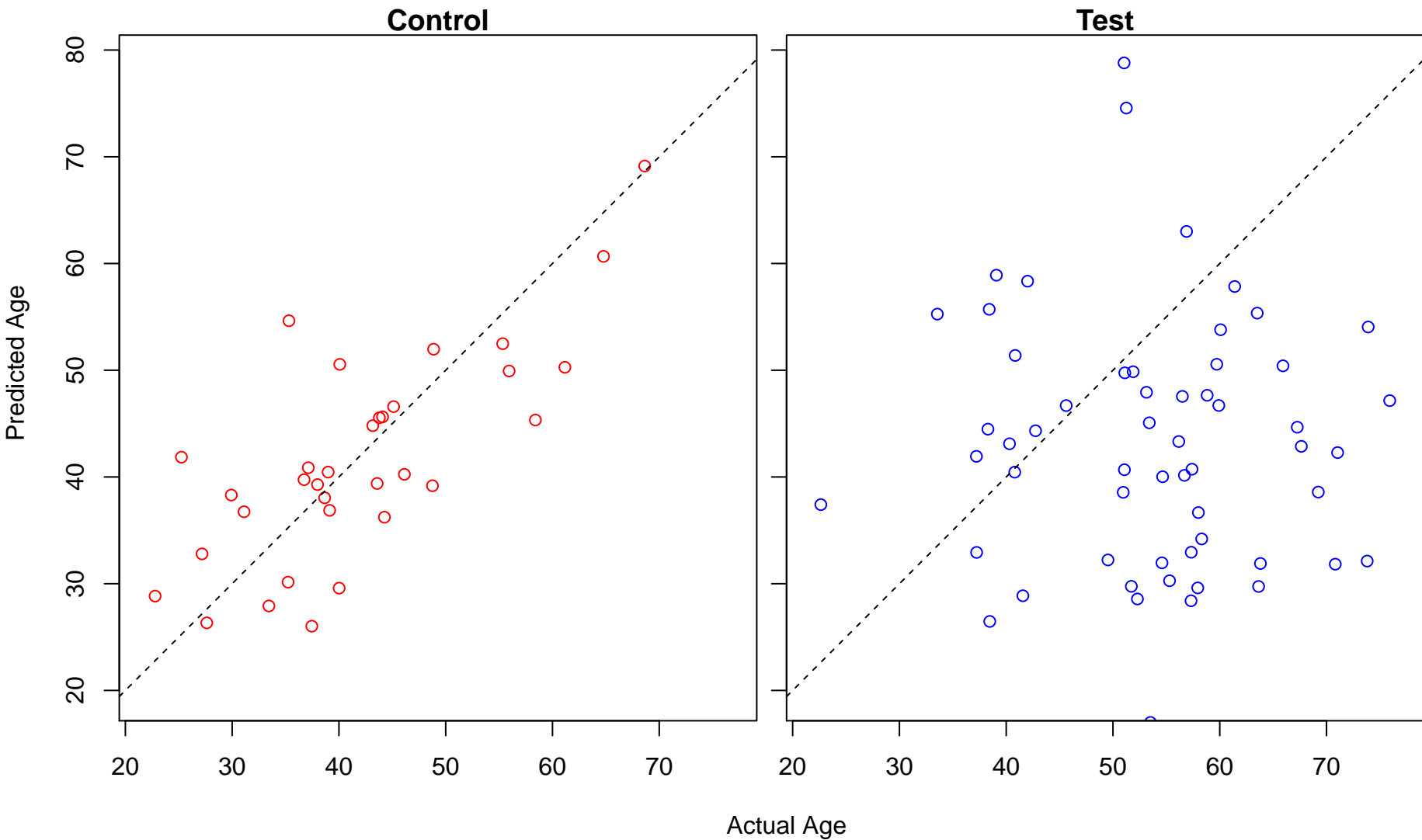
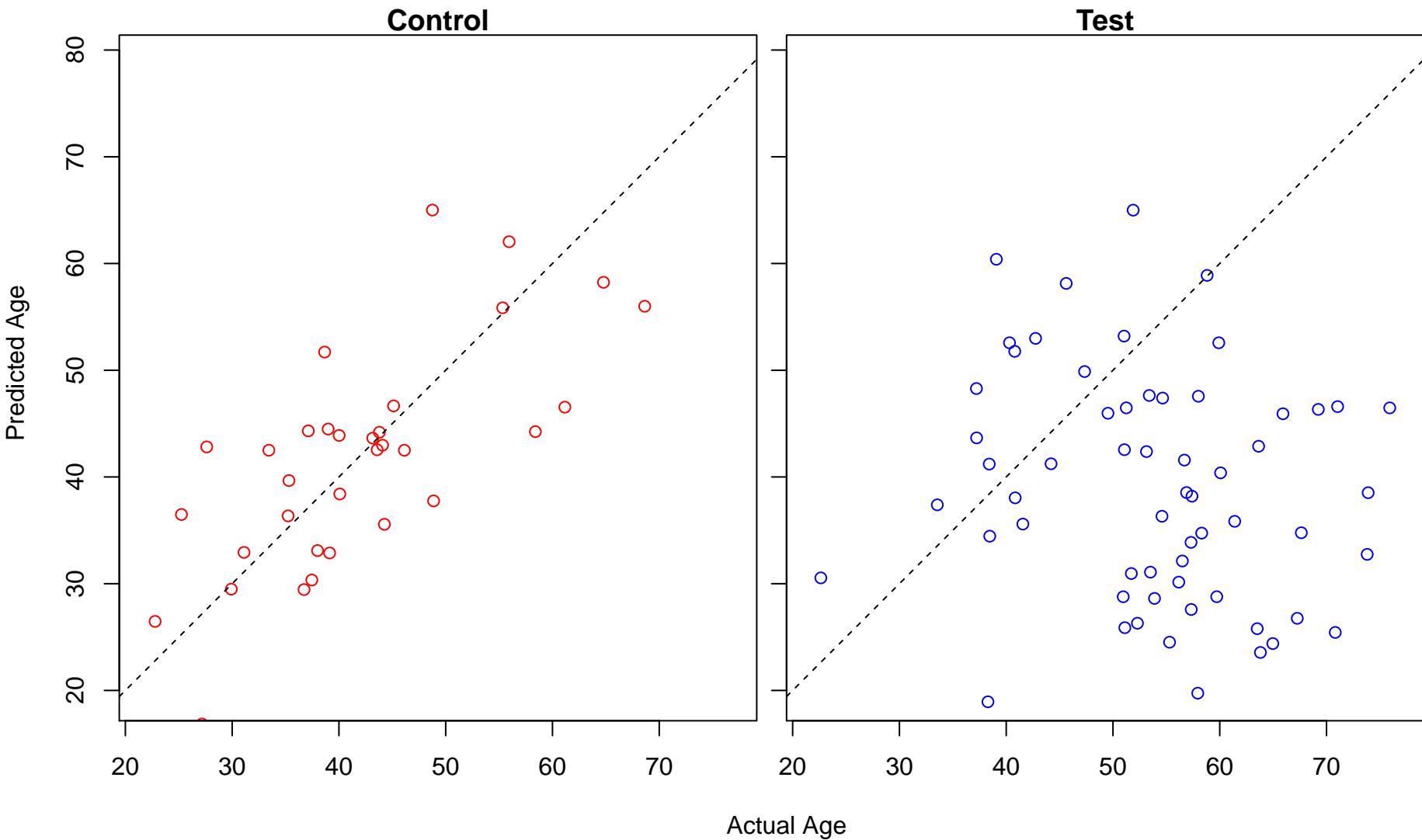


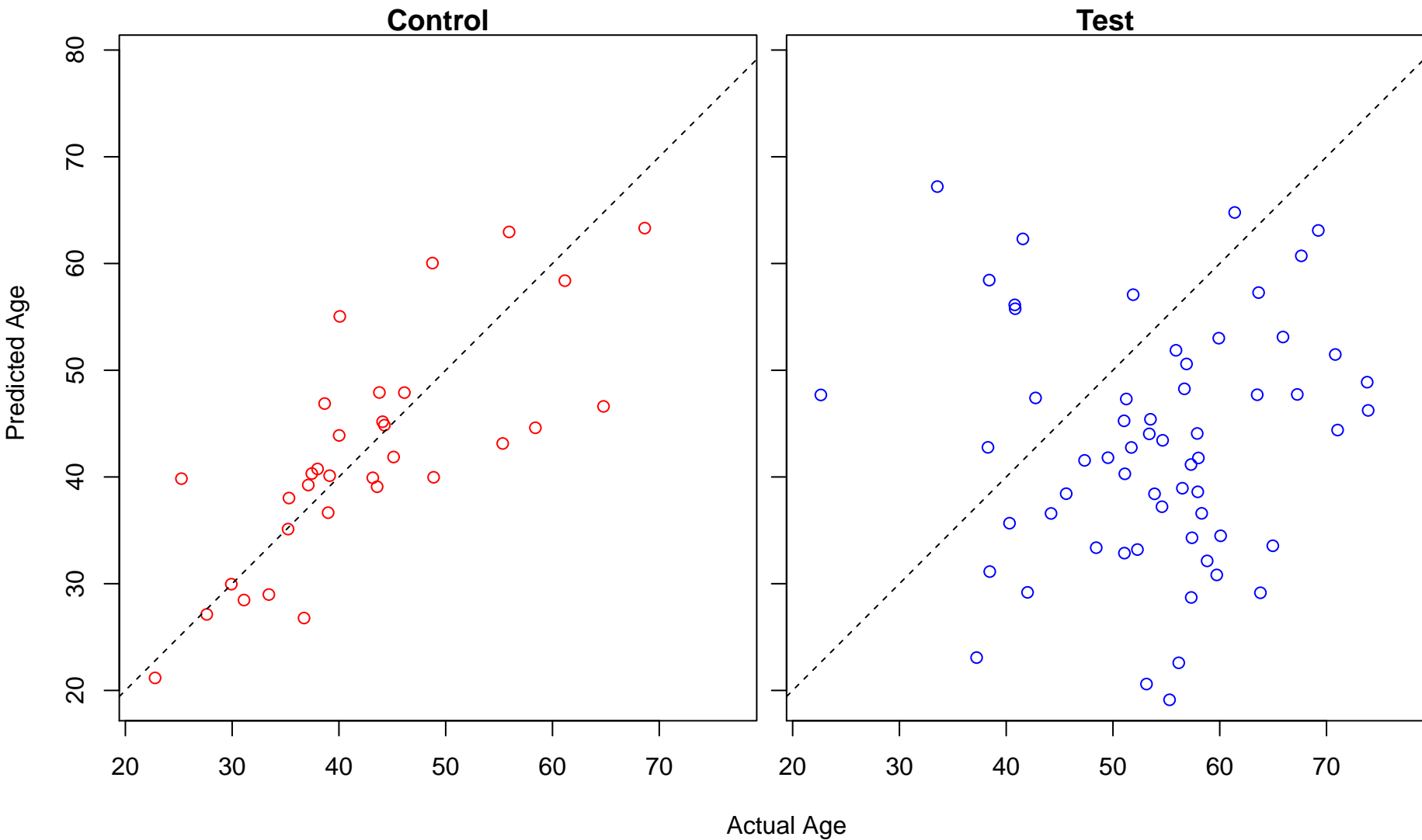
negative regulation of DNA recombination (Score: 4.273286)



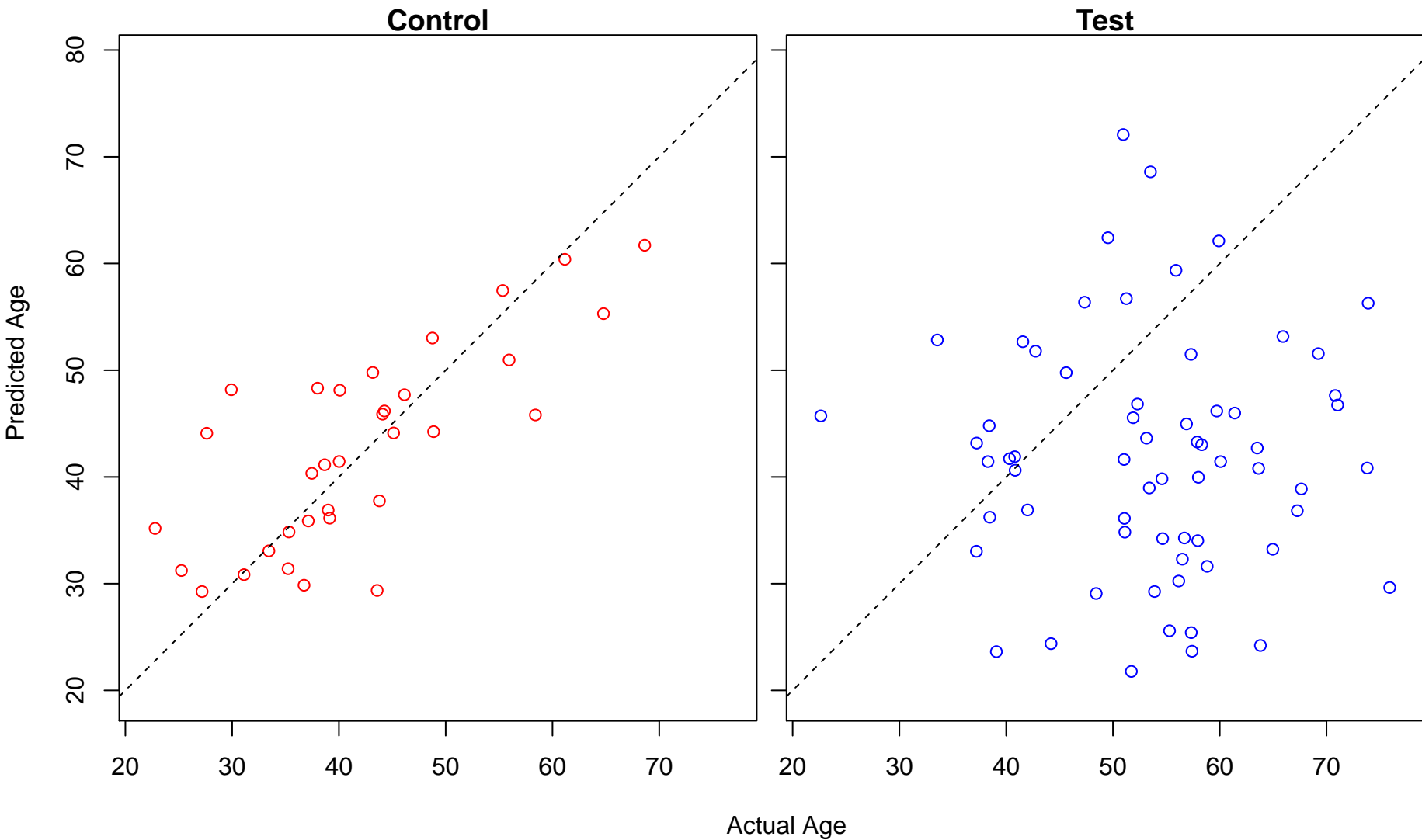
positive regulation of sodium ion transmembrane transport (Score: 3.451872)



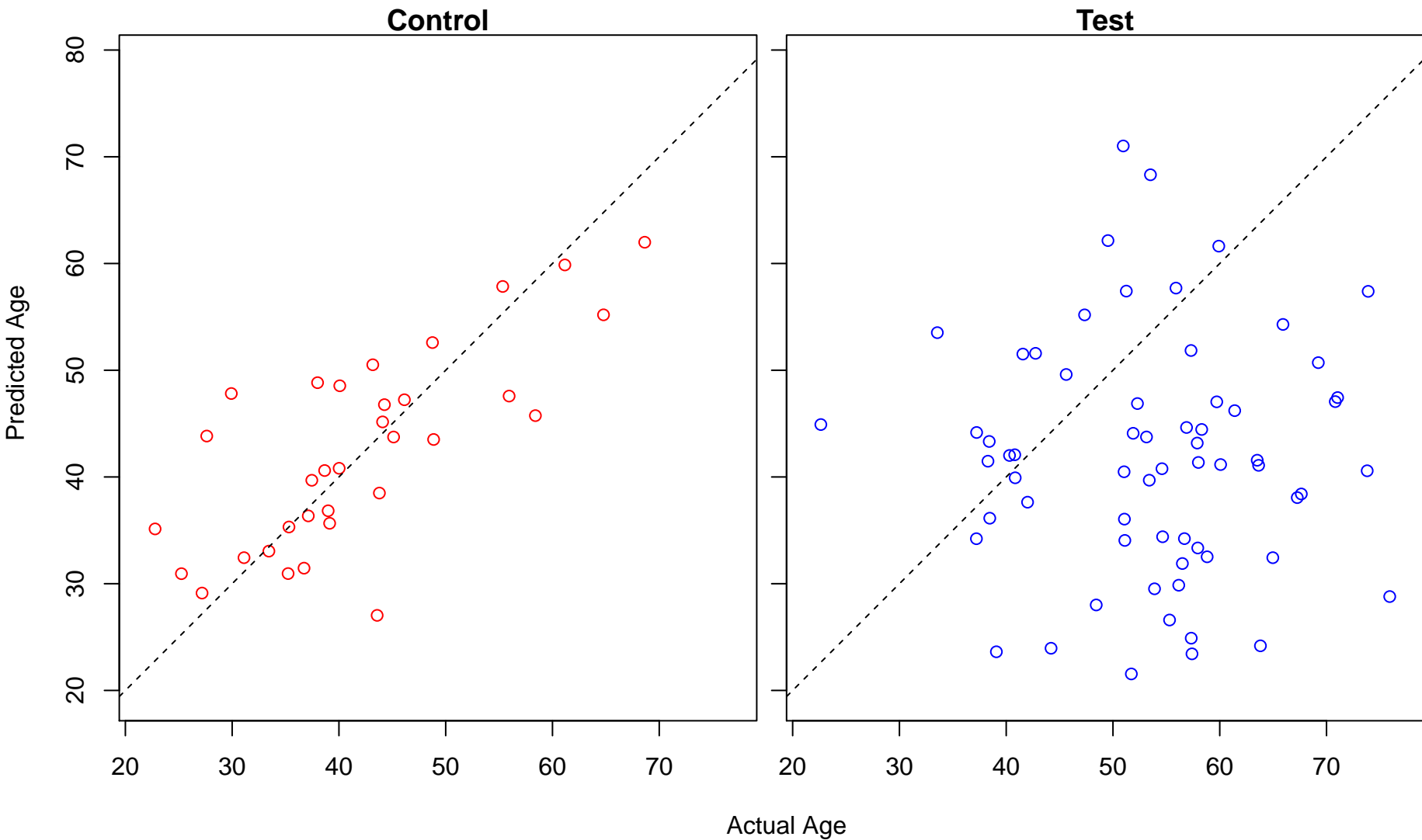
telomere maintenance via recombination (Score: 3.421698)



