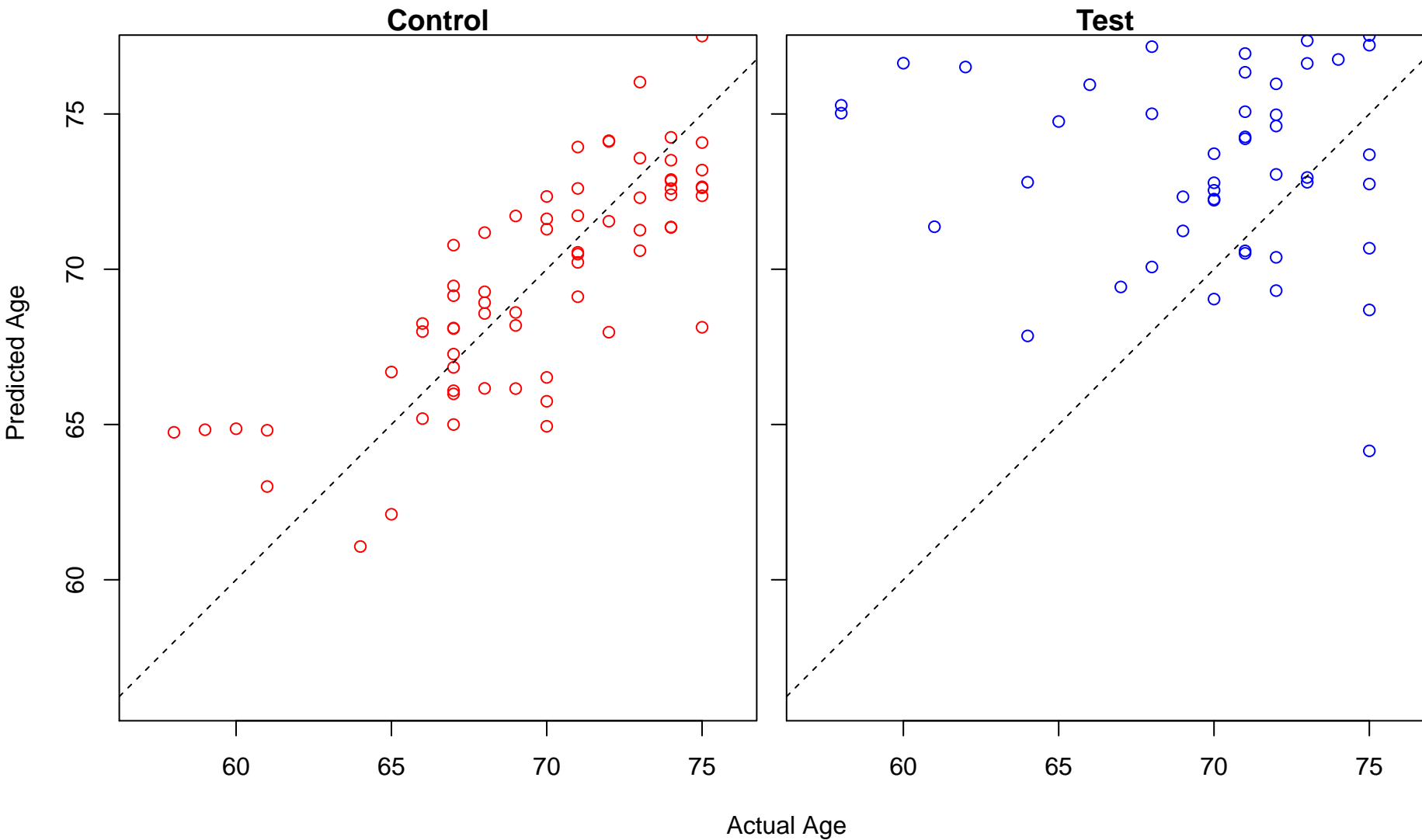
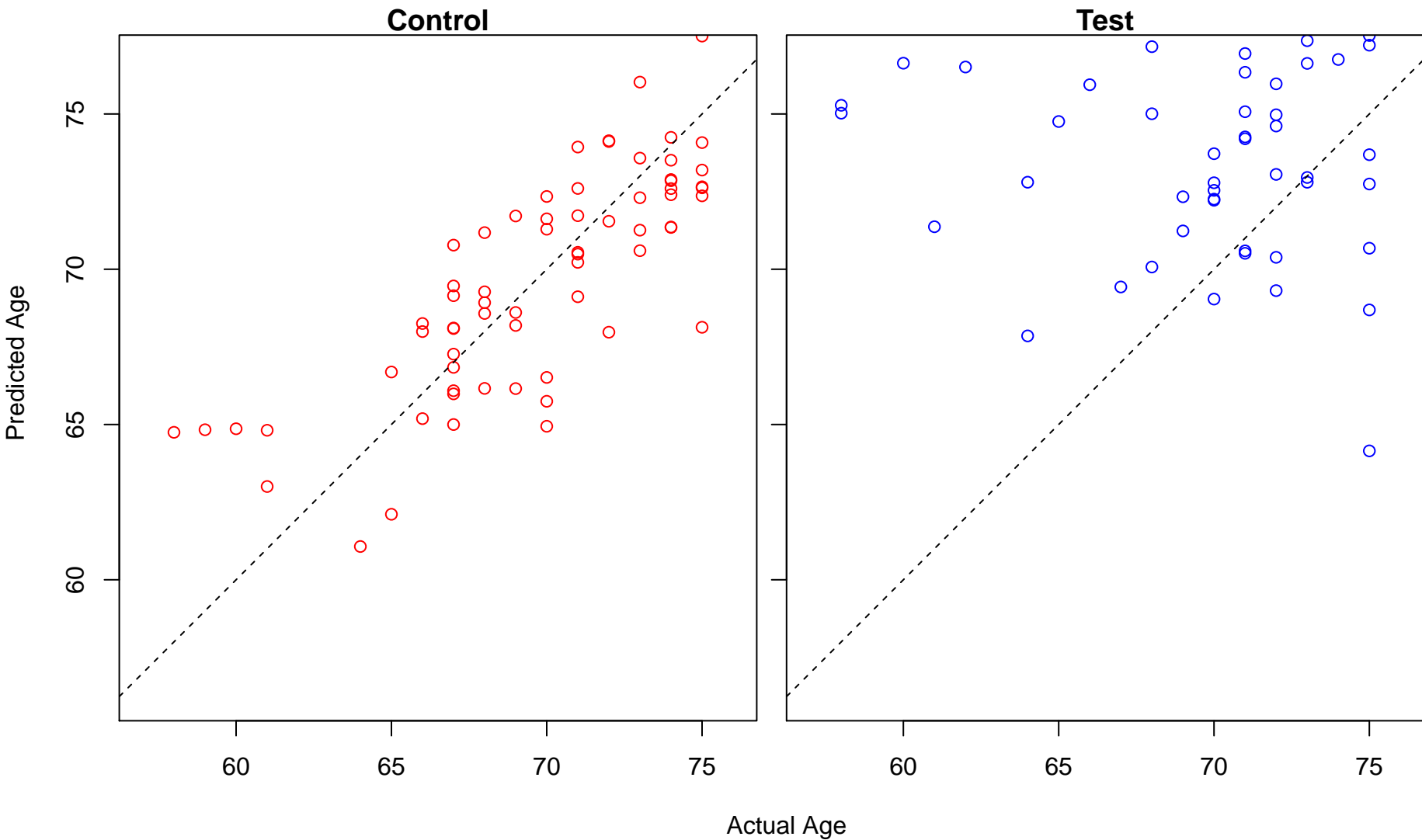


peptidyl-tyrosine phosphorylation (Score: 2.972314)

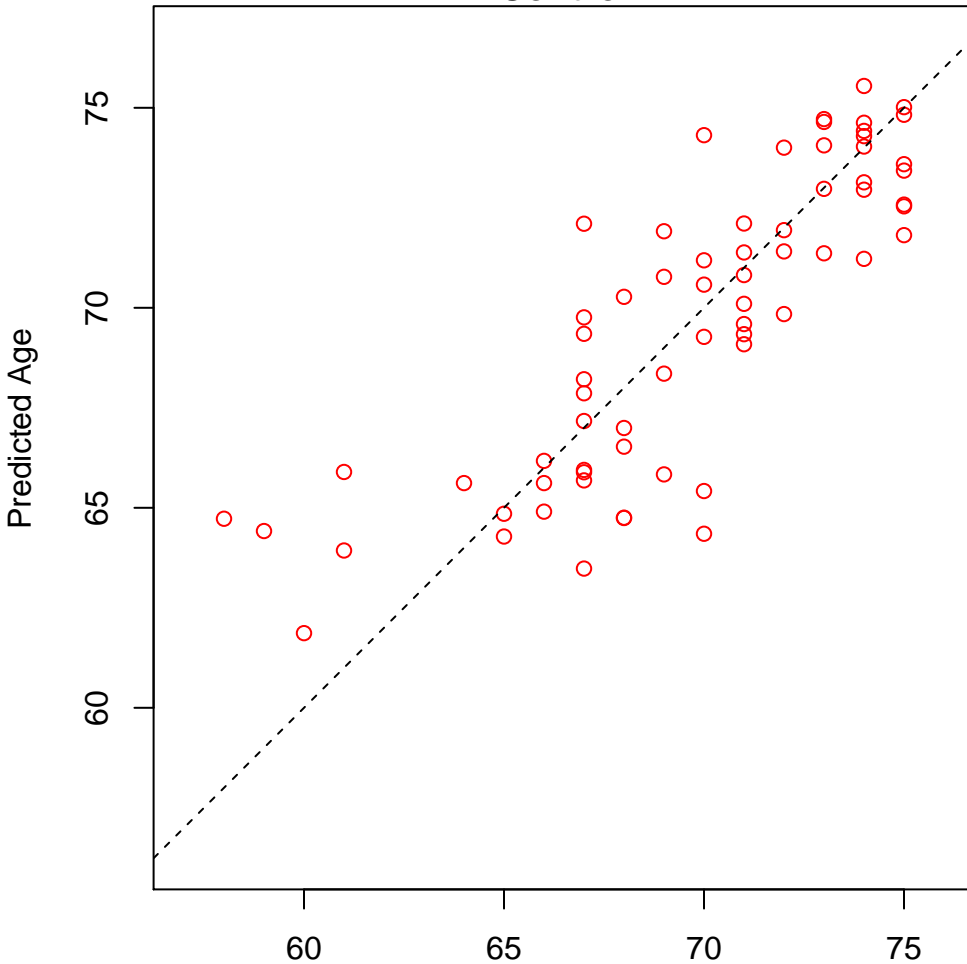


peptidyl-tyrosine modification (Score: 2.972314)

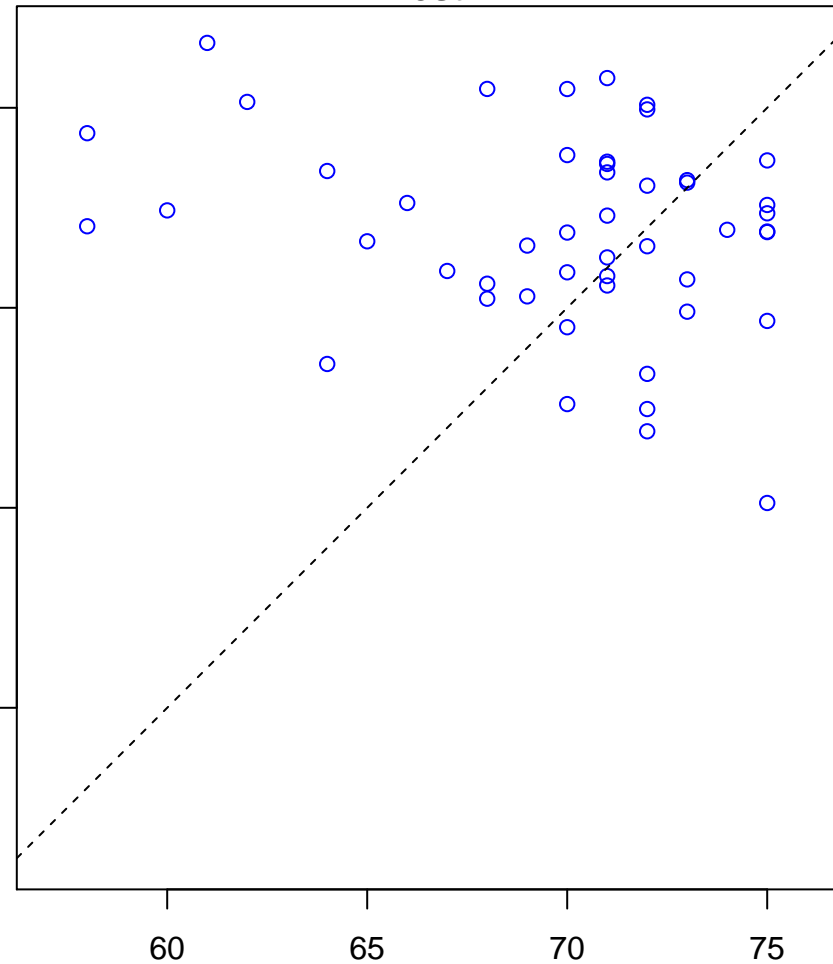


phosphatidylcholine metabolic process (Score: 2.851289)

Control

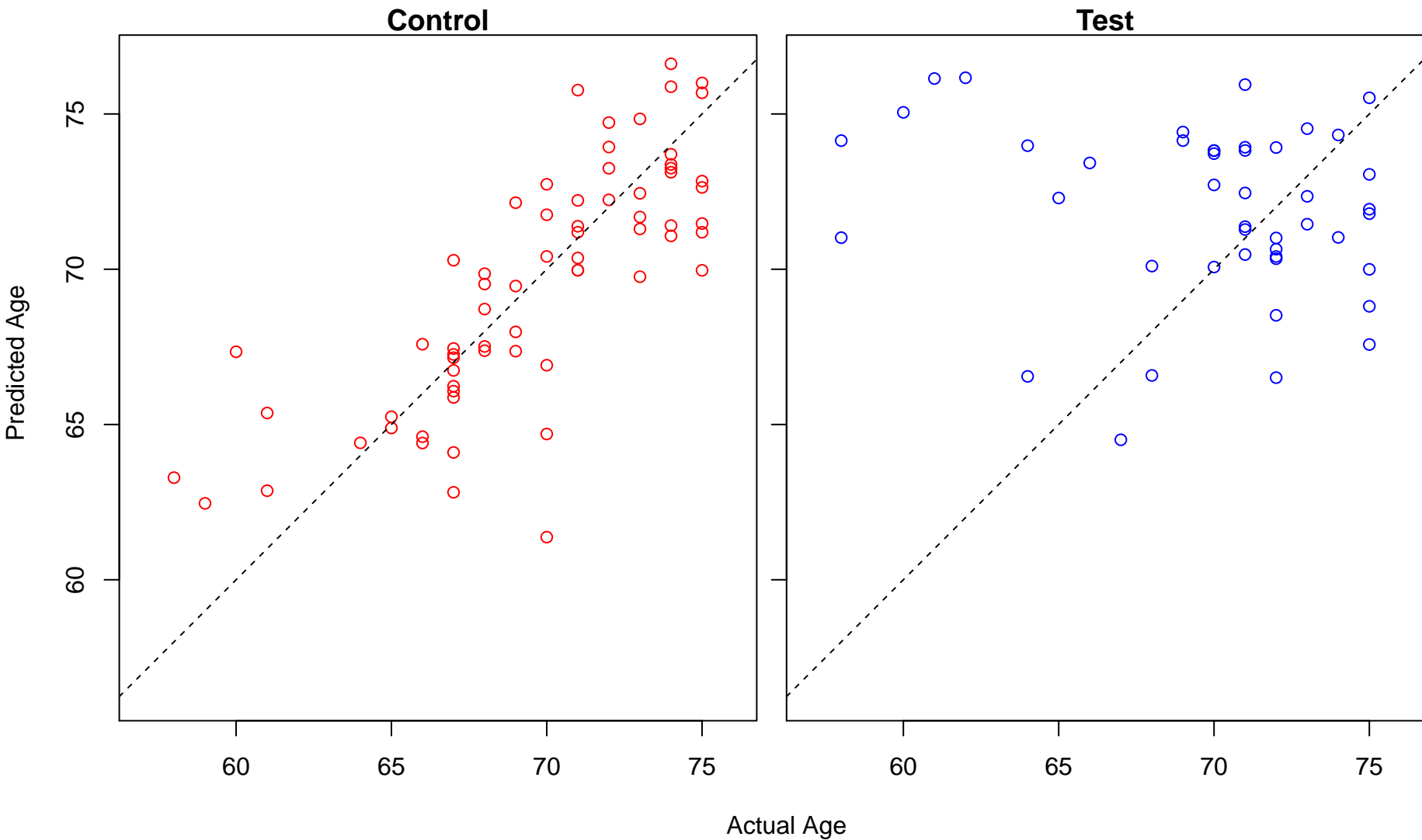


Test

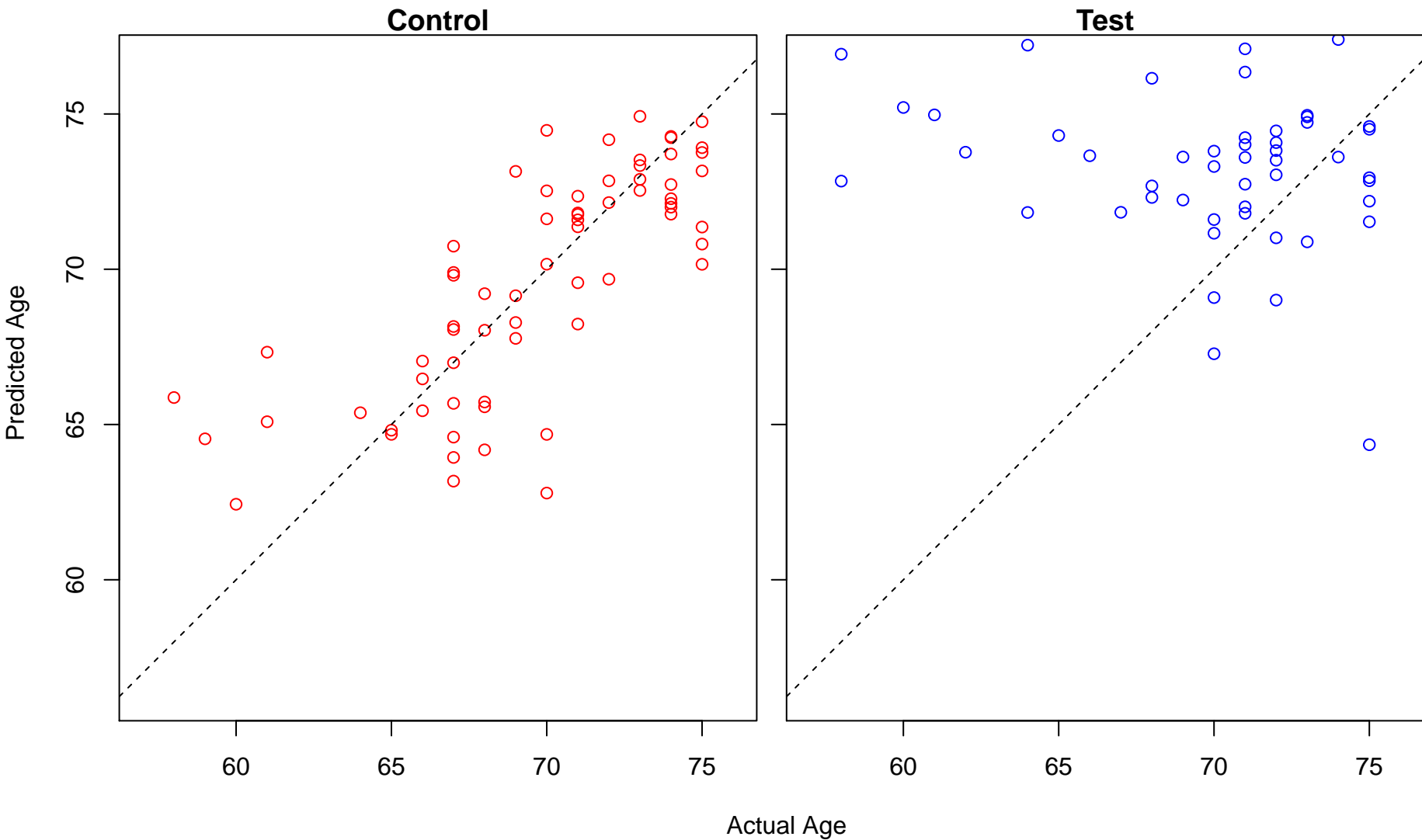


Actual Age

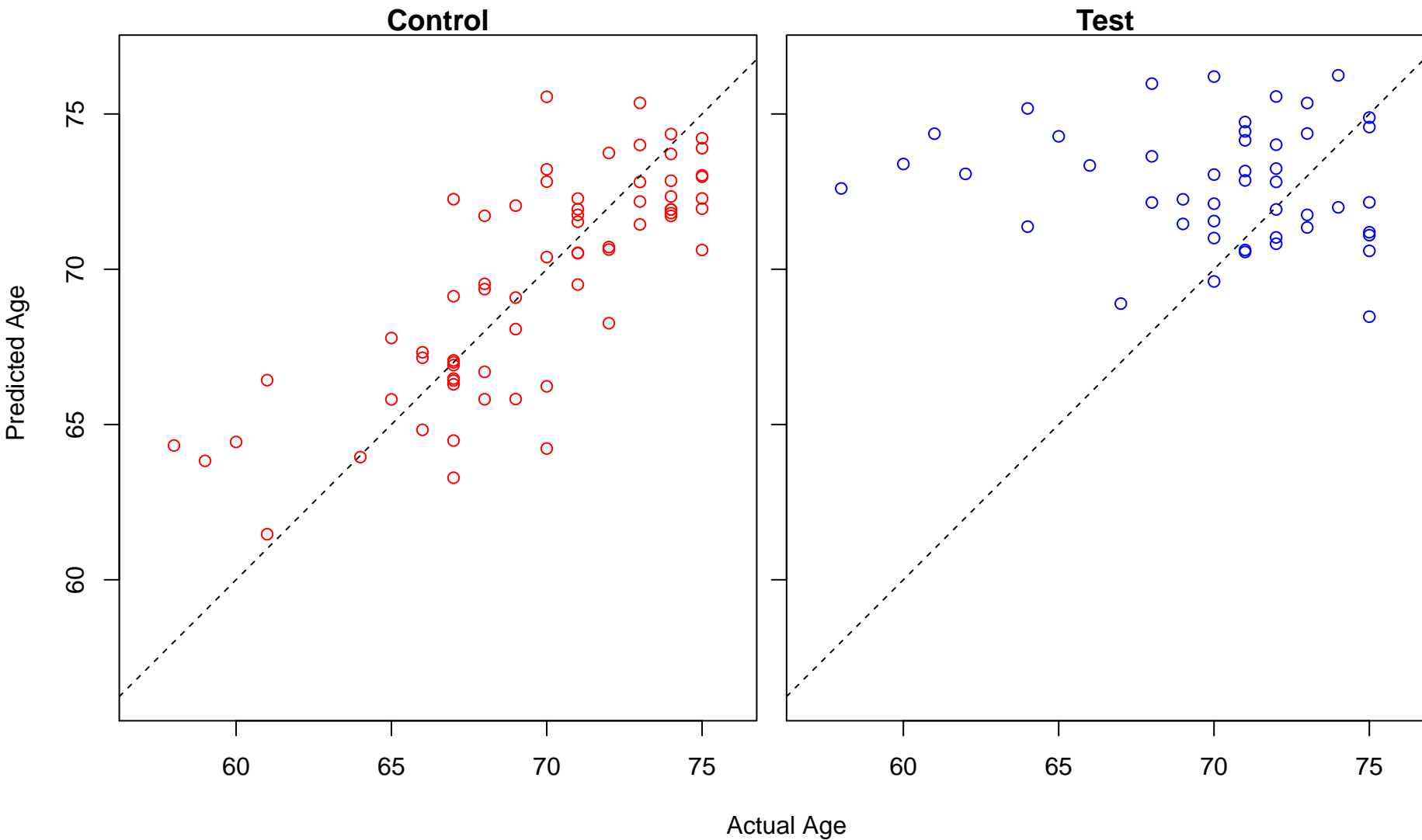
transcription elongation from RNA polymerase II promoter (Score: 2.728676)



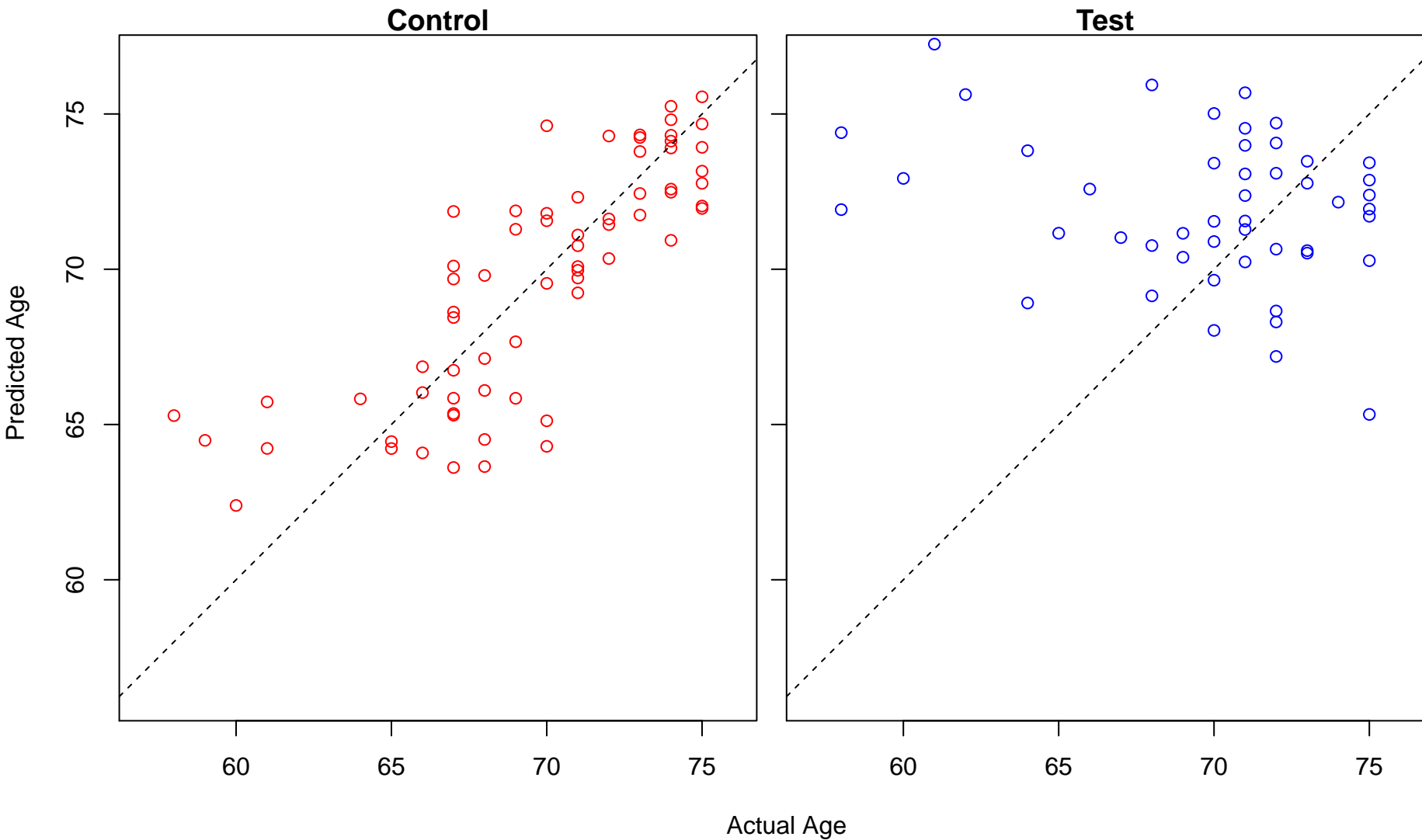
ammonium ion metabolic process (Score: 2.649021)



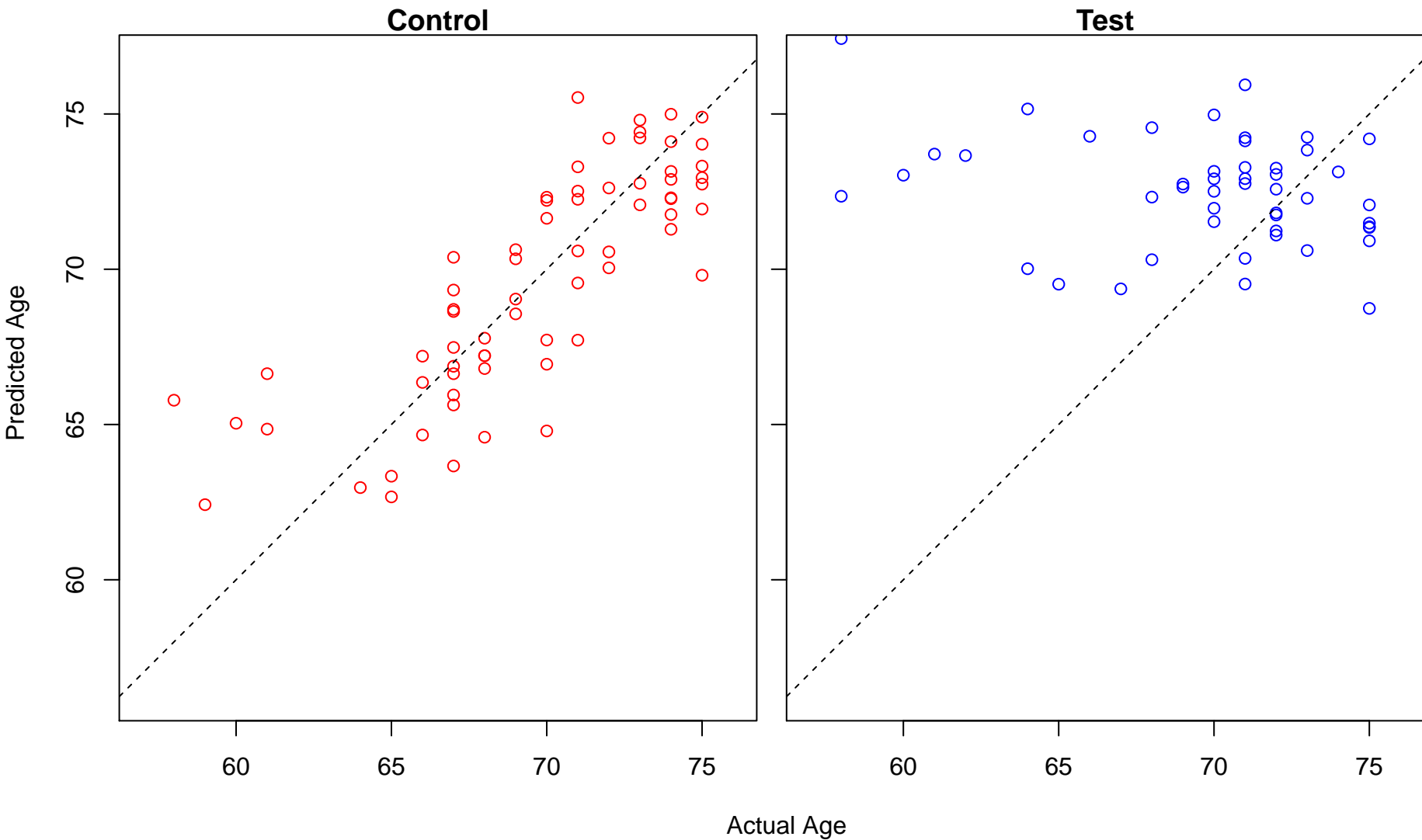
double-strand break repair via nonhomologous end joining (Score: 2.646962)



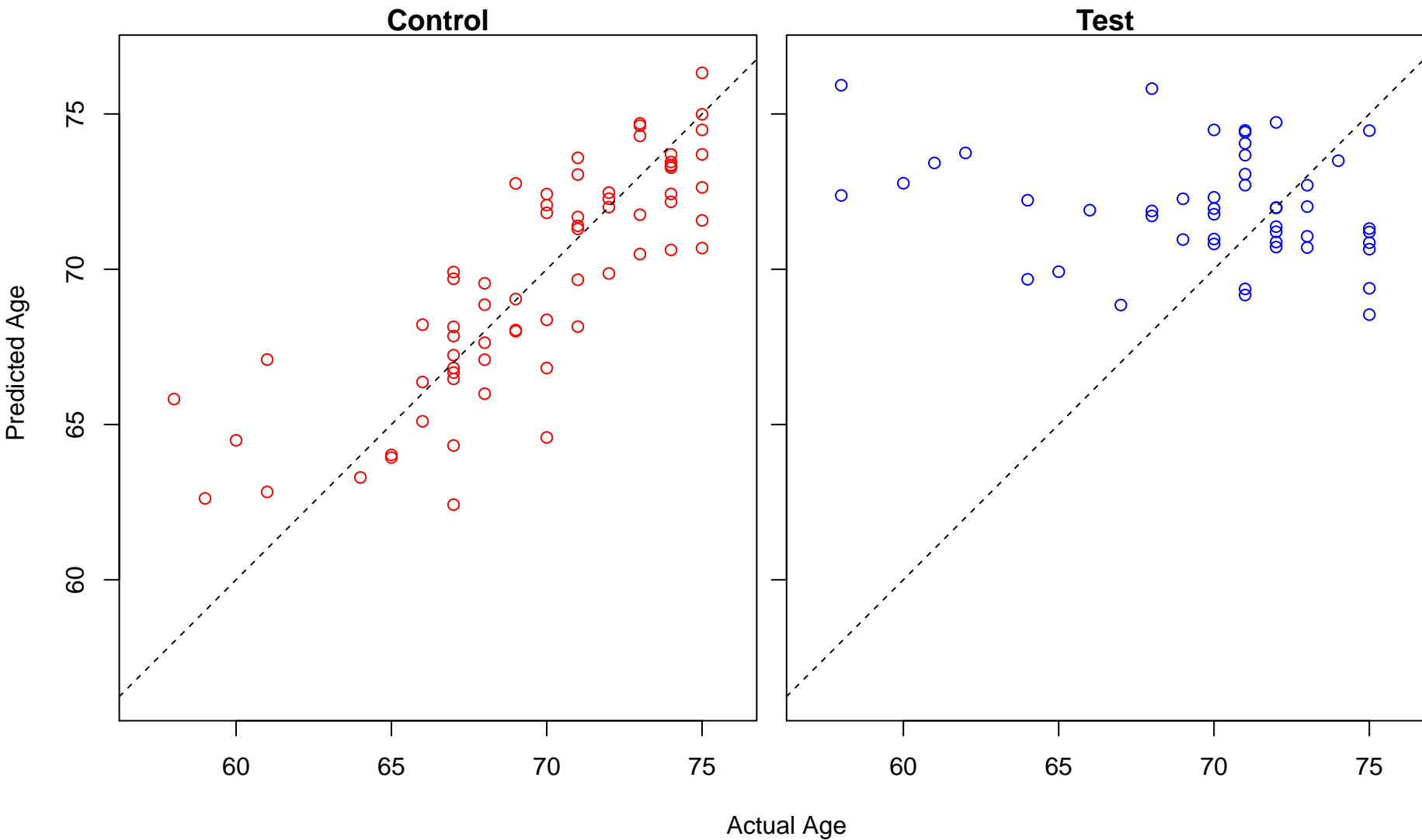
ethanolamine-containing compound metabolic process (Score: 2.621627)



positive regulation of apoptotic signaling pathway (Score: 2.601258)

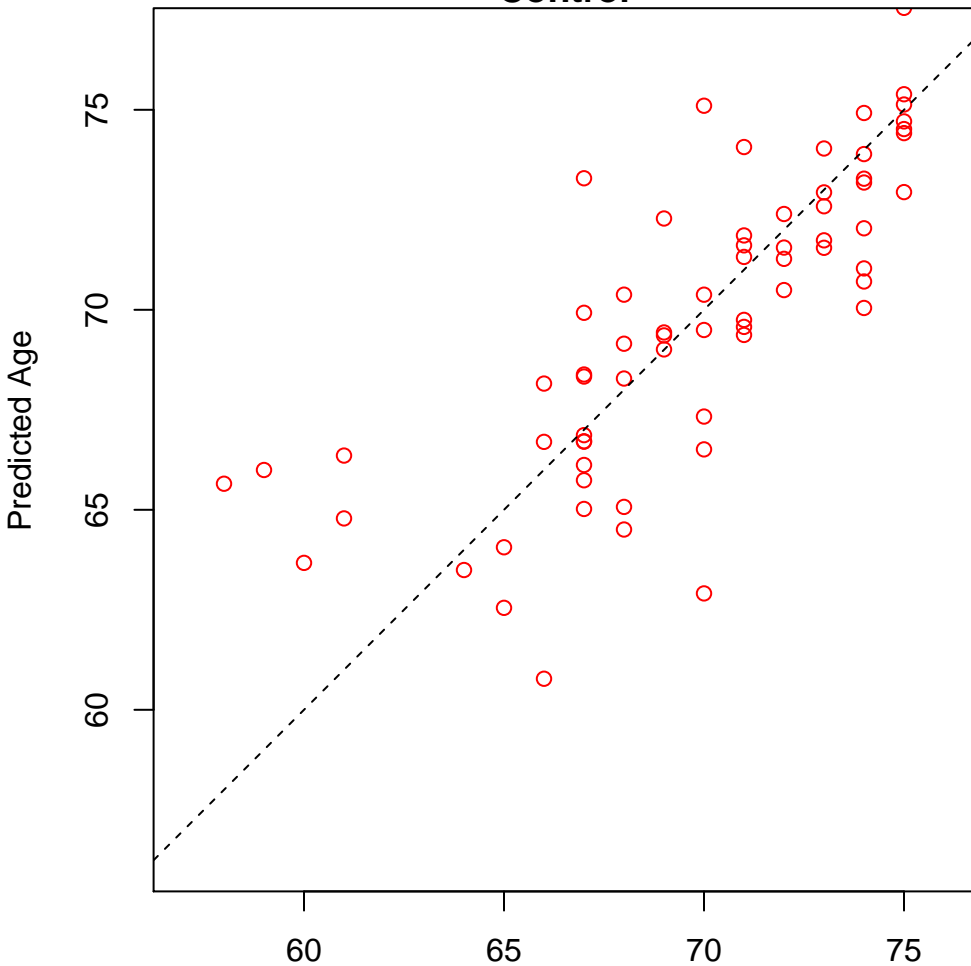


regulation of apoptotic signaling pathway (Score: 2.594848)

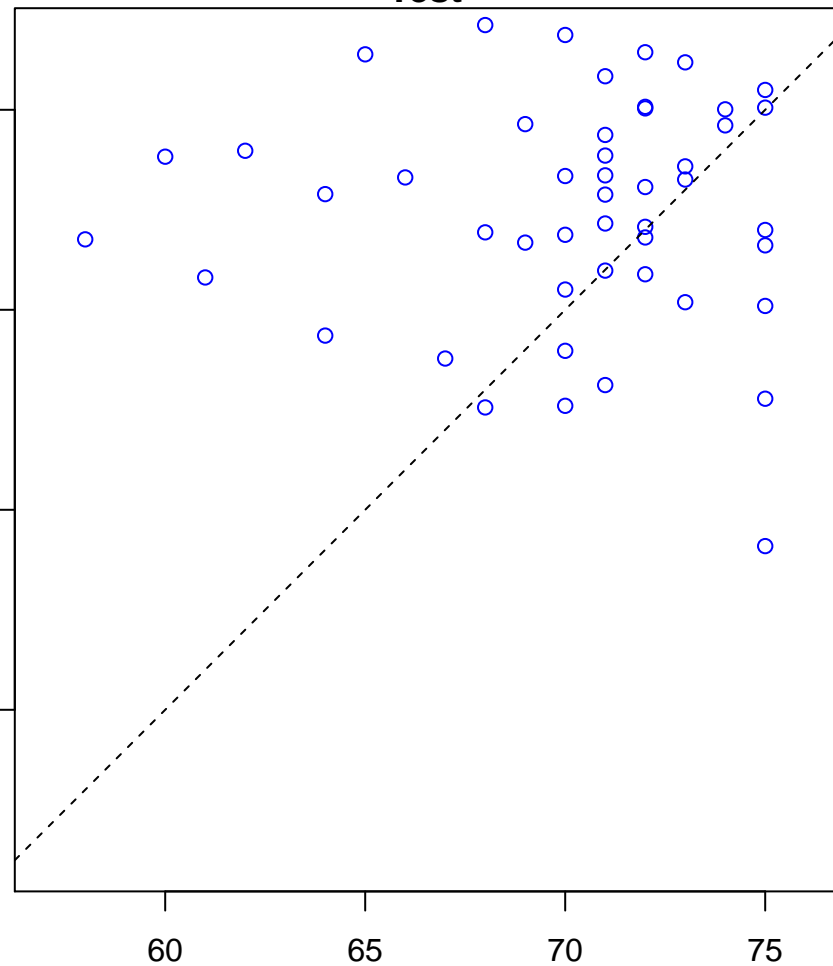


regulation of myeloid cell differentiation (Score: 2.586323)

Control

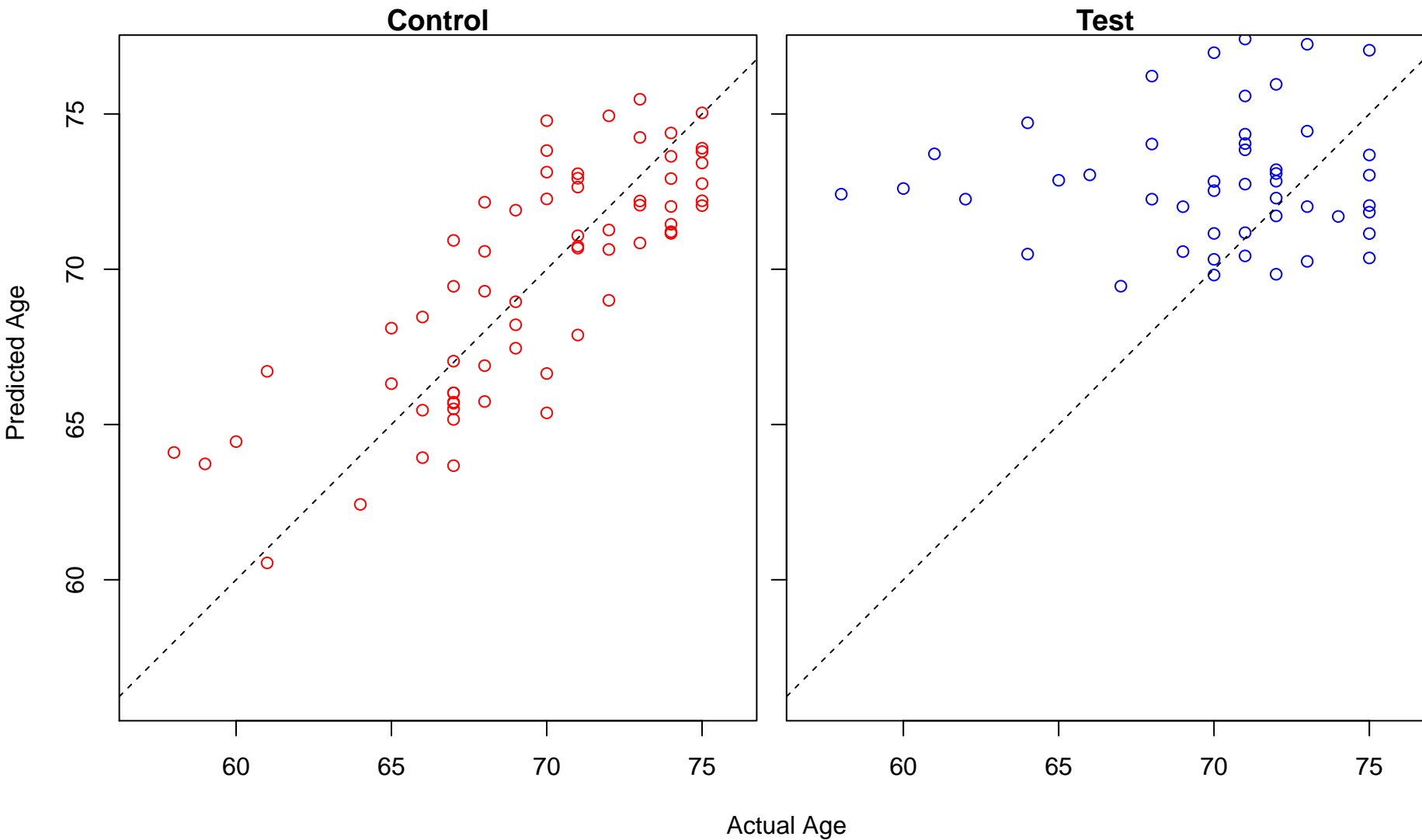


Test

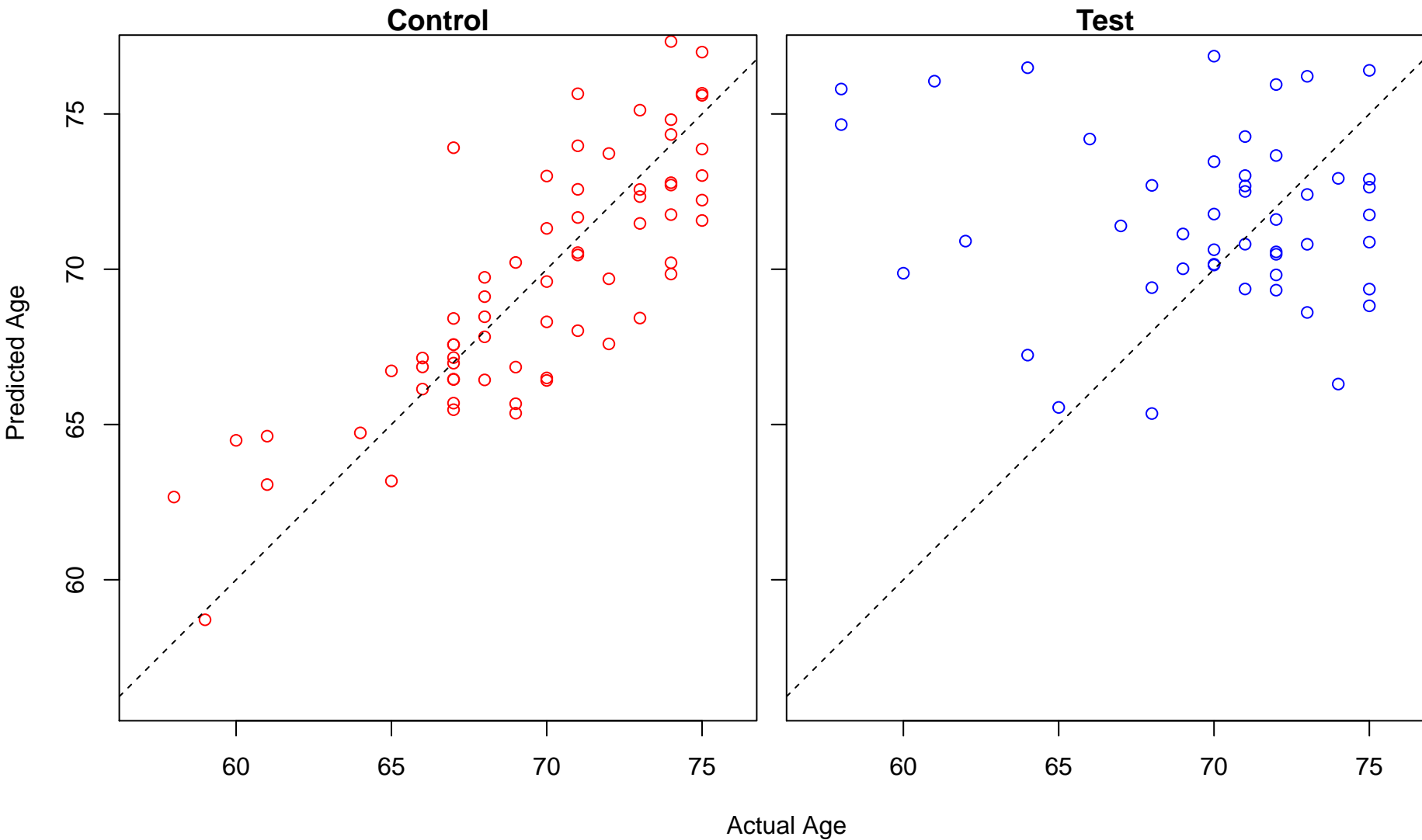


Actual Age

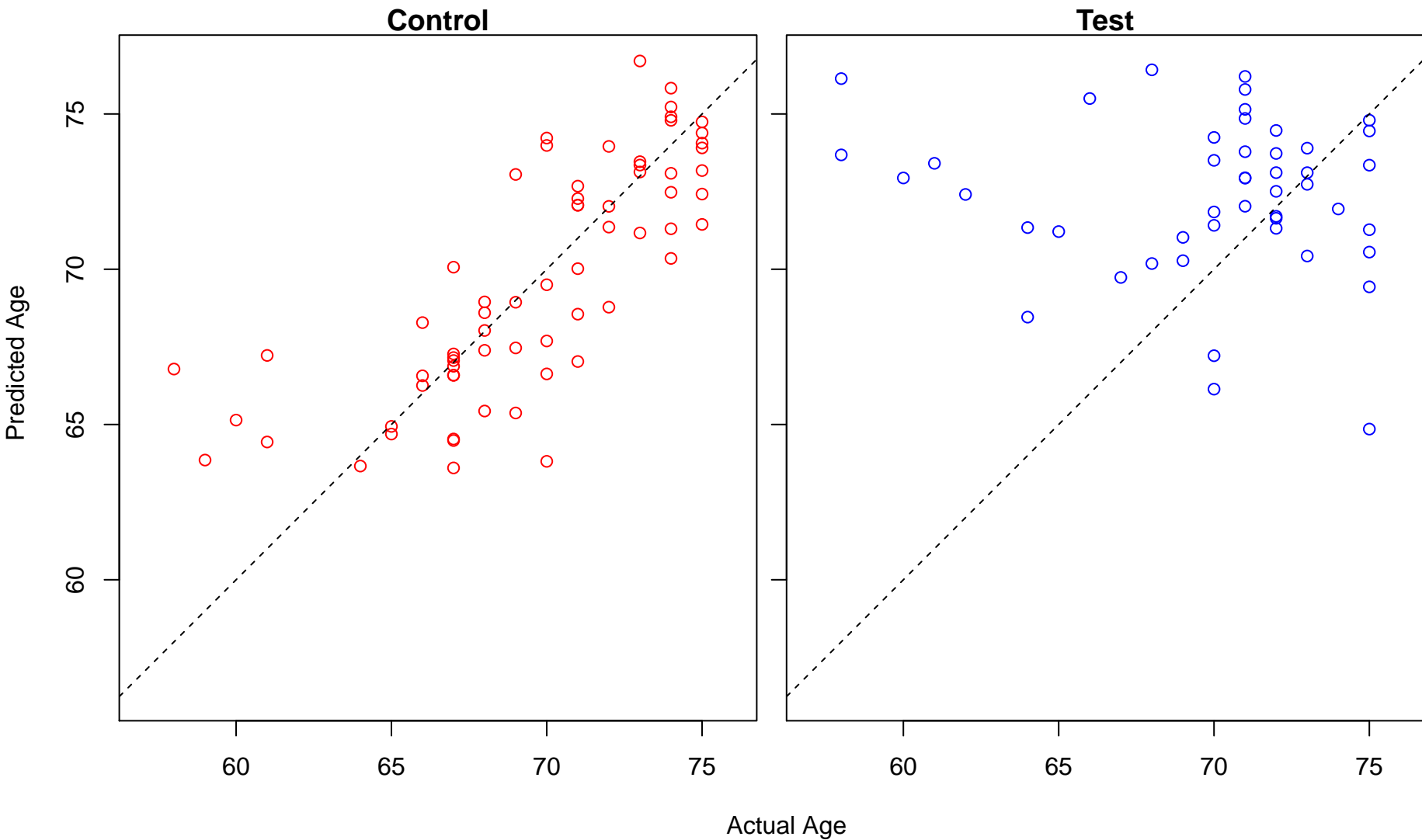
non-recombinational repair (Score: 2.561398)



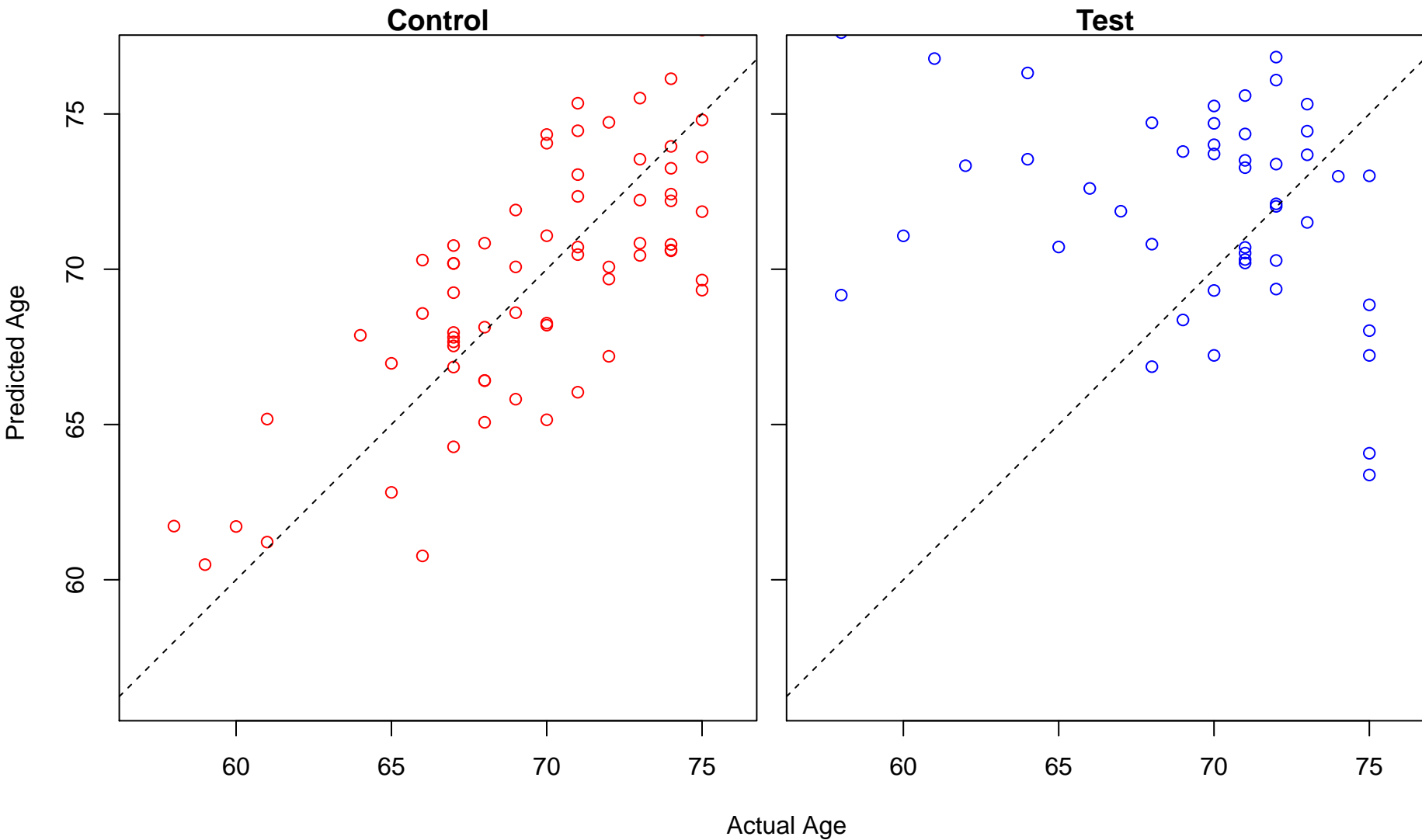
protein monoubiquitination (Score: 2.553711)



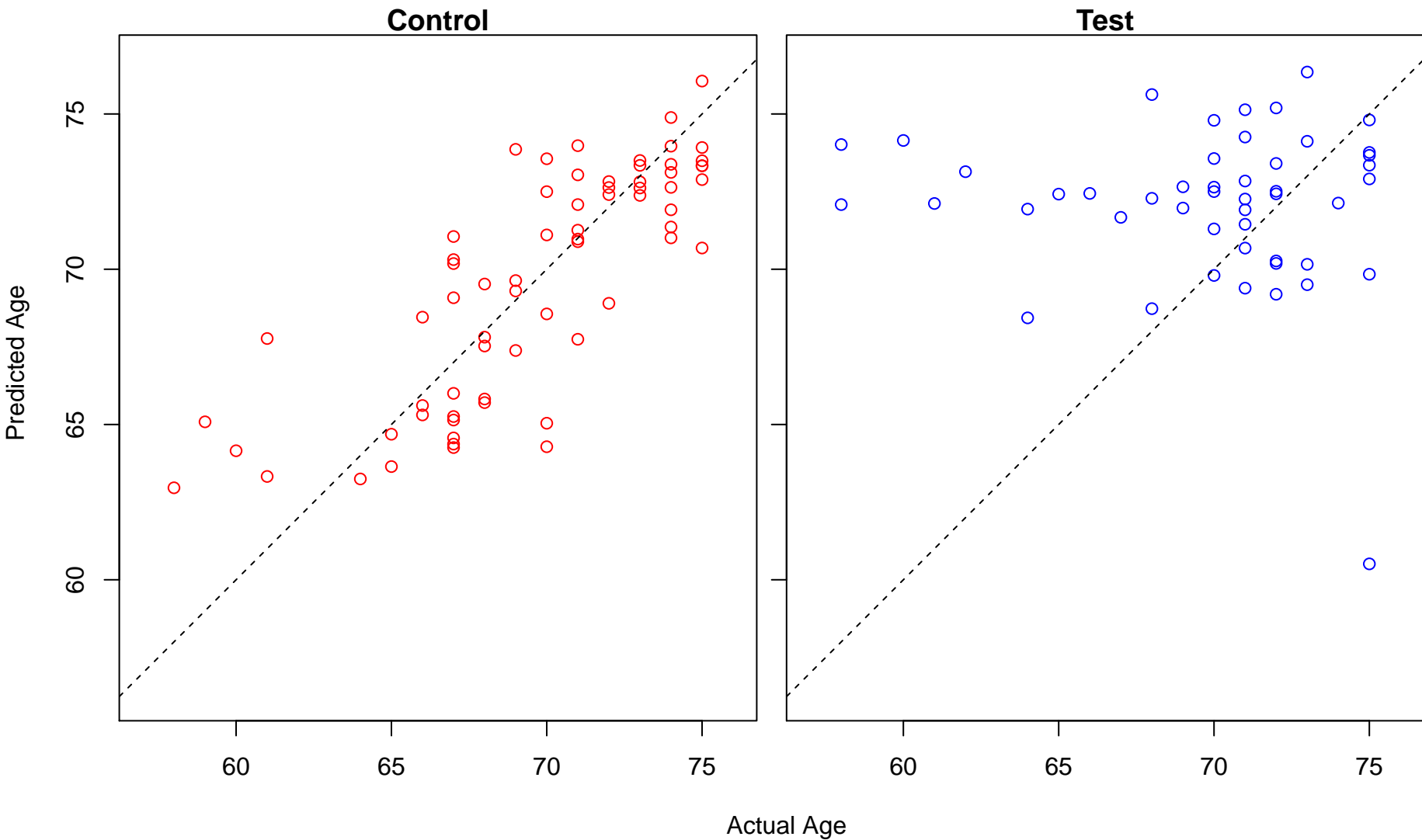
leukocyte cell-cell adhesion (Score: 2.537390)



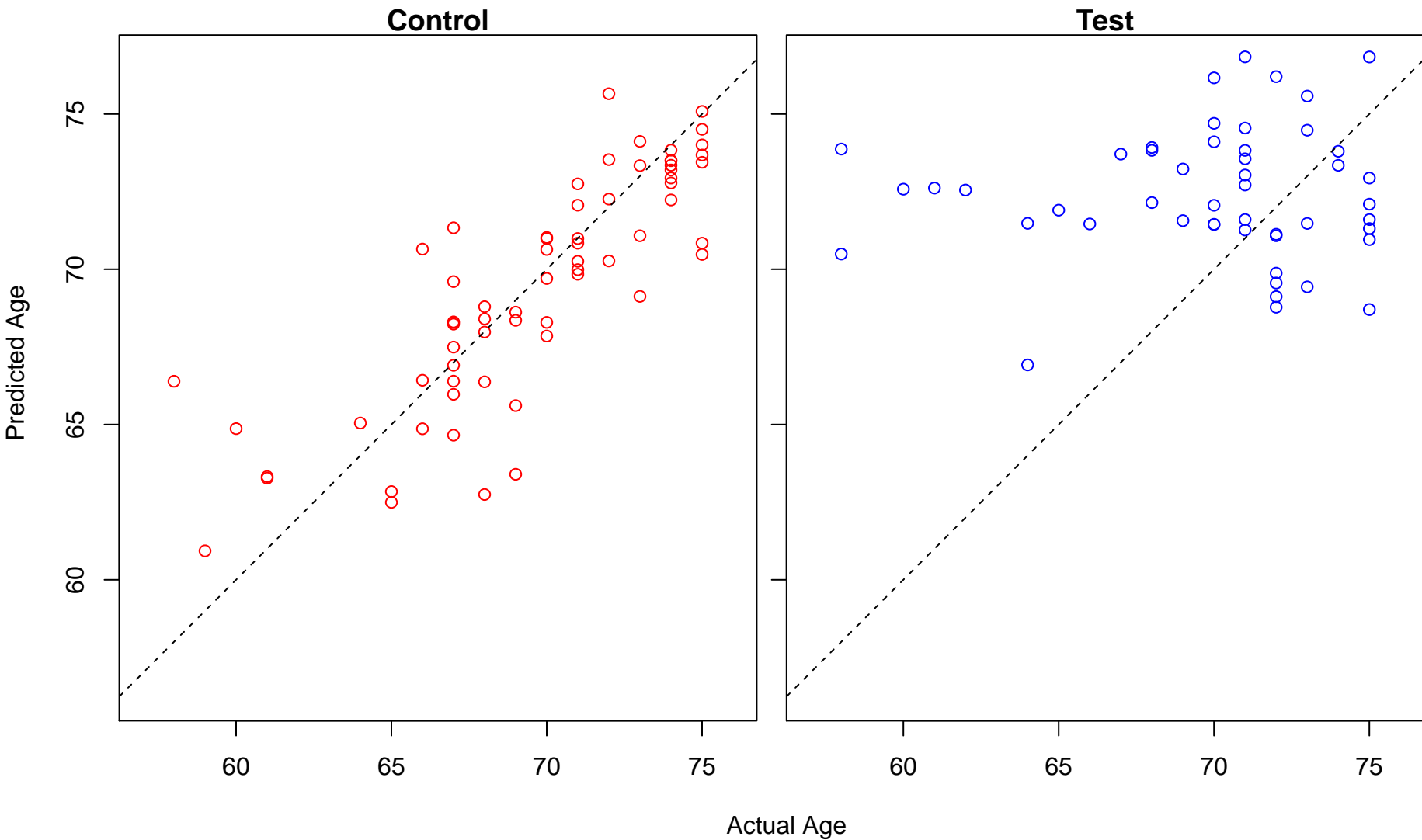
positive regulation of transporter activity (Score: 2.527508)



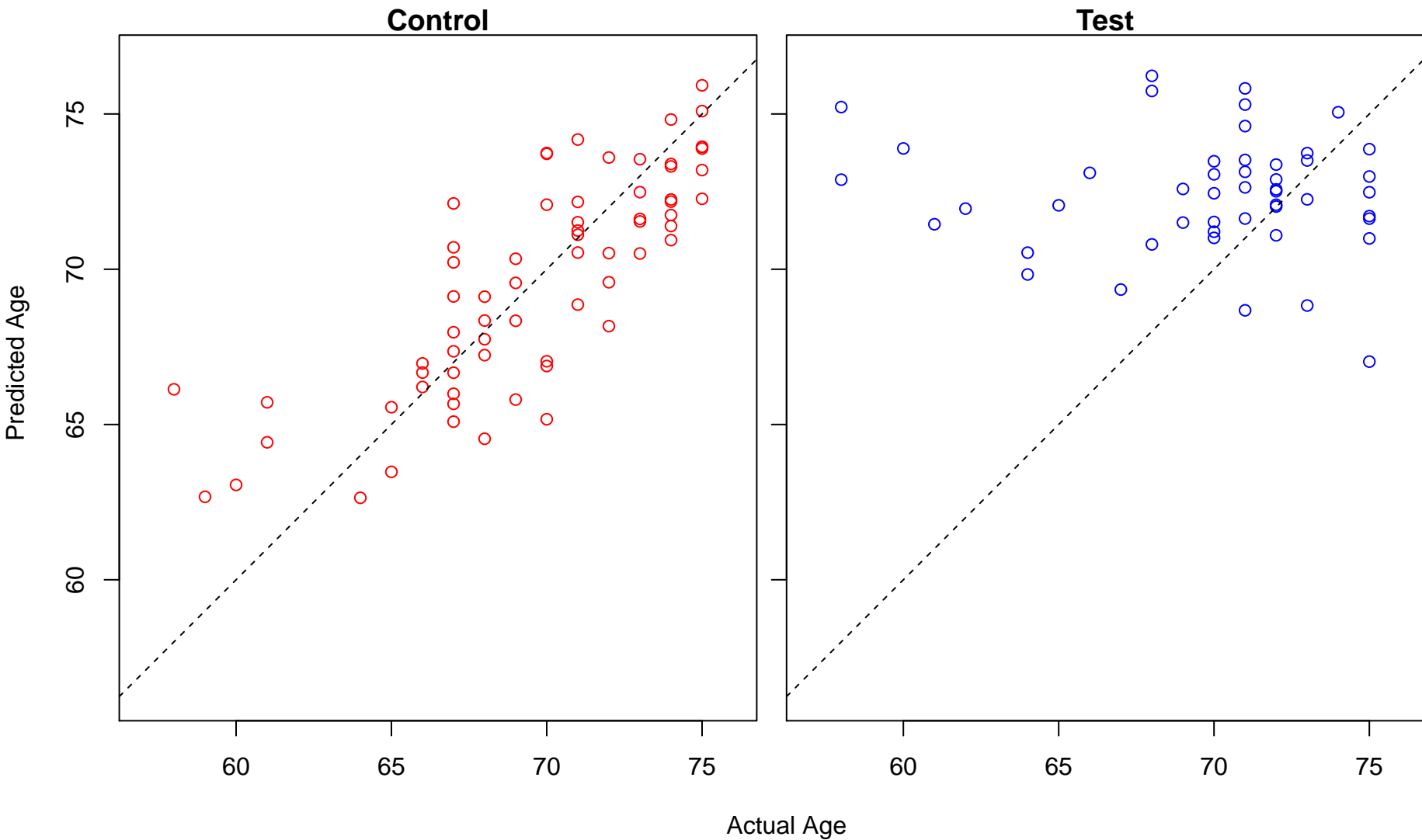
alcohol metabolic process (Score: 2.515535)



