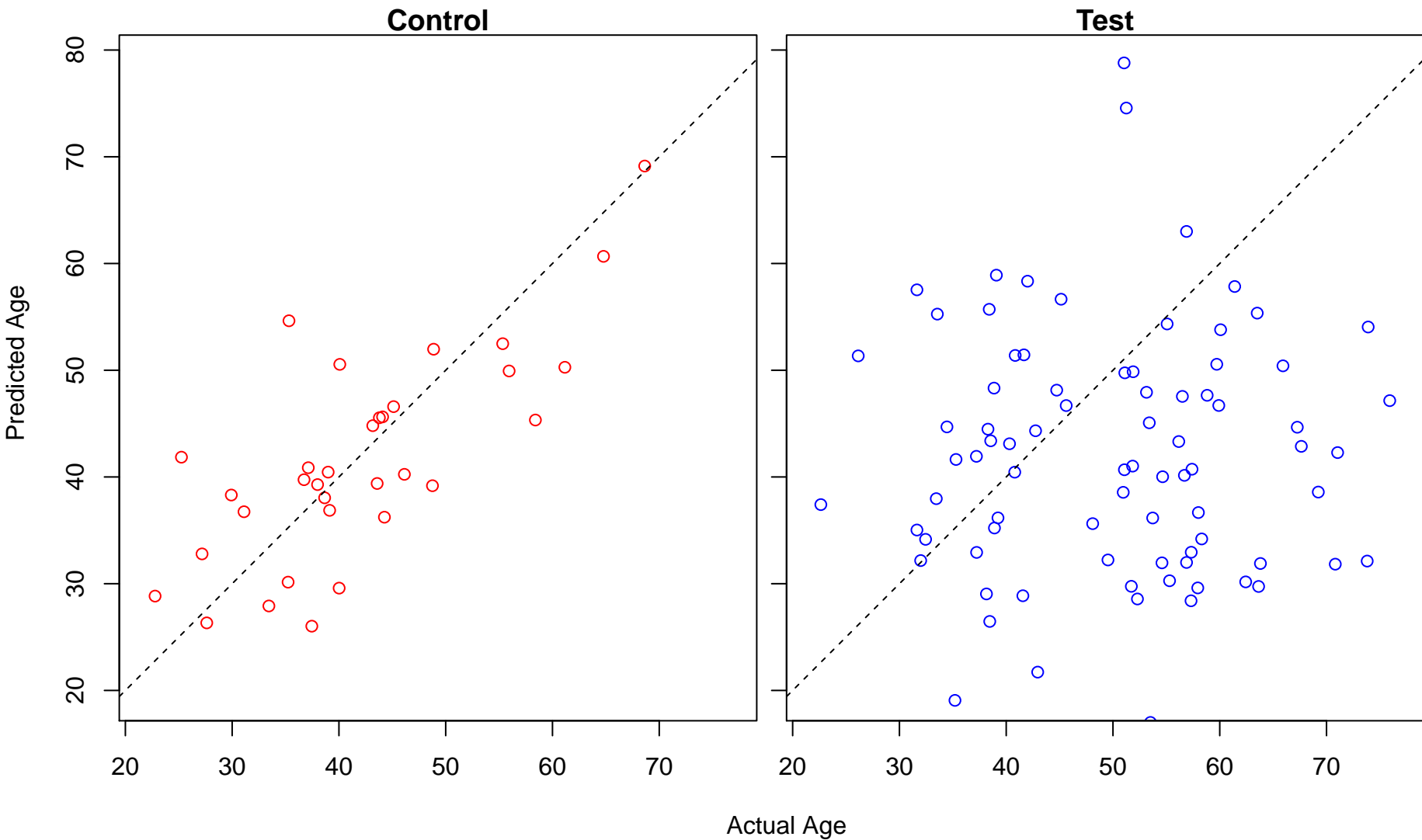
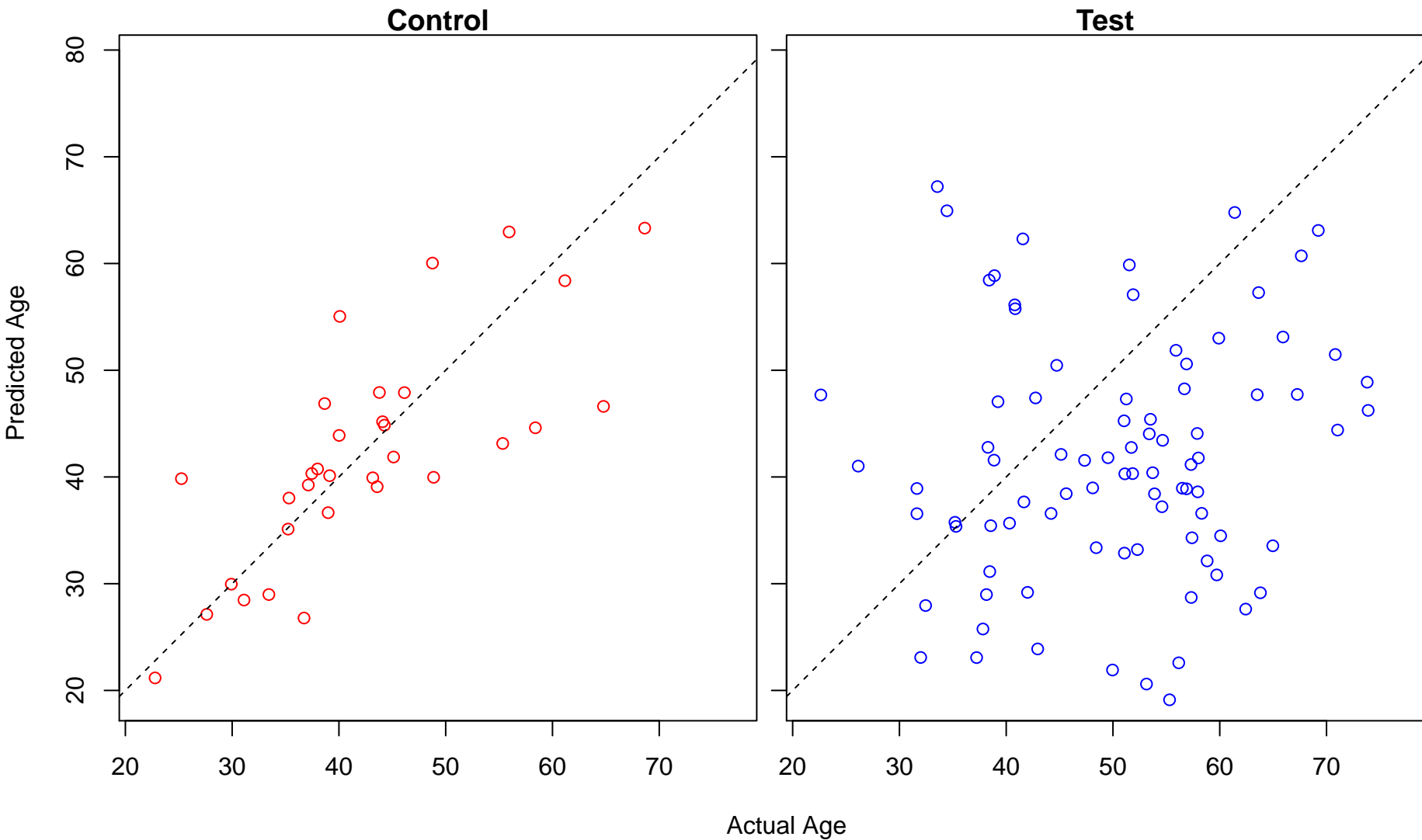


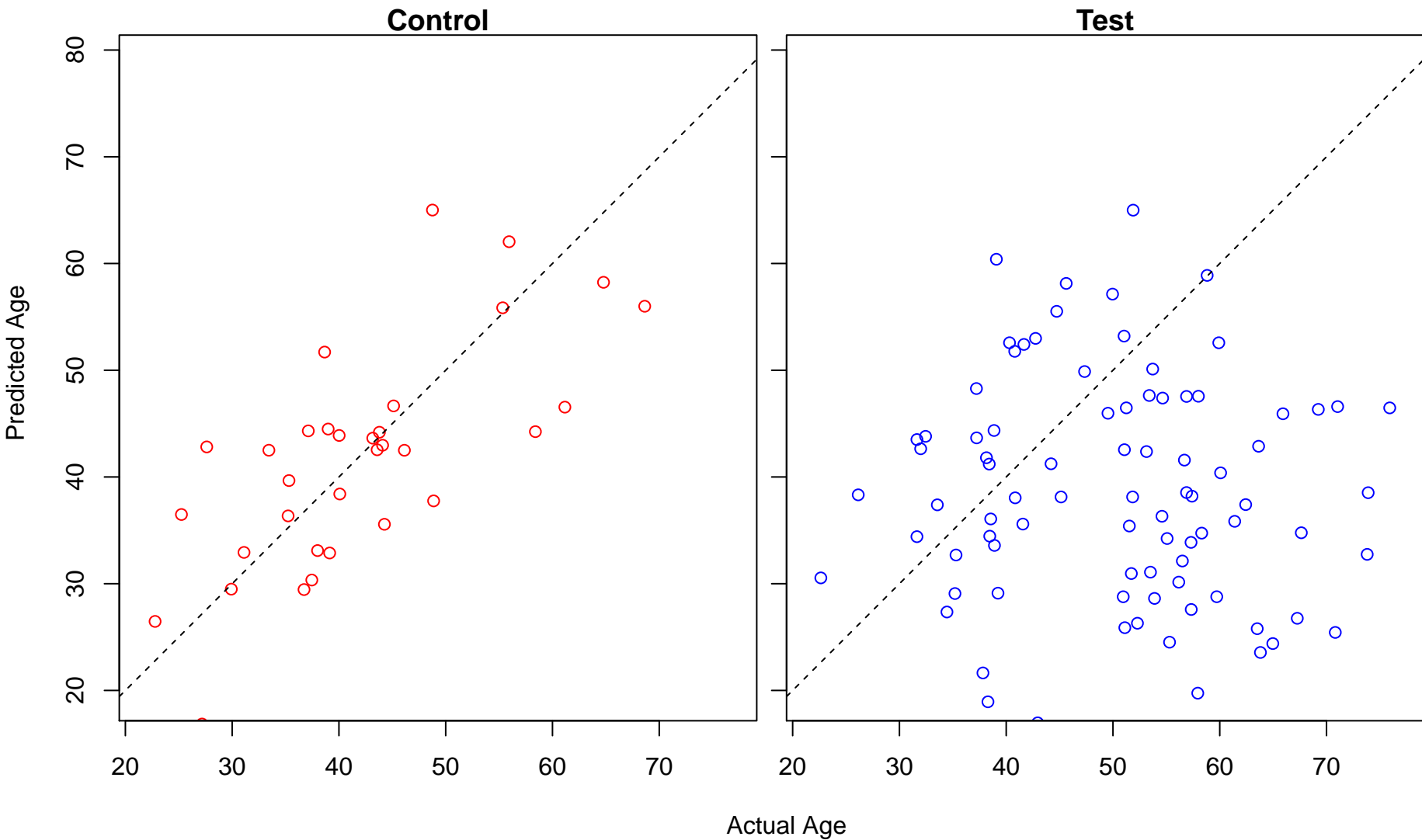
negative regulation of DNA recombination (Score: 3.829675)



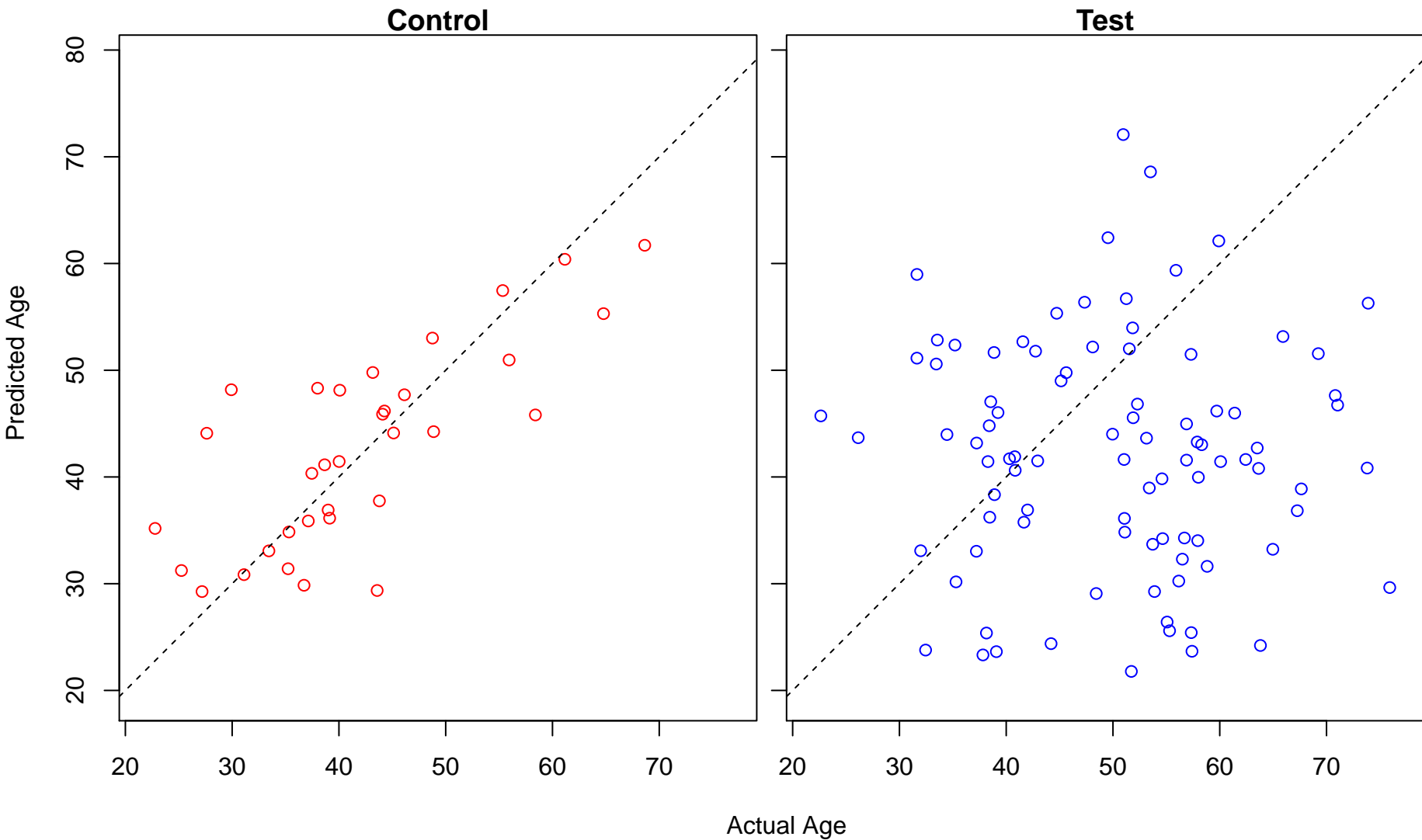
telomere maintenance via recombination (Score: 3.214893)



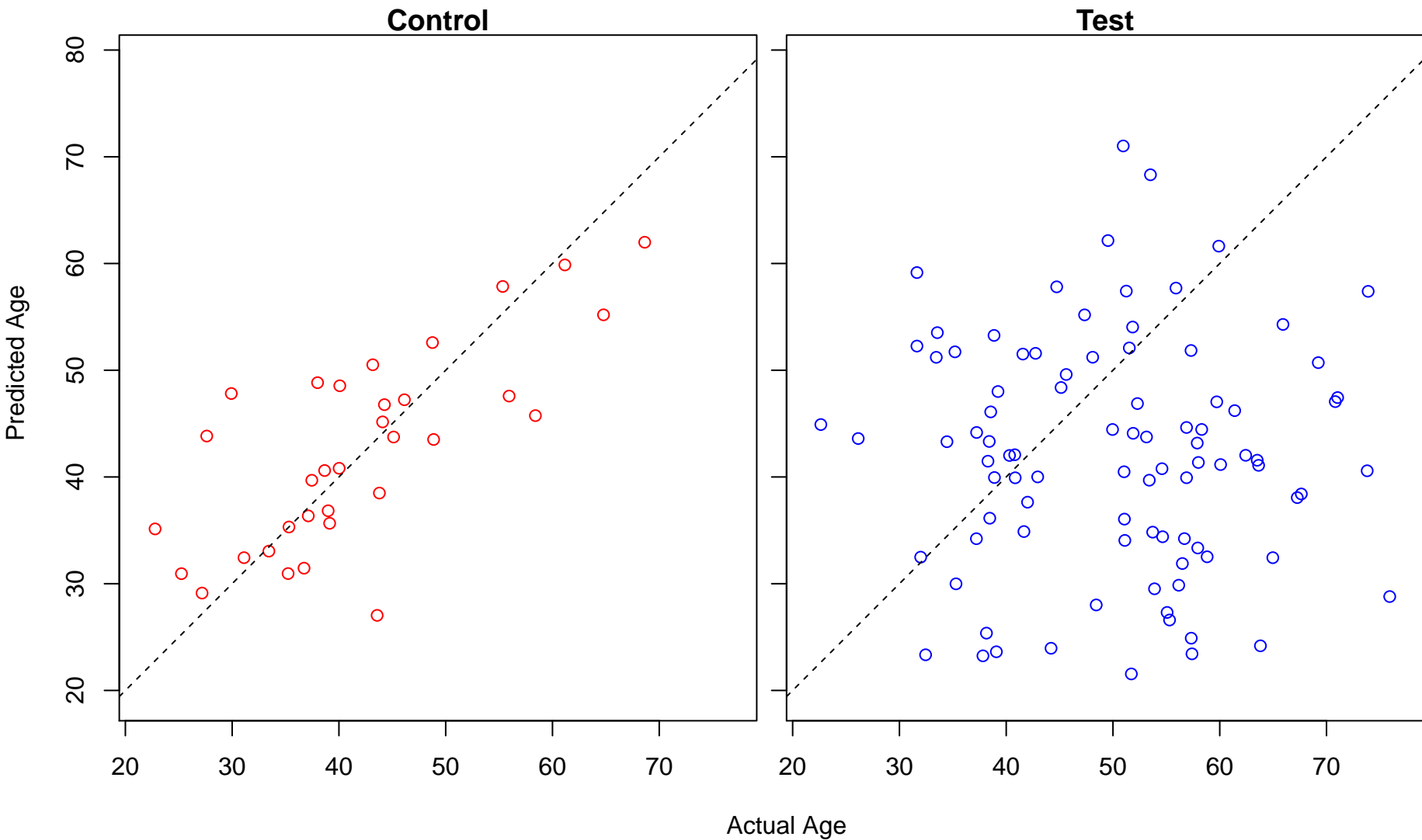
positive regulation of sodium ion transmembrane transport (Score: 2.982268)



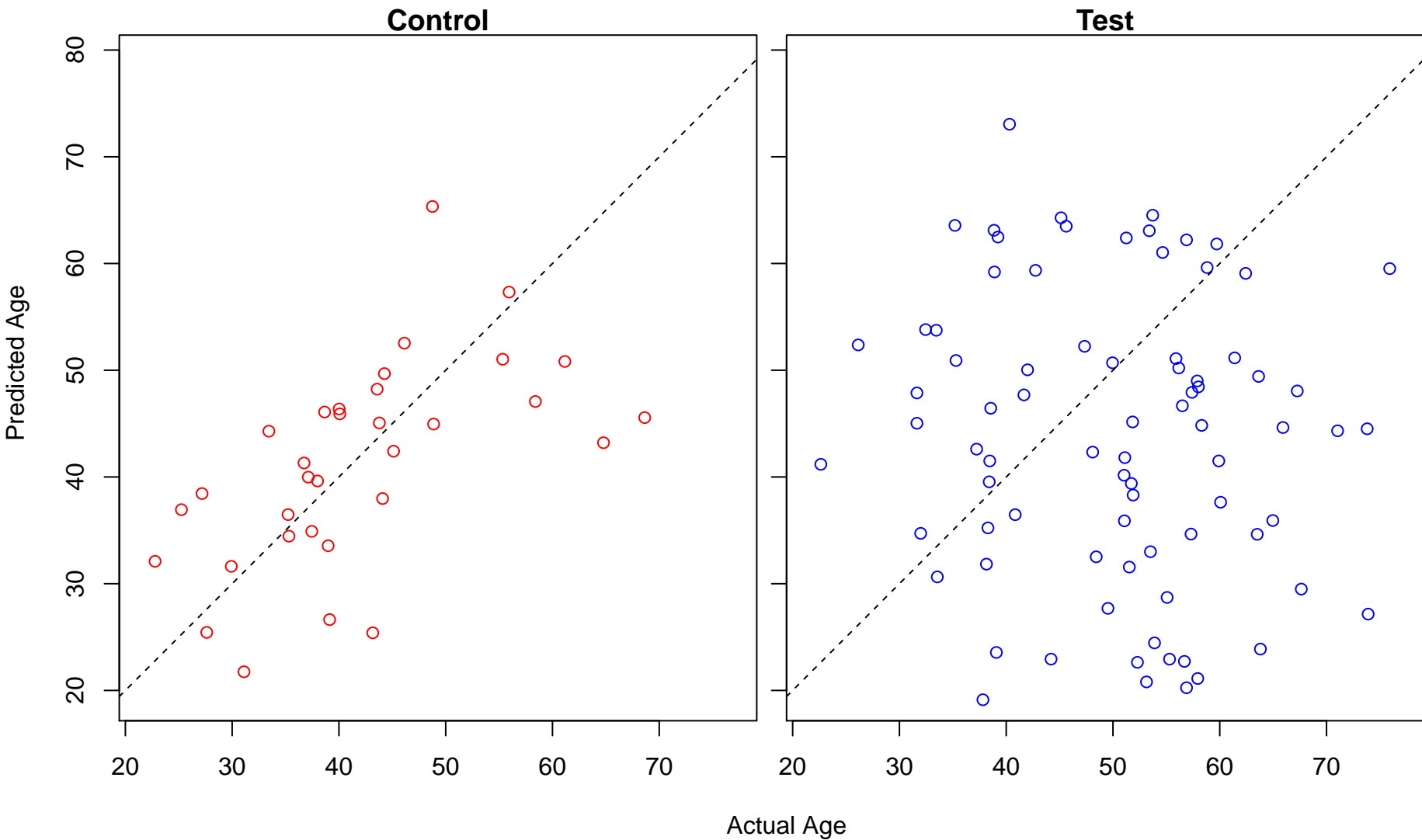
phototransduction, visible light (Score: 2.957197)



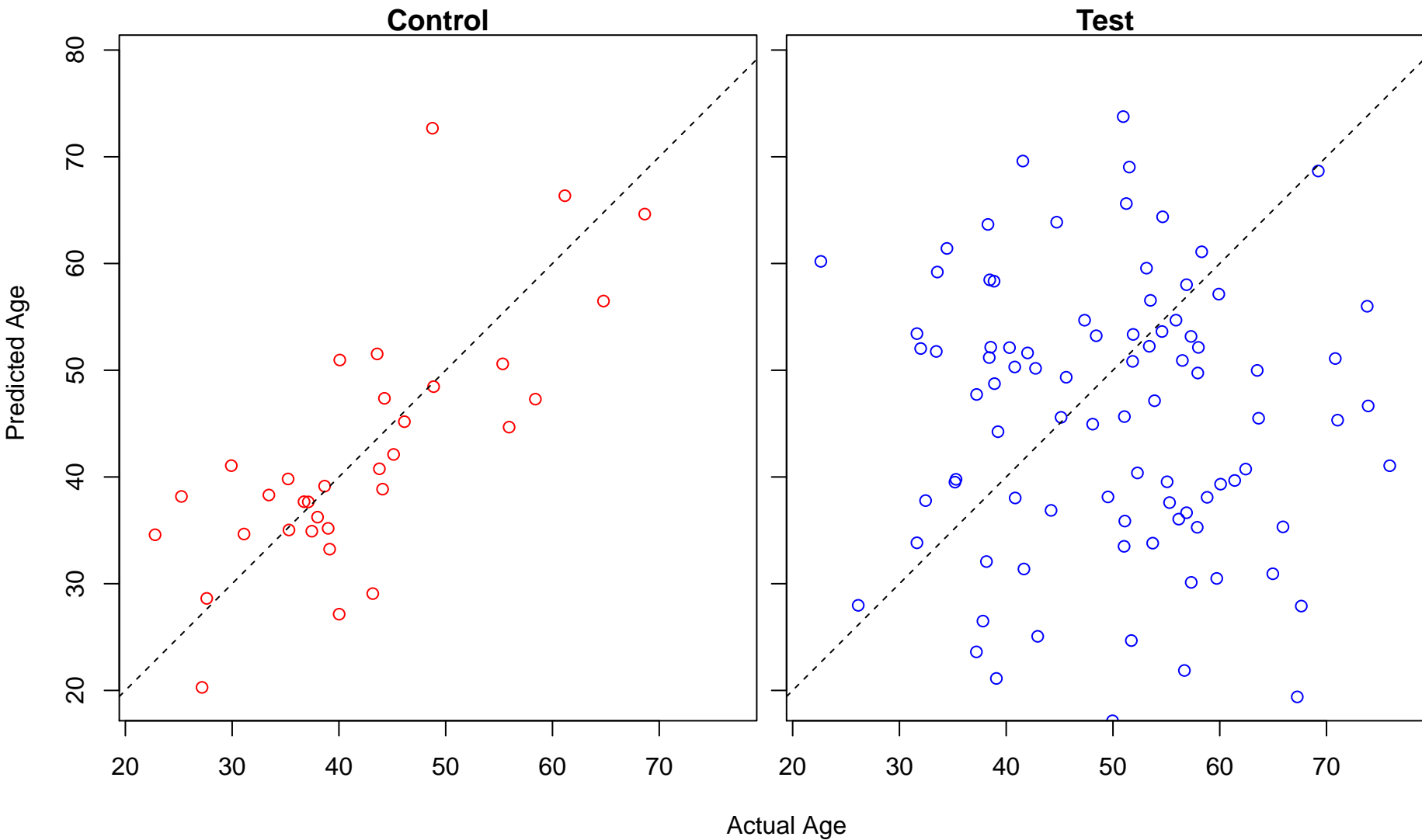
phototransduction (Score: 2.835202)



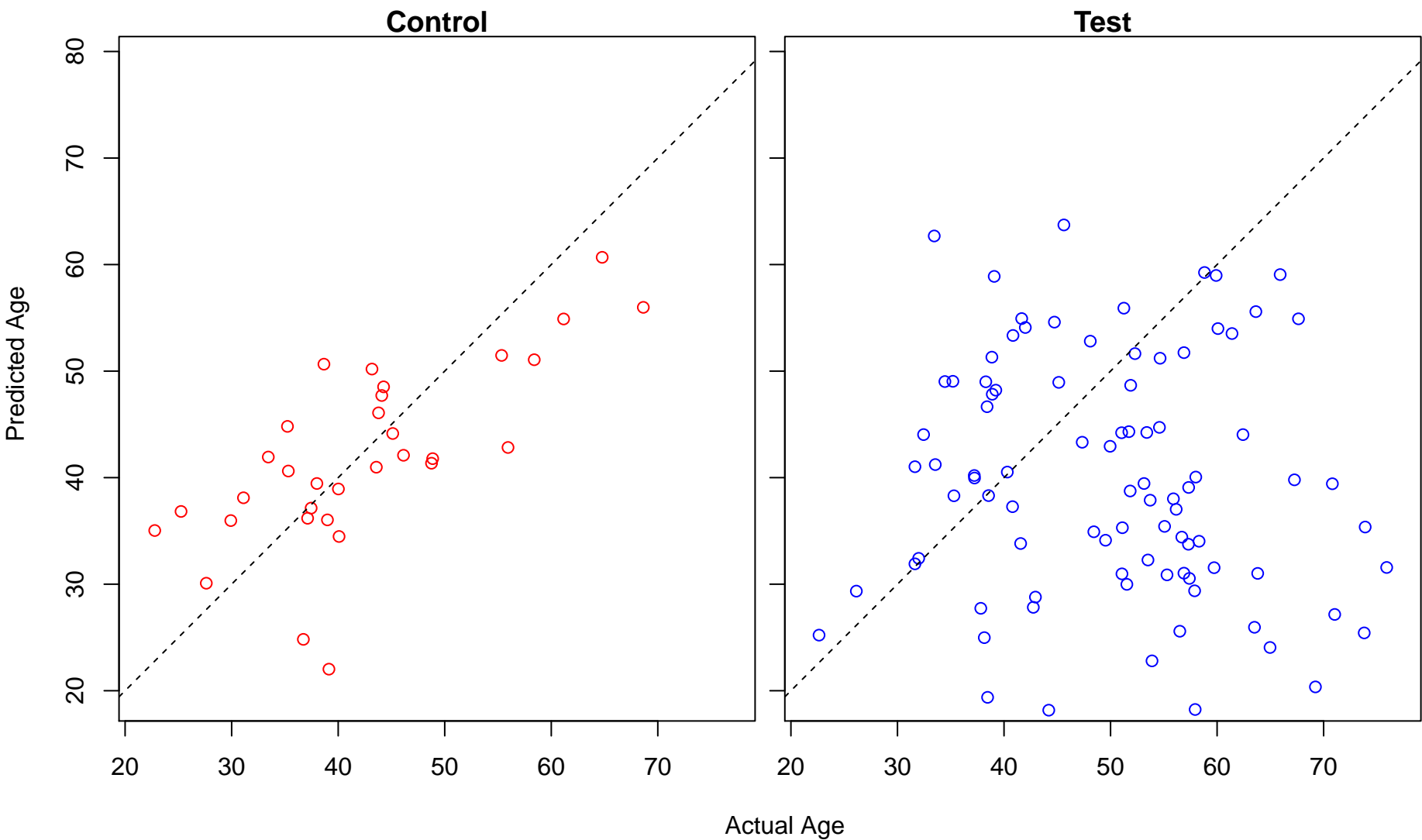
regulation of anion transport (Score: 2.813328)



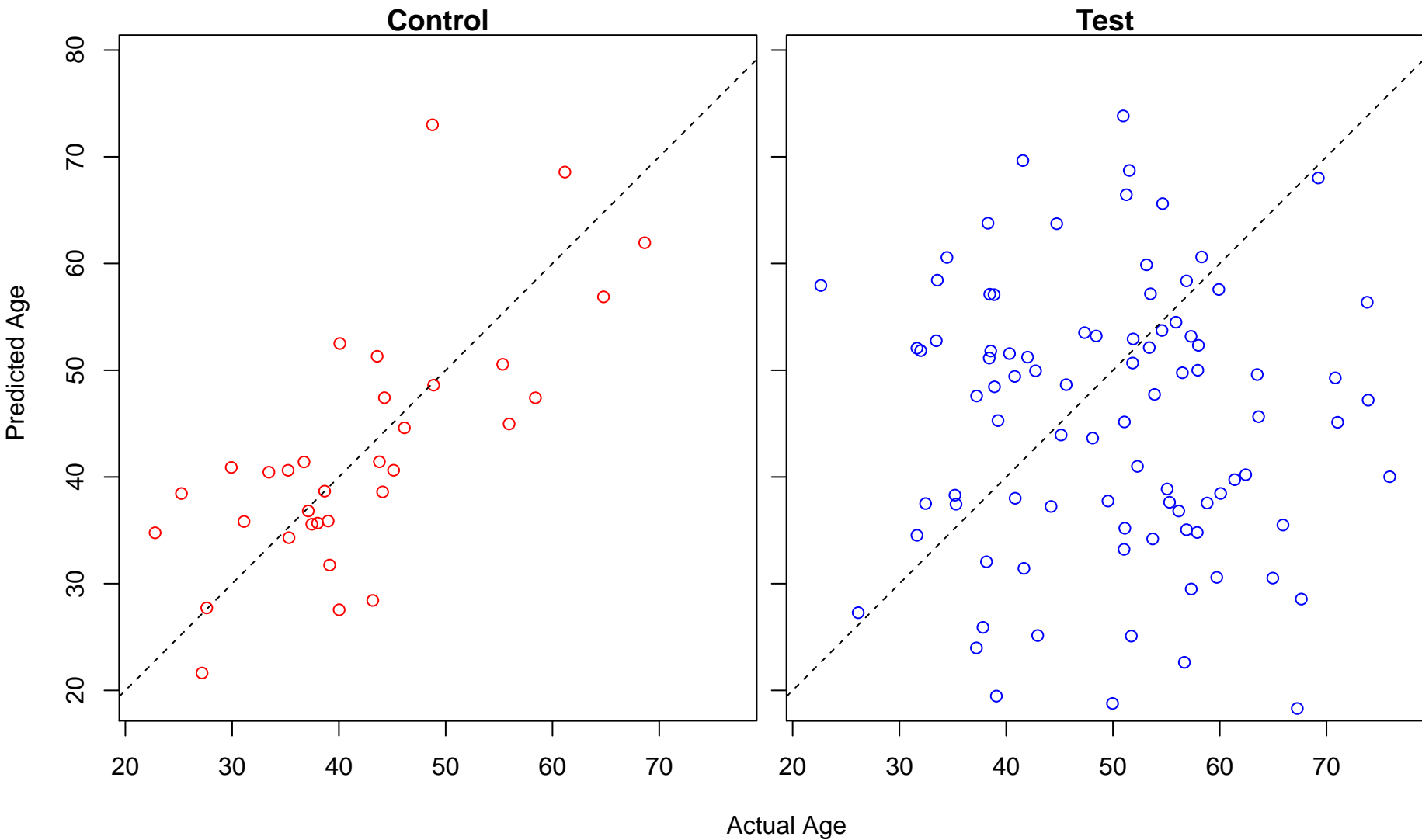
regulation of epidermal growth factor receptor signaling pathway (Score: 2.739069)



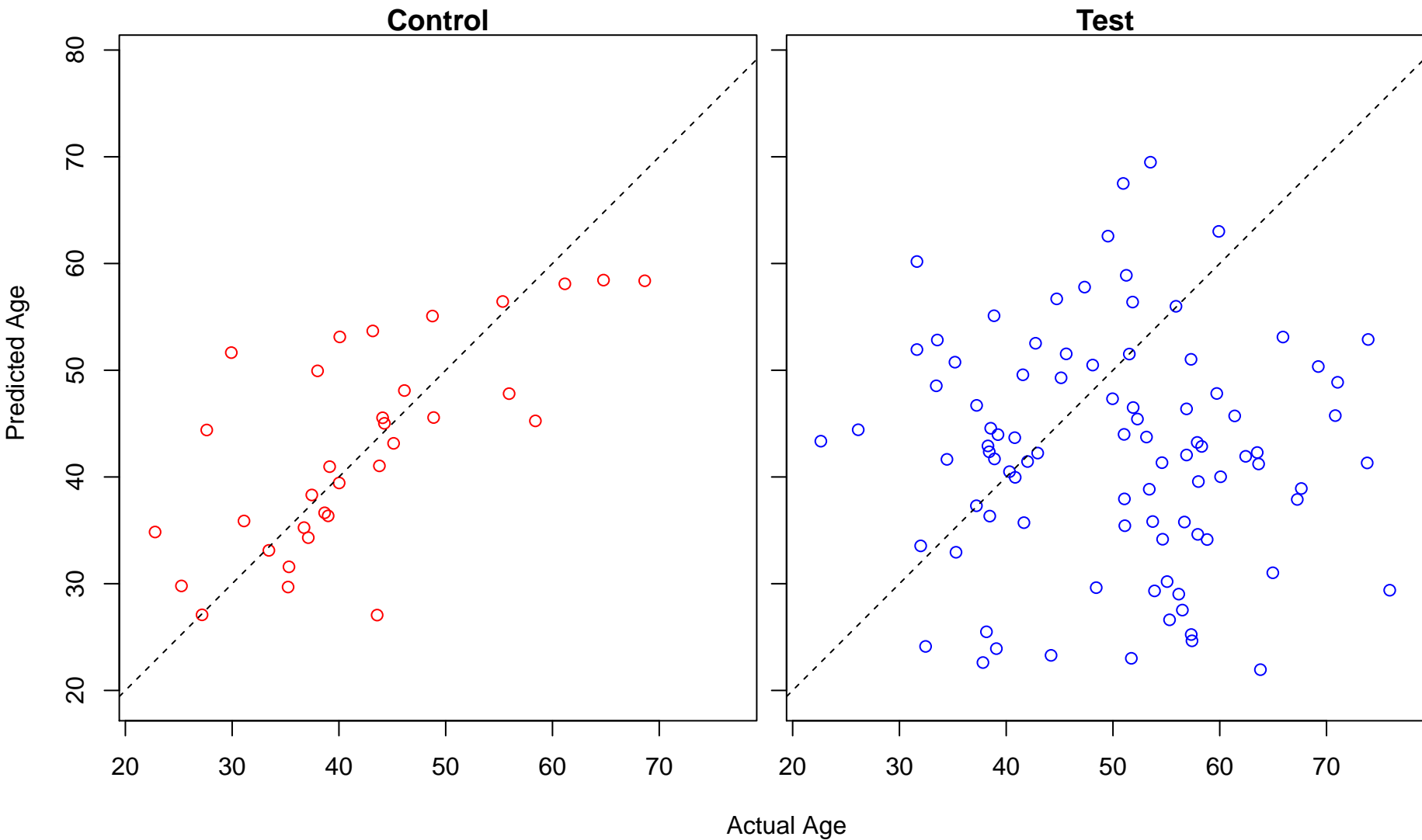
negative regulation of transcription from RNA polymerase II promoter in response to stress (Score: 2.65)



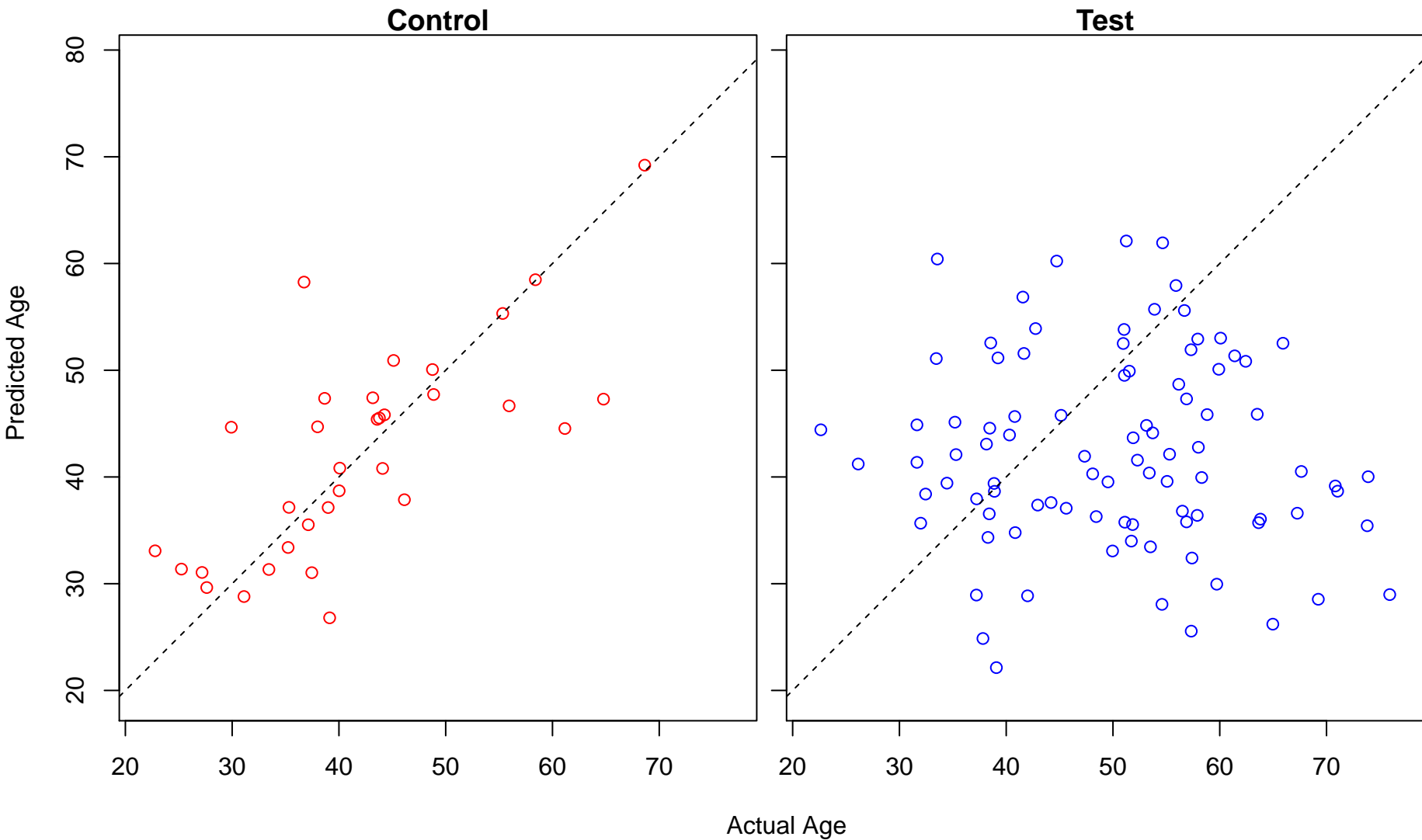
regulation of ERBB signaling pathway (Score: 2.557476)



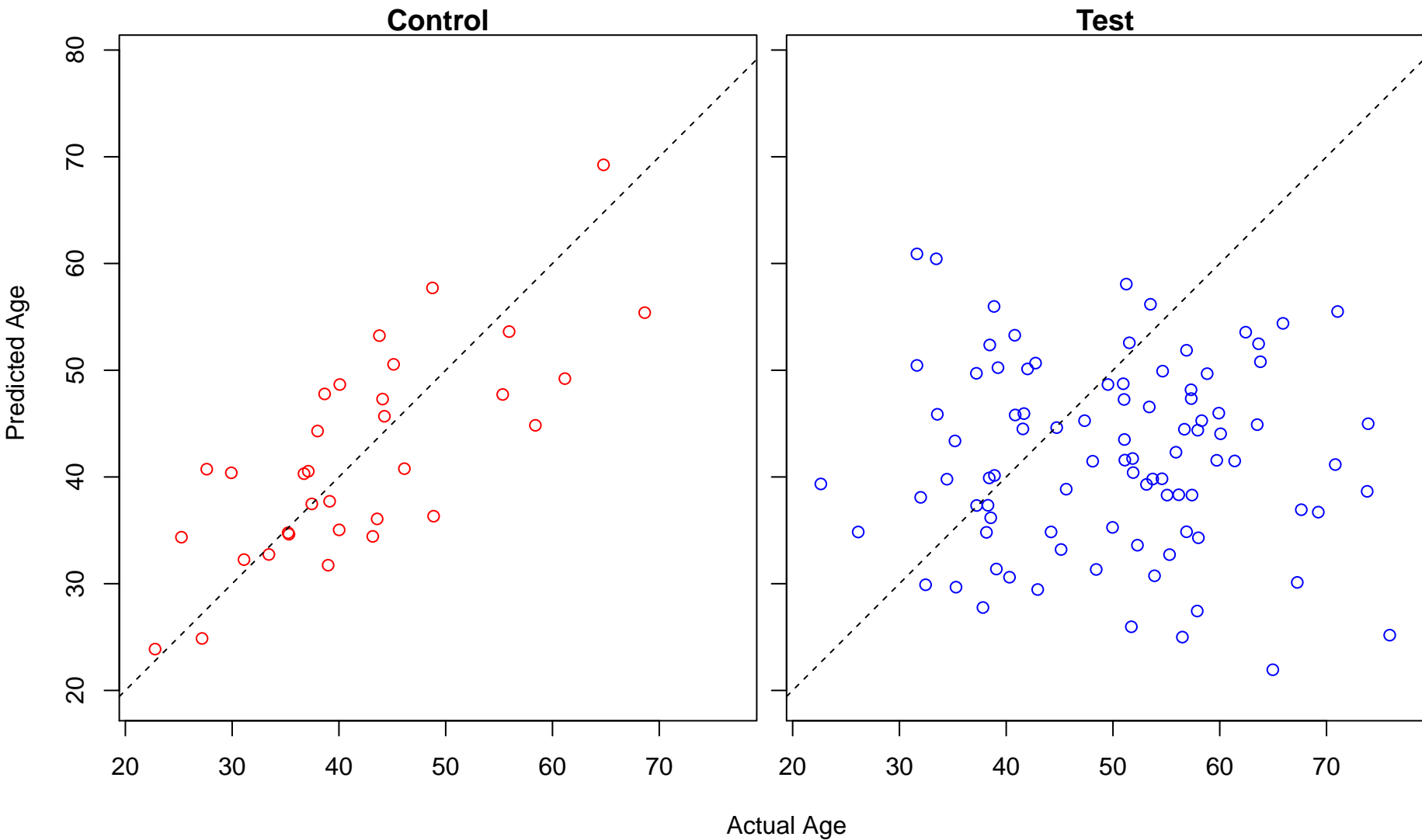
detection of visible light (Score: 2.518682)



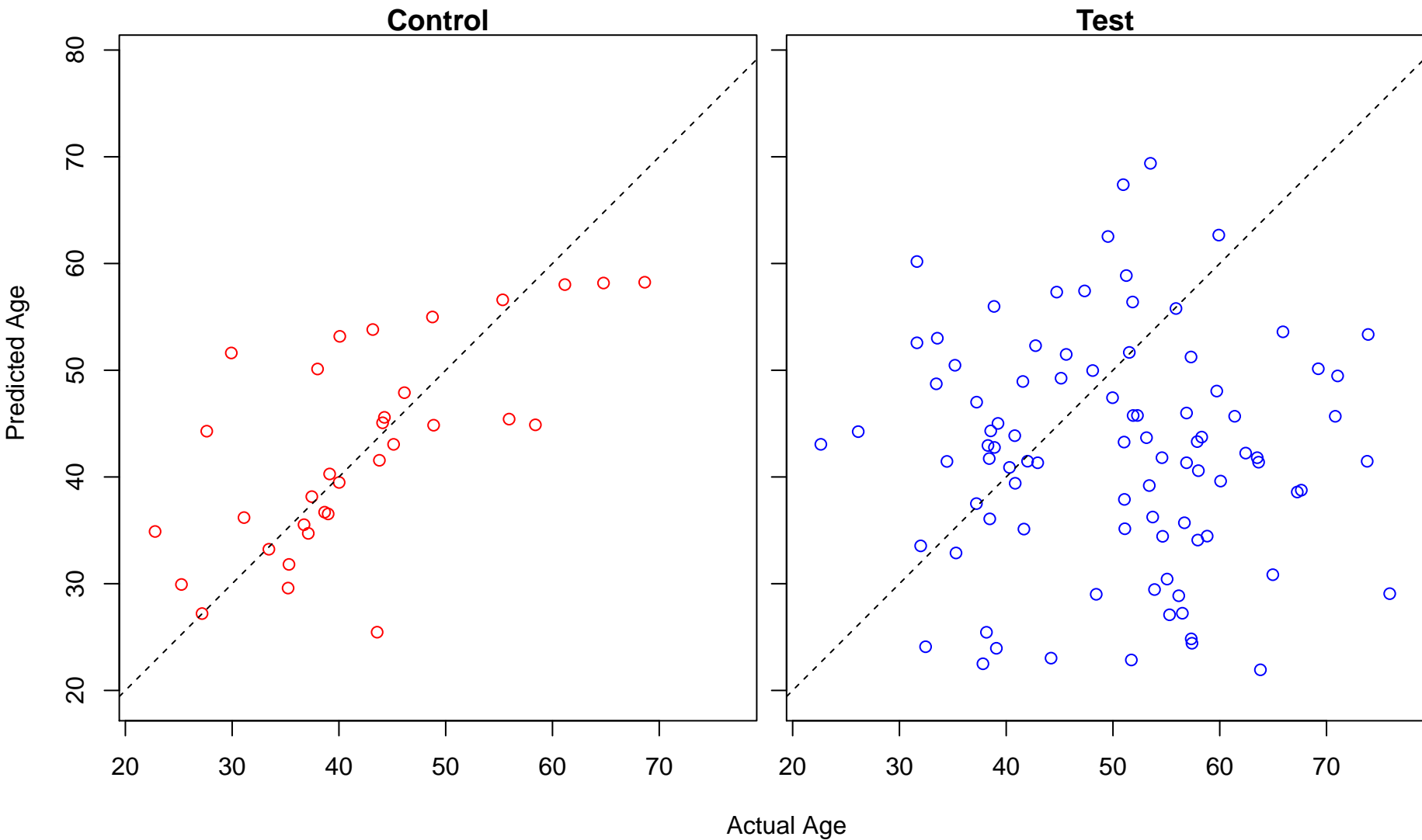
tumor necrosis factor-mediated signaling pathway (Score: 2.486408)



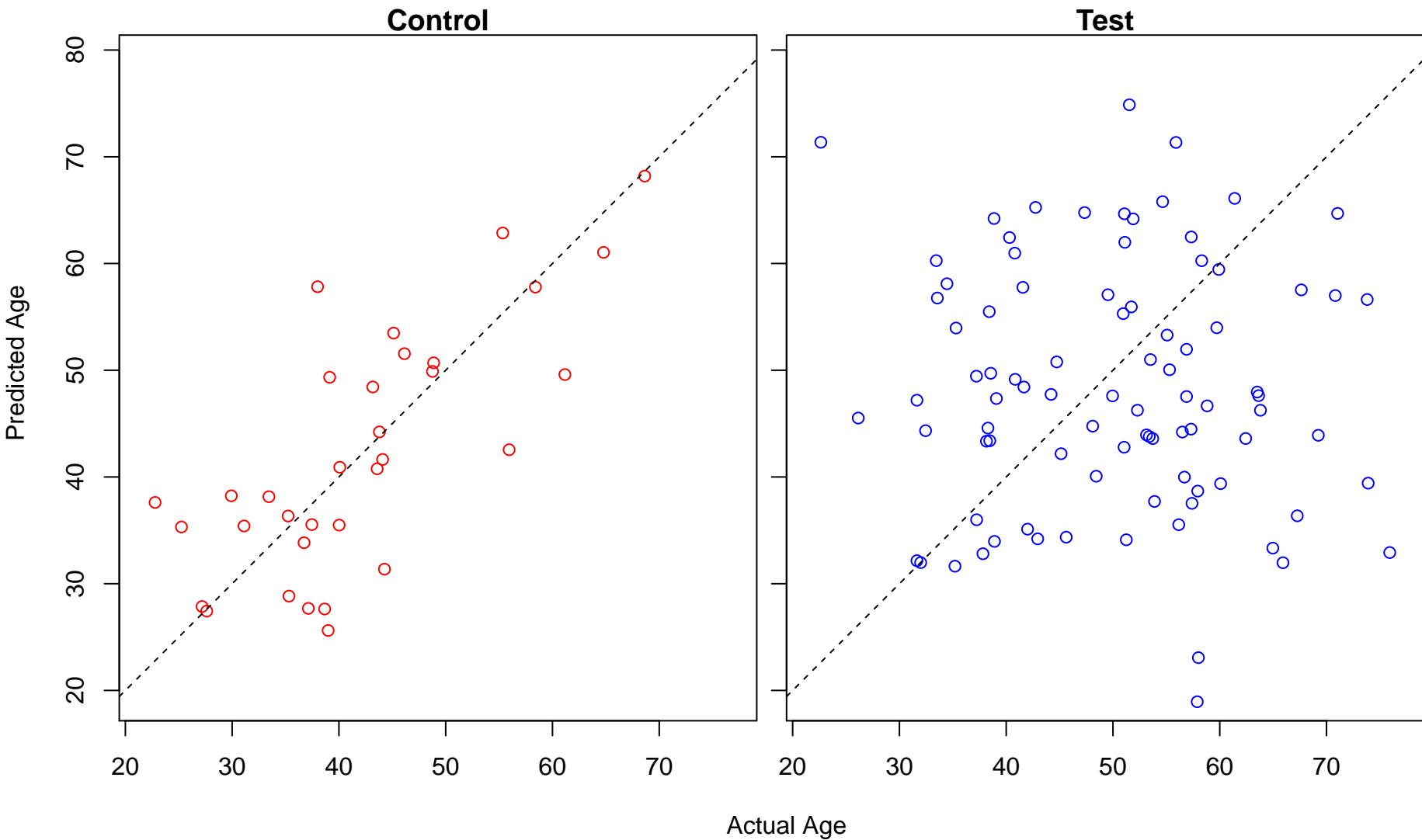
ammonium ion metabolic process (Score: 2.472630)



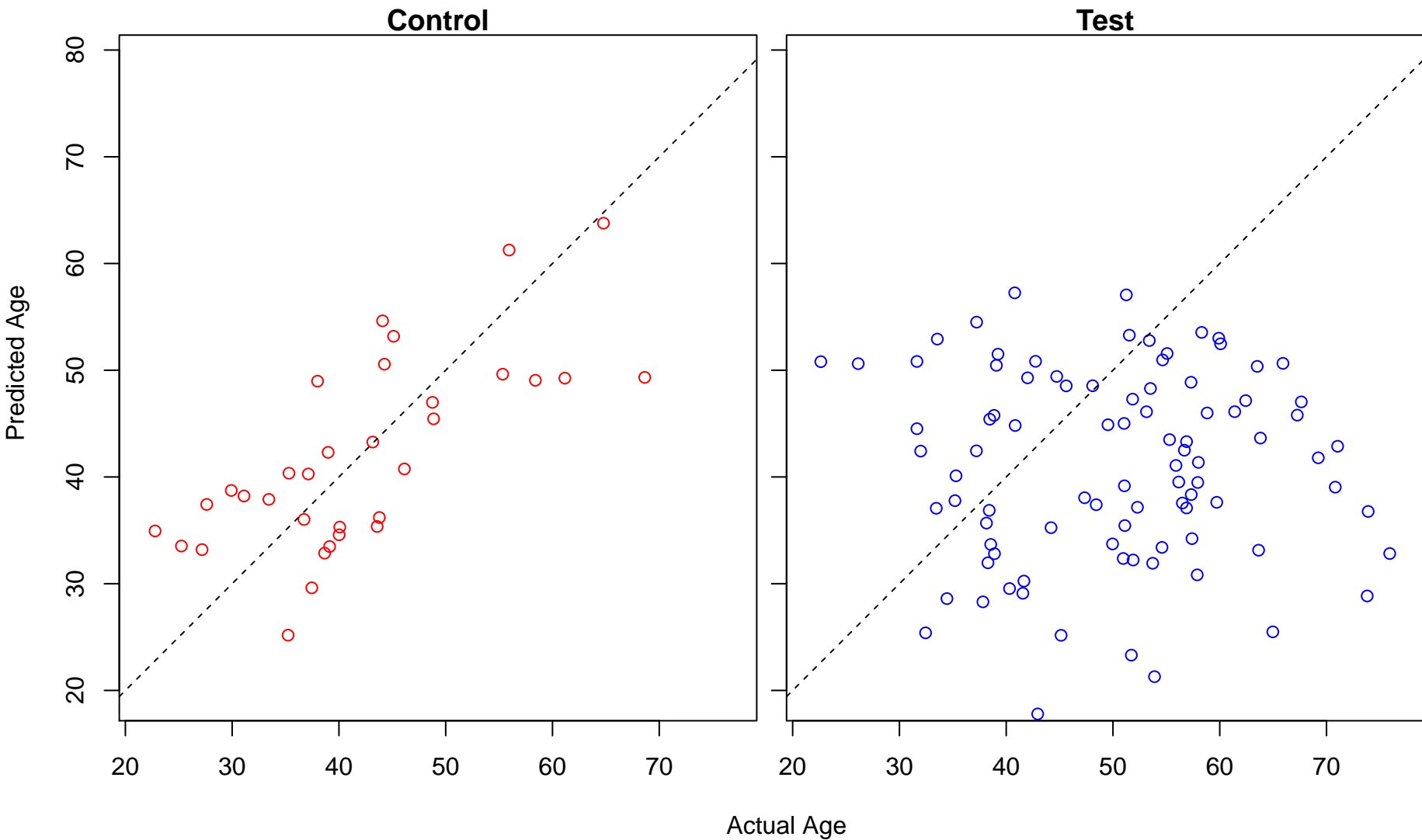
detection of light stimulus (Score: 2.427063)



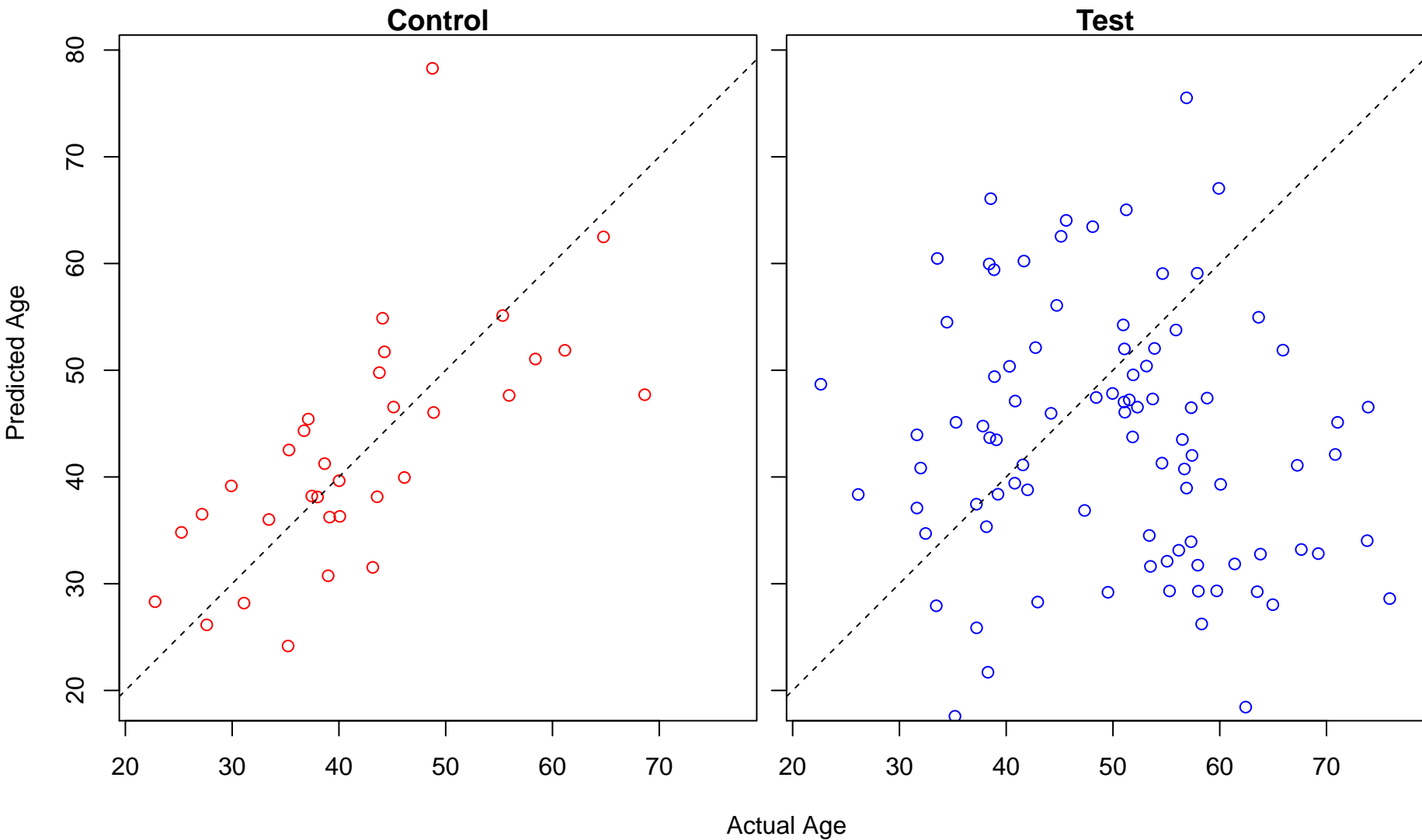
negative regulation of cation channel activity (Score: 2.421026)



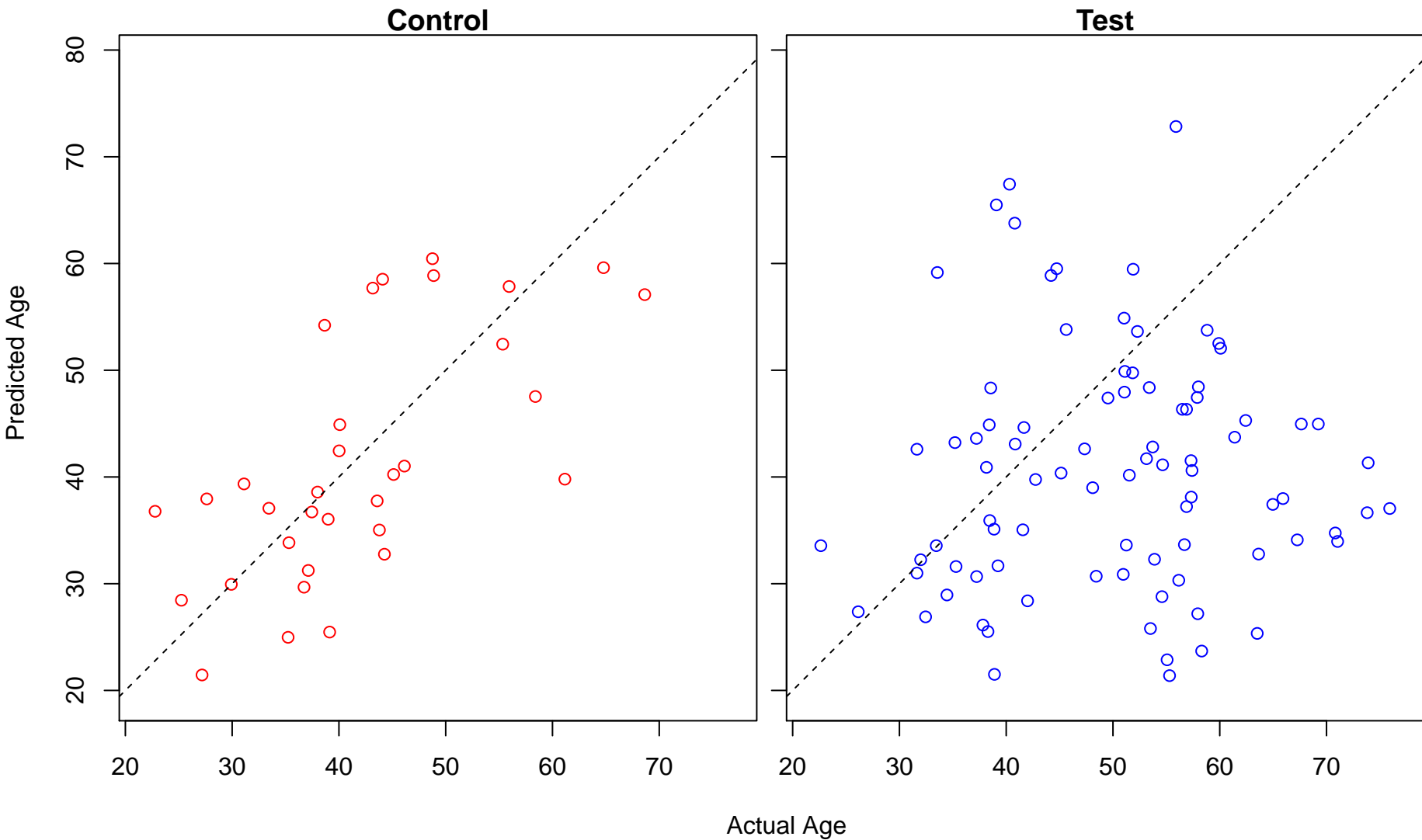
intestinal absorption (Score: 2.338839)



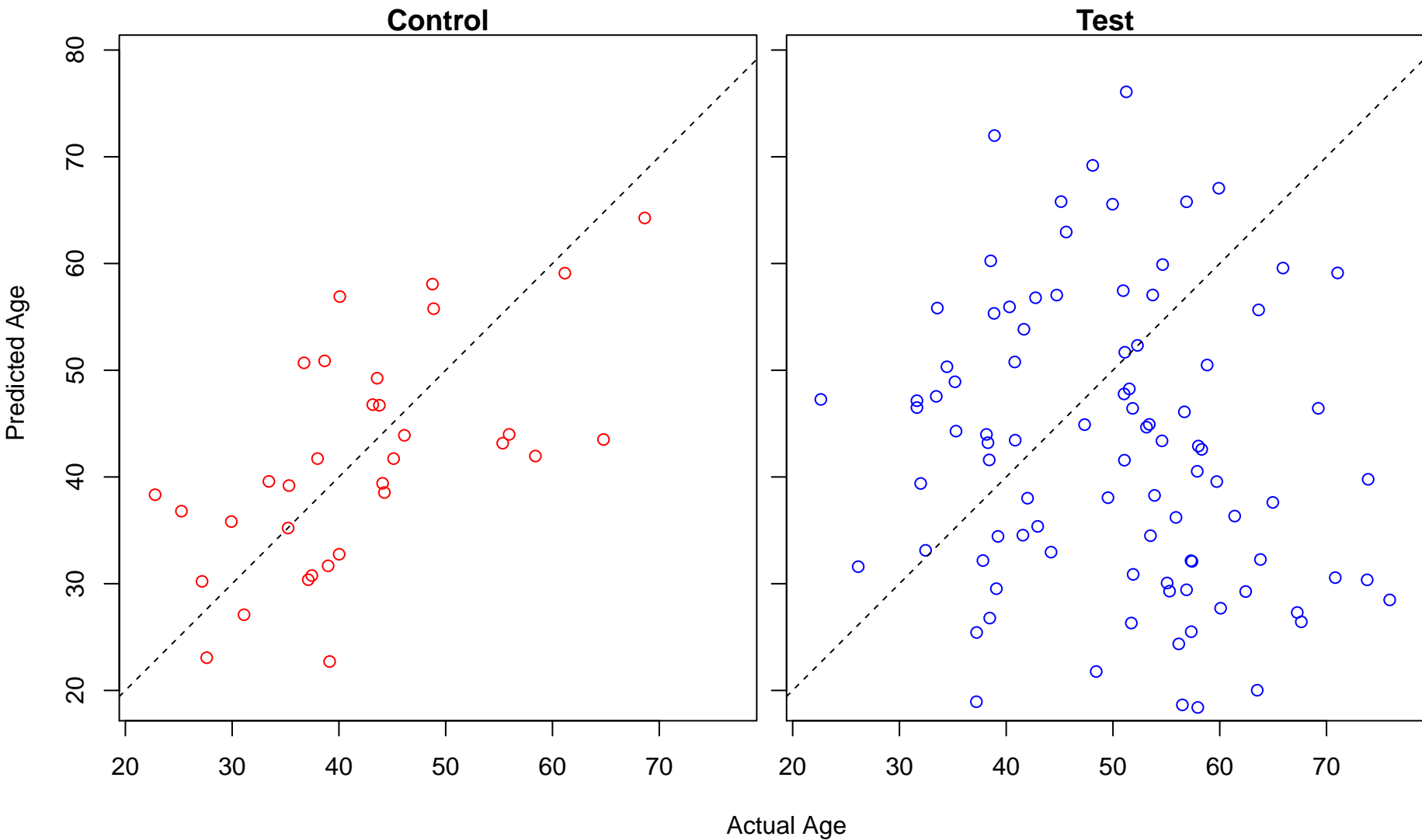
negative regulation of protein acetylation (Score: 2.329704)



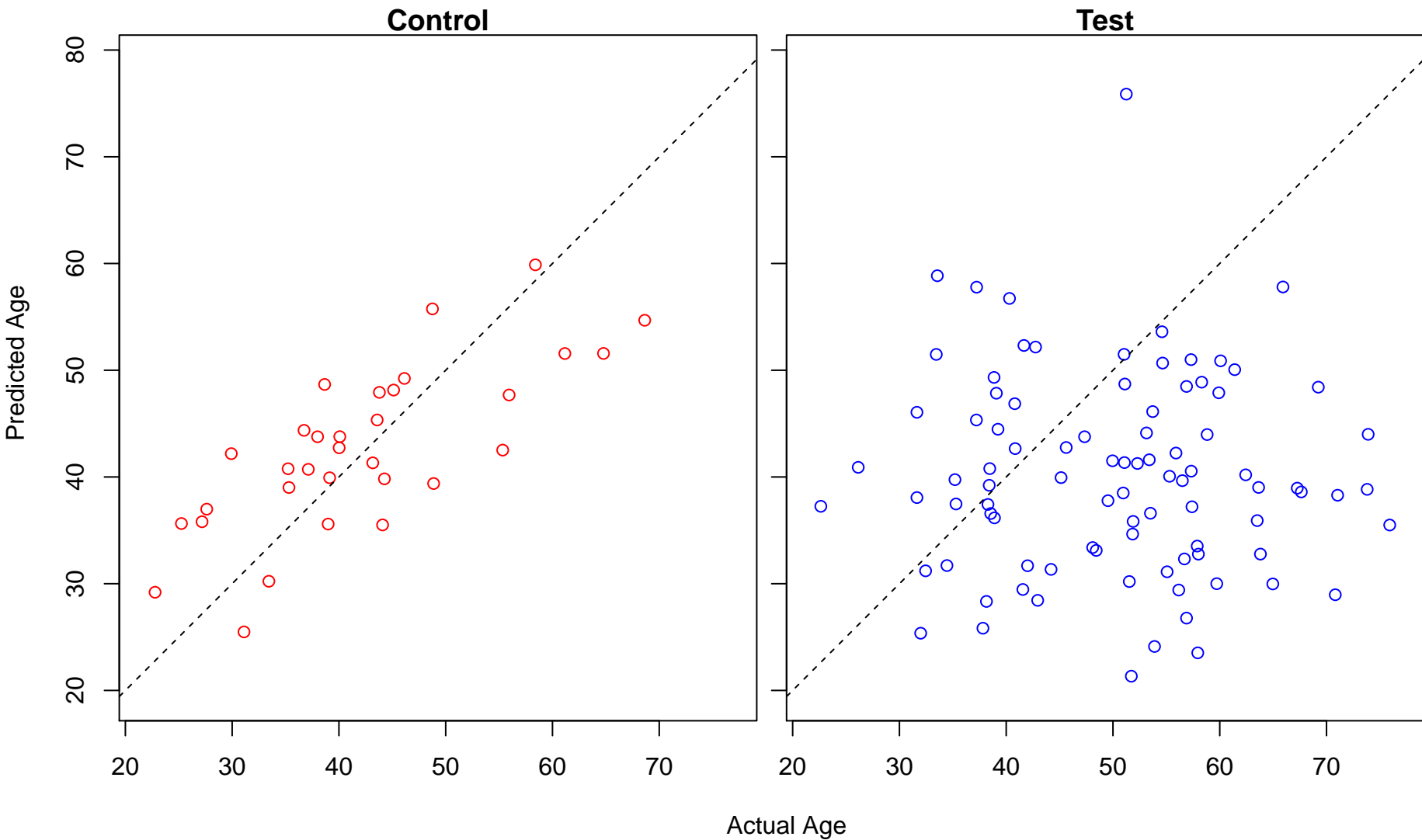
regulation of sodium ion transmembrane transporter activity (Score: 2.326888)



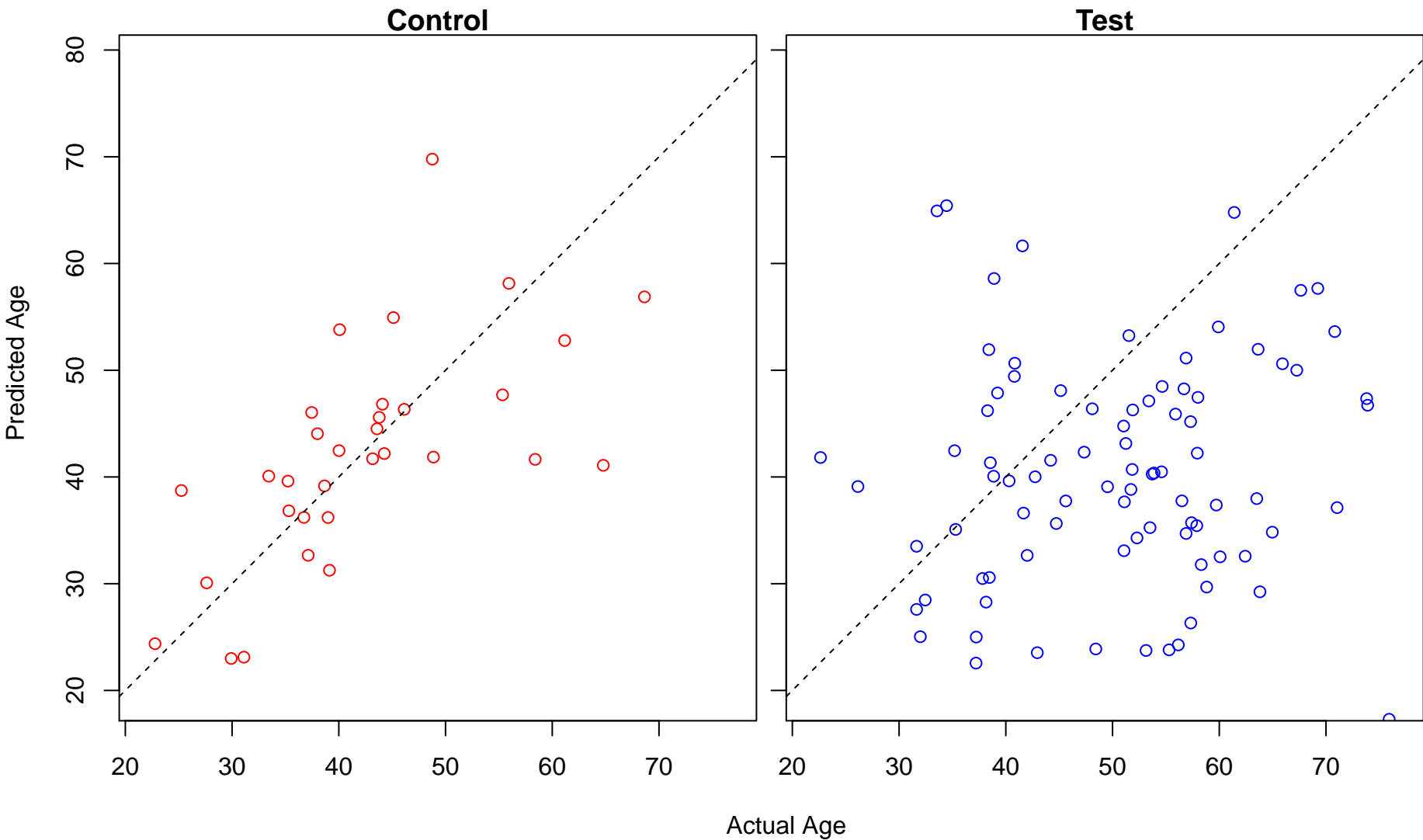
regulation of peptidyl-lysine acetylation (Score: 2.309511)



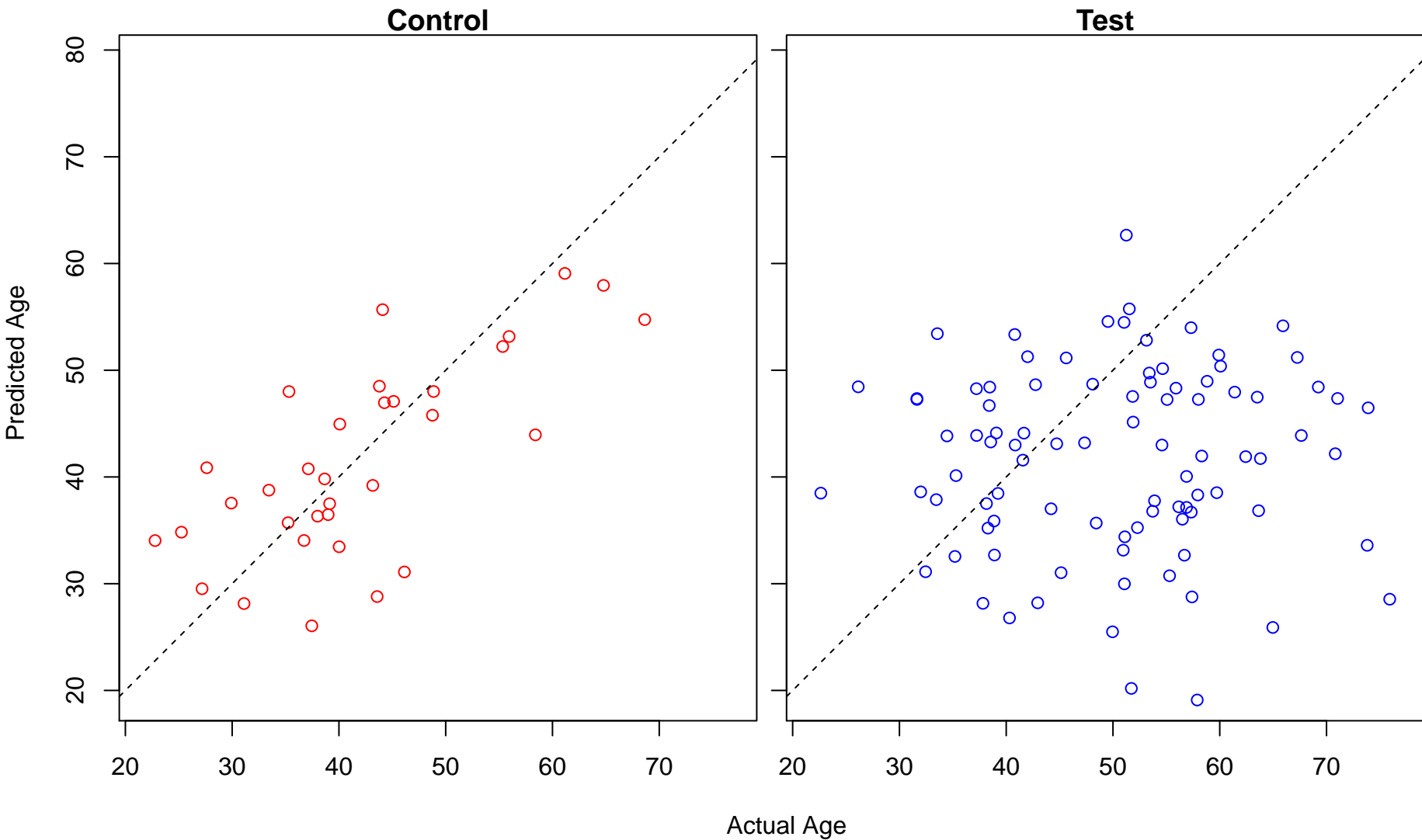
regulation of cholesterol metabolic process (Score: 2.303944)



