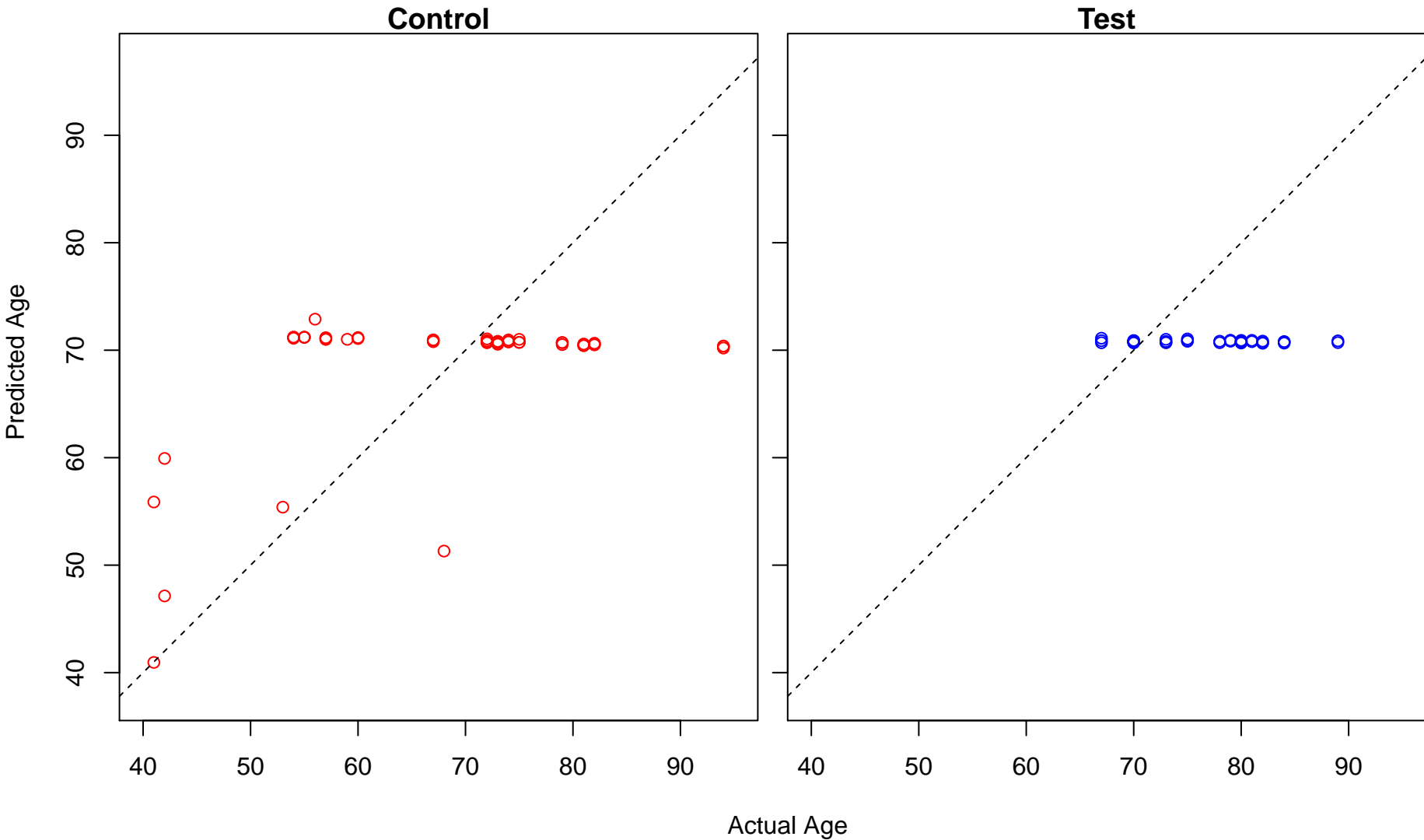
kidney development (Score: 0.793750)



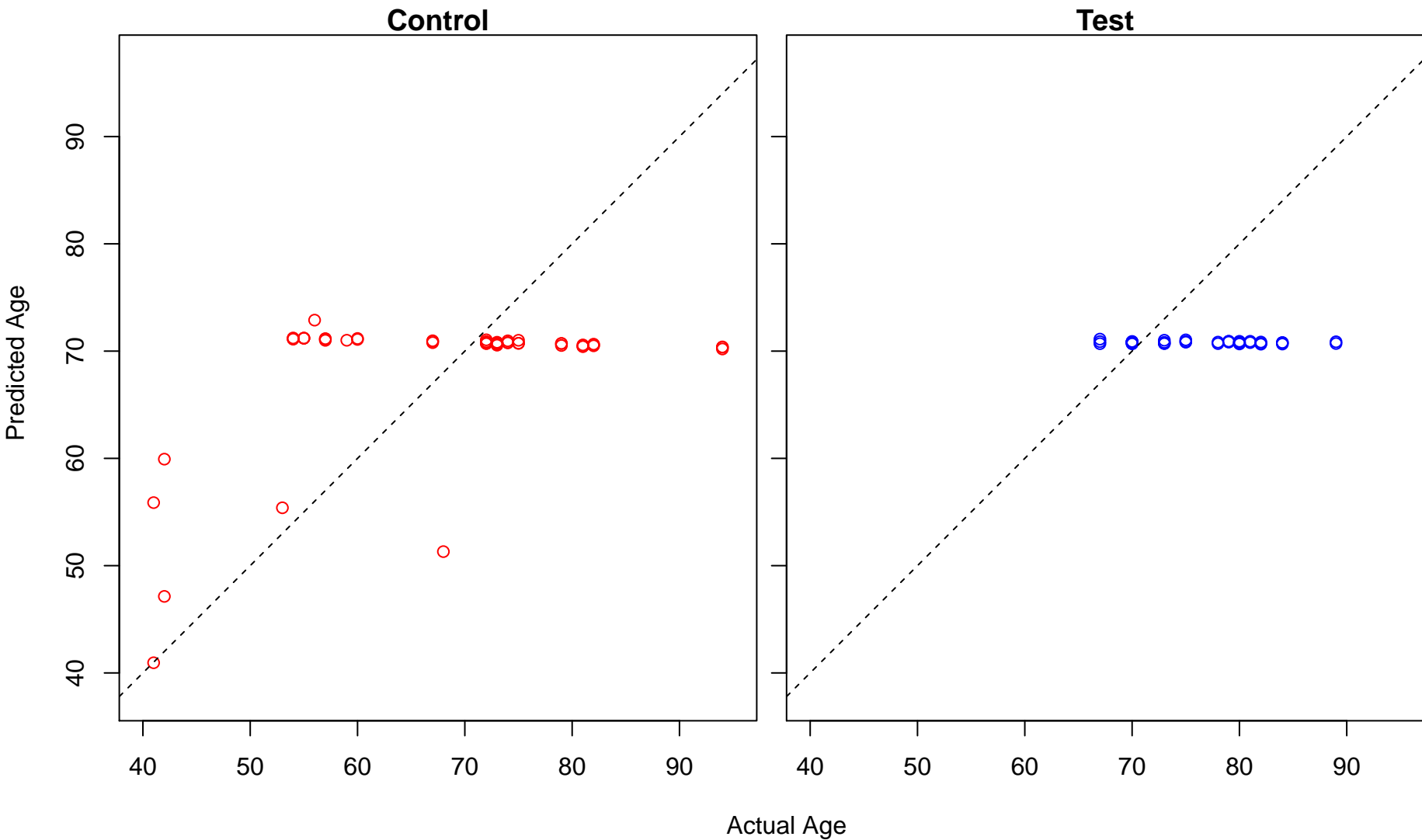
epithelial cell differentiation involved in kidney development (Score: 0.793750)



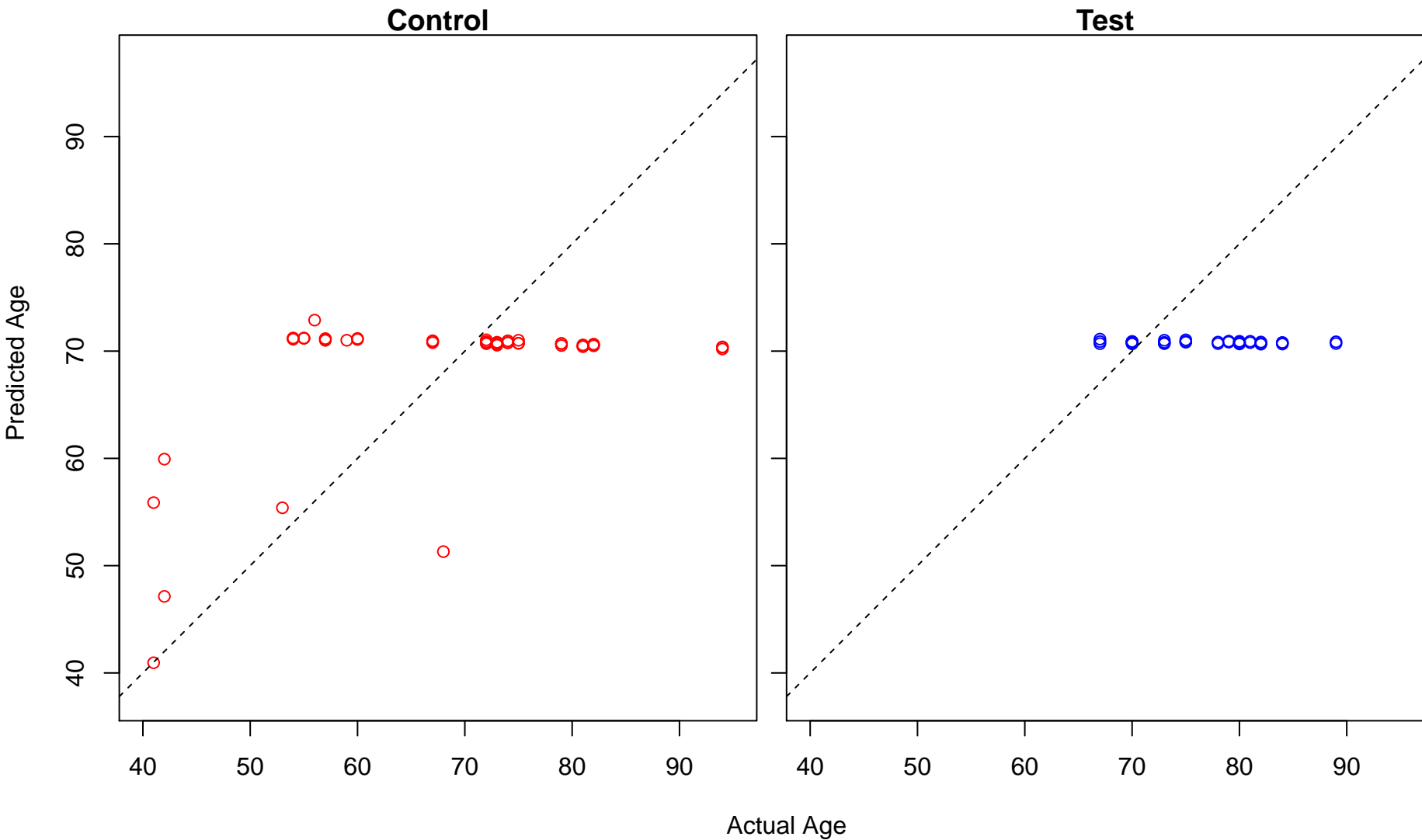
cell differentiation involved in kidney development (Score: 0.793750)



renal system development (Score: 0.793750)

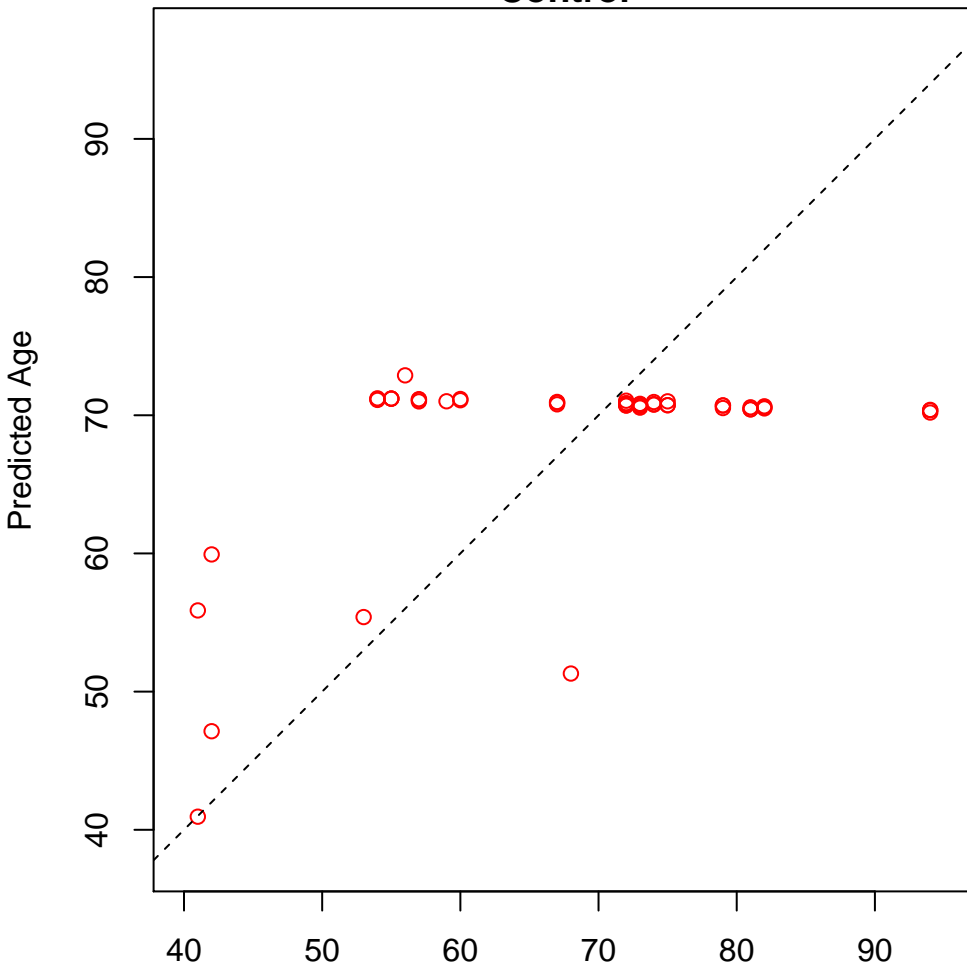


nephron development (Score: 0.793750)

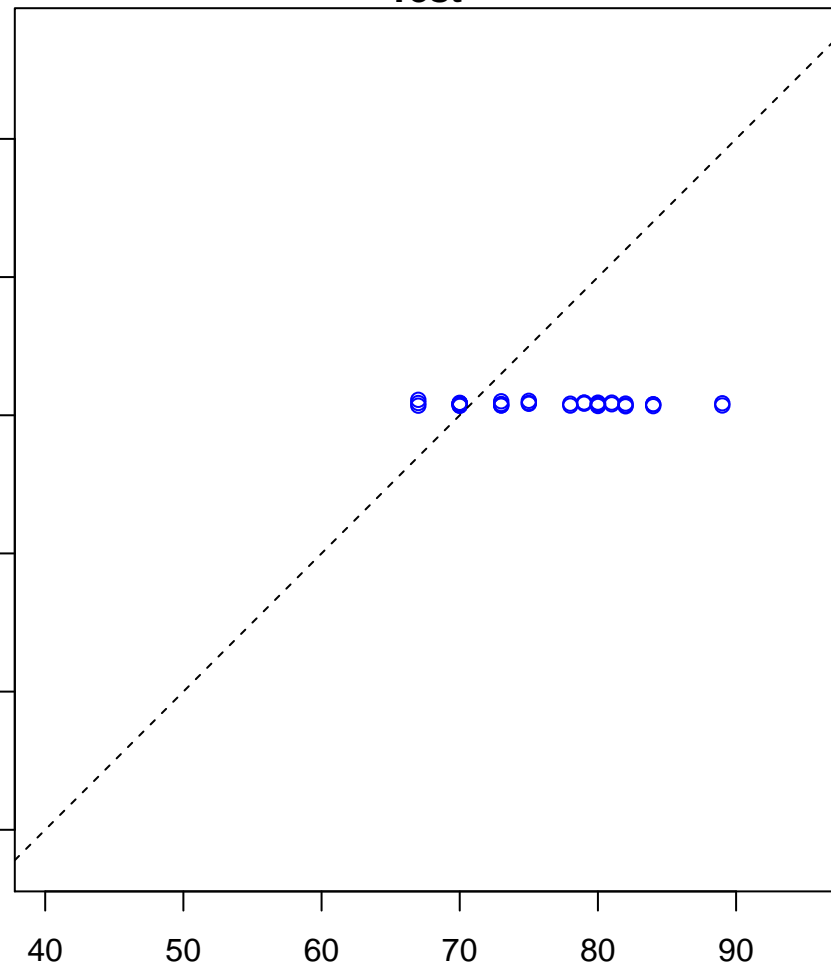


nephron epithelium development (Score: 0.793750)

Control



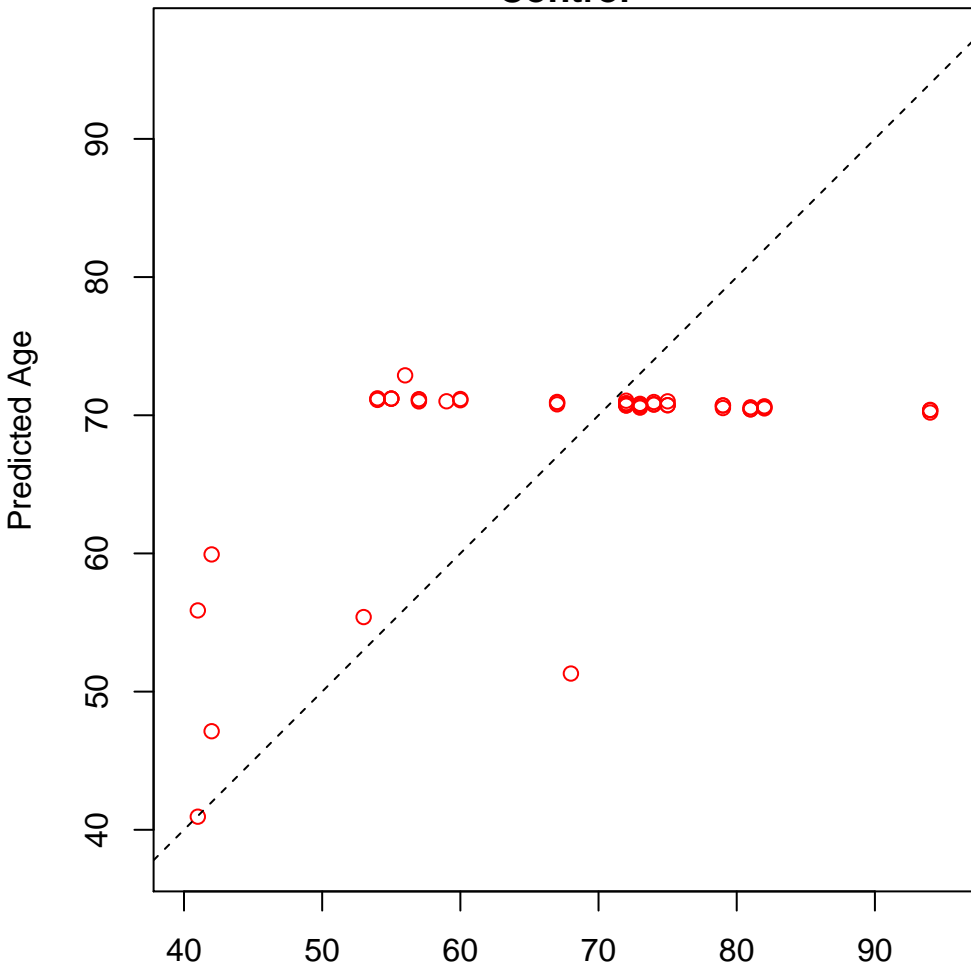
Test



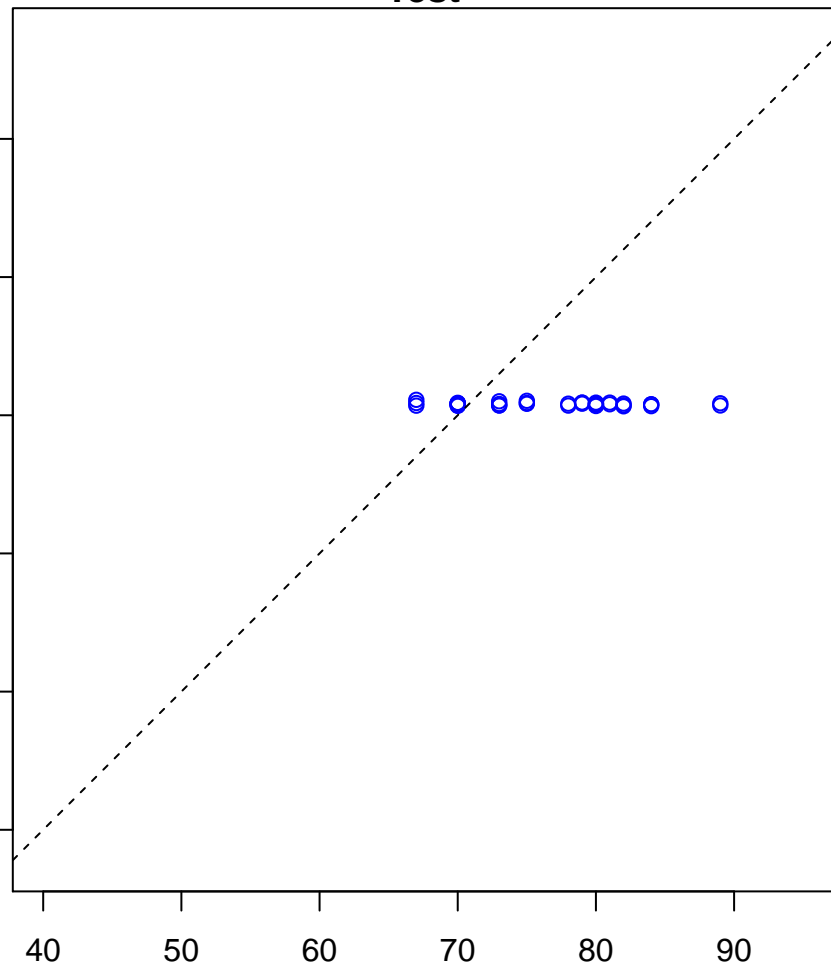
Actual Age

kidney epithelium development (Score: 0.793750)

Control

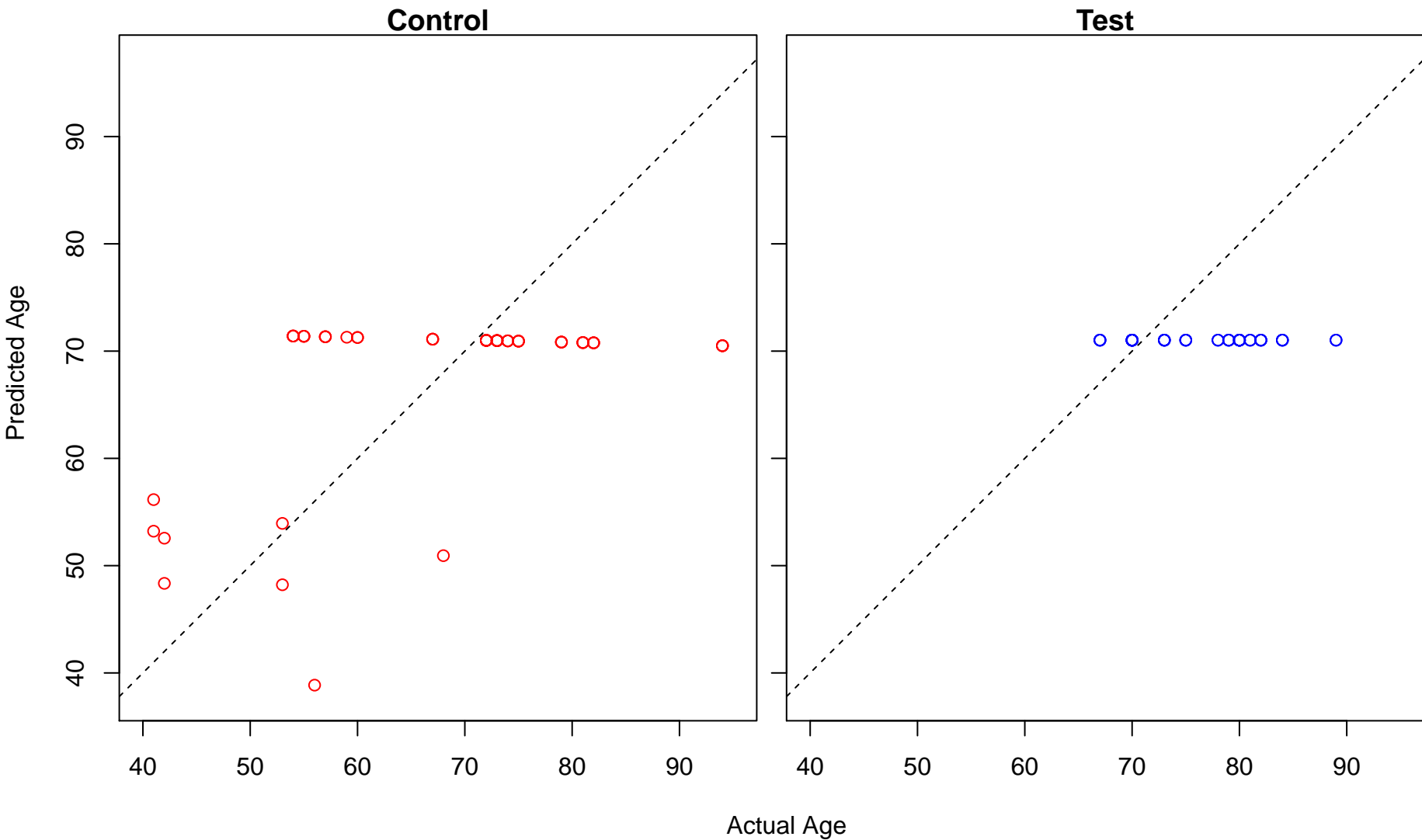


Test

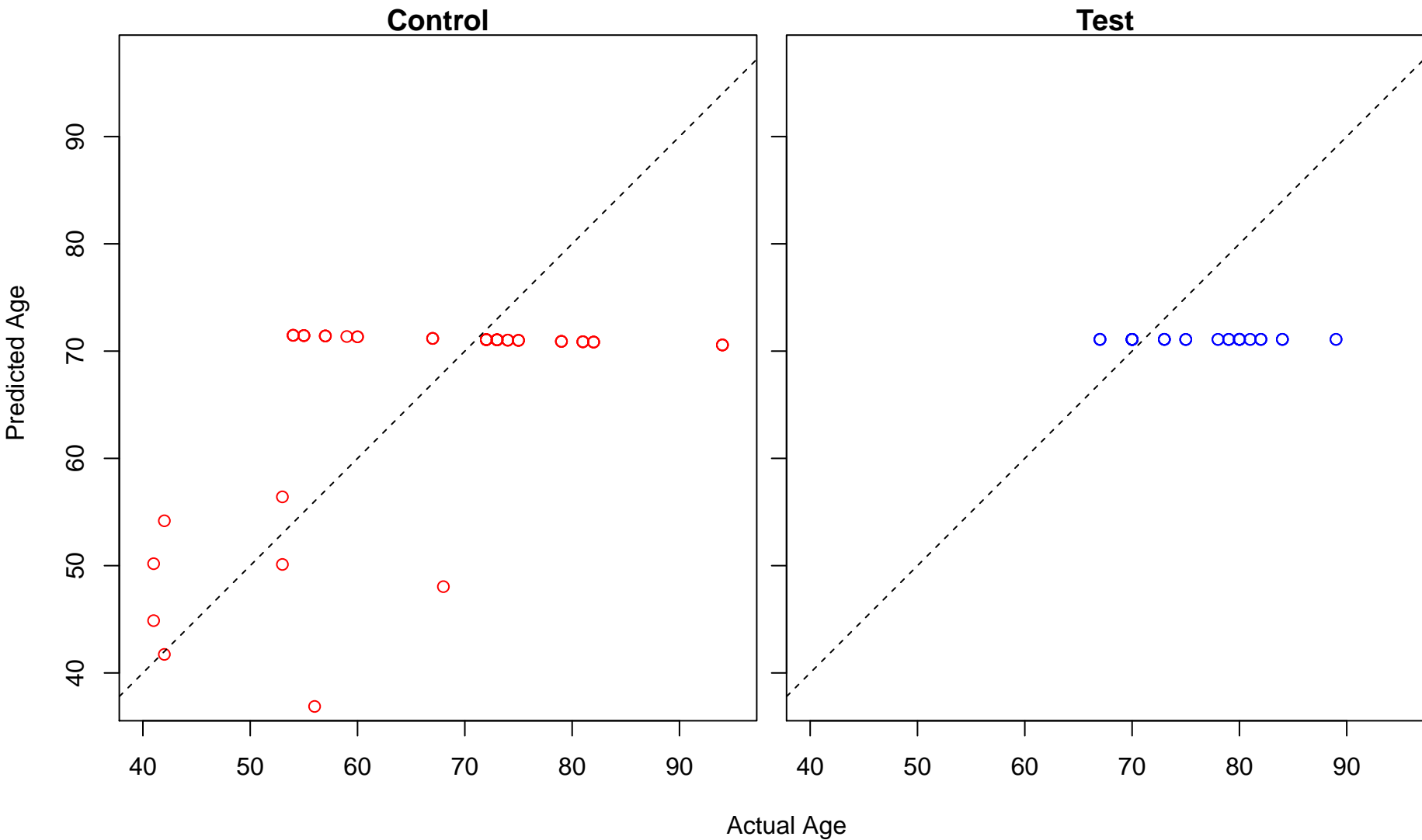


Actual Age

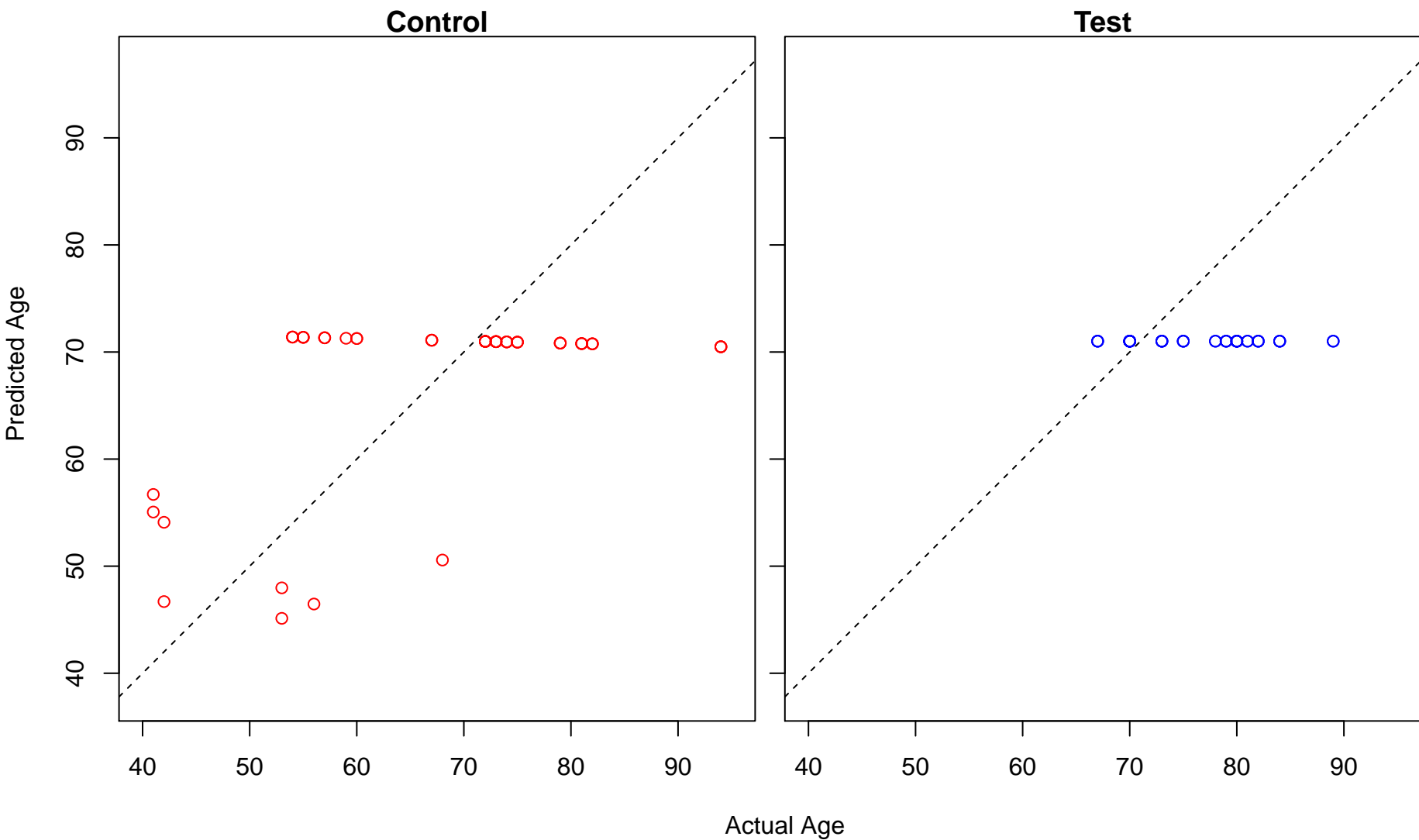
detection of stimulus (Score: 0.793707)



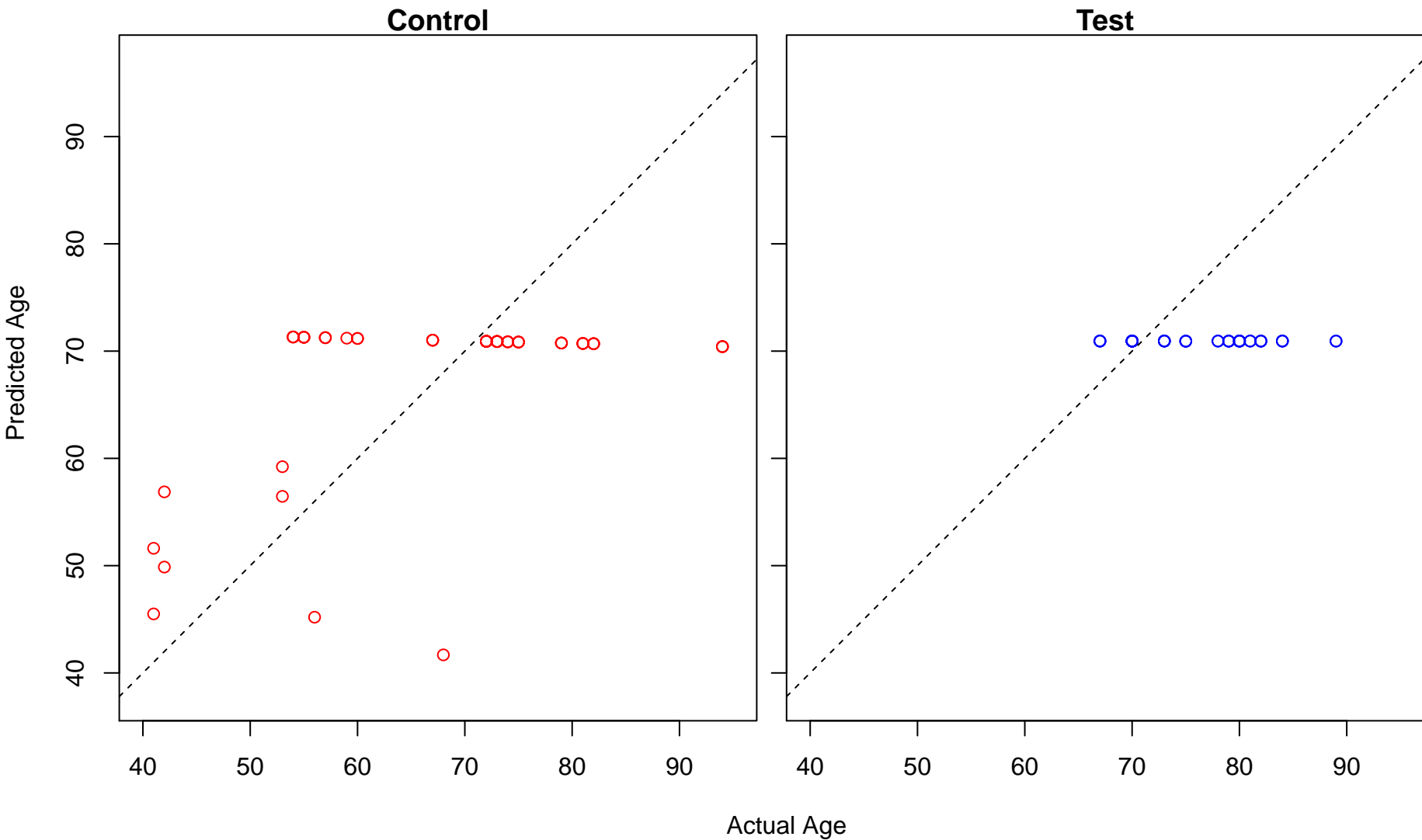
nuclear import (Score: 0.793455)



response to bacterium (Score: 0.793342)

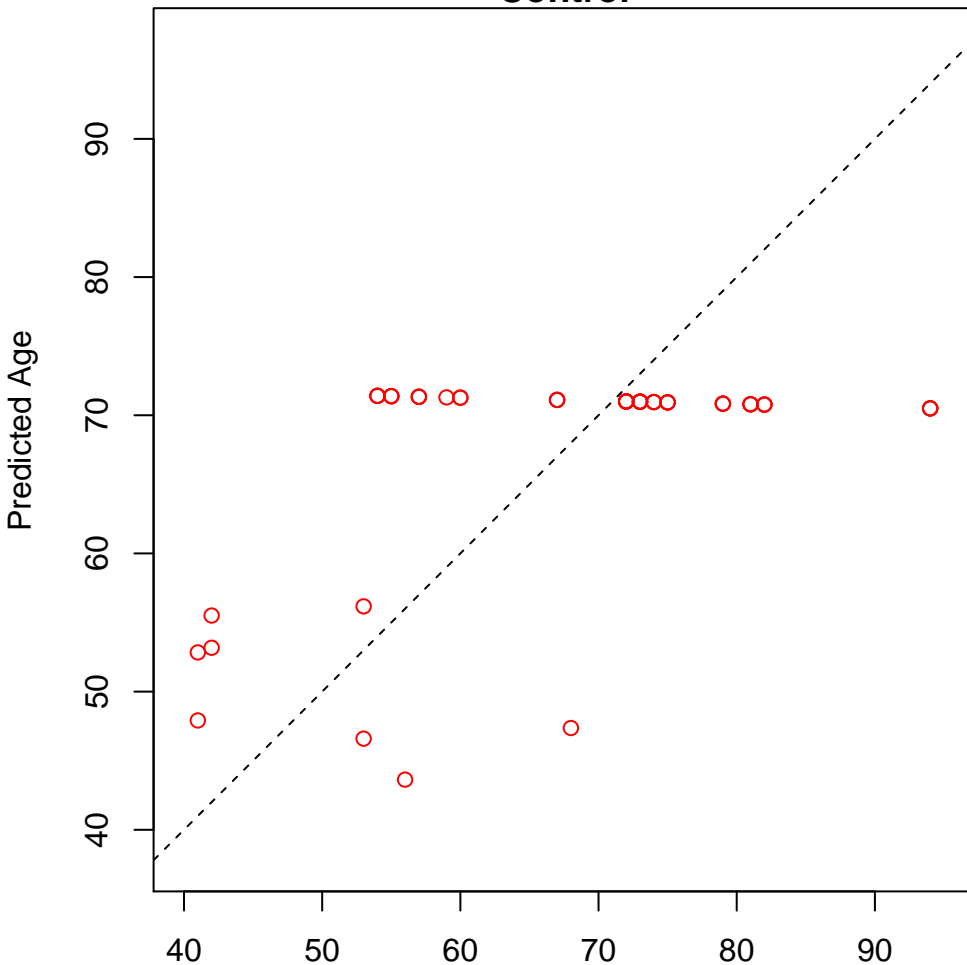


protein refolding (Score: 0.793278)

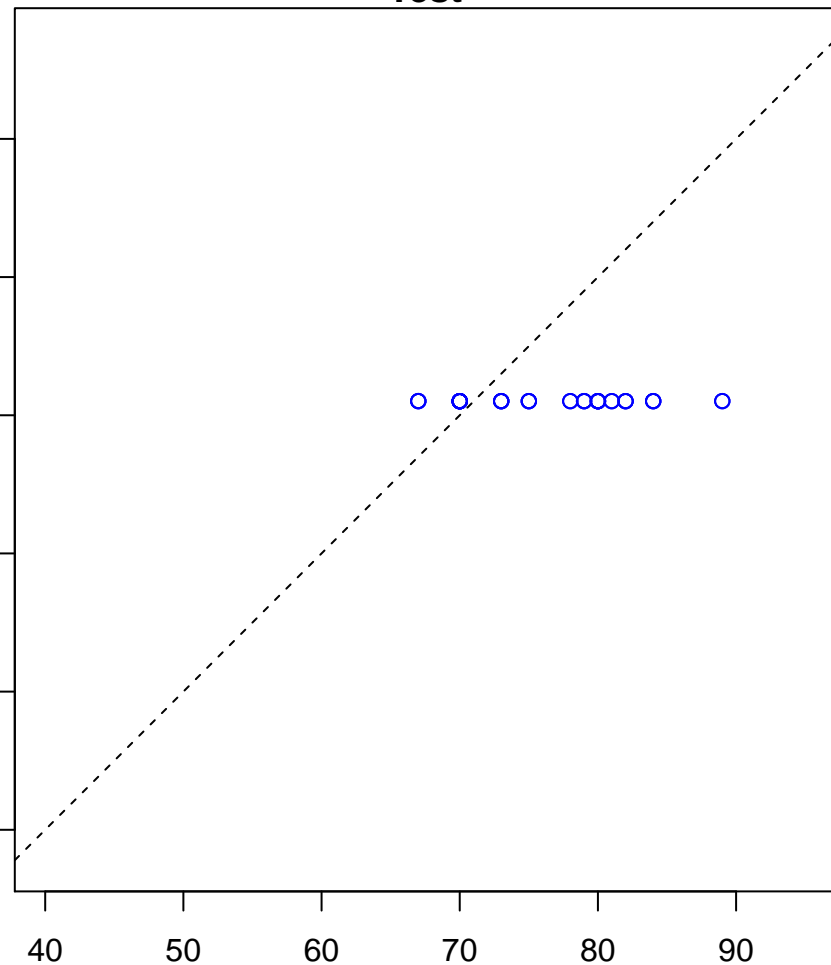


regulation of lymphocyte activation (Score: 0.793262)

Control

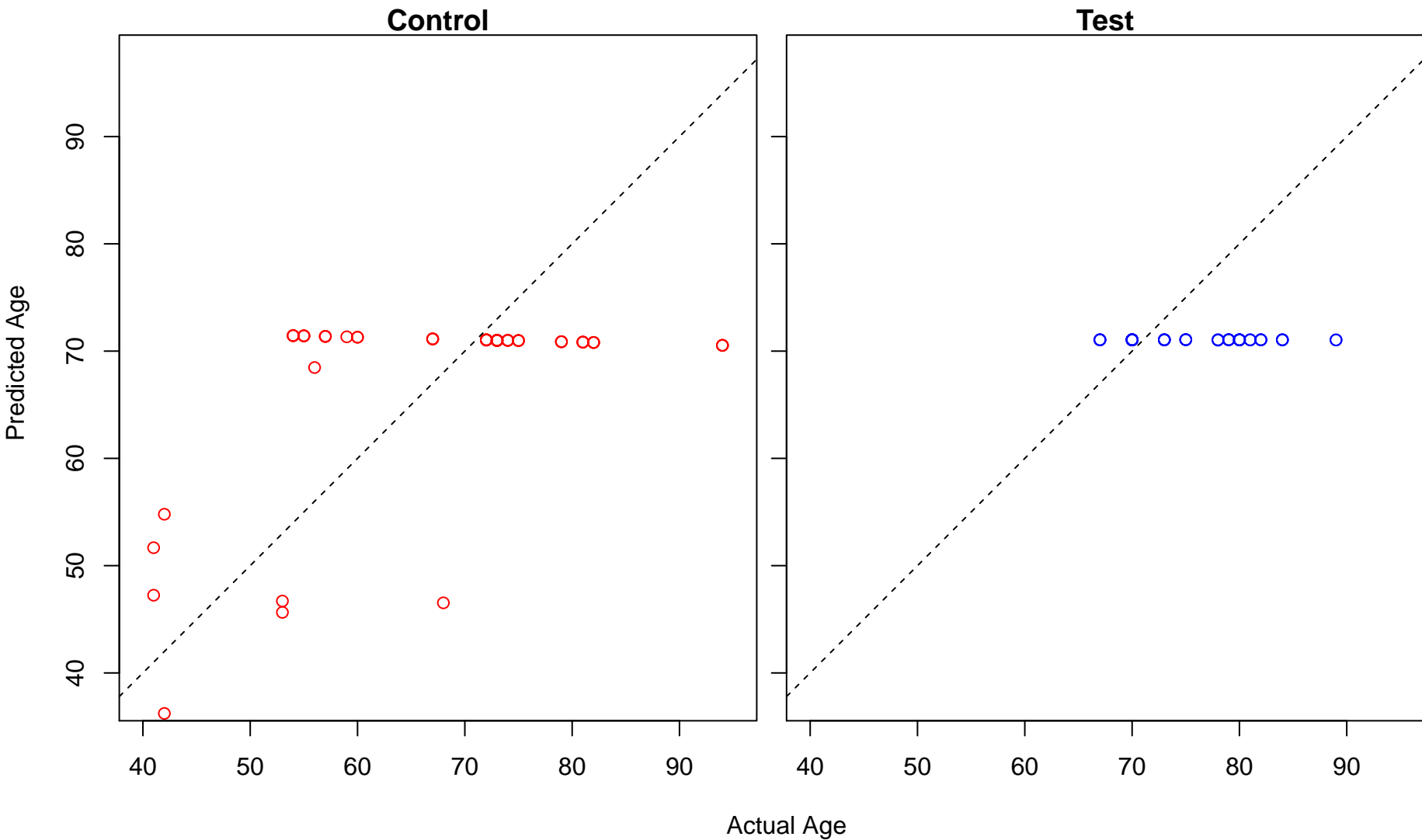


Test



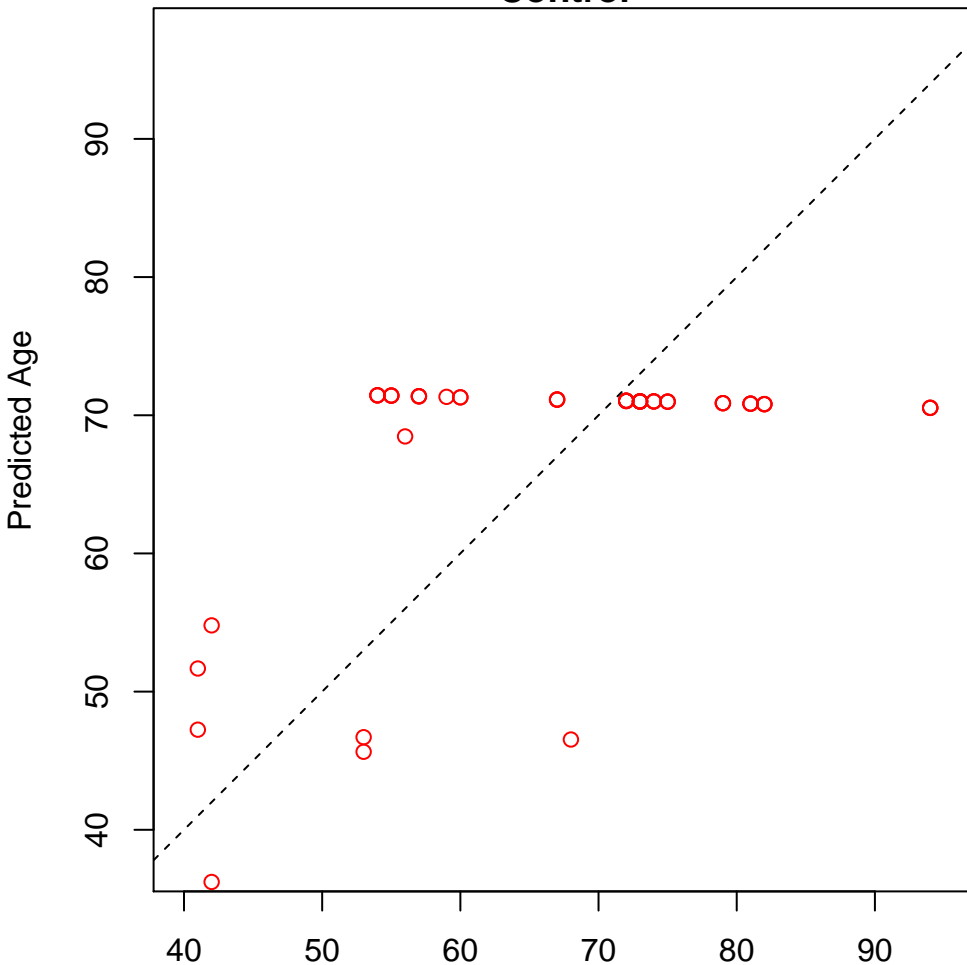
Actual Age

response to glucagon (Score: 0.793178)

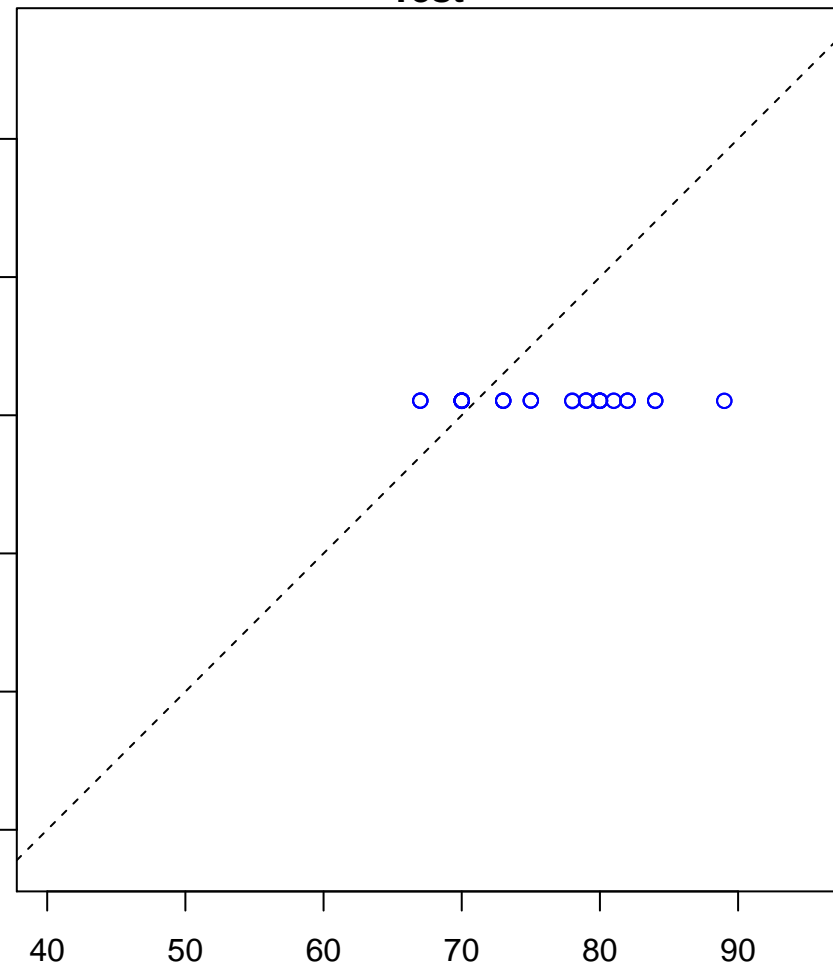


cellular response to glucagon stimulus (Score: 0.793178)

Control

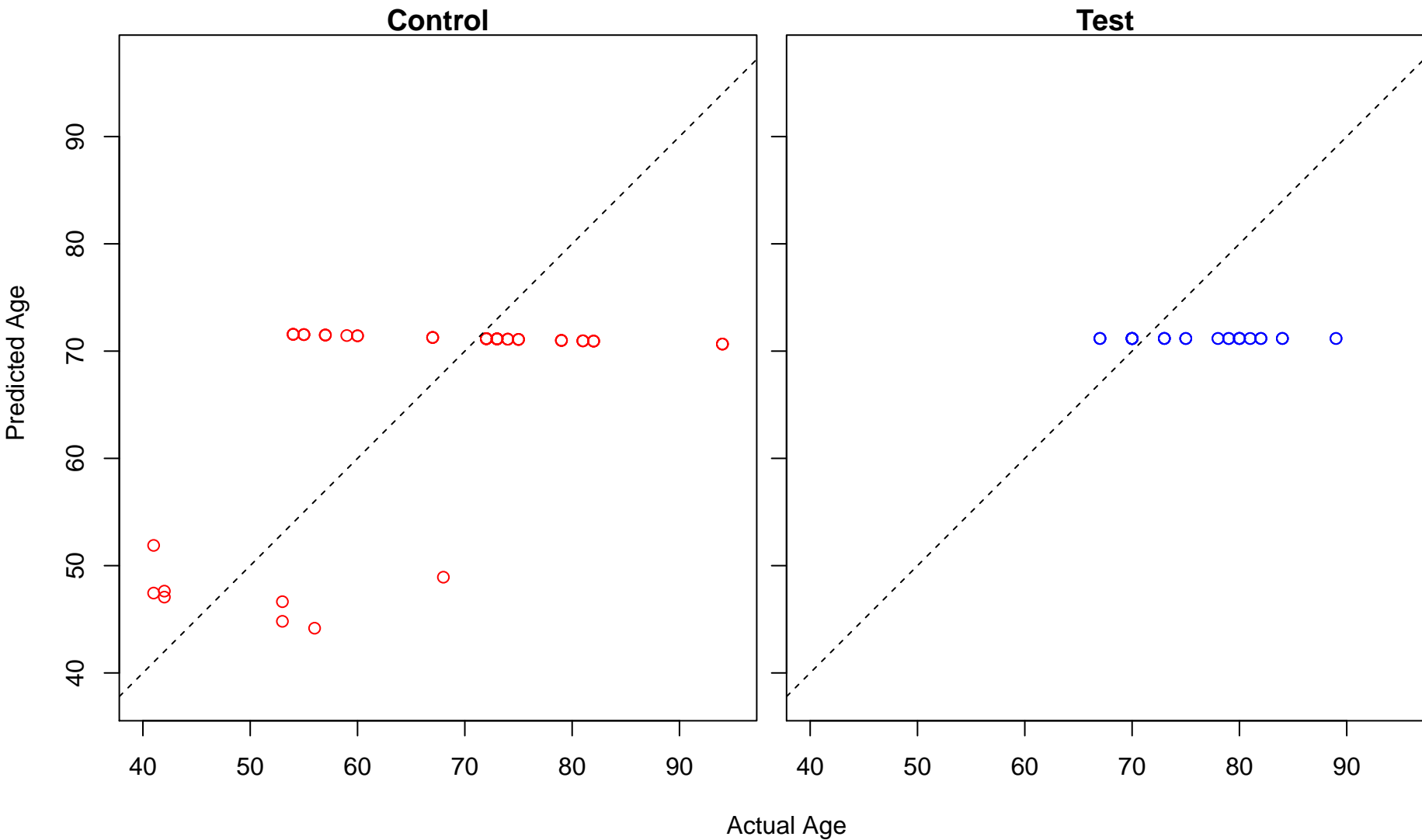


Test

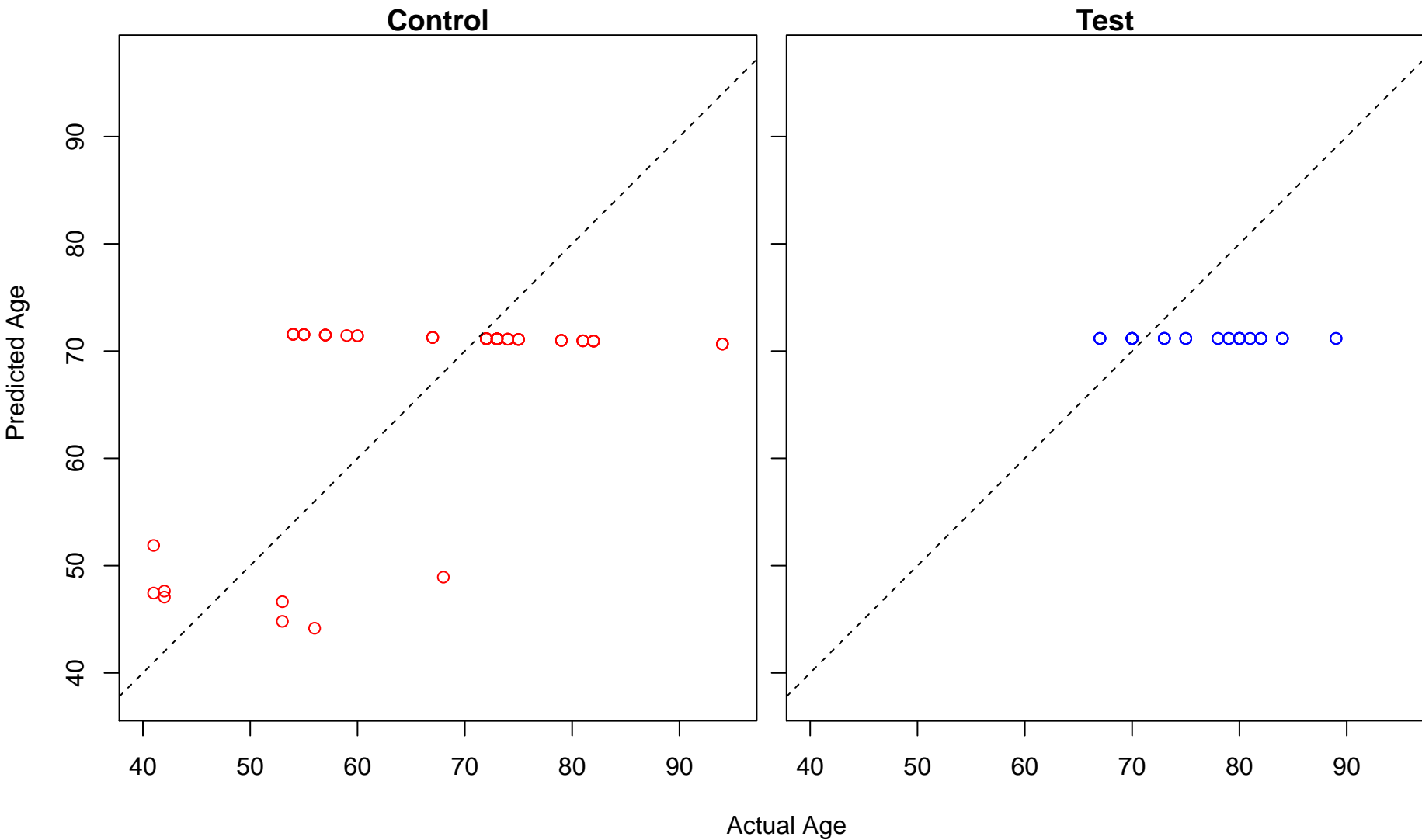


Actual Age

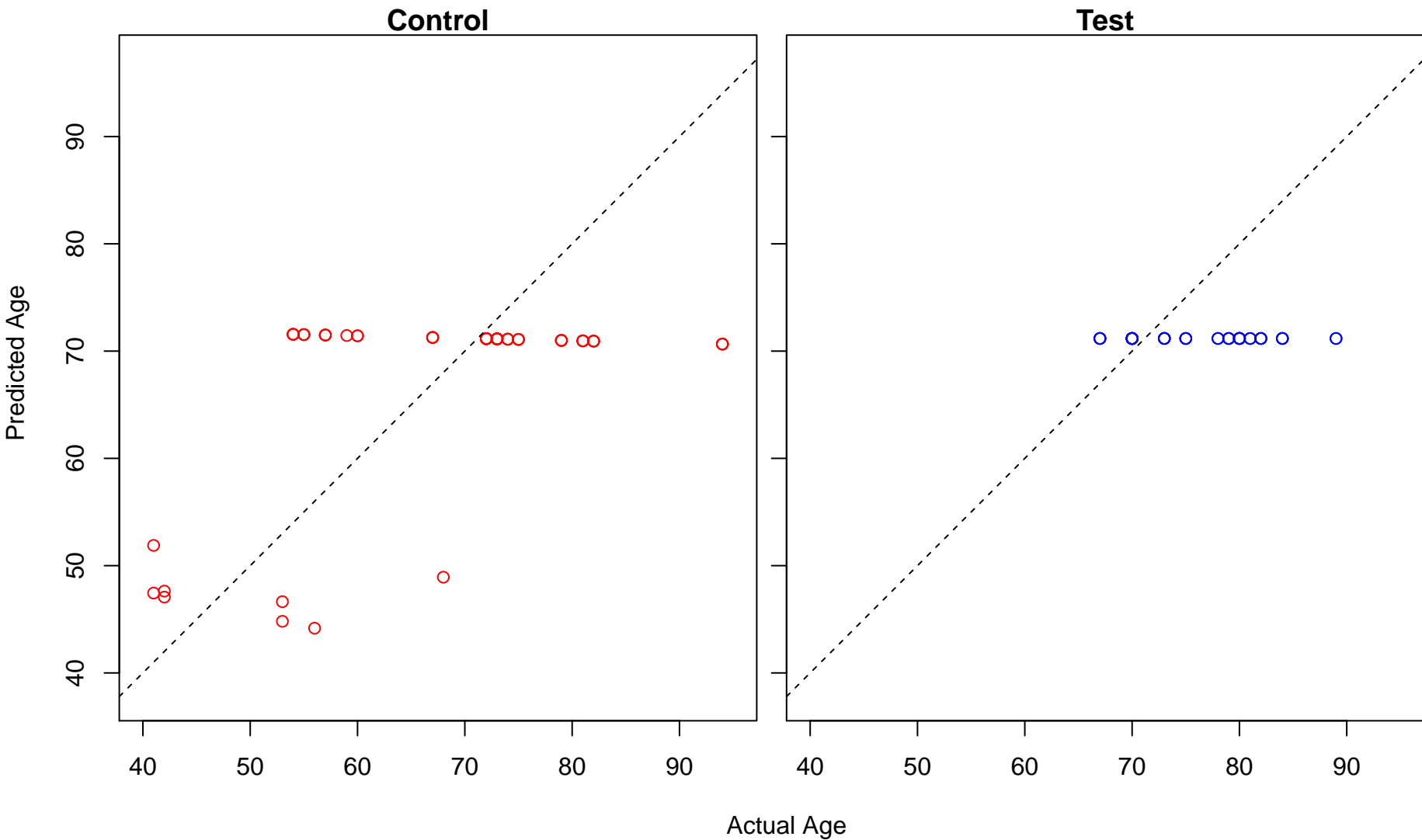
protein transport (Score: 0.793090)



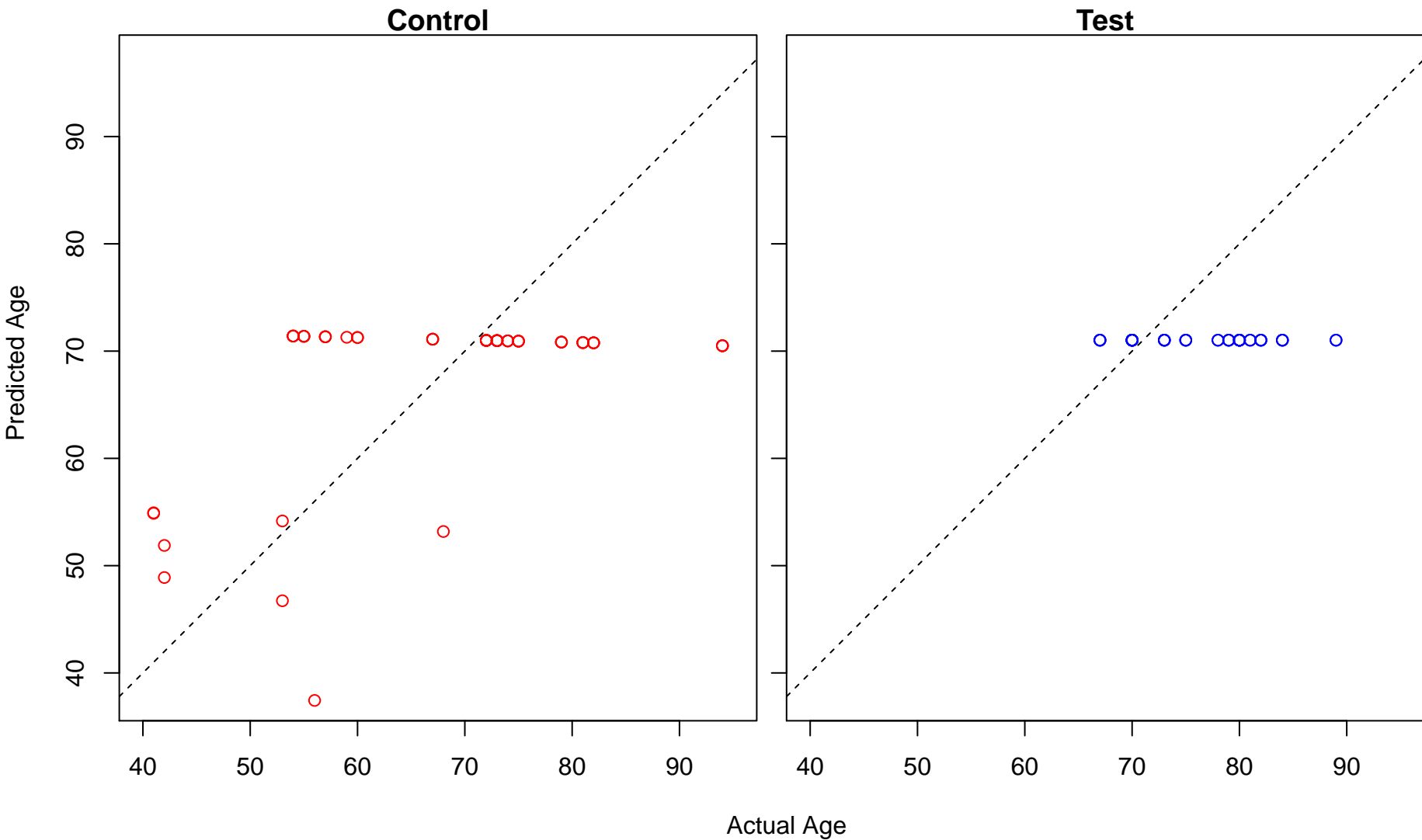
peptide transport (Score: 0.793090)



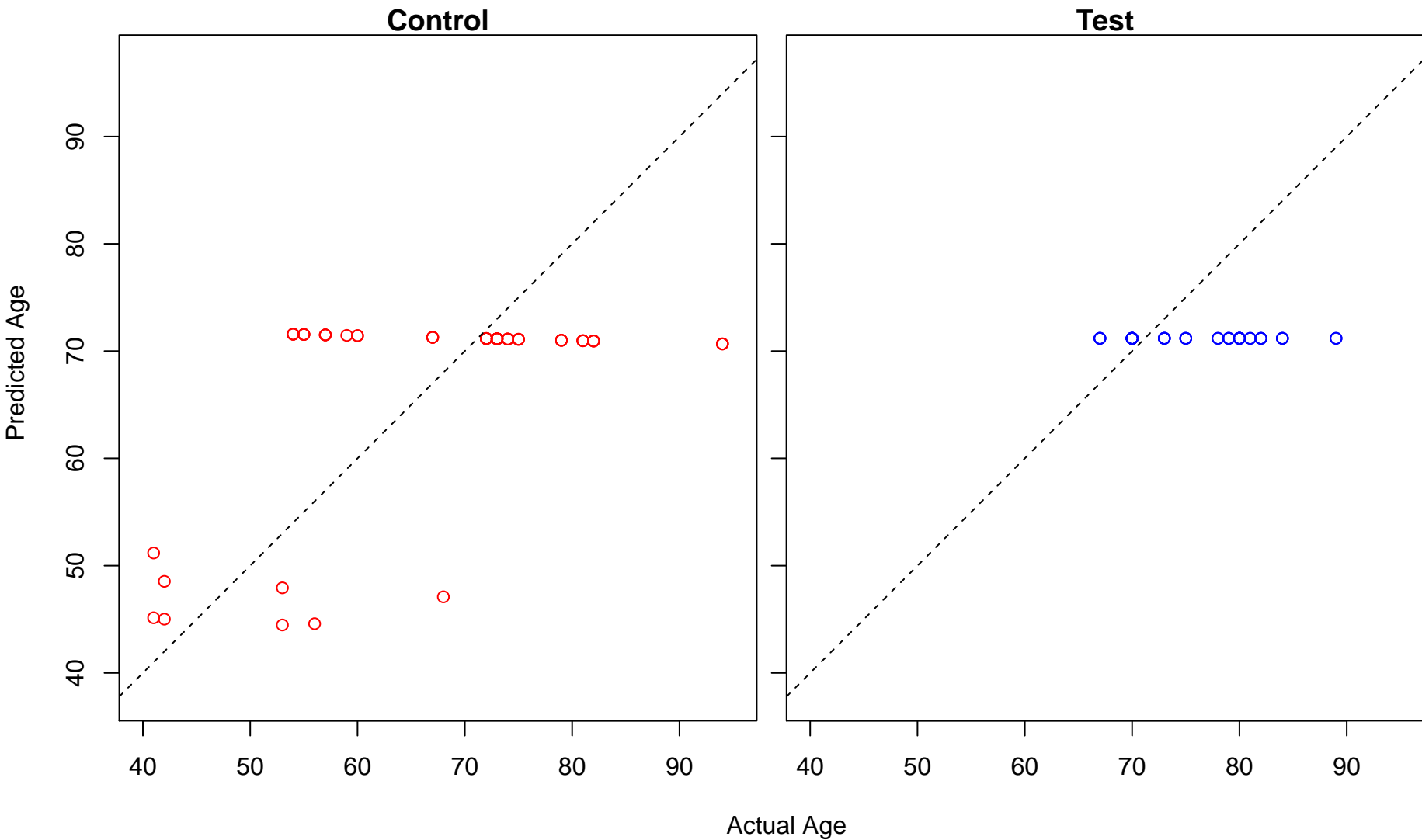
amide transport (Score: 0.793090)



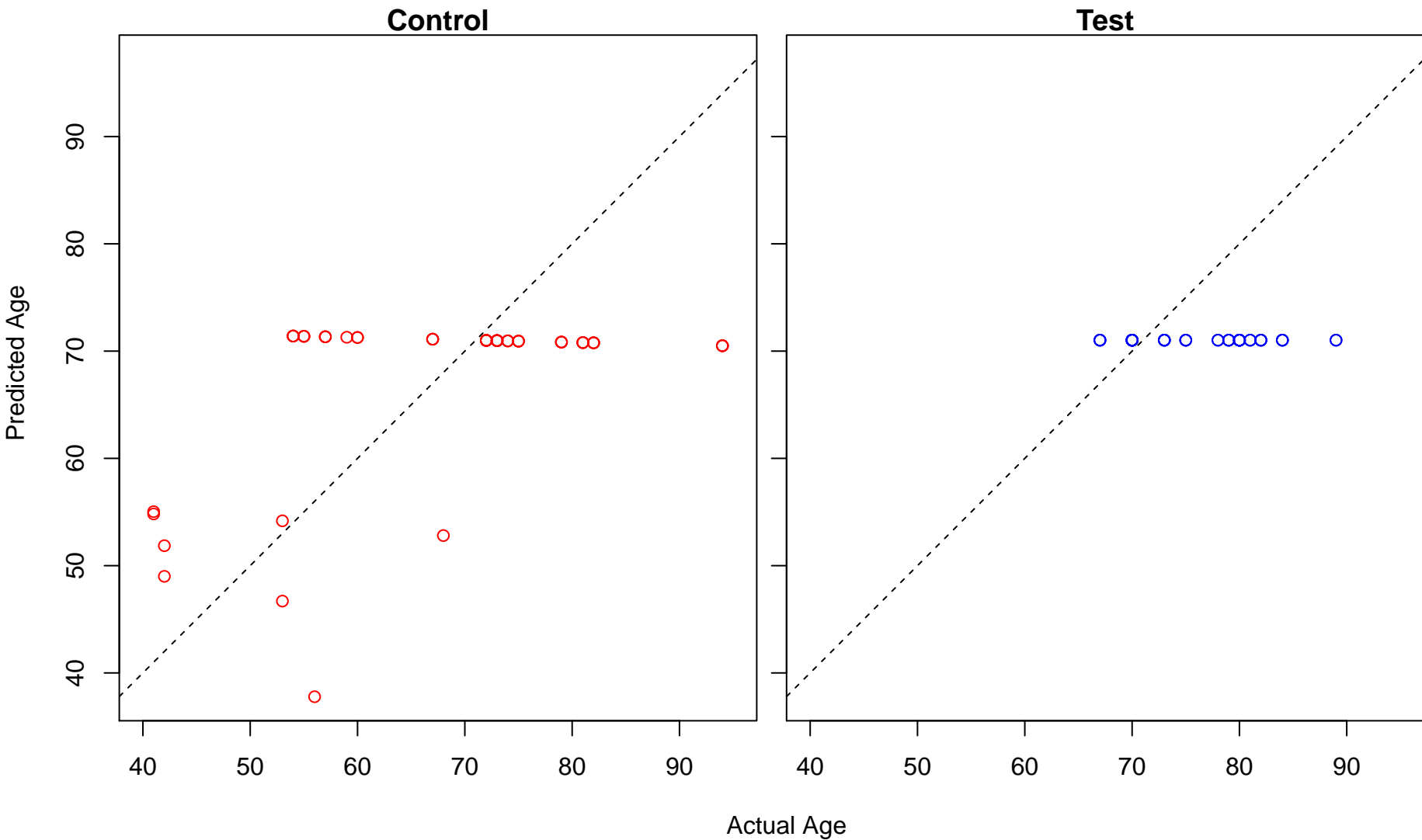
transmembrane receptor protein serine/threonine kinase signaling pathway (Score: 0.792984)



regulation of nitrogen compound metabolic process (Score: 0.792919)

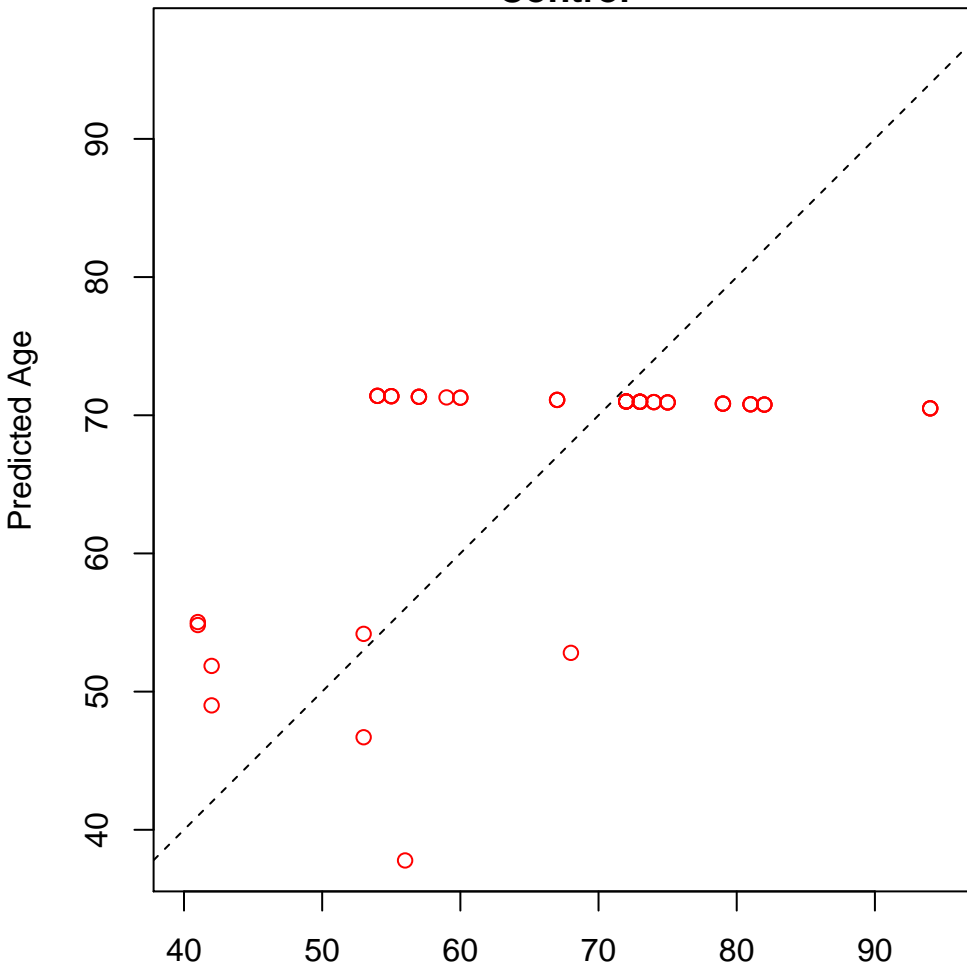


response to growth factor (Score: 0.792885)

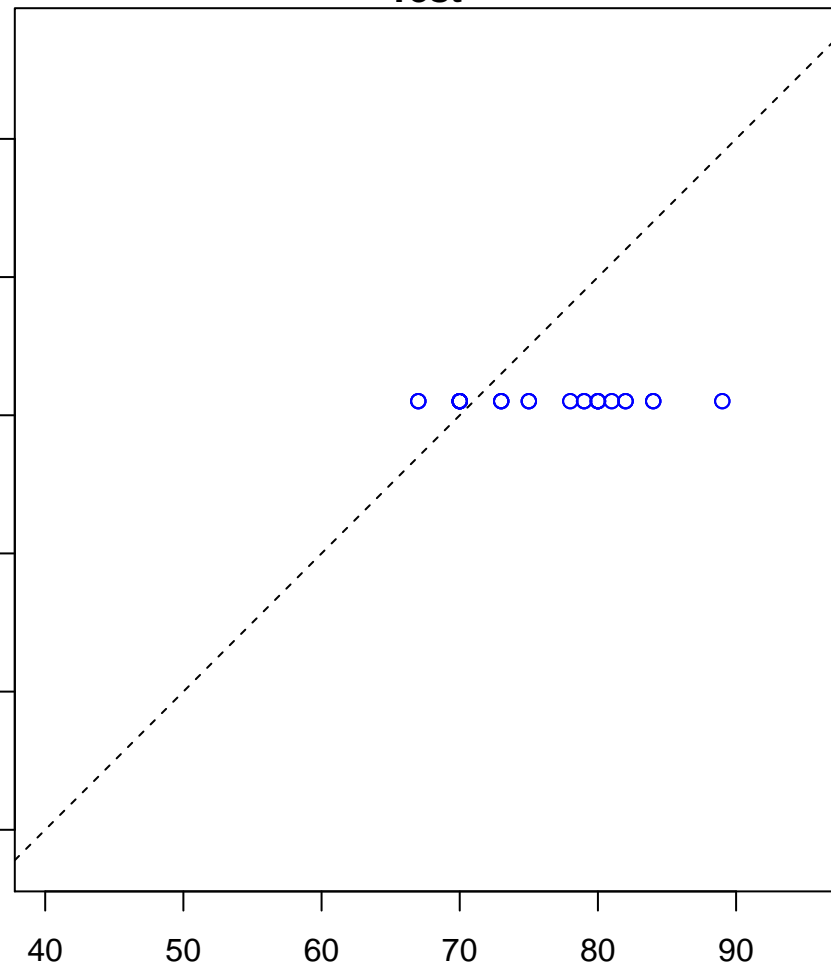


cellular response to growth factor stimulus (Score: 0.792885)

Control



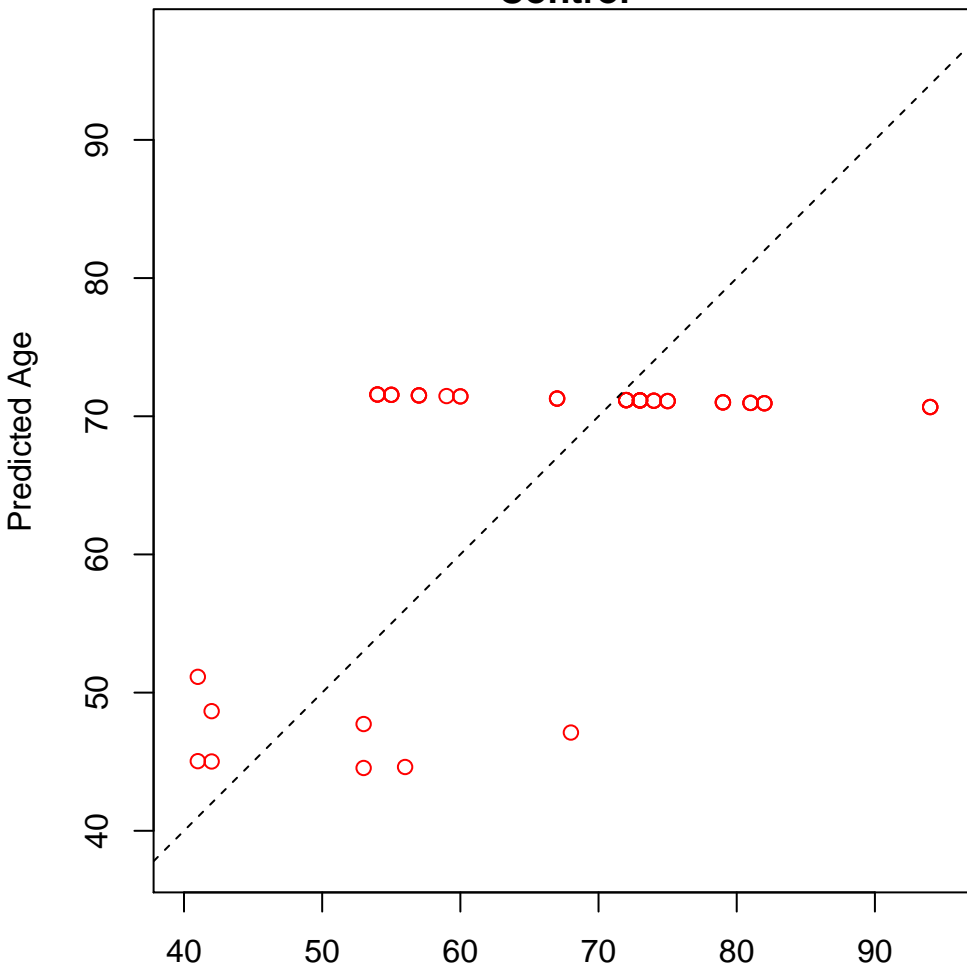
Test



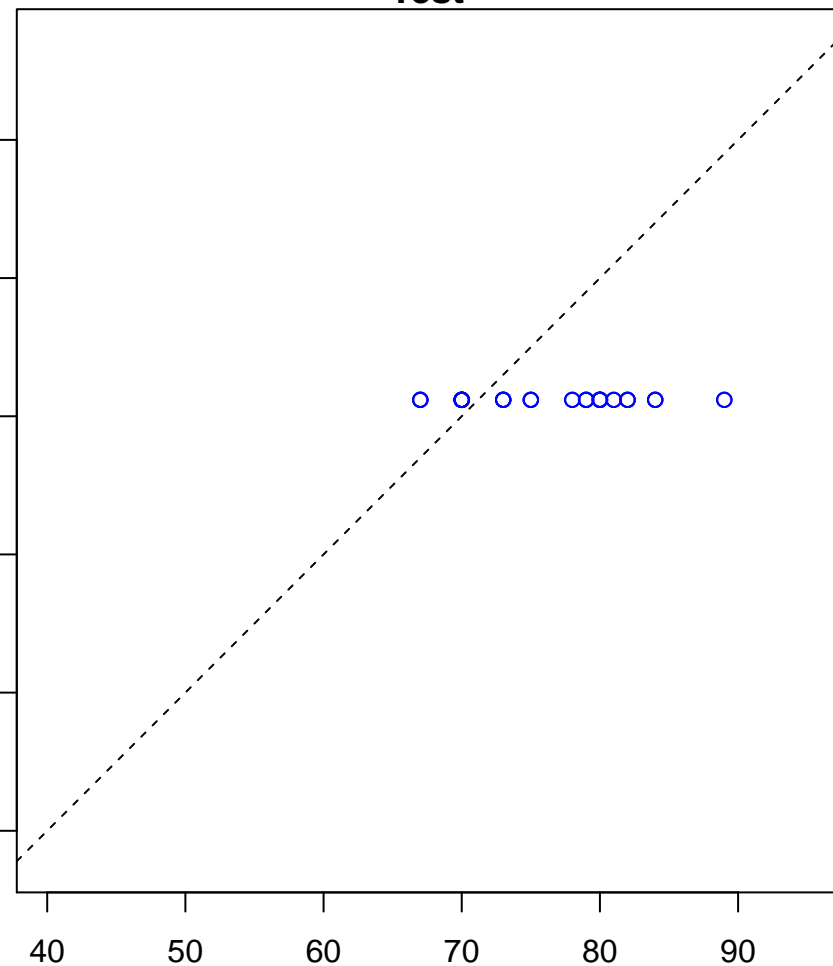
Actual Age

regulation of primary metabolic process (Score: 0.792845)

Control

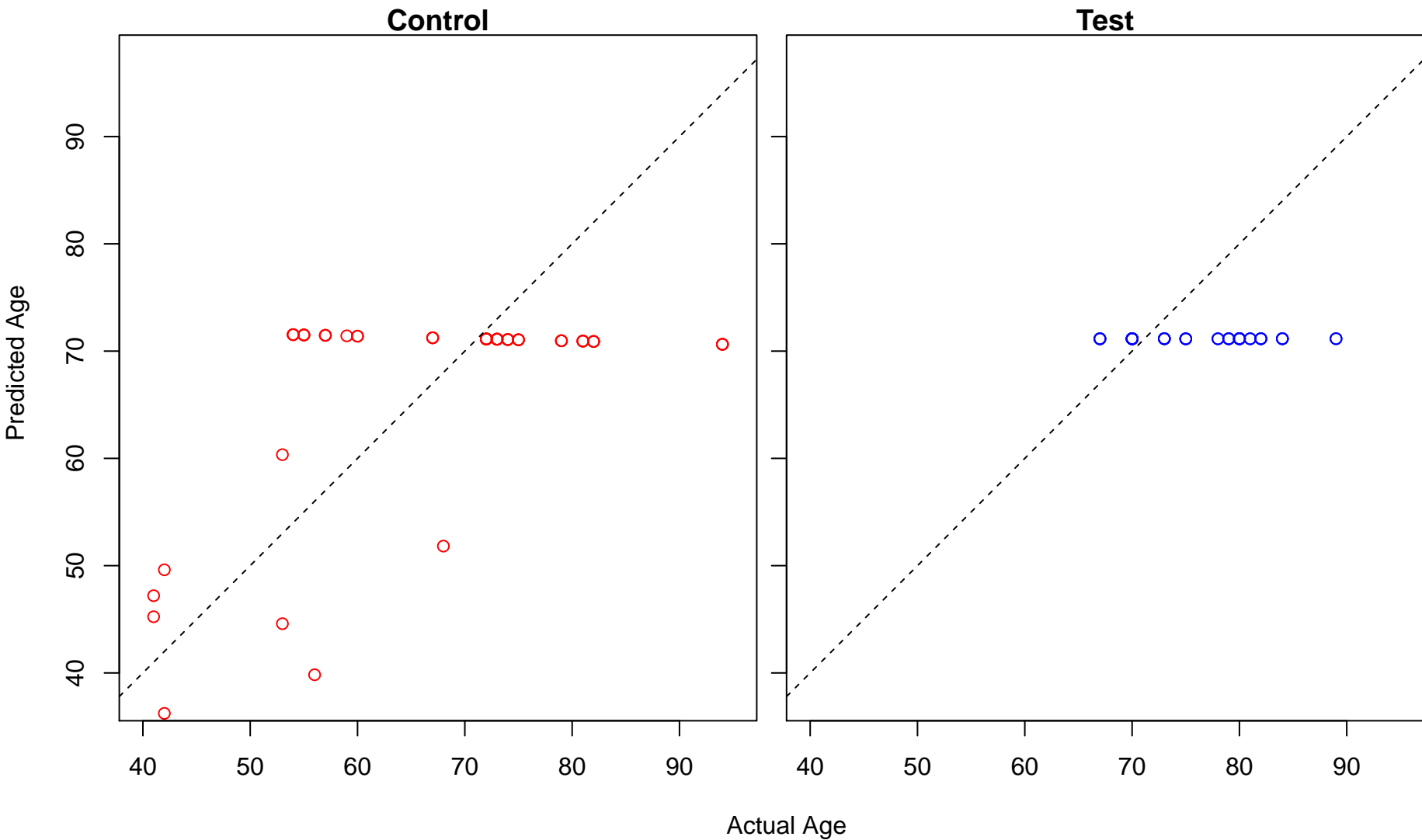


Test

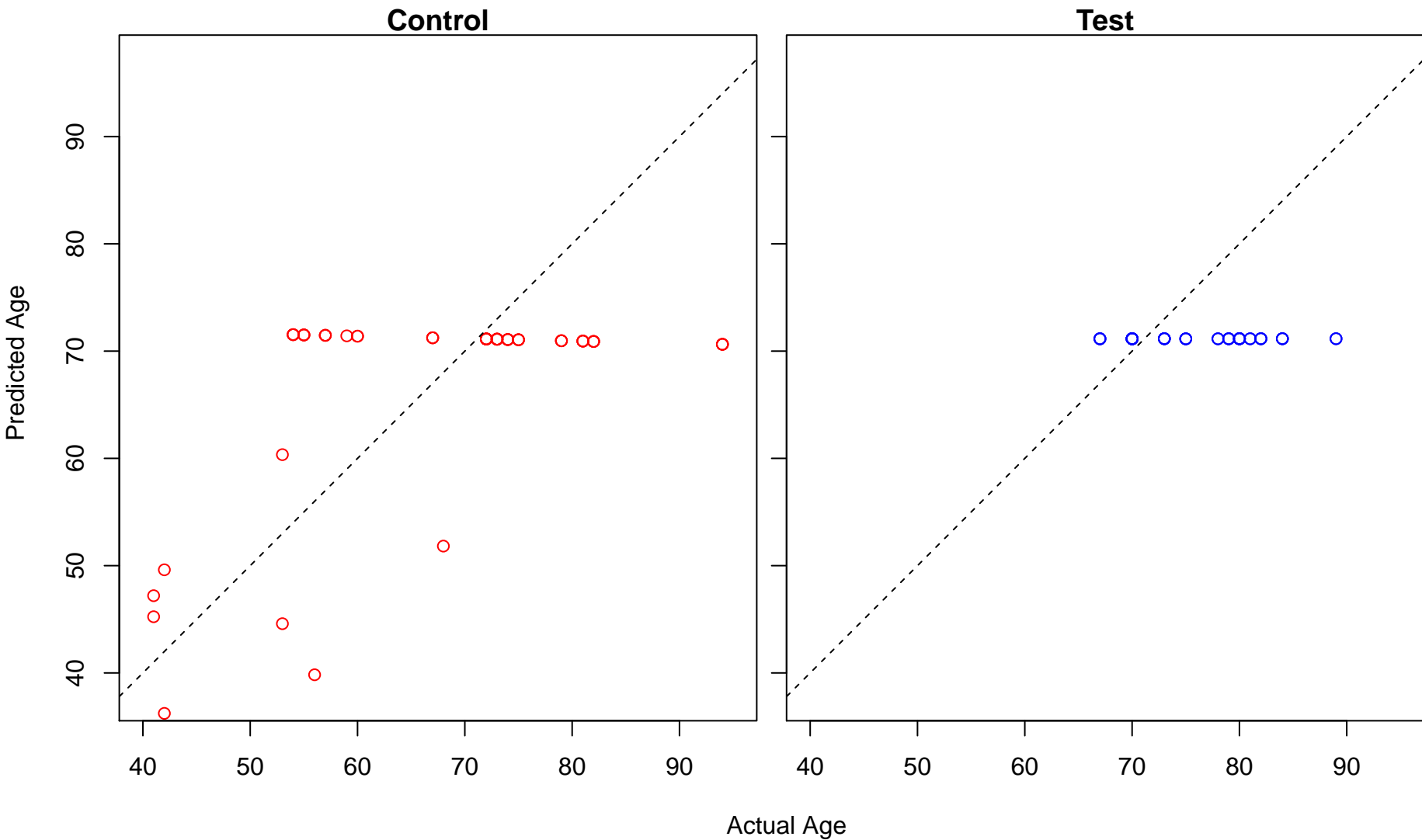


Actual Age

regulation of posttranscriptional gene silencing (Score: 0.792781)

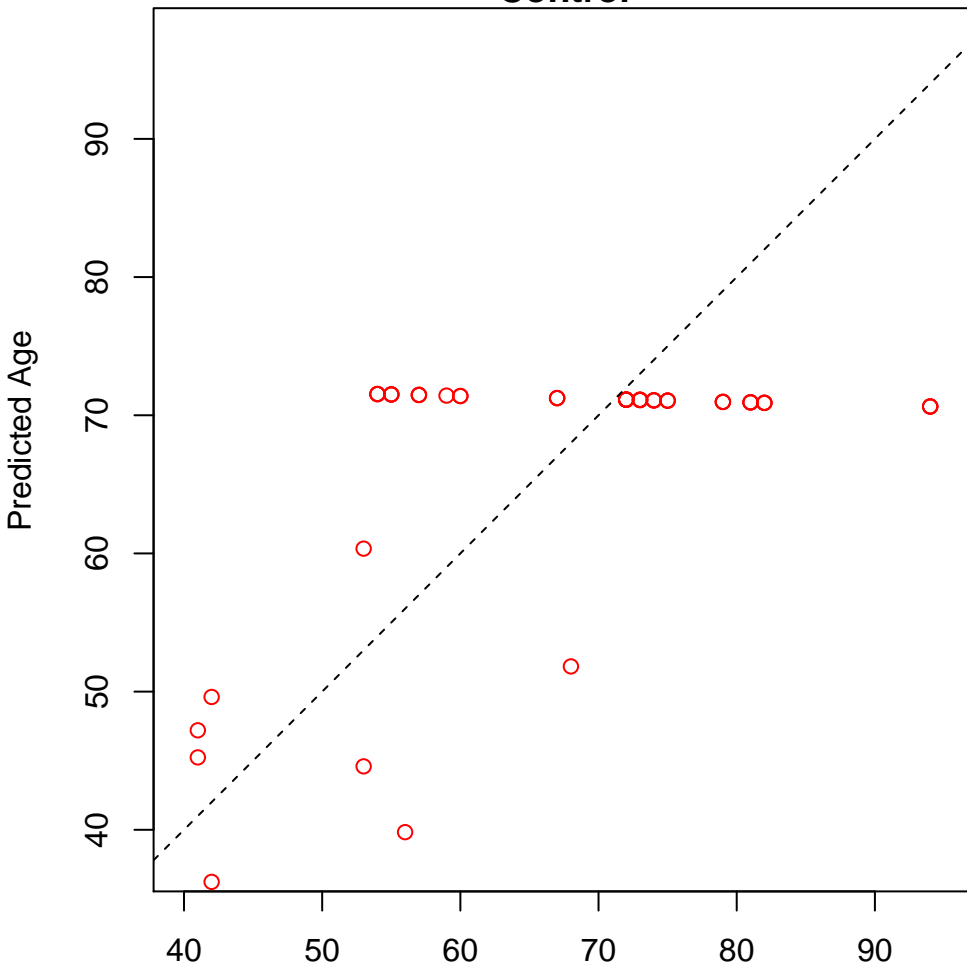


regulation of gene silencing by miRNA (Score: 0.792781)

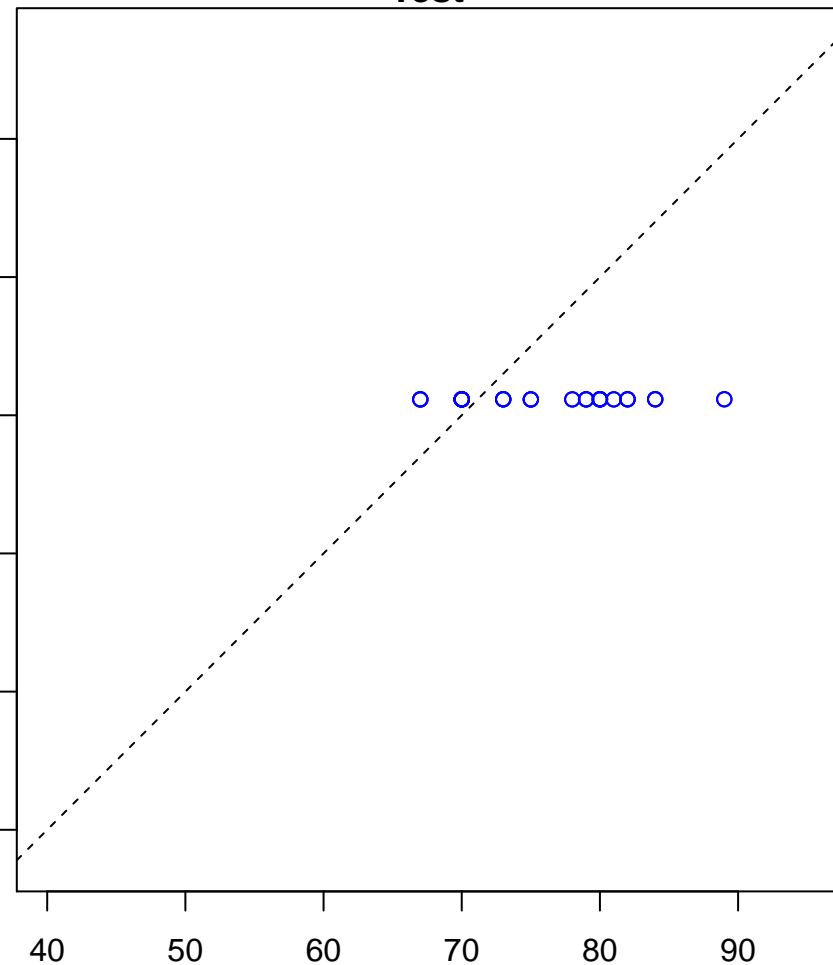


regulation of gene silencing by RNA (Score: 0.792781)

Control

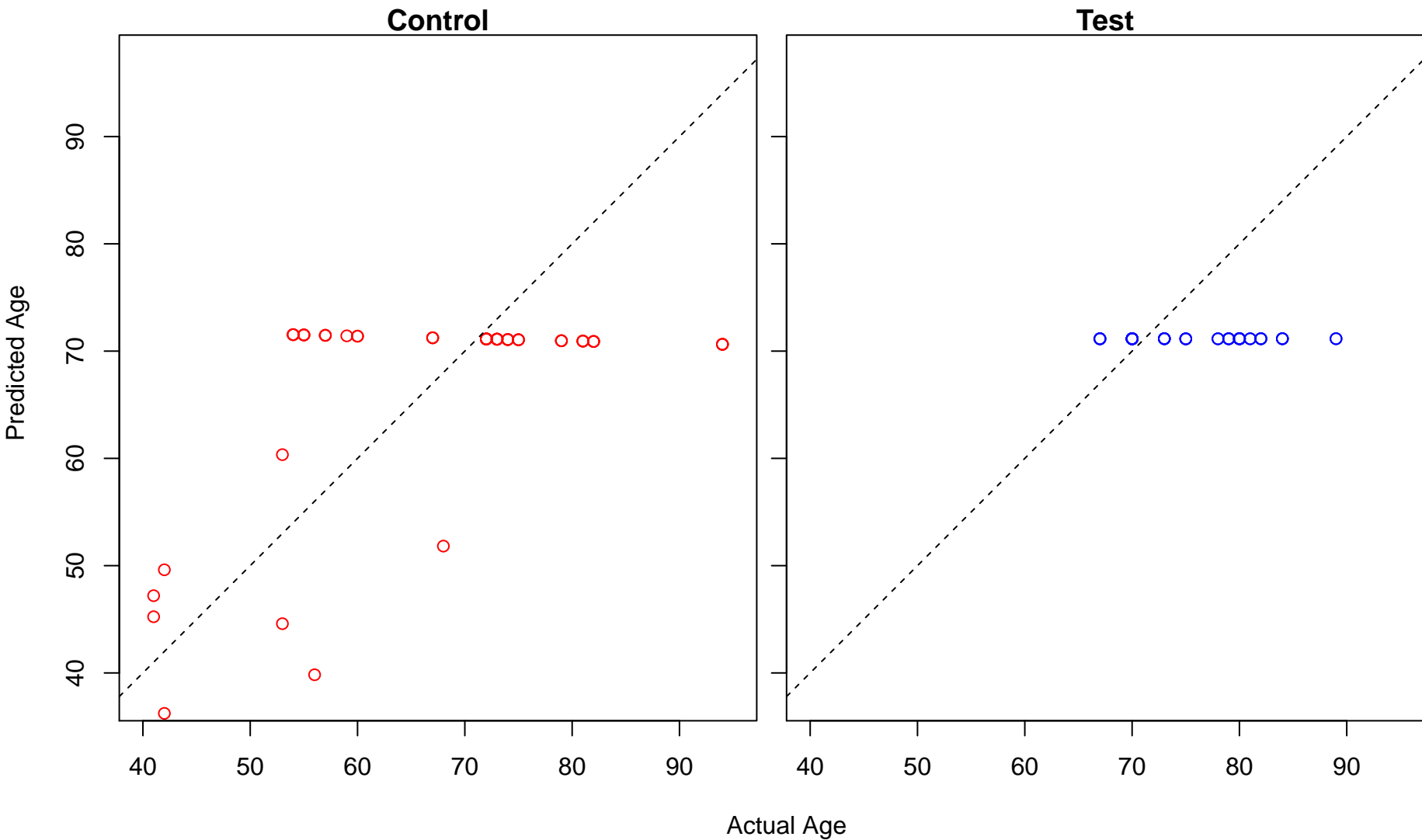


Test

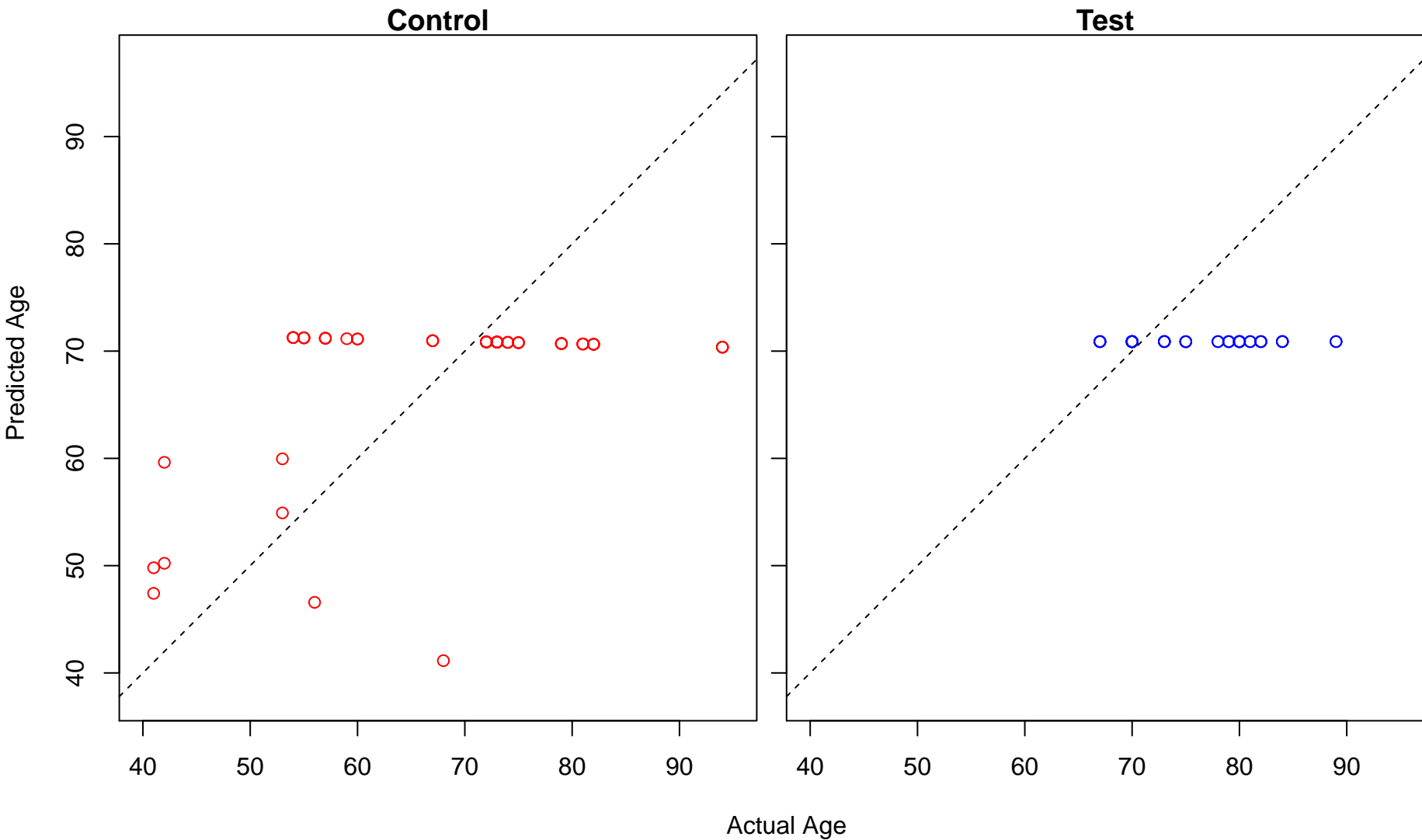


Actual Age

regulation of gene silencing (Score: 0.792781)

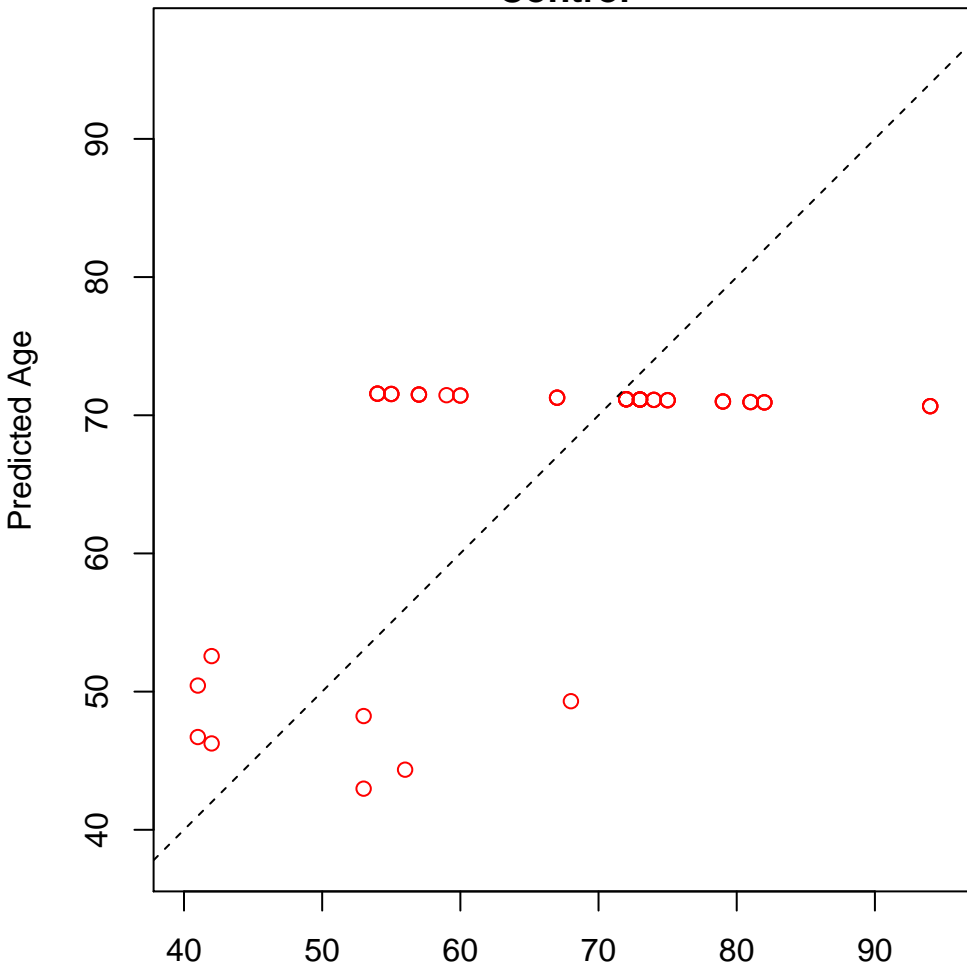


positive regulation of DNA biosynthetic process (Score: 0.792744)

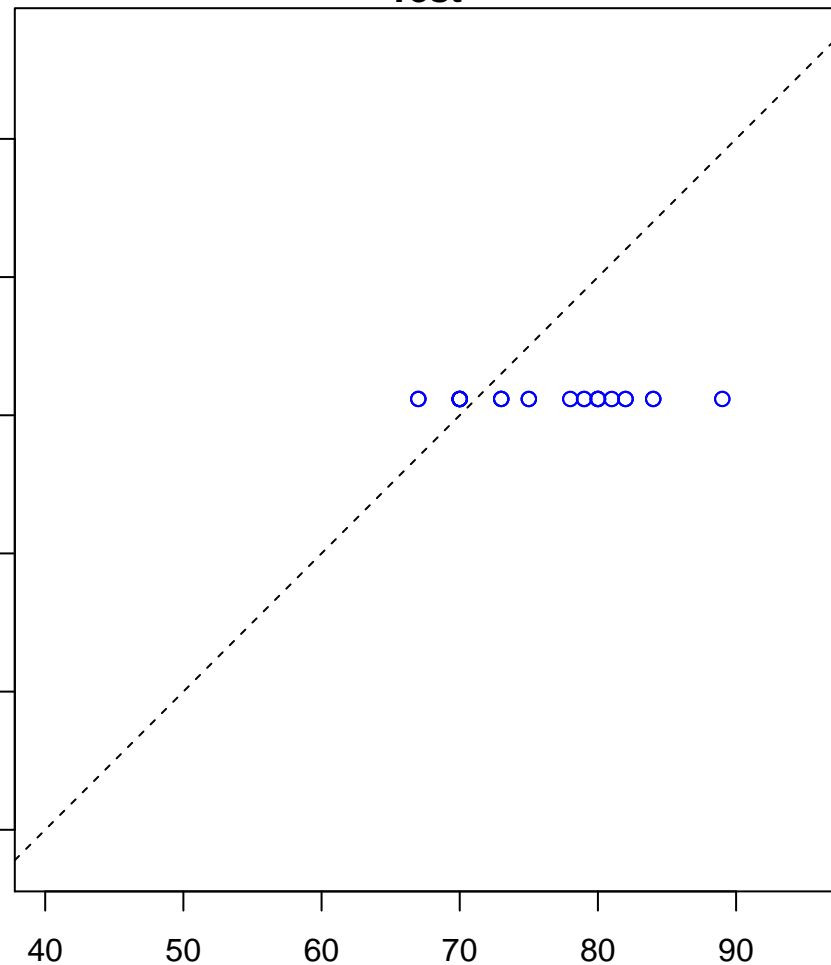


nitrogen compound metabolic process (Score: 0.792688)

Control

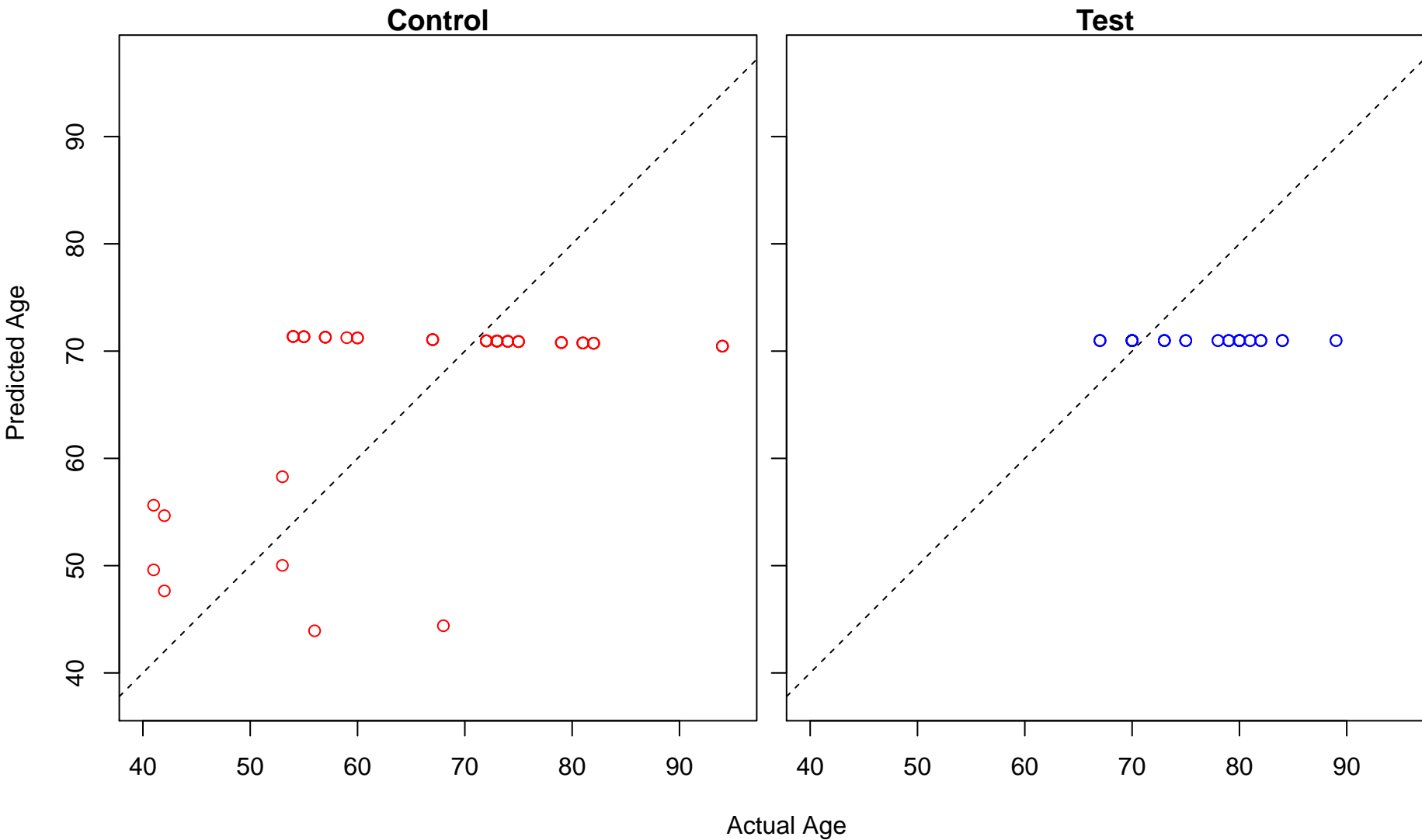


Test



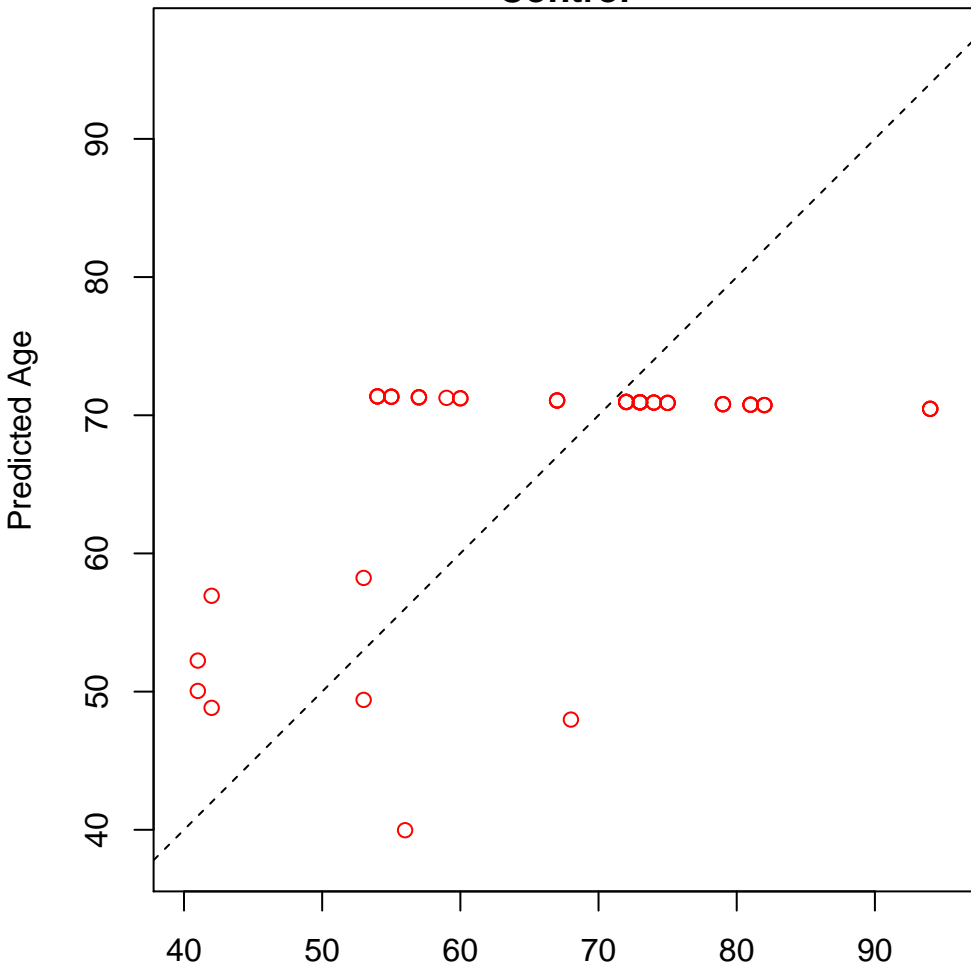
Actual Age

positive regulation of receptor-mediated endocytosis (Score: 0.792513)

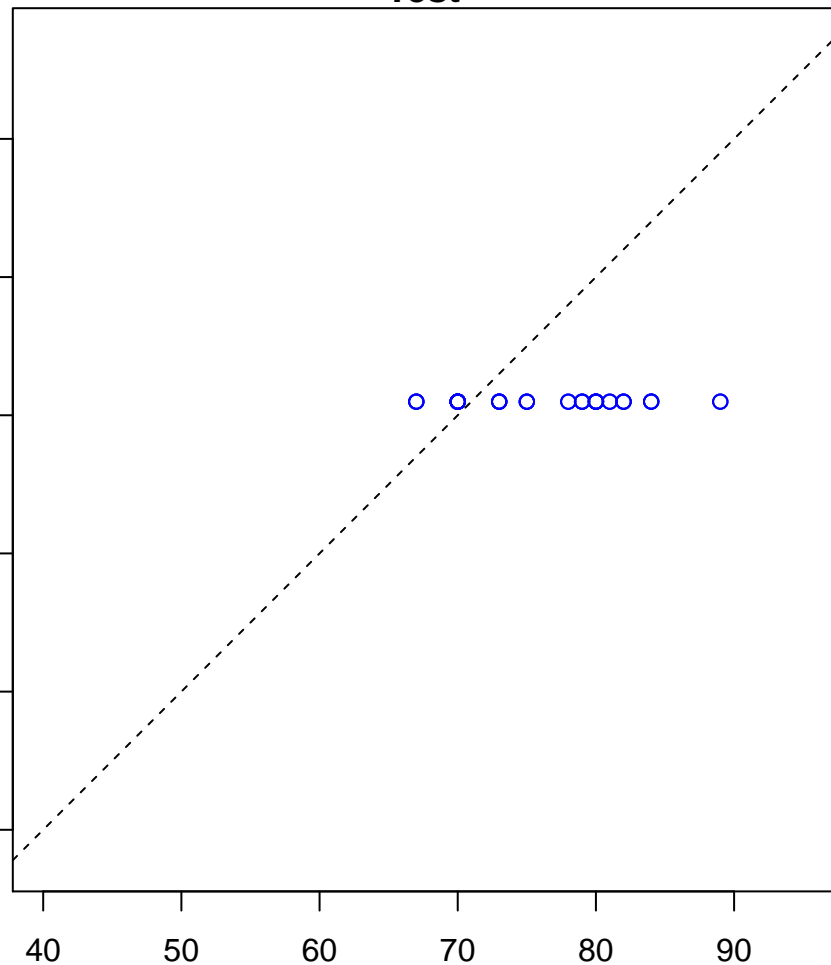


response to ammonium ion (Score: 0.792230)

Control



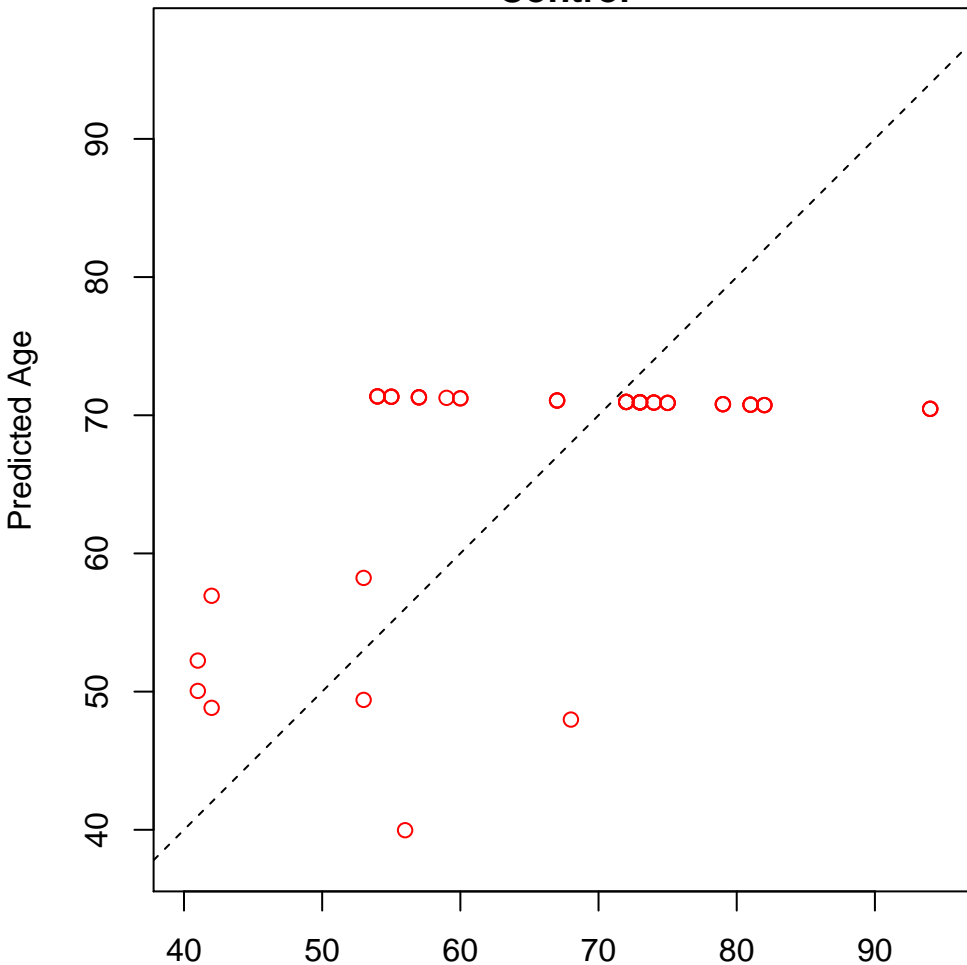
Test



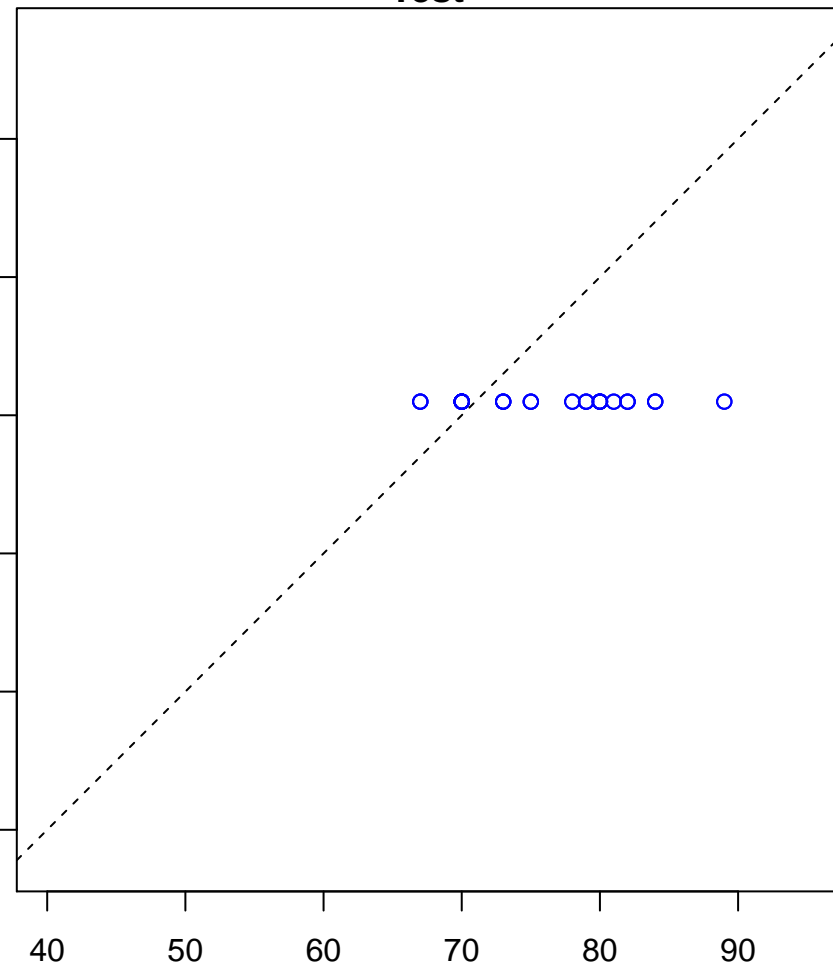
Actual Age

cellular response to ammonium ion (Score: 0.792230)

Control

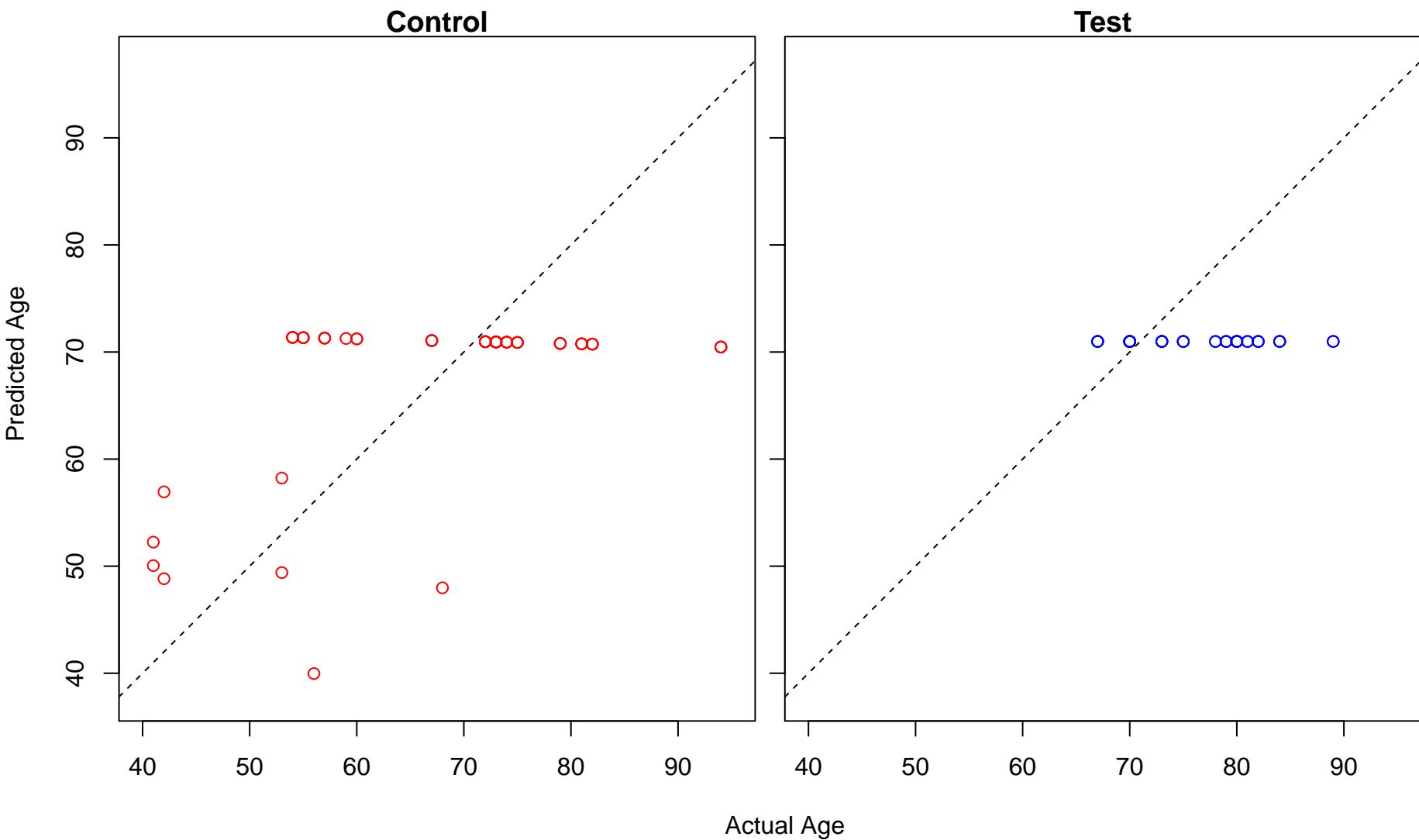


Test



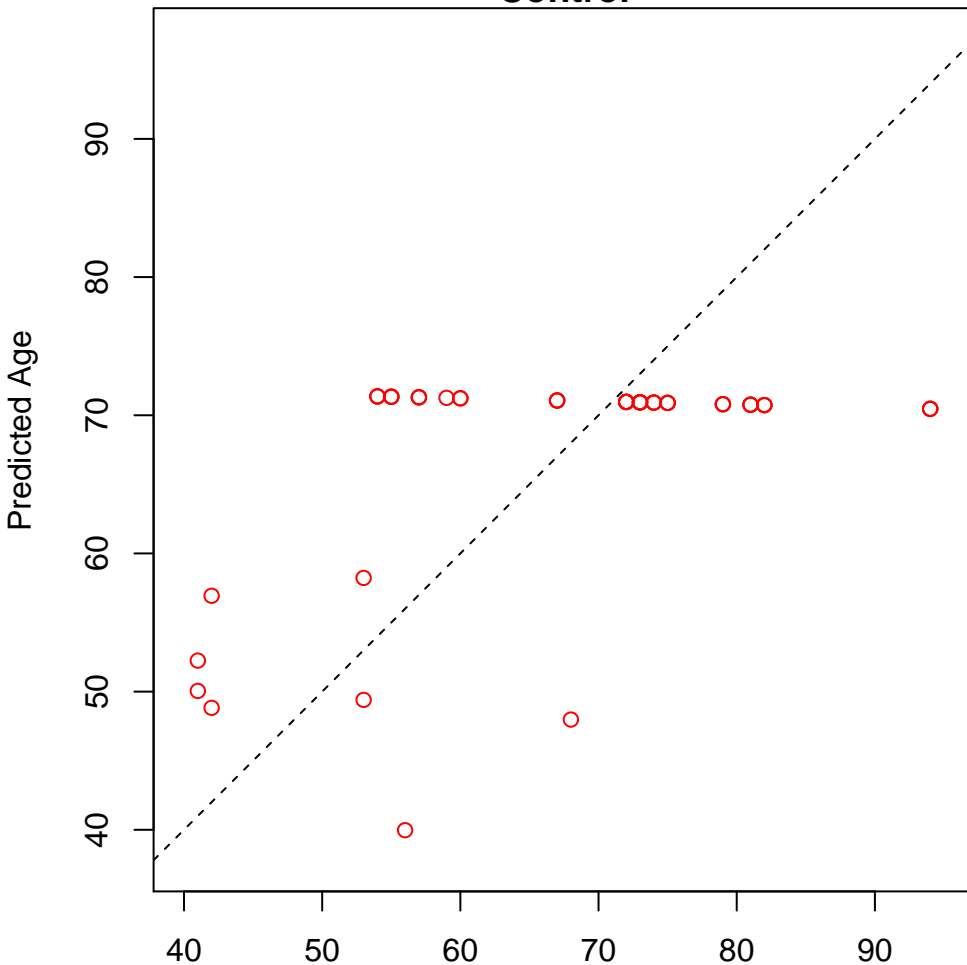
Actual Age

response to monoamine (Score: 0.792230)

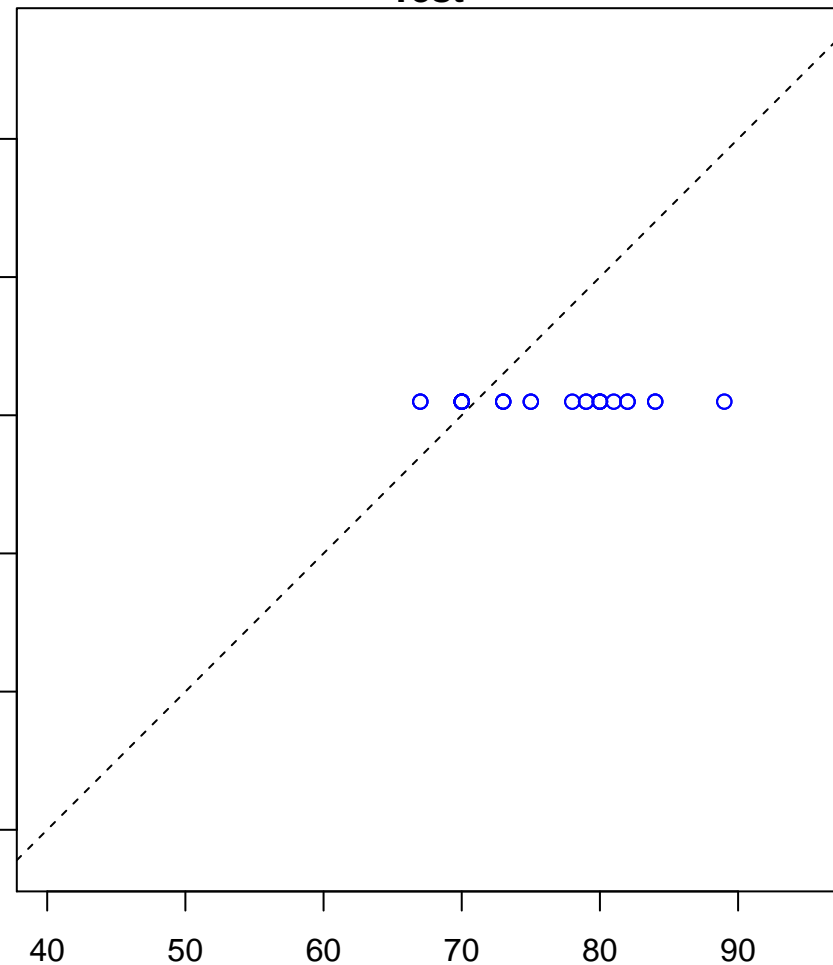


cellular response to monoamine stimulus (Score: 0.792230)

Control

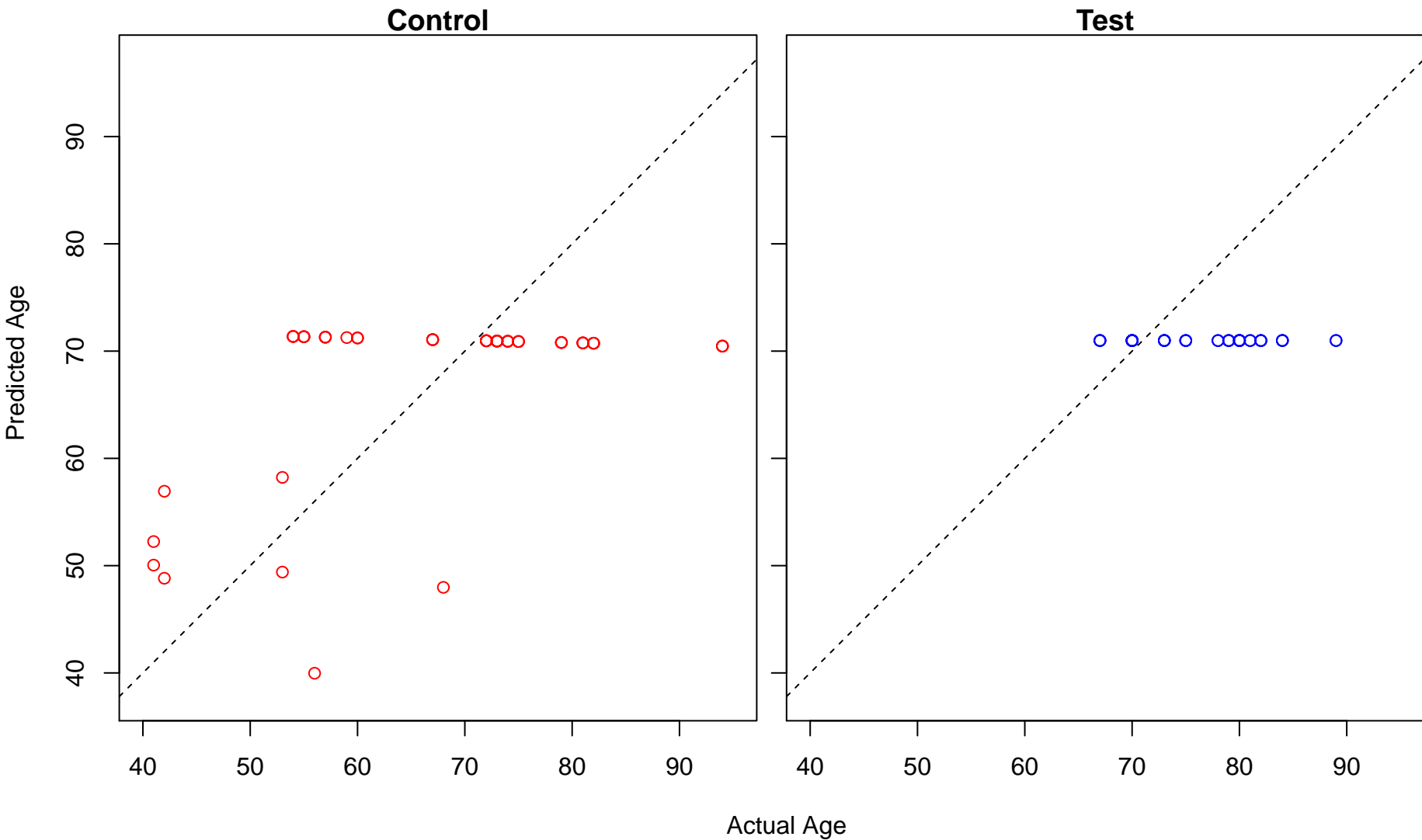


Test

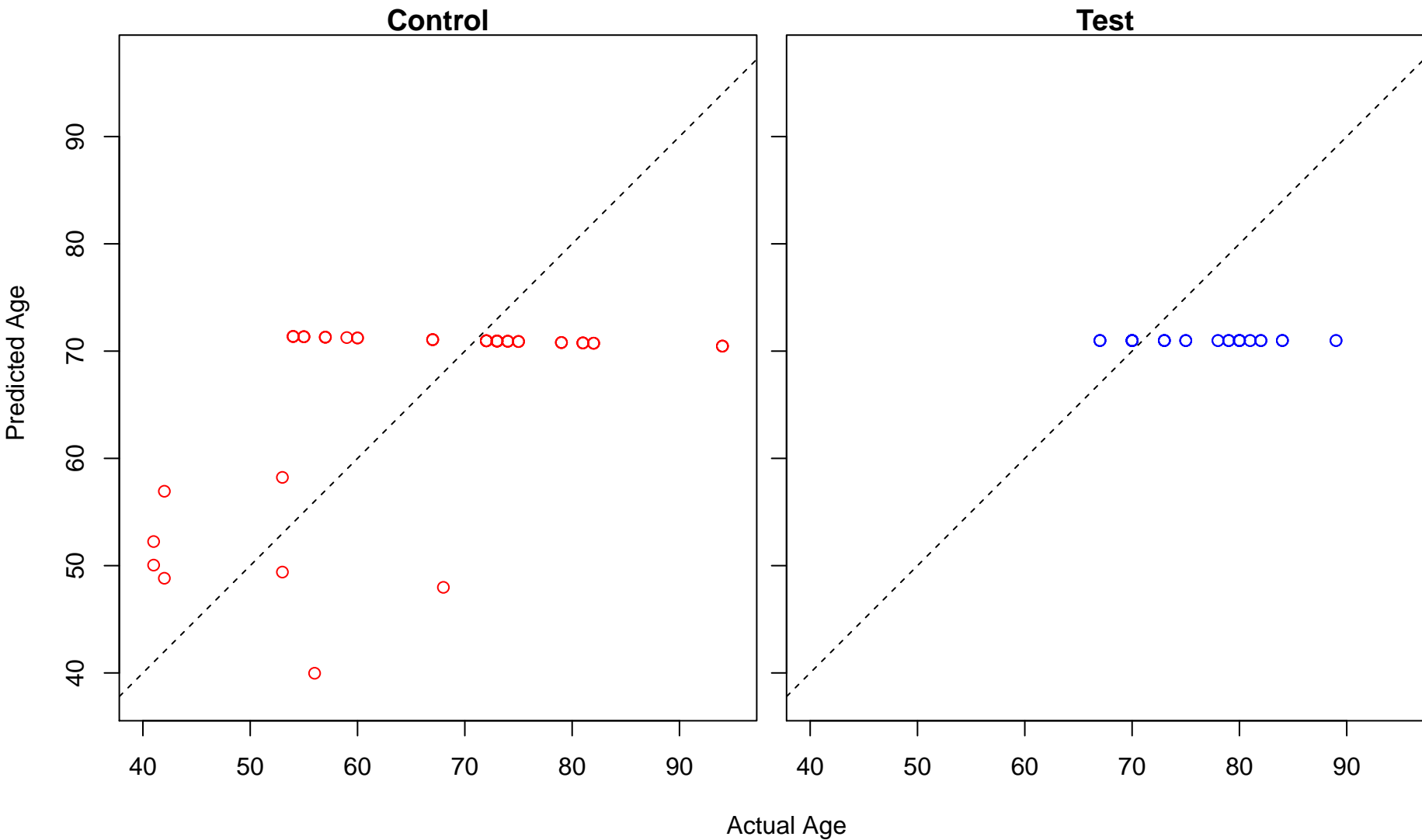


Actual Age

response to catecholamine (Score: 0.792230)

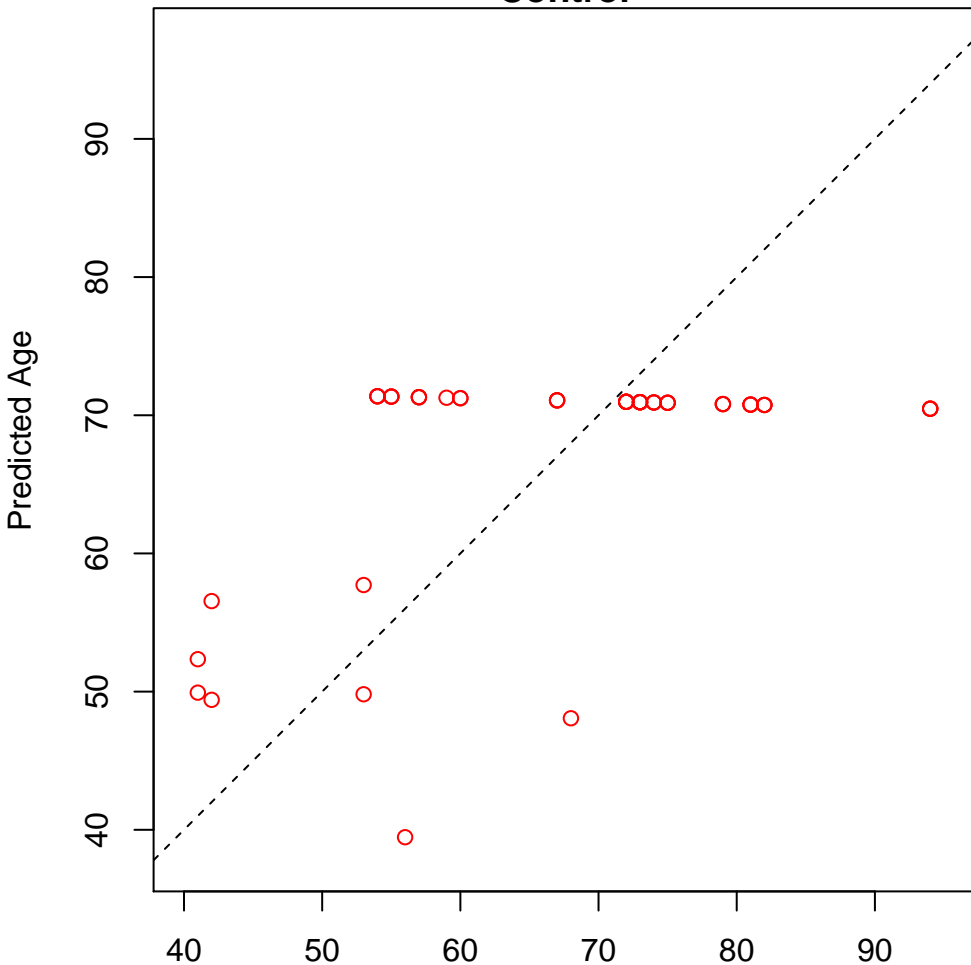


cellular response to catecholamine stimulus (Score: 0.792230)

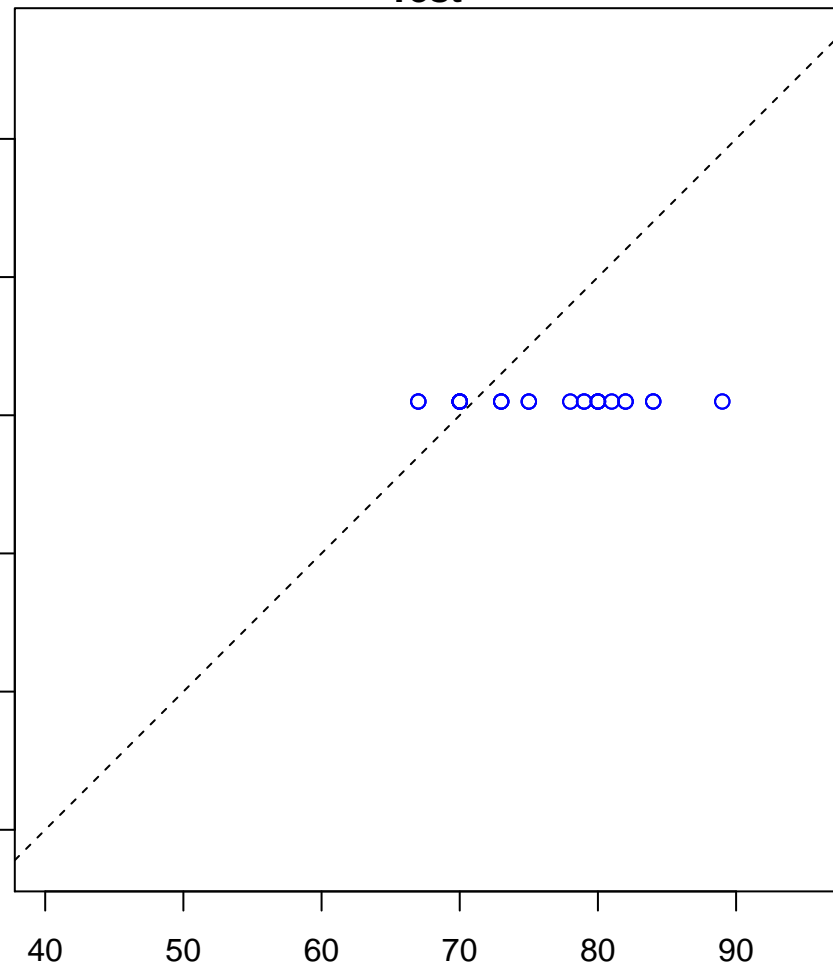


cellular response to light stimulus (Score: 0.792199)

Control



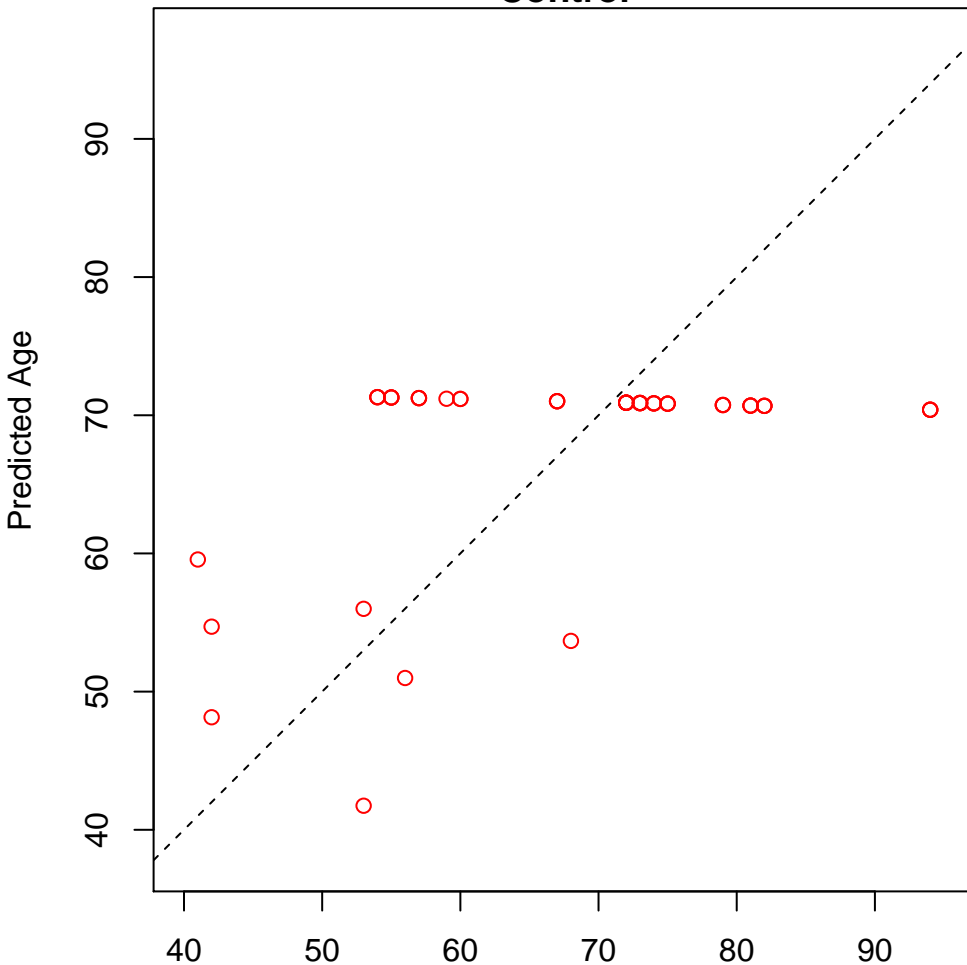
Test



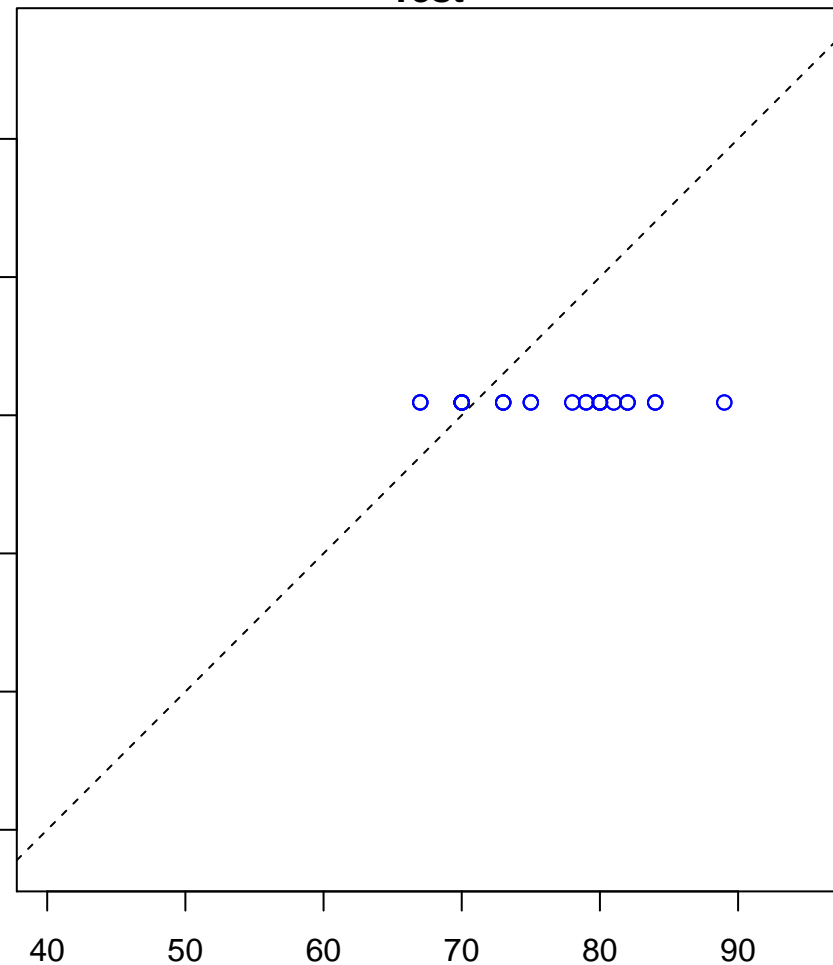
Actual Age

actin cytoskeleton reorganization (Score: 0.792131)

Control



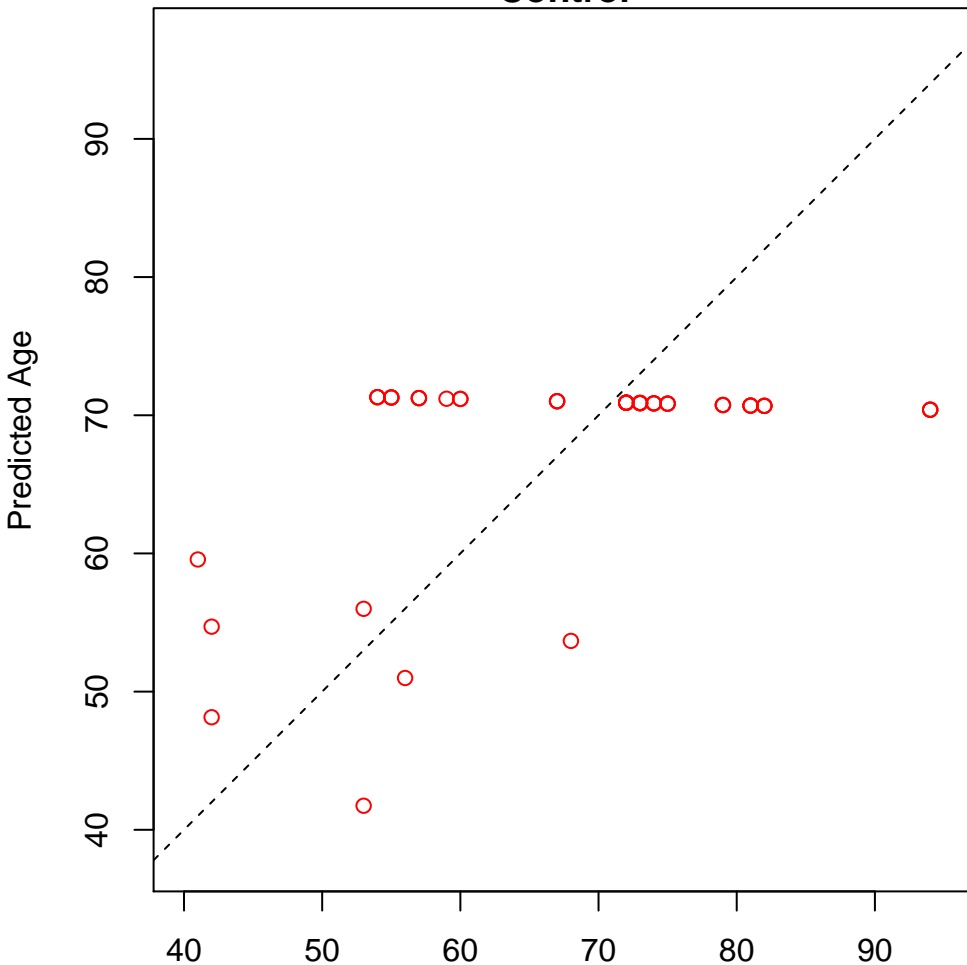
Test



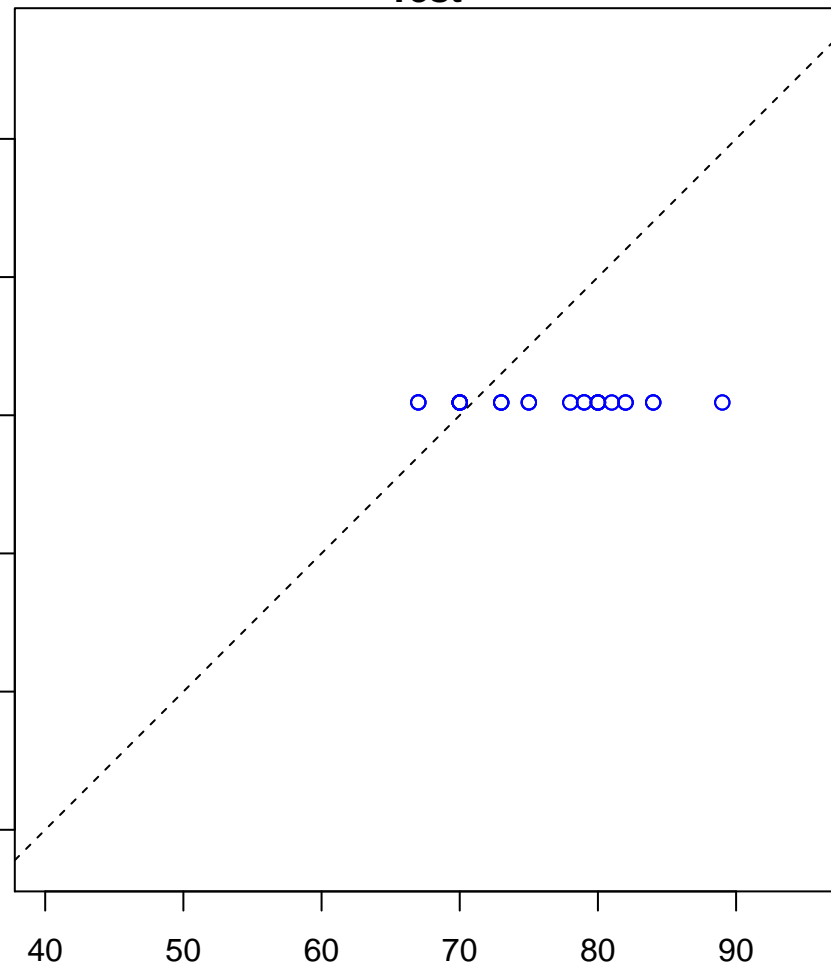
Actual Age

plasma membrane invagination (Score: 0.792131)

Control



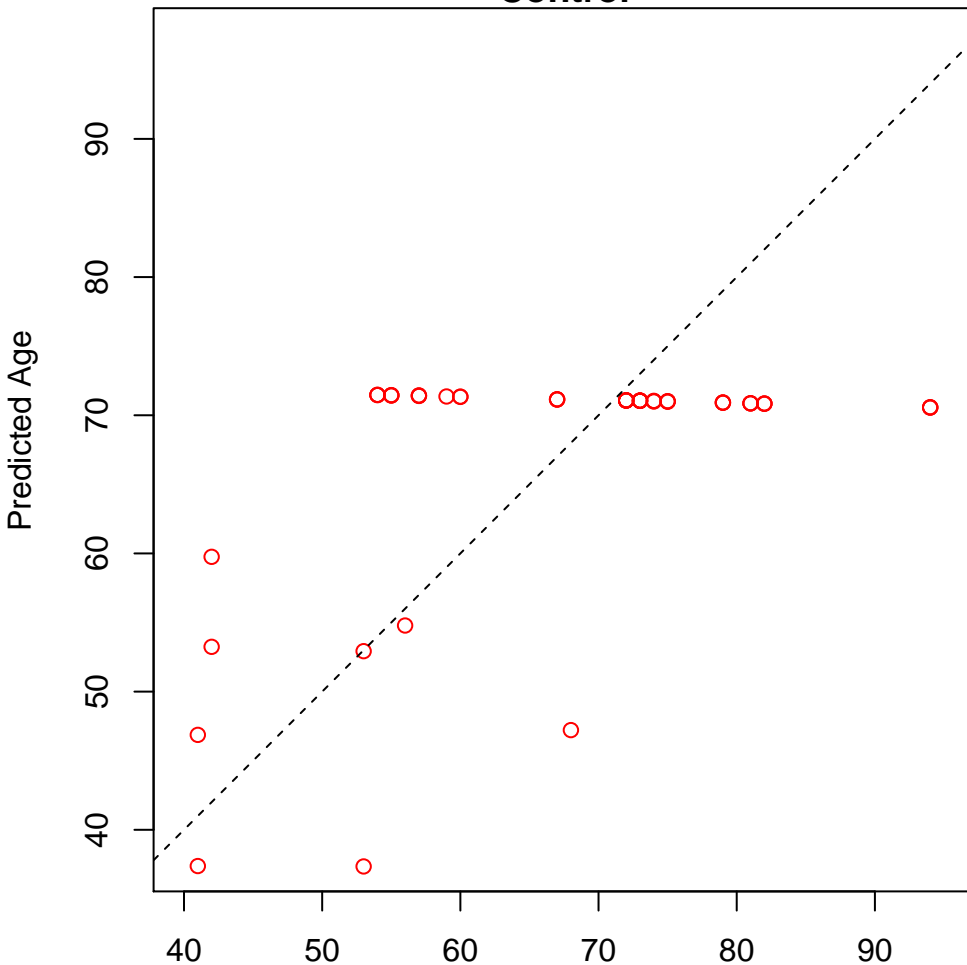
Test



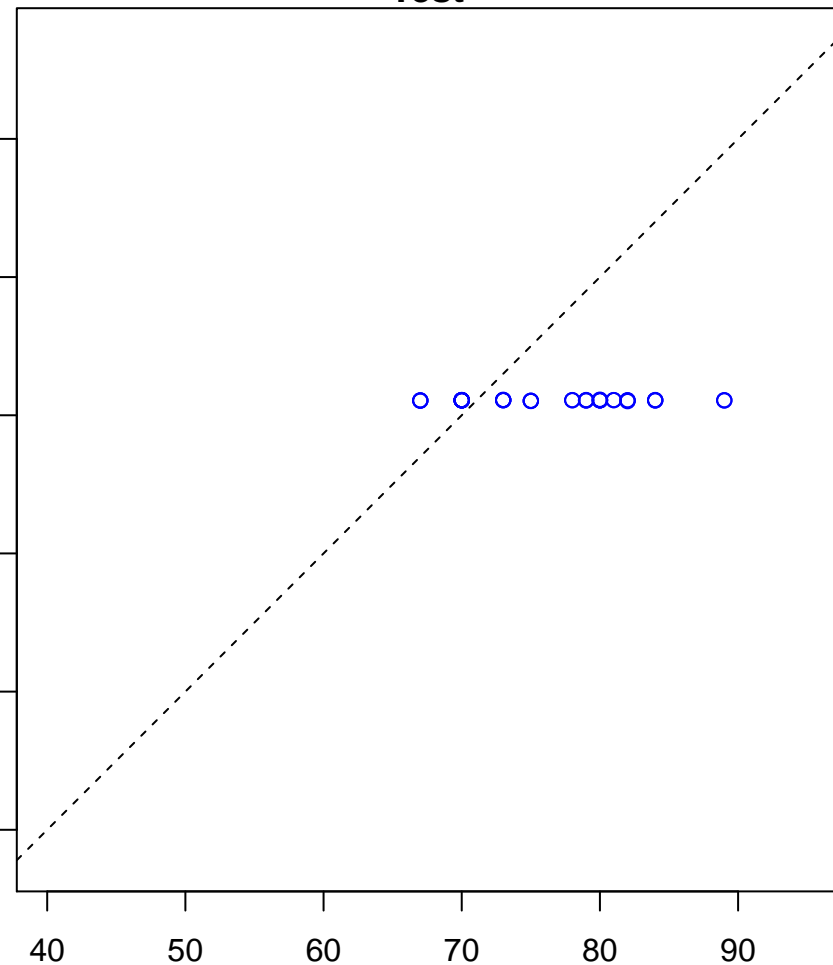
Actual Age

response to acid chemical (Score: 0.792066)

Control



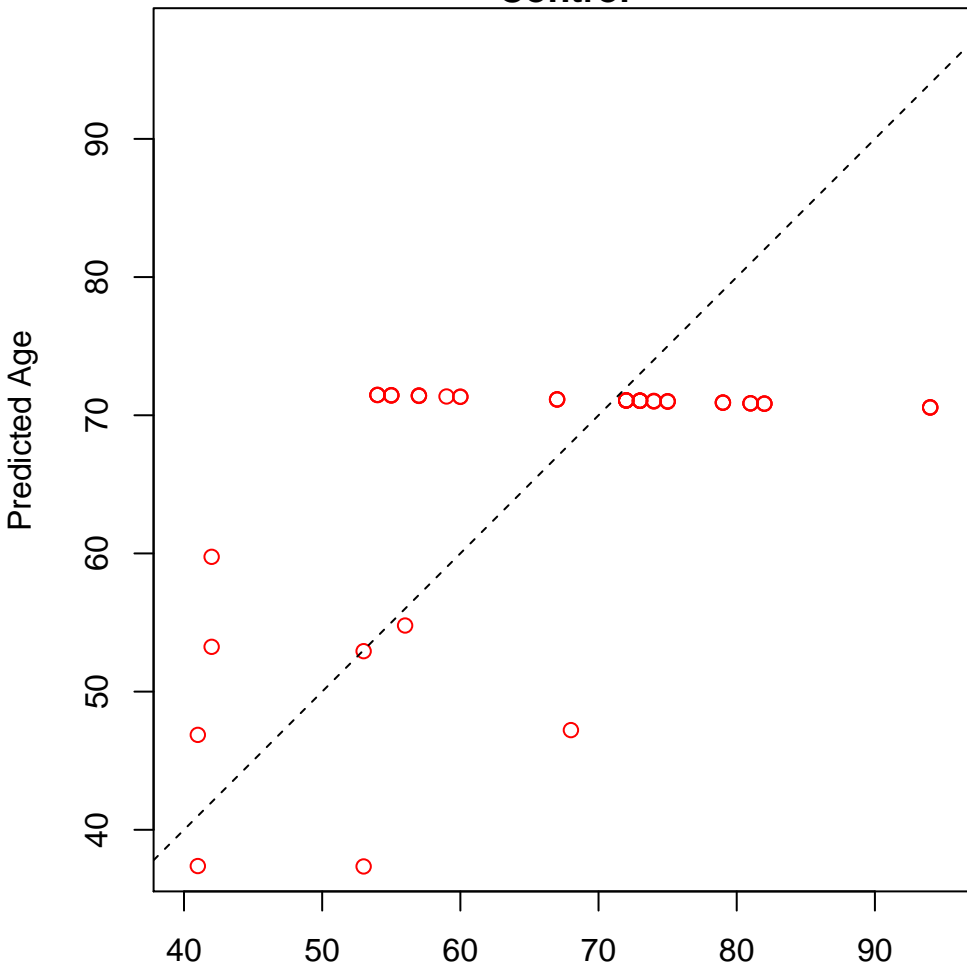
Test



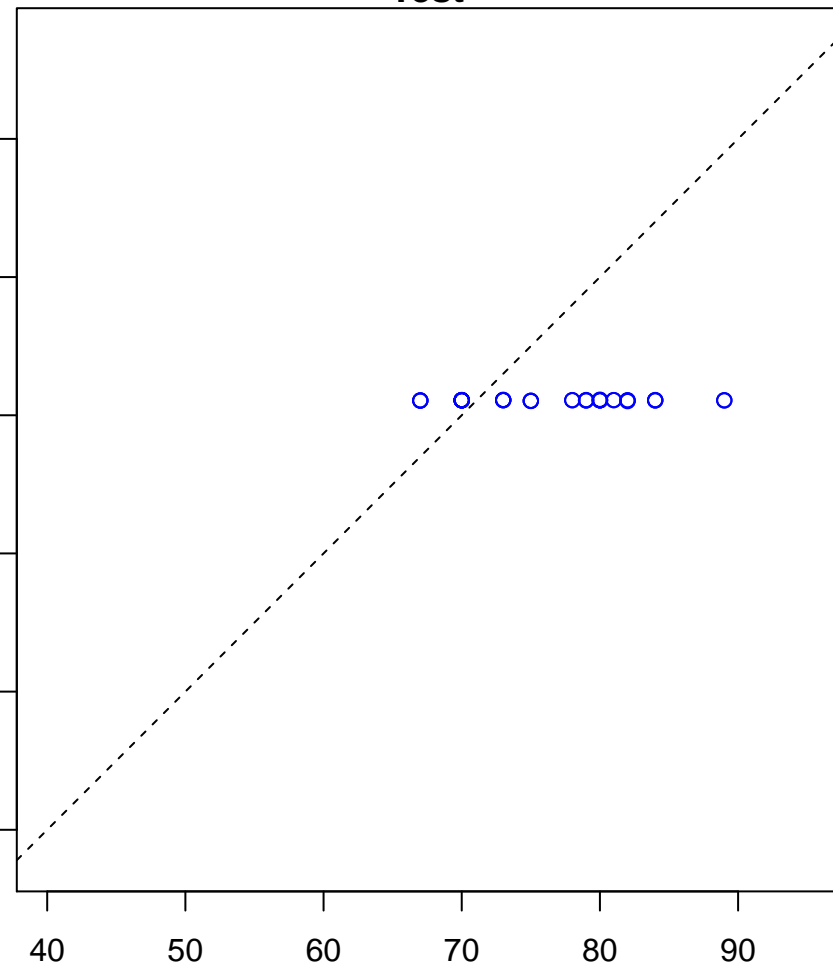
Actual Age

cellular response to acid chemical (Score: 0.792066)

Control



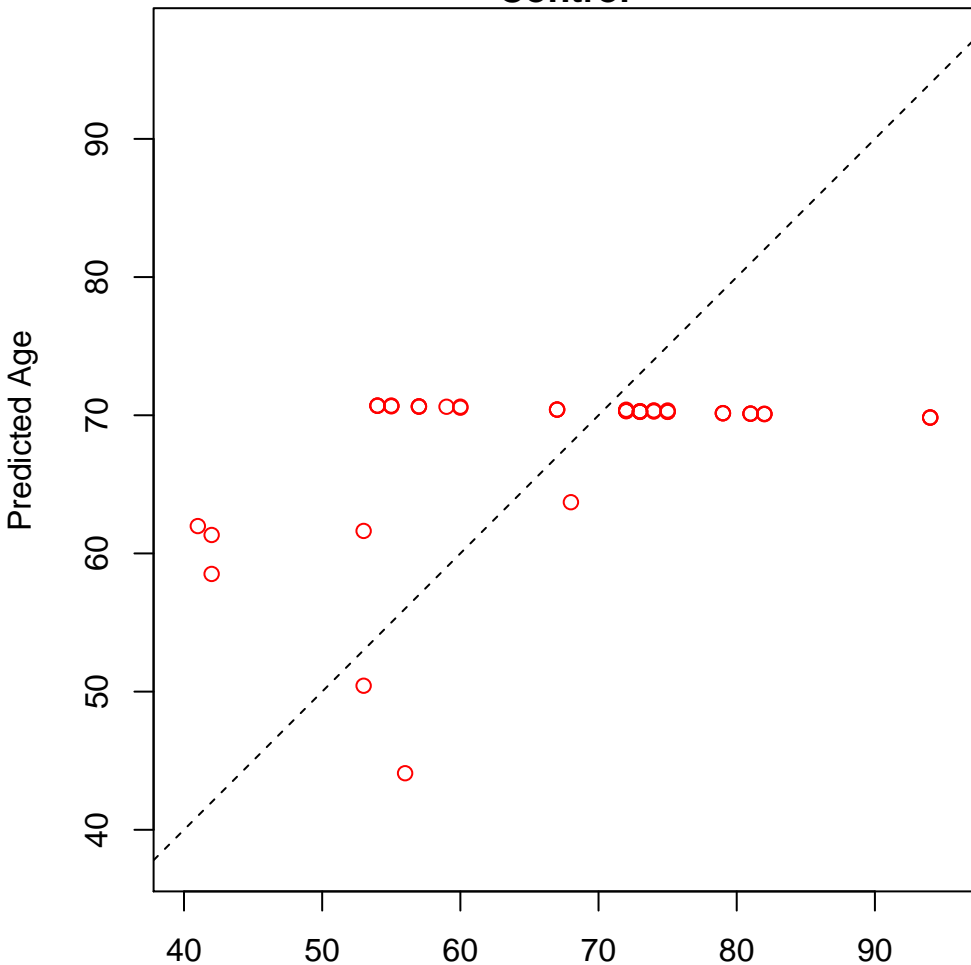
Test



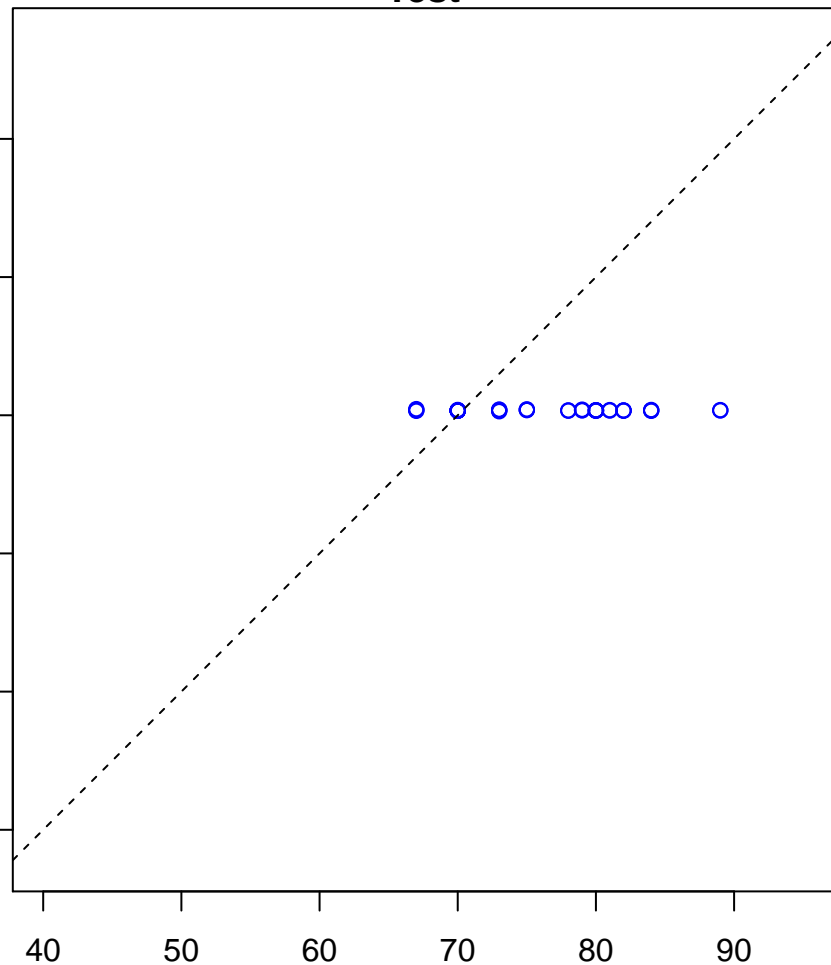
Actual Age

regulation of epithelial cell differentiation (Score: 0.791956)

Control

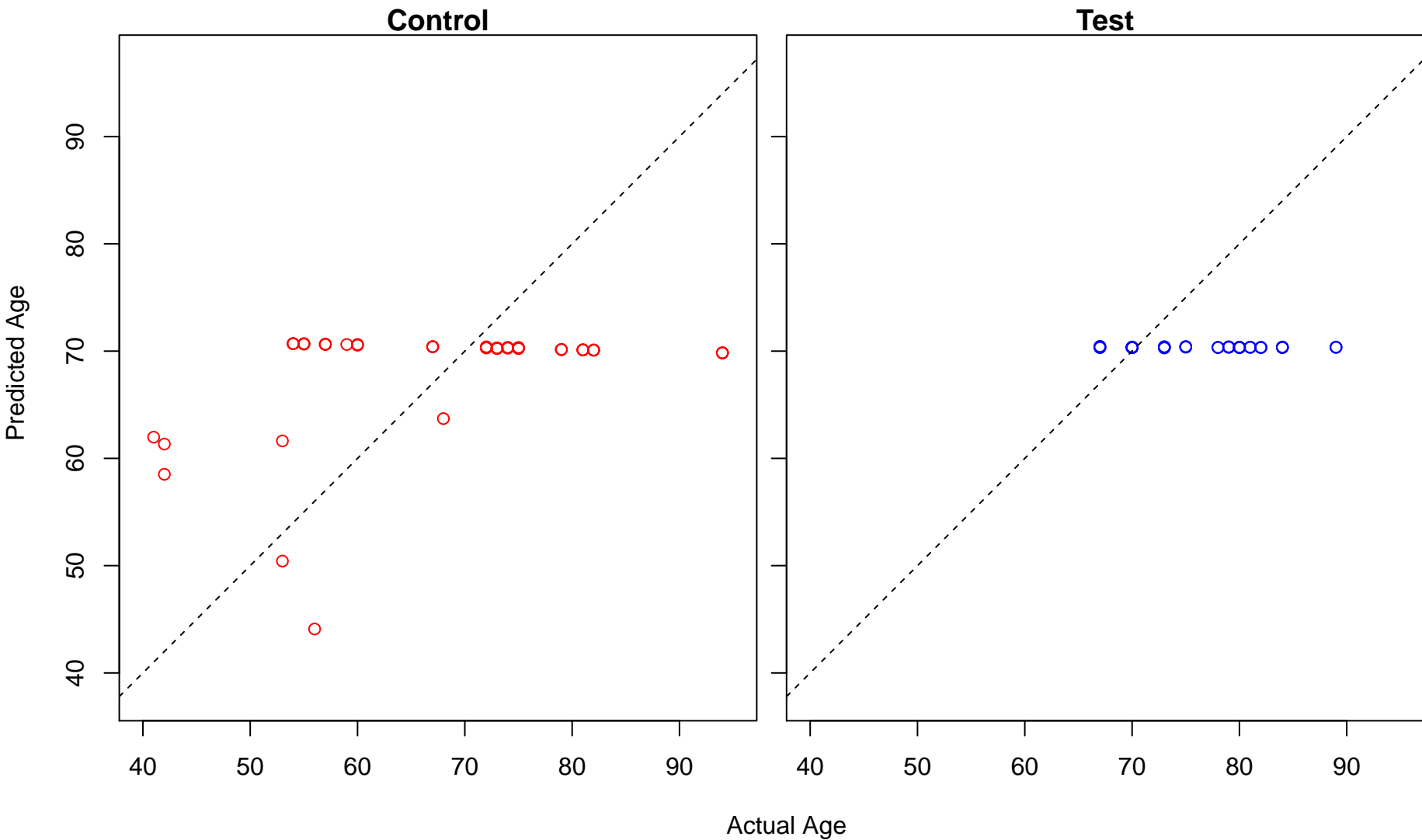


Test



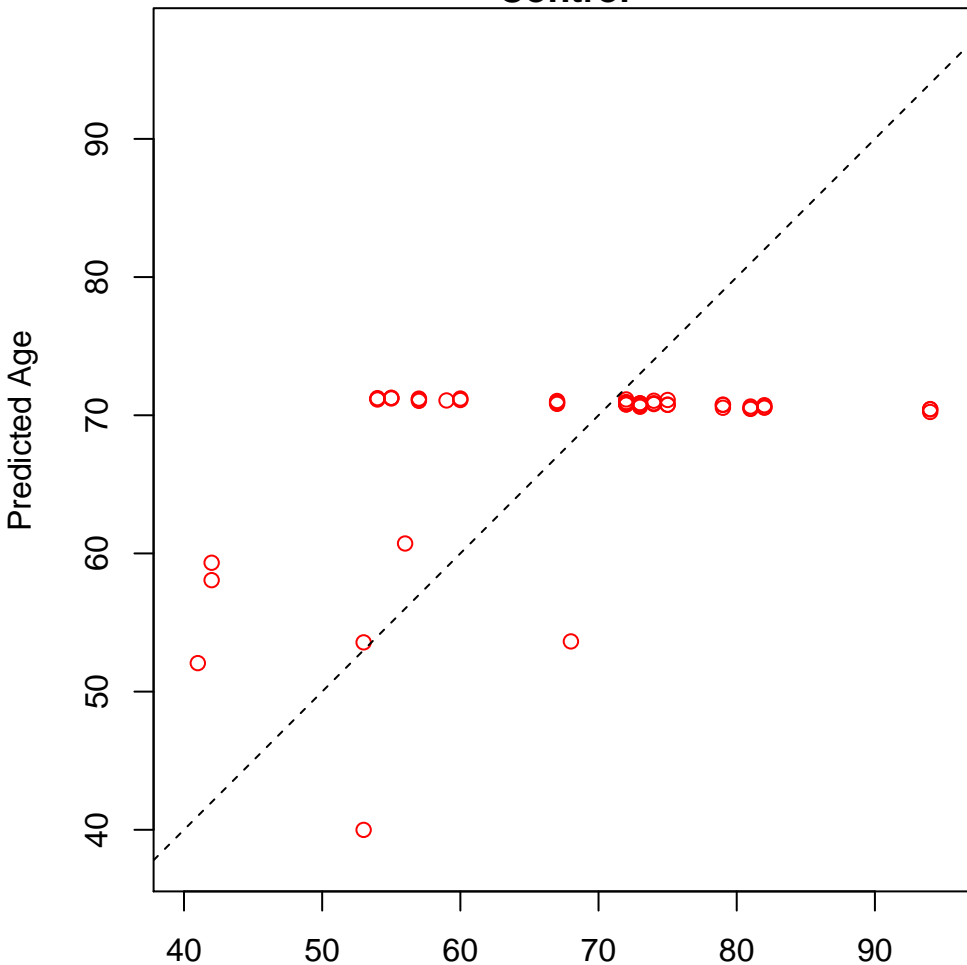
Actual Age

positive regulation of epithelial cell differentiation (Score: 0.791956)

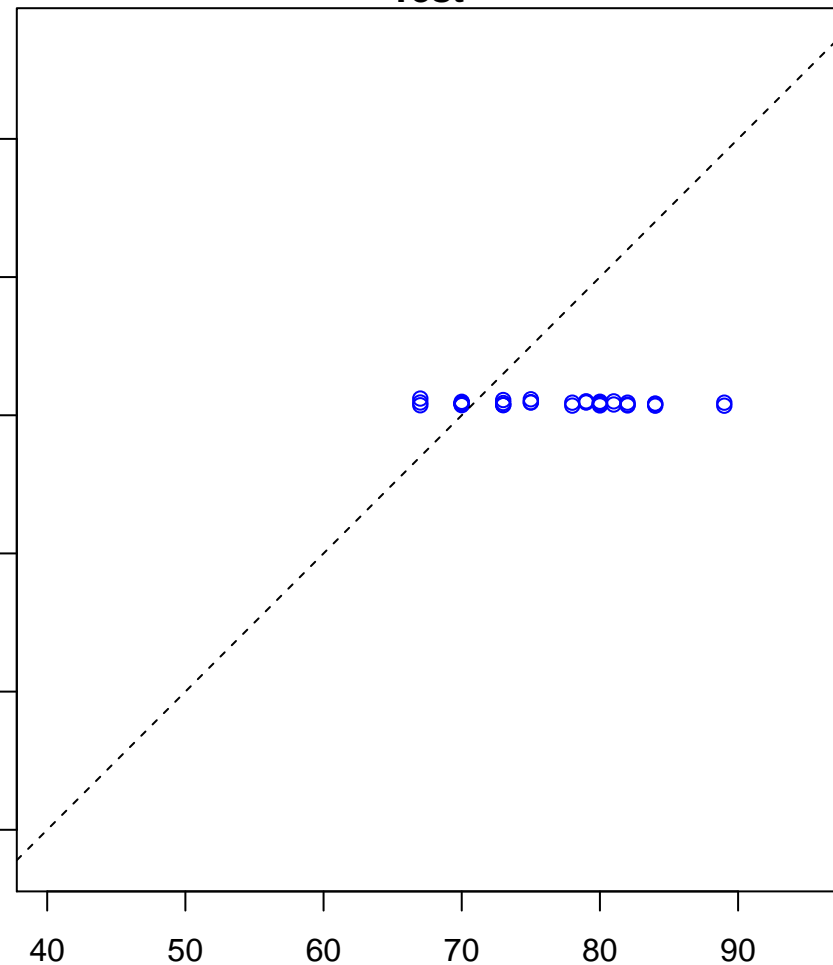


urogenital system development (Score: 0.791954)

Control



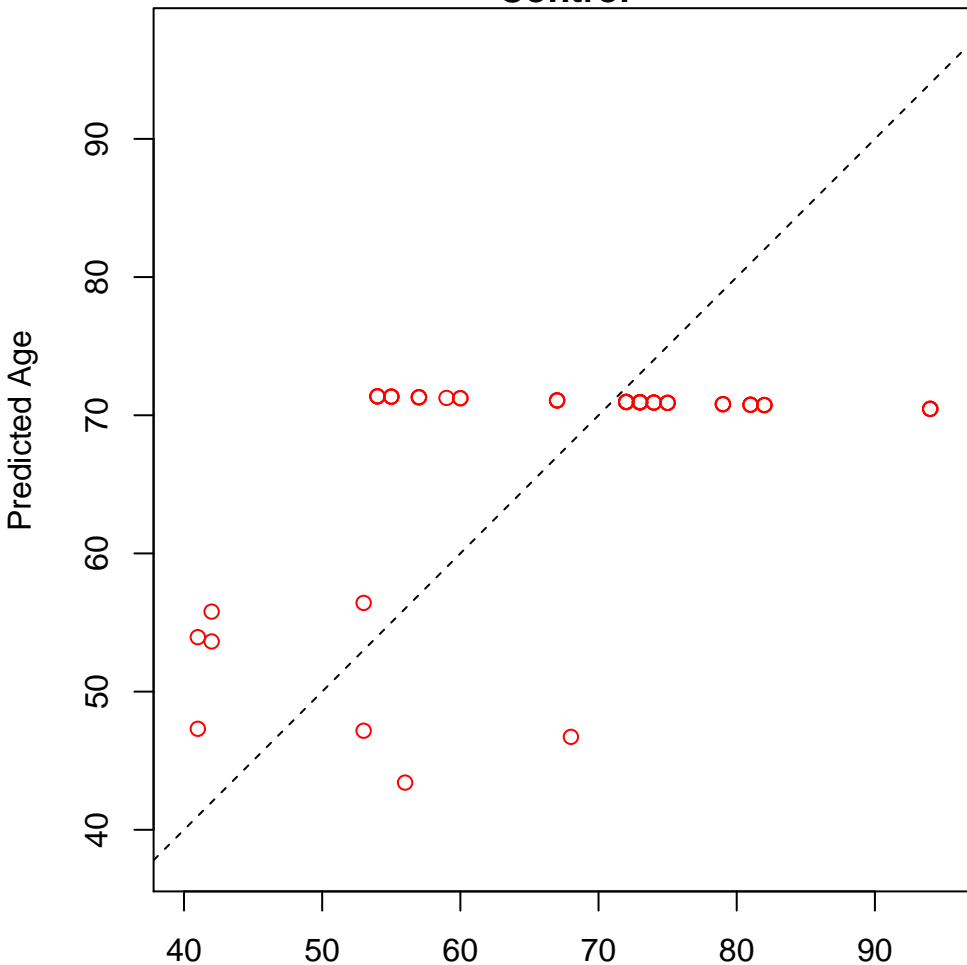
Test



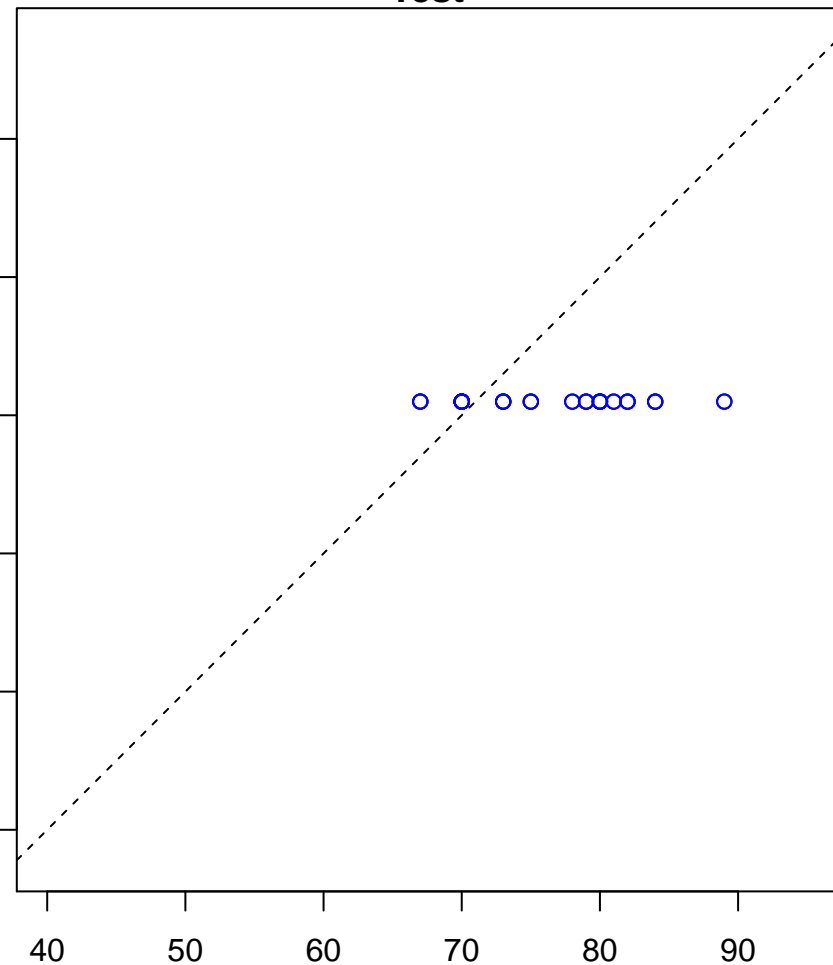
Actual Age

regulation of mononuclear cell proliferation (Score: 0.791873)

Control



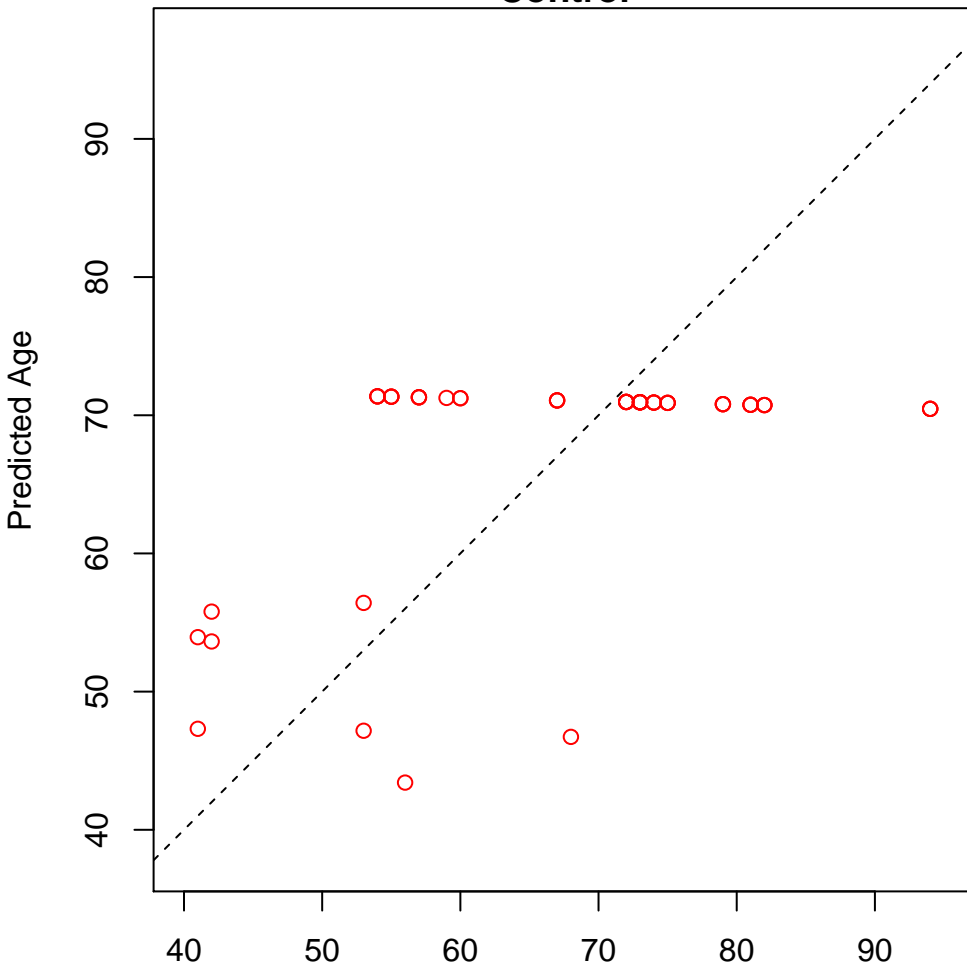
Test



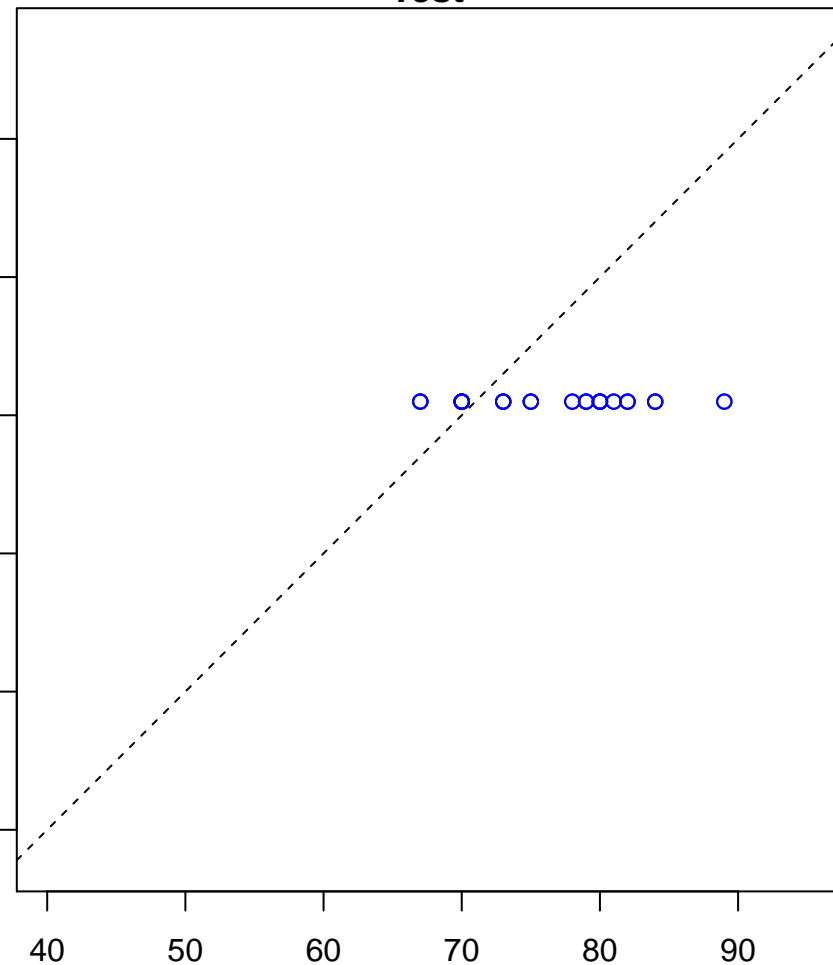
Actual Age

regulation of lymphocyte proliferation (Score: 0.791873)

Control



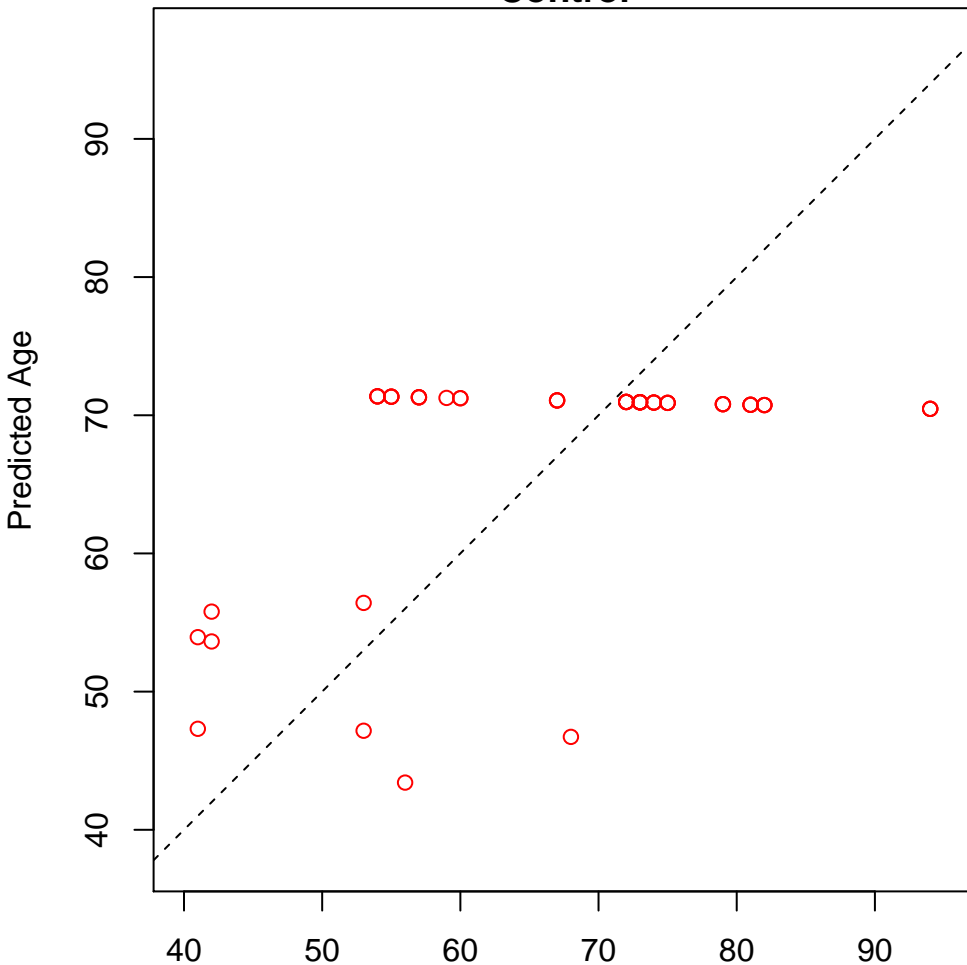
Test



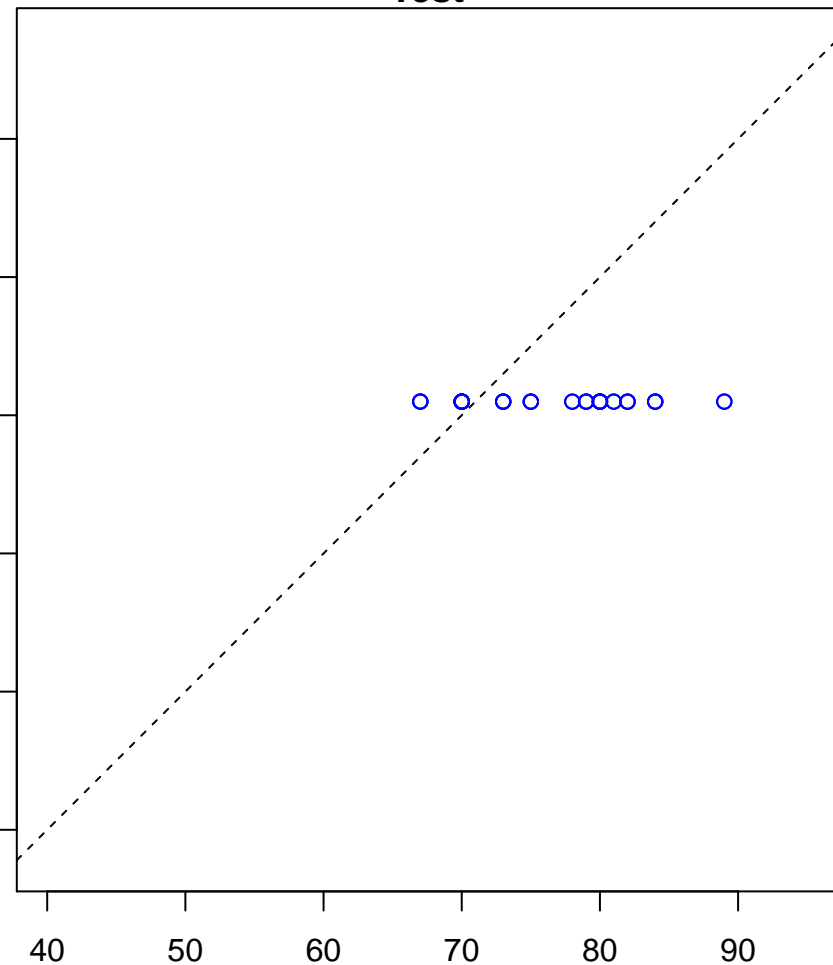
Actual Age

regulation of leukocyte proliferation (Score: 0.791873)