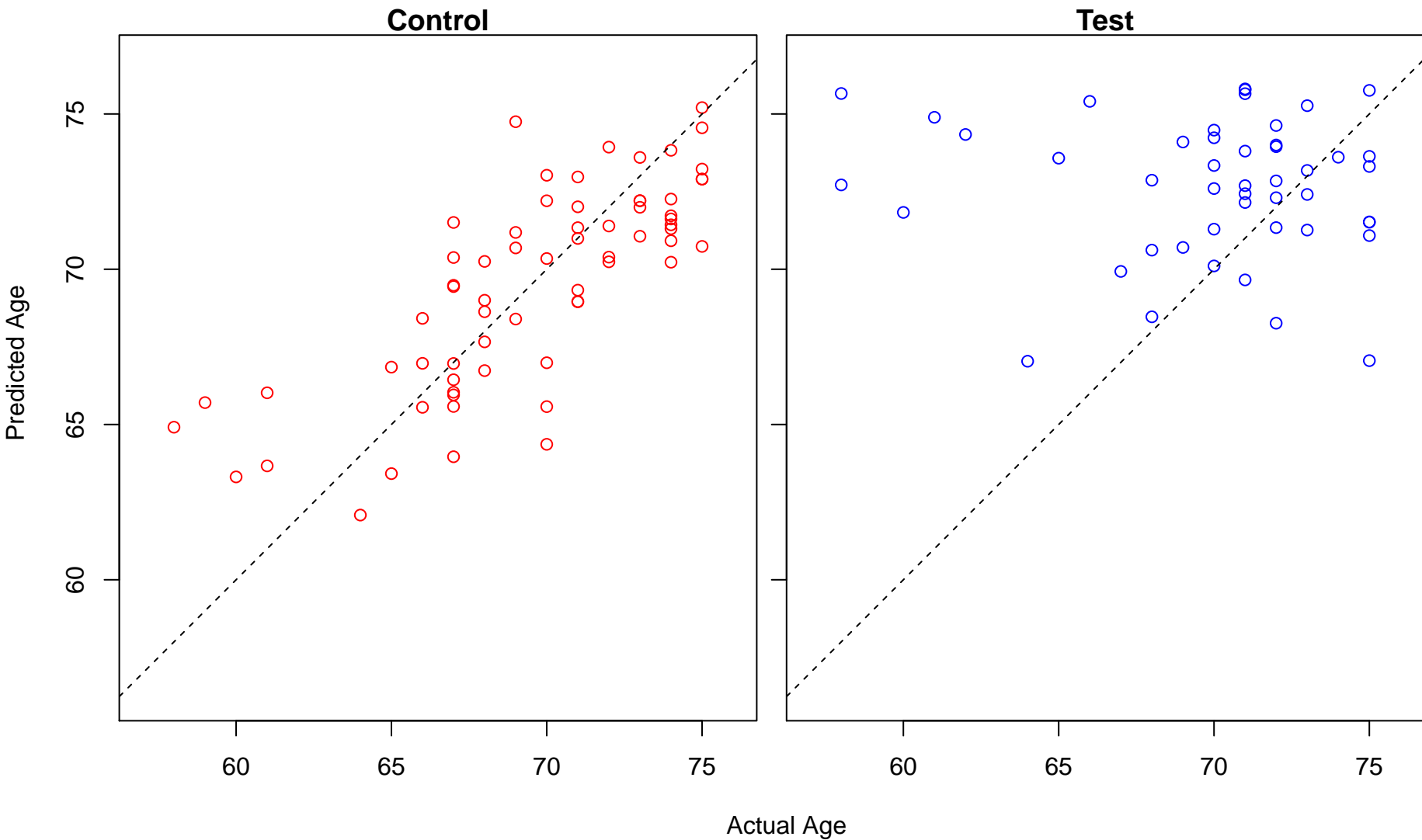
cell cycle arrest (Score: 2.483351)



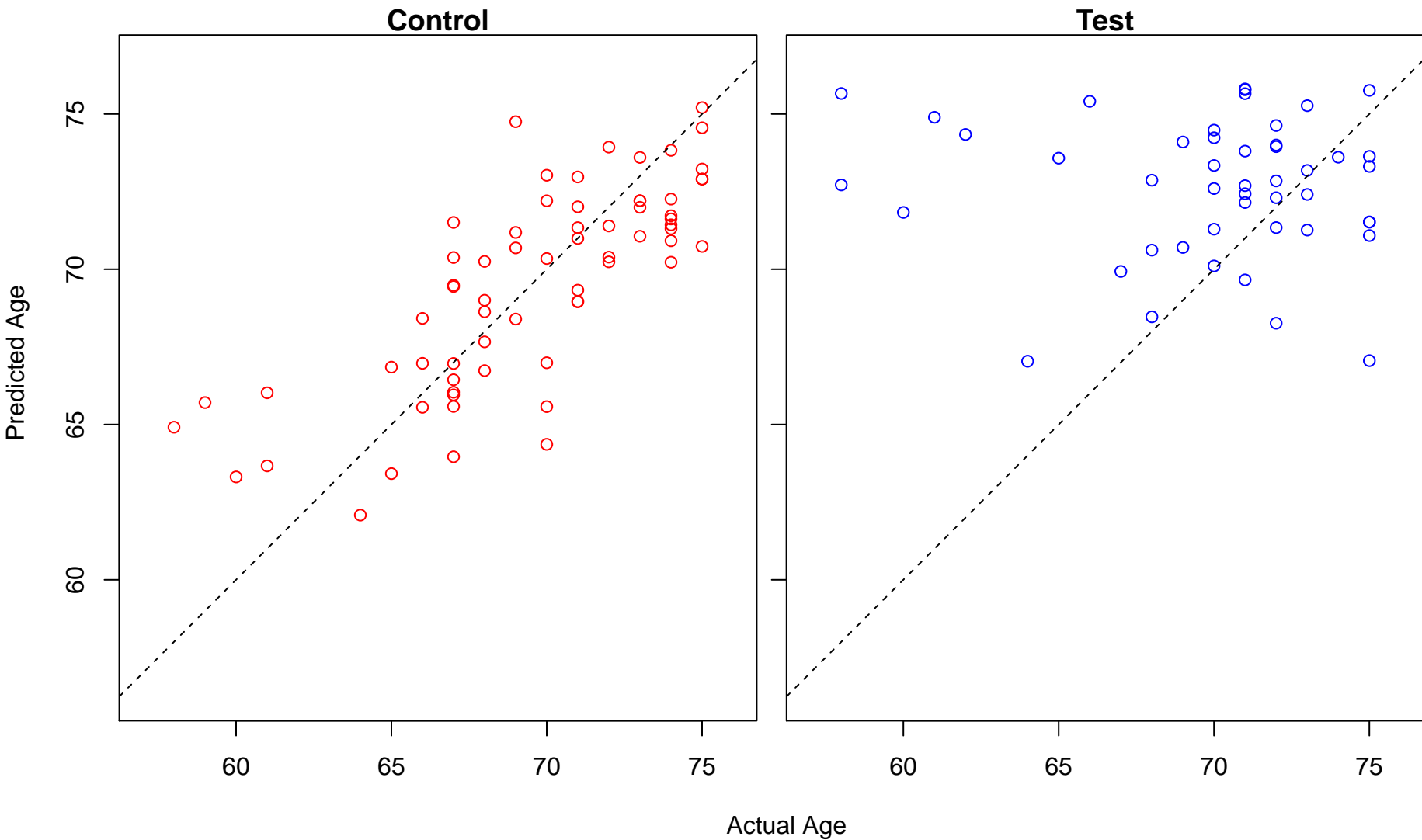
intrinsic apoptotic signaling pathway (Score: 2.477730)



stress-activated protein kinase signaling cascade (Score: 2.454550)

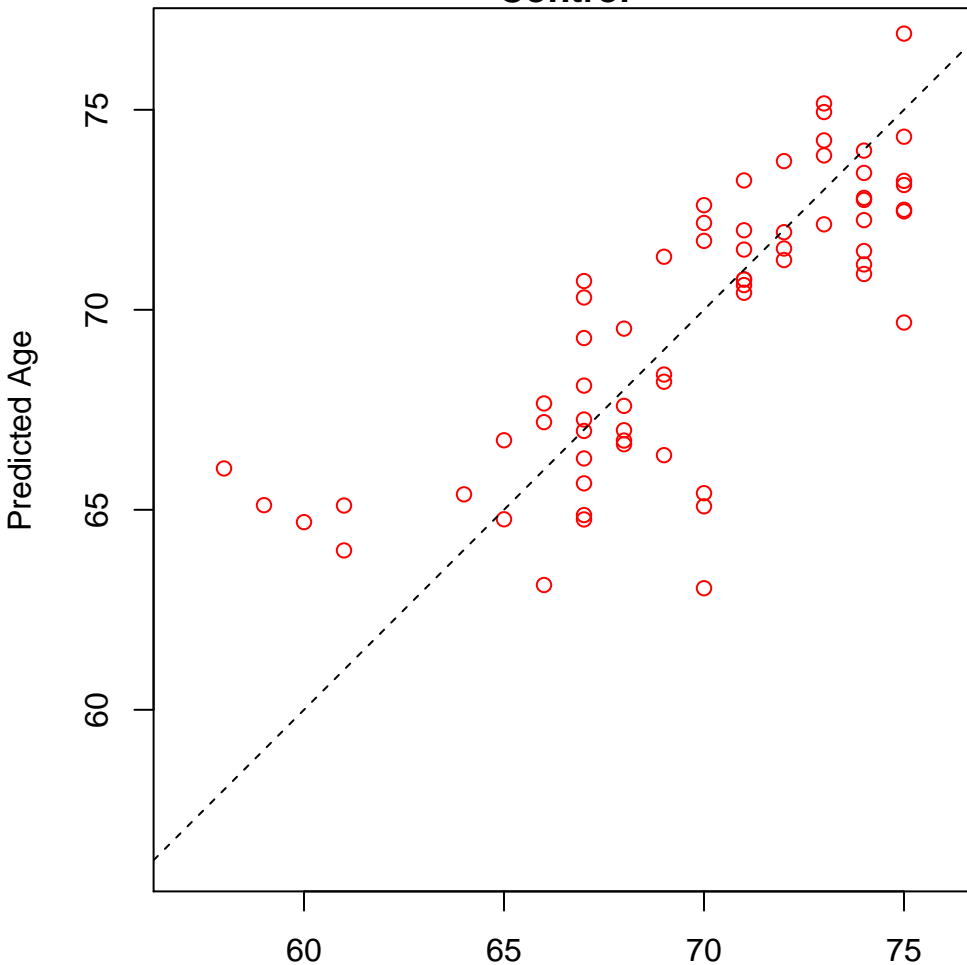


stress-activated MAPK cascade (Score: 2.454550)

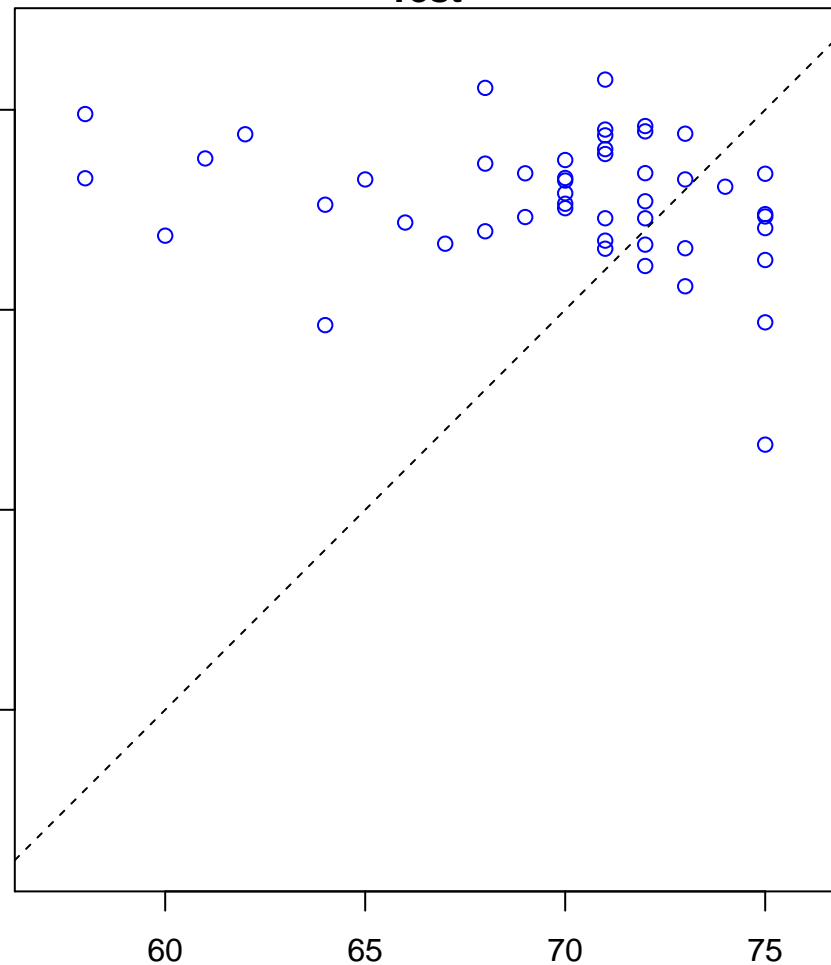


glycerophospholipid metabolic process (Score: 2.447317)

Control

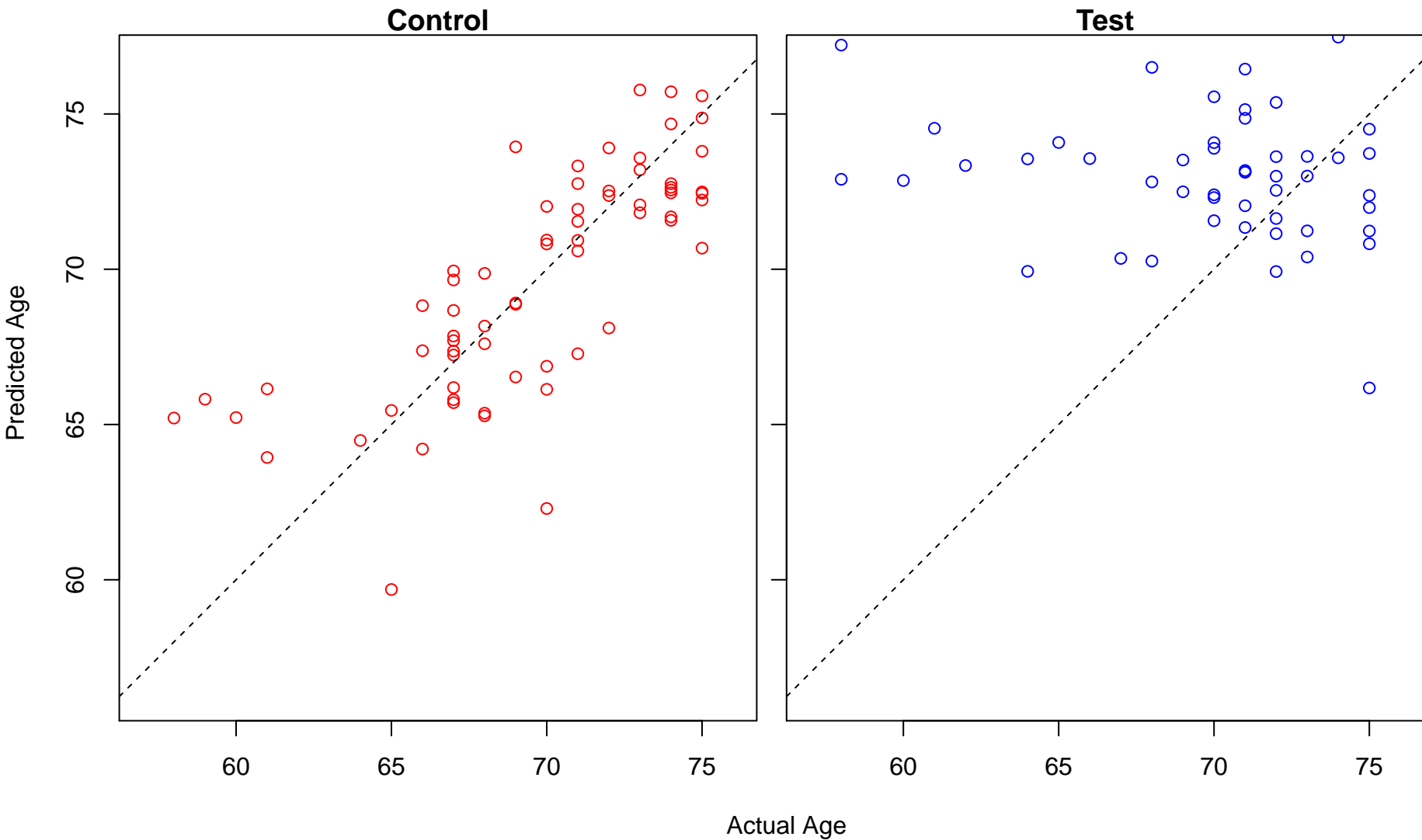


Test

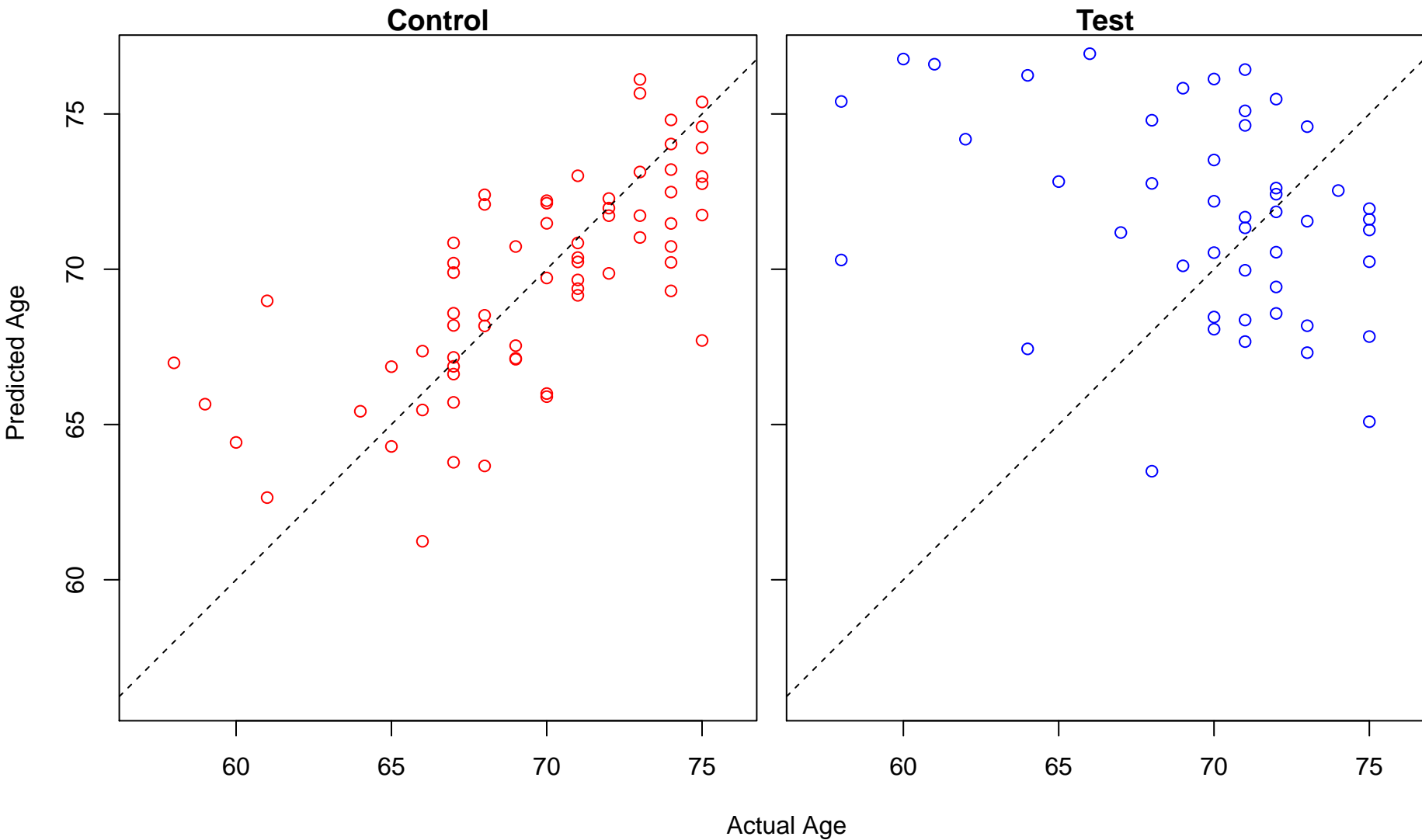


Actual Age

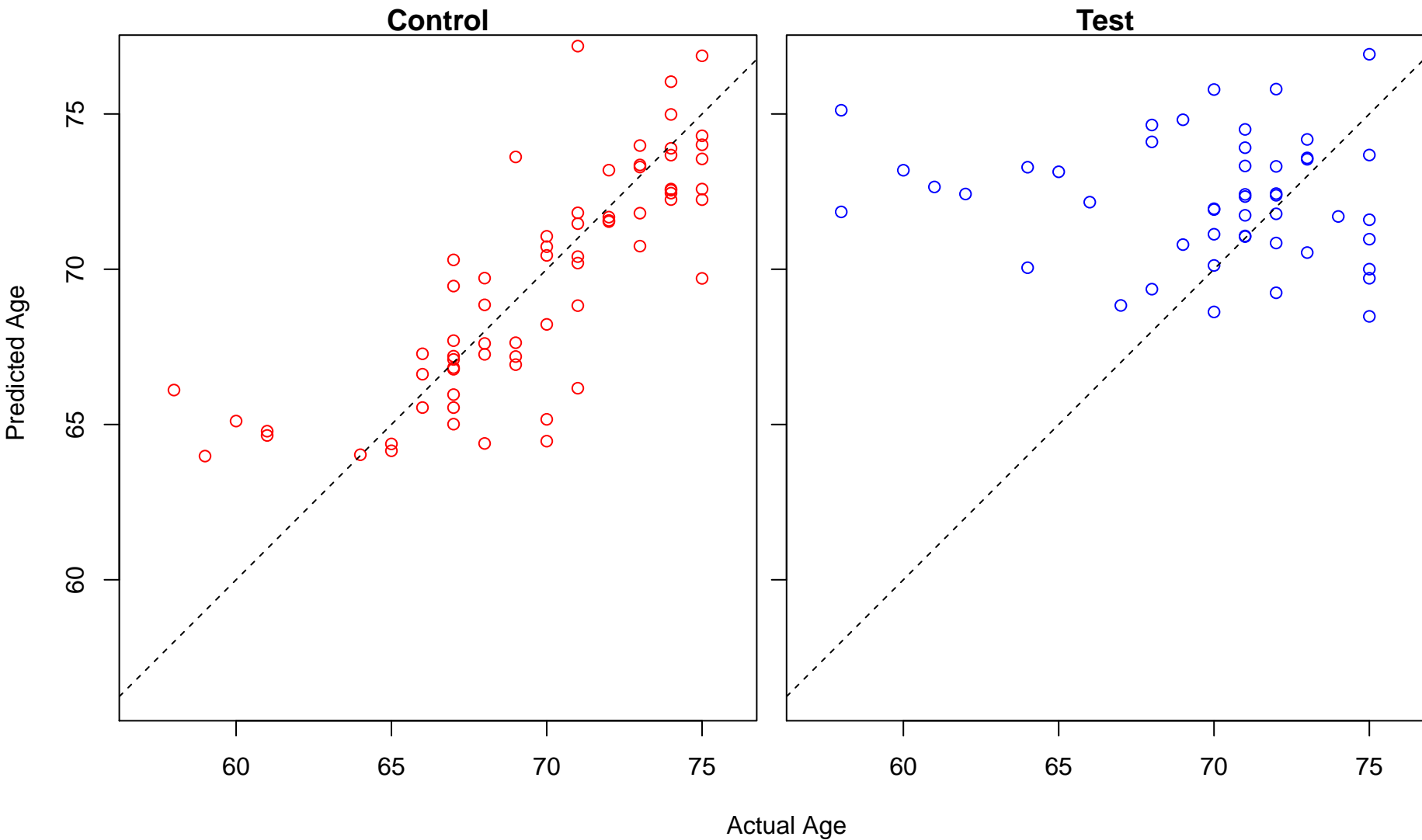
regulation of leukocyte differentiation (Score: 2.438654)



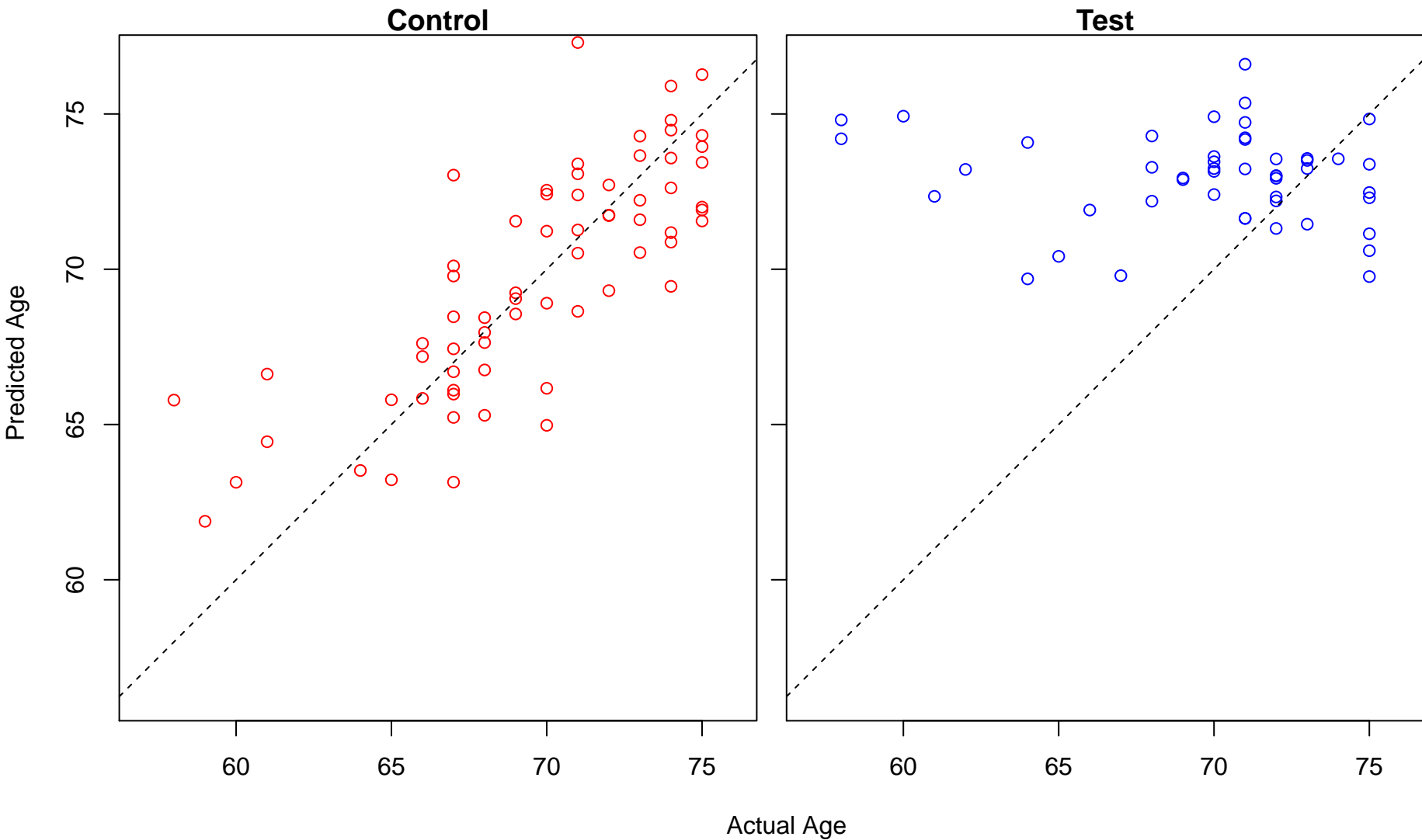
phosphatidylserine acyl-chain remodeling (Score: 2.420388)



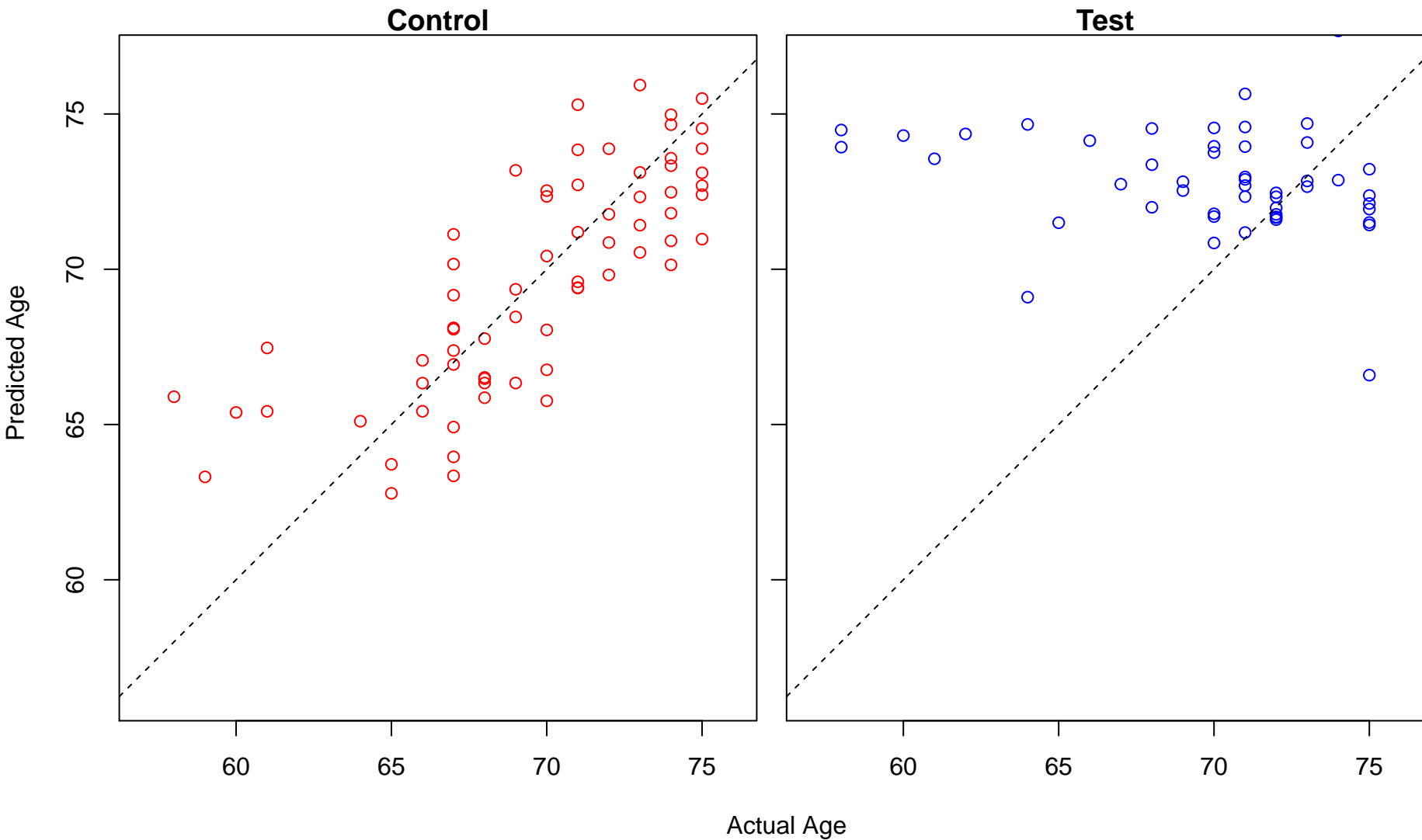
negative regulation of cell proliferation (Score: 2.419677)



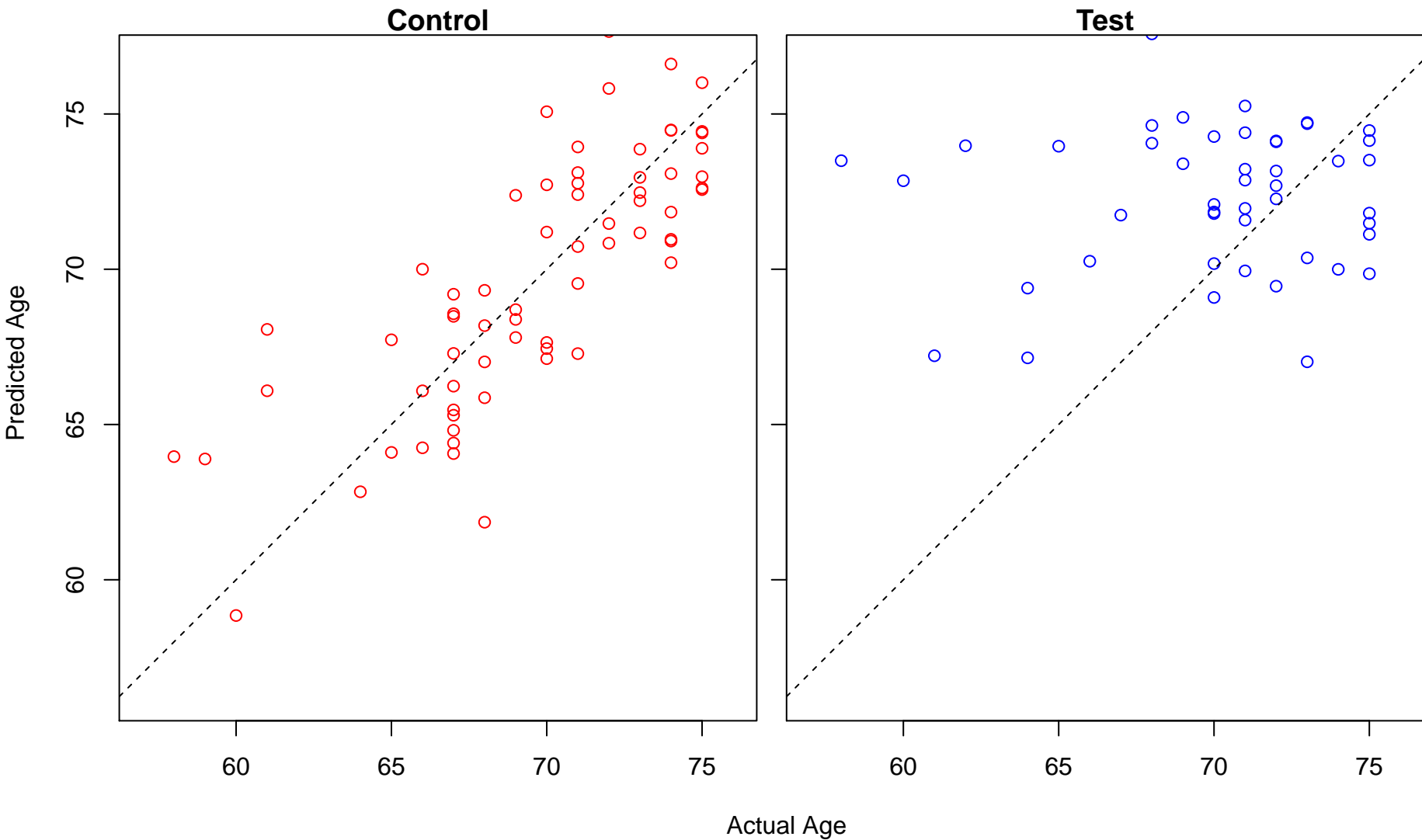
positive regulation of mitochondrion organization (Score: 2.380345)



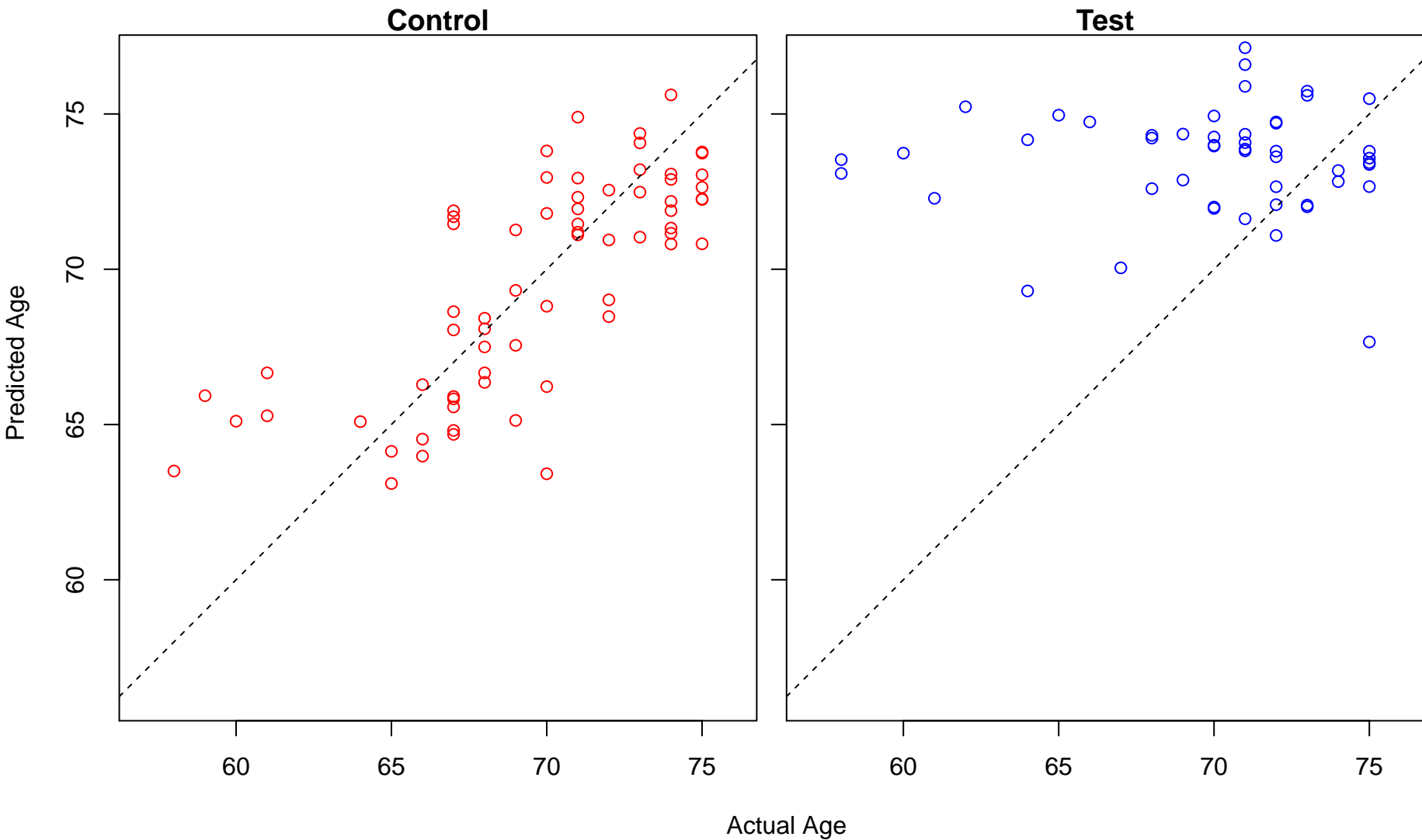
regulation of intrinsic apoptotic signaling pathway (Score: 2.368510)



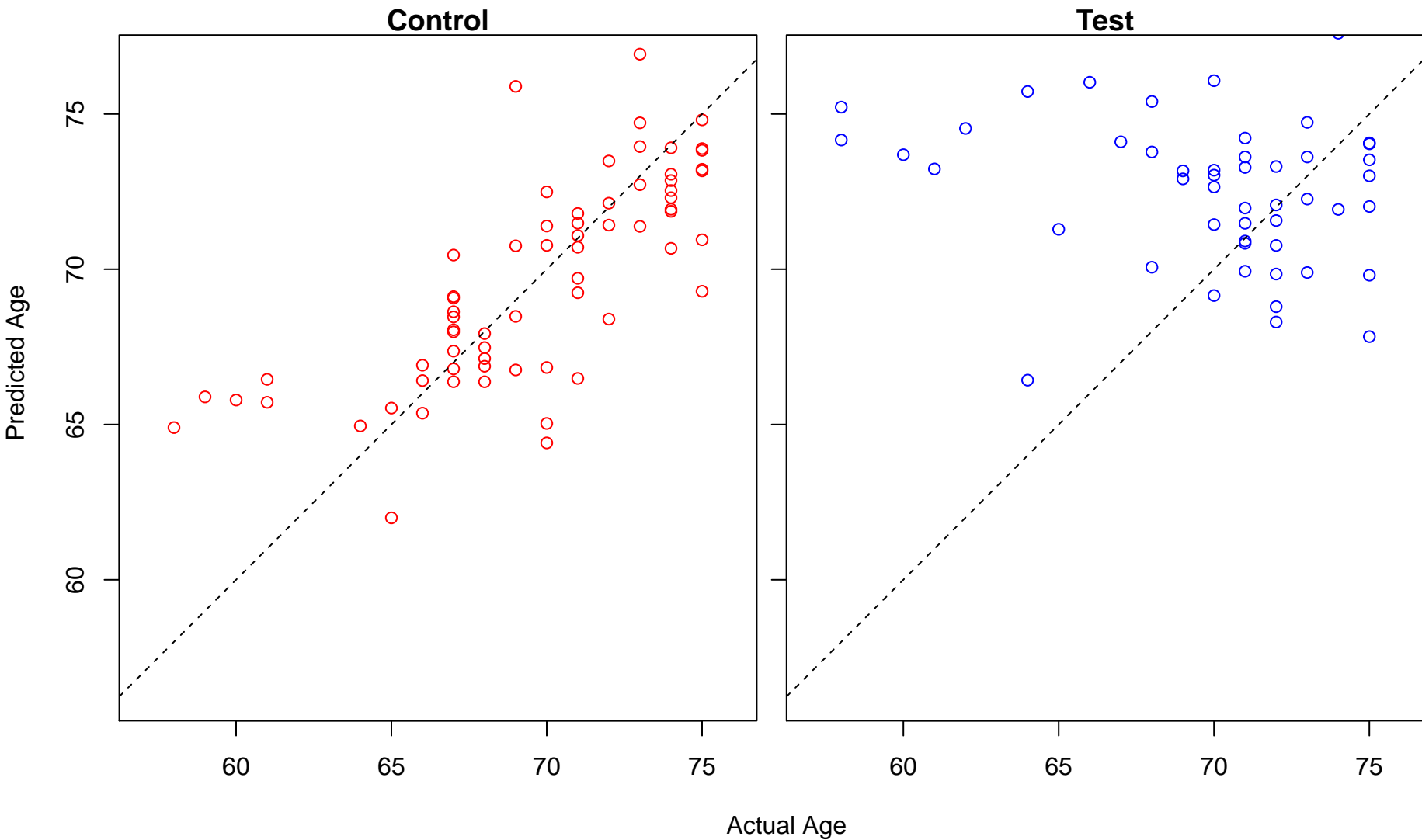
nuclear import (Score: 2.352674)



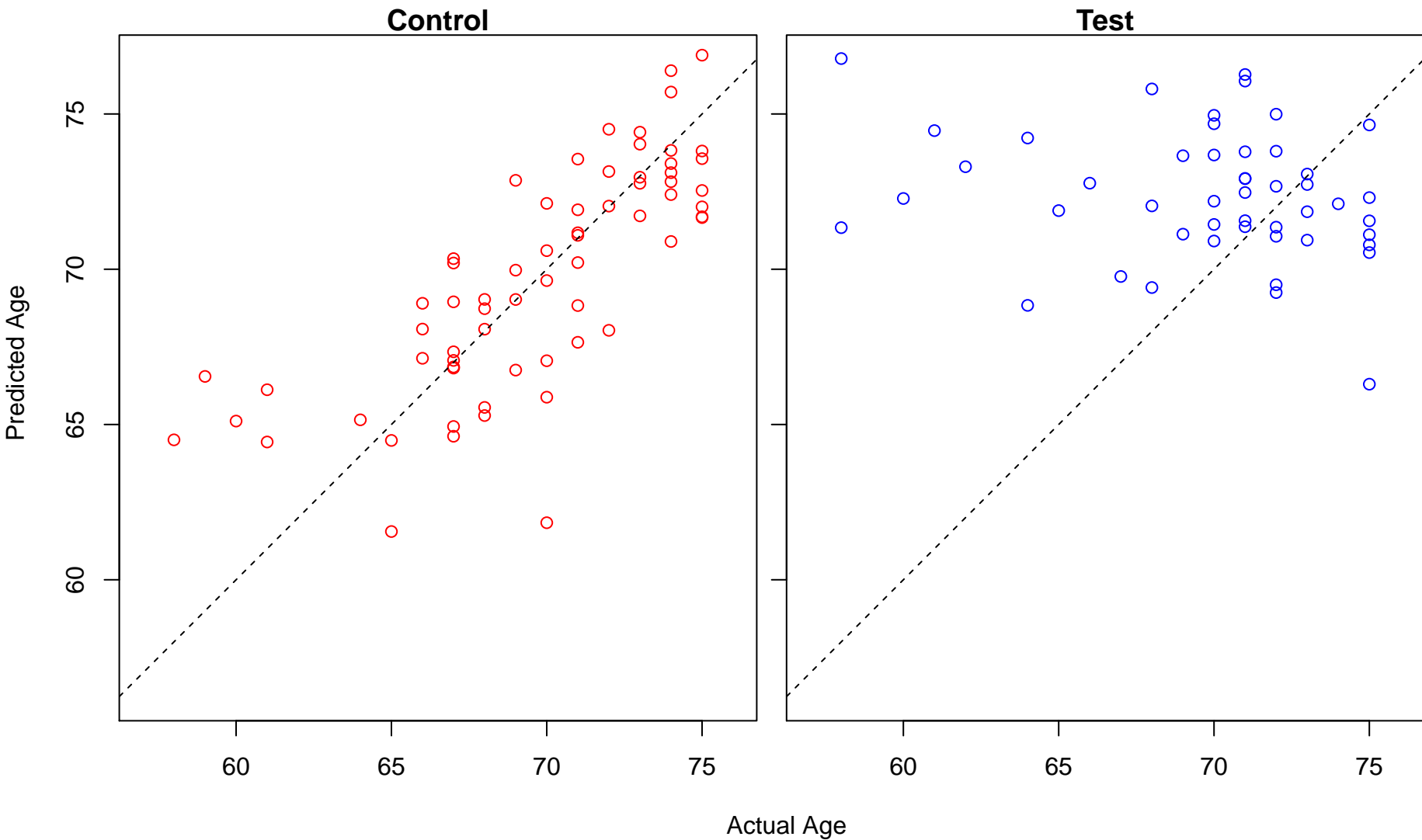
protein acetylation (Score: 2.320174)



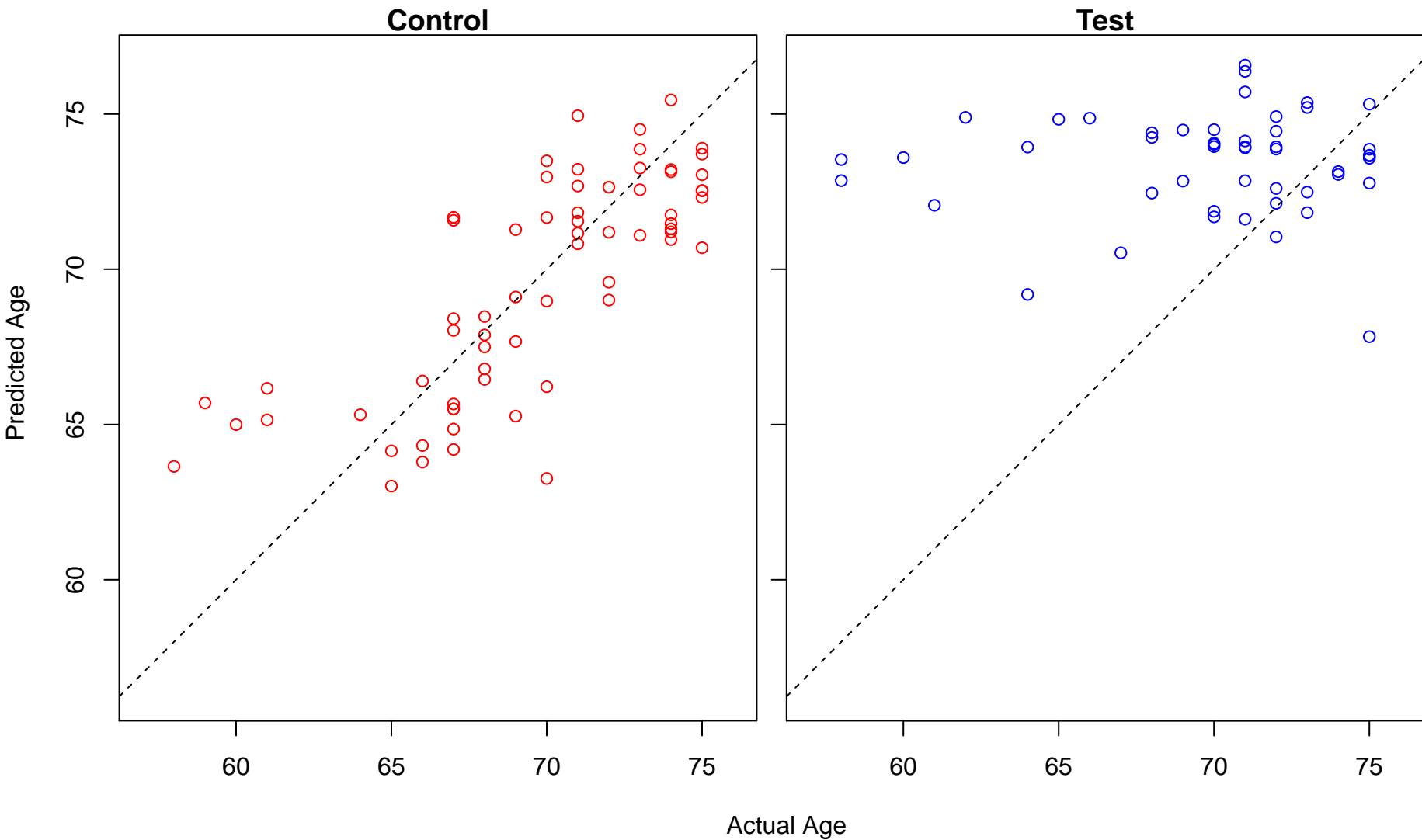
leukocyte migration involved in inflammatory response (Score: 2.309936)



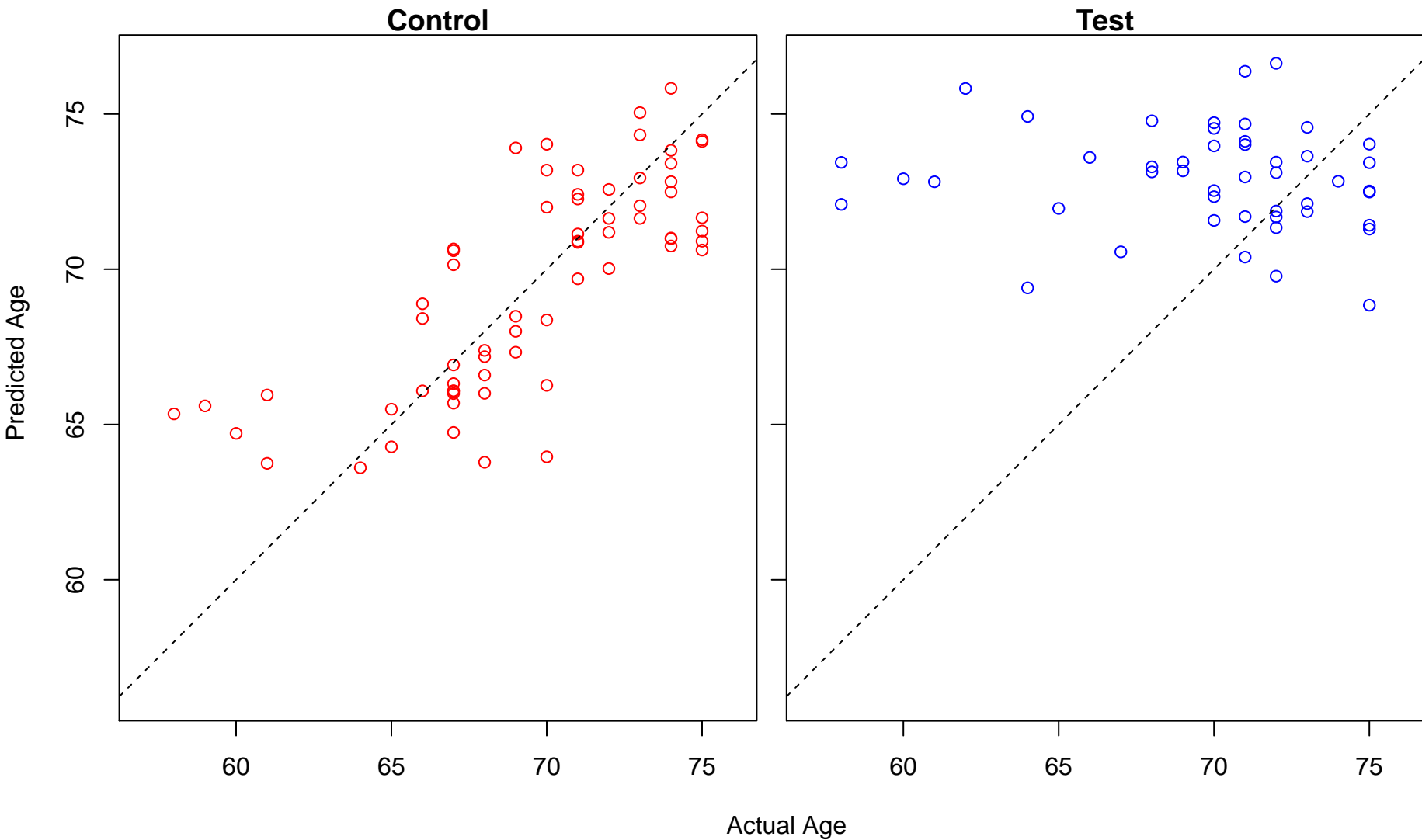
positive regulation of leukocyte differentiation (Score: 2.308740)



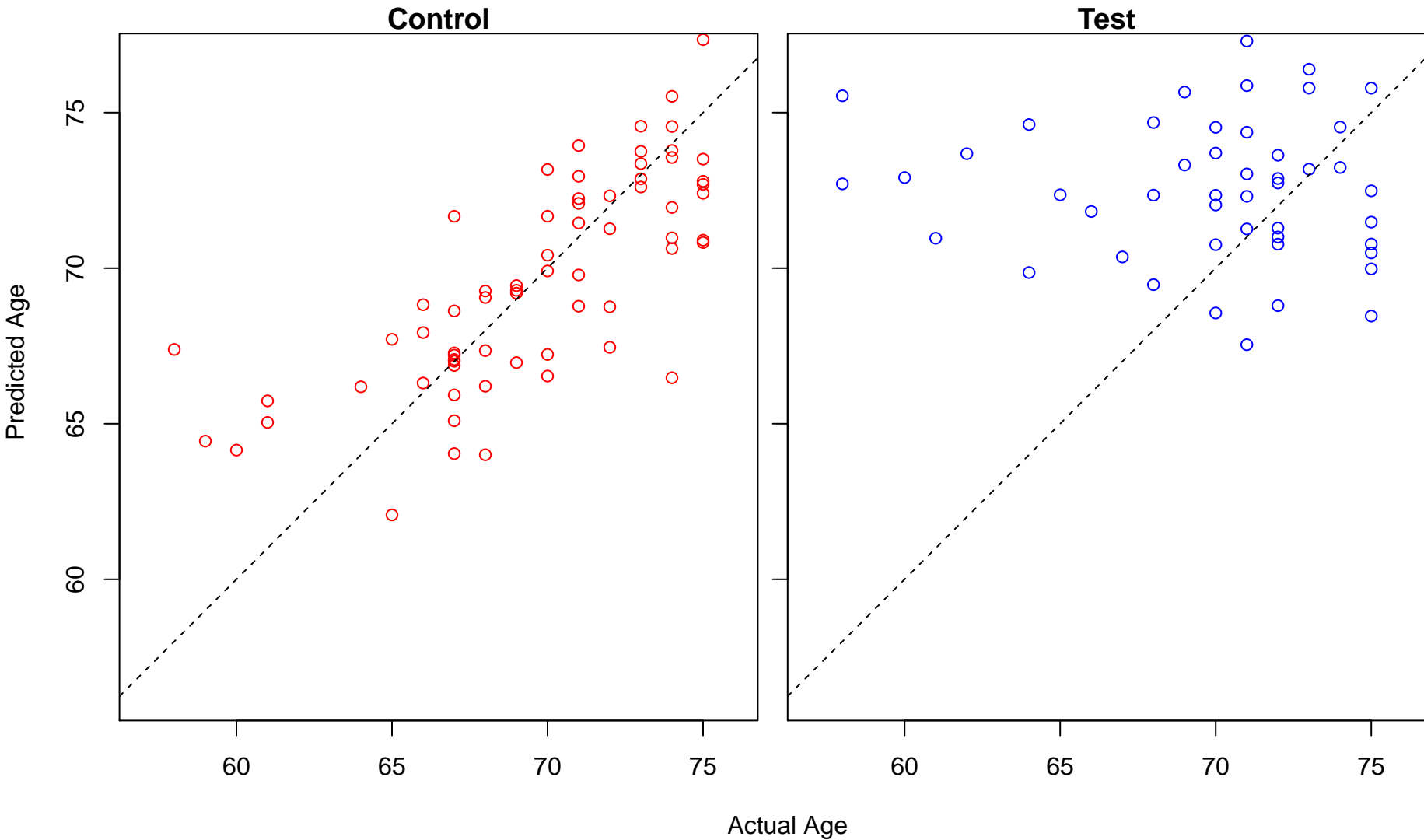
peptidyl-lysine acetylation (Score: 2.301800)



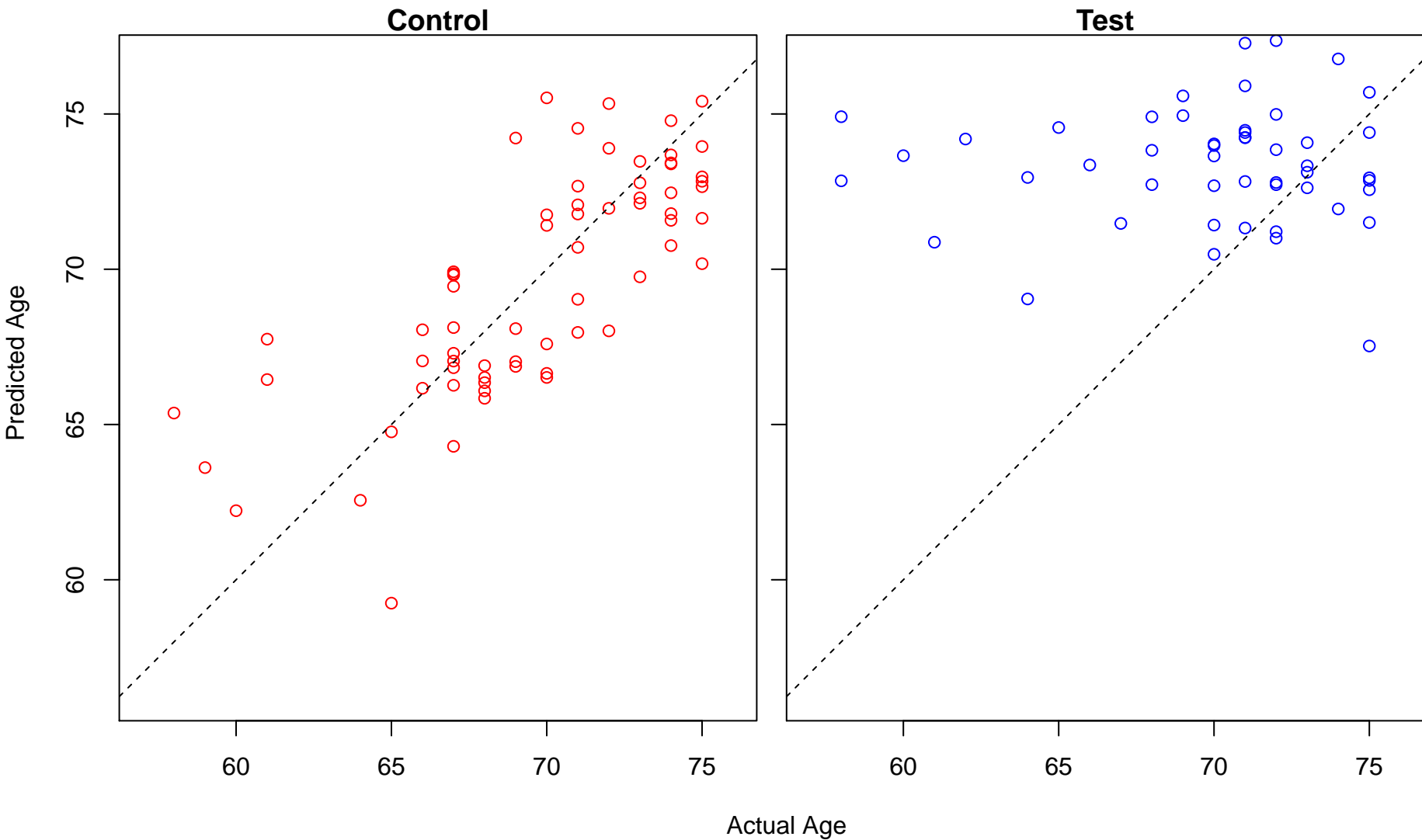
membrane budding (Score: 2.296105)



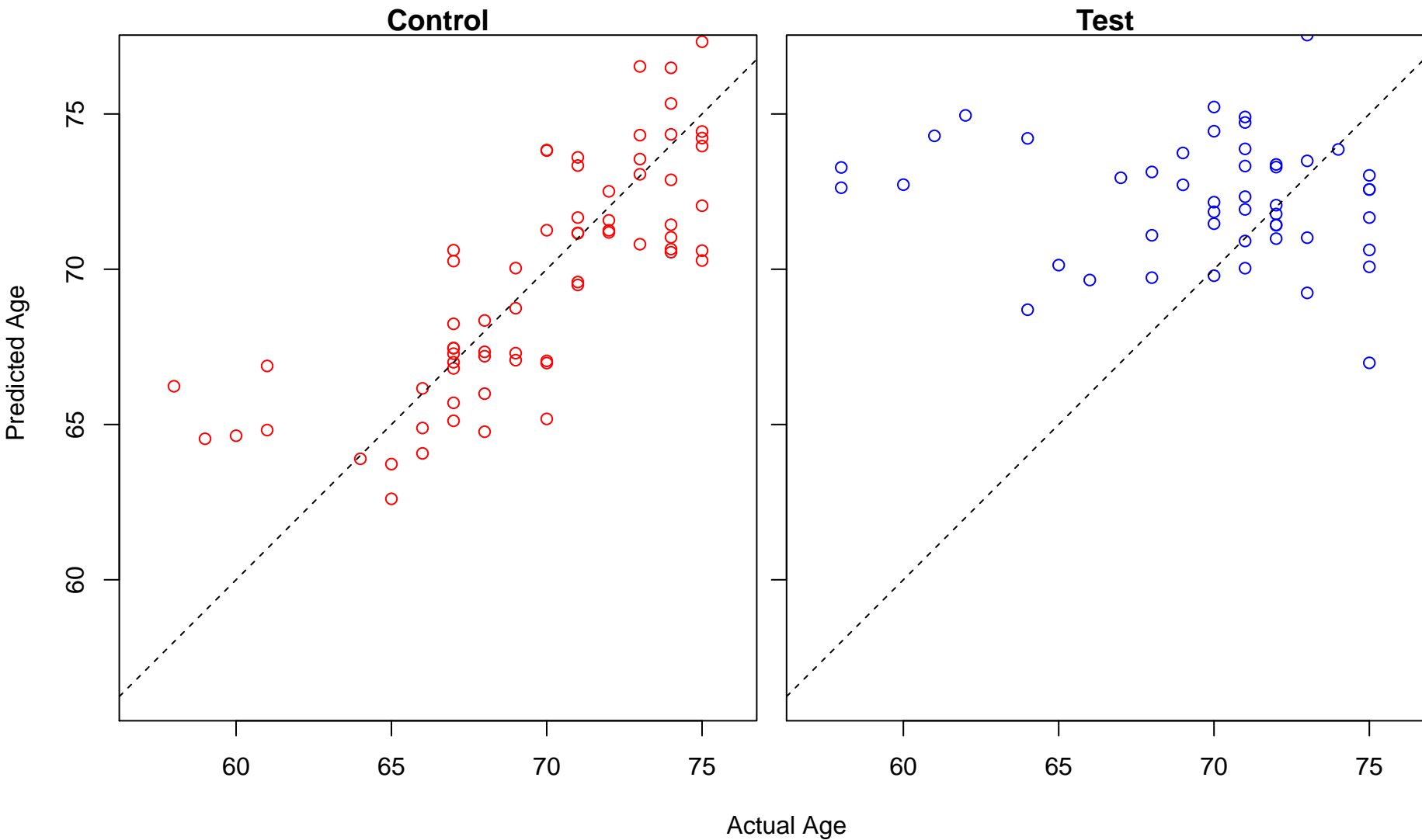
regulation of Ras protein signal transduction (Score: 2.293632)



protein import (Score: 2.287925)

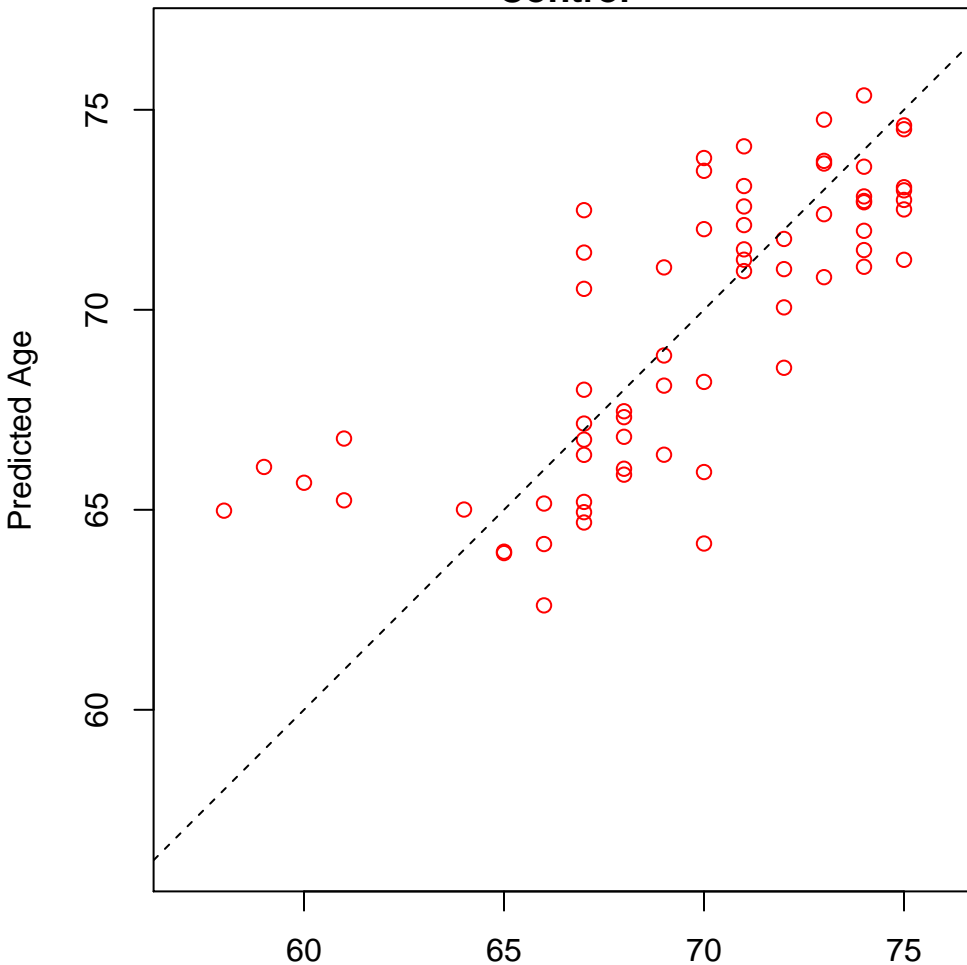


regulation of organelle assembly (Score: 2.274574)

