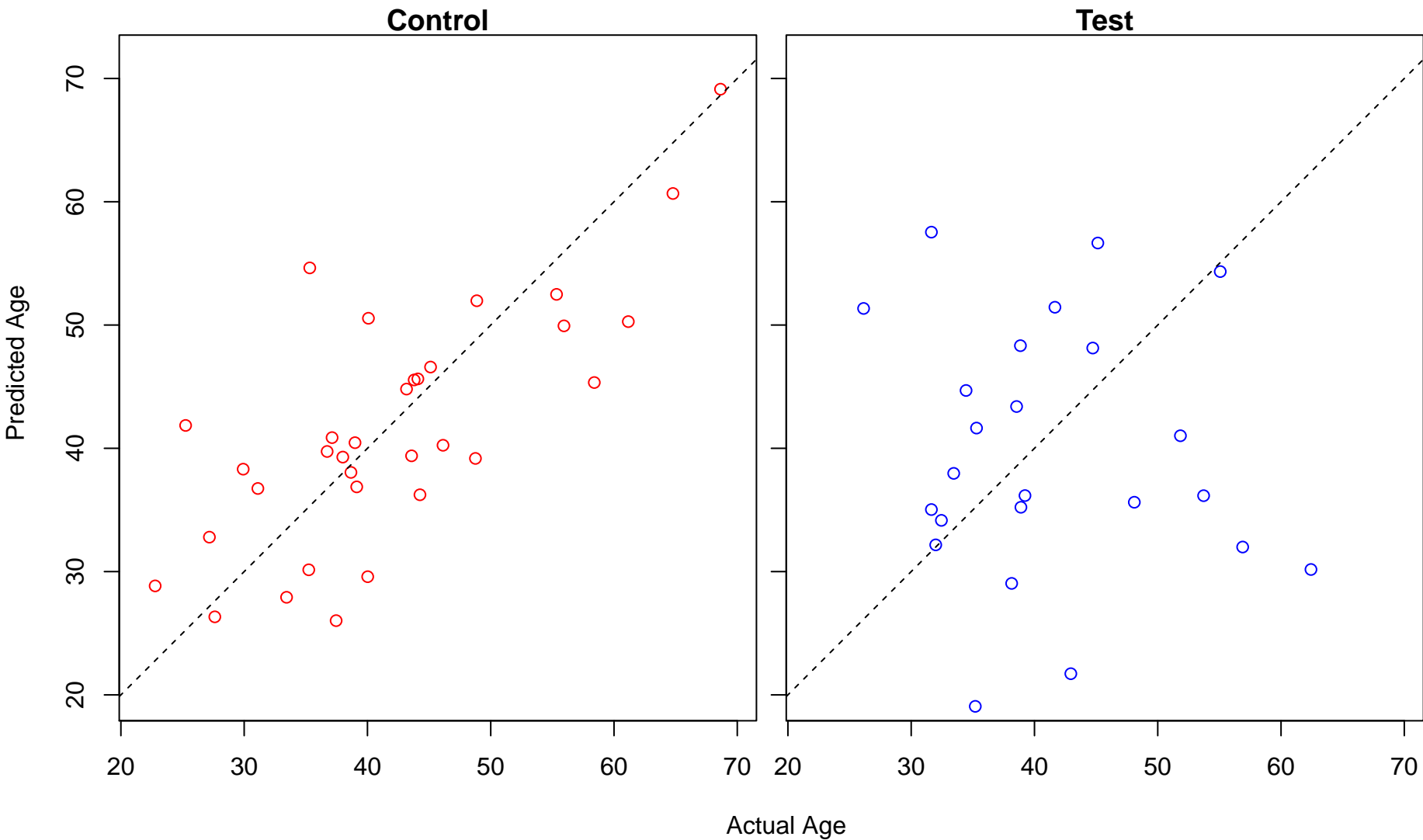
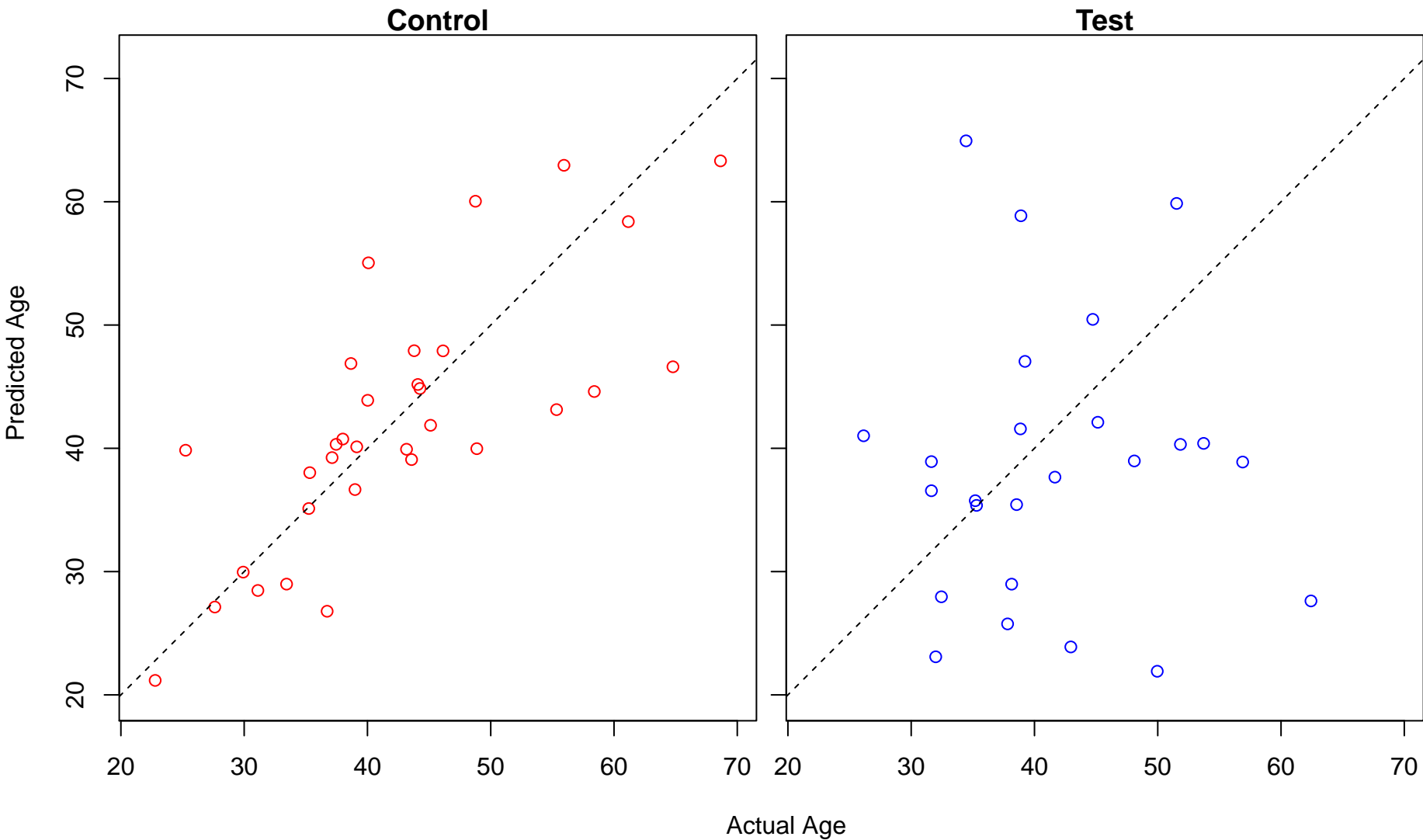


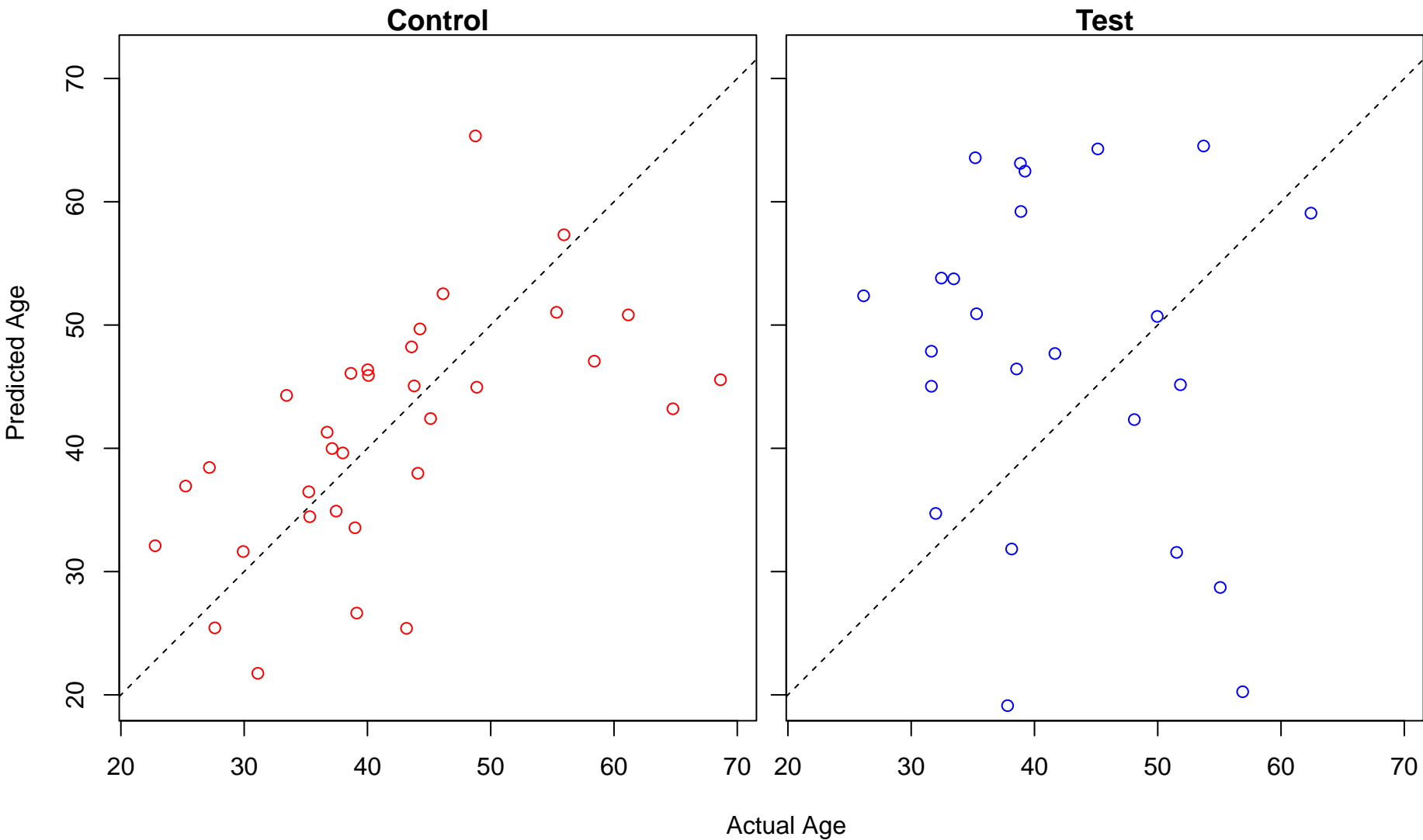
negative regulation of DNA recombination (Score: 2.778153)



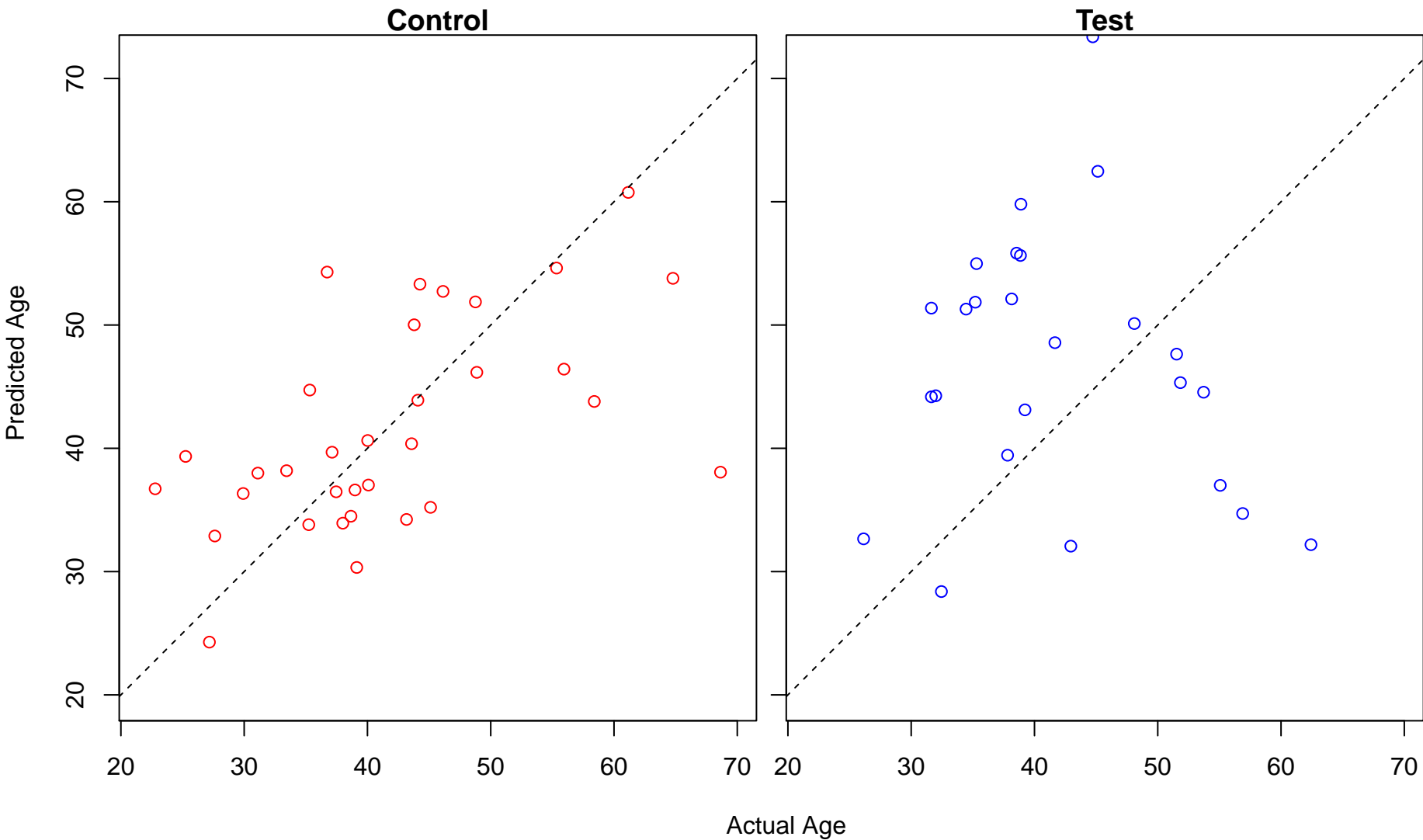
telomere maintenance via recombination (Score: 2.724690)



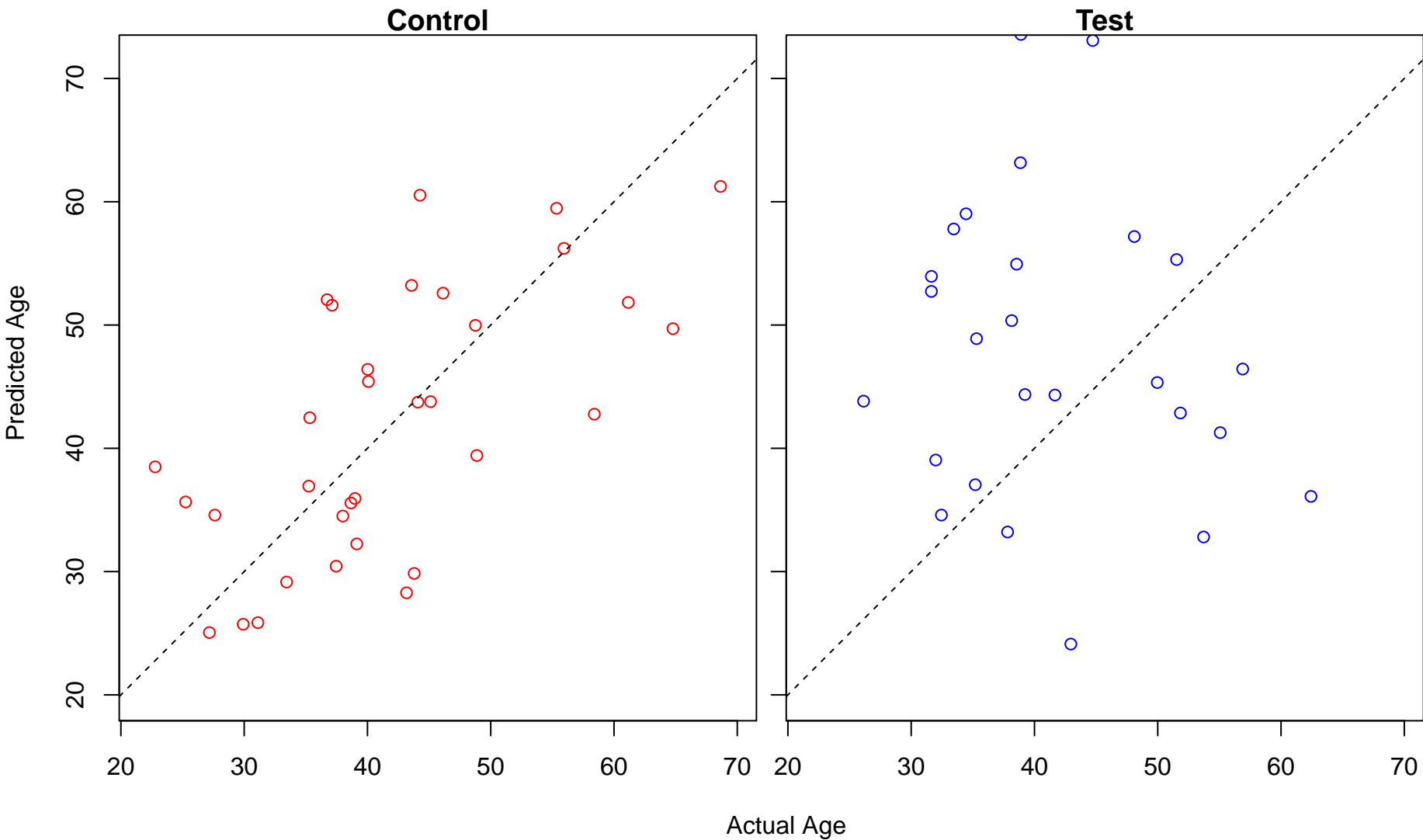
regulation of anion transport (Score: 2.418190)



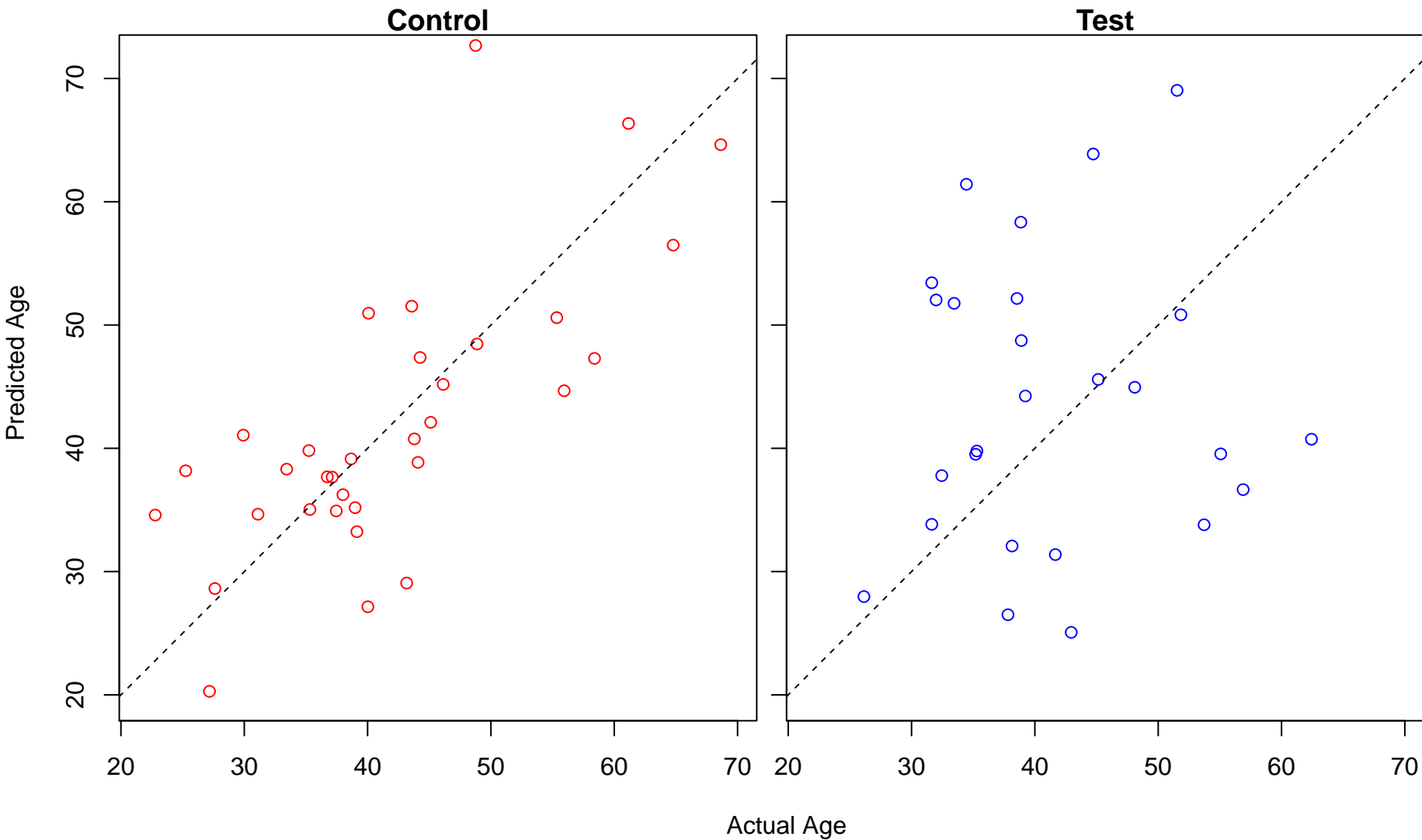
negative regulation of reactive oxygen species biosynthetic process (Score: 2.103974)



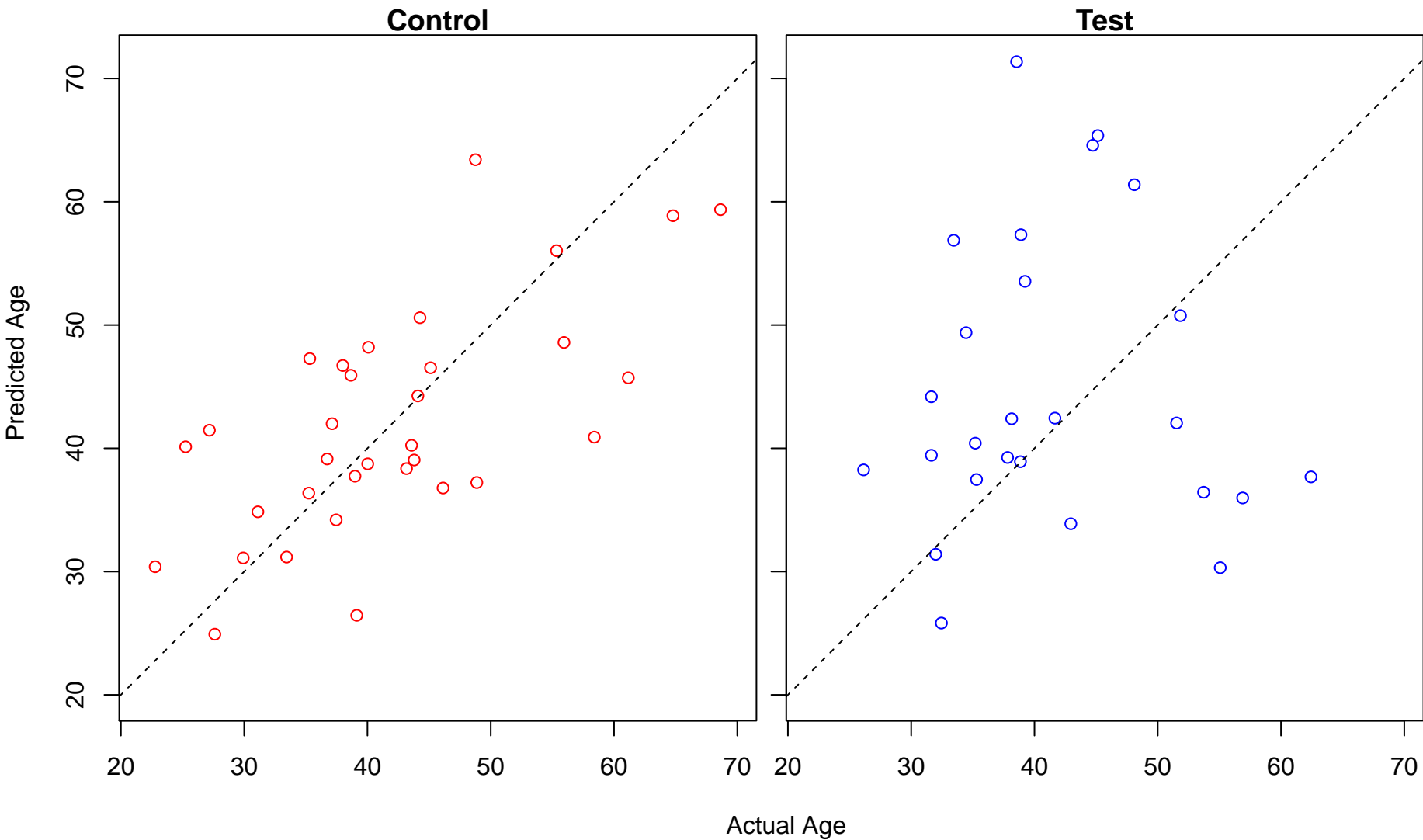
regulation of nitric oxide biosynthetic process (Score: 2.090749)



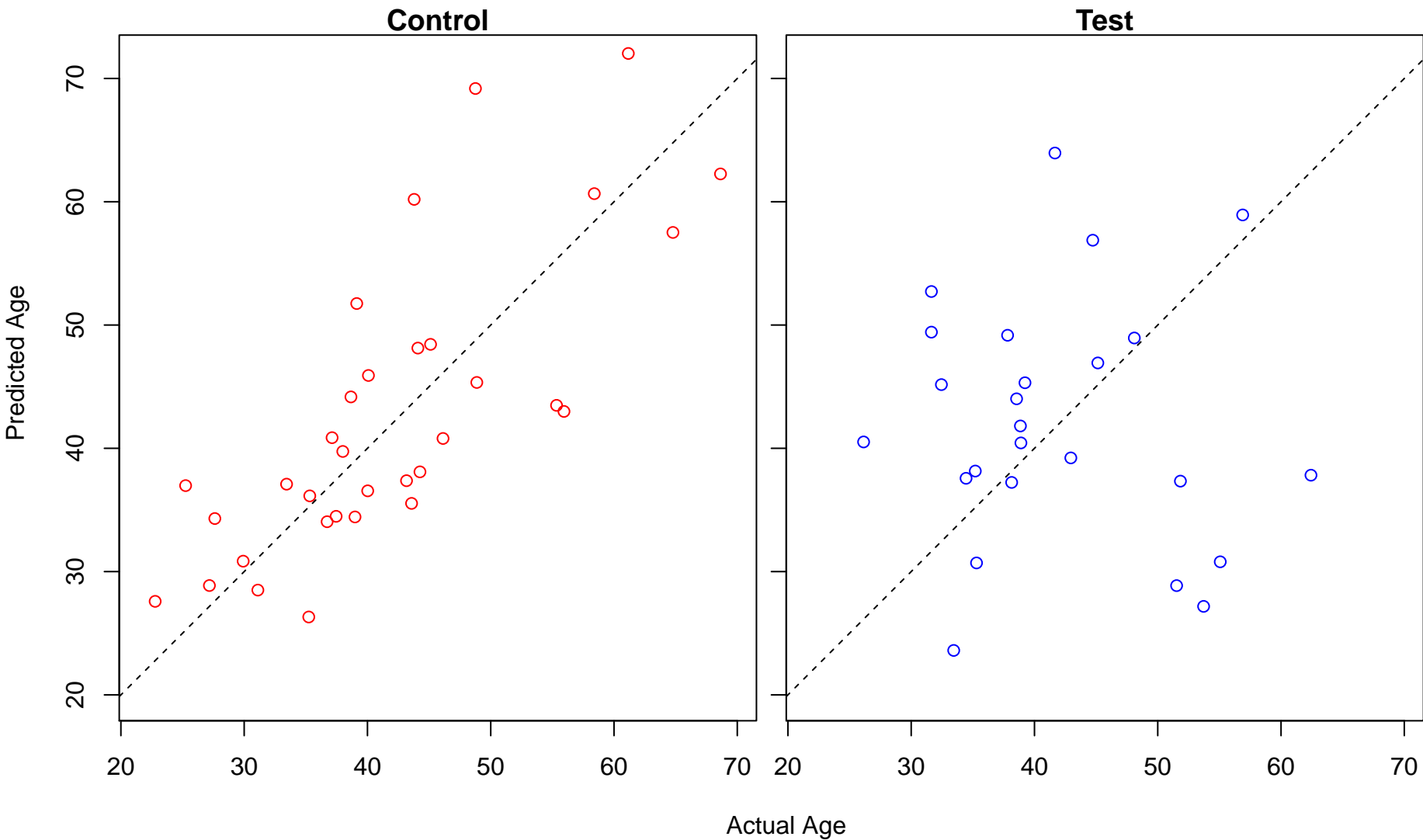
regulation of epidermal growth factor receptor signaling pathway (Score: 2.027198)



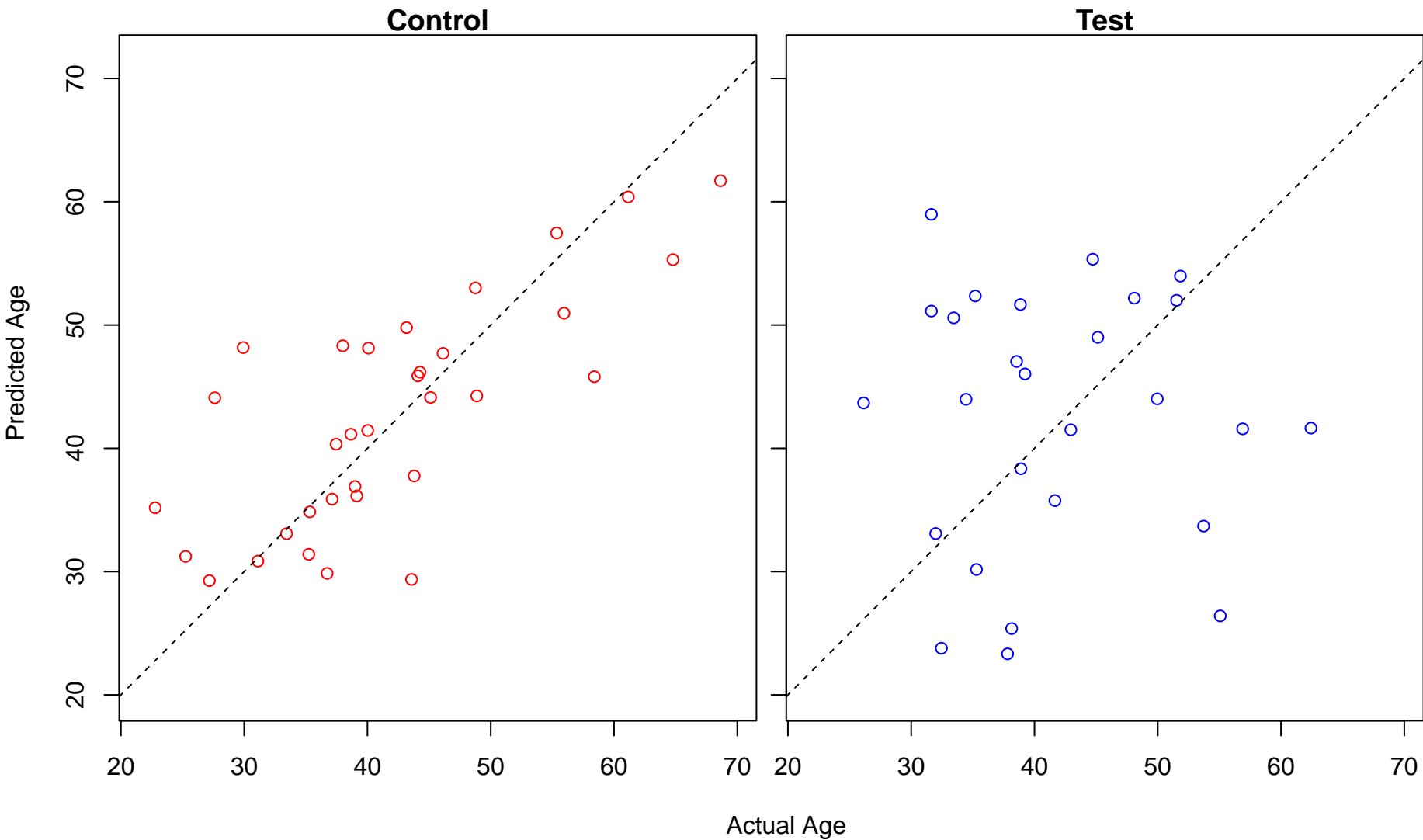
intracellular protein transmembrane import (Score: 2.000334)



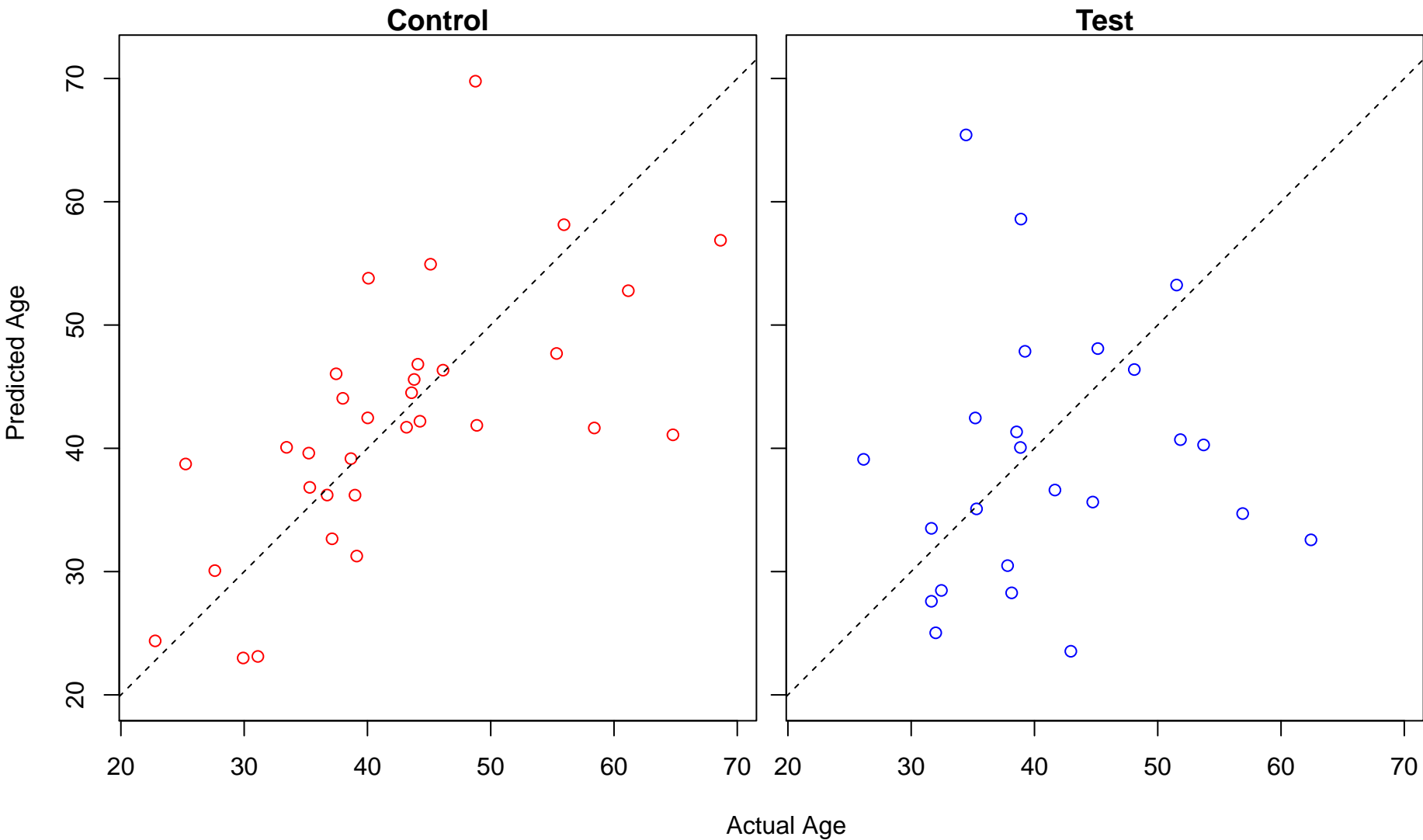
regulation of leukocyte degranulation (Score: 1.970425)



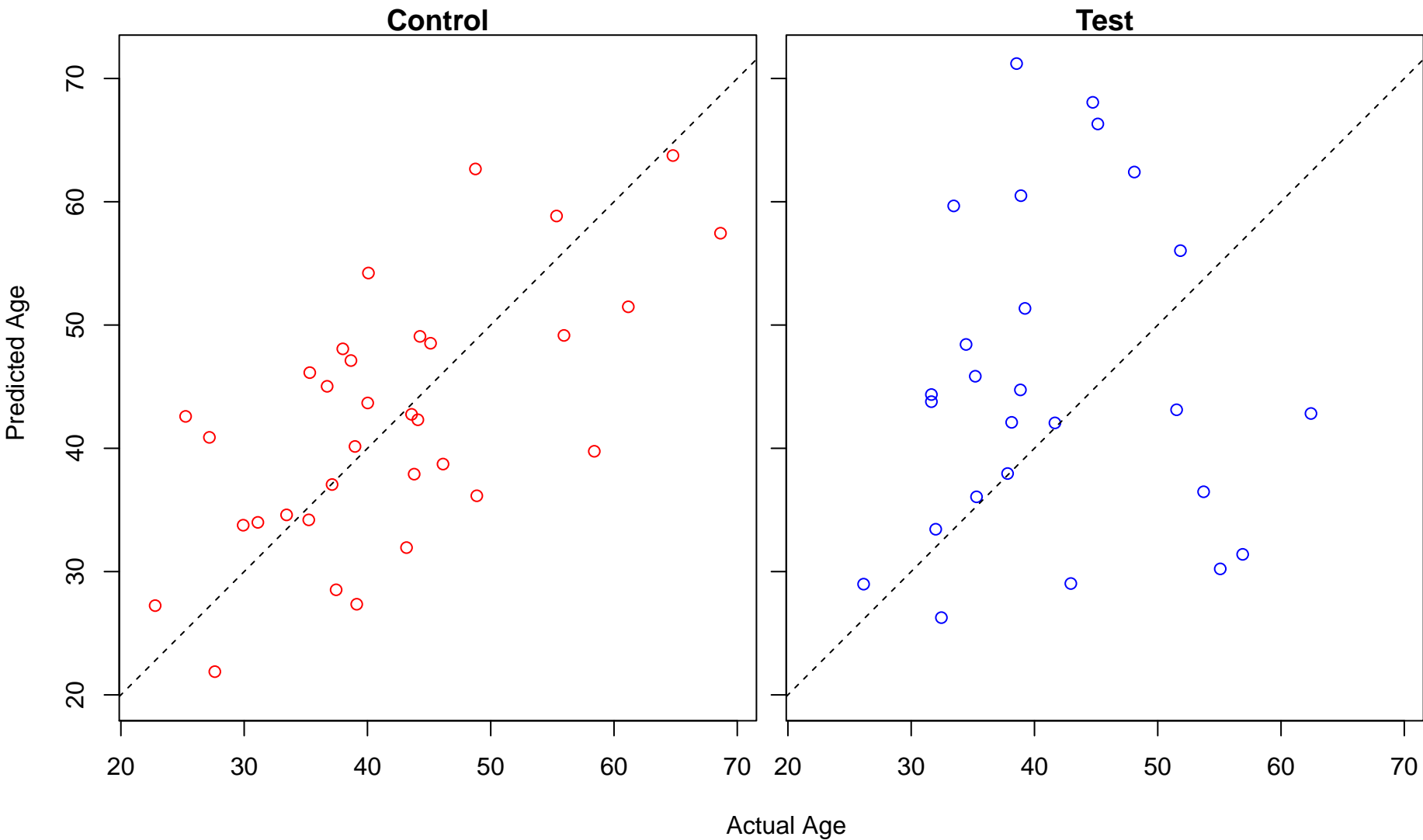
phototransduction, visible light (Score: 1.966733)



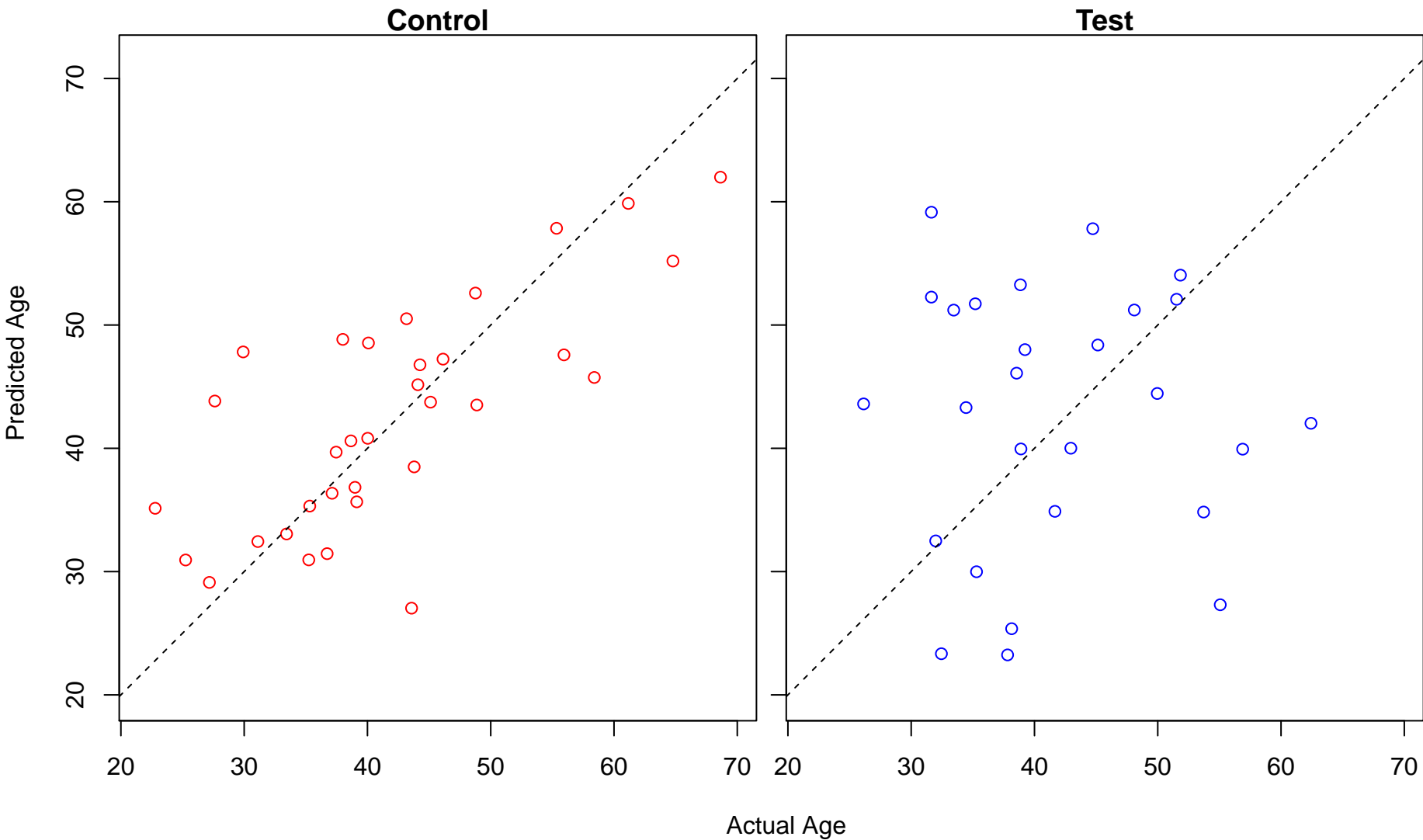
mitotic recombination (Score: 1.959502)



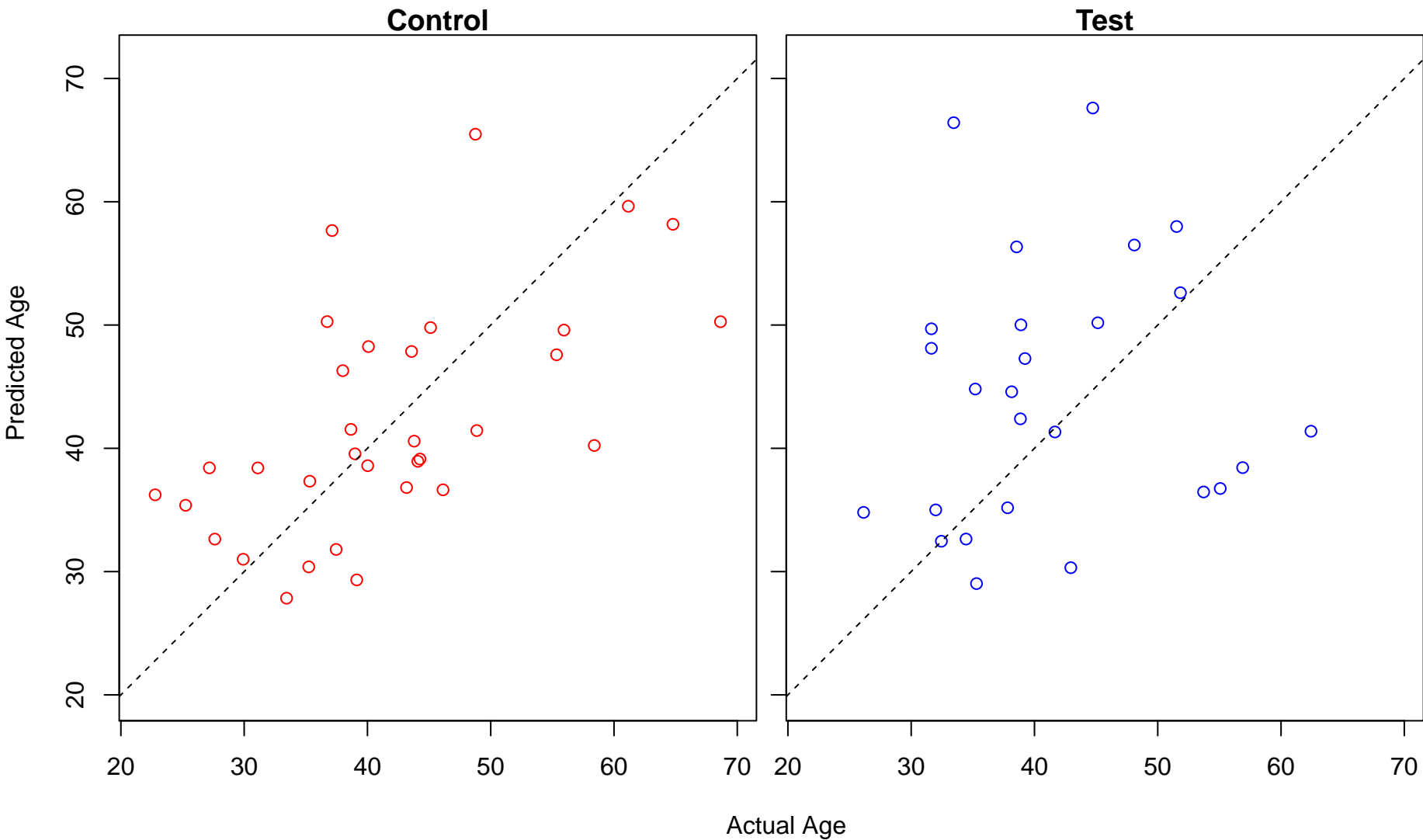
intracellular protein transmembrane transport (Score: 1.937223)



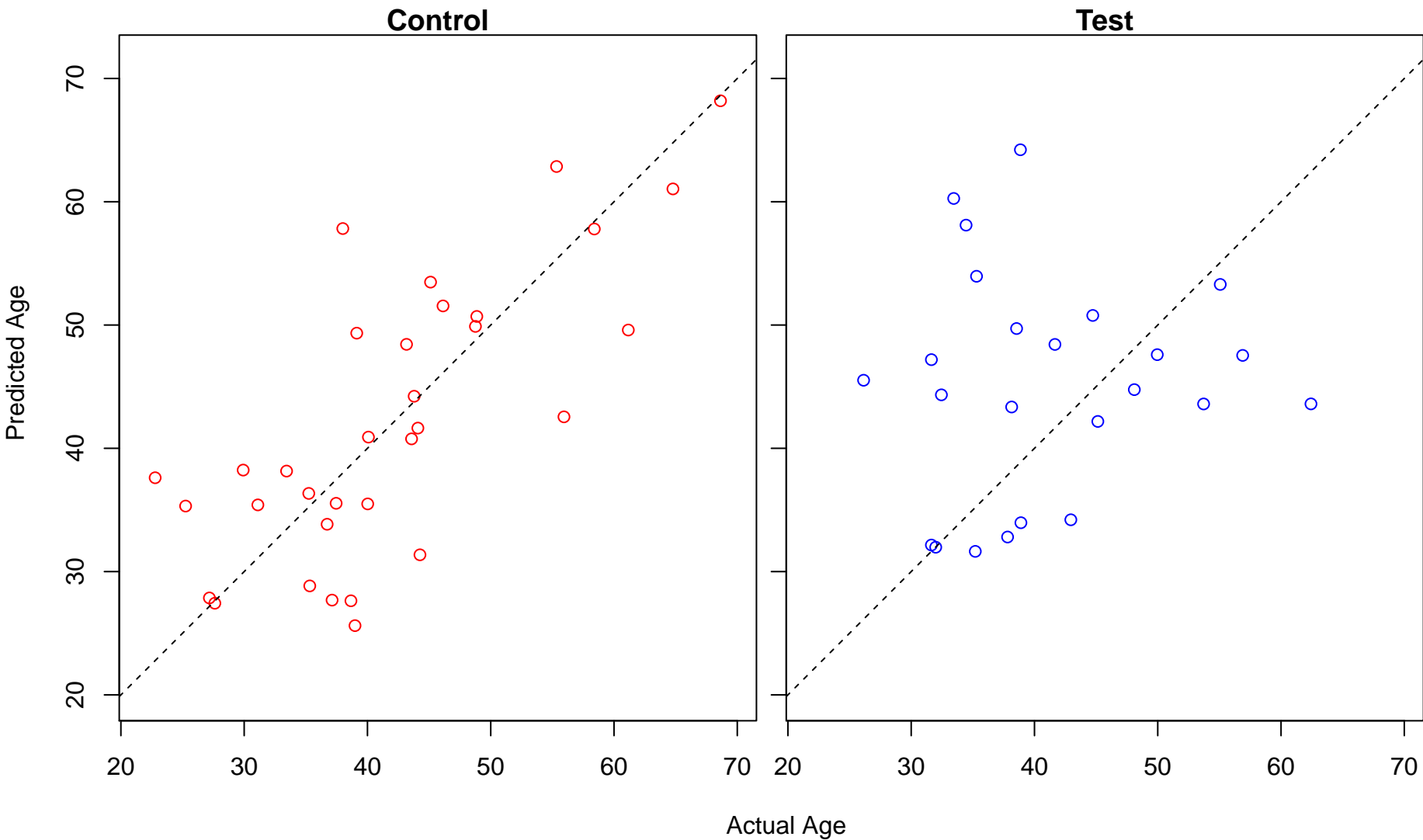
phototransduction (Score: 1.934286)



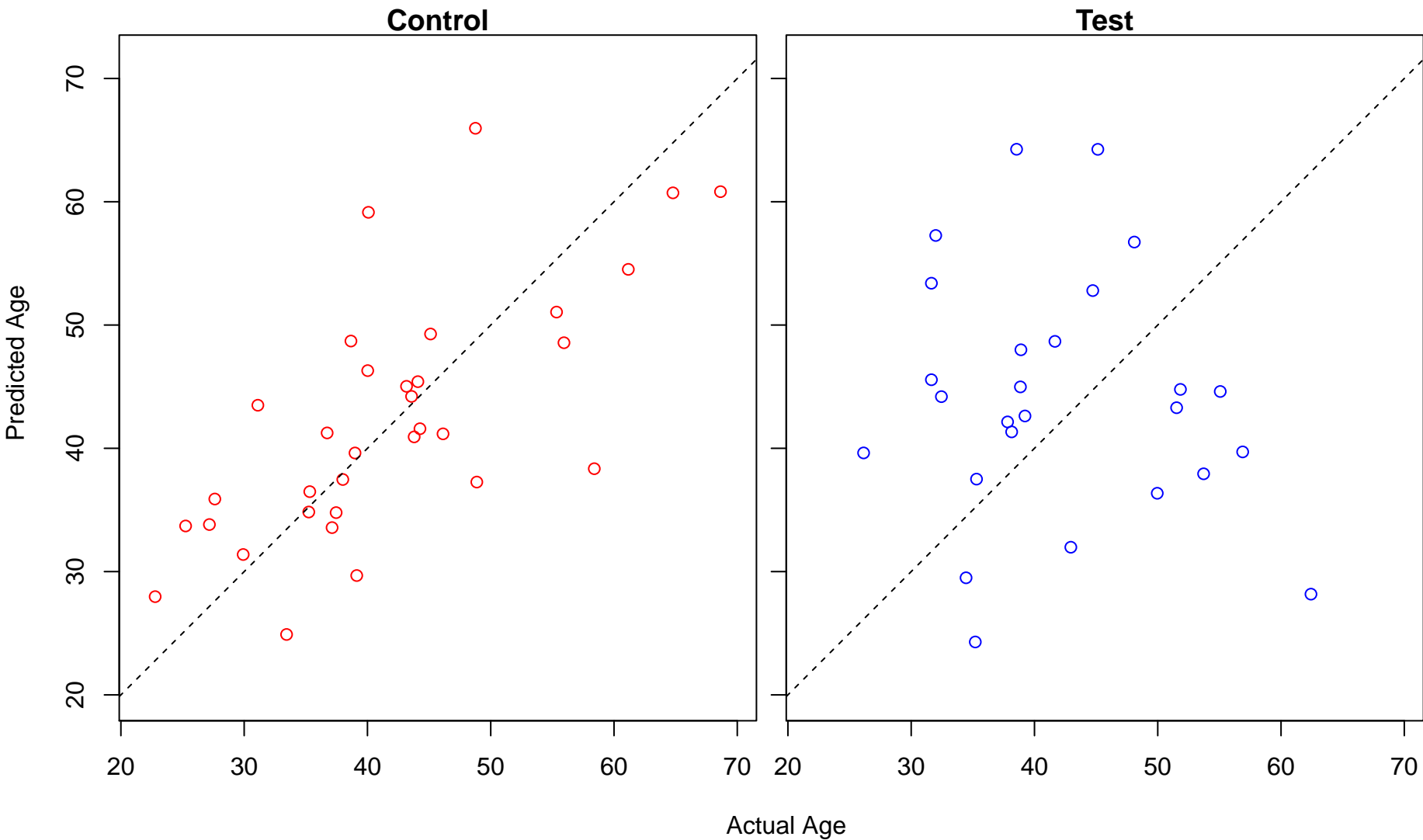
negative regulation of telomere capping (Score: 1.914508)



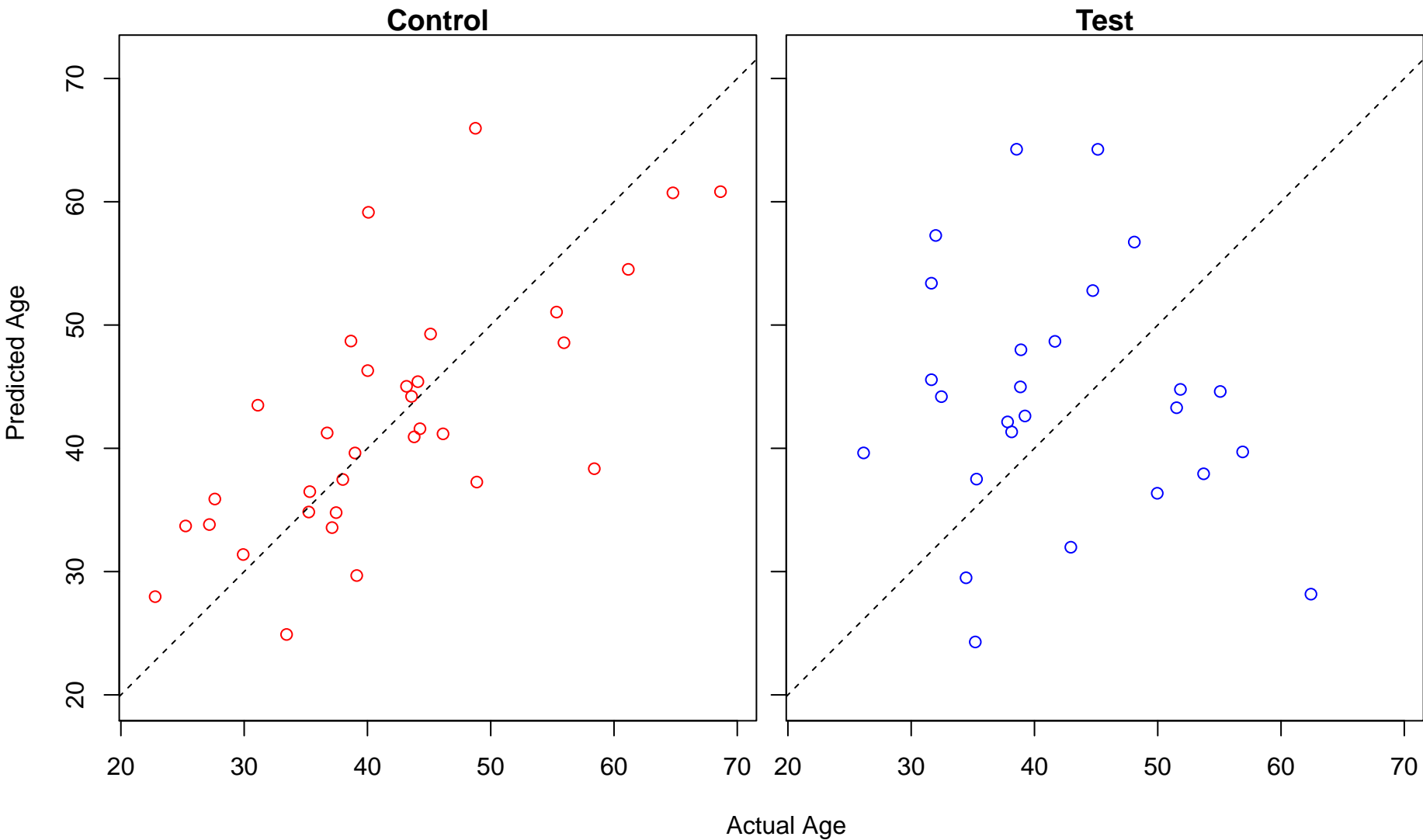
negative regulation of cation channel activity (Score: 1.906014)



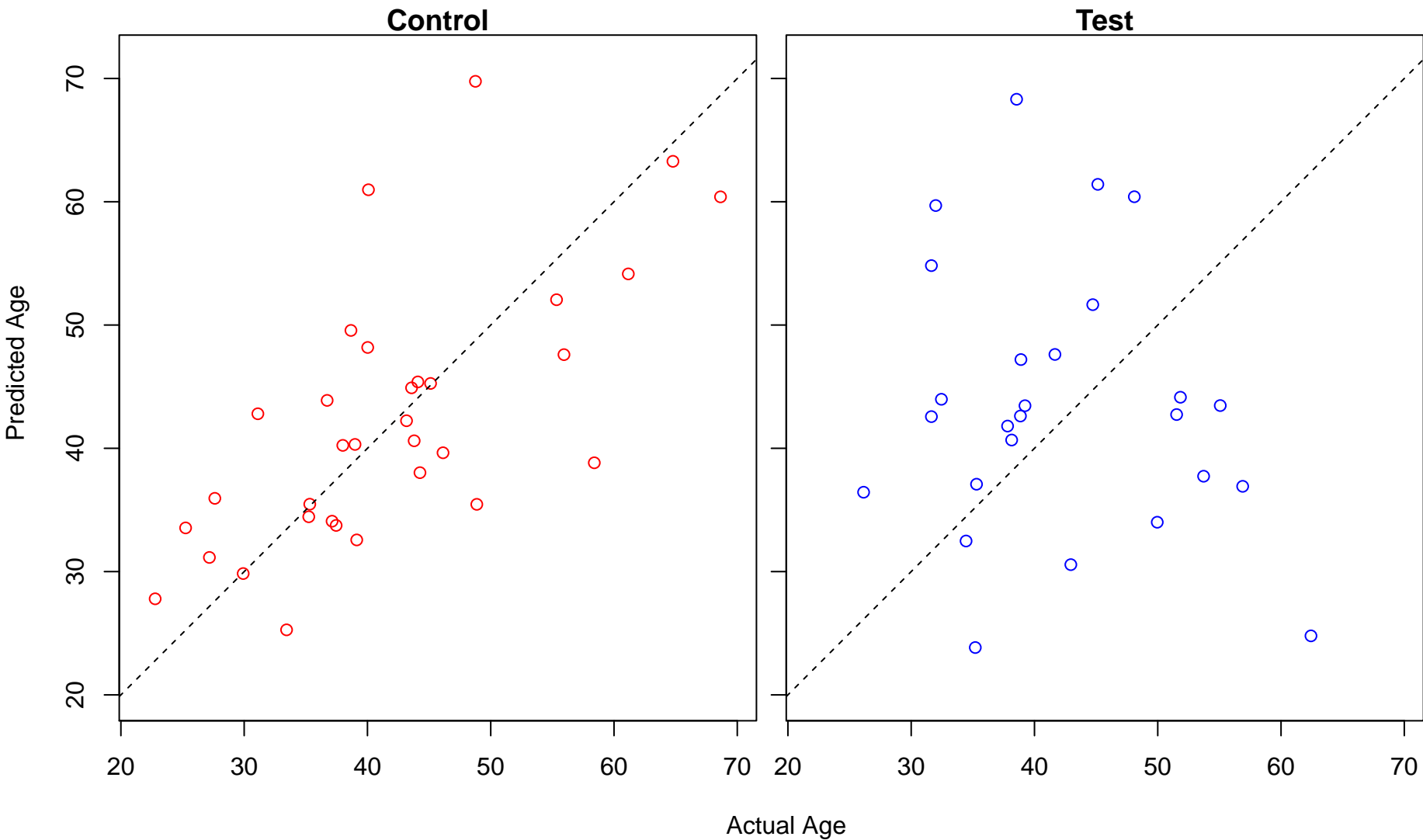
negative regulation of protein exit from endoplasmic reticulum (Score: 1.905926)



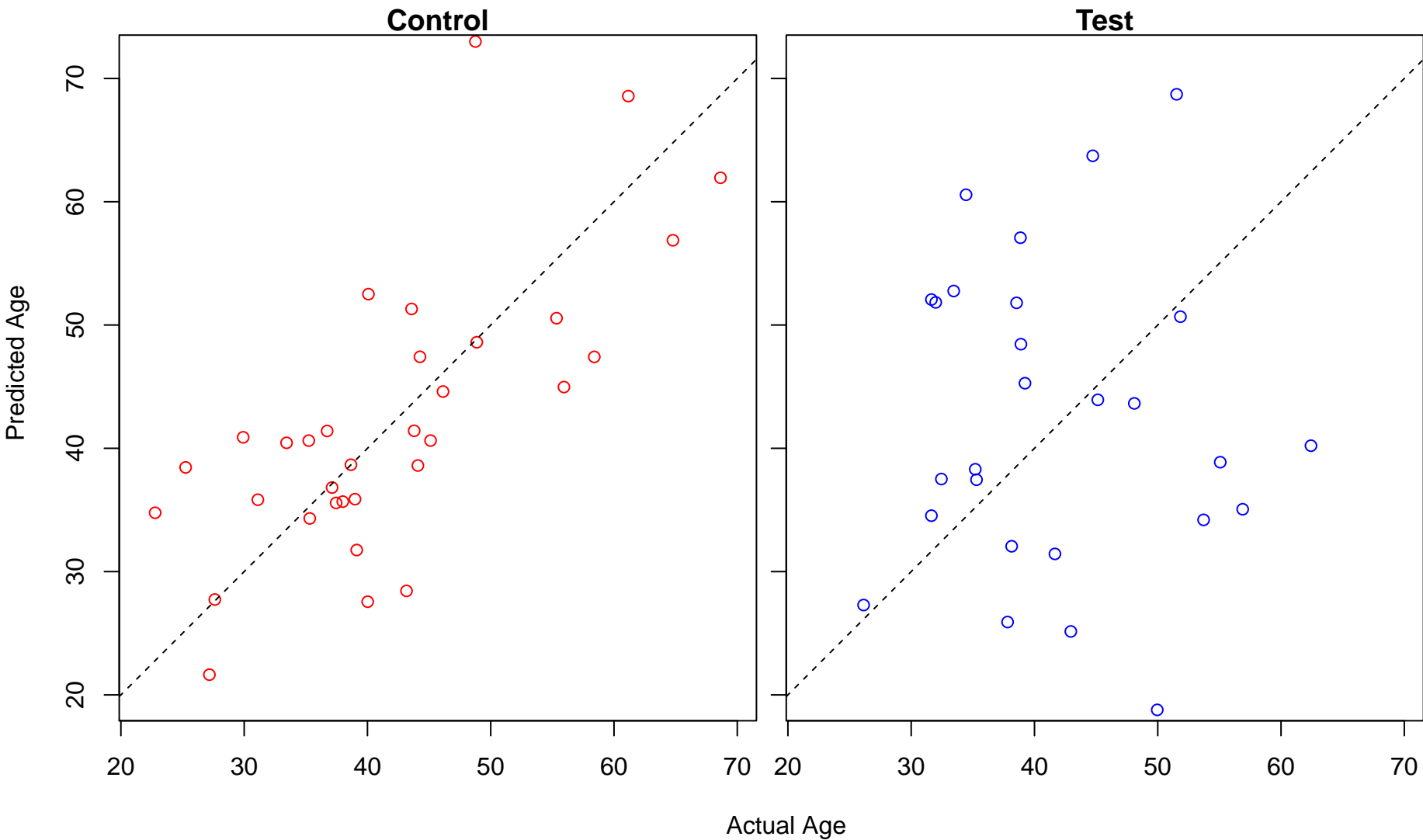
negative regulation of retrograde protein transport, ER to cytosol (Score: 1.905926)



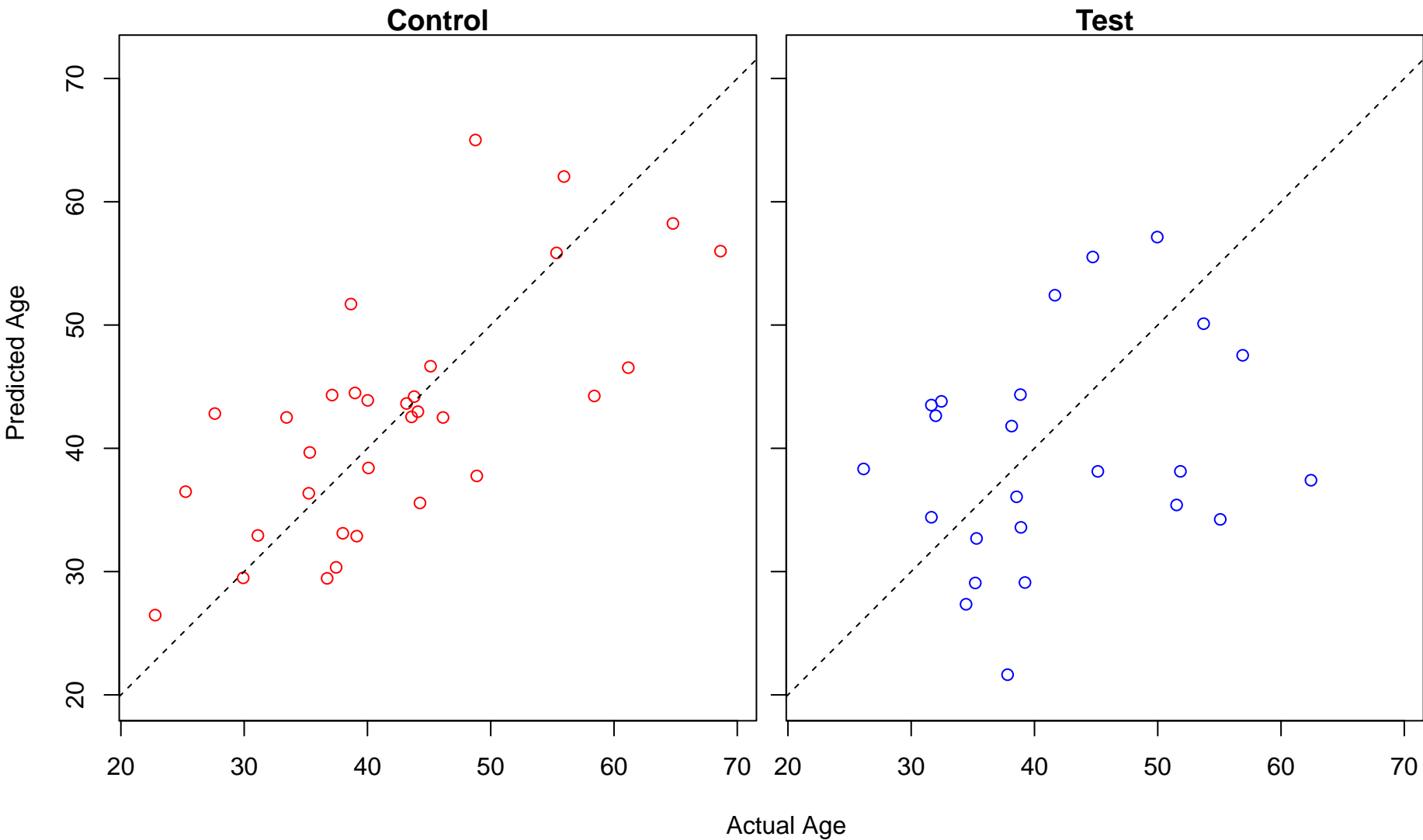
negative regulation of ERAD pathway (Score: 1.897780)