Control

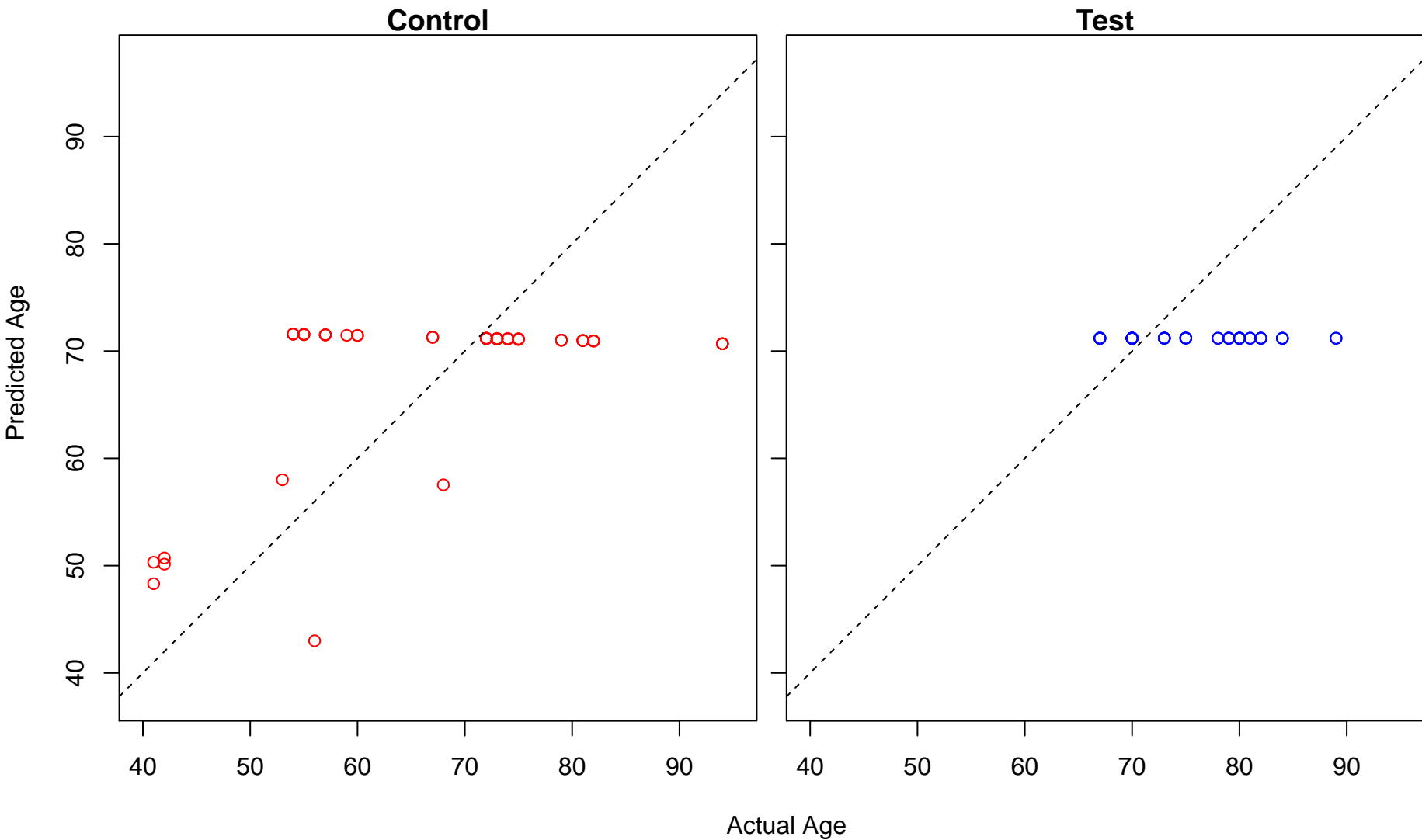


Test

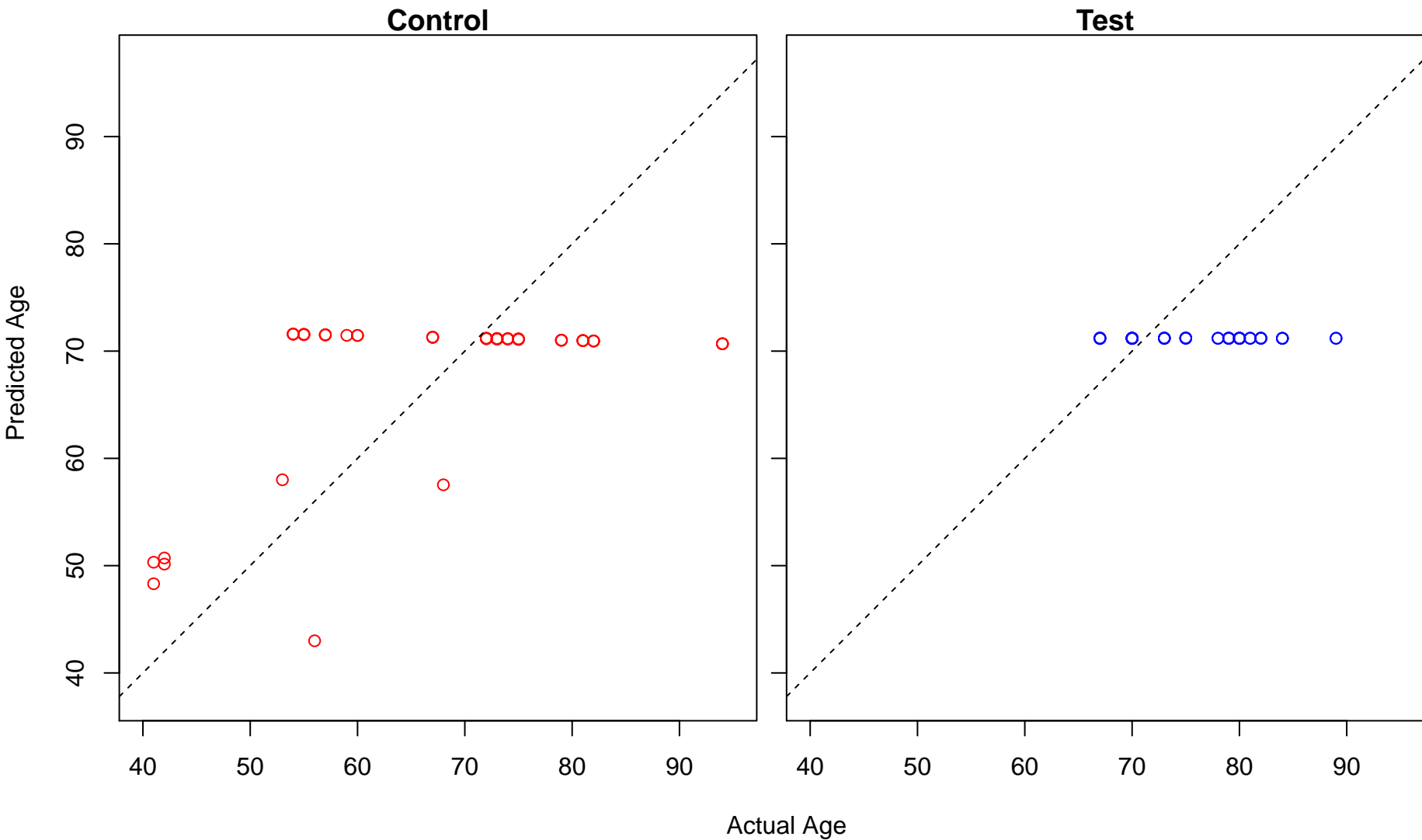


Actual Age

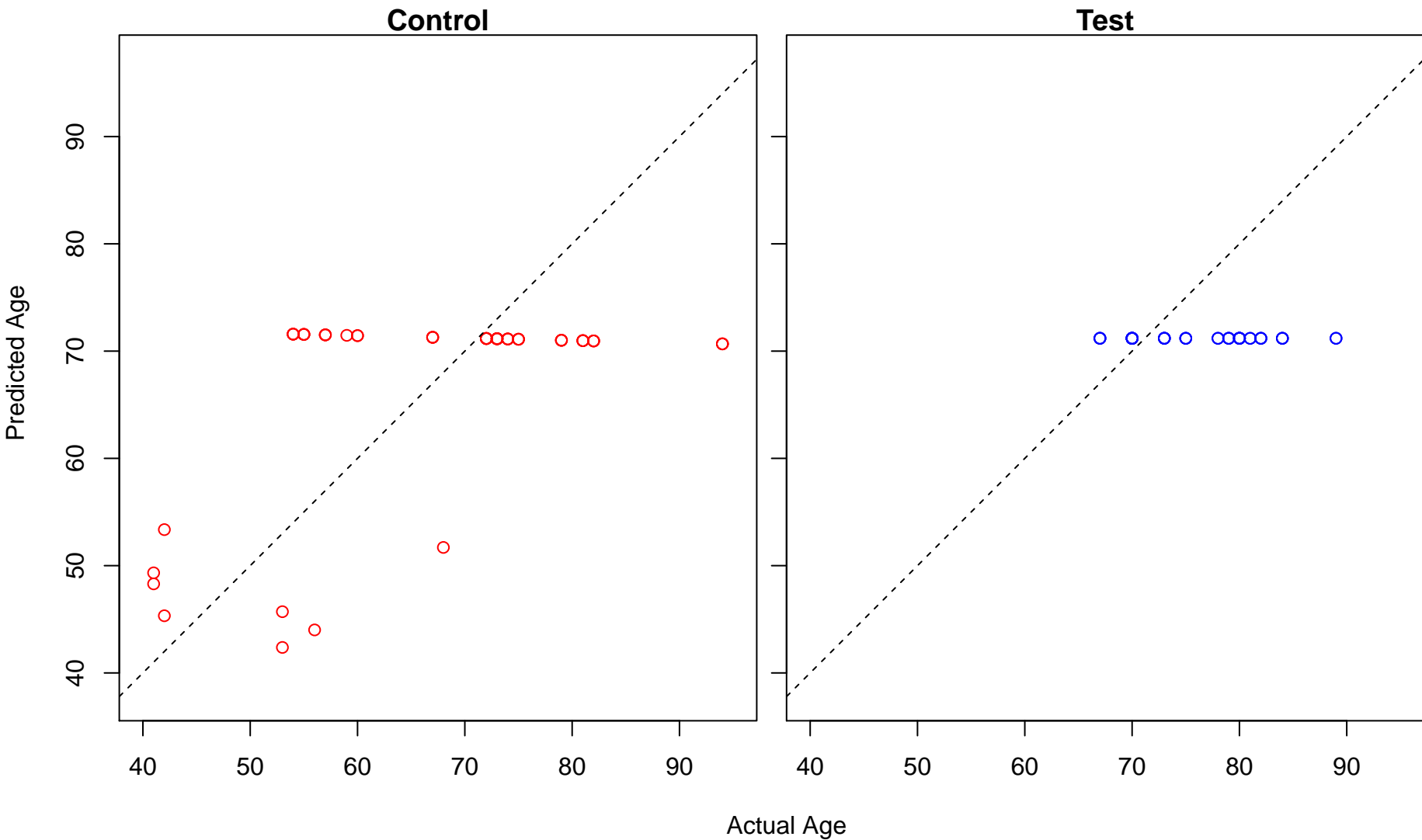
regulation of peptidyl-serine phosphorylation (Score: 0.791853)



positive regulation of peptidyl-serine phosphorylation (Score: 0.791853)

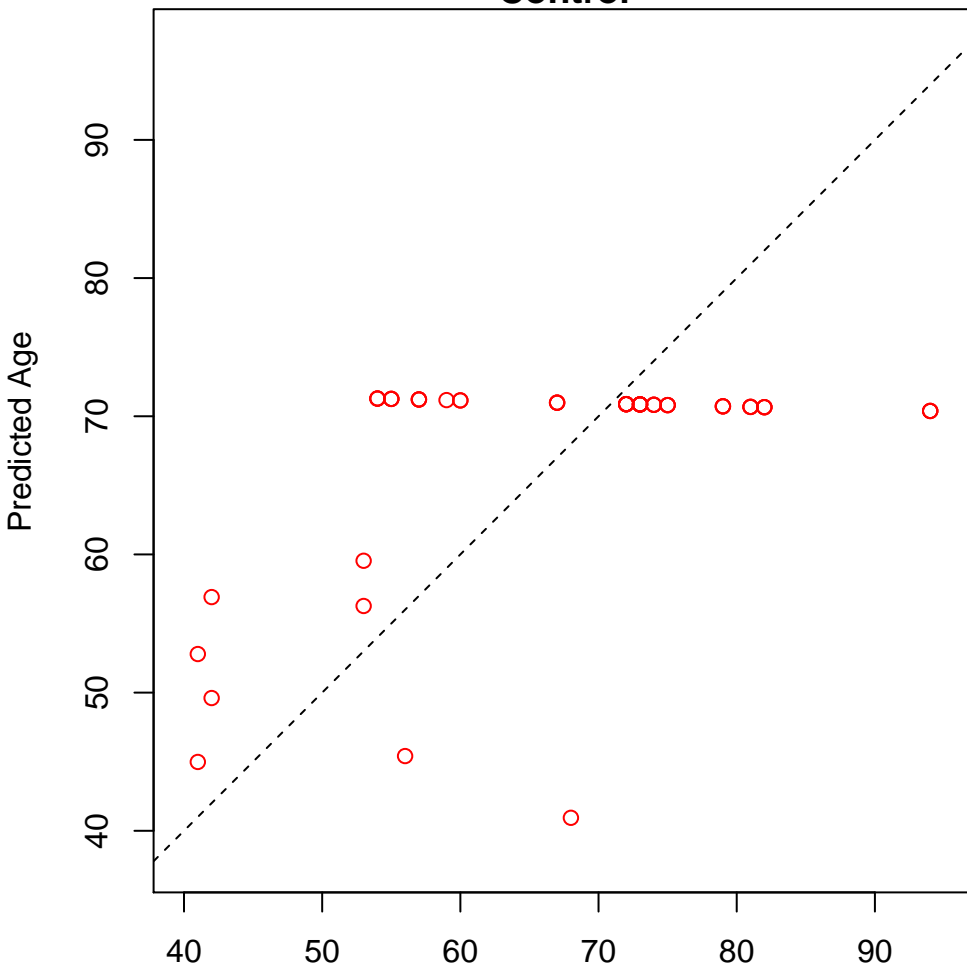


regulation of cellular process (Score: 0.791840)

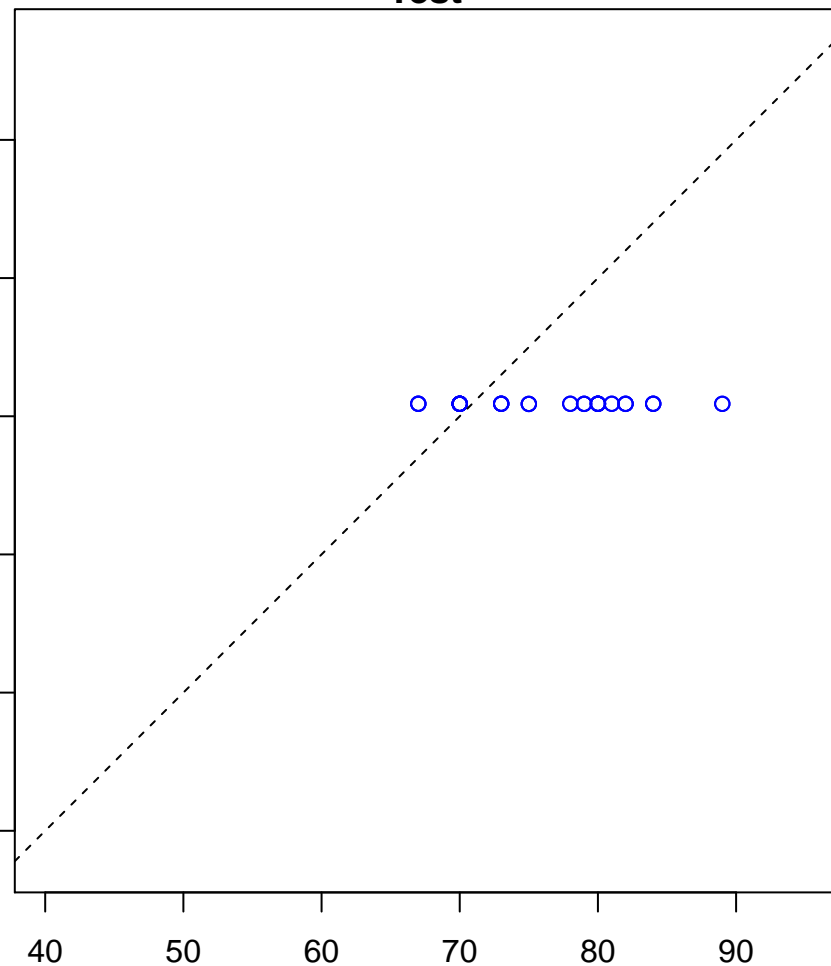


chaperone-mediated protein folding (Score: 0.791766)

Control

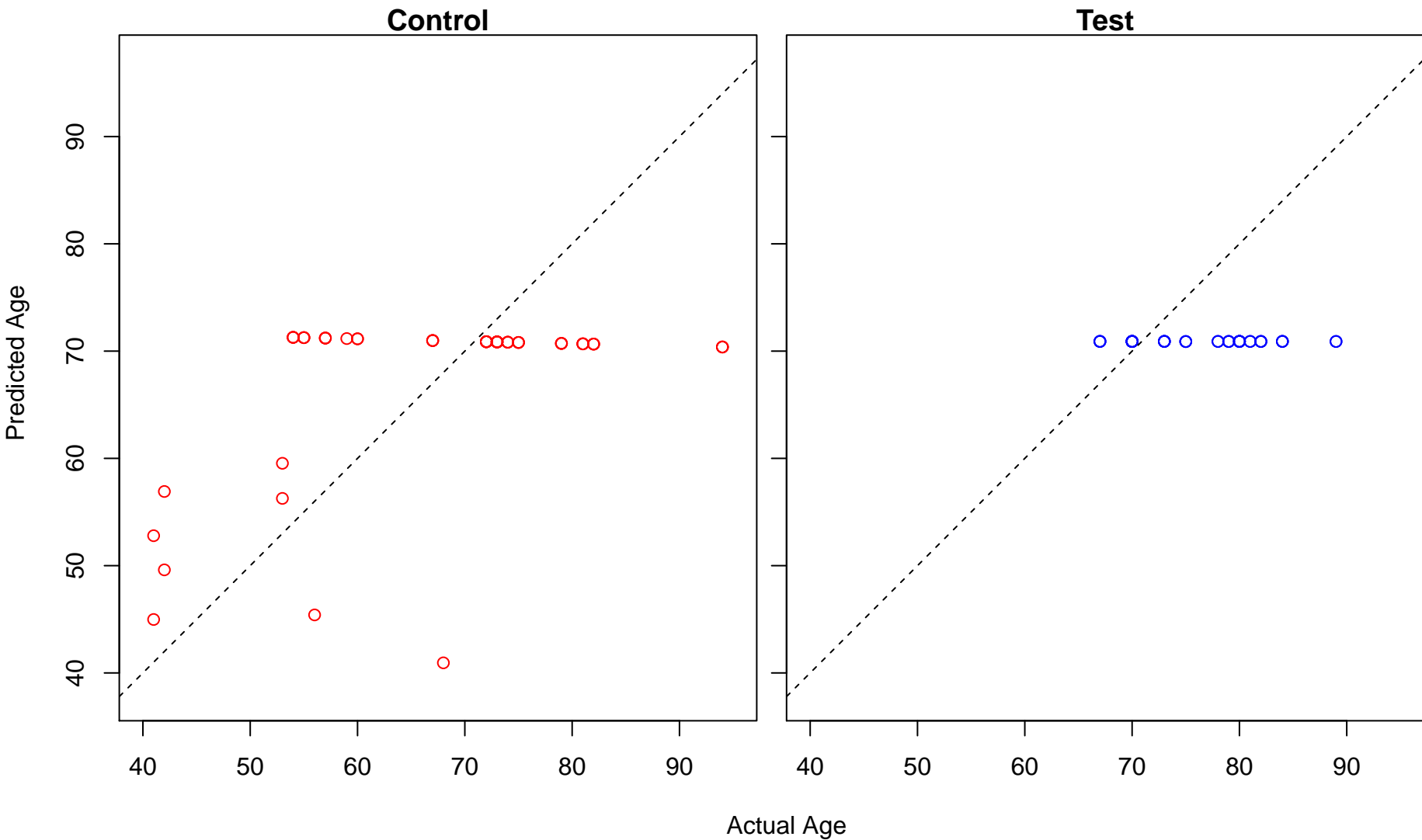


Test



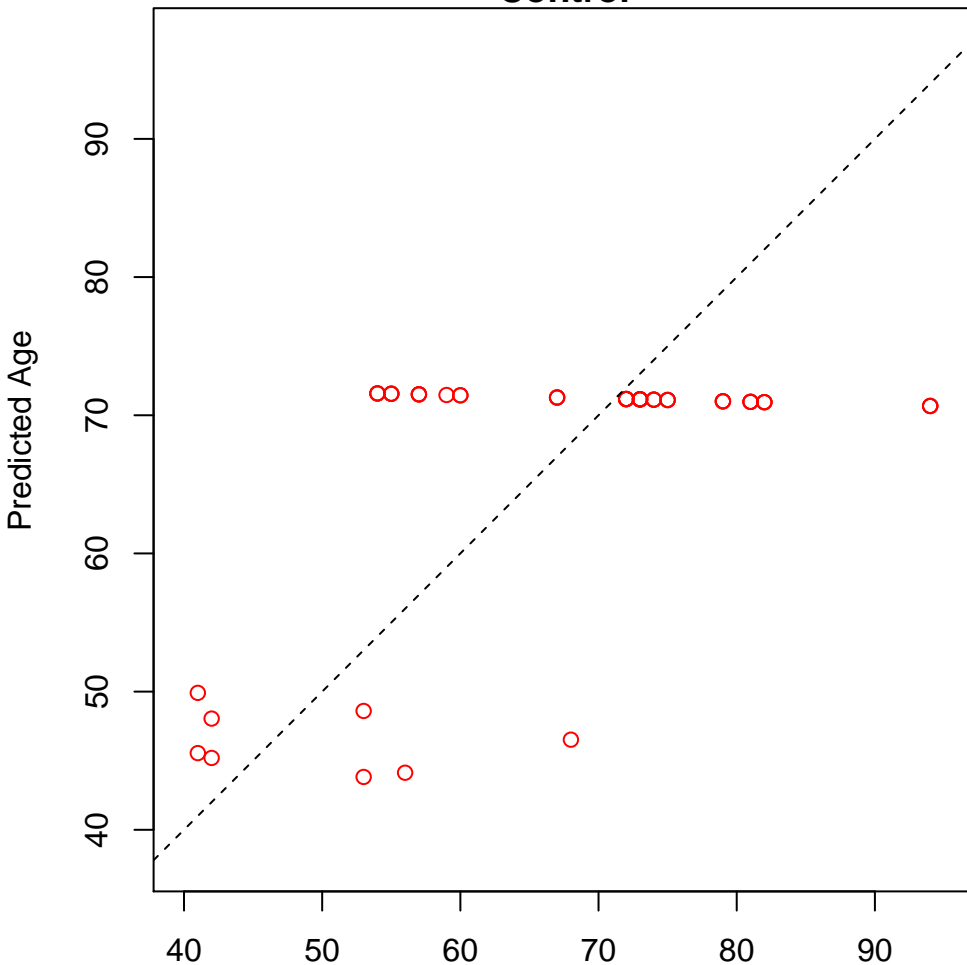
Actual Age

chaperone cofactor-dependent protein refolding (Score: 0.791766)

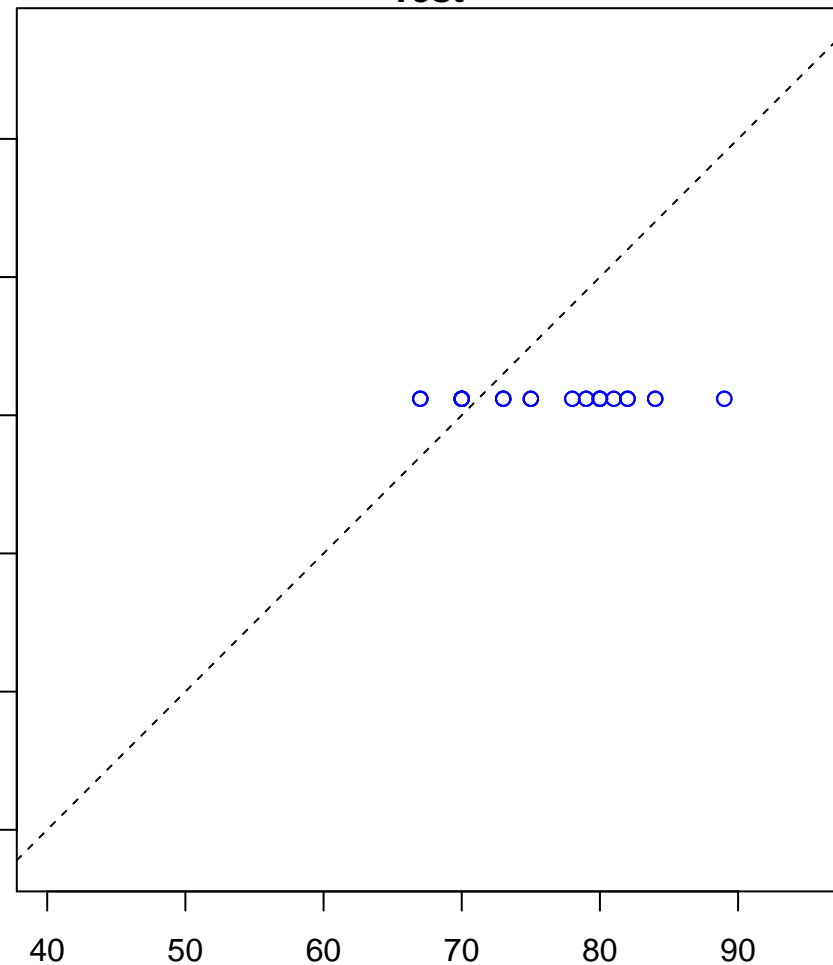


regulation of biosynthetic process (Score: 0.791737)

Control

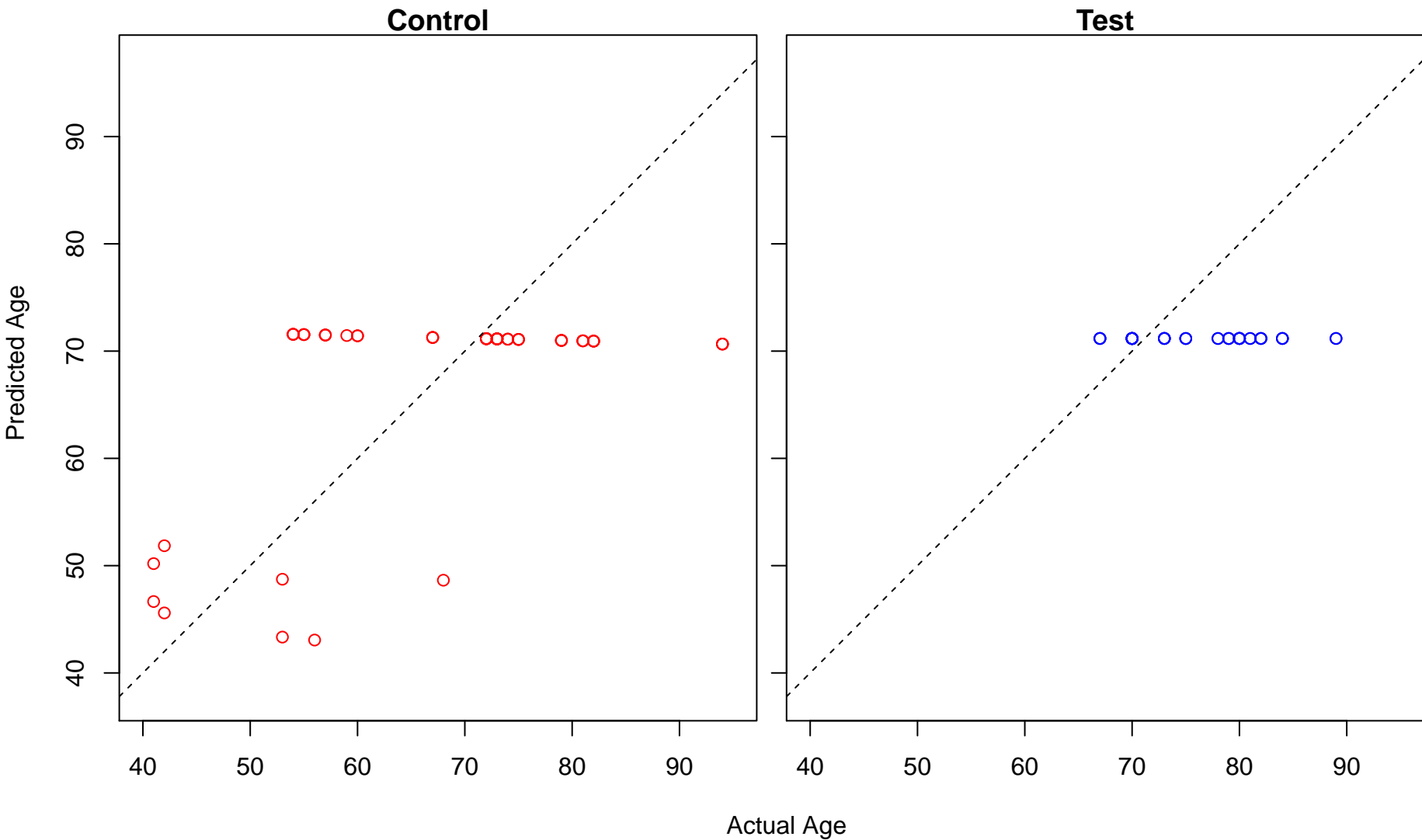


Test



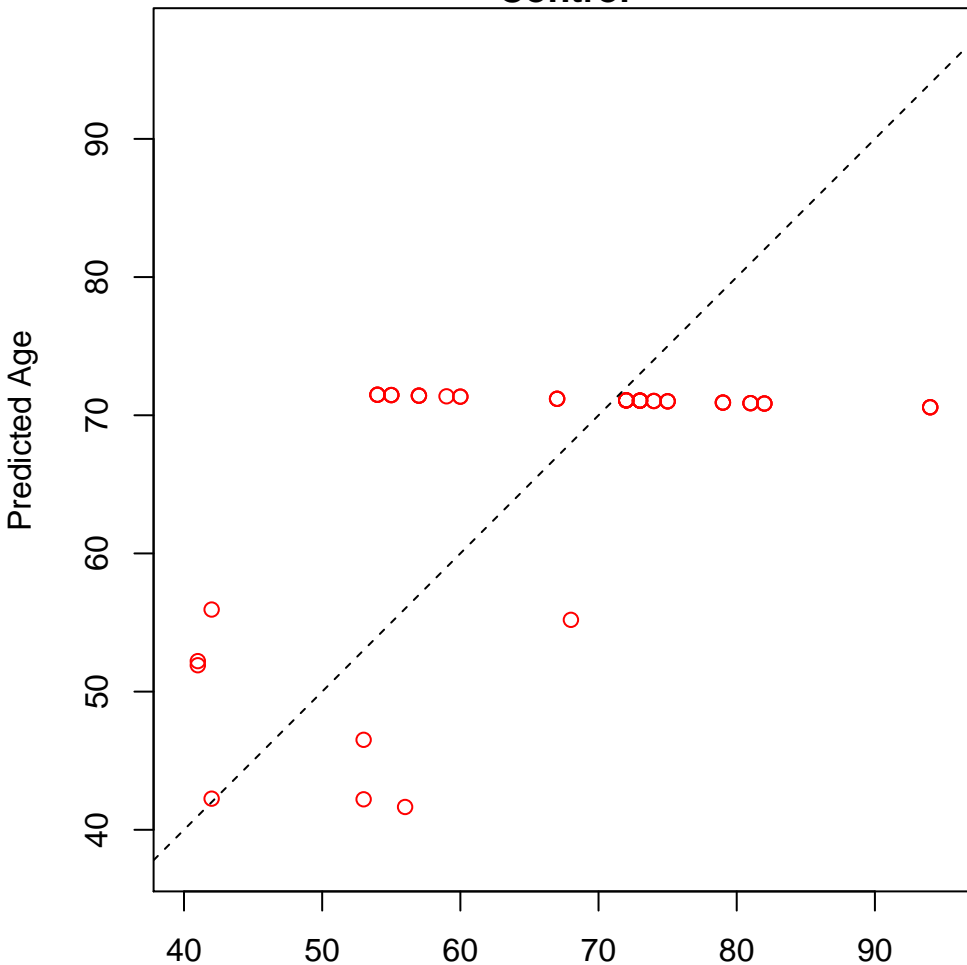
Actual Age

cellular nitrogen compound metabolic process (Score: 0.791403)

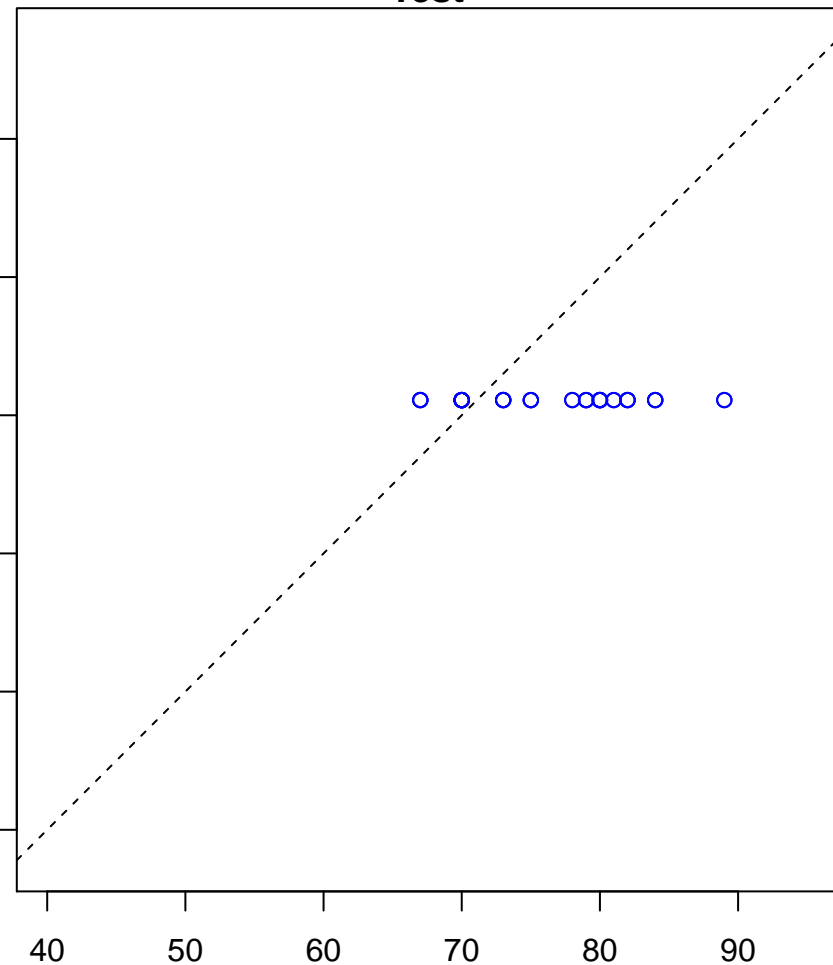


negative regulation of phosphorylation (Score: 0.791375)

Control

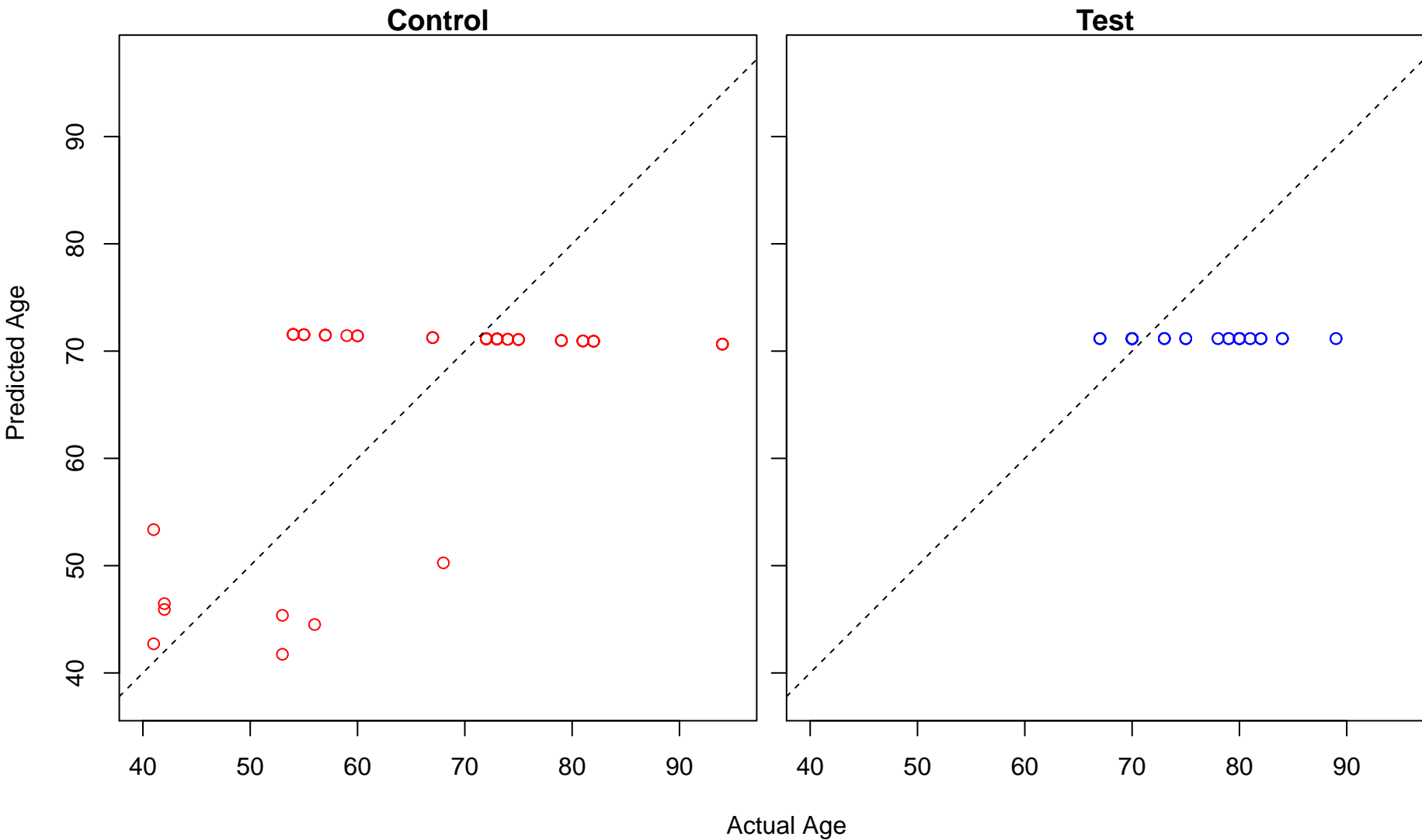


Test



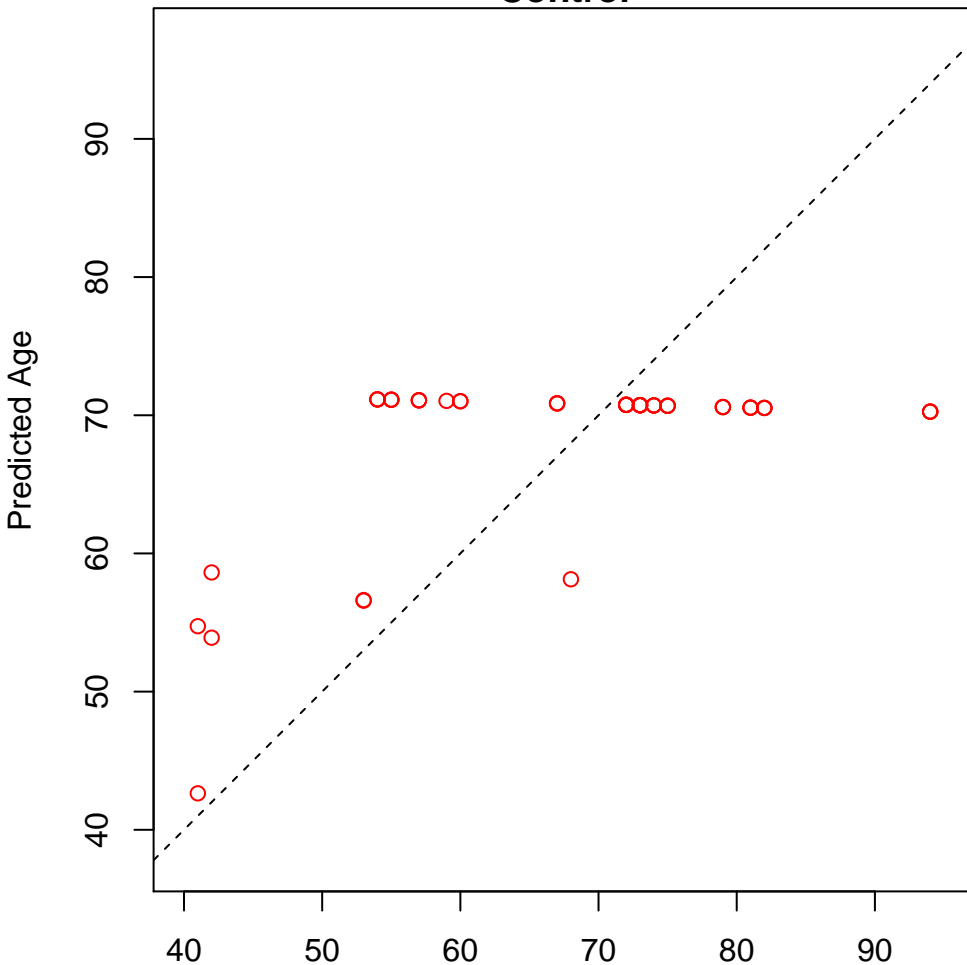
Actual Age

positive regulation of immune system process (Score: 0.791233)

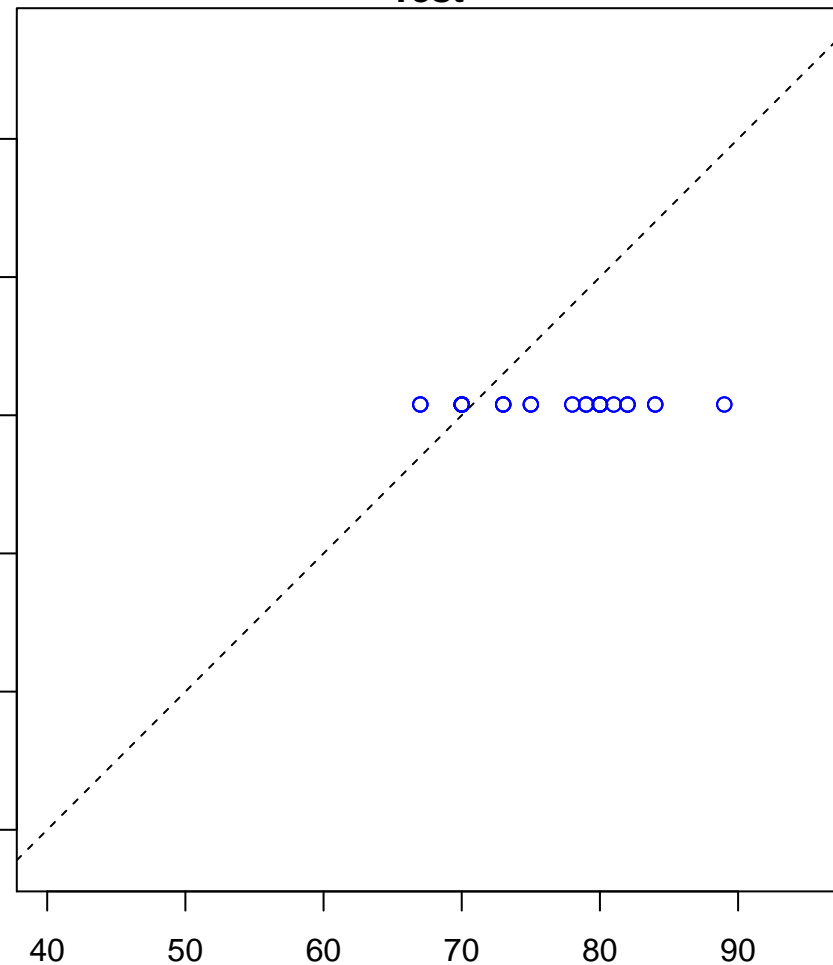


circulatory system development (Score: 0.791227)

Control

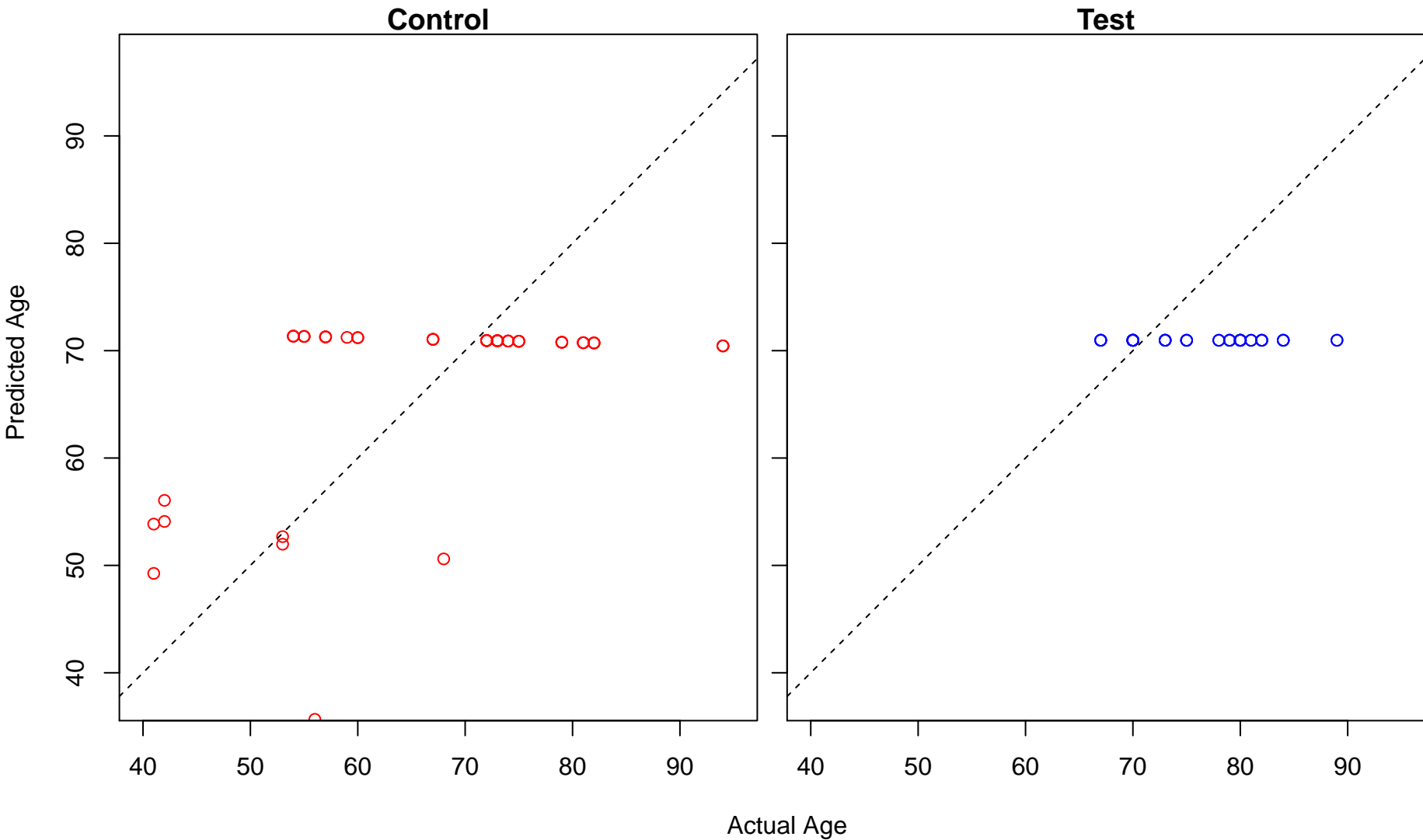


Test

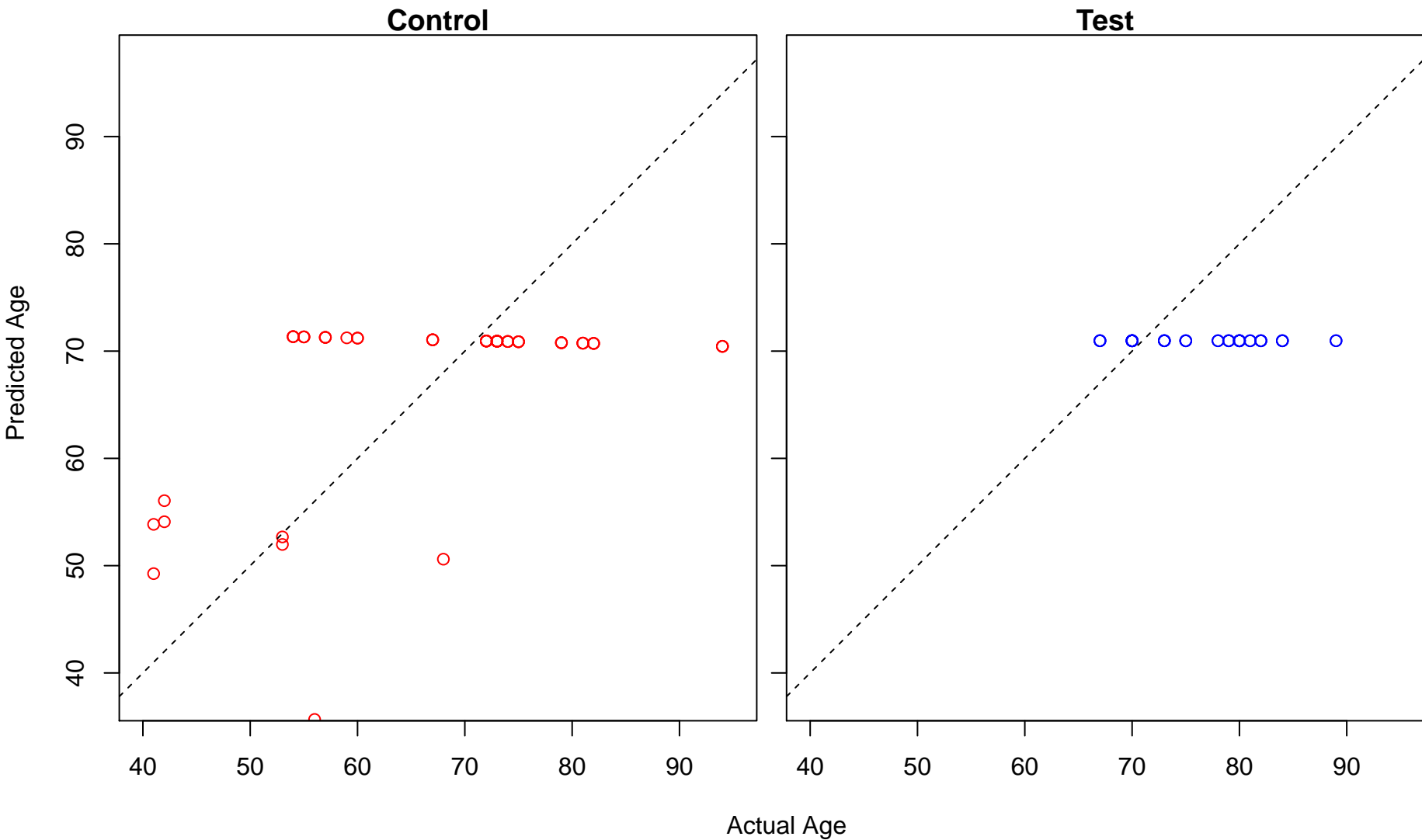


Actual Age

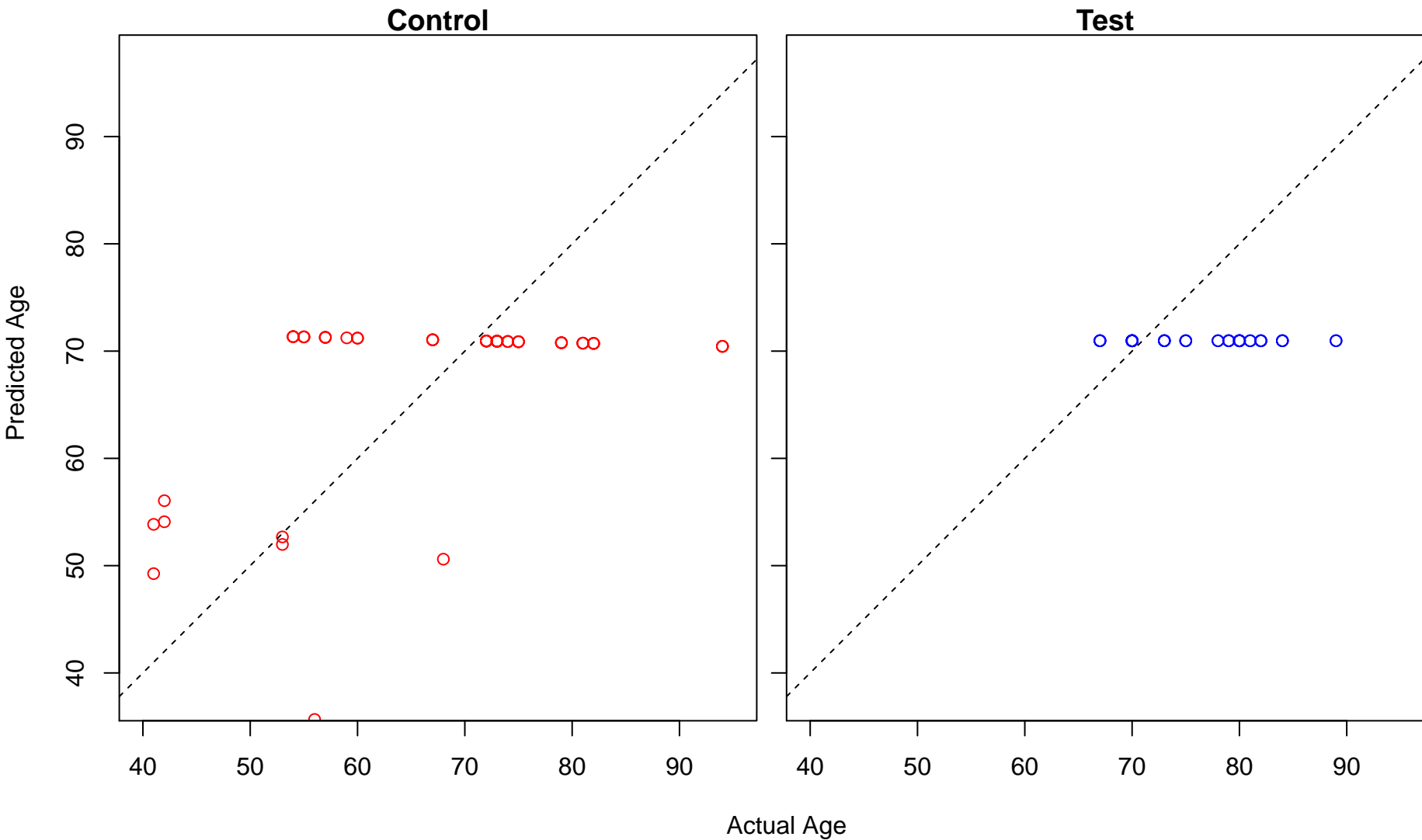
positive regulation of lymphocyte migration (Score: 0.791221)



regulation of T cell migration (Score: 0.791221)

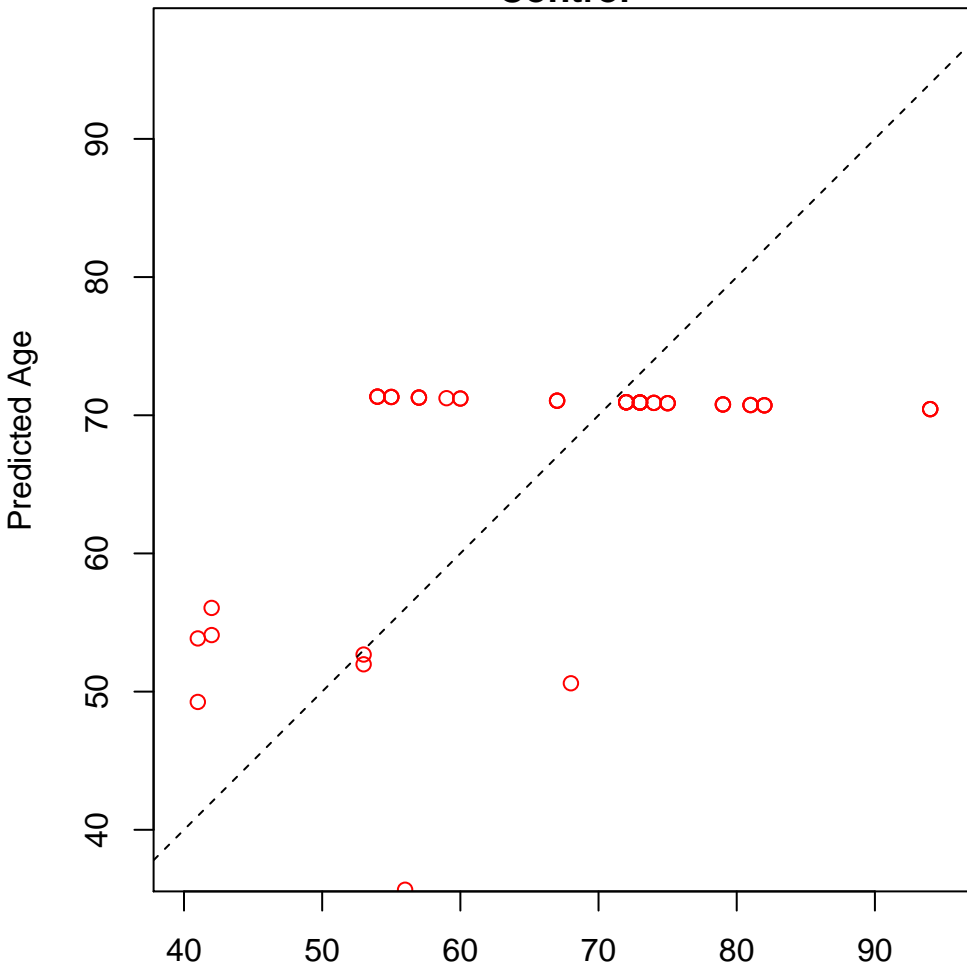


positive regulation of T cell migration (Score: 0.791221)

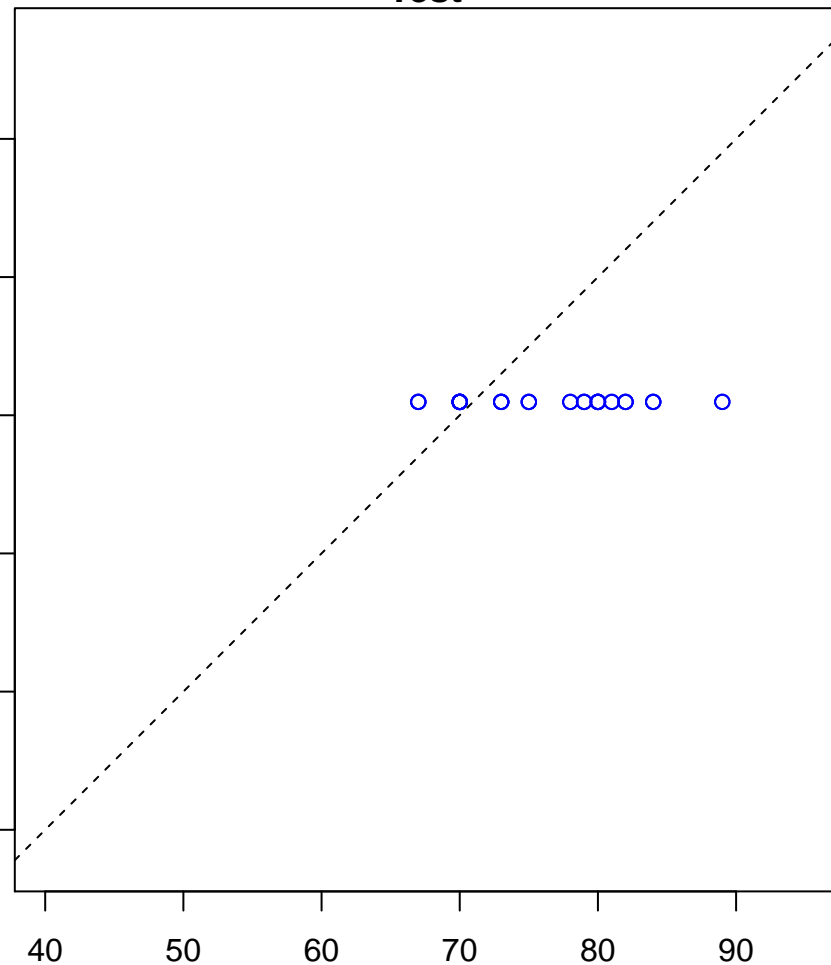


anatomical structure maturation (Score: 0.791221)

Control

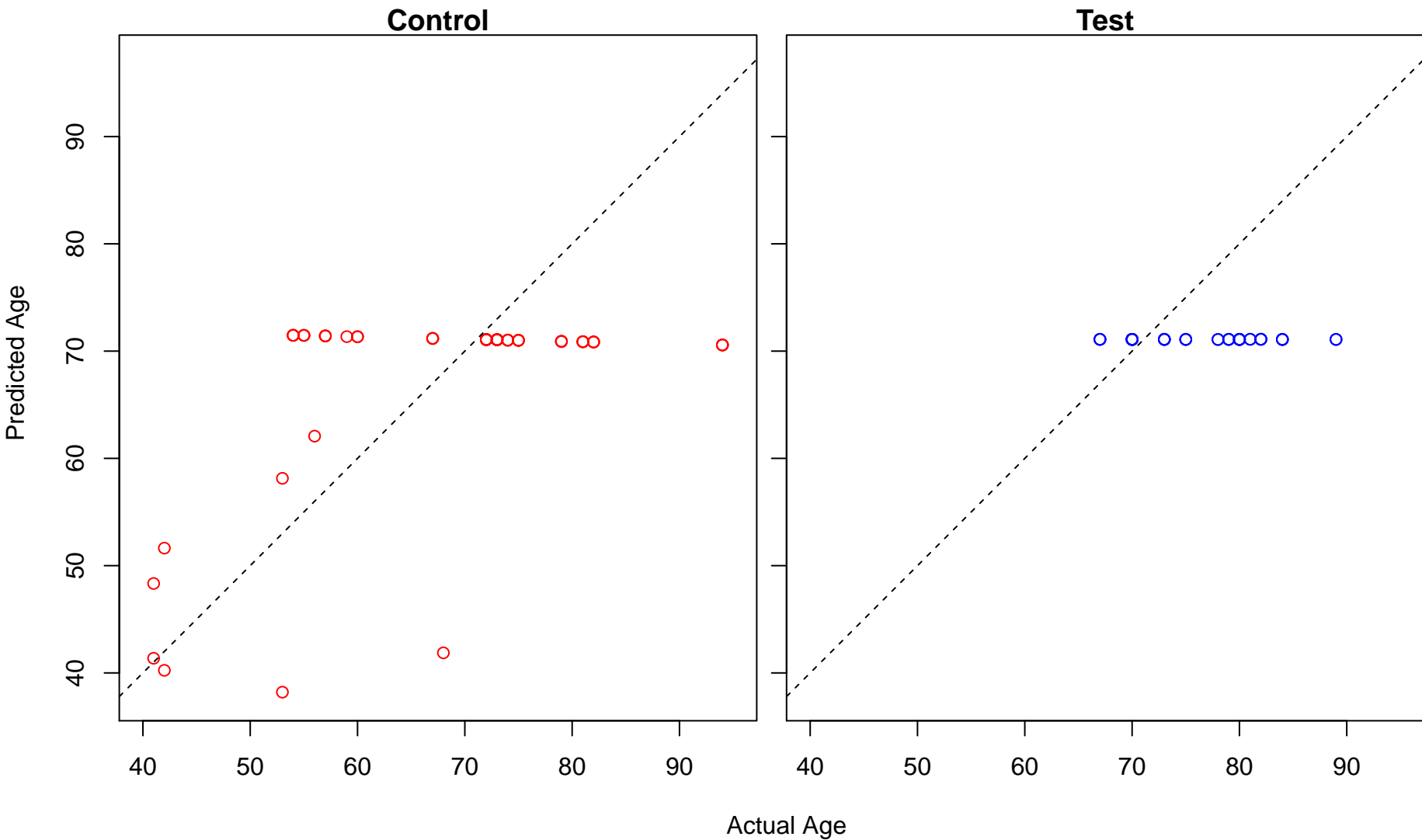


Test

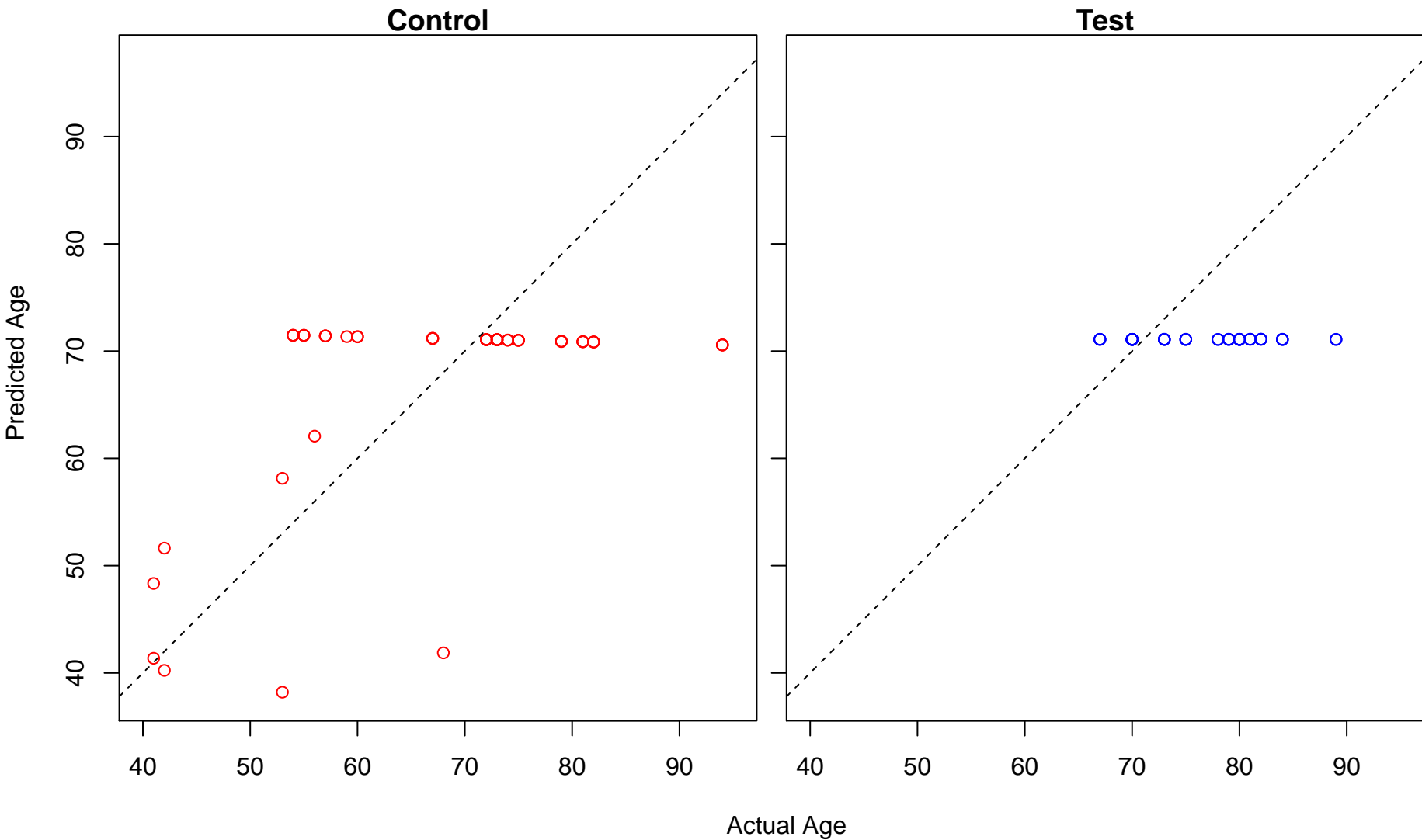


Actual Age

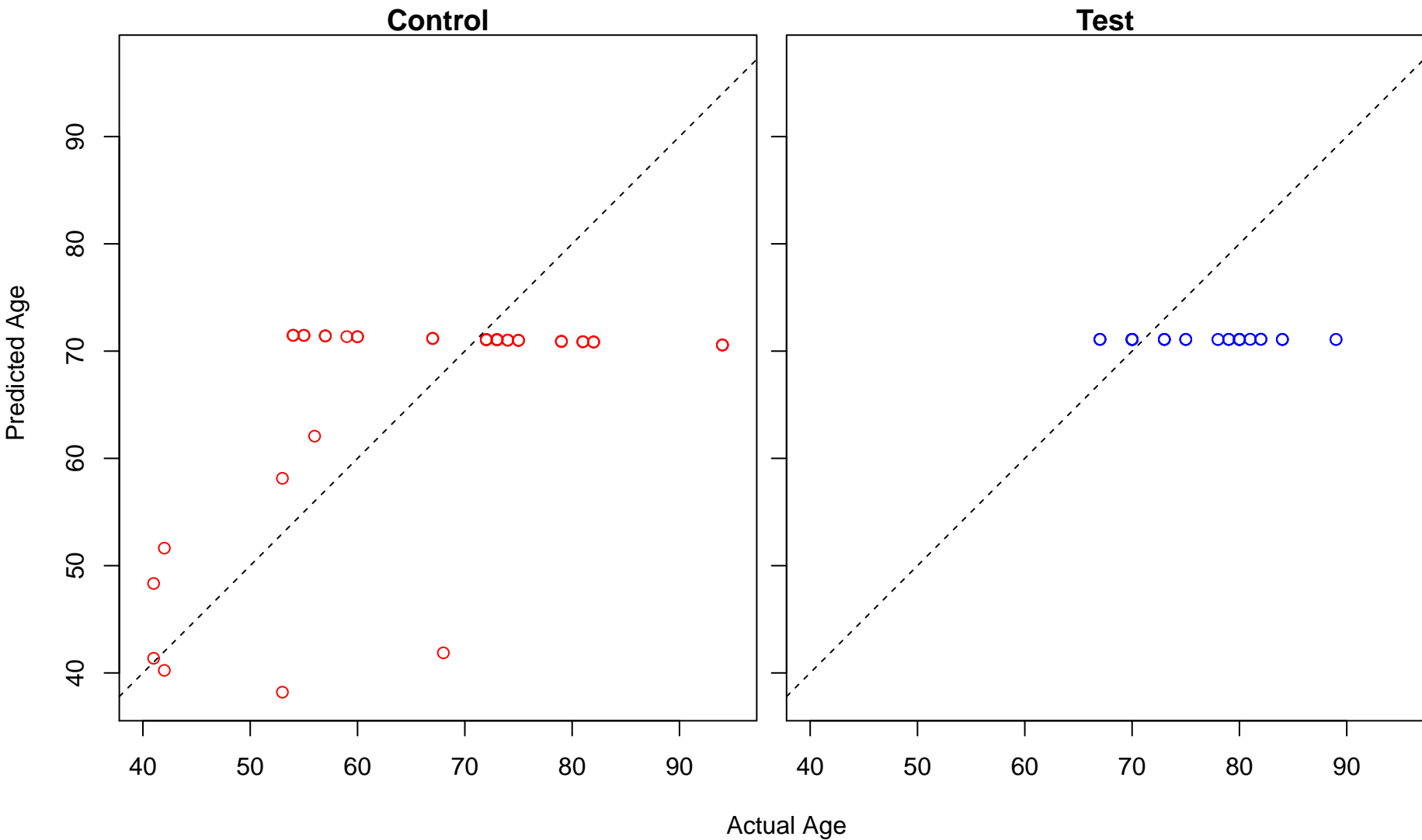
RNA stabilization (Score: 0.791205)



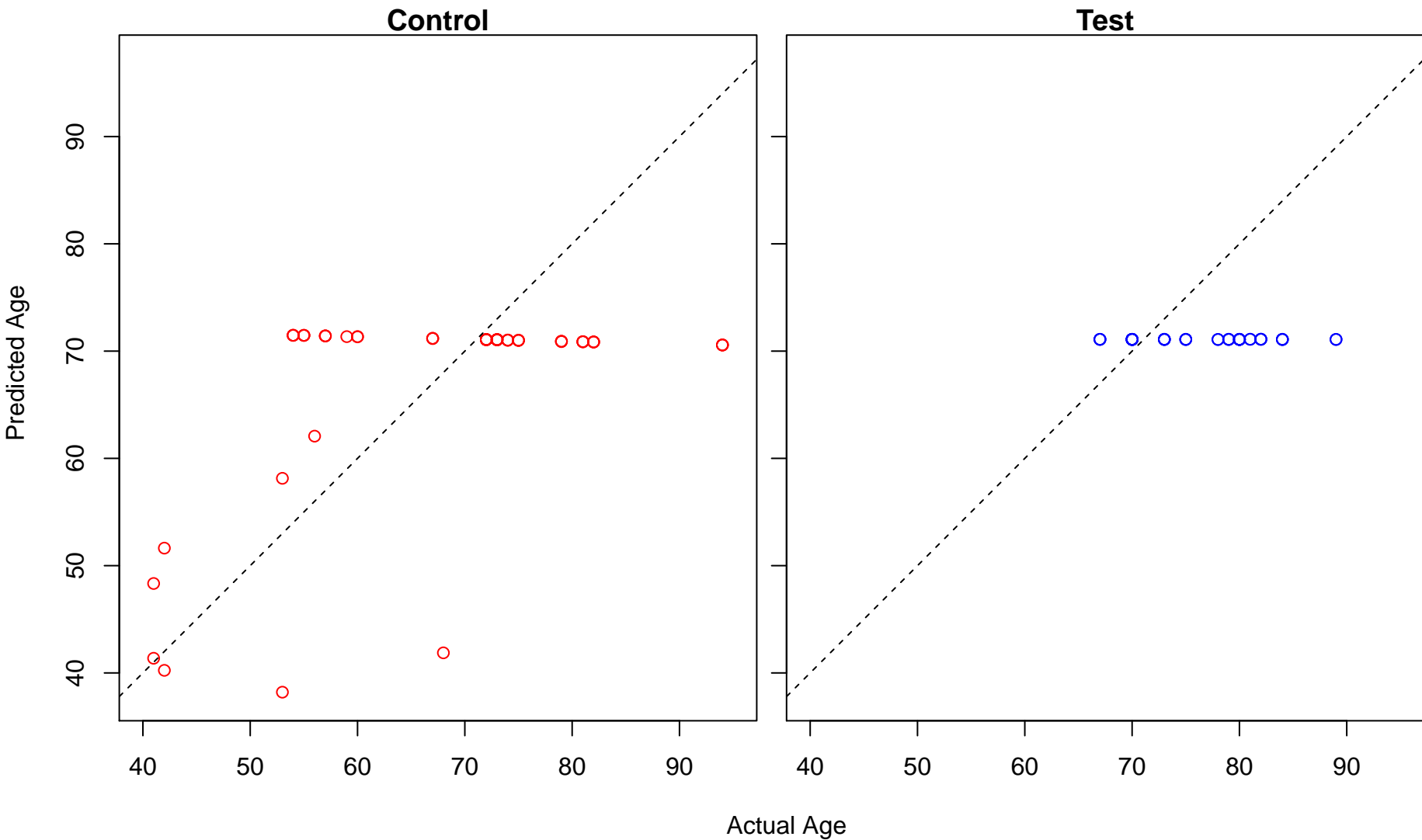
mRNA stabilization (Score: 0.791205)



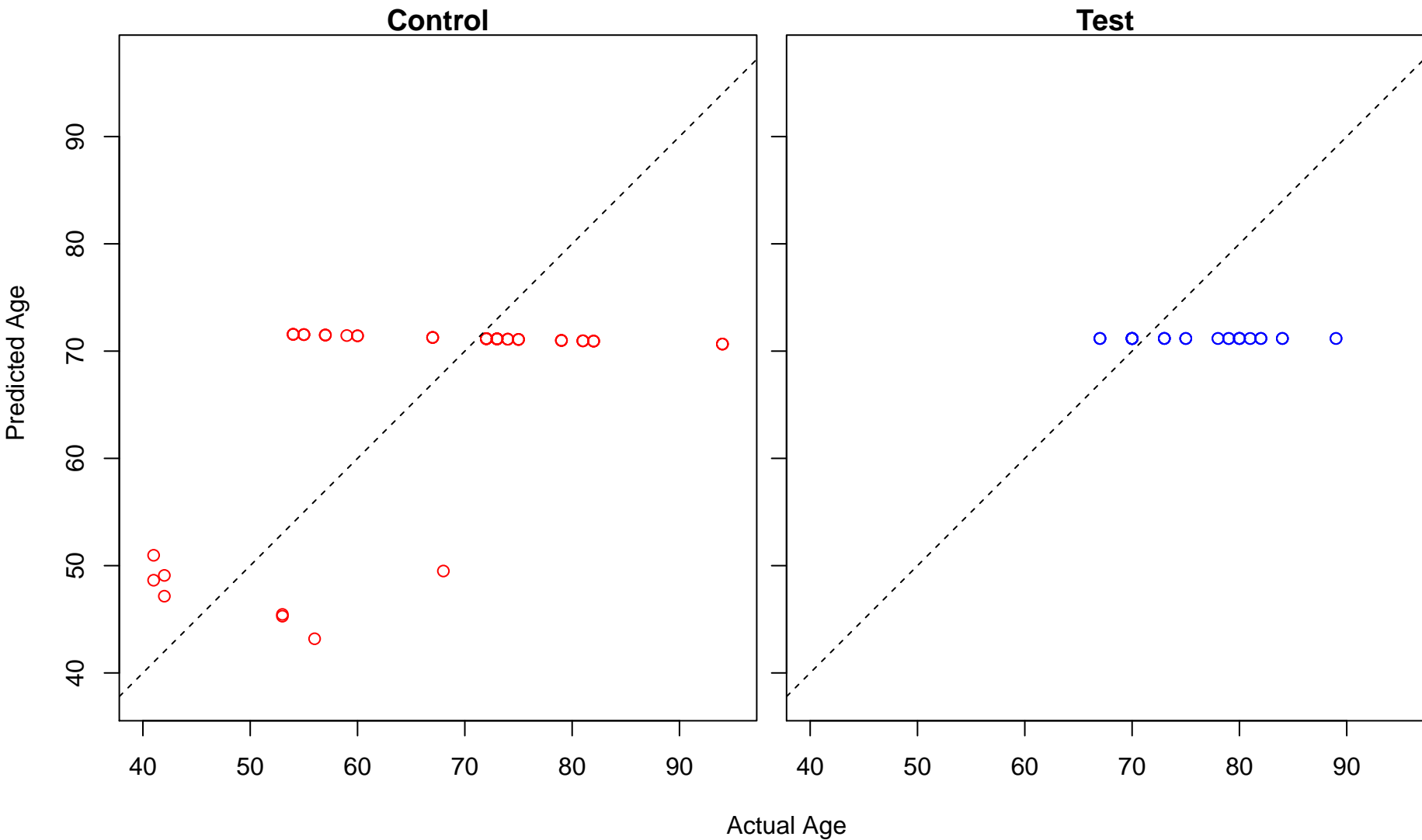
negative regulation of RNA catabolic process (Score: 0.791205)



negative regulation of mRNA catabolic process (Score: 0.791205)



catabolic process (Score: 0.791176)

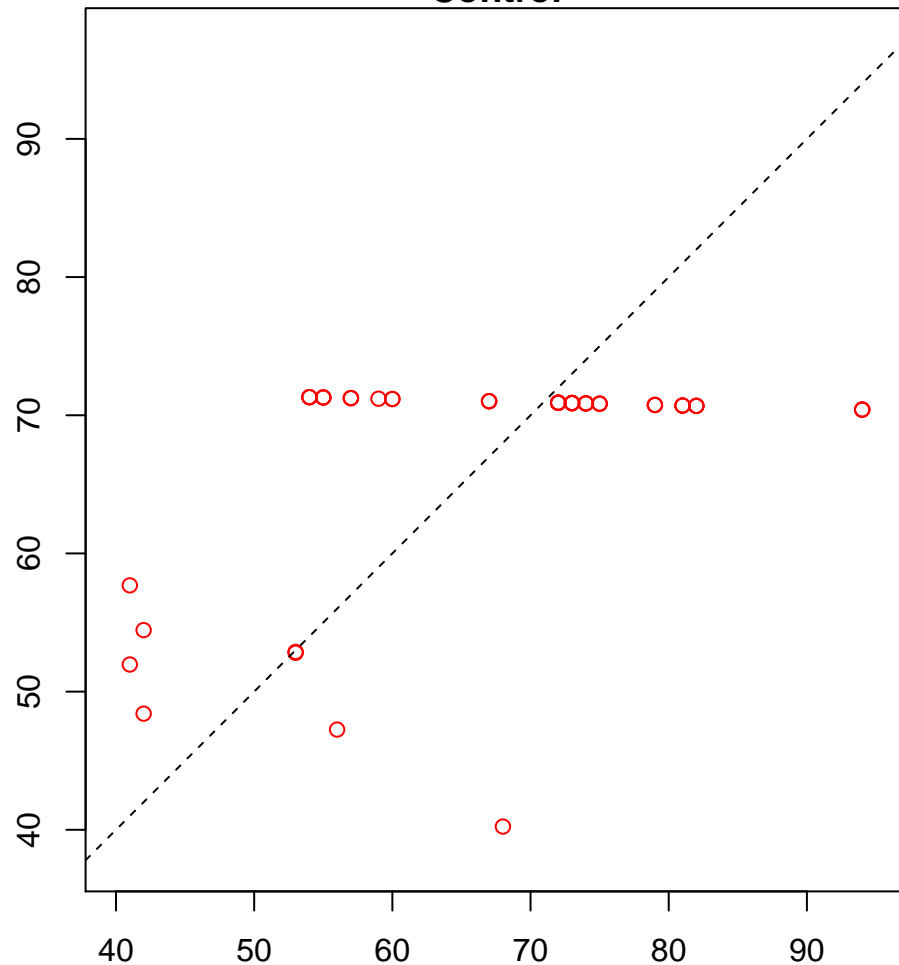


negative regulation of ion transport (Score: 0.791107)

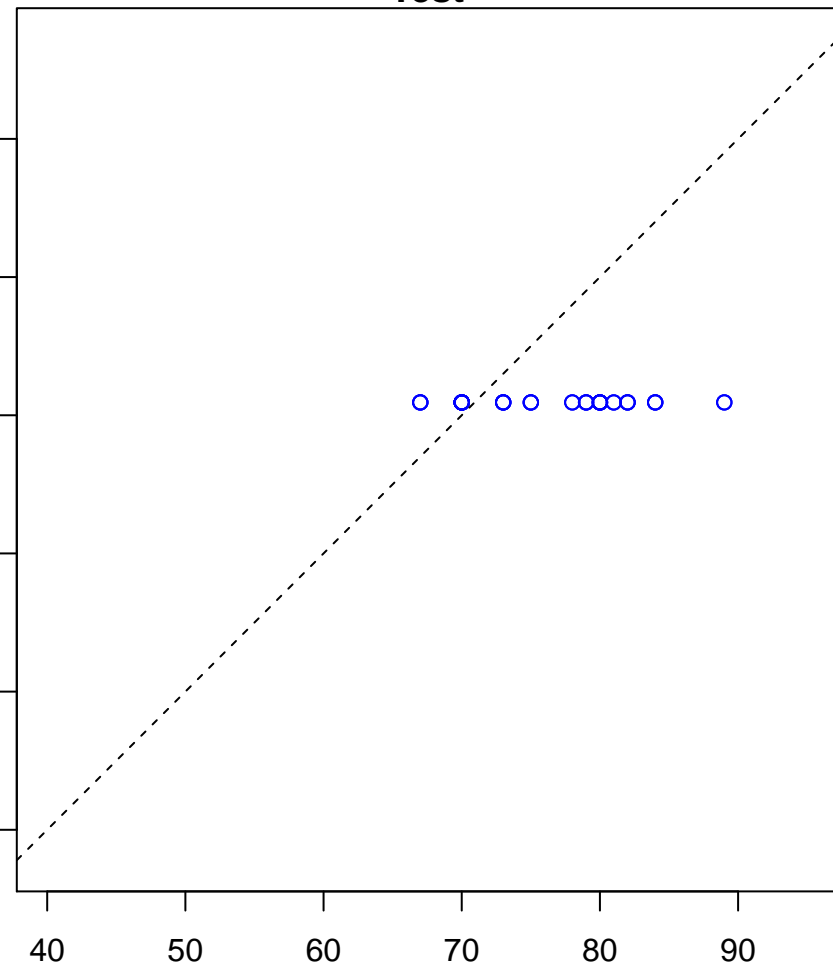
Control

Test

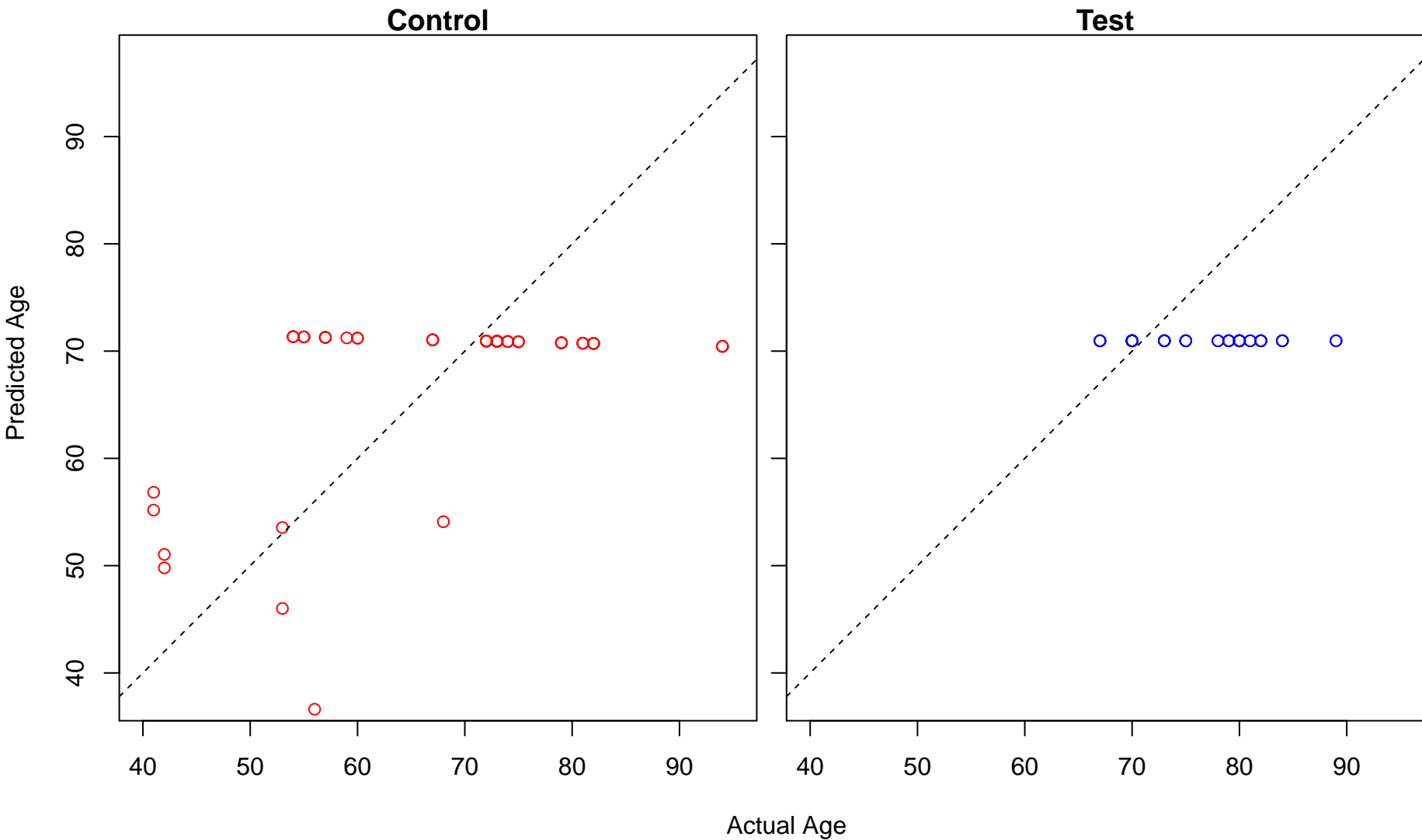
Predicted Age



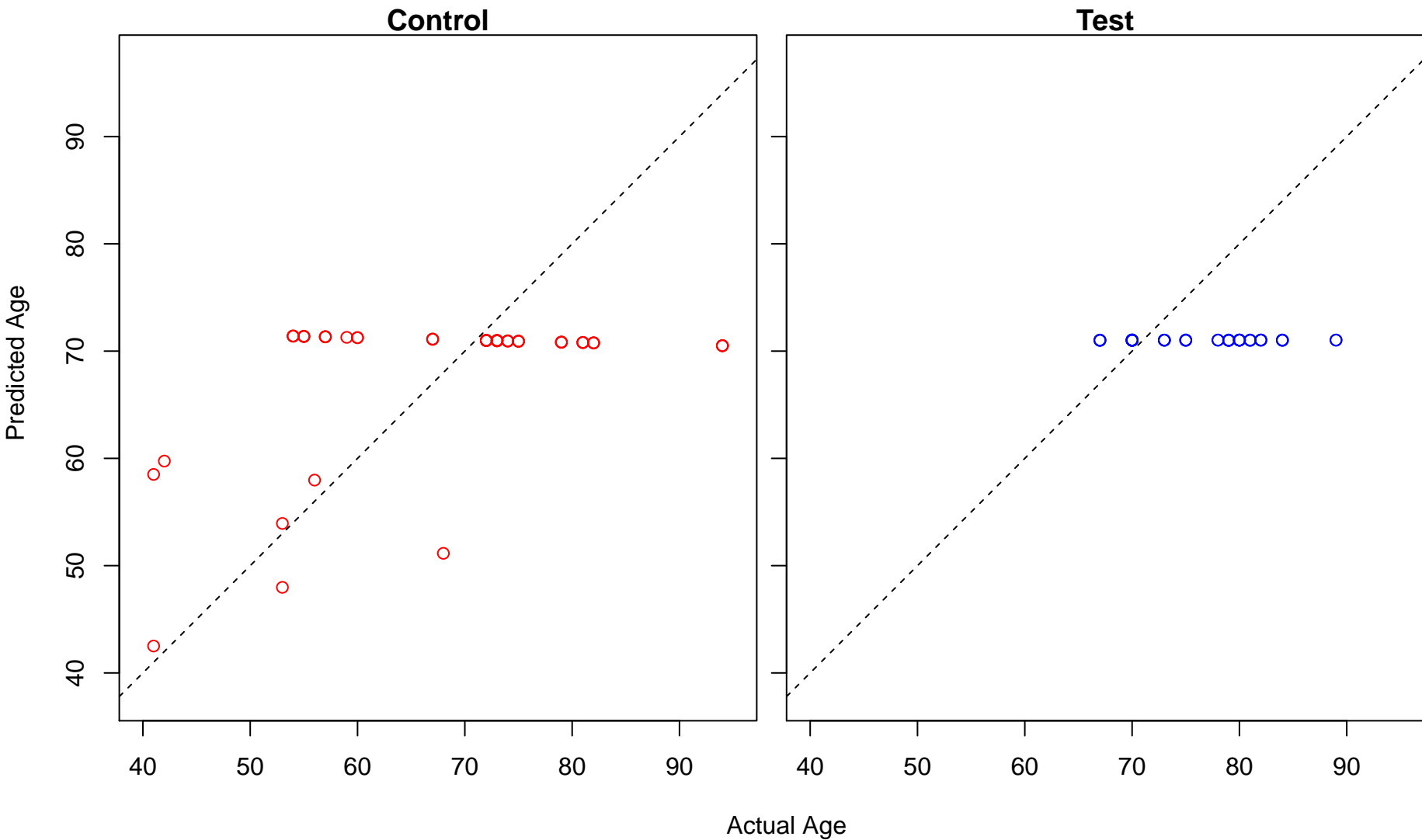
Actual Age



regulation of intrinsic apoptotic signaling pathway by p53 class mediator (Score: 0.791092)

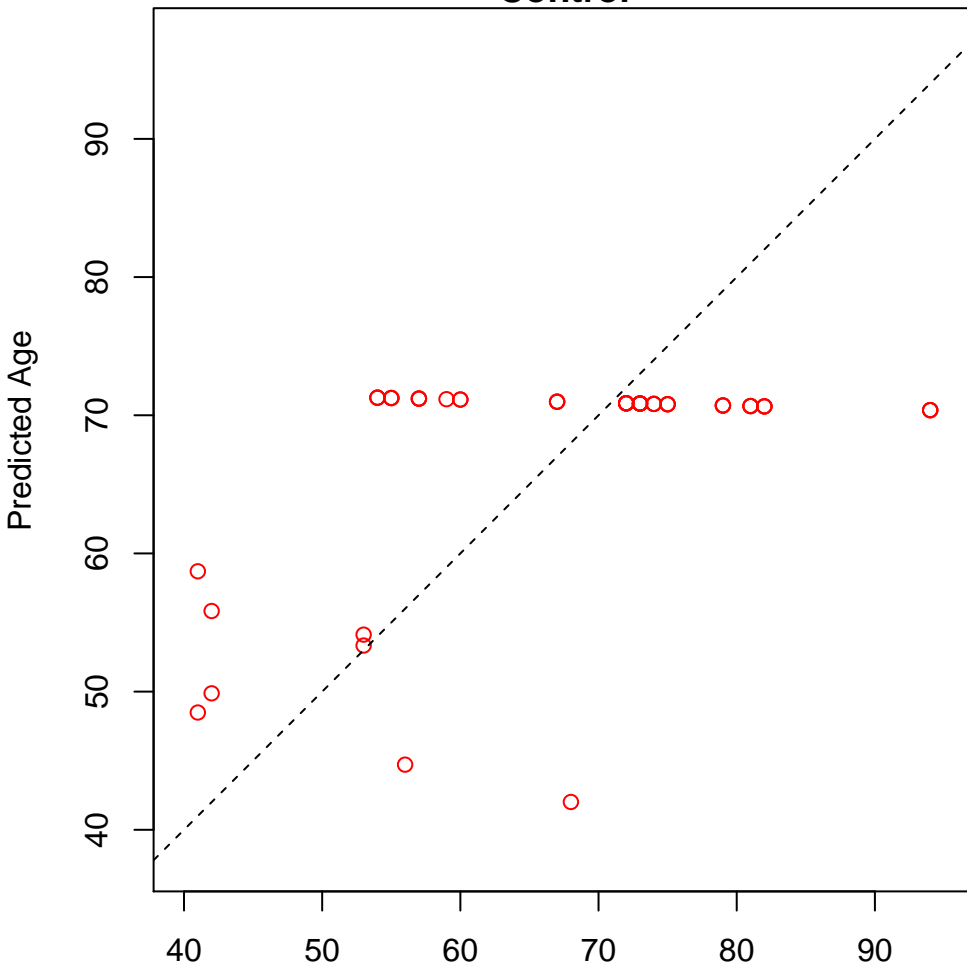


regulation of G-protein coupled receptor protein signaling pathway (Score: 0.791049)

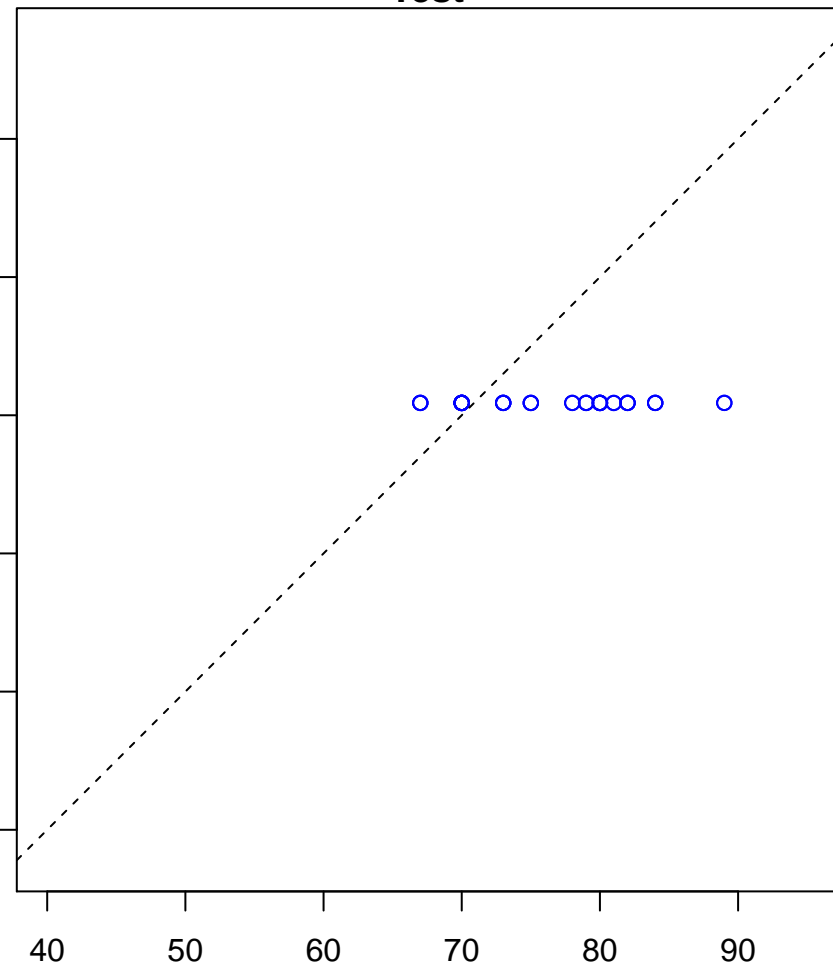


regulation of transmembrane transport (Score: 0.790809)

Control

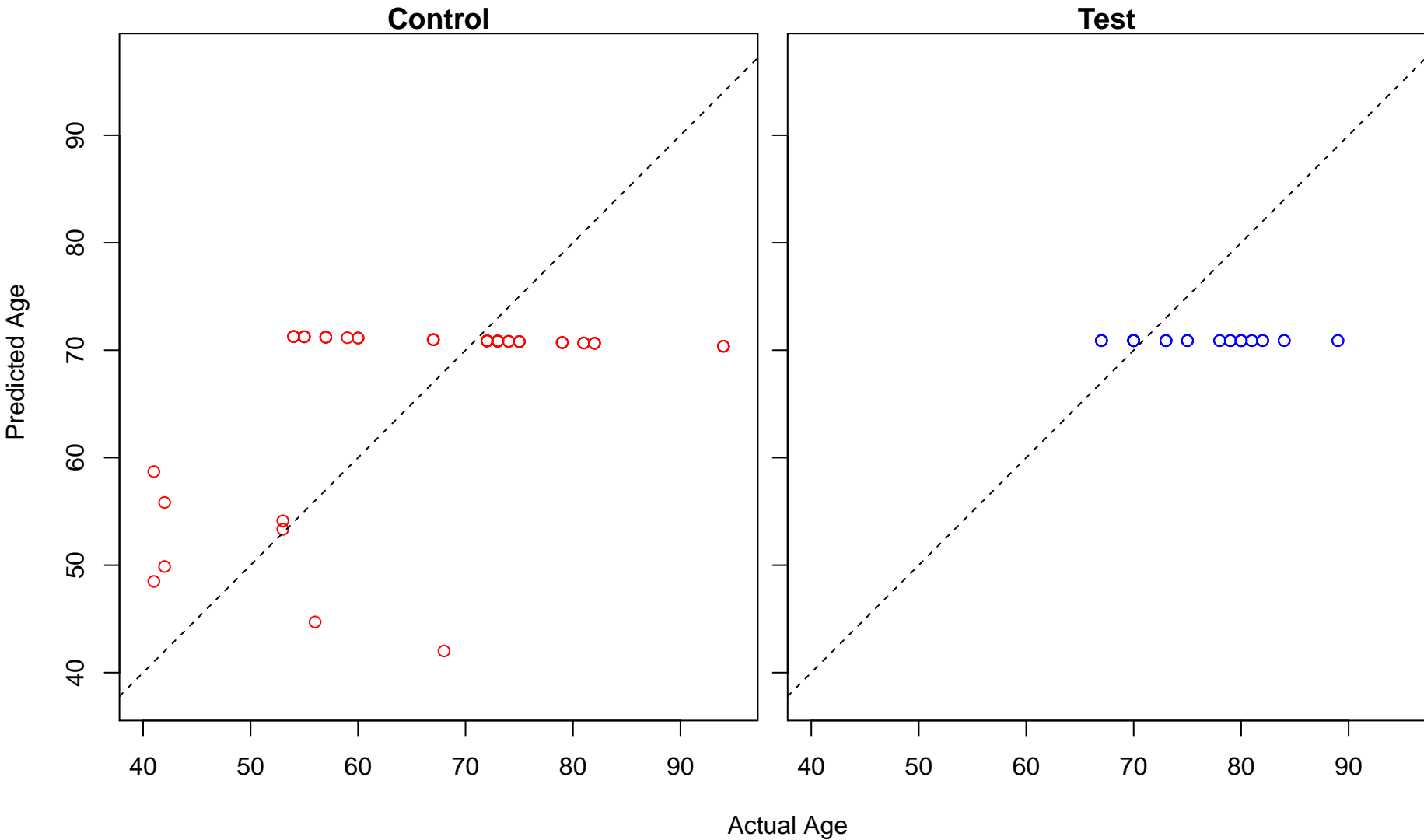


Test



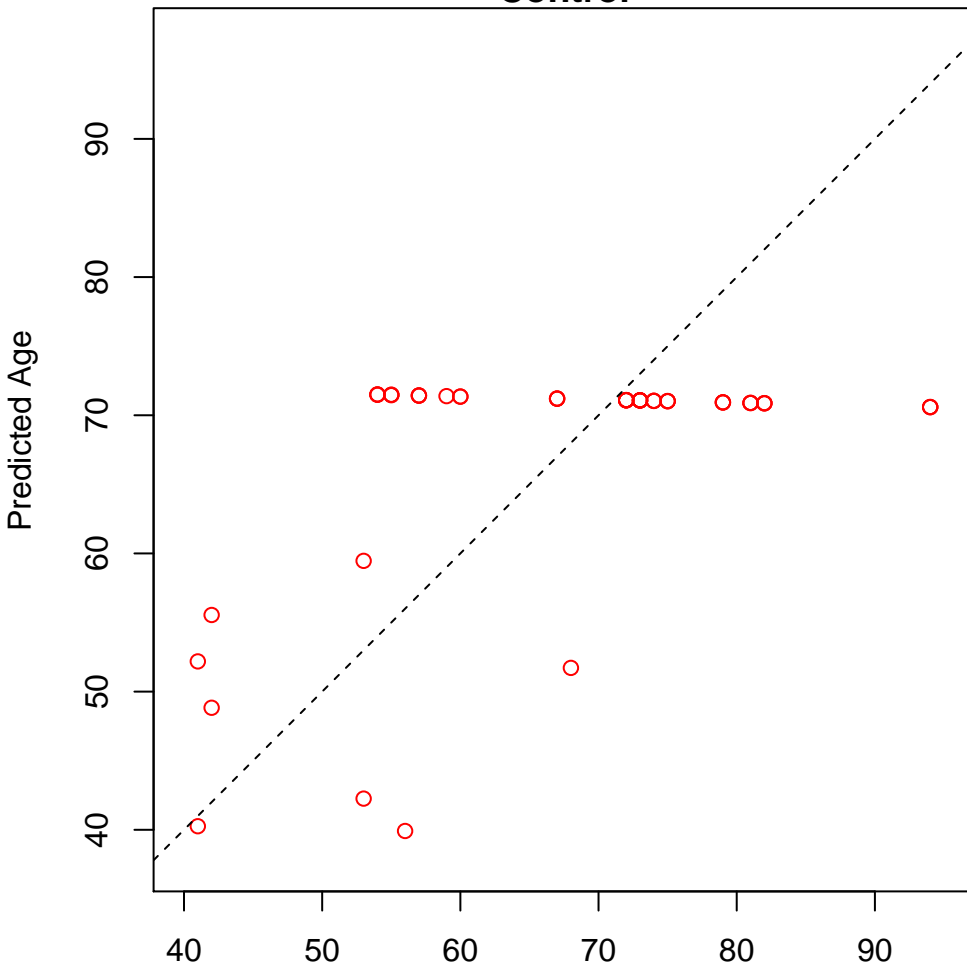
Actual Age

regulation of ion transmembrane transport (Score: 0.790809)

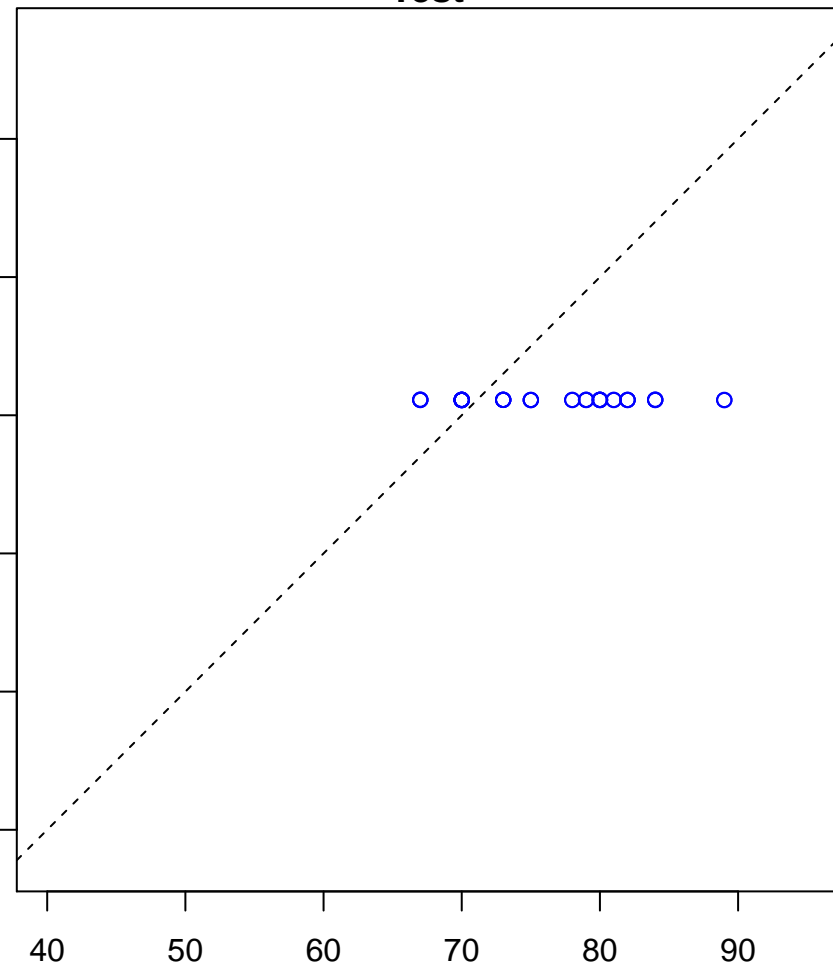


chromatin assembly or disassembly (Score: 0.790789)

Control

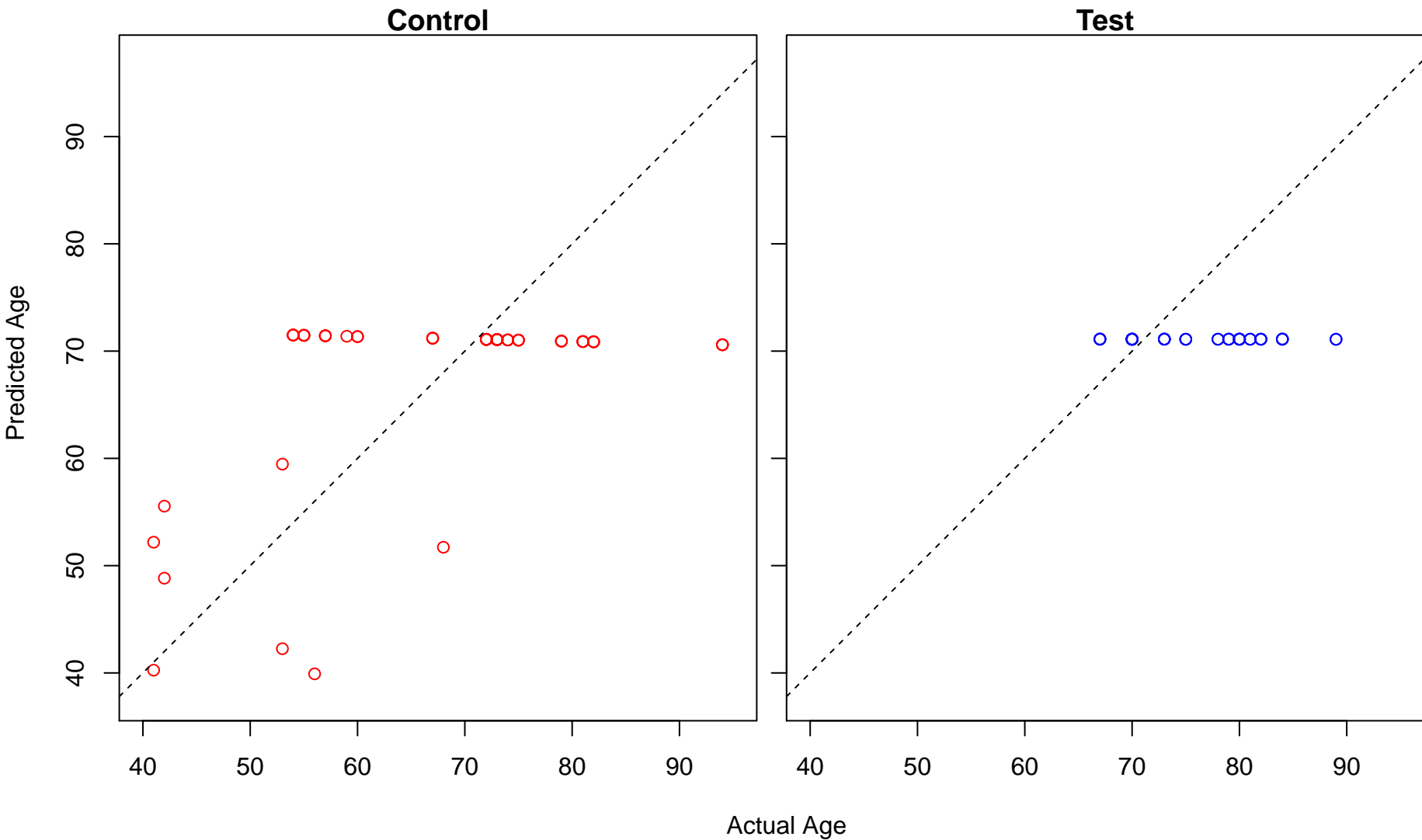


Test

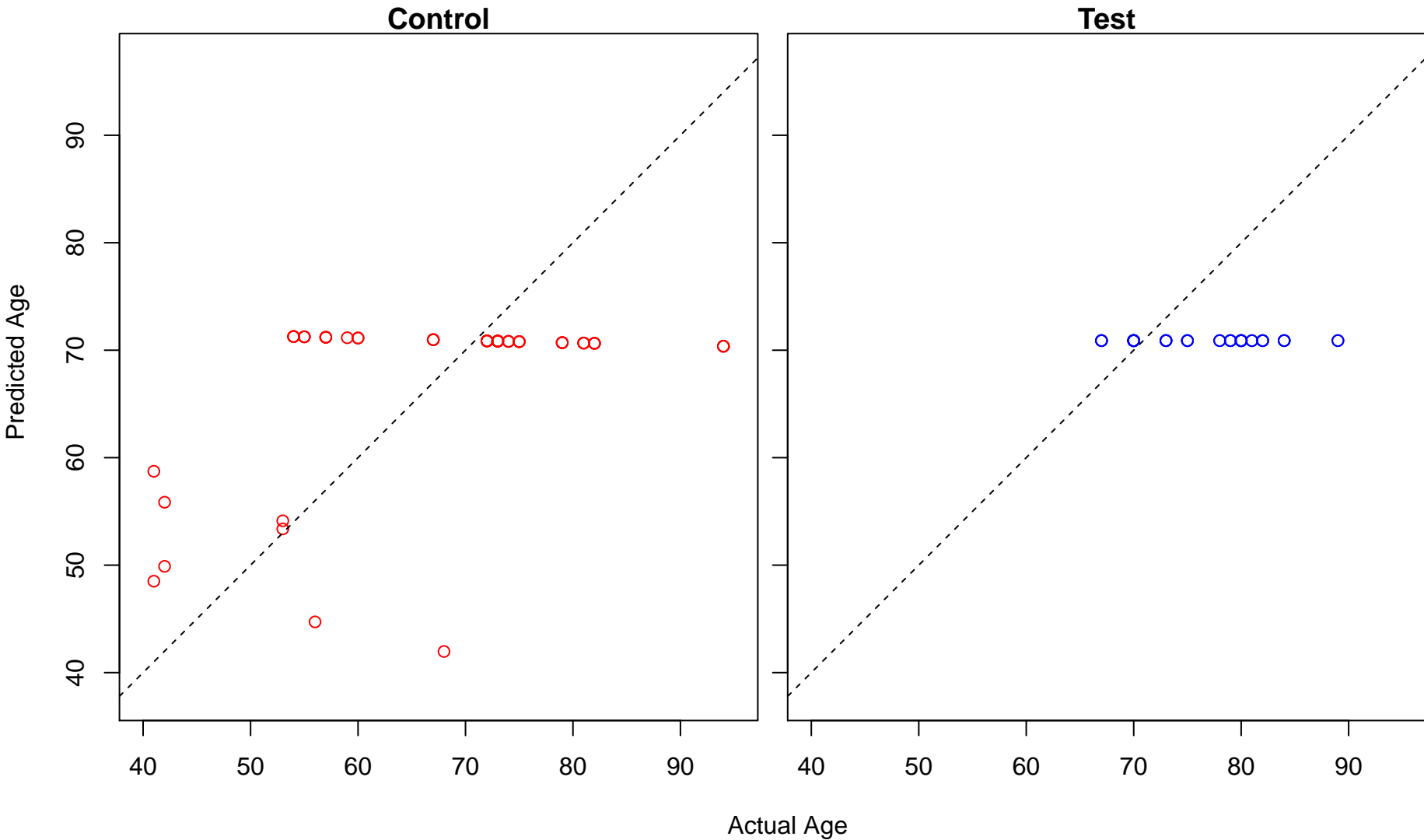


Actual Age

nucleosome organization (Score: 0.790789)

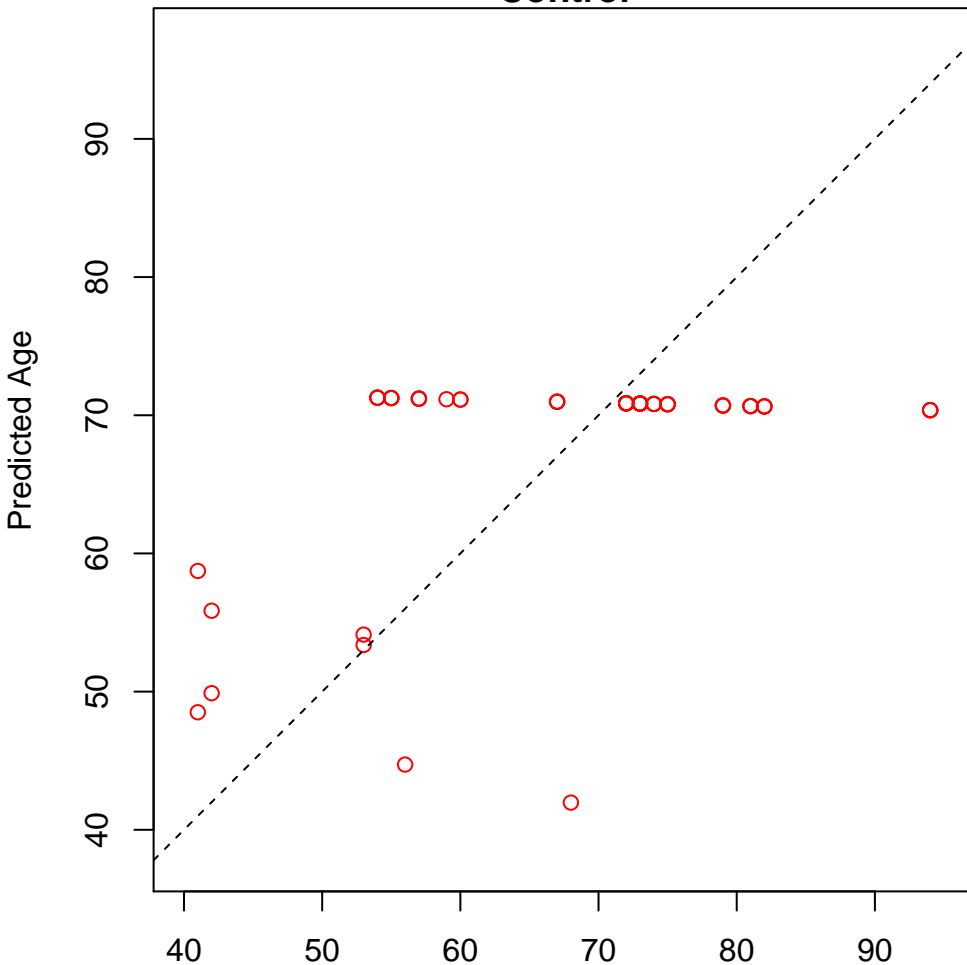


regulation of transmembrane transporter activity (Score: 0.790689)

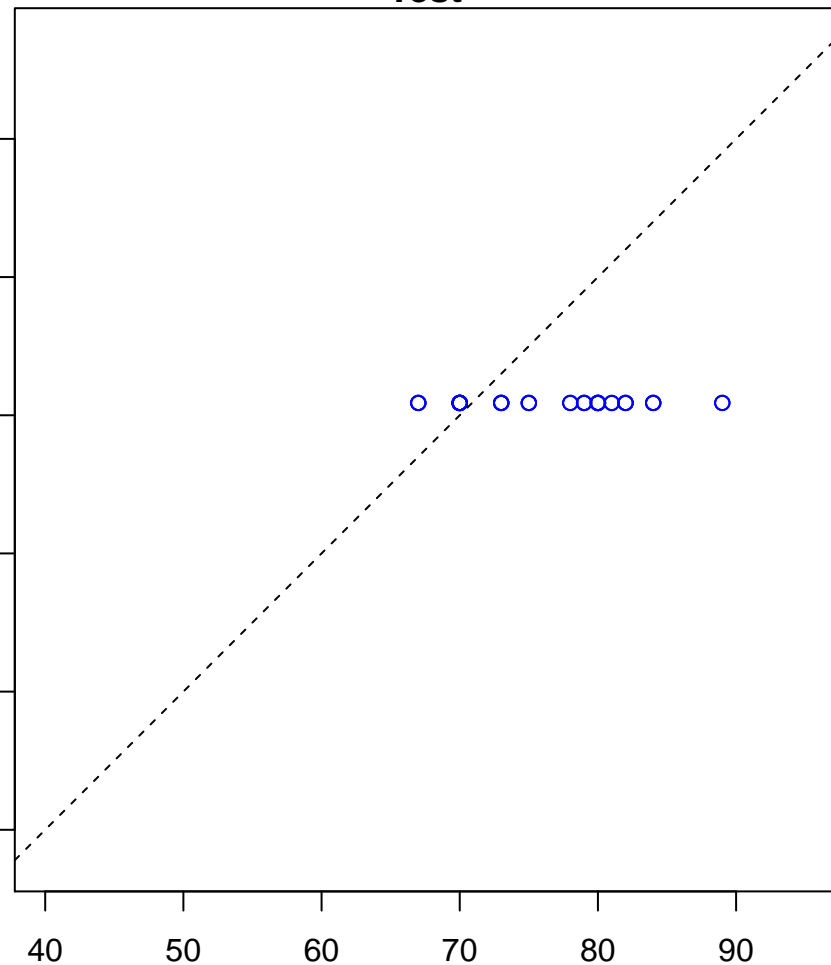


regulation of transporter activity (Score: 0.790689)

Control

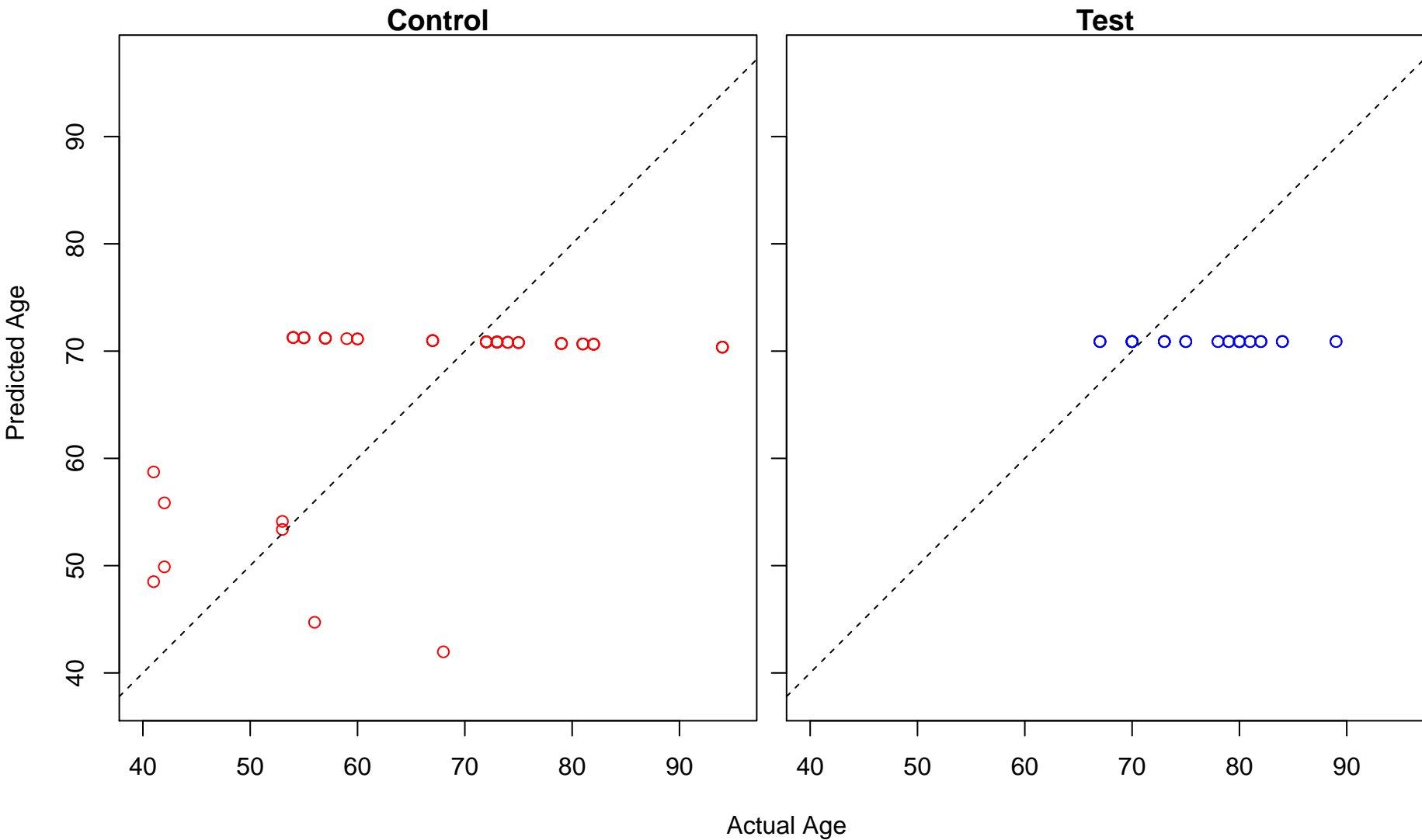


Test

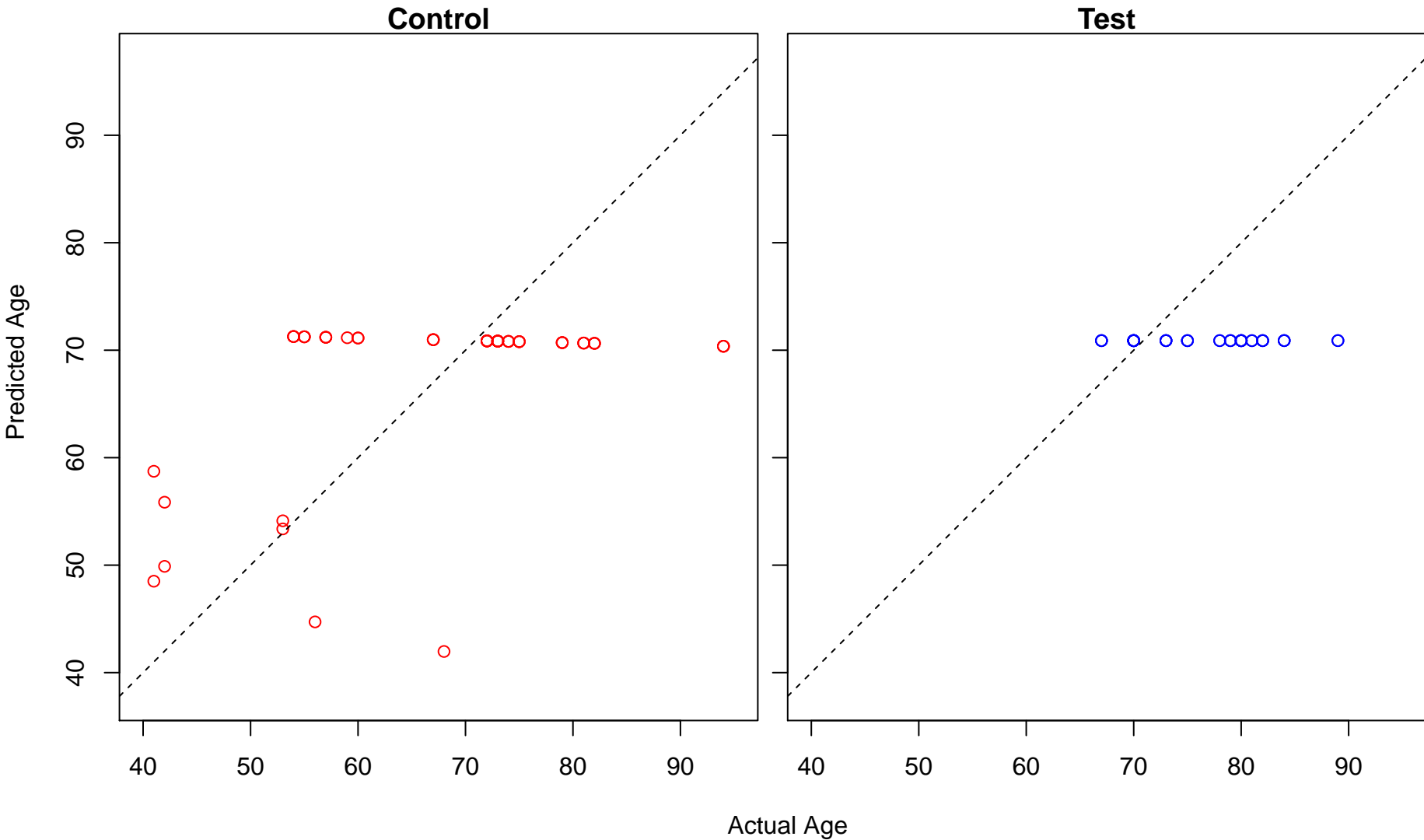


Actual Age

regulation of ion transmembrane transporter activity (Score: 0.790689)

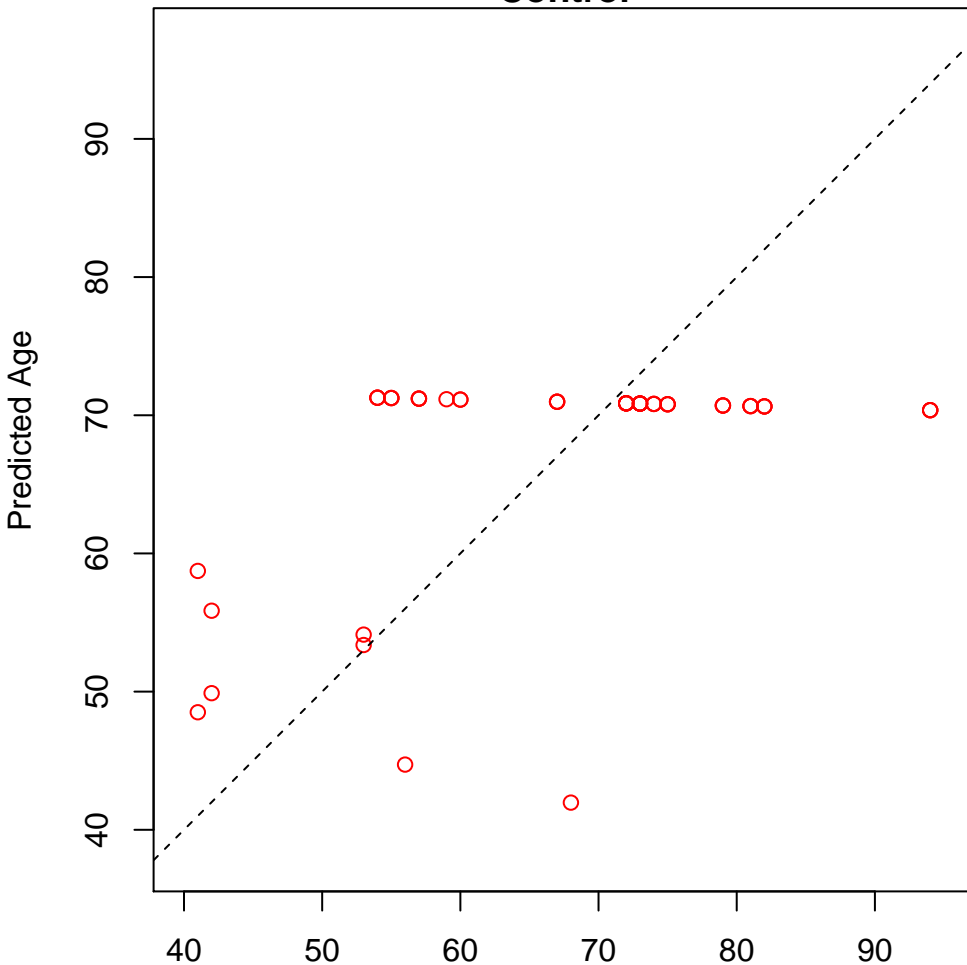


regulation of cation transmembrane transport (Score: 0.790689)

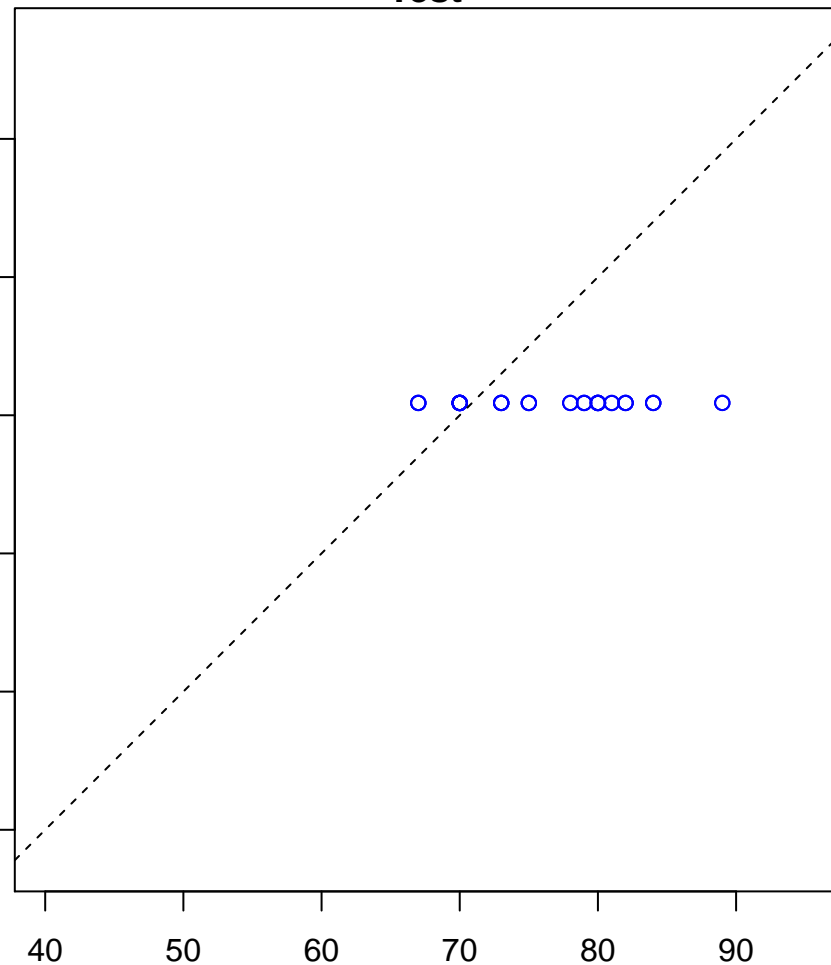


regulation of cation channel activity (Score: 0.790689)

Control

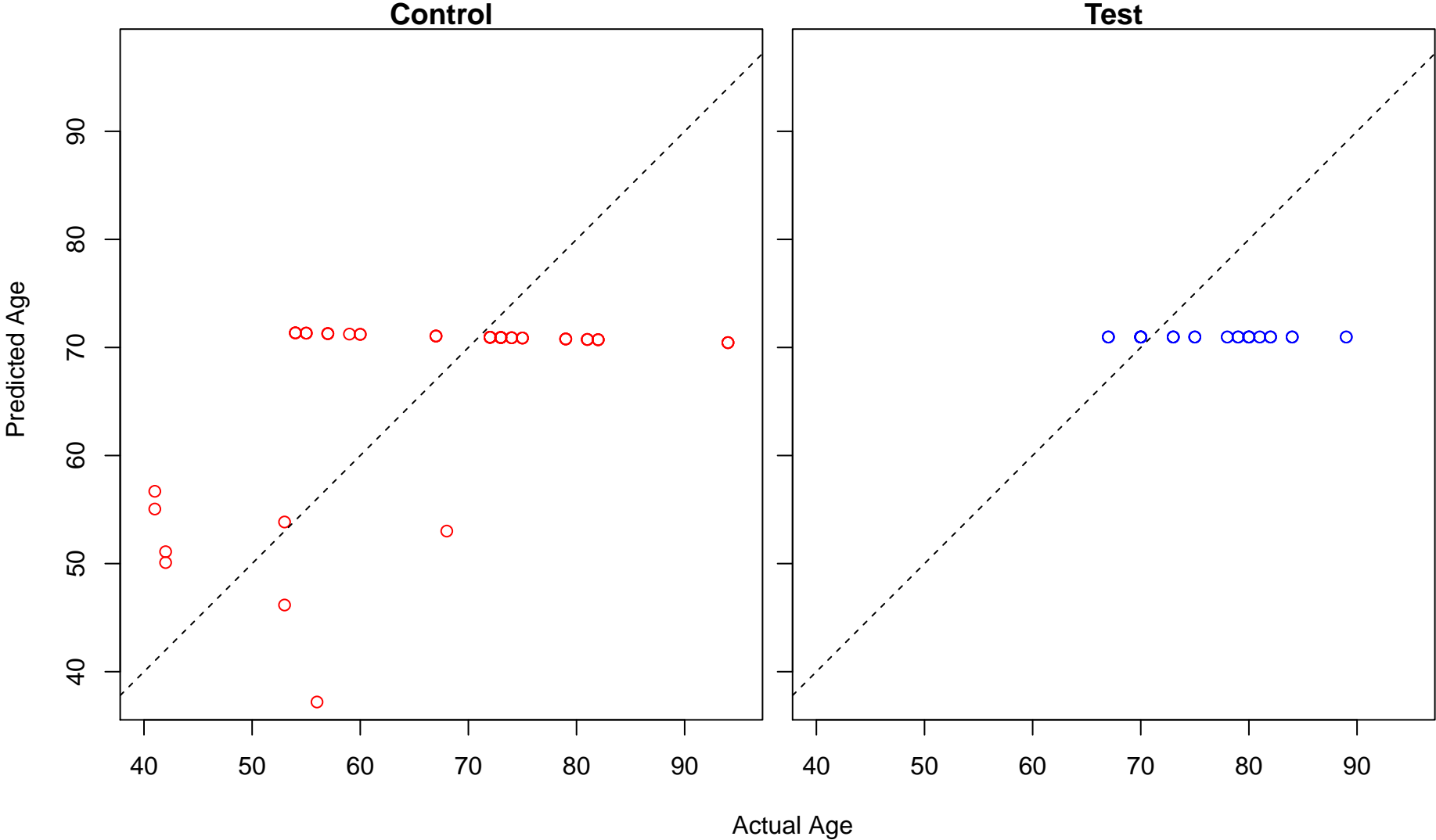


Test

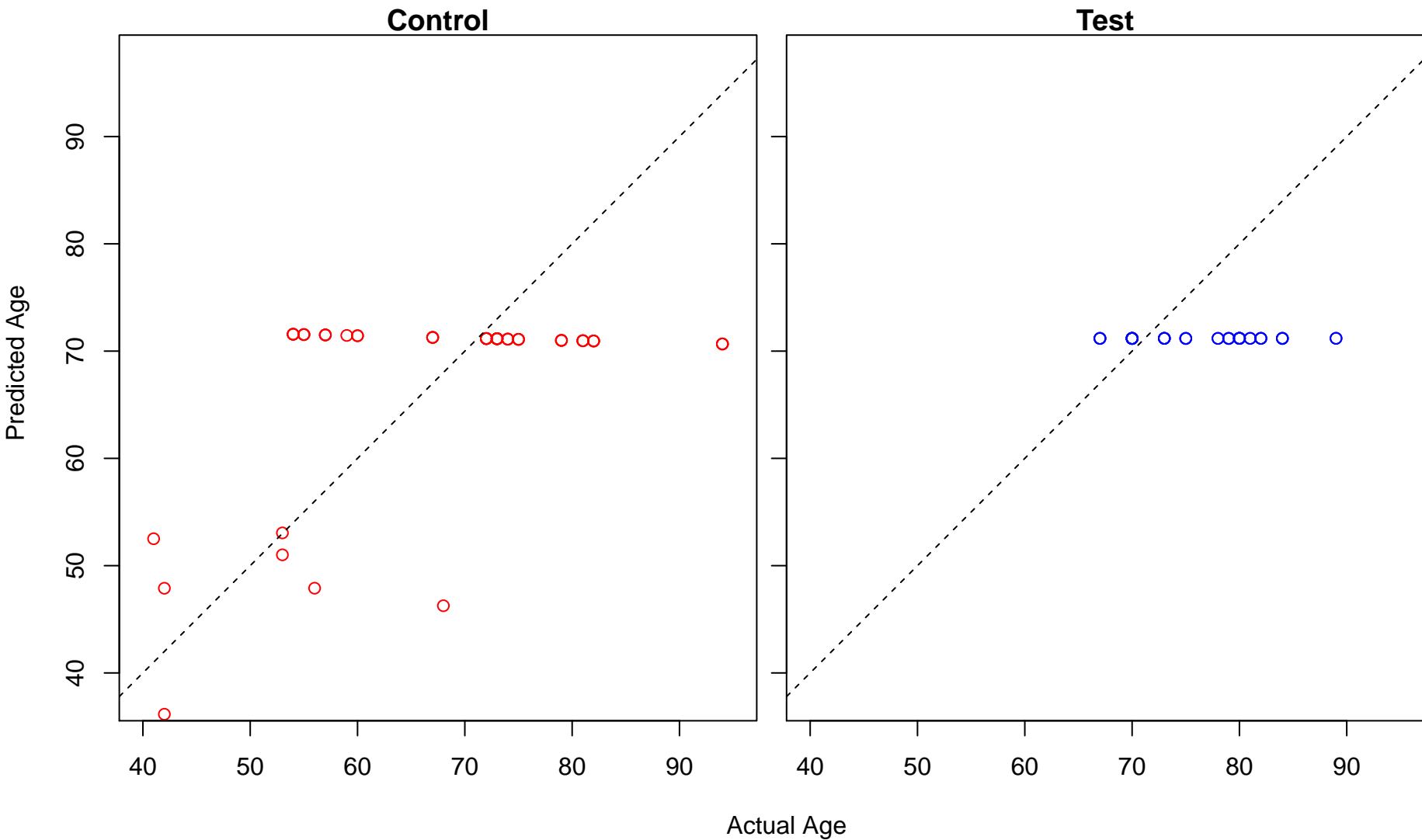


Actual Age

positive regulation of signal transduction by p53 class mediator (Score: 0.790588)

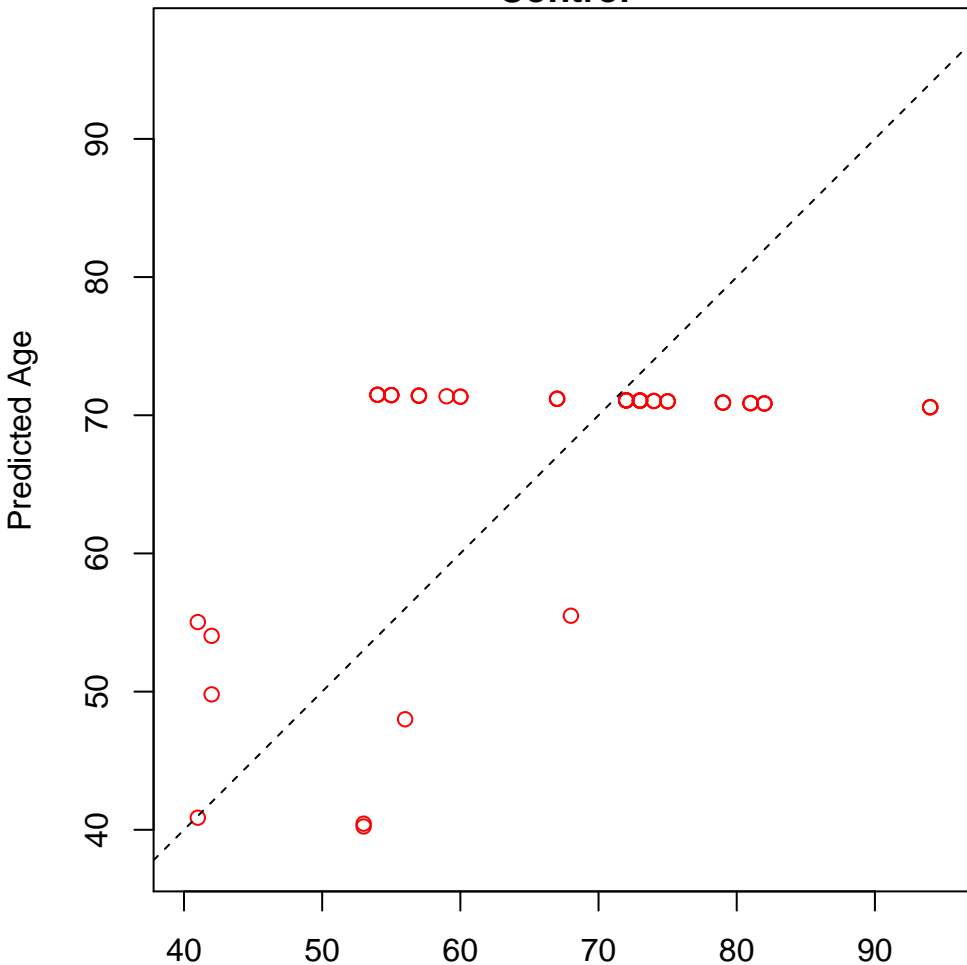


enzyme linked receptor protein signaling pathway (Score: 0.790586)

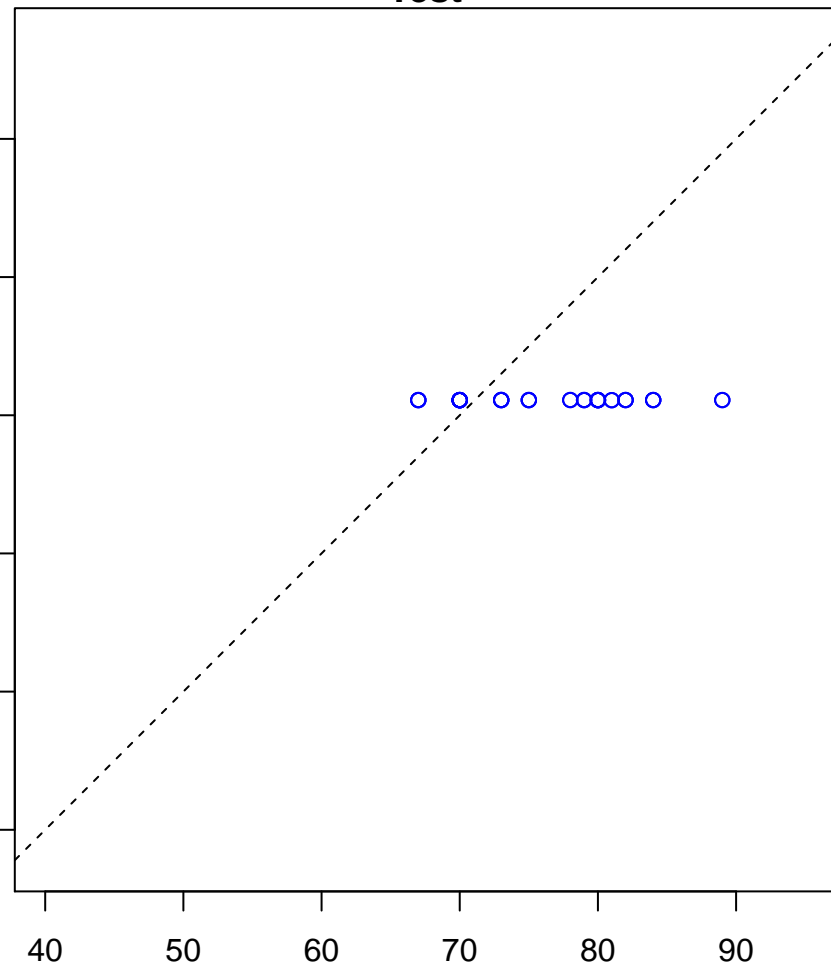


cellular calcium ion homeostasis (Score: 0.790583)

Control

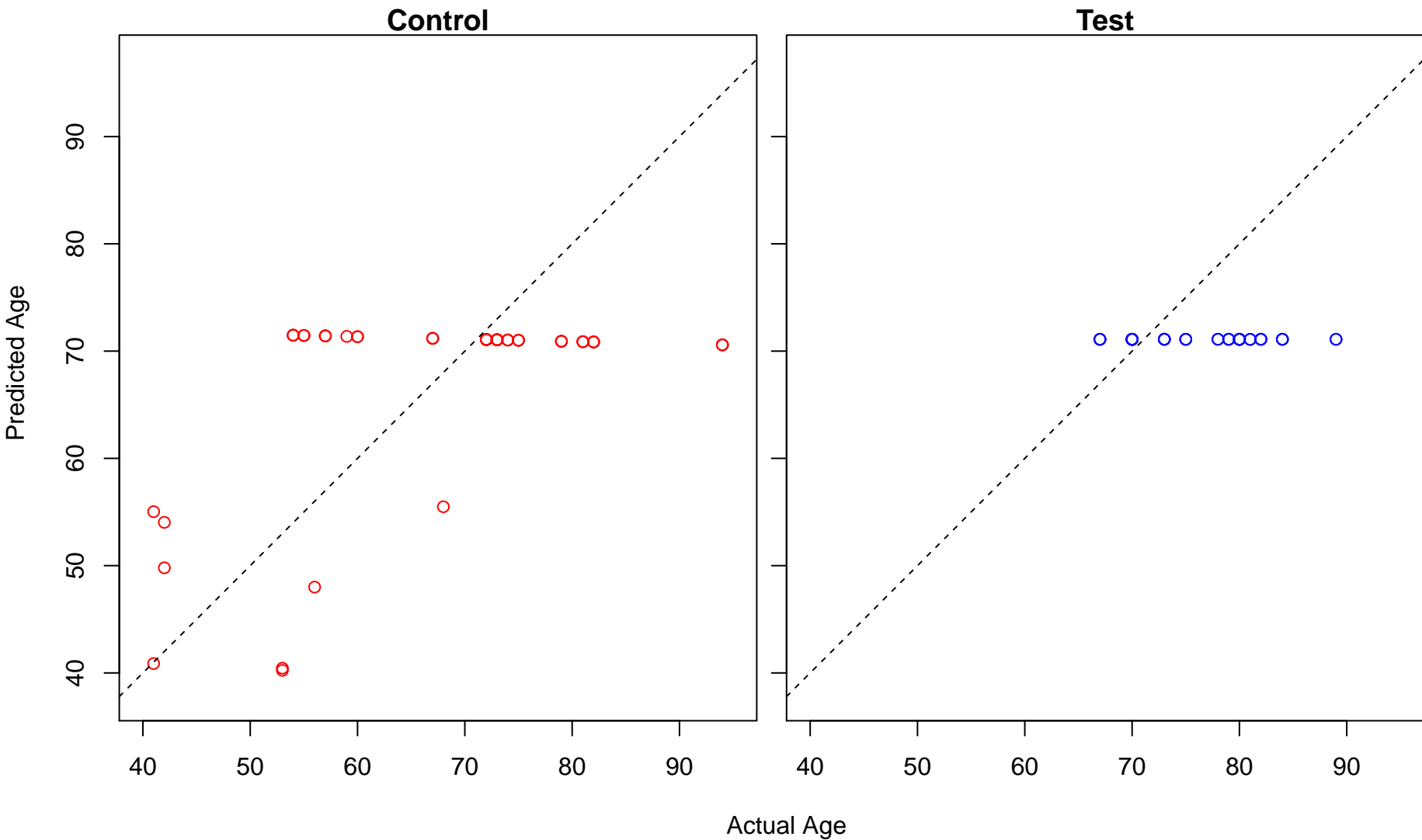


Test

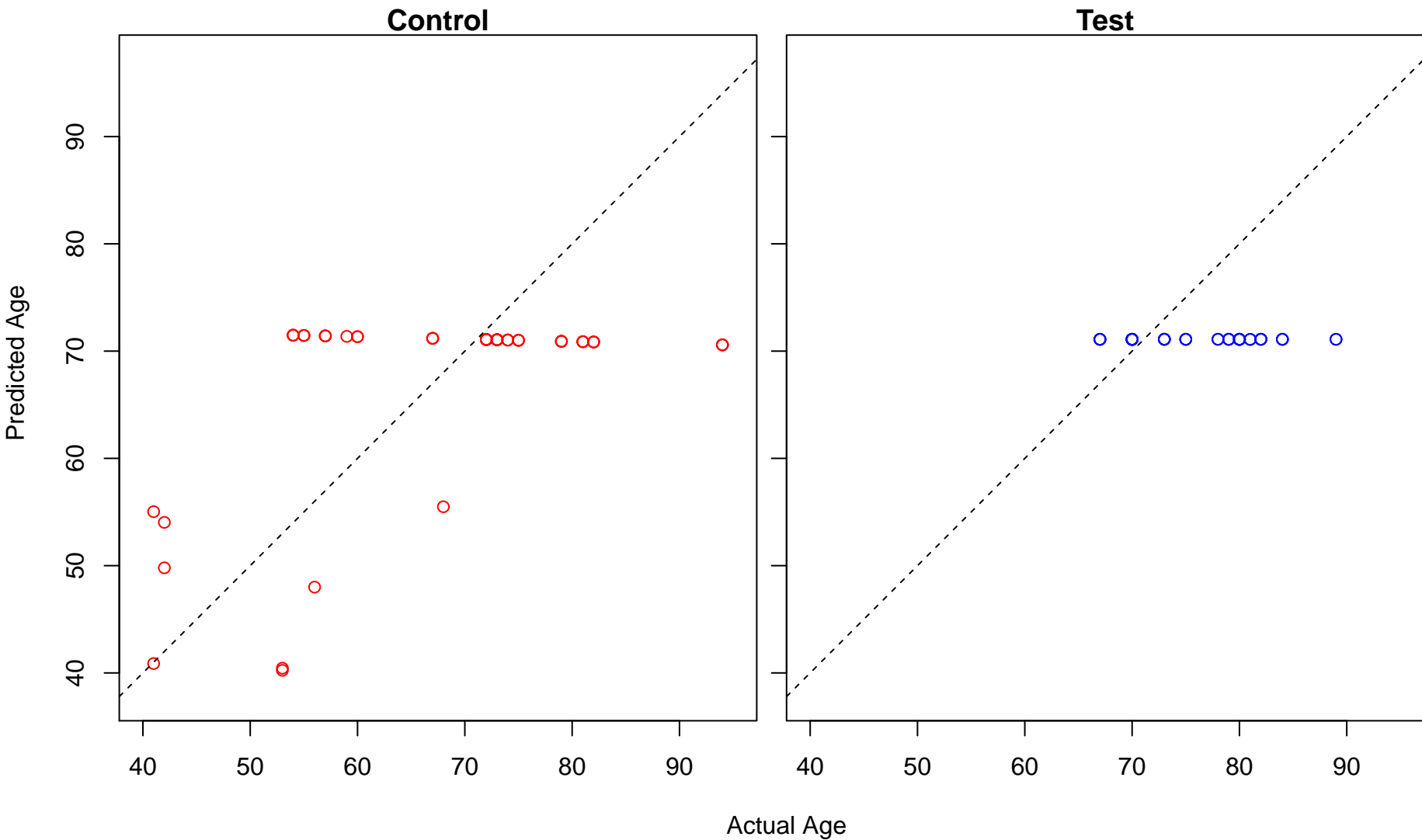


Actual Age

calcium ion homeostasis (Score: 0.790583)

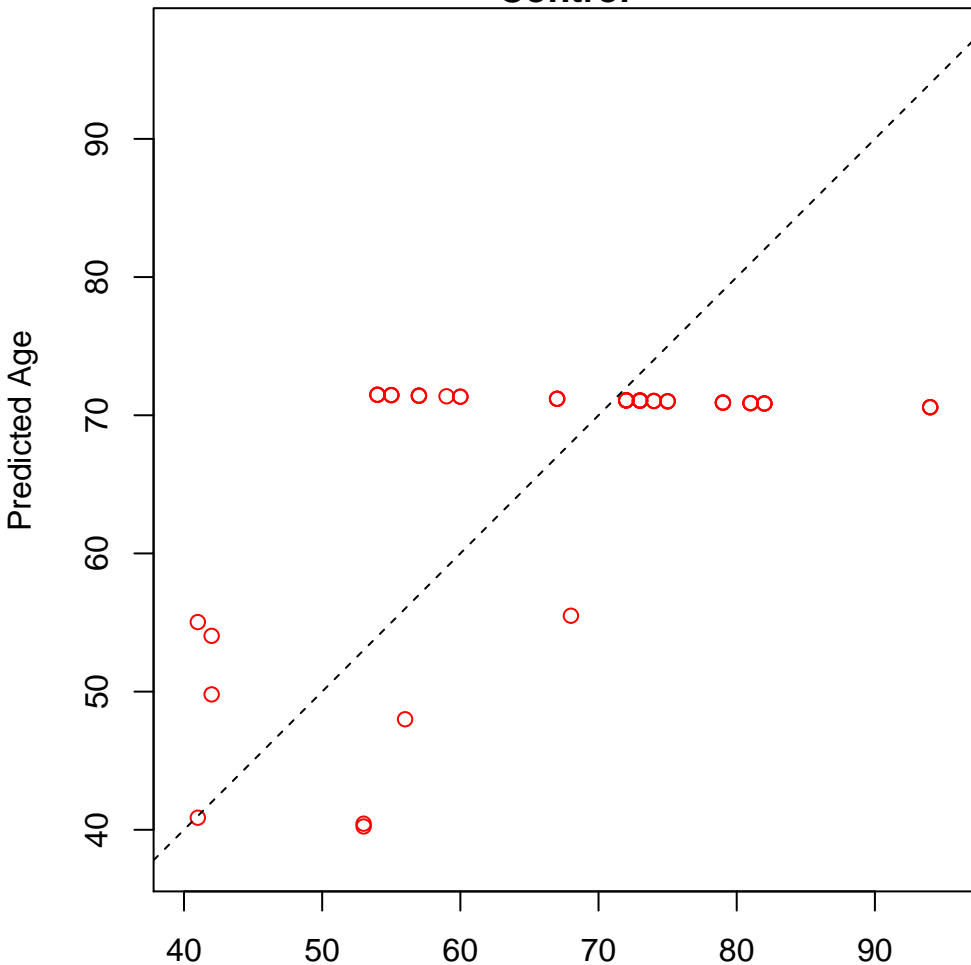


cellular divalent inorganic cation homeostasis (Score: 0.790583)

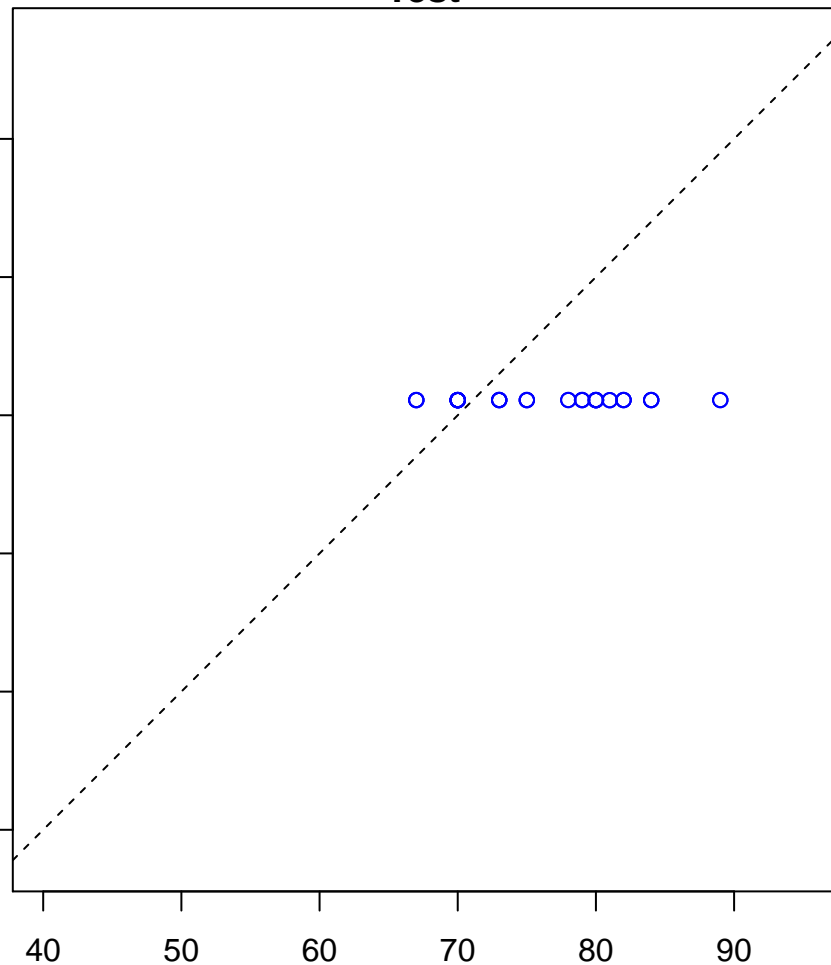


divalent inorganic cation homeostasis (Score: 0.790583)

Control

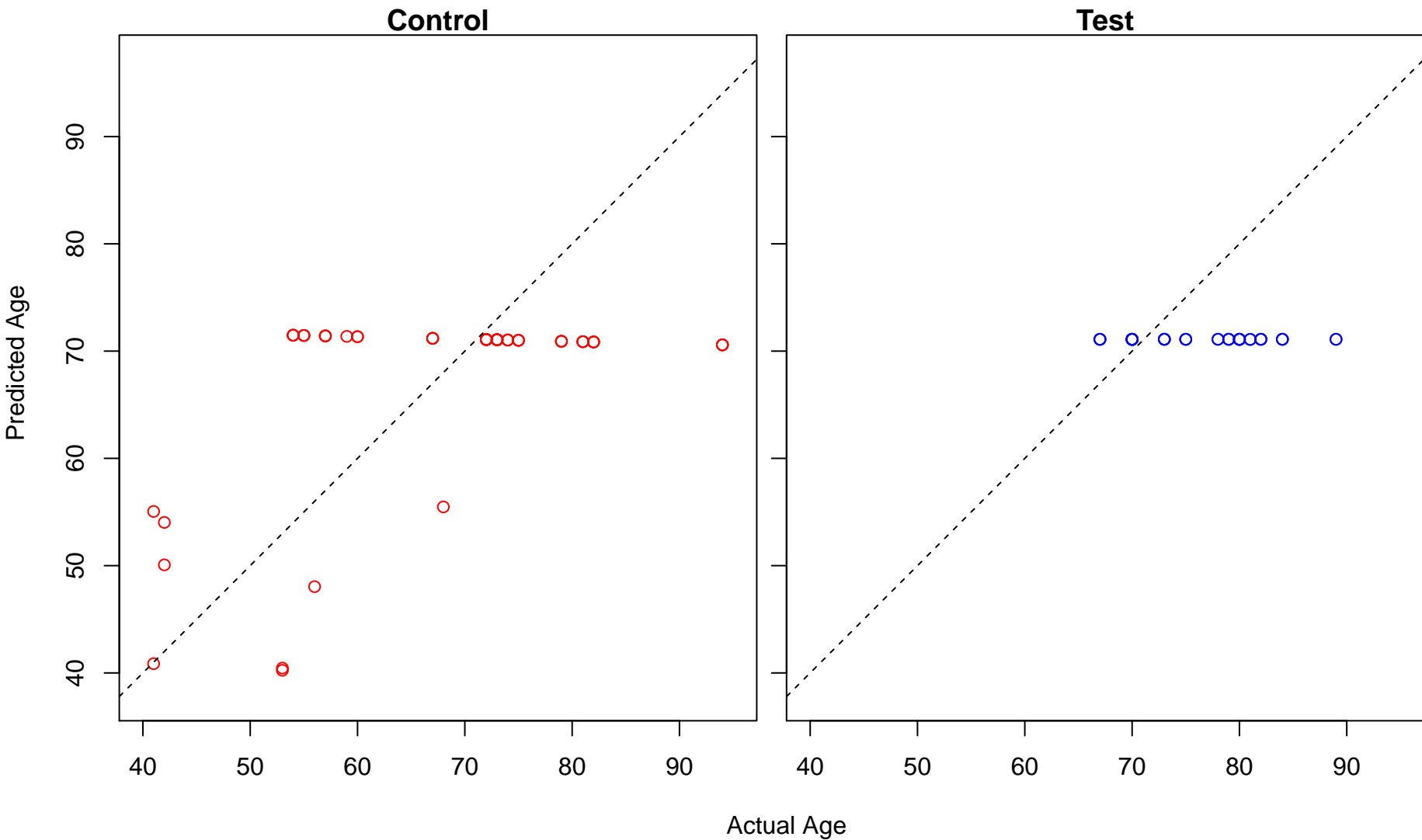


Test

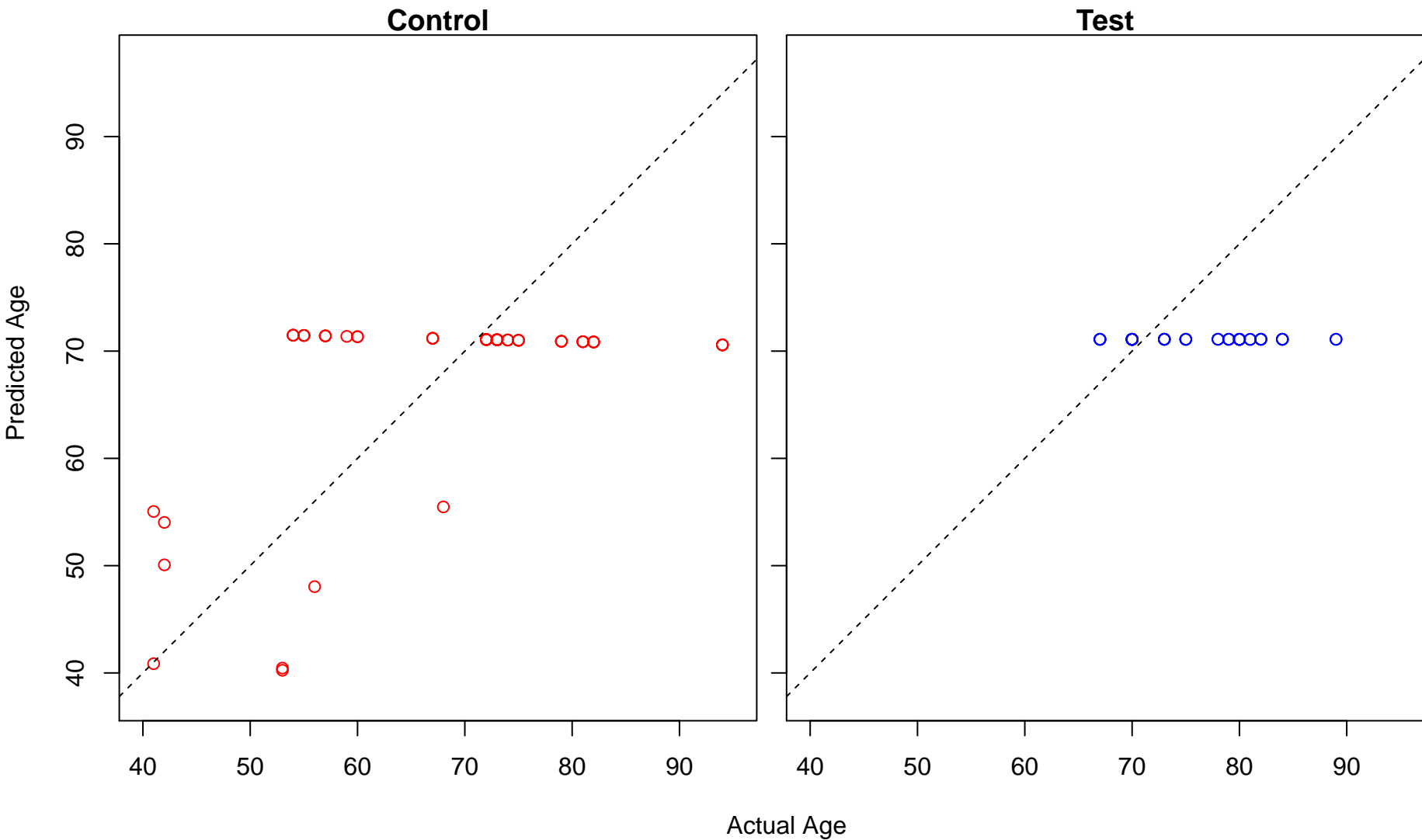


Actual Age

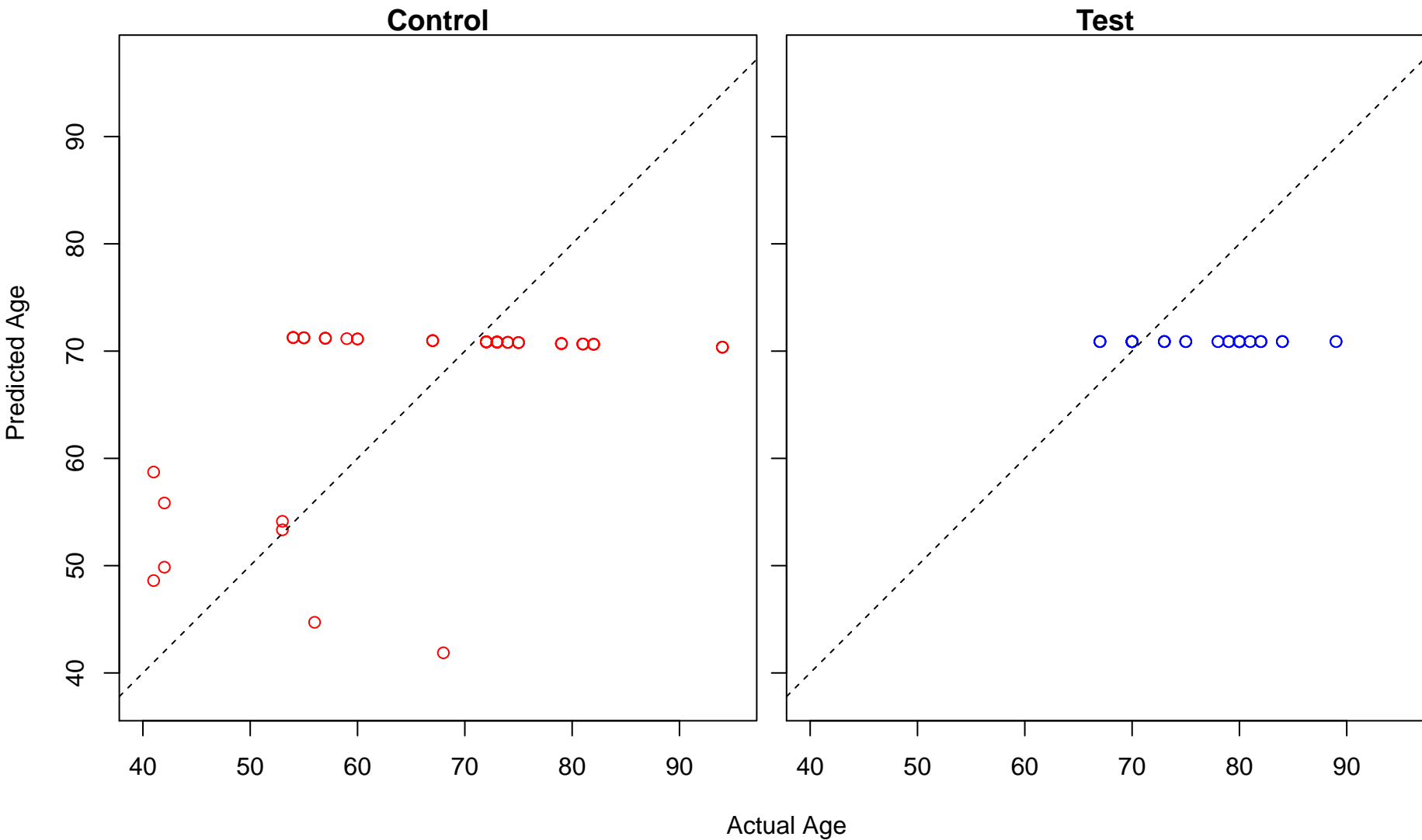
positive regulation of cytosolic calcium ion concentration (Score: 0.790525)



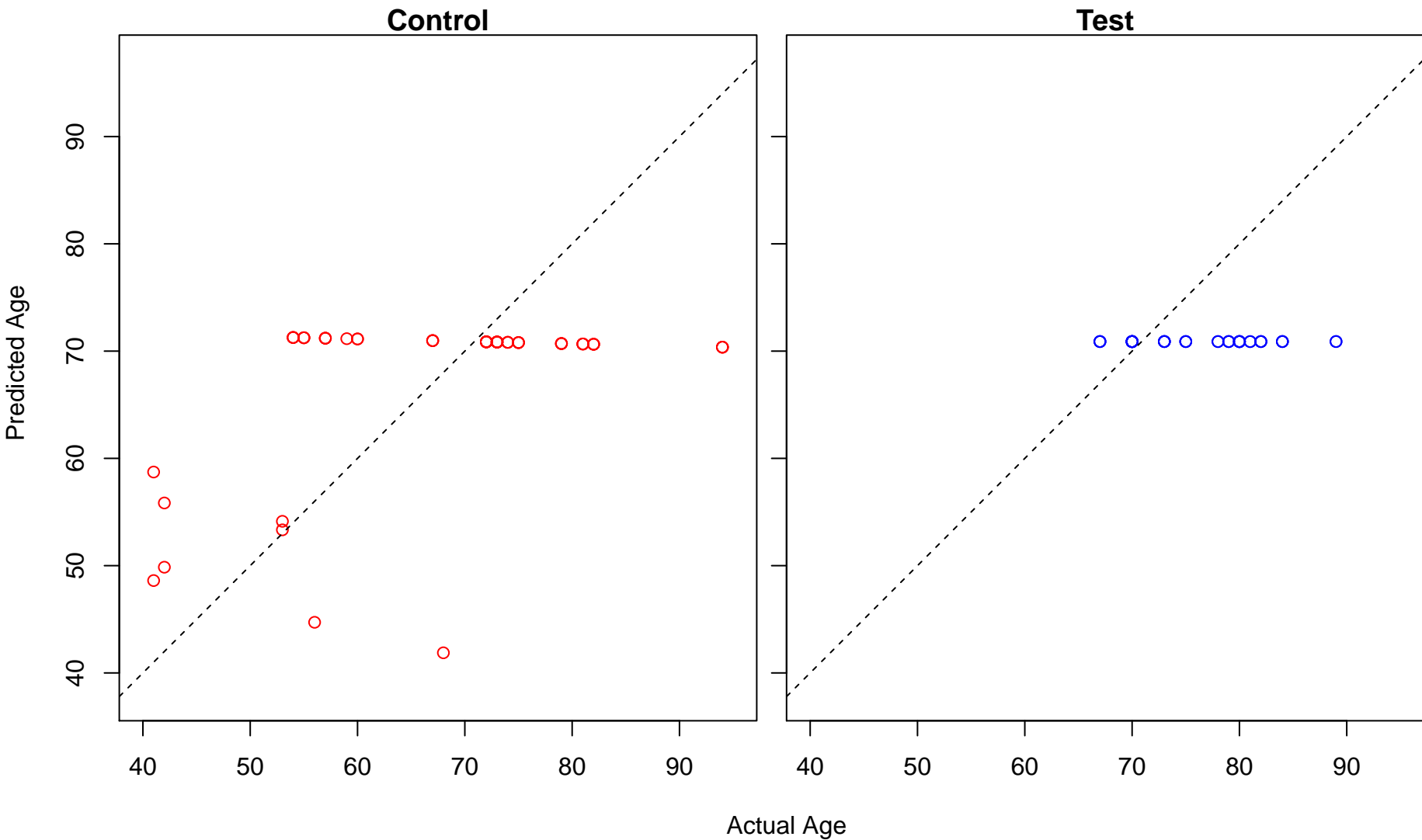
regulation of cytosolic calcium ion concentration (Score: 0.790525)



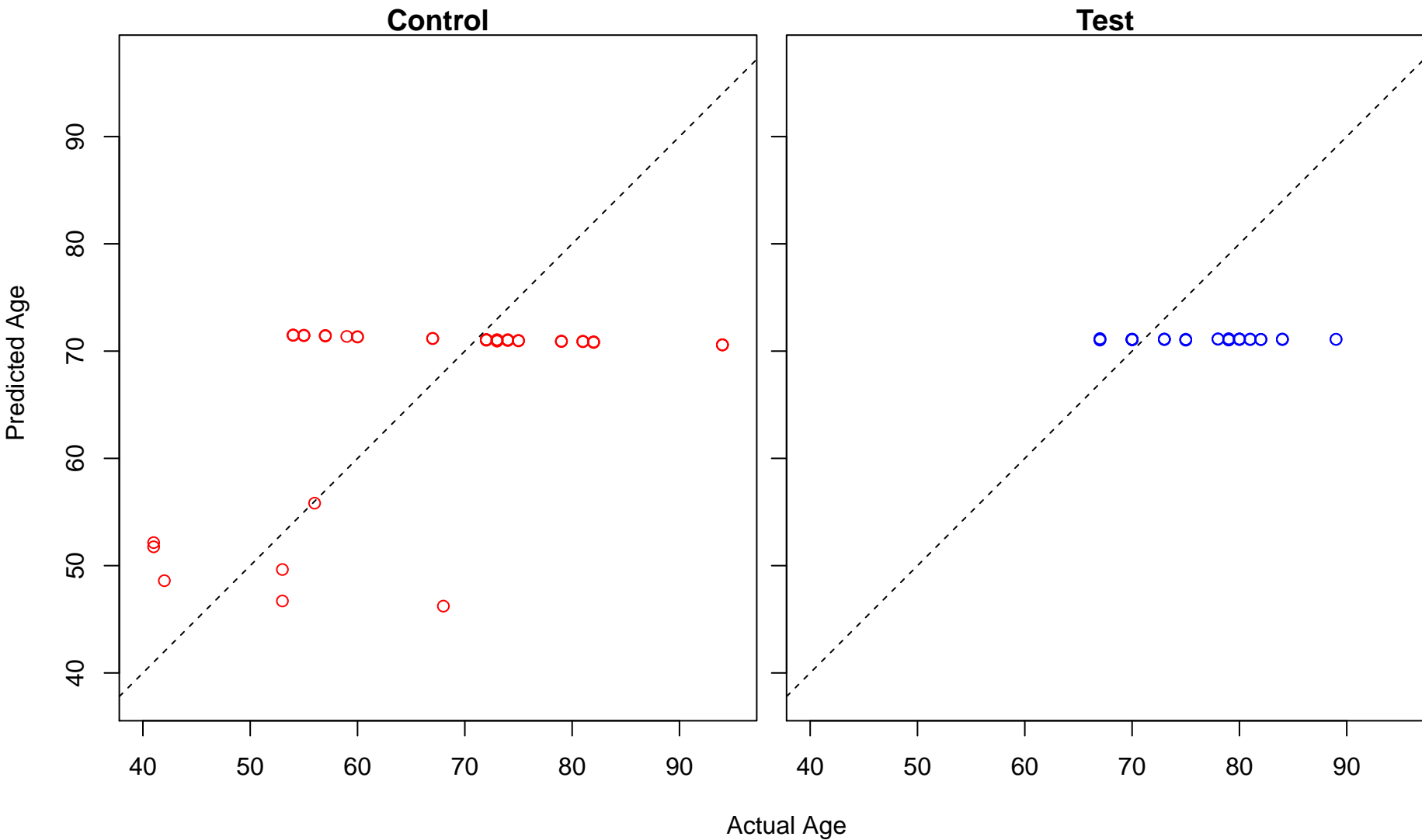
regulation of peptidyl–threonine phosphorylation (Score: 0.790508)



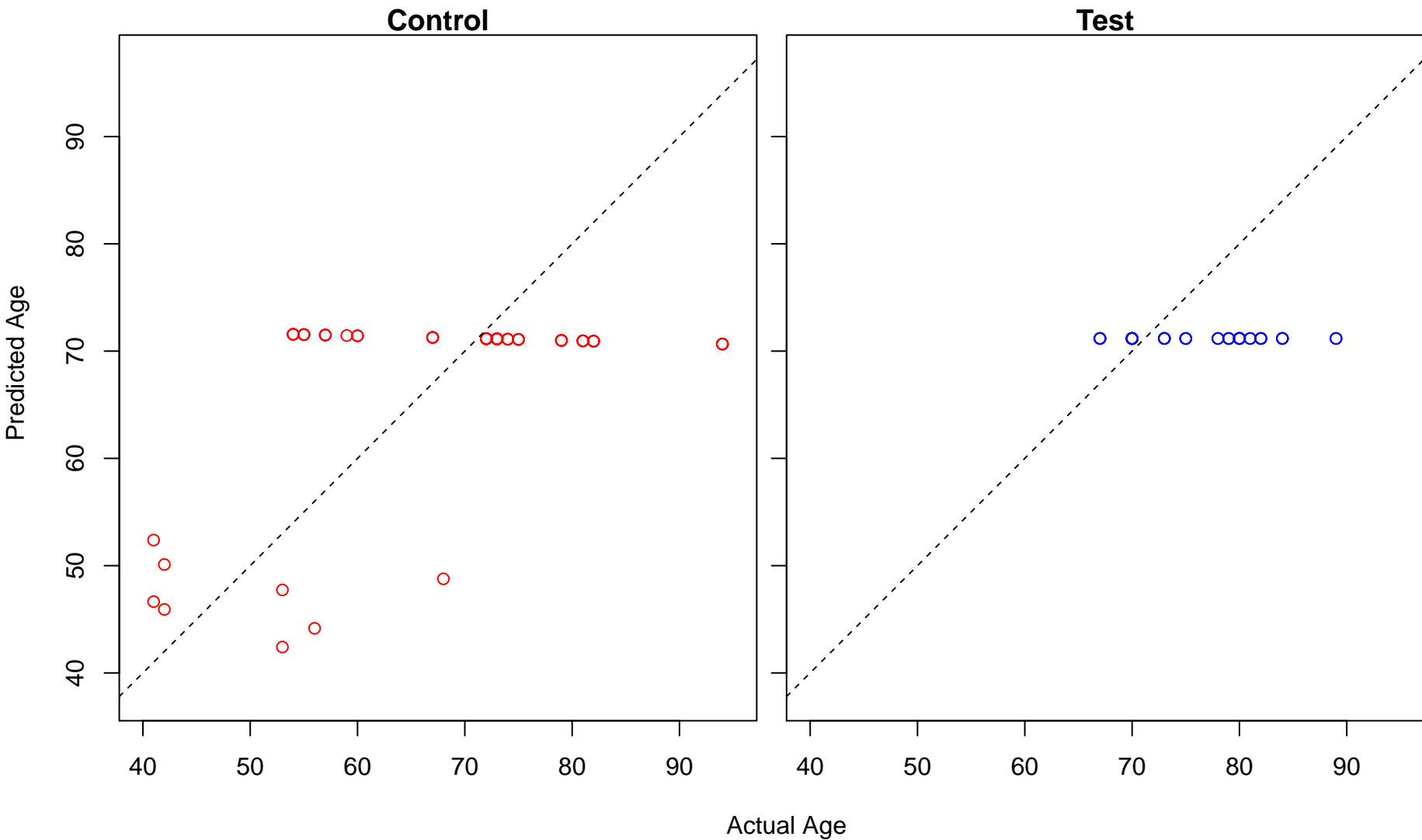
positive regulation of peptidyl–threonine phosphorylation (Score: 0.790508)



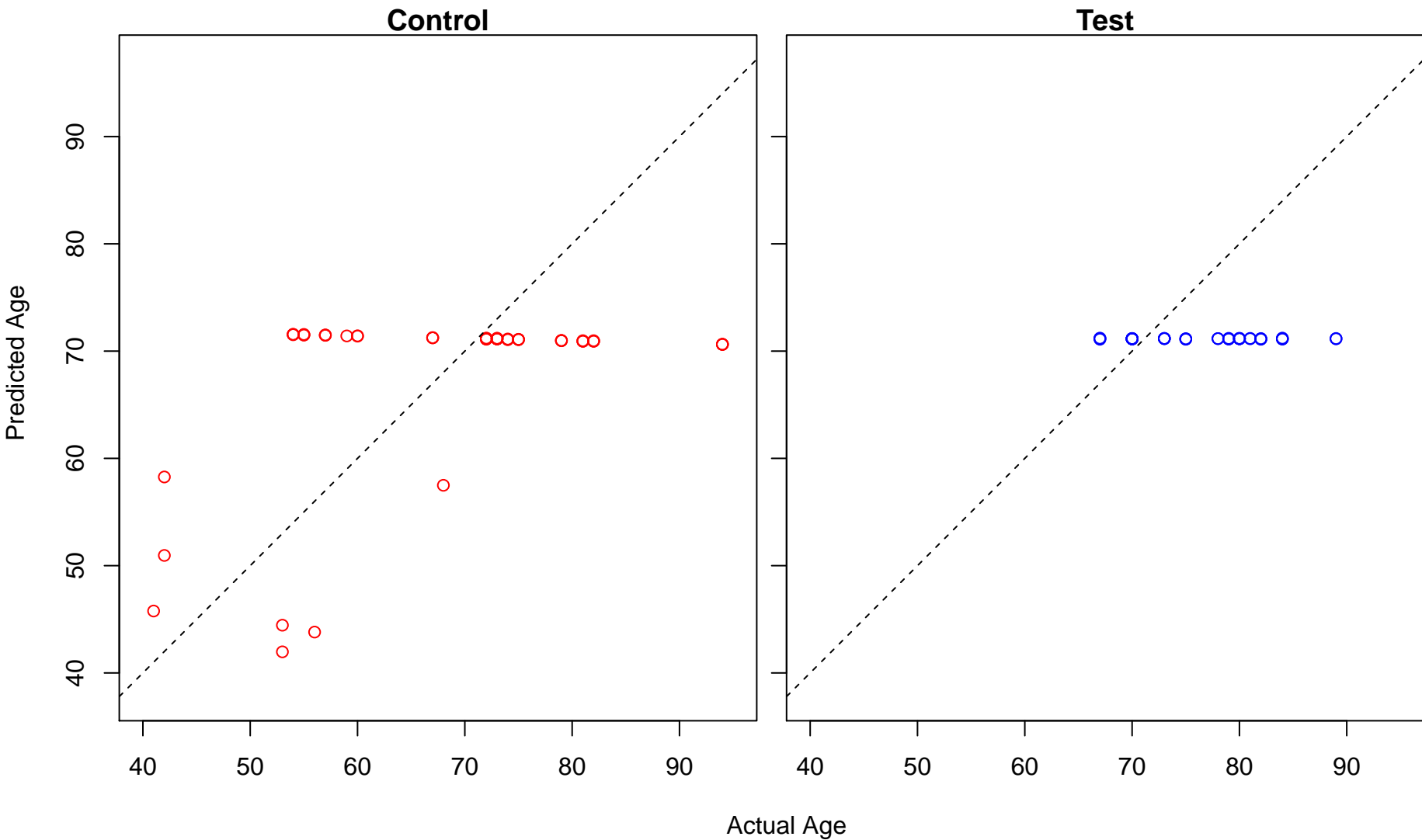
alternative mRNA splicing, via spliceosome (Score: 0.790495)



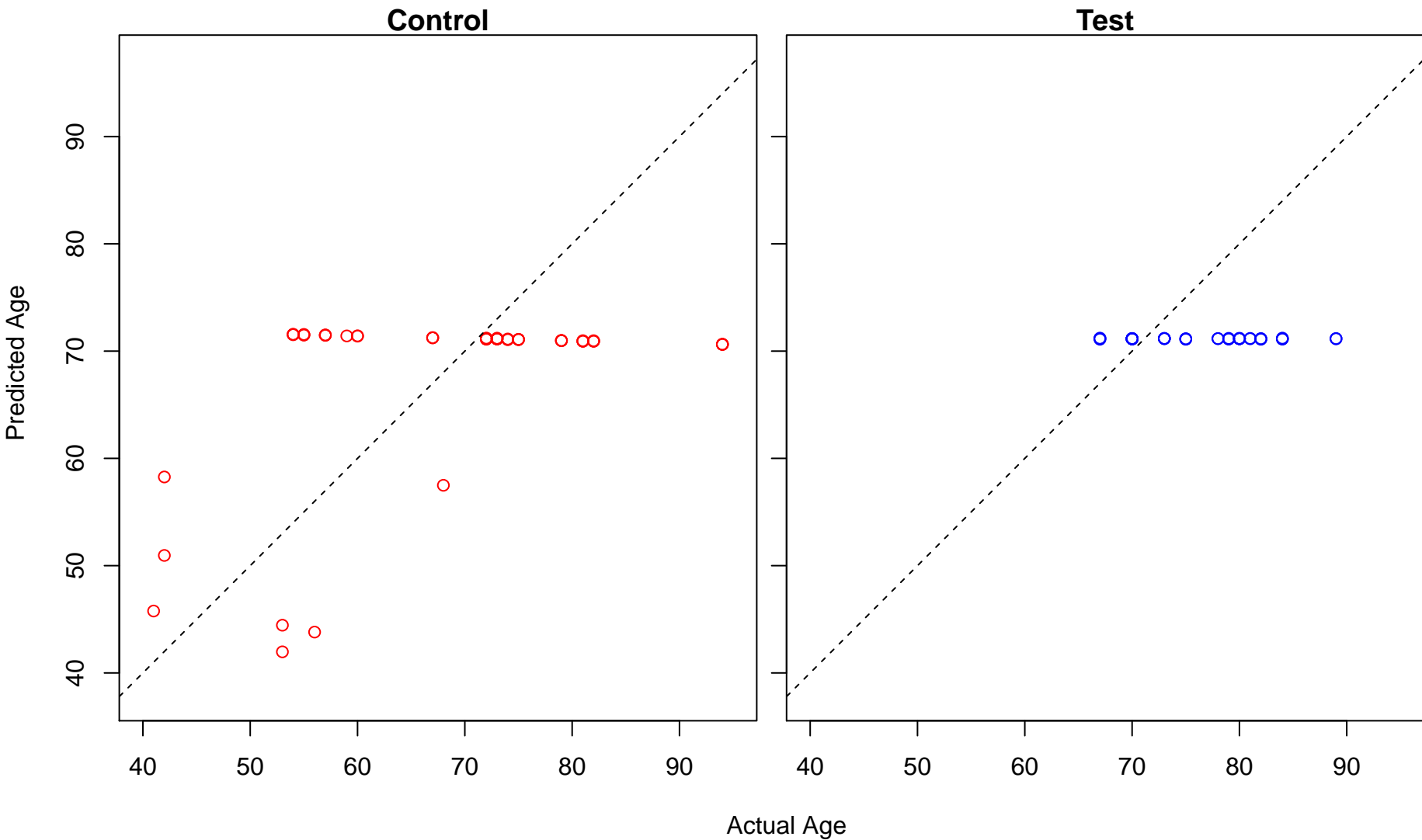
intracellular protein transport (Score: 0.790349)



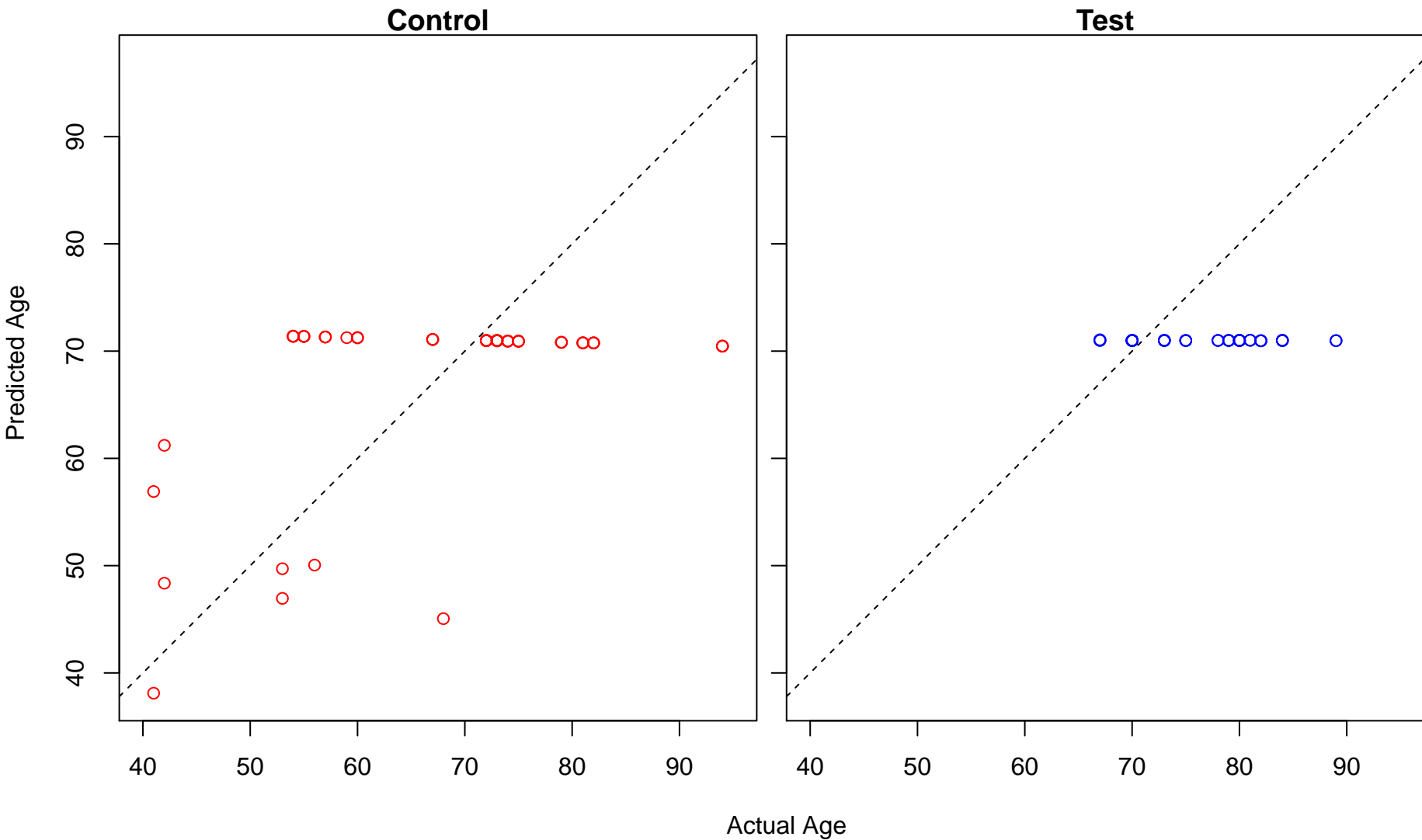
response to lipid (Score: 0.790297)



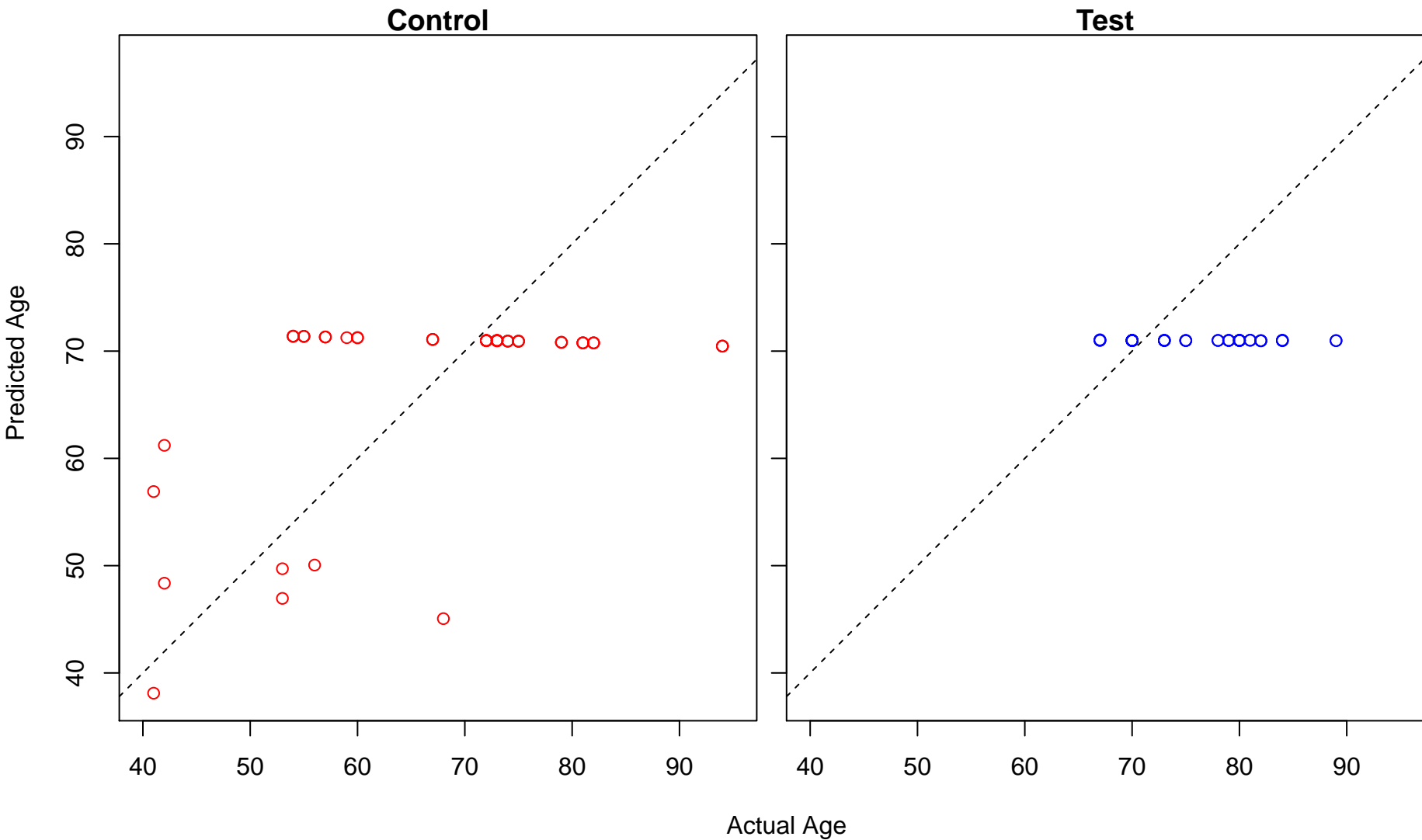
cellular response to lipid (Score: 0.790297)



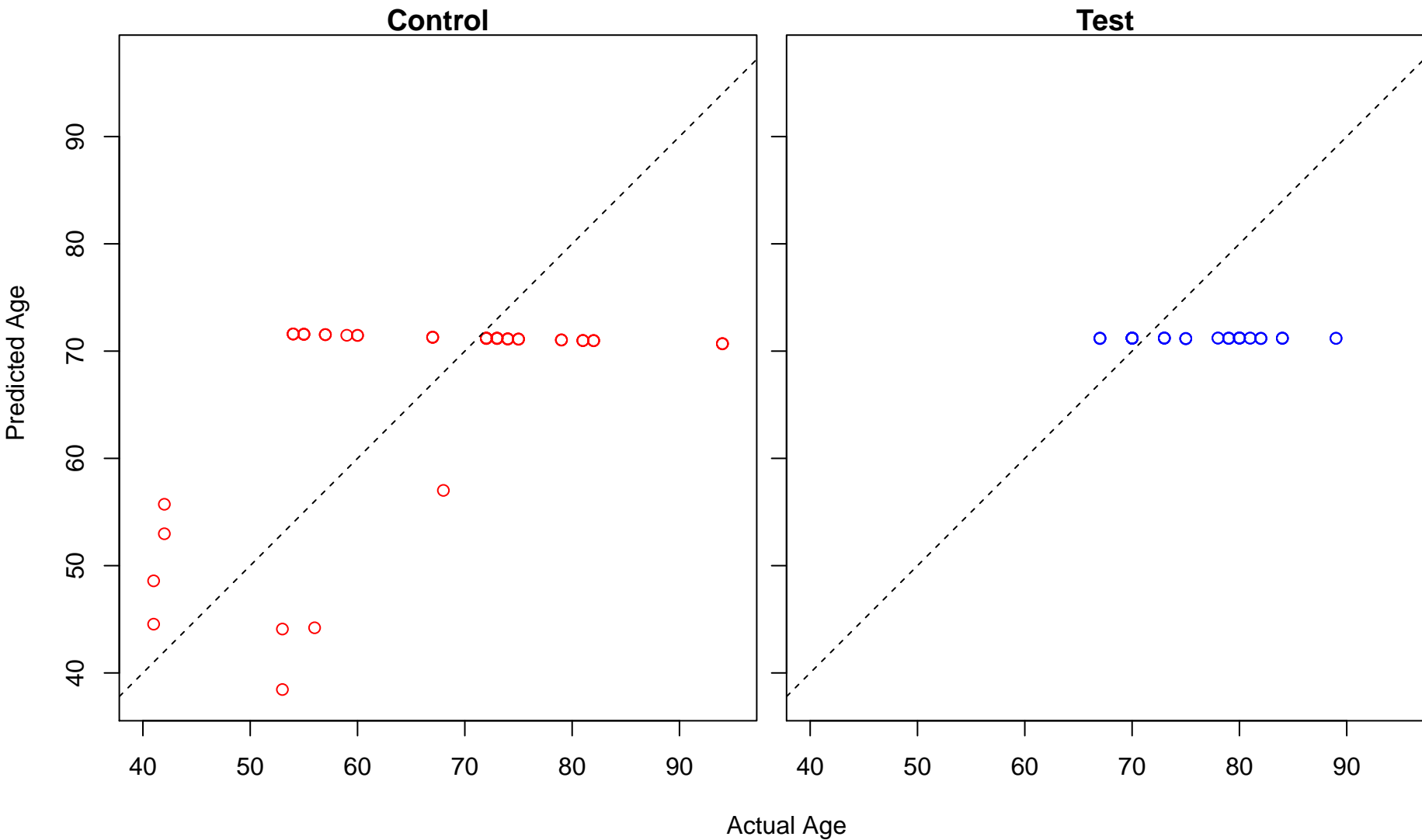
T cell activation (Score: 0.790237)



lymphocyte activation (Score: 0.790237)

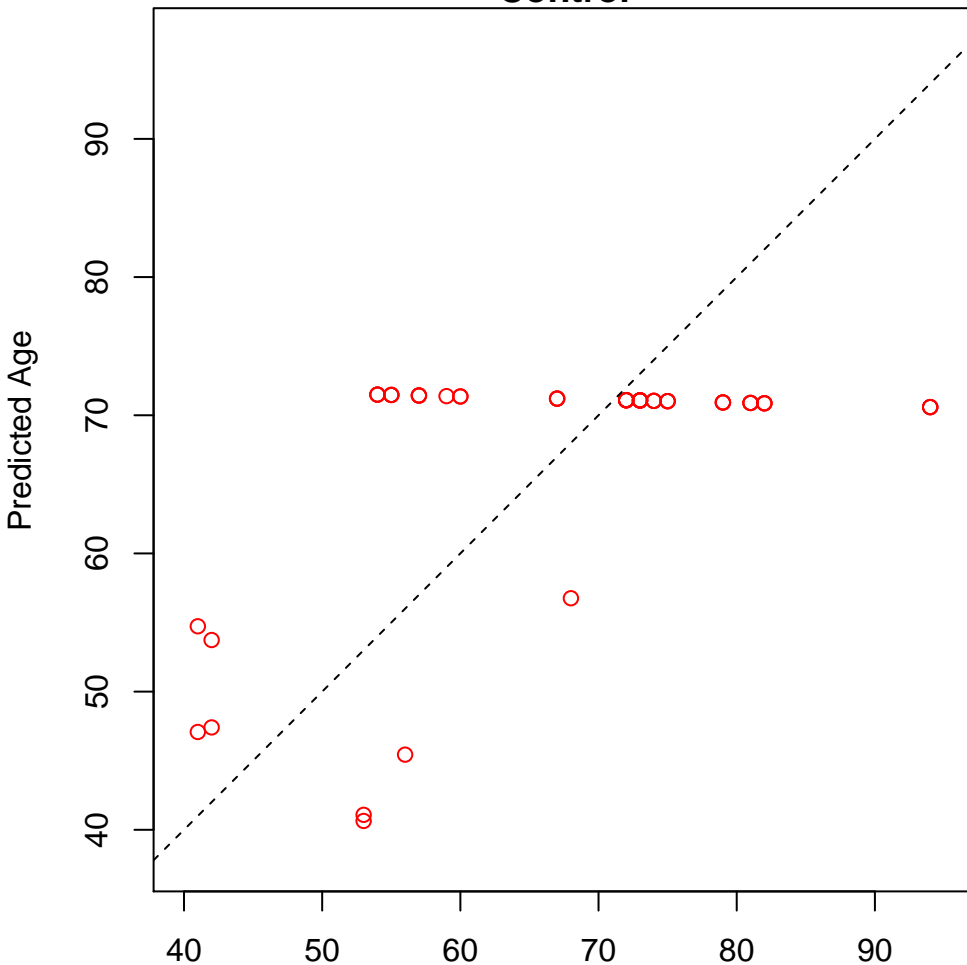


ER-nucleus signaling pathway (Score: 0.790150)

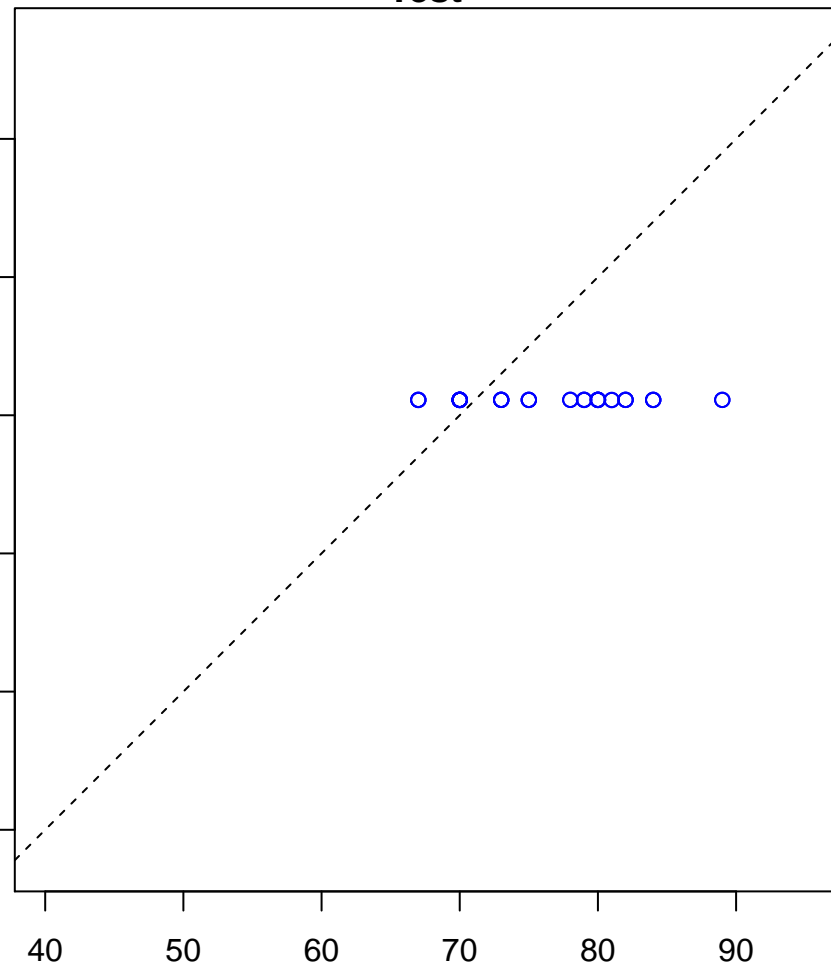


leukocyte differentiation (Score: 0.790082)

Control

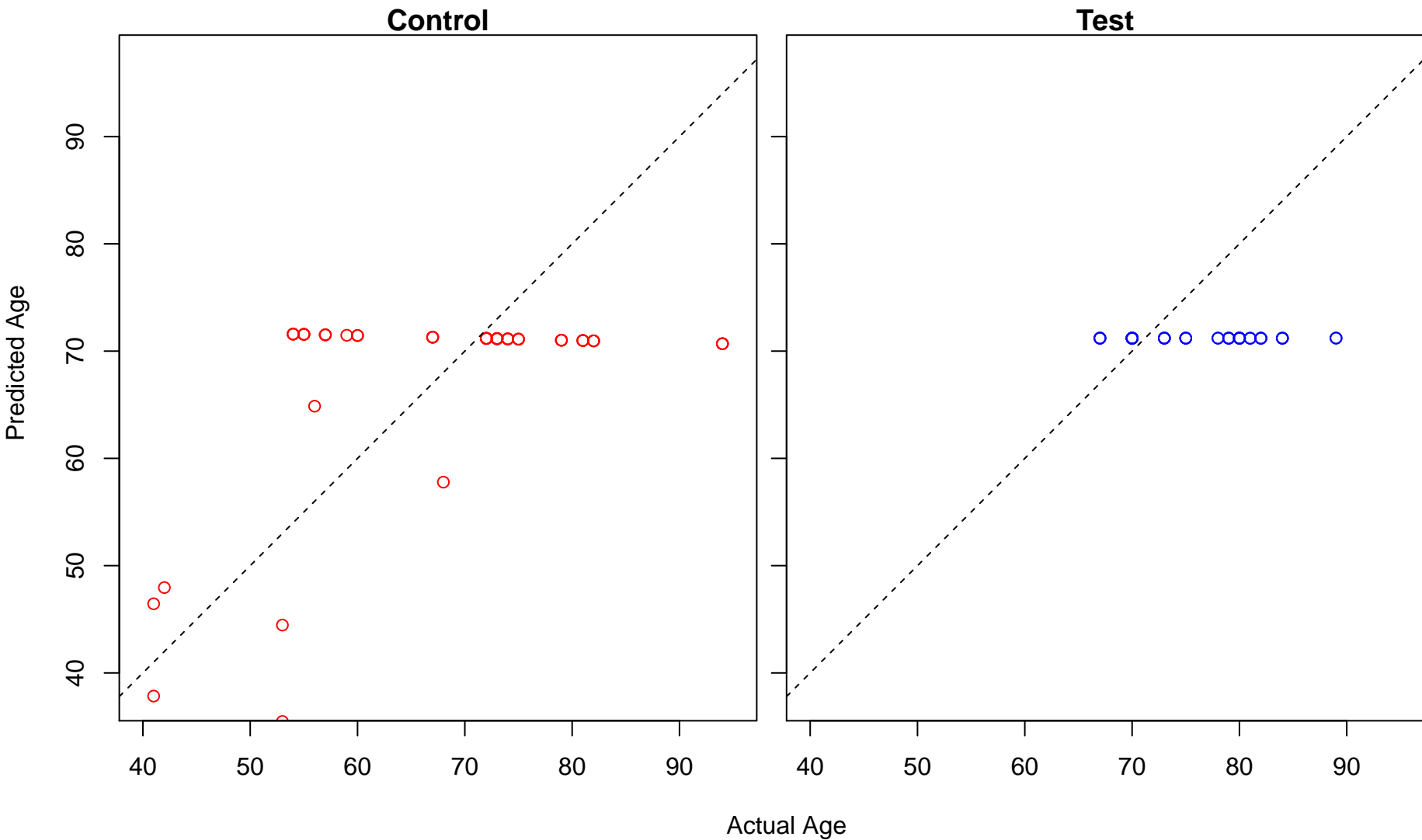


Test

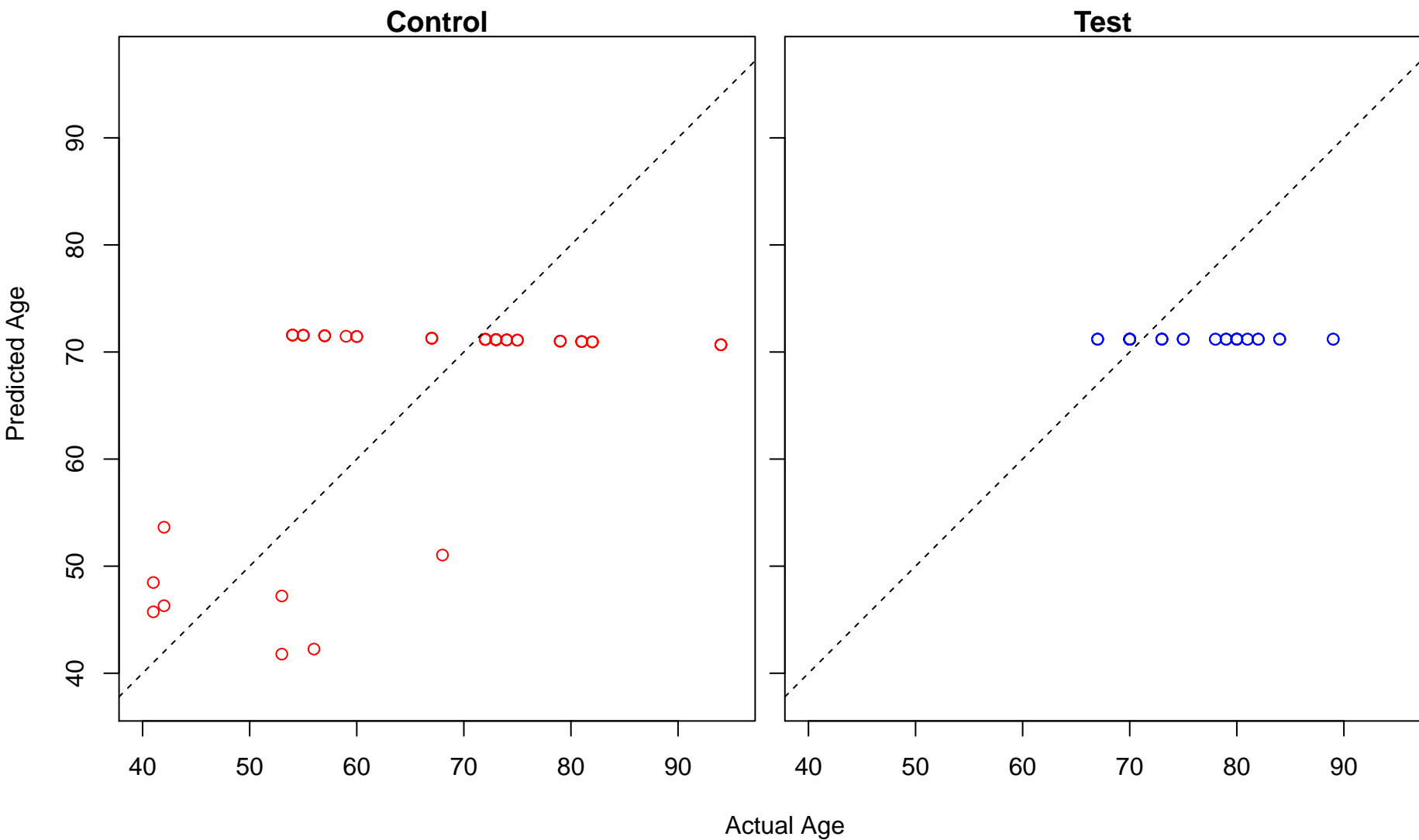


Actual Age

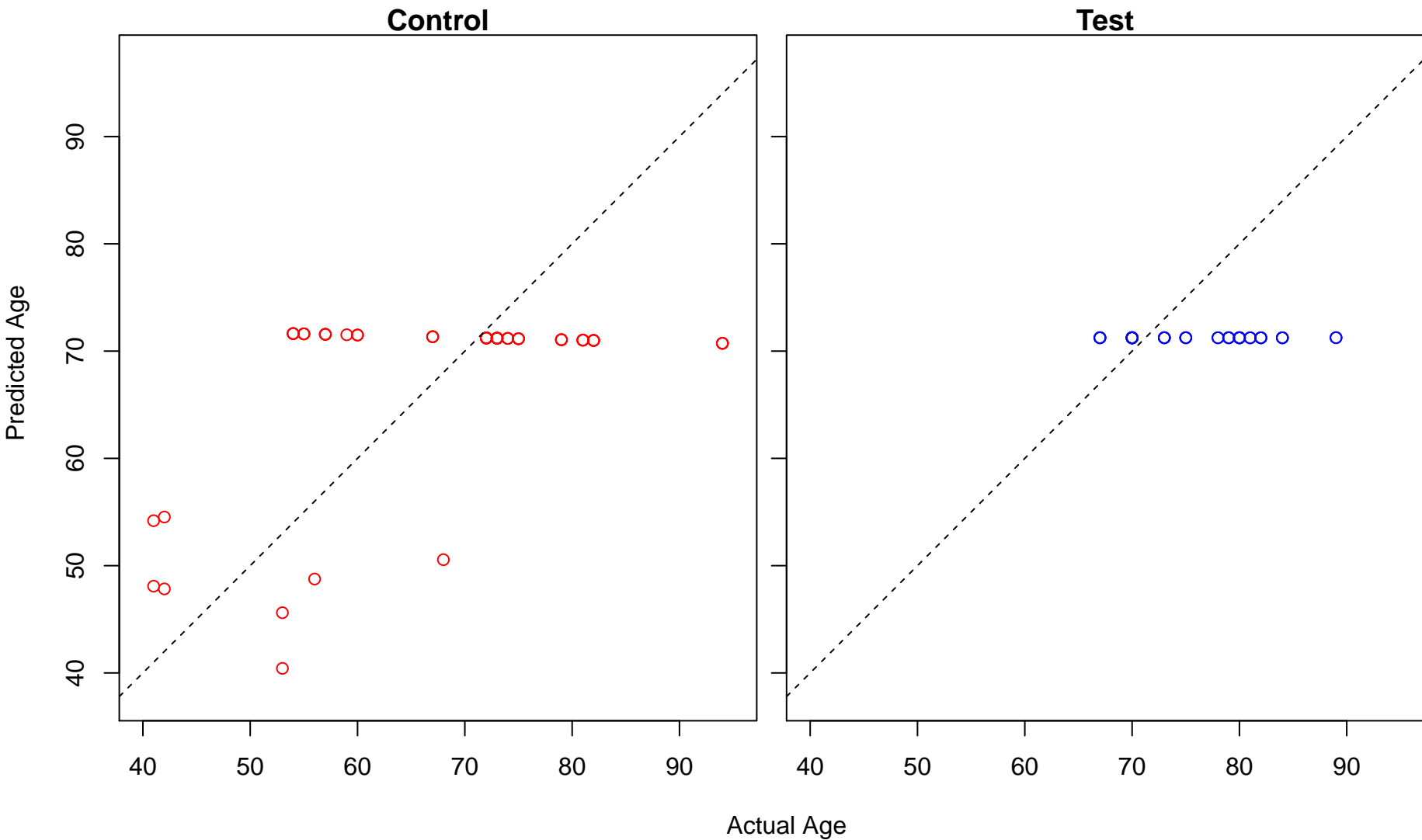
protein phosphorylation (Score: 0.790030)



response to stimulus (Score: 0.789994)