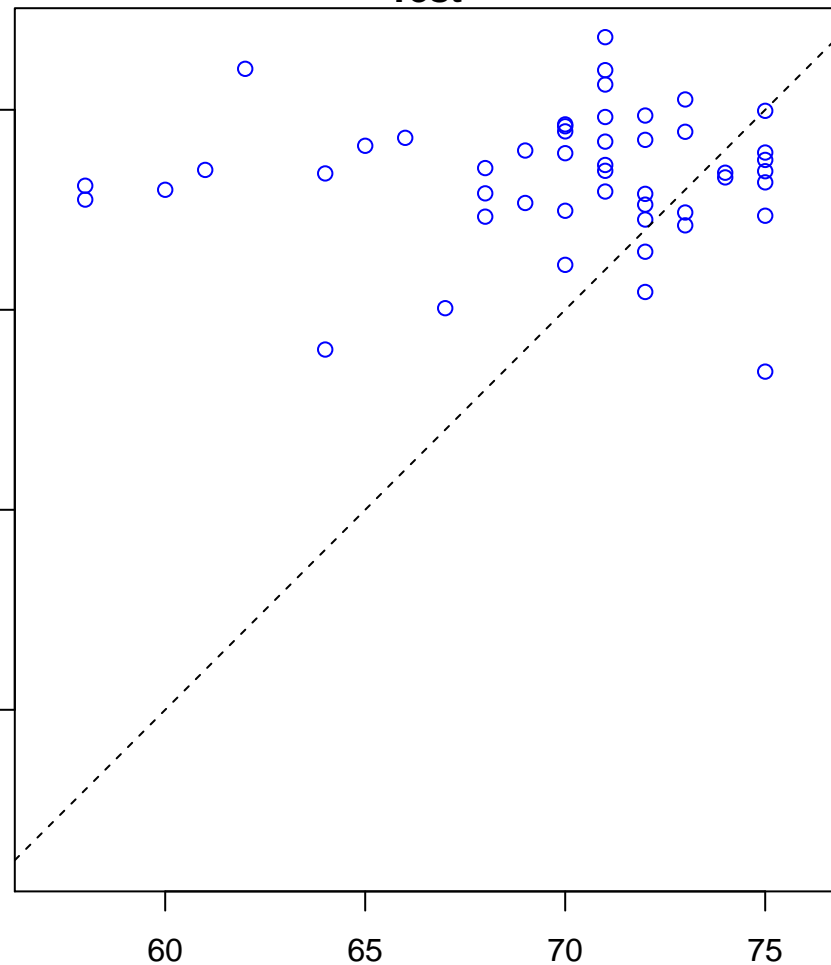


internal protein amino acid acetylation (Score: 2.260107)

Control

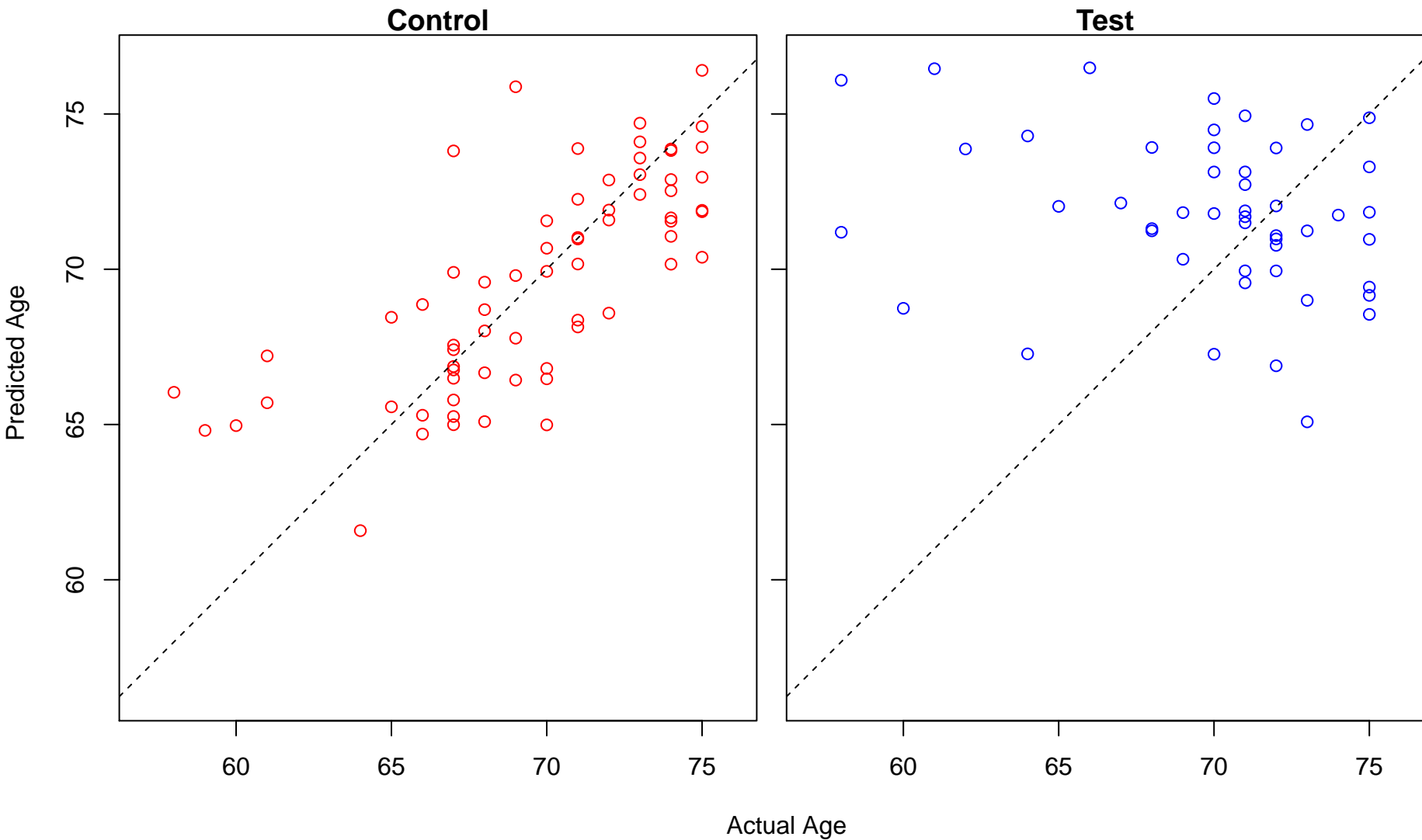


Test

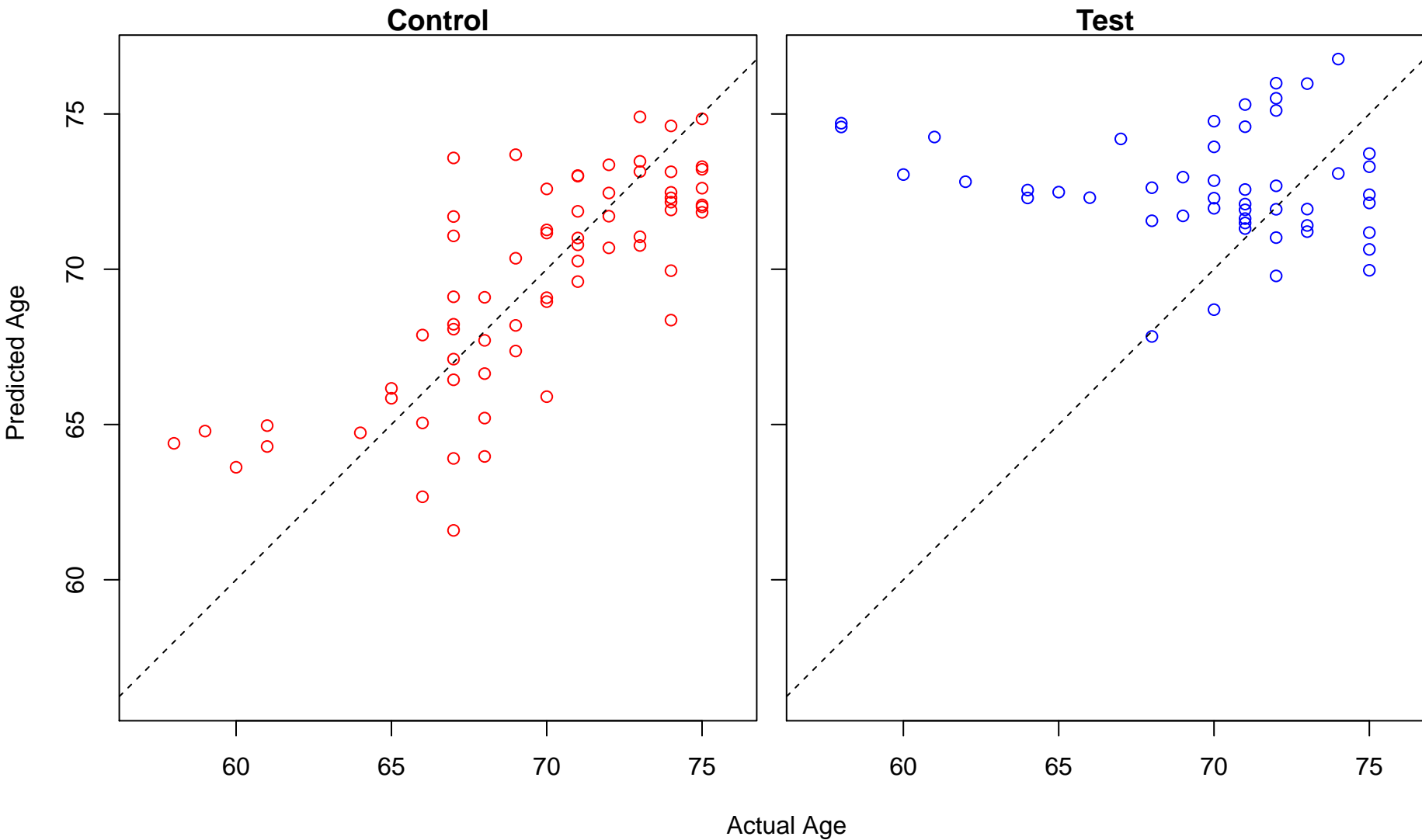


Actual Age

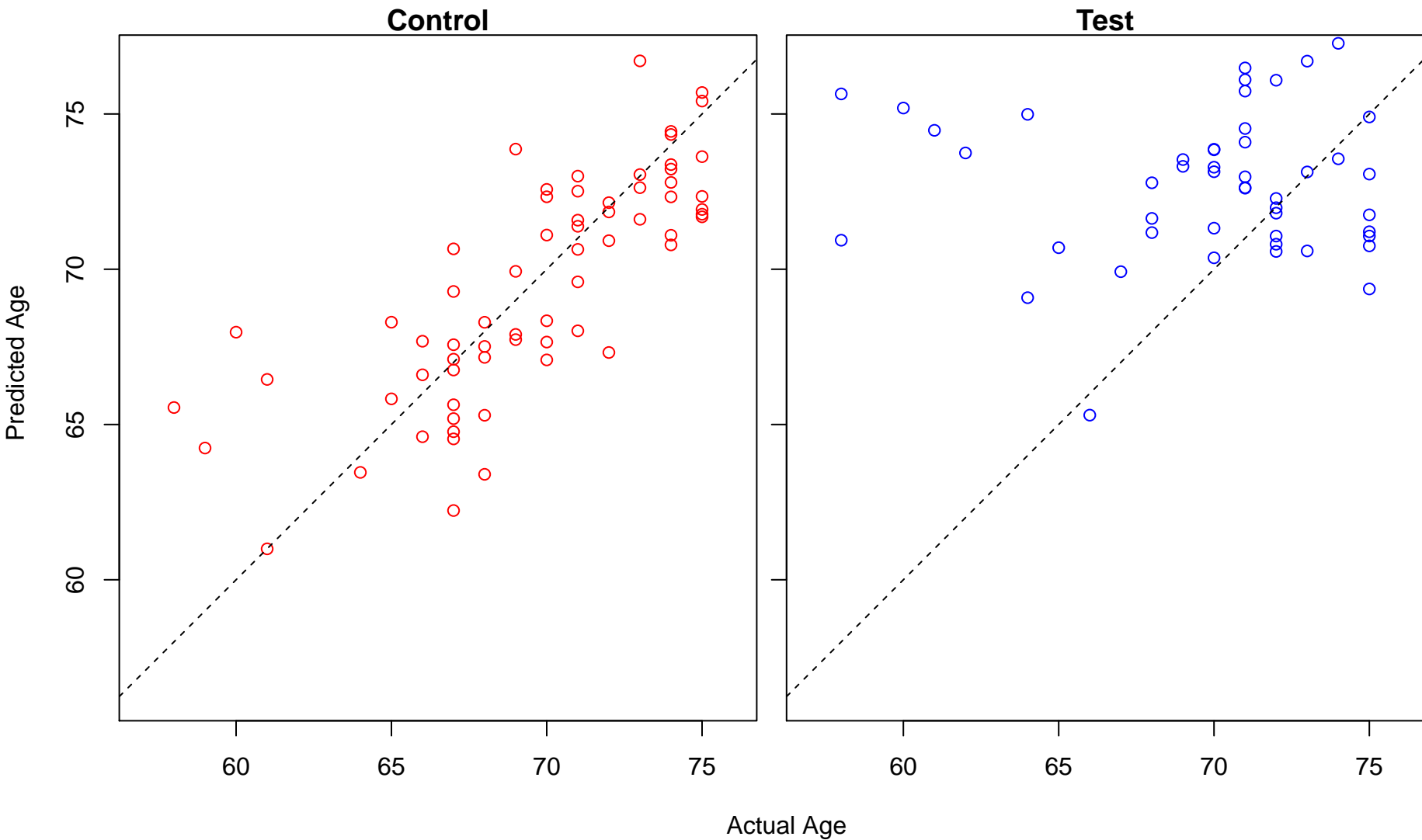
negative regulation of viral genome replication (Score: 2.252328)



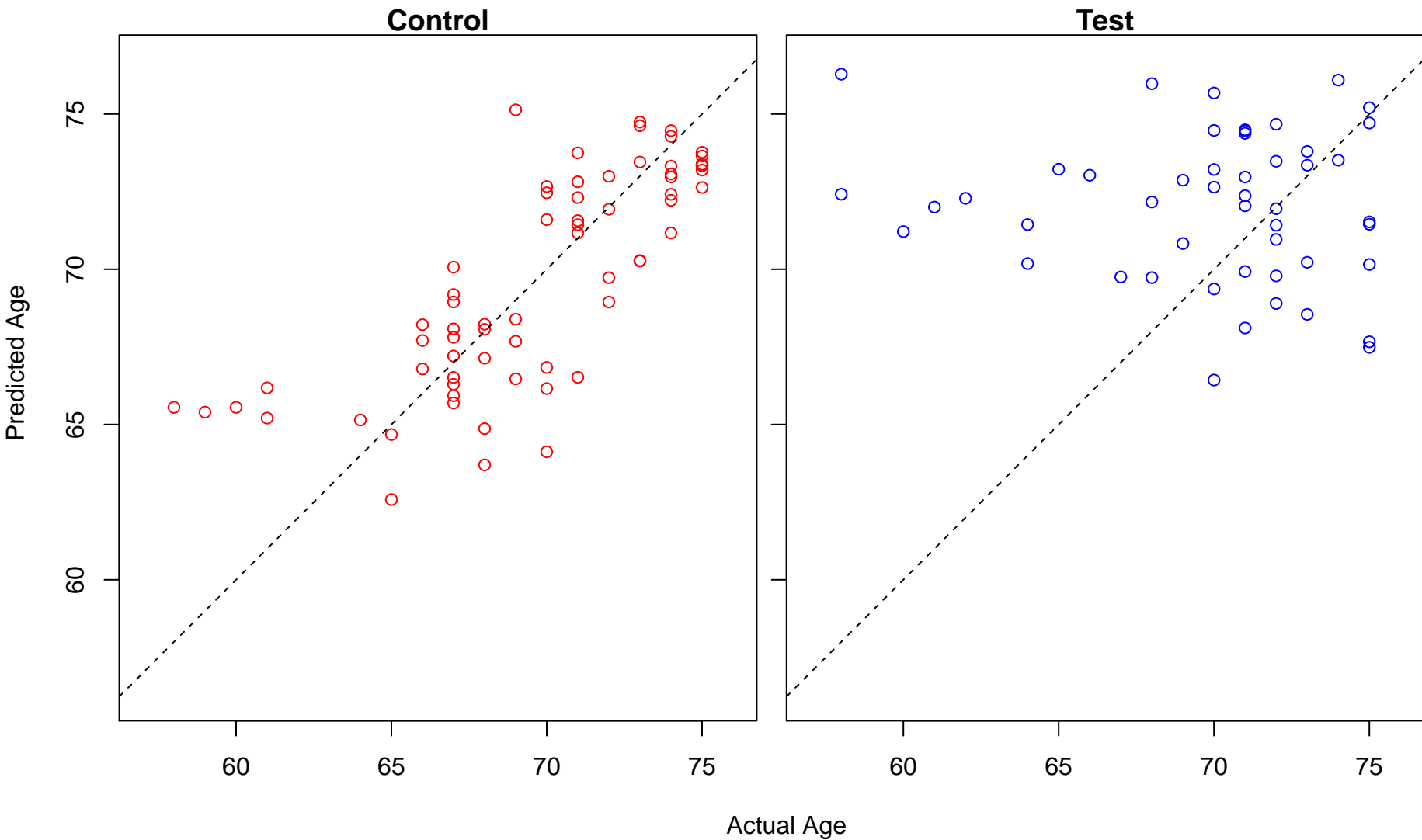
mitochondrial fusion (Score: 2.244797)



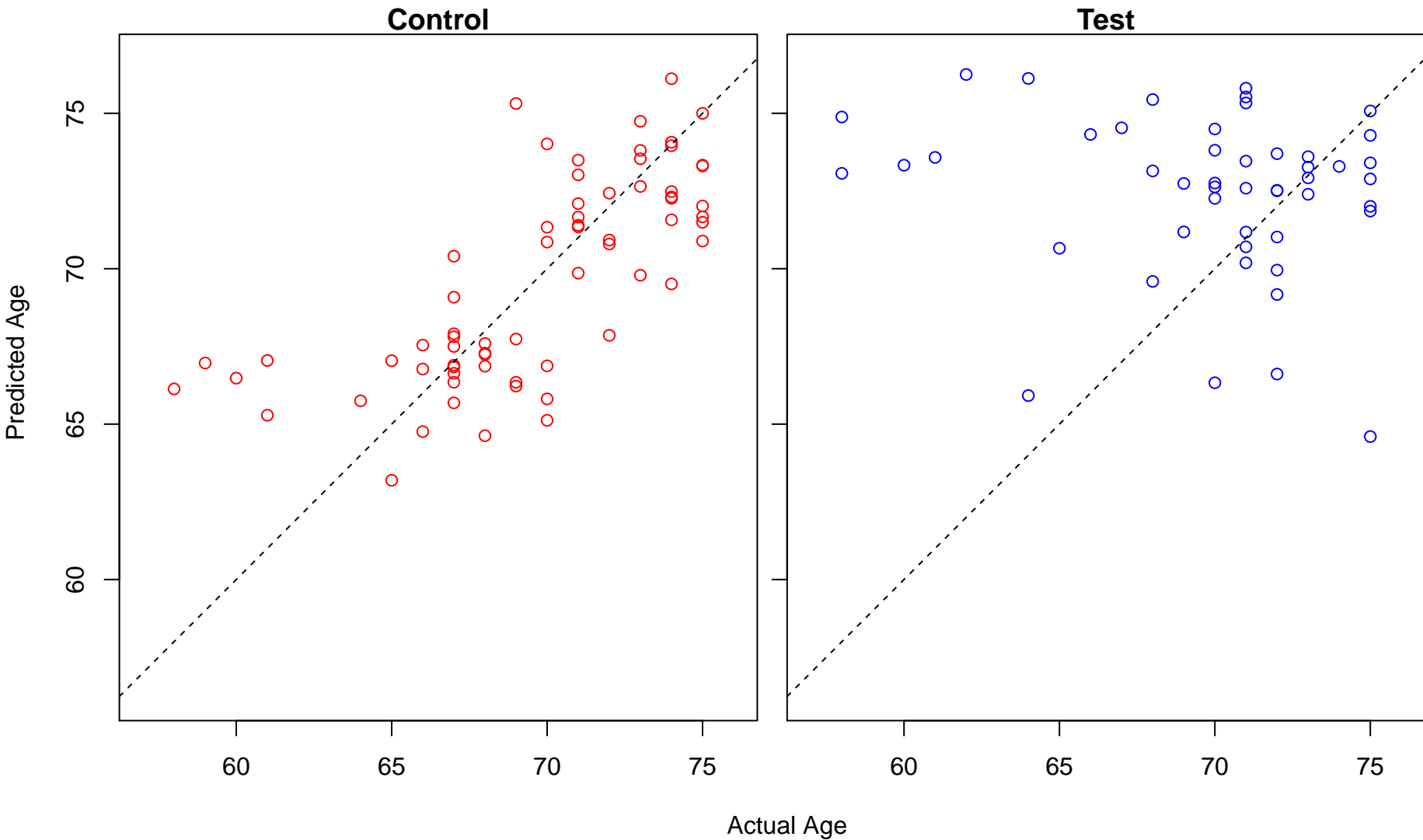
protein targeting to mitochondrion (Score: 2.244362)



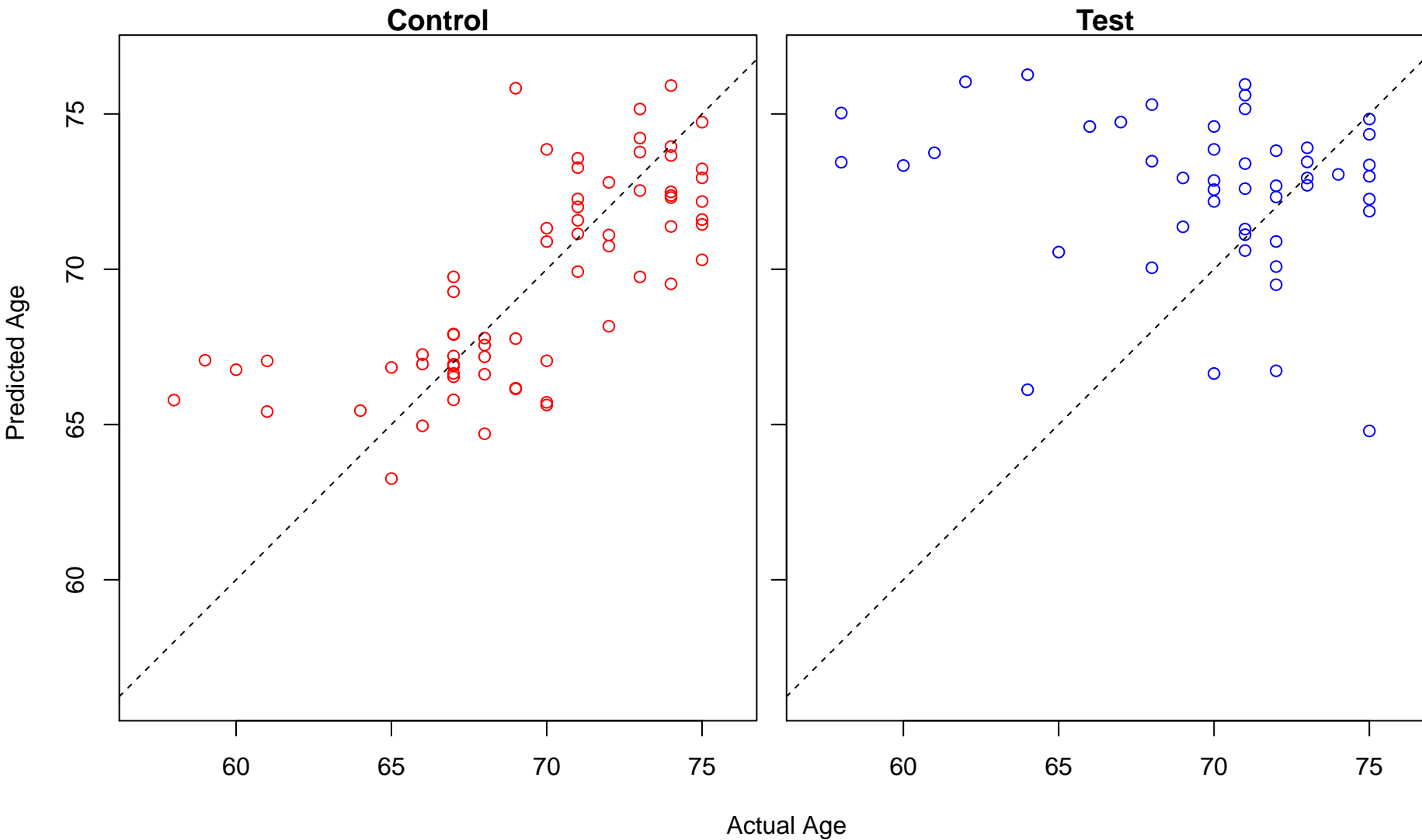
regulation of myeloid leukocyte differentiation (Score: 2.237221)



positive regulation of lymphocyte migration (Score: 2.219028)

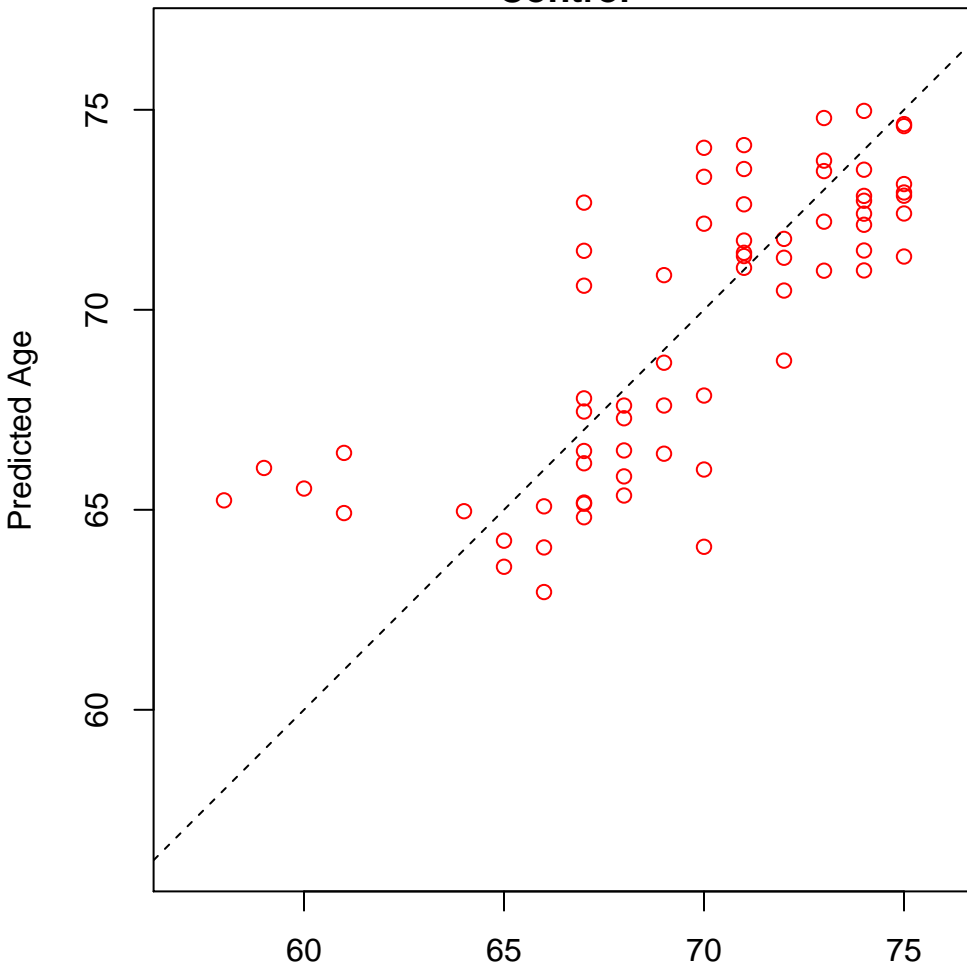


regulation of T cell migration (Score: 2.215157)

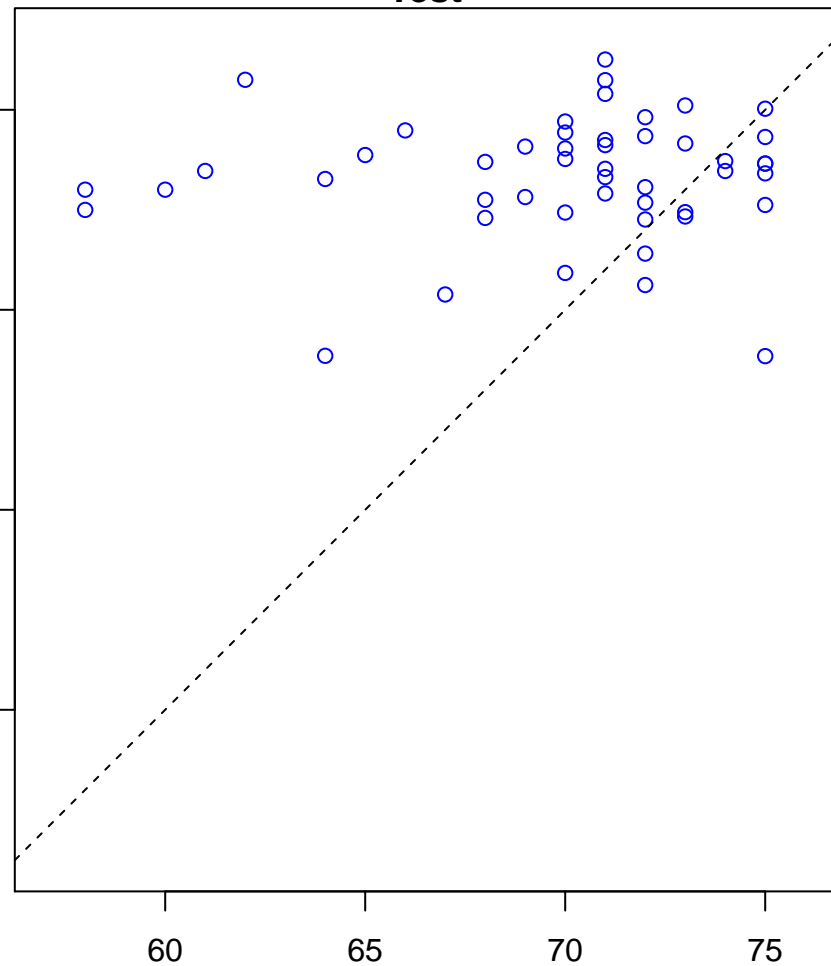


internal peptidyl-lysine acetylation (Score: 2.209610)

Control

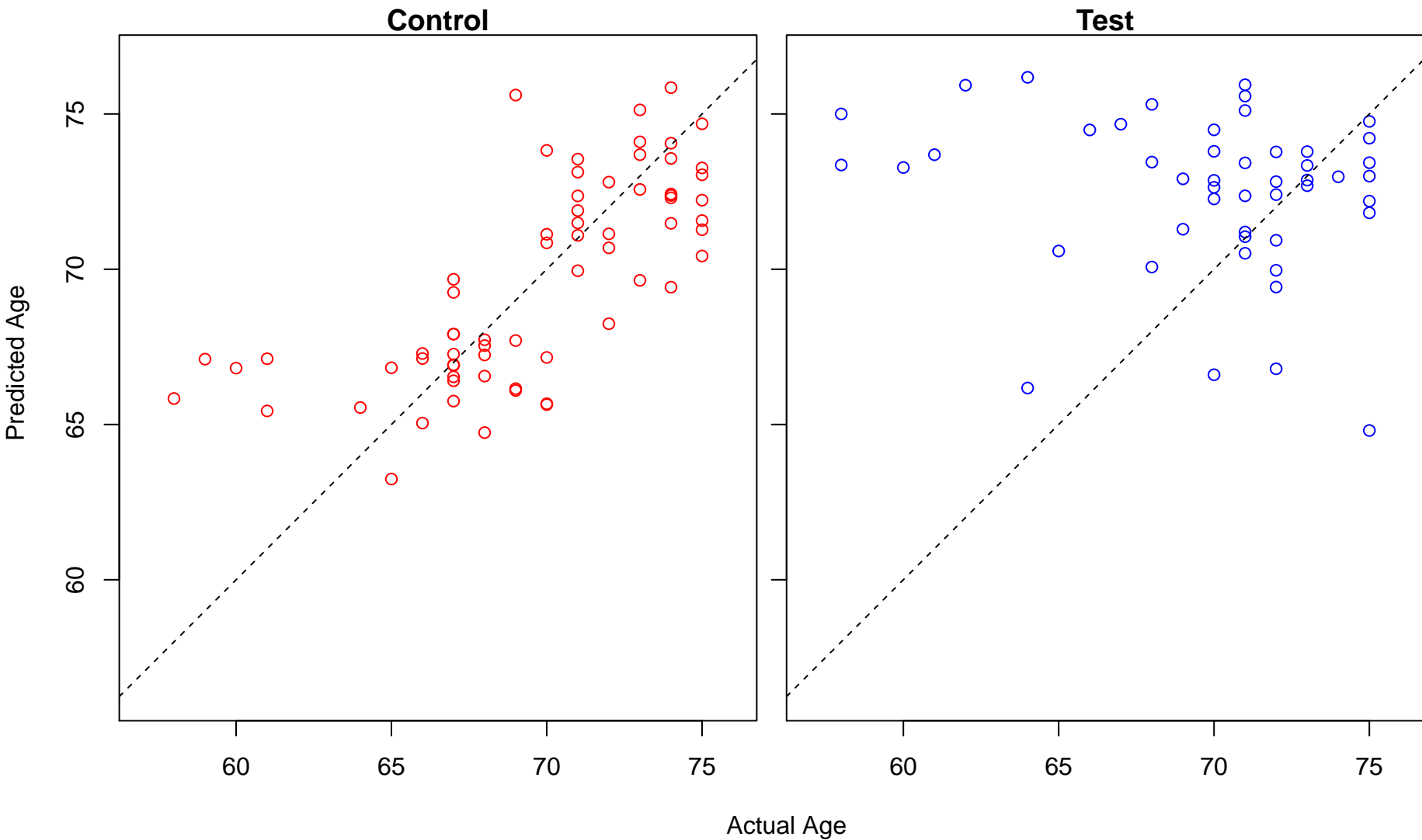


Test

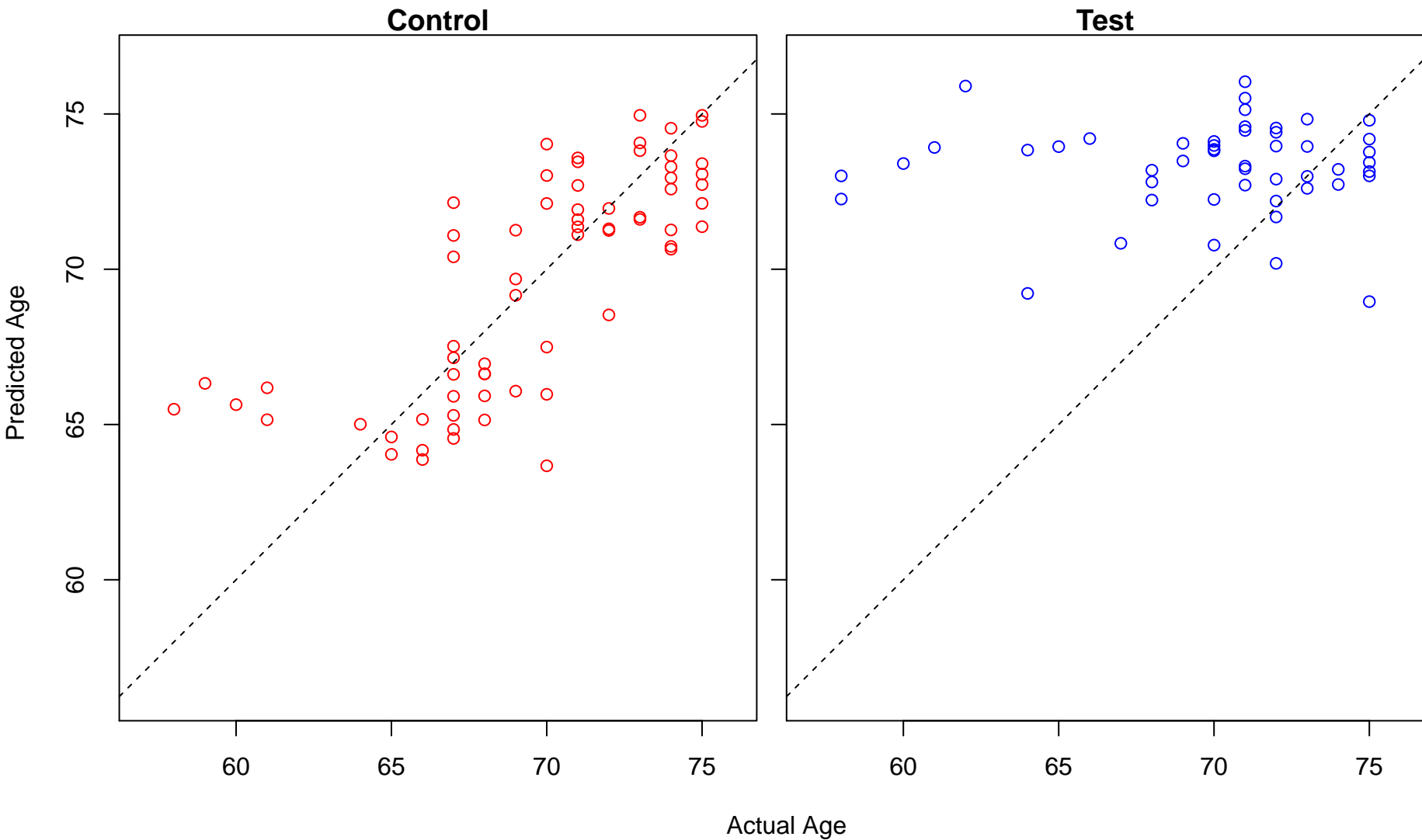


Actual Age

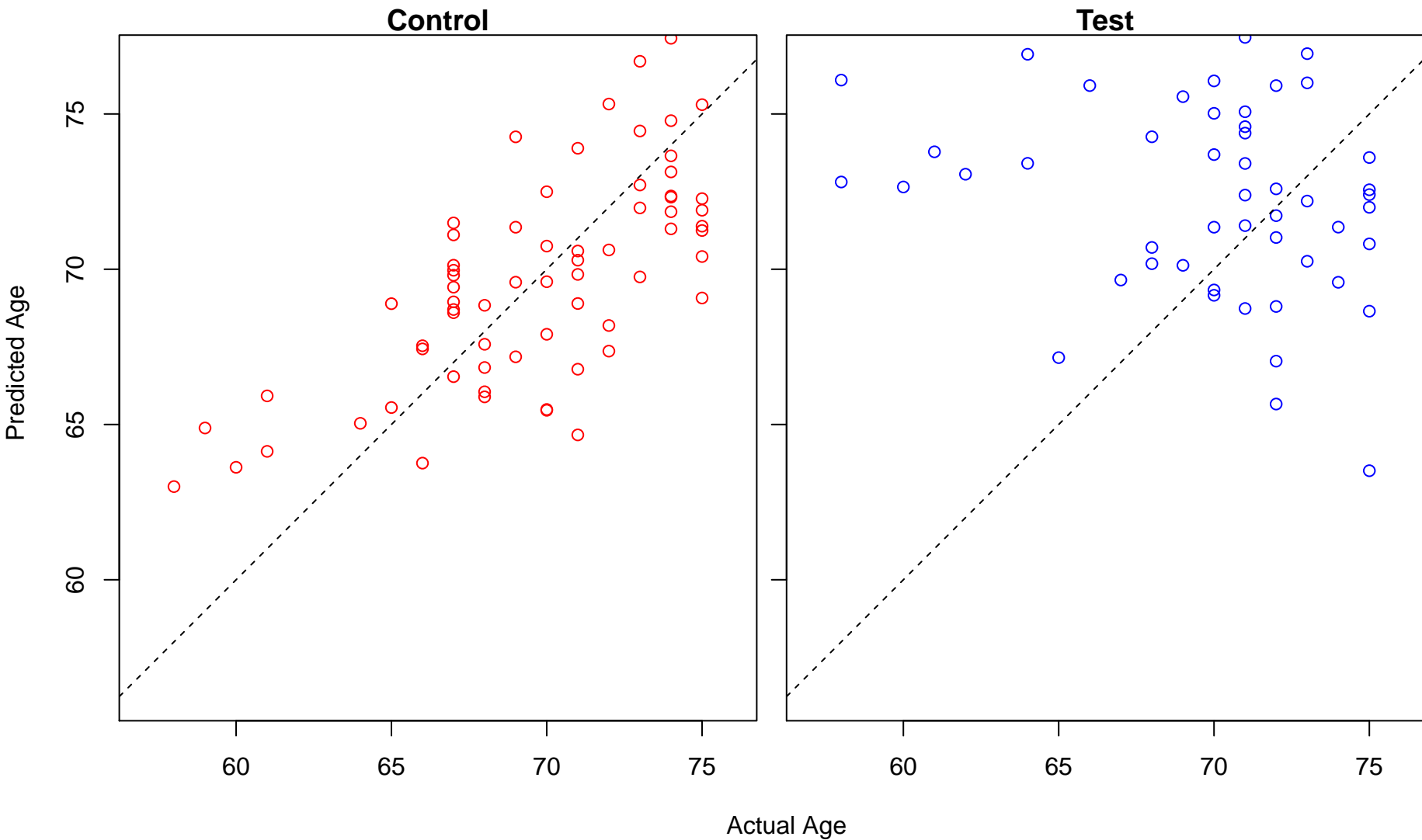
positive regulation of T cell migration (Score: 2.209432)



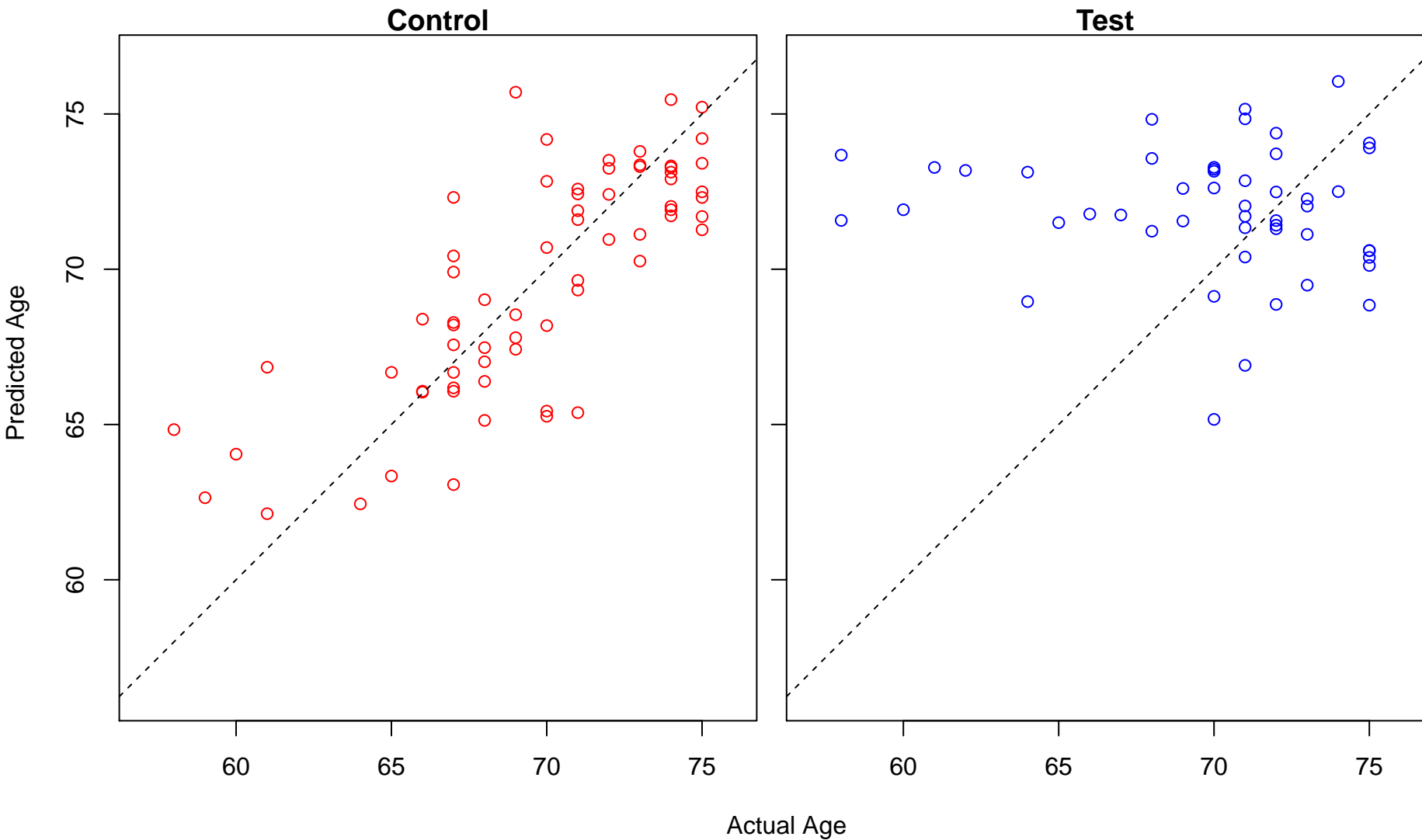
histone acetylation (Score: 2.207403)



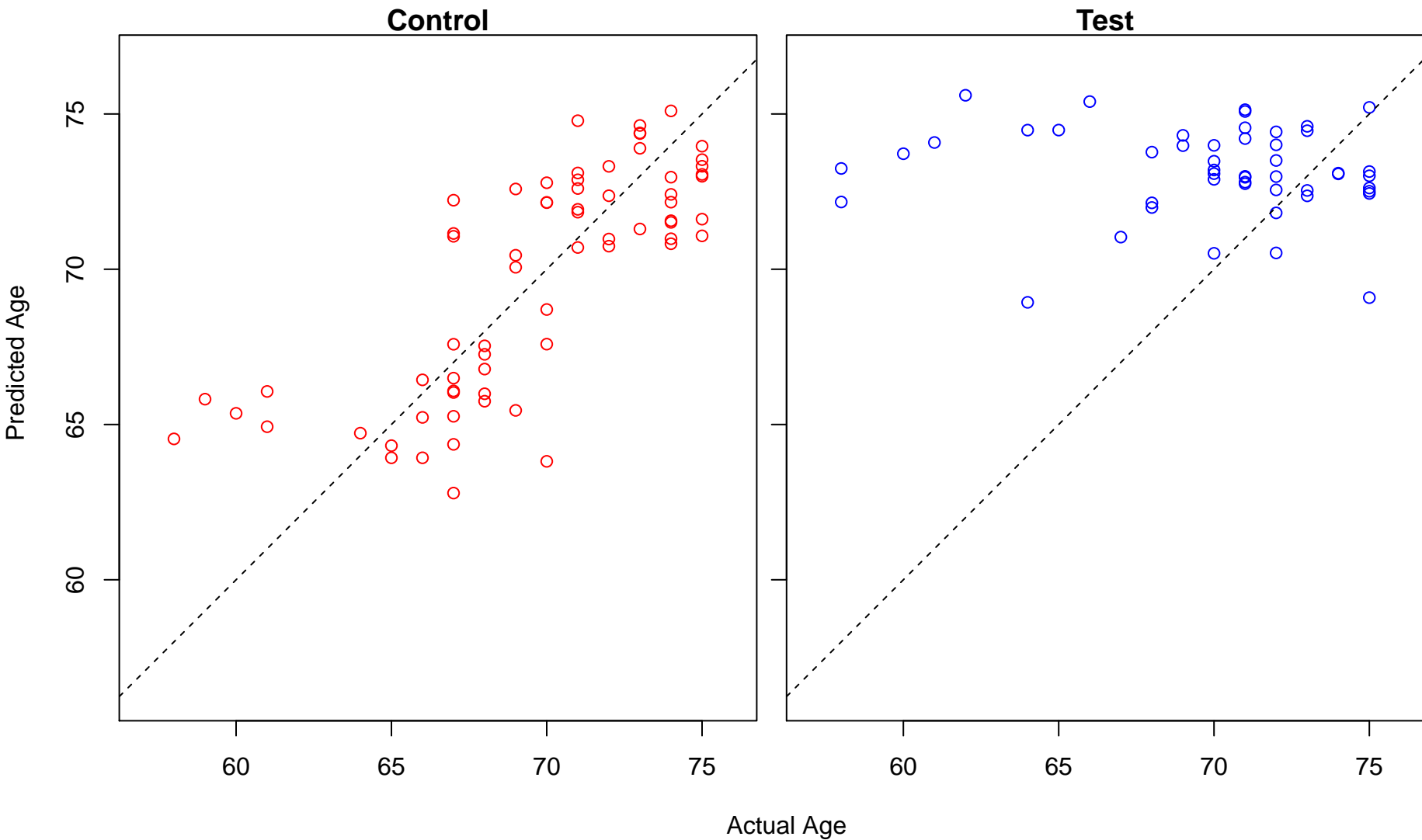
regulation of thymocyte apoptotic process (Score: 2.202633)



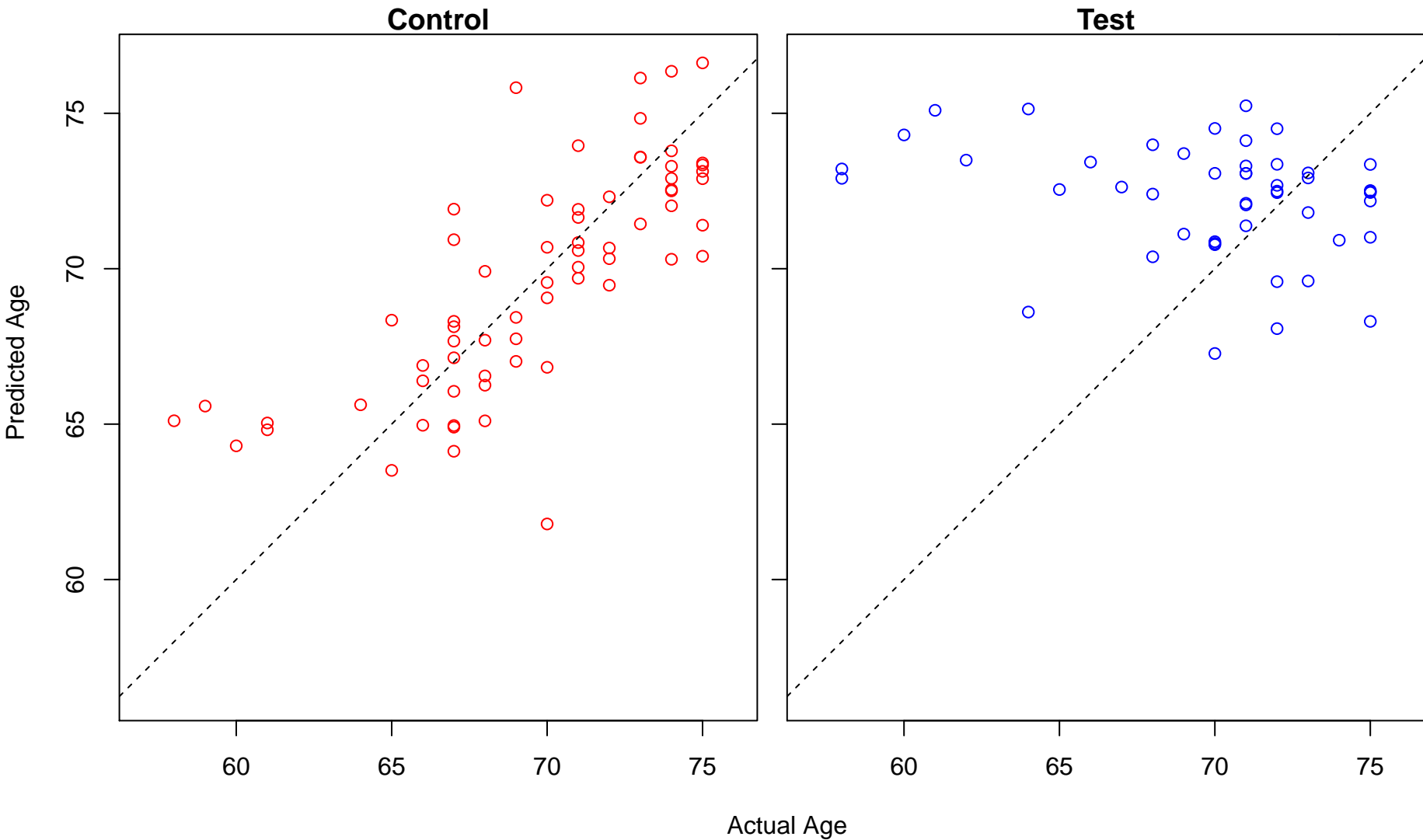
apoptotic mitochondrial changes (Score: 2.200079)



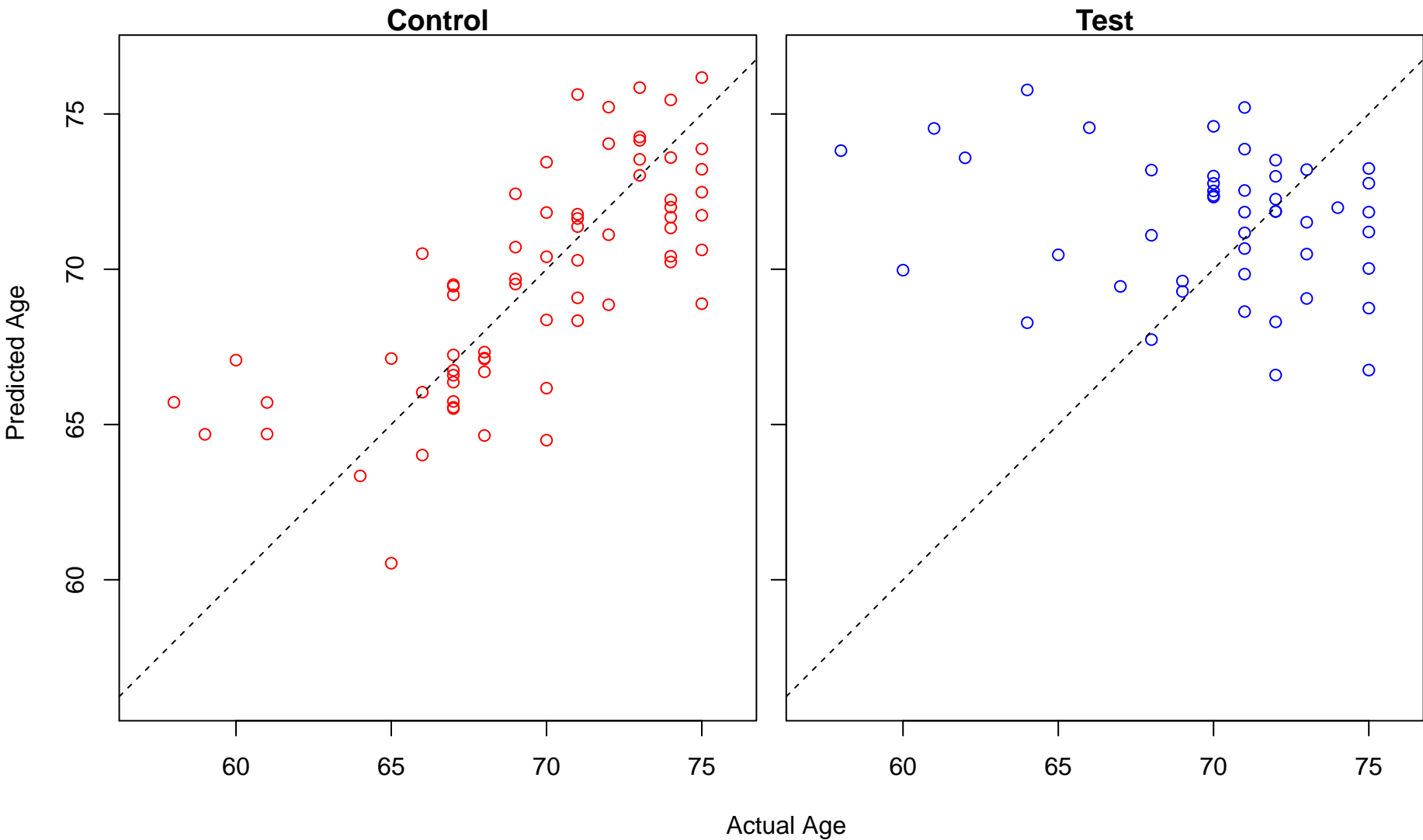
histone H4 acetylation (Score: 2.198775)



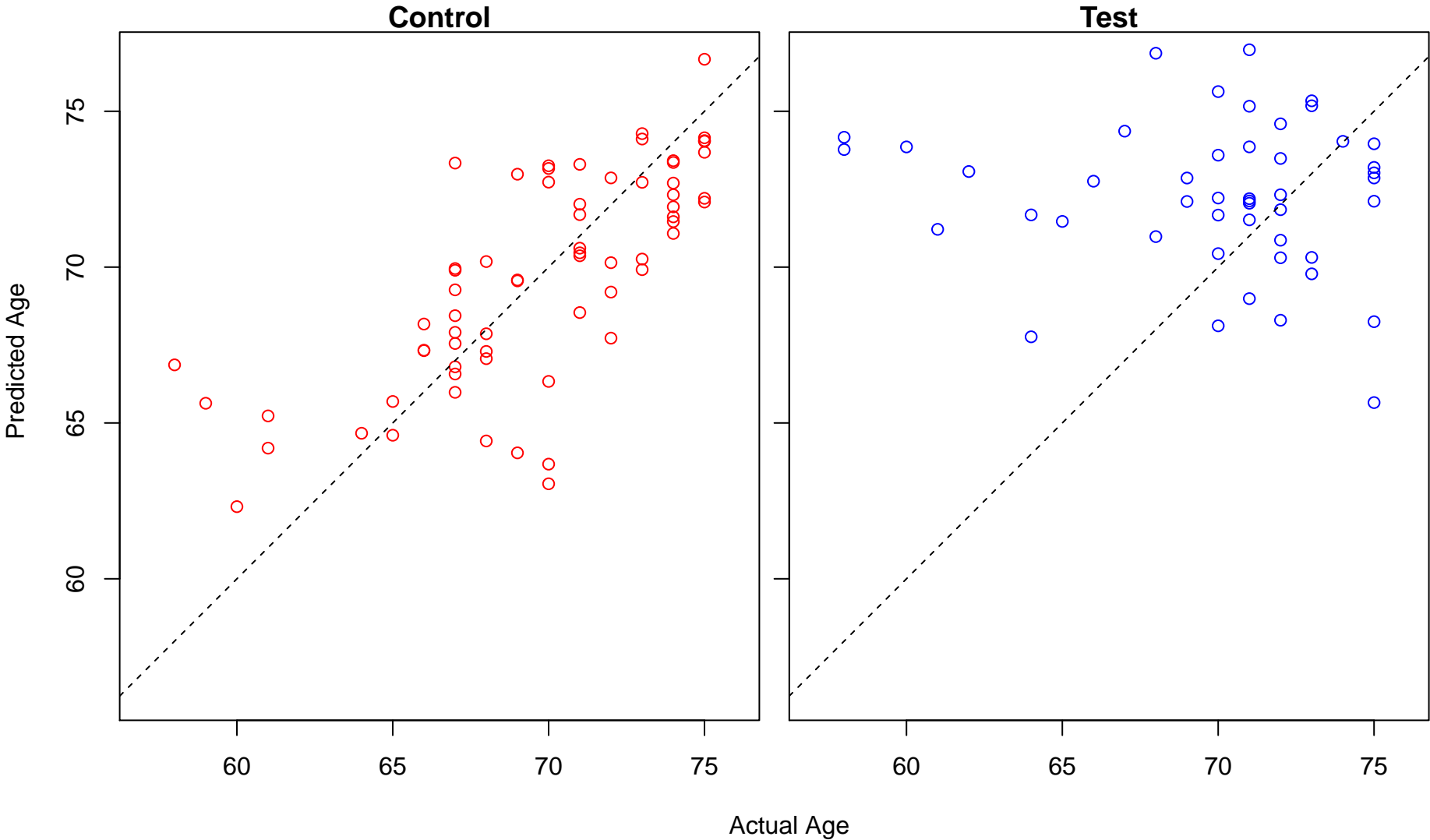
phosphatidylcholine acyl-chain remodeling (Score: 2.182806)



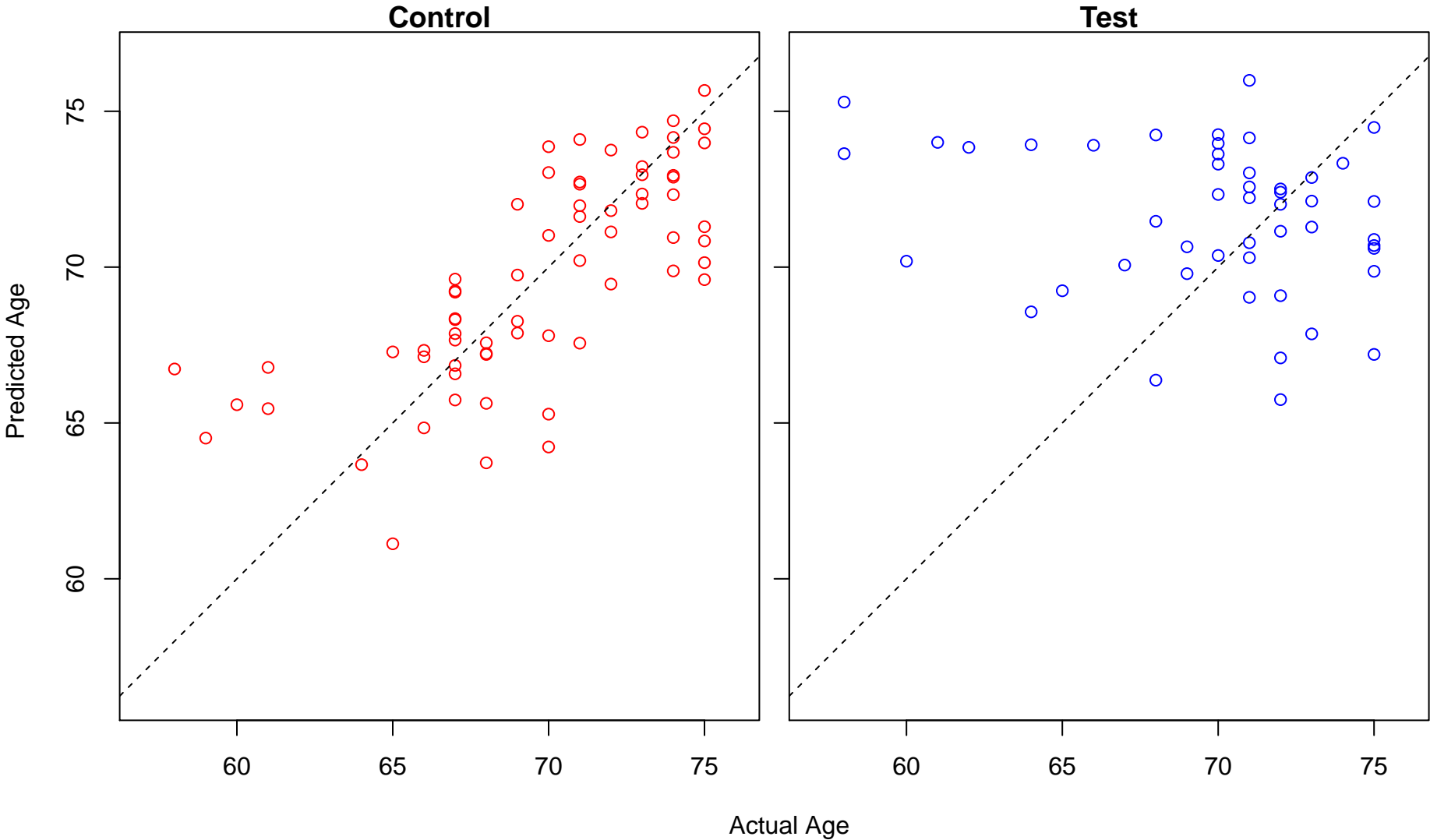
positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 1.0)



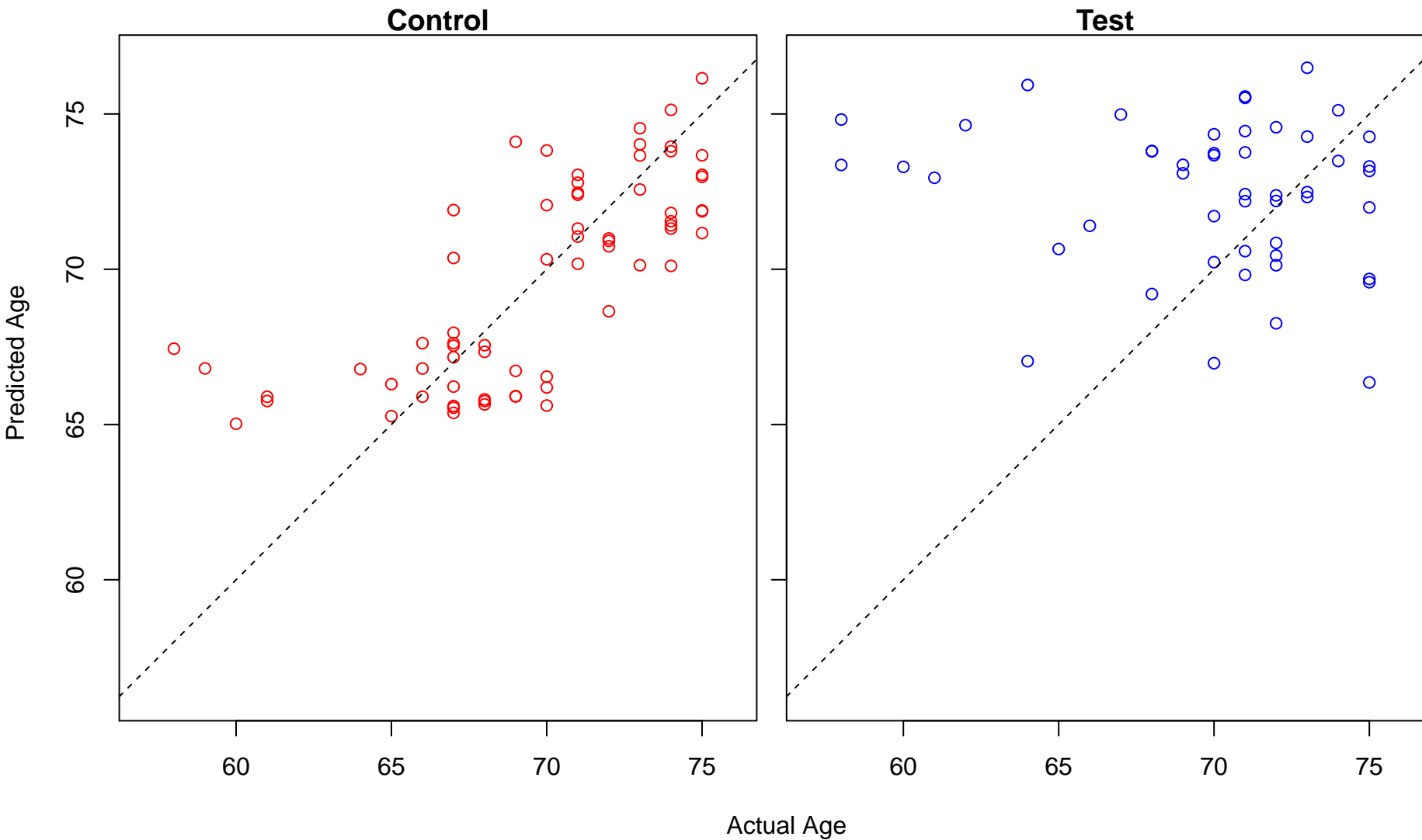
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (Score: 2.155)