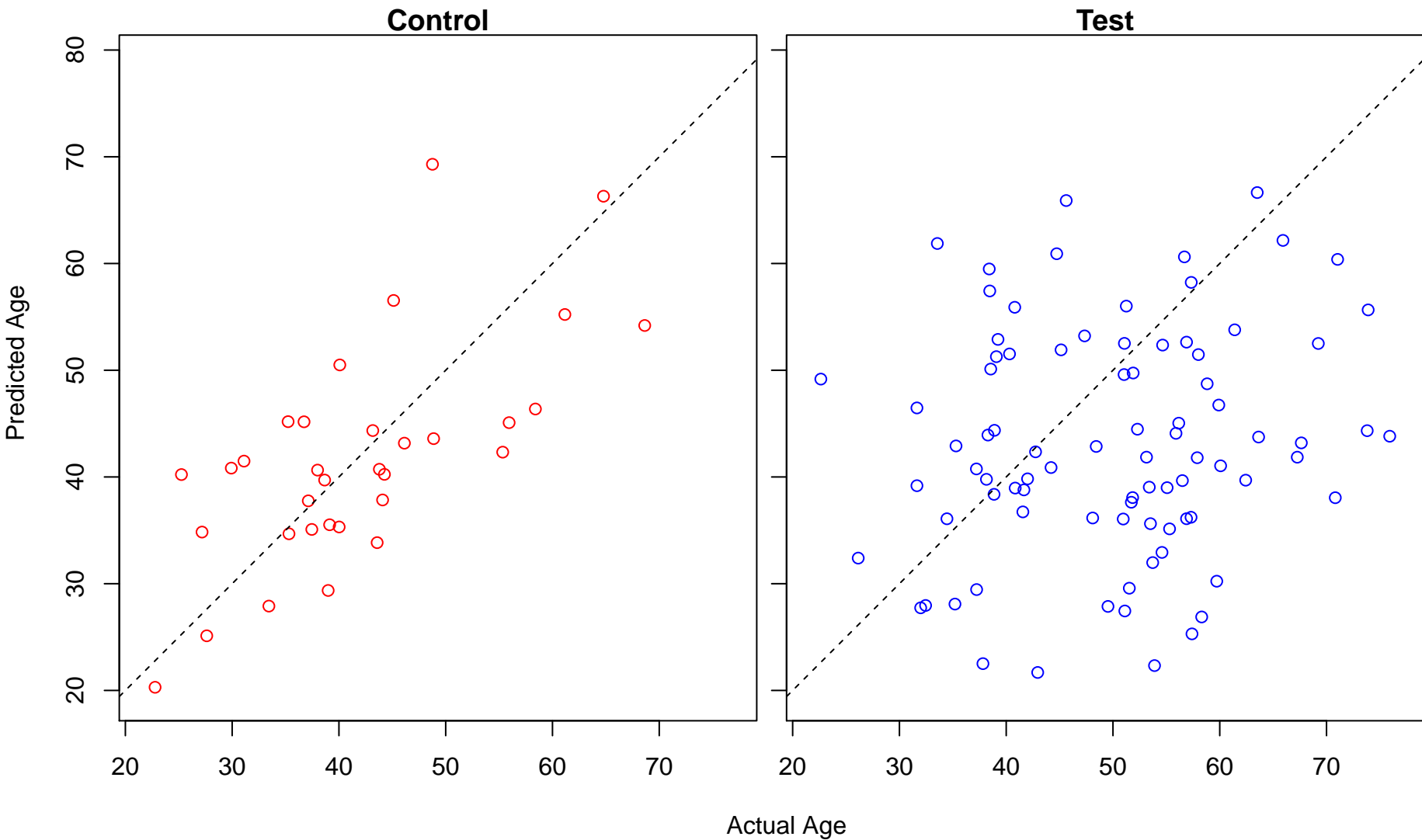
mitotic recombination (Score: 2.302113)



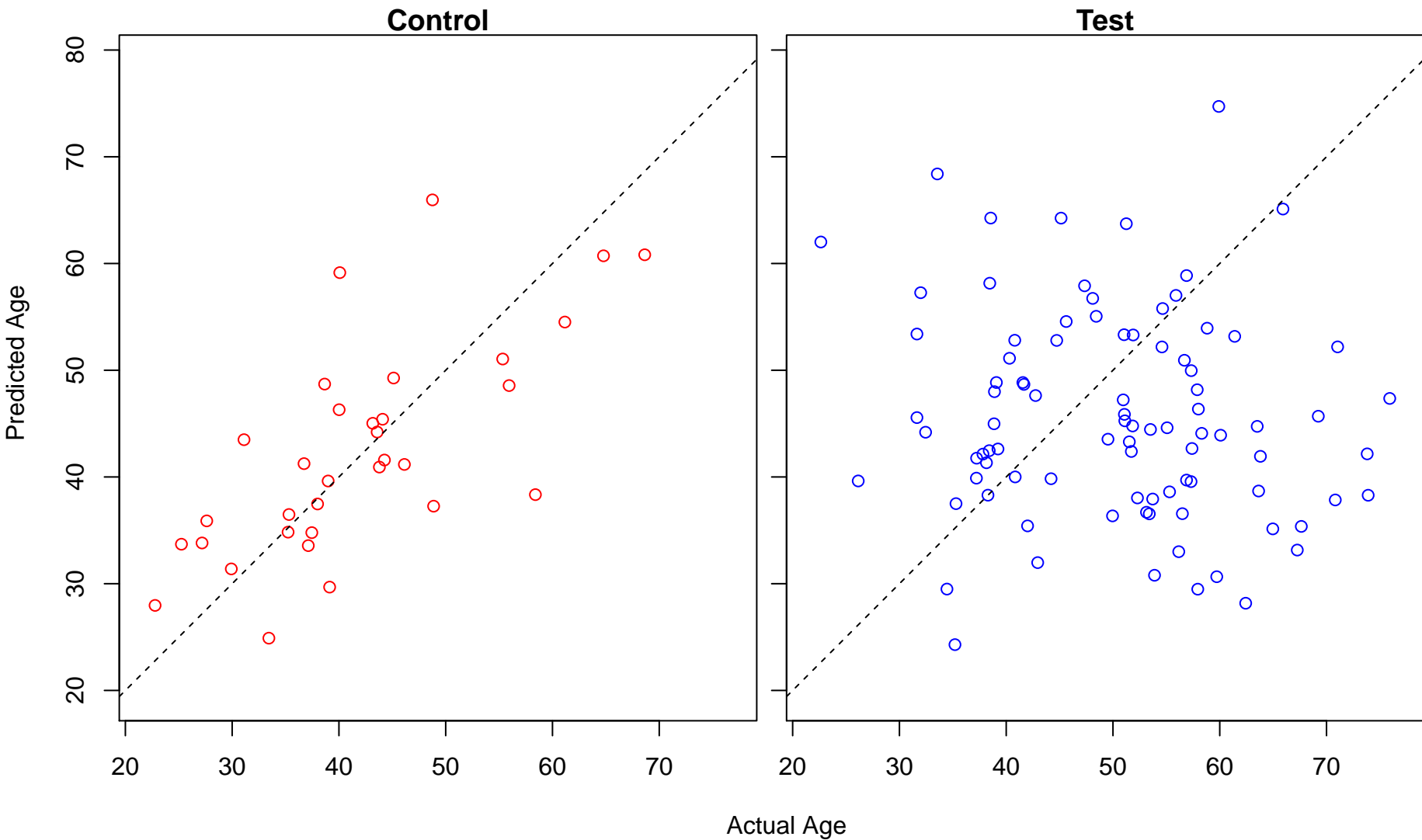
digestion (Score: 2.247896)



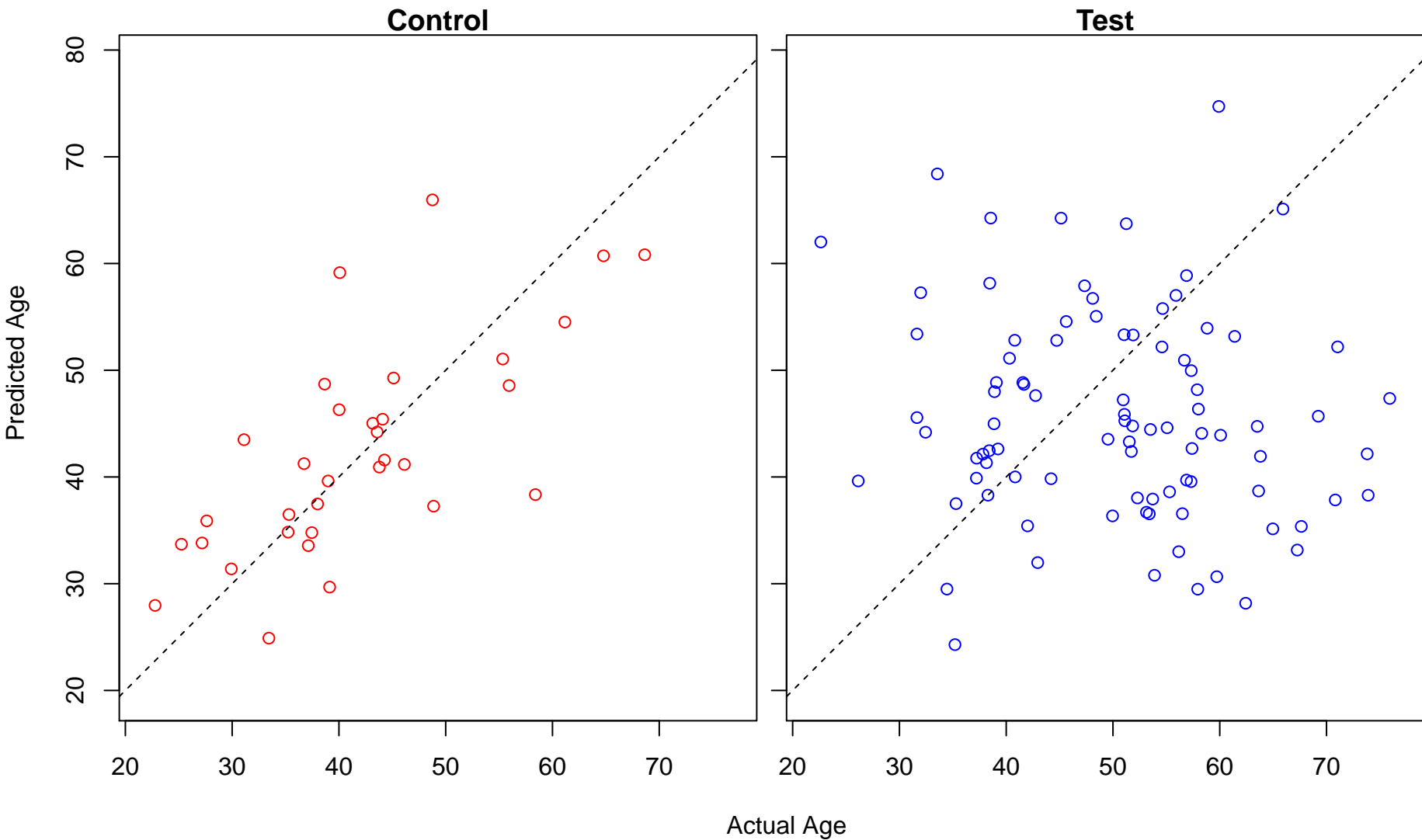
cellular response to biotic stimulus (Score: 2.241736)



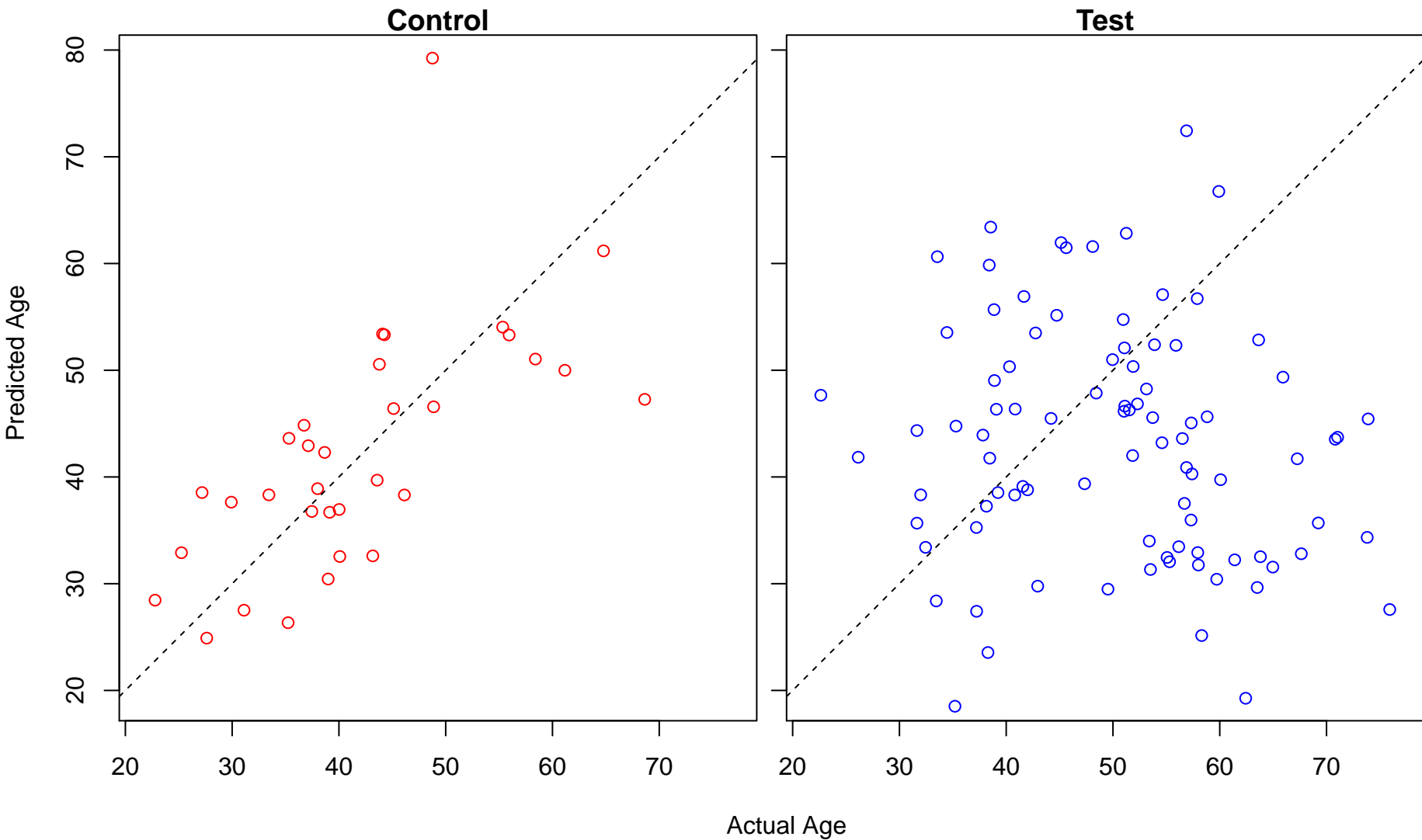
negative regulation of protein exit from endoplasmic reticulum (Score: 2.222812)



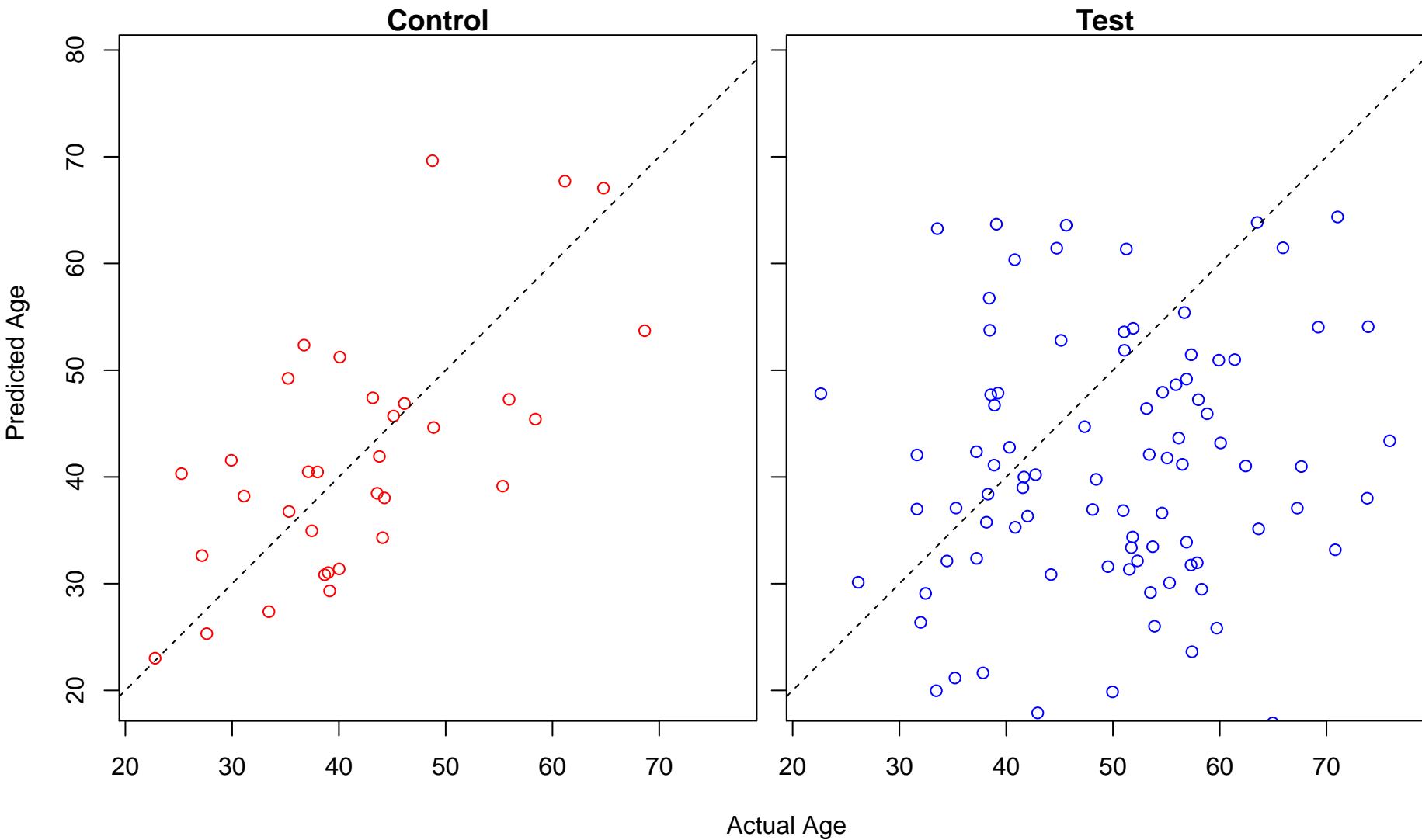
negative regulation of retrograde protein transport, ER to cytosol (Score: 2.222812)



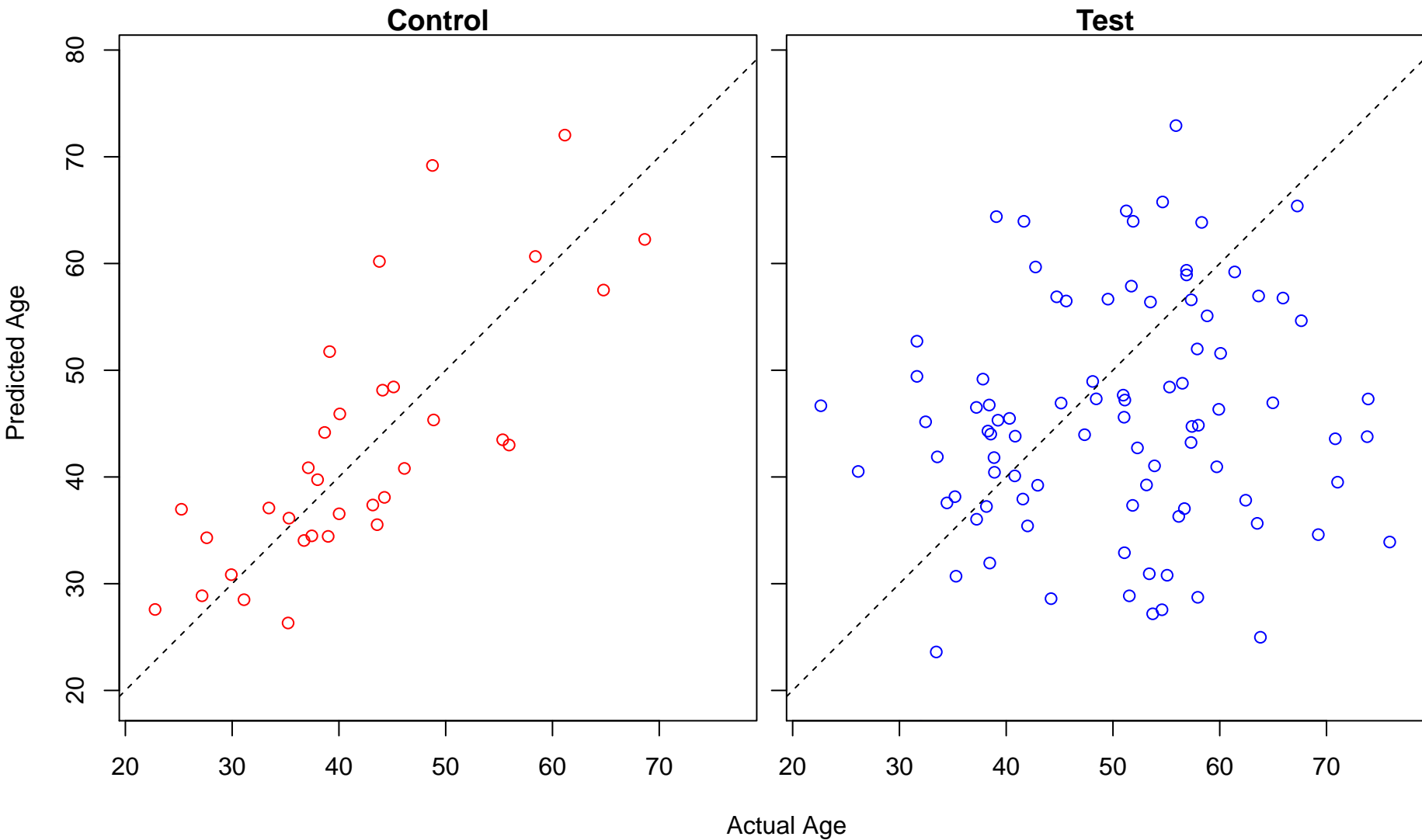
negative regulation of peptidyl-lysine acetylation (Score: 2.203685)



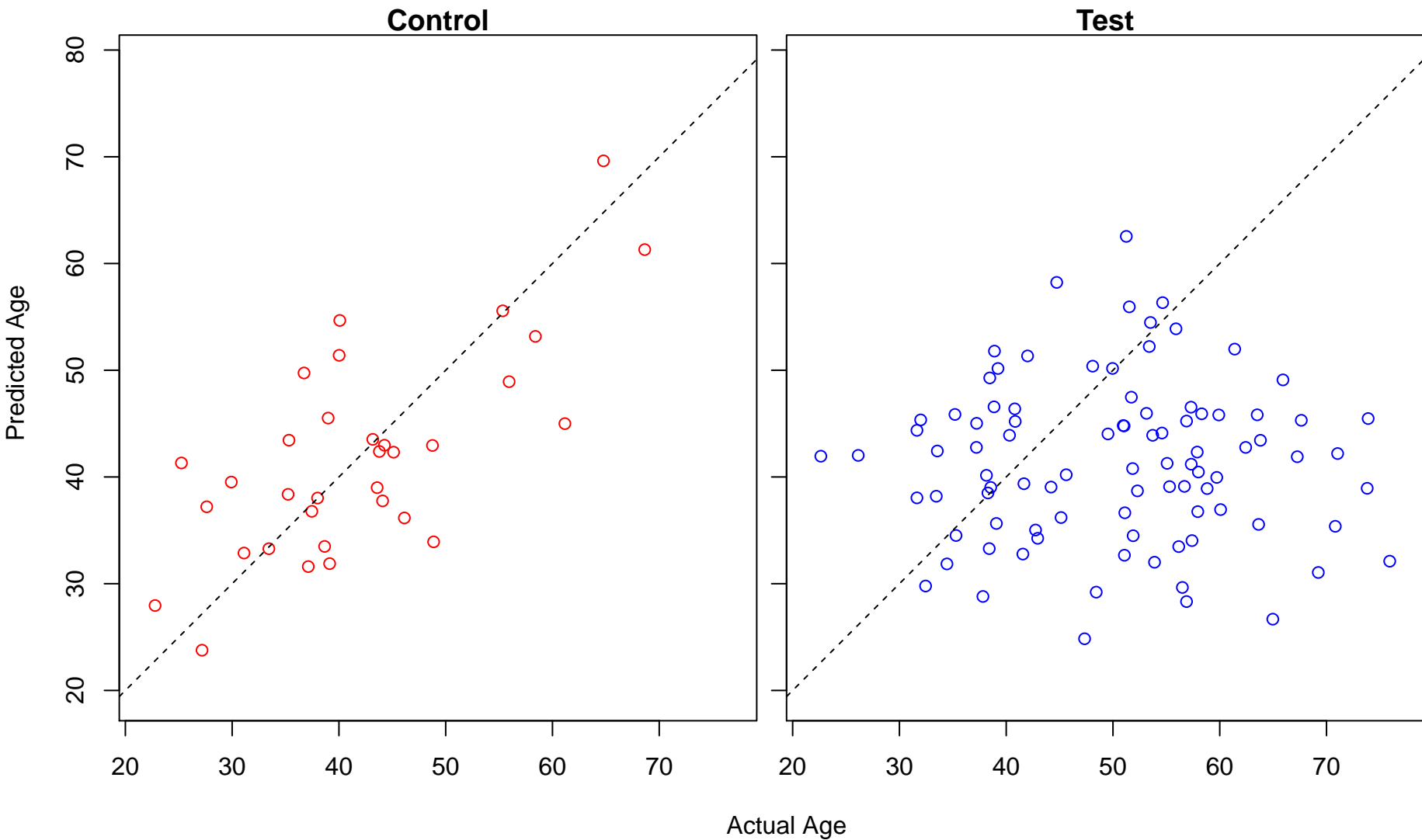
cellular response to molecule of bacterial origin (Score: 2.191727)



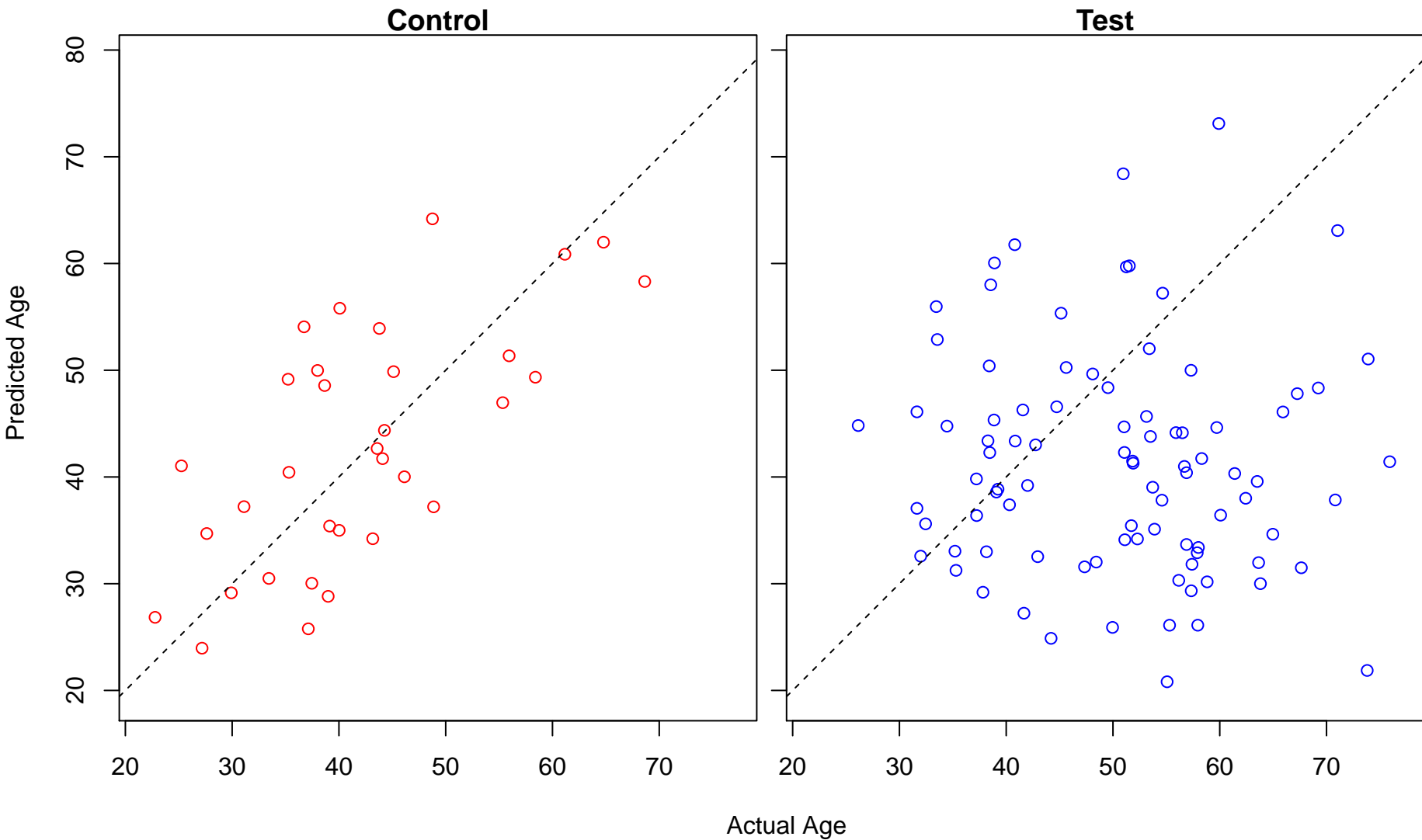
regulation of leukocyte degranulation (Score: 2.186430)



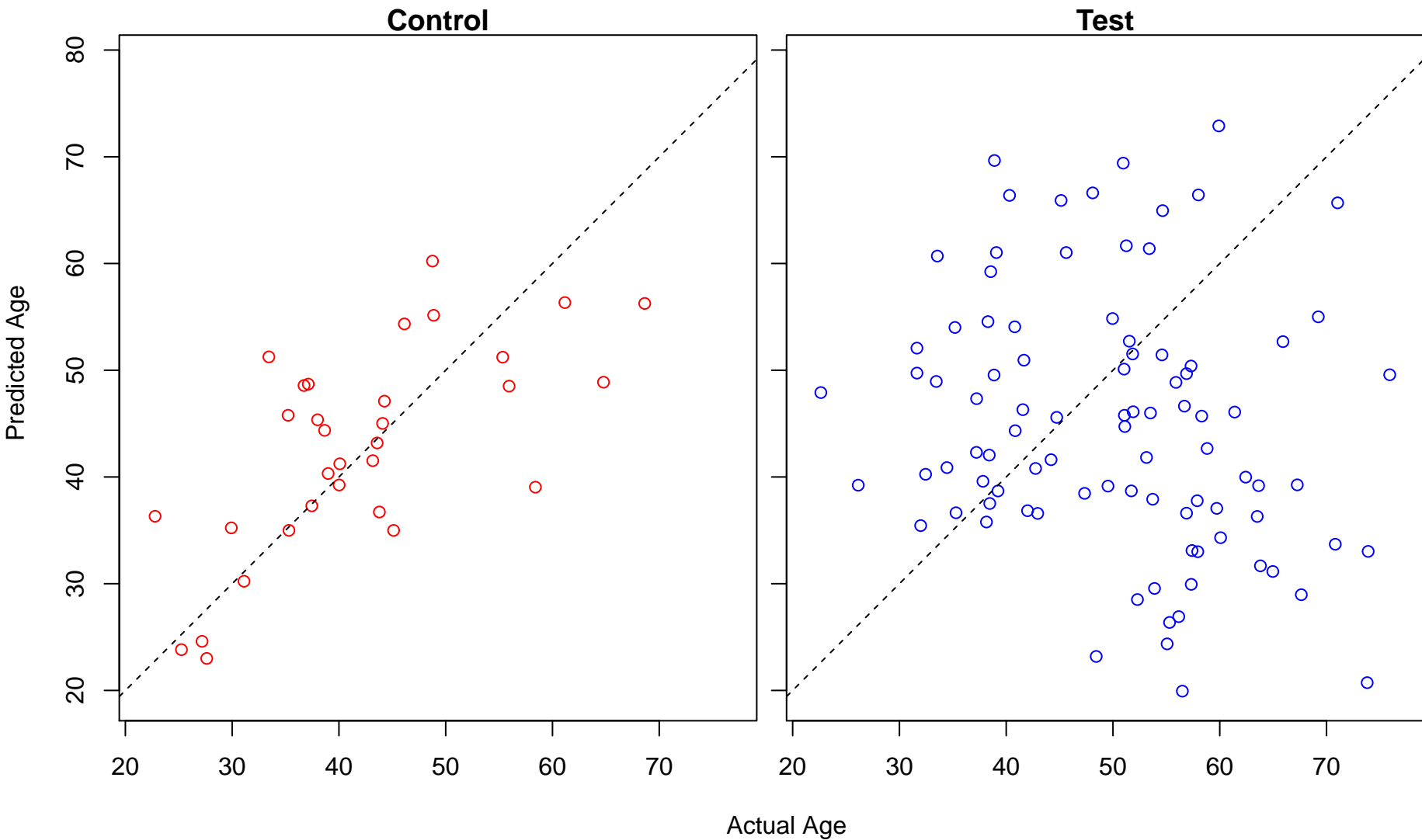
bile acid and bile salt transport (Score: 2.175692)



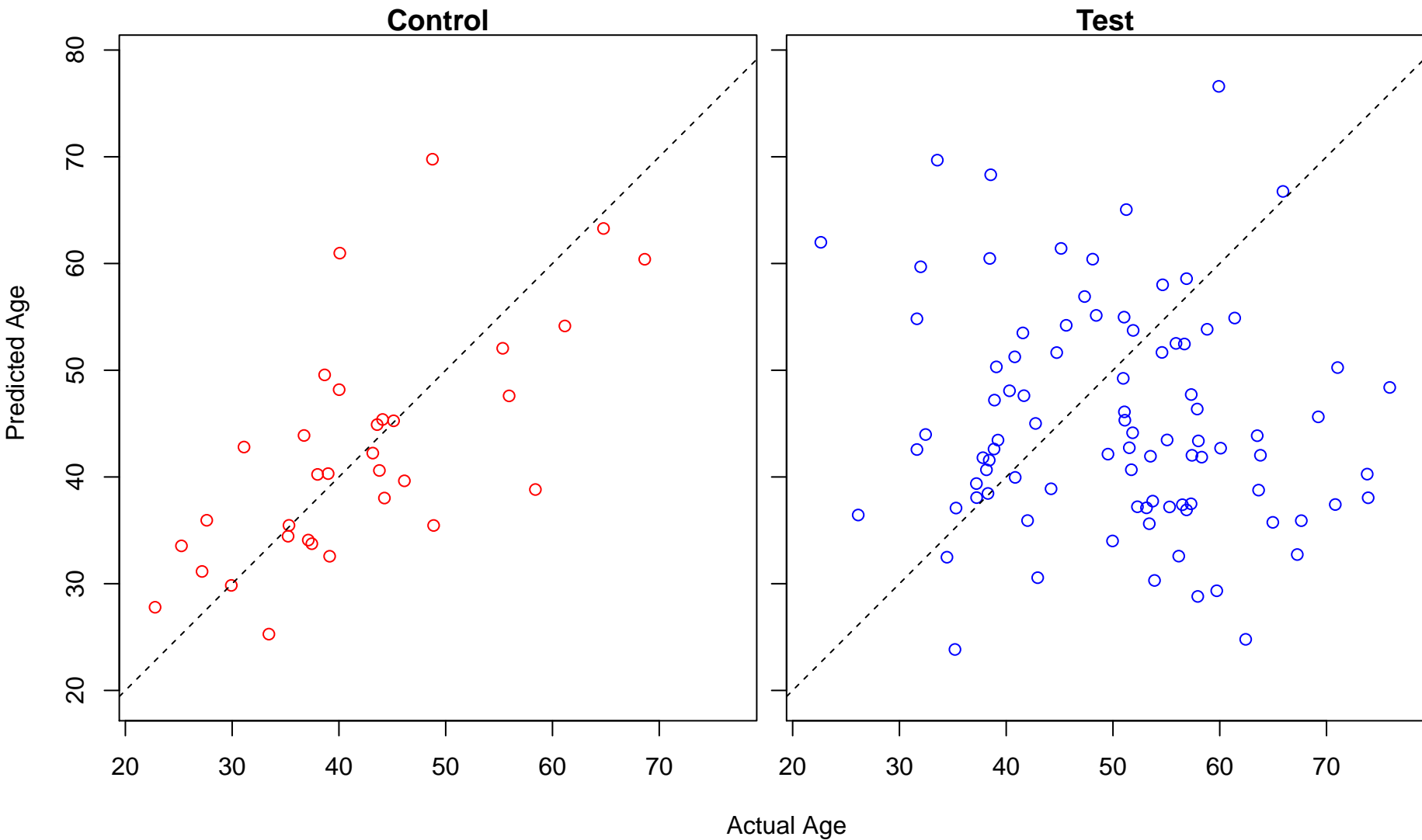
organophosphate catabolic process (Score: 2.173843)



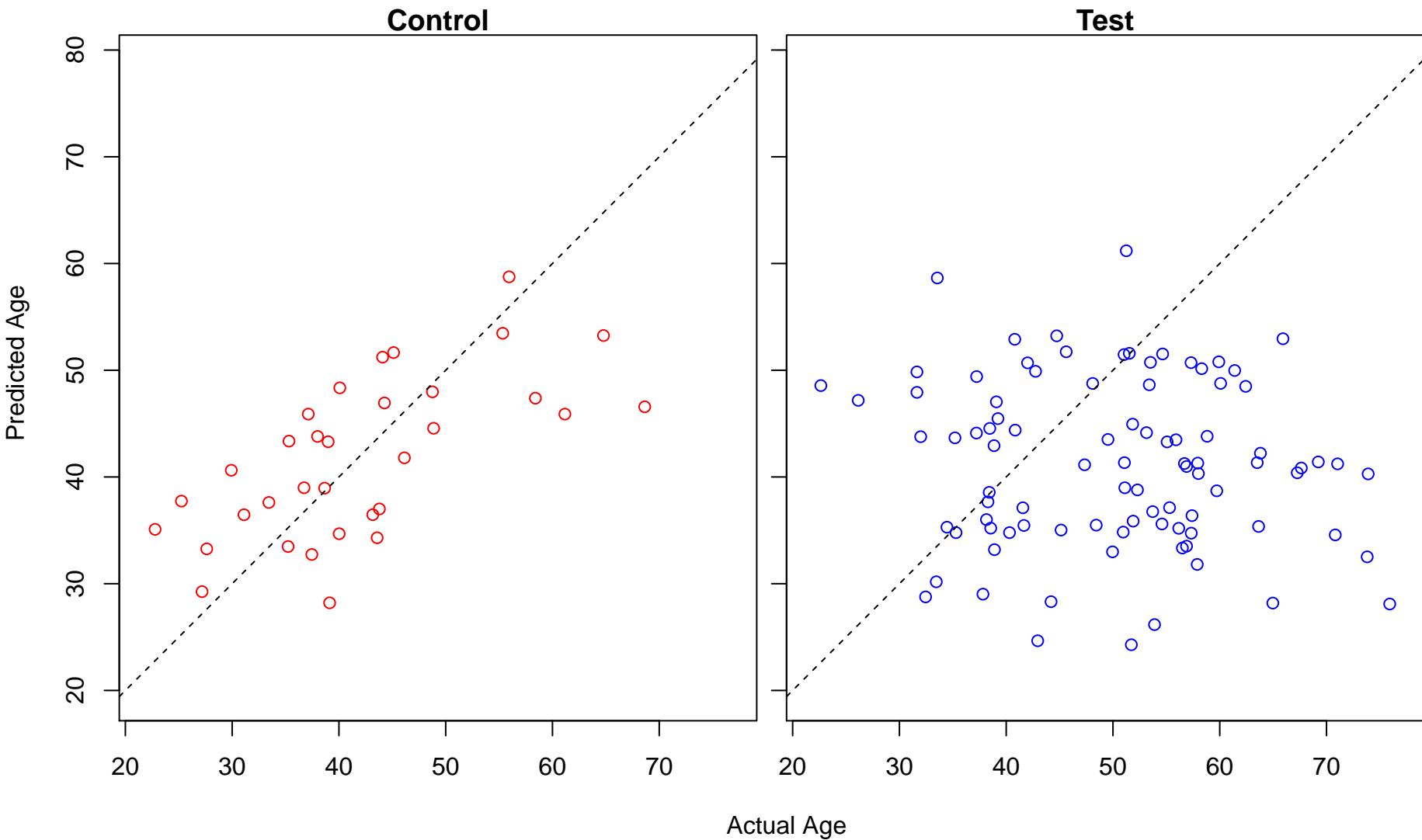
regulation of transcription from RNA polymerase I promoter (Score: 2.171239)



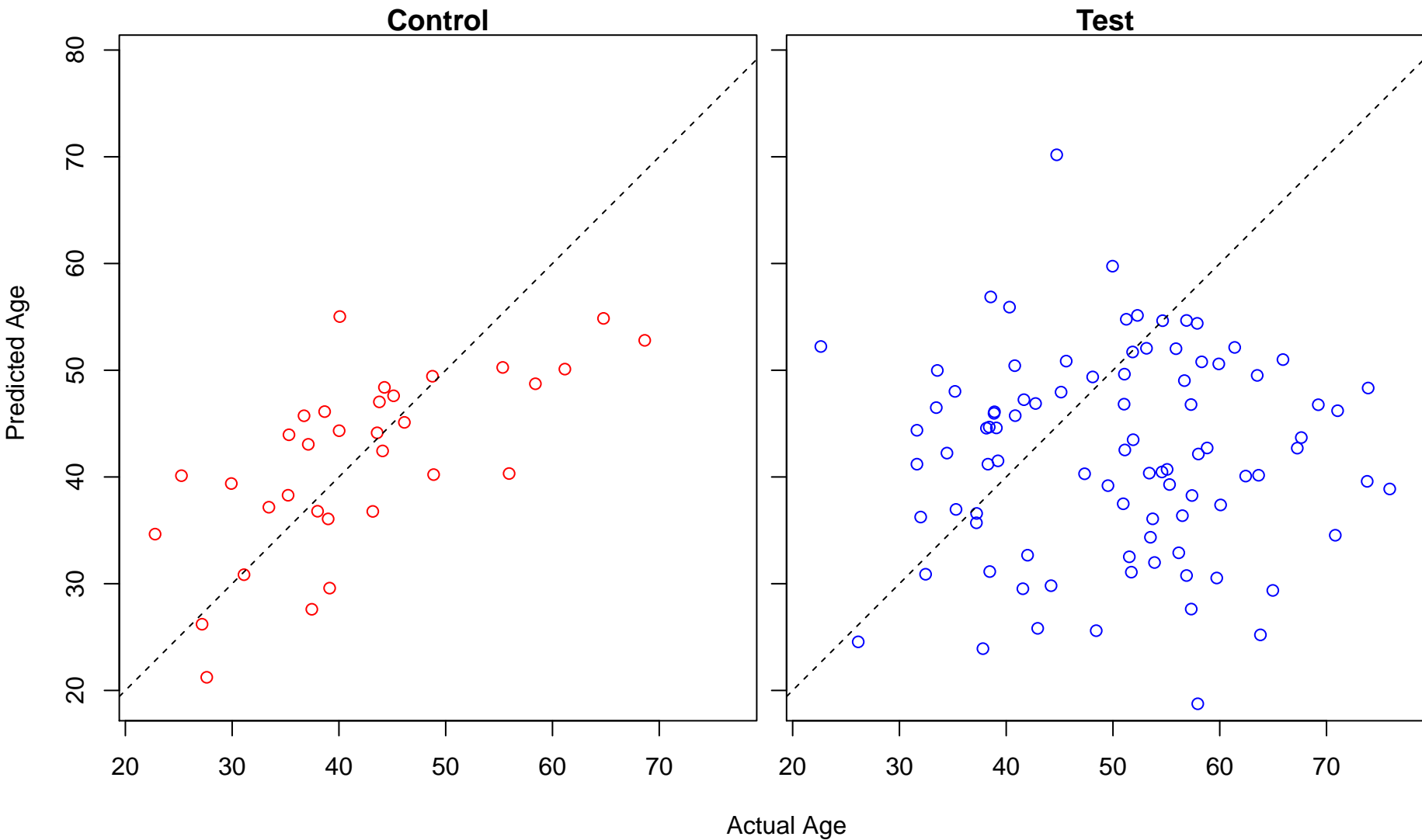
negative regulation of ERAD pathway (Score: 2.165816)



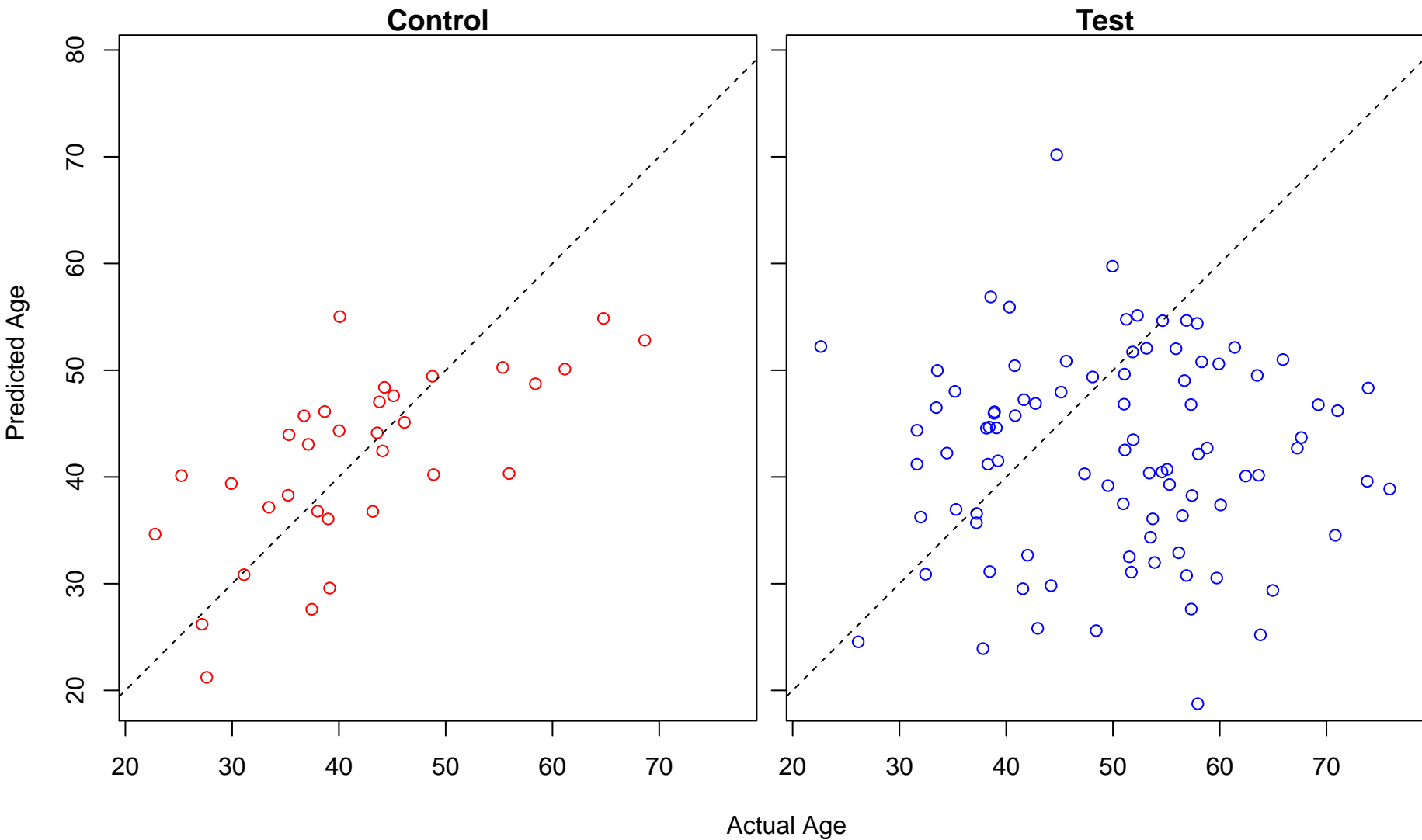
digestive system process (Score: 2.154327)



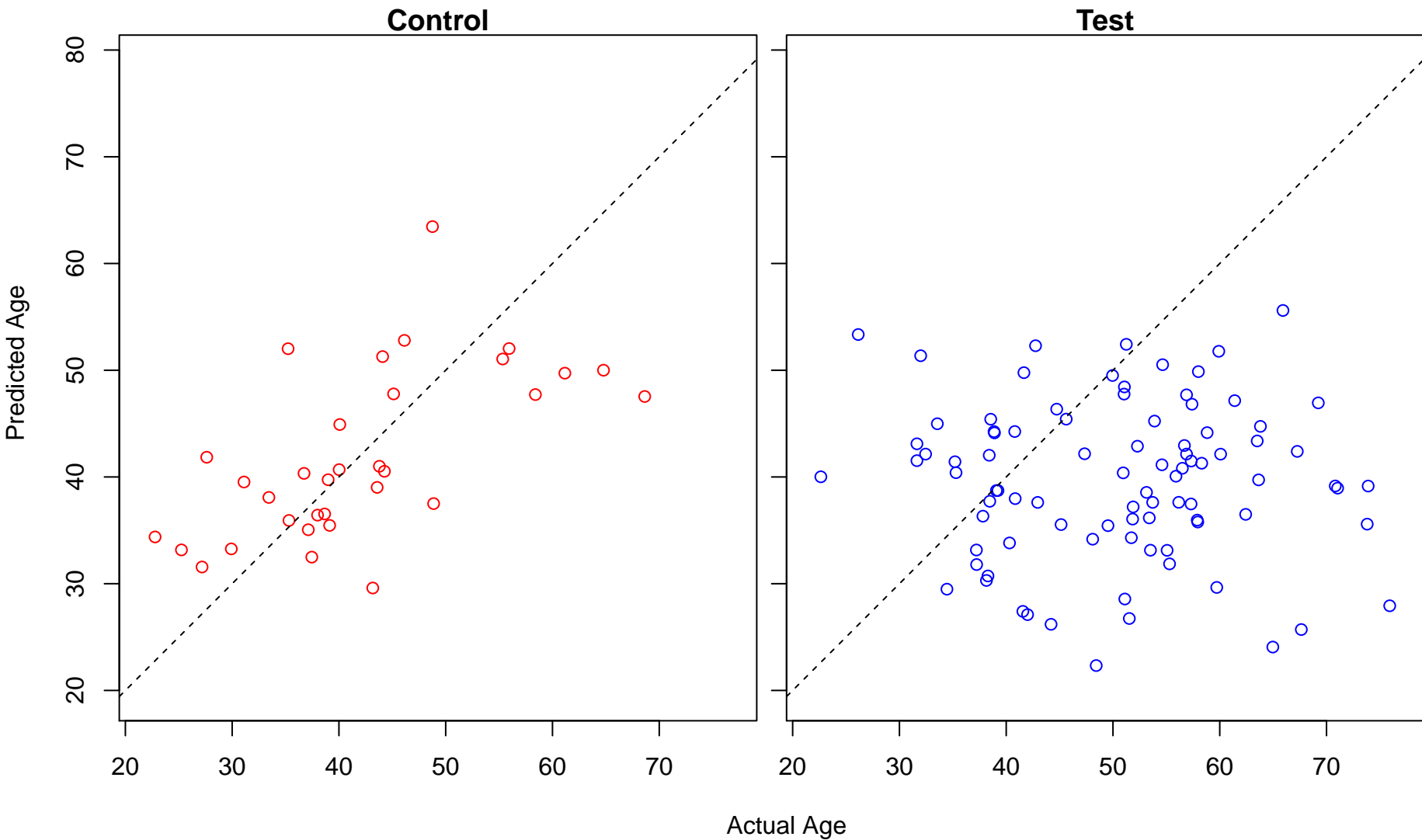
peroxisomal membrane transport (Score: 2.137529)



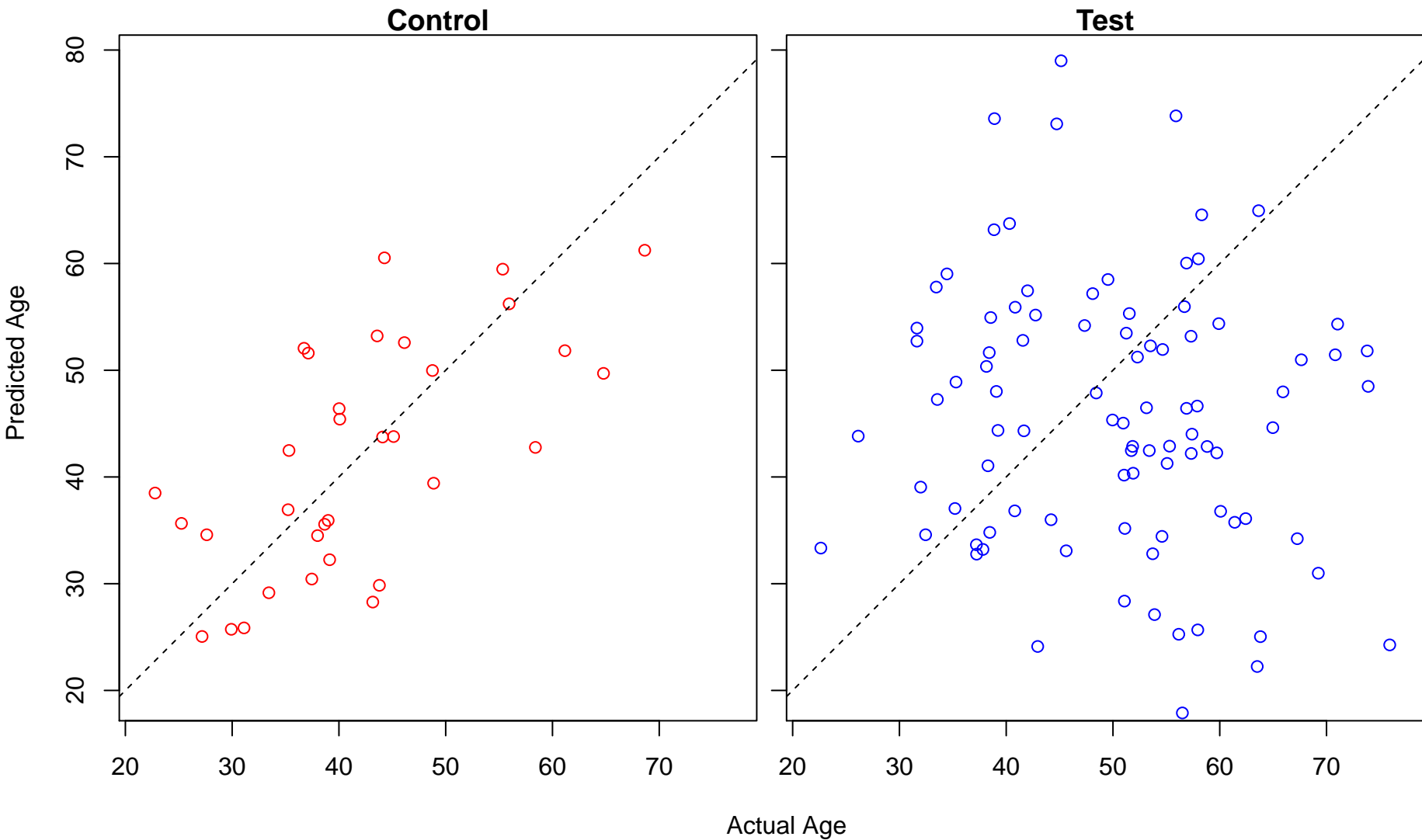
protein import into peroxisome membrane (Score: 2.137529)



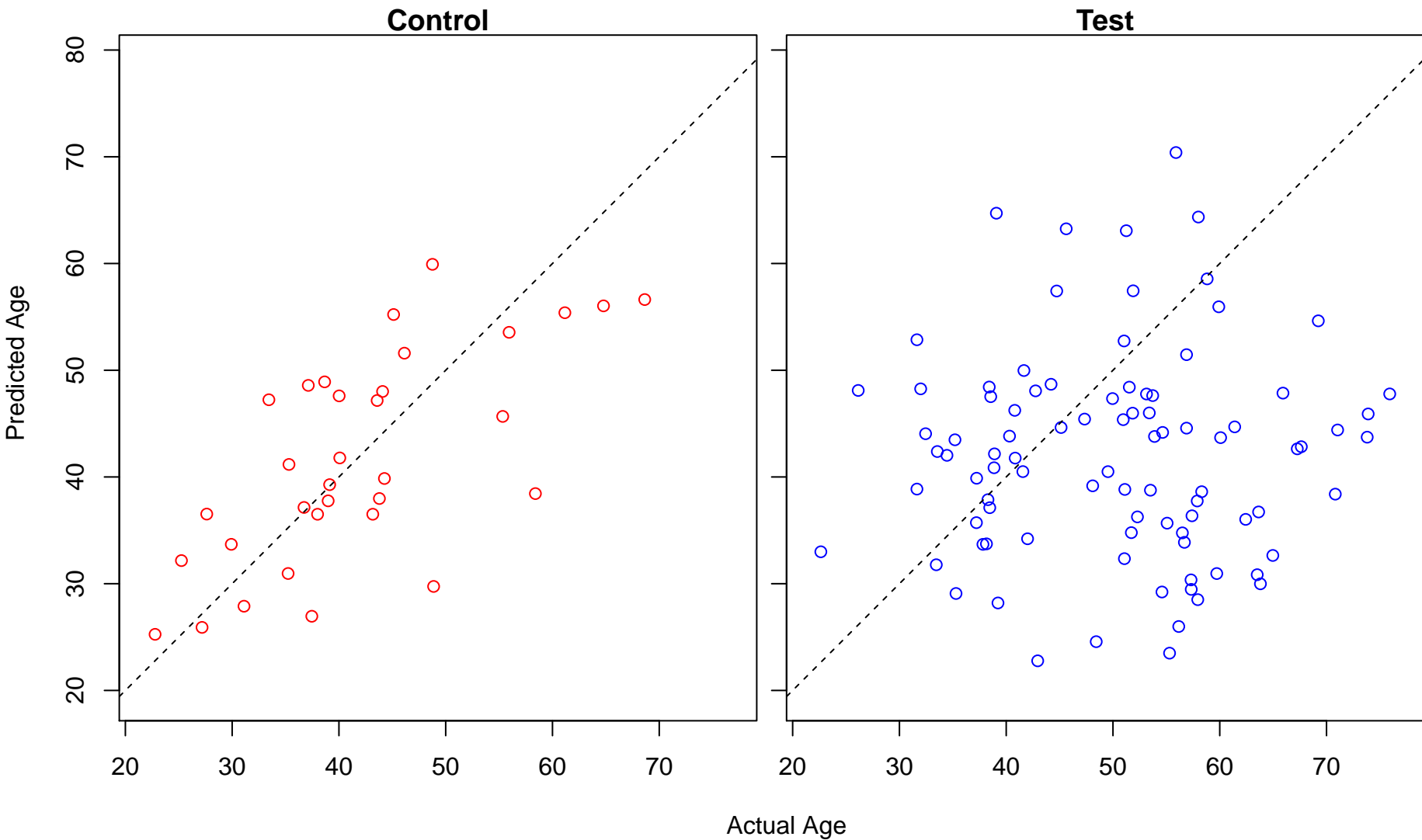
cell communication involved in cardiac conduction (Score: 2.109232)



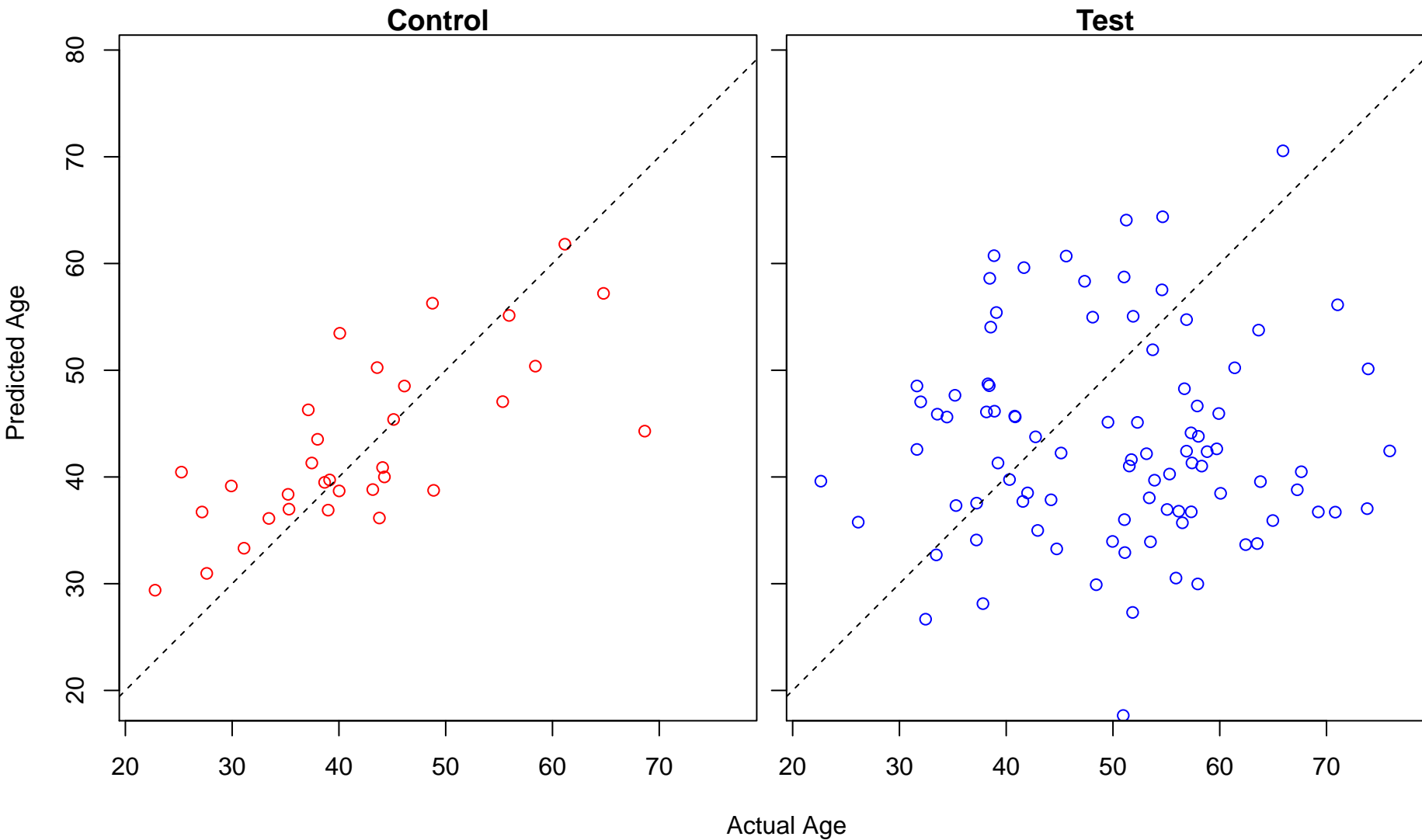
regulation of nitric oxide biosynthetic process (Score: 2.104044)



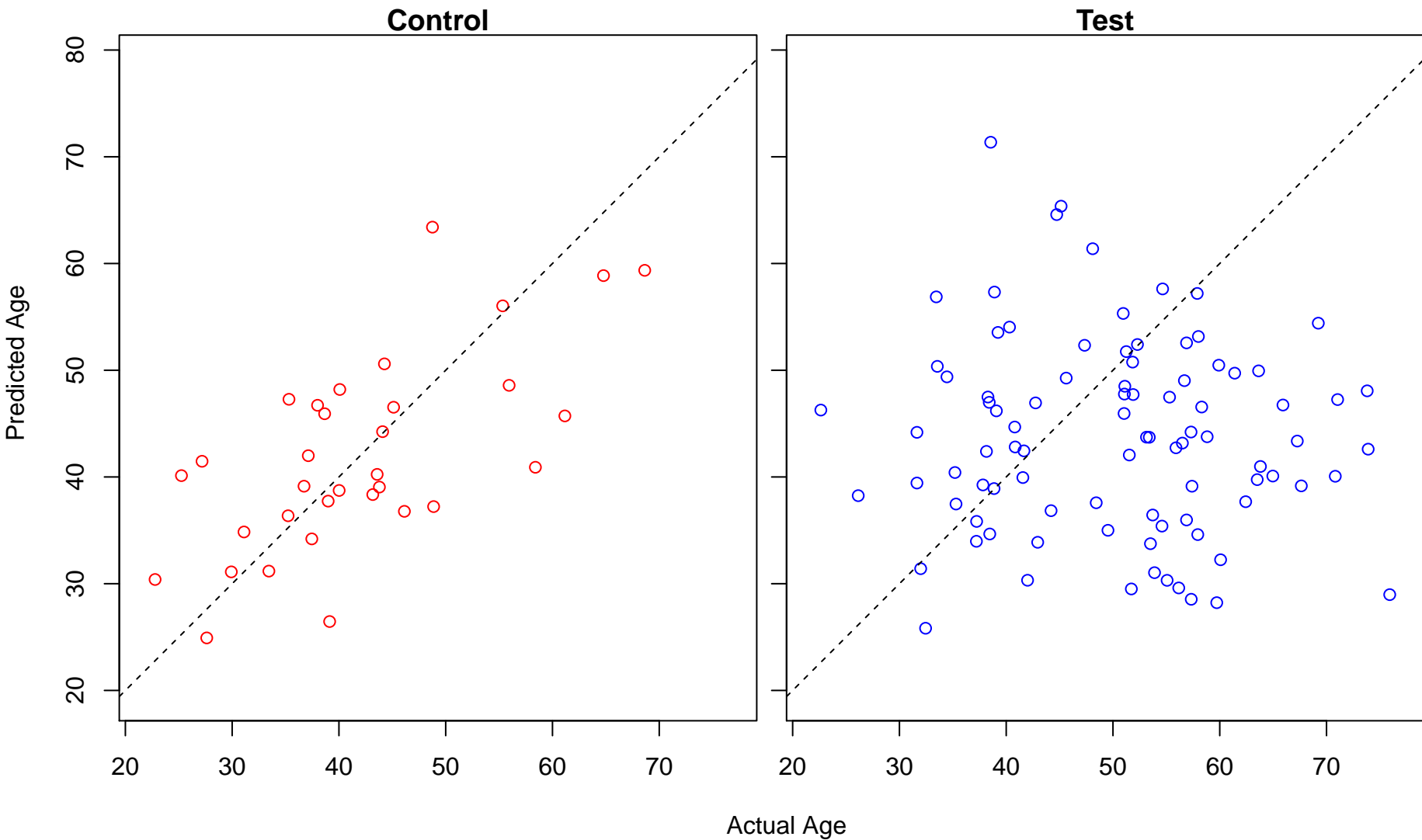
positive regulation of ion transmembrane transporter activity (Score: 2.095944)



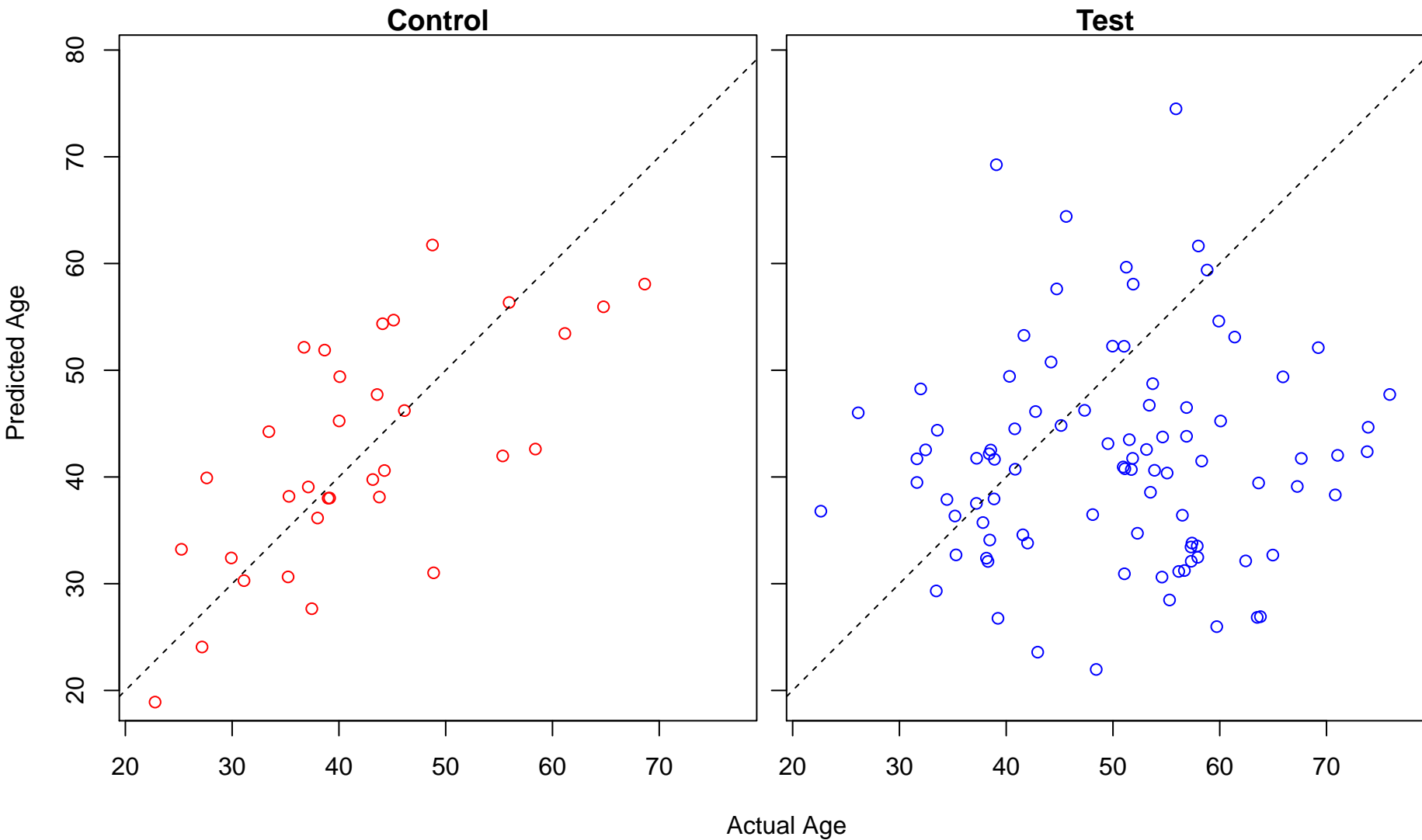
CDP-choline pathway (Score: 2.084766)



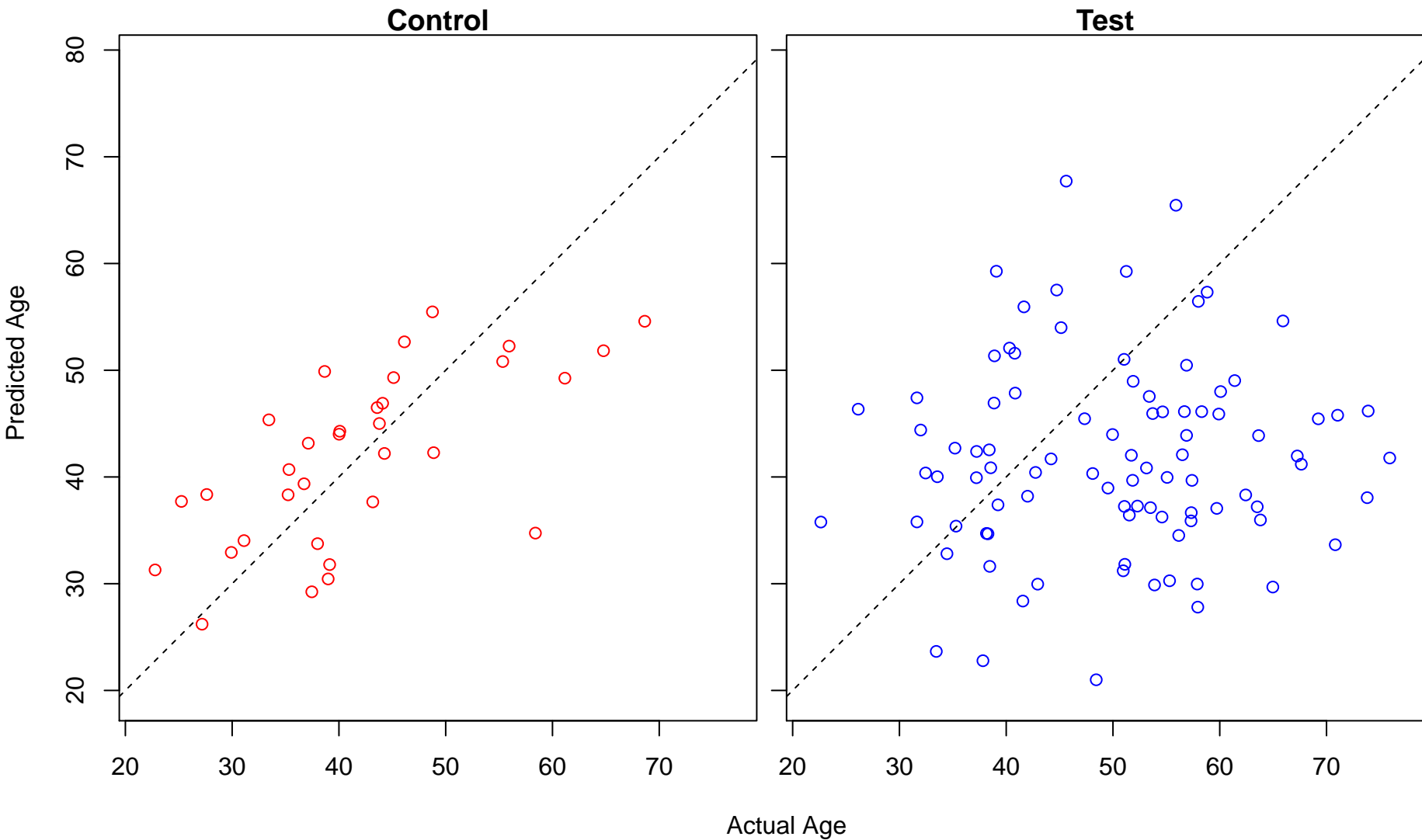
intracellular protein transmembrane import (Score: 2.074781)