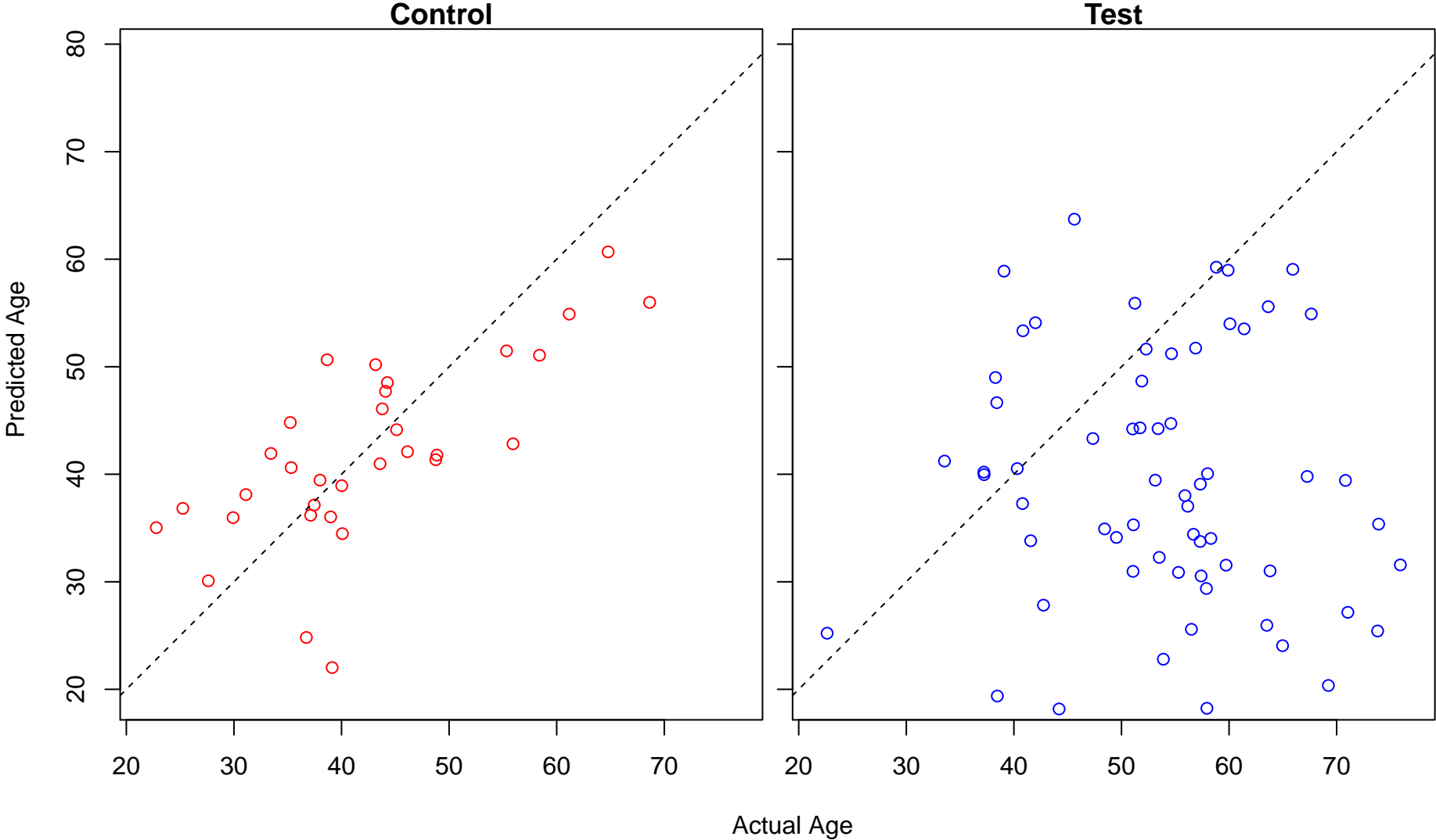
phototransduction, visible light (Score: 3.375049)



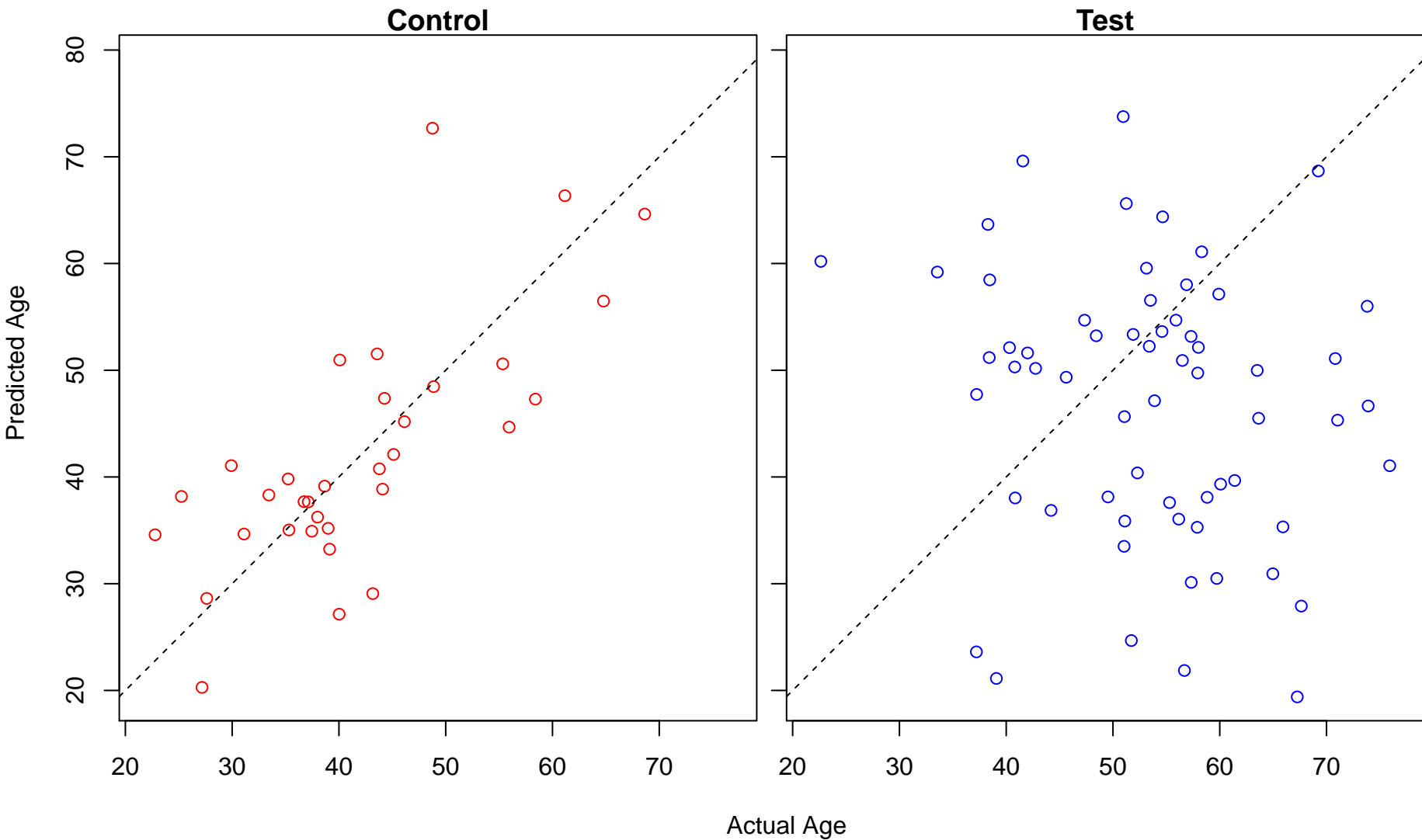
phototransduction (Score: 3.215275)



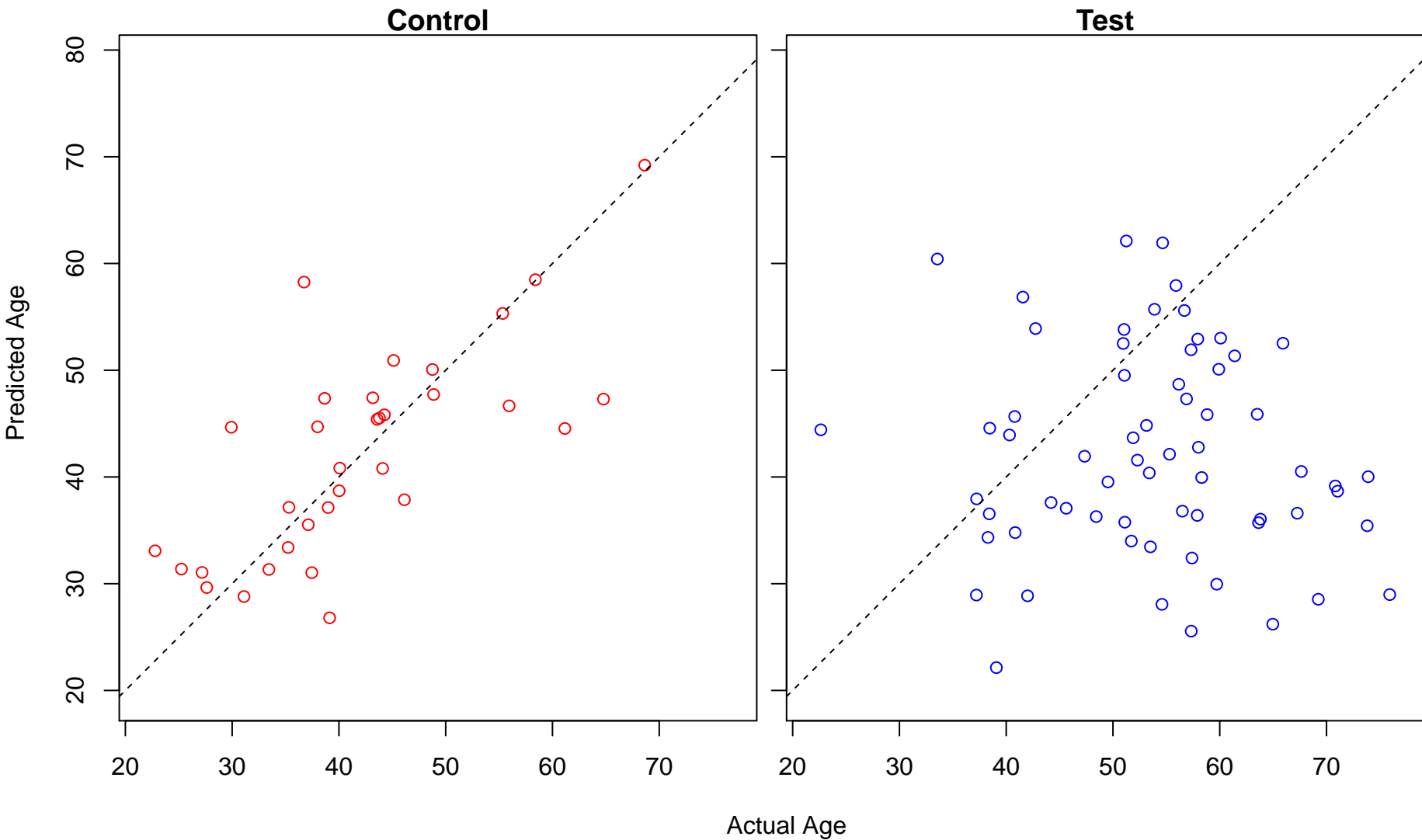
negative regulation of transcription from RNA polymerase II promoter in response to stress (Score: 3.07)



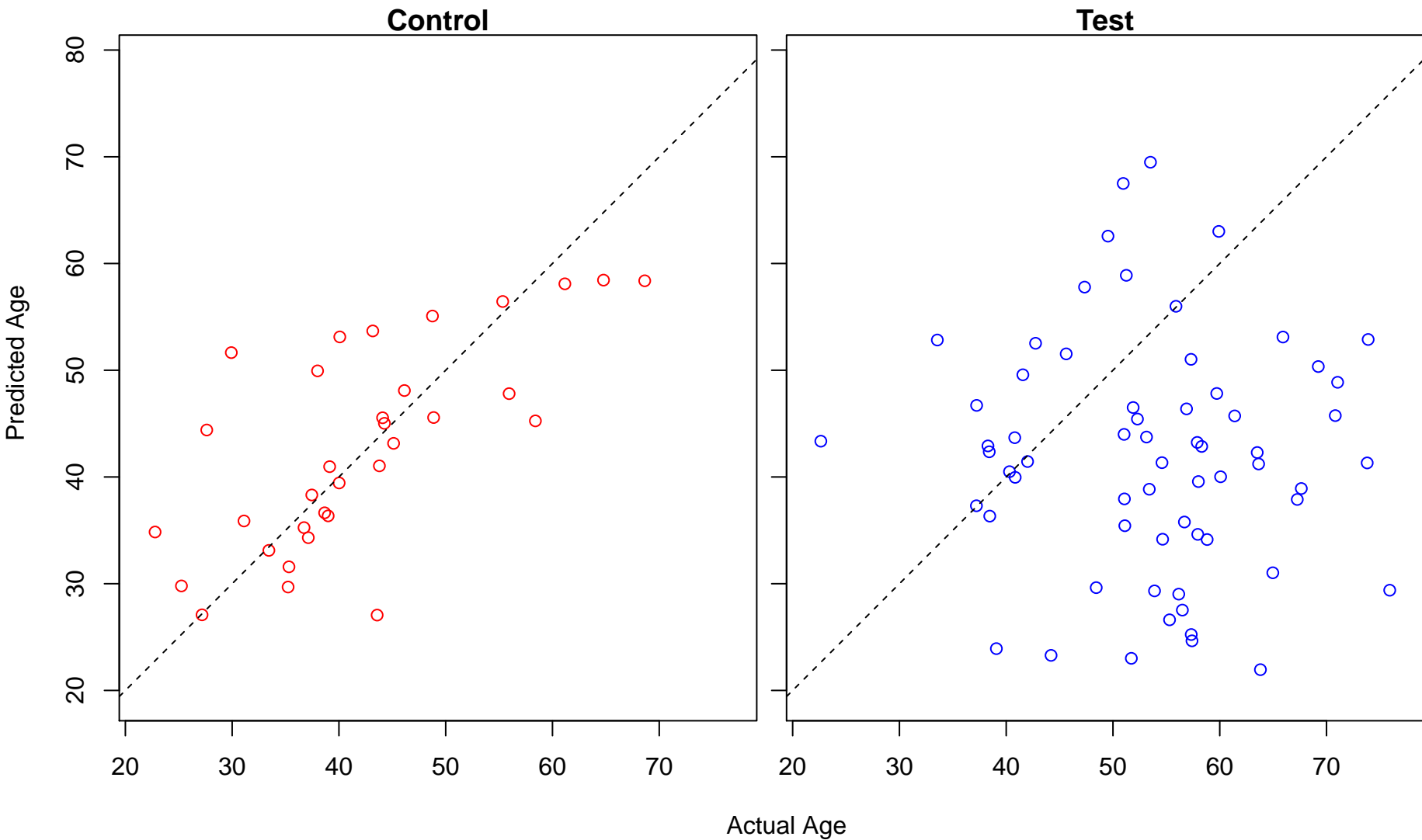
regulation of epidermal growth factor receptor signaling pathway (Score: 3.039390)



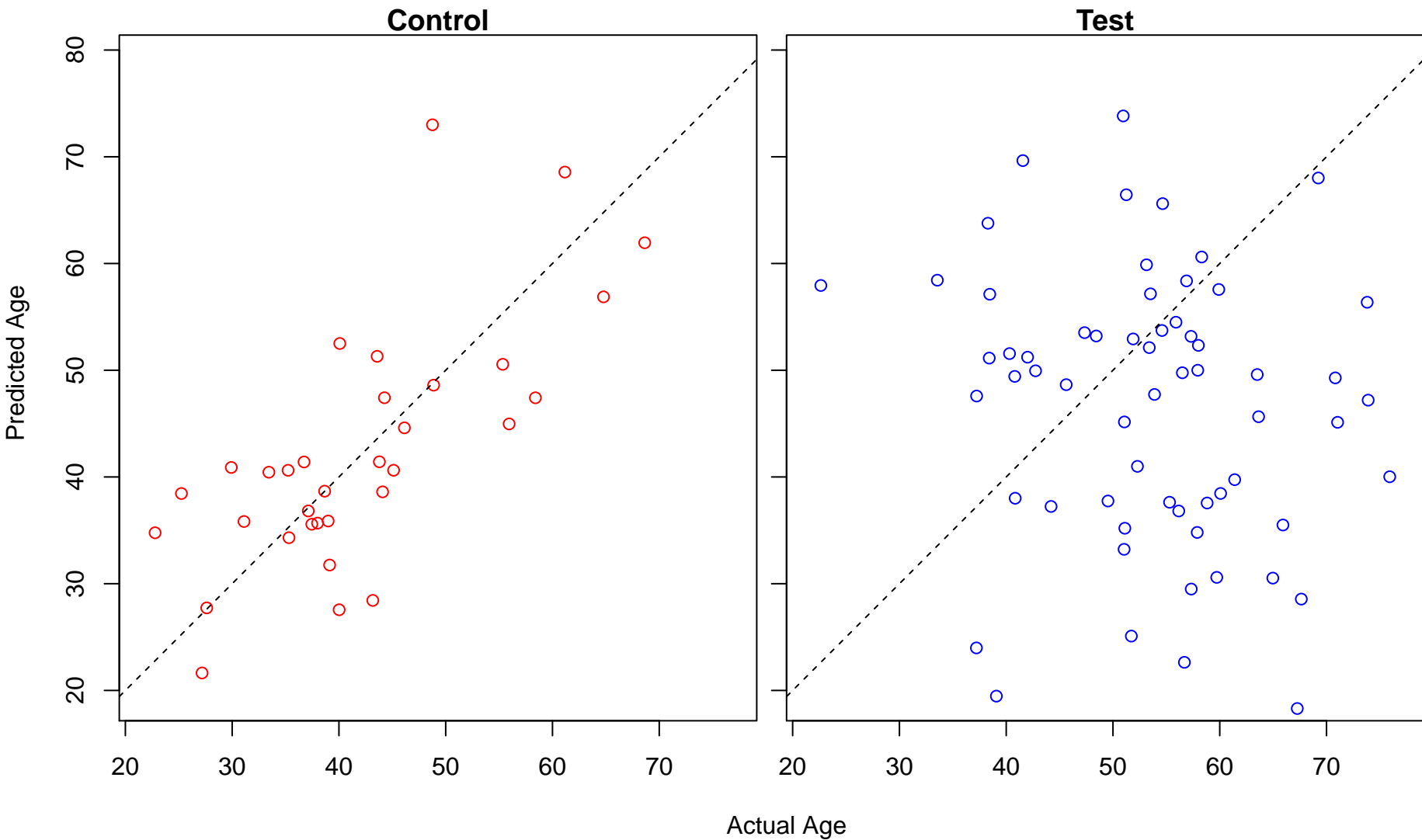
tumor necrosis factor-mediated signaling pathway (Score: 2.893633)