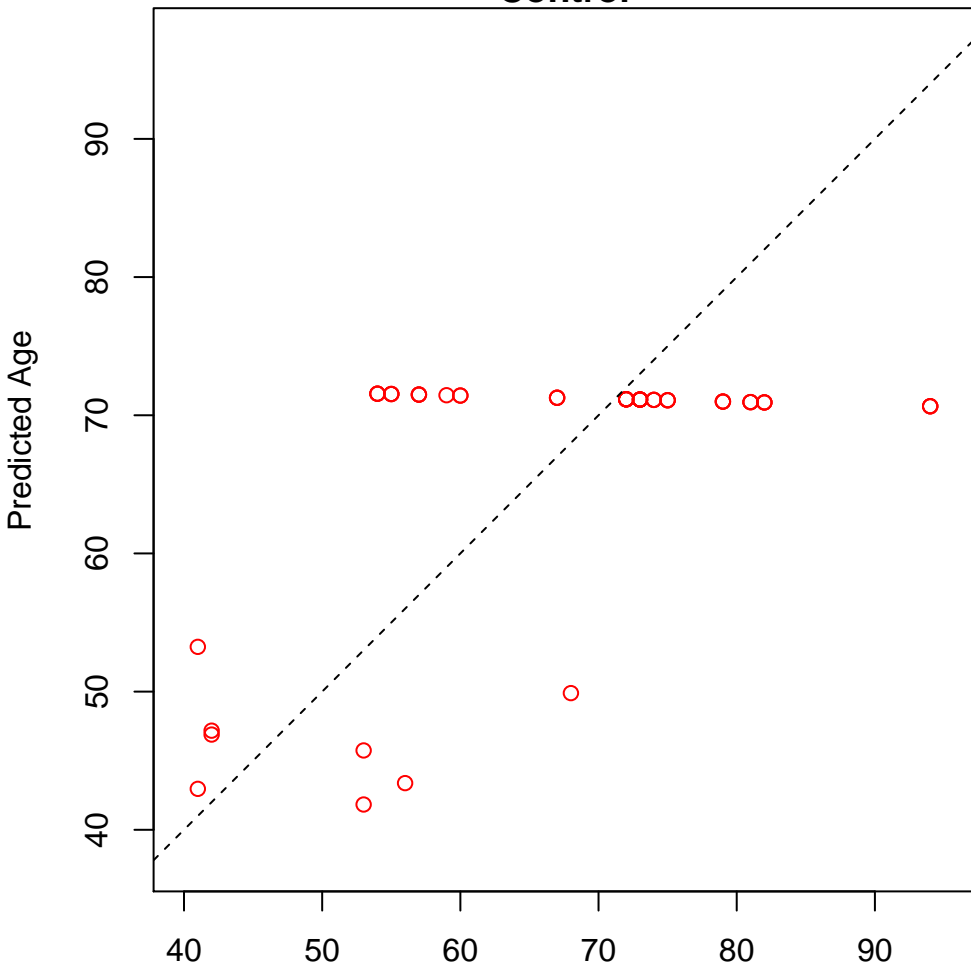


telomere maintenance (Score: 0.789854)

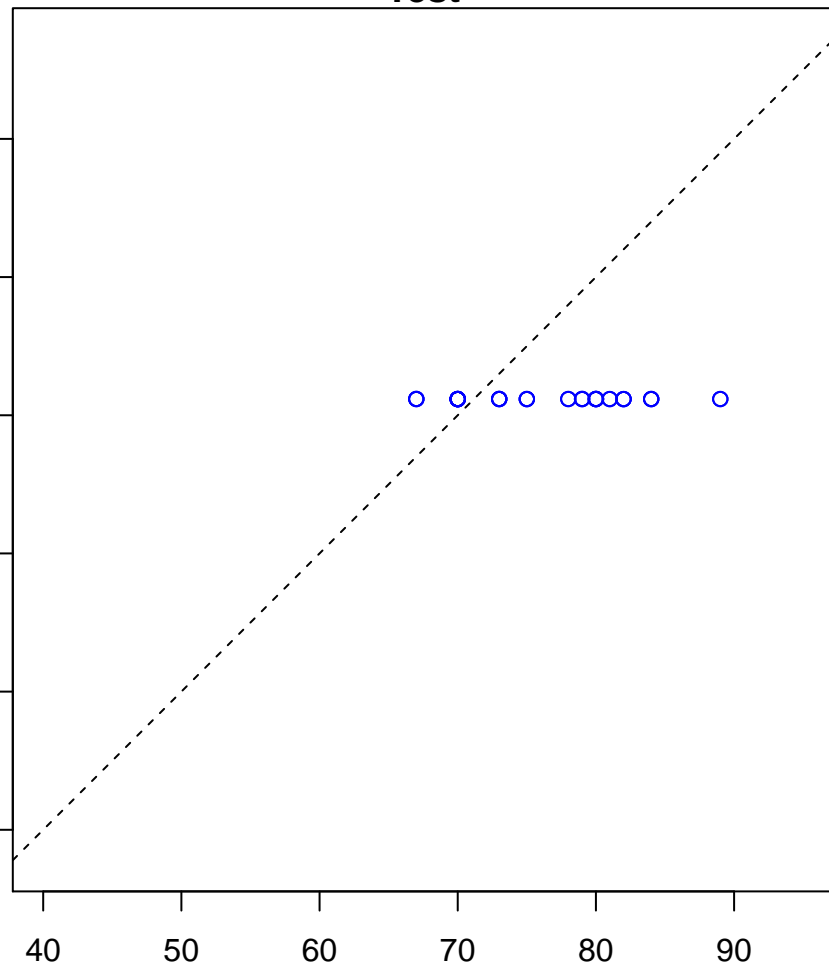


regulation of immune system process (Score: 0.789105)

Control



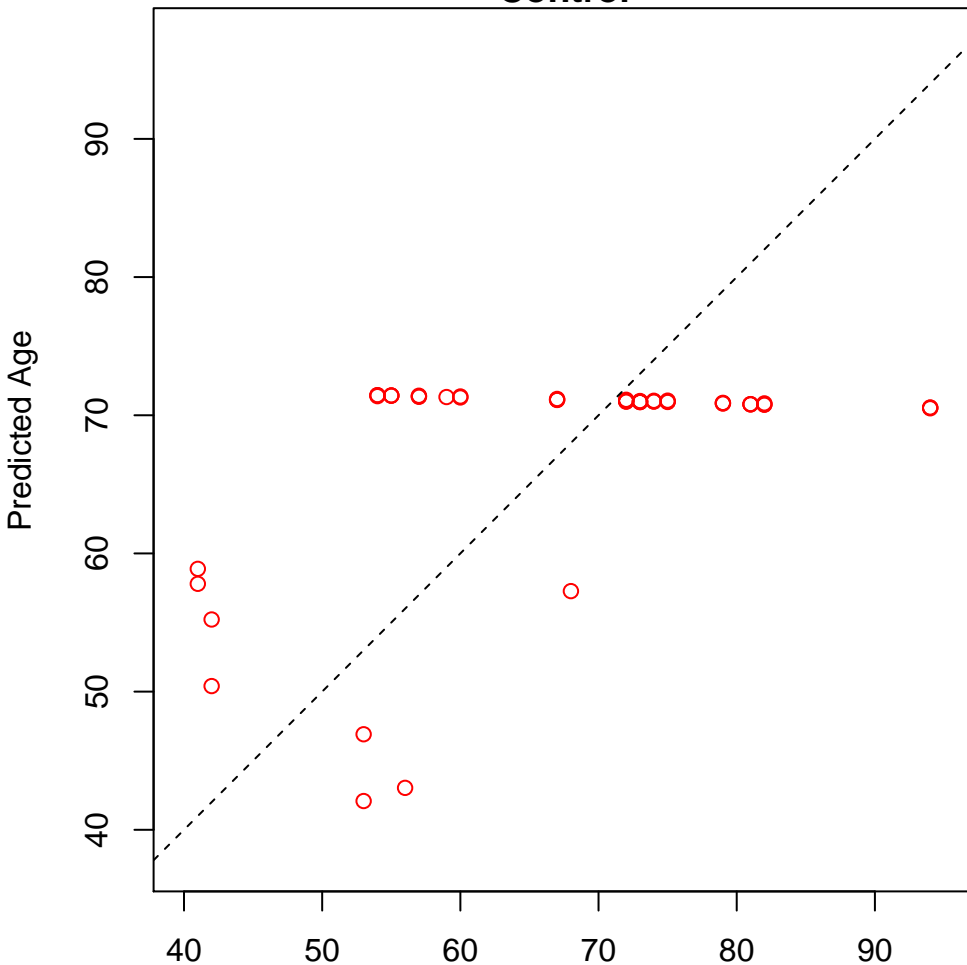
Test



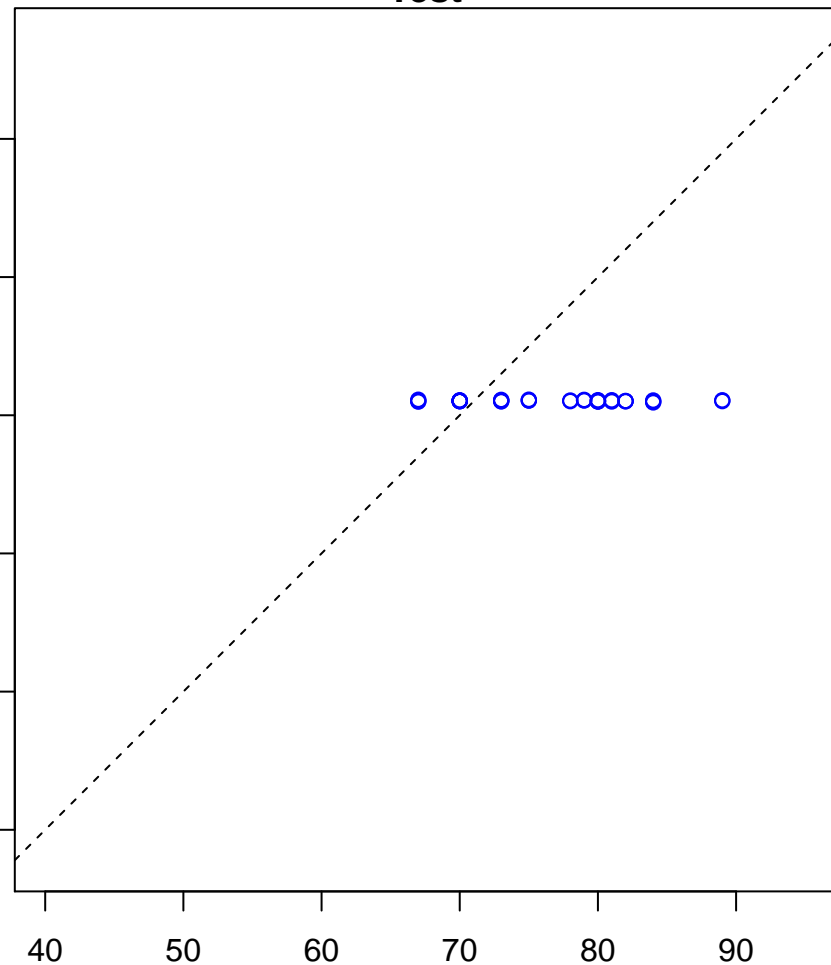
Actual Age

regulation of phospholipase activity (Score: 0.788779)

Control

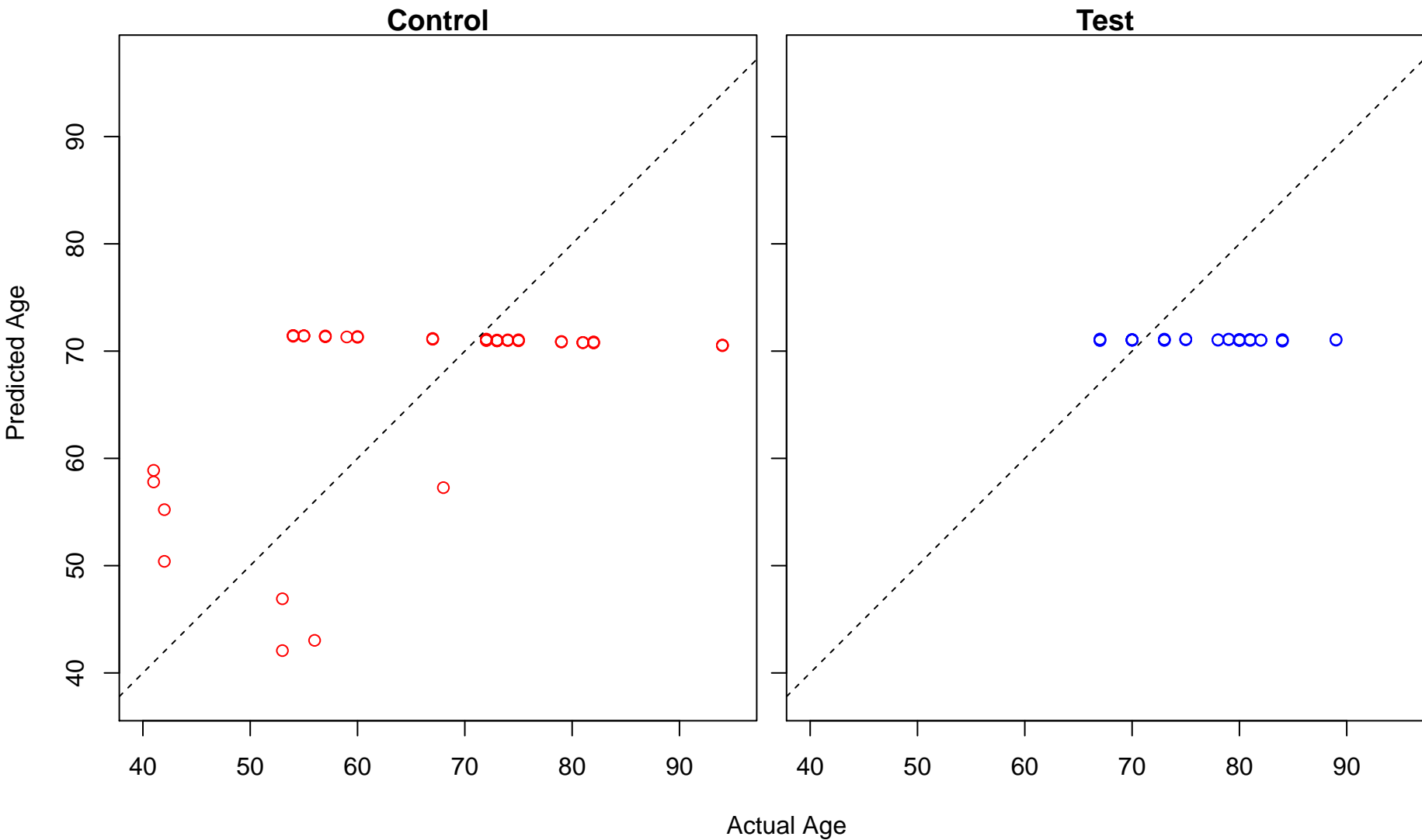


Test

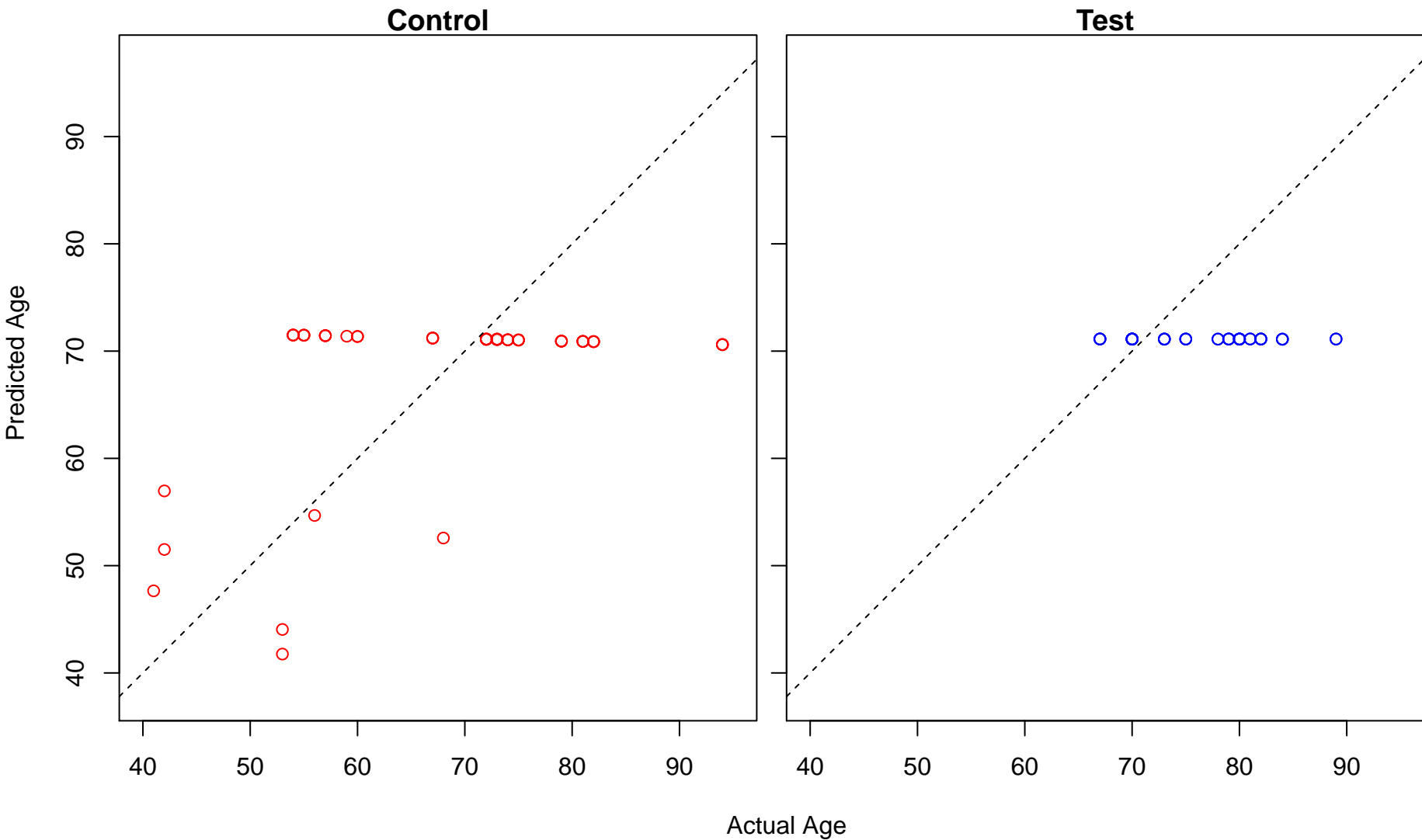


Actual Age

regulation of smooth muscle cell migration (Score: 0.788779)

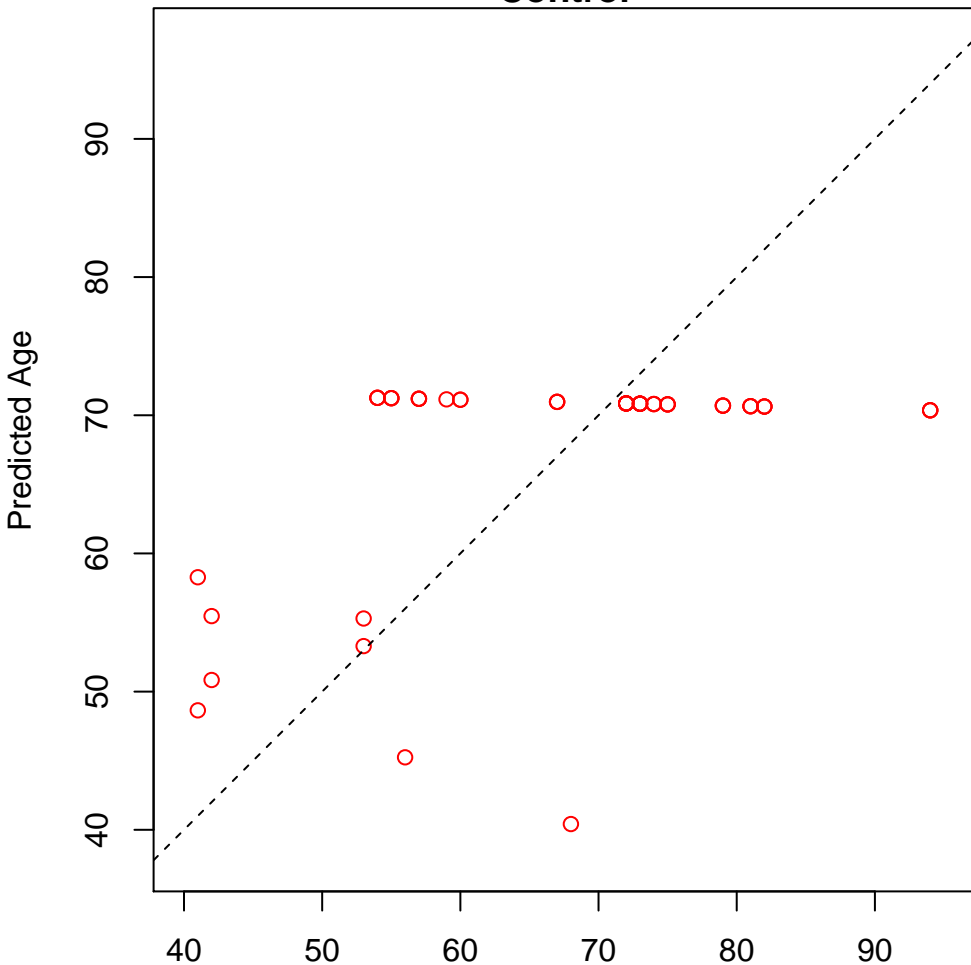


regulation of alternative mRNA splicing, via spliceosome (Score: 0.788710)

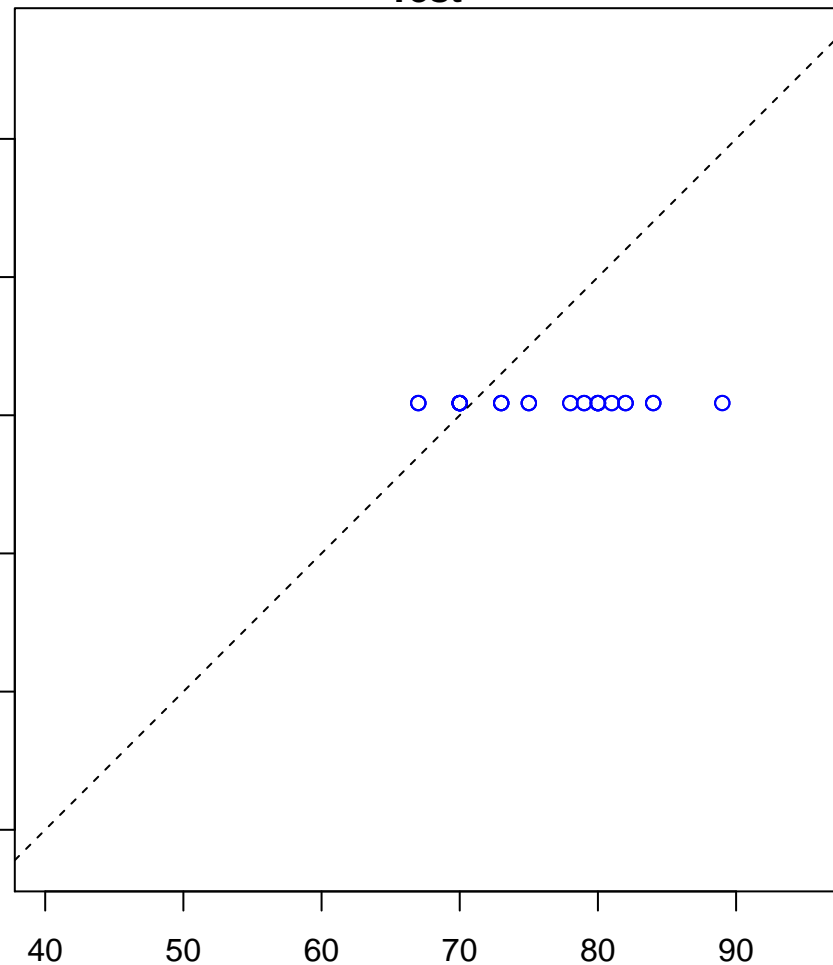


regulation of phosphatase activity (Score: 0.788376)

Control

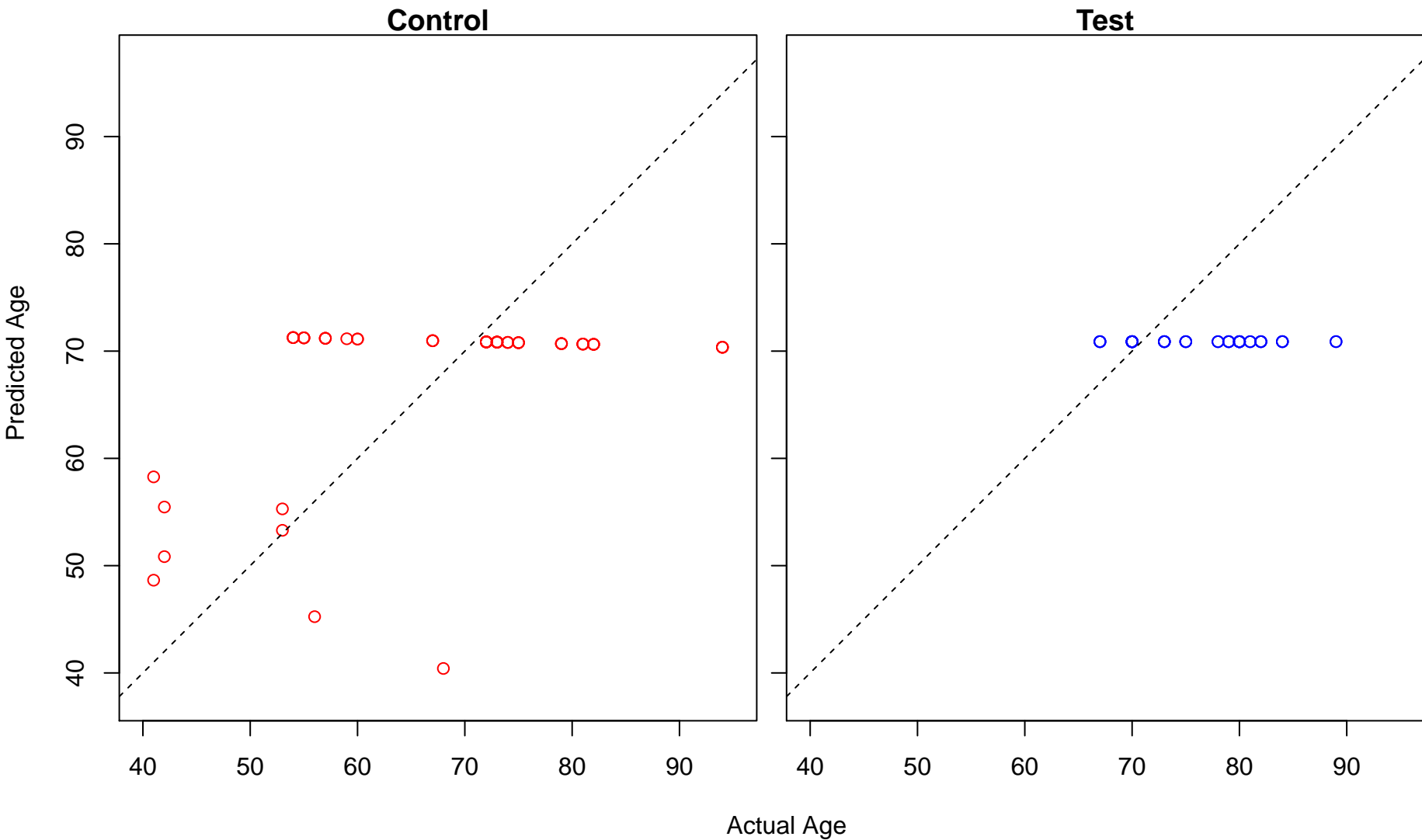


Test



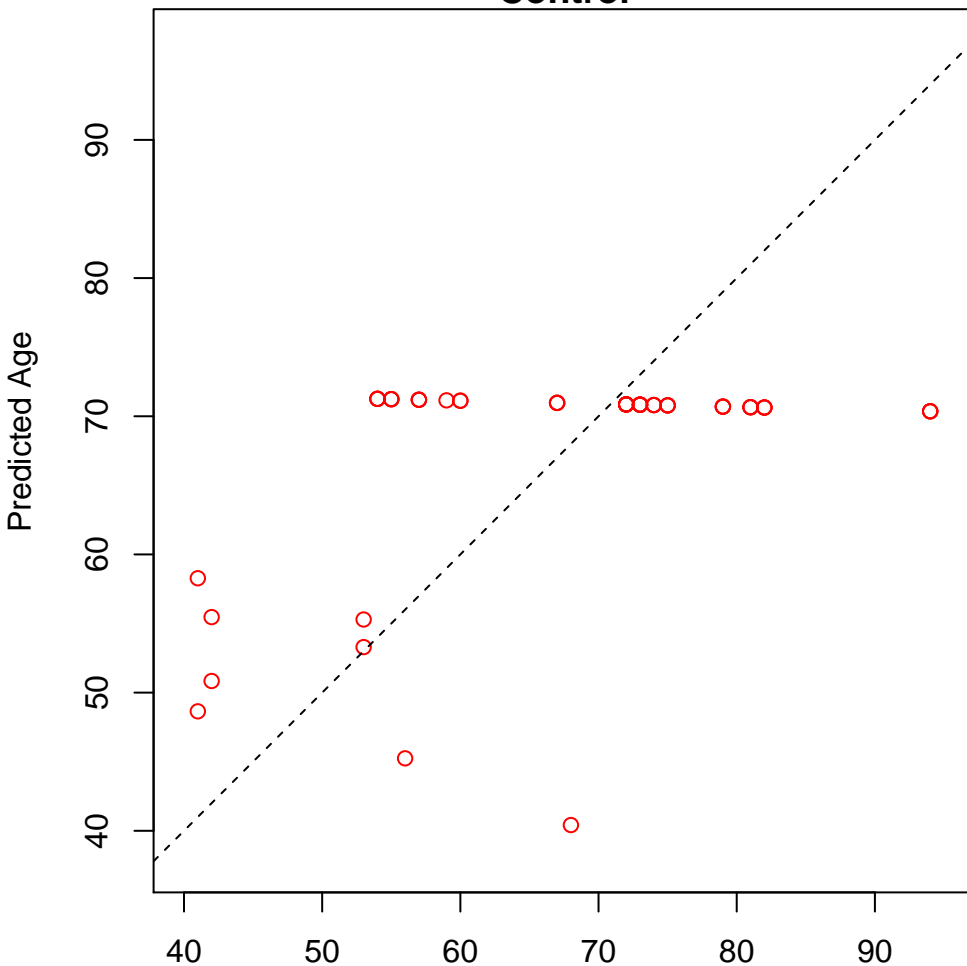
Actual Age

regulation of dephosphorylation (Score: 0.788376)

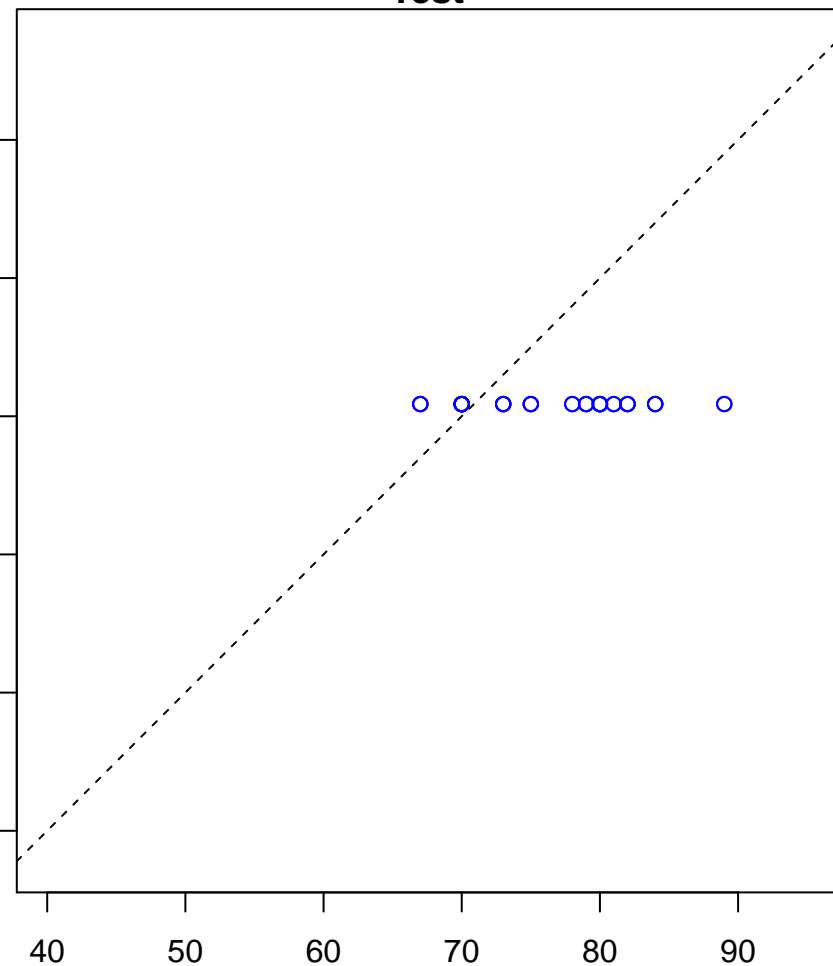


regulation of protein dephosphorylation (Score: 0.788376)

Control

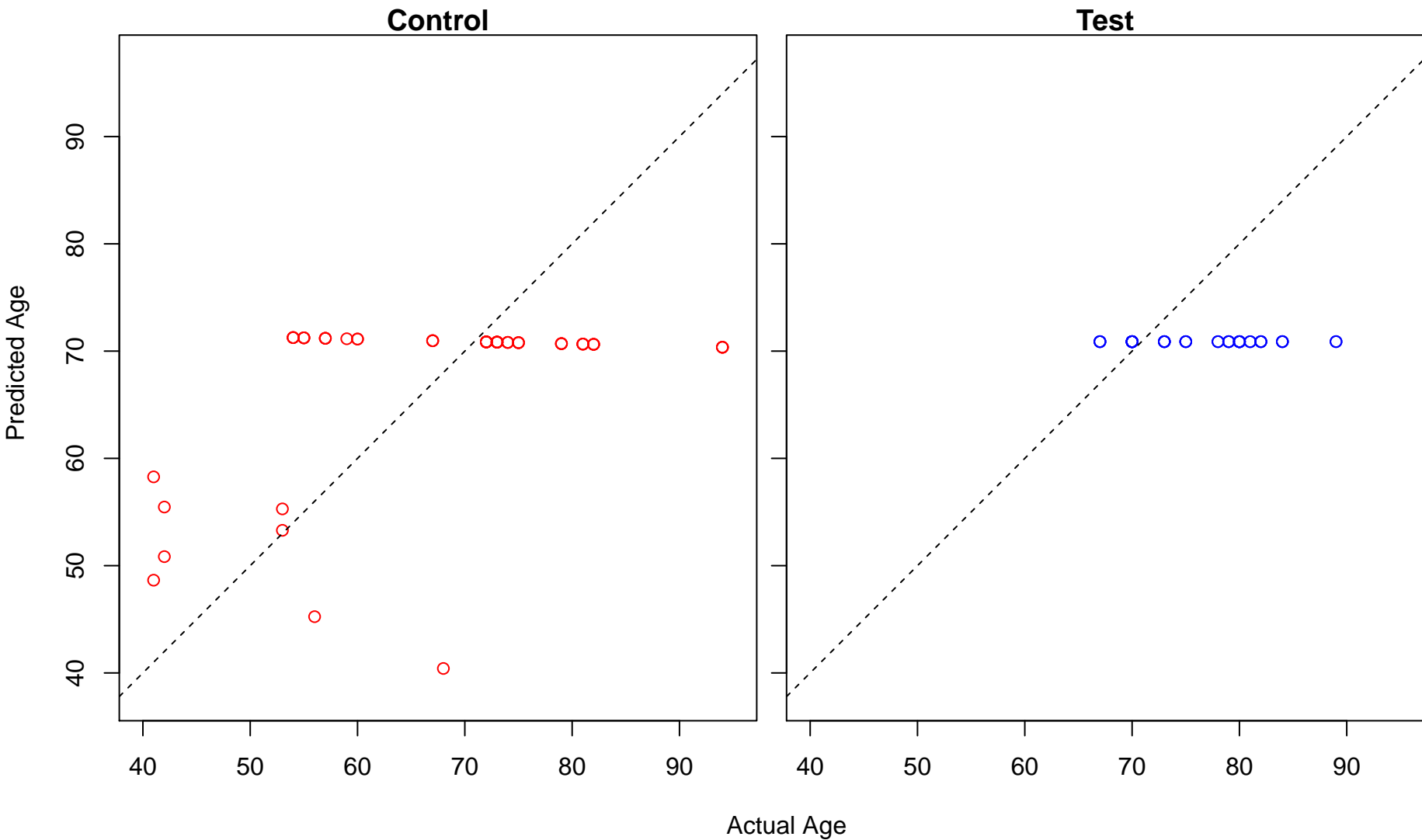


Test

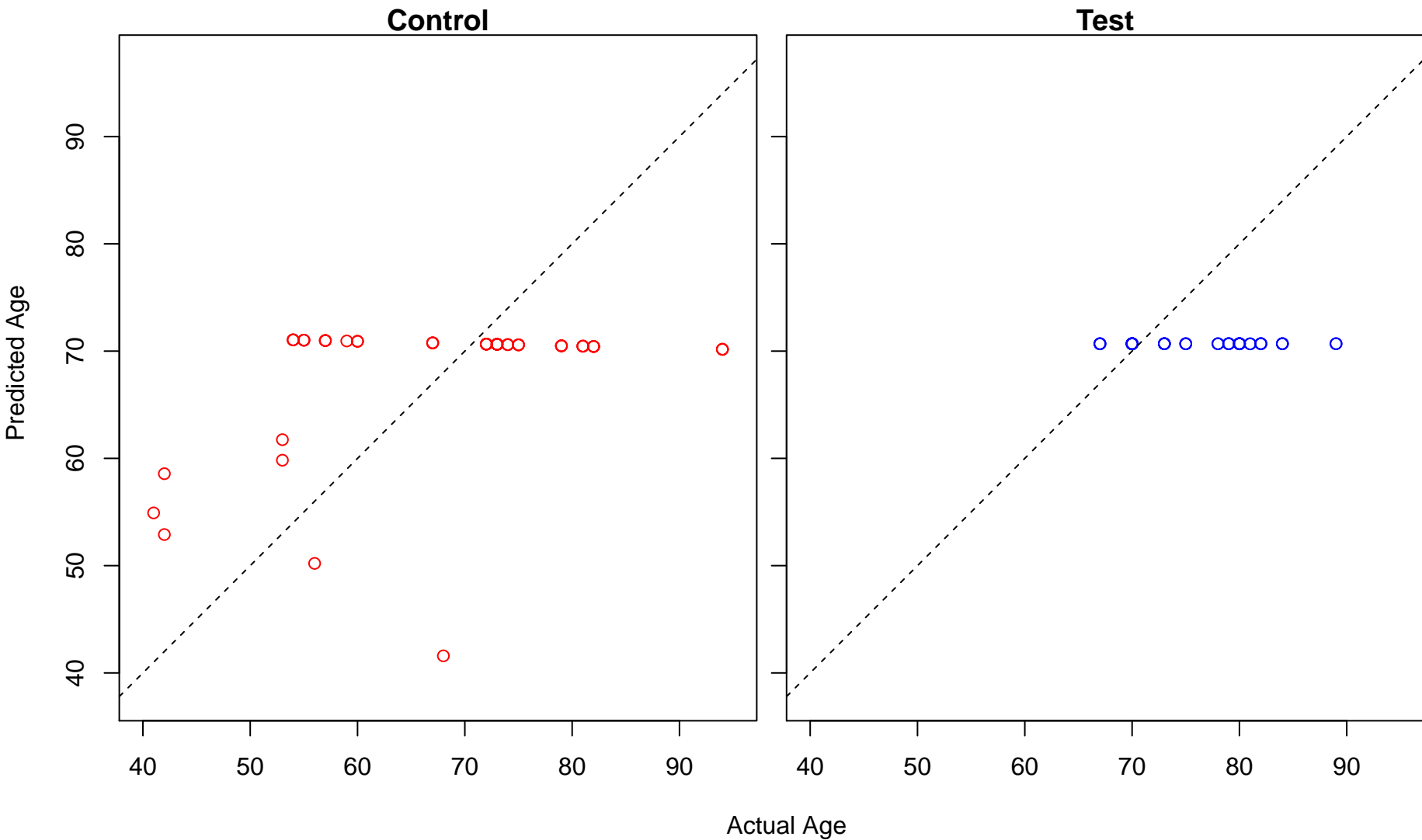


Actual Age

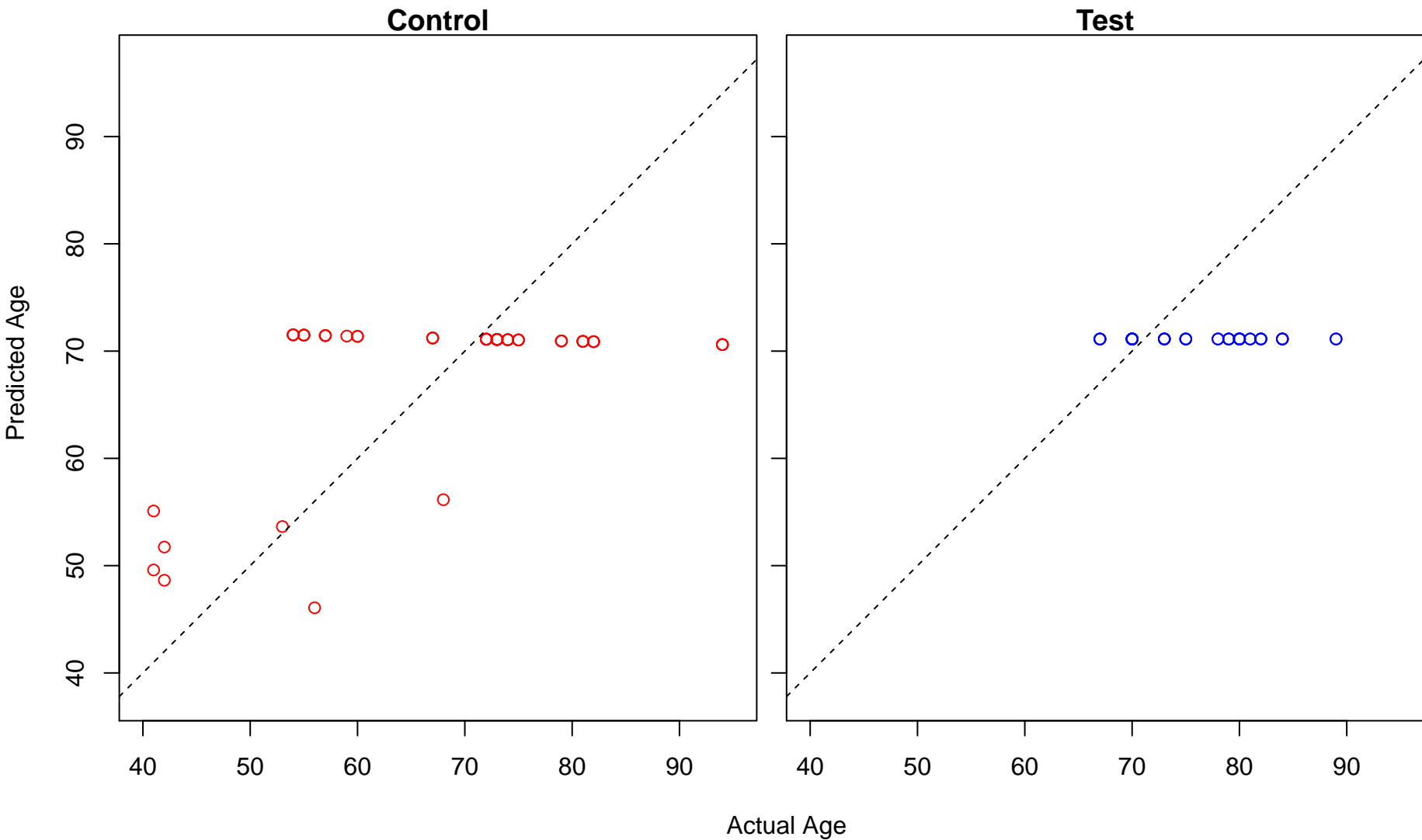
regulation of phosphoprotein phosphatase activity (Score: 0.788376)



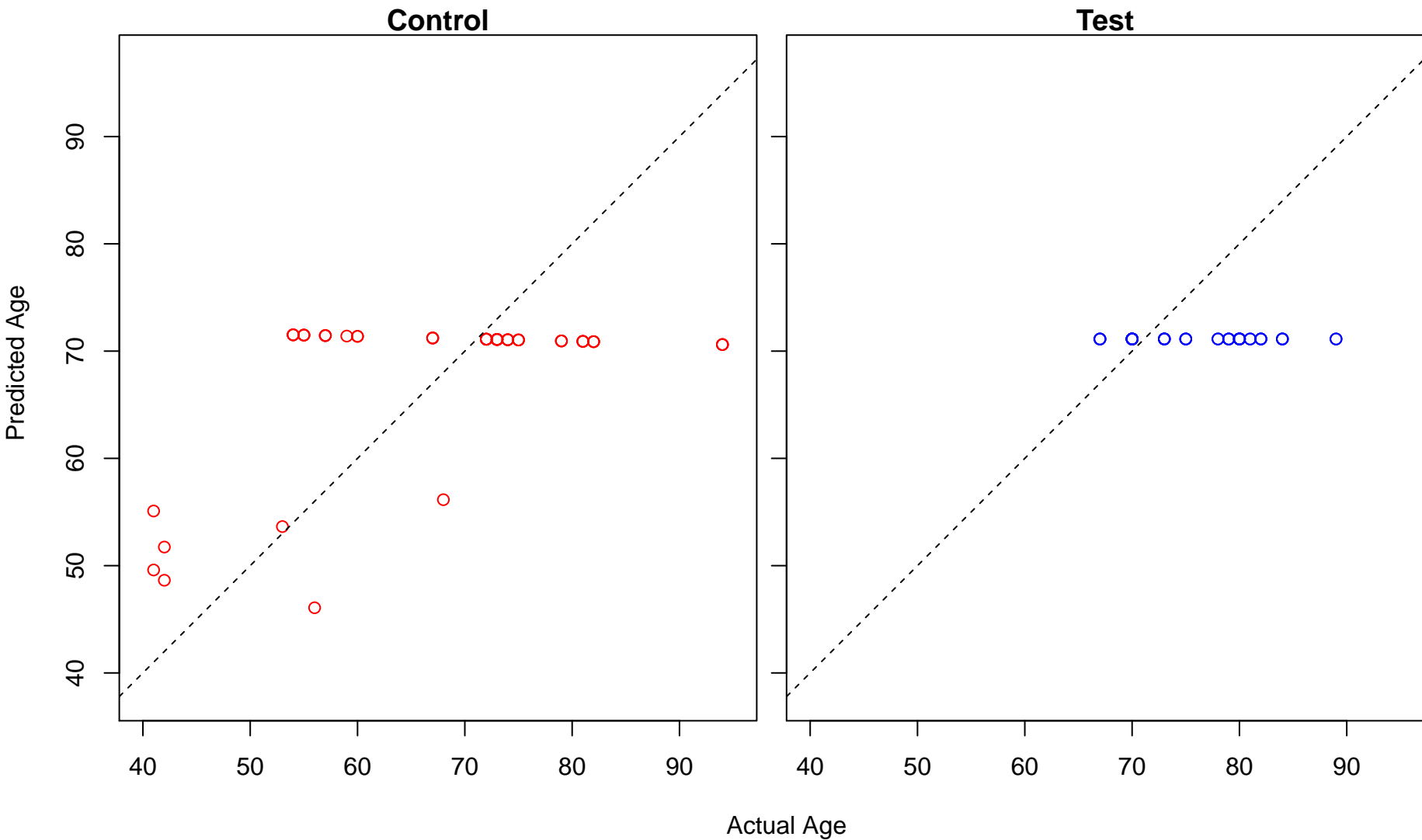
Golgi organization (Score: 0.788347)



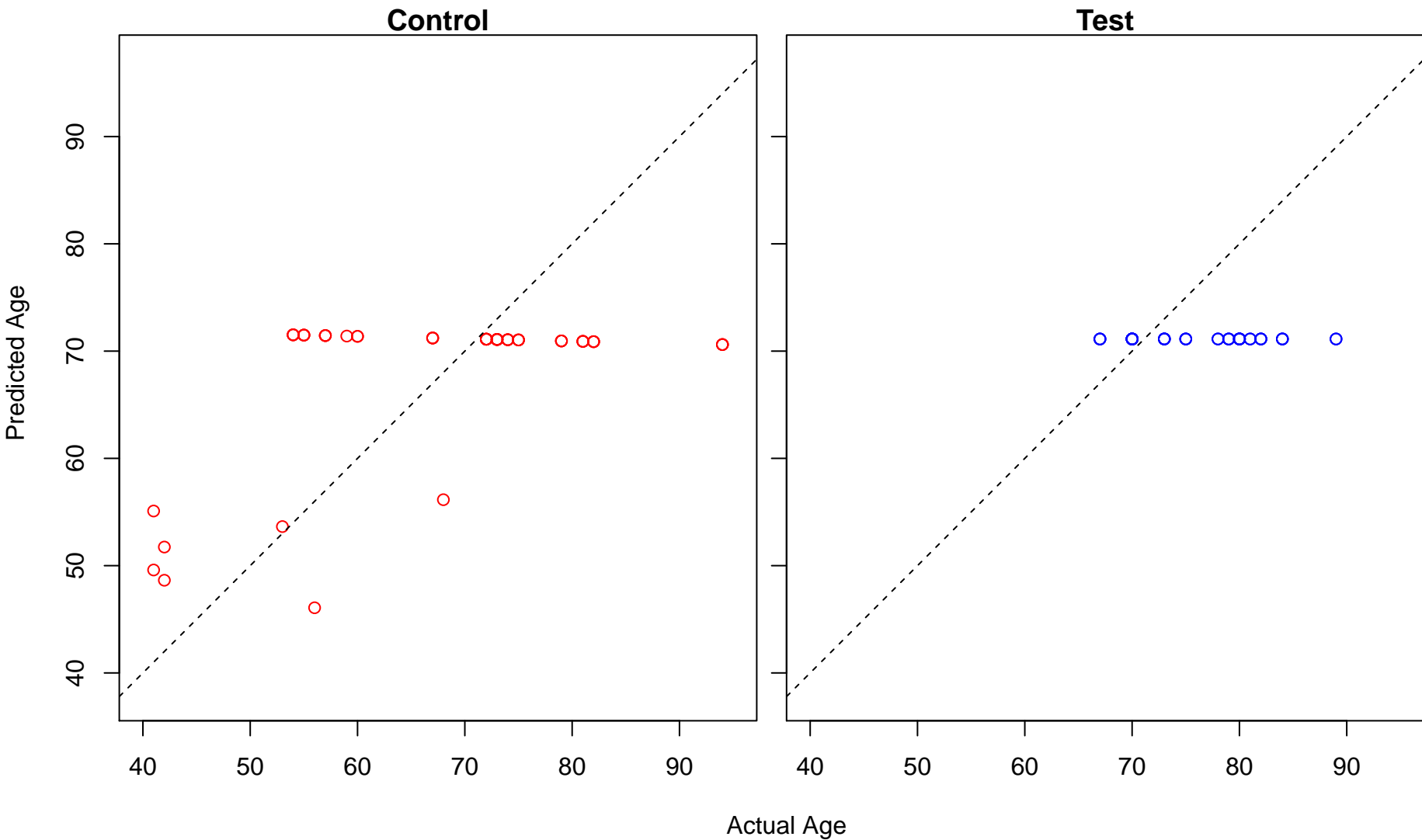
regulation of nucleotide metabolic process (Score: 0.788233)



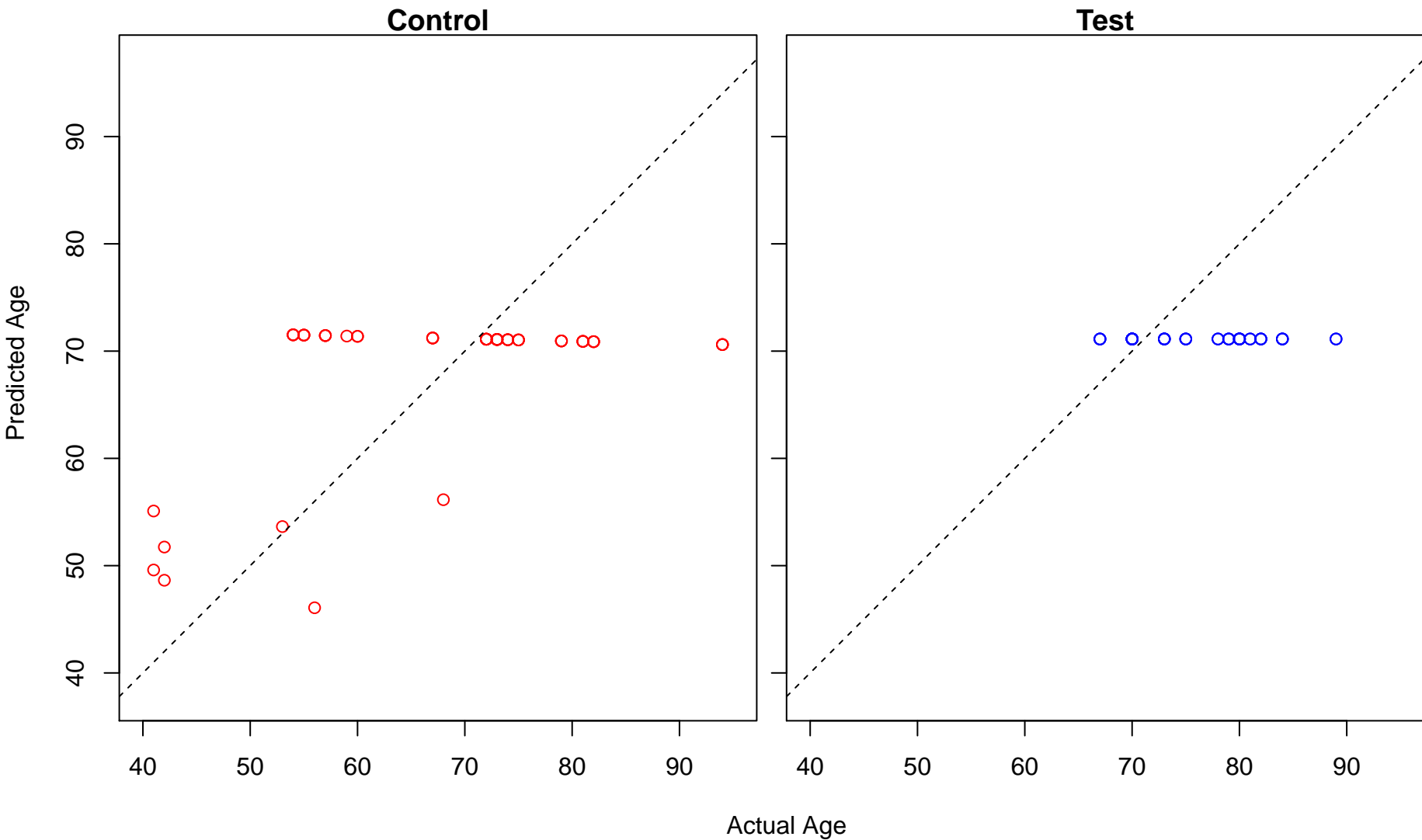
positive regulation of nucleotide metabolic process (Score: 0.788233)



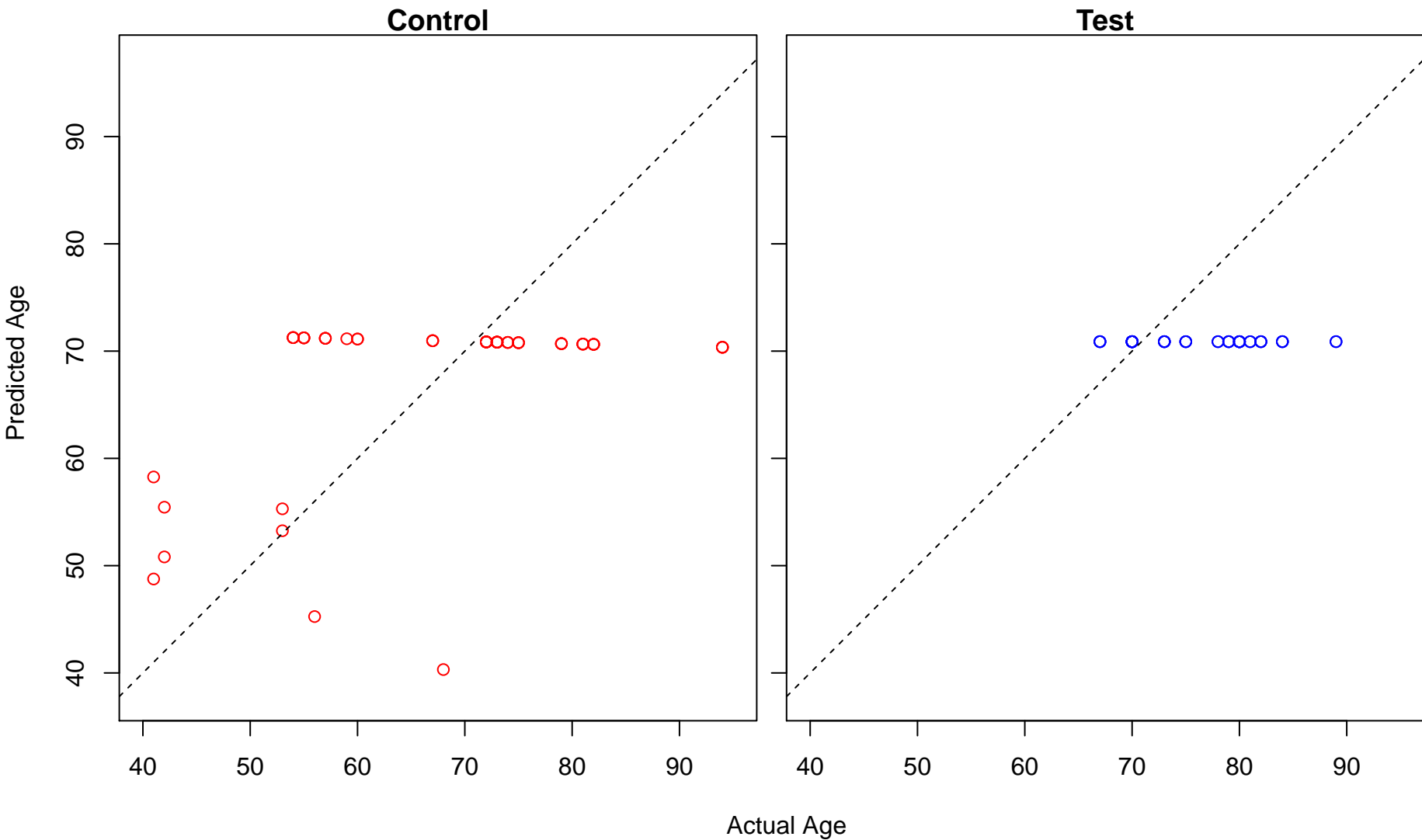
regulation of purine nucleotide metabolic process (Score: 0.788233)



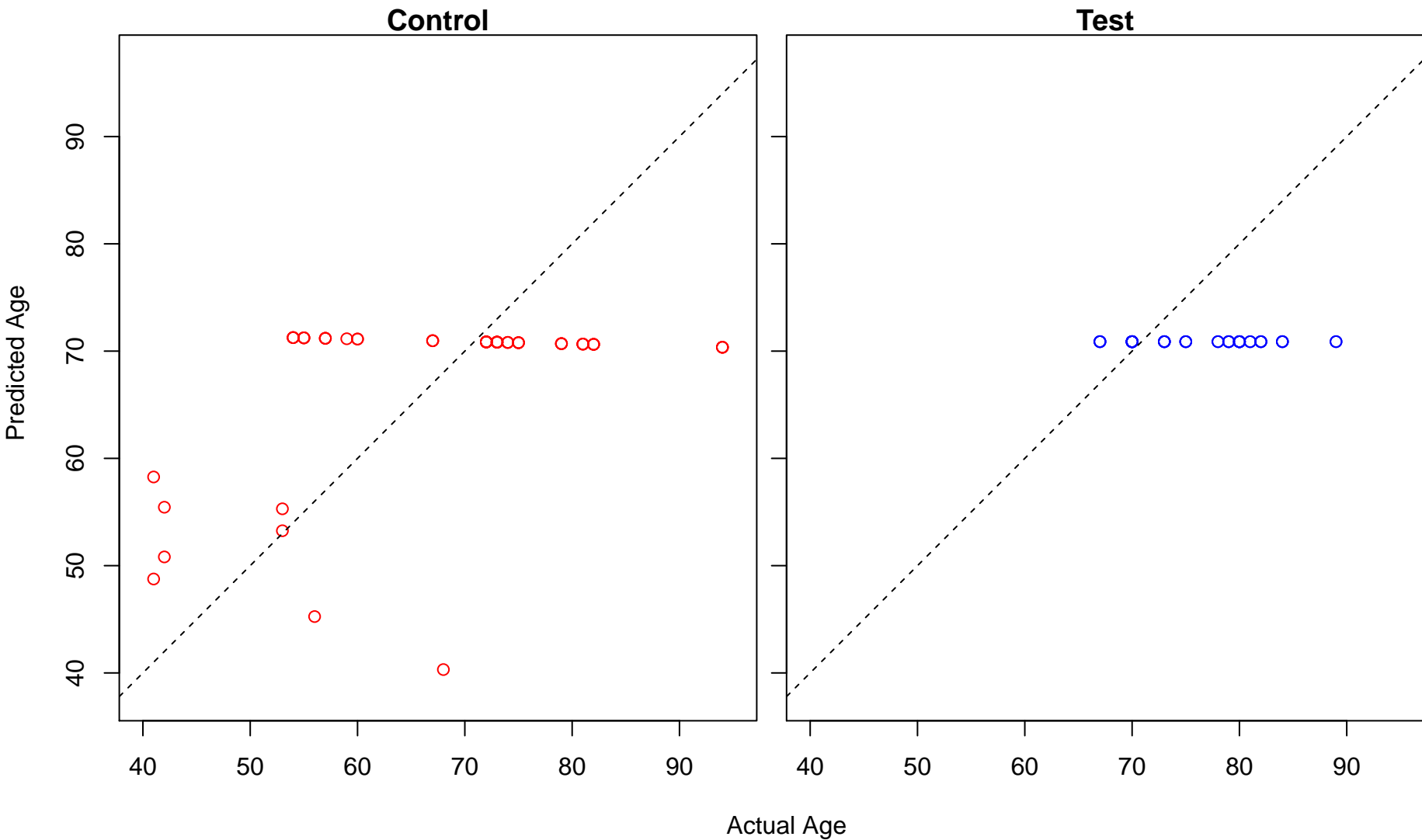
positive regulation of purine nucleotide metabolic process (Score: 0.788233)



positive regulation of phosphatase activity (Score: 0.788179)

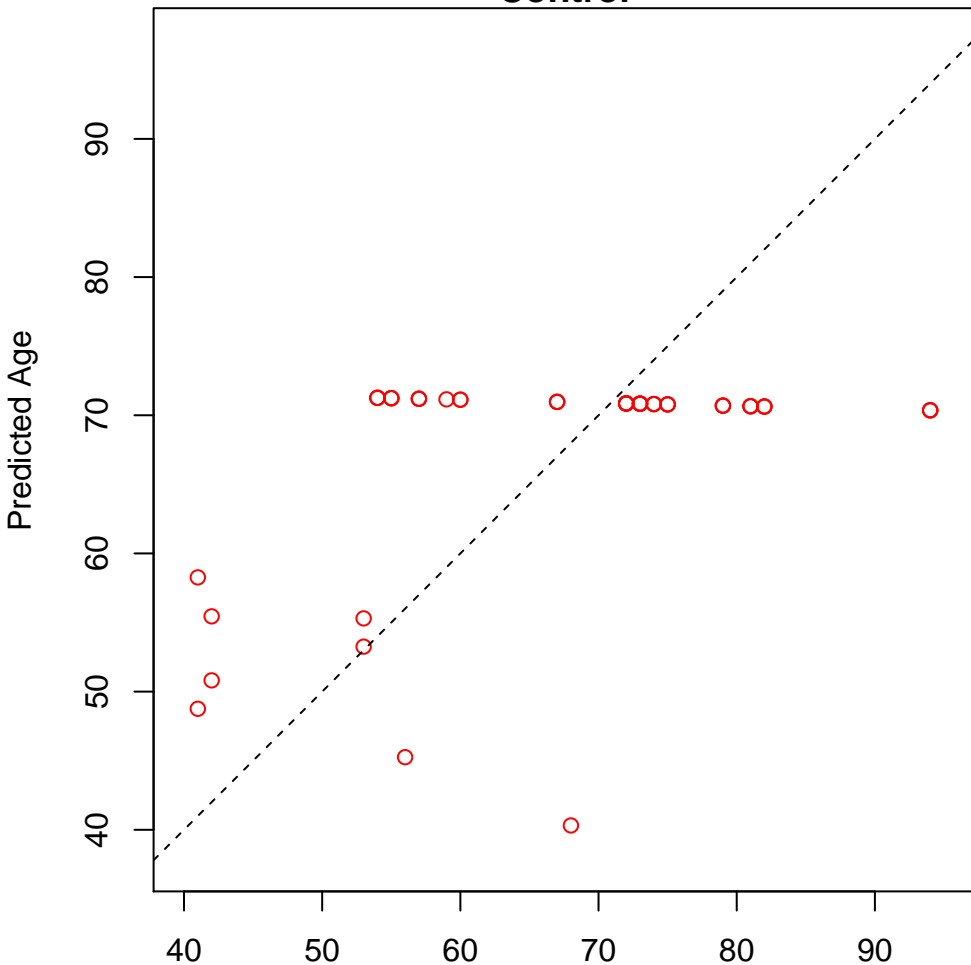


positive regulation of phosphoprotein phosphatase activity (Score: 0.788179)

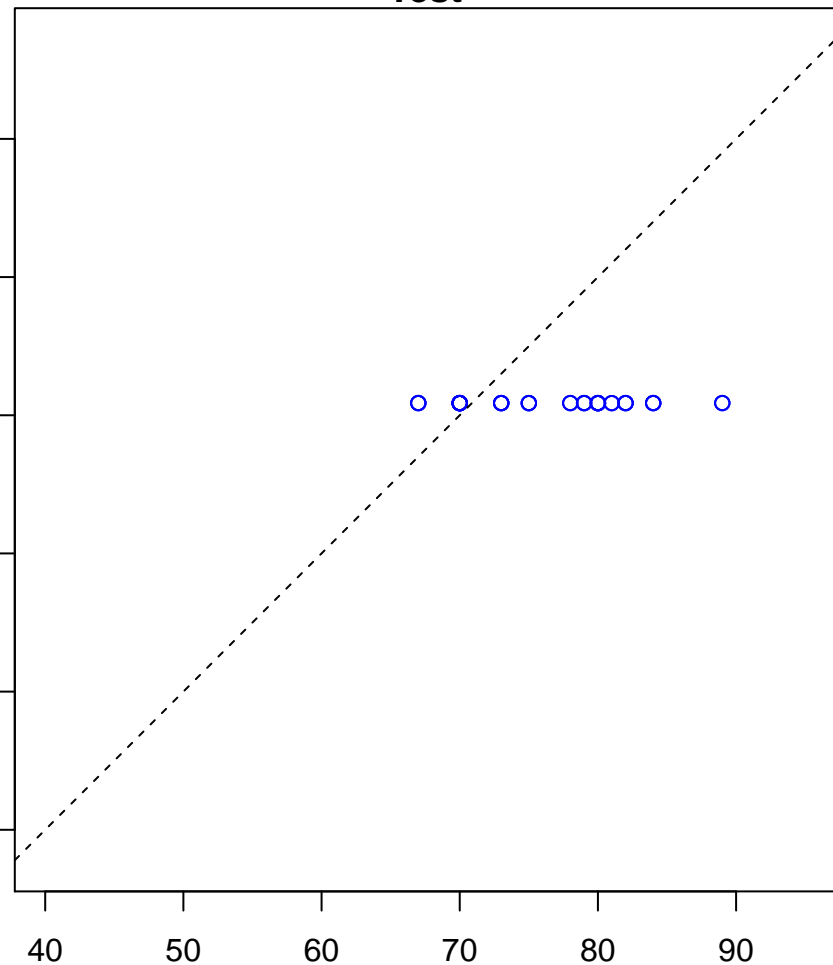


positive regulation of dephosphorylation (Score: 0.788179)

Control

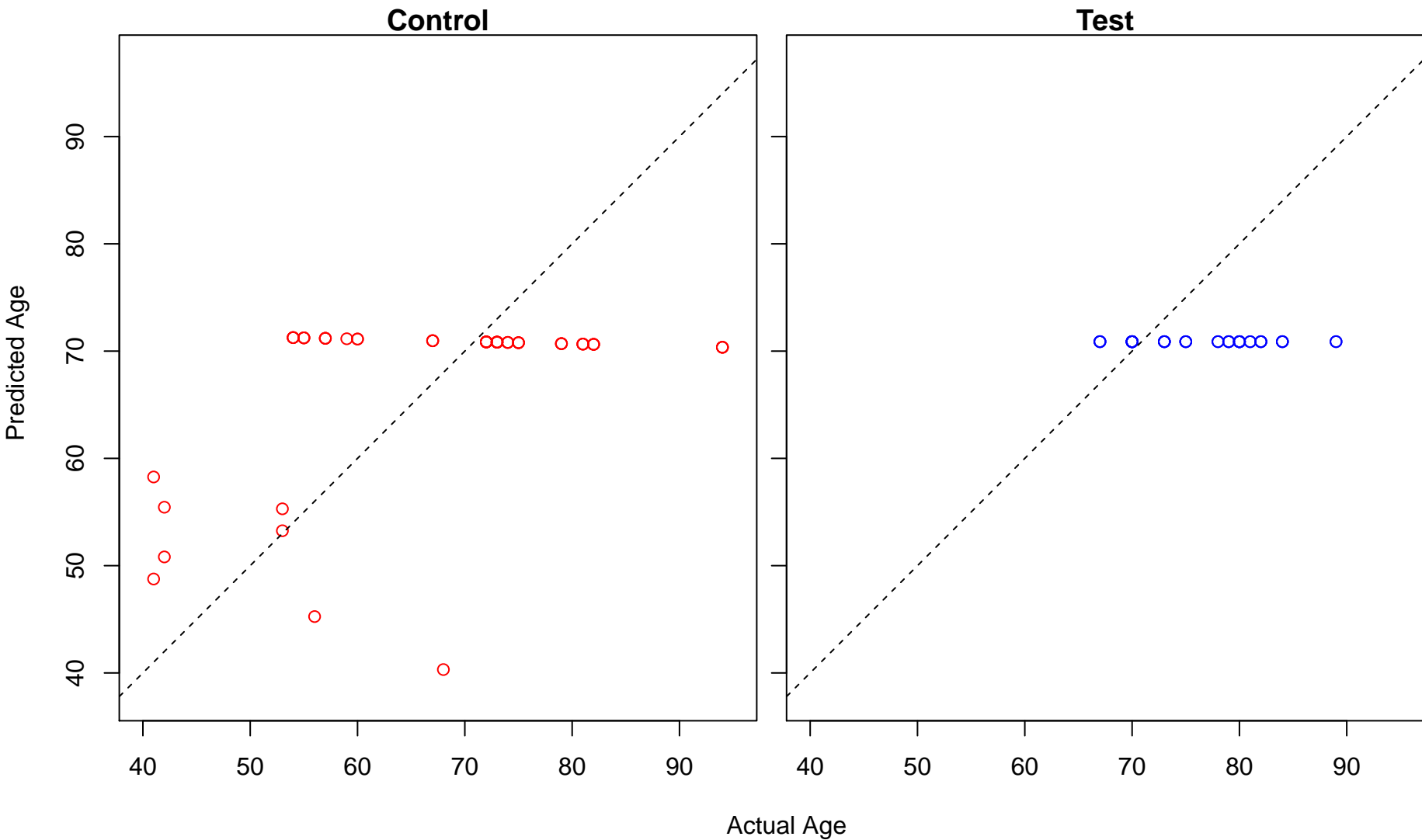


Test

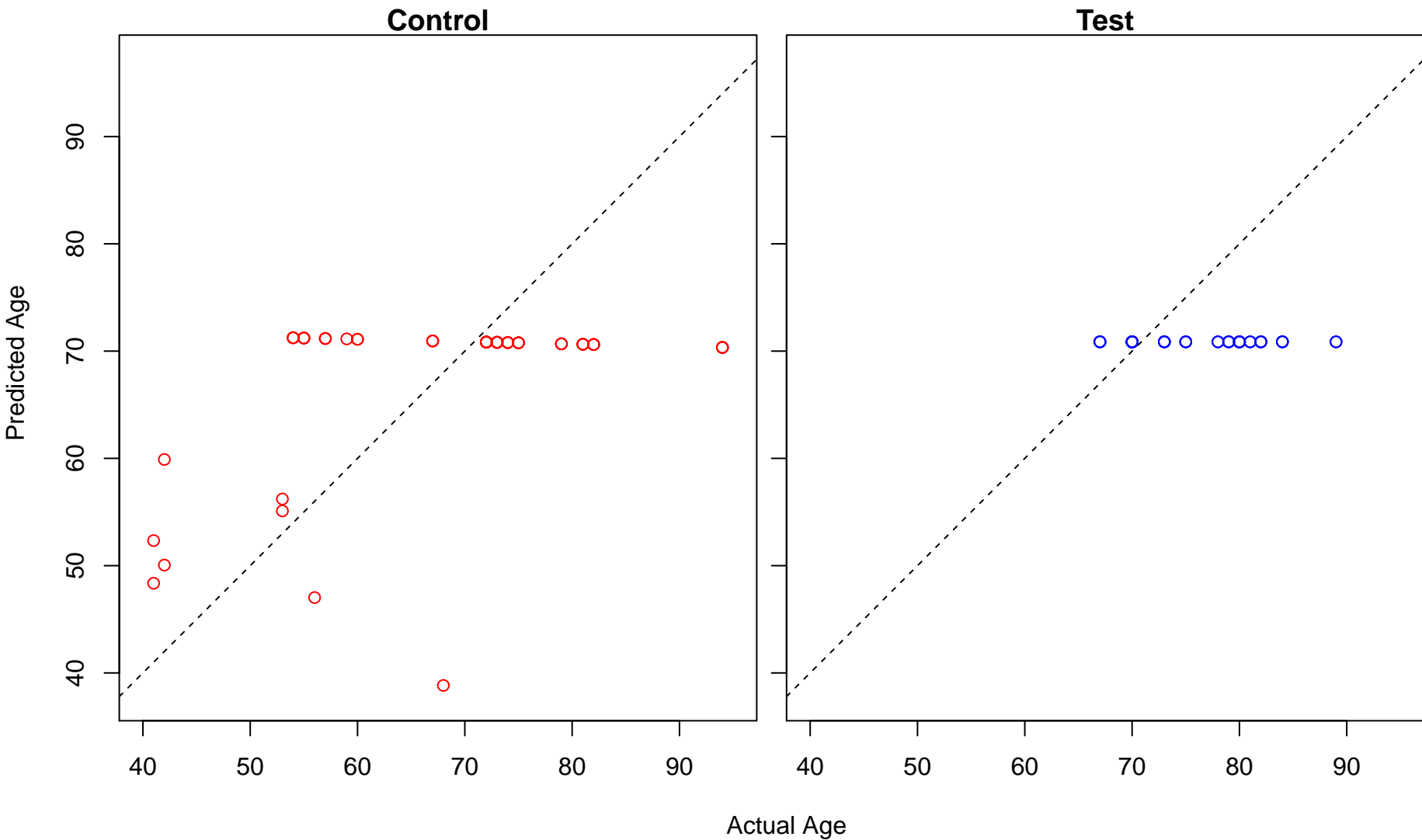


Actual Age

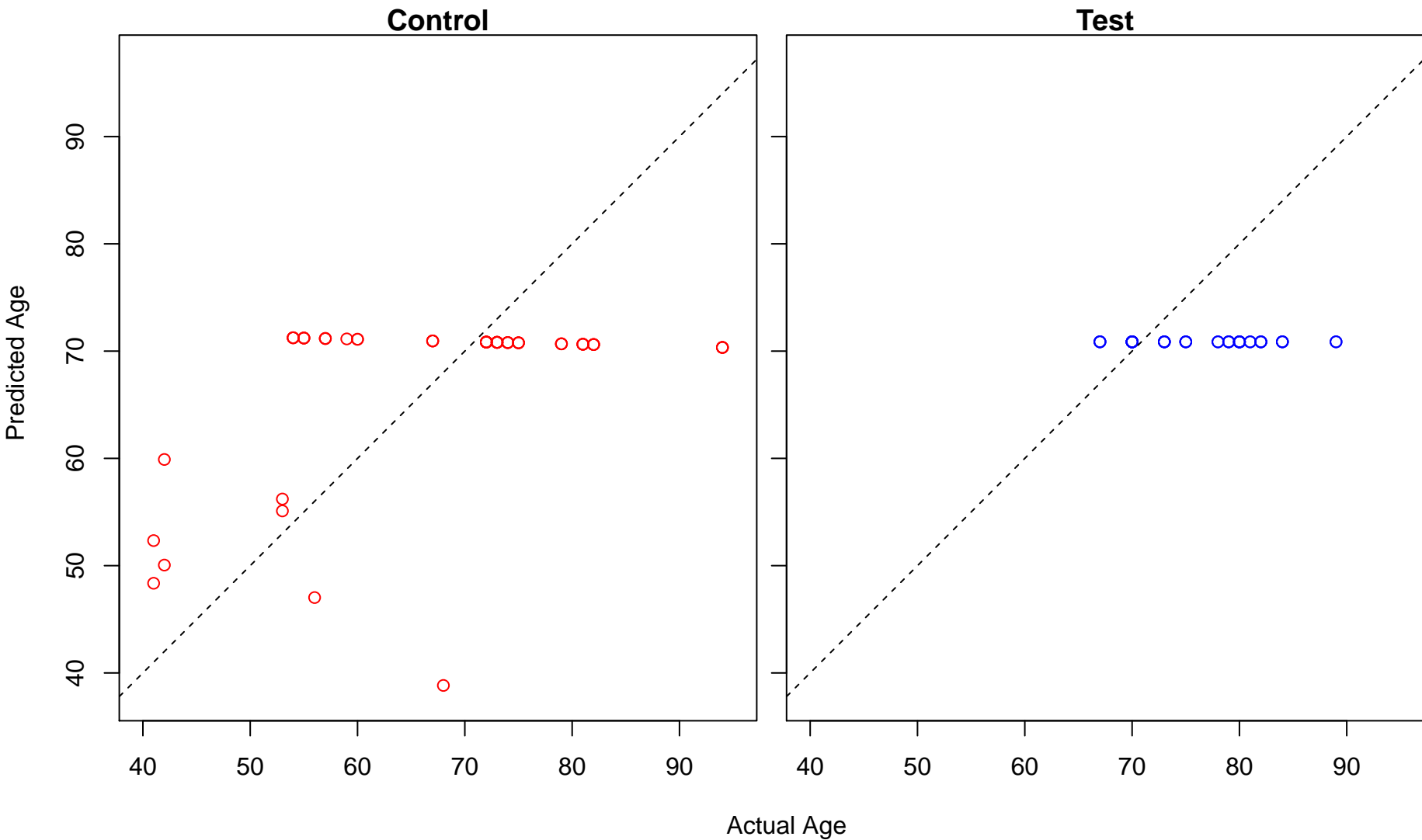
positive regulation of protein dephosphorylation (Score: 0.788179)



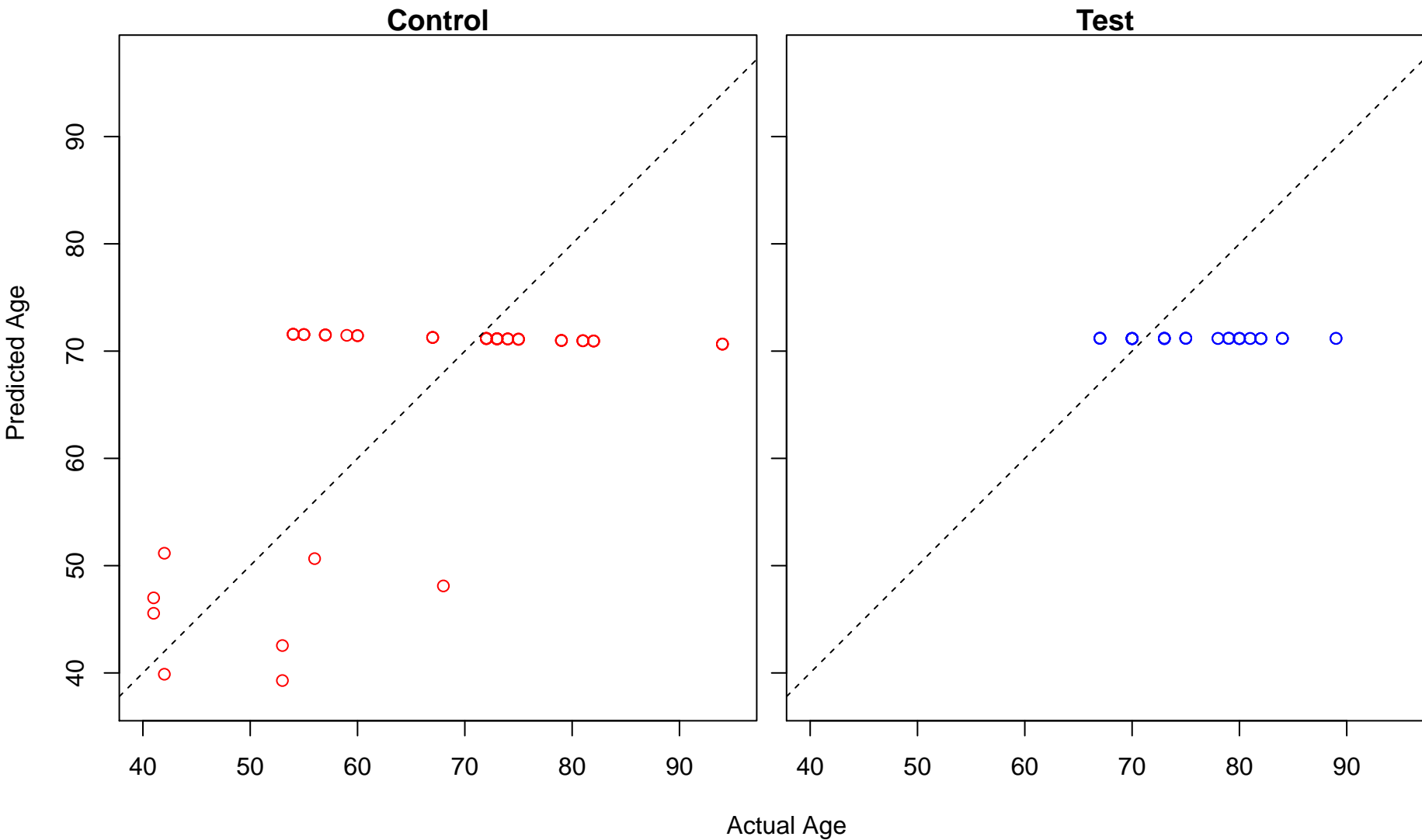
response to ketone (Score: 0.788172)



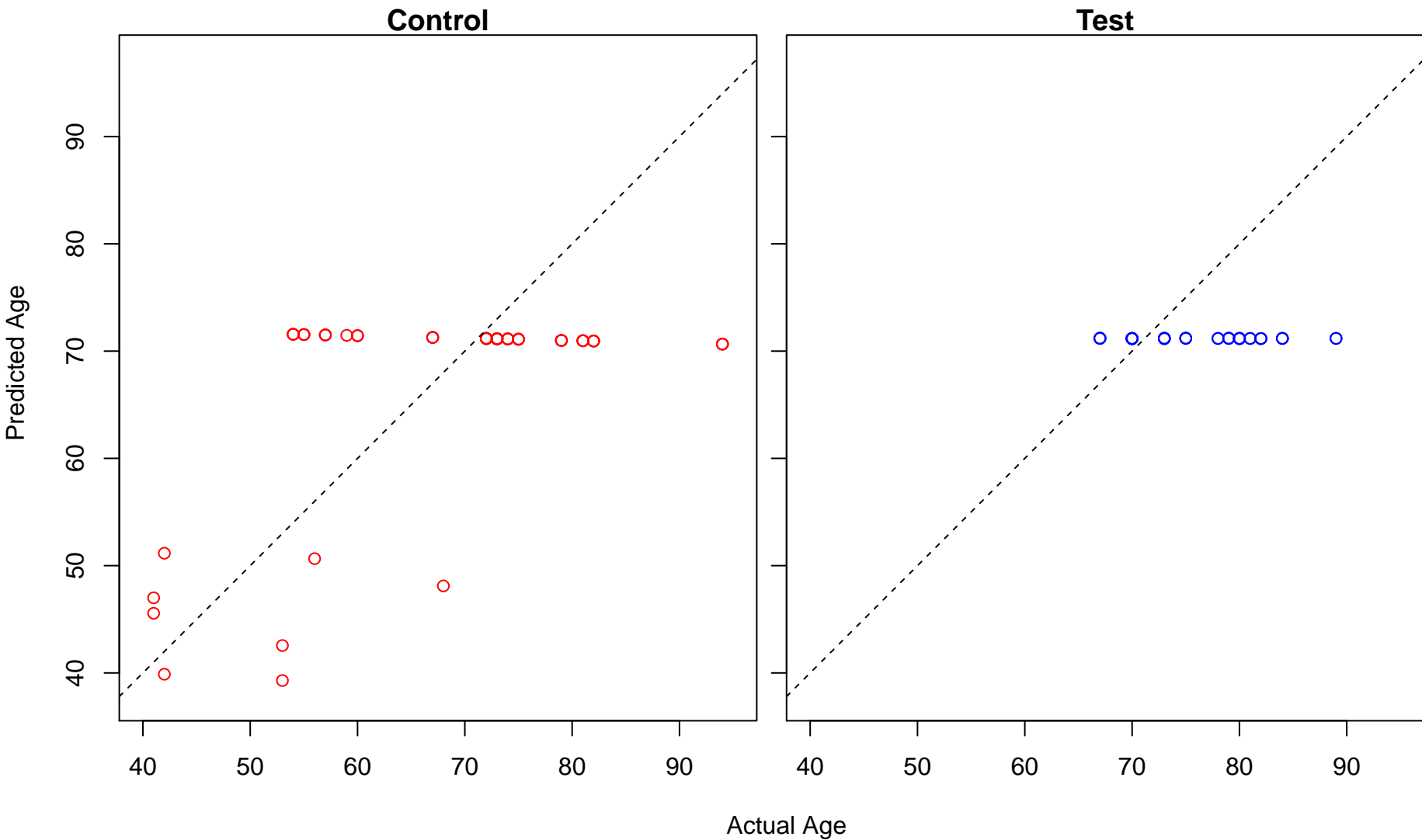
cellular response to ketone (Score: 0.788172)



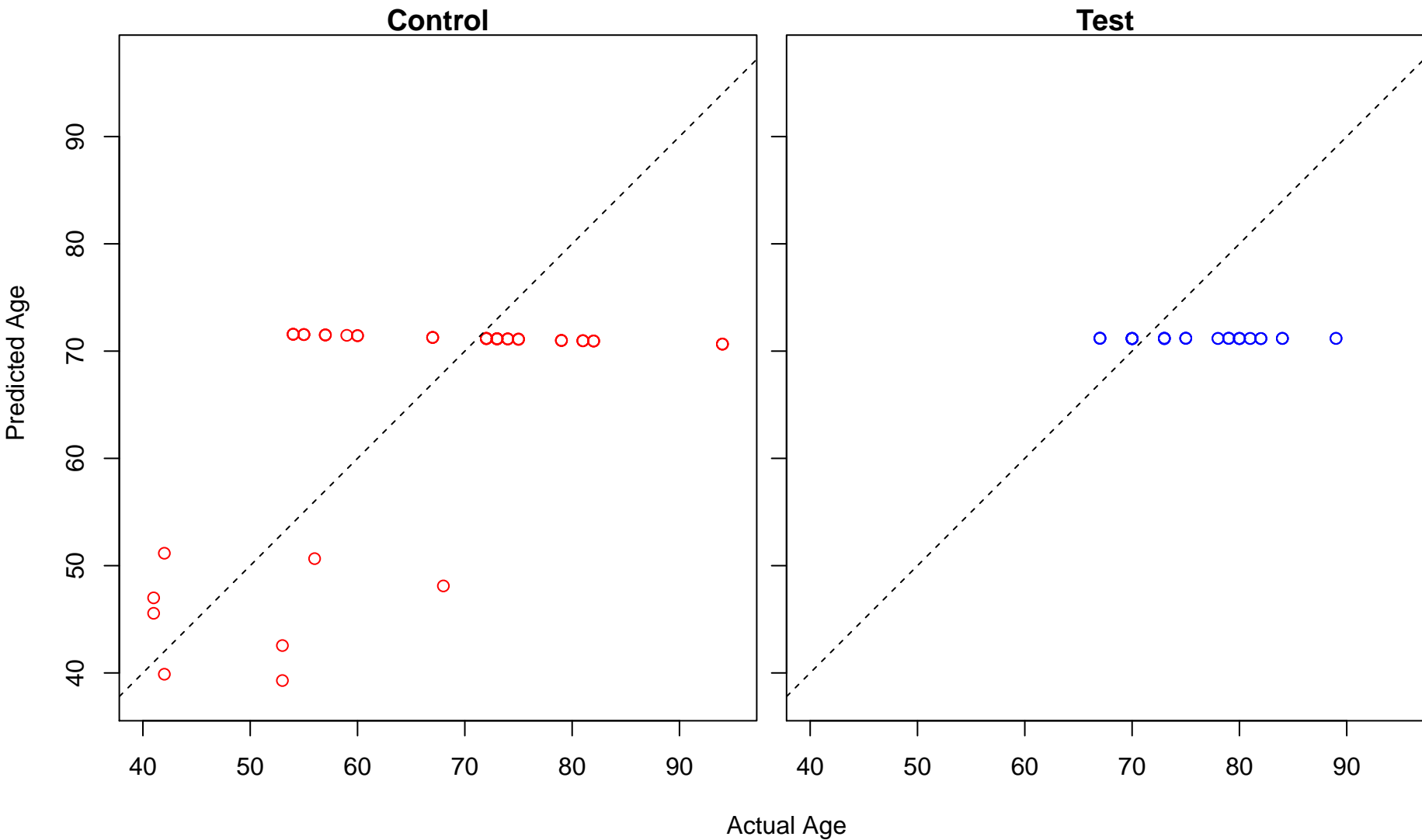
regulation of cell migration (Score: 0.788129)



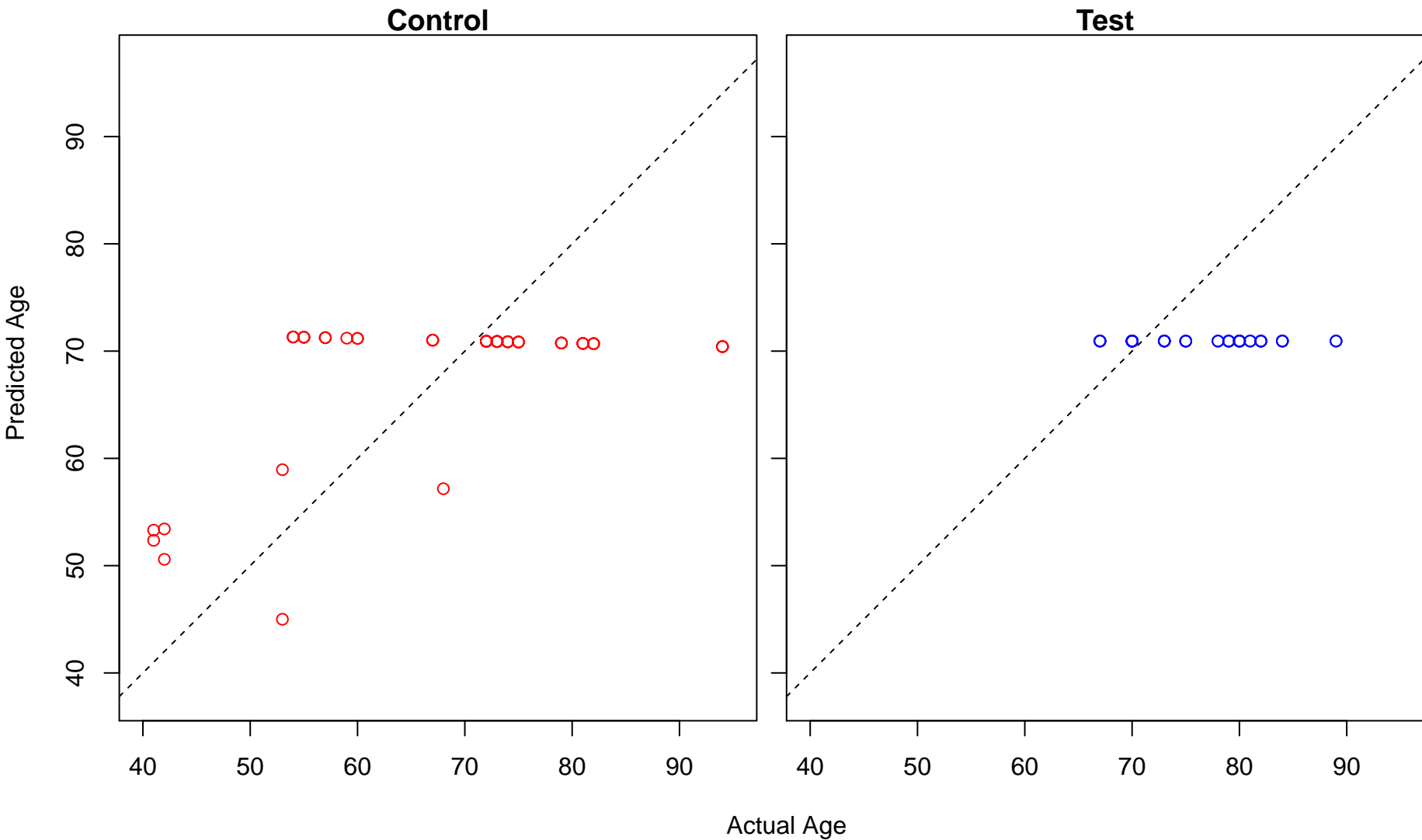
regulation of locomotion (Score: 0.788129)



regulation of cell motility (Score: 0.788129)

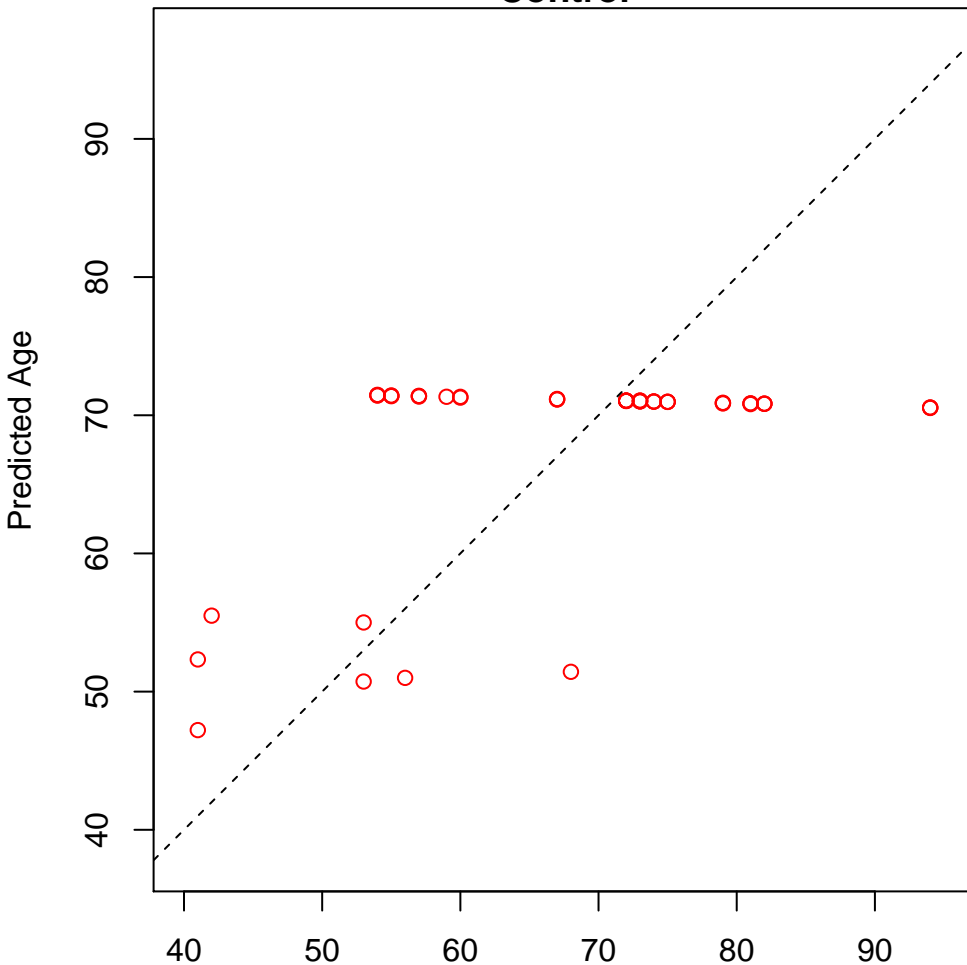


cellular response to UV (Score: 0.787919)

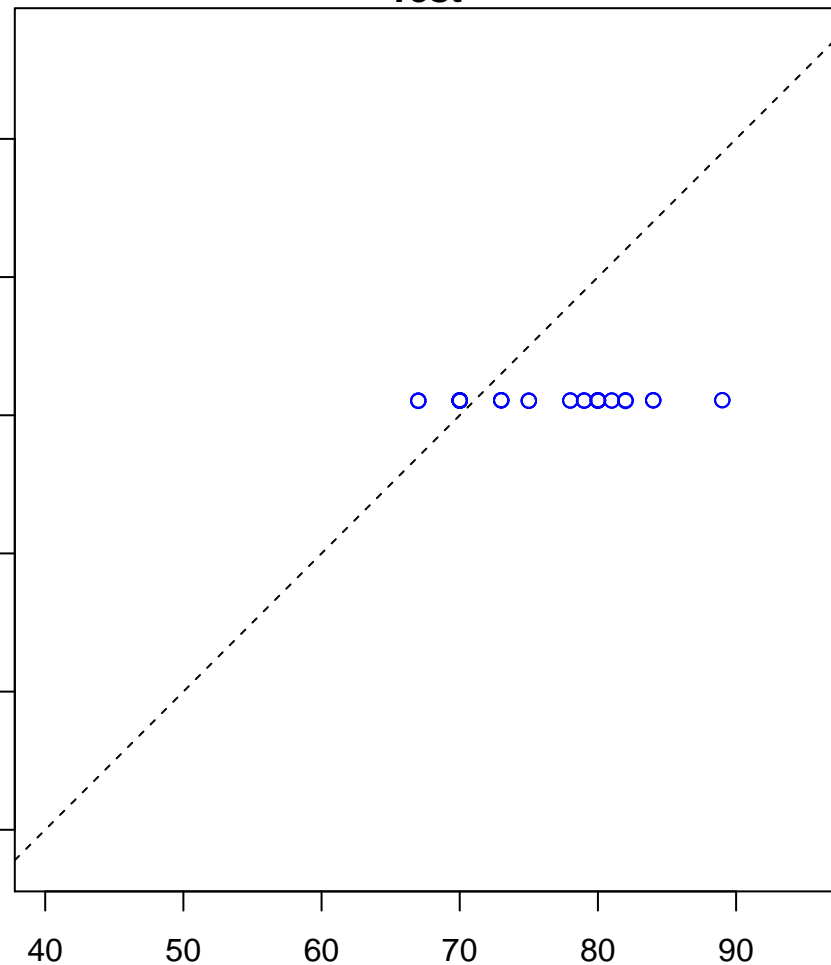


negative regulation of hemopoiesis (Score: 0.787915)

Control

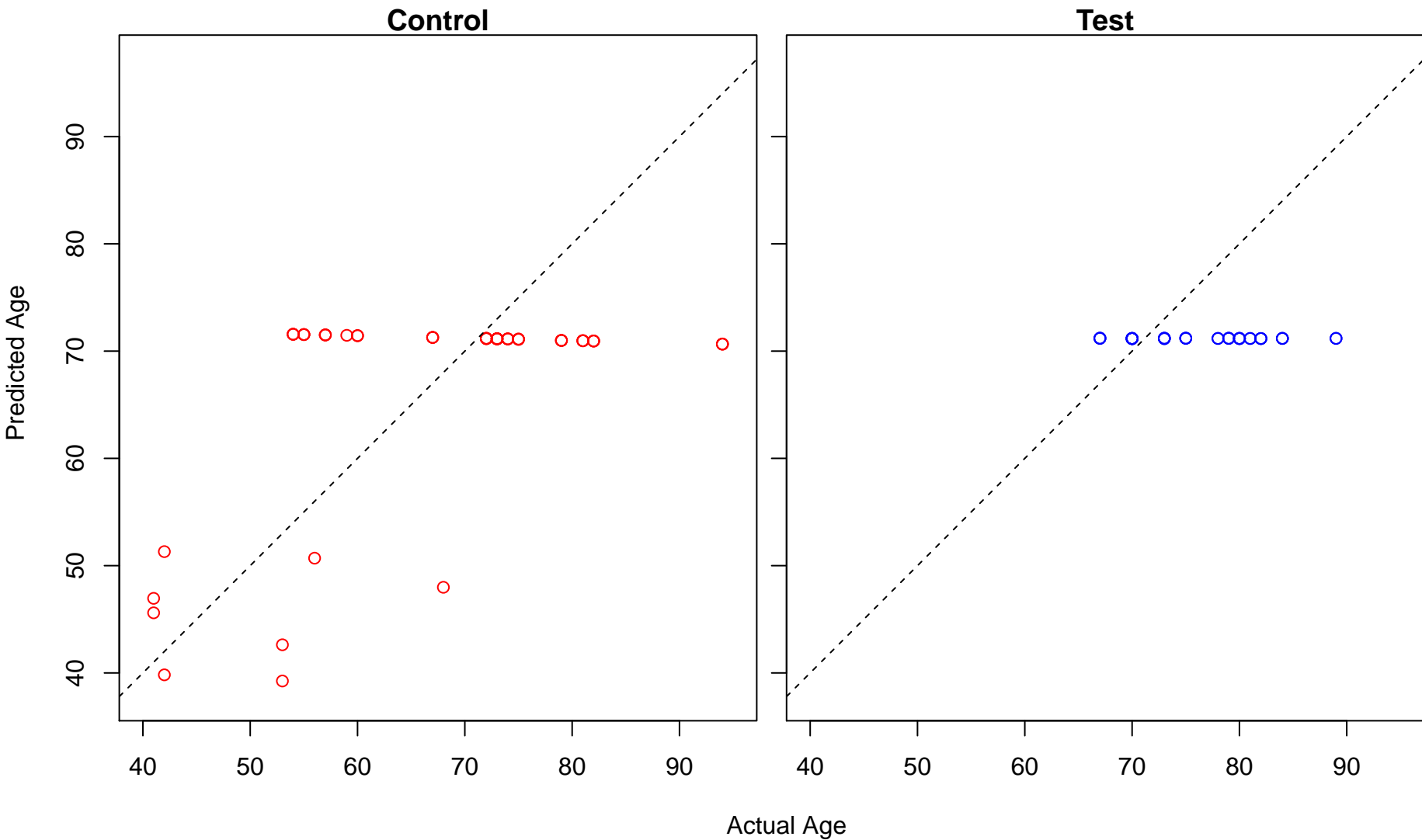


Test

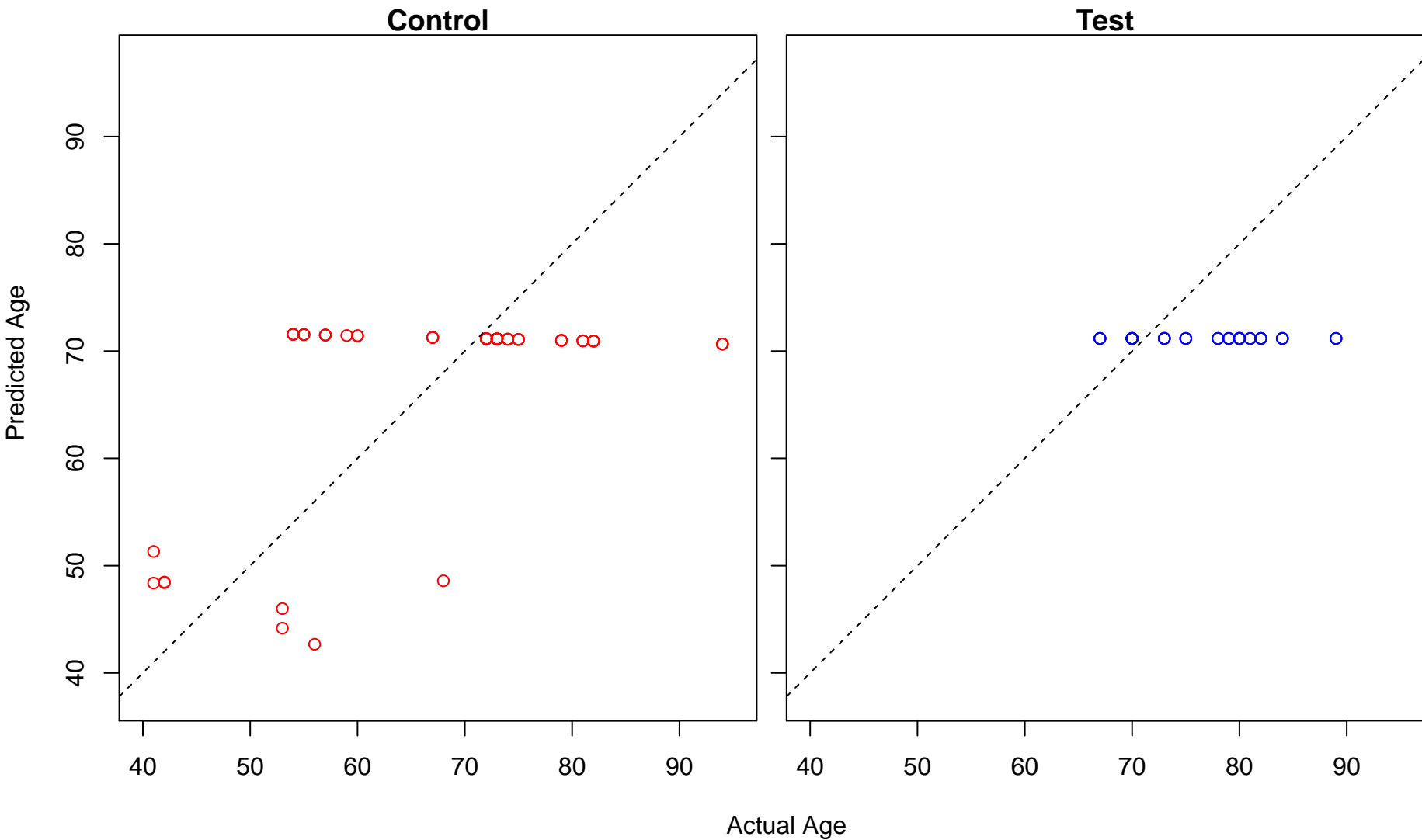


Actual Age

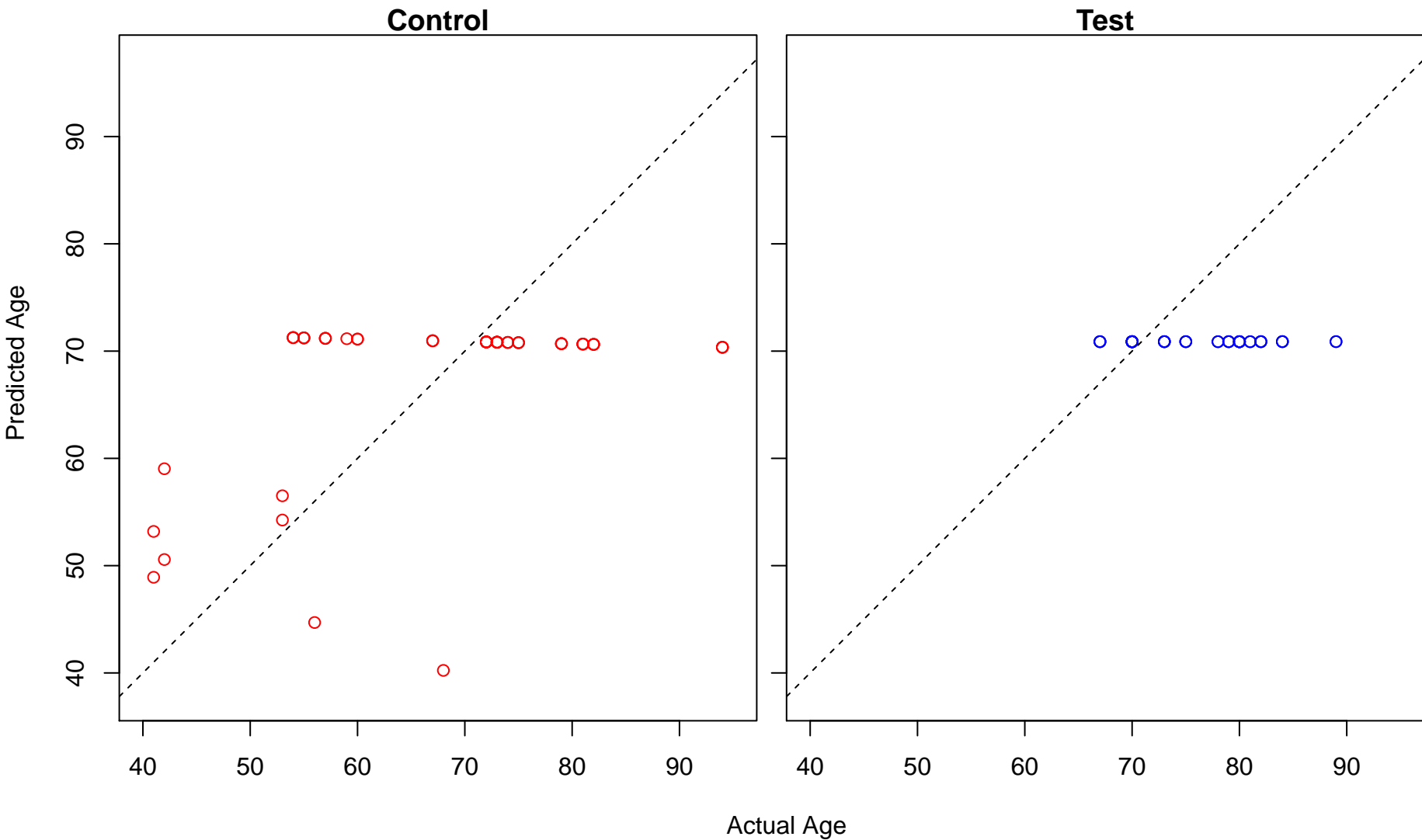
regulation of cellular component movement (Score: 0.787866)



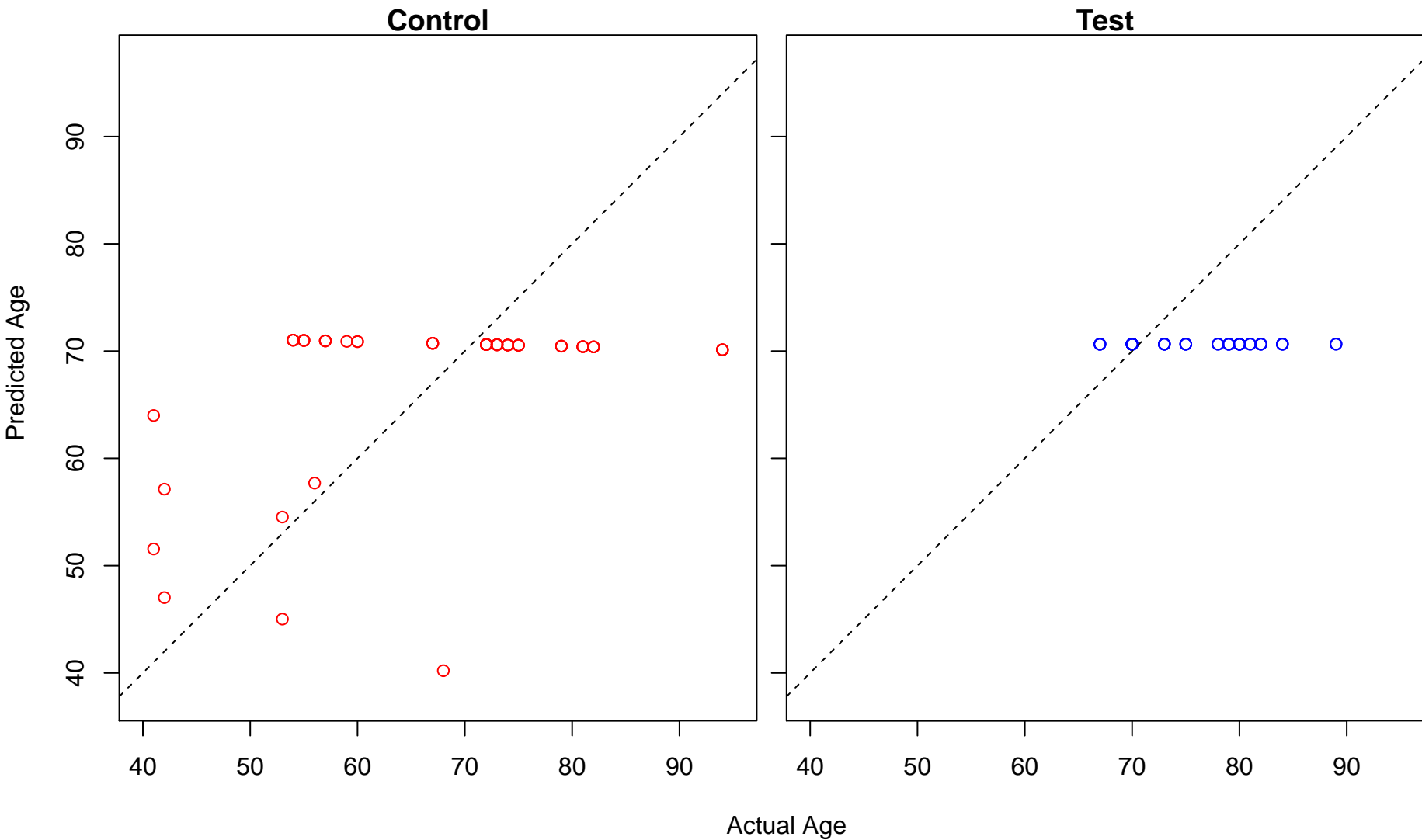
cellular catabolic process (Score: 0.787820)



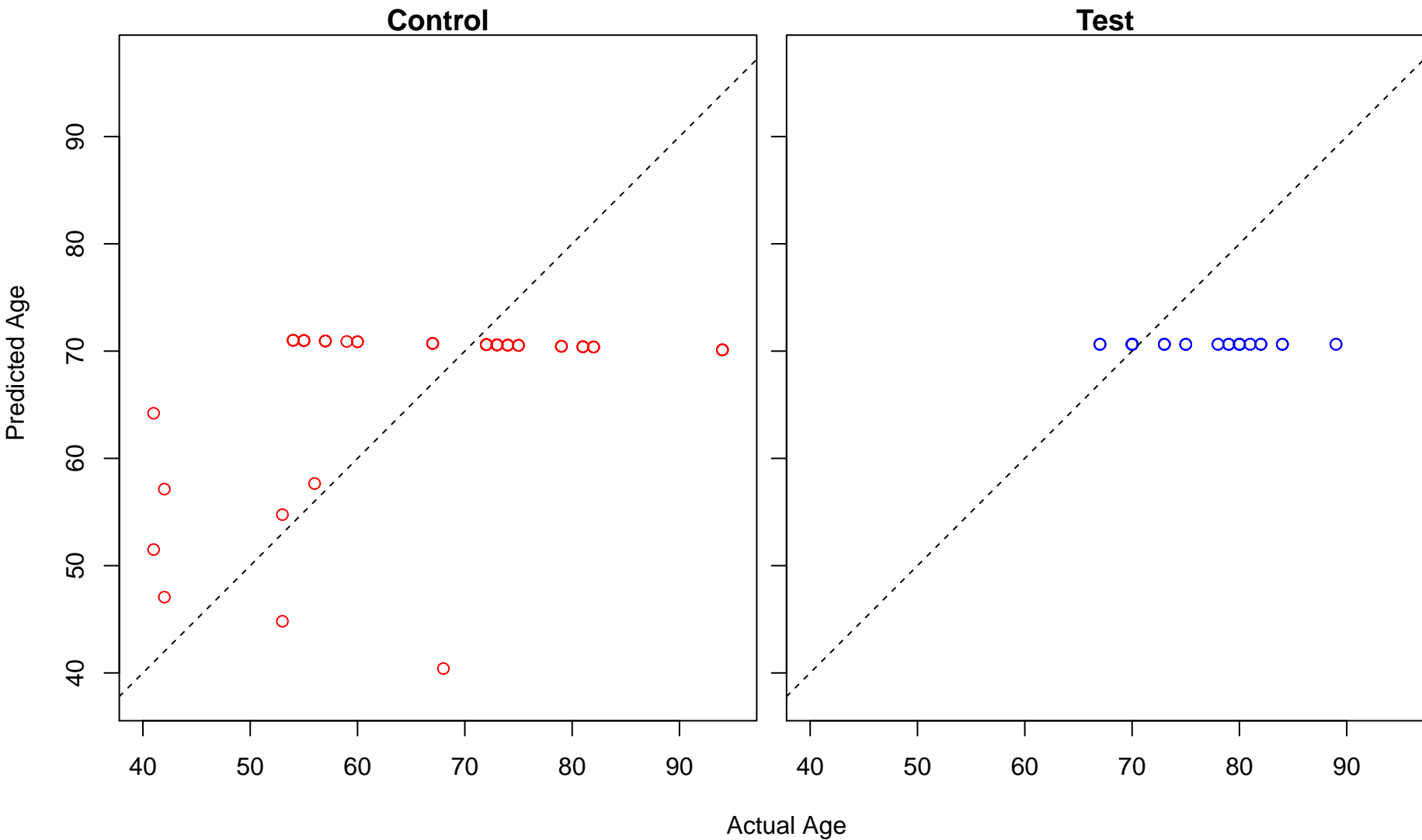
cellular response to alcohol (Score: 0.787594)



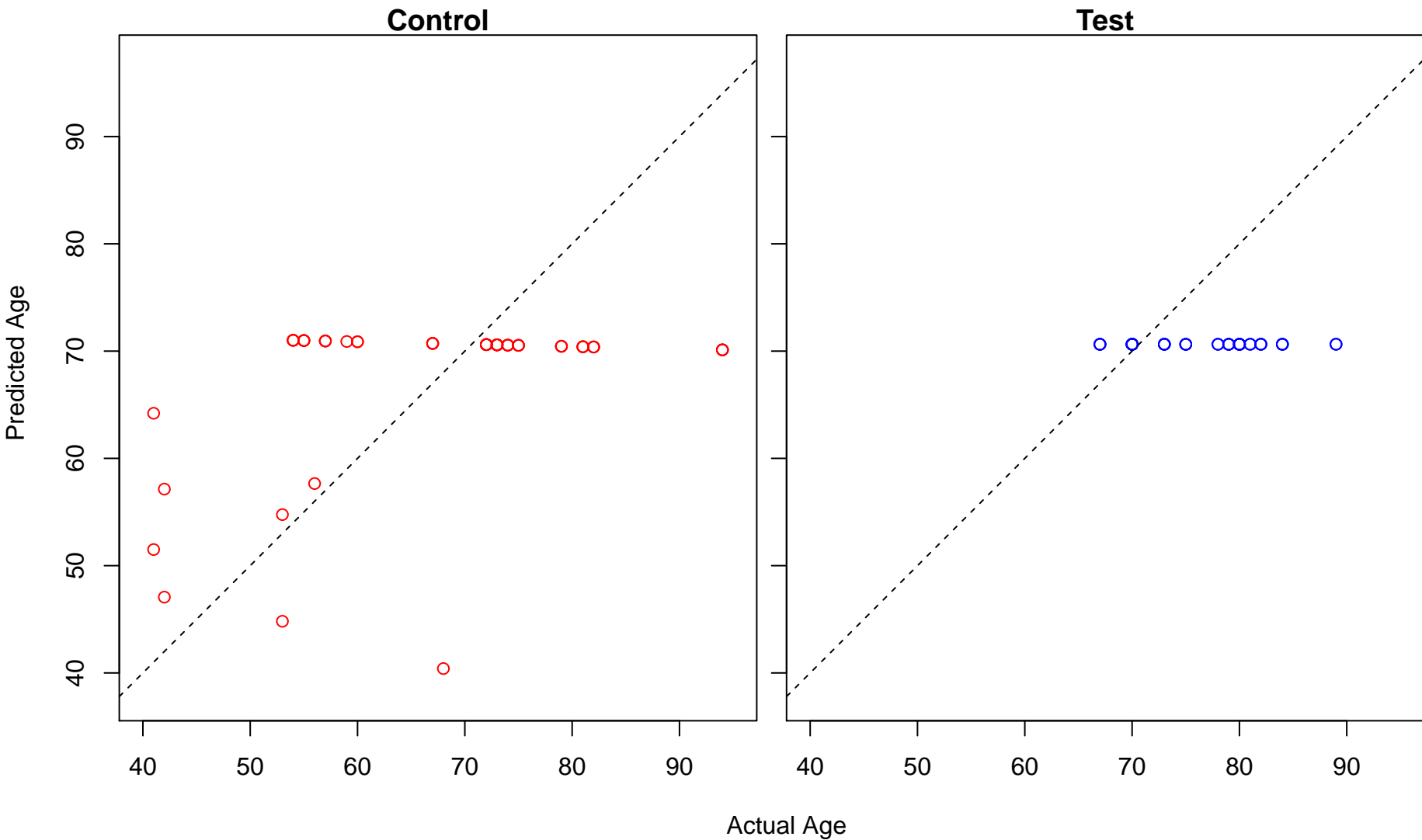
regulation of rhodopsin mediated signaling pathway (Score: 0.787457)



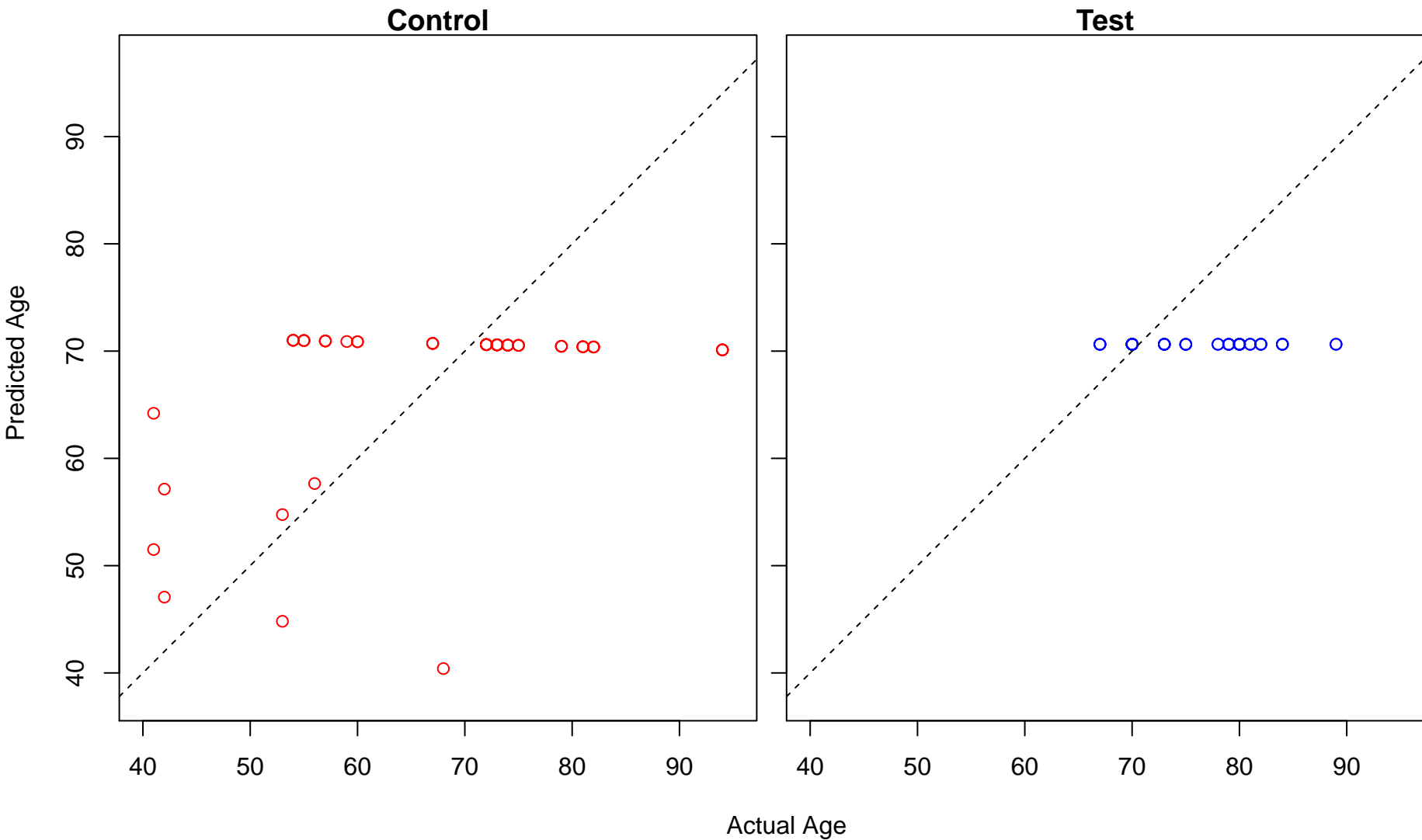
protein prenylation (Score: 0.787412)



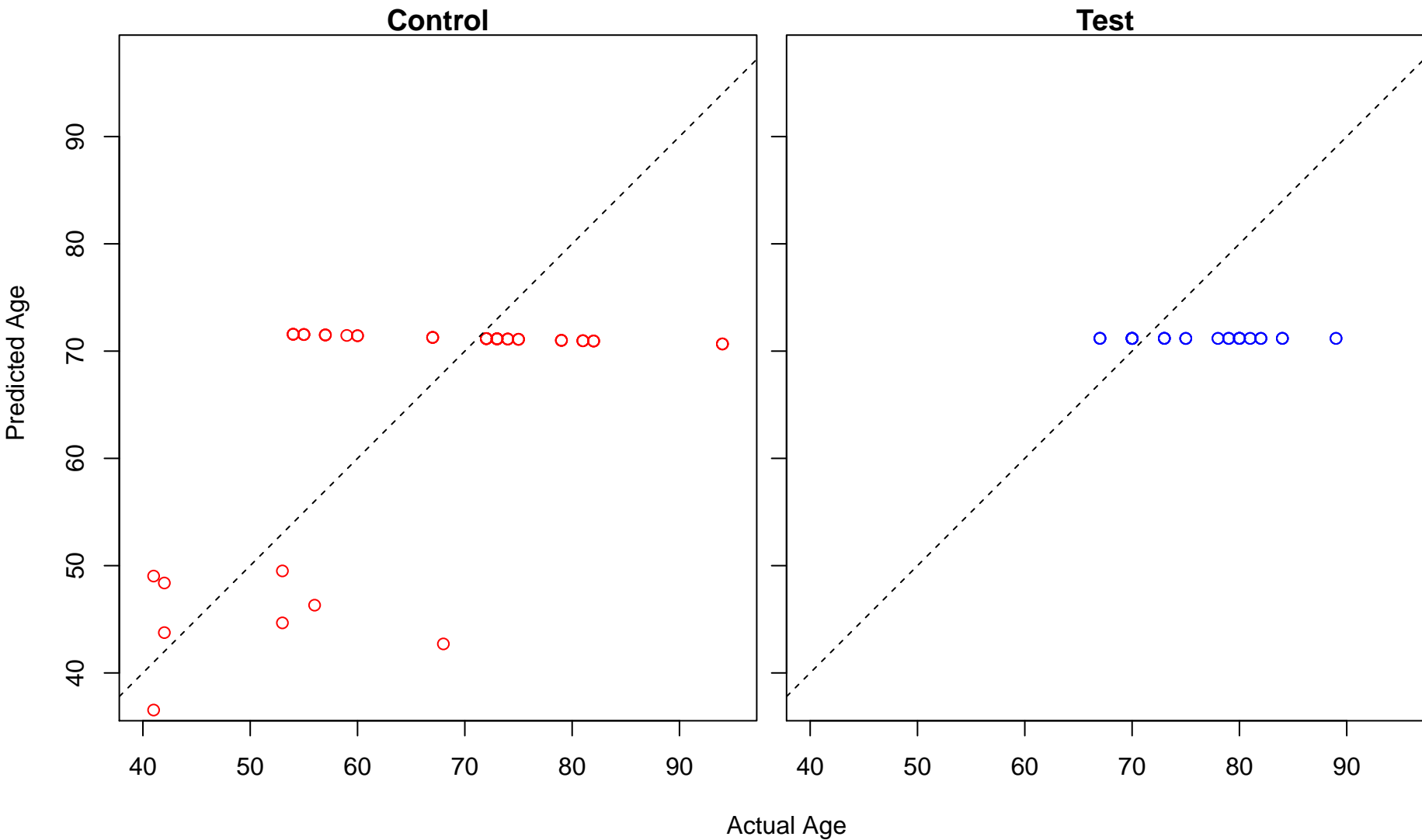
protein farnesylation (Score: 0.787412)



prenylation (Score: 0.787412)

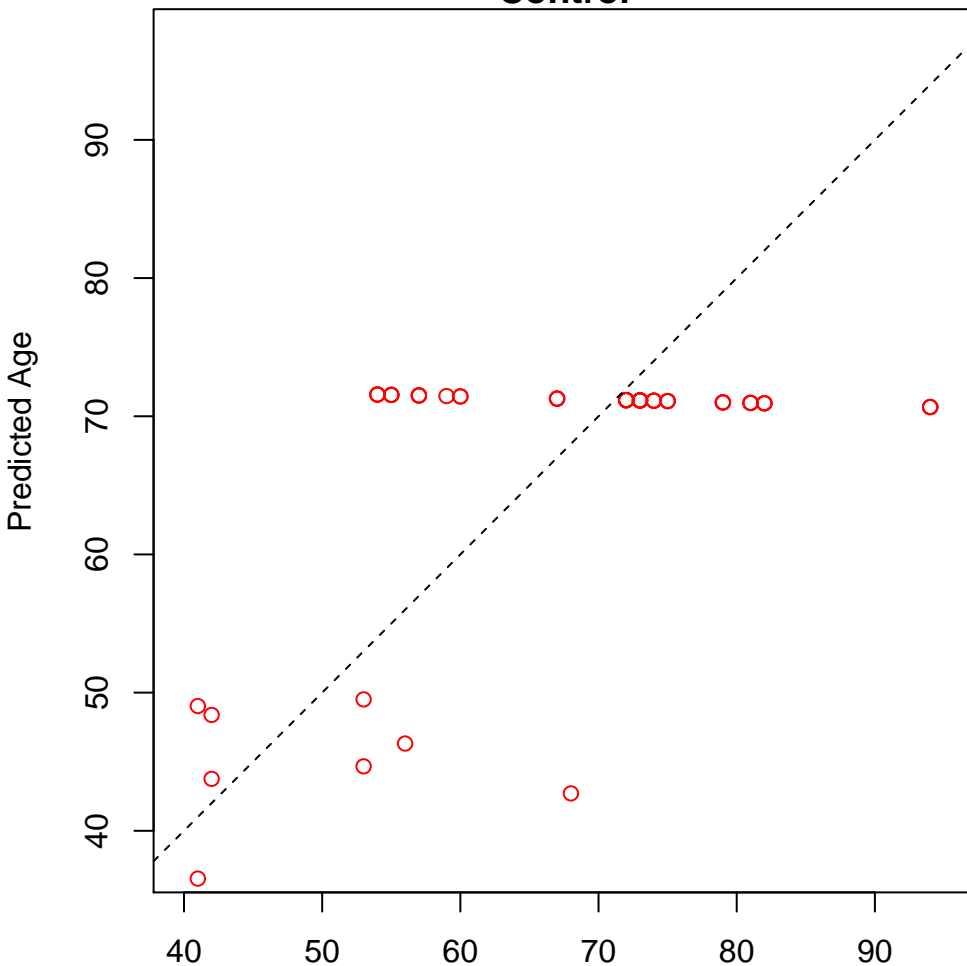


heterocycle biosynthetic process (Score: 0.787408)

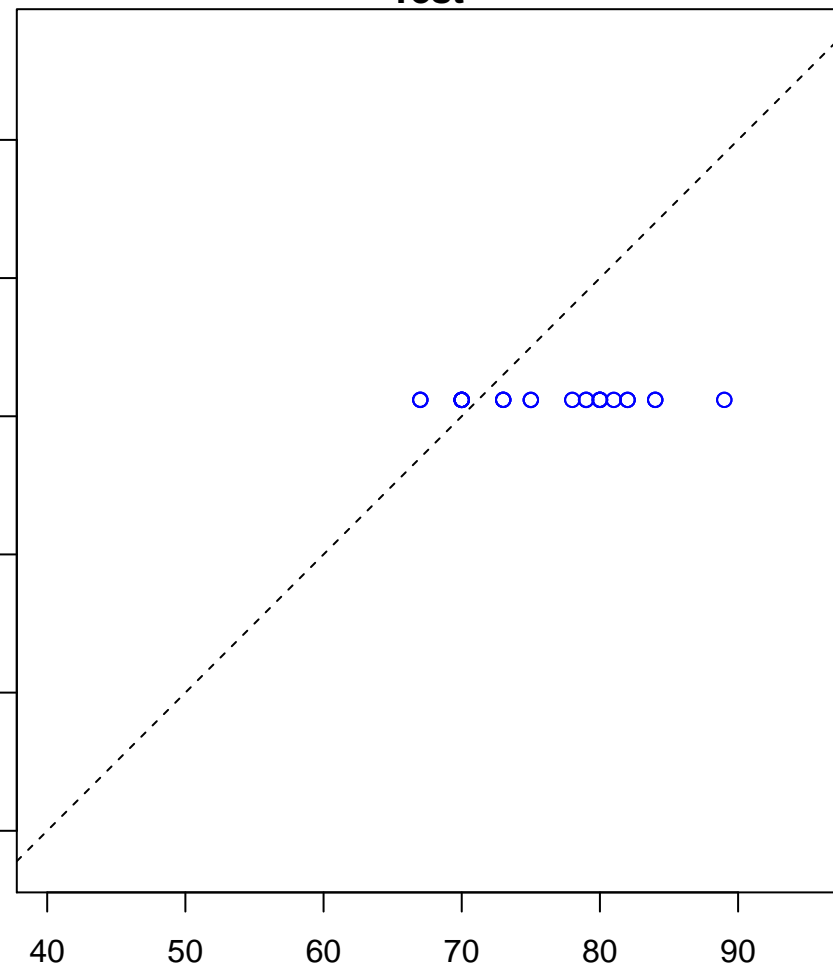


aromatic compound biosynthetic process (Score: 0.787408)

Control

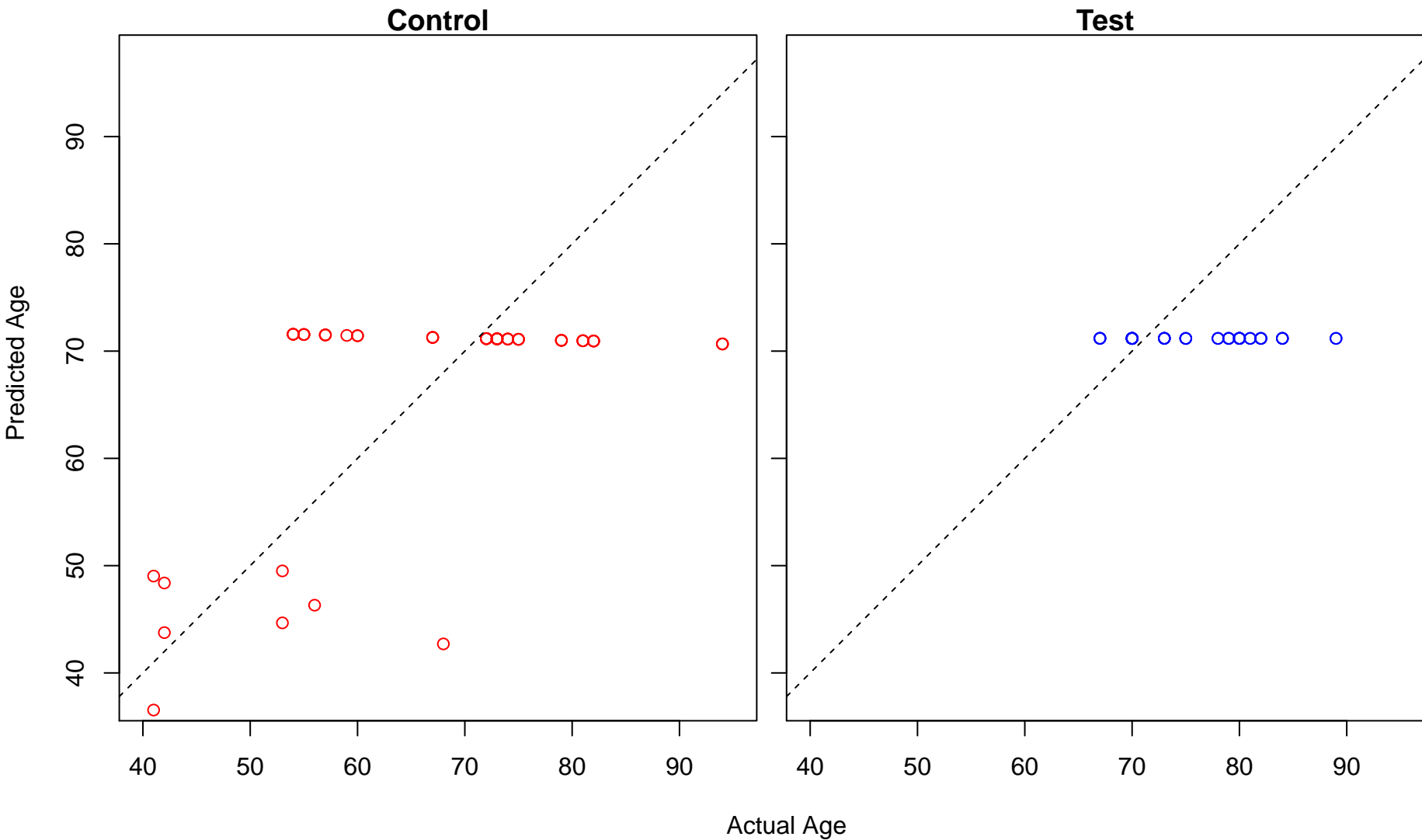


Test

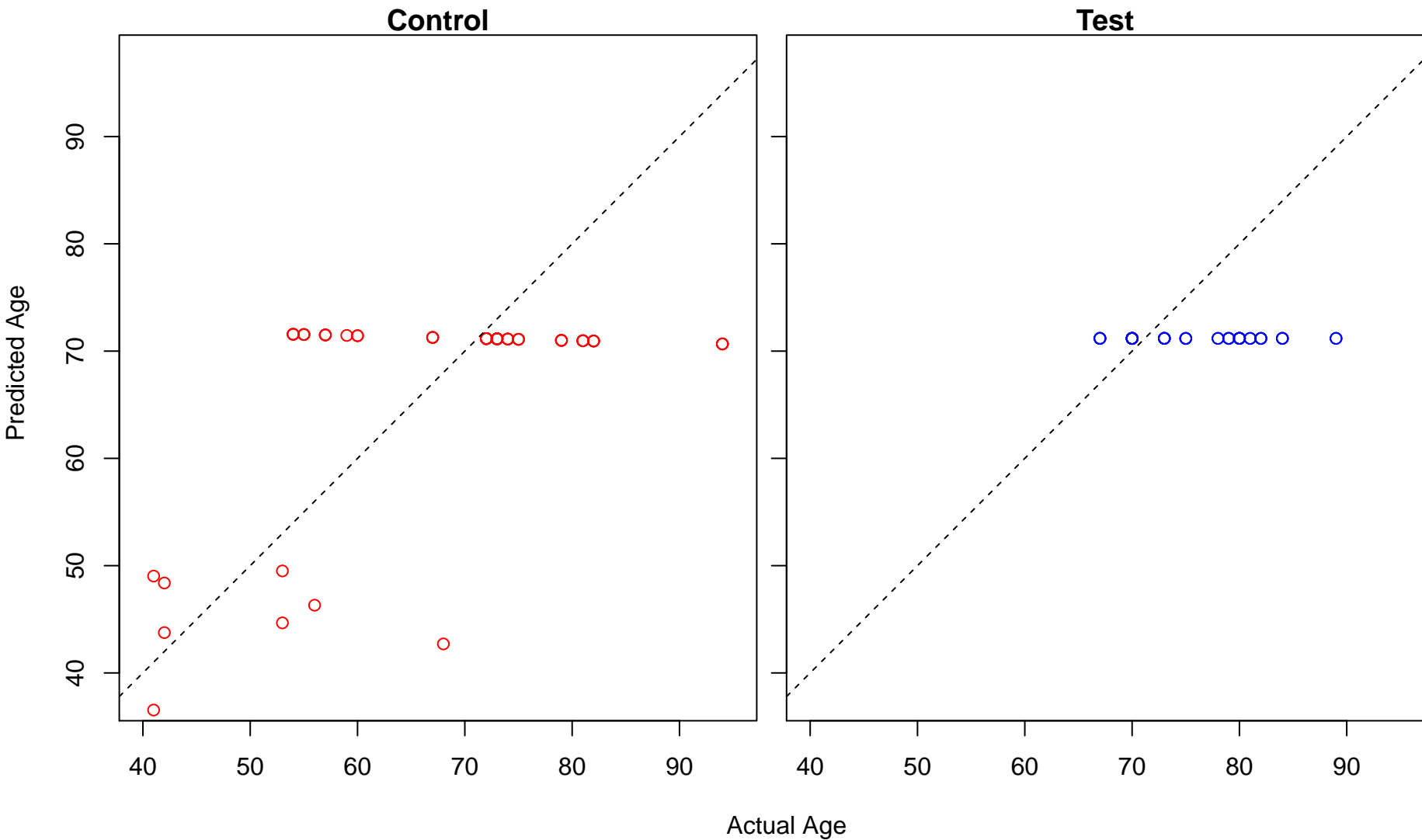


Actual Age

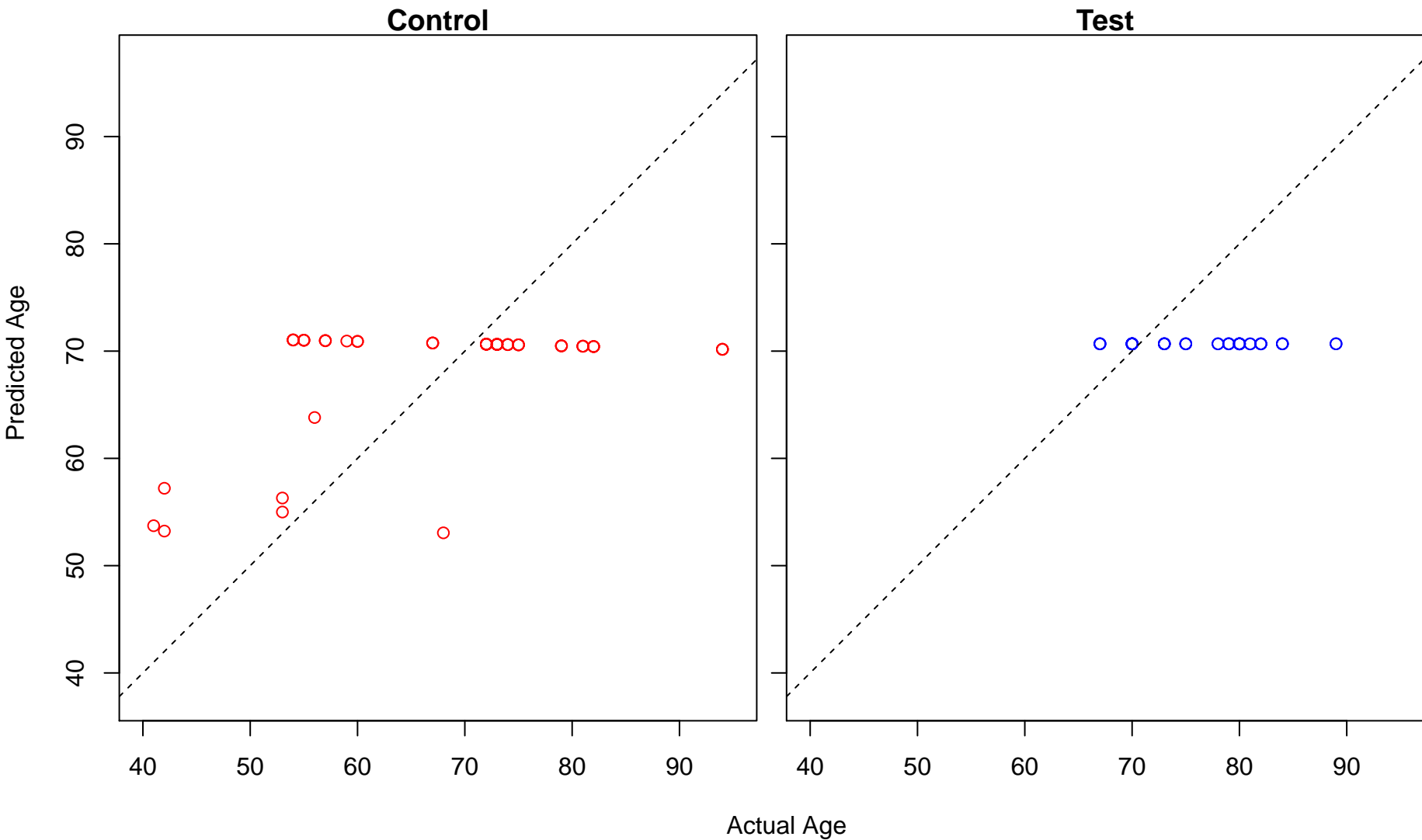
nucleobase-containing compound biosynthetic process (Score: 0.787408)



organic cyclic compound biosynthetic process (Score: 0.787408)

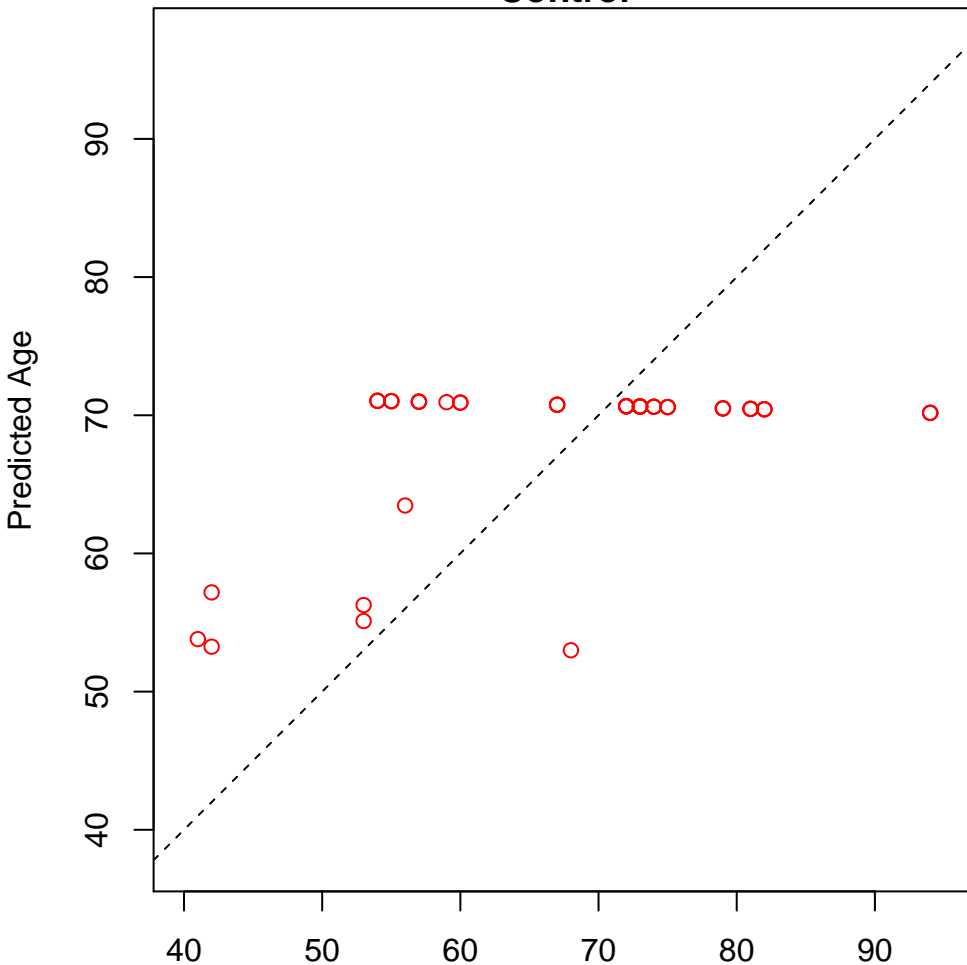


dendritic spine organization (Score: 0.786966)

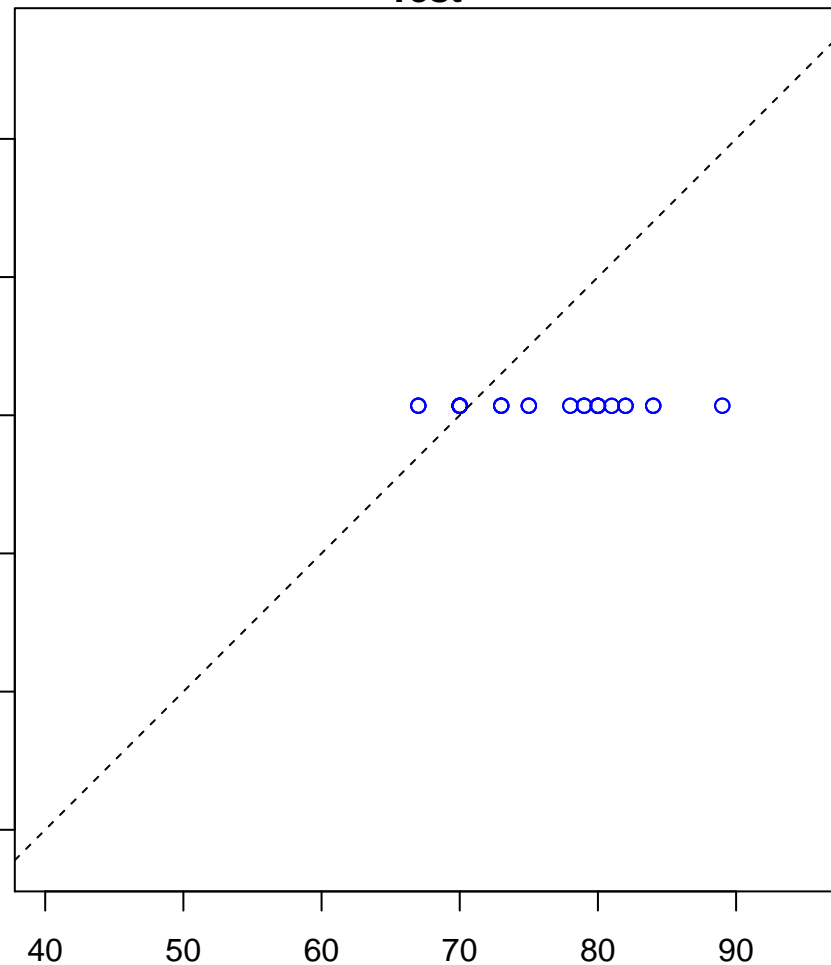


post-Golgi vesicle-mediated transport (Score: 0.786943)

Control

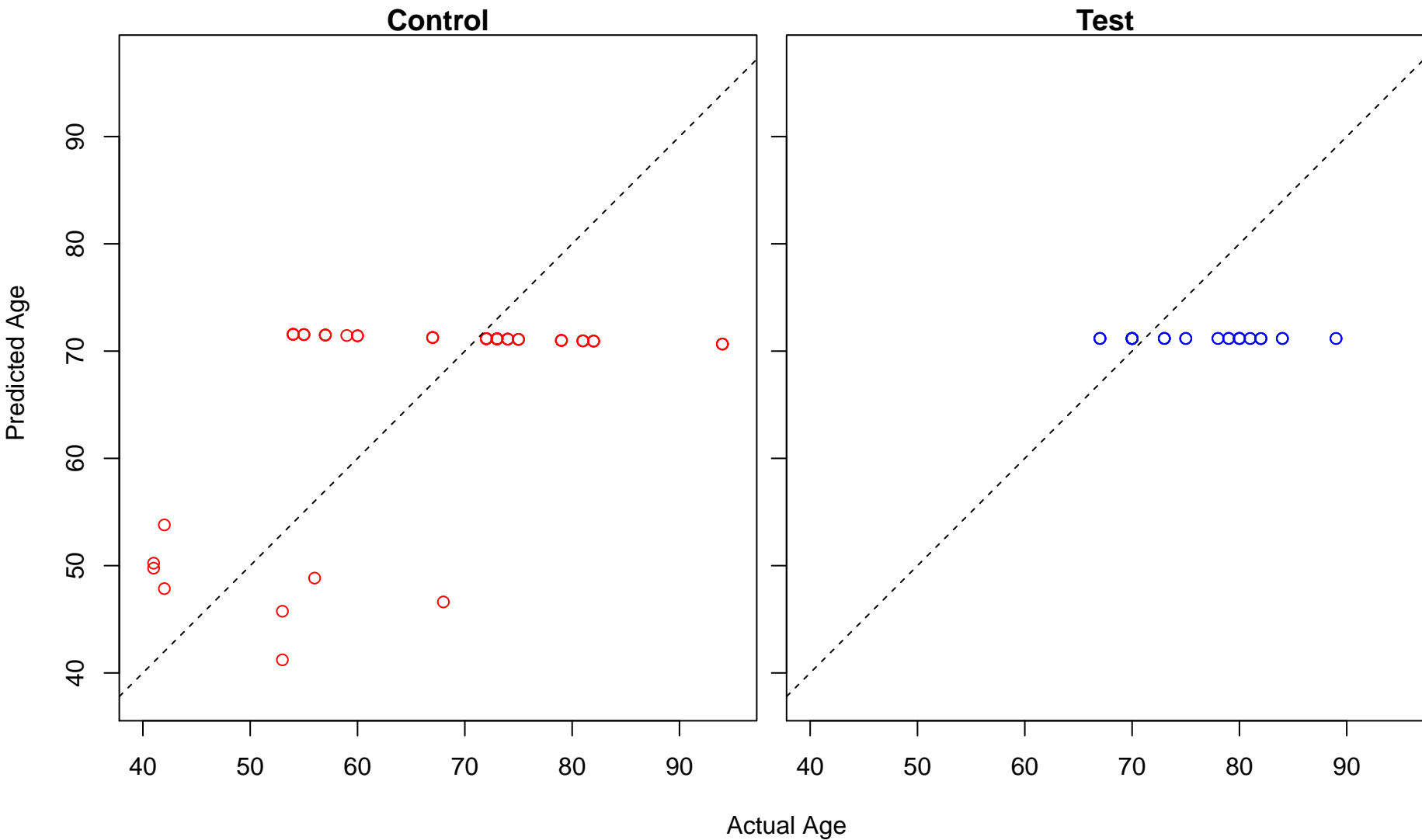


Test



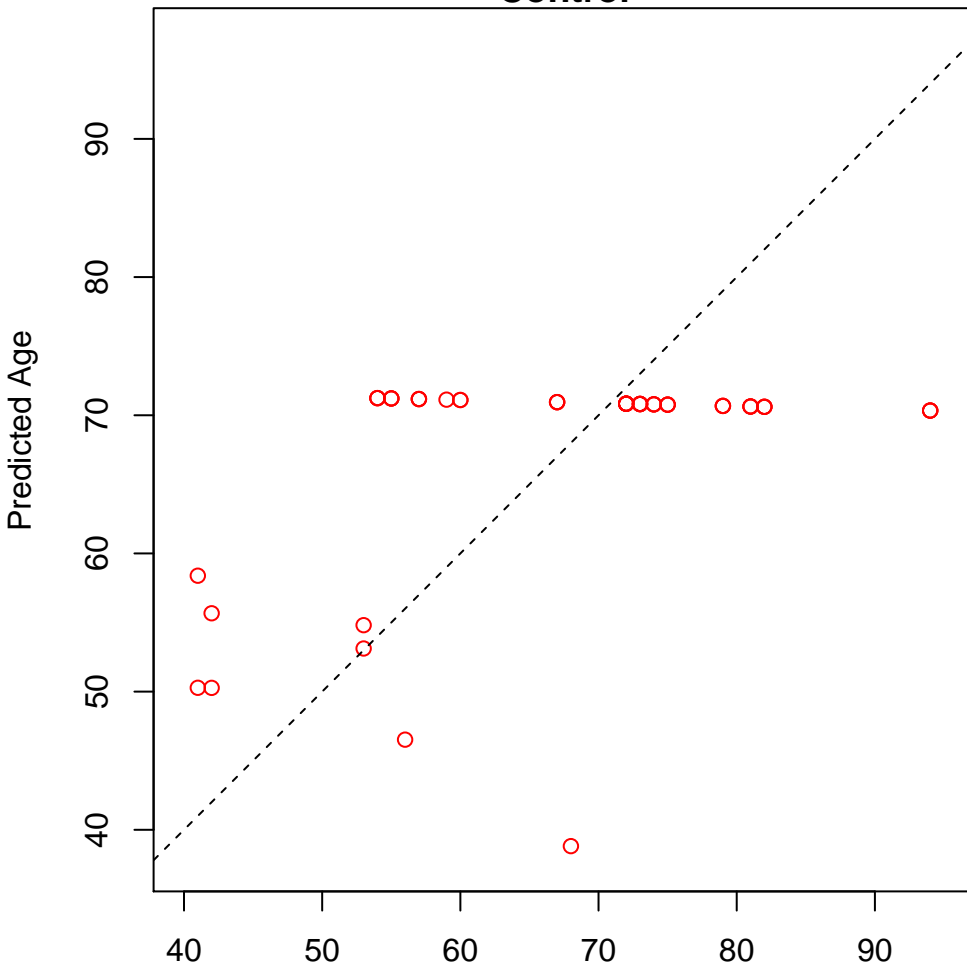
Actual Age

regulation of cellular component biogenesis (Score: 0.786610)

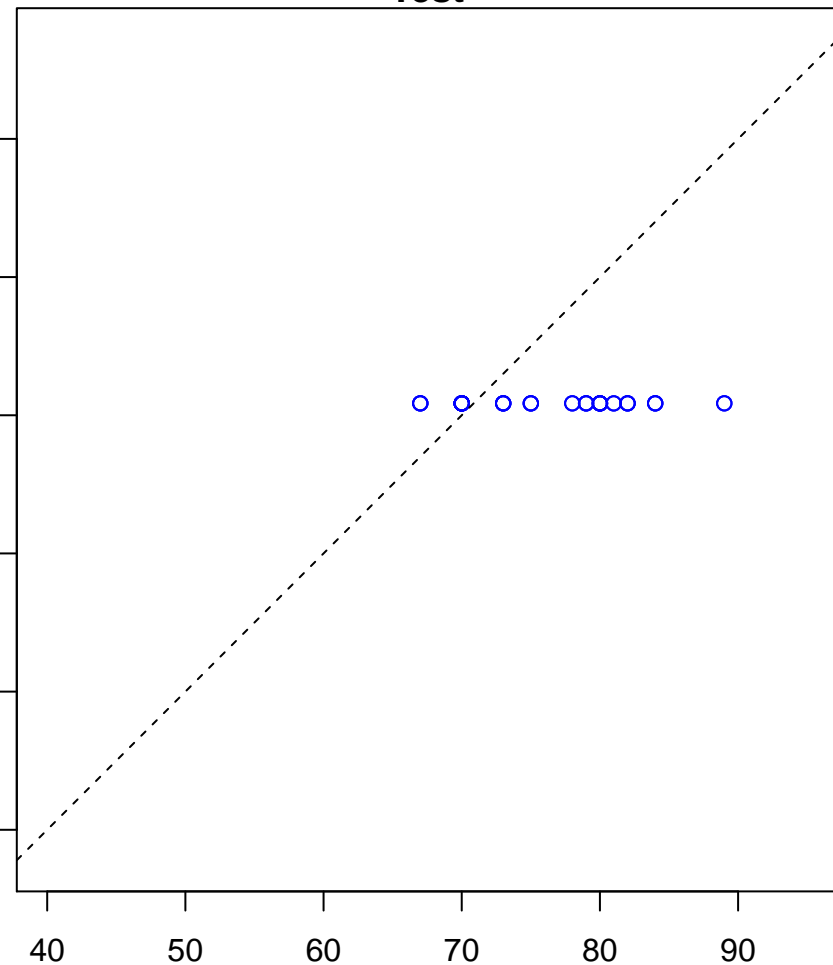


regulation of homeostatic process (Score: 0.786574)

Control

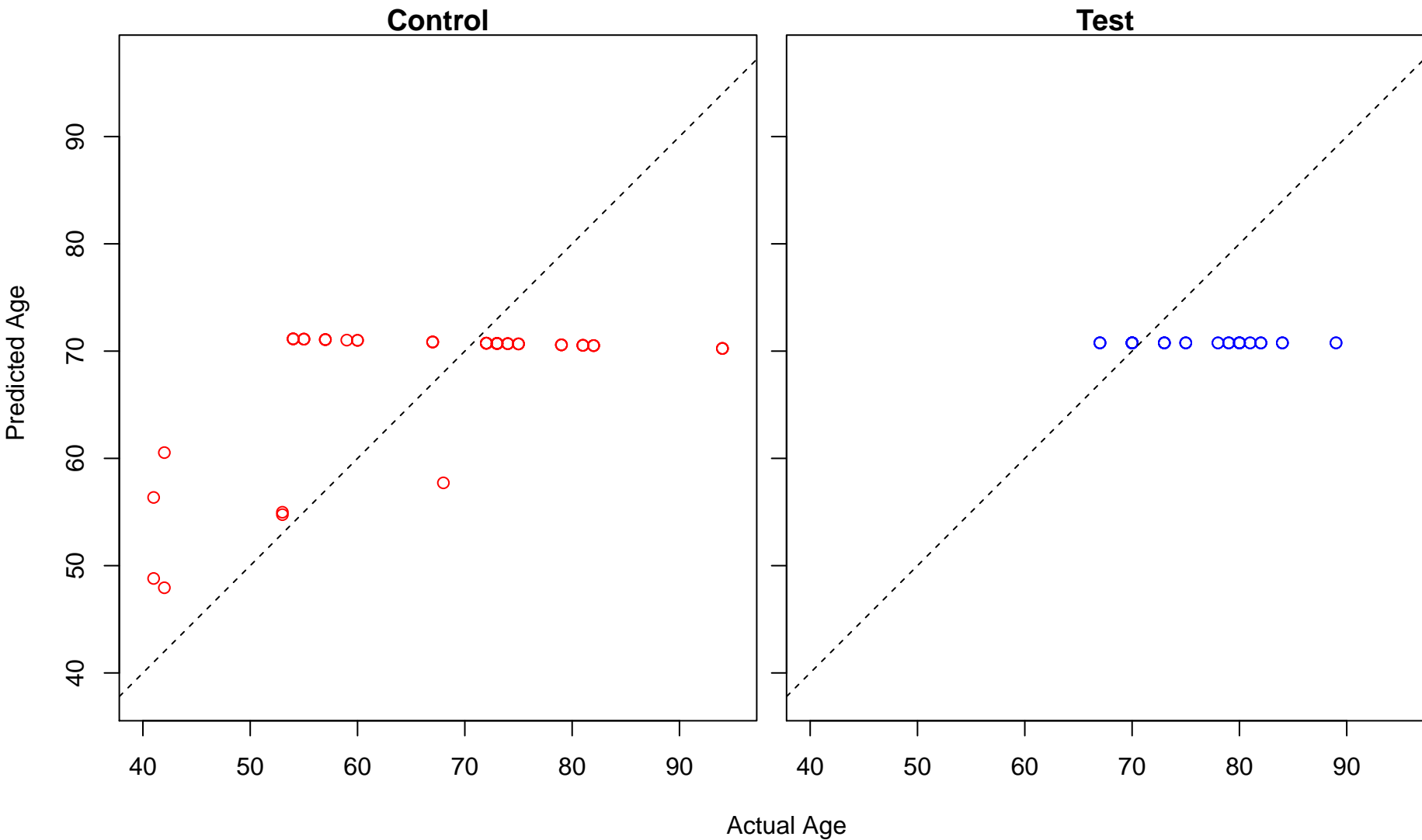


Test

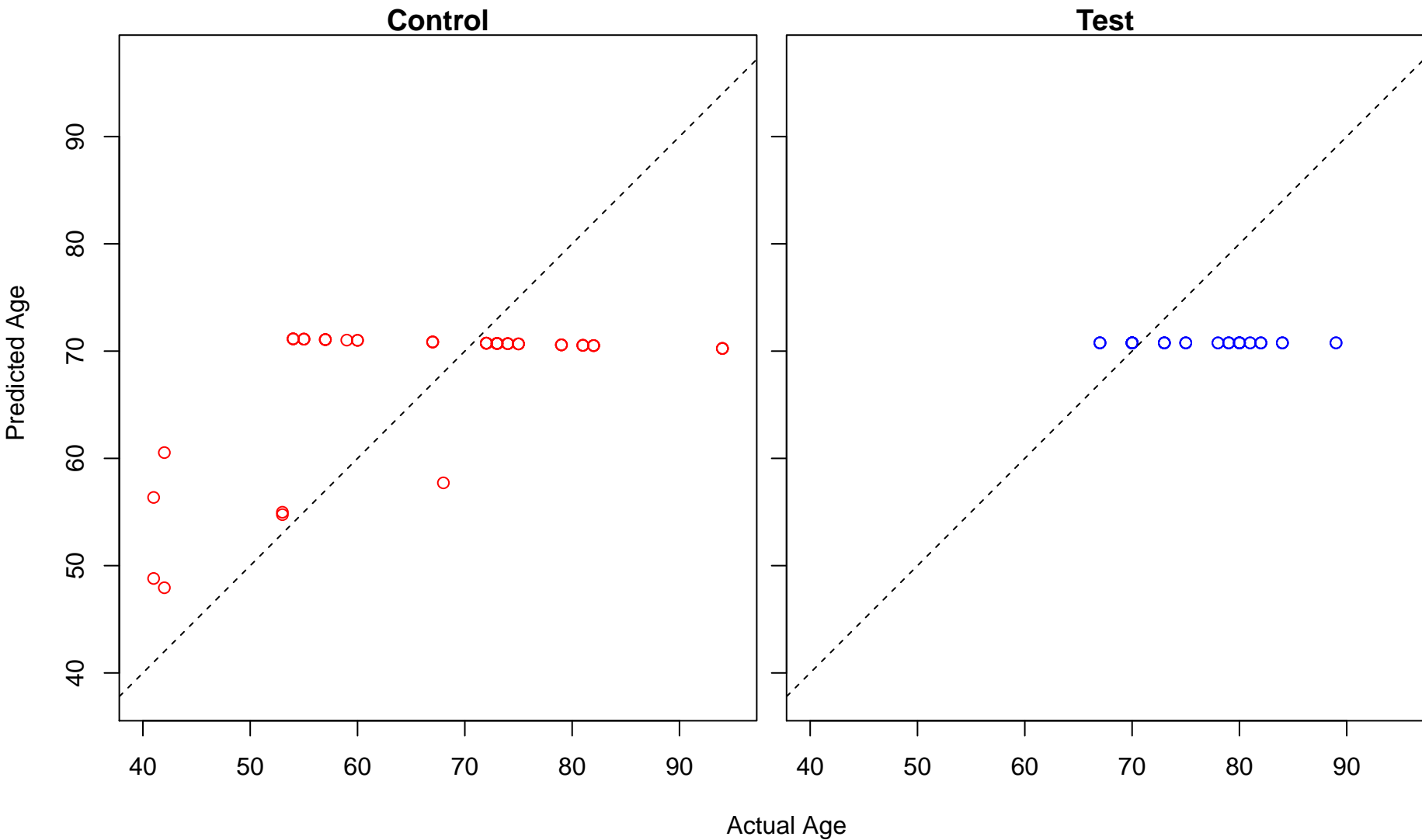


Actual Age

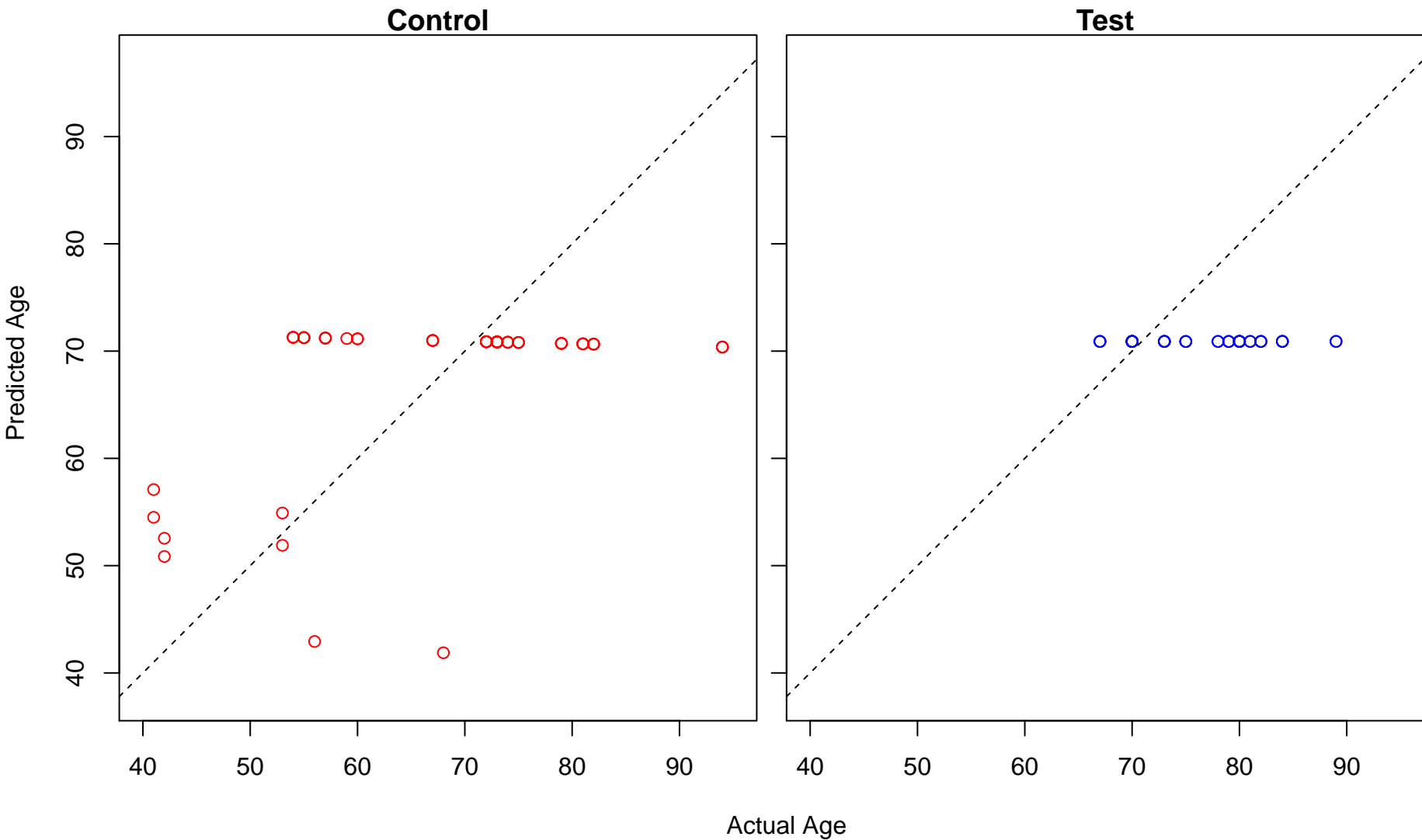
DNA replication-independent nucleosome assembly (Score: 0.786514)



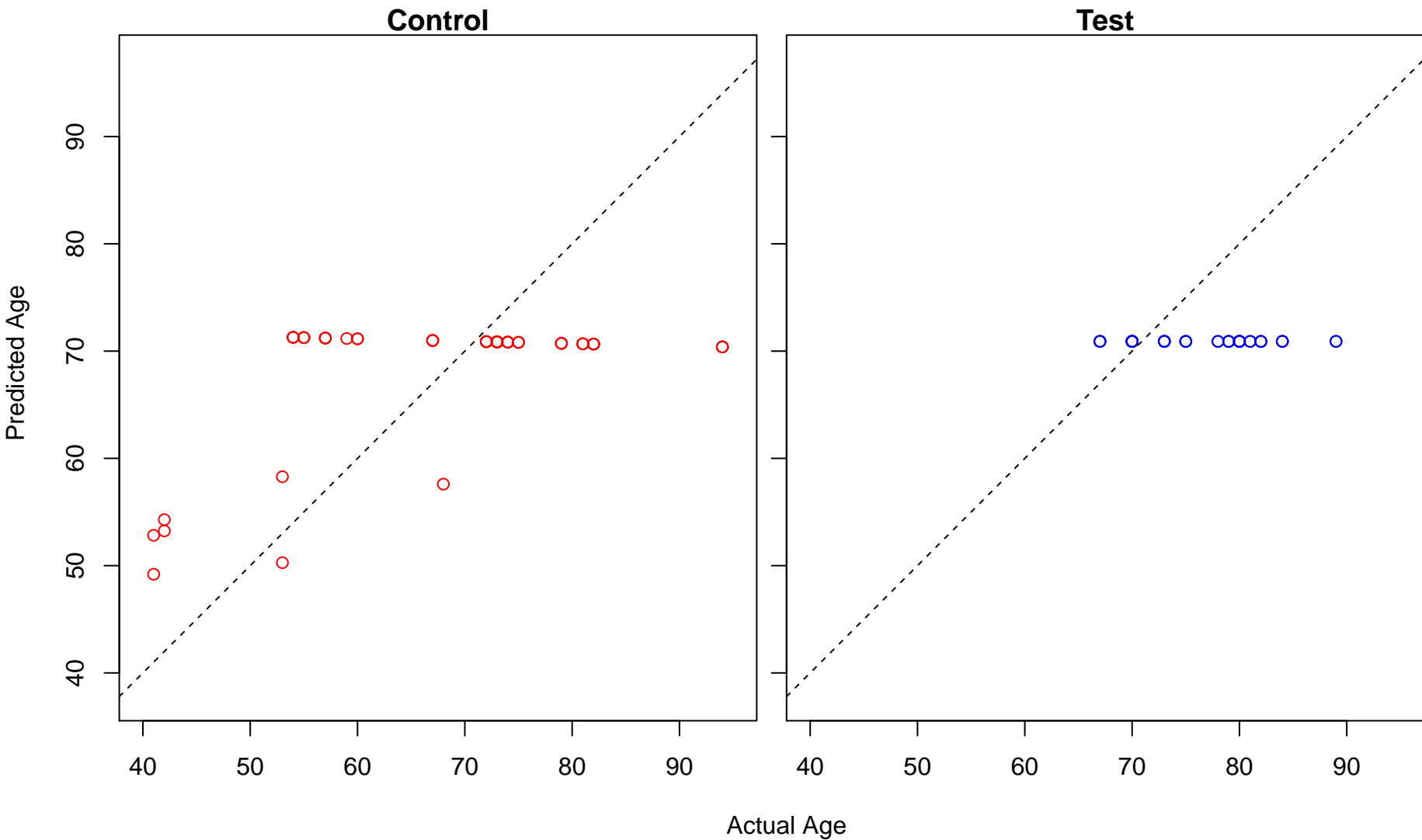
DNA replication-independent nucleosome organization (Score: 0.786514)



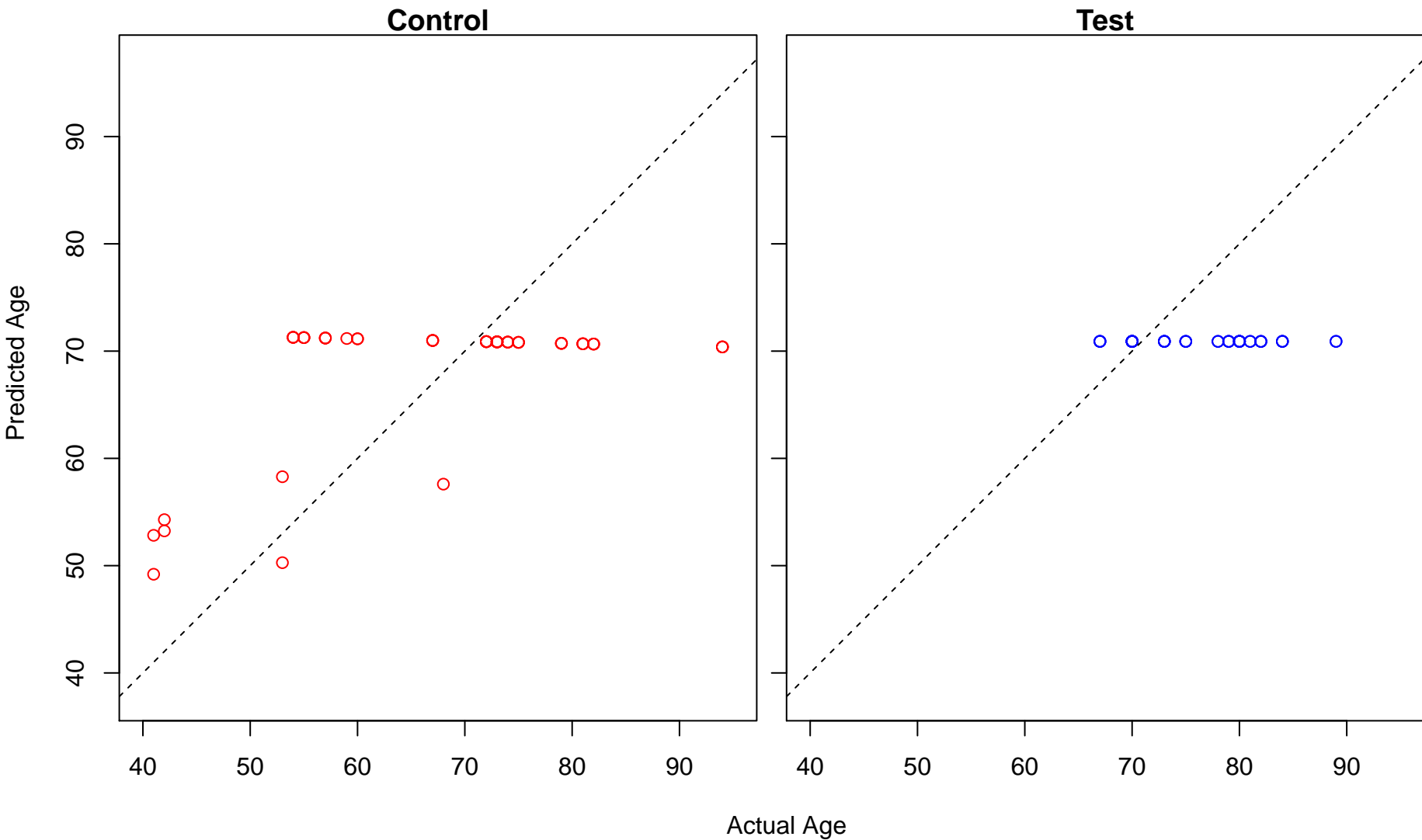
circadian rhythm (Score: 0.786463)



regulation of transcription from RNA polymerase I promoter (Score: 0.786444)

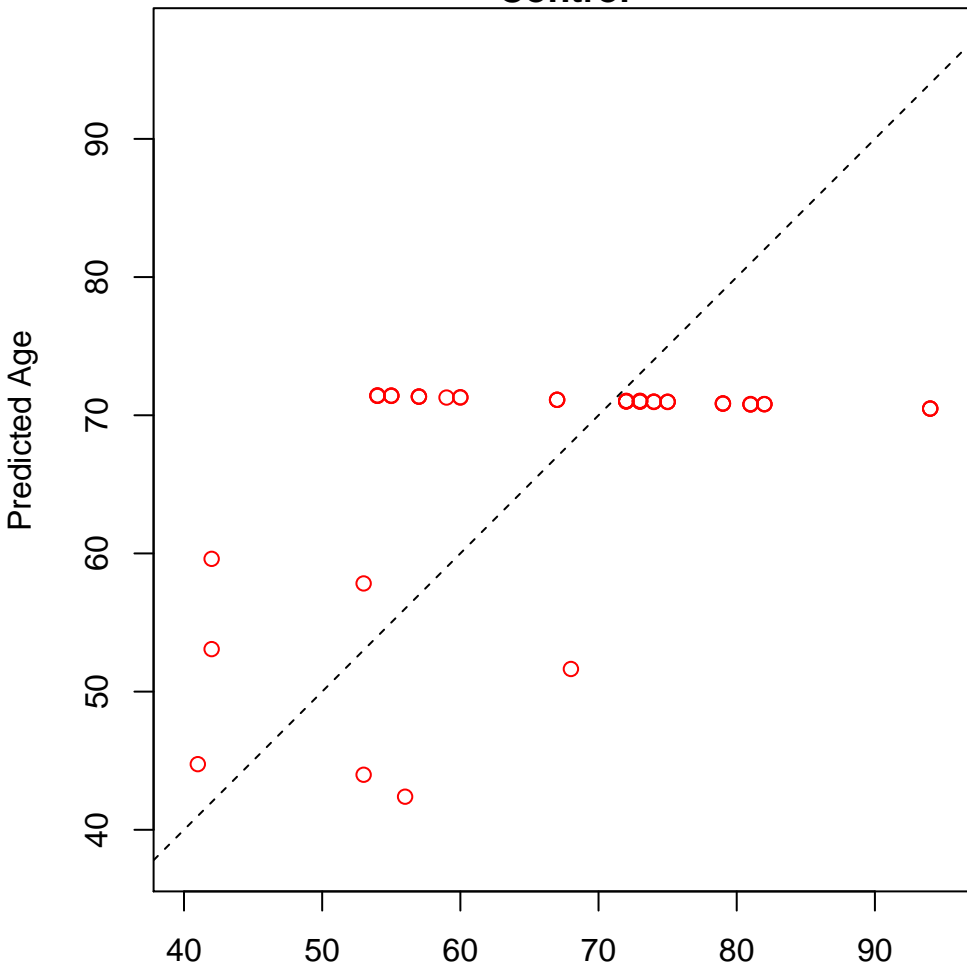


positive regulation of transcription from RNA polymerase I promoter (Score: 0.786444)

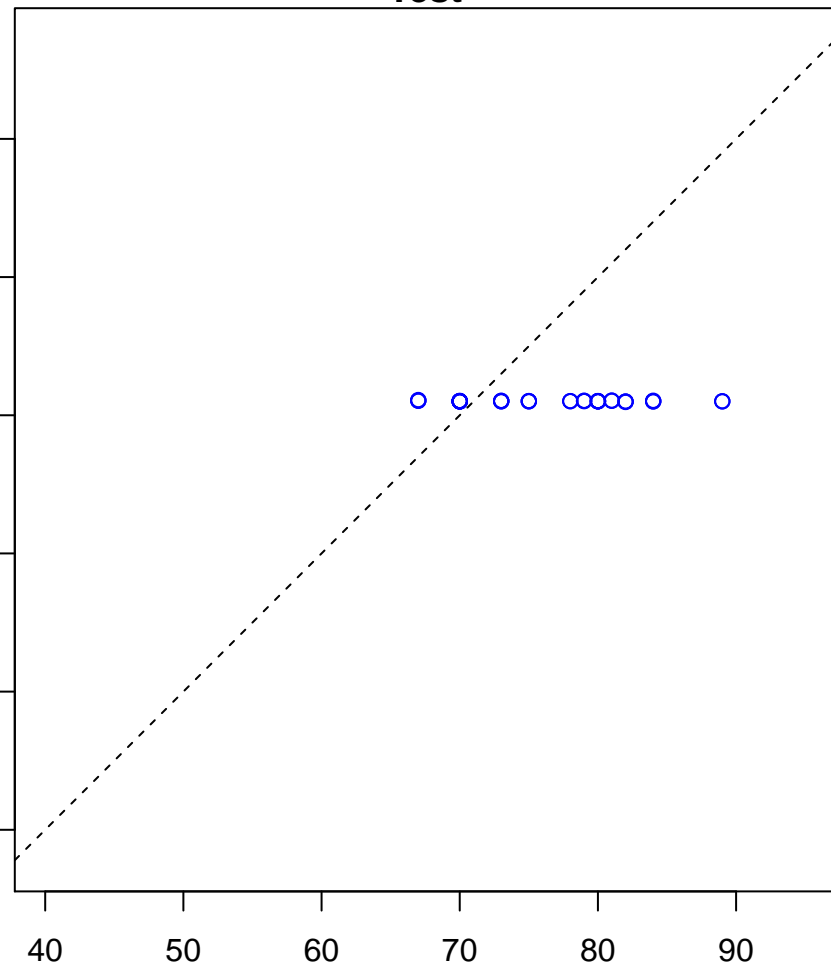


morphogenesis of an epithelium (Score: 0.786416)

Control



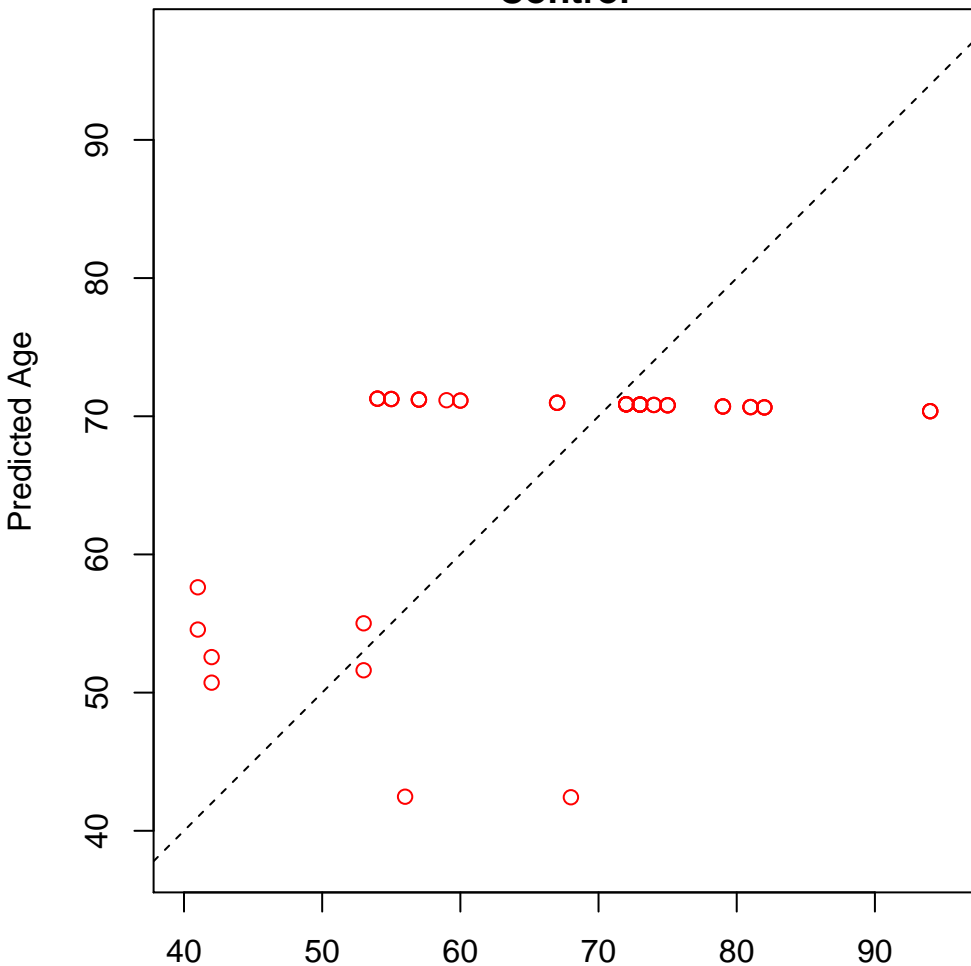
Test



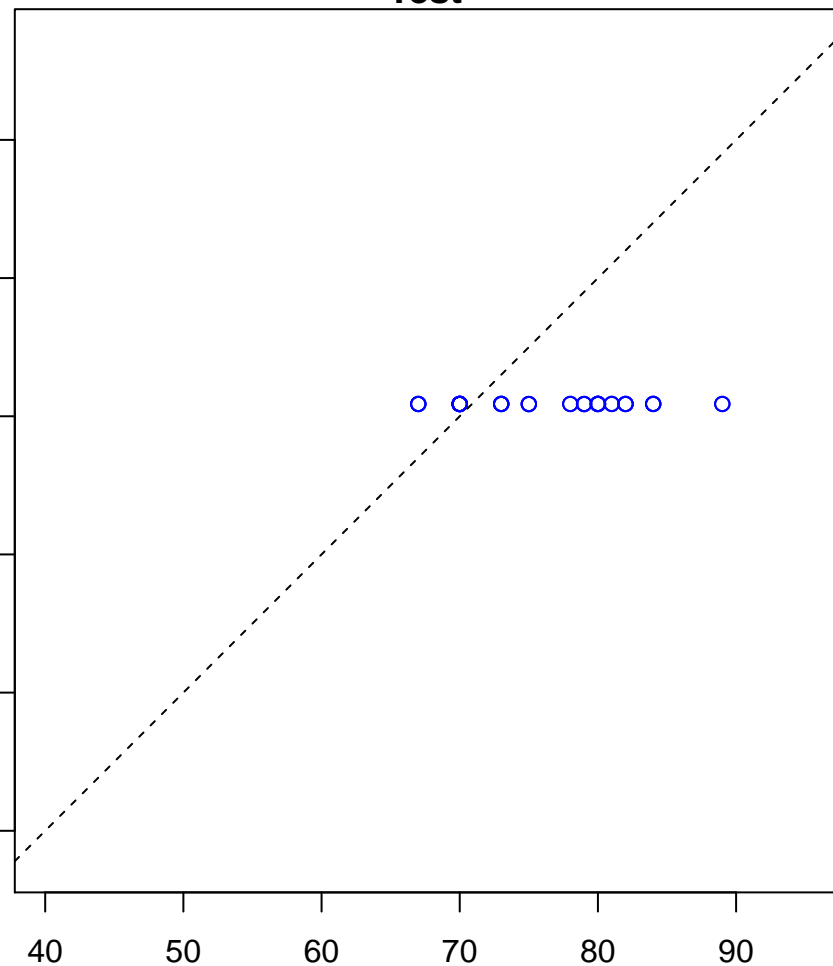
Actual Age

circadian regulation of gene expression (Score: 0.786260)

Control

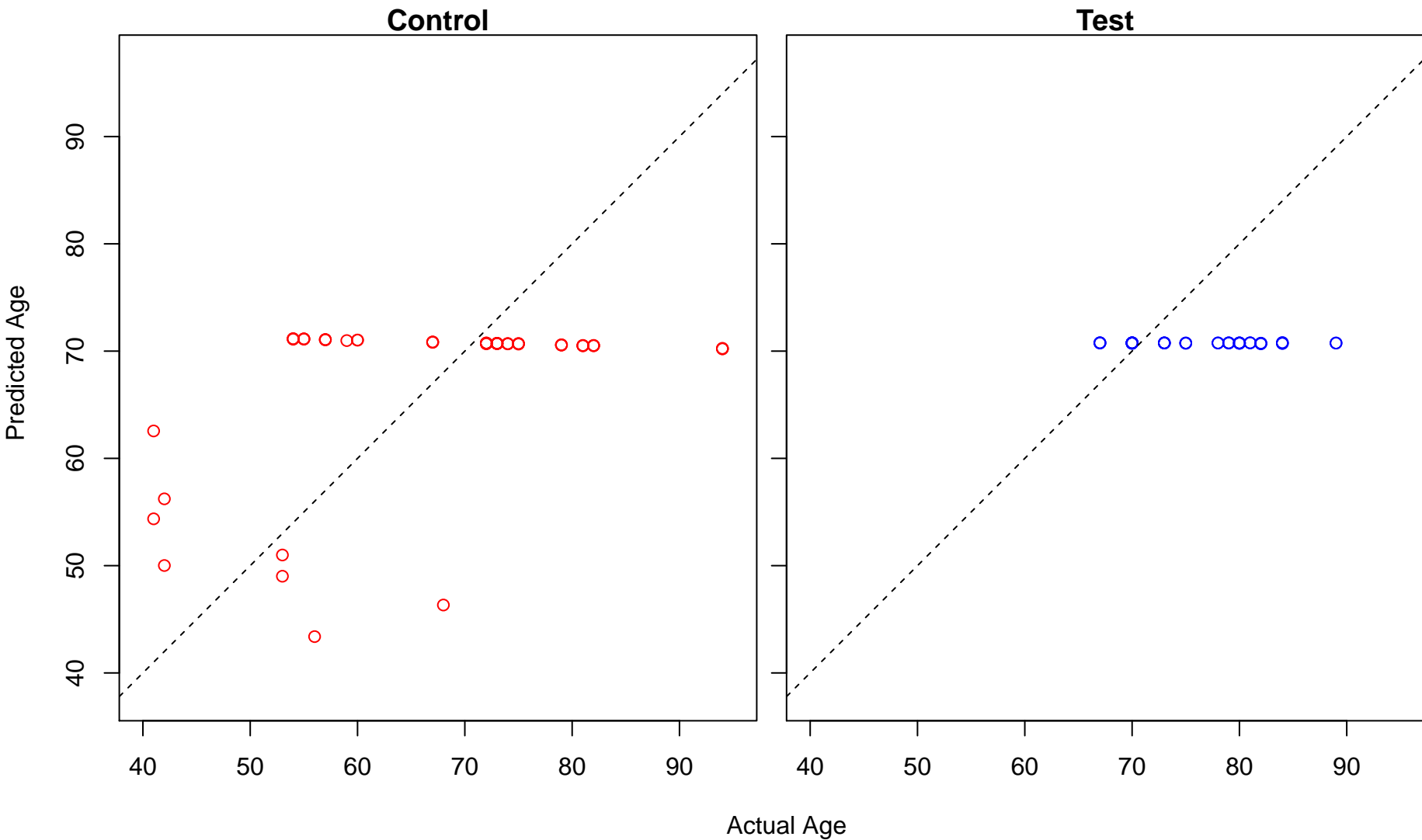


Test

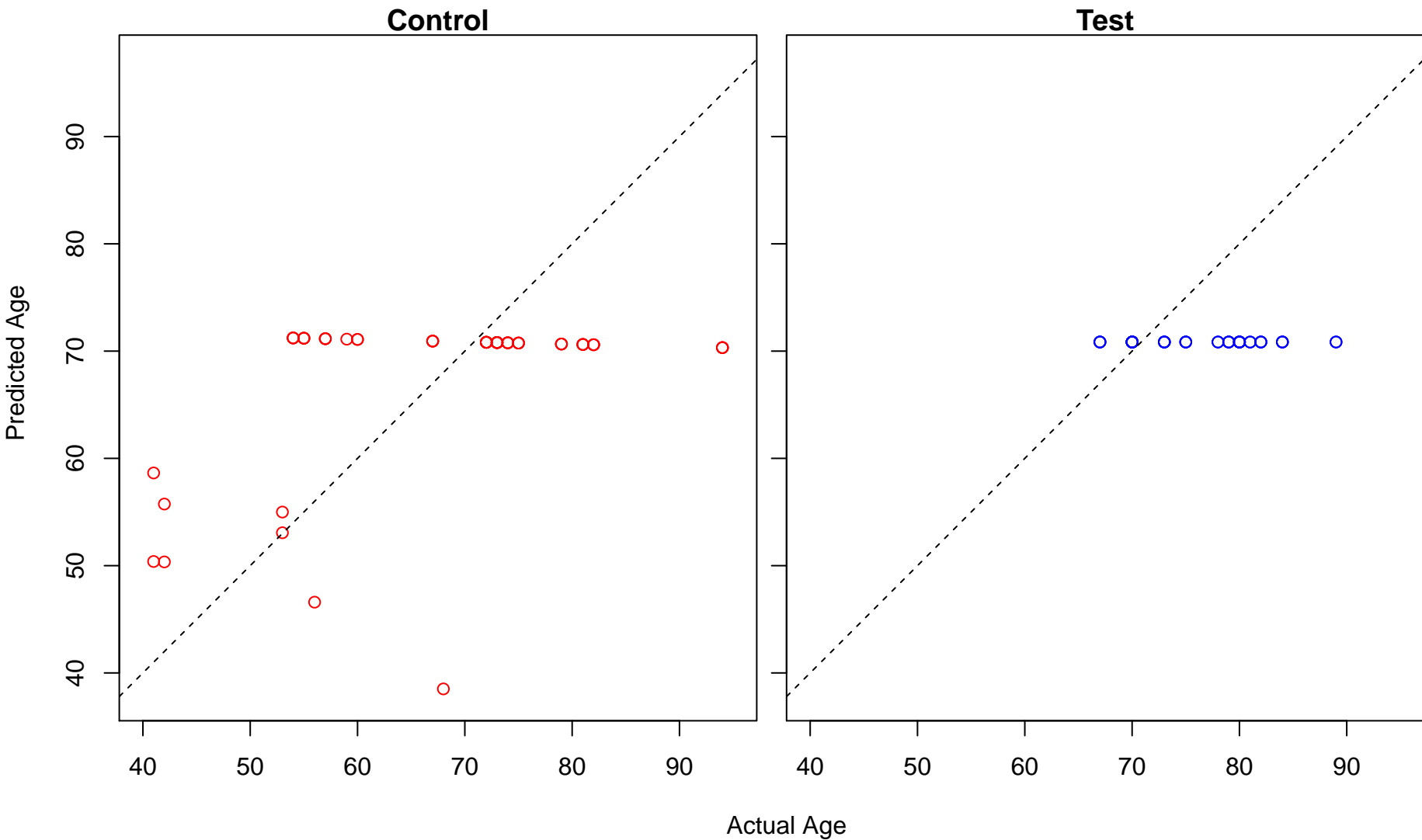


Actual Age

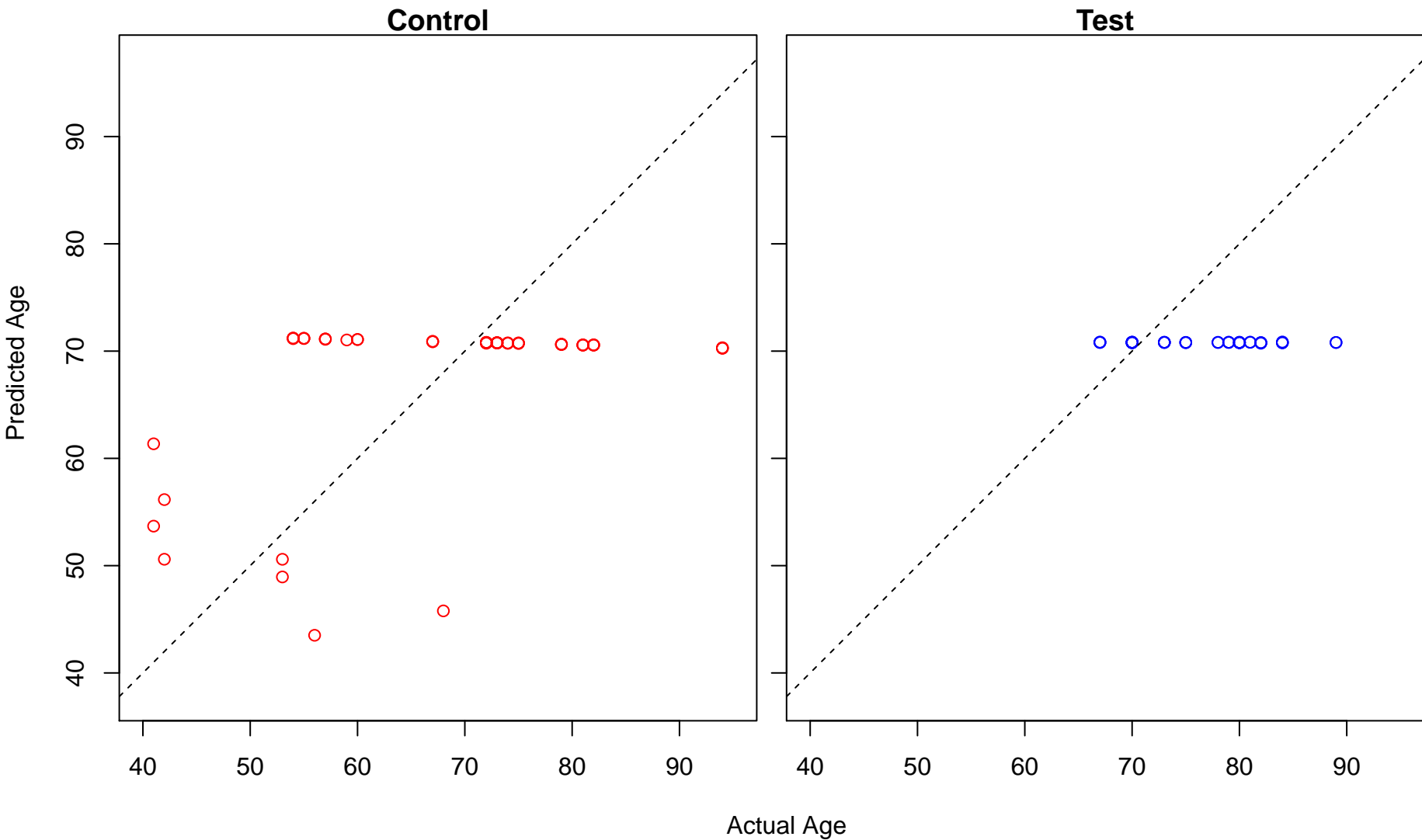
endoderm development (Score: 0.785944)