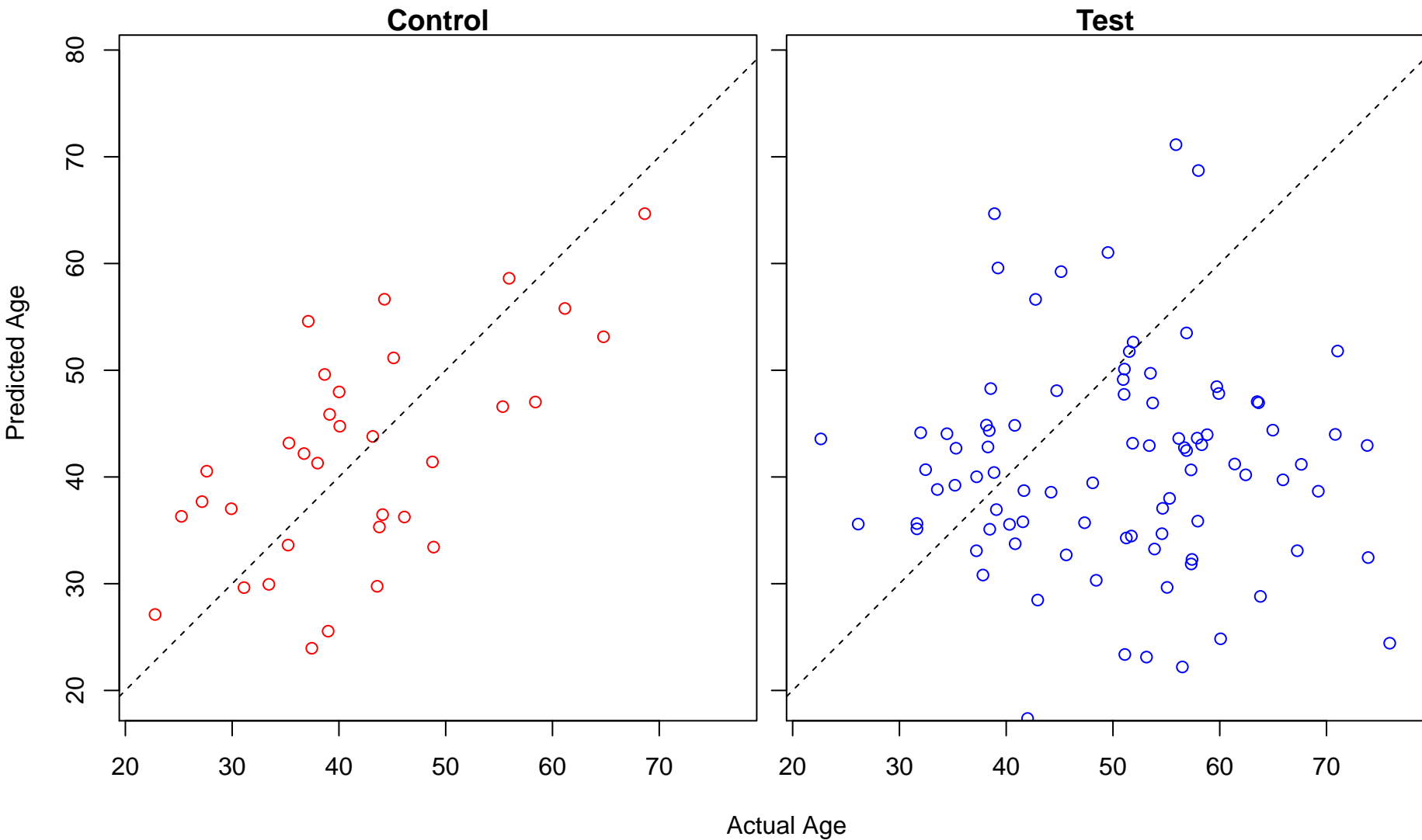
positive regulation of transporter activity (Score: 2.073830)



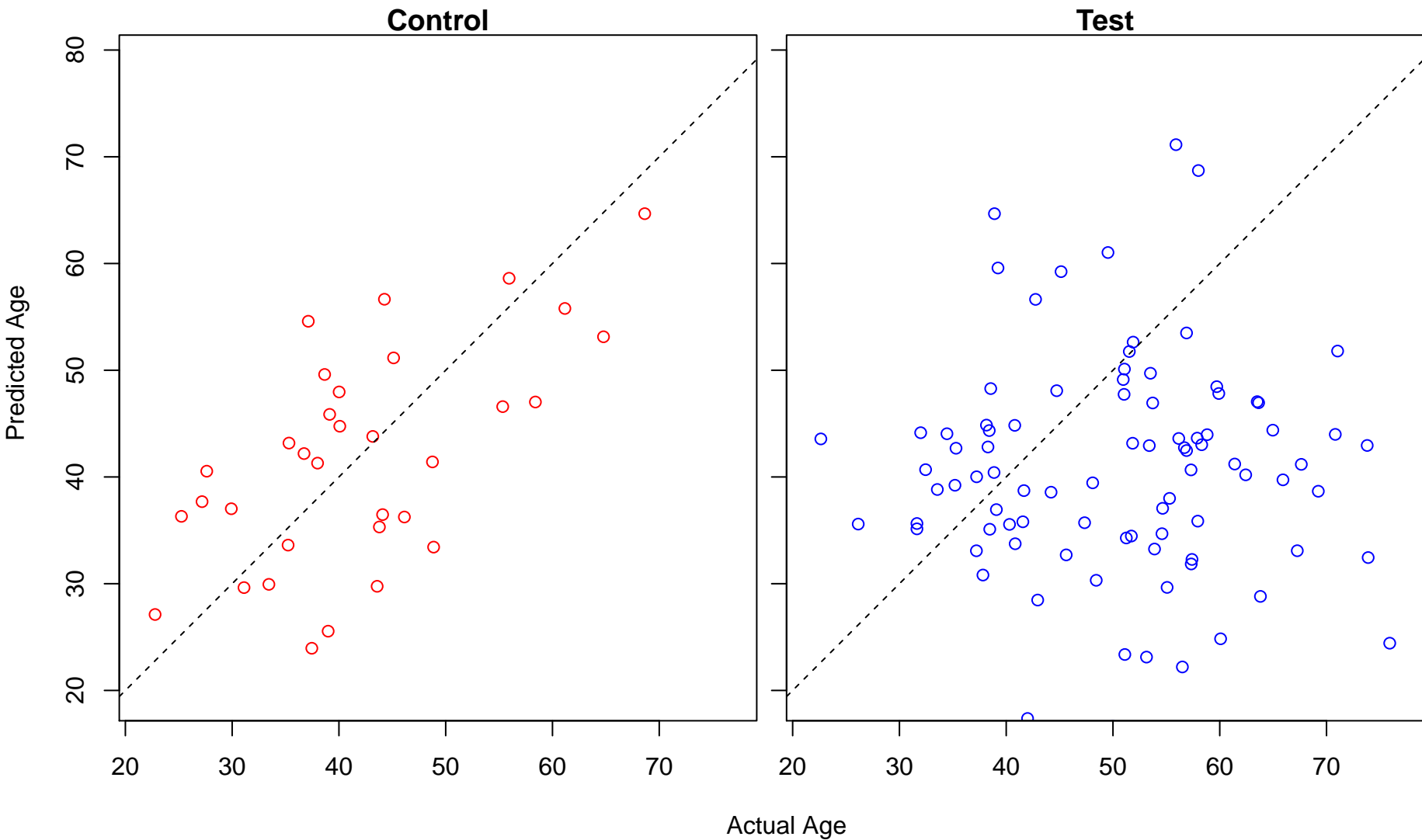
positive regulation of cation transmembrane transport (Score: 2.064155)



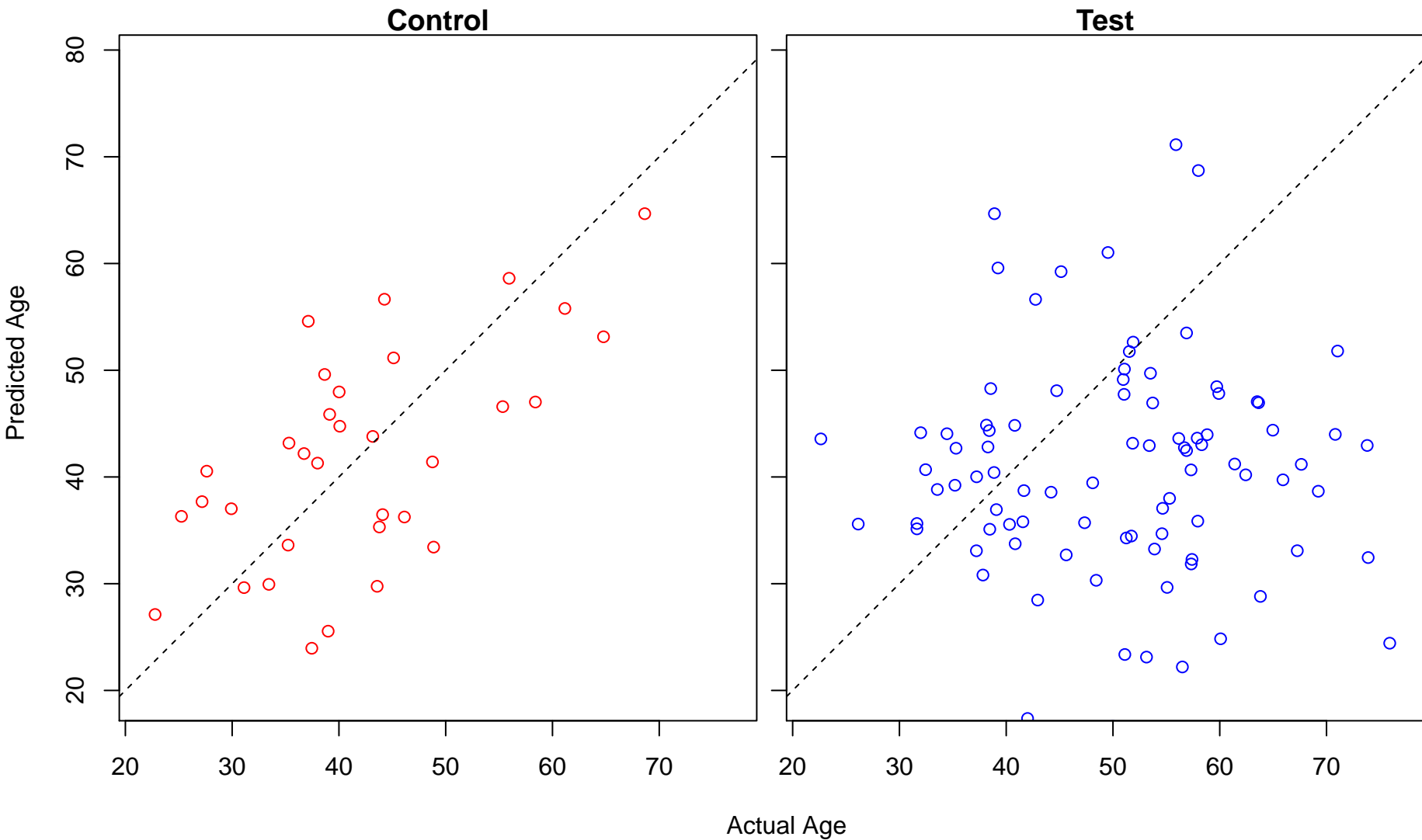
ferric iron transport (Score: 2.057467)



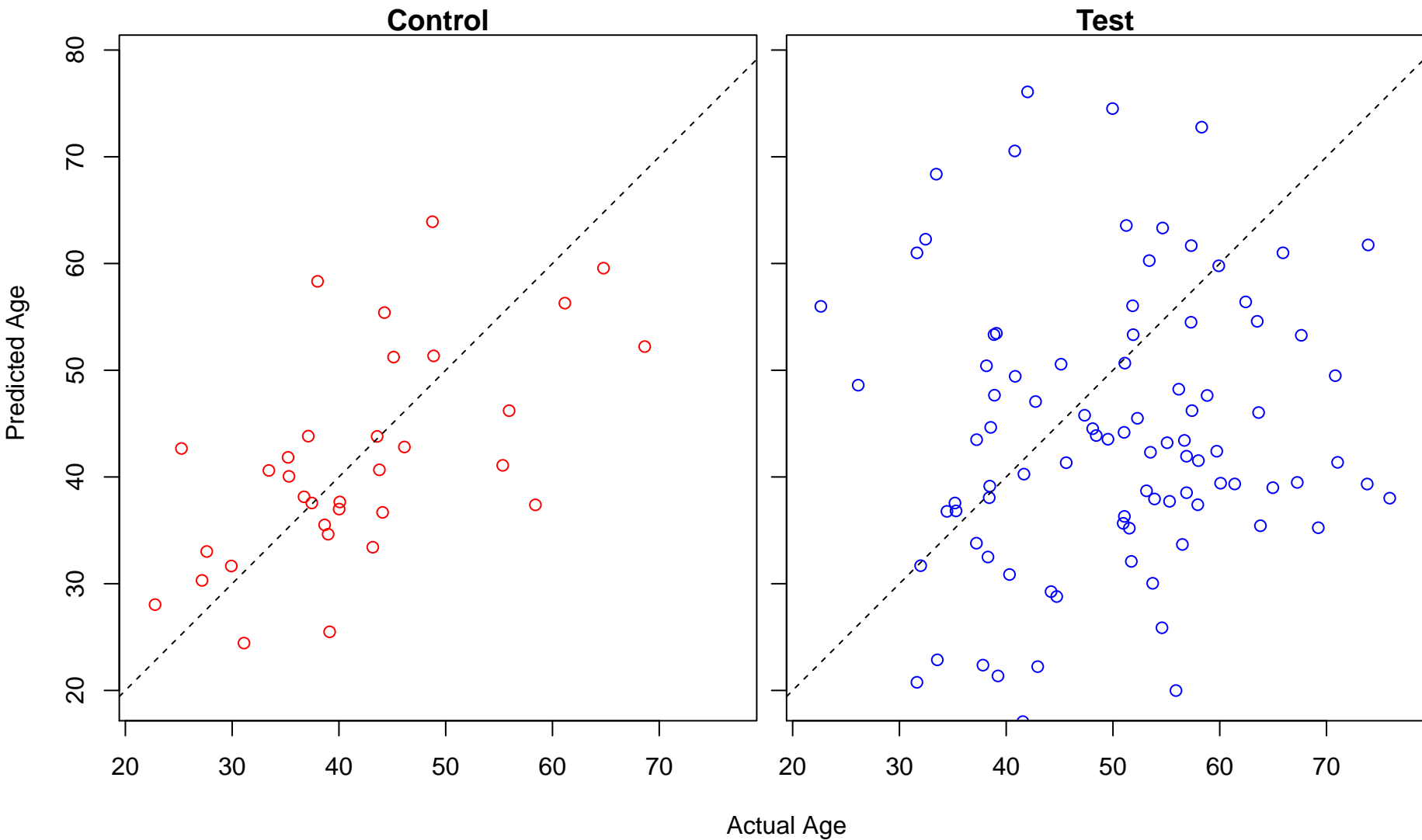
transferrin transport (Score: 2.057467)



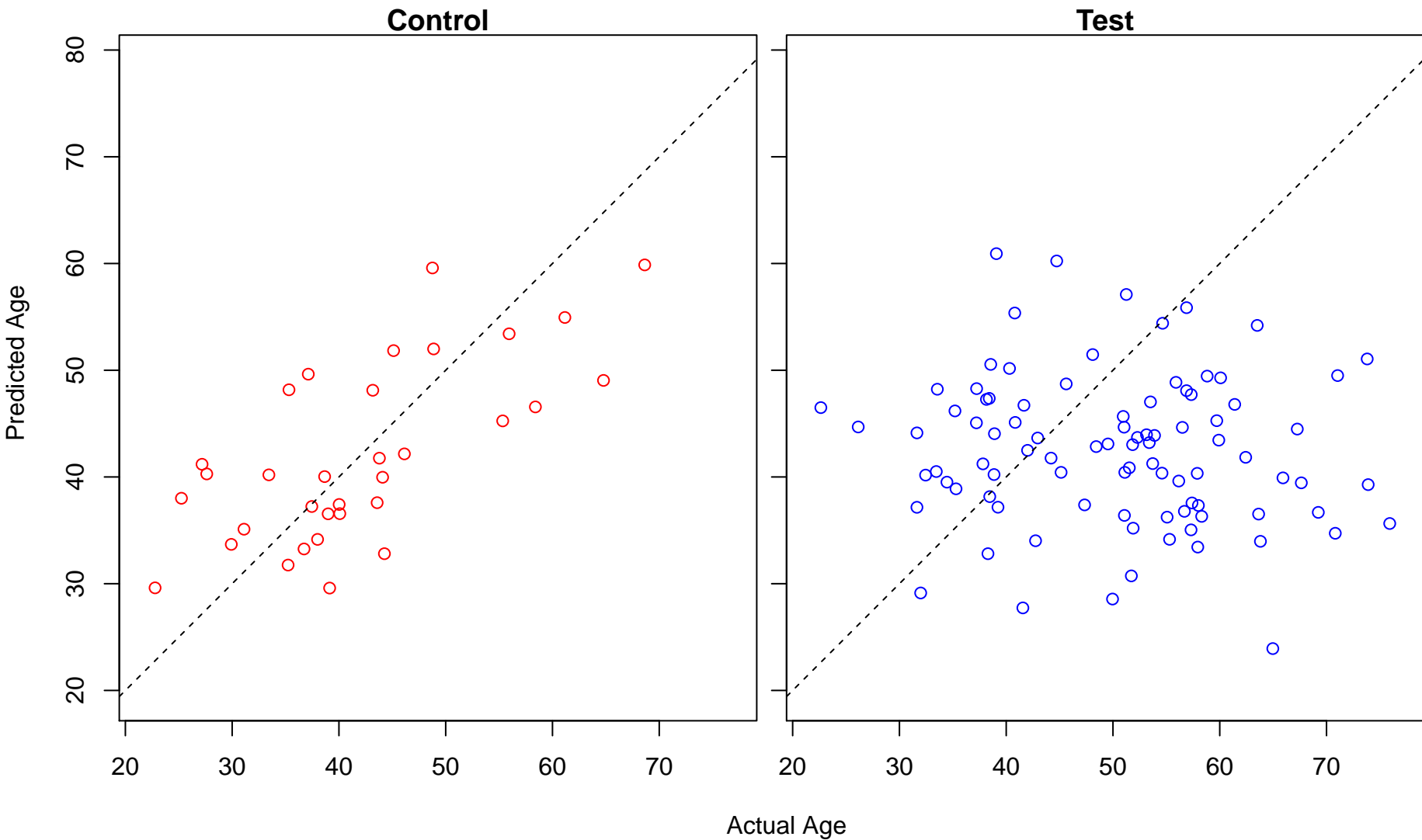
trivalent inorganic cation transport (Score: 2.057467)



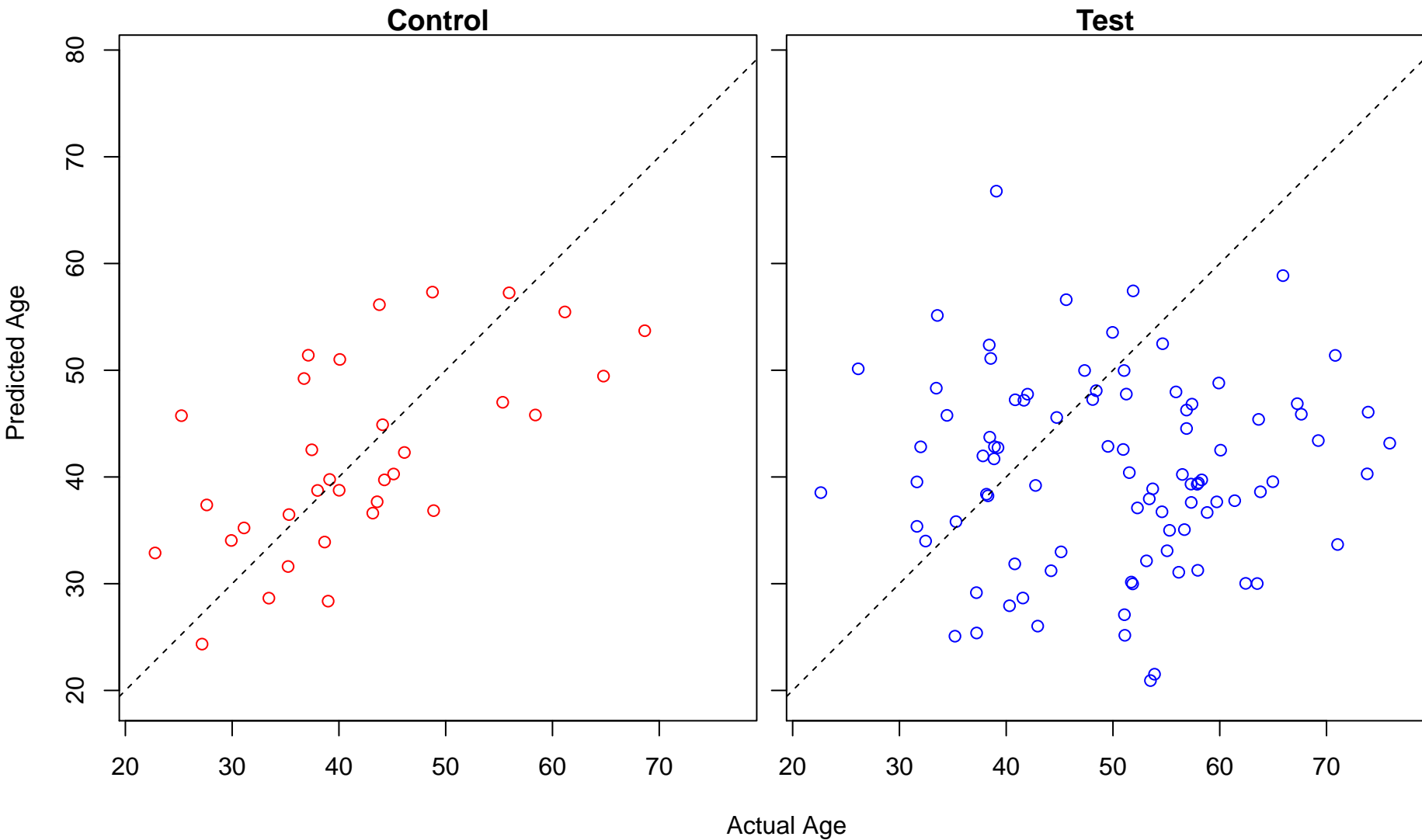
mitotic G2/M transition checkpoint (Score: 2.056037)



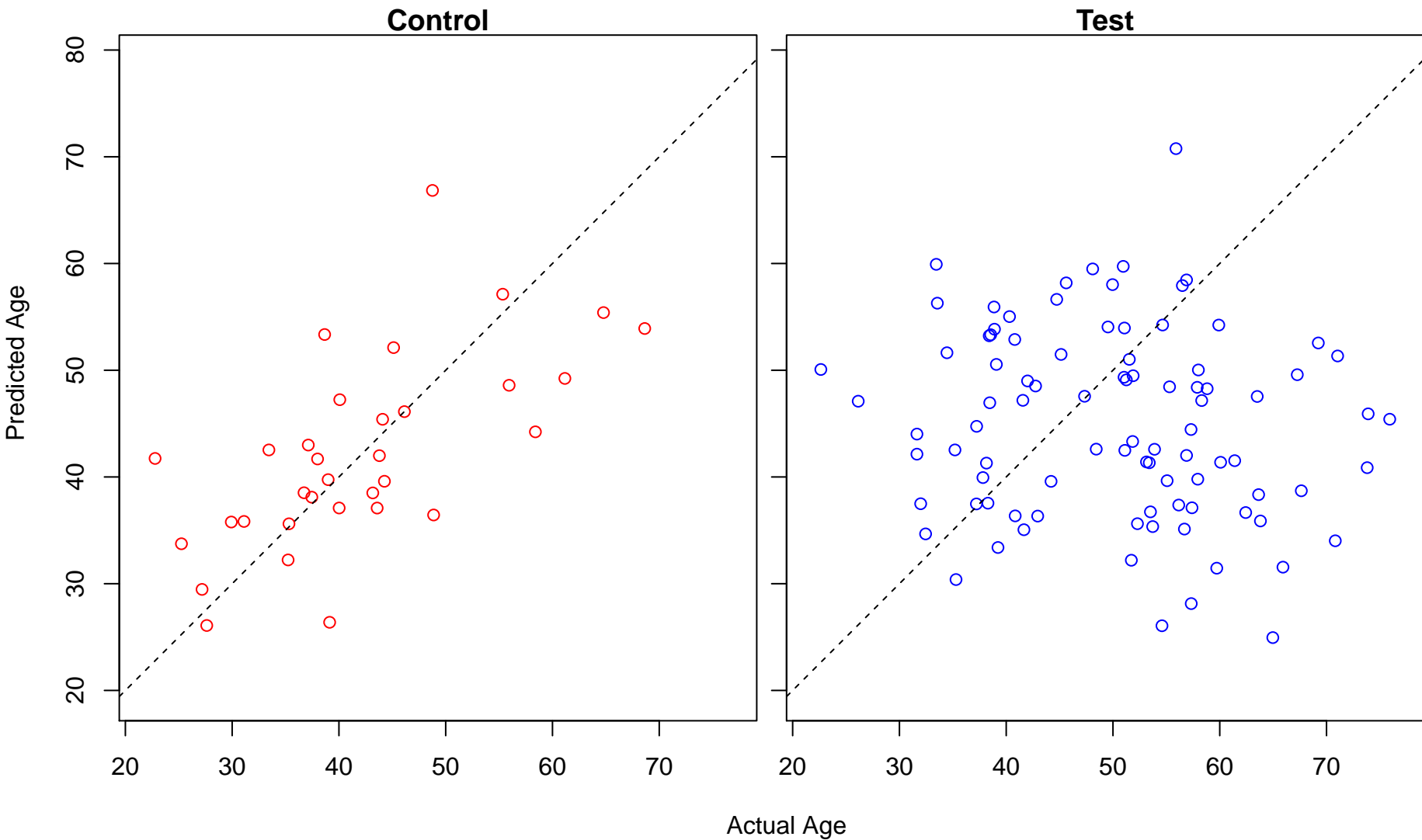
locomotor rhythm (Score: 2.053942)



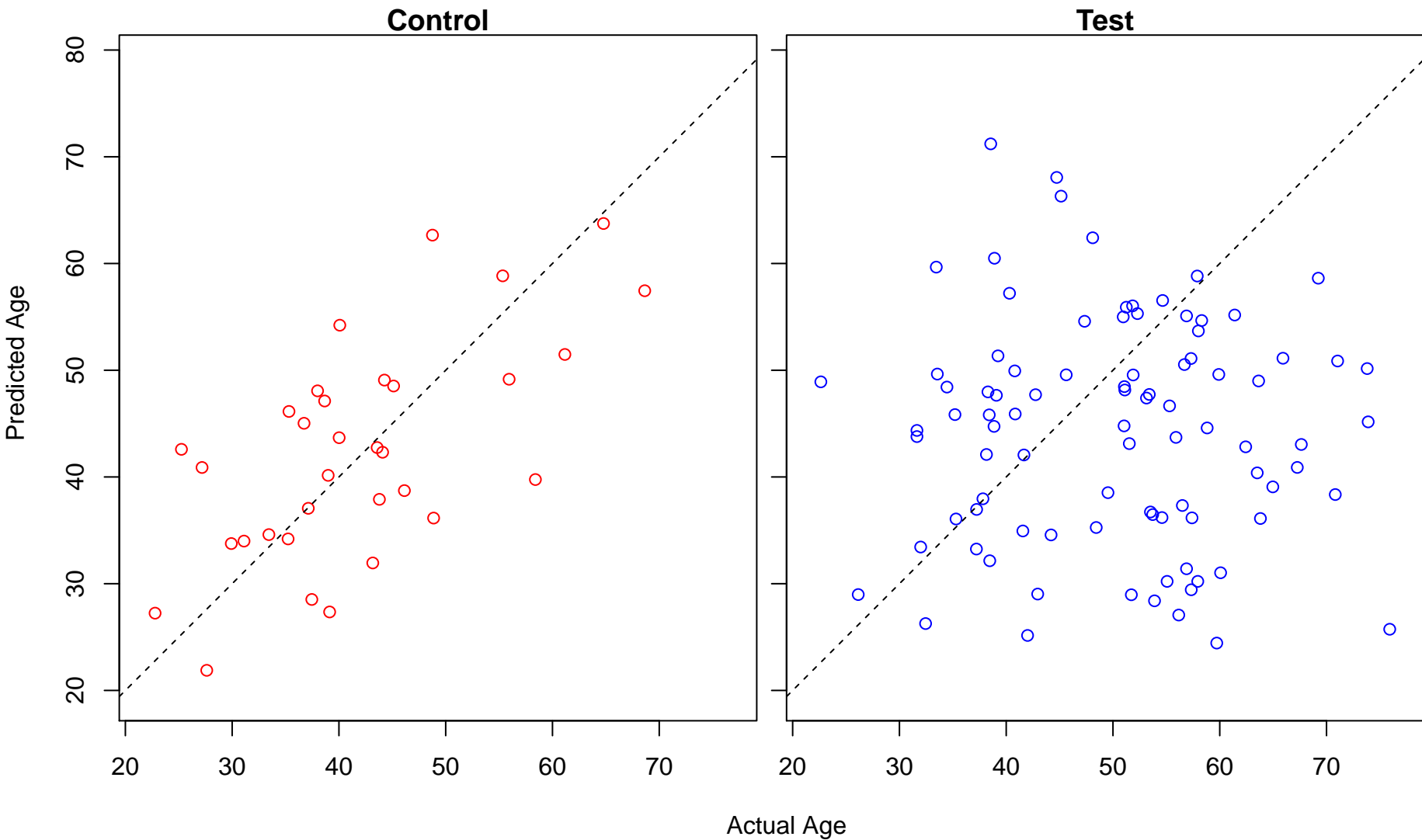
blood coagulation, intrinsic pathway (Score: 2.043903)



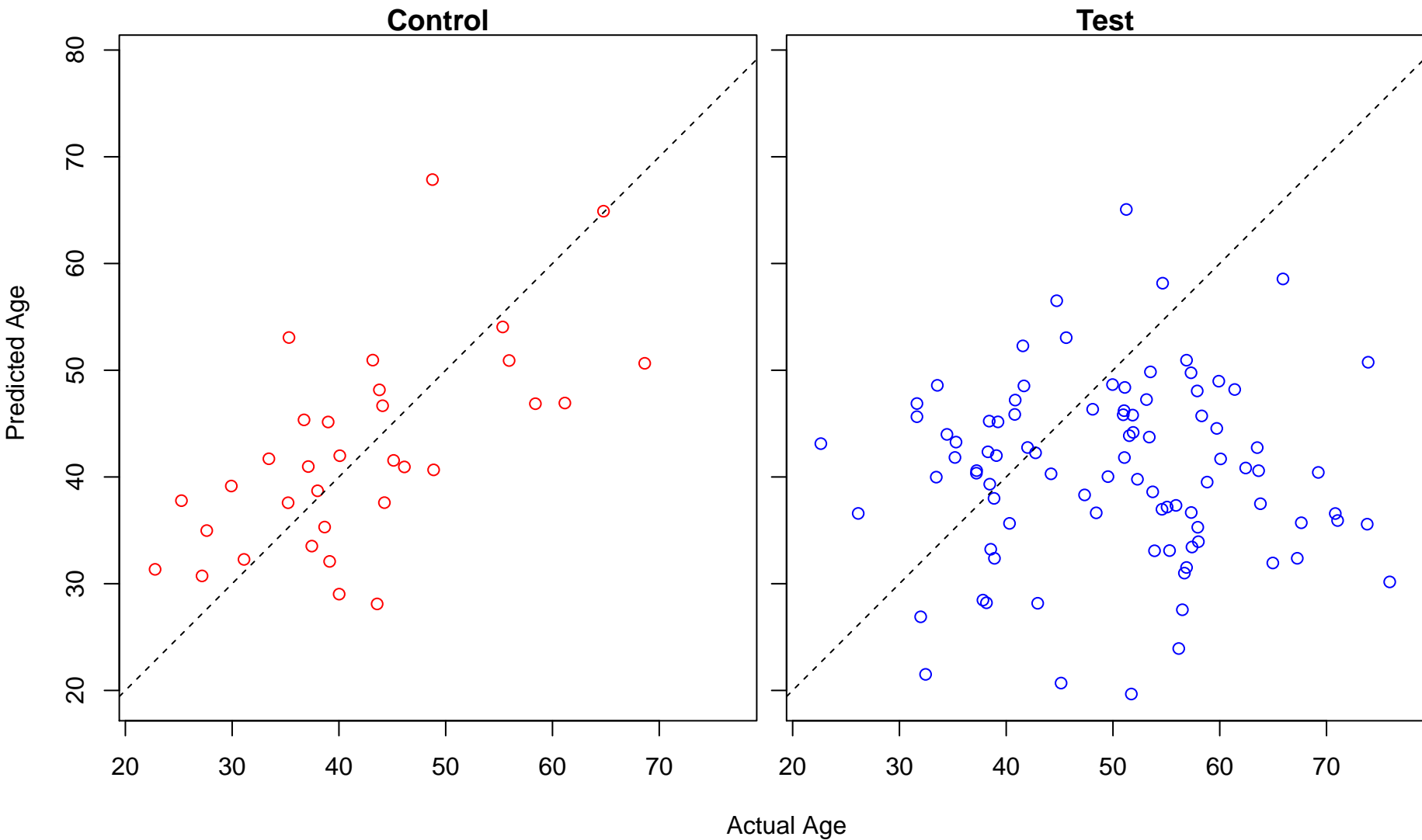
positive regulation of tumor necrosis factor production (Score: 2.012353)



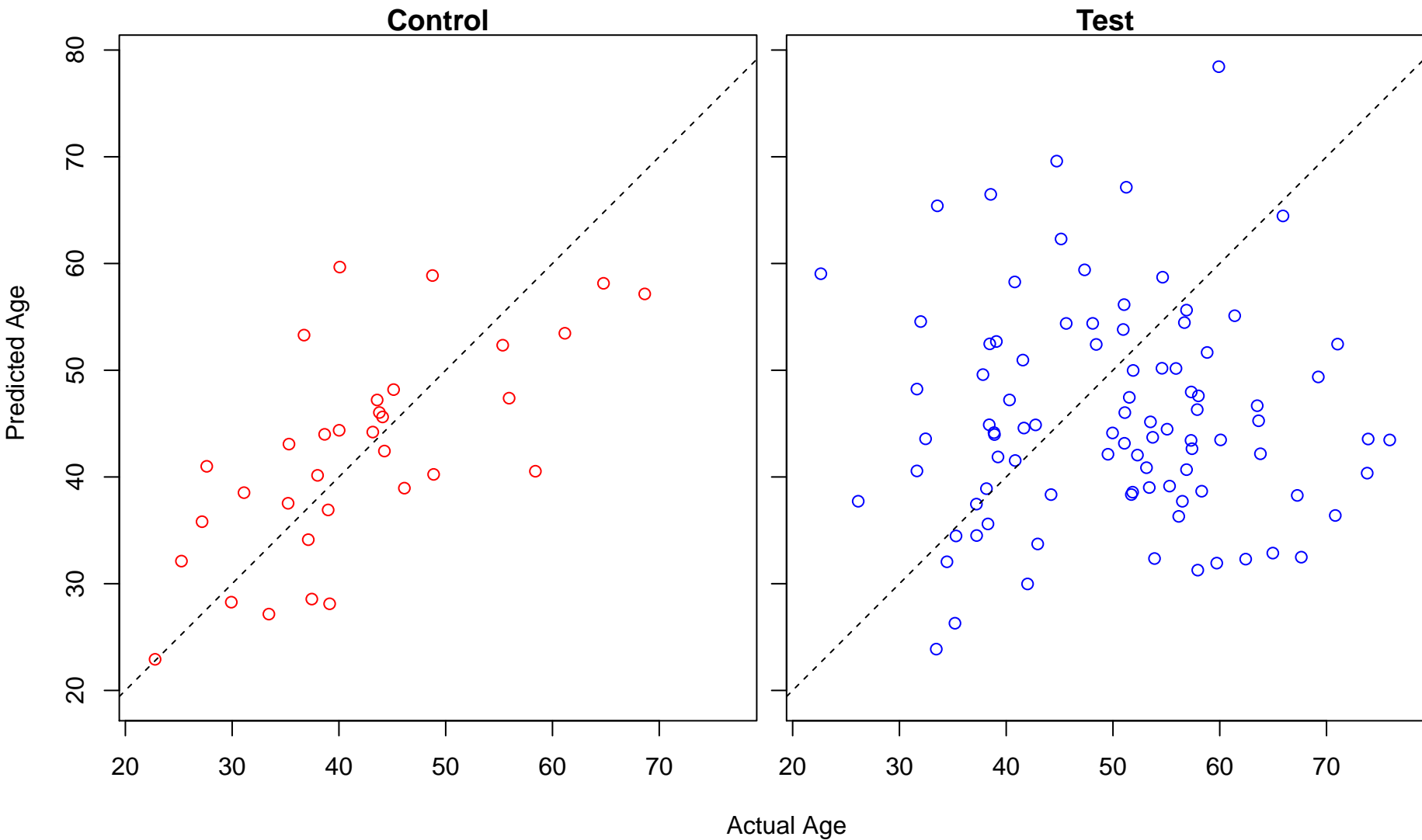
intracellular protein transmembrane transport (Score: 2.012031)



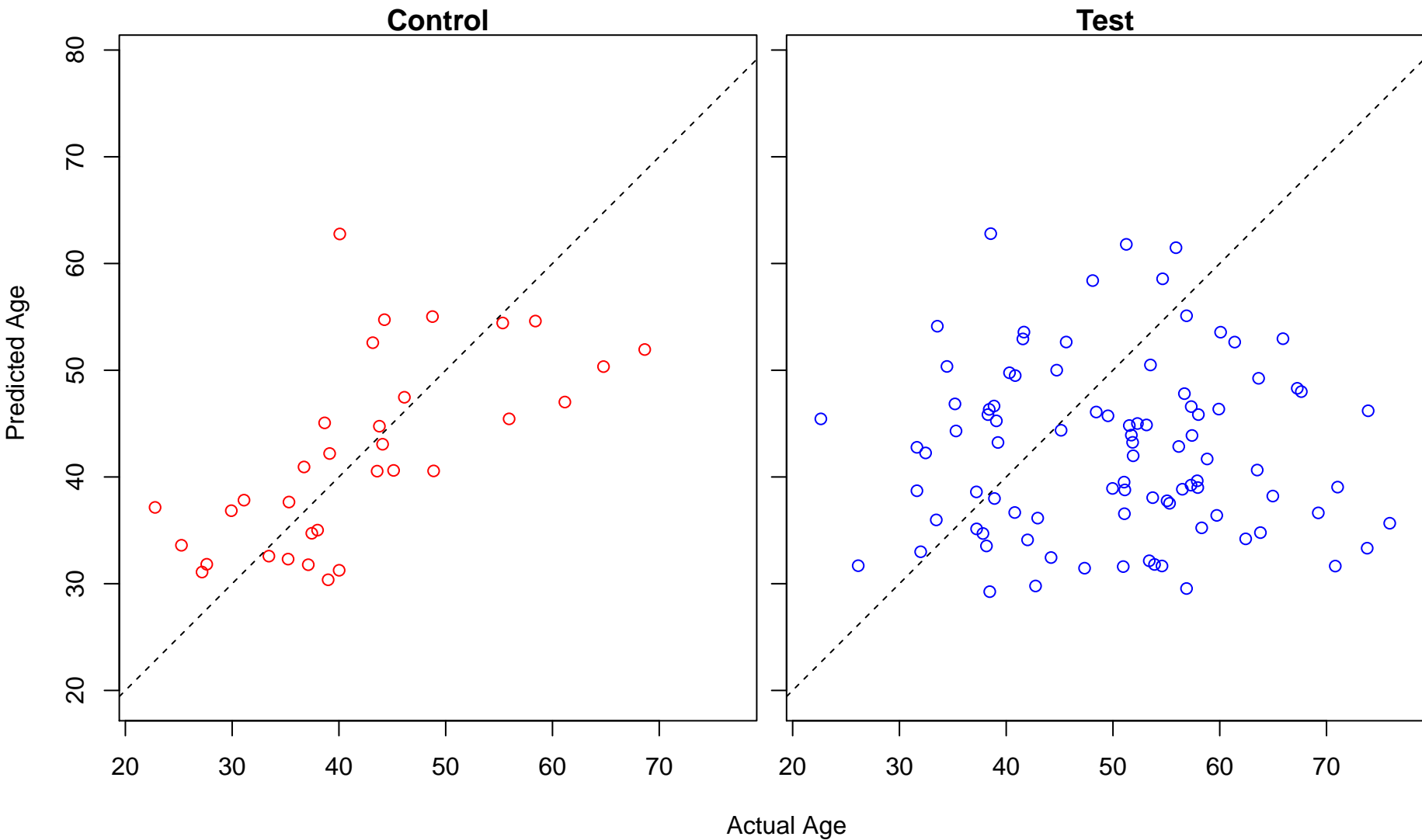
cellular aldehyde metabolic process (Score: 2.010668)



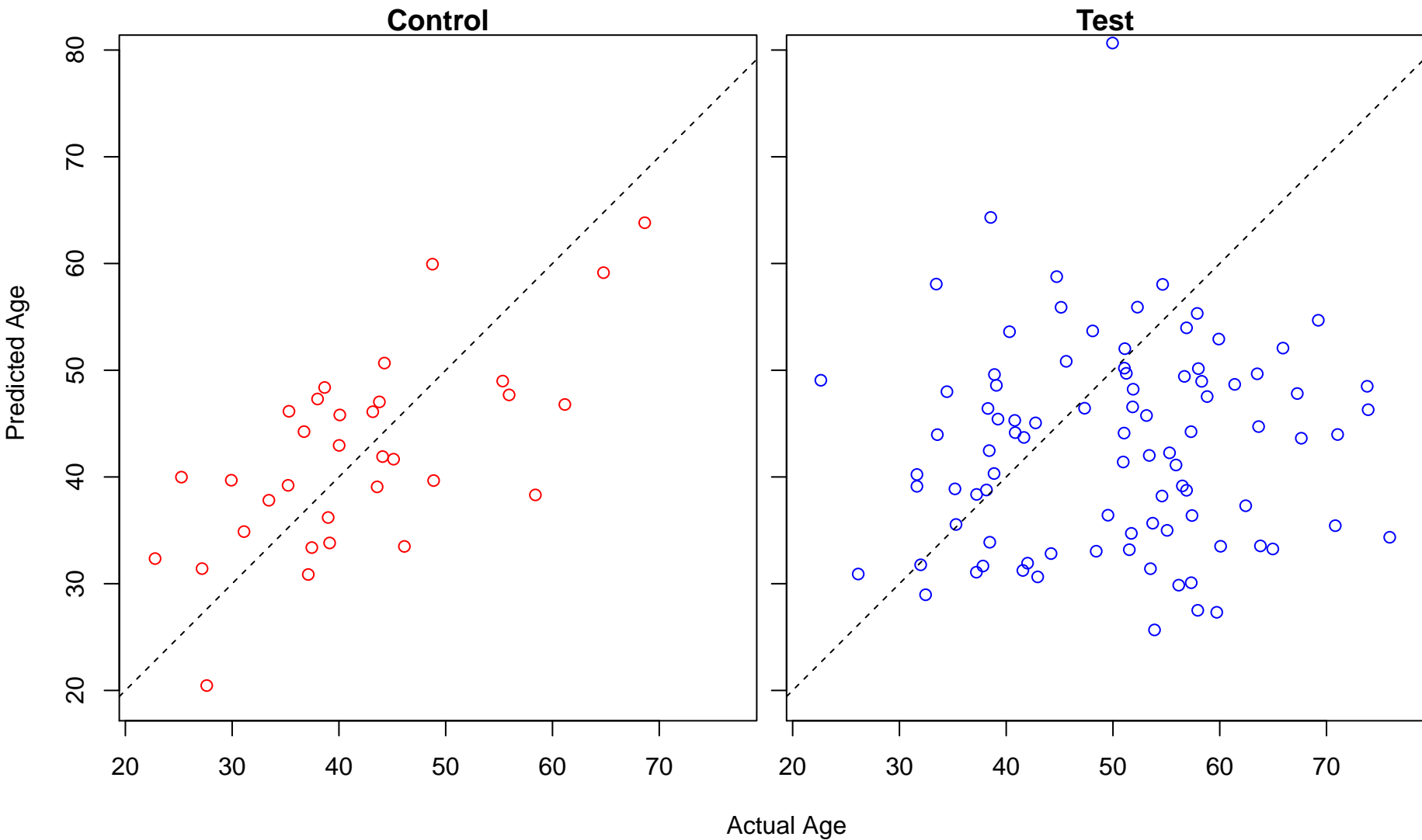
regulation of retrograde protein transport, ER to cytosol (Score: 2.010319)



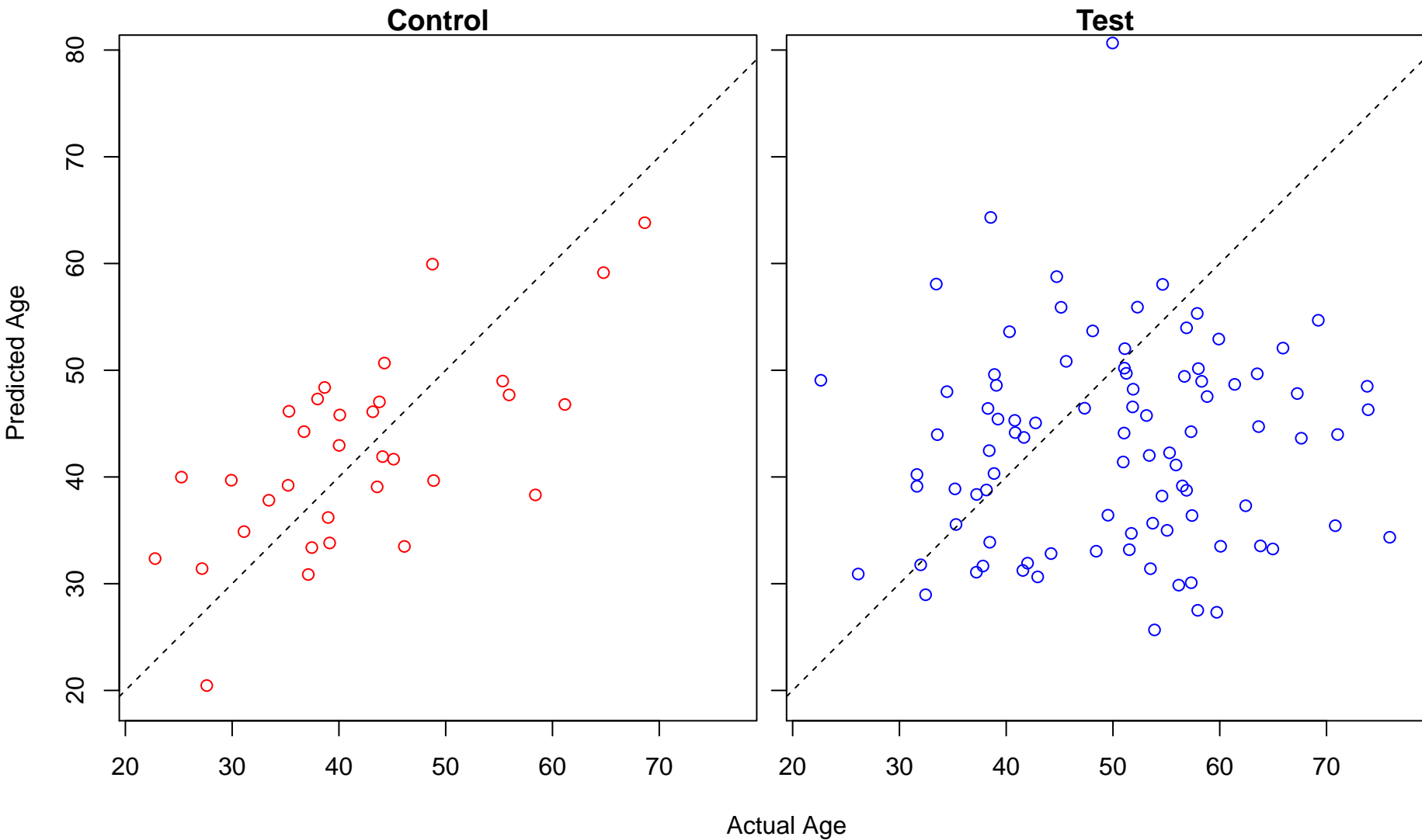
regulation of metalloendopeptidase activity (Score: 1.998594)



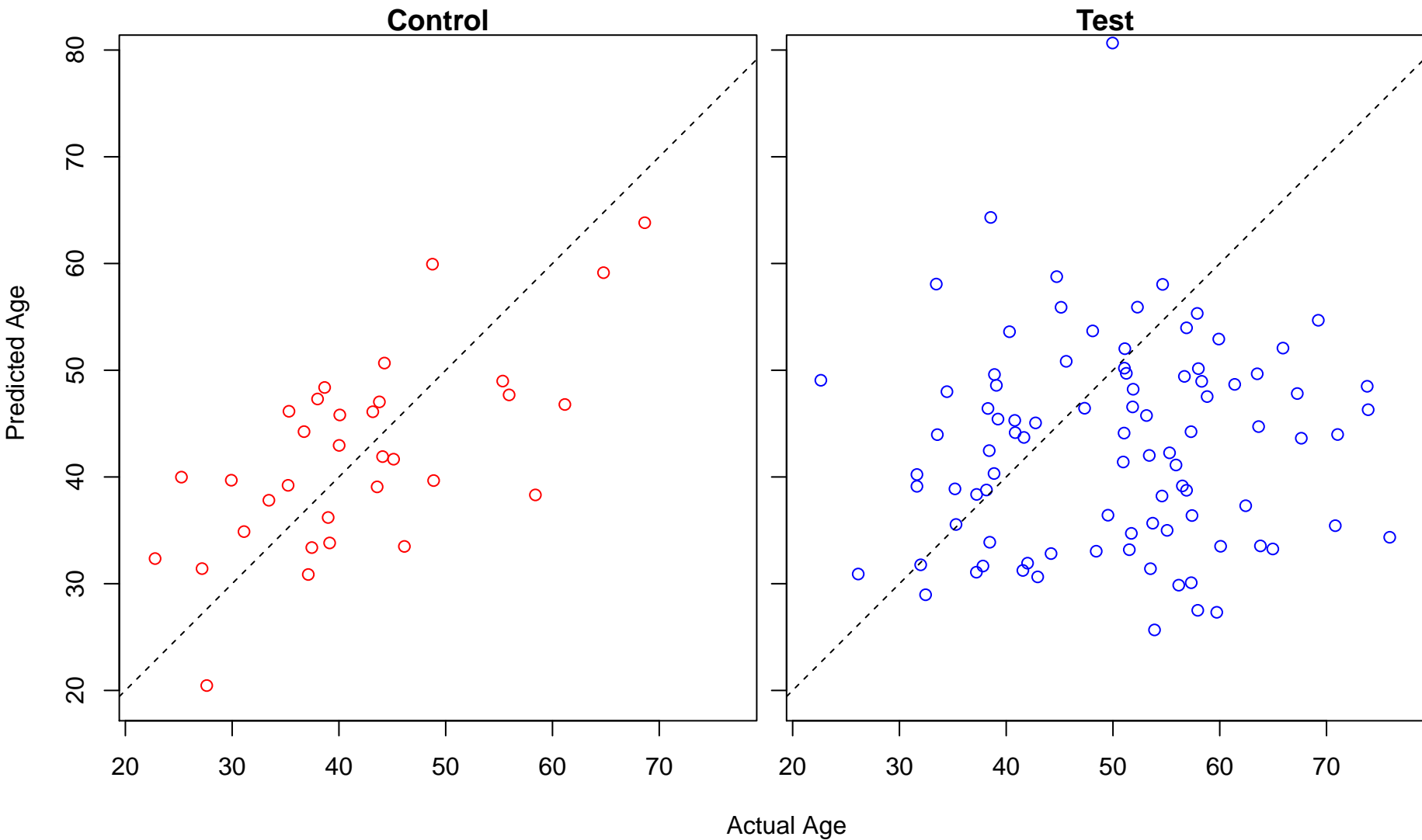
protein targeting to peroxisome (Score: 1.994493)



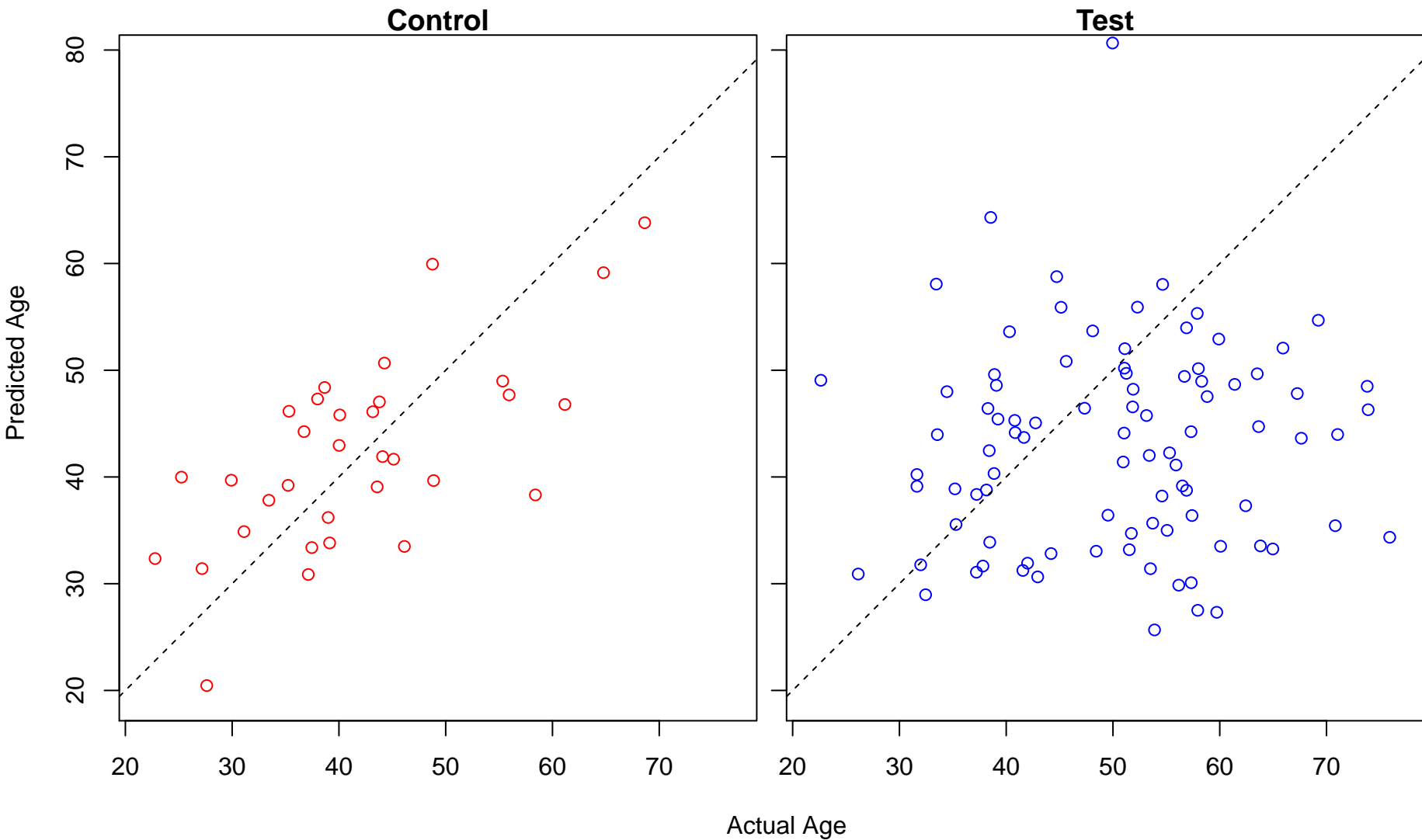
peroxisomal transport (Score: 1.994493)



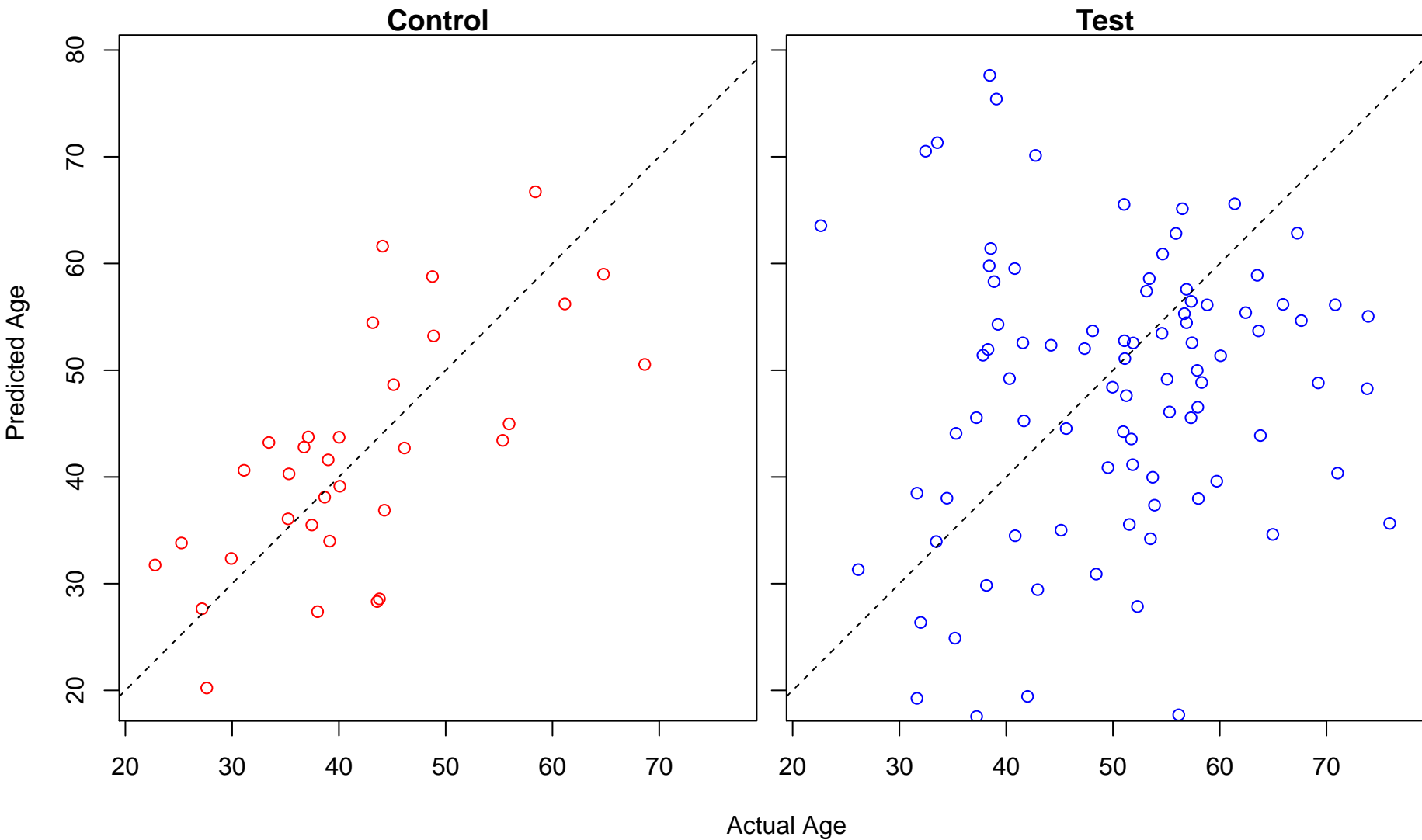
protein localization to peroxisome (Score: 1.994493)



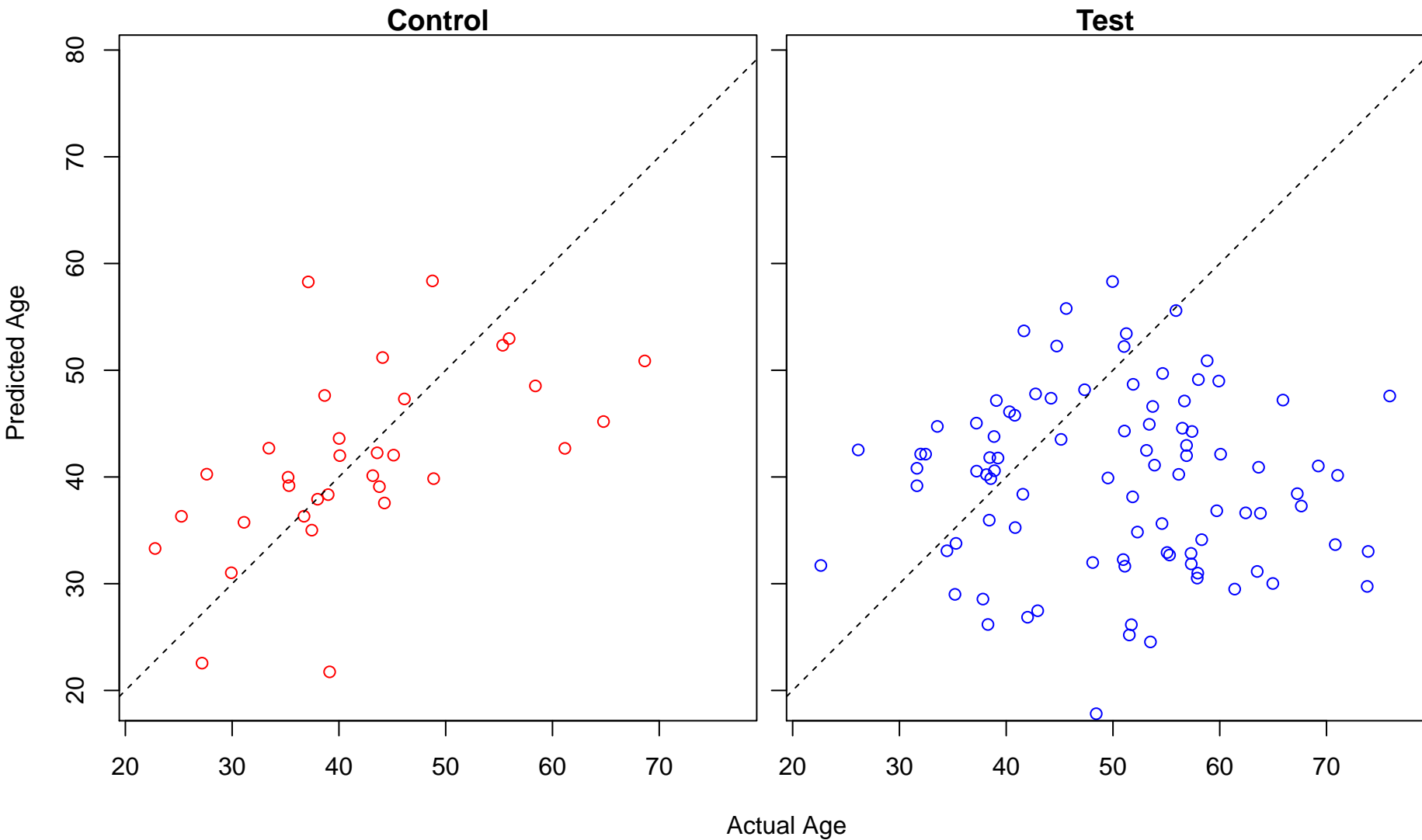
establishment of protein localization to peroxisome (Score: 1.994493)



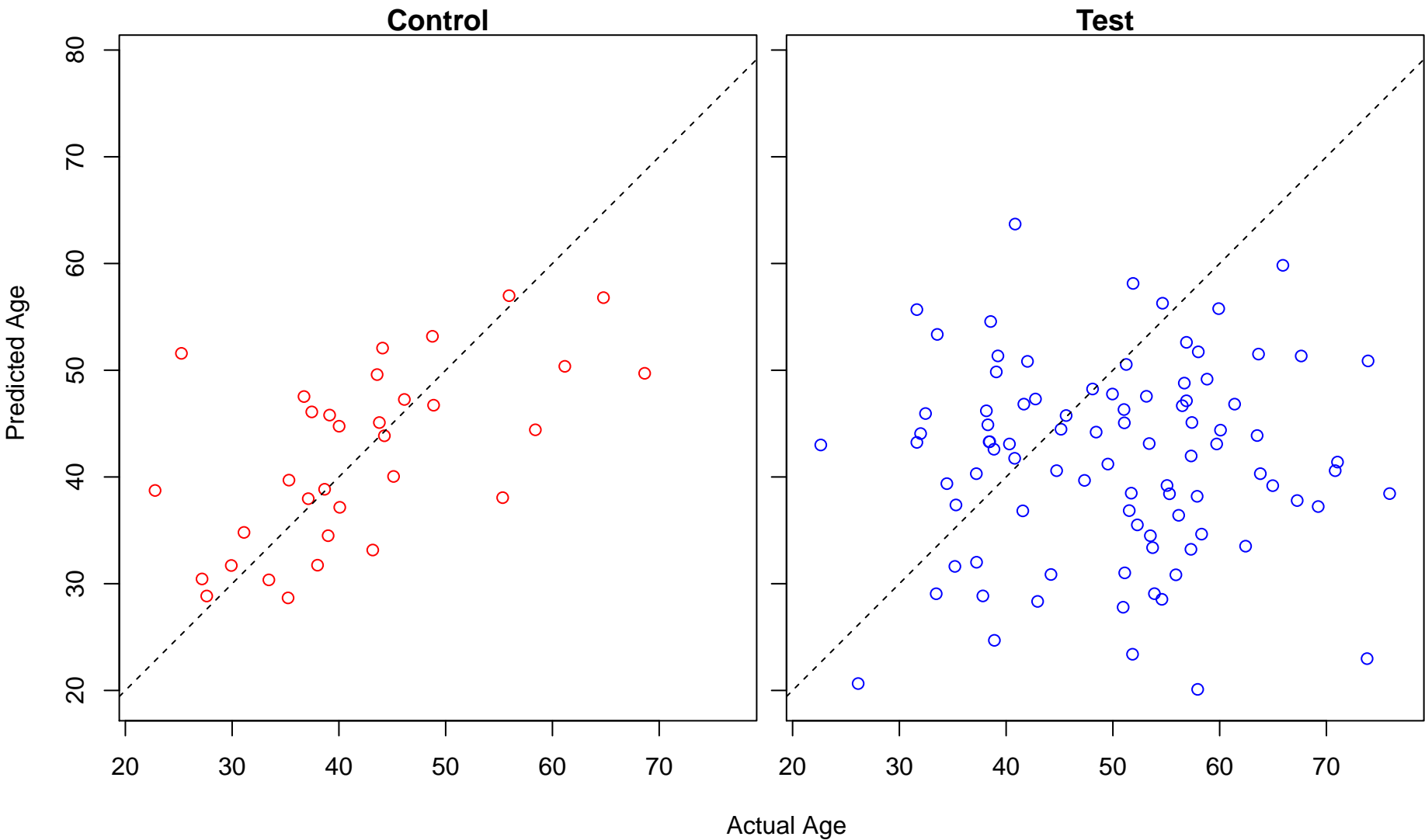
acute inflammatory response (Score: 1.984921)



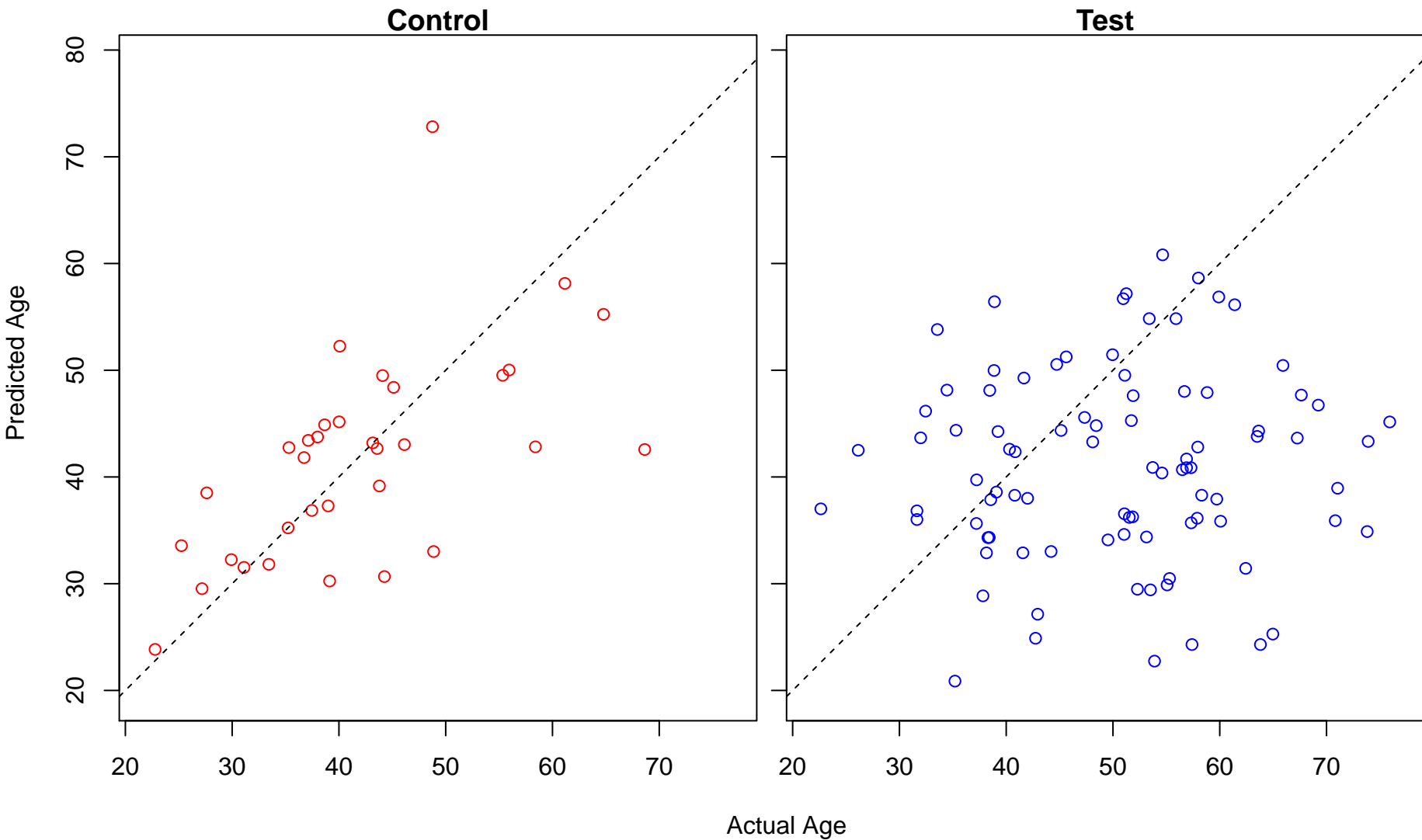
positive regulation of sodium ion transport (Score: 1.980938)



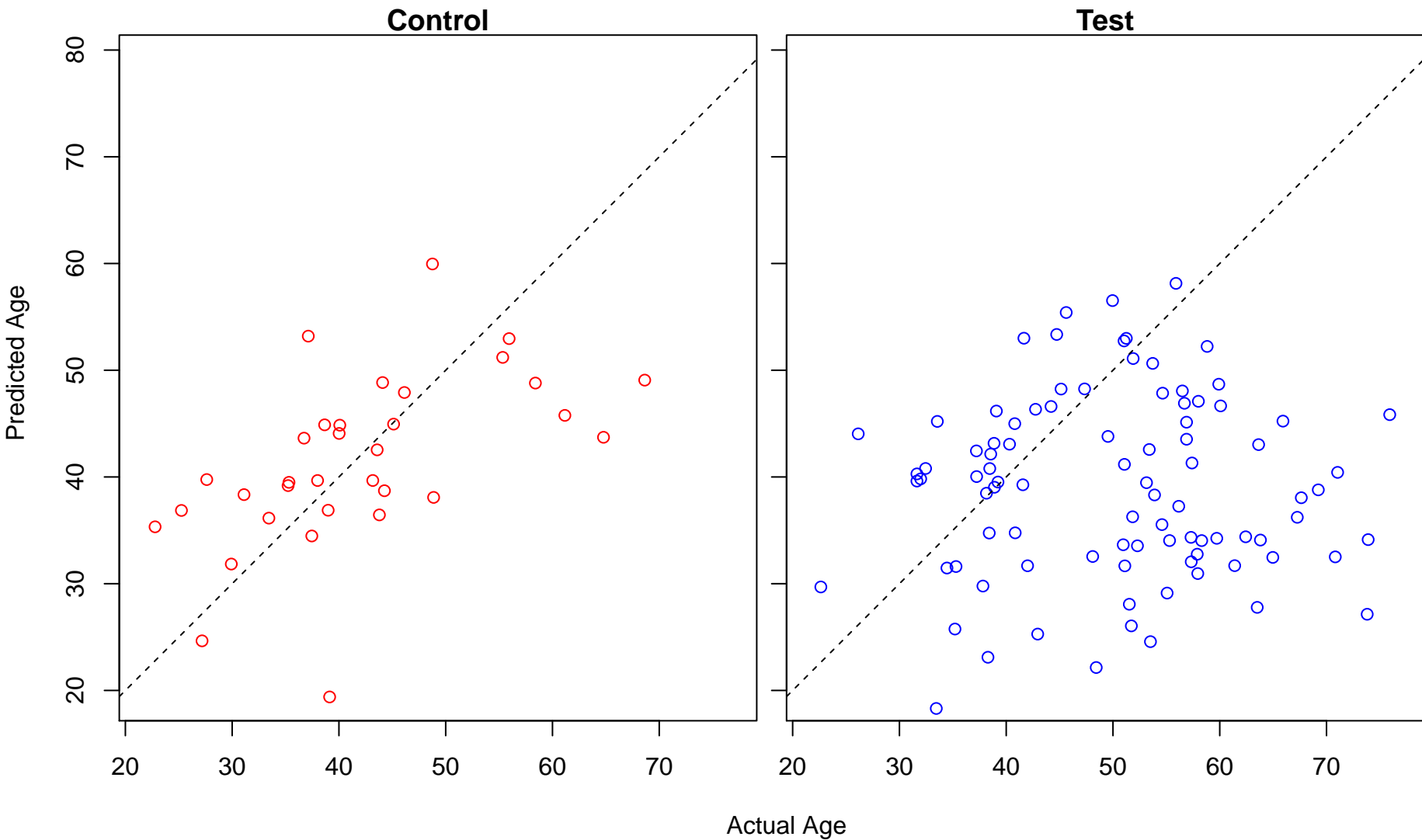
activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c (Score: 1)



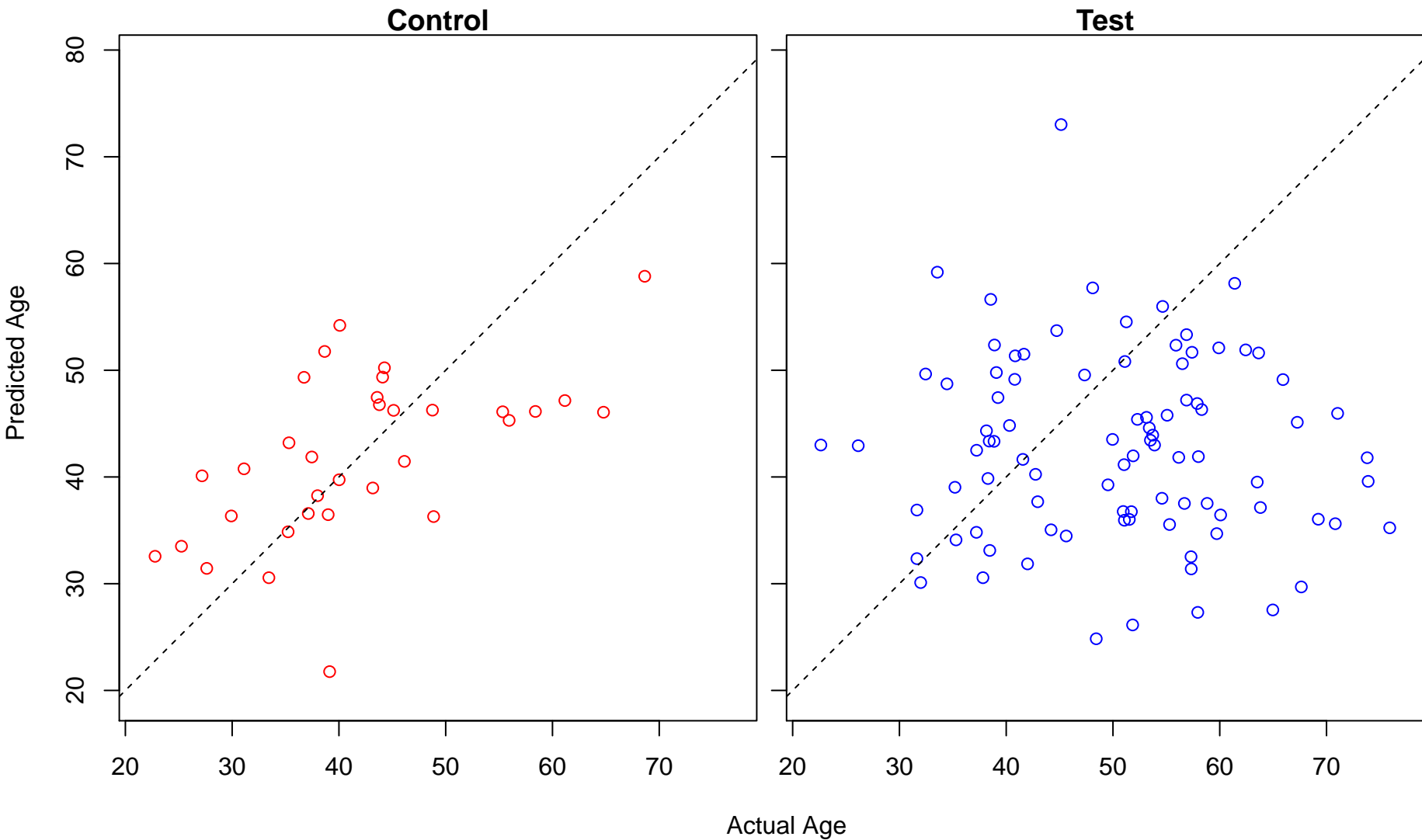
protein autophosphorylation (Score: 1.970510)