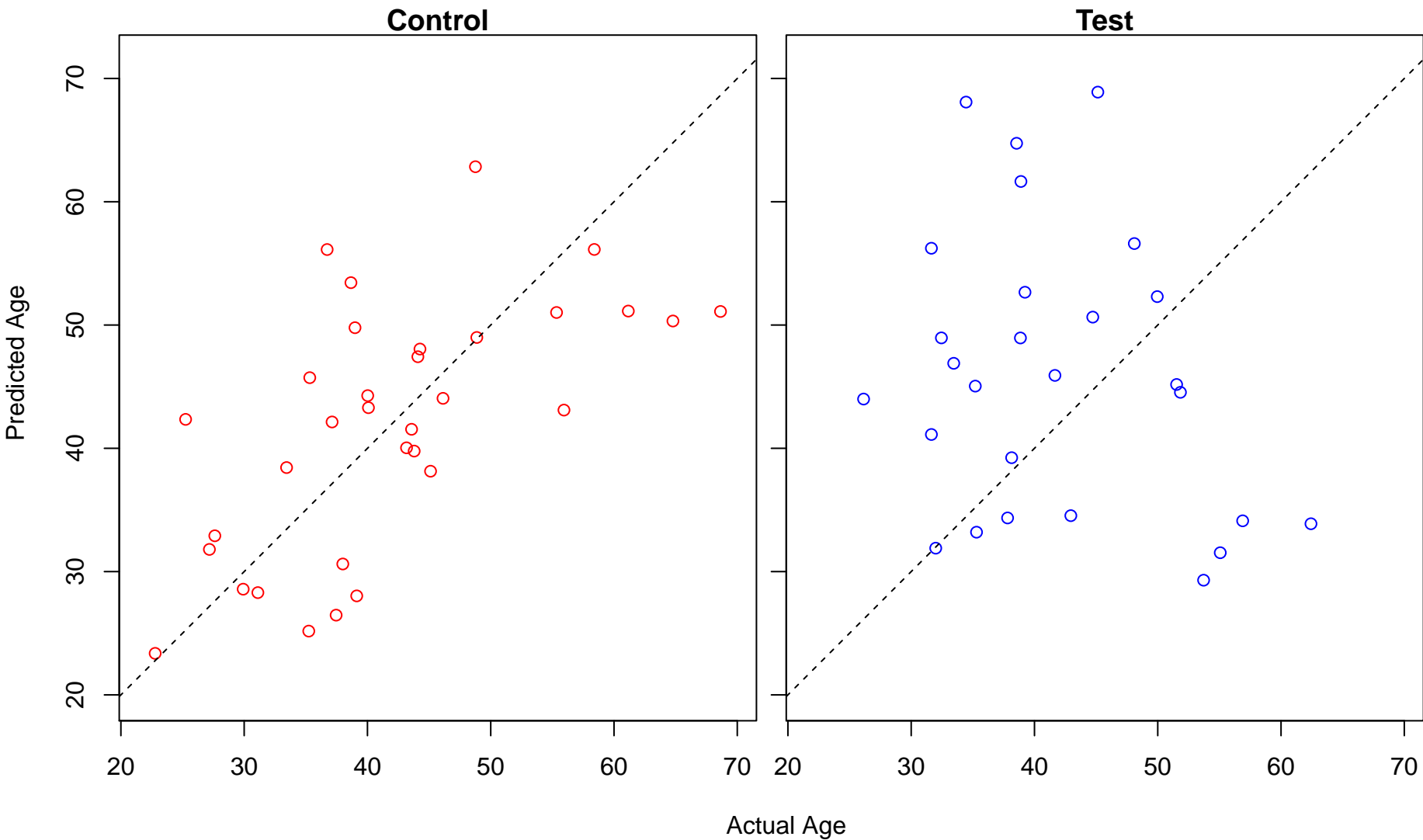
regulation of ERBB signaling pathway (Score: 1.879608)



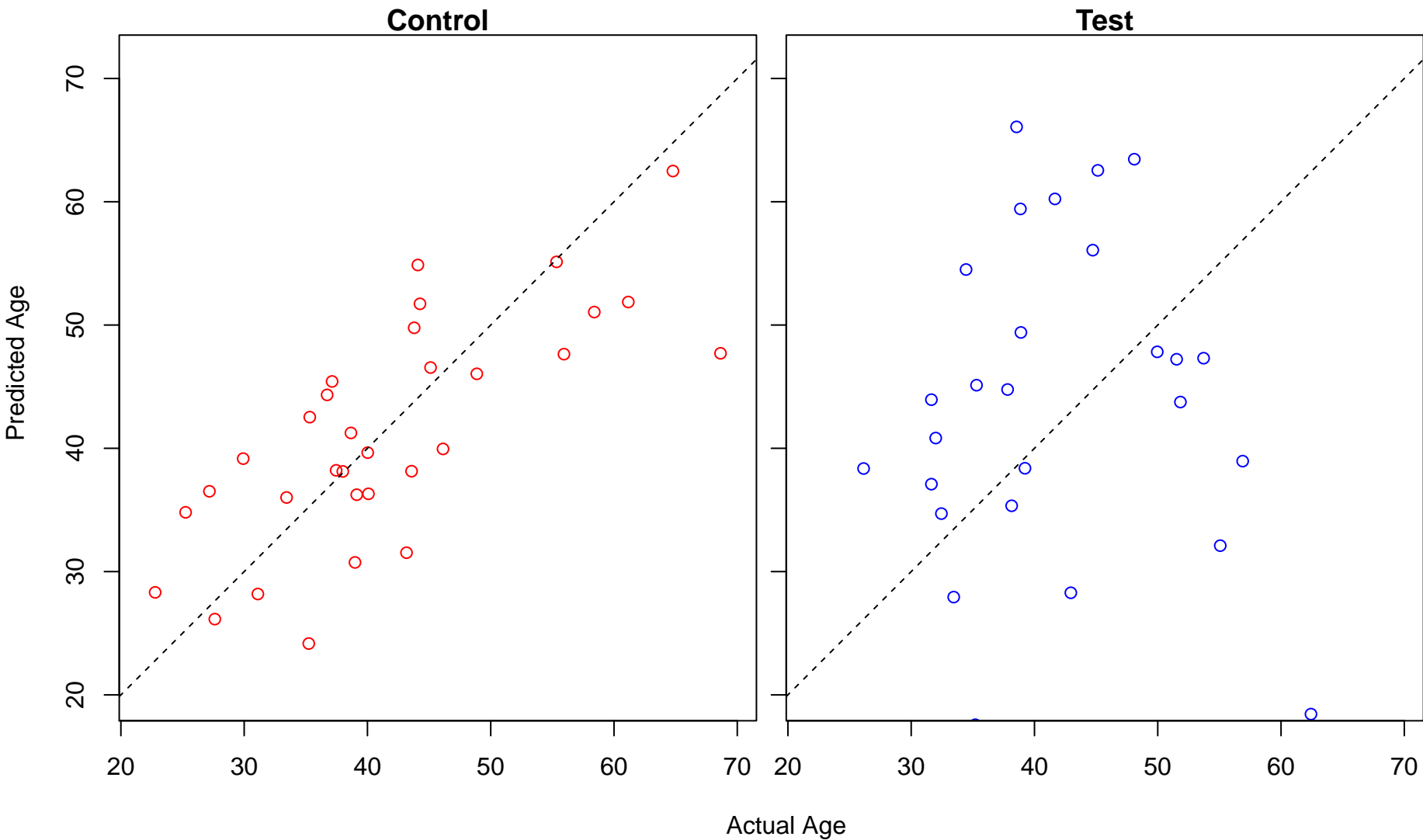
positive regulation of sodium ion transmembrane transport (Score: 1.869131)



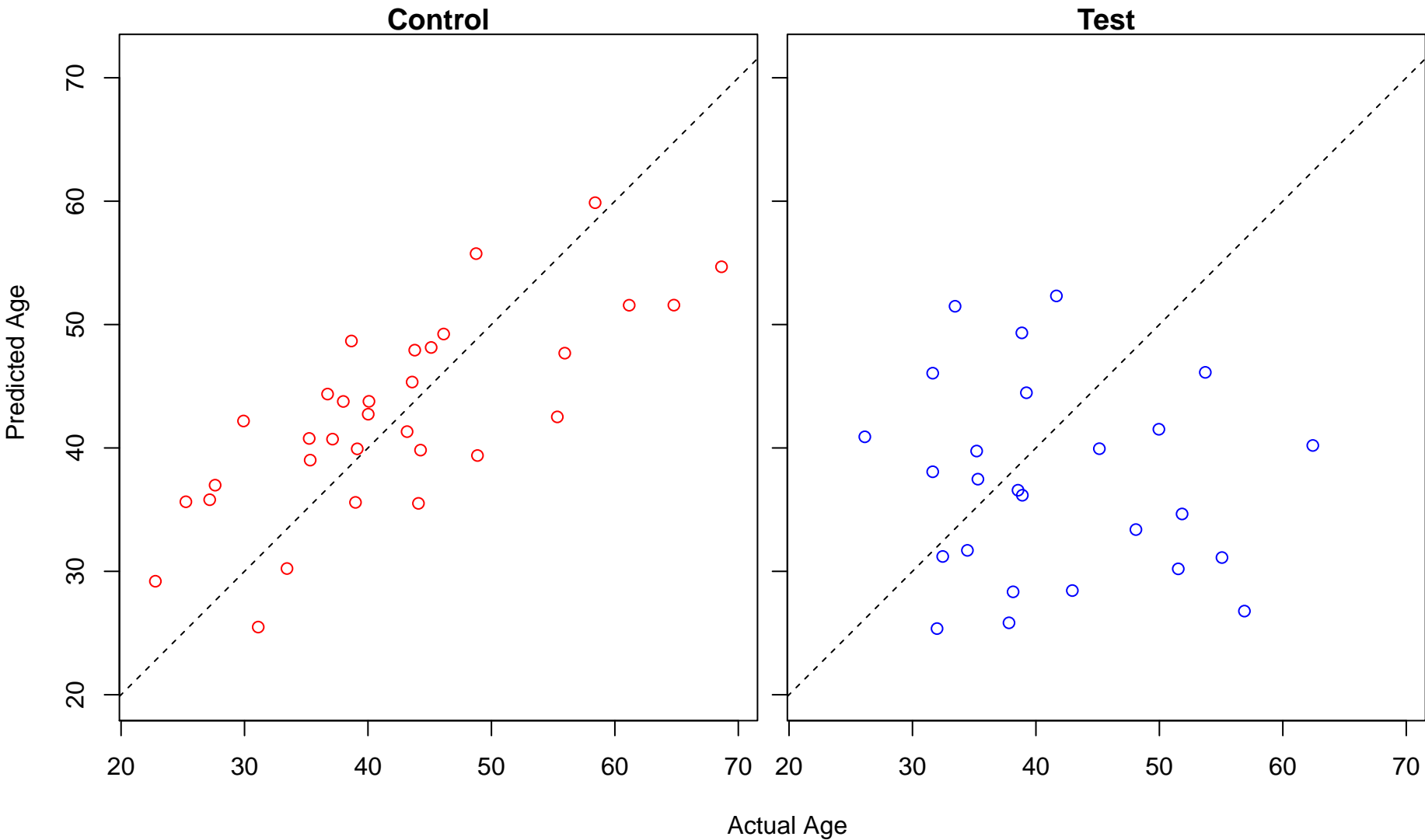
cellular glucose homeostasis (Score: 1.851818)



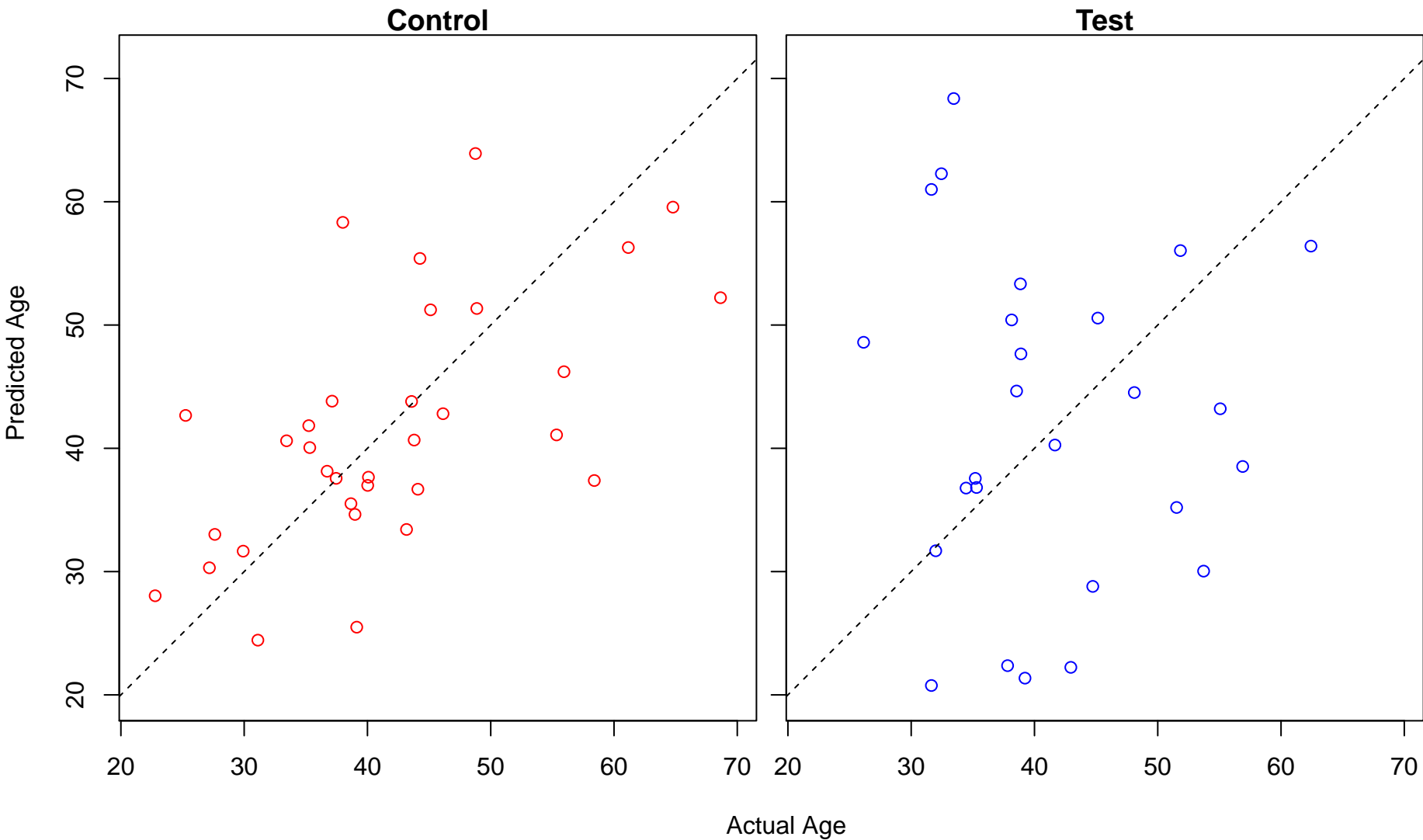
negative regulation of protein acetylation (Score: 1.803012)



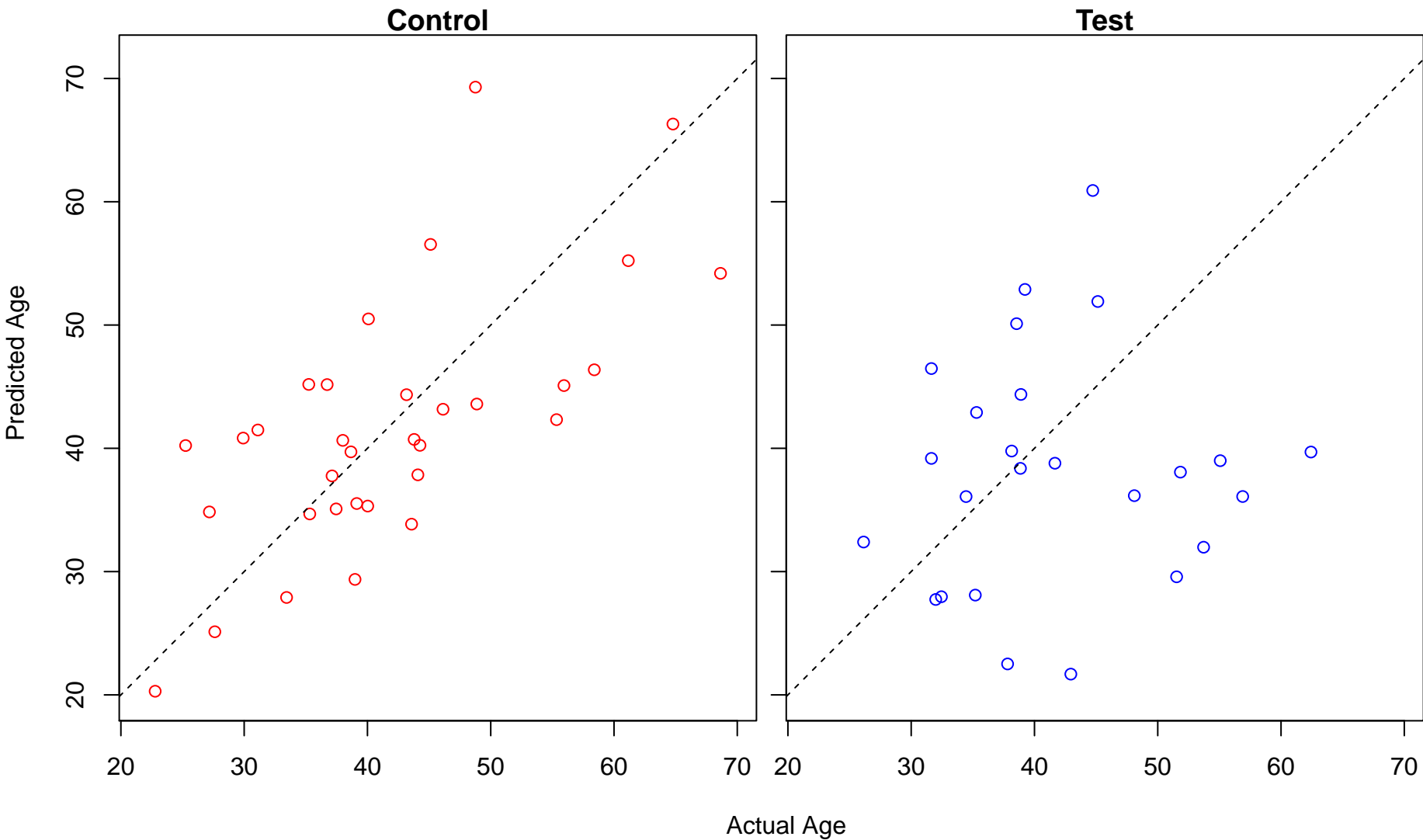
regulation of cholesterol metabolic process (Score: 1.799067)



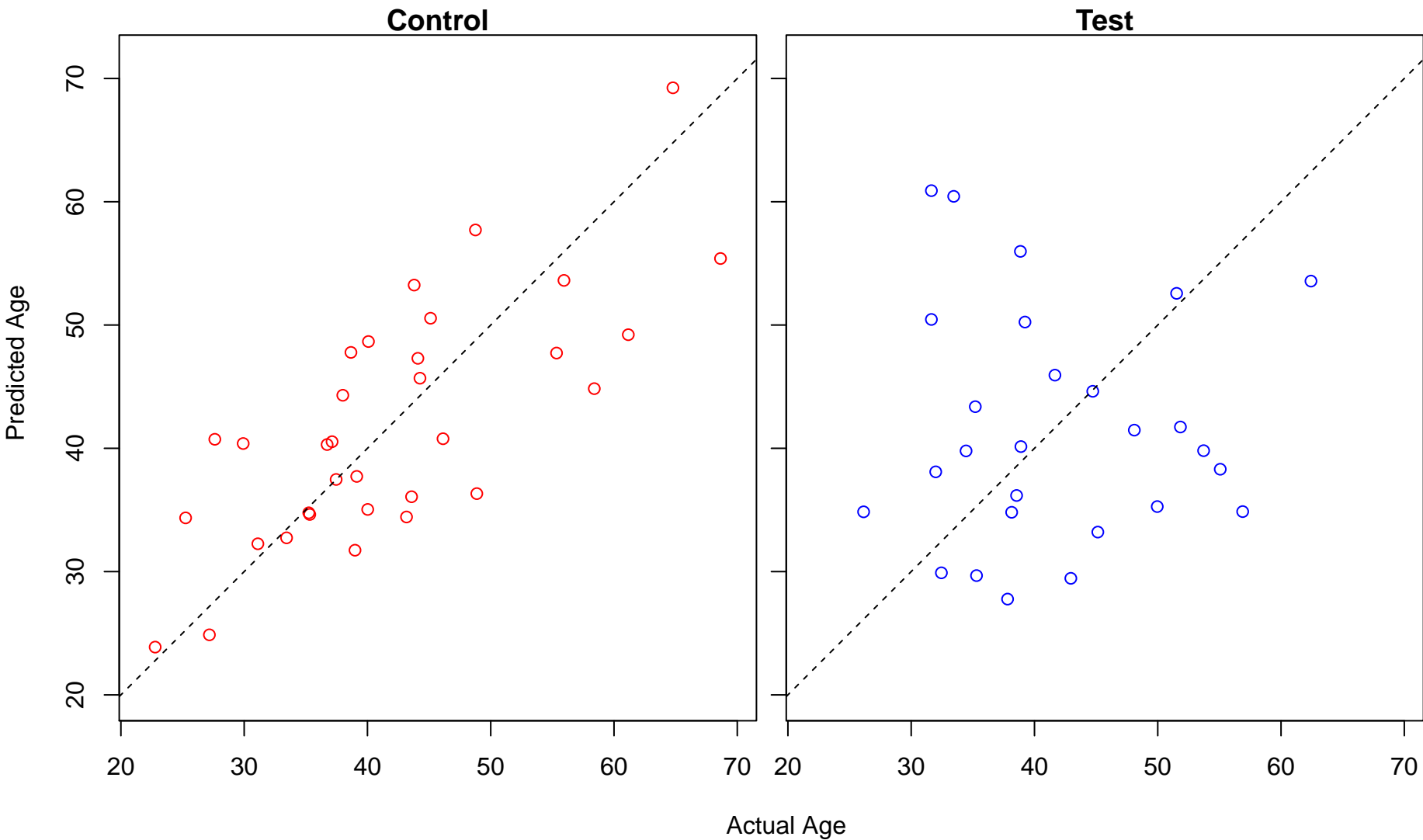
mitotic G2/M transition checkpoint (Score: 1.794525)



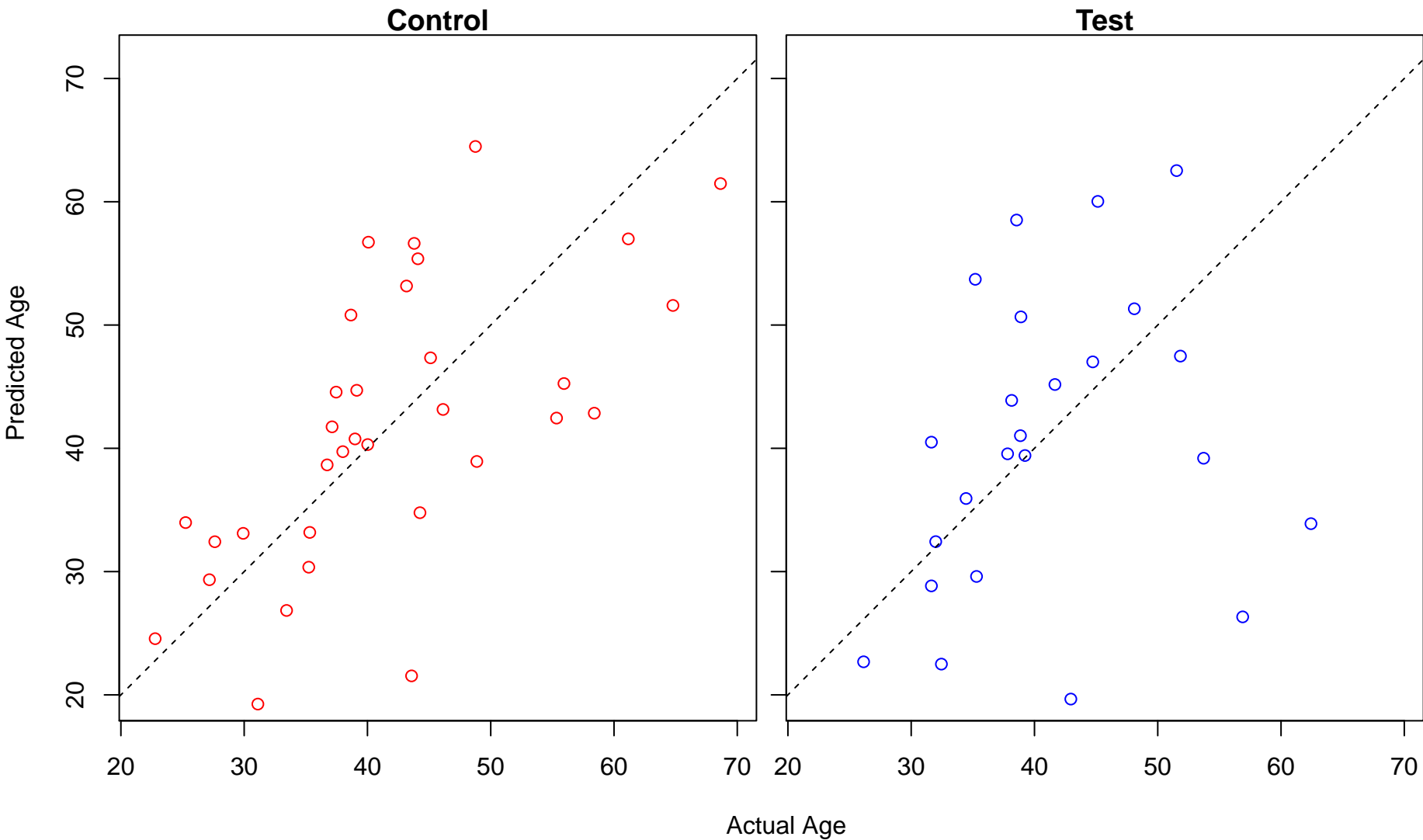
cellular response to biotic stimulus (Score: 1.740526)



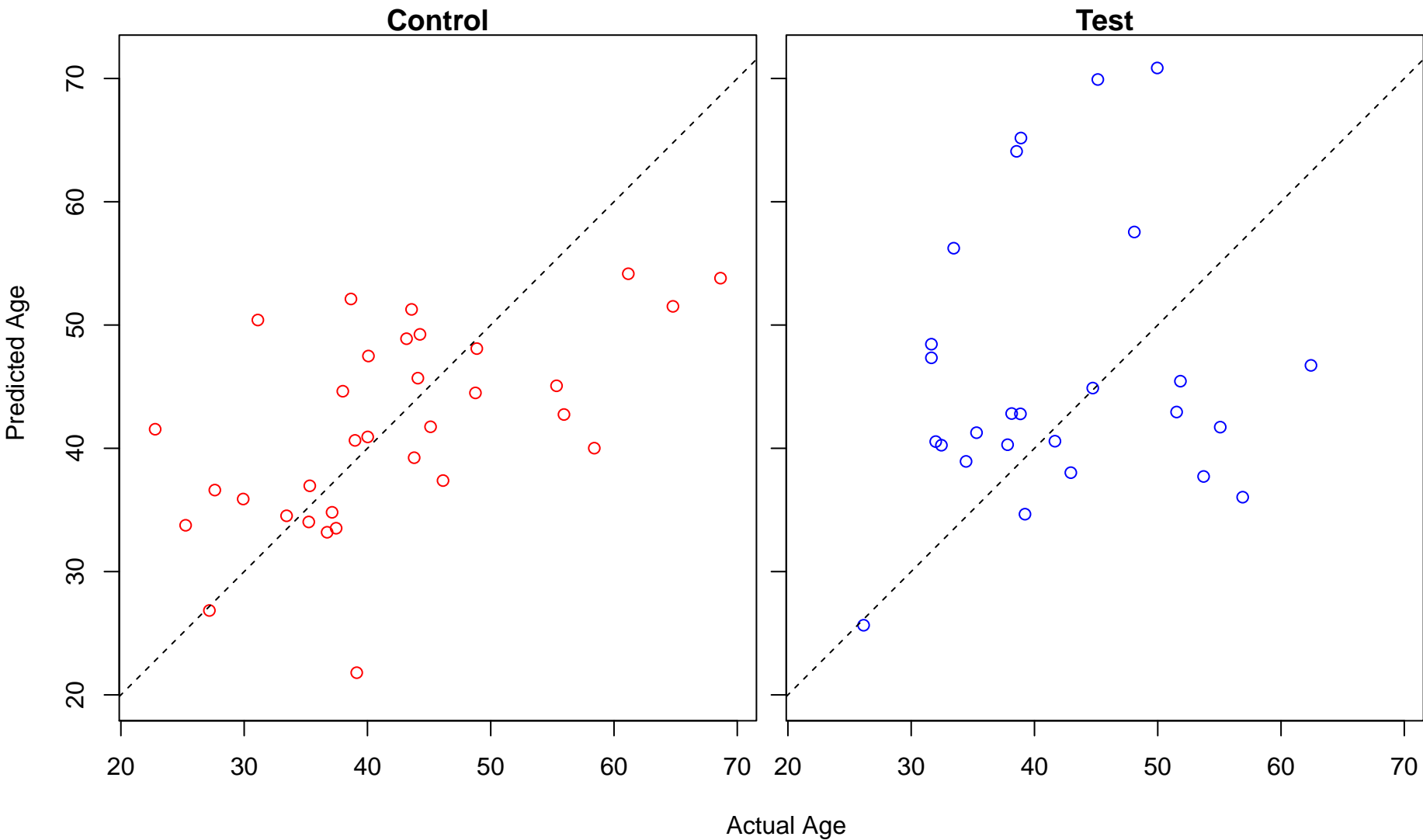
ammonium ion metabolic process (Score: 1.739265)



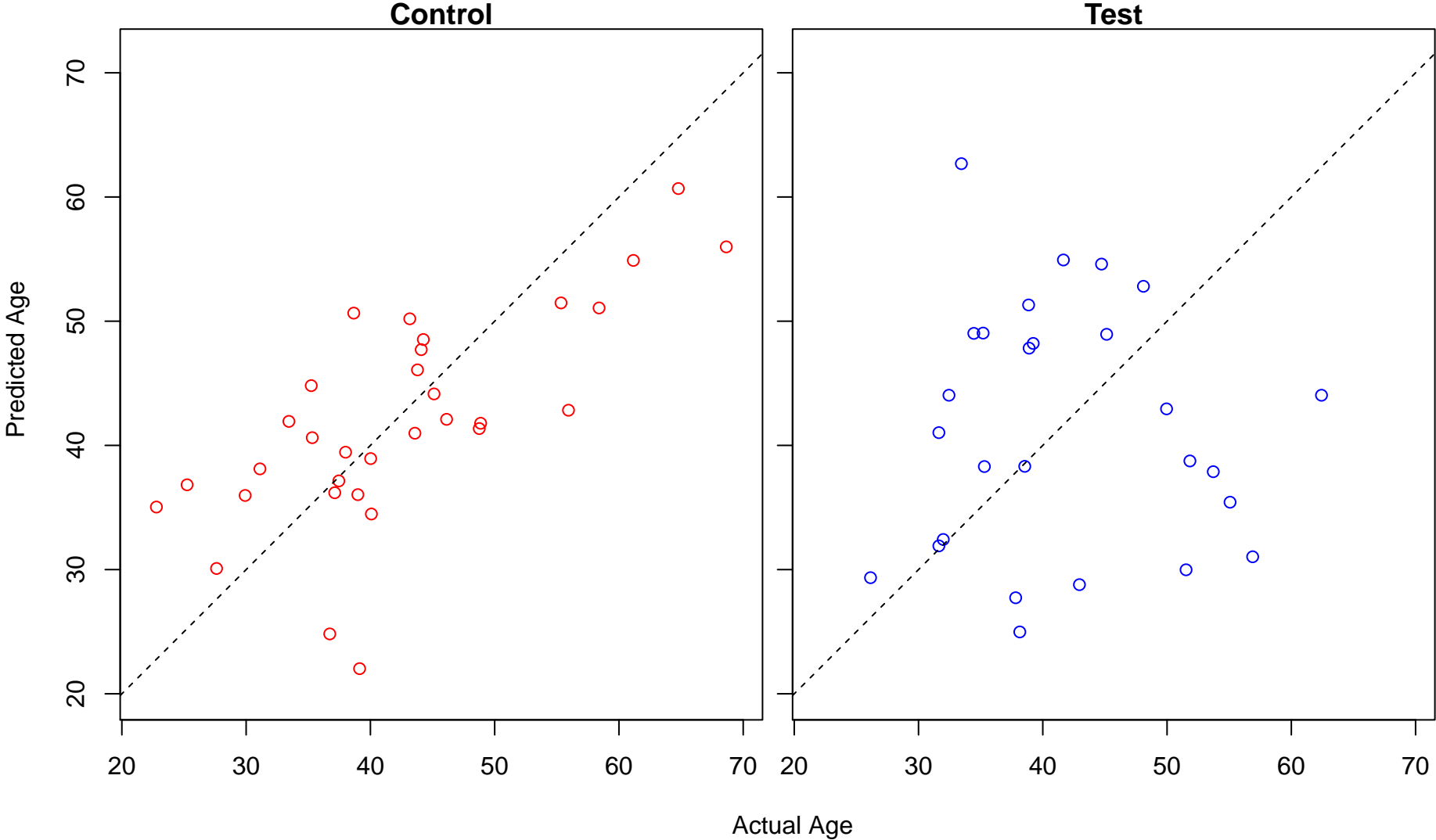
DNA strand elongation (Score: 1.702783)



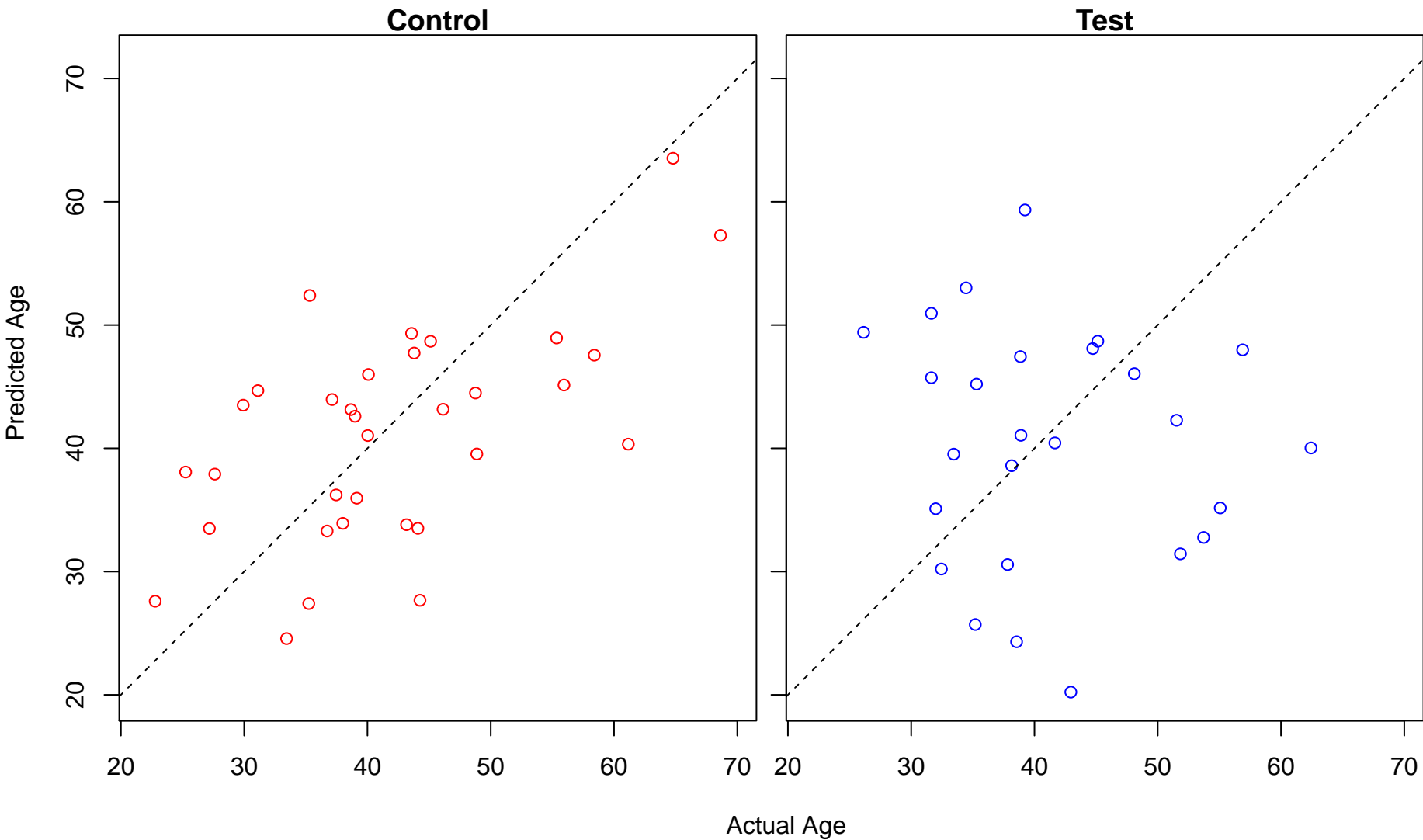
negative regulation of histone H3-K9 methylation (Score: 1.695332)



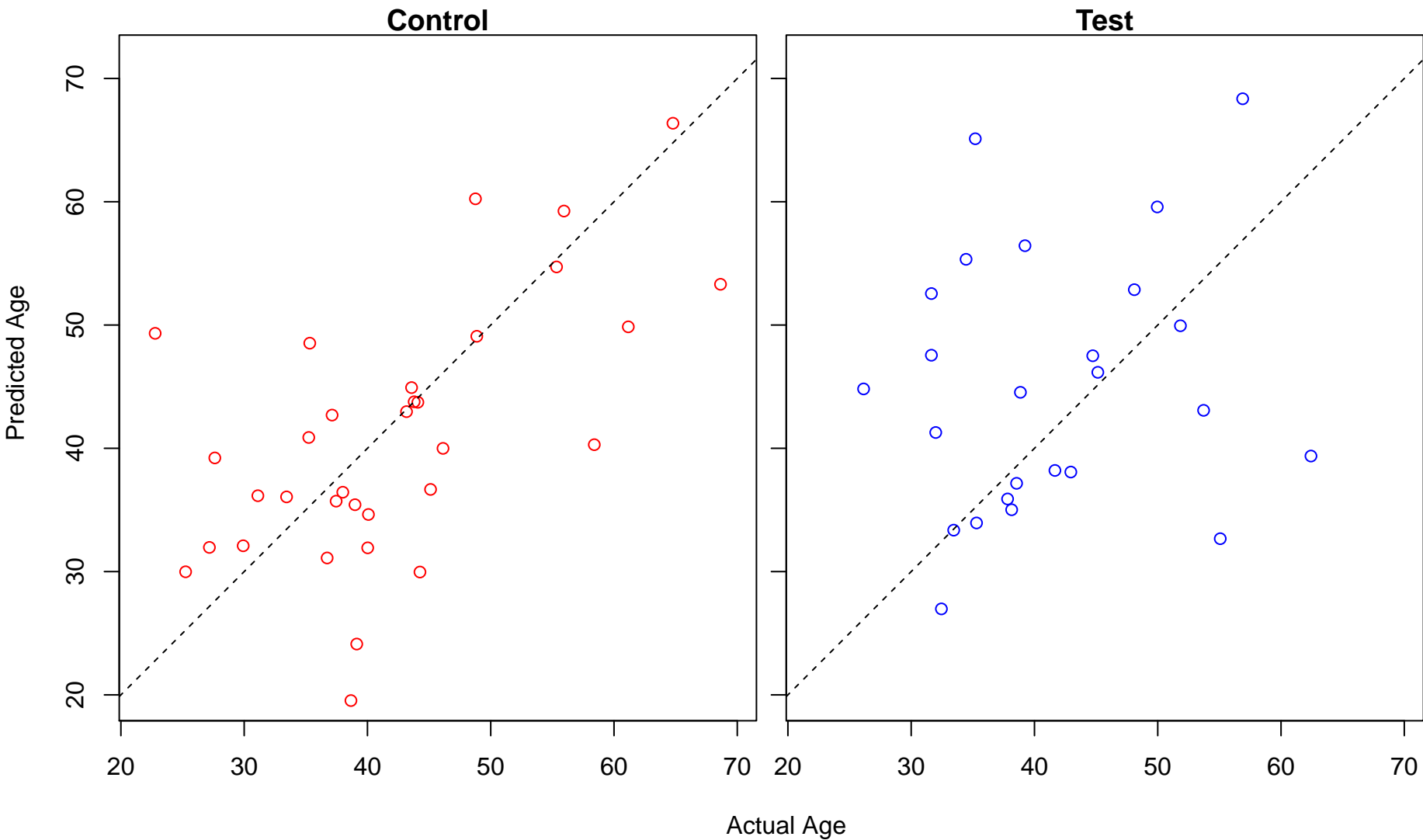
negative regulation of transcription from RNA polymerase II promoter in response to stress (Score: 1.68)



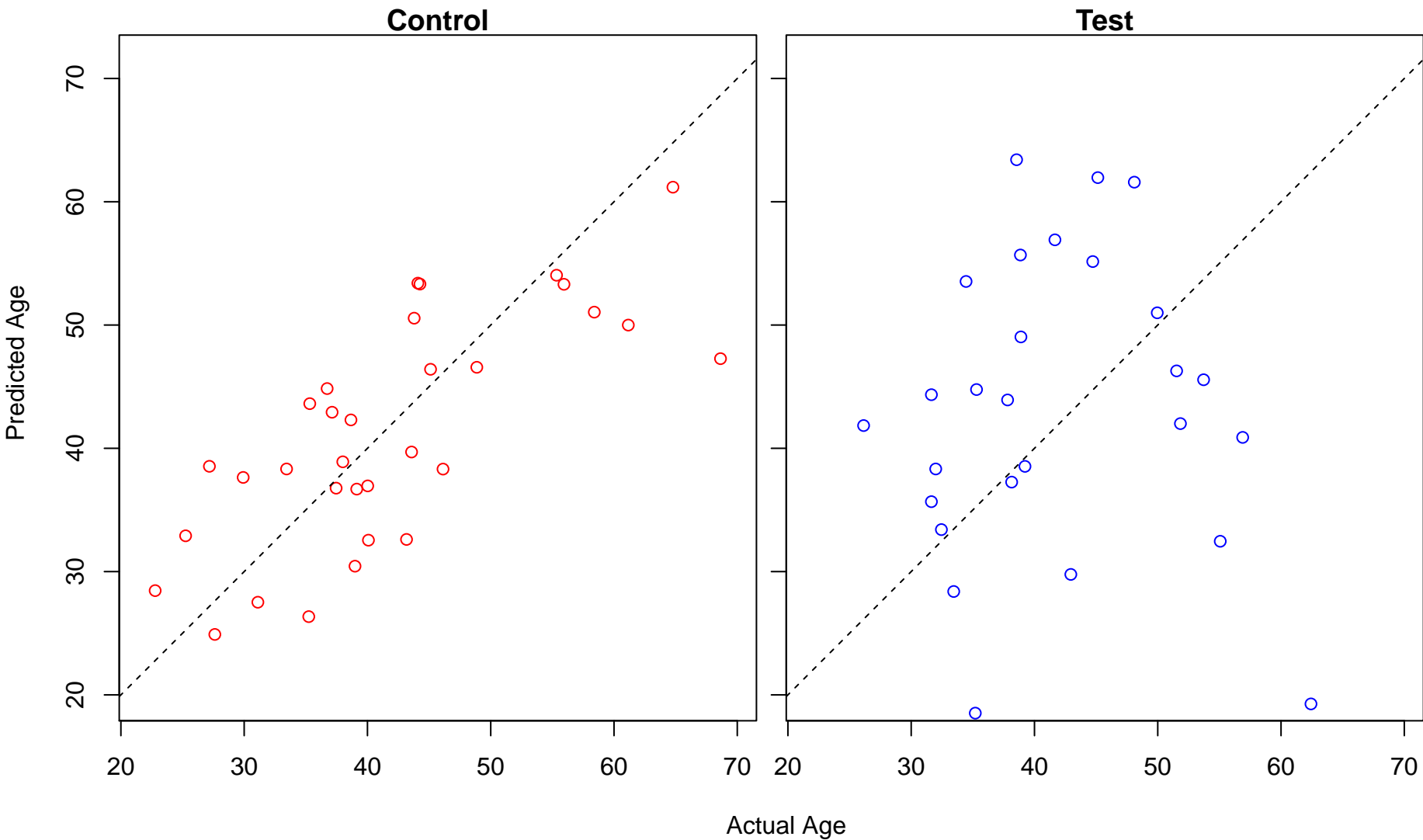
phosphatidylethanolamine acyl-chain remodeling (Score: 1.664764)



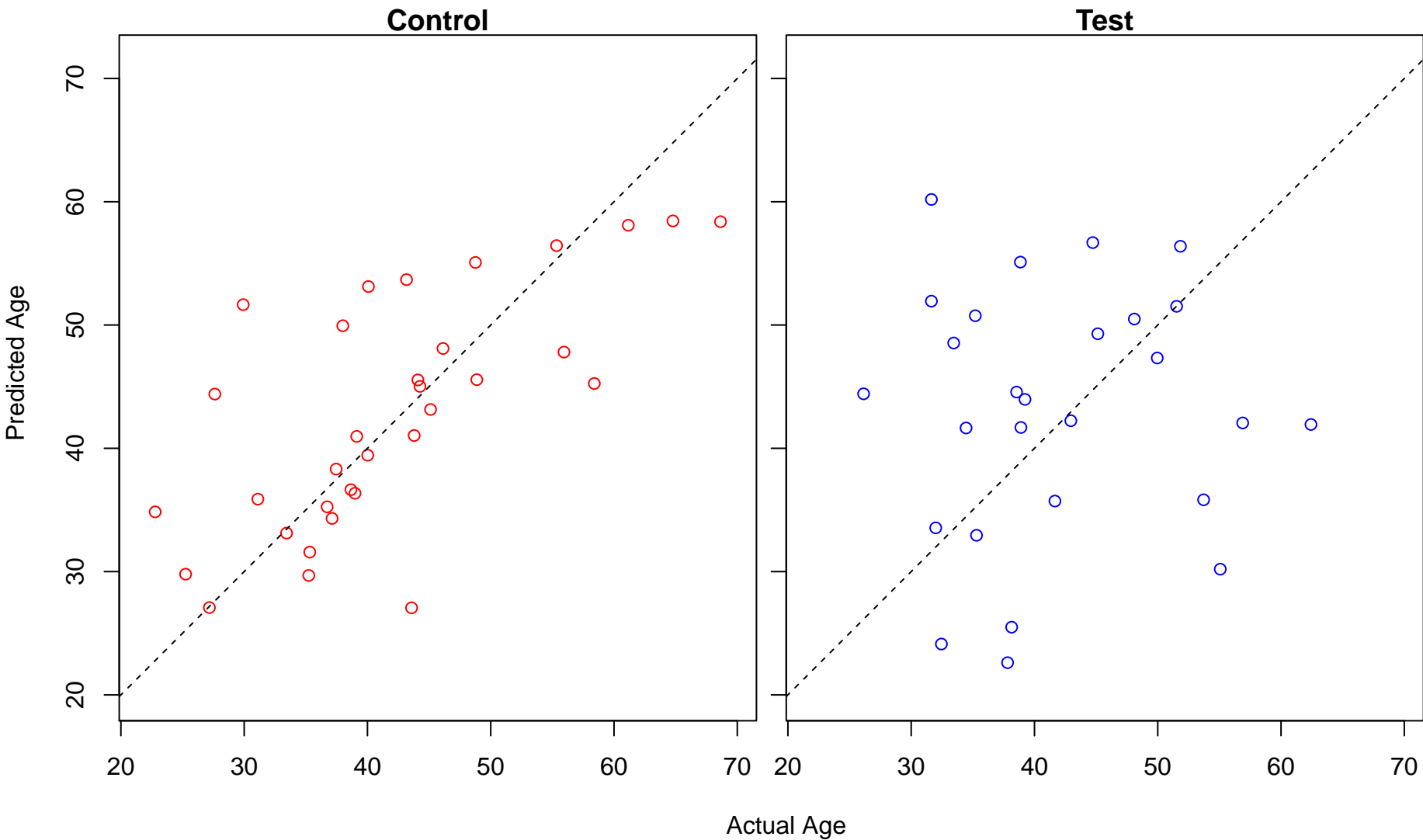
protein heterooligomerization (Score: 1.662099)



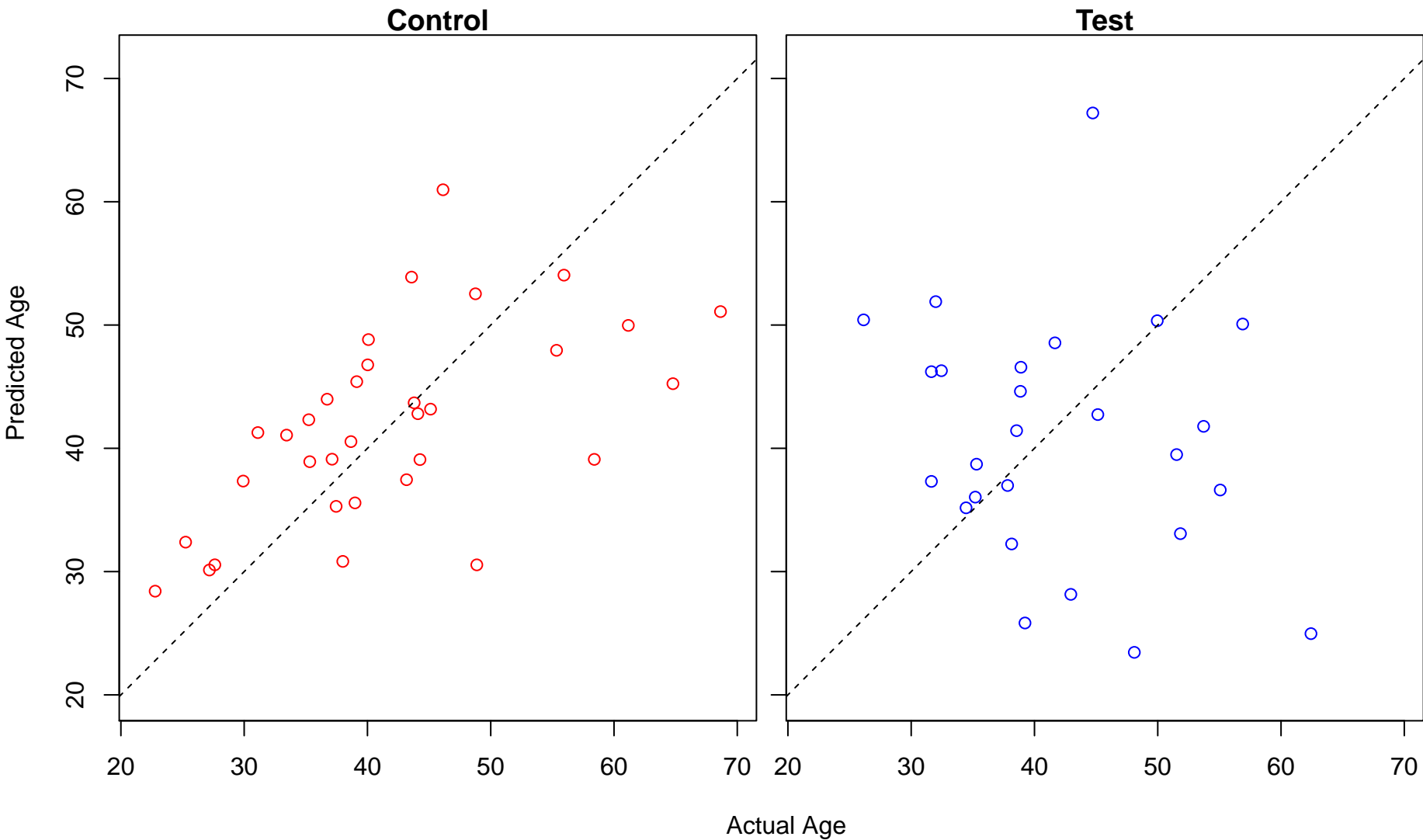
negative regulation of peptidyl-lysine acetylation (Score: 1.649902)



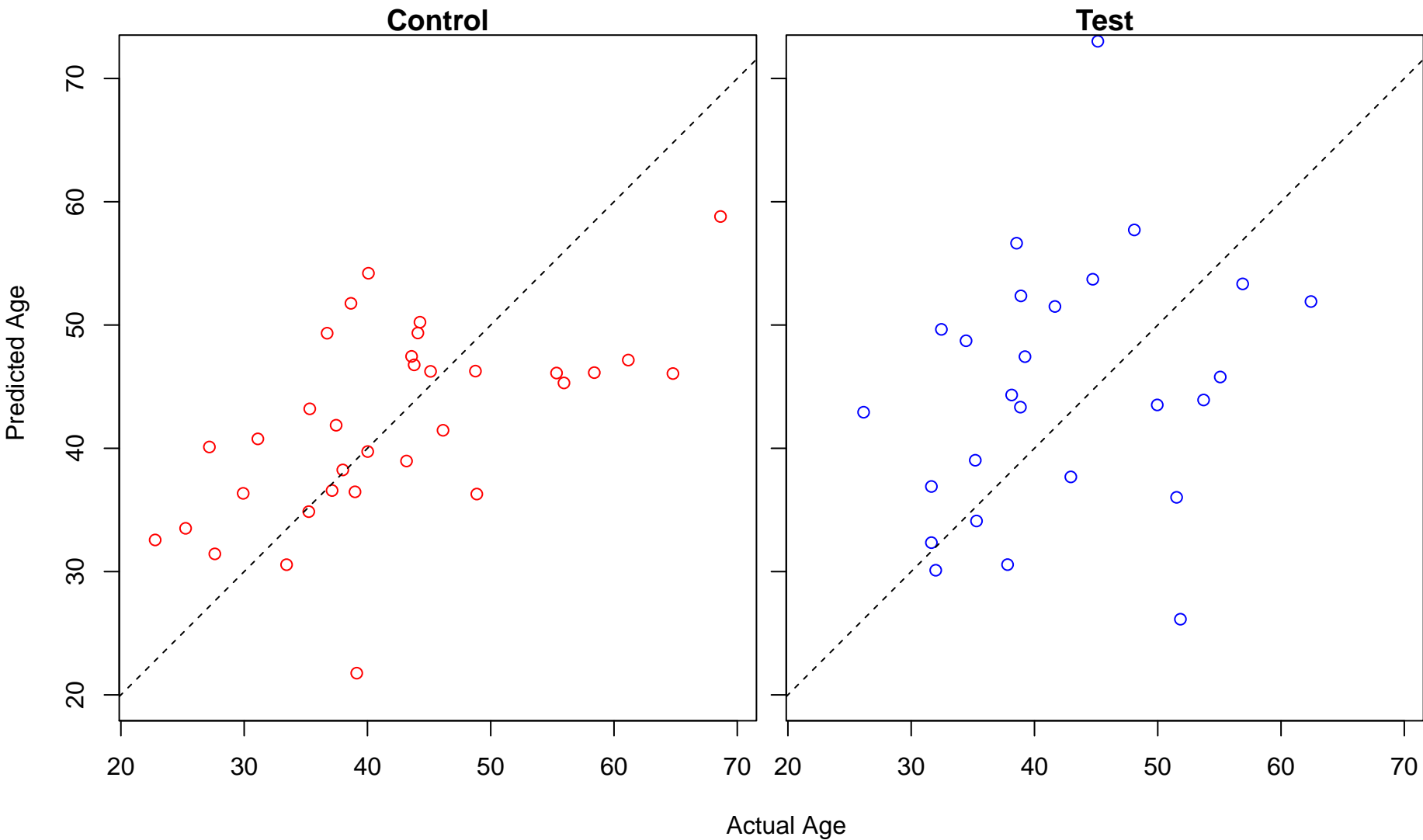
detection of visible light (Score: 1.648864)



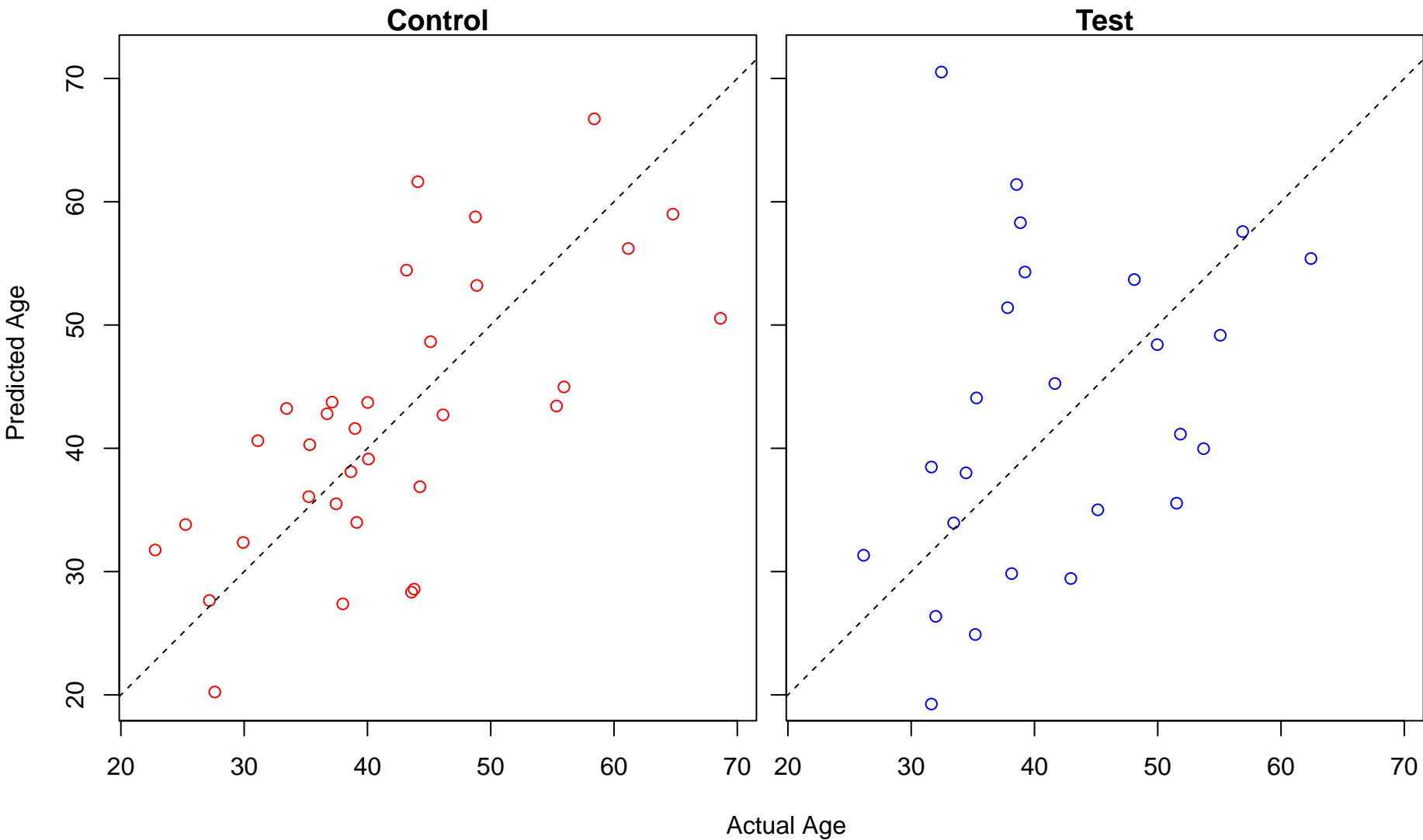
positive regulation of potassium ion transmembrane transport (Score: 1.637097)



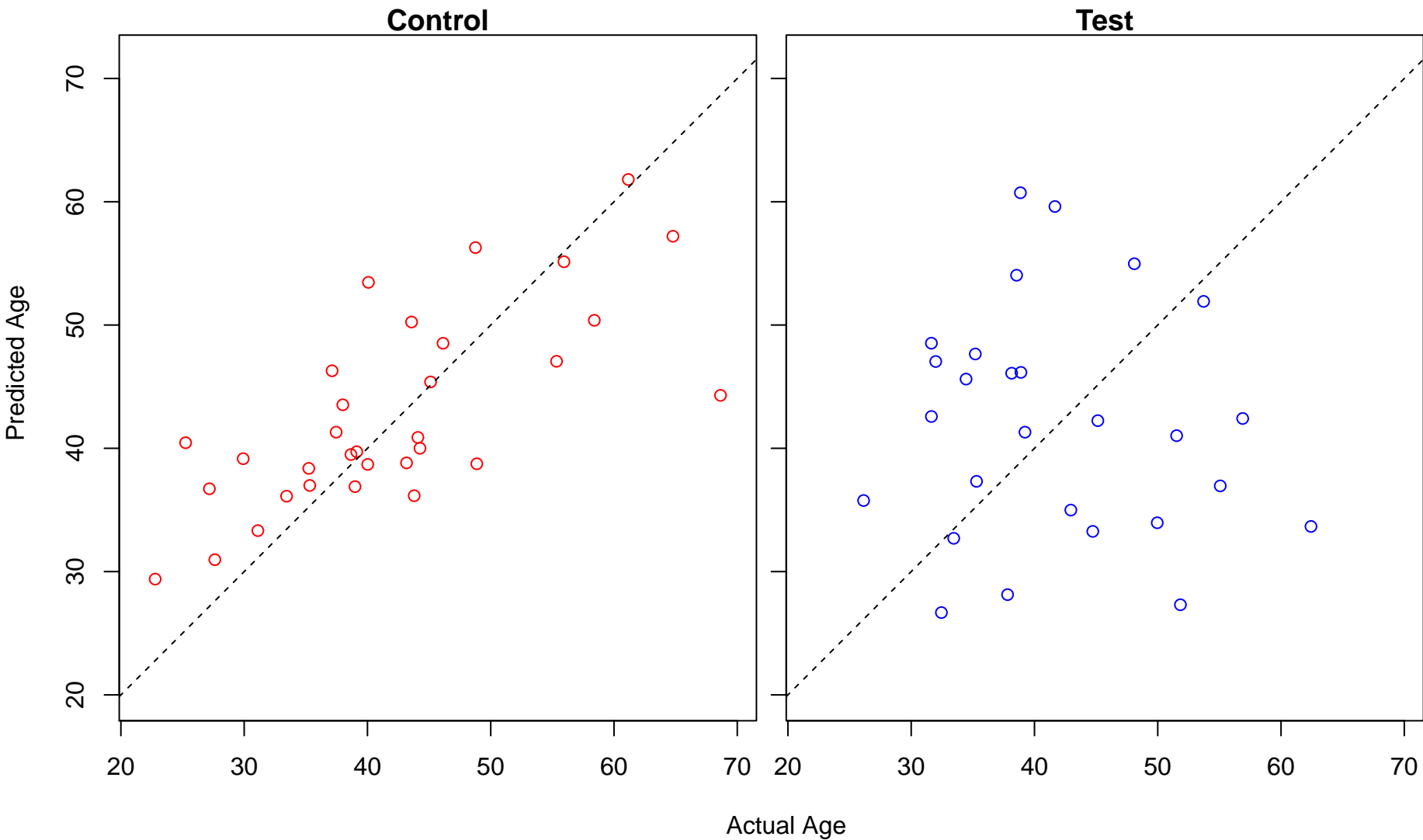
developmental process involved in reproduction (Score: 1.632736)



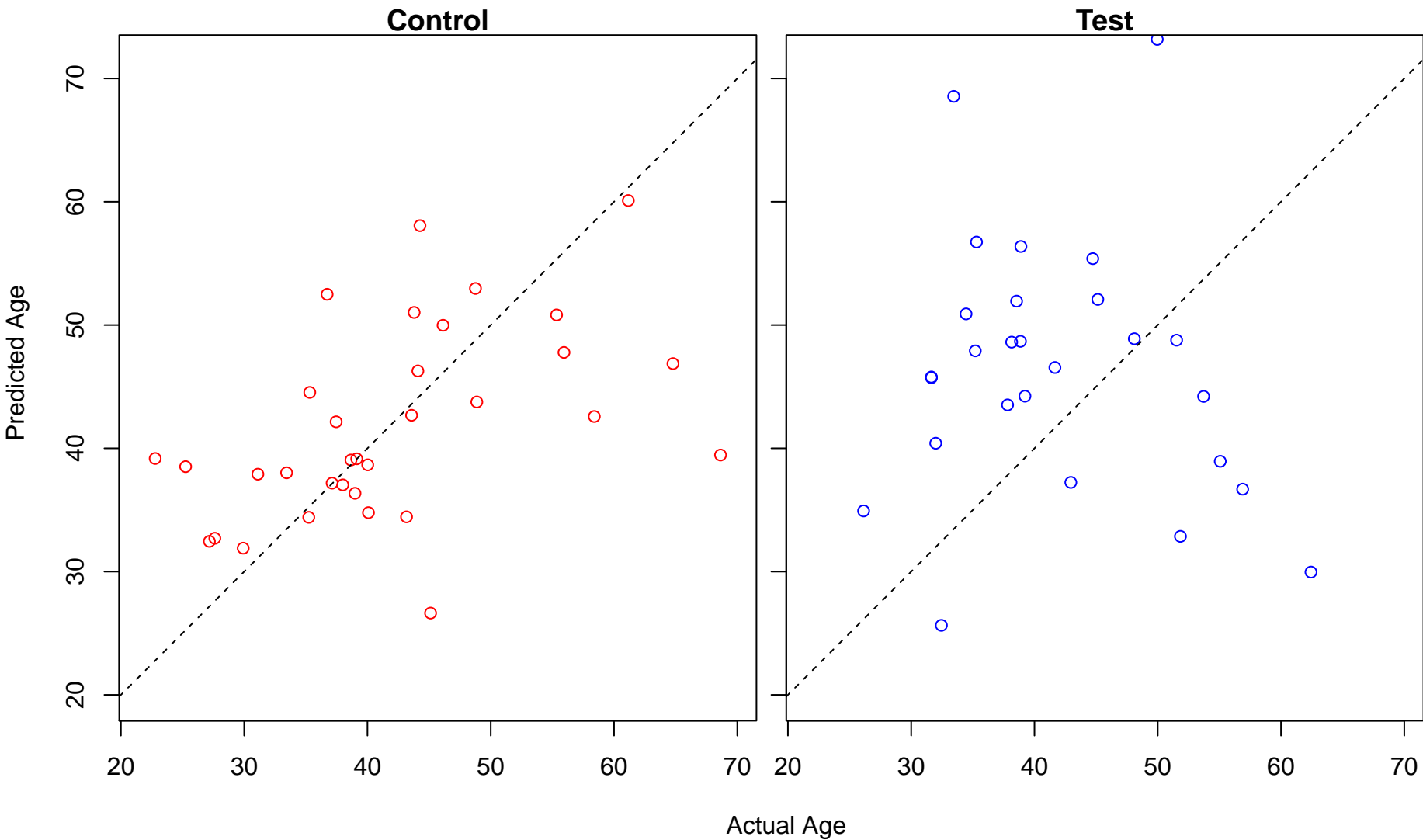
acute inflammatory response (Score: 1.632607)



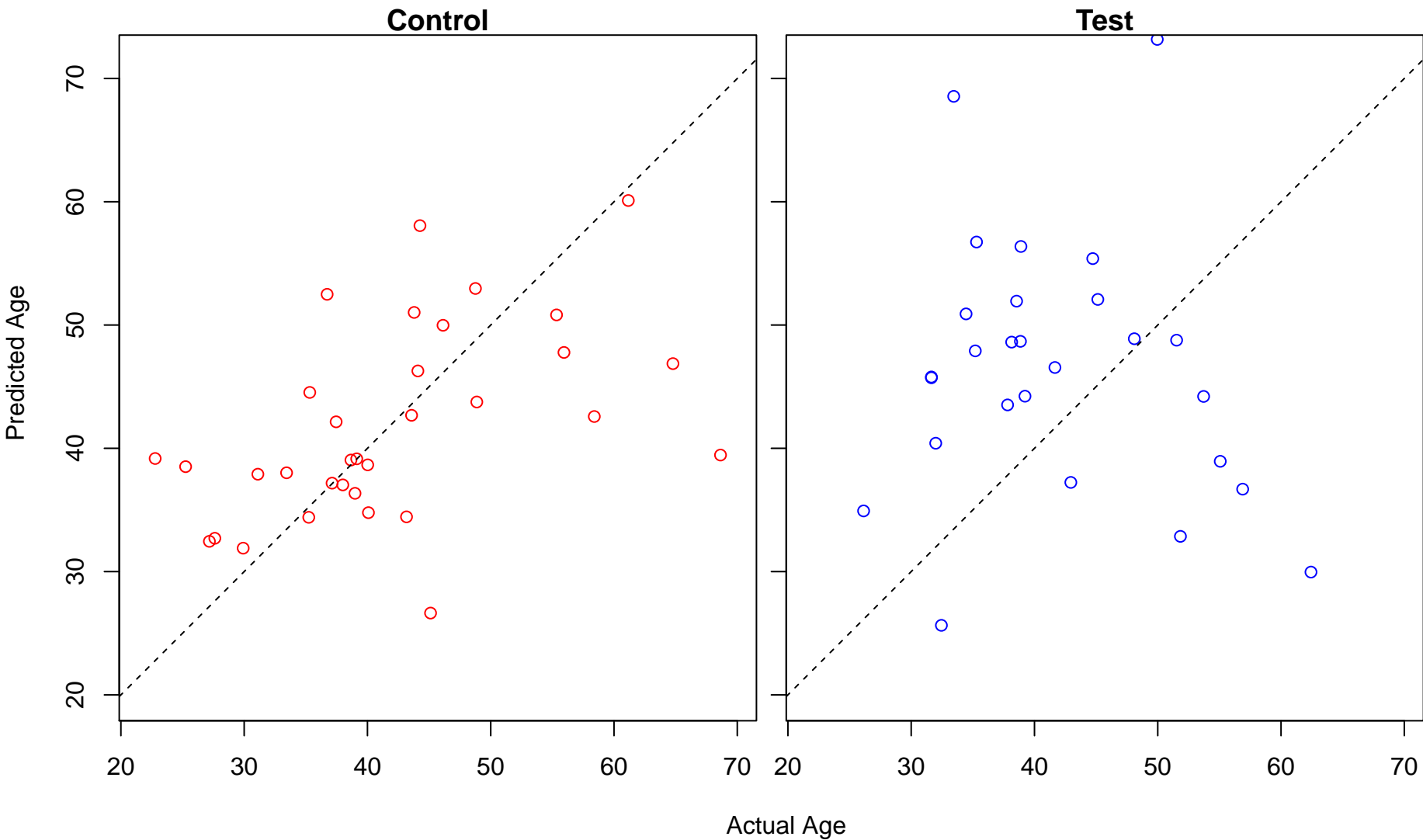
CDP-choline pathway (Score: 1.631798)



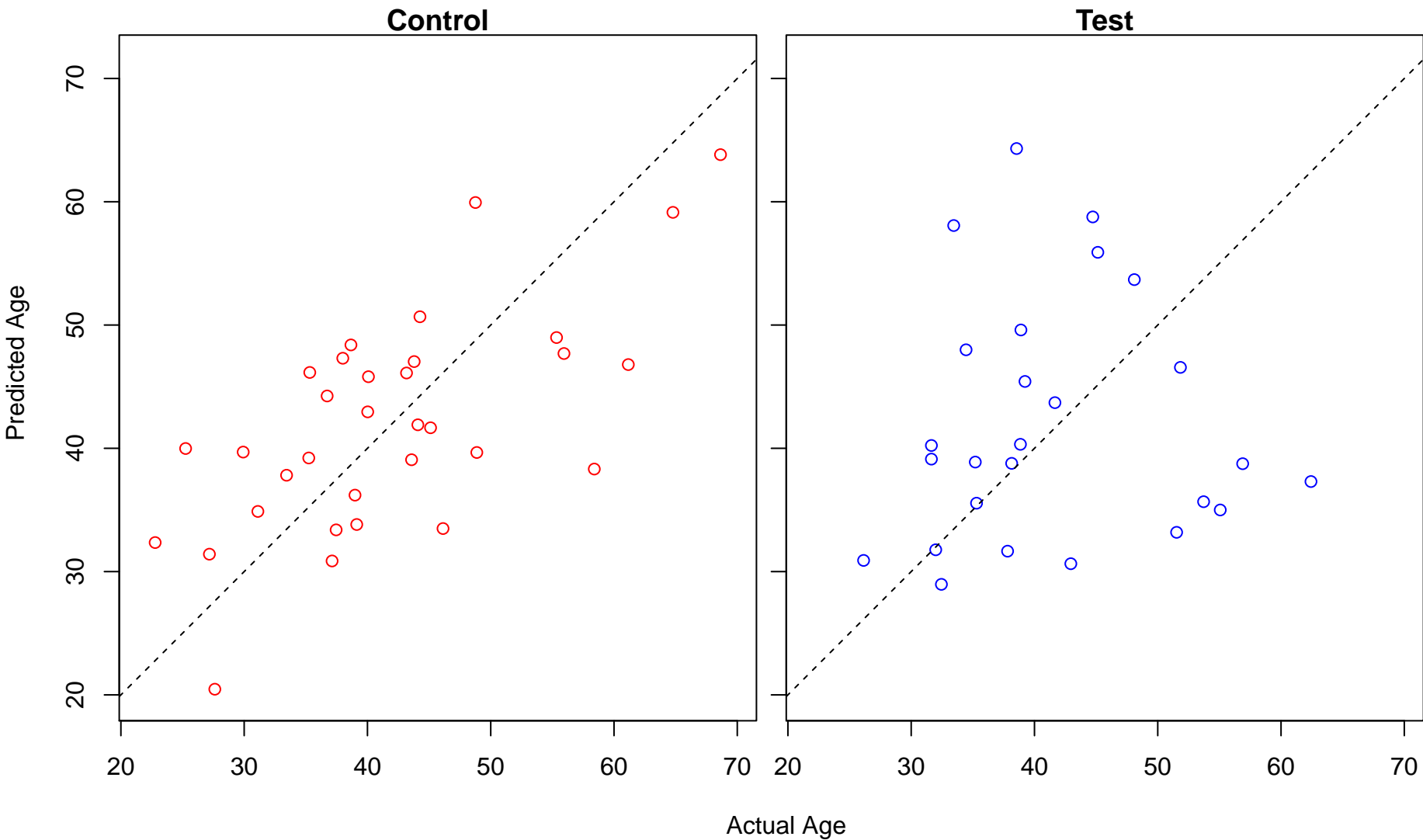
negative regulation of nitric oxide biosynthetic process (Score: 1.628870)