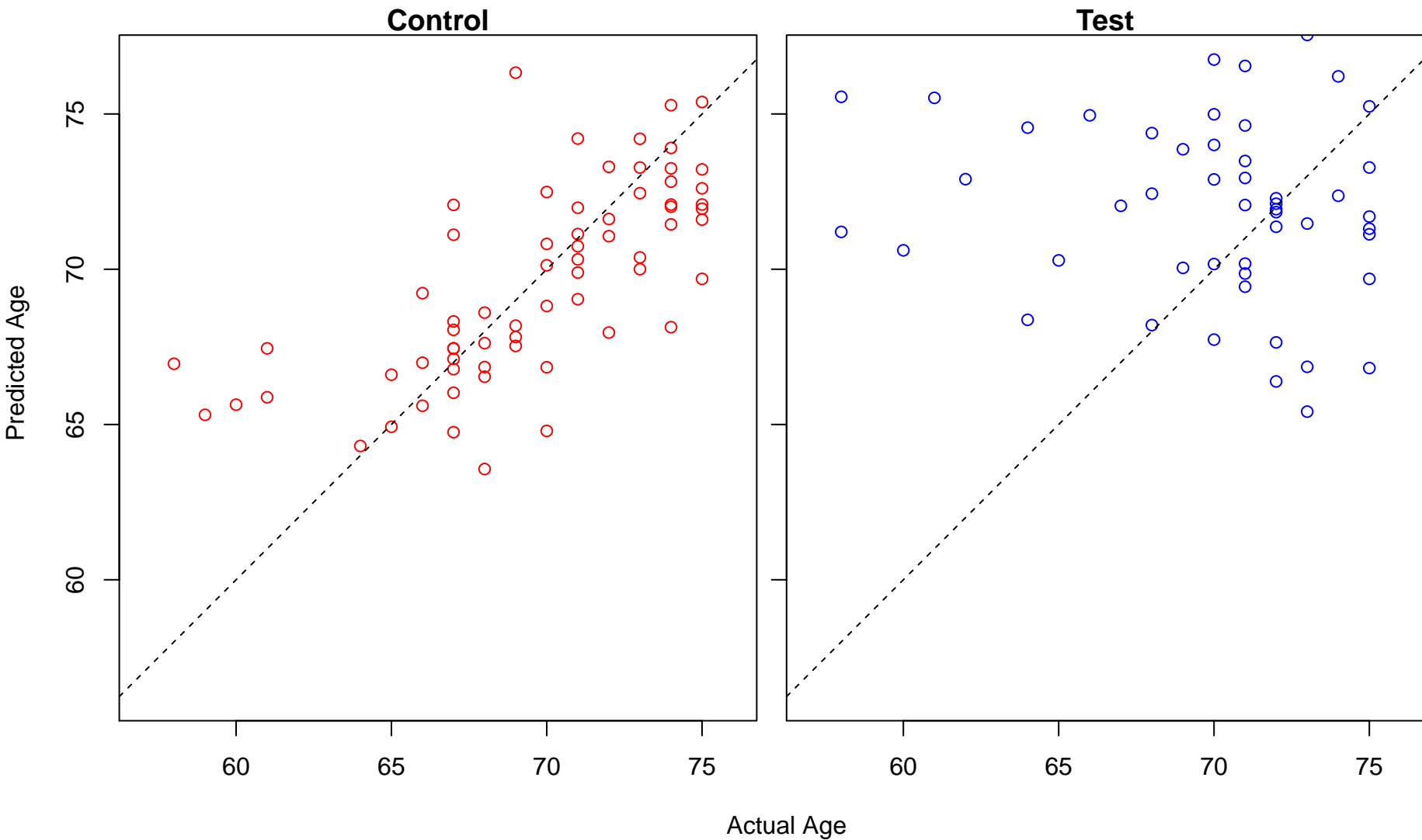
regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (Score: 2.15)



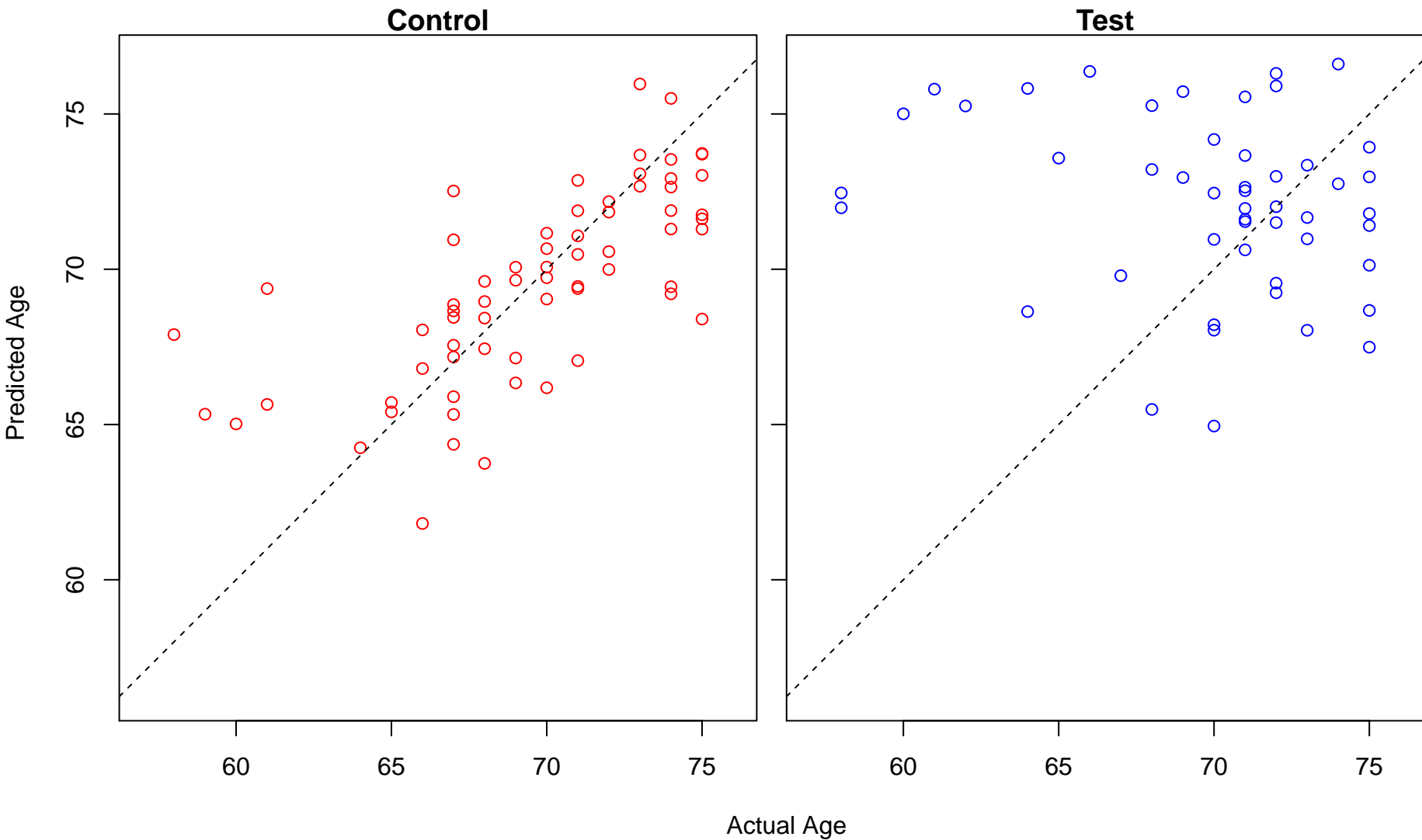
negative regulation of smooth muscle cell proliferation (Score: 2.150033)



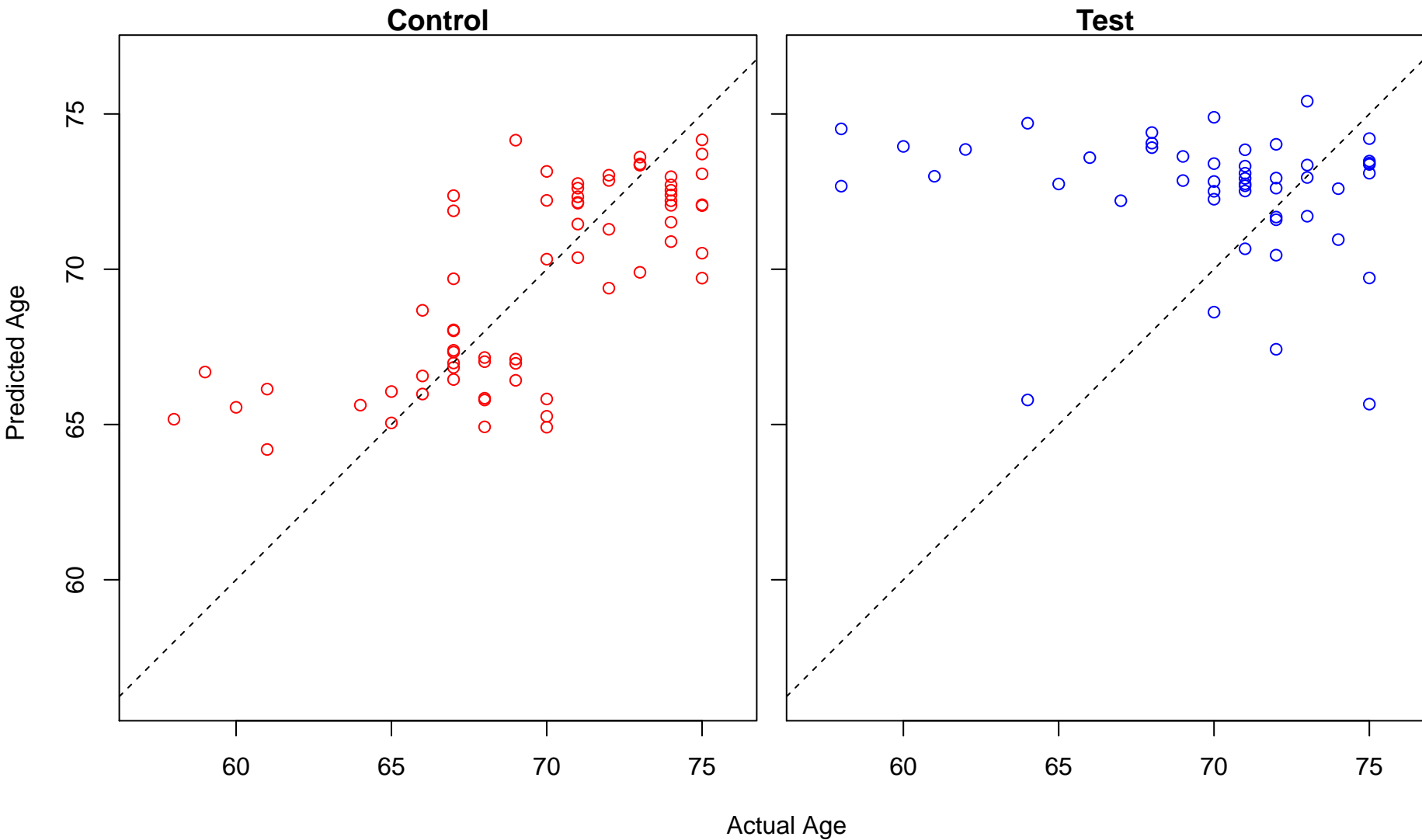
negative regulation of defense response to virus (Score: 2.141329)



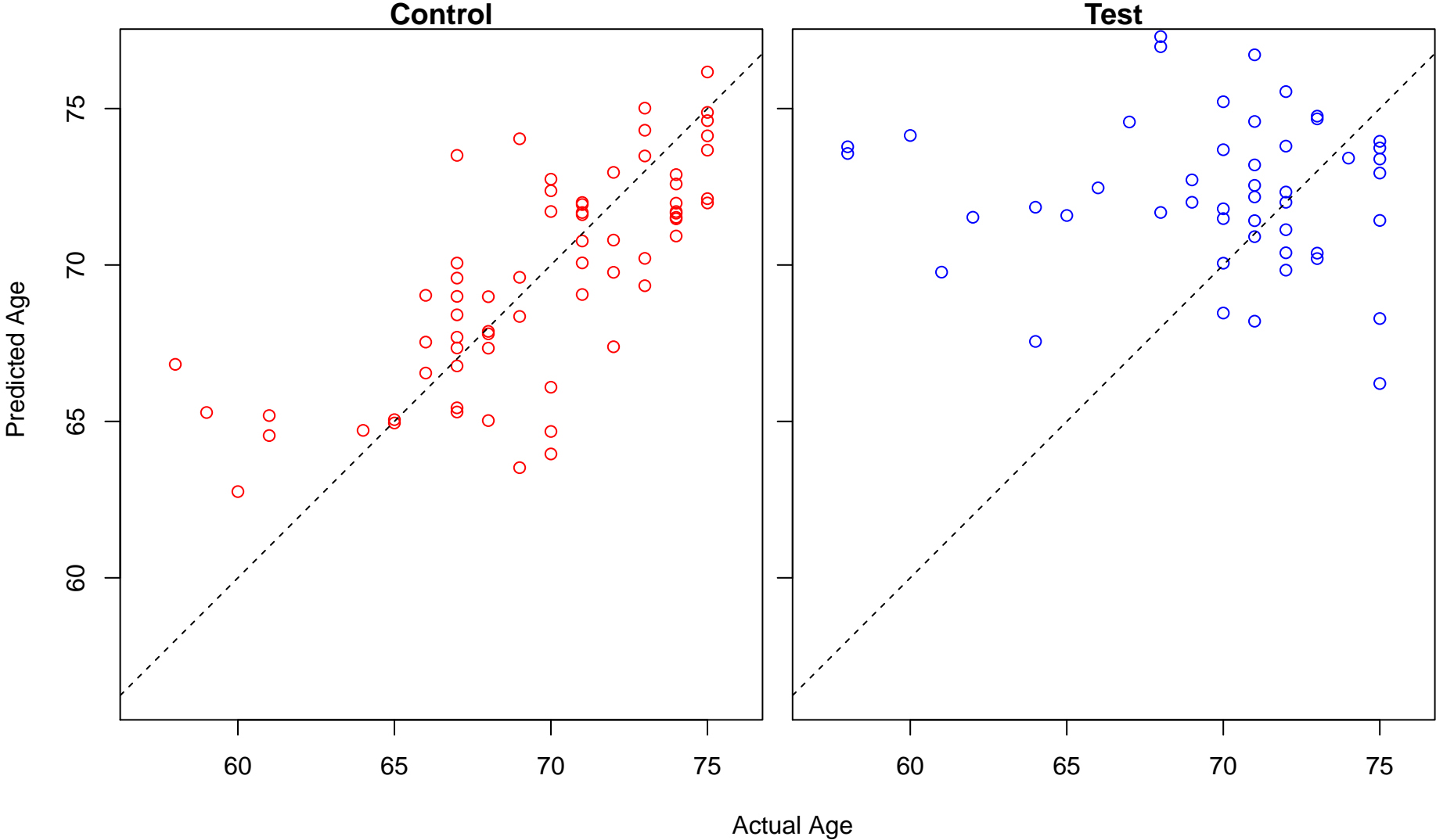
phosphatidylethanolamine acyl-chain remodeling (Score: 2.135091)



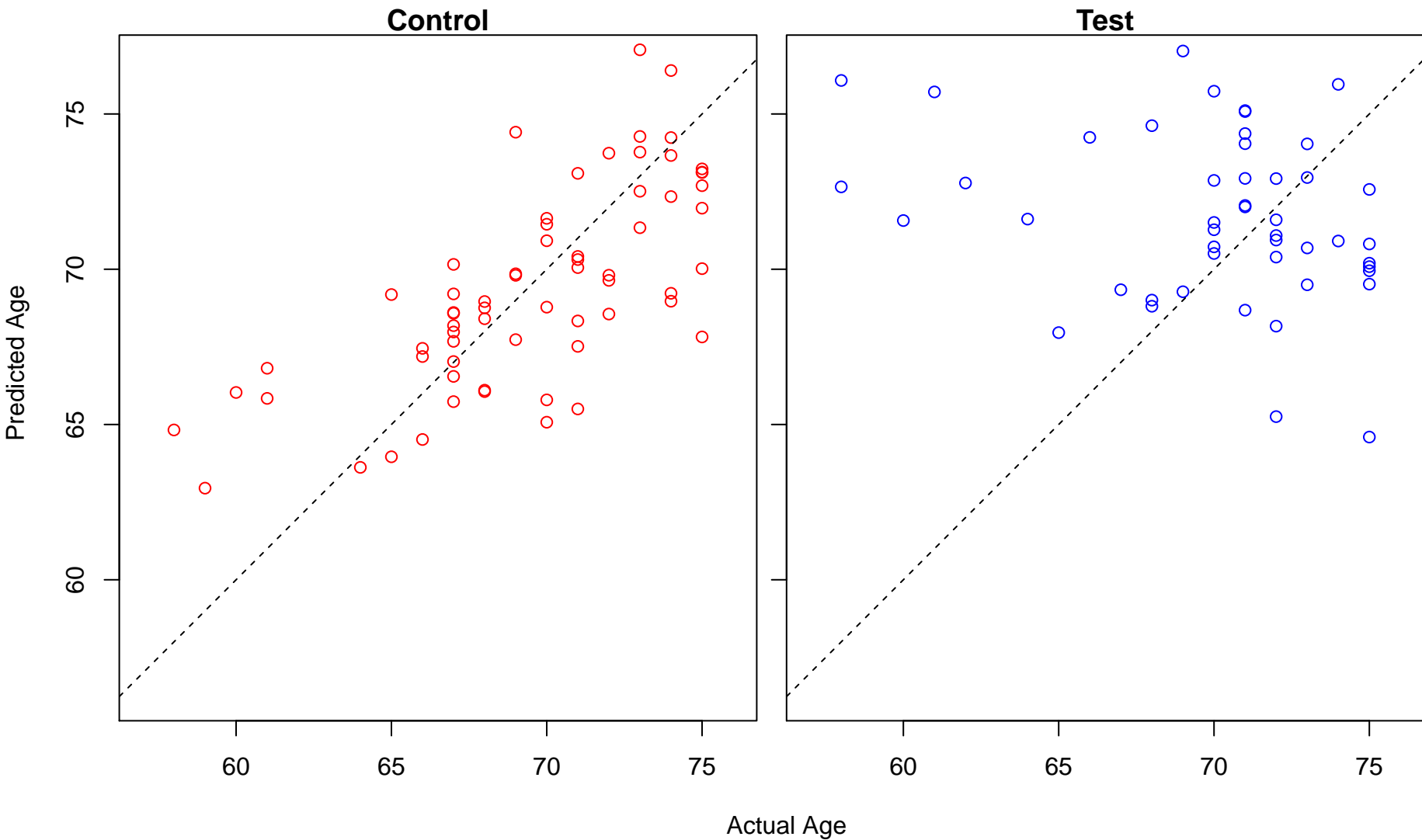
cyclic-nucleotide-mediated signaling (Score: 2.127839)



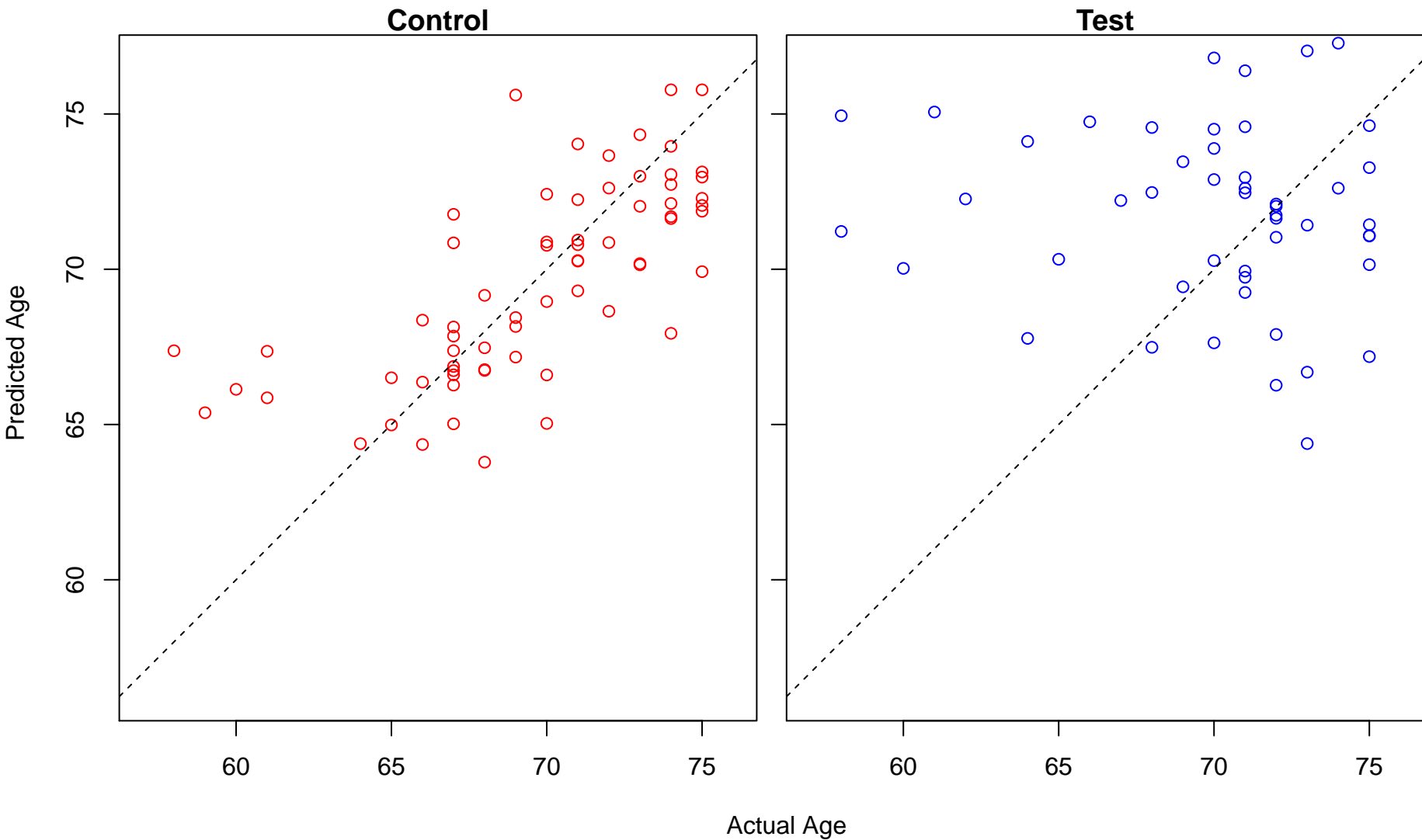
intrinsic apoptotic signaling pathway by p53 class mediator (Score: 2.122041)



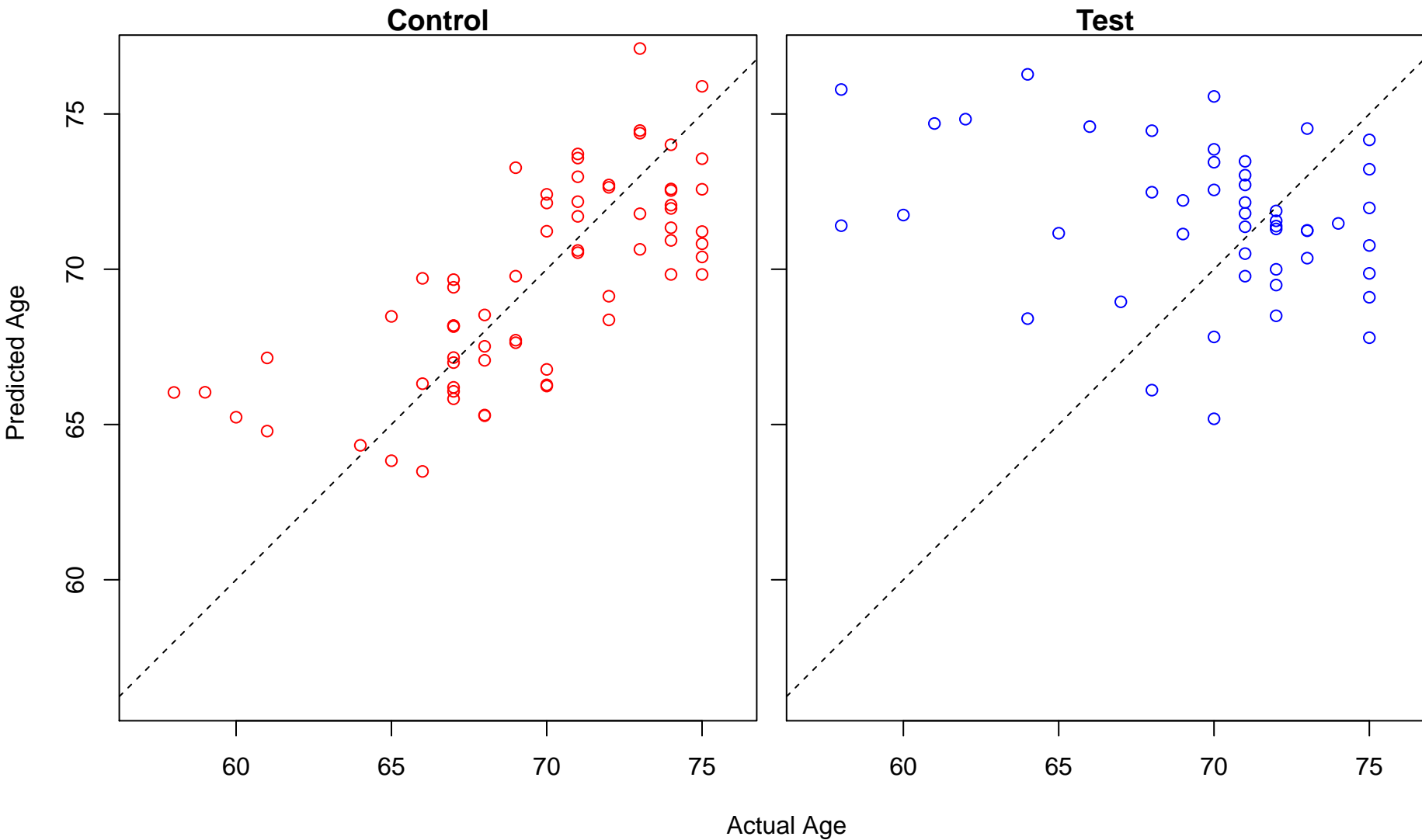
positive regulation of lymphocyte apoptotic process (Score: 2.121678)



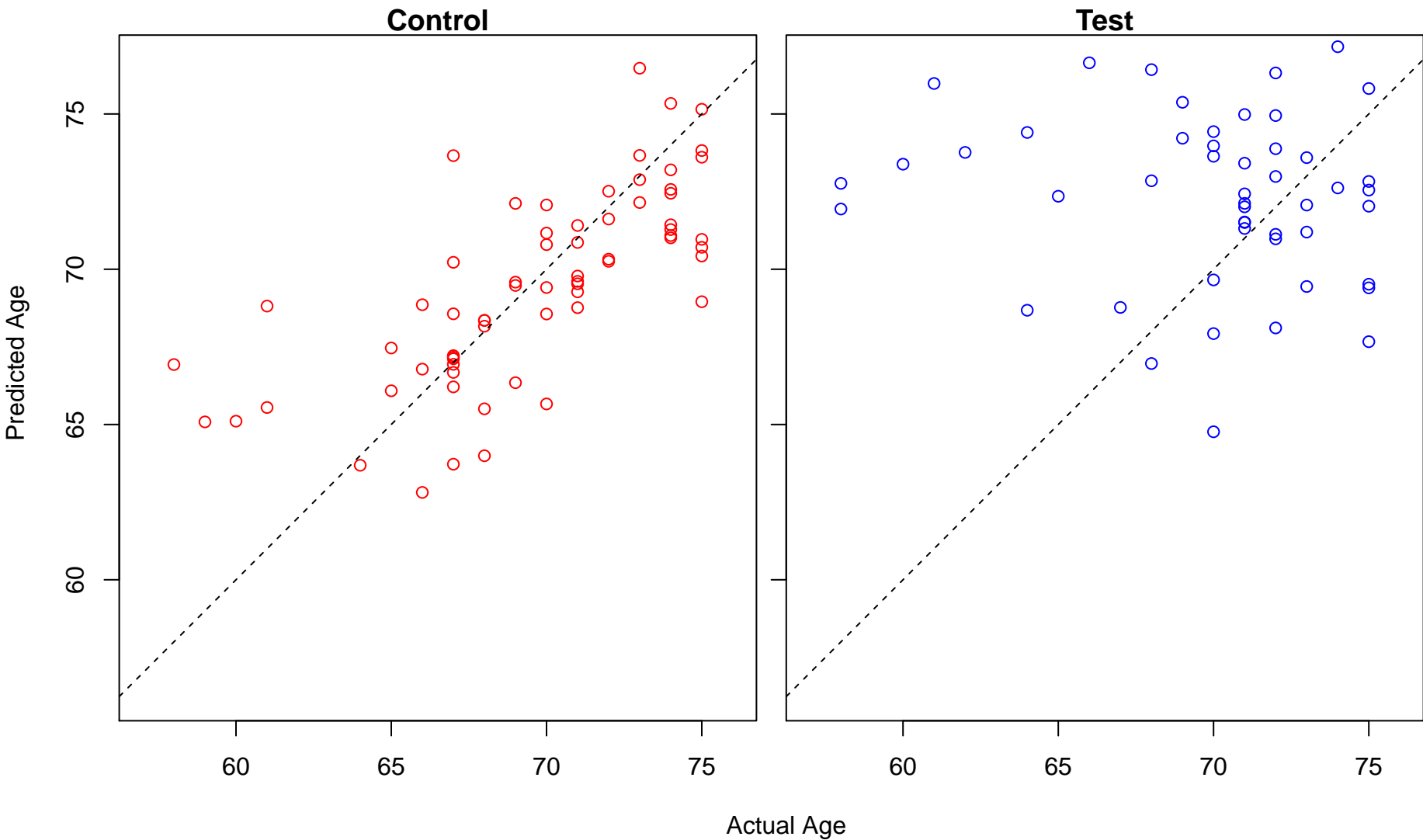
negative regulation of response to biotic stimulus (Score: 2.119999)



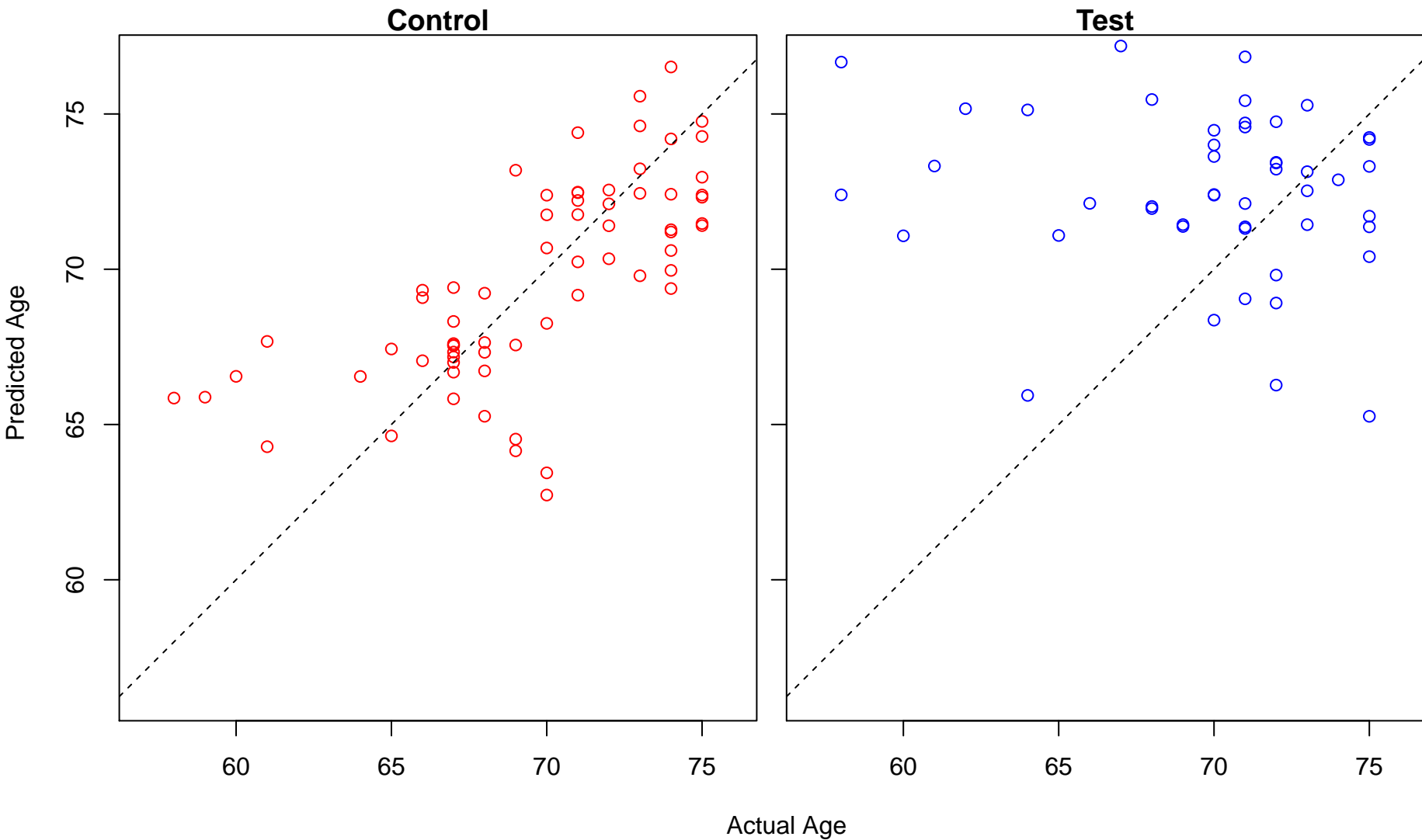
fatty acid beta-oxidation using acyl-CoA dehydrogenase (Score: 2.108718)



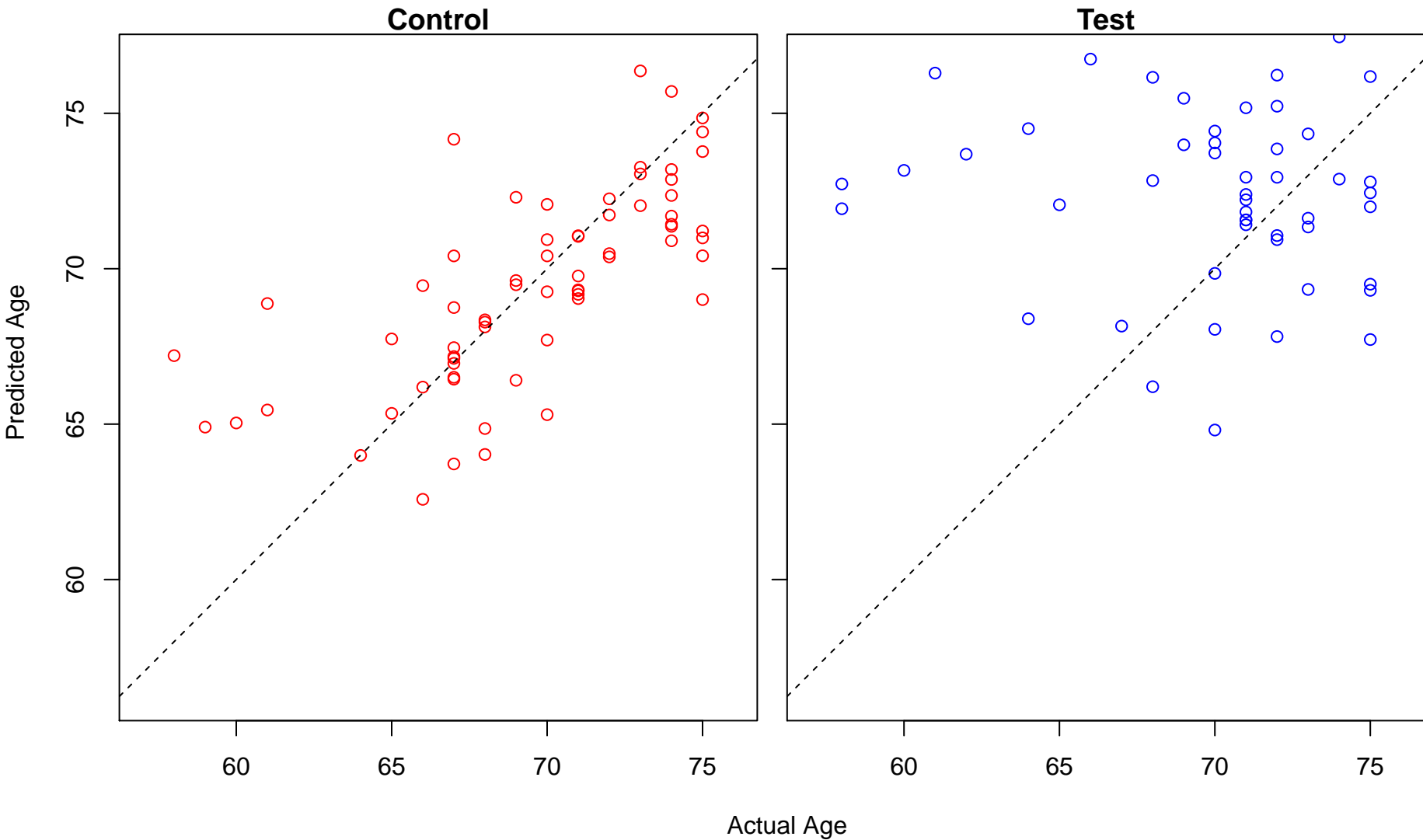
phosphatidylserine metabolic process (Score: 2.108001)



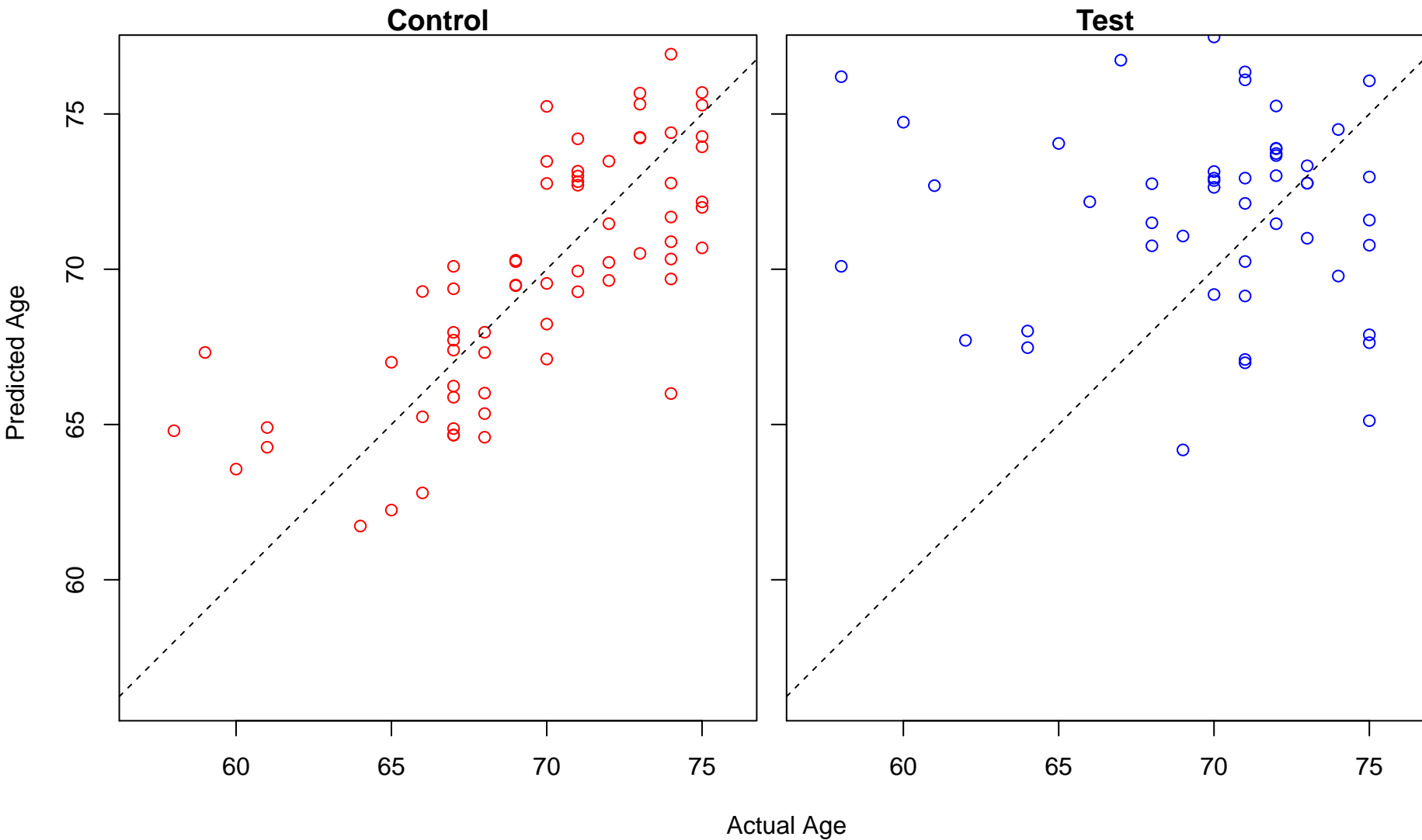
positive regulation of G1/S transition of mitotic cell cycle (Score: 2.101229)



alditol phosphate metabolic process (Score: 2.093461)

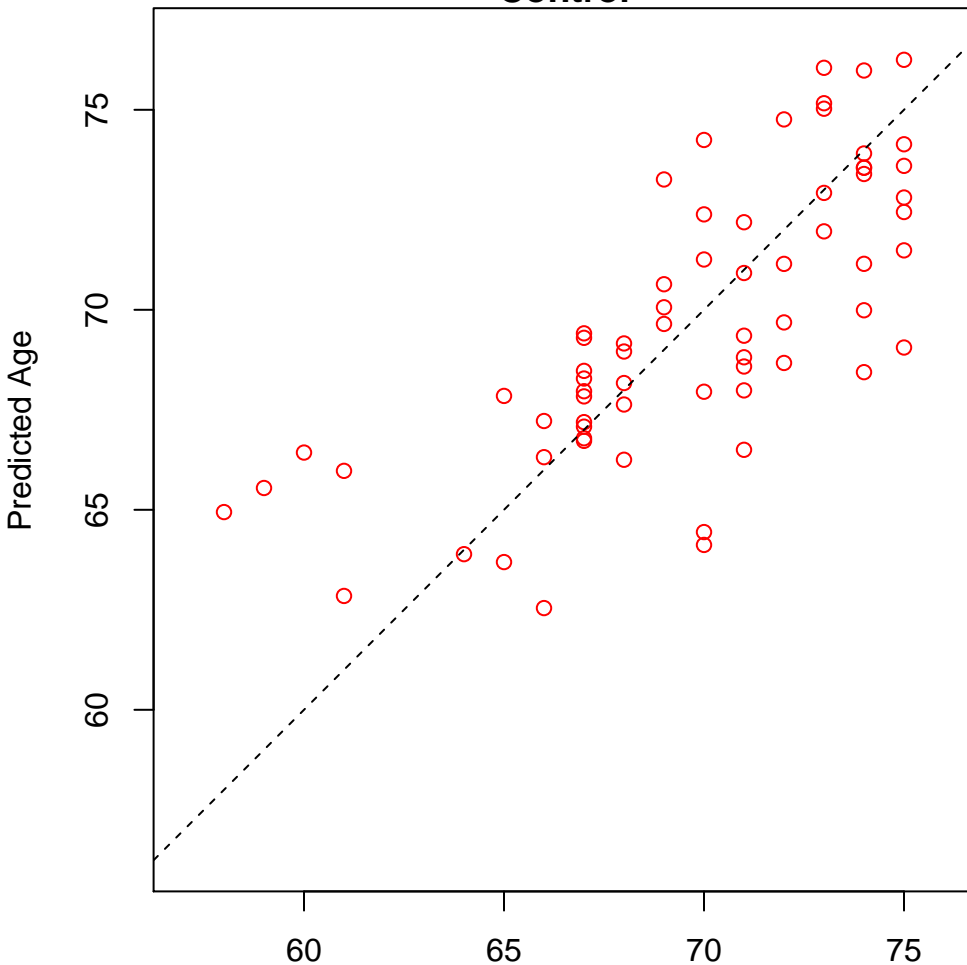


regulation of necrotic cell death (Score: 2.092329)

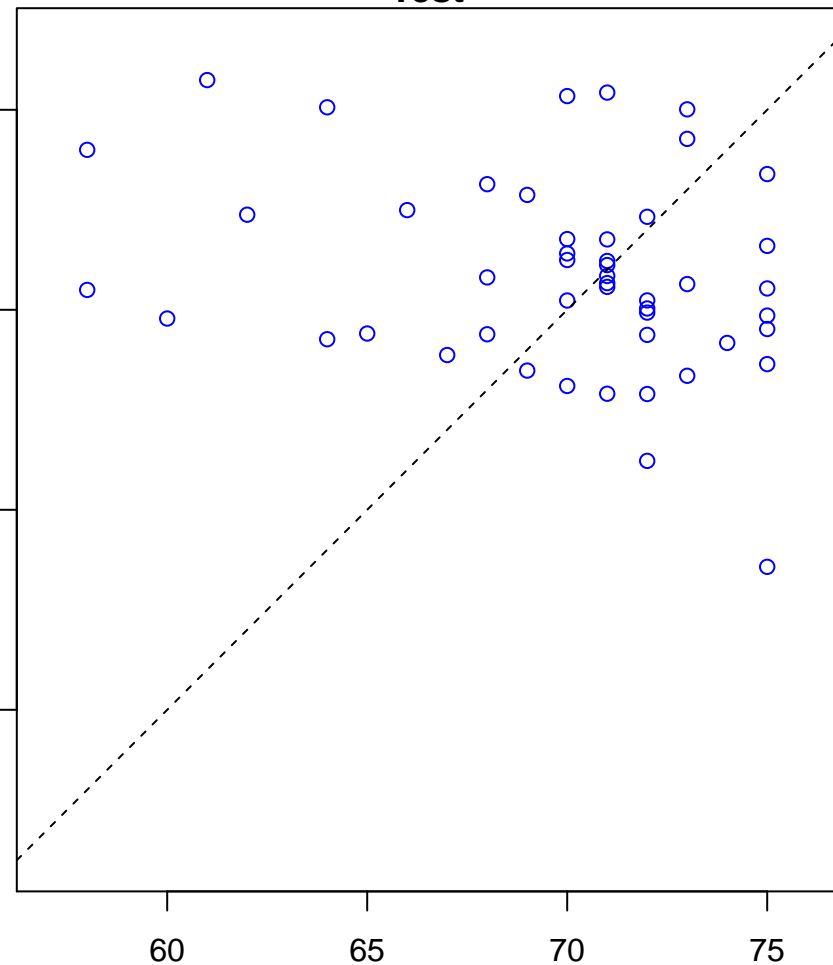


regulation of T cell apoptotic process (Score: 2.081361)

Control

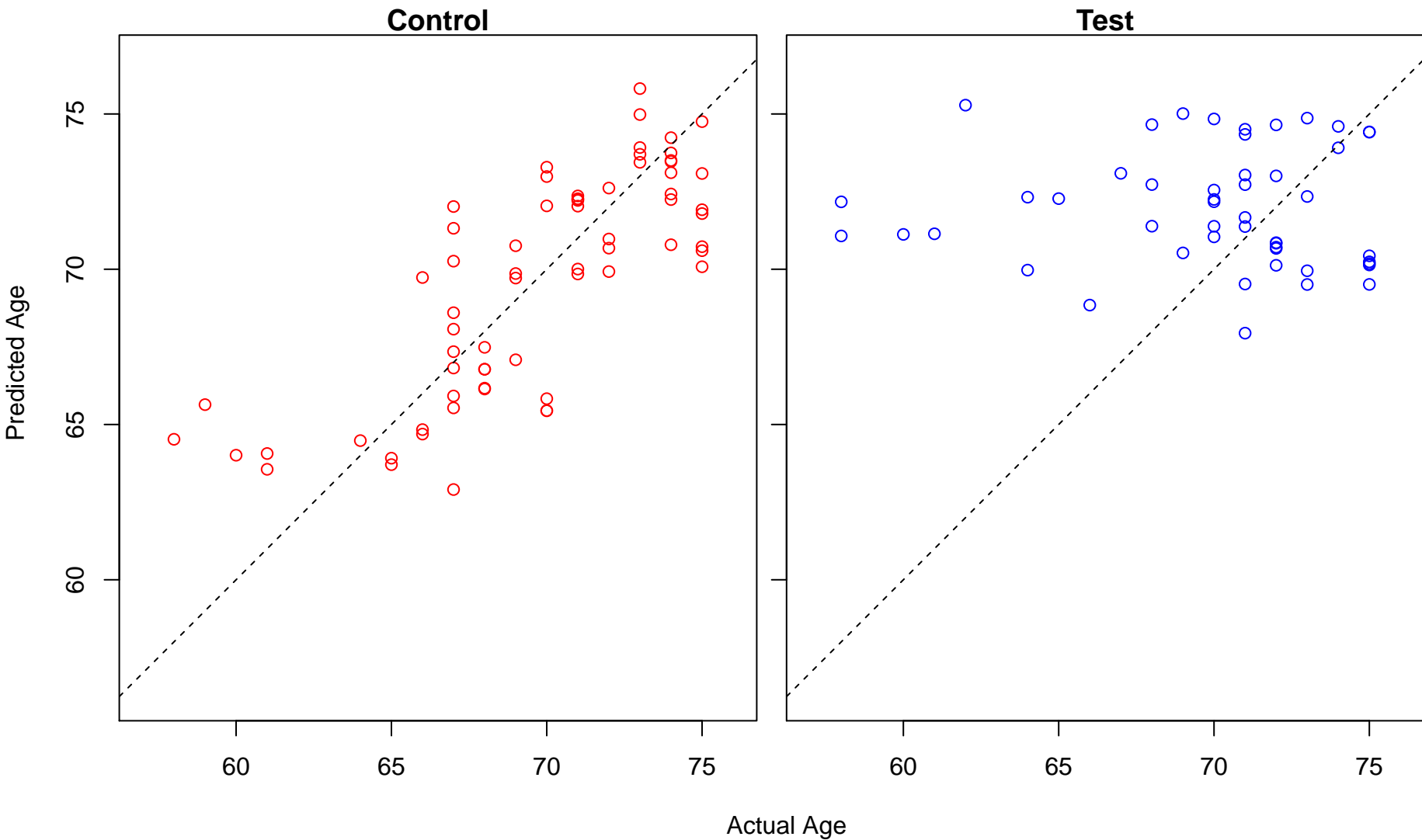


Test



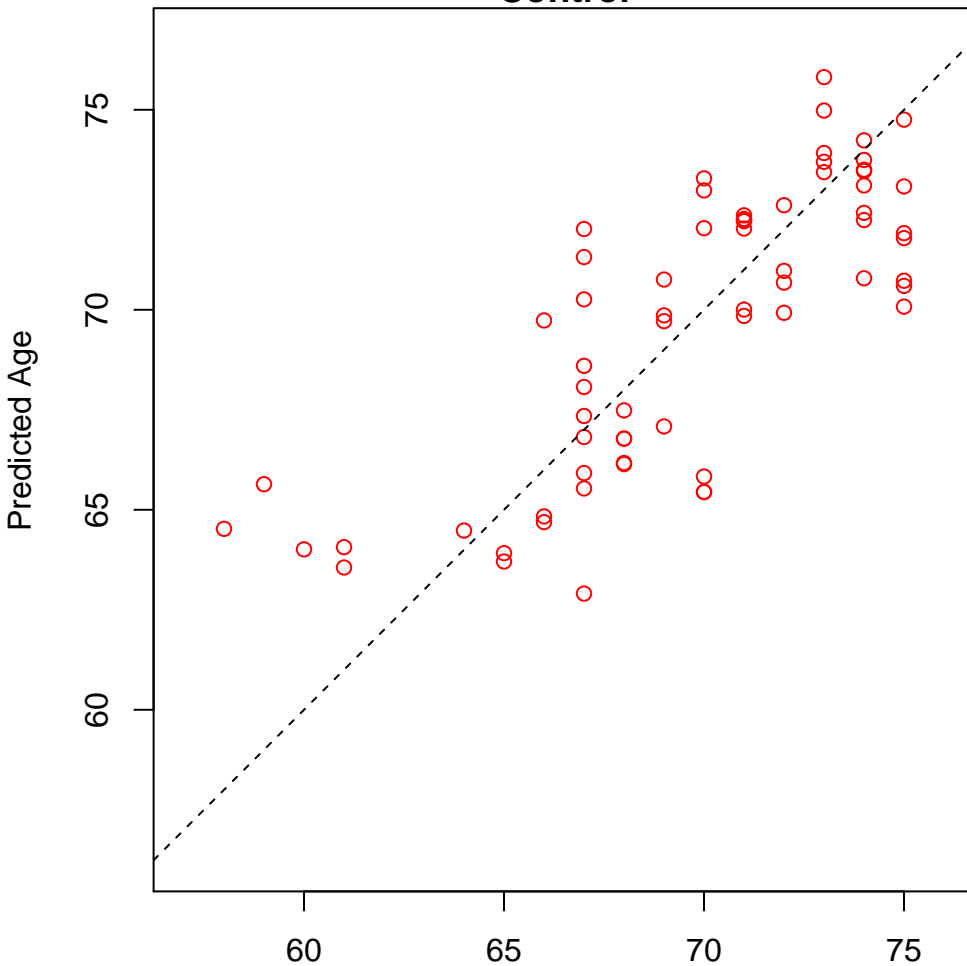
Actual Age

viral budding (Score: 2.071559)

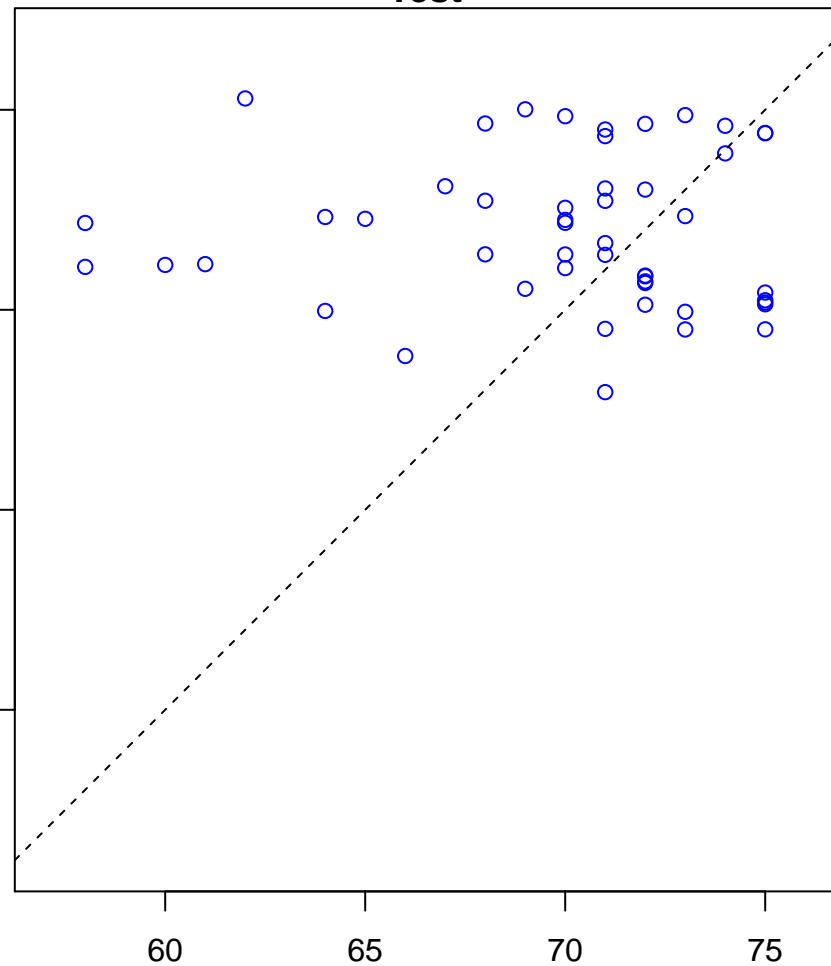


multi-organism organelle organization (Score: 2.071559)

Control

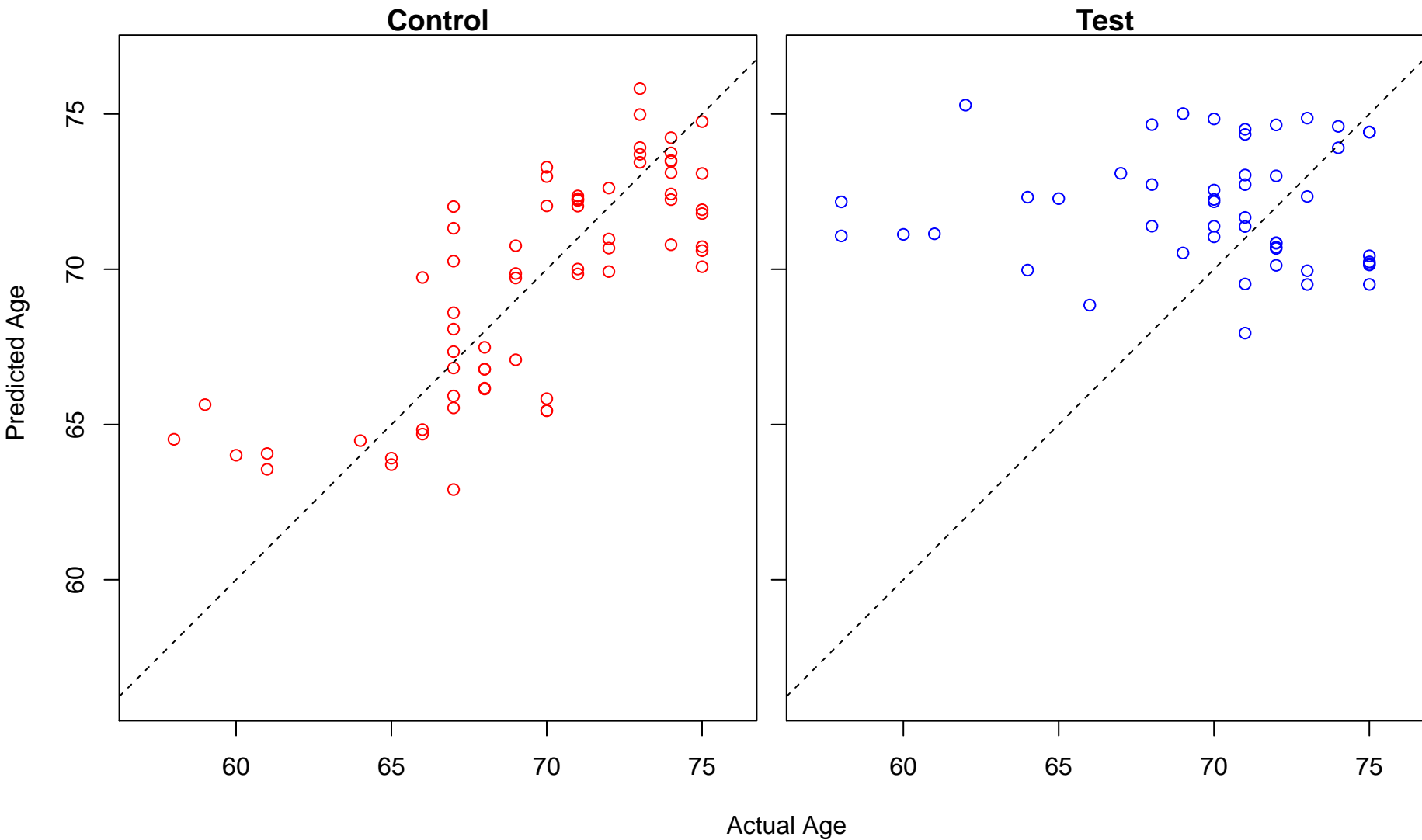


Test

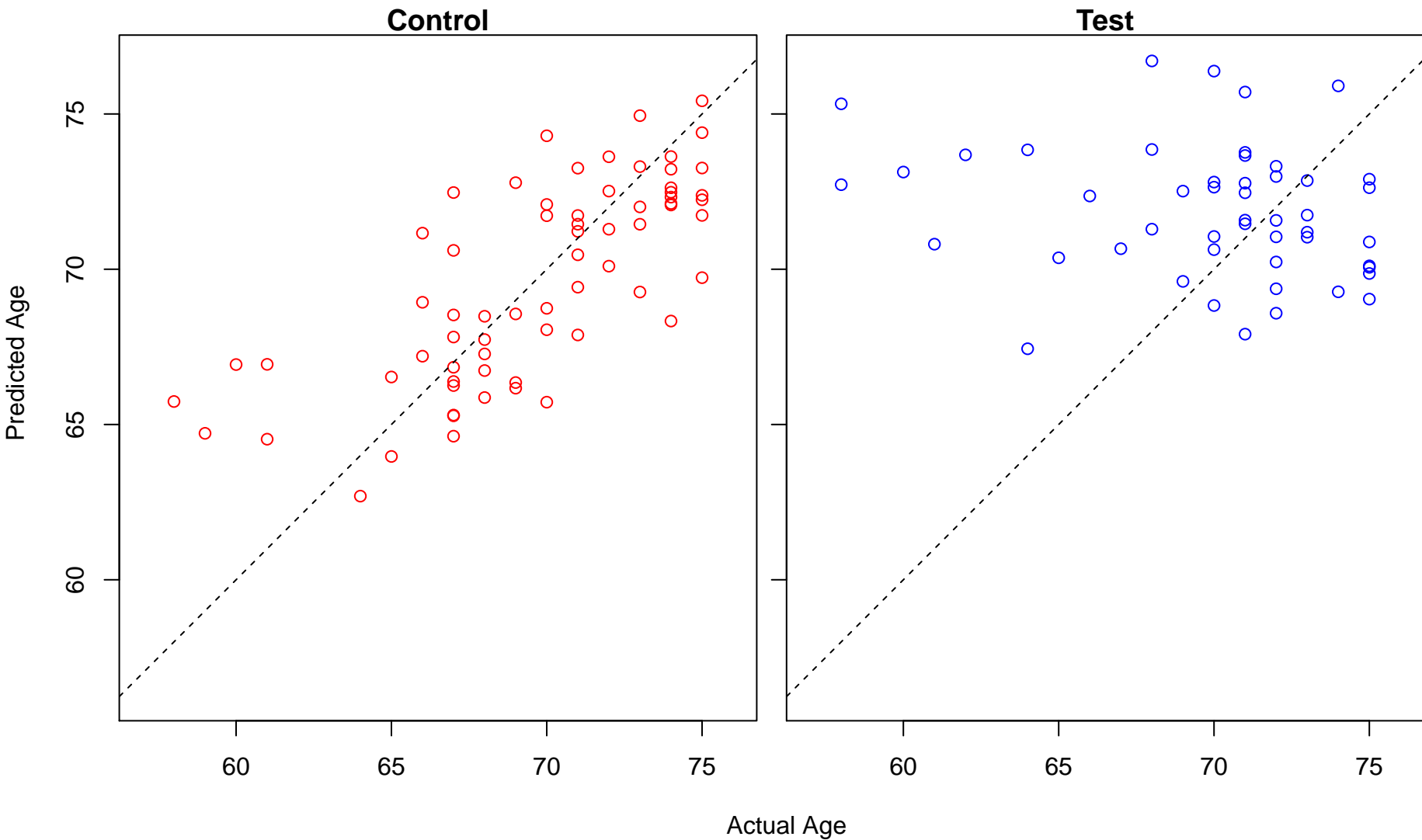


Actual Age

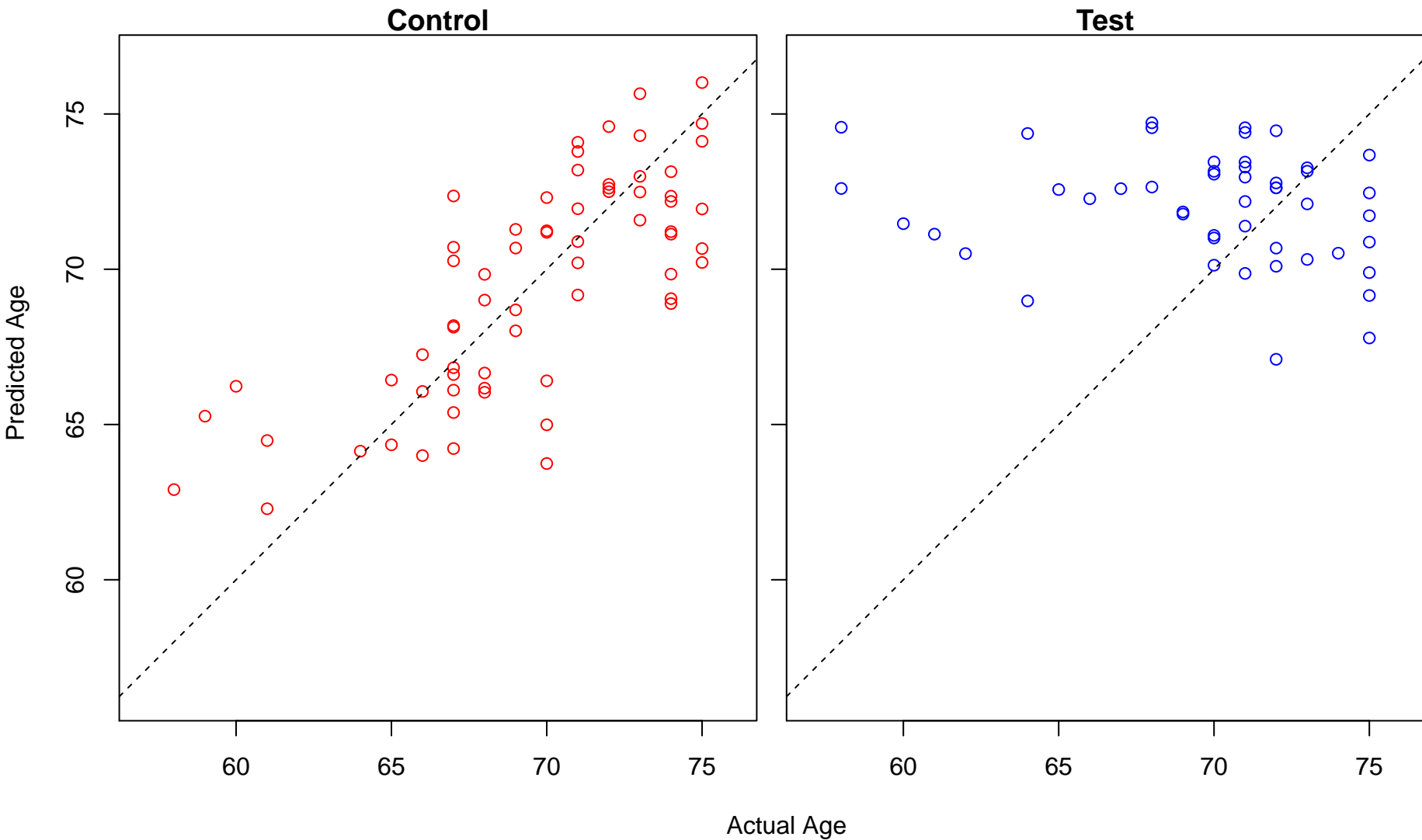
multi-organism membrane budding (Score: 2.071559)



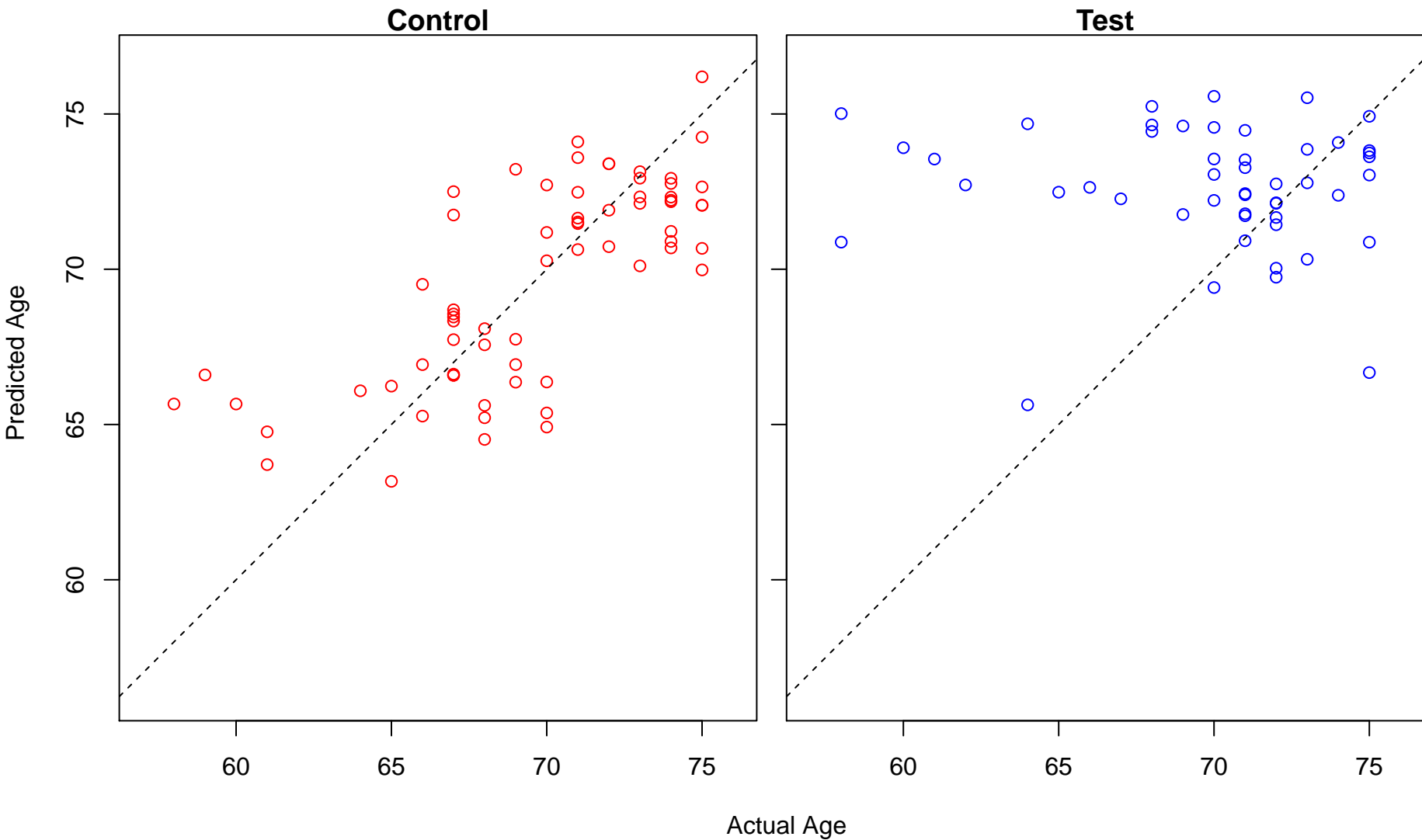
chromosome condensation (Score: 2.067387)