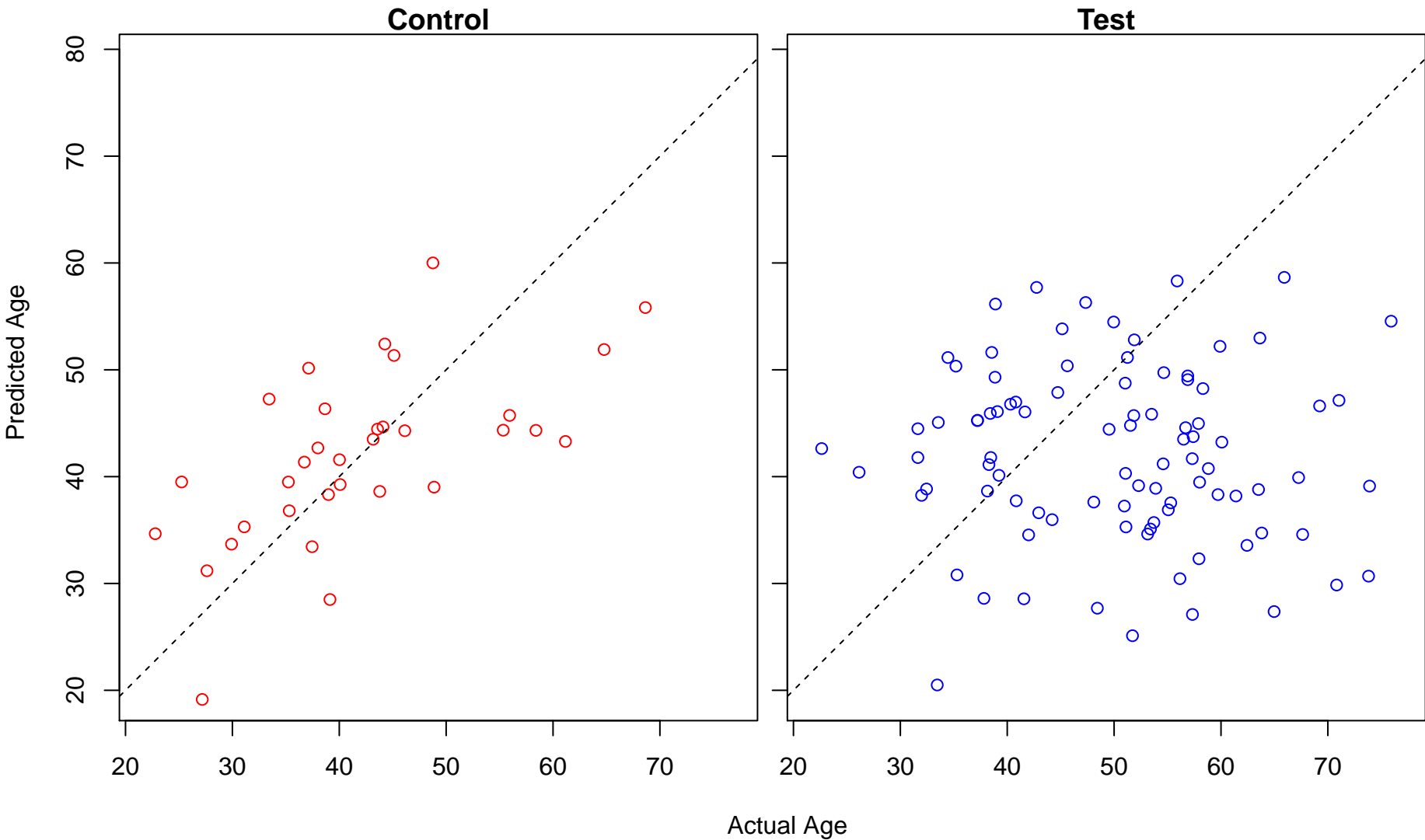
regulation of sodium ion transmembrane transport (Score: 1.961005)



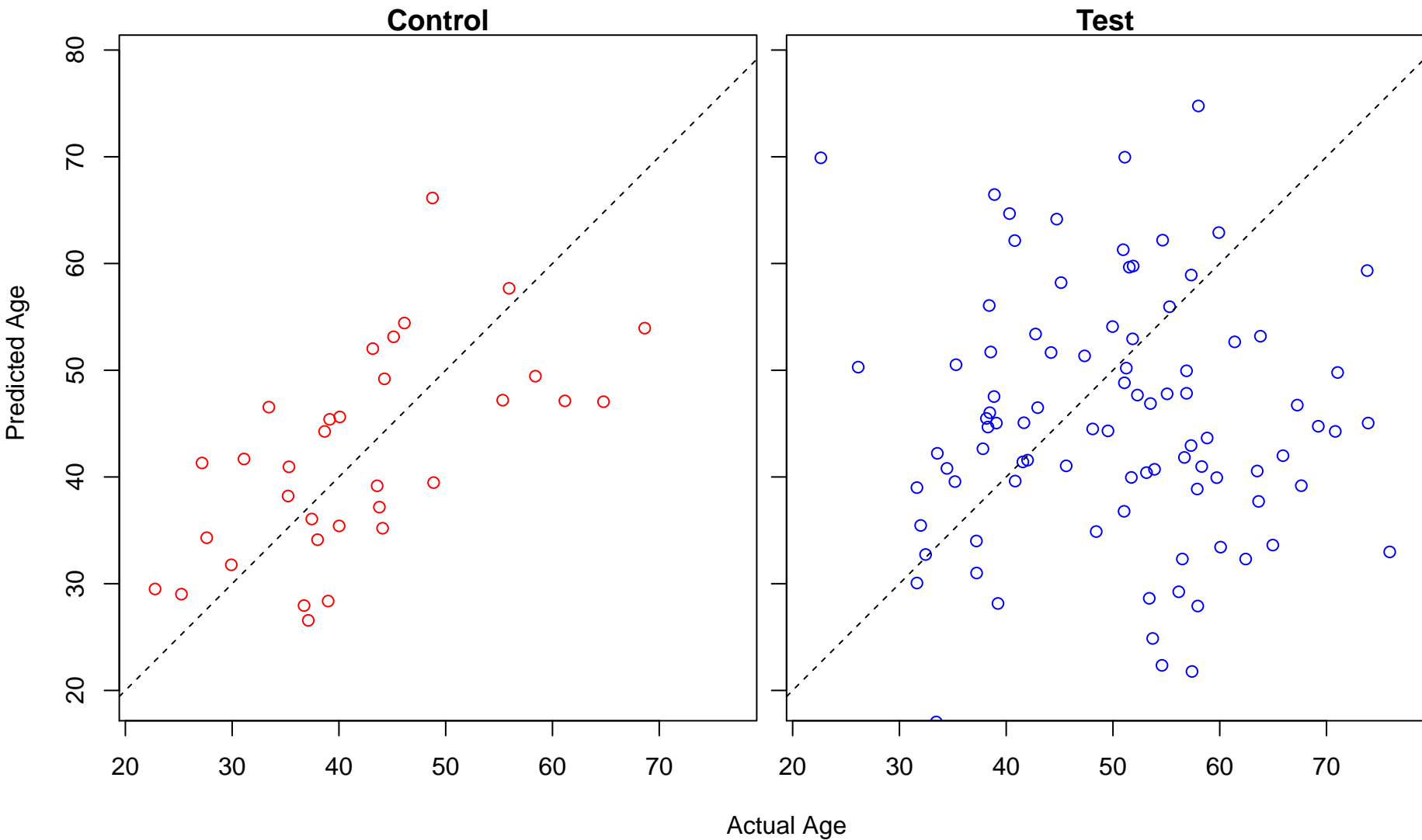
developmental process involved in reproduction (Score: 1.959633)



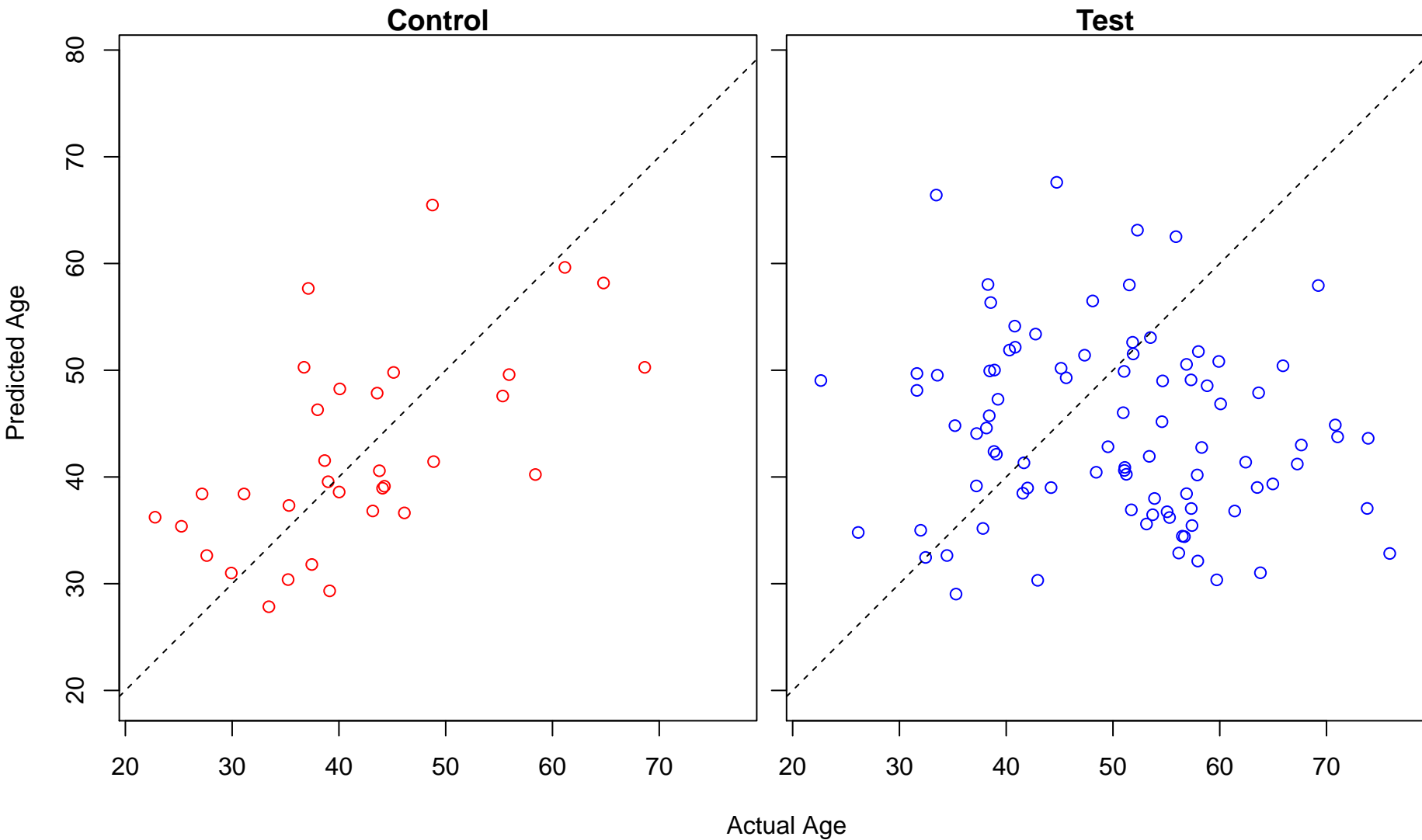
positive regulation of ATPase activity (Score: 1.947230)



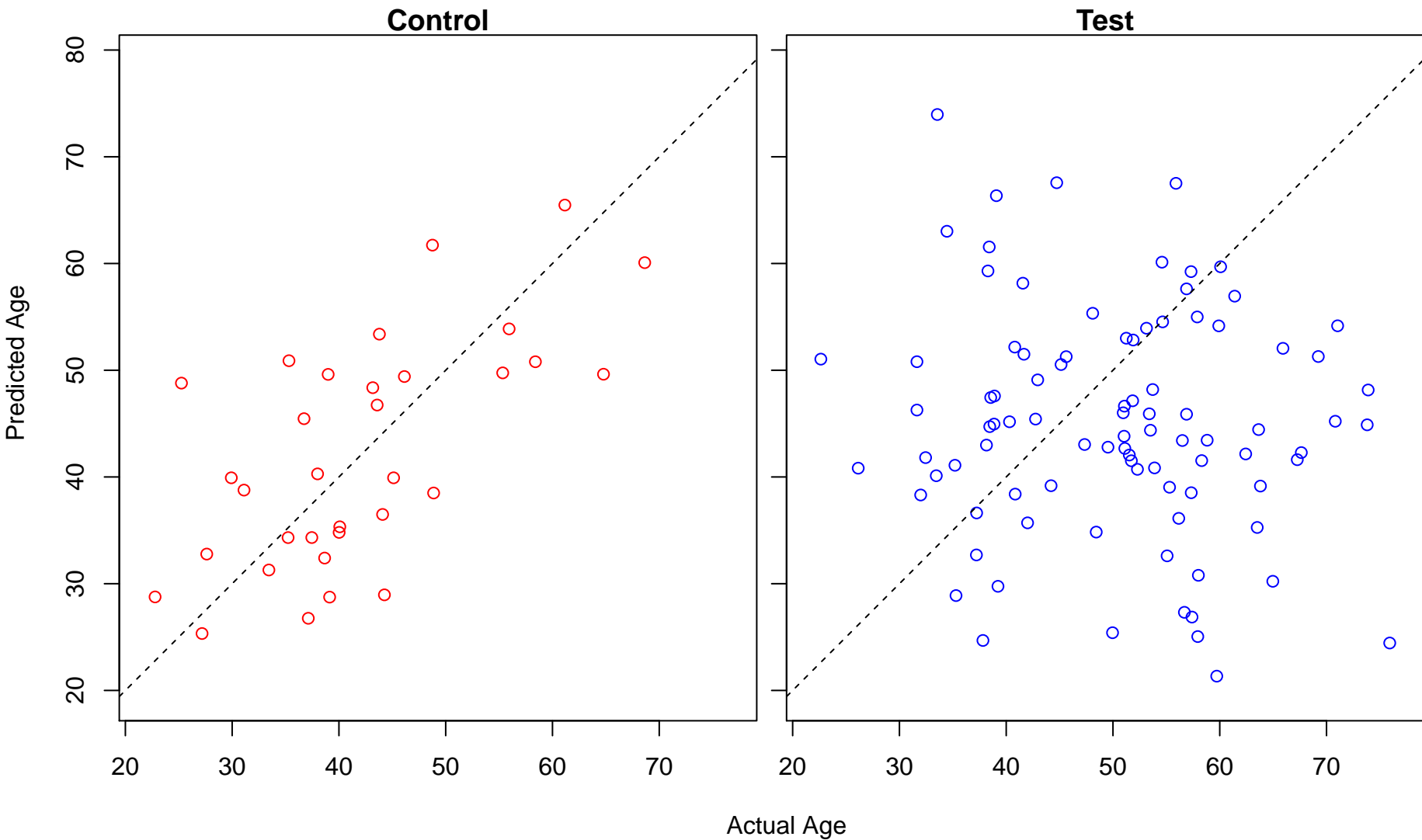
negative regulation of potassium ion transmembrane transporter activity (Score: 1.943514)



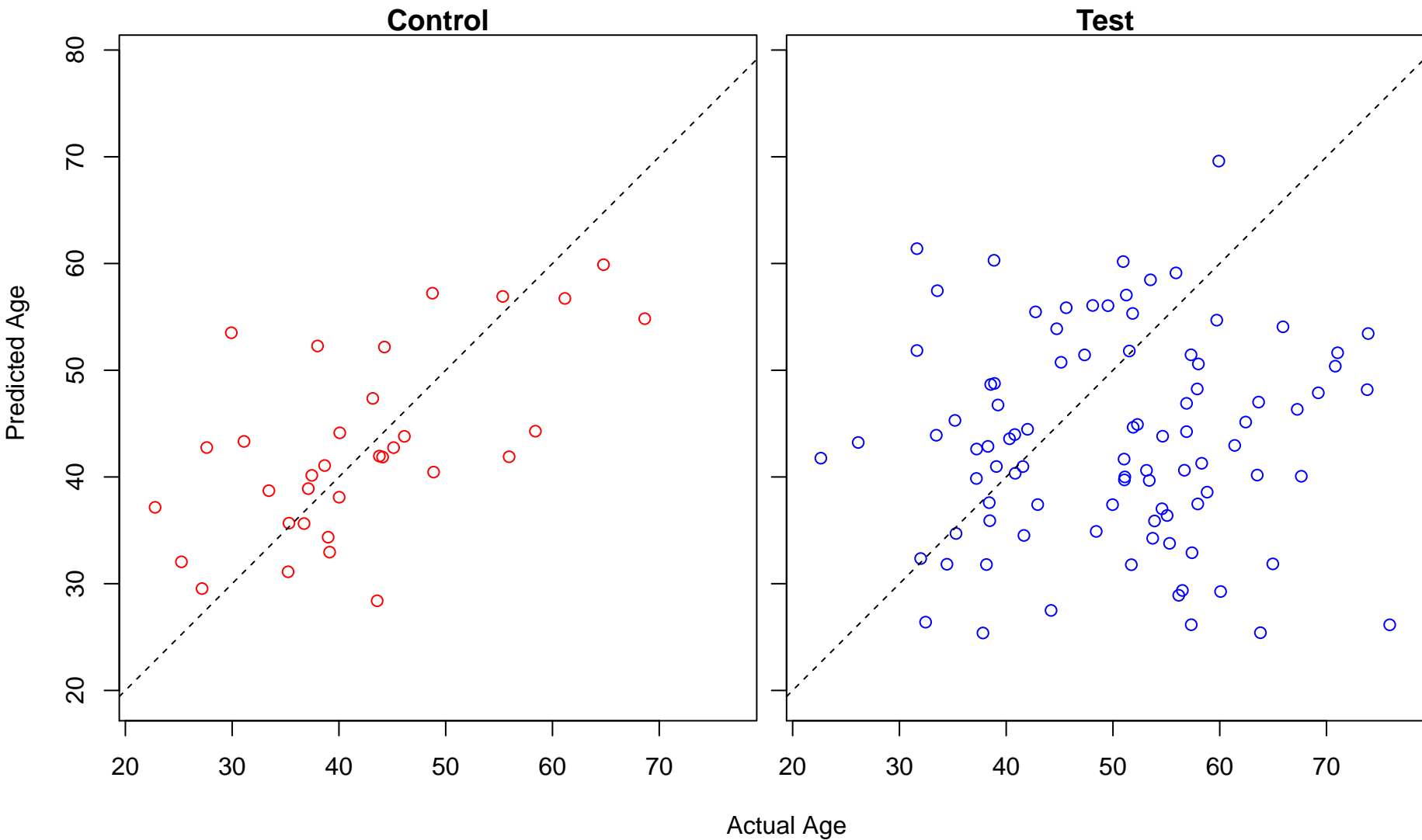
negative regulation of telomere capping (Score: 1.941992)



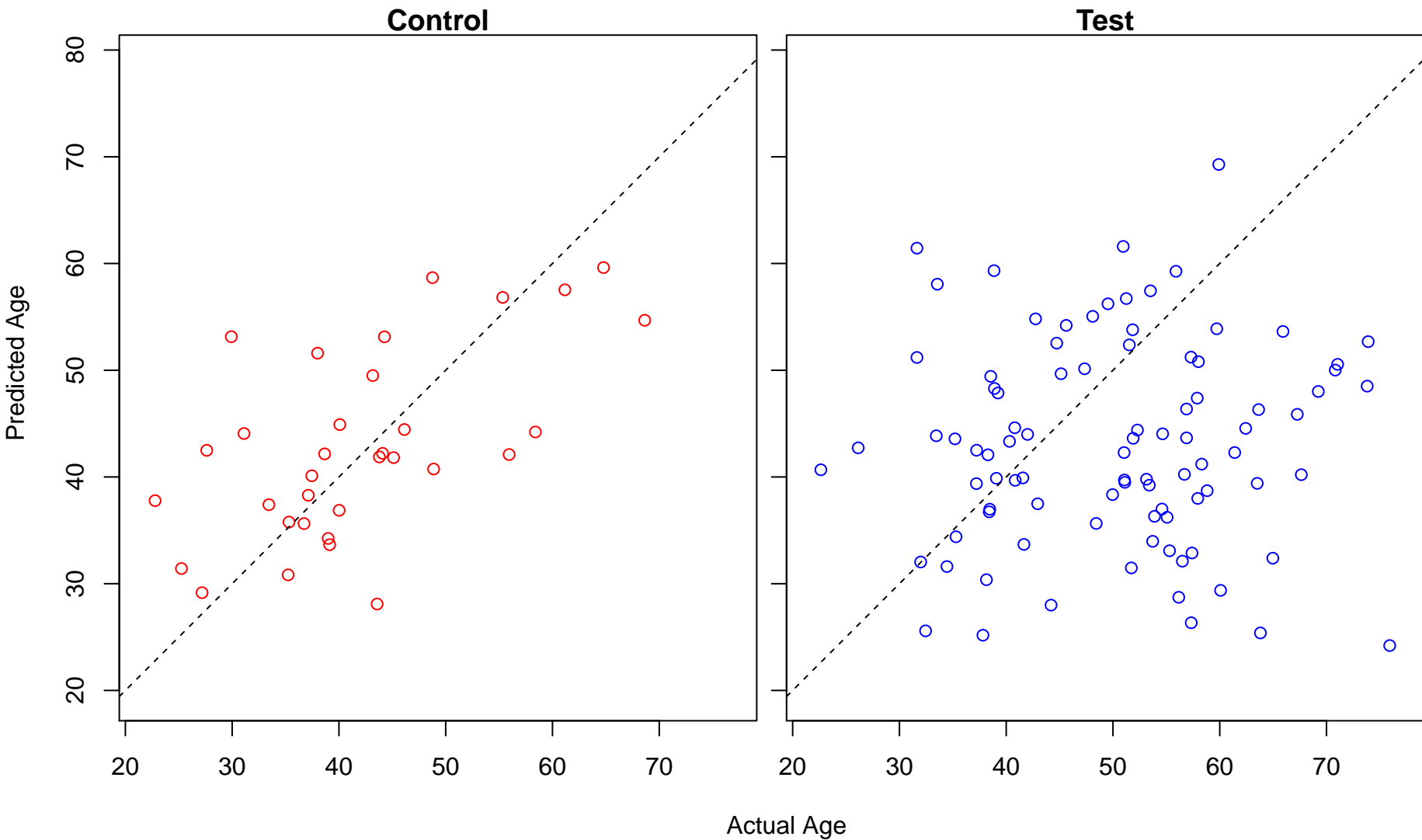
spermatid development (Score: 1.938607)



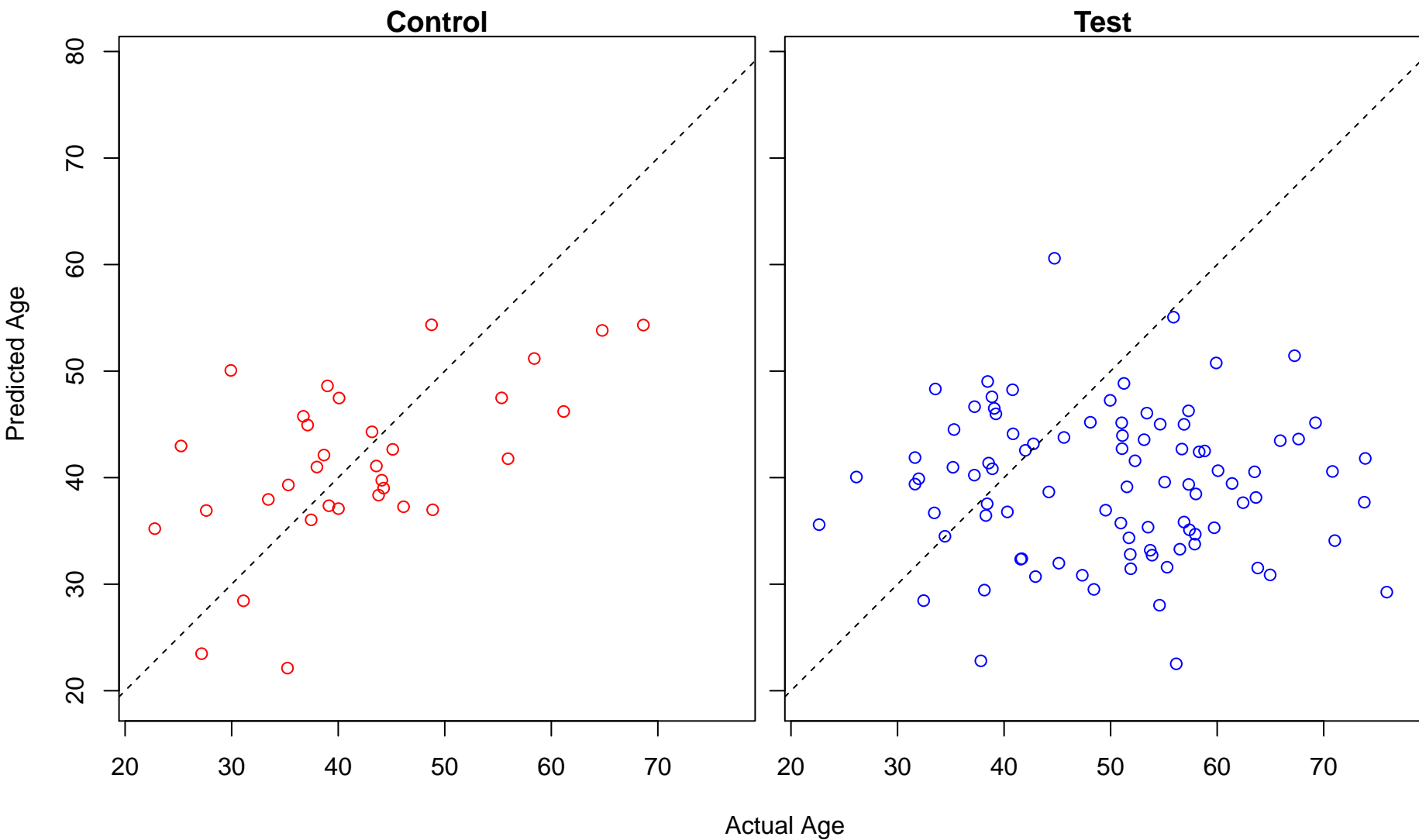
detection of external stimulus (Score: 1.932226)



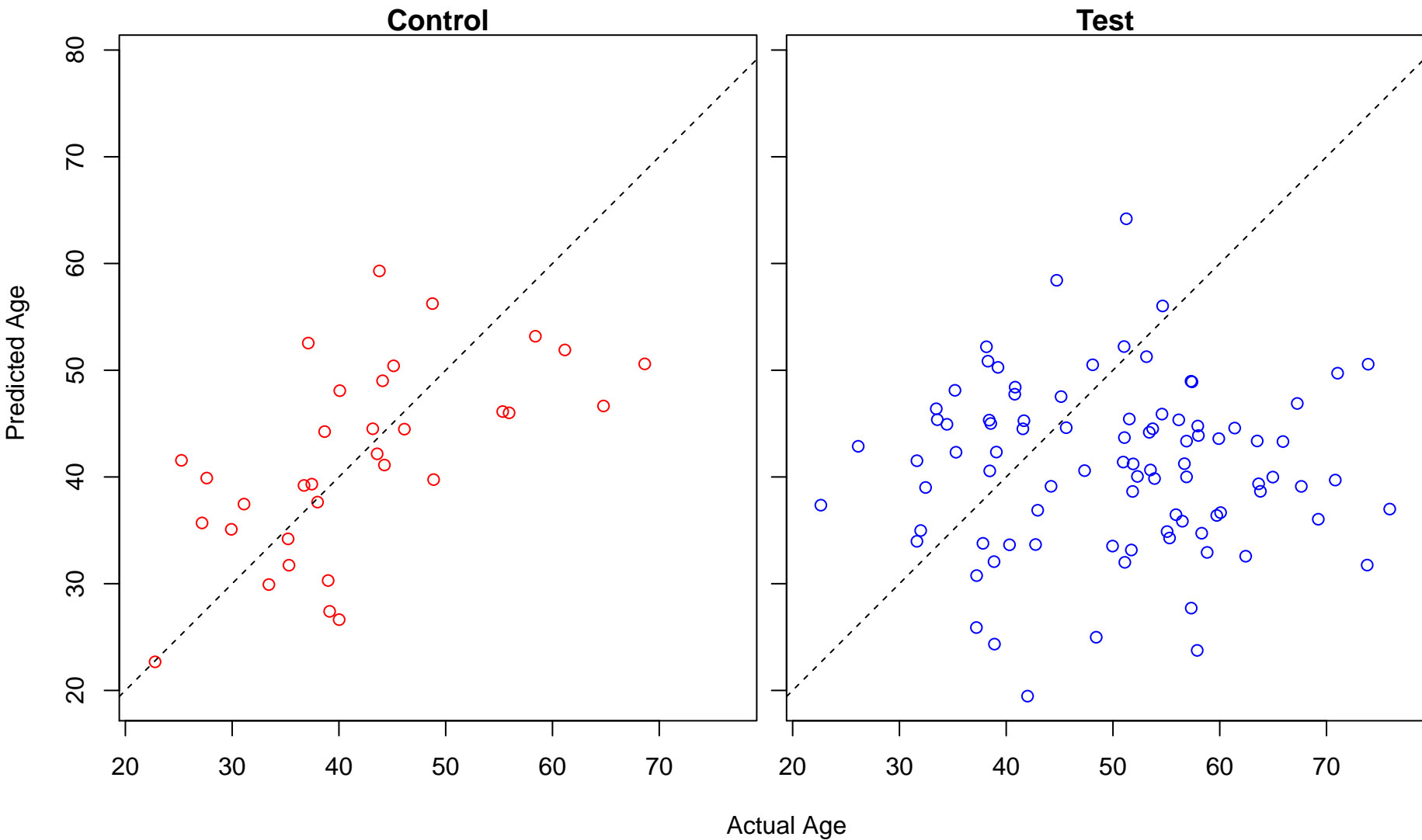
detection of abiotic stimulus (Score: 1.917654)



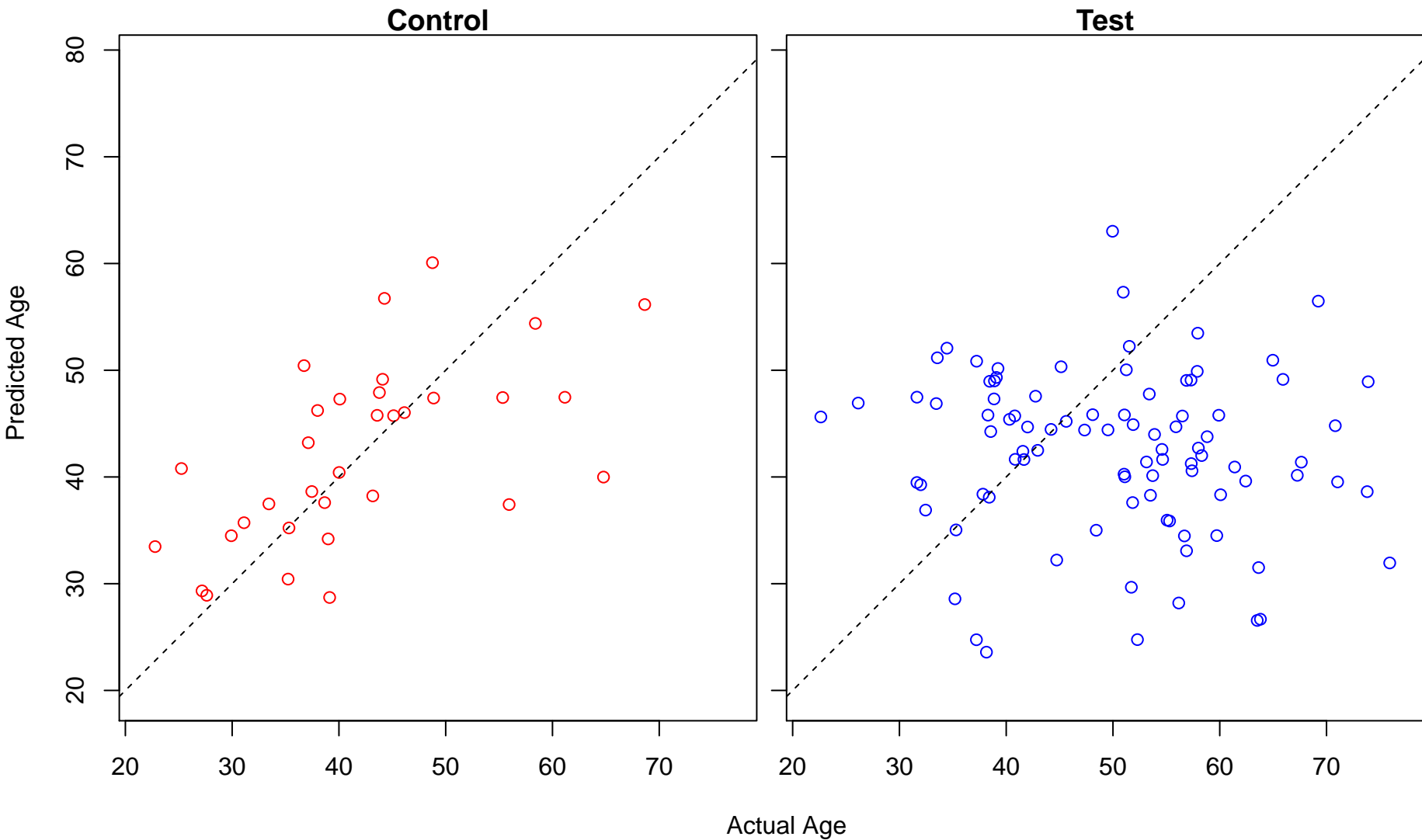
lipid homeostasis (Score: 1.912839)



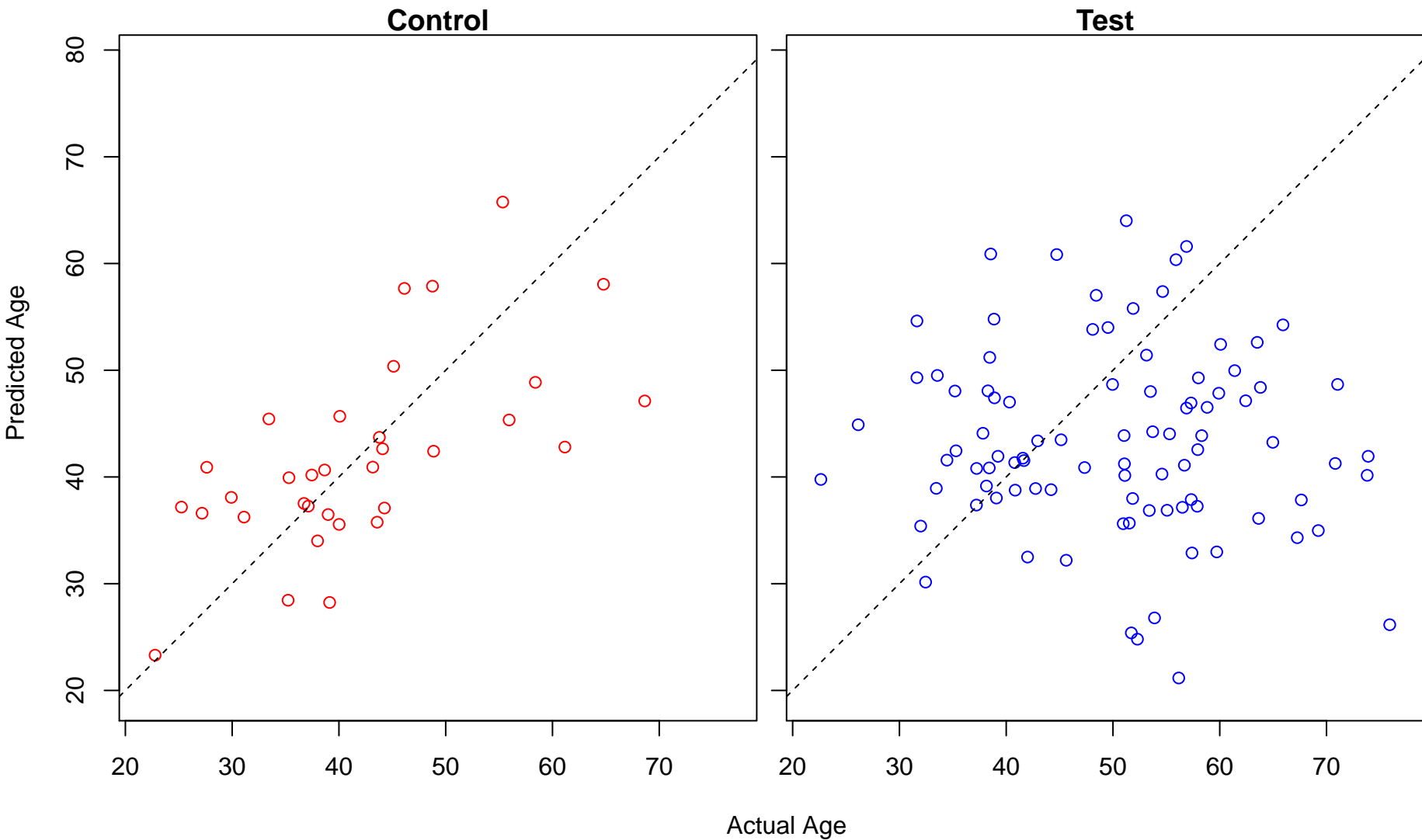
phosphatidylethanolamine metabolic process (Score: 1.912485)



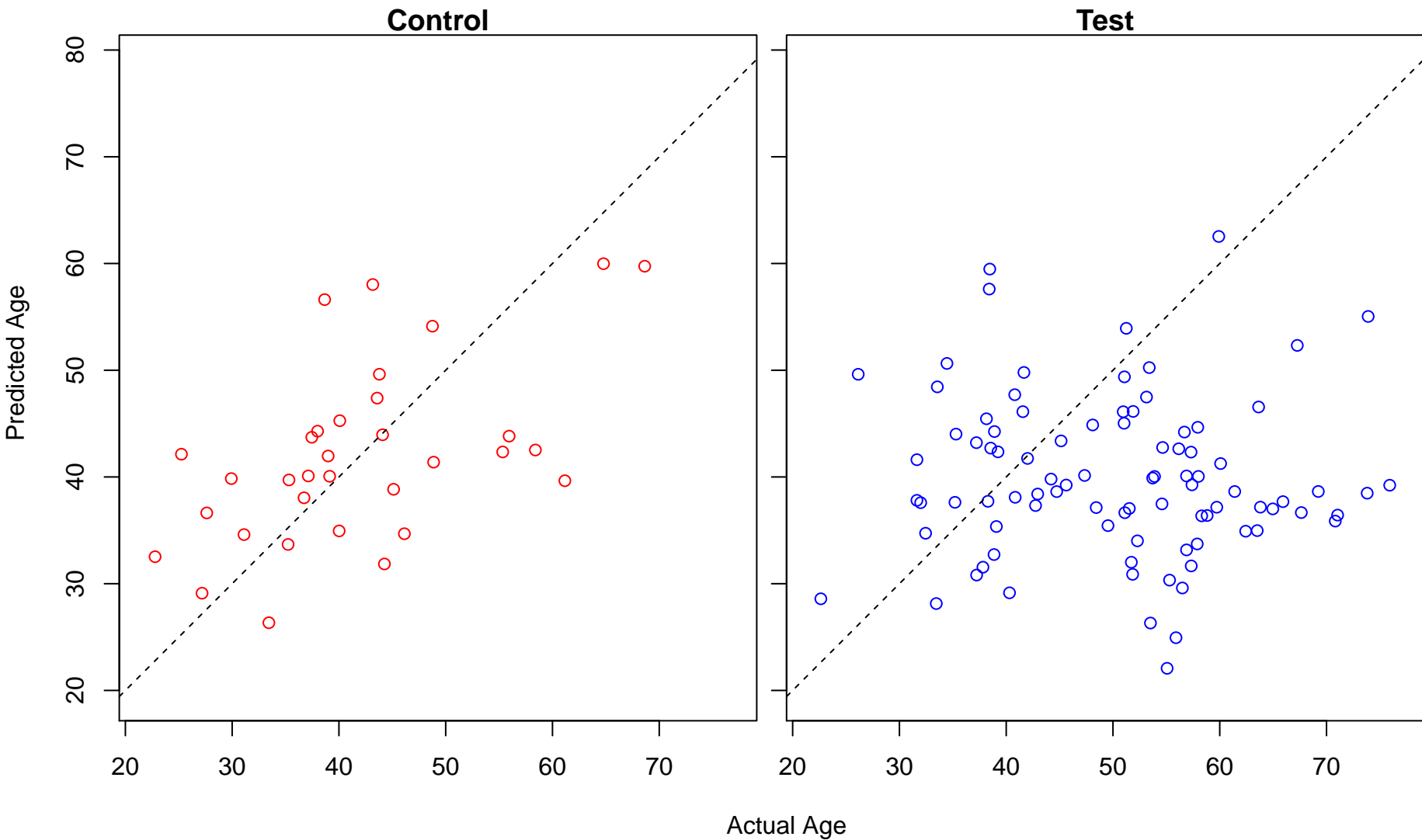
protein activation cascade (Score: 1.911821)



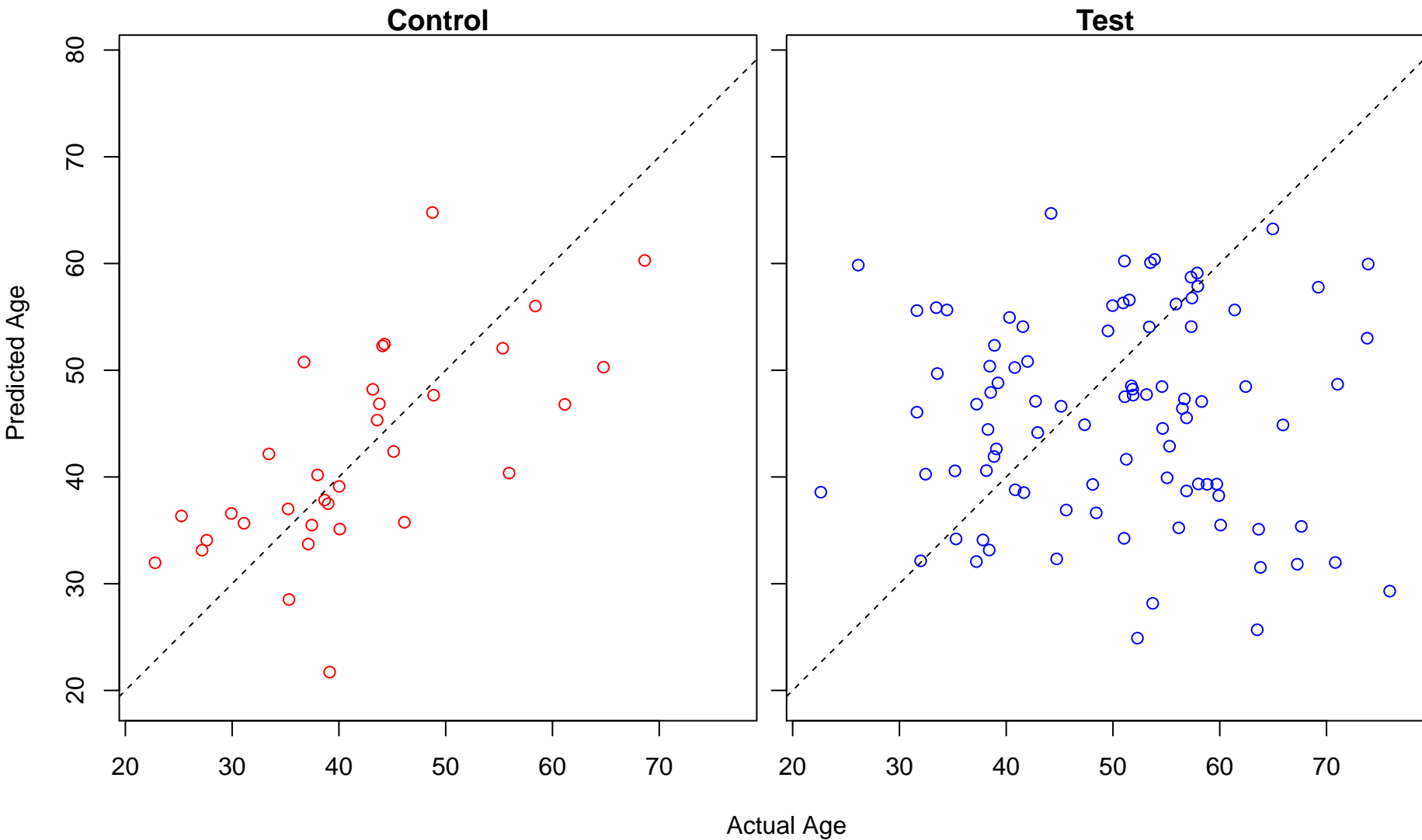
microtubule organizing center organization (Score: 1.910722)



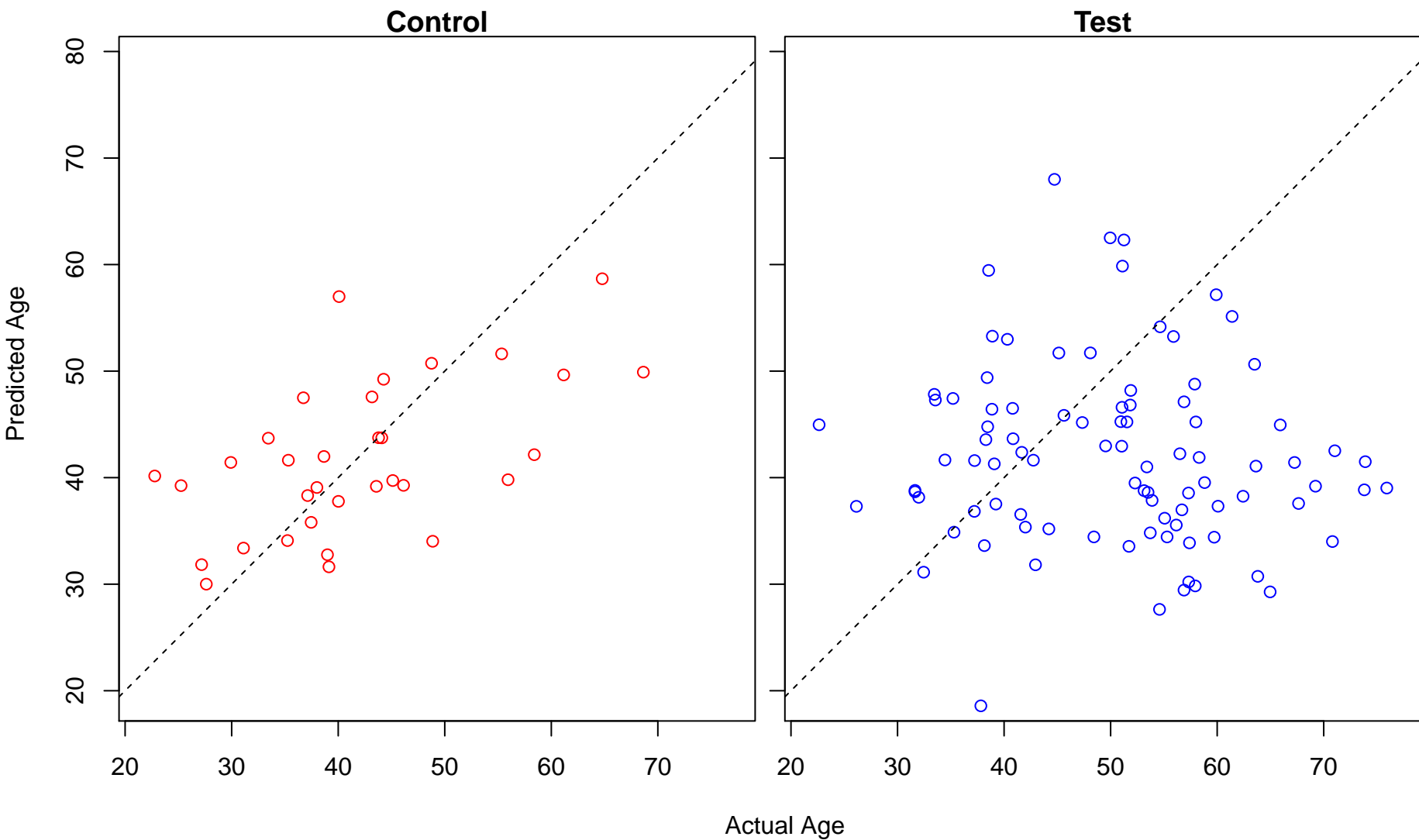
phospholipid catabolic process (Score: 1.910189)



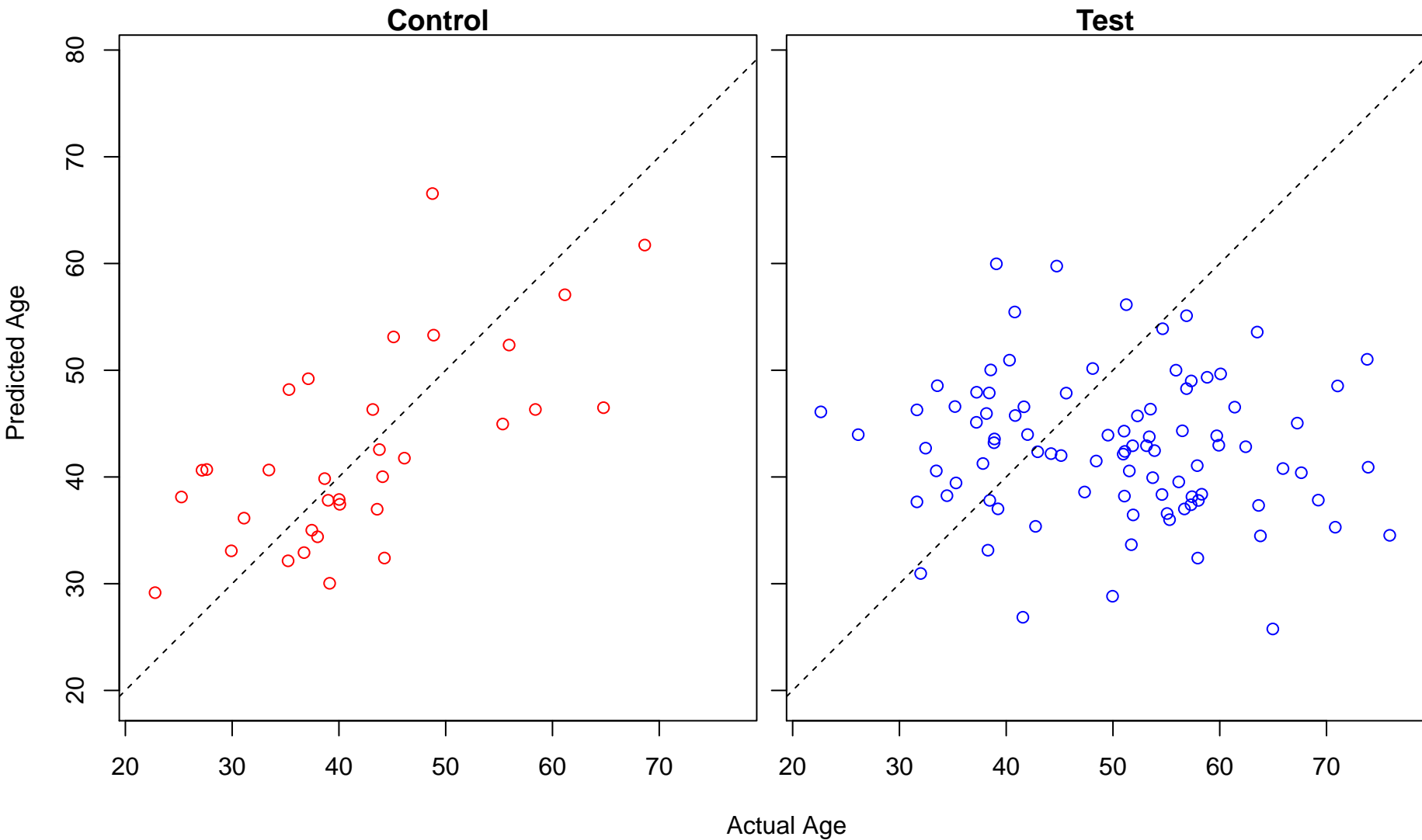
humoral immune response mediated by circulating immunoglobulin (Score: 1.908018)



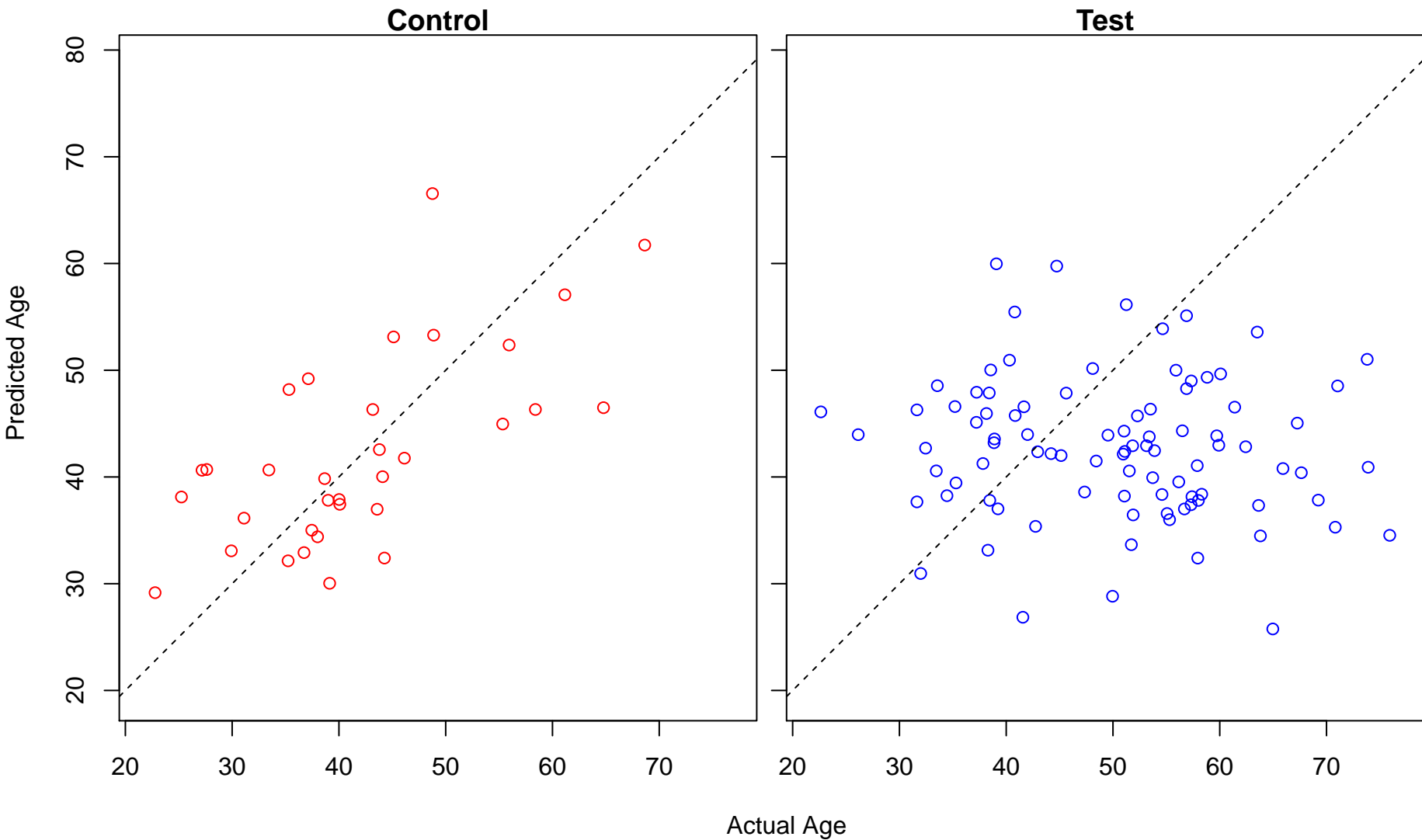
viral mRNA export from host cell nucleus (Score: 1.901717)



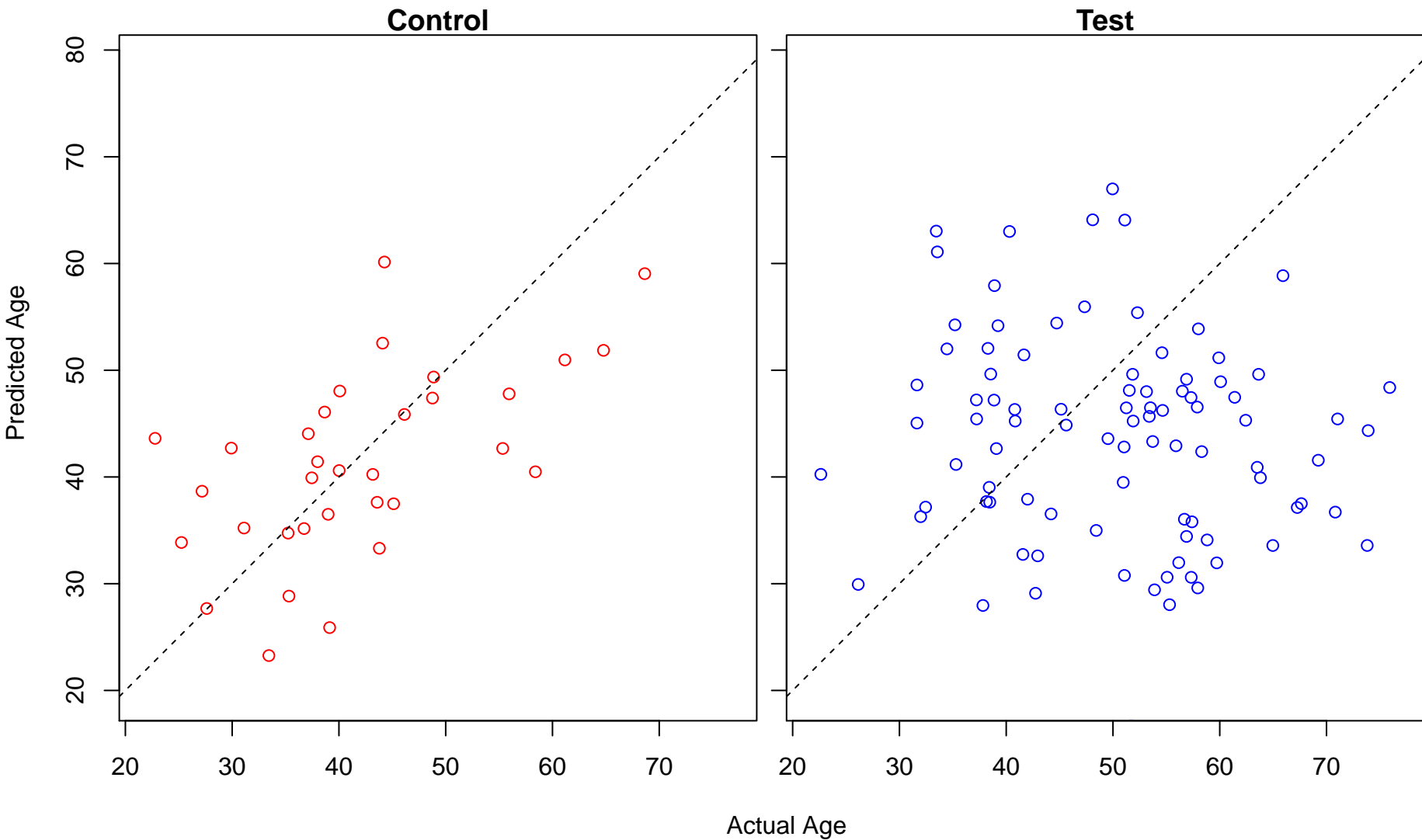
rhythmic behavior (Score: 1.901539)



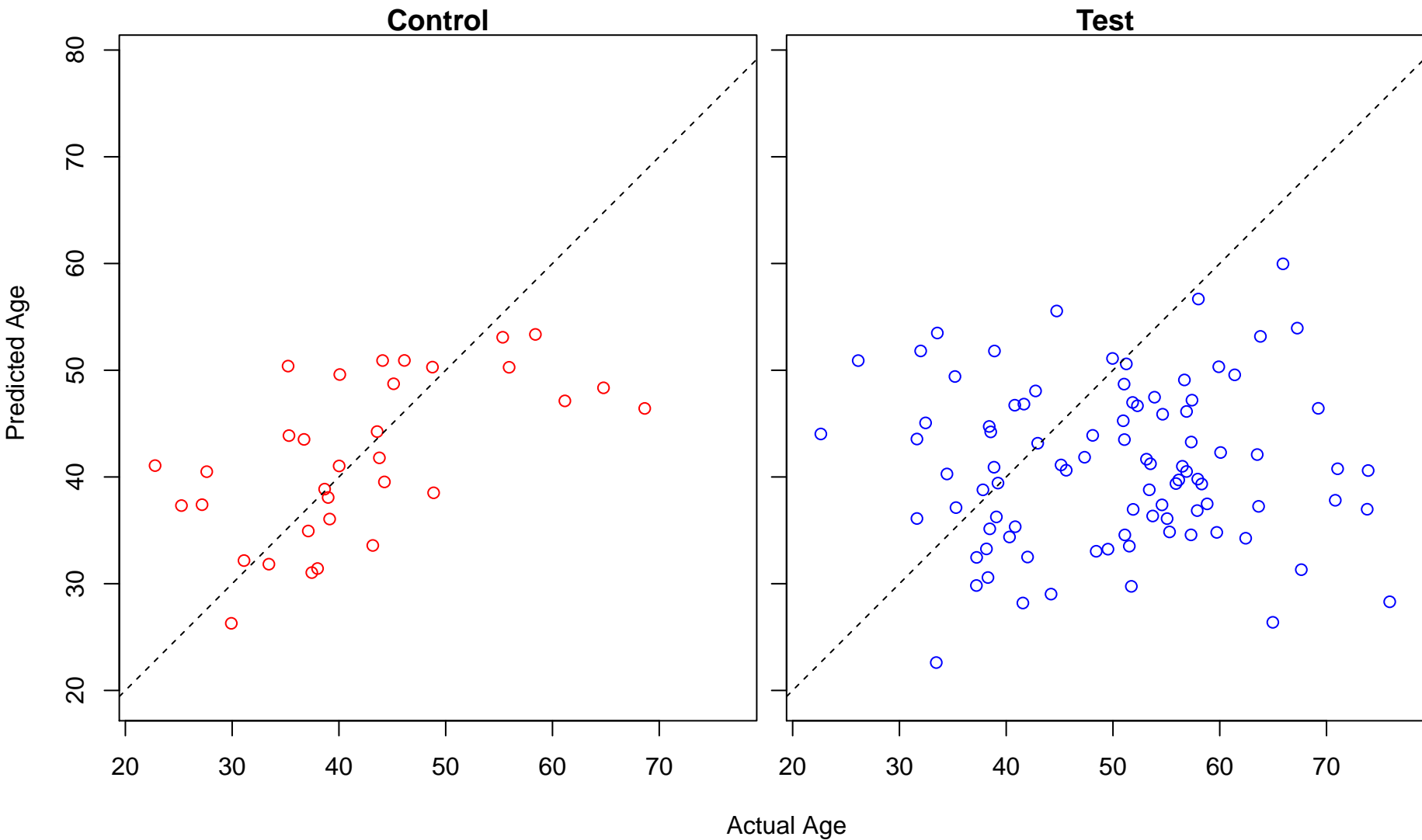
circadian behavior (Score: 1.901539)



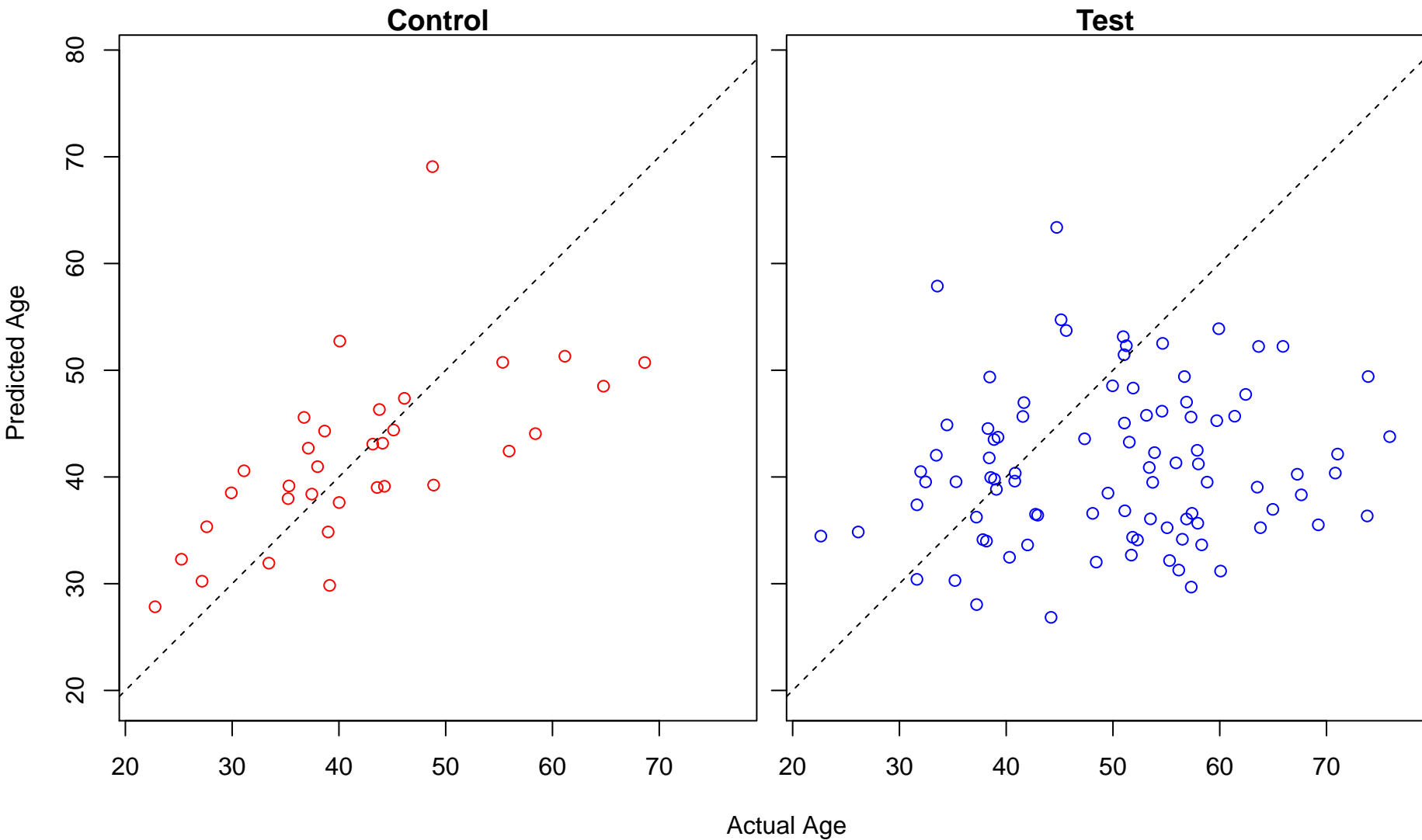
peptidyl-arginine N-methylation (Score: 1.900711)



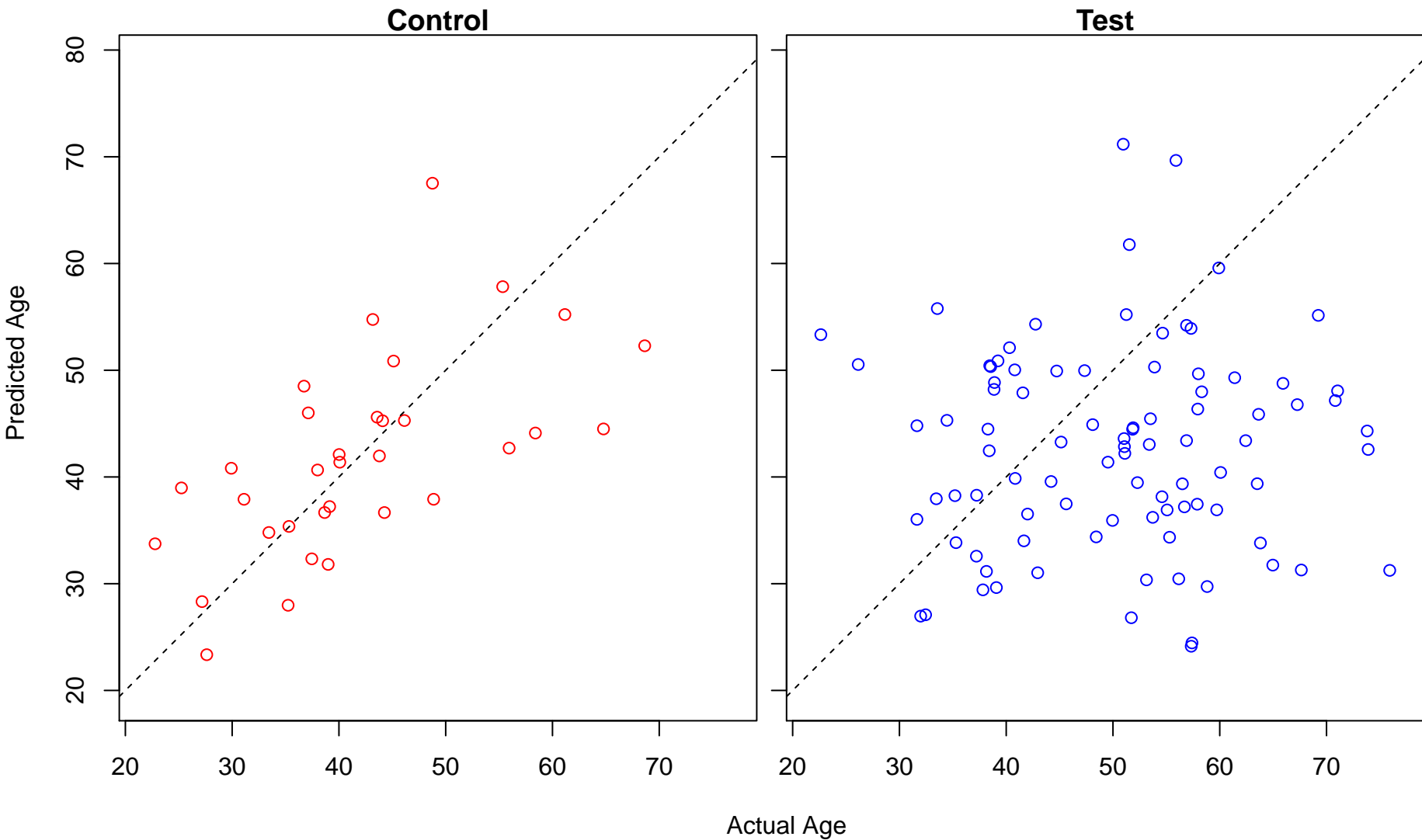
cell-cell signaling involved in cardiac conduction (Score: 1.893092)



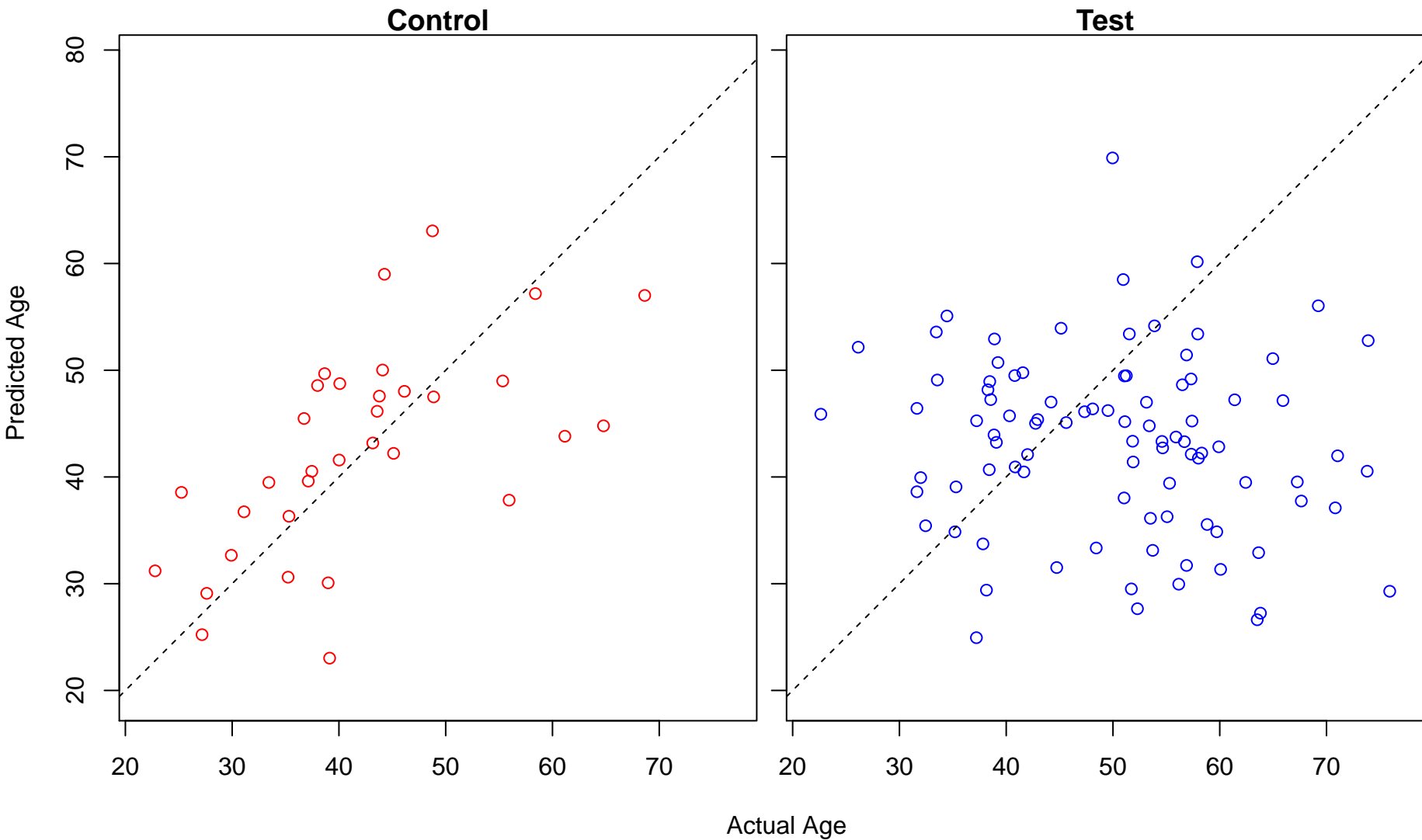
epidermal growth factor receptor signaling pathway (Score: 1.893083)



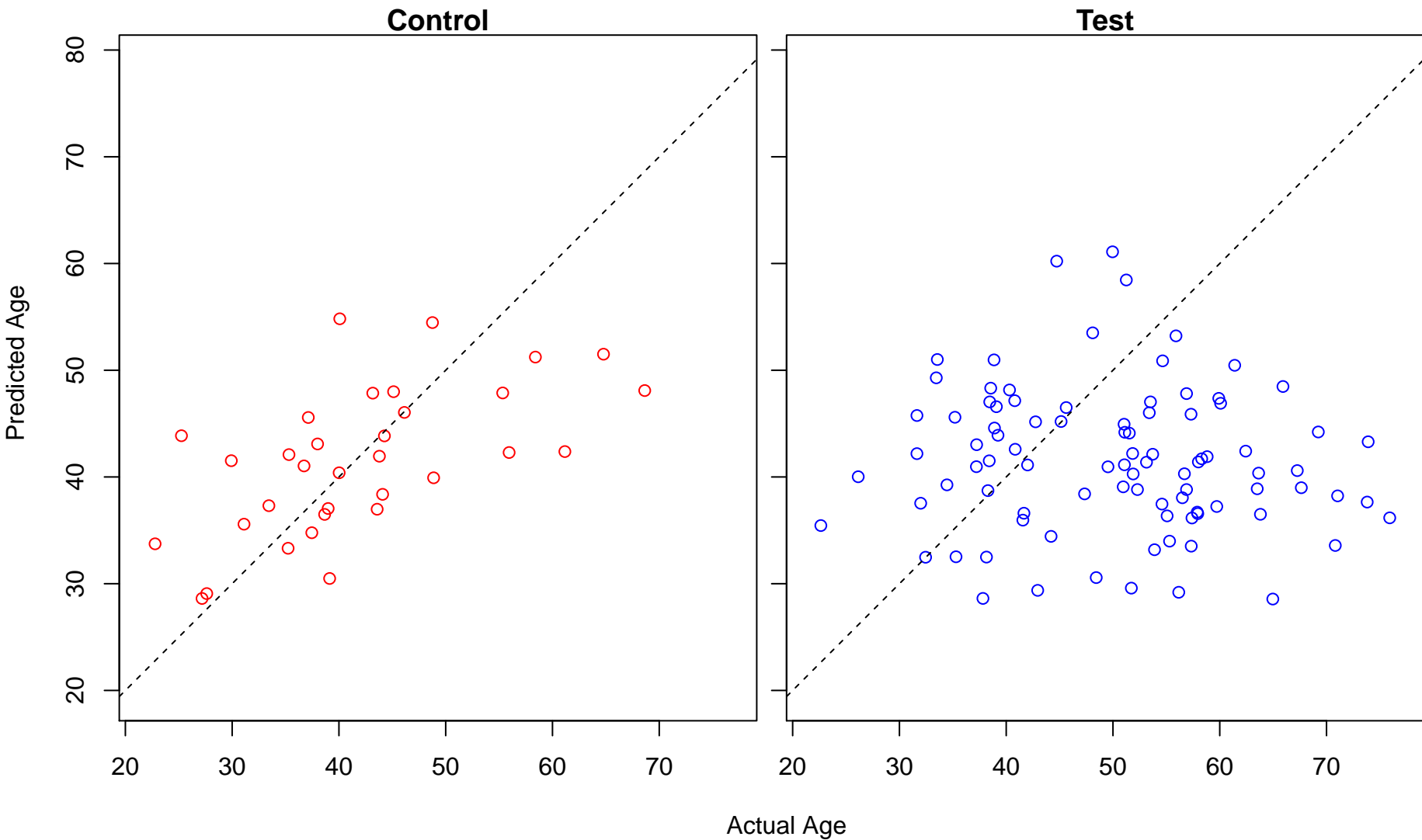
DNA damage response, detection of DNA damage (Score: 1.891359)