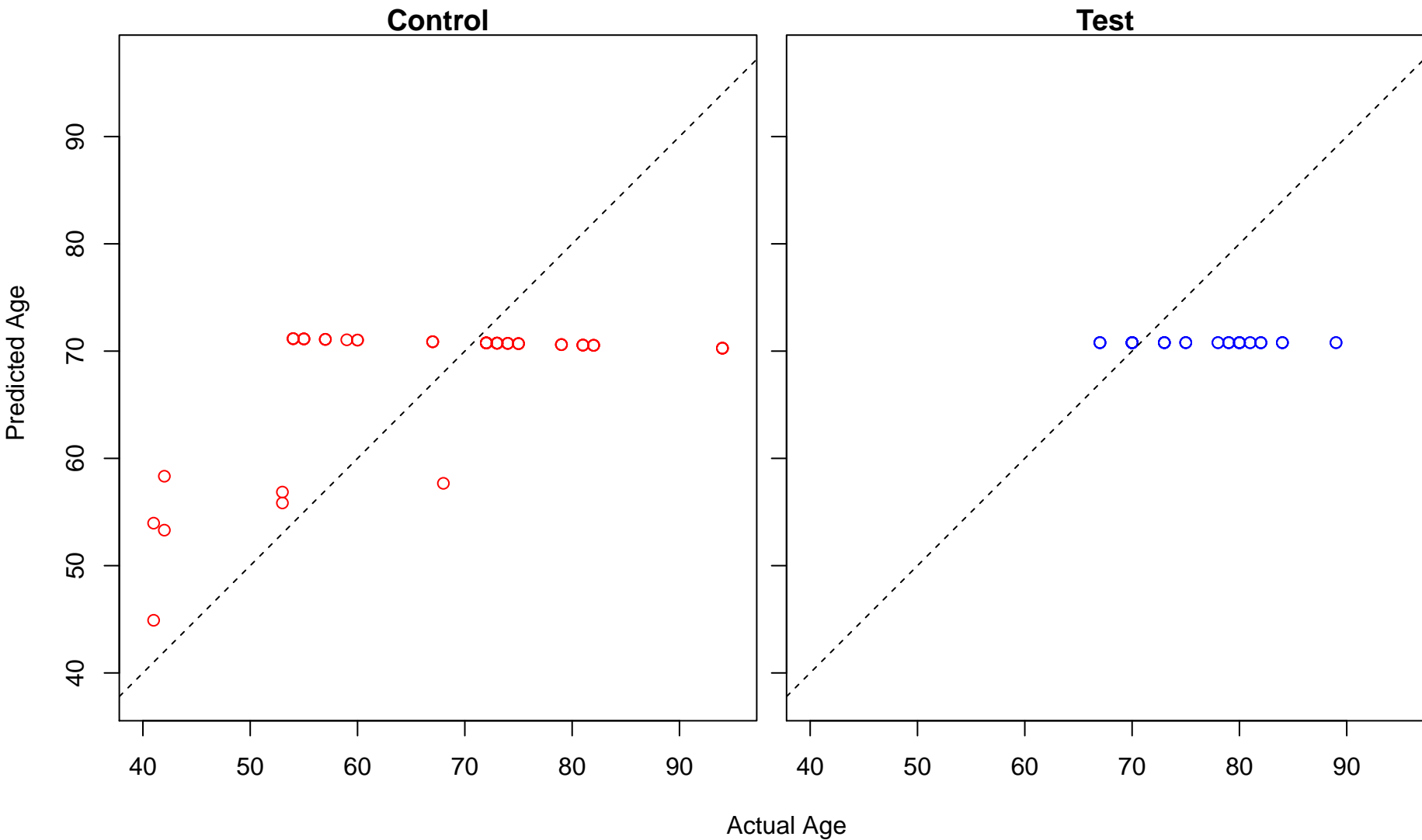
positive regulation of homeostatic process (Score: 0.785819)



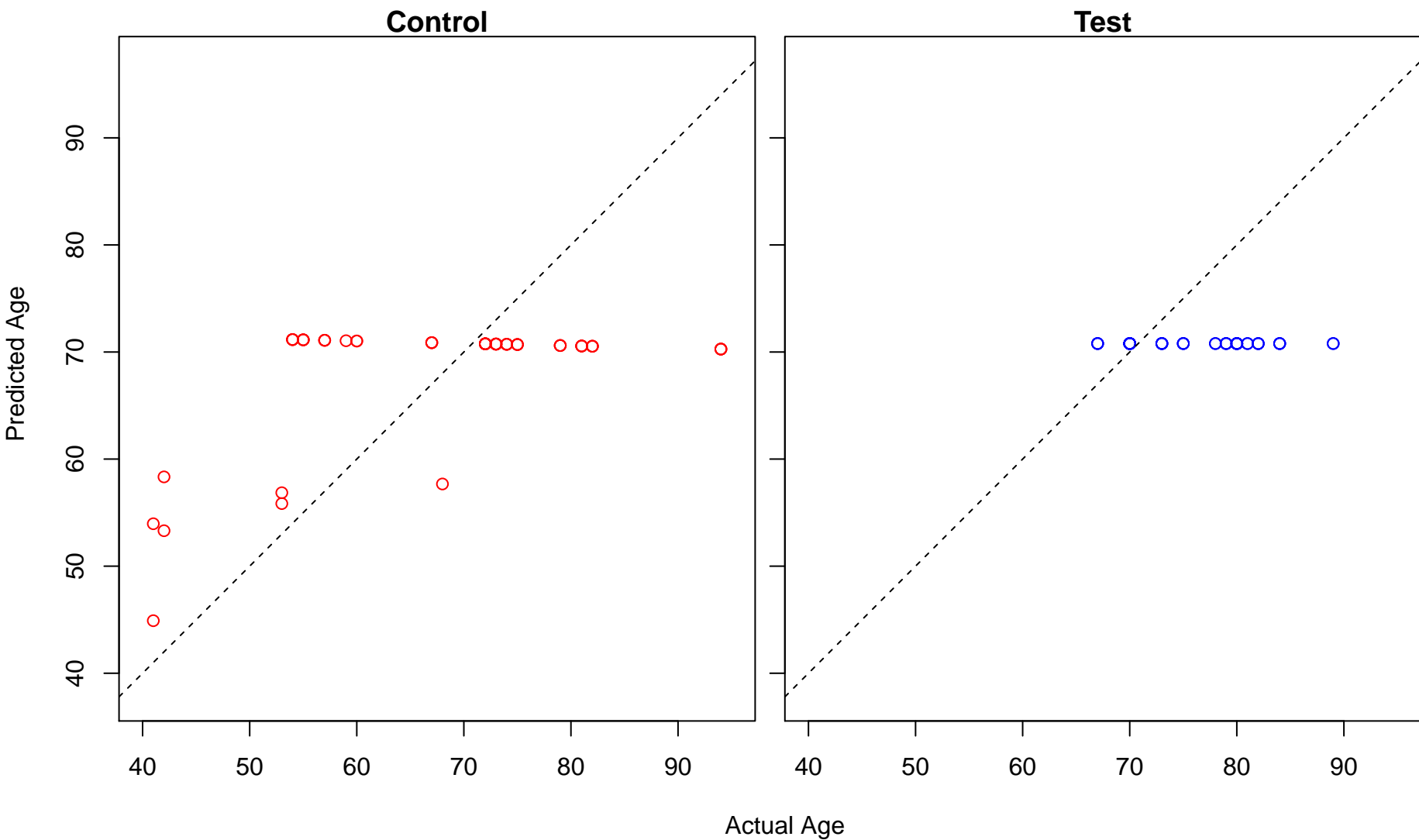
substrate adhesion-dependent cell spreading (Score: 0.785480)



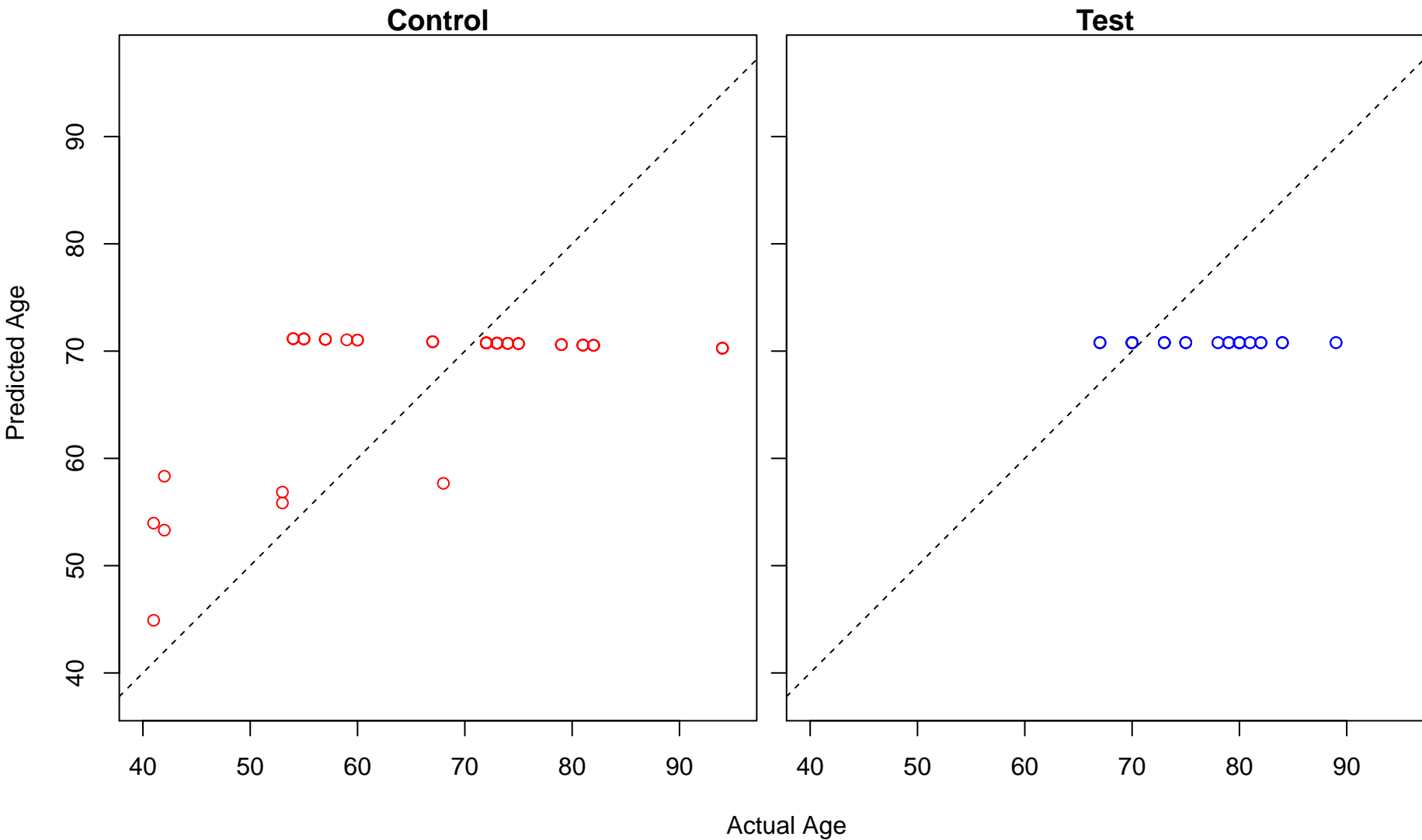
blood vessel development (Score: 0.784801)



vasculature development (Score: 0.784801)

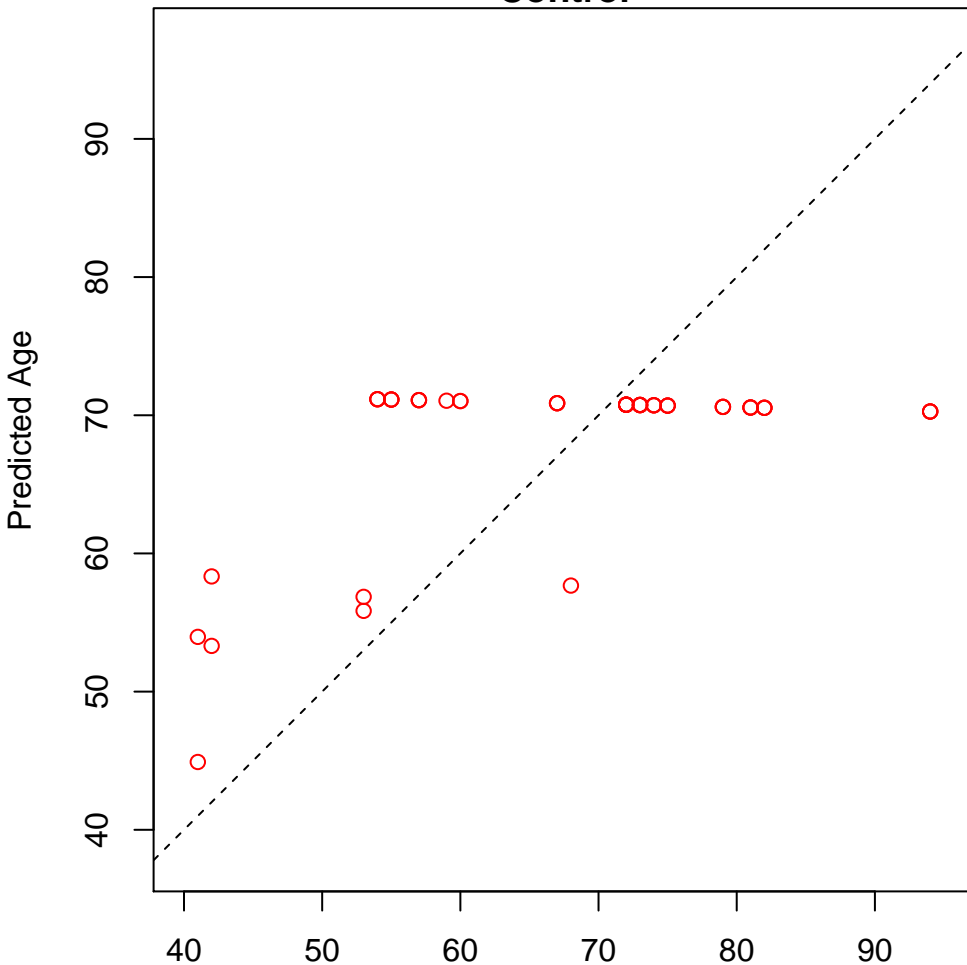


blood vessel morphogenesis (Score: 0.784801)

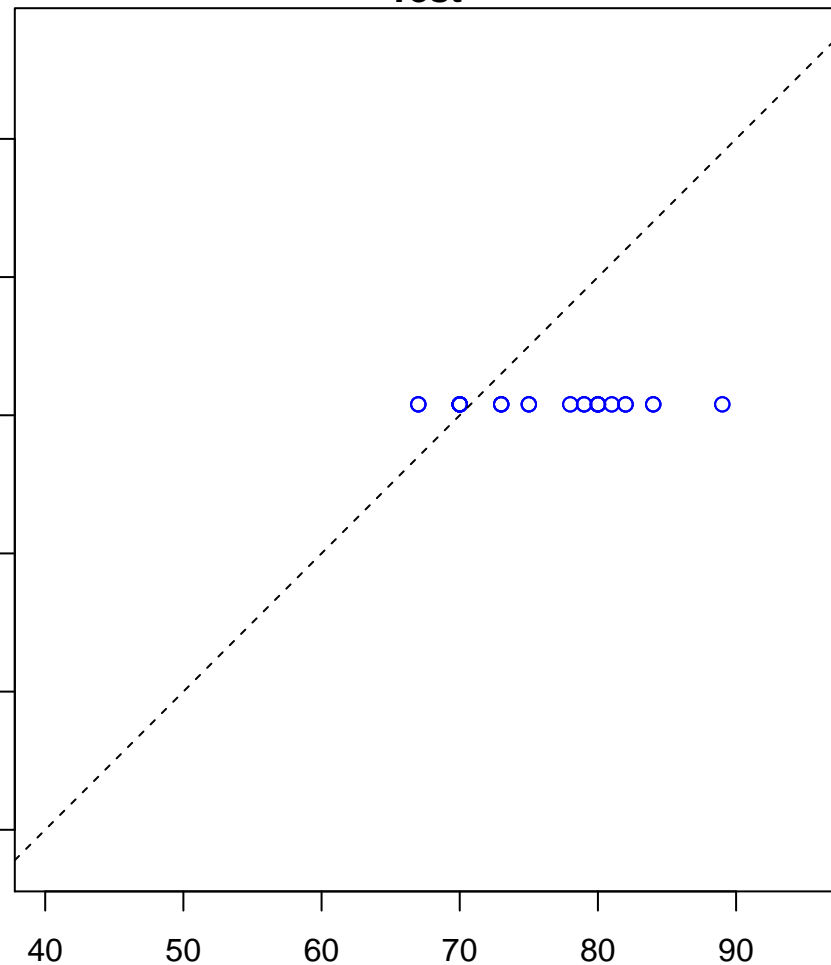


cardiovascular system development (Score: 0.784801)

Control

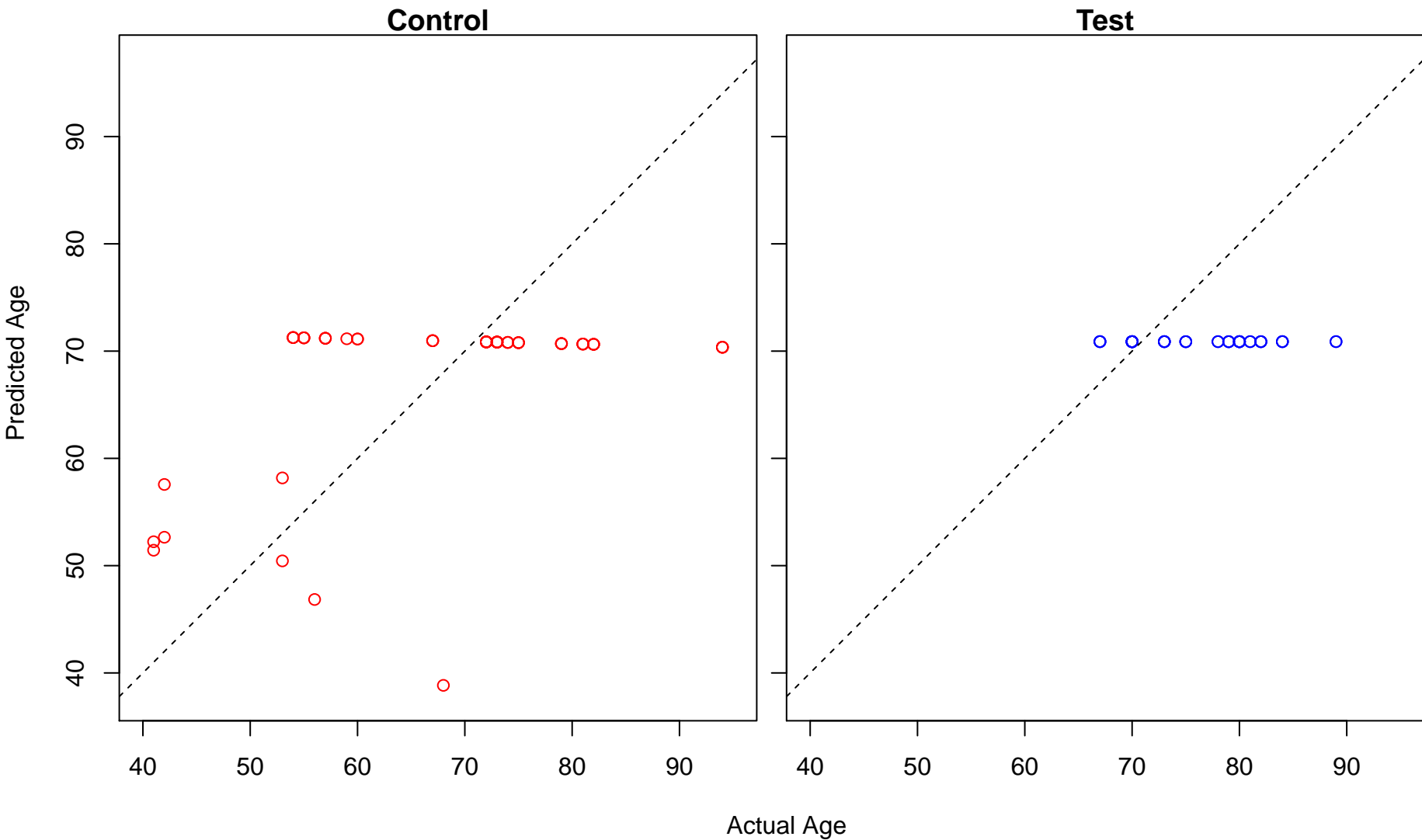


Test

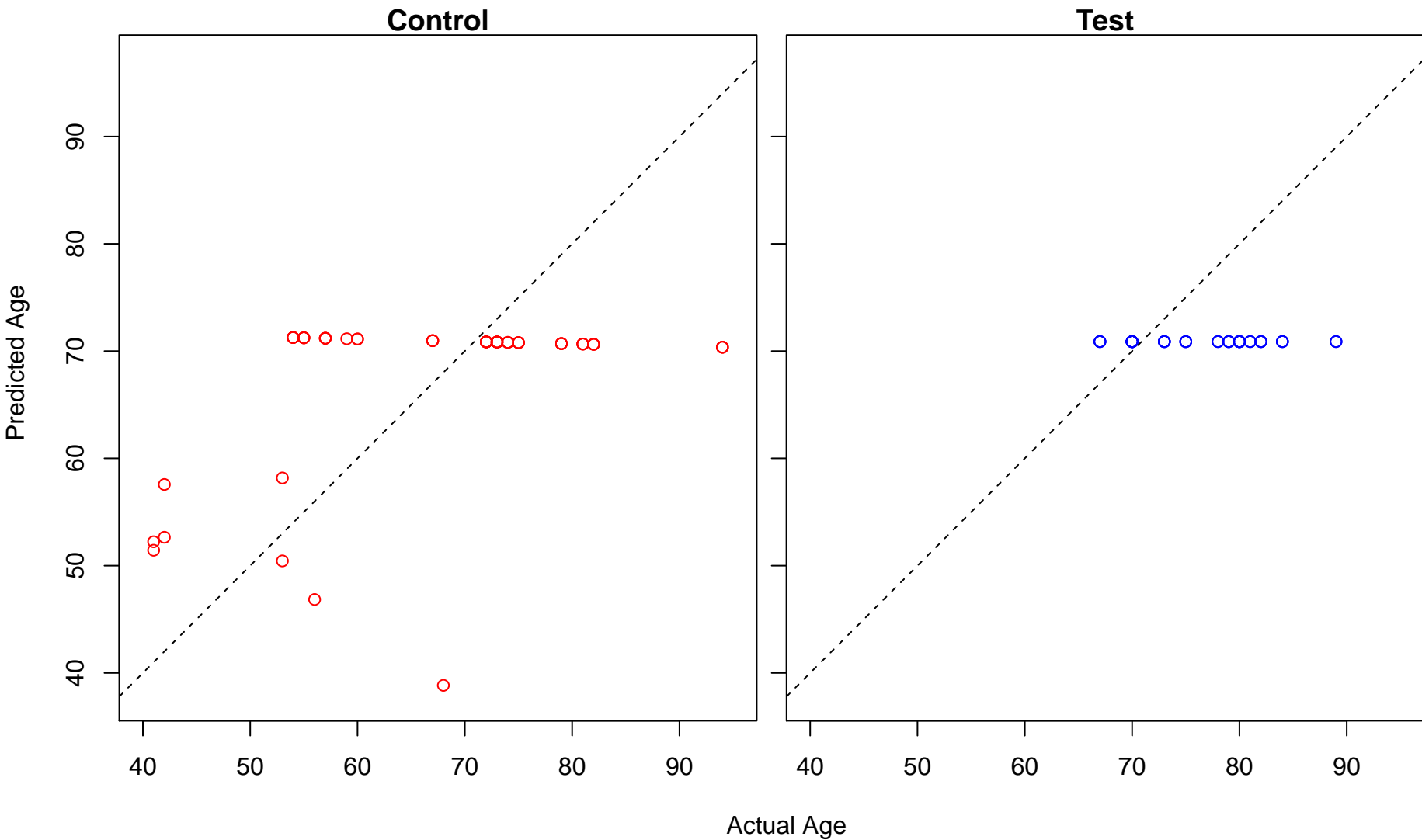


Actual Age

transcription, DNA-templated (Score: 0.784469)

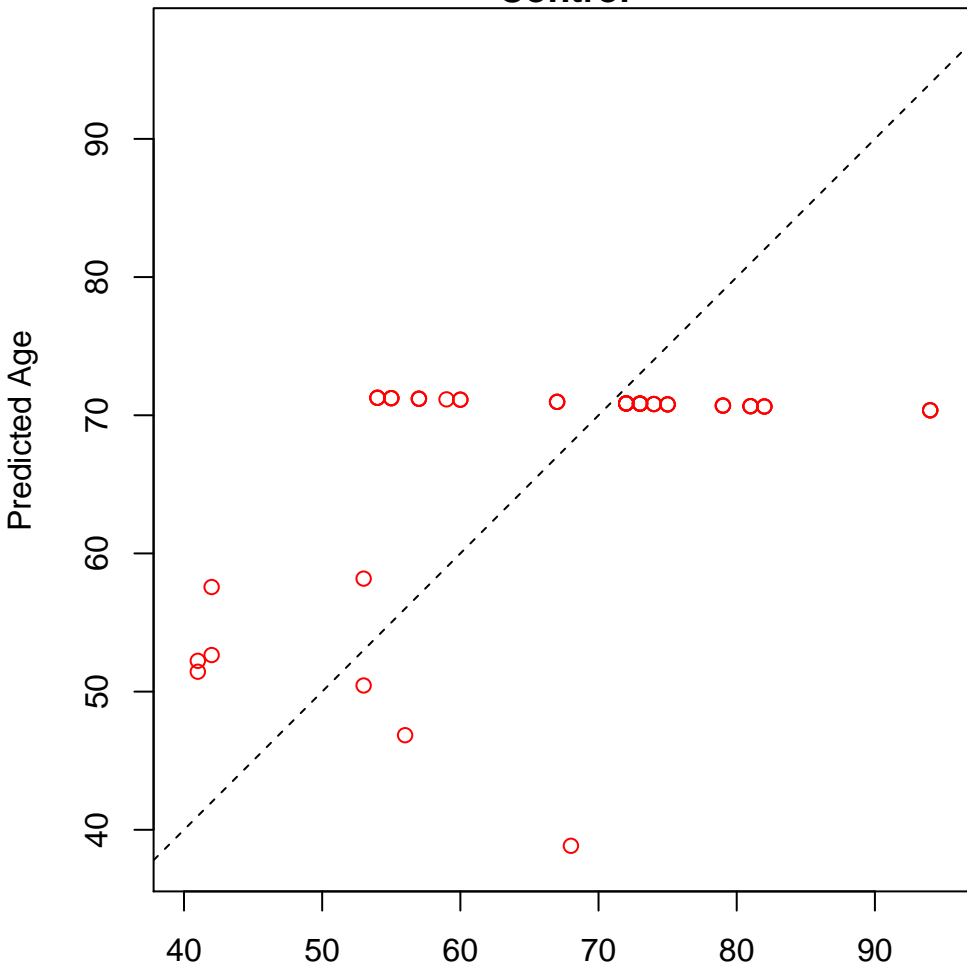


RNA biosynthetic process (Score: 0.784469)

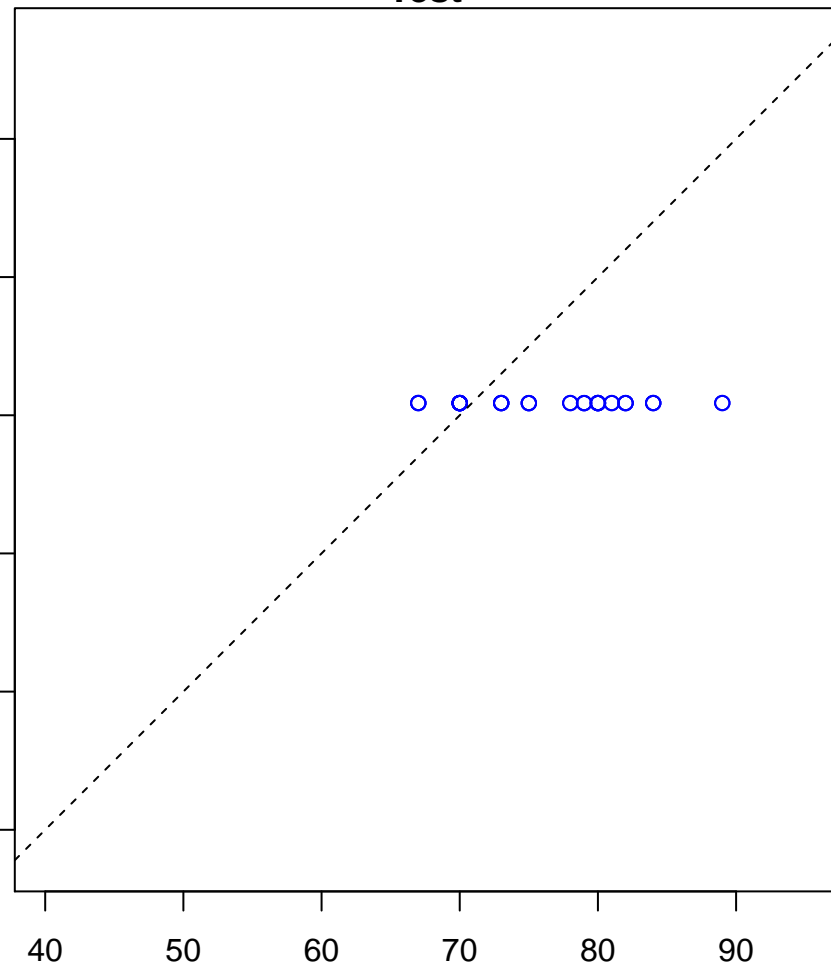


nucleic acid-templated transcription (Score: 0.784469)

Control

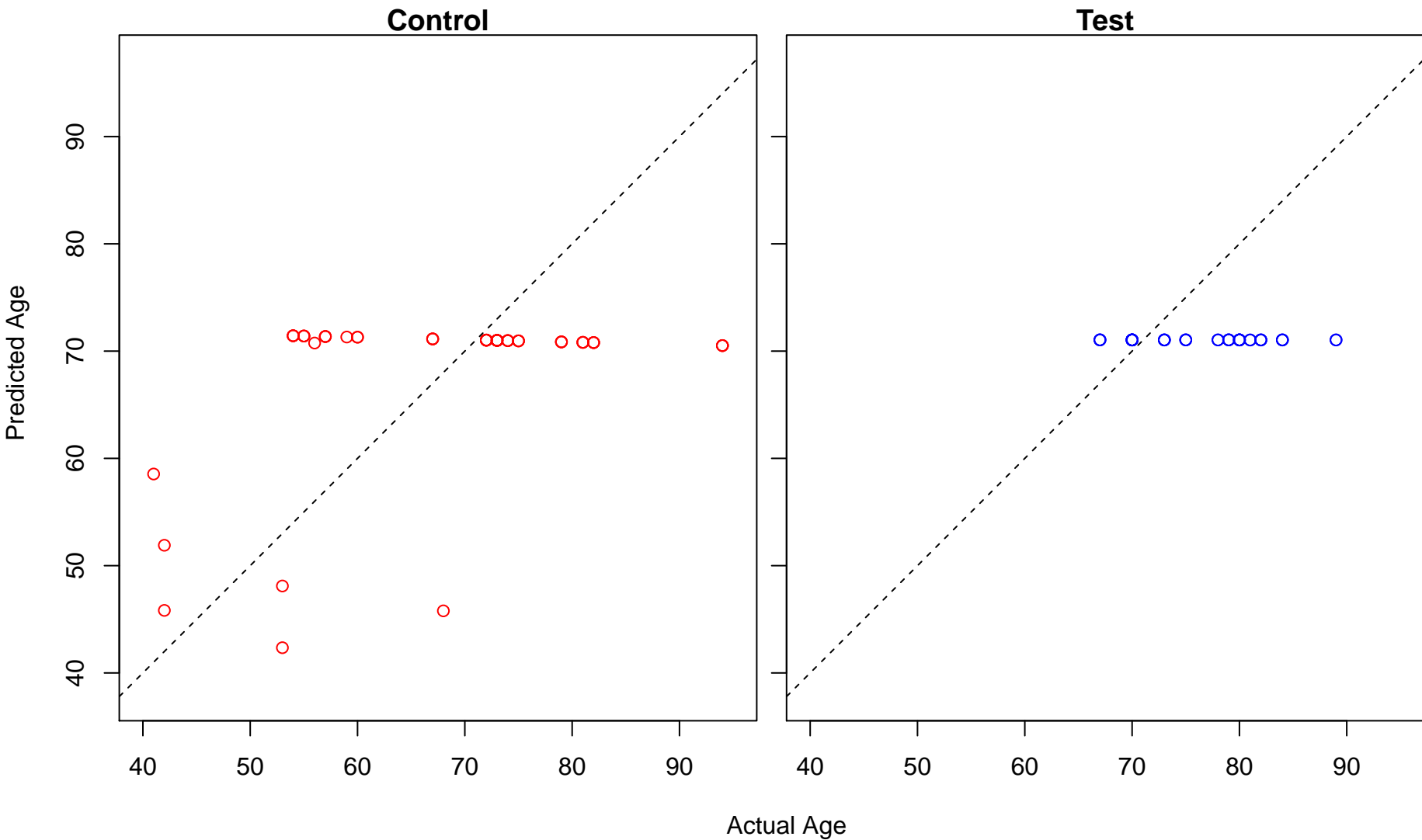


Test



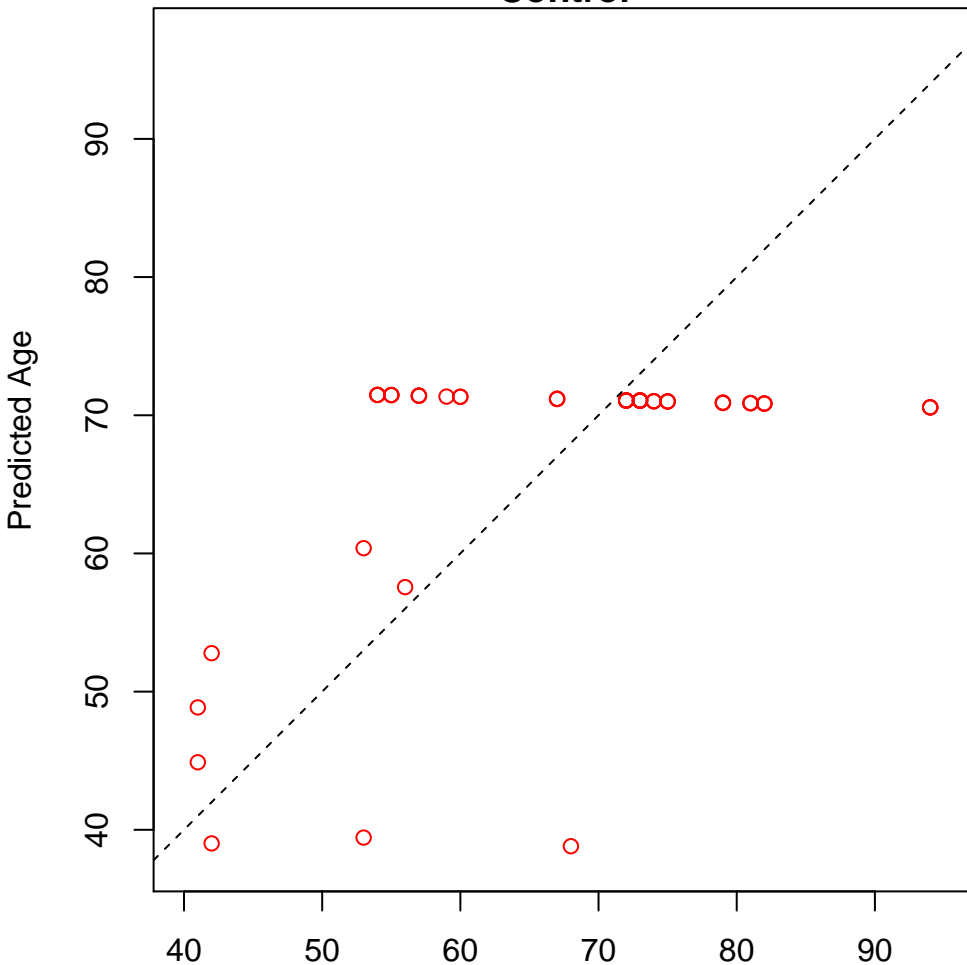
Actual Age

membrane invagination (Score: 0.784455)

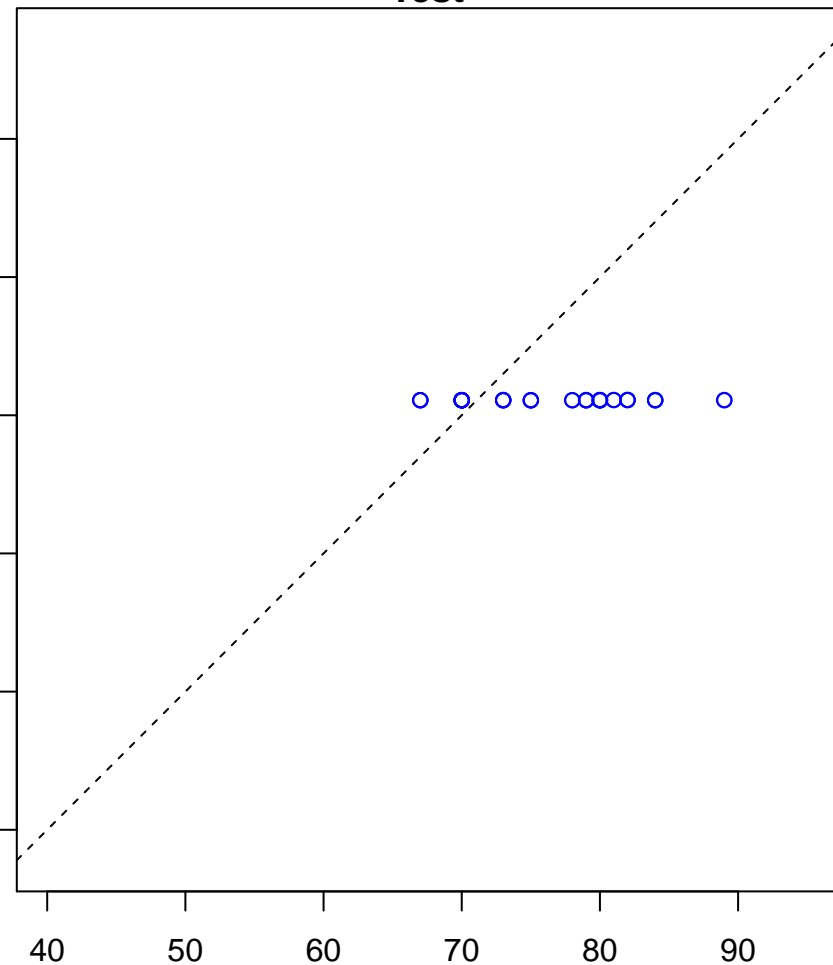


regulation of telomere maintenance (Score: 0.784425)

Control



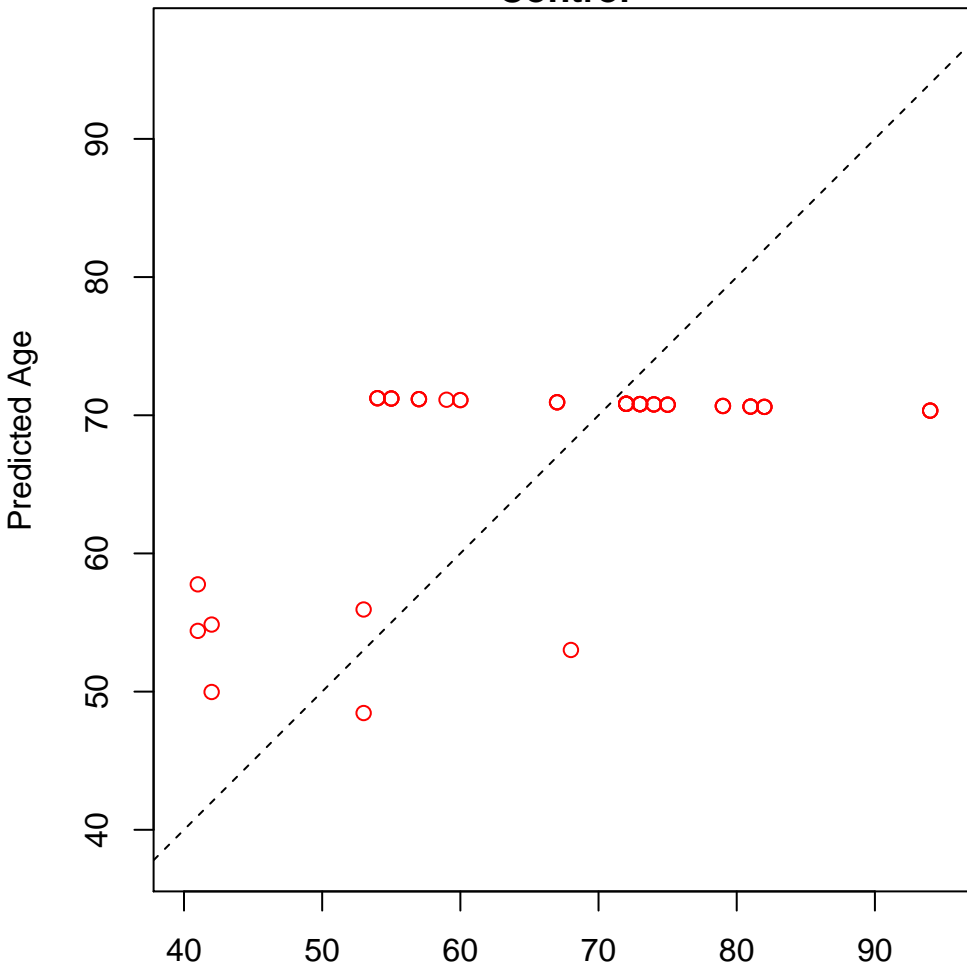
Test



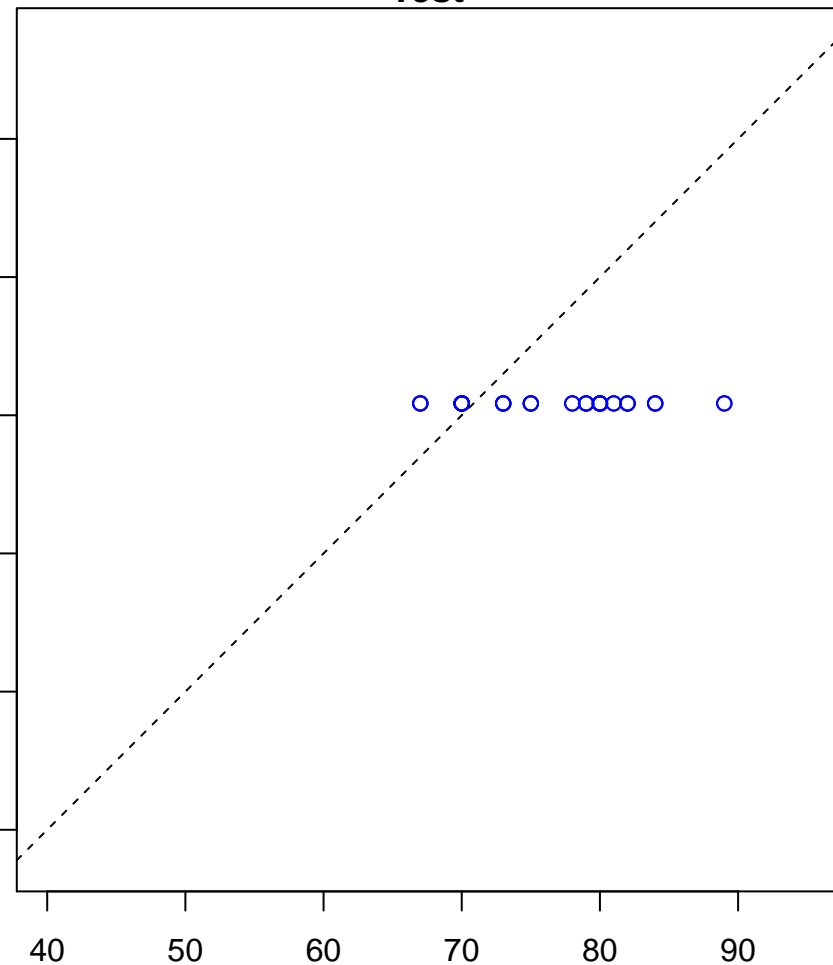
Actual Age

ribosomal small subunit biogenesis (Score: 0.784367)

Control



Test



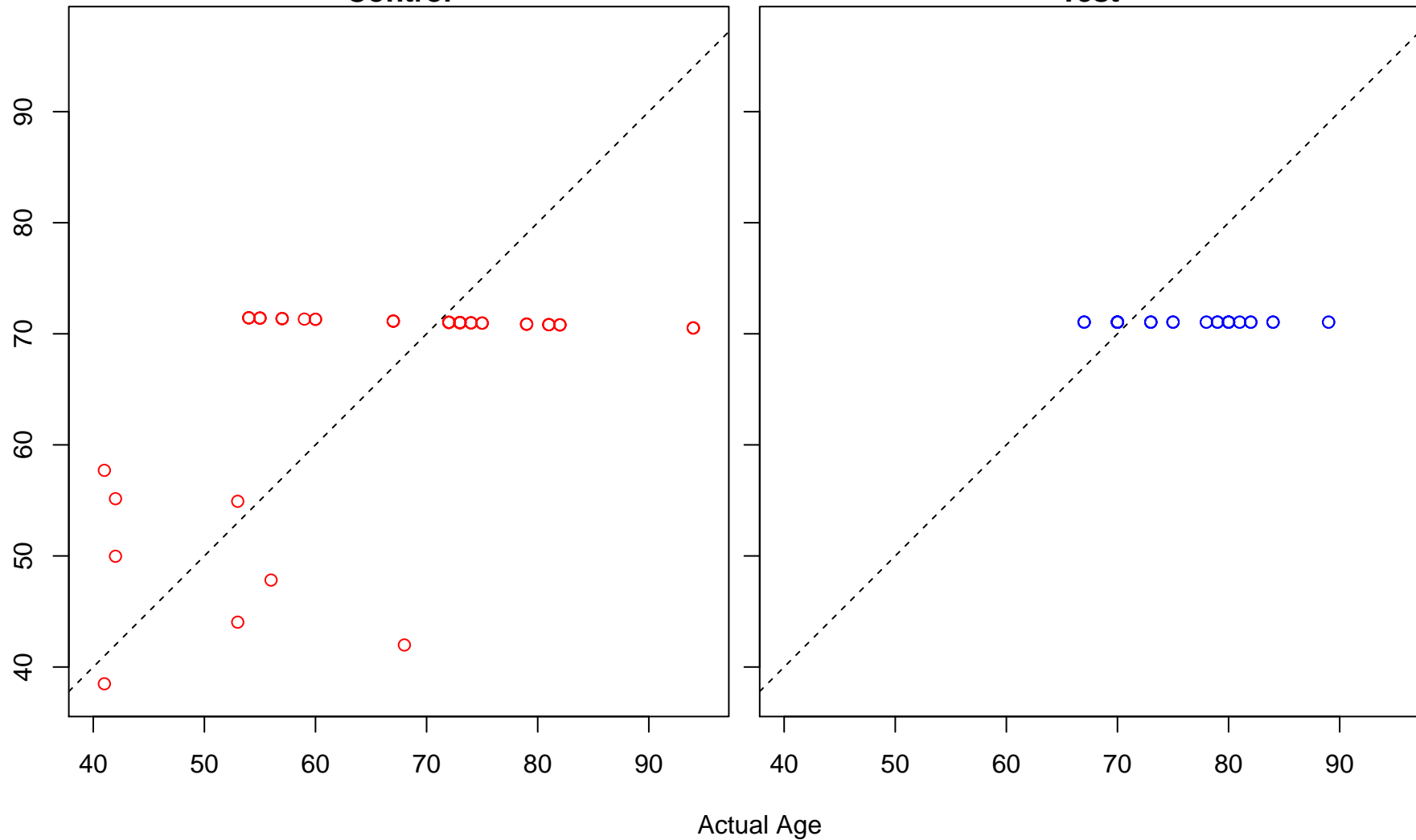
Actual Age

negative regulation of viral life cycle (Score: 0.783575)

Control

Test

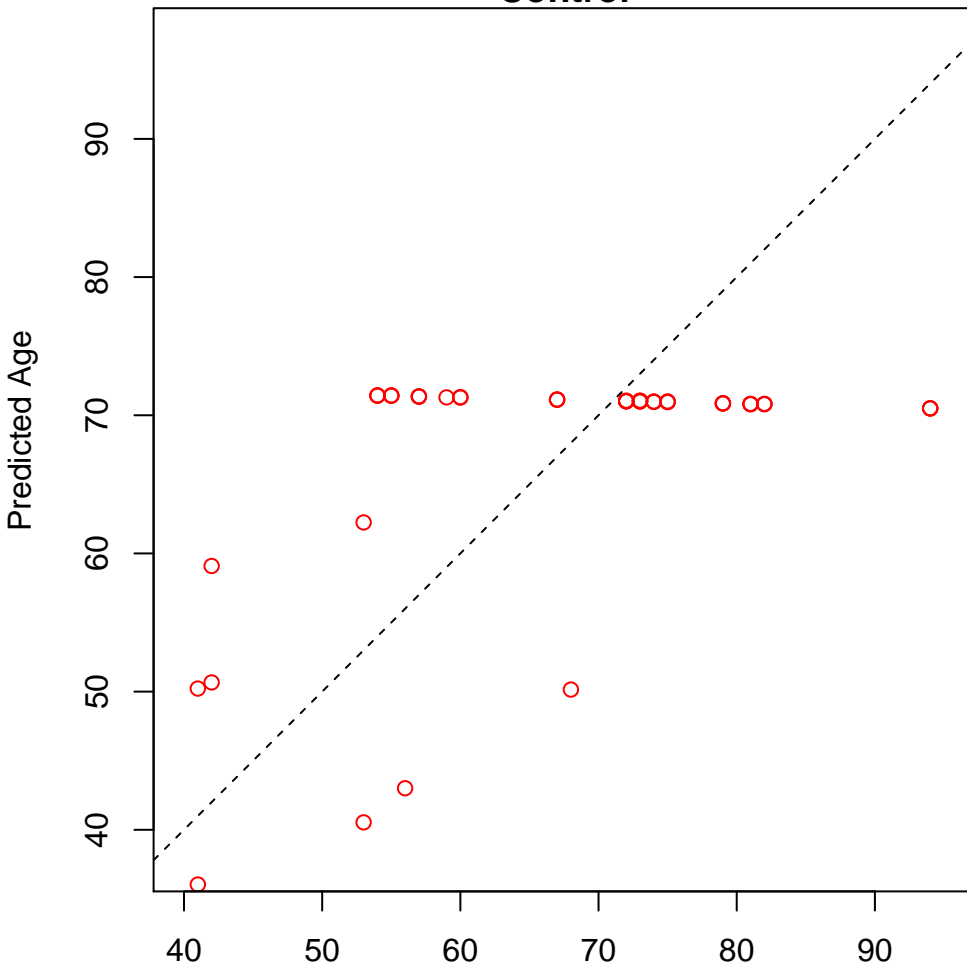
Predicted Age



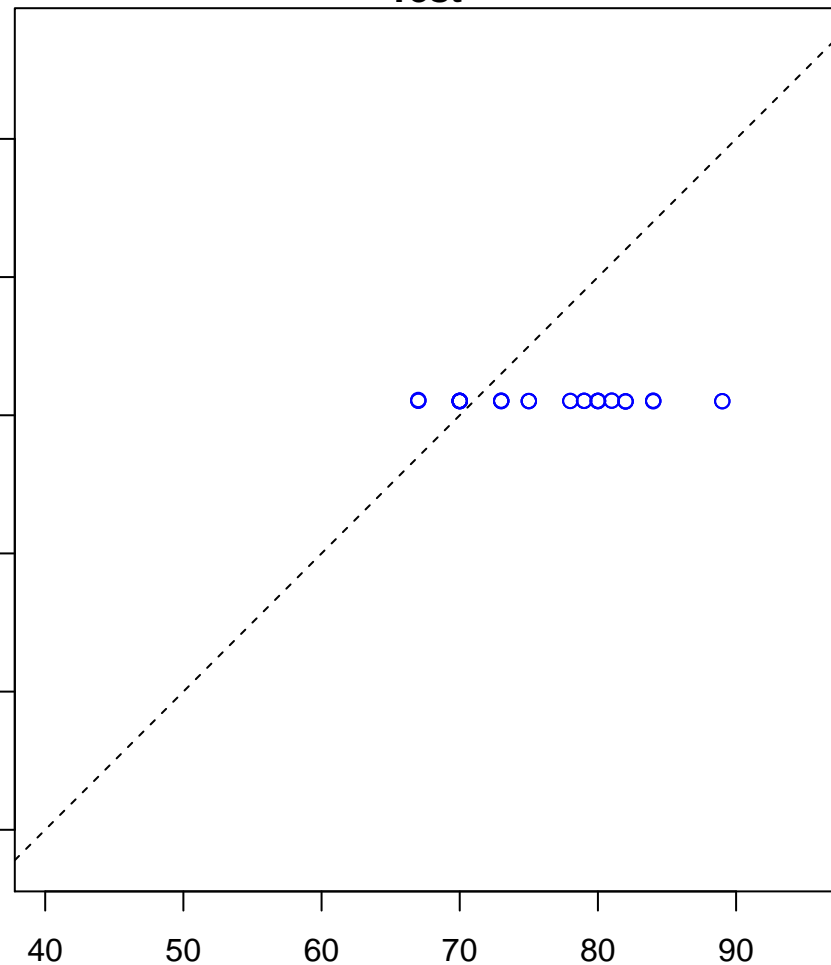
Actual Age

regulation of lymphocyte migration (Score: 0.783558)

Control

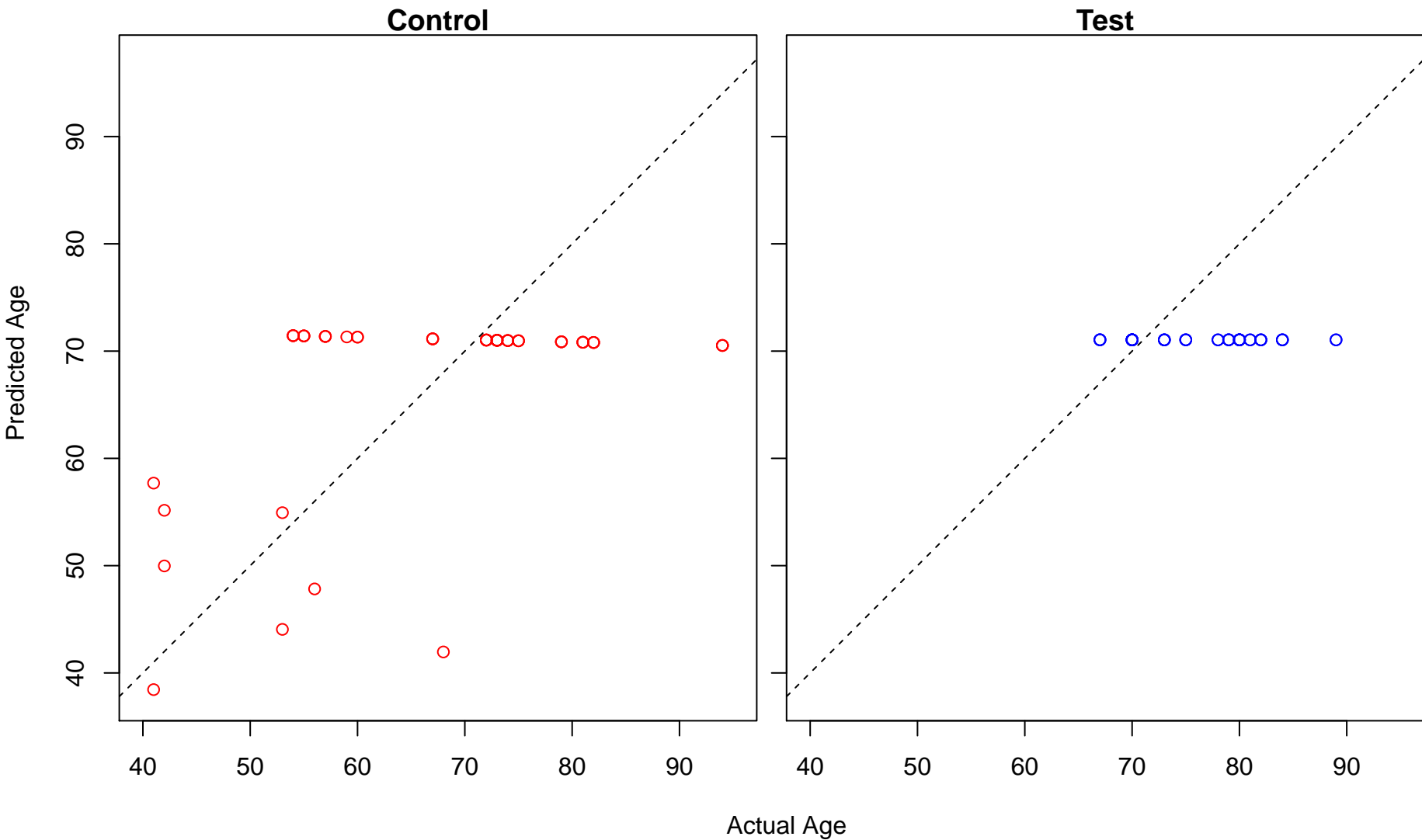


Test

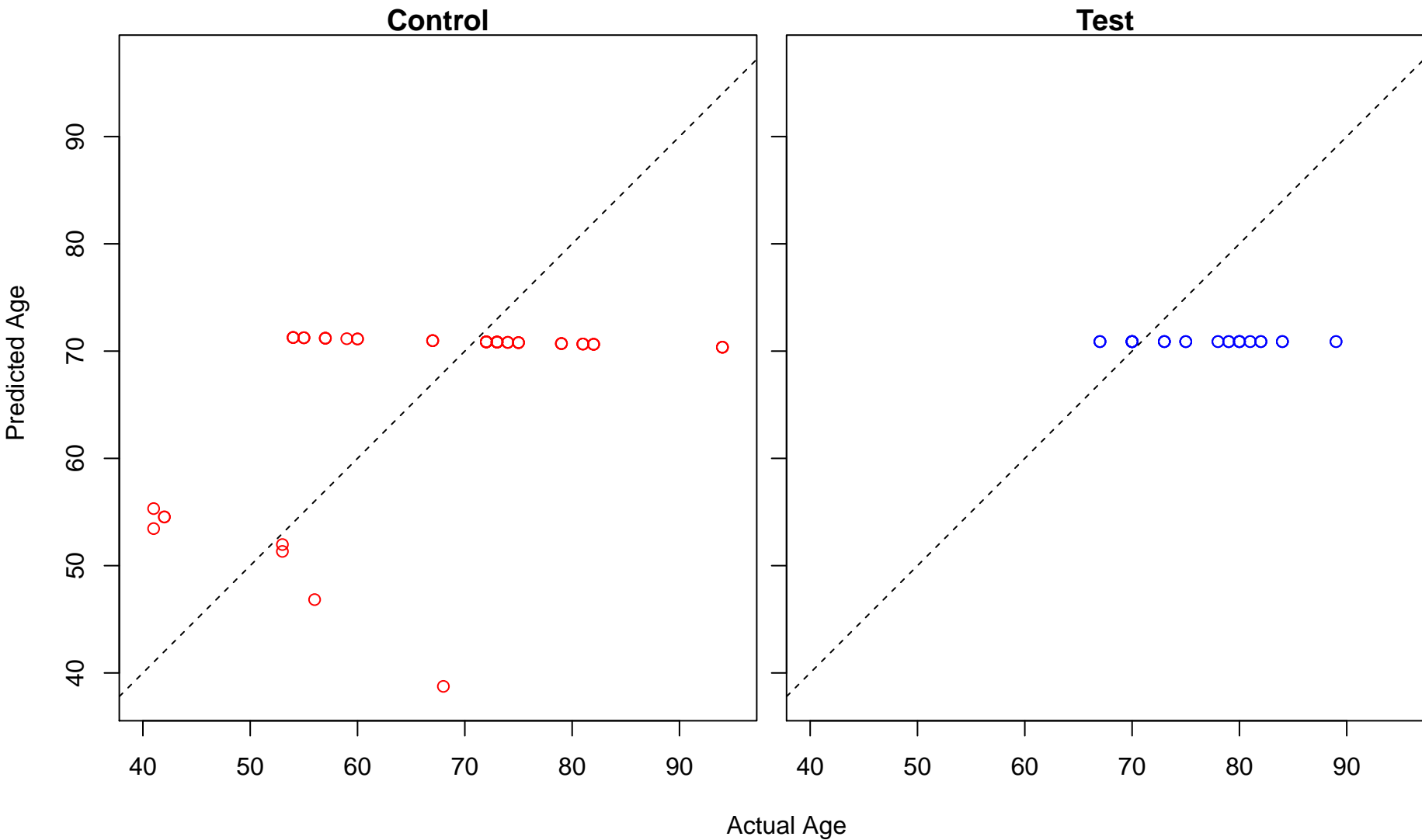


Actual Age

negative regulation of viral entry into host cell (Score: 0.783504)

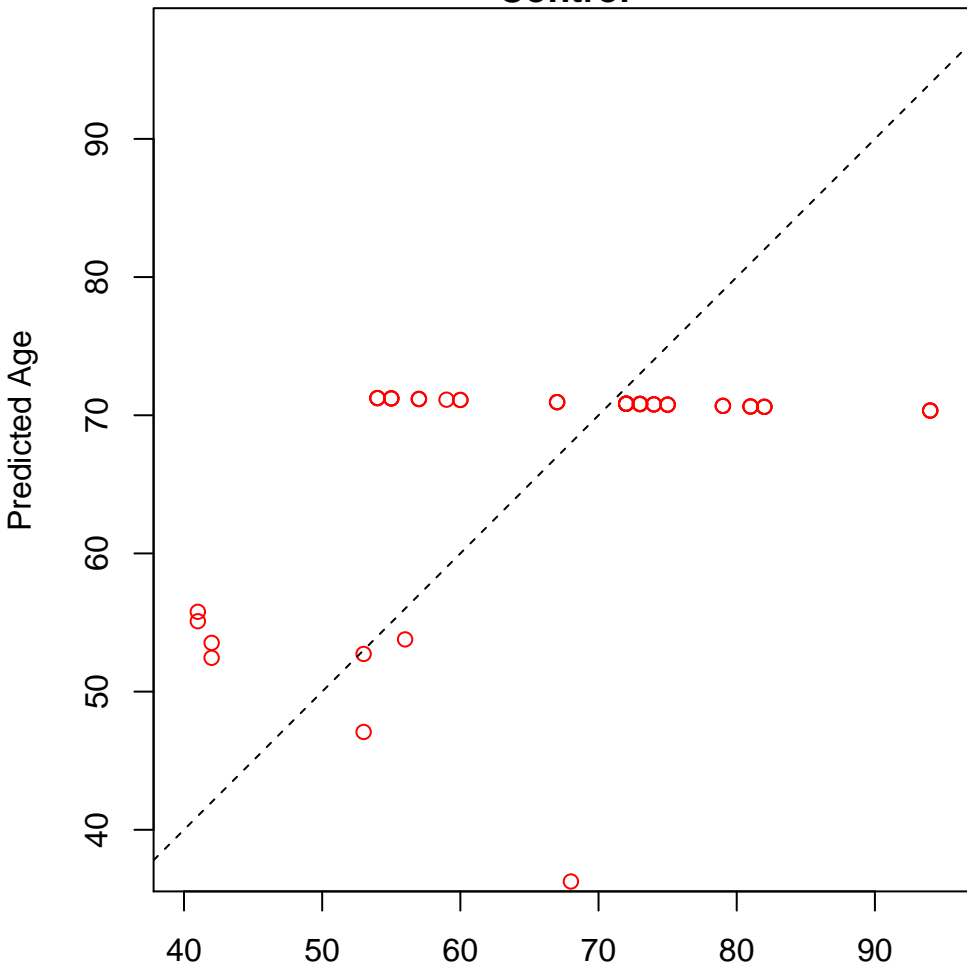


positive regulation of cell projection organization (Score: 0.783494)

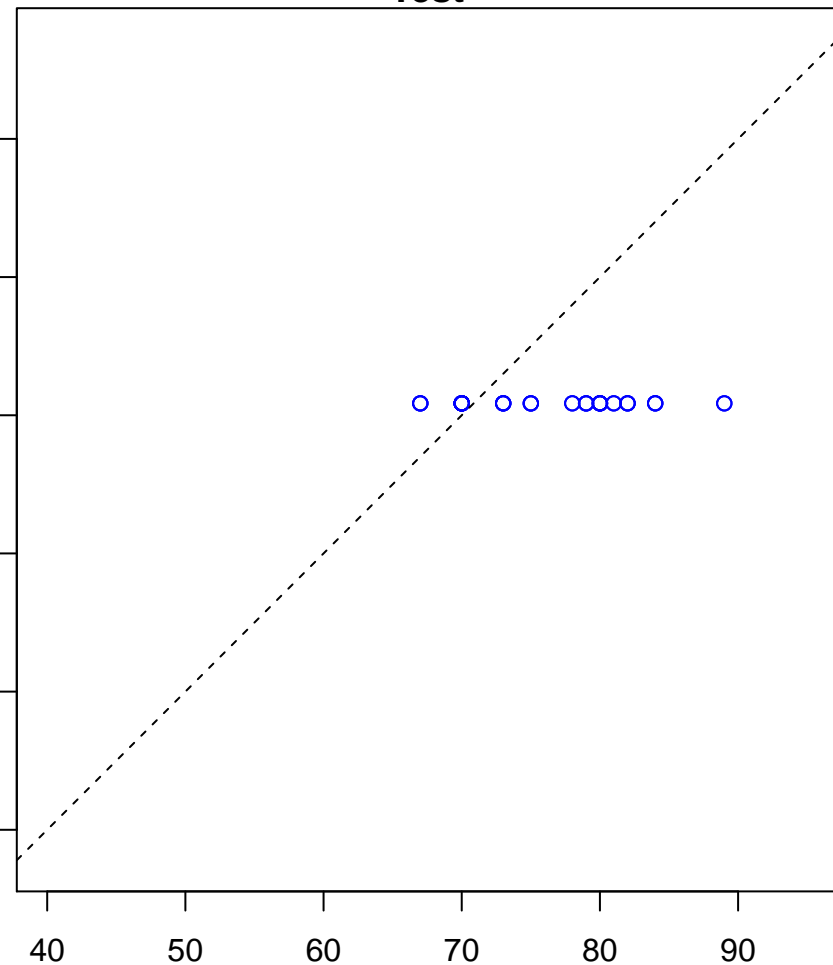


regulation of cytoplasmic transport (Score: 0.783198)

Control

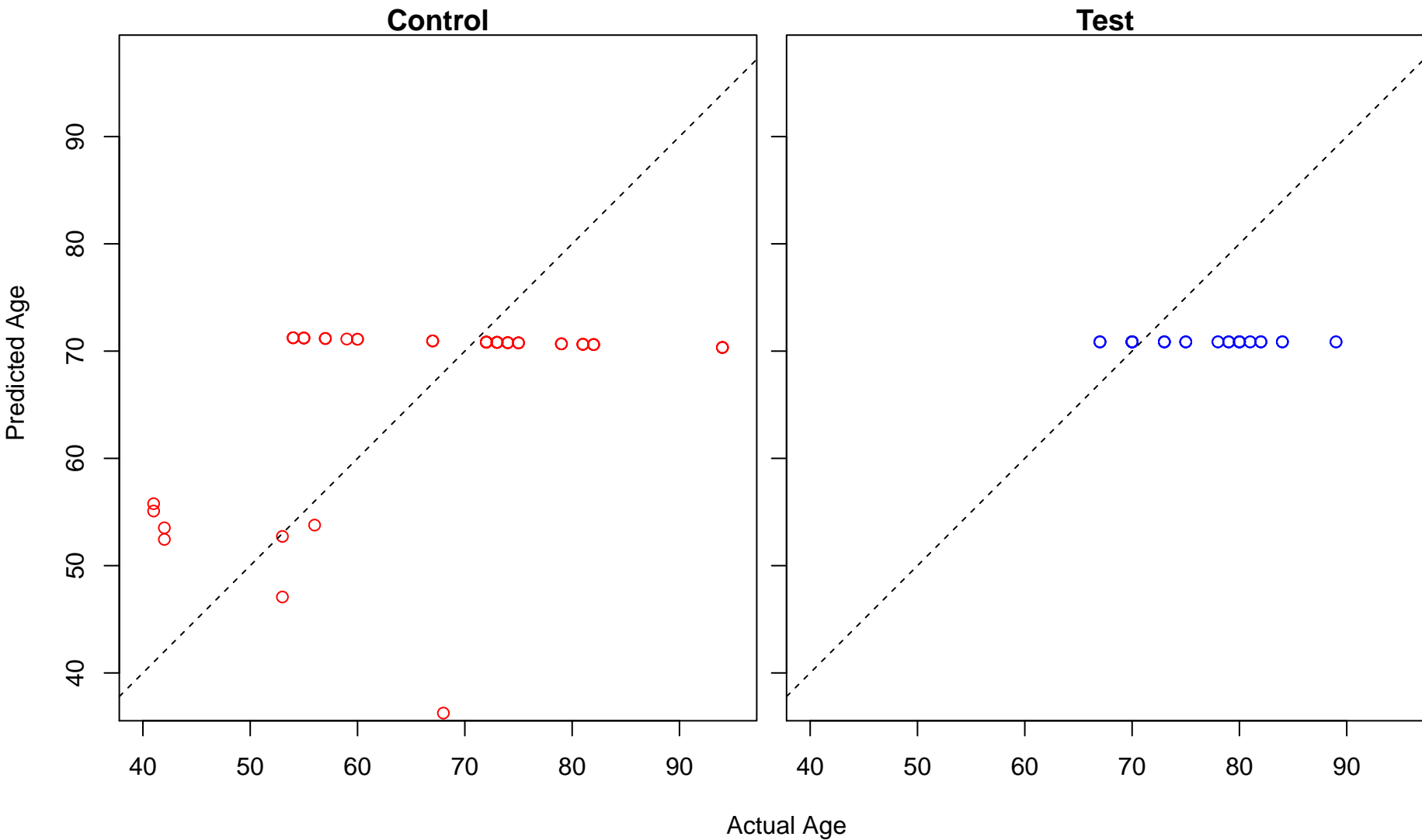


Test



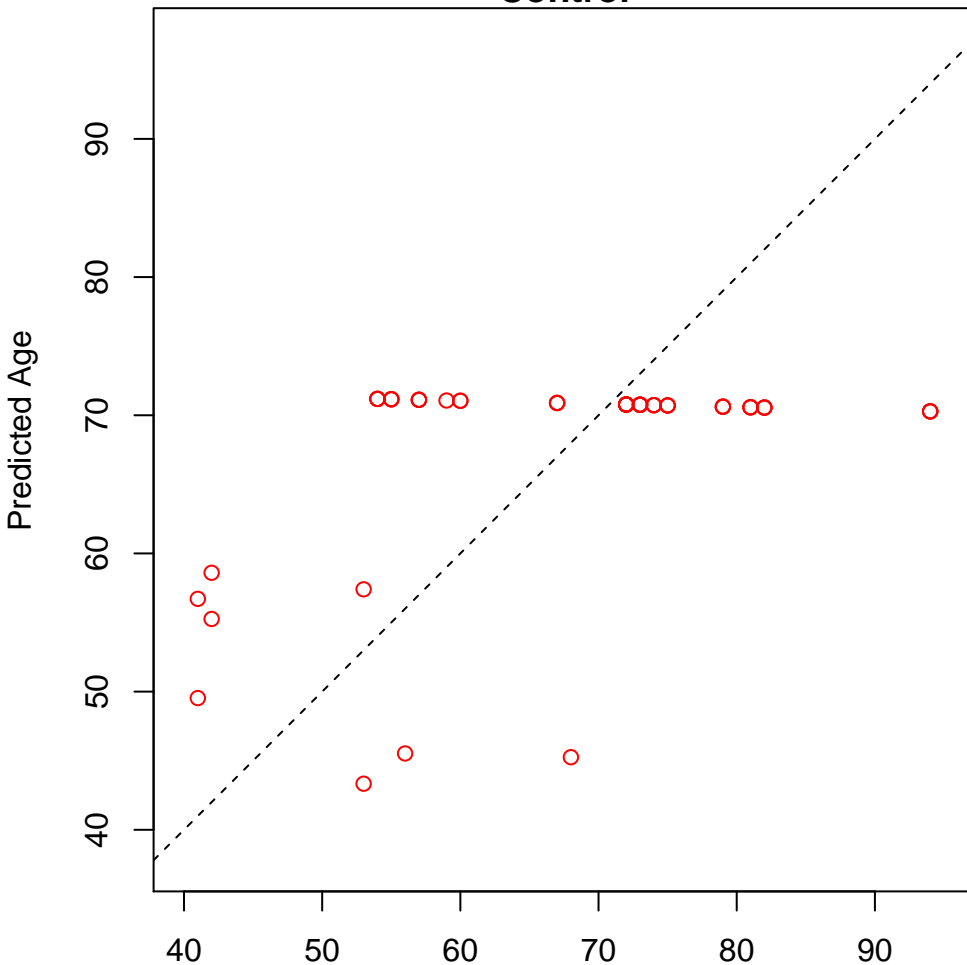
Actual Age

regulation of early endosome to late endosome transport (Score: 0.783198)

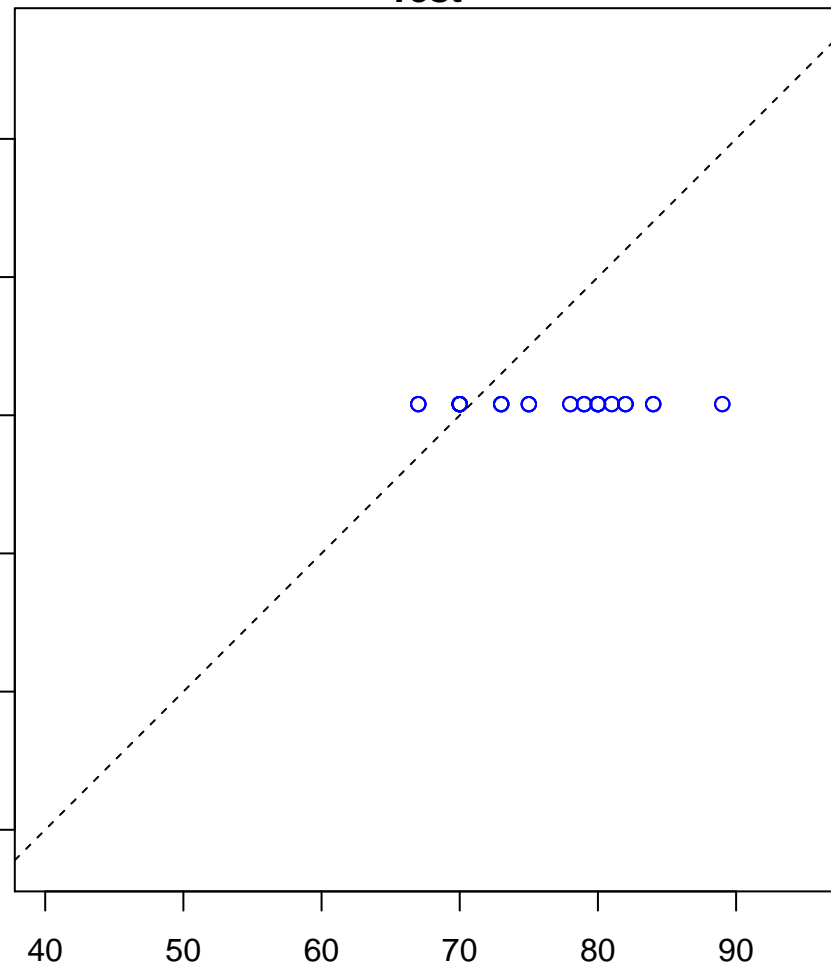


negative regulation of angiogenesis (Score: 0.783138)

Control

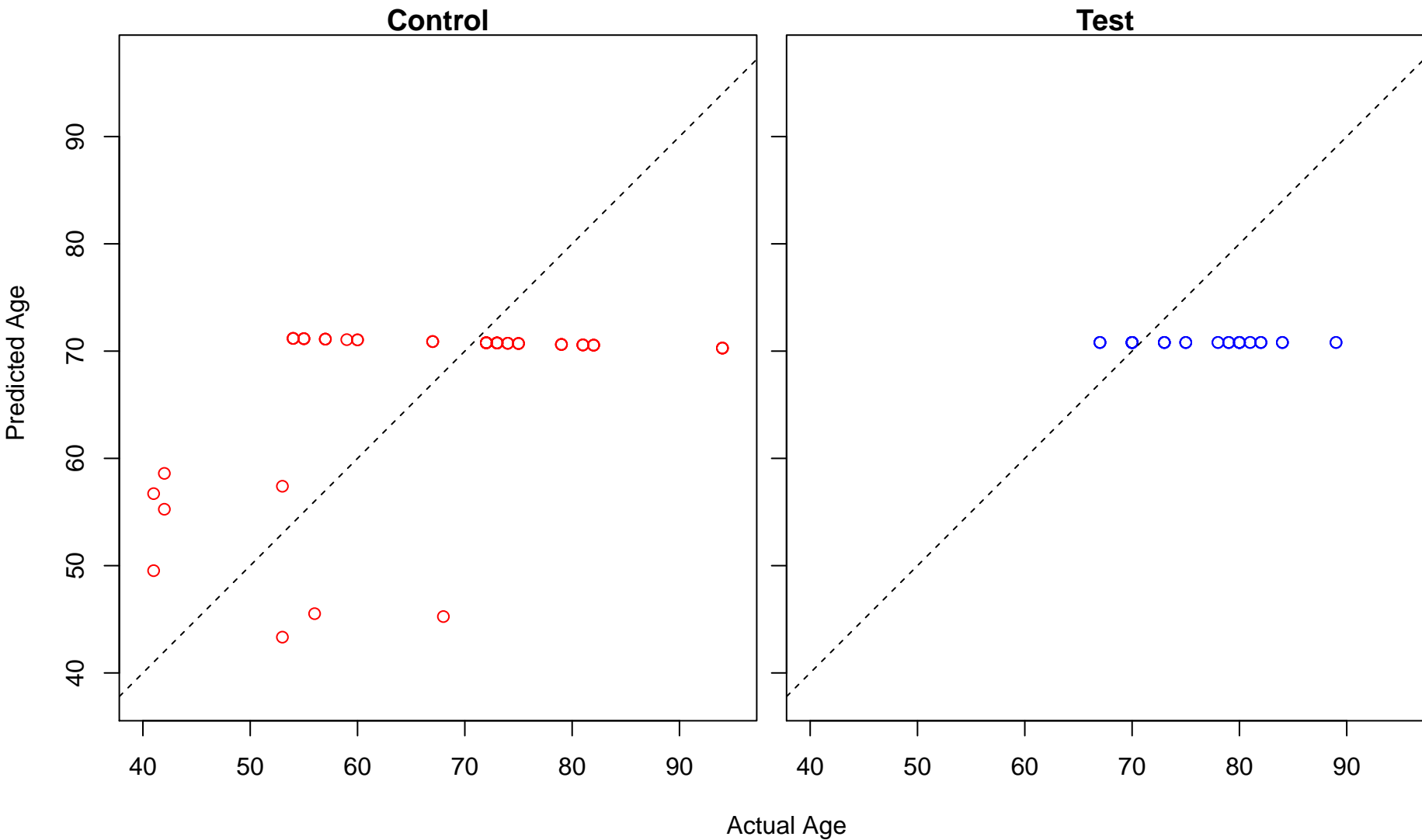


Test

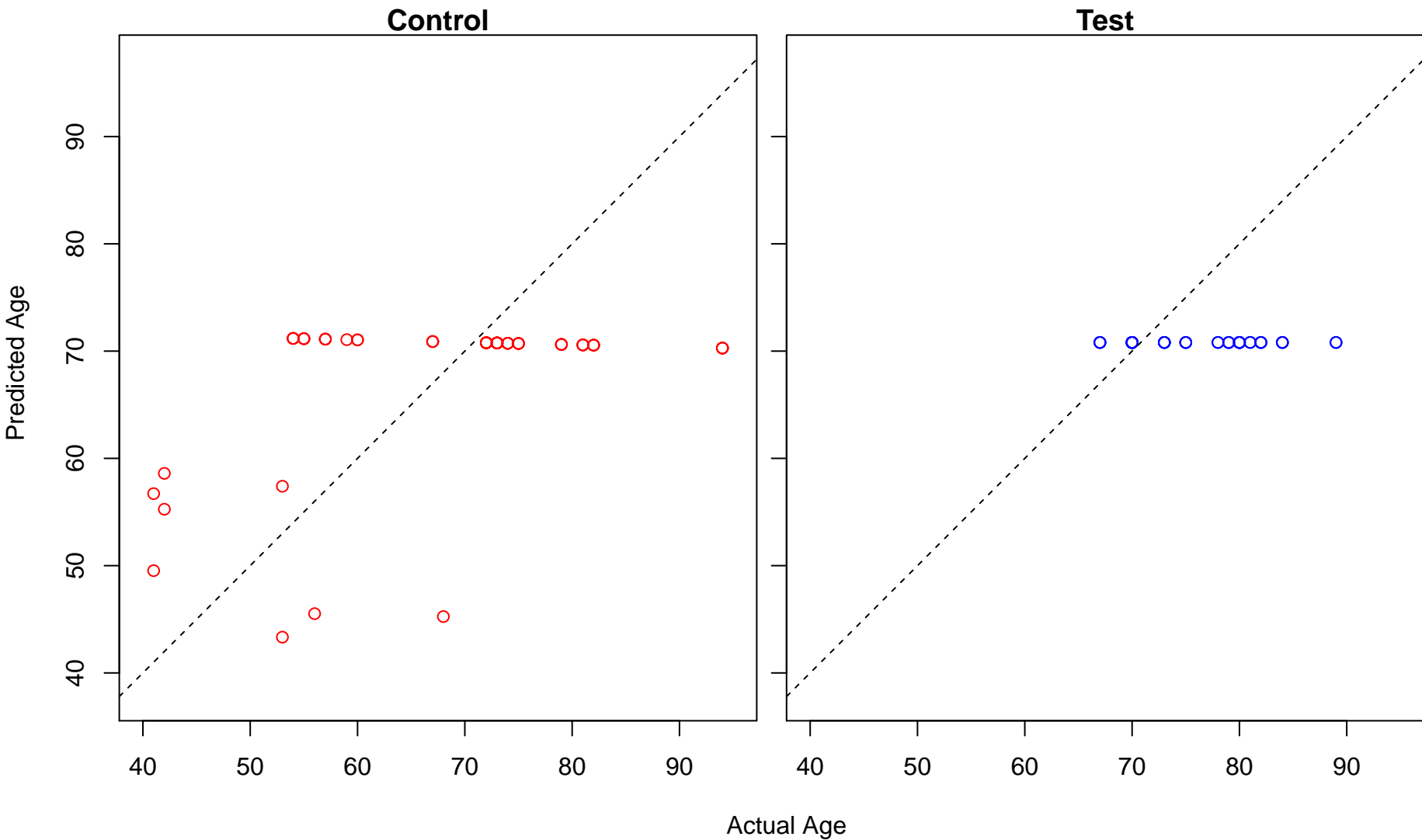


Actual Age

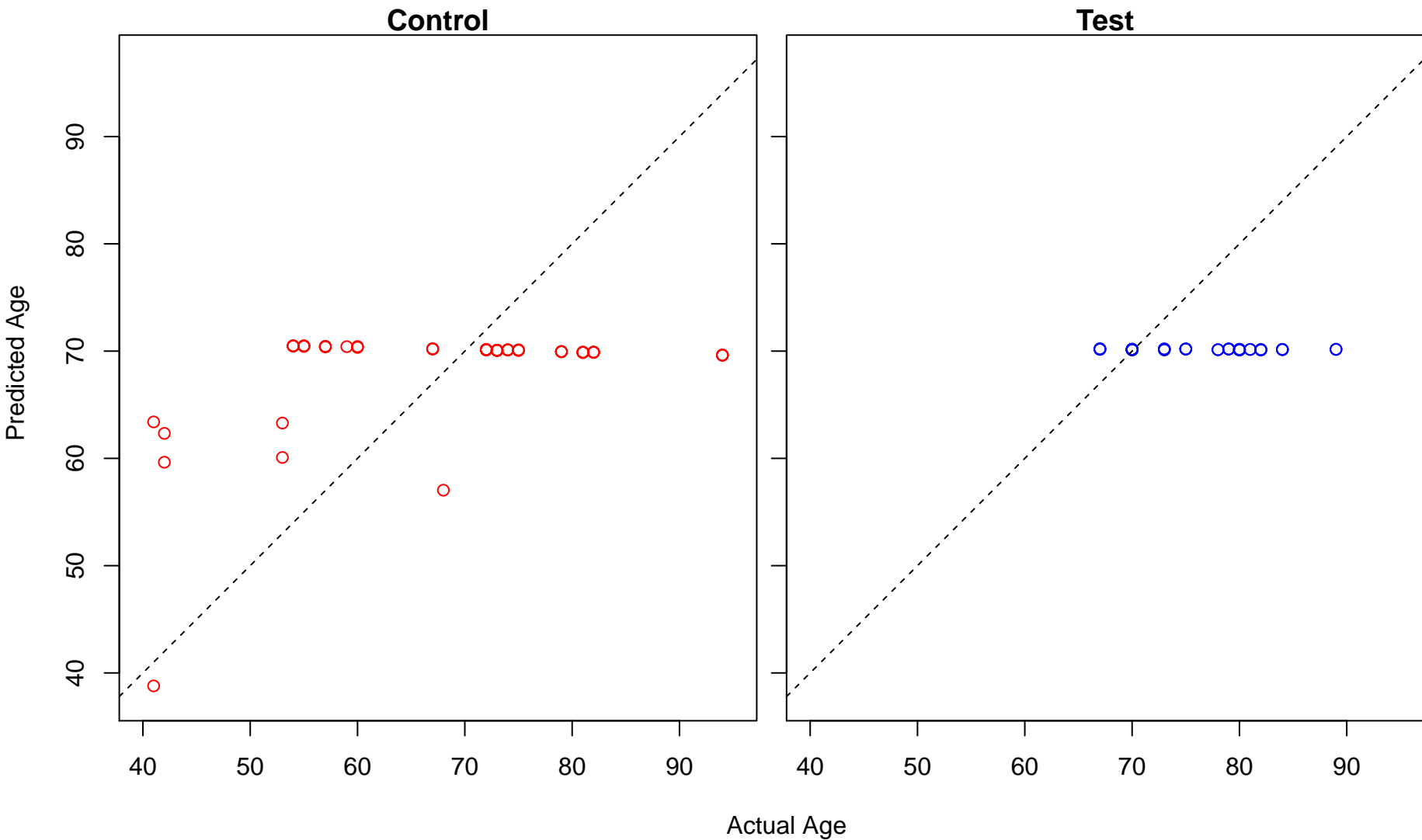
negative regulation of vasculature development (Score: 0.783138)



negative regulation of blood vessel morphogenesis (Score: 0.783138)

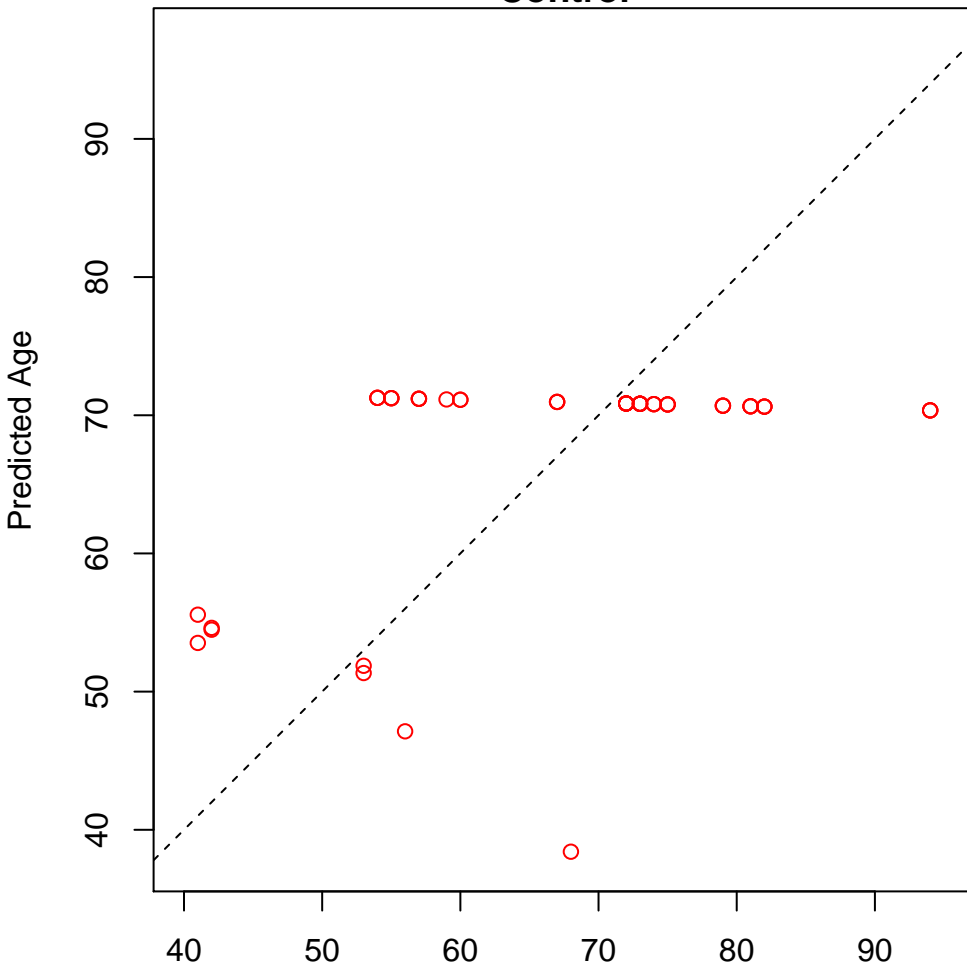


positive regulation of protein localization to cell periphery (Score: 0.783044)

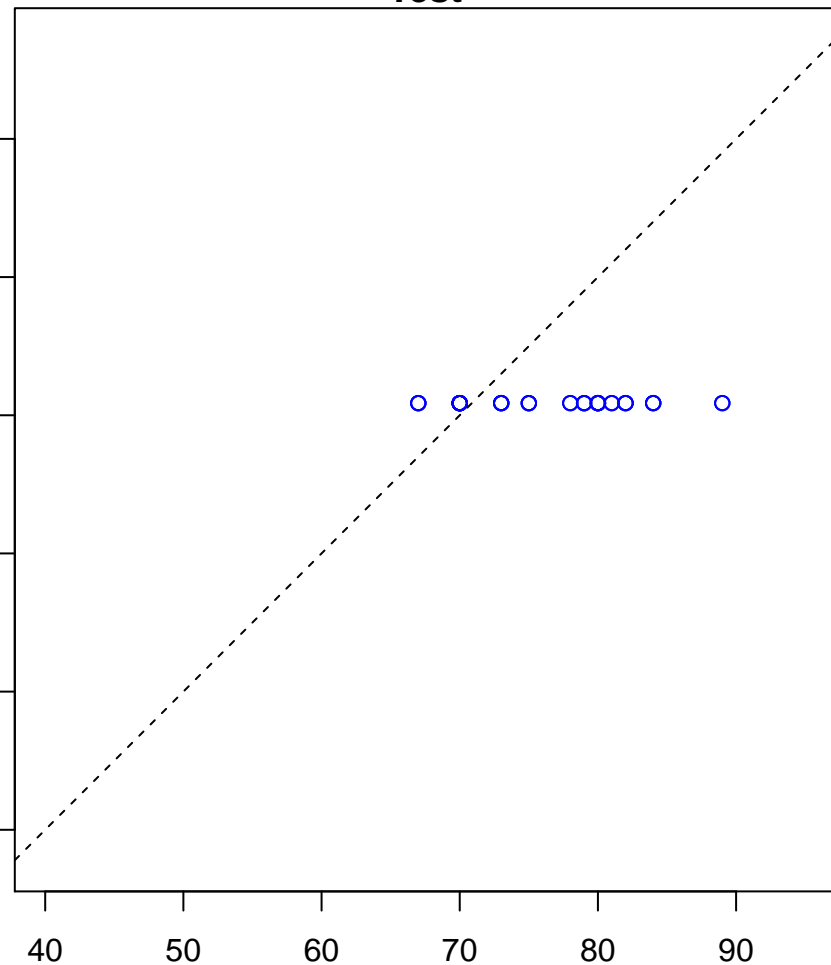


positive regulation of cell development (Score: 0.782993)

Control

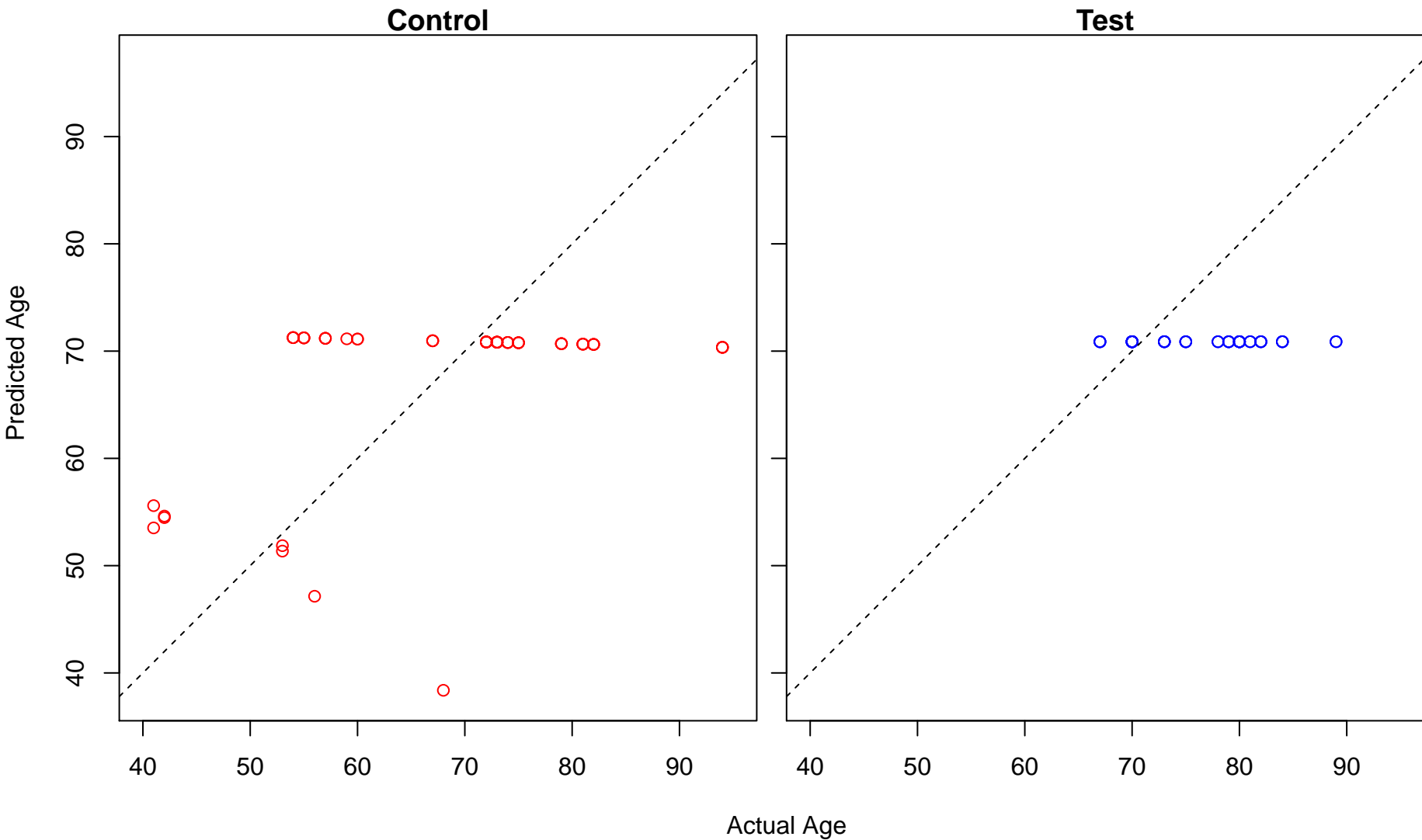


Test

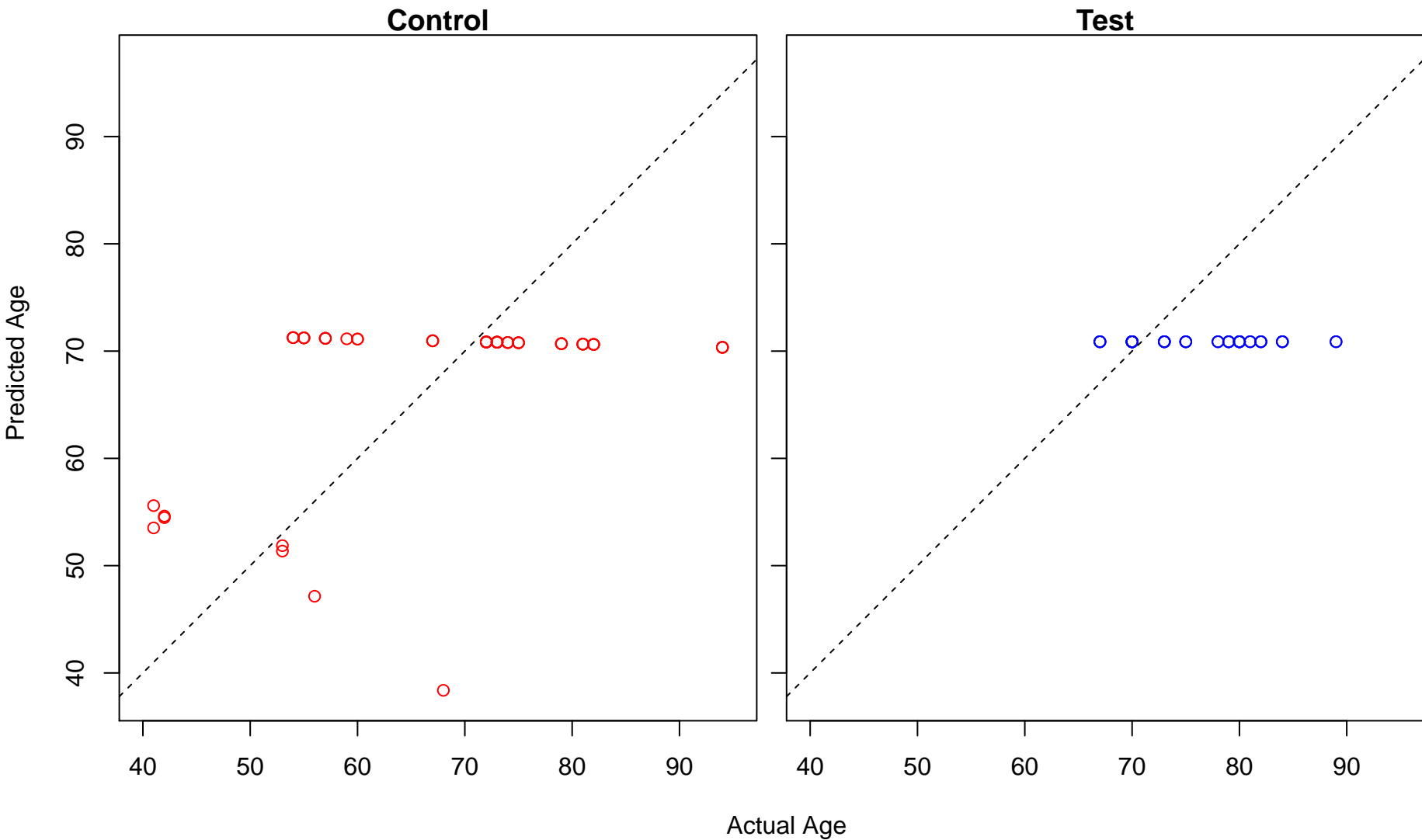


Actual Age

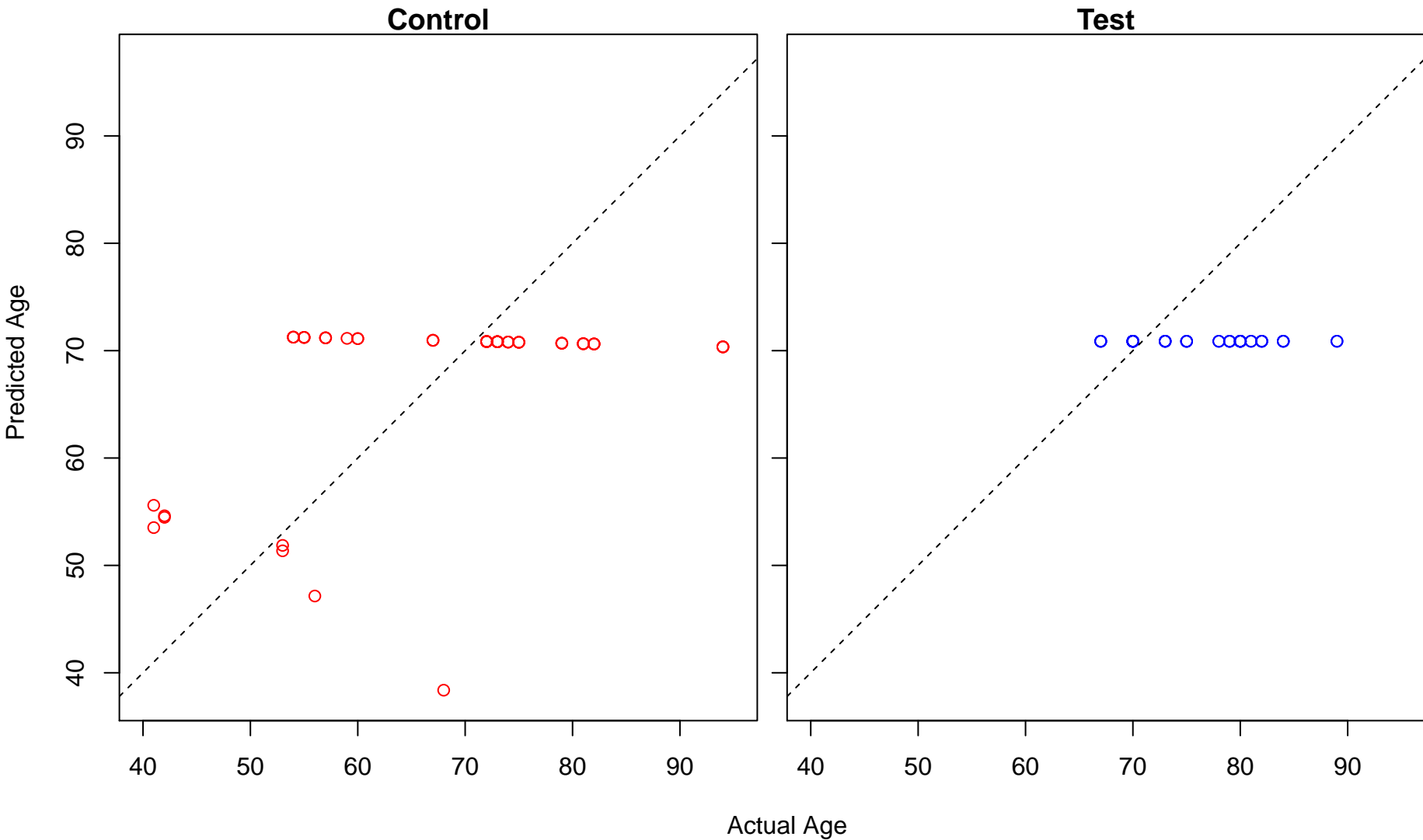
positive regulation of nervous system development (Score: 0.782952)



positive regulation of neuron projection development (Score: 0.782951)

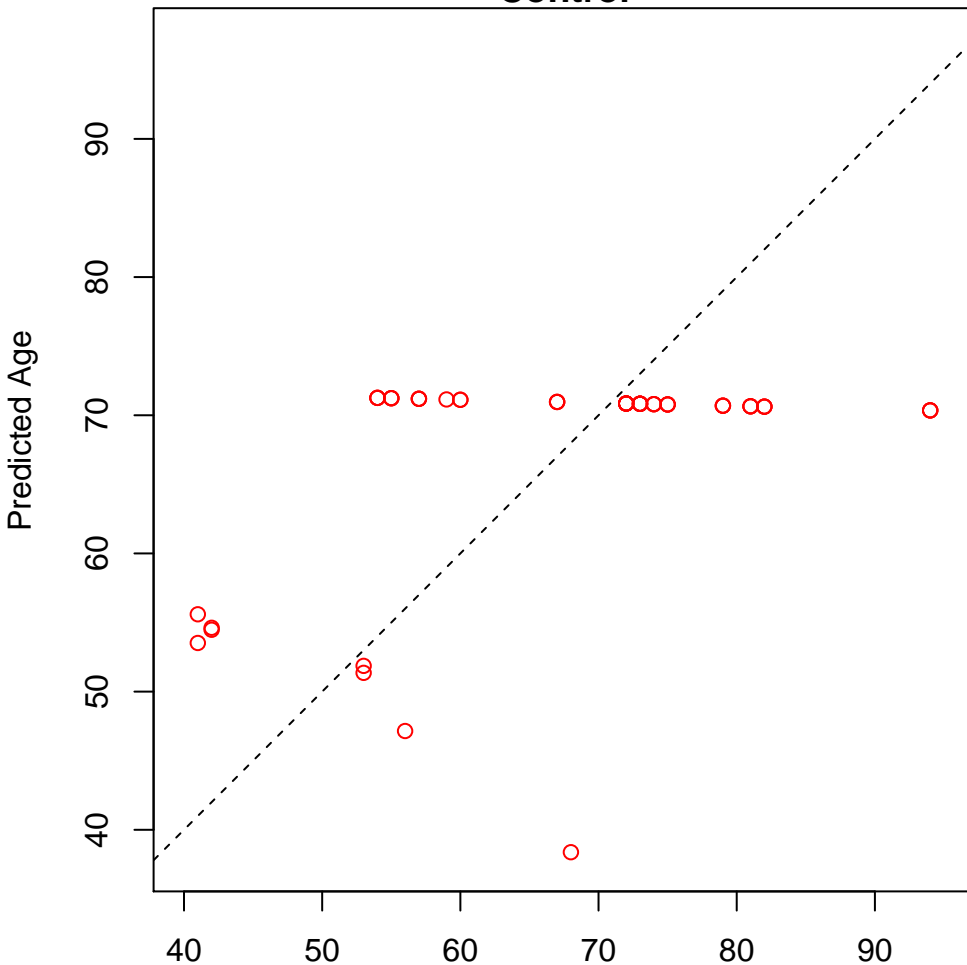


positive regulation of neuron differentiation (Score: 0.782951)

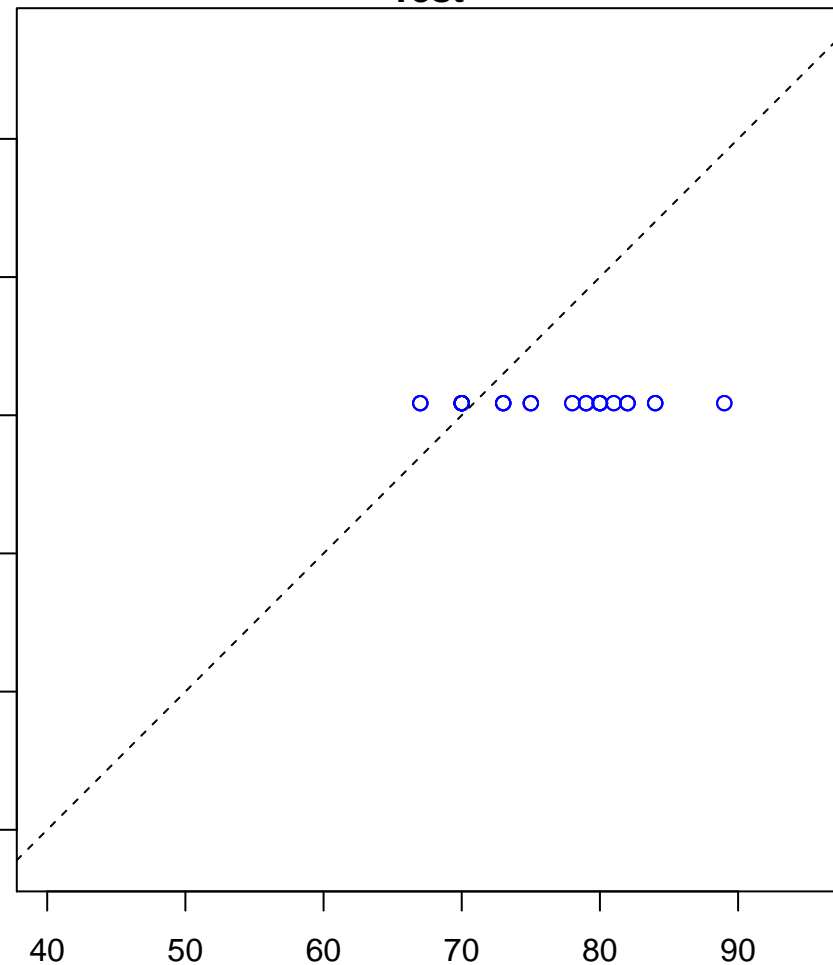


positive regulation of neurogenesis (Score: 0.782951)

Control

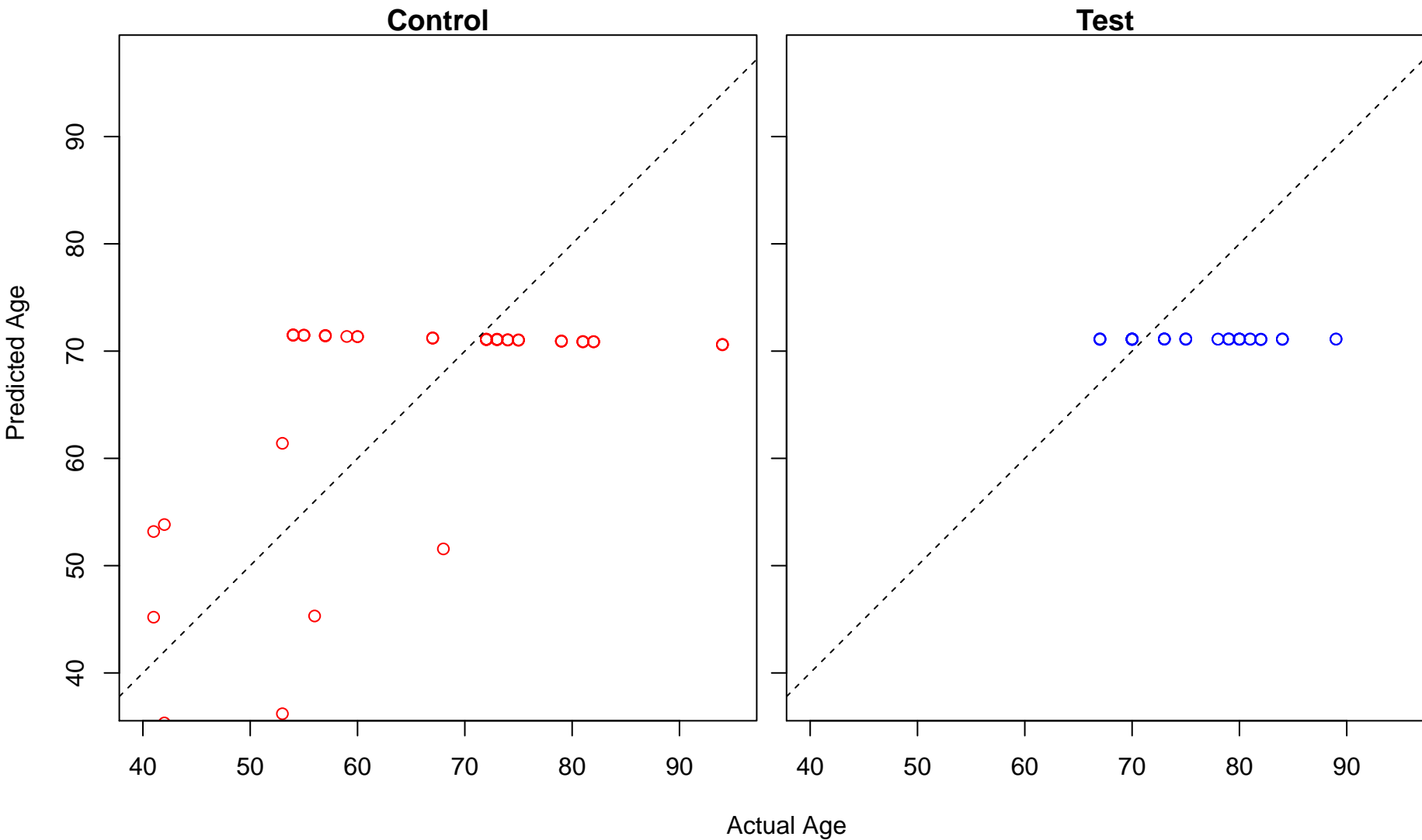


Test

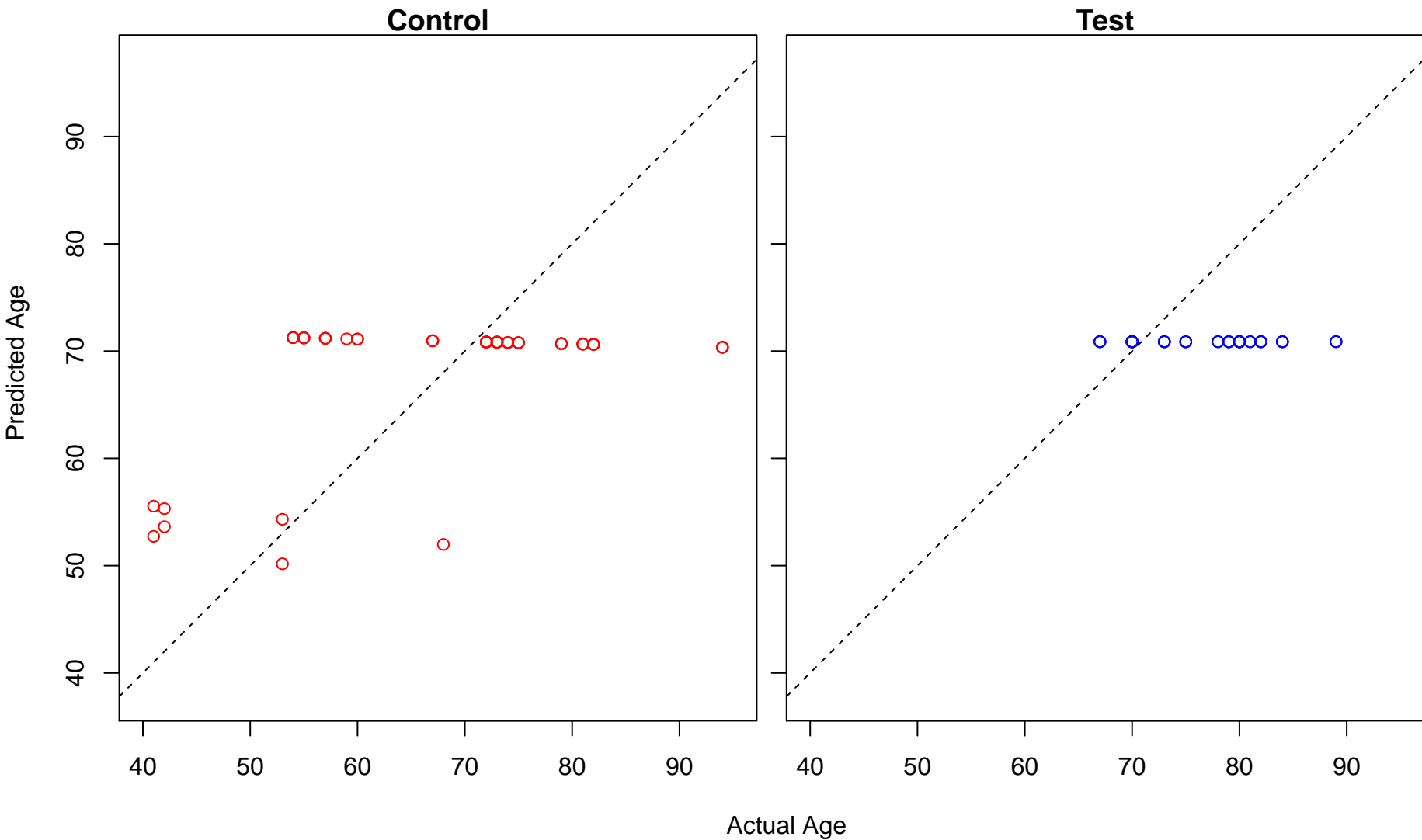


Actual Age

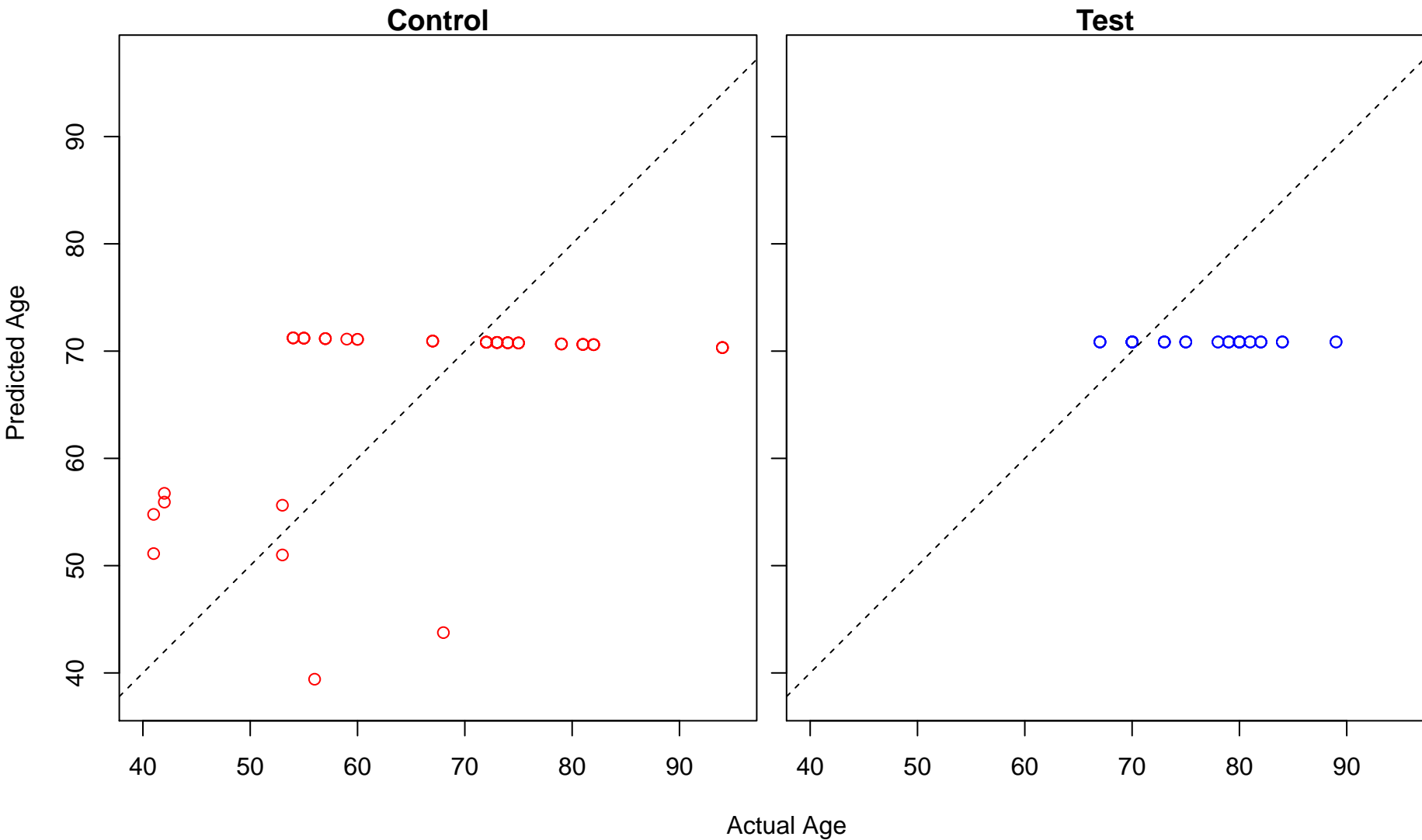
negative regulation of protein kinase activity (Score: 0.782805)



positive regulation of muscle cell differentiation (Score: 0.782593)

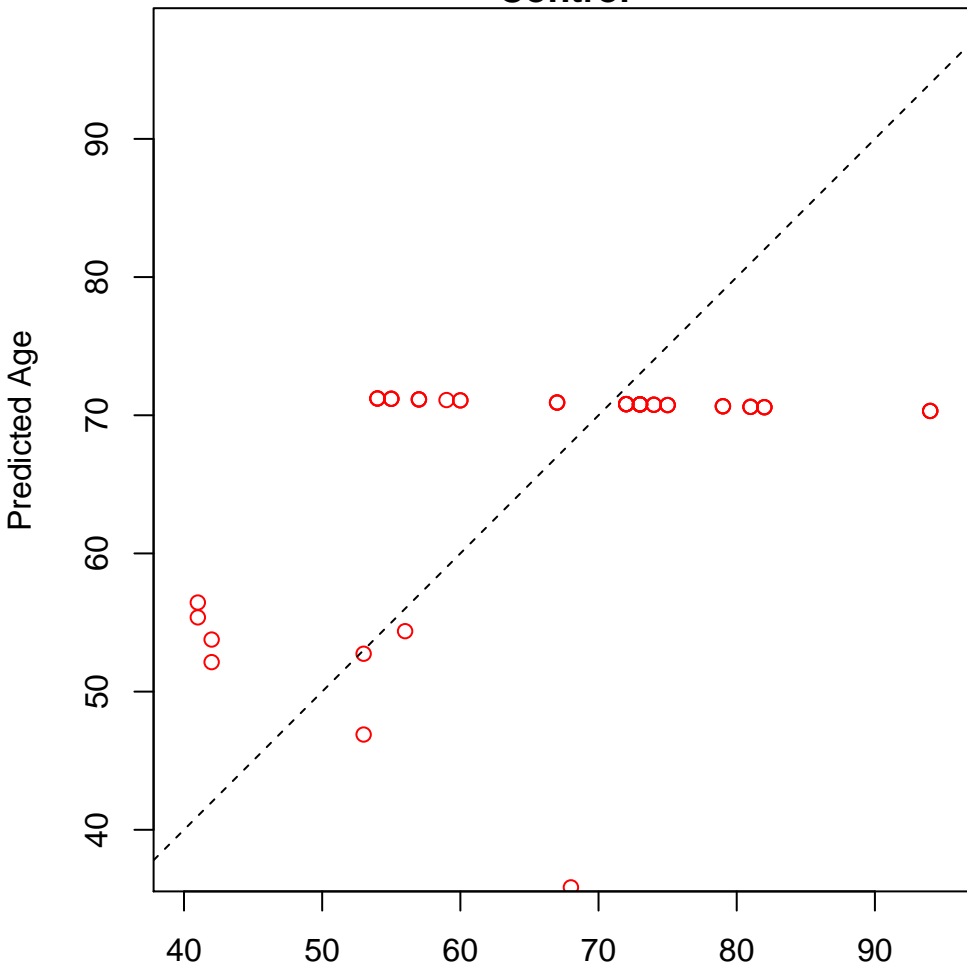


tissue morphogenesis (Score: 0.782419)

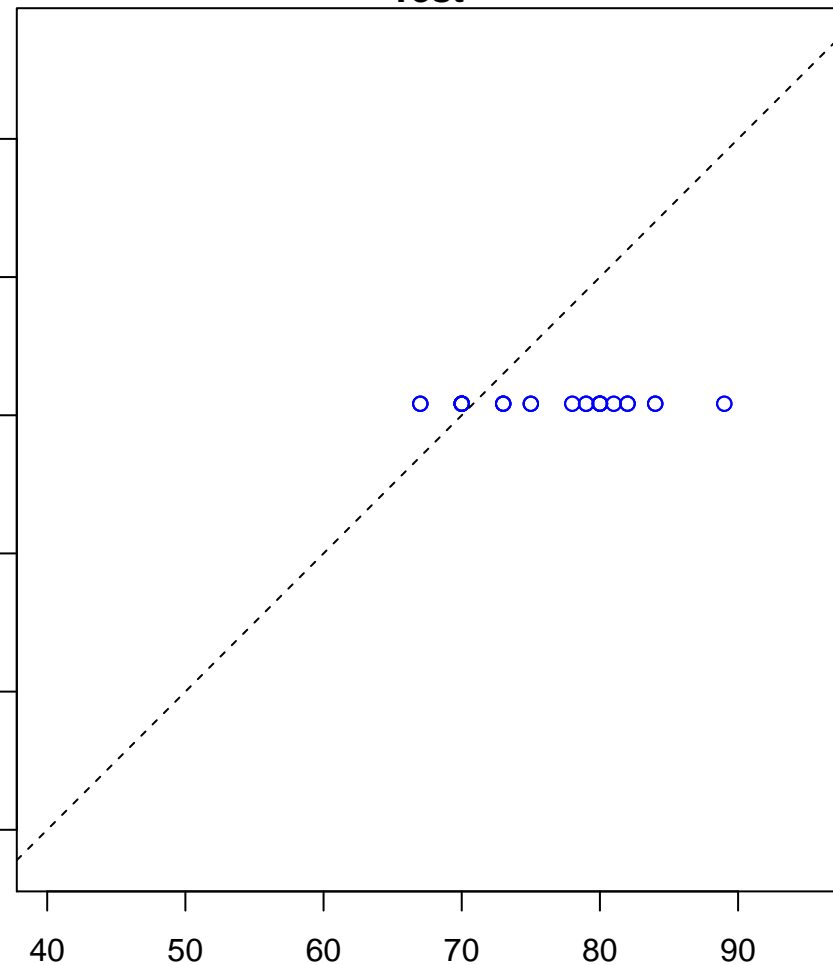


vesicle budding from membrane (Score: 0.782390)

Control



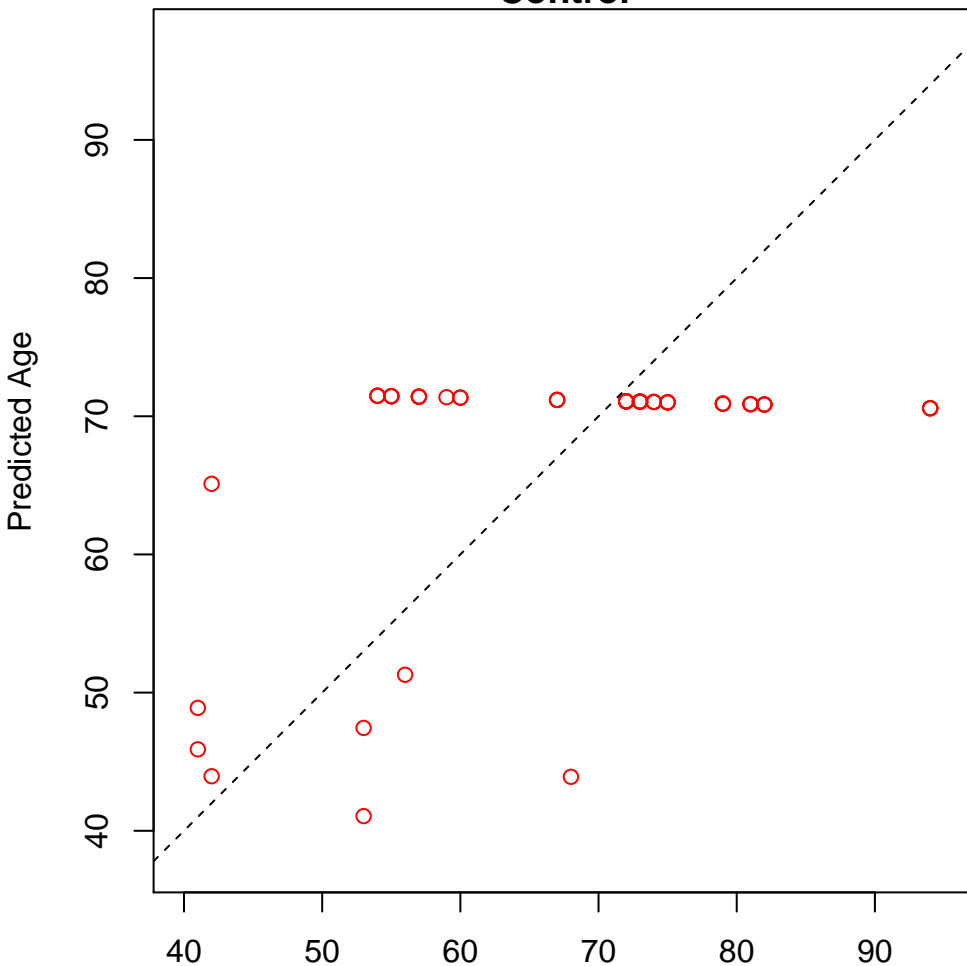
Test



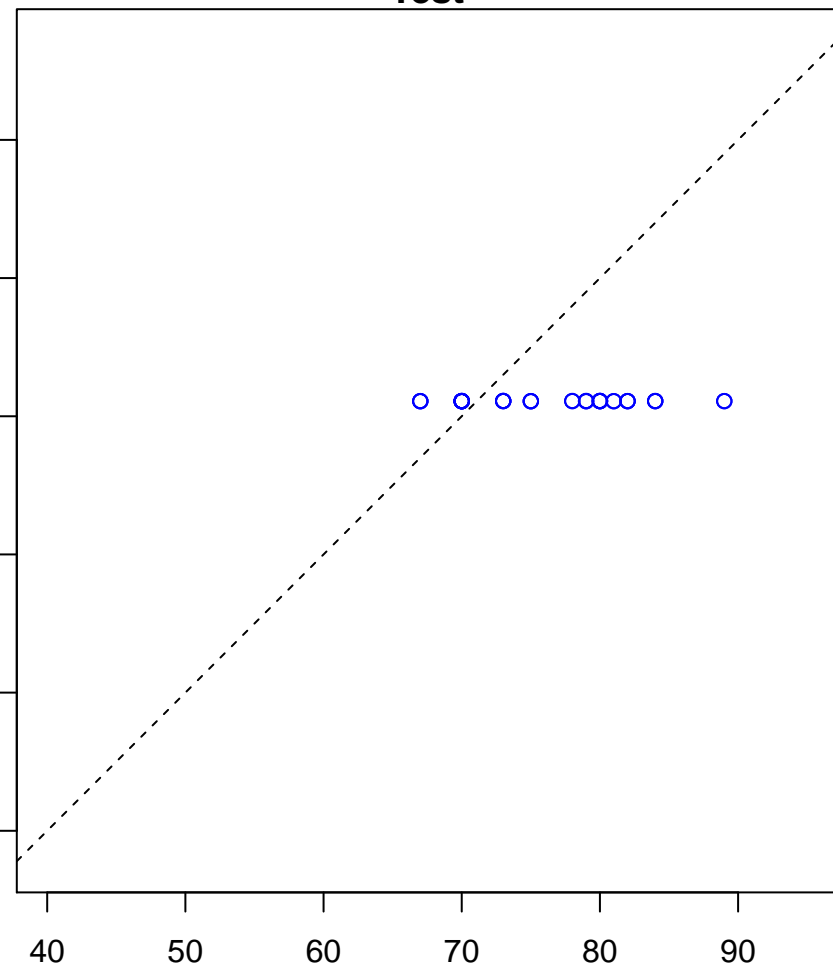
Actual Age

positive regulation of cell differentiation (Score: 0.782155)

Control

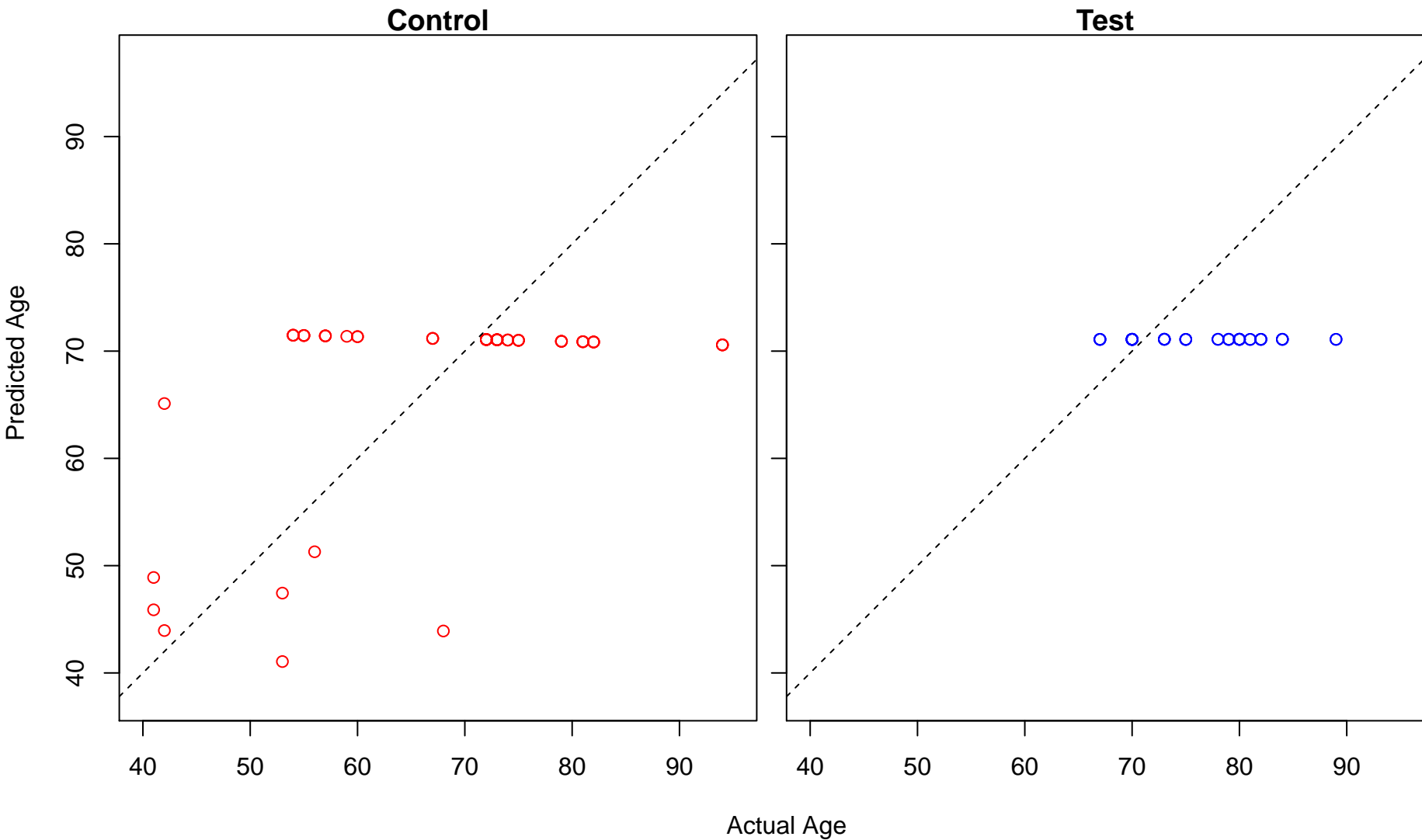


Test

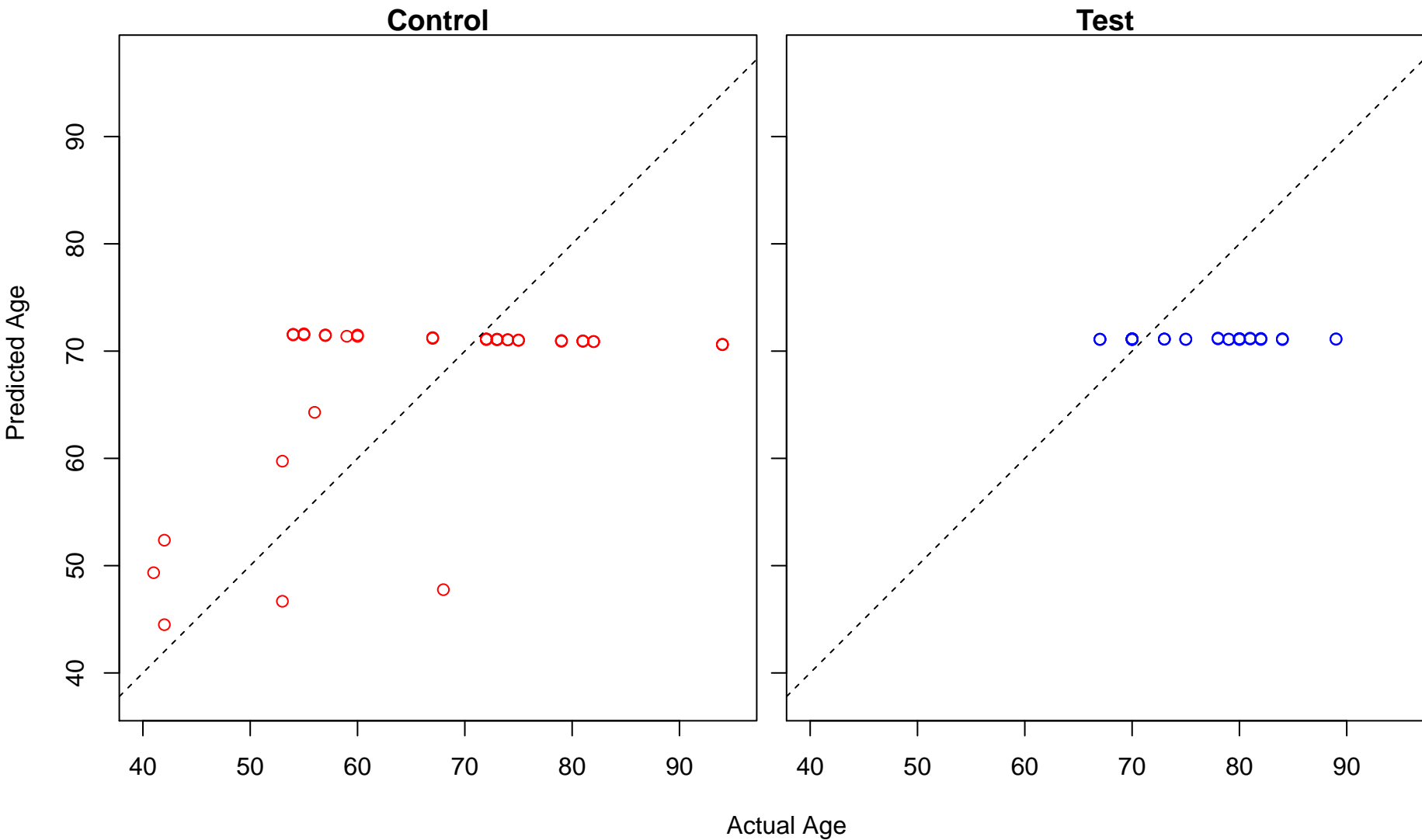


Actual Age

positive regulation of developmental process (Score: 0.782152)

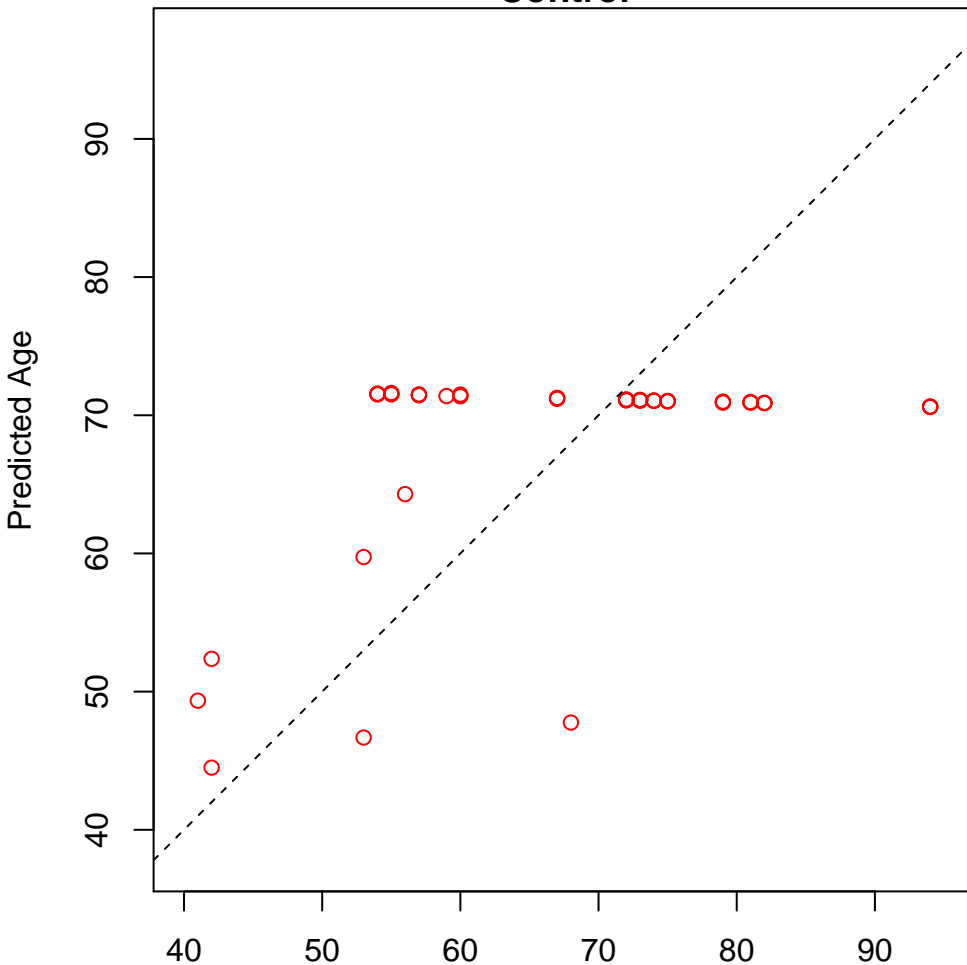


vesicle localization (Score: 0.782023)

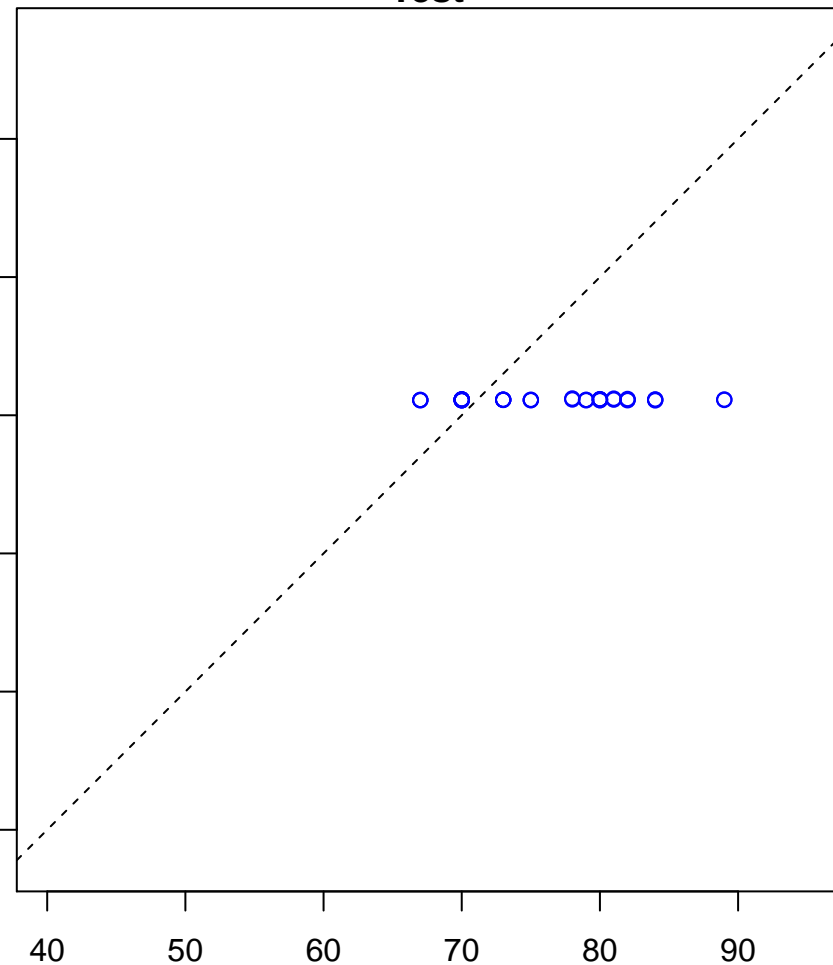


establishment of vesicle localization (Score: 0.782023)

Control

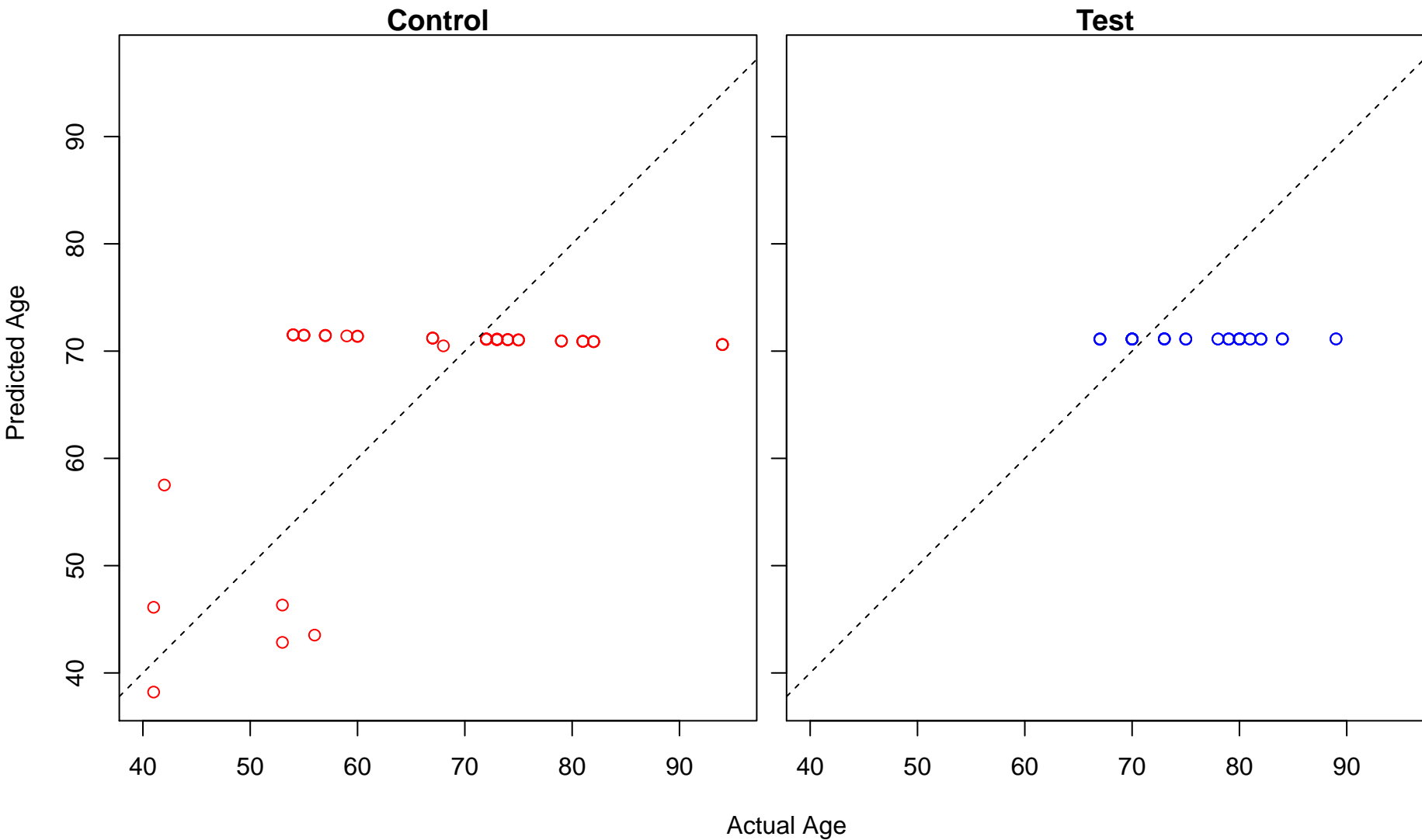


Test



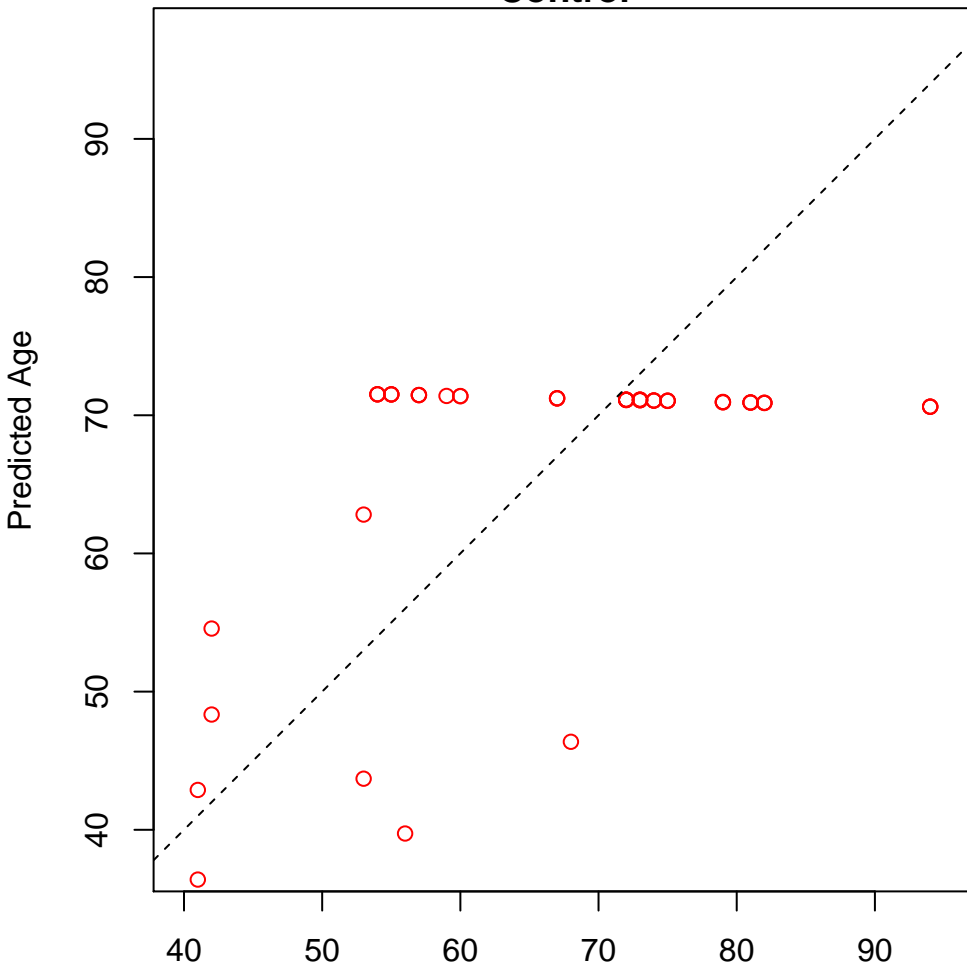
Actual Age

negative regulation of developmental process (Score: 0.781800)

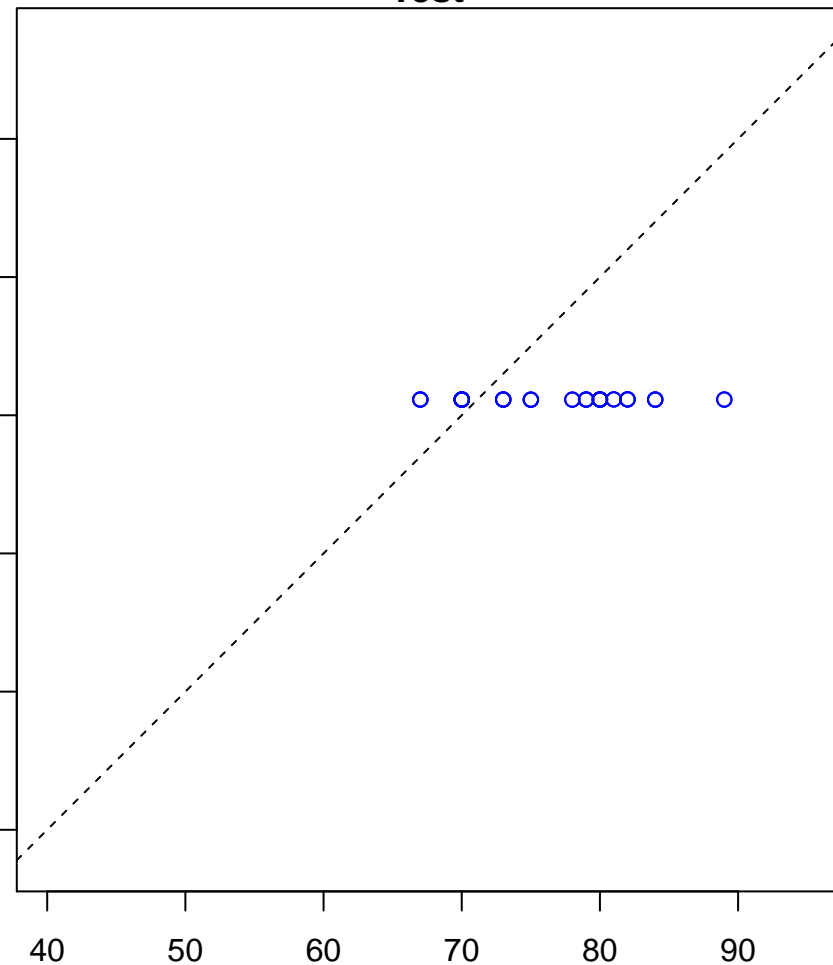


regulation of DNA biosynthetic process (Score: 0.781354)

Control



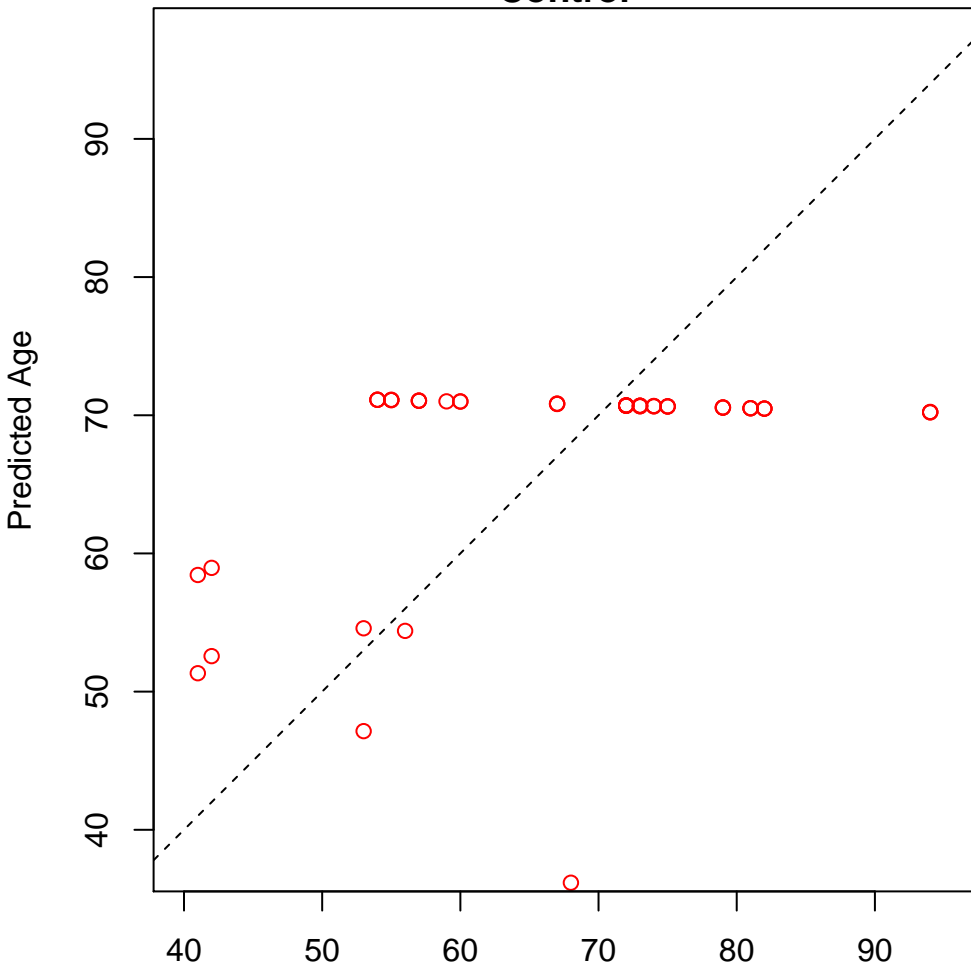
Test



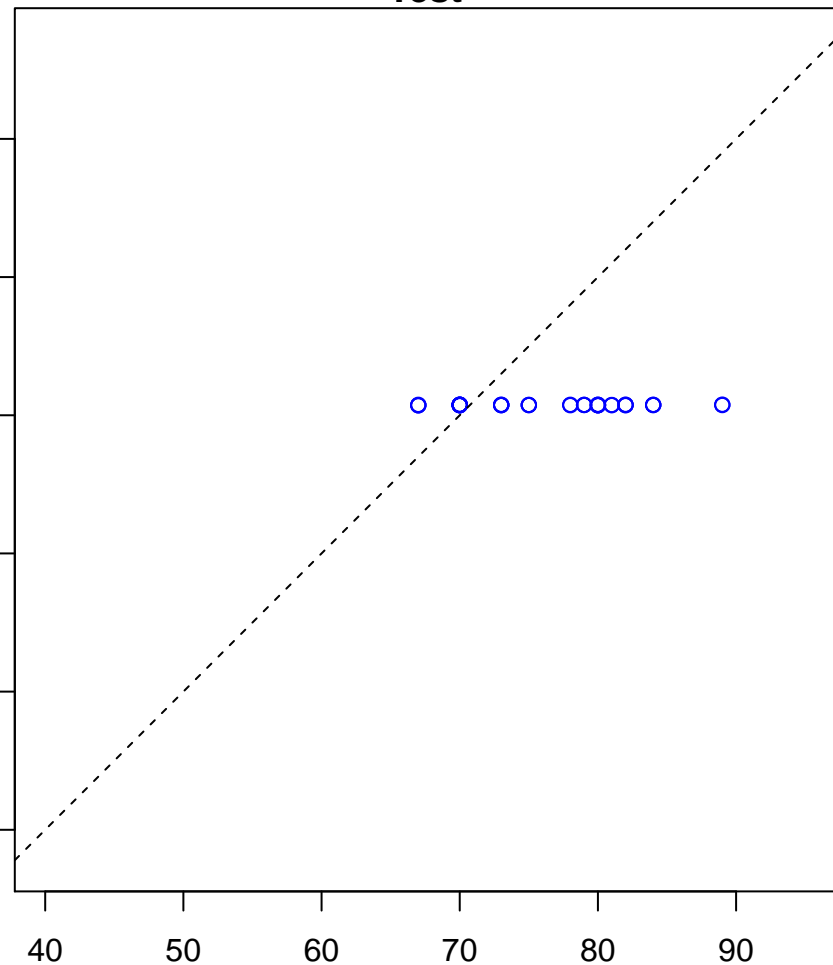
Actual Age

cellular response to inorganic substance (Score: 0.781311)

Control

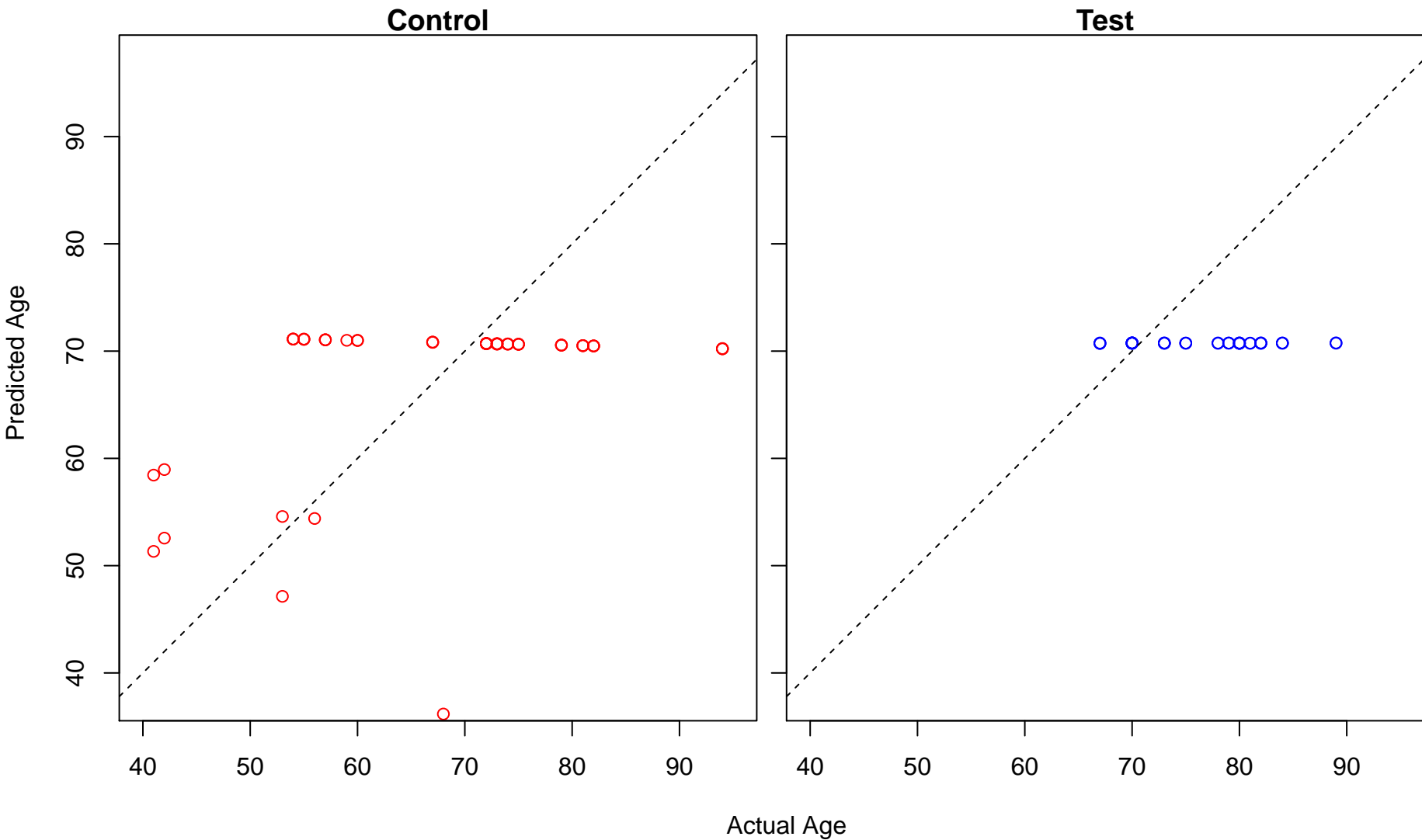


Test

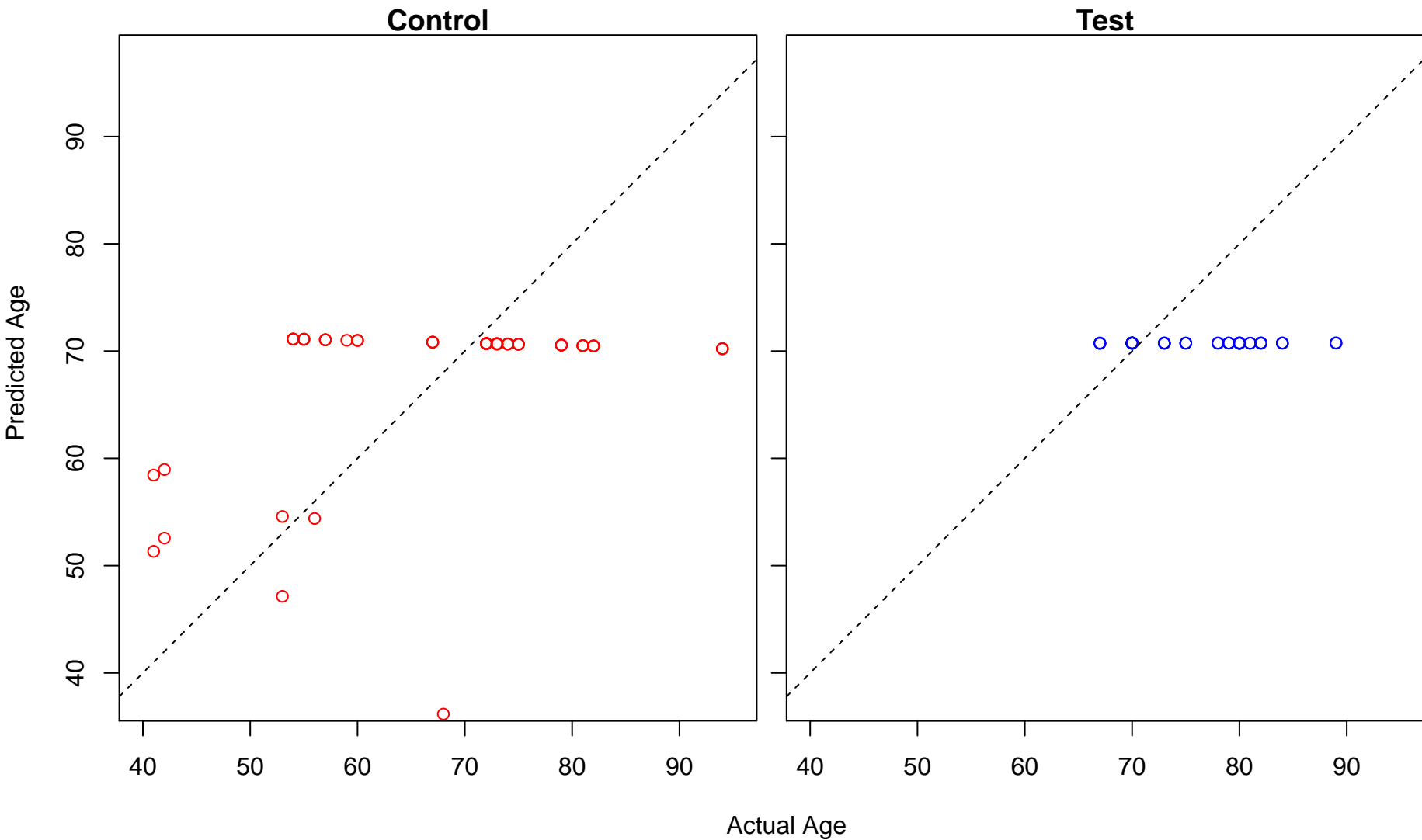


Actual Age

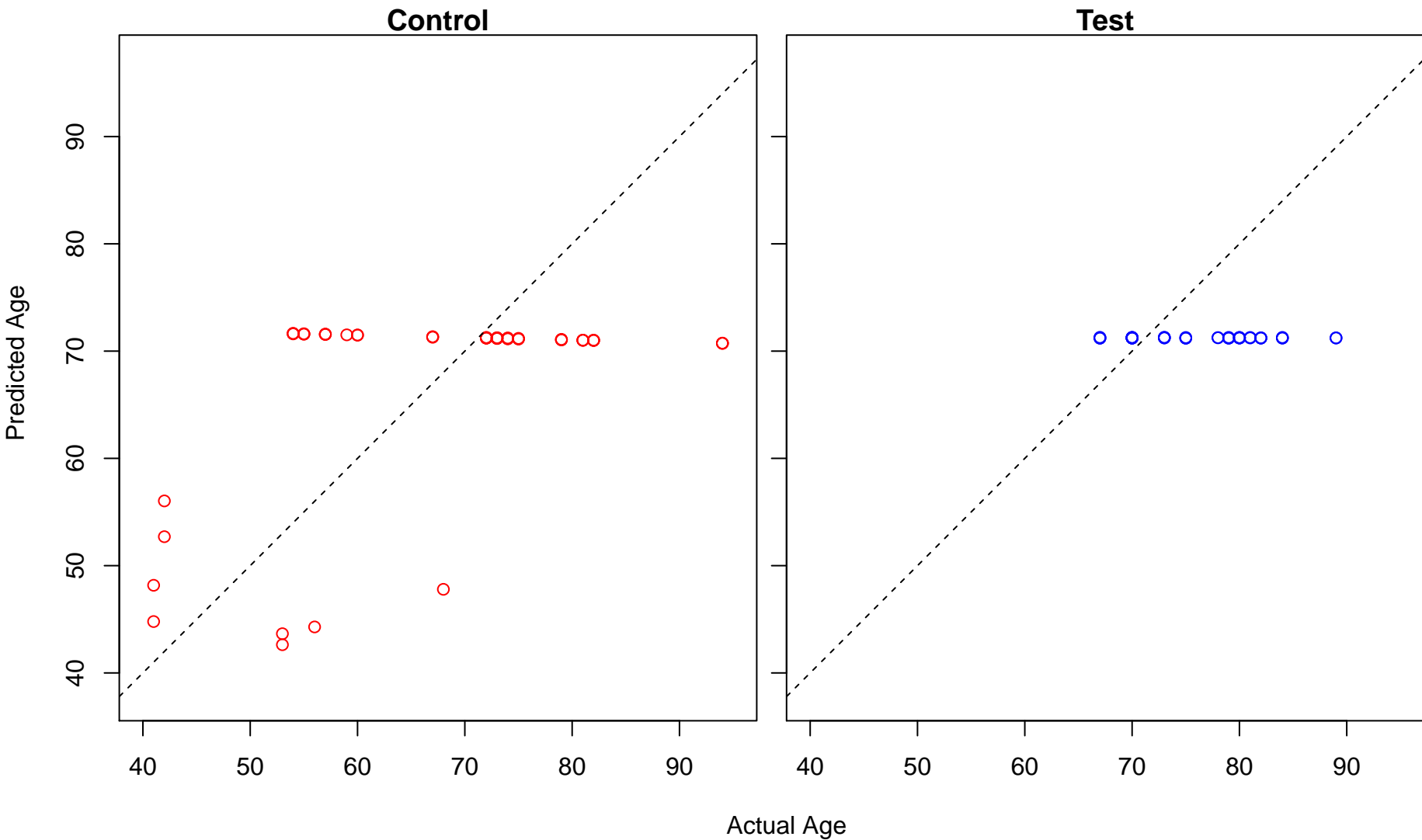
cellular response to metal ion (Score: 0.781311)



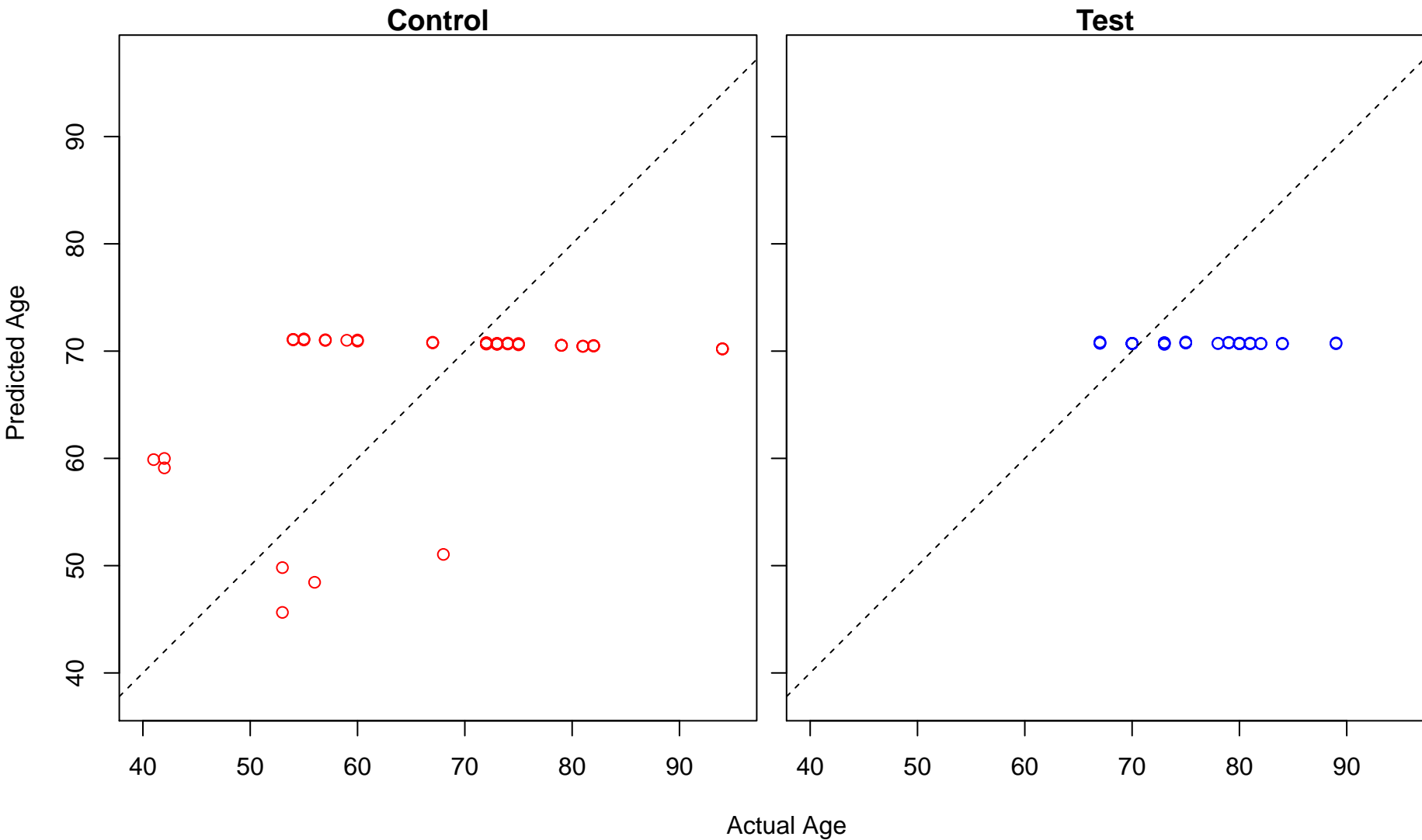
cellular response to calcium ion (Score: 0.781311)



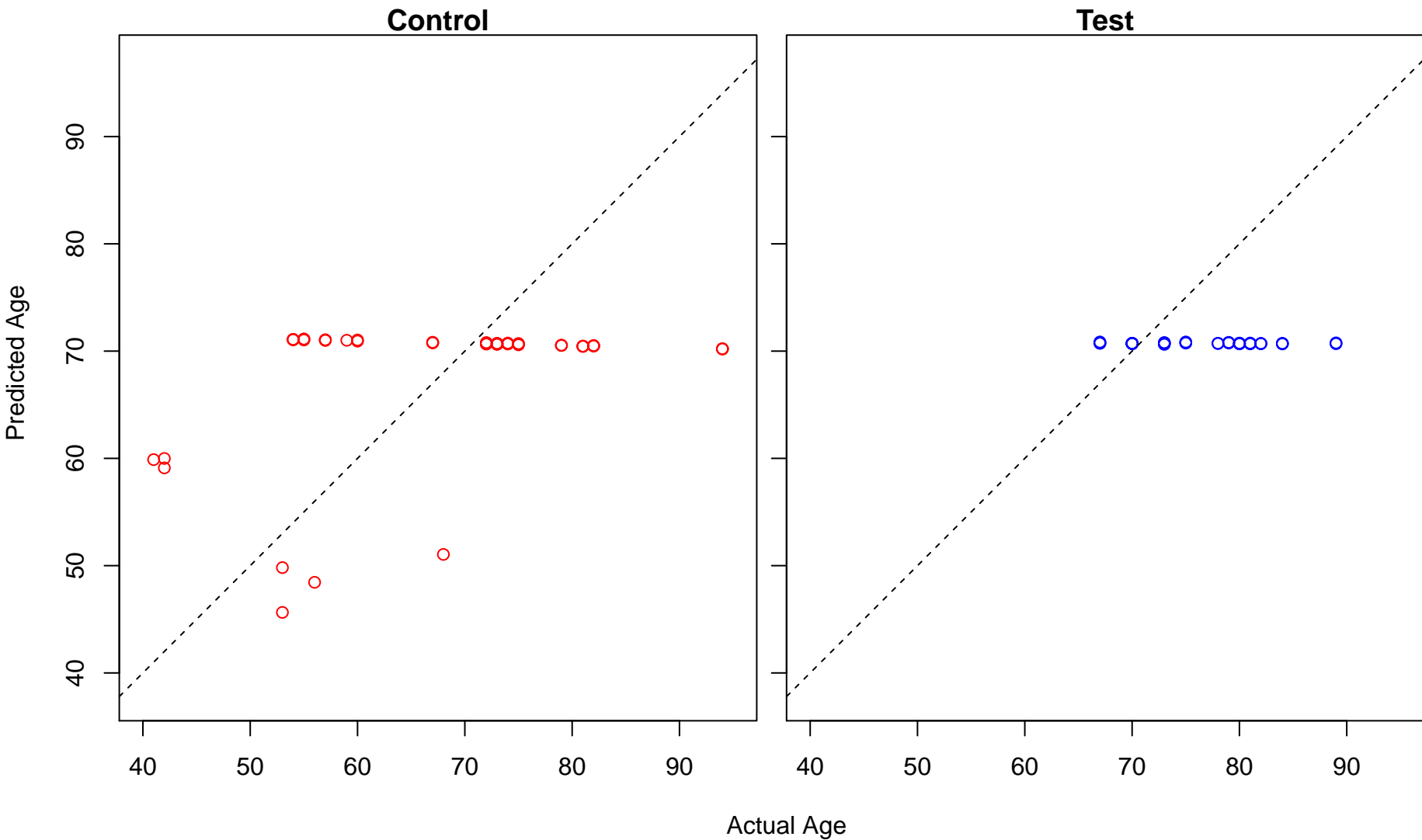
positive regulation of growth (Score: 0.781133)



isoprenoid metabolic process (Score: 0.780568)

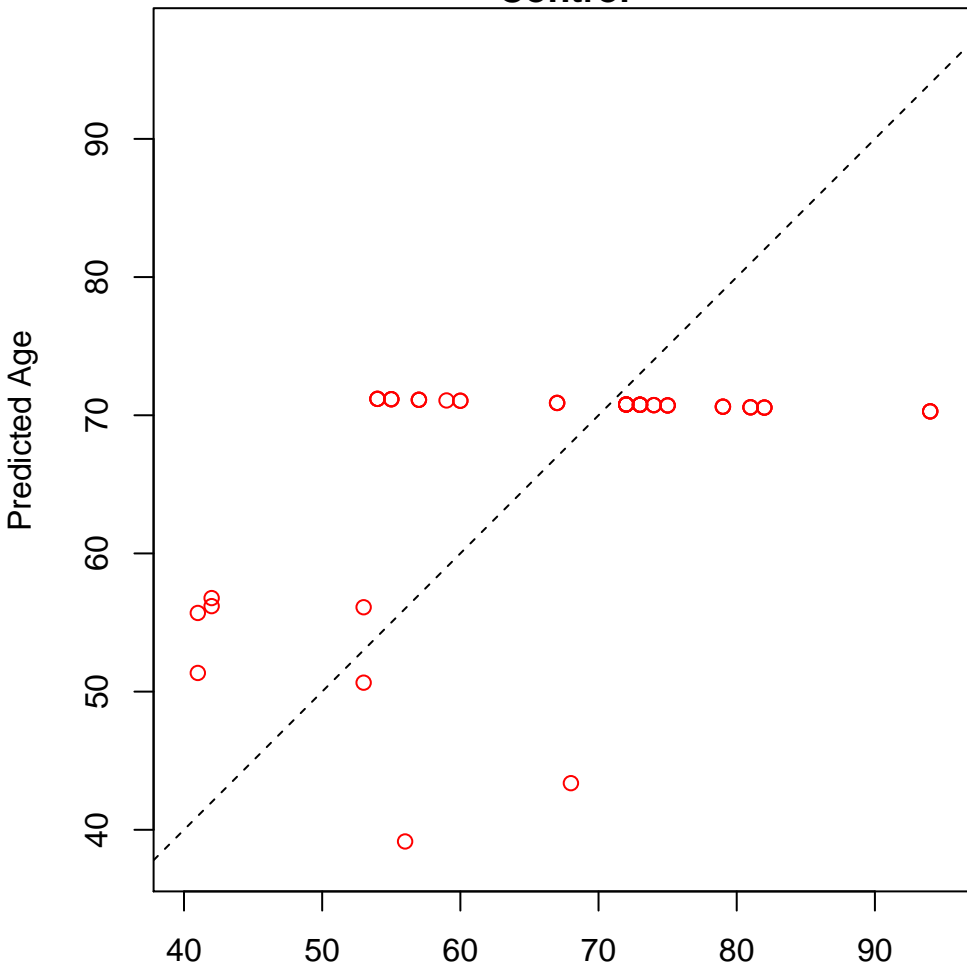


terpenoid metabolic process (Score: 0.780568)

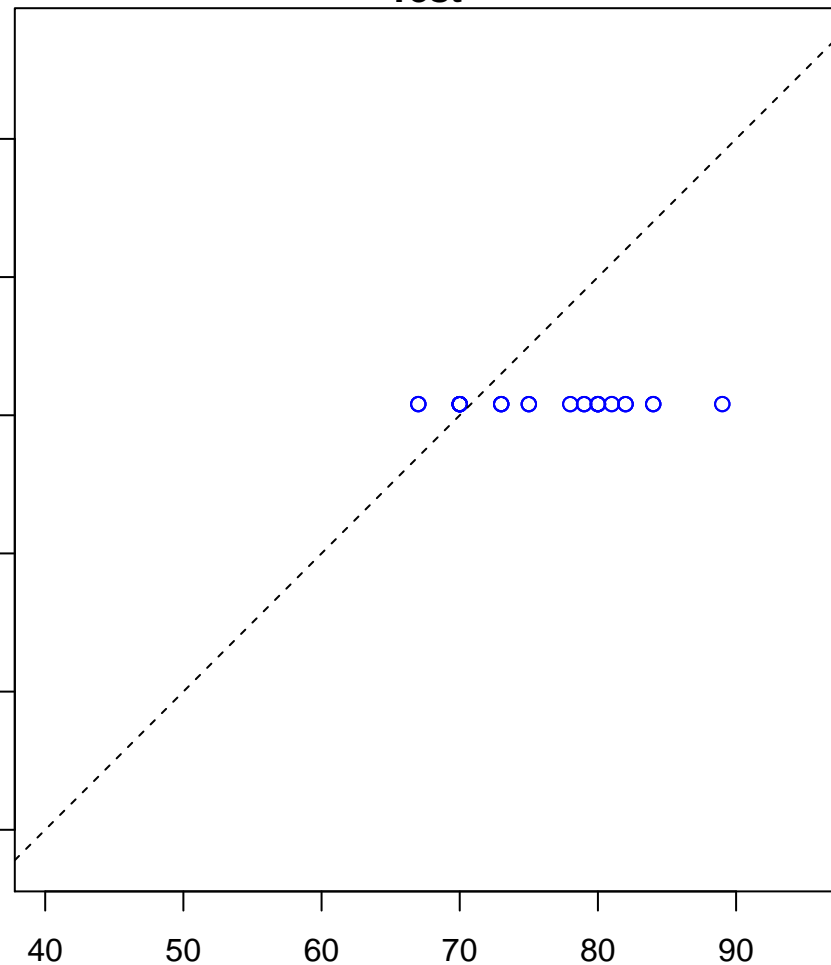


morphogenesis of an epithelial sheet (Score: 0.780284)

Control



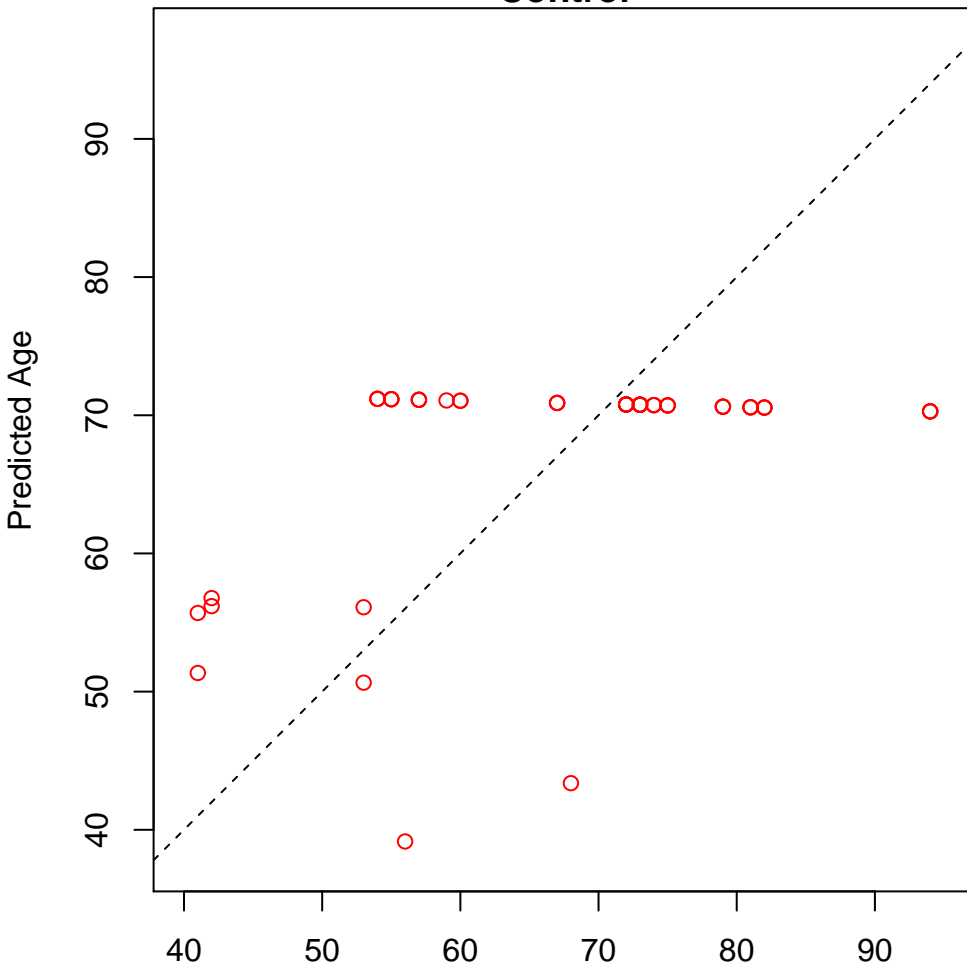
Test



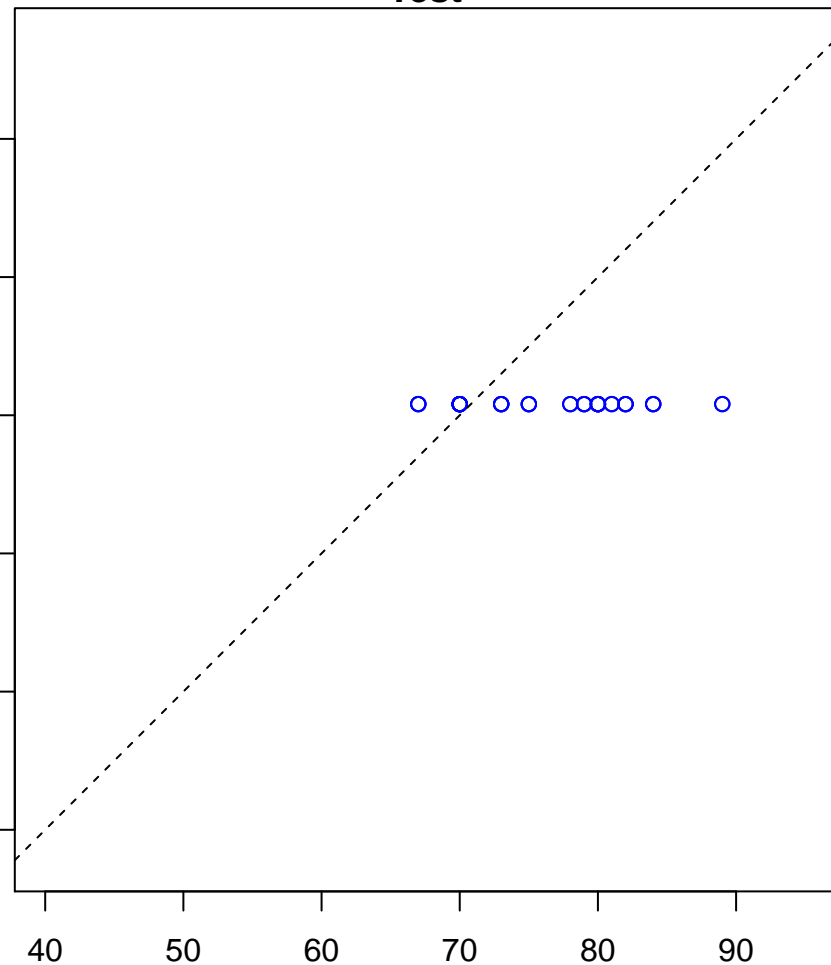
Actual Age

wound healing, spreading of cells (Score: 0.780284)

Control

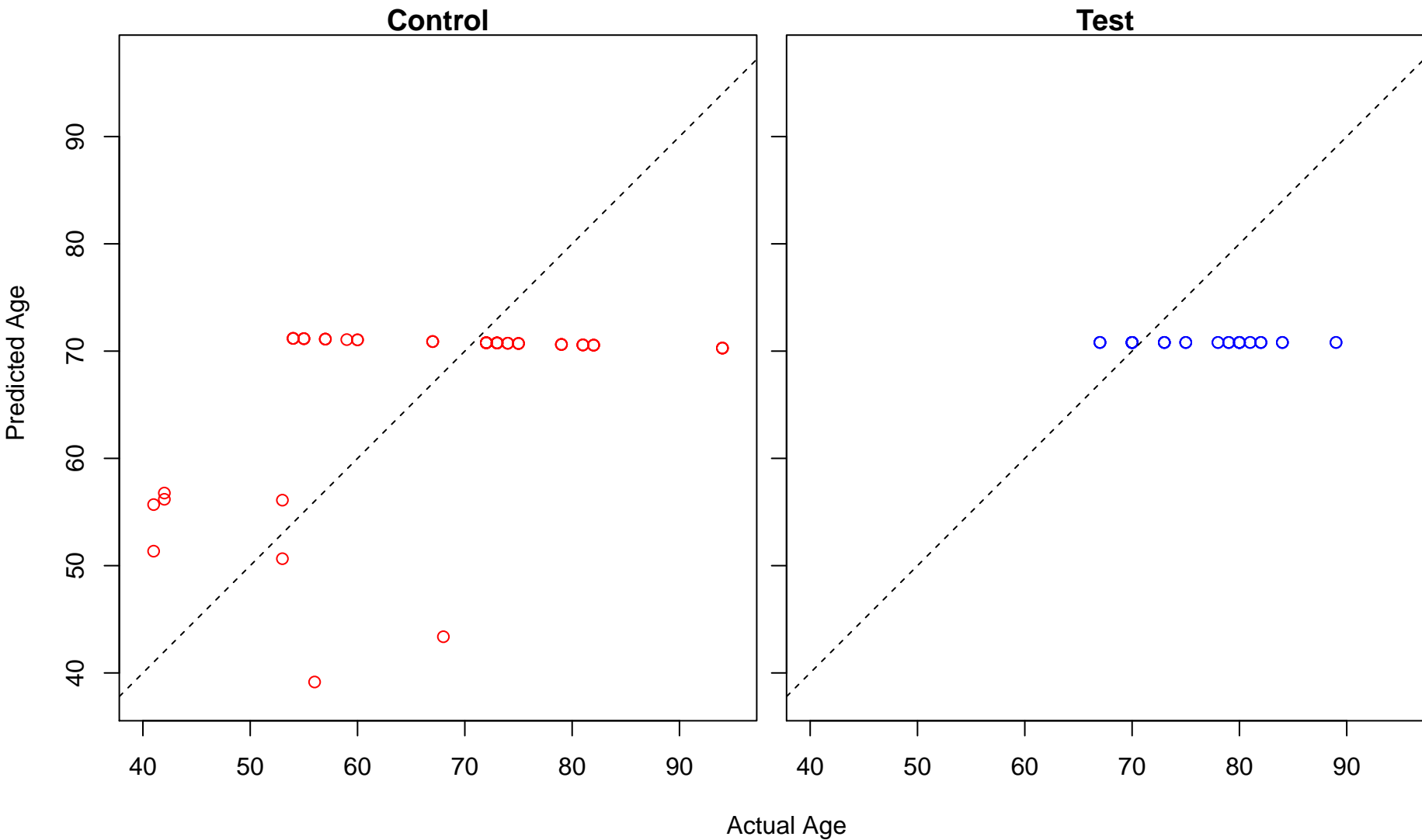


Test



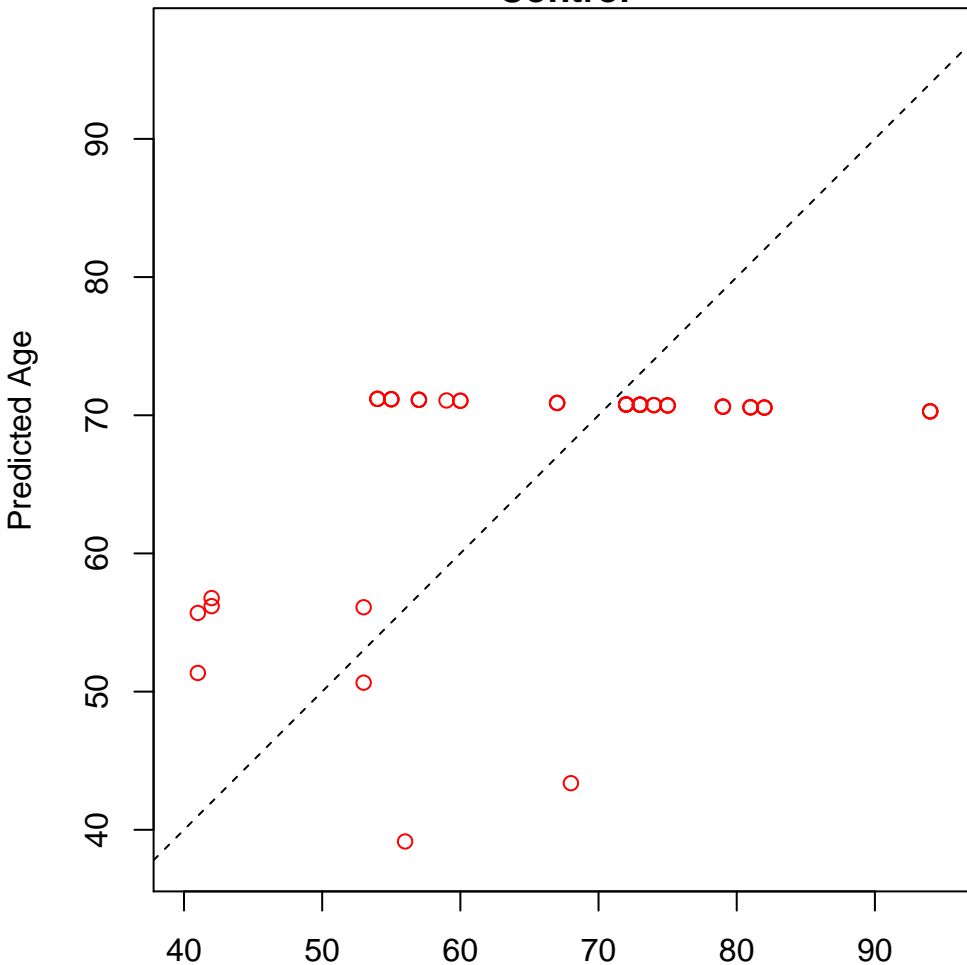
Actual Age

epiboly (Score: 0.780284)

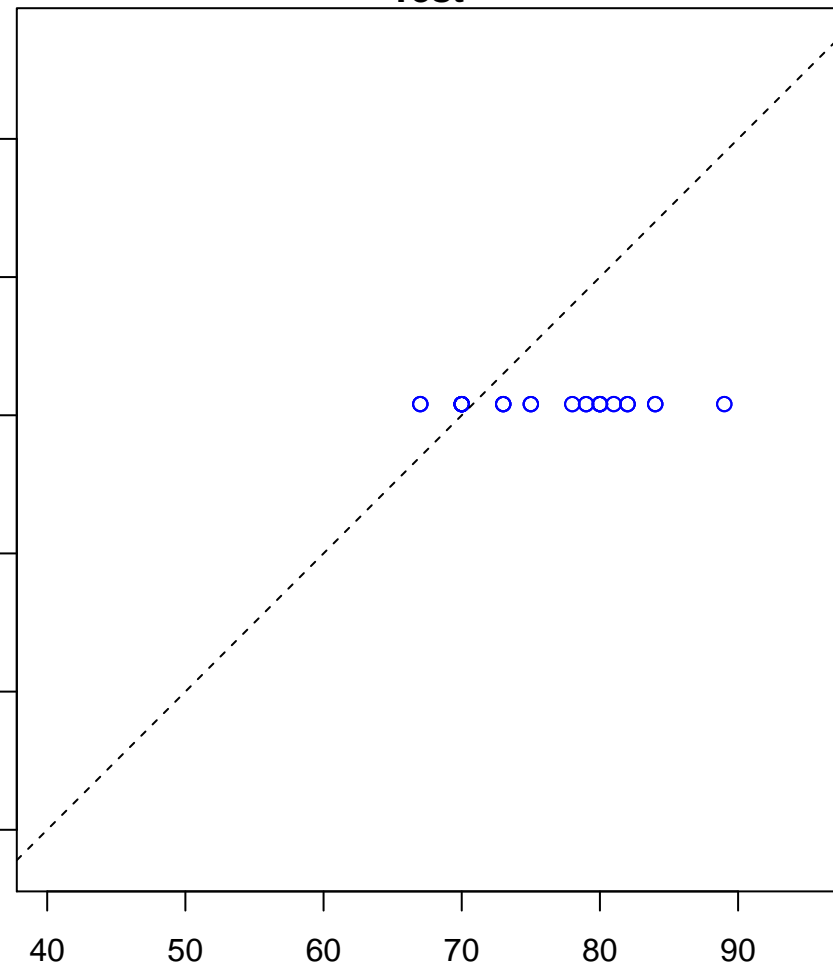


epiboly involved in wound healing (Score: 0.780284)

Control

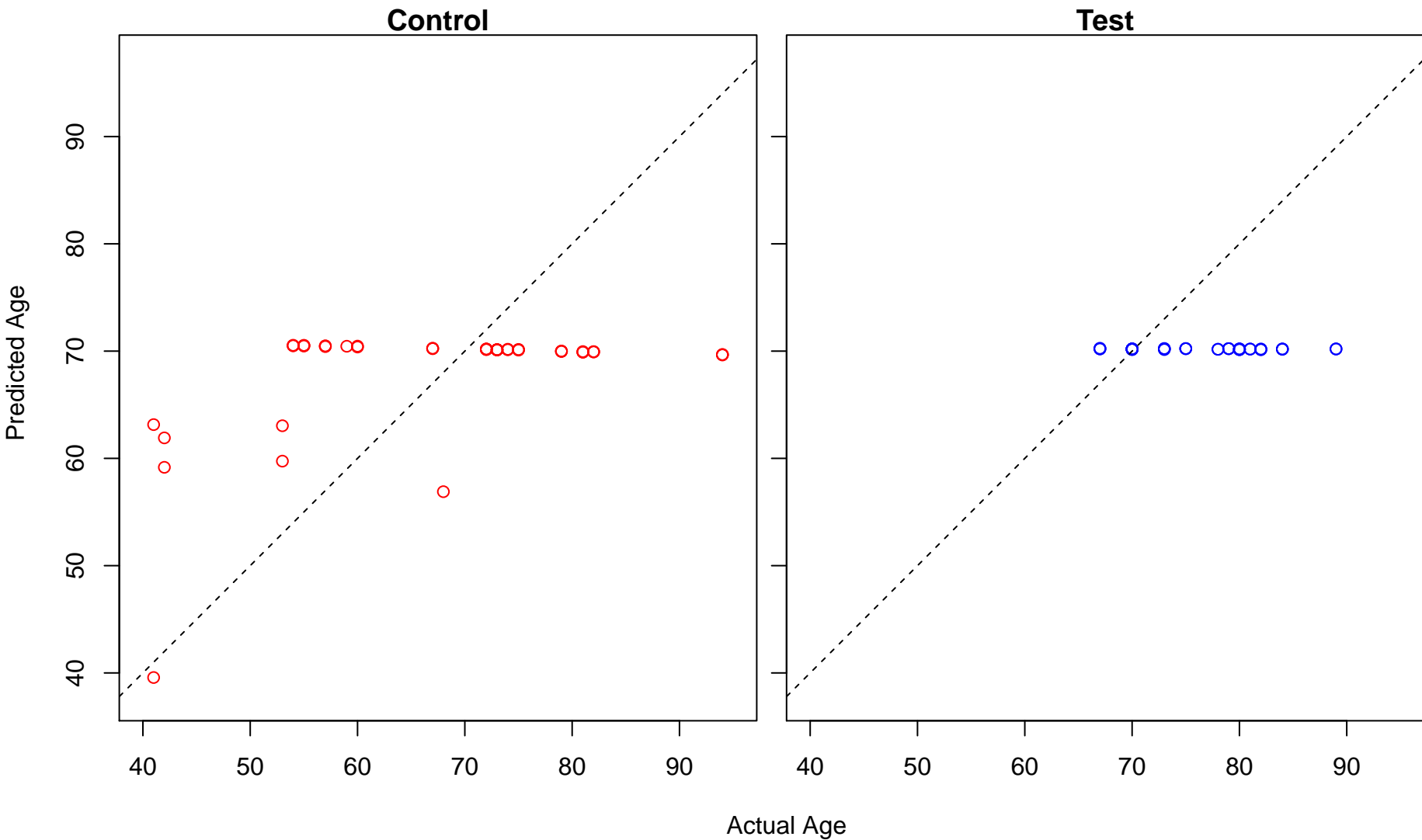


Test

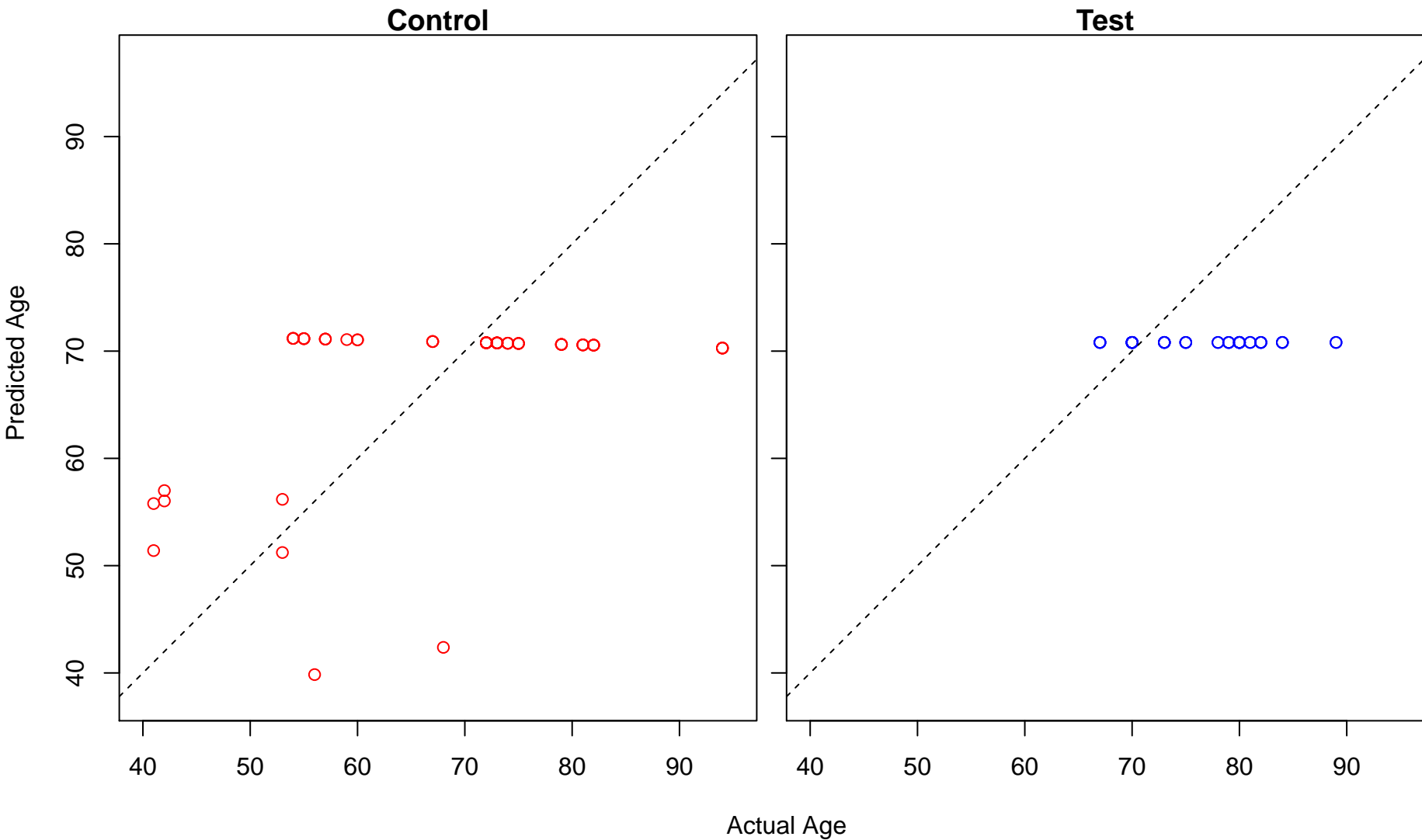


Actual Age

positive regulation of protein localization to plasma membrane (Score: 0.780116)