C-terminal protein lipidation (Score: 2.052867)

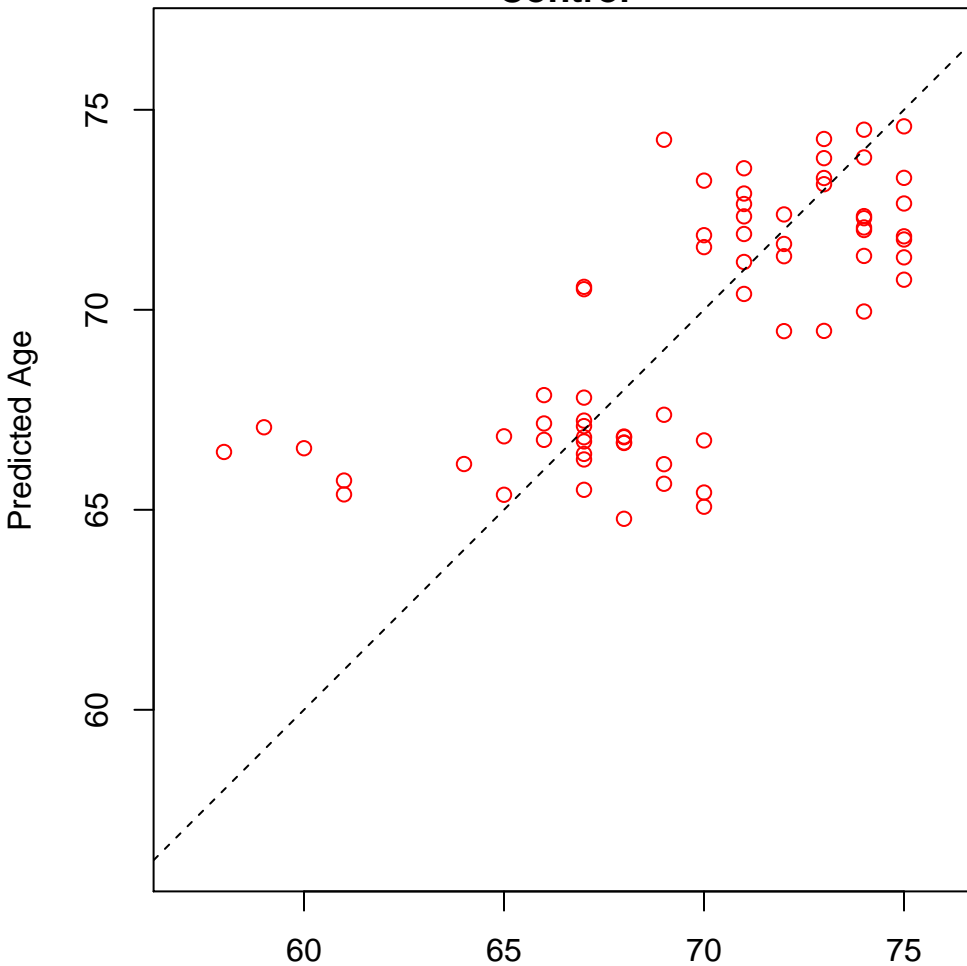


cAMP-mediated signaling (Score: 2.040064)

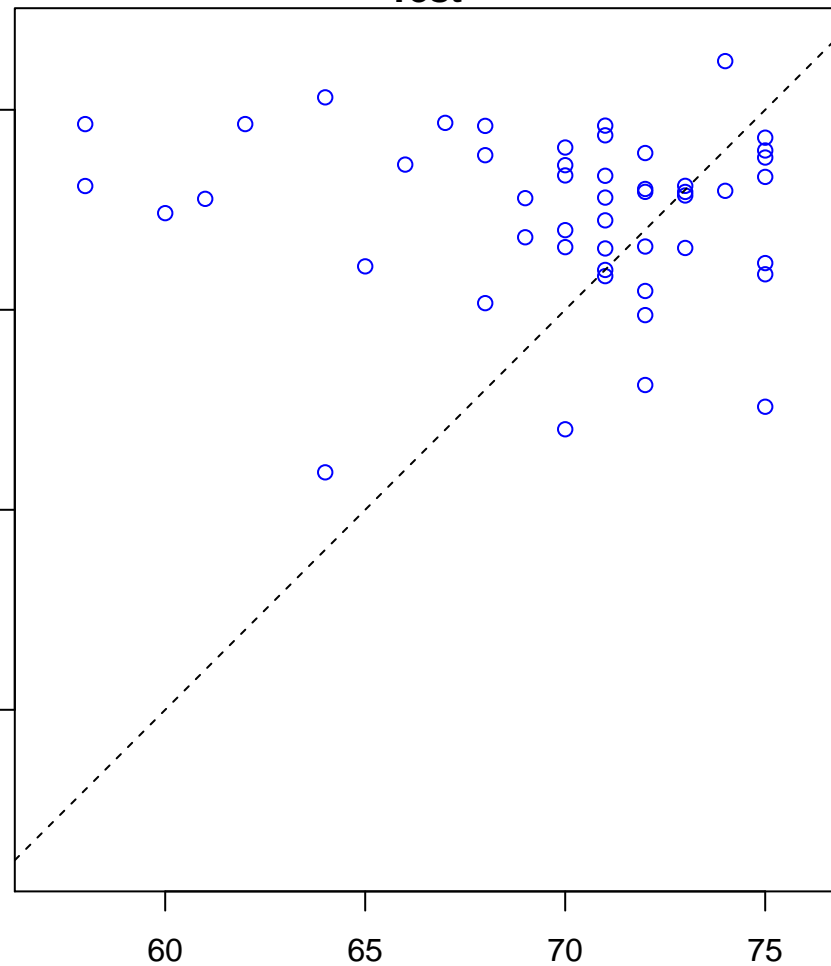


actin polymerization or depolymerization (Score: 2.026498)

Control



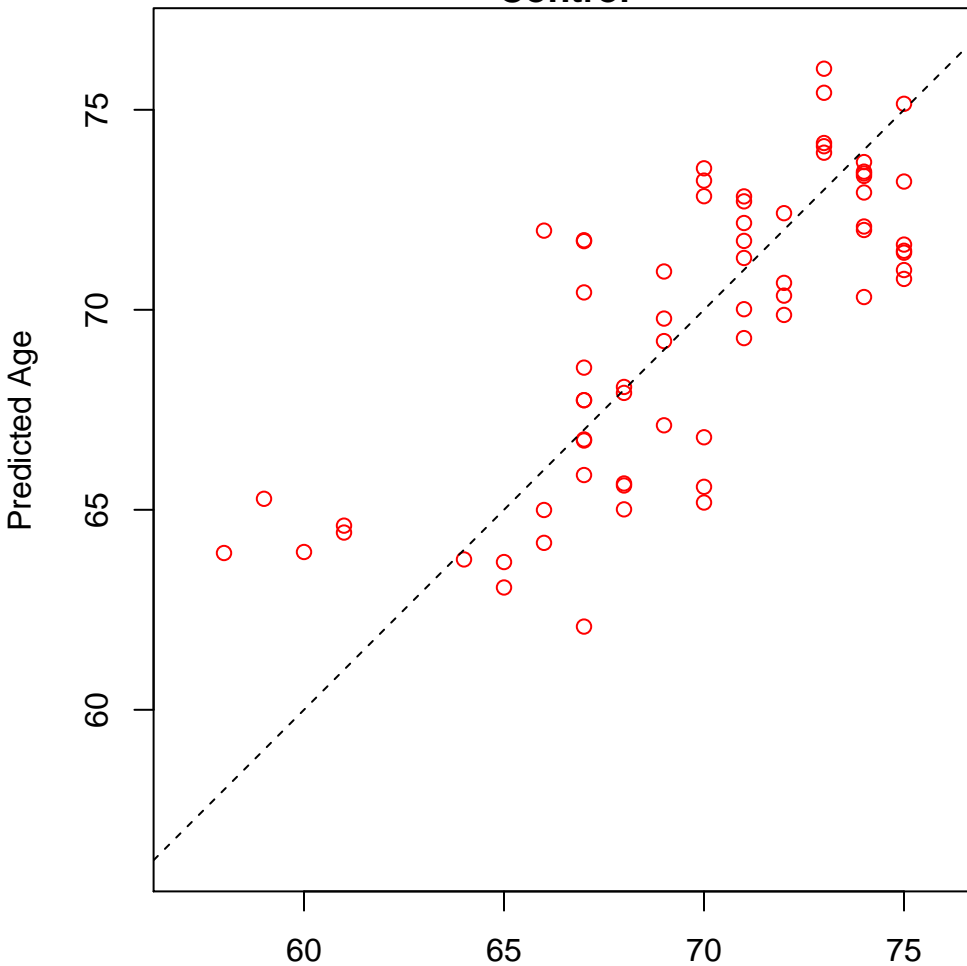
Test



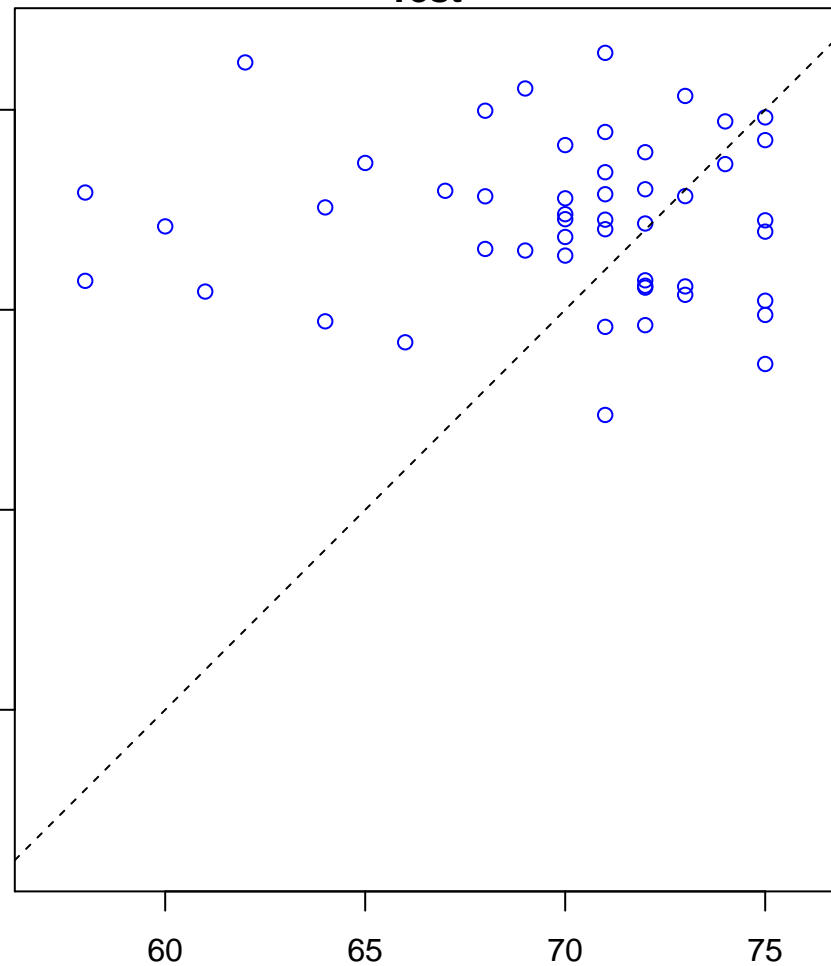
Actual Age

multi-organism membrane organization (Score: 2.023182)

Control

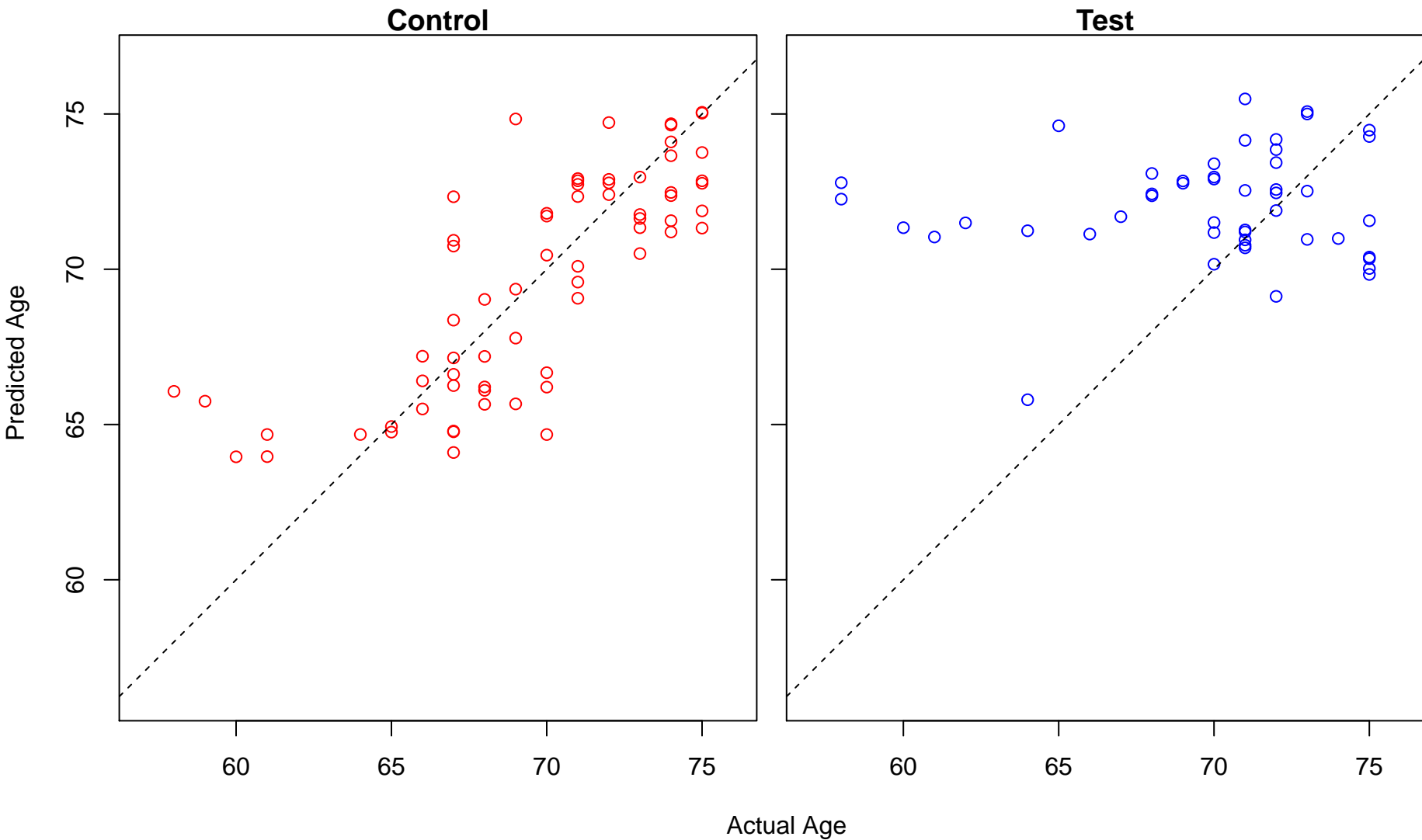


Test

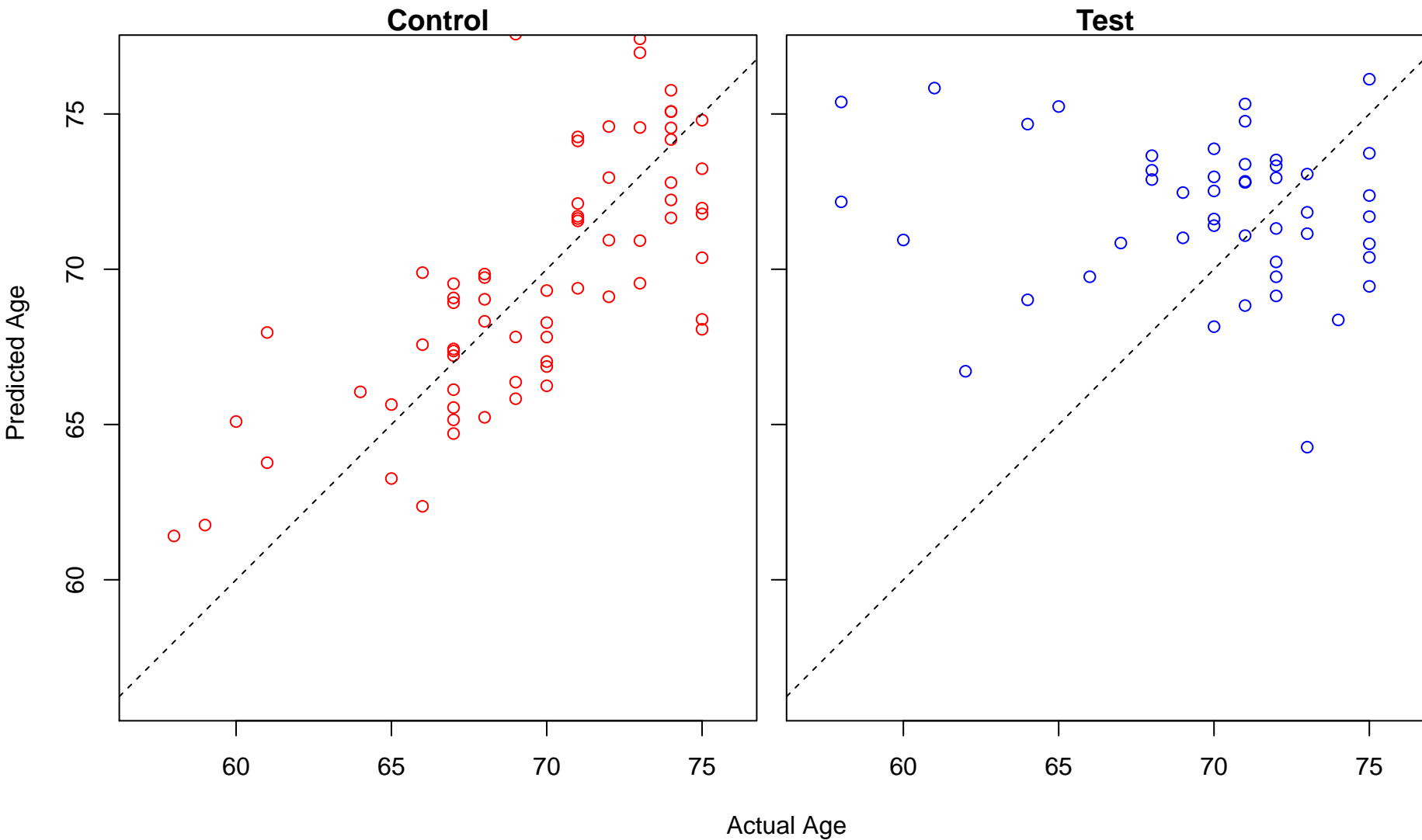


Actual Age

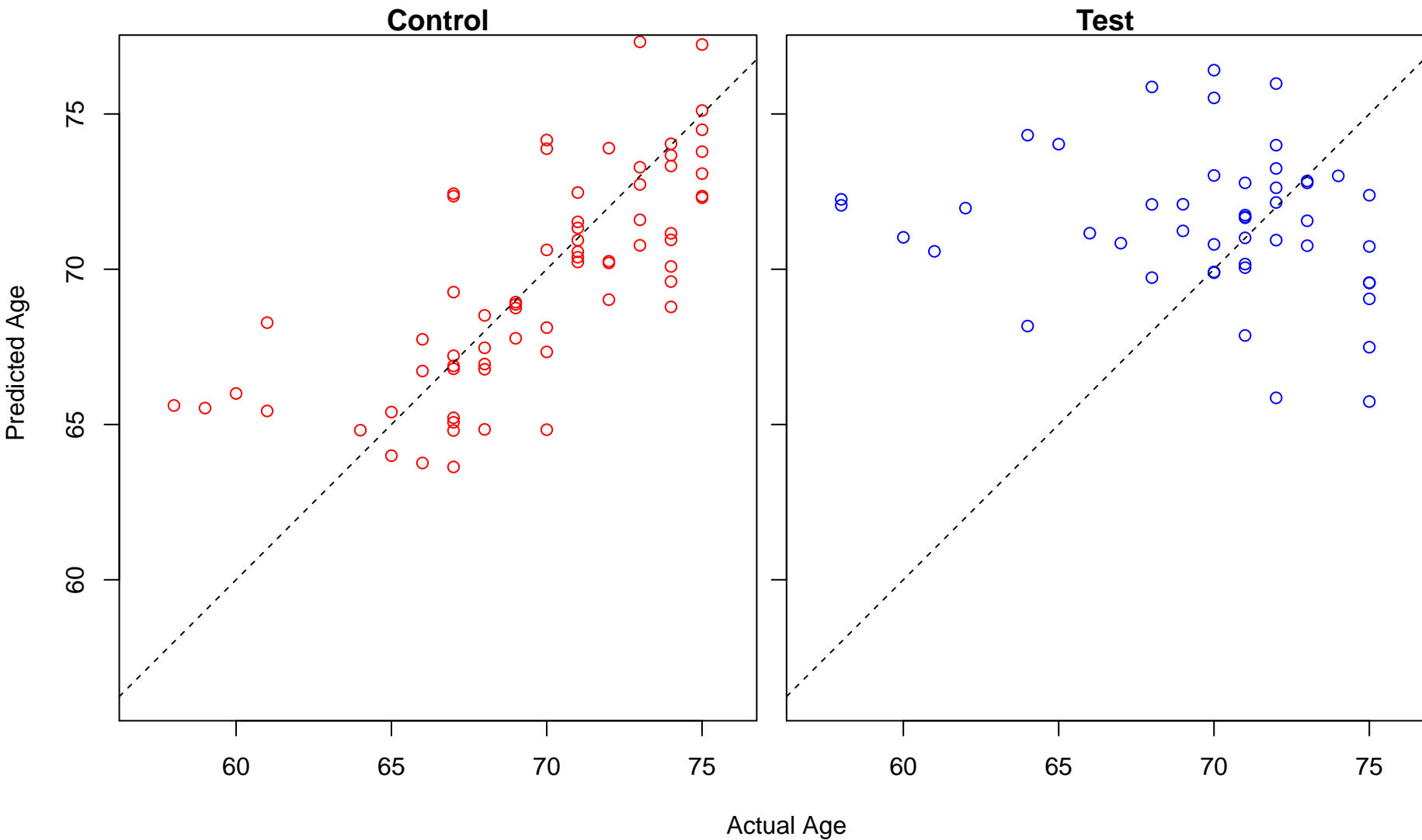
nuclear-transcribed mRNA catabolic process, exonucleolytic (Score: 2.022756)



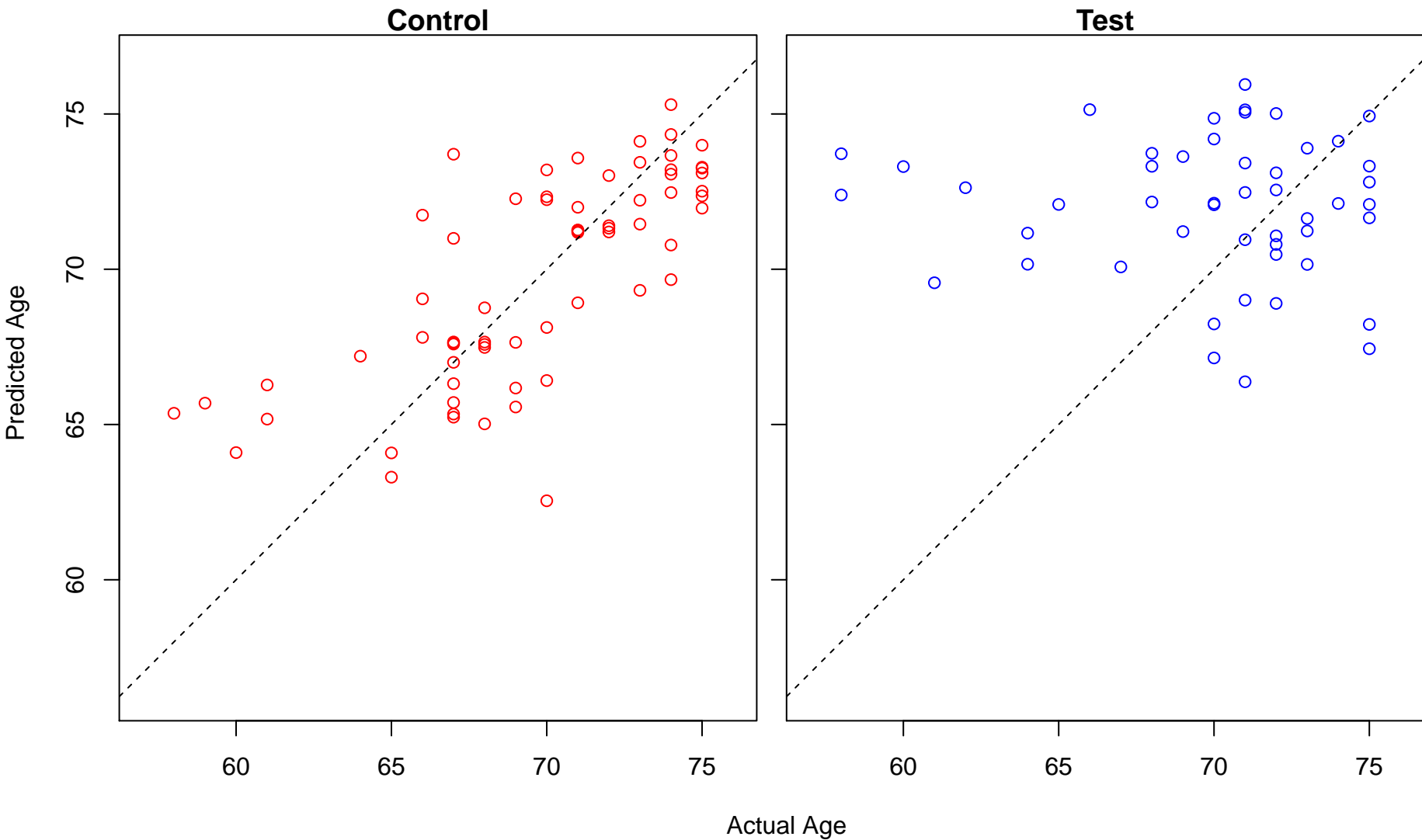
branched-chain amino acid catabolic process (Score: 2.018971)



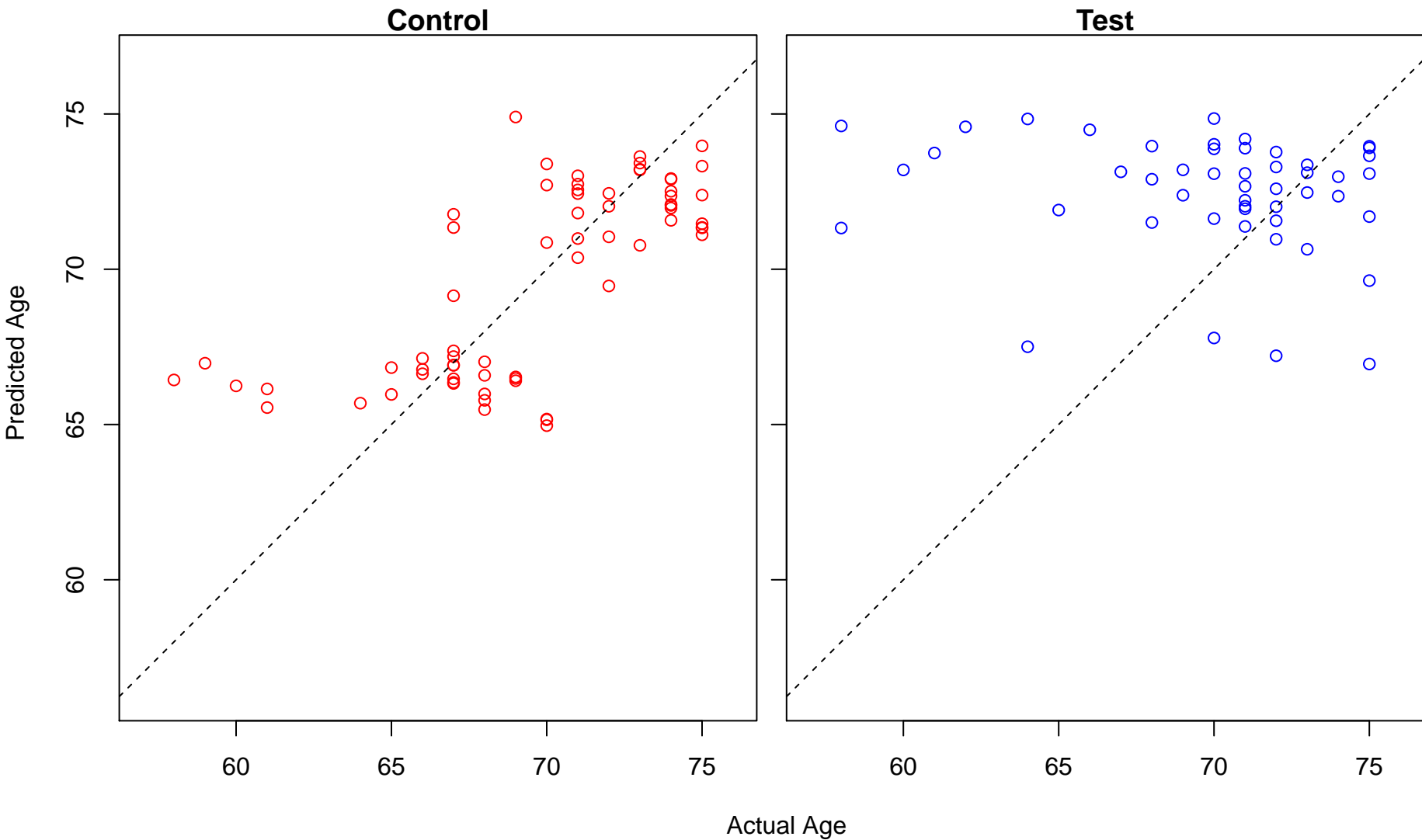
regulation of DNA-dependent DNA replication (Score: 2.014257)



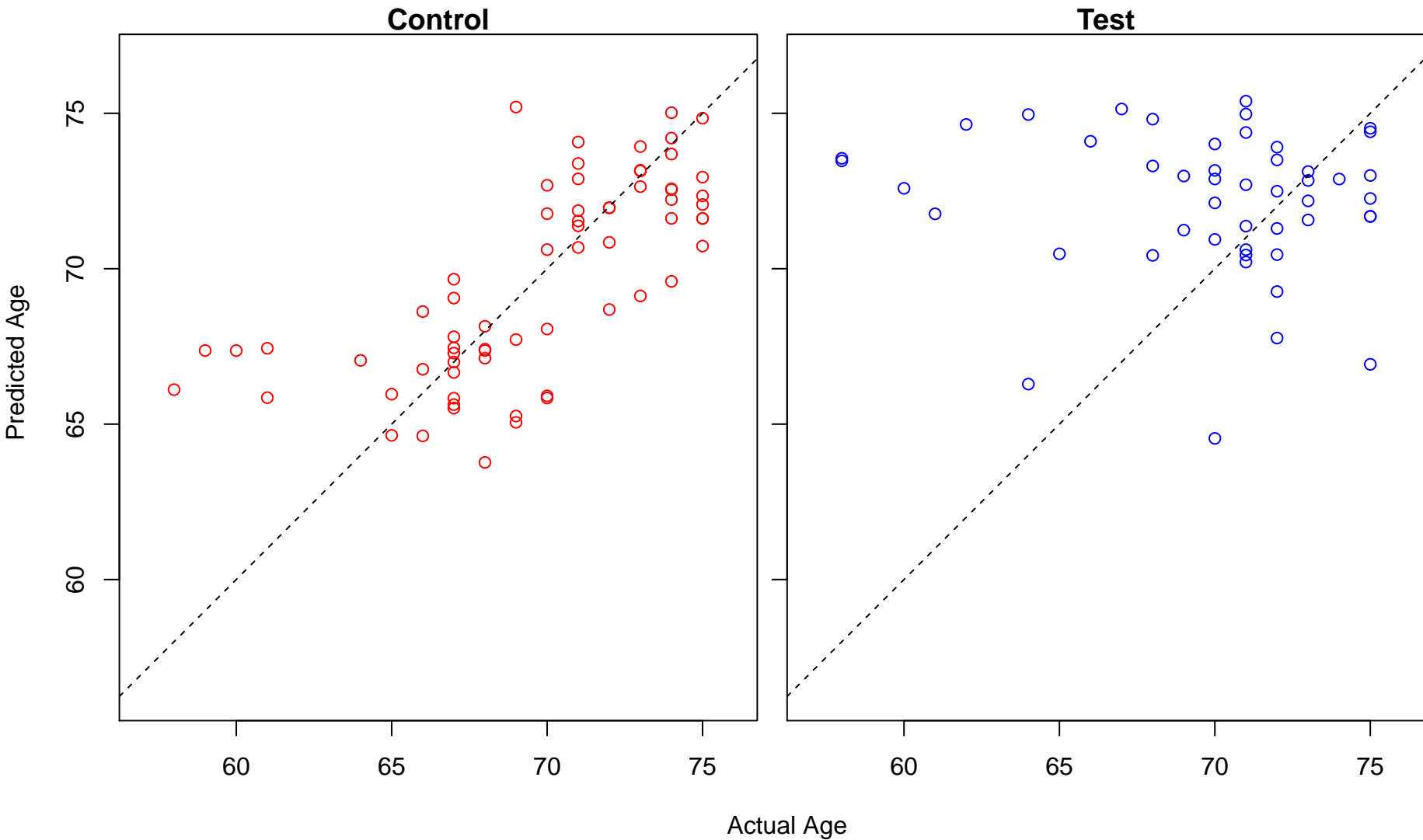
positive regulation of myeloid leukocyte differentiation (Score: 2.013541)



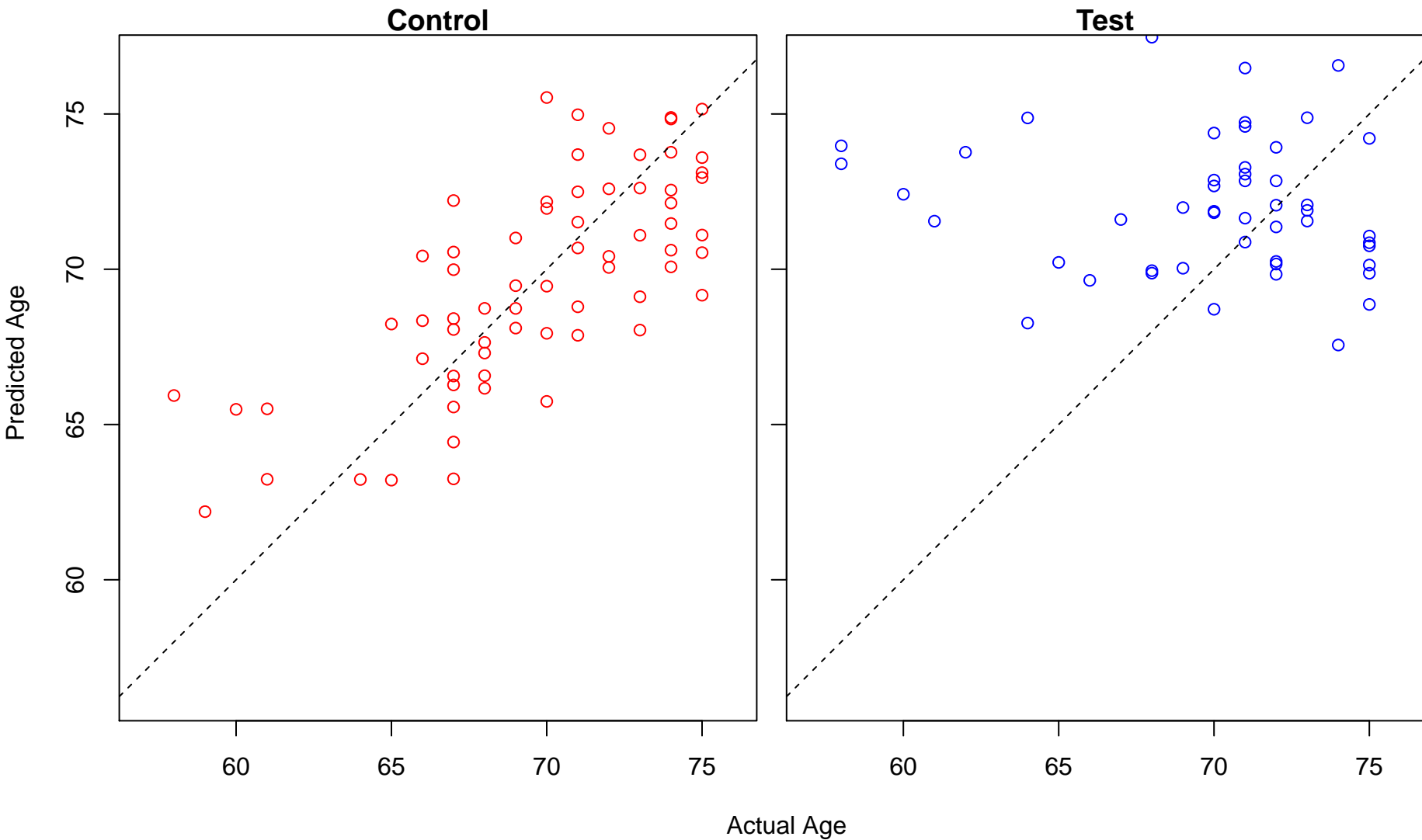
NADH dehydrogenase complex assembly (Score: 2.009560)



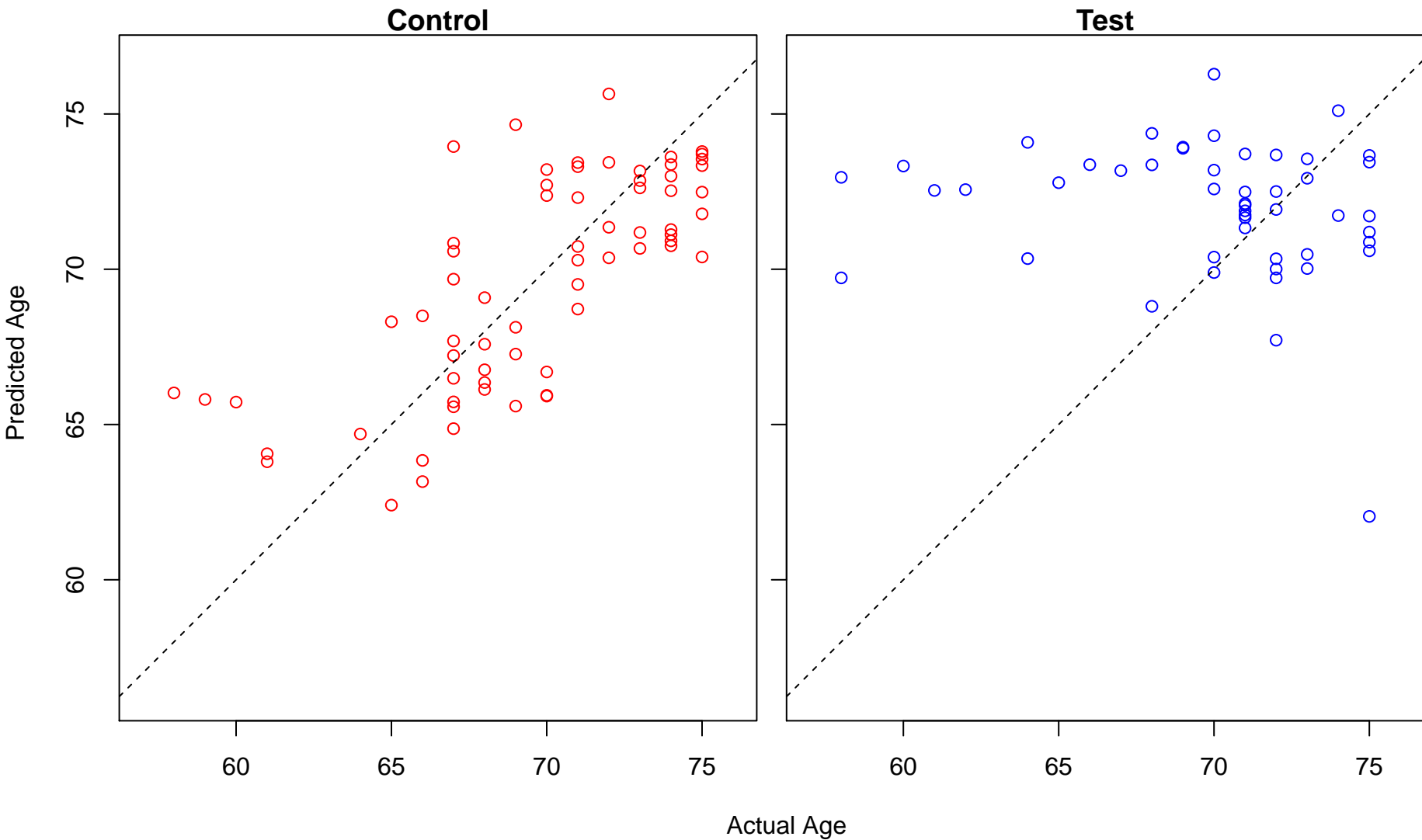
positive regulation of monocyte chemotaxis (Score: 1.994253)



negative regulation of RNA splicing (Score: 1.992932)

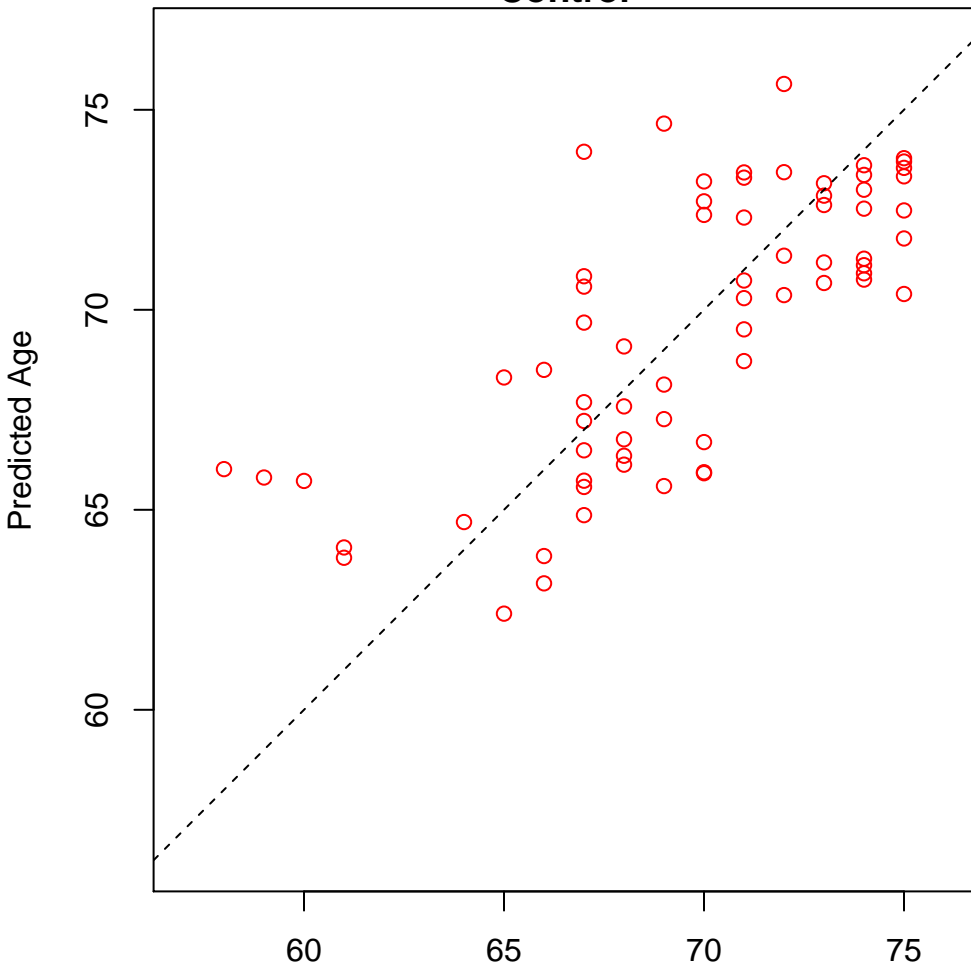


protein mannosylation (Score: 1.991270)

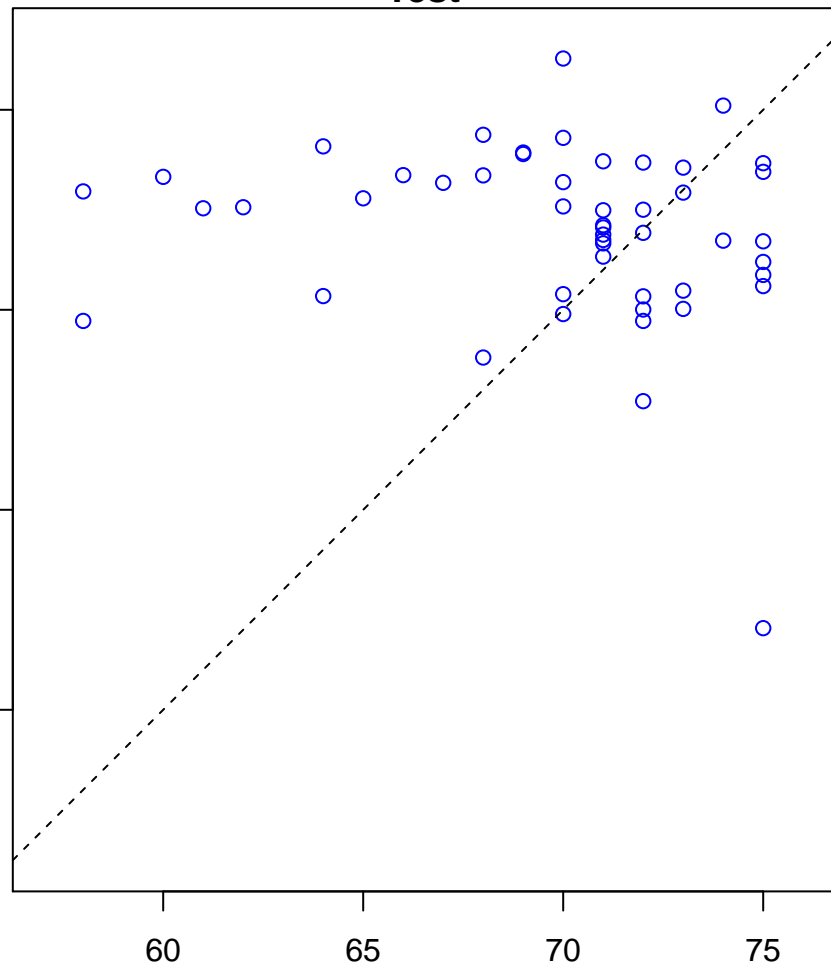


protein O-linked mannosylation (Score: 1.991270)

Control



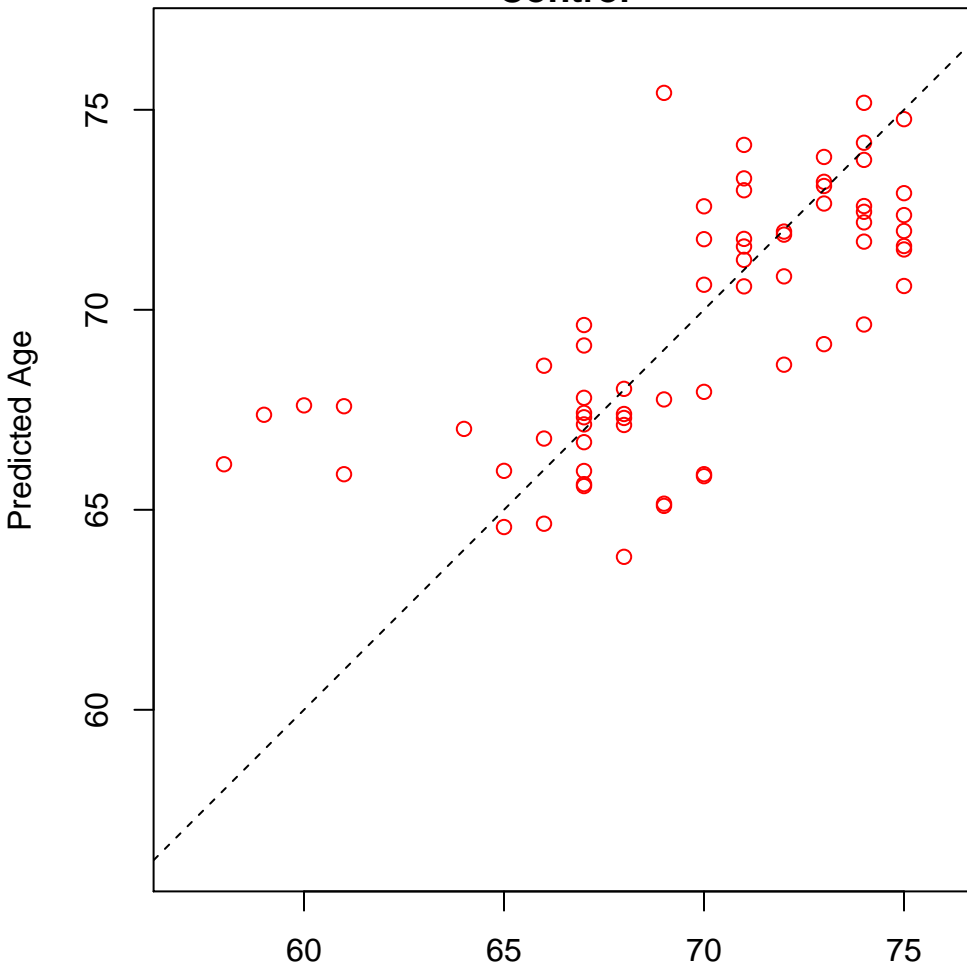
Test



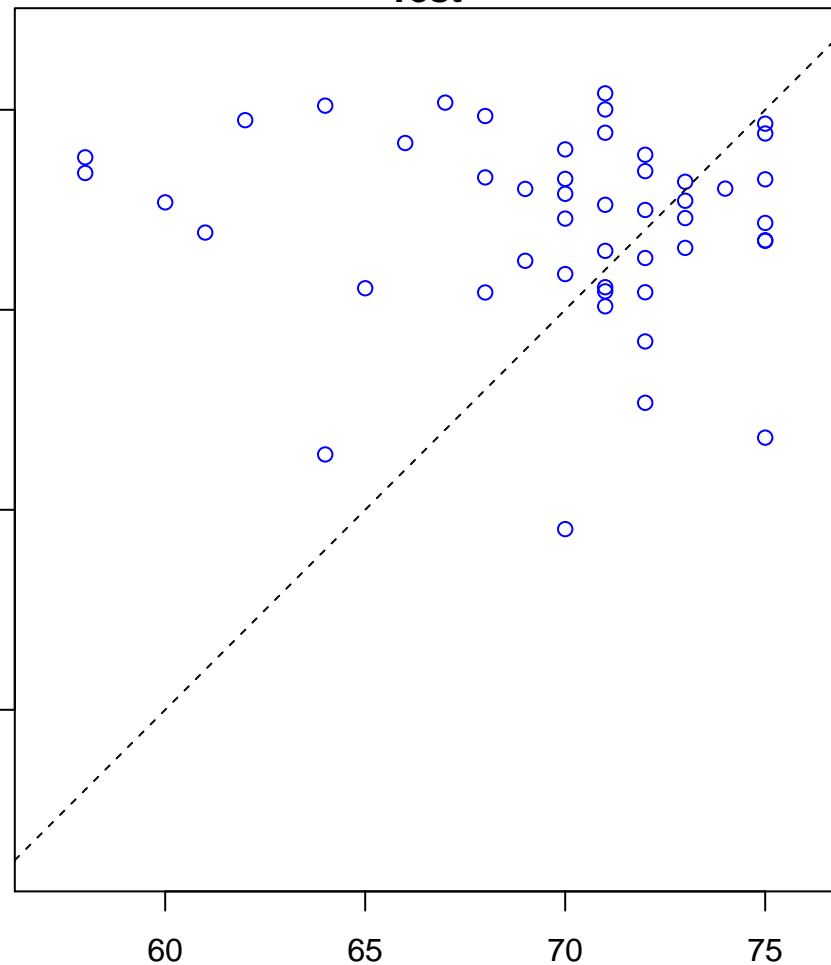
Actual Age

regulation of monocyte chemotaxis (Score: 1.990305)

Control

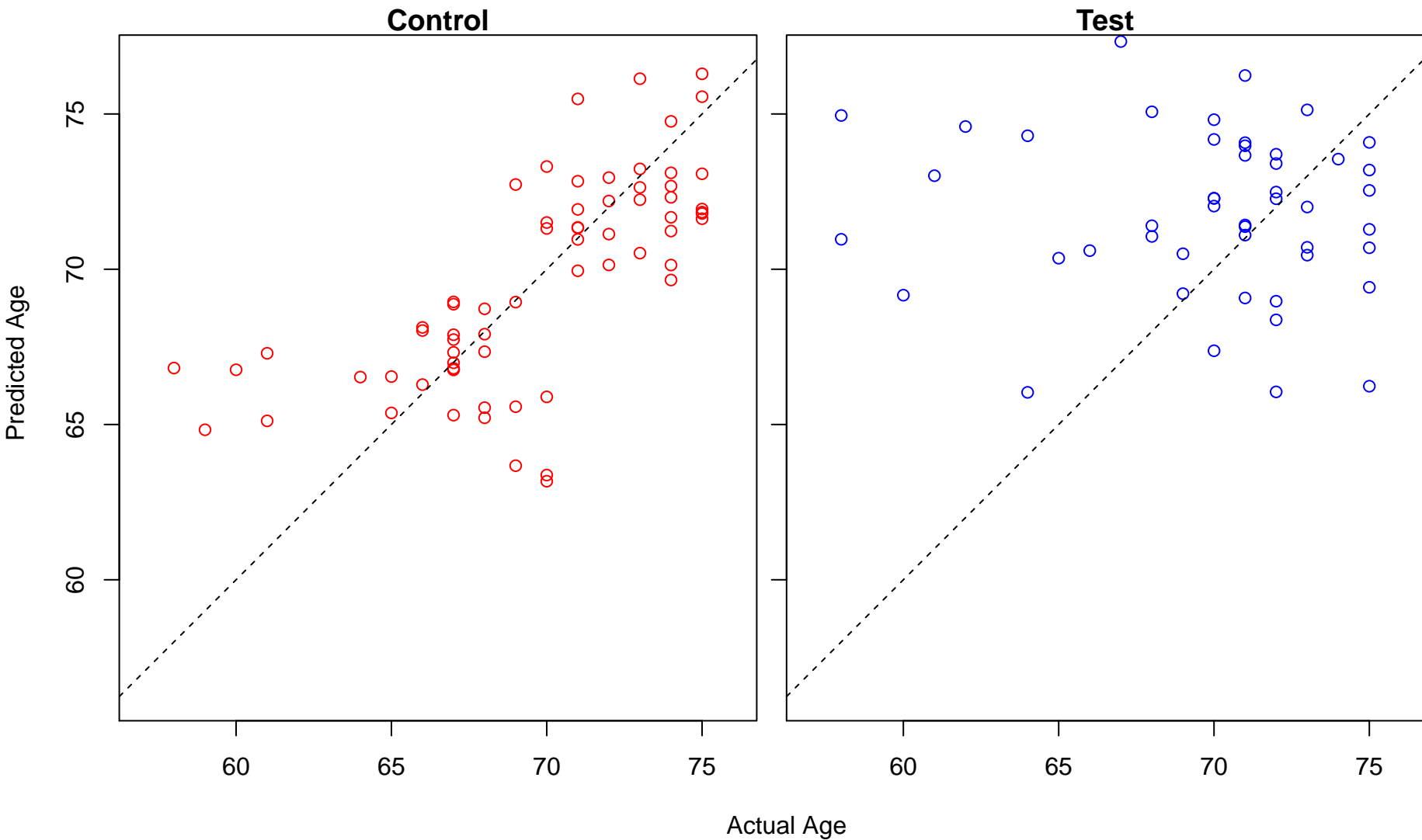


Test



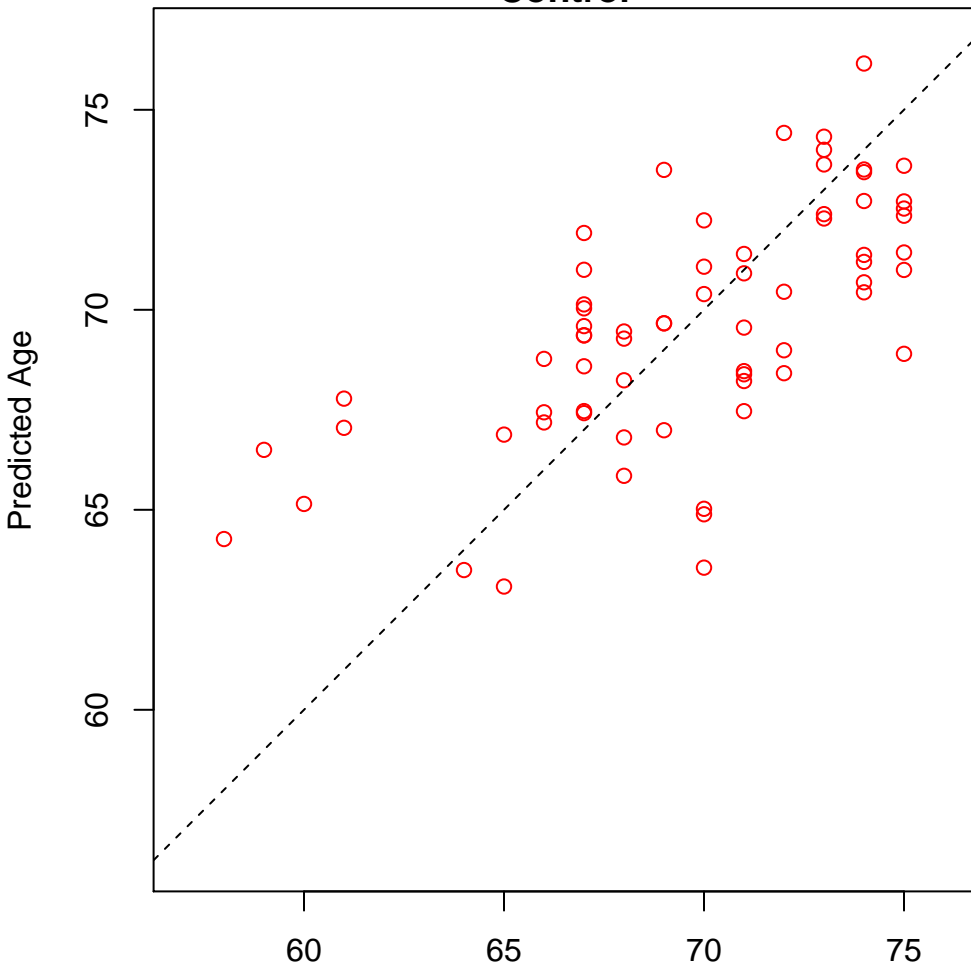
Actual Age

positive regulation of cell cycle G1/S phase transition (Score: 1.988185)

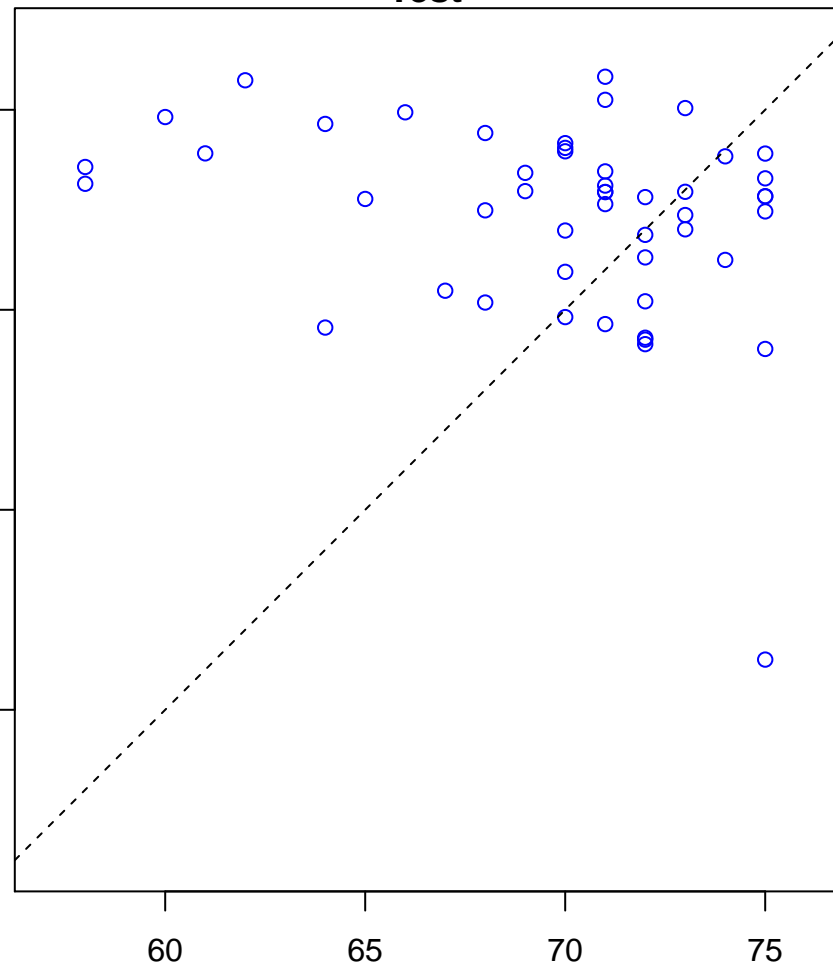


positive regulation of bone resorption (Score: 1.985937)

Control



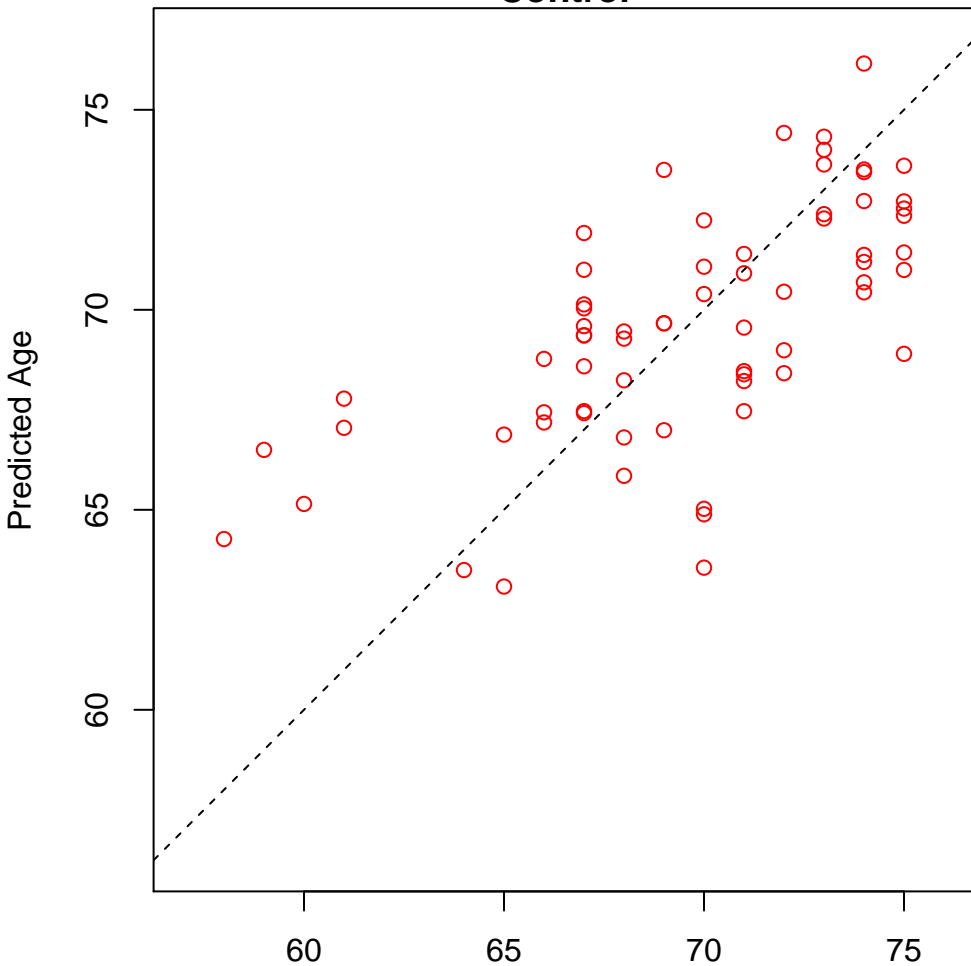
Test



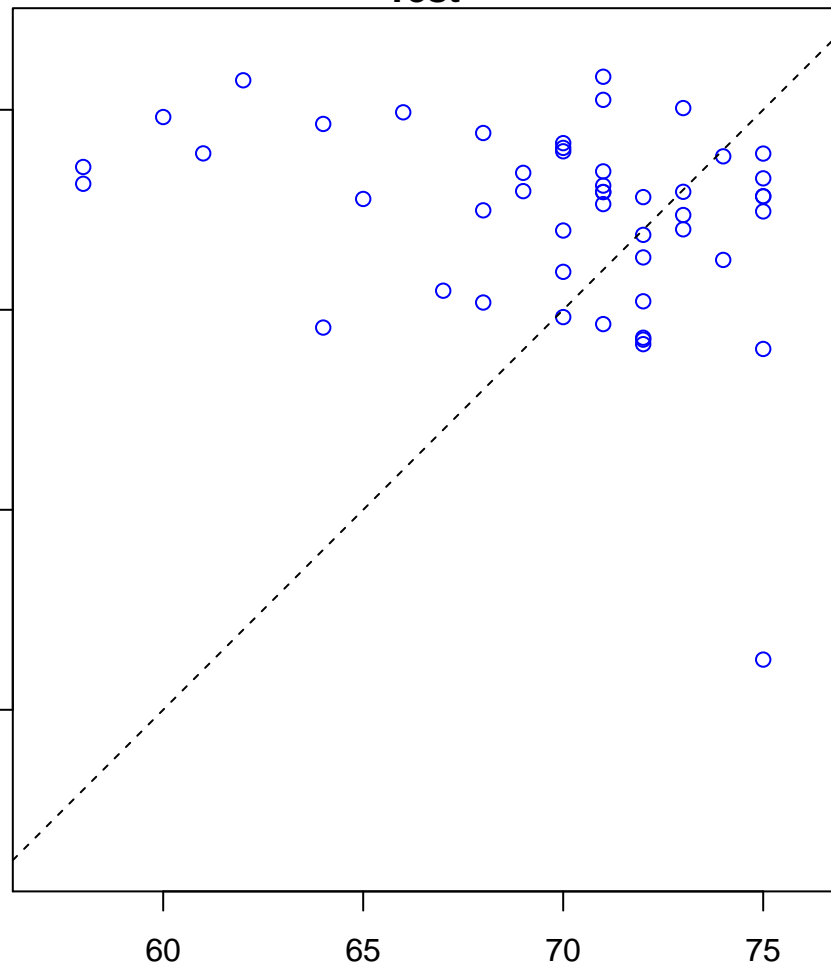
Actual Age

positive regulation of bone remodeling (Score: 1.985937)