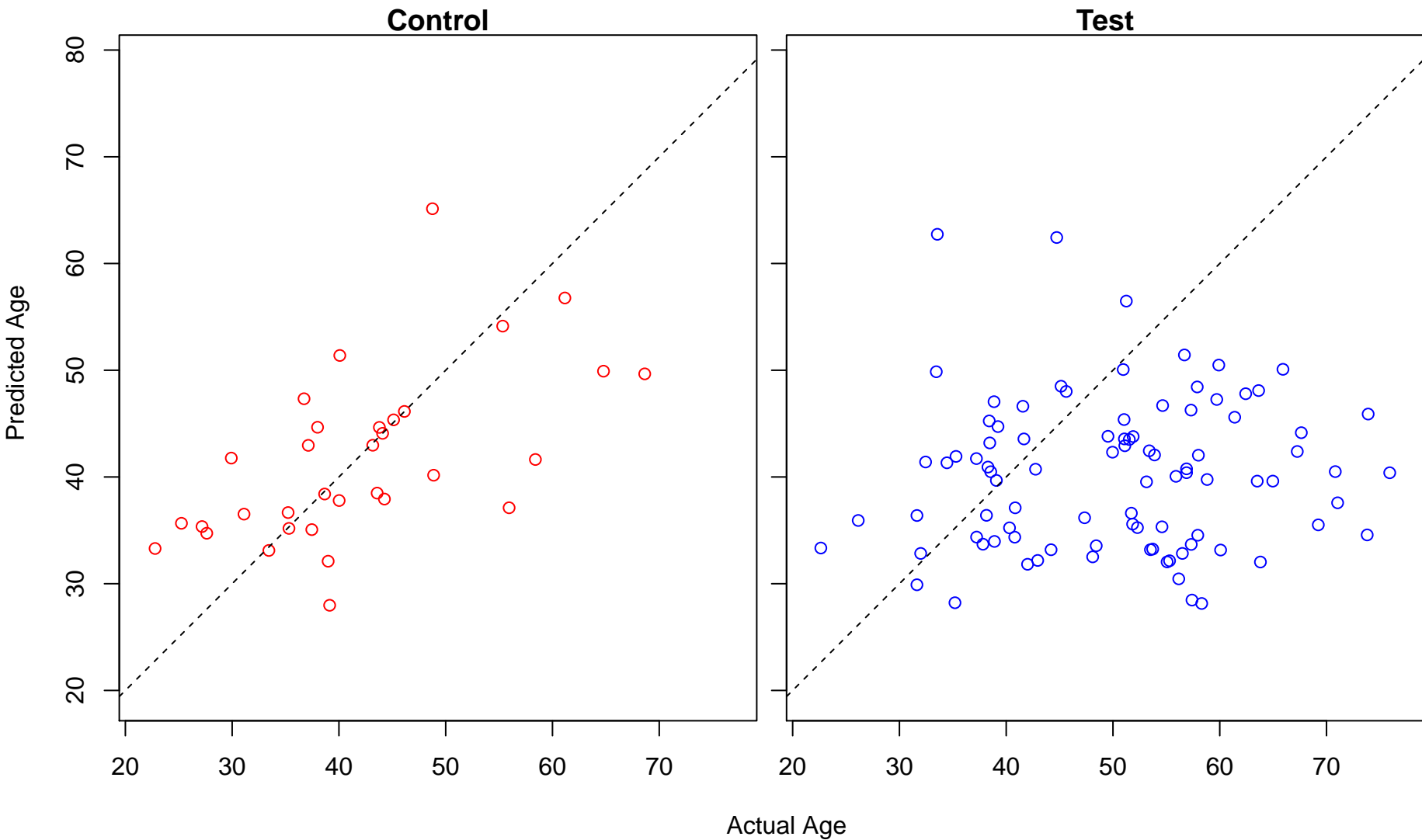
complement activation (Score: 1.888191)



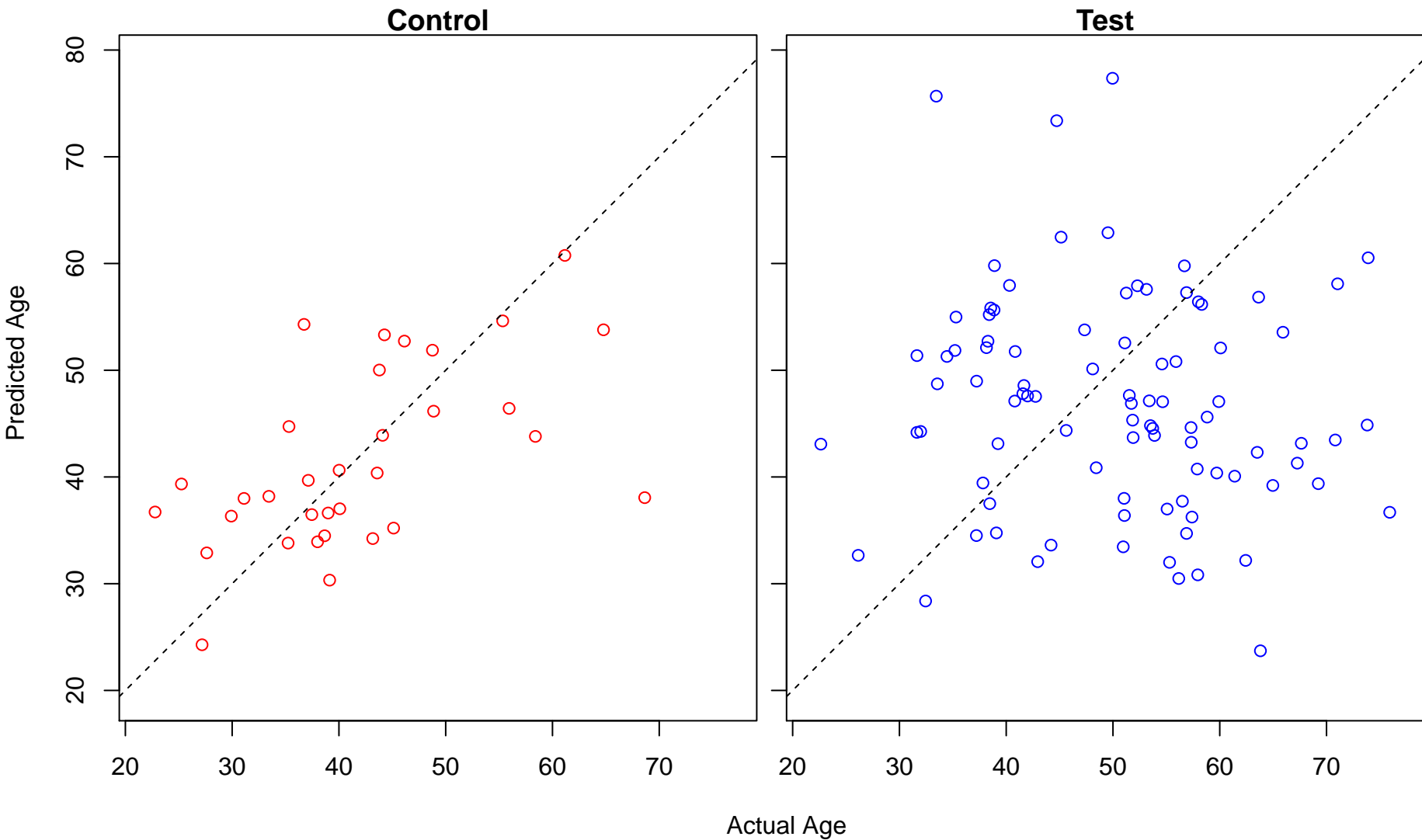
organic hydroxy compound transport (Score: 1.888066)



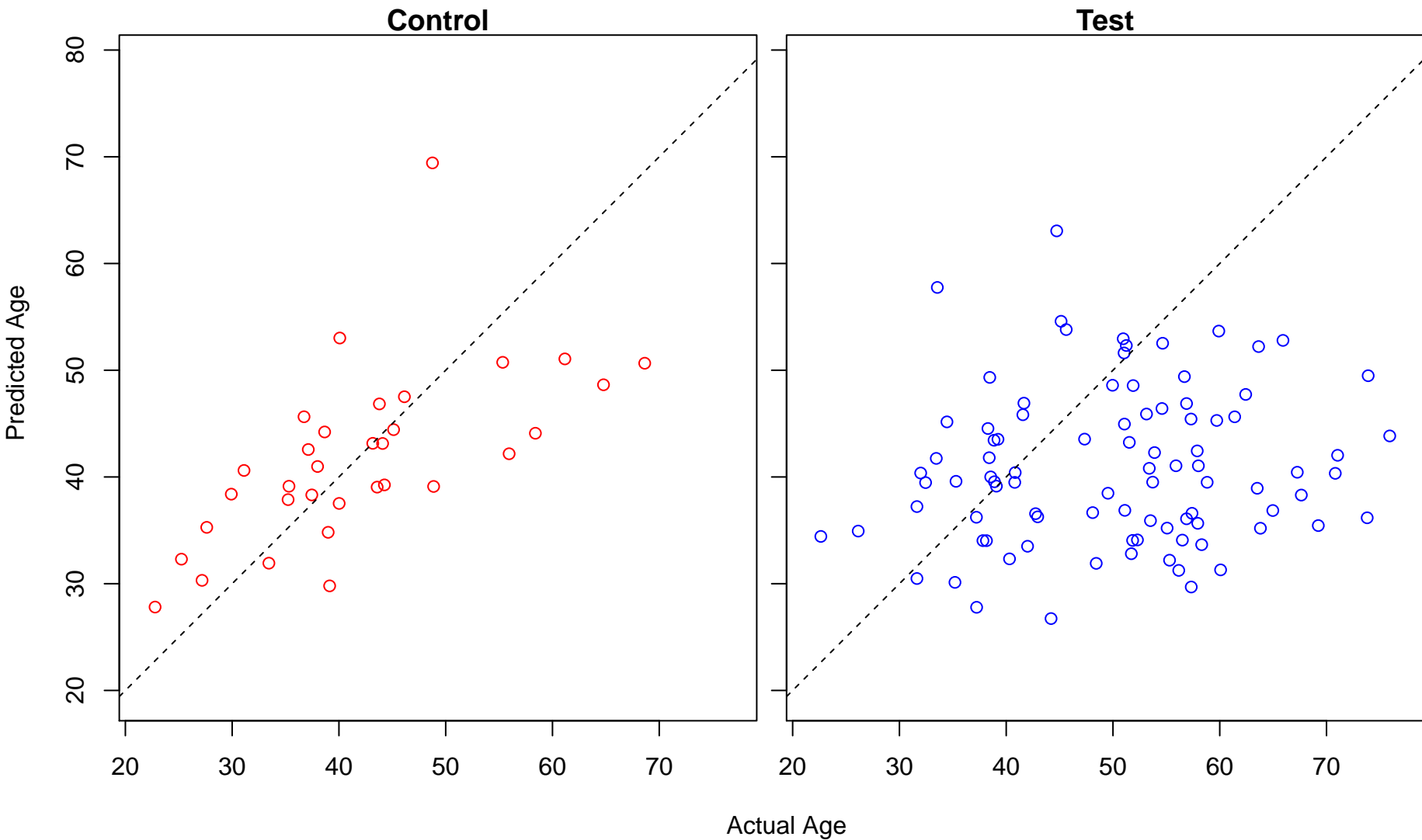
fibroblast growth factor receptor signaling pathway (Score: 1.886654)



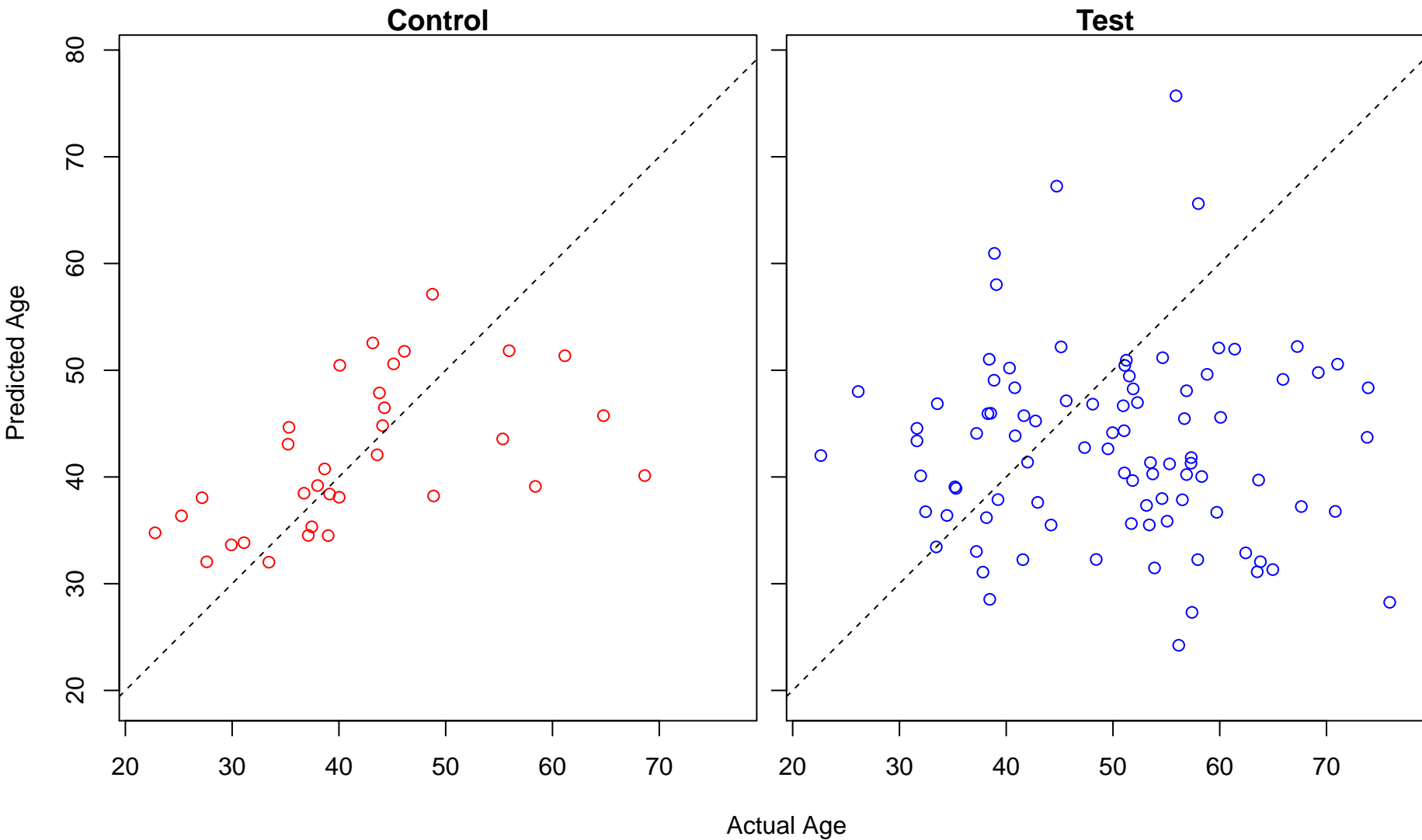
negative regulation of reactive oxygen species biosynthetic process (Score: 1.881353)



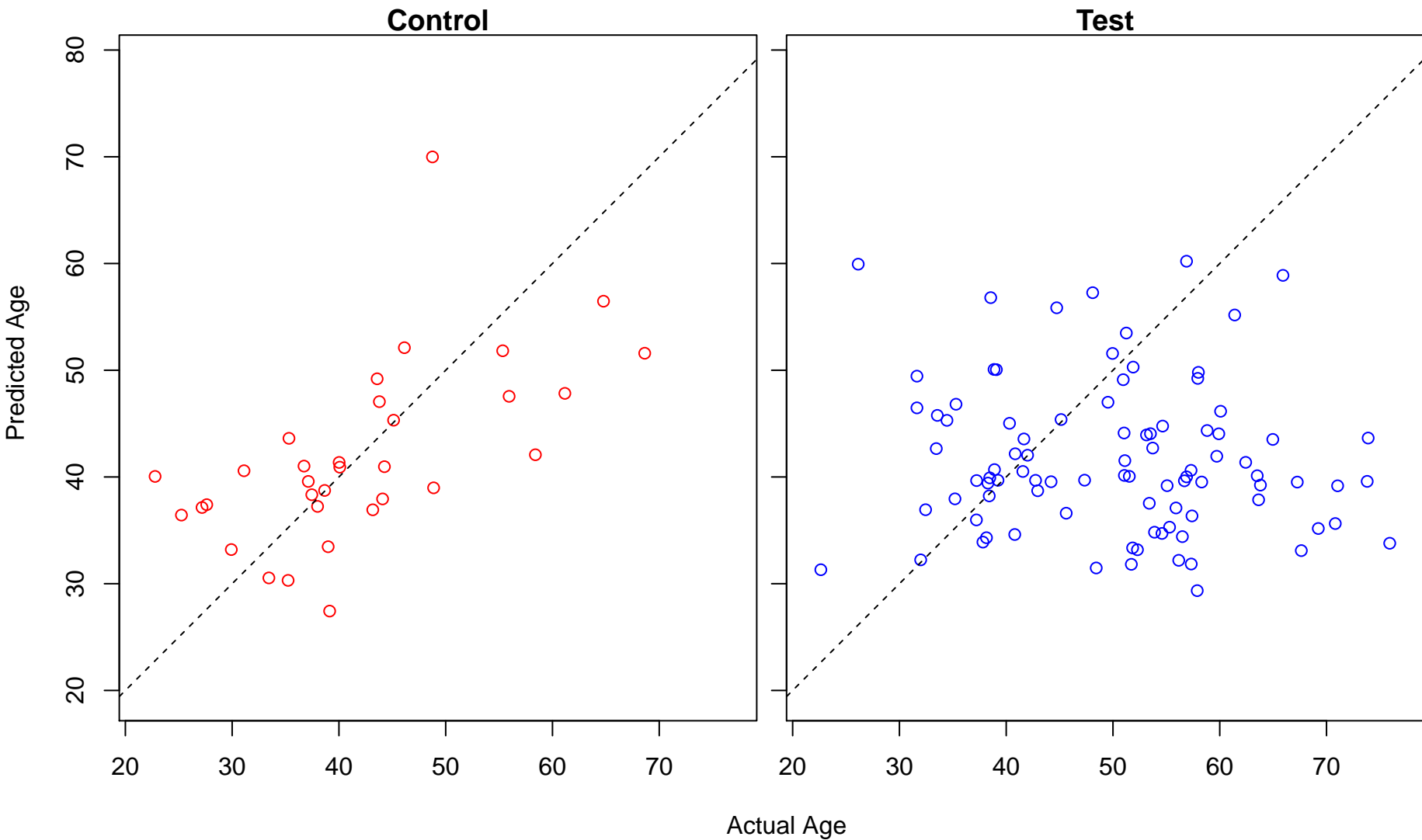
ERBB signaling pathway (Score: 1.880268)



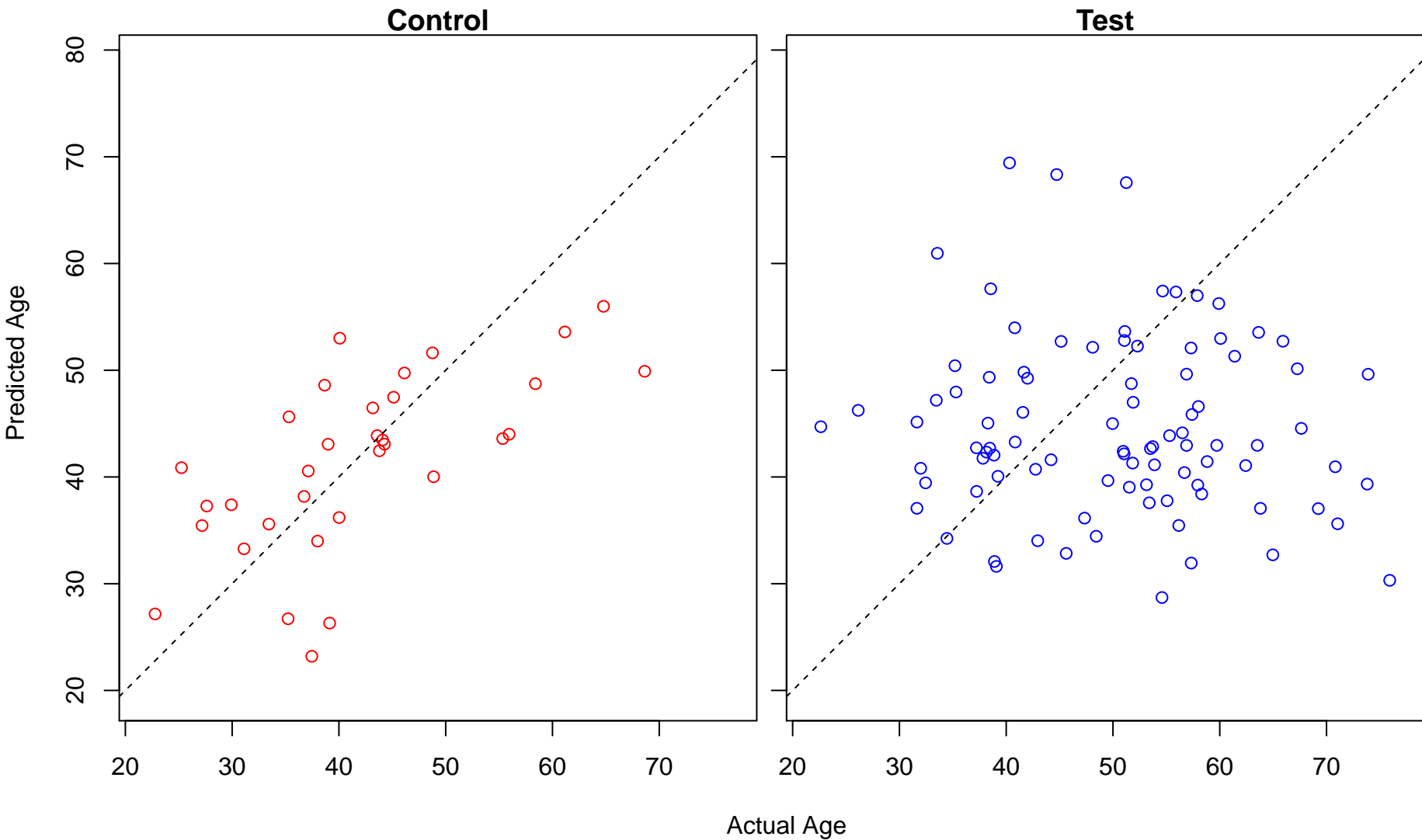
negative regulation of potassium ion transport (Score: 1.876141)



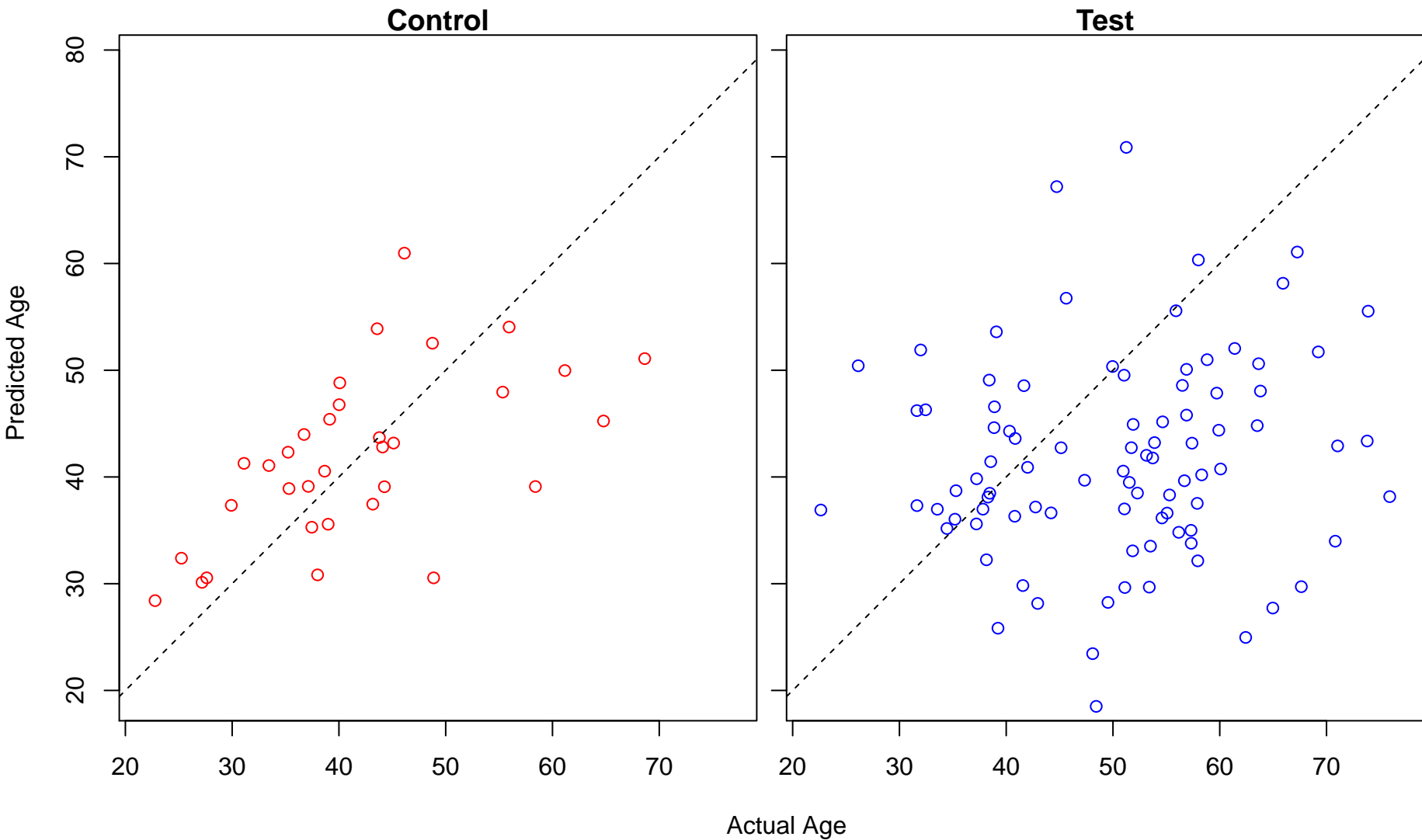
G2 DNA damage checkpoint (Score: 1.875130)



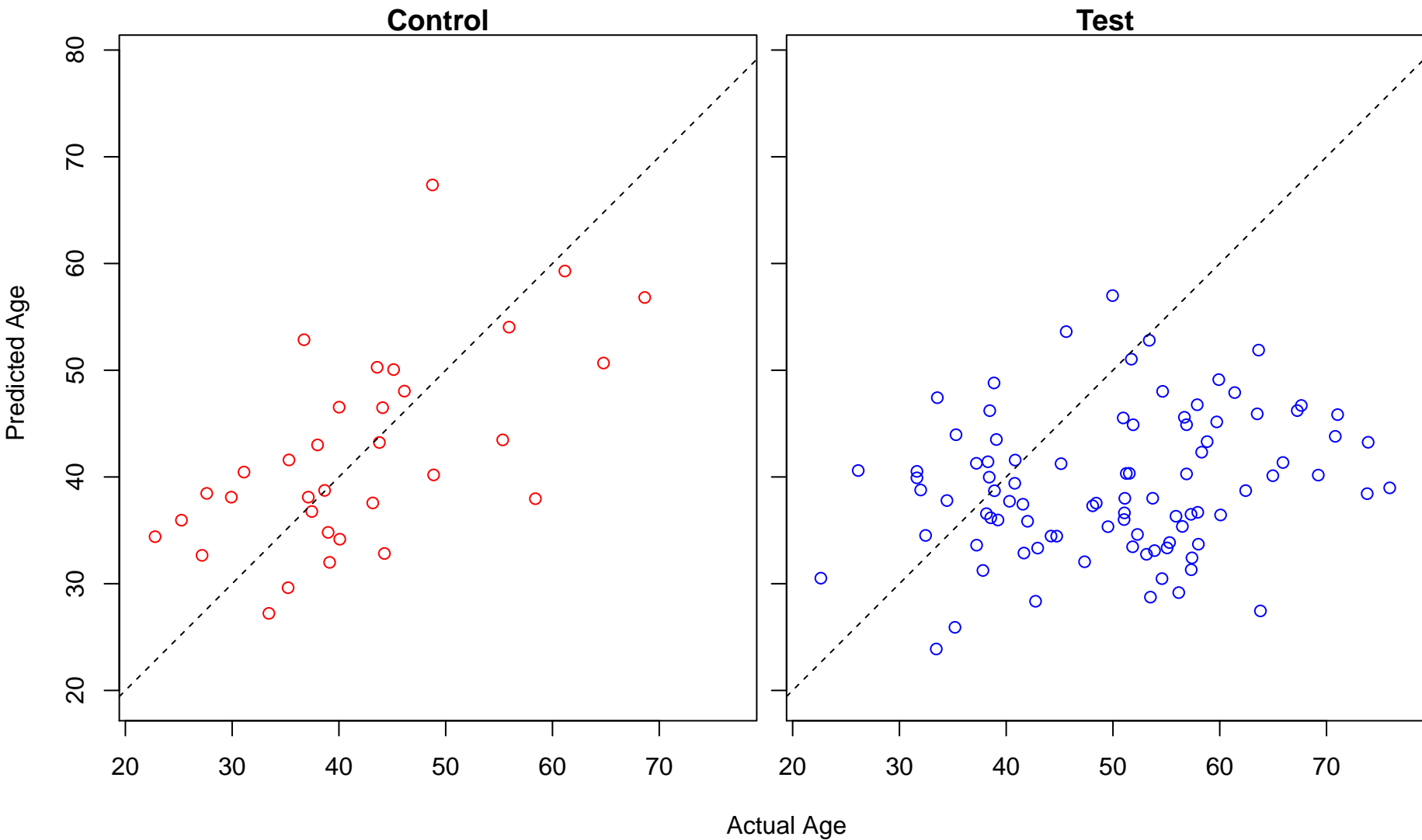
temperature homeostasis (Score: 1.871888)



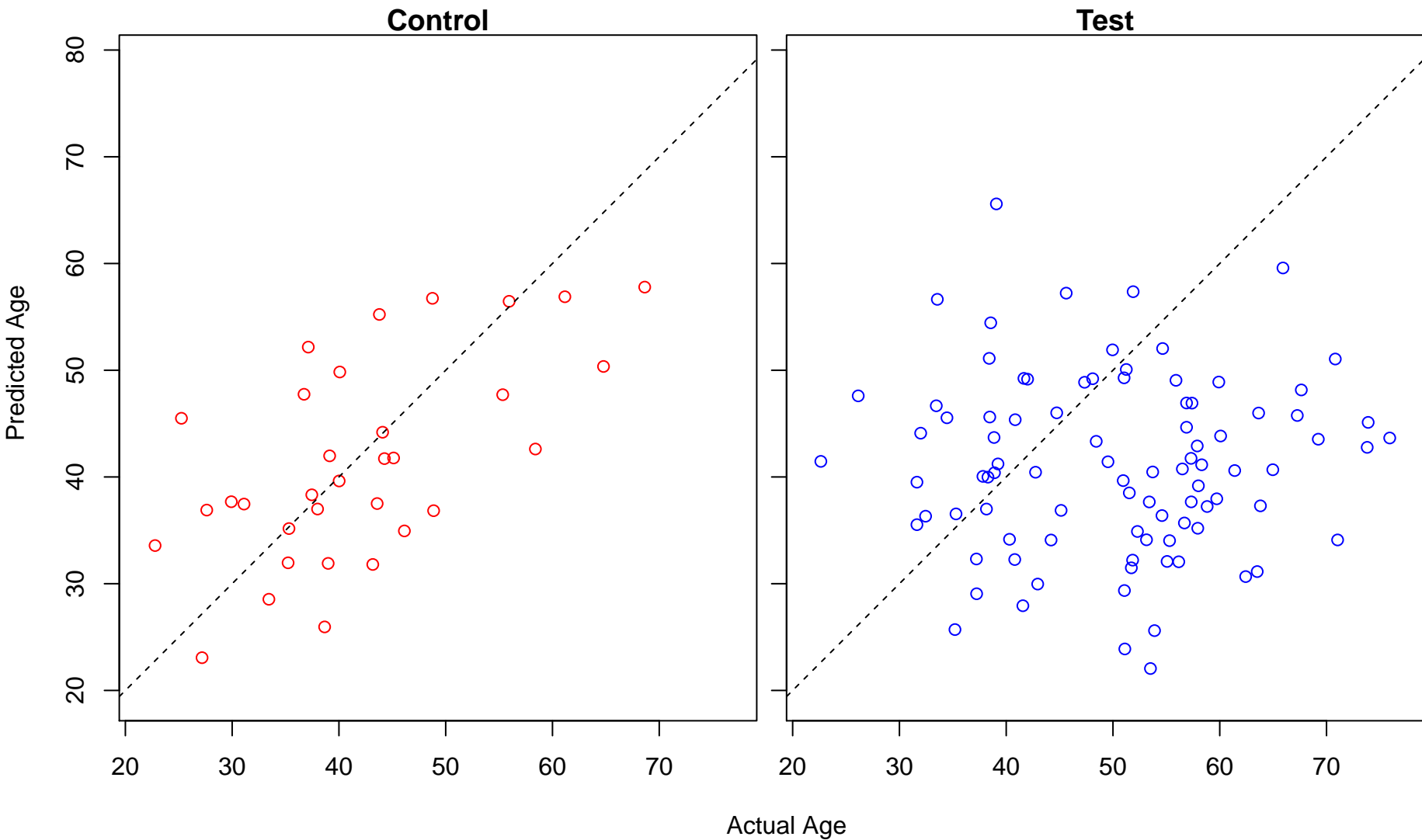
positive regulation of potassium ion transmembrane transport (Score: 1.868239)



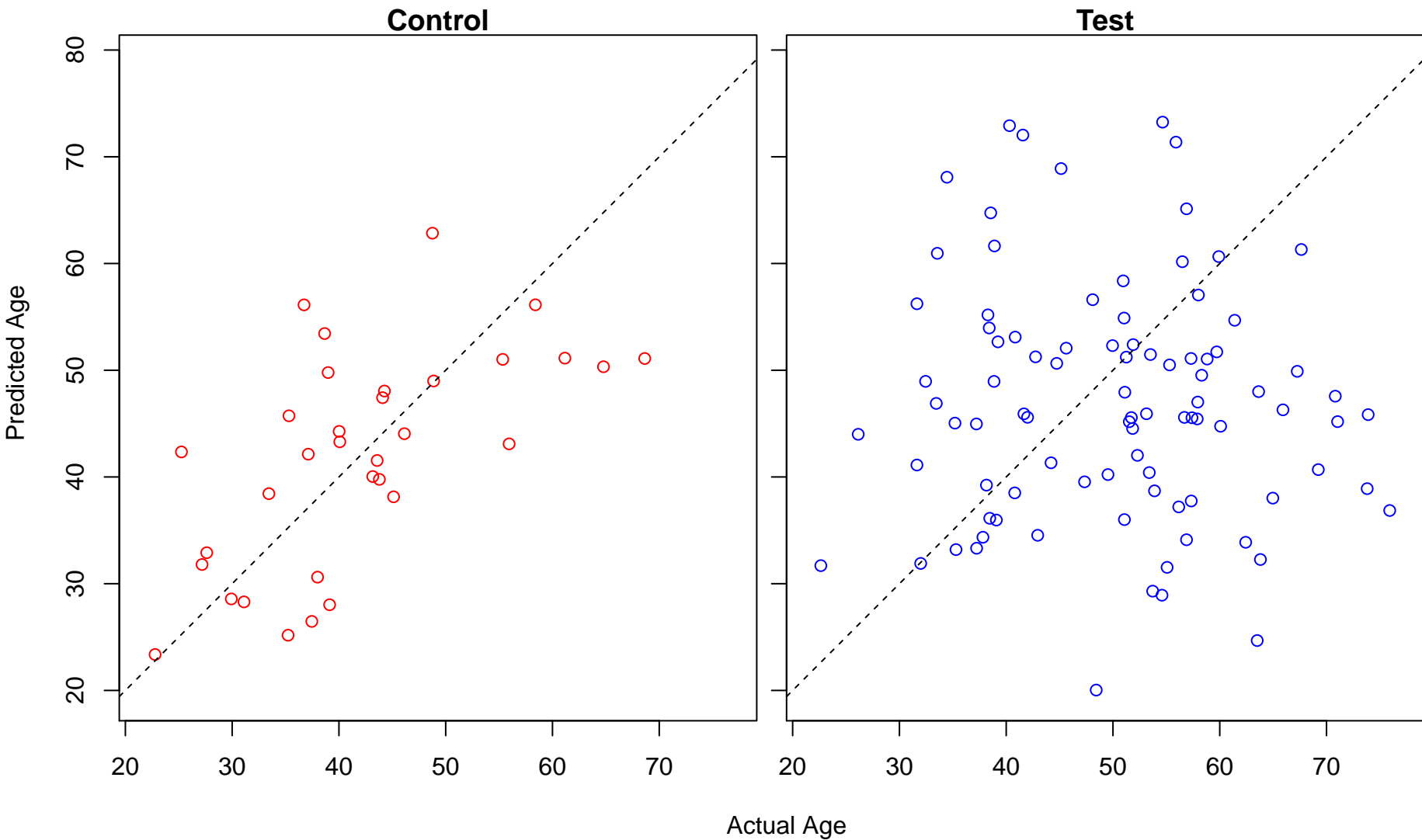
positive regulation of adherens junction organization (Score: 1.866248)



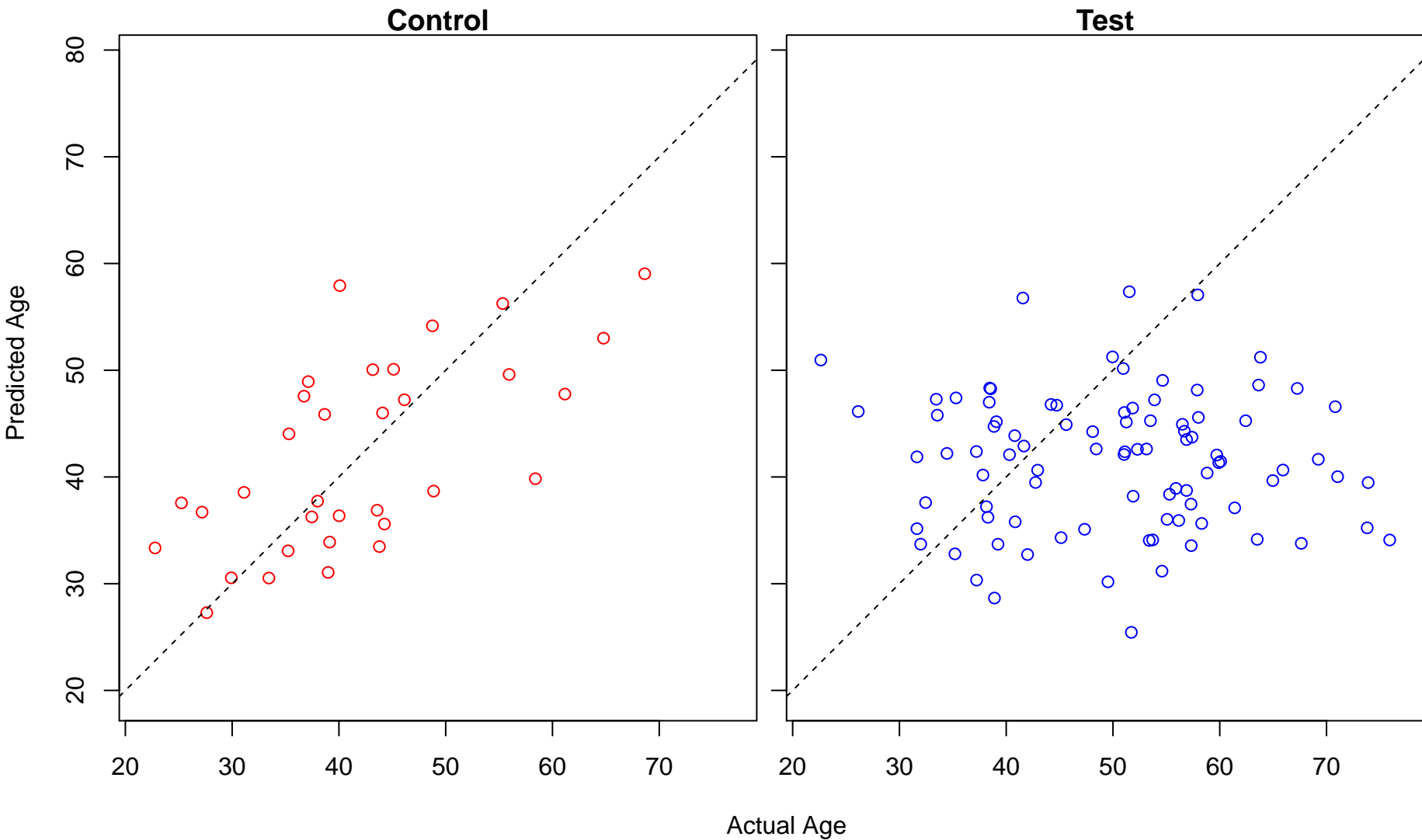
blood coagulation, fibrin clot formation (Score: 1.865453)



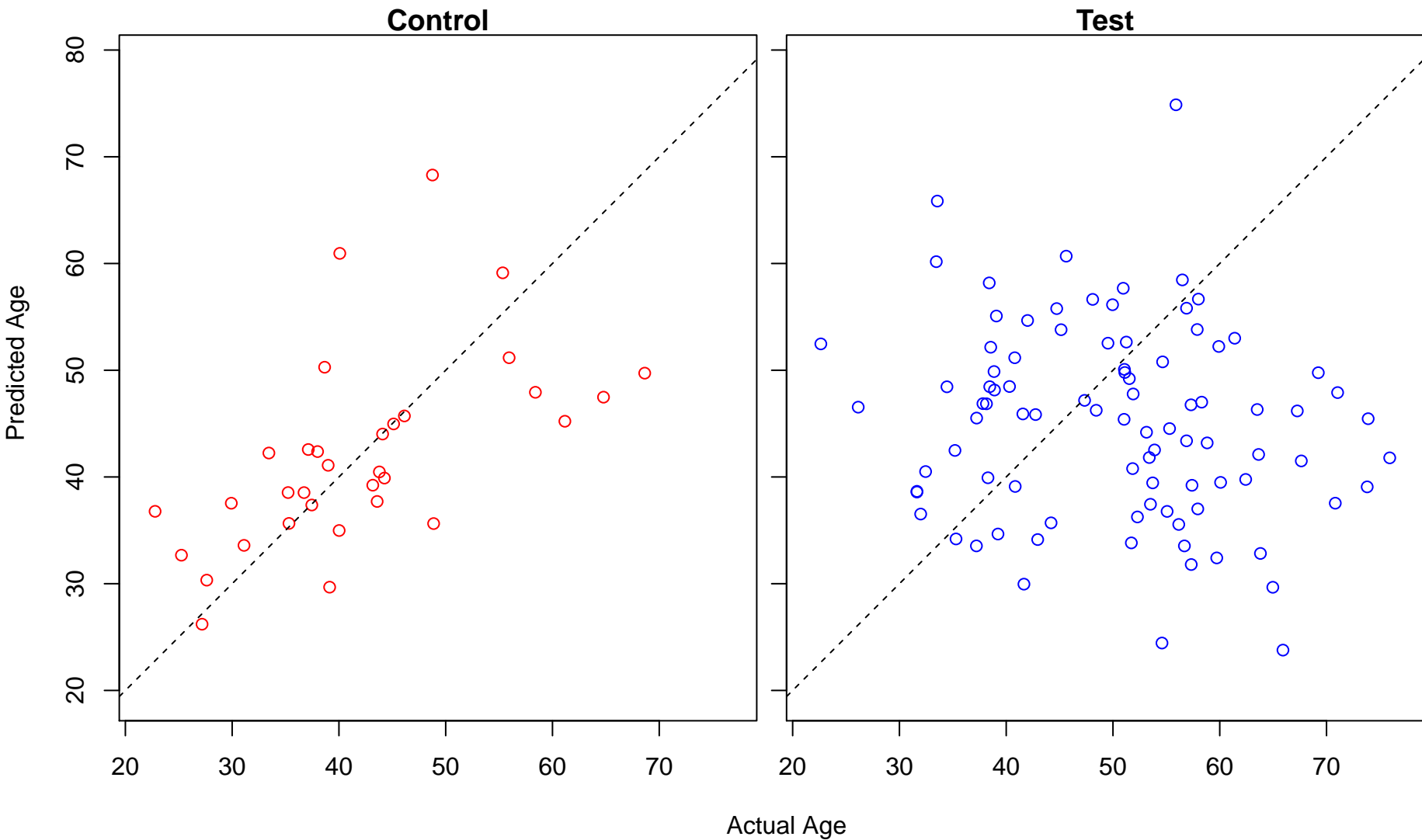
cellular glucose homeostasis (Score: 1.865366)



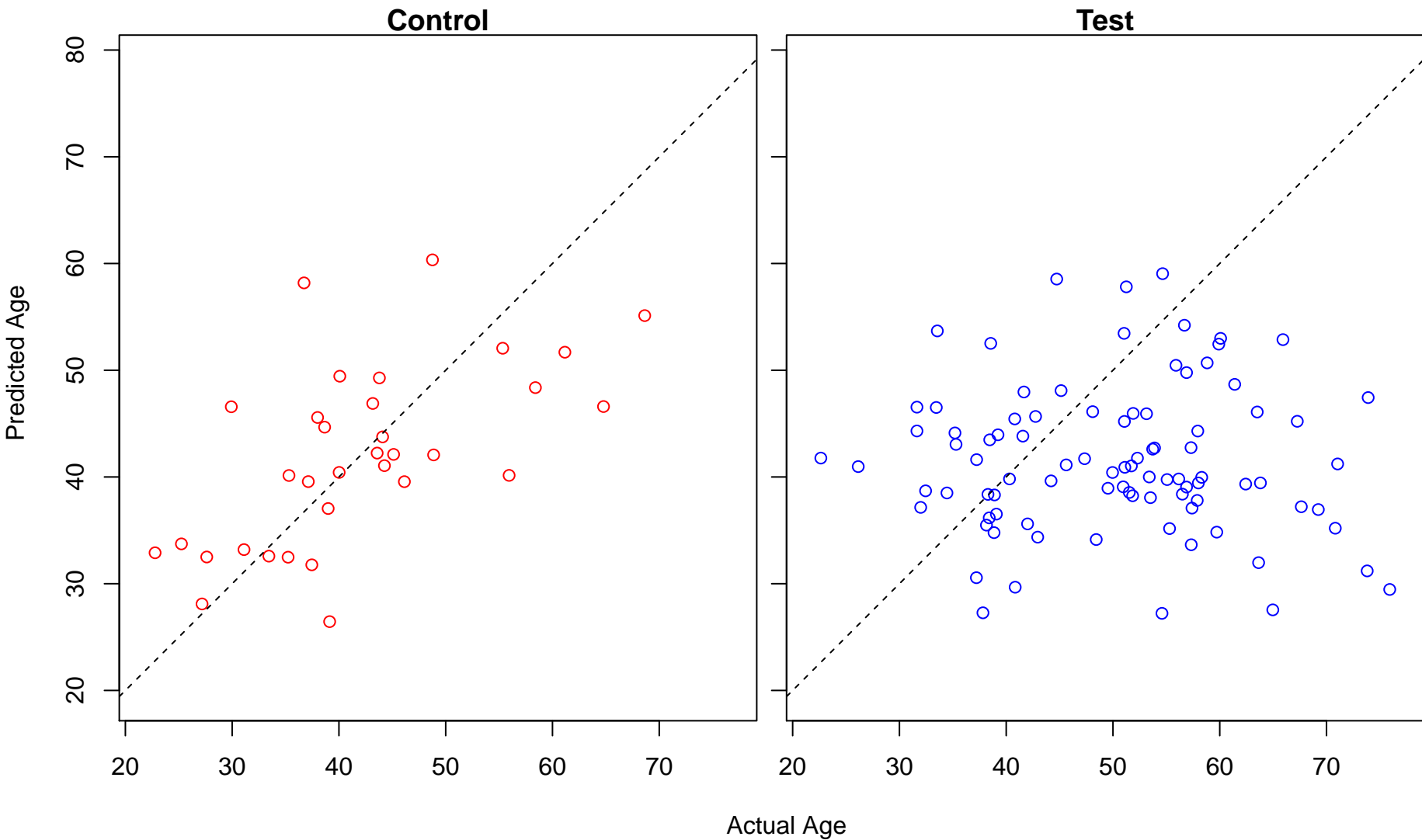
transmission of nerve impulse (Score: 1.860541)



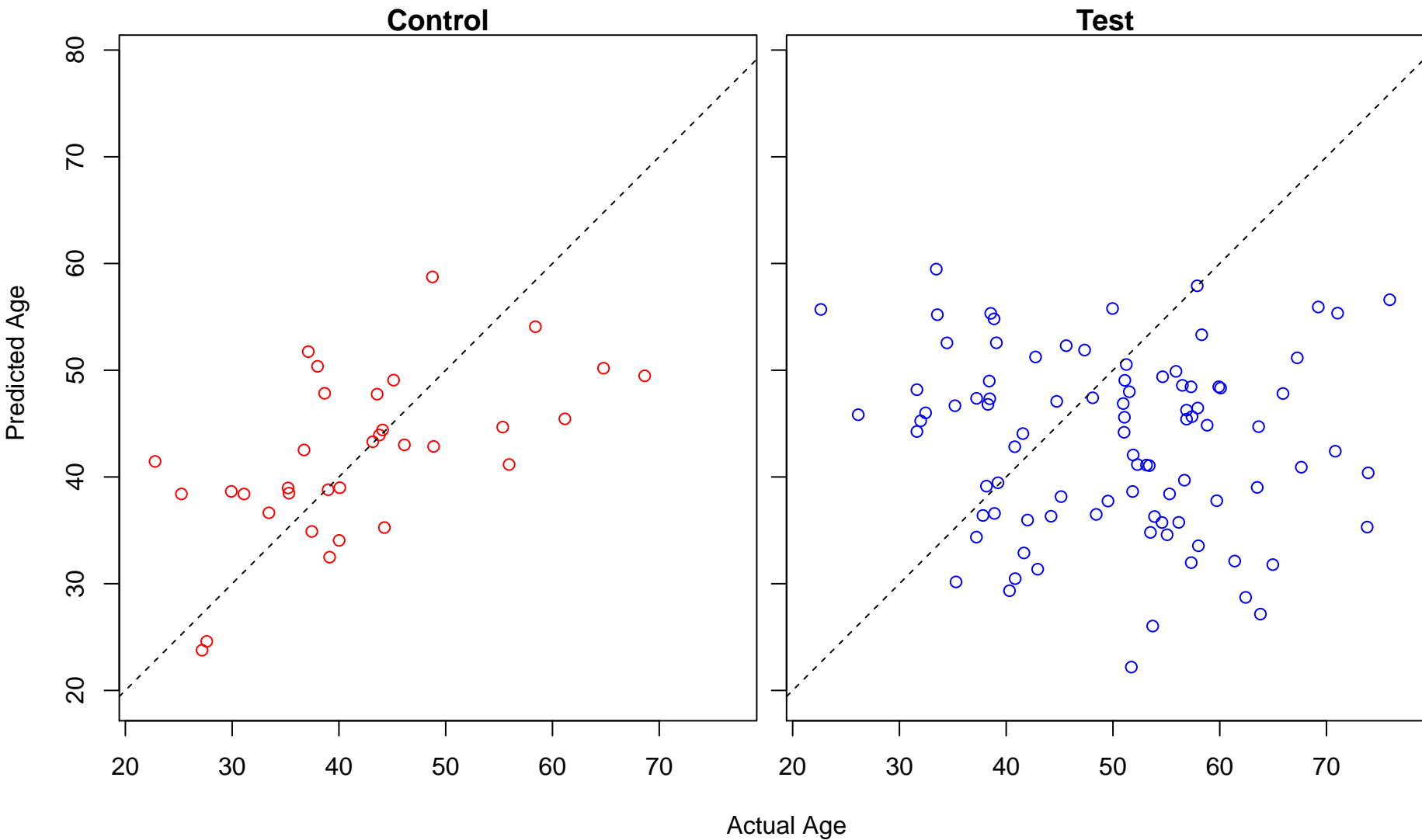
regulation of tumor necrosis factor production (Score: 1.859892)



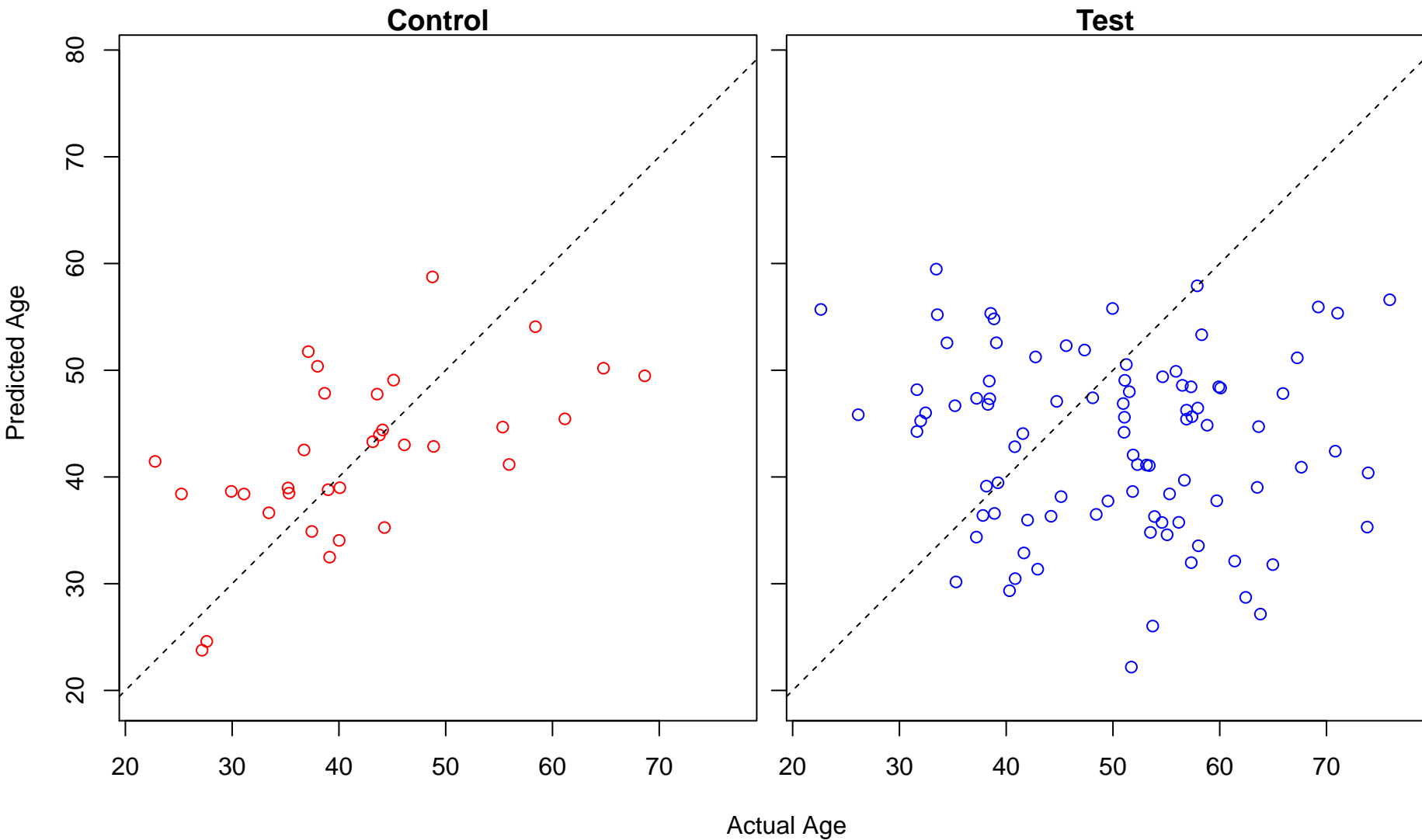
cellular response to tumor necrosis factor (Score: 1.857309)



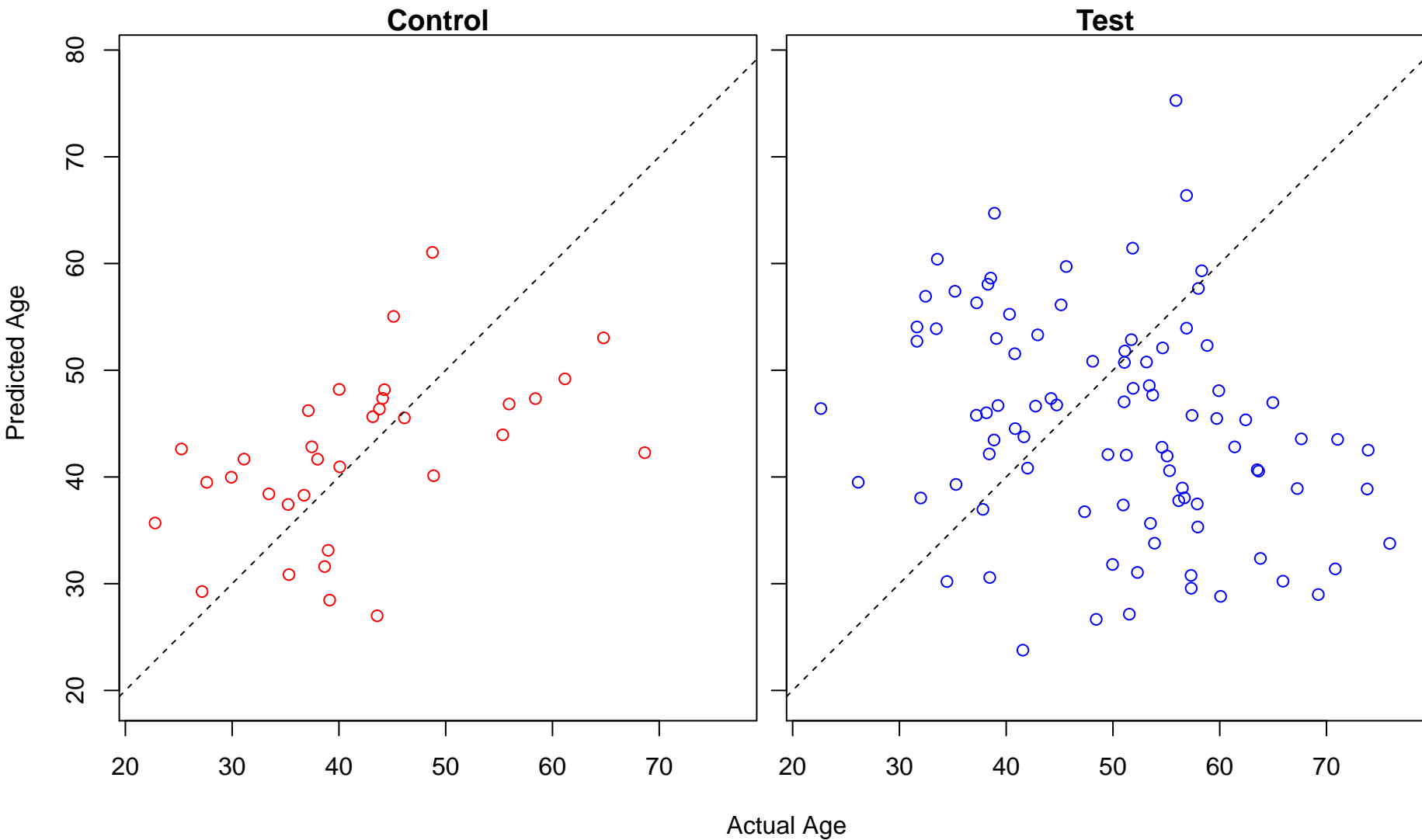
central nervous system myelination (Score: 1.856137)



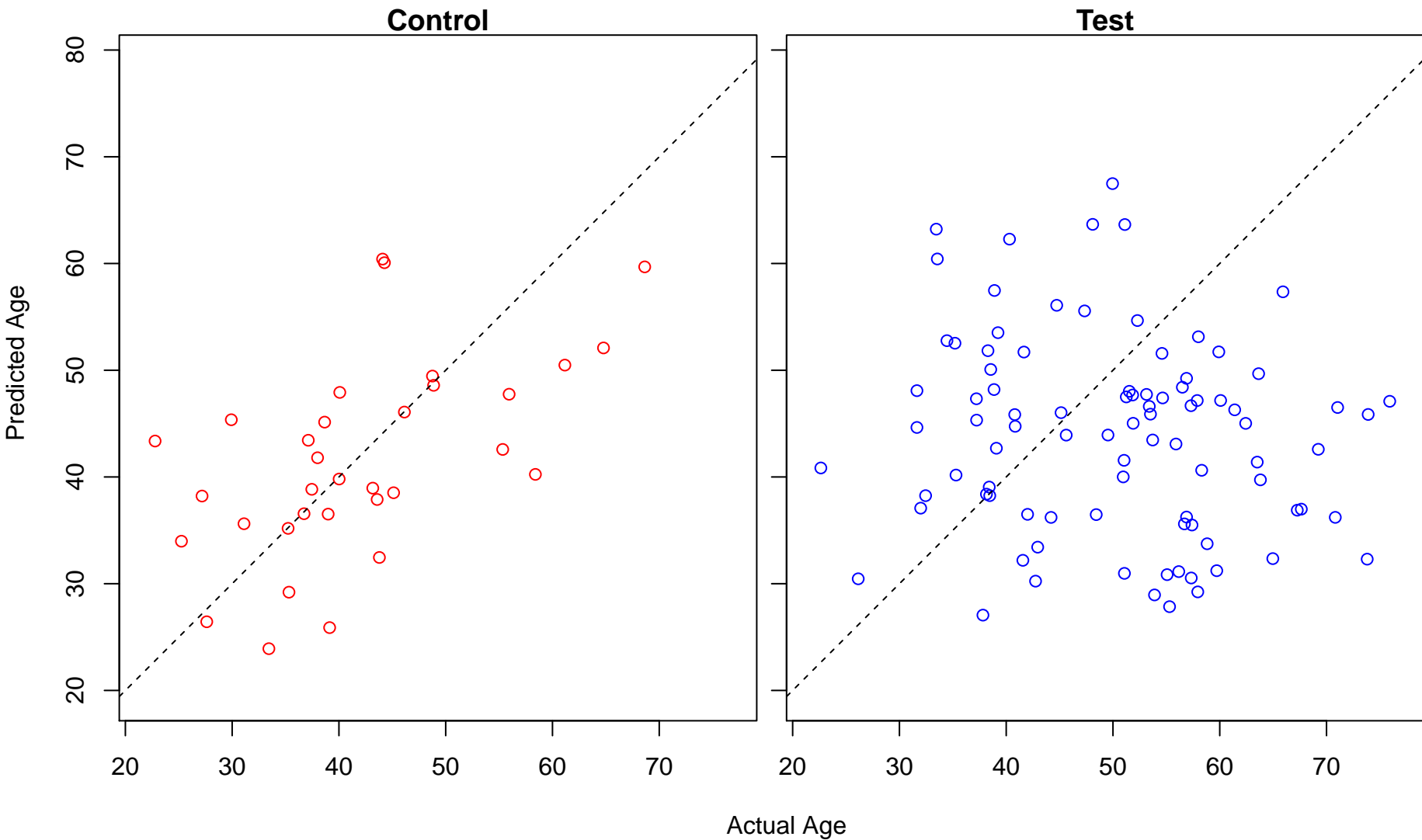
axon ensheathment in central nervous system (Score: 1.856137)



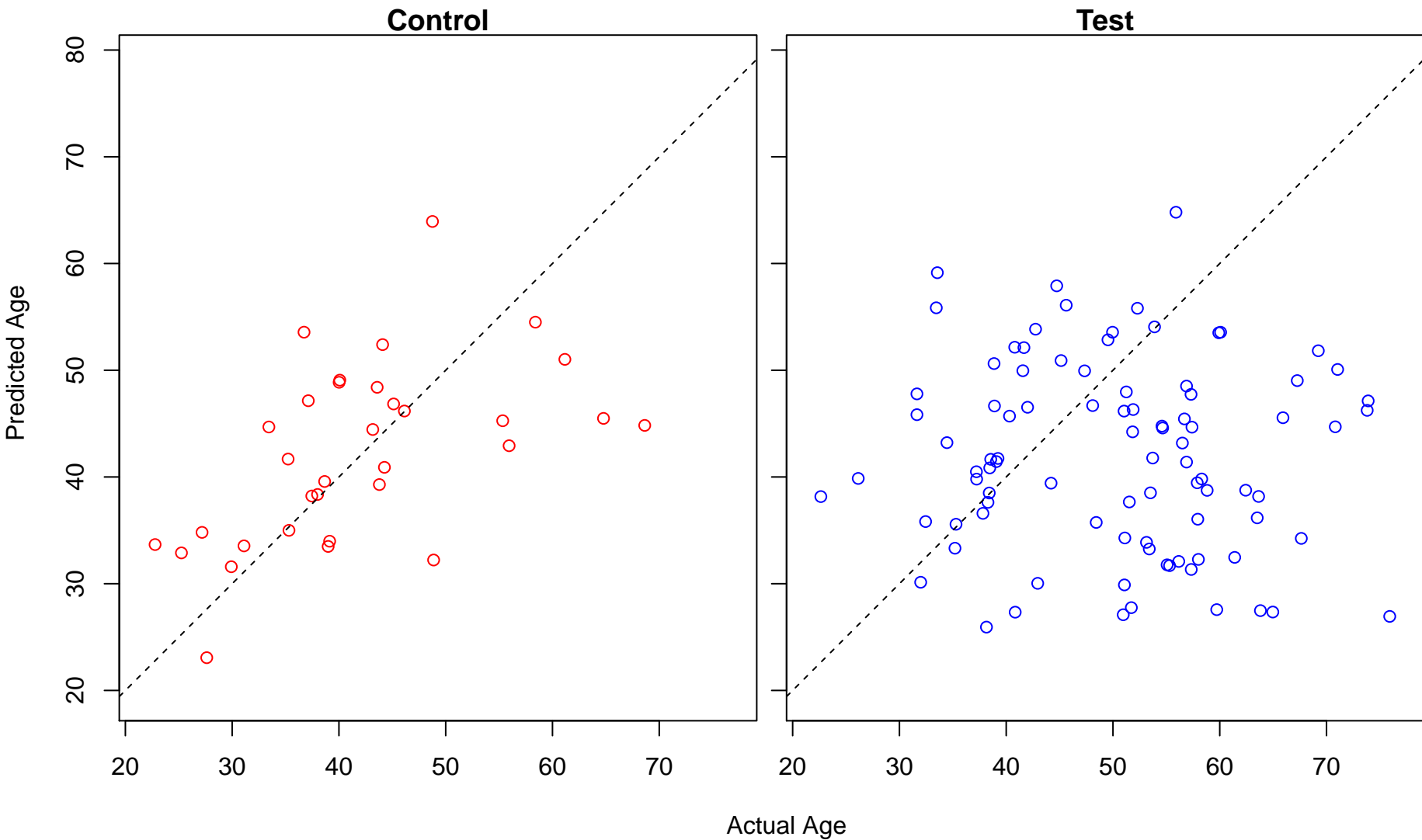
regulation of immature T cell proliferation in thymus (Score: 1.852196)



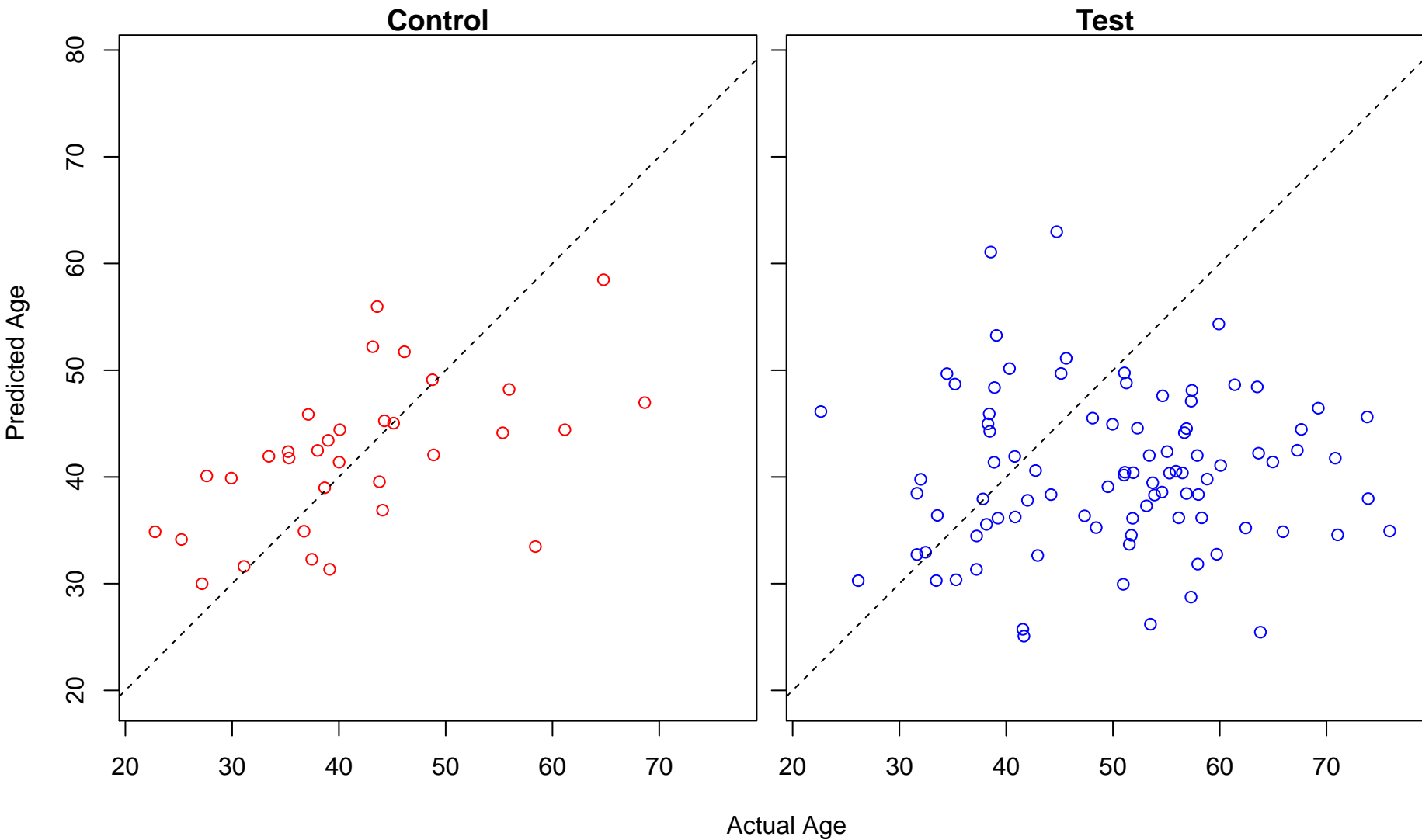
peptidyl-arginine methylation (Score: 1.848595)



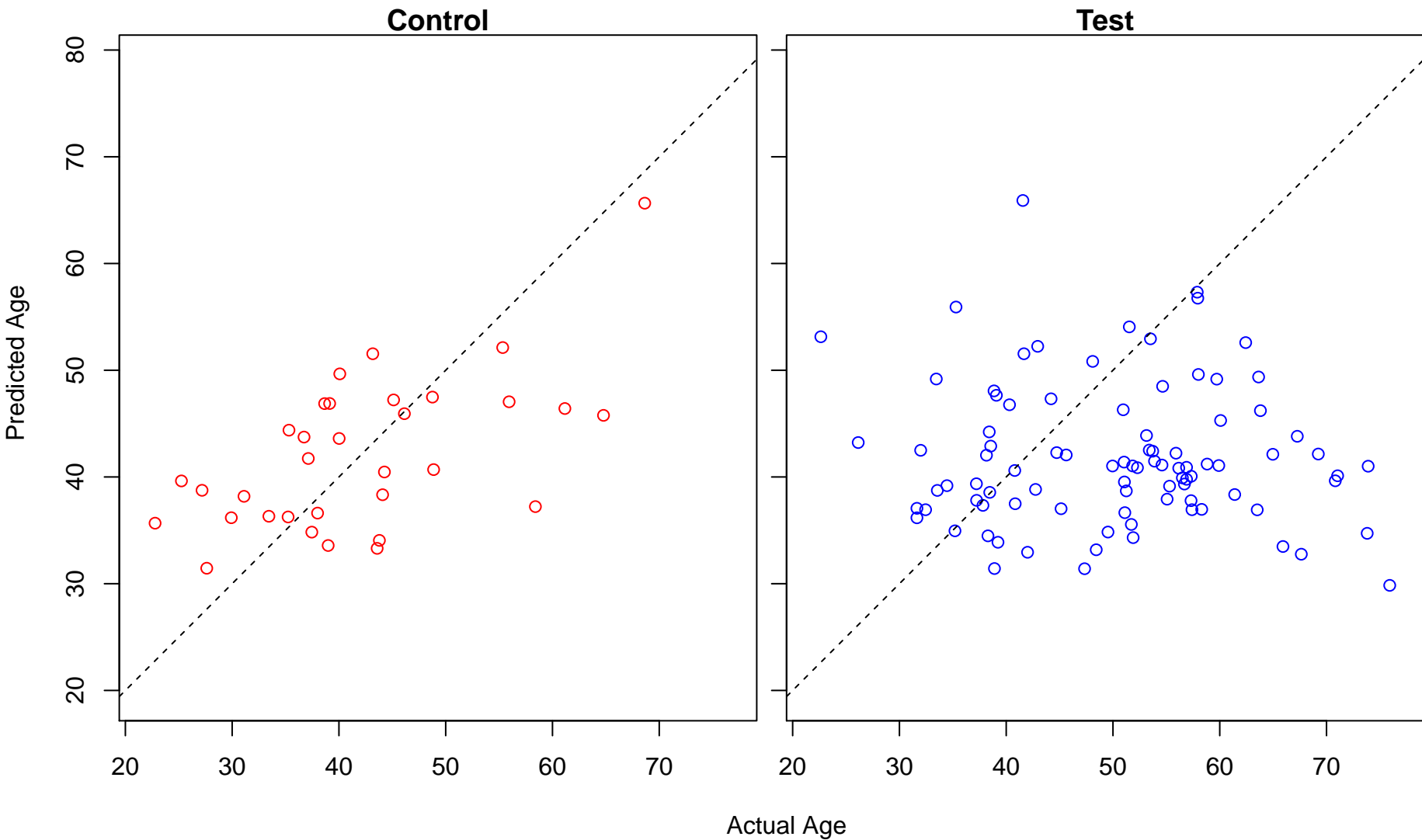
membrane depolarization (Score: 1.847159)