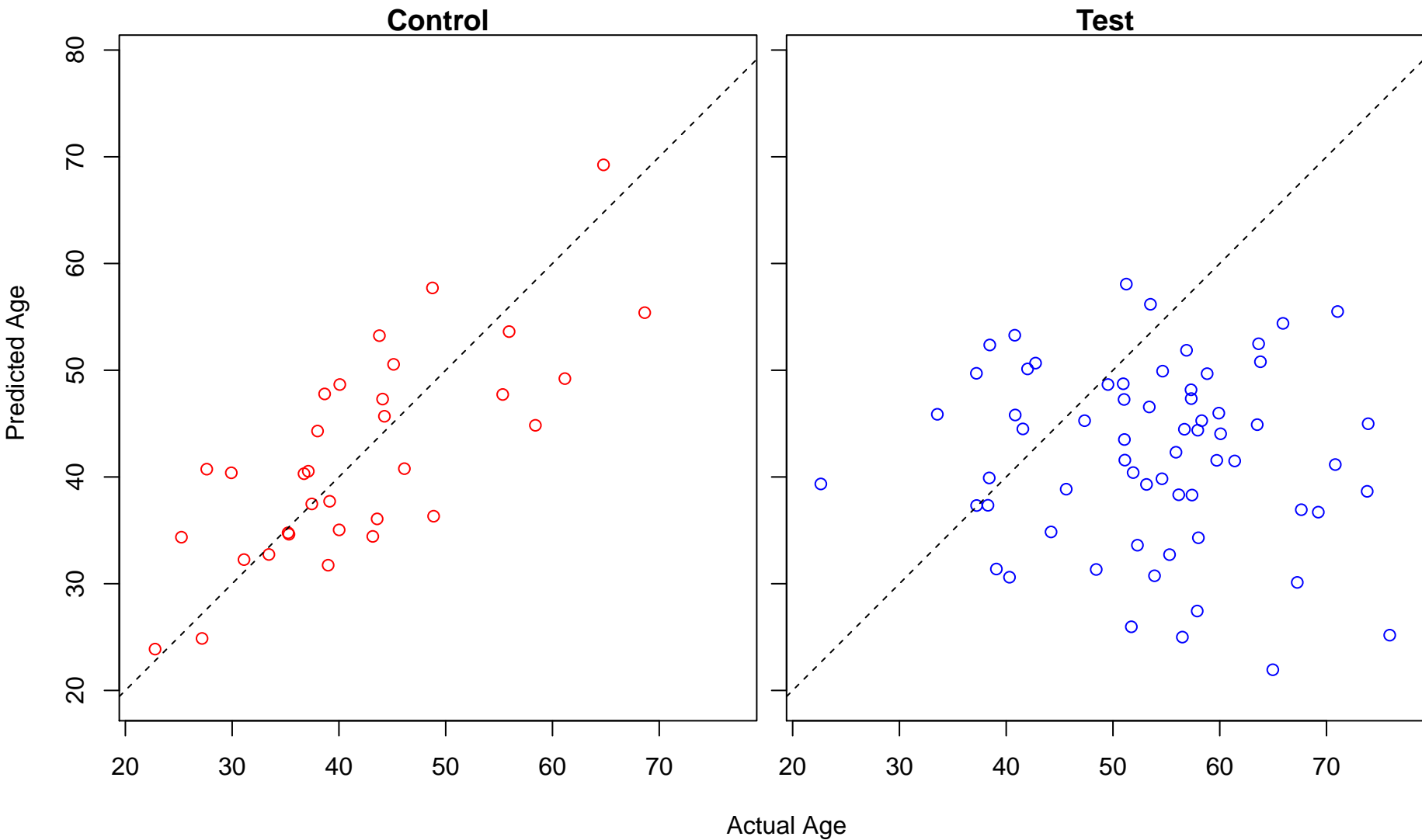
detection of visible light (Score: 2.885637)



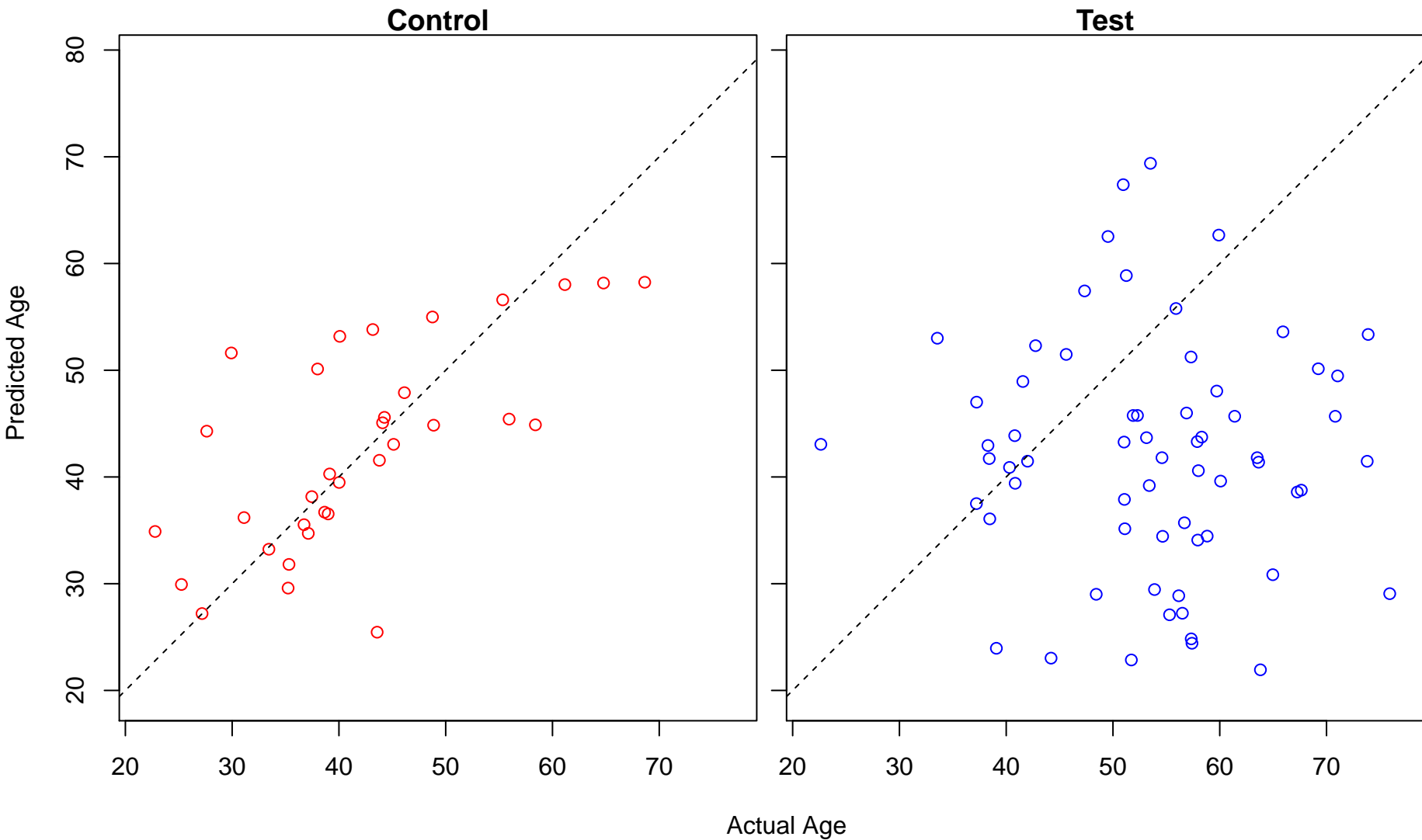
regulation of ERBB signaling pathway (Score: 2.843452)



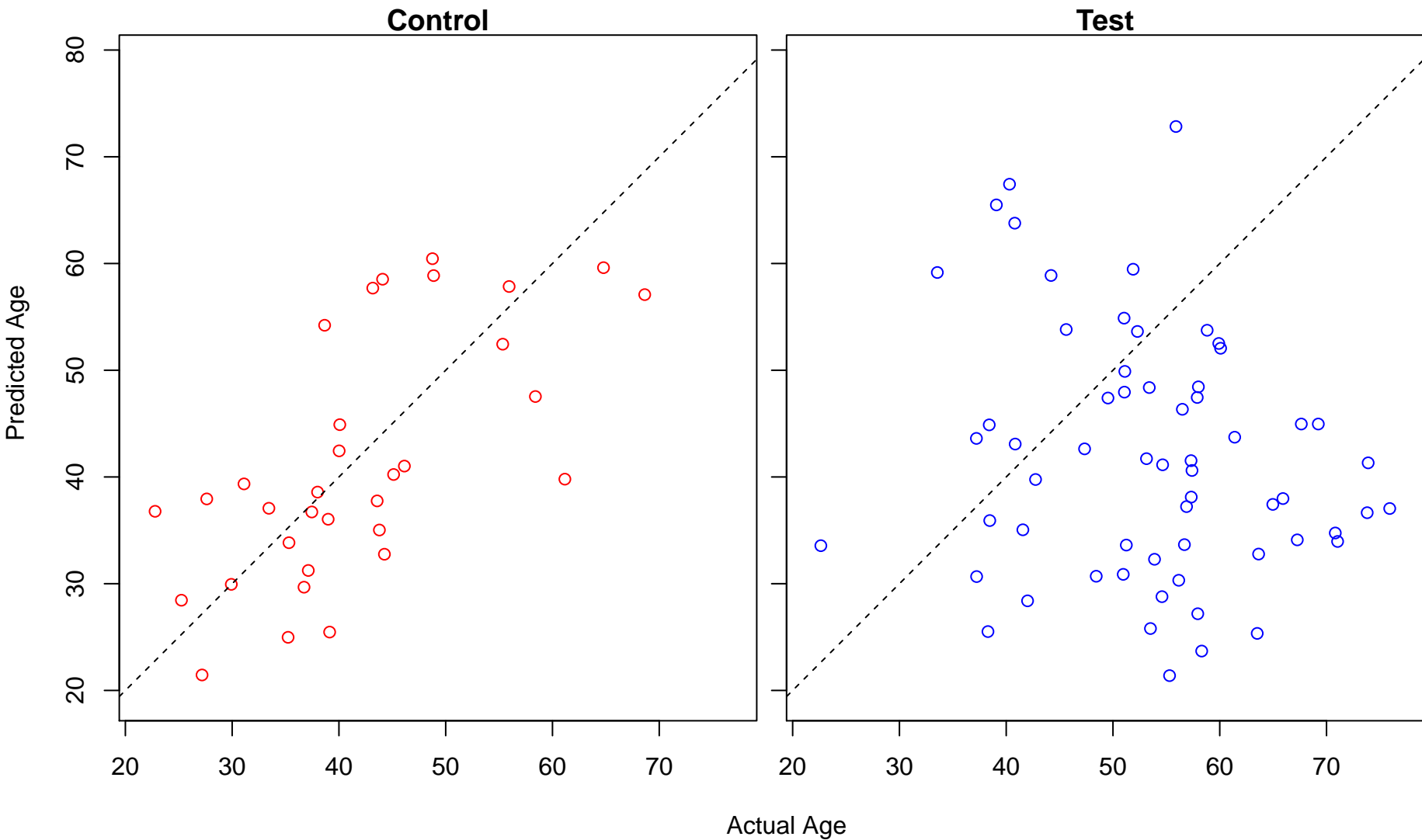
ammonium ion metabolic process (Score: 2.782018)



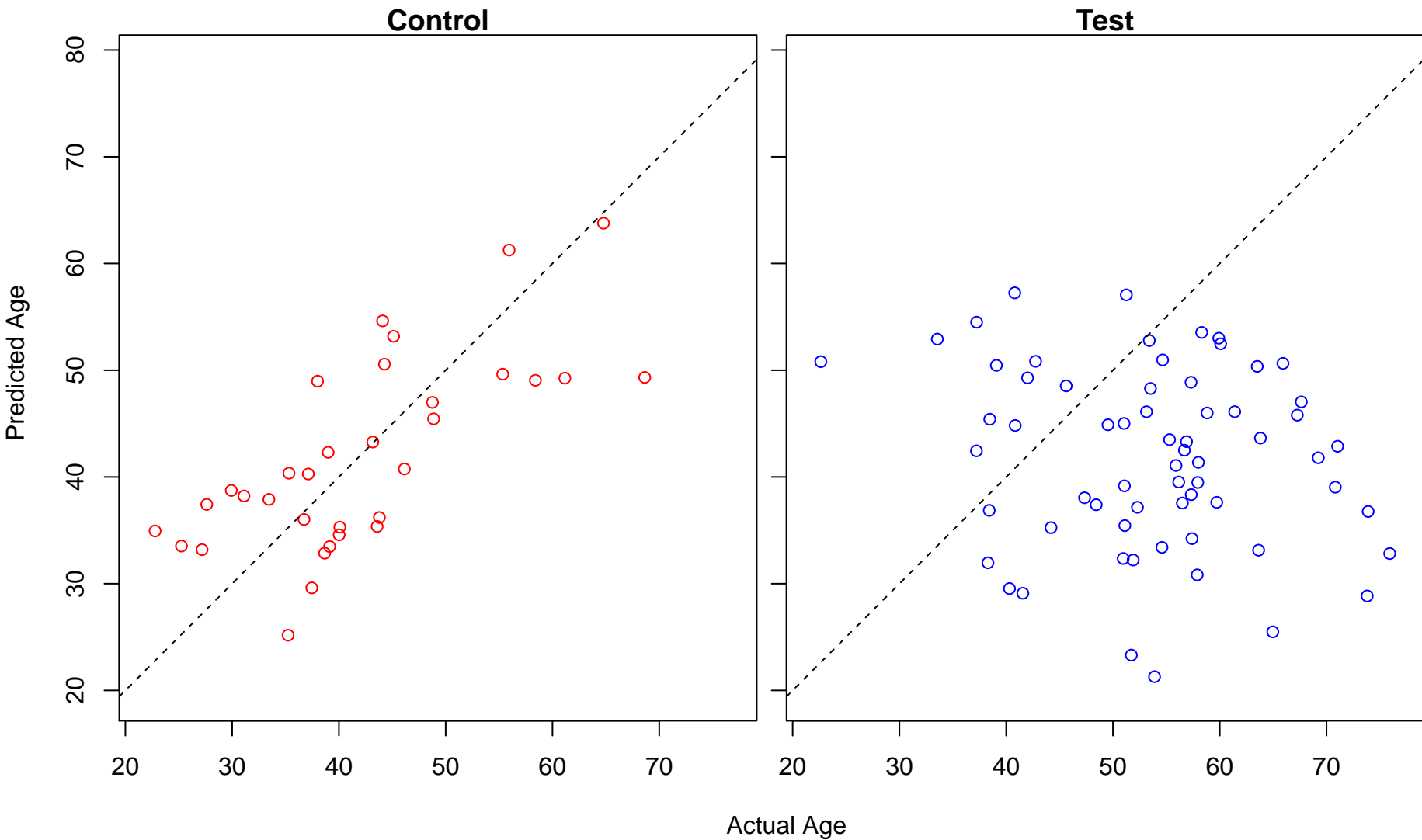
detection of light stimulus (Score: 2.766865)



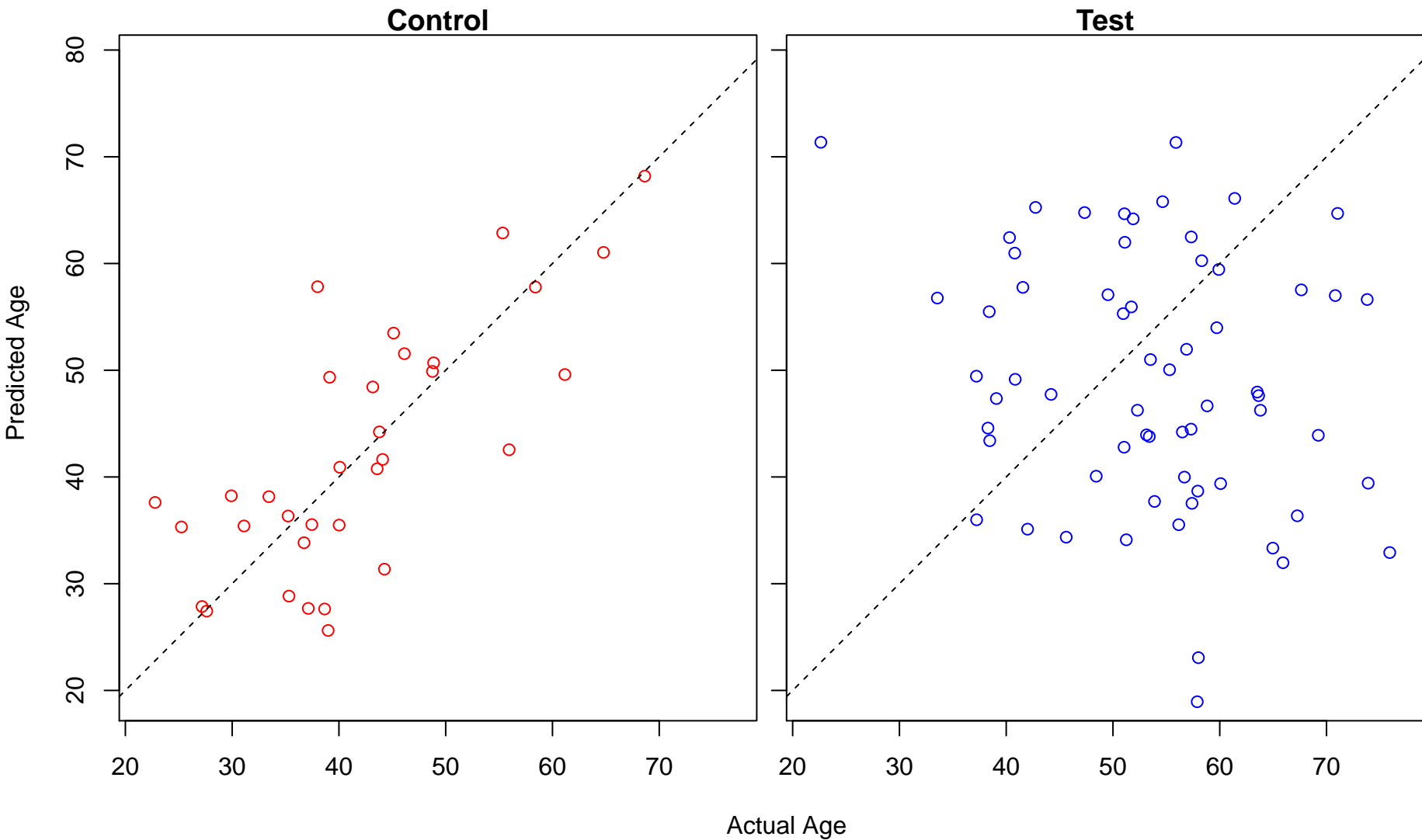
regulation of sodium ion transmembrane transporter activity (Score: 2.718957)