Control

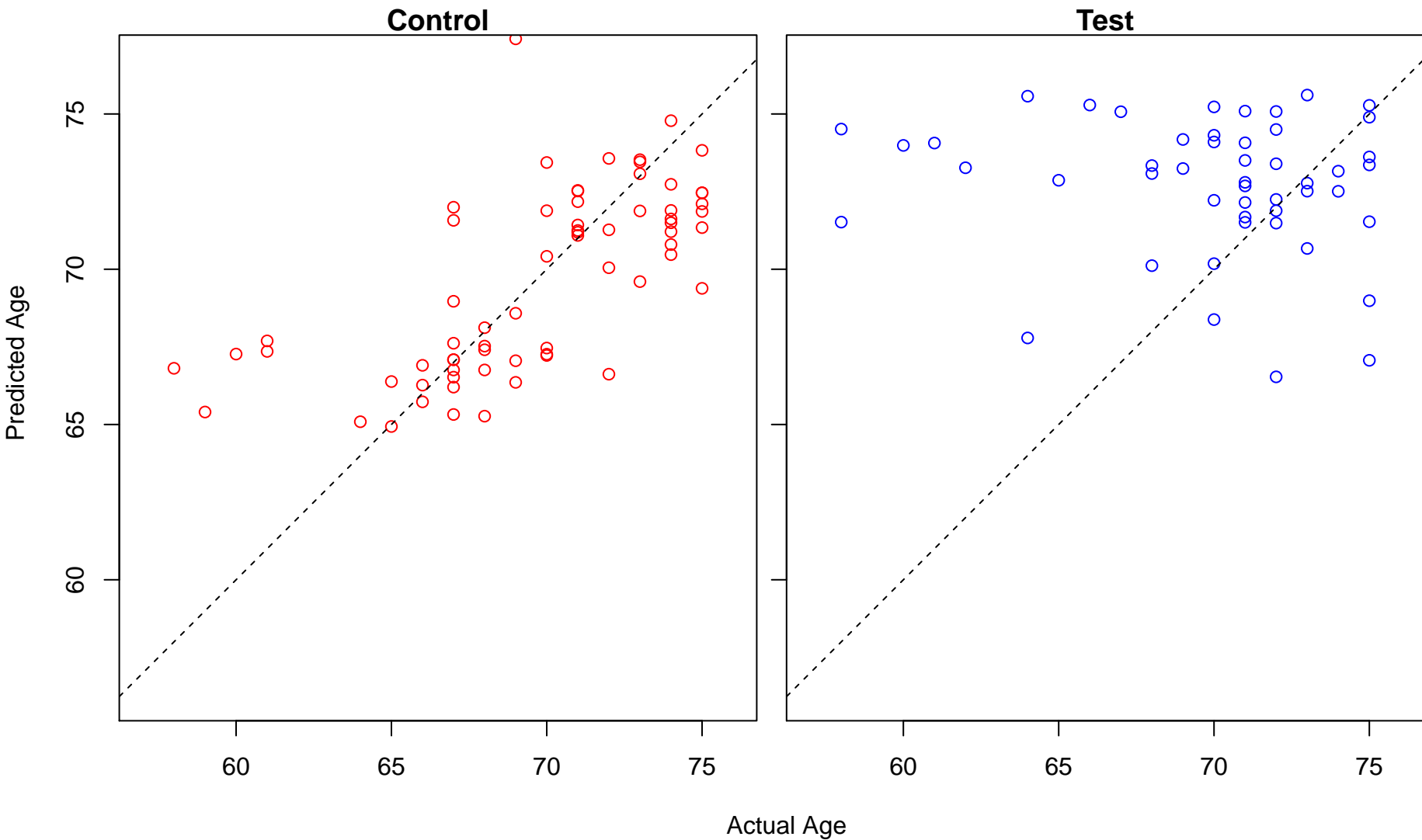


Test

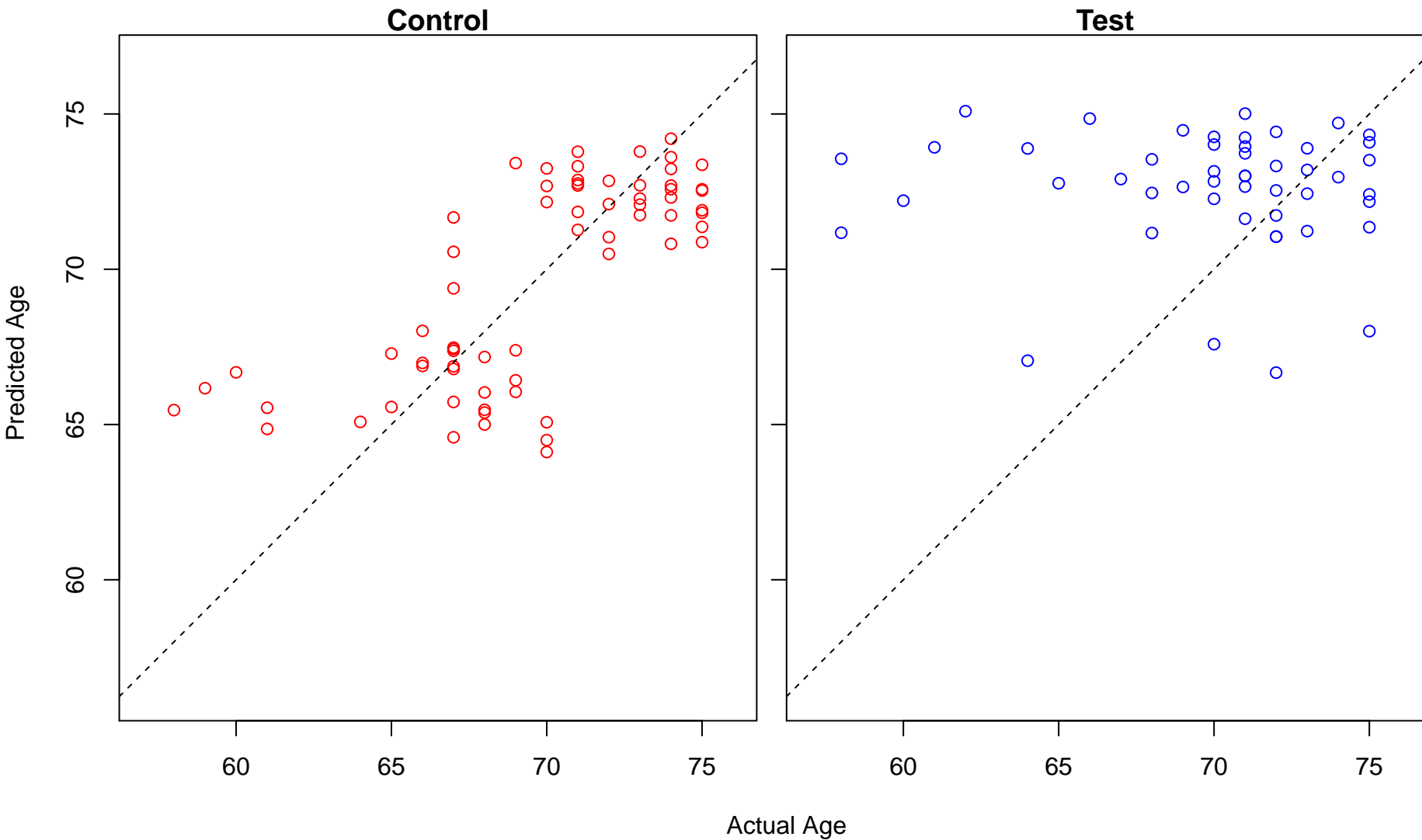


Actual Age

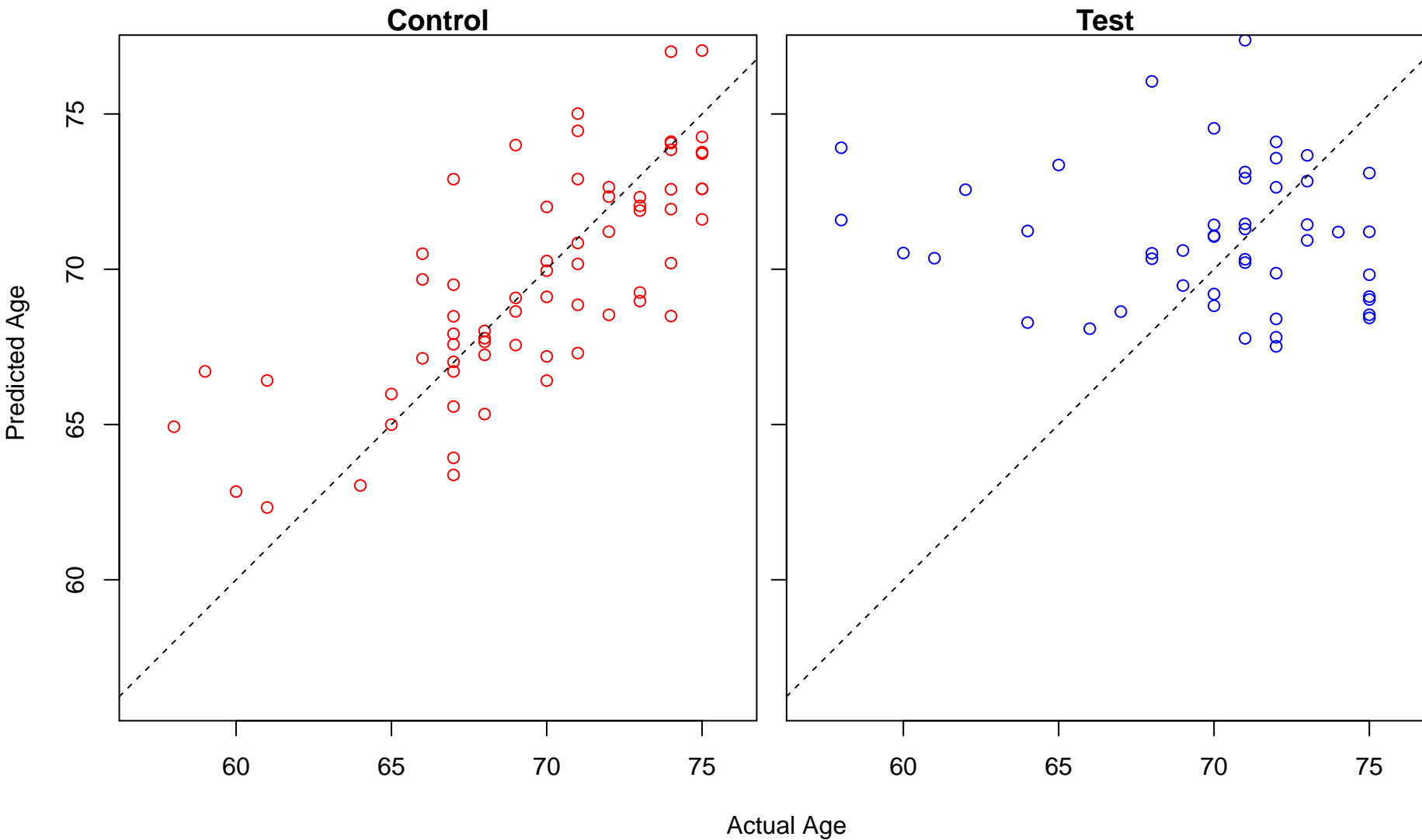
negative regulation of JUN kinase activity (Score: 1.985314)



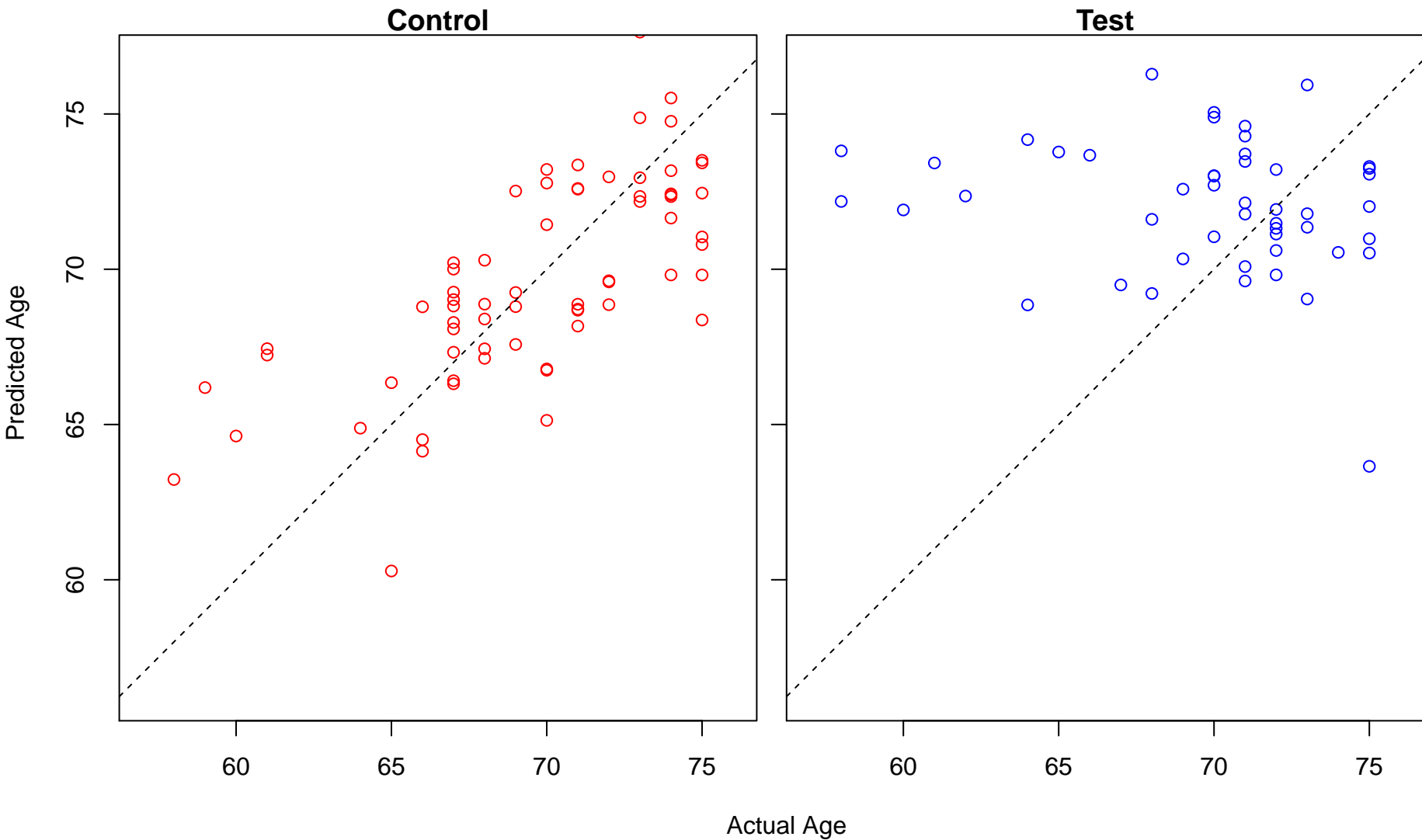
histone deubiquitination (Score: 1.984809)



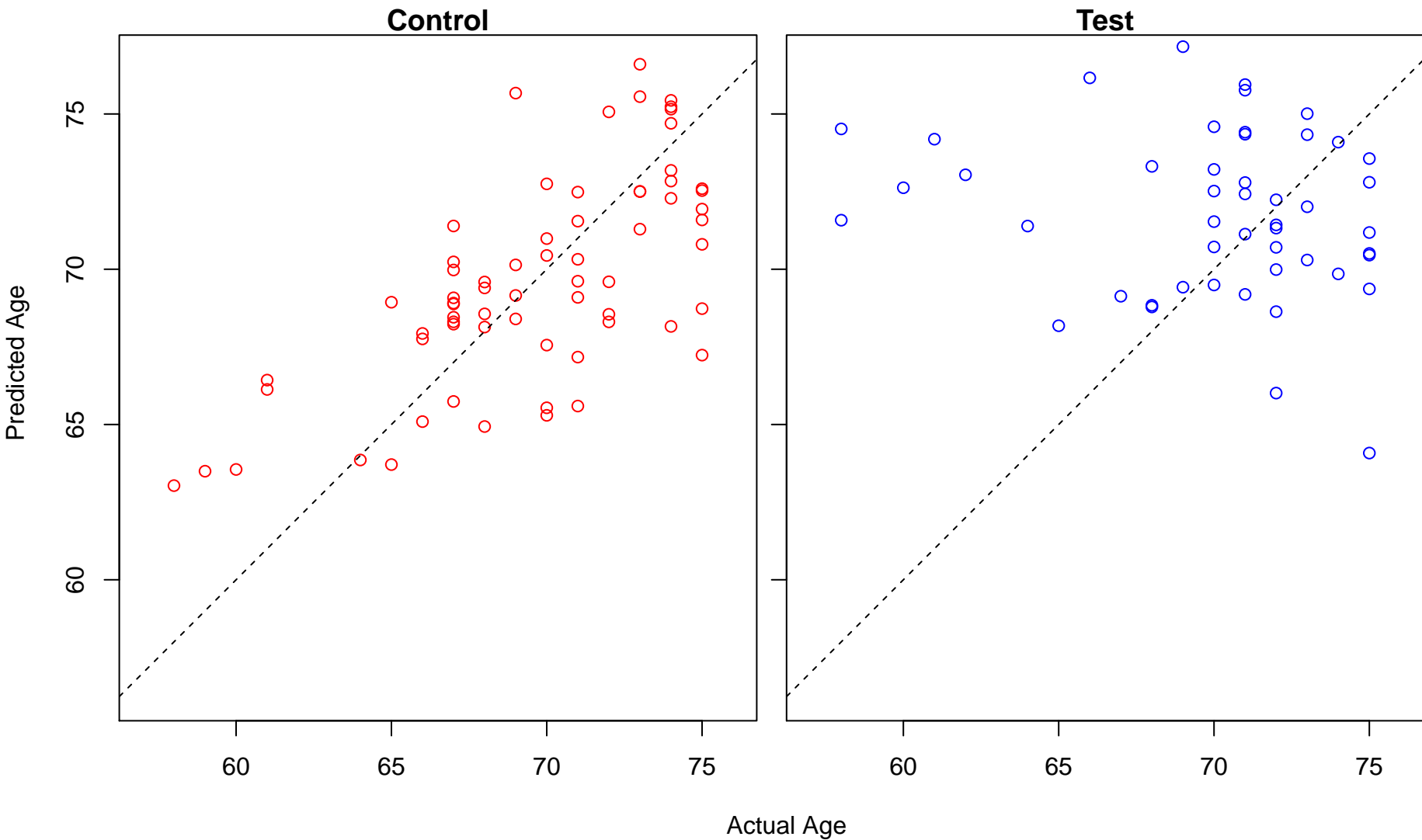
regulation of monocyte differentiation (Score: 1.980704)



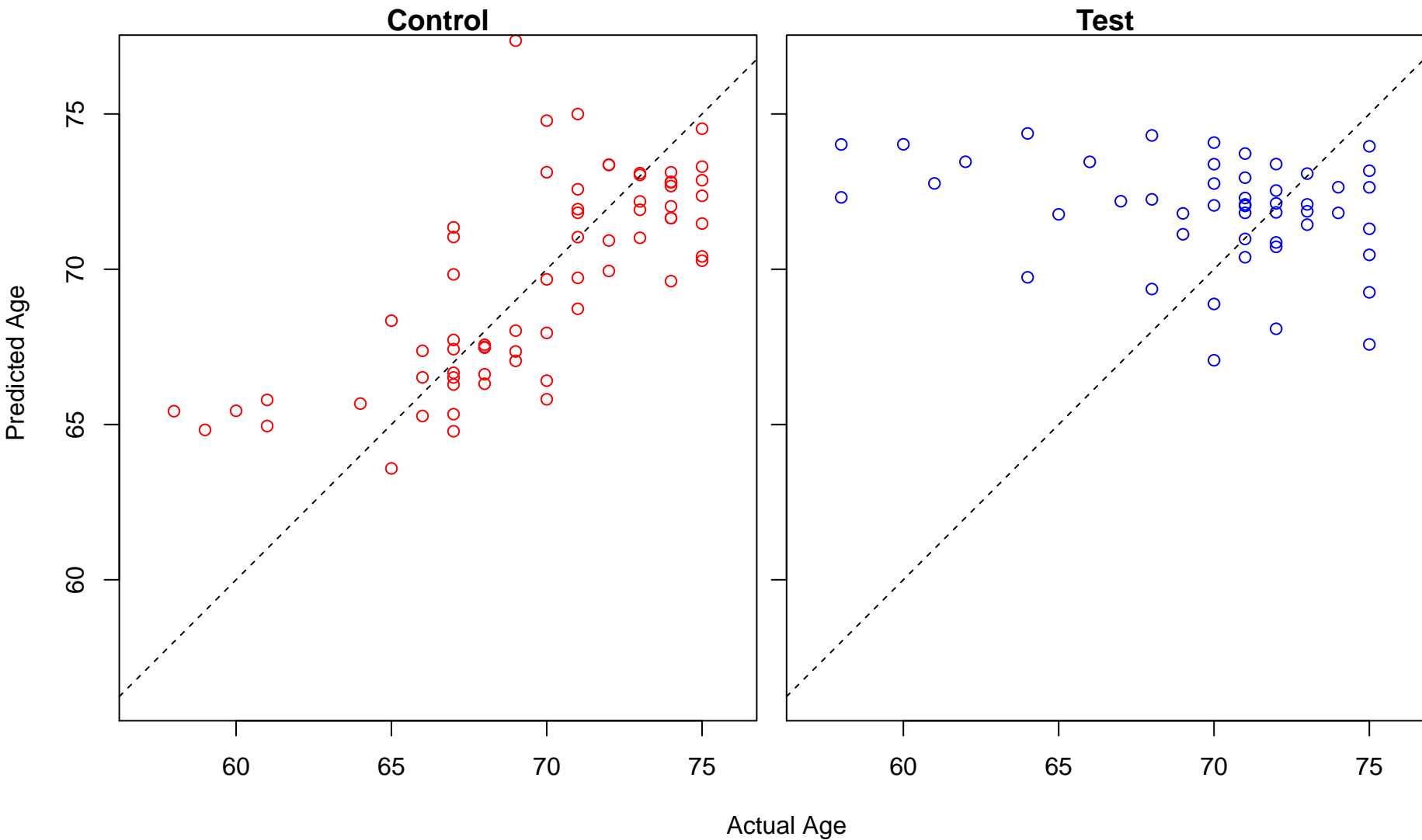
regulation of neutrophil migration (Score: 1.977601)



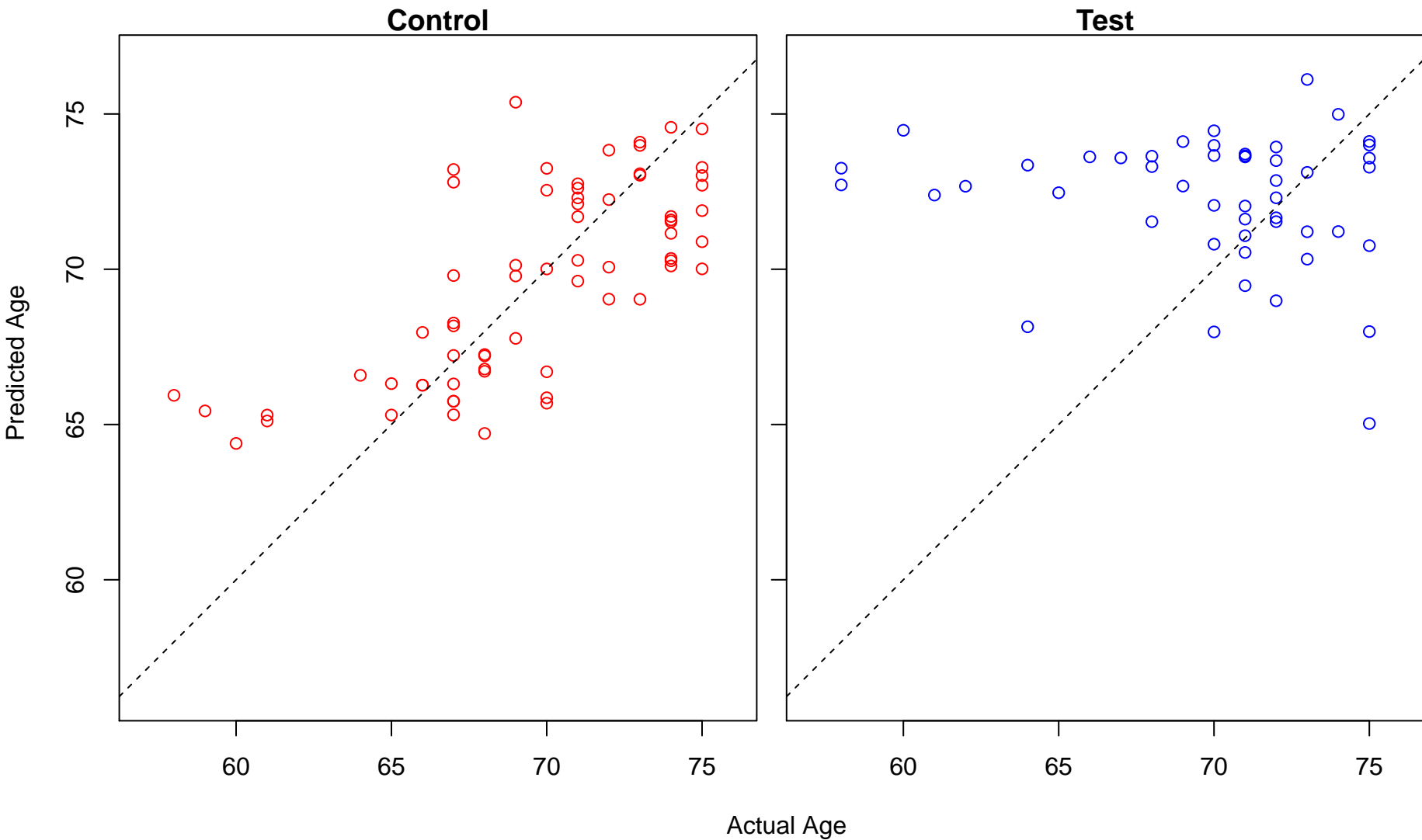
positive regulation of T cell apoptotic process (Score: 1.976334)



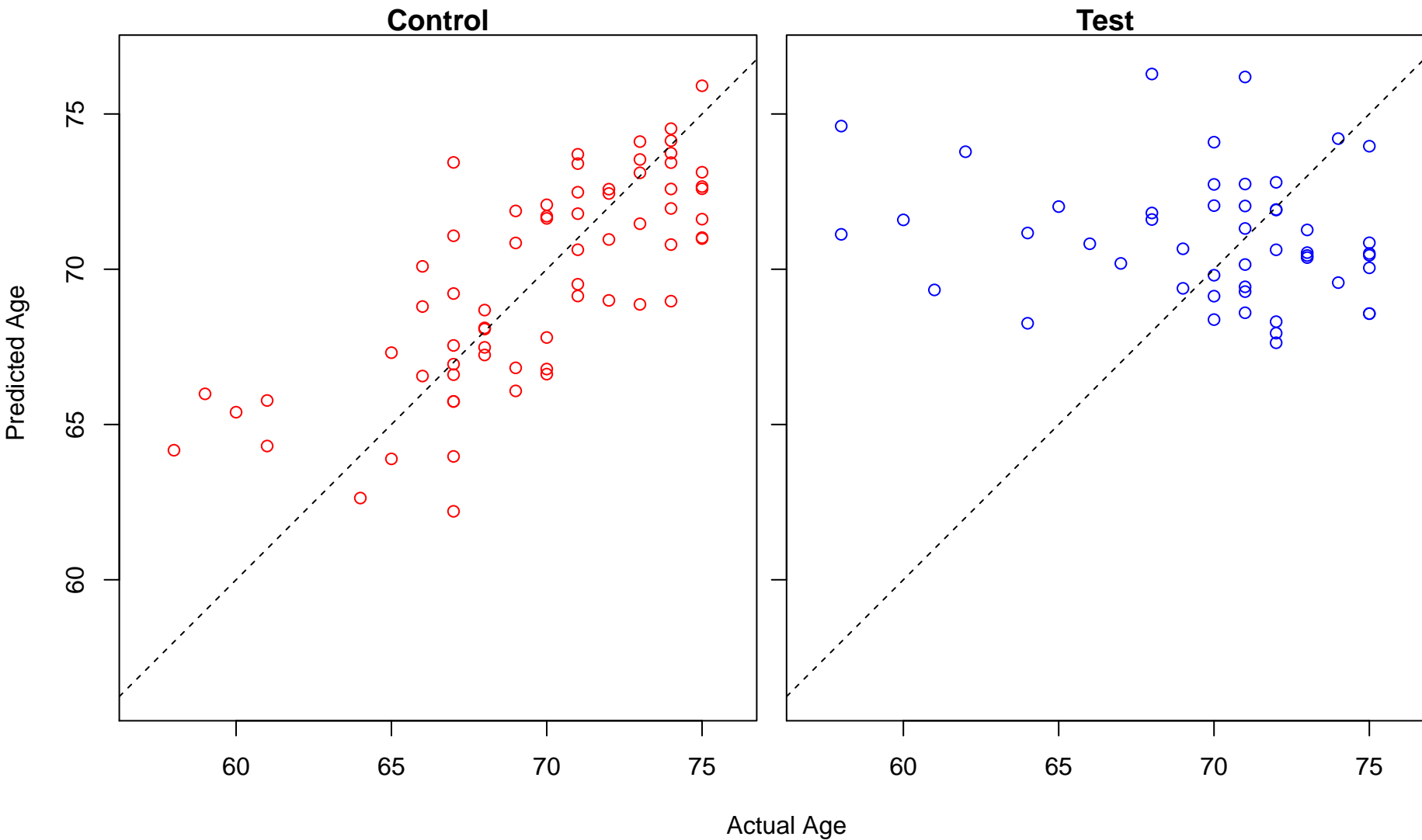
regulation of IRE1-mediated unfolded protein response (Score: 1.975474)



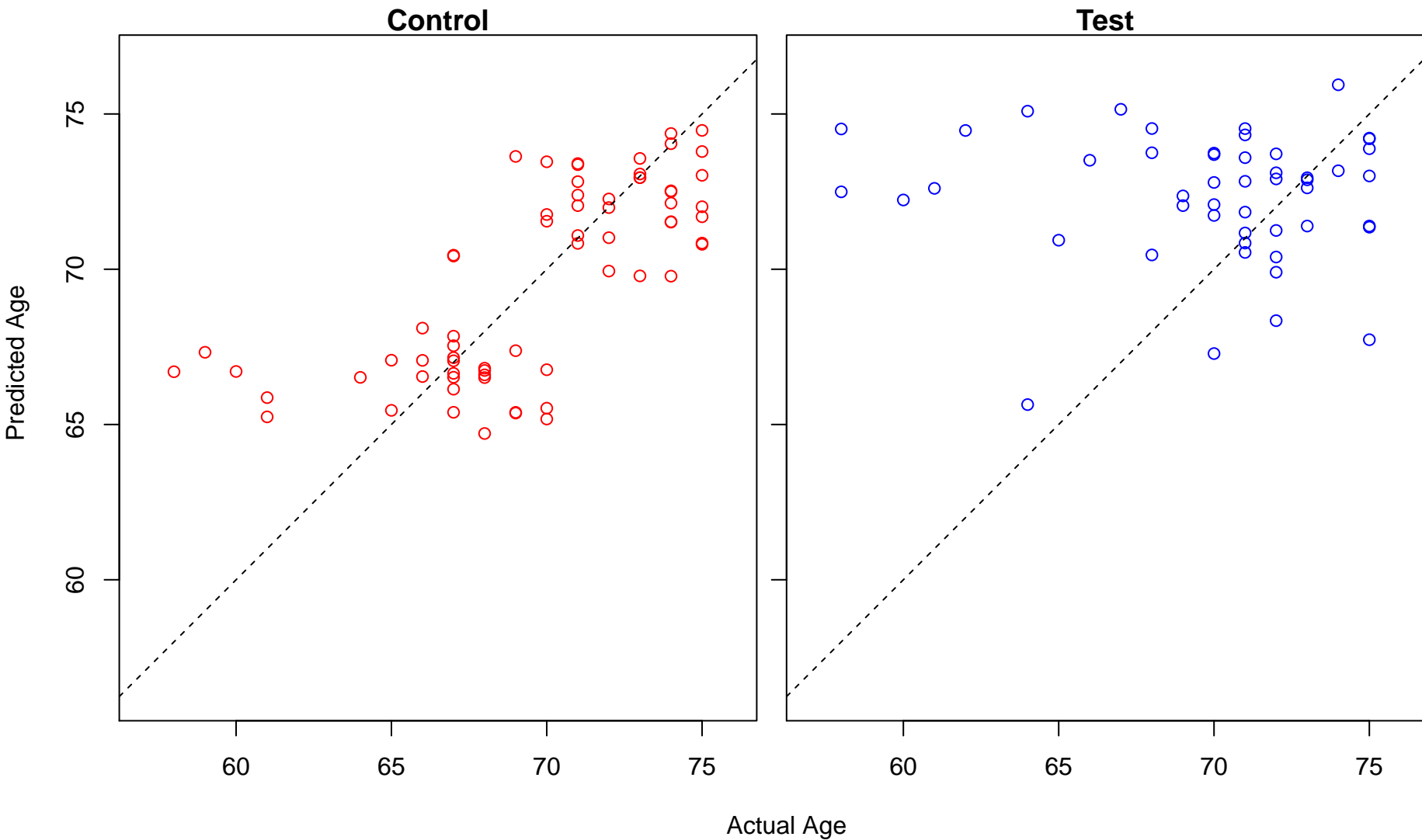
polyprenol metabolic process (Score: 1.974029)



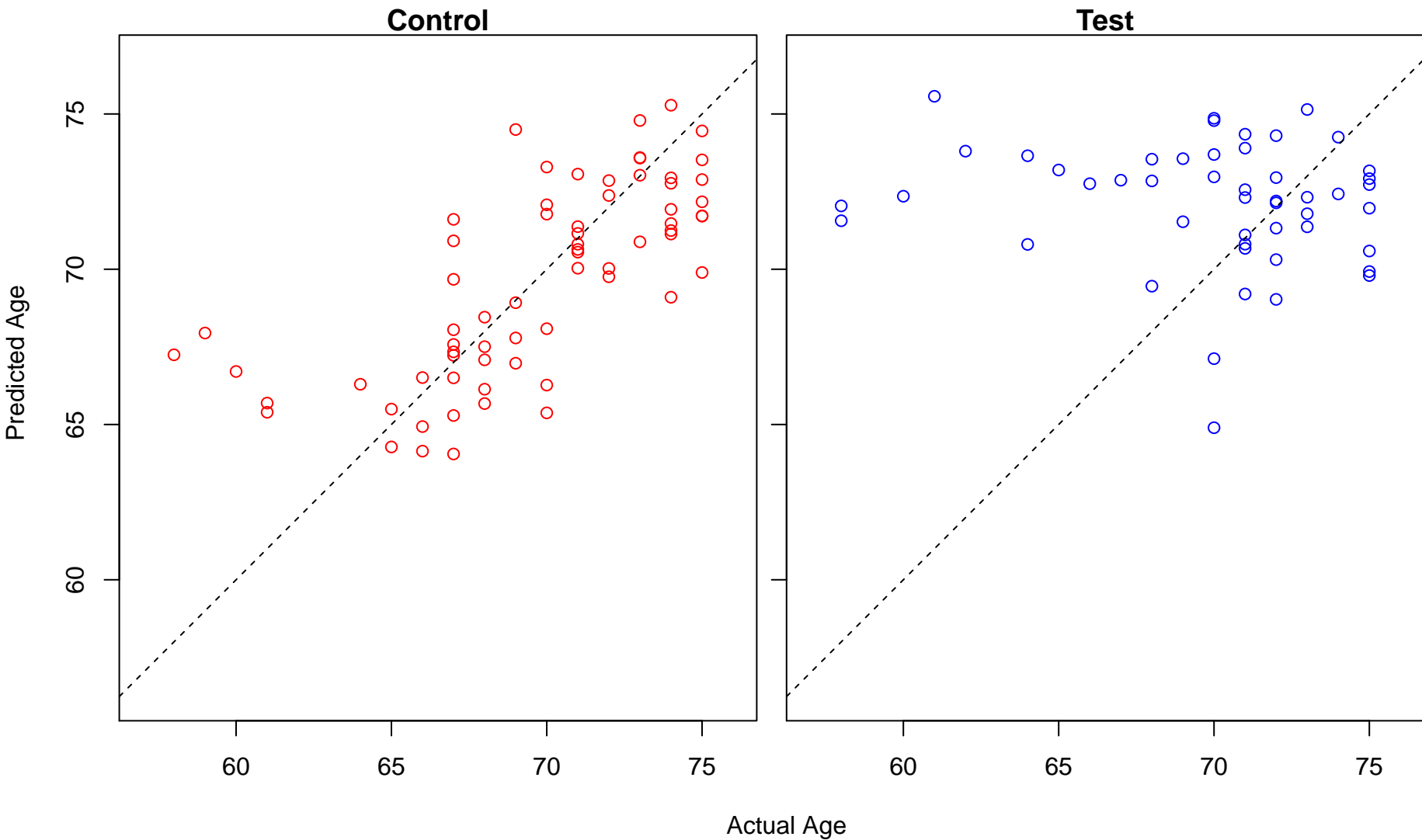
positive regulation of monocyte differentiation (Score: 1.967587)



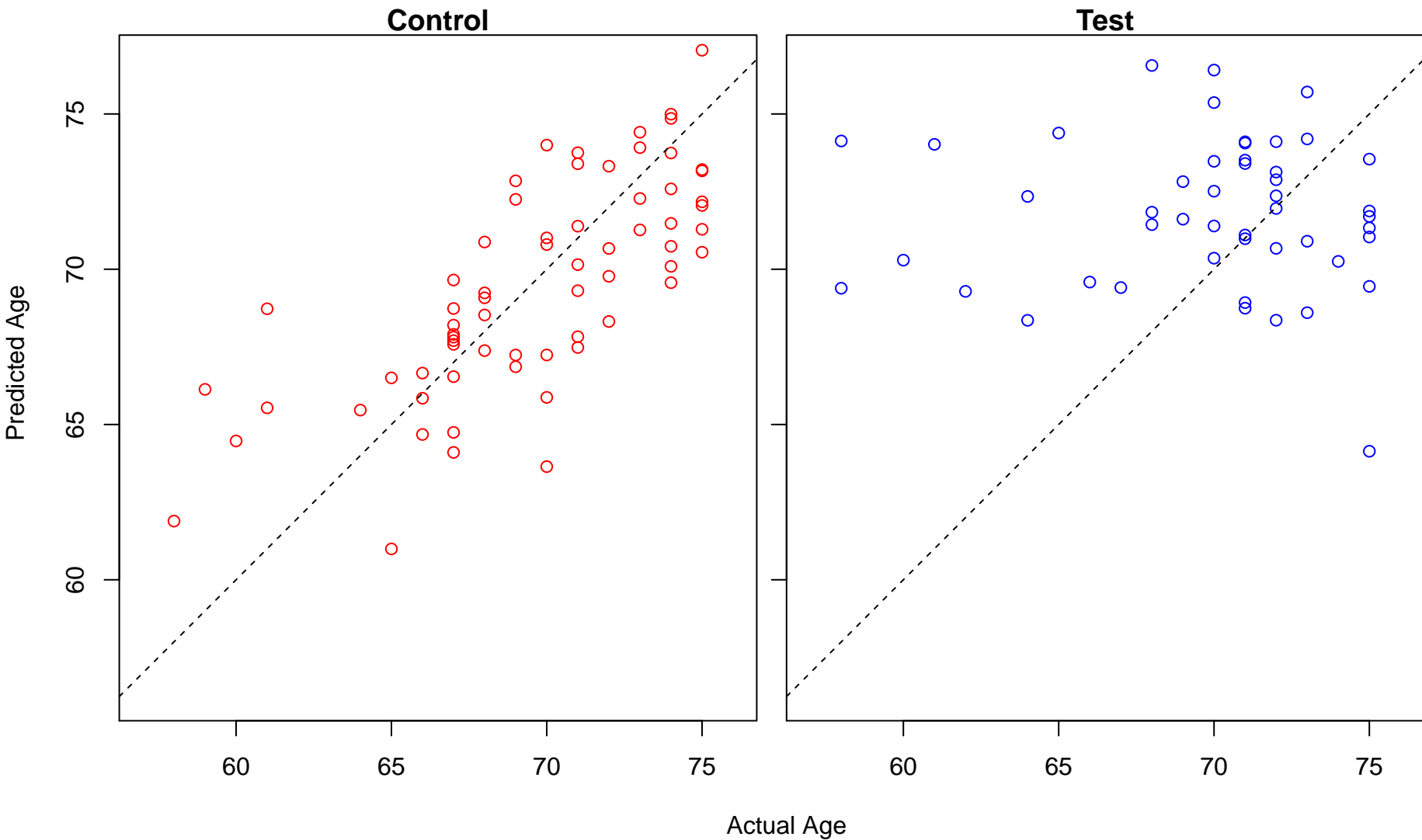
actin filament polymerization (Score: 1.964504)



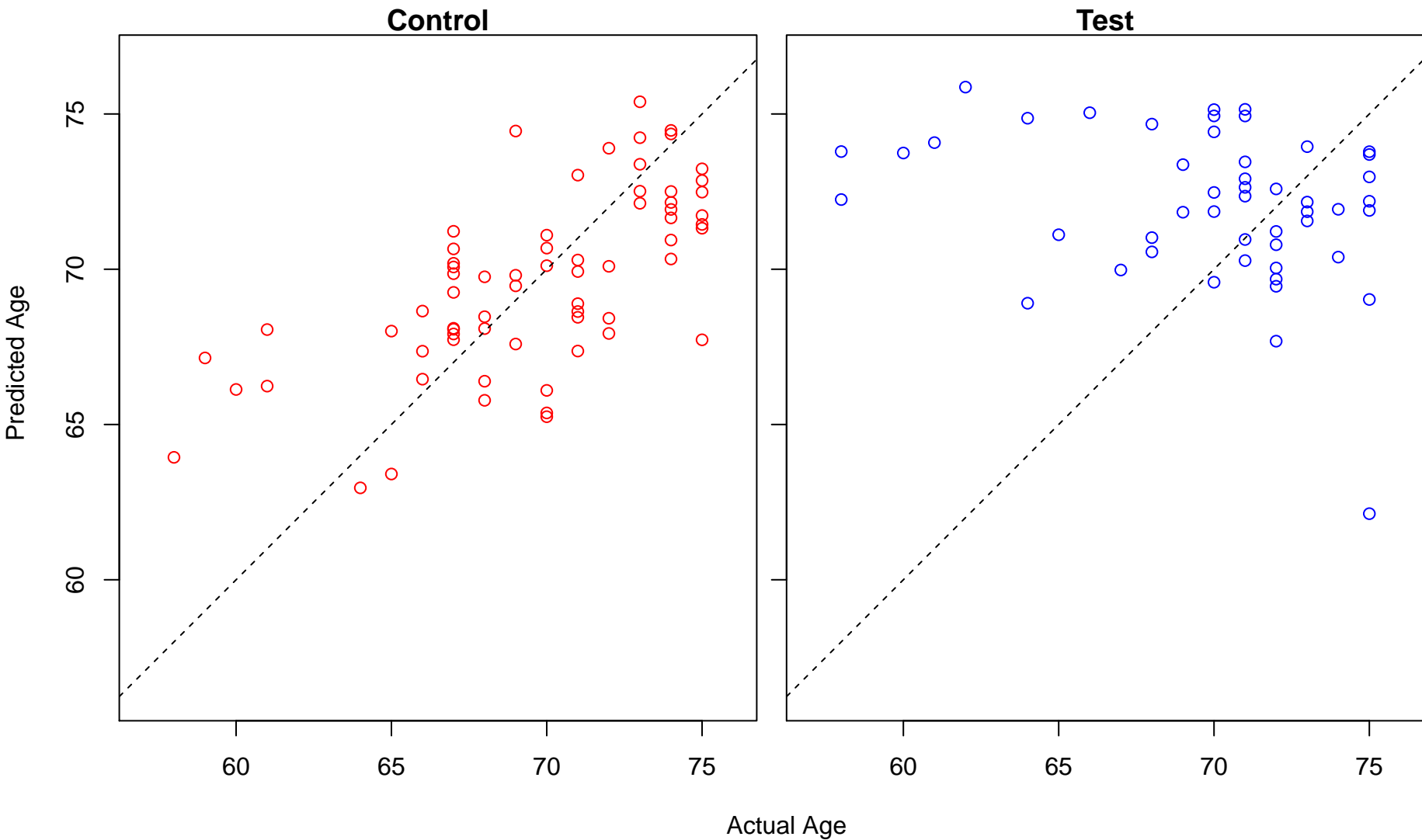
histone H2A acetylation (Score: 1.962588)



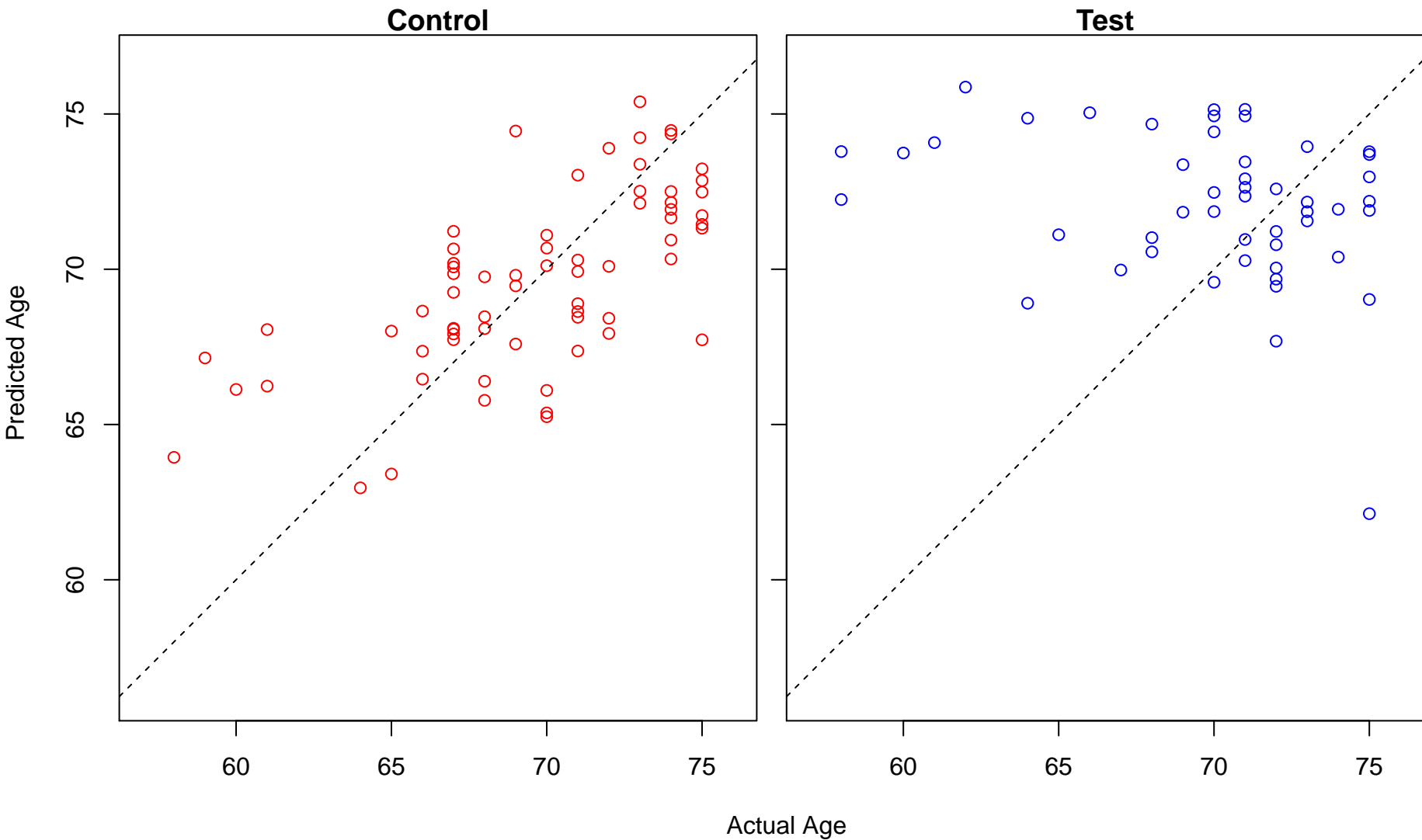
positive regulation of neutrophil migration (Score: 1.961443)



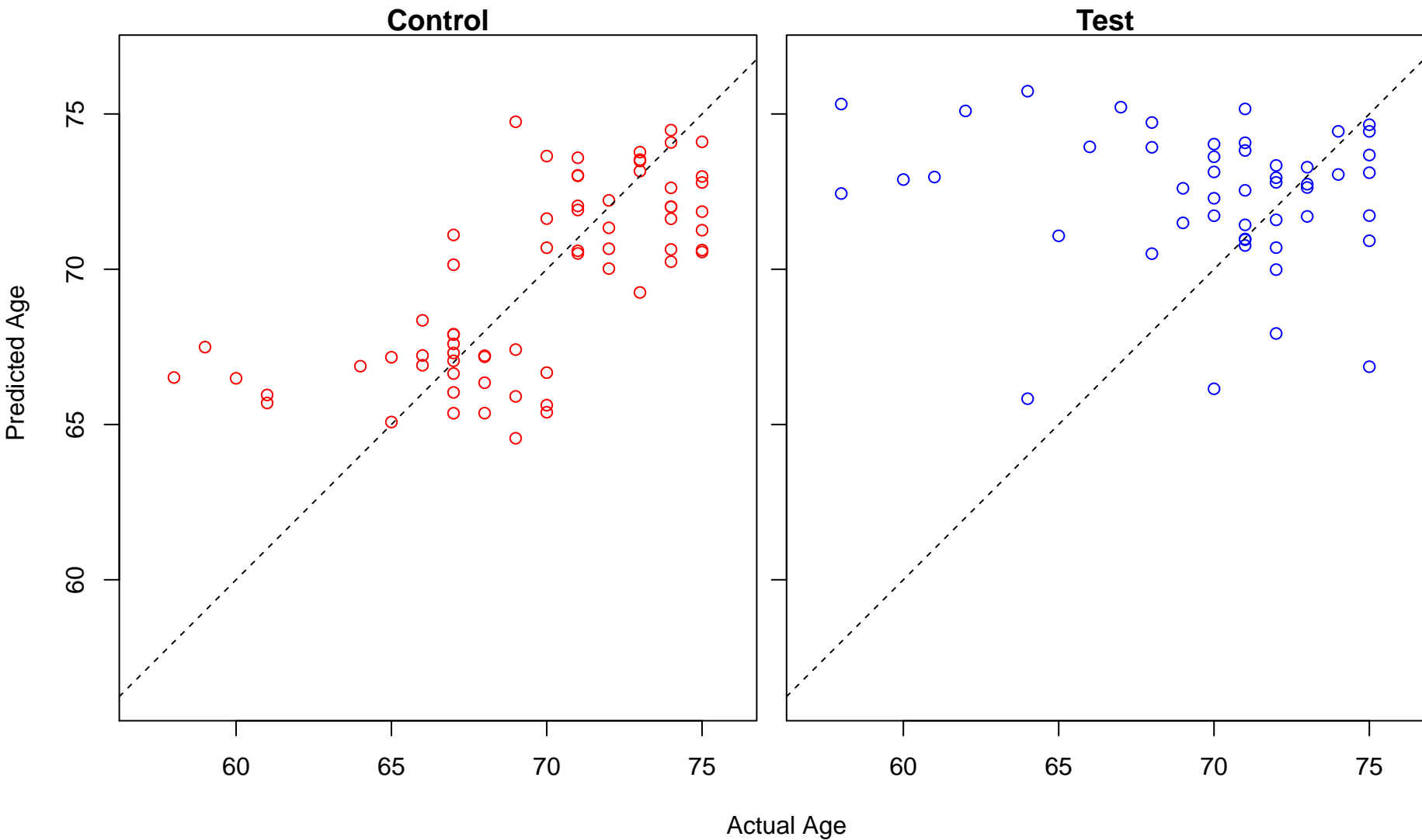
positive regulation of T cell differentiation in thymus (Score: 1.961318)



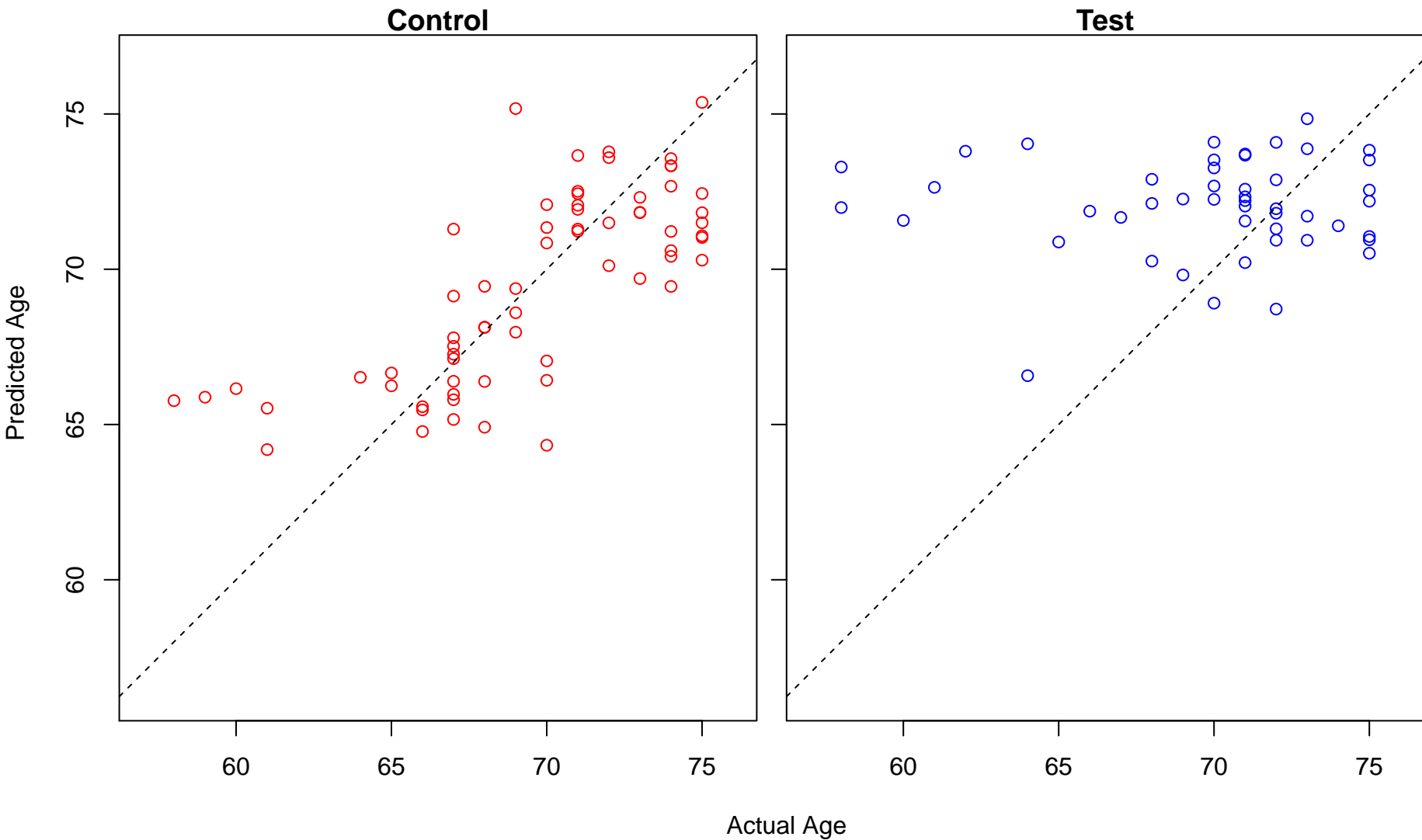
positive regulation of thymocyte aggregation (Score: 1.961318)



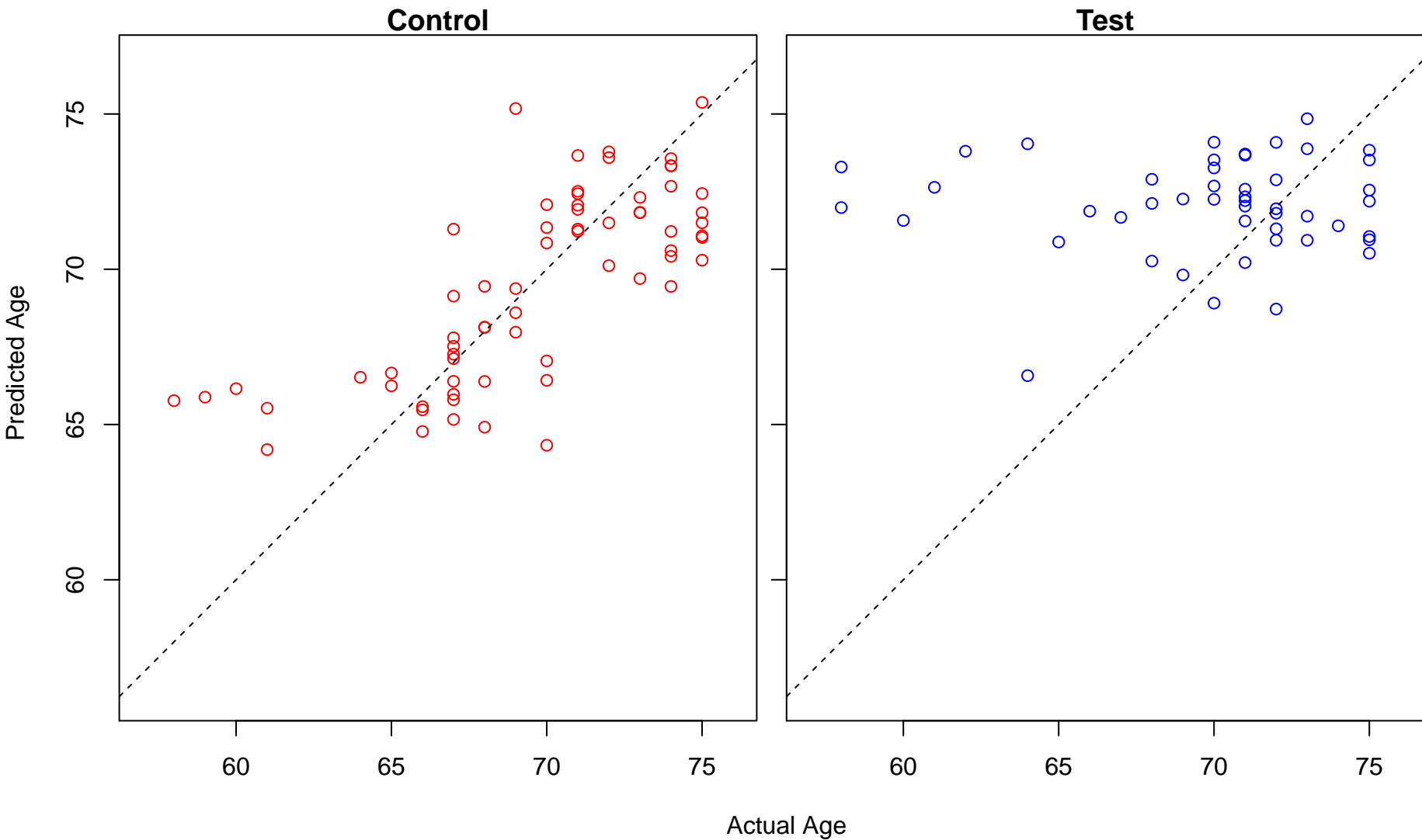
phagocytosis, engulfment (Score: 1.958000)



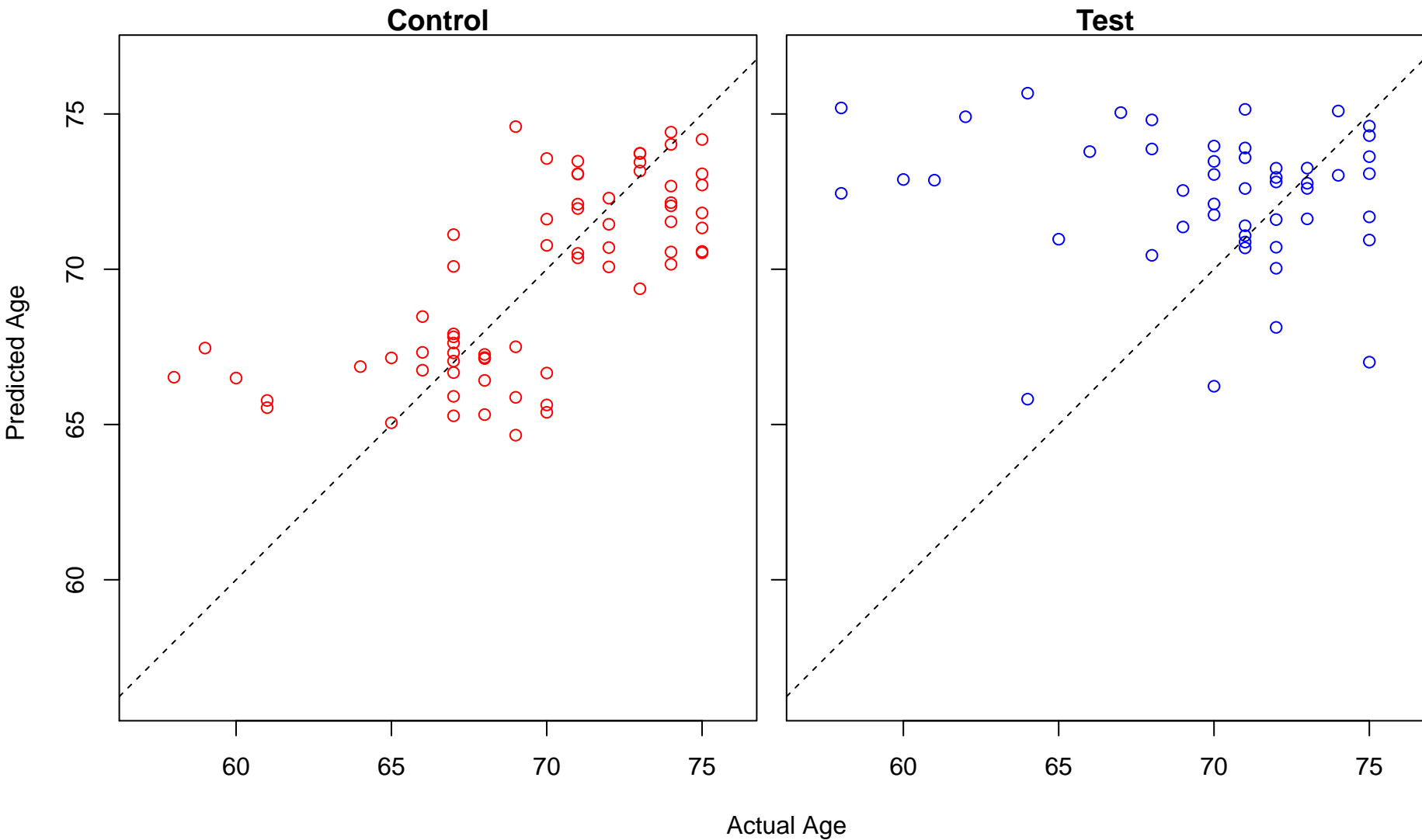
Arp2/3 complex-mediated actin nucleation (Score: 1.957615)



actin nucleation (Score: 1.957615)

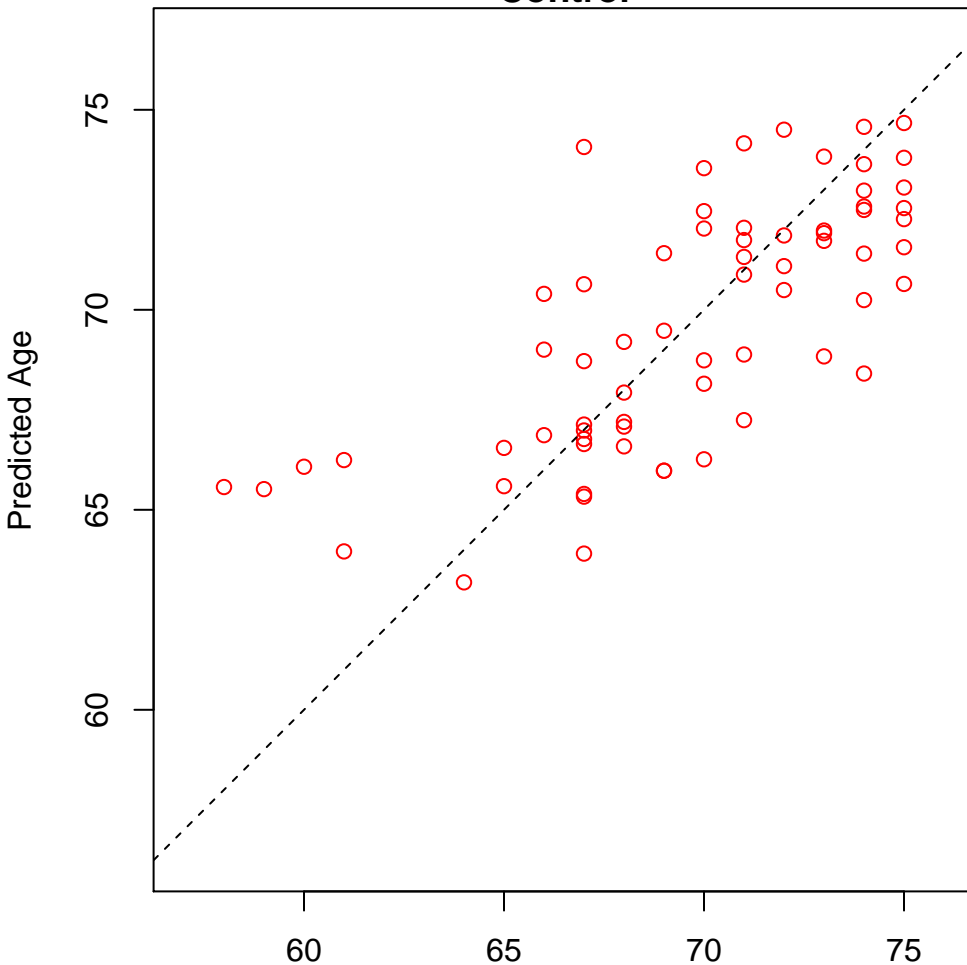


membrane invagination (Score: 1.949269)

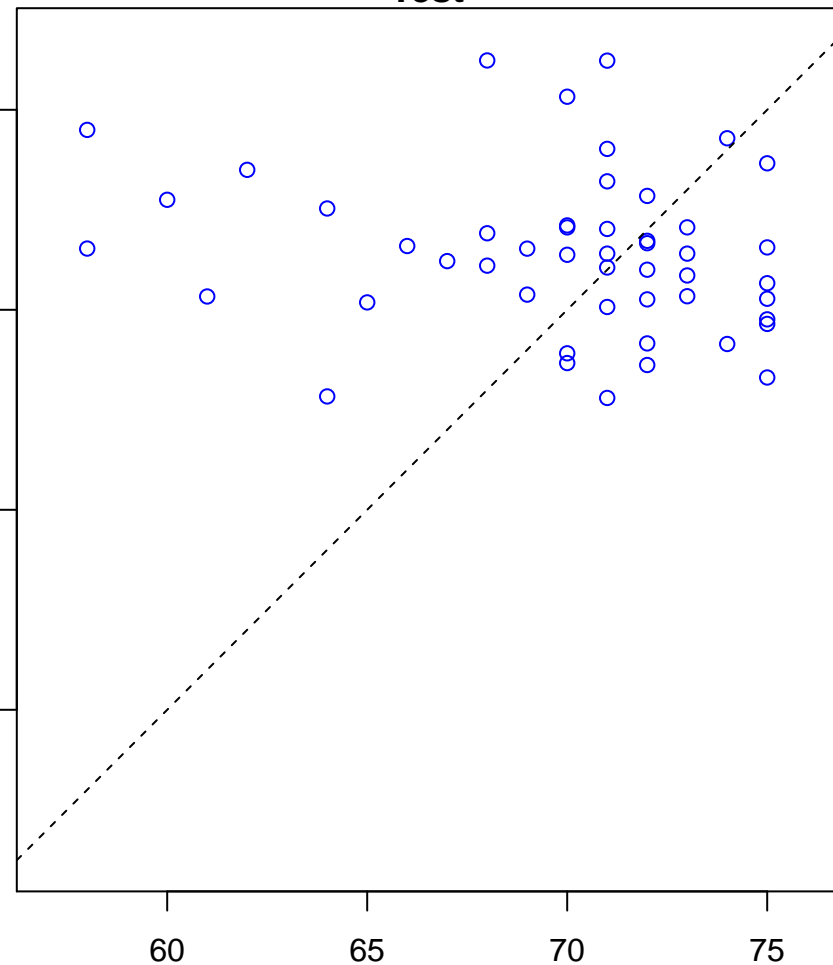


apoptotic chromosome condensation (Score: 1.945977)