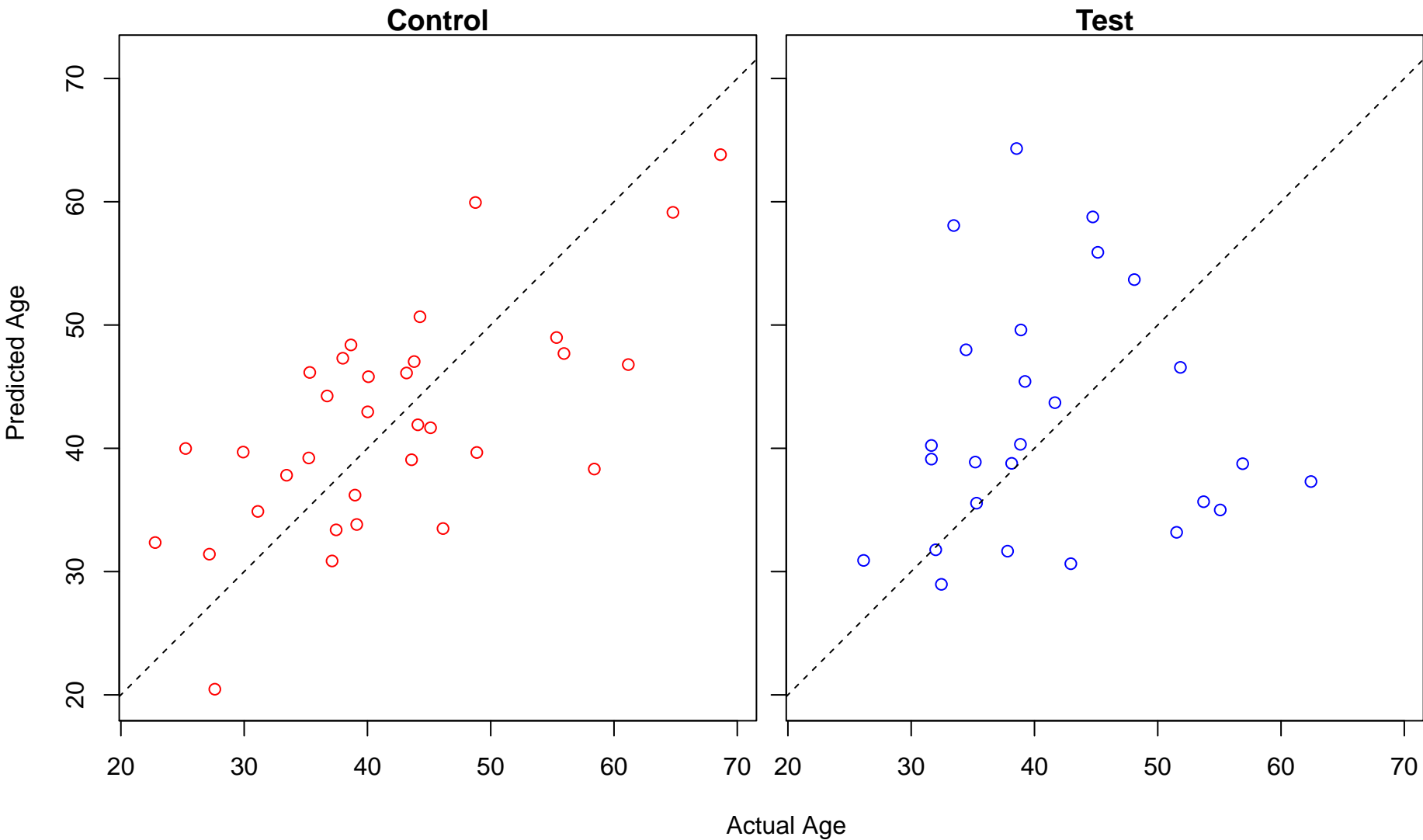
negative regulation of nitric oxide metabolic process (Score: 1.628870)



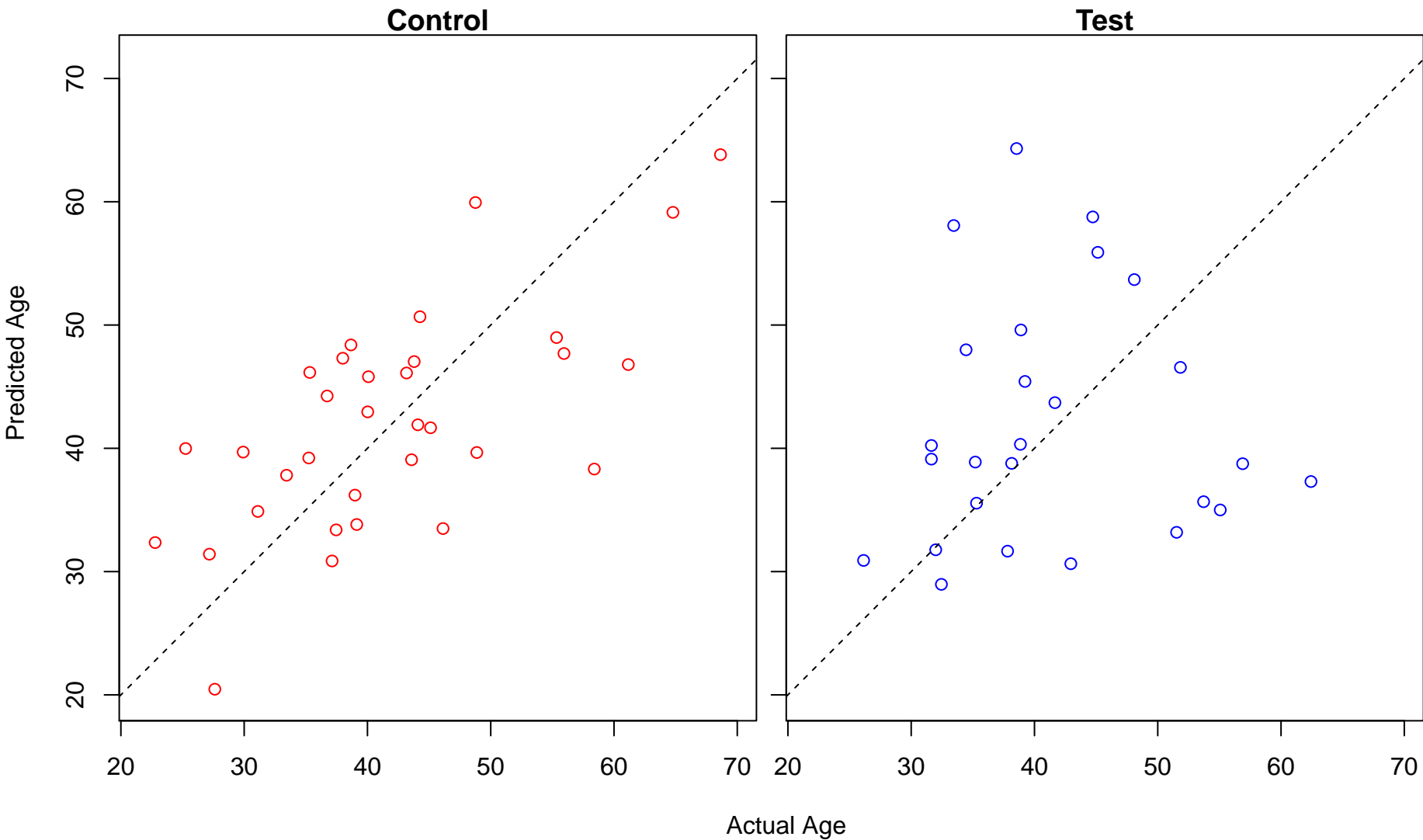
protein targeting to peroxisome (Score: 1.628801)



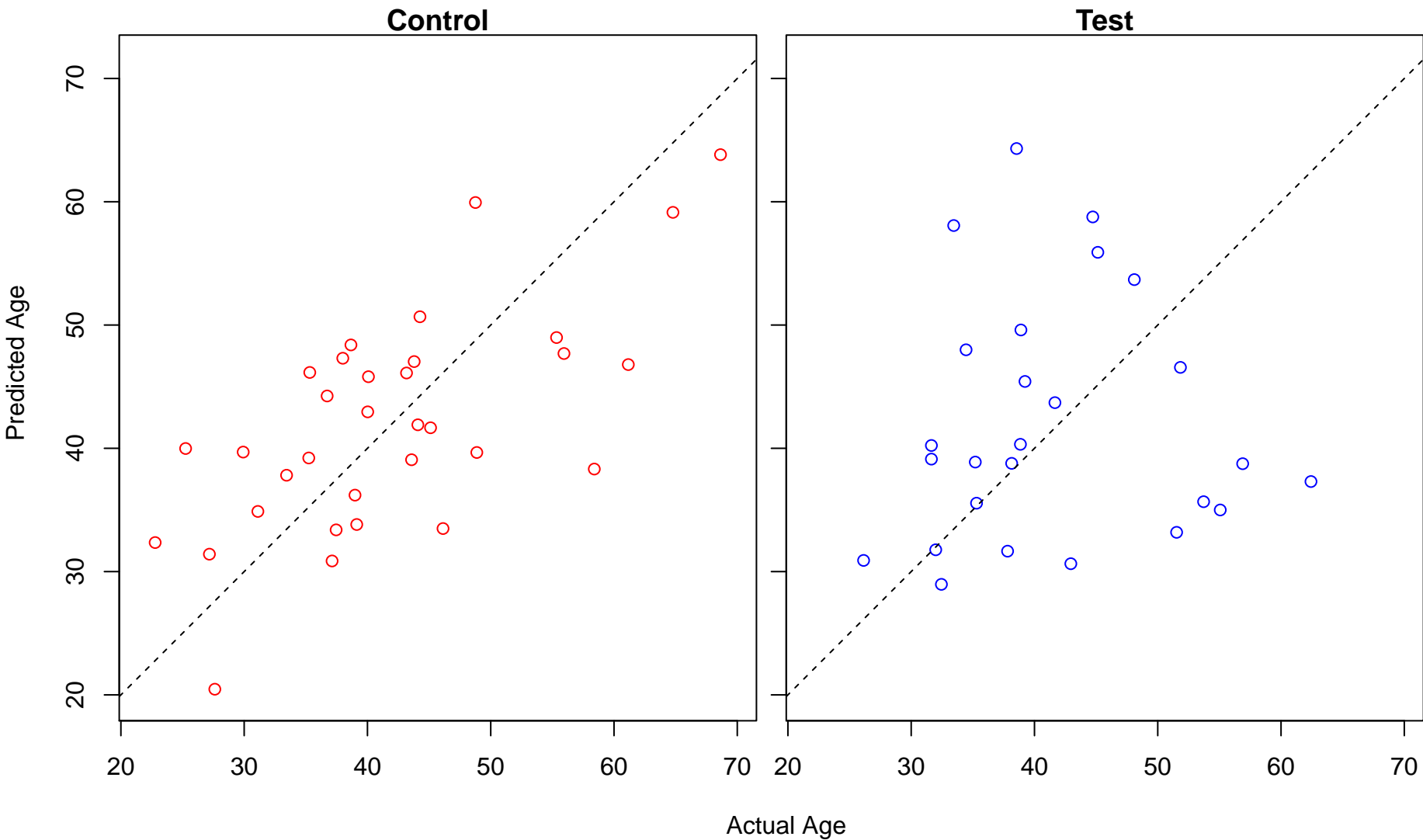
peroxisomal transport (Score: 1.628801)



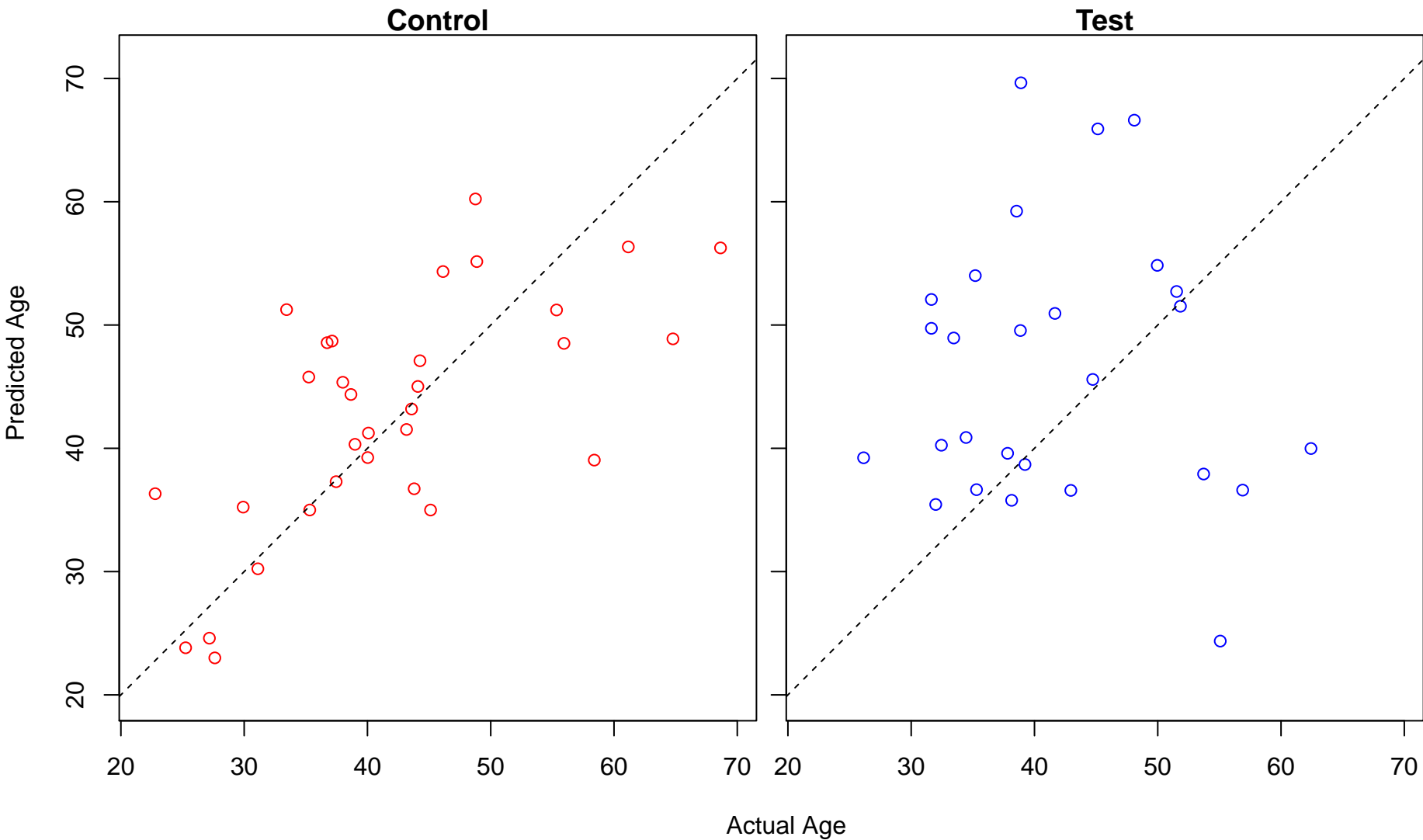
protein localization to peroxisome (Score: 1.628801)



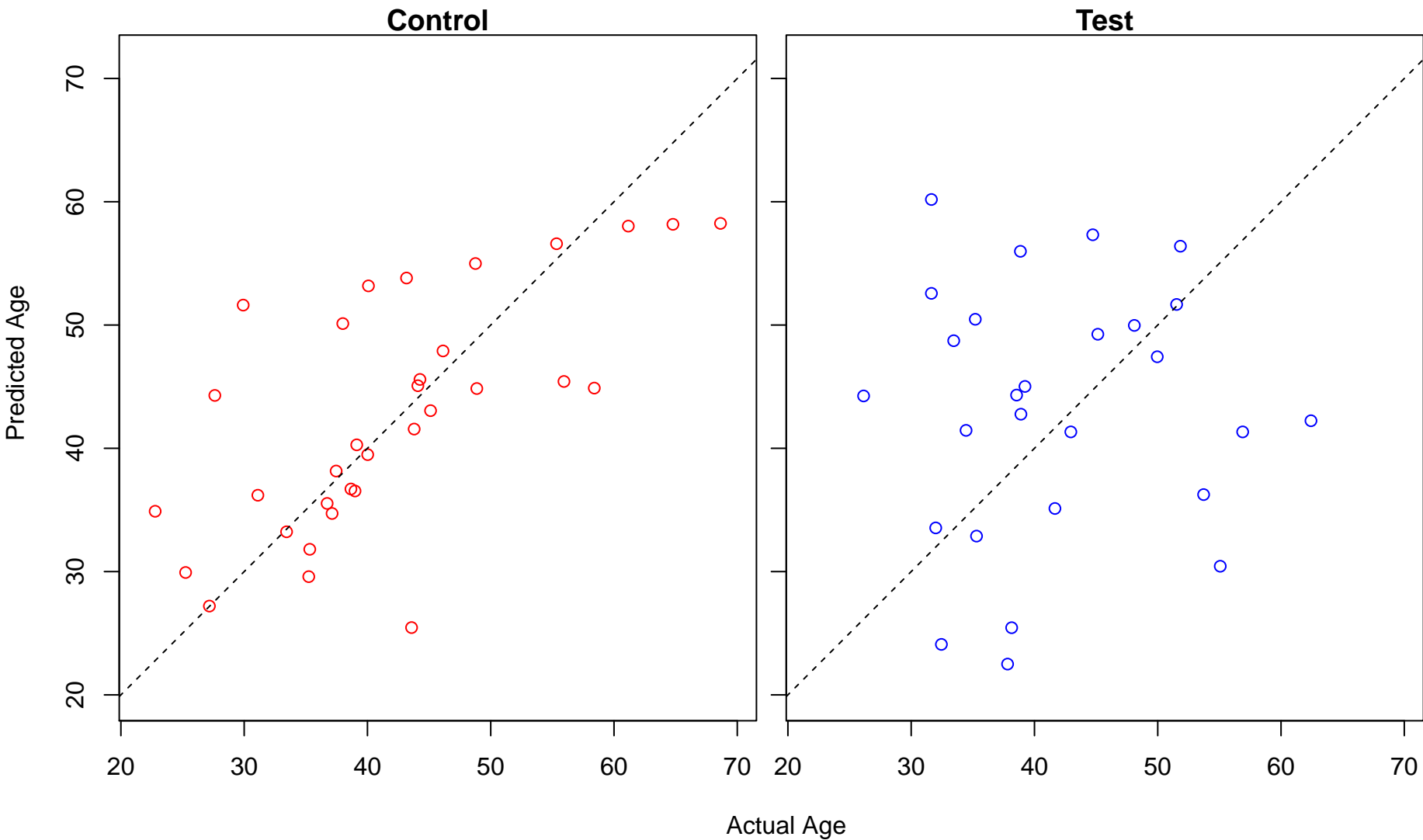
establishment of protein localization to peroxisome (Score: 1.628801)



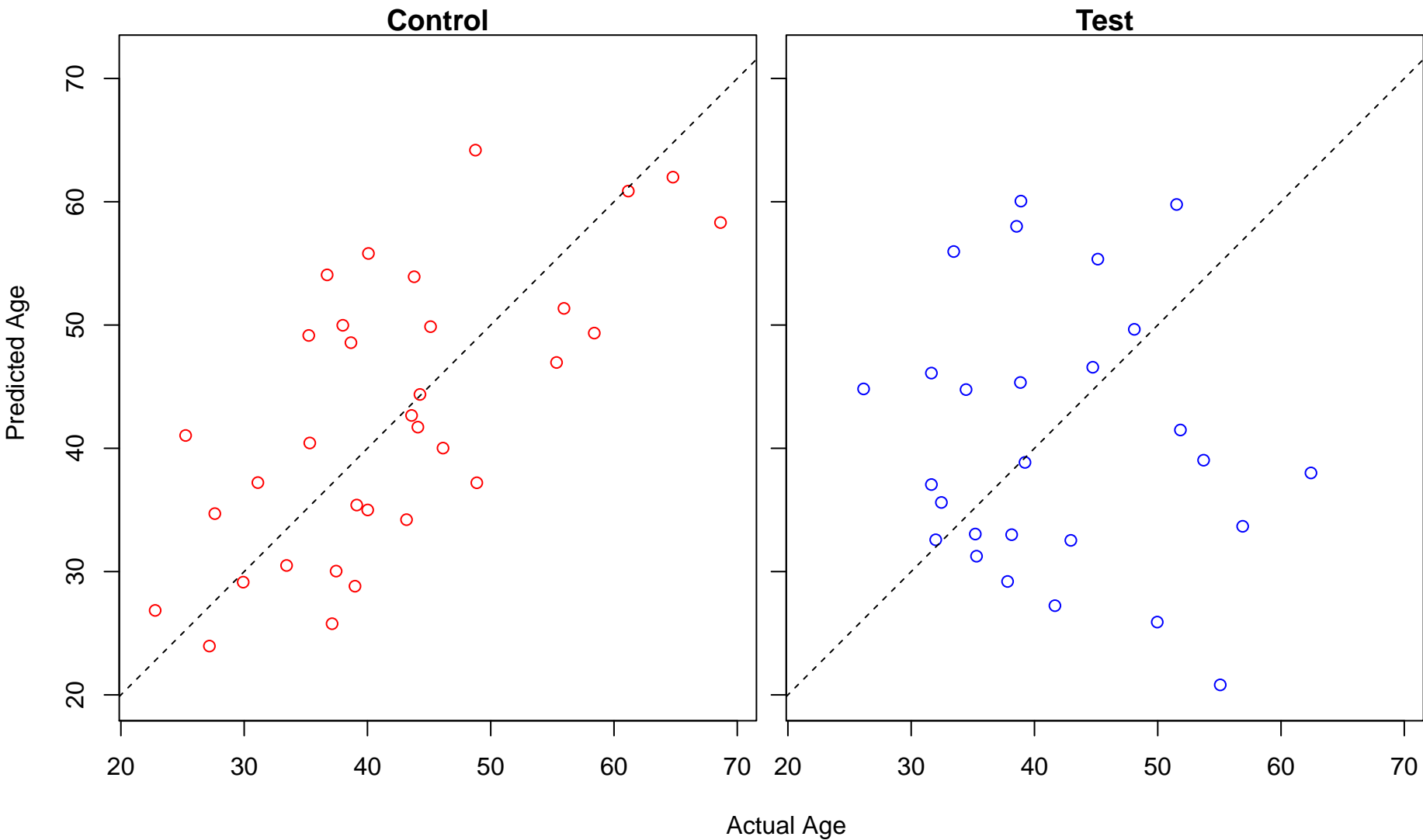
regulation of transcription from RNA polymerase I promoter (Score: 1.621873)



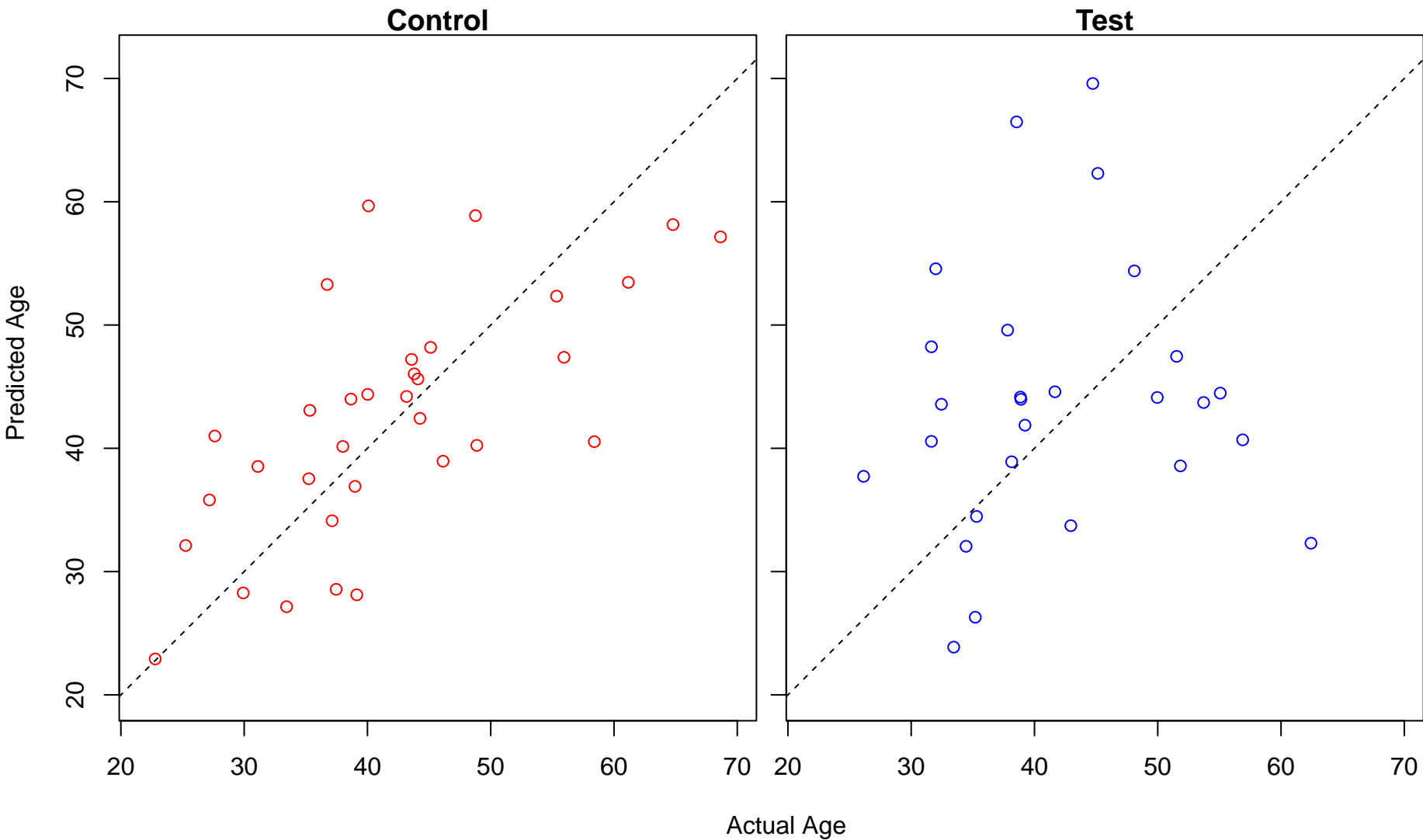
detection of light stimulus (Score: 1.621609)



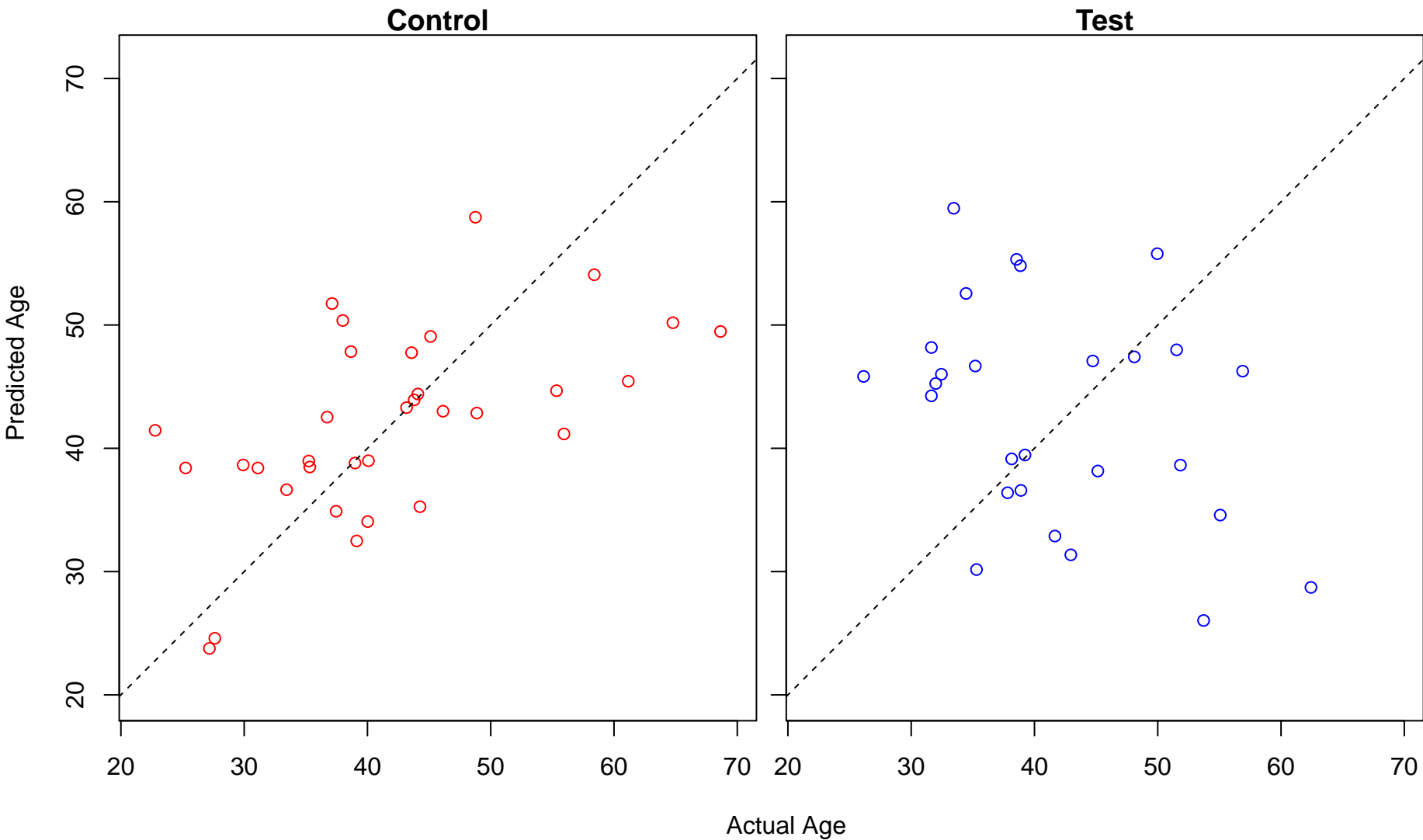
organophosphate catabolic process (Score: 1.618532)



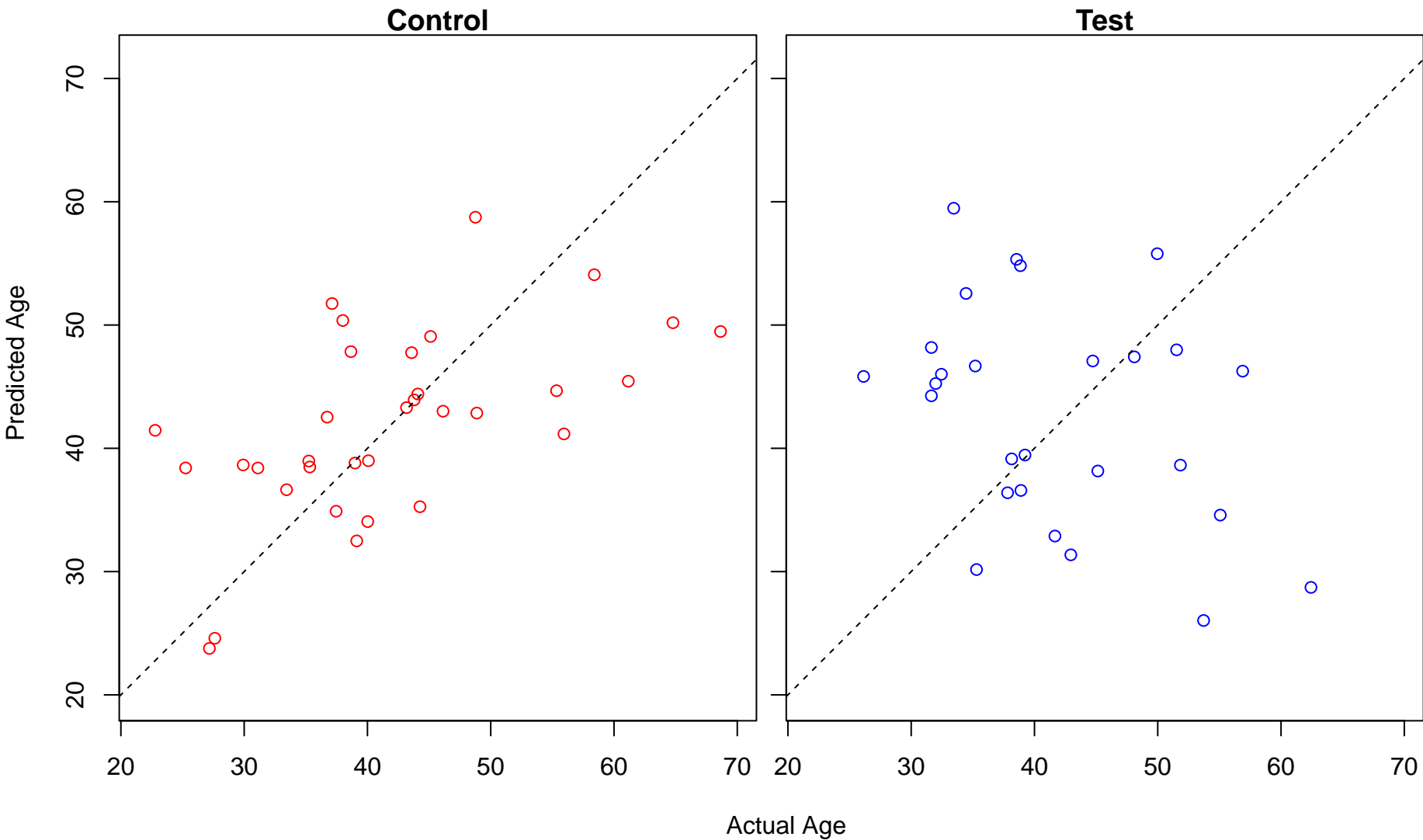
regulation of retrograde protein transport, ER to cytosol (Score: 1.606062)



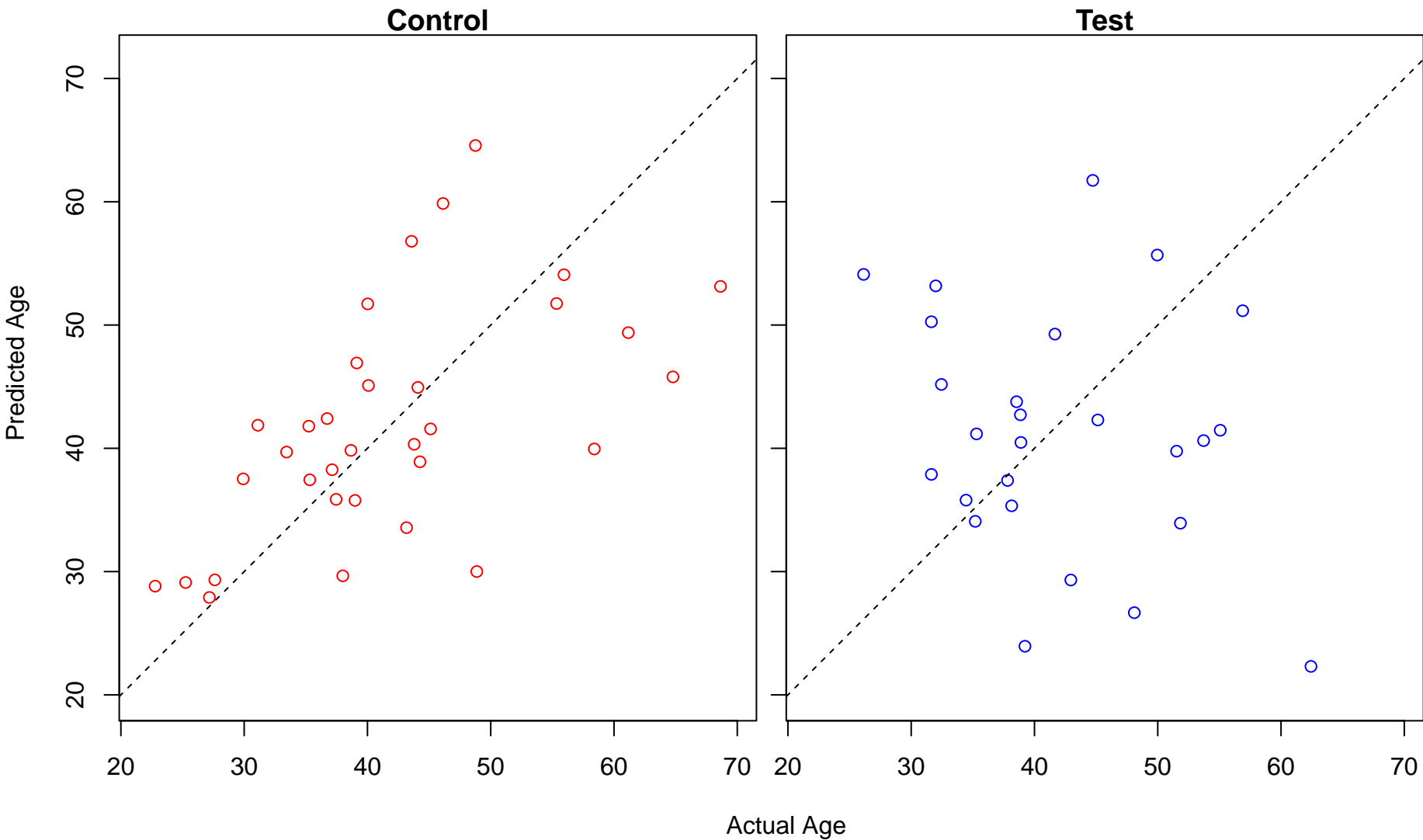
central nervous system myelination (Score: 1.603915)



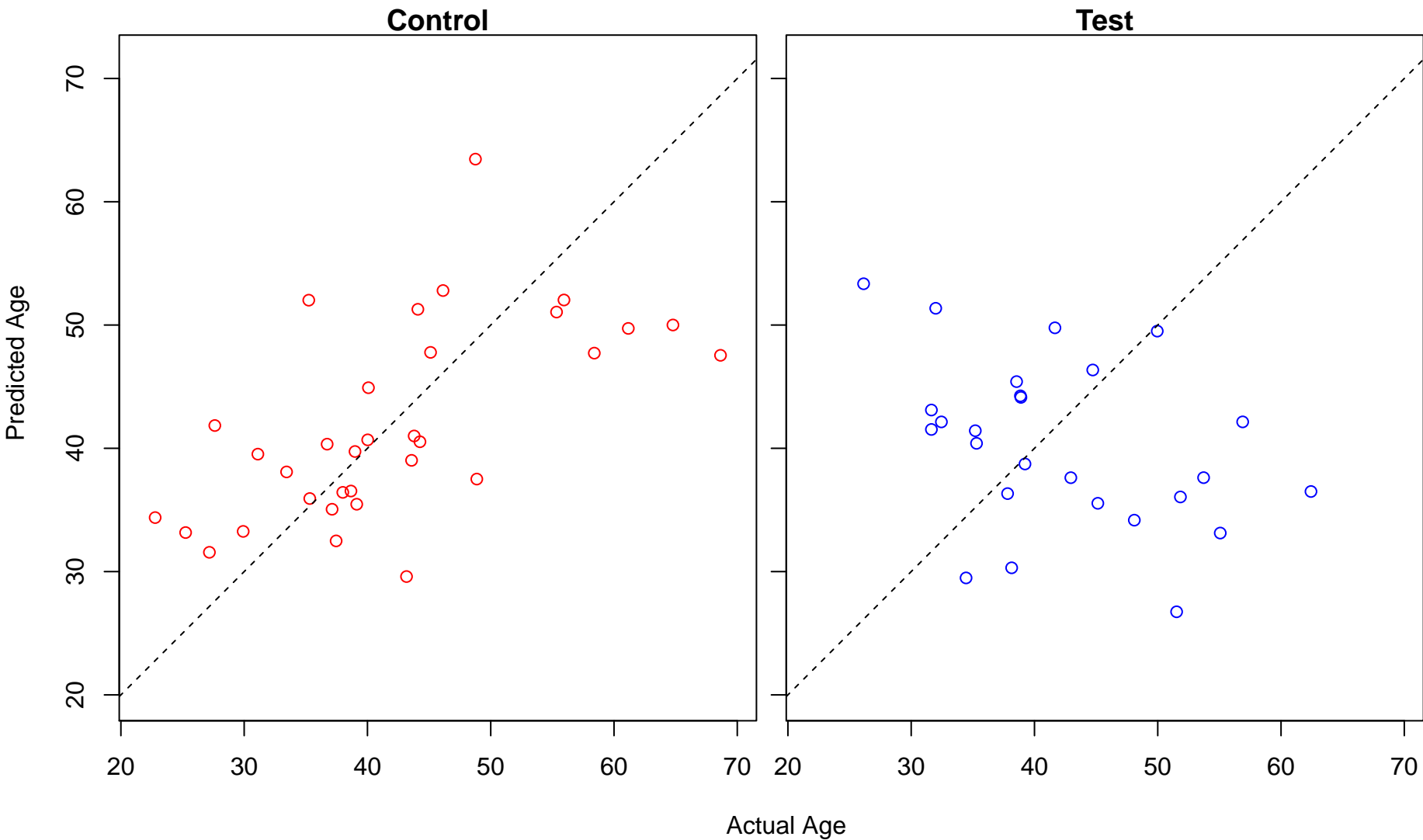
axon ensheathment in central nervous system (Score: 1.603915)



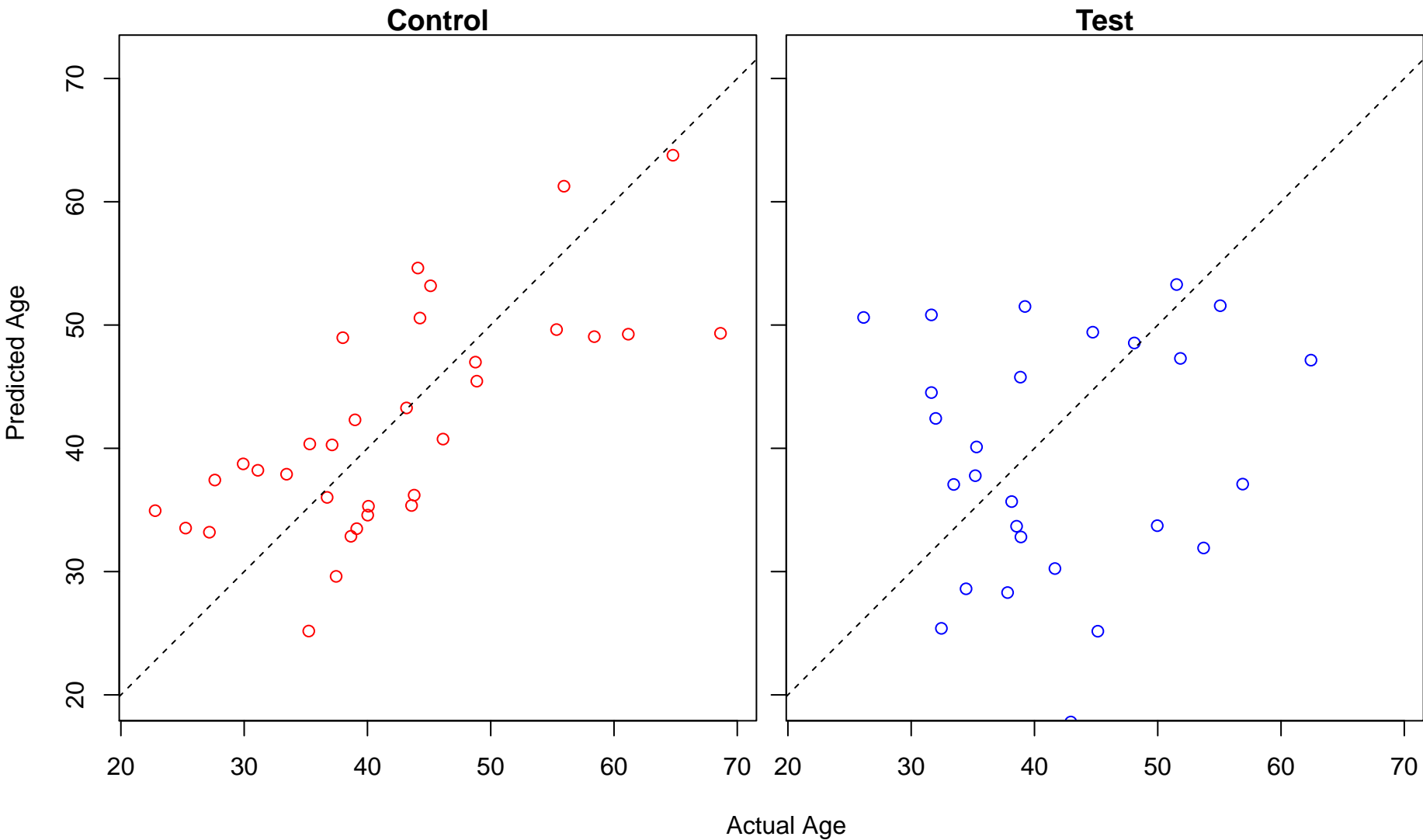
positive regulation of potassium ion transport (Score: 1.579151)



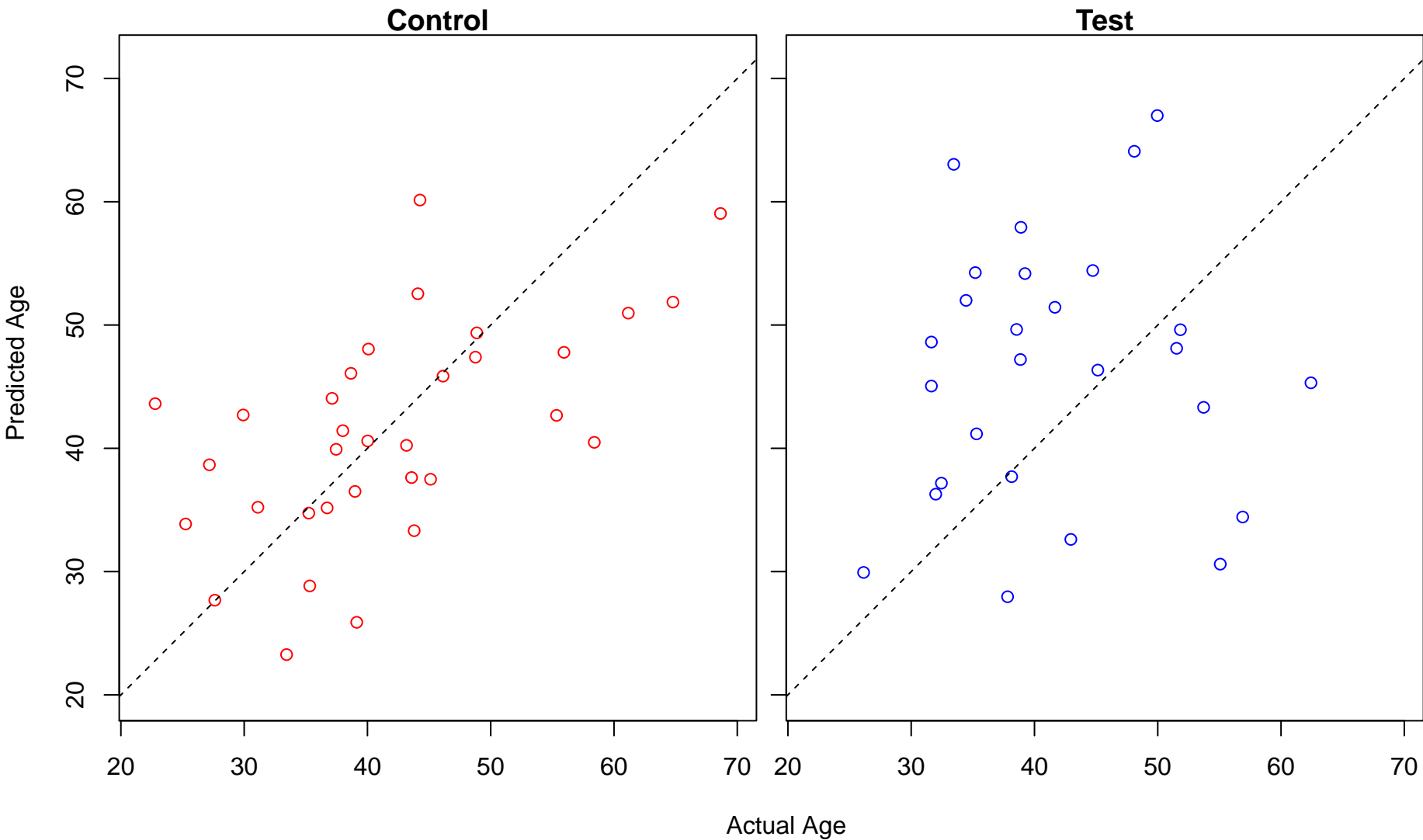
cell communication involved in cardiac conduction (Score: 1.570042)



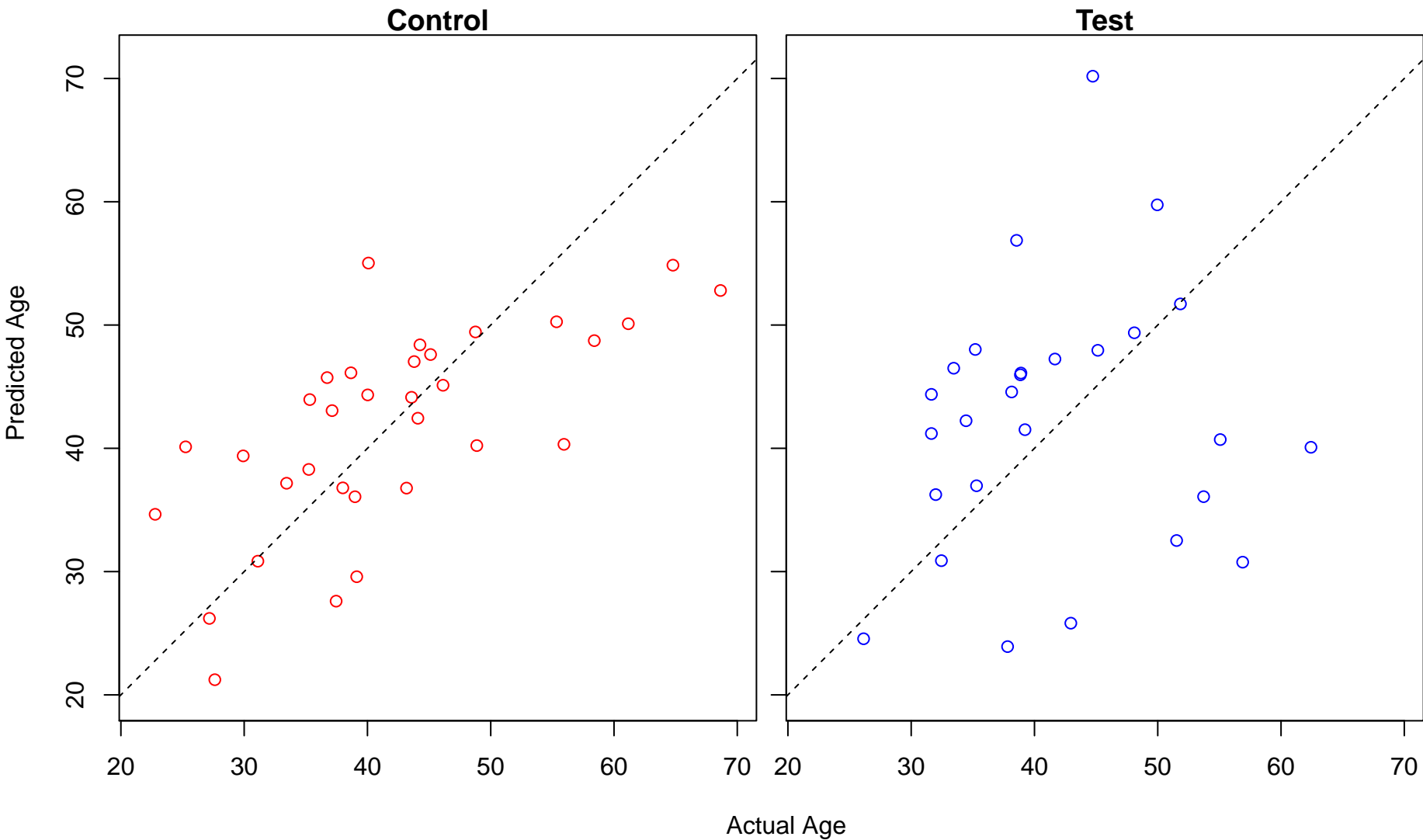
intestinal absorption (Score: 1.564920)



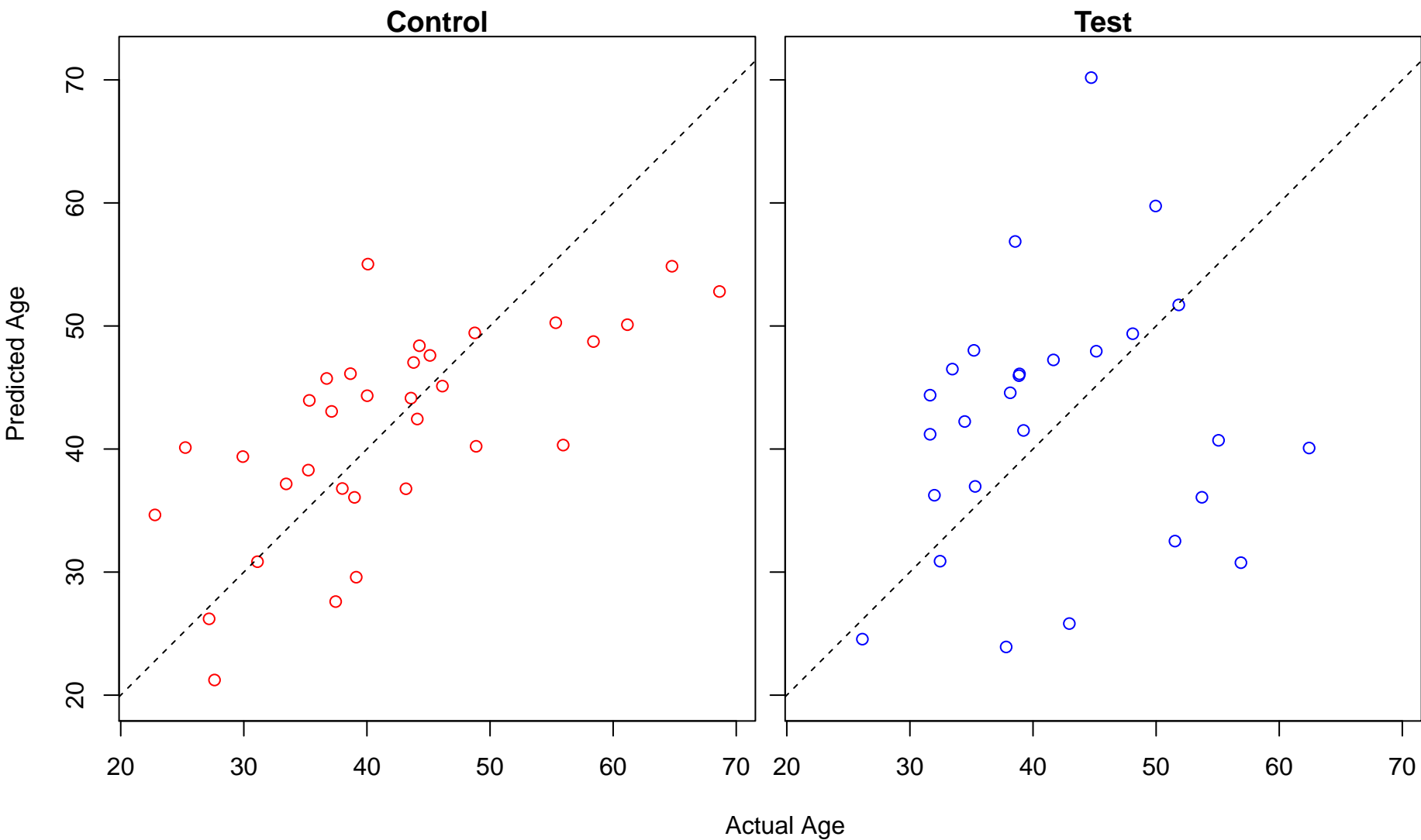
peptidyl-arginine N-methylation (Score: 1.563580)



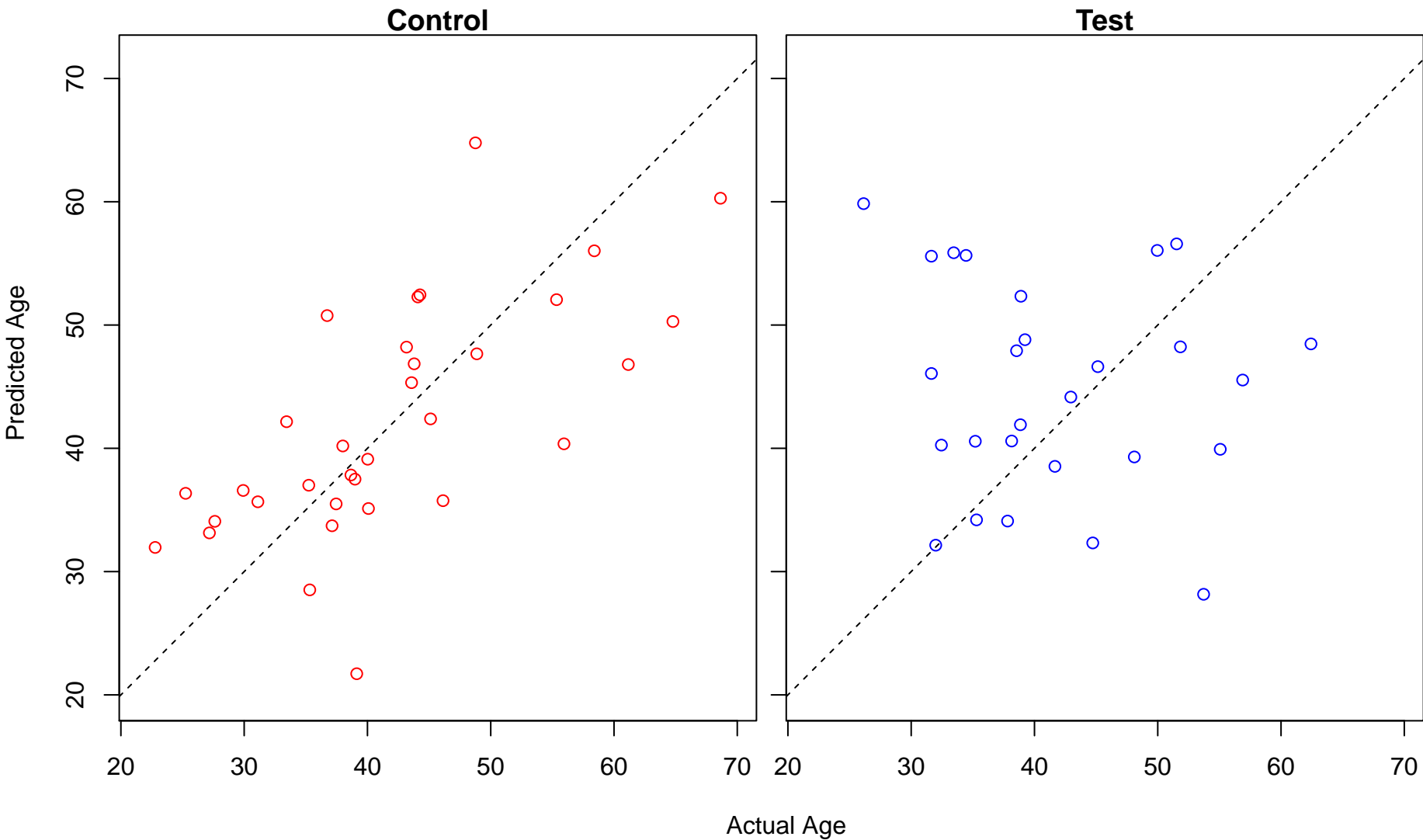
peroxisomal membrane transport (Score: 1.560743)



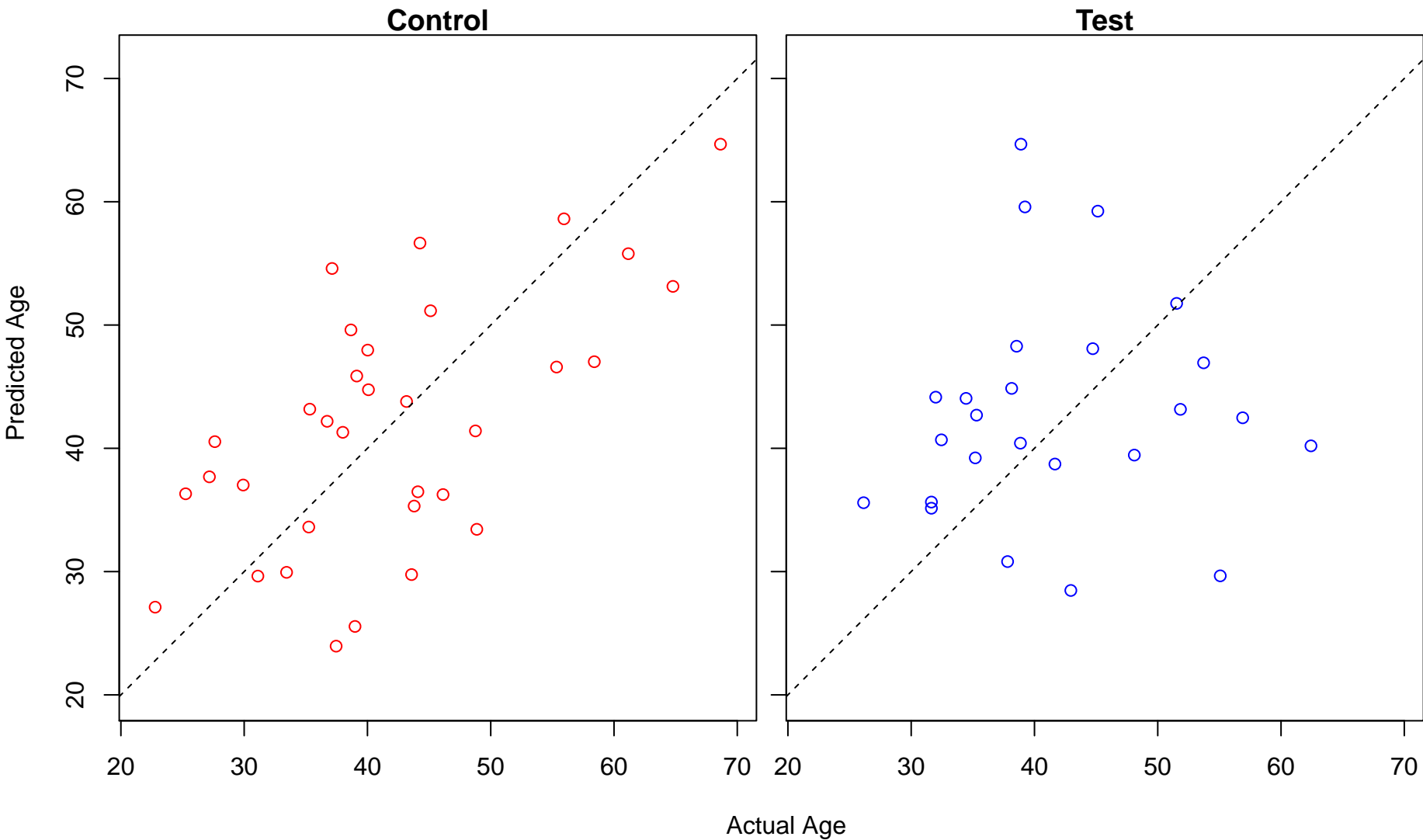
protein import into peroxisome membrane (Score: 1.560743)



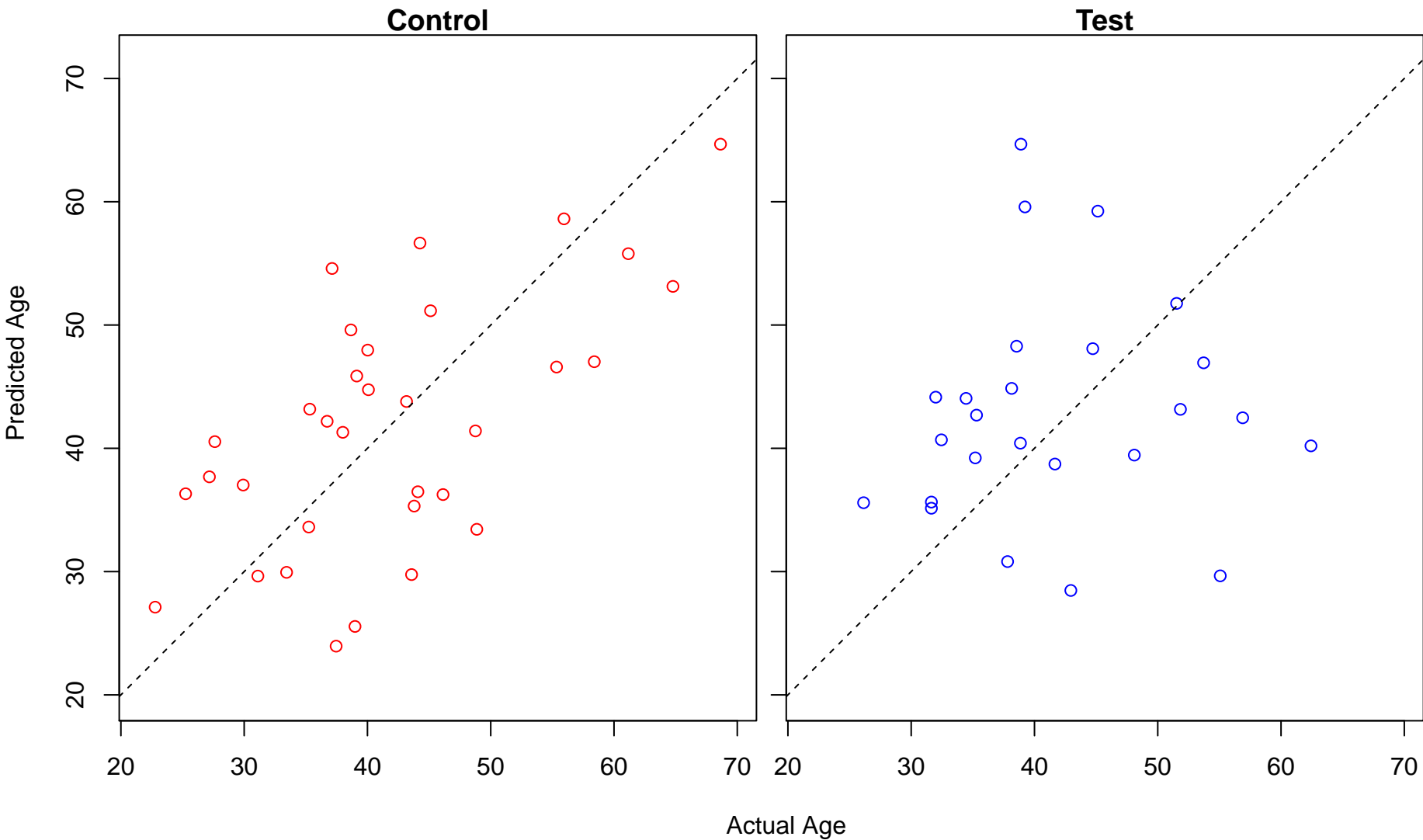
humoral immune response mediated by circulating immunoglobulin (Score: 1.557738)



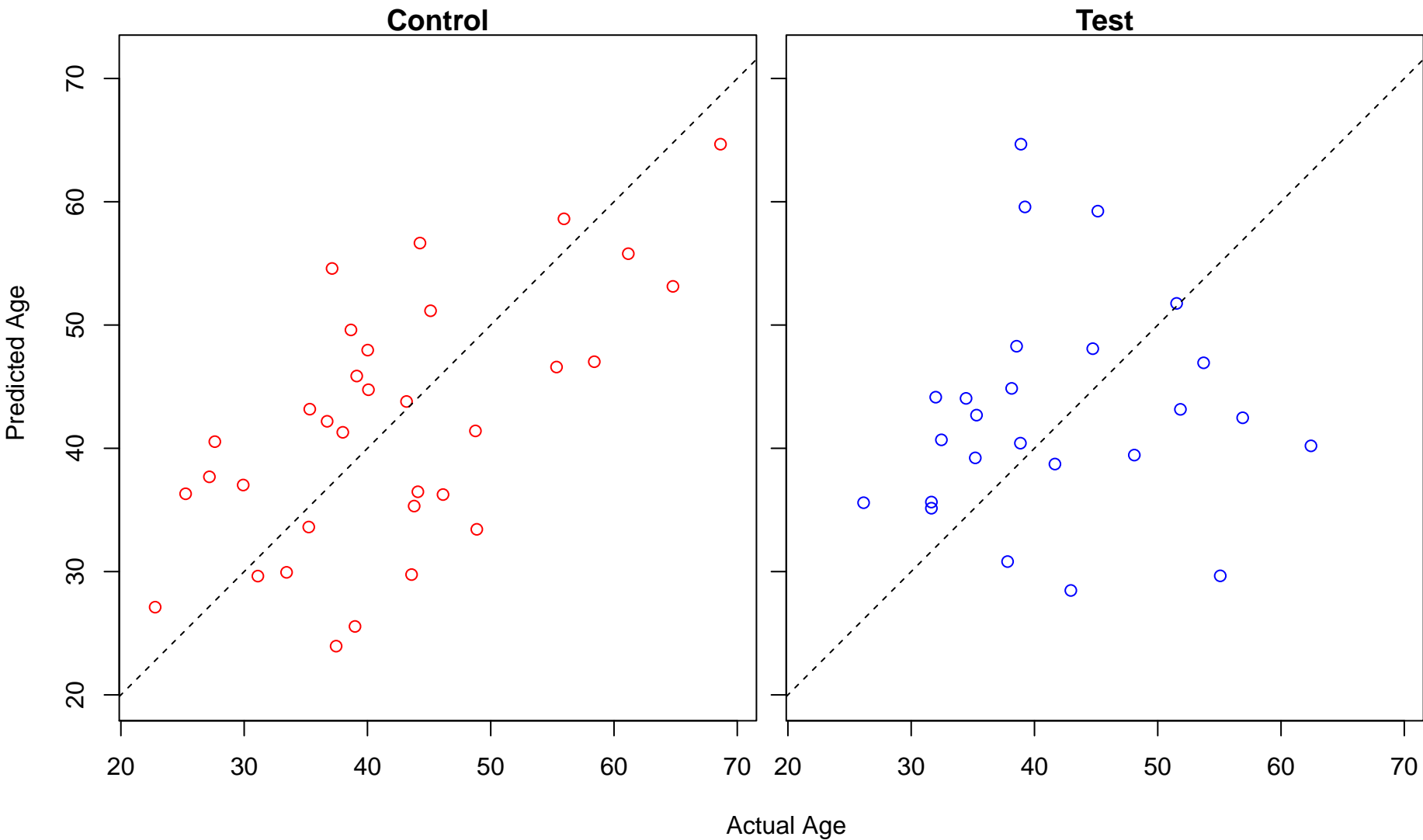
ferric iron transport (Score: 1.556343)