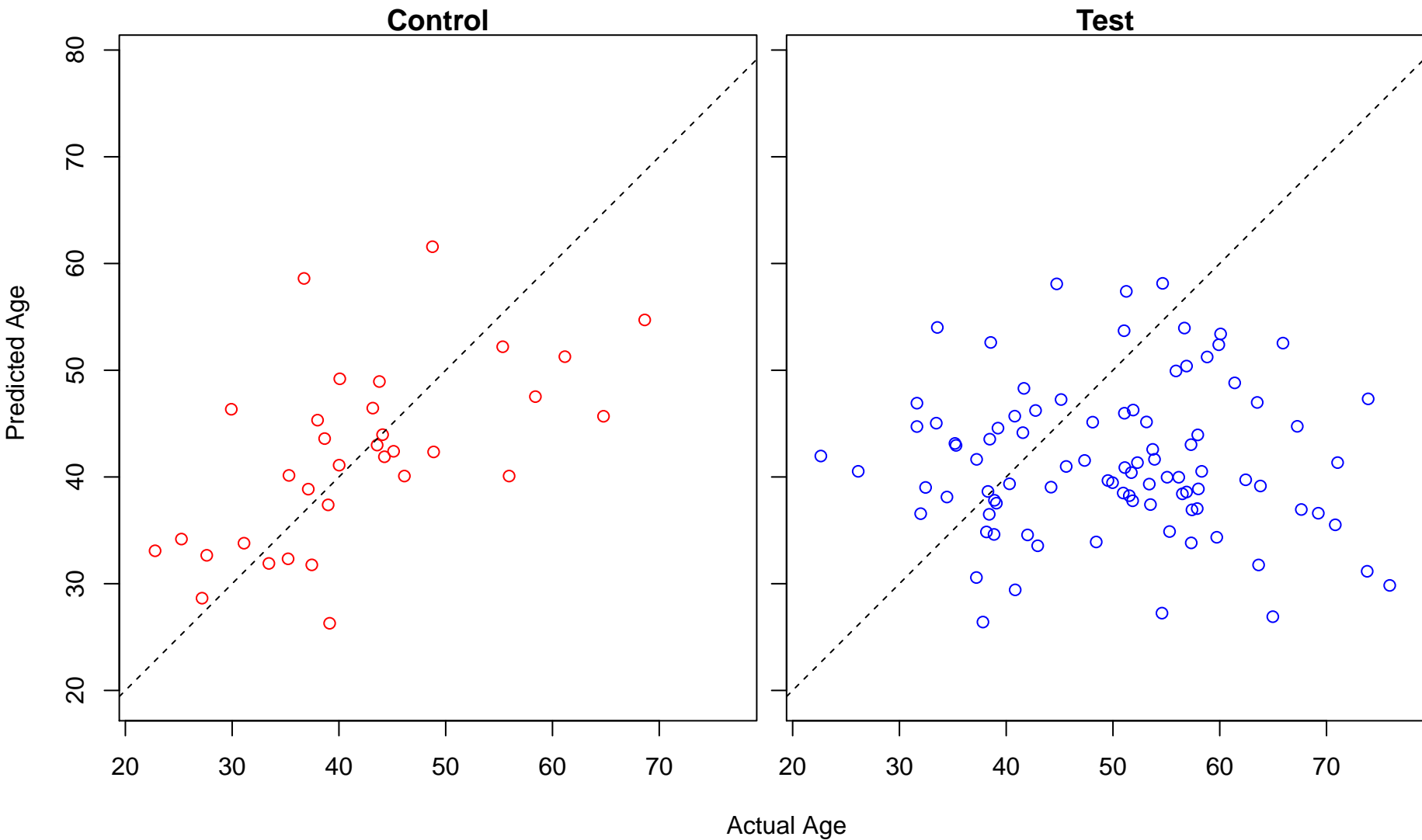
receptor guanylyl cyclase signaling pathway (Score: 1.847157)



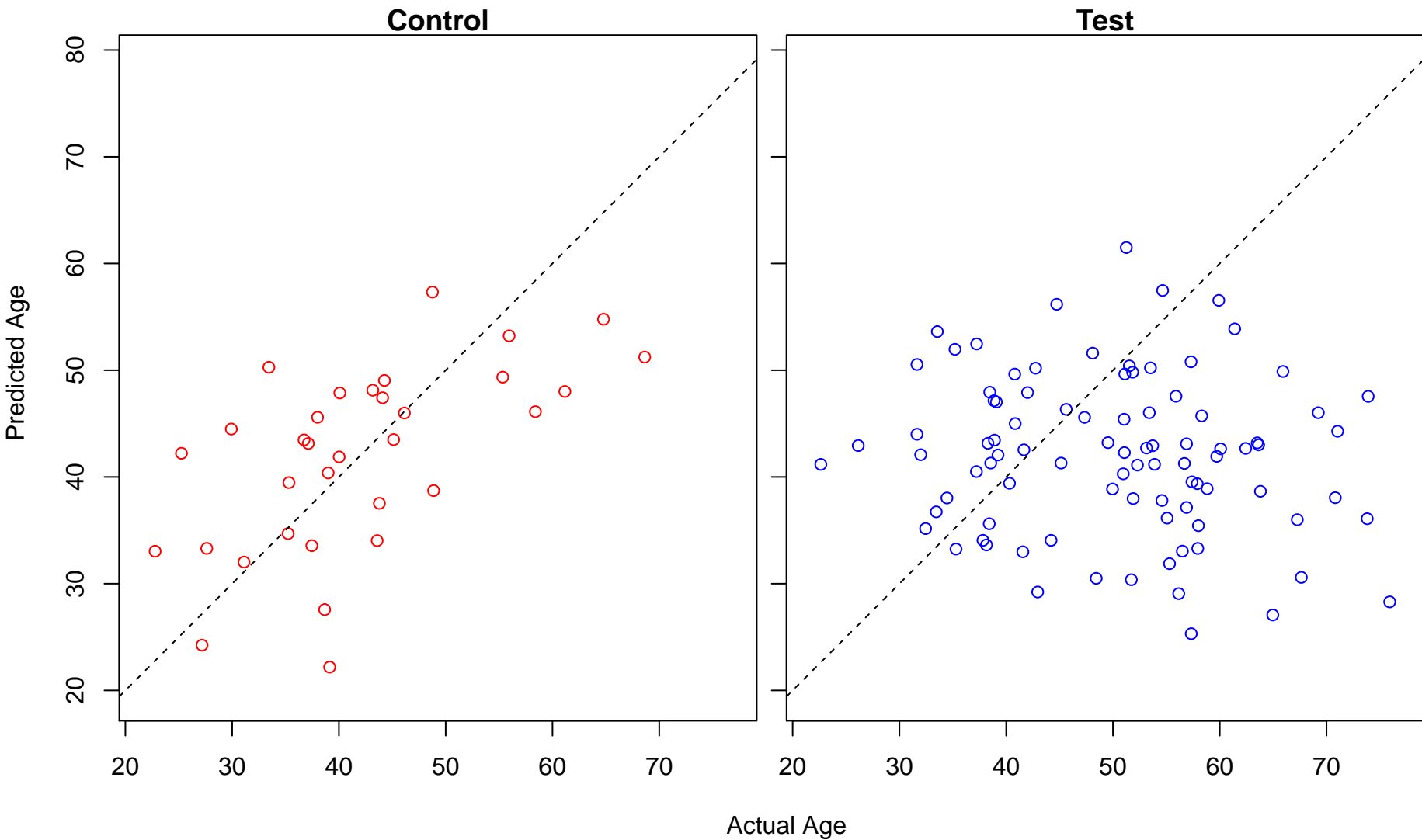
detection of calcium ion (Score: 1.842519)



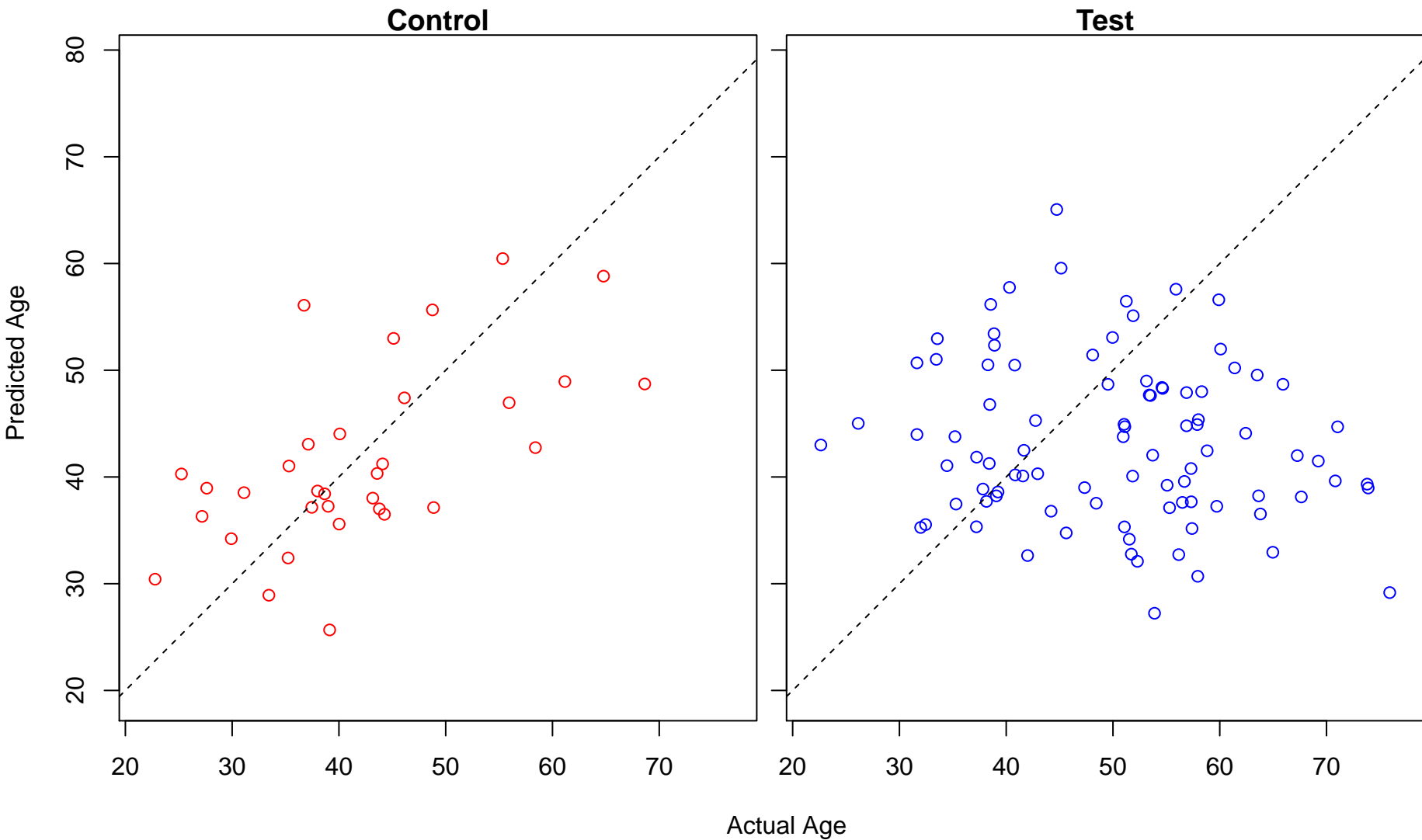
response to tumor necrosis factor (Score: 1.841980)



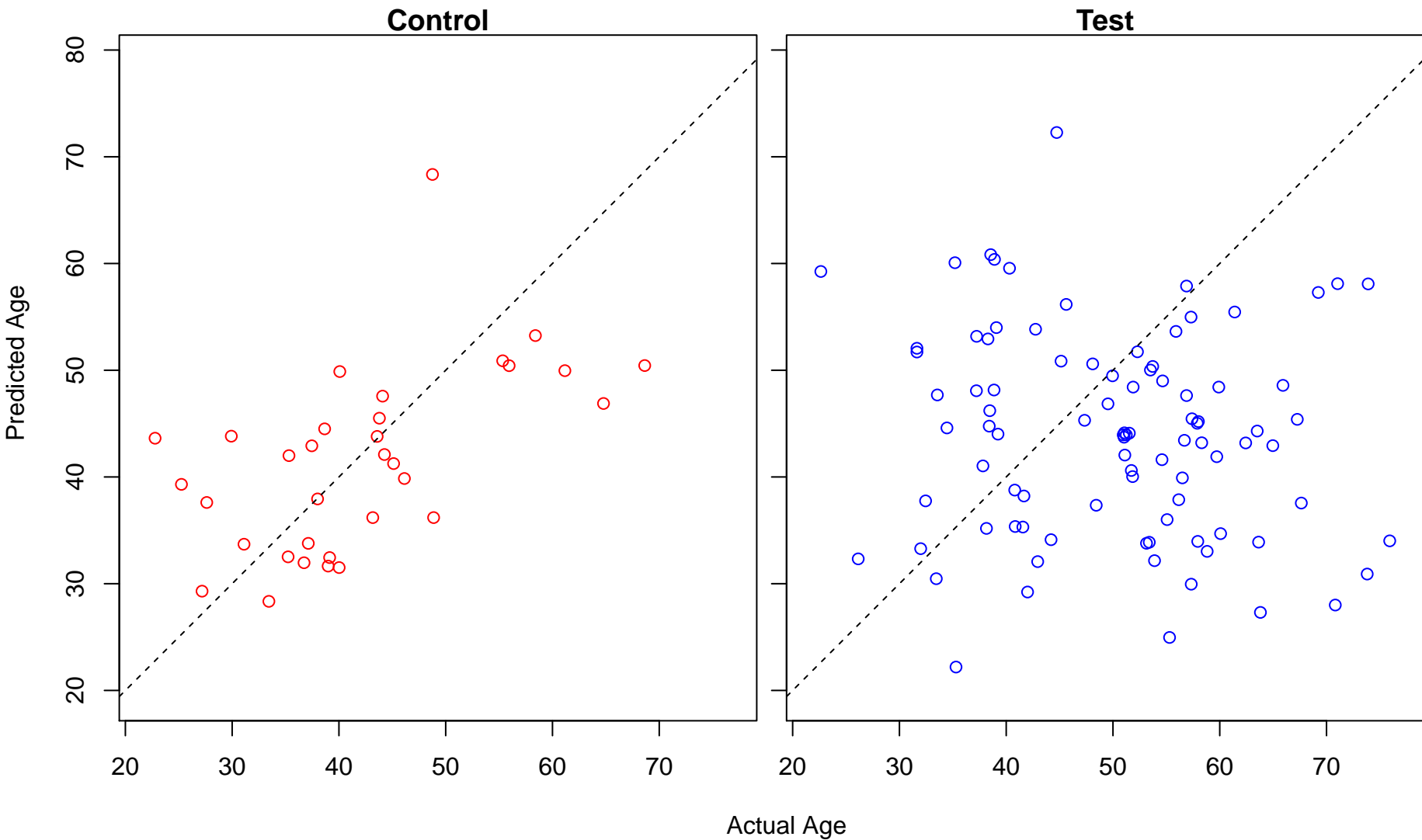
response to organophosphorus (Score: 1.839830)



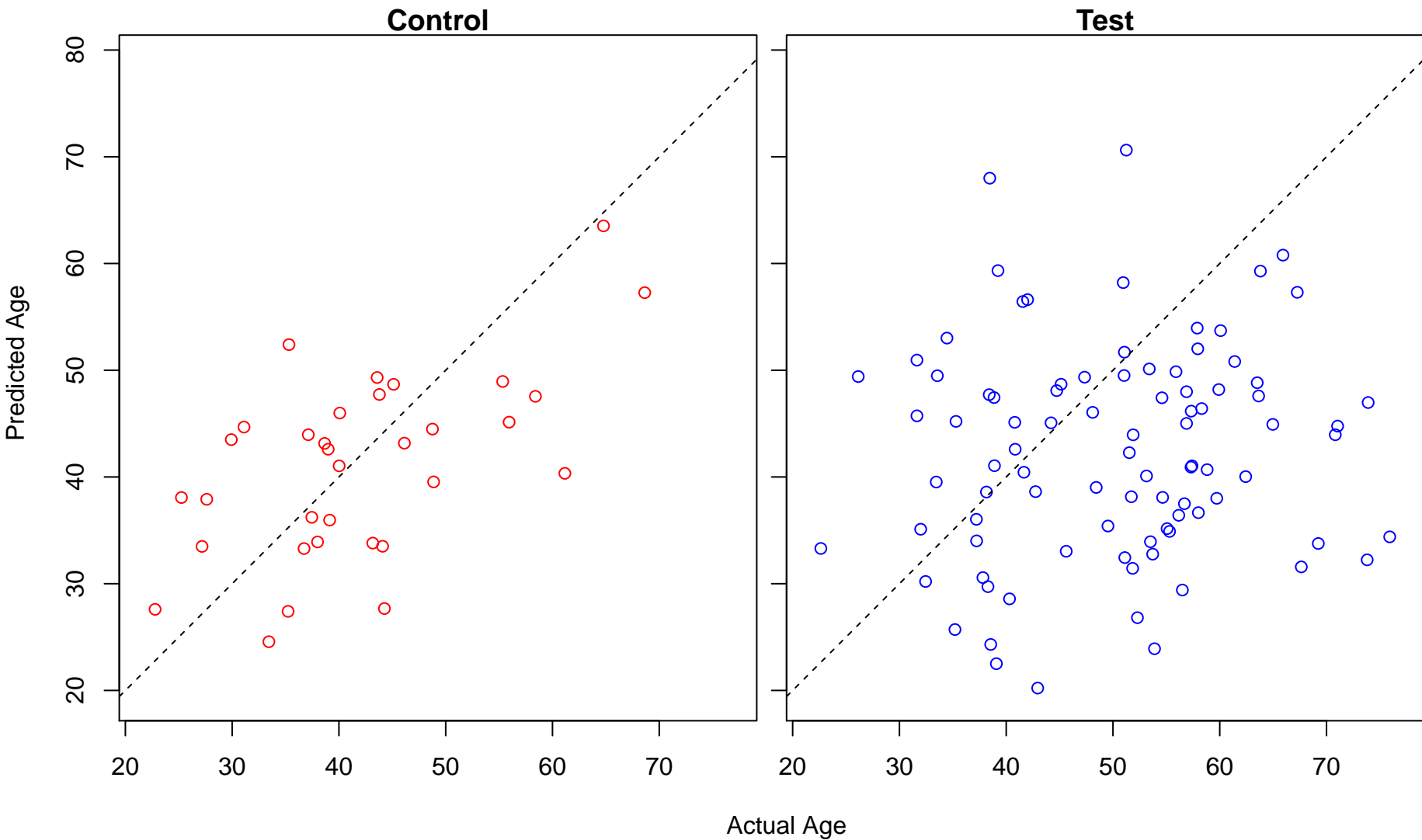
microtubule cytoskeleton organization (Score: 1.832989)



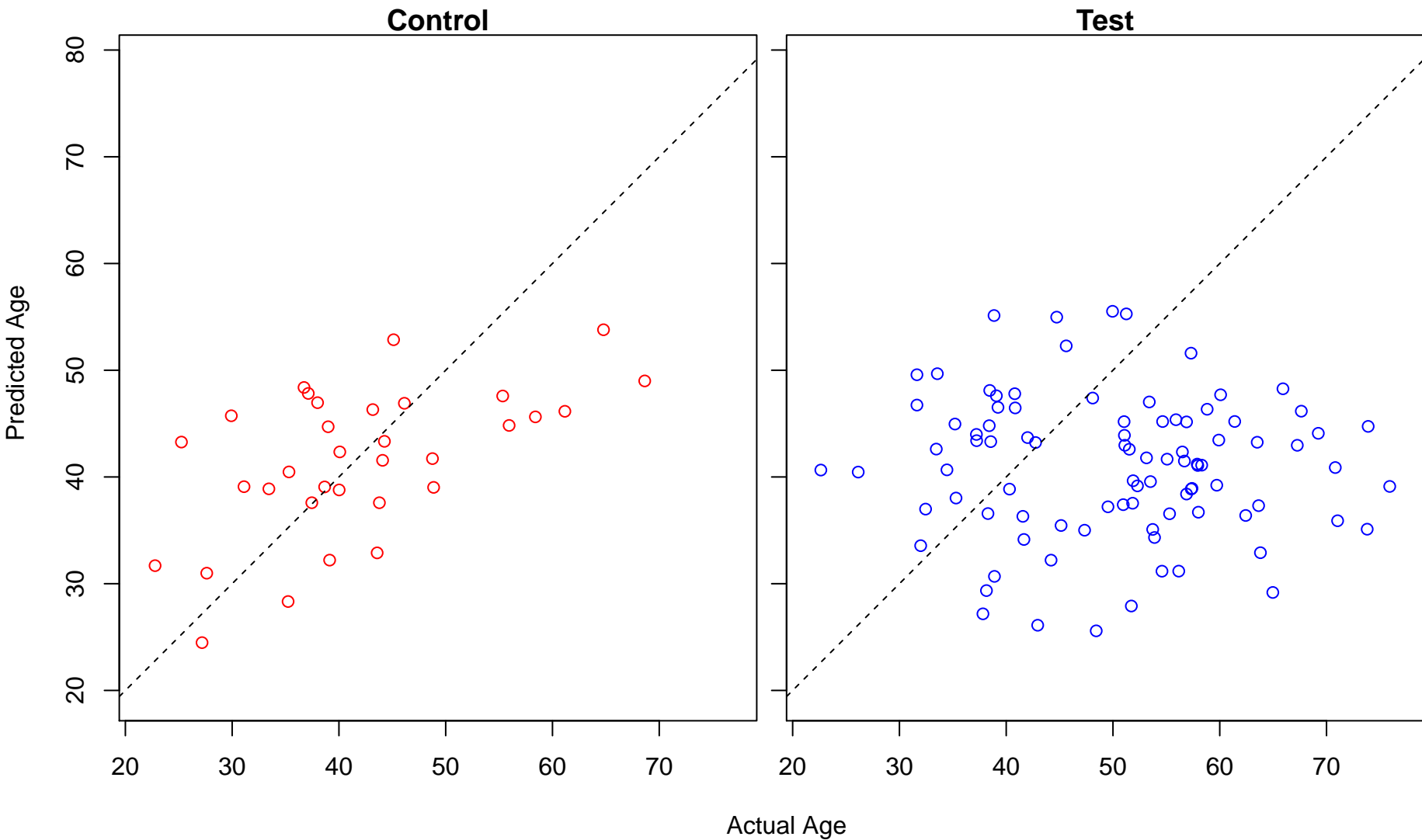
receptor clustering (Score: 1.822455)



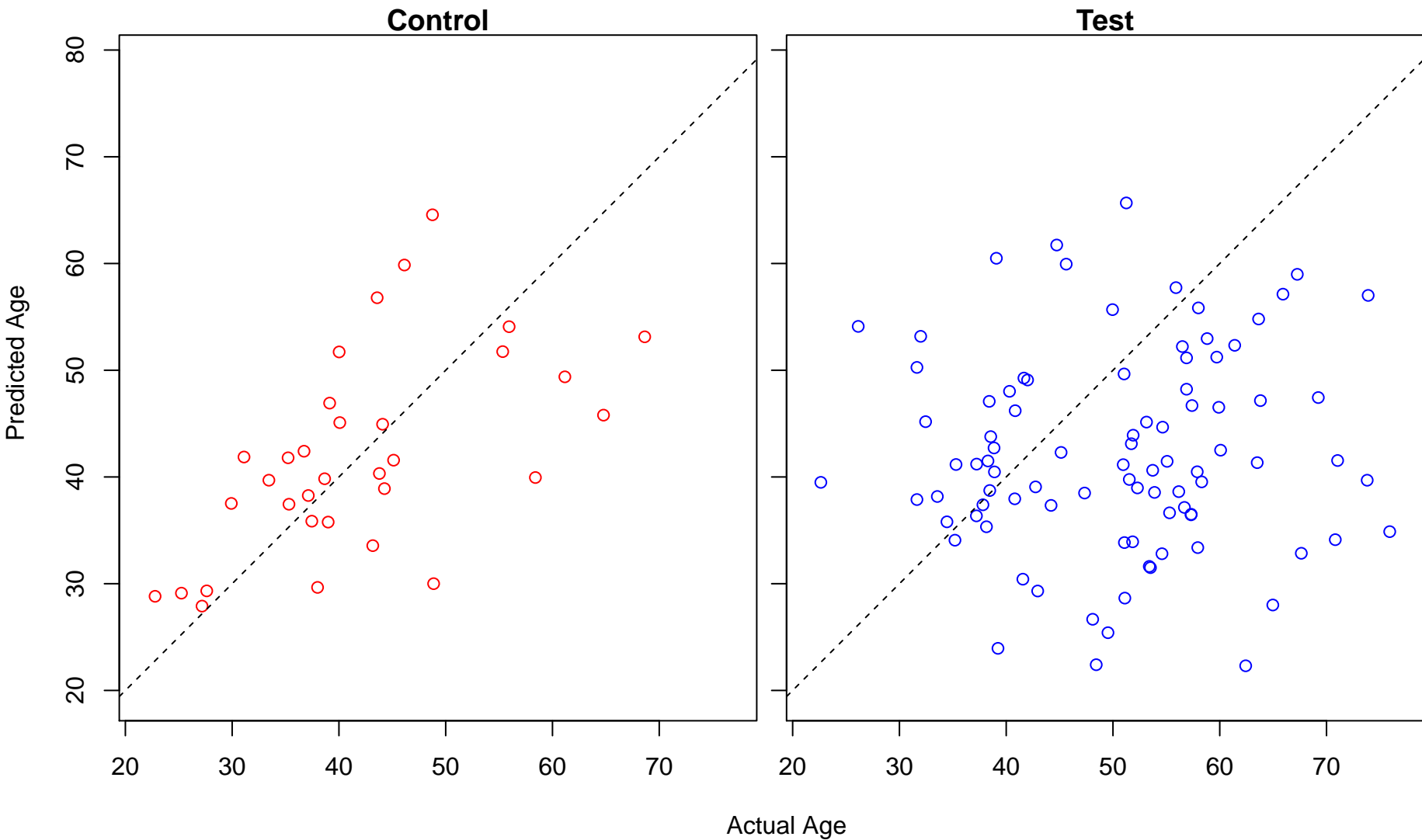
phosphatidylethanolamine acyl-chain remodeling (Score: 1.819376)



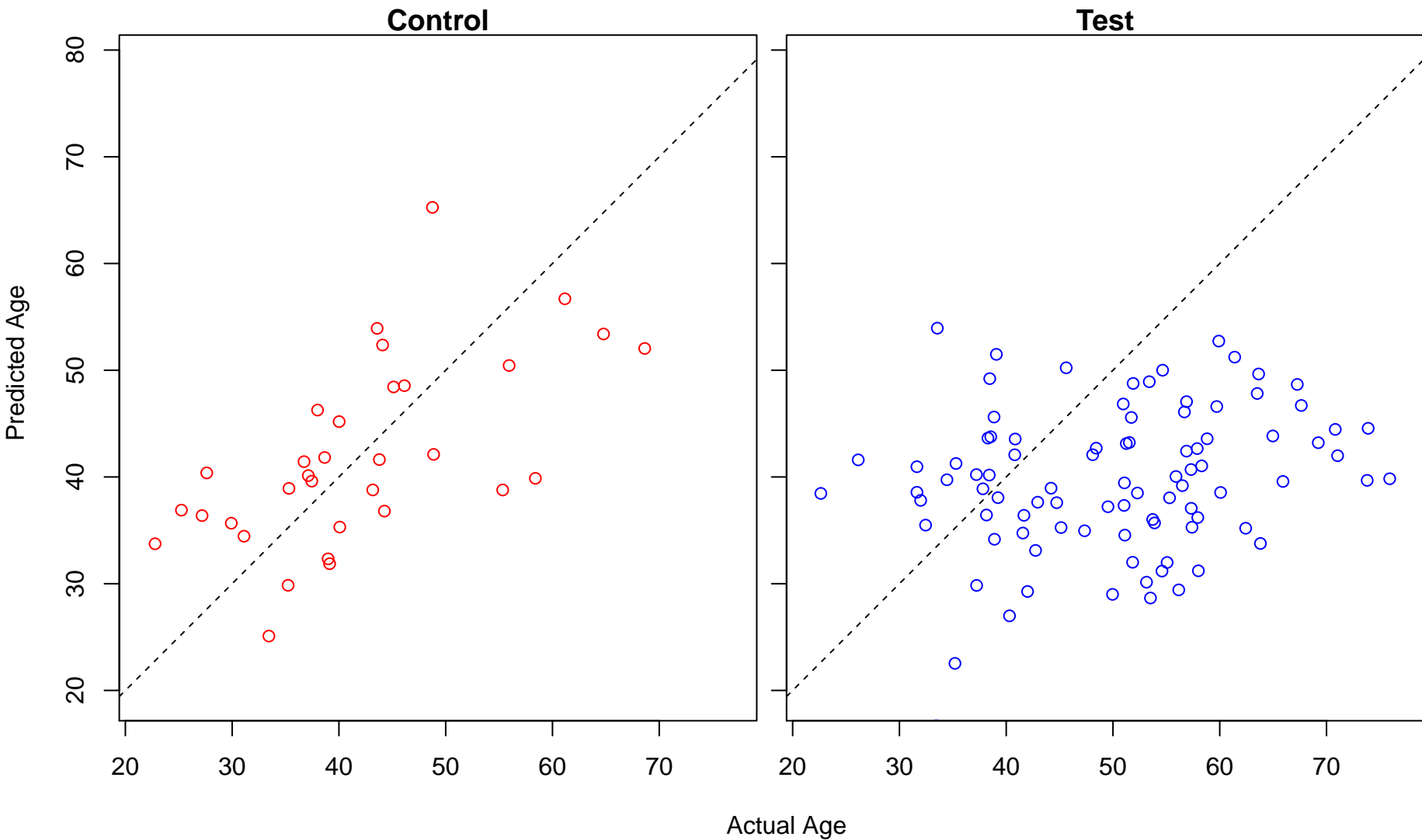
cholesterol transport (Score: 1.817263)



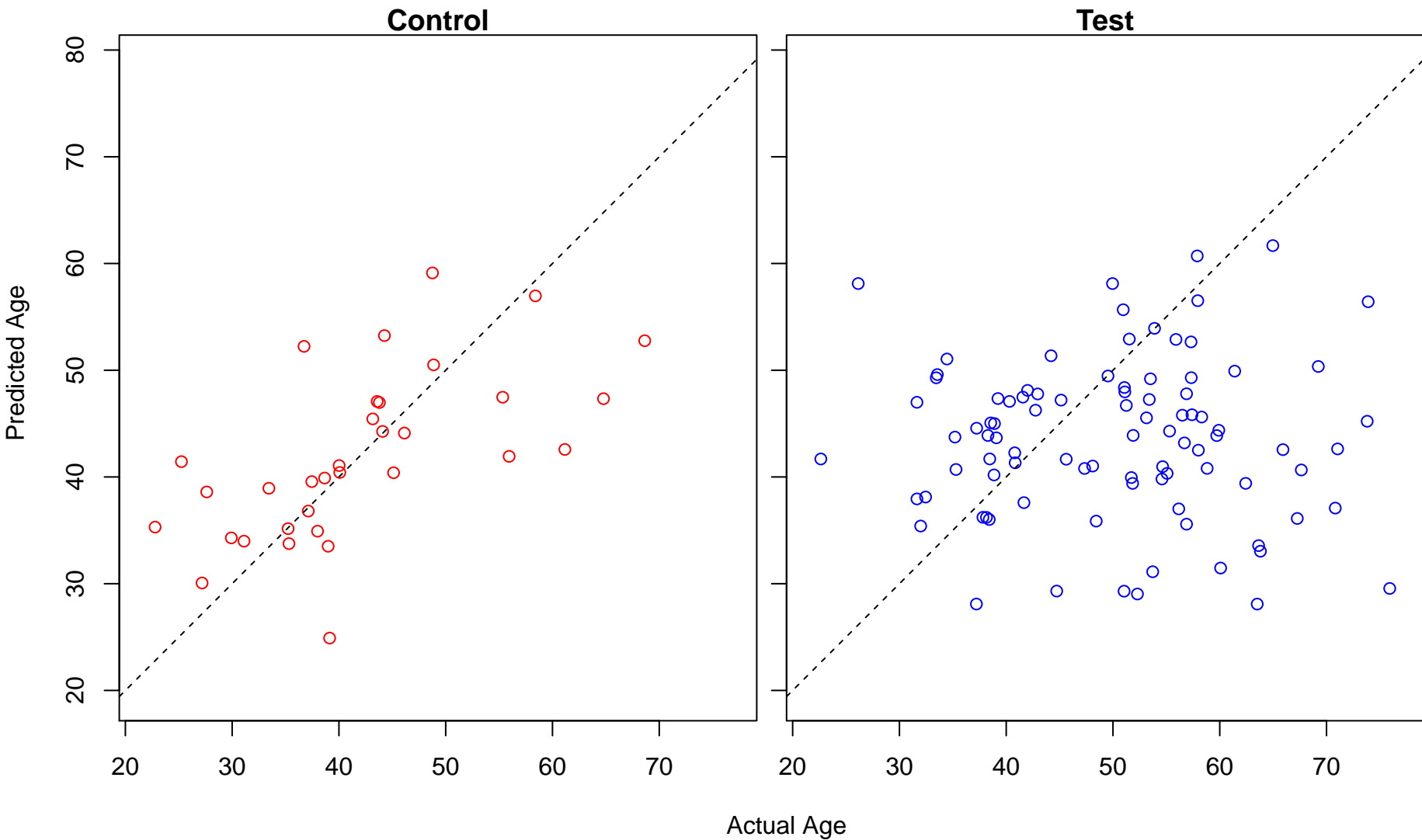
positive regulation of potassium ion transport (Score: 1.817191)



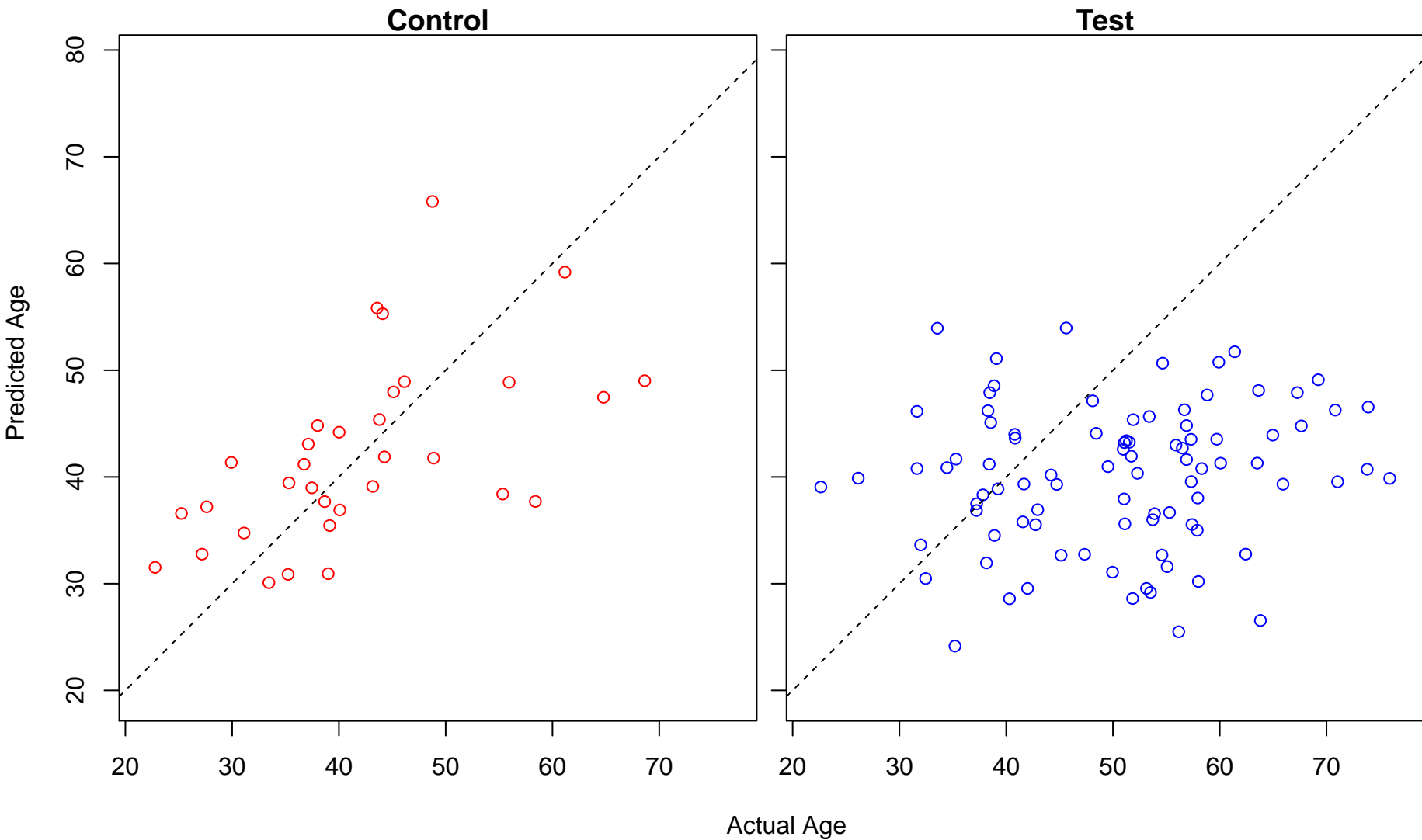
positive regulation of focal adhesion assembly (Score: 1.809400)



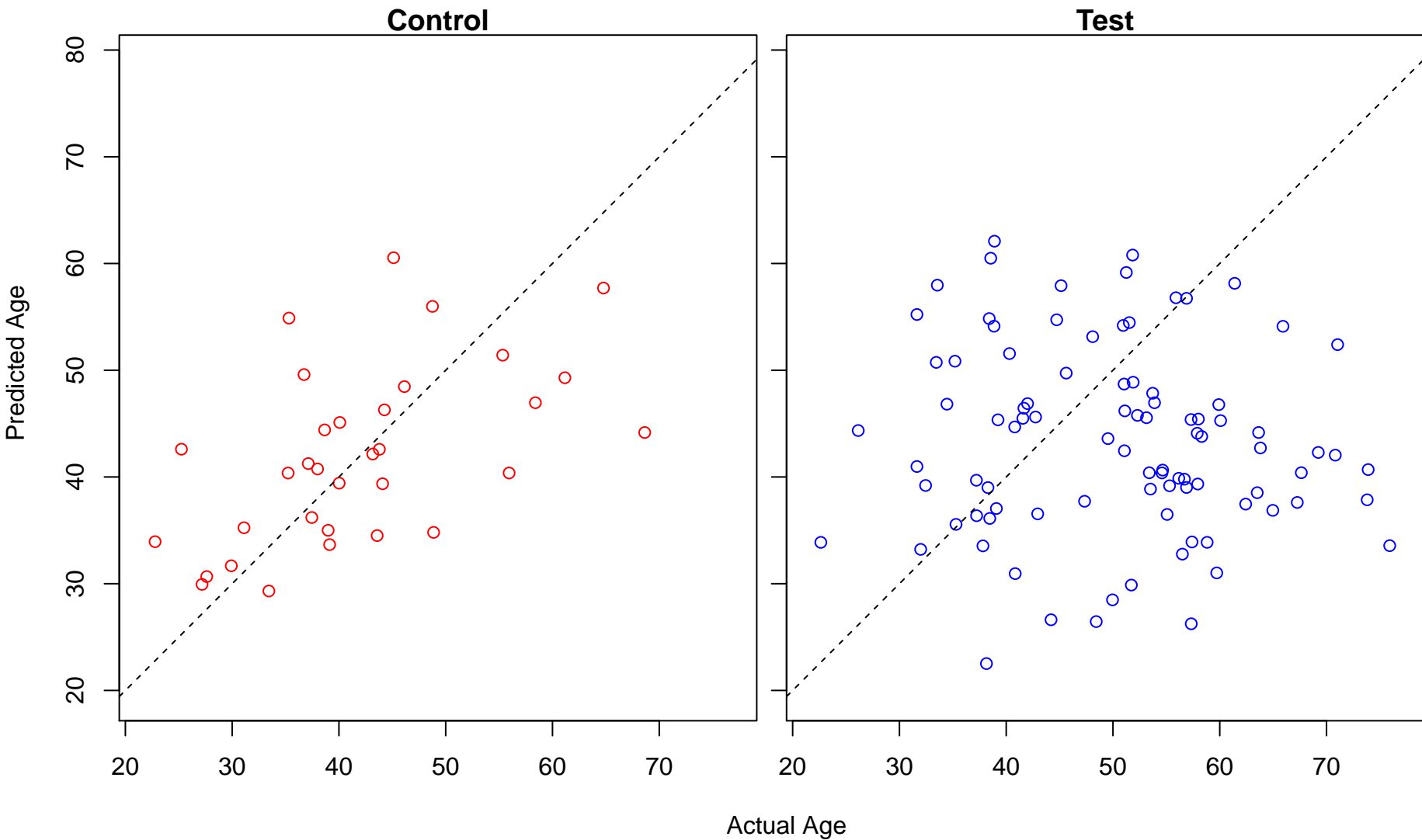
complement activation, classical pathway (Score: 1.808181)



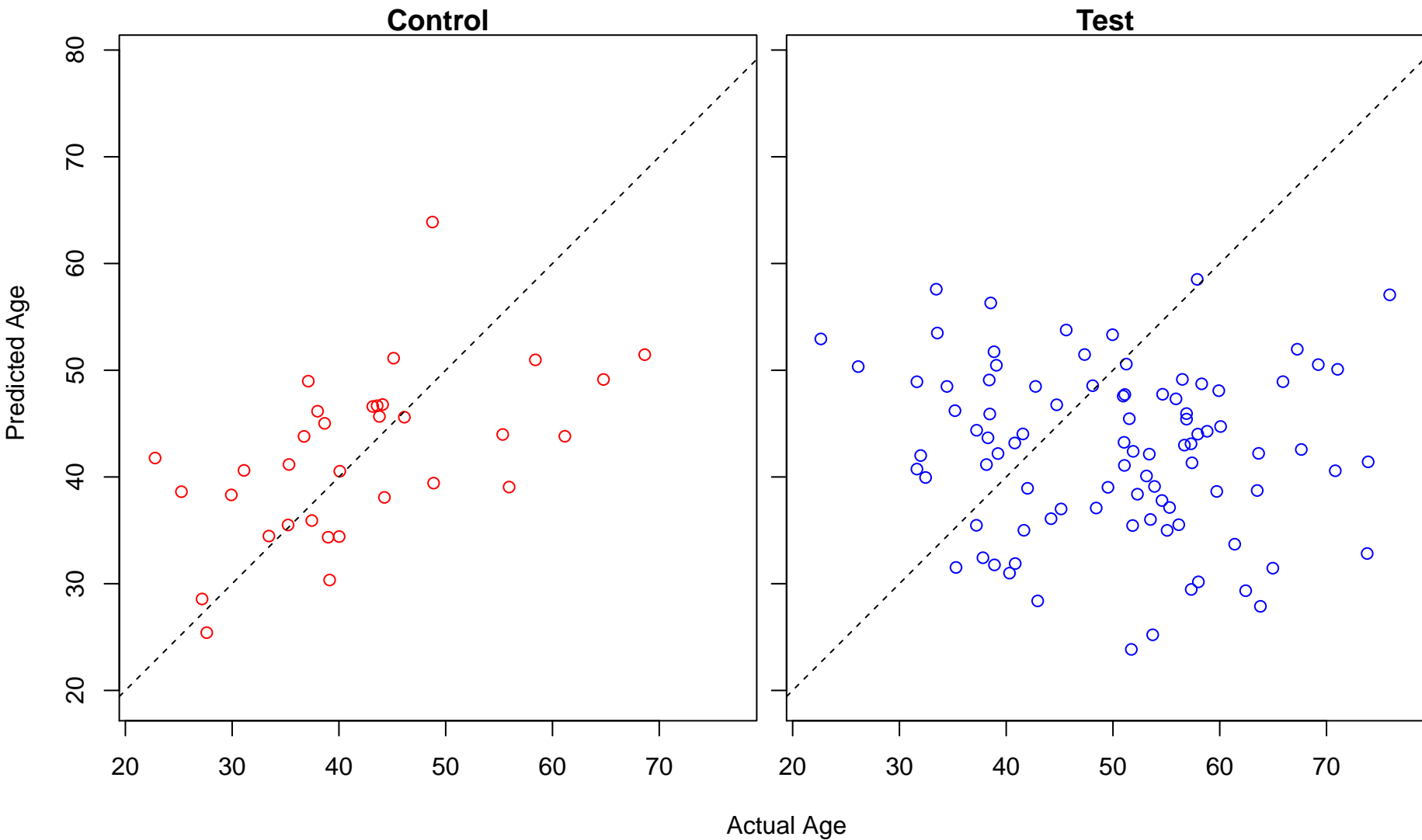
positive regulation of cell junction assembly (Score: 1.798924)



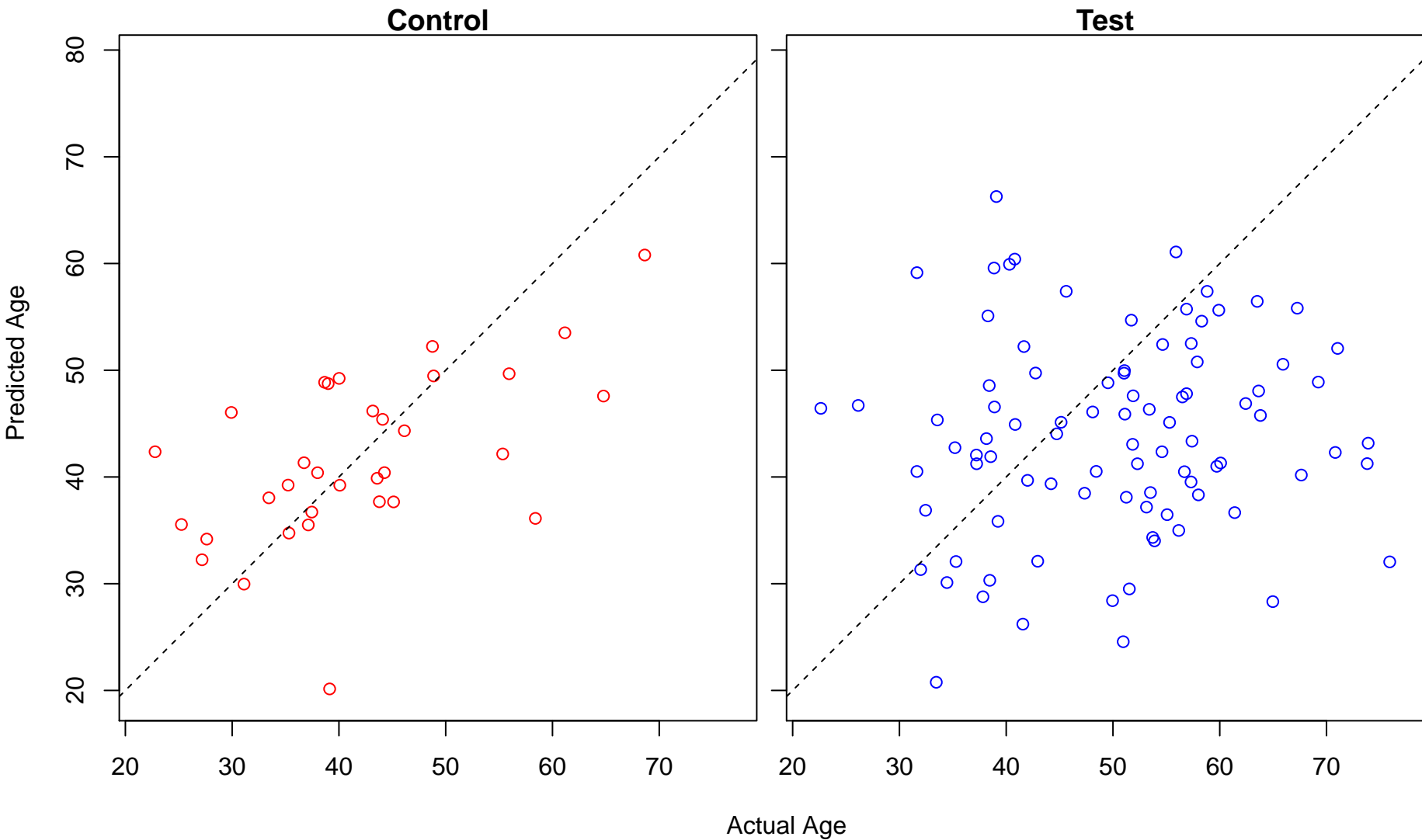
spinal cord development (Score: 1.798070)



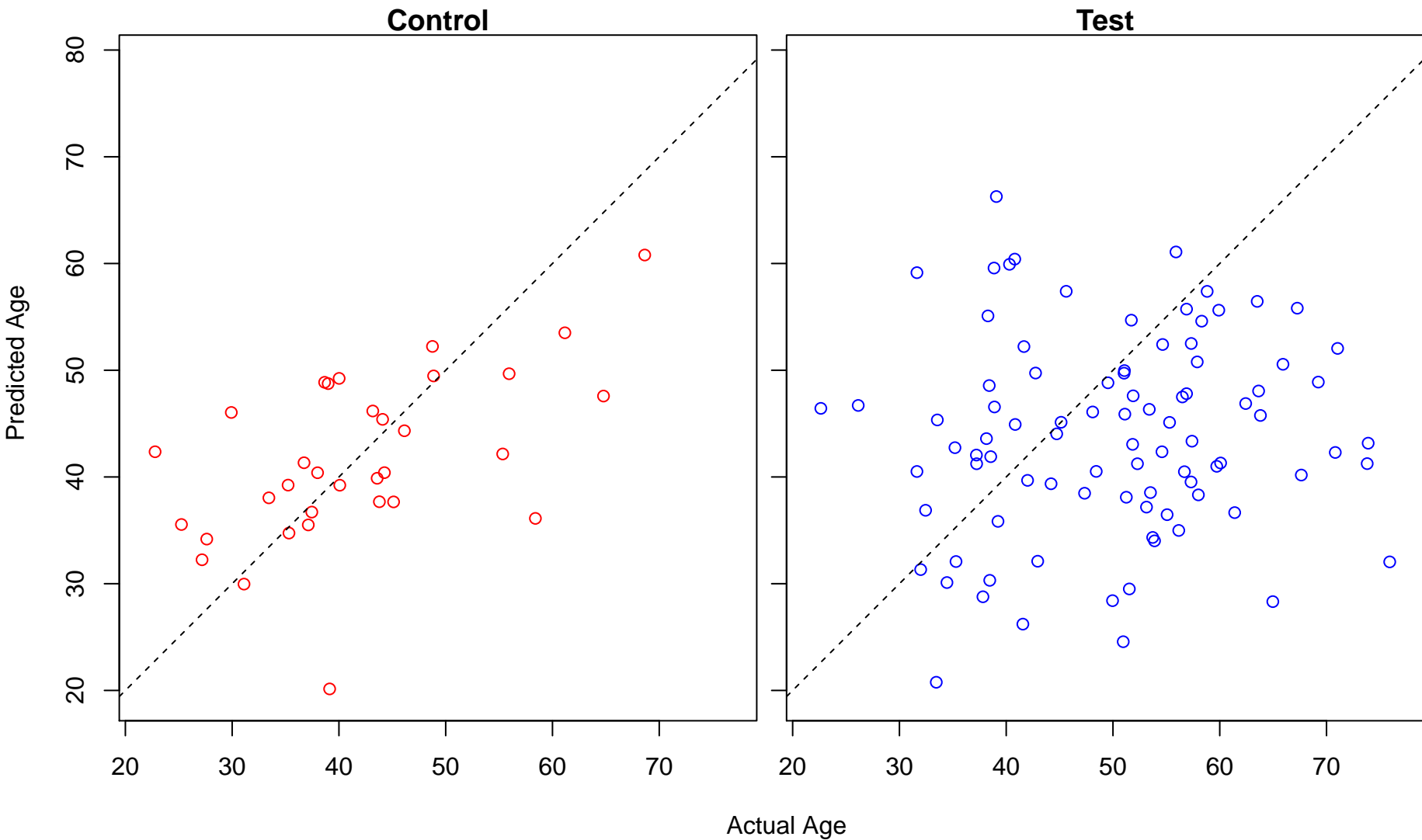
myelin maintenance (Score: 1.797878)



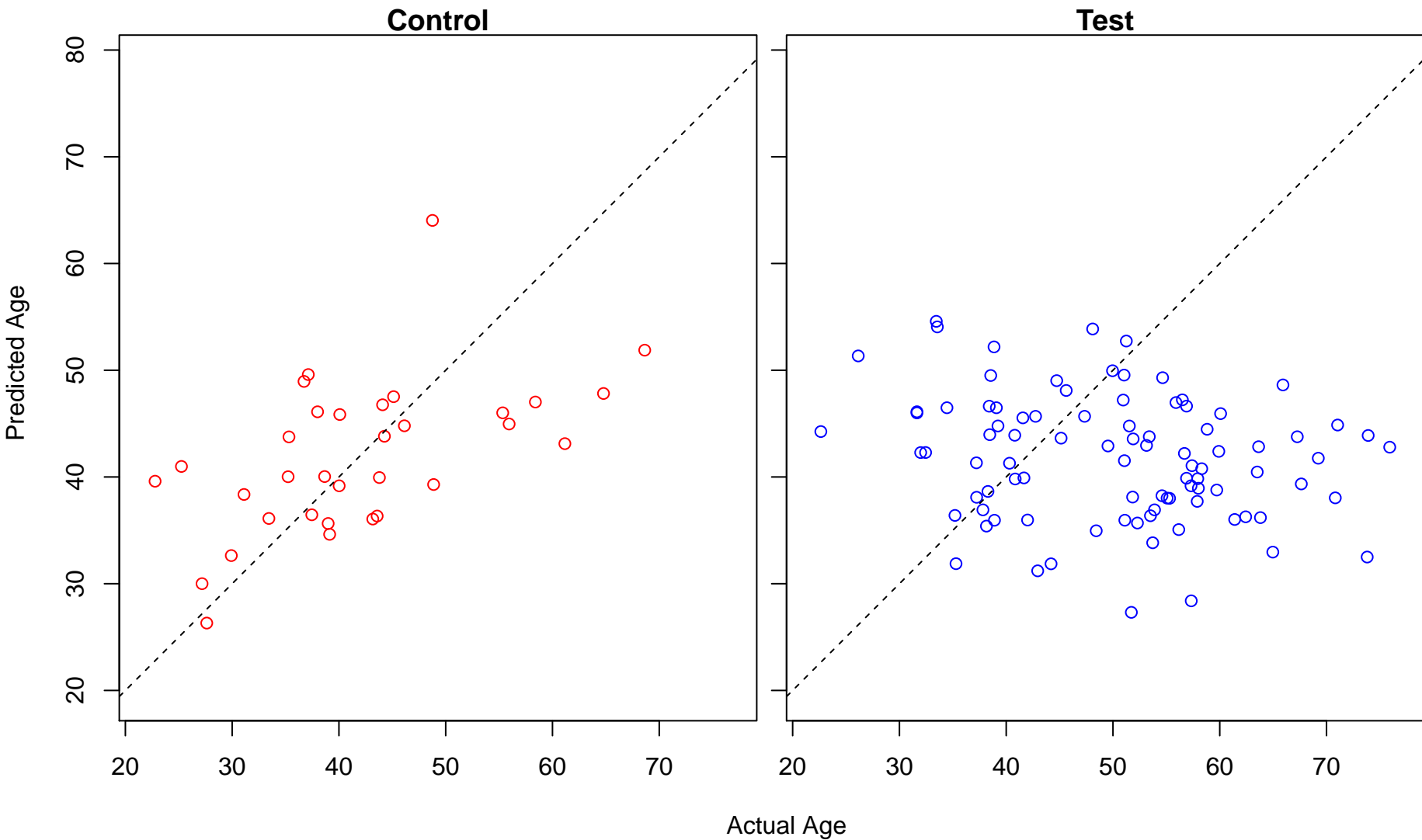
subpallium development (Score: 1.792062)



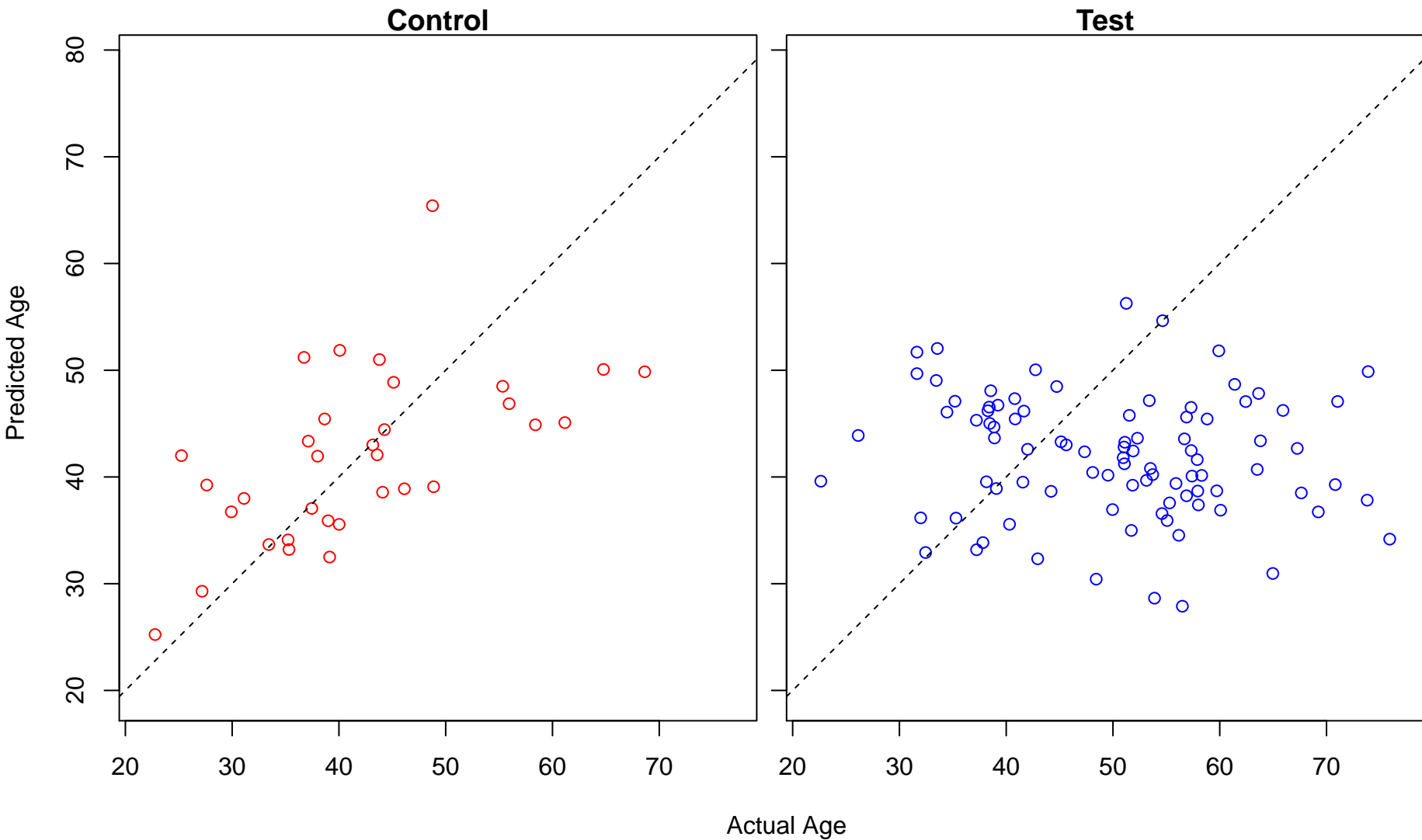
striatum development (Score: 1.792062)



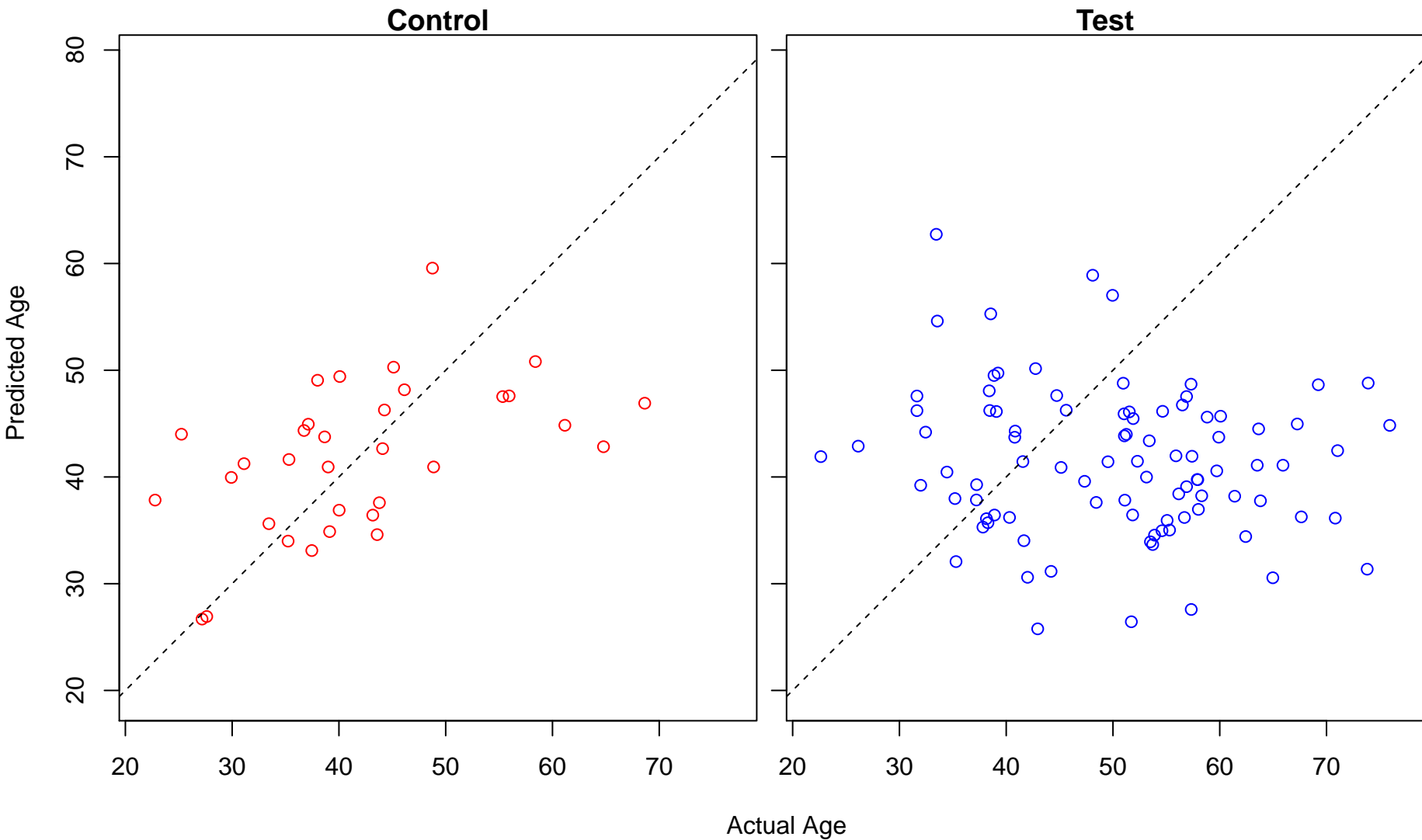
negative regulation of protein oligomerization (Score: 1.791964)



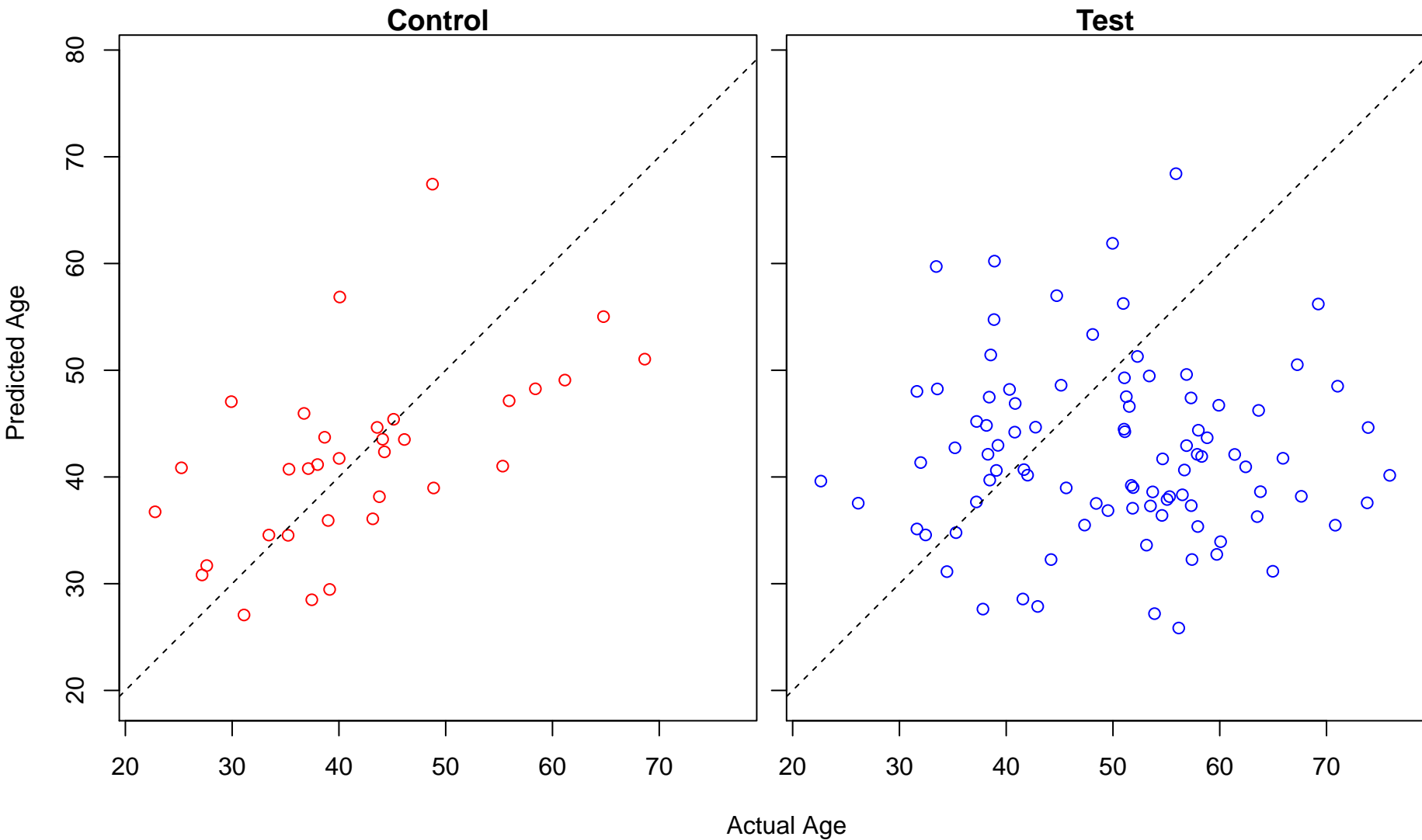
organic hydroxy compound metabolic process (Score: 1.782740)



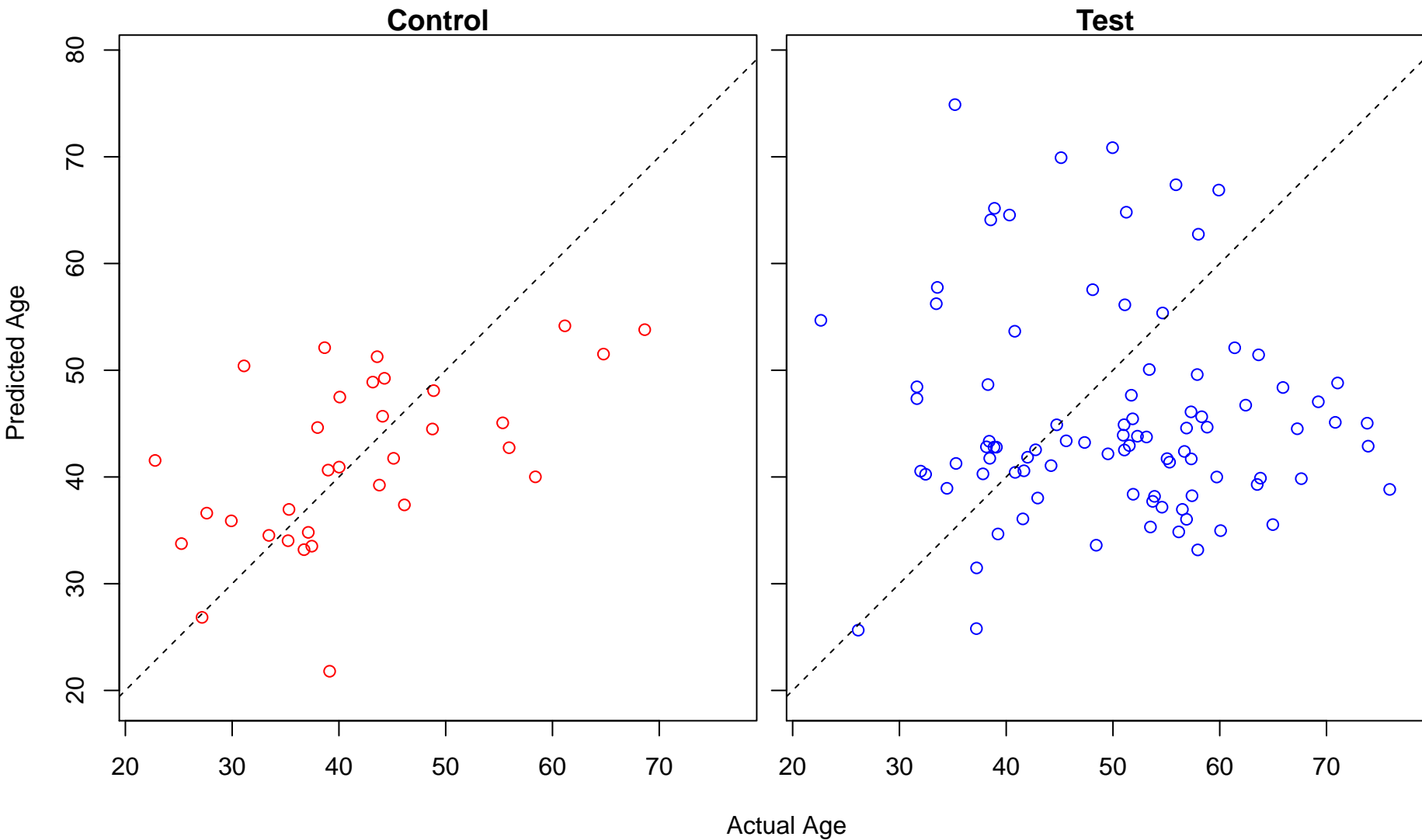
regulation of inclusion body assembly (Score: 1.777480)



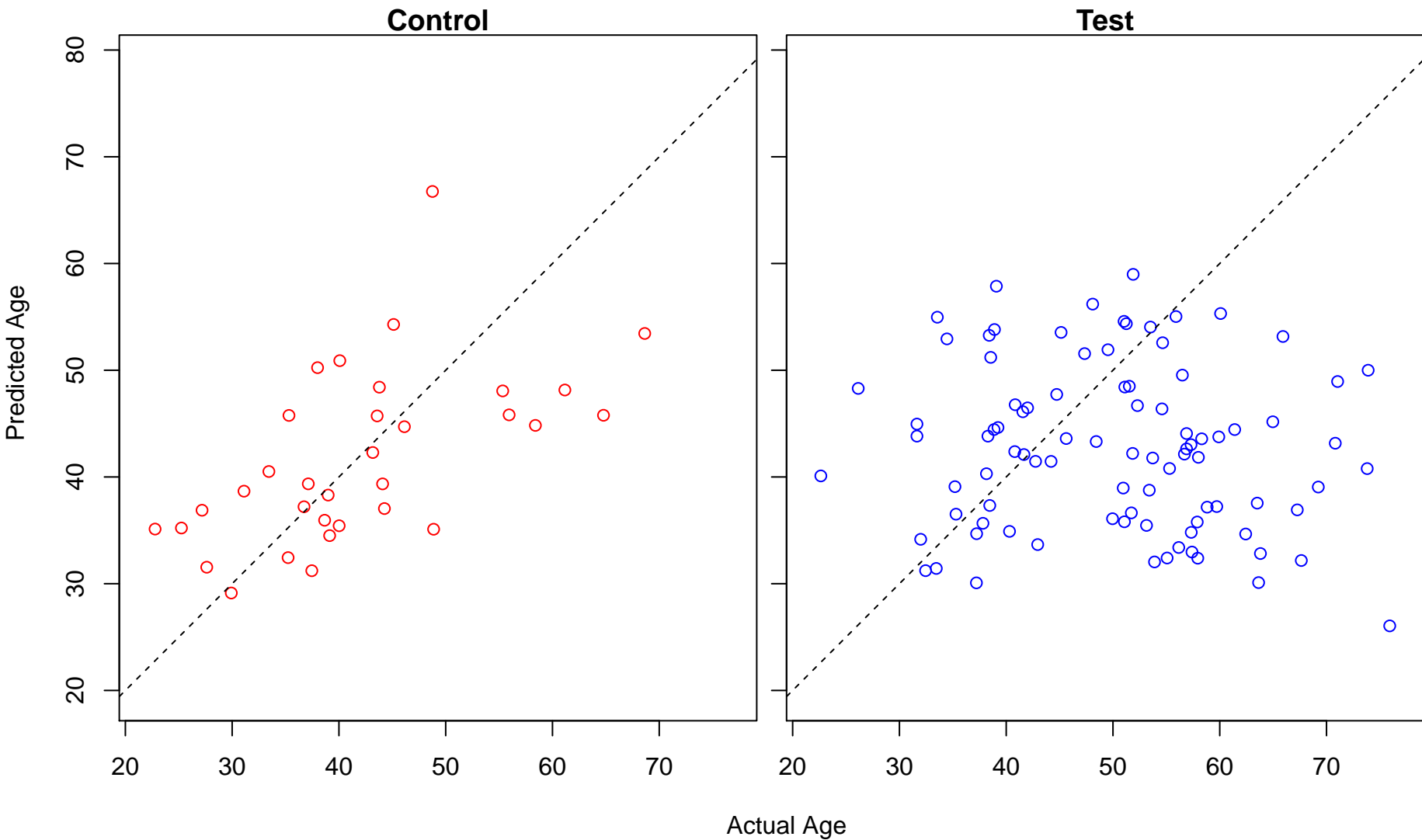
regulation of cholesterol transport (Score: 1.776634)



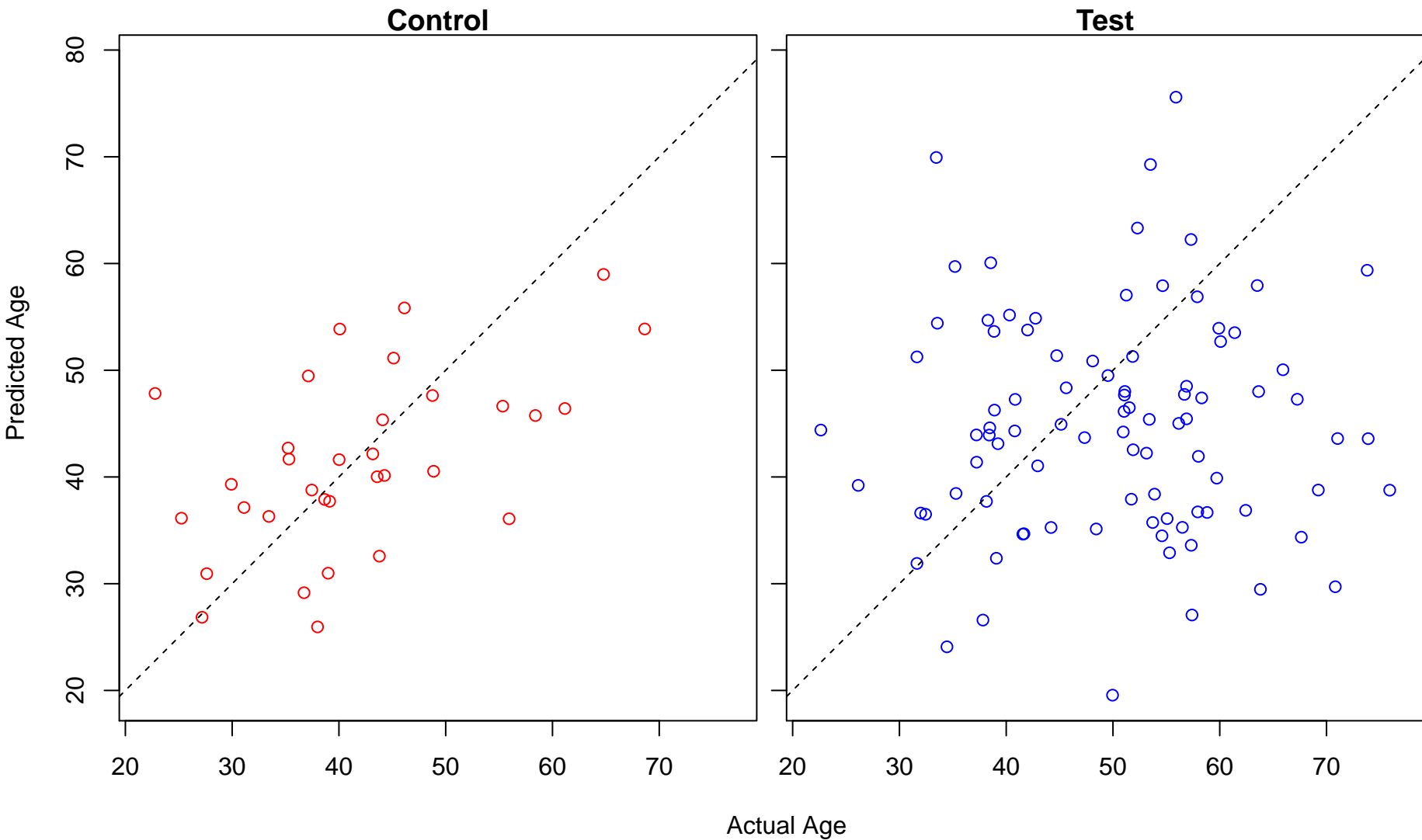
negative regulation of histone H3-K9 methylation (Score: 1.775716)