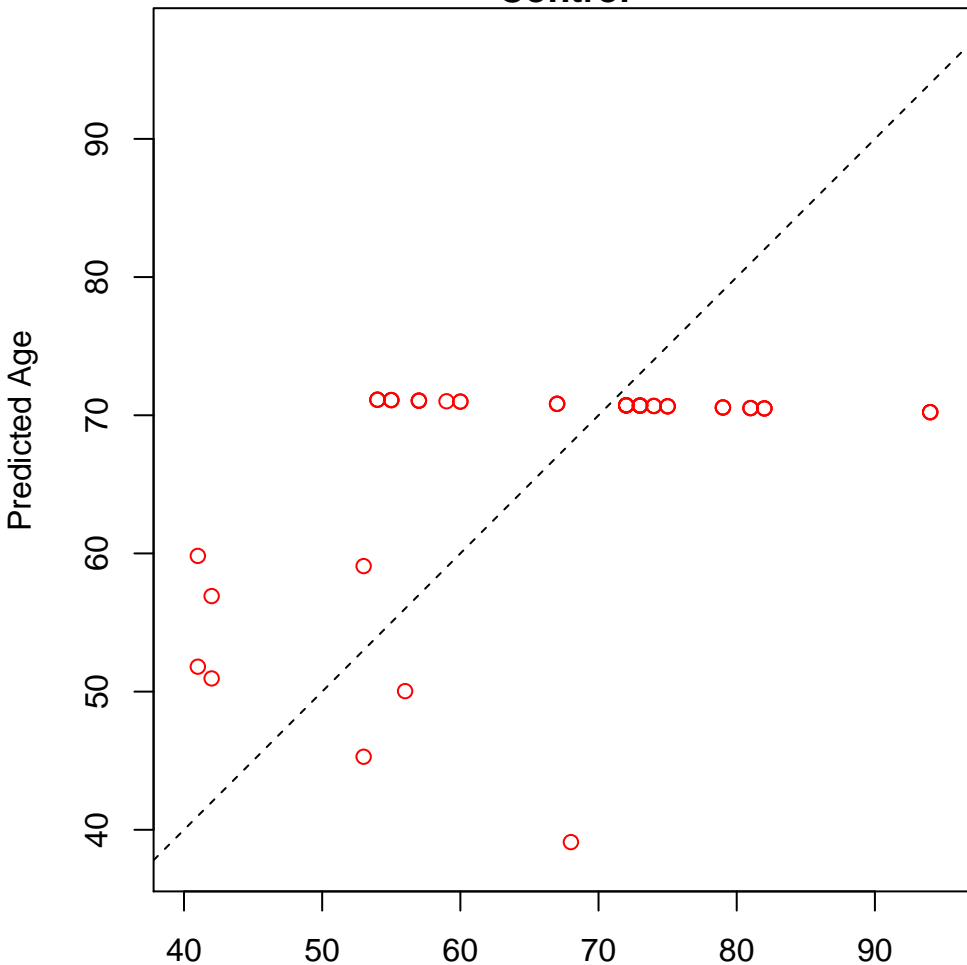


trabecula morphogenesis (Score: 0.780078)

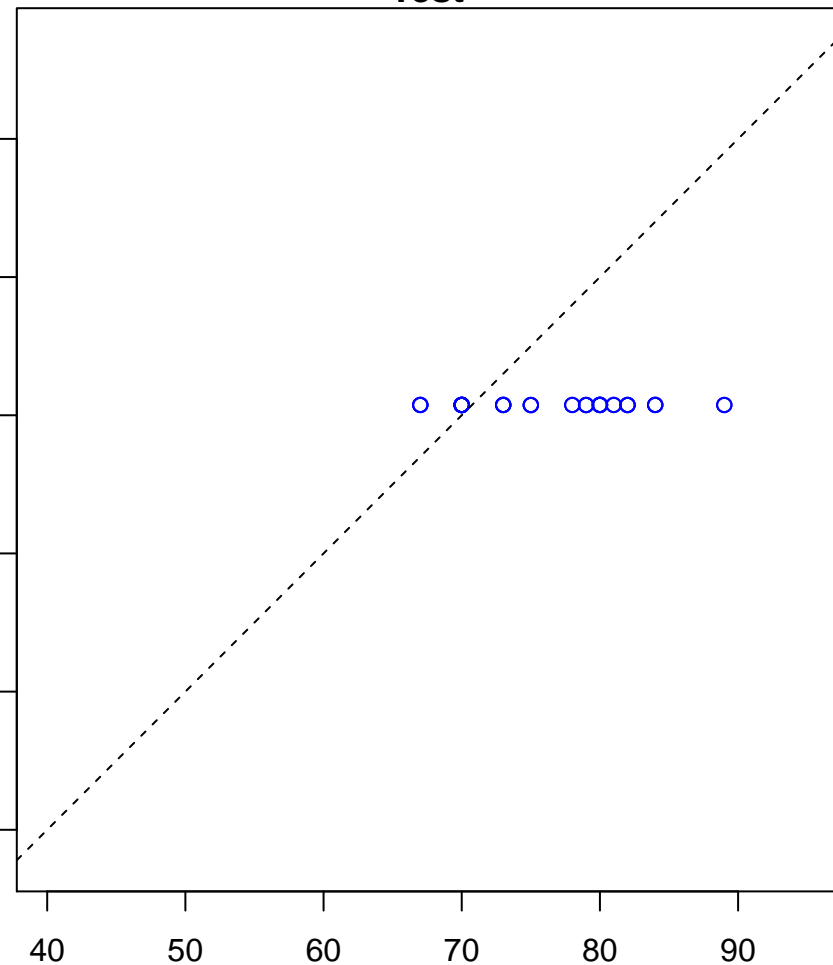


response to arsenic-containing substance (Score: 0.779995)

Control

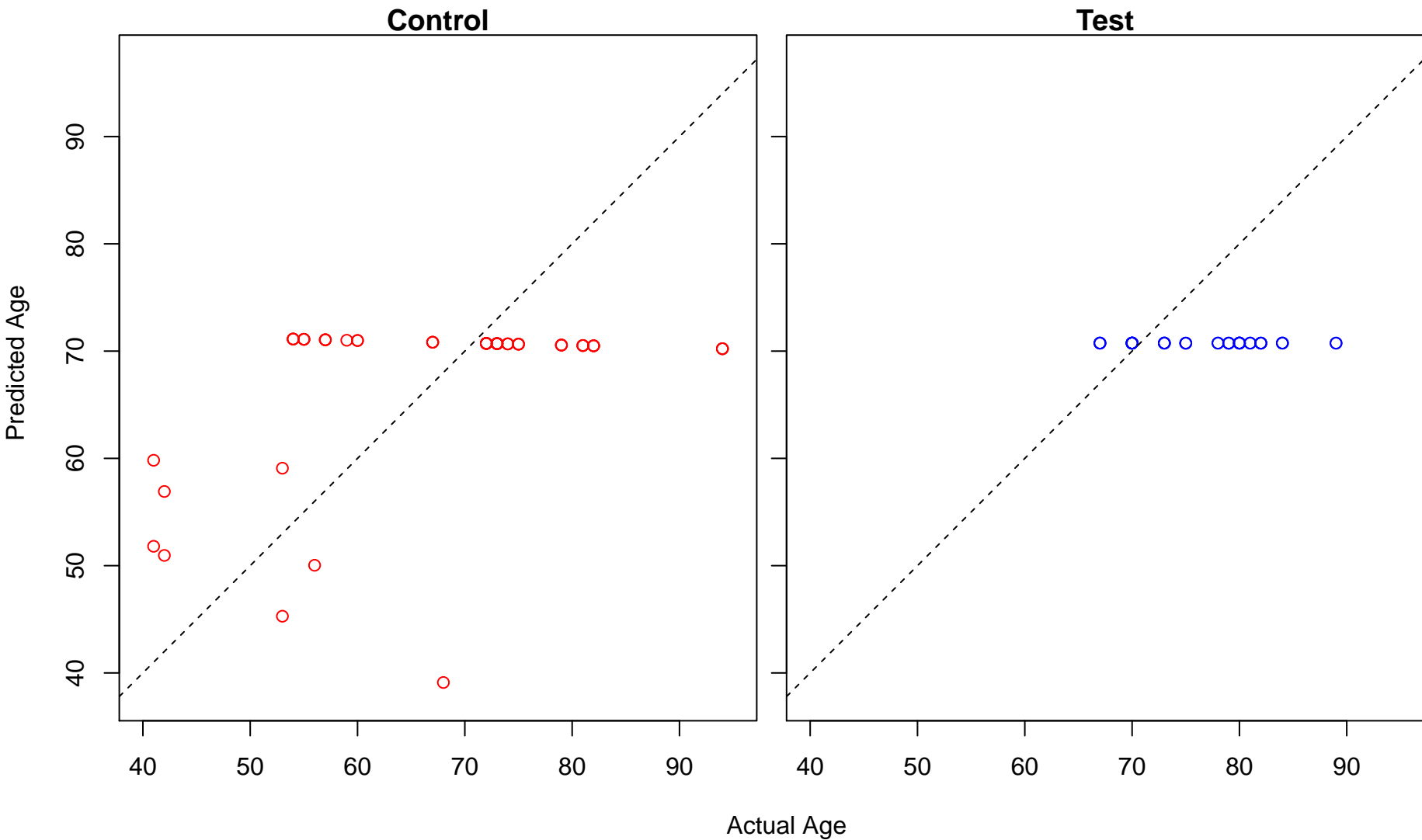


Test



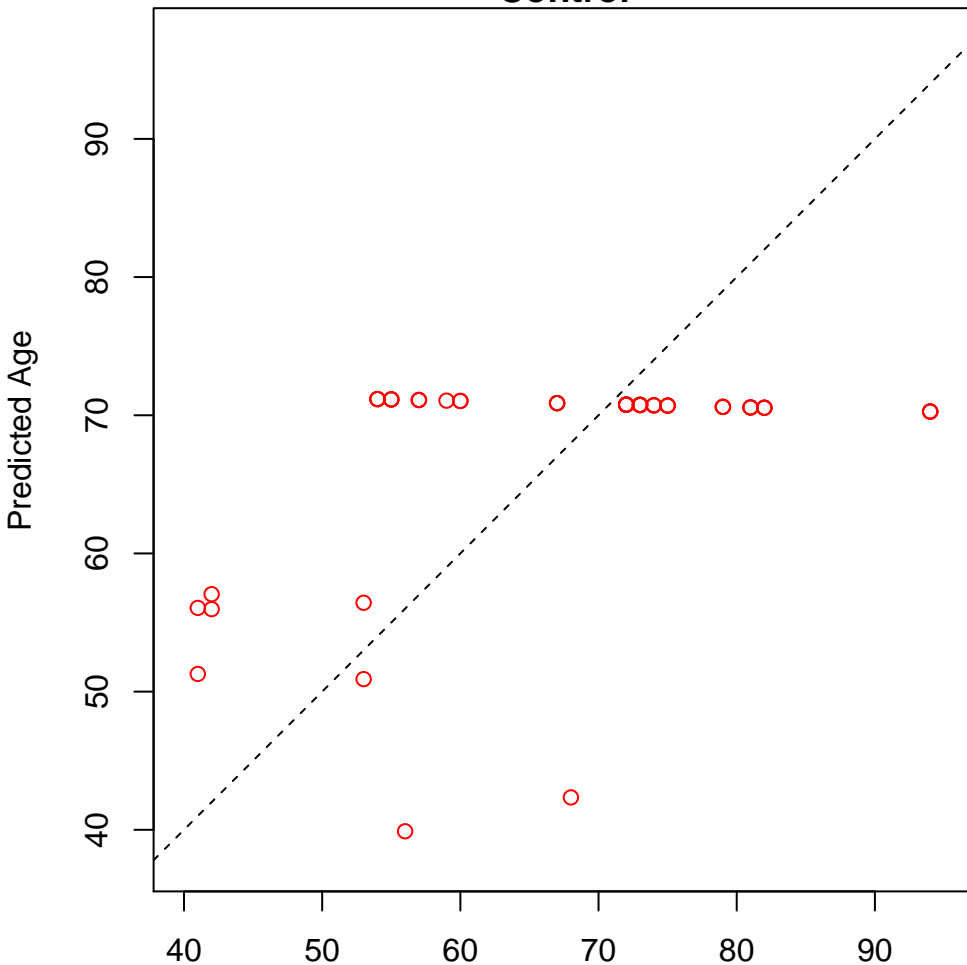
Actual Age

cellular response to arsenic-containing substance (Score: 0.779995)

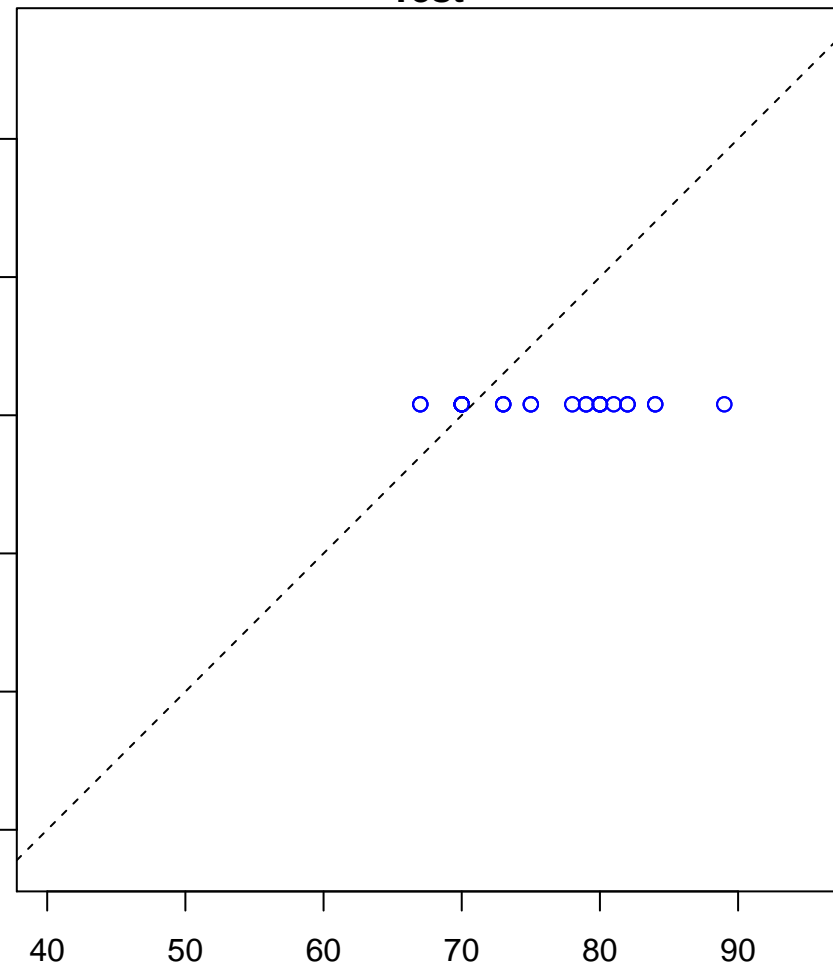


negative regulation of cell development (Score: 0.779623)

Control

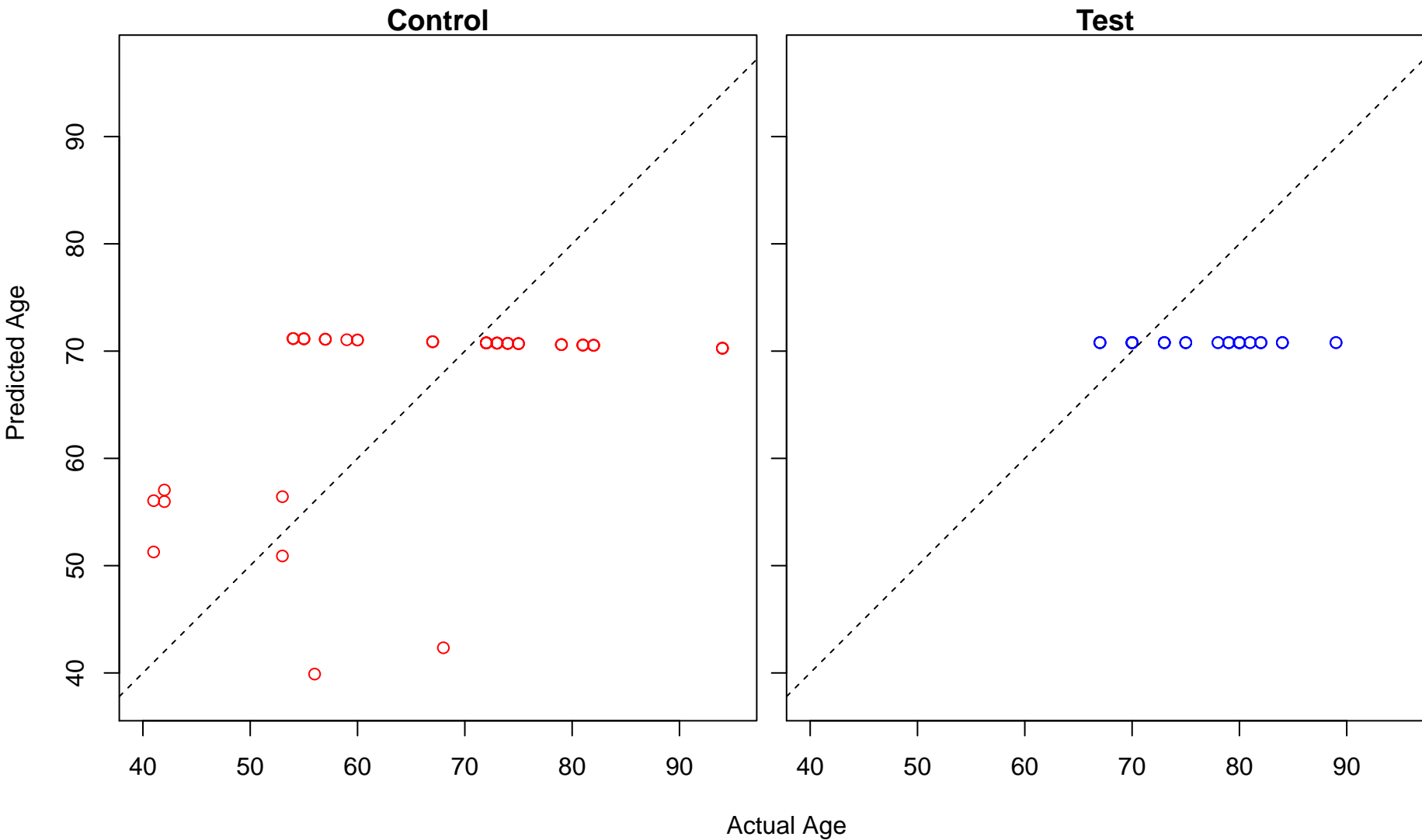


Test

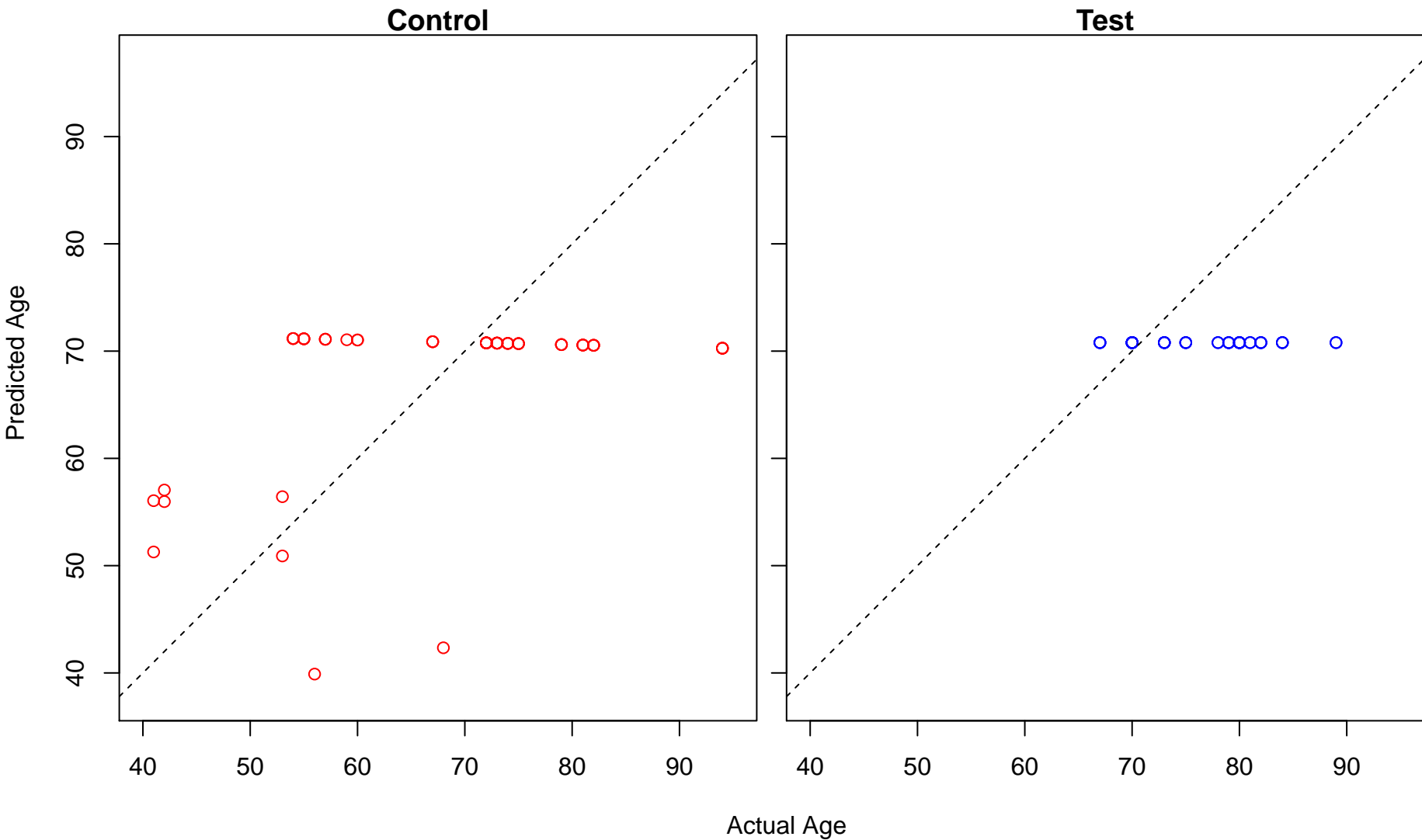


Actual Age

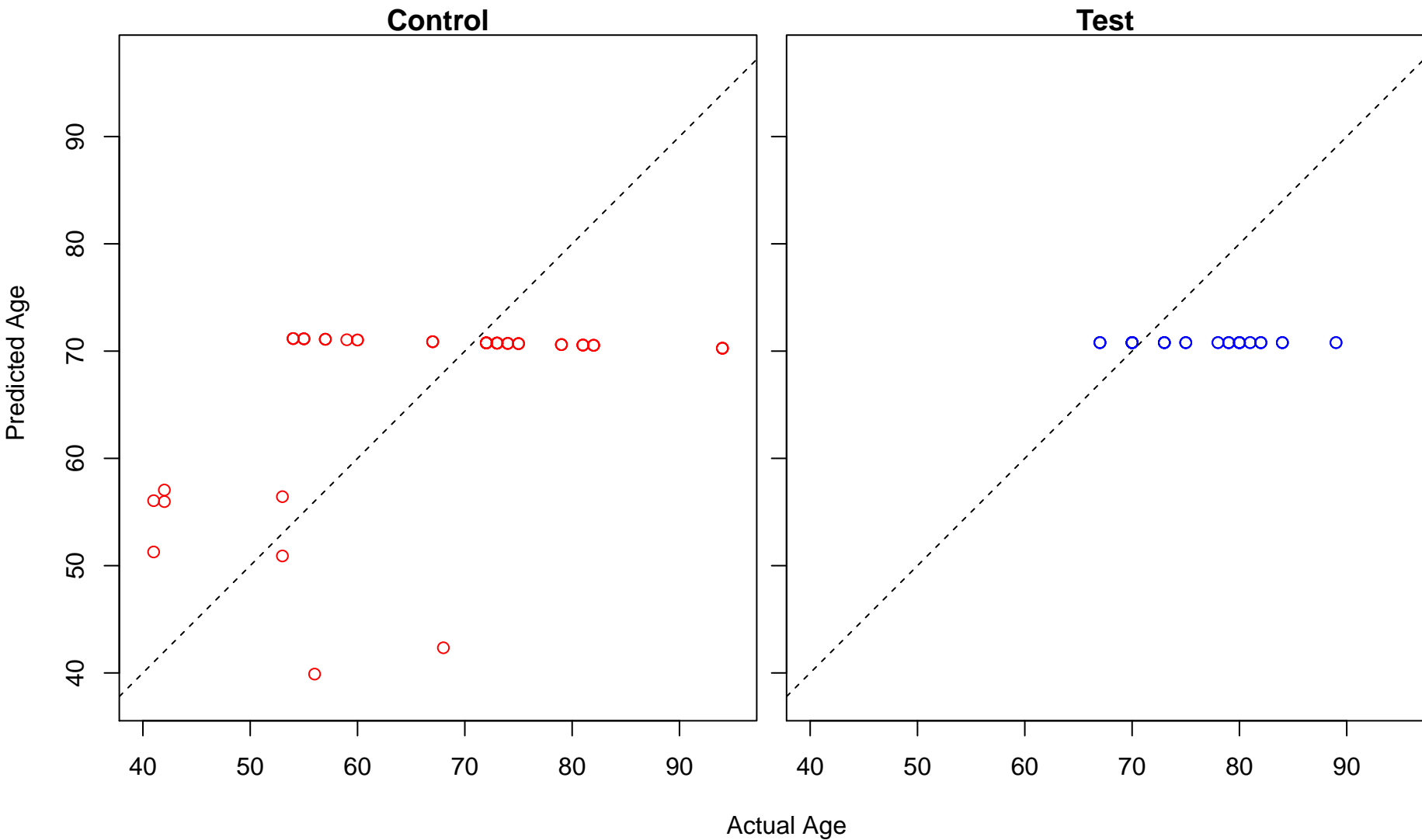
negative regulation of cell morphogenesis involved in differentiation (Score: 0.779623)



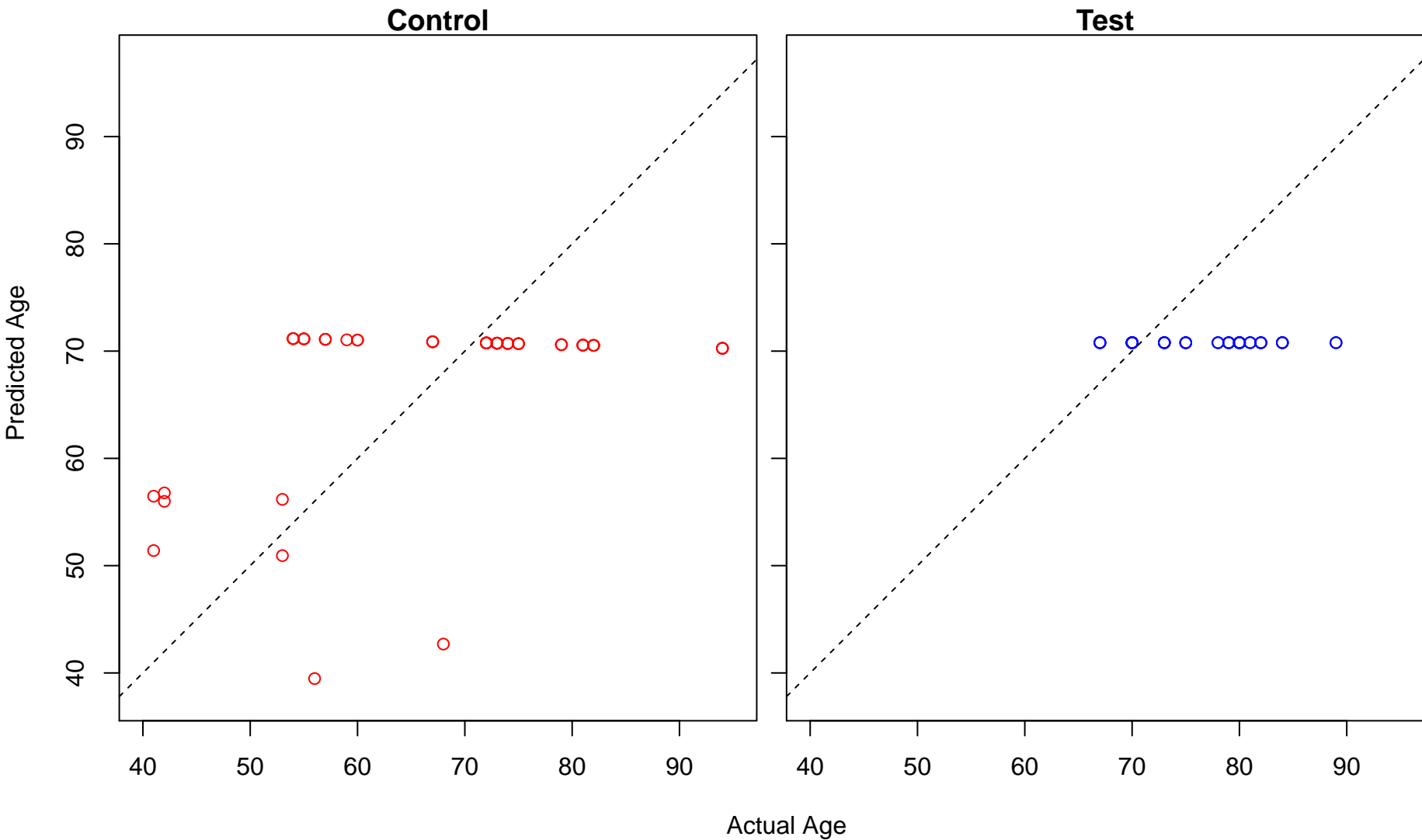
regulation of cell-substrate adhesion (Score: 0.779623)



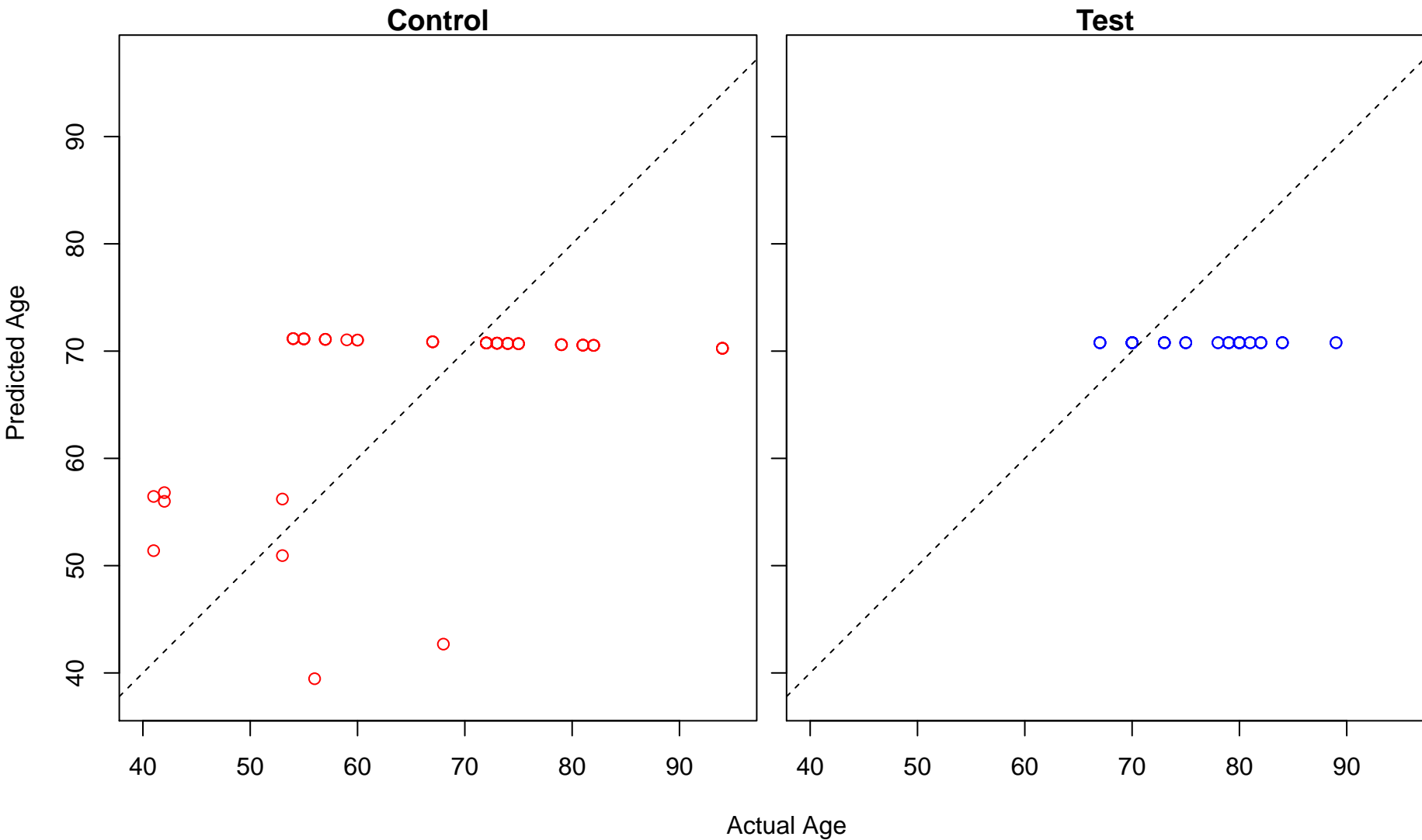
negative regulation of cell-substrate adhesion (Score: 0.779623)



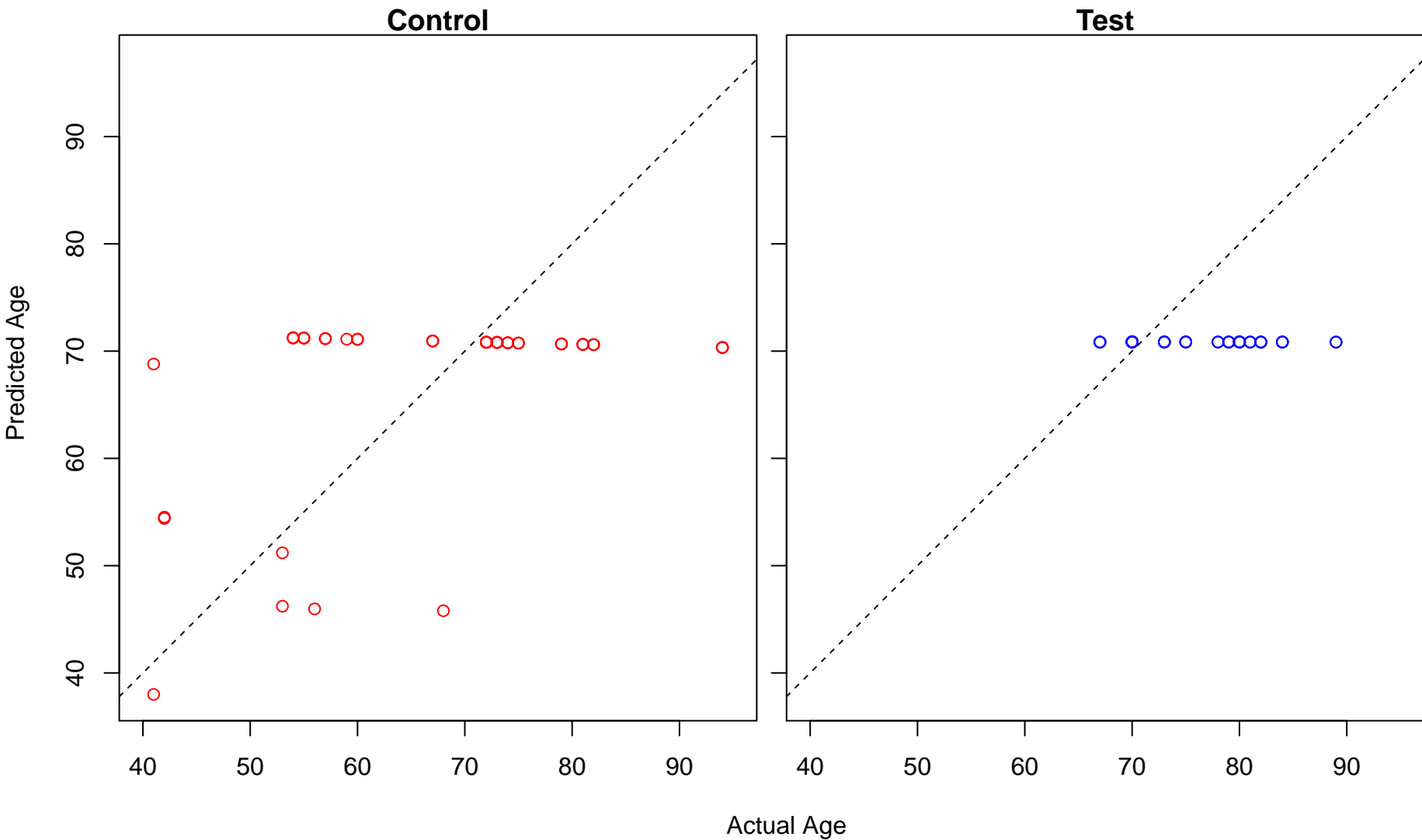
cell junction organization (Score: 0.779574)



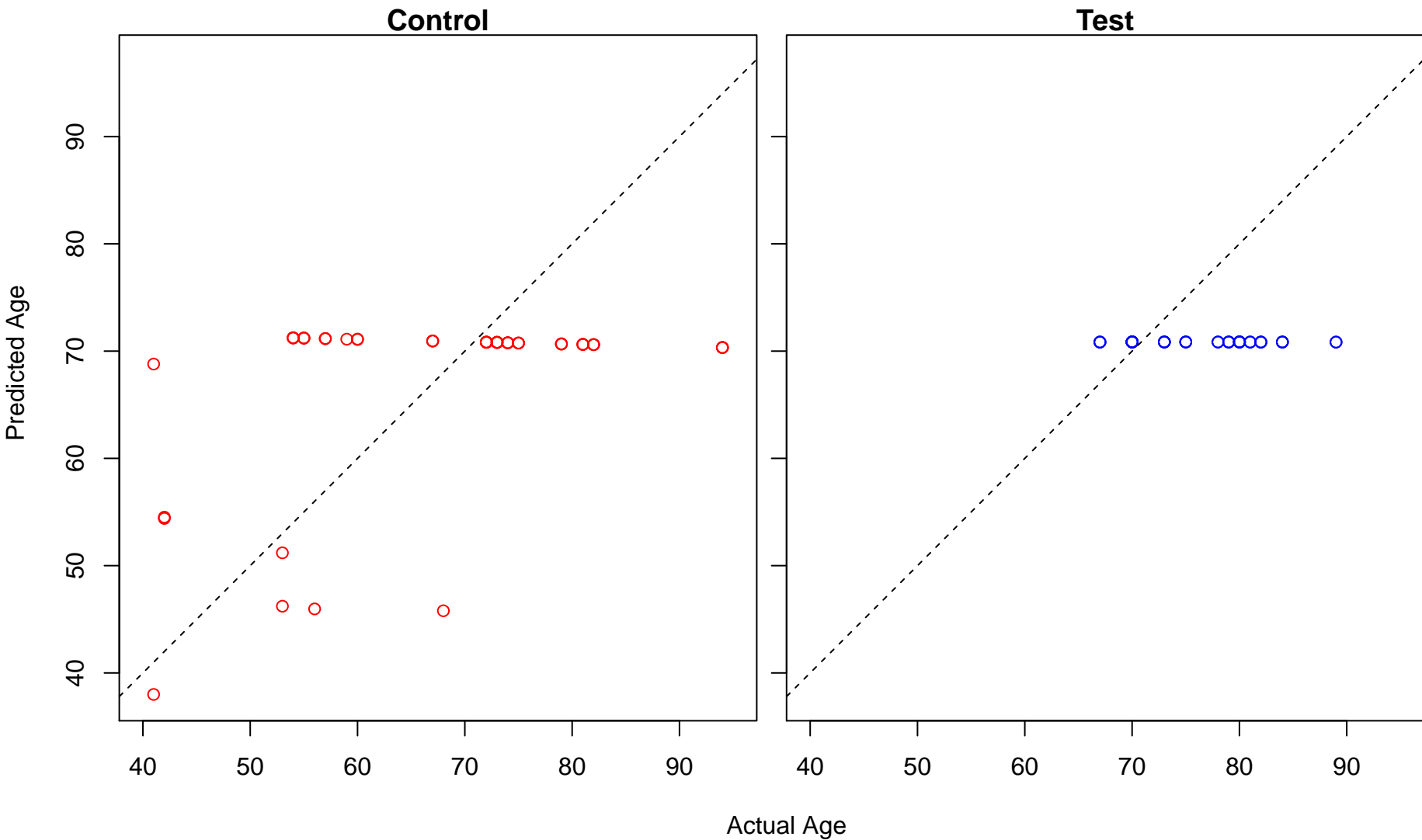
cell-cell junction organization (Score: 0.779545)



nuclear division (Score: 0.779472)

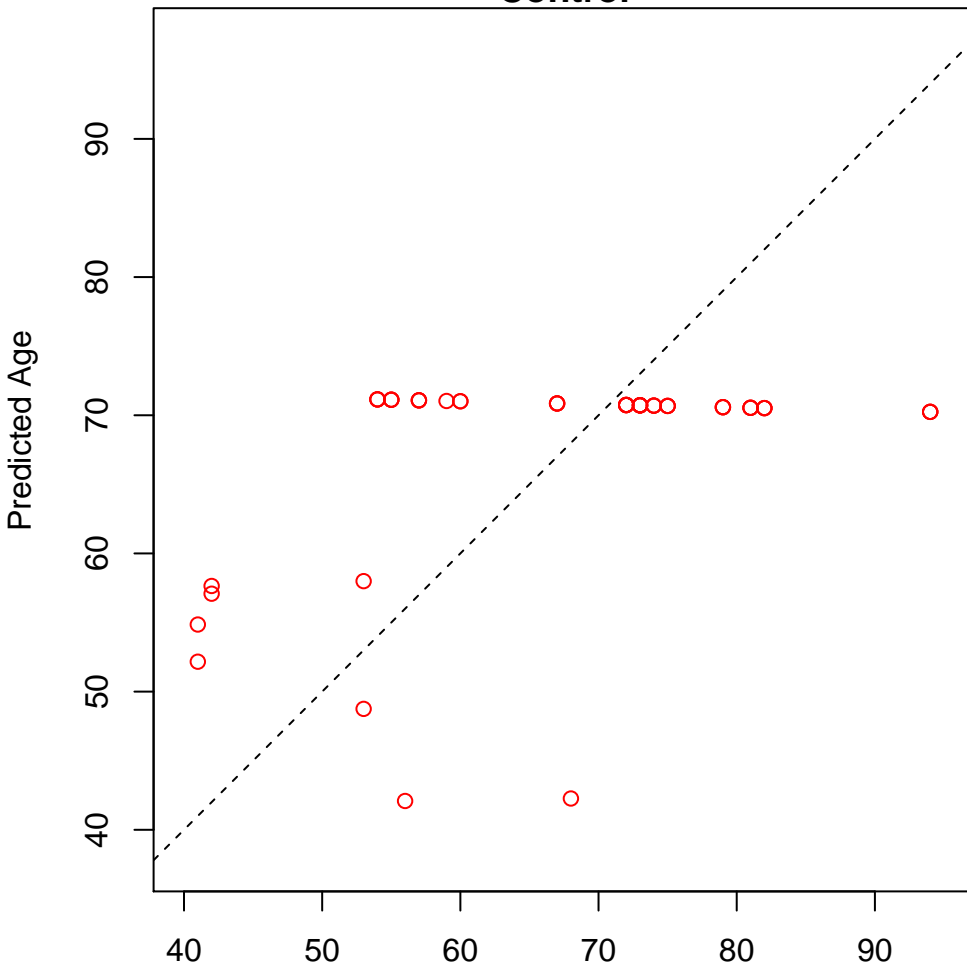


organelle fission (Score: 0.779472)

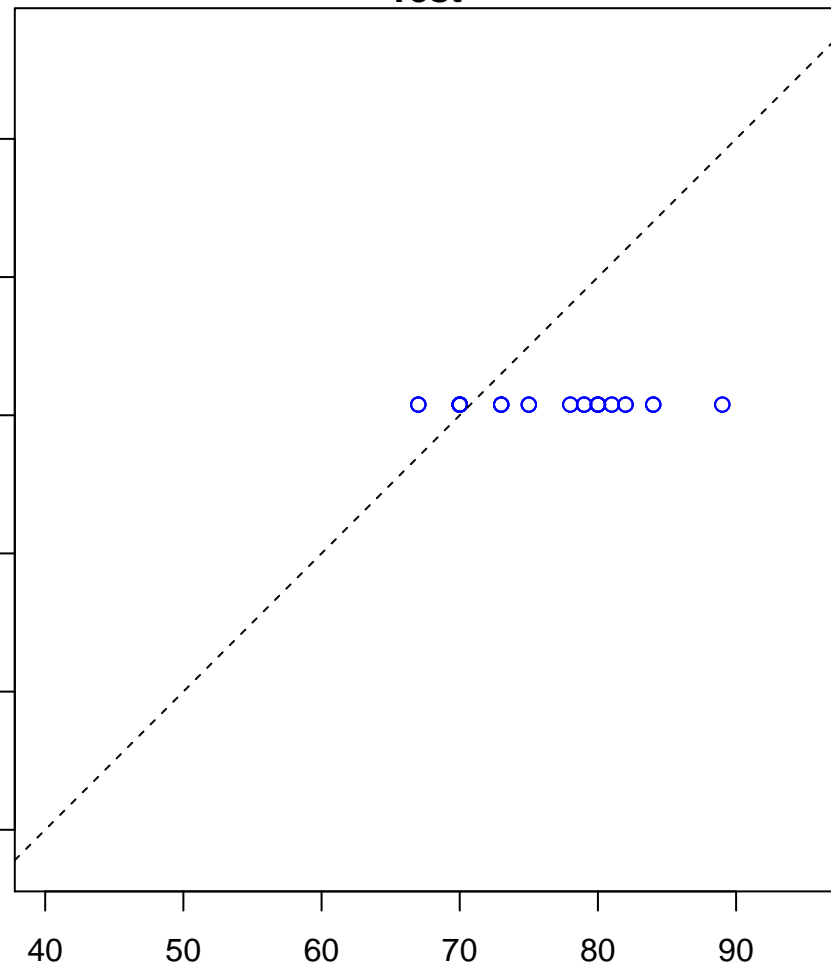


regulation of epithelial cell migration (Score: 0.779376)

Control



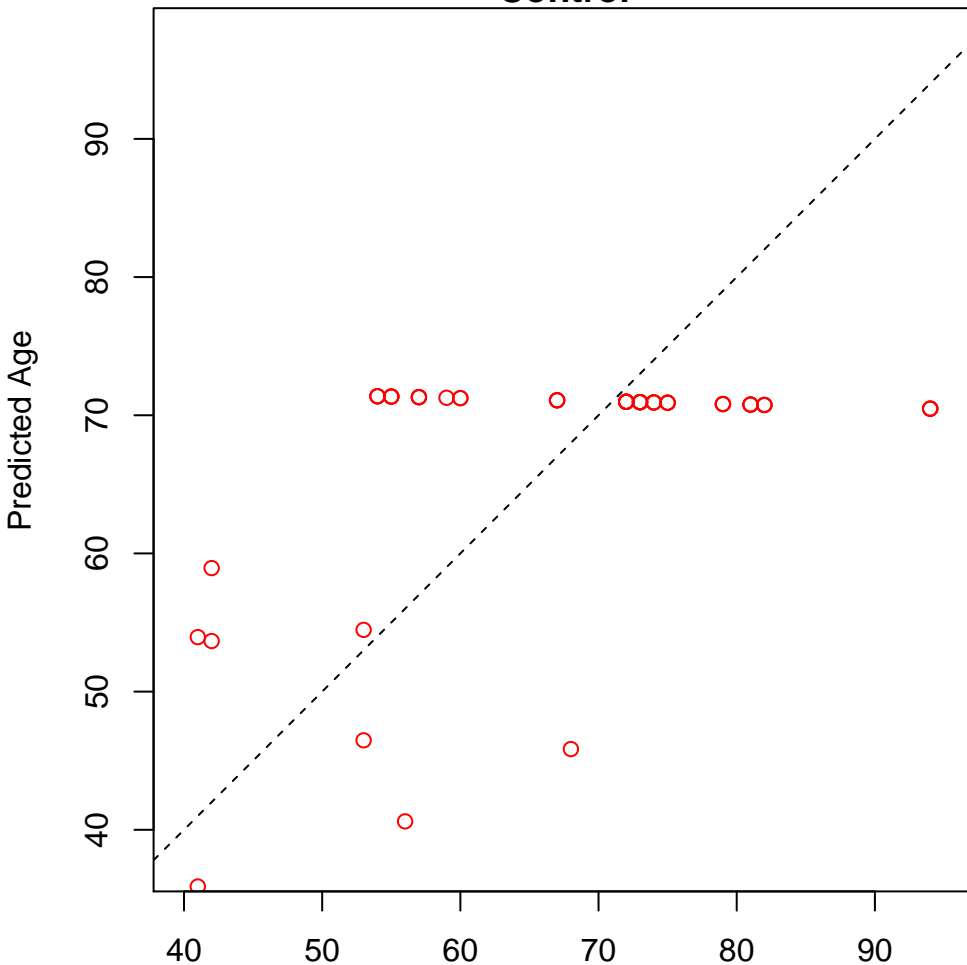
Test



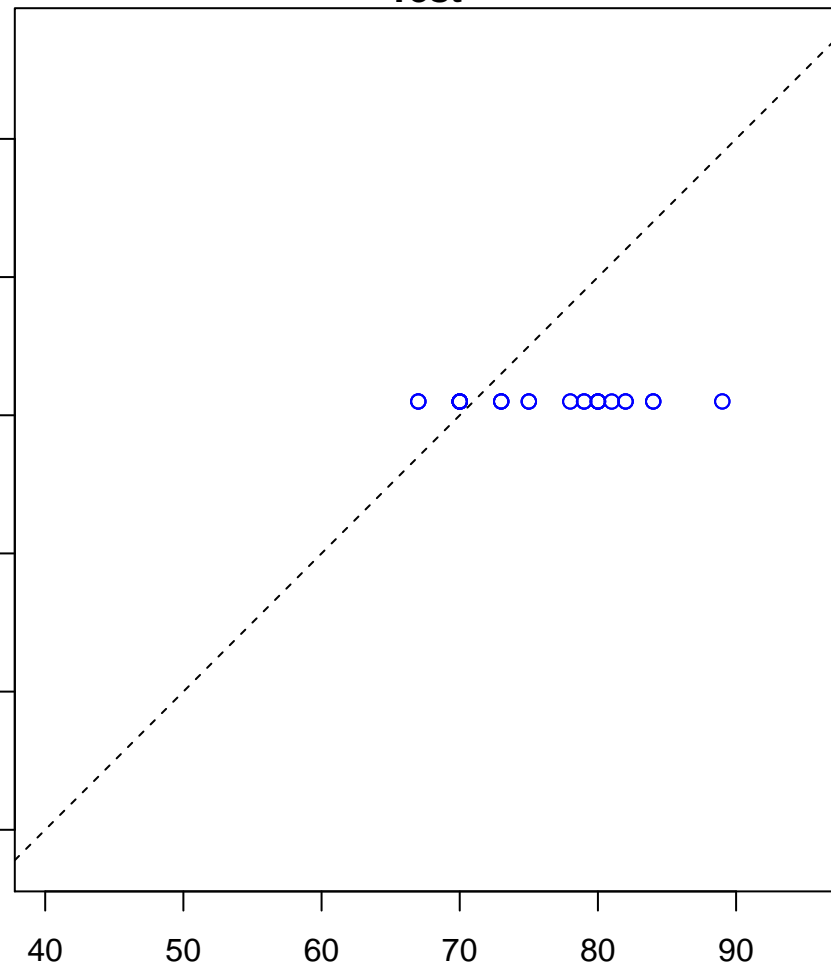
Actual Age

response to calcium ion (Score: 0.779314)

Control

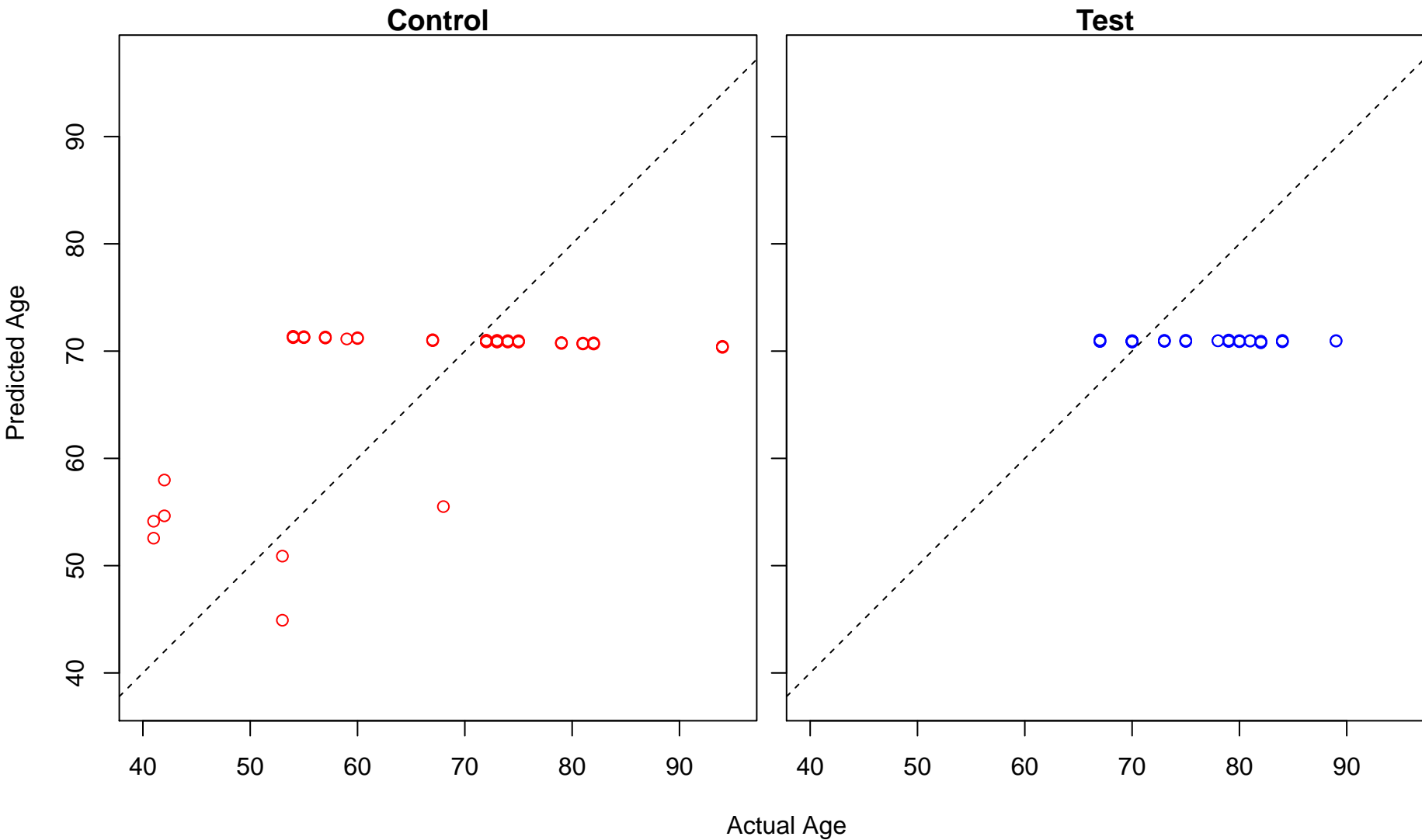


Test



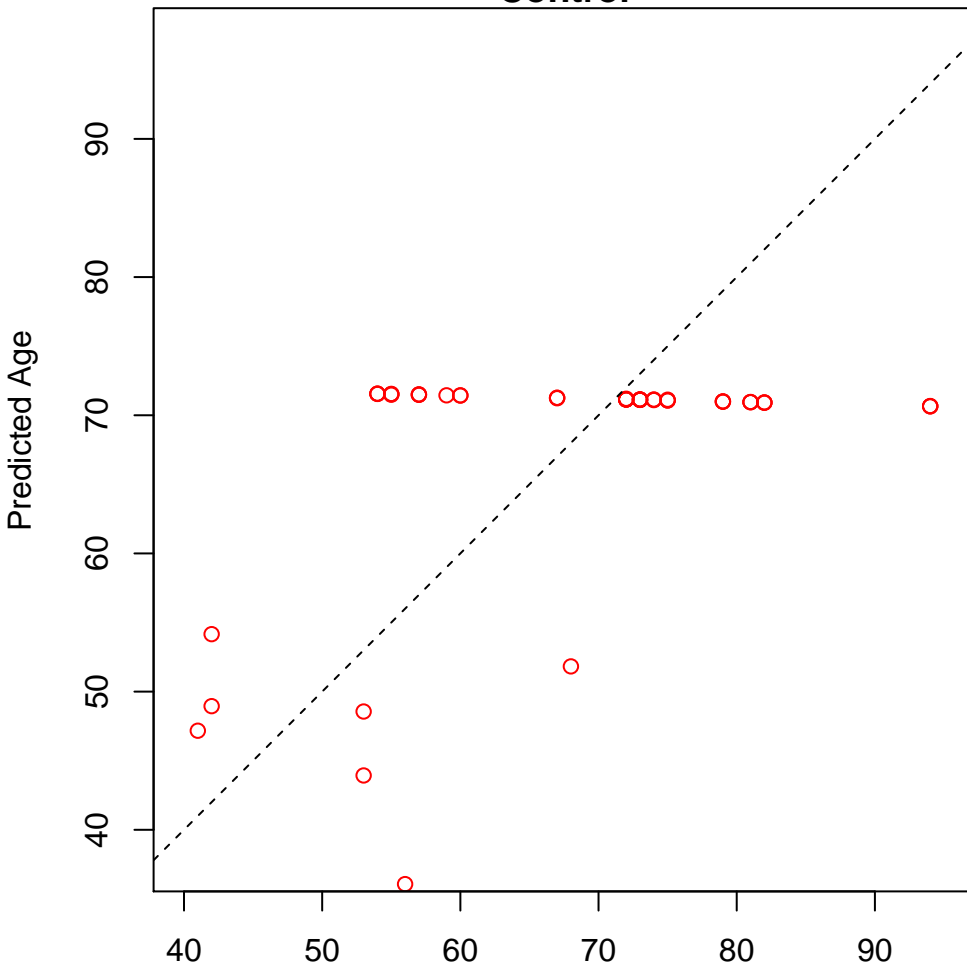
Actual Age

cell junction assembly (Score: 0.779164)

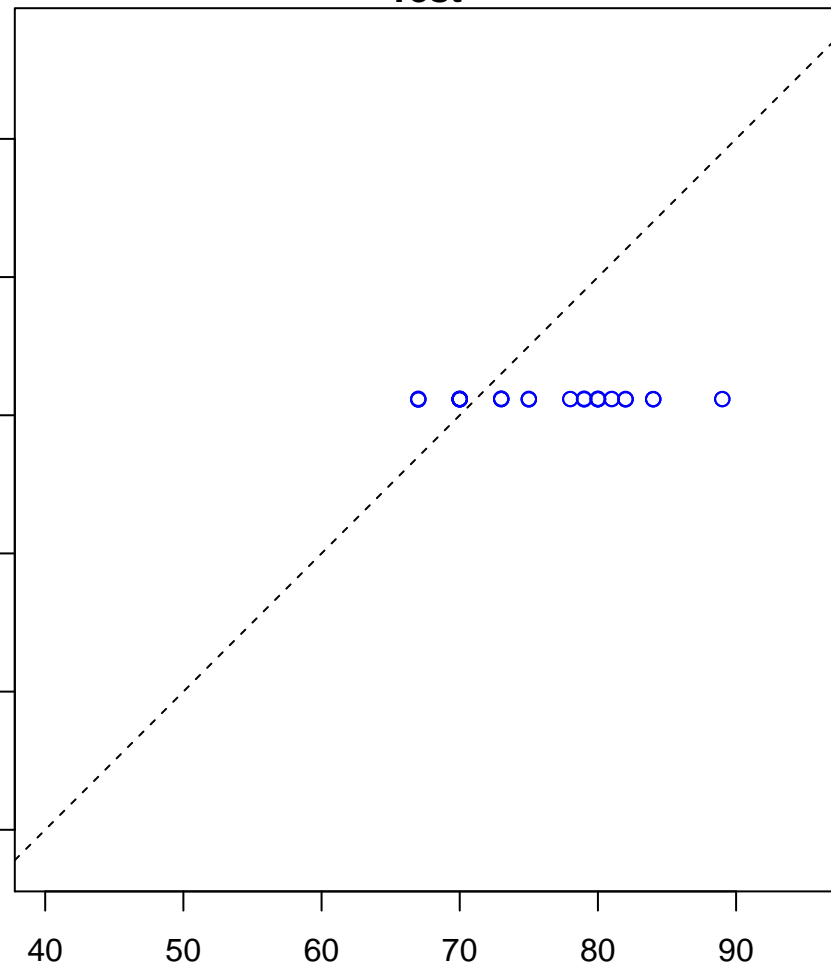


response to extracellular stimulus (Score: 0.779162)

Control

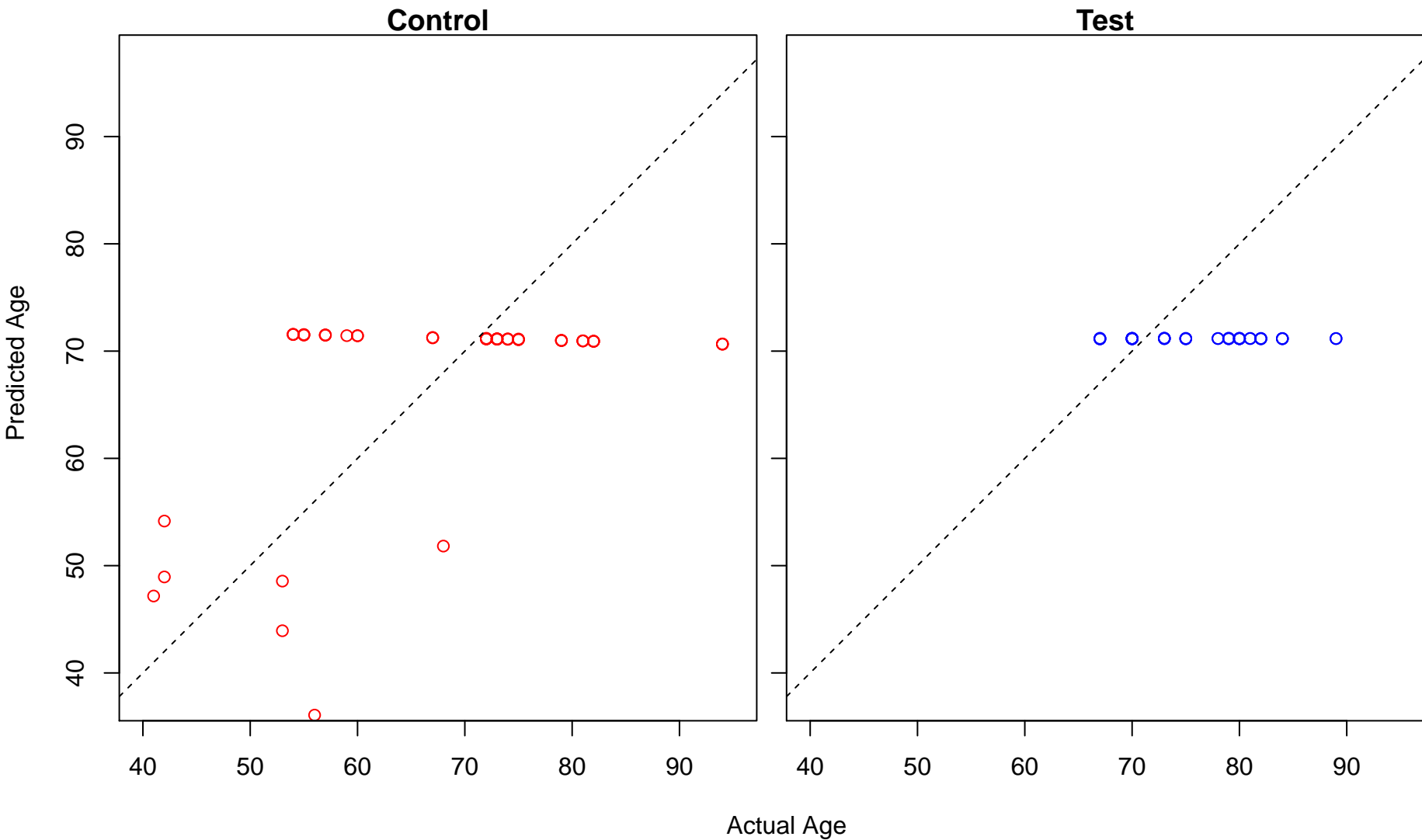


Test



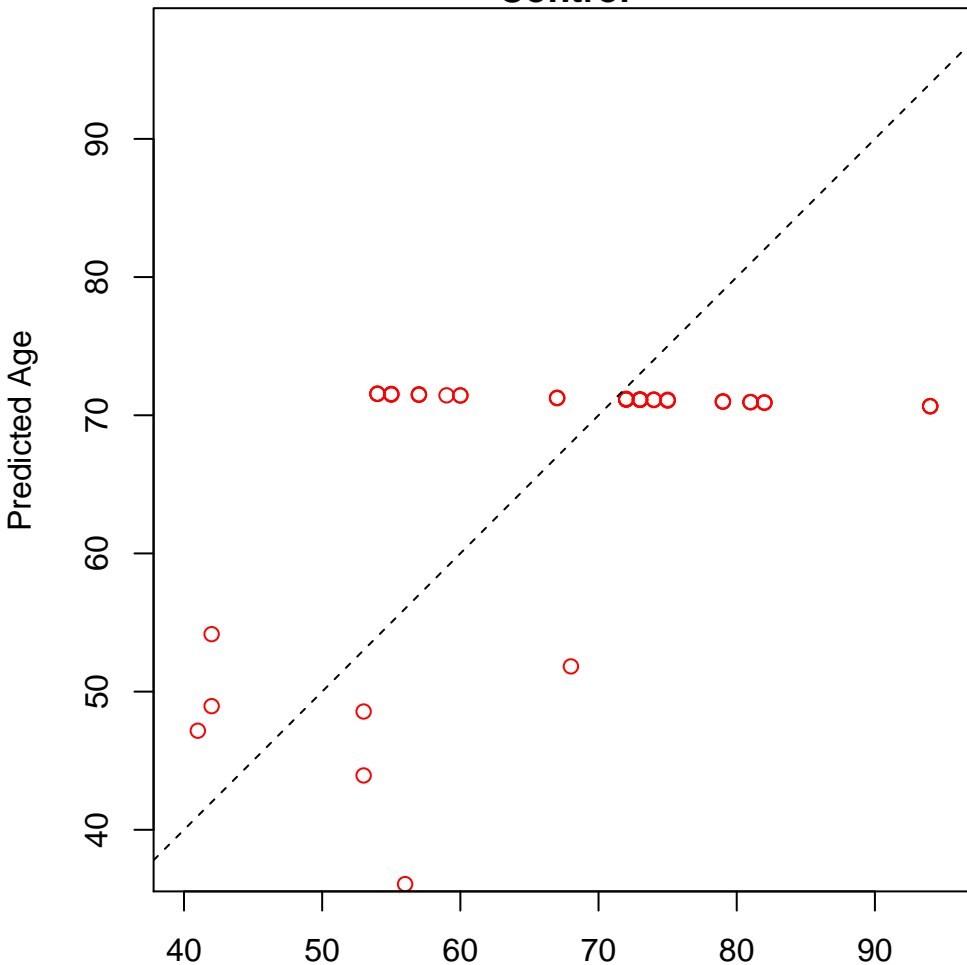
Actual Age

response to nutrient levels (Score: 0.779162)

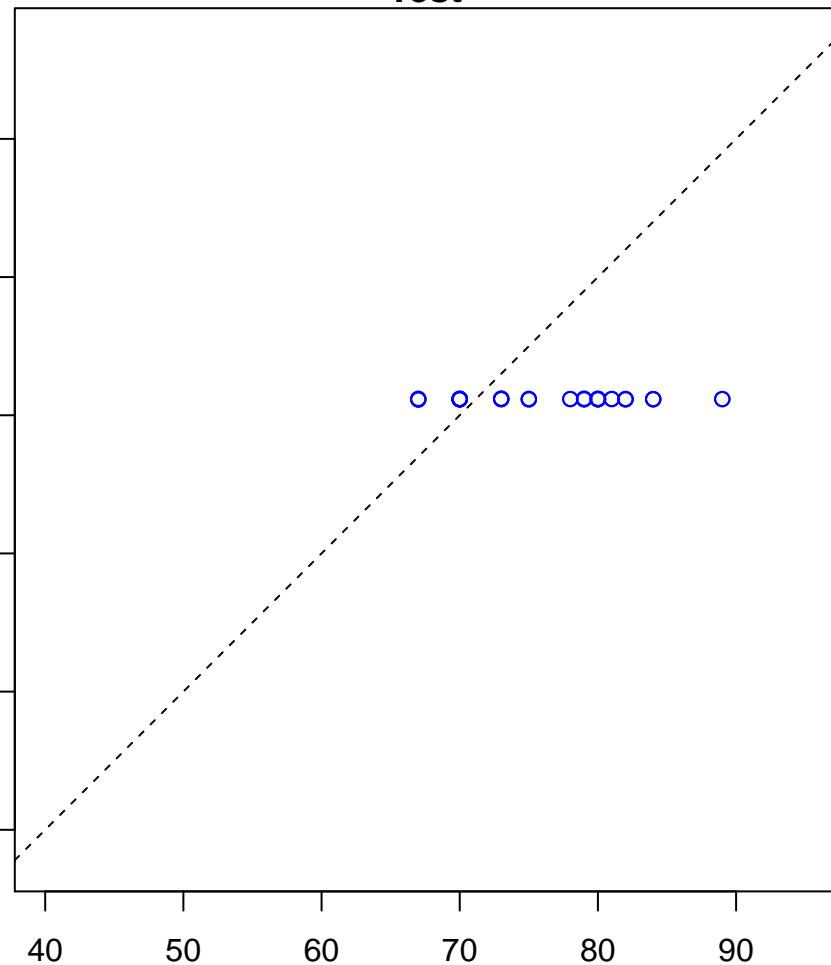


cellular response to extracellular stimulus (Score: 0.779162)

Control



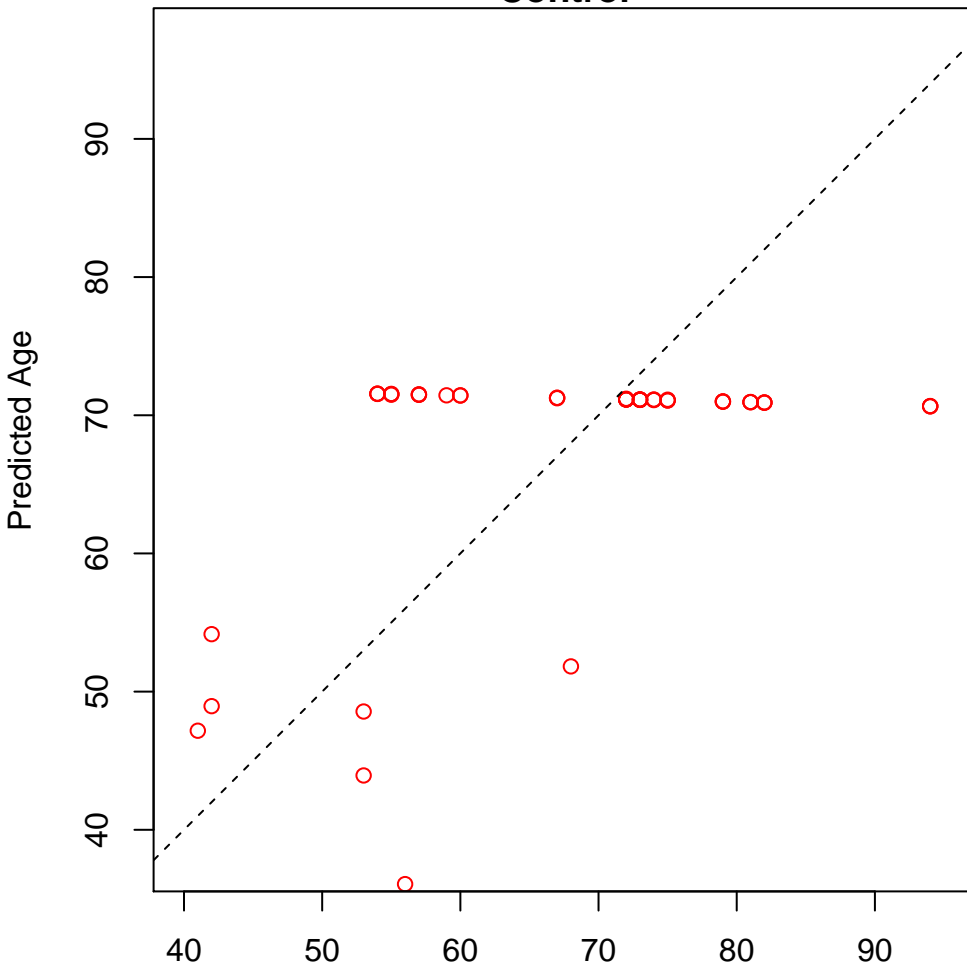
Test



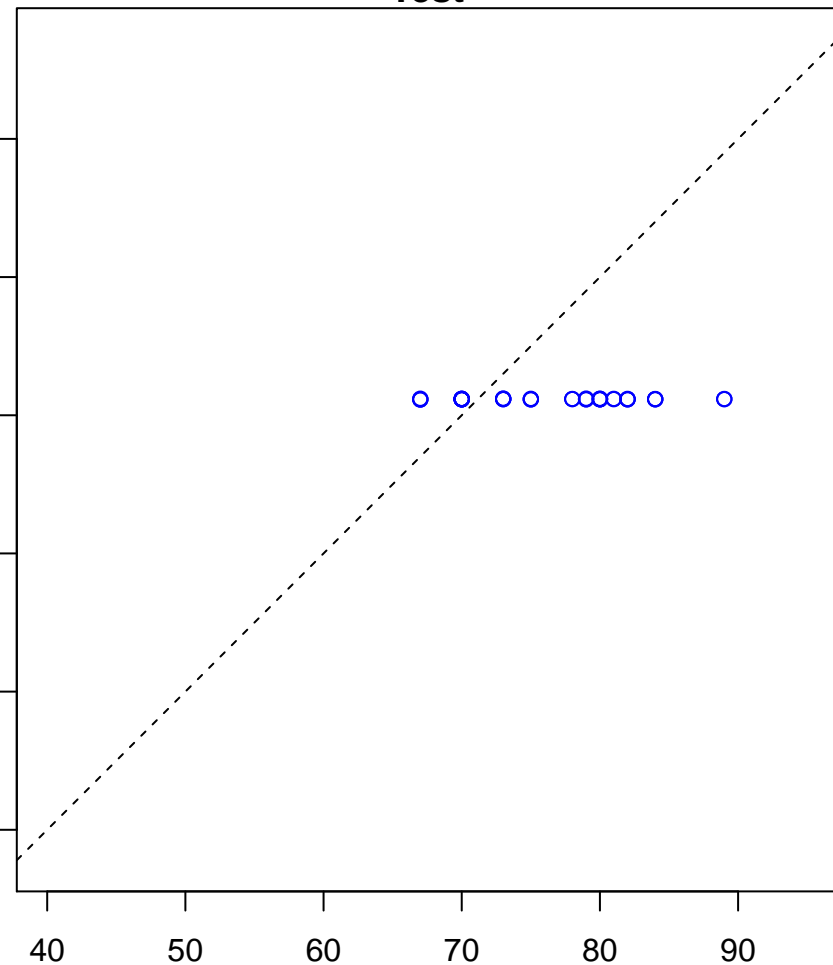
Actual Age

cellular response to nutrient levels (Score: 0.779162)

Control

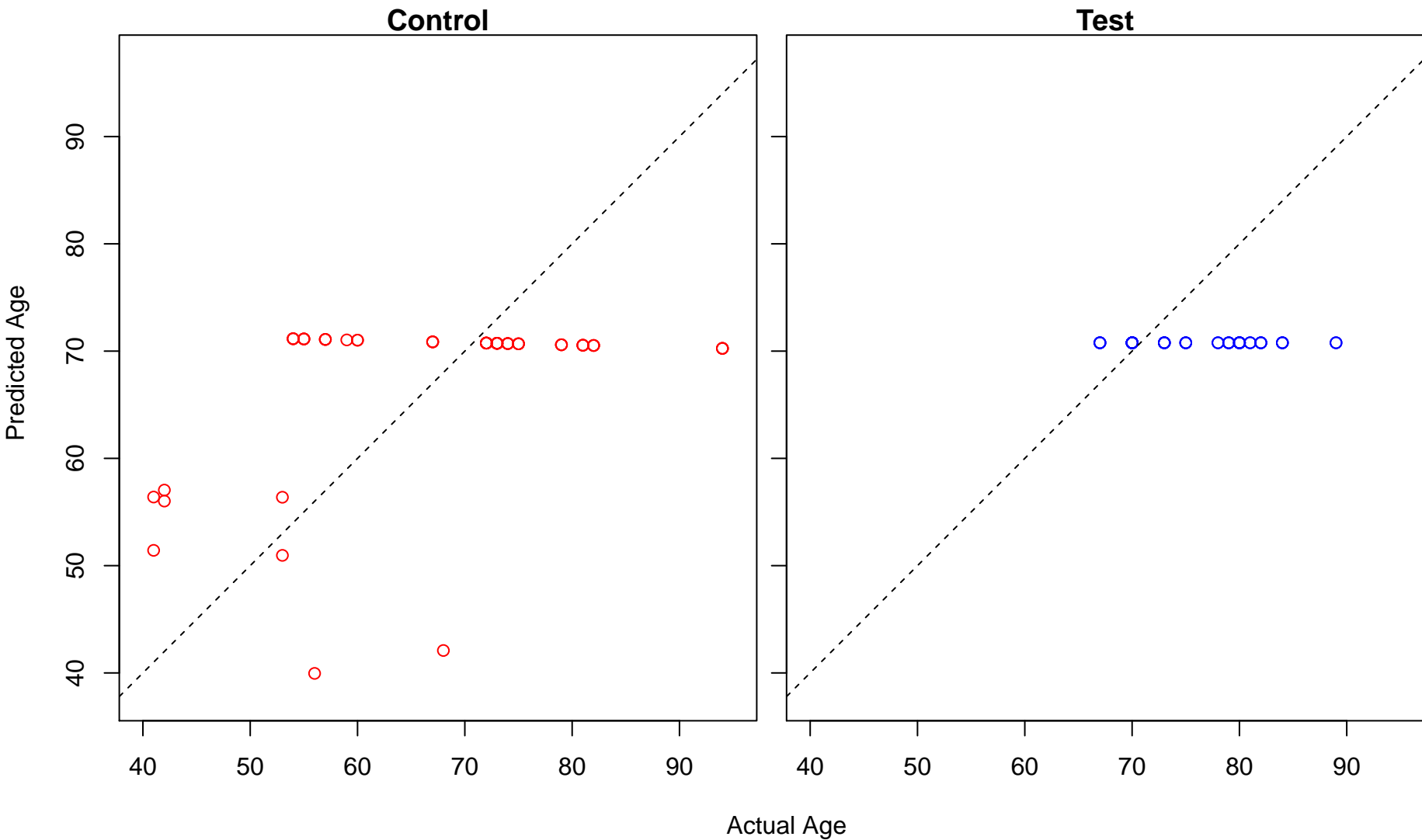


Test

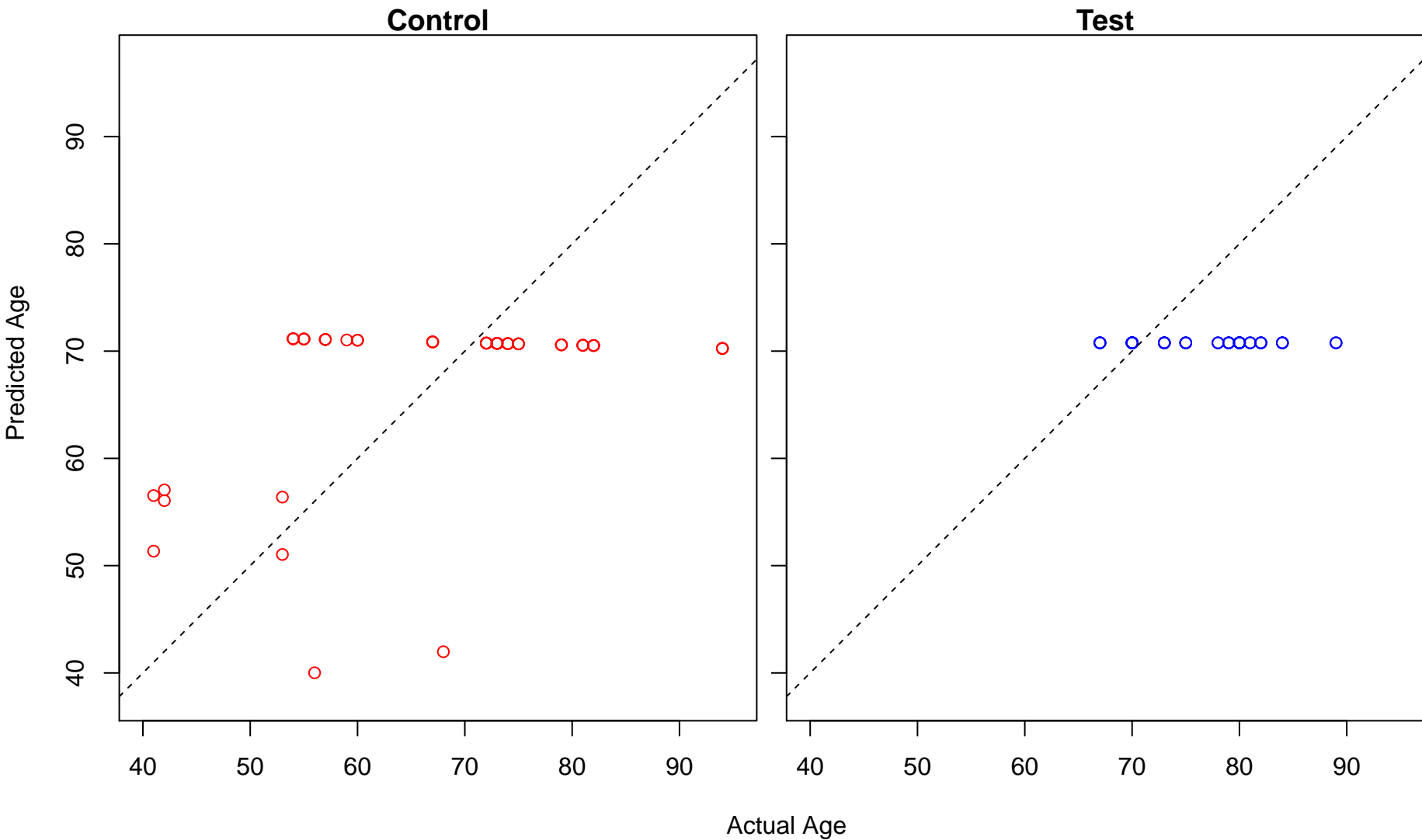


Actual Age

positive regulation of cell morphogenesis involved in differentiation (Score: 0.779118)

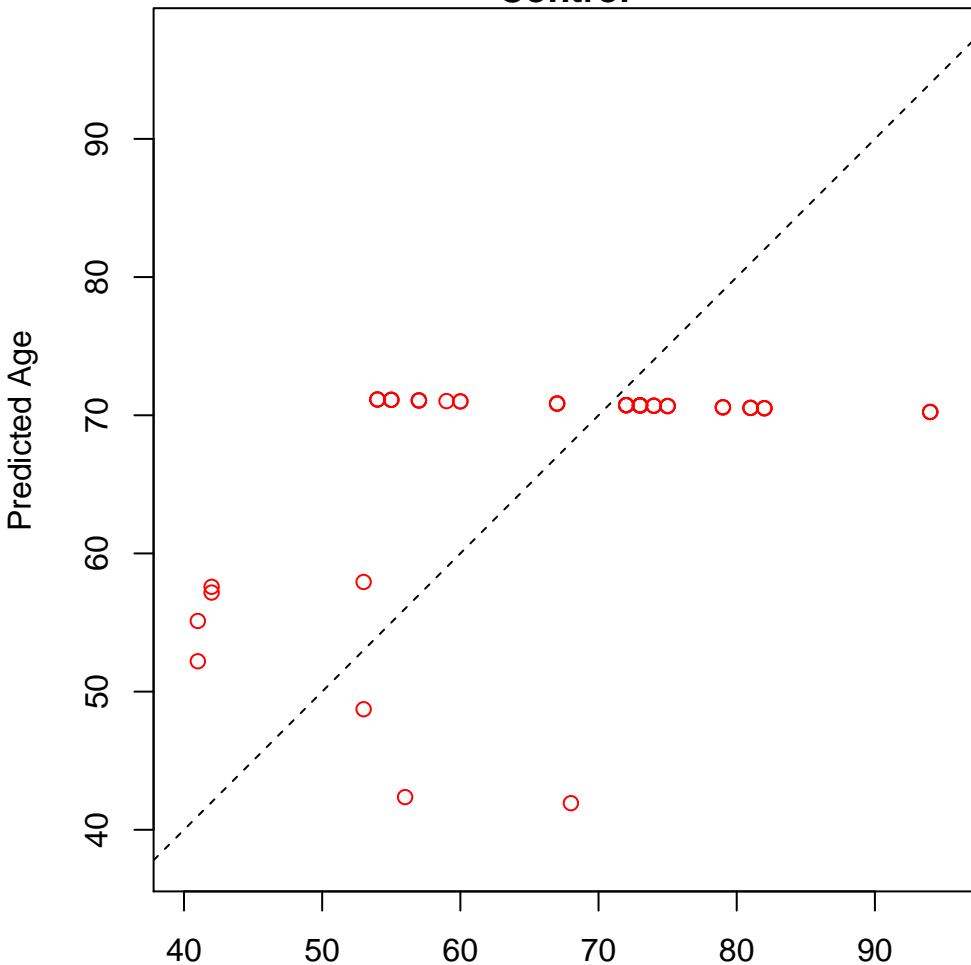


regulation of lipase activity (Score: 0.779024)

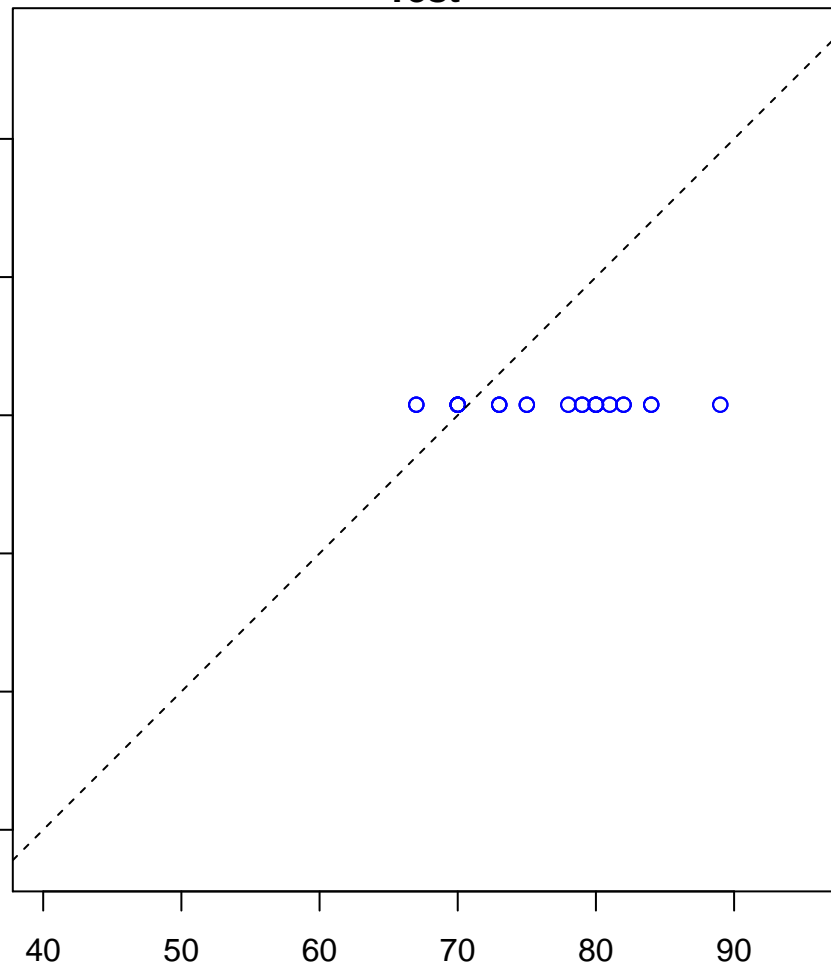


regulation of endothelial cell migration (Score: 0.779015)

Control



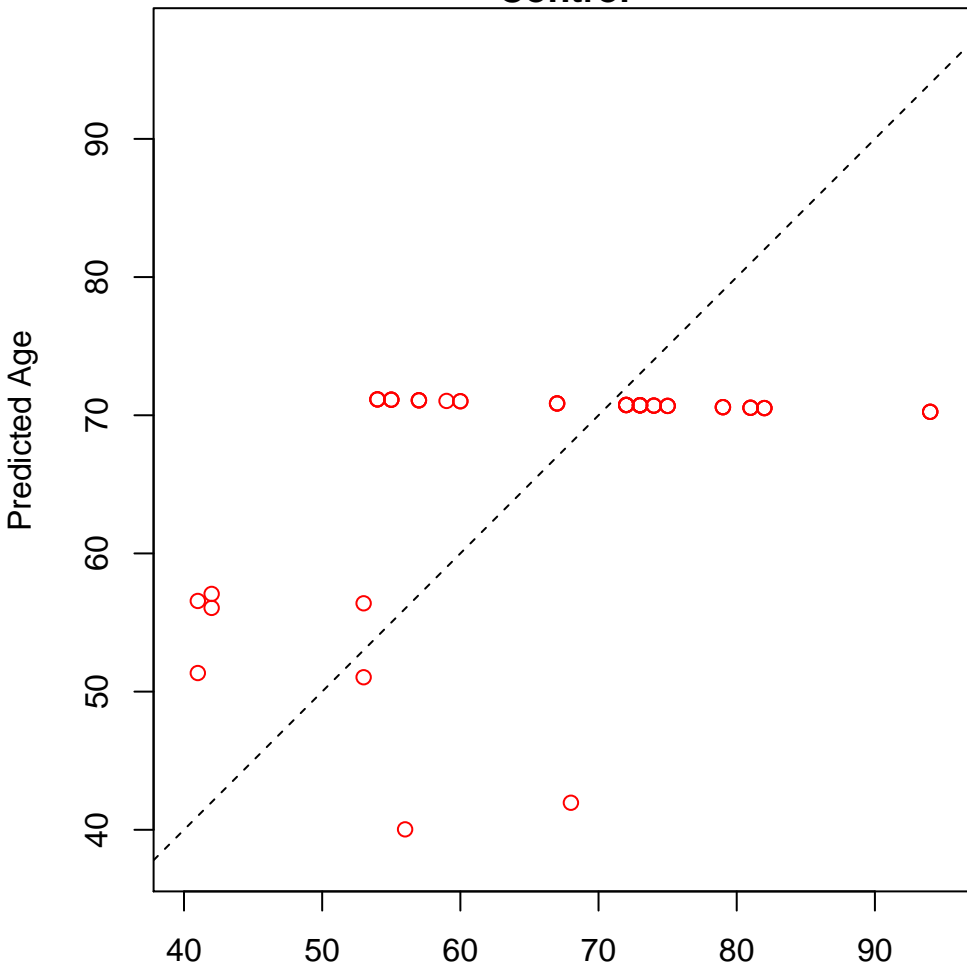
Test



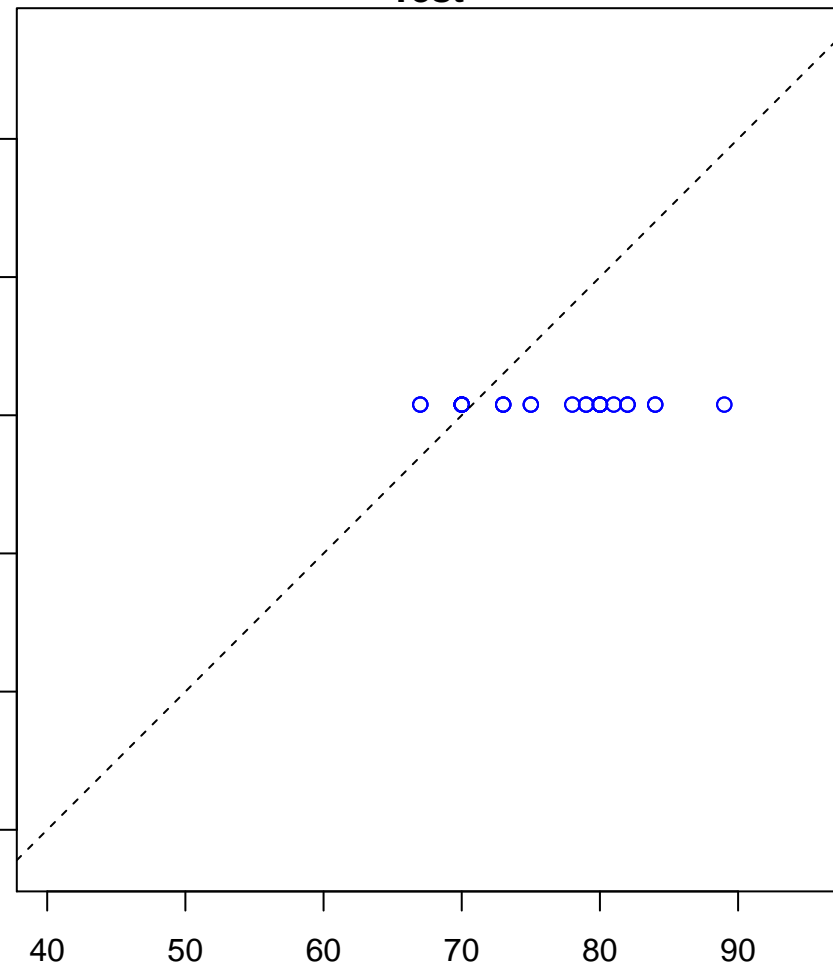
Actual Age

positive regulation of lipase activity (Score: 0.779007)

Control

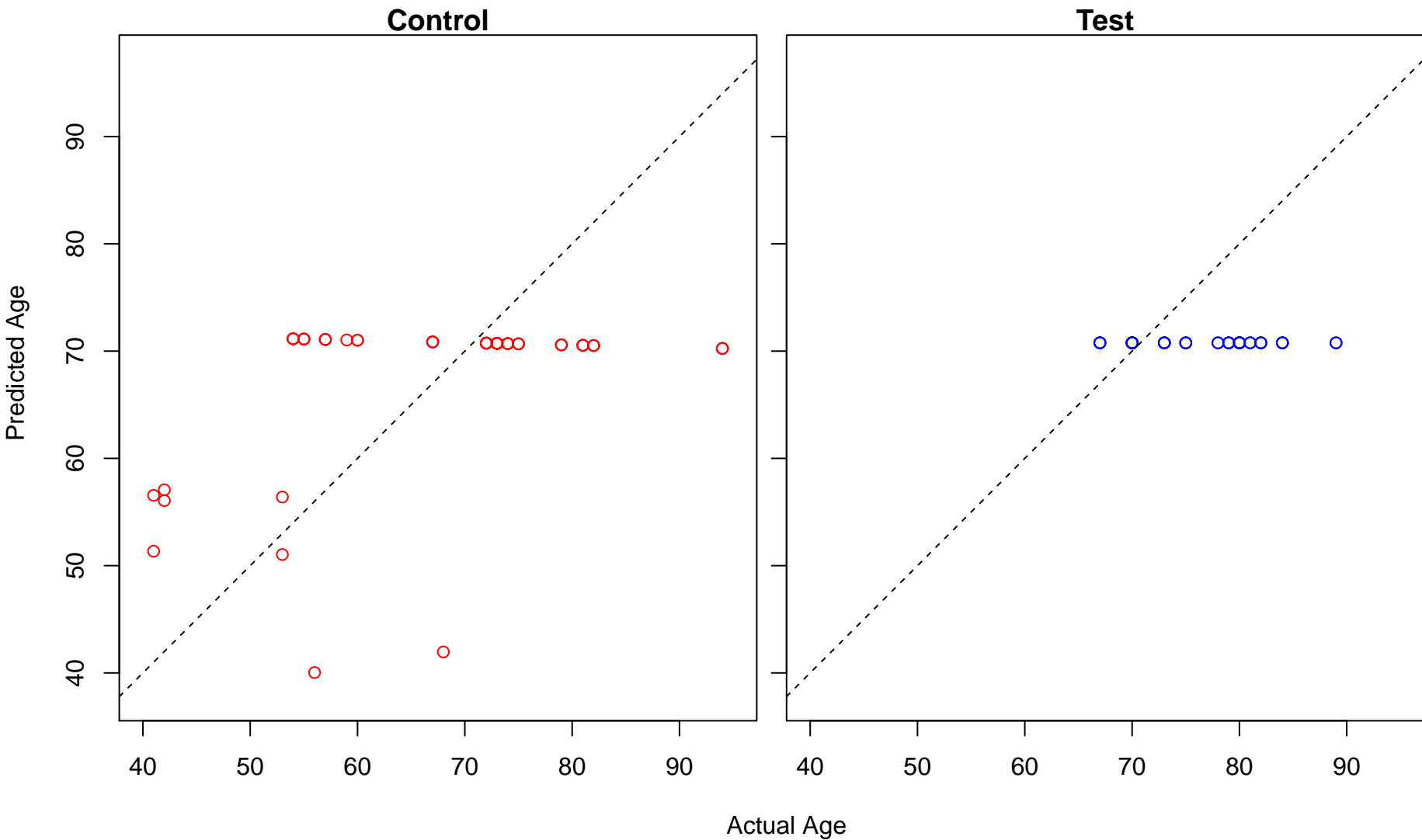


Test

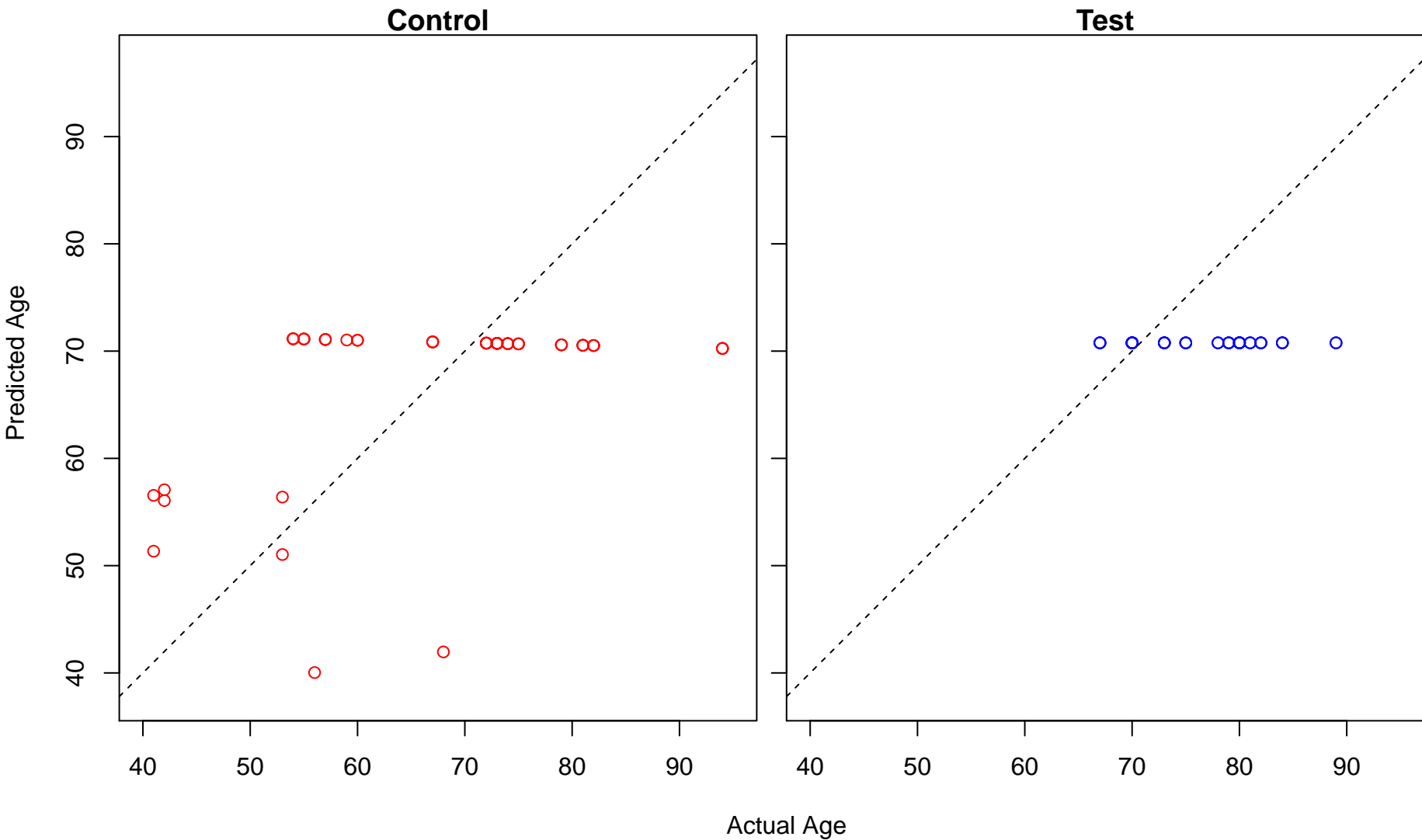


Actual Age

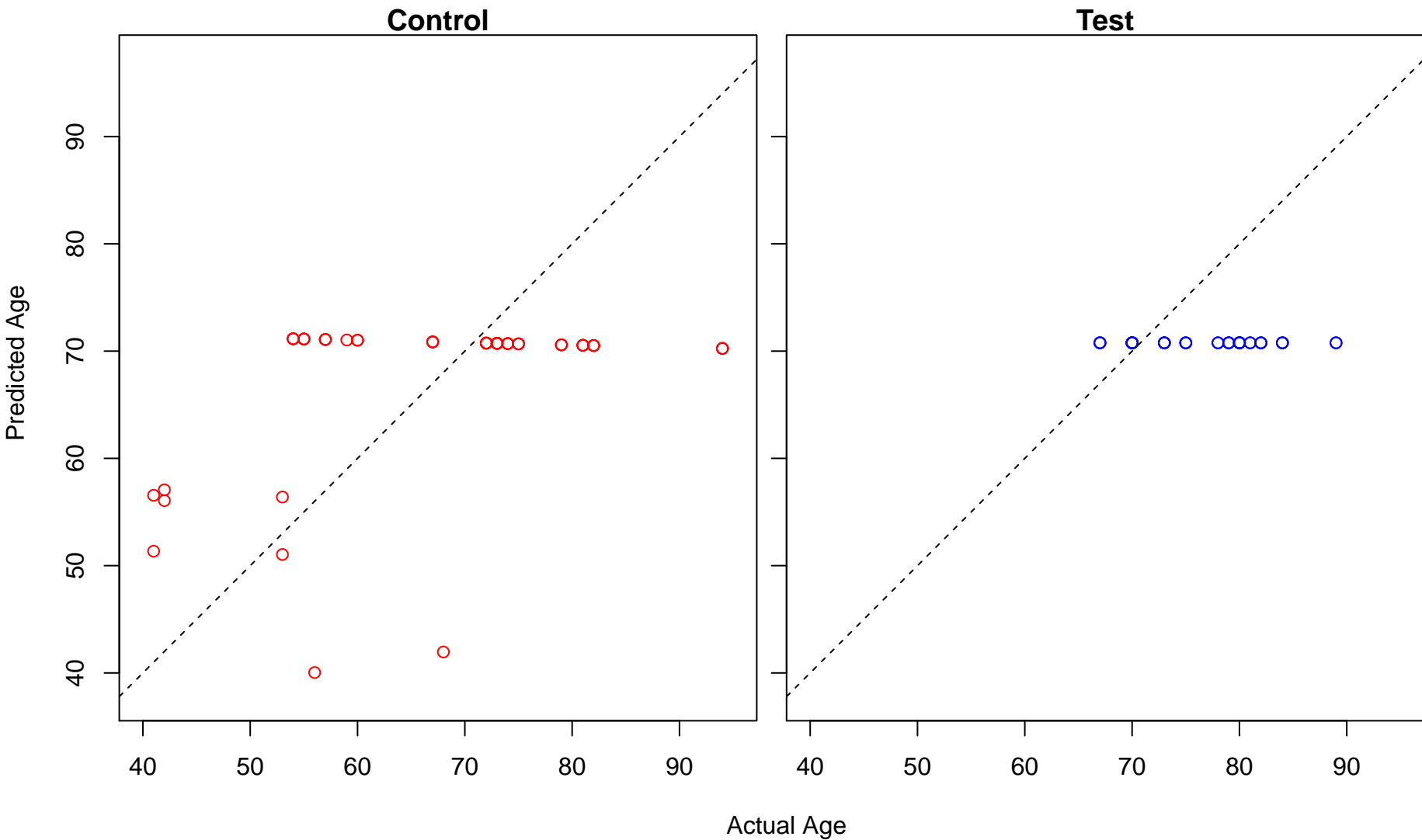
tube morphogenesis (Score: 0.779006)



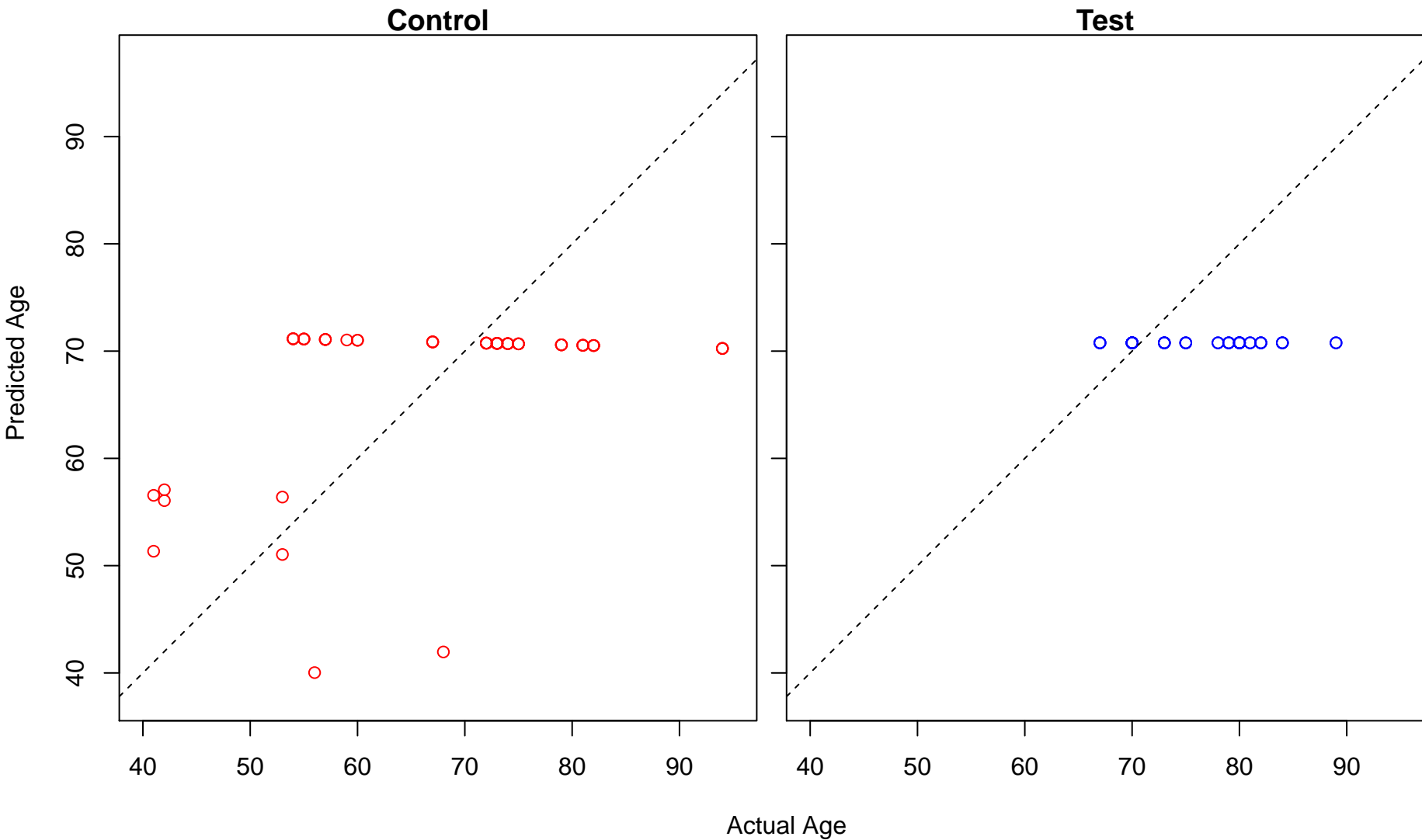
tube development (Score: 0.779006)



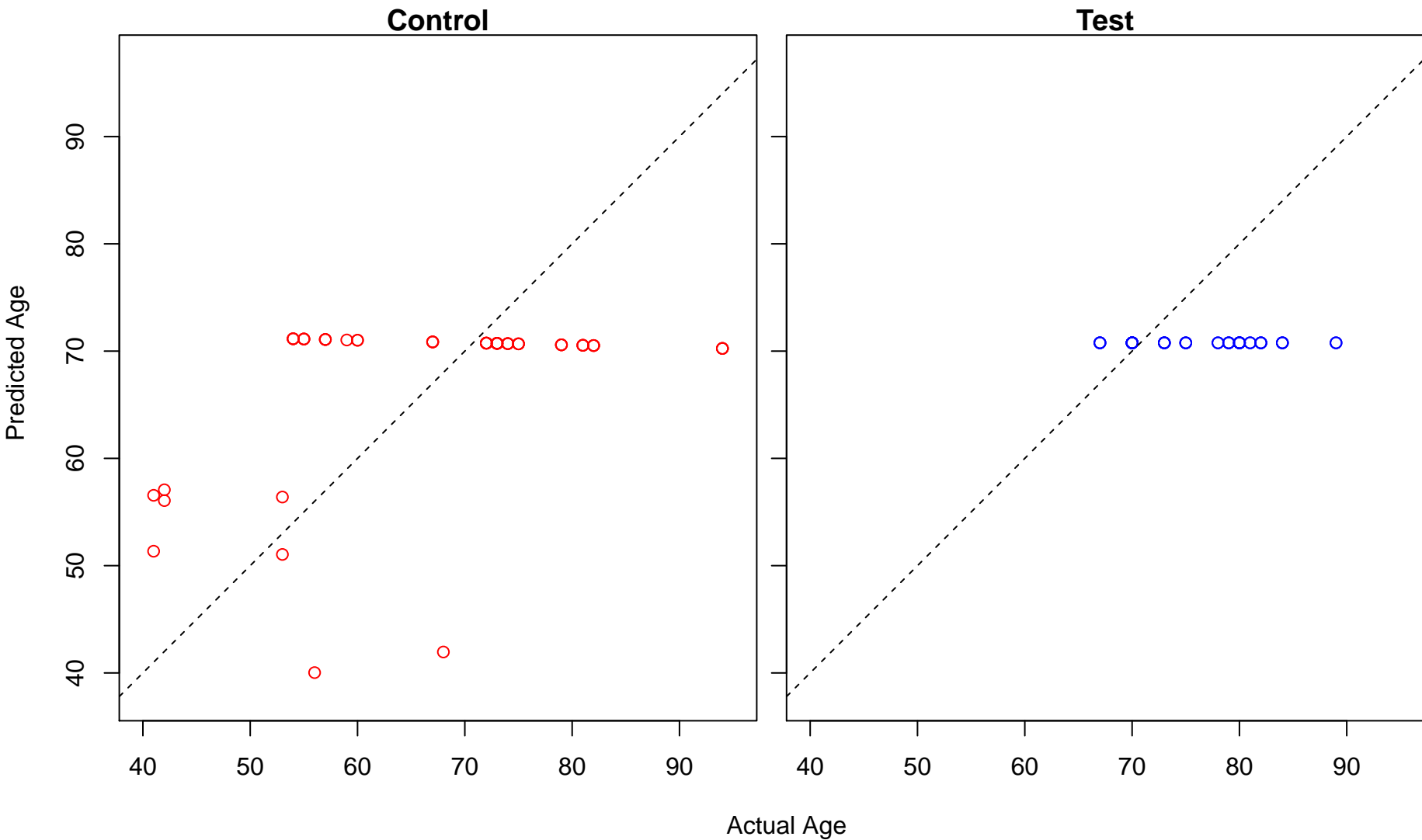
epithelial tube morphogenesis (Score: 0.779002)



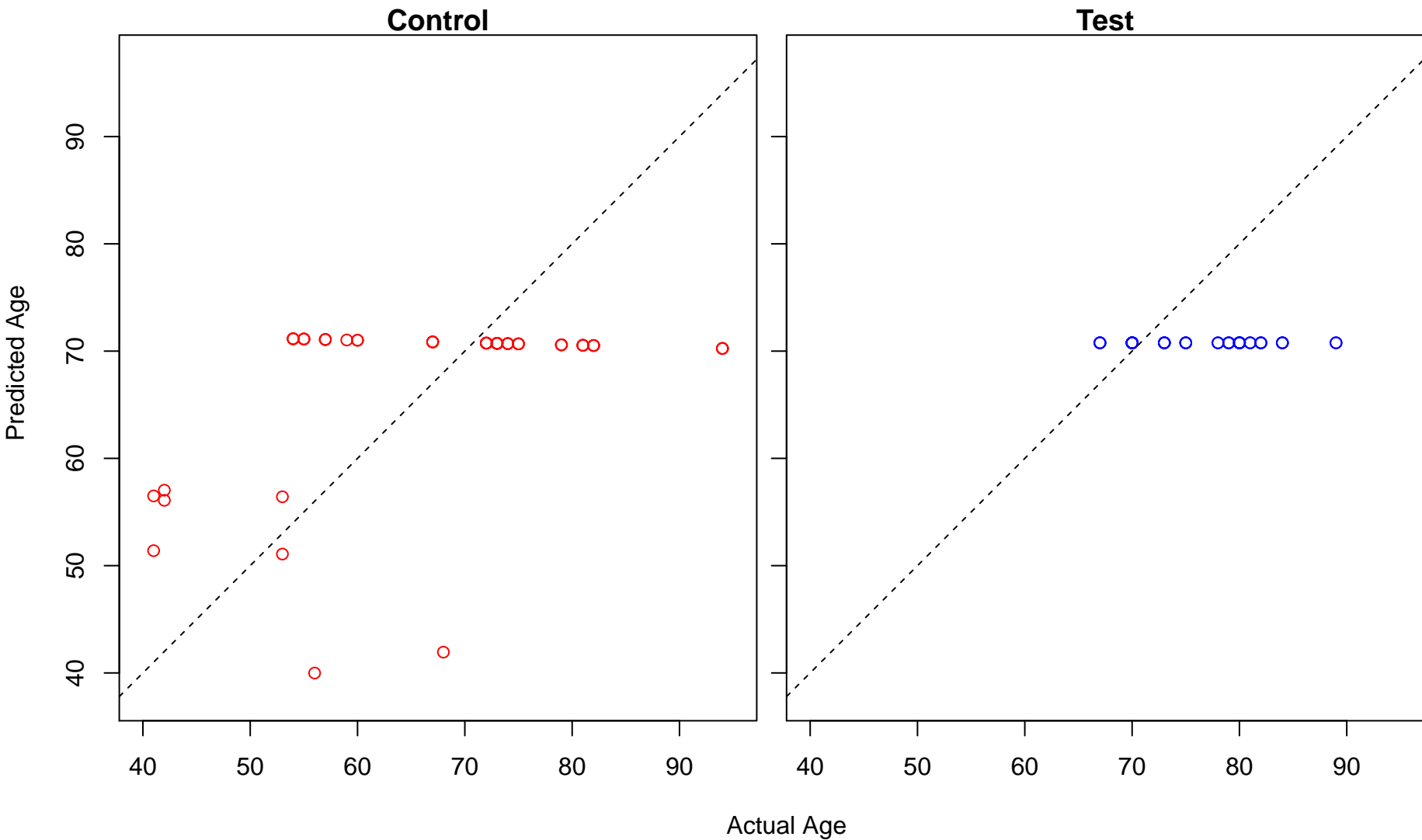
regulation of axonogenesis (Score: 0.779001)



spindle assembly (Score: 0.778997)

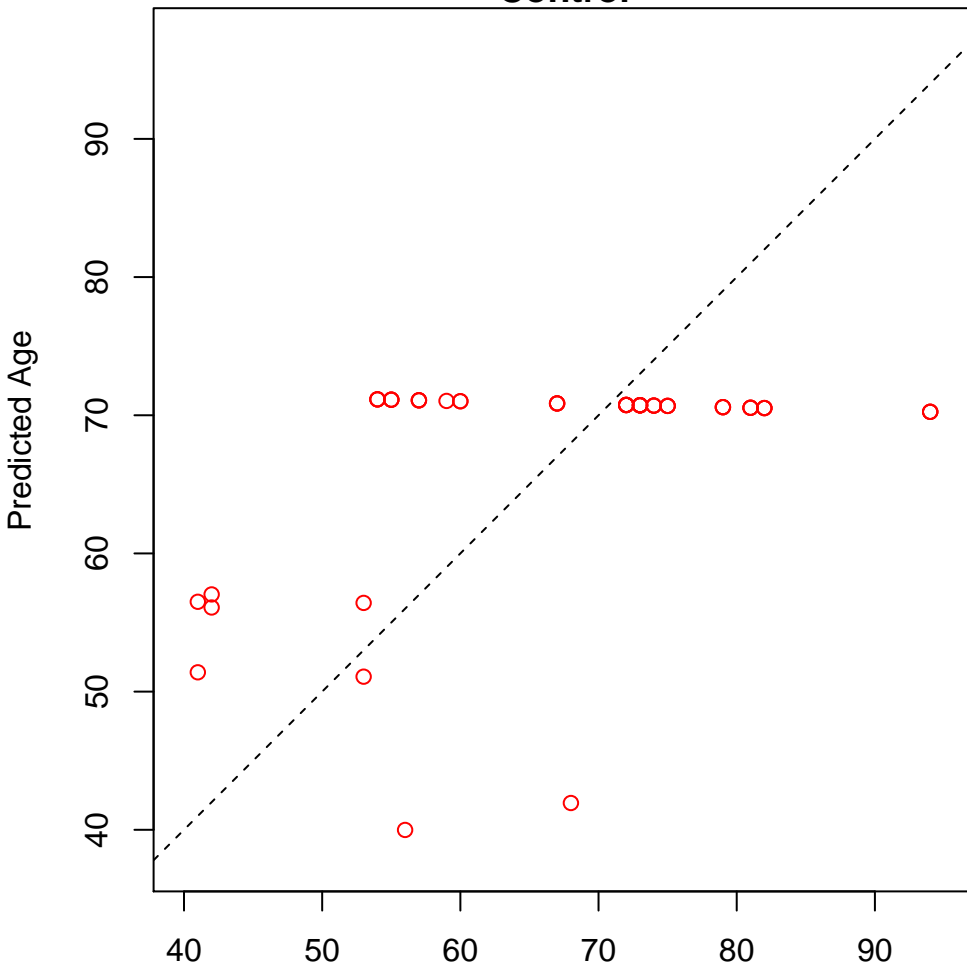


actin filament bundle assembly (Score: 0.778963)

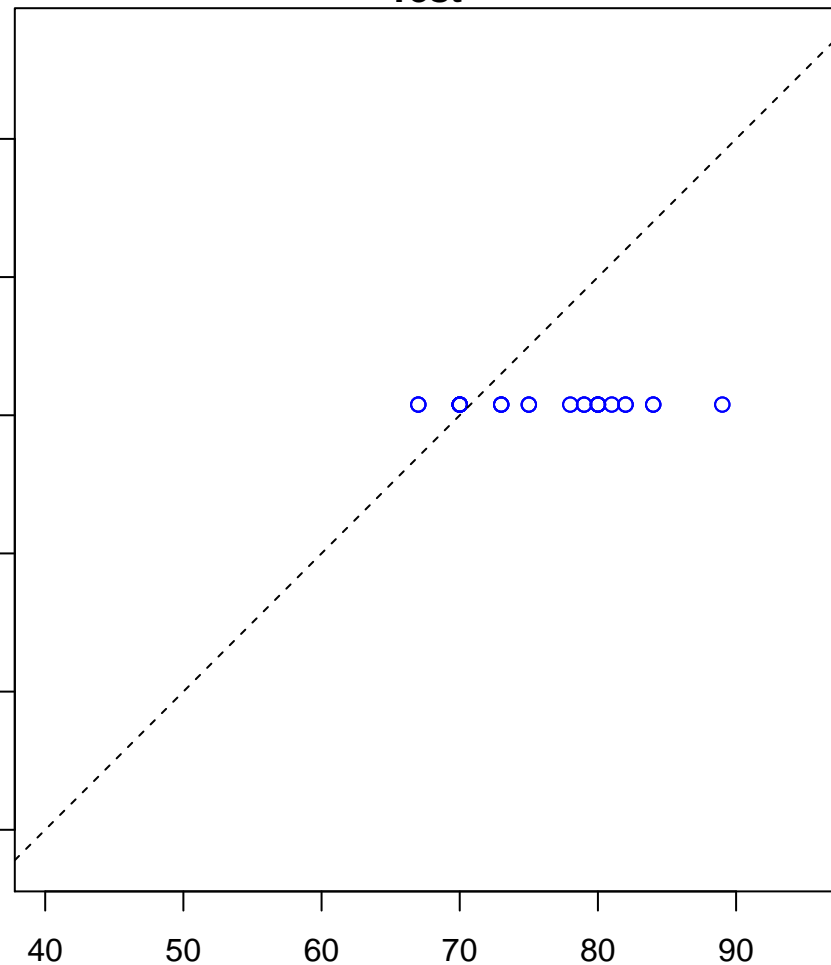


actin filament bundle organization (Score: 0.778963)

Control



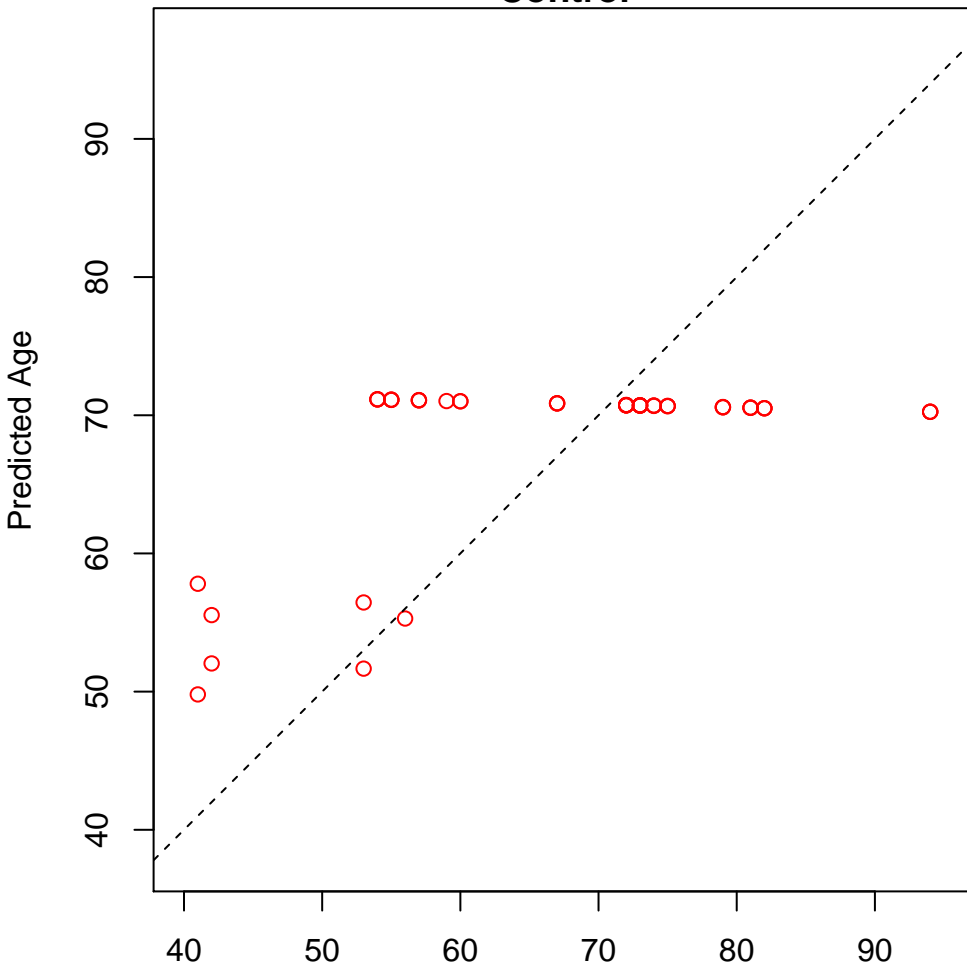
Test



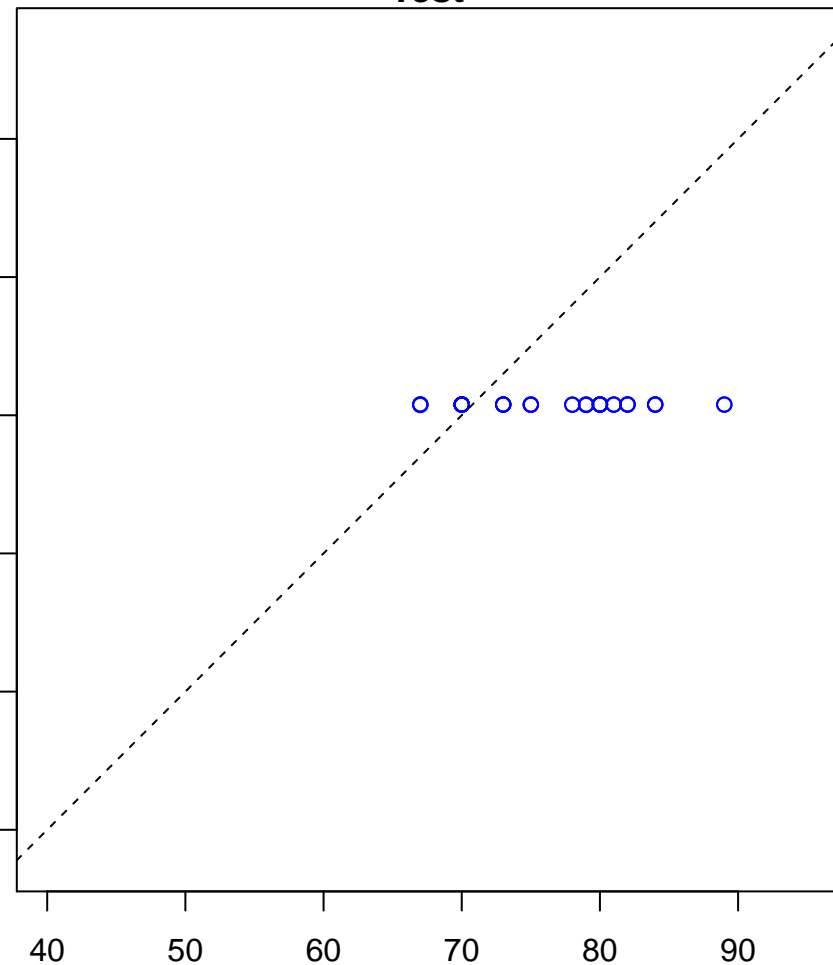
Actual Age

regulation of chromosome separation (Score: 0.778912)

Control

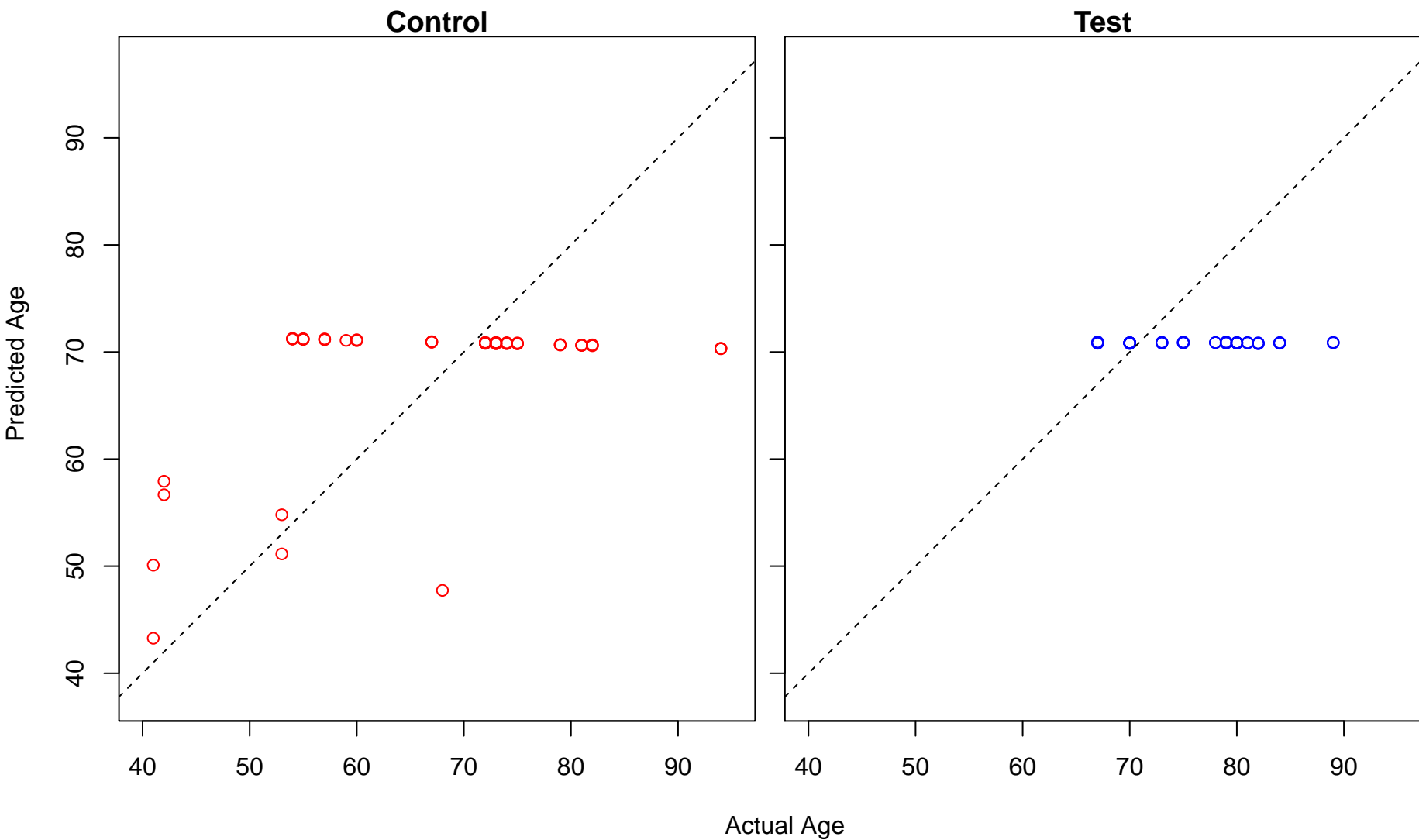


Test

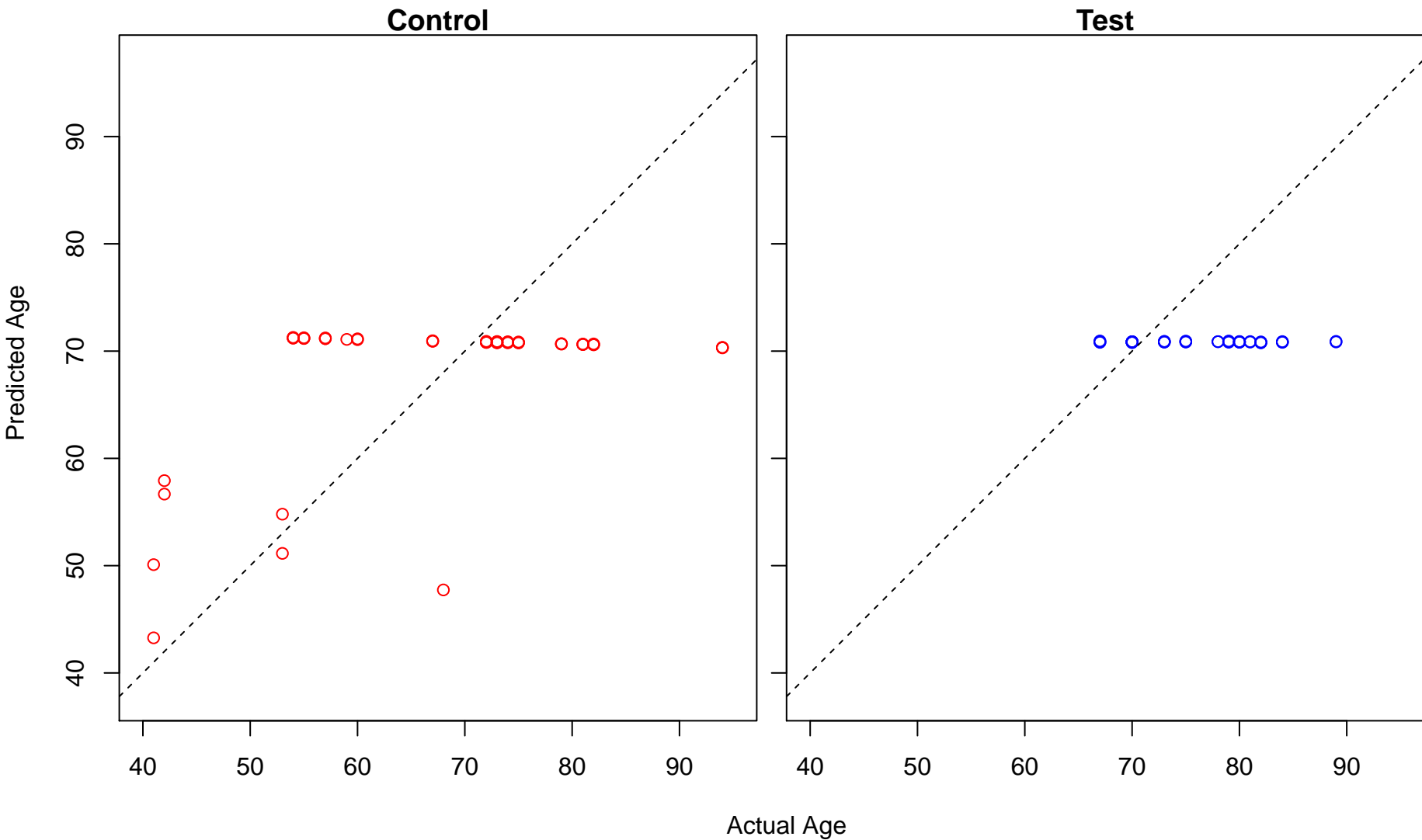


Actual Age

cell-cell junction assembly (Score: 0.777781)

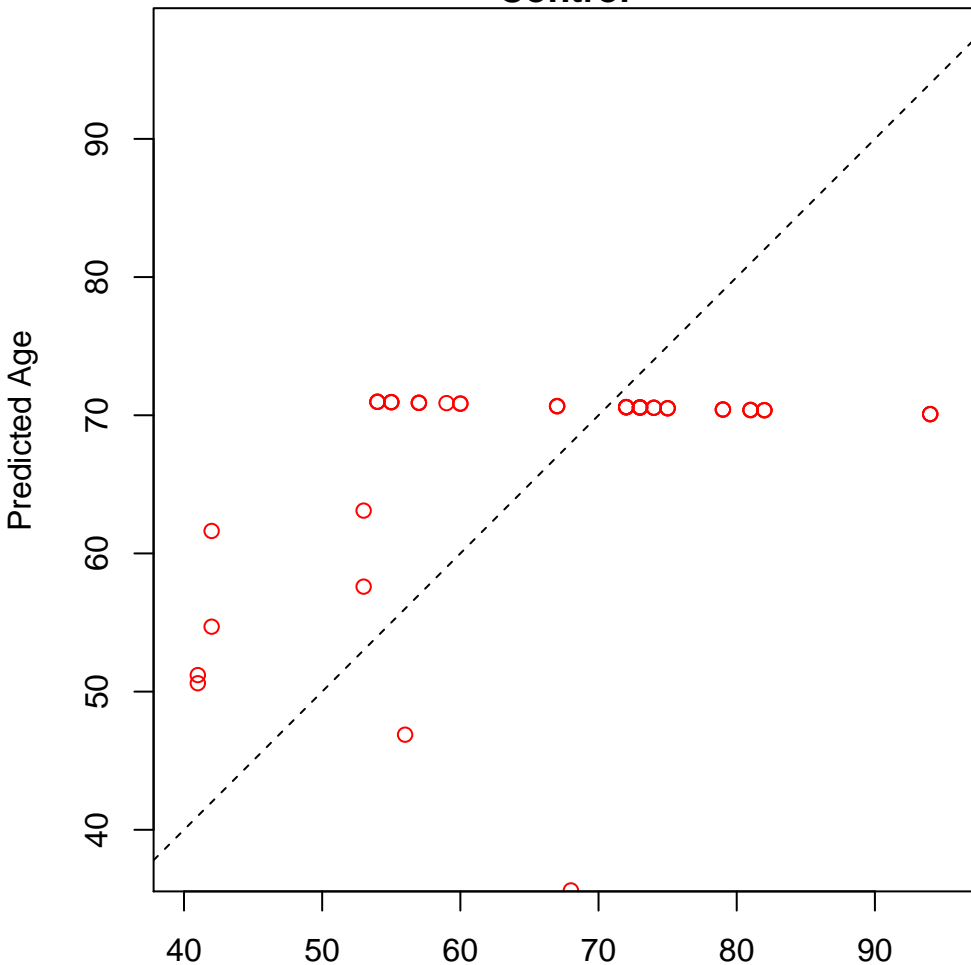


apical junction assembly (Score: 0.777781)

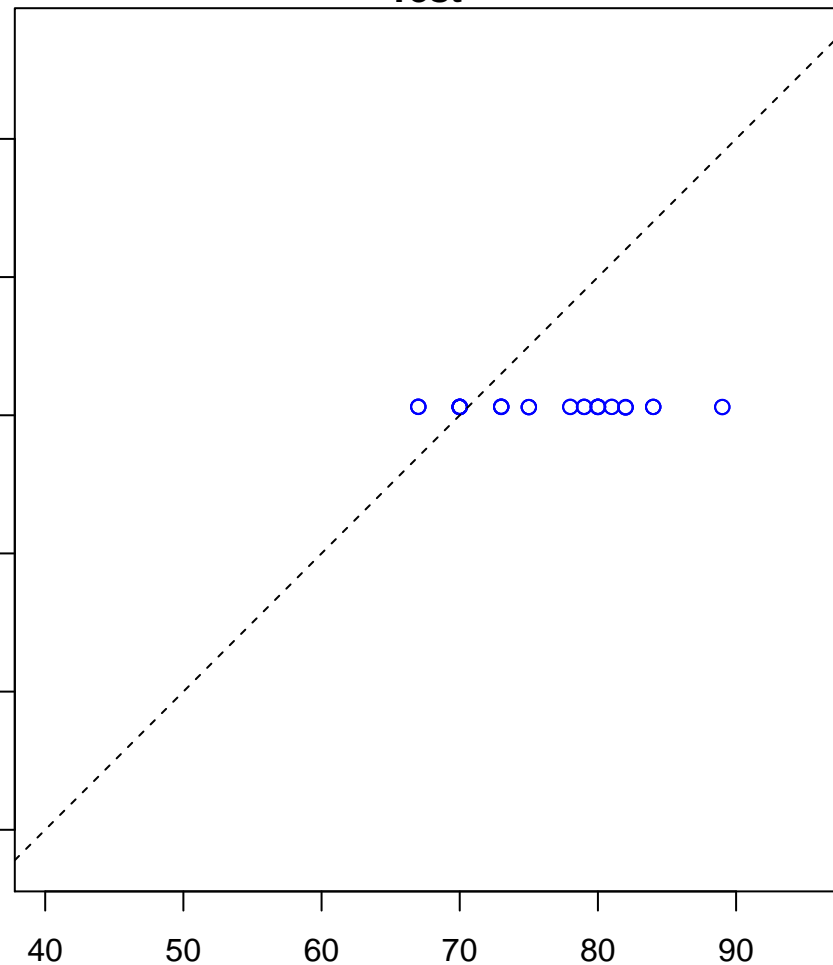


positive regulation of ATPase activity (Score: 0.777618)

Control

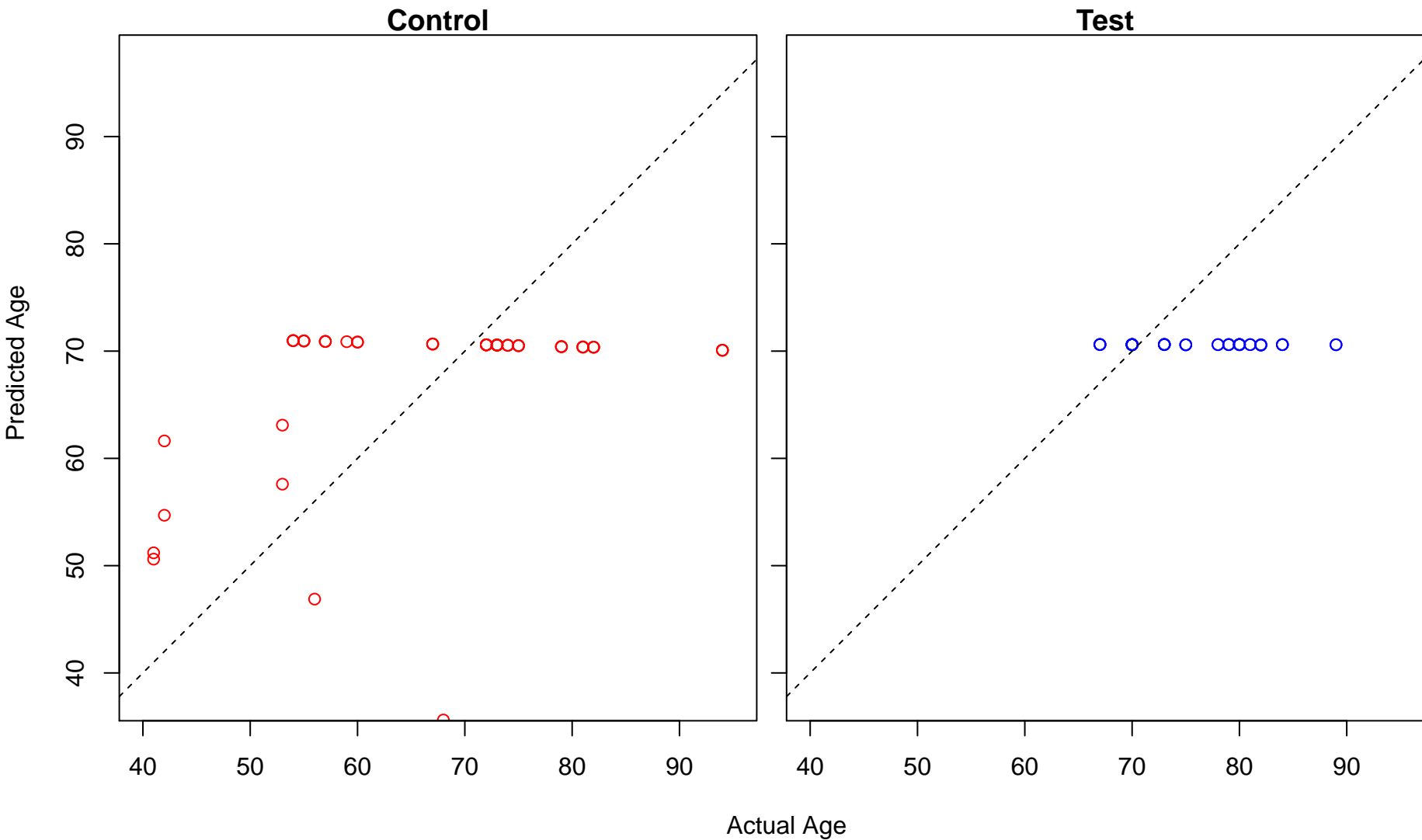


Test

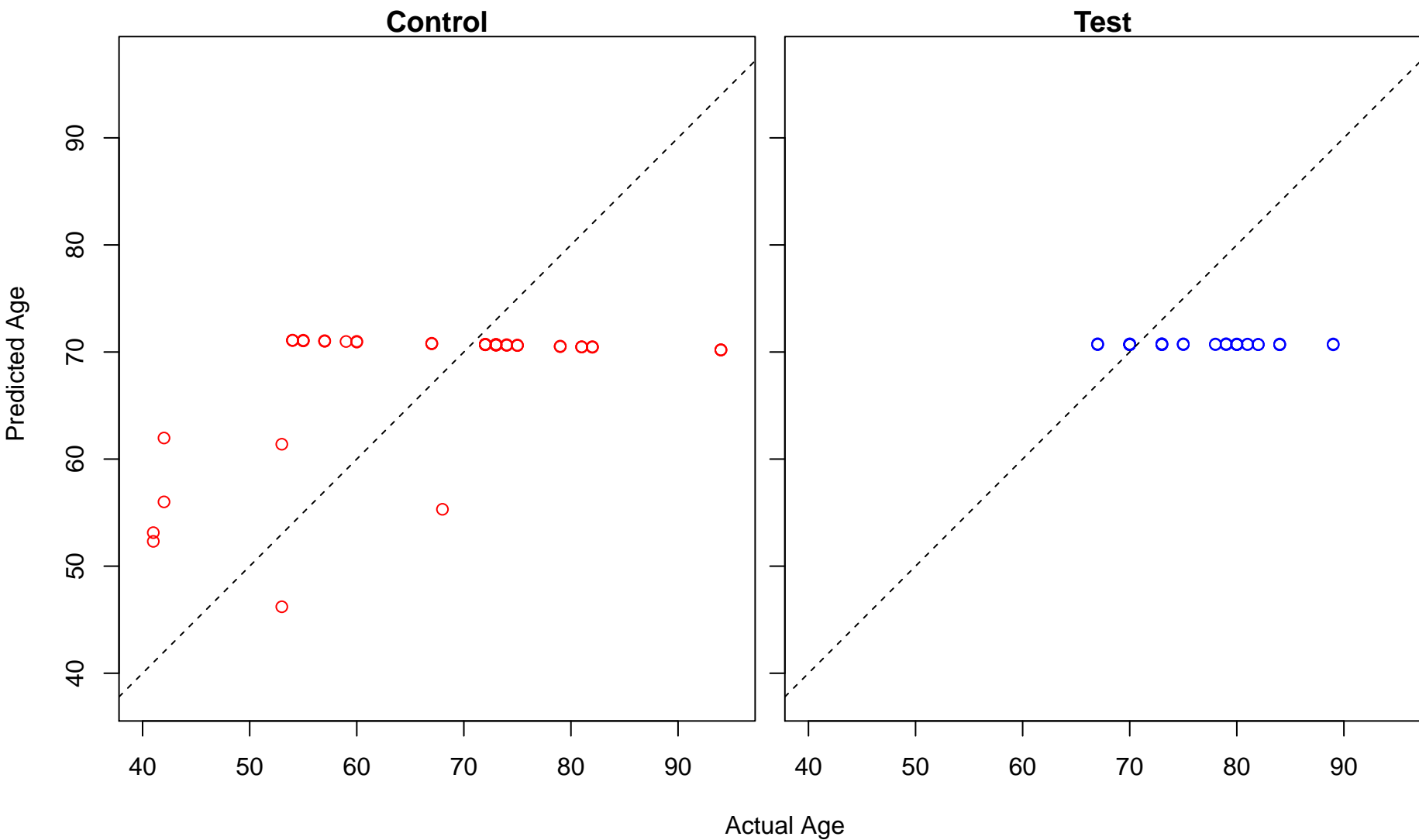


Actual Age

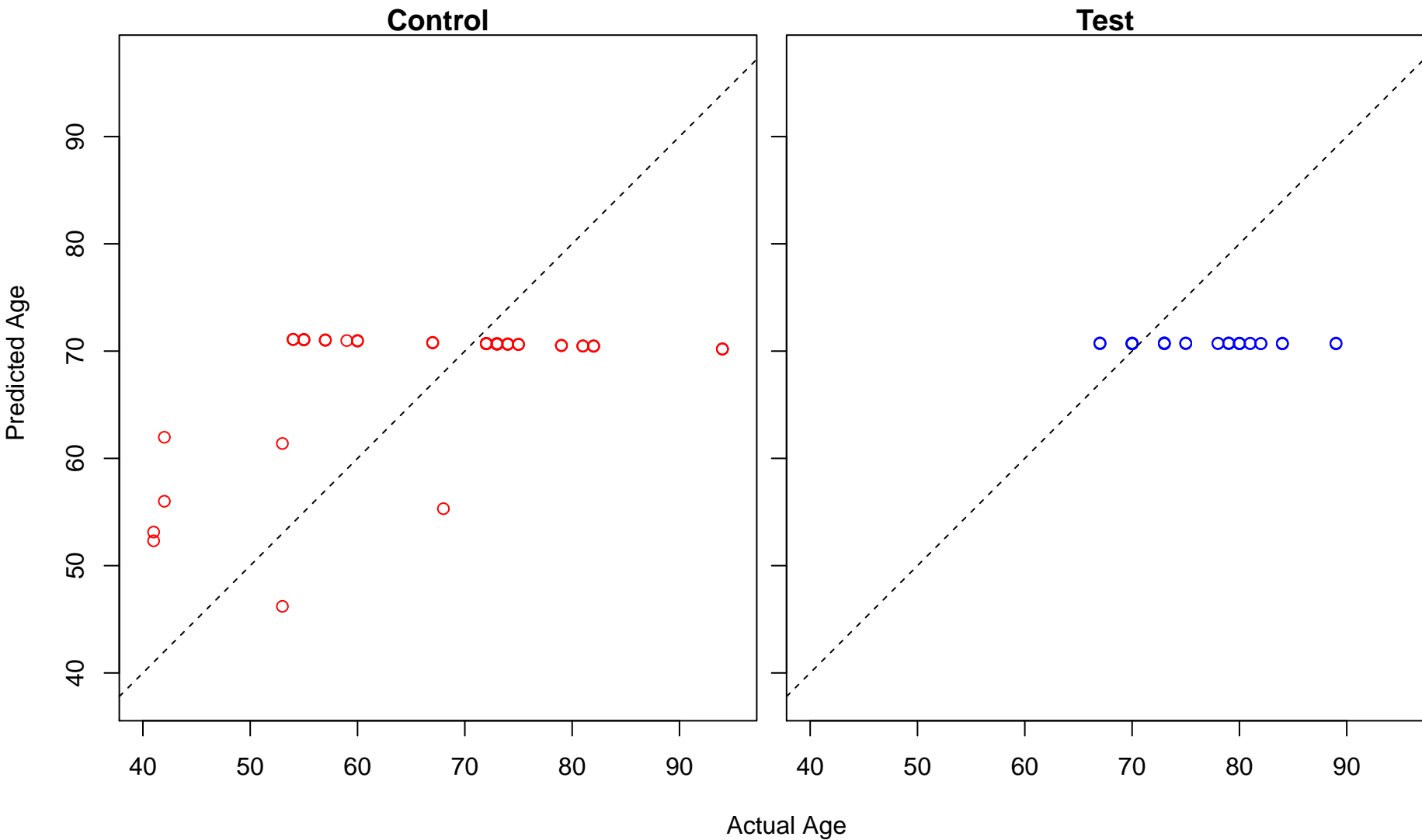
regulation of ATPase activity (Score: 0.777618)



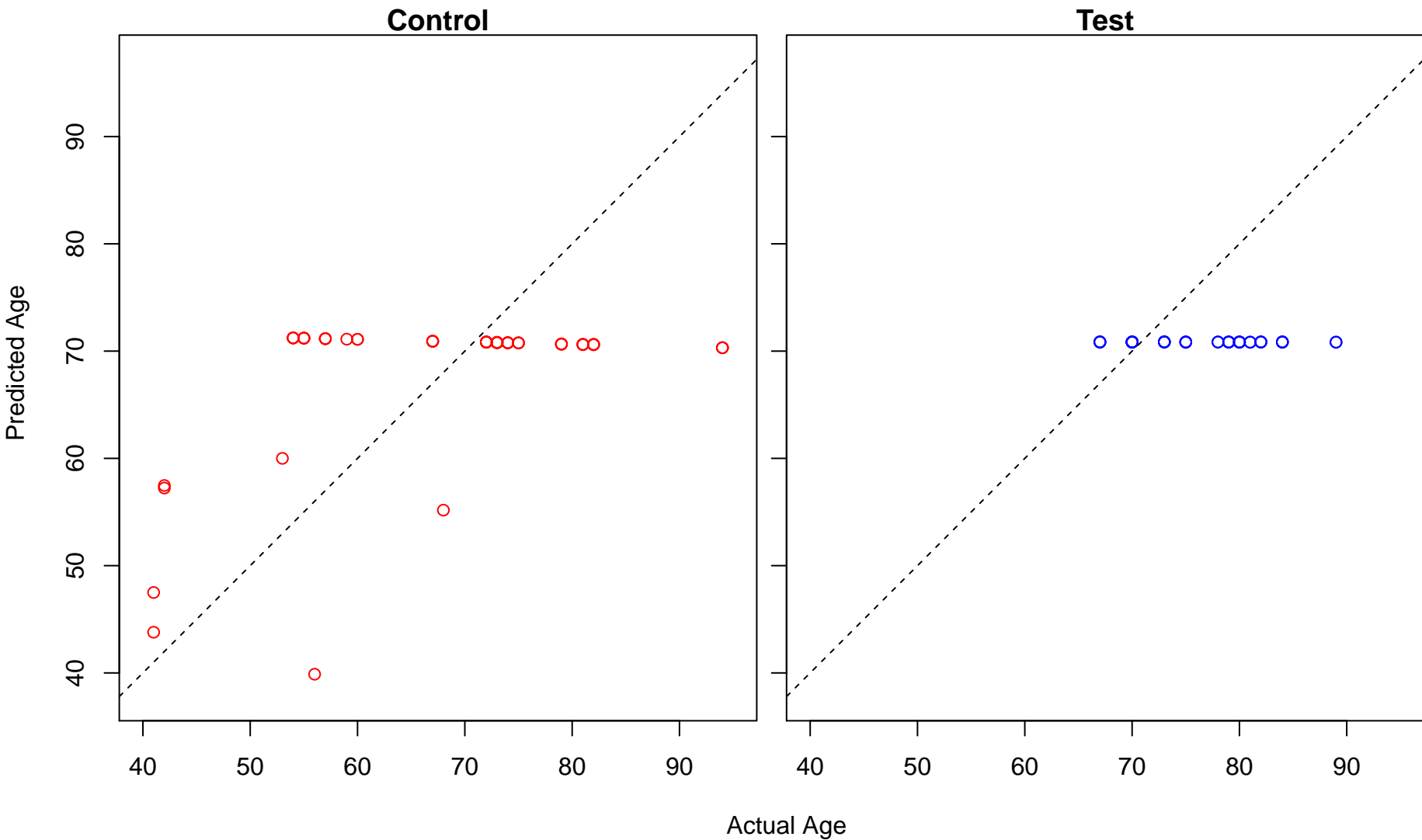
regulation of cell projection assembly (Score: 0.777429)



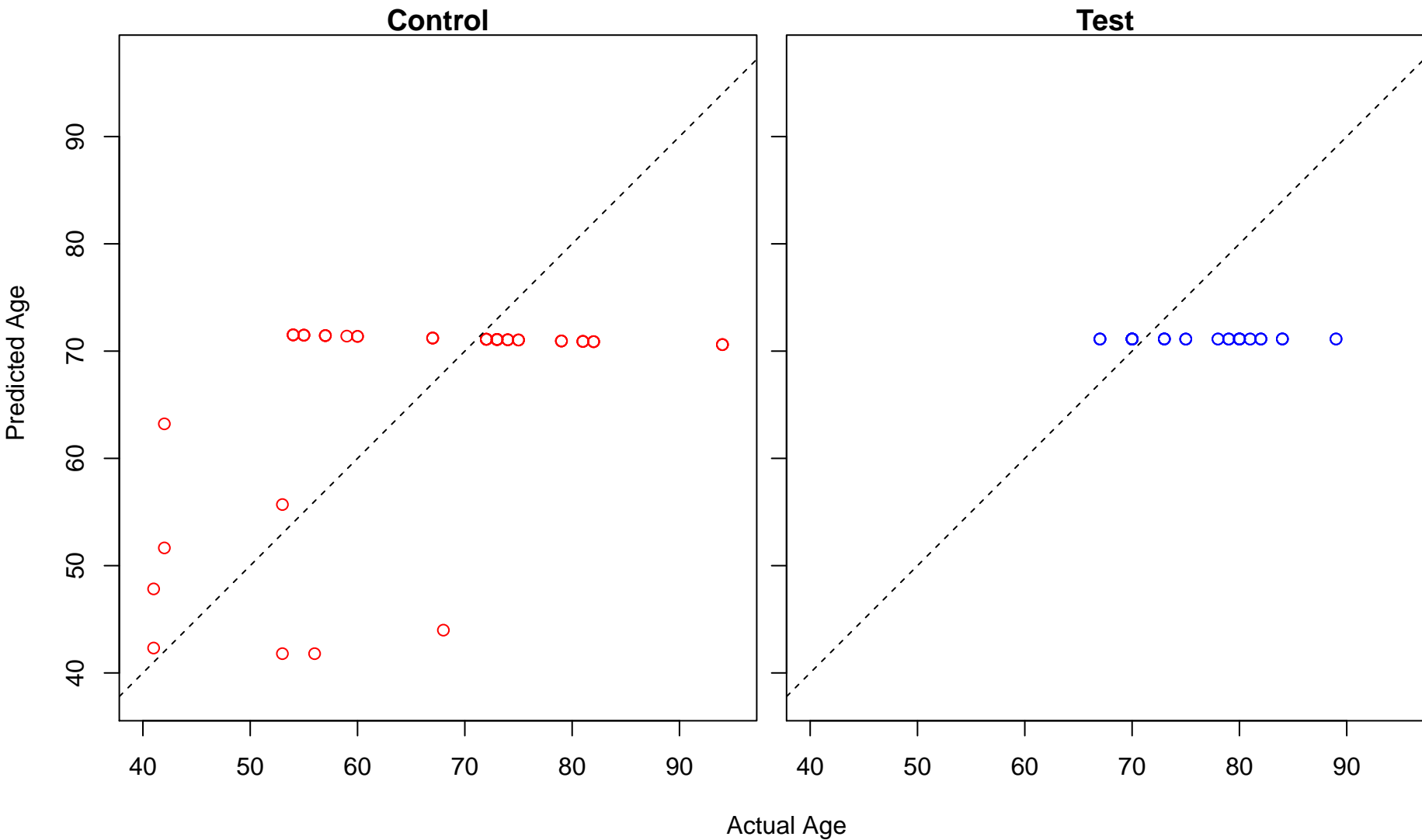
regulation of plasma membrane bounded cell projection assembly (Score: 0.777429)



tissue remodeling (Score: 0.777070)

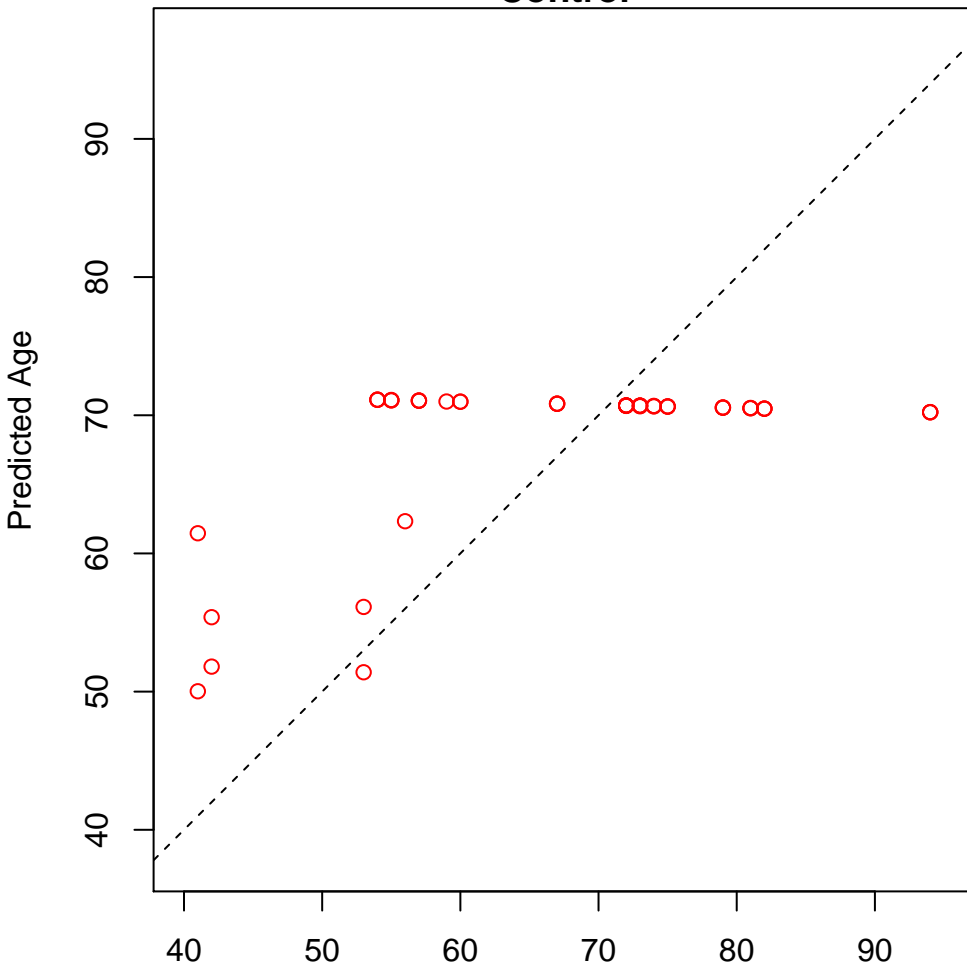


negative regulation of homeostatic process (Score: 0.776754)

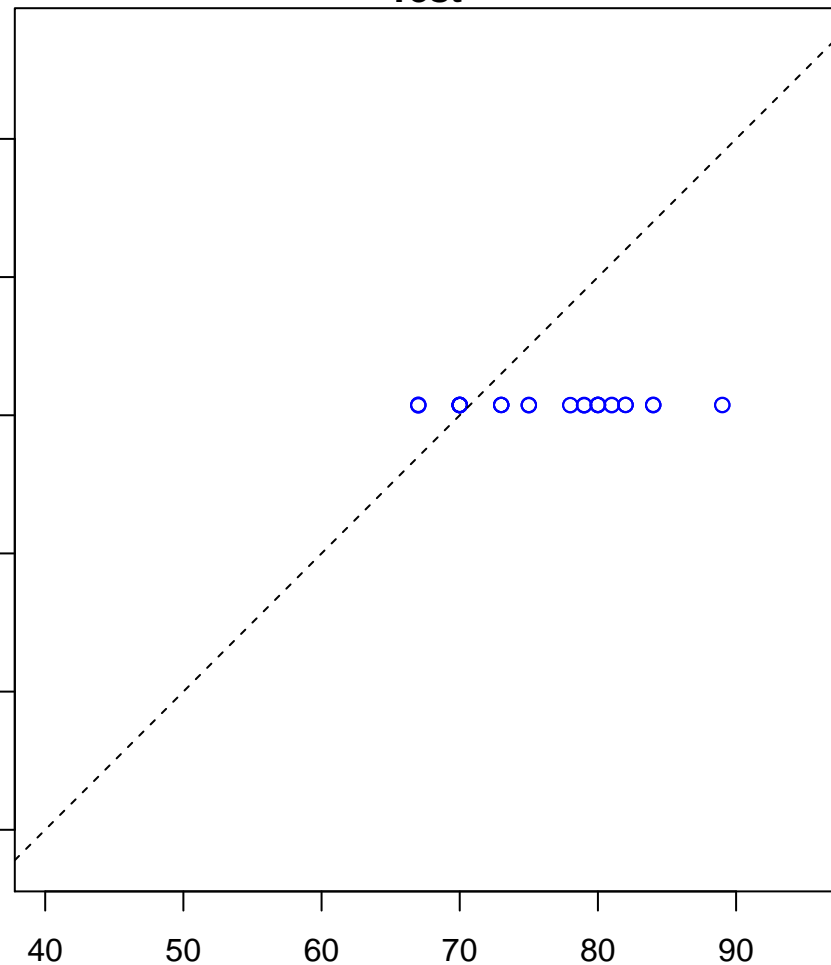


protein localization to chromosome (Score: 0.776711)

Control

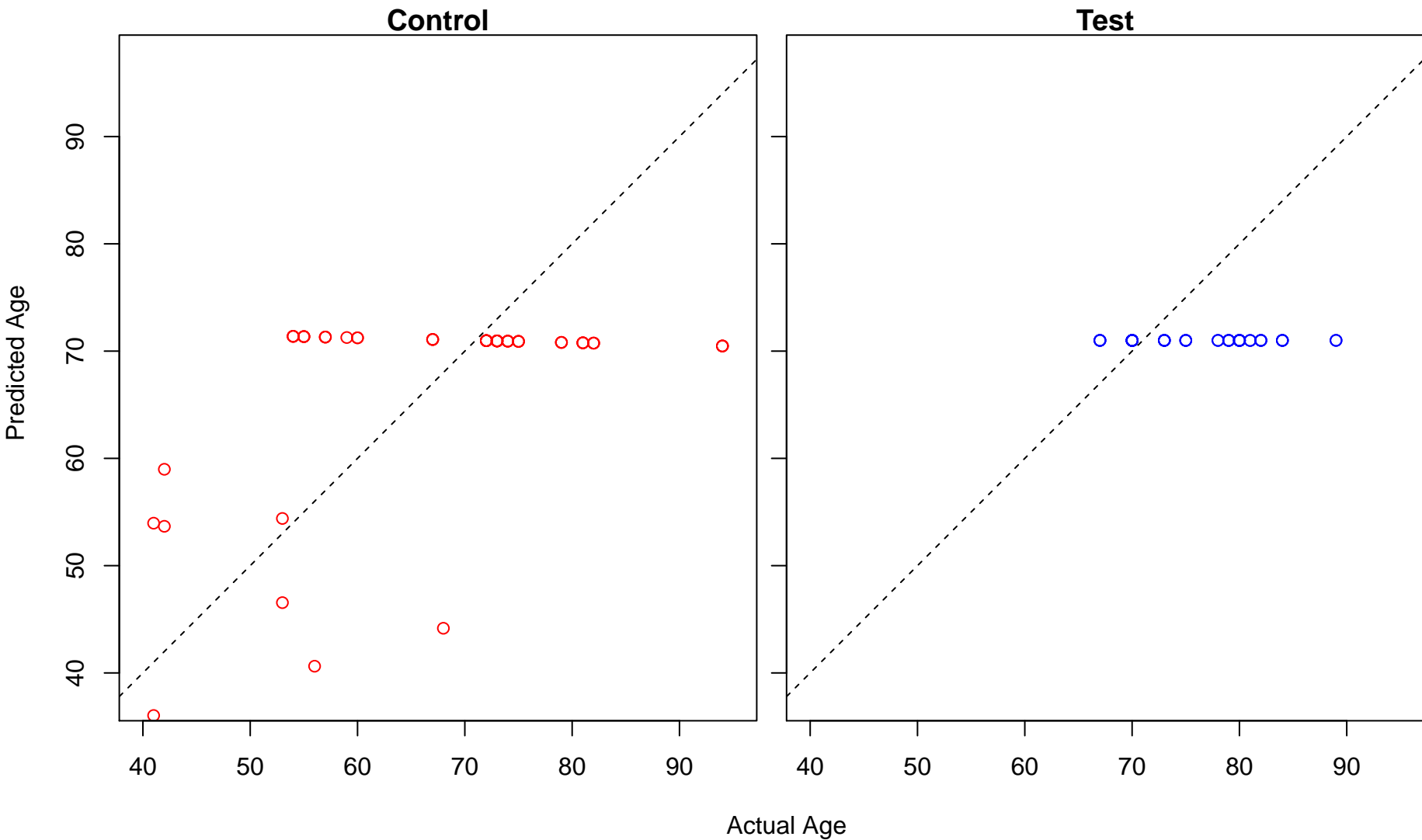


Test



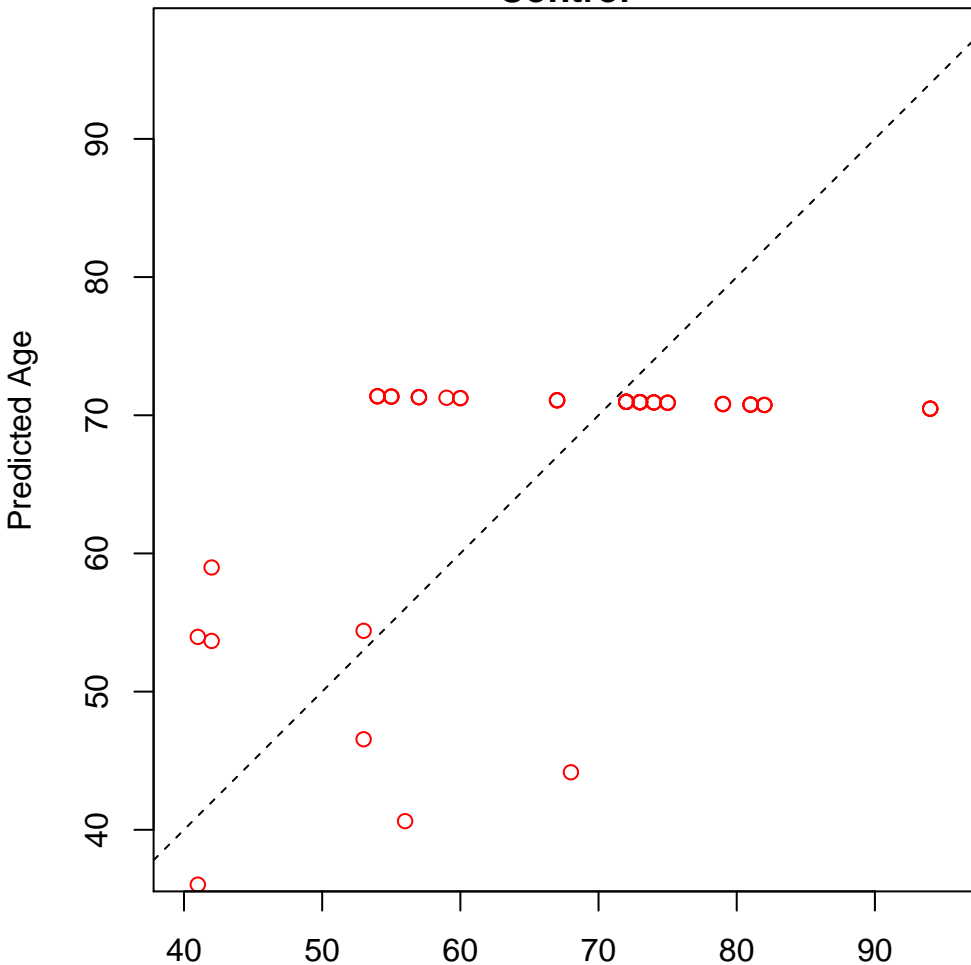
Actual Age

regulation of heart rate (Score: 0.776692)

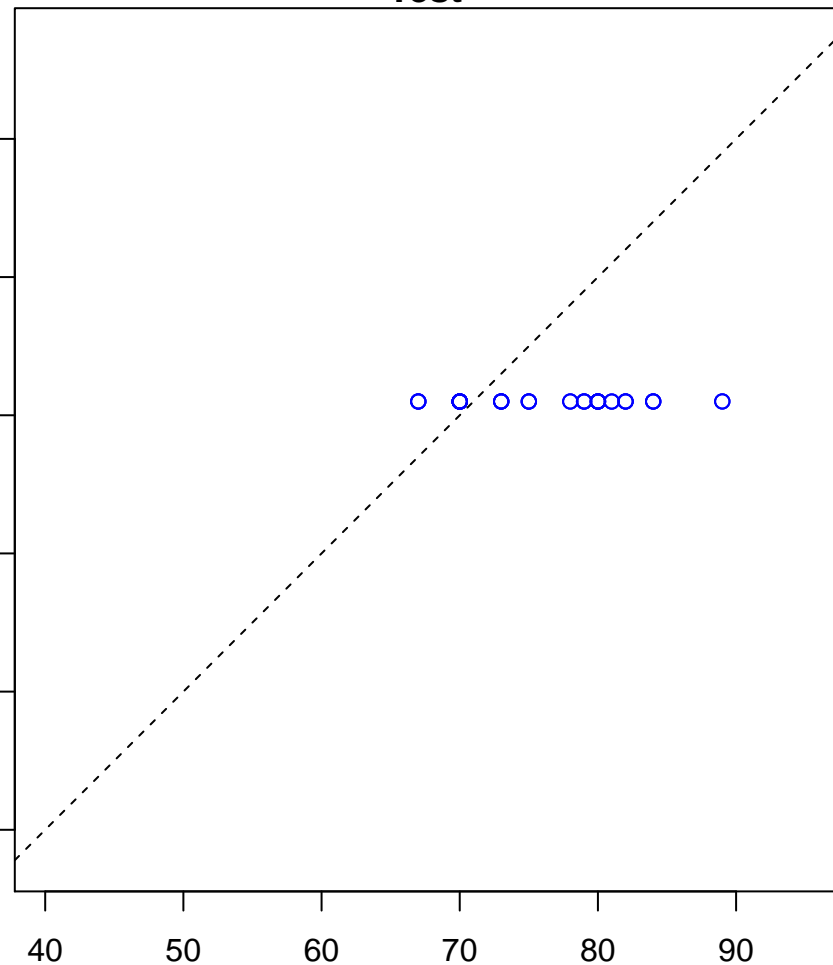


regulation of striated muscle contraction (Score: 0.776692)

Control



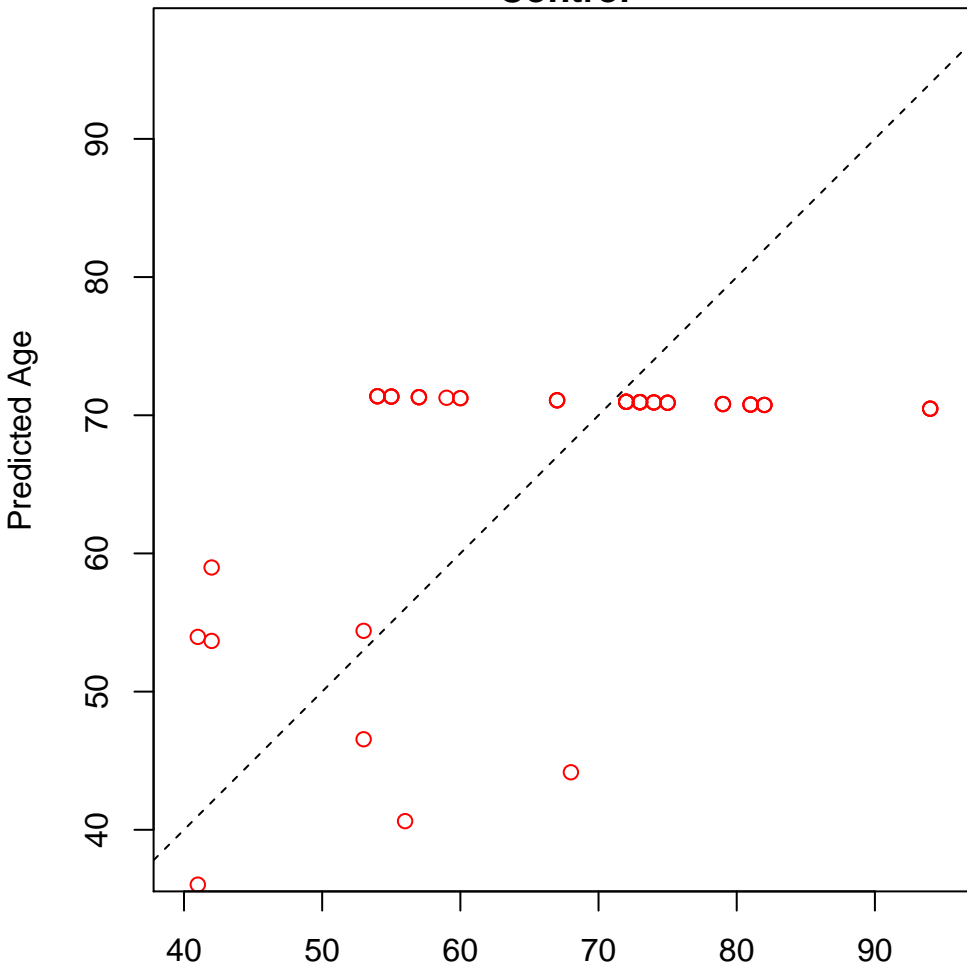
Test



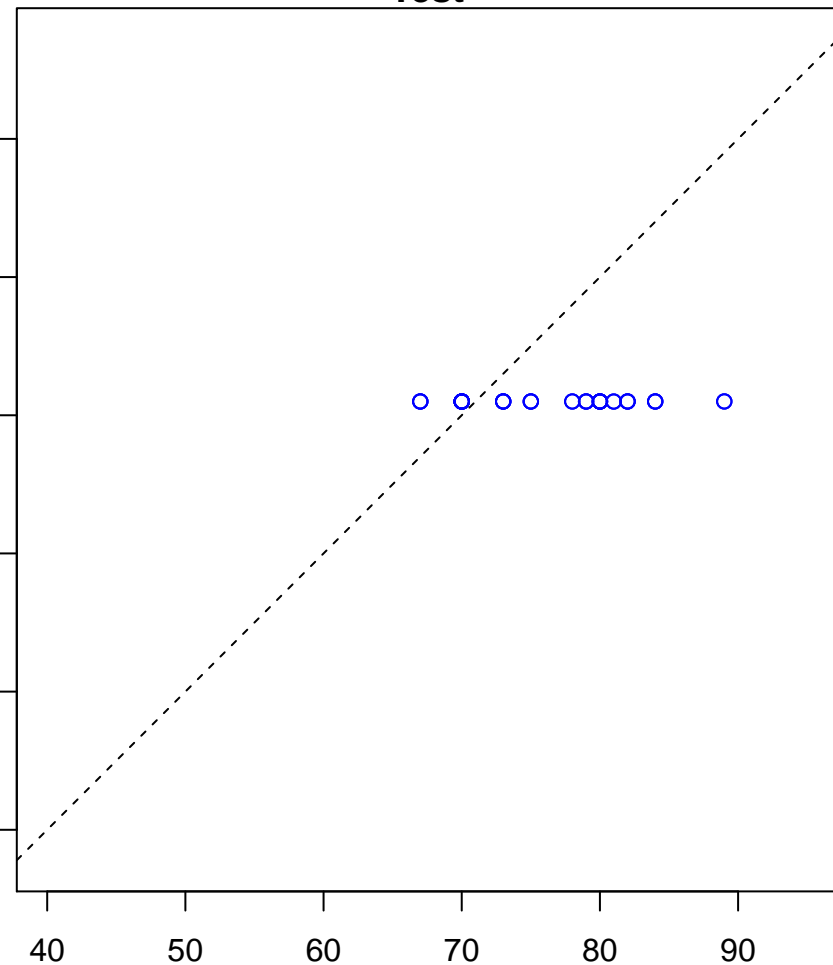
Actual Age

regulation of heart contraction (Score: 0.776692)

Control



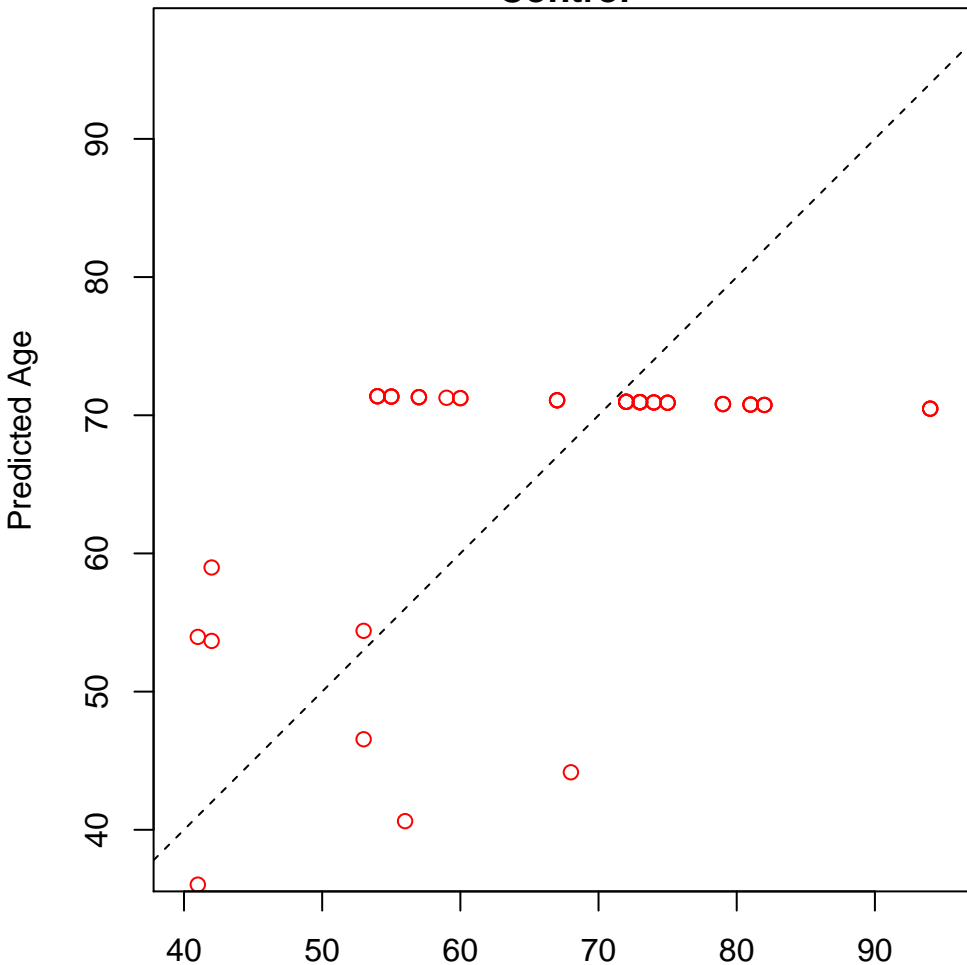
Test



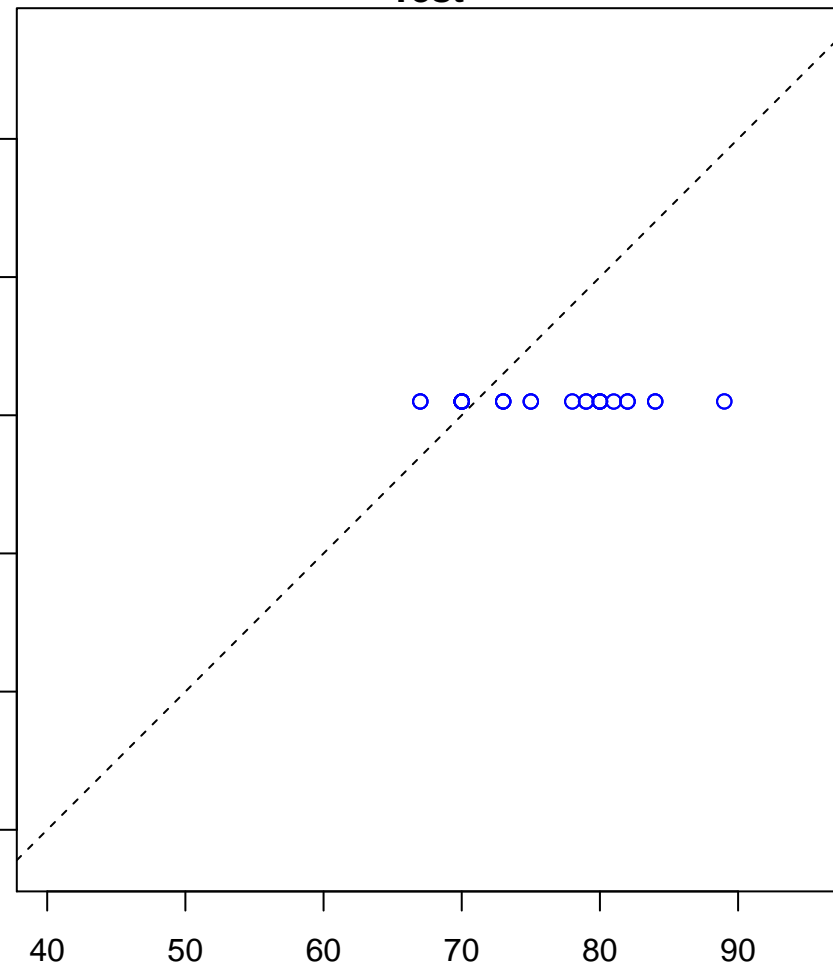
Actual Age

regulation of cardiac muscle contraction (Score: 0.776692)

Control



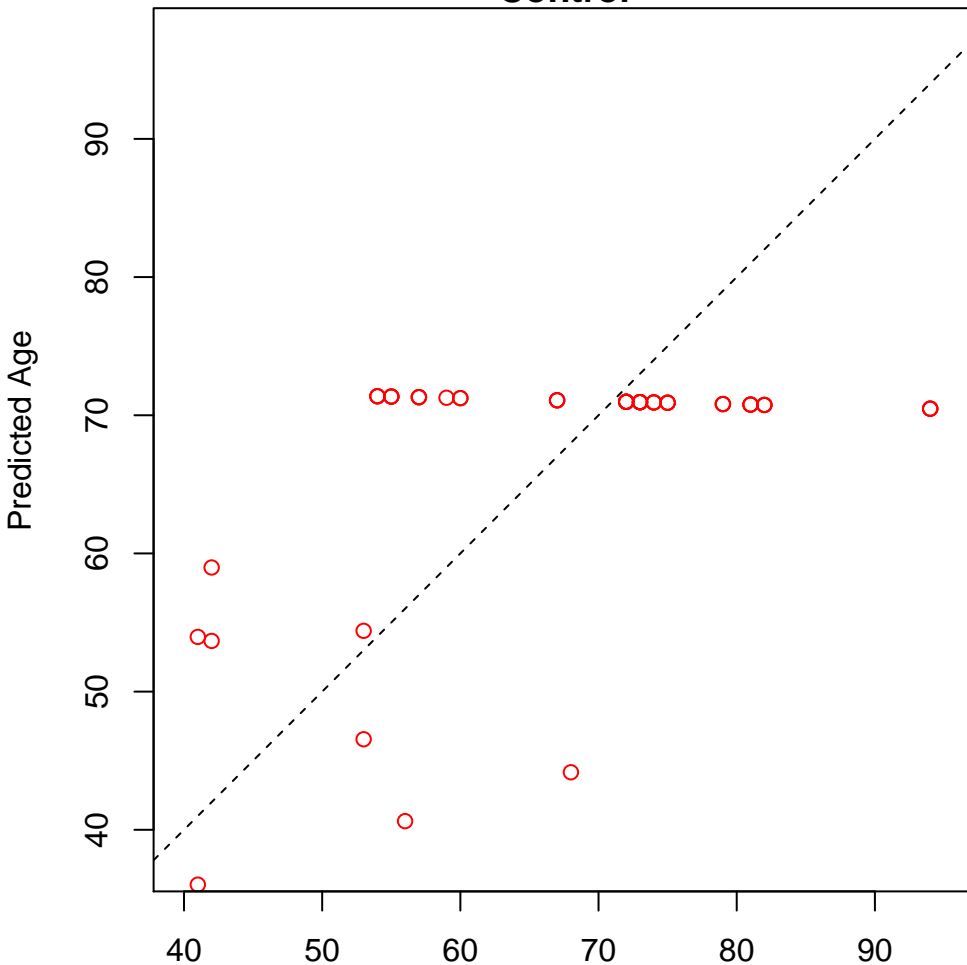
Test



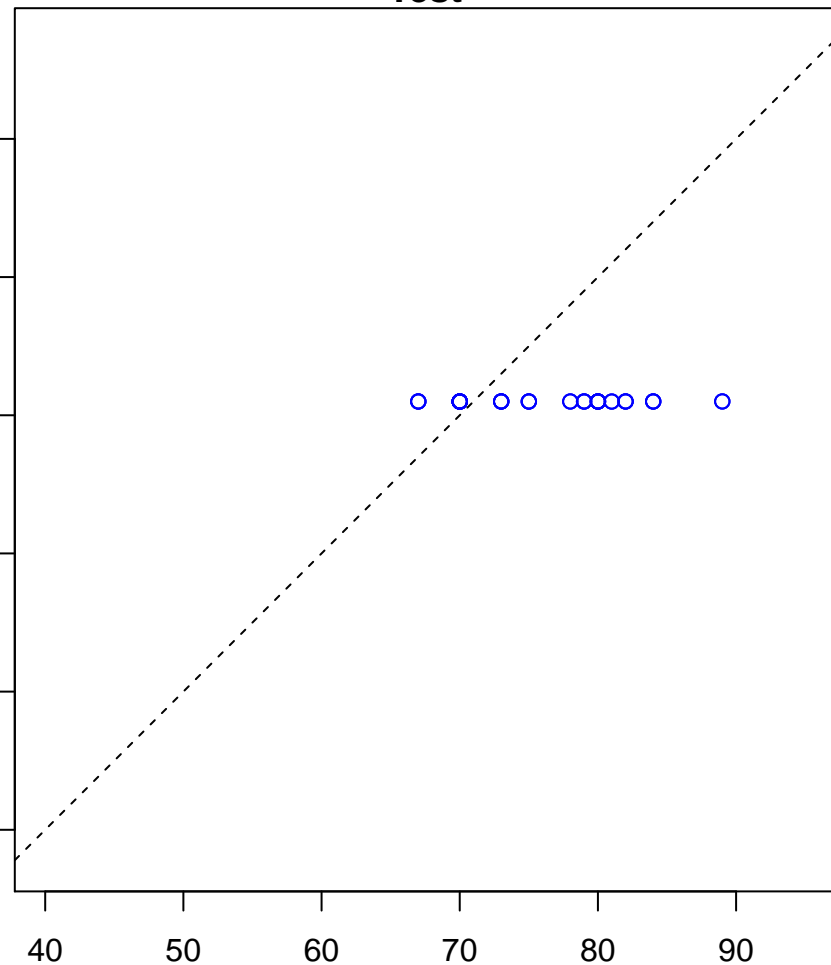
Actual Age

regulation of blood circulation (Score: 0.776692)

Control

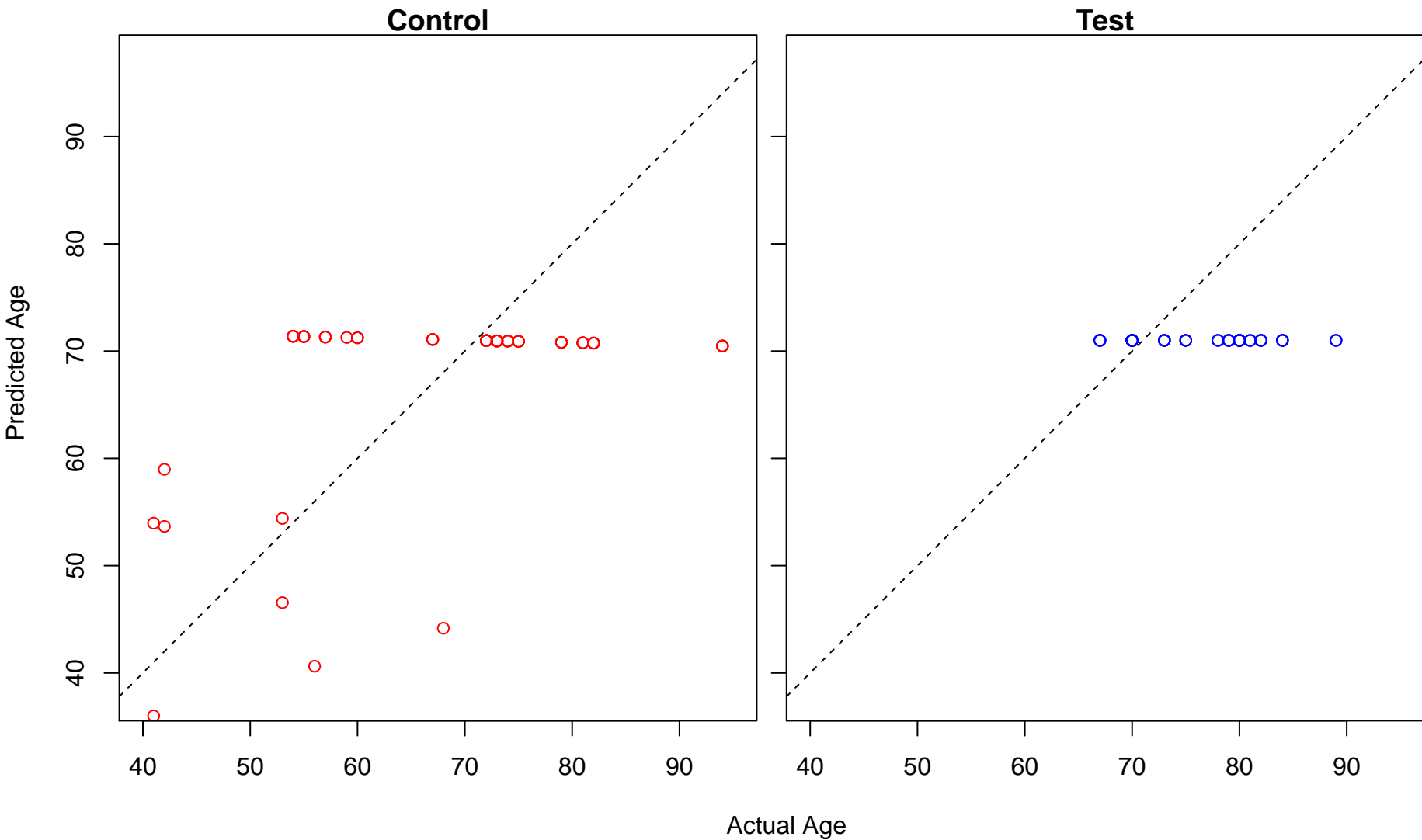


Test

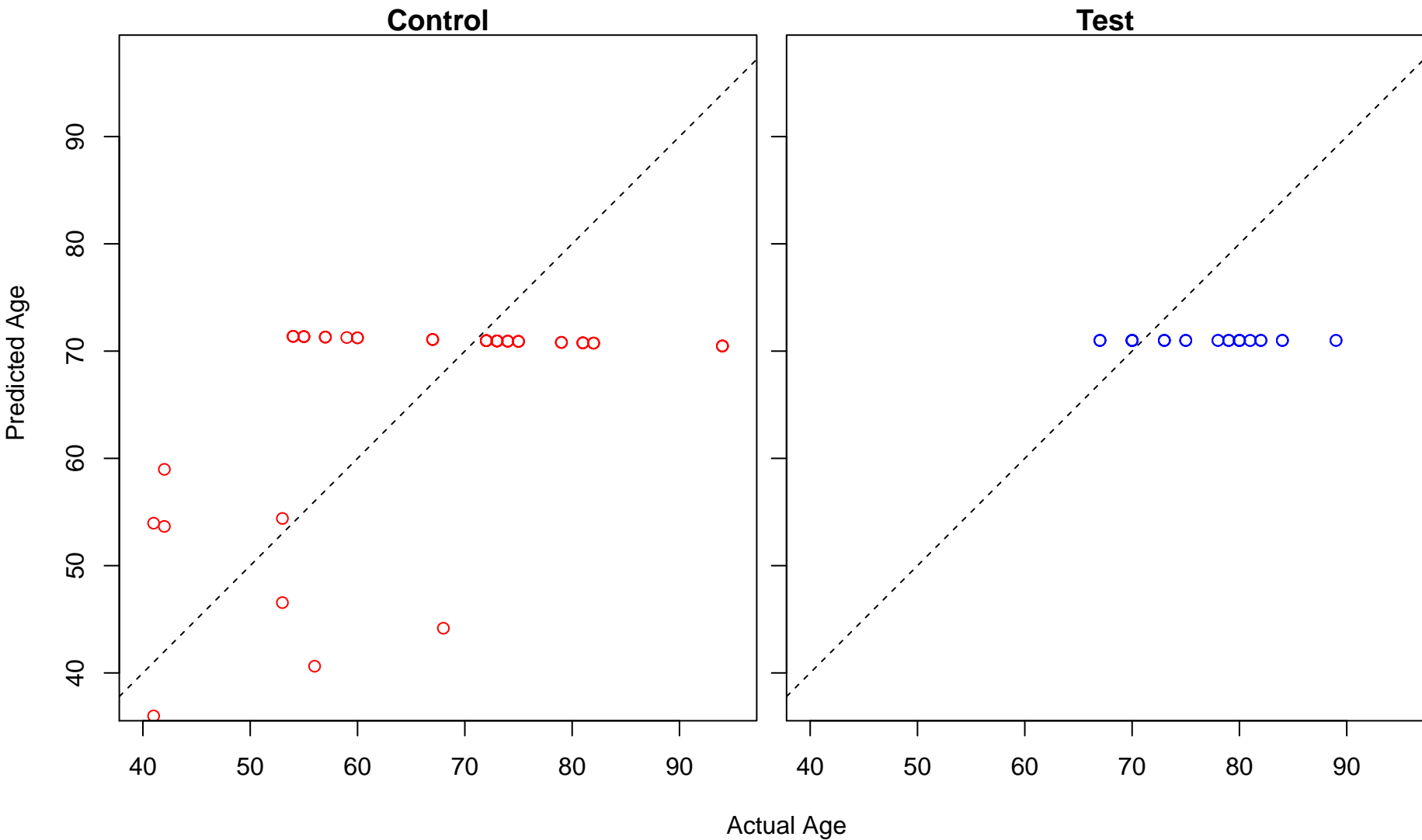


Actual Age

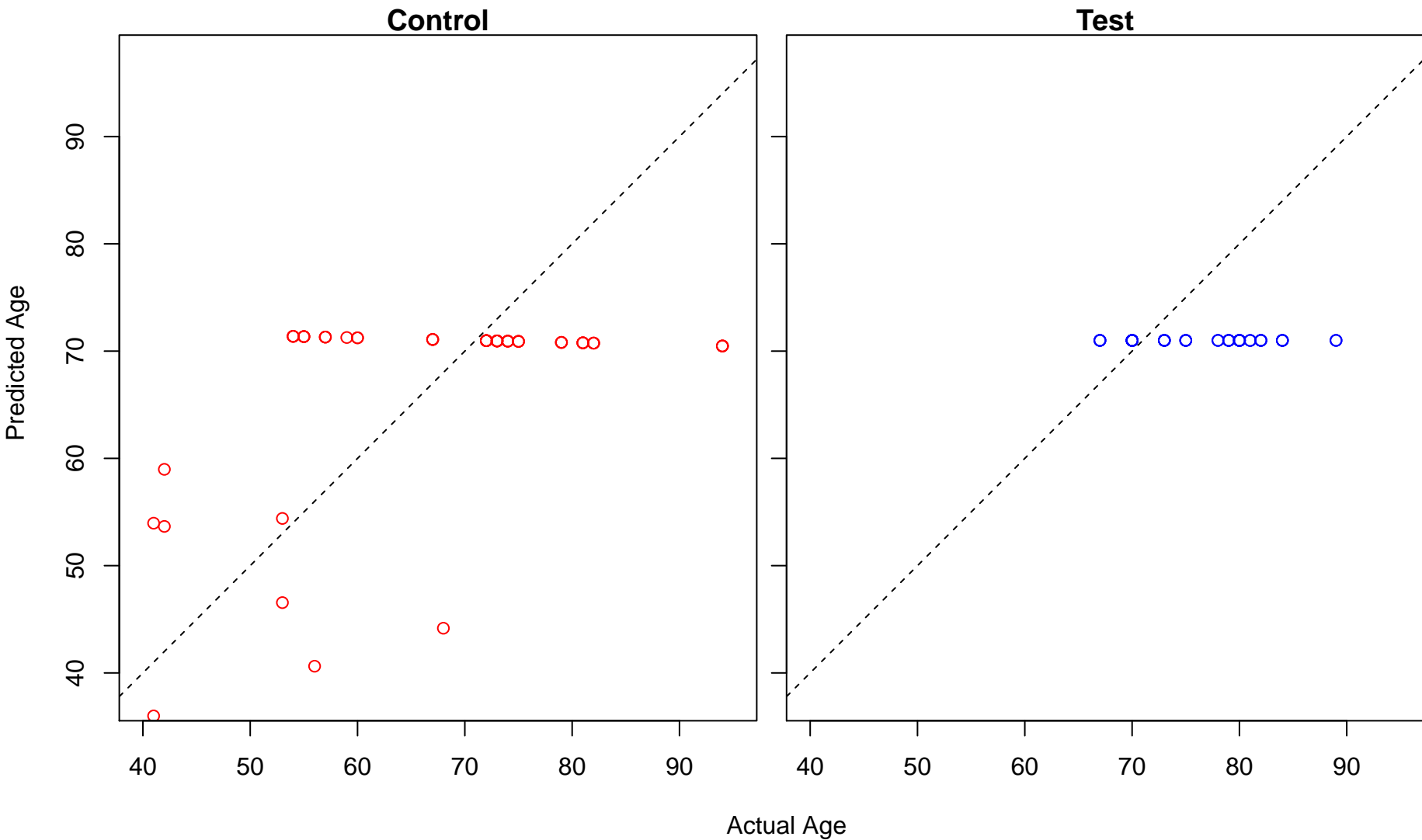
detection of calcium ion (Score: 0.776661)



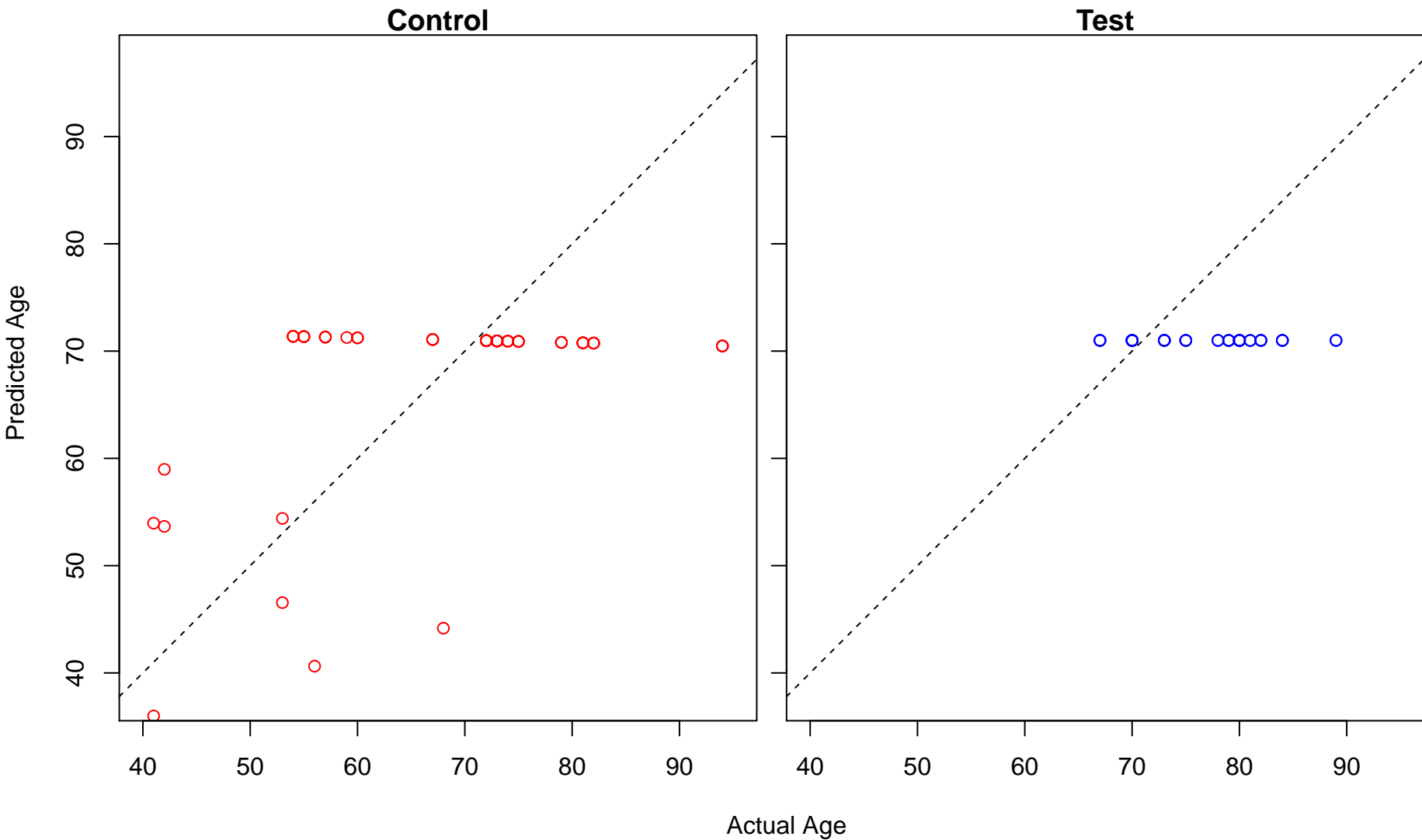
detection of chemical stimulus (Score: 0.776661)