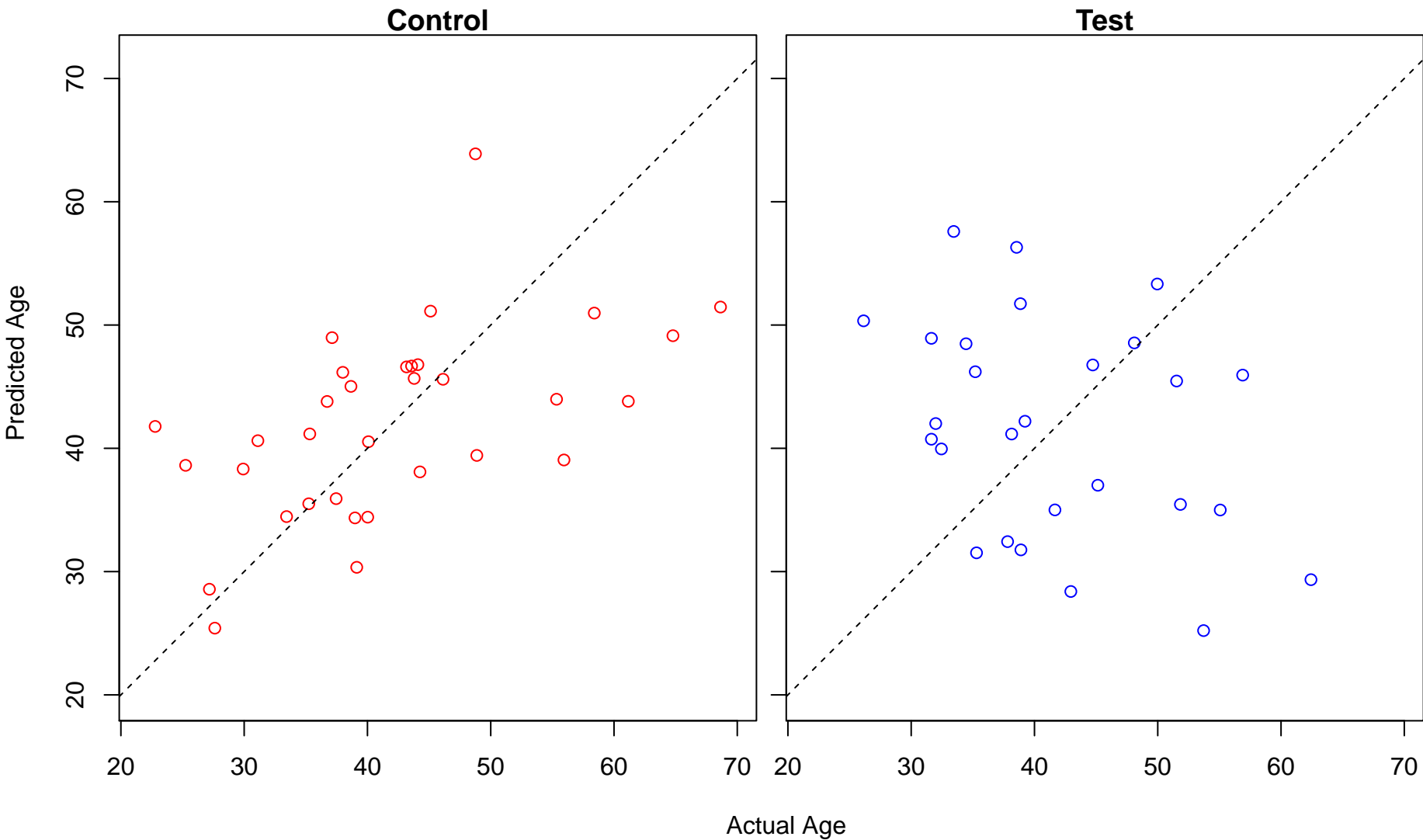
transferrin transport (Score: 1.556343)



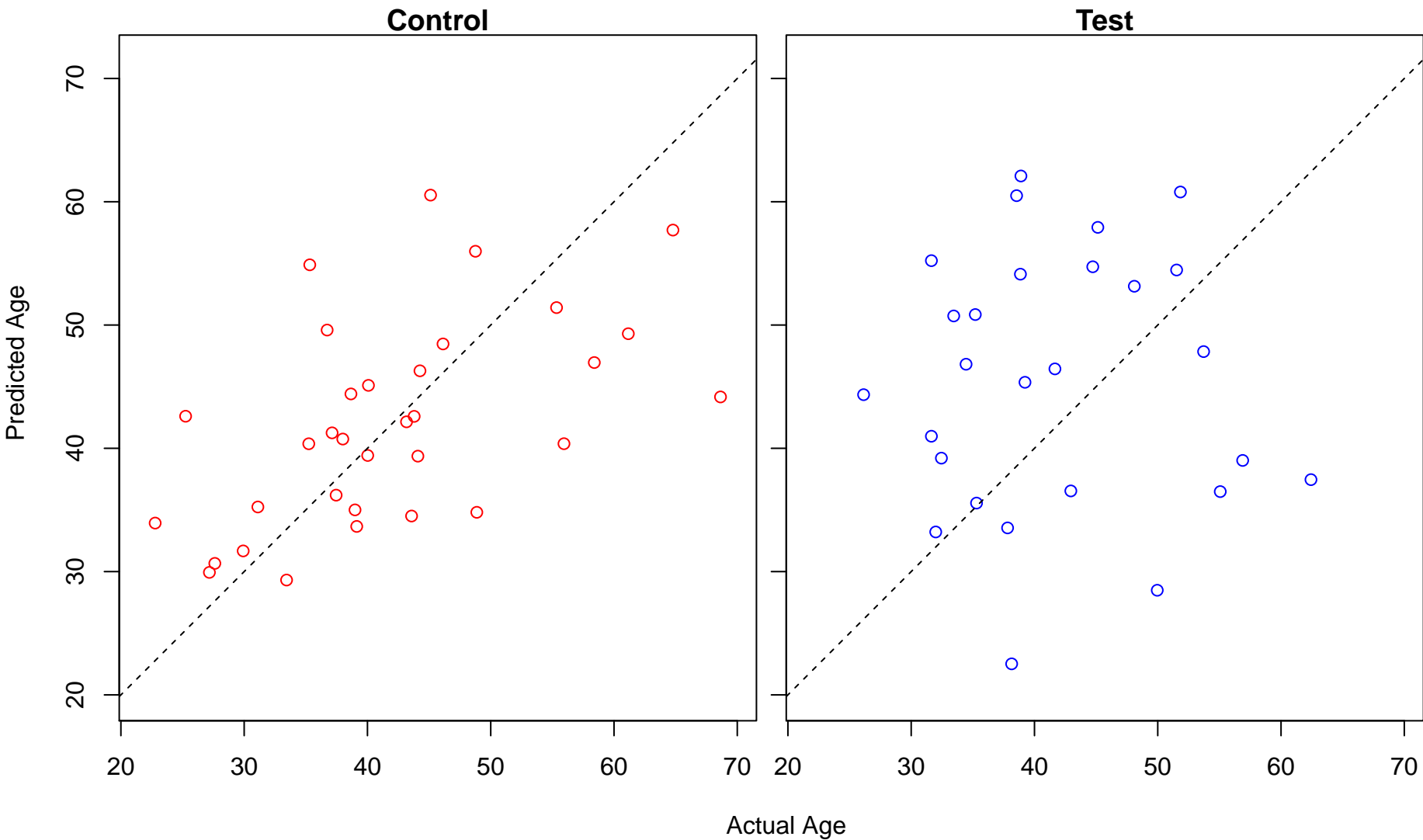
trivalent inorganic cation transport (Score: 1.556343)



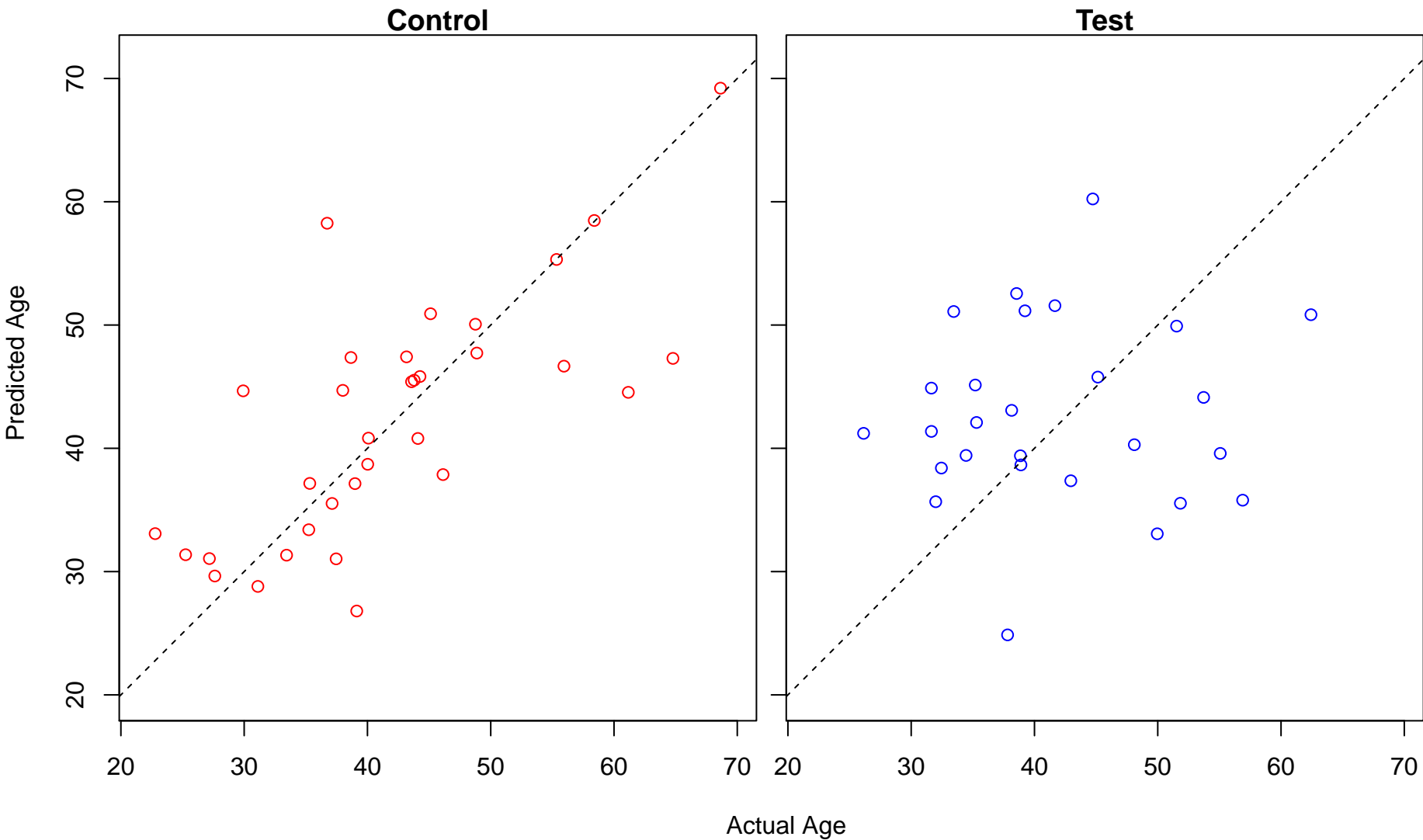
myelin maintenance (Score: 1.528748)



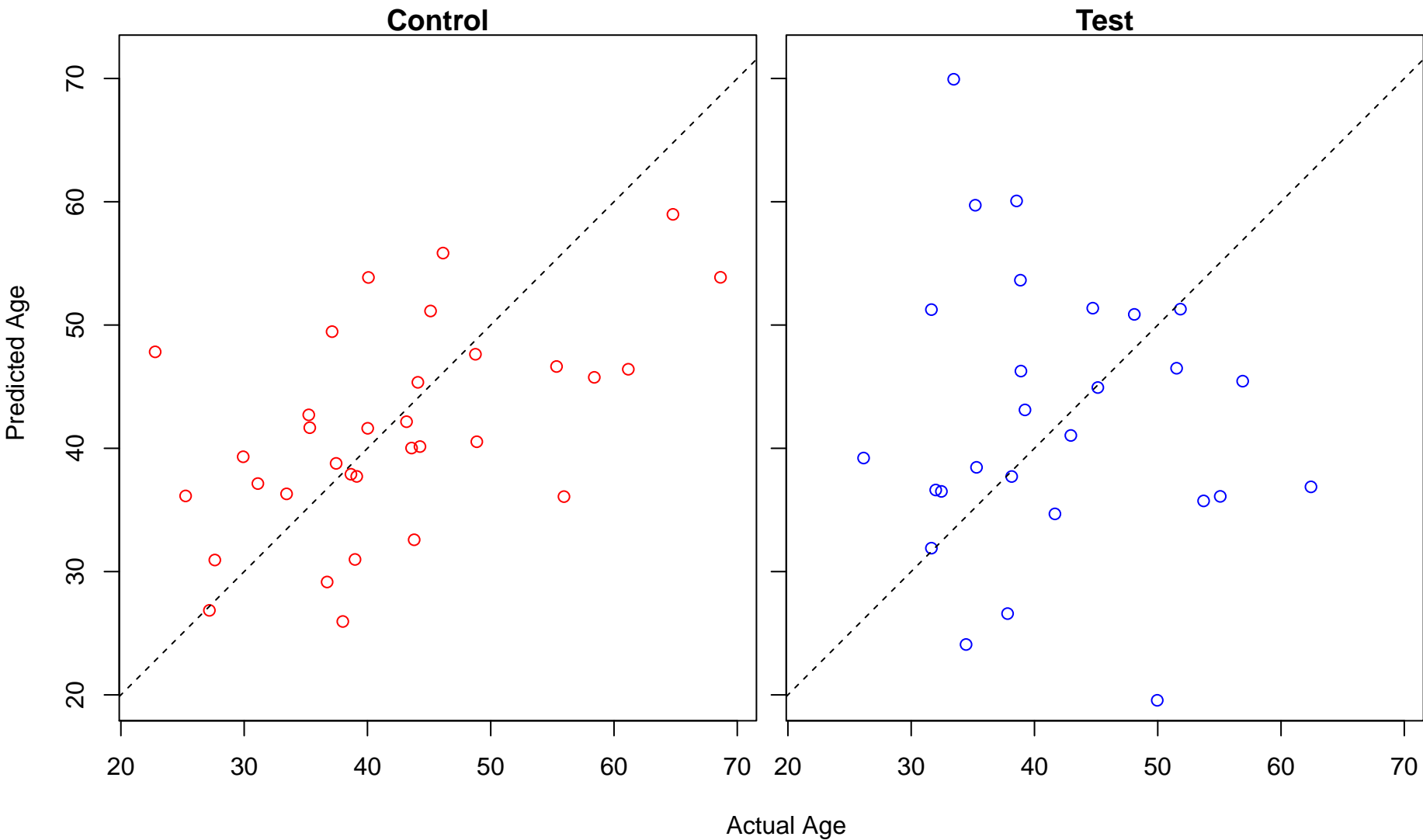
spinal cord development (Score: 1.522825)



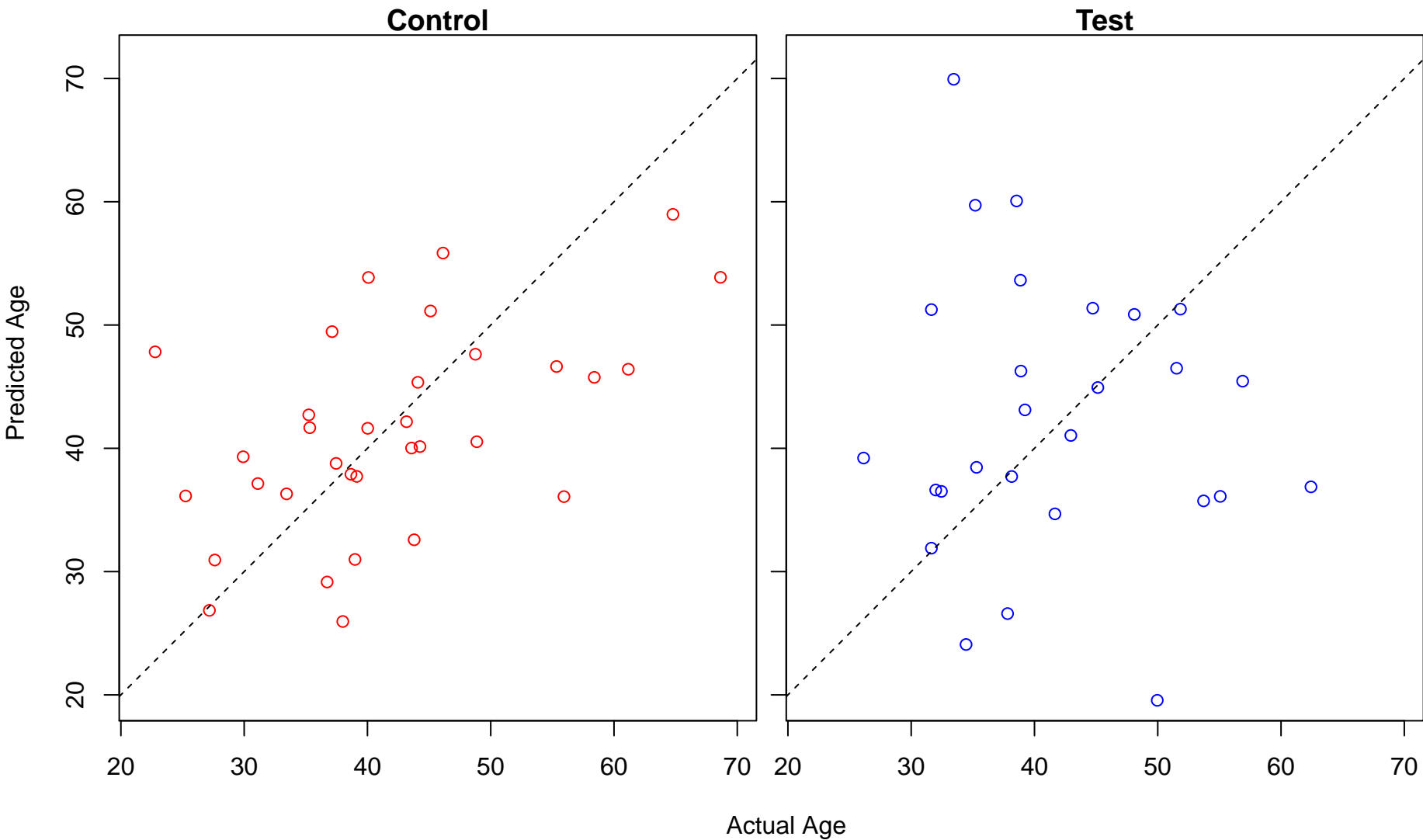
tumor necrosis factor-mediated signaling pathway (Score: 1.521133)



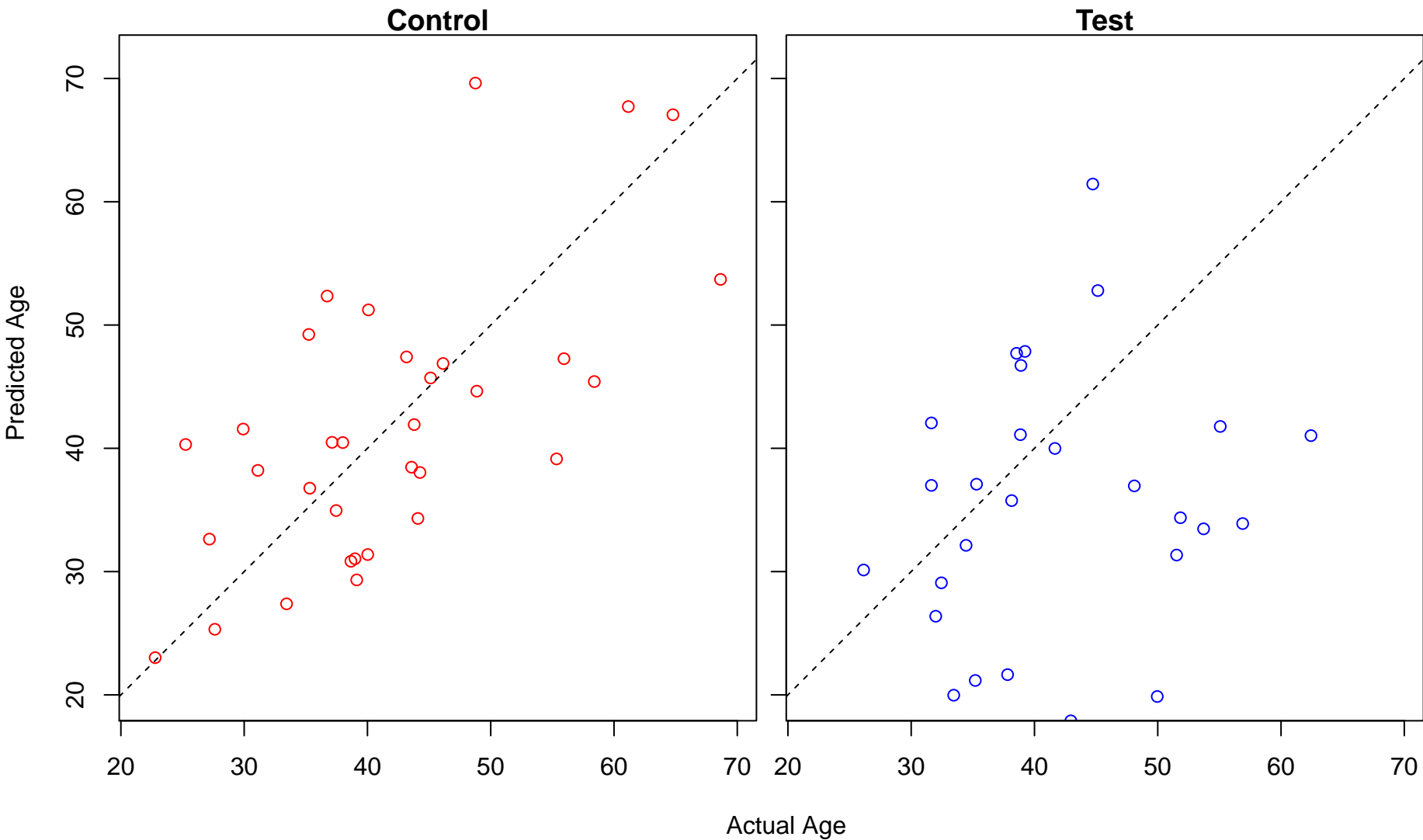
glycogen biosynthetic process (Score: 1.508678)



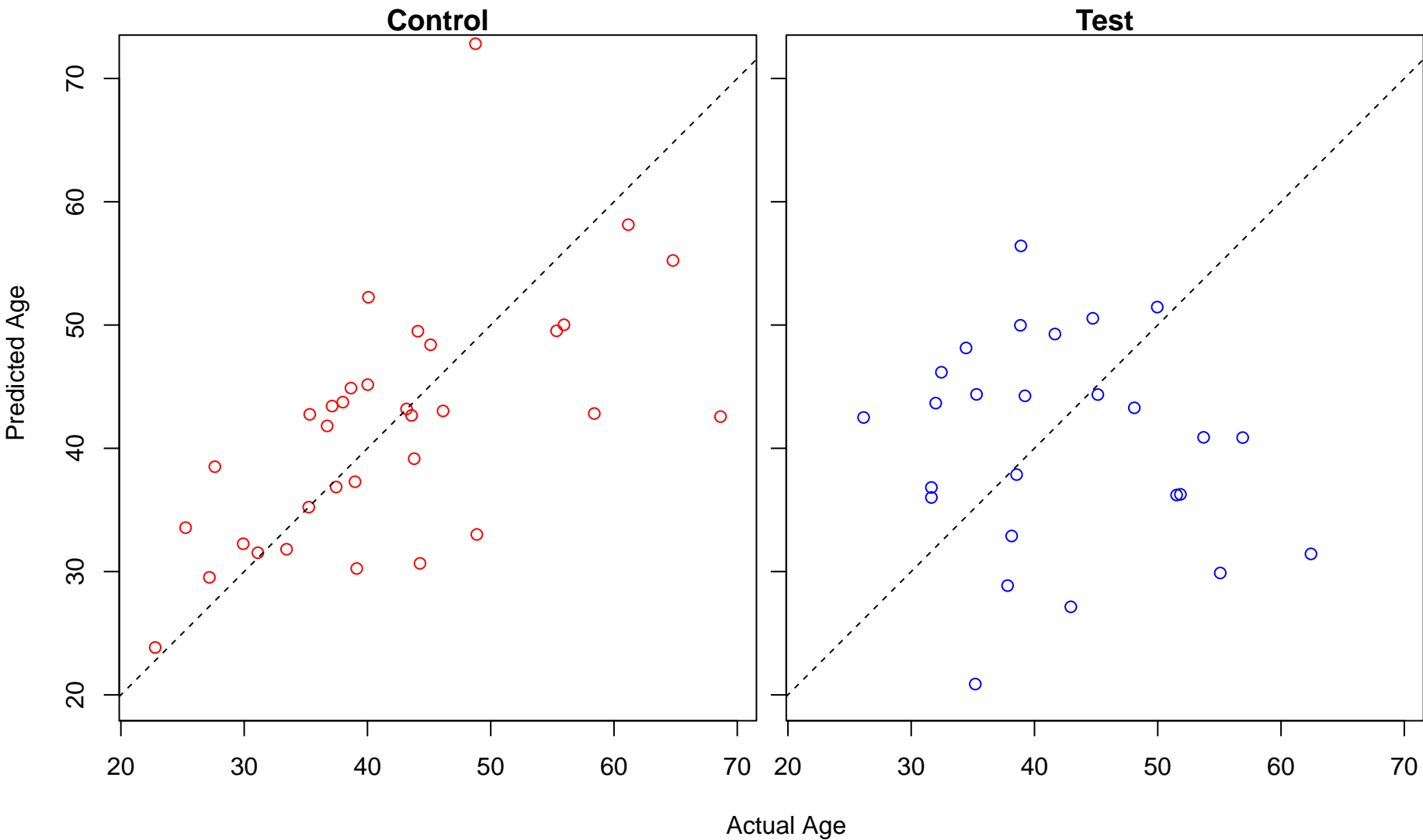
glucan biosynthetic process (Score: 1.508678)



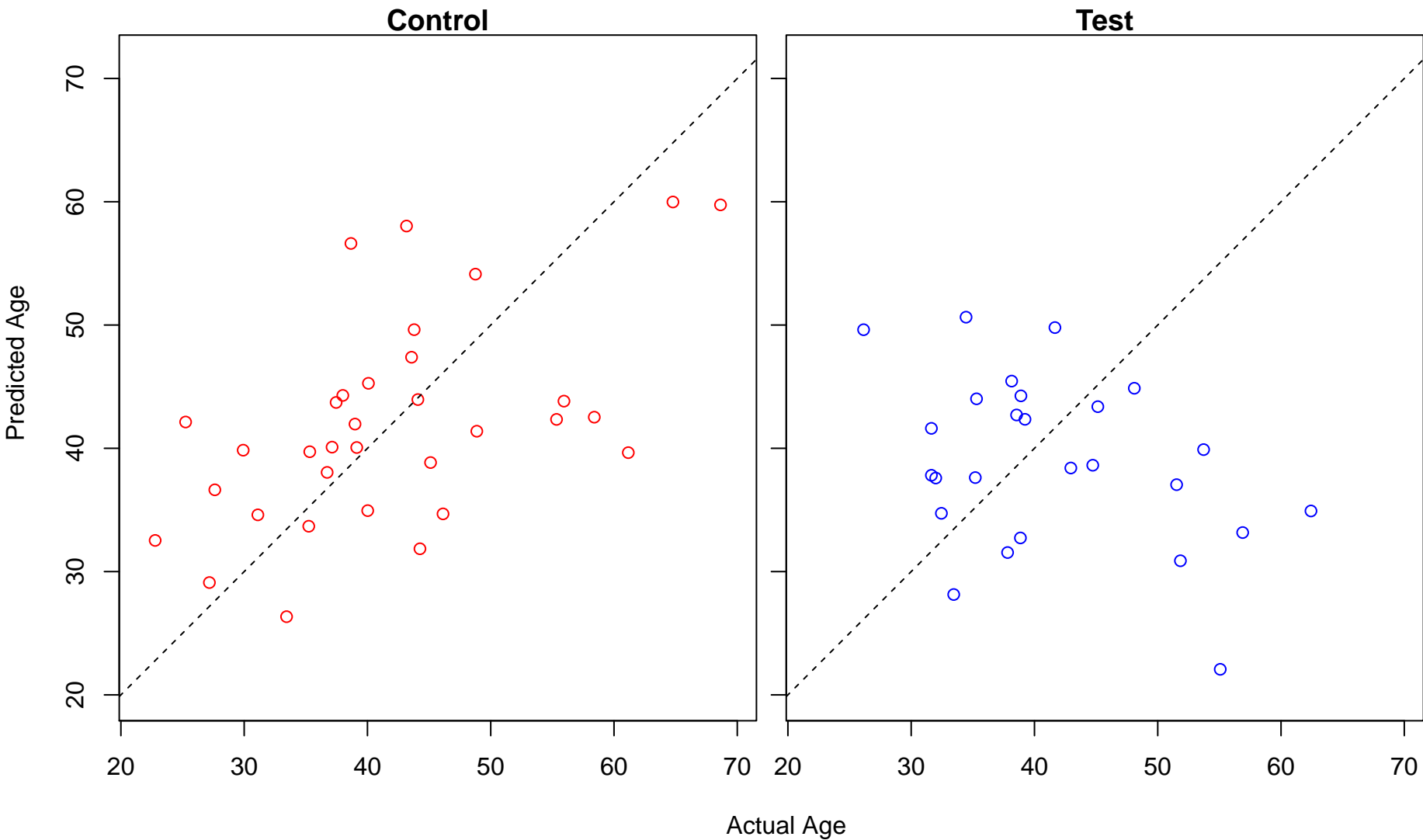
cellular response to molecule of bacterial origin (Score: 1.508005)



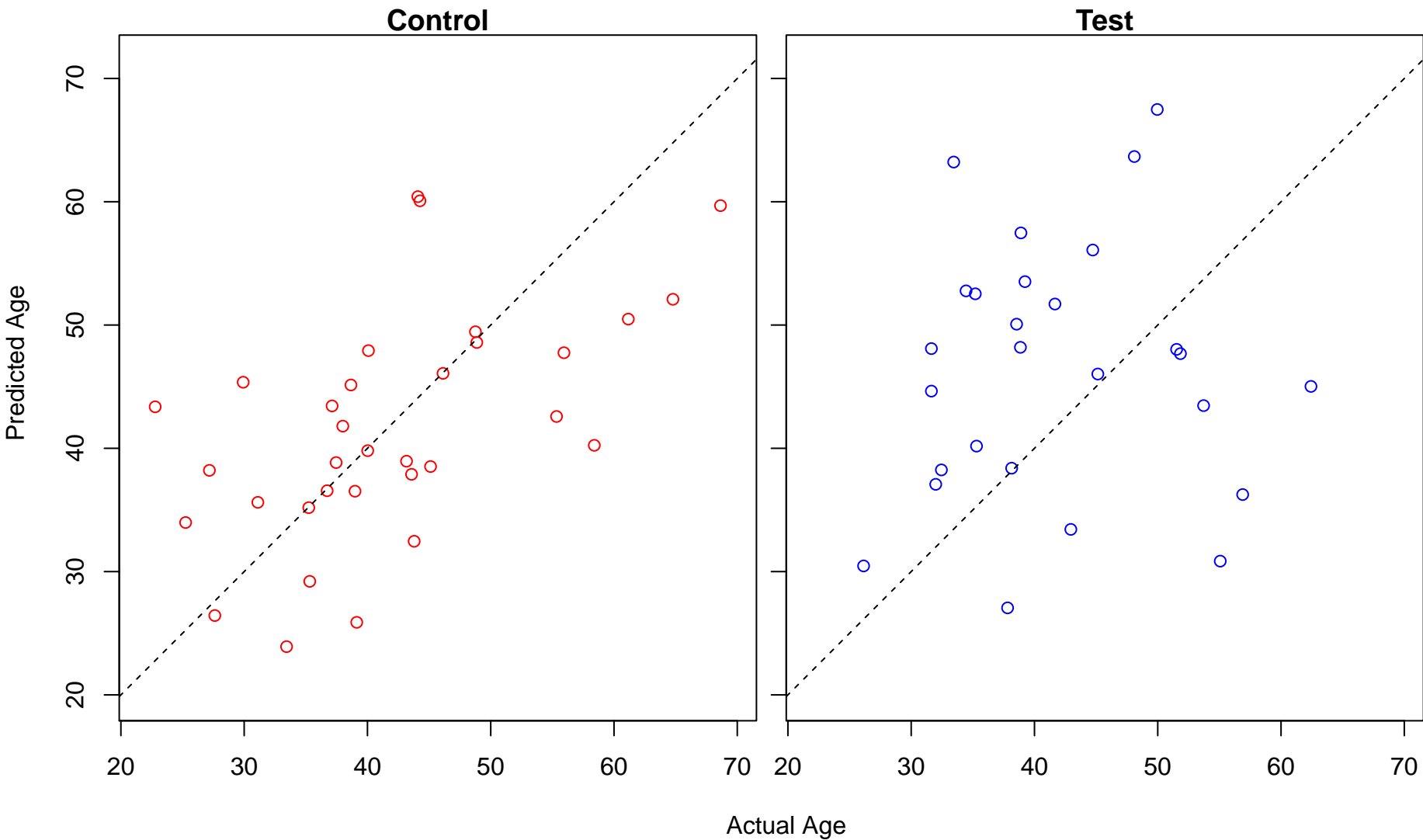
protein autophosphorylation (Score: 1.506643)



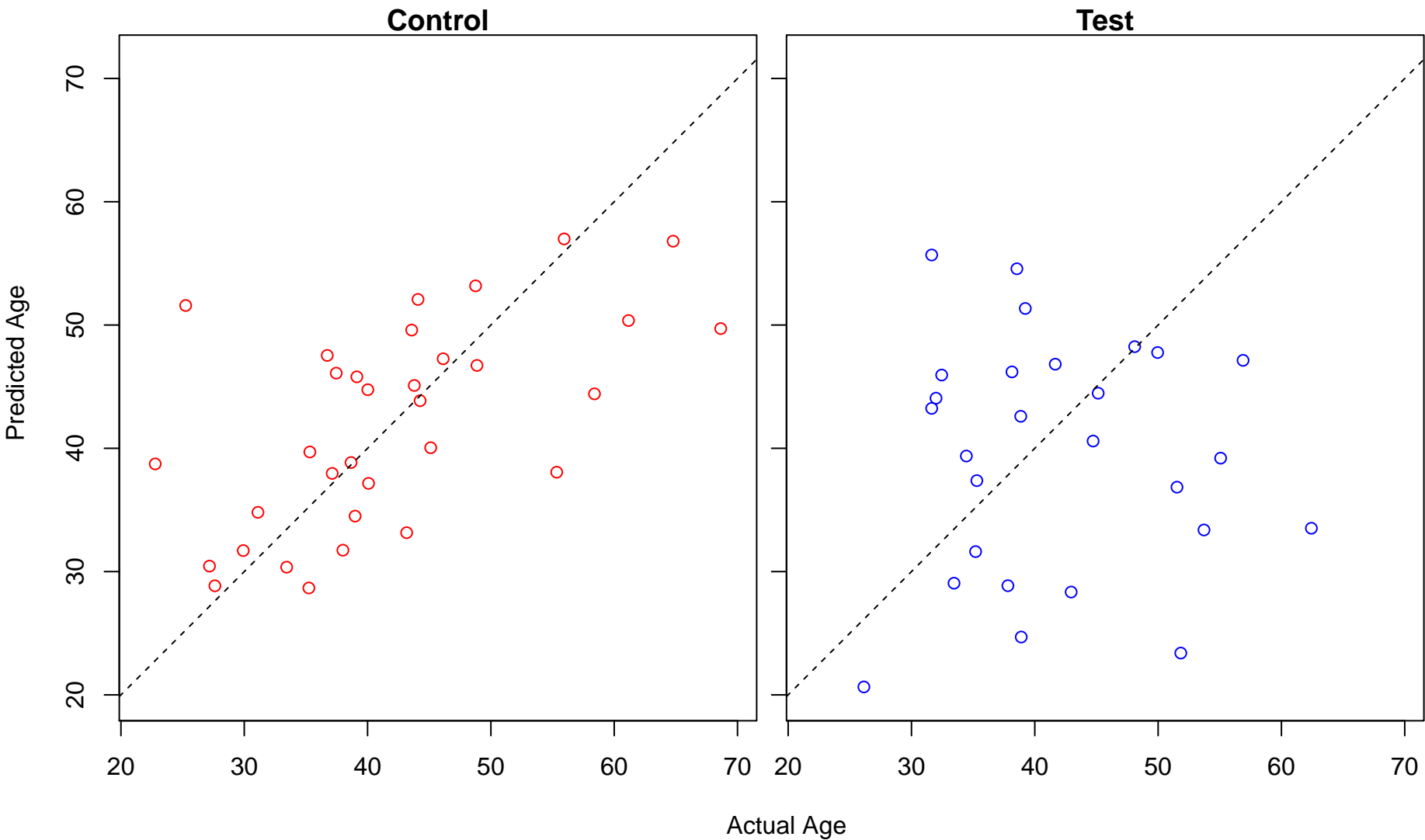
phospholipid catabolic process (Score: 1.501088)



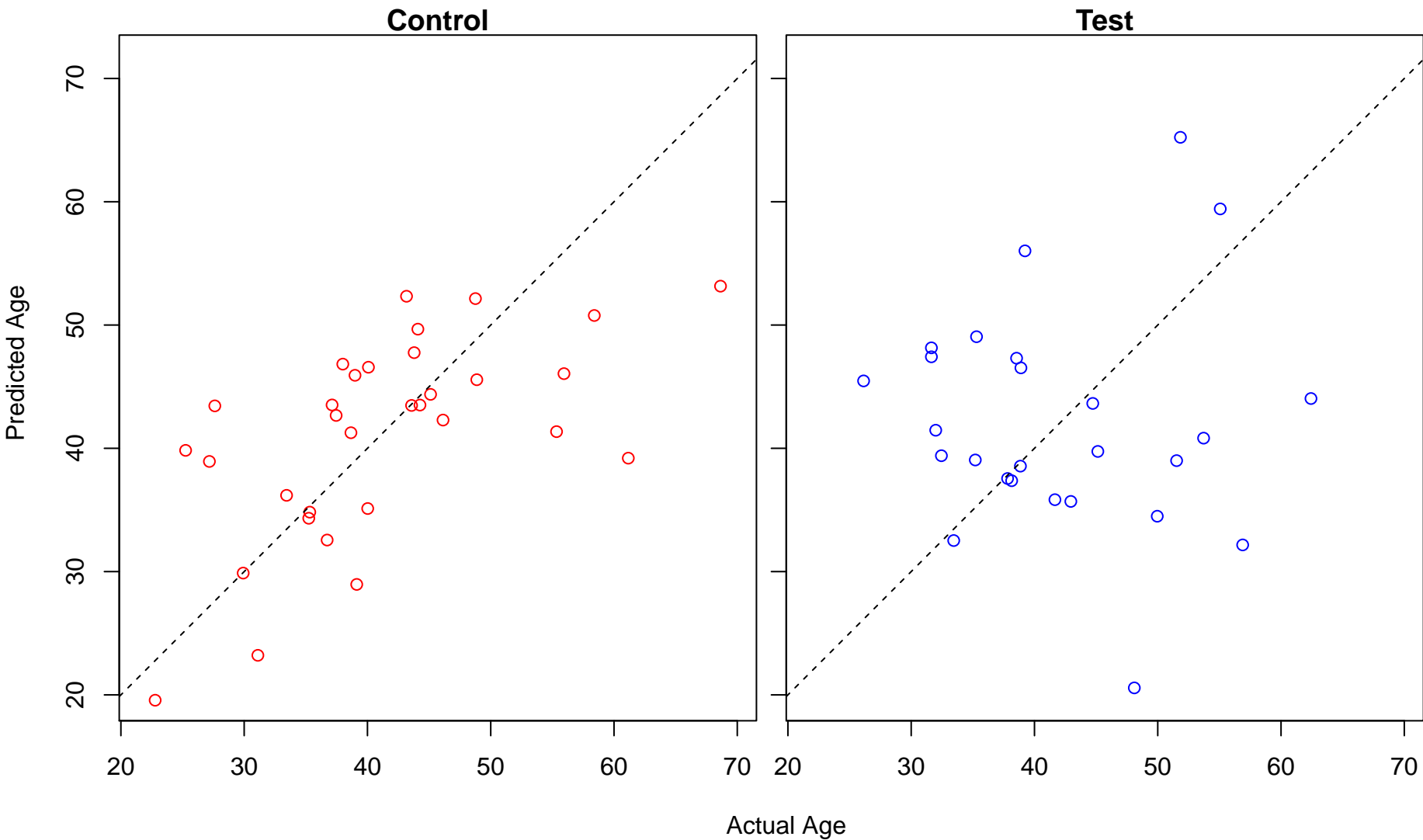
peptidyl-arginine methylation (Score: 1.489316)



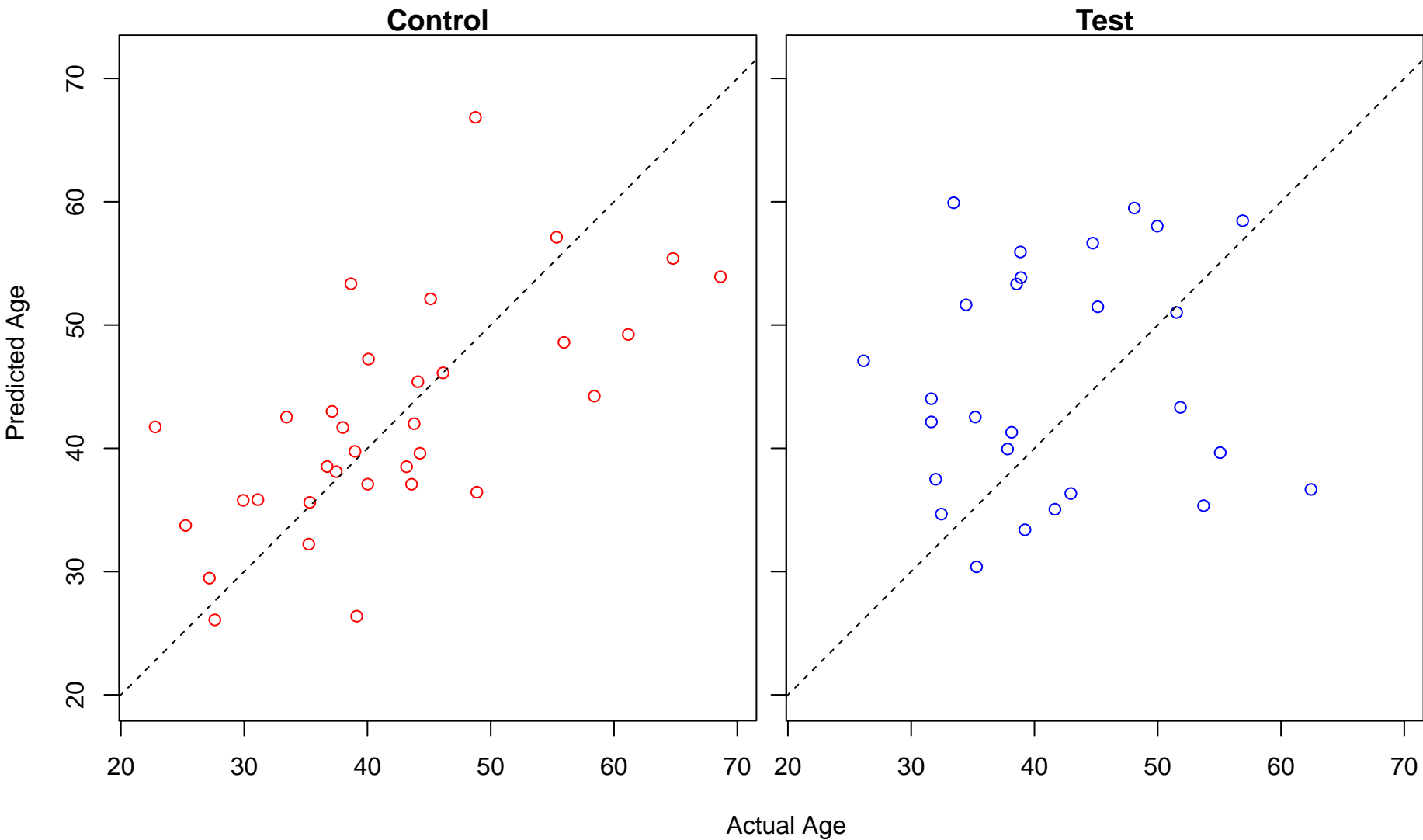
activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c (Score: 1)



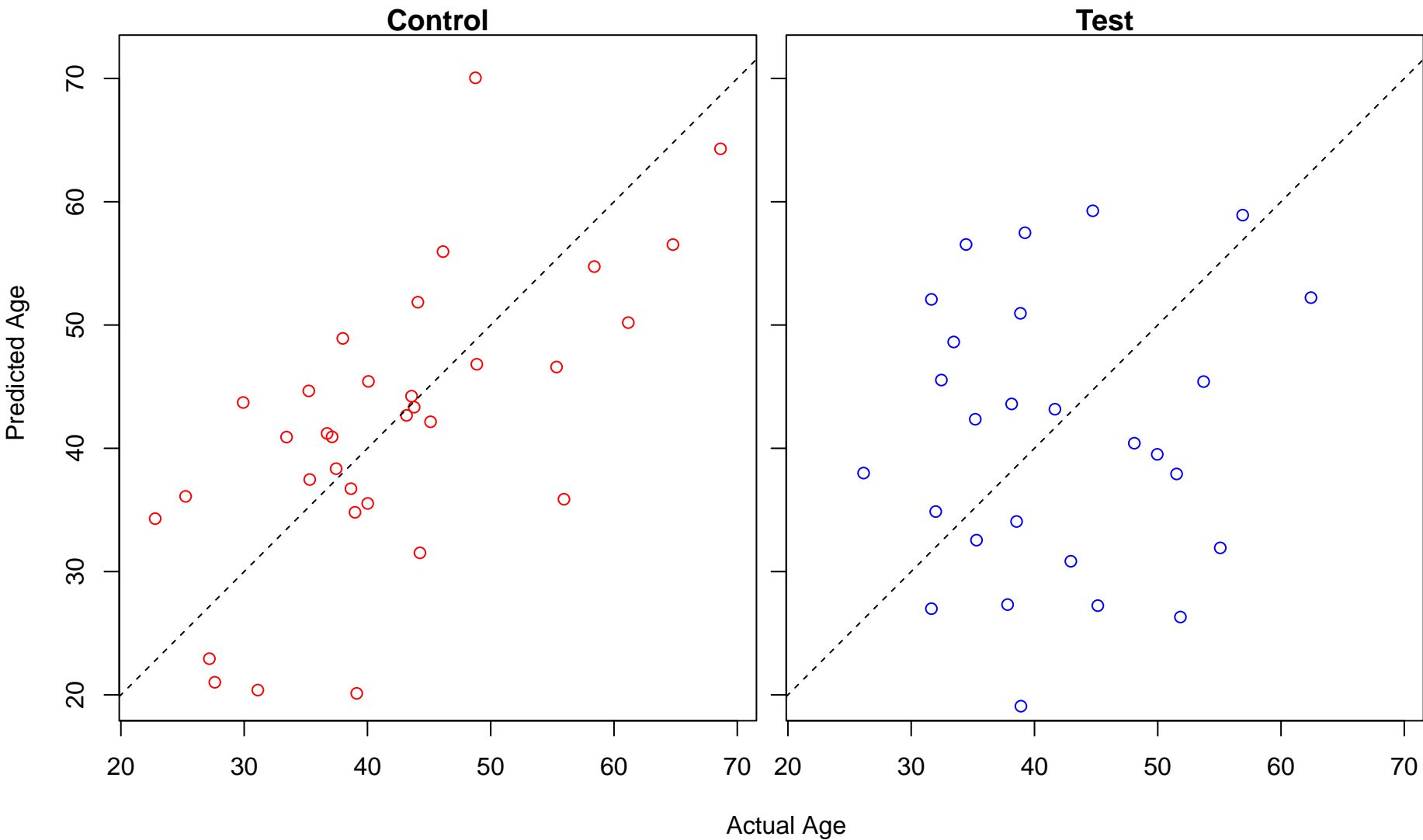
dorsal/ventral pattern formation (Score: 1.489273)



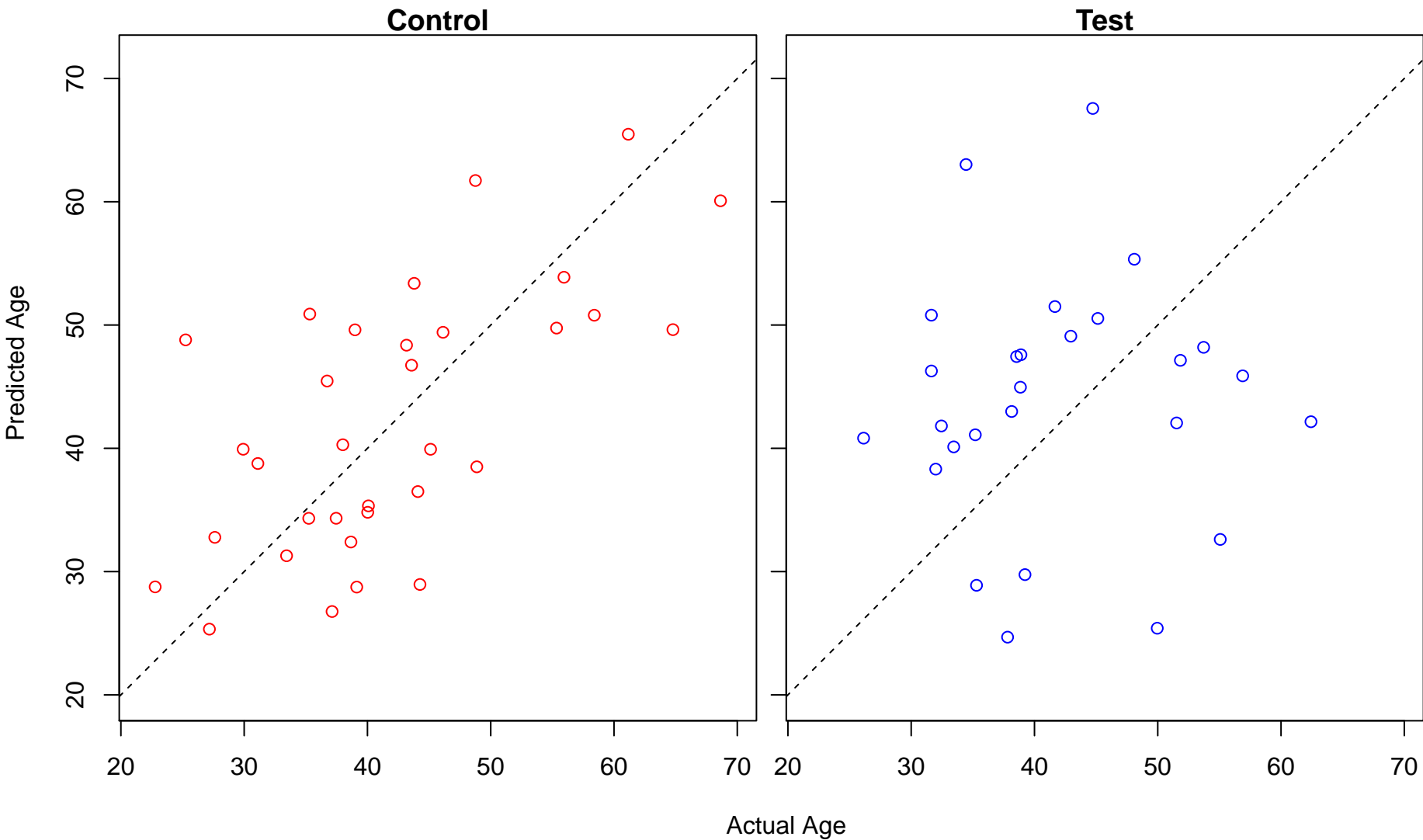
positive regulation of tumor necrosis factor production (Score: 1.488015)



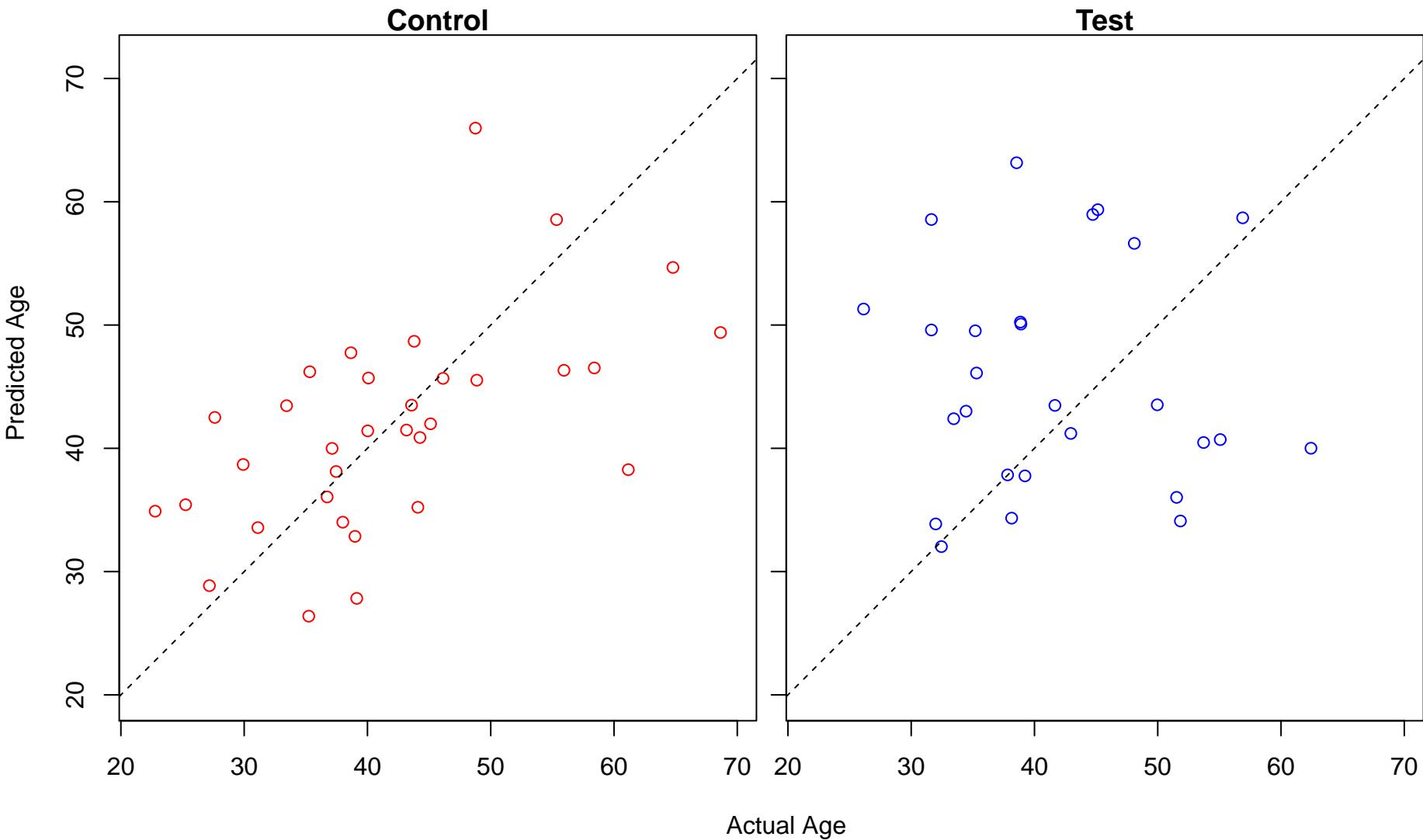
regulation of transcription from RNA polymerase II promoter in response to stress (Score: 1.46750)



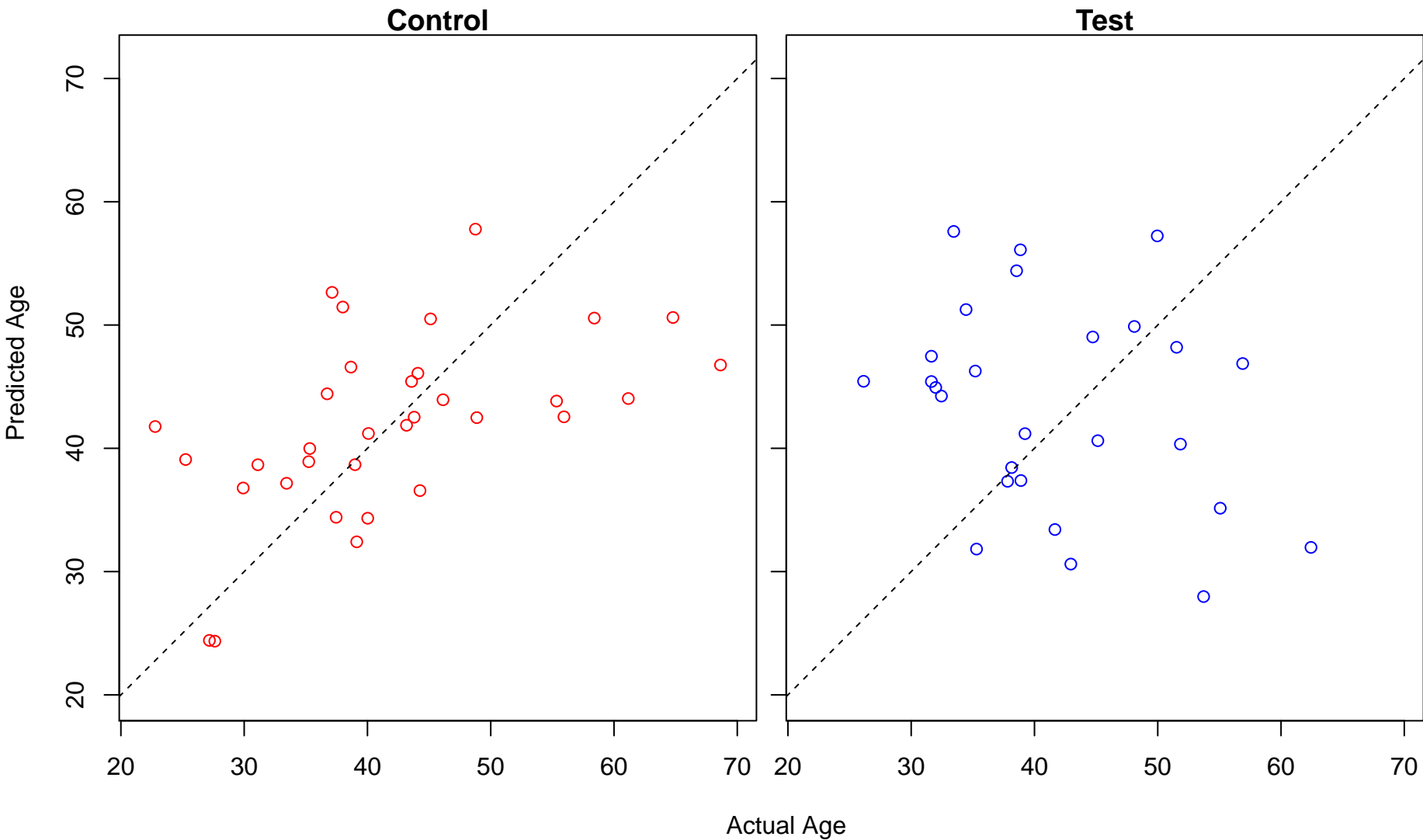
spermatid development (Score: 1.463482)



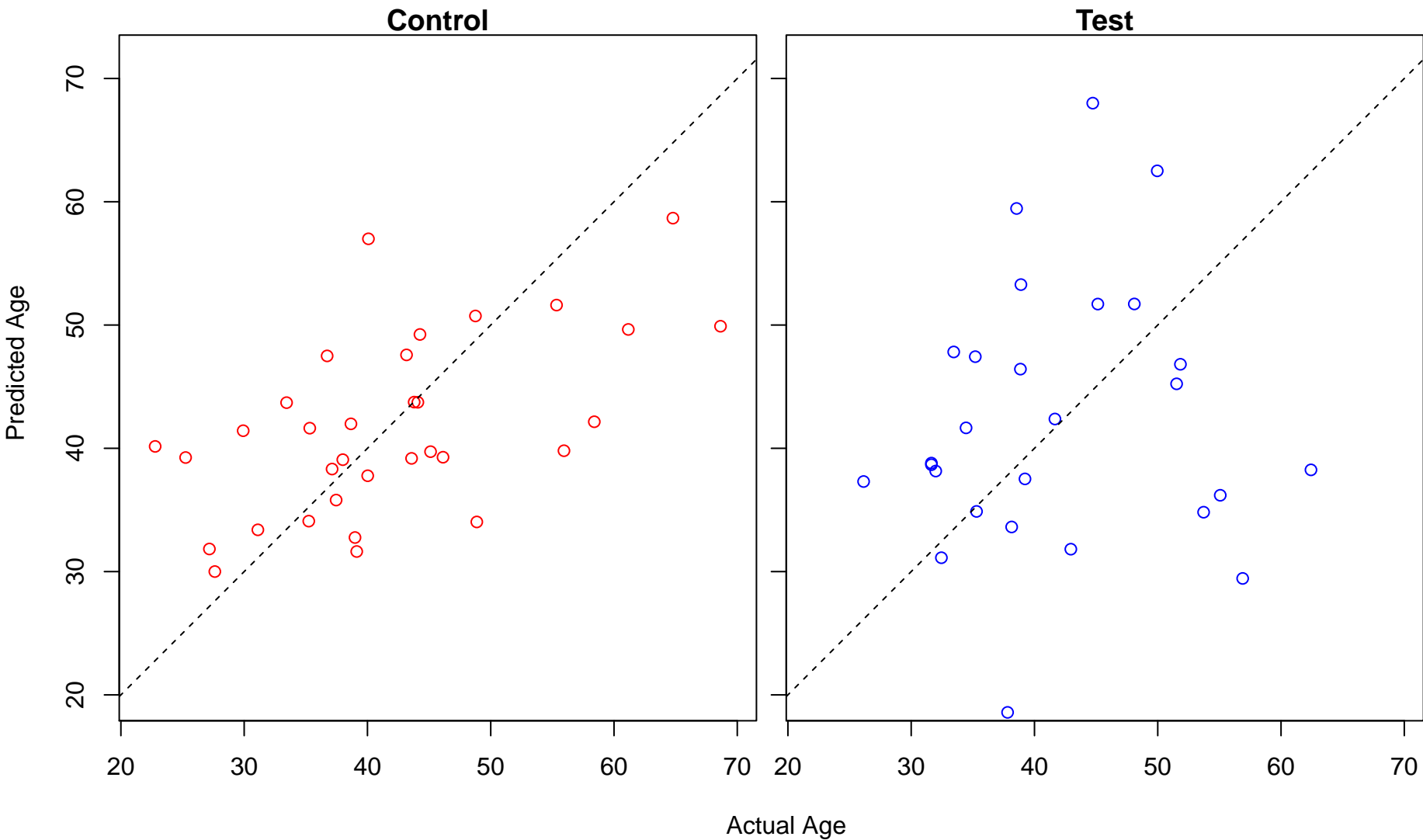
centrosome duplication (Score: 1.460578)



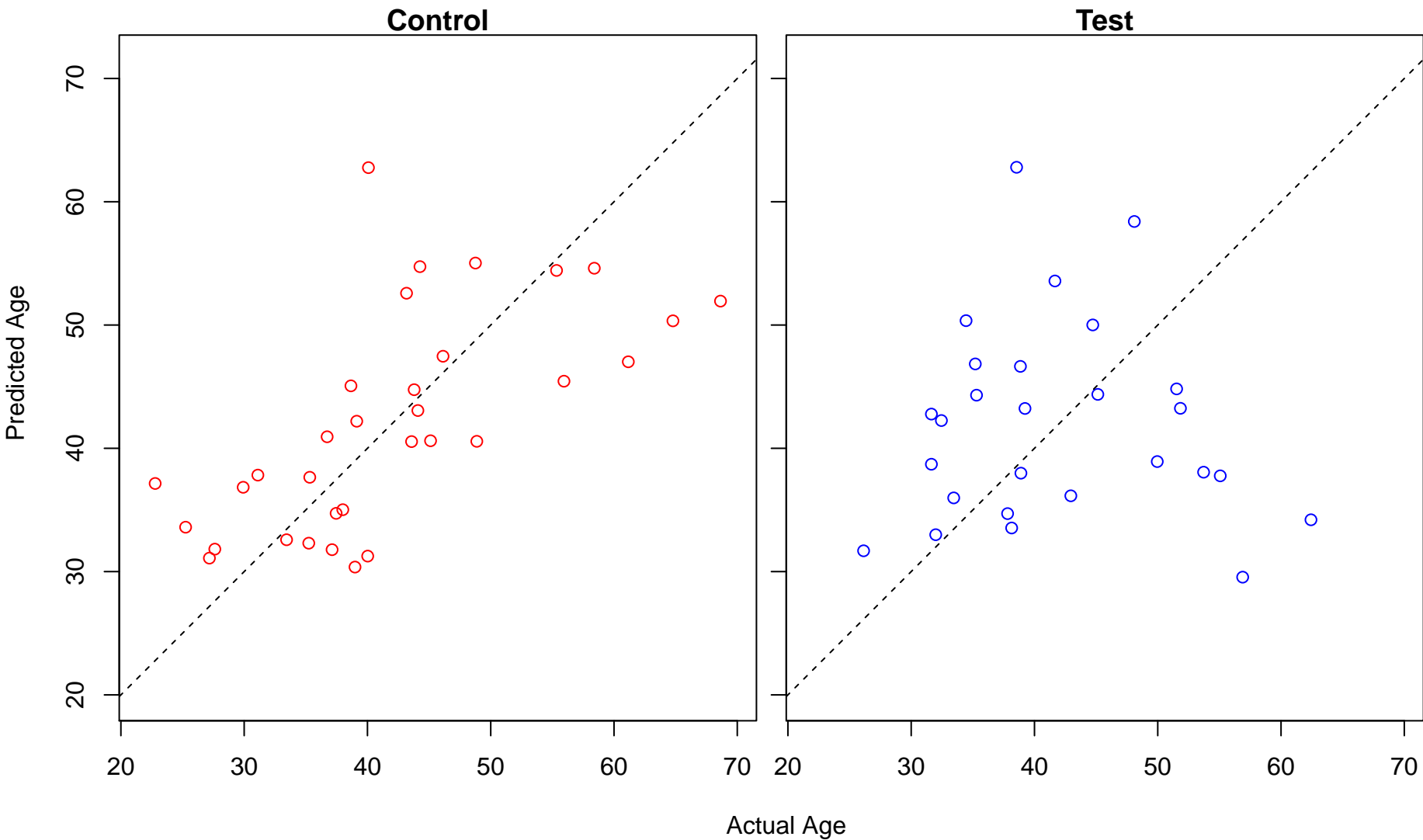
oligodendrocyte development (Score: 1.451666)



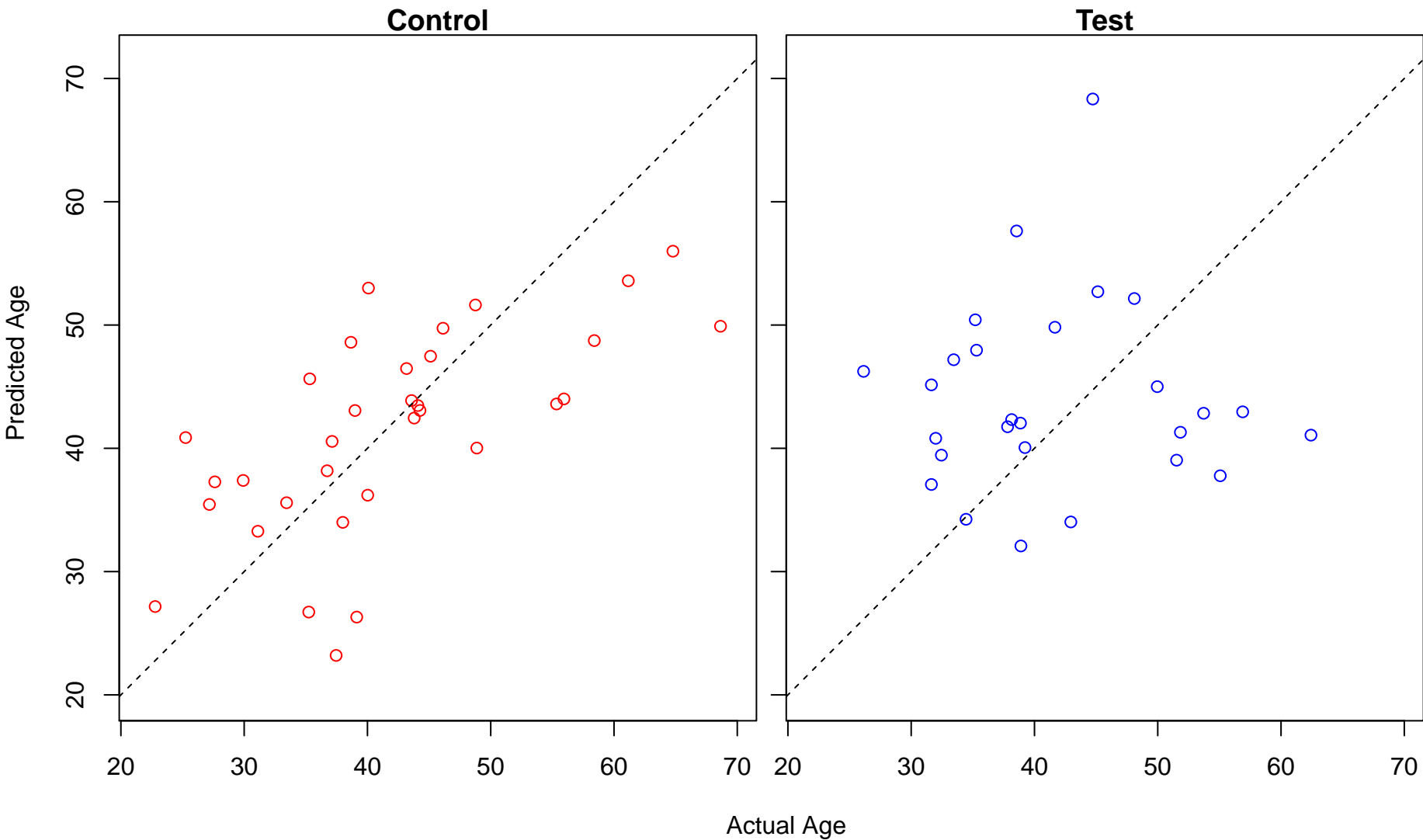
viral mRNA export from host cell nucleus (Score: 1.445860)



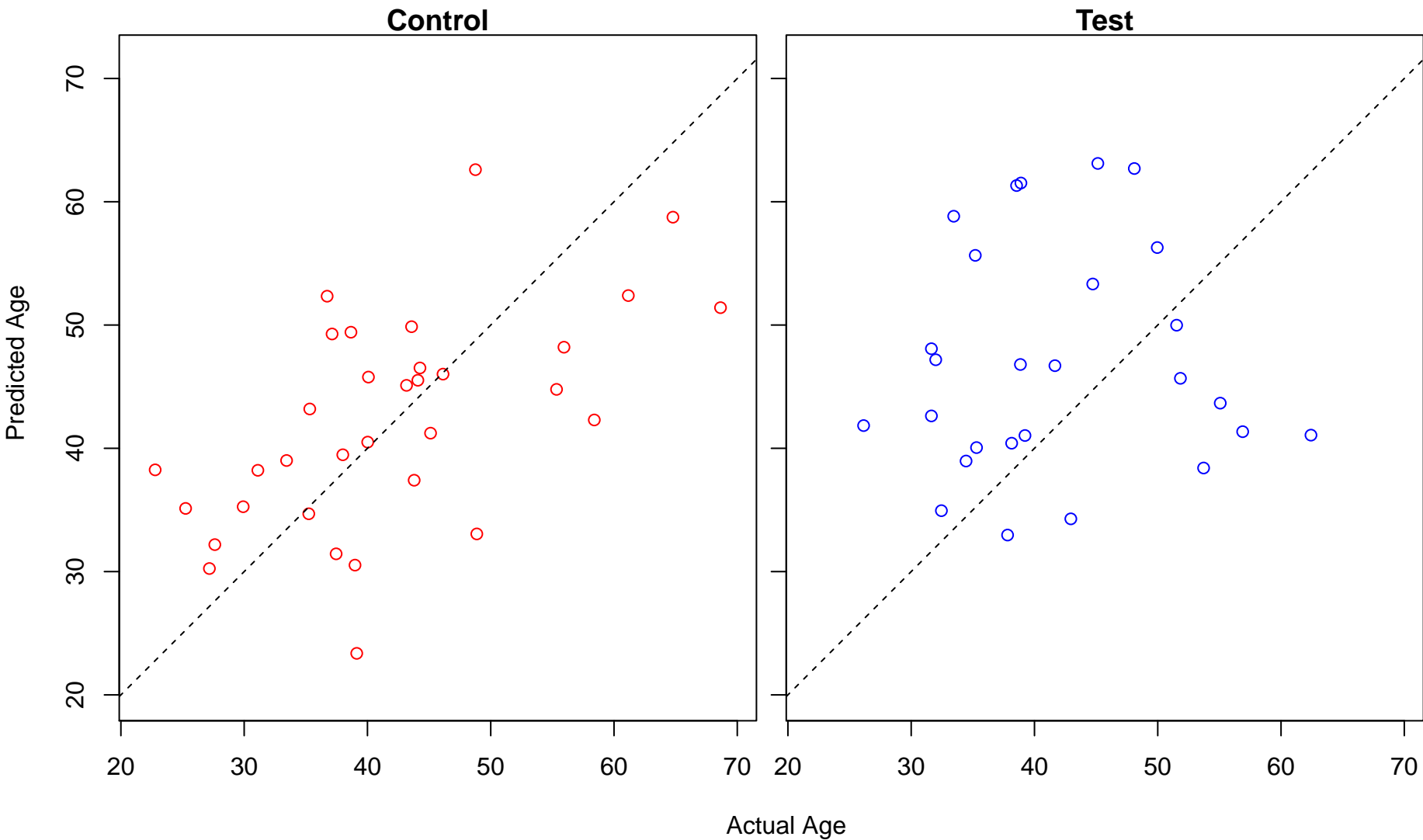
regulation of metalloendopeptidase activity (Score: 1.438845)