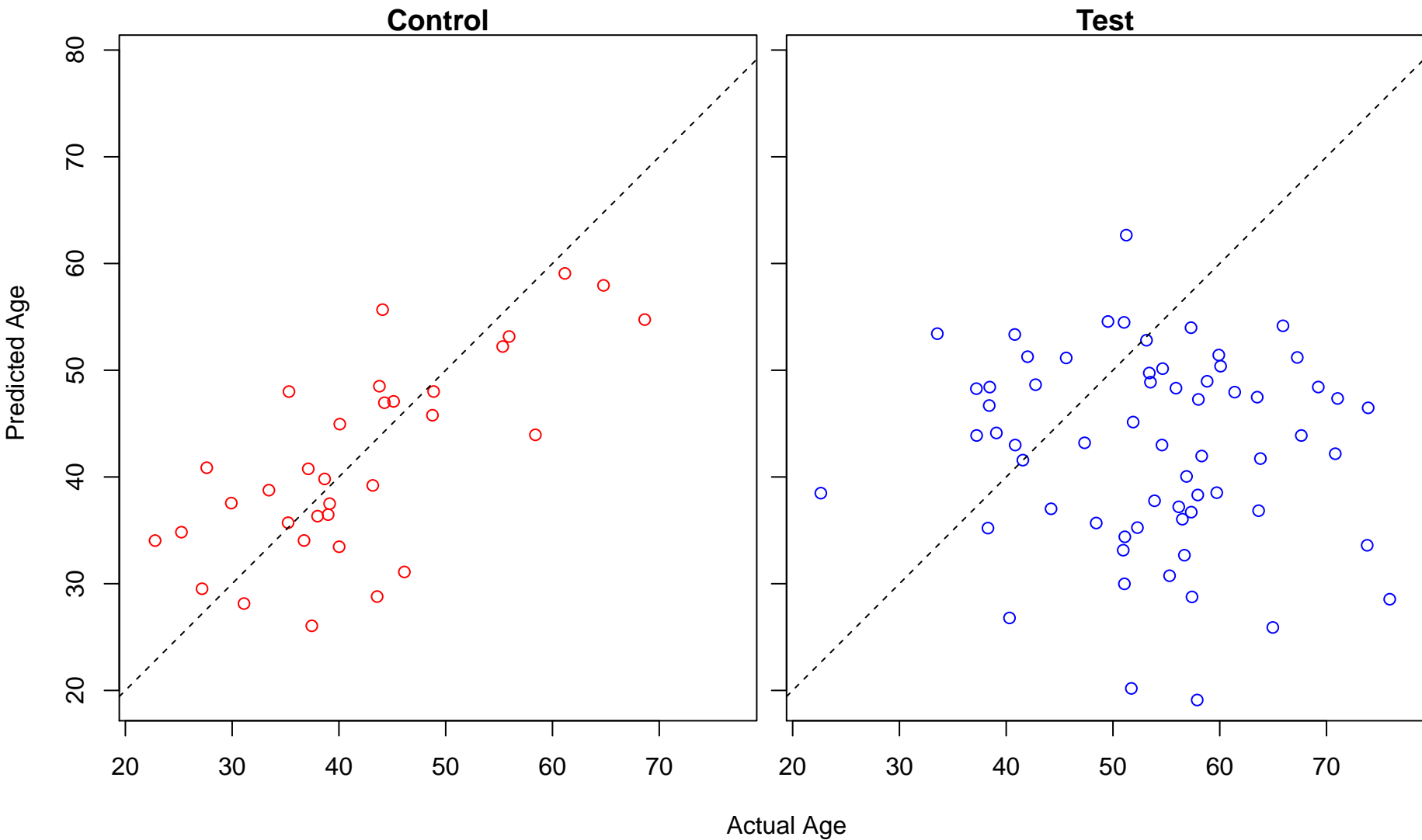
intestinal absorption (Score: 2.665336)



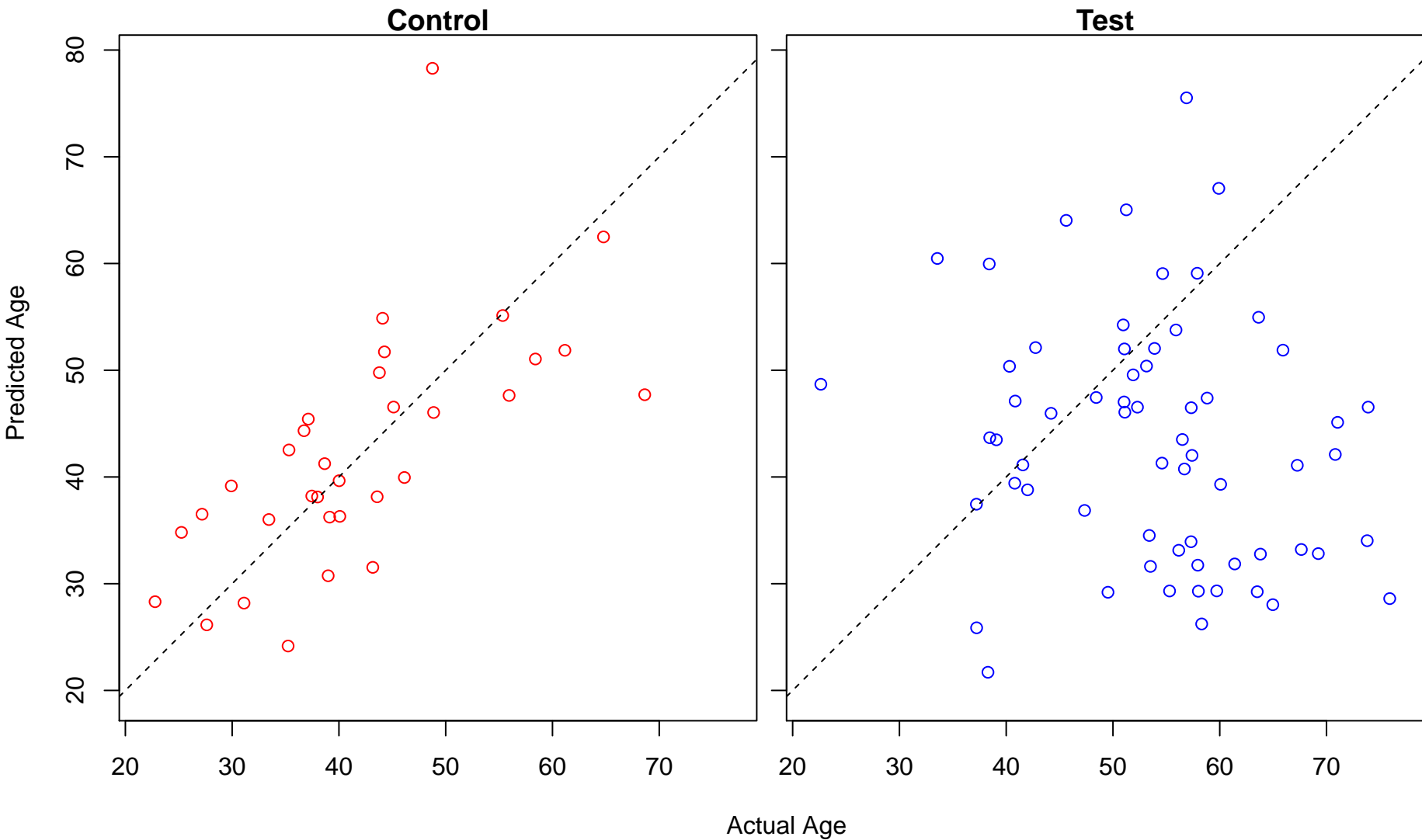
negative regulation of cation channel activity (Score: 2.638297)



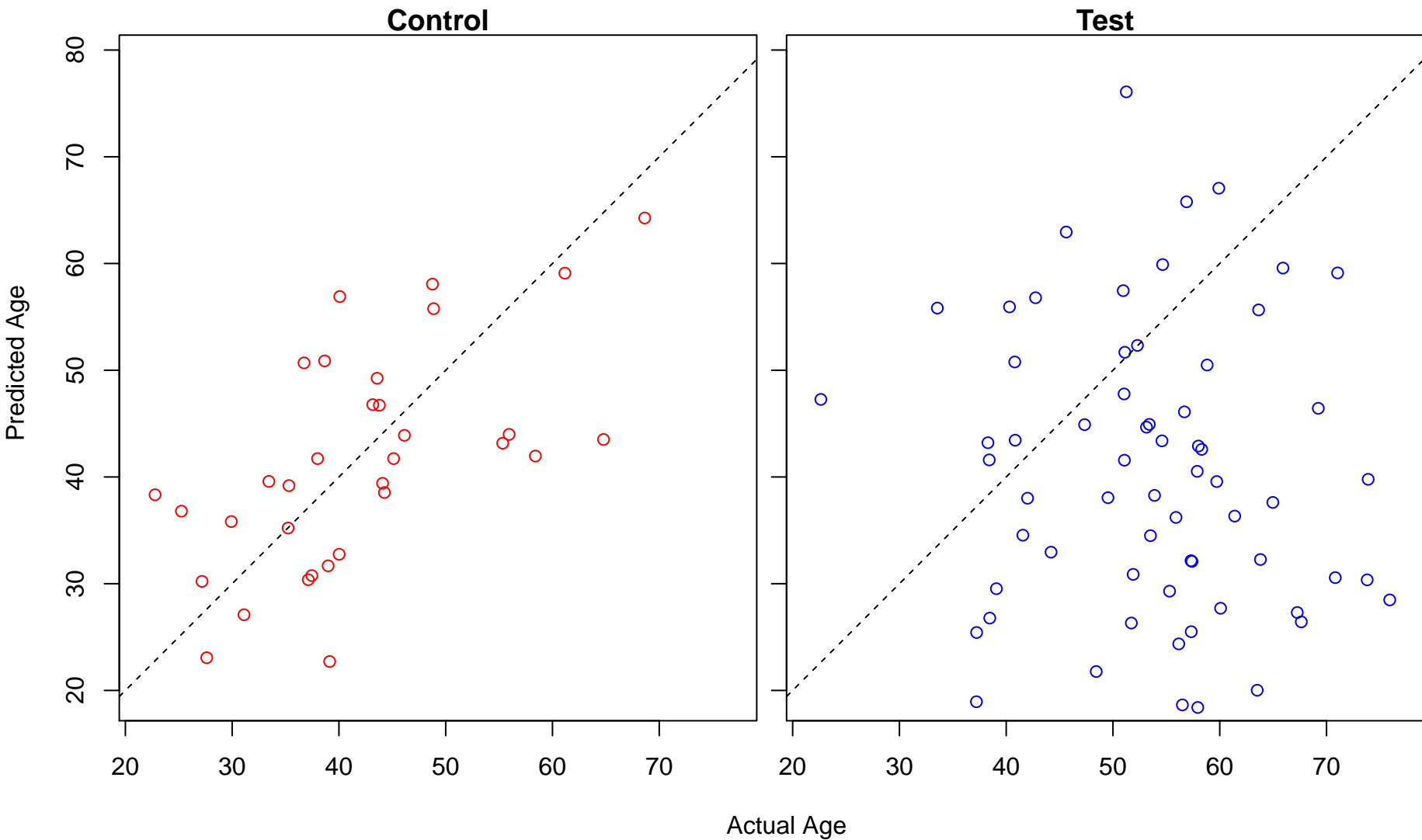
digestion (Score: 2.595113)



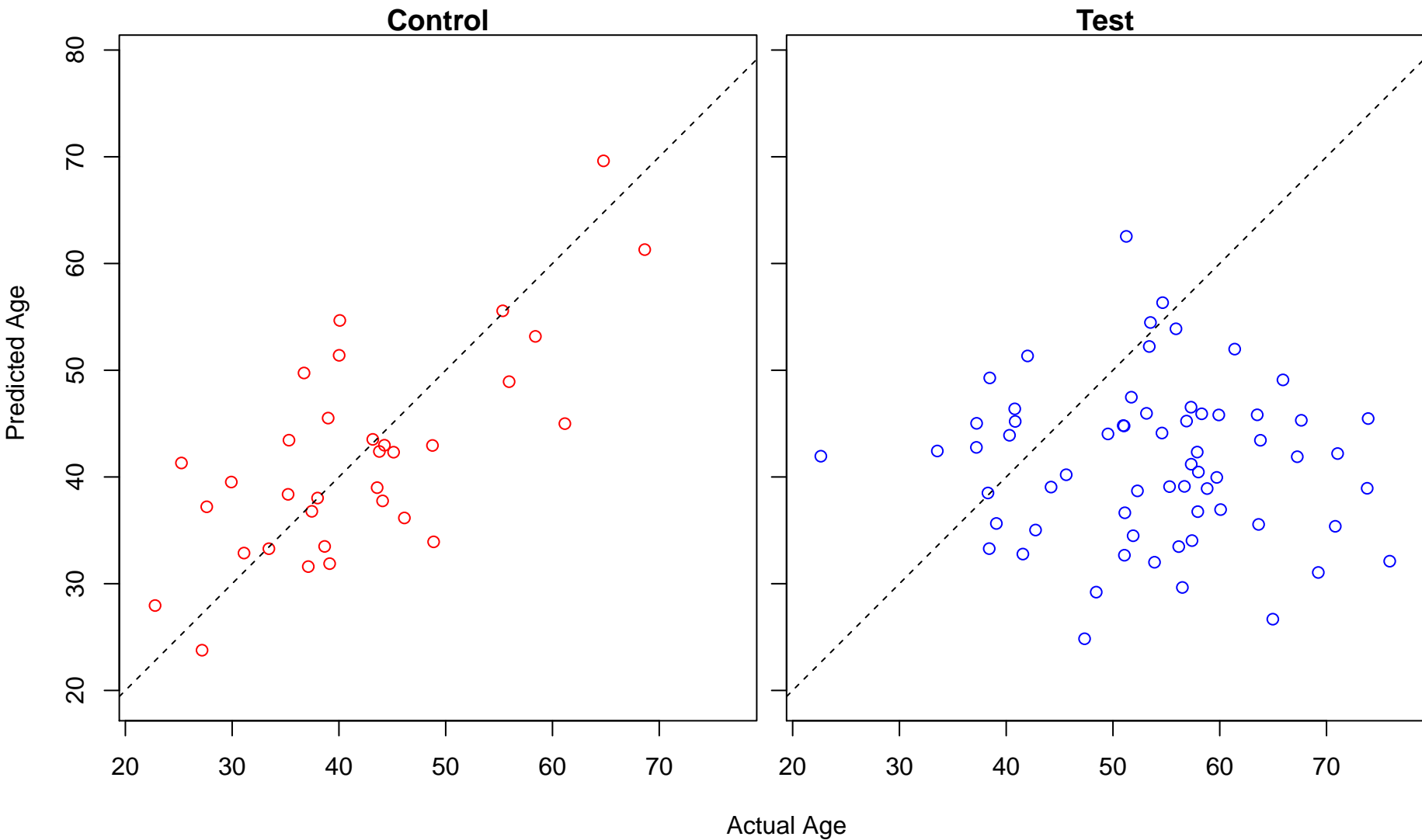
negative regulation of protein acetylation (Score: 2.551901)



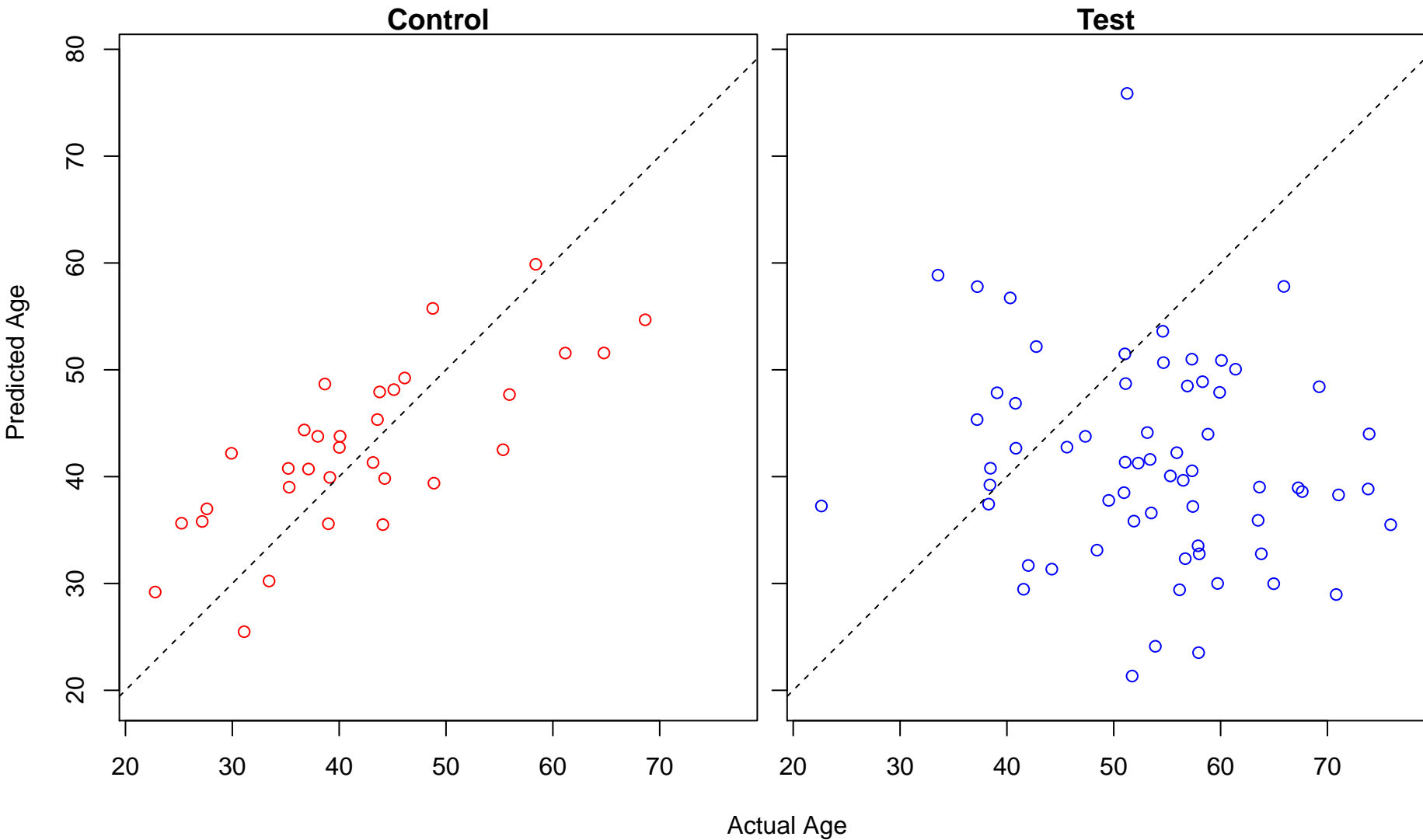
regulation of peptidyl-lysine acetylation (Score: 2.538116)