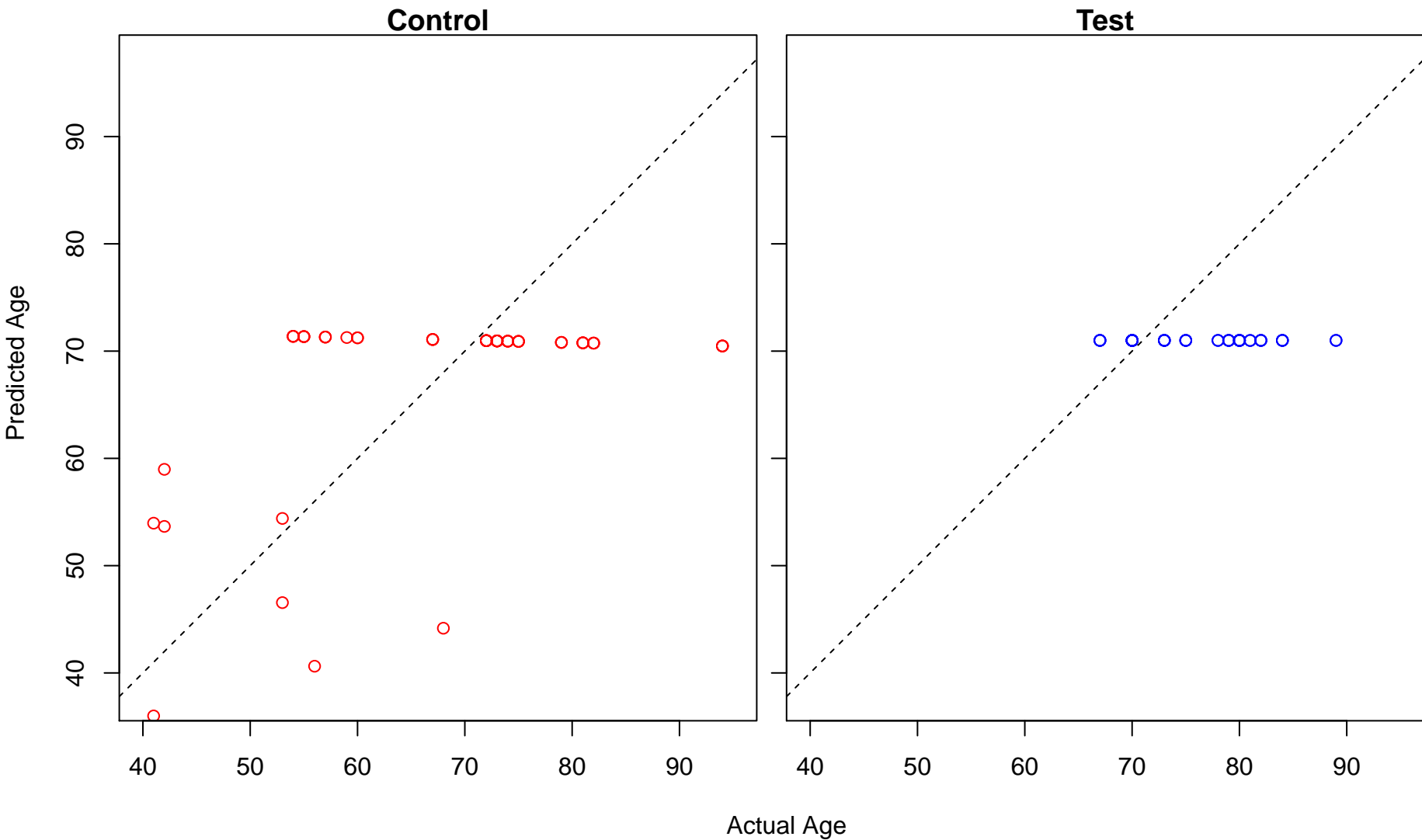
negative regulation of calcium ion transport into cytosol (Score: 0.776661)



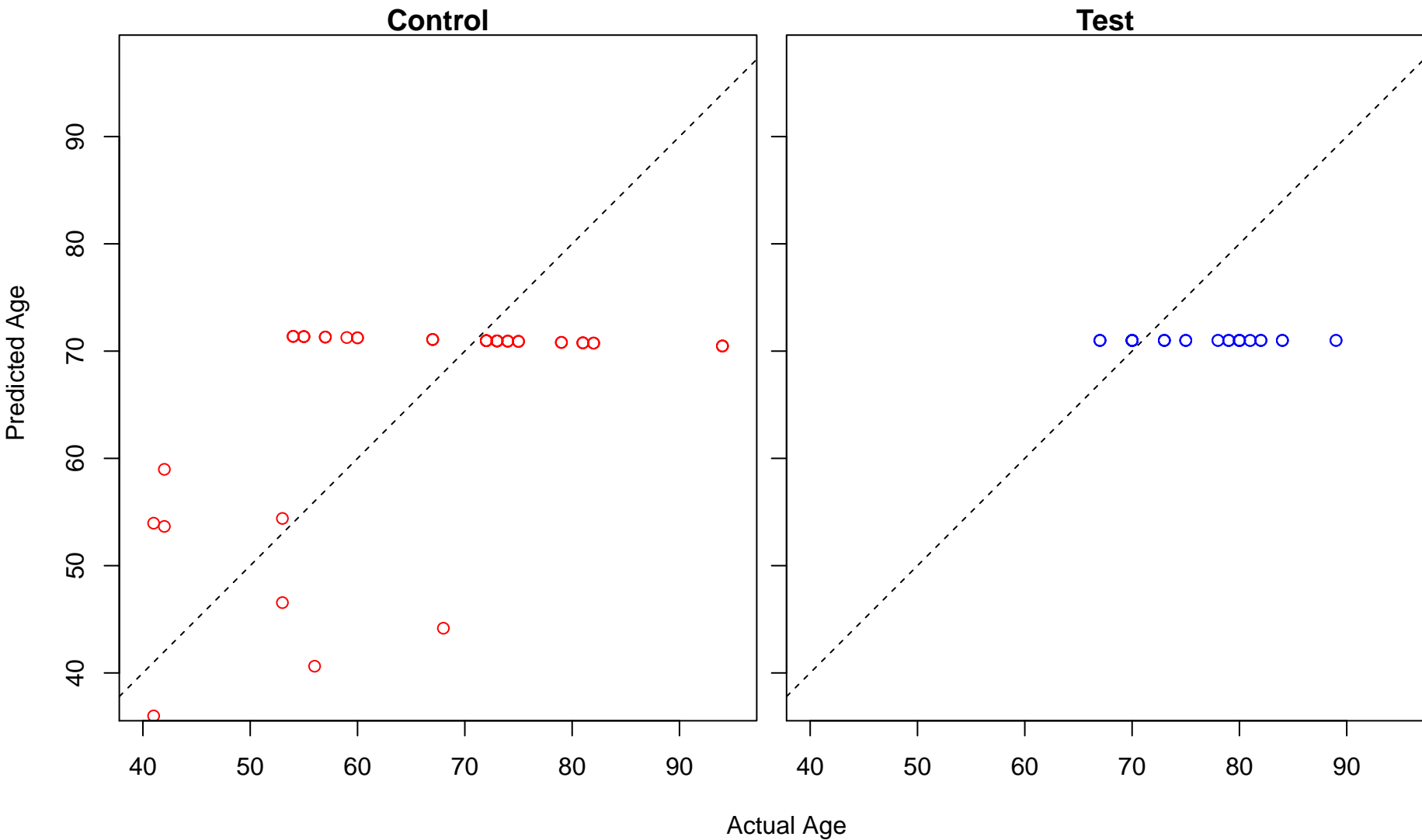
positive regulation of calcium ion transport into cytosol (Score: 0.776661)



negative regulation of peptidyl–threonine phosphorylation (Score: 0.776661)

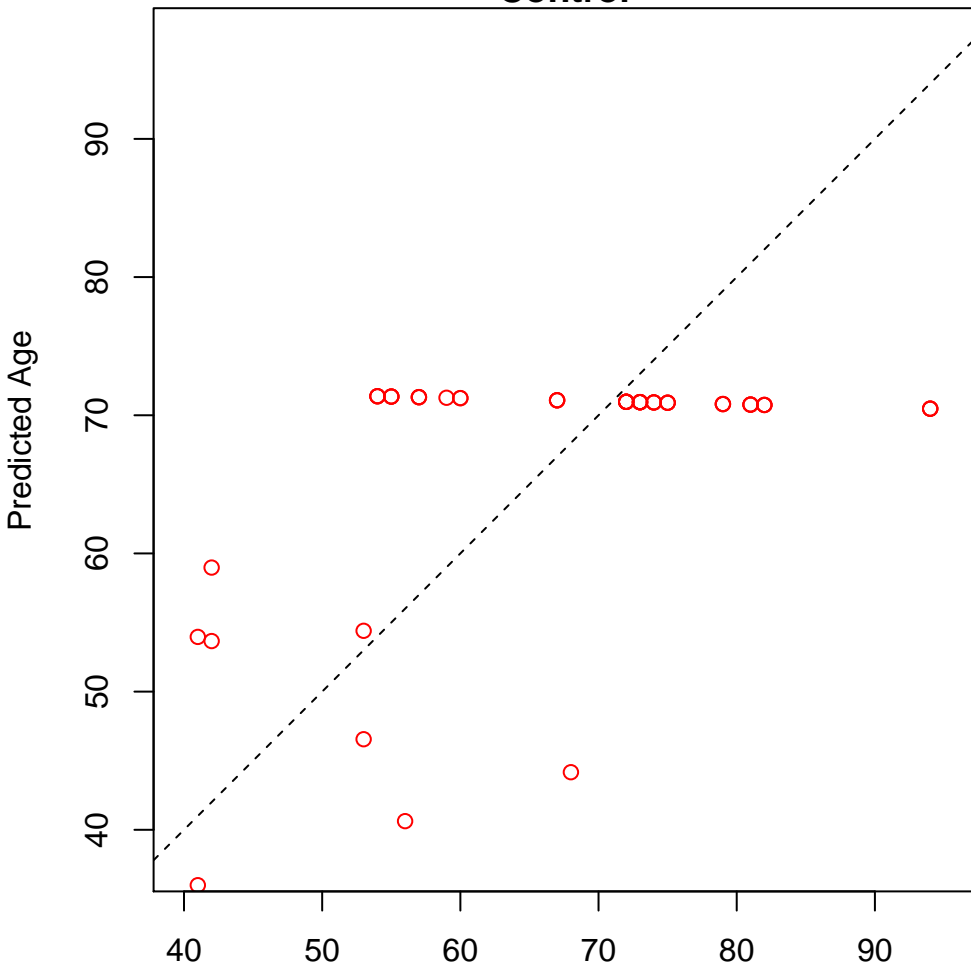


regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum (Score: 0.776)

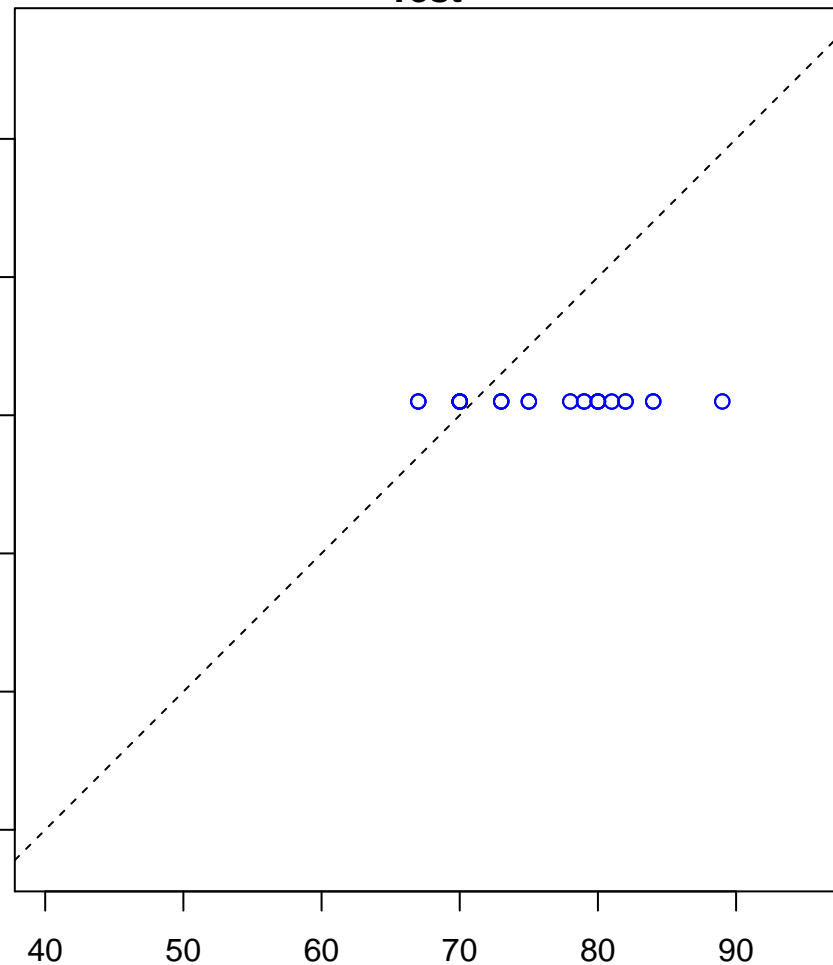


regulation of protein autophosphorylation (Score: 0.776661)

Control

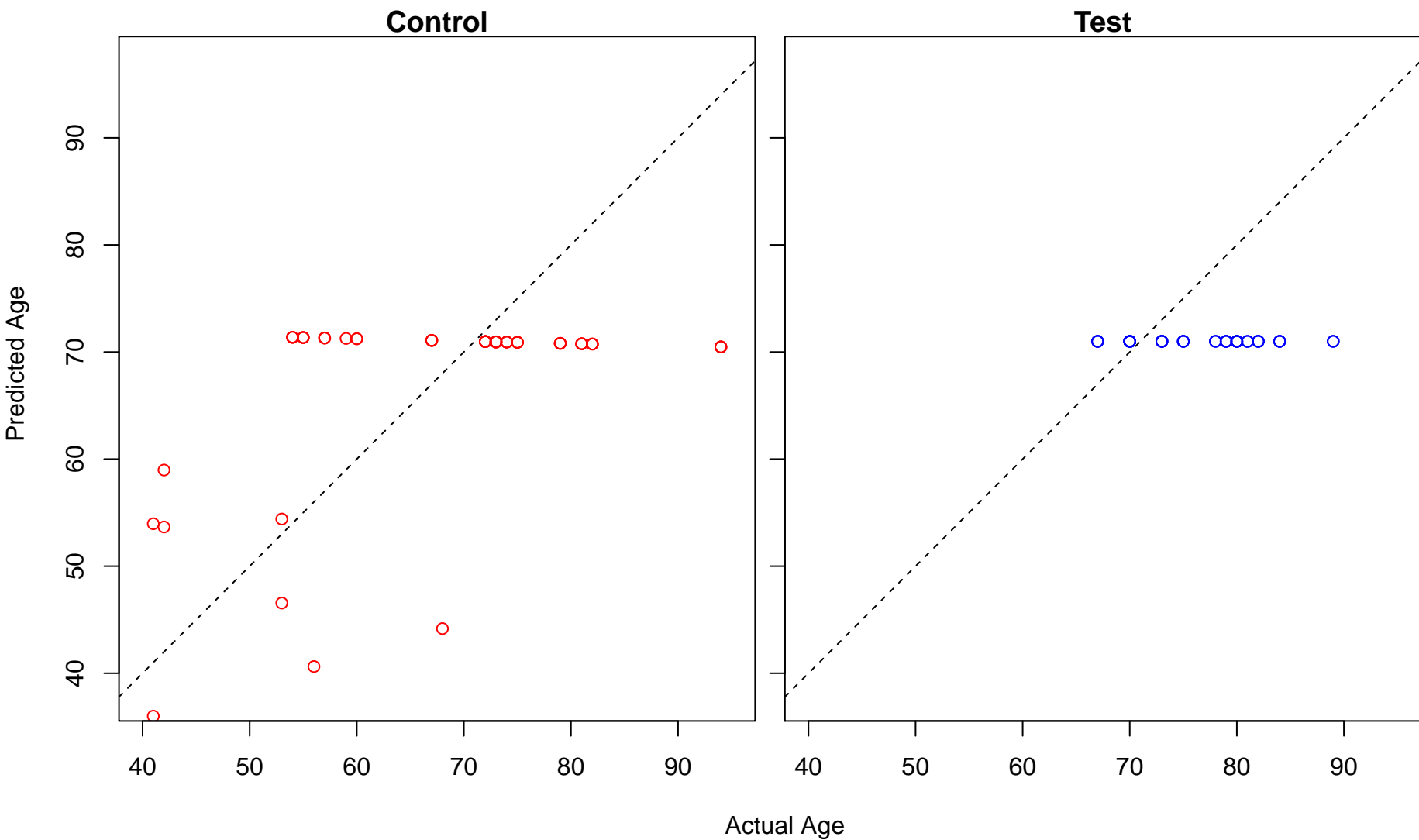


Test



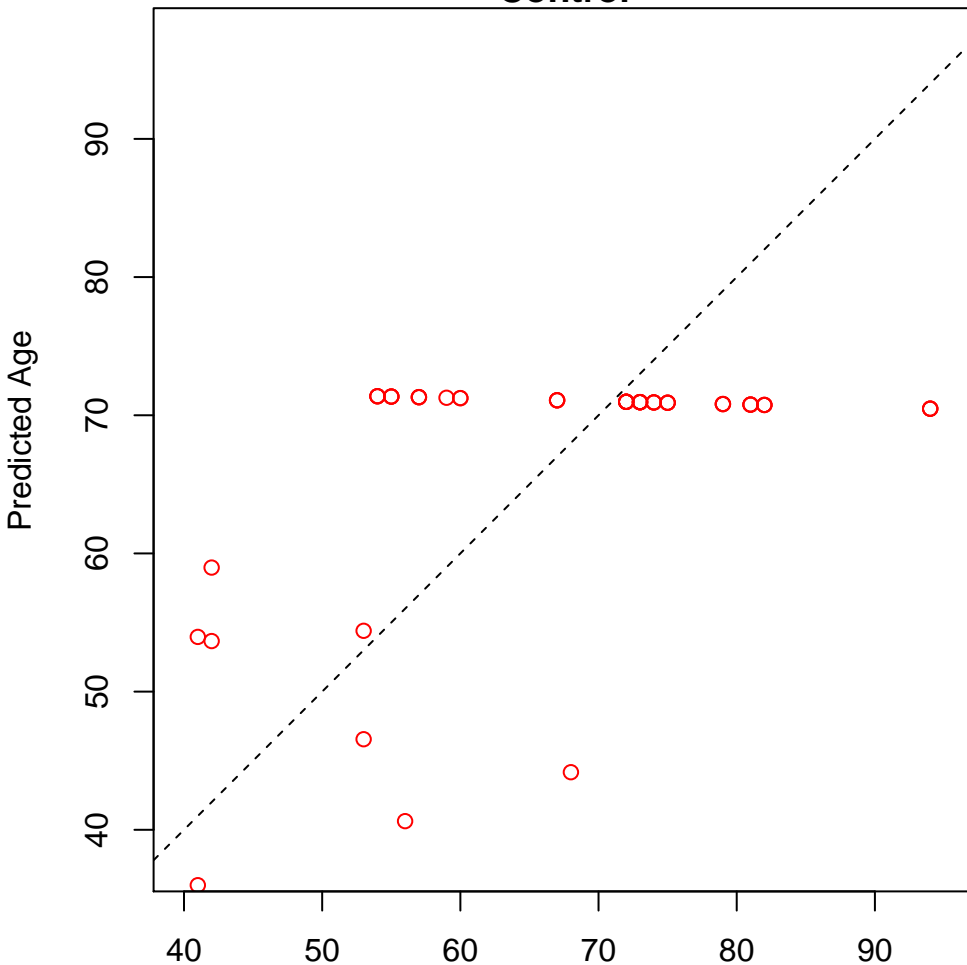
Actual Age

positive regulation of protein autophosphorylation (Score: 0.776661)

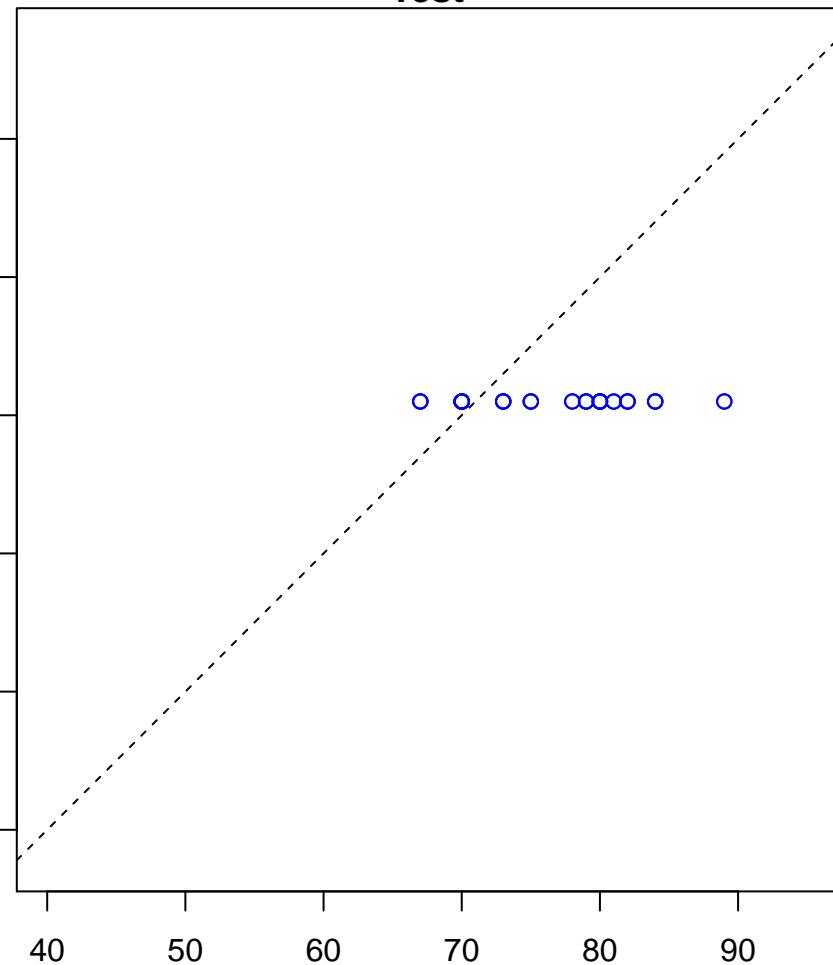


negative regulation of transporter activity (Score: 0.776661)

Control



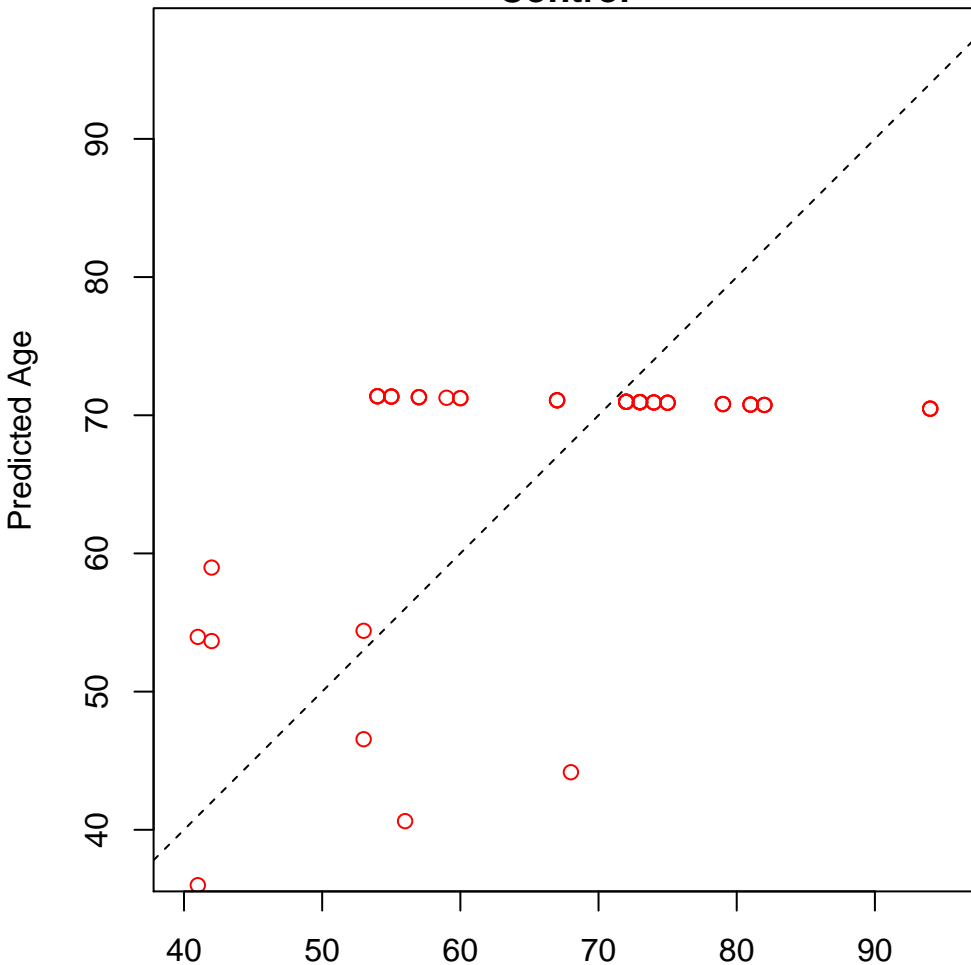
Test



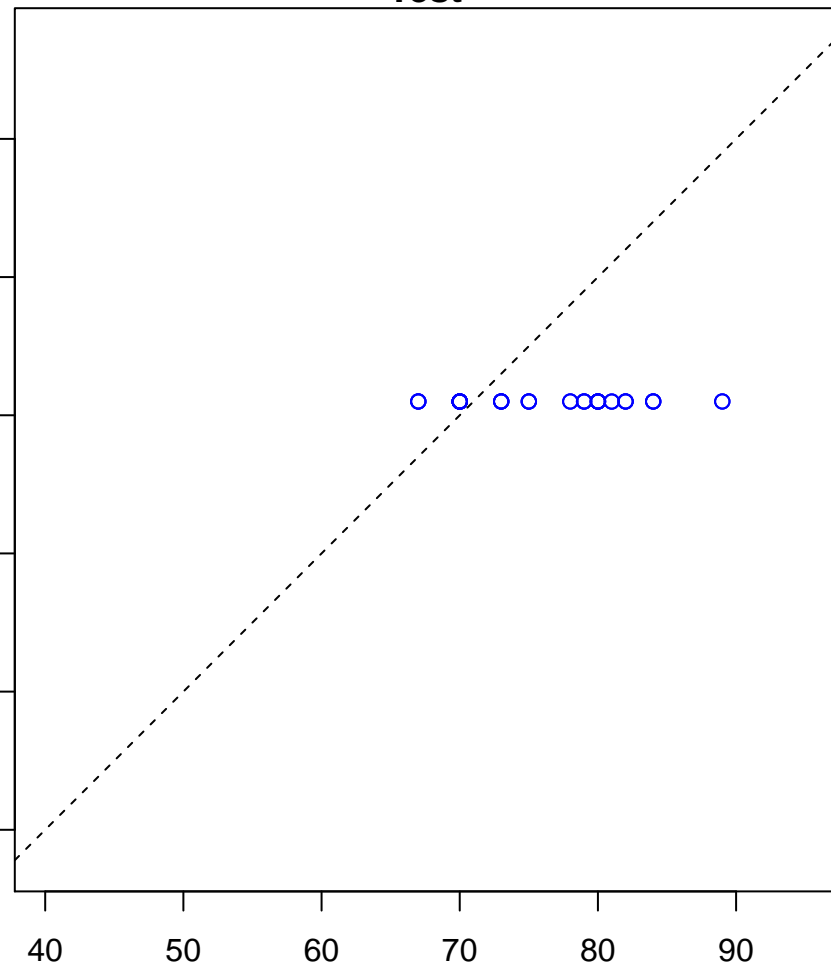
Actual Age

positive regulation of transporter activity (Score: 0.776661)

Control

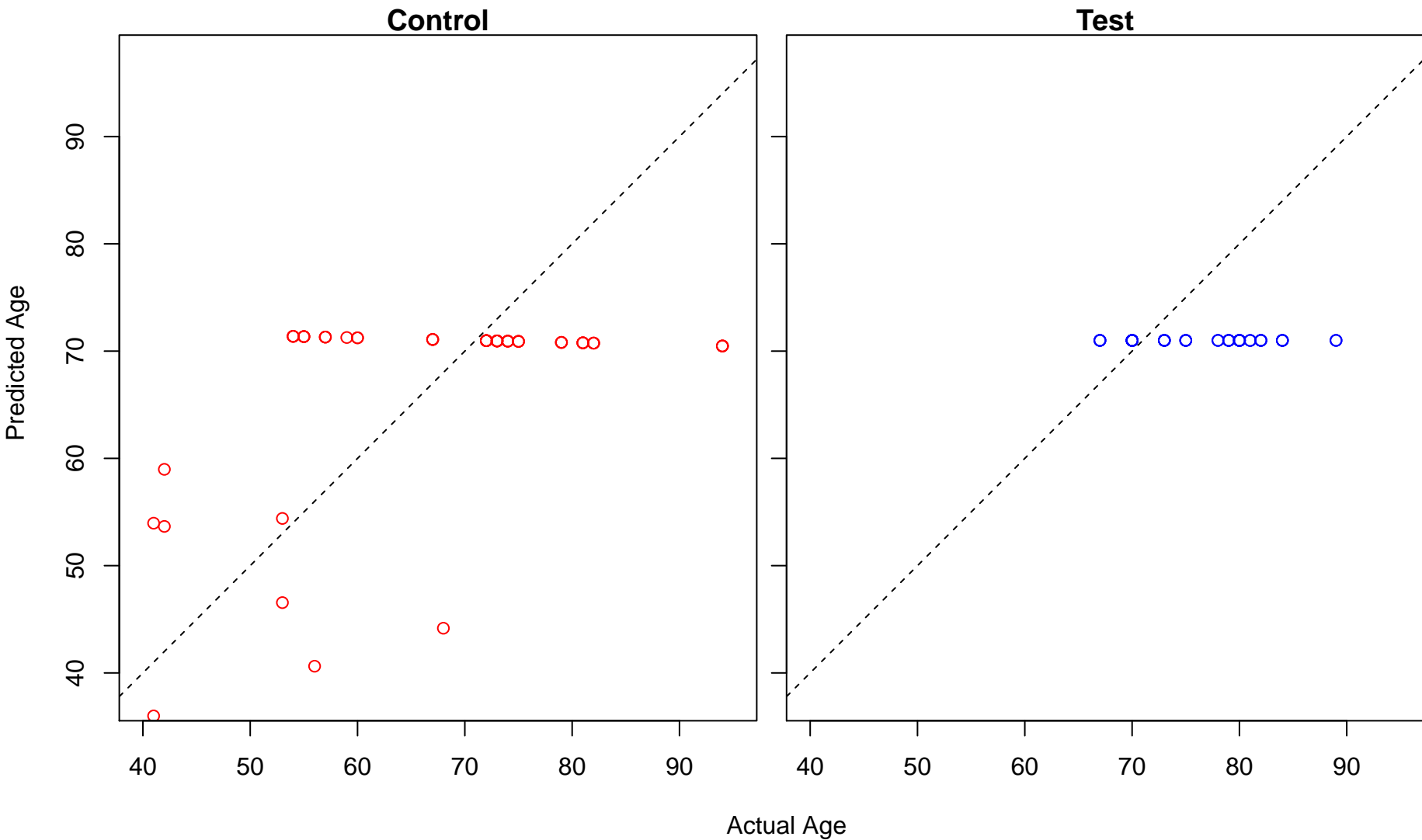


Test

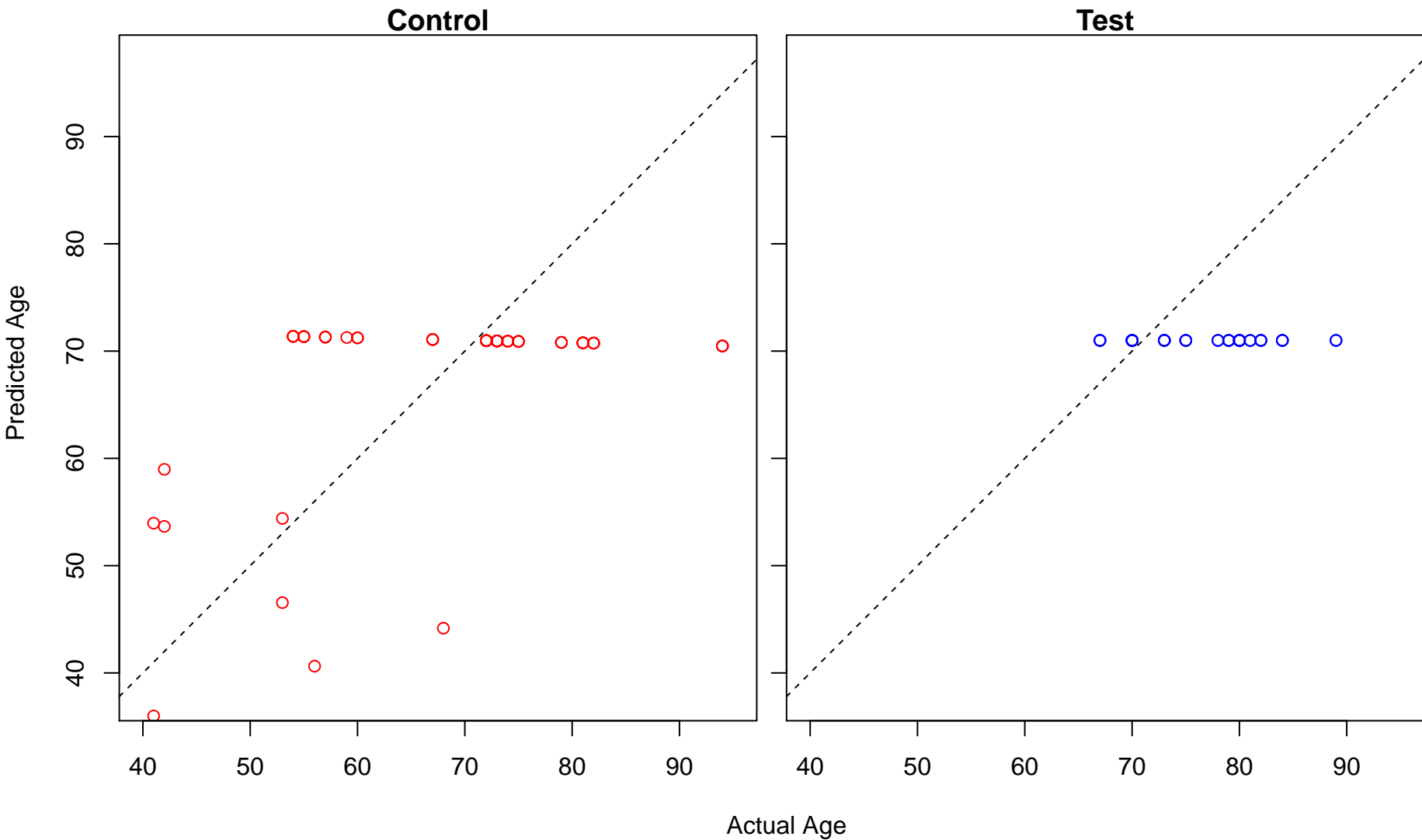


Actual Age

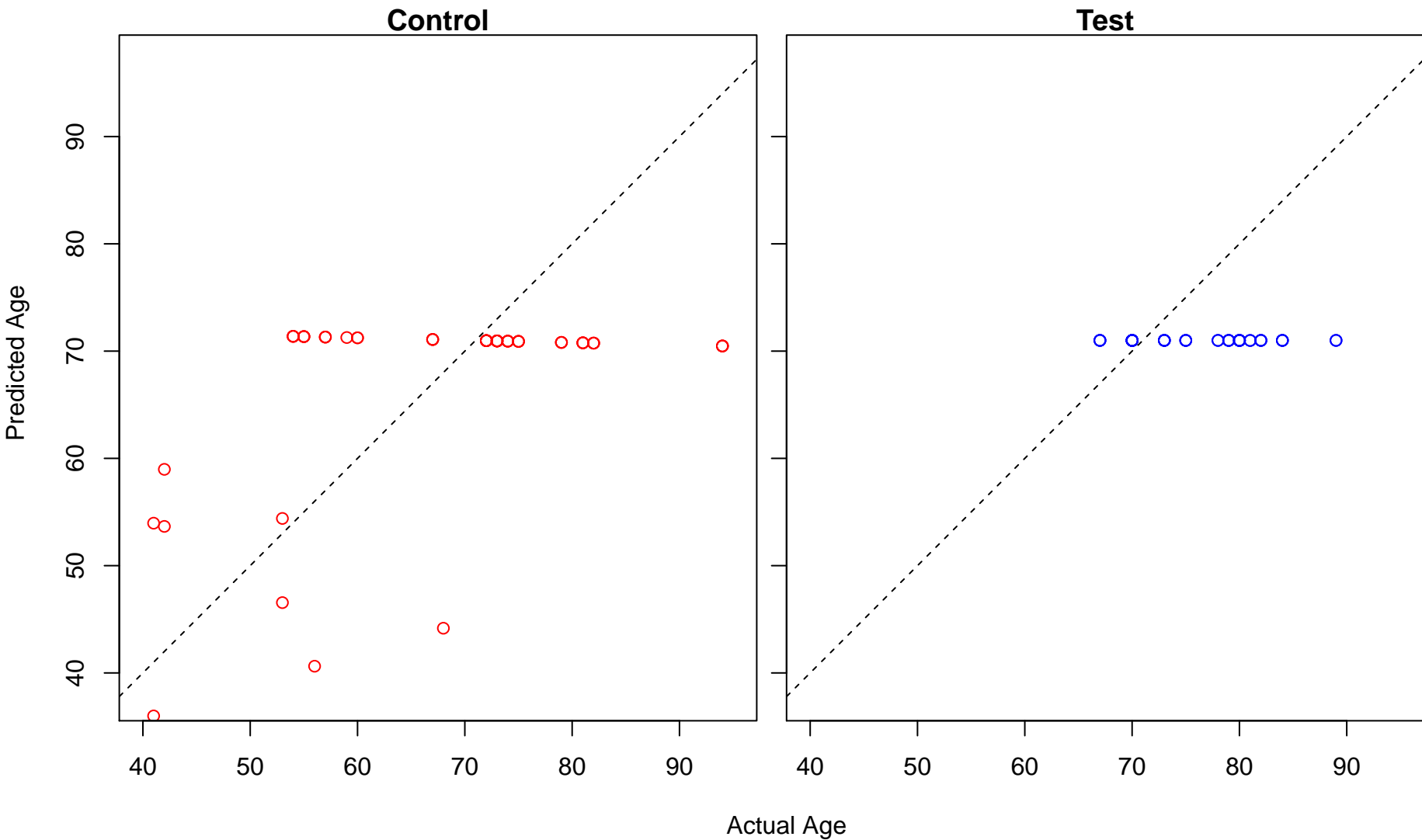
negative regulation of ion transmembrane transporter activity (Score: 0.776661)



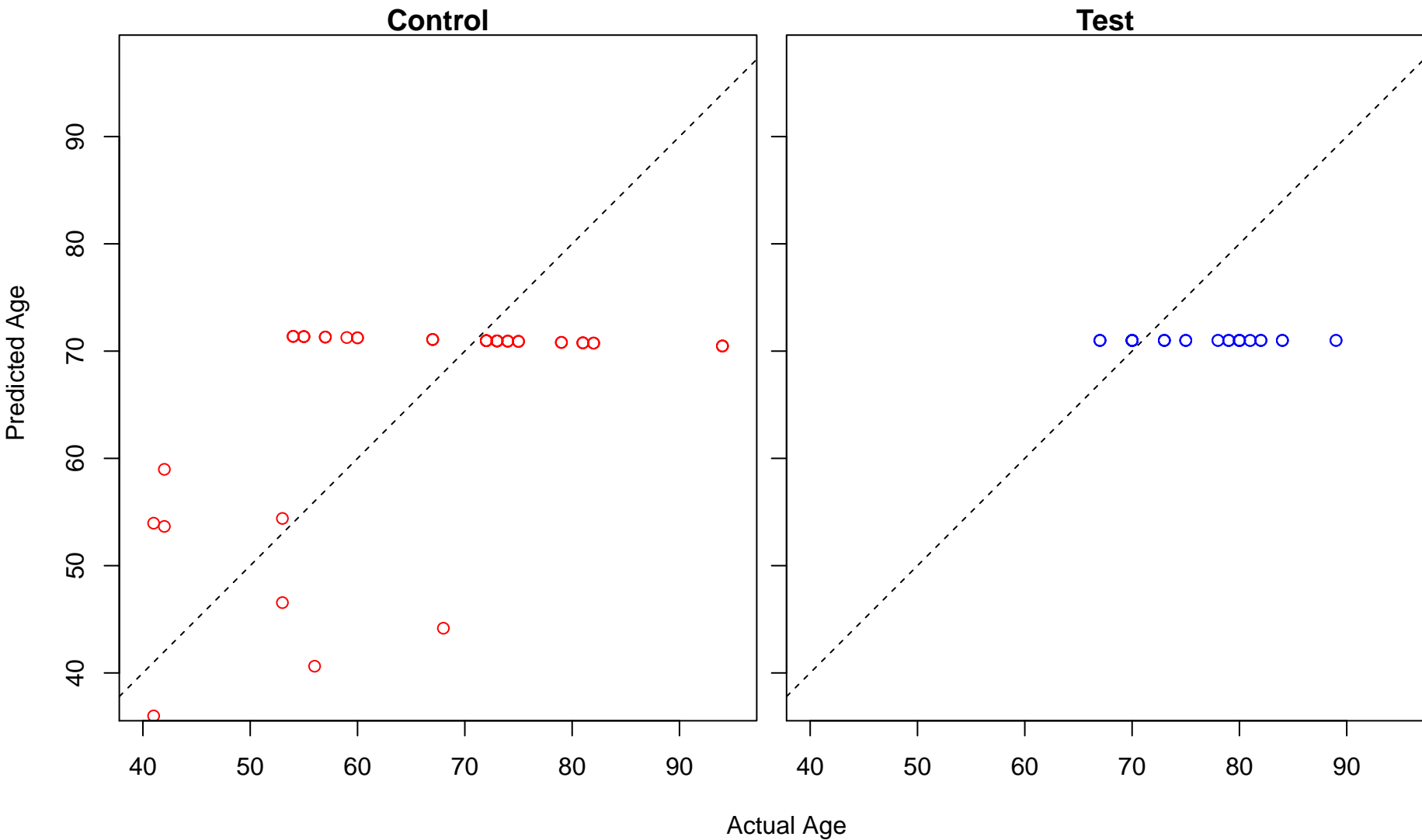
positive regulation of ion transmembrane transporter activity (Score: 0.776661)



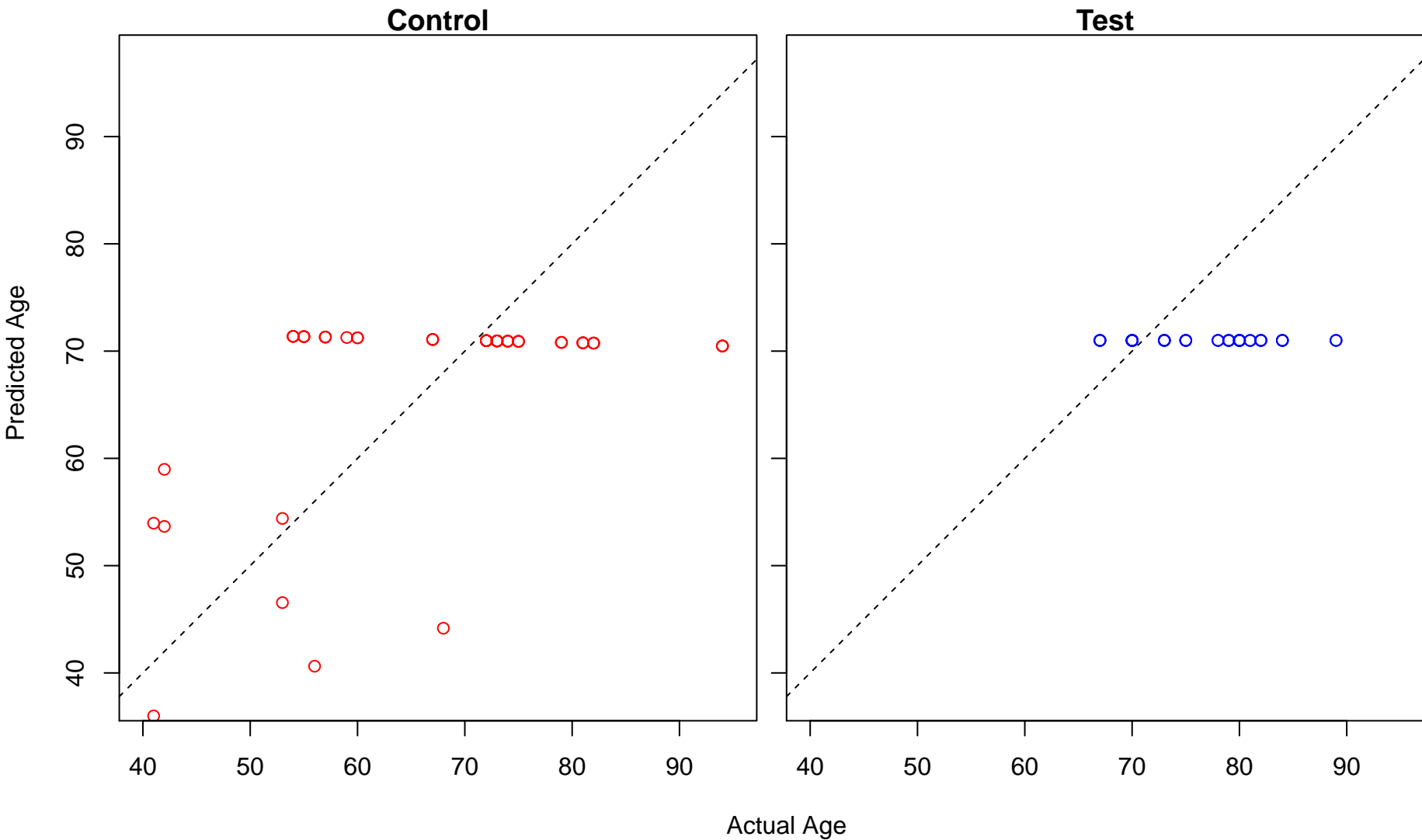
negative regulation of transmembrane transport (Score: 0.776661)



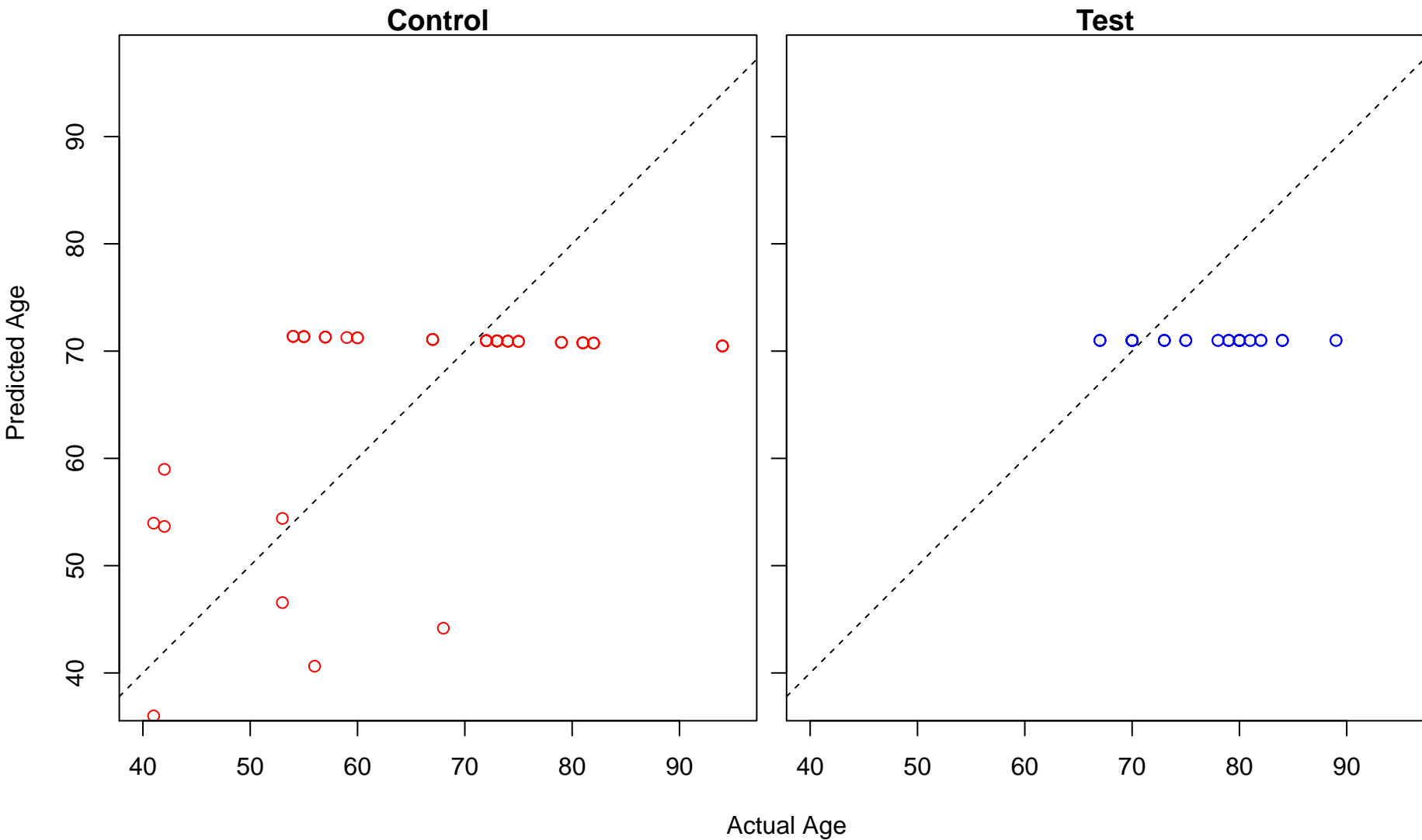
positive regulation of transmembrane transport (Score: 0.776661)



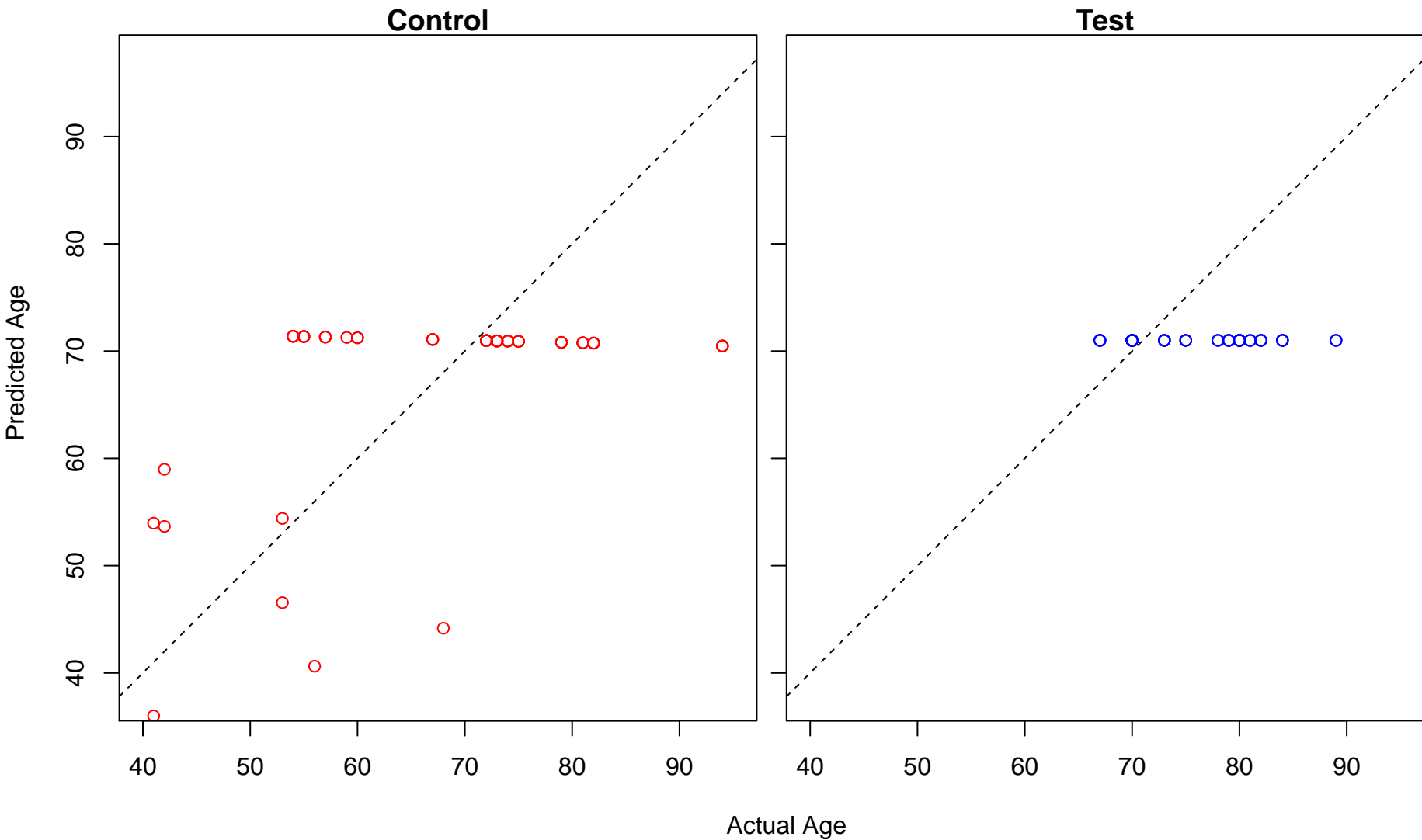
negative regulation of ion transmembrane transport (Score: 0.776661)



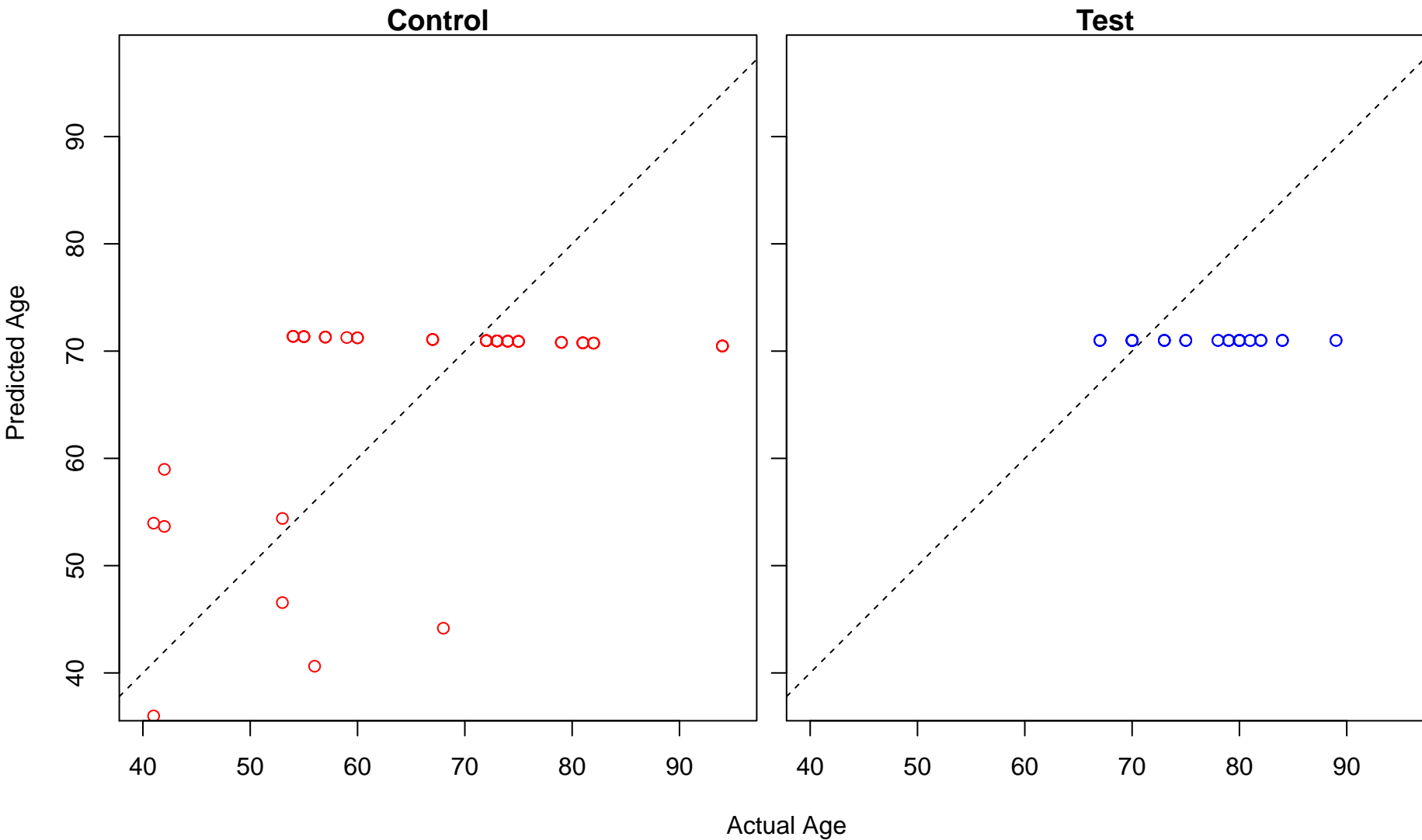
positive regulation of ion transmembrane transport (Score: 0.776661)



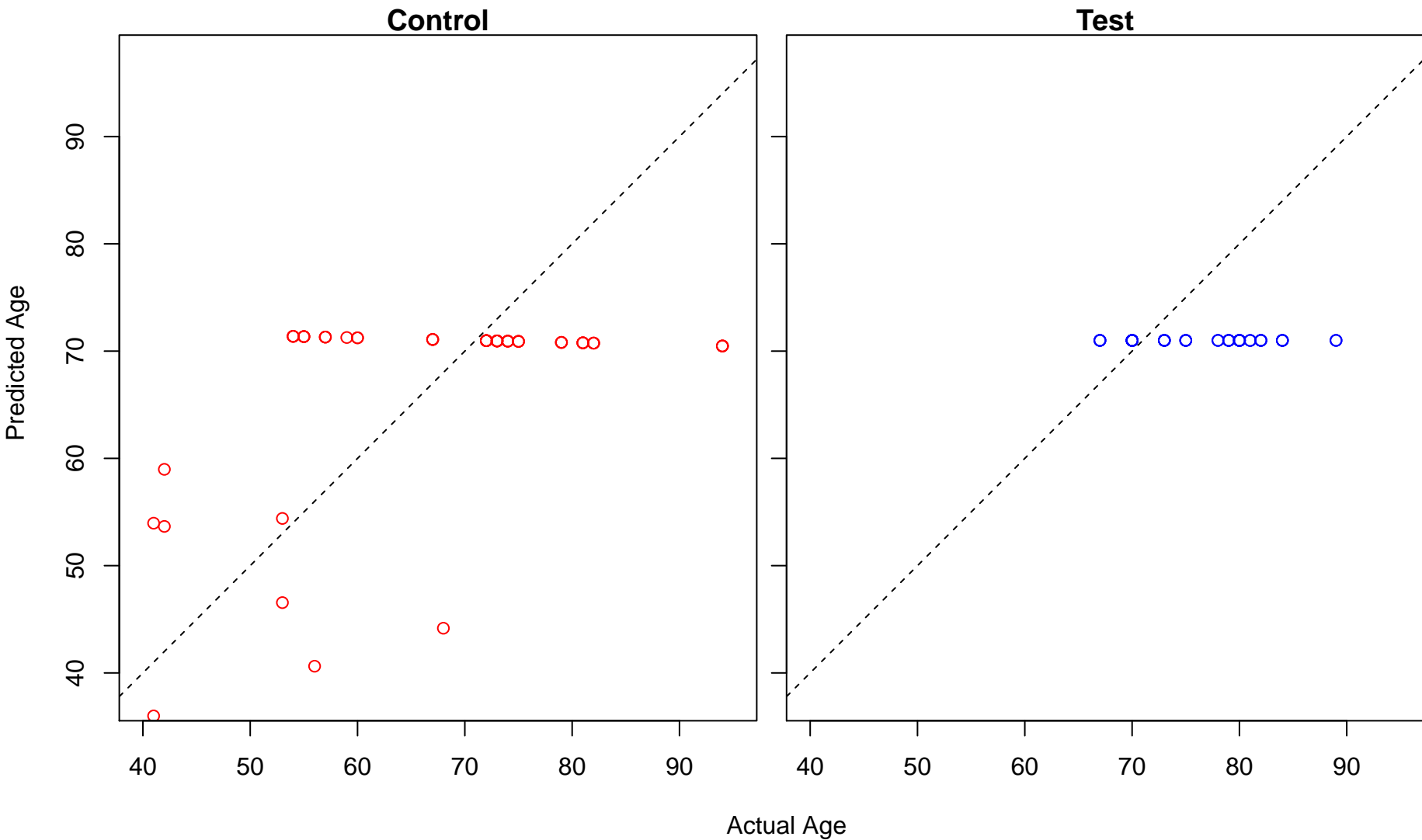
negative regulation of calcium-mediated signaling (Score: 0.776661)



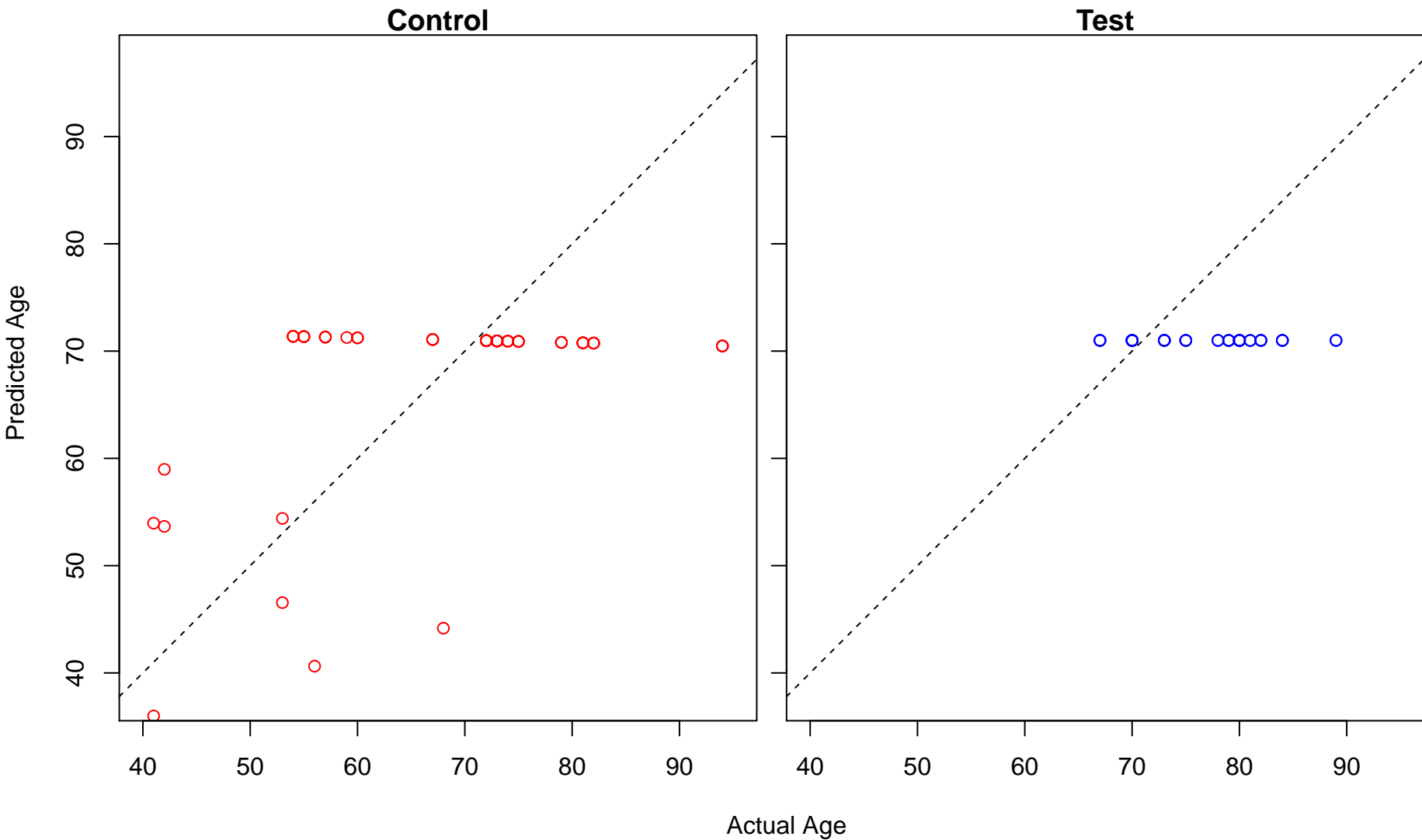
positive regulation of calcium-mediated signaling (Score: 0.776661)



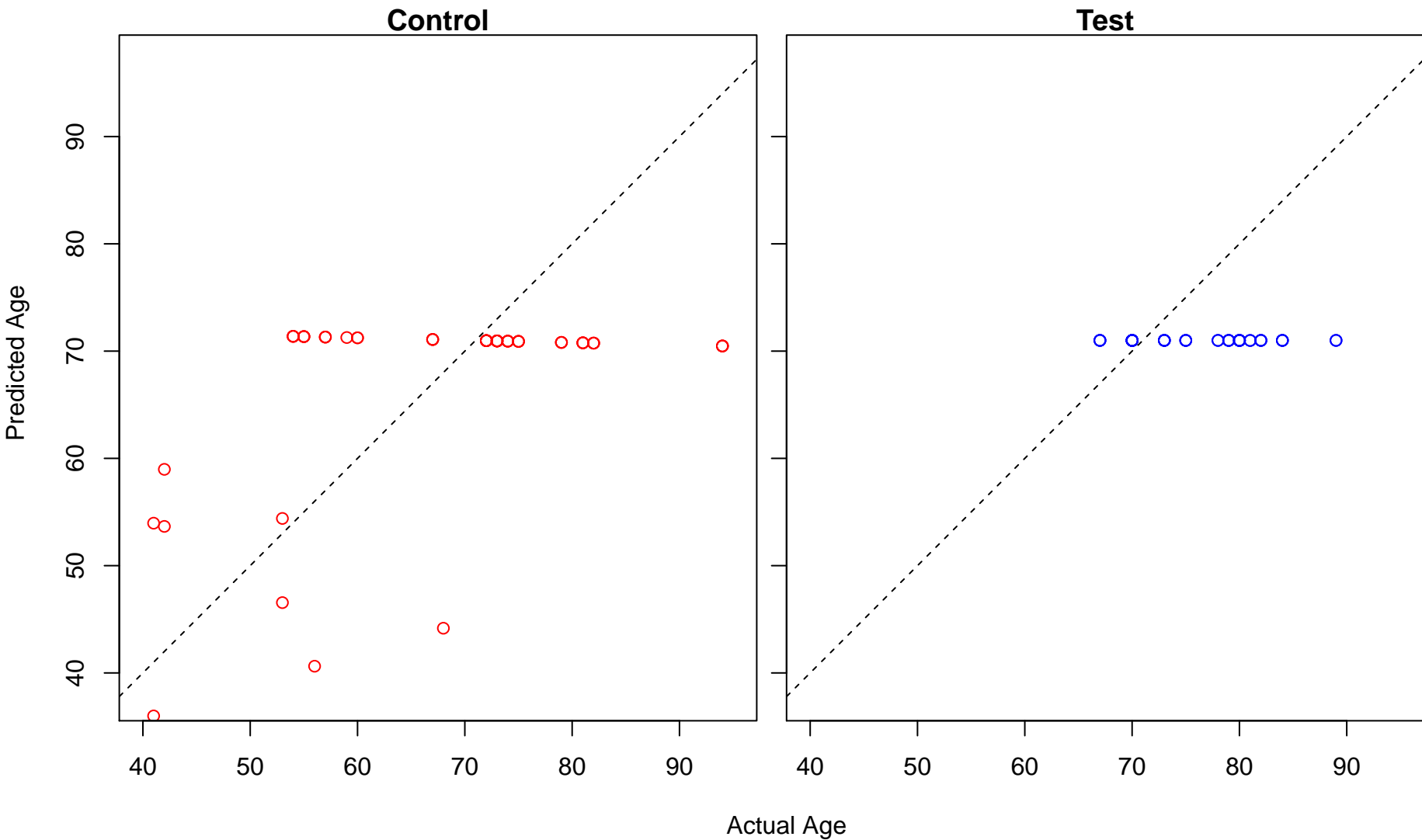
negative regulation of release of sequestered calcium ion into cytosol (Score: 0.776661)



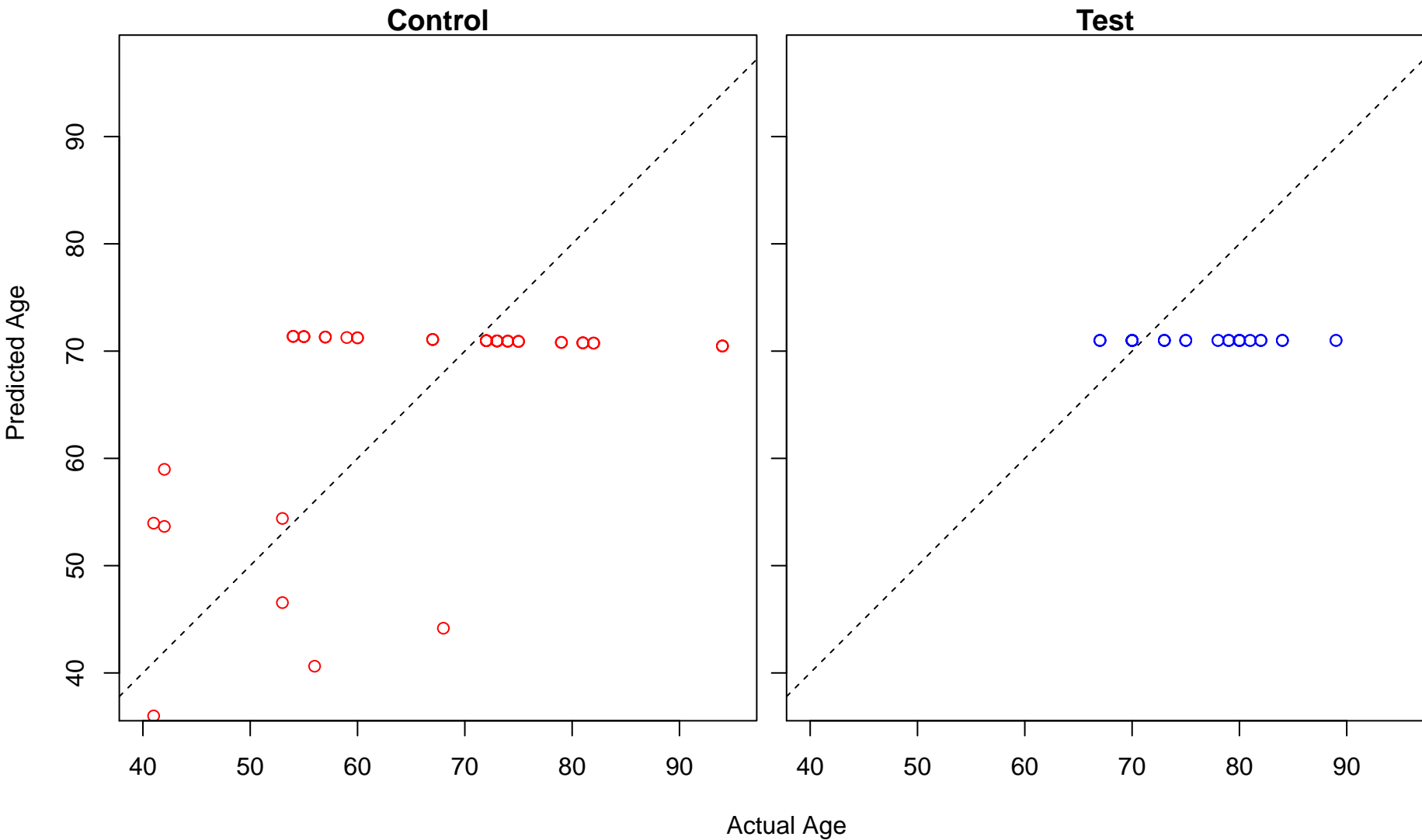
positive regulation of release of sequestered calcium ion into cytosol (Score: 0.776661)



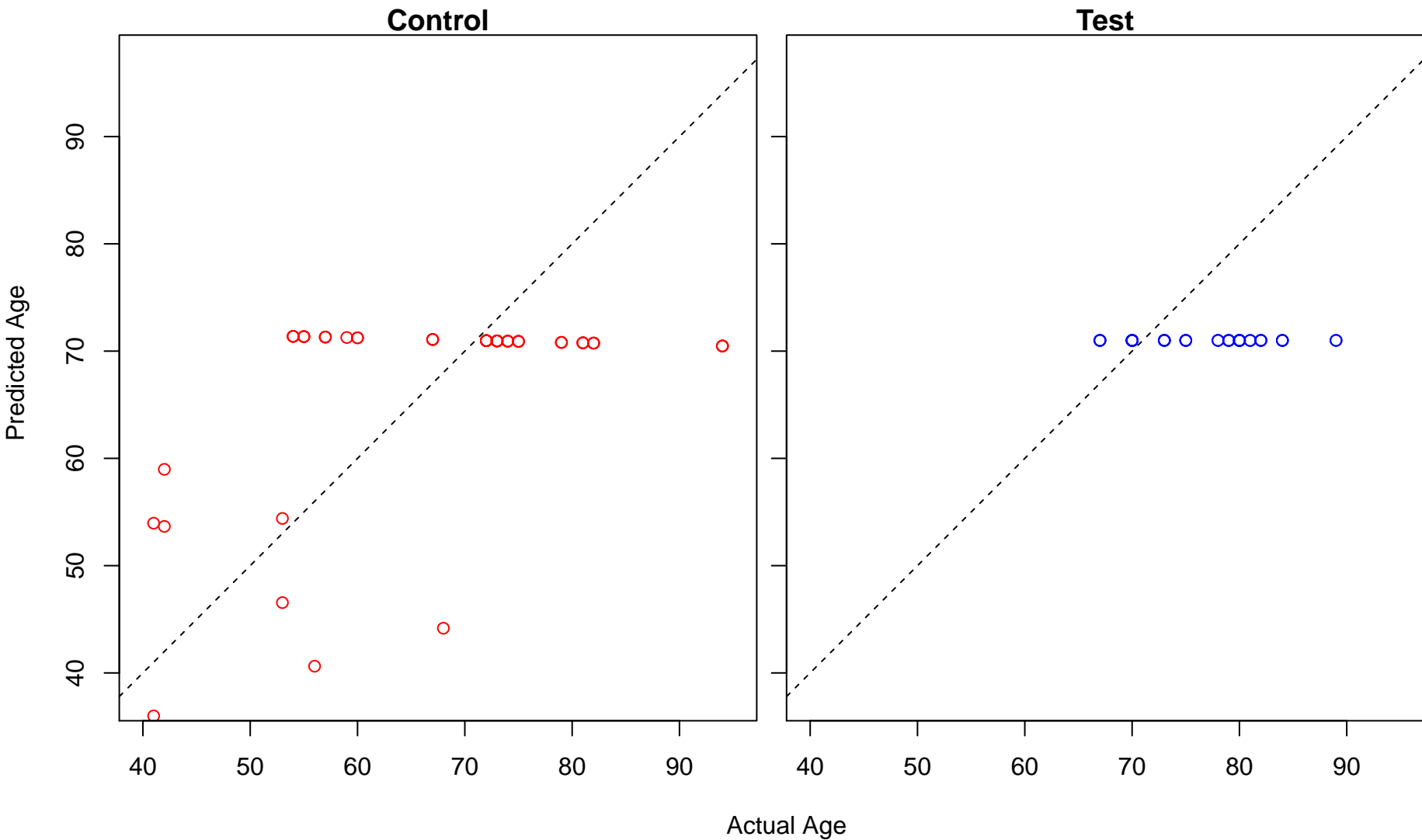
positive regulation of sequestering of calcium ion (Score: 0.776661)



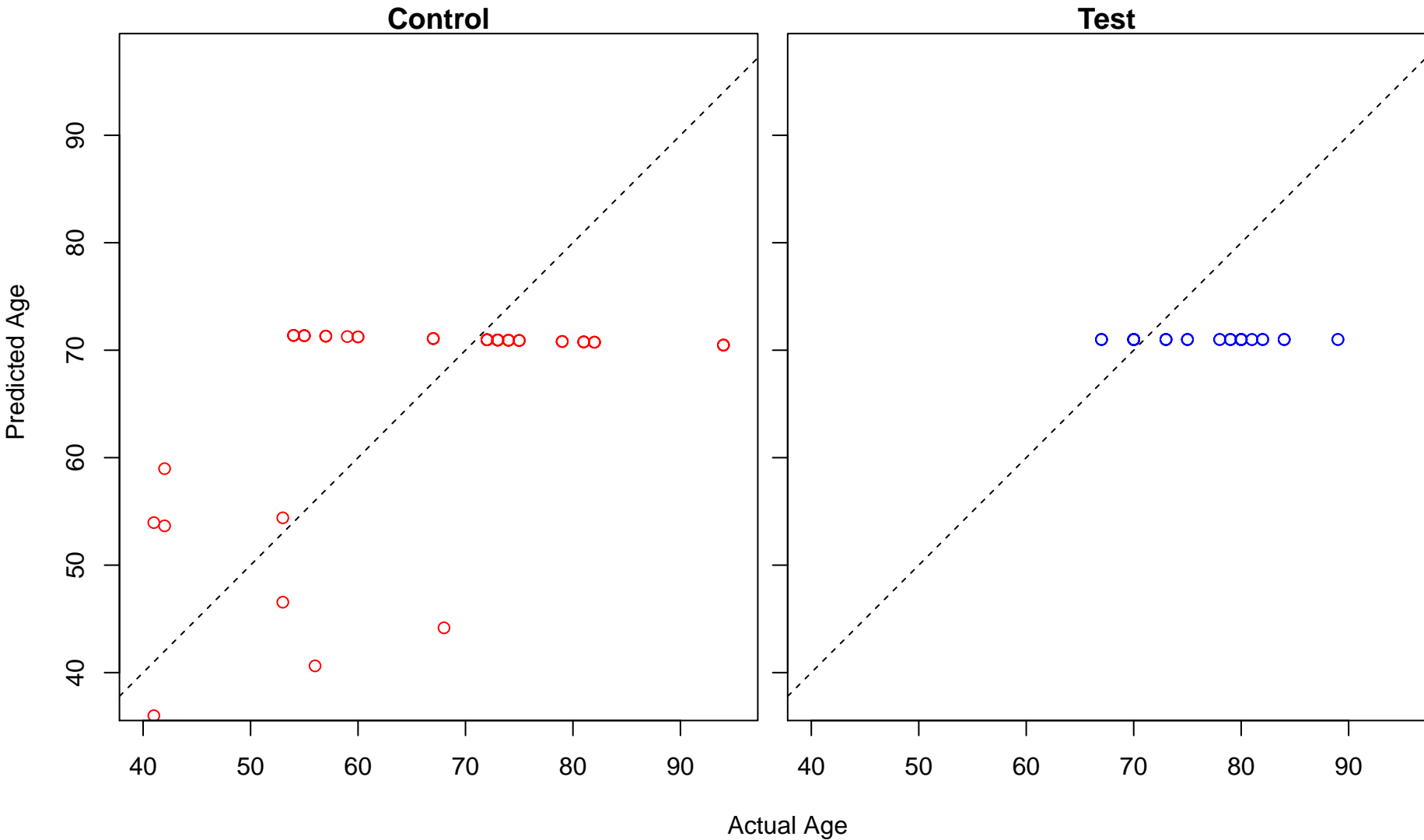
regulation of cyclic-nucleotide phosphodiesterase activity (Score: 0.776661)



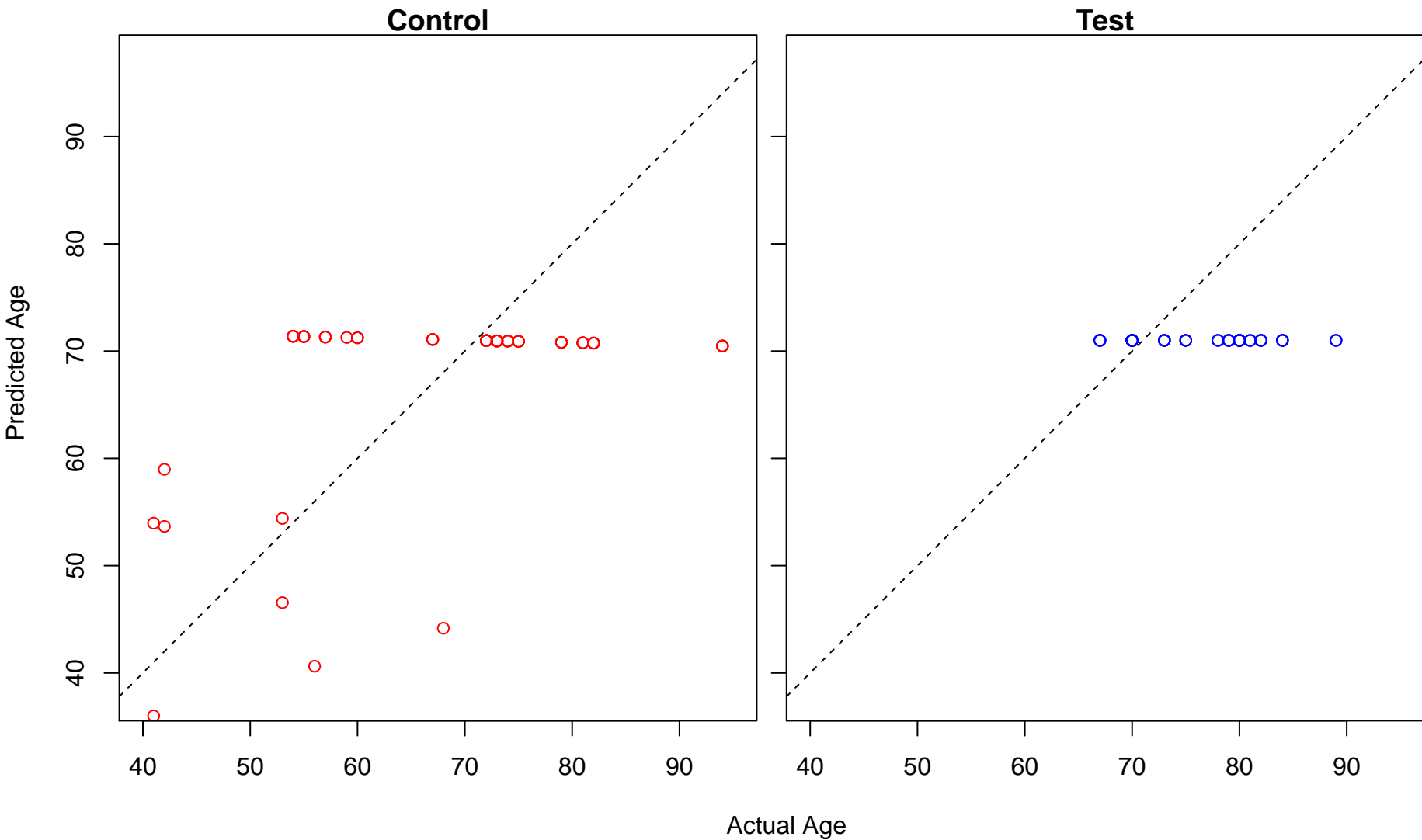
positive regulation of cyclic-nucleotide phosphodiesterase activity (Score: 0.776661)



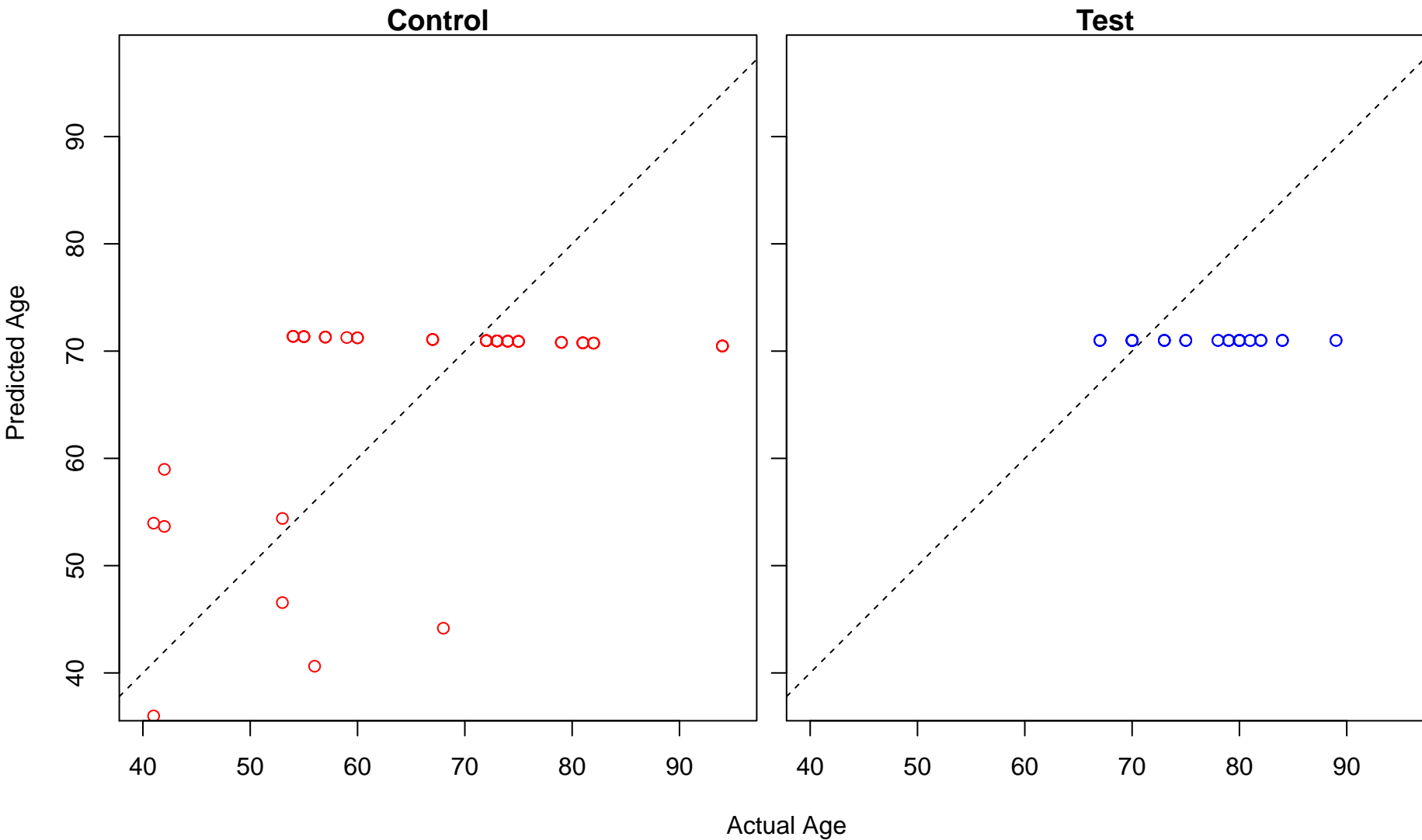
negative regulation of calcium ion transport (Score: 0.776661)



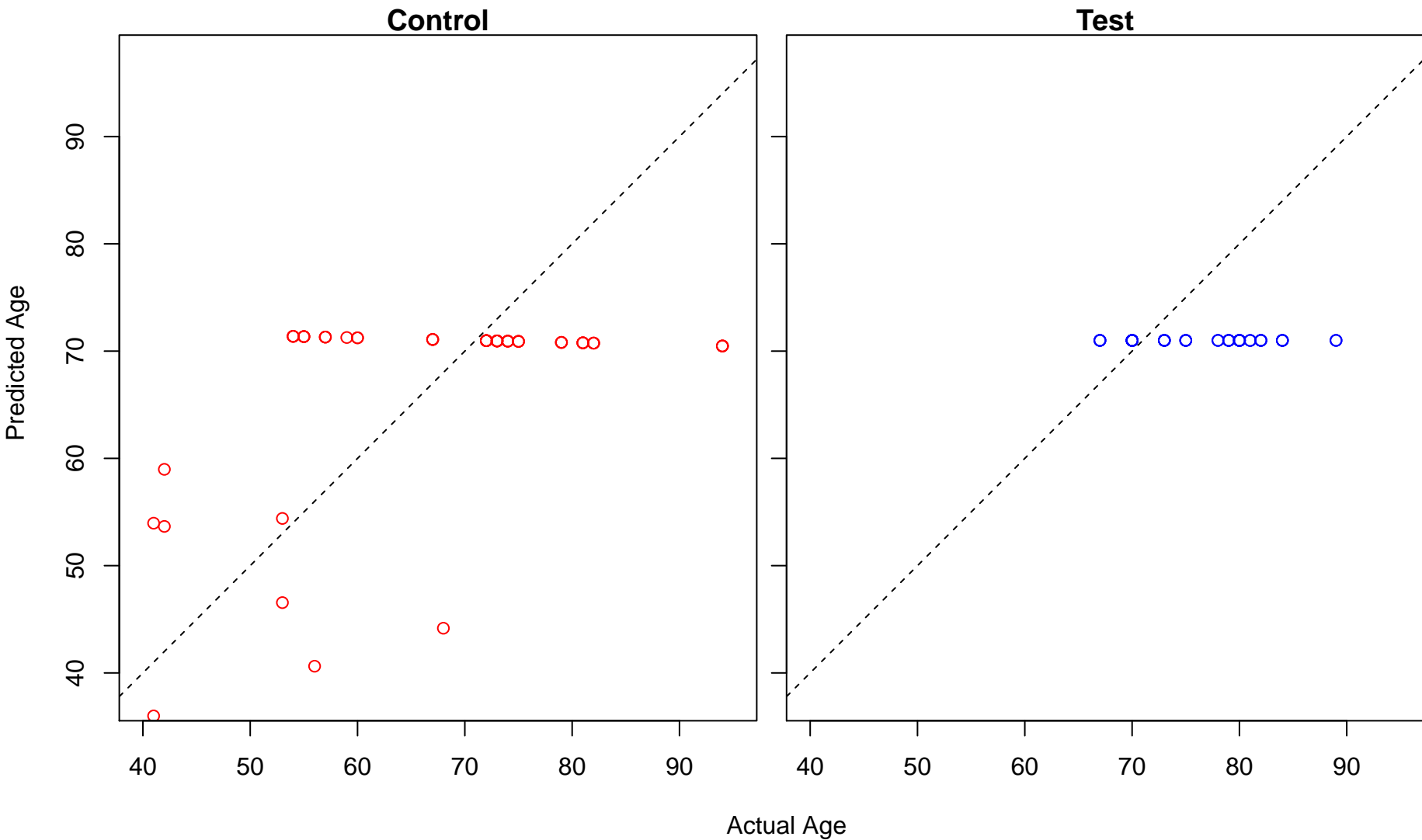
negative regulation of ryanodine-sensitive calcium-release channel activity (Score: 0.776661)



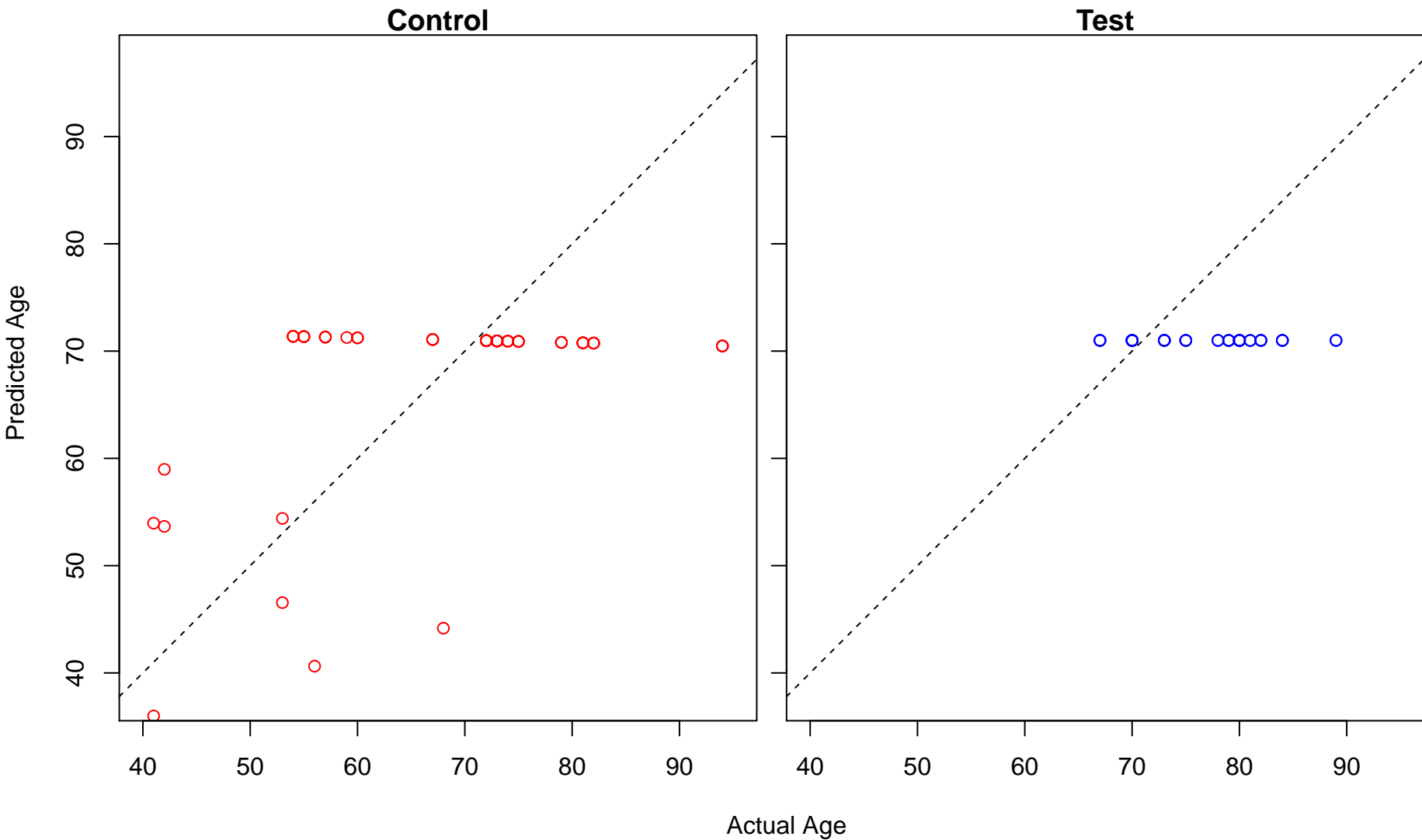
positive regulation of ryanodine-sensitive calcium-release channel activity (Score: 0.776661)



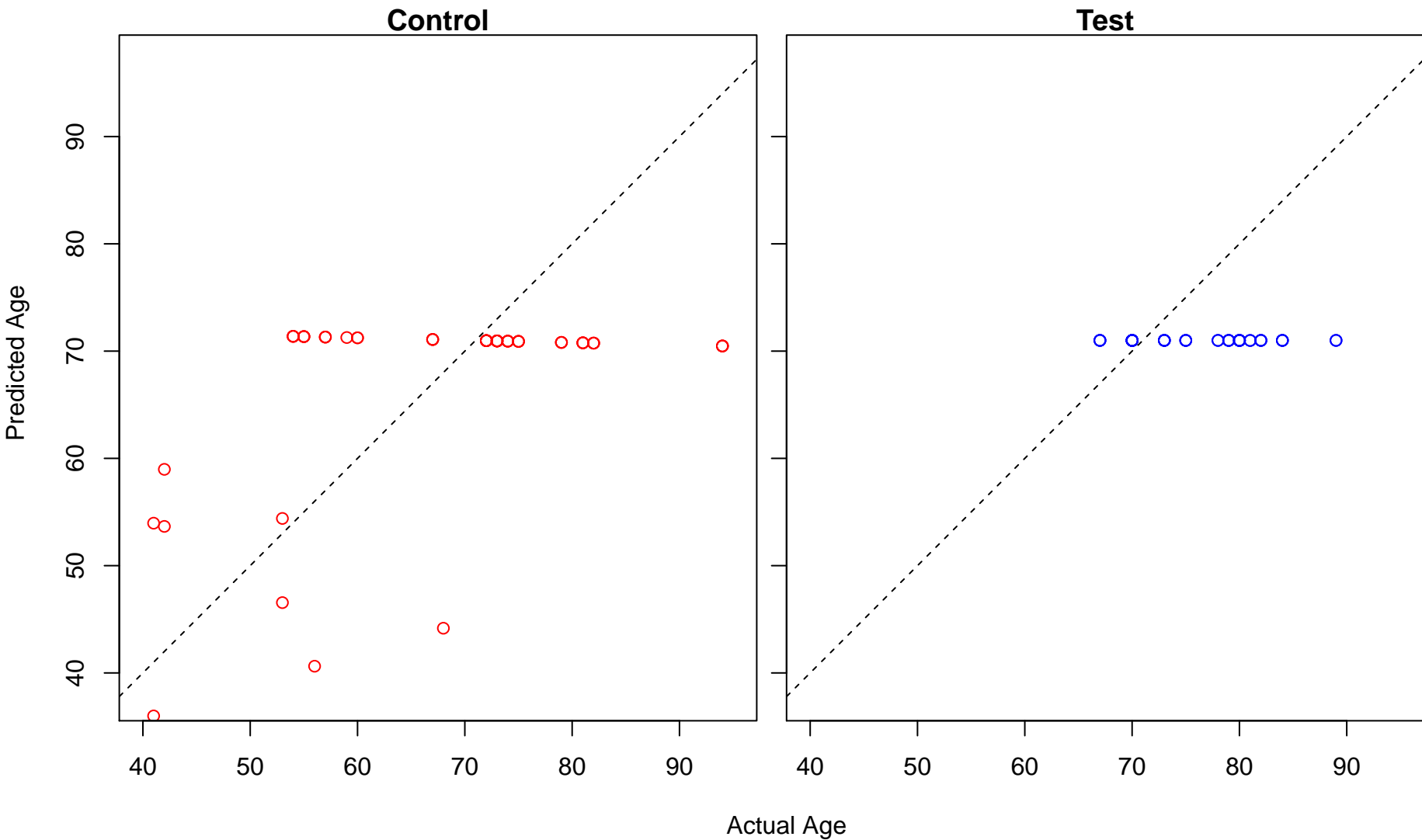
negative regulation of calcium ion transmembrane transporter activity (Score: 0.776661)



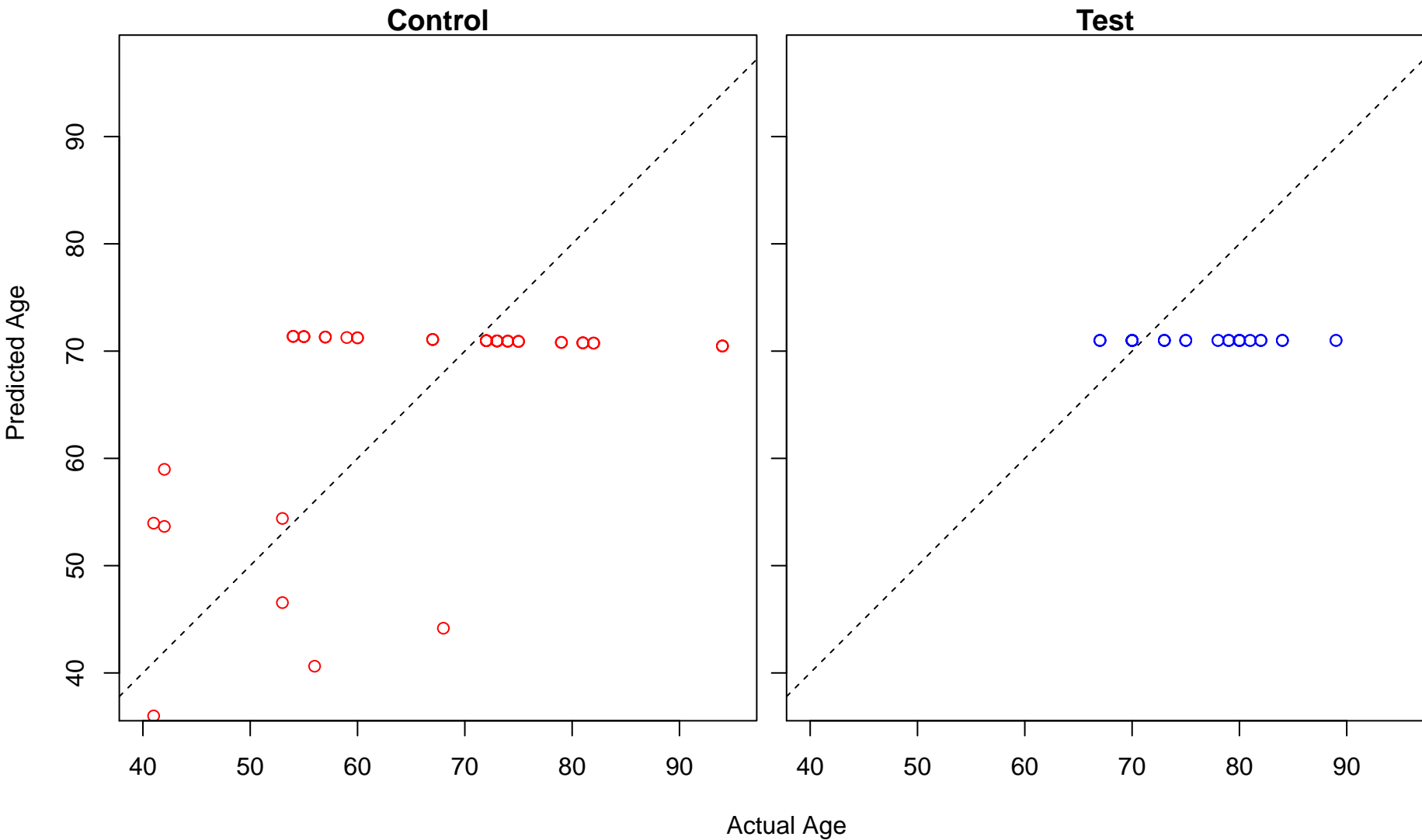
positive regulation of calcium ion transmembrane transporter activity (Score: 0.776661)



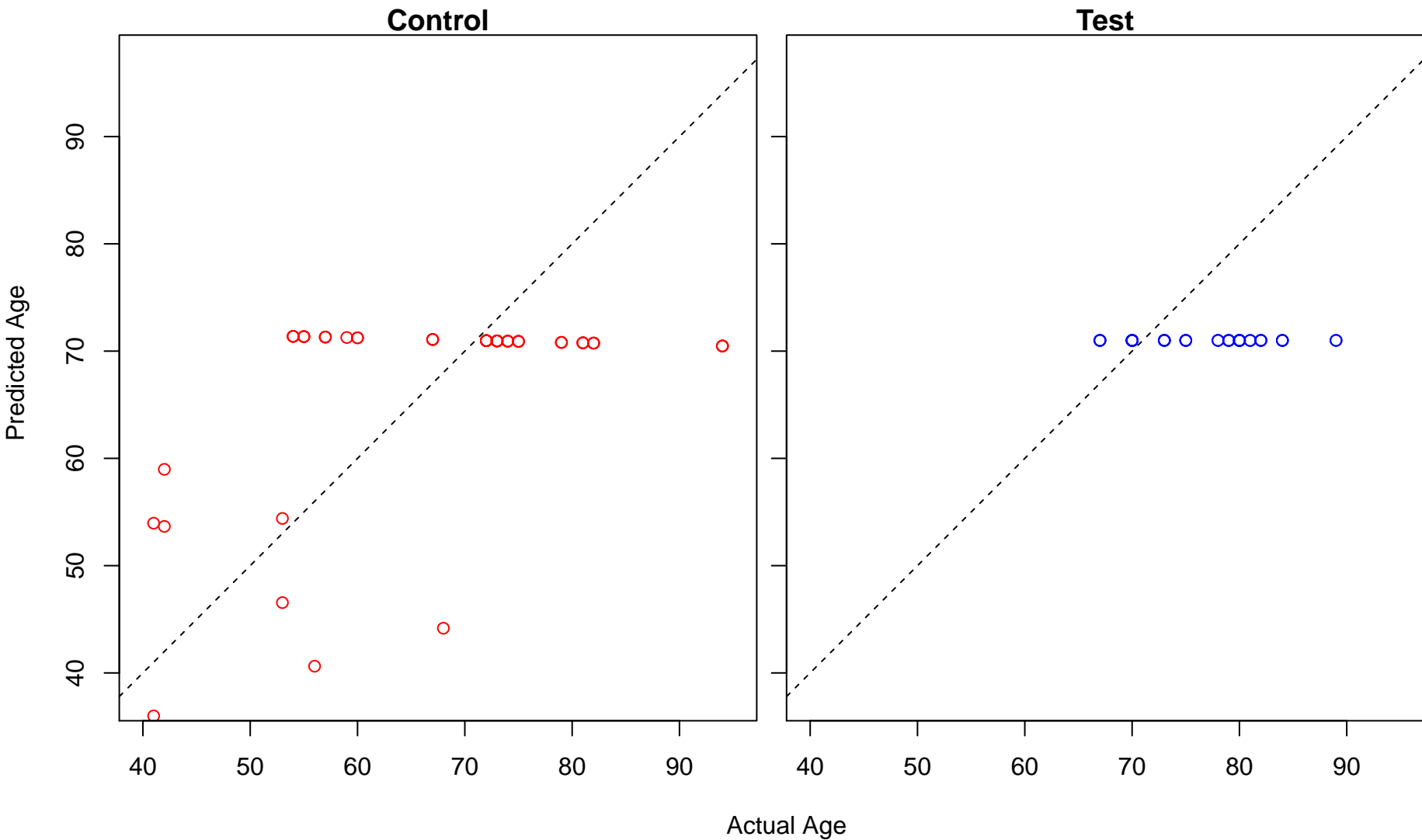
negative regulation of calcium ion transmembrane transport (Score: 0.776661)



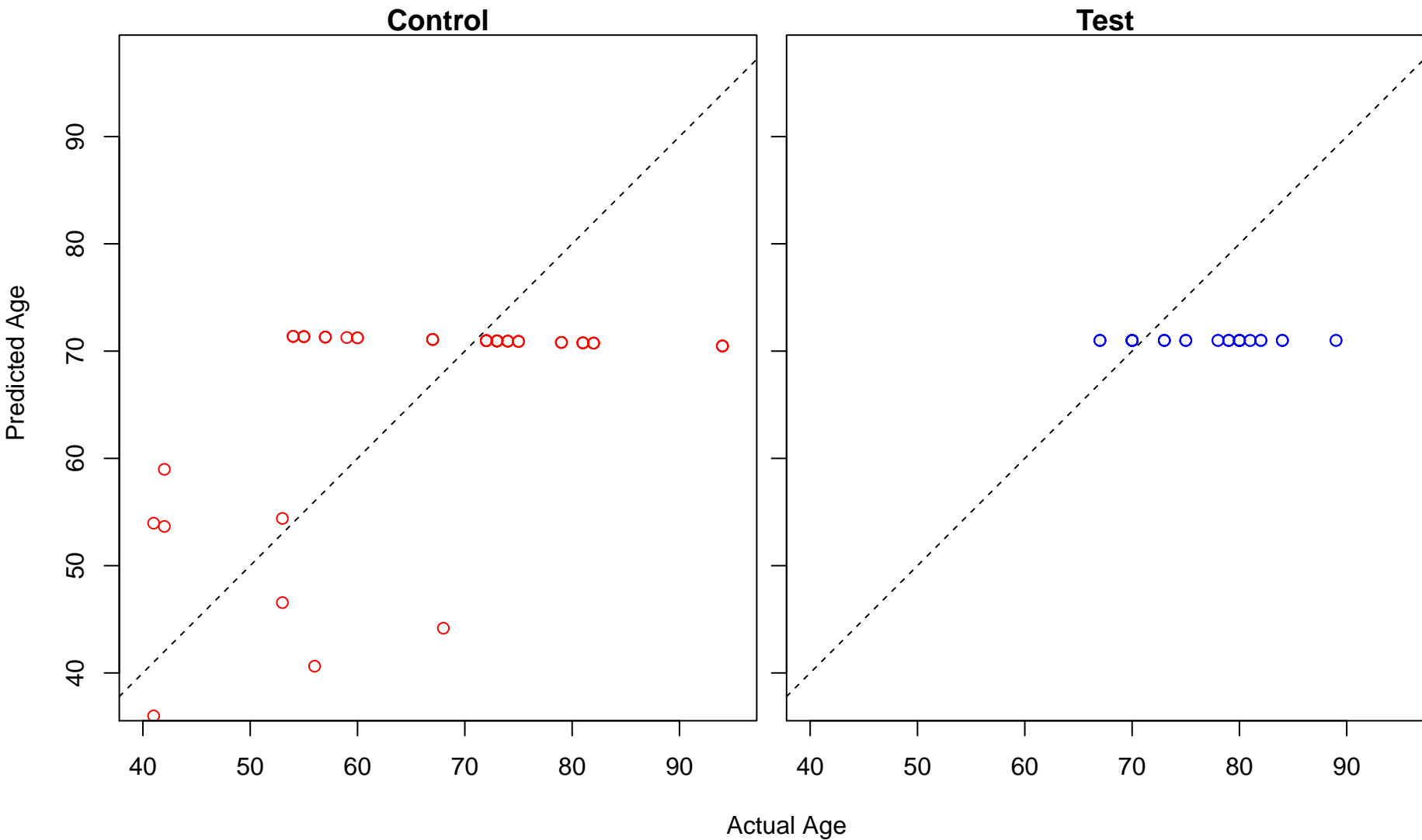
negative regulation of cation transmembrane transport (Score: 0.776661)



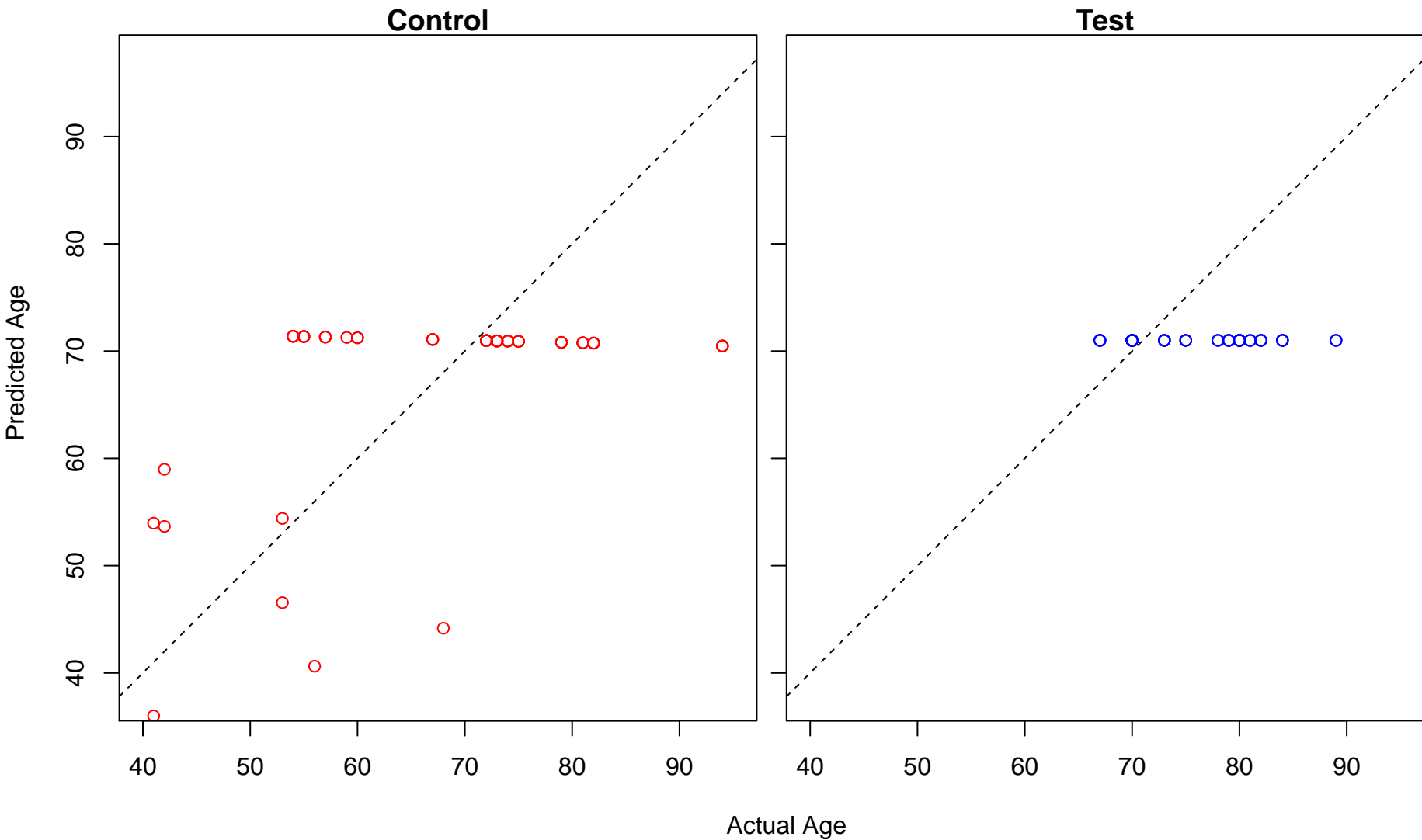
positive regulation of cation transmembrane transport (Score: 0.776661)



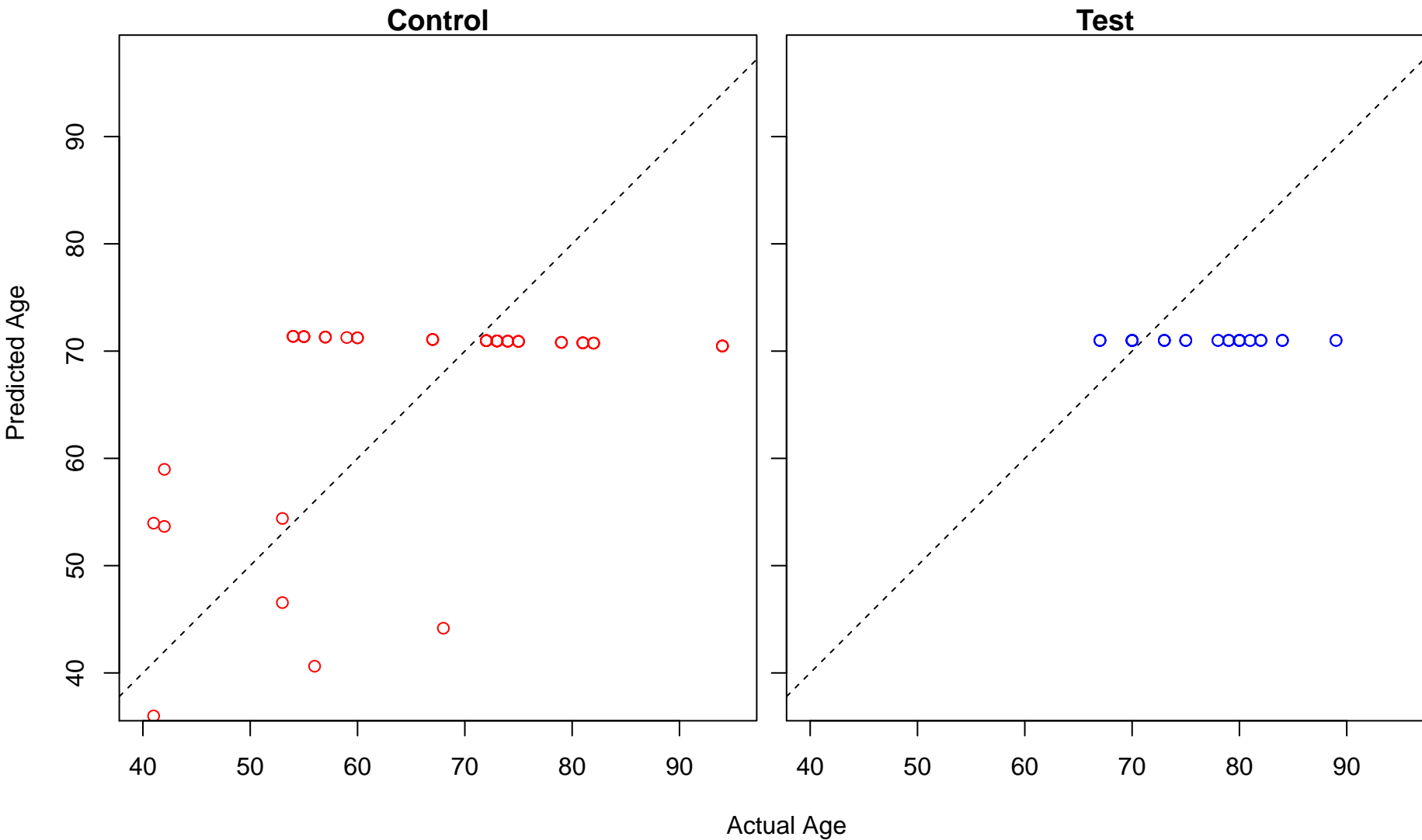
positive regulation of calcium ion transmembrane transport (Score: 0.776661)



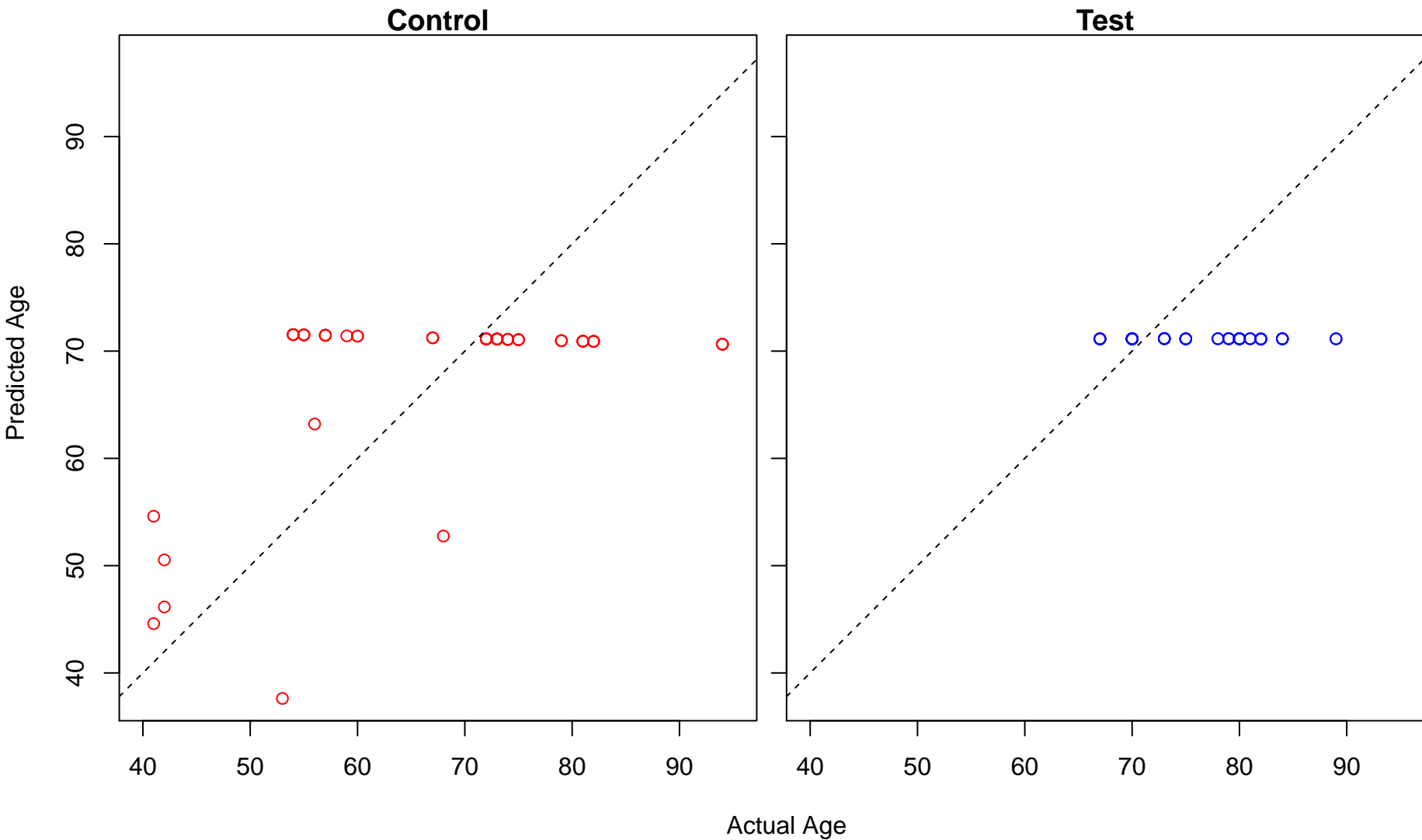
negative regulation of cation channel activity (Score: 0.776661)



positive regulation of cation channel activity (Score: 0.776661)

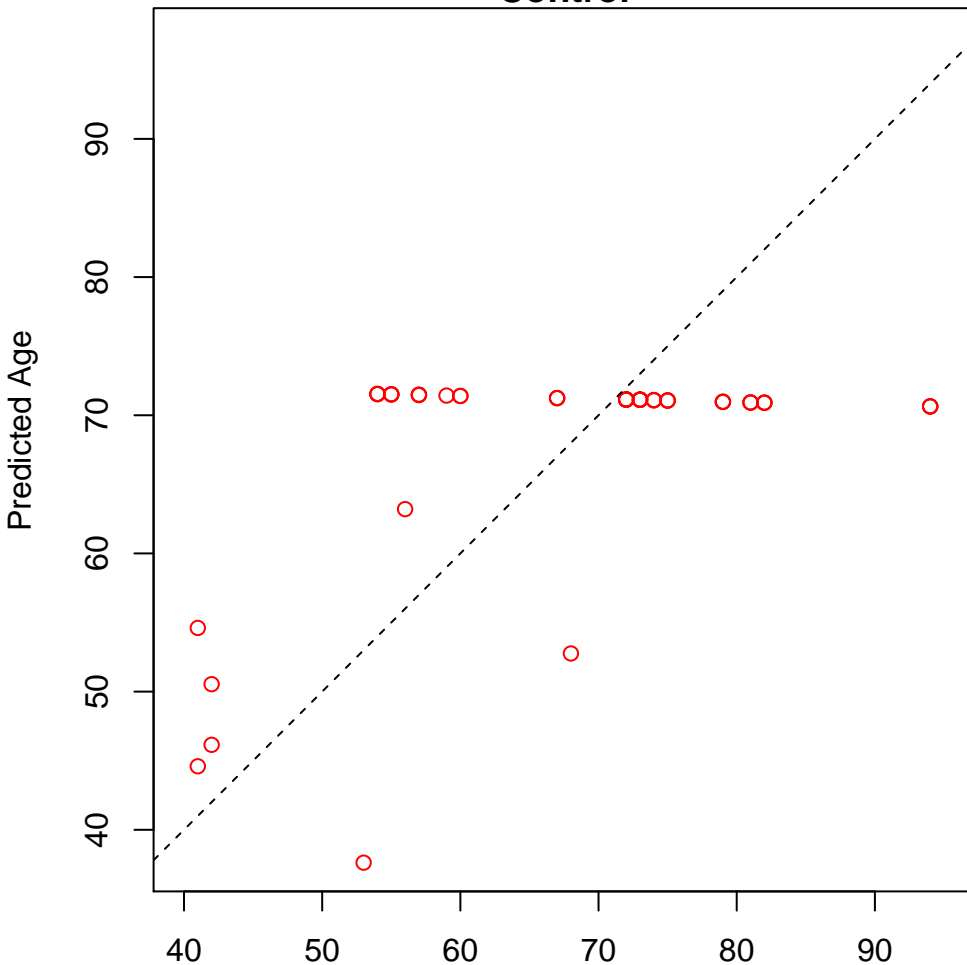


regulation of angiogenesis (Score: 0.776618)

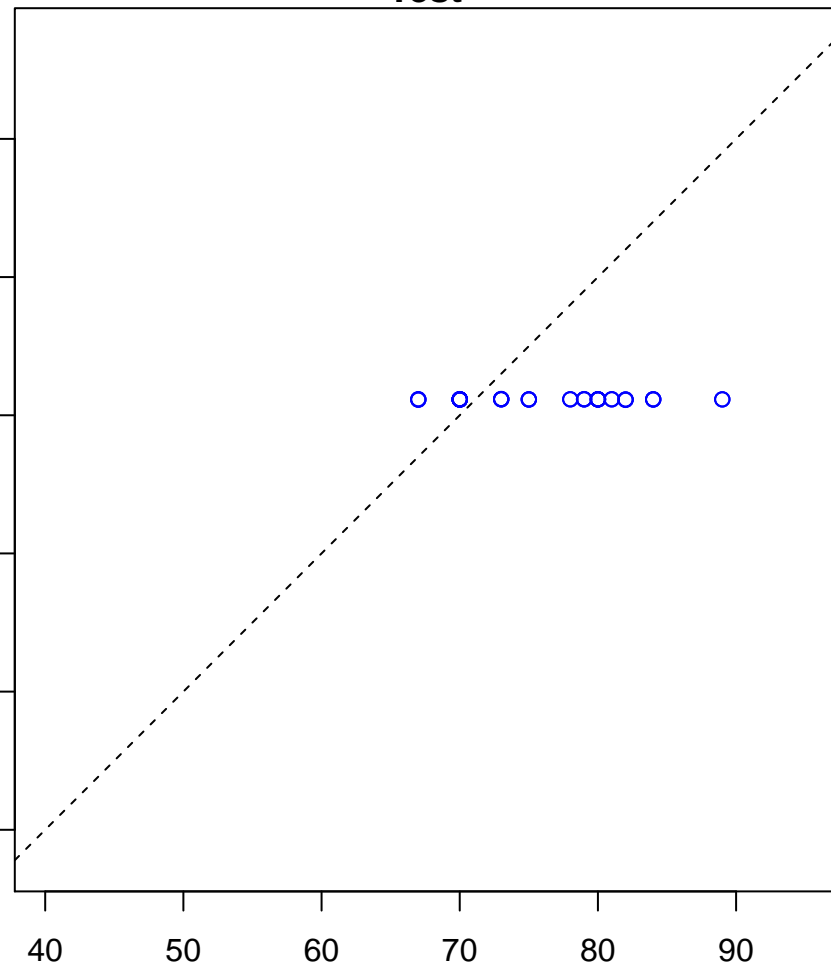


regulation of vasculature development (Score: 0.776618)

Control



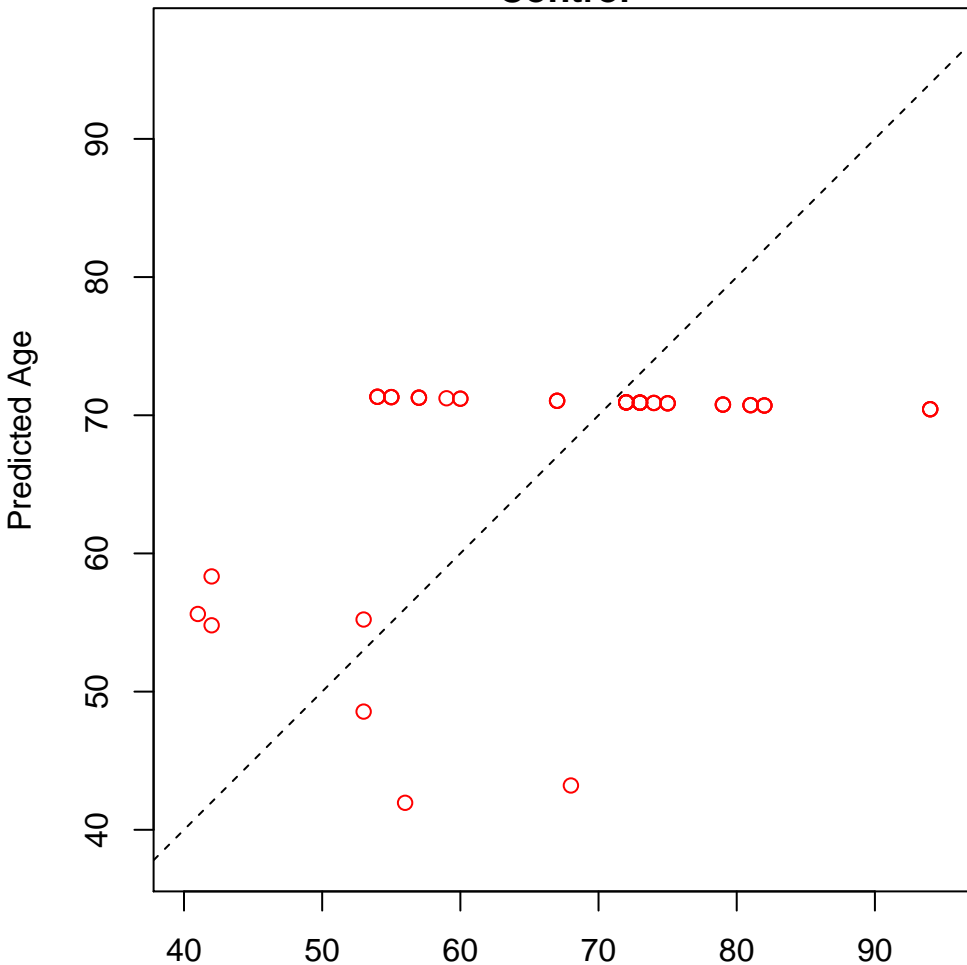
Test



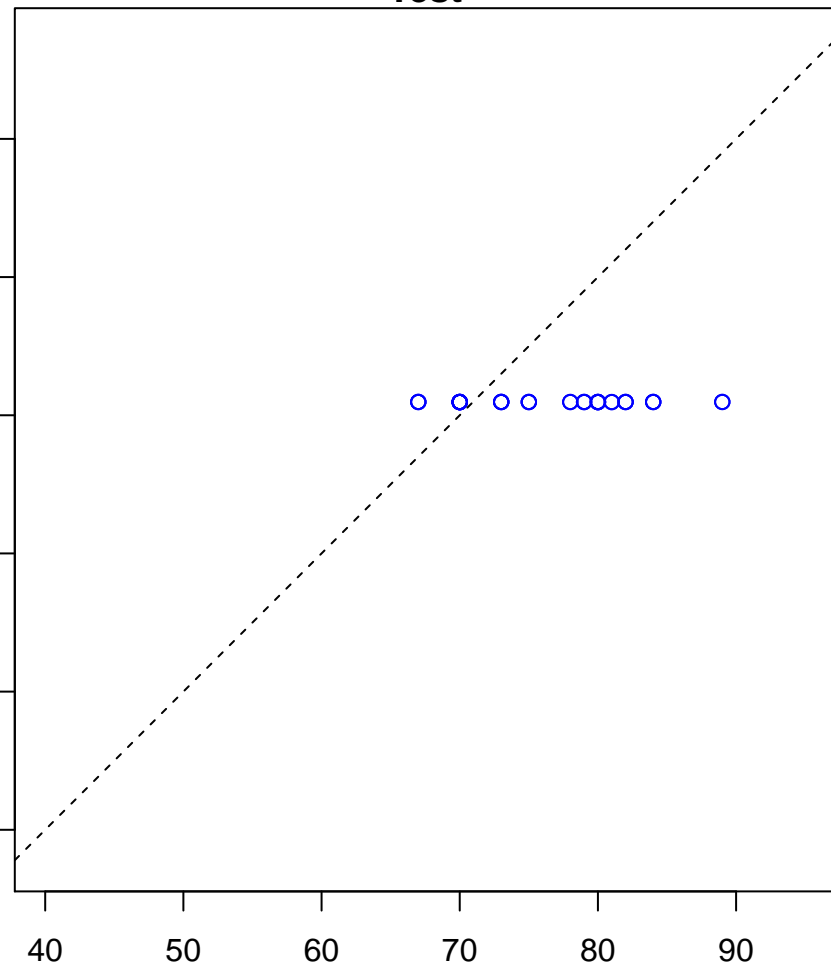
Actual Age

regulation of calcium ion transport (Score: 0.776042)

Control

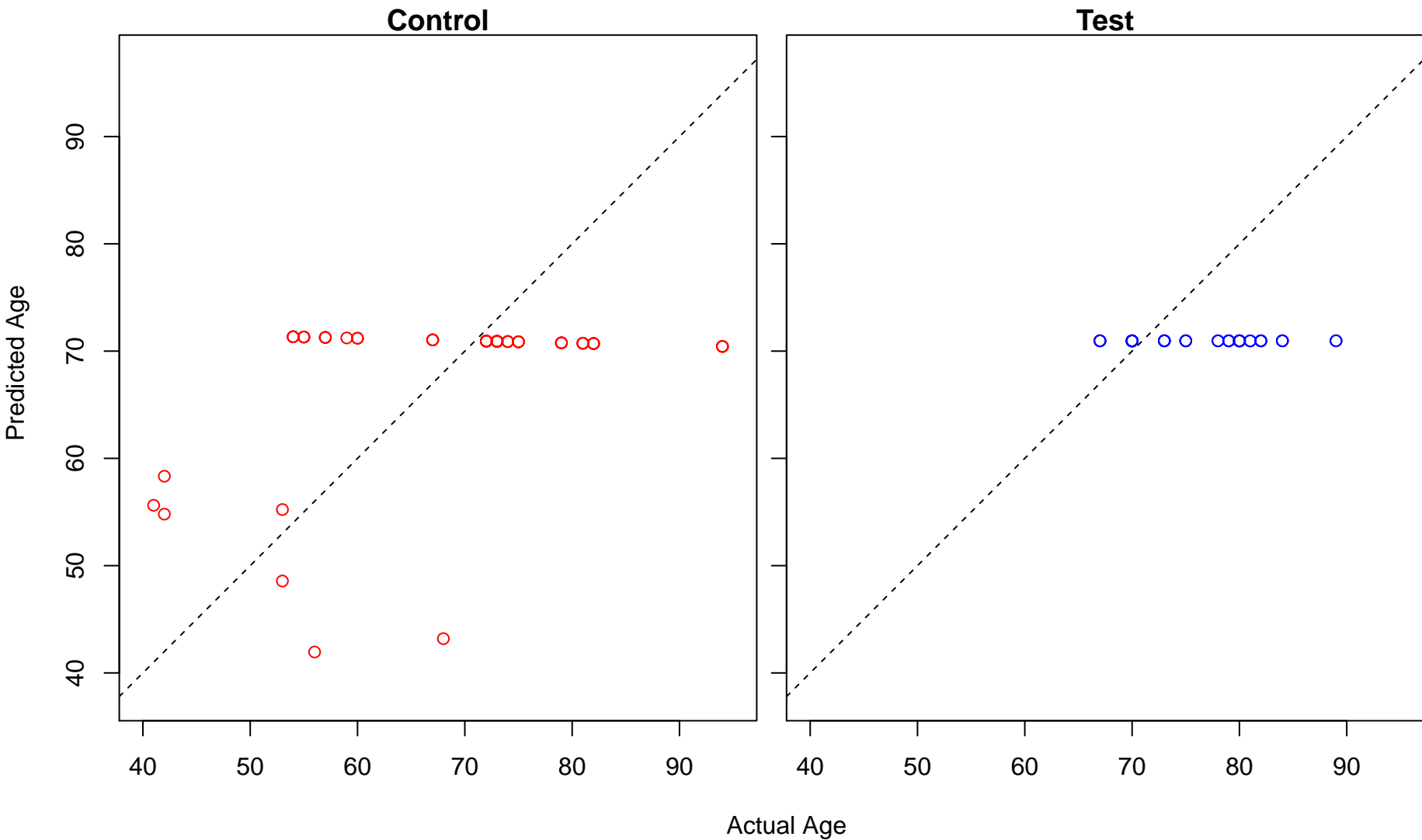


Test



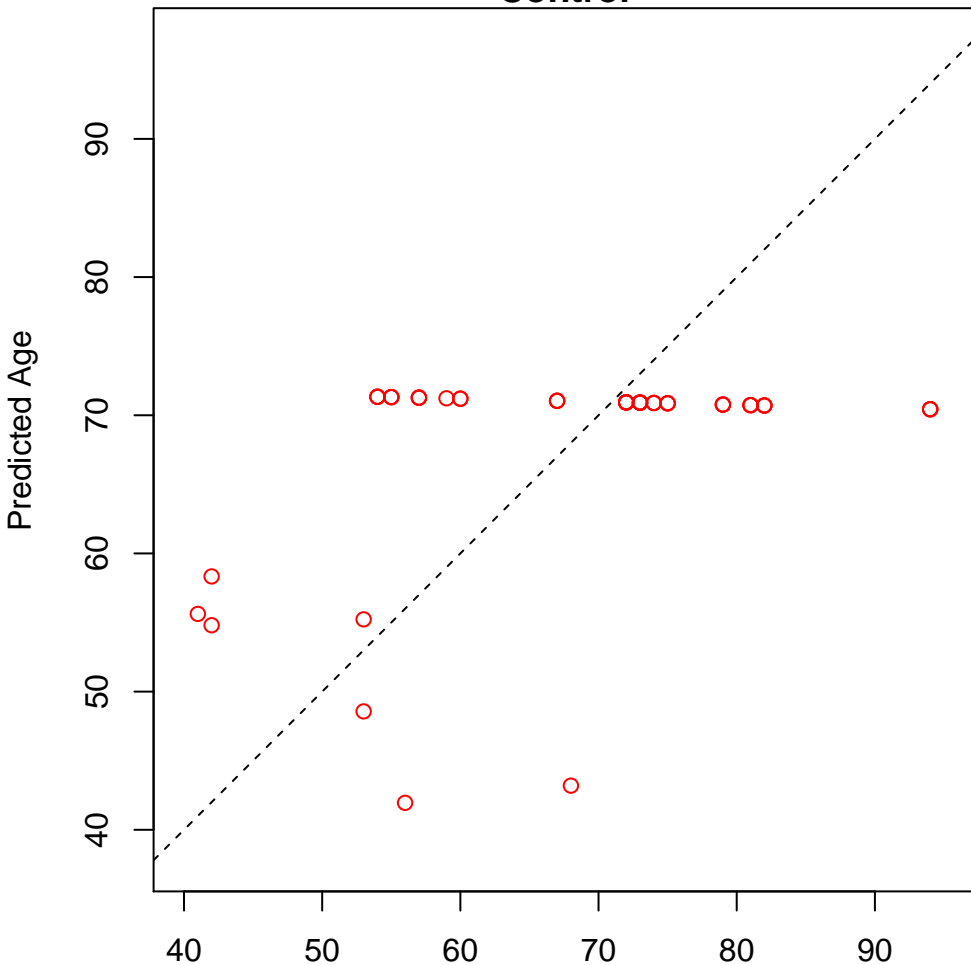
Actual Age

regulation of calcium ion transport into cytosol (Score: 0.775992)

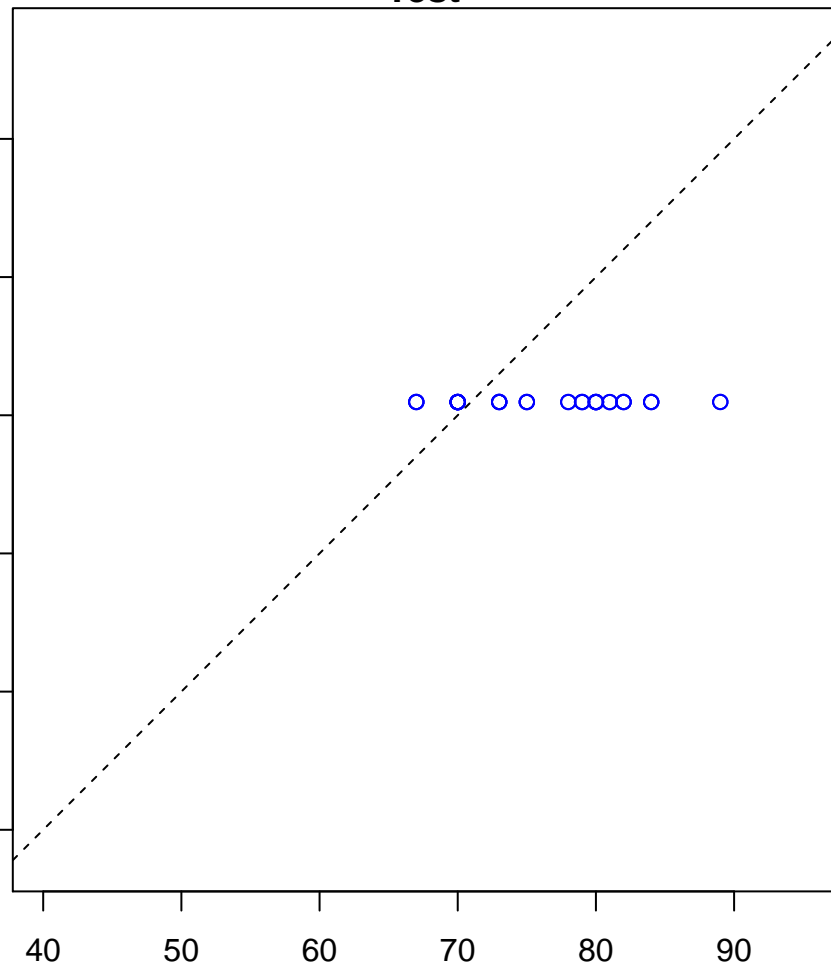


regulation of calcium-mediated signaling (Score: 0.775992)

Control

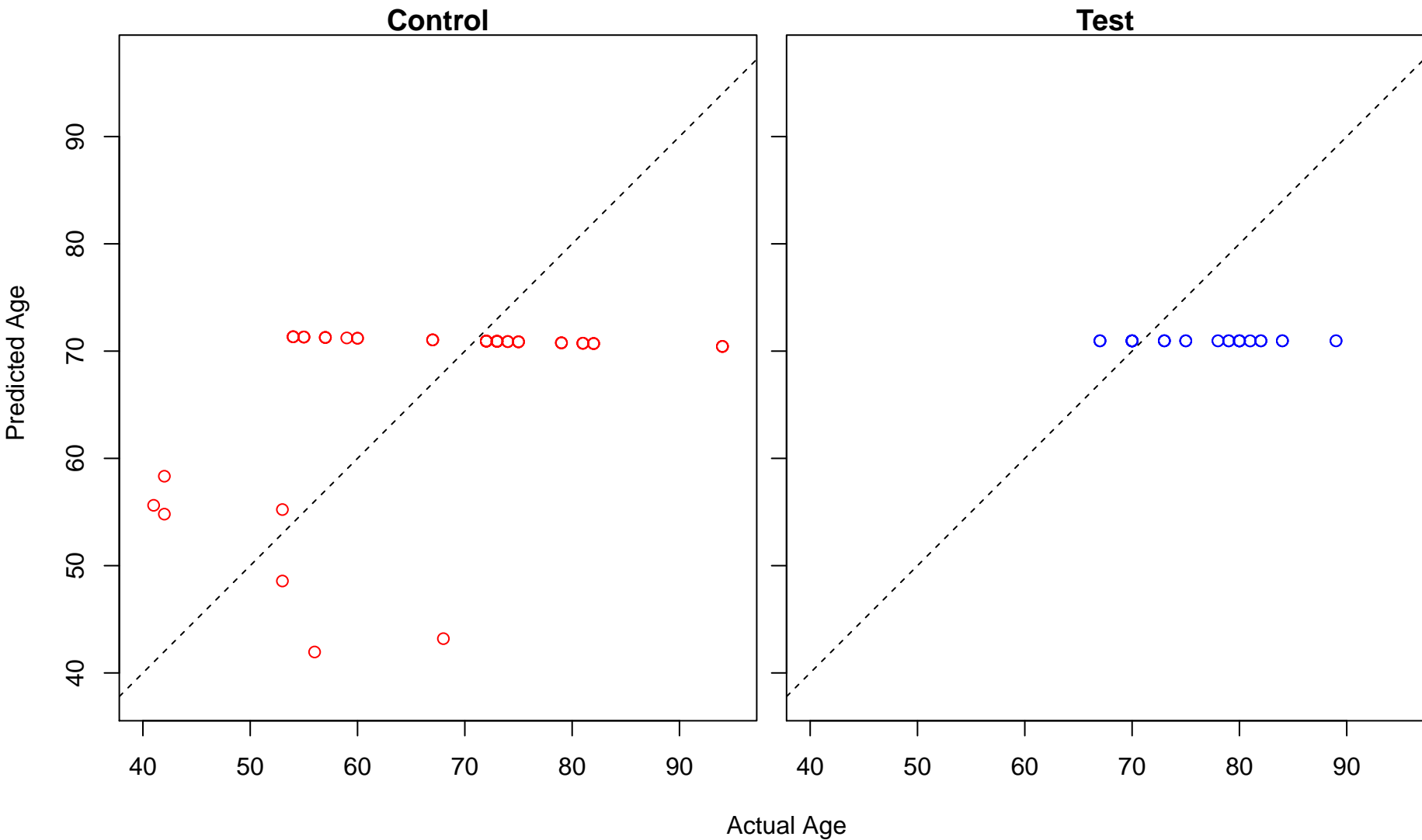


Test



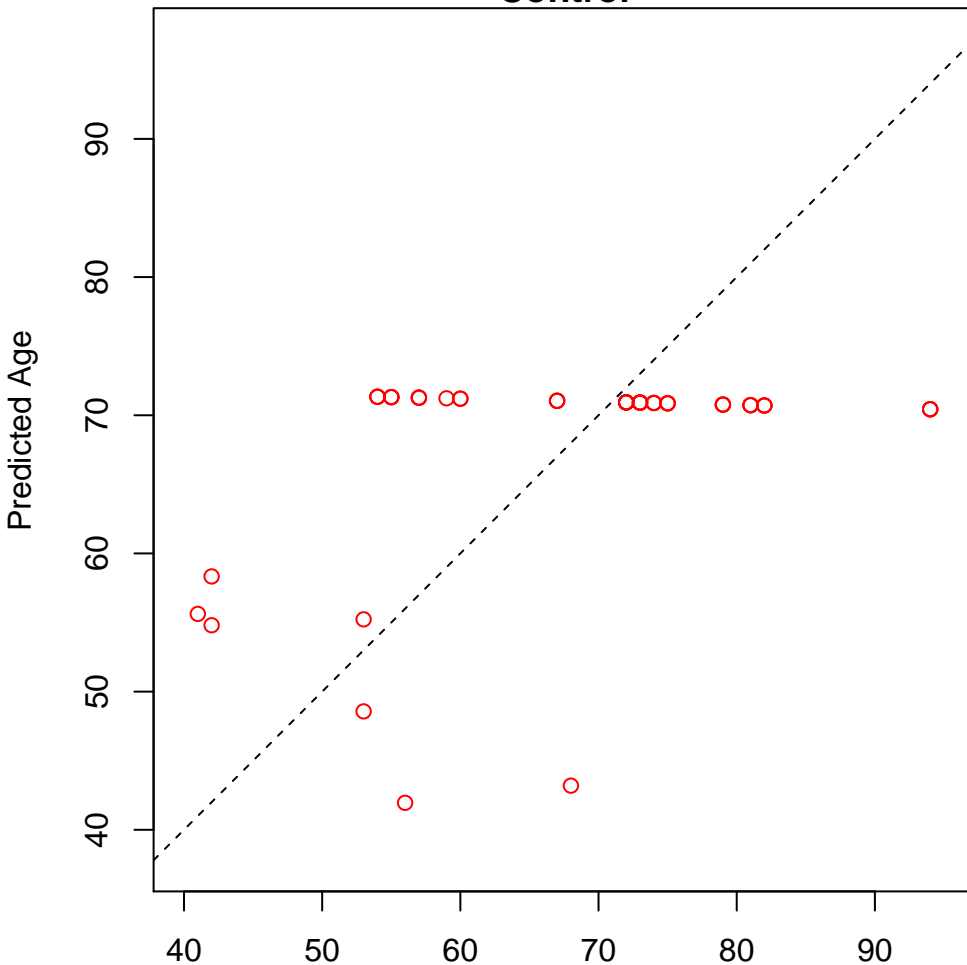
Actual Age

regulation of release of sequestered calcium ion into cytosol (Score: 0.775992)

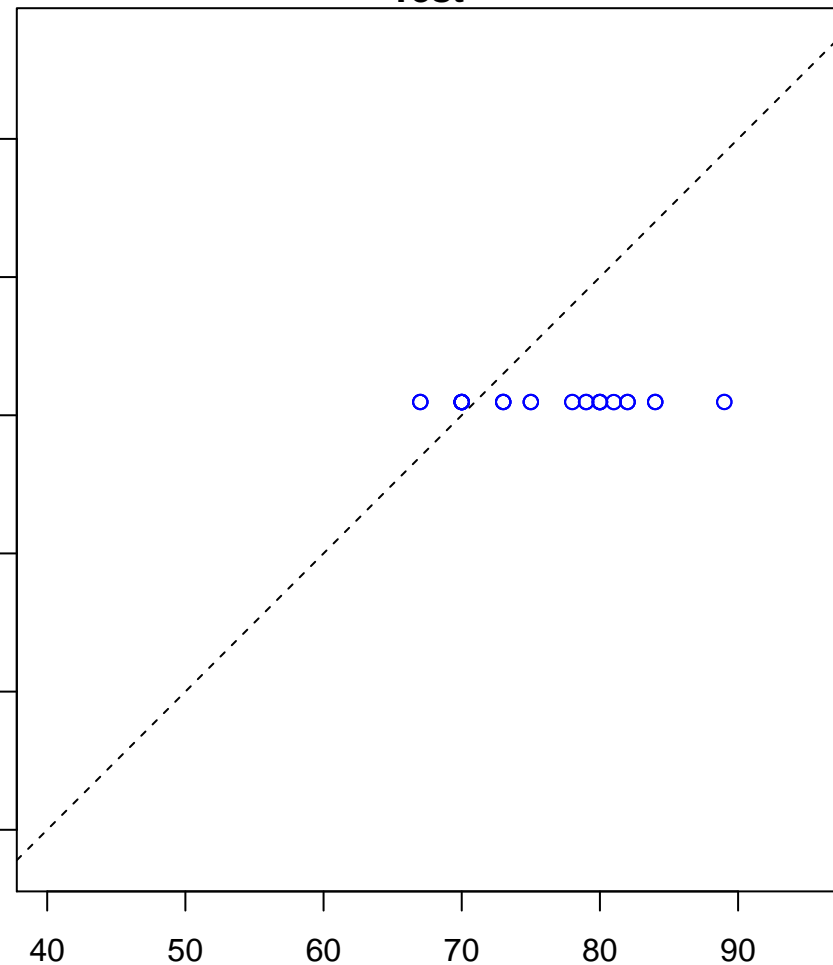


regulation of sequestering of calcium ion (Score: 0.775992)

Control

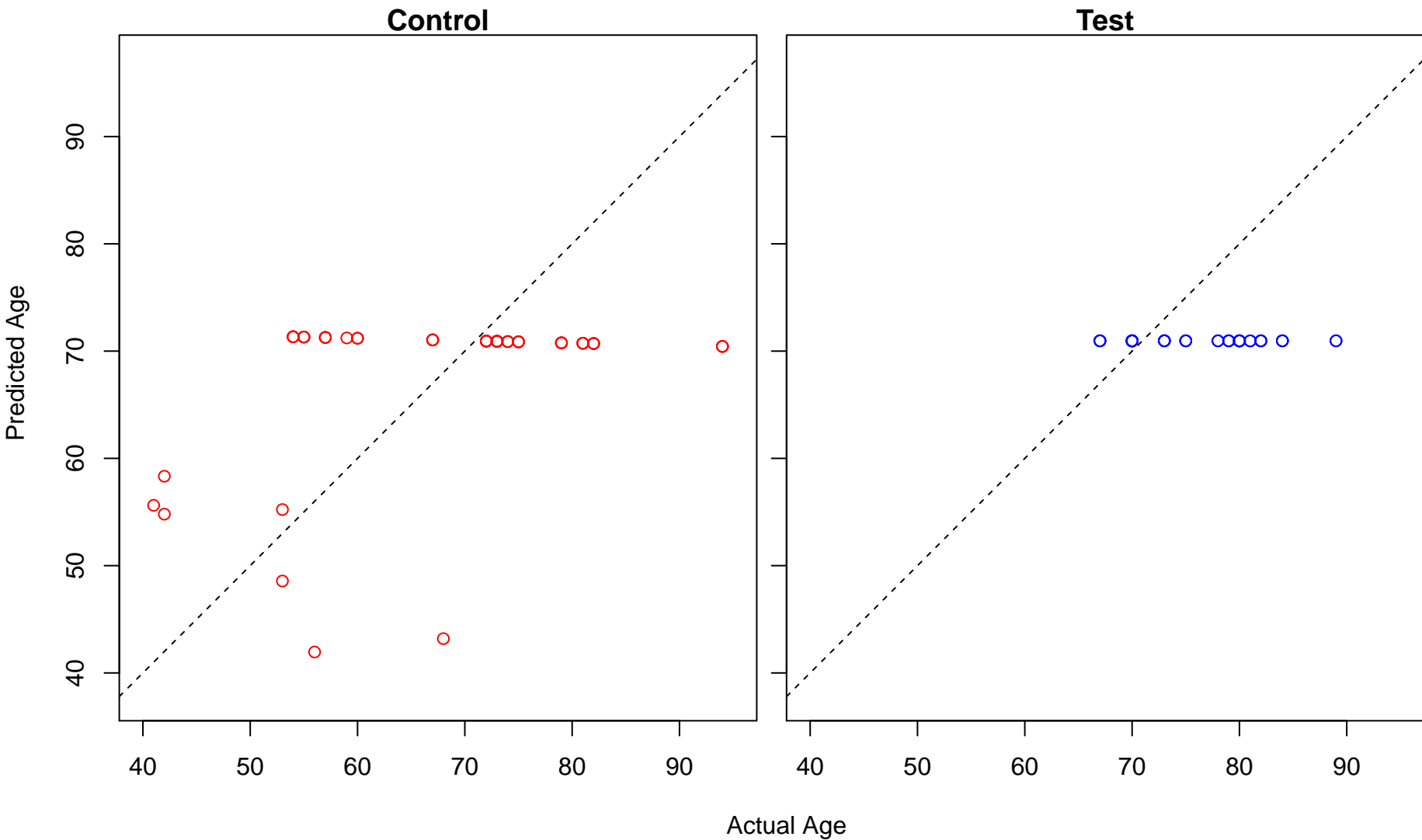


Test

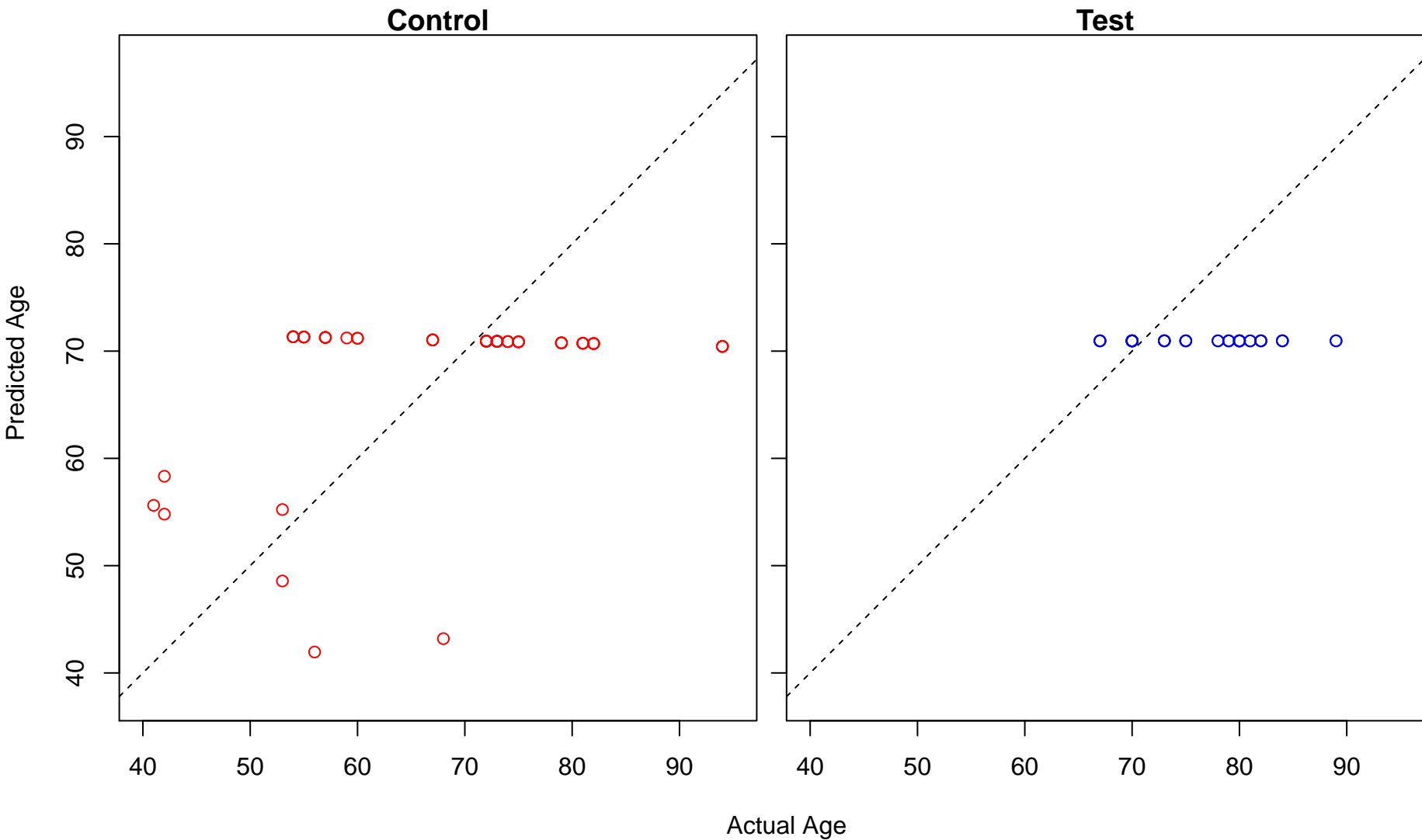


Actual Age

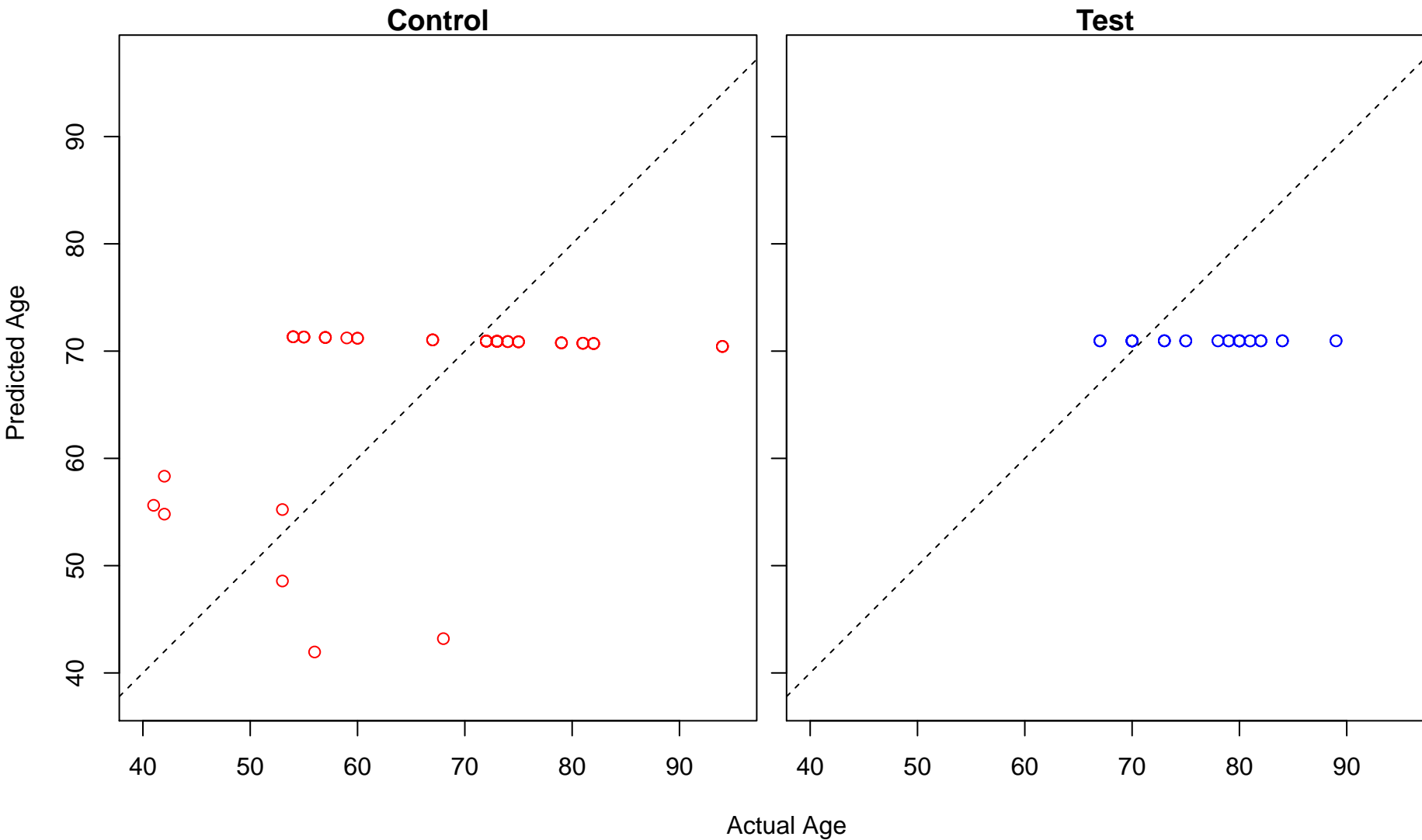
regulation of ryanodine-sensitive calcium-release channel activity (Score: 0.775992)



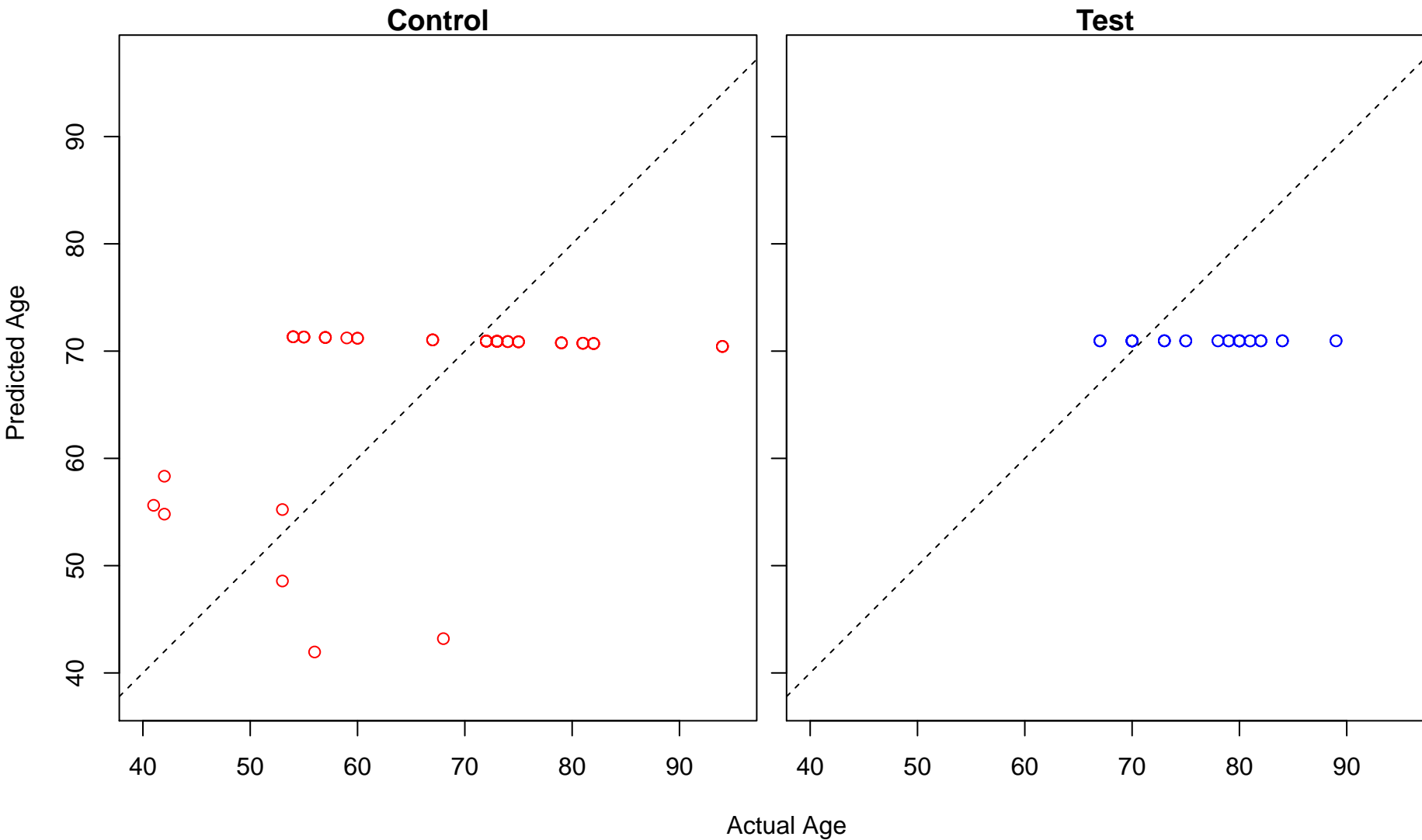
regulation of calcium ion transmembrane transporter activity (Score: 0.775992)



regulation of calcium ion transmembrane transport (Score: 0.775992)

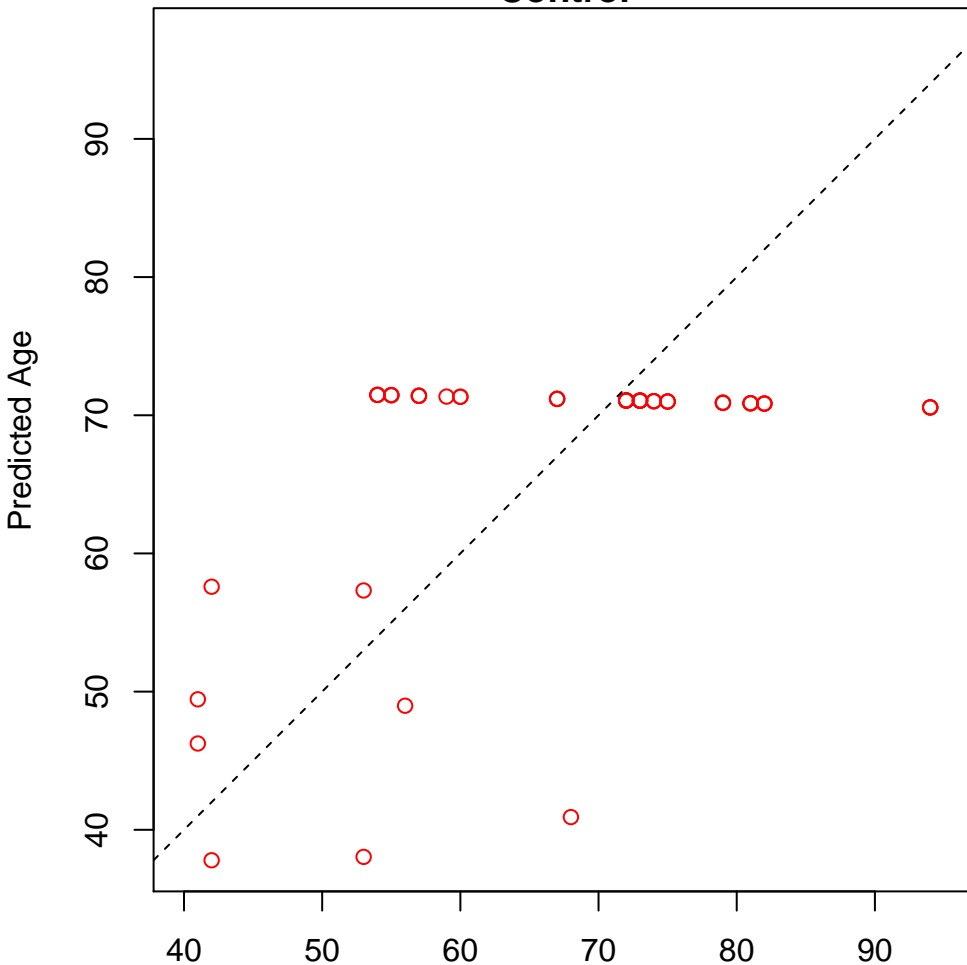


regulation of ion homeostasis (Score: 0.775992)

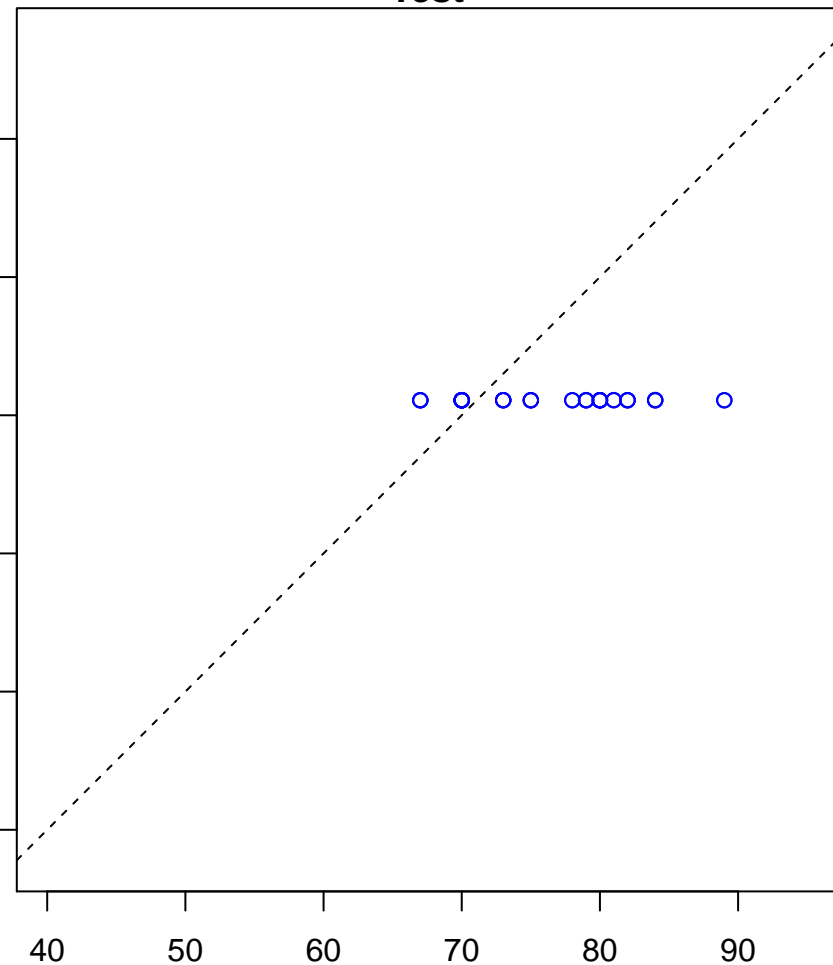


regulation of chromosome organization (Score: 0.775793)

Control

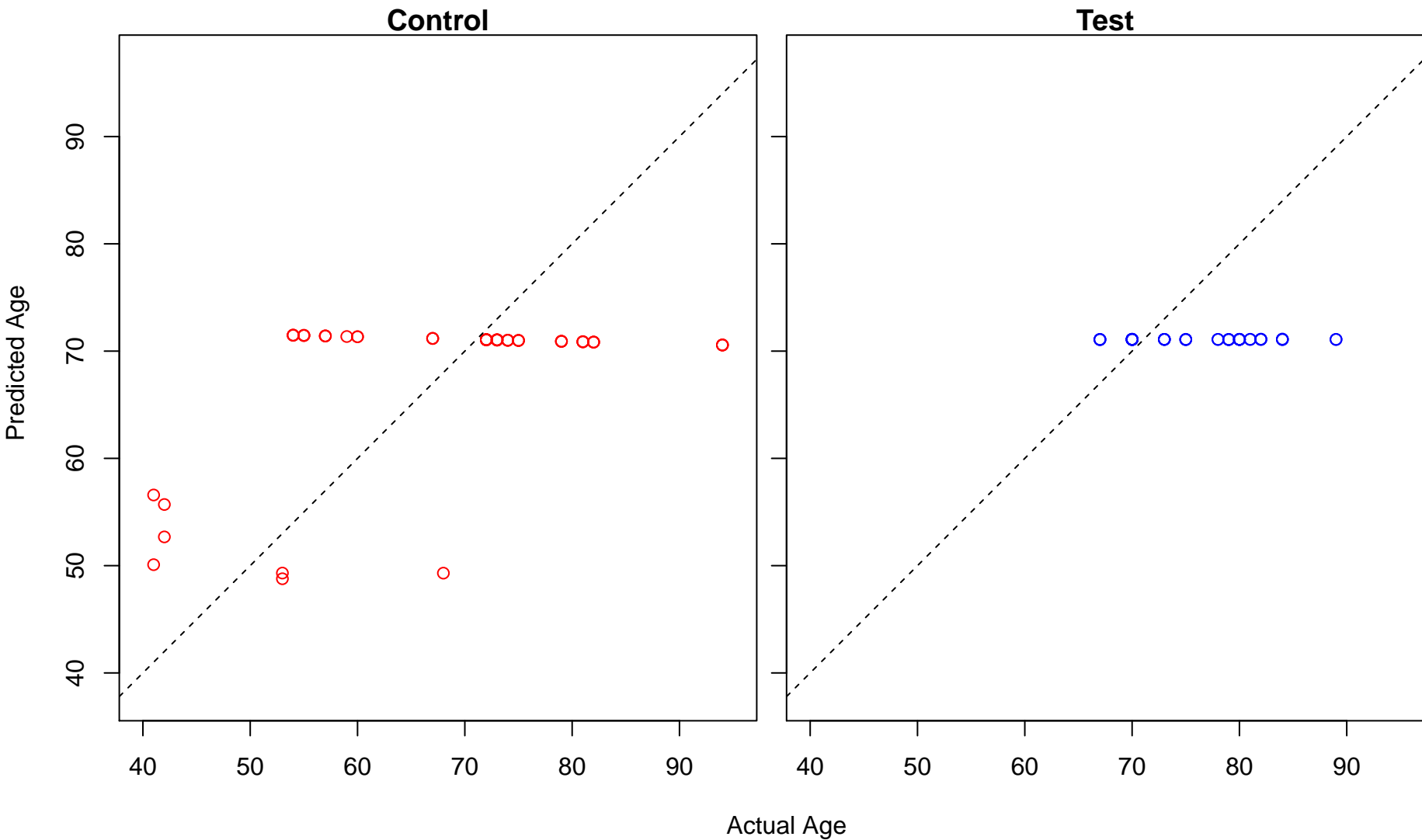


Test

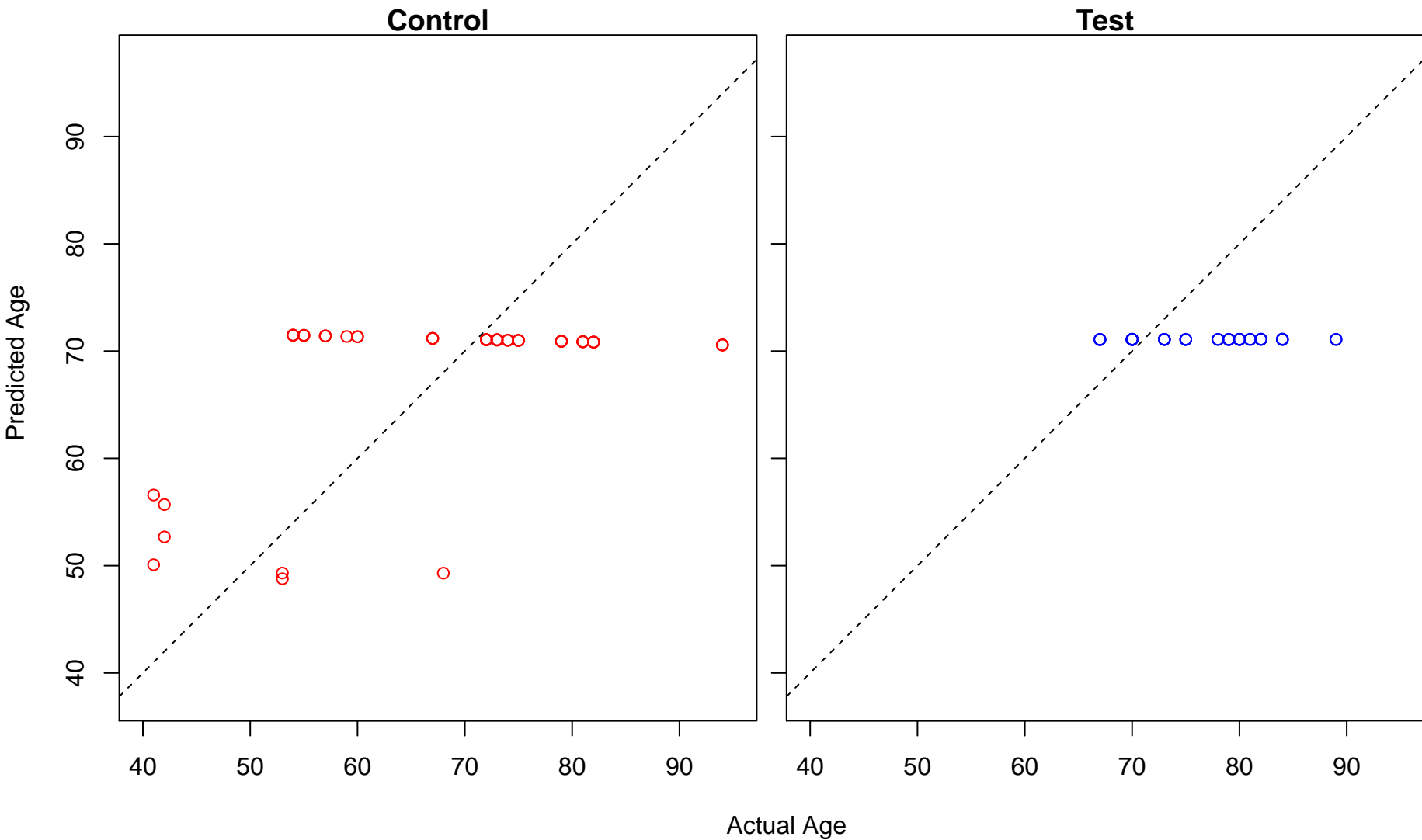


Actual Age

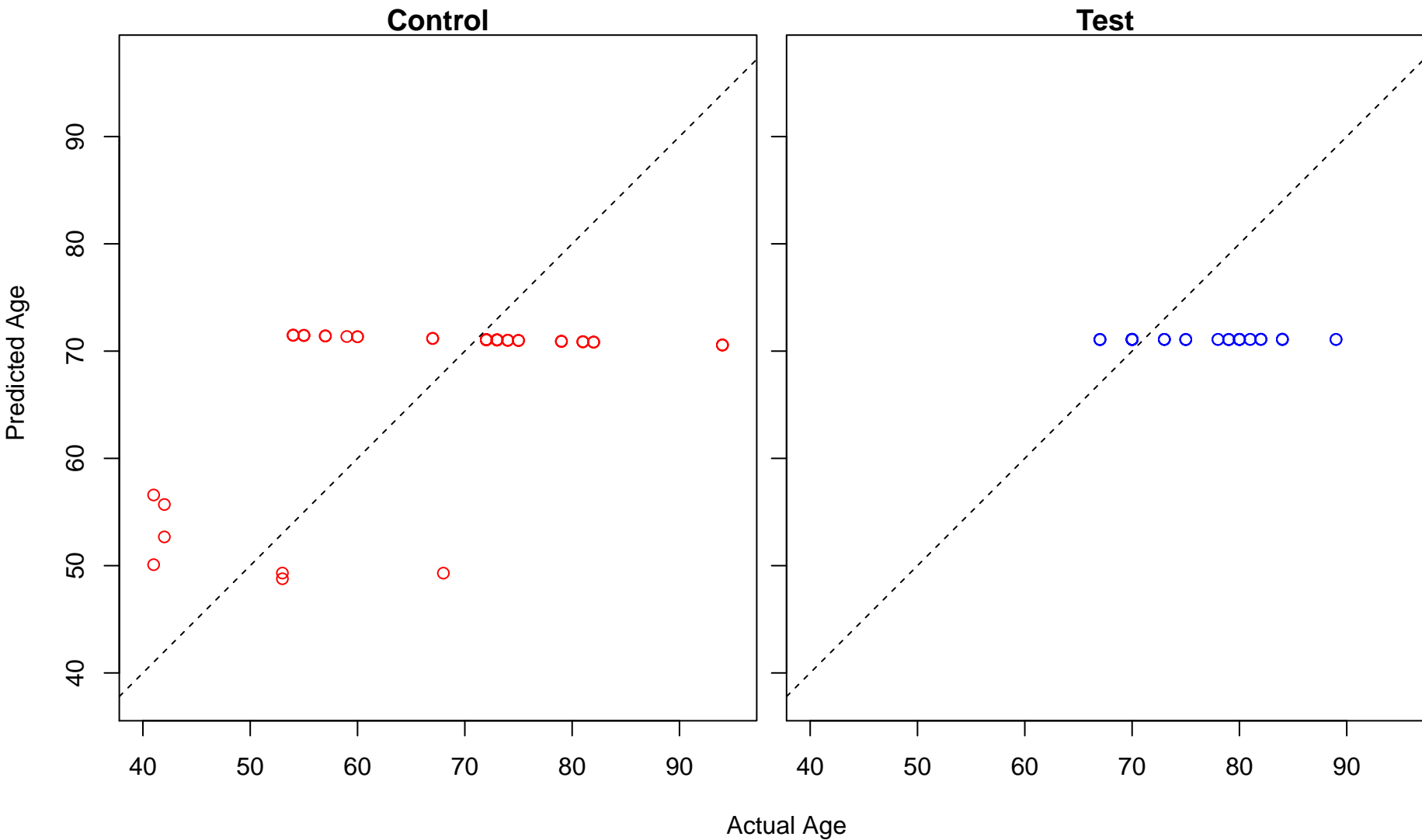
DNA packaging (Score: 0.775575)



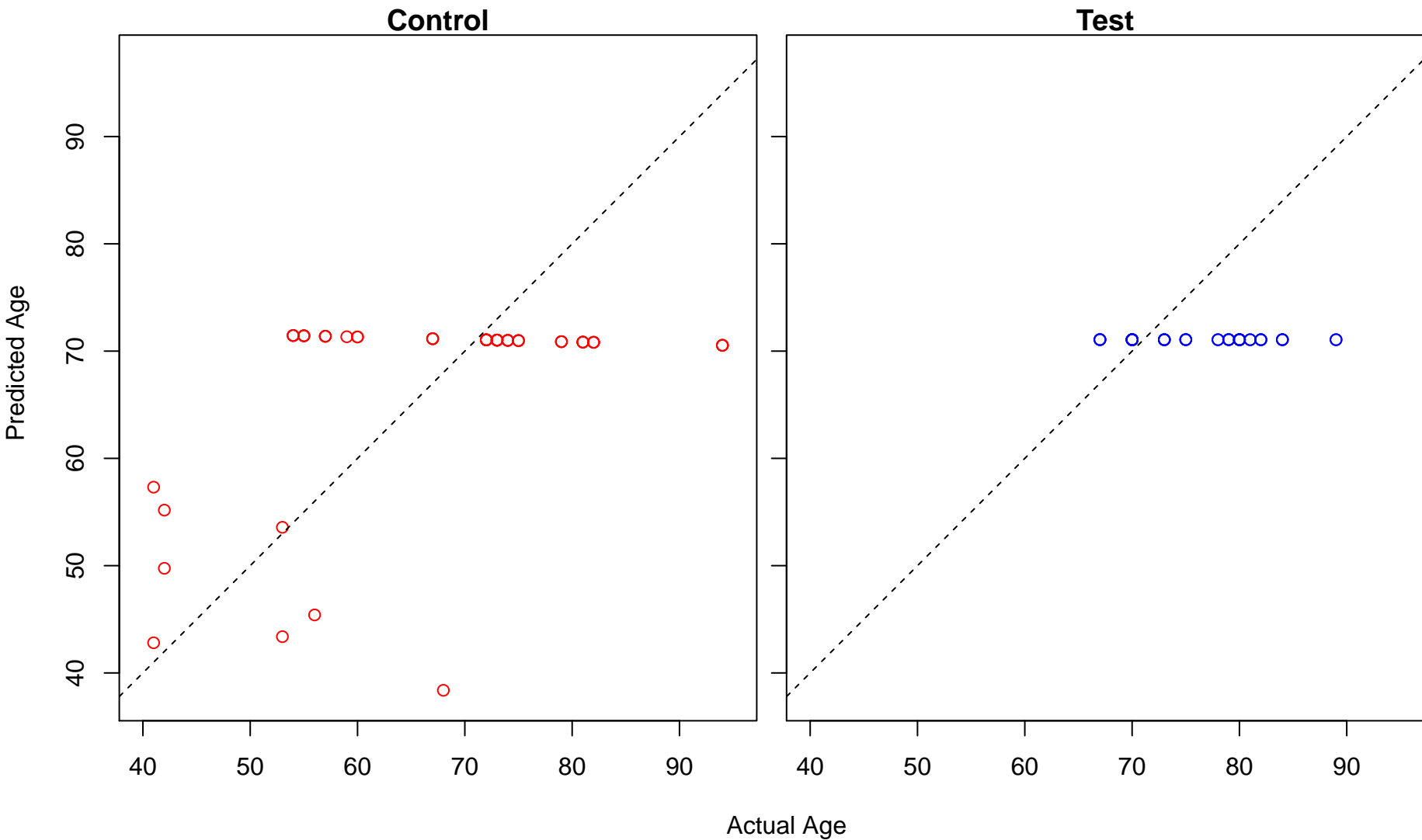
nucleosome assembly (Score: 0.775575)



chromatin assembly (Score: 0.775575)

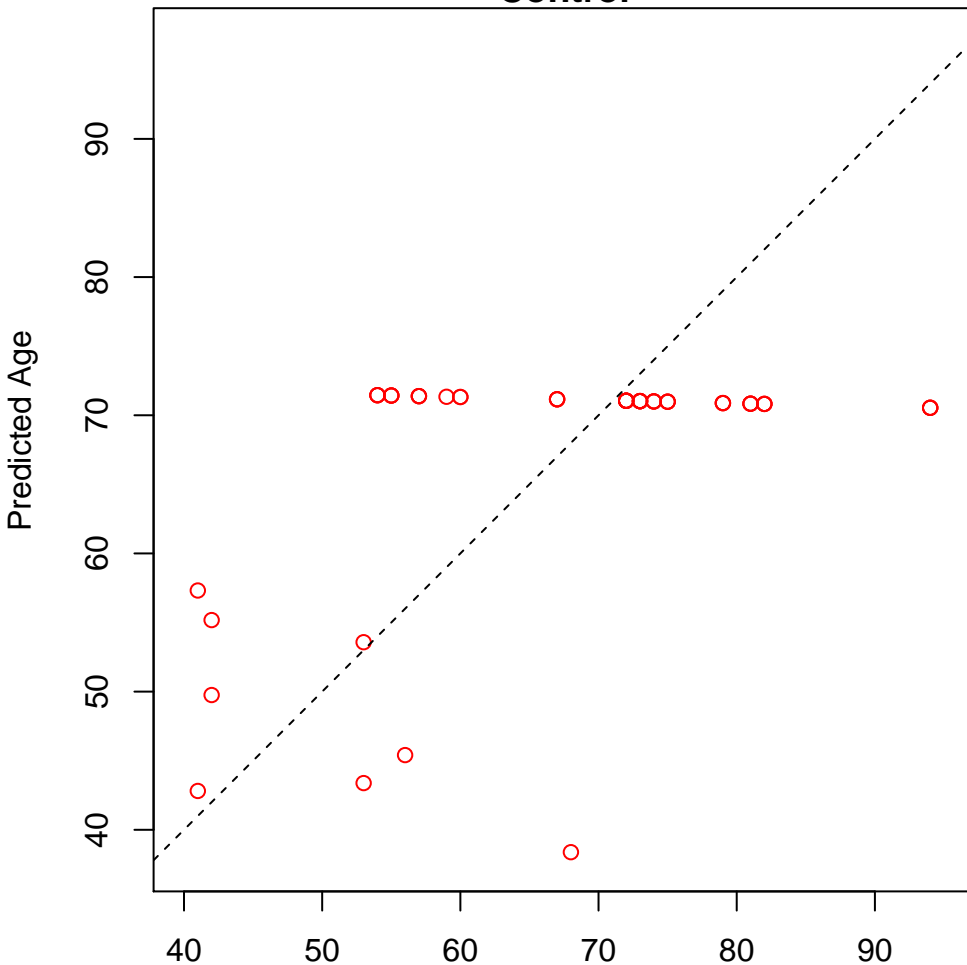


negative regulation of multi-organism process (Score: 0.775456)

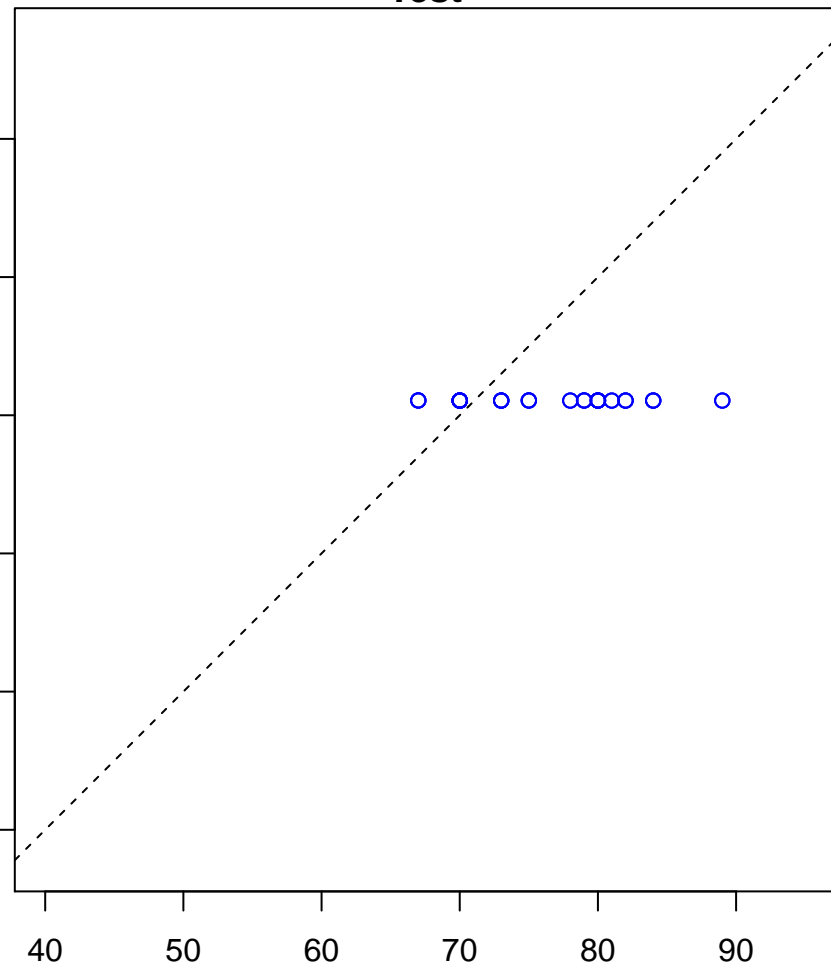


negative regulation of viral process (Score: 0.775456)

Control



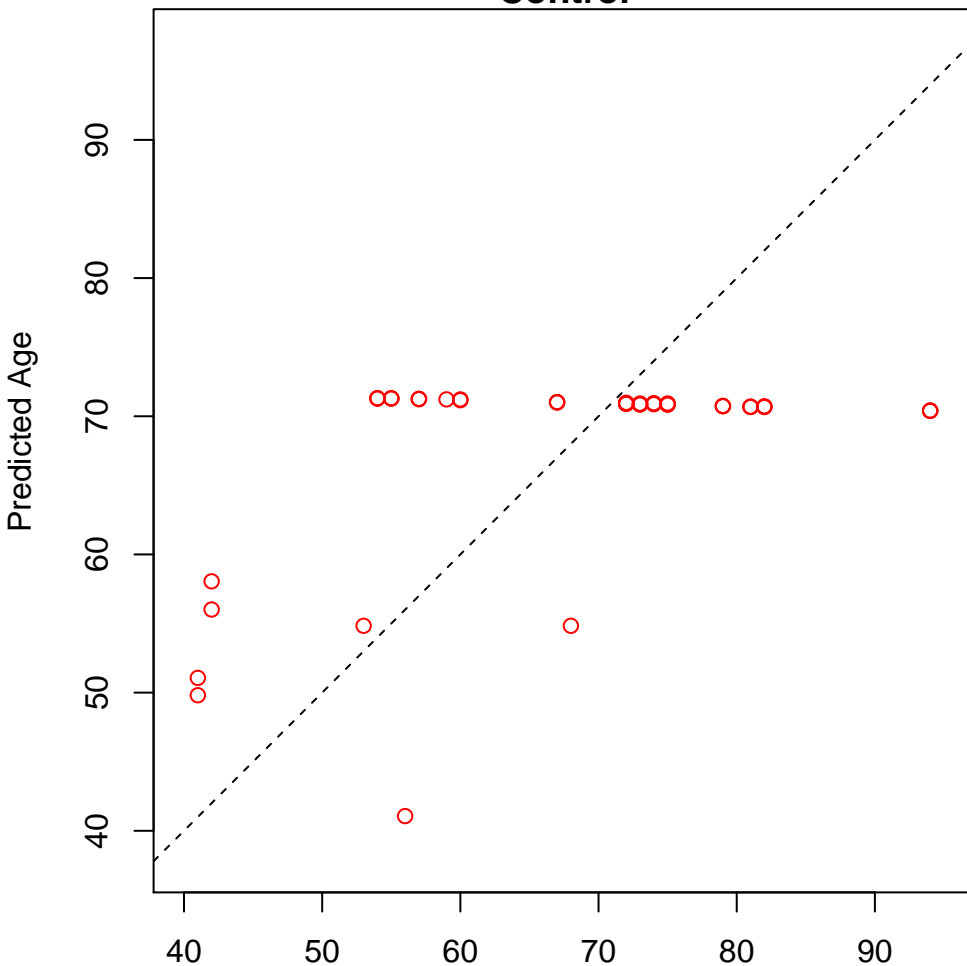
Test



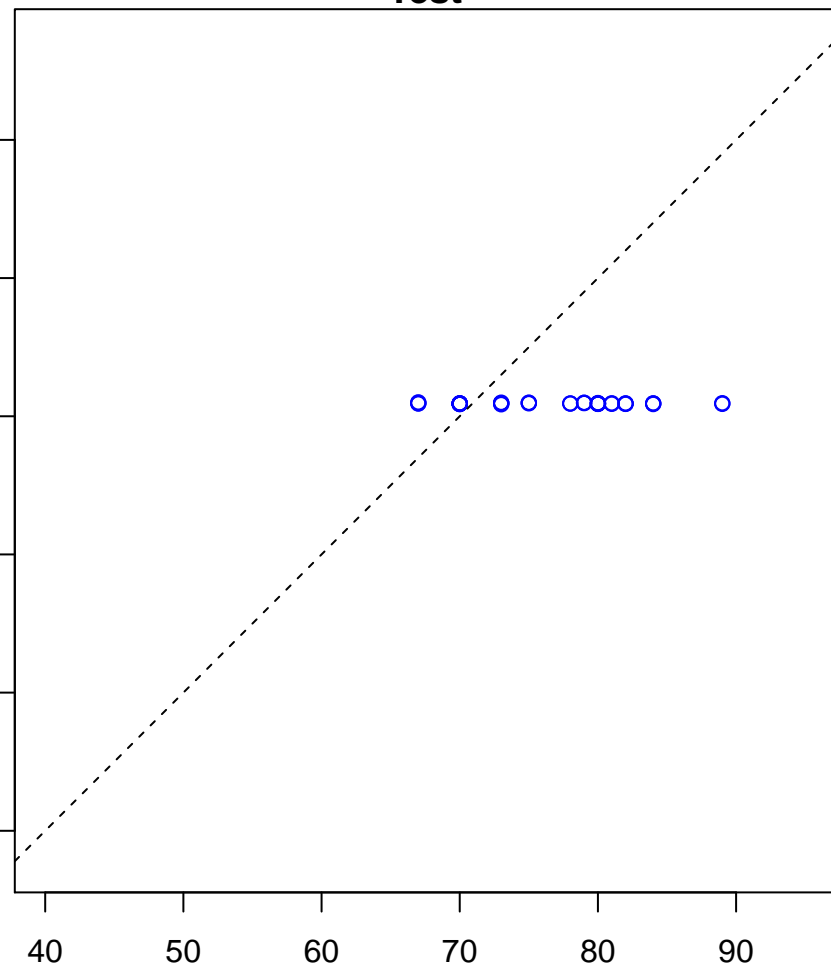
Actual Age

negative regulation of cell migration (Score: 0.775125)

Control

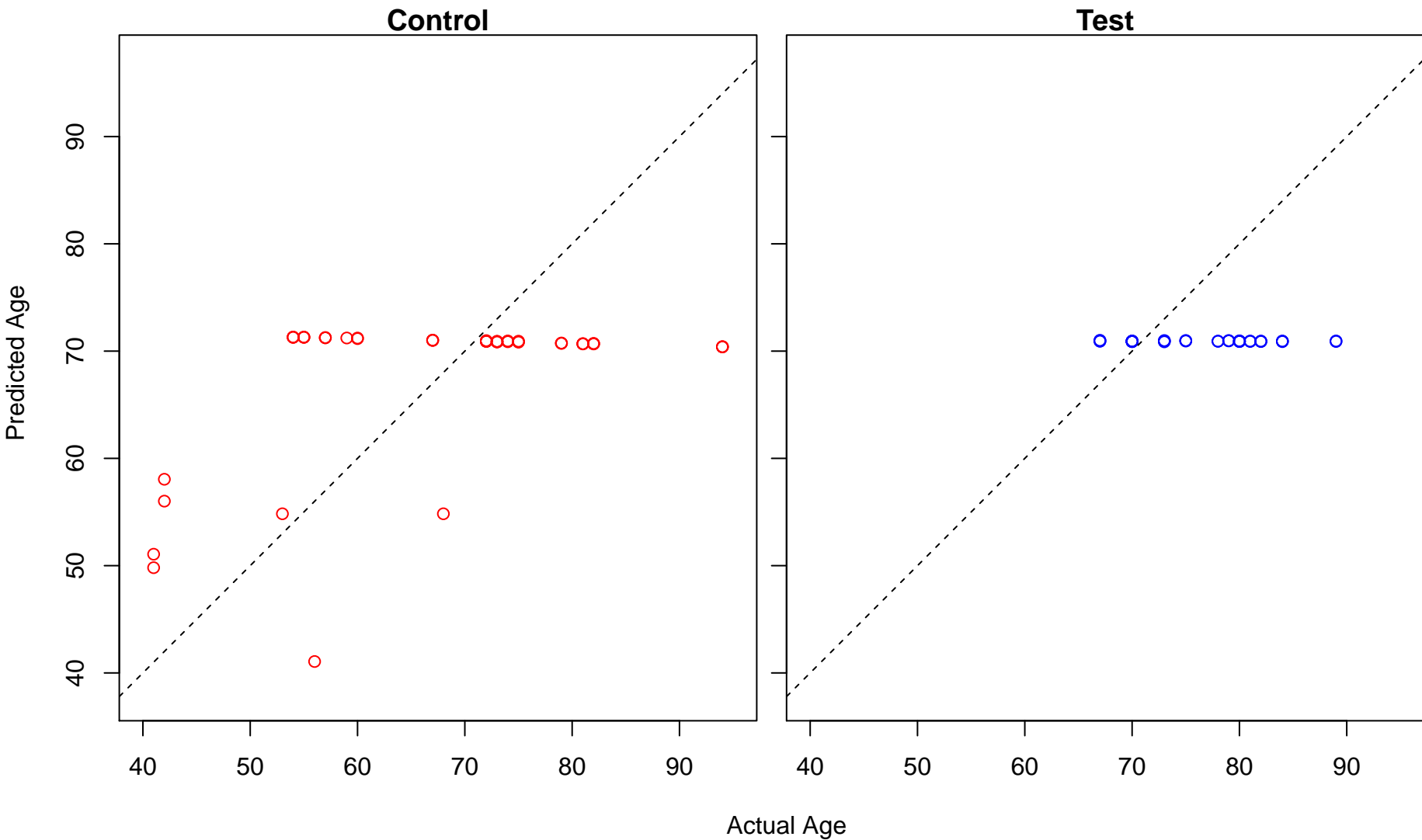


Test

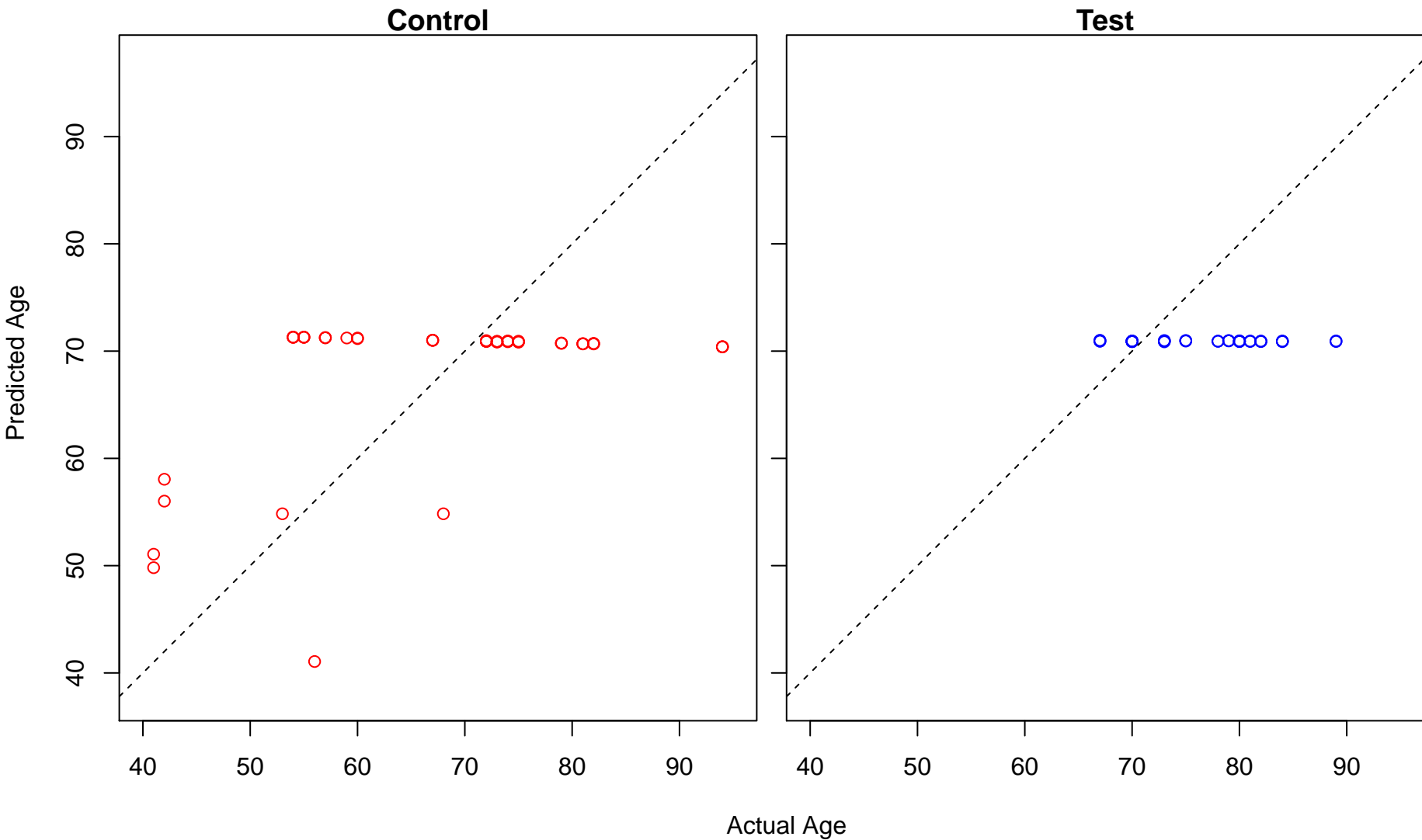


Actual Age

negative regulation of locomotion (Score: 0.775125)

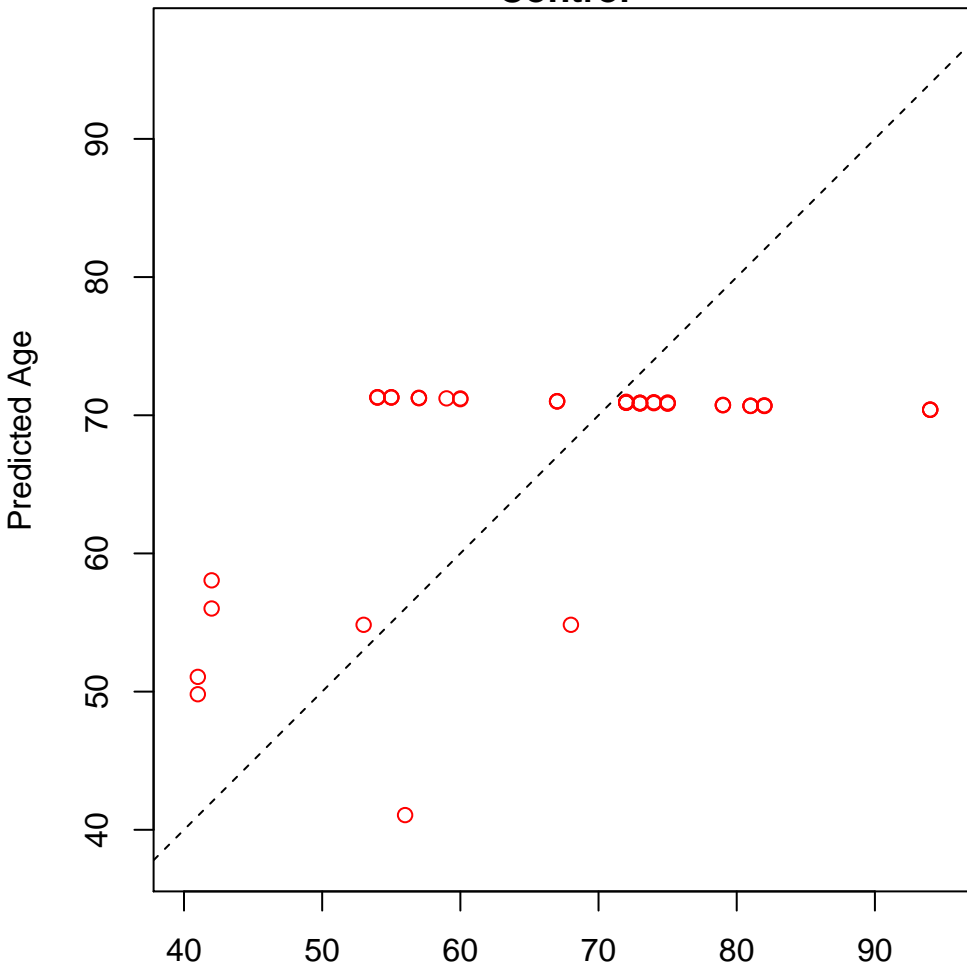


negative regulation of cellular component movement (Score: 0.775125)