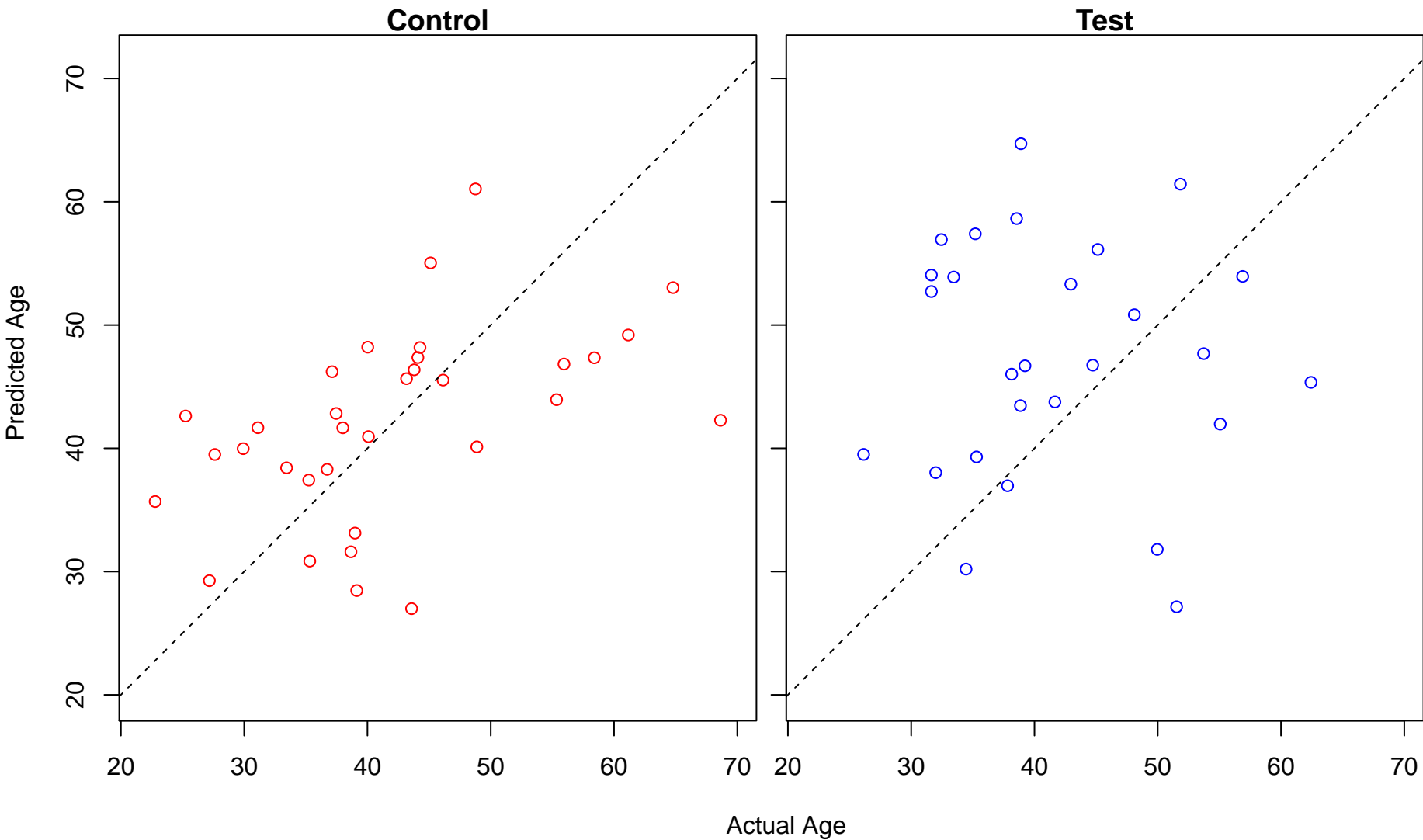
temperature homeostasis (Score: 1.434685)



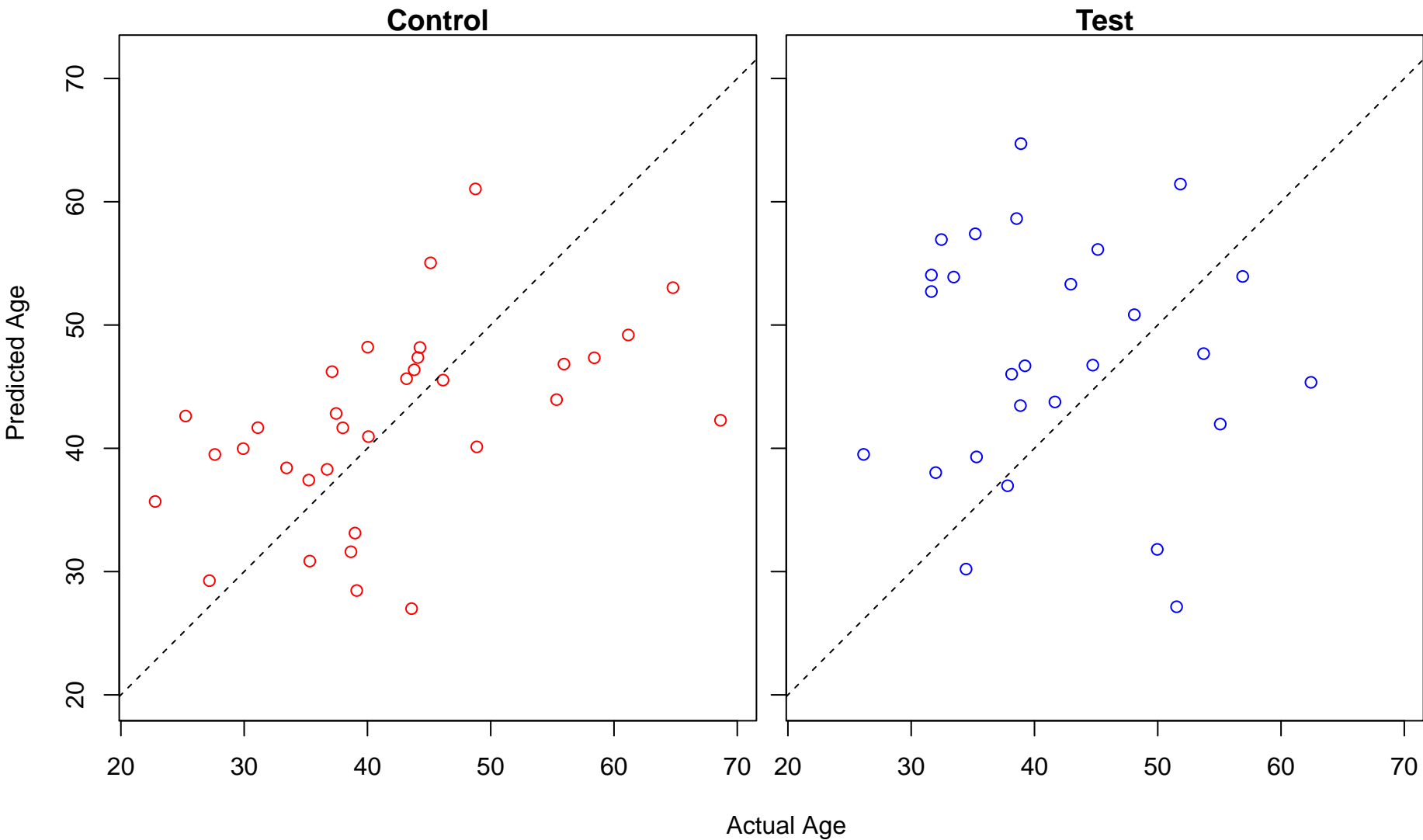
negative regulation of transcription factor import into nucleus (Score: 1.433139)



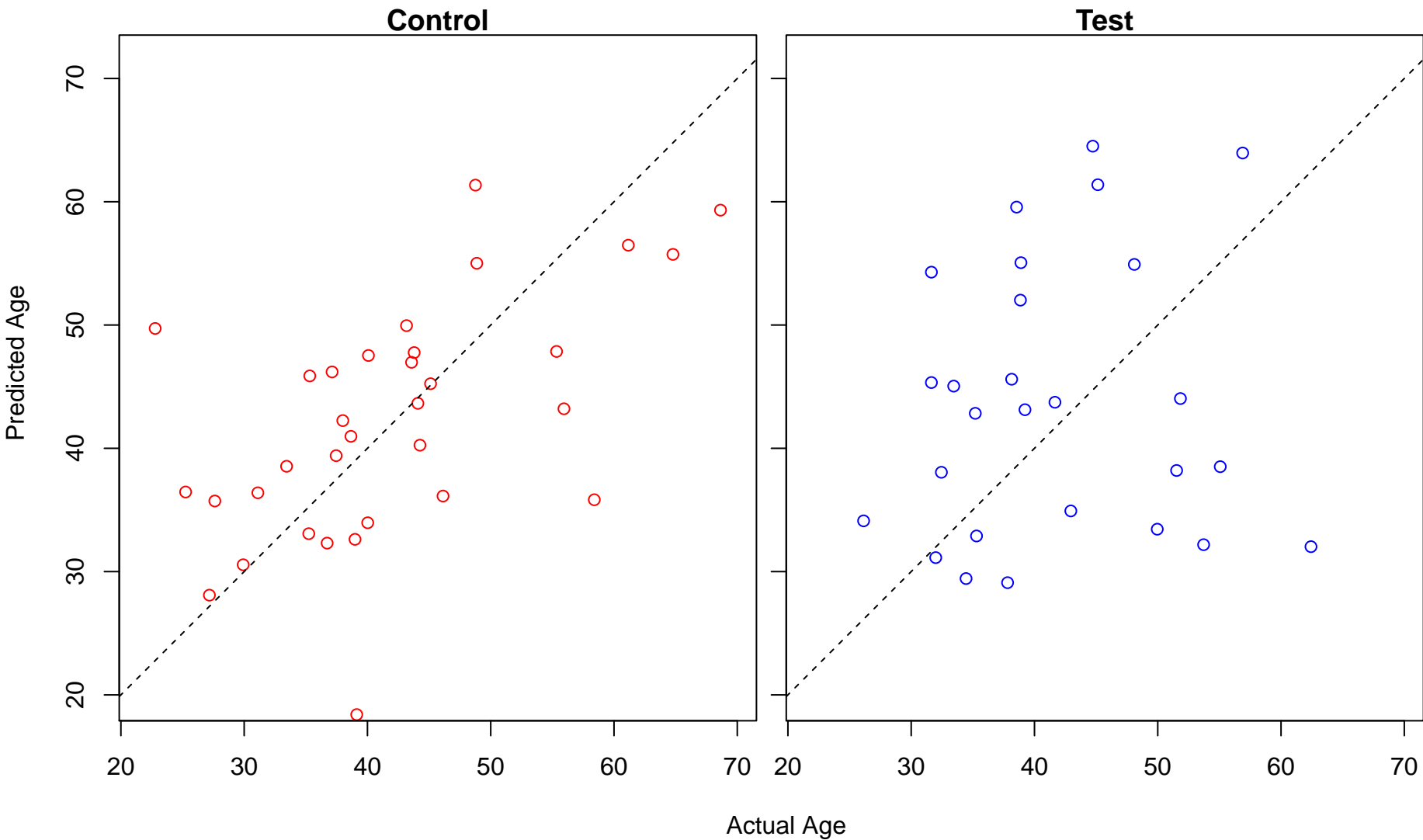
regulation of immature T cell proliferation (Score: 1.432991)



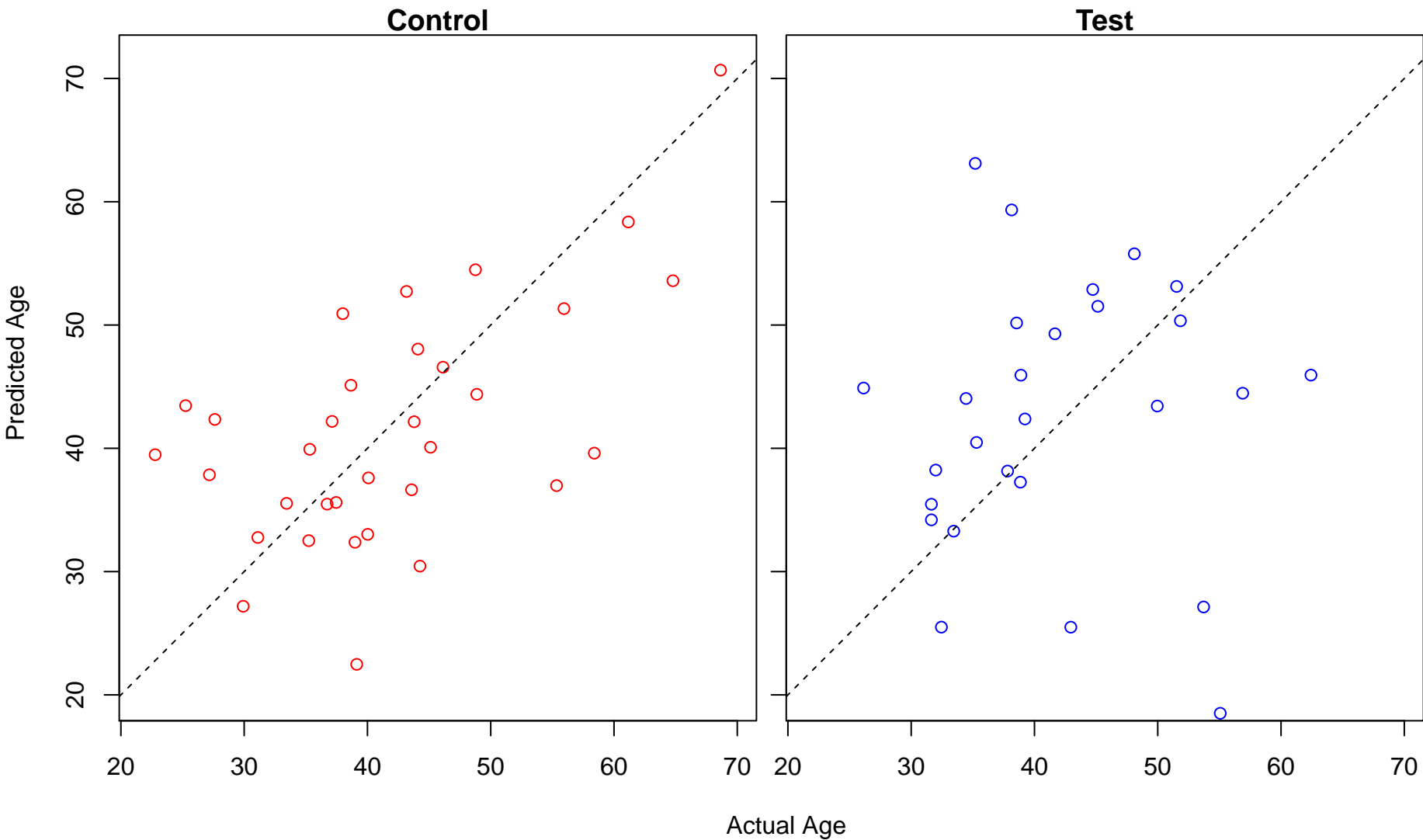
regulation of immature T cell proliferation in thymus (Score: 1.432991)



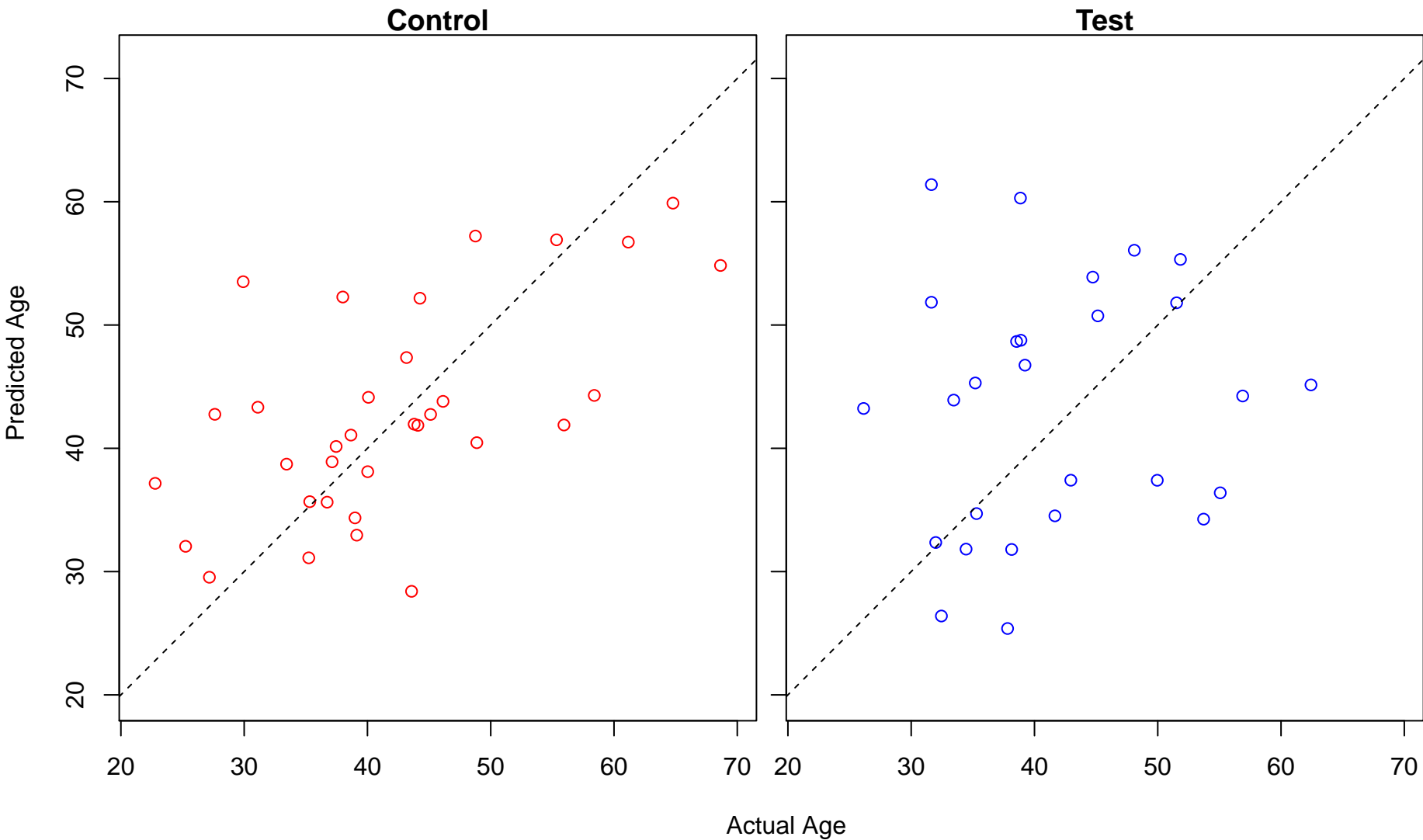
retrograde transport, endosome to plasma membrane (Score: 1.421821)



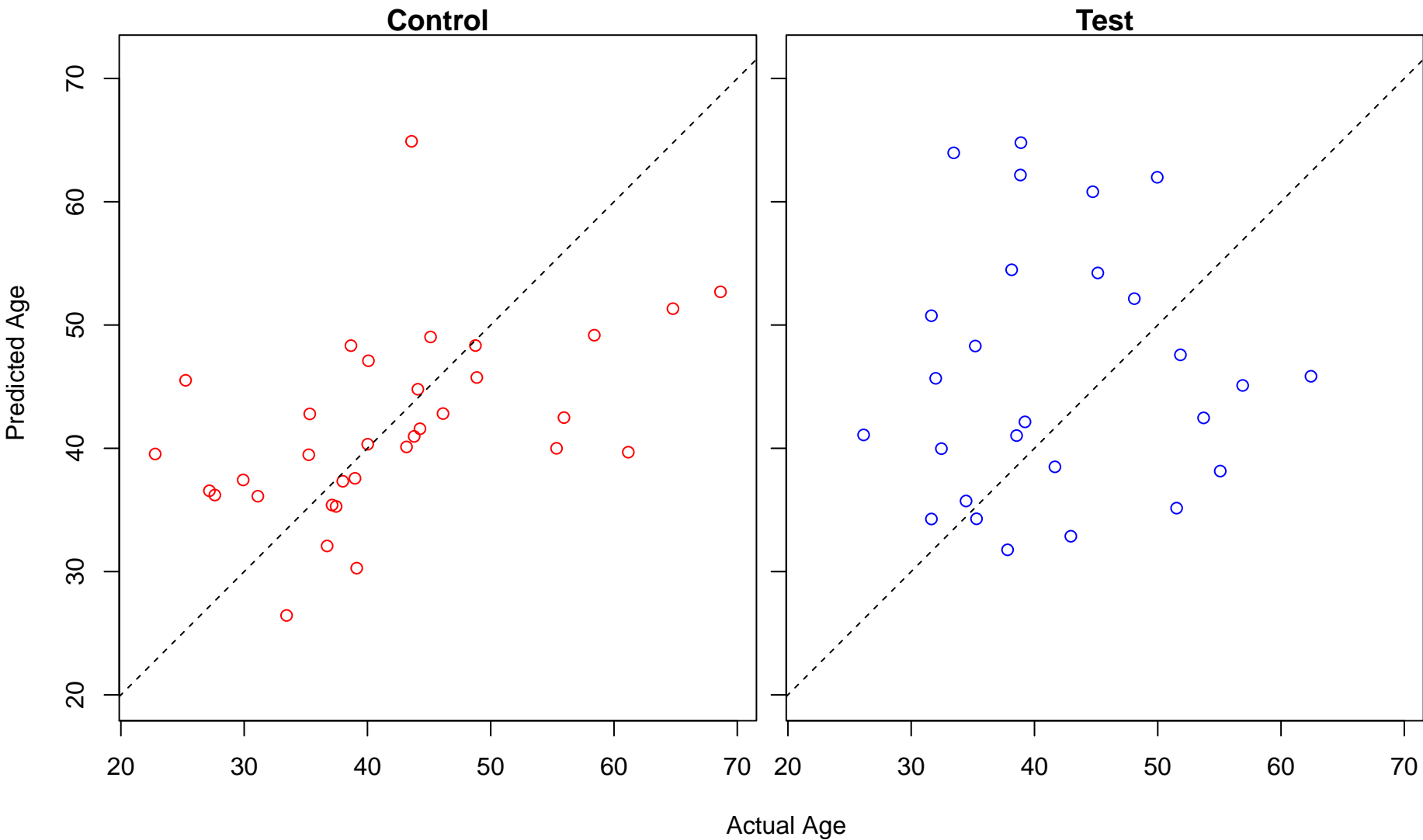
response to antibiotic (Score: 1.419158)



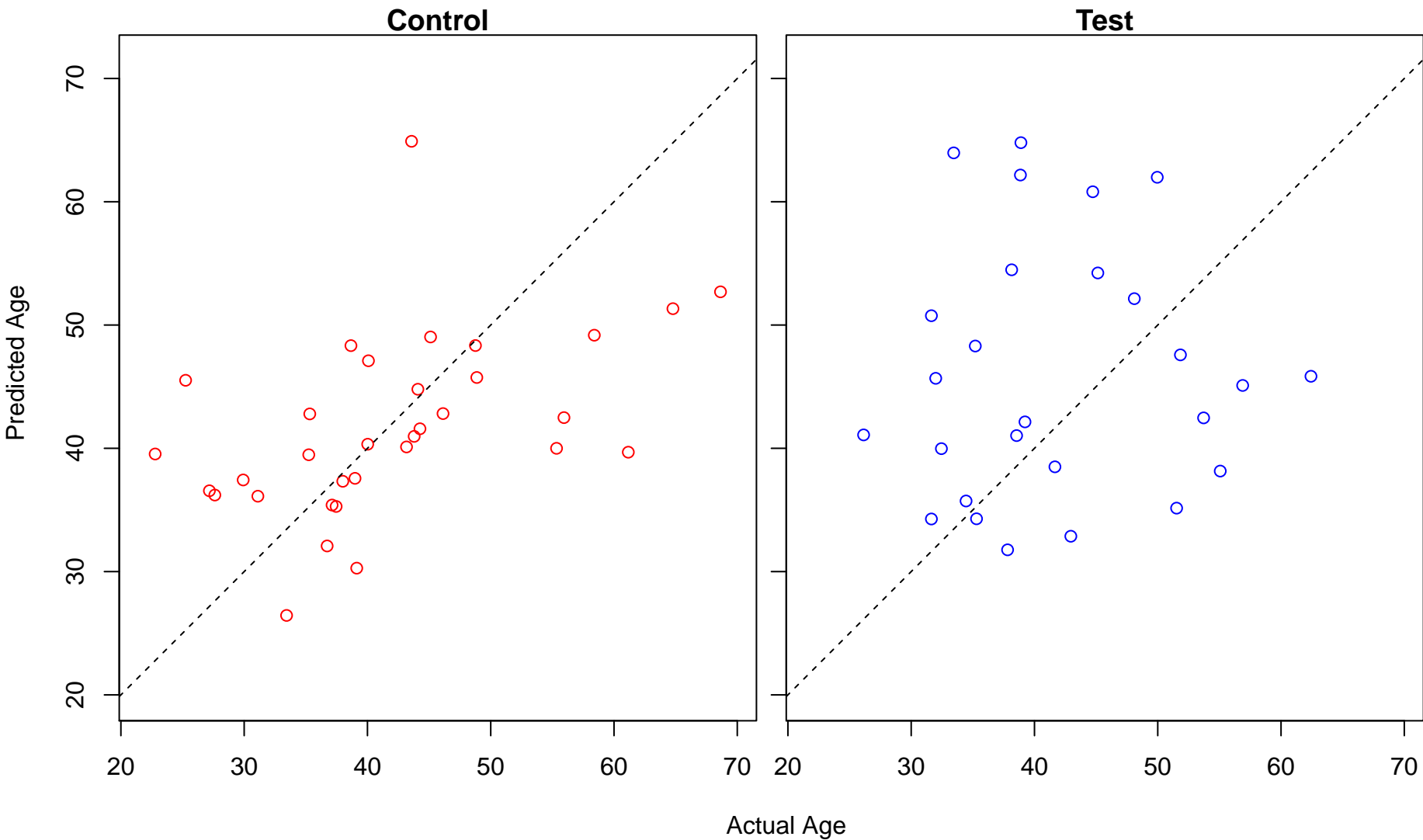
detection of external stimulus (Score: 1.416191)



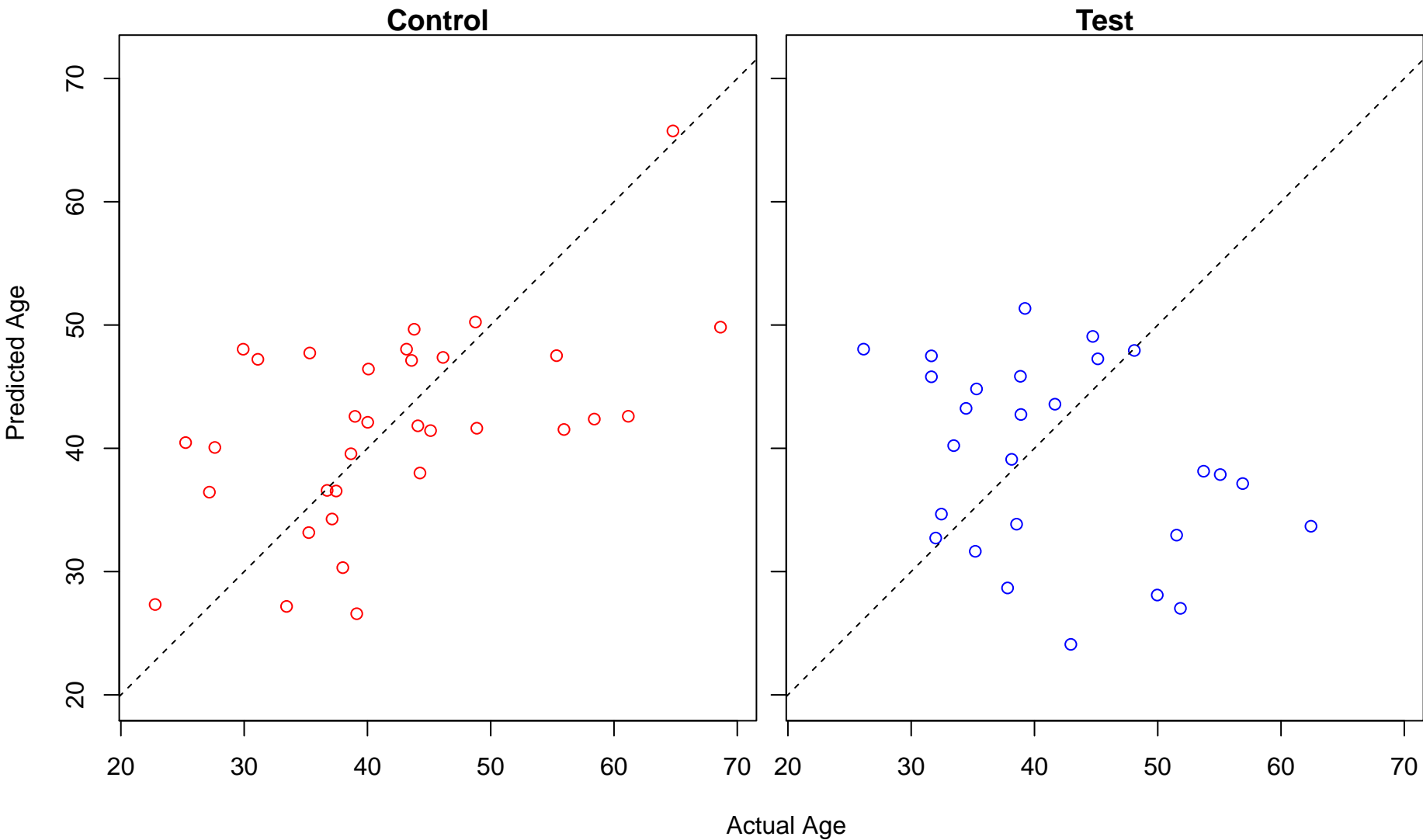
lipid translocation (Score: 1.416144)



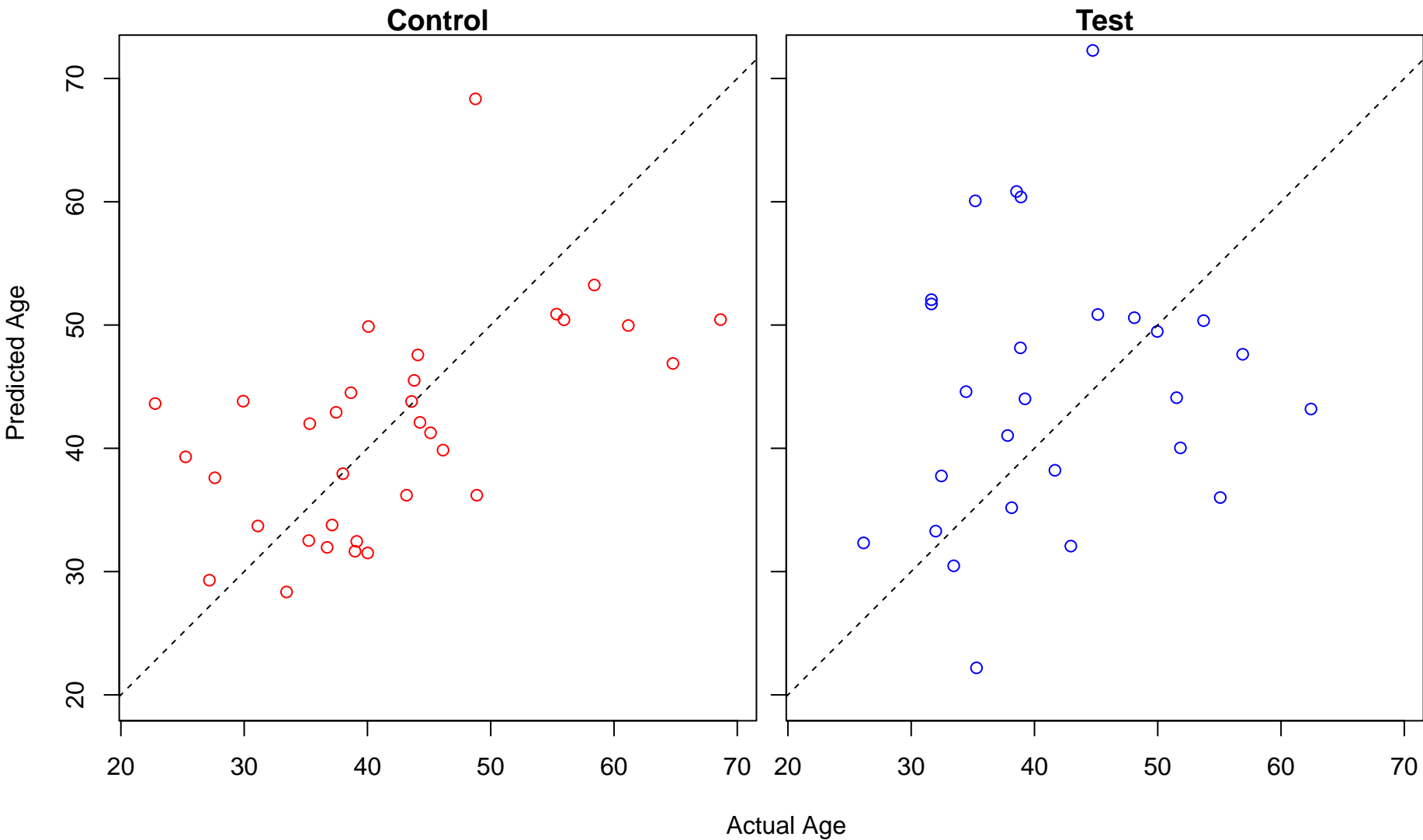
phospholipid translocation (Score: 1.416144)



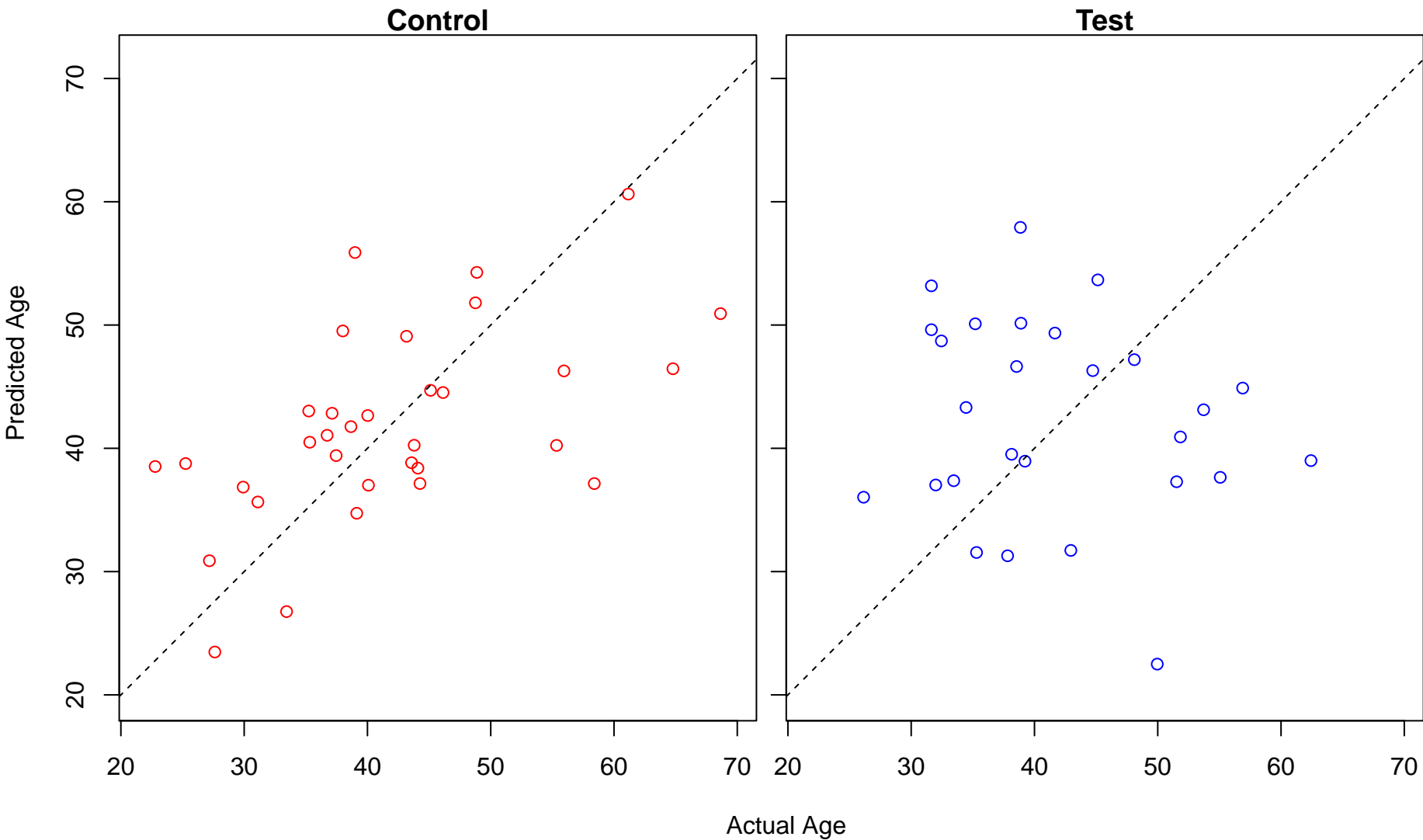
phosphatidylserine acyl-chain remodeling (Score: 1.412293)



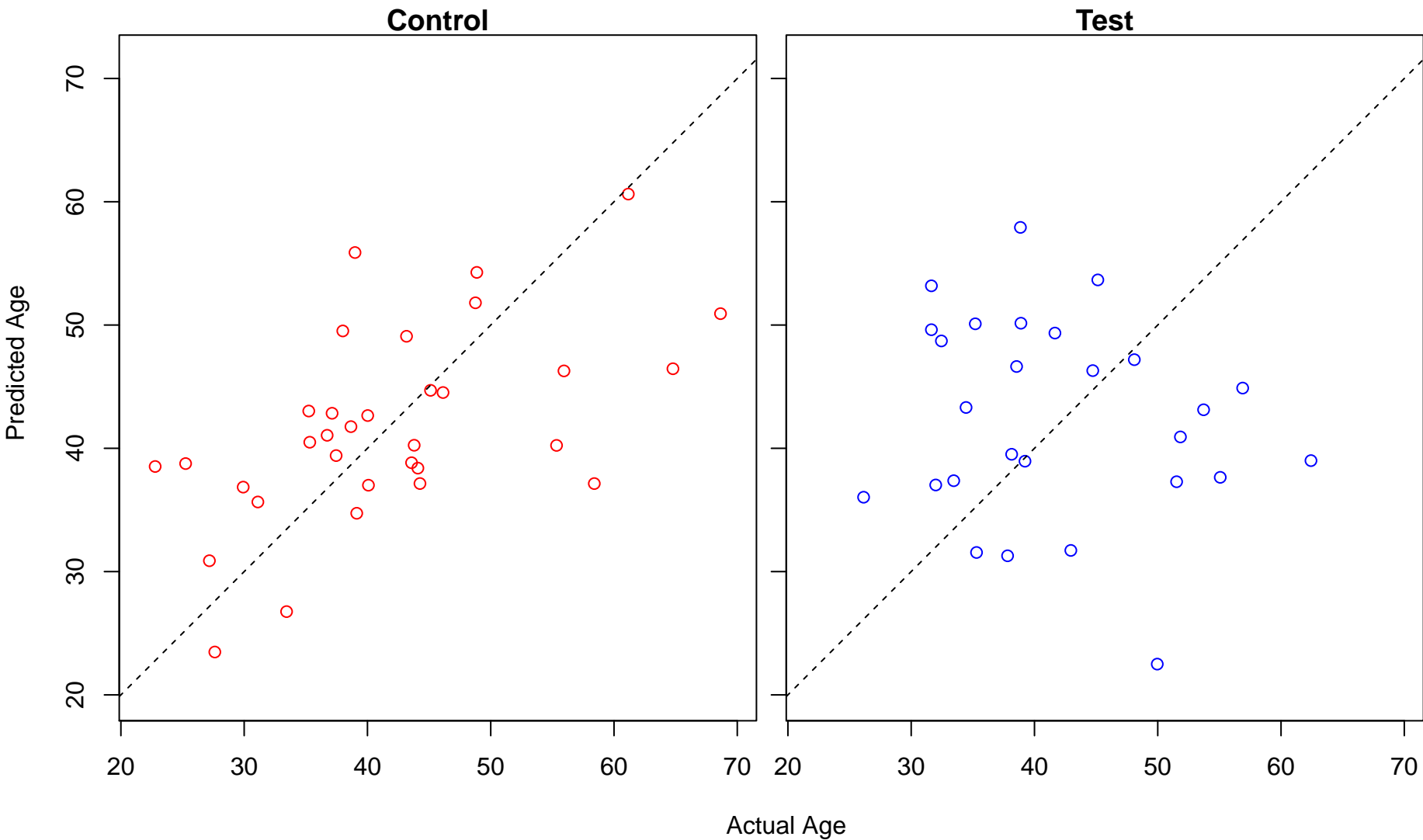
receptor clustering (Score: 1.405002)



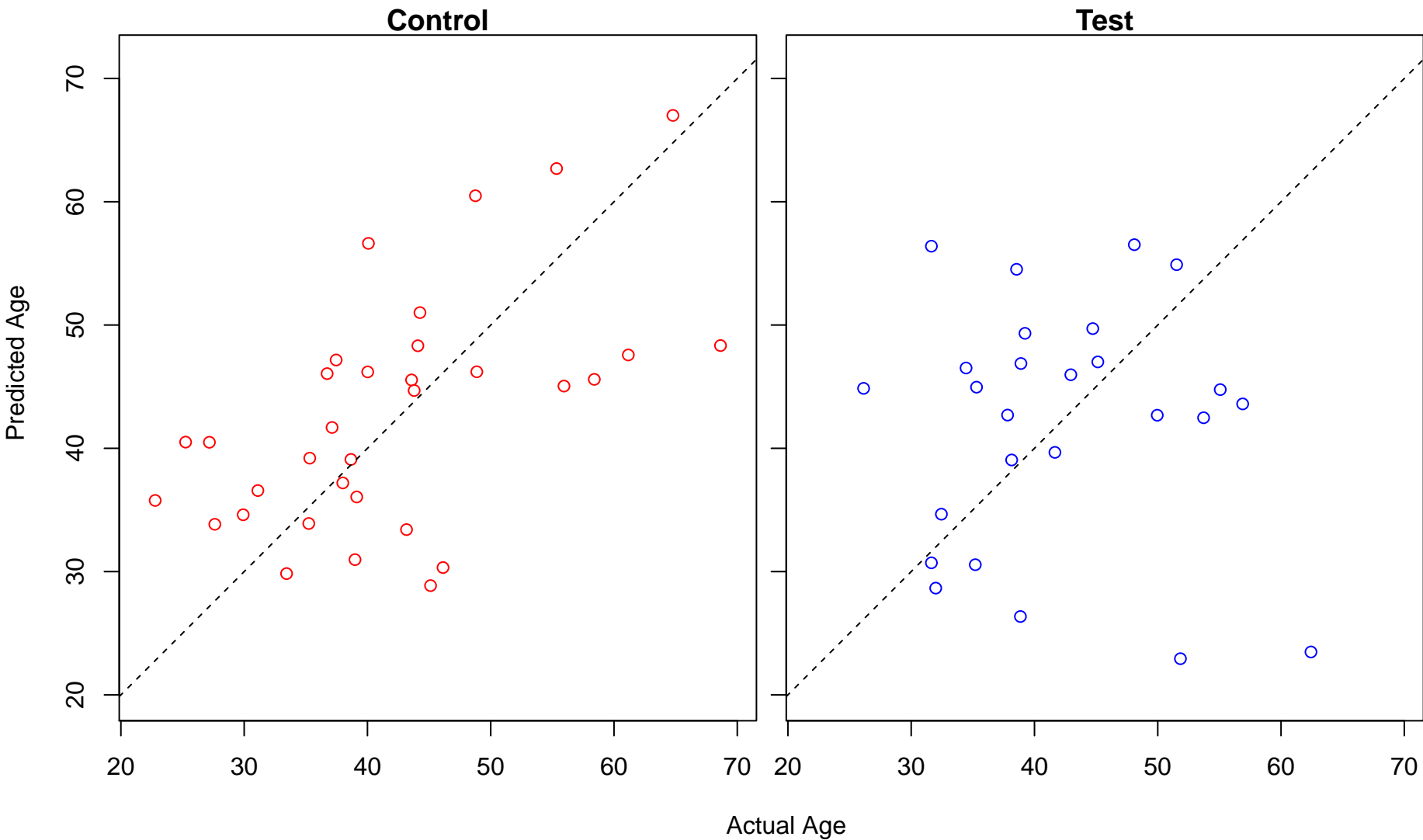
negative regulation of response to food (Score: 1.401825)



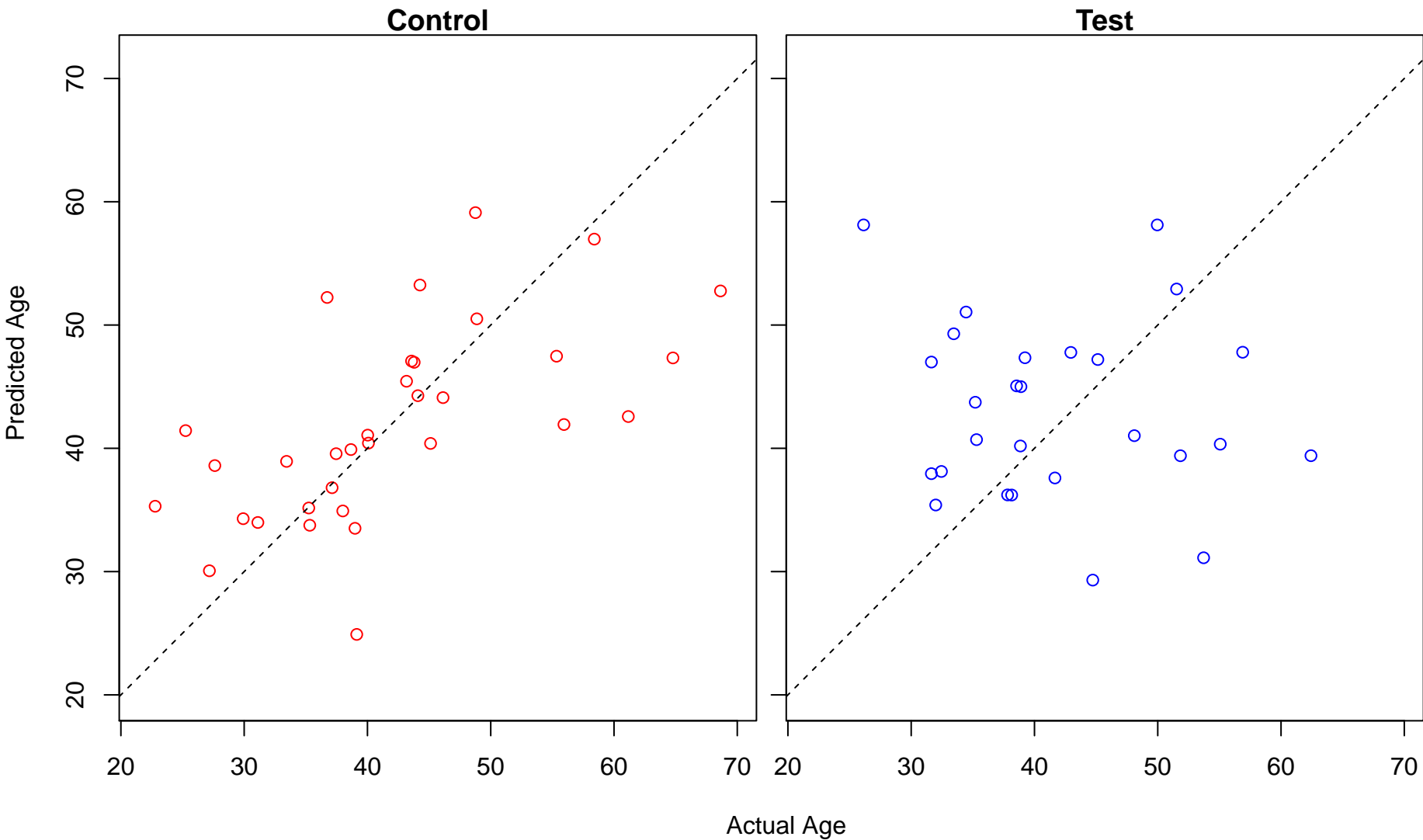
negative regulation of appetite (Score: 1.401825)



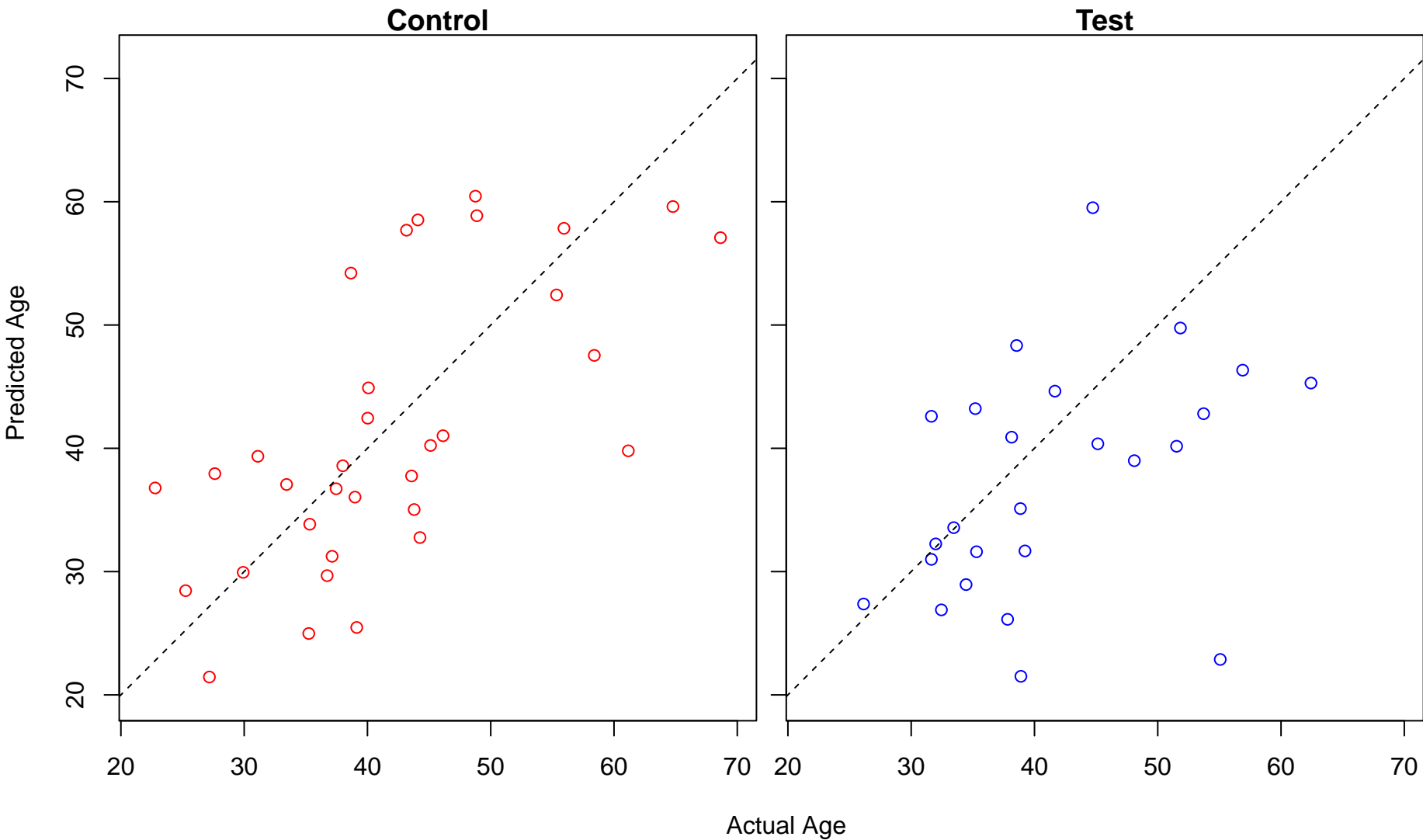
mitochondrion morphogenesis (Score: 1.401588)



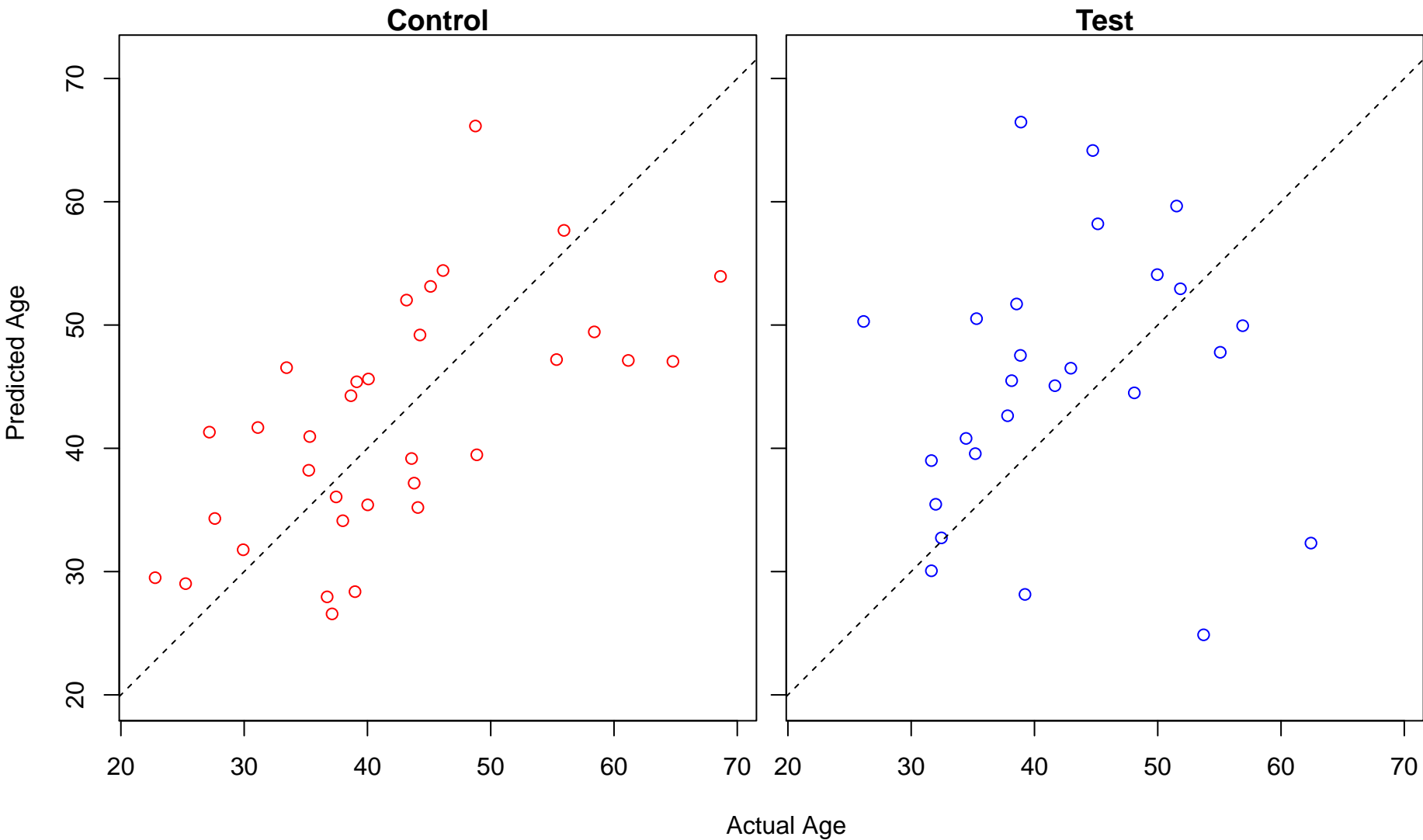
complement activation, classical pathway (Score: 1.400153)



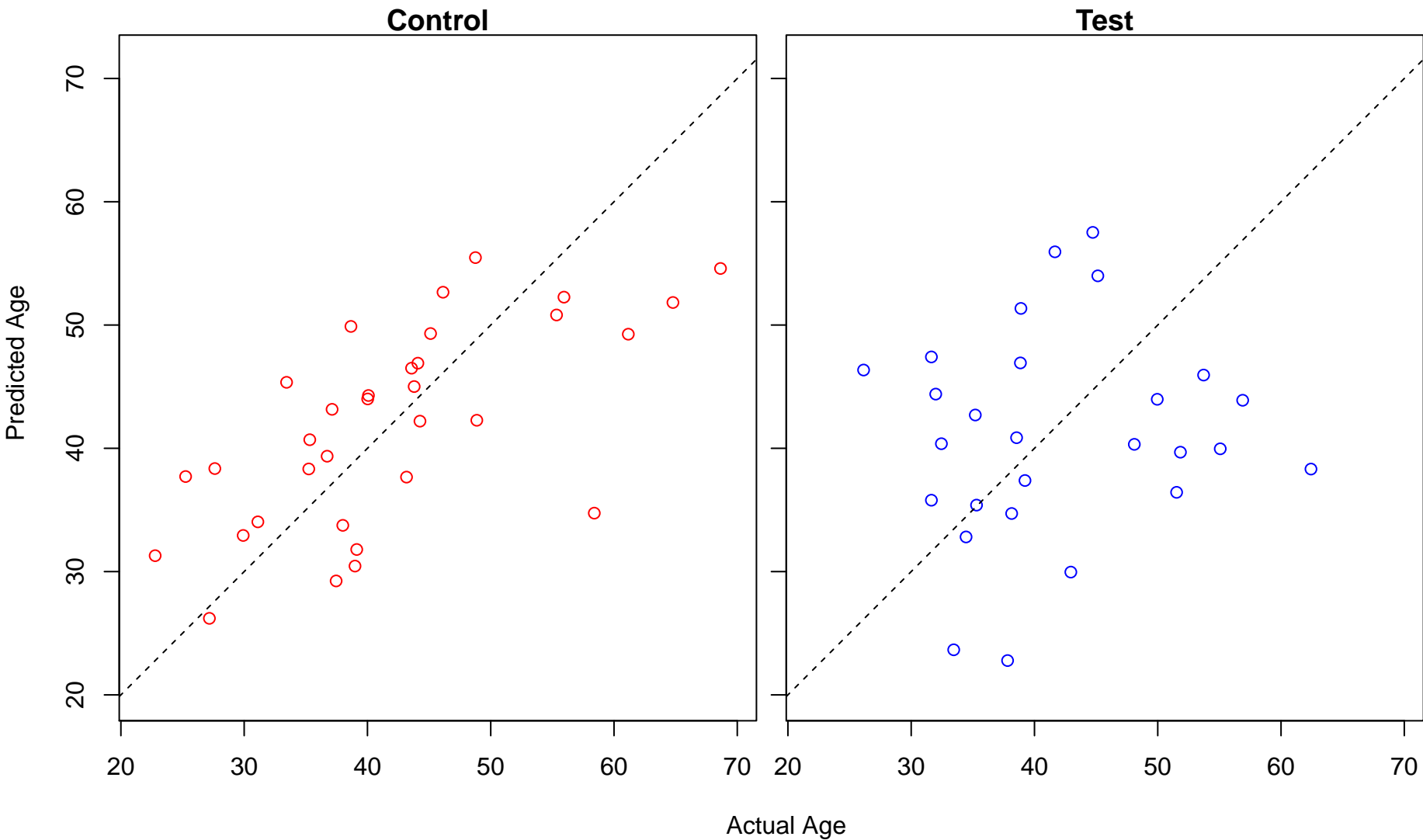
regulation of sodium ion transmembrane transporter activity (Score: 1.397538)



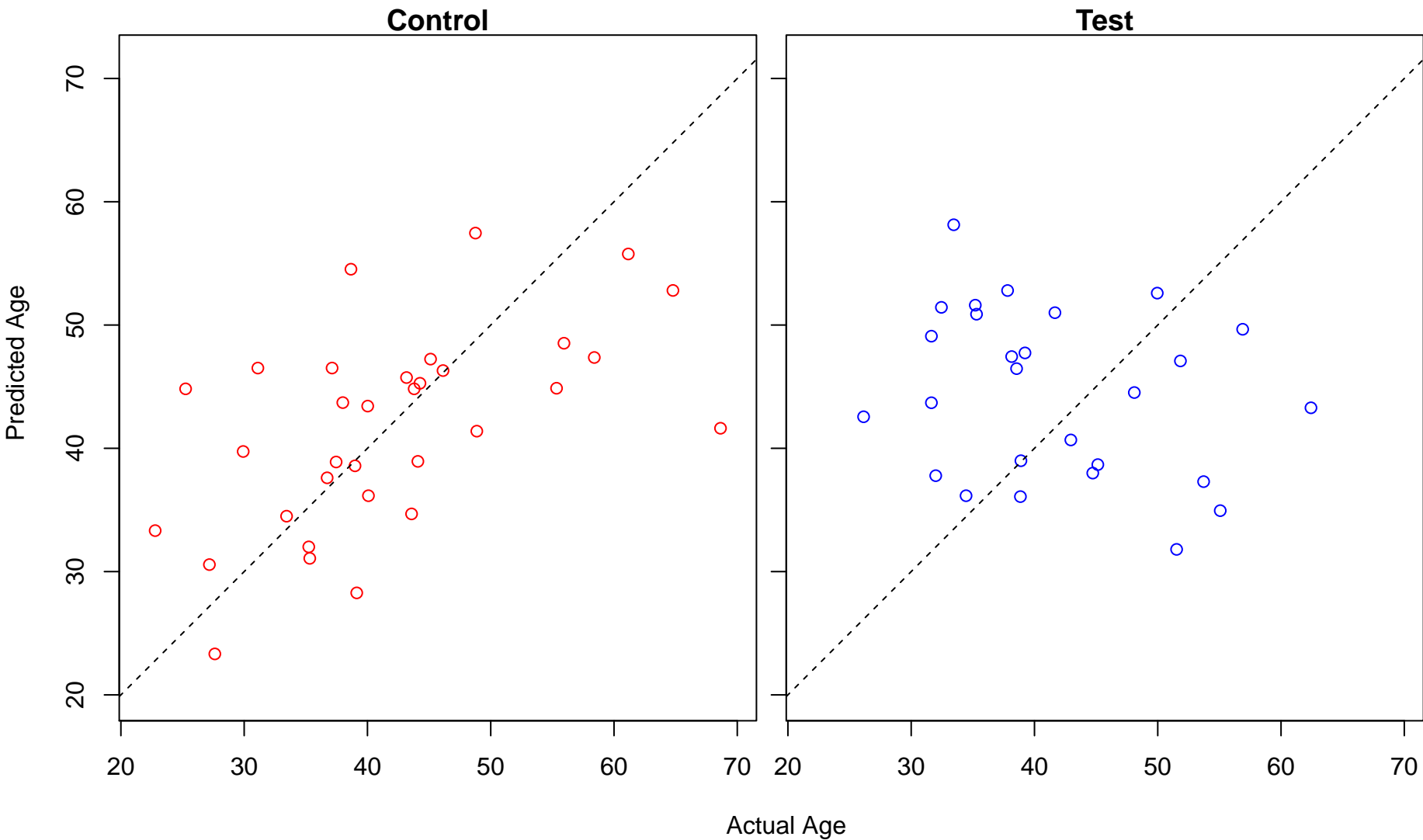
negative regulation of potassium ion transmembrane transporter activity (Score: 1.391578)



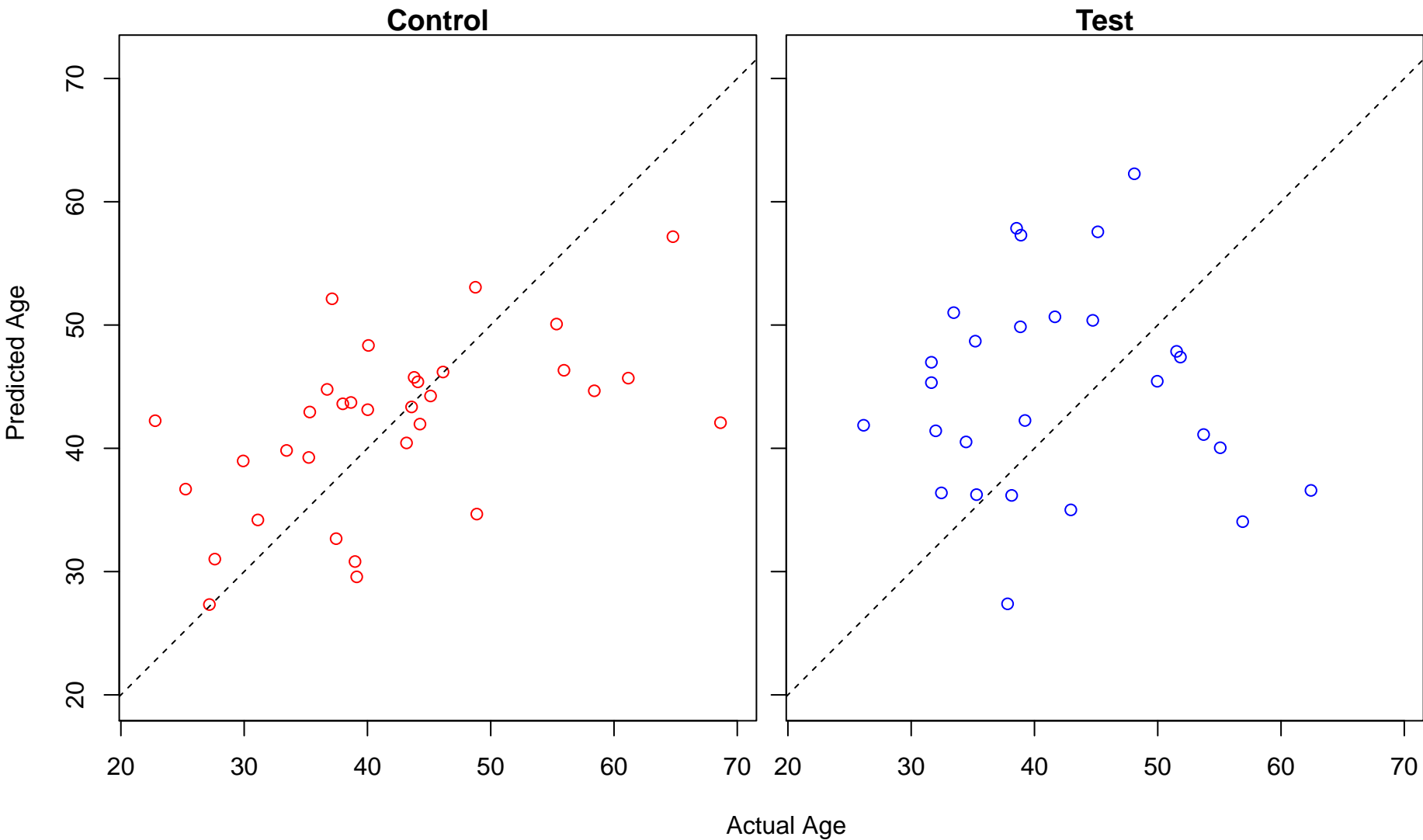
positive regulation of cation transmembrane transport (Score: 1.390638)



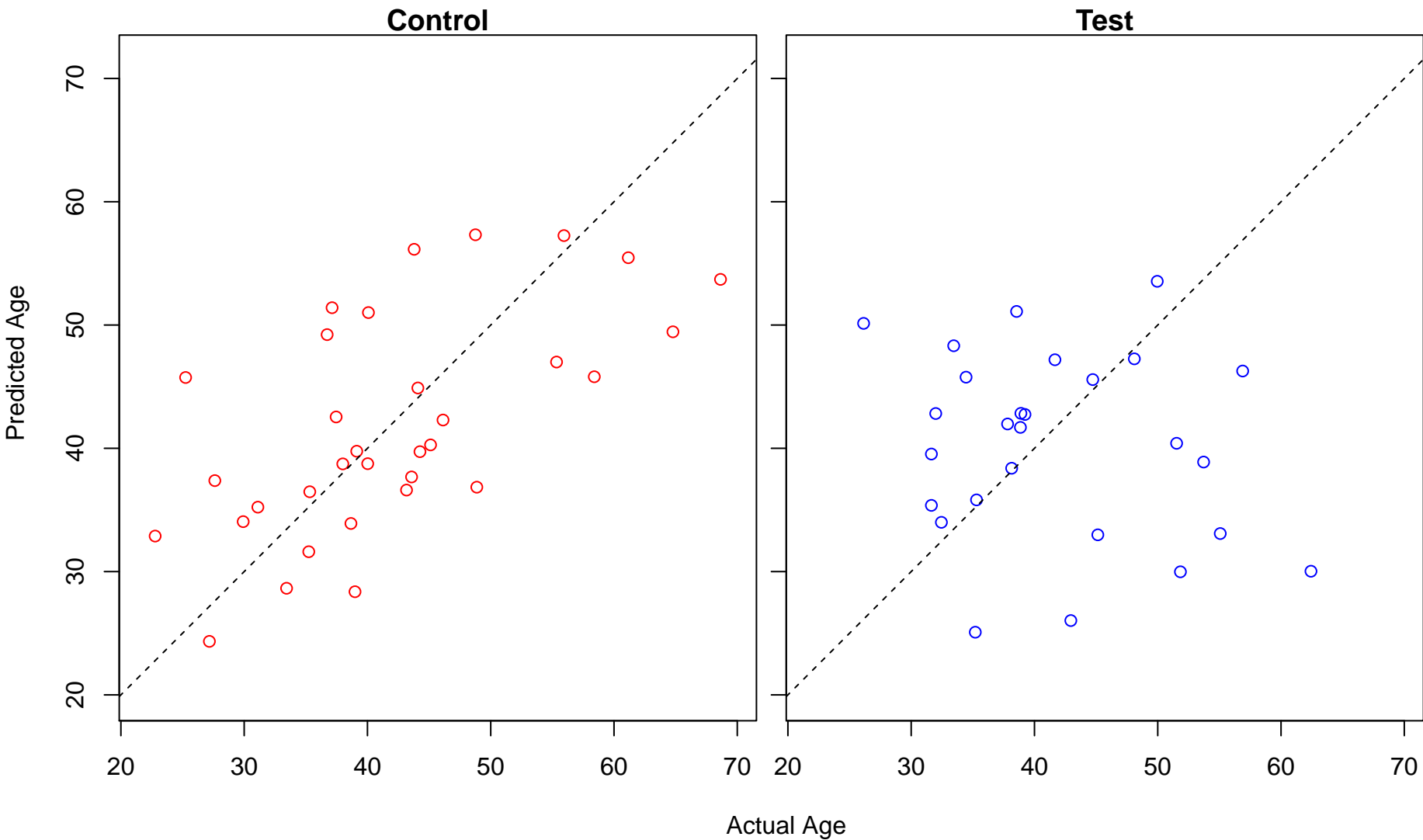
endocrine pancreas development (Score: 1.390526)