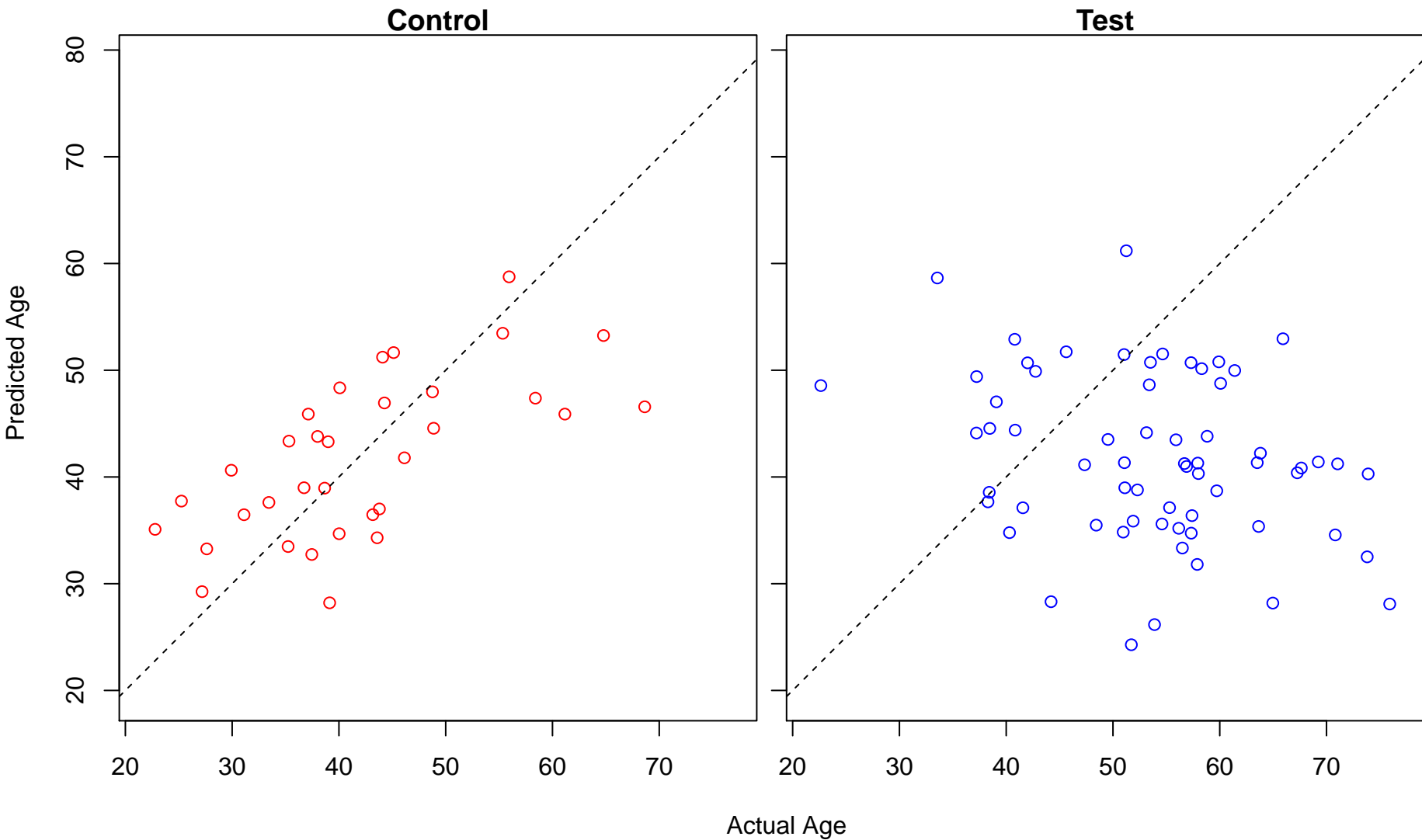
bile acid and bile salt transport (Score: 2.527508)



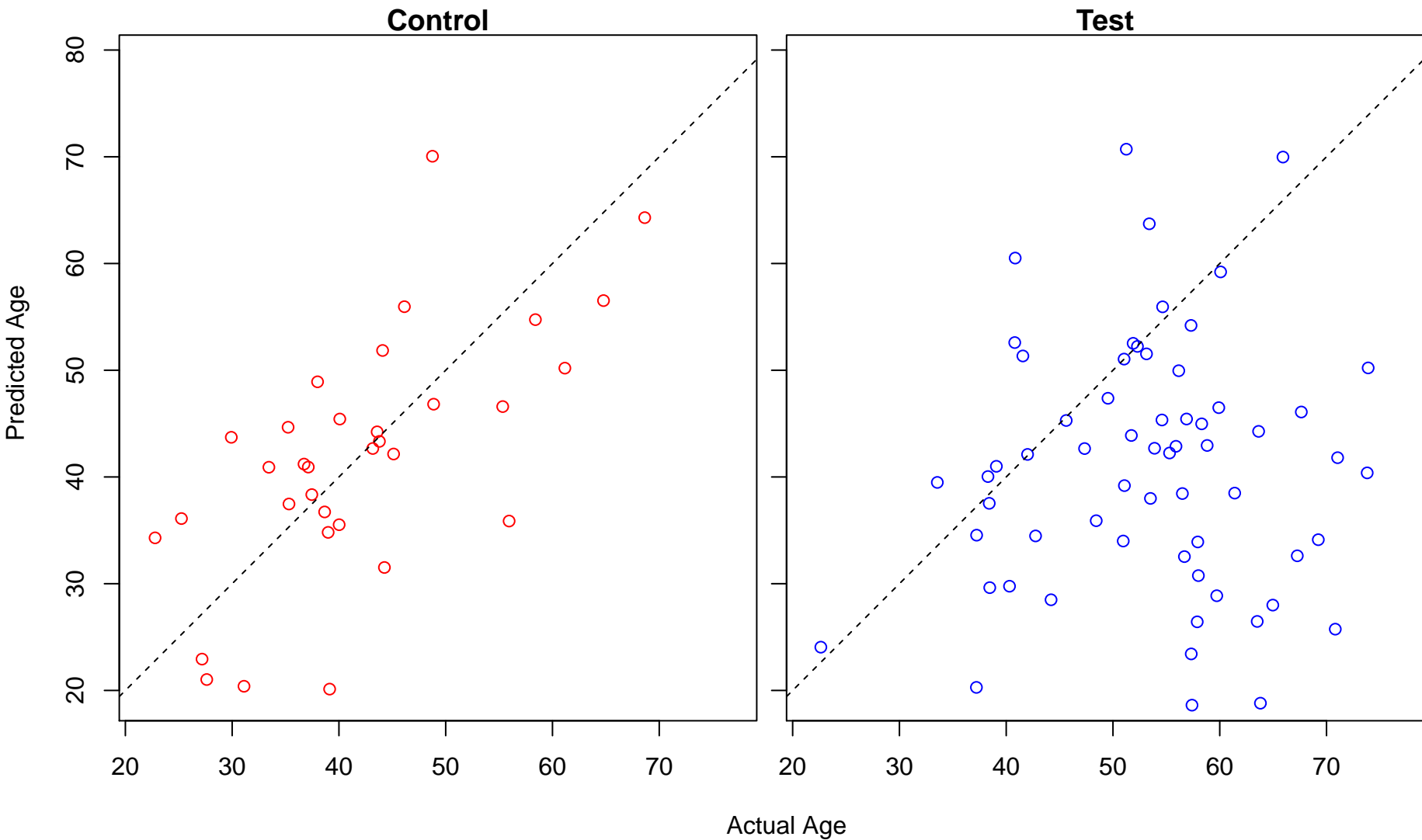
regulation of cholesterol metabolic process (Score: 2.516940)



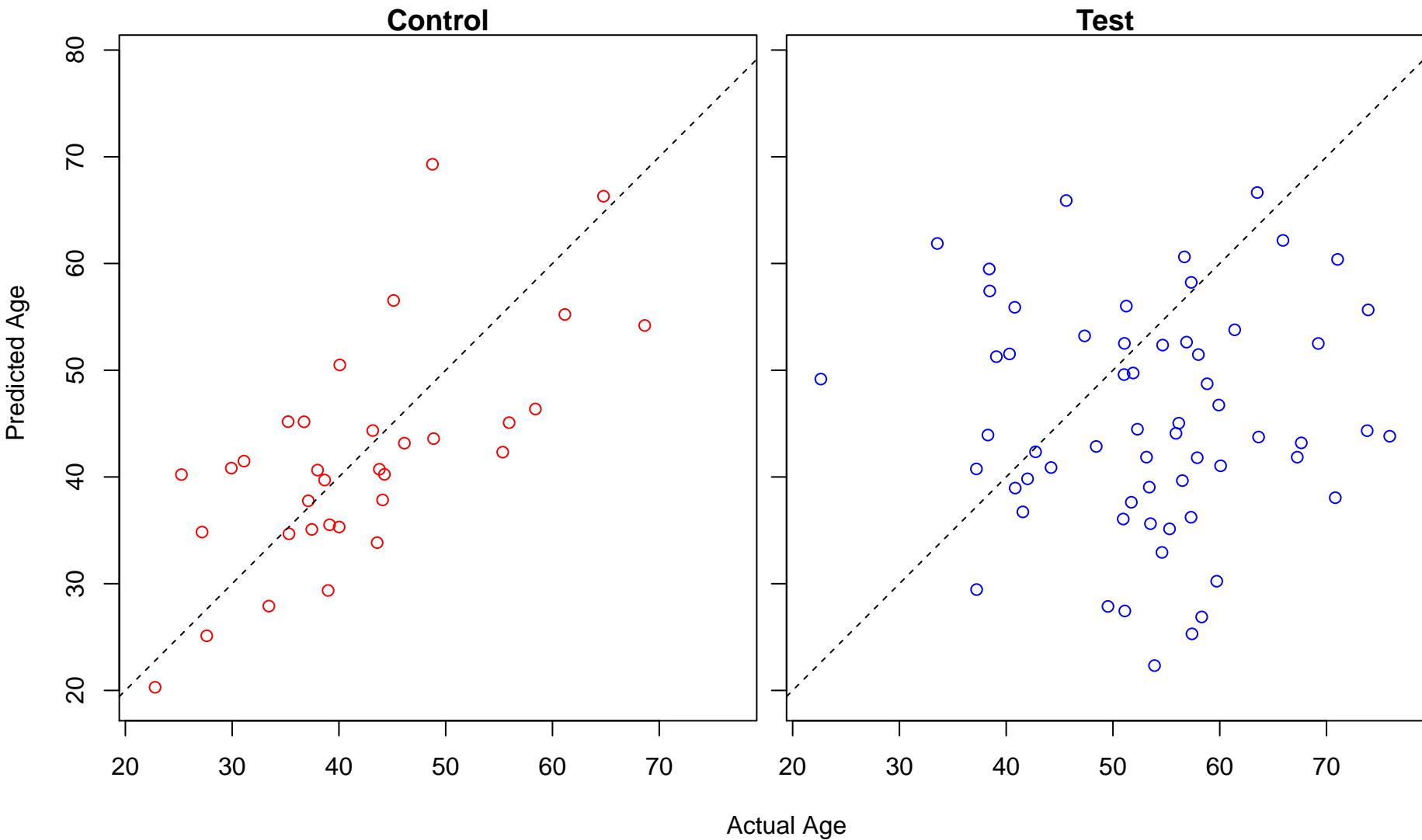
digestive system process (Score: 2.504424)



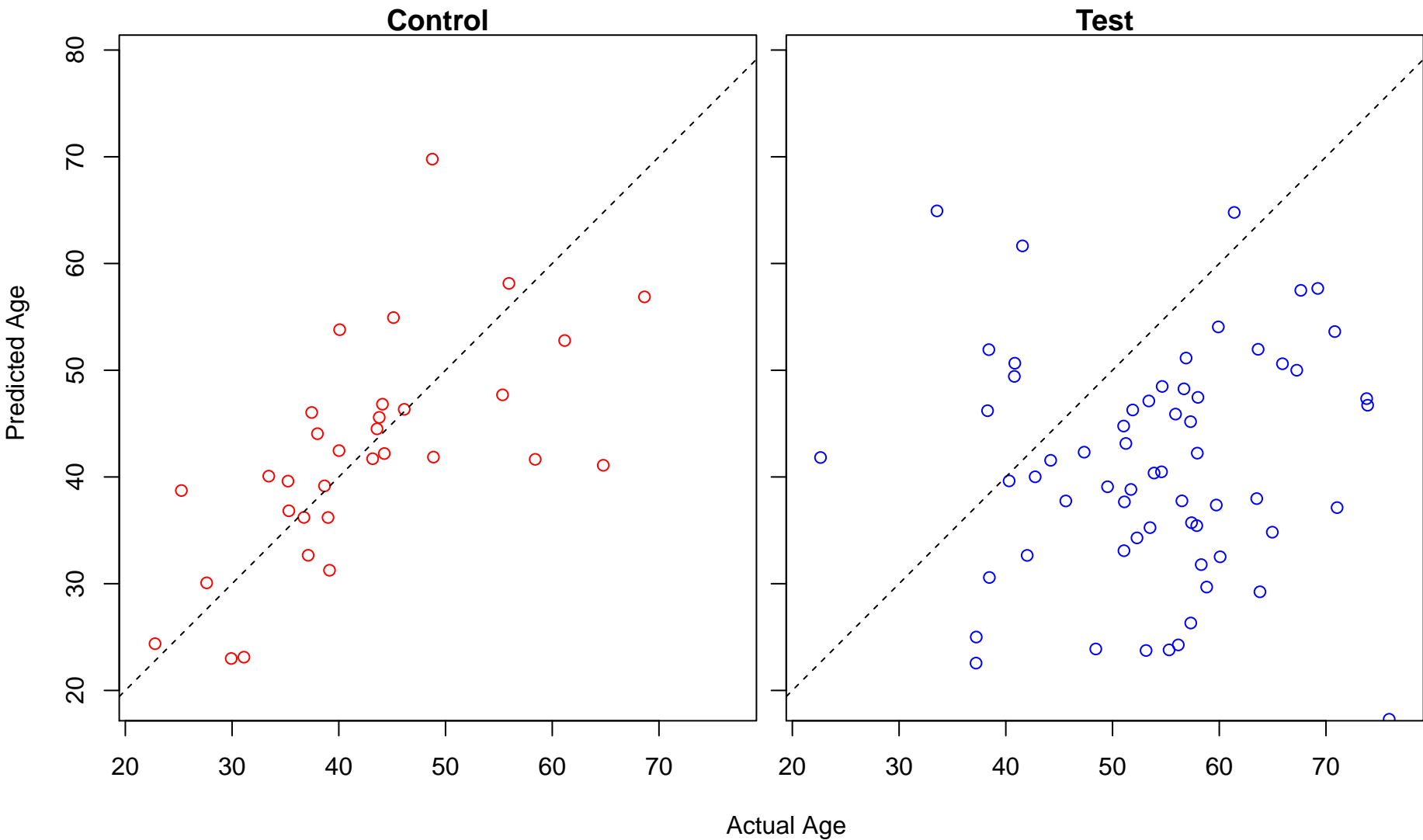
regulation of transcription from RNA polymerase II promoter in response to stress (Score: 2.46520)



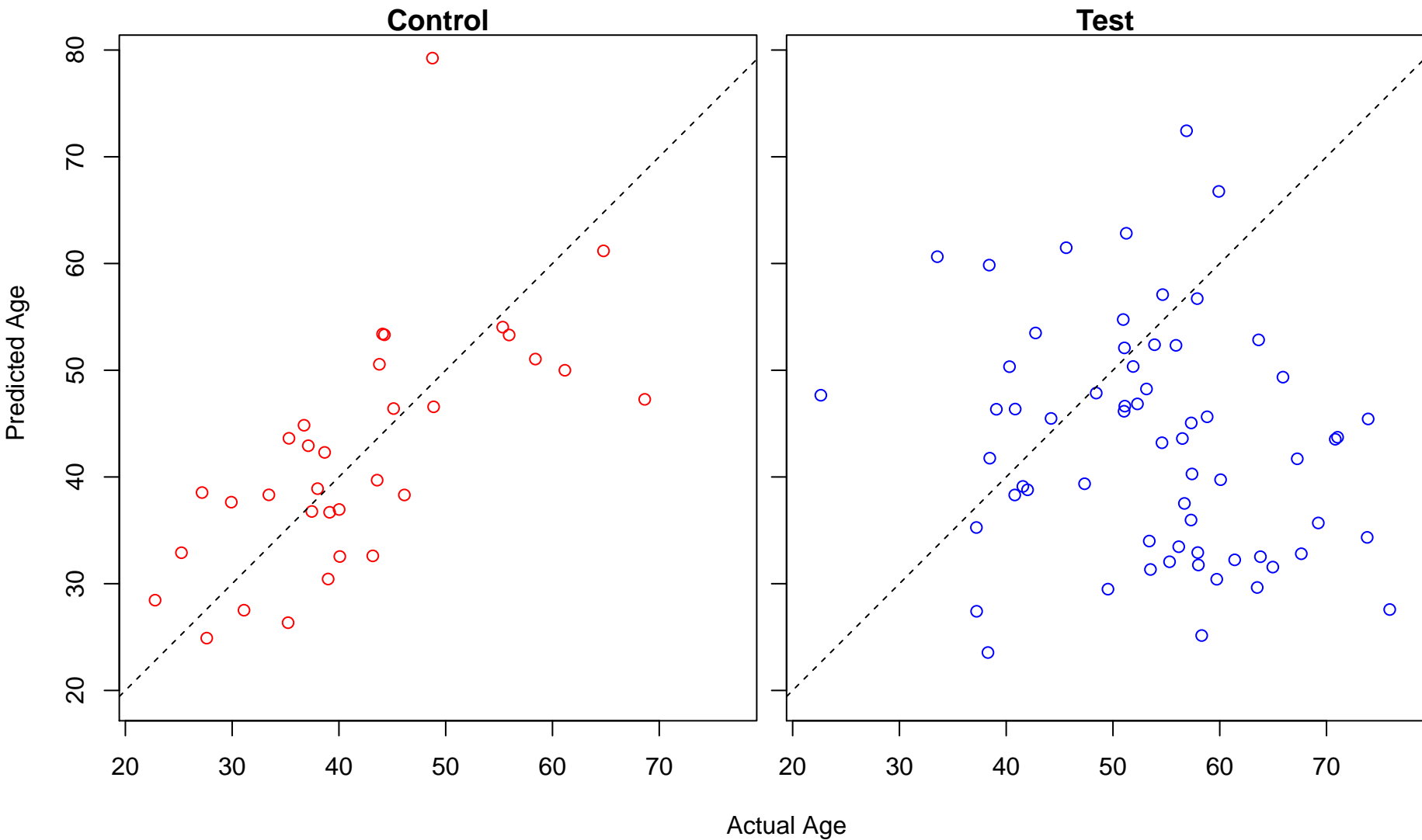
cellular response to biotic stimulus (Score: 2.453184)