Control

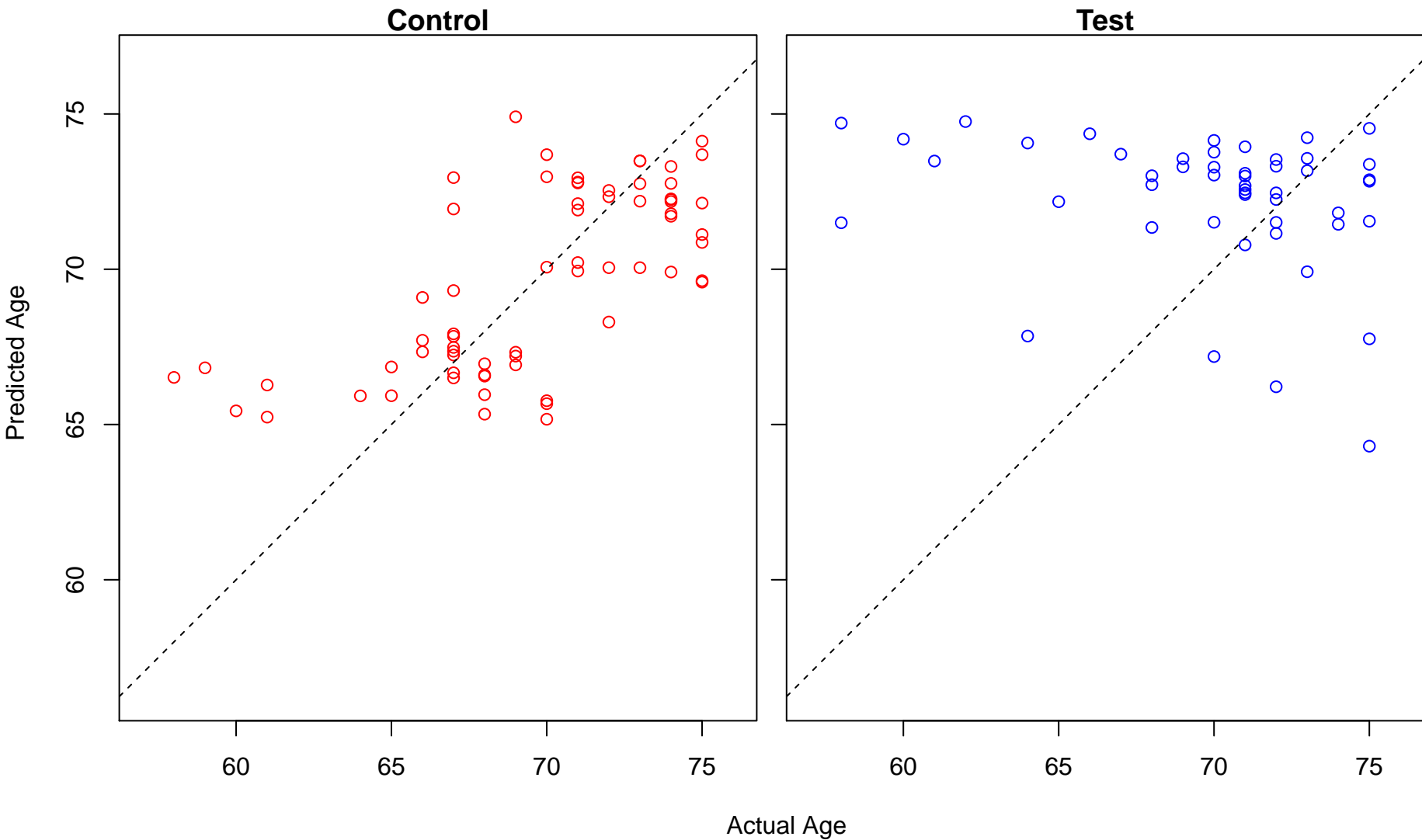


Test

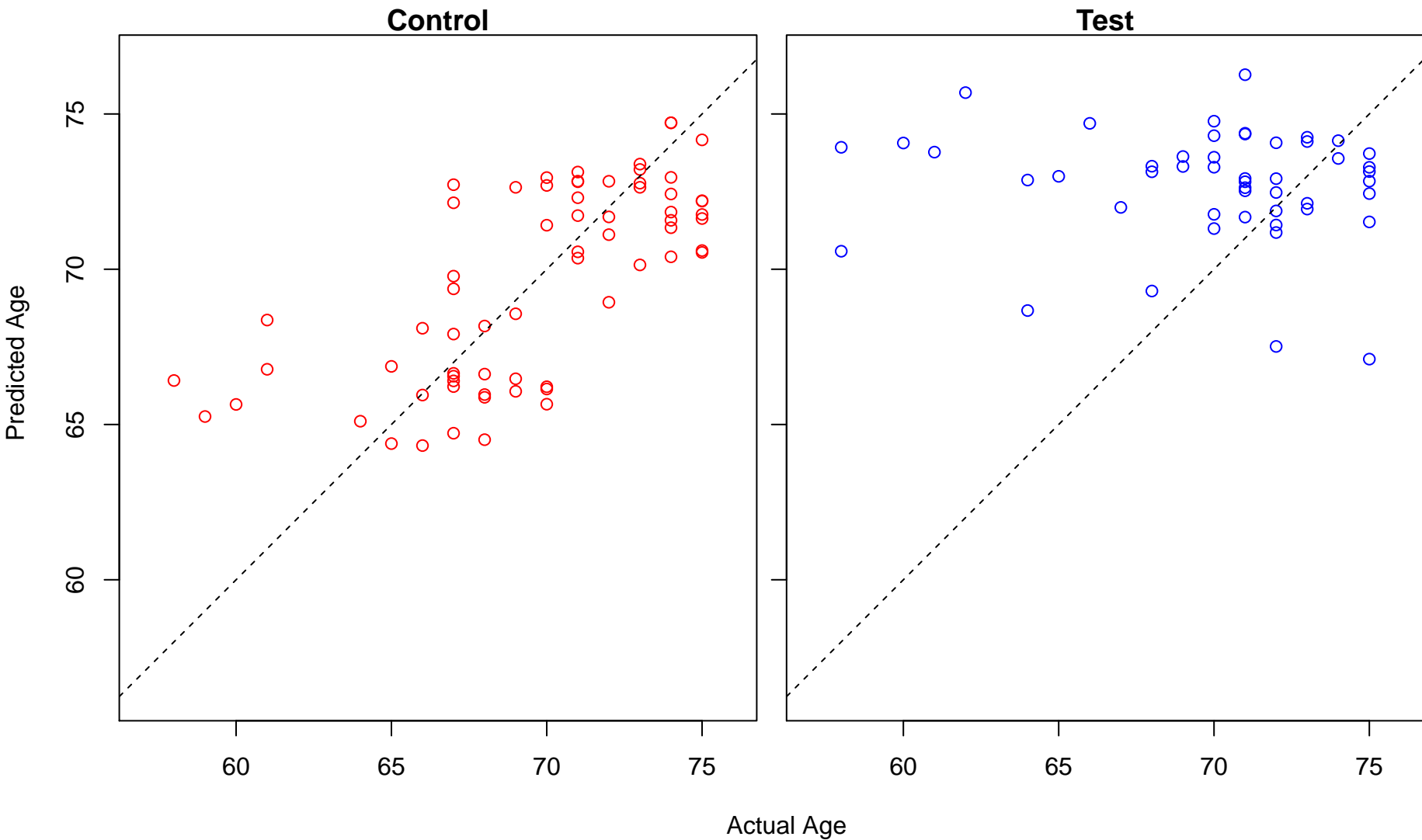


Actual Age

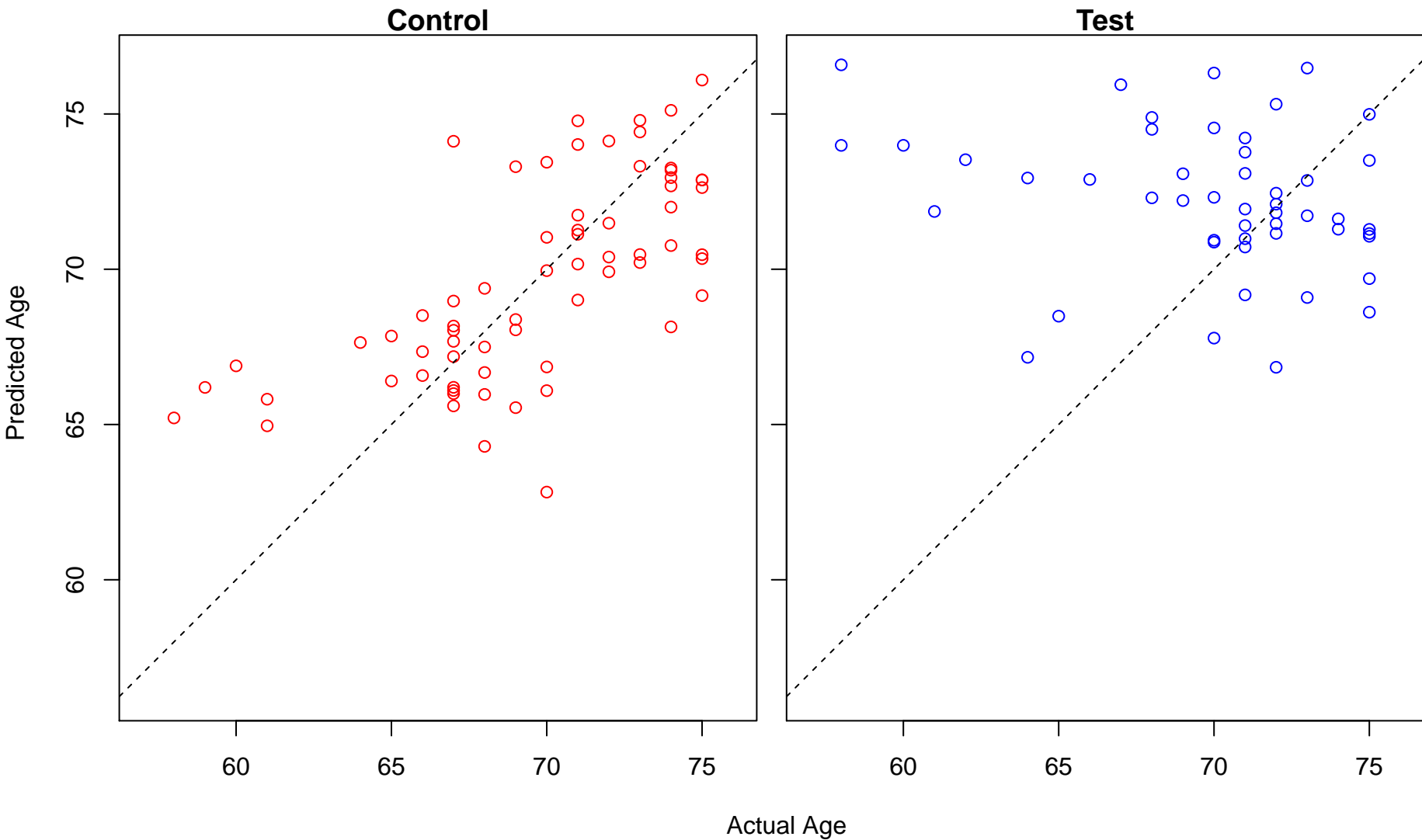
ribosomal large subunit biogenesis (Score: 1.942820)



protein localization to cytoplasmic stress granule (Score: 1.931610)

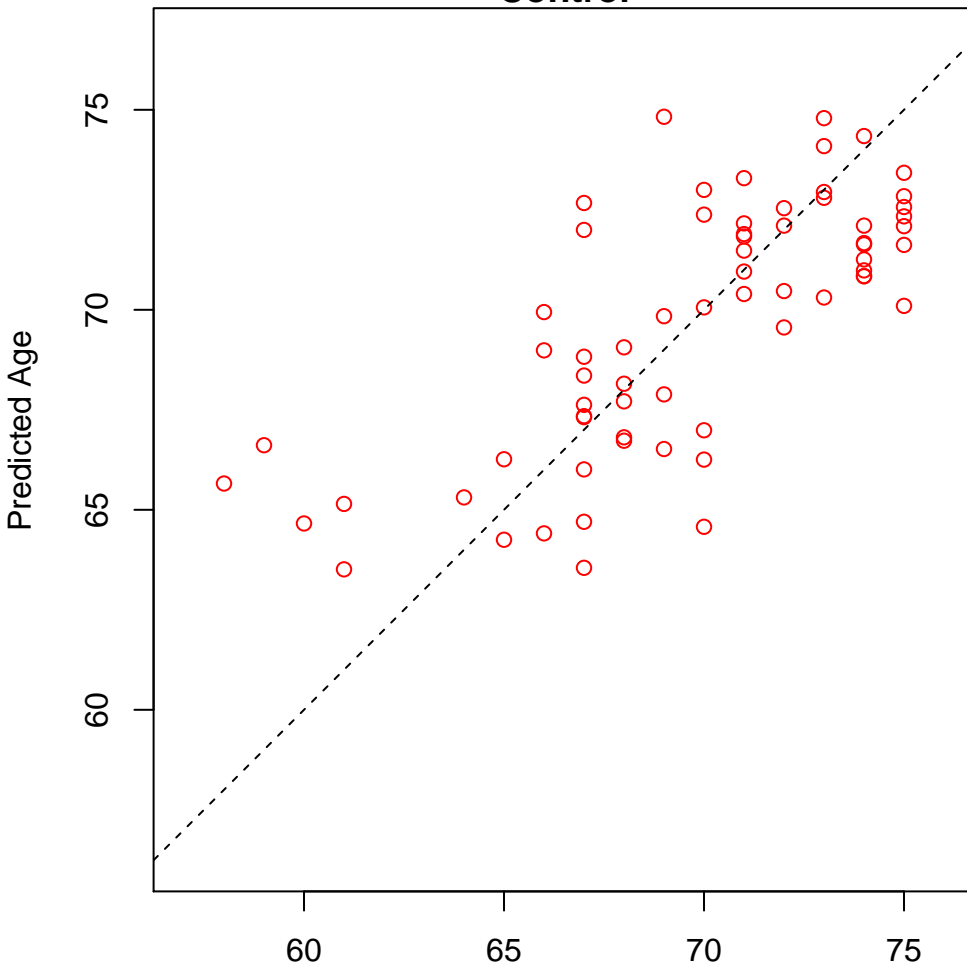


sequestering of metal ion (Score: 1.924469)

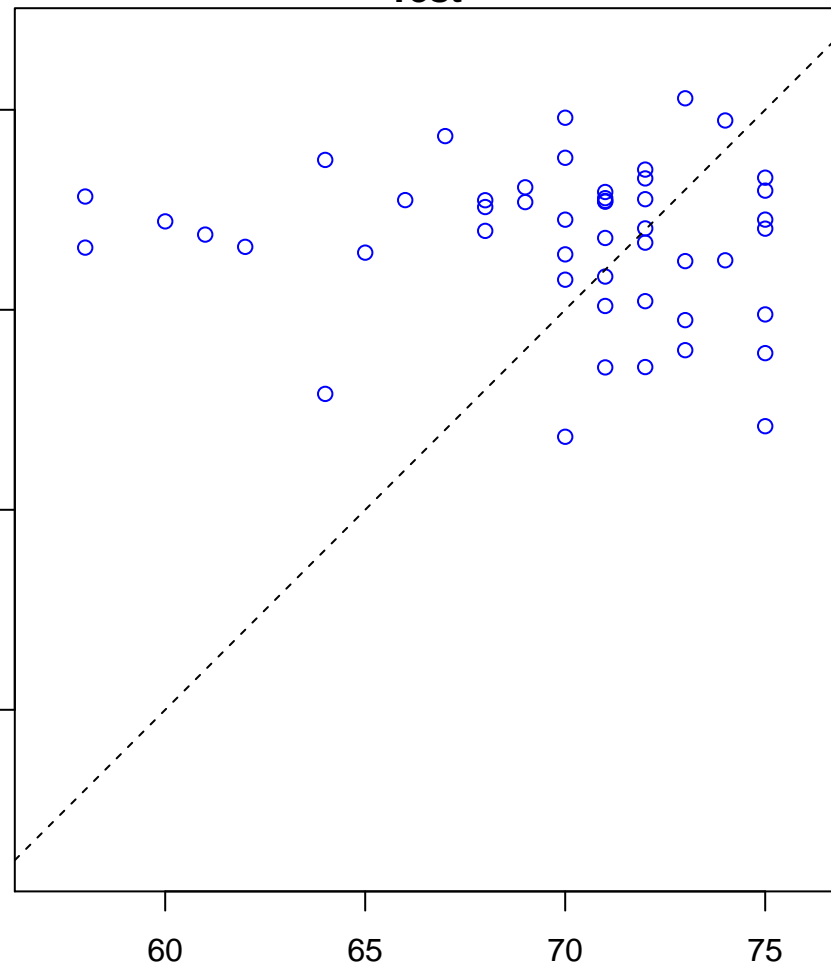


multivesicular body sorting pathway (Score: 1.915578)

Control

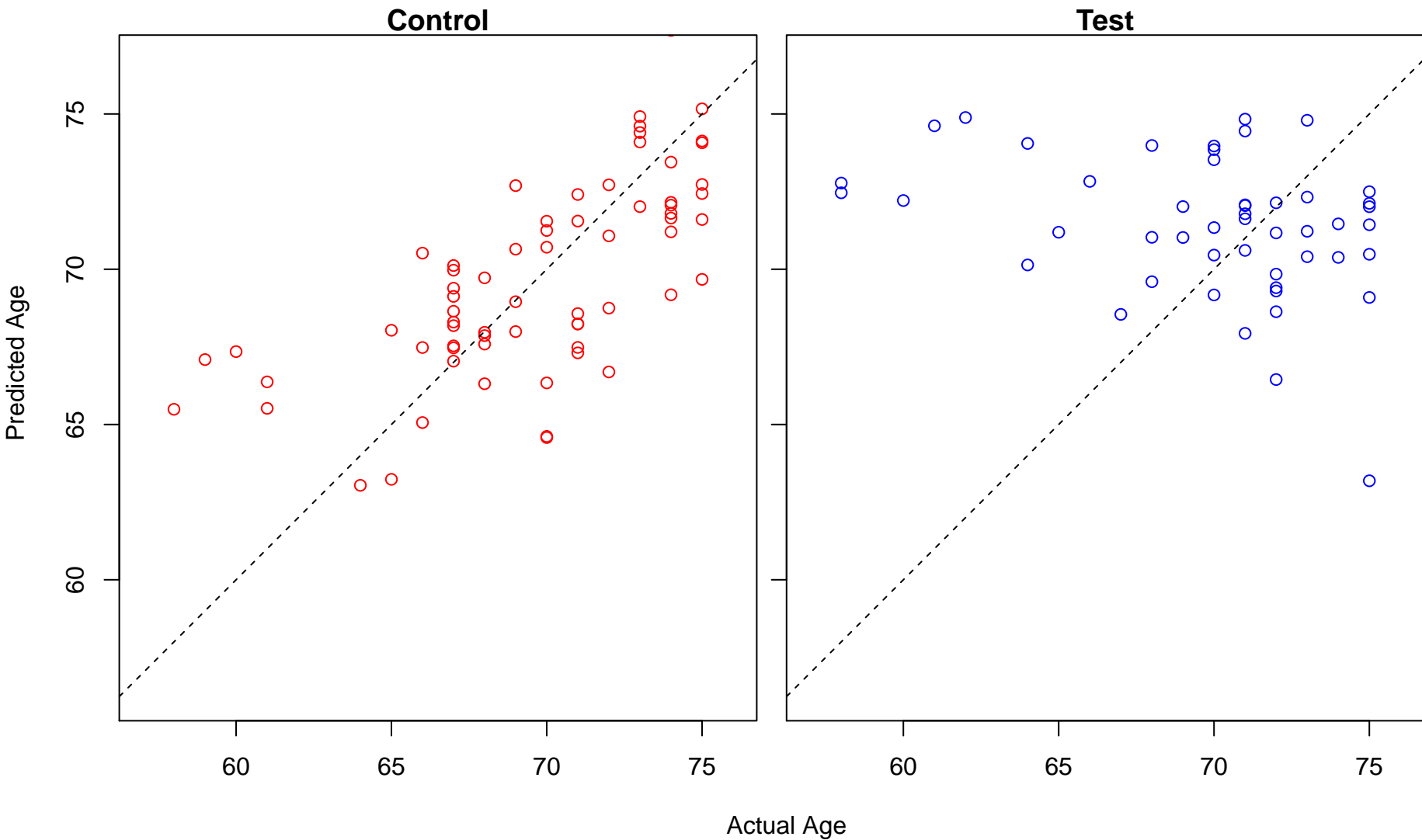


Test

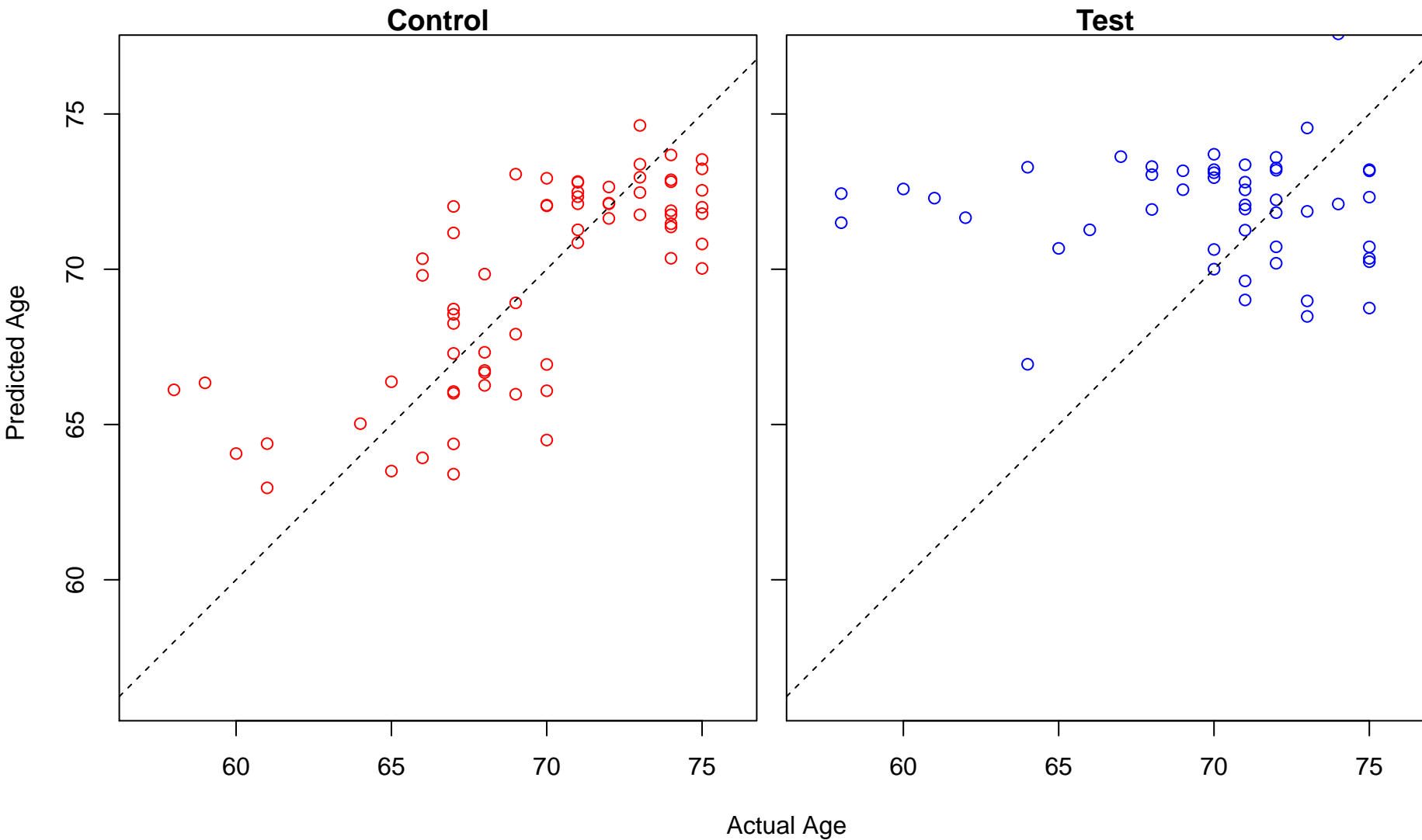


Actual Age

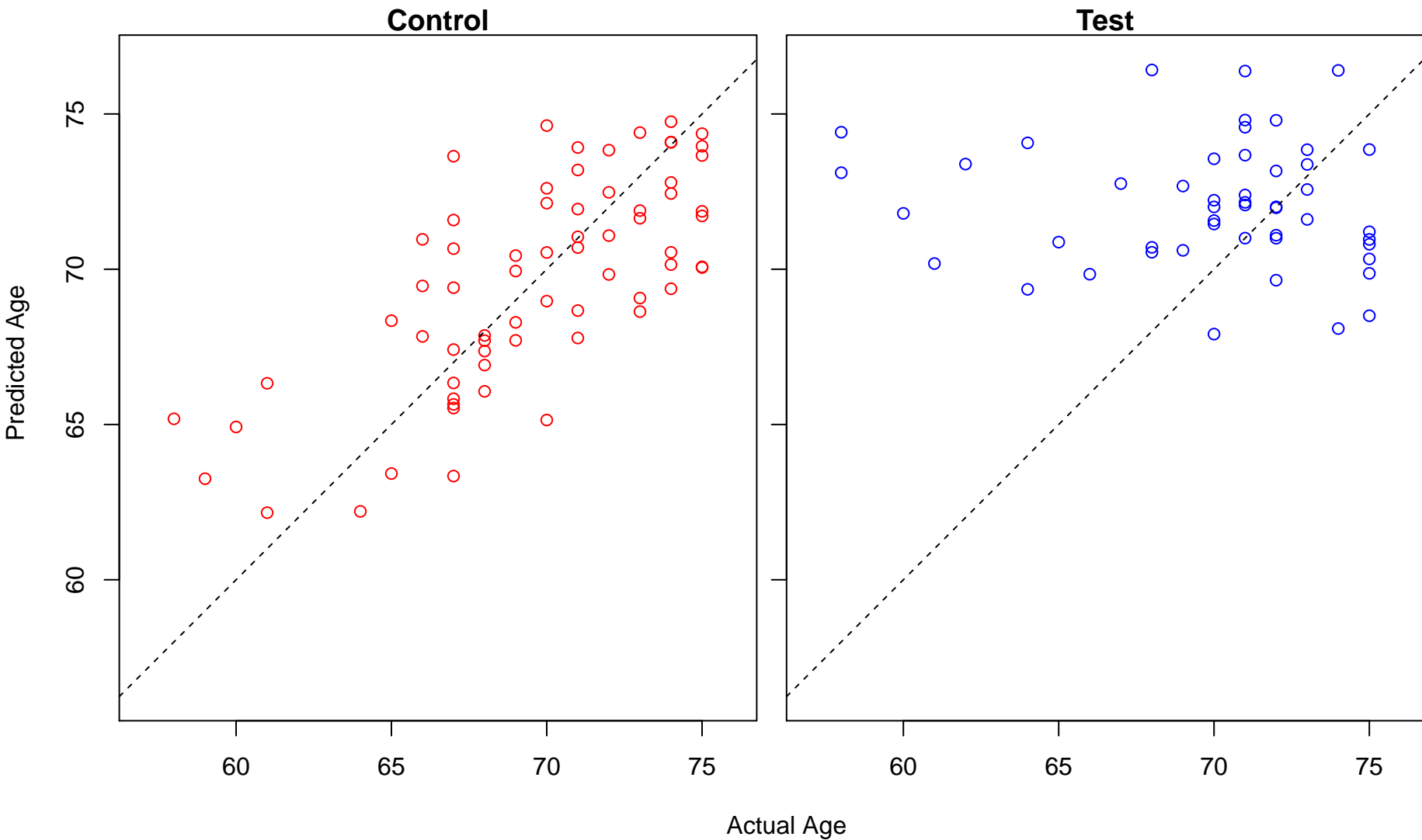
positive regulation of cellular extravasation (Score: 1.914924)



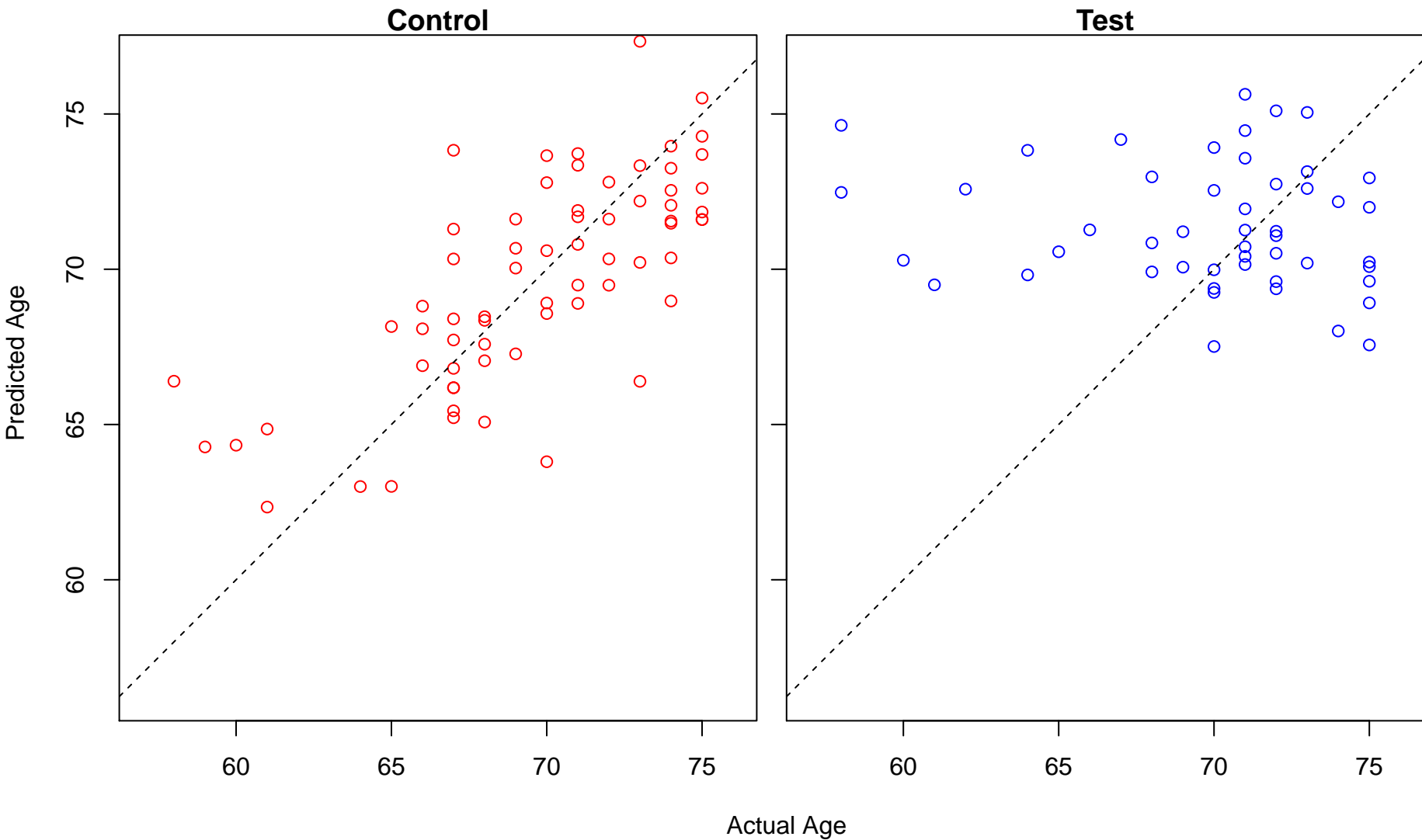
regulation of spindle assembly (Score: 1.896463)



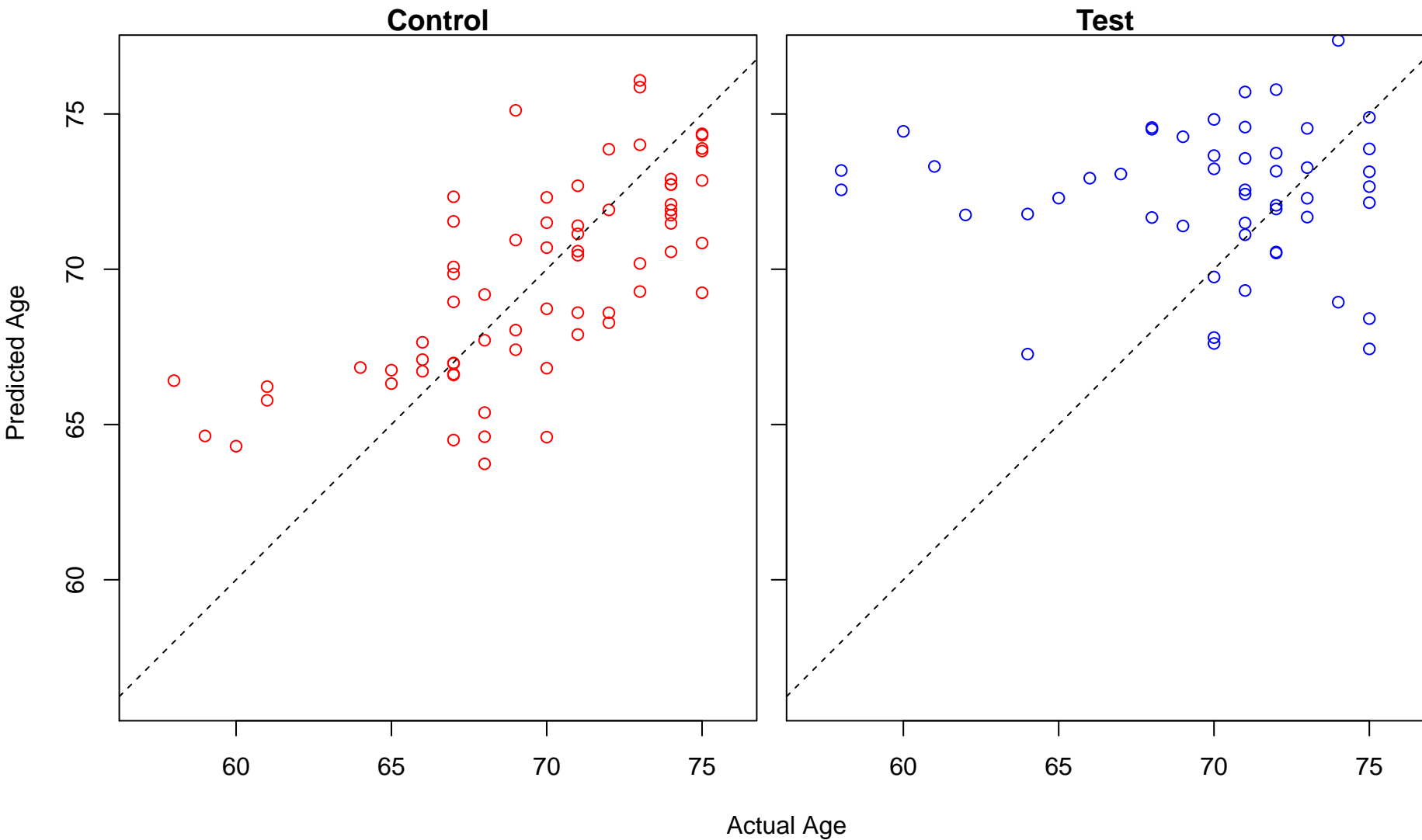
negative regulation of mRNA splicing, via spliceosome (Score: 1.892632)



negative regulation of mRNA processing (Score: 1.888588)

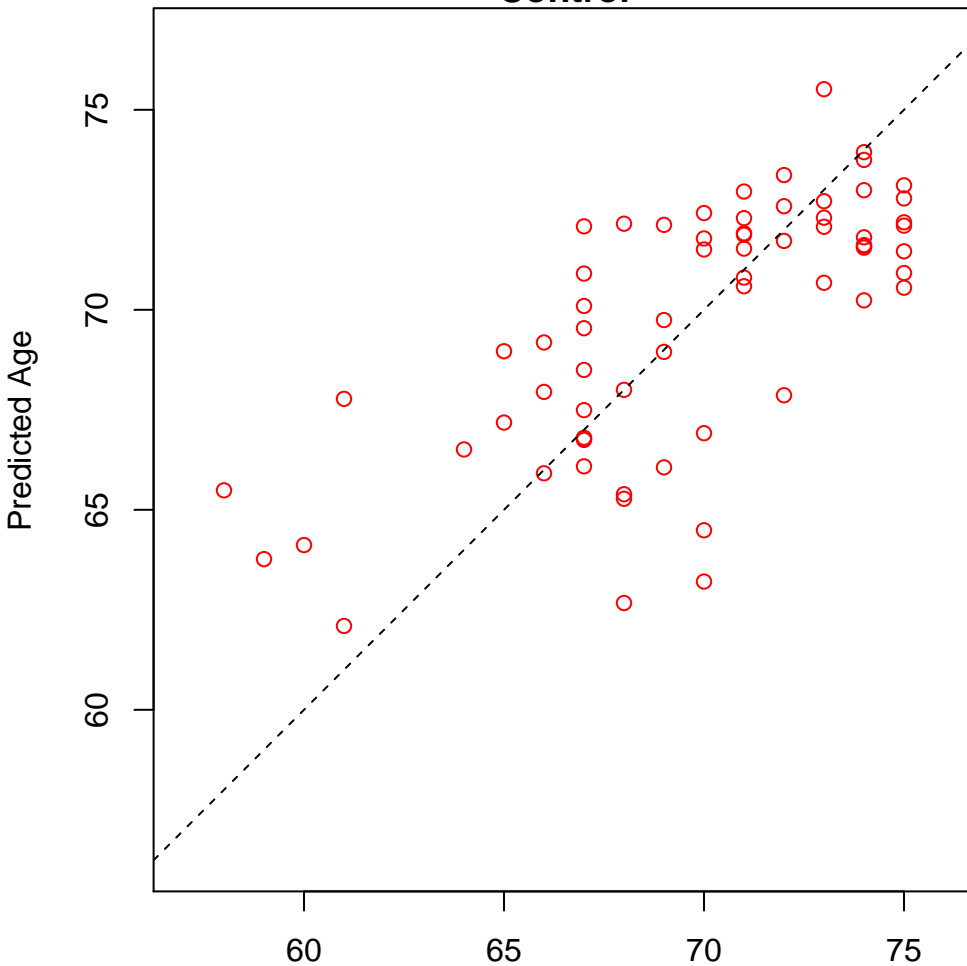


thymic T cell selection (Score: 1.884263)

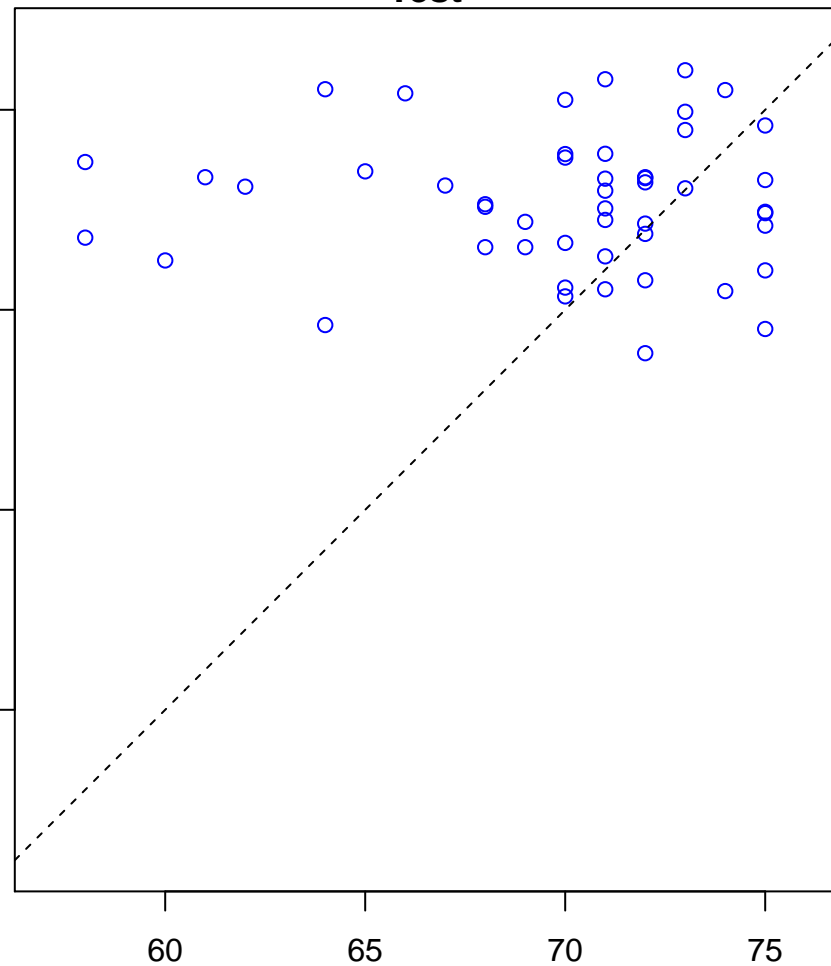


DNA double-strand break processing (Score: 1.876043)

Control

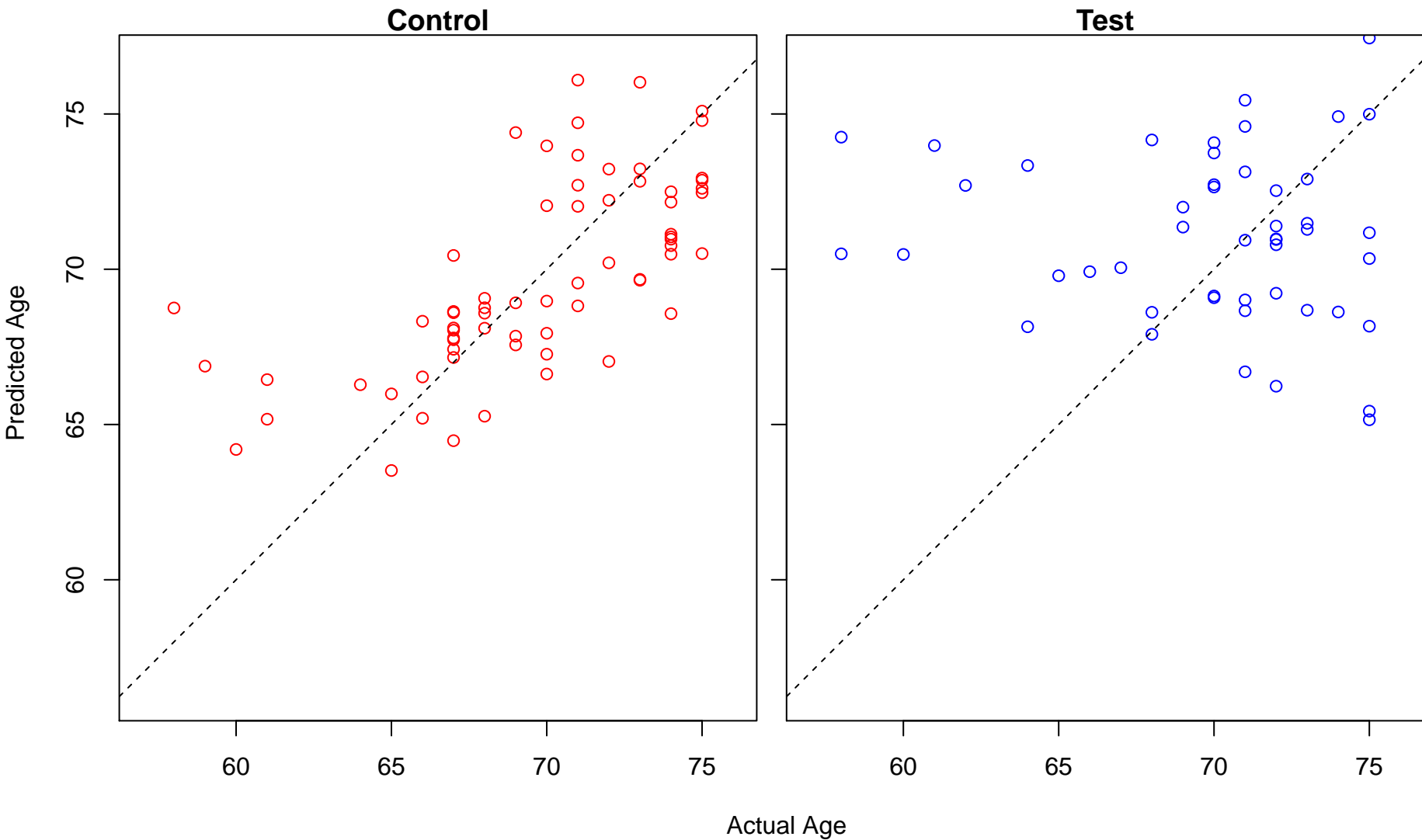


Test



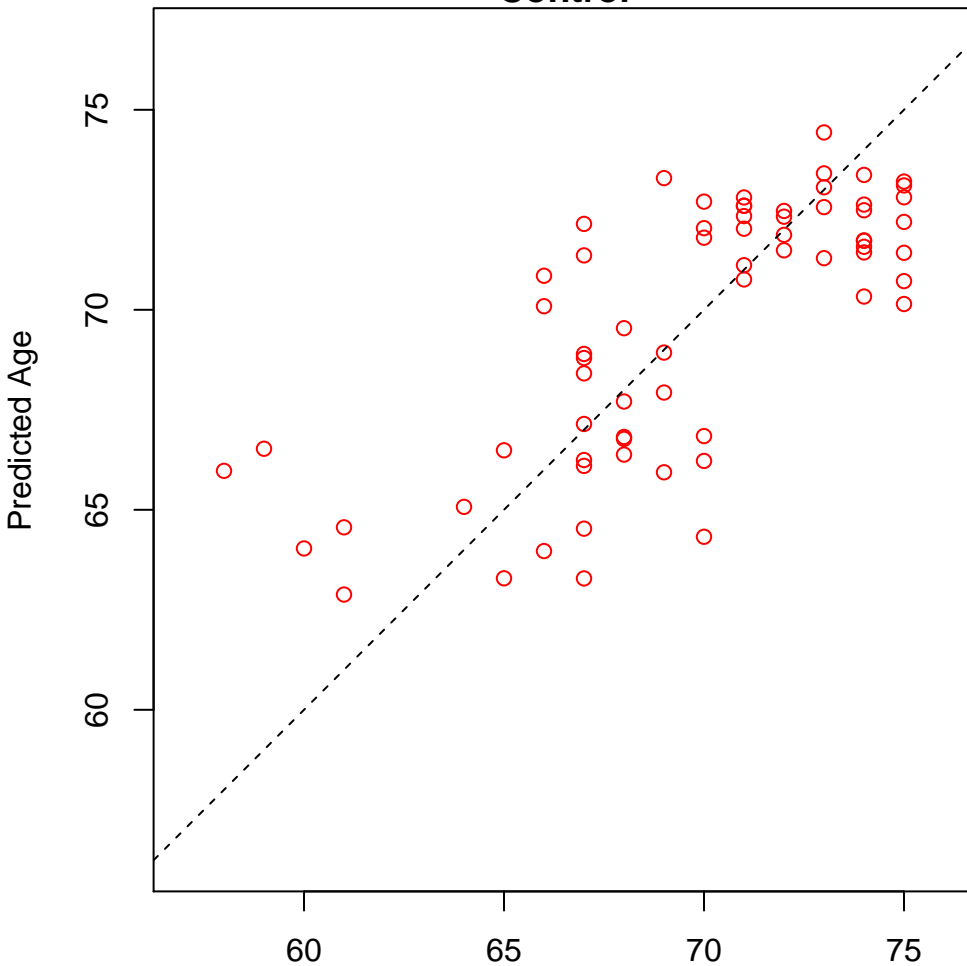
Actual Age

rRNA-containing ribonucleoprotein complex export from nucleus (Score: 1.872435)

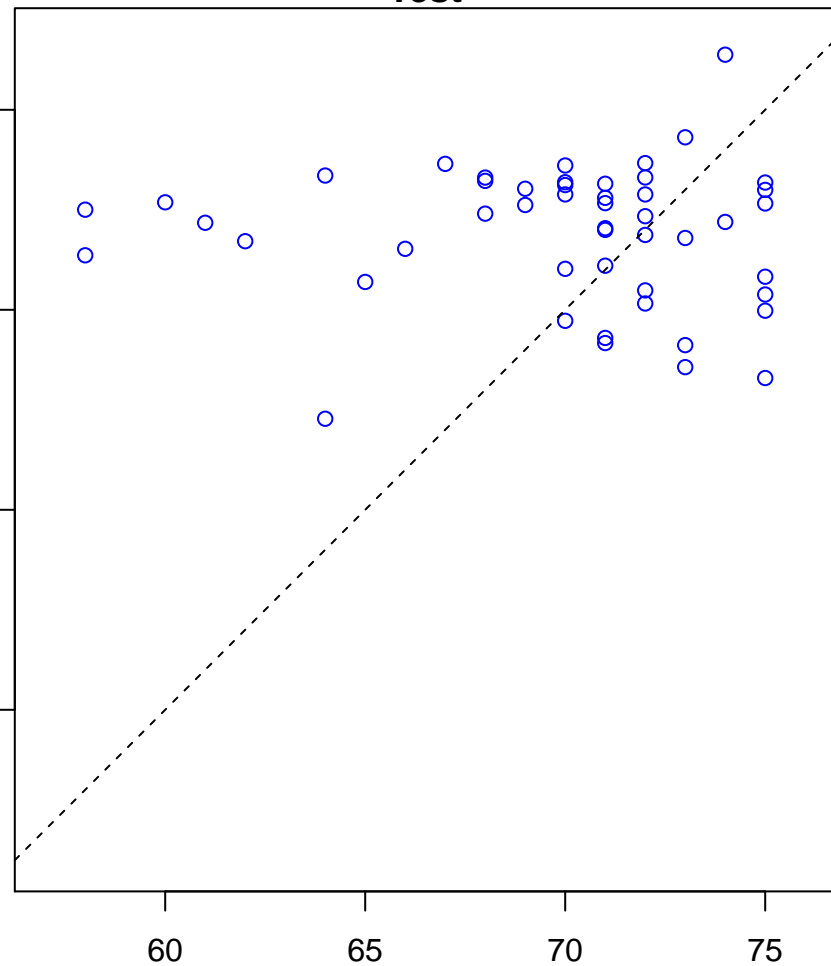


regulation of mitotic spindle assembly (Score: 1.869961)

Control

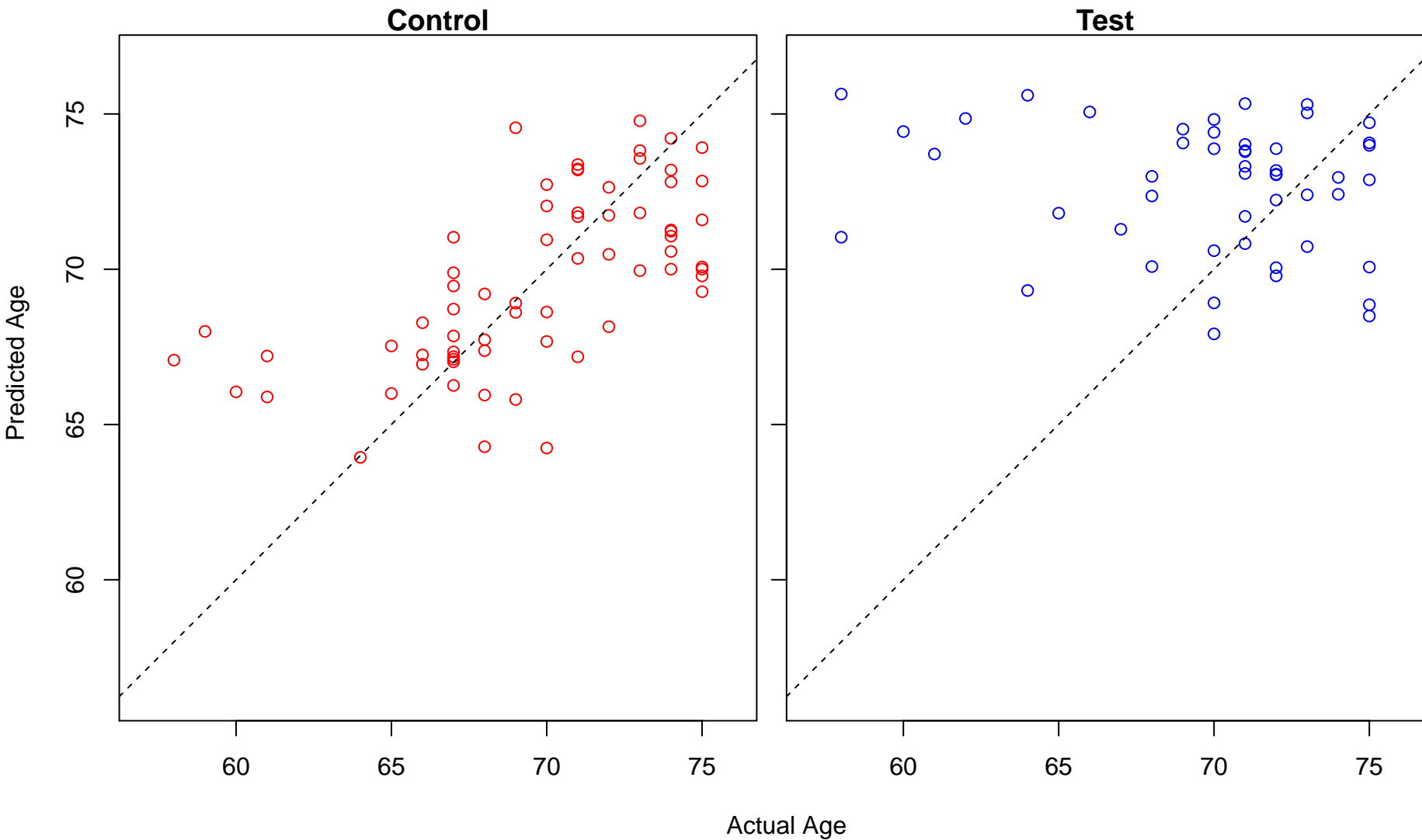


Test

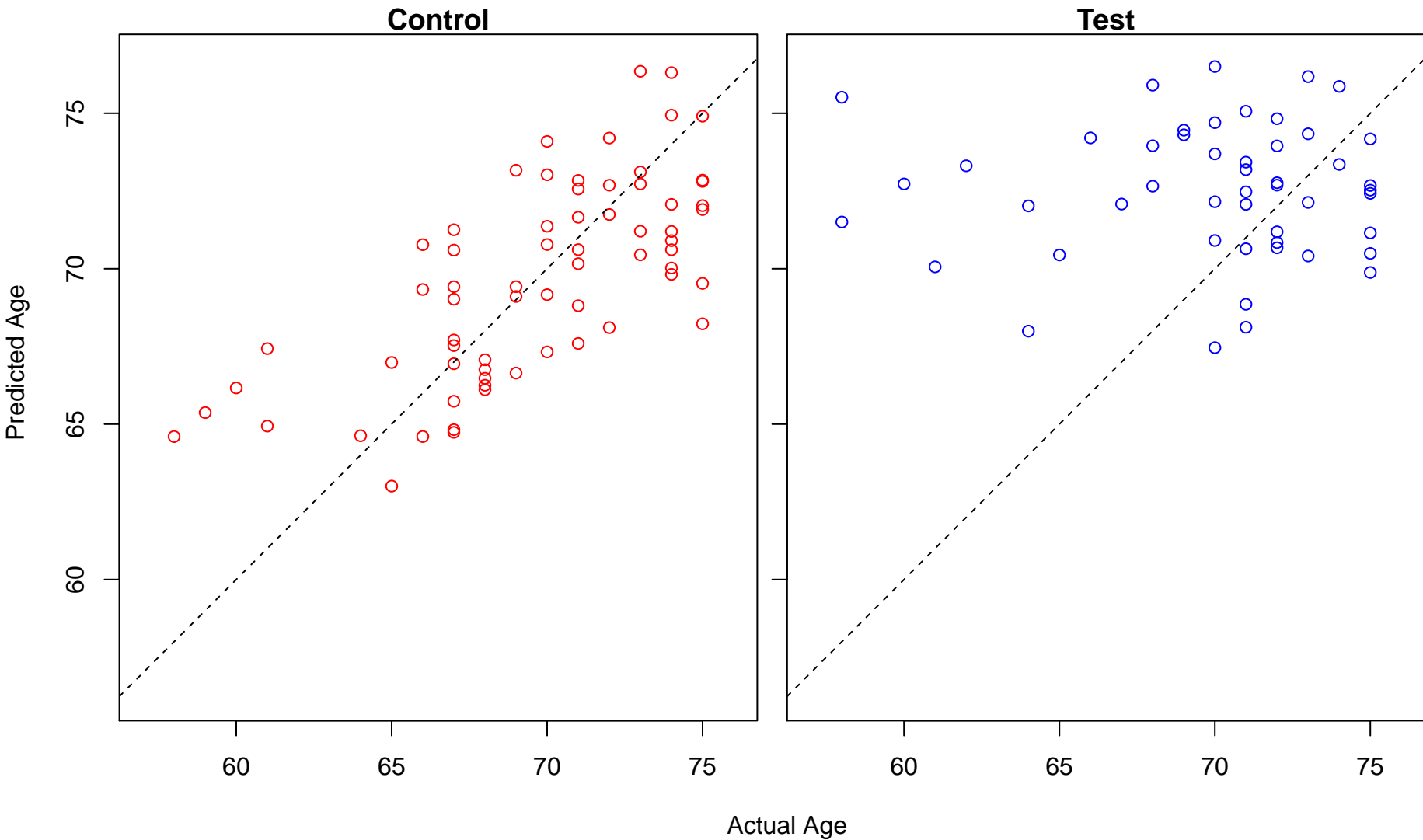


Actual Age

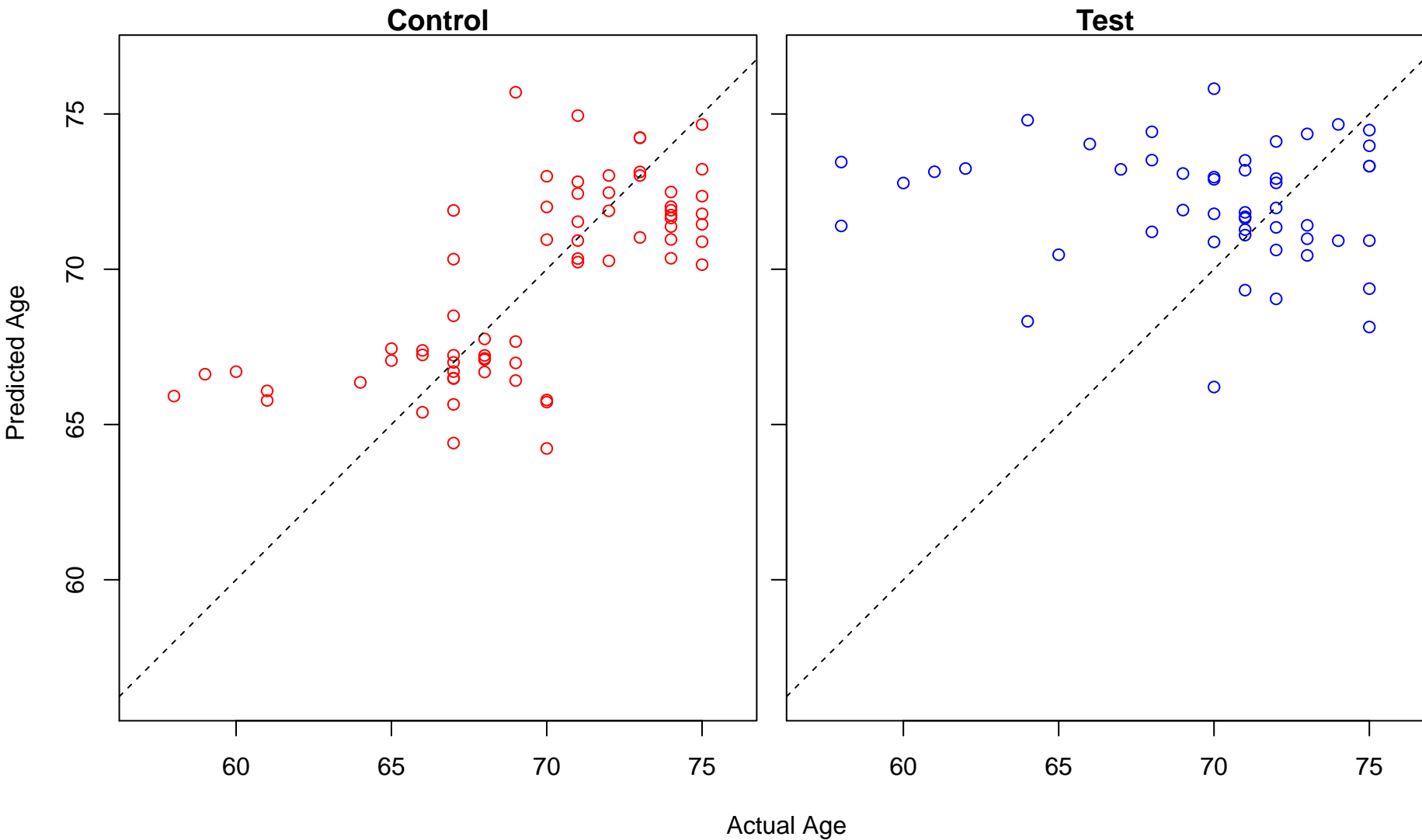
protein ufmylation (Score: 1.867511)



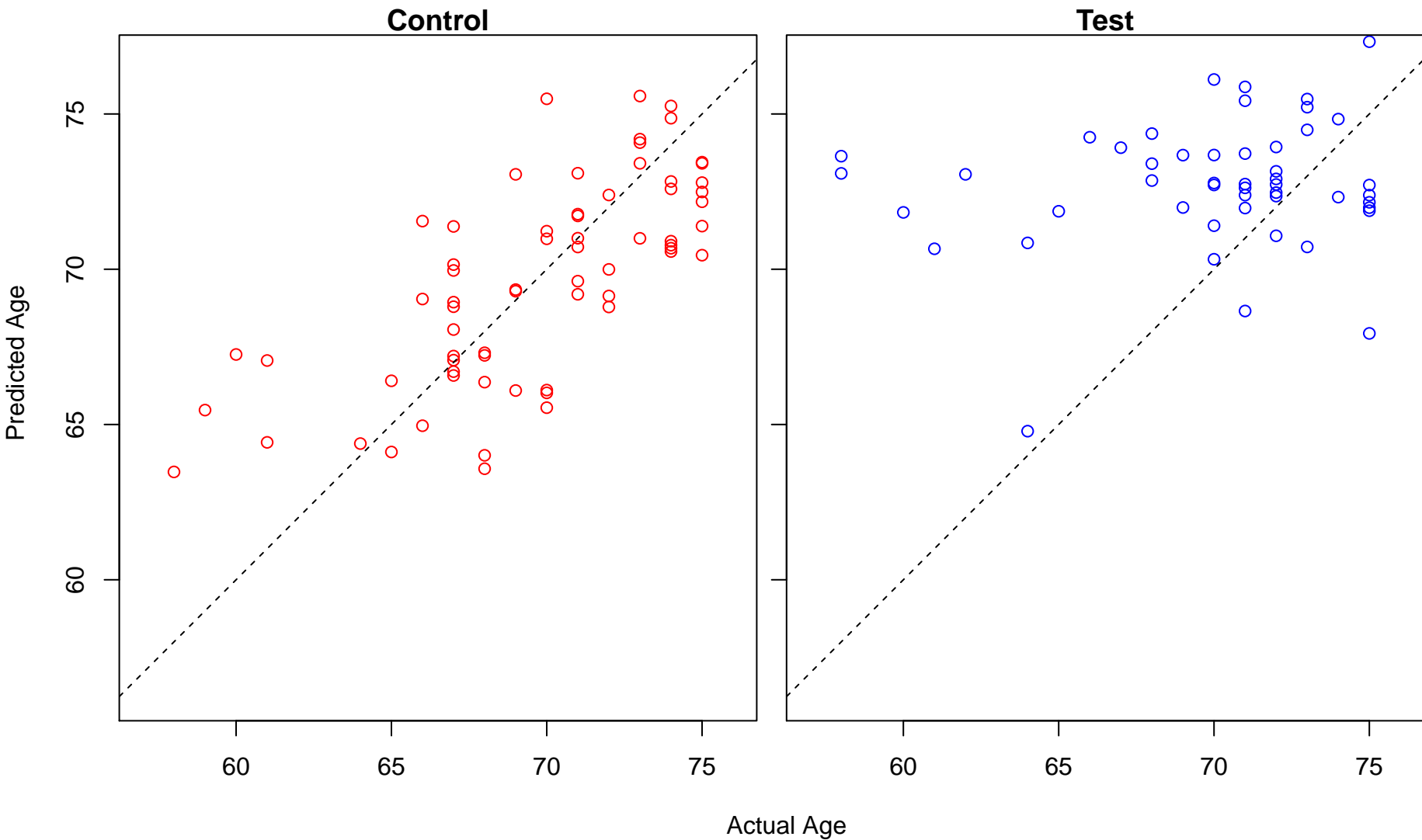
positive regulation of mitochondrial membrane permeability (Score: 1.855018)



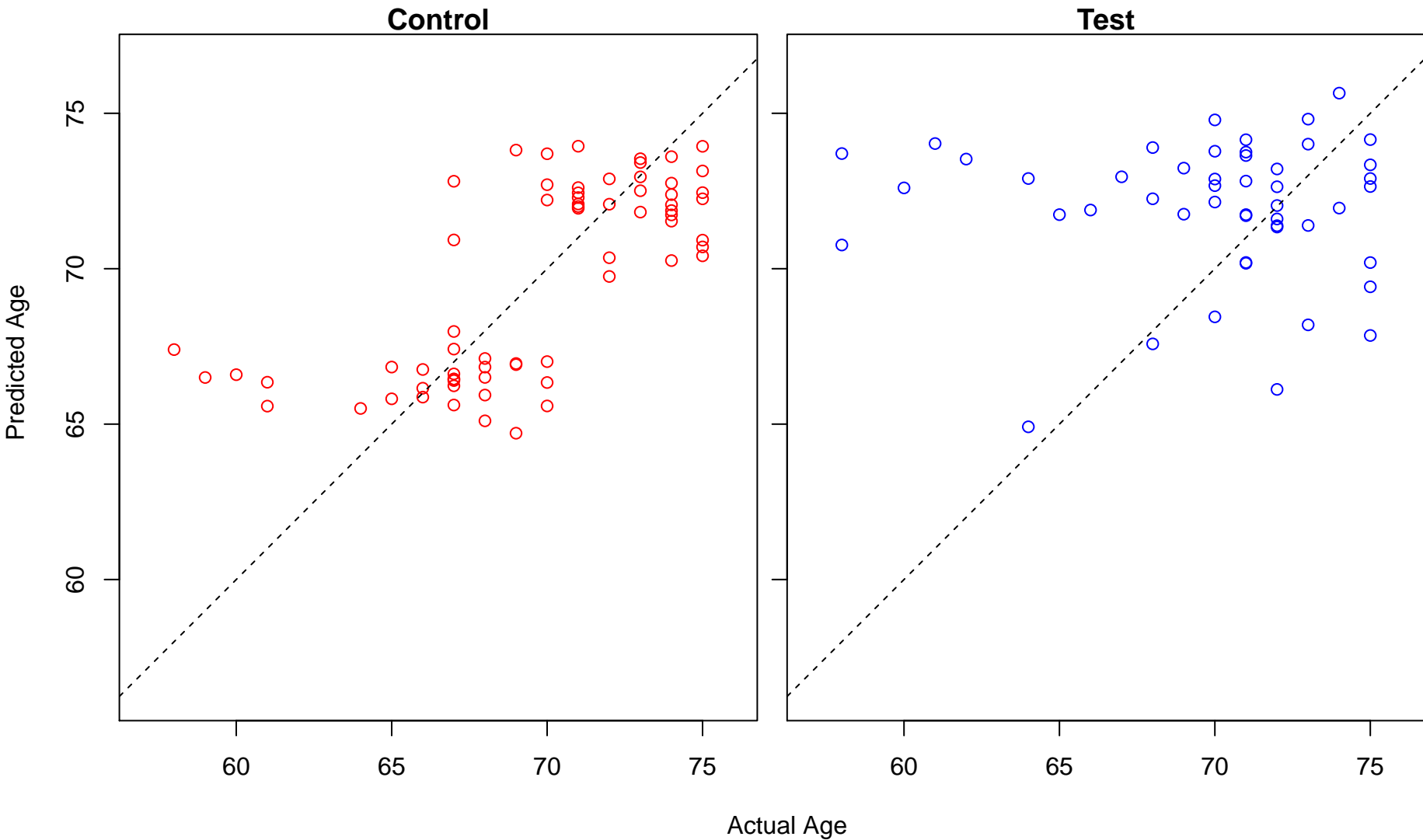
protein repair (Score: 1.847029)