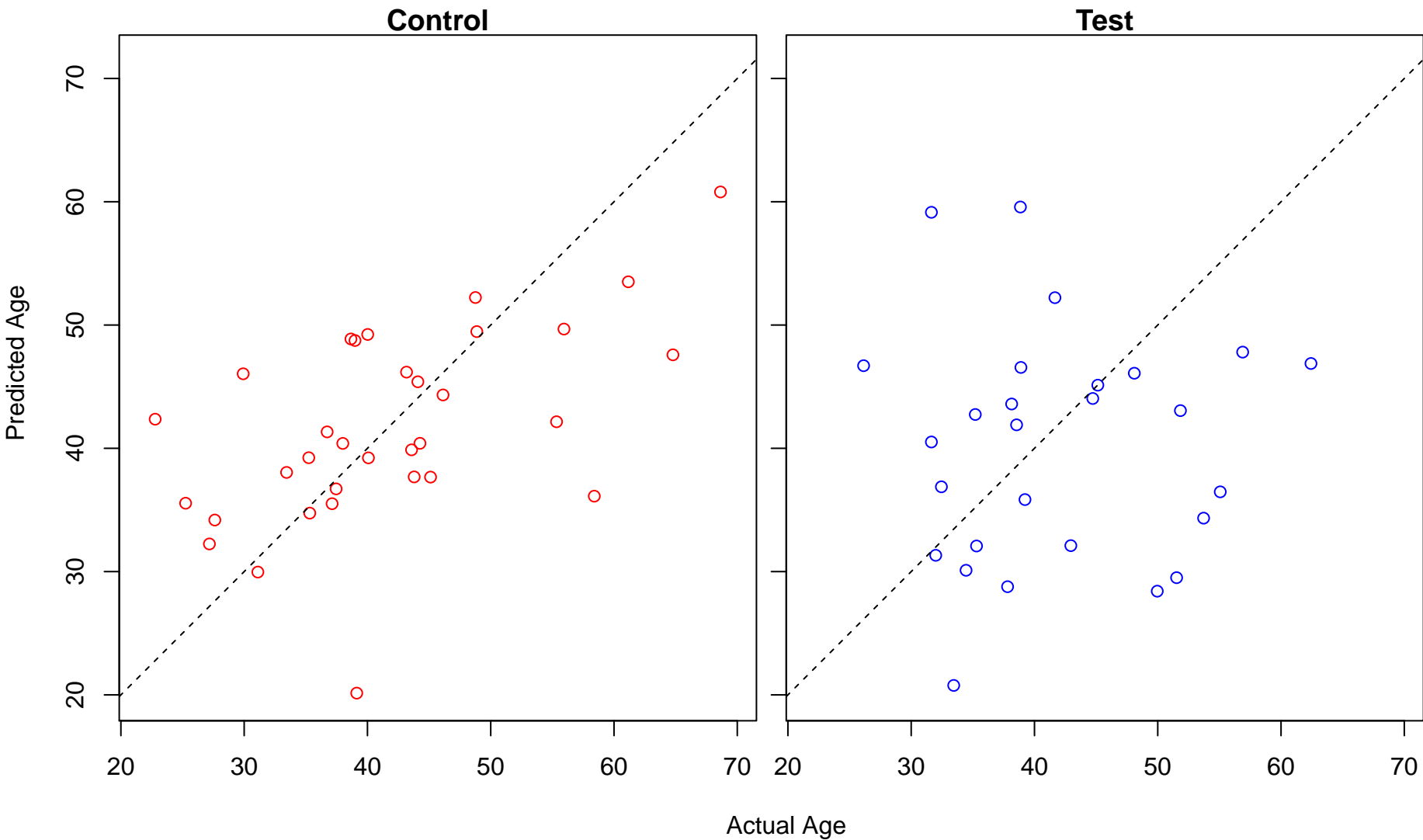
cytoplasmic sequestering of transcription factor (Score: 1.386692)



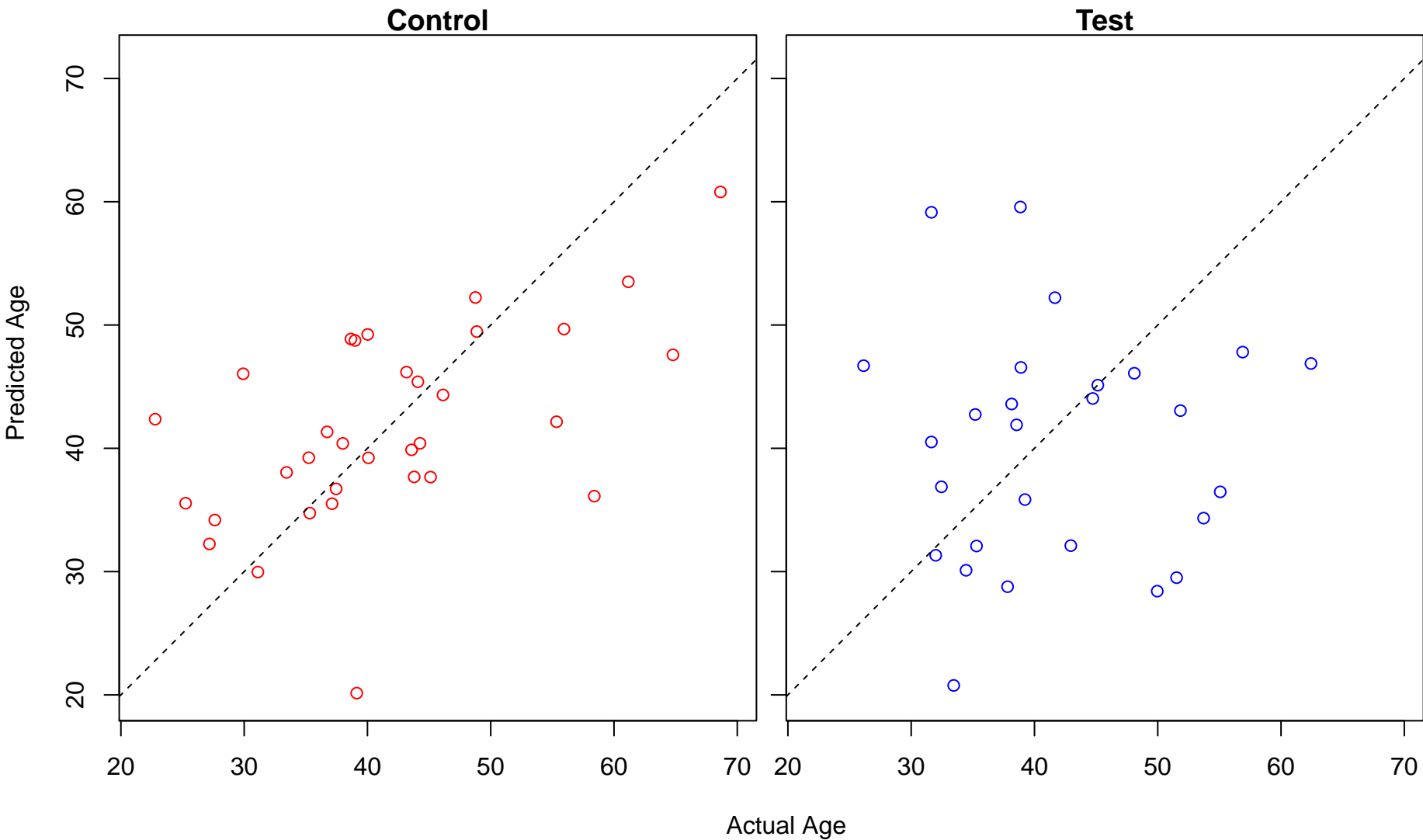
blood coagulation, intrinsic pathway (Score: 1.380789)



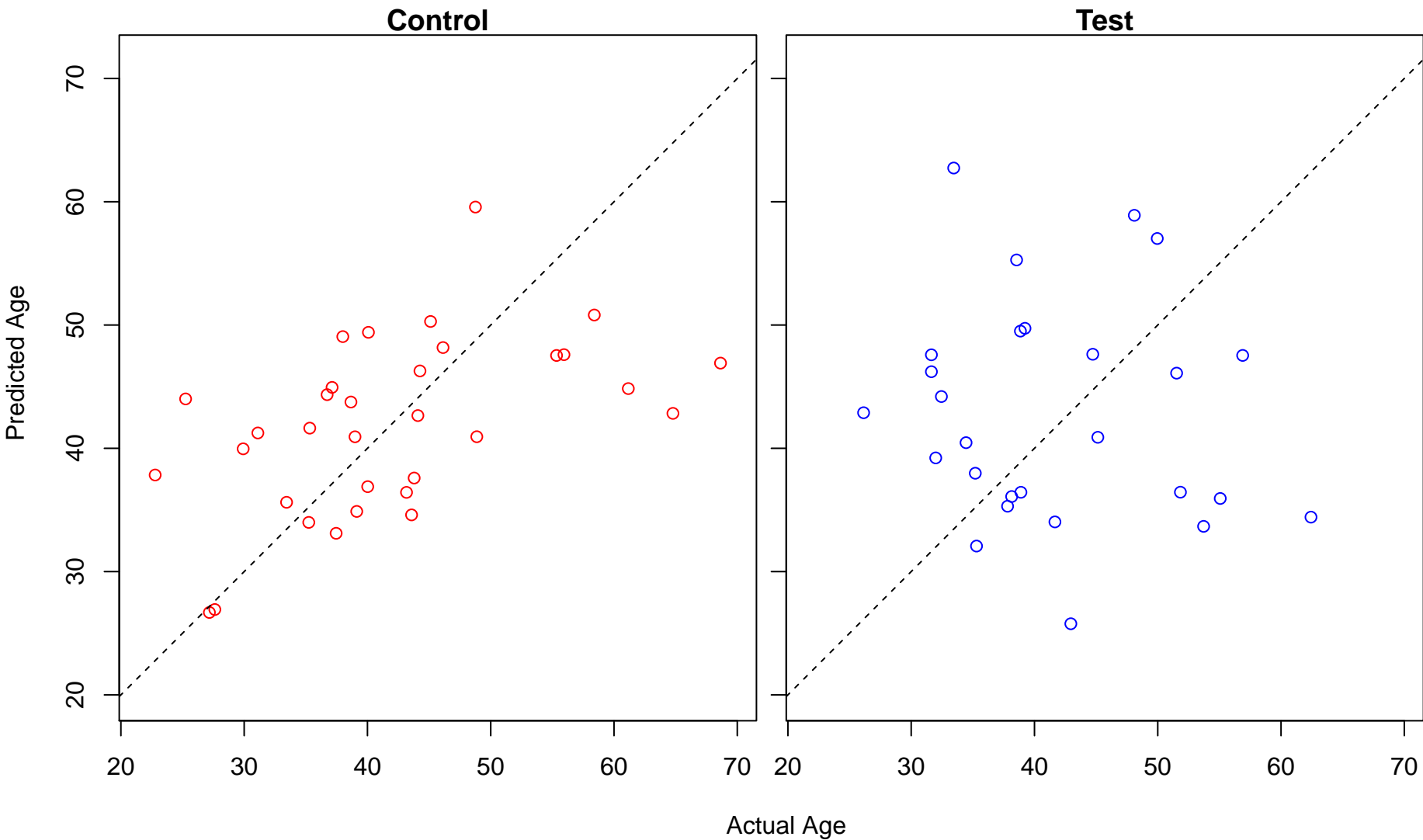
subpallium development (Score: 1.377051)



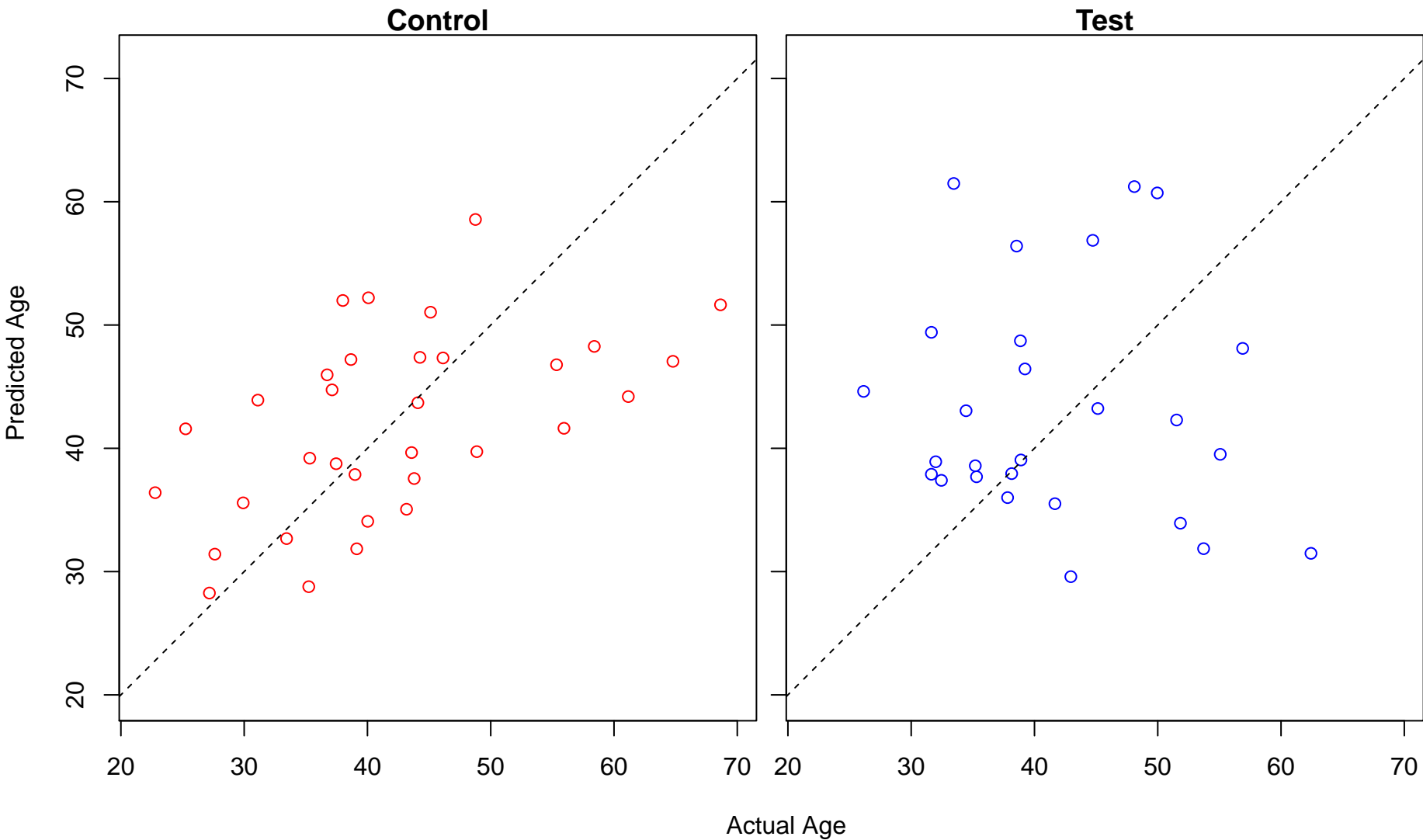
striatum development (Score: 1.377051)



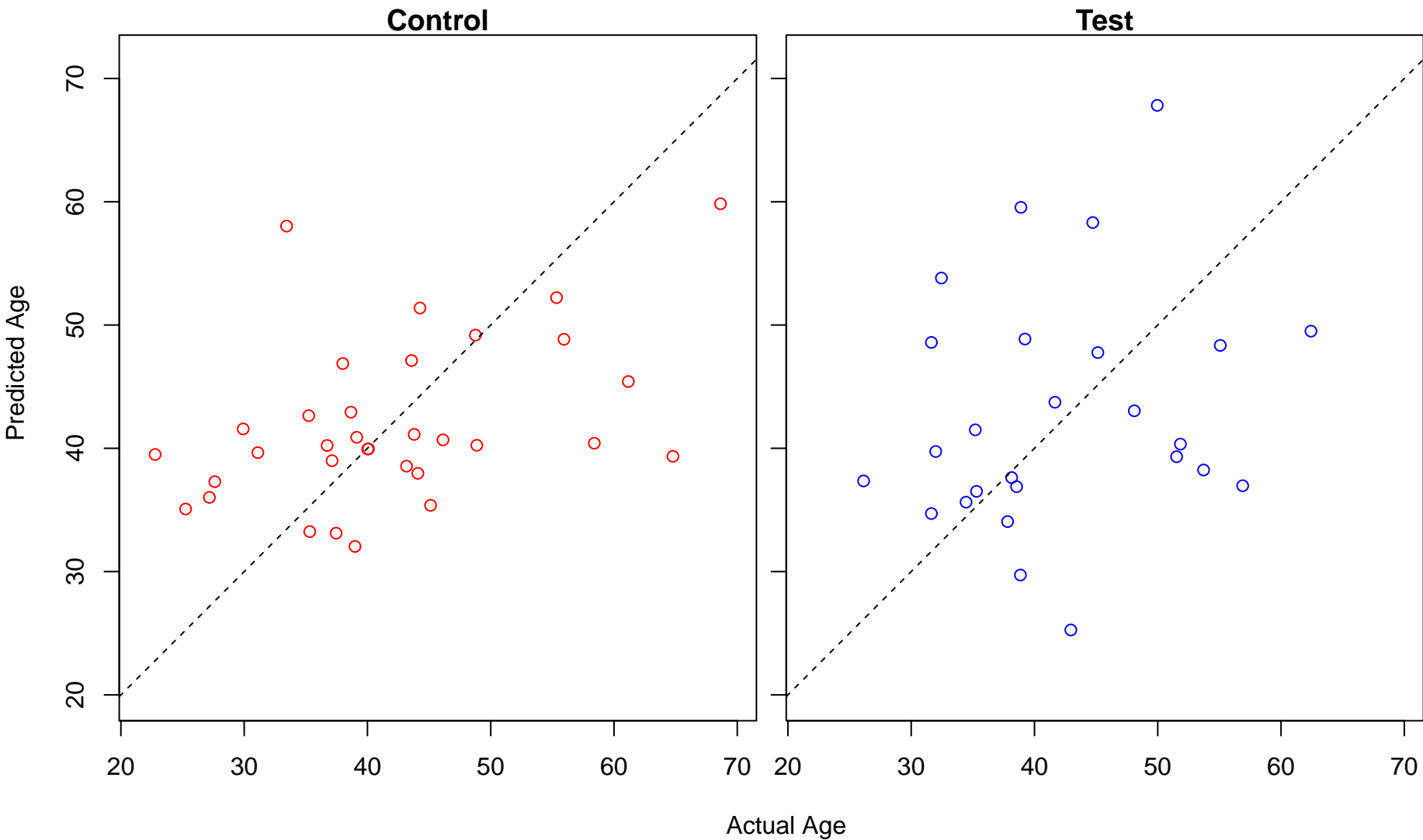
regulation of inclusion body assembly (Score: 1.376986)



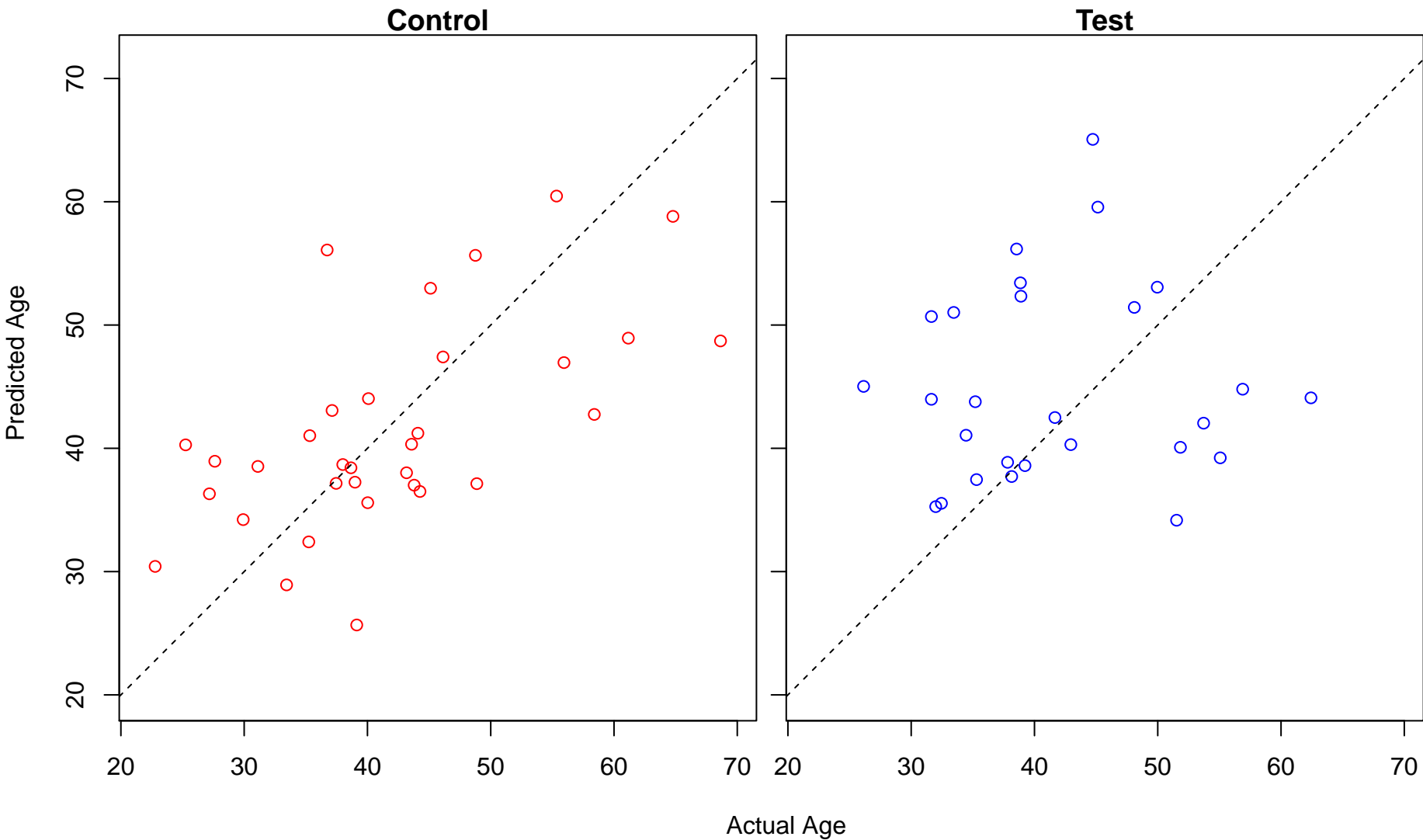
regulation of beta-amyloid formation (Score: 1.370661)



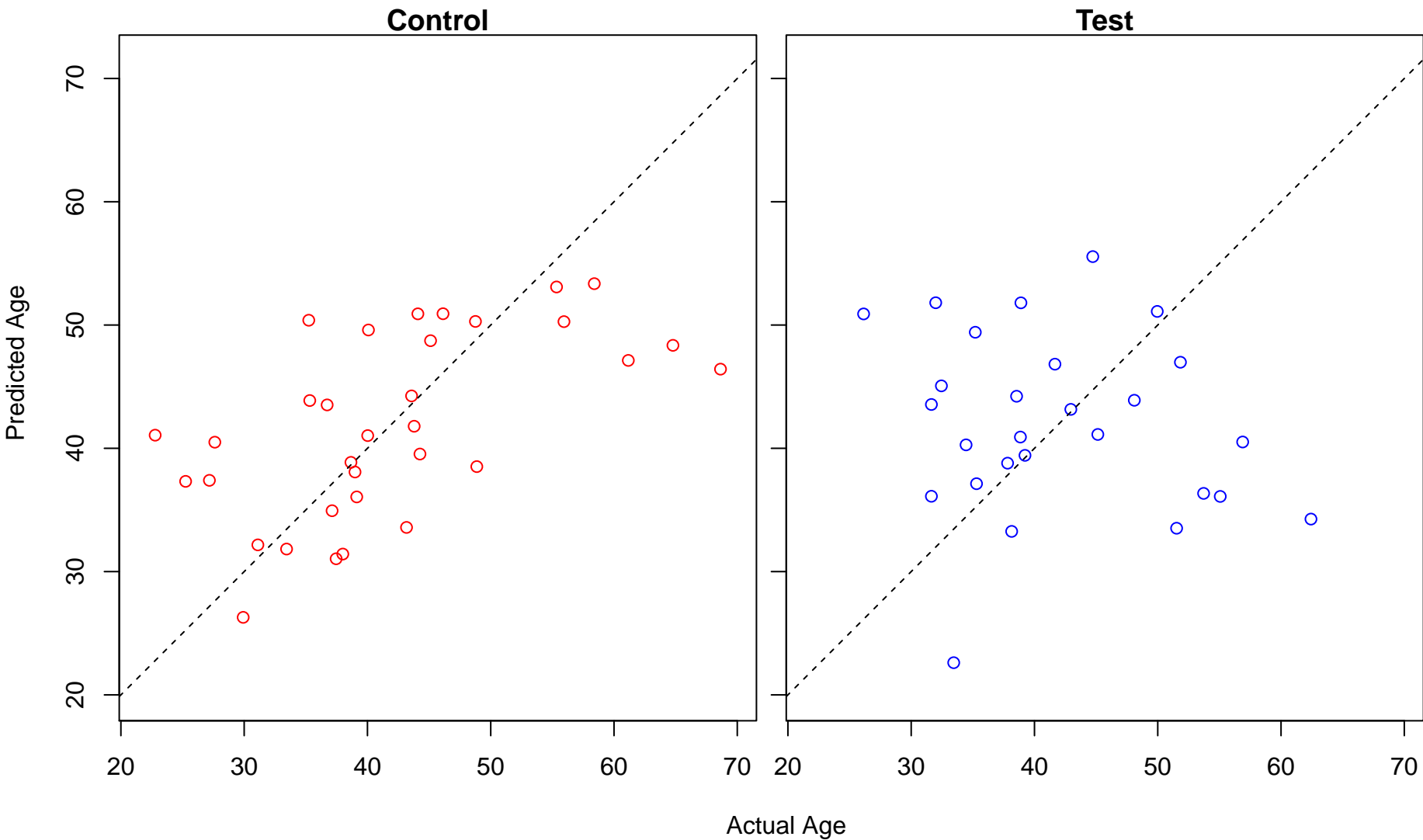
regulation of G0 to G1 transition (Score: 1.360680)



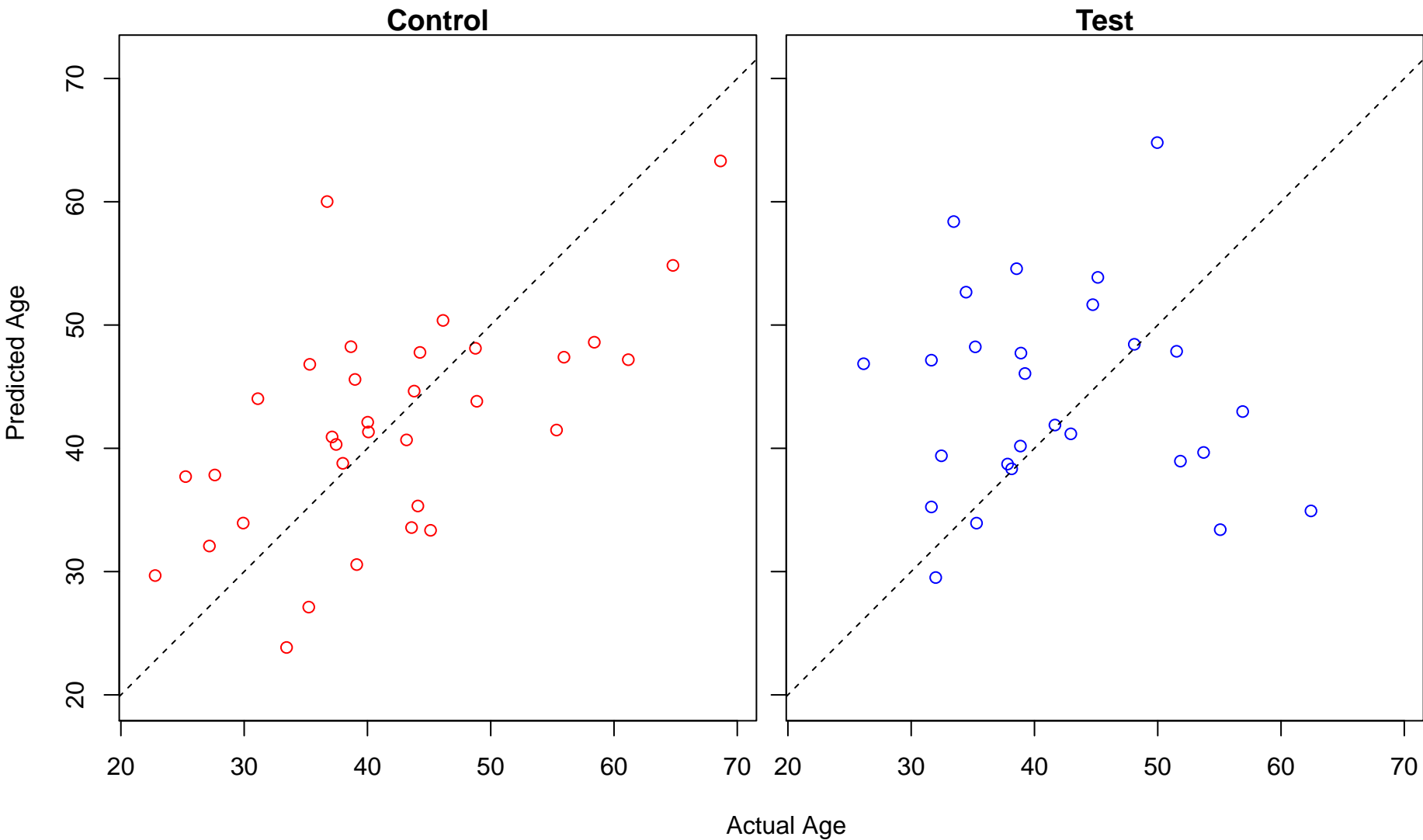
microtubule cytoskeleton organization (Score: 1.358008)



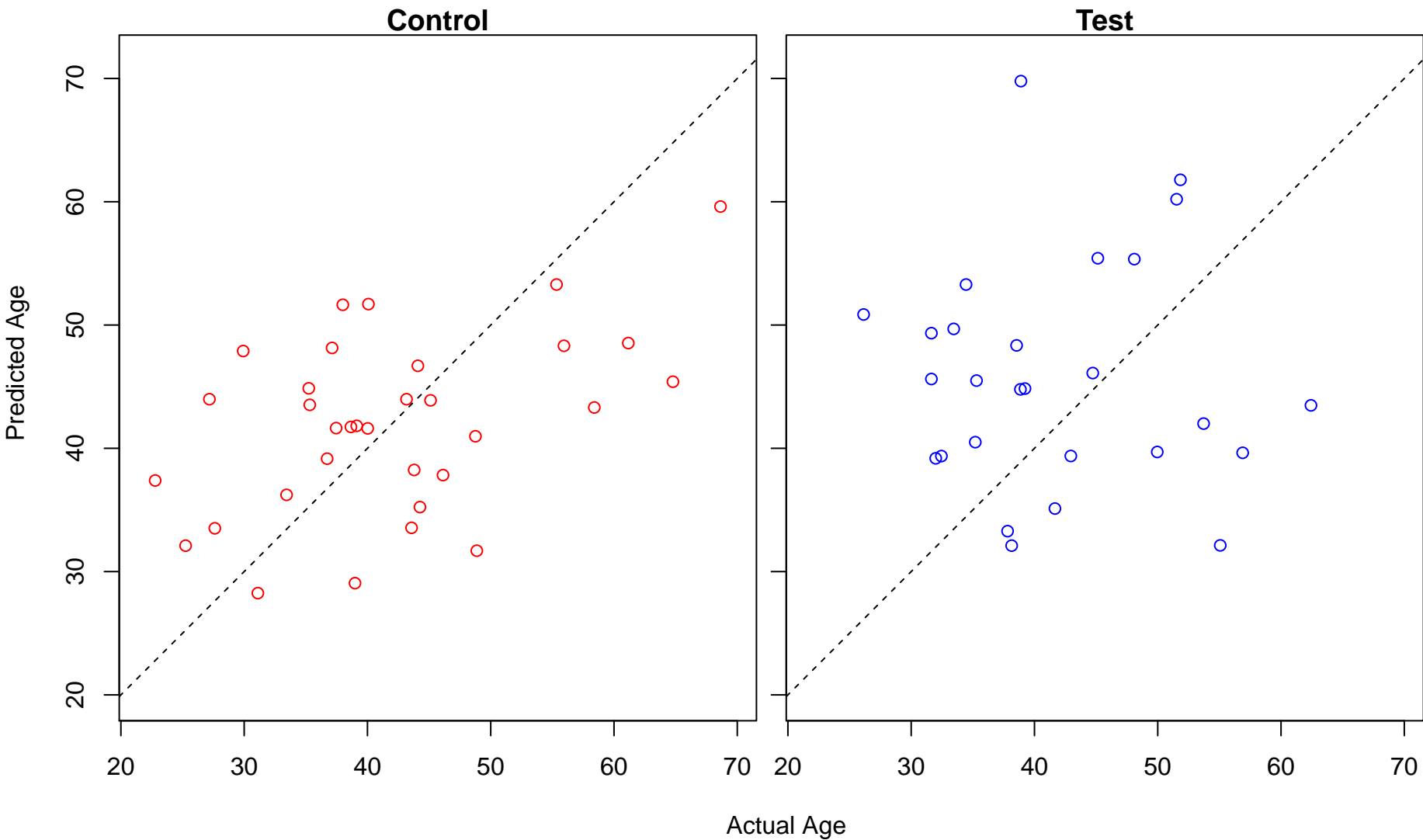
cell-cell signaling involved in cardiac conduction (Score: 1.356856)



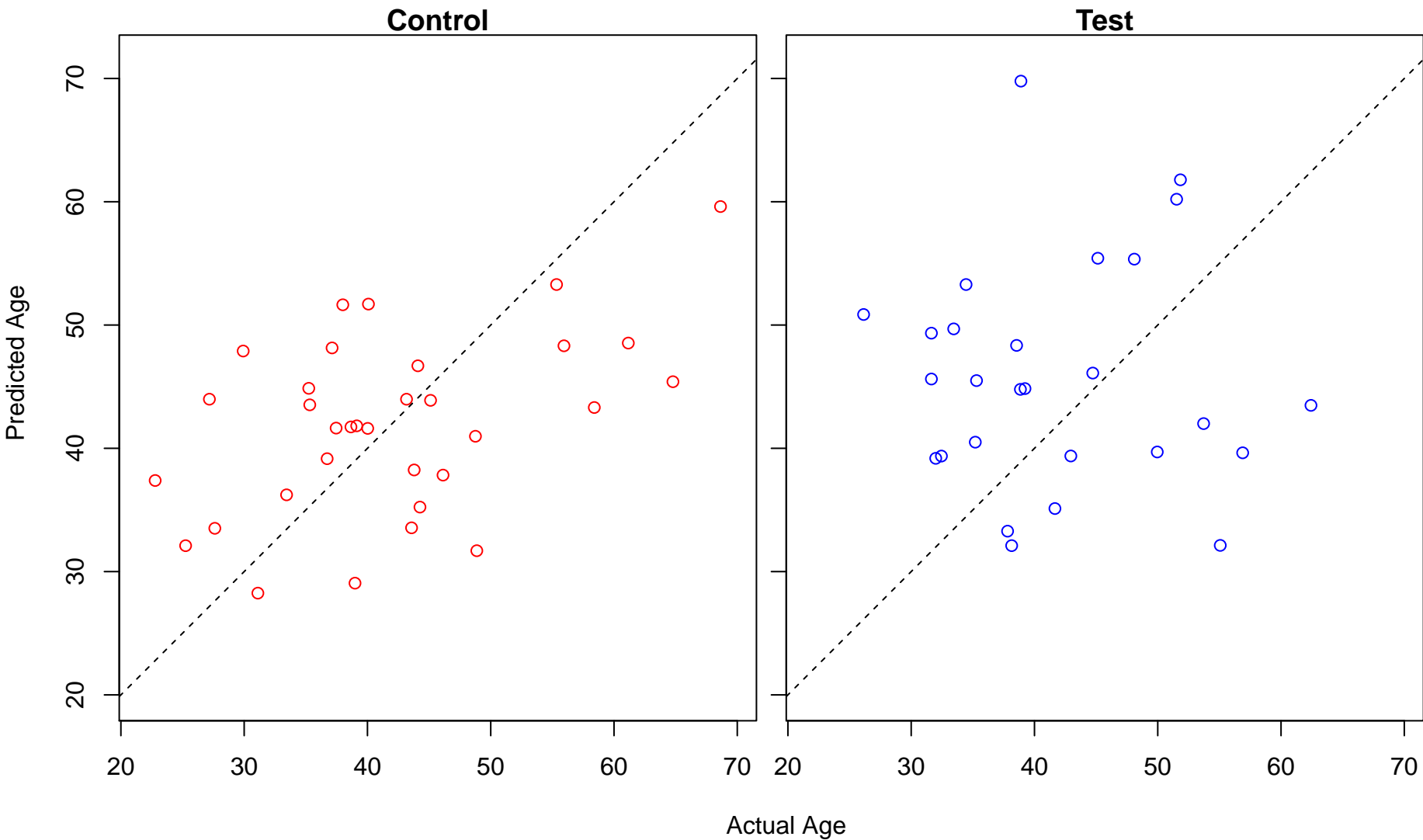
cellular response to cold (Score: 1.354264)



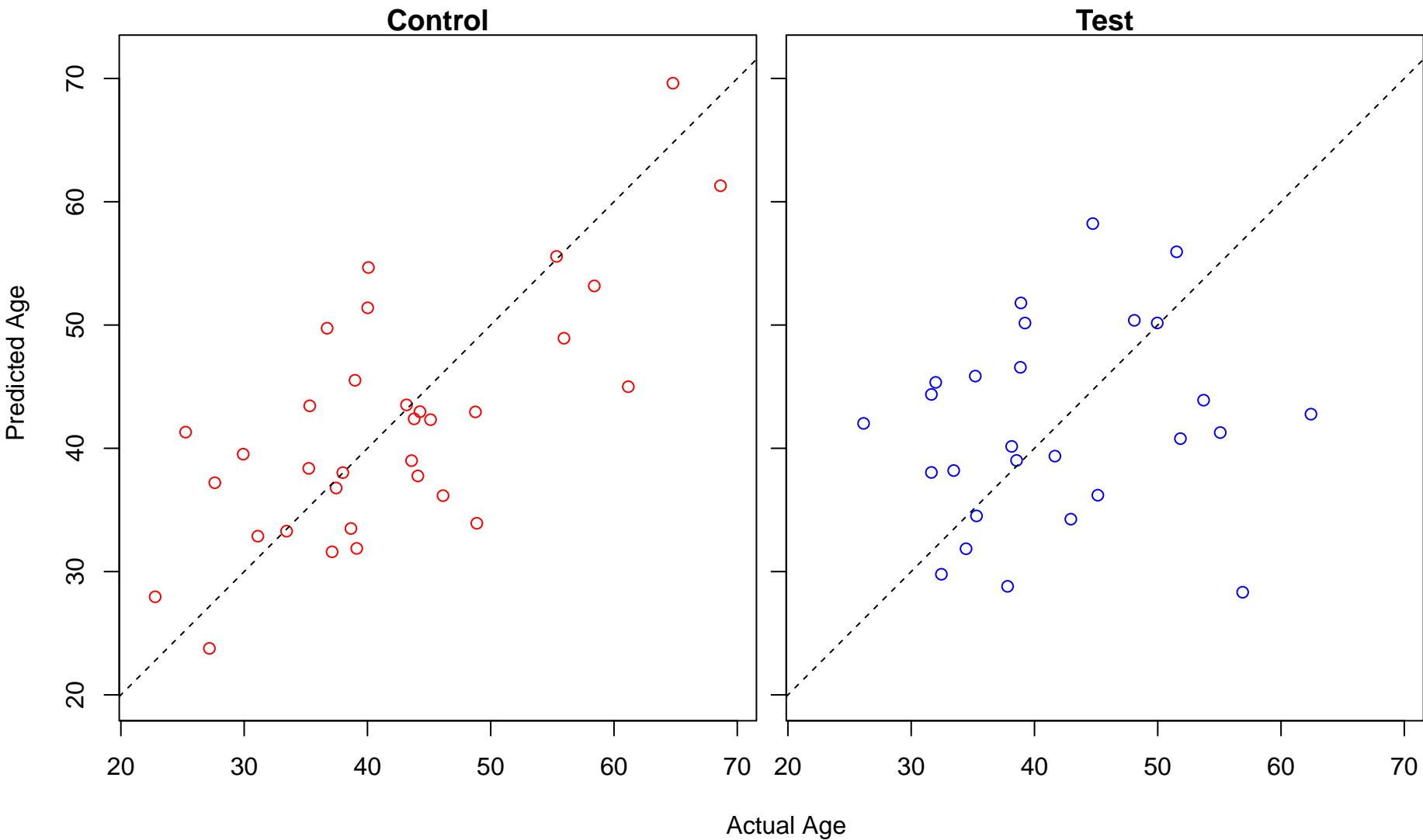
renal system vasculature morphogenesis (Score: 1.348381)



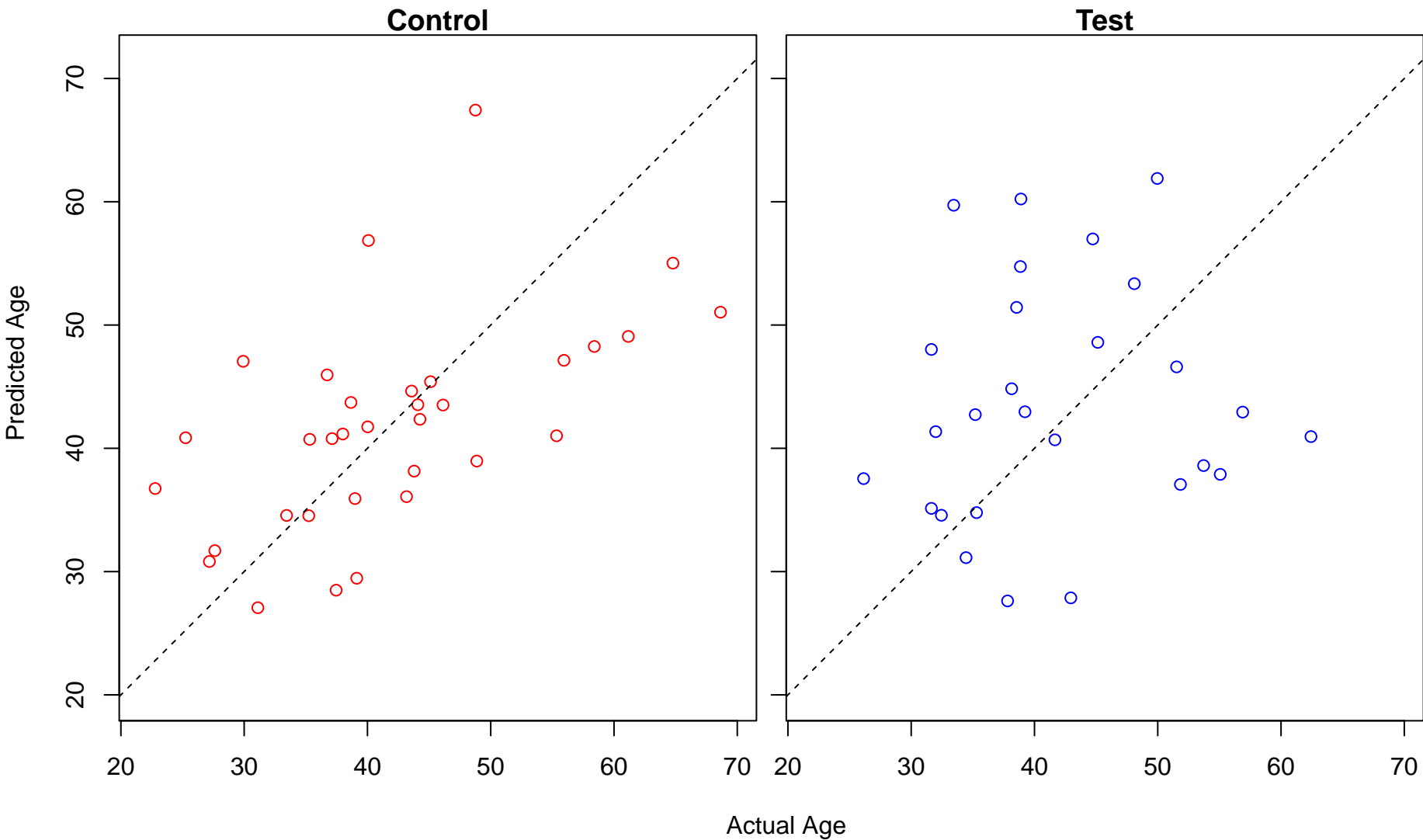
kidney vasculature morphogenesis (Score: 1.348381)



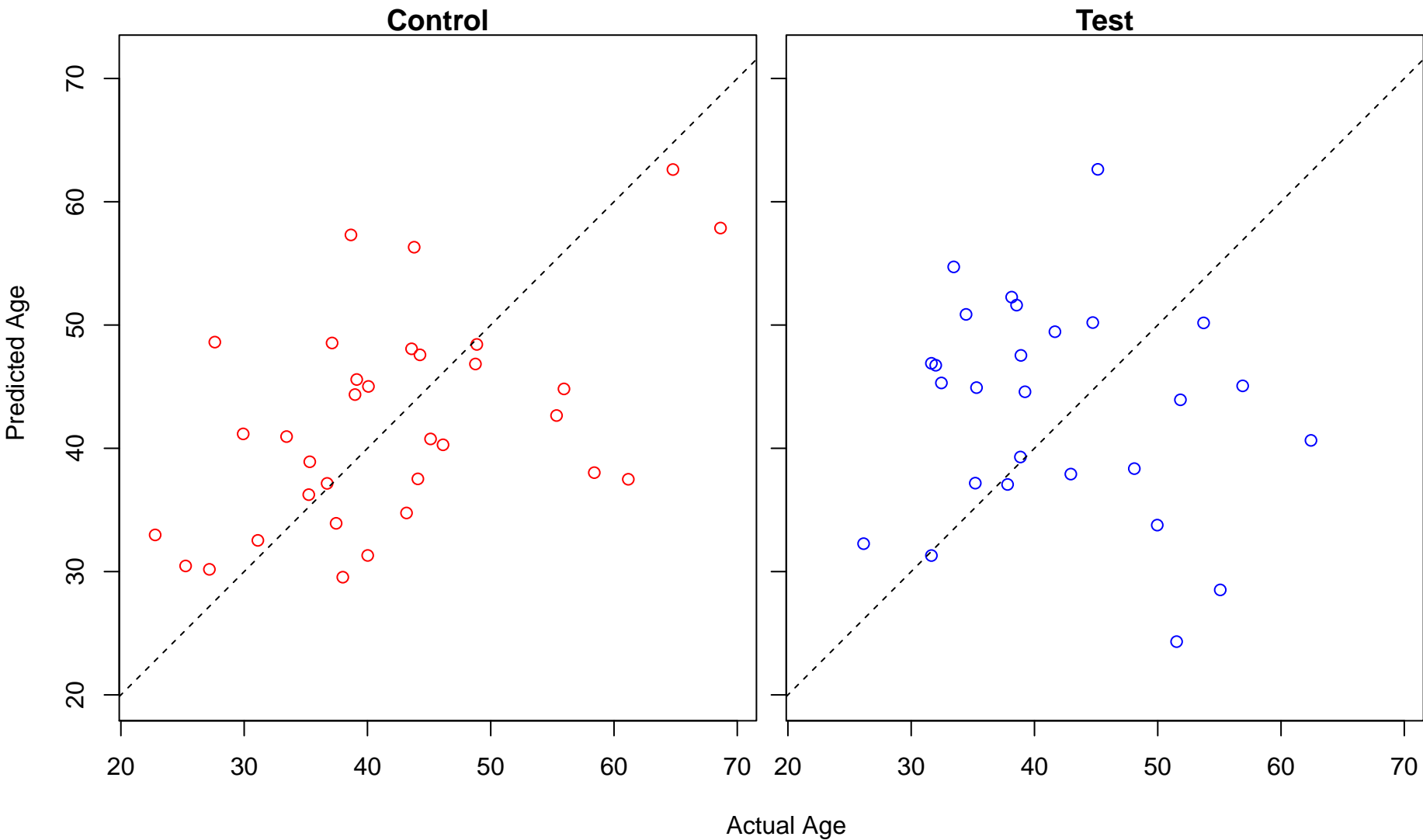
bile acid and bile salt transport (Score: 1.341760)



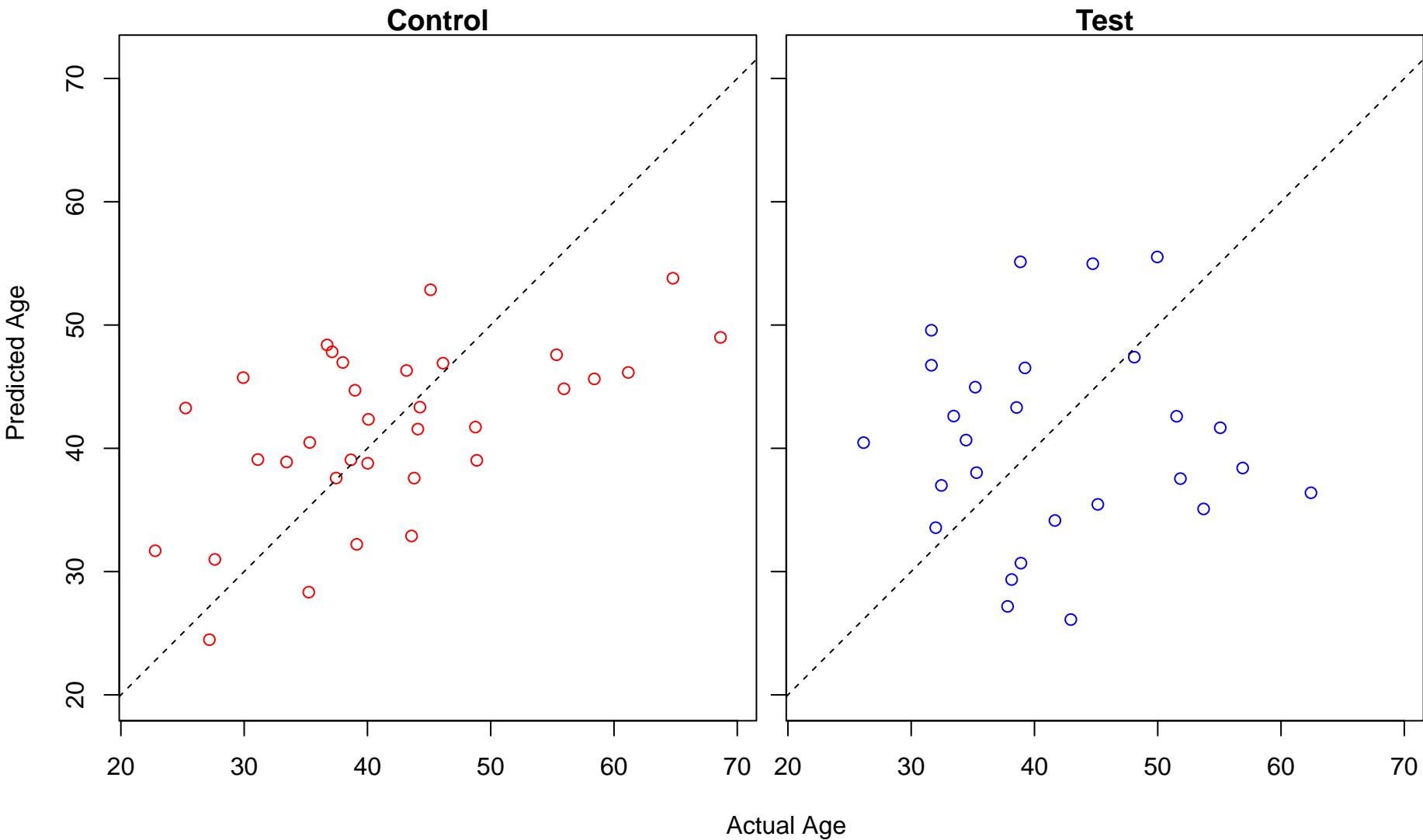
regulation of sterol transport (Score: 1.340081)



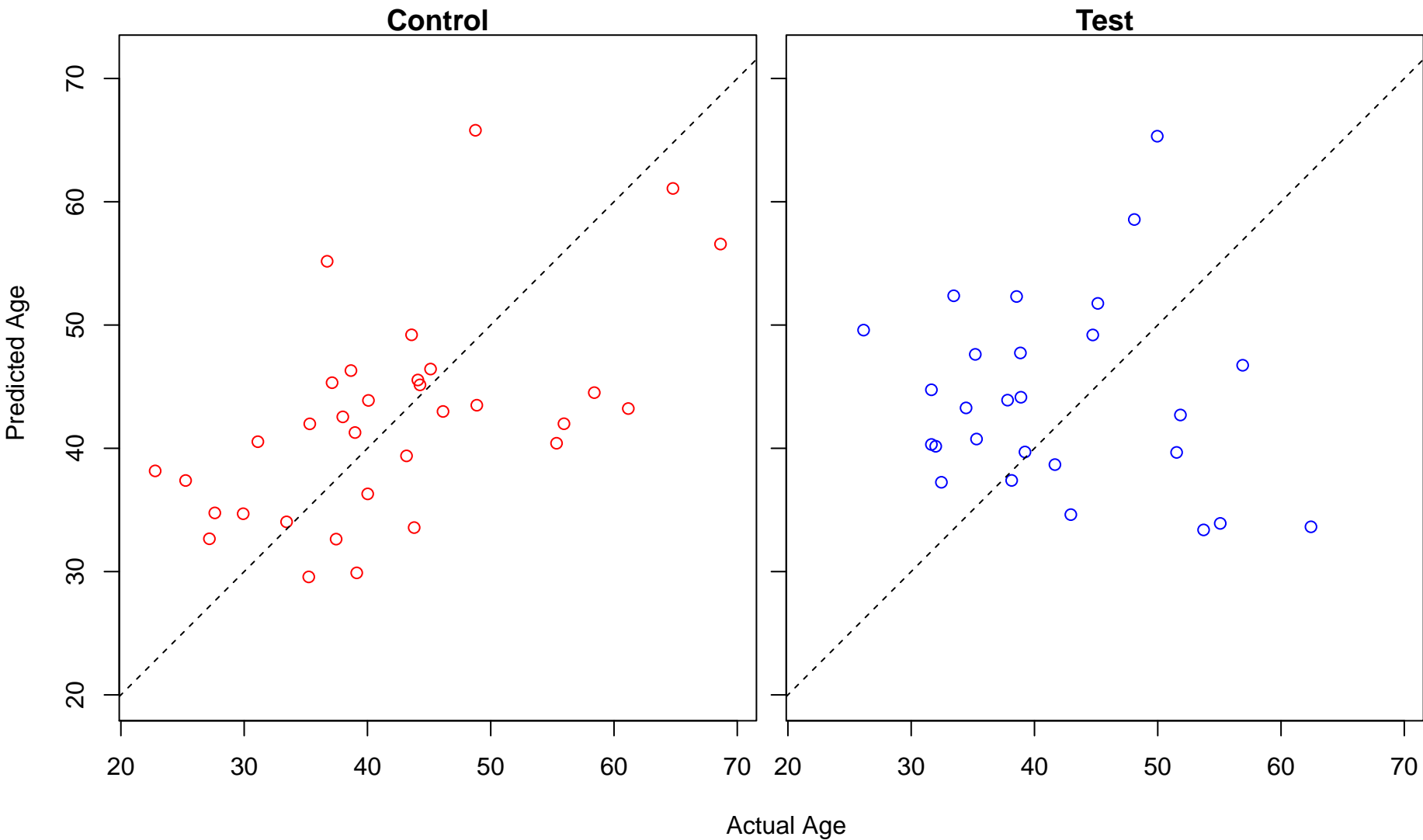
sphingolipid catabolic process (Score: 1.335256)



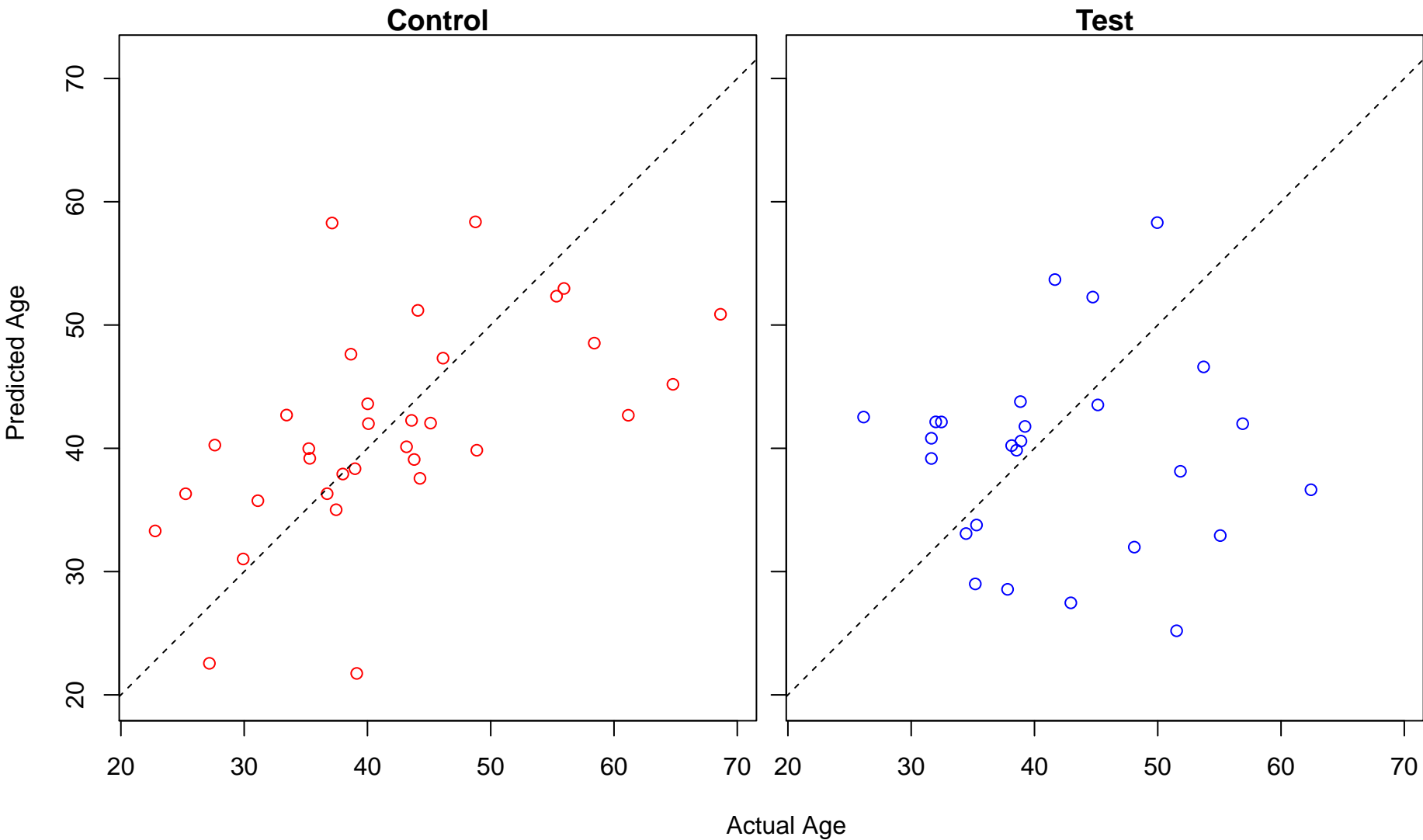
cholesterol transport (Score: 1.331132)



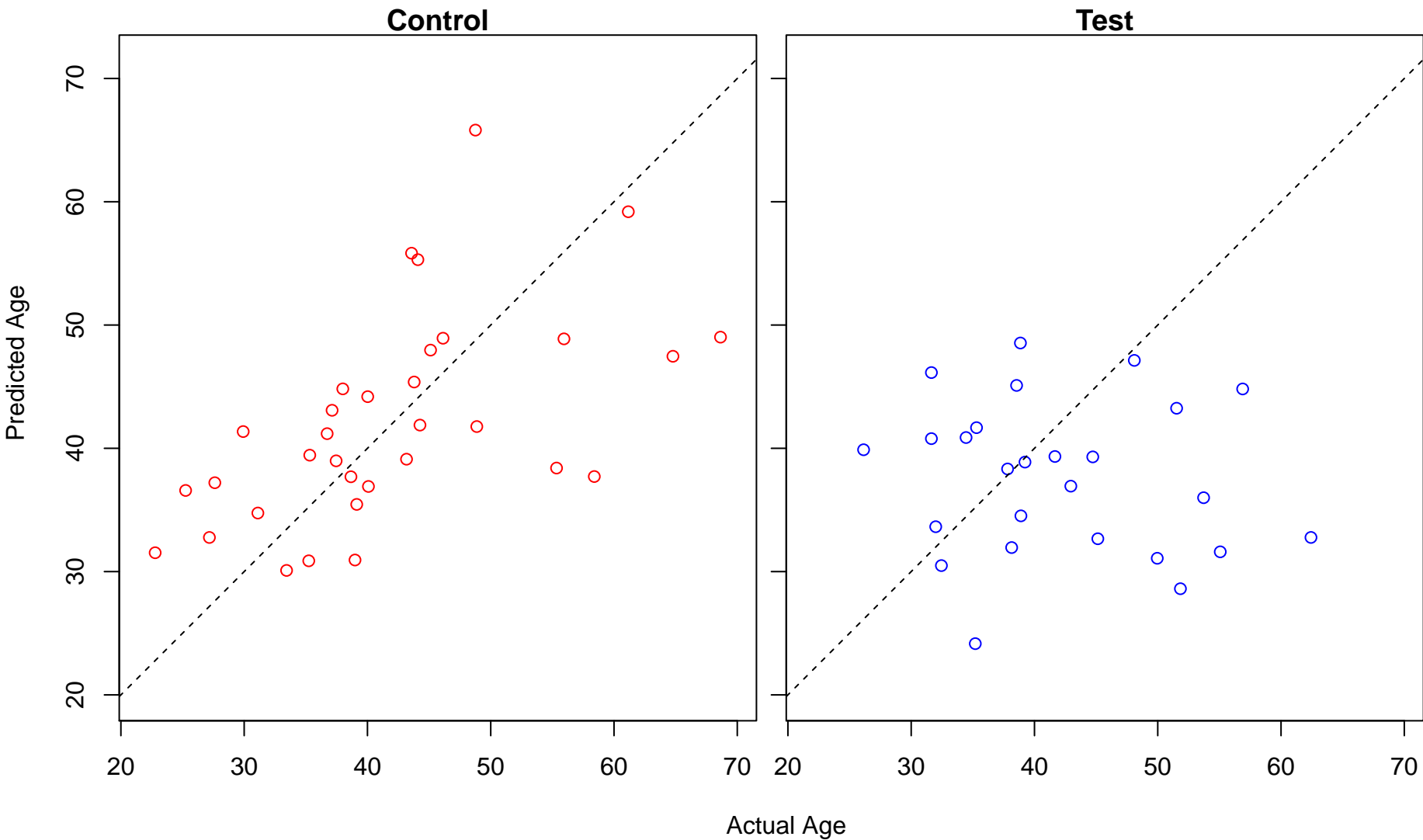
response to nitric oxide (Score: 1.331117)



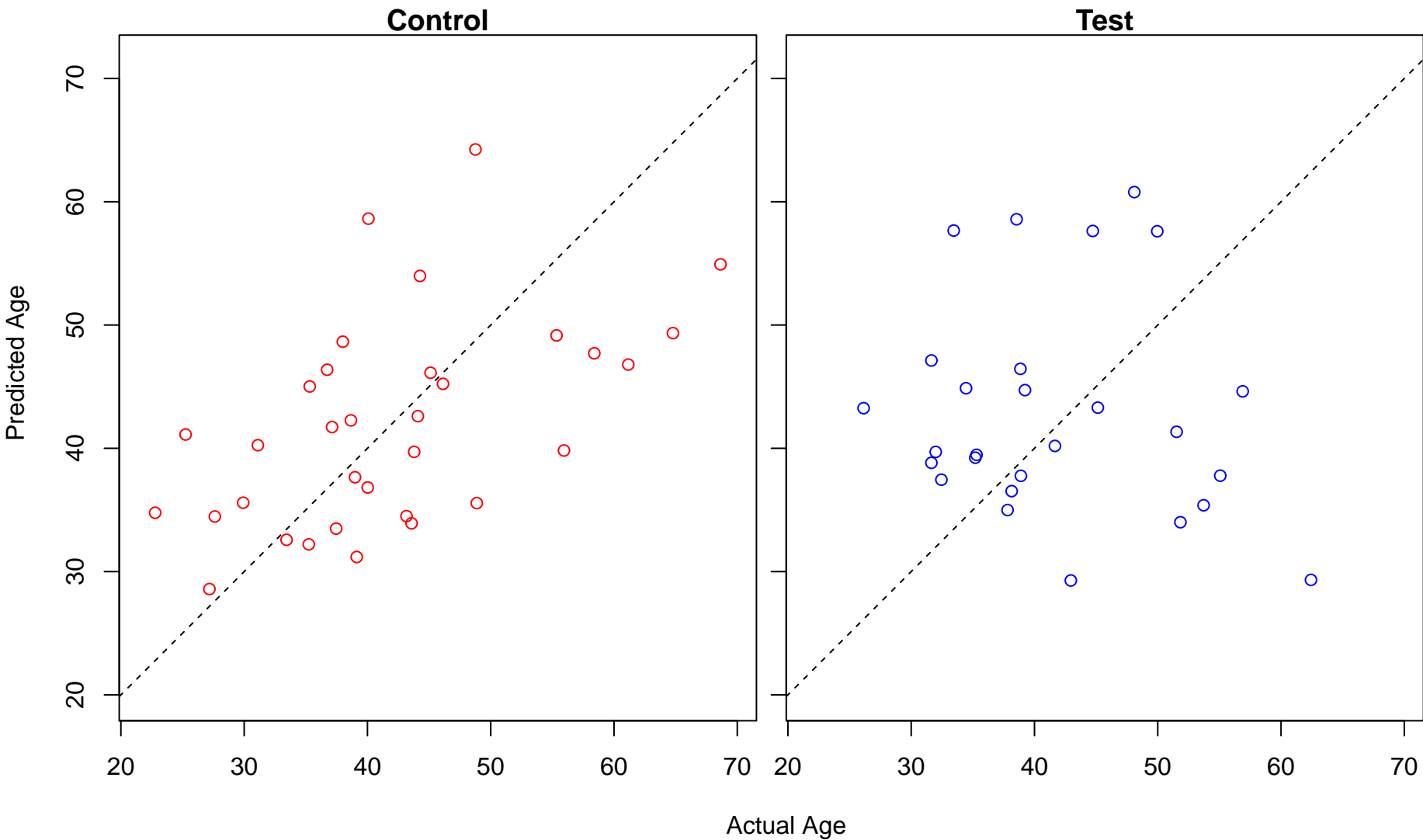
positive regulation of sodium ion transport (Score: 1.330790)



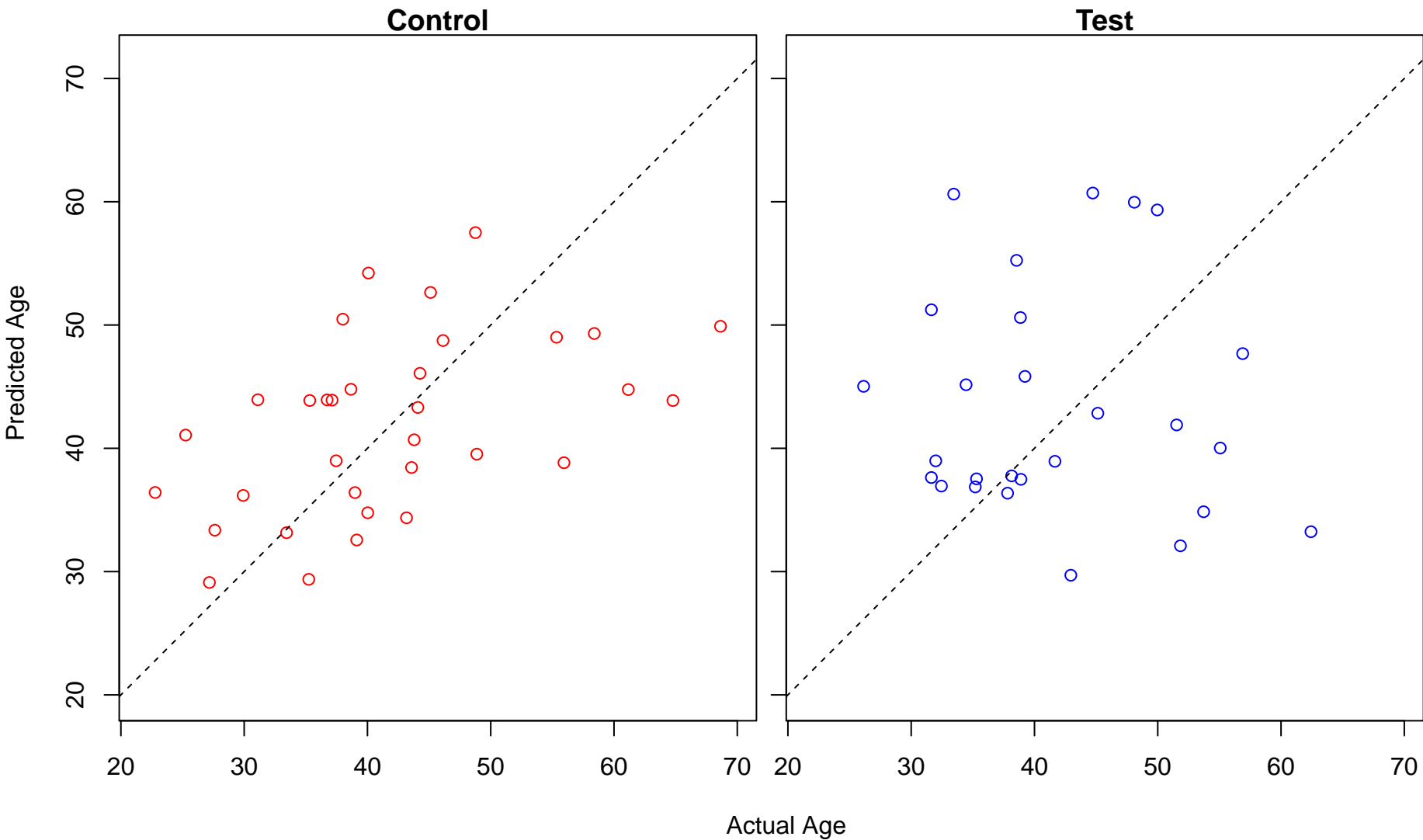
positive regulation of cell junction assembly (Score: 1.329772)