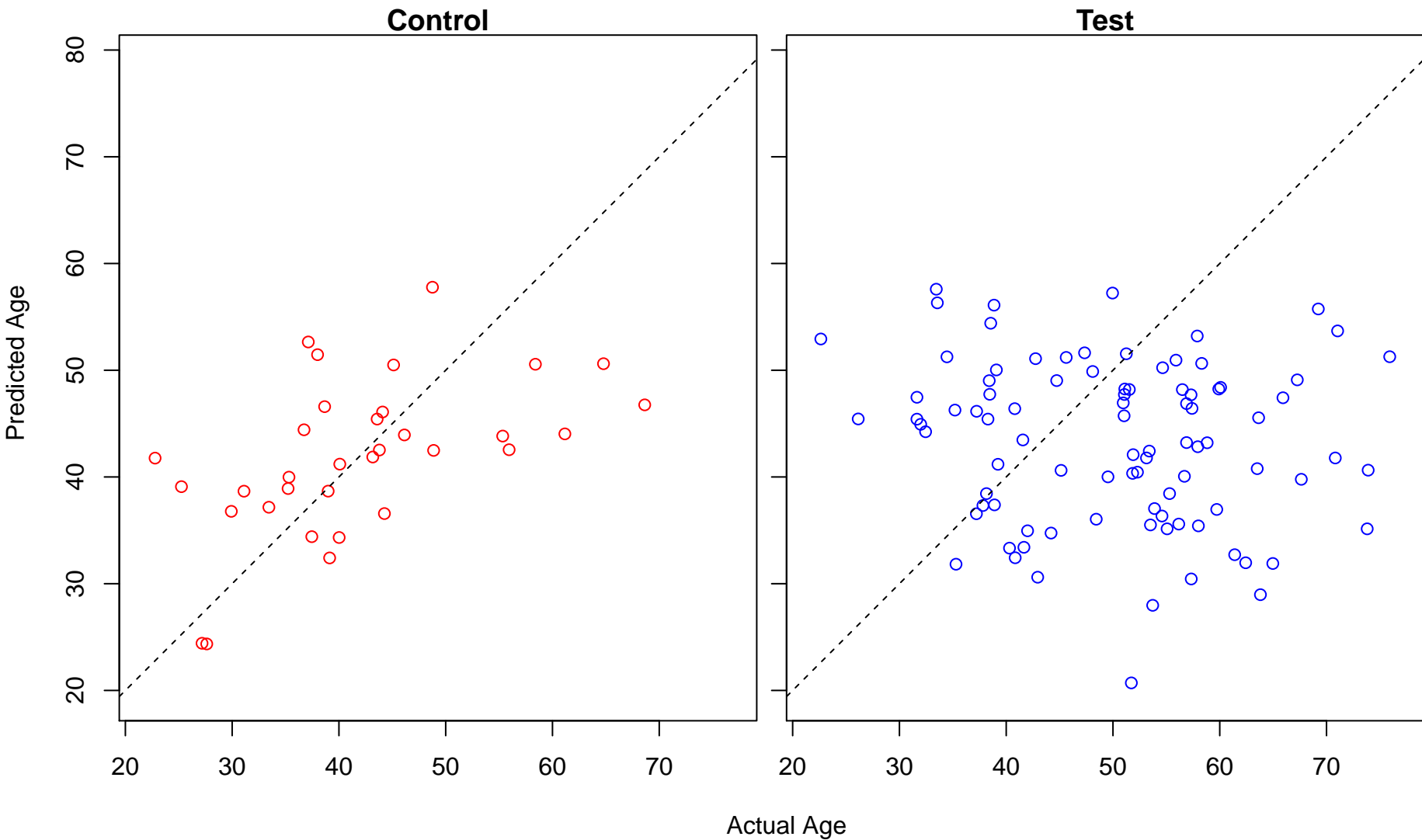
snRNA transcription from RNA polymerase II promoter (Score: 1.775117)



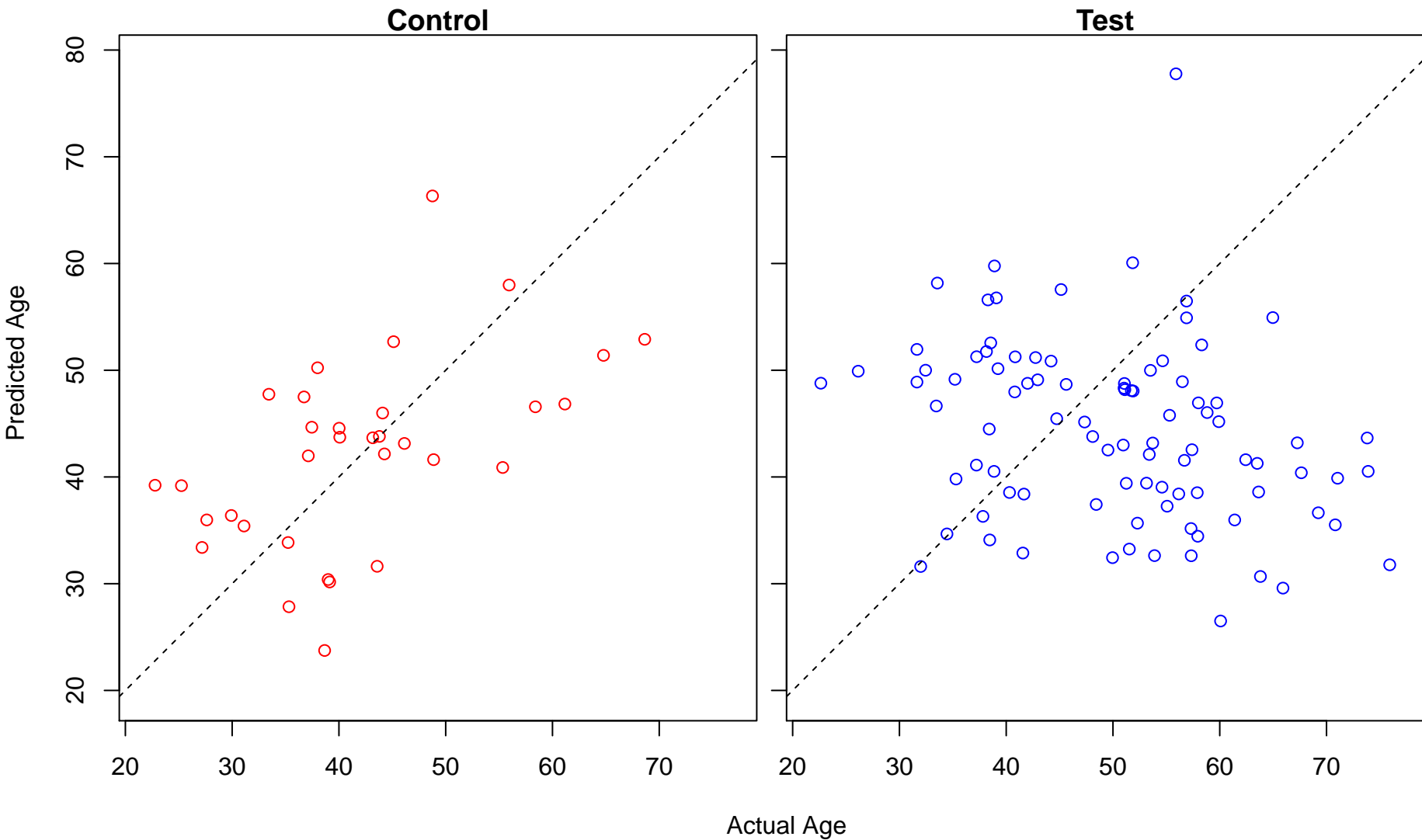
glucan biosynthetic process (Score: 1.767942)



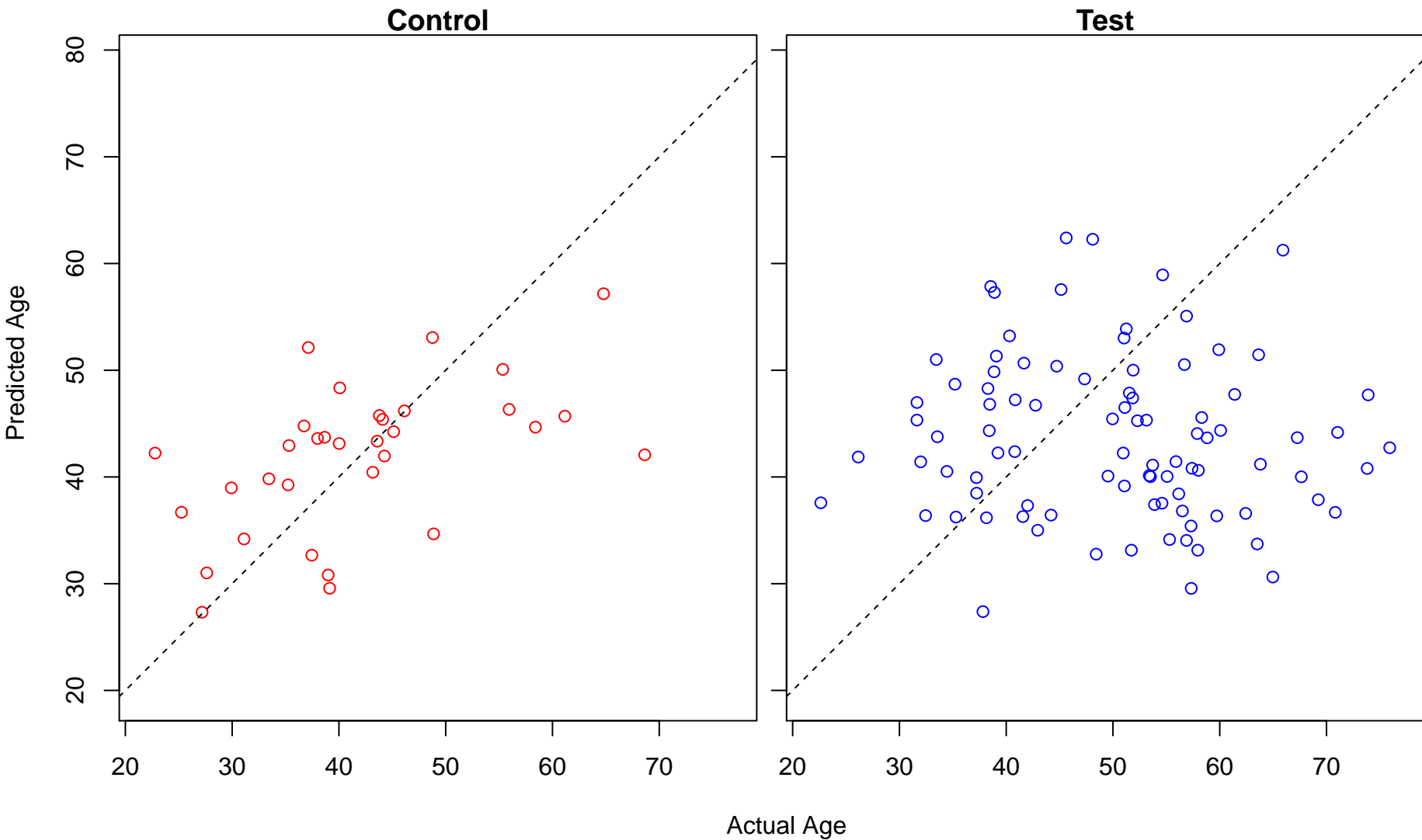
oligodendrocyte development (Score: 1.745343)



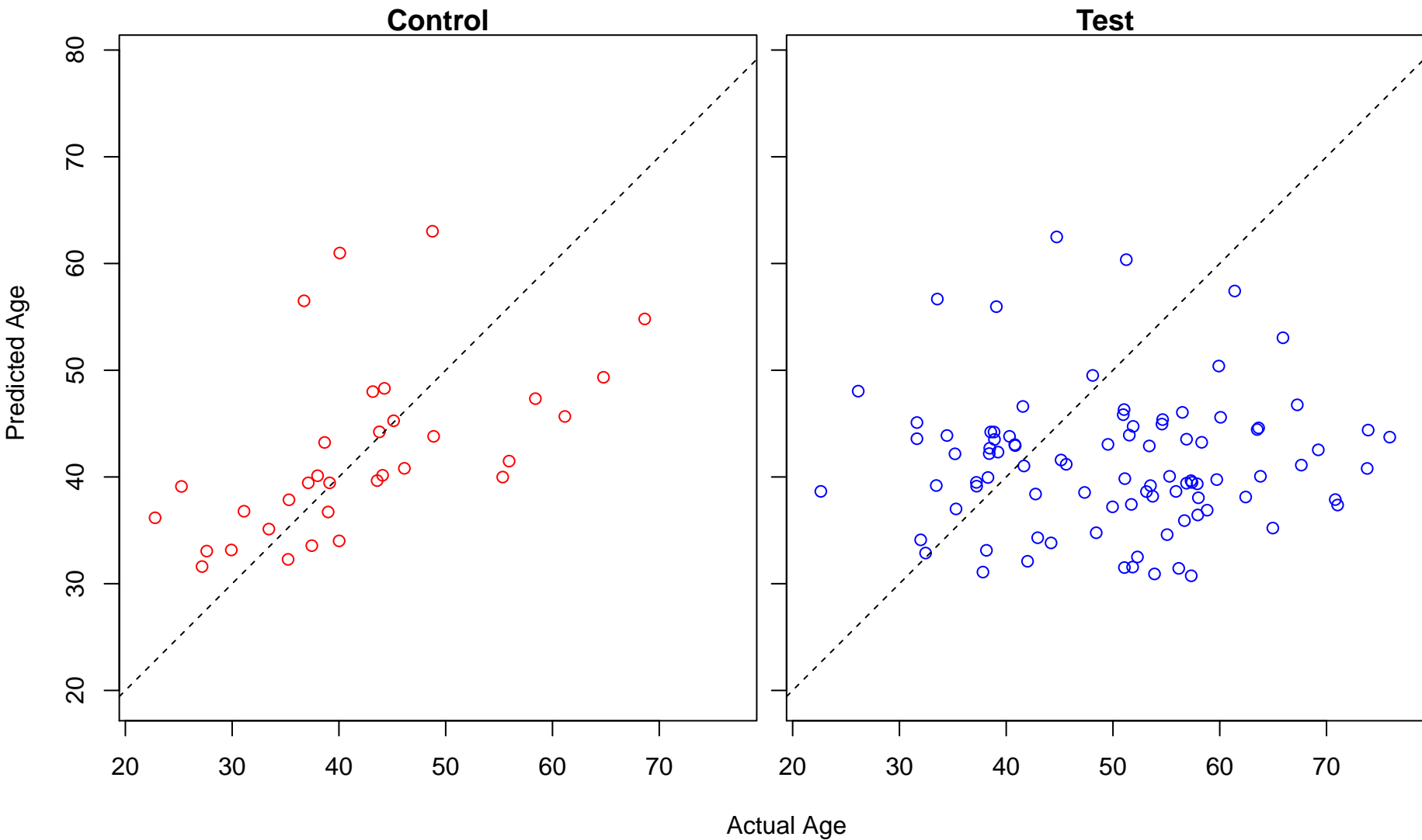
negative regulation of T cell differentiation in thymus (Score: 1.737459)



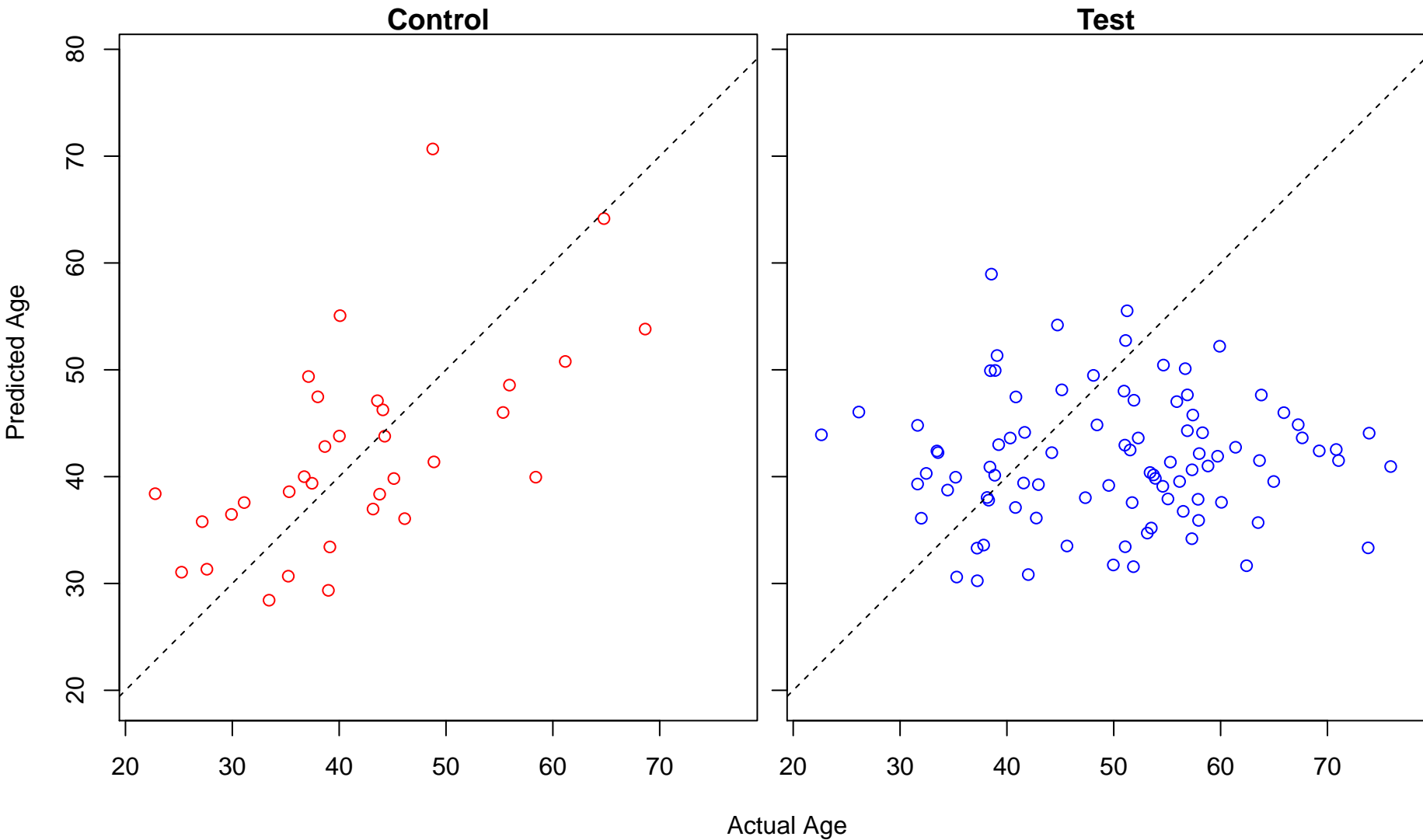
cytoplasmic sequestering of transcription factor (Score: 1.731616)



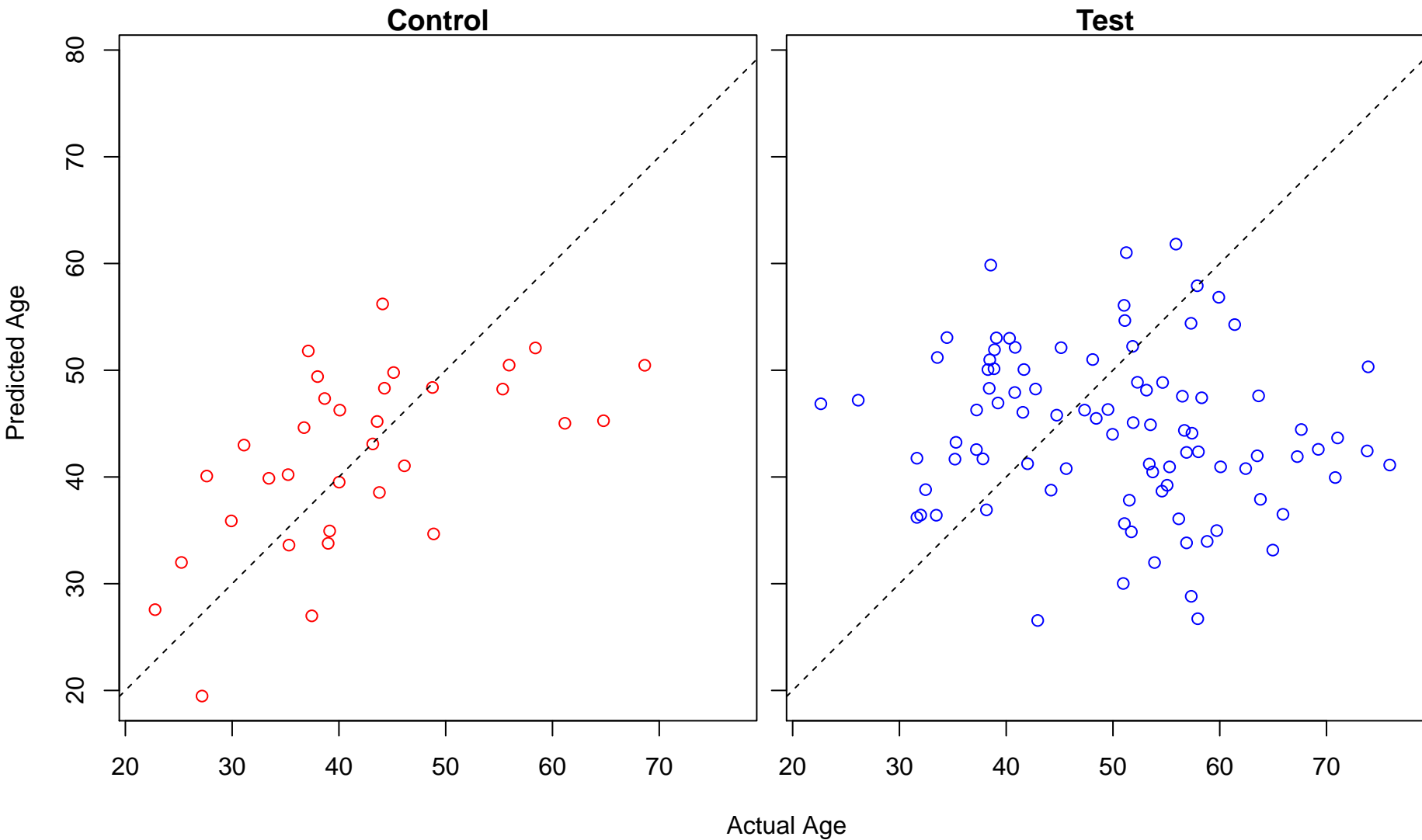
negative regulation of skeletal muscle tissue development (Score: 1.729553)



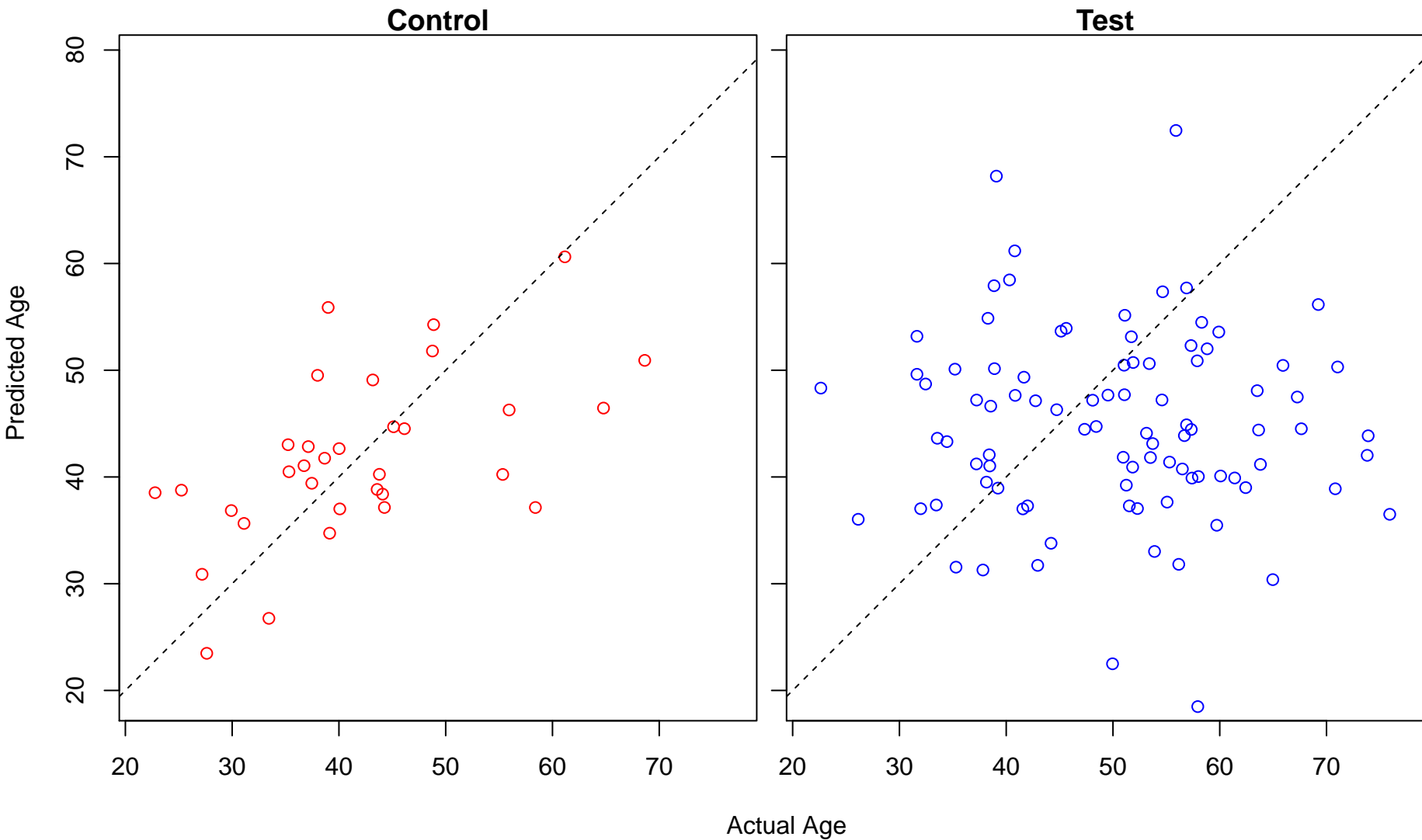
positive regulation of mitochondrial fission (Score: 1.729137)



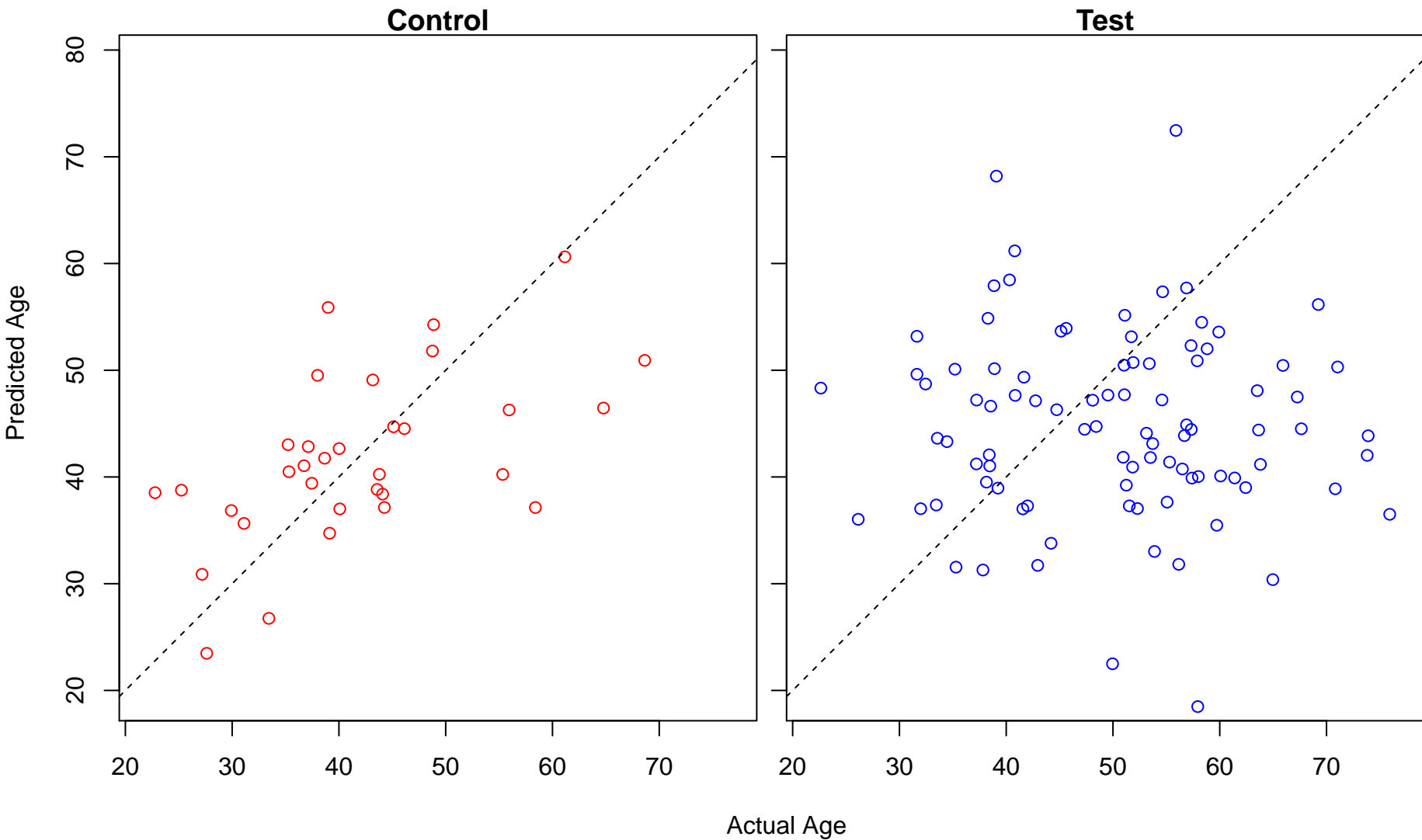
vasoconstriction (Score: 1.726104)



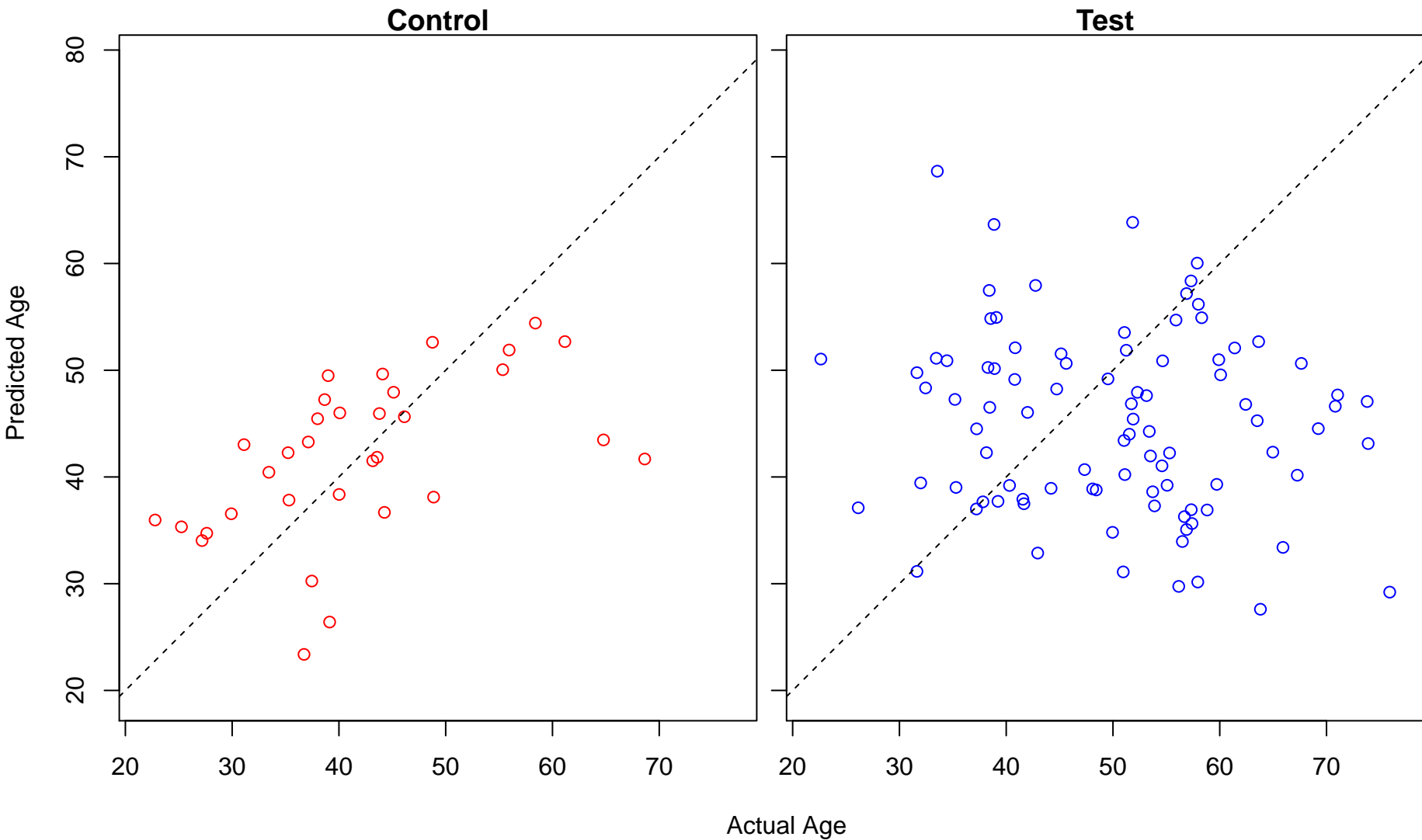
negative regulation of response to food (Score: 1.718973)



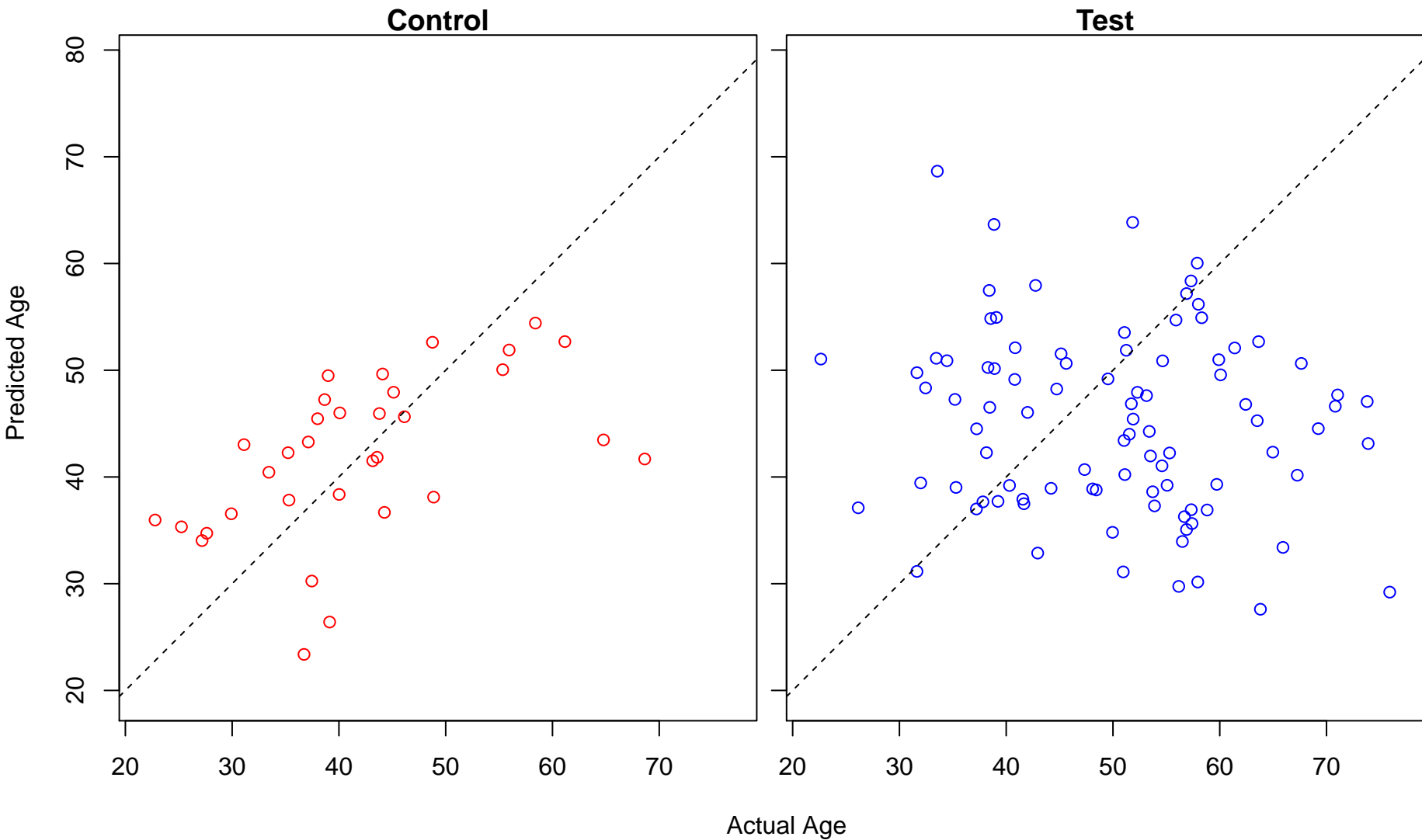
negative regulation of appetite (Score: 1.718973)



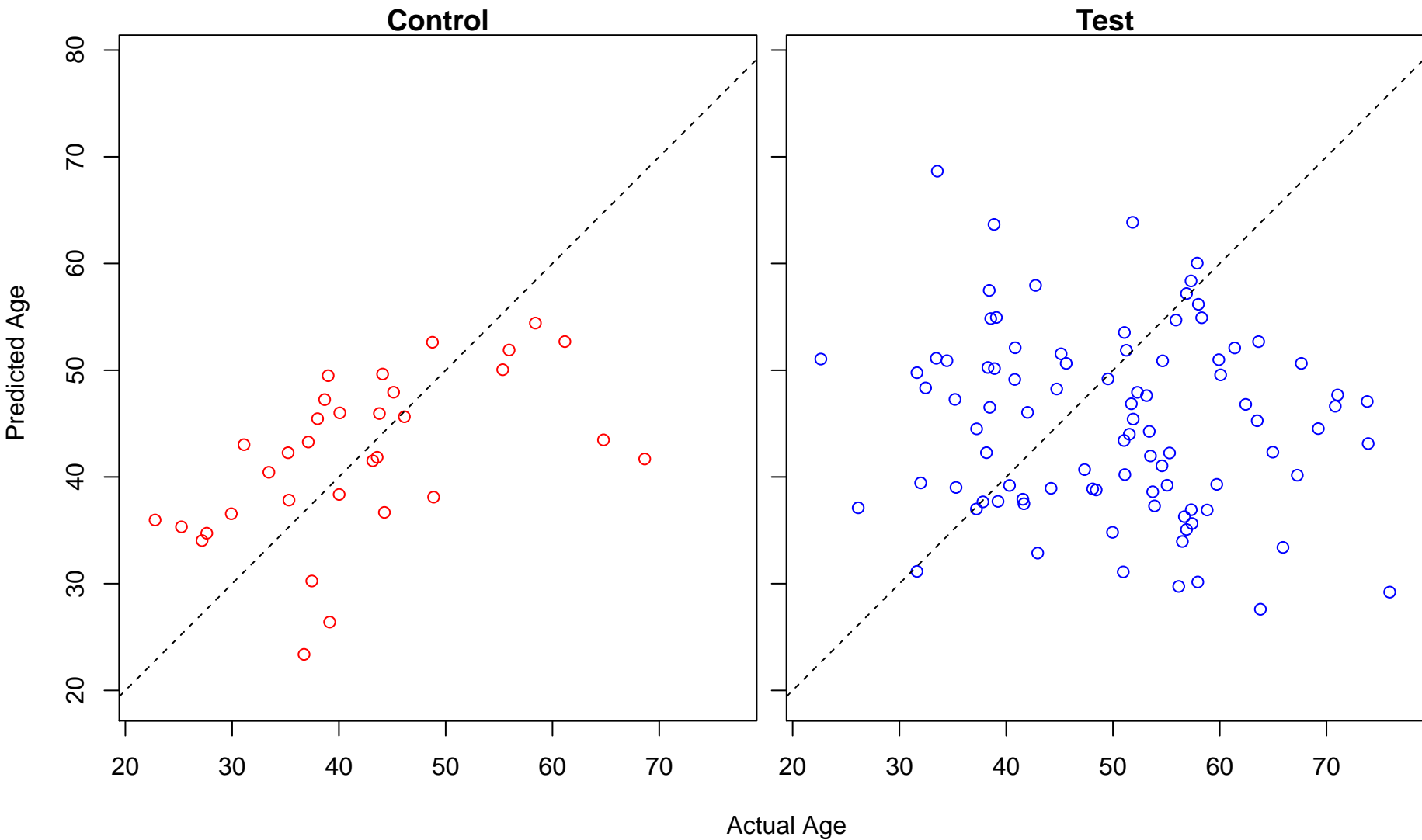
response to caffeine (Score: 1.708828)



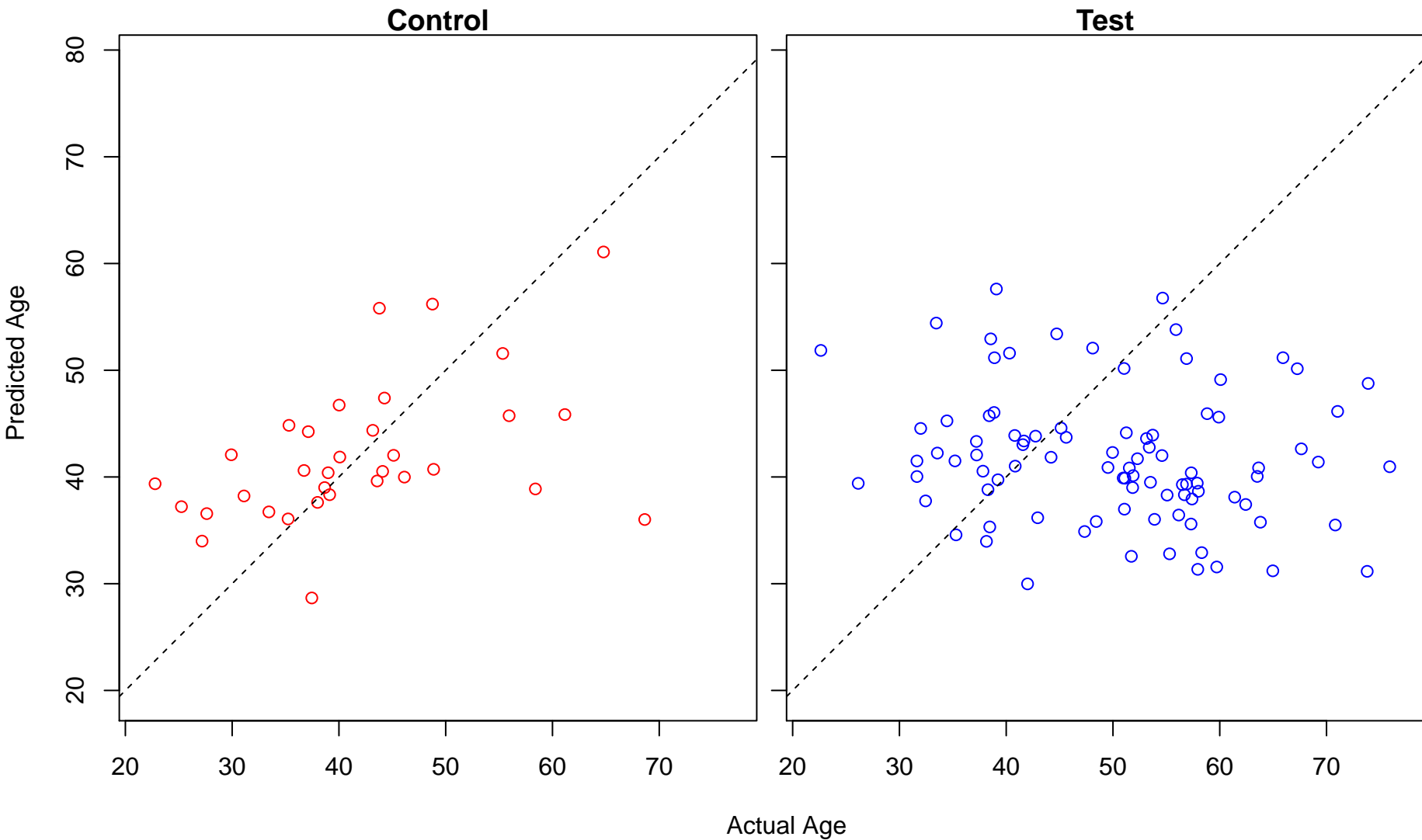
cellular response to caffeine (Score: 1.708828)



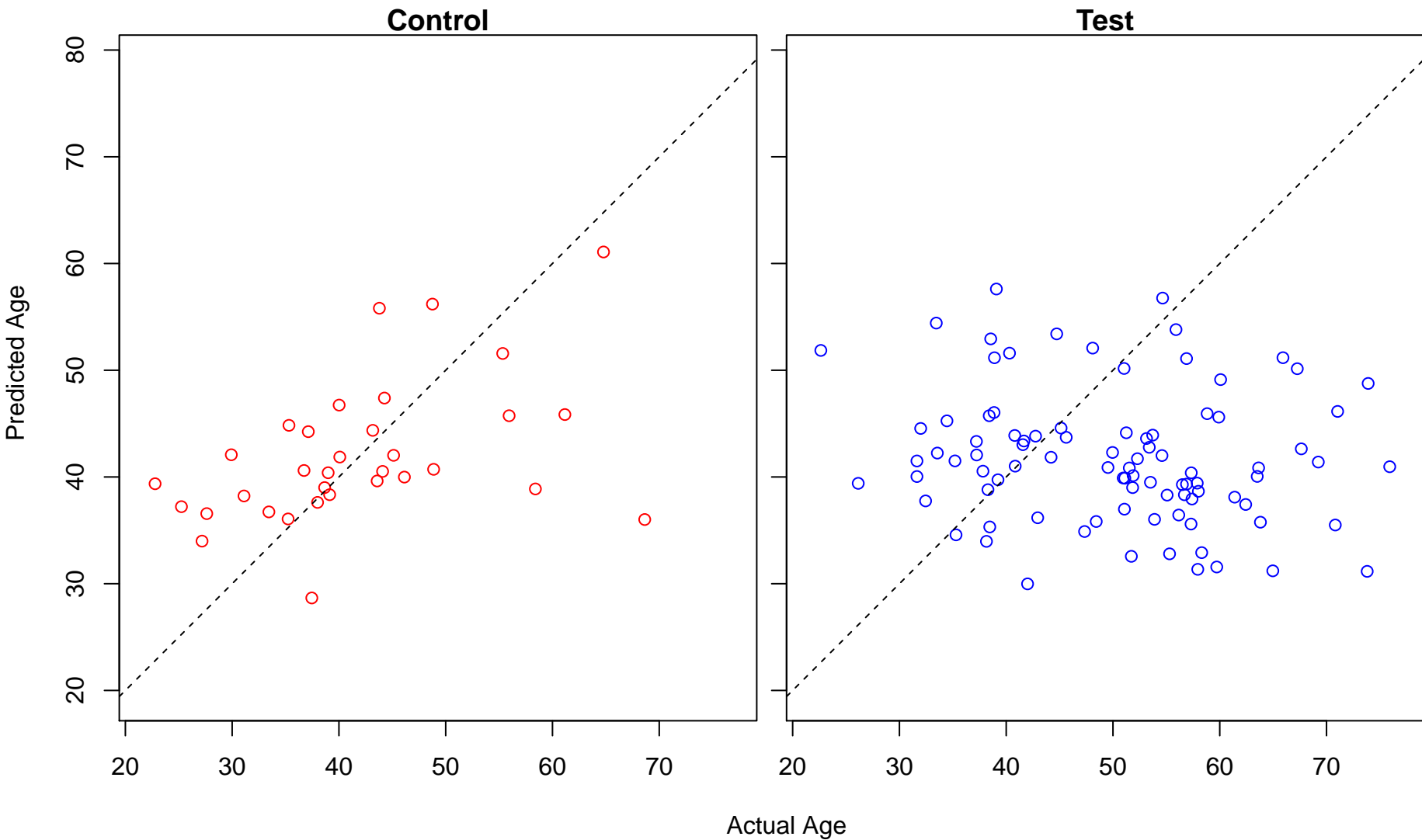
cellular response to purine-containing compound (Score: 1.708828)



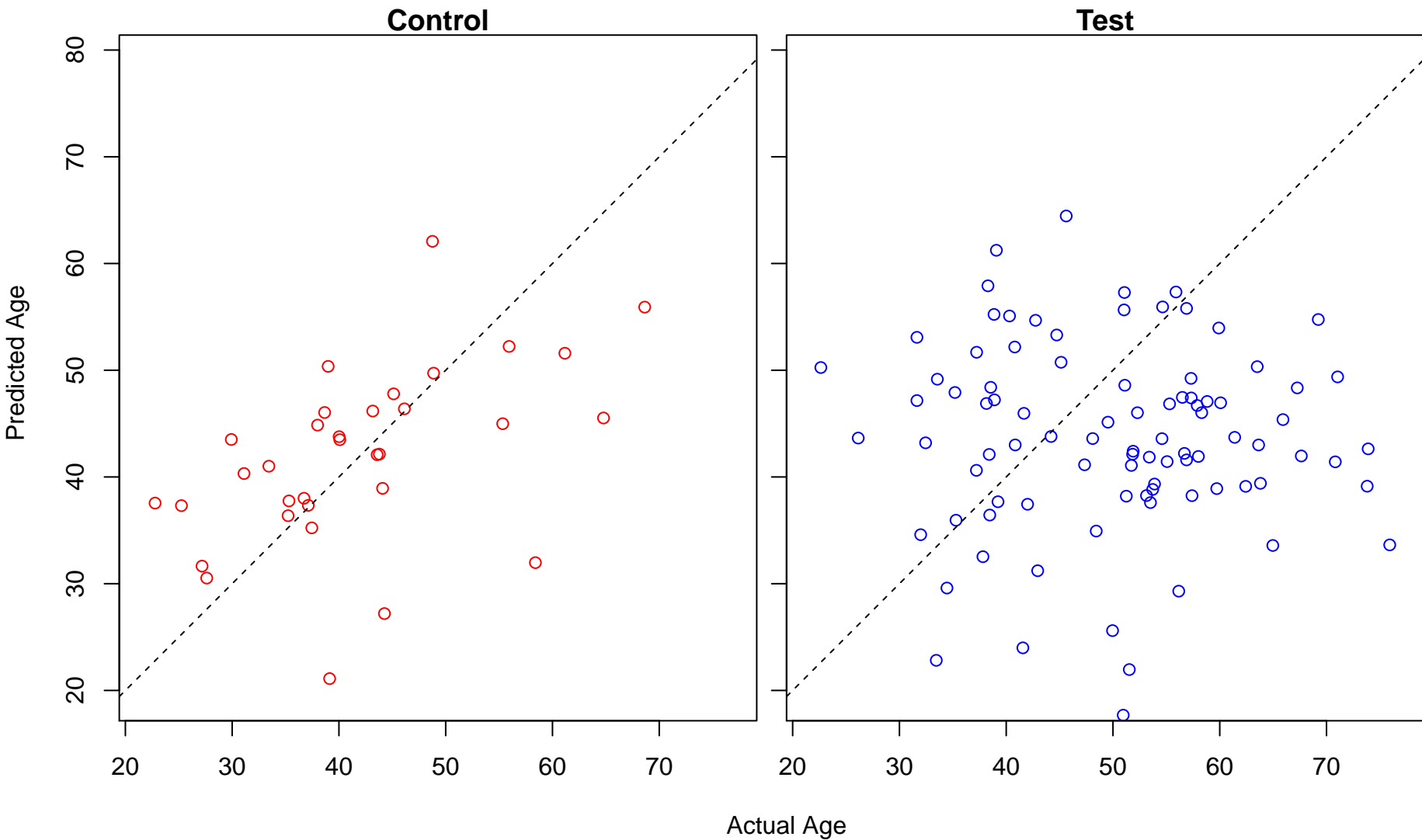
cartilage condensation (Score: 1.708803)



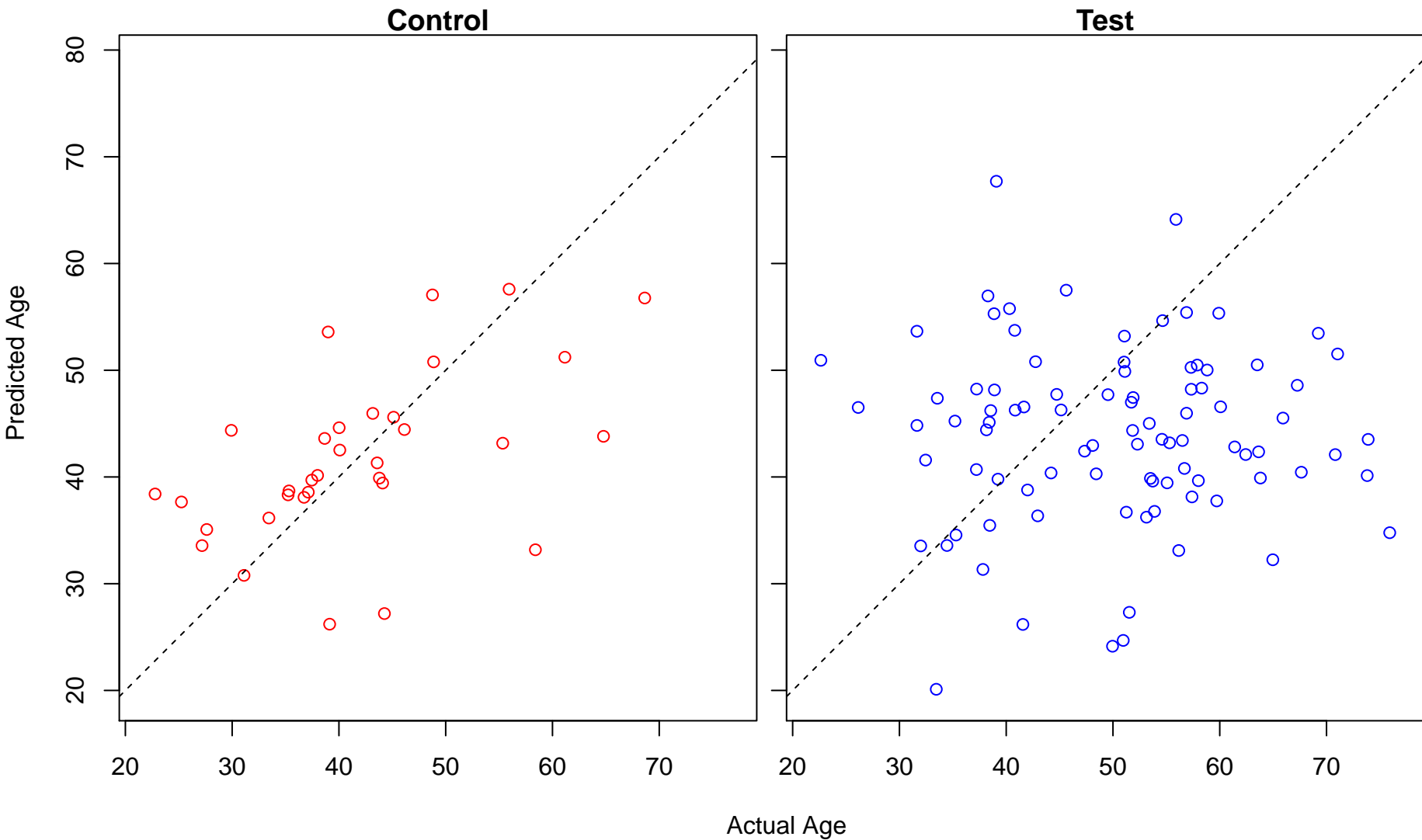
cell aggregation (Score: 1.708803)



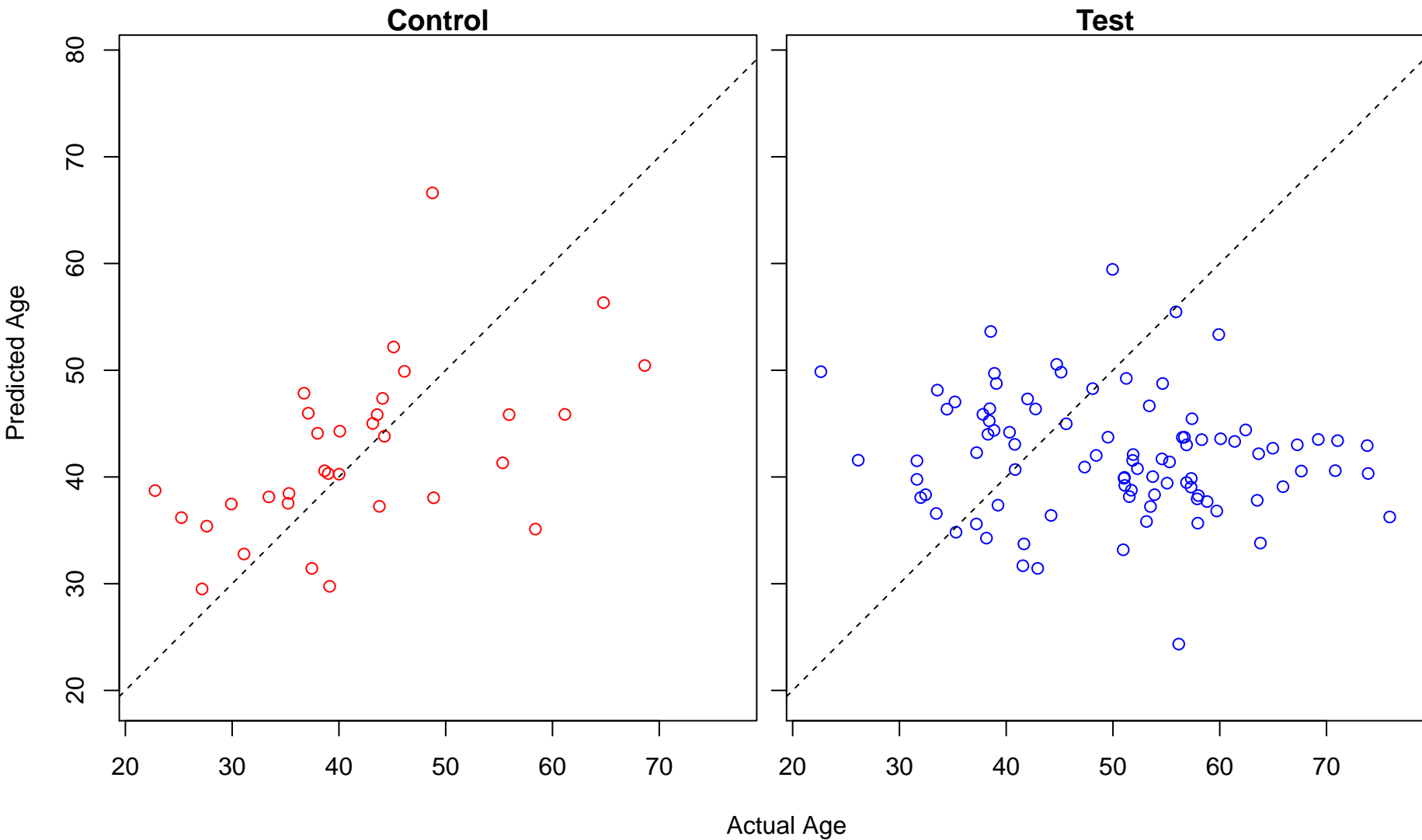
cellular response to leptin stimulus (Score: 1.705833)



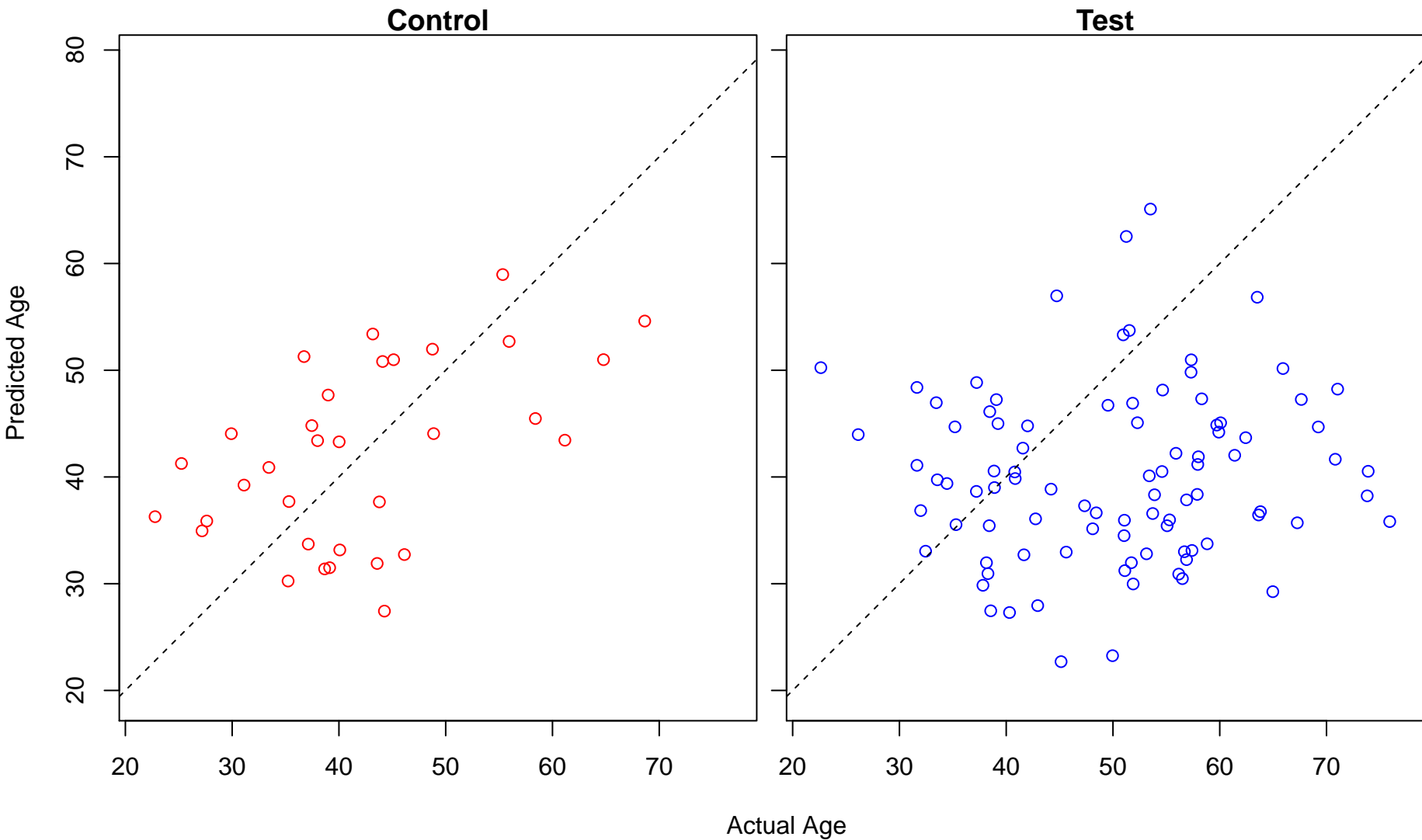
leptin-mediated signaling pathway (Score: 1.702601)



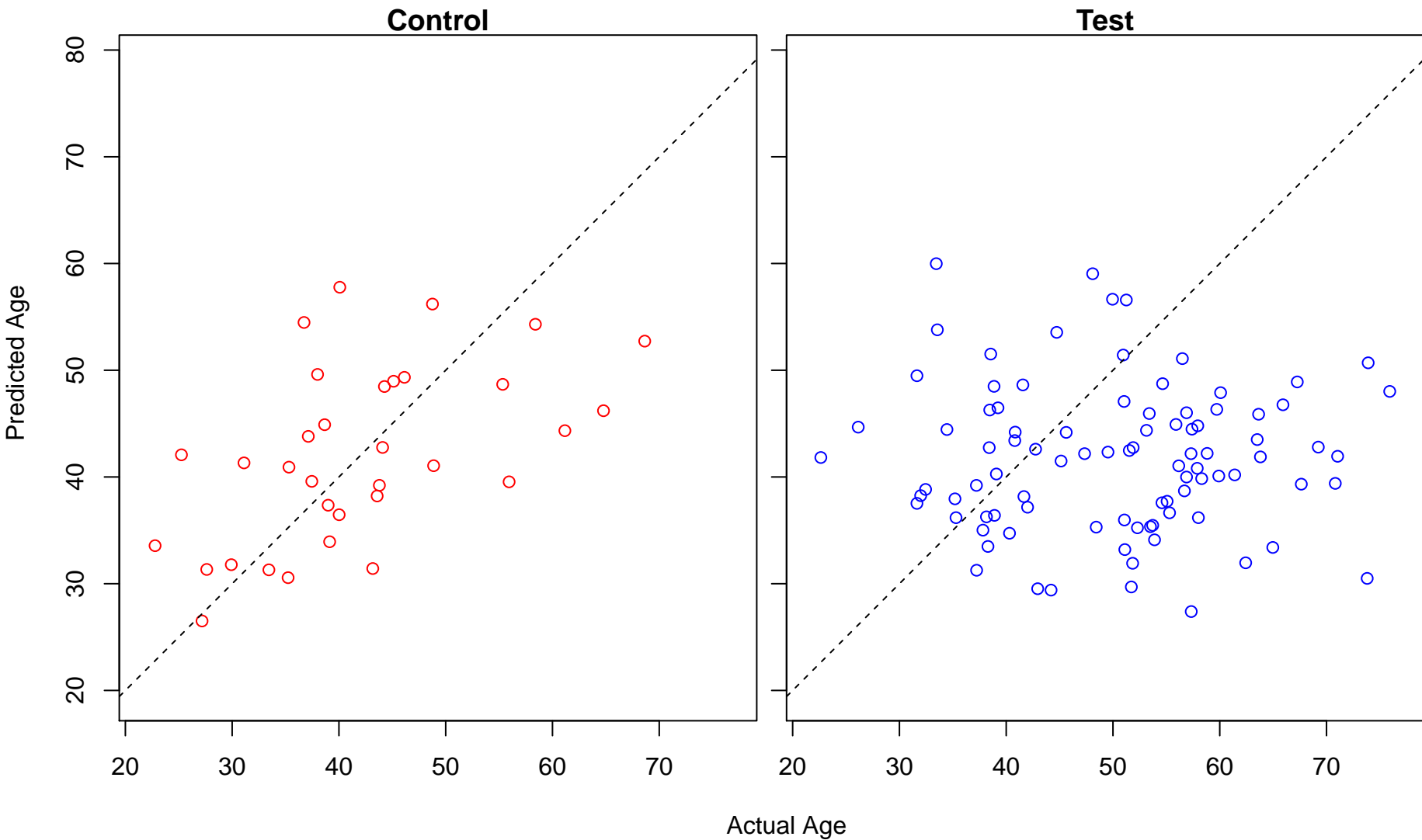
cGMP biosynthetic process (Score: 1.695015)



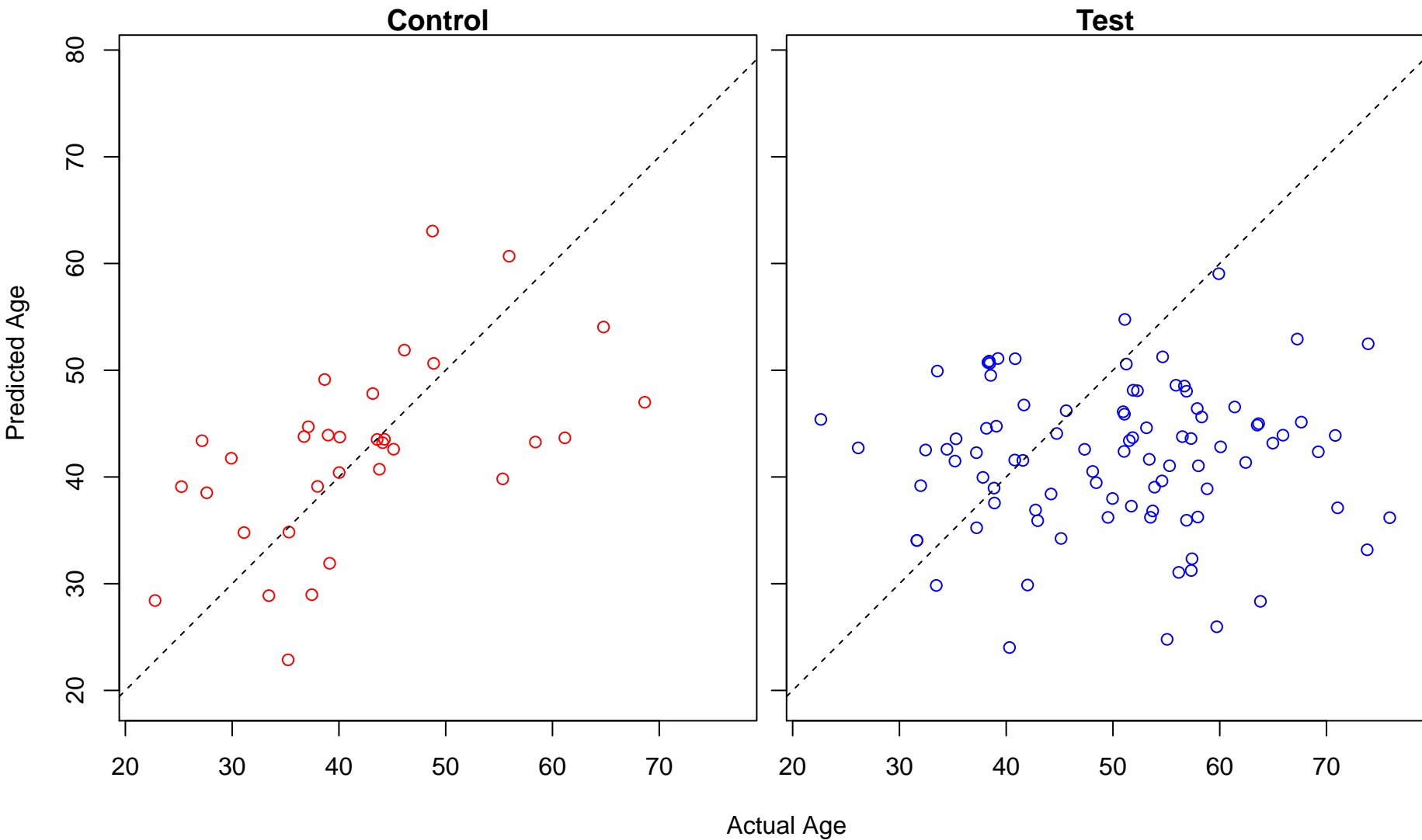
retinal metabolic process (Score: 1.682973)



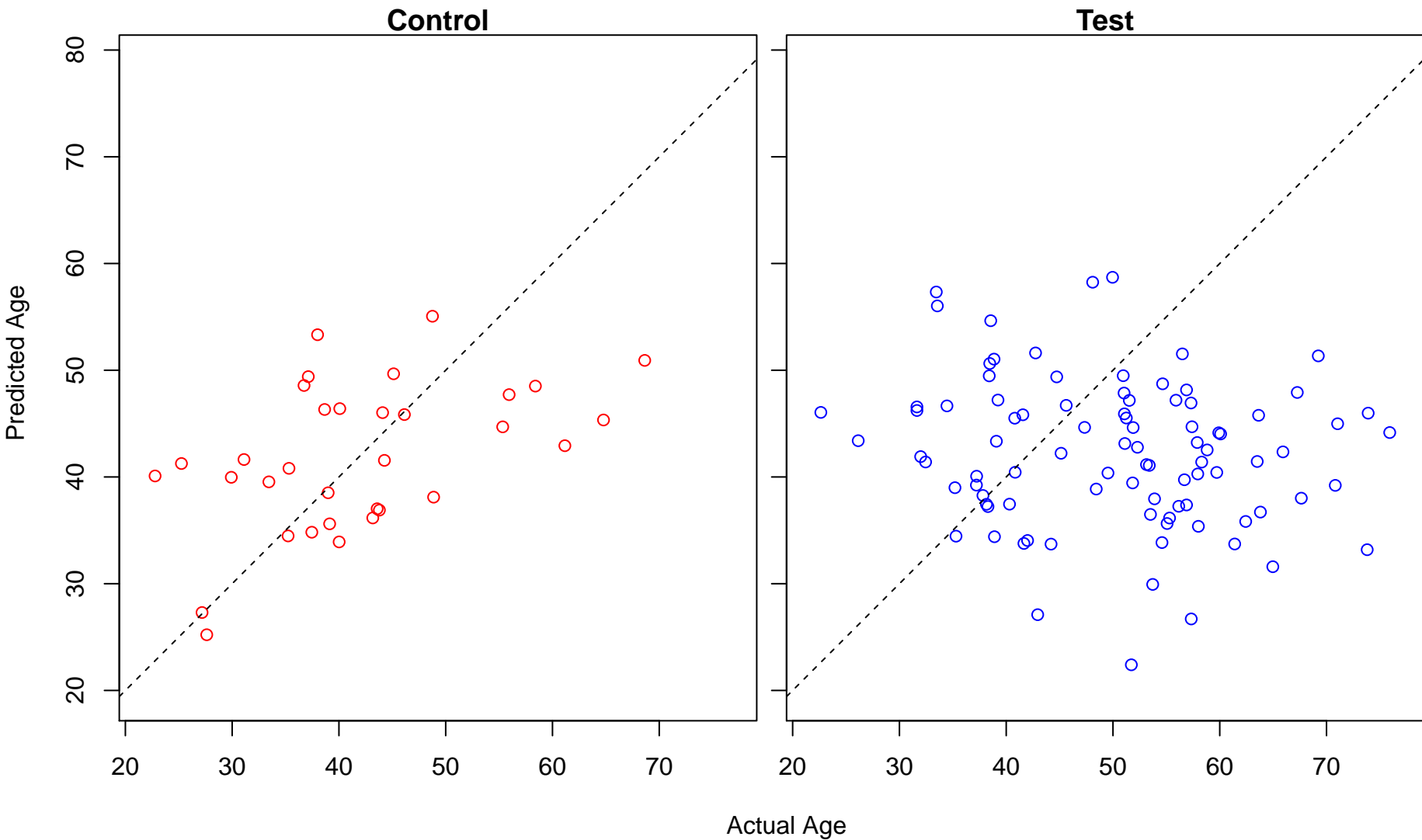
negative regulation of beta-amyloid formation (Score: 1.682823)