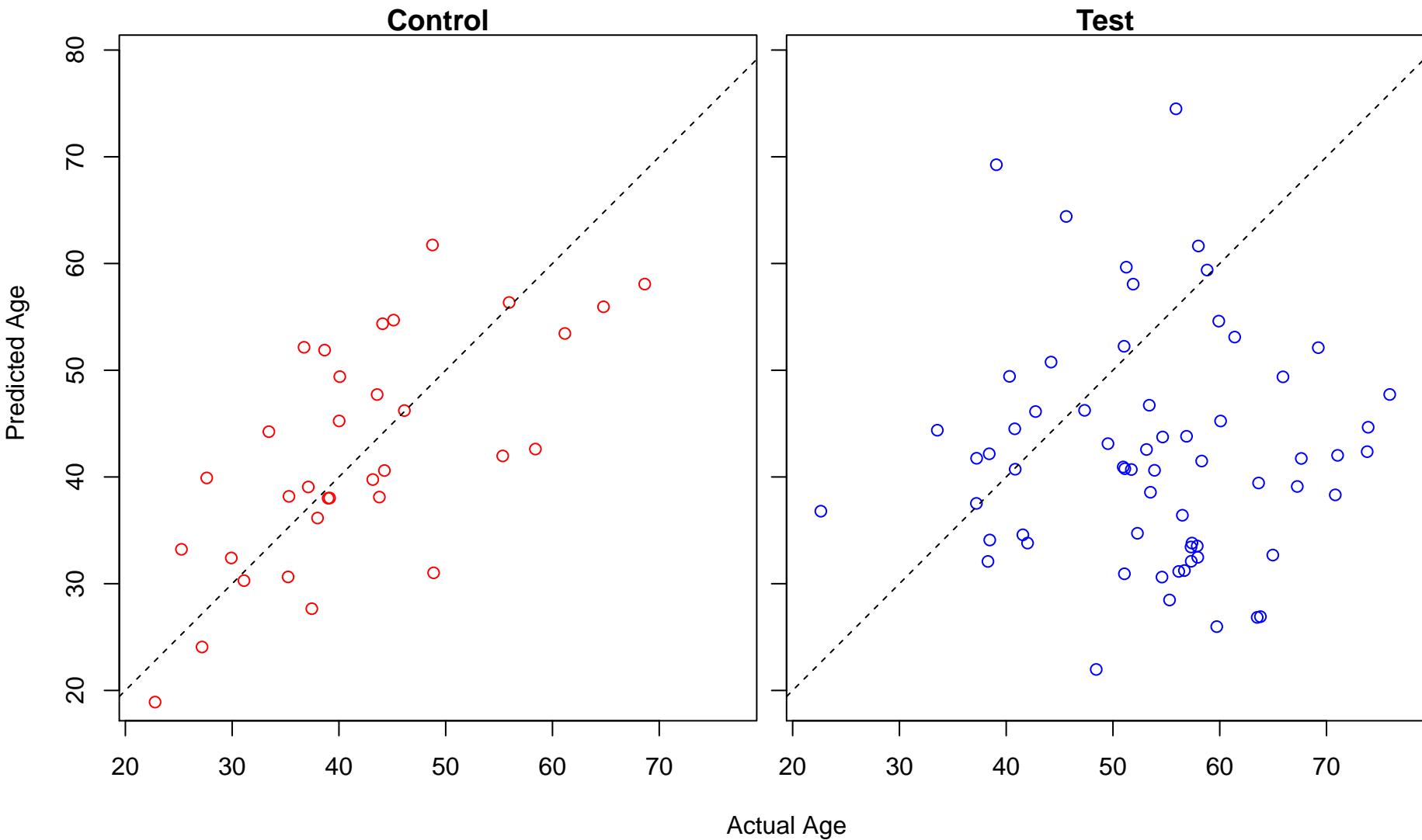
mitotic recombination (Score: 2.446651)



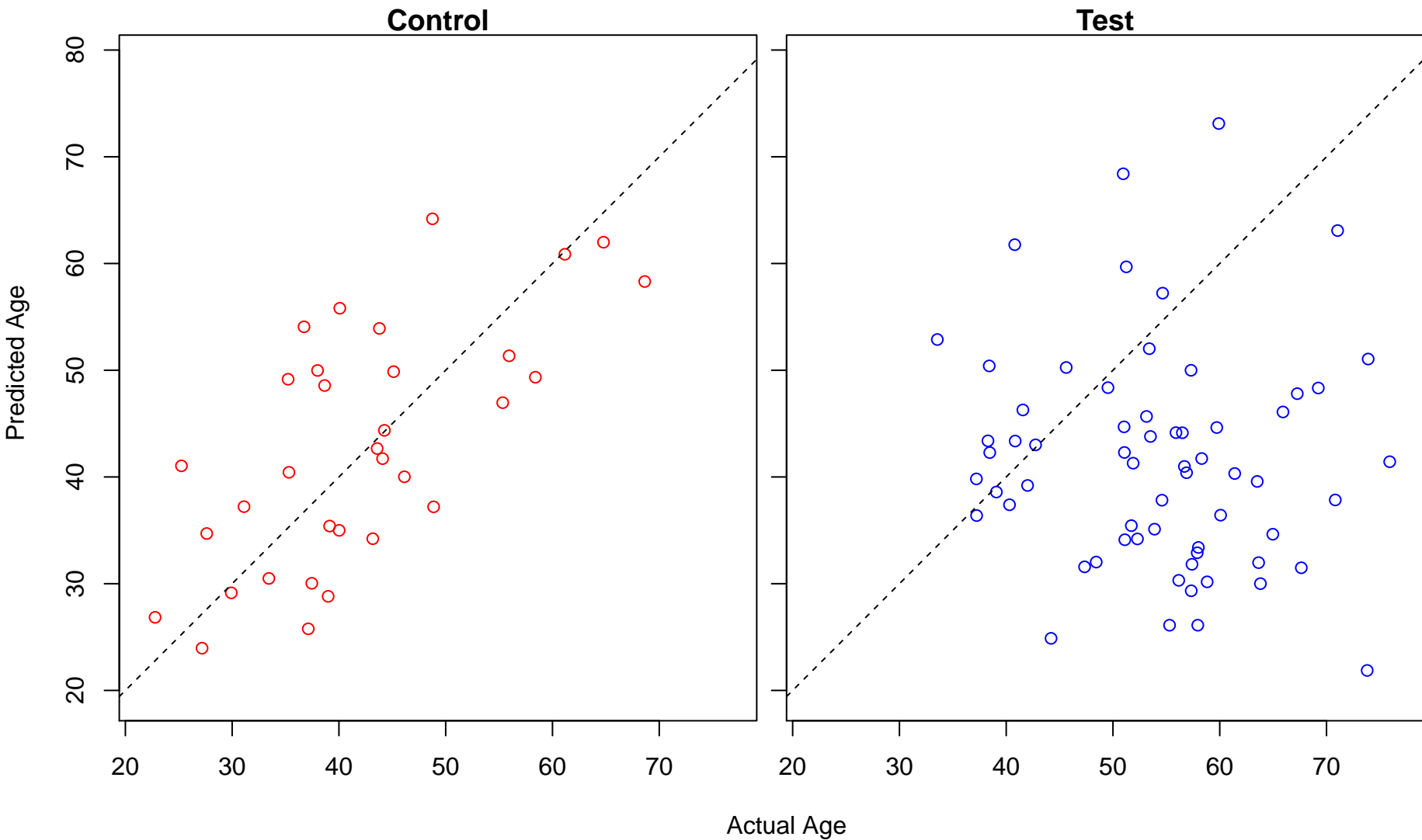
negative regulation of peptidyl-lysine acetylation (Score: 2.437312)



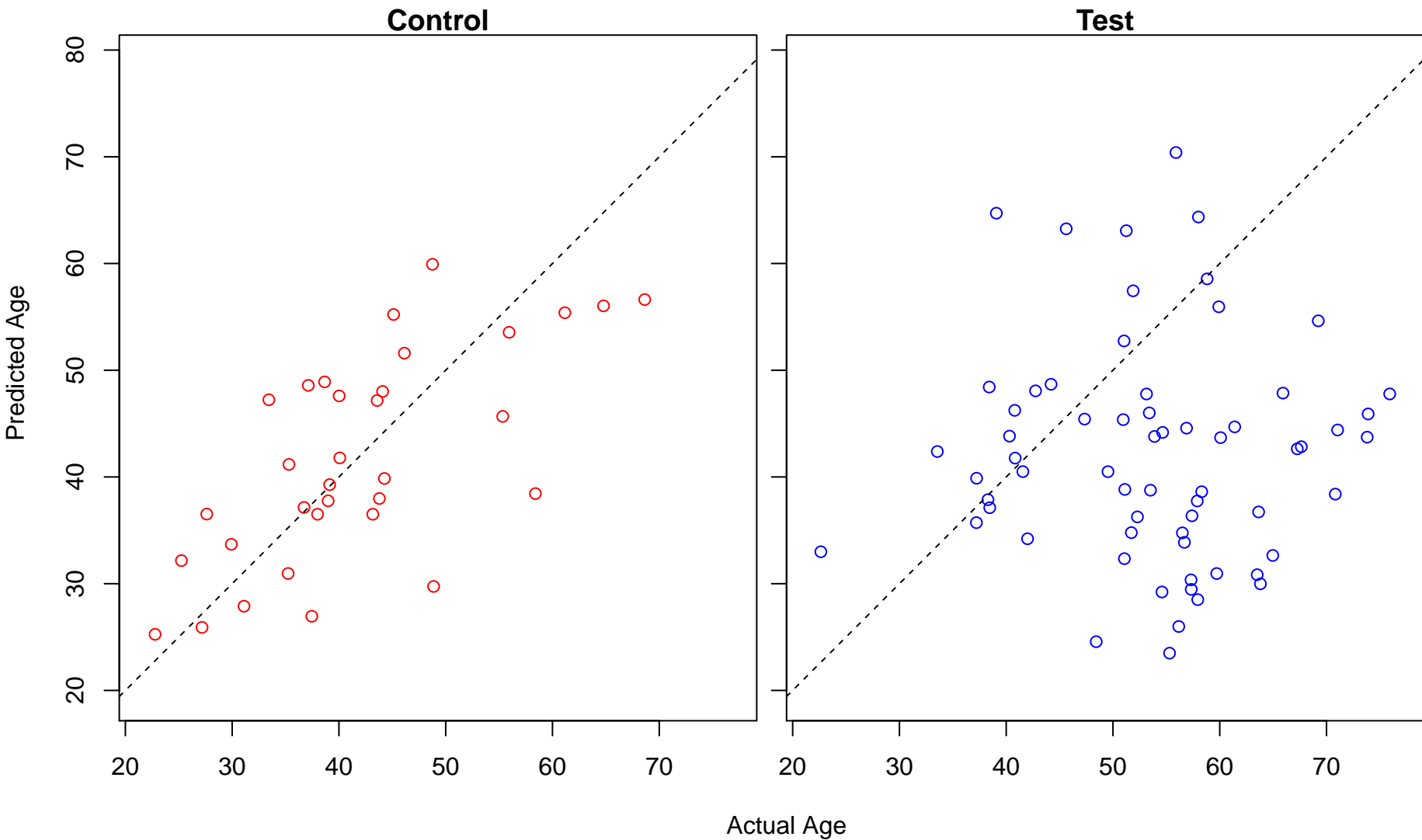
positive regulation of transporter activity (Score: 2.416531)



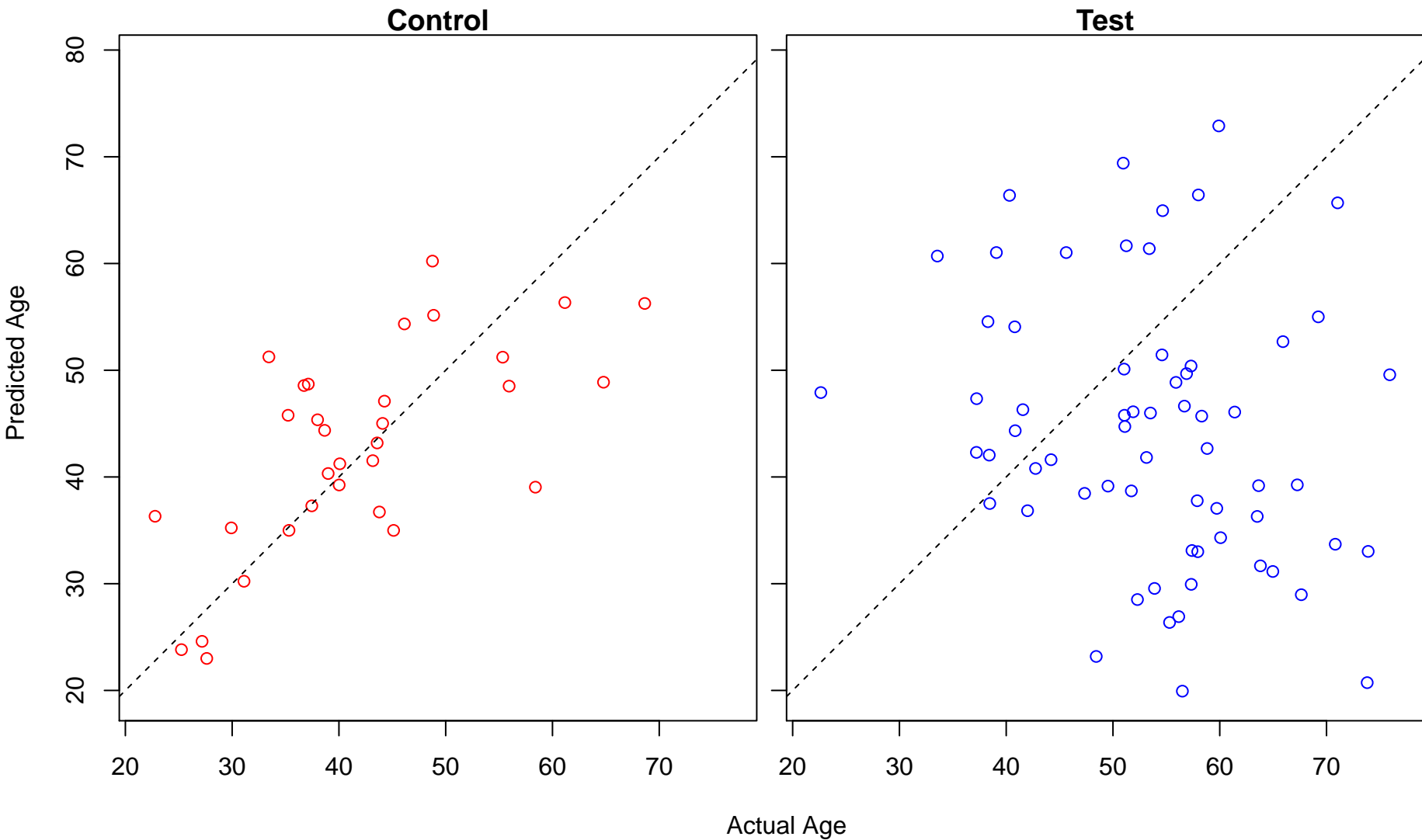
organophosphate catabolic process (Score: 2.408115)



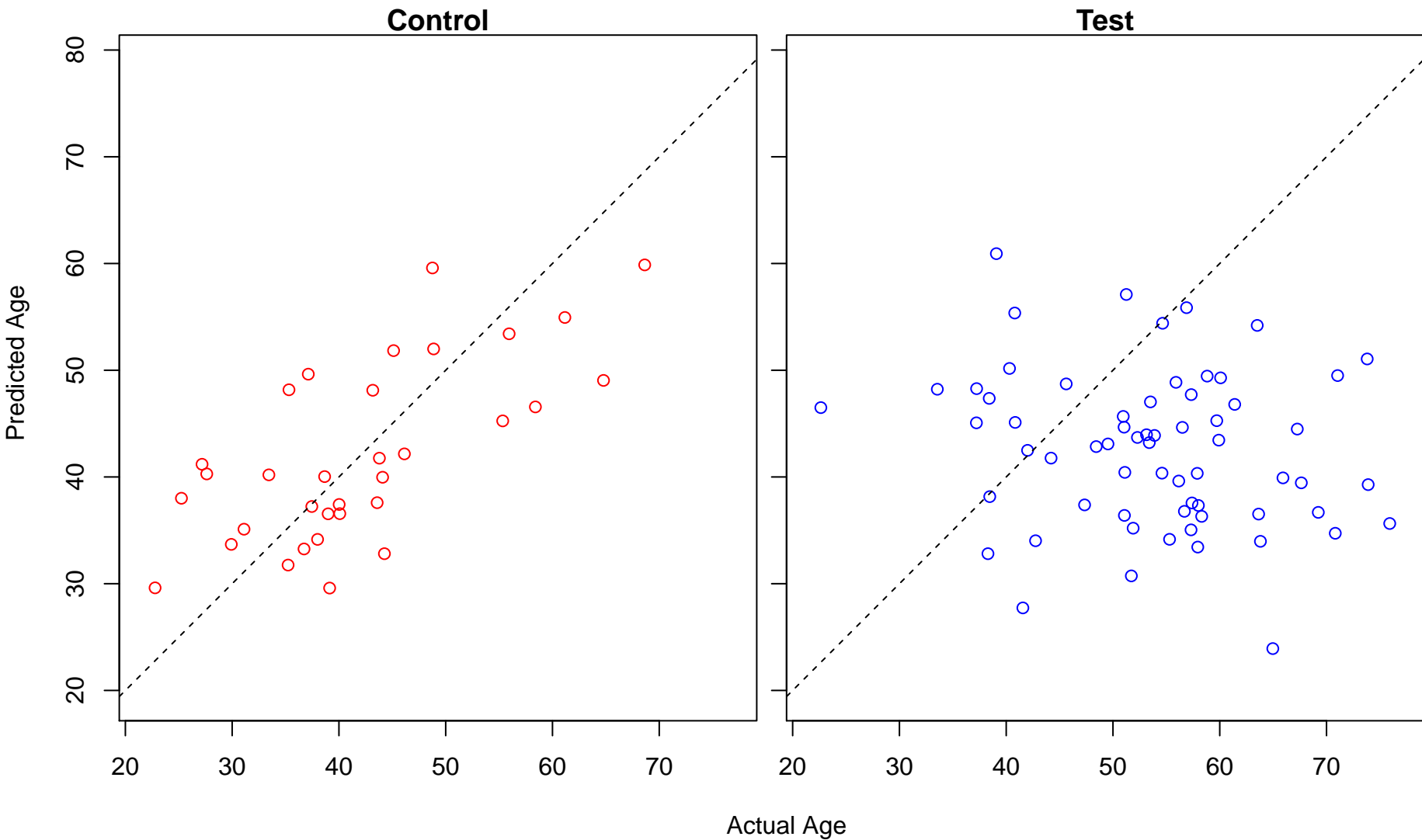
positive regulation of ion transmembrane transporter activity (Score: 2.405078)