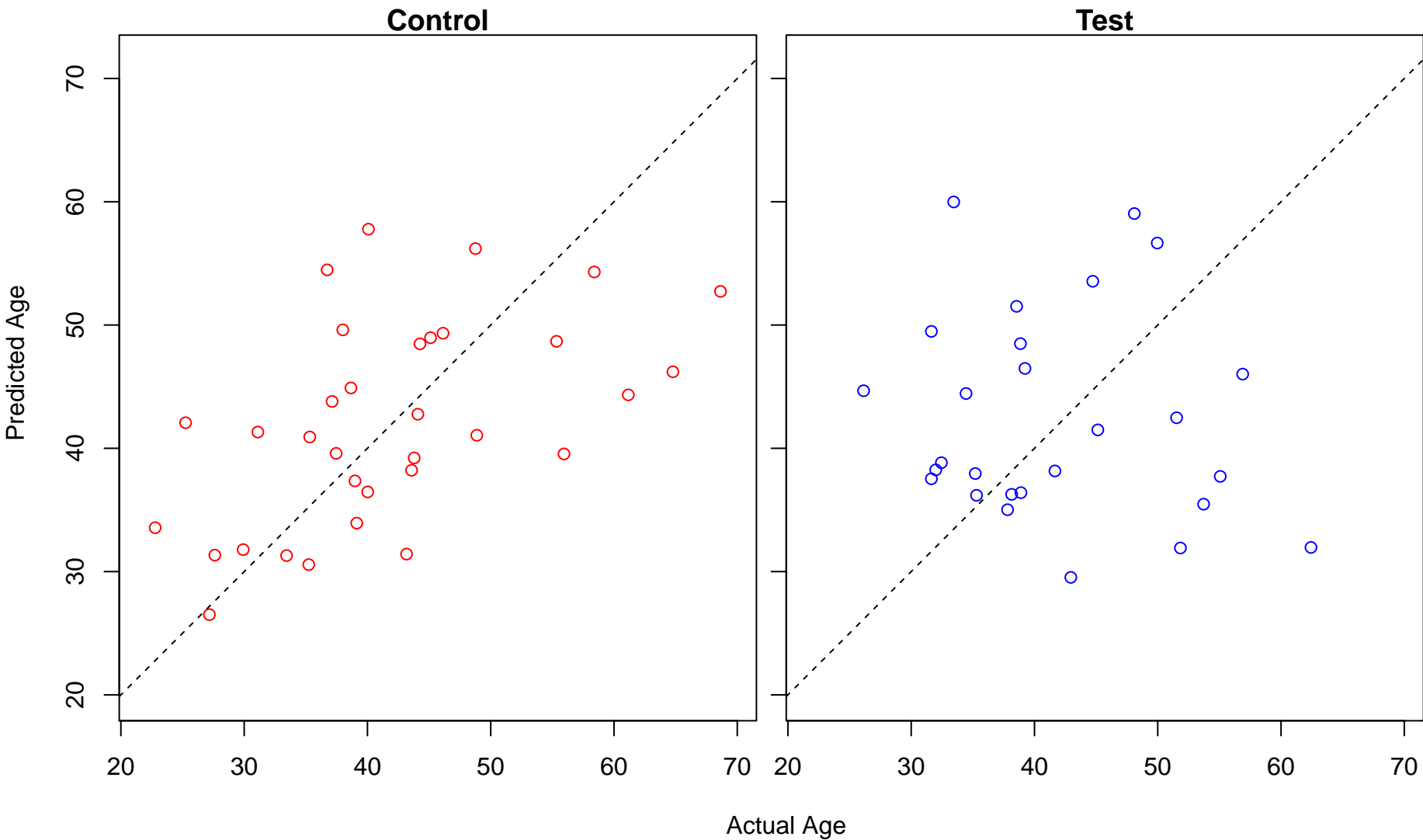
negative regulation of amyloid precursor protein catabolic process (Score: 1.328277)



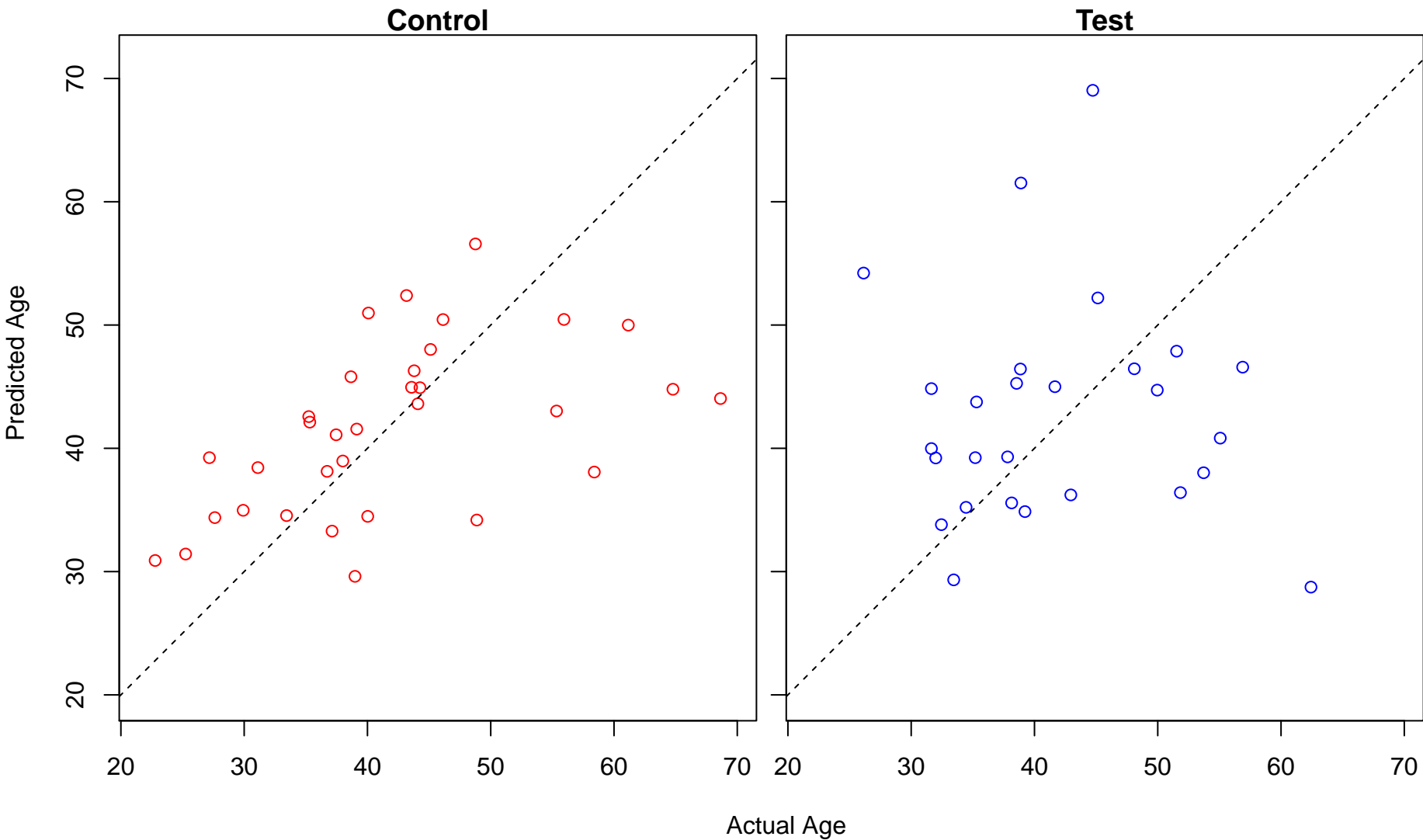
regulation of amyloid precursor protein catabolic process (Score: 1.318329)



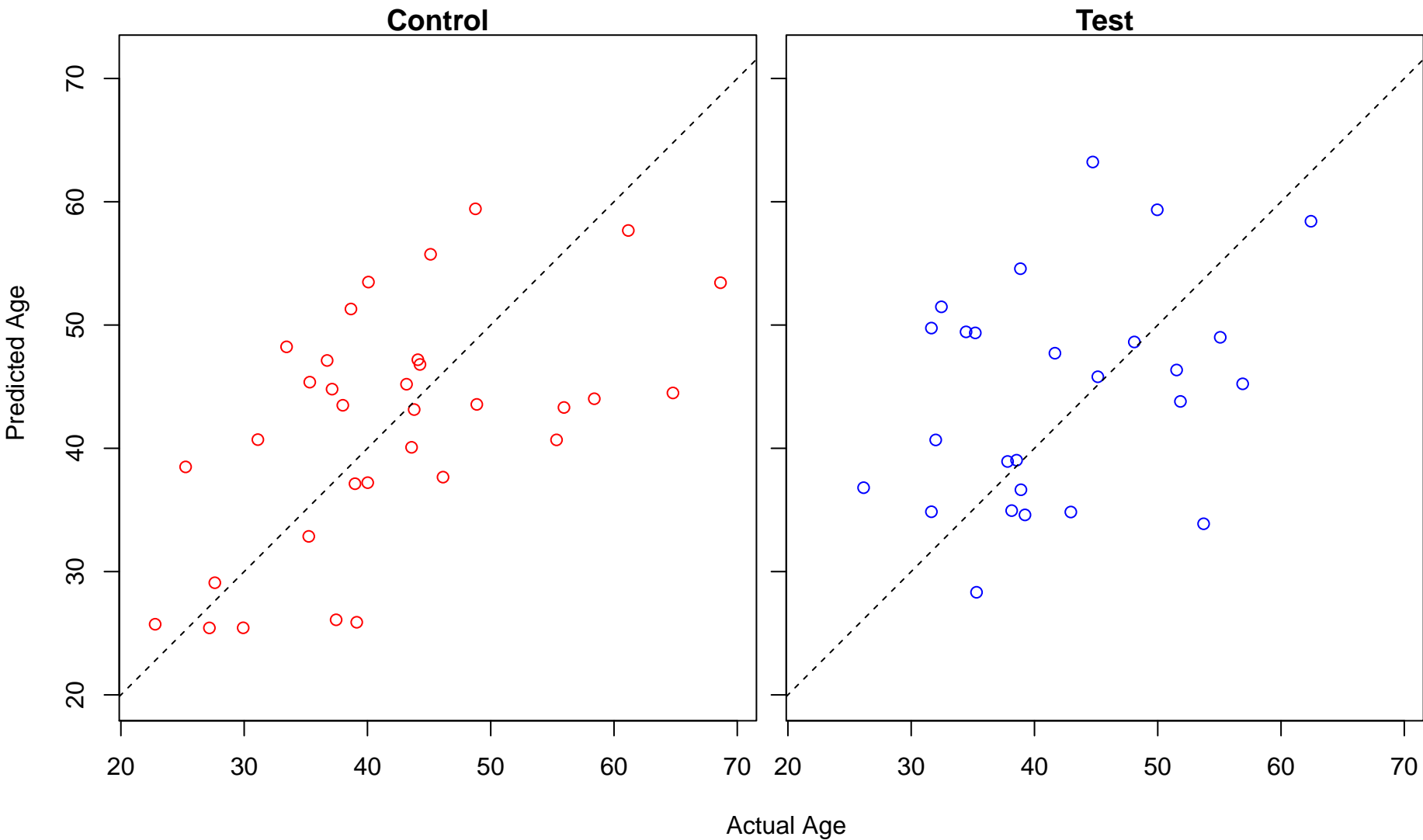
negative regulation of beta-amyloid formation (Score: 1.318072)



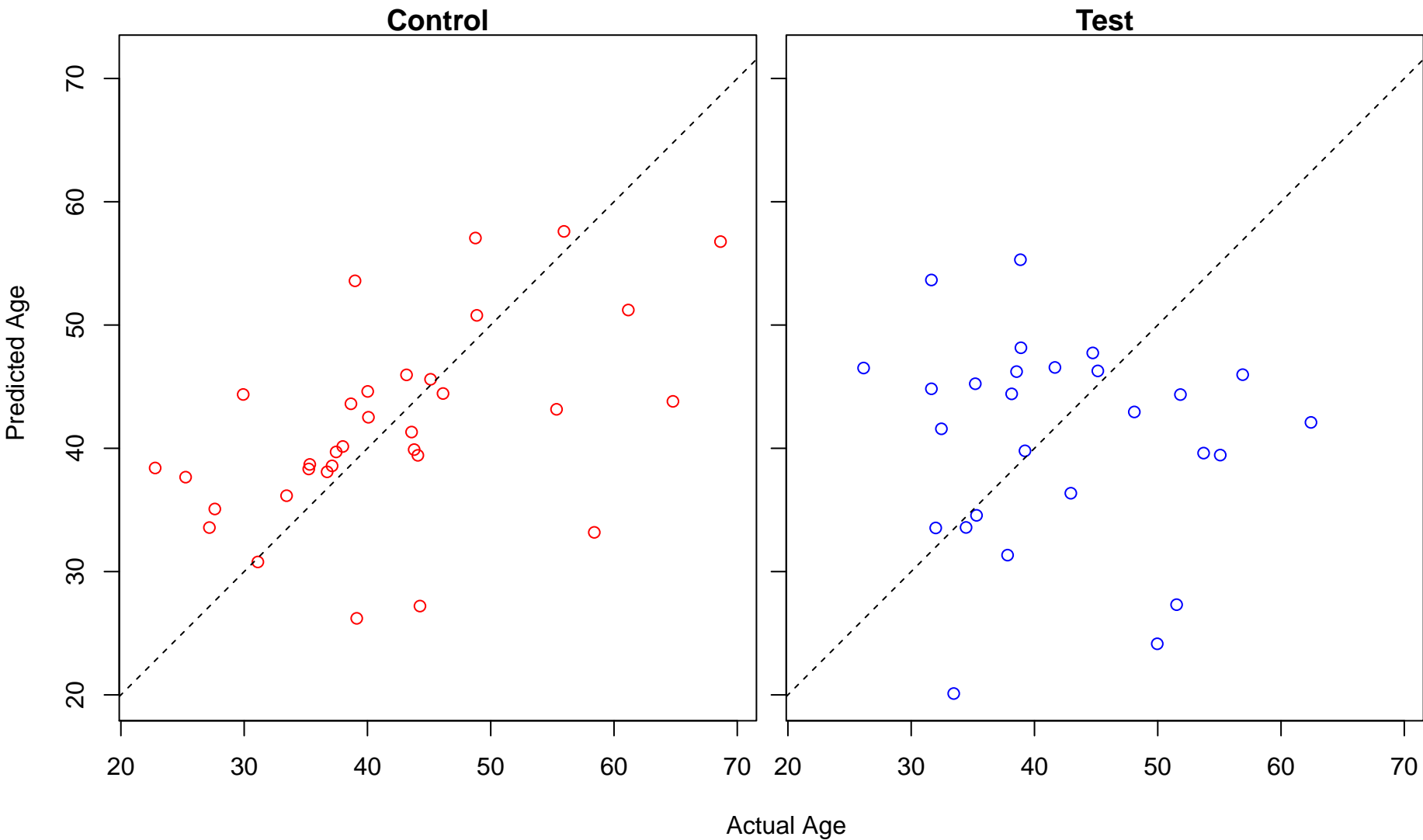
negative regulation of potassium ion transmembrane transport (Score: 1.317778)



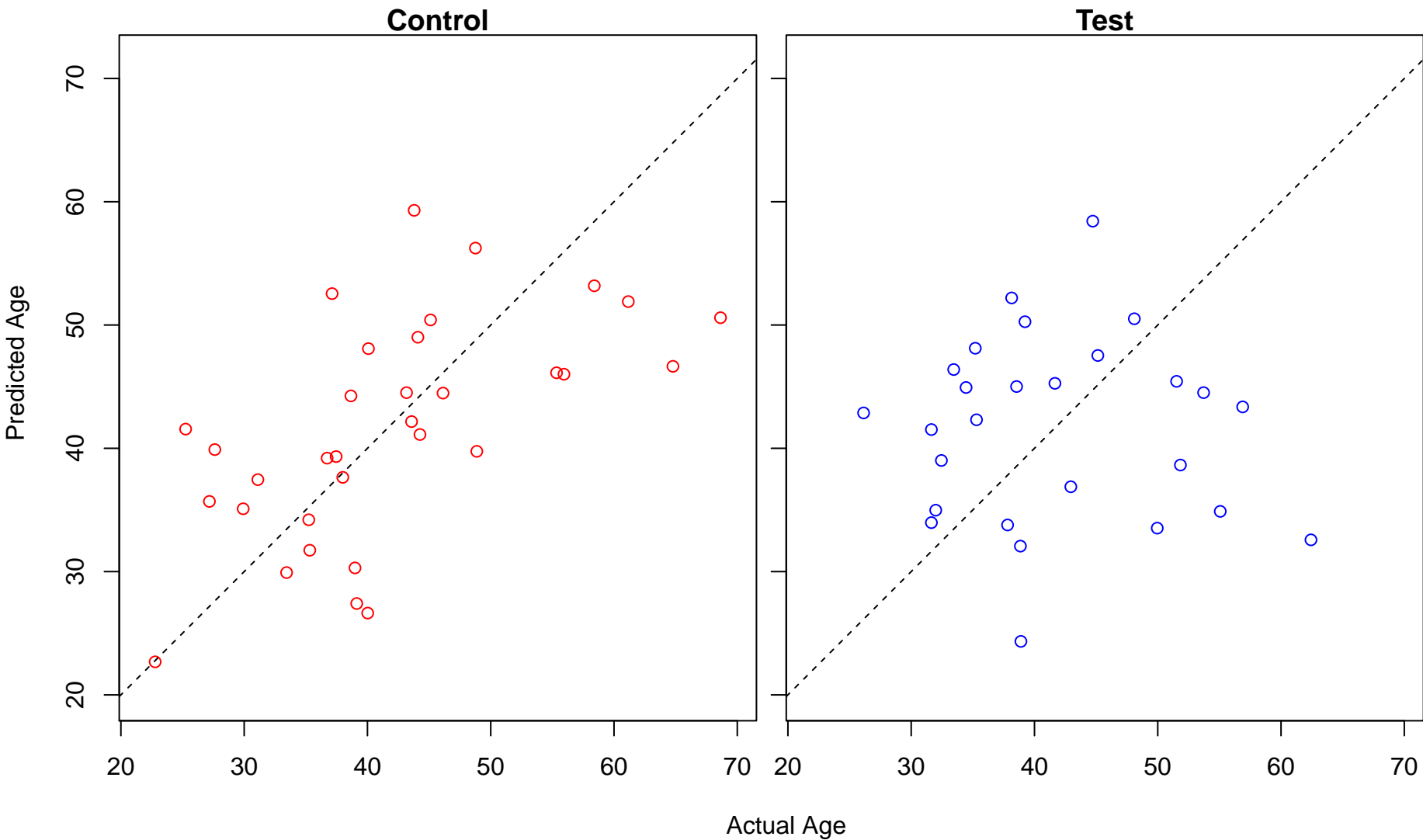
positive regulation of synaptic transmission (Score: 1.313660)



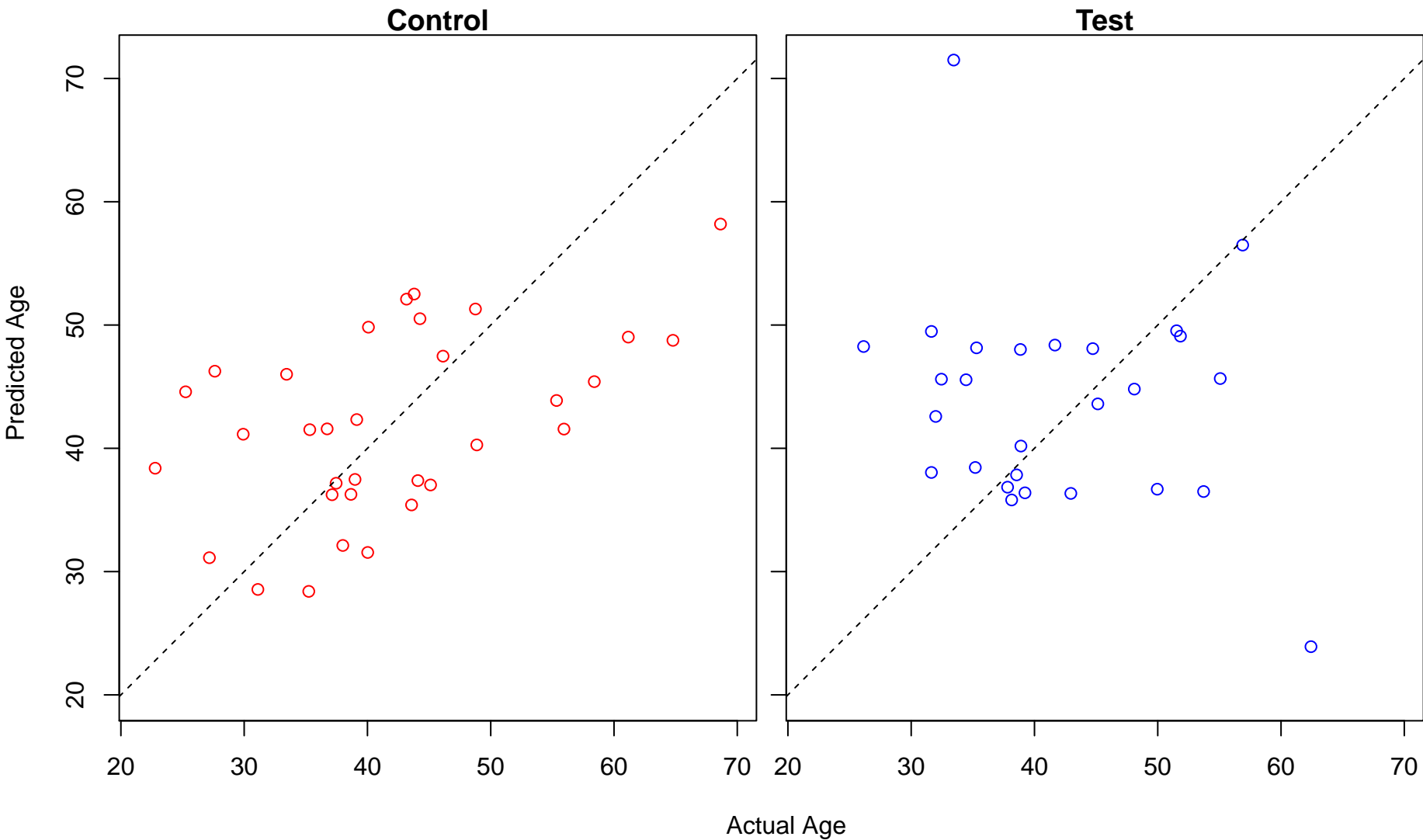
leptin-mediated signaling pathway (Score: 1.311197)



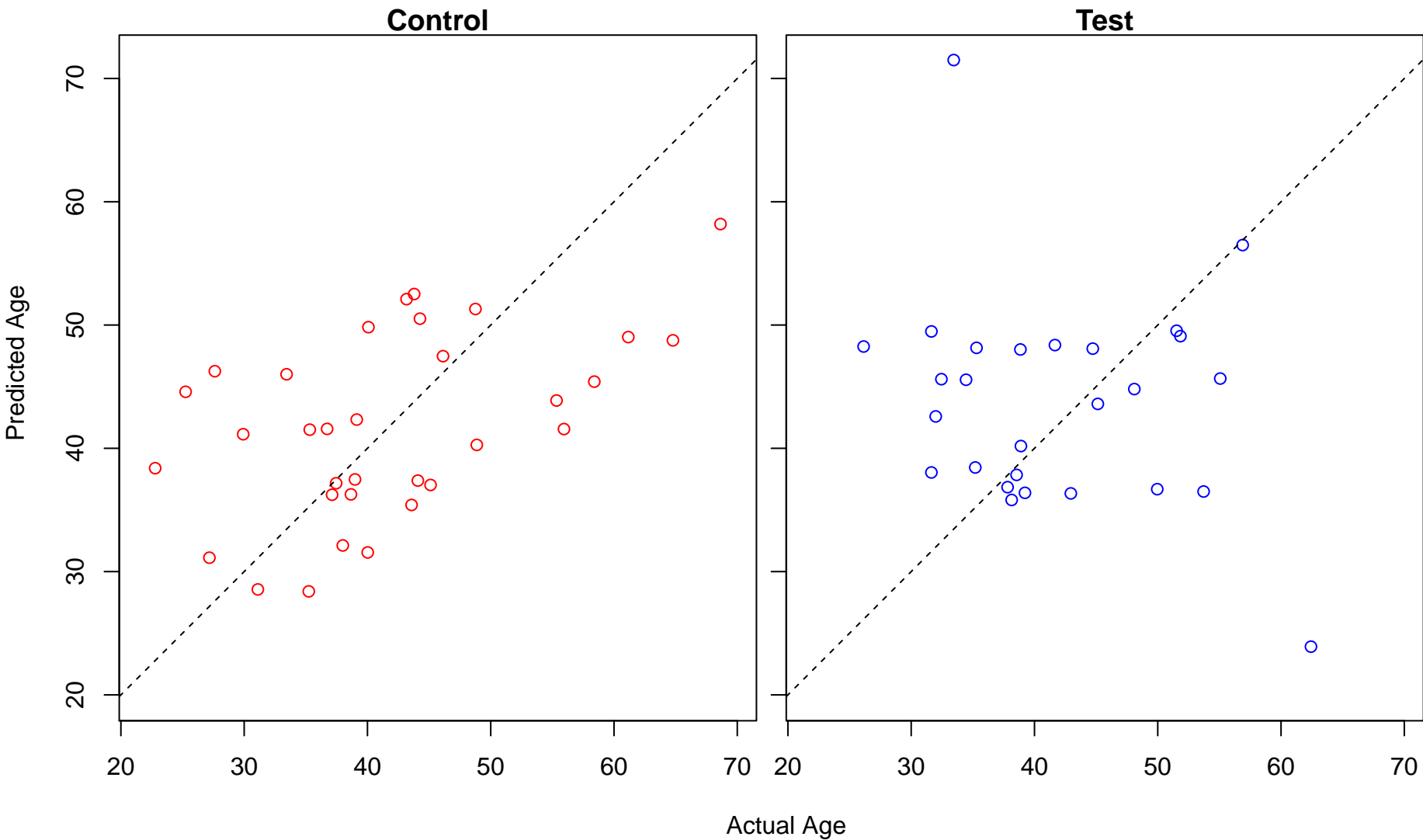
phosphatidylethanolamine metabolic process (Score: 1.311032)



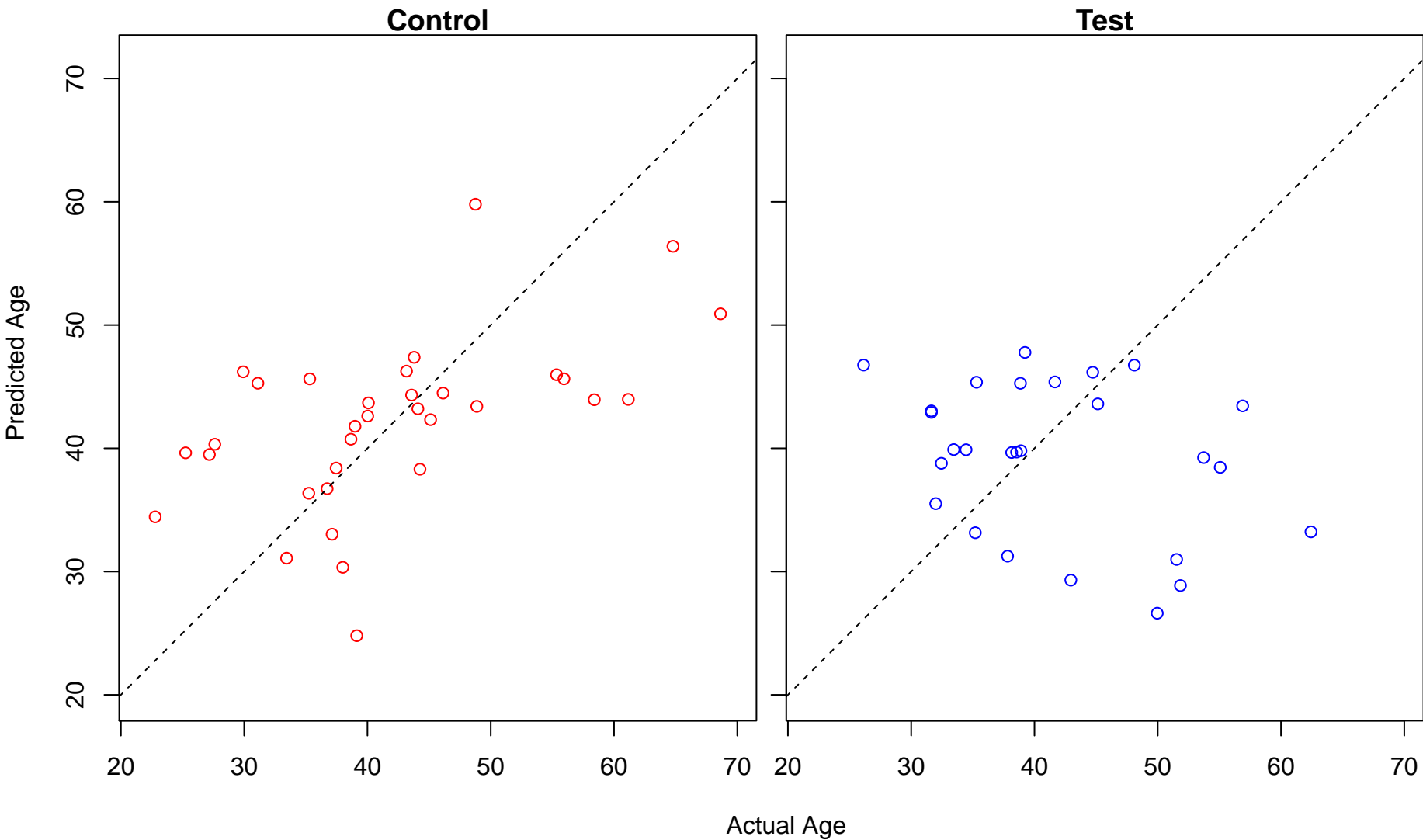
pulmonary valve development (Score: 1.310727)



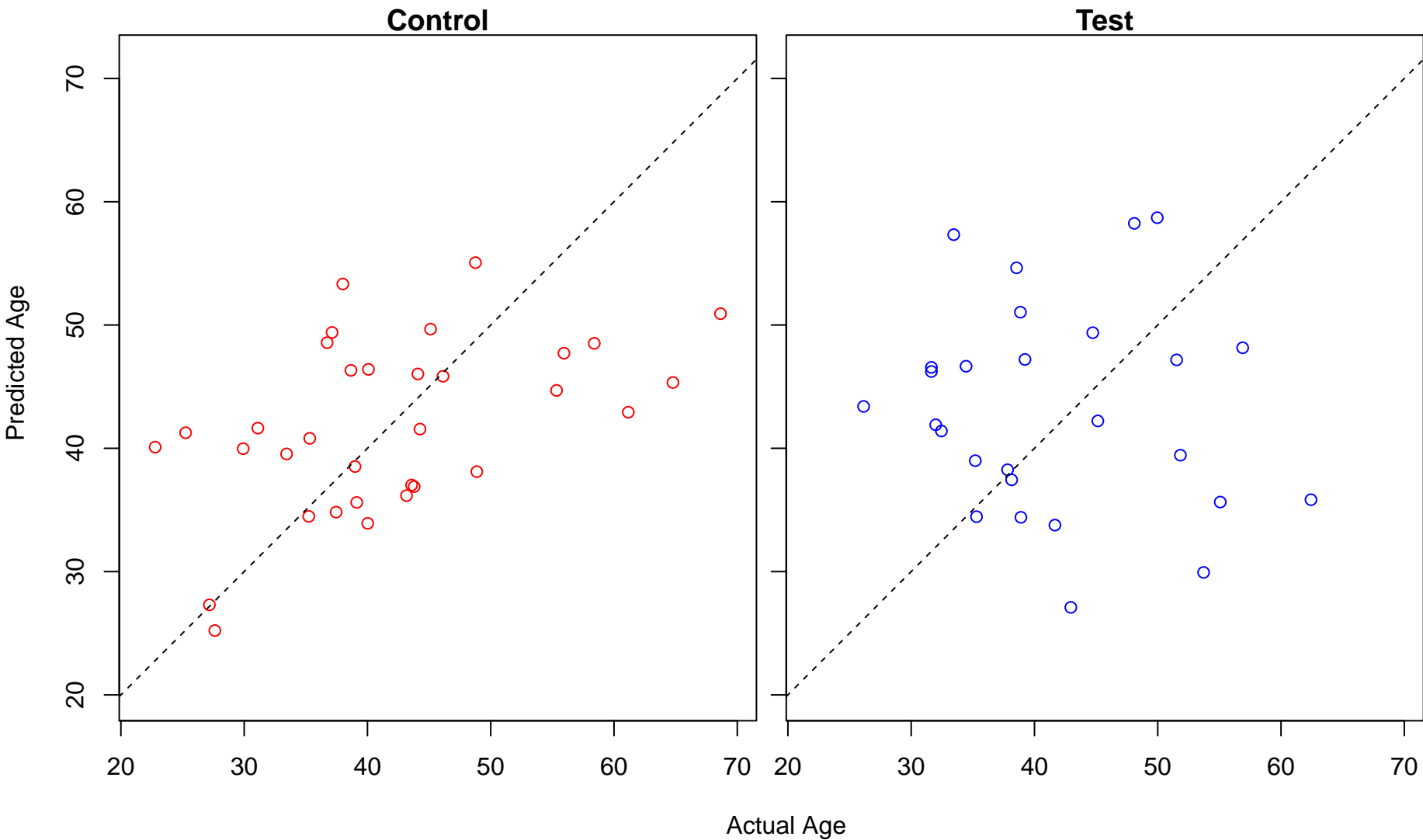
pulmonary valve morphogenesis (Score: 1.310727)



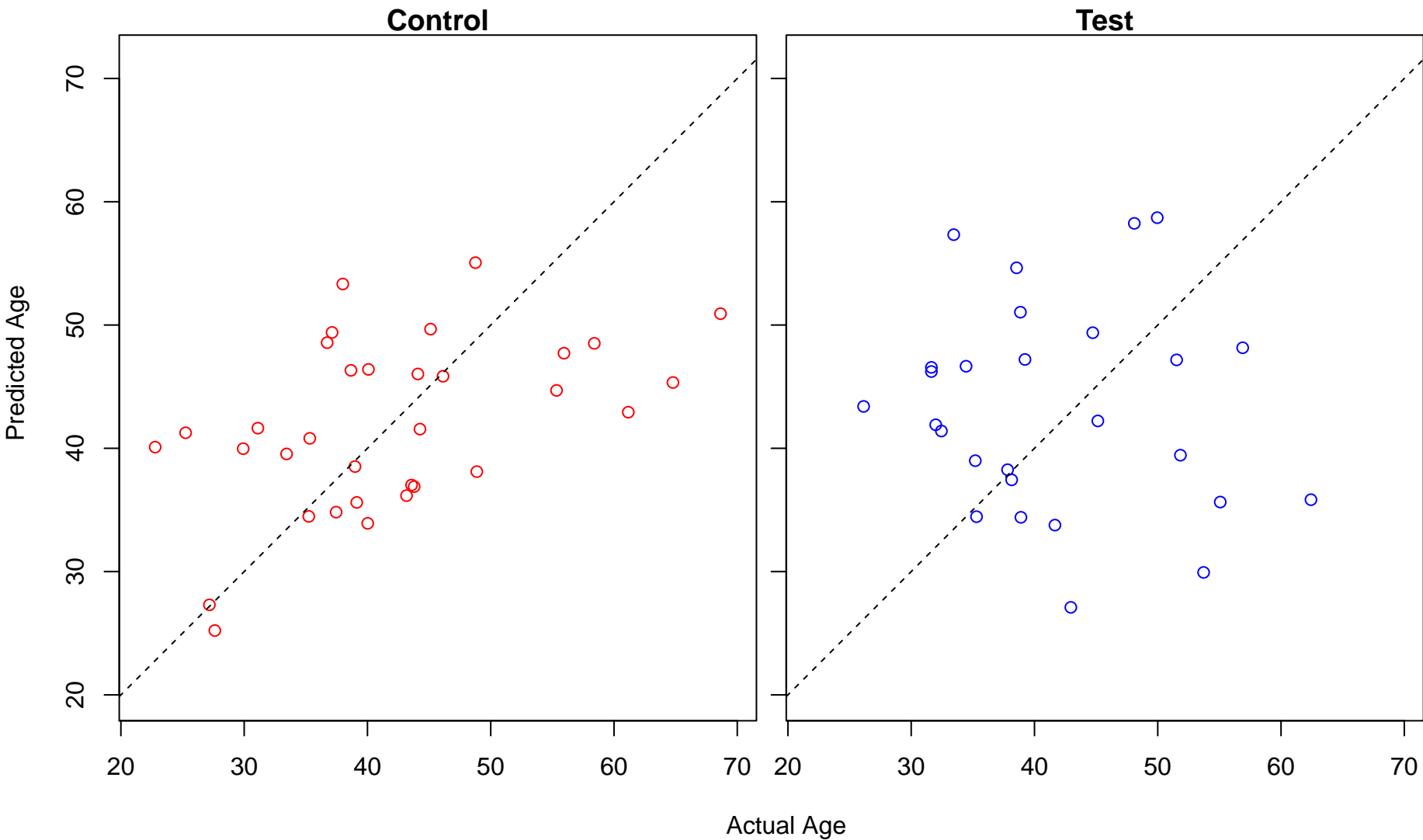
phosphatidylglycerol acyl-chain remodeling (Score: 1.308543)



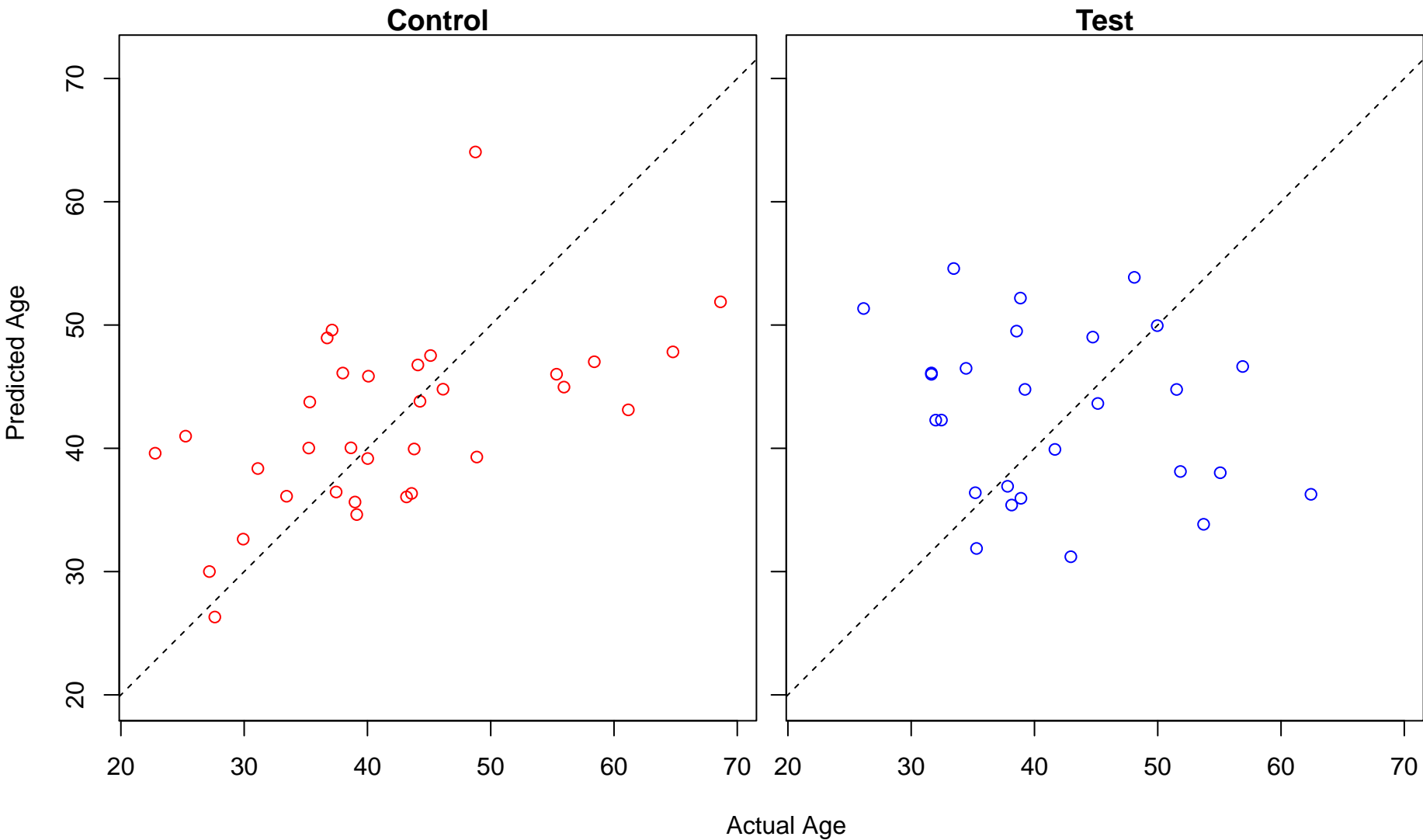
positive regulation of beta-amyloid formation (Score: 1.303425)



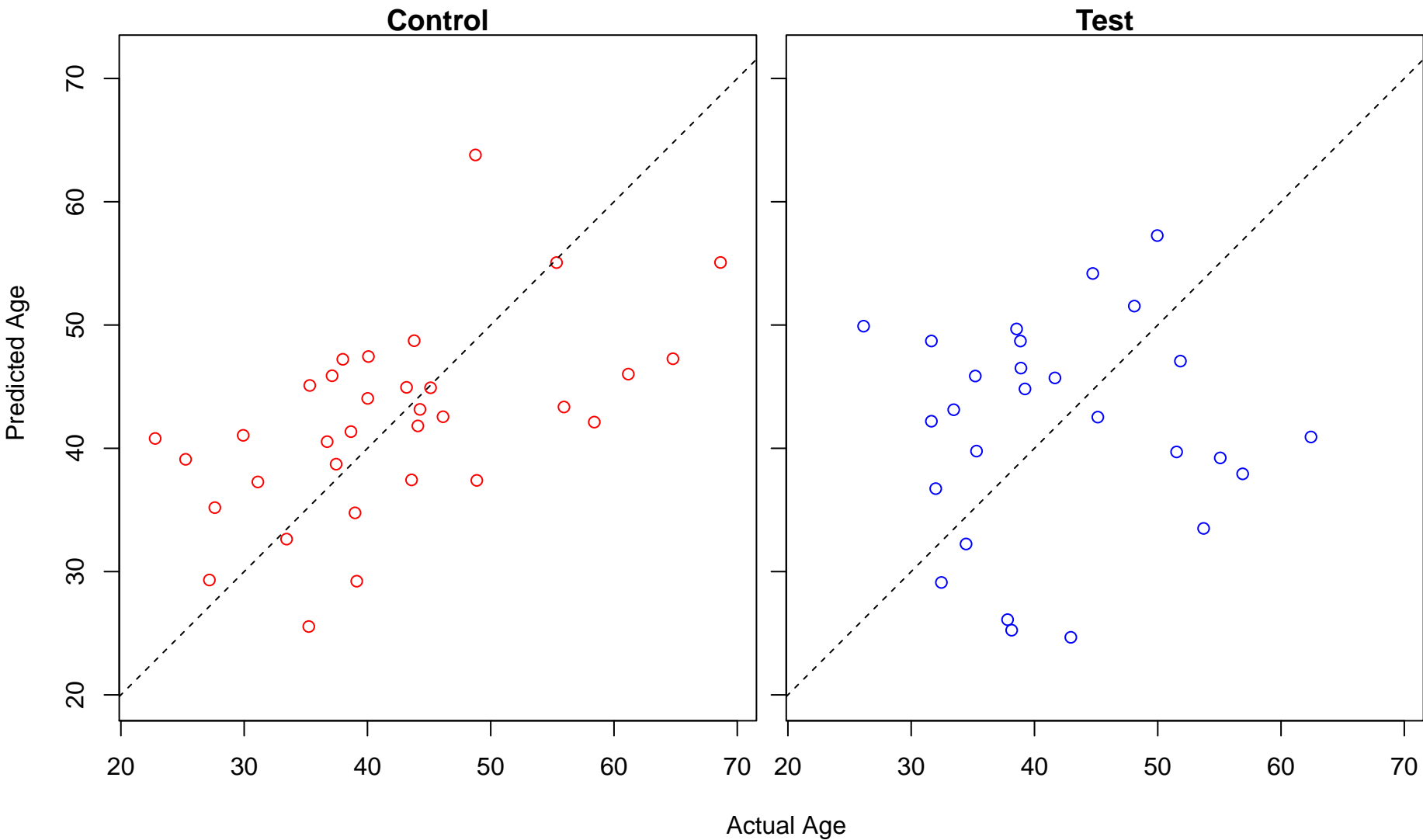
positive regulation of amyloid precursor protein catabolic process (Score: 1.303425)



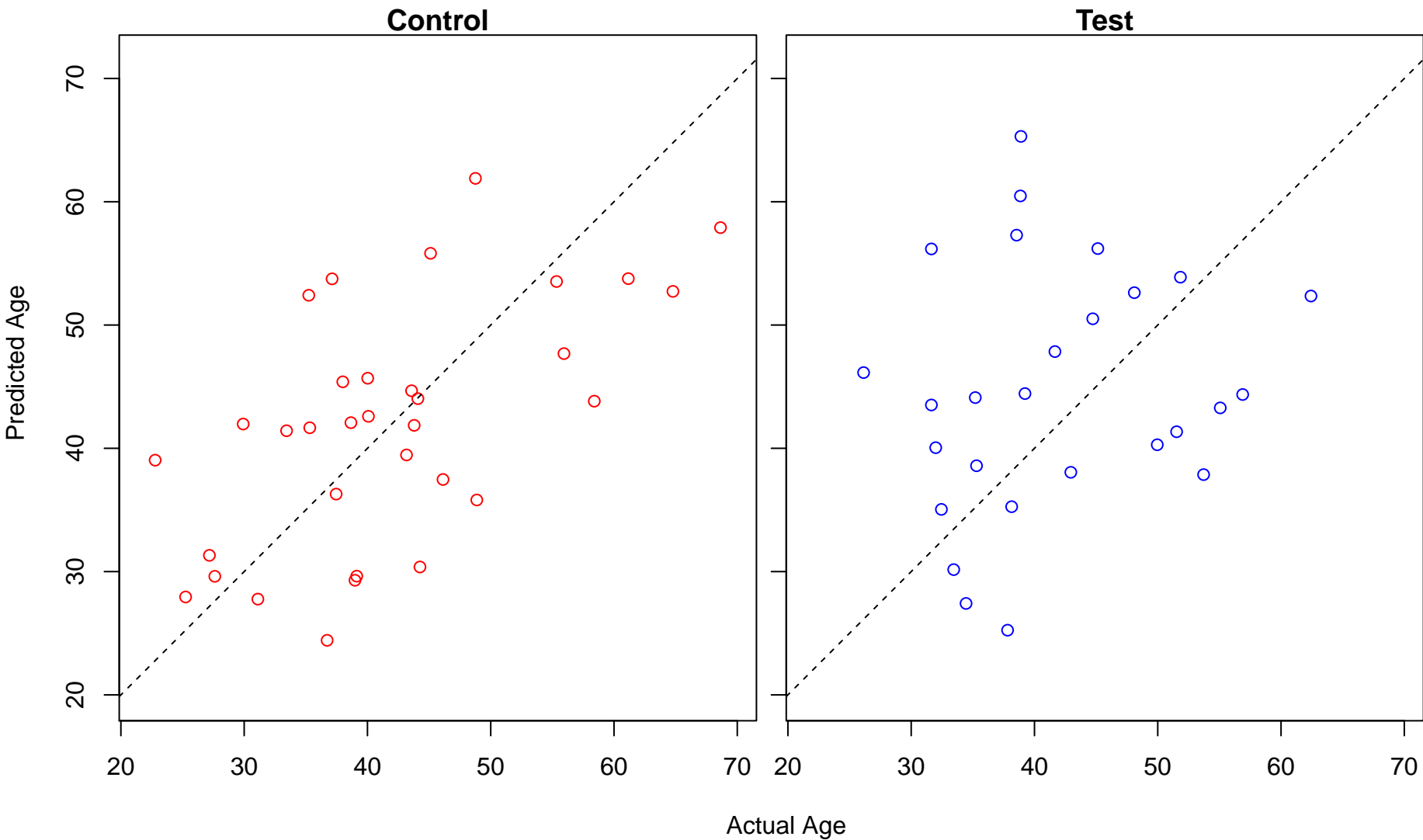
negative regulation of protein oligomerization (Score: 1.298104)



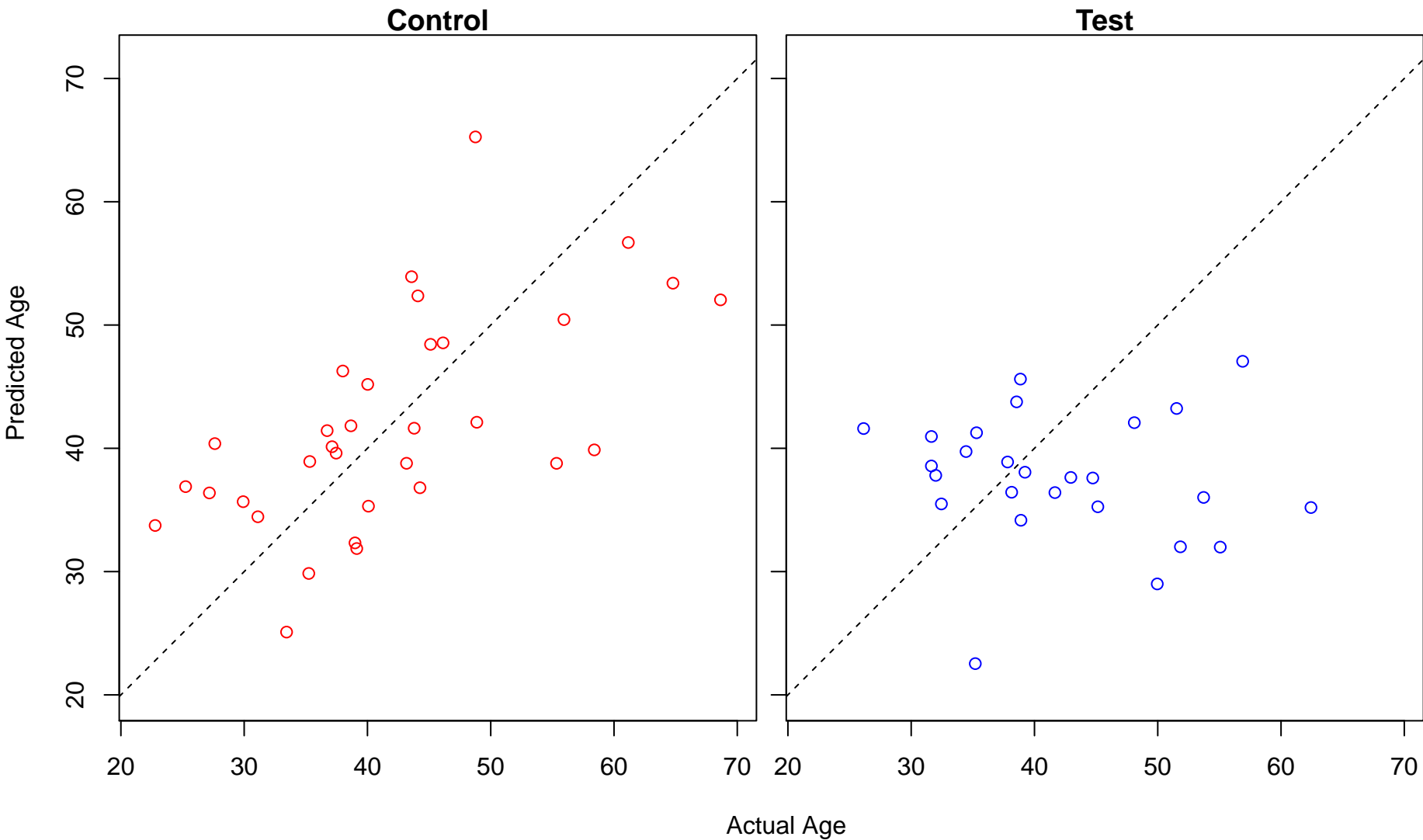
response to radiation (Score: 1.293679)



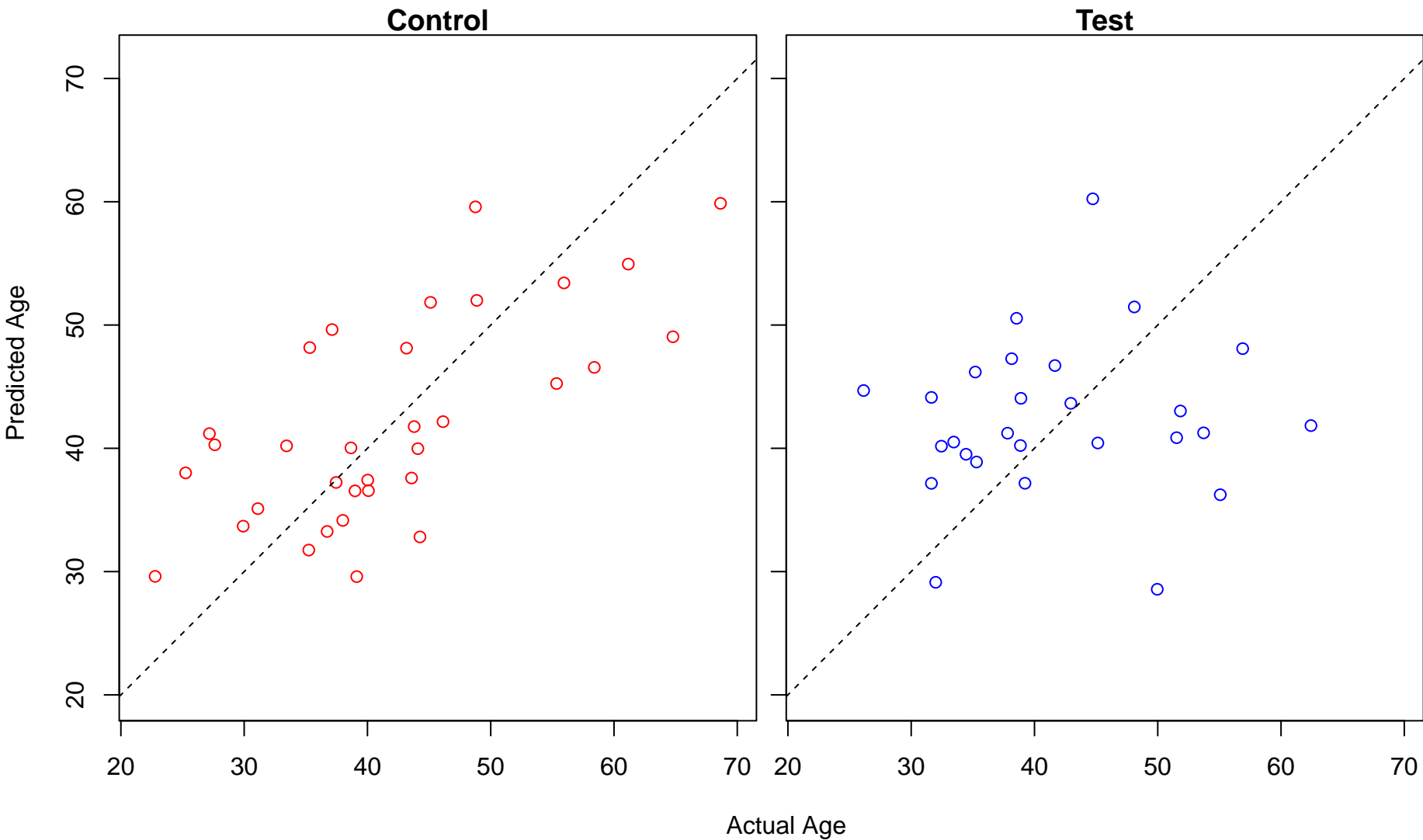
detection of mechanical stimulus (Score: 1.290472)



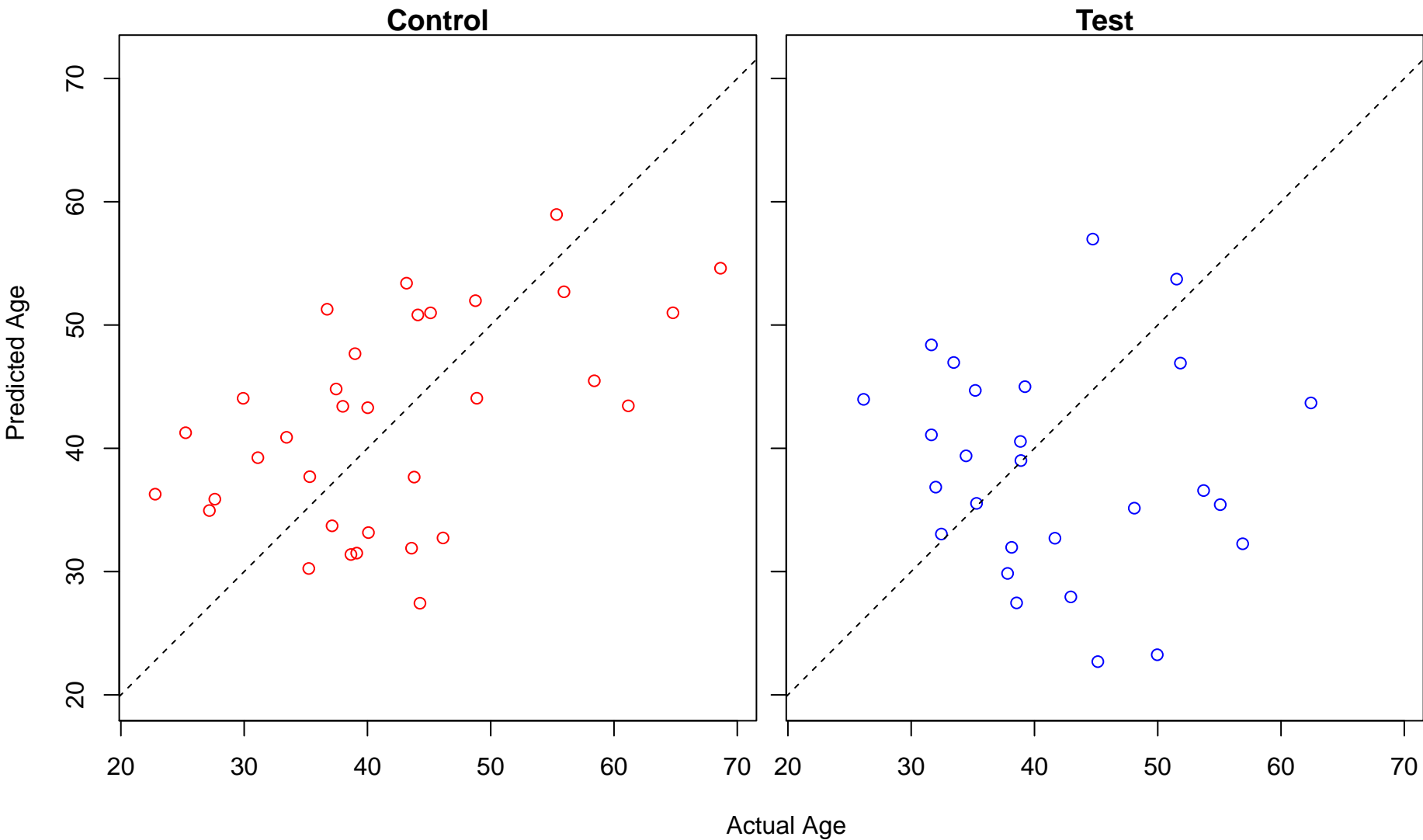
positive regulation of focal adhesion assembly (Score: 1.288197)



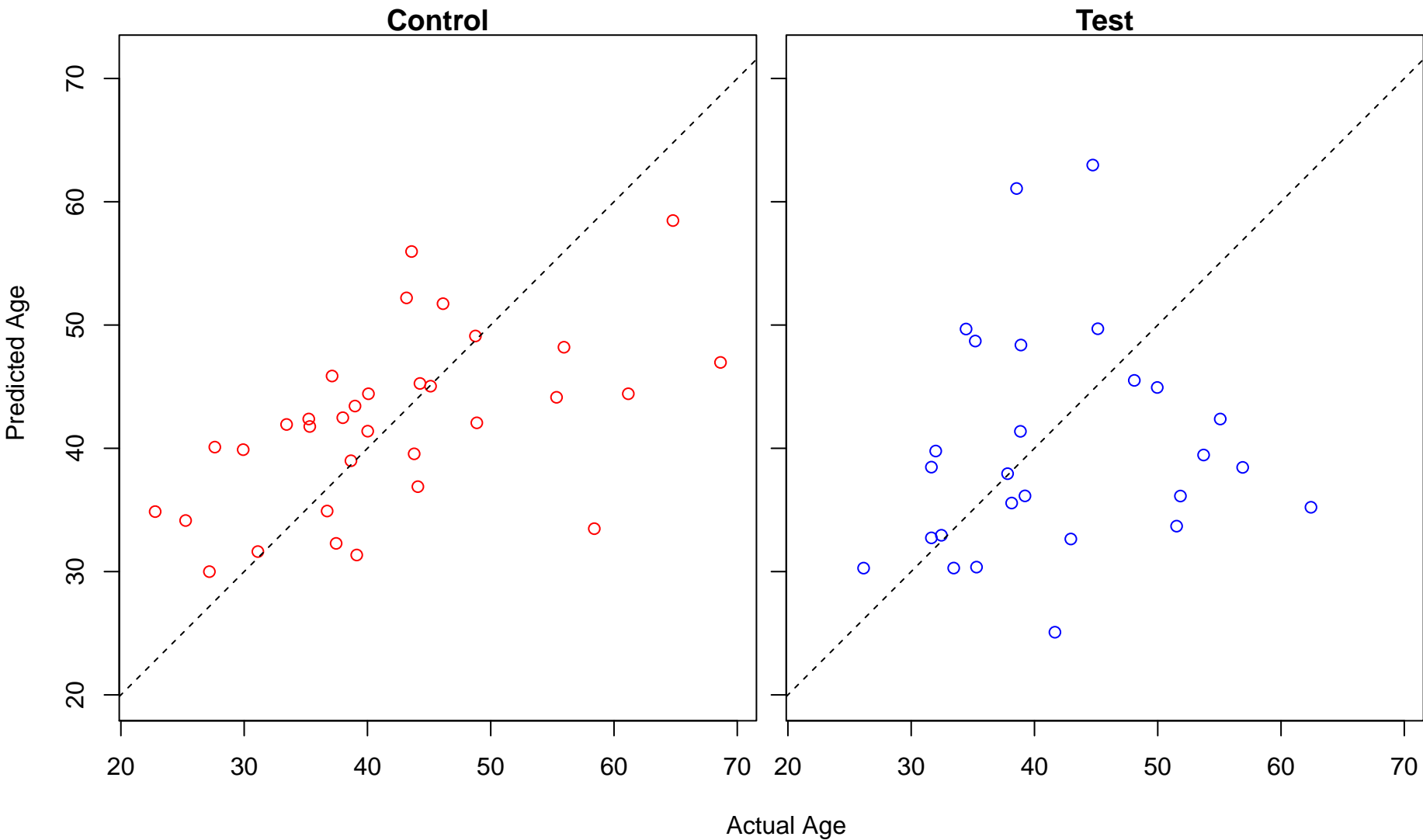
locomotor rhythm (Score: 1.275530)



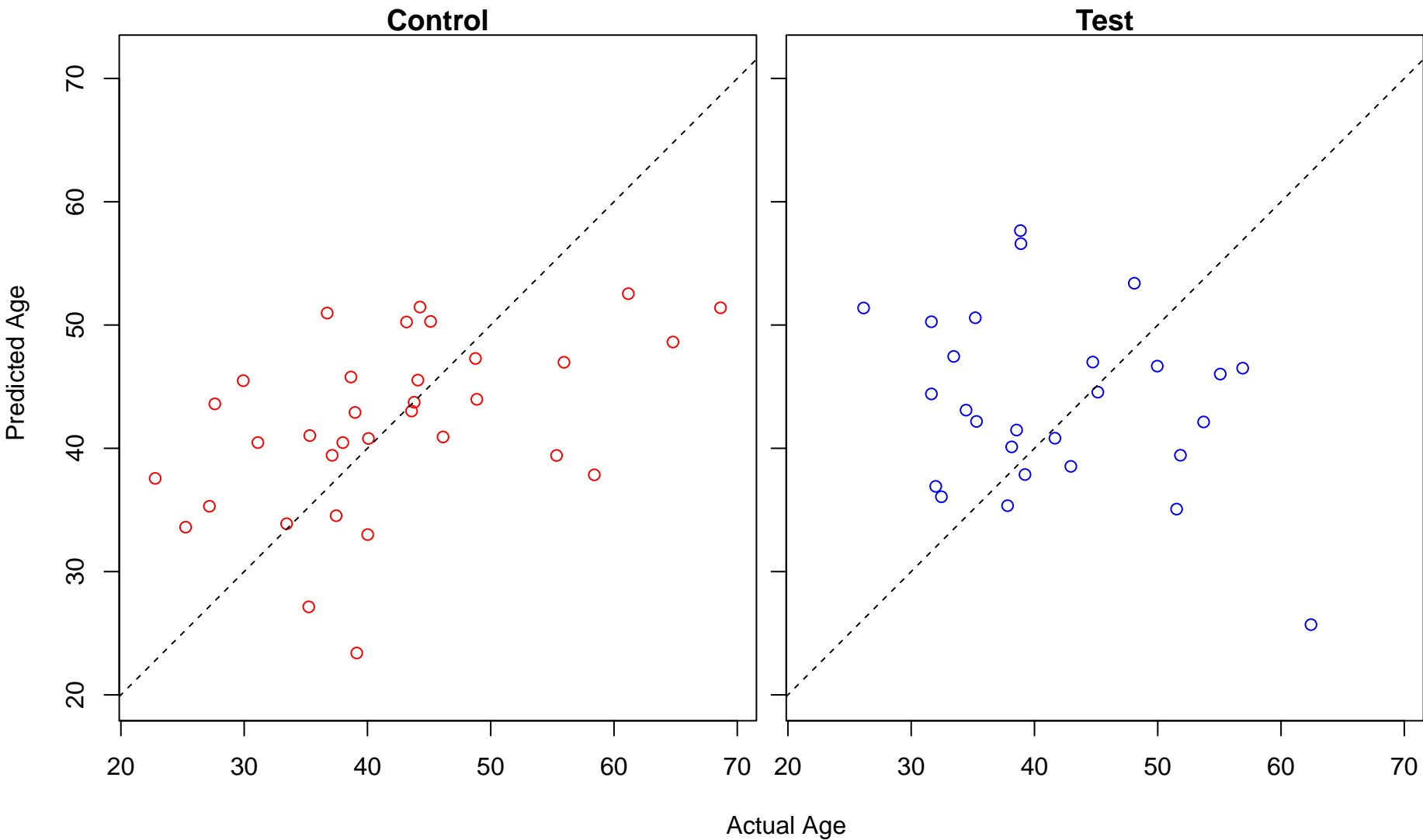
retinal metabolic process (Score: 1.274115)



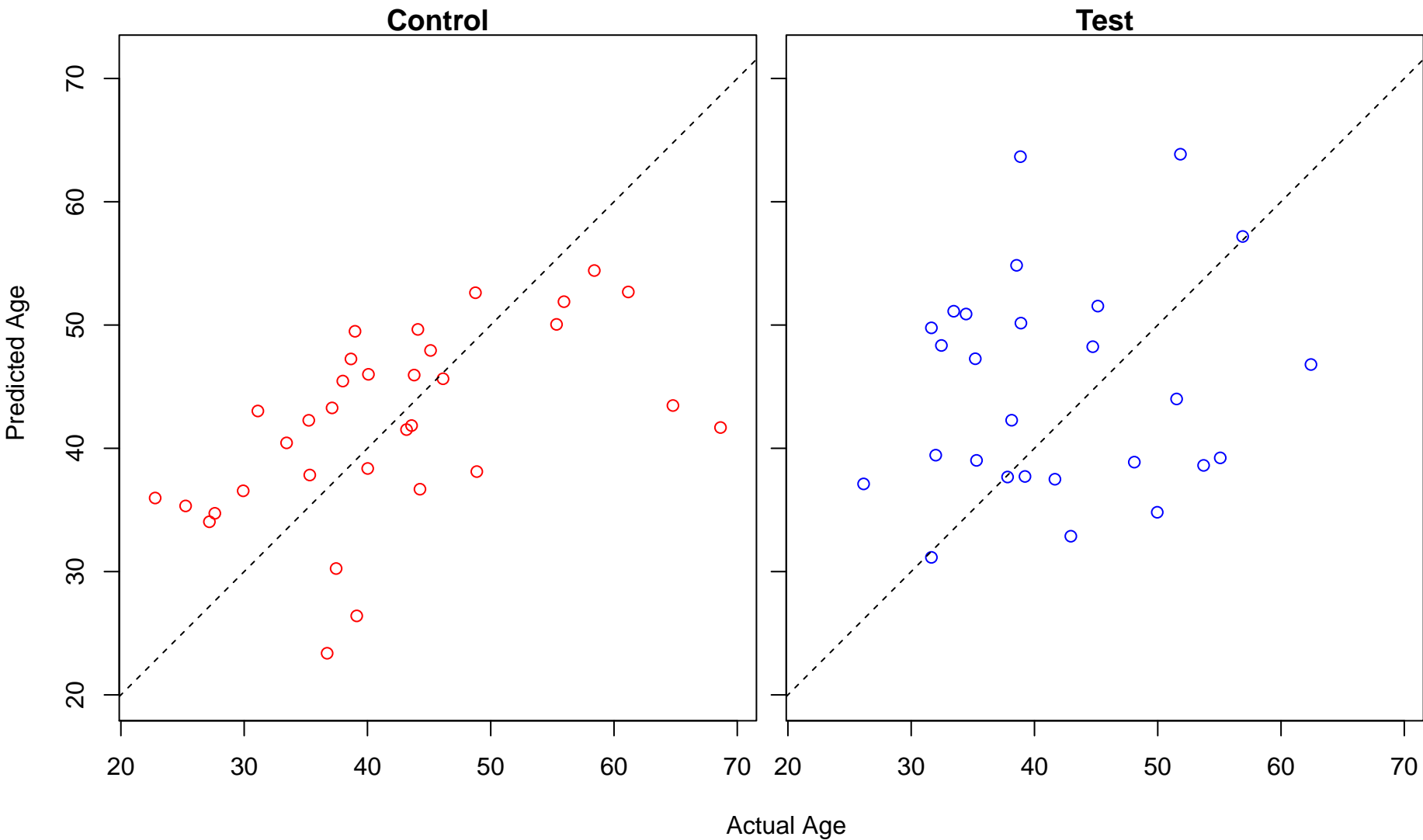
receptor guanylyl cyclase signaling pathway (Score: 1.271069)



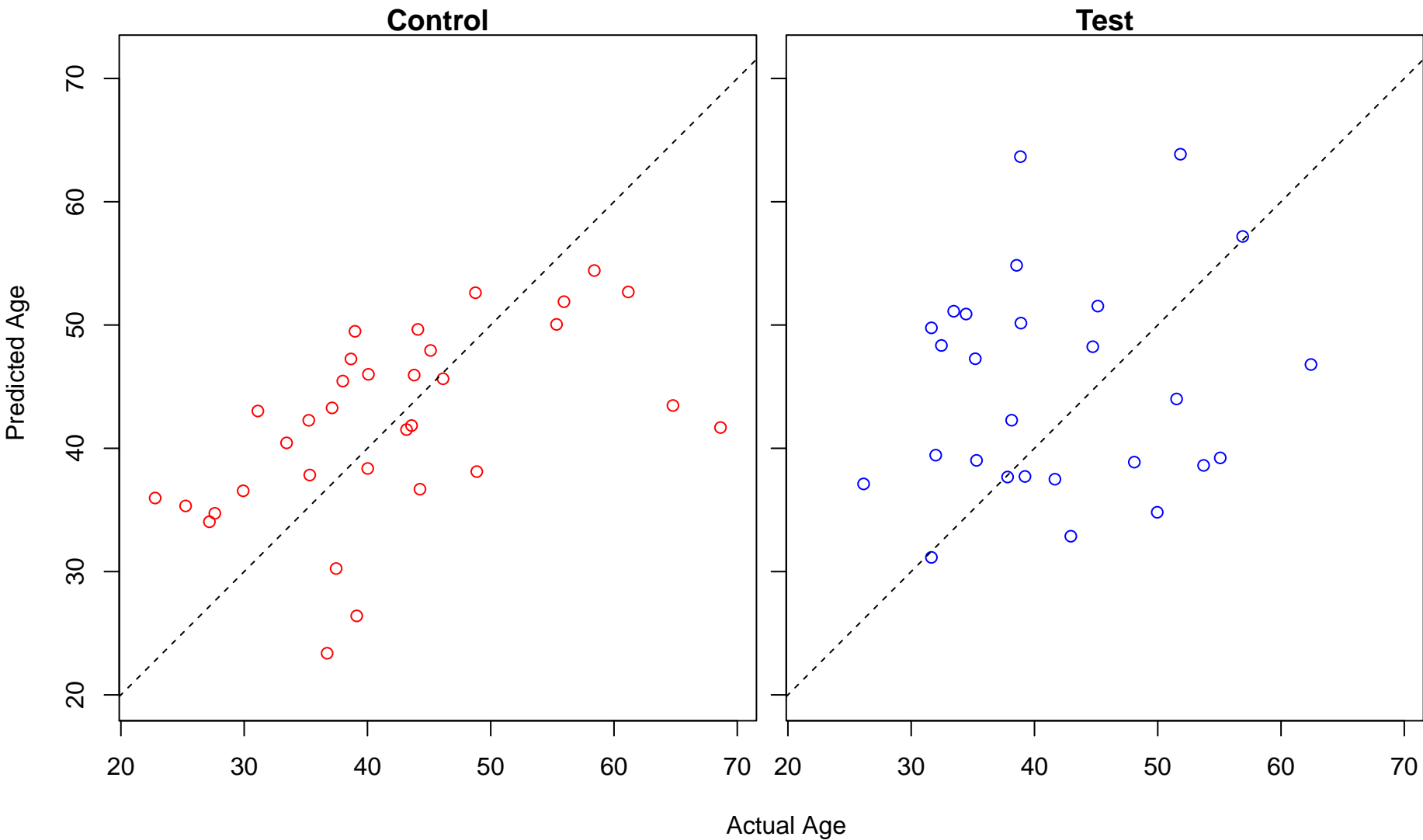
alkaloid metabolic process (Score: 1.267085)