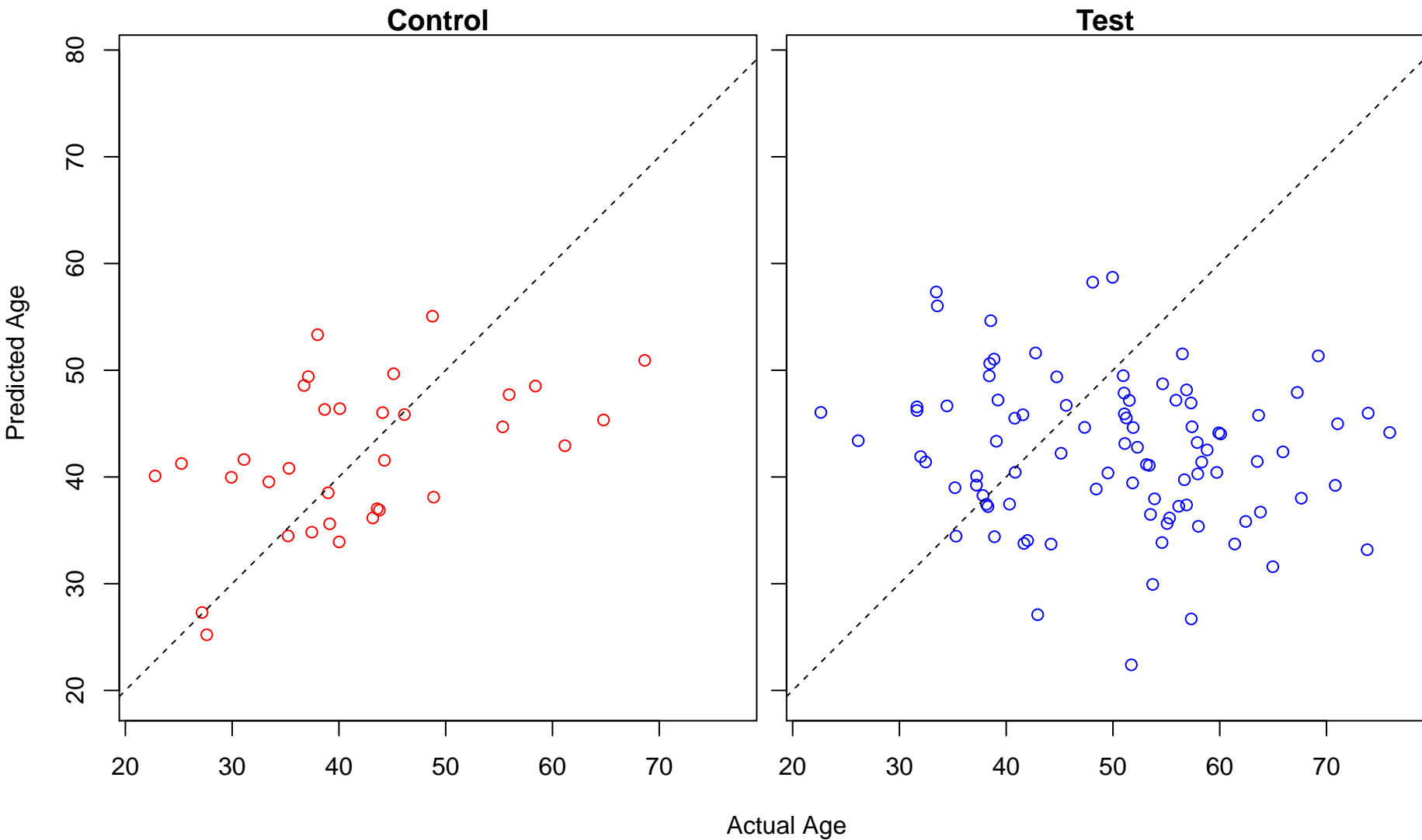
regulation of macrophage cytokine production (Score: 1.682414)



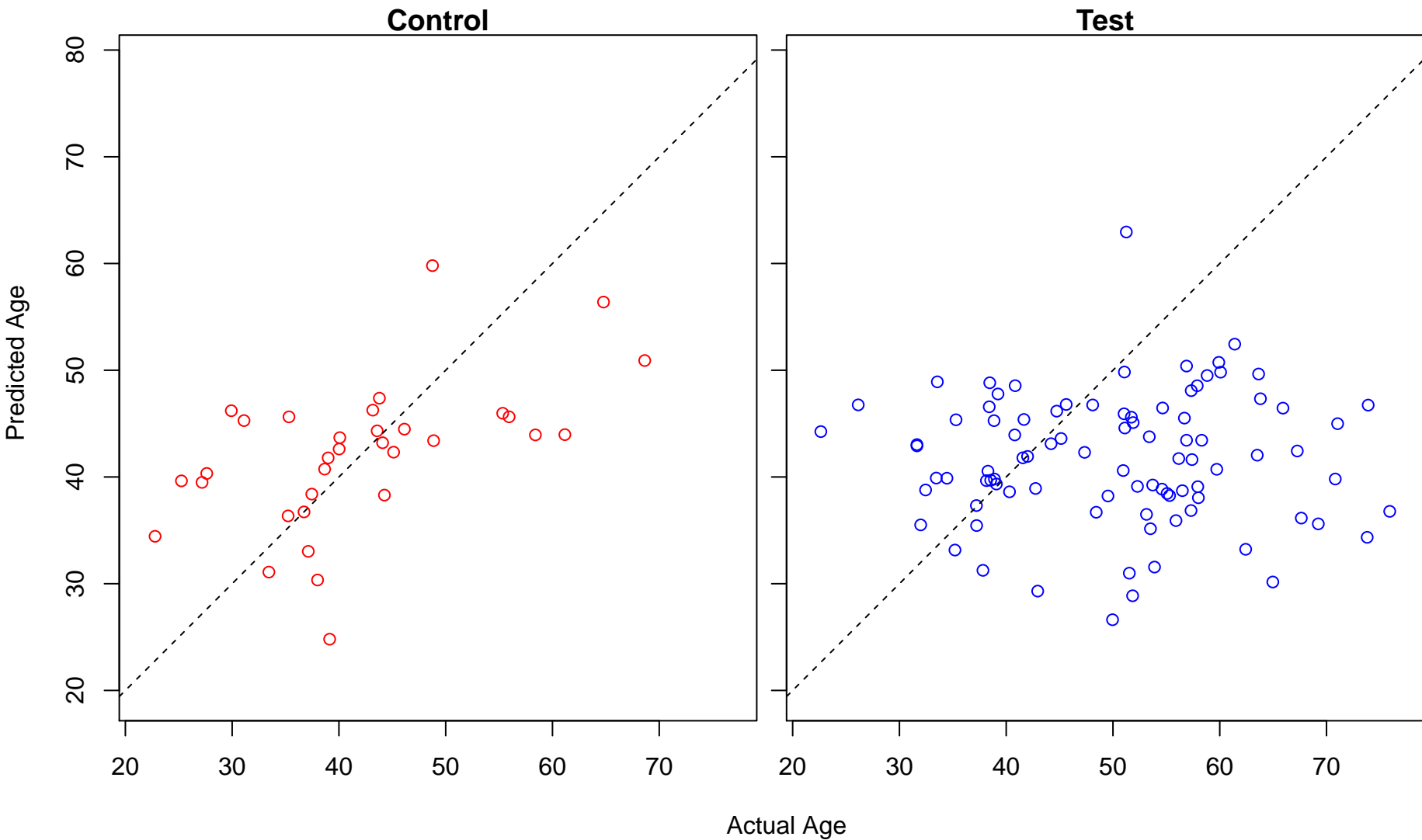
positive regulation of beta-amyloid formation (Score: 1.675123)



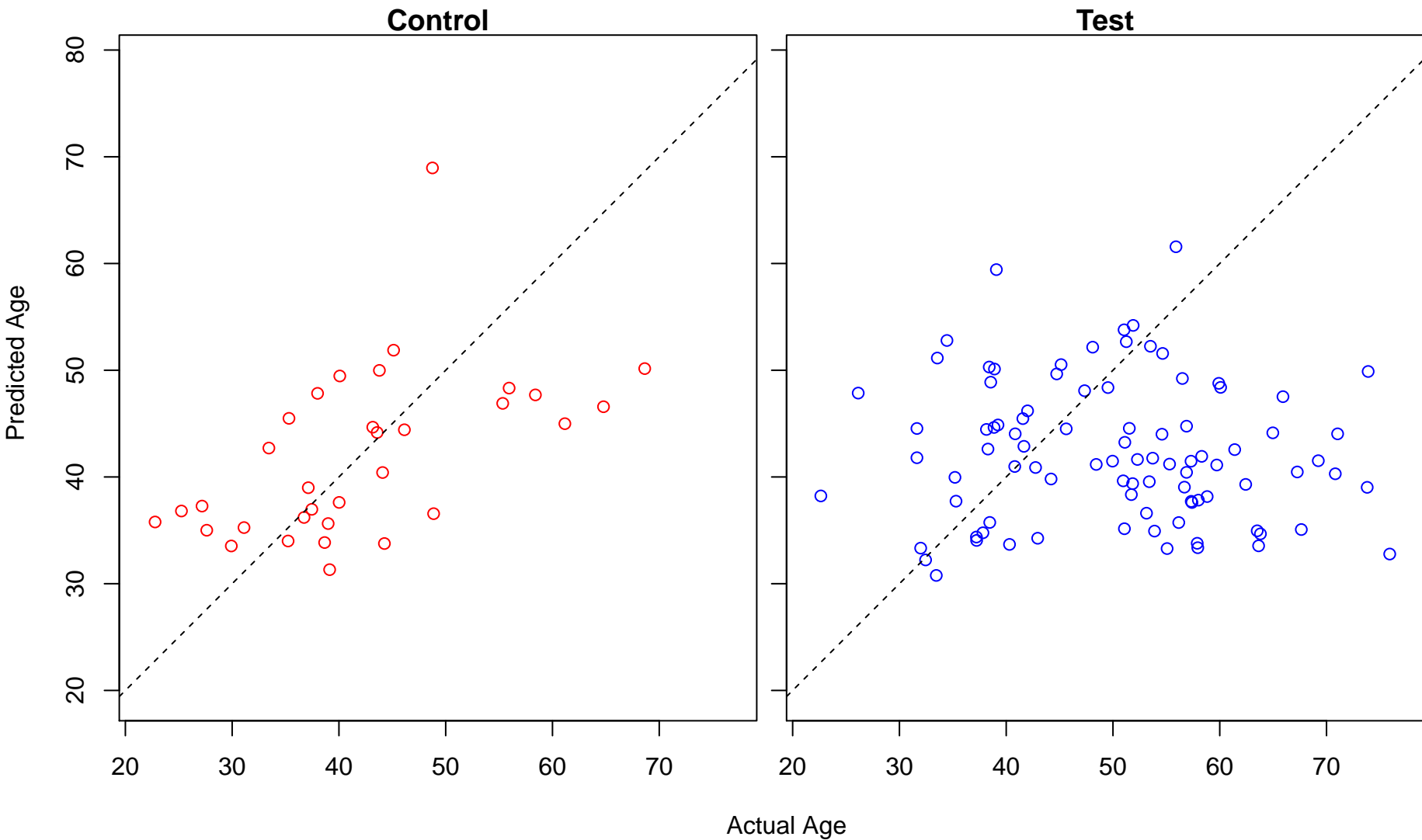
positive regulation of amyloid precursor protein catabolic process (Score: 1.675123)



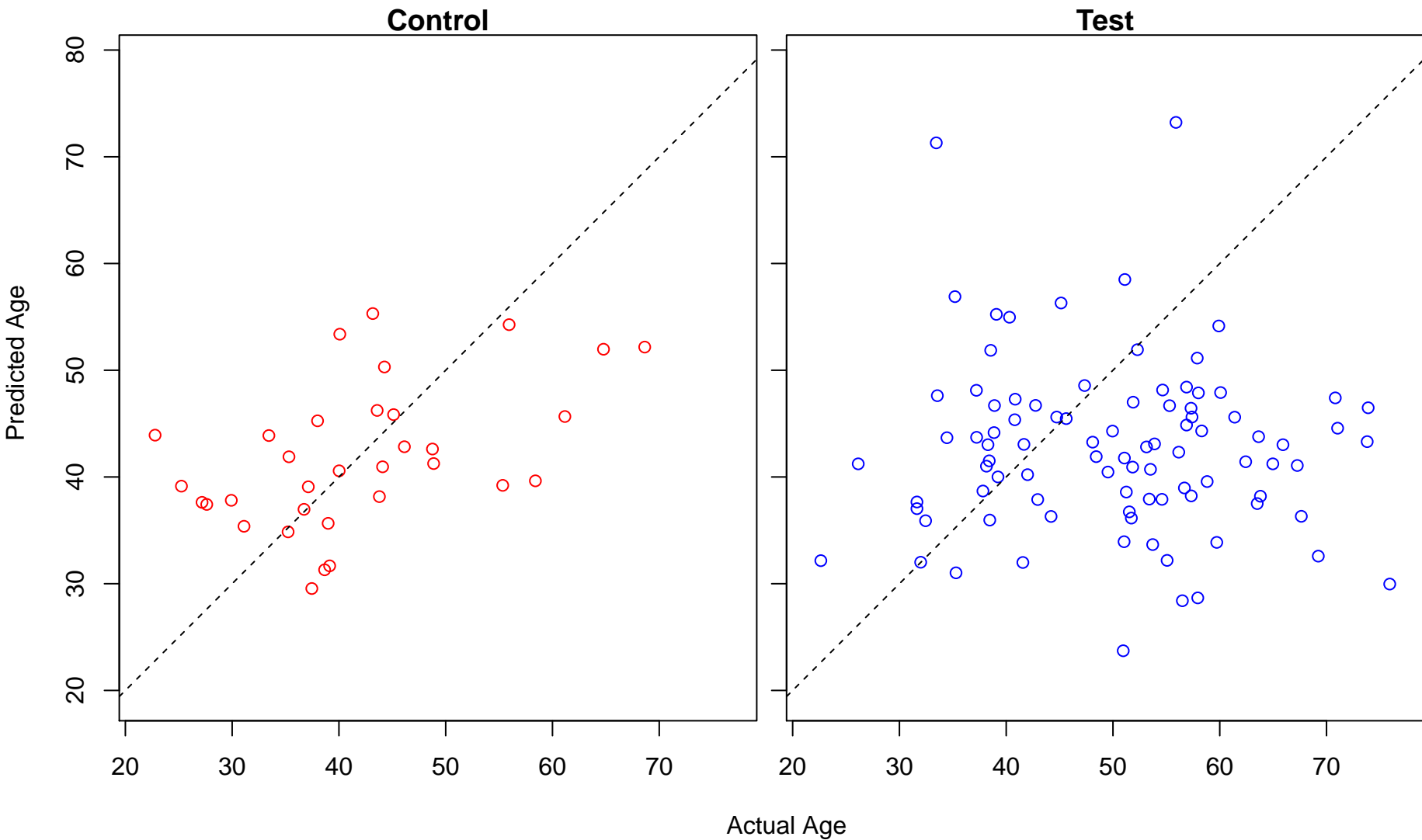
phosphatidylglycerol acyl-chain remodeling (Score: 1.673221)



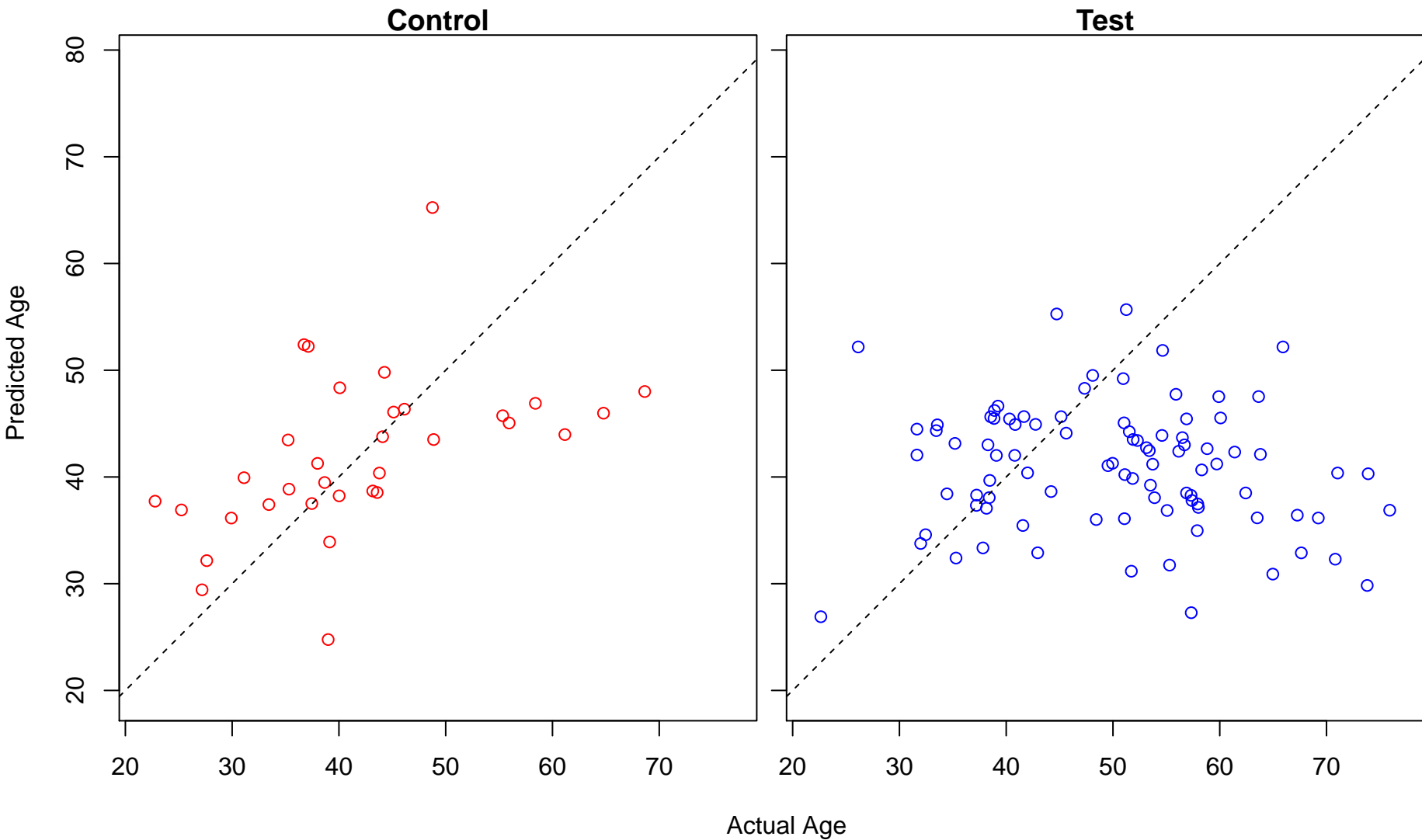
snRNA transcription from RNA polymerase III promoter (Score: 1.662237)



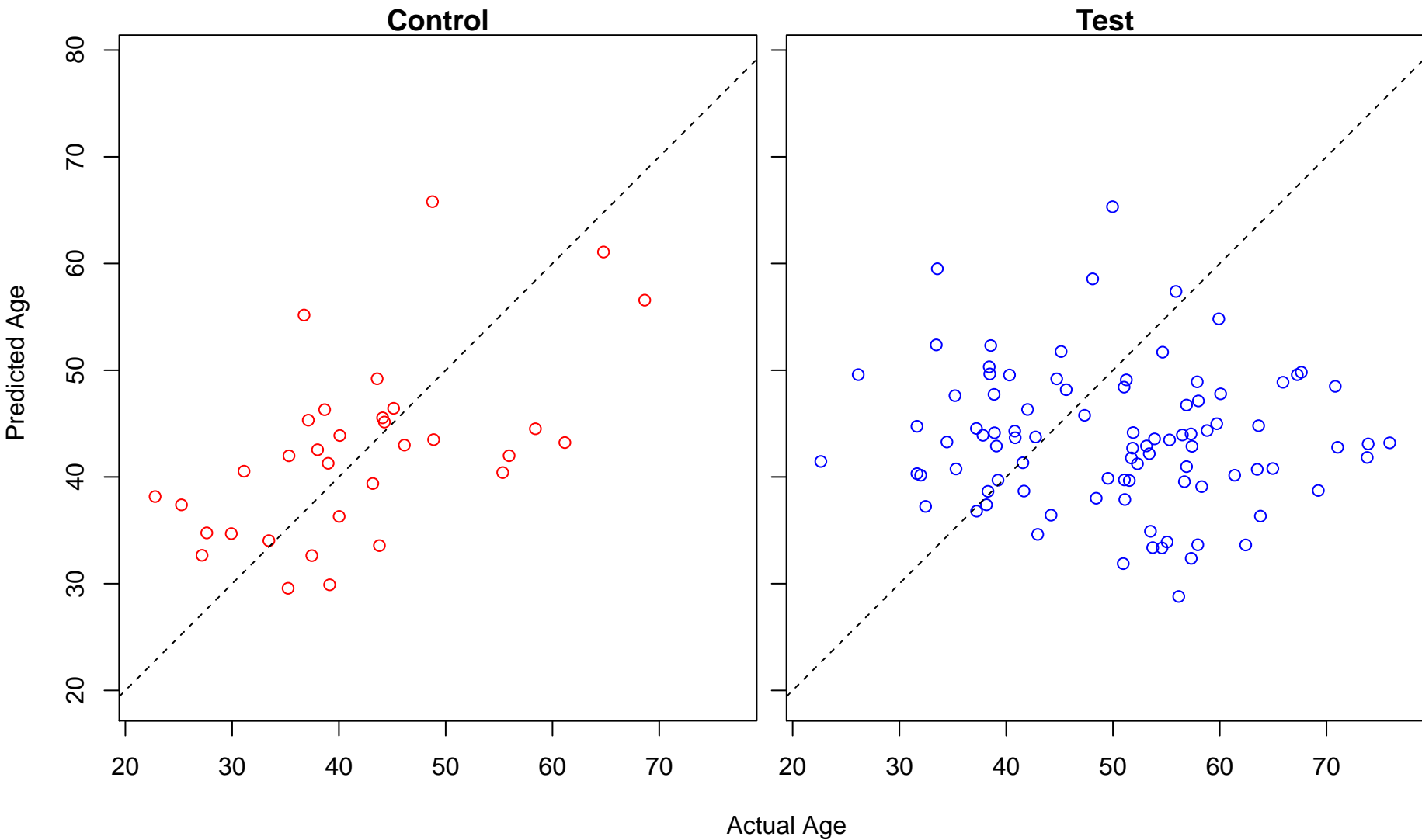
heterochromatin assembly (Score: 1.661120)



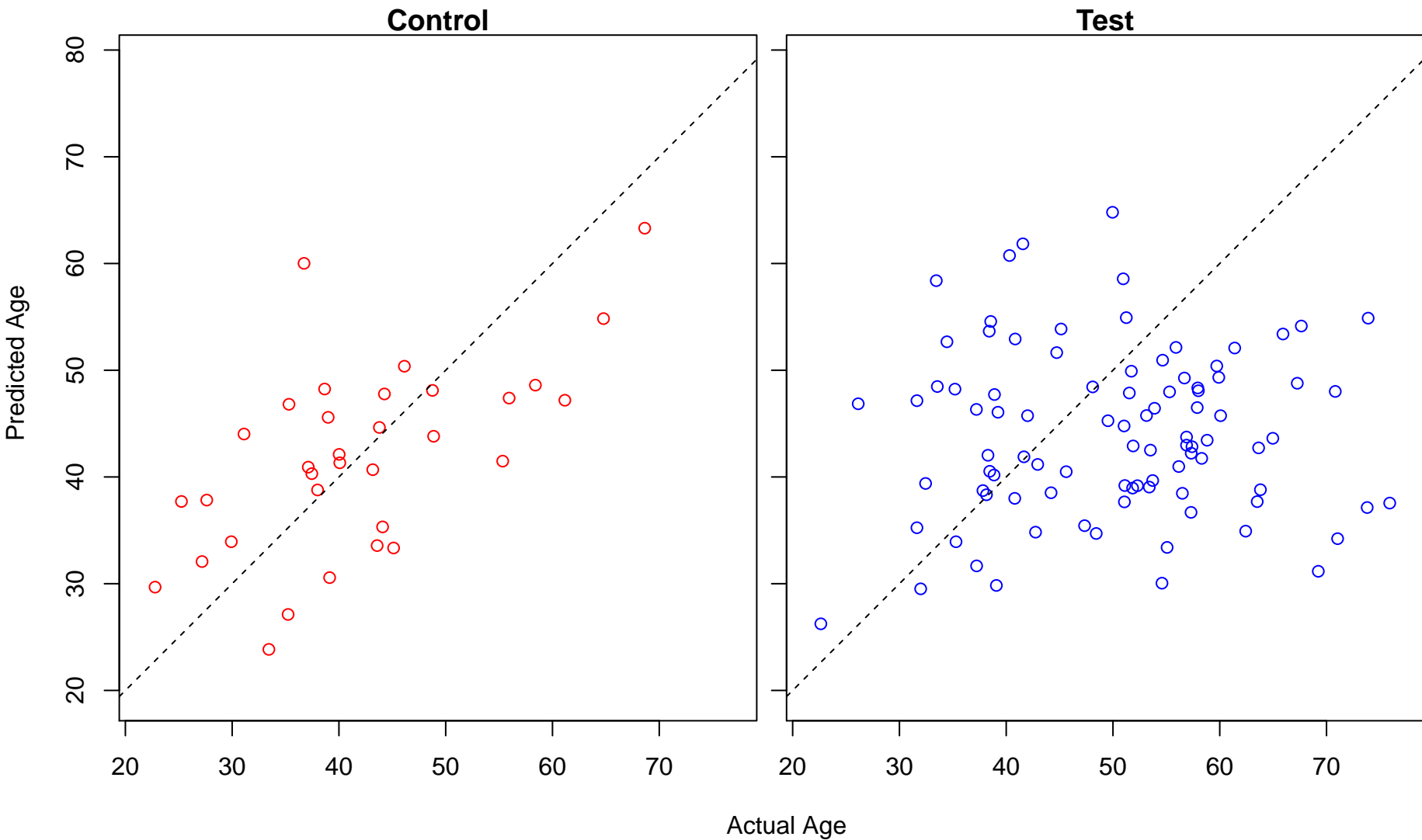
erythrocyte development (Score: 1.657540)



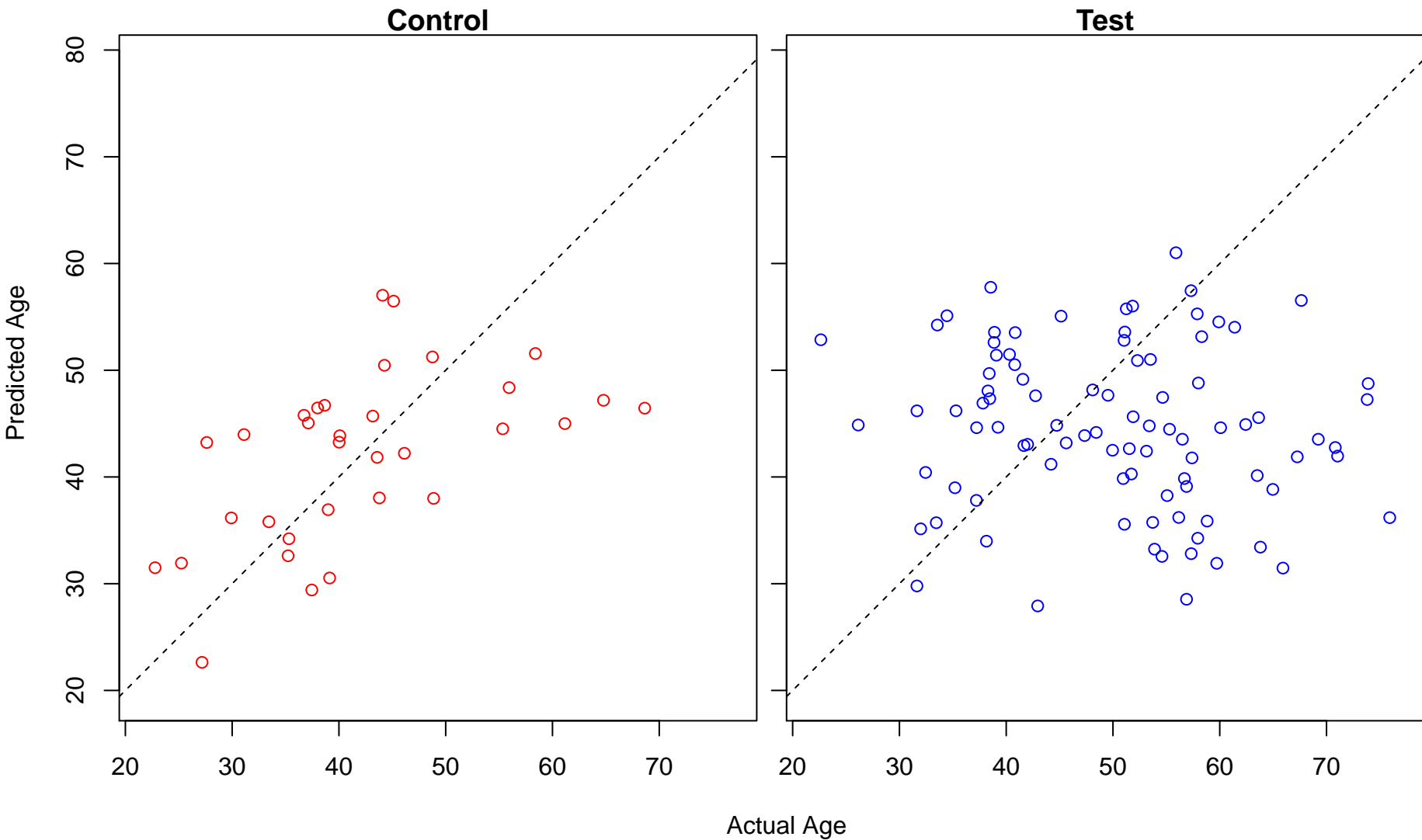
response to nitric oxide (Score: 1.65559)



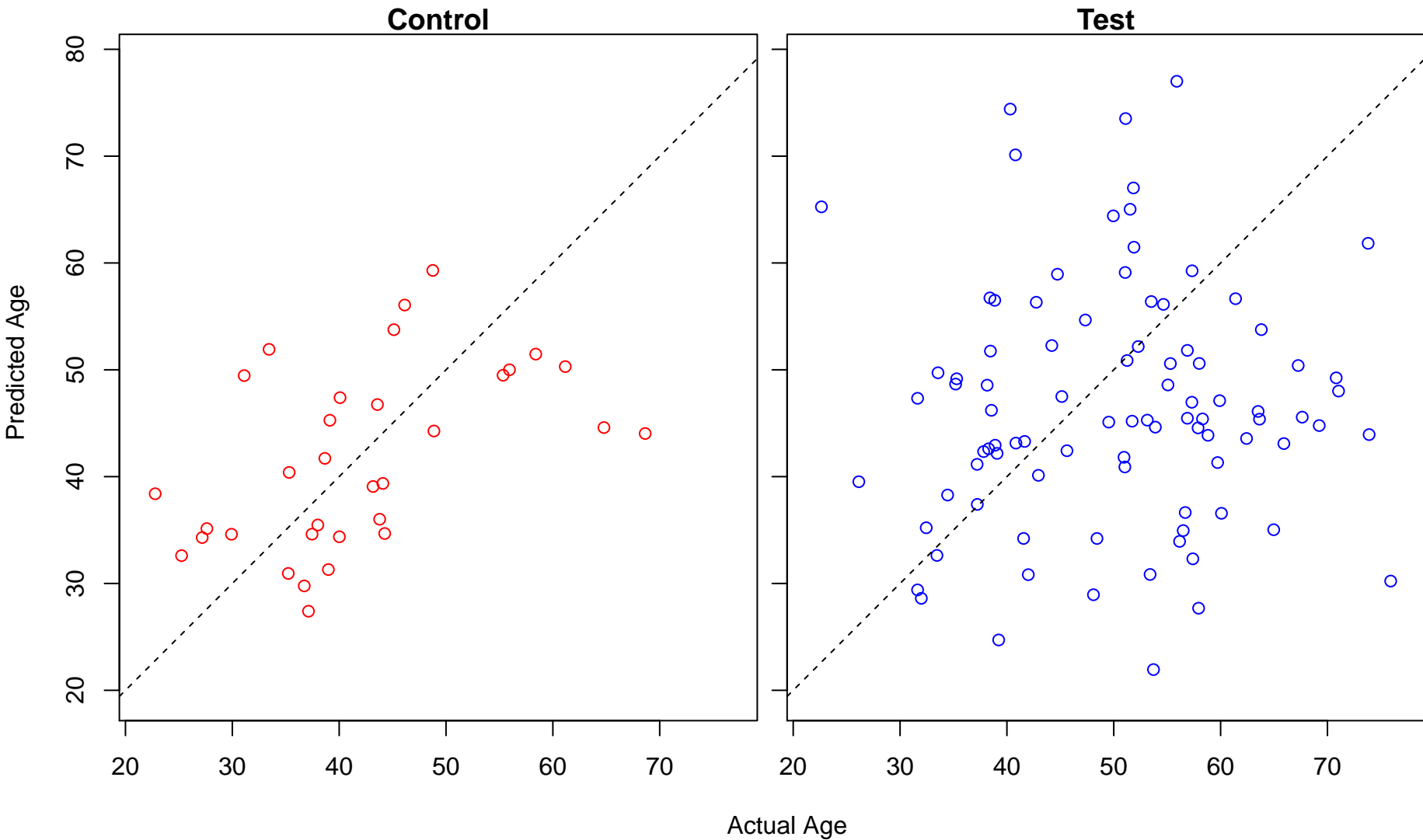
cellular response to cold (Score: 1.651879)



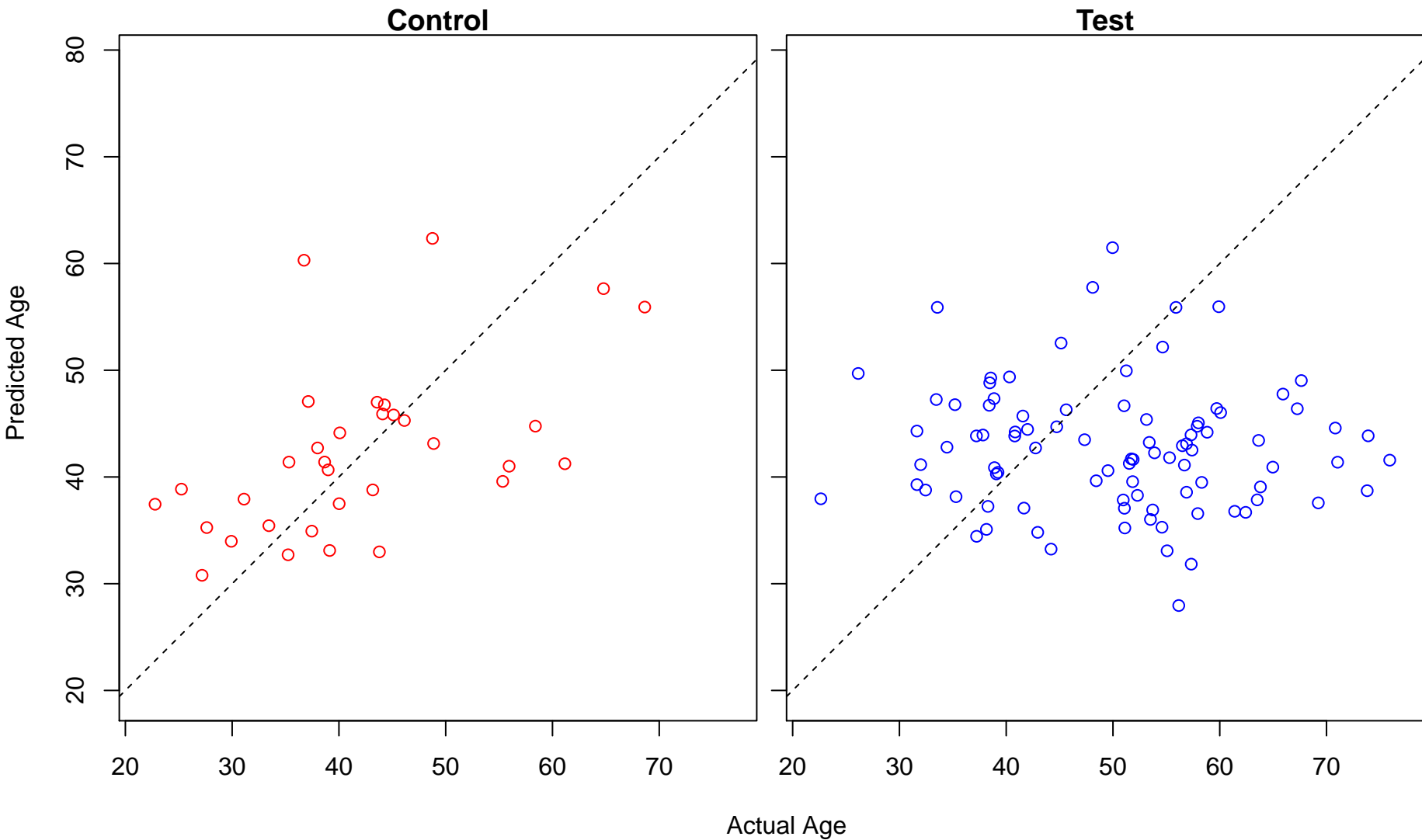
vascular smooth muscle contraction (Score: 1.651377)



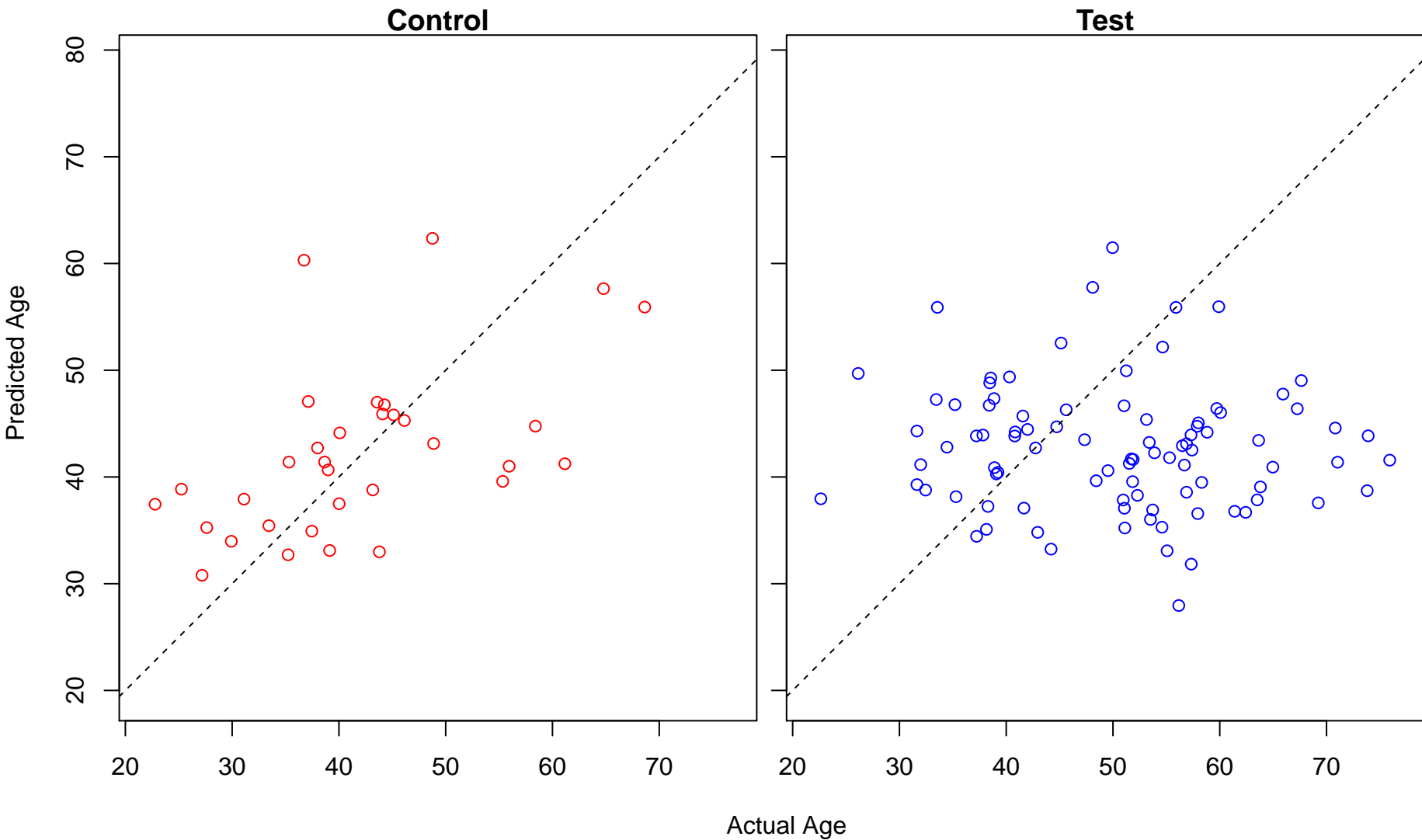
negative regulation of delayed rectifier potassium channel activity (Score: 1.649083)



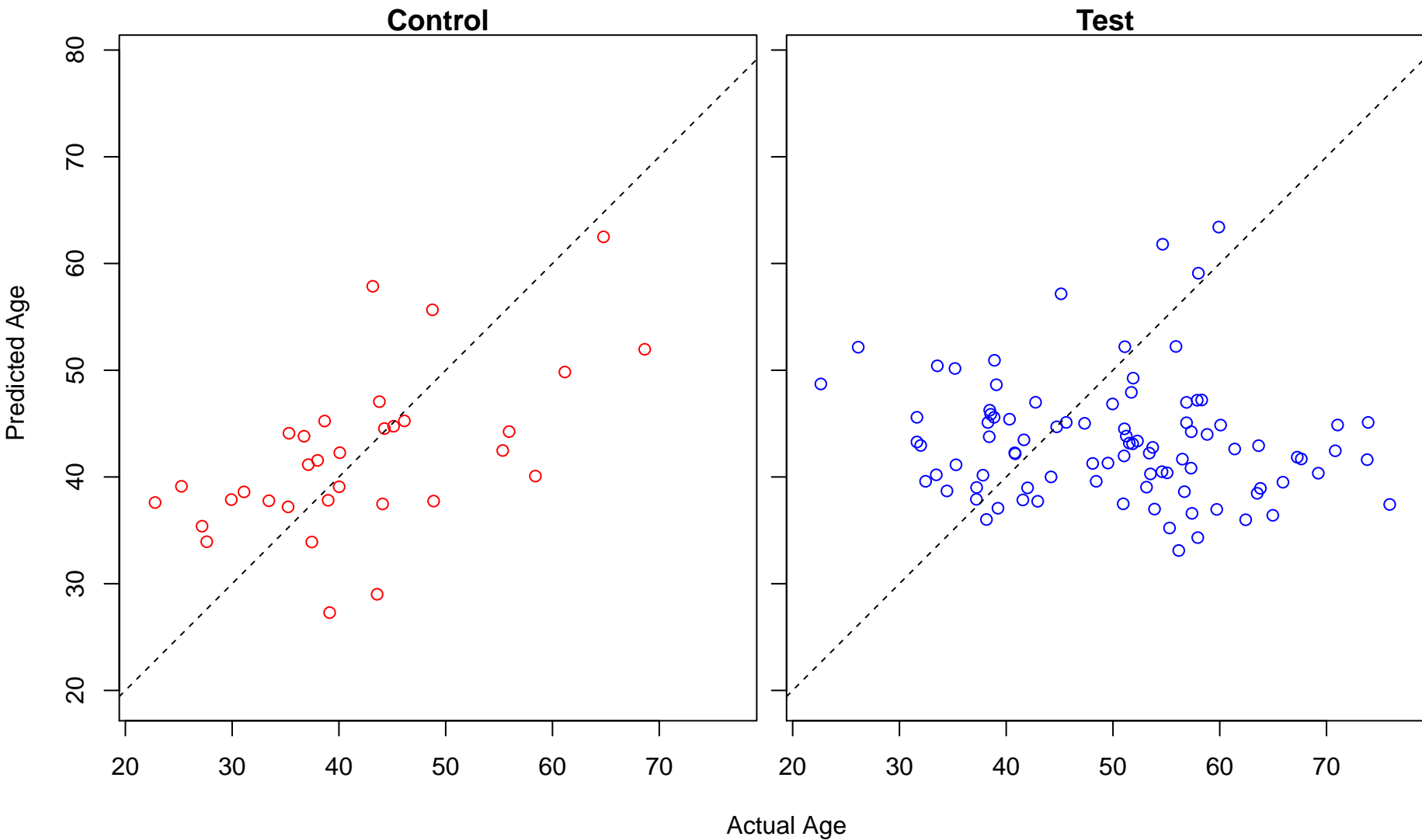
cellular response to nitric oxide (Score: 1.648089)



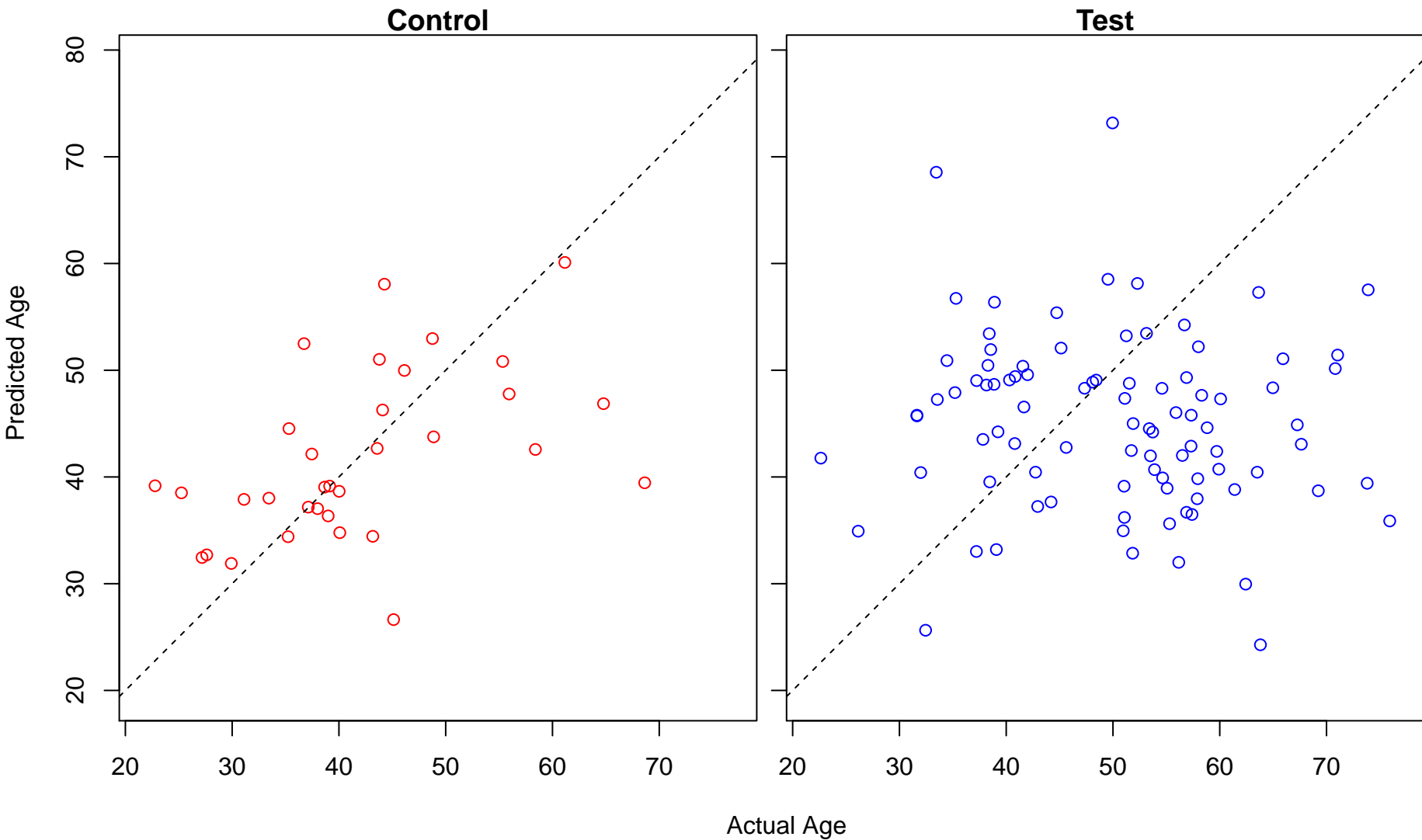
cellular response to reactive nitrogen species (Score: 1.648089)



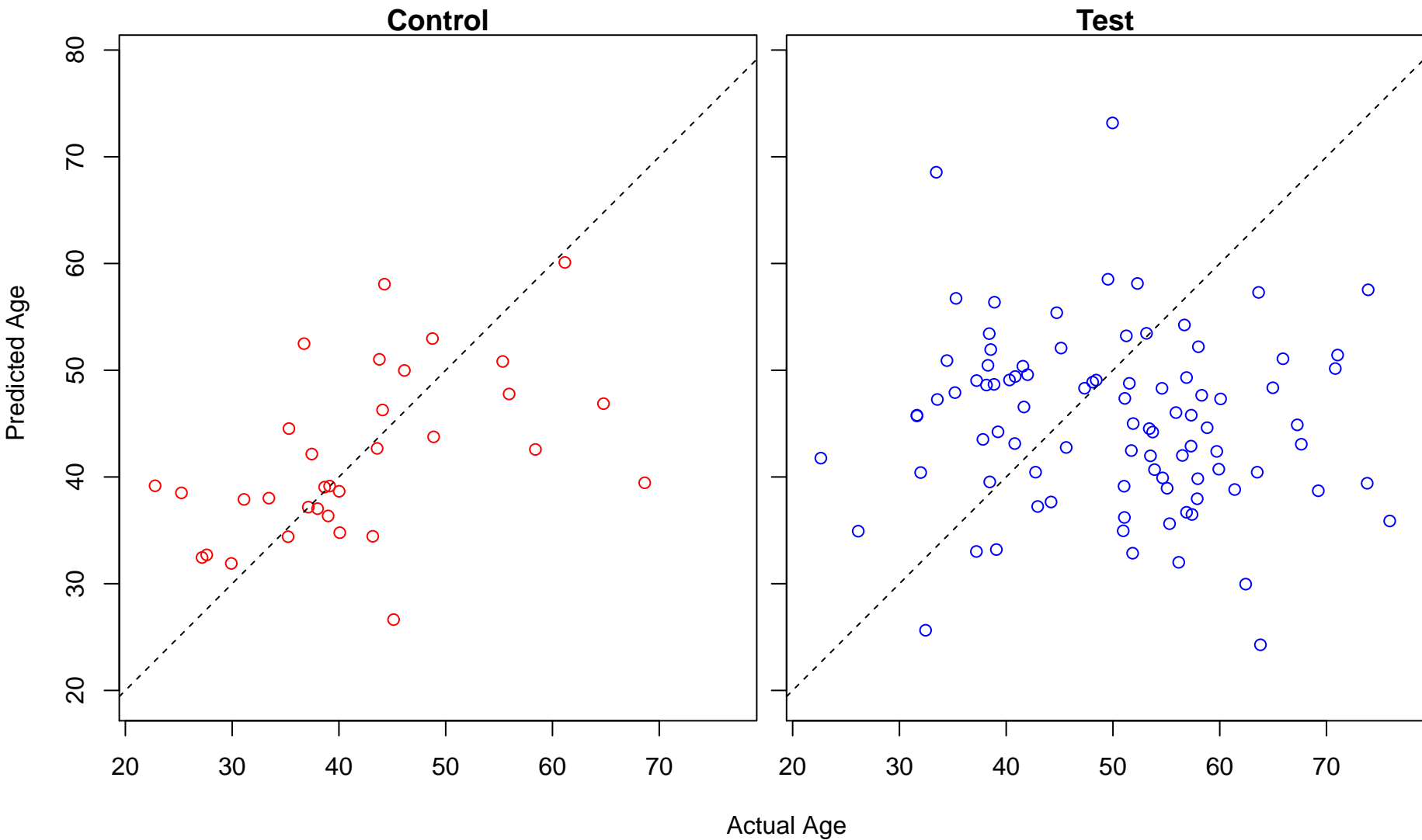
positive regulation of nuclear cell cycle DNA replication (Score: 1.646309)



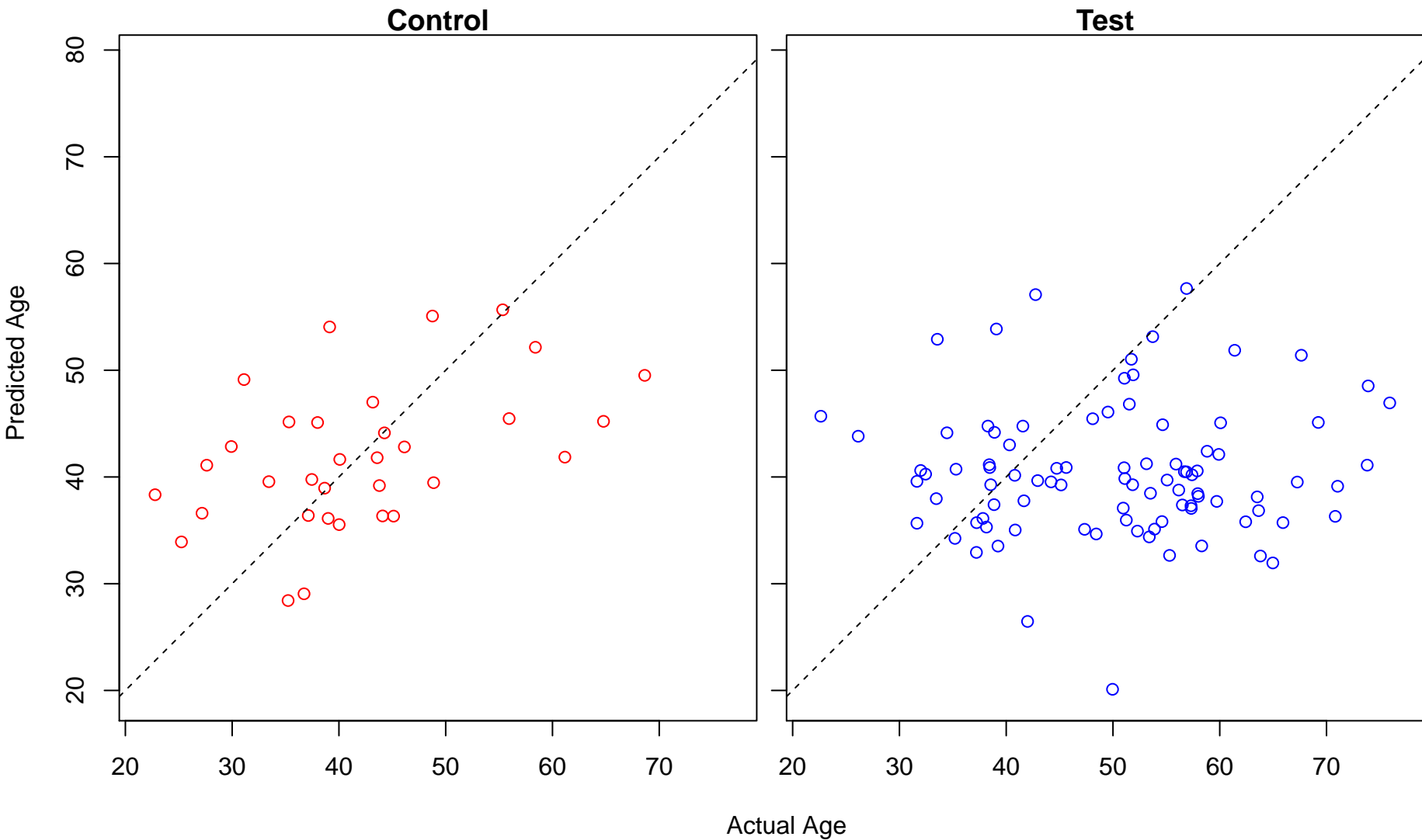
negative regulation of nitric oxide biosynthetic process (Score: 1.642777)



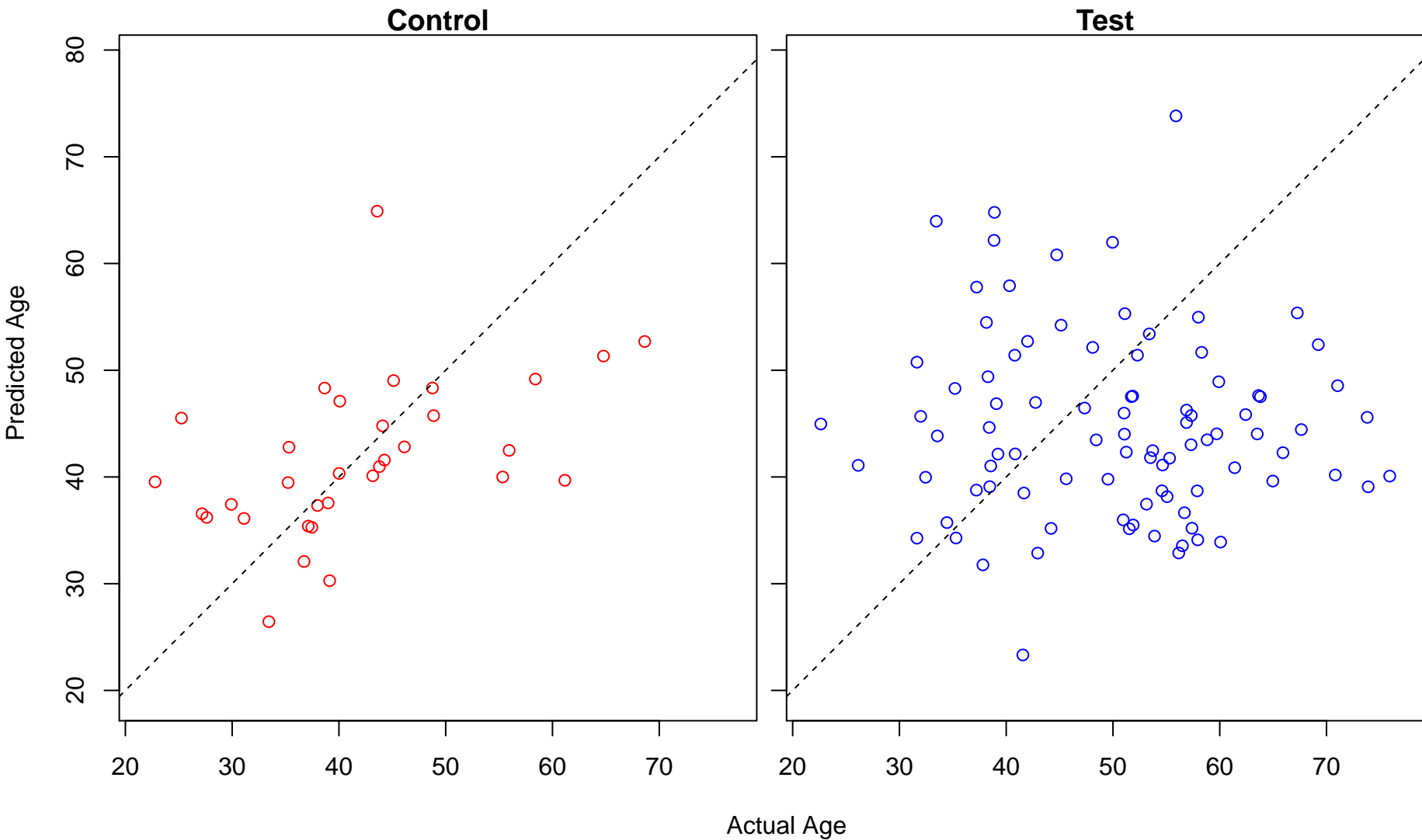
negative regulation of nitric oxide metabolic process (Score: 1.642777)



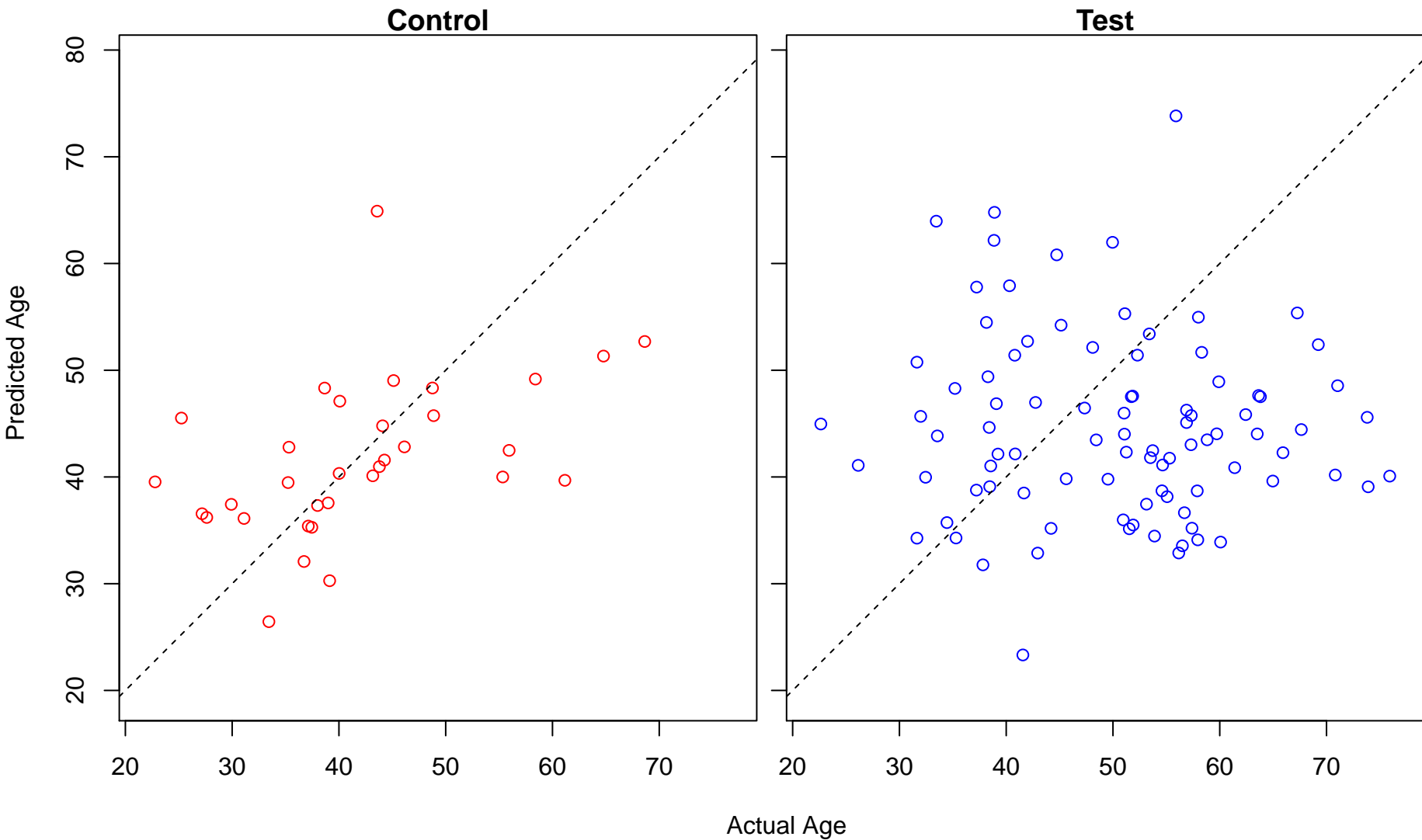
Notch signaling involved in heart development (Score: 1.637176)



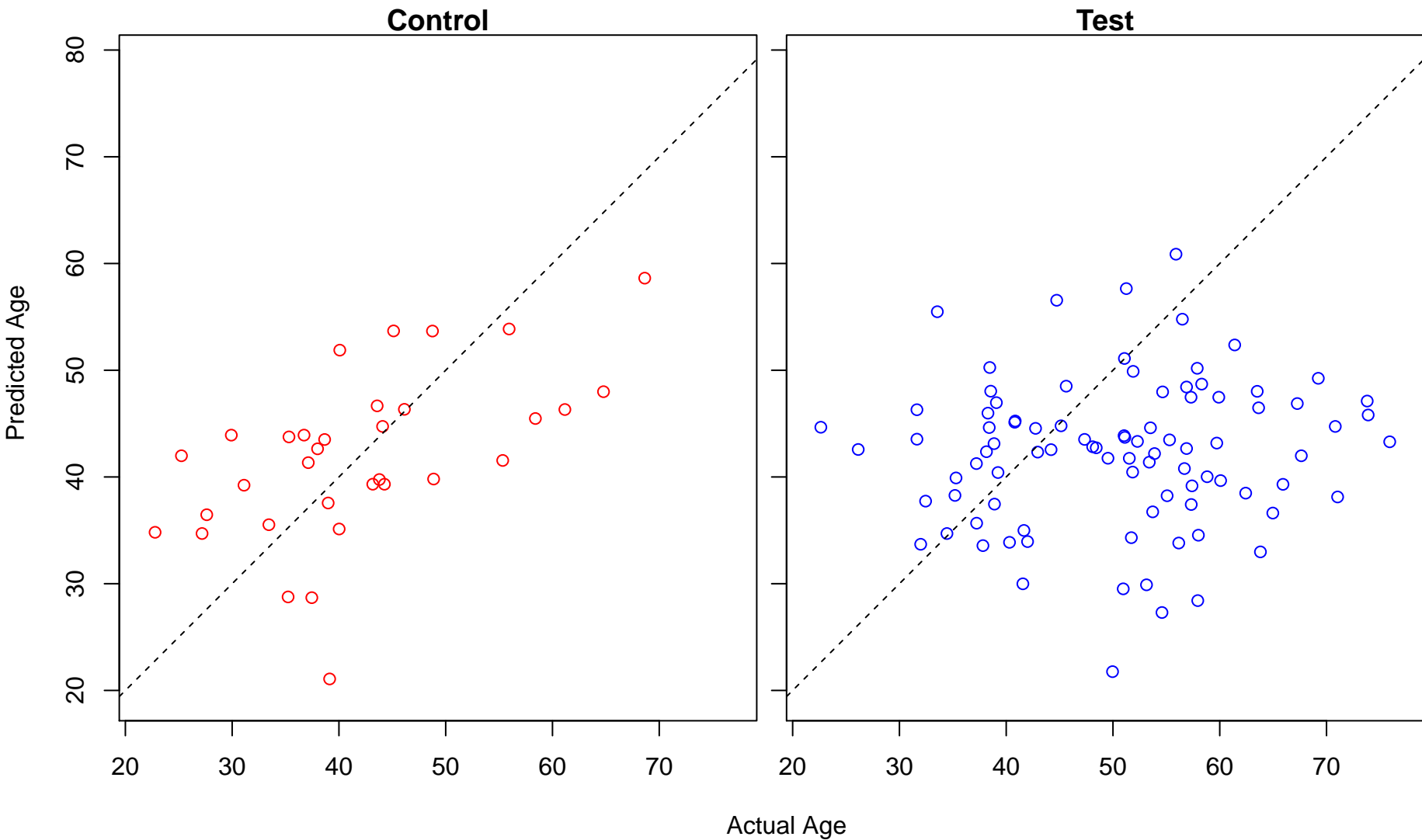
lipid translocation (Score: 1.625815)



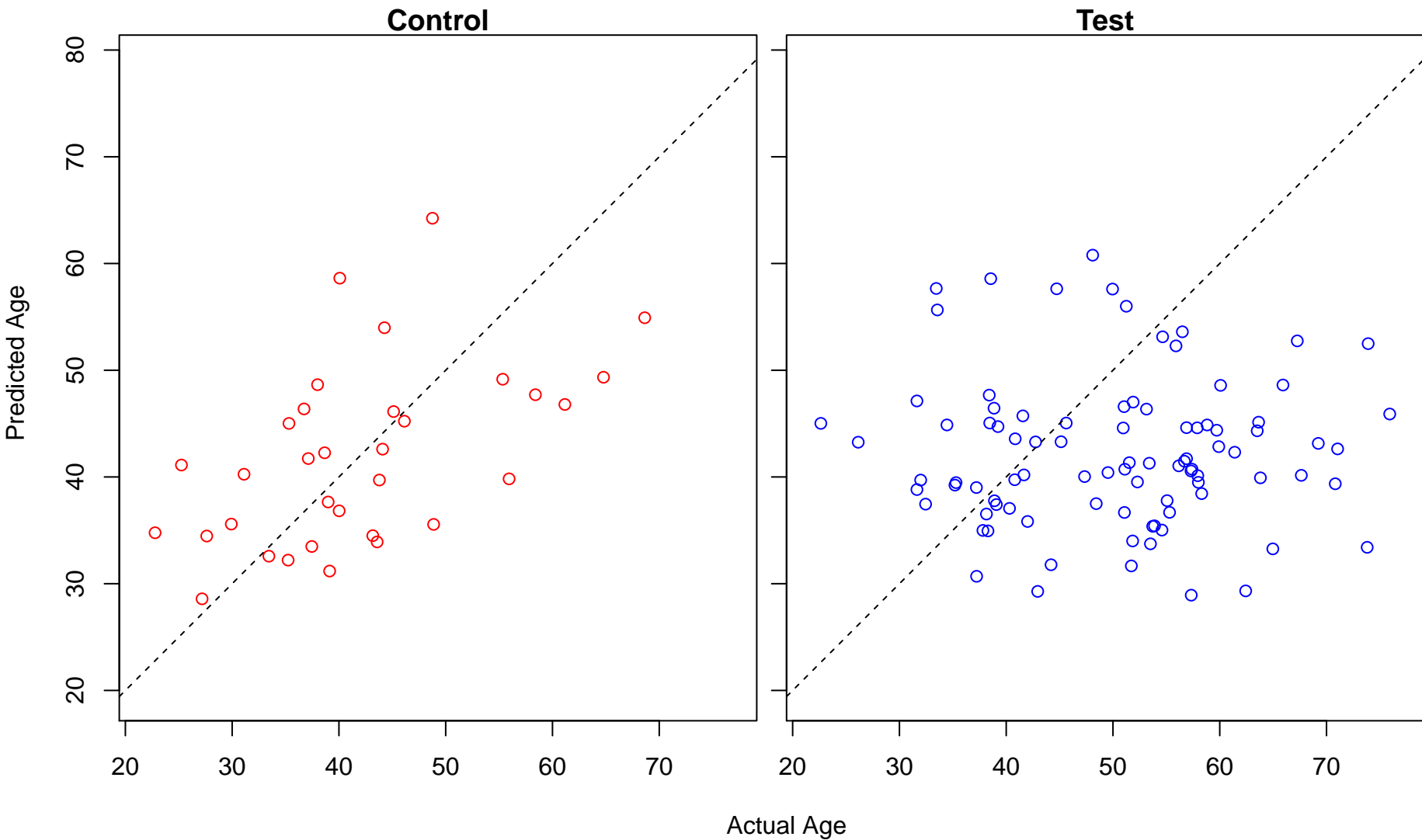
phospholipid translocation (Score: 1.625815)



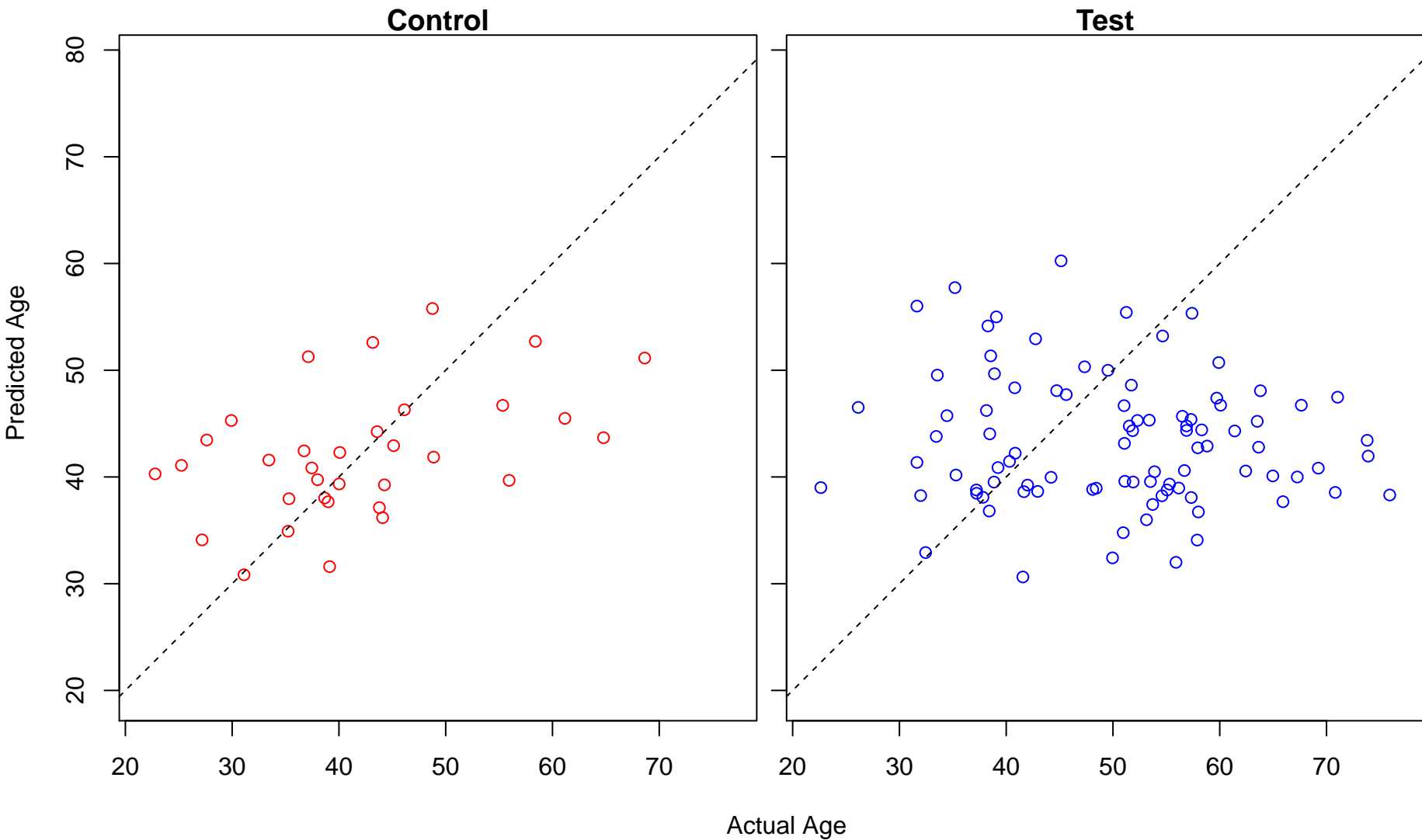
glutamine metabolic process (Score: 1.615352)



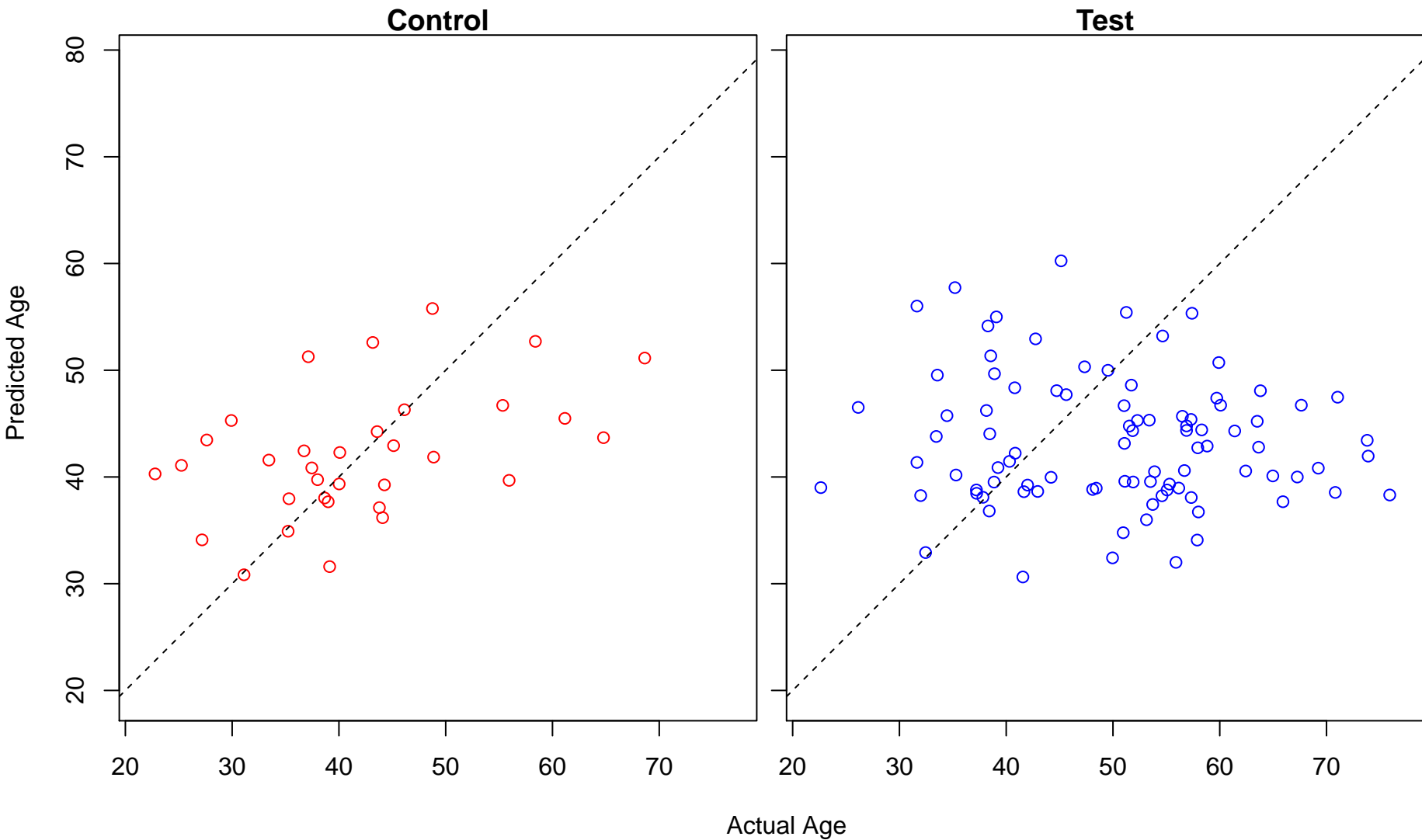
negative regulation of amyloid precursor protein catabolic process (Score: 1.602529)



response to potassium ion (Score: 1.574560)



cellular response to potassium ion (Score: 1.574560)



sarcomere organization (Score: 1.570747)