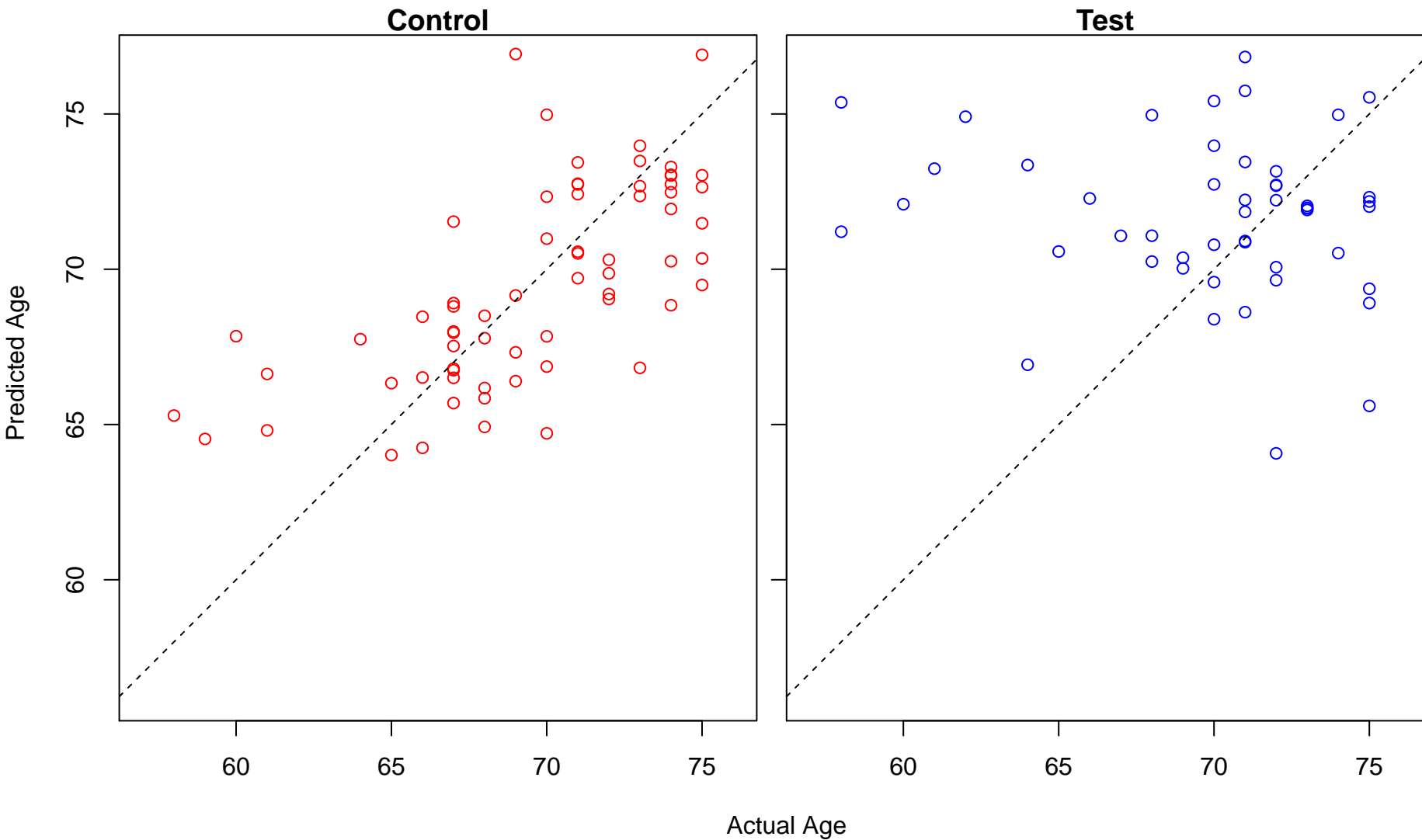
Golgi to endosome transport (Score: 1.845027)



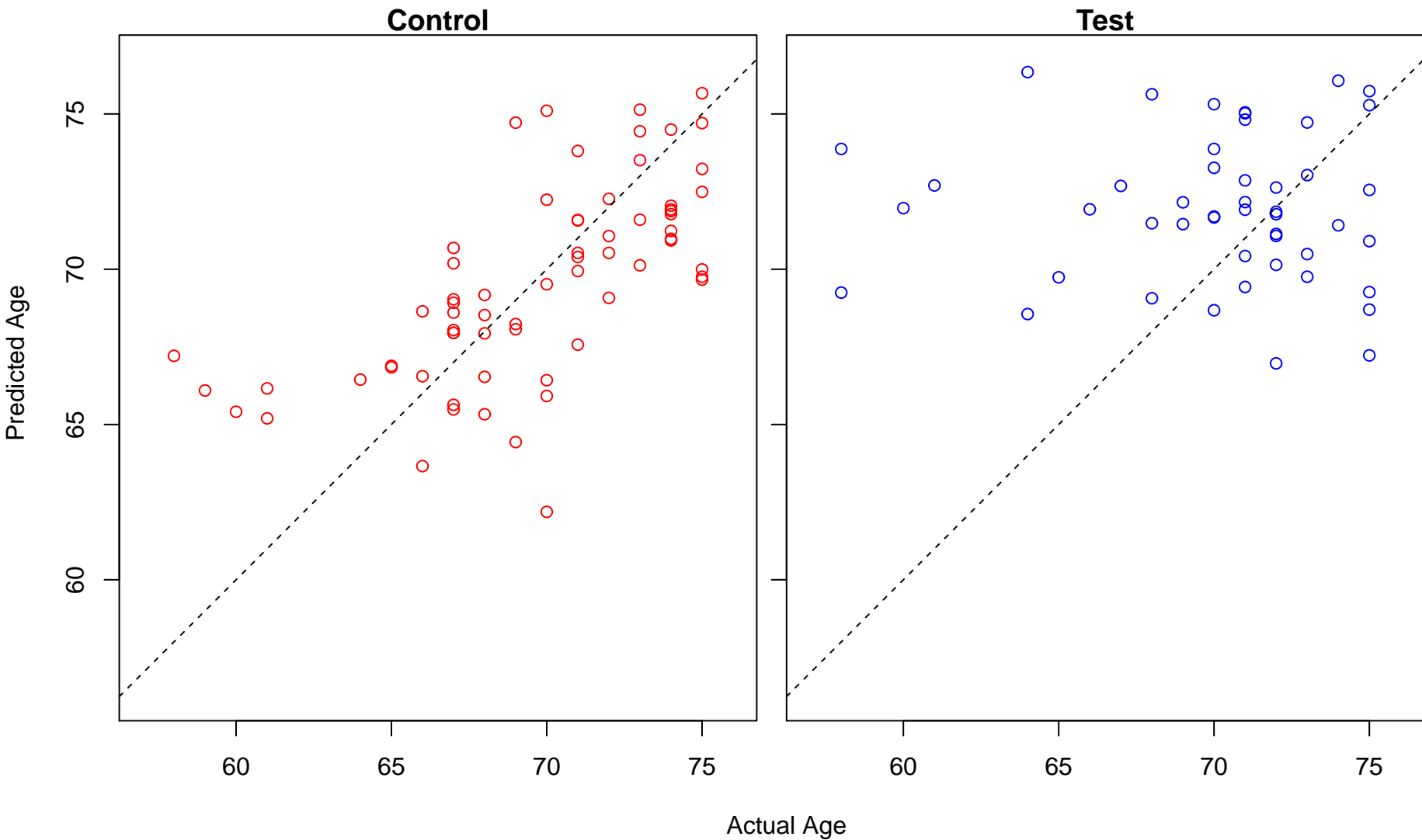
alternative mRNA splicing, via spliceosome (Score: 1.842414)



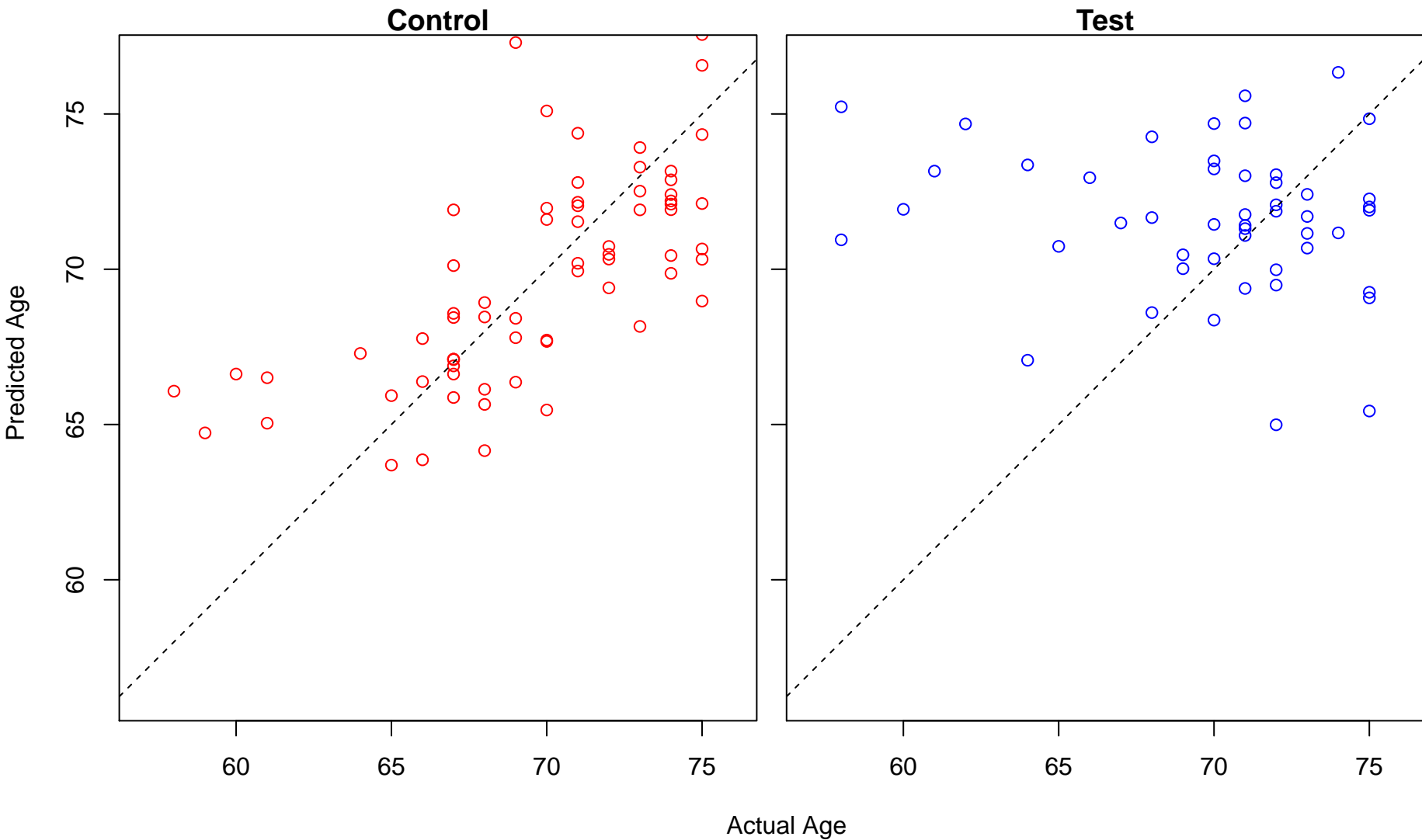
protein deneddylation (Score: 1.835985)



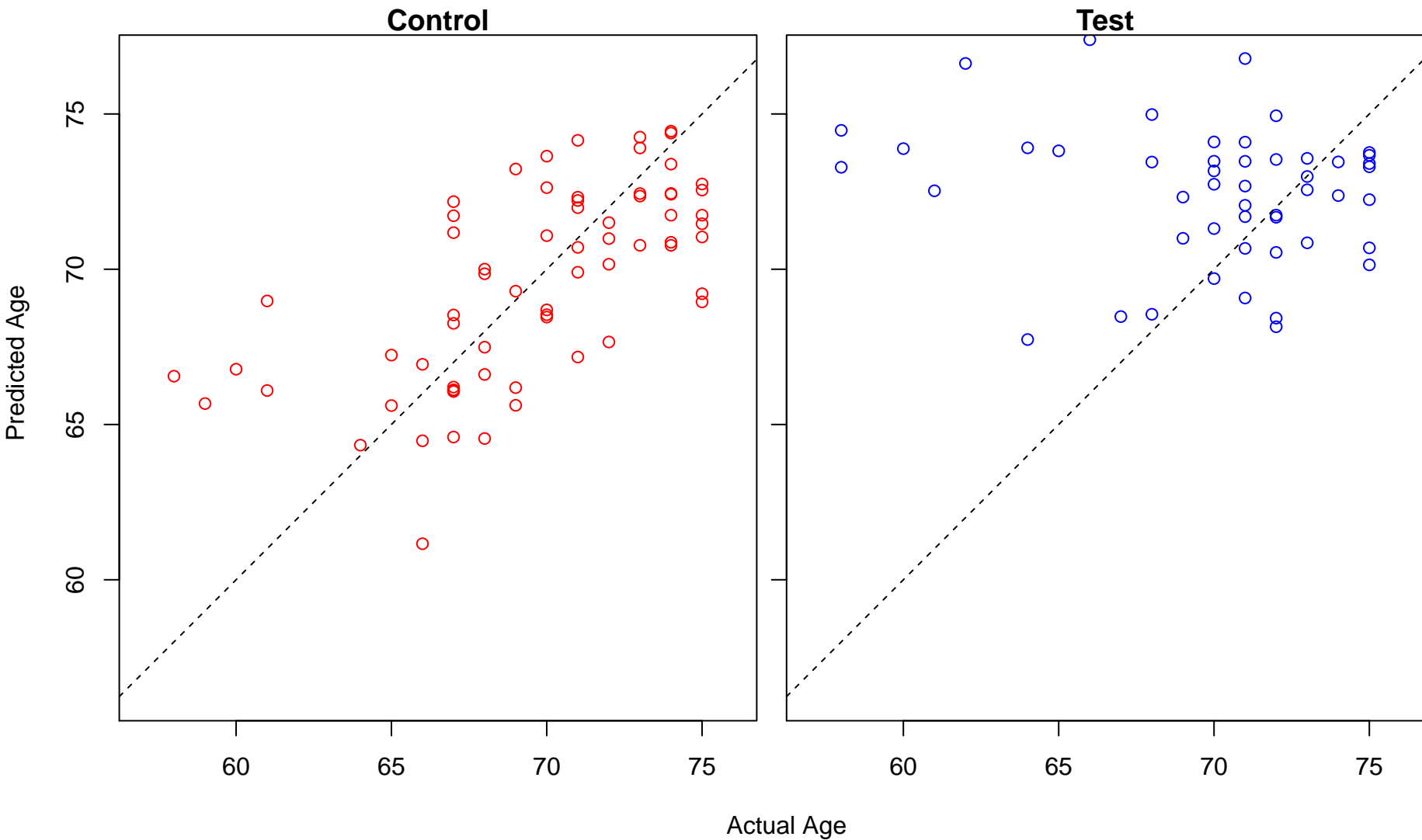
protein neddylation (Score: 1.829838)



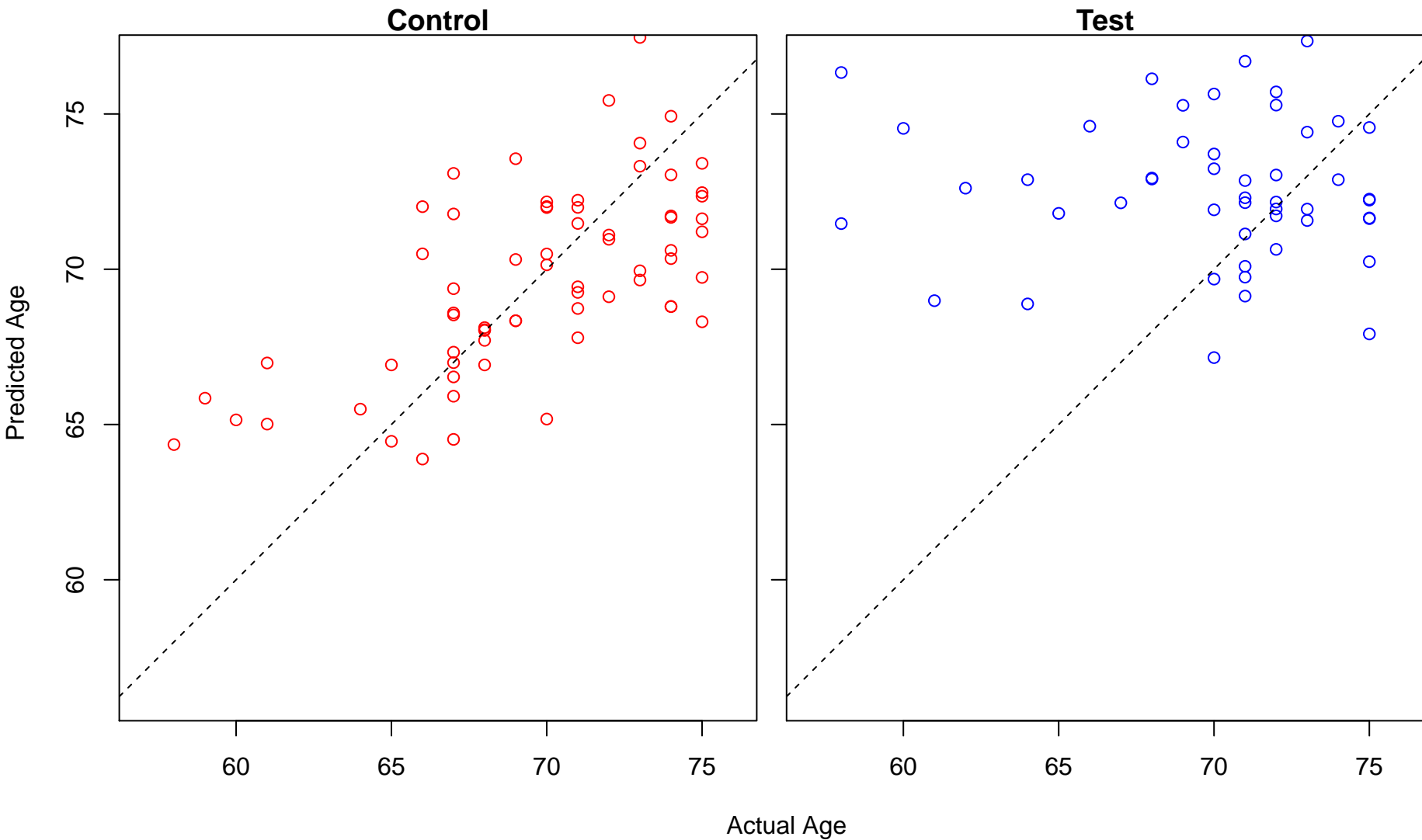
cullin deneddylation (Score: 1.828413)



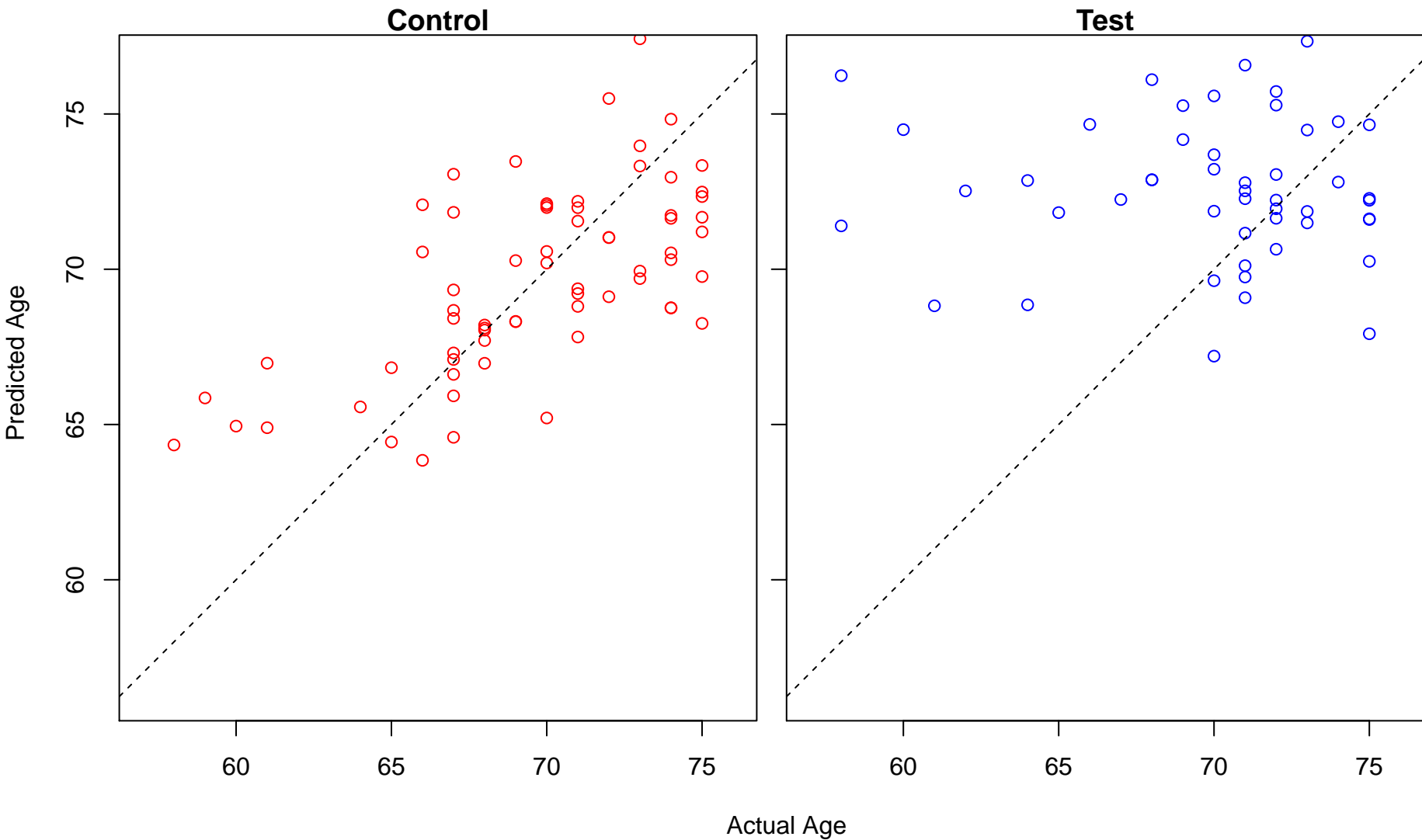
histone H3-K4 trimethylation (Score: 1.826060)



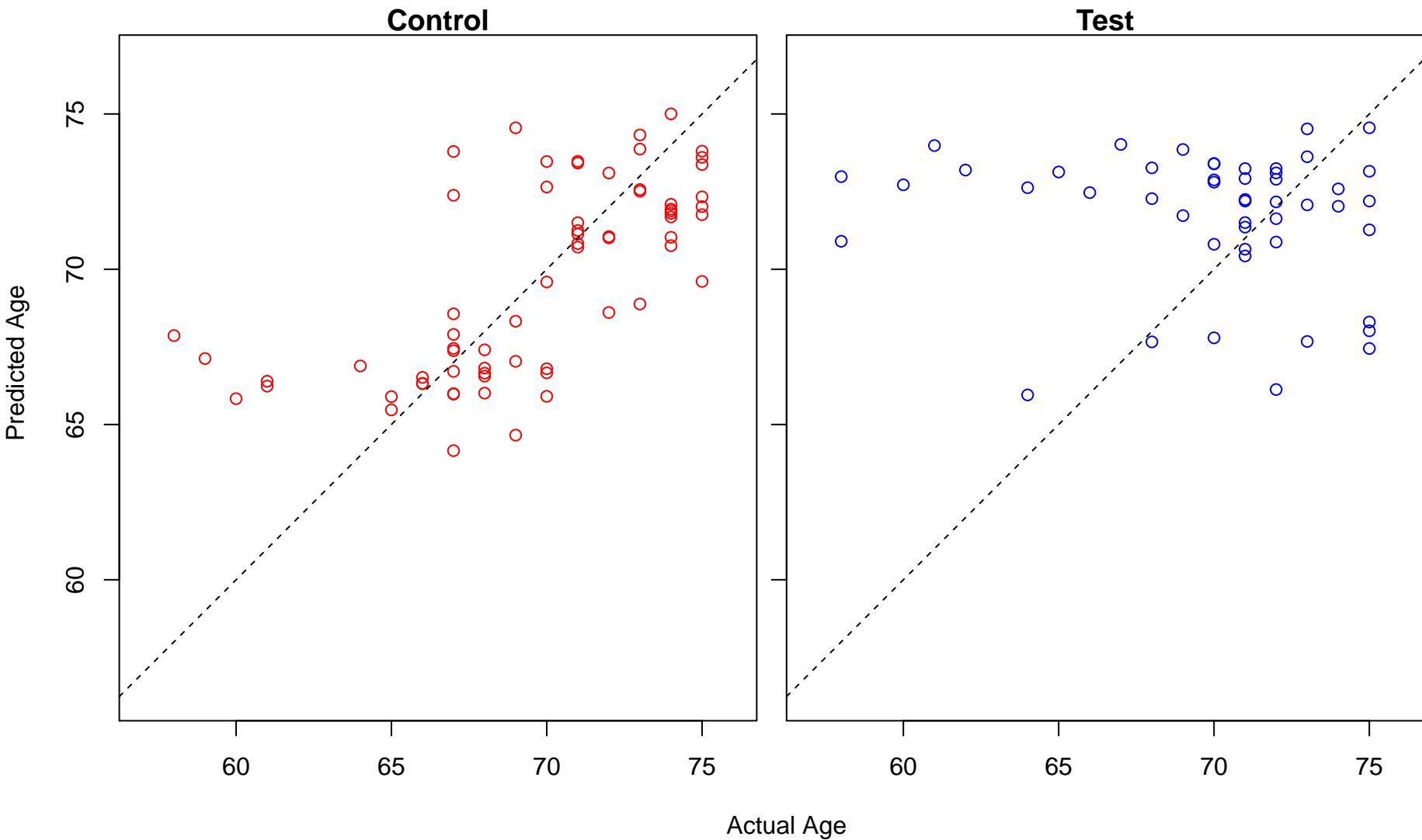
mitochondrial outer membrane permeabilization involved in programmed cell death (Score: 1.79928)



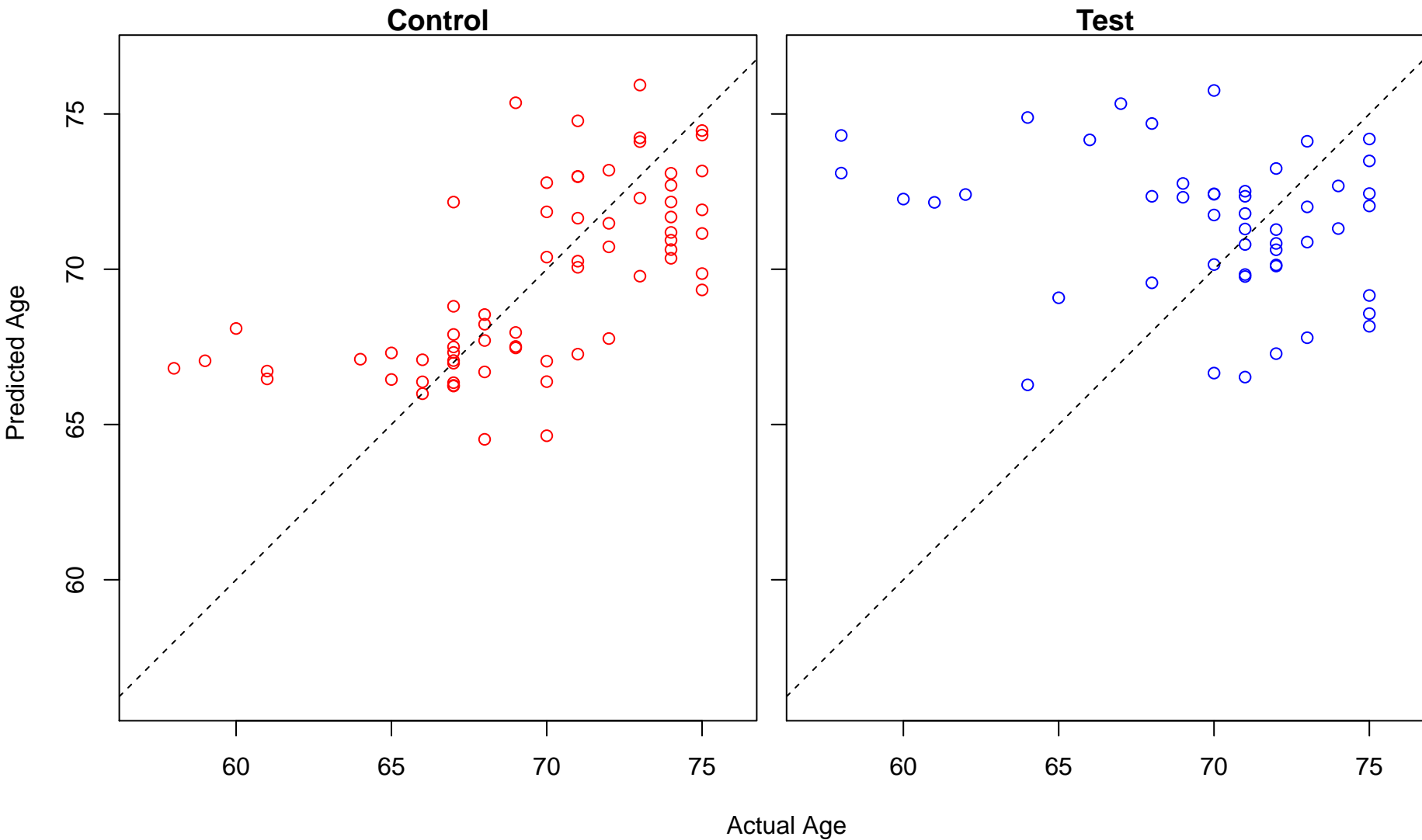
mitochondrial outer membrane permeabilization (Score: 1.796809)



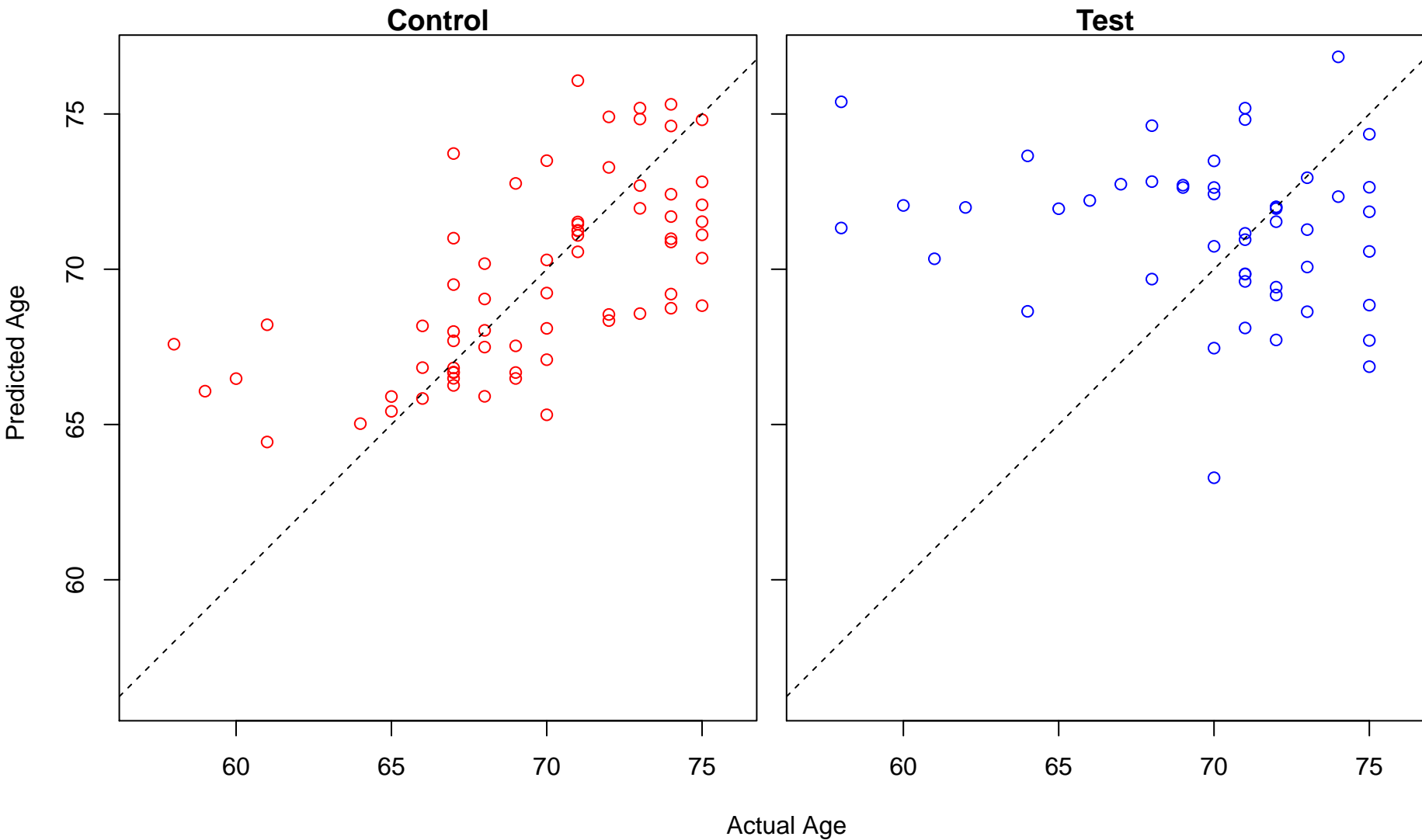
mRNA 3'-splice site recognition (Score: 1.786397)



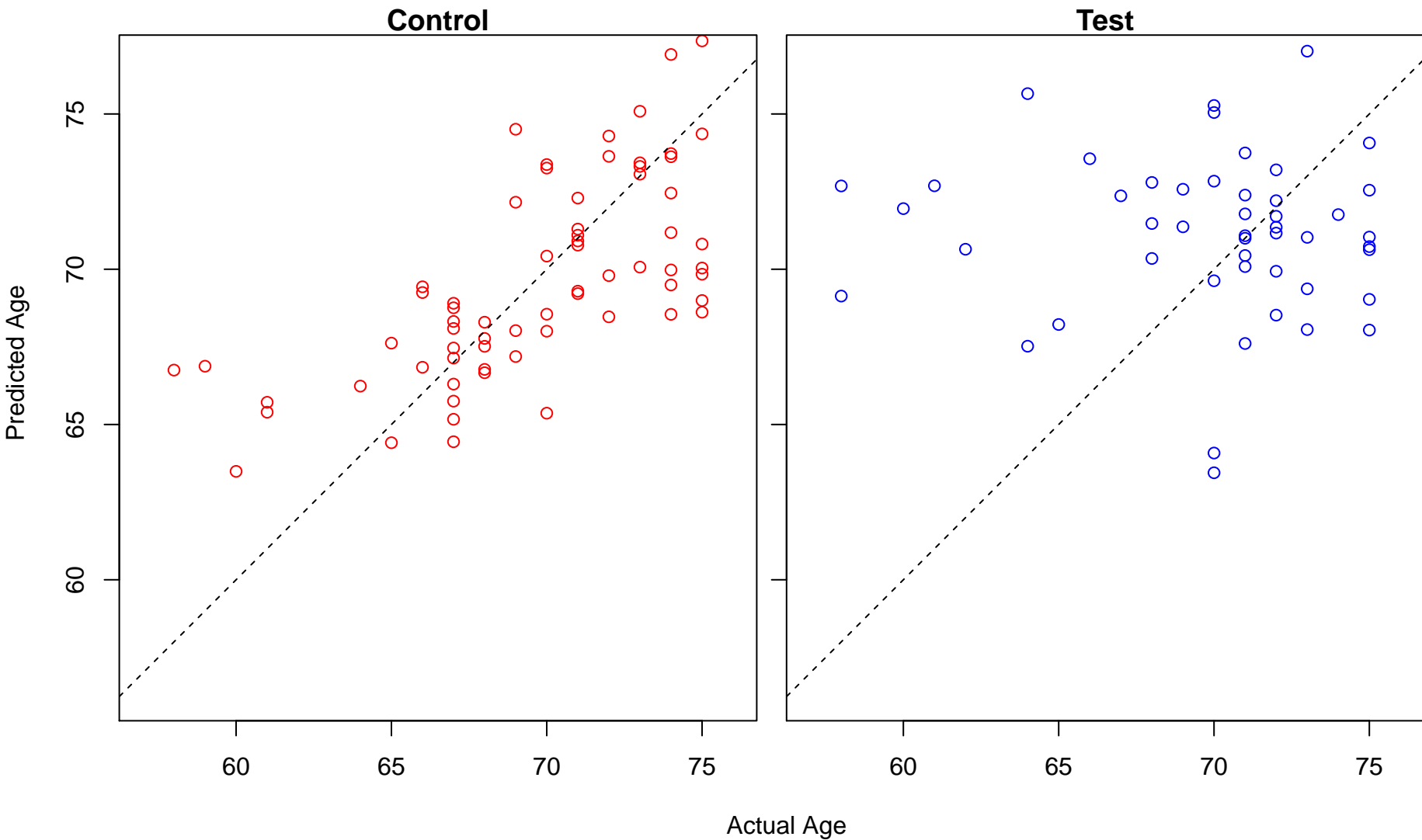
protein nitrosylation (Score: 1.782669)



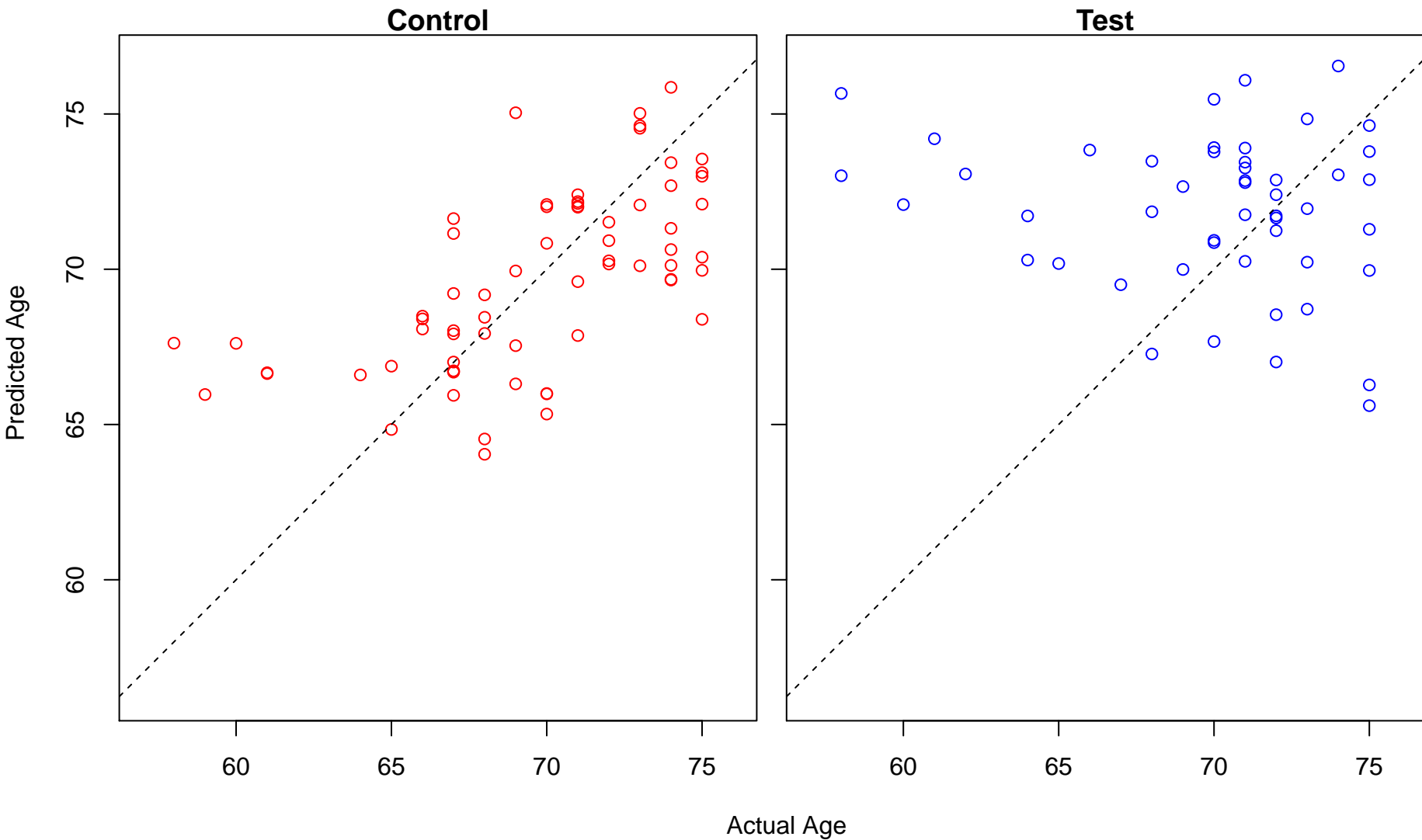
spliceosomal tri-snRNP complex assembly (Score: 1.766197)



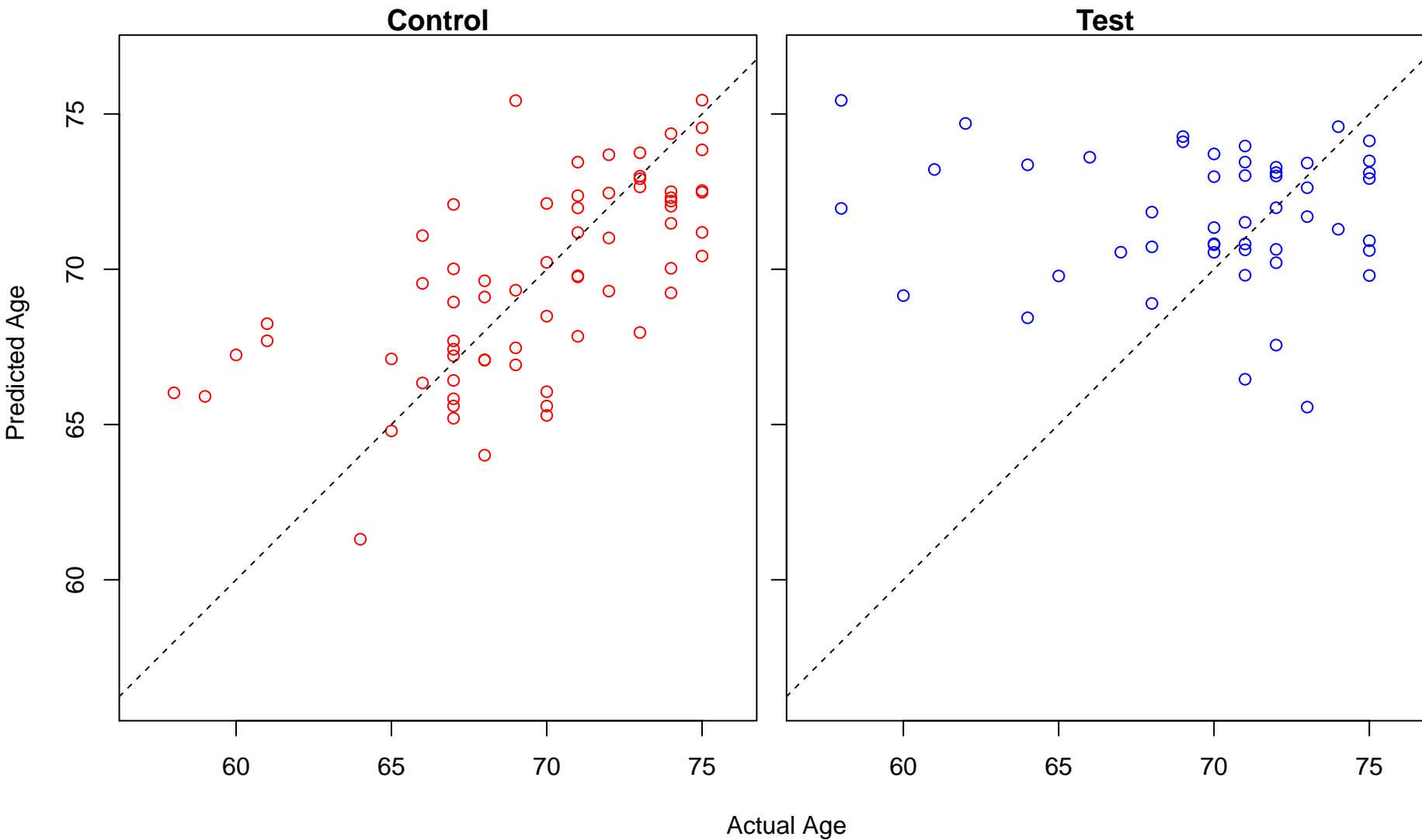
negative regulation of fatty acid oxidation (Score: 1.760042)



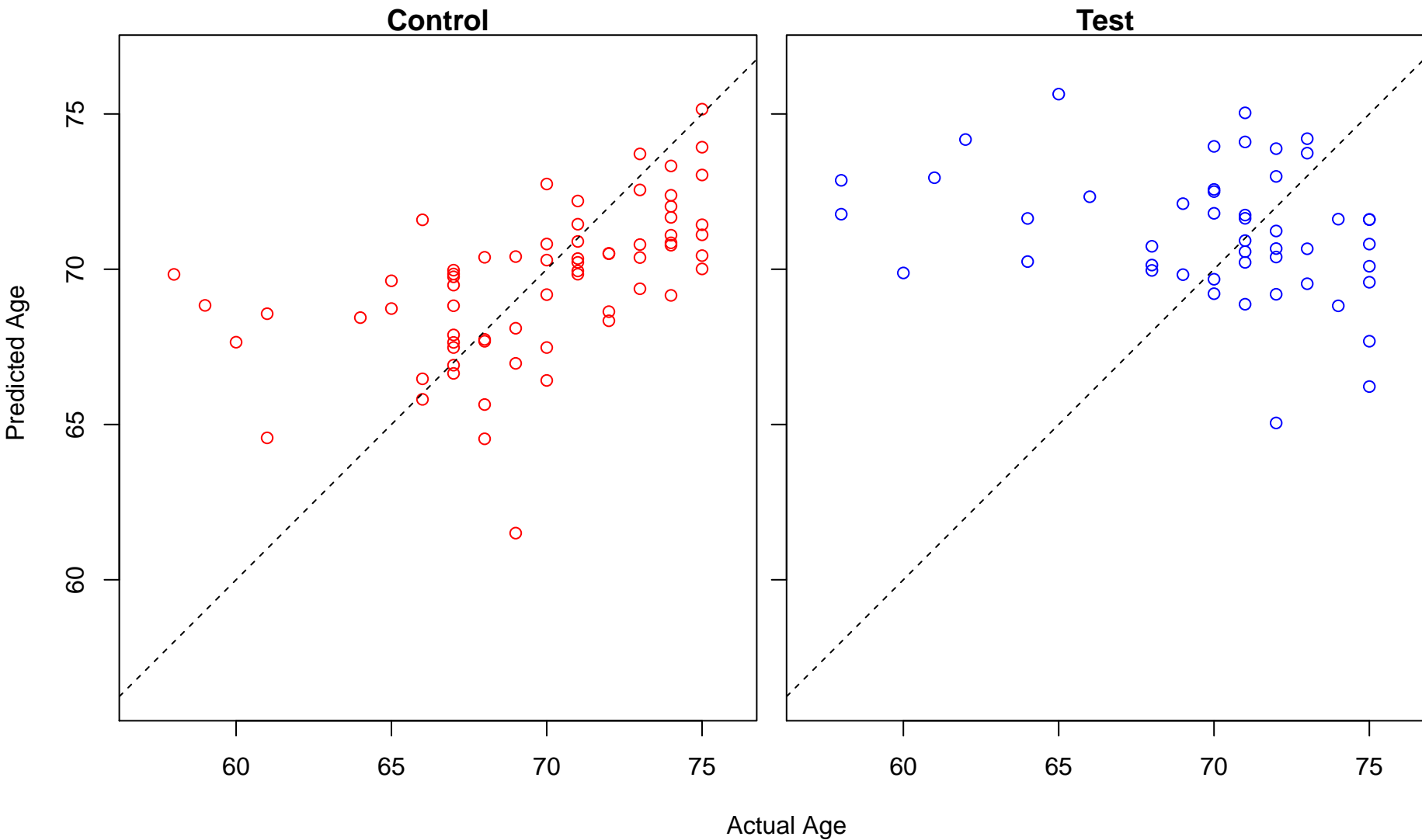
regulation of bone development (Score: 1.751570)



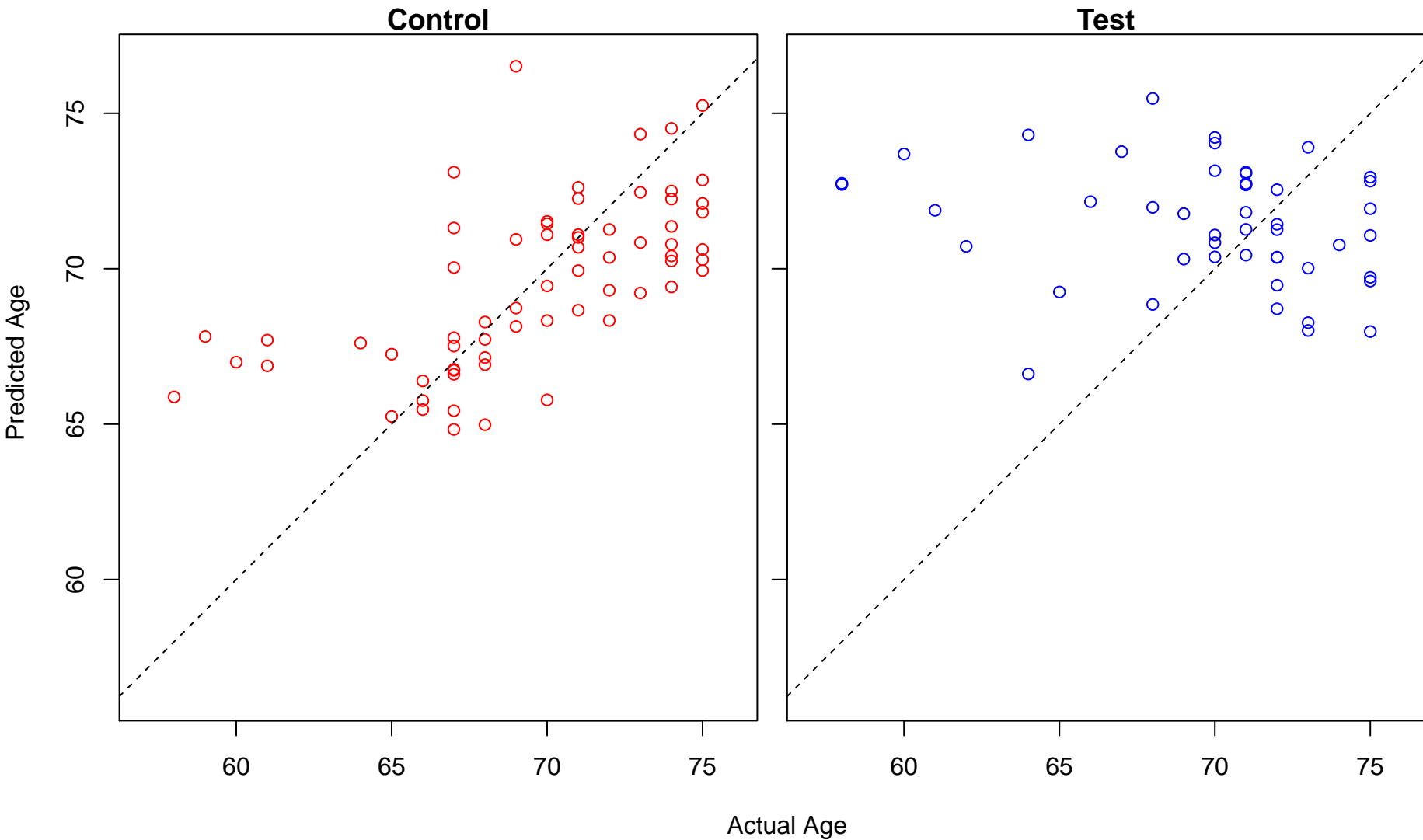
sybiont intracellular protein transport in host (Score: 1.673430)



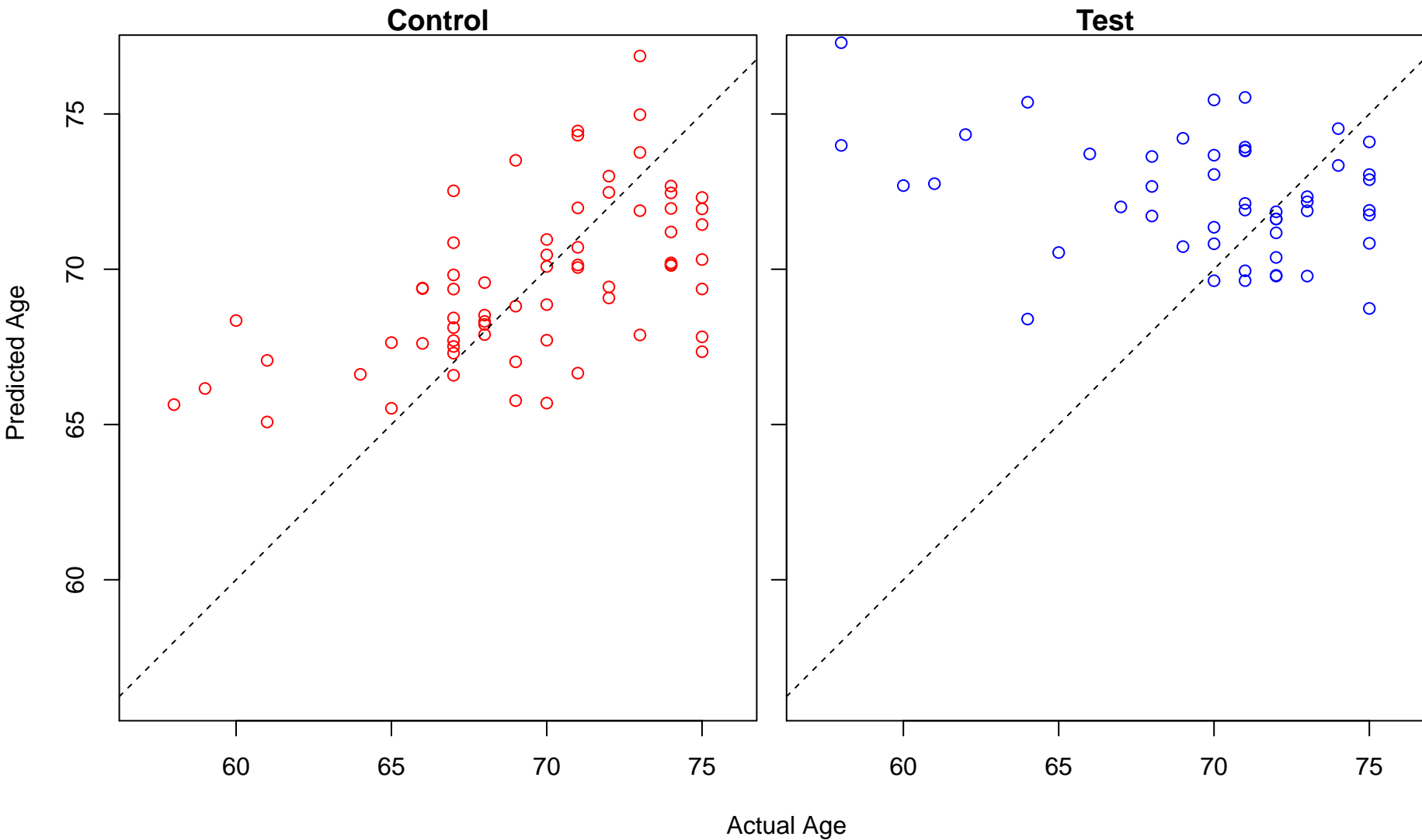
positive regulation of double-strand break repair (Score: 1.659347)



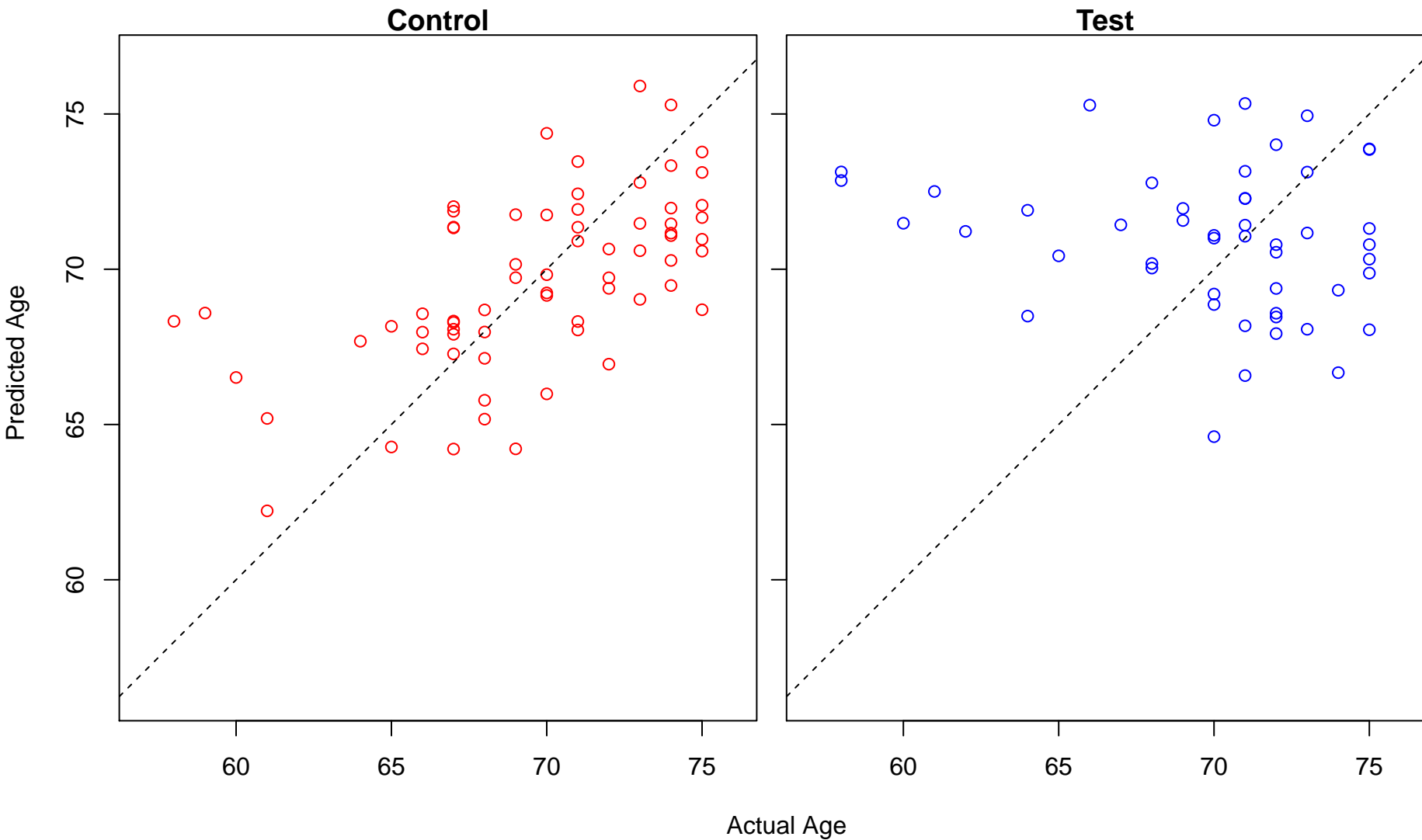
positive regulation of vesicle fusion (Score: 1.652676)



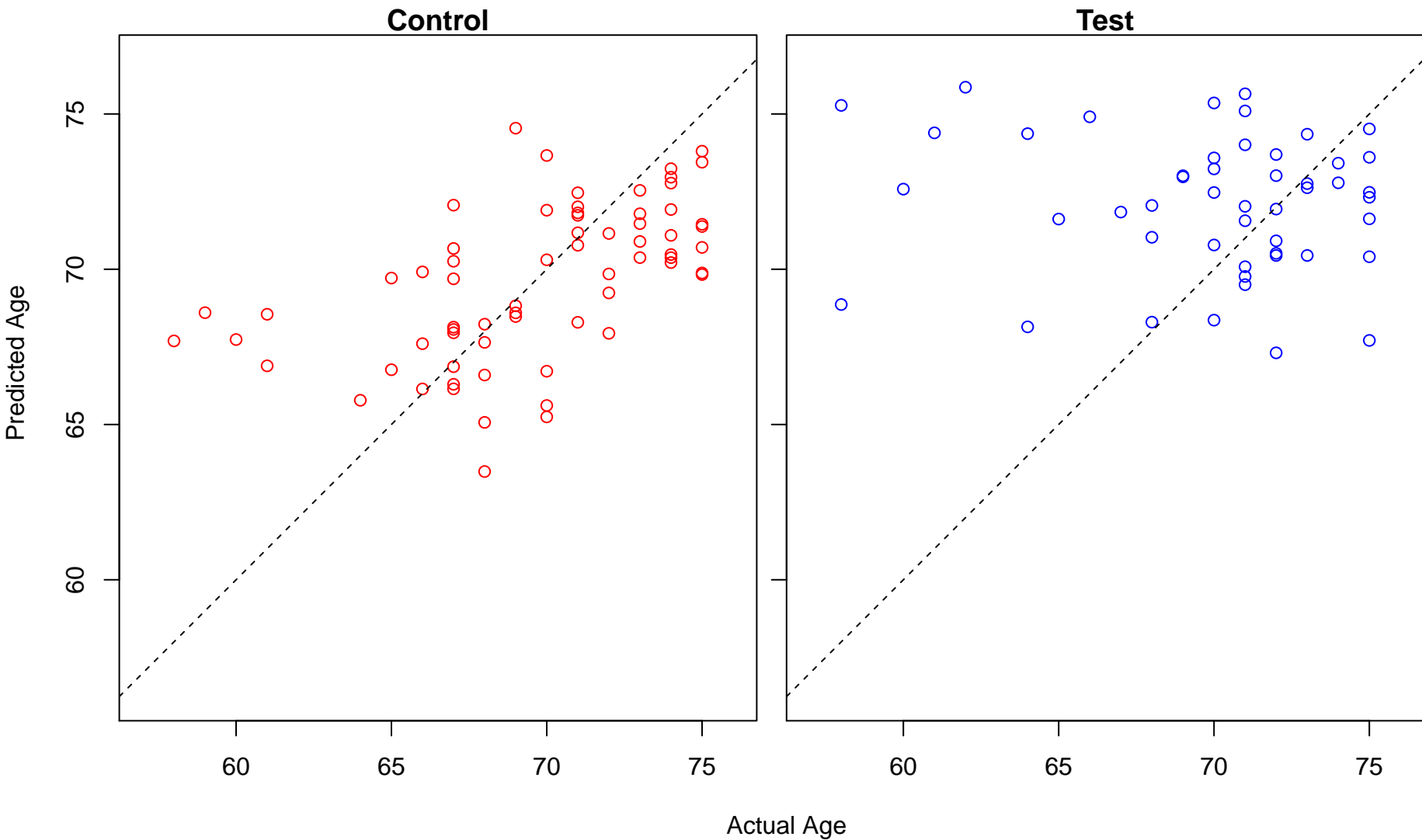
snRNA transcription from RNA polymerase III promoter (Score: 1.646420)



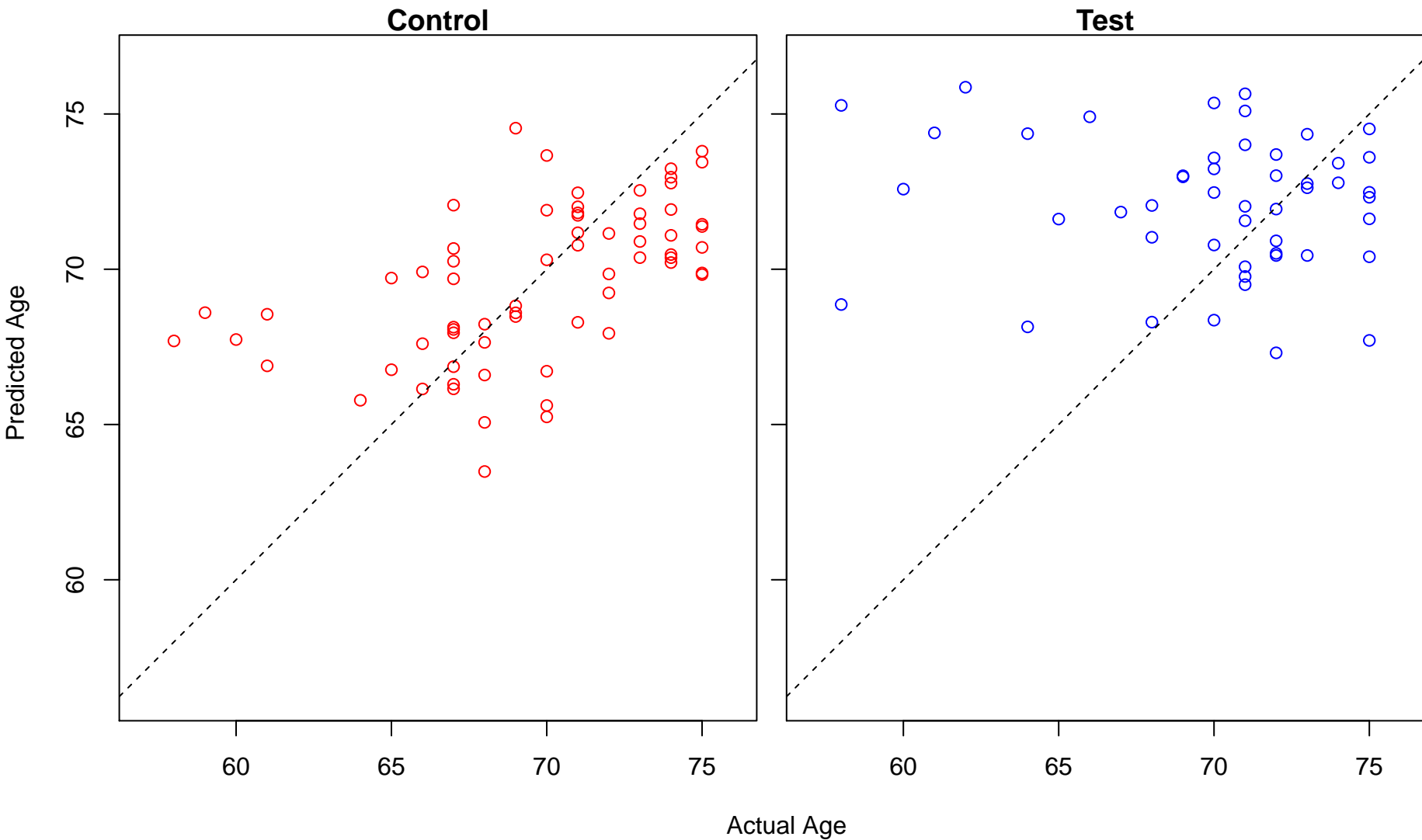
GTP metabolic process (Score: 1.614202)



protein polyufmylation (Score: 1.578232)



protein K69-linked ufmylation (Score: 1.578232)



astral microtubule organization (Score: 1.536596)