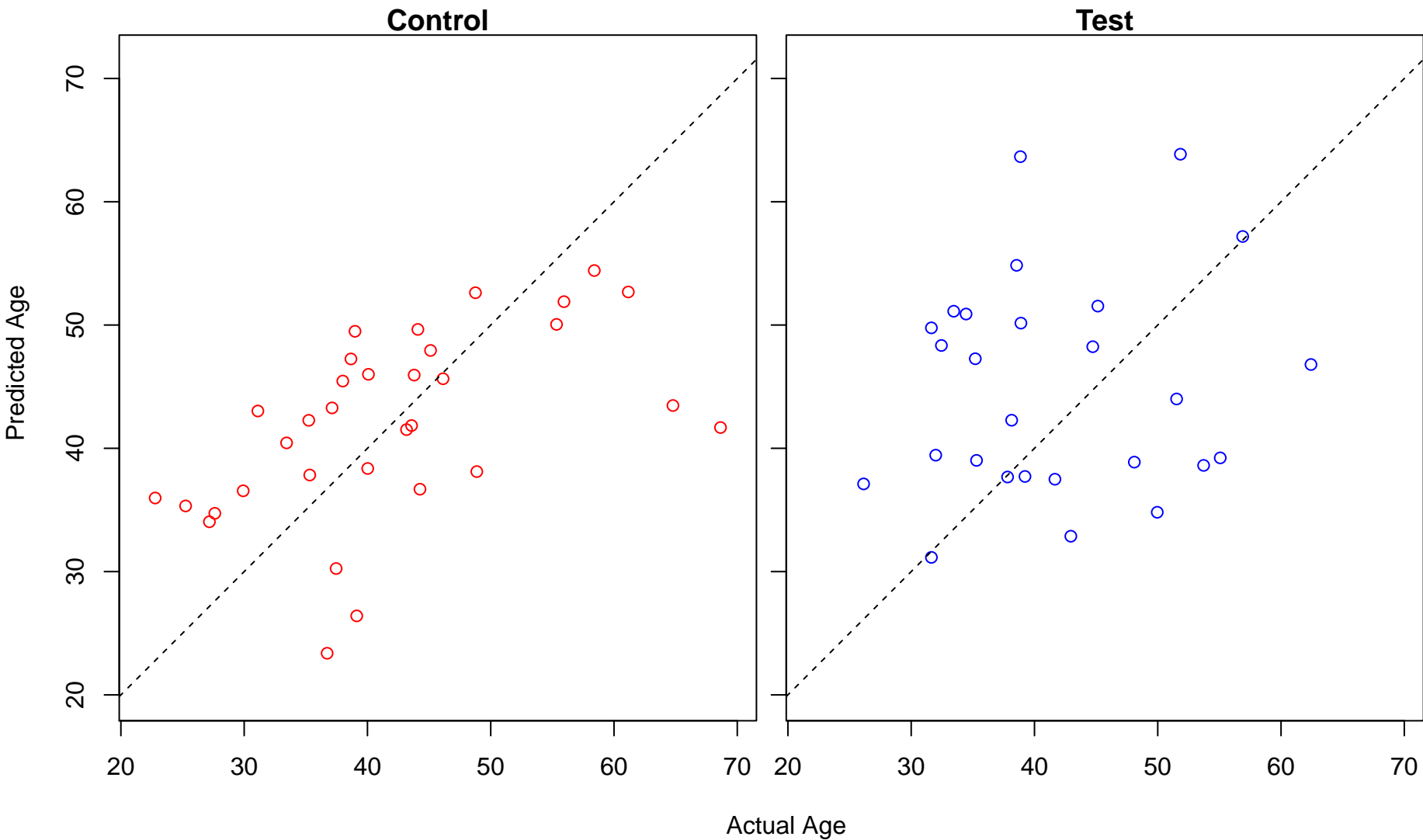
response to caffeine (Score: 1.266047)



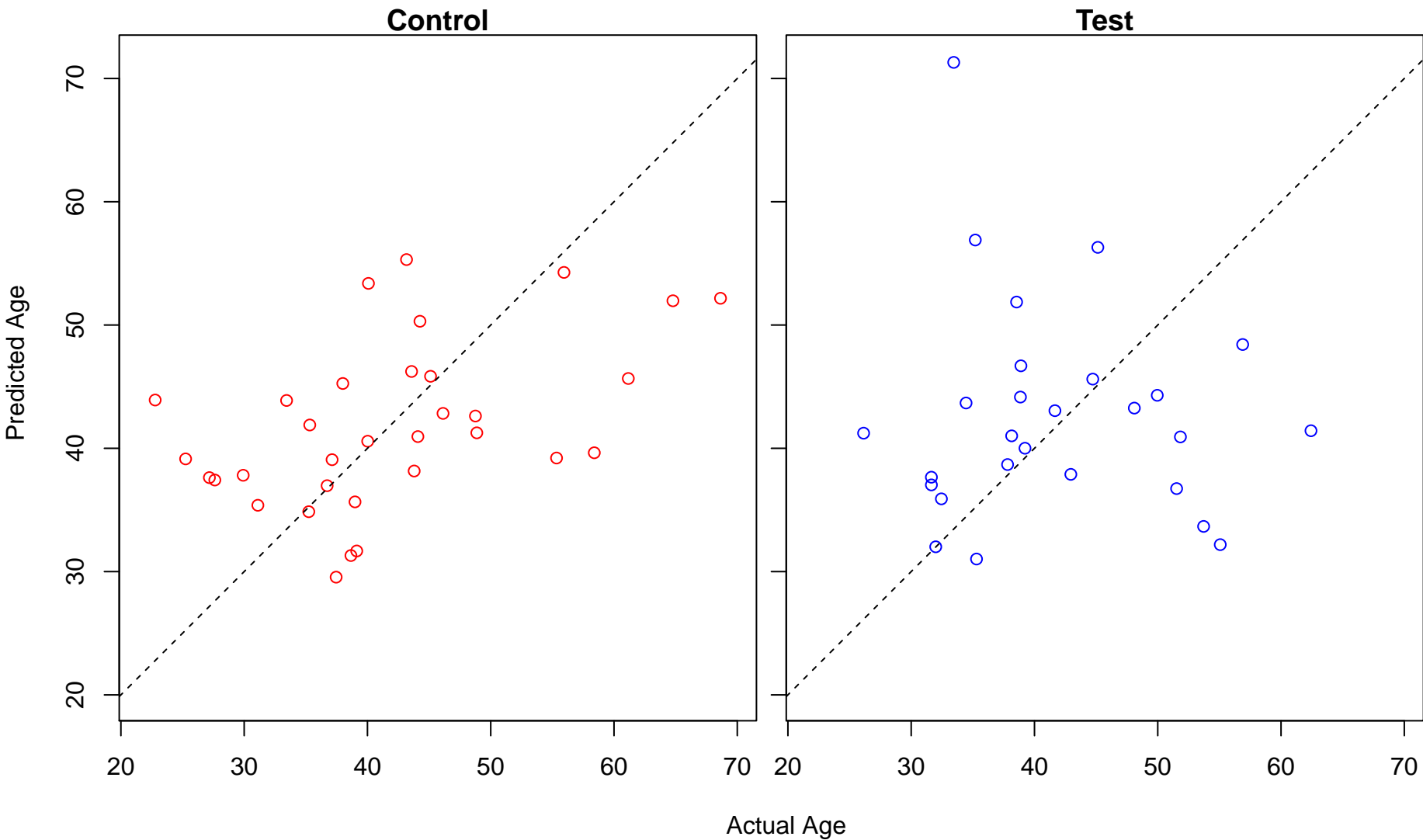
cellular response to caffeine (Score: 1.266047)



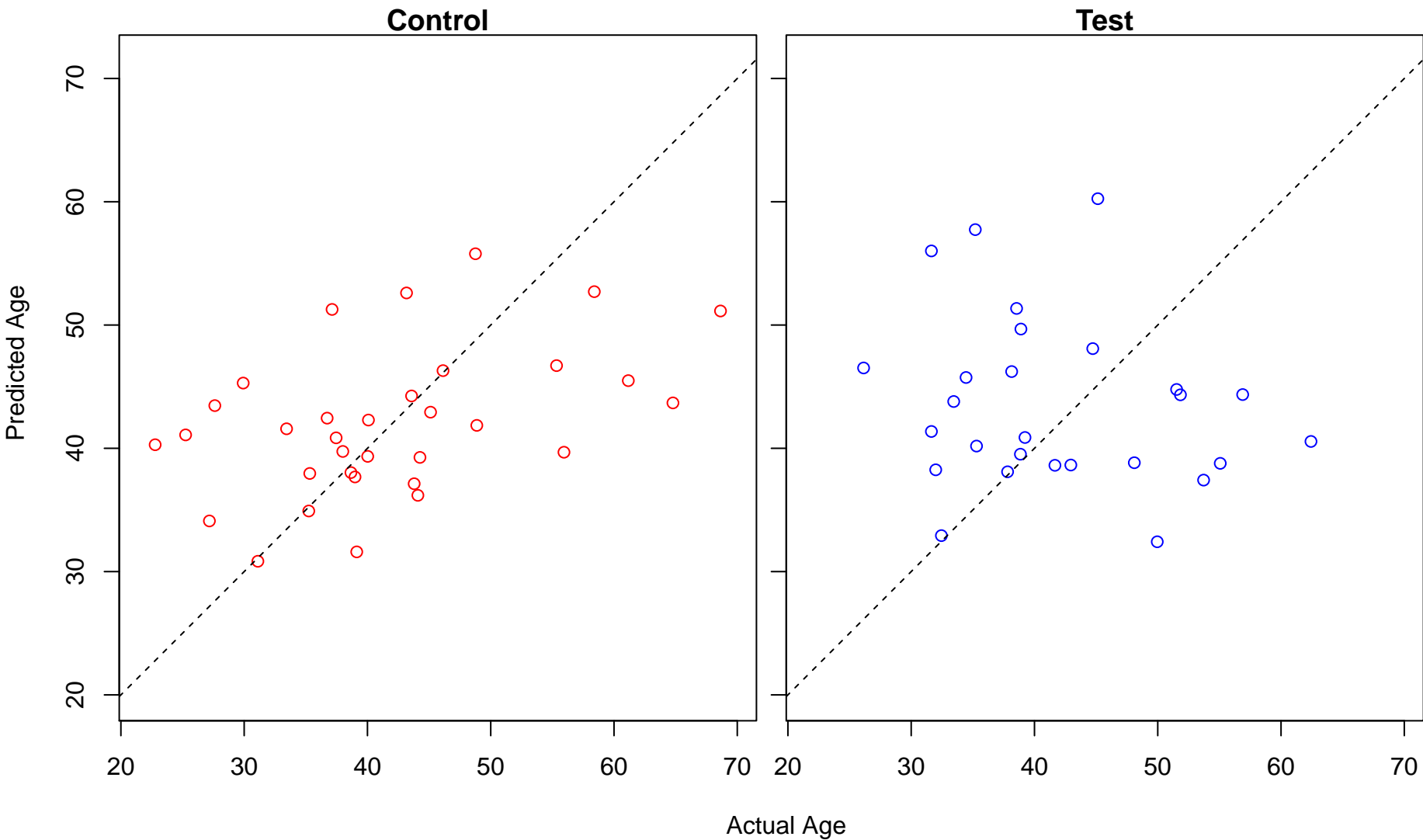
cellular response to purine-containing compound (Score: 1.266047)



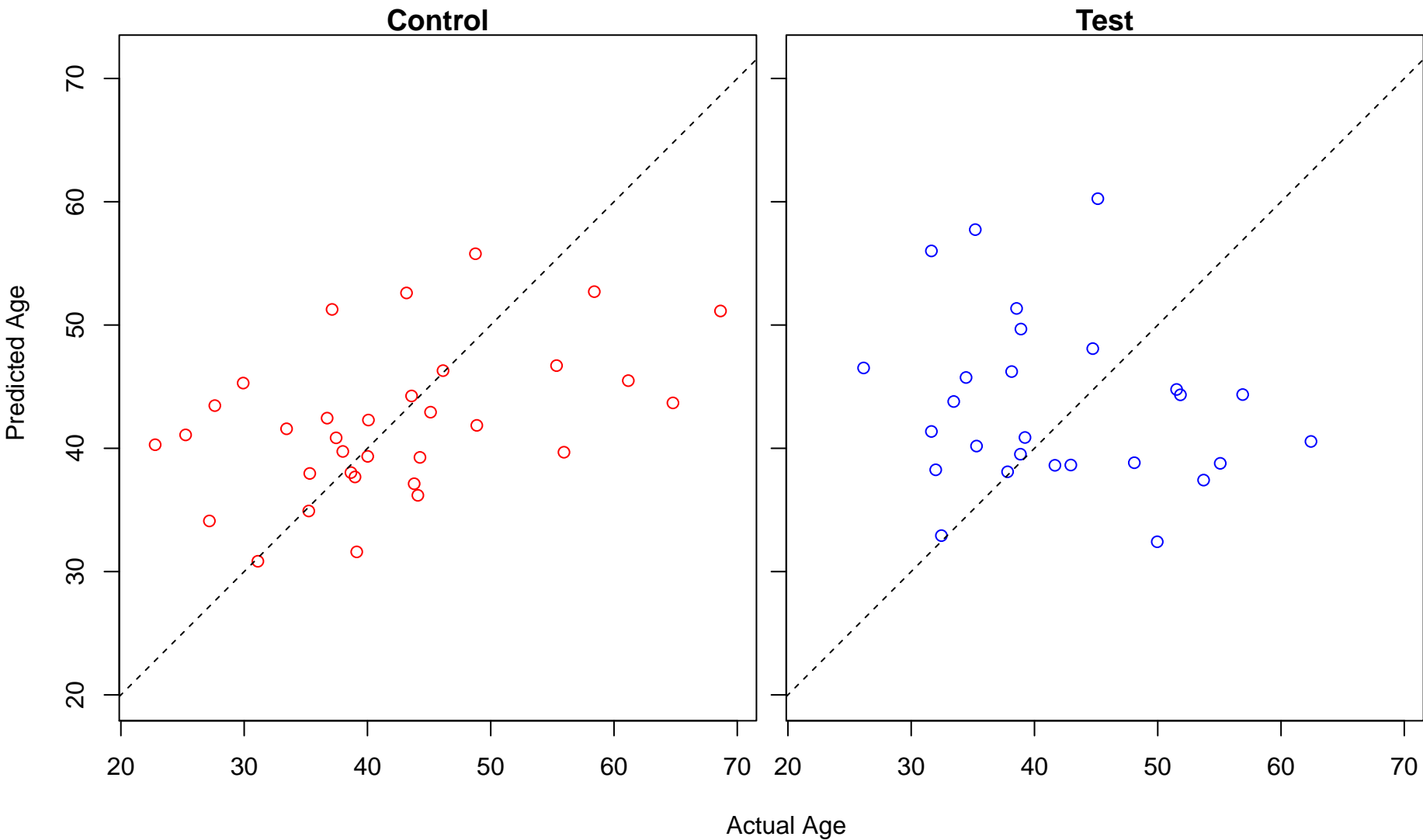
heterochromatin assembly (Score: 1.265481)



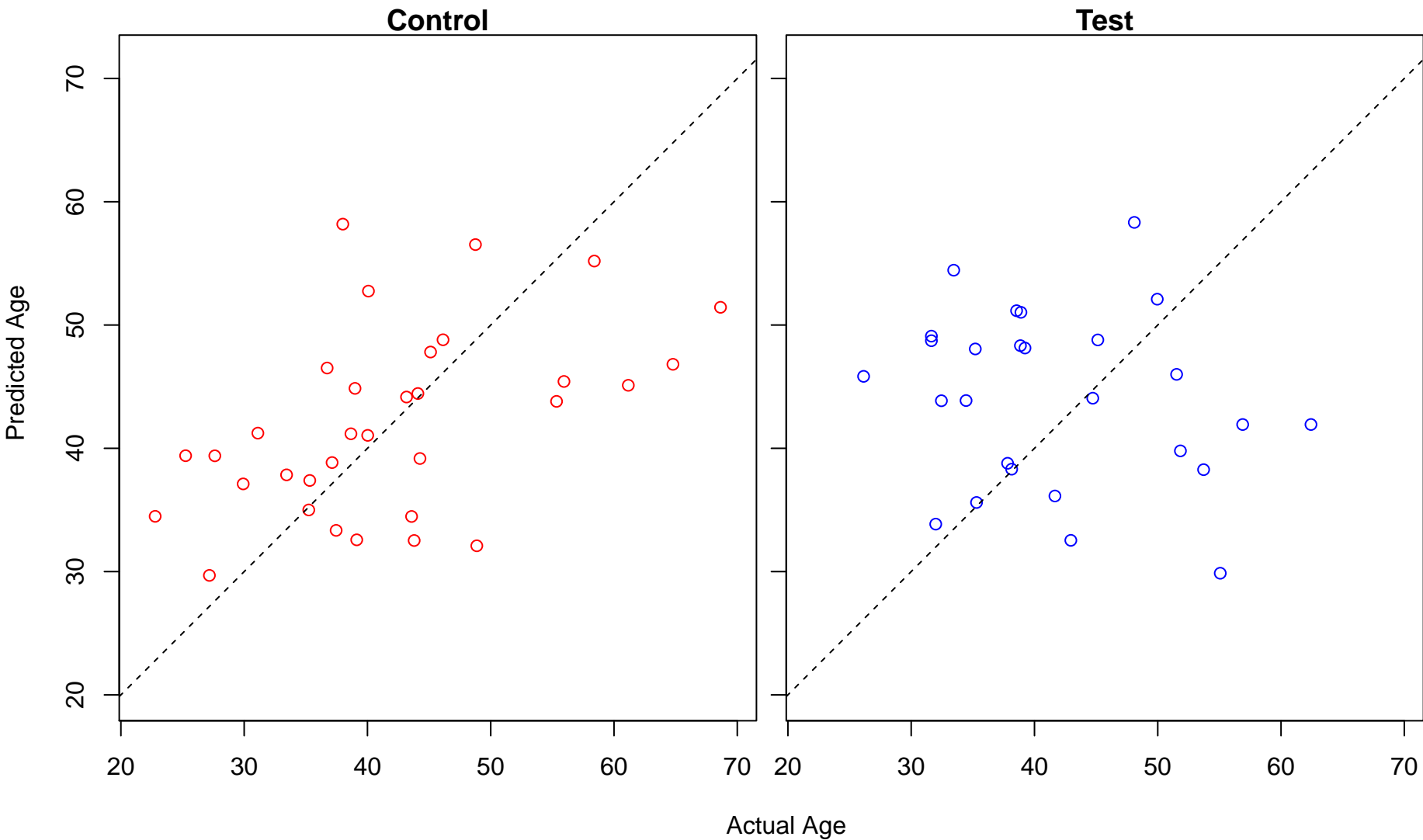
response to potassium ion (Score: 1.264975)



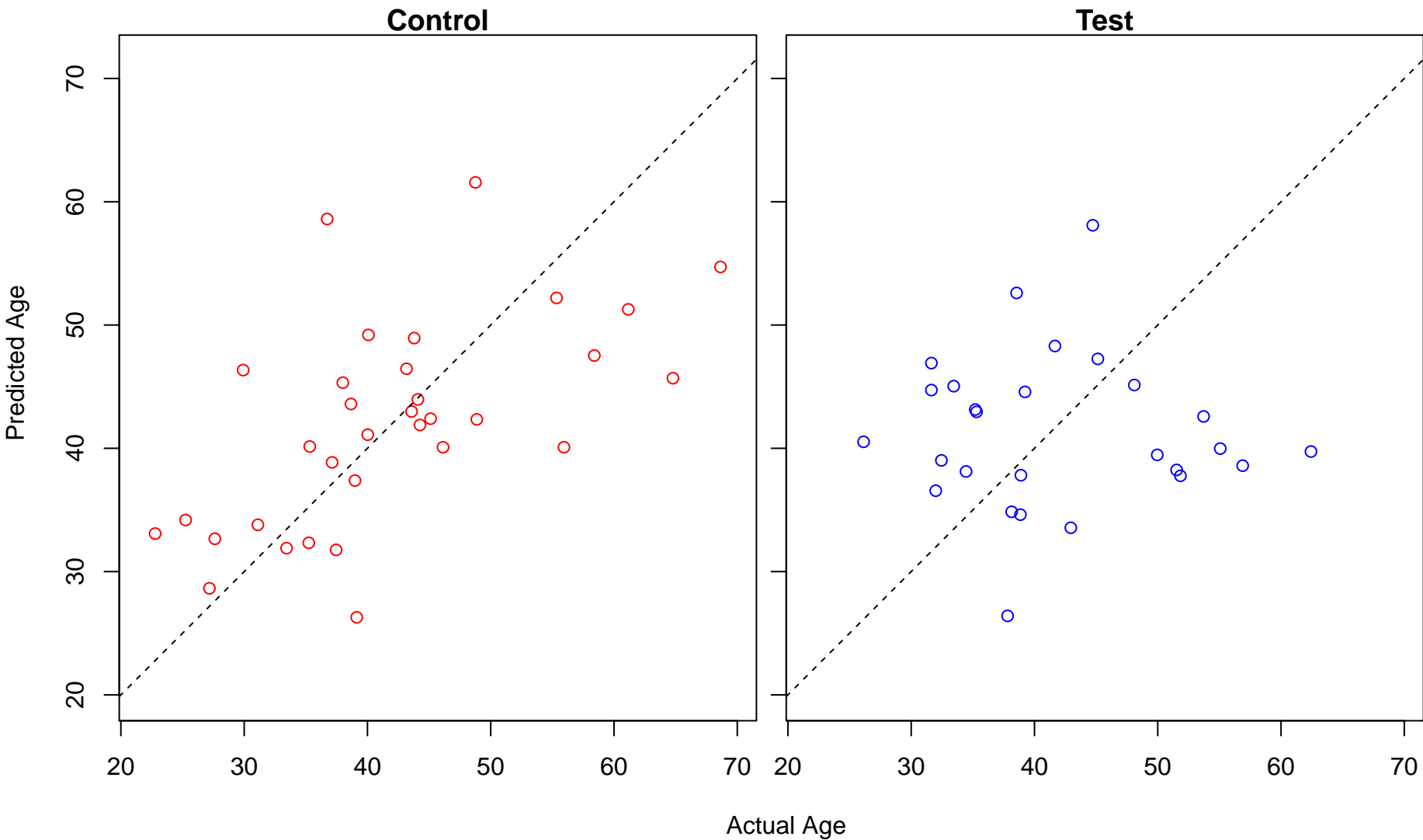
cellular response to potassium ion (Score: 1.264975)



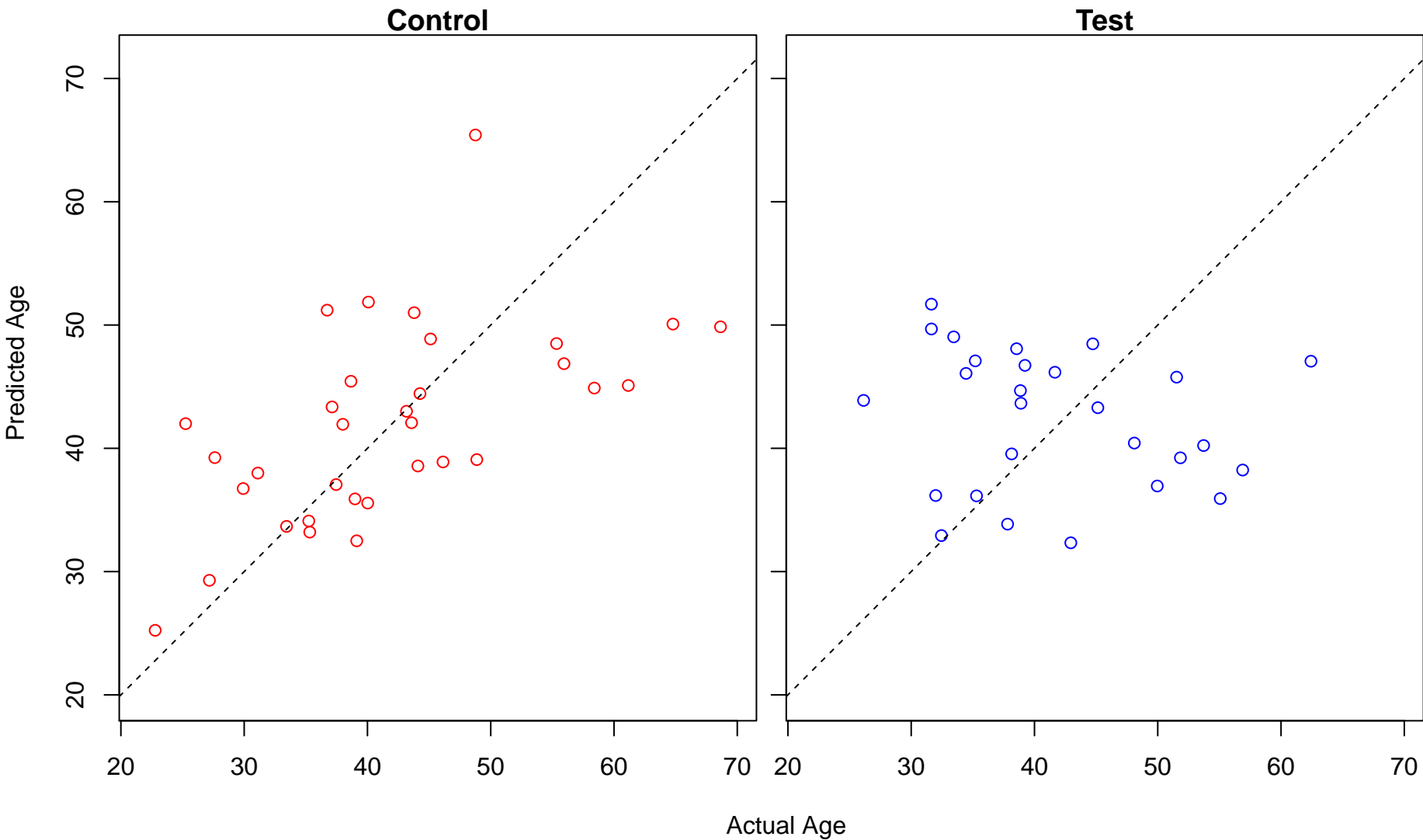
cGMP-mediated signaling (Score: 1.259372)



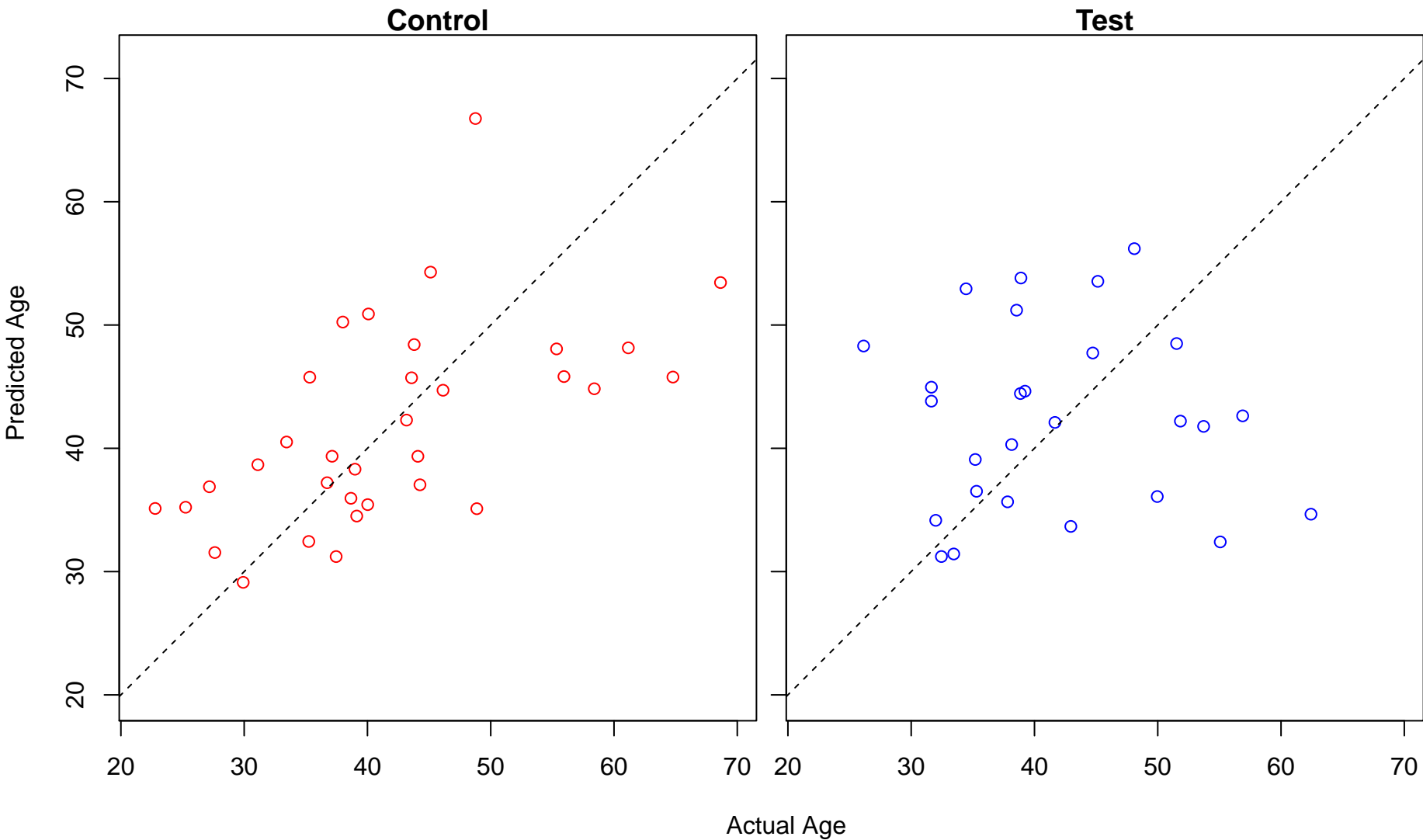
response to tumor necrosis factor (Score: 1.251839)



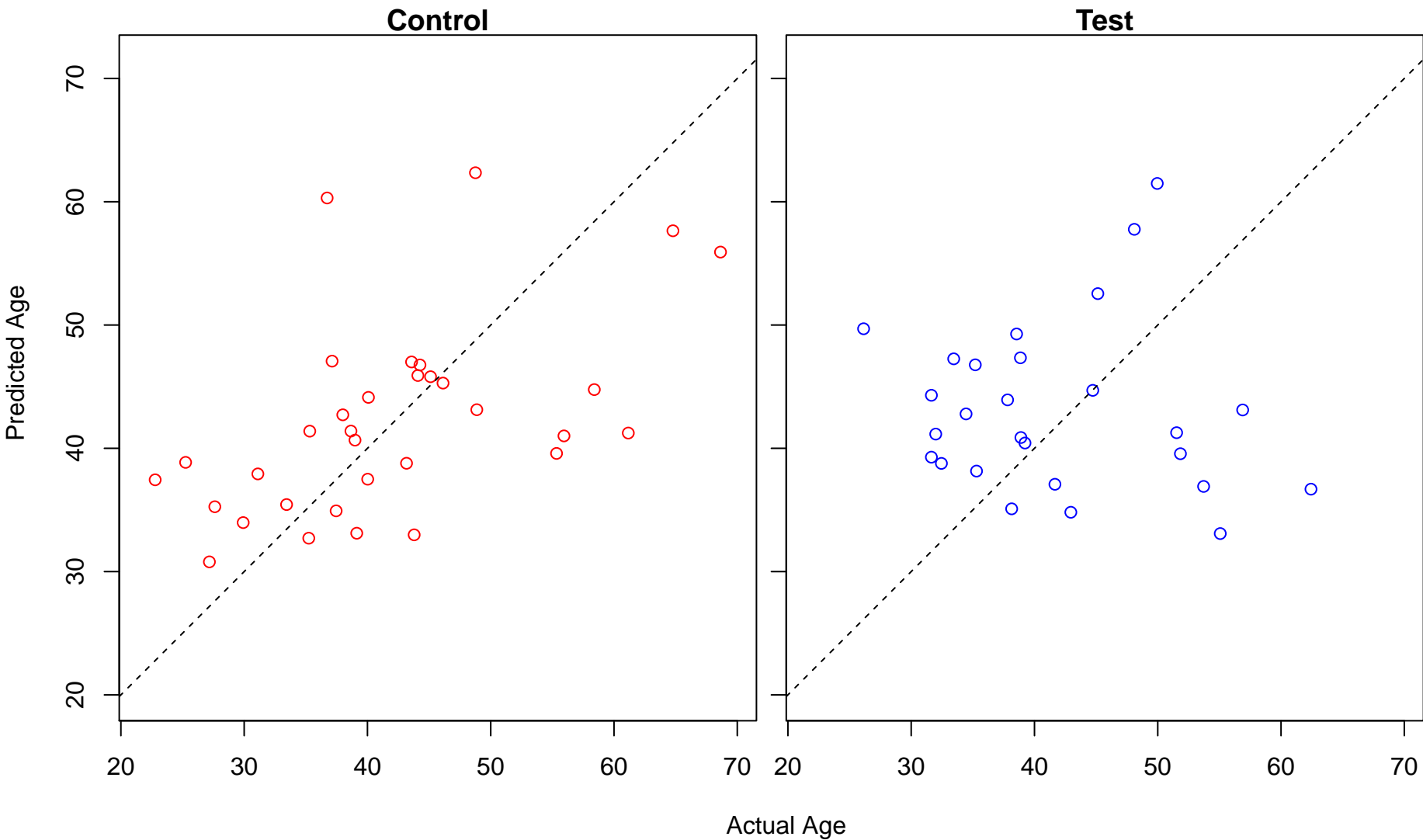
organic hydroxy compound metabolic process (Score: 1.251185)



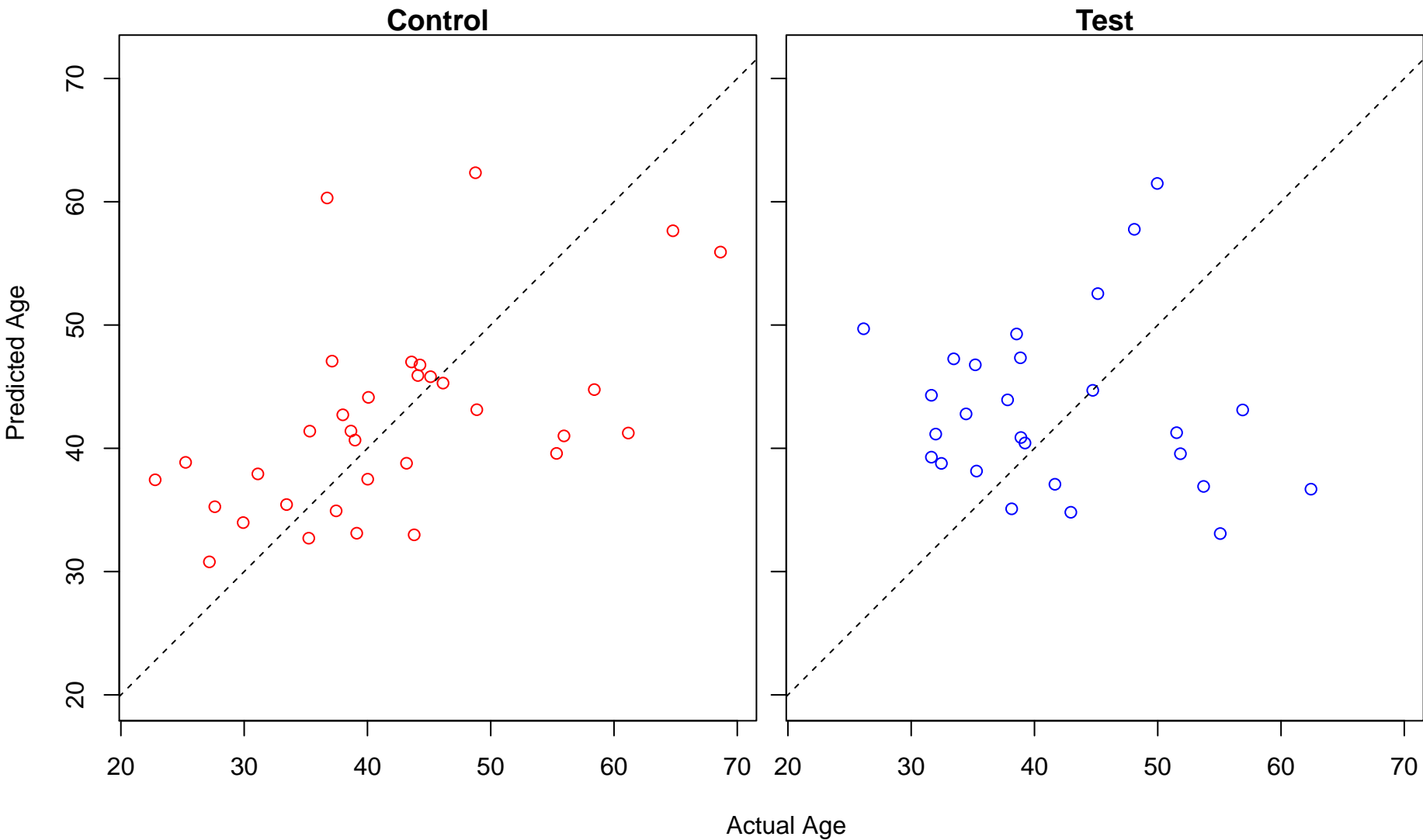
snRNA transcription from RNA polymerase II promoter (Score: 1.248734)



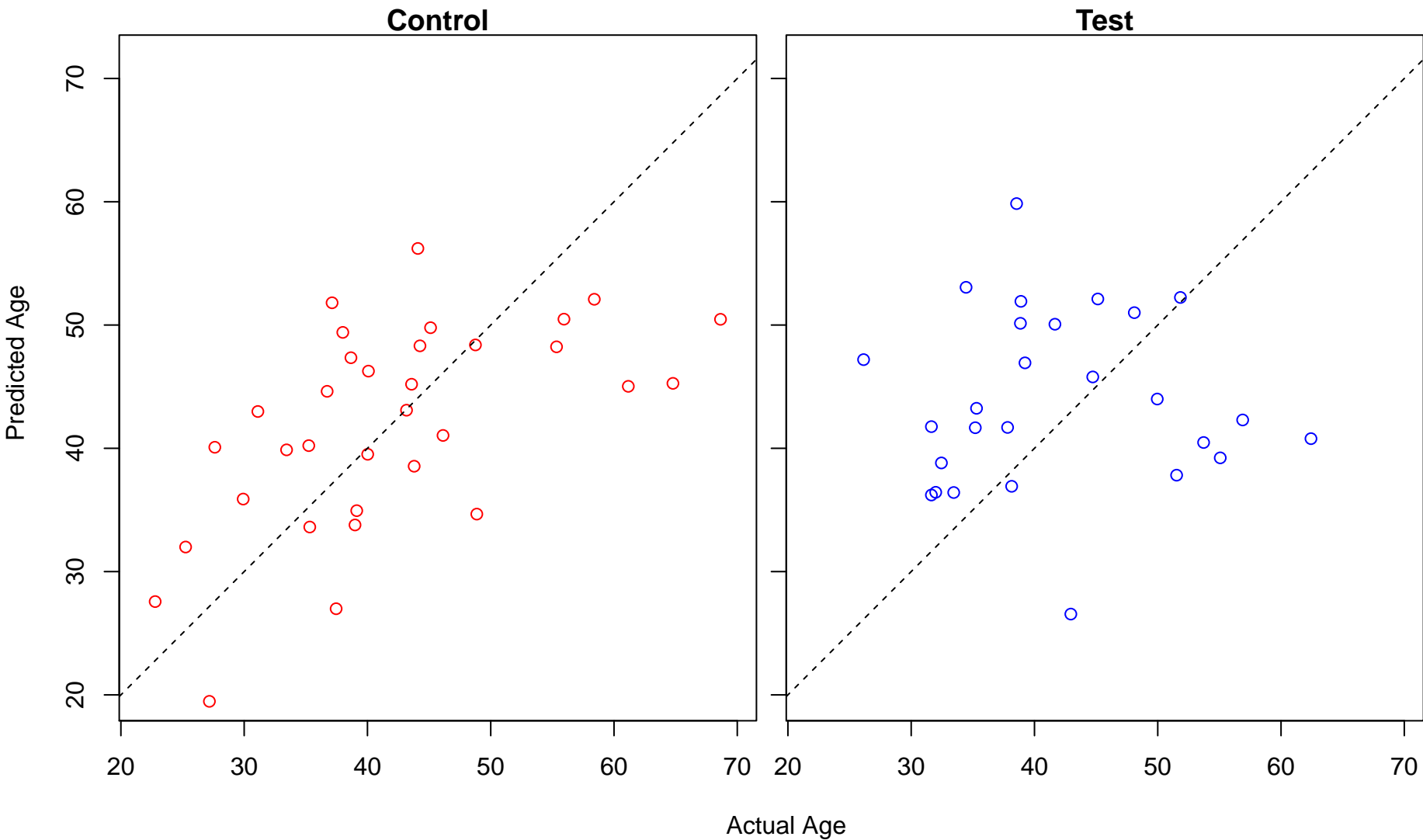
cellular response to nitric oxide (Score: 1.24731)



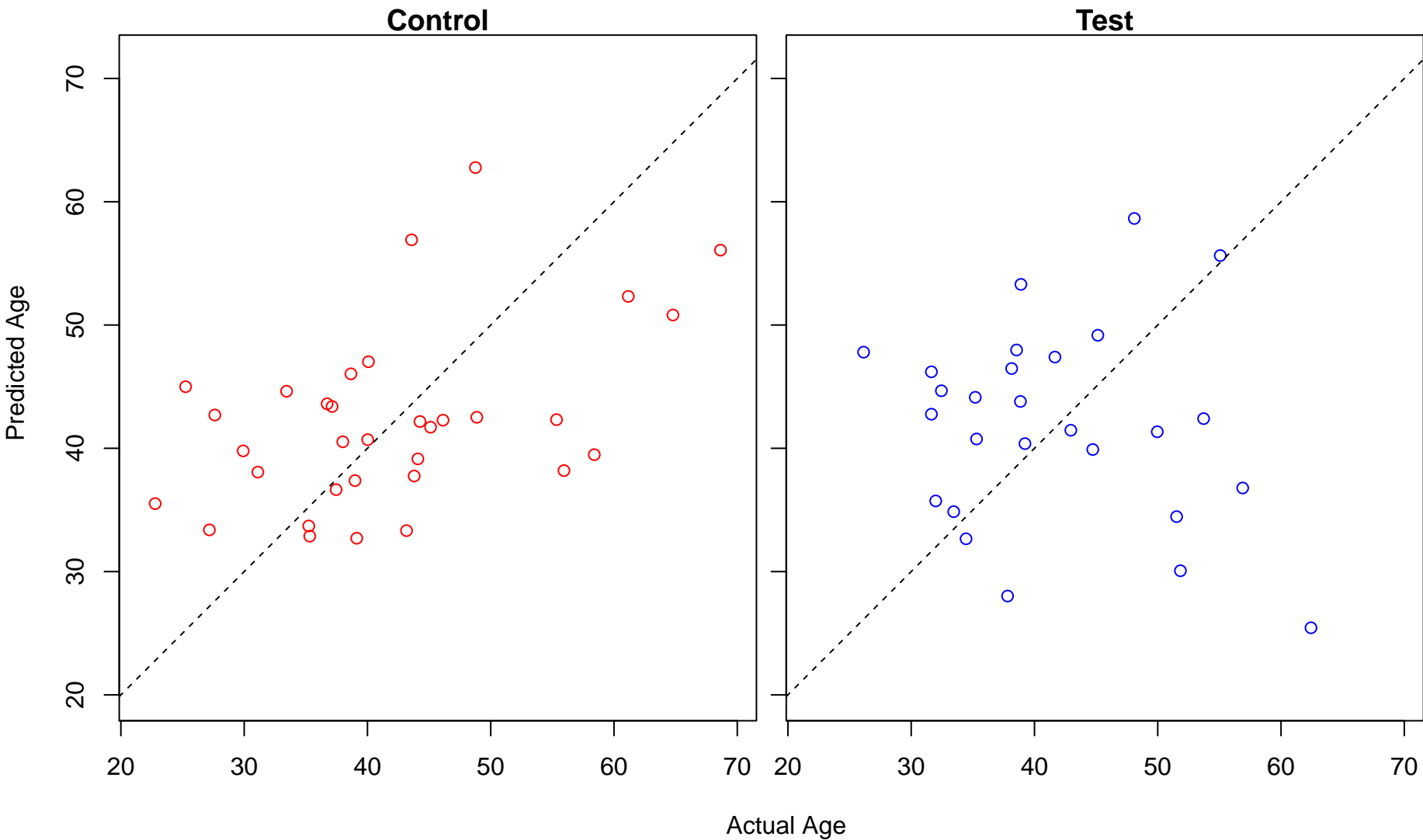
cellular response to reactive nitrogen species (Score: 1.243731)



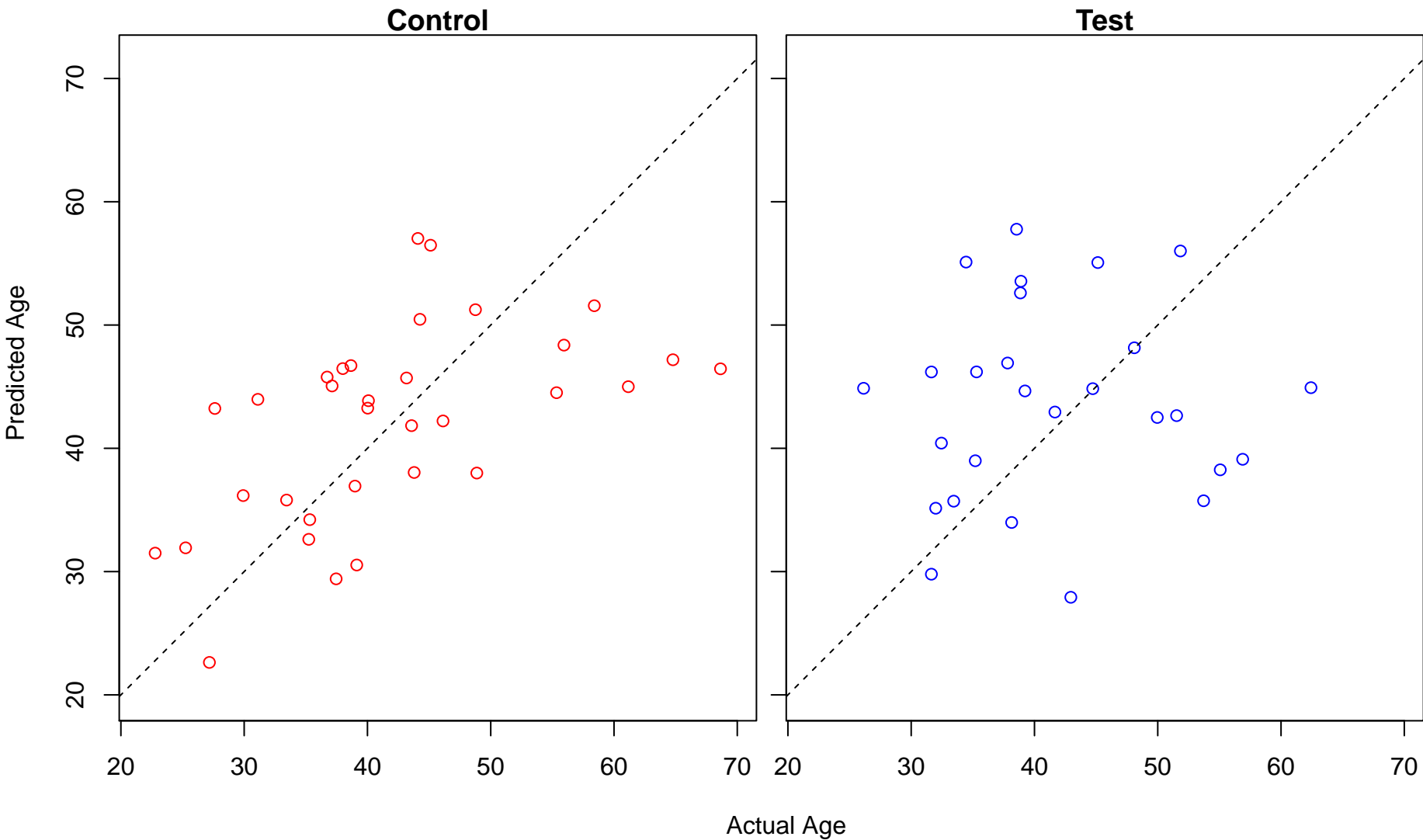
vasoconstriction (Score: 1.243555)



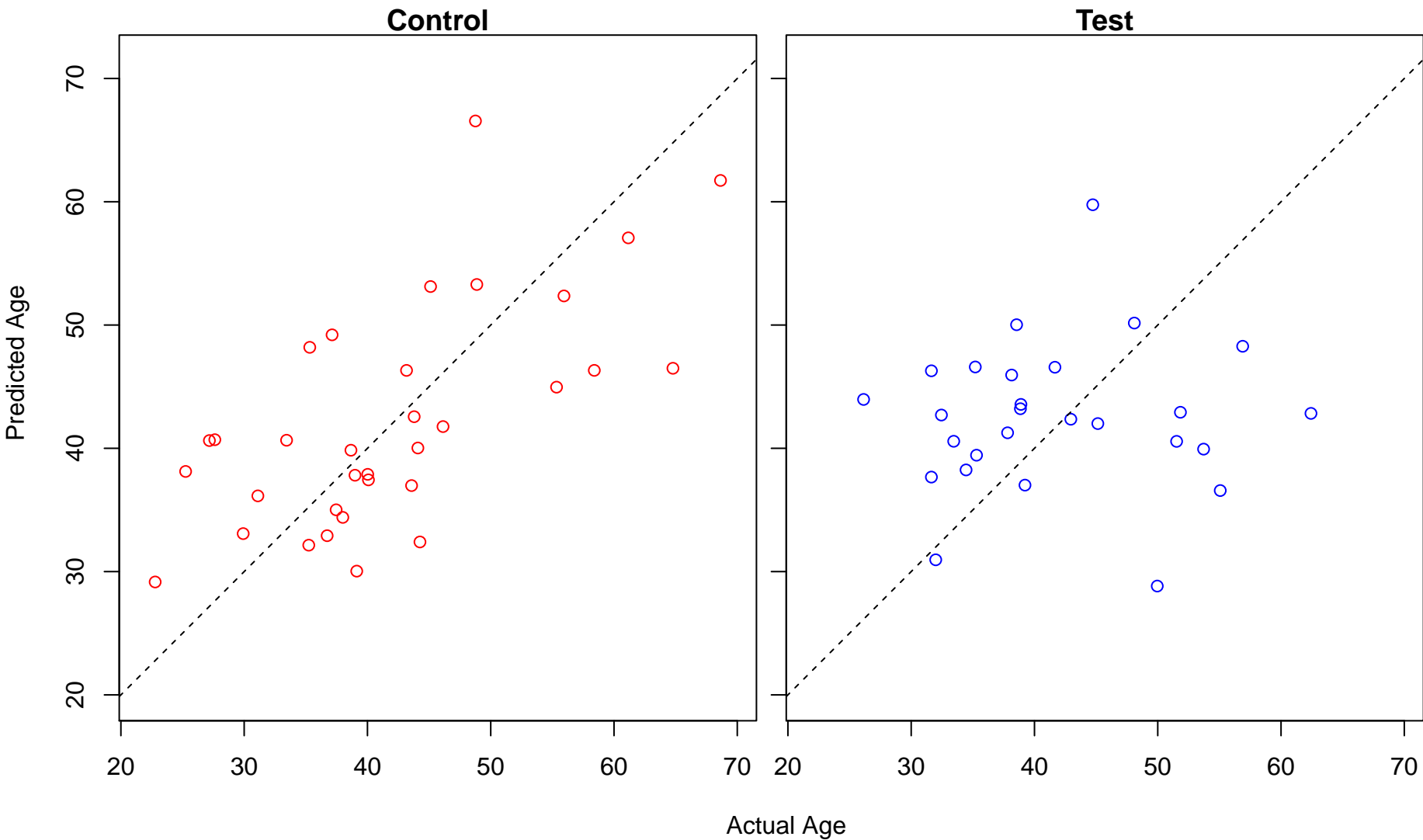
positive regulation of intracellular estrogen receptor signaling pathway (Score: 1.240668)



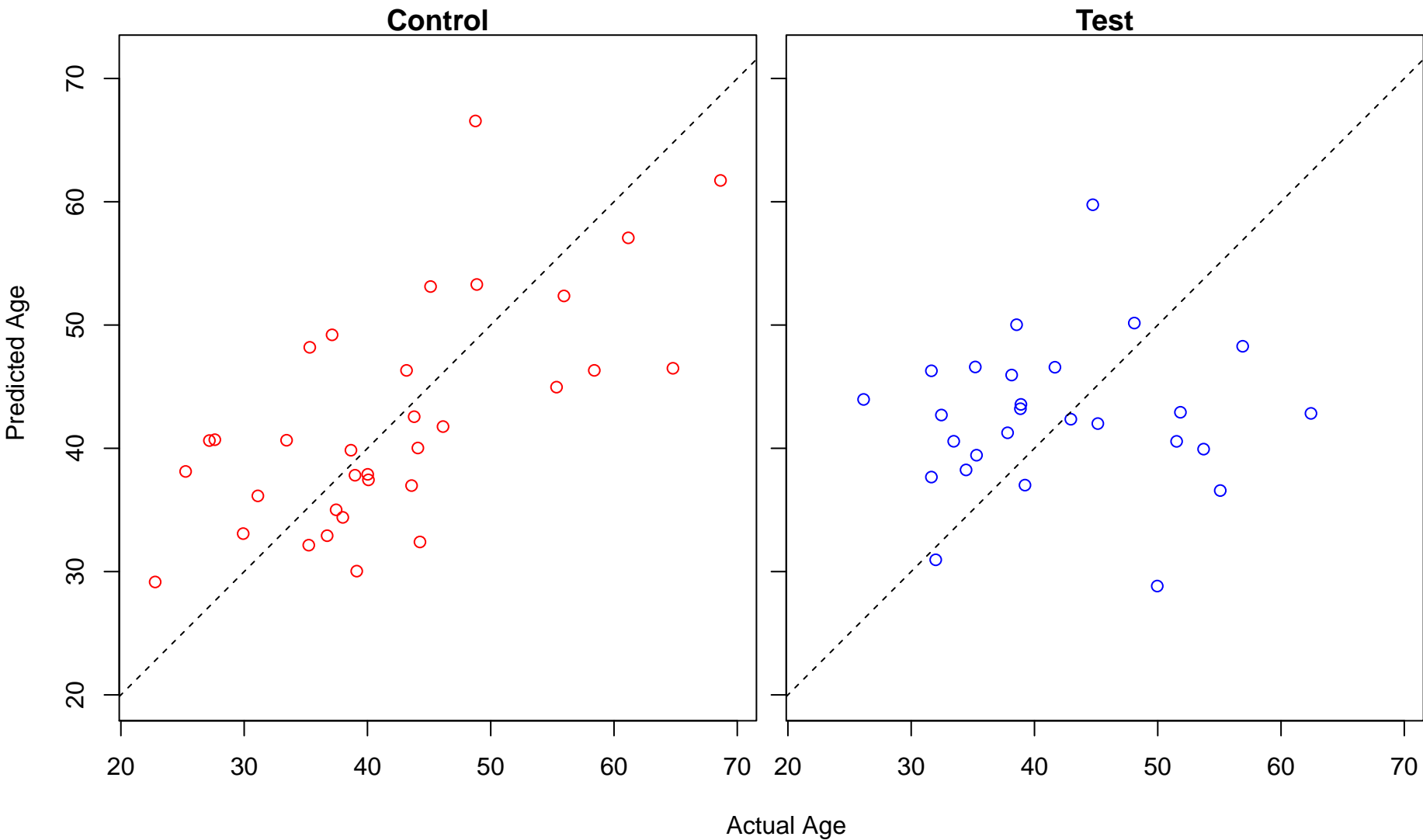
vascular smooth muscle contraction (Score: 1.238722)



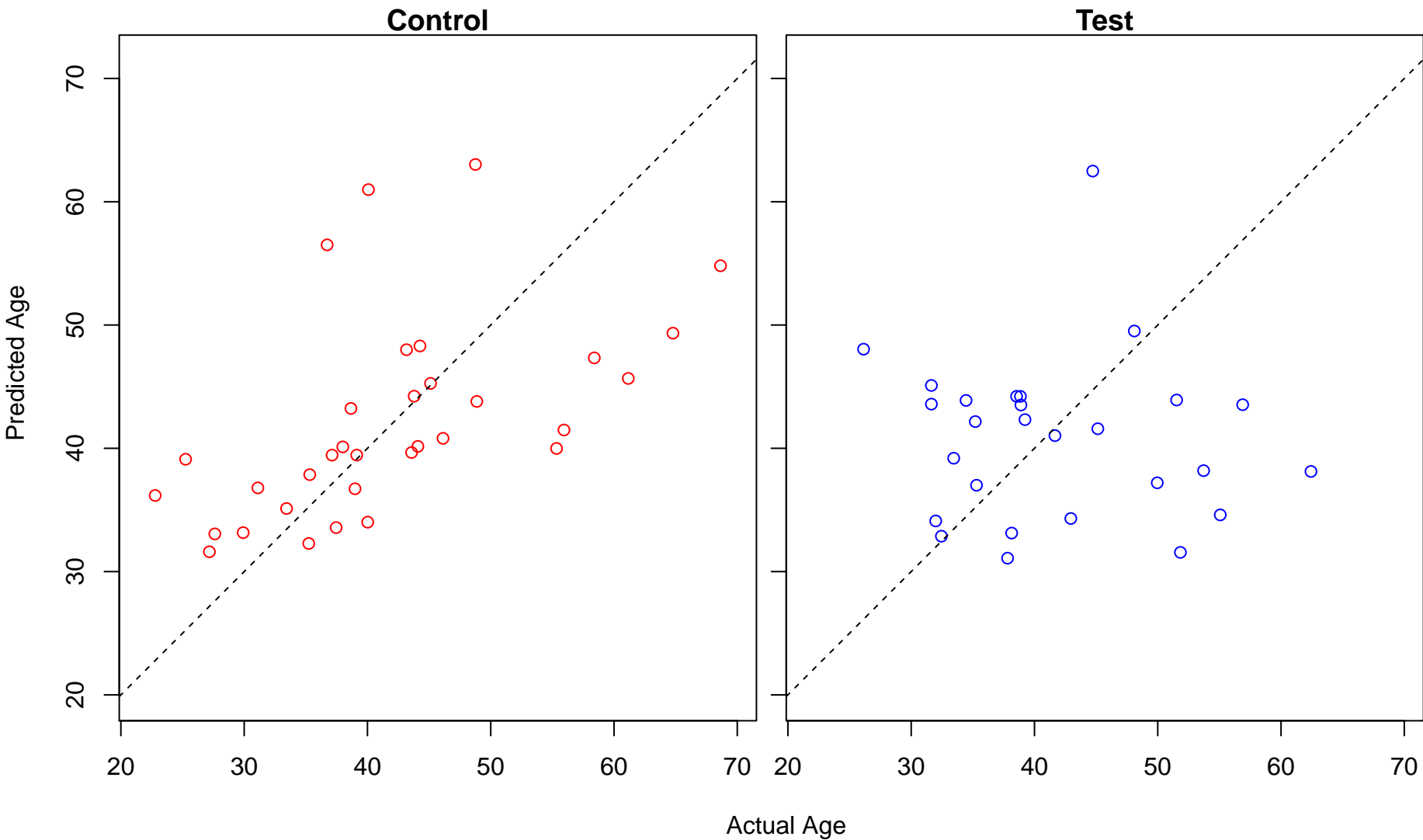
rhythmic behavior (Score: 1.210104)



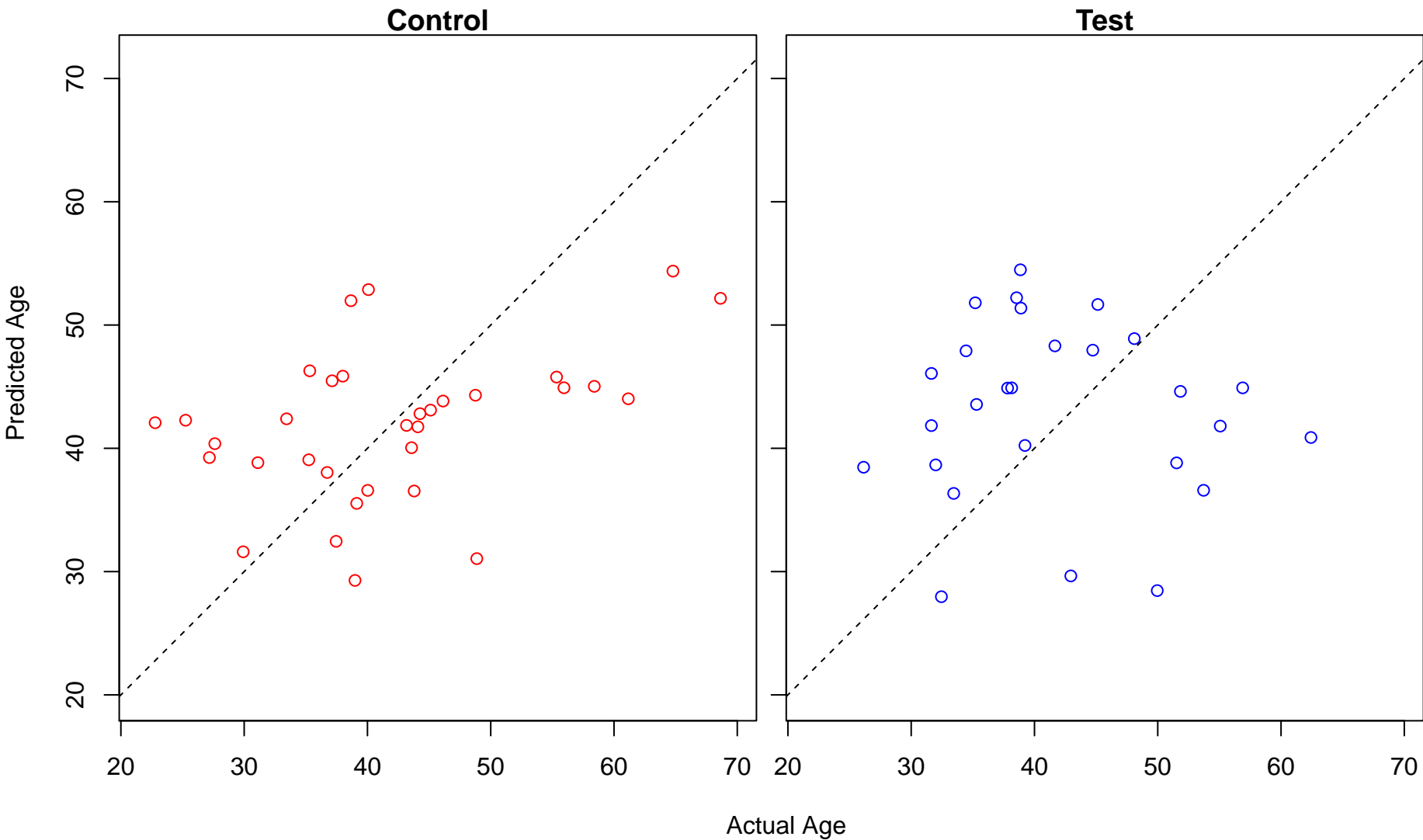
circadian behavior (Score: 1.210104)



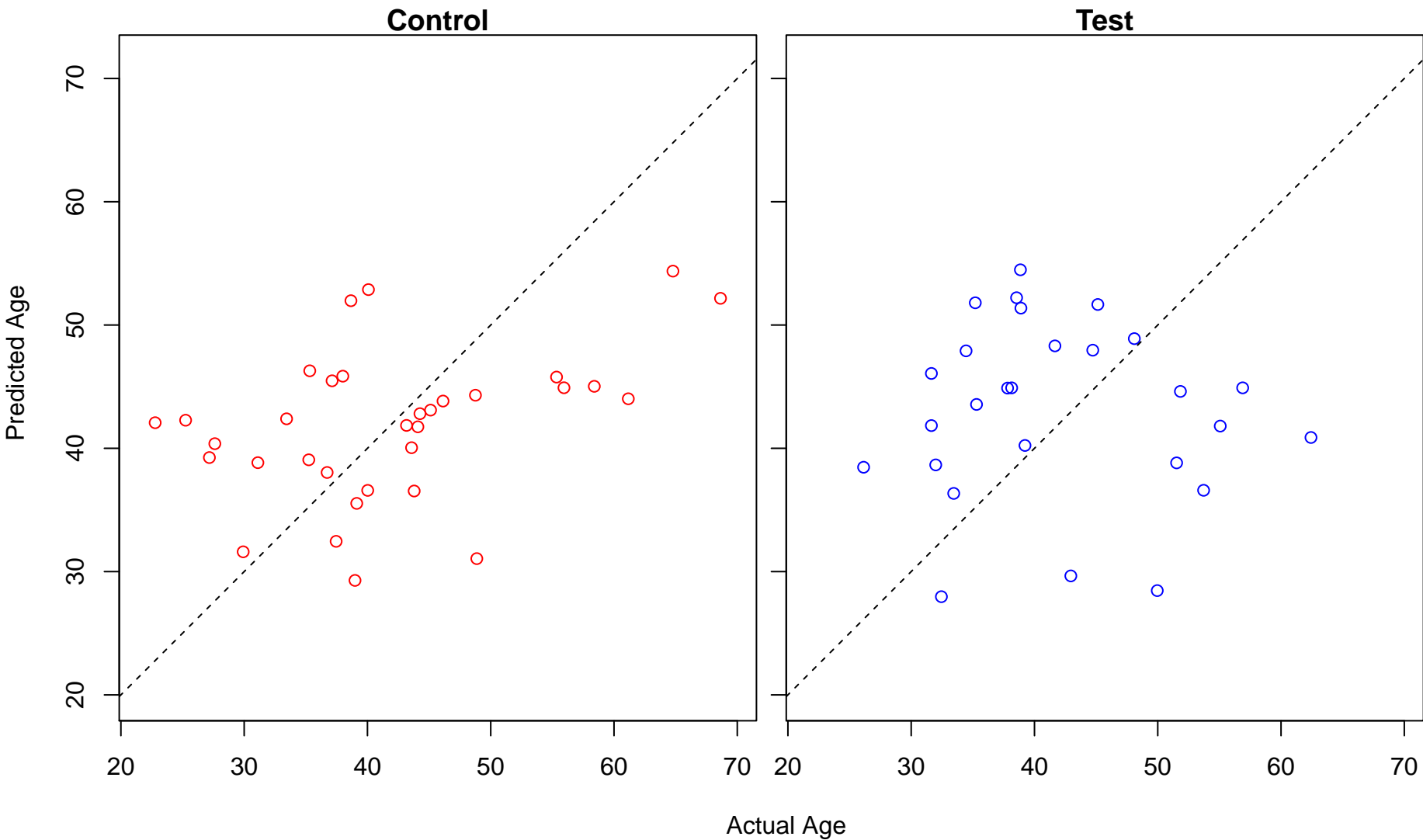
negative regulation of skeletal muscle tissue development (Score: 1.206411)



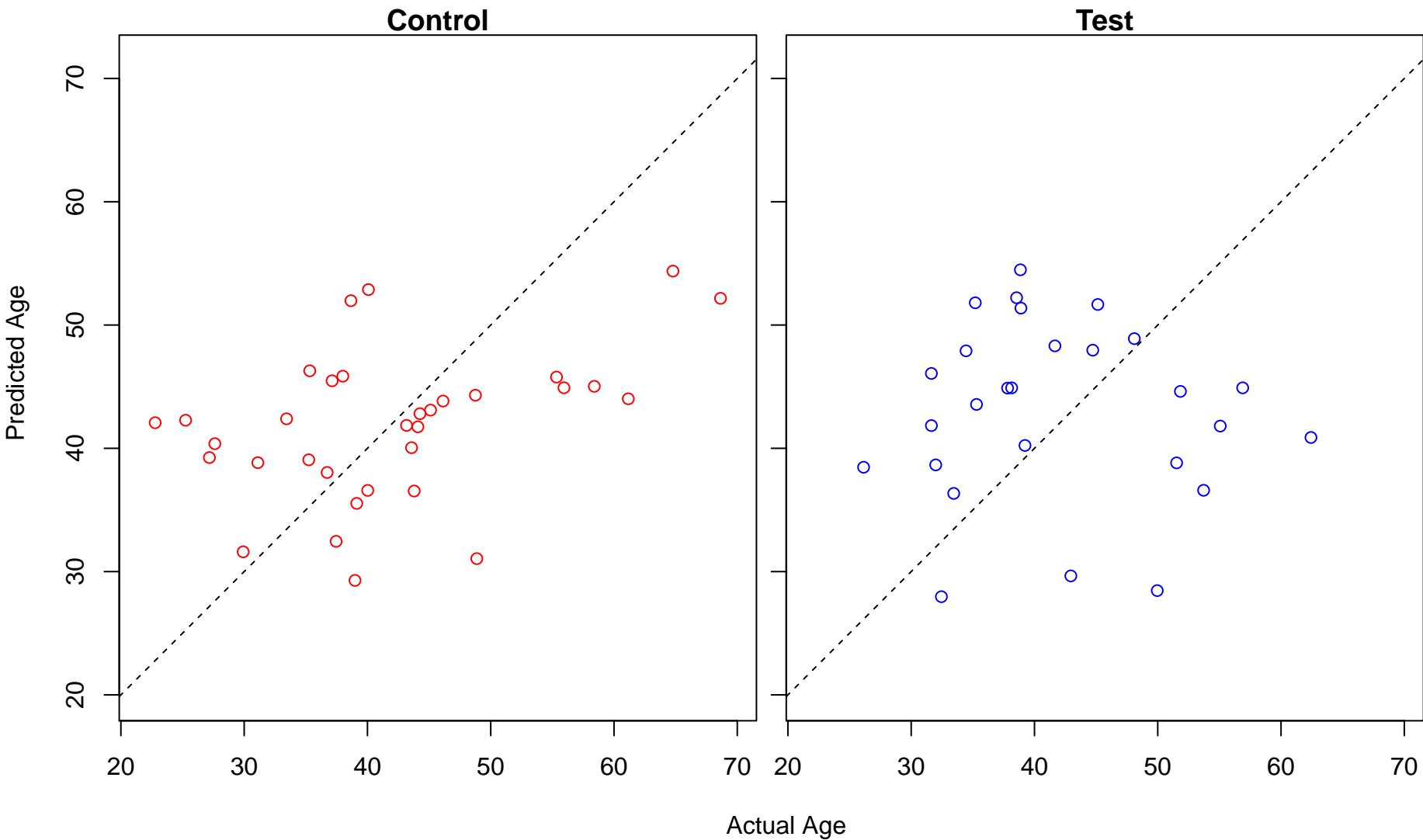
regulation of synaptic transmission, dopaminergic (Score: 1.171842)



regulation of dopamine uptake involved in synaptic transmission (Score: 1.171842)



regulation of catecholamine uptake involved in synaptic transmission (Score: 1.171842)



cell aggregation (Score: 1.152395)