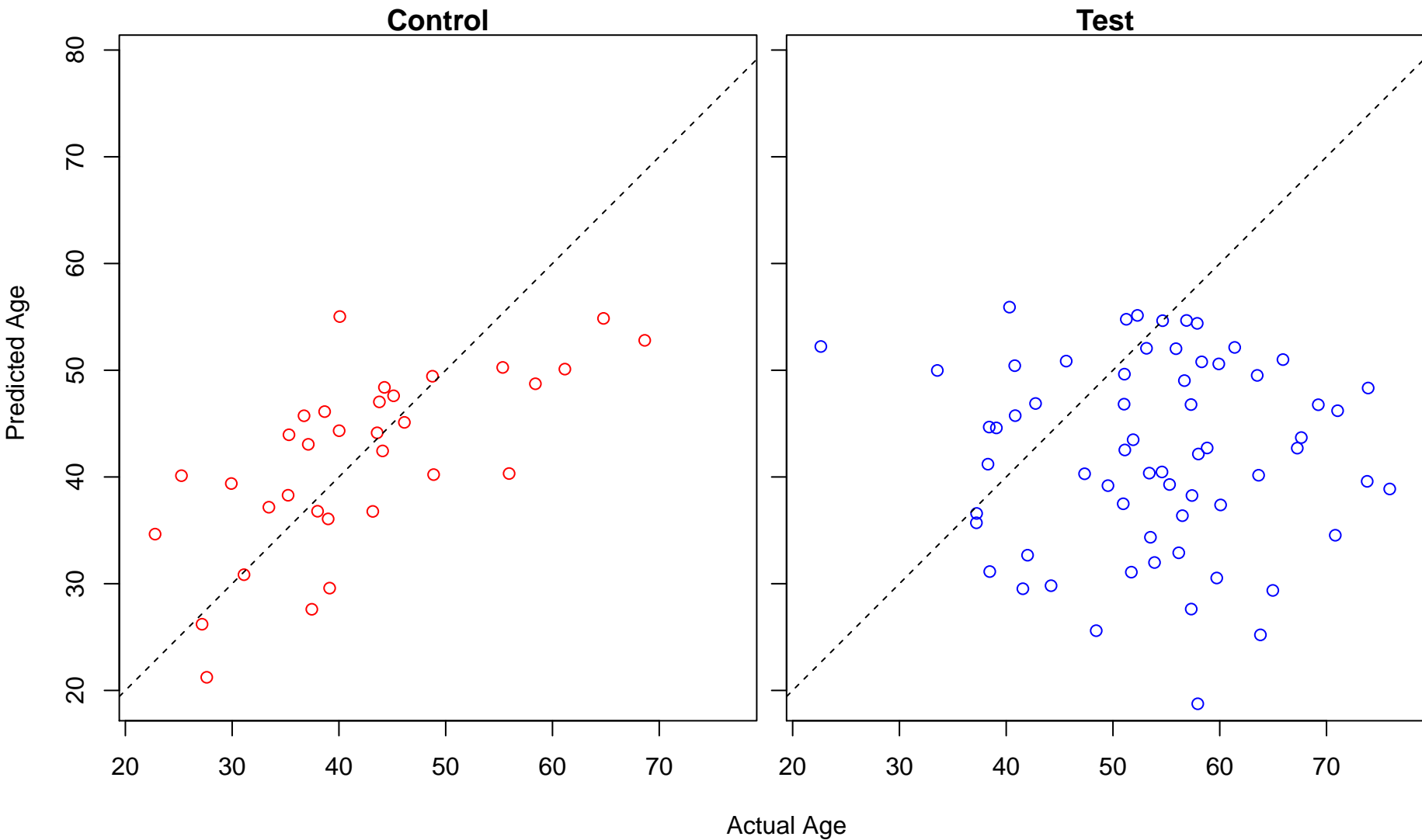
regulation of transcription from RNA polymerase I promoter (Score: 2.403003)



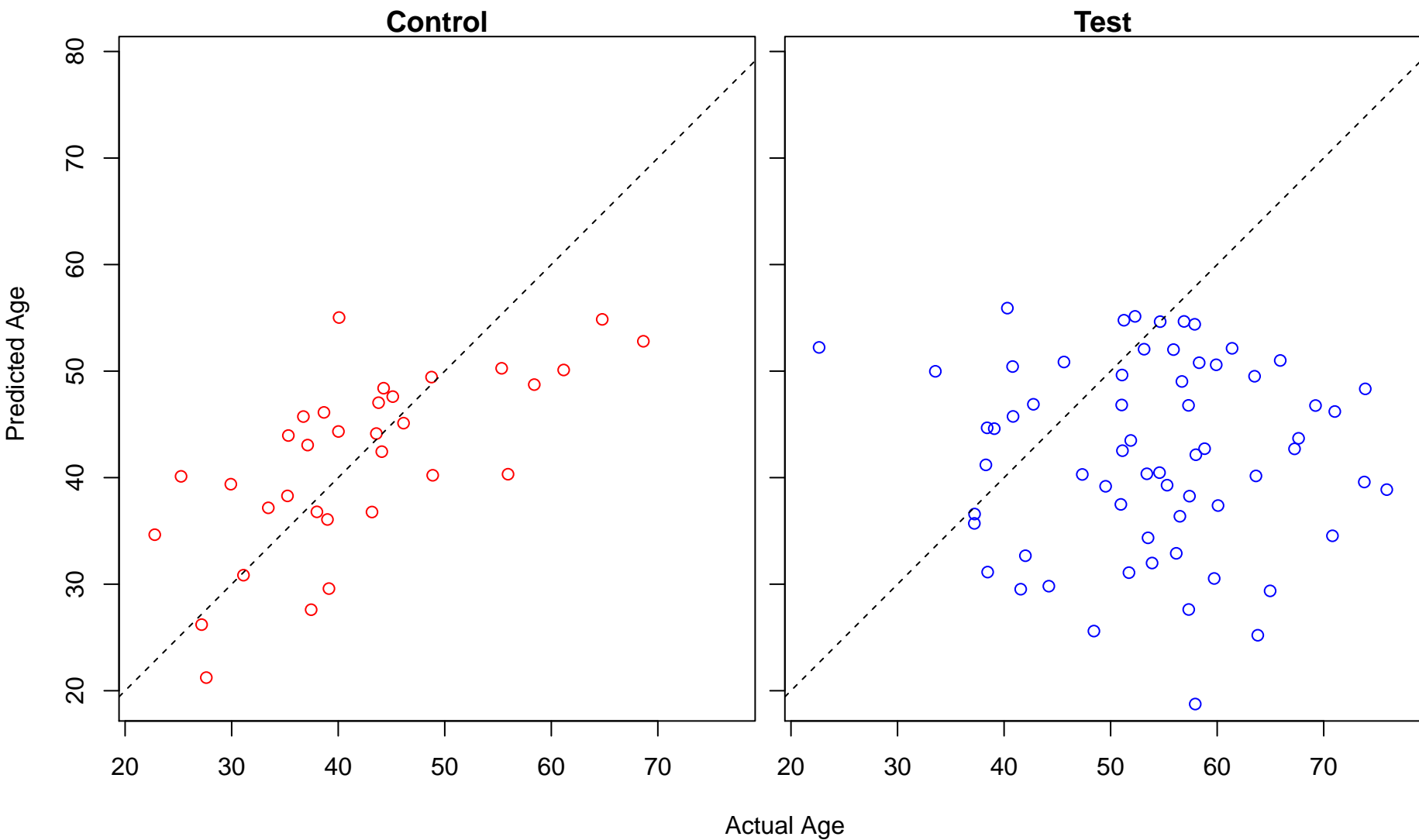
locomotor rhythm (Score: 2.382335)



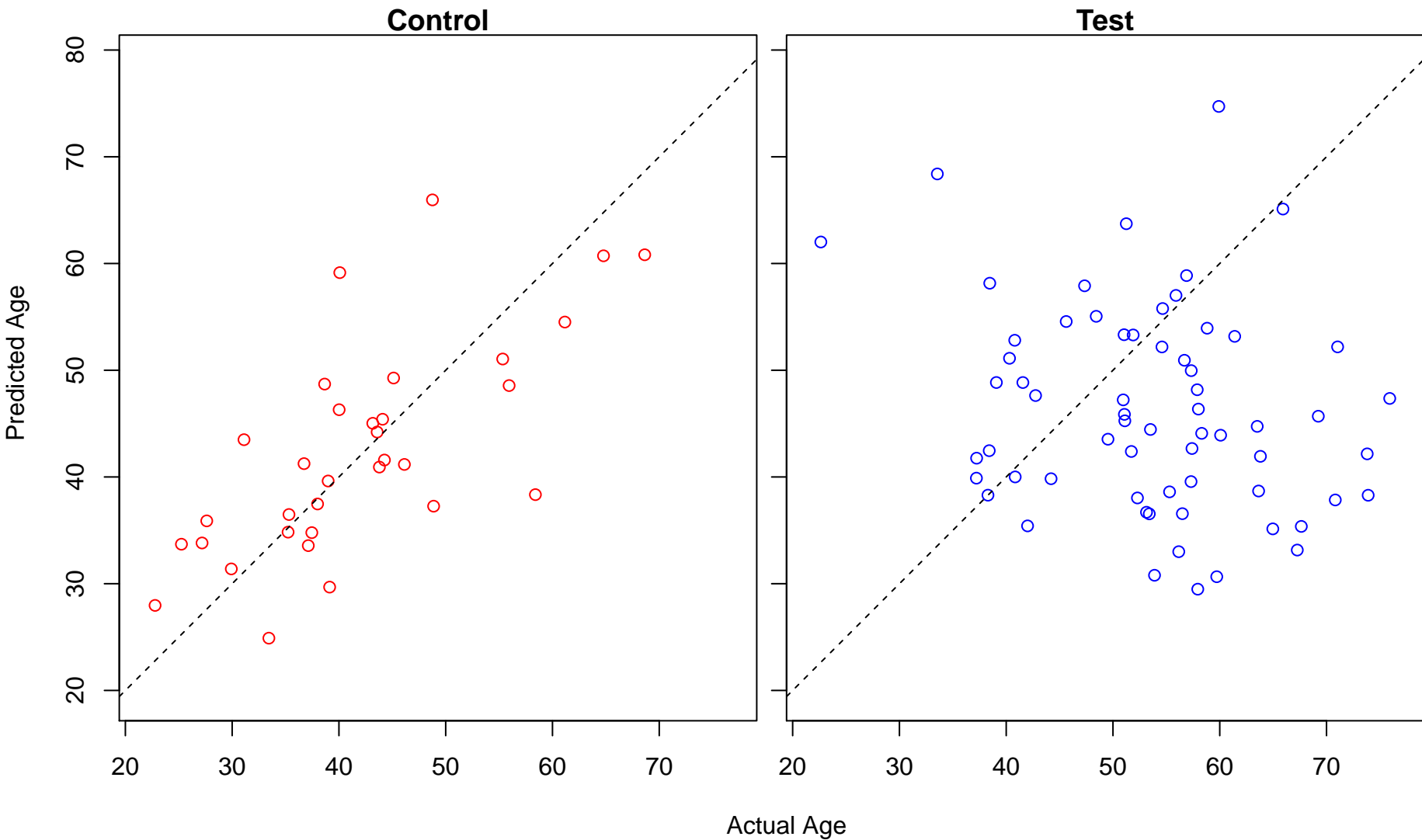
peroxisomal membrane transport (Score: 2.380861)



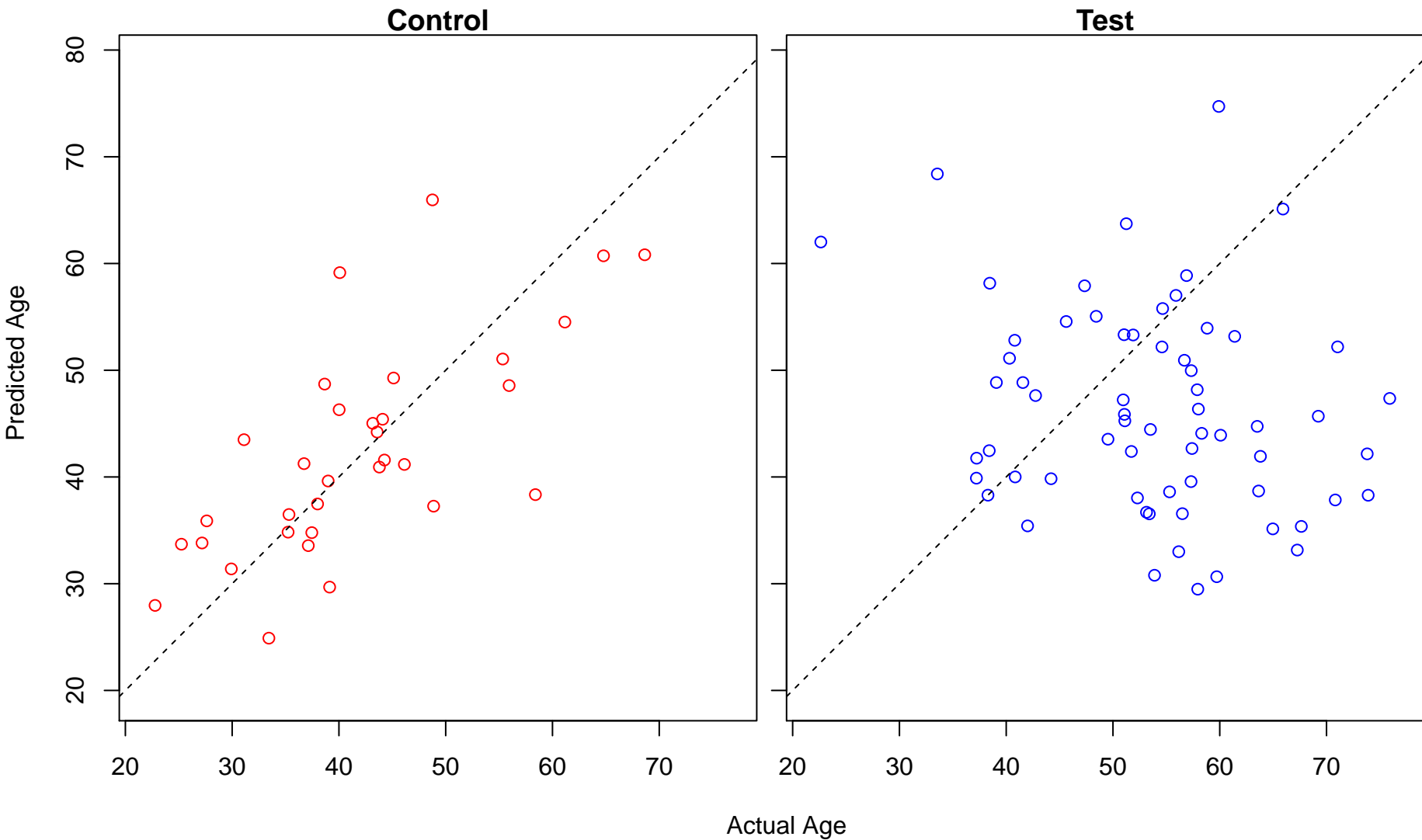
protein import into peroxisome membrane (Score: 2.380861)



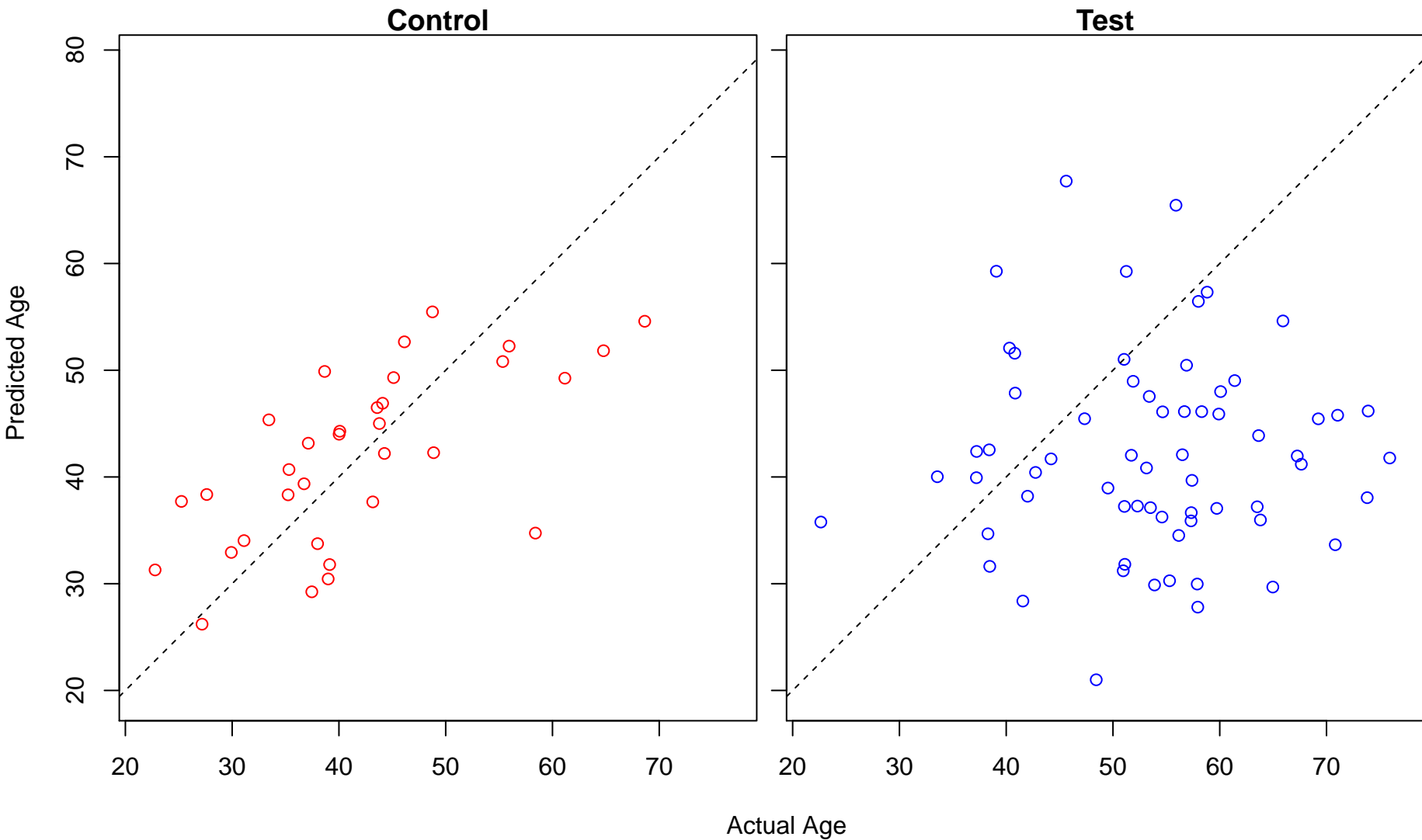
negative regulation of protein exit from endoplasmic reticulum (Score: 2.356499)