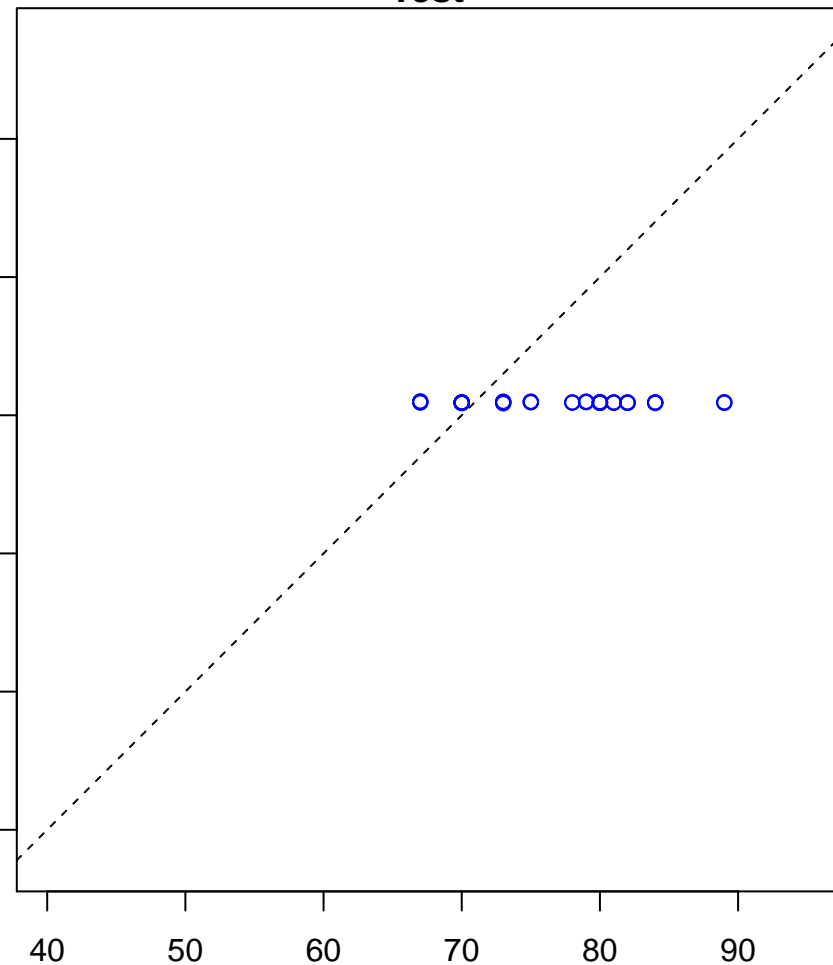


negative regulation of cell motility (Score: 0.775125)

Control



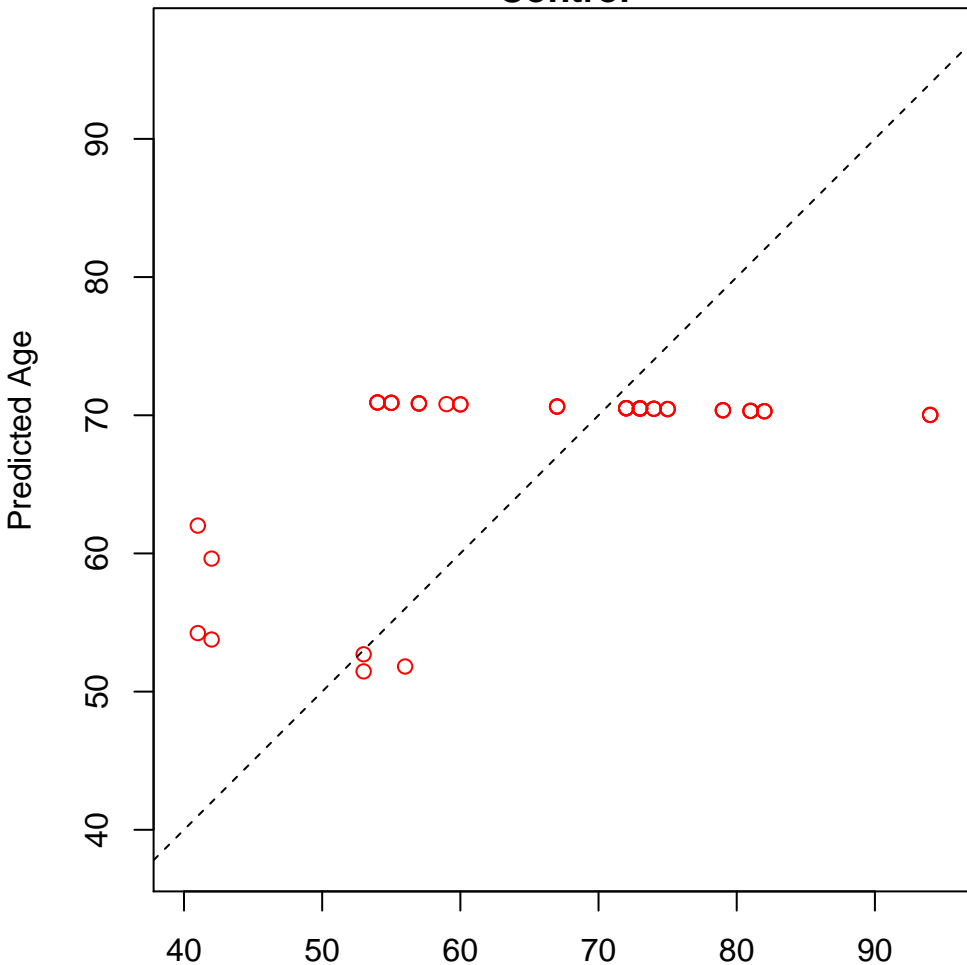
Test



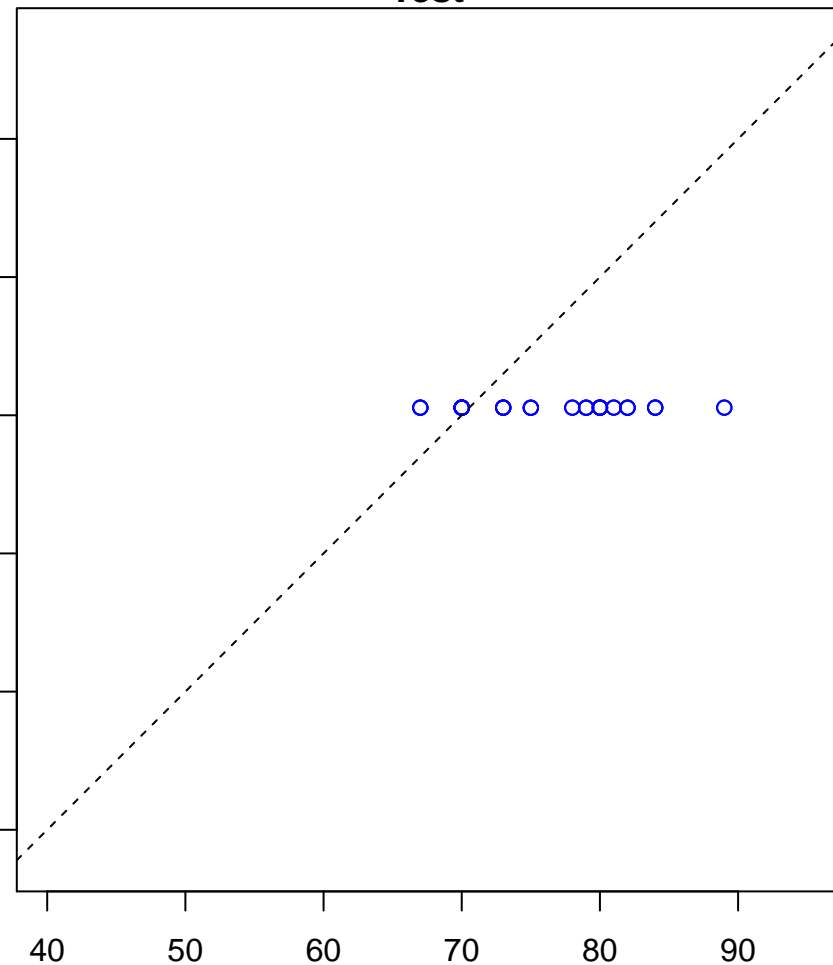
Actual Age

protein localization to microtubule (Score: 0.773862)

Control



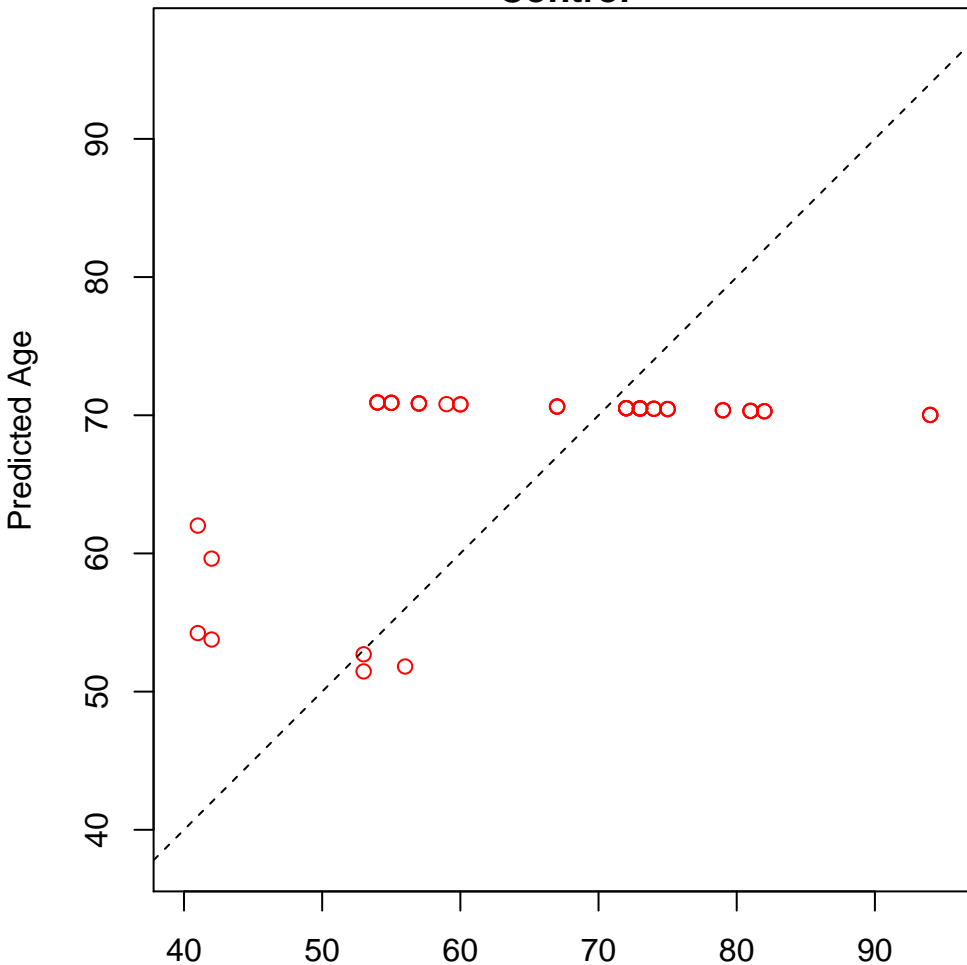
Test



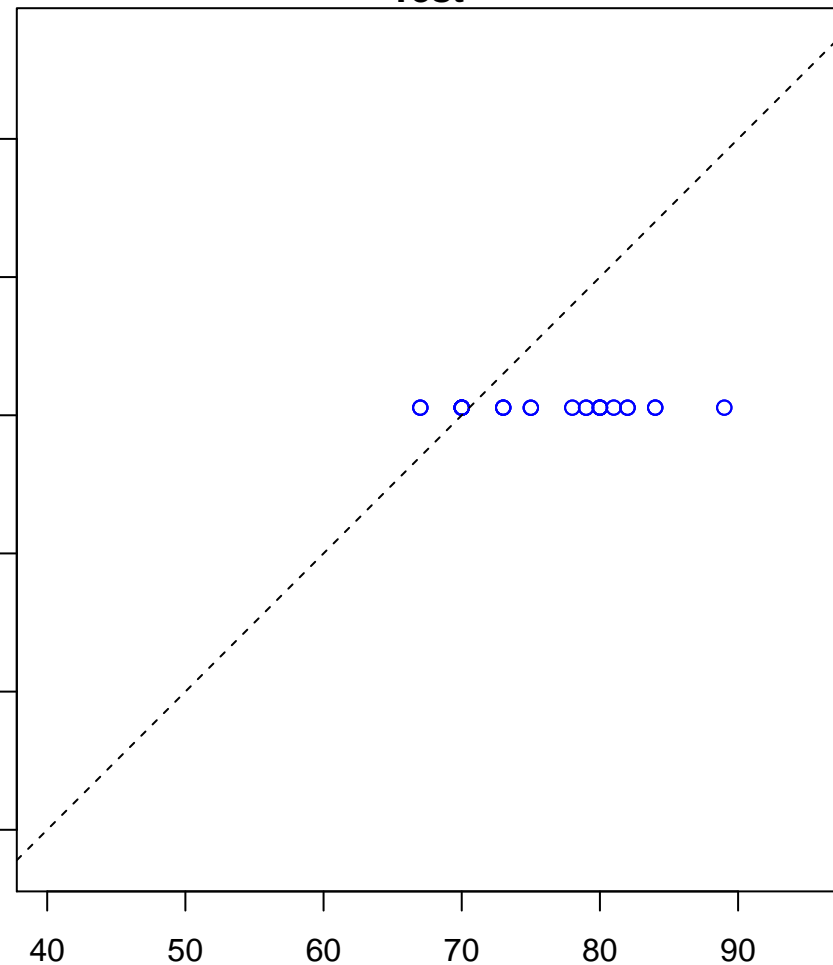
Actual Age

protein localization to cytoskeleton (Score: 0.773862)

Control

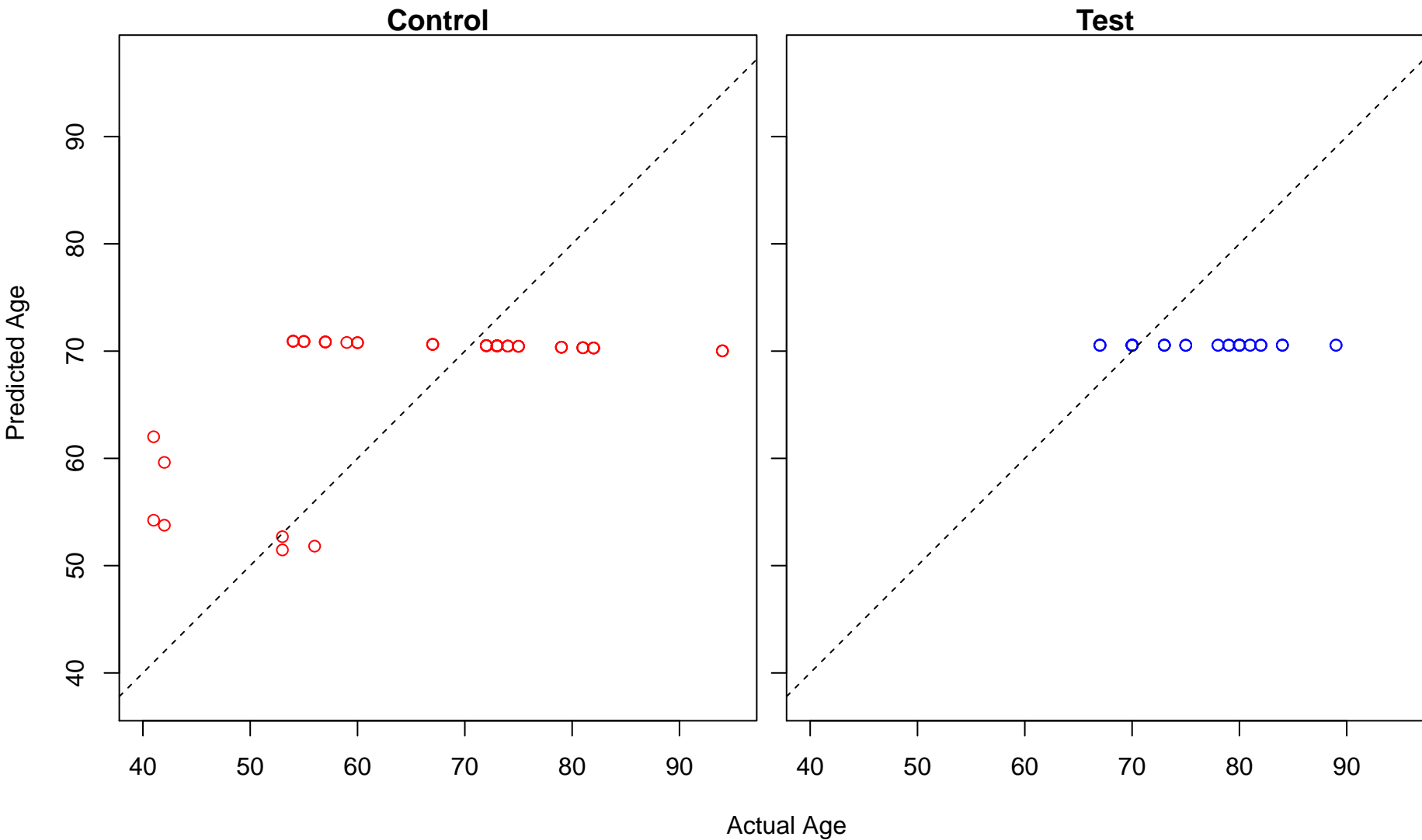


Test



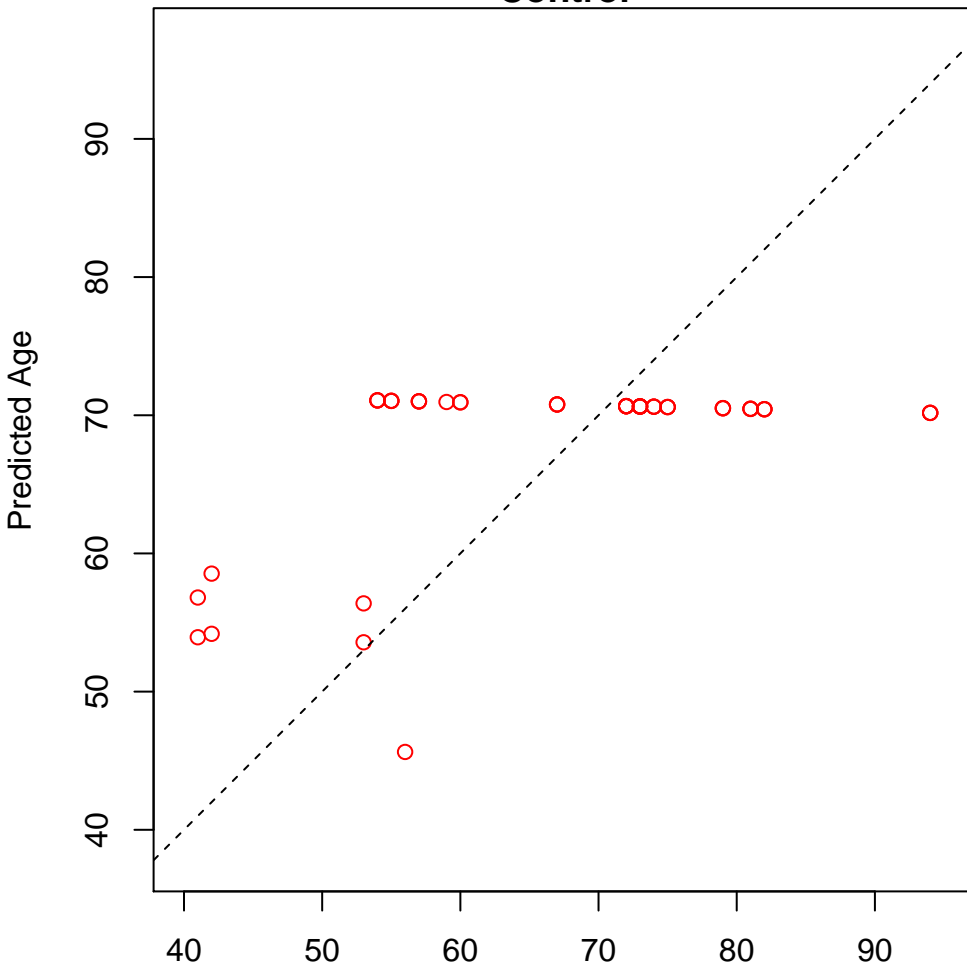
Actual Age

protein localization to microtubule cytoskeleton (Score: 0.773862)

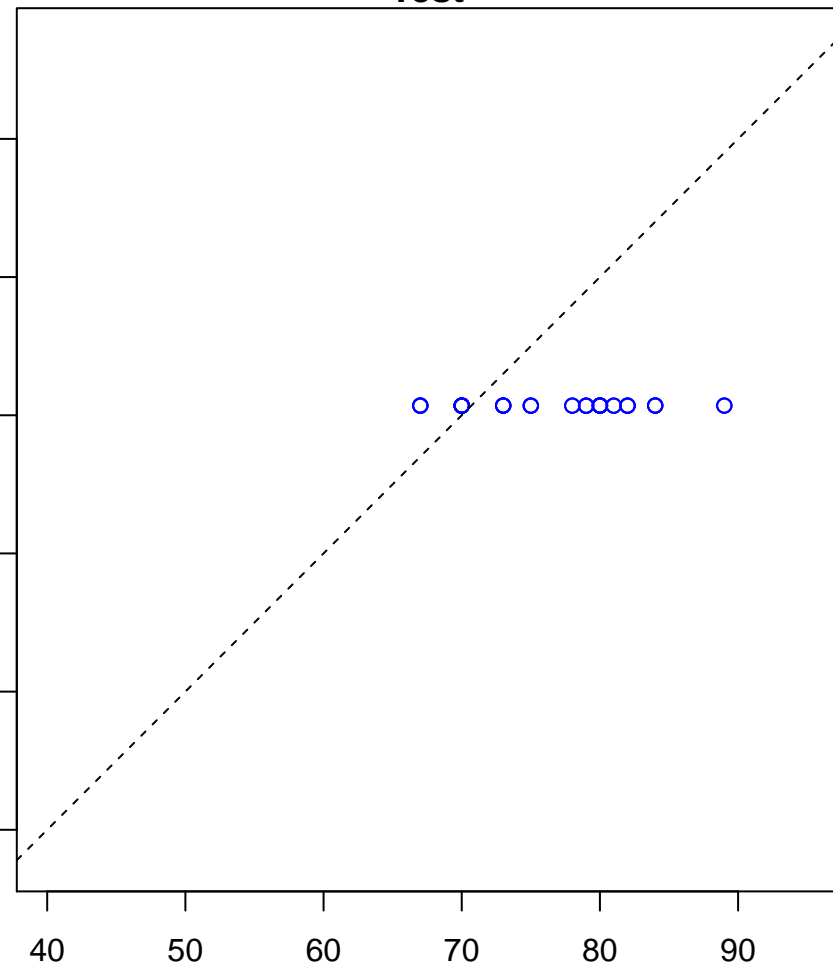


regulation of mitotic nuclear division (Score: 0.773544)

Control

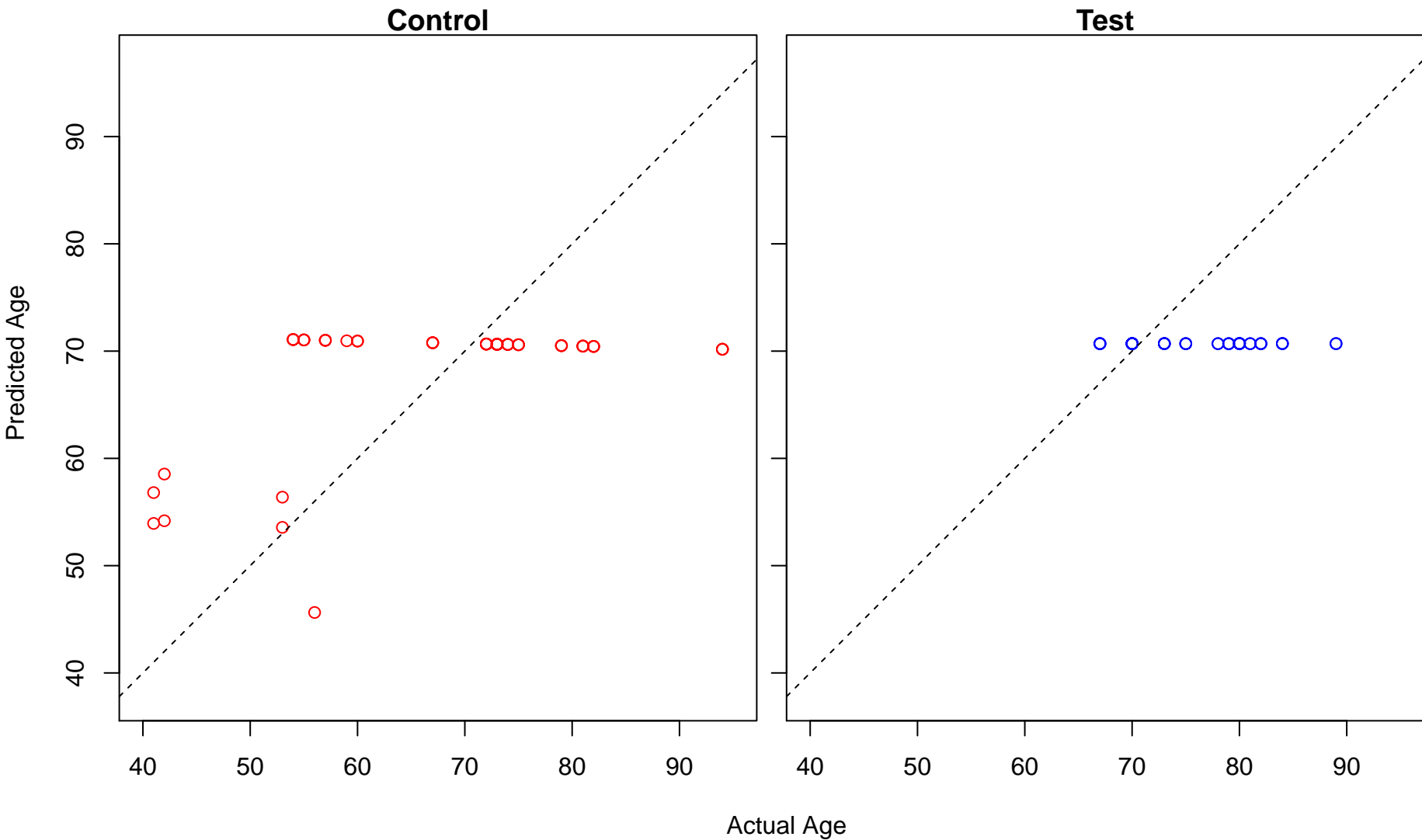


Test

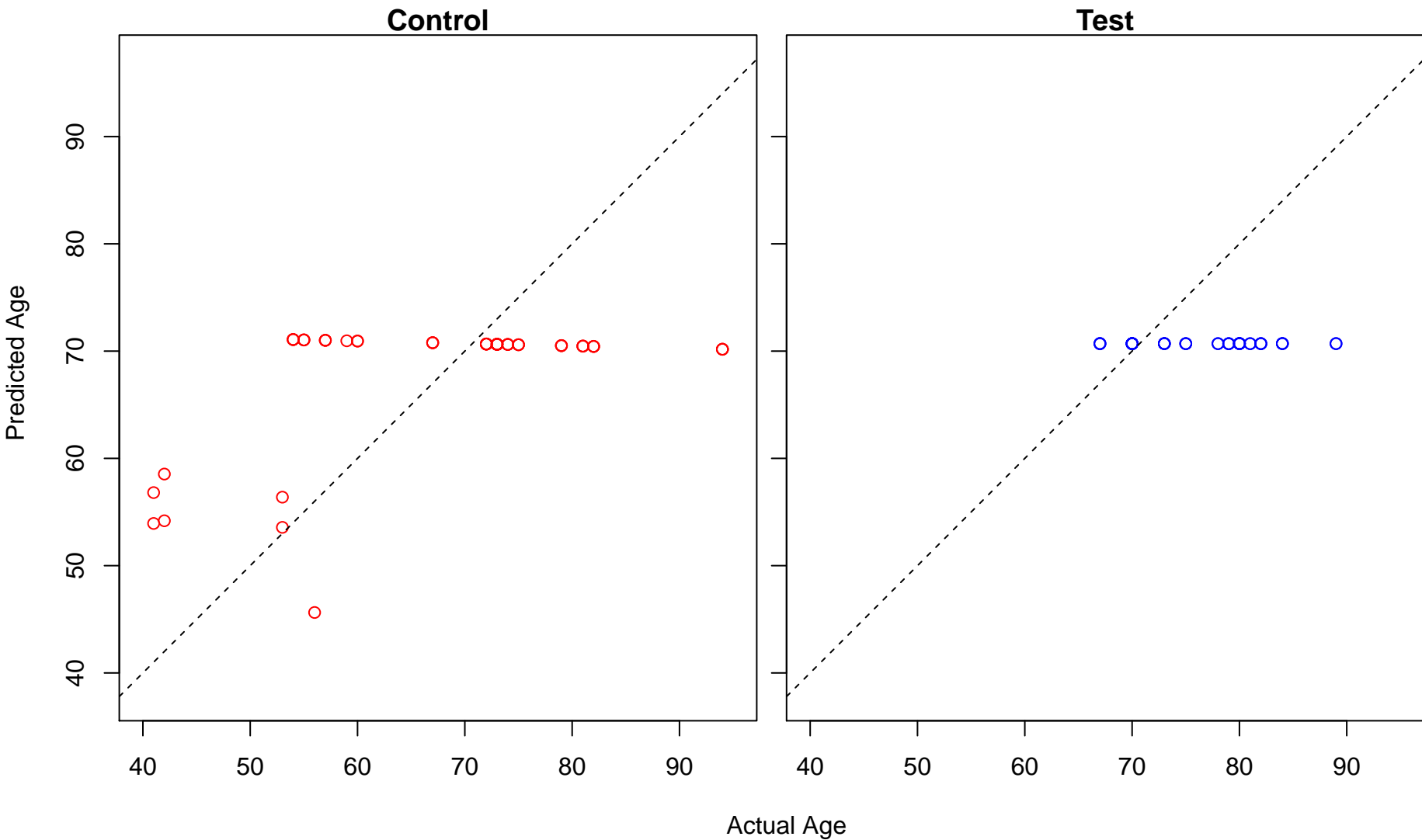


Actual Age

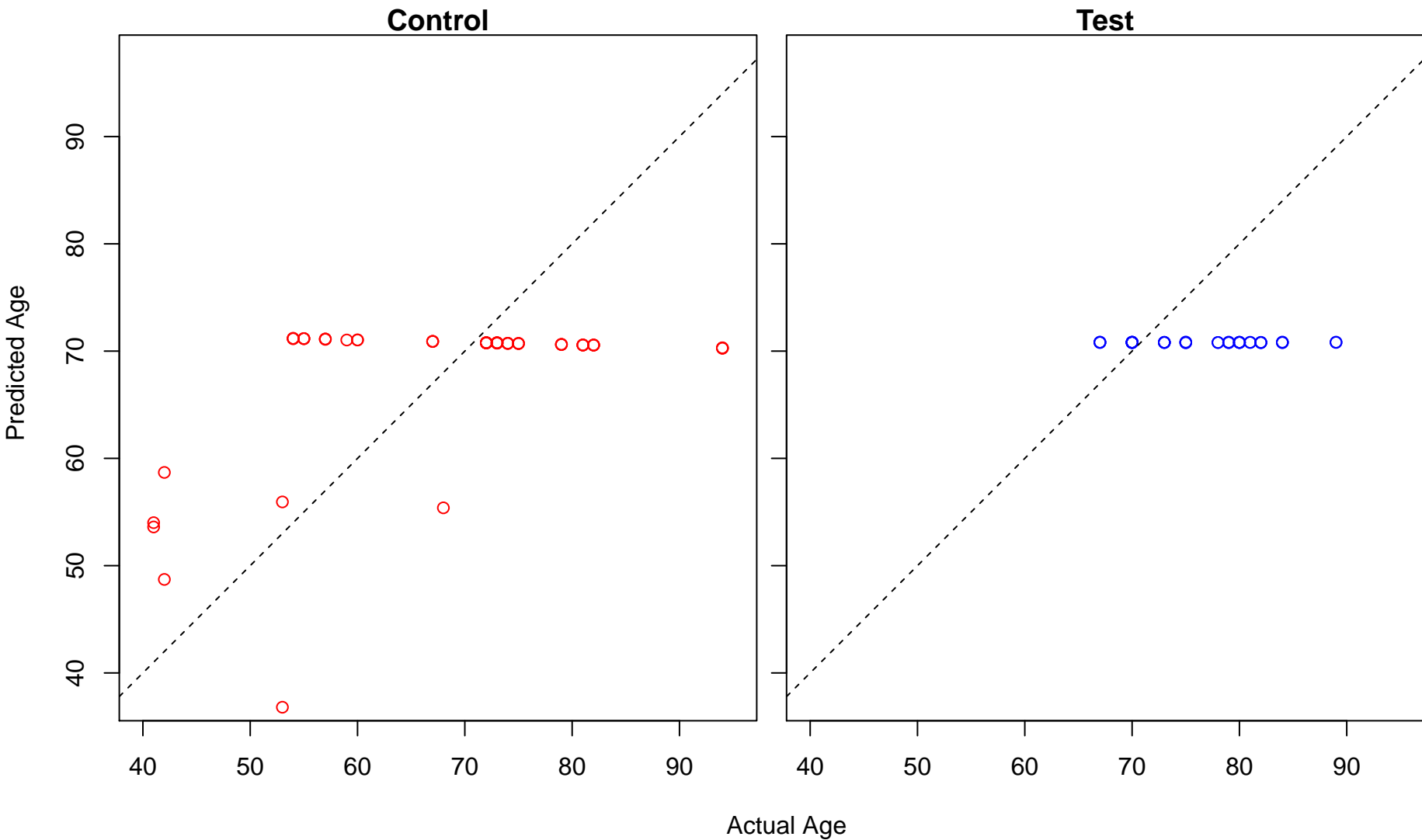
regulation of mitotic sister chromatid segregation (Score: 0.773544)



regulation of nuclear division (Score: 0.773544)

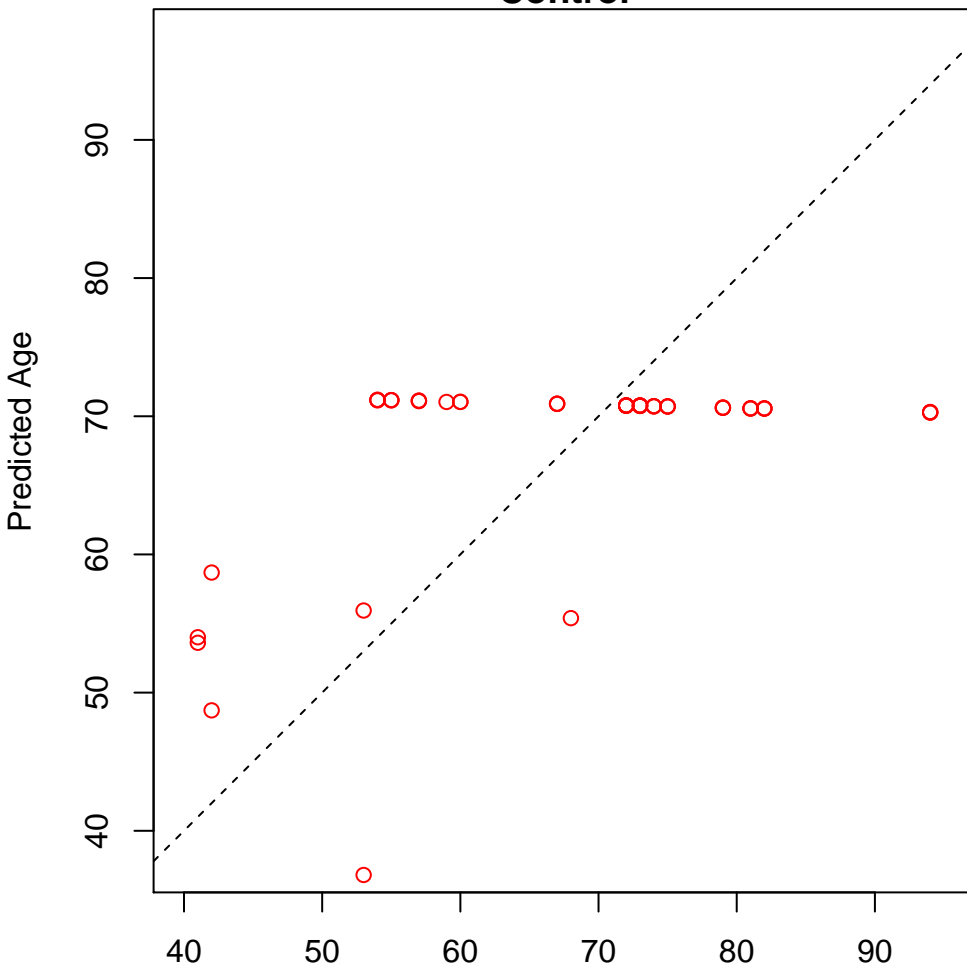


regulation of nuclease activity (Score: 0.772381)

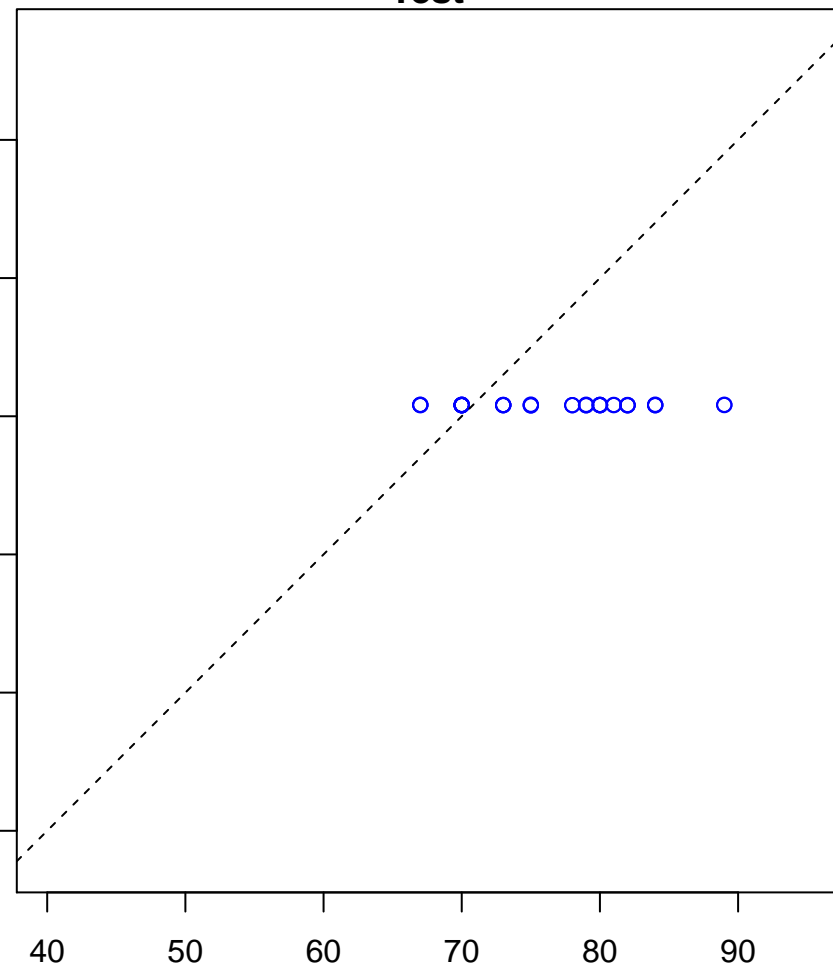


regulation of deoxyribonuclease activity (Score: 0.772381)

Control

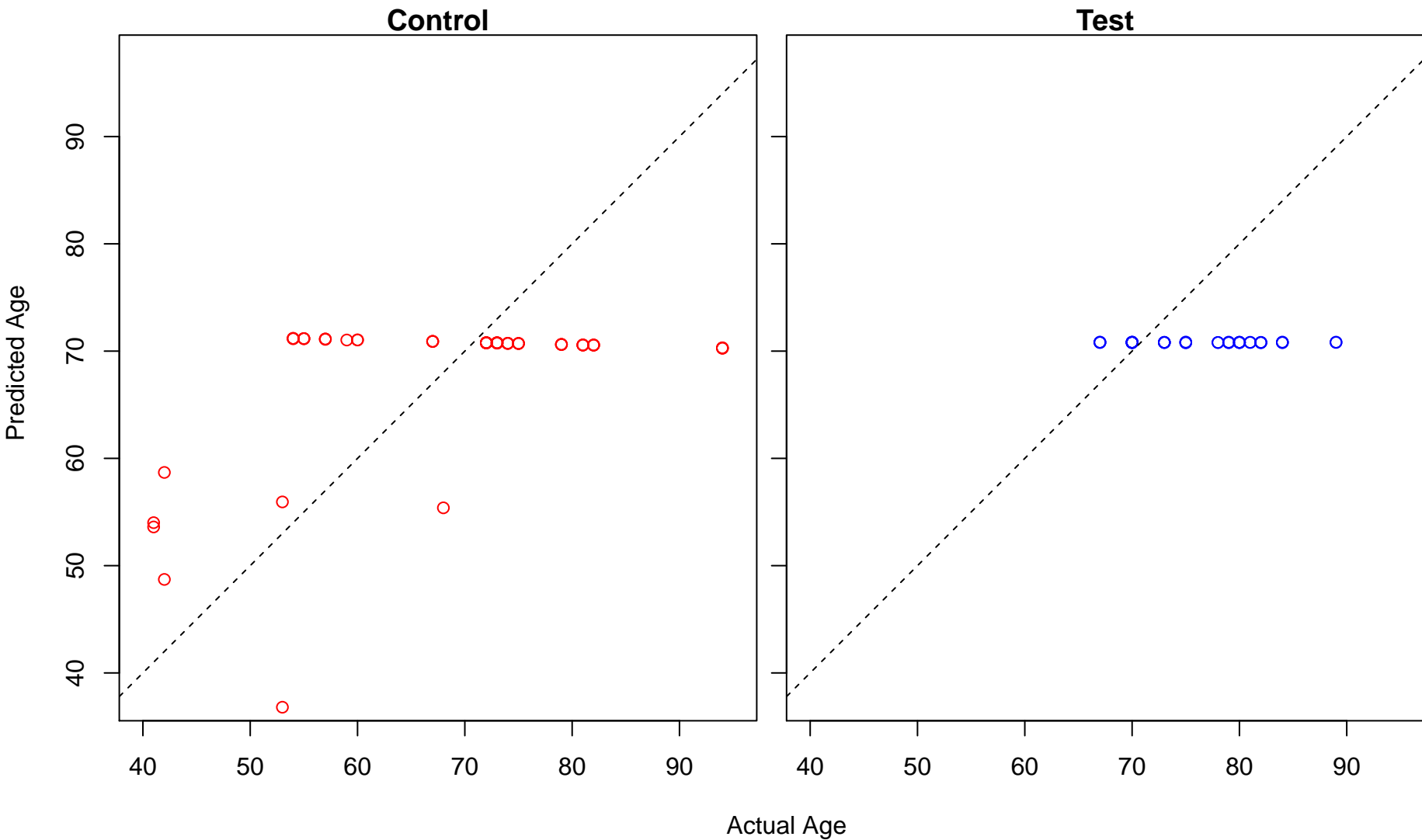


Test

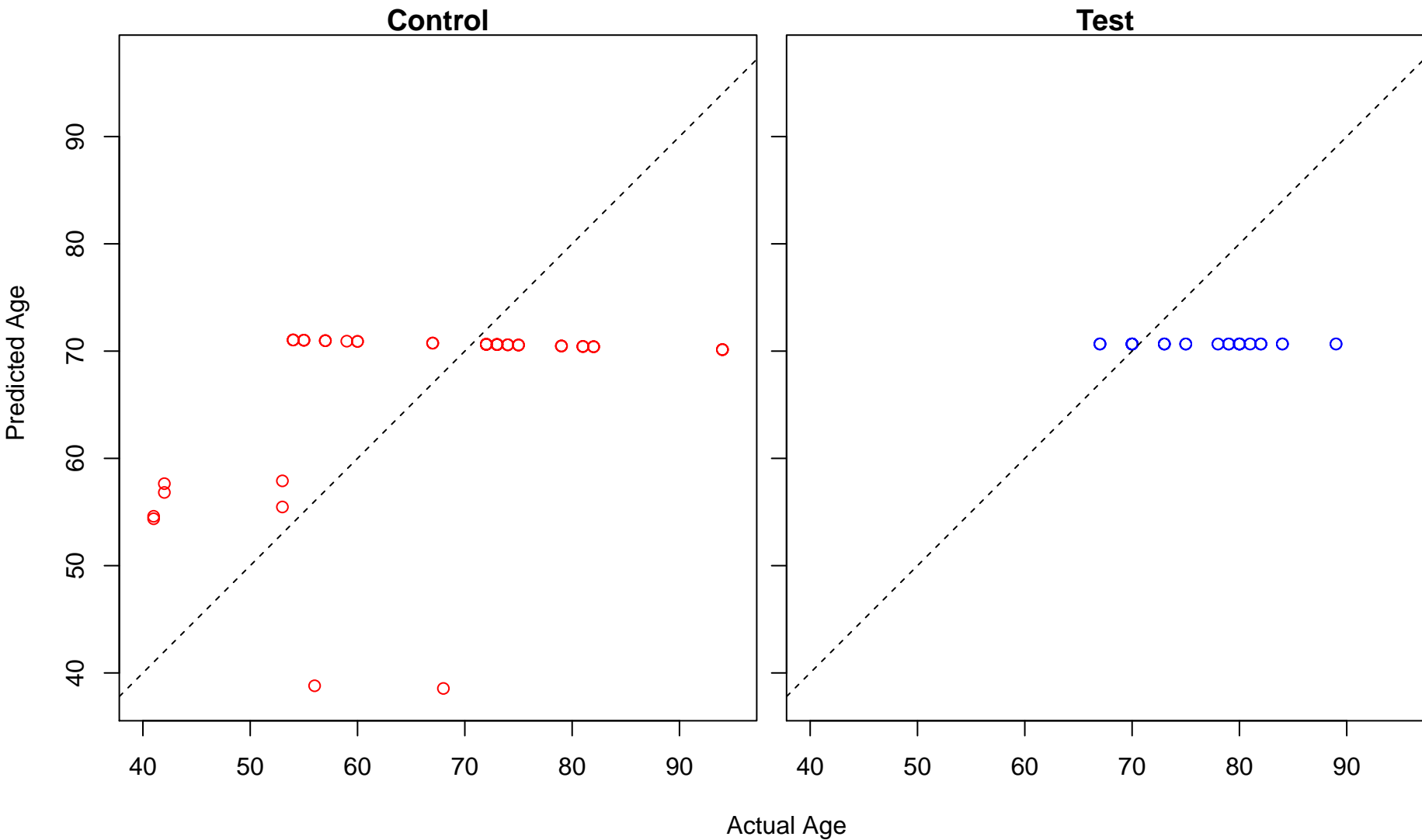


Actual Age

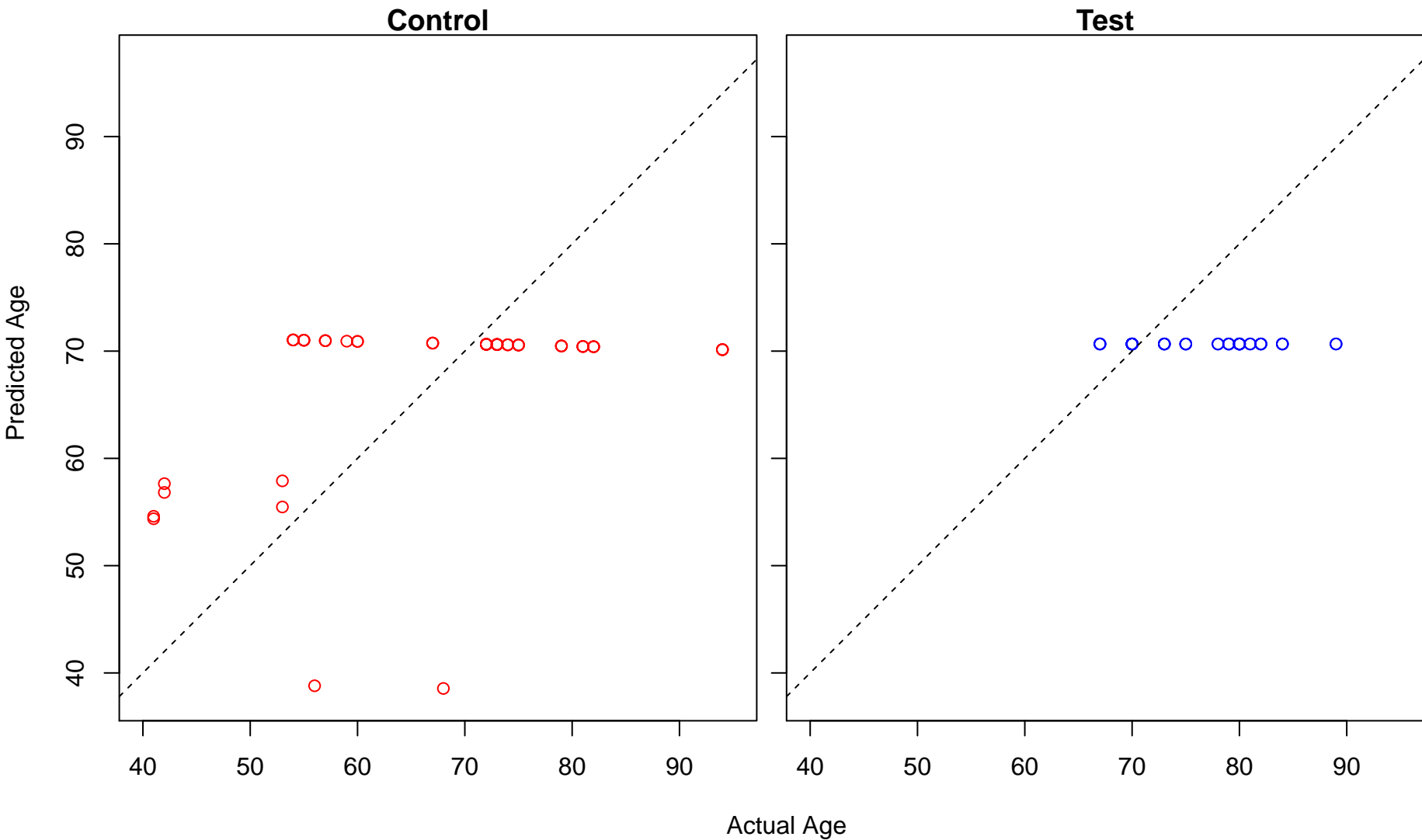
regulation of endodeoxyribonuclease activity (Score: 0.772381)



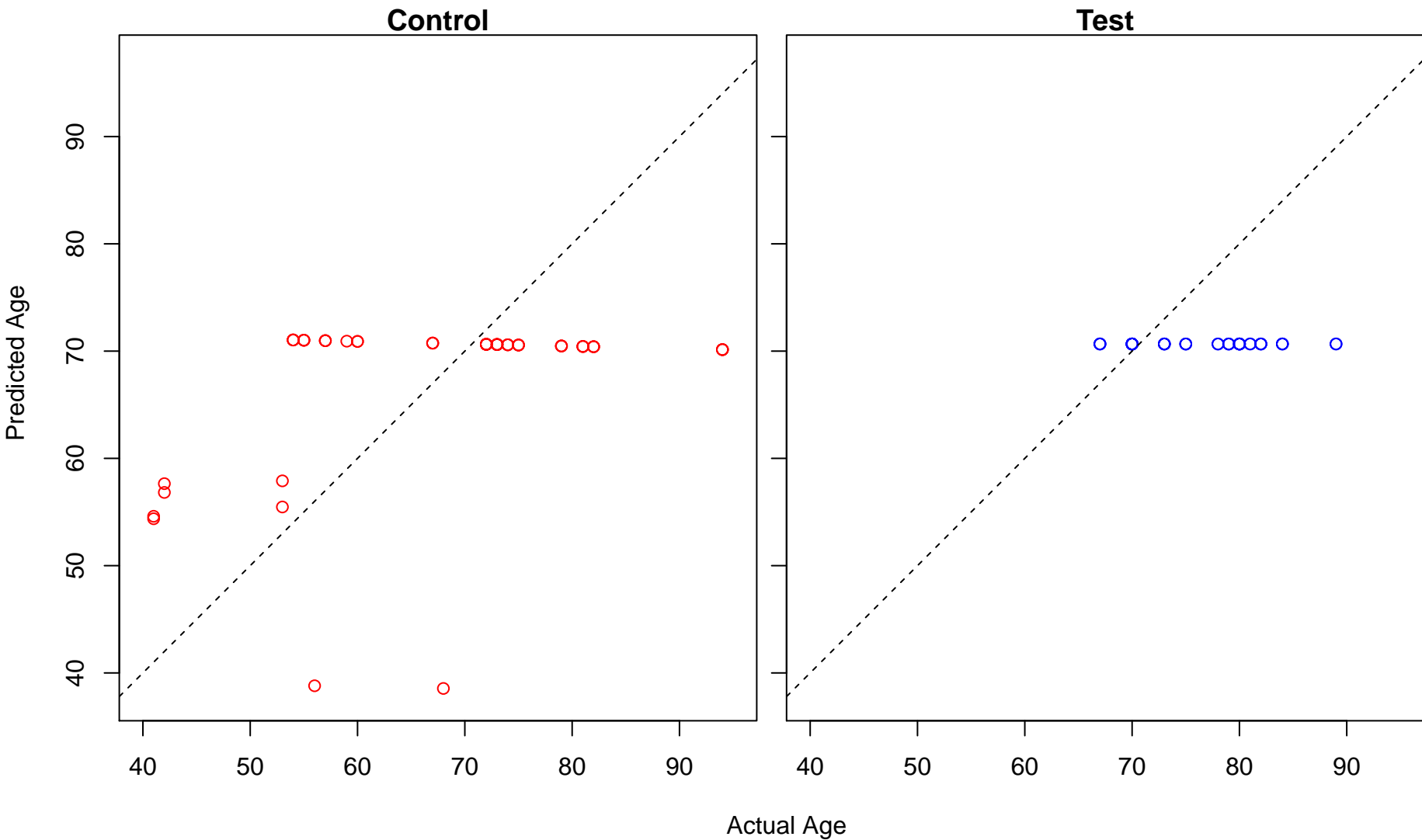
negative regulation of endothelial cell migration (Score: 0.771769)



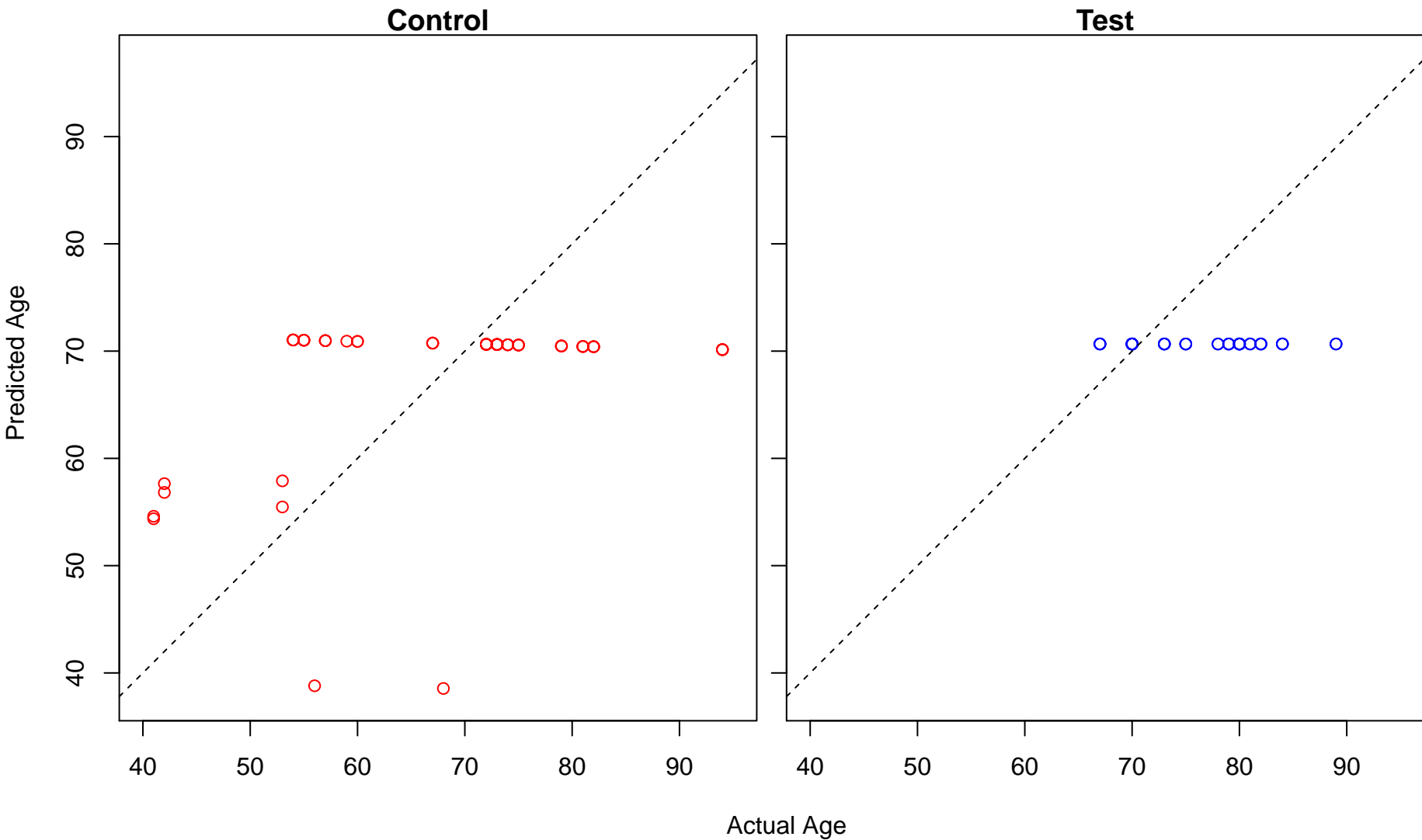
negative regulation of epithelial cell migration (Score: 0.771769)



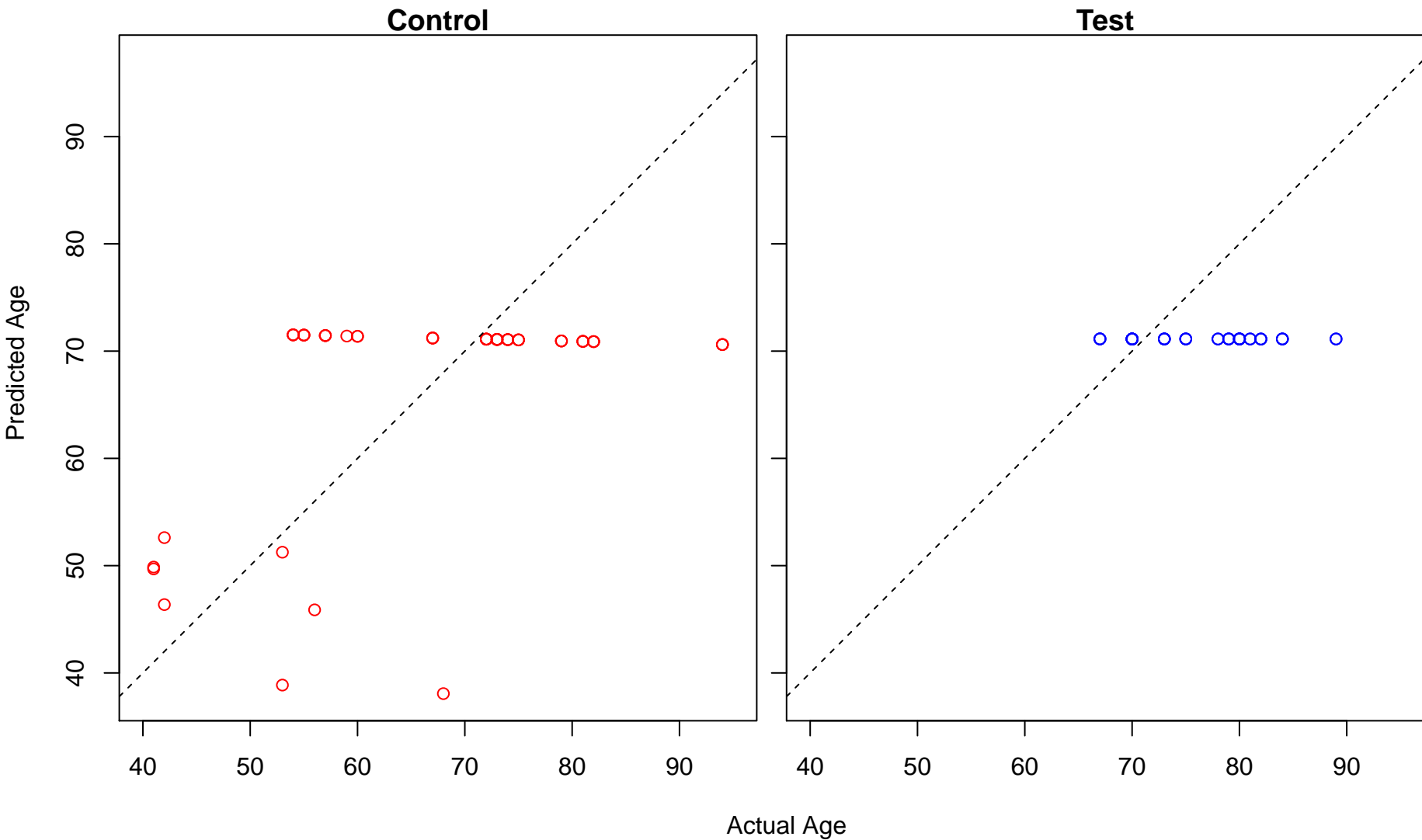
regulation of blood vessel endothelial cell migration (Score: 0.771769)



negative regulation of blood vessel endothelial cell migration (Score: 0.771769)

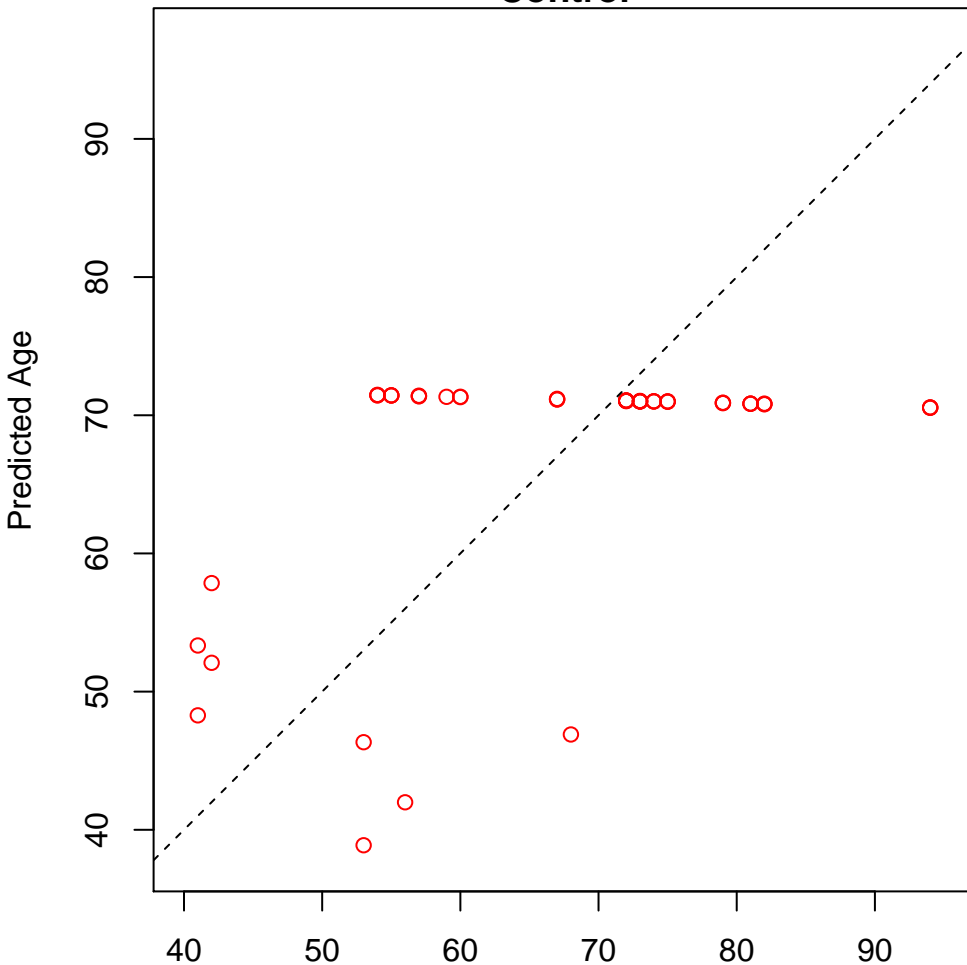


transcription from RNA polymerase II promoter (Score: 0.771586)

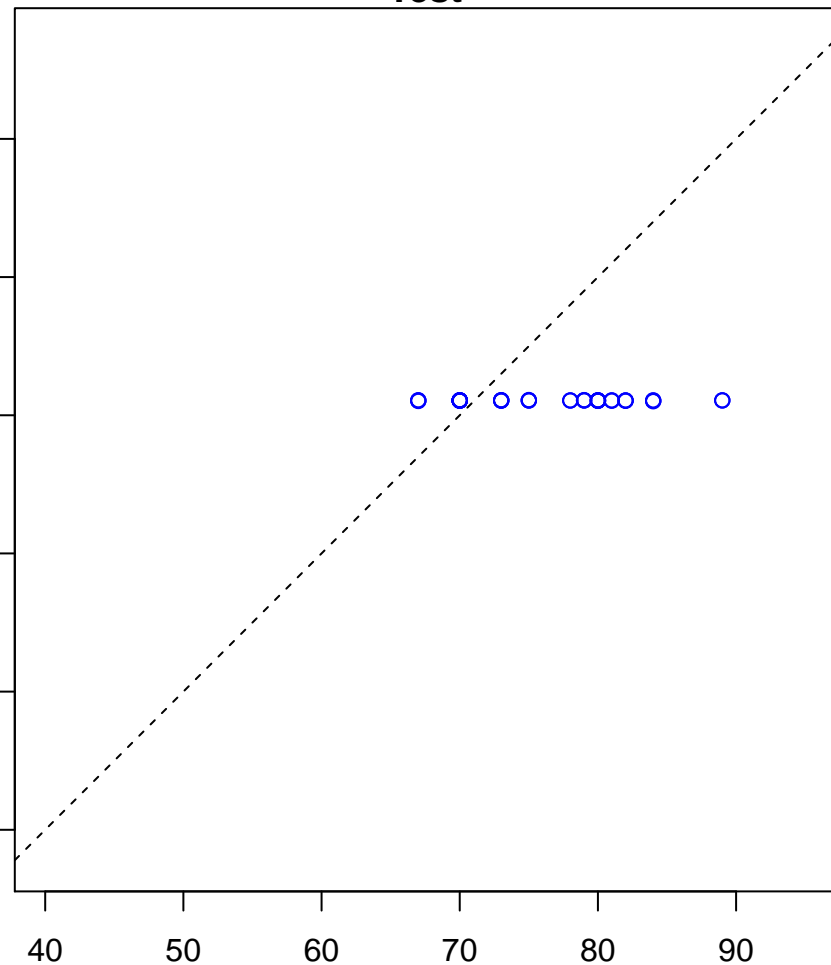


positive regulation of ion transport (Score: 0.771258)

Control

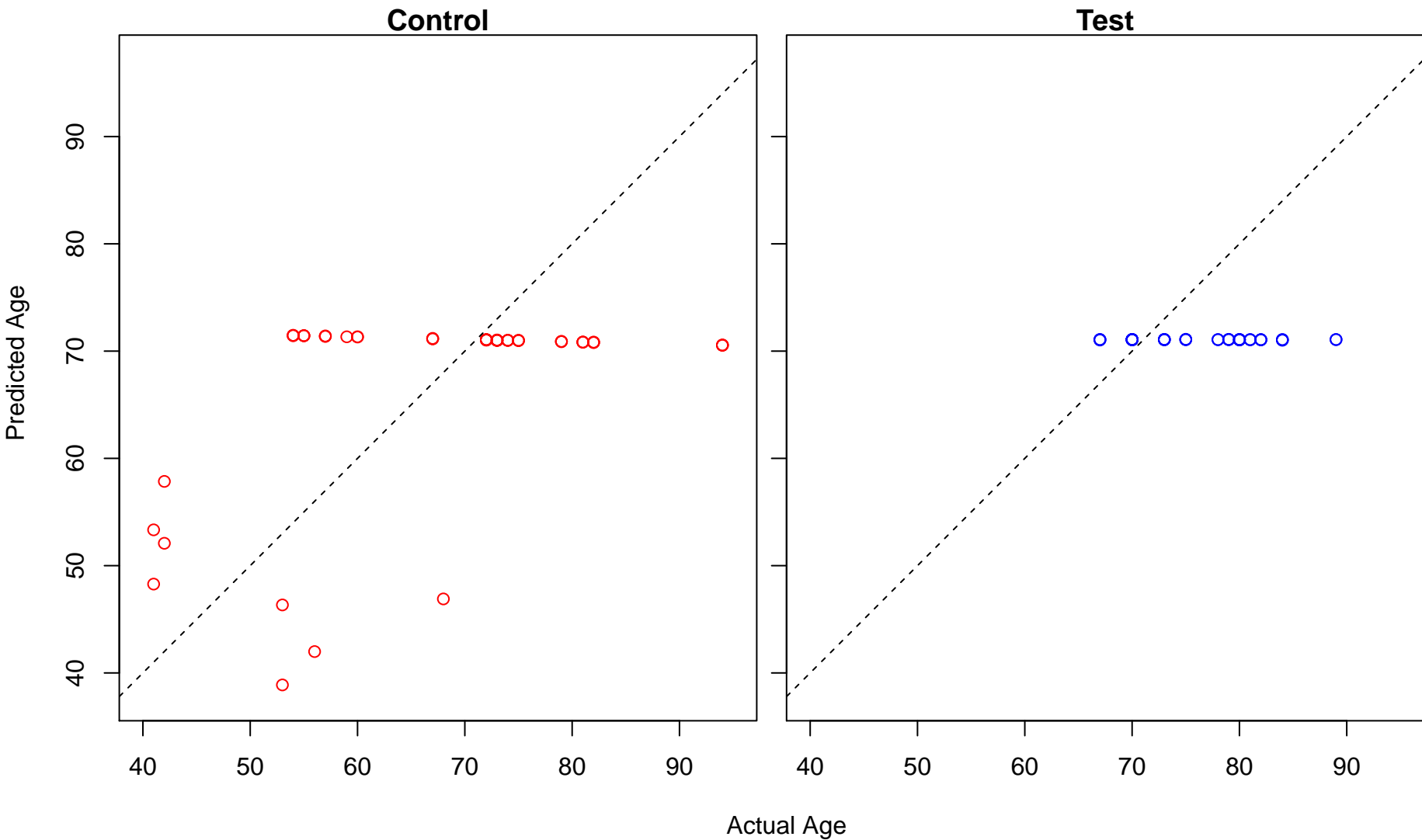


Test



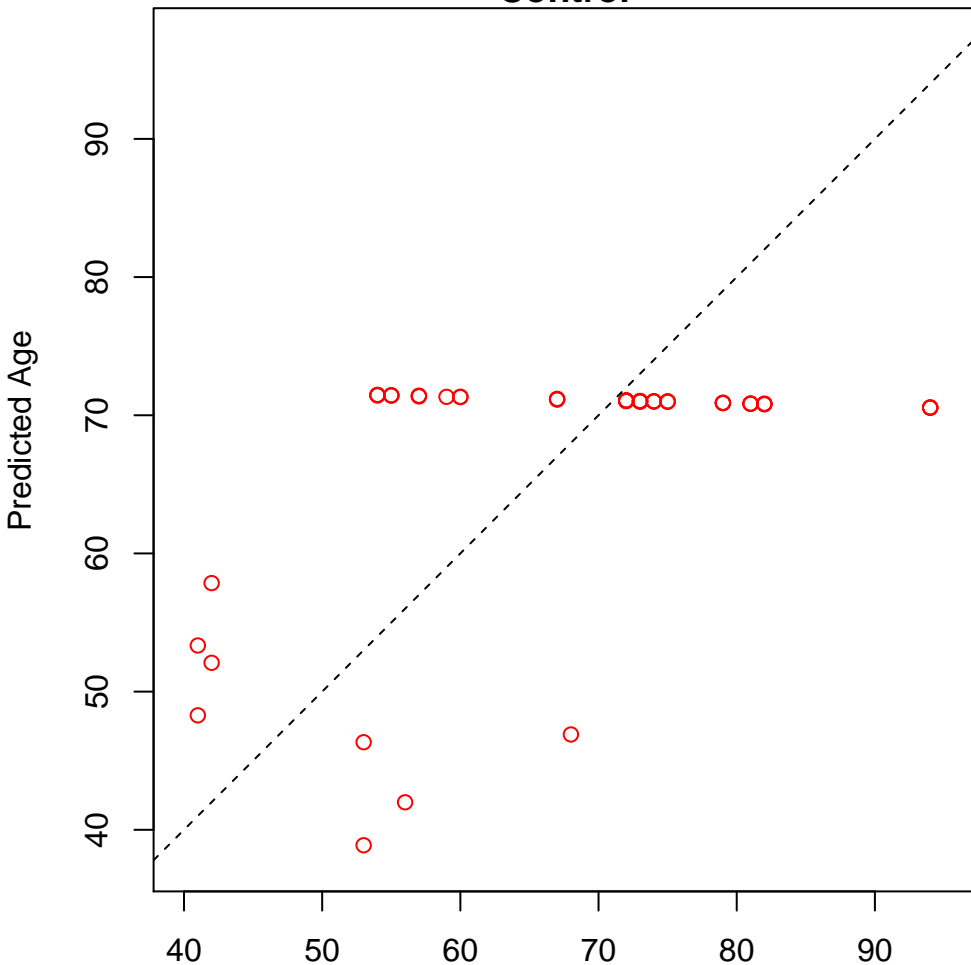
Actual Age

positive regulation of calcium ion transport (Score: 0.771258)

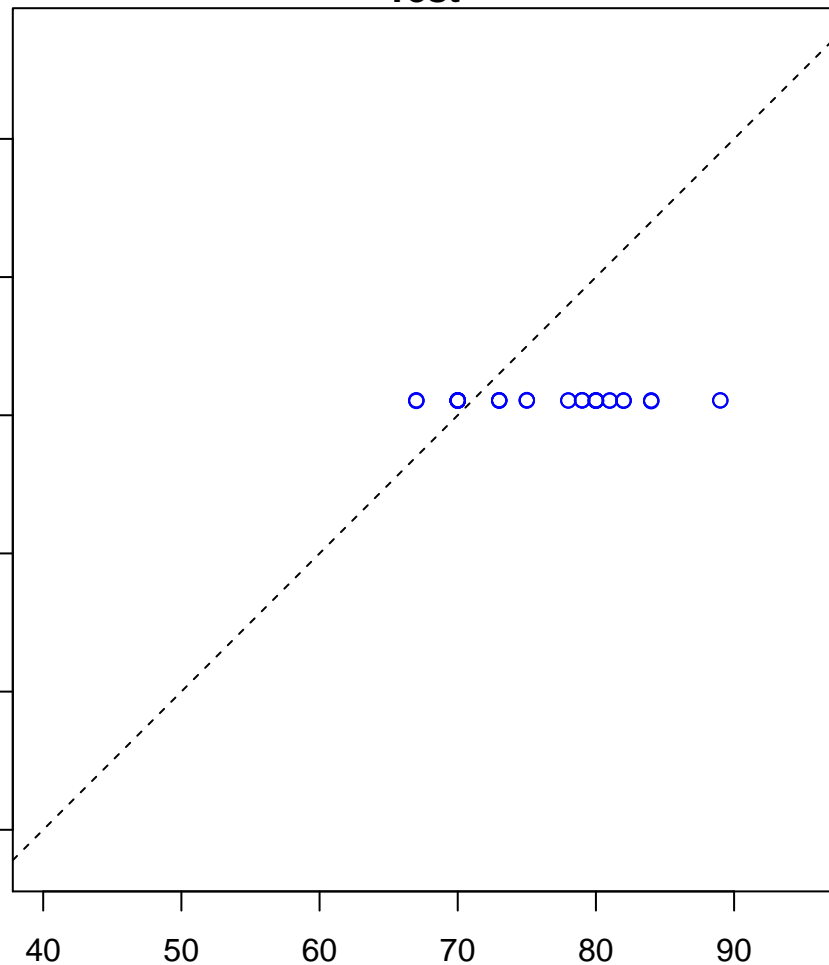


negative regulation of receptor activity (Score: 0.771258)

Control

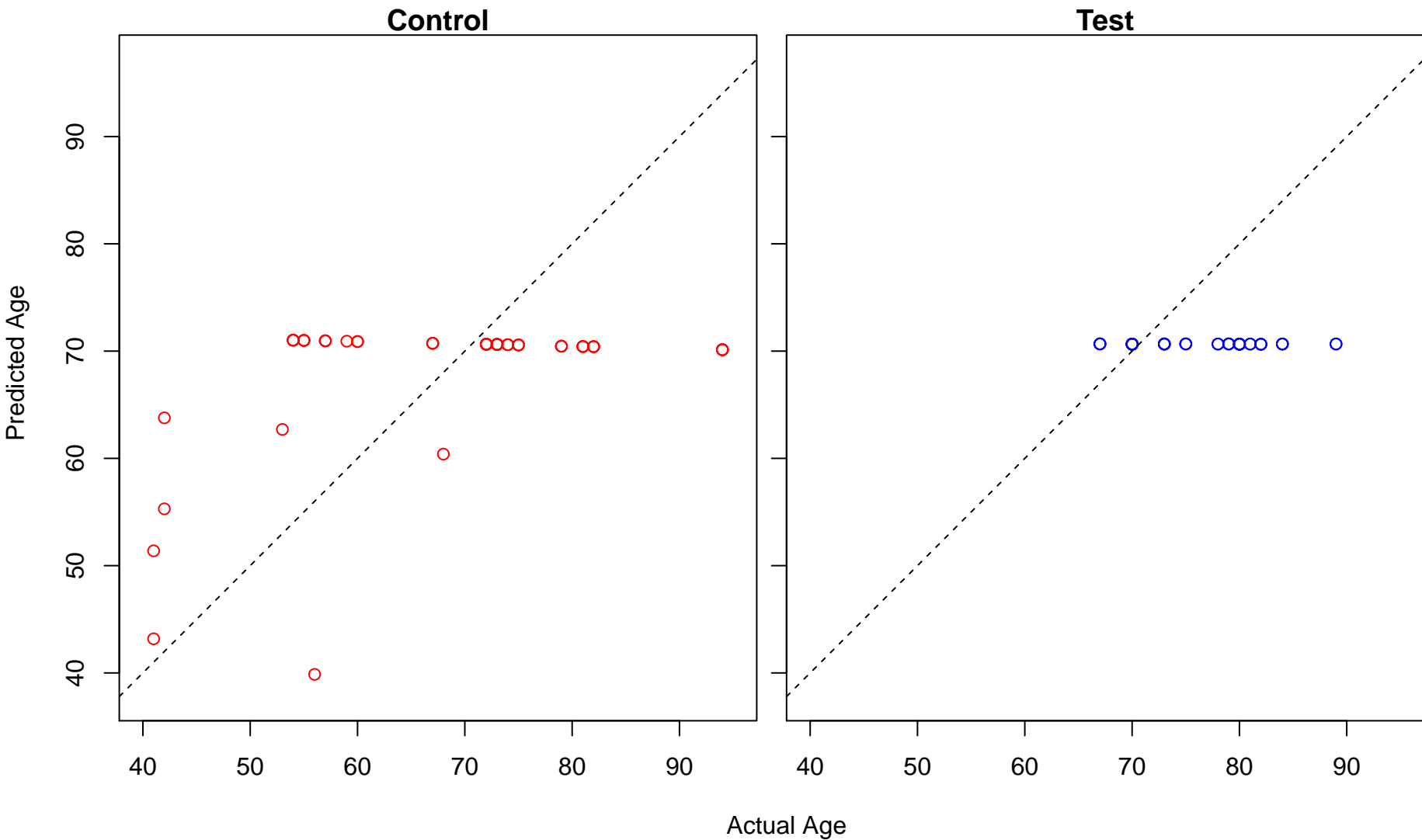


Test

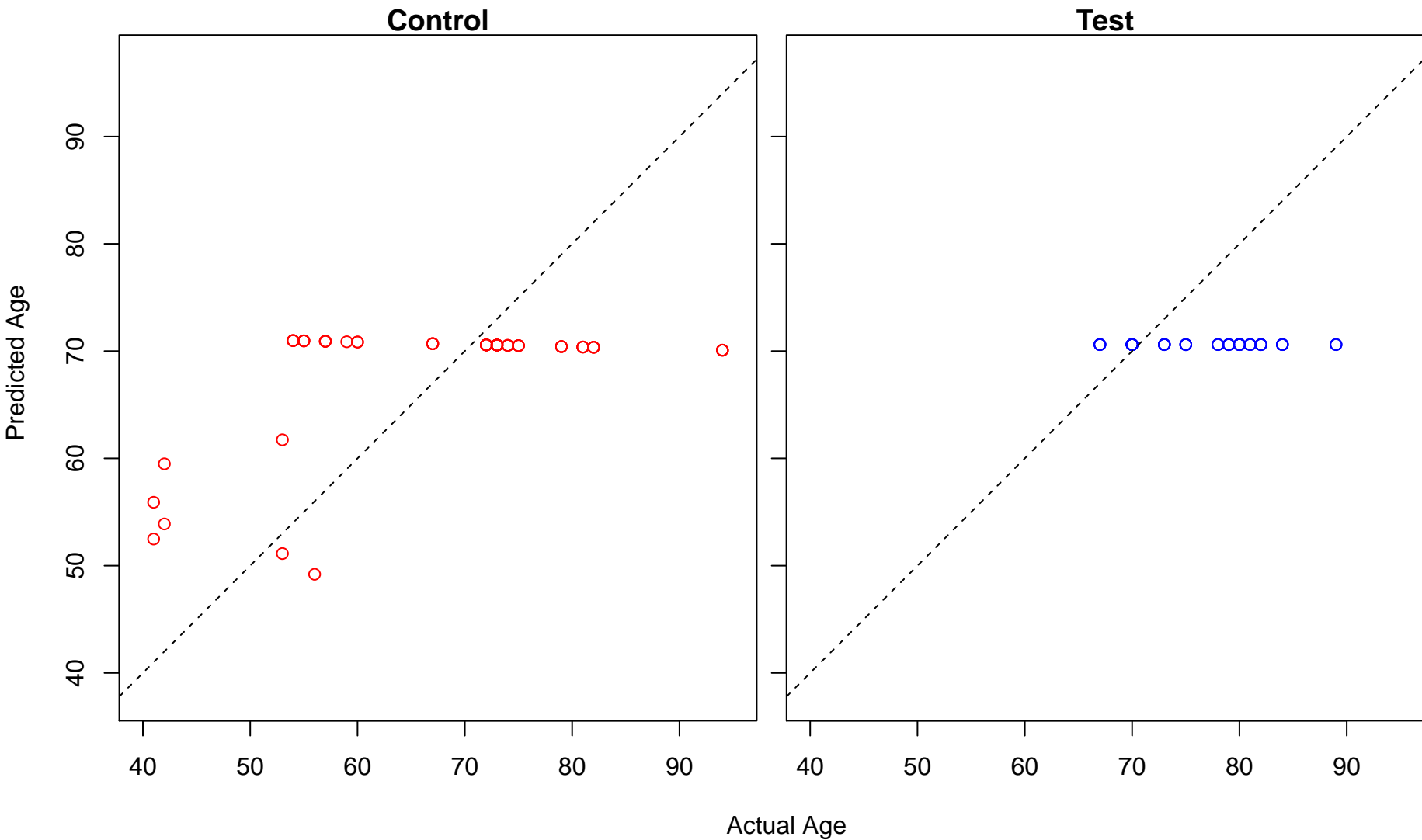


Actual Age

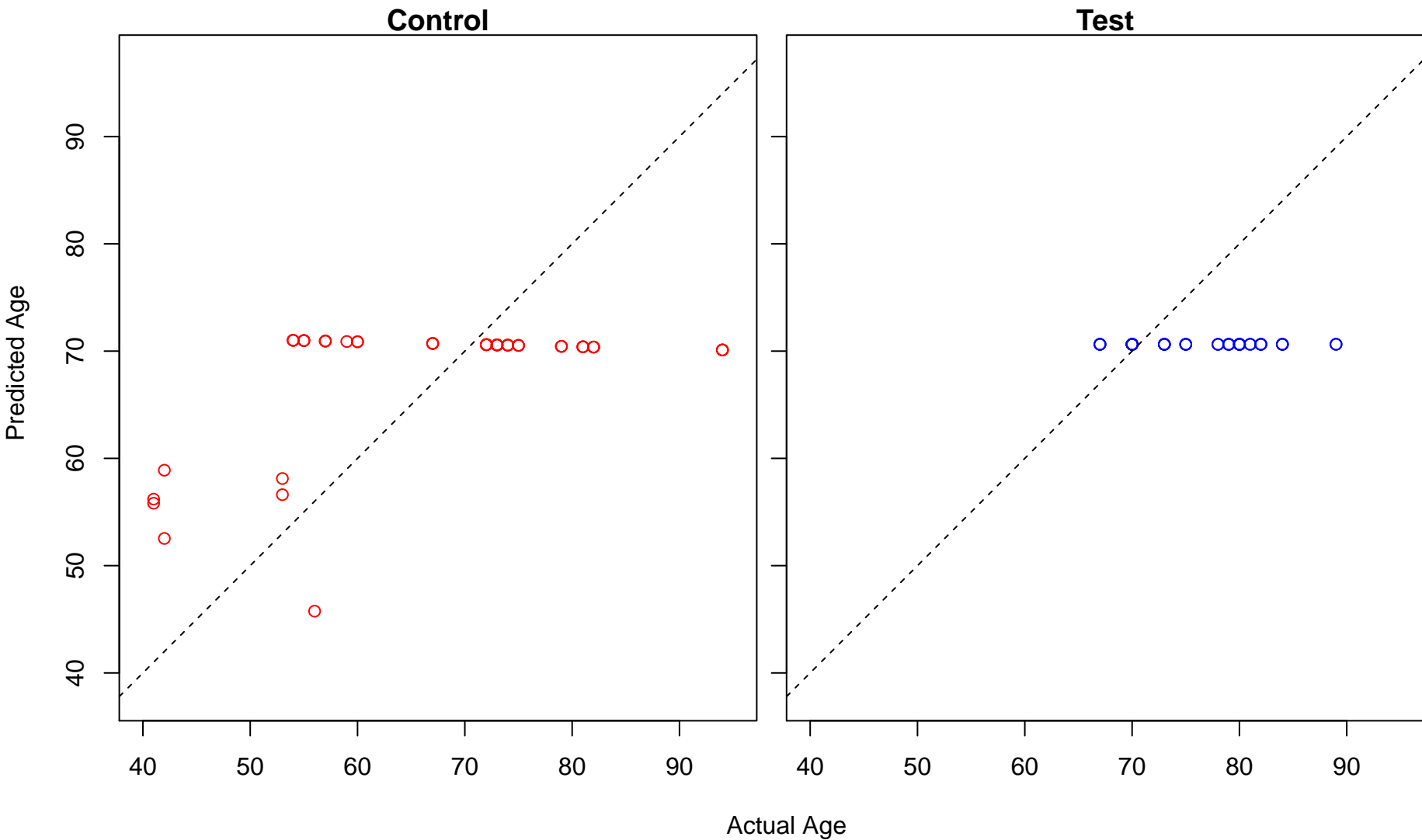
positive regulation of epithelial cell migration (Score: 0.770640)



mRNA transcription (Score: 0.770500)

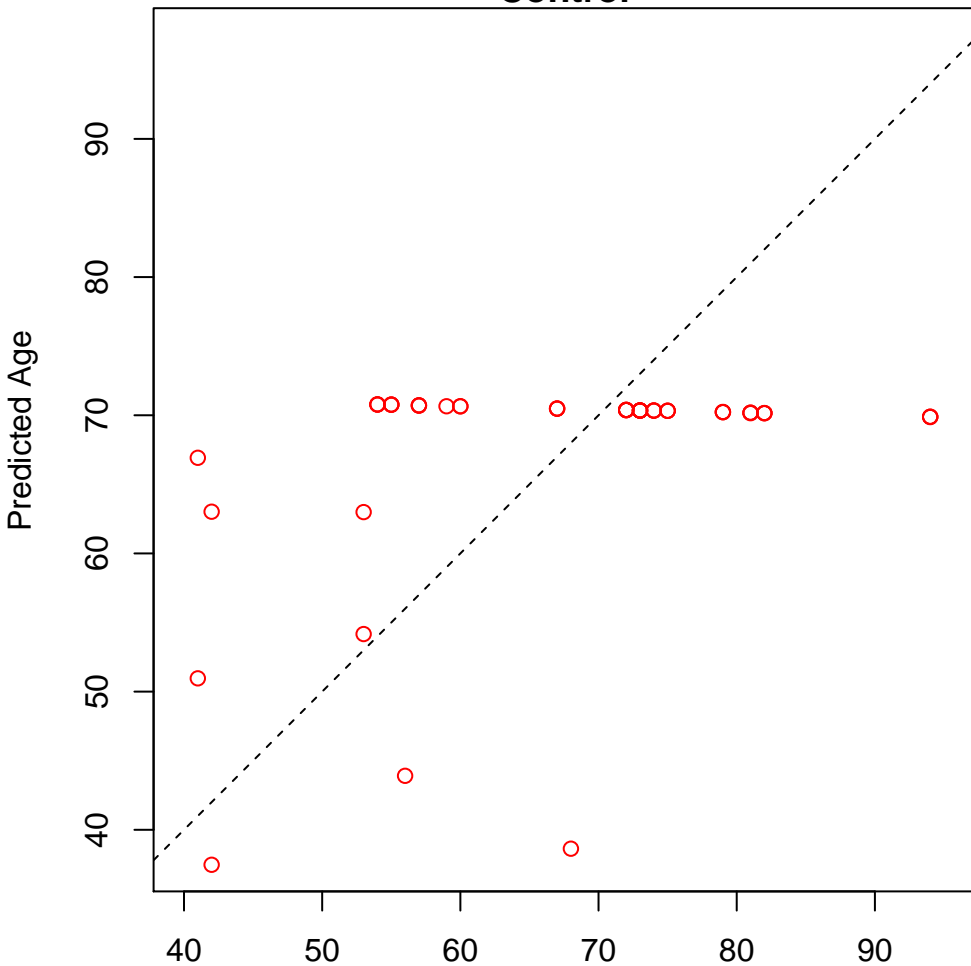


execution phase of apoptosis (Score: 0.769156)

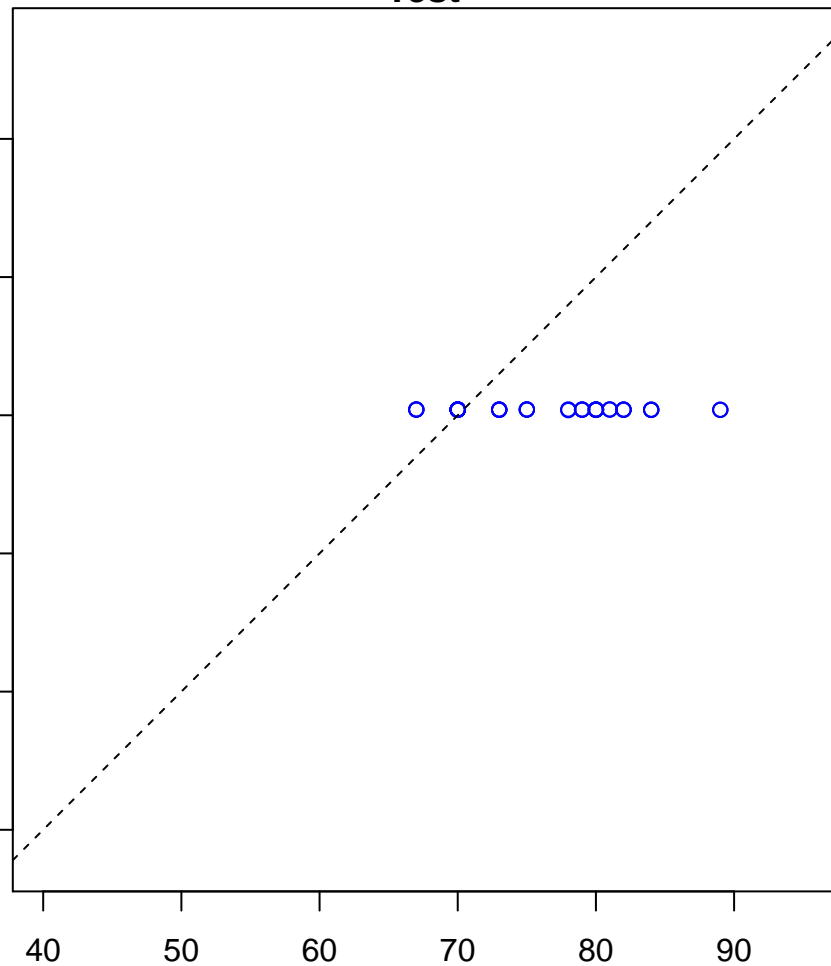


negative regulation of leukocyte activation (Score: 0.768947)

Control



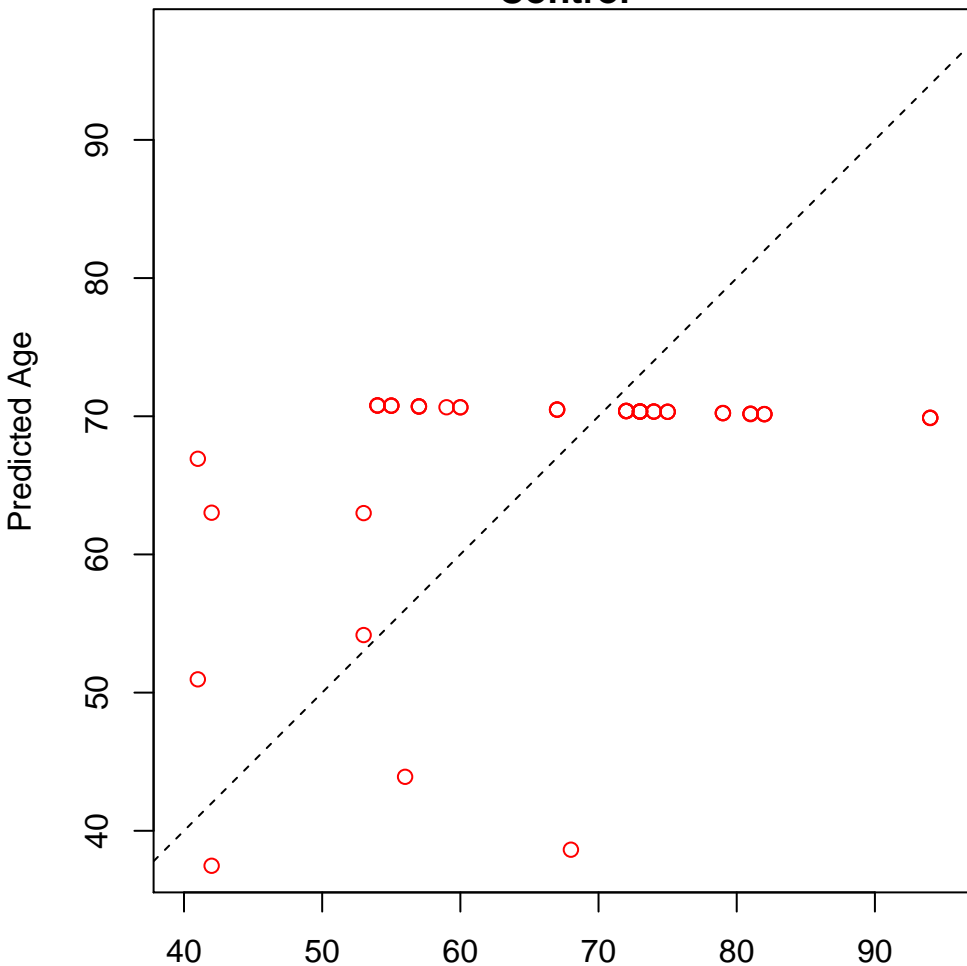
Test



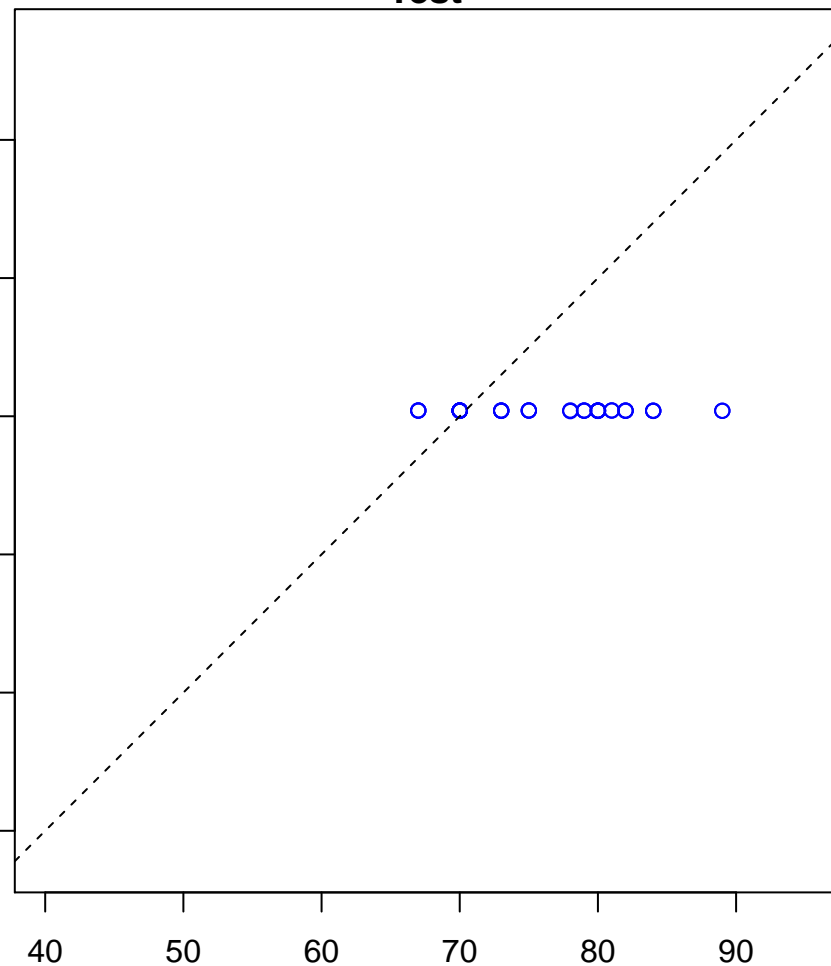
Actual Age

negative regulation of cell-cell adhesion (Score: 0.768947)

Control



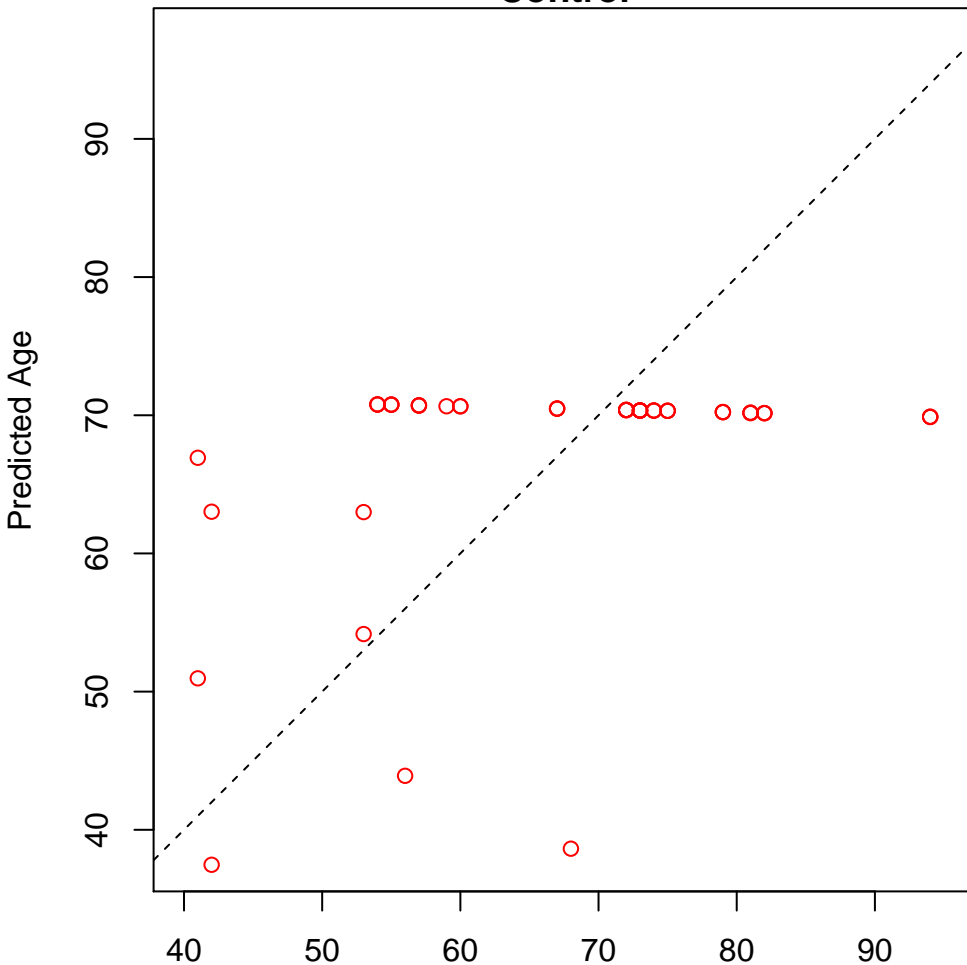
Test



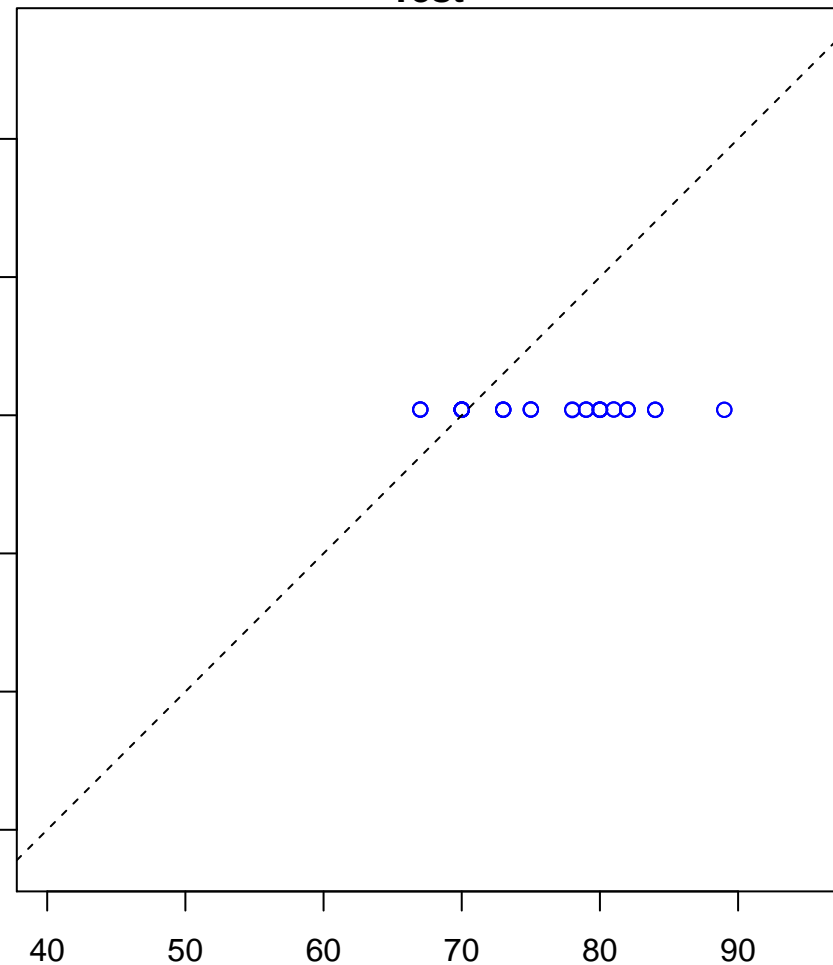
Actual Age

regulation of activated T cell proliferation (Score: 0.768947)

Control



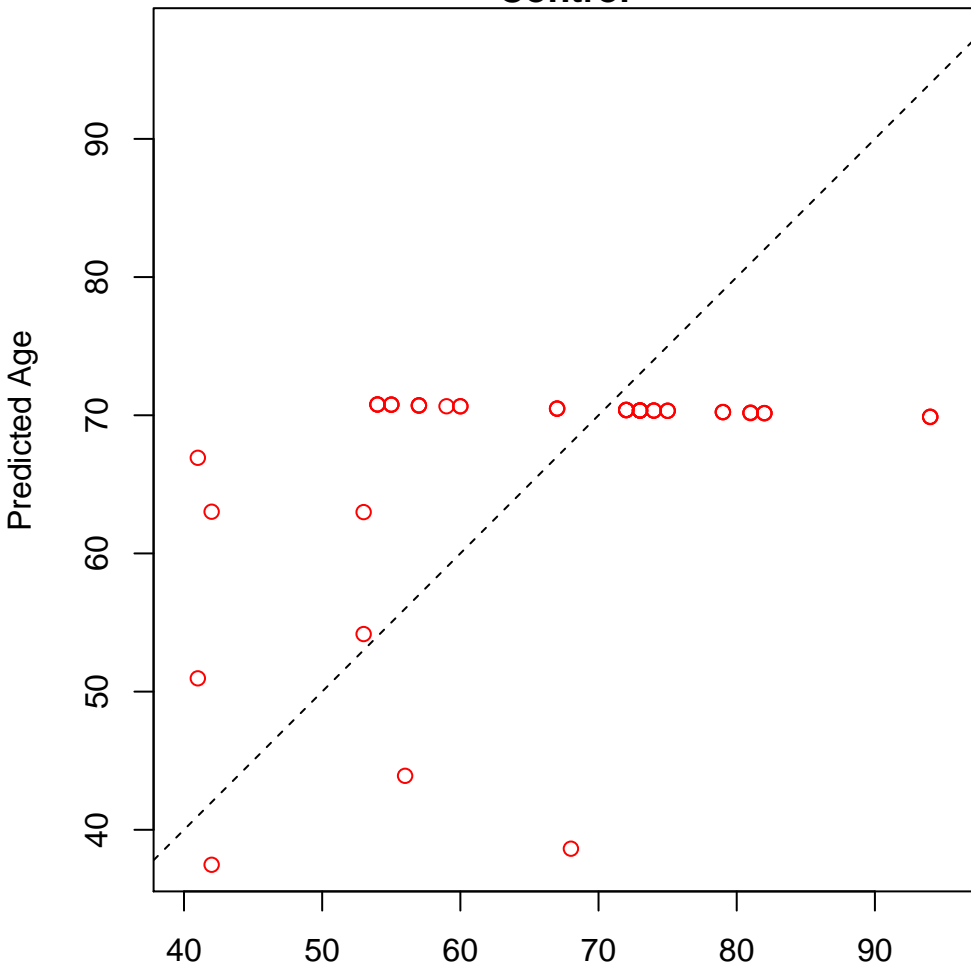
Test



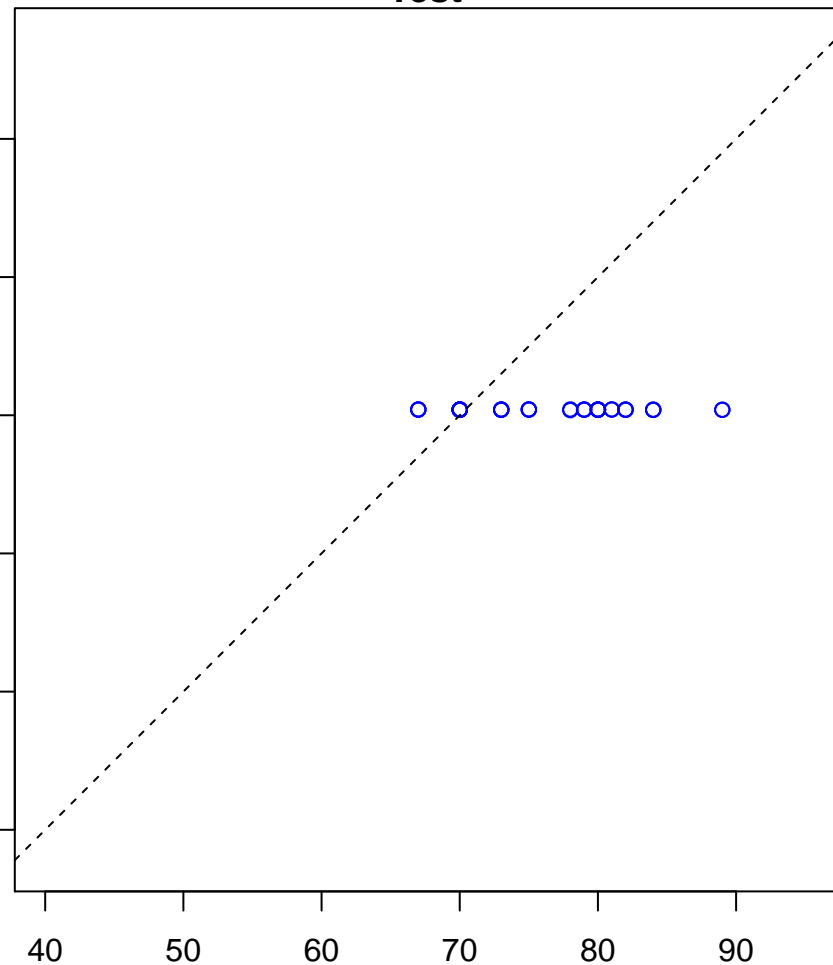
Actual Age

negative regulation of cell activation (Score: 0.768947)

Control



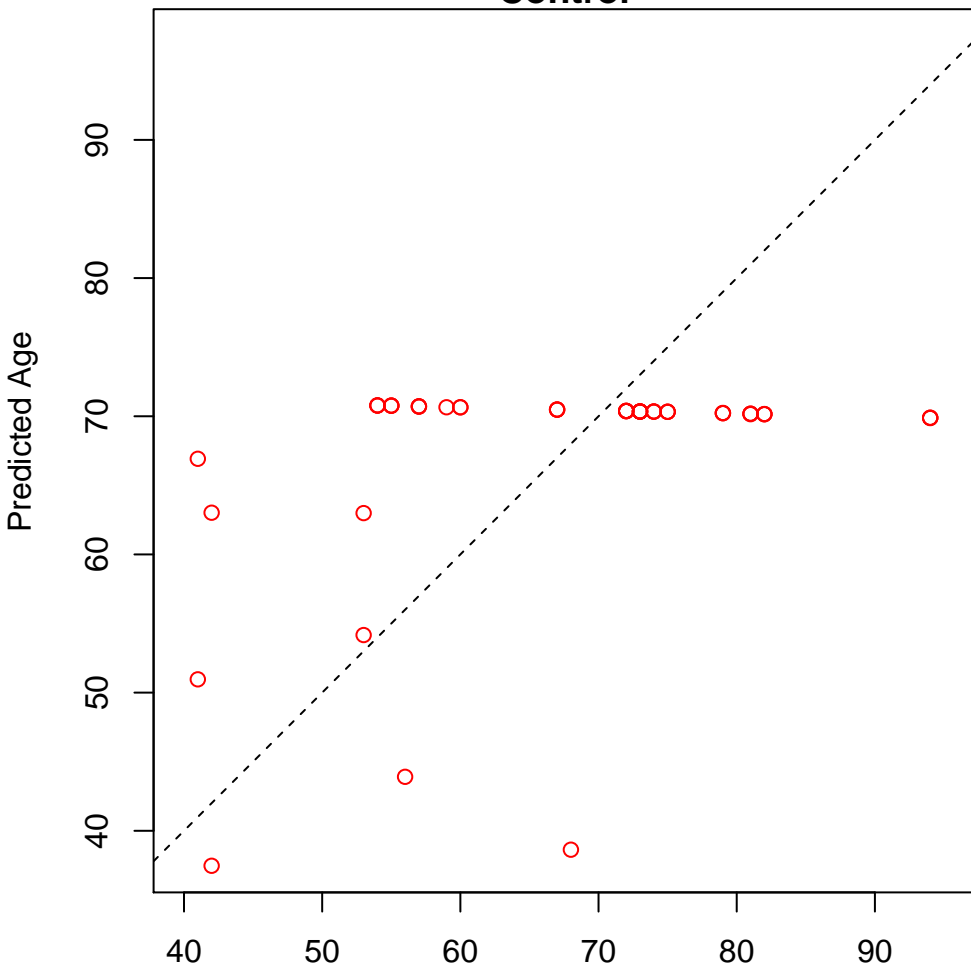
Test



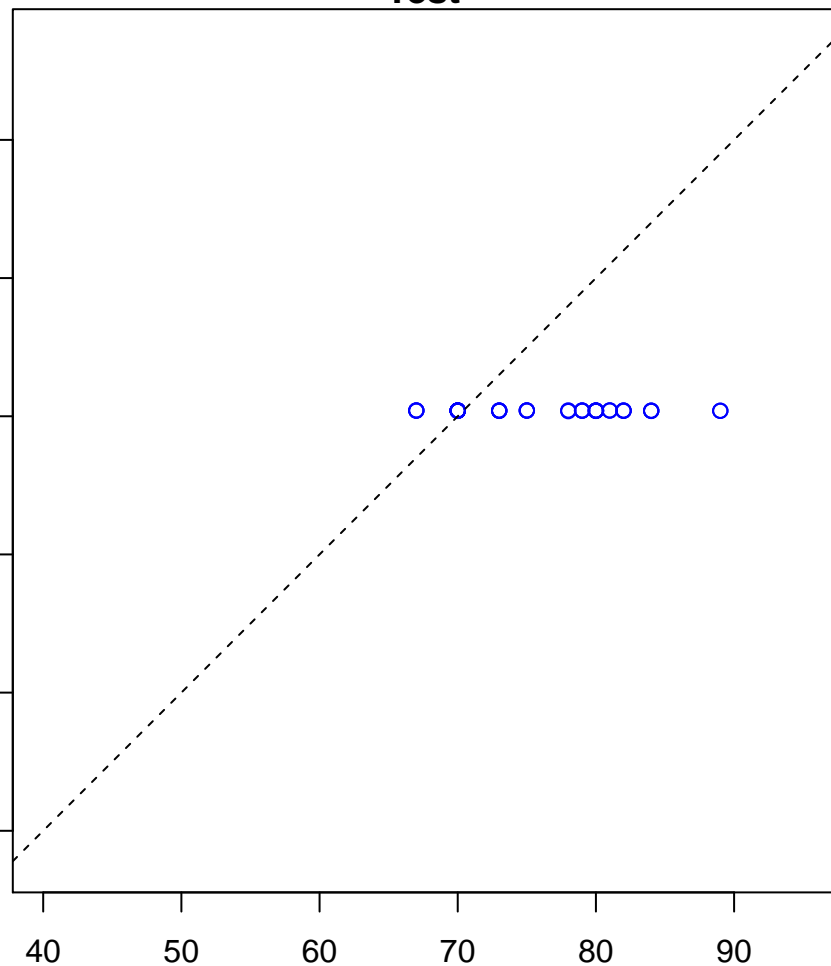
Actual Age

negative regulation of T cell activation (Score: 0.768947)

Control

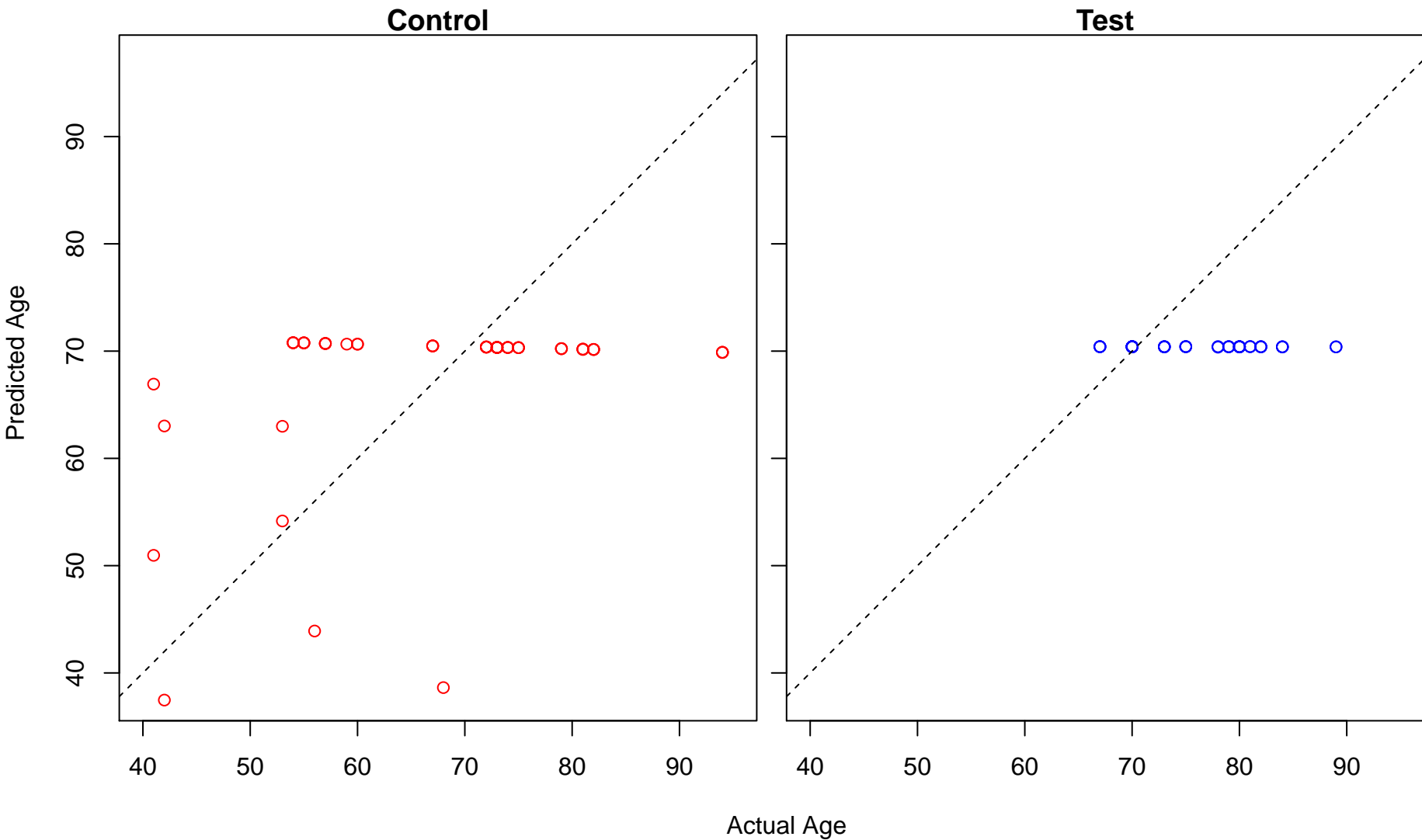


Test

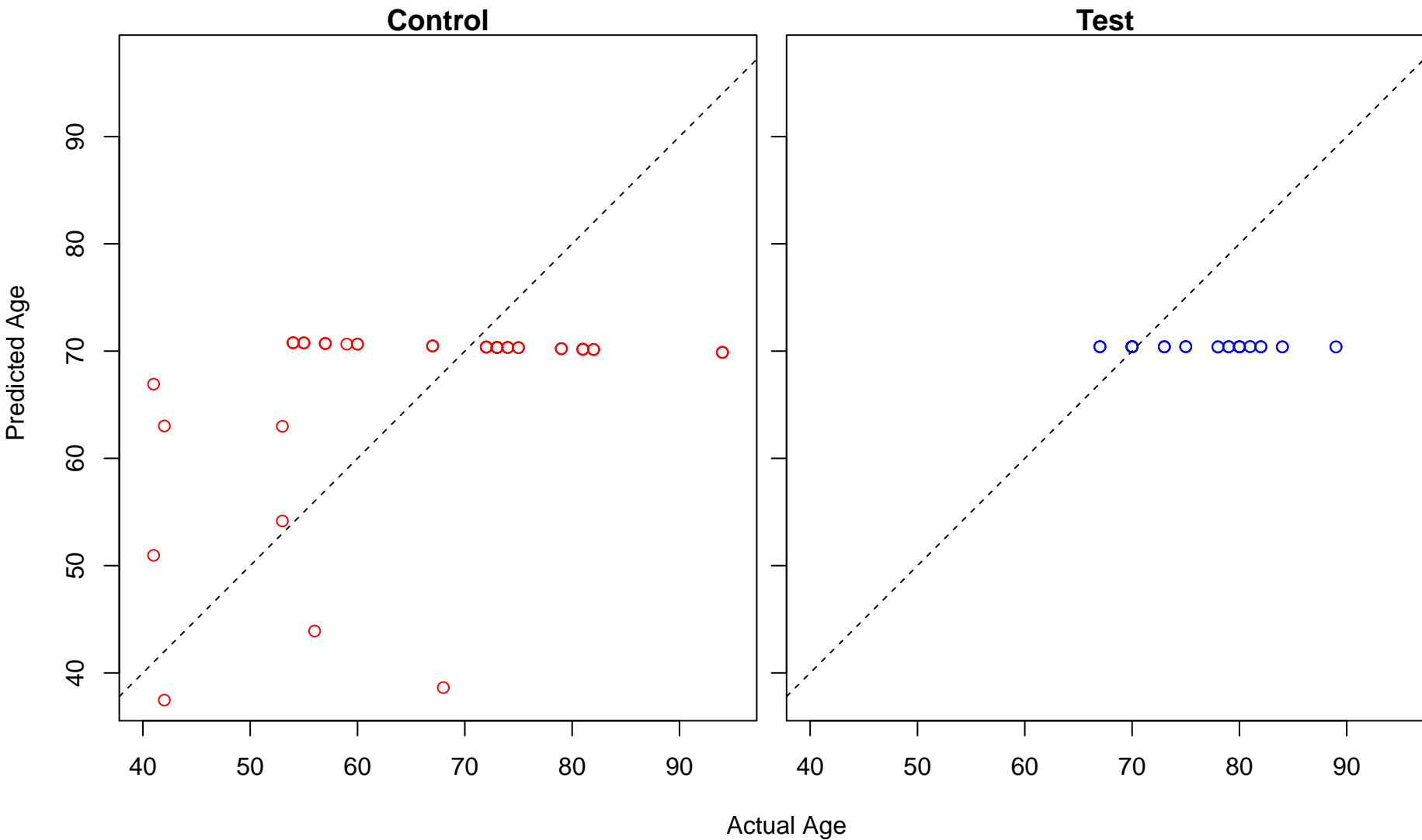


Actual Age

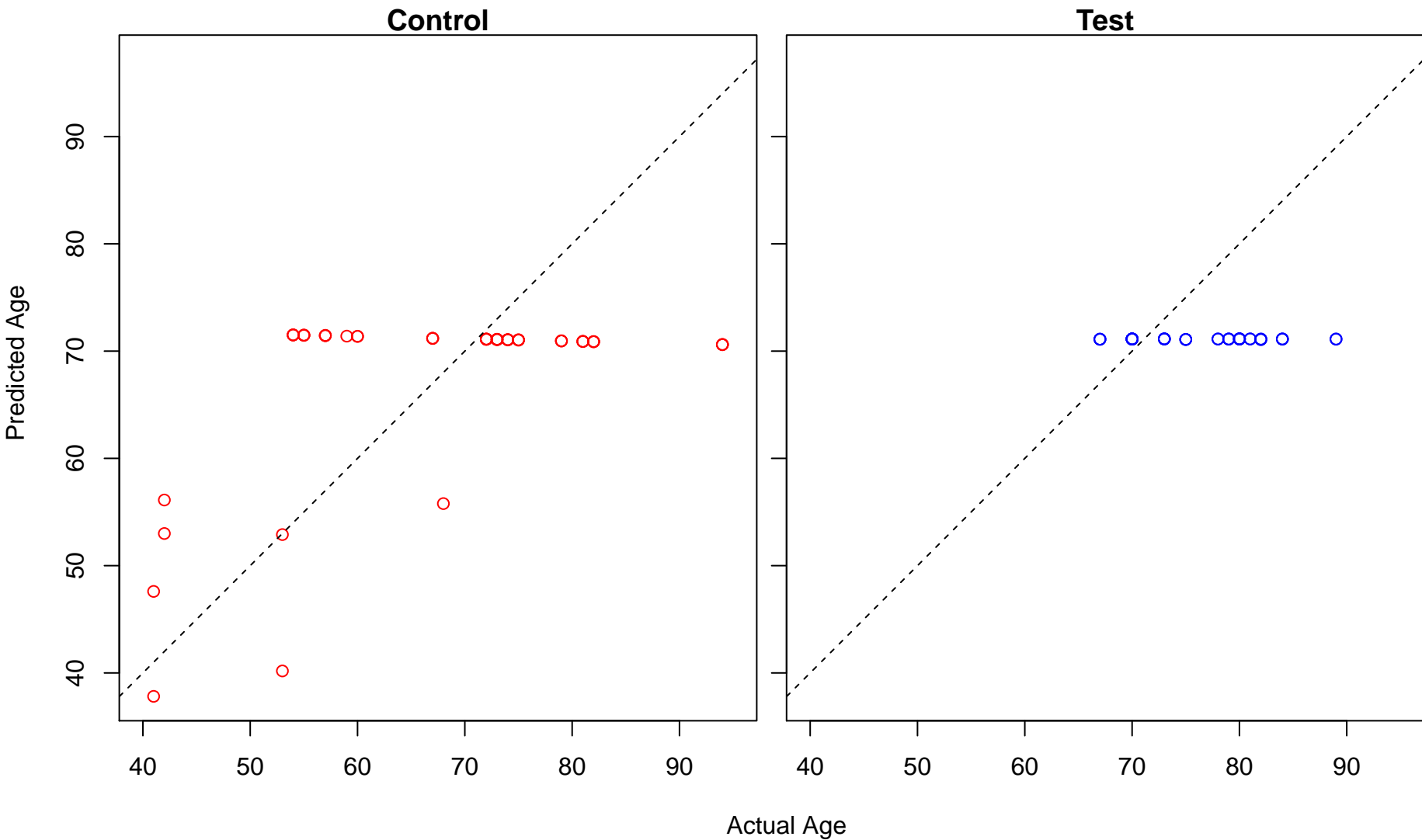
negative regulation of lymphocyte activation (Score: 0.768947)



negative regulation of leukocyte cell-cell adhesion (Score: 0.768947)

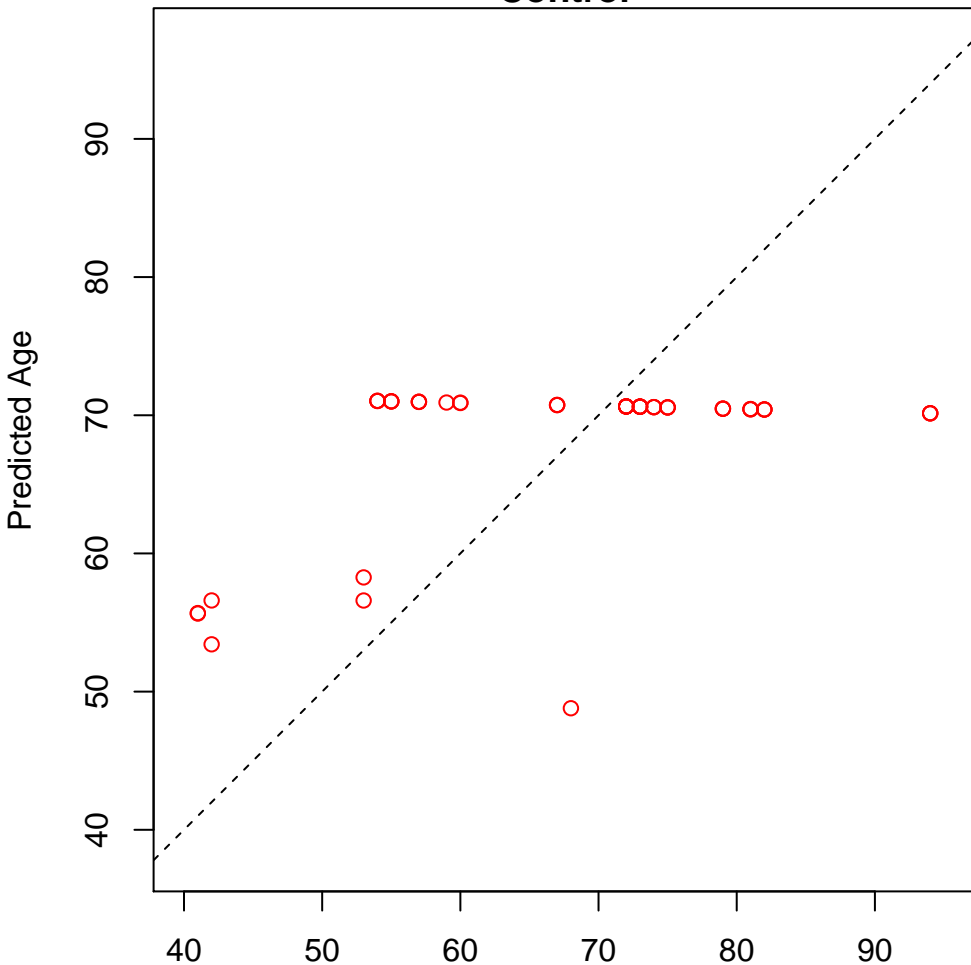


angiogenesis (Score: 0.768734)

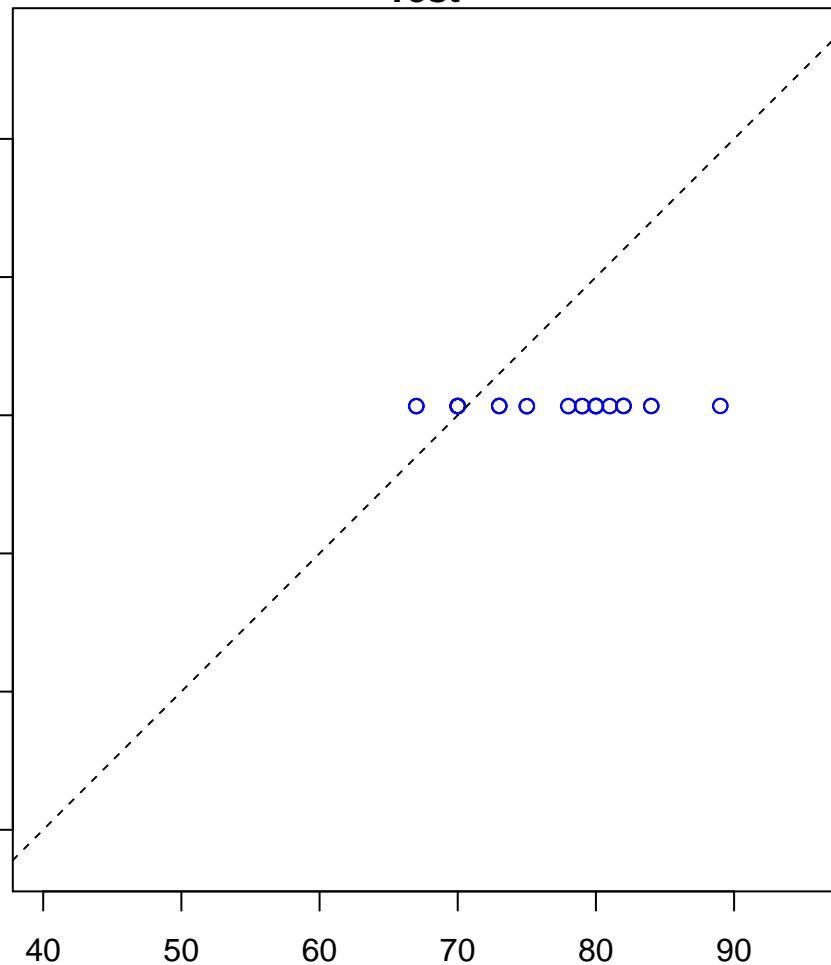


protein folding in endoplasmic reticulum (Score: 0.768651)

Control

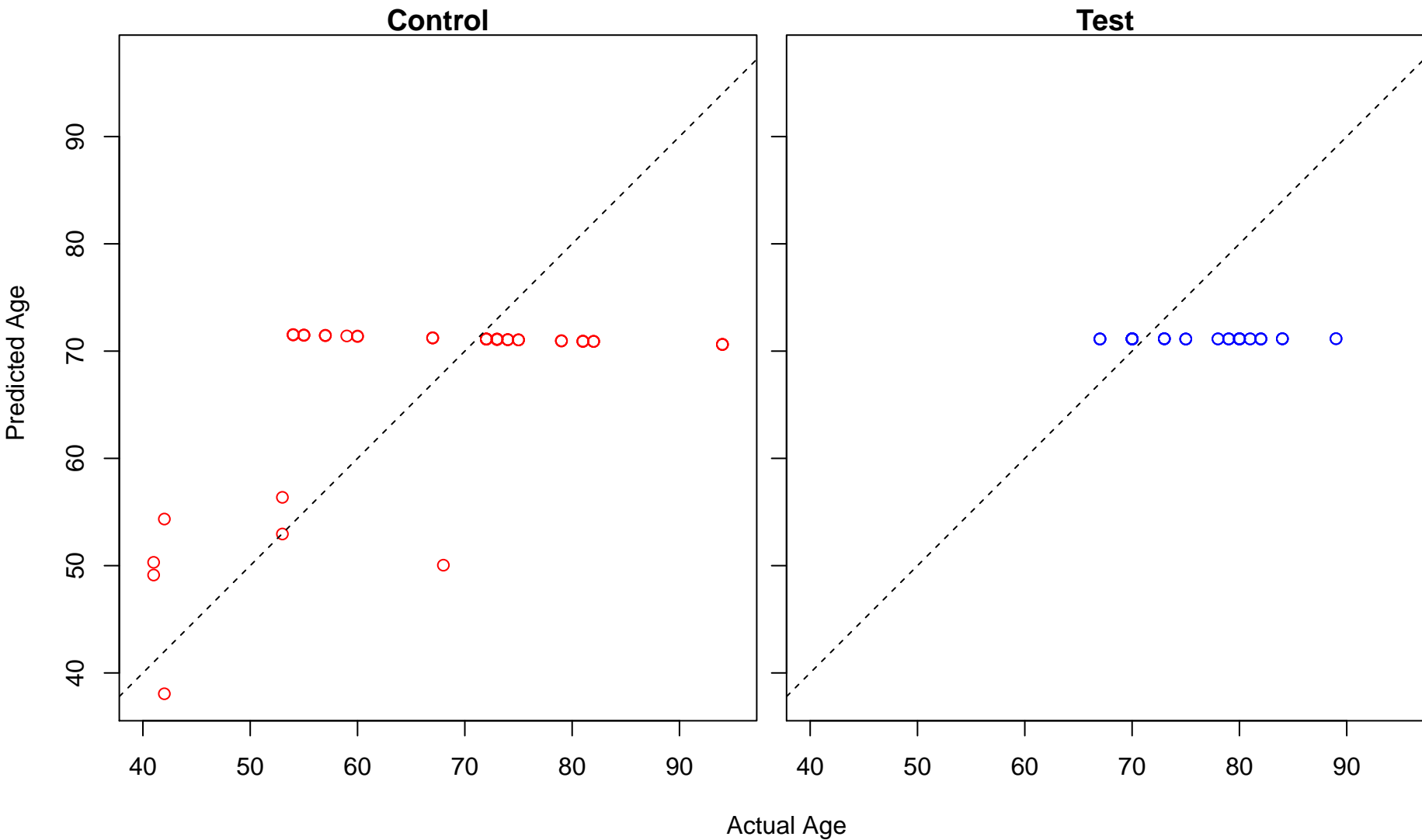


Test

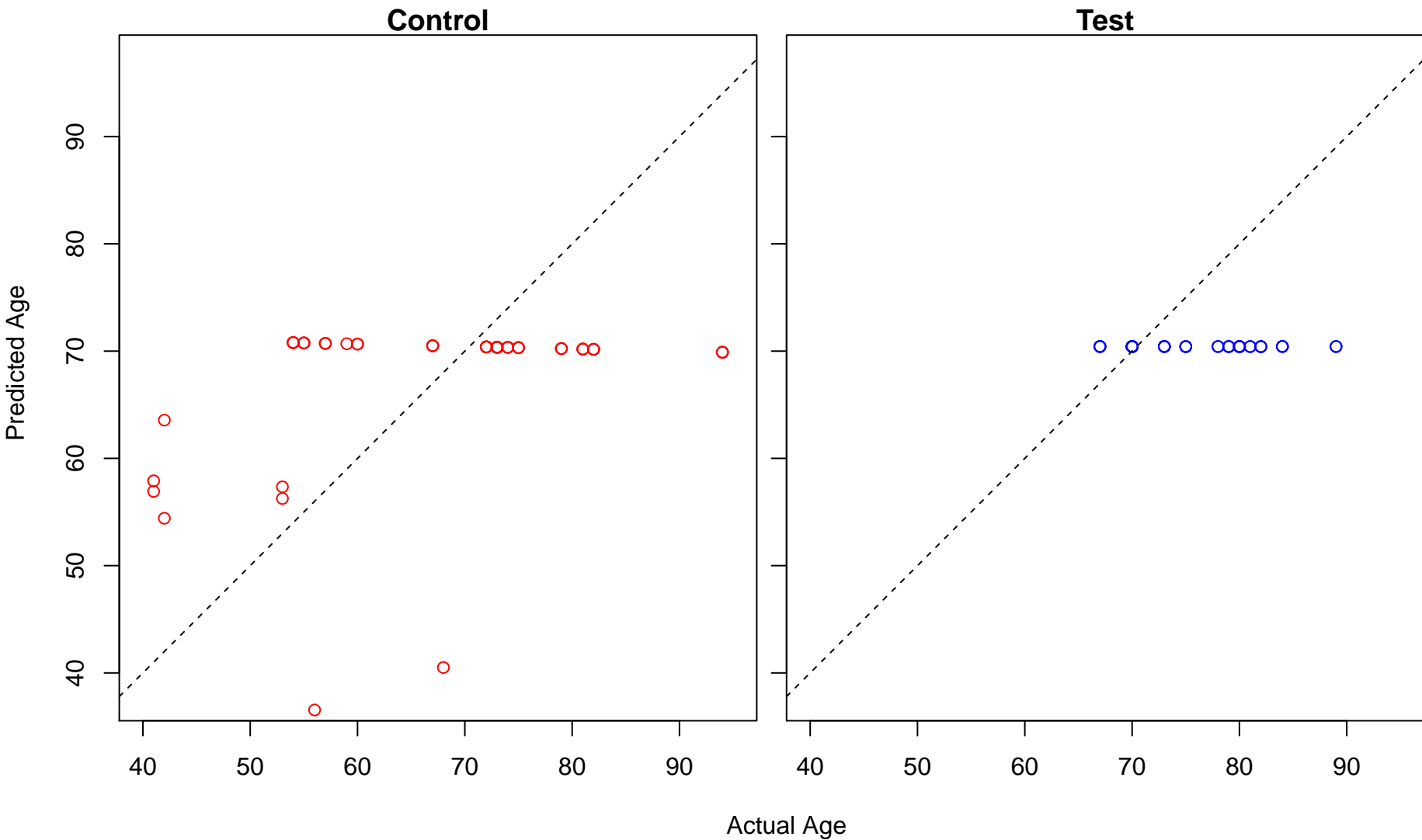


Actual Age

erythrocyte homeostasis (Score: 0.768466)

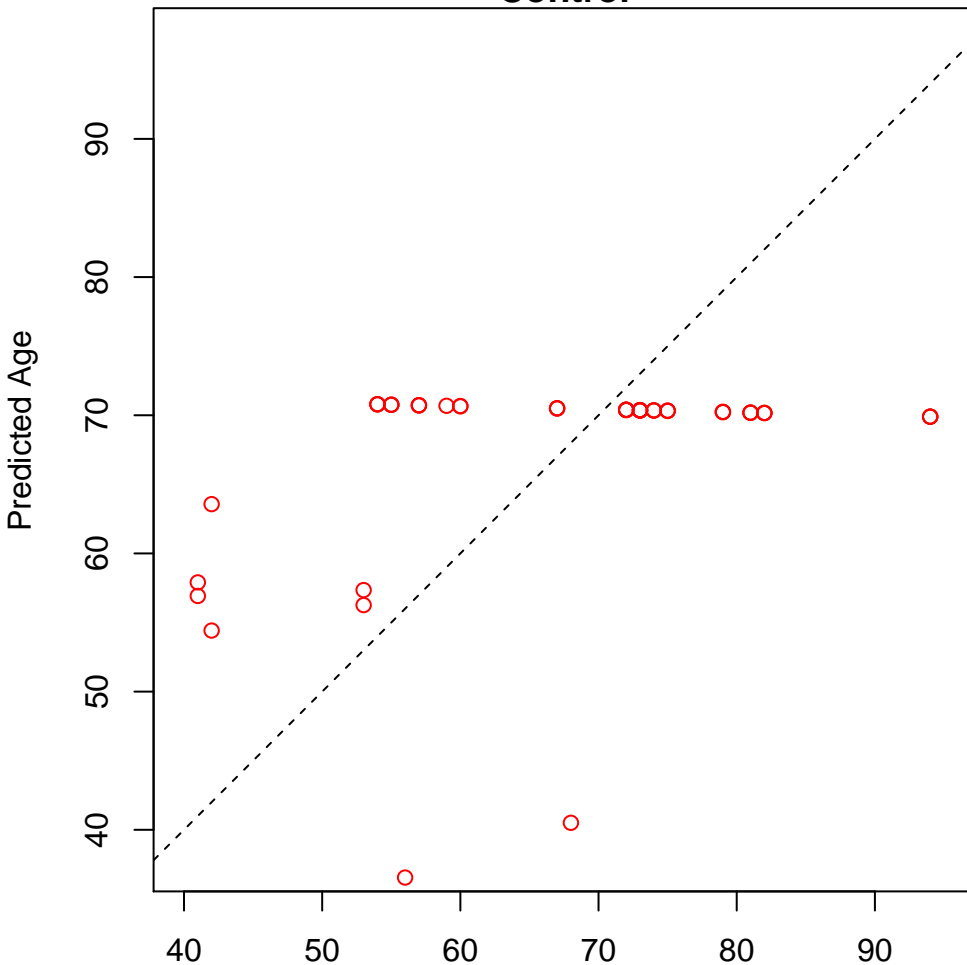


positive regulation of mitotic nuclear division (Score: 0.767588)

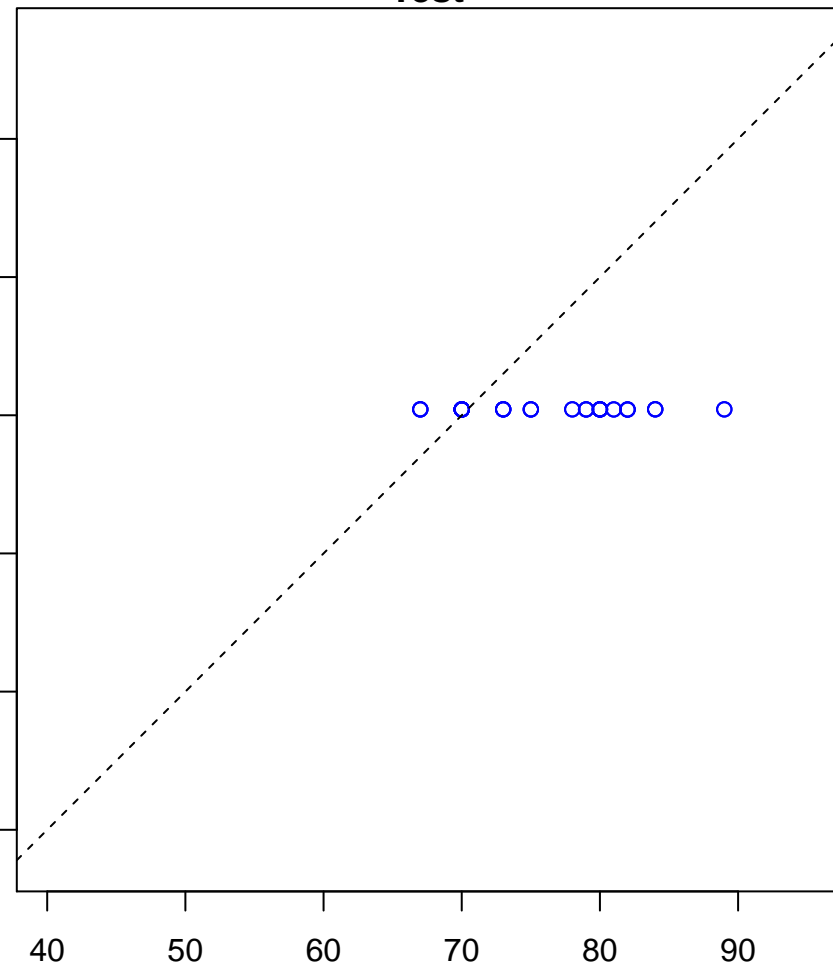


positive regulation of nuclear division (Score: 0.767588)

Control

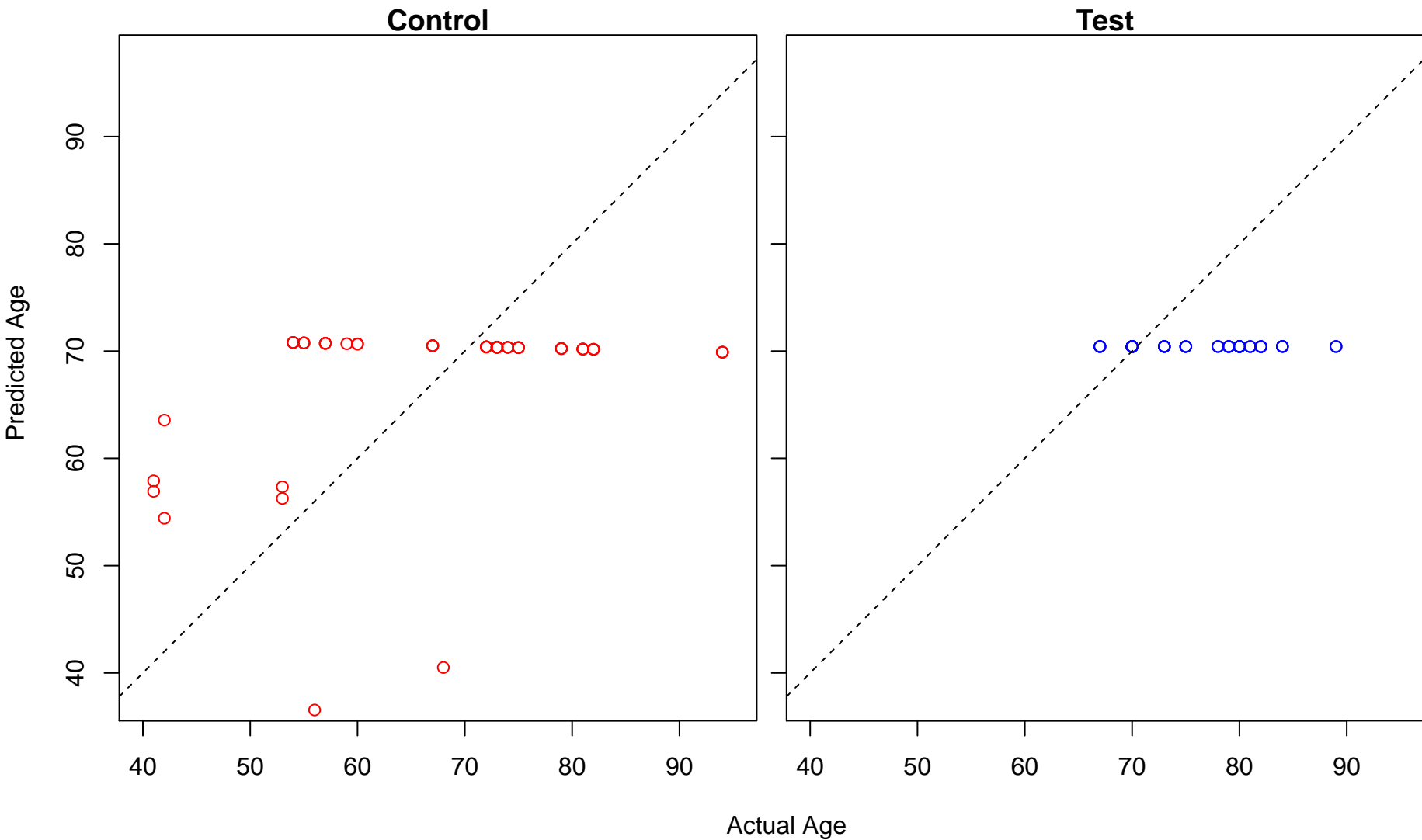


Test



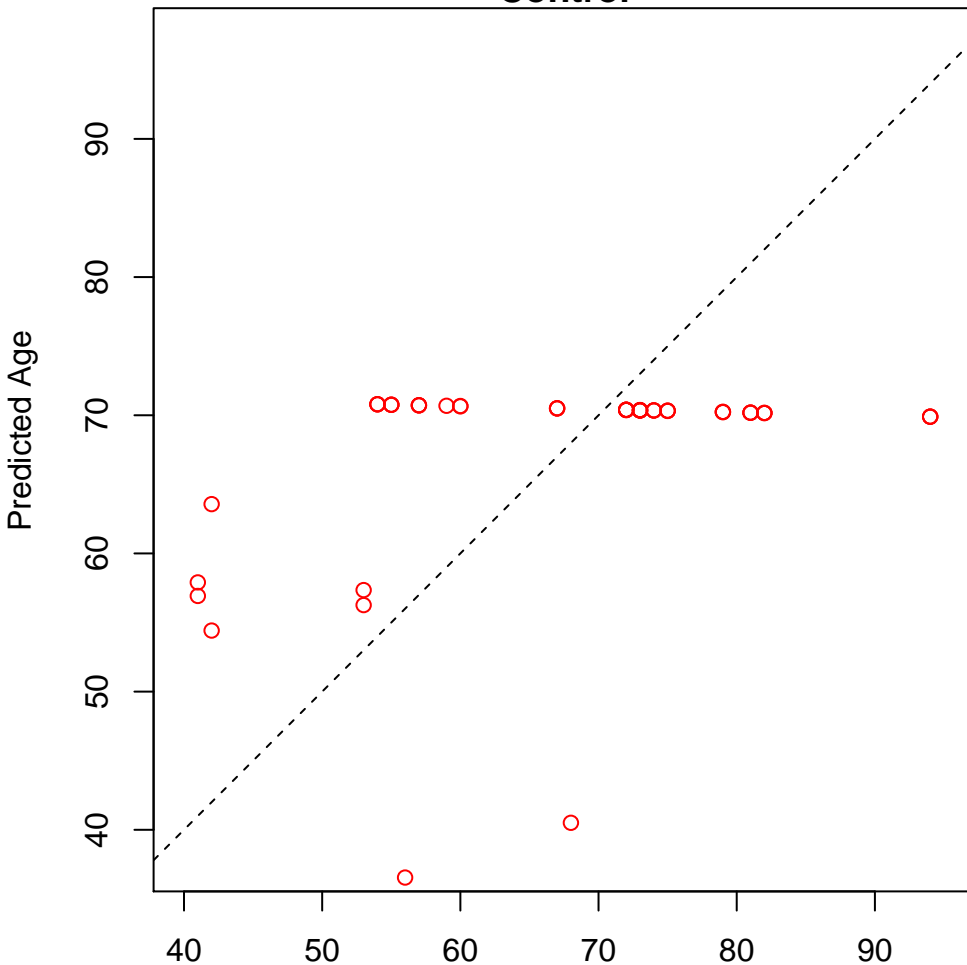
Actual Age

regulation of spindle assembly (Score: 0.767588)

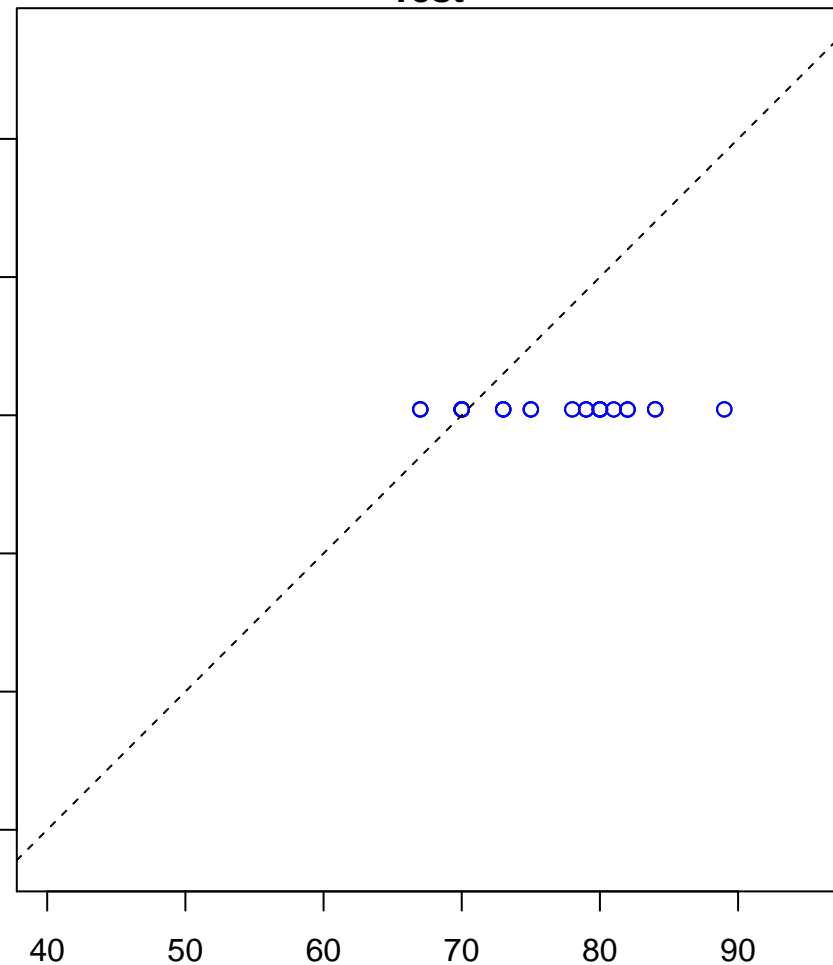


regulation of metaphase plate congression (Score: 0.767588)

Control



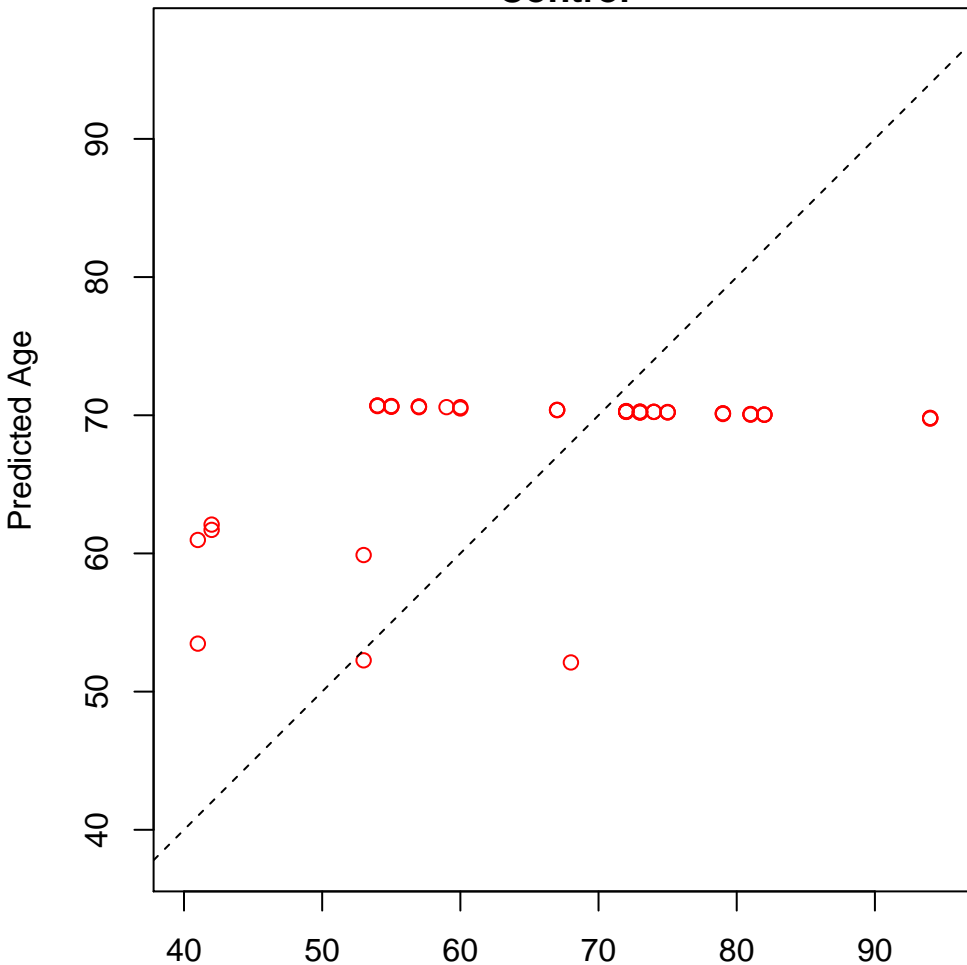
Test



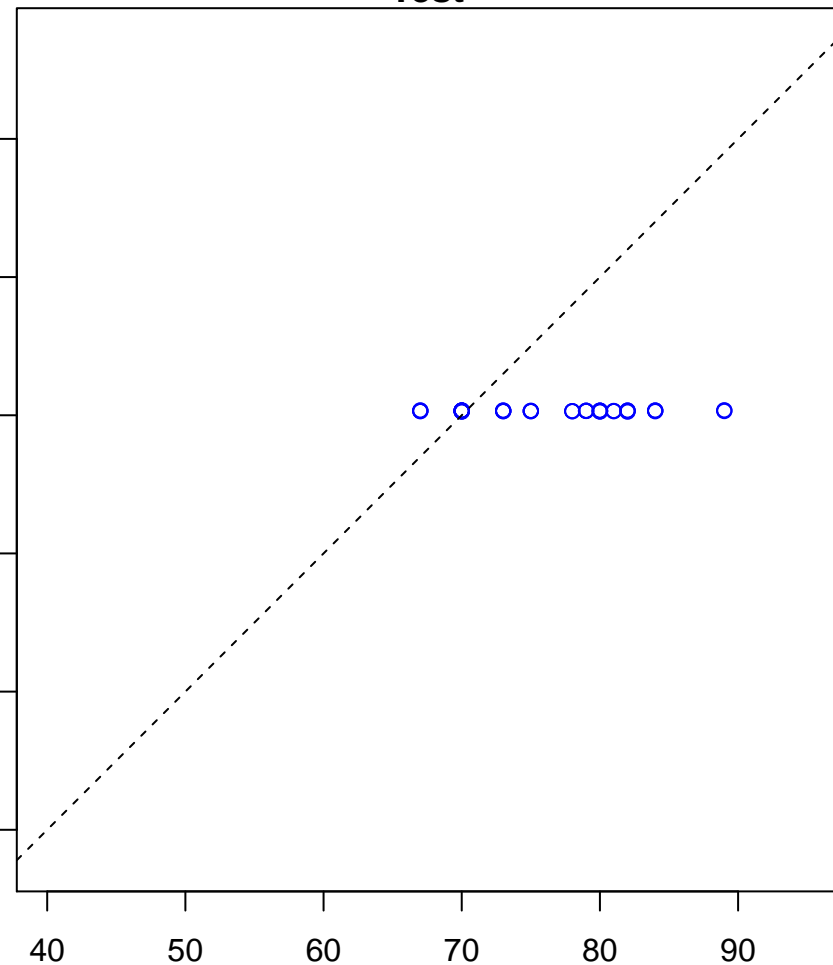
Actual Age

negative regulation of GTPase activity (Score: 0.766888)

Control



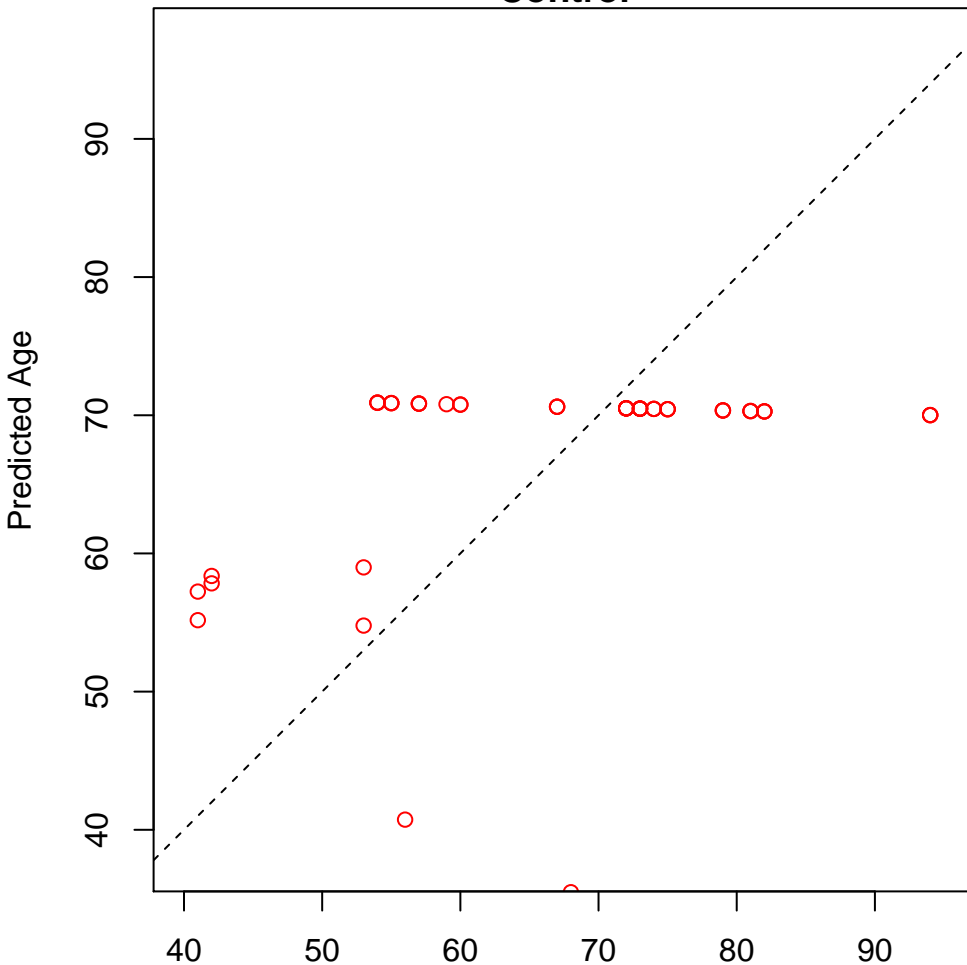
Test



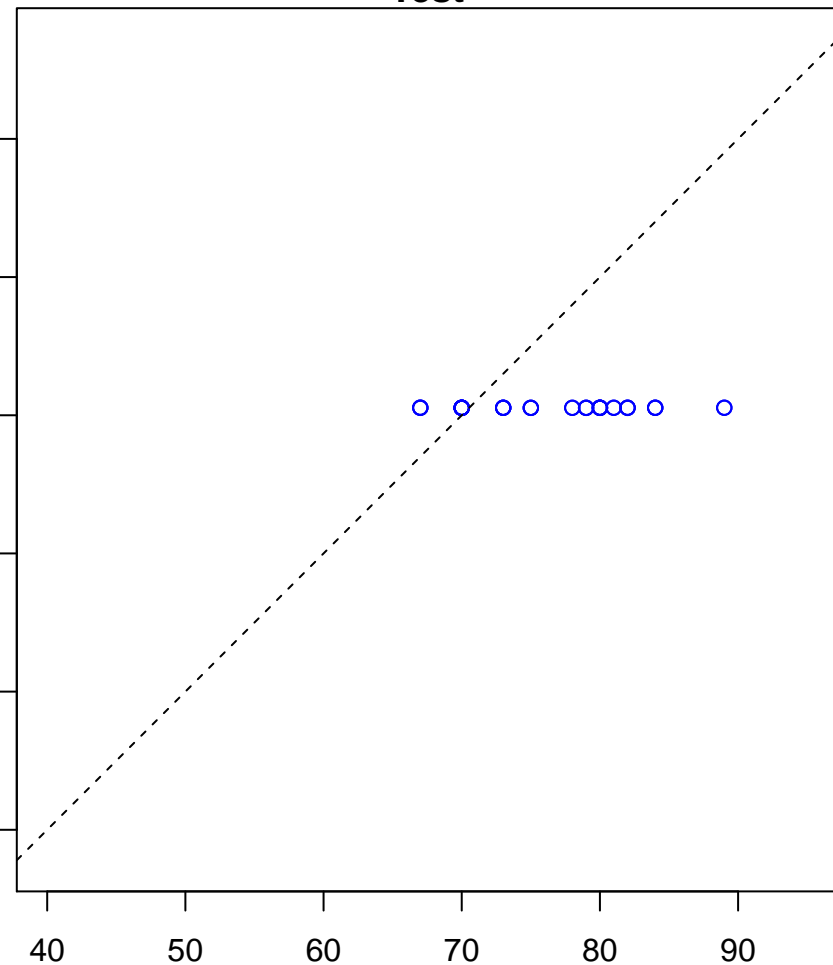
Actual Age

regulation of sister chromatid segregation (Score: 0.766585)

Control



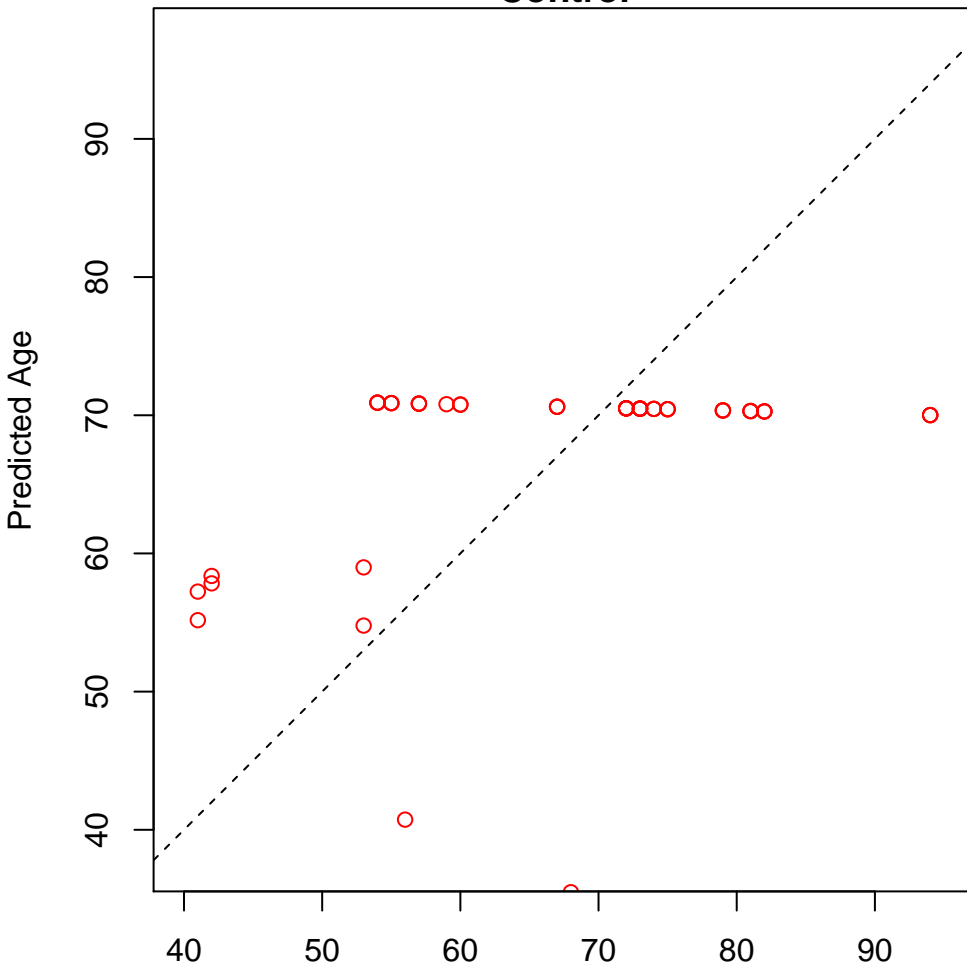
Test



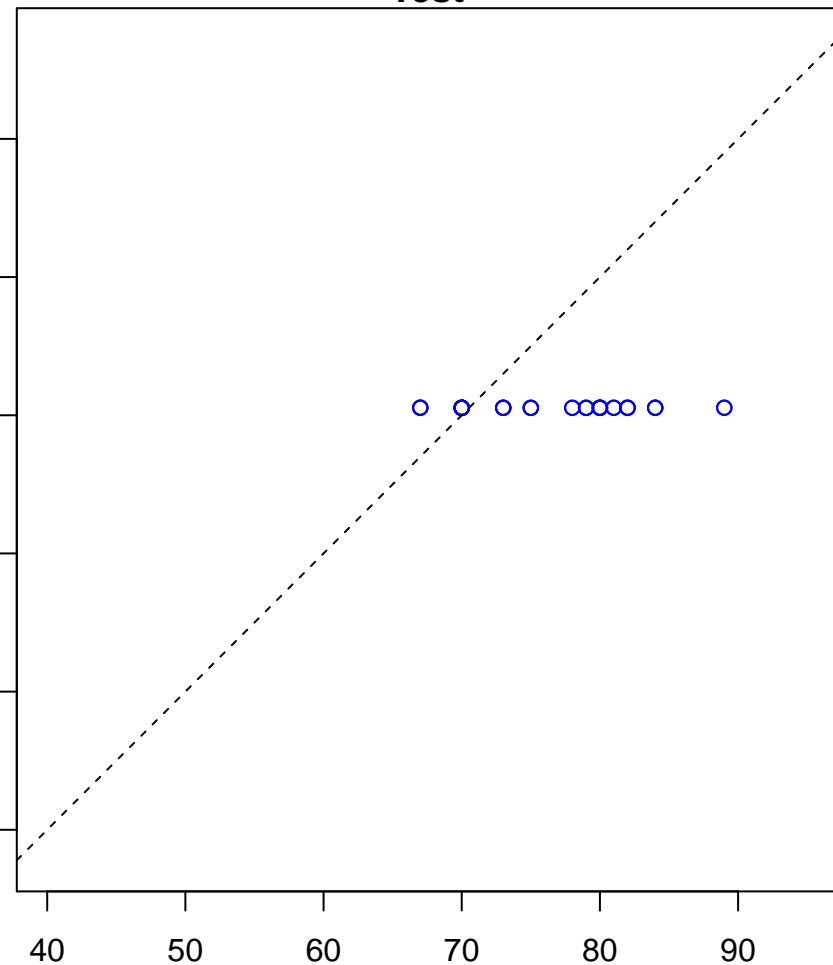
Actual Age

regulation of chromosome segregation (Score: 0.766585)

Control

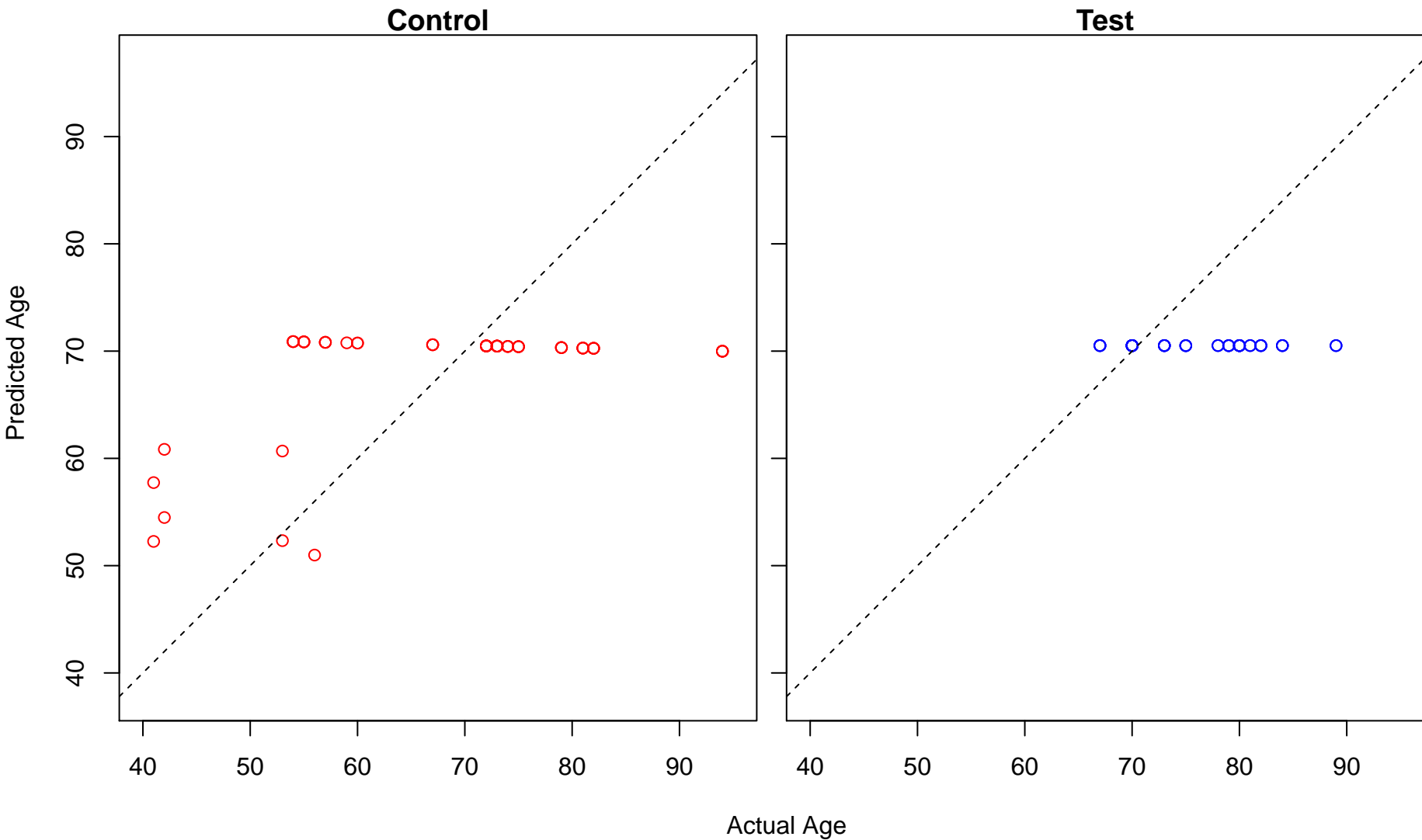


Test



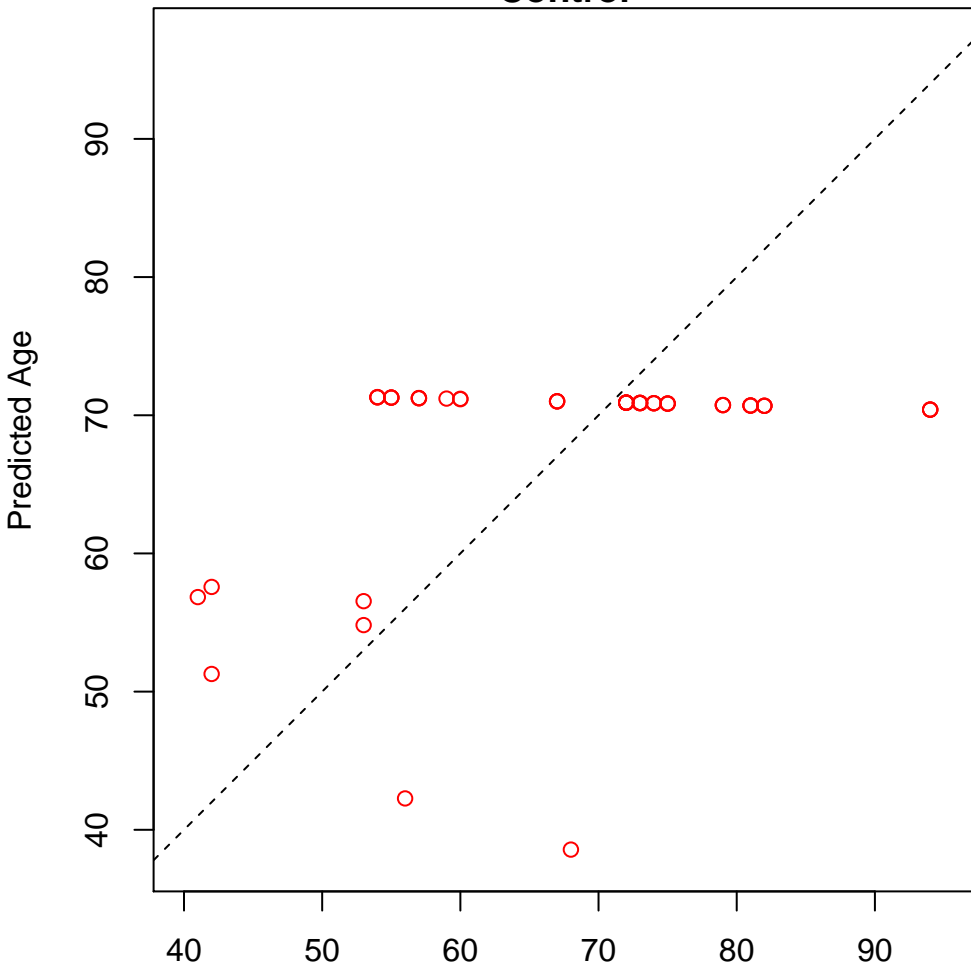
Actual Age

regulation of DNA damage response, signal transduction by p53 class mediator (Score: 0.766533)

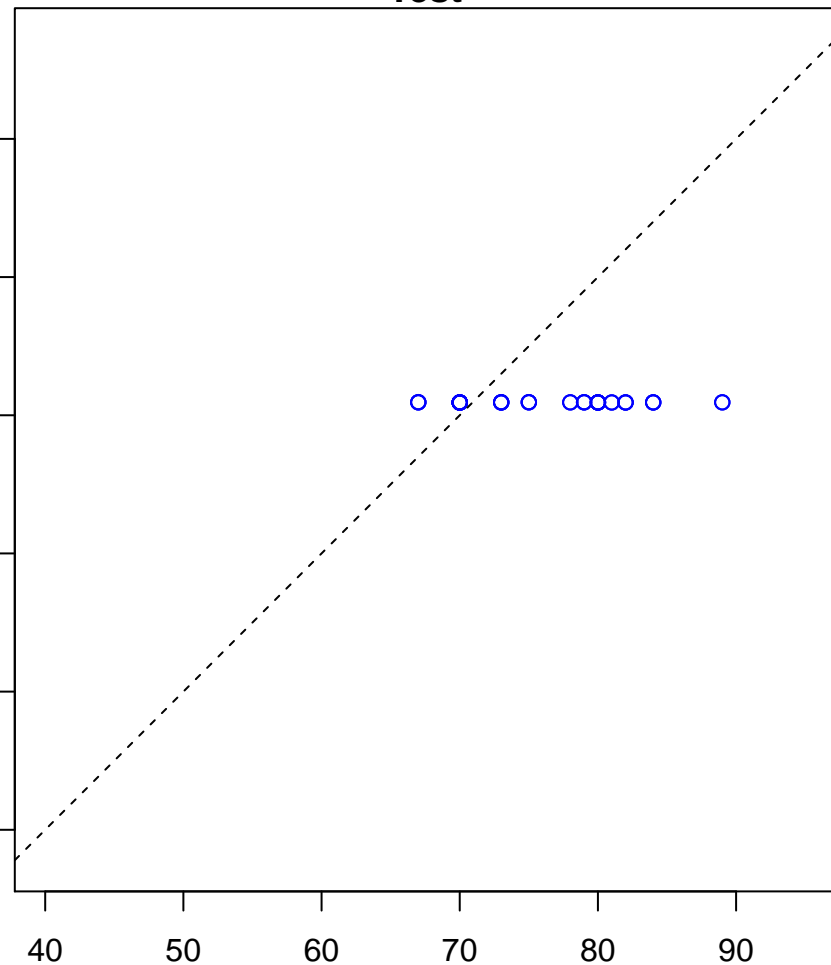


protein dephosphorylation (Score: 0.765774)

Control

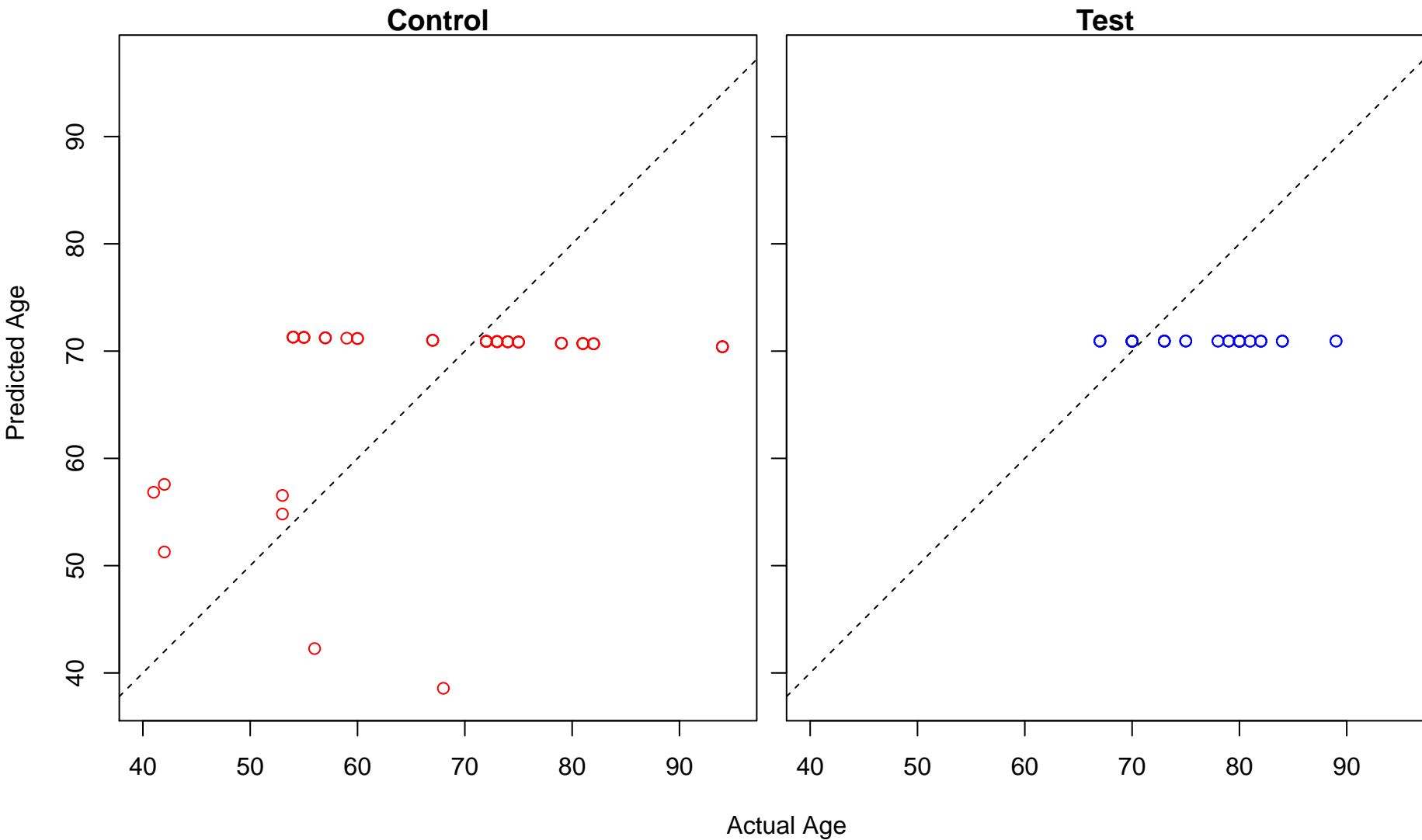


Test

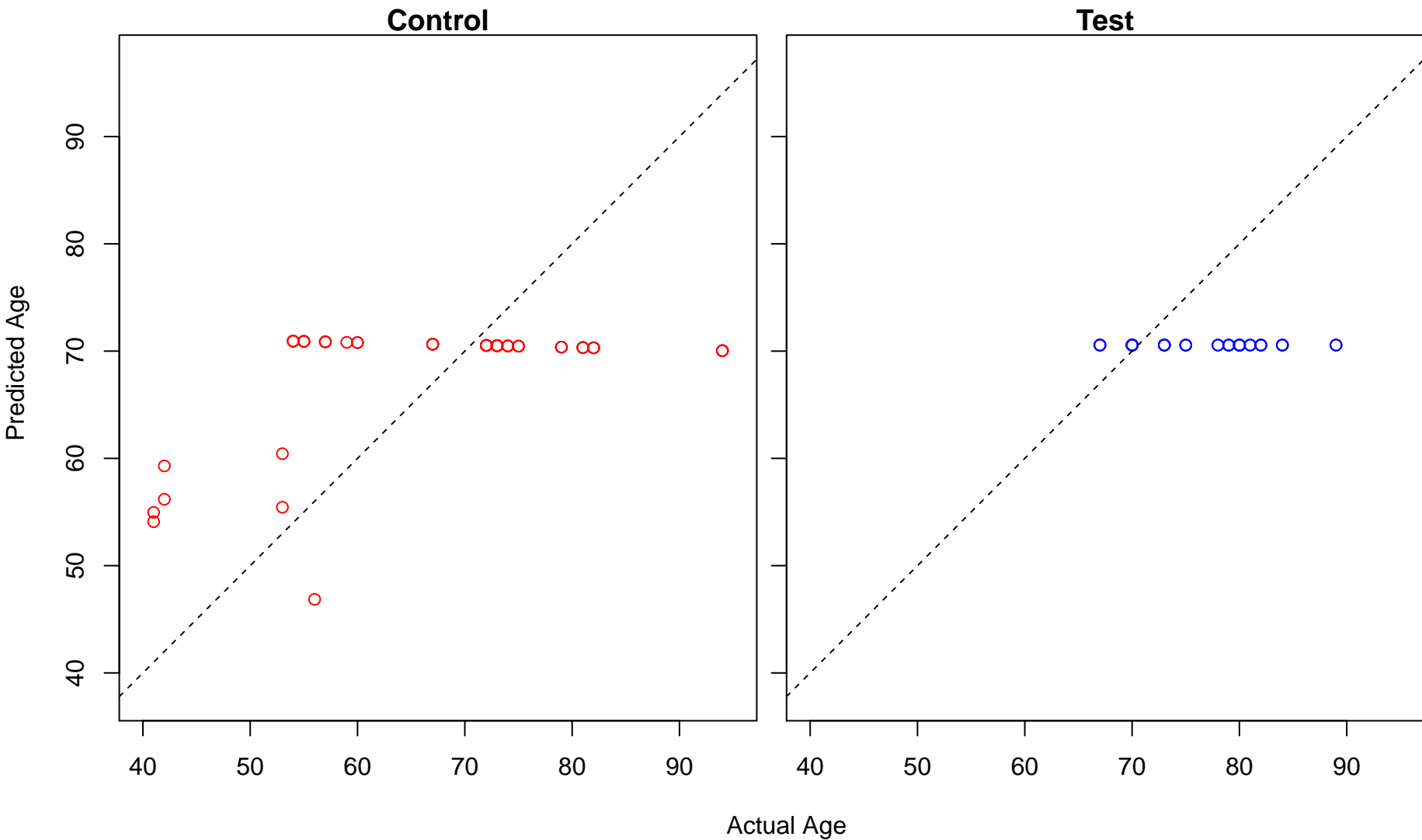


Actual Age

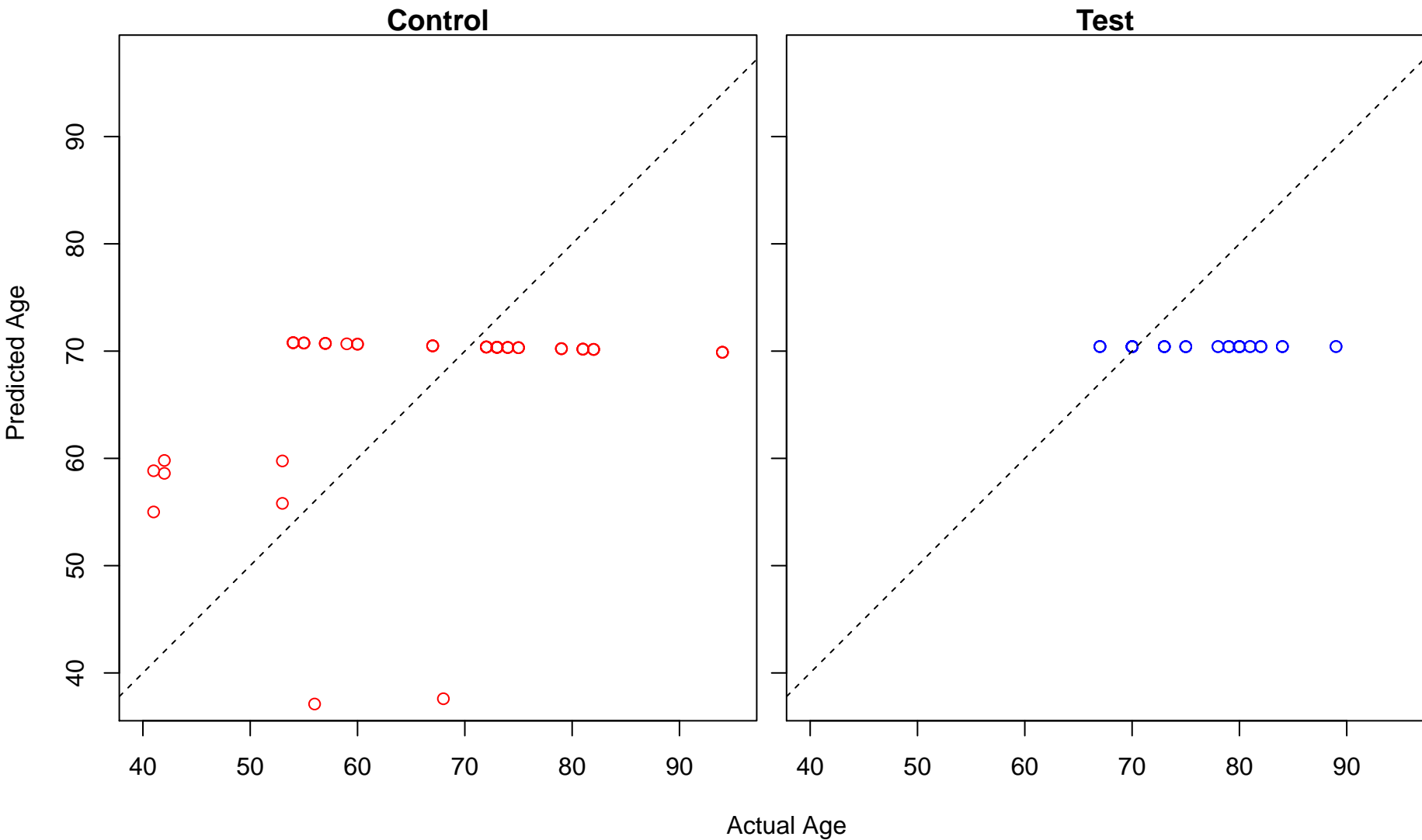
dephosphorylation (Score: 0.765774)



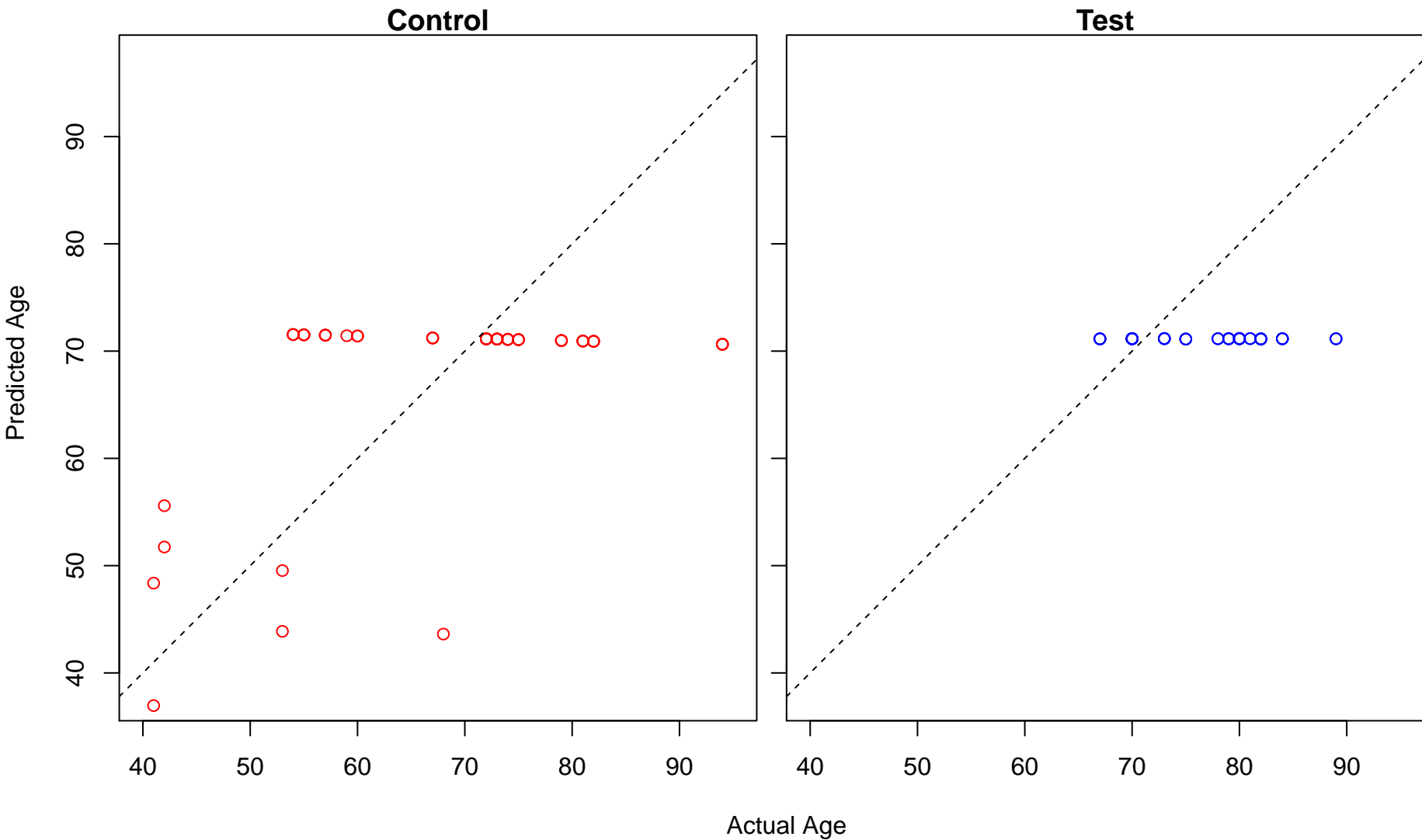
regulation of response to DNA damage stimulus (Score: 0.765052)



positive regulation of chromosome segregation (Score: 0.763611)

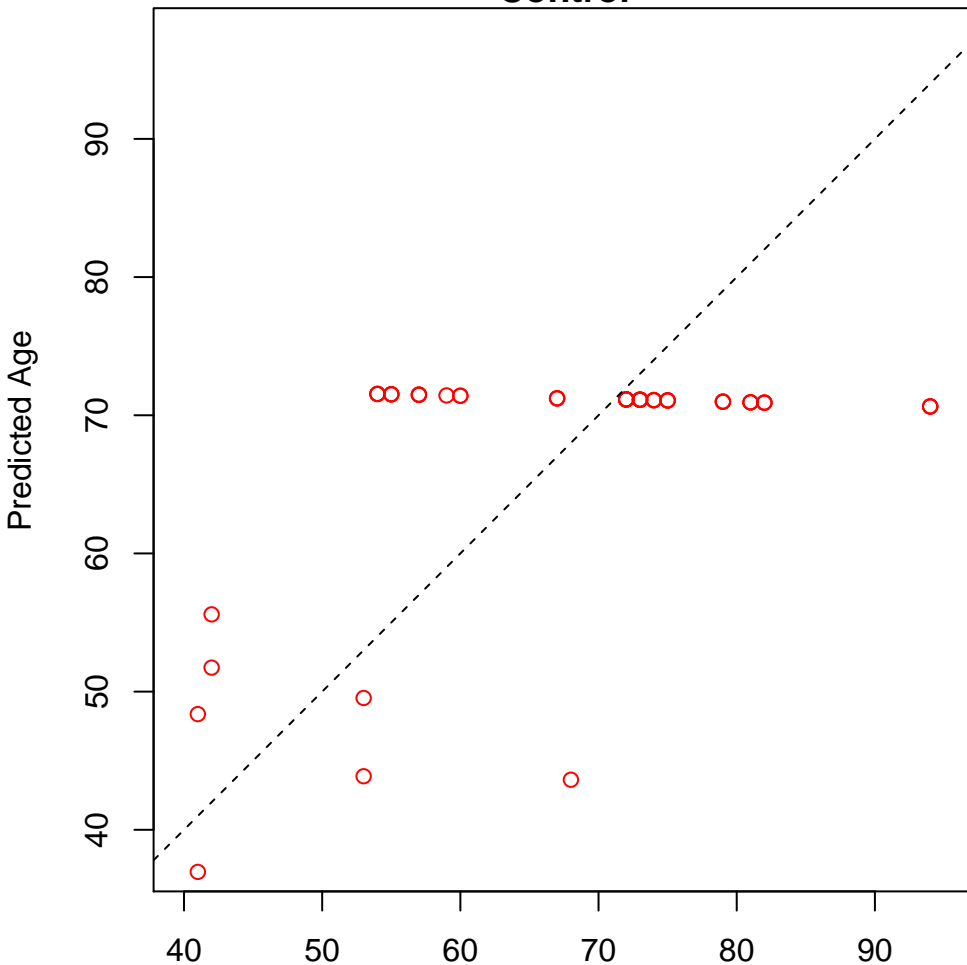


cellular response to starvation (Score: 0.763543)

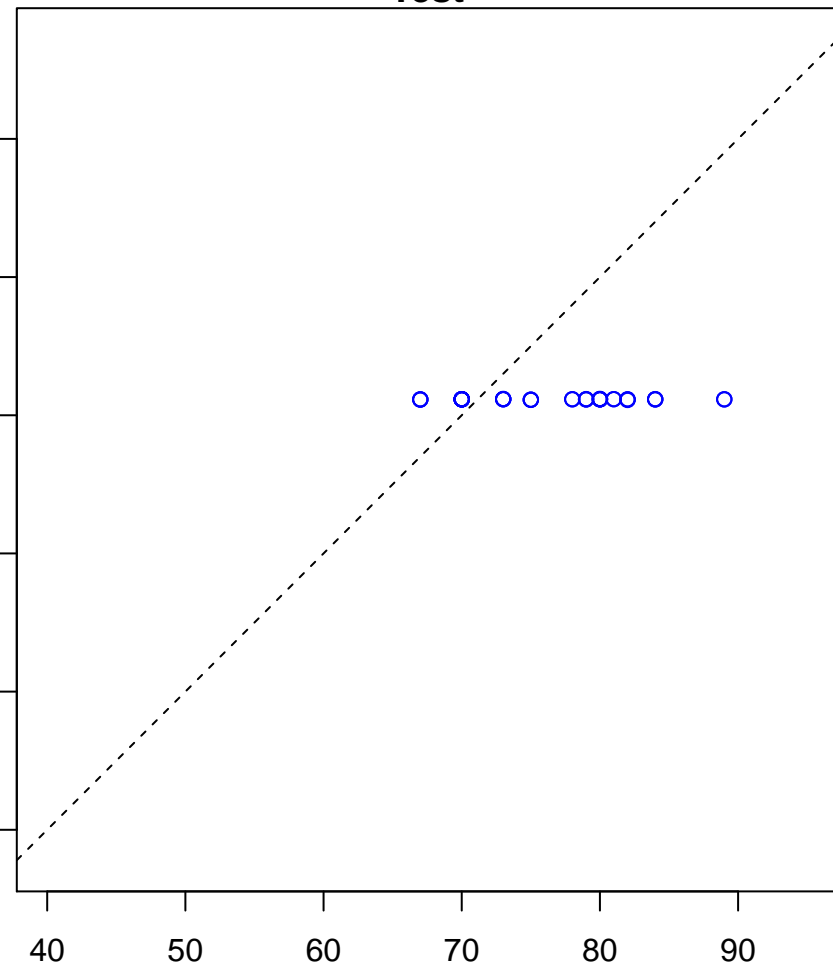


cellular response to glucose starvation (Score: 0.763543)

Control

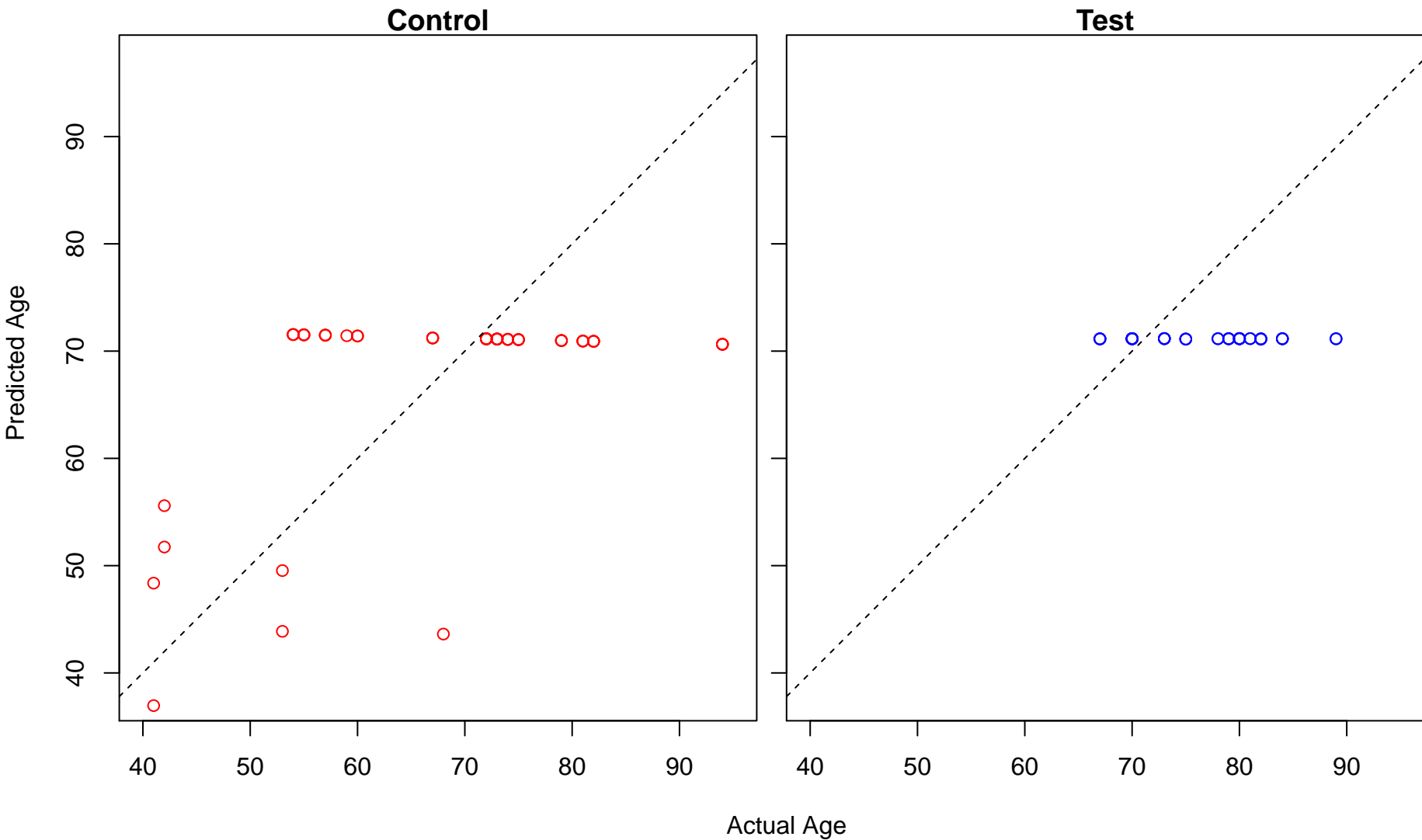


Test

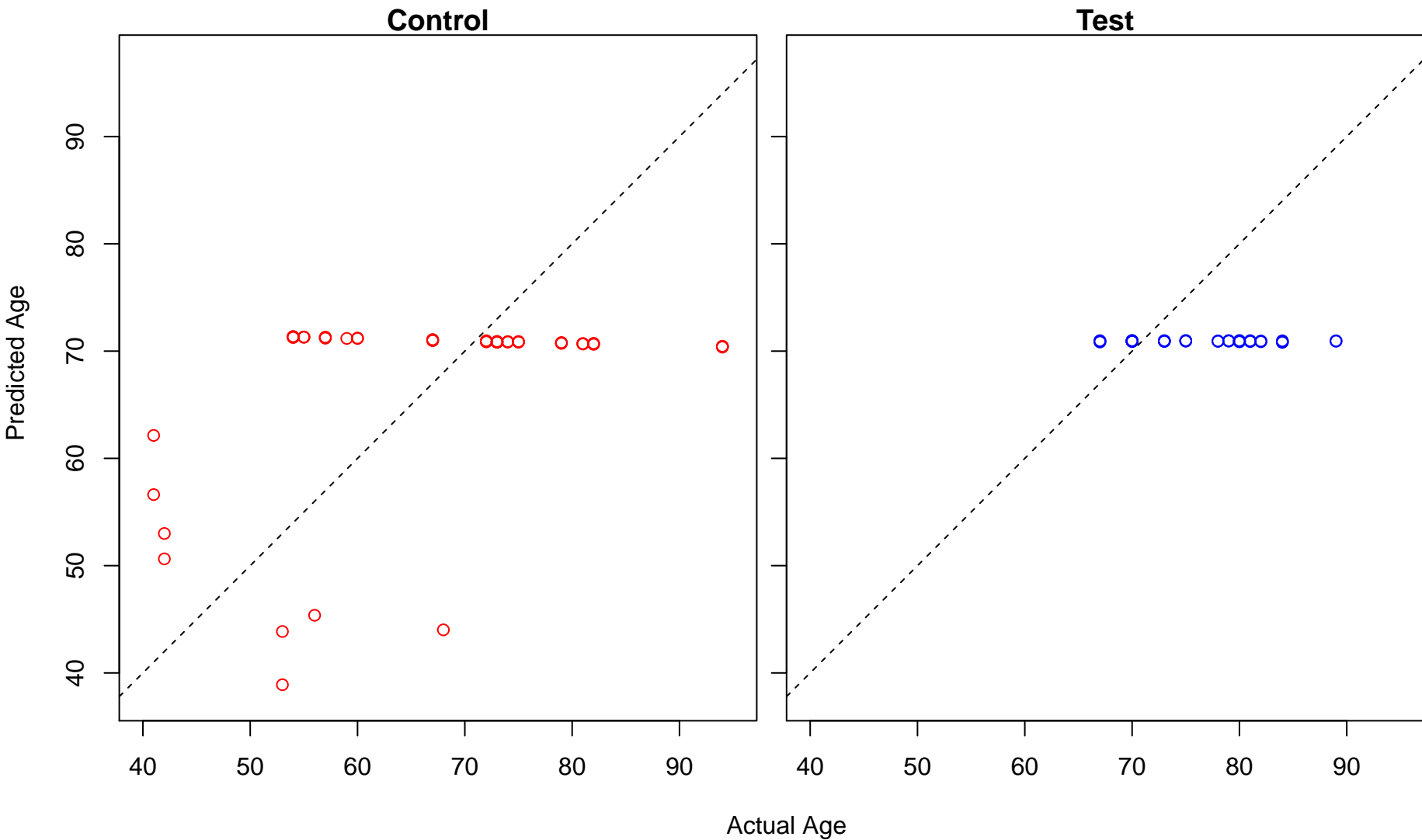


Actual Age

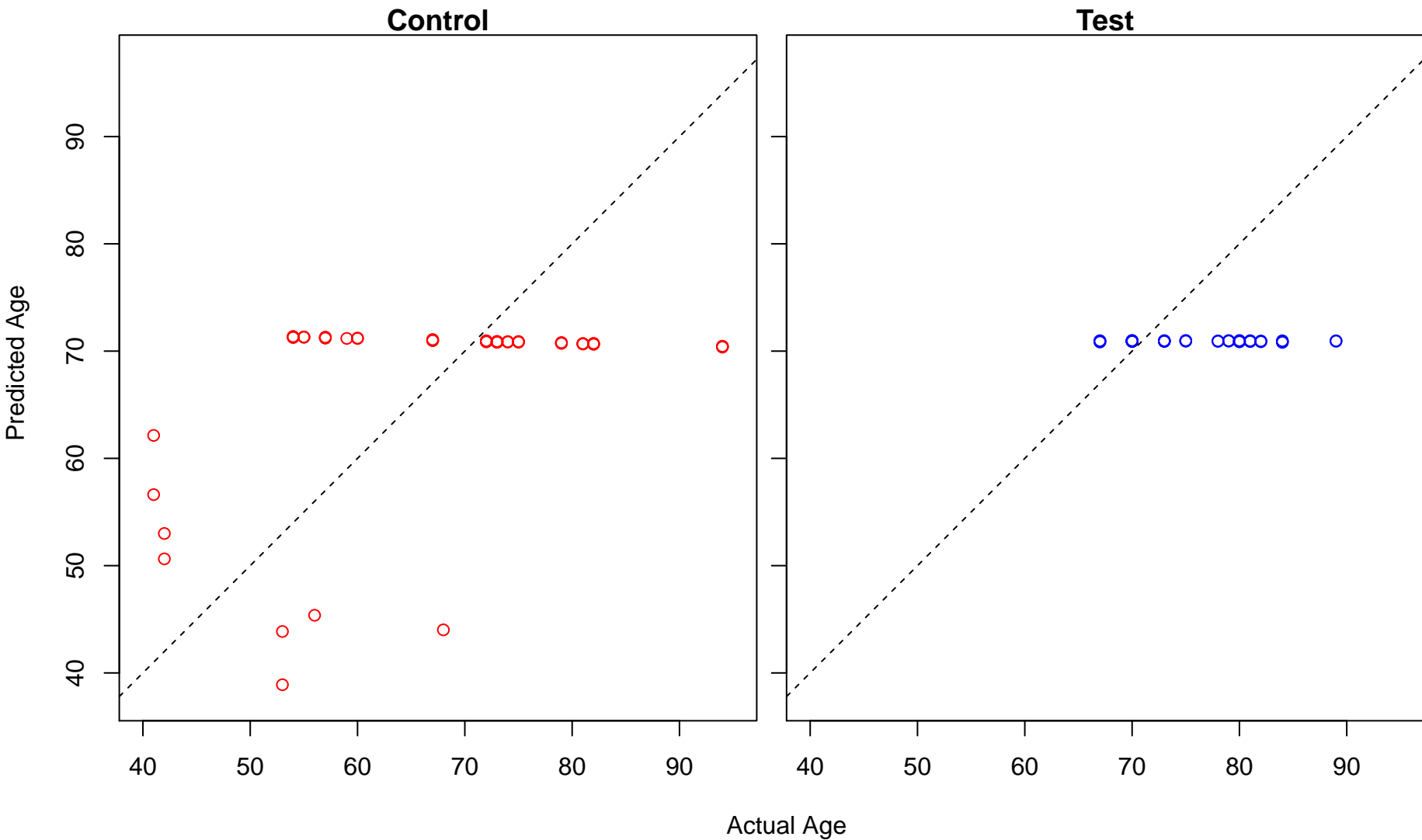
response to starvation (Score: 0.763543)



dendritic cell chemotaxis (Score: 0.763261)

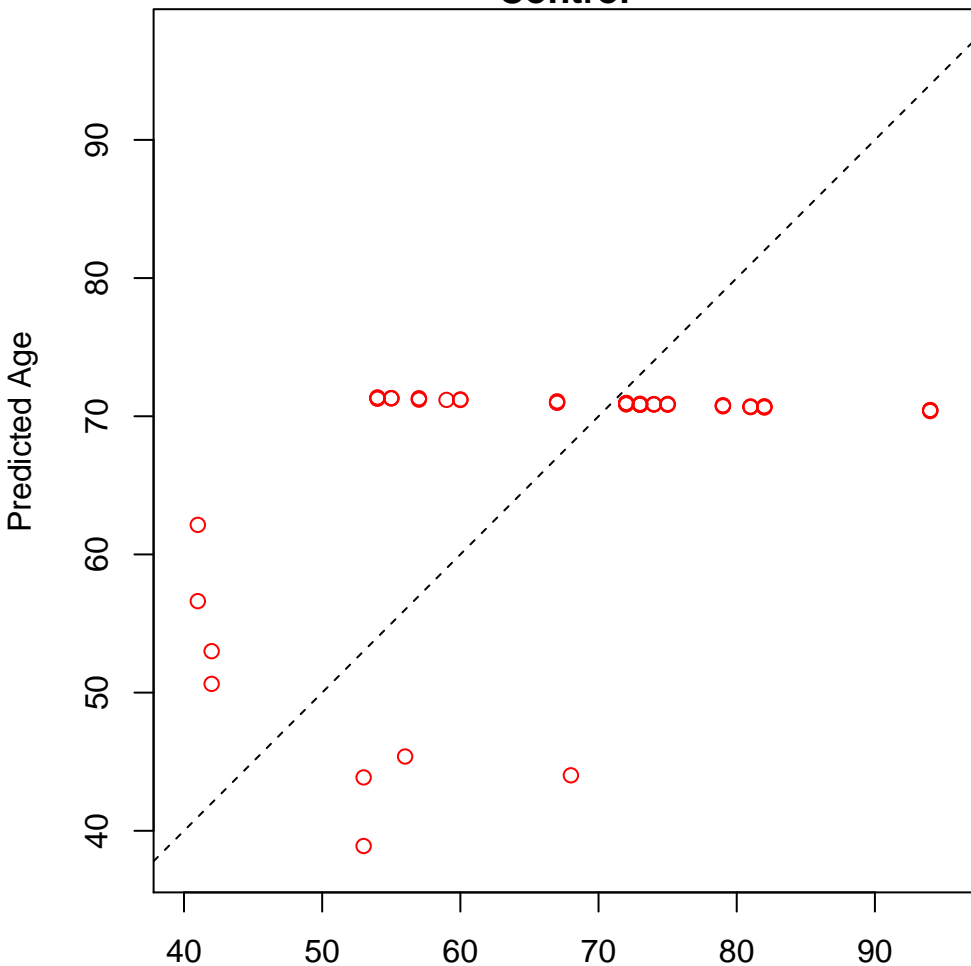


dendritic cell migration (Score: 0.763261)

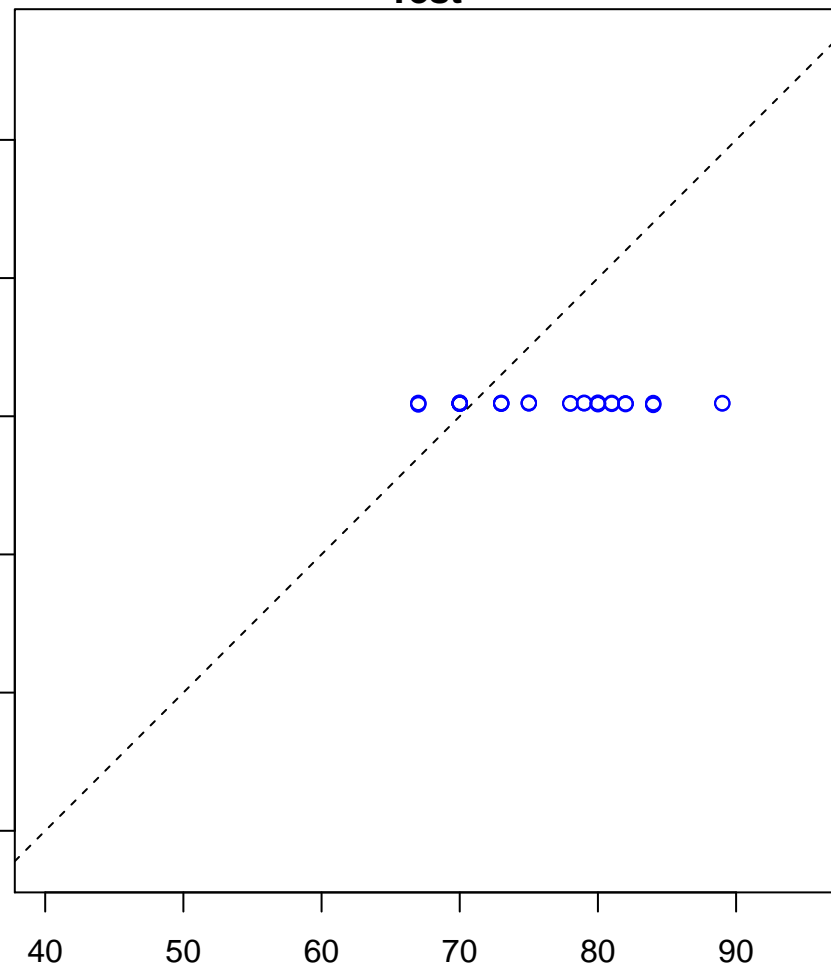


positive regulation of T cell proliferation (Score: 0.763261)

Control

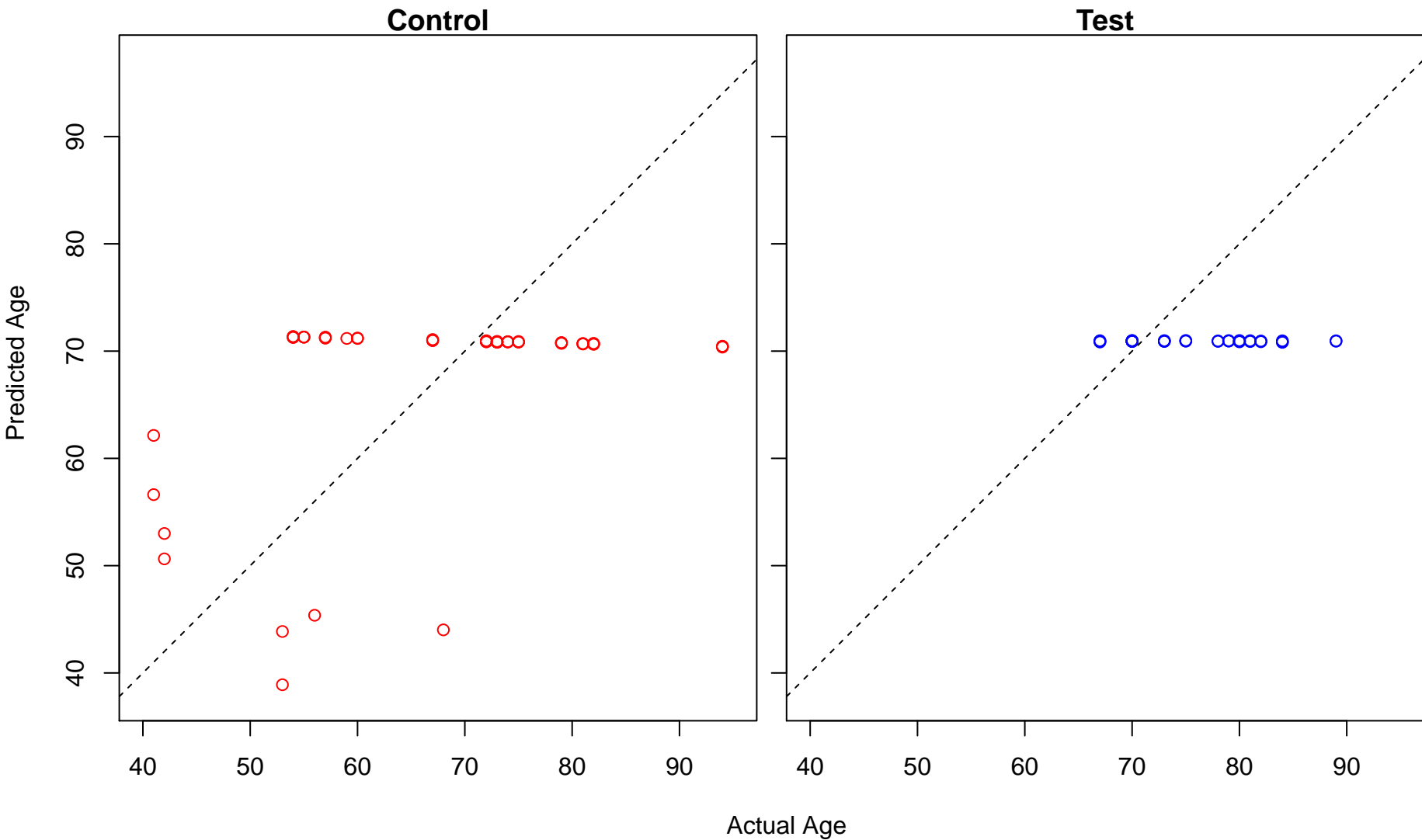


Test

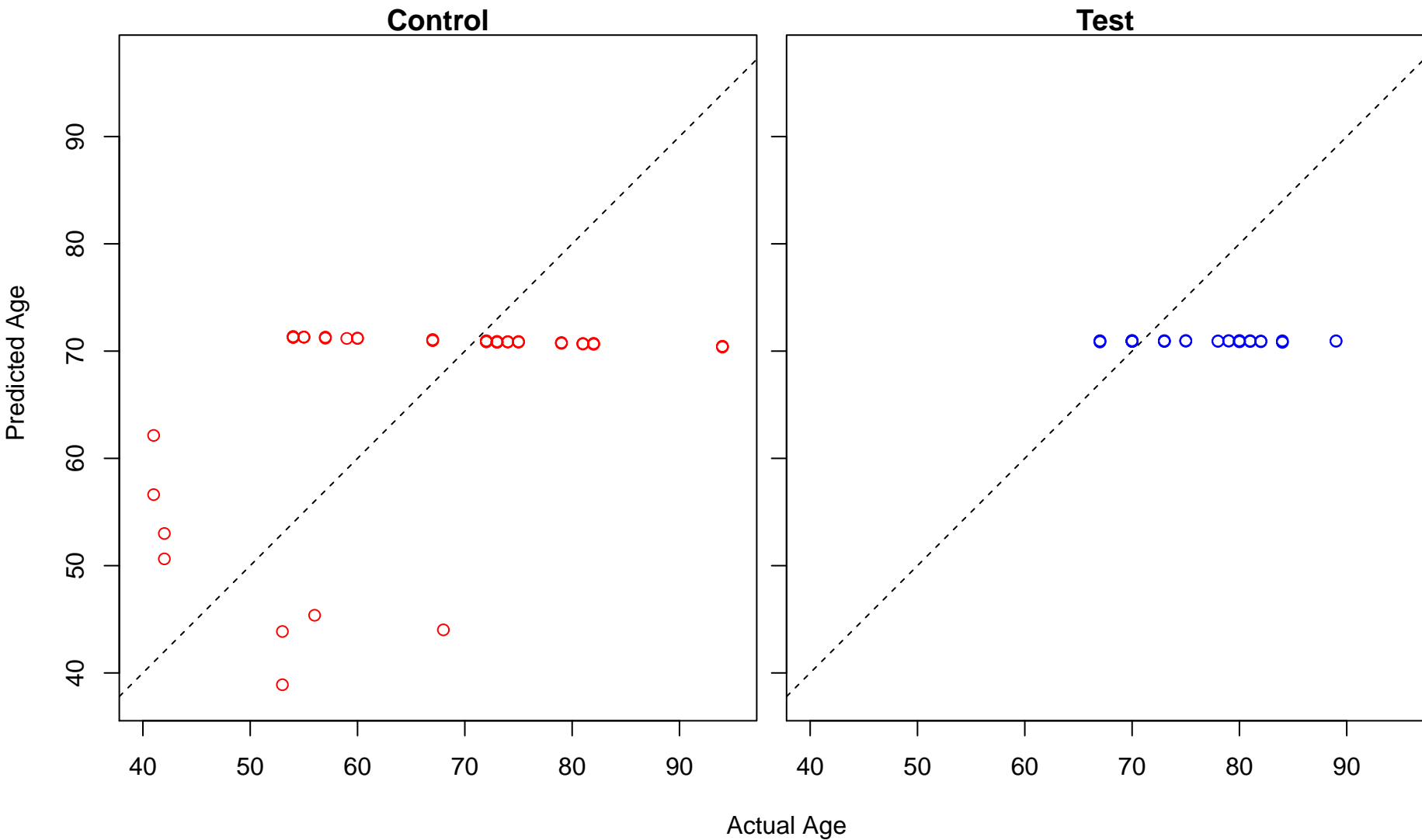


Actual Age

positive chemotaxis (Score: 0.763261)

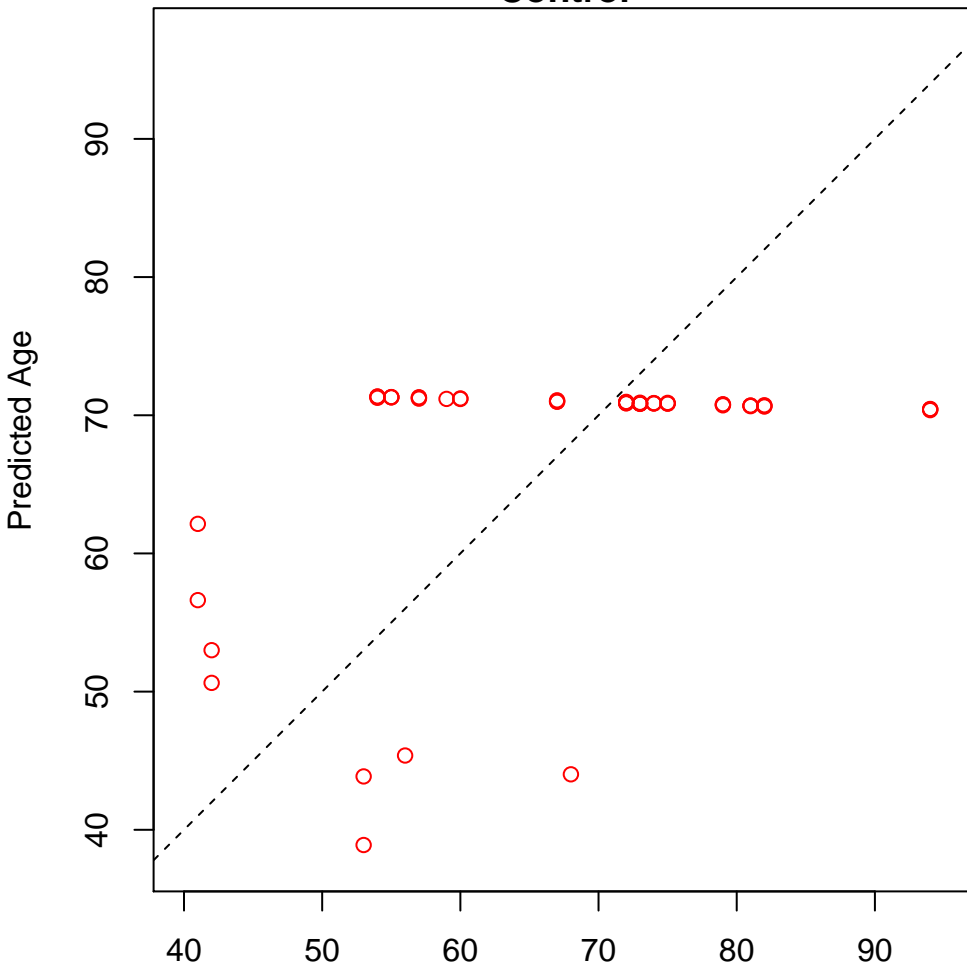


positive regulation of mononuclear cell migration (Score: 0.763261)

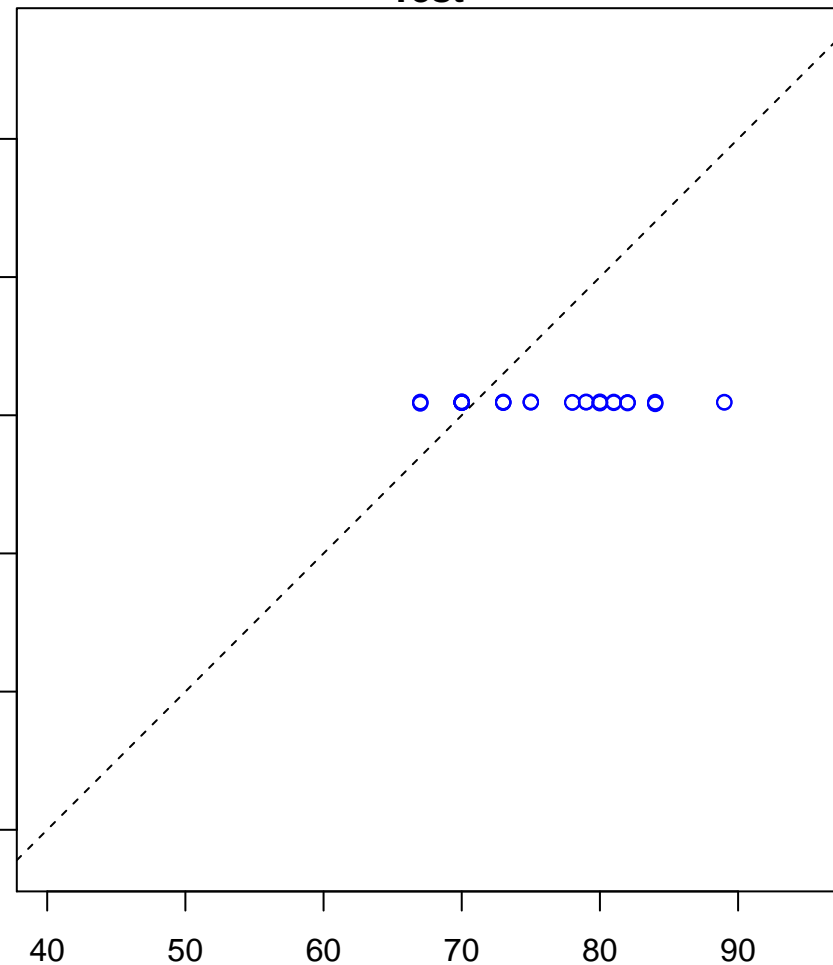


regulation of monocyte chemotaxis (Score: 0.763261)

Control

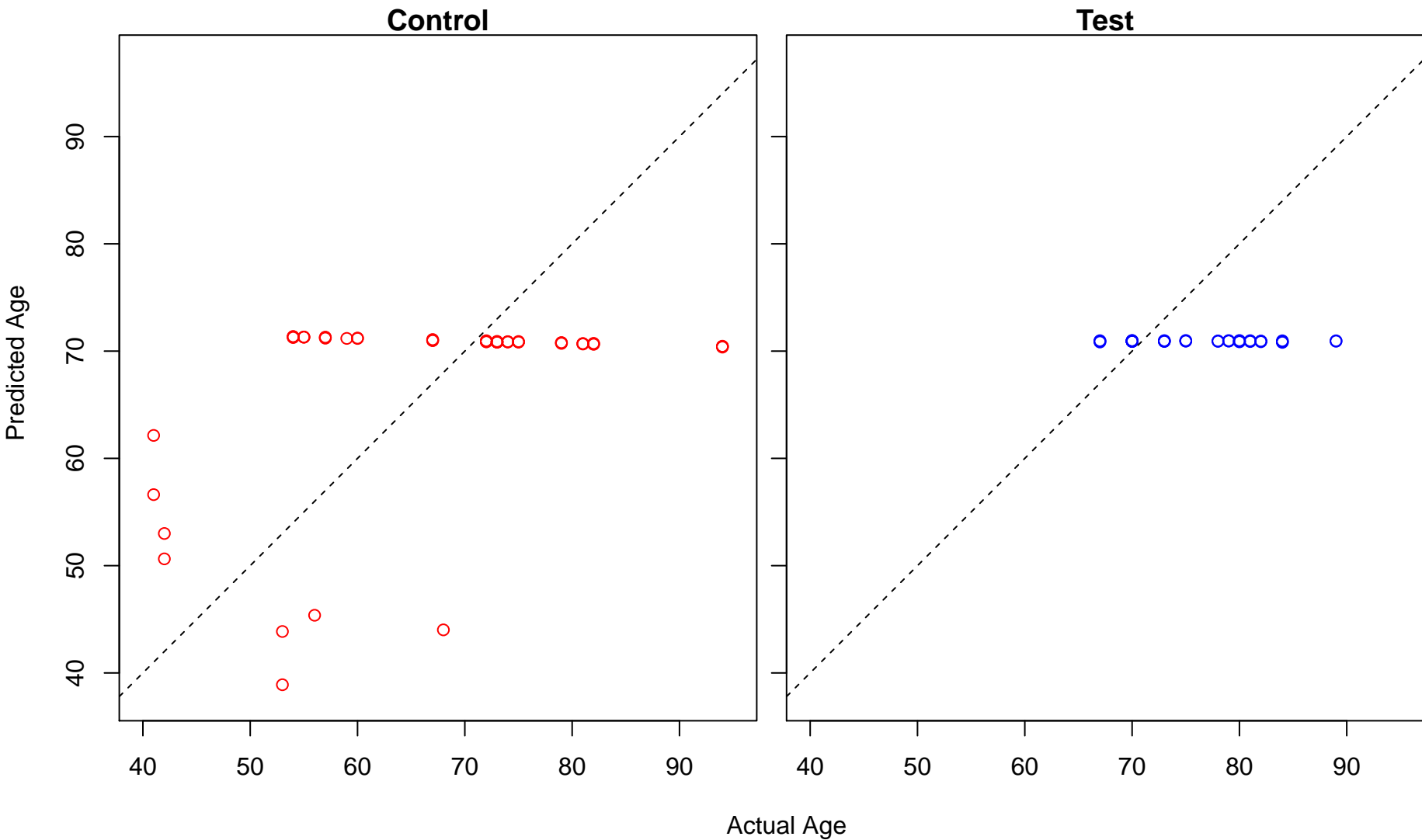


Test

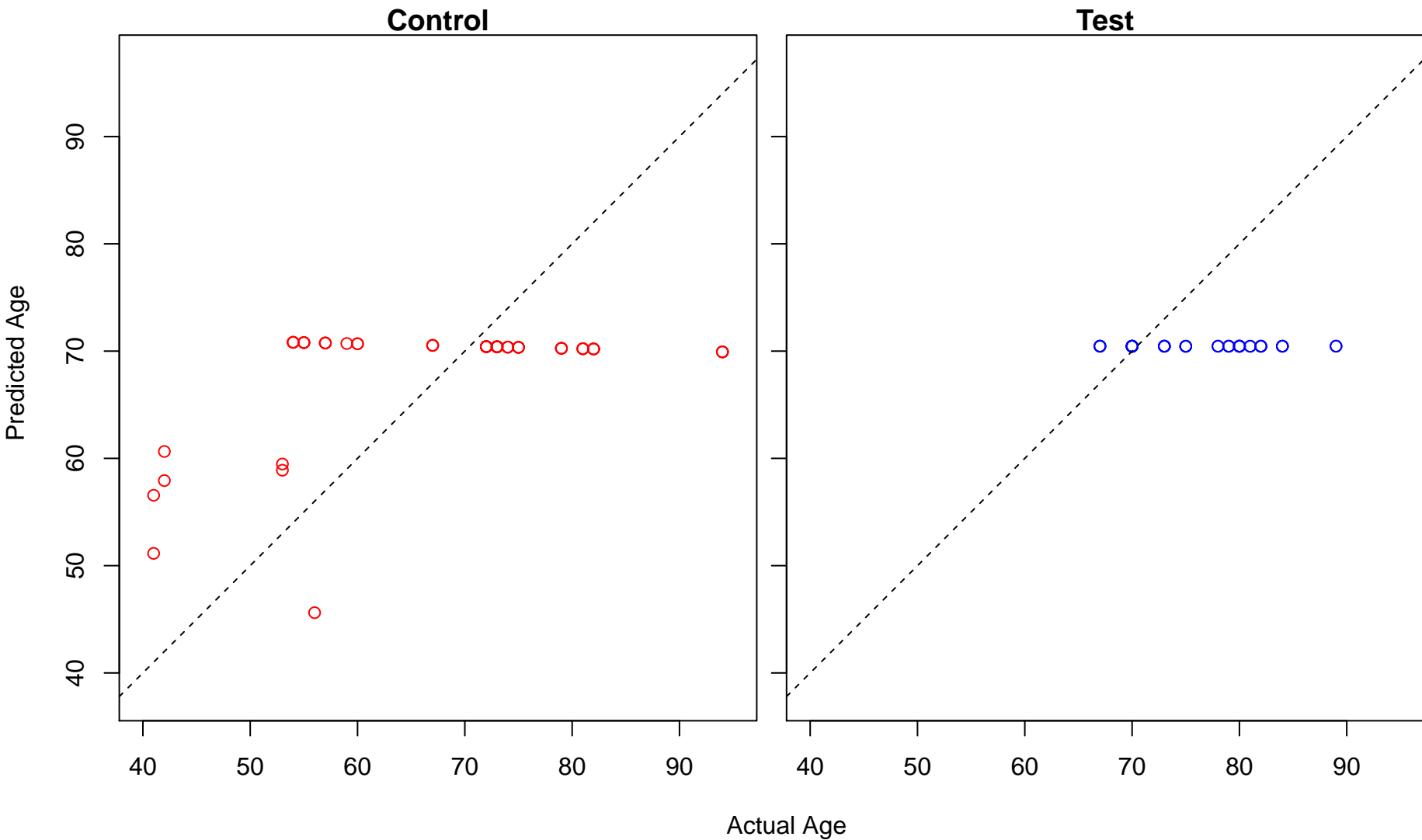


Actual Age

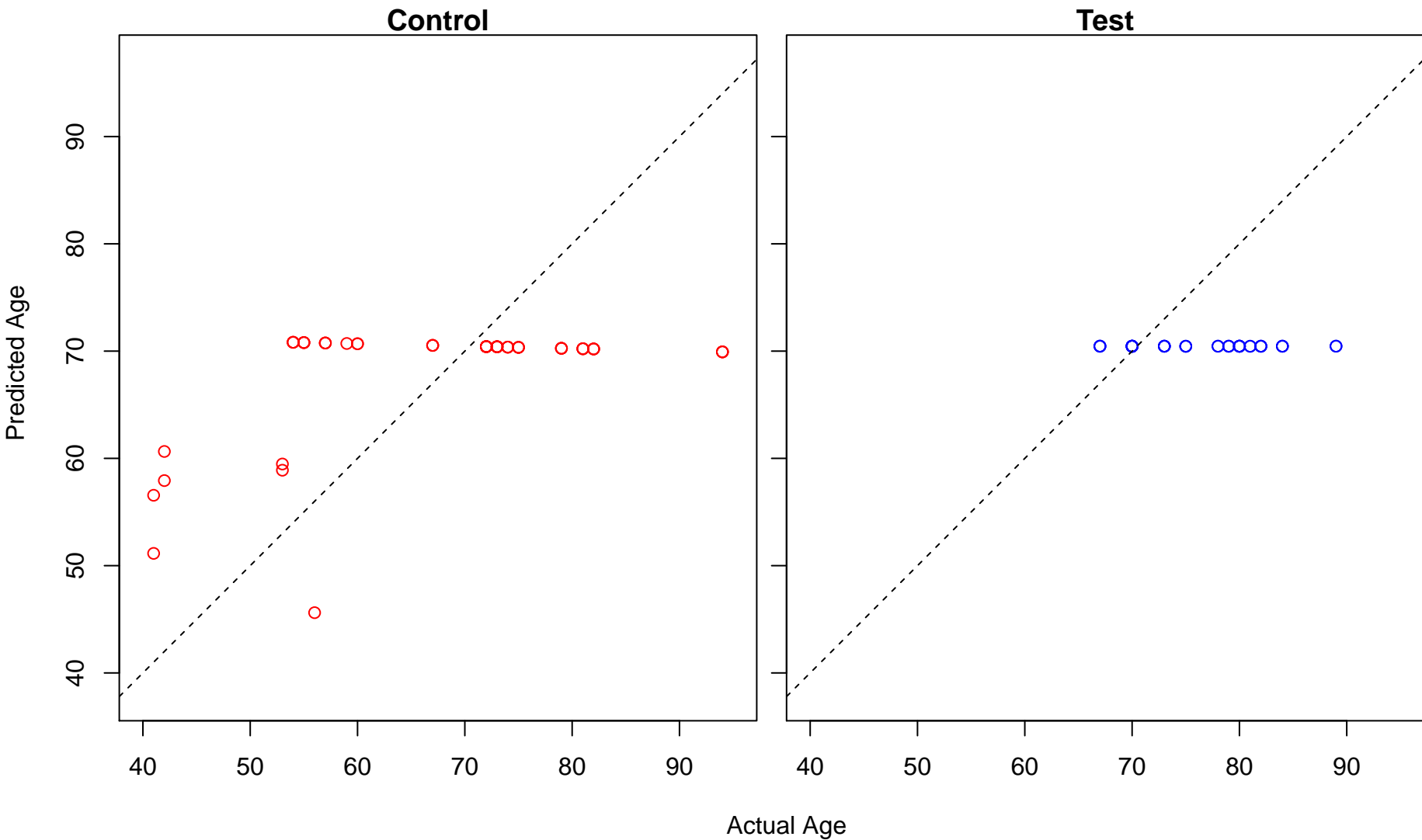
positive regulation of monocyte chemotaxis (Score: 0.763261)



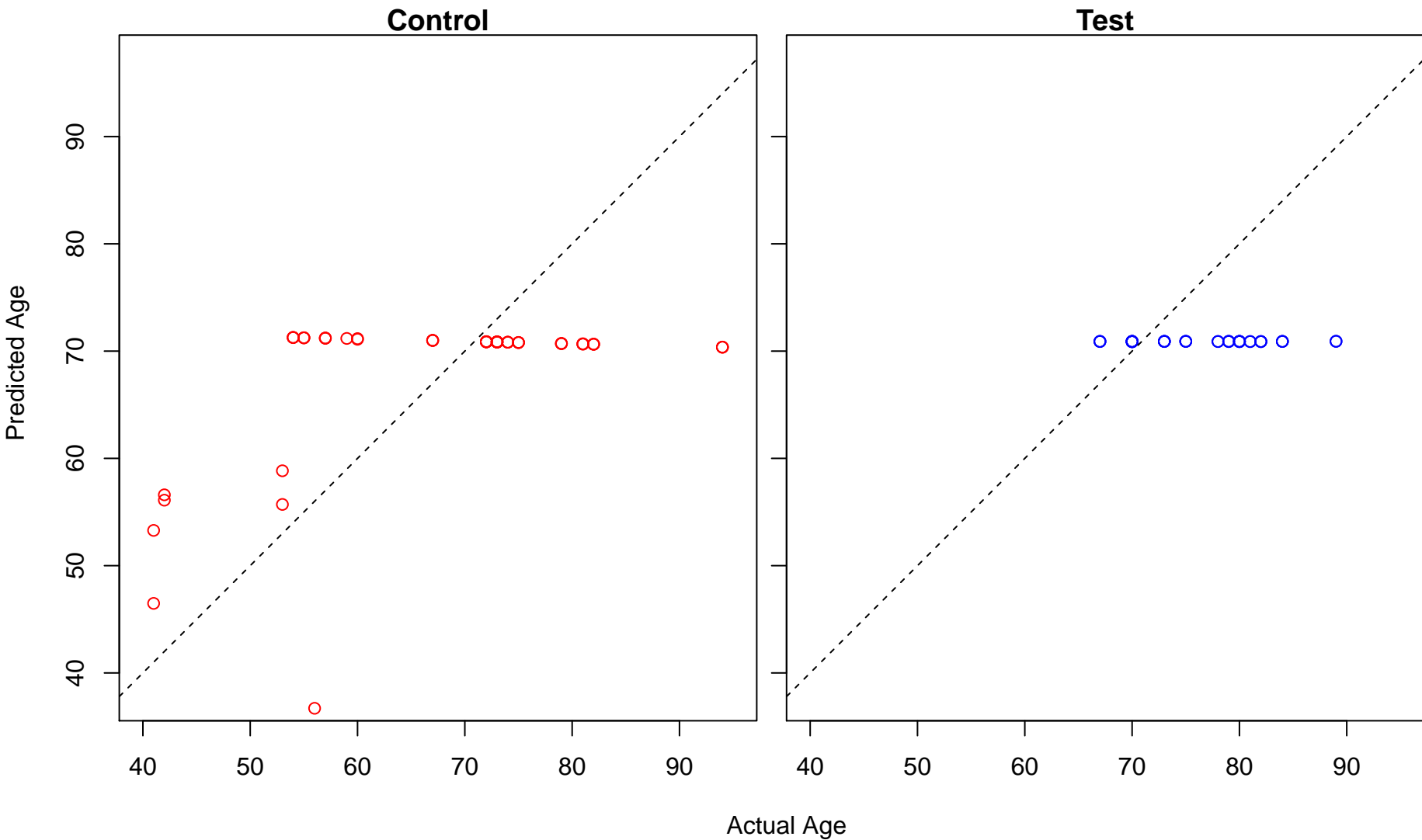
regulation of lipid transport (Score: 0.762702)



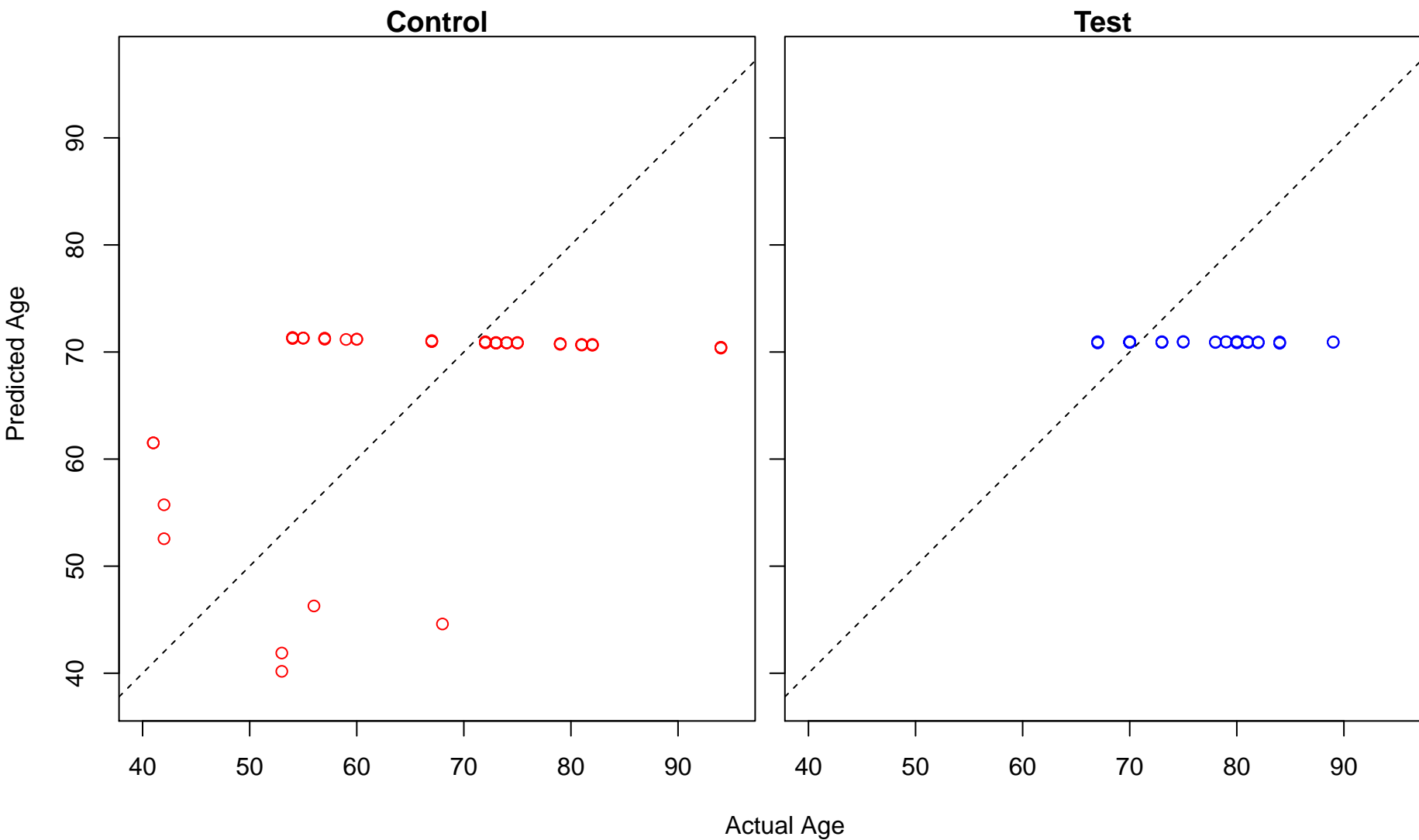
regulation of lipid localization (Score: 0.762702)



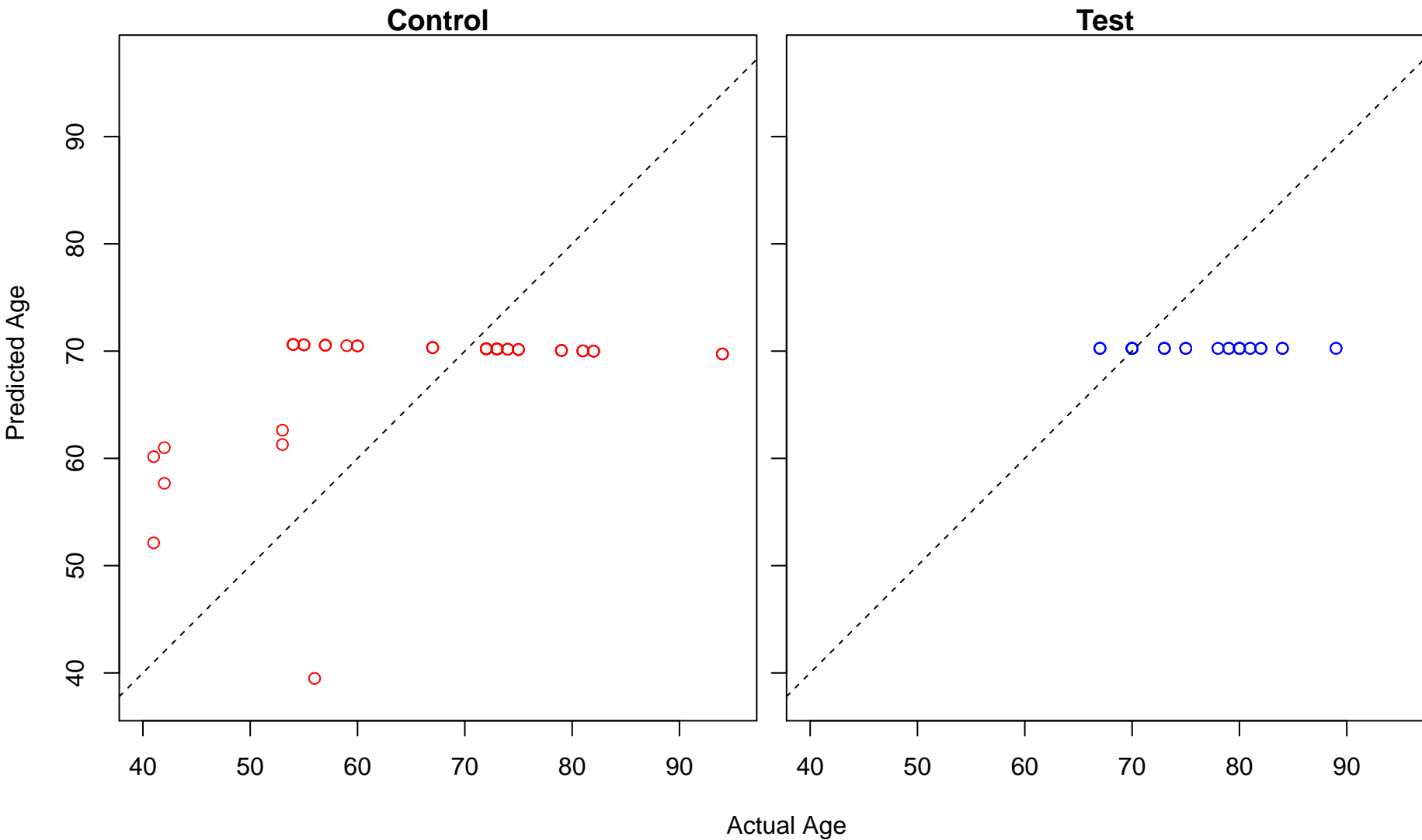
regulation of circadian rhythm (Score: 0.761975)



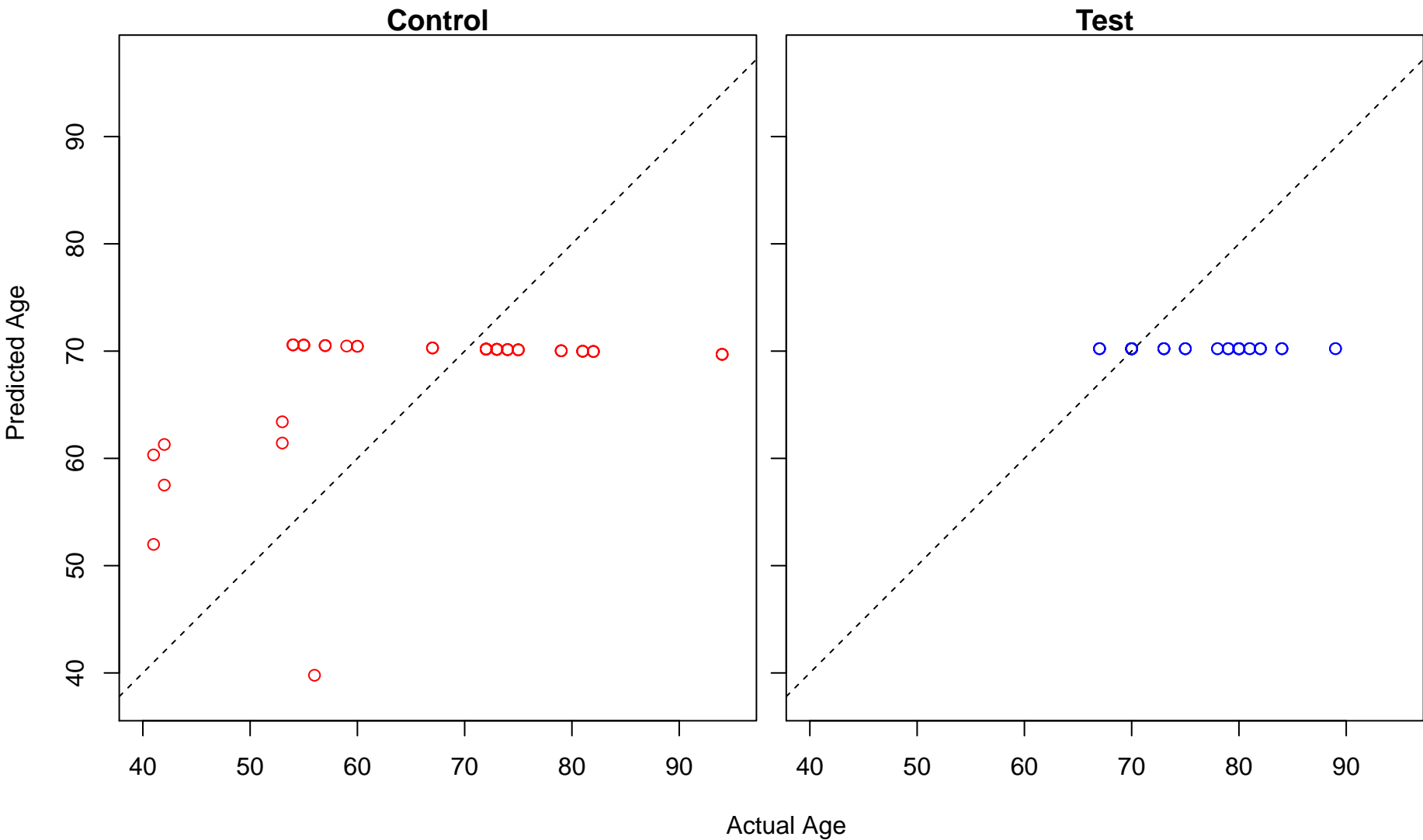
regulation of T cell proliferation (Score: 0.760804)



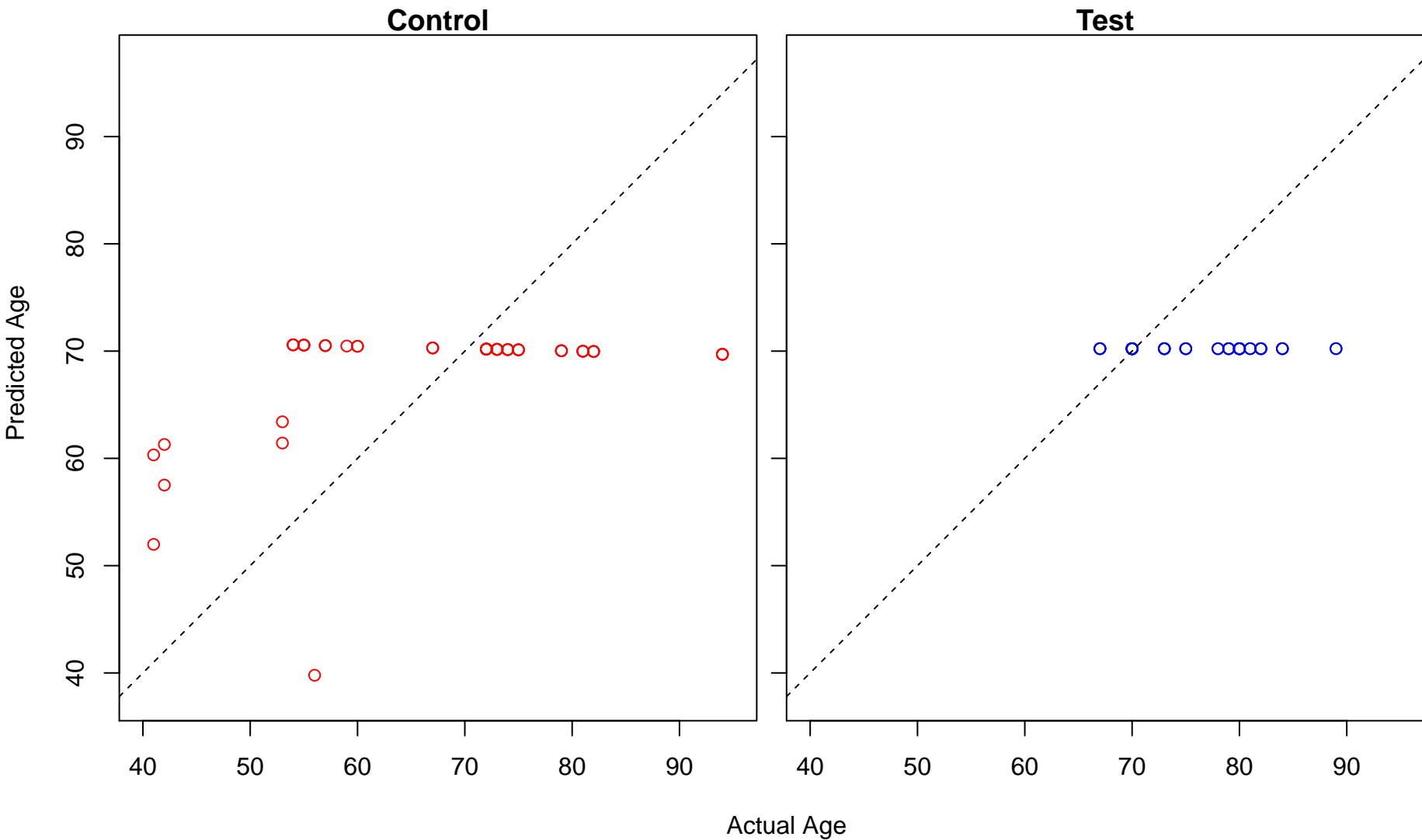
DNA recombination (Score: 0.760195)



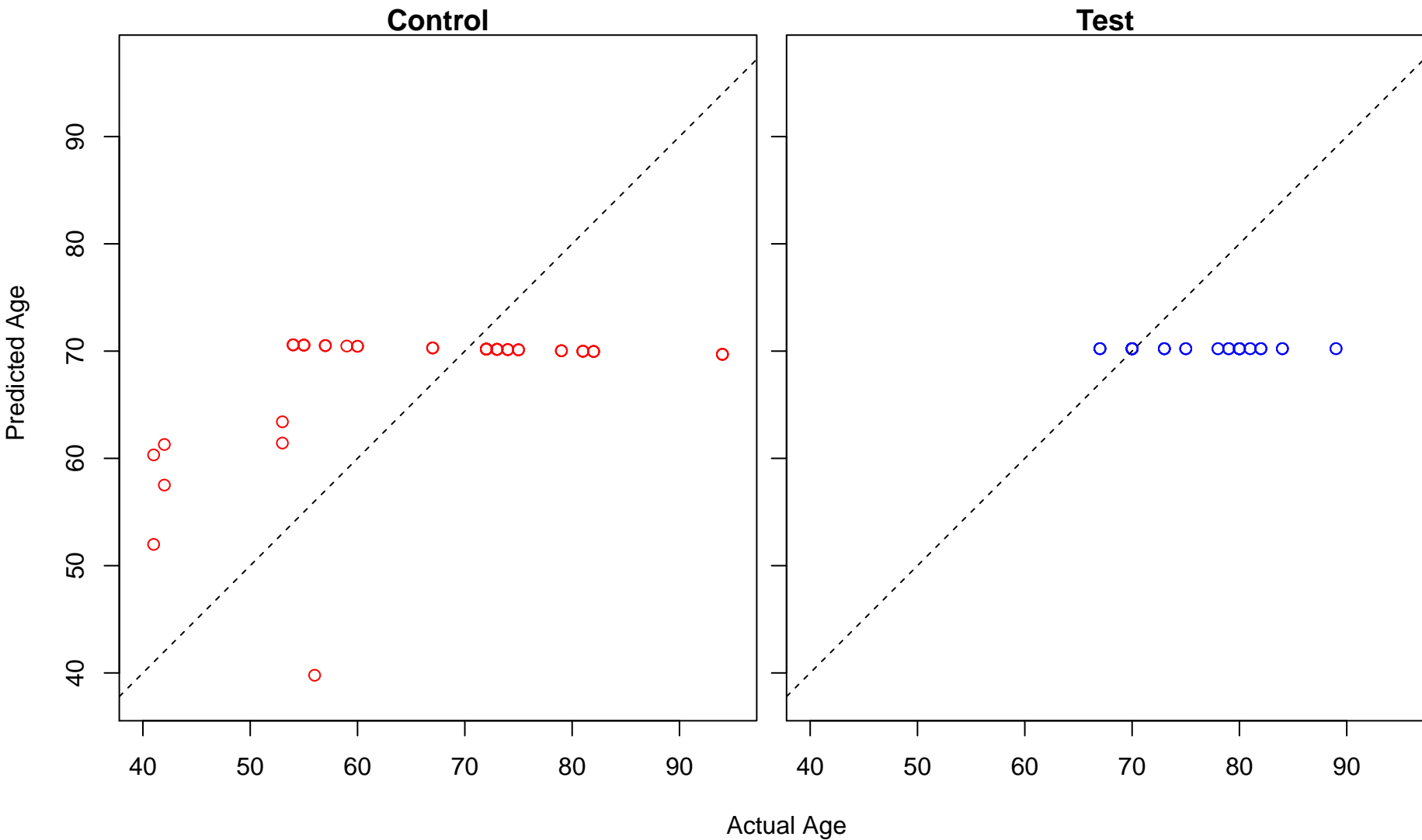
negative regulation of RNA polymerase II transcriptional preinitiation complex assembly (Score: 0.760)



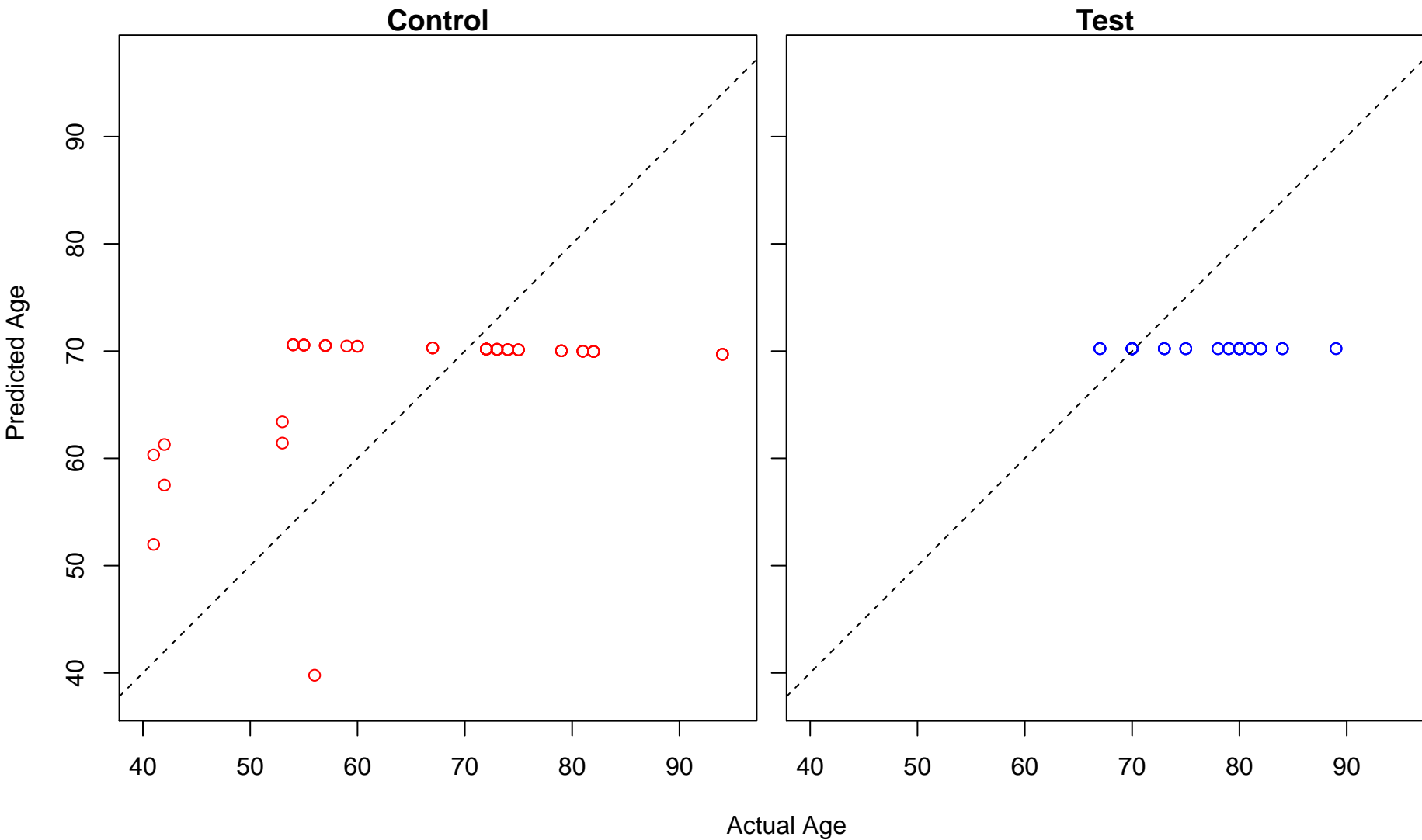
regulation of RNA polymerase II transcriptional preinitiation complex assembly (Score: 0.760131)



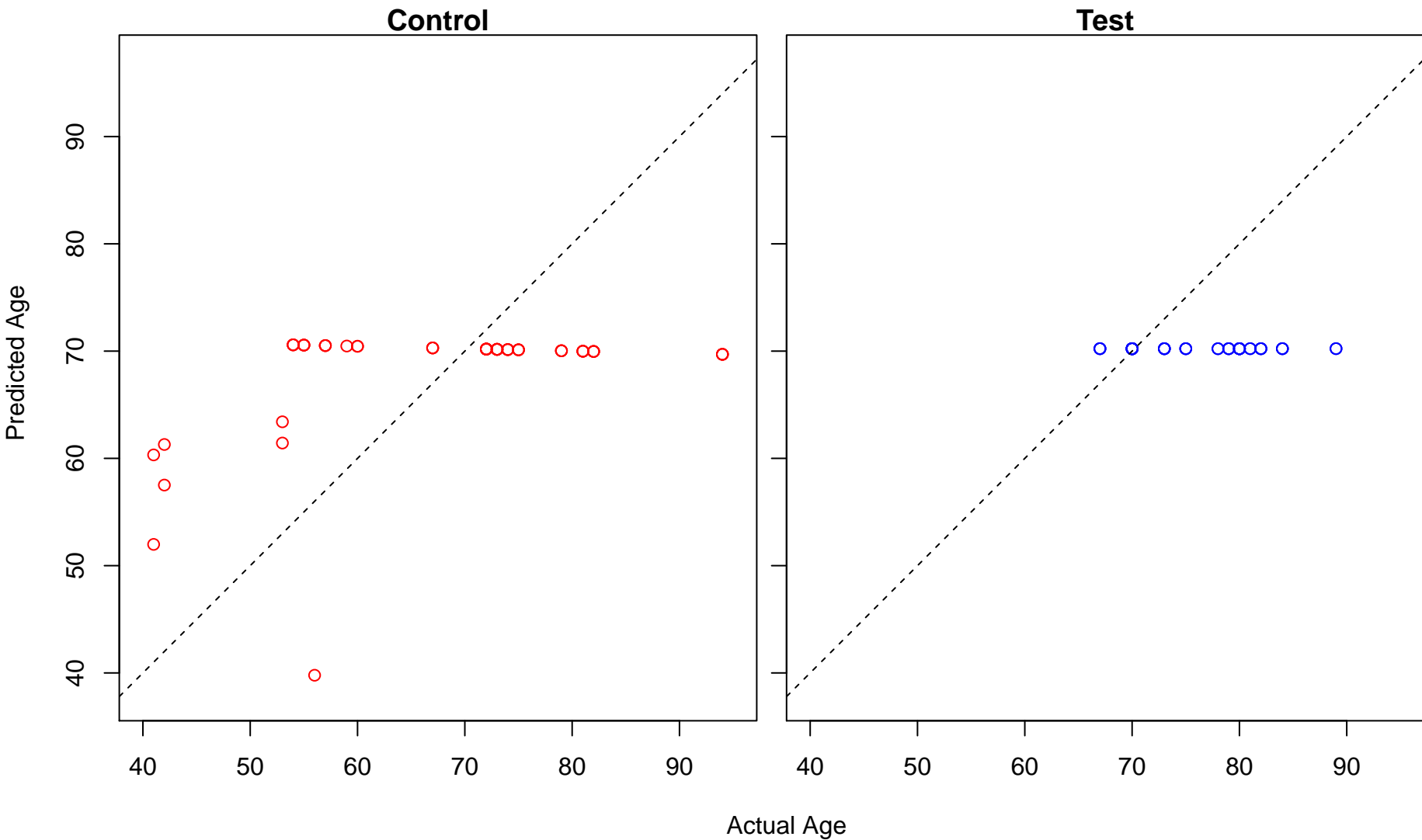
regulation of transcription initiation from RNA polymerase II promoter (Score: 0.760131)



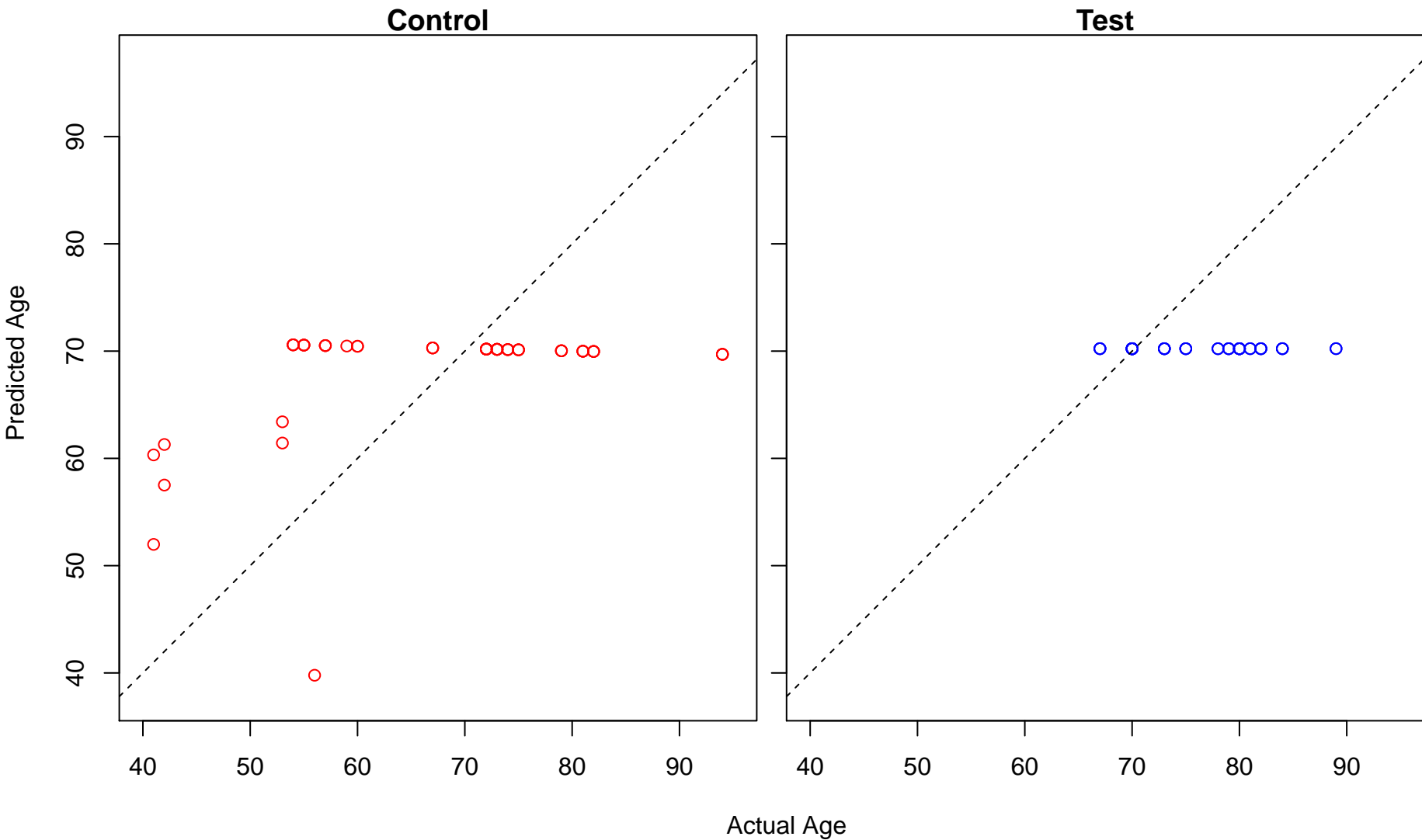
negative regulation of transcription initiation from RNA polymerase II promoter (Score: 0.760131)



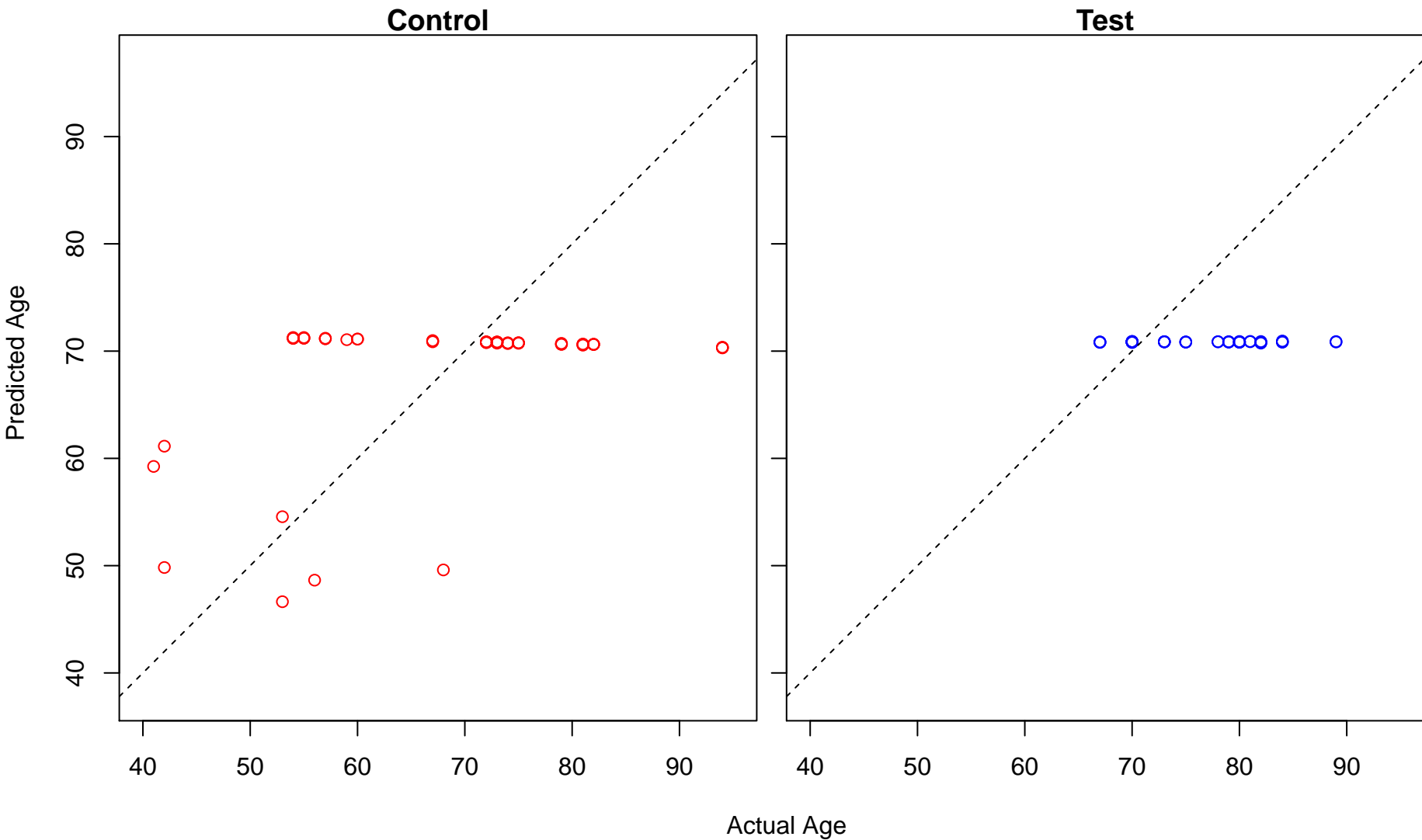
regulation of DNA-templated transcription, initiation (Score: 0.760131)



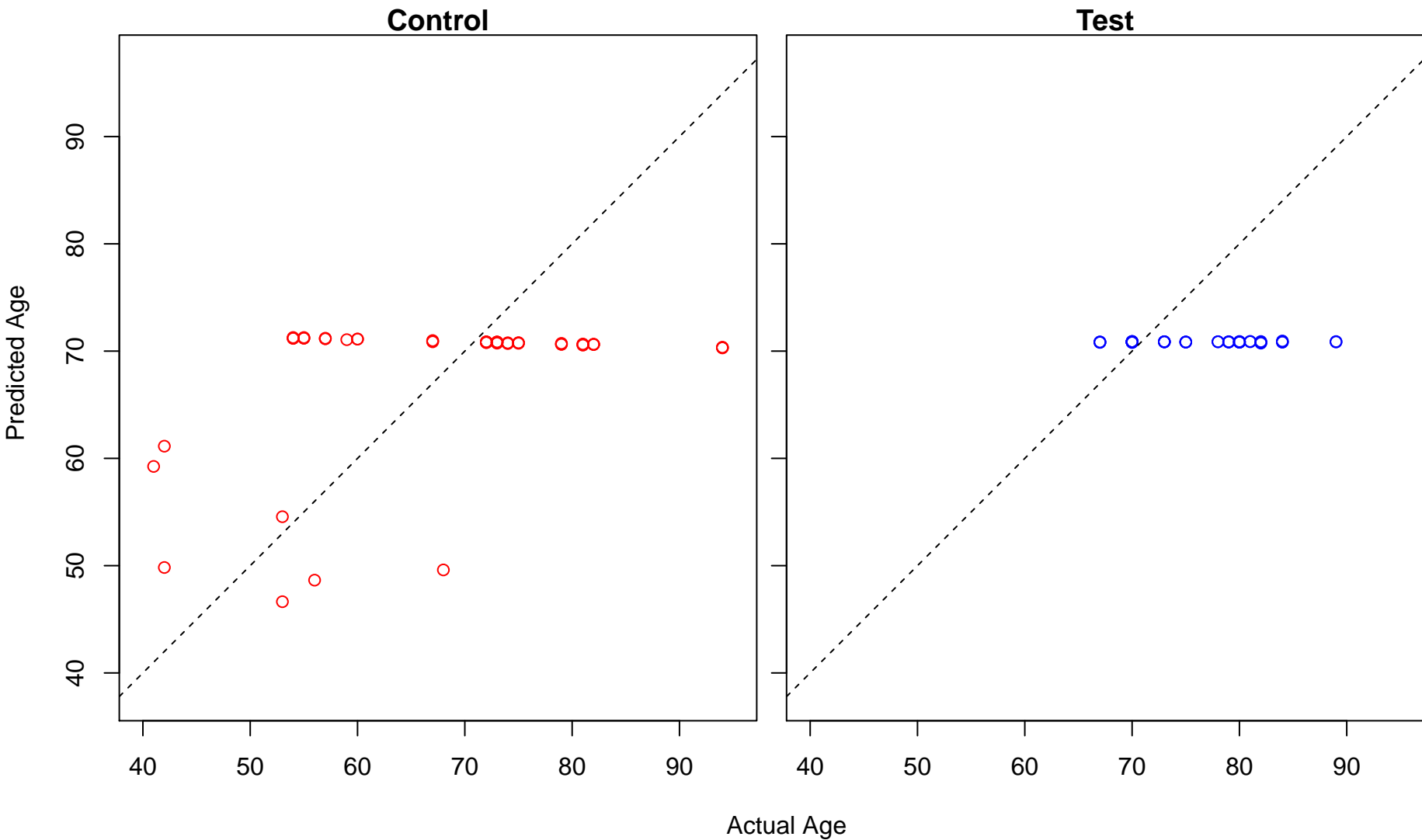
negative regulation of DNA-templated transcription, initiation (Score: 0.760131)



heart morphogenesis (Score: 0.758860)

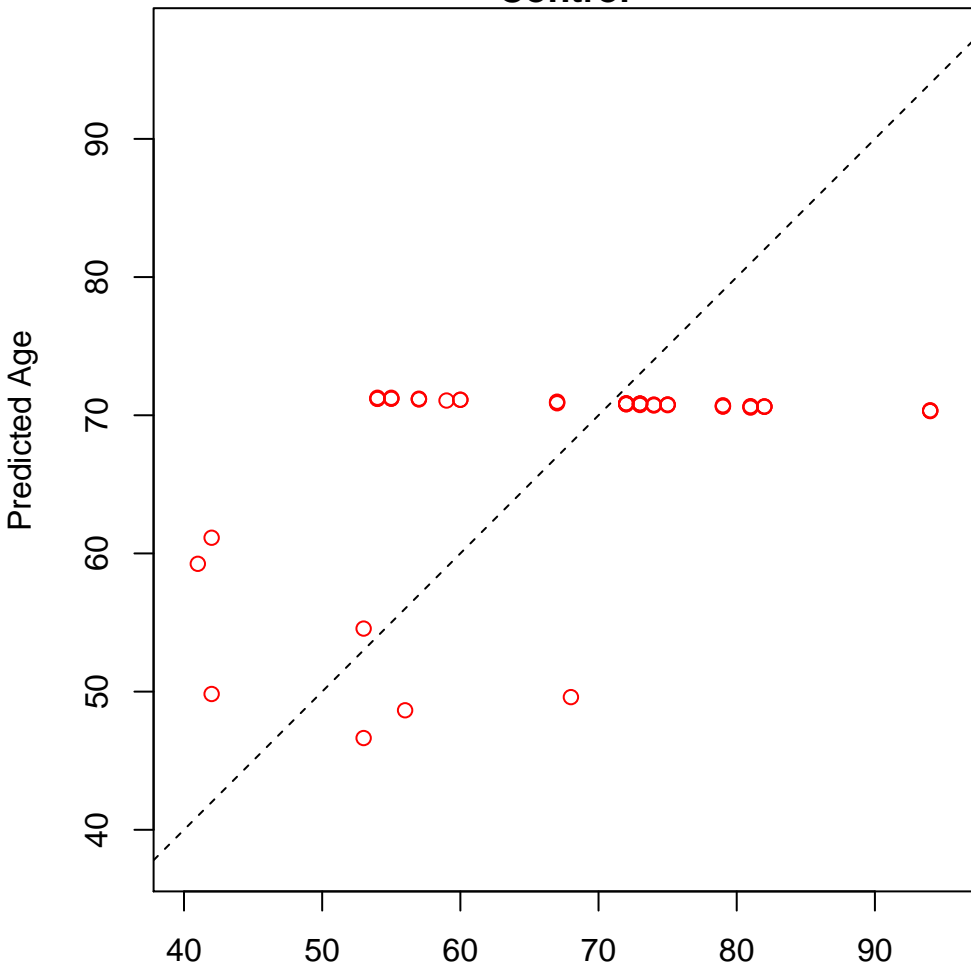


cardiac chamber development (Score: 0.758860)

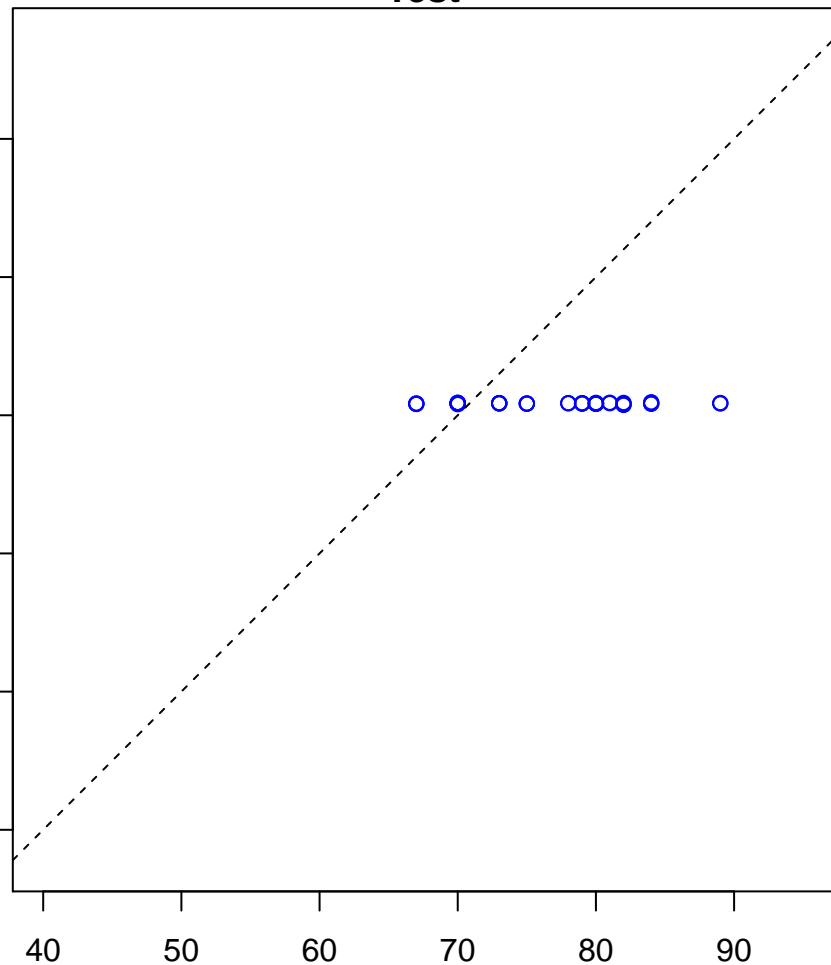


cardiac chamber morphogenesis (Score: 0.758860)

Control



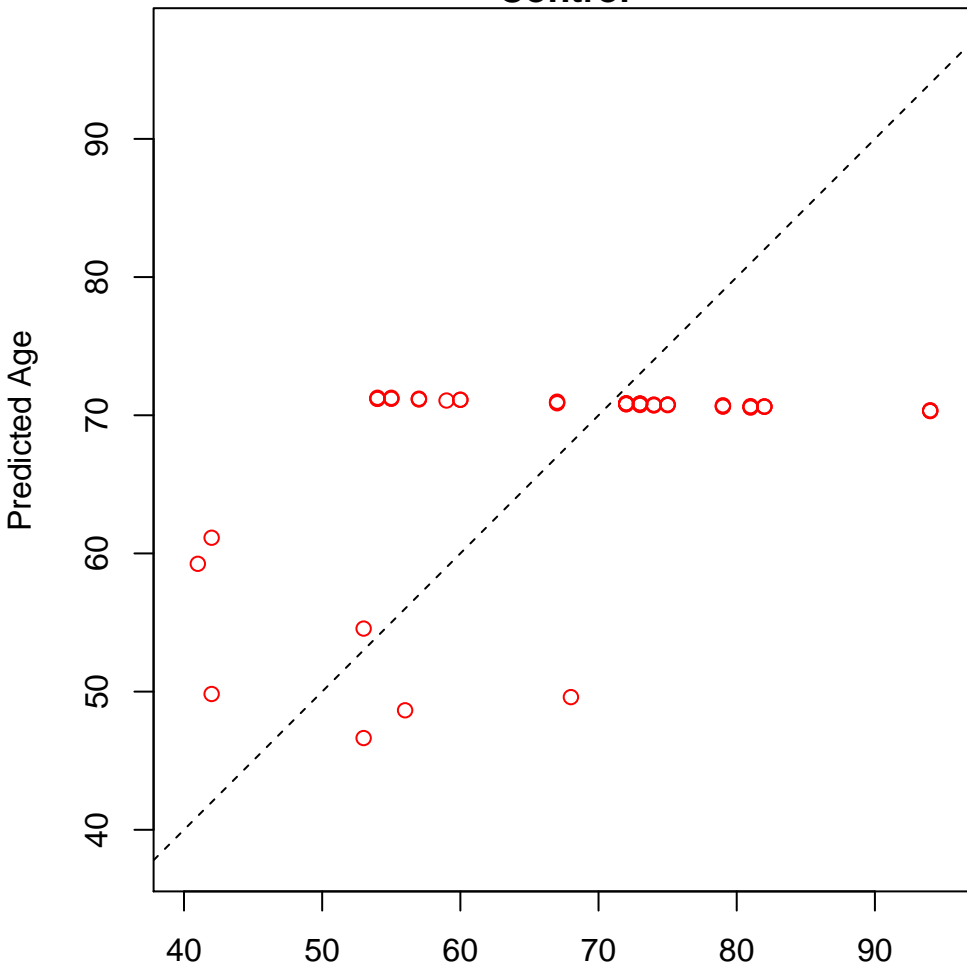
Test



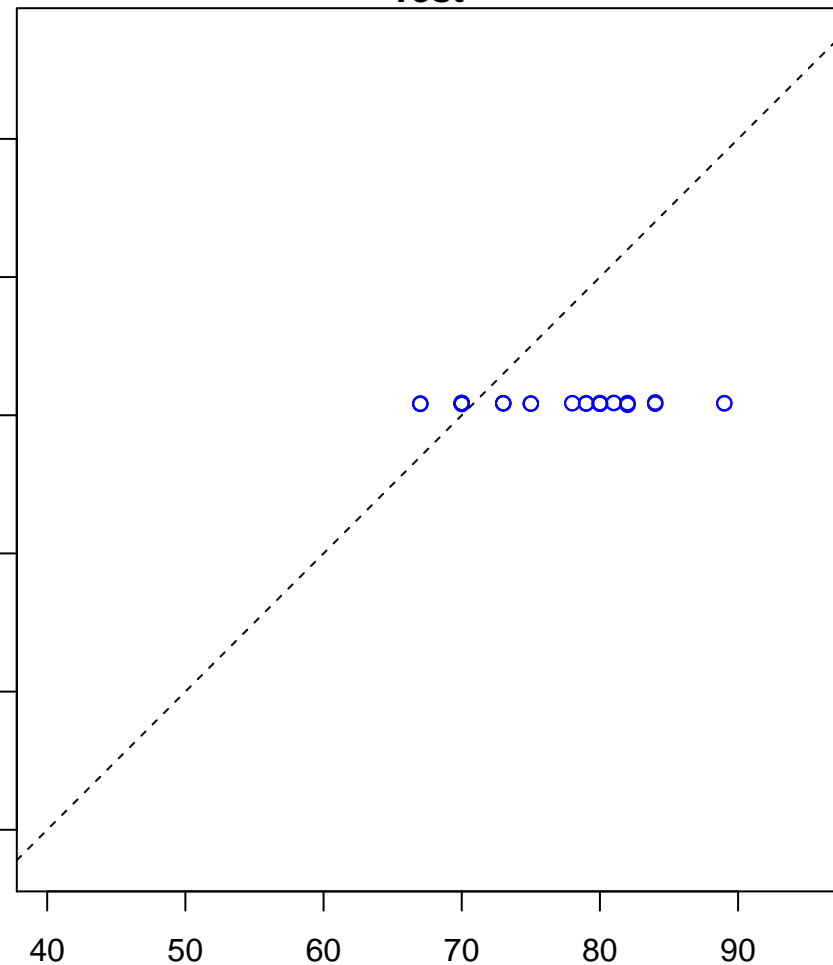
Actual Age

cardiac ventricle morphogenesis (Score: 0.758860)

Control

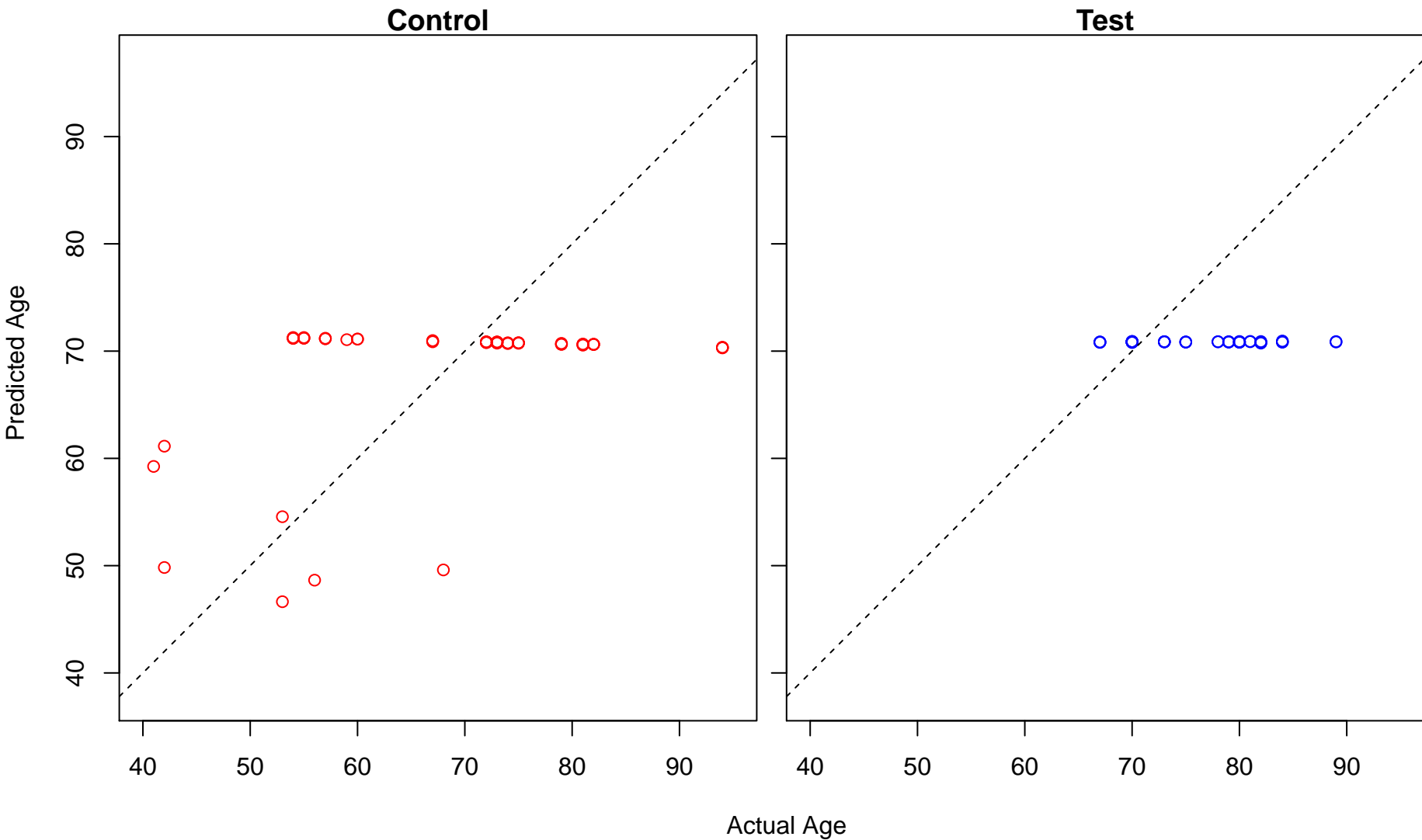


Test



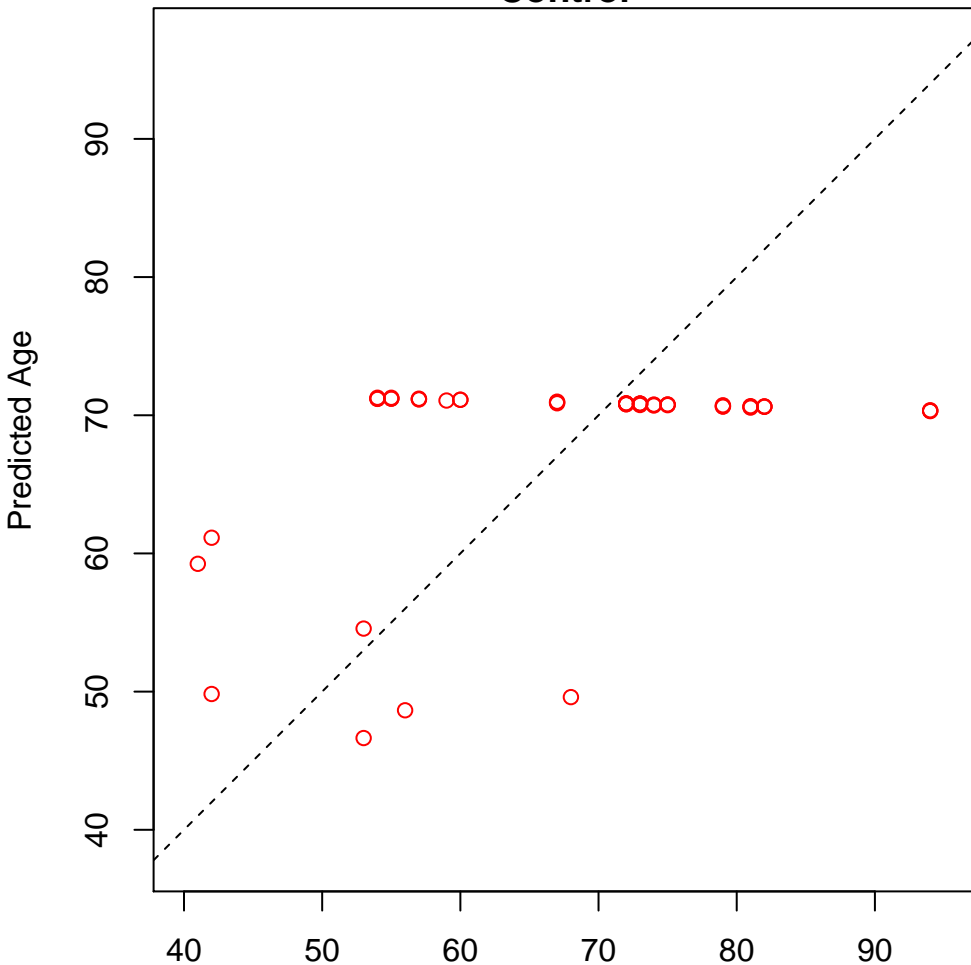
Actual Age

ventricular cardiac muscle tissue development (Score: 0.758860)

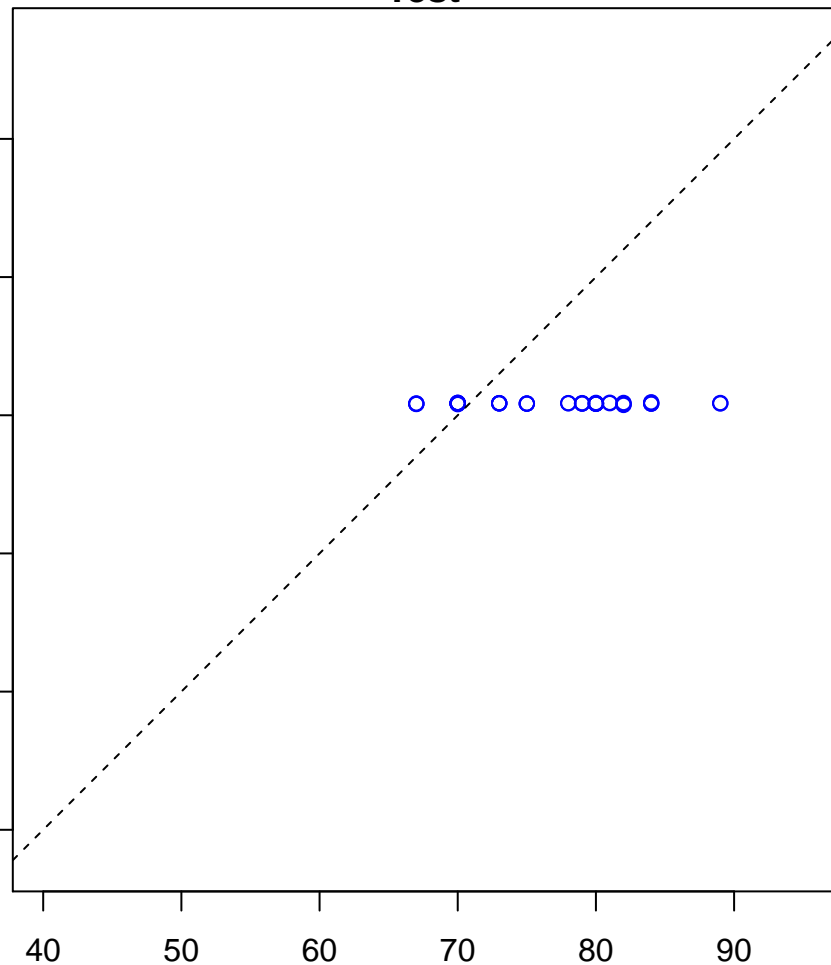


cardiac ventricle development (Score: 0.758860)

Control

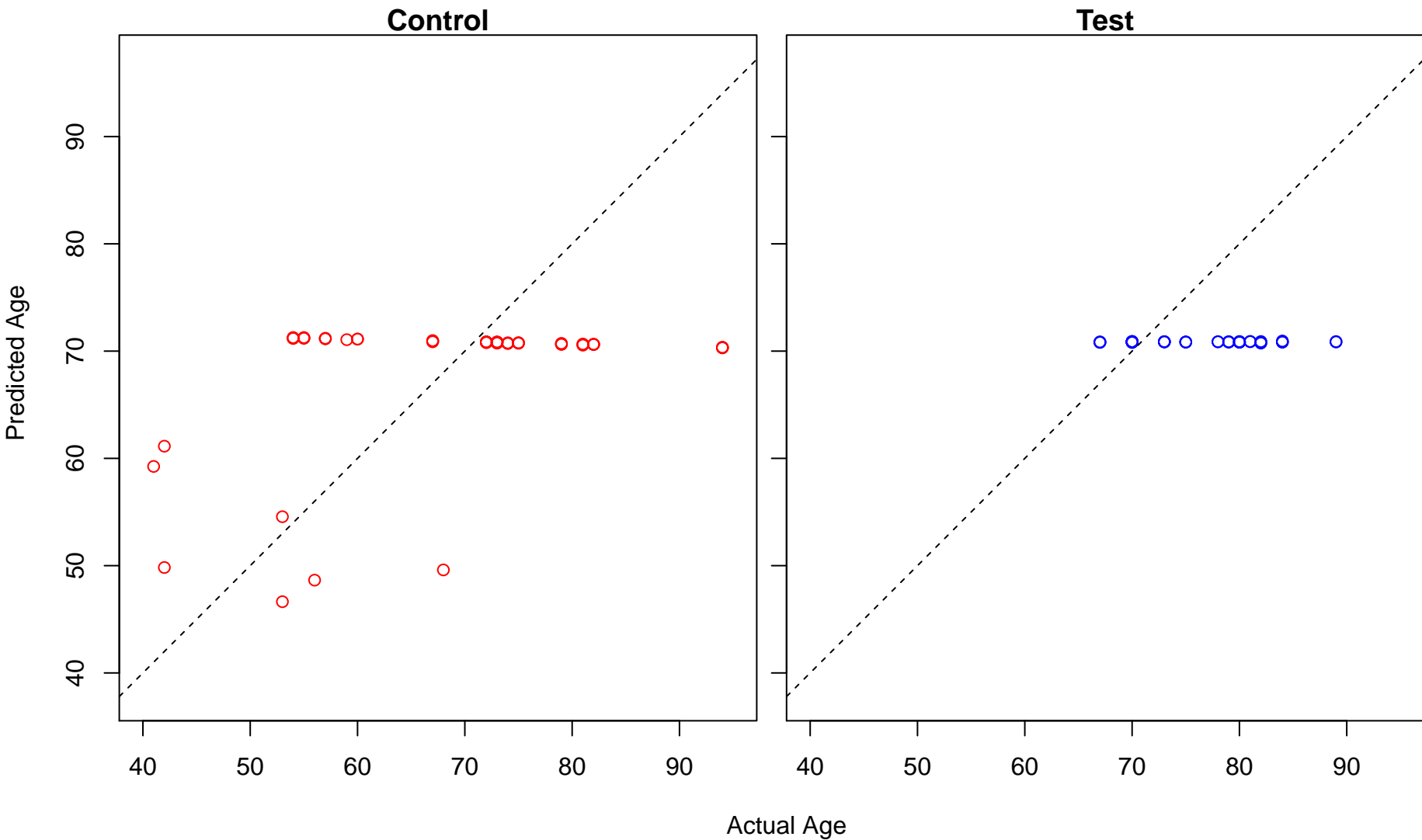


Test

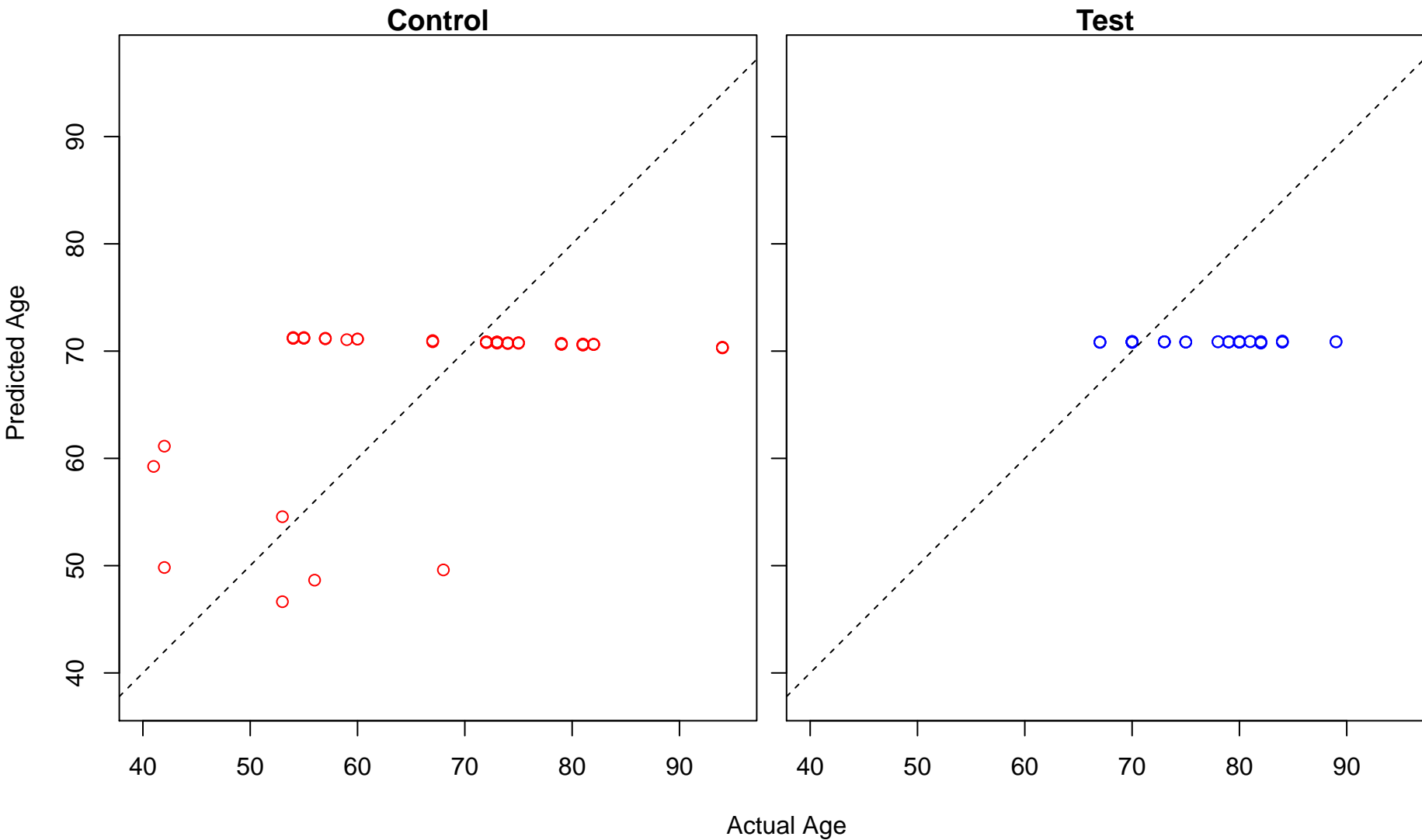


Actual Age

heart development (Score: 0.758860)

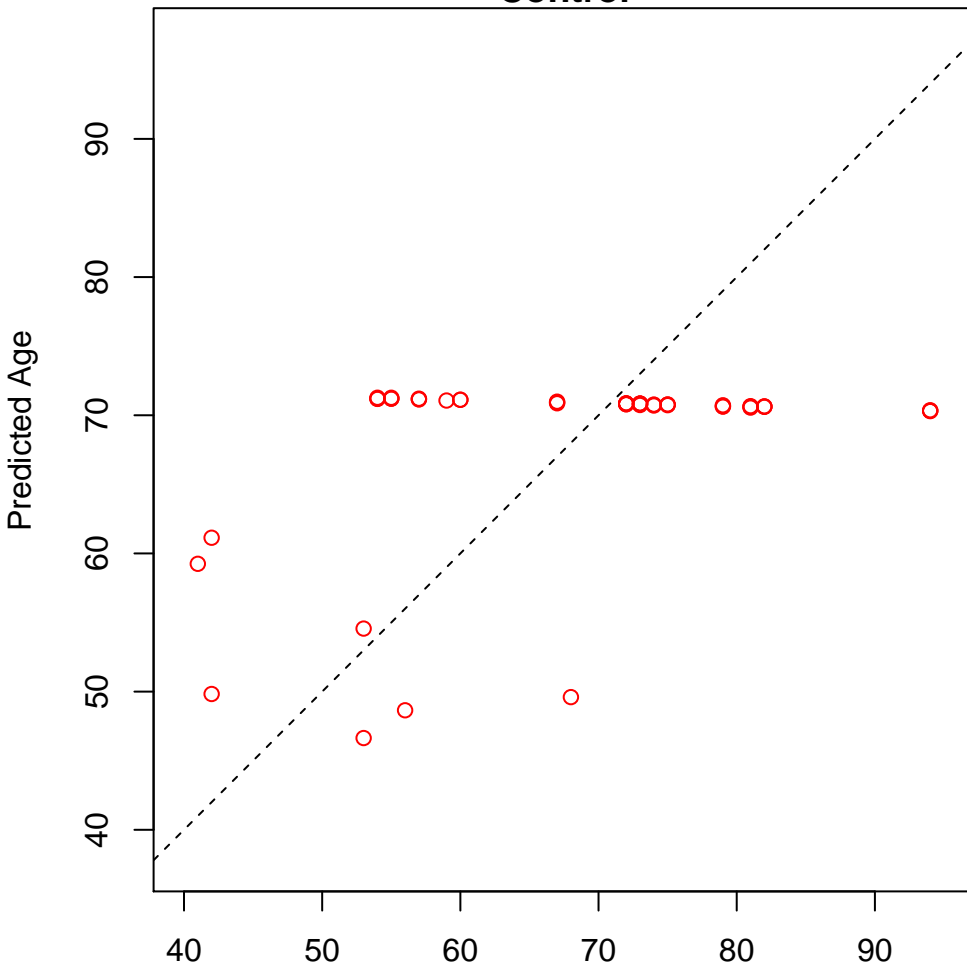


muscle organ development (Score: 0.758860)

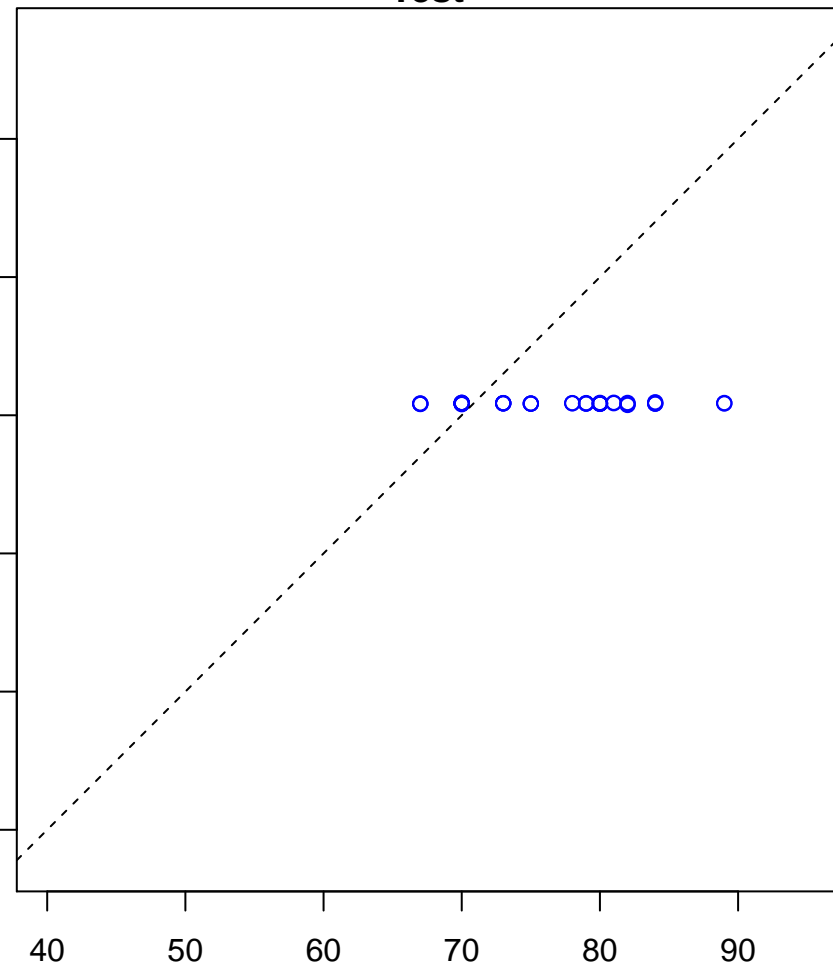


striated muscle tissue development (Score: 0.758860)

Control



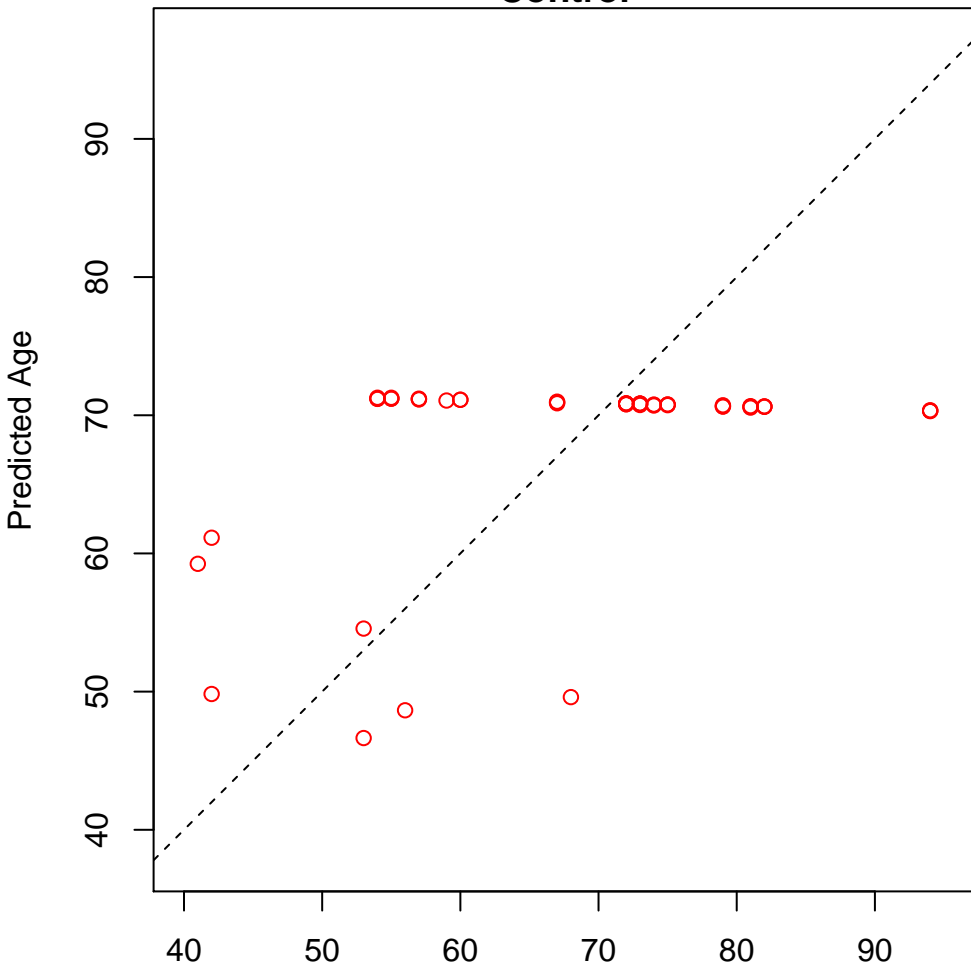
Test



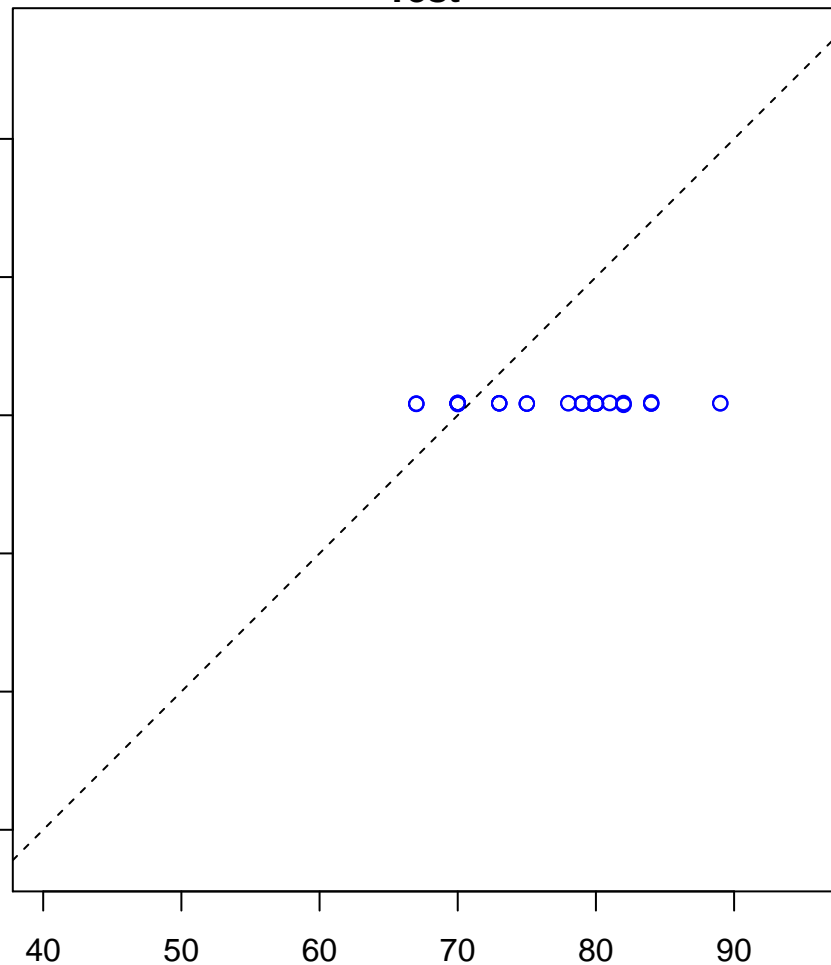
Actual Age

muscle organ morphogenesis (Score: 0.758860)

Control



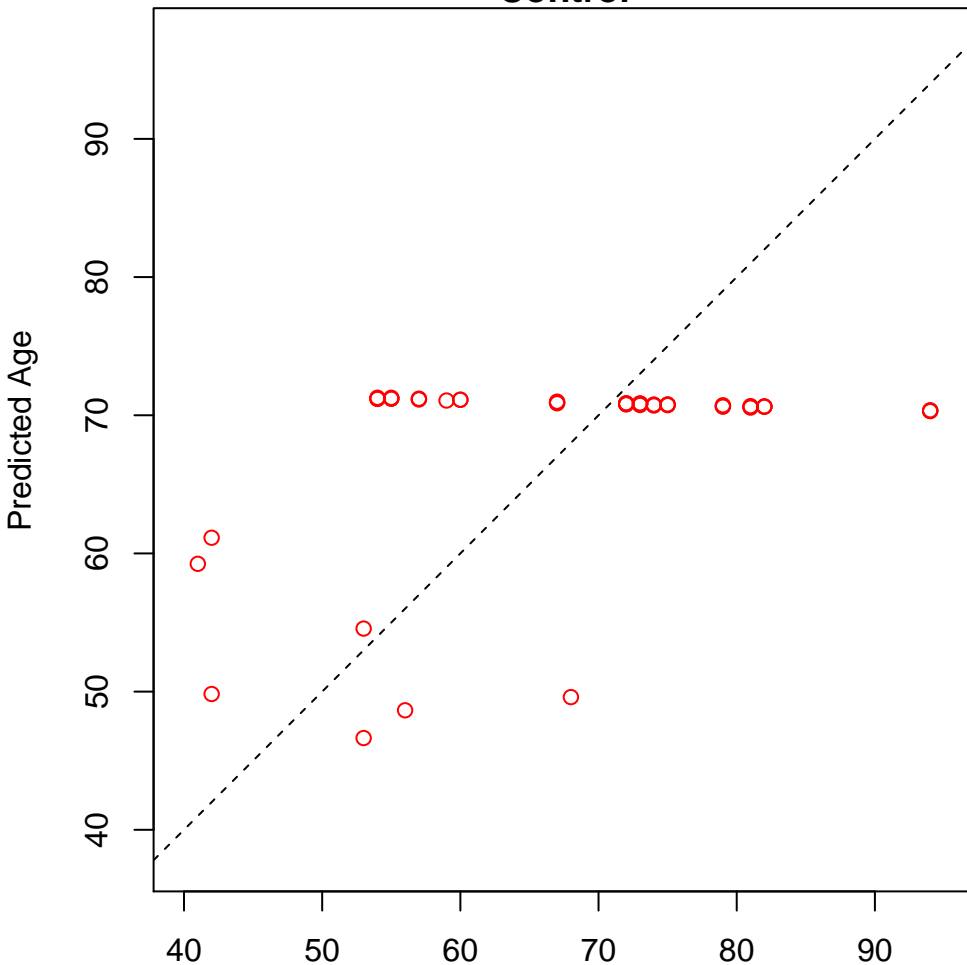
Test



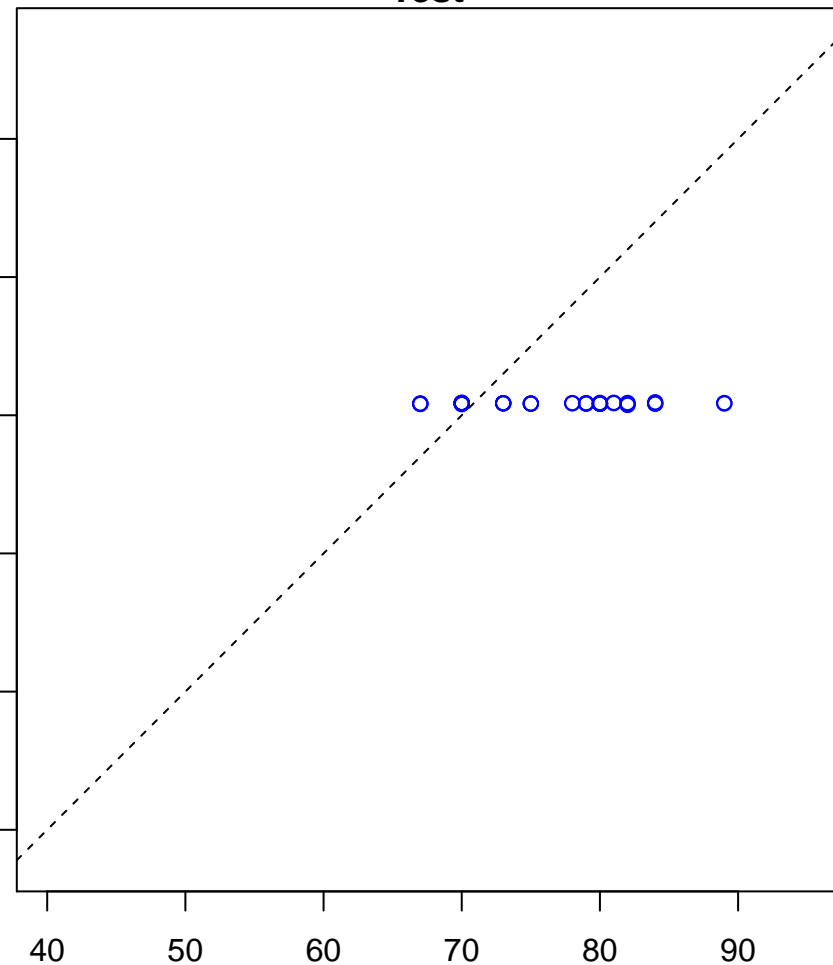
Actual Age

cardiac muscle tissue development (Score: 0.758860)

Control



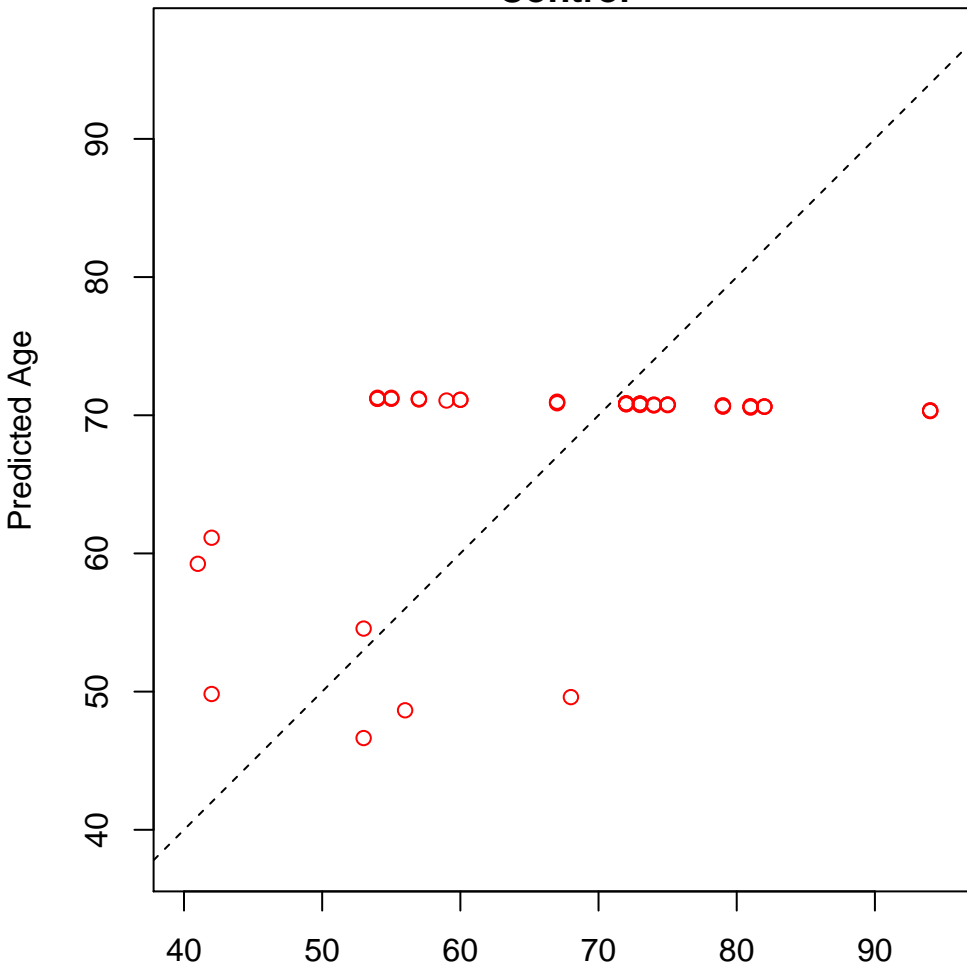
Test



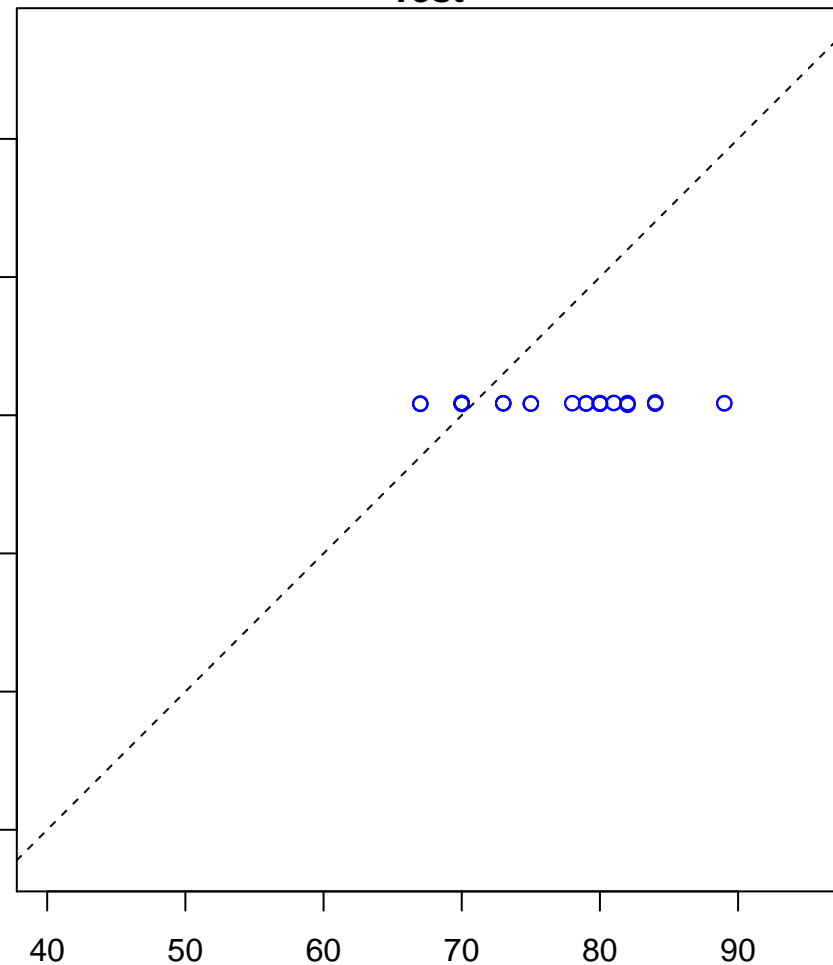
Actual Age

cardiac muscle tissue morphogenesis (Score: 0.758860)

Control

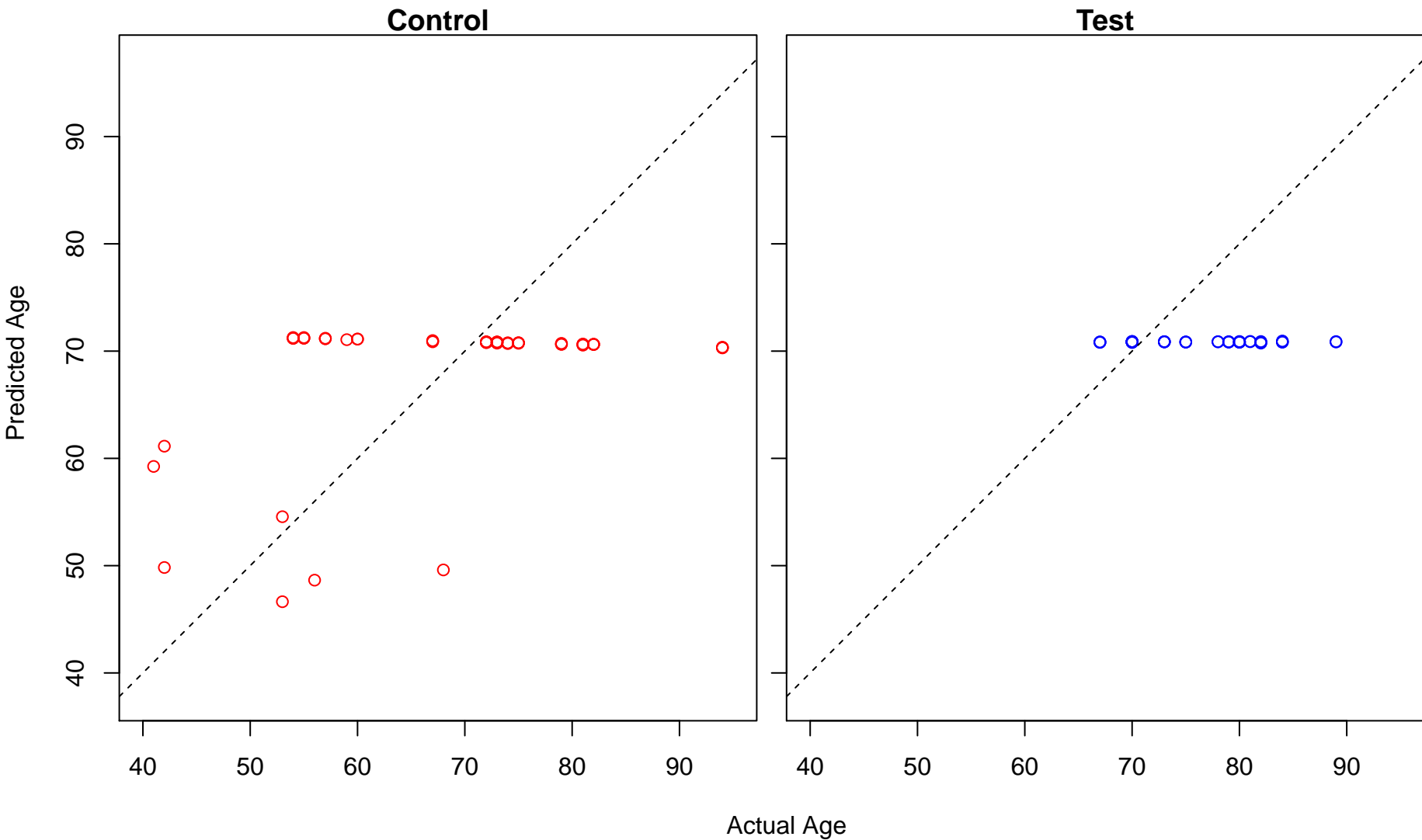


Test

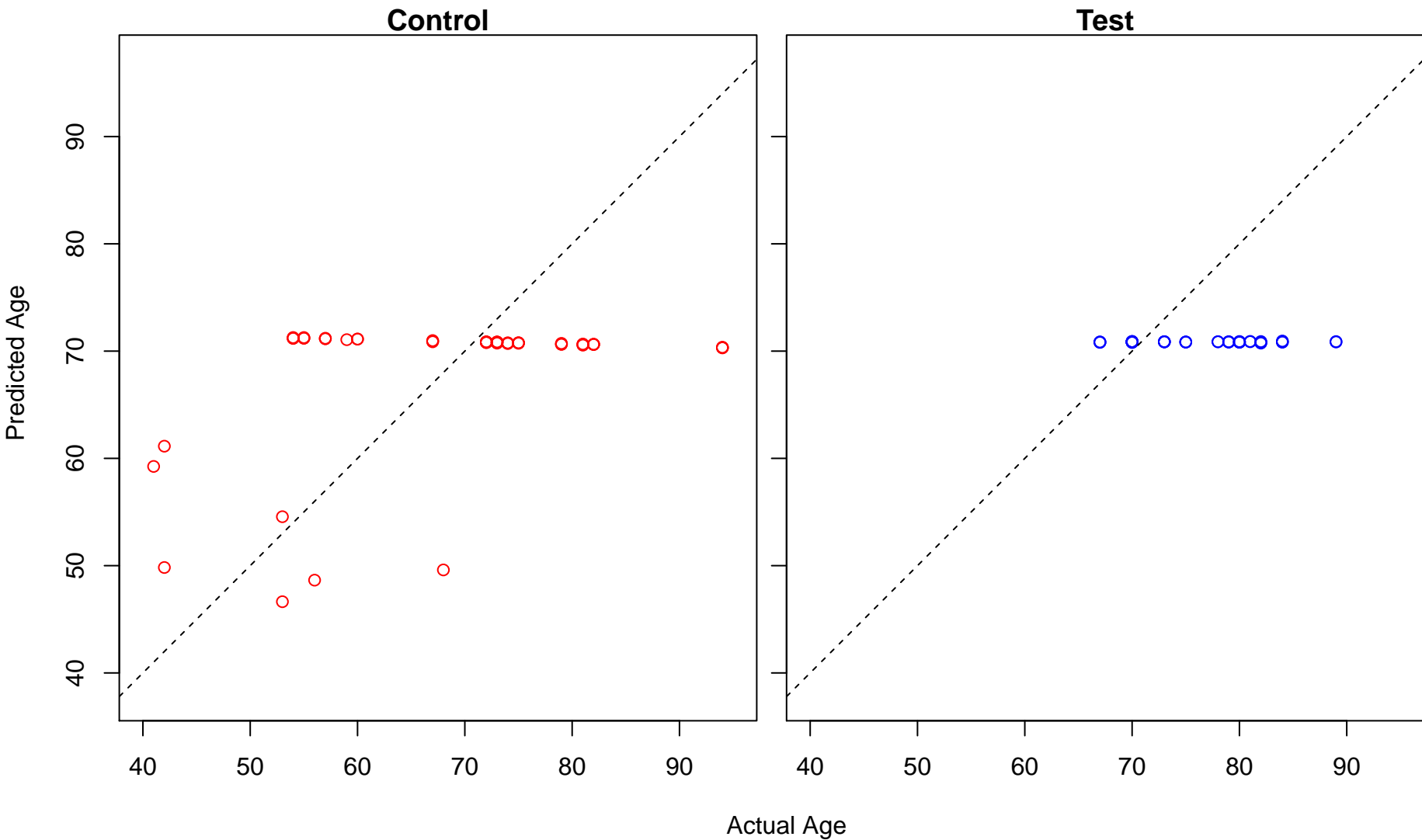


Actual Age

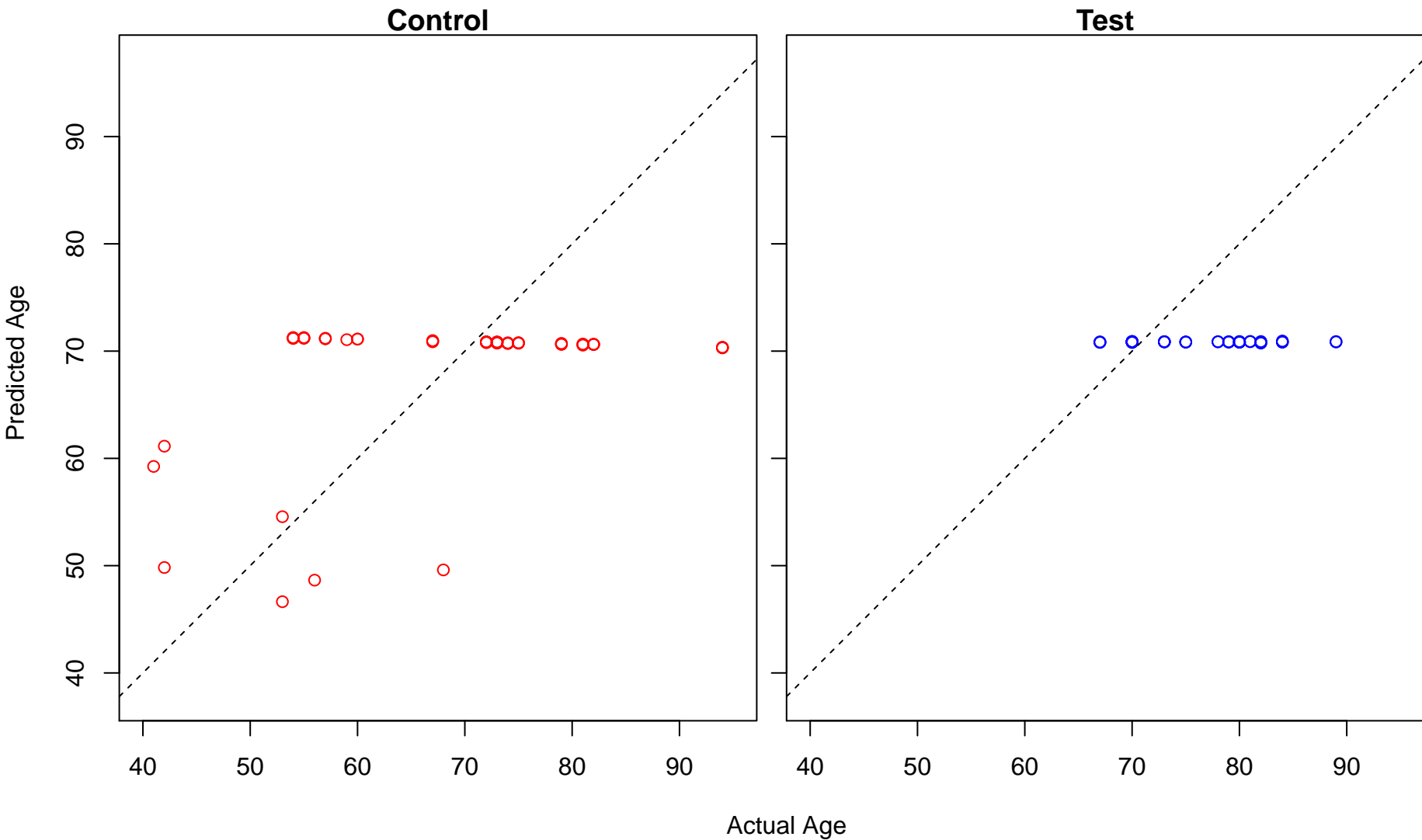
ventricular cardiac muscle tissue morphogenesis (Score: 0.758860)



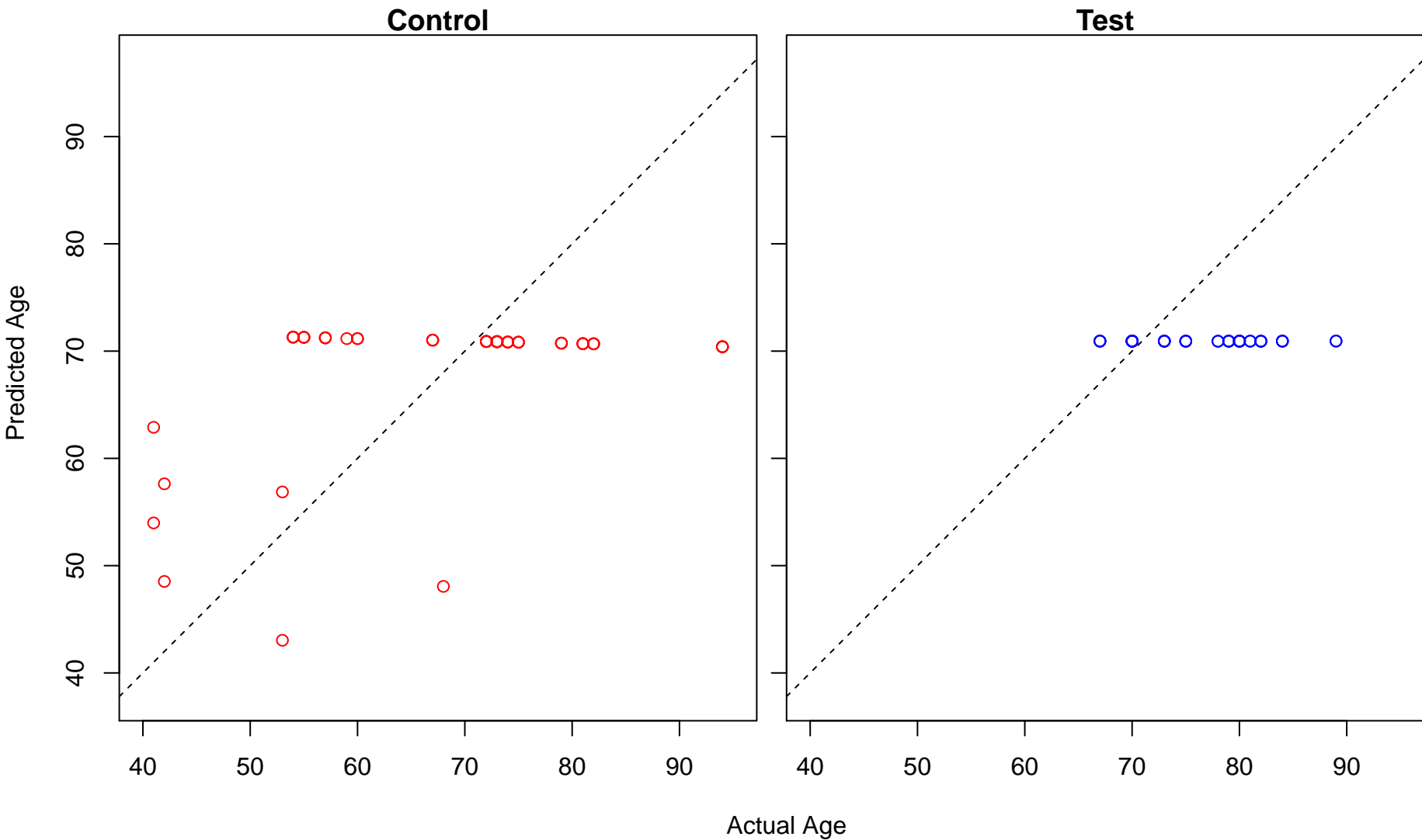
muscle tissue morphogenesis (Score: 0.758860)



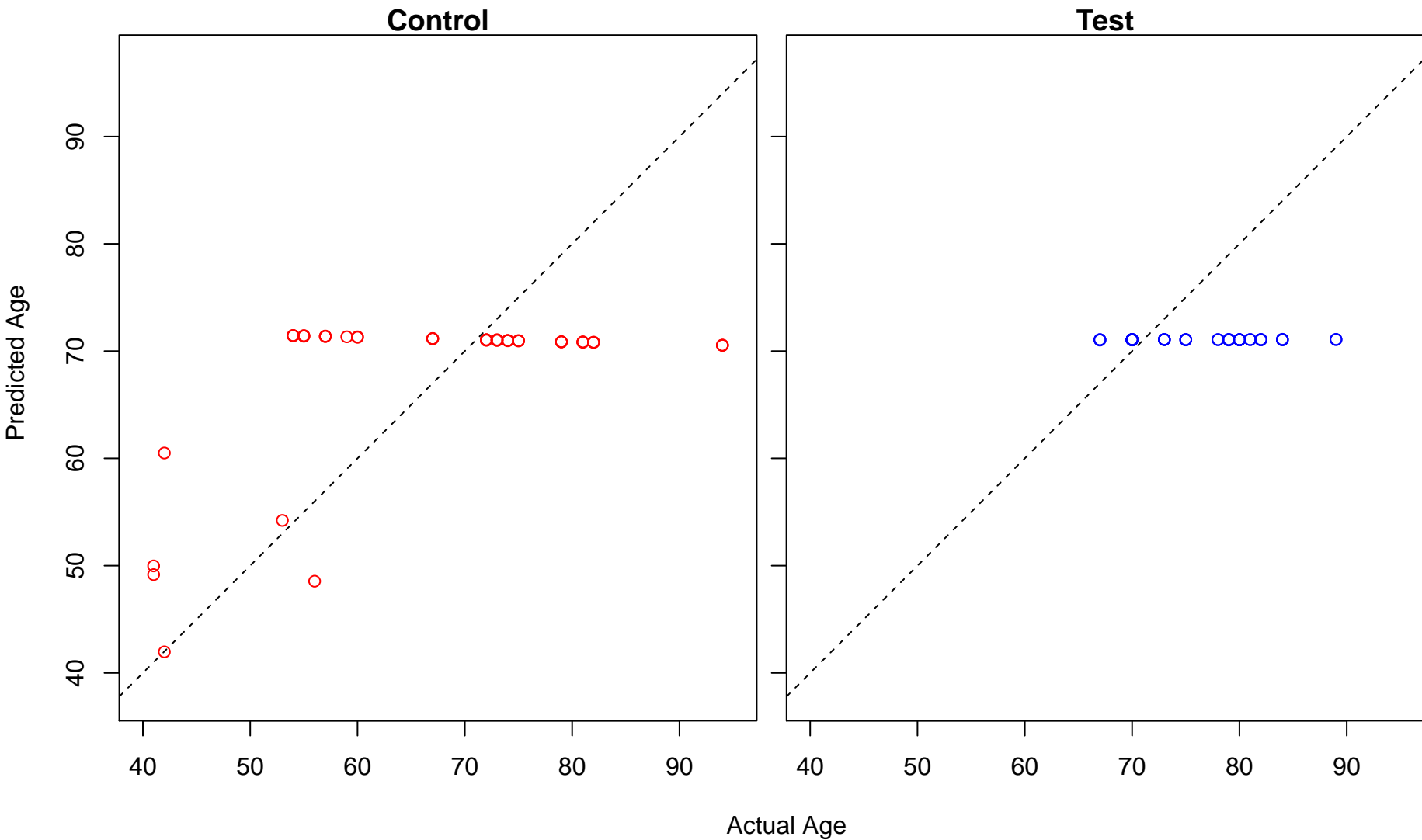
muscle tissue development (Score: 0.758860)



ribosome assembly (Score: 0.757091)

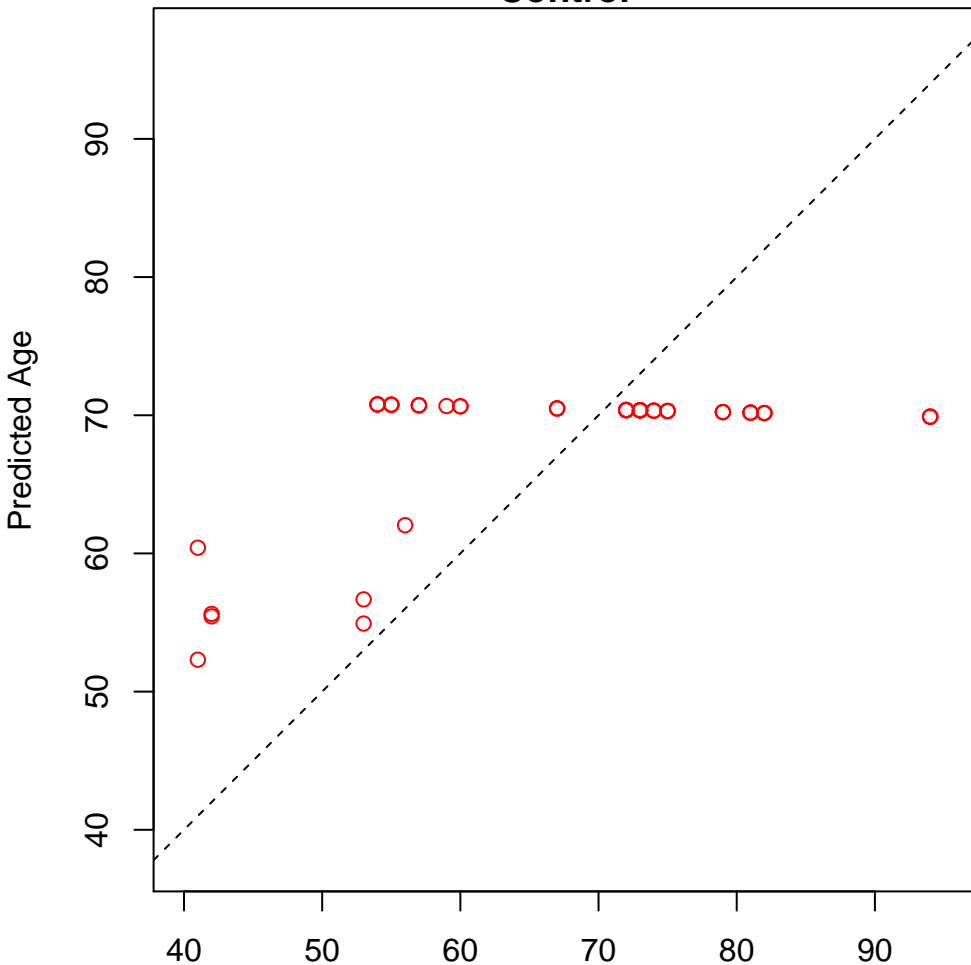


positive regulation of chromosome organization (Score: 0.755227)

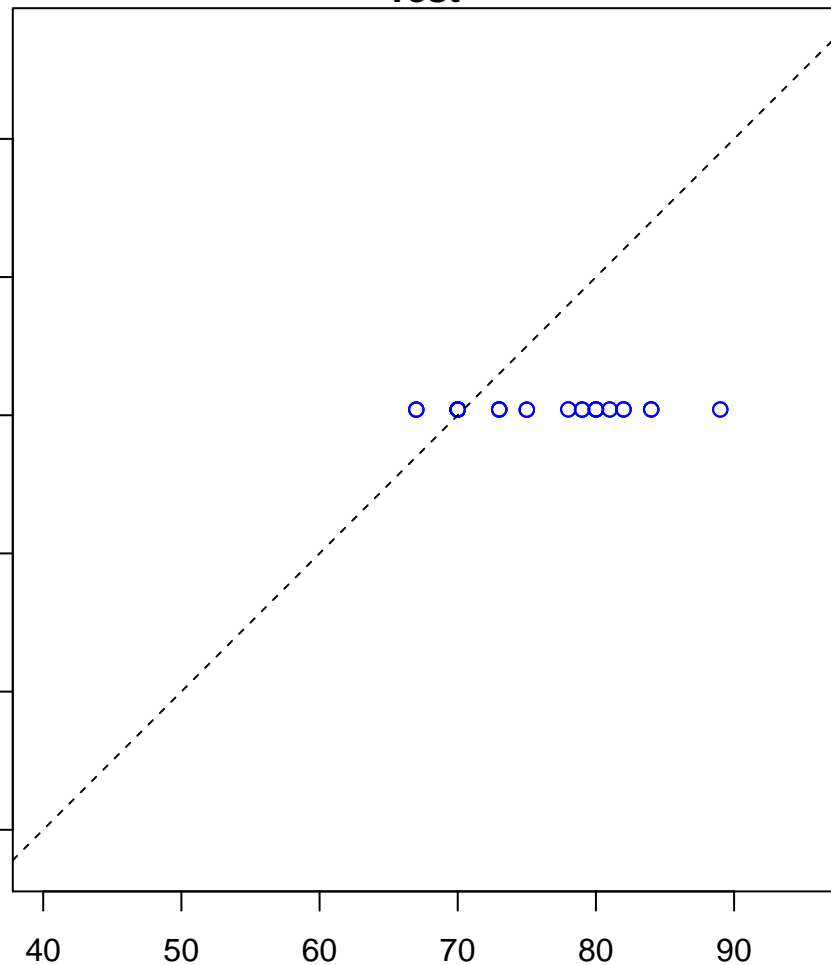


negative regulation of viral transcription (Score: 0.754385)

Control



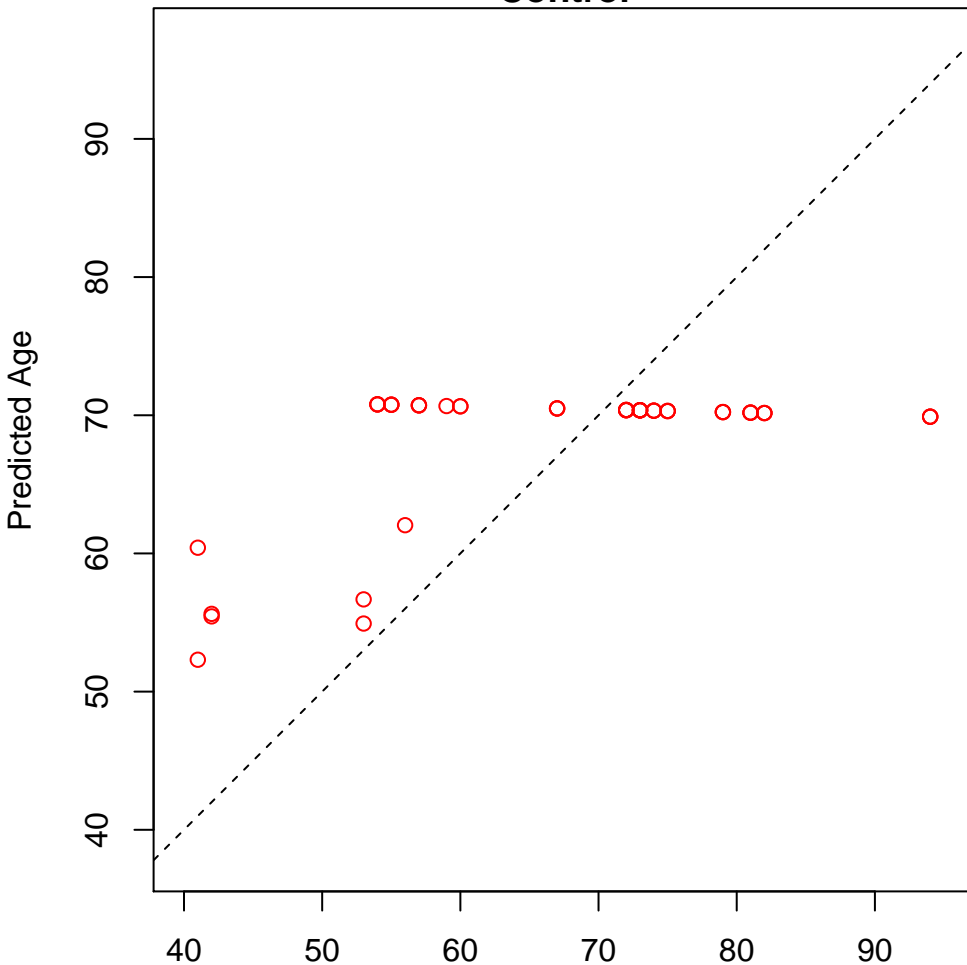
Test



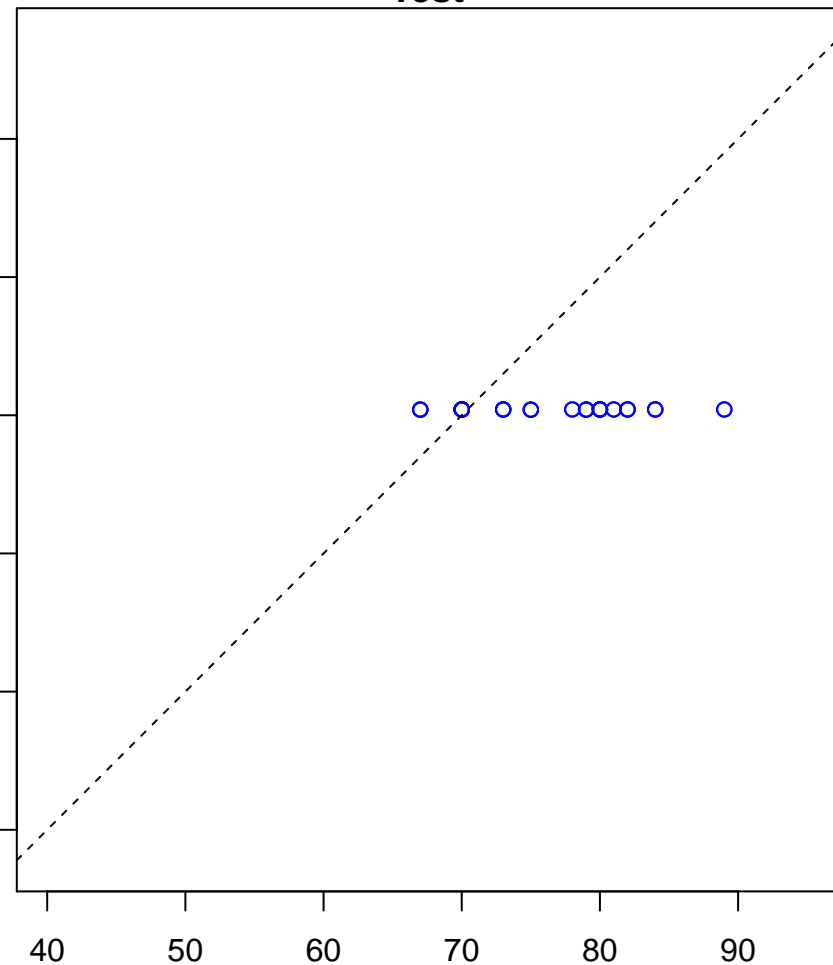
Actual Age

modulation by host of viral transcription (Score: 0.754385)

Control

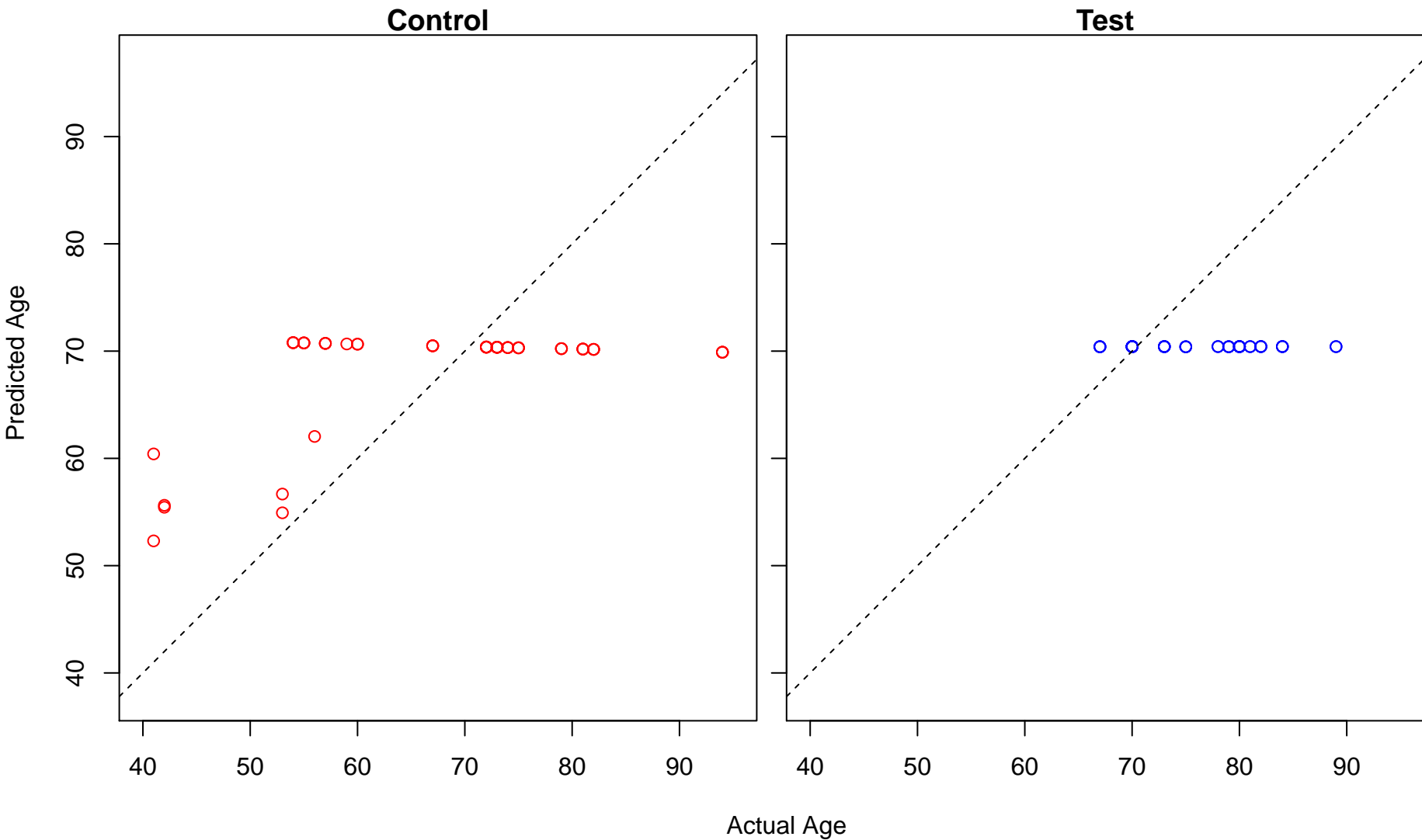


Test

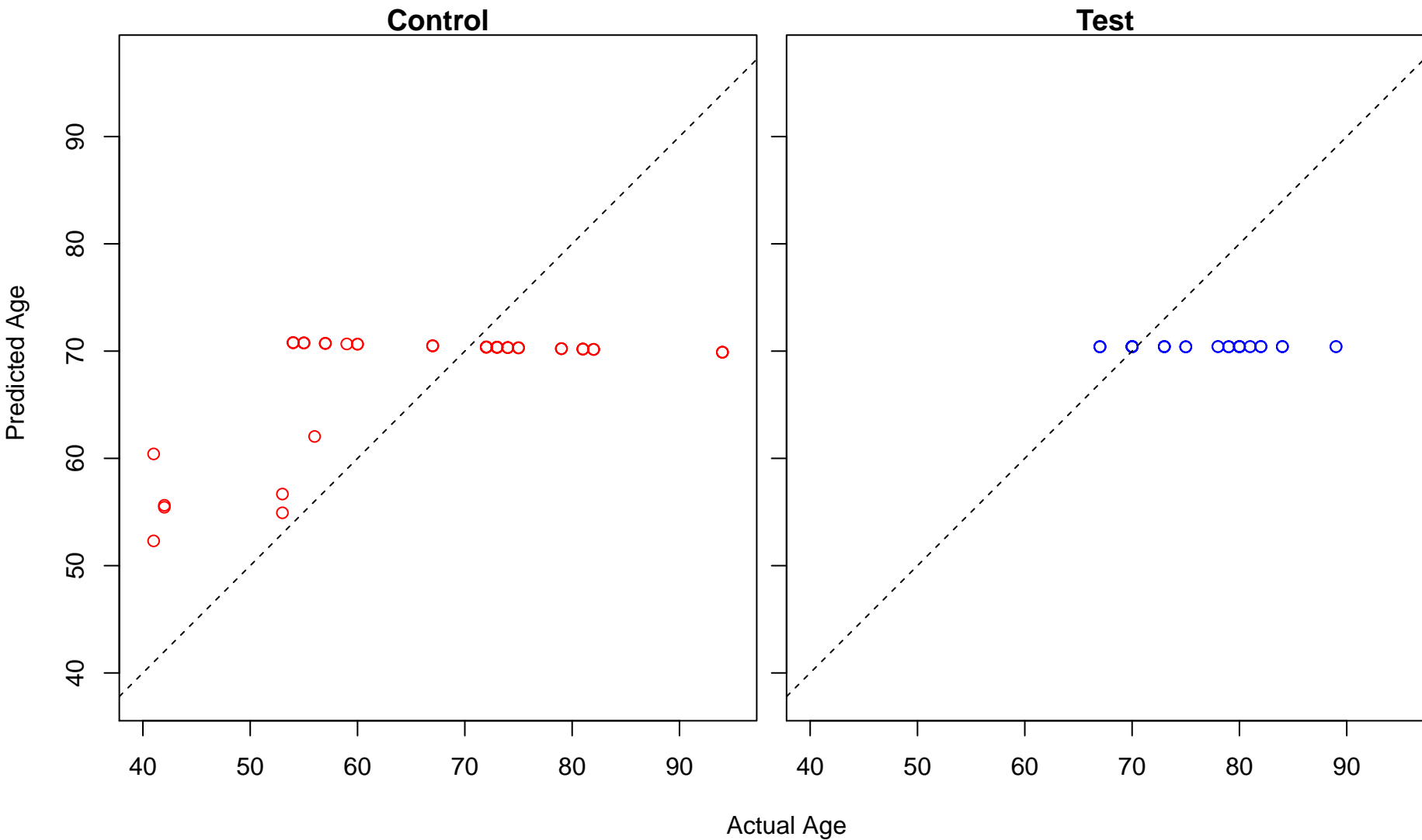


Actual Age

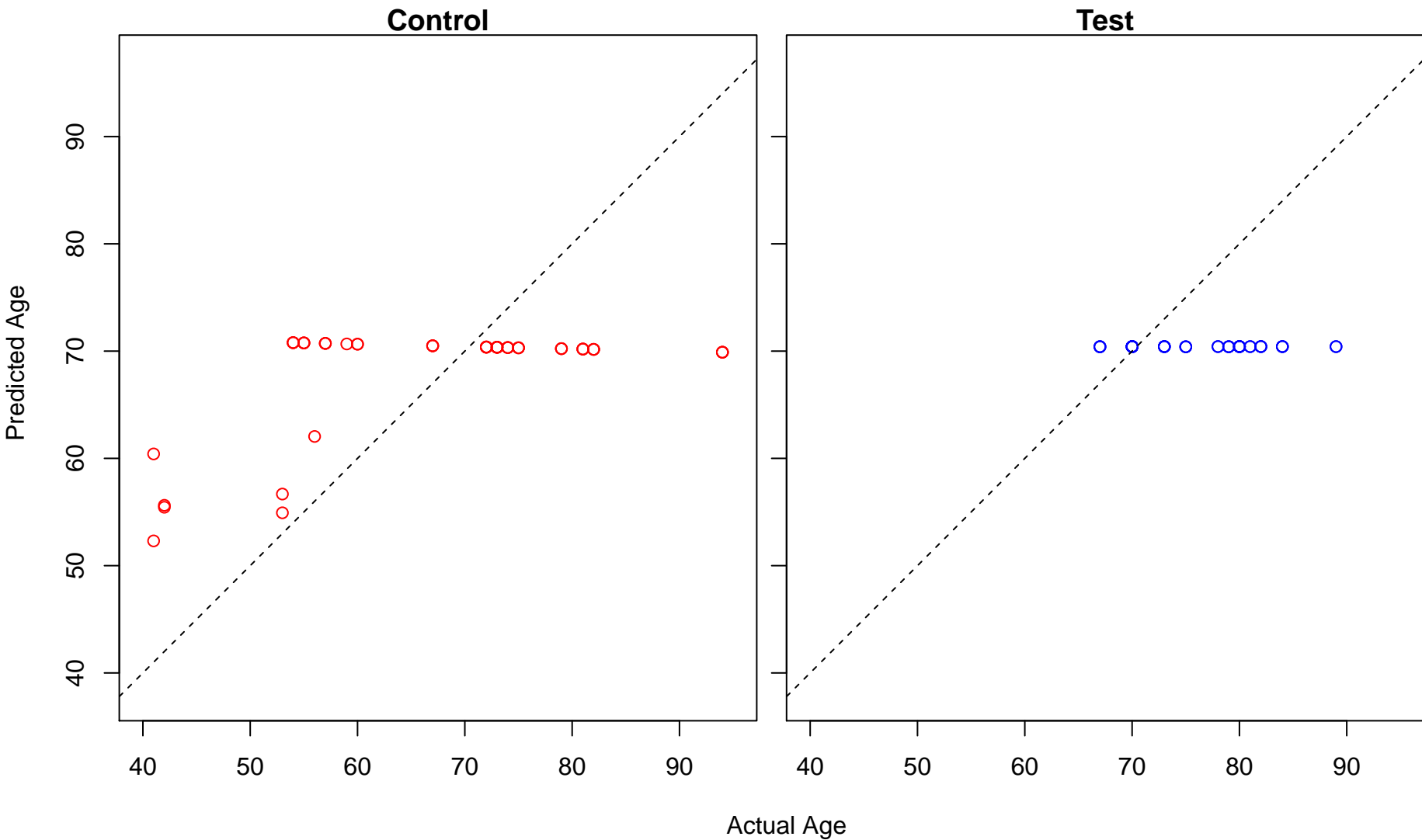
negative regulation by host of viral transcription (Score: 0.754385)



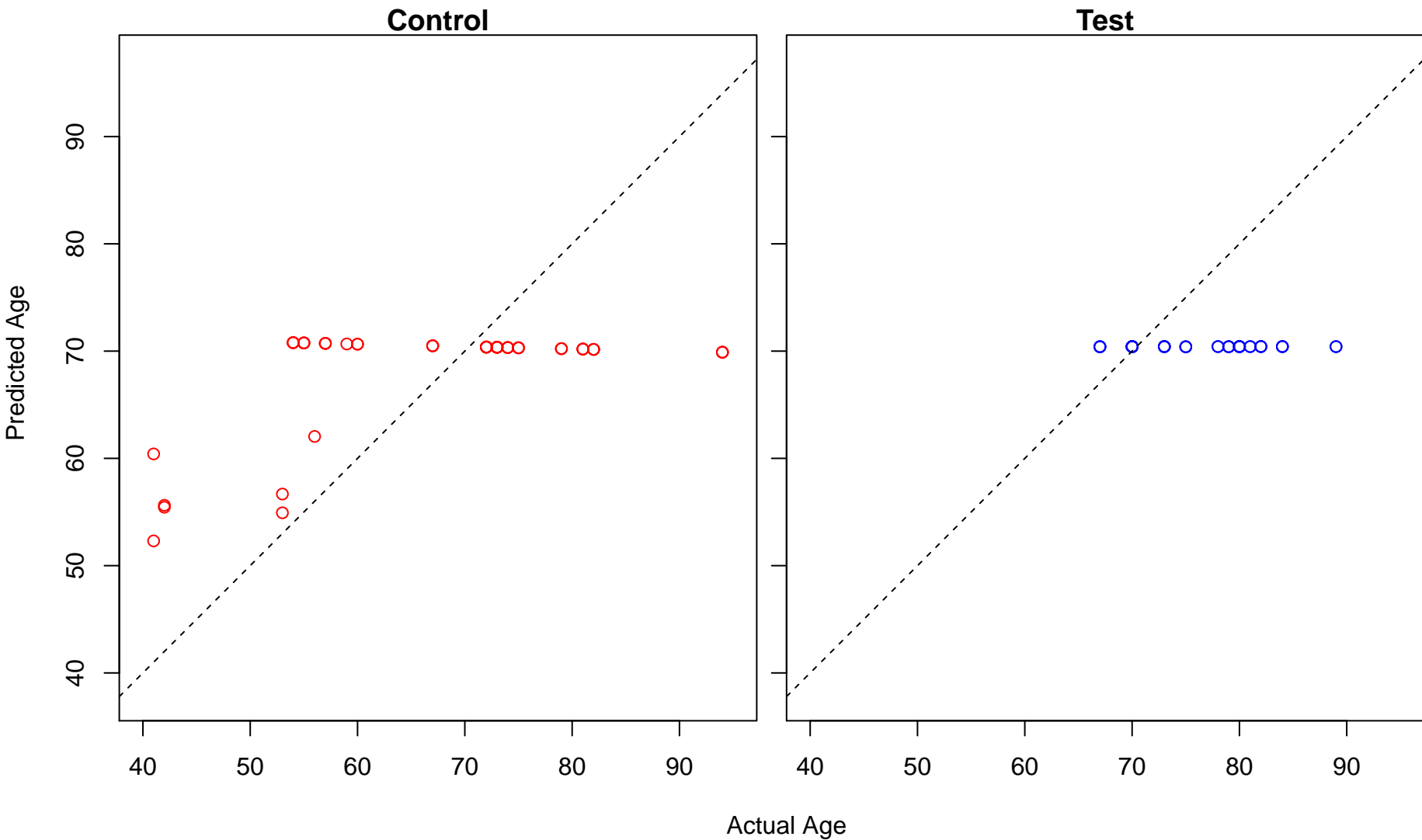
regulation of viral transcription (Score: 0.754385)



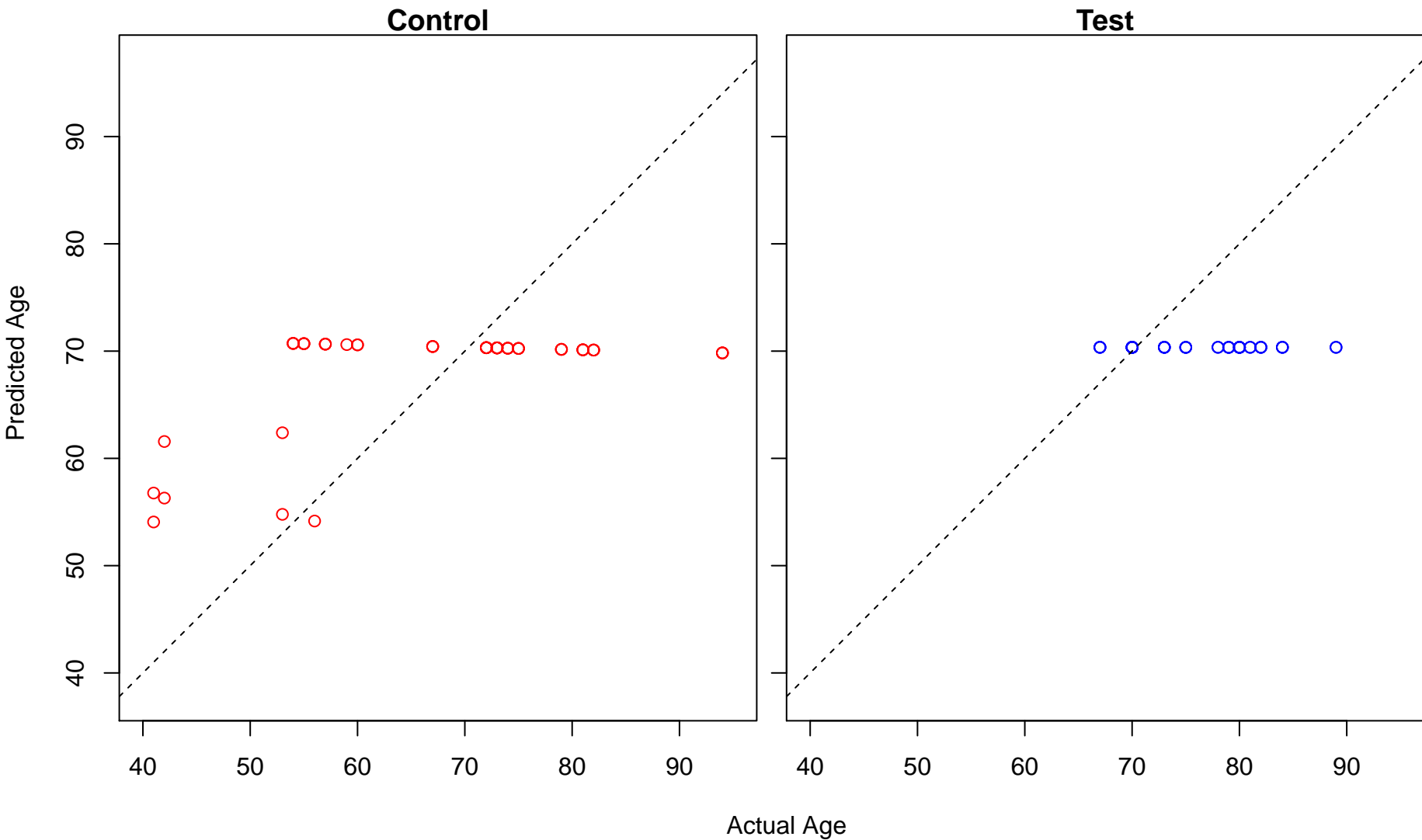
modulation of transcription in other organism involved in symbiotic interaction (Score: 0.754385)



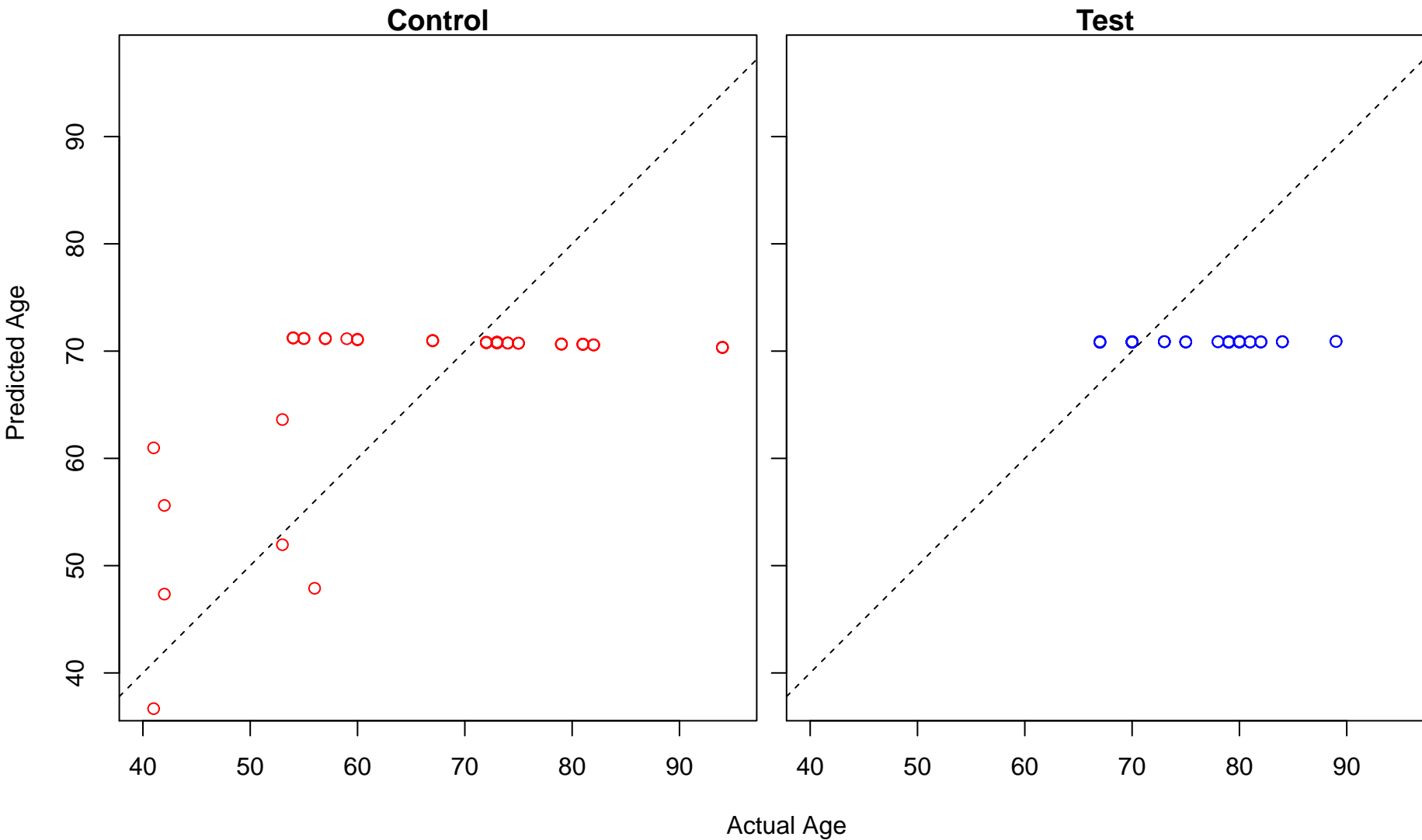
modulation by host of symbiont transcription (Score: 0.754385)



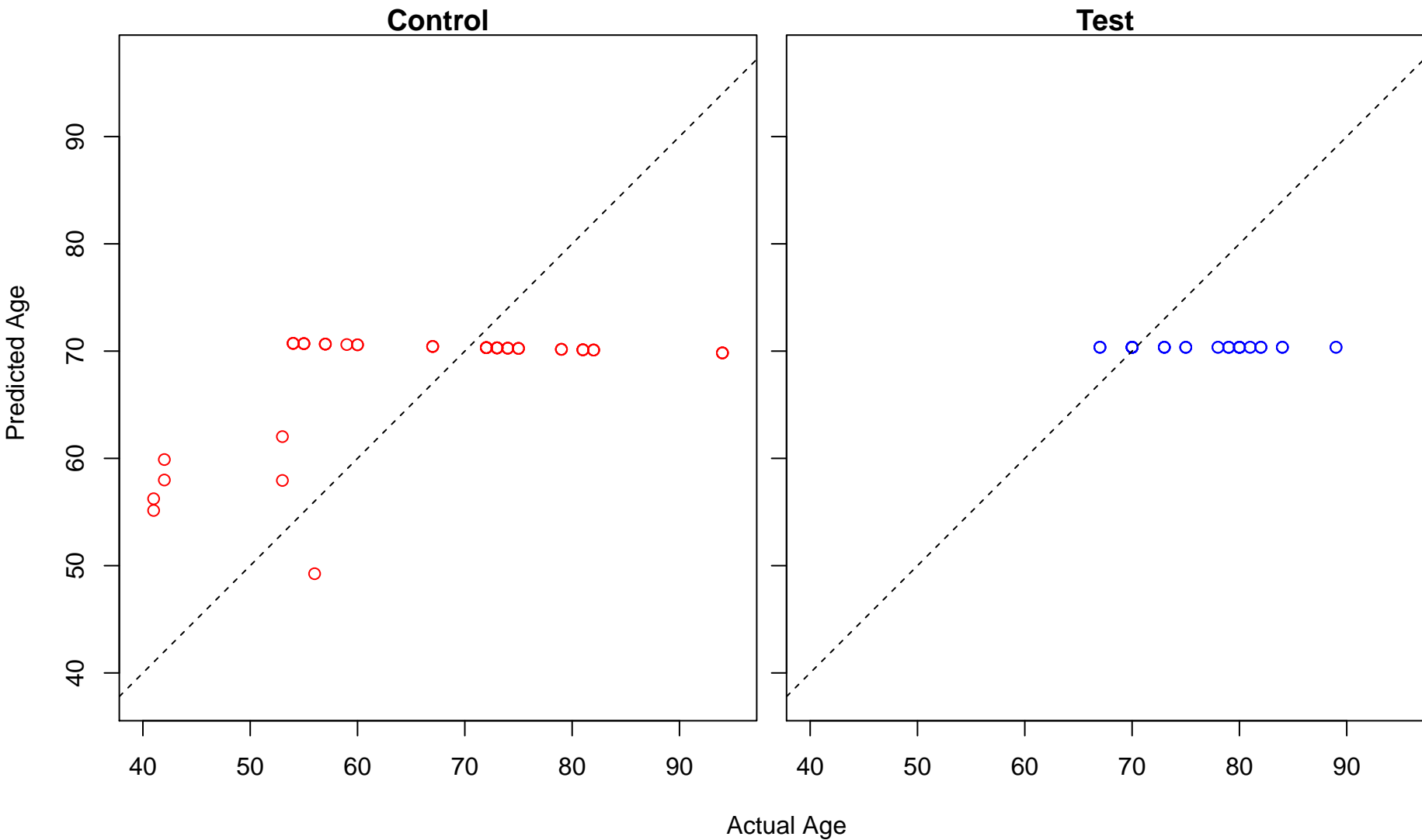
muscle structure development (Score: 0.753226)



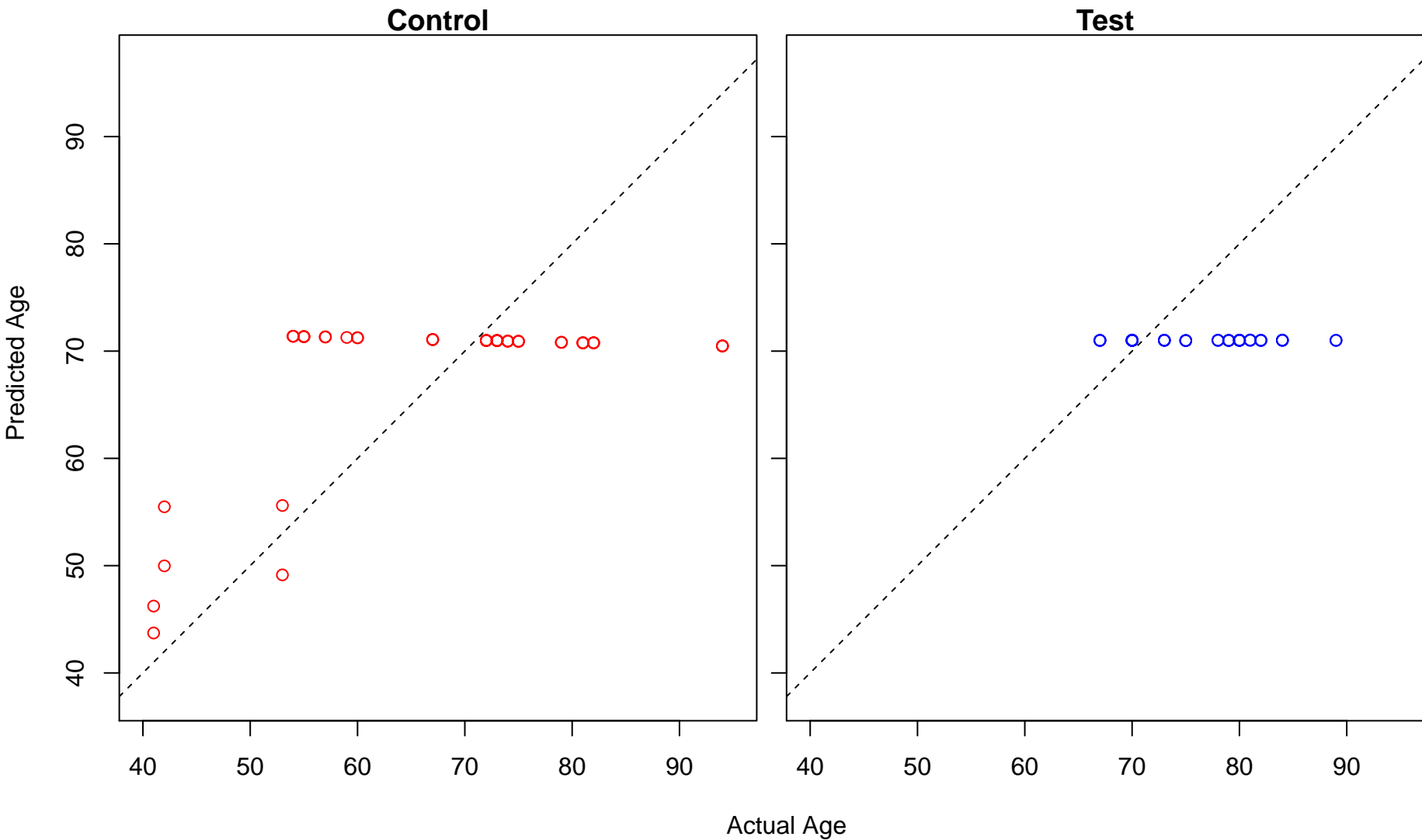
positive regulation of telomere maintenance (Score: 0.752680)



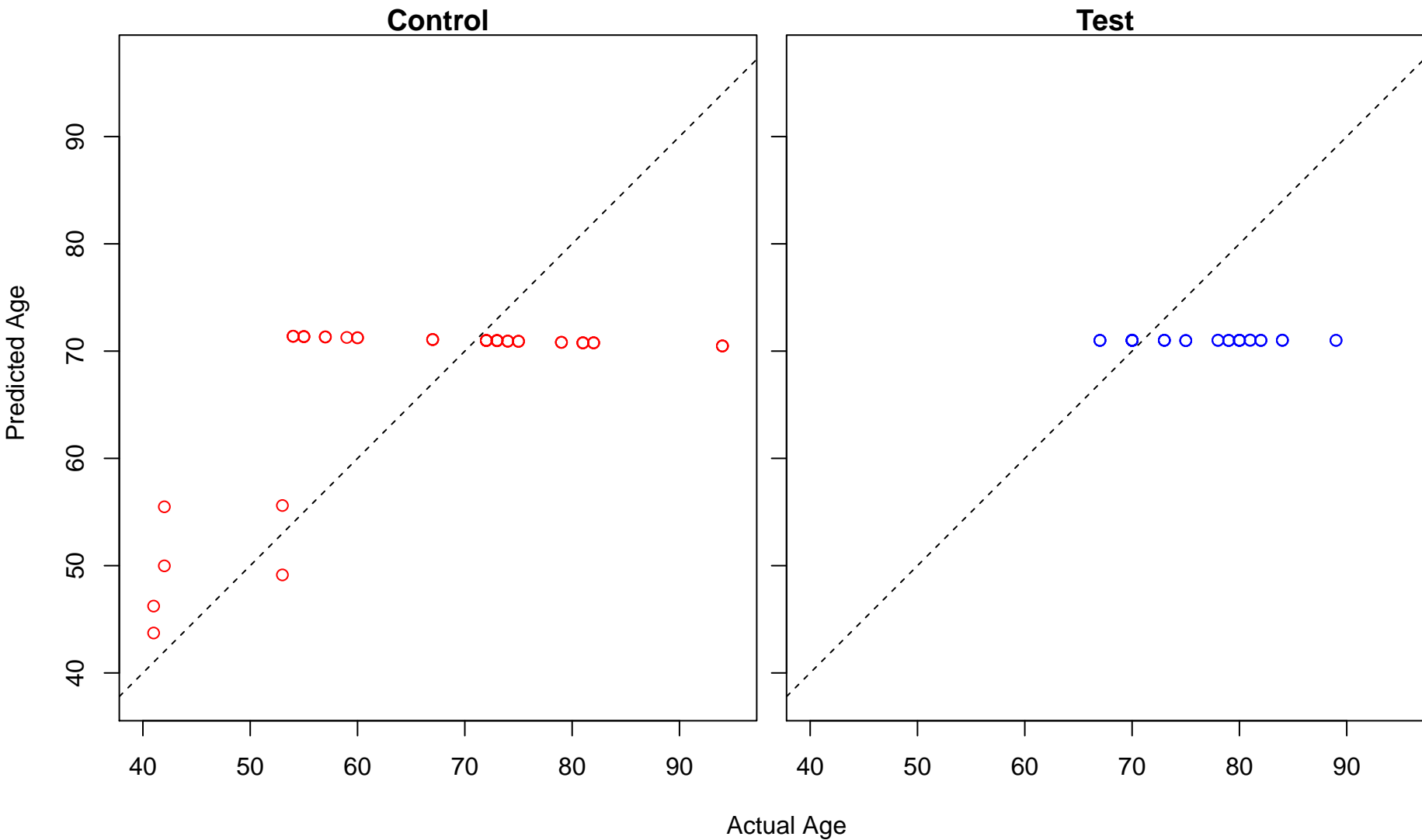
positive regulation of response to DNA damage stimulus (Score: 0.752126)



BMP signaling pathway (Score: 0.749355)

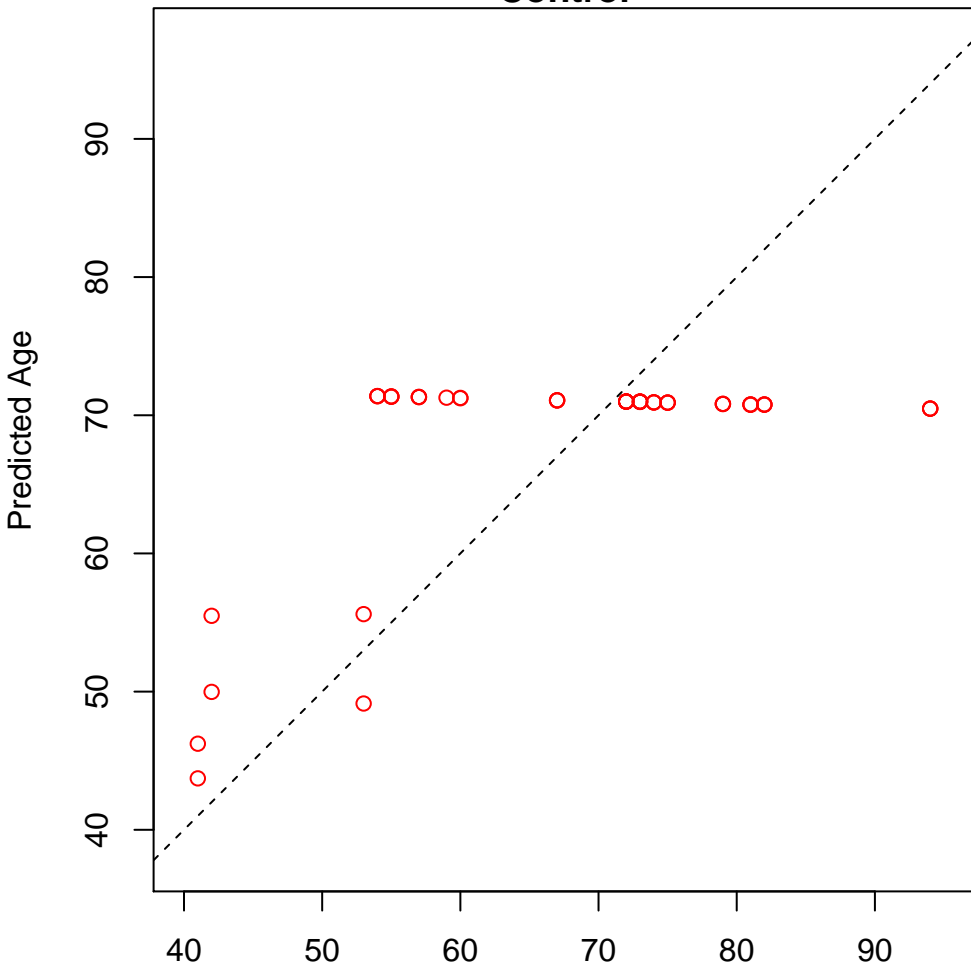


response to BMP (Score: 0.749355)

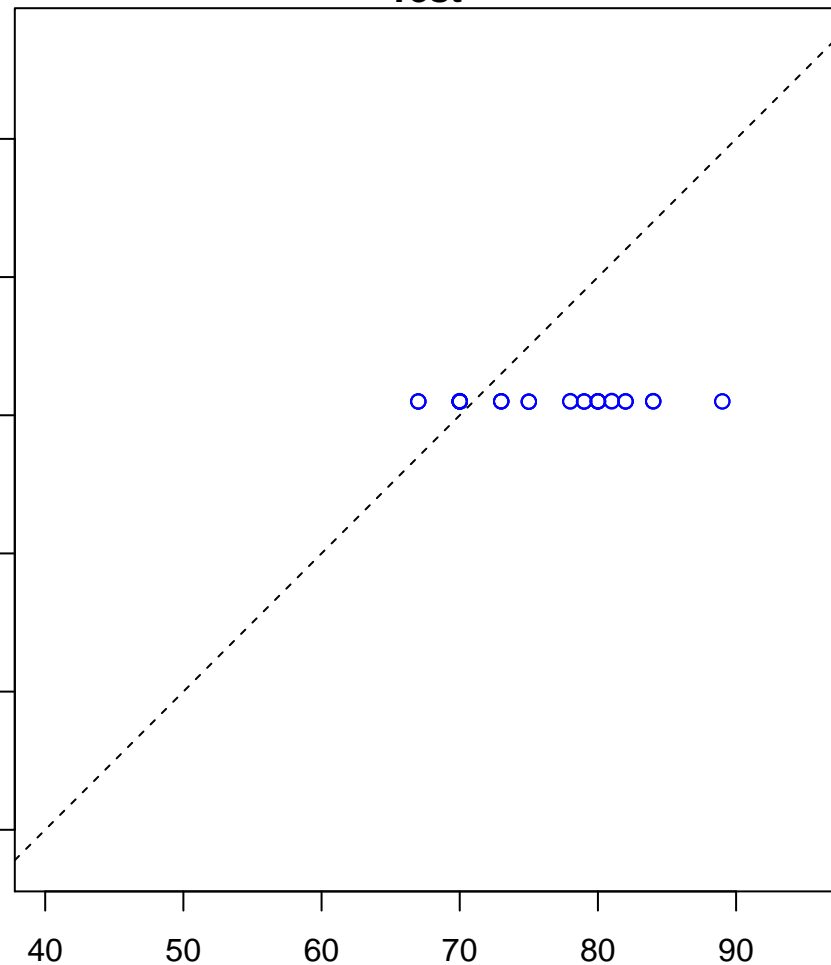


cellular response to BMP stimulus (Score: 0.749355)

Control

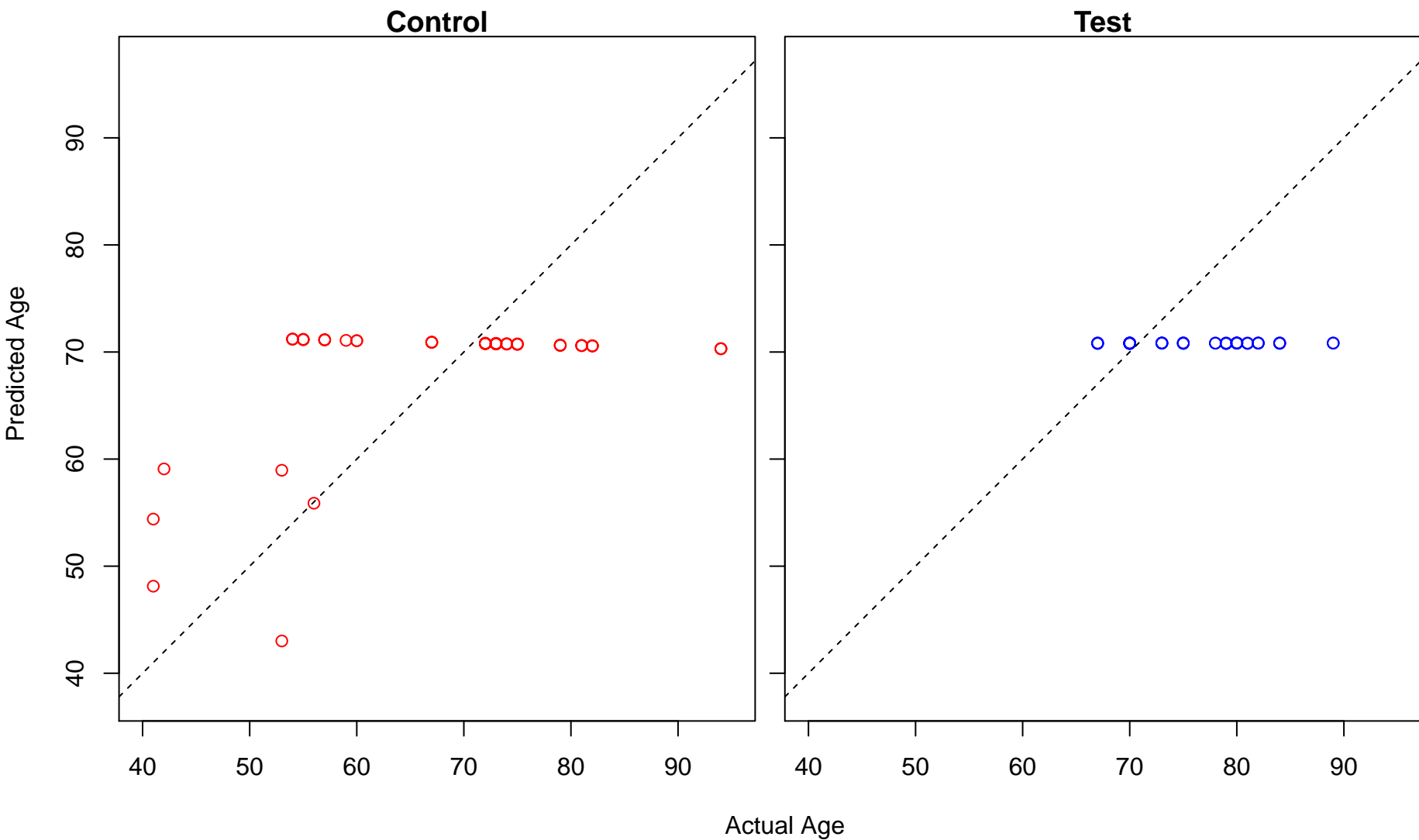


Test

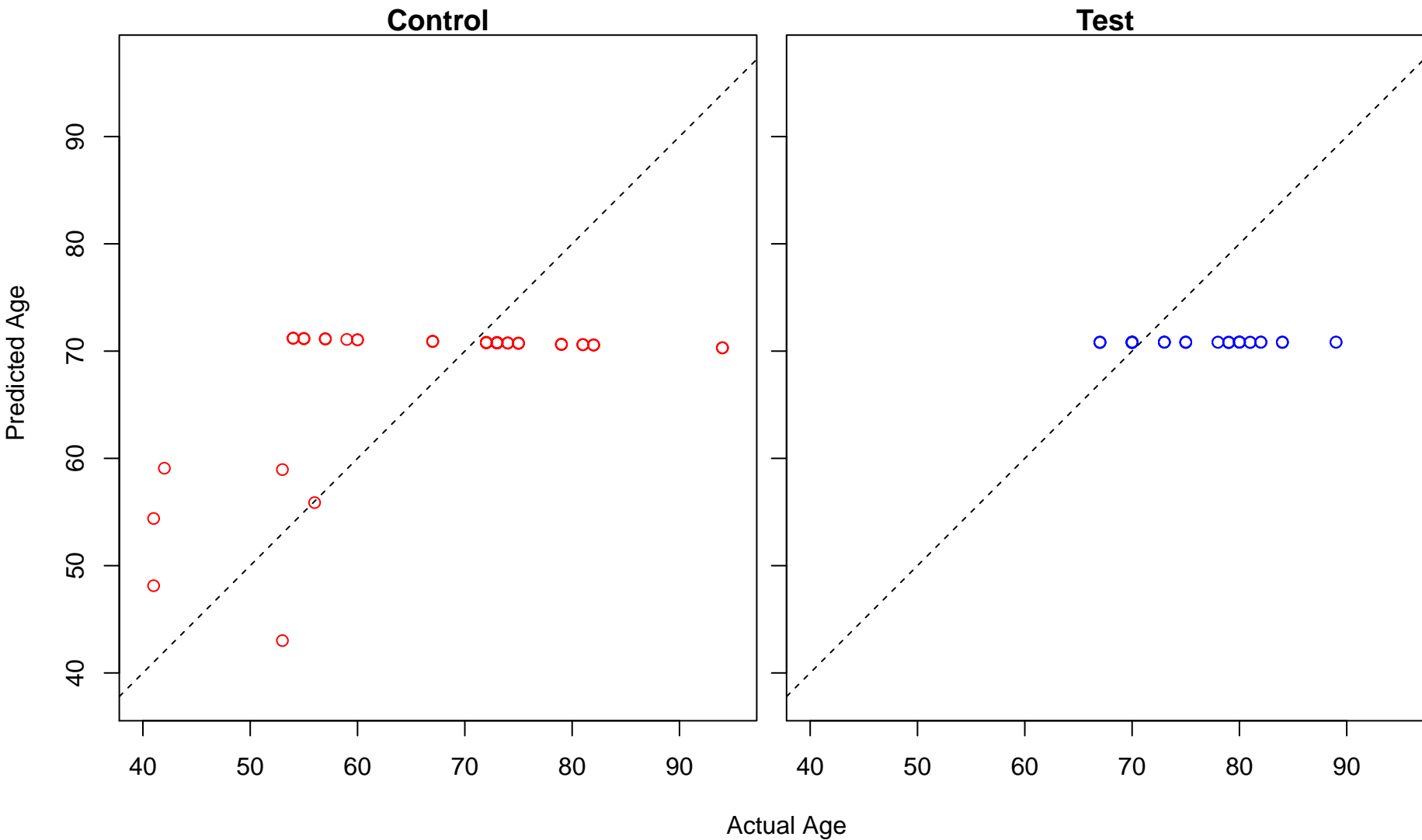


Actual Age

intracellular steroid hormone receptor signaling pathway (Score: 0.743941)

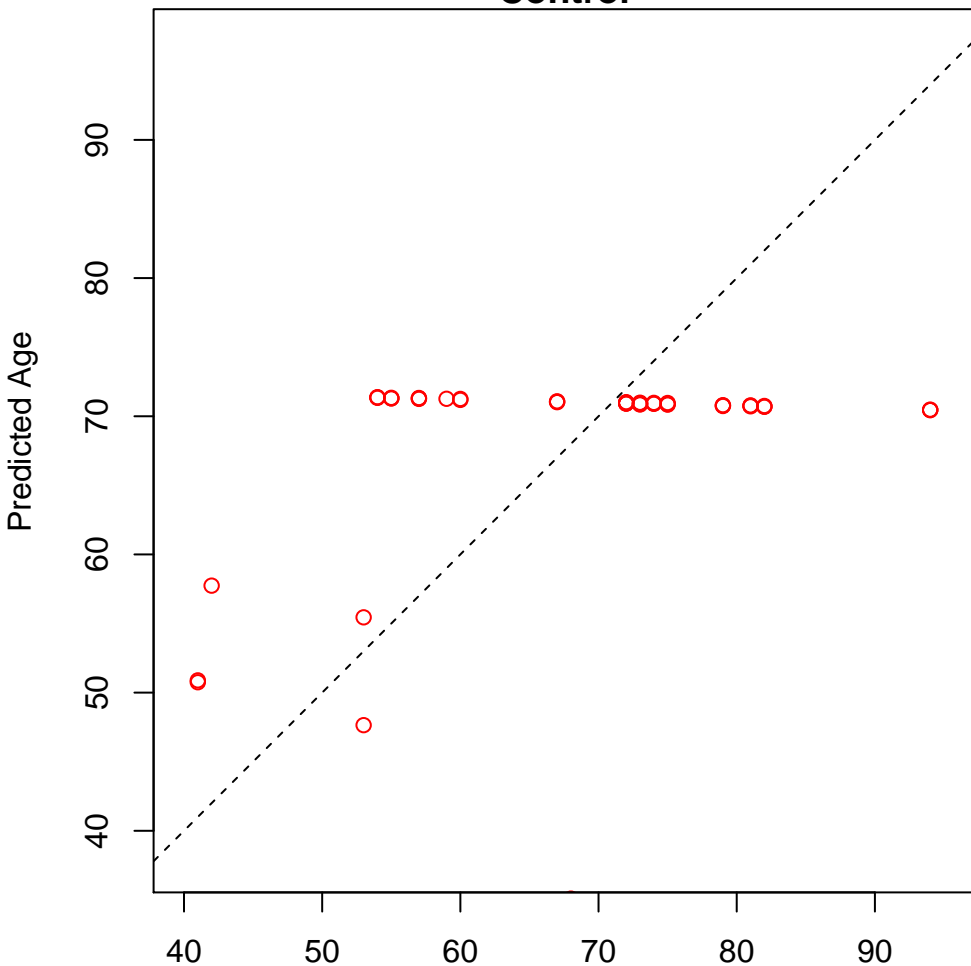


steroid hormone mediated signaling pathway (Score: 0.743941)

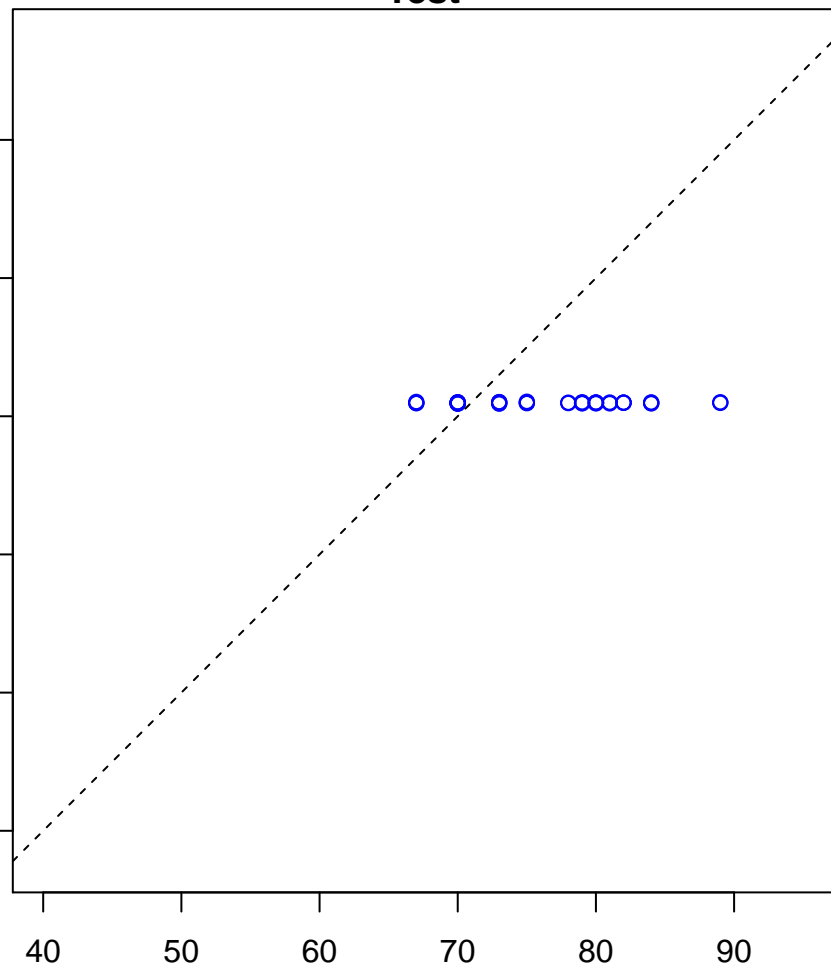


hormone-mediated signaling pathway (Score: 0.735099)

Control



Test



Actual Age