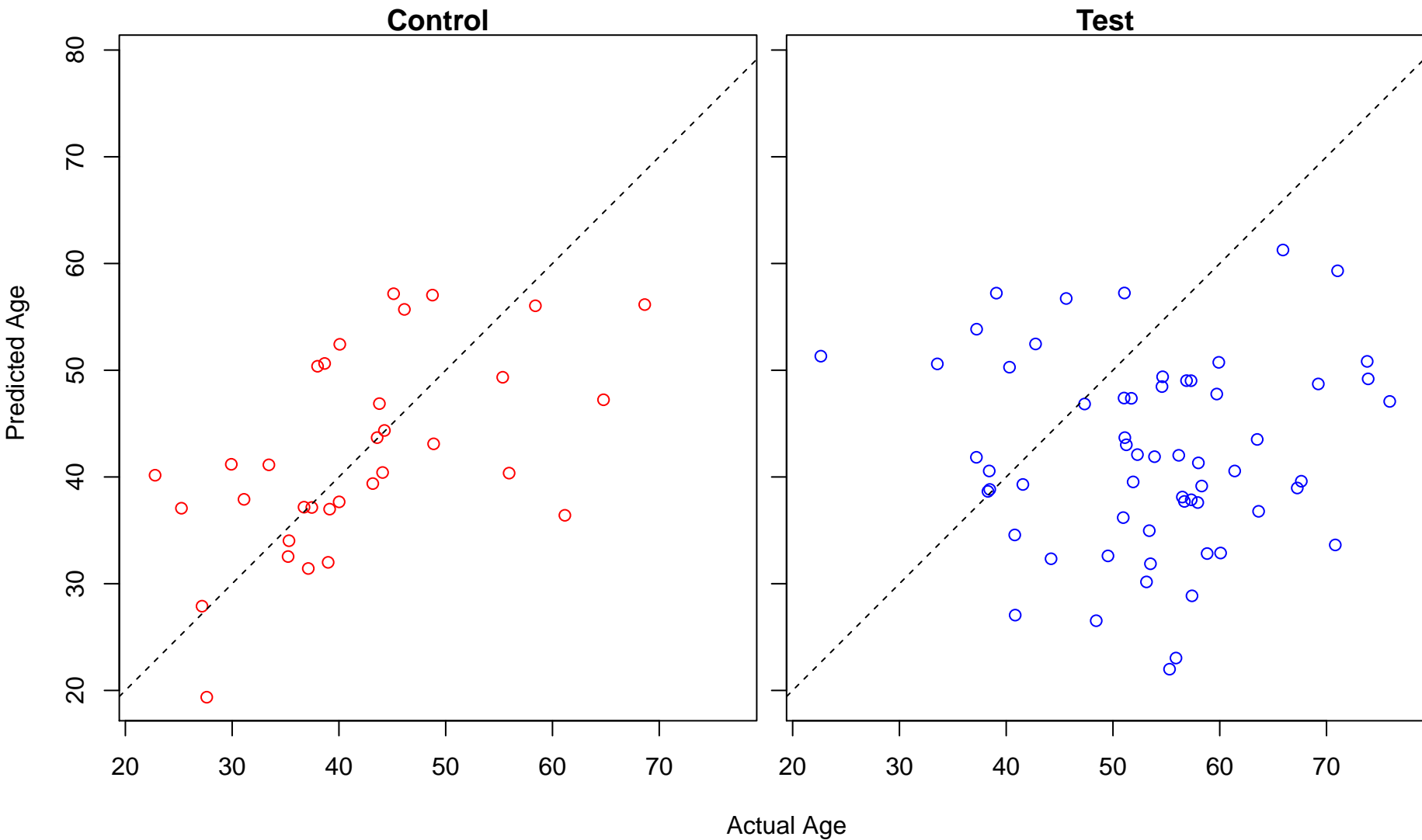
negative regulation of retrograde protein transport, ER to cytosol (Score: 2.356499)



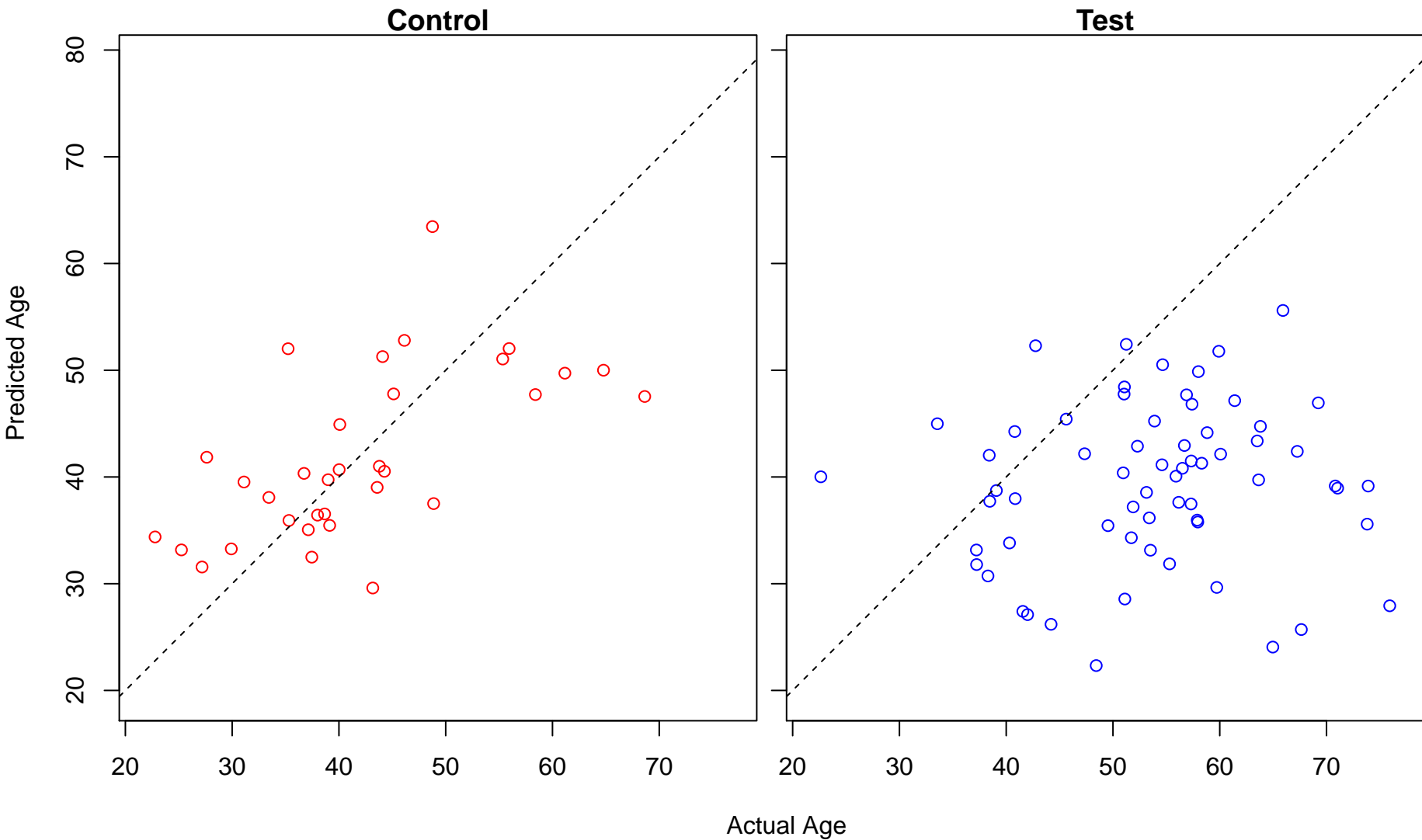
positive regulation of cation transmembrane transport (Score: 2.348296)



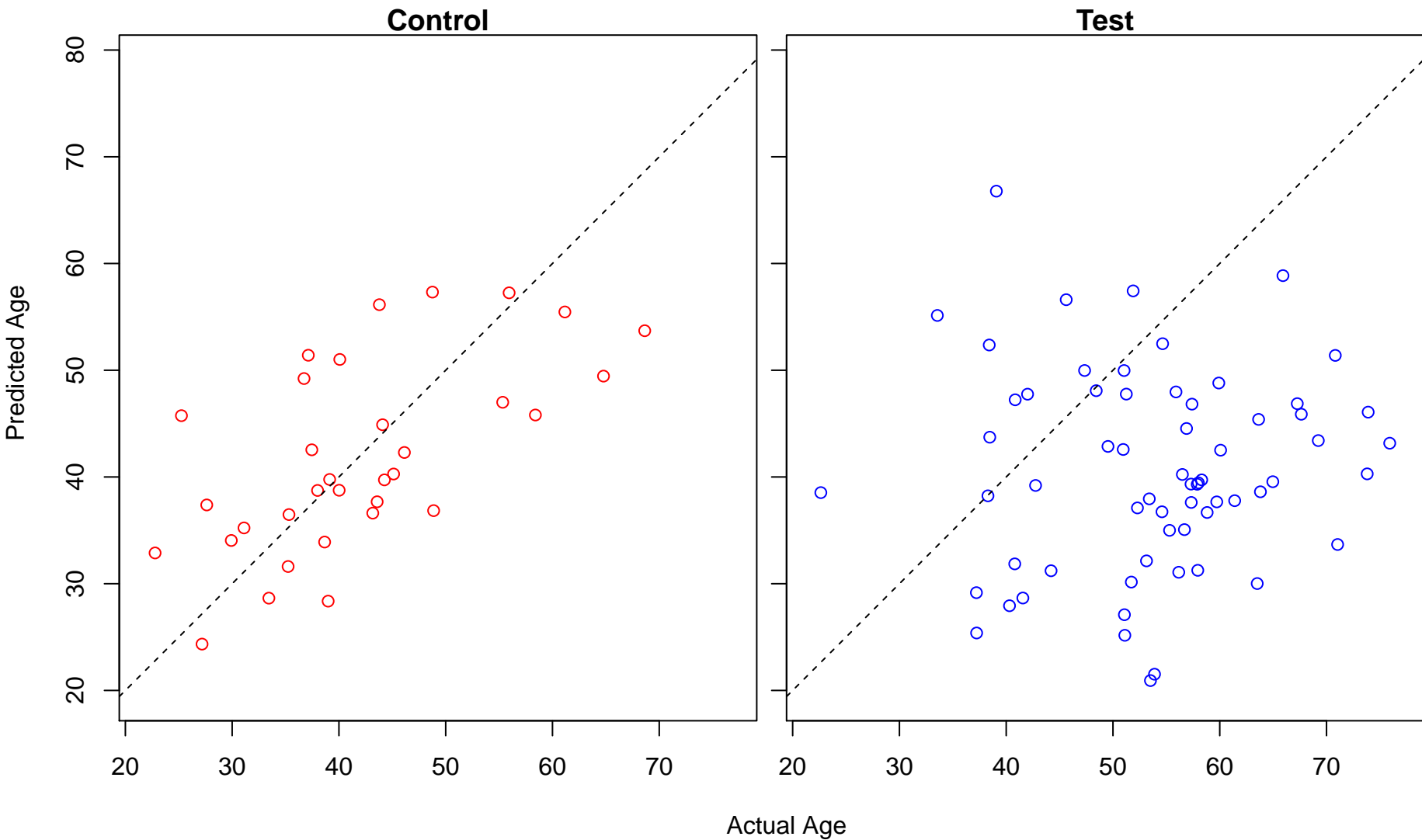
synapse organization (Score: 2.342178)



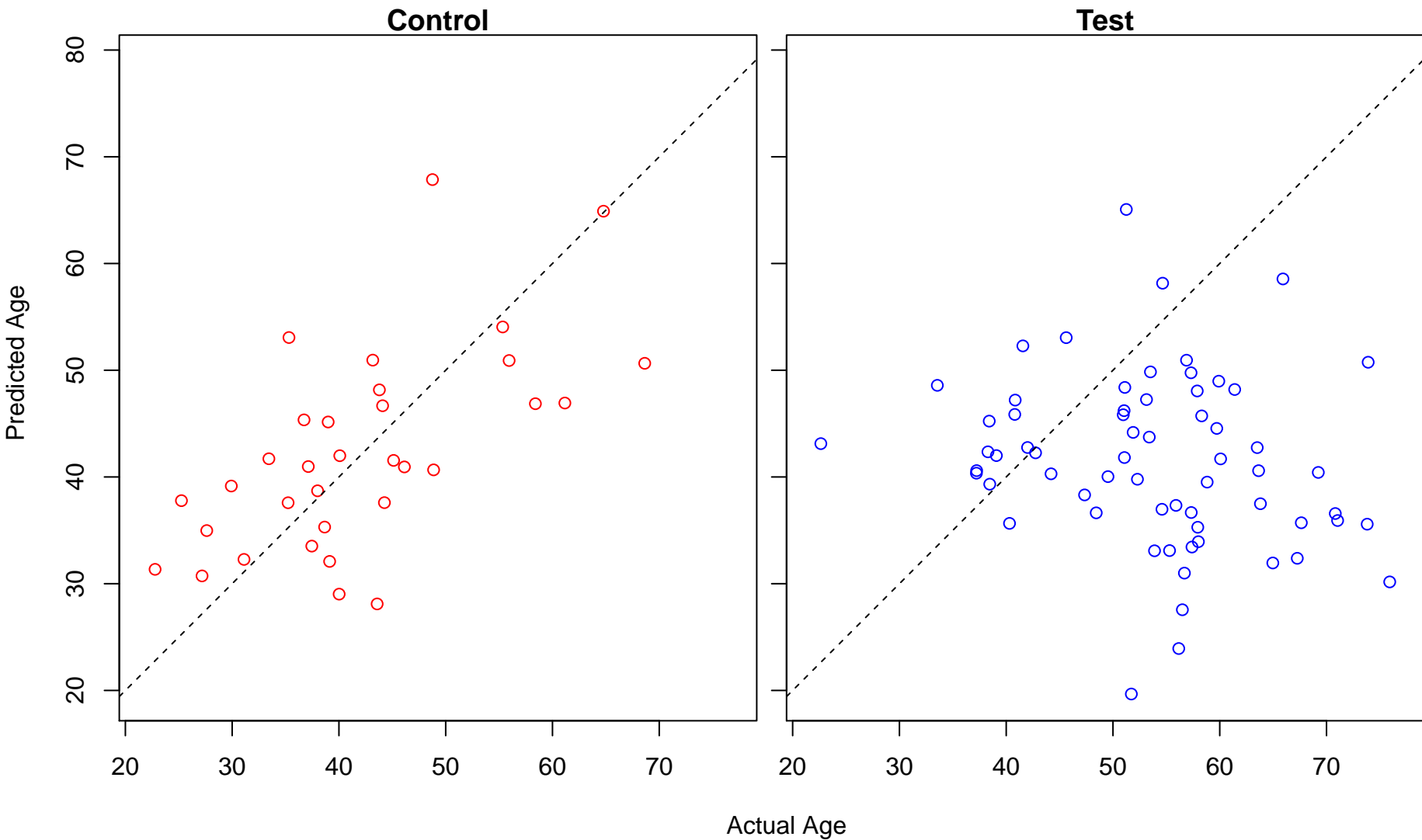
cell communication involved in cardiac conduction (Score: 2.336703)



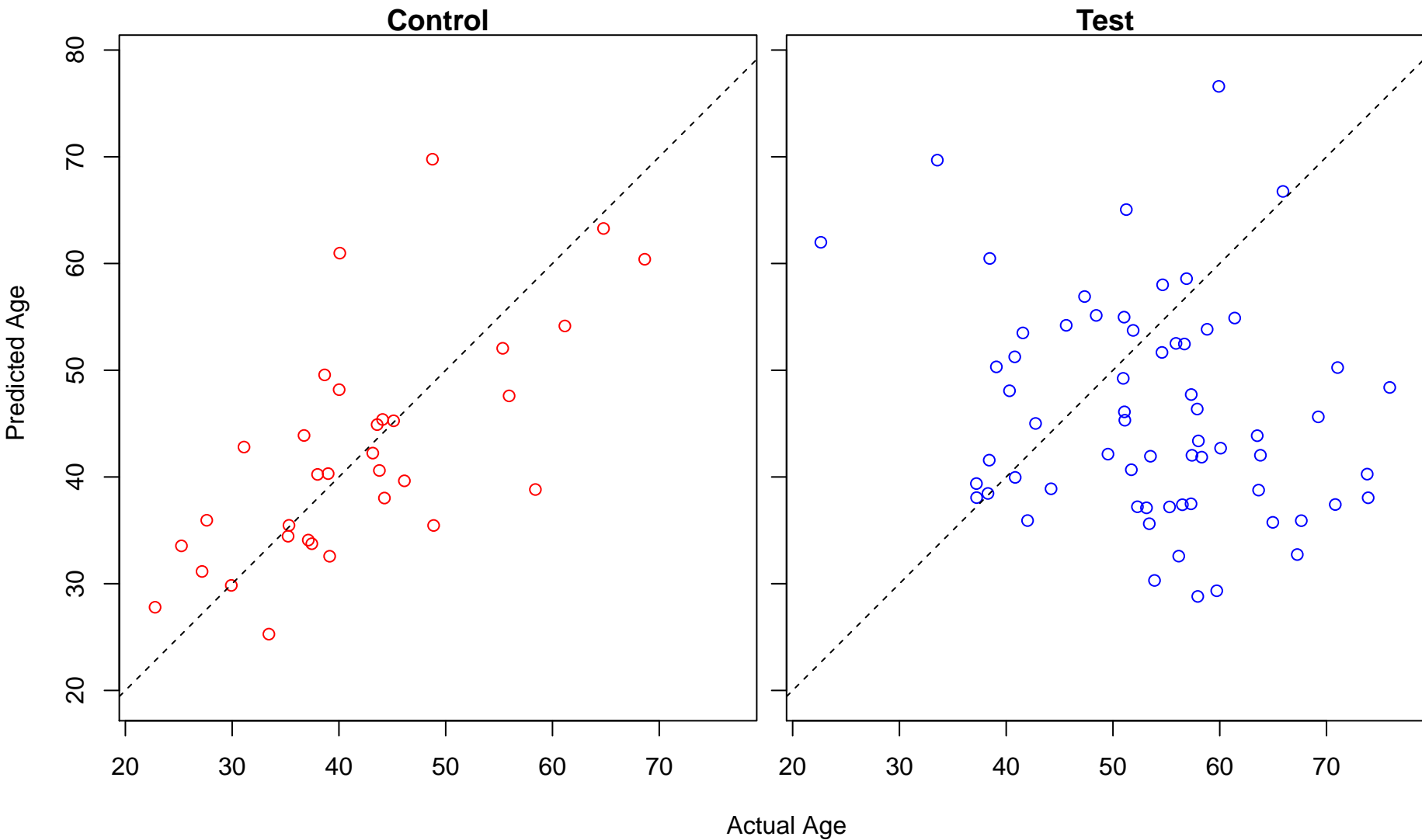
blood coagulation, intrinsic pathway (Score: 2.323655)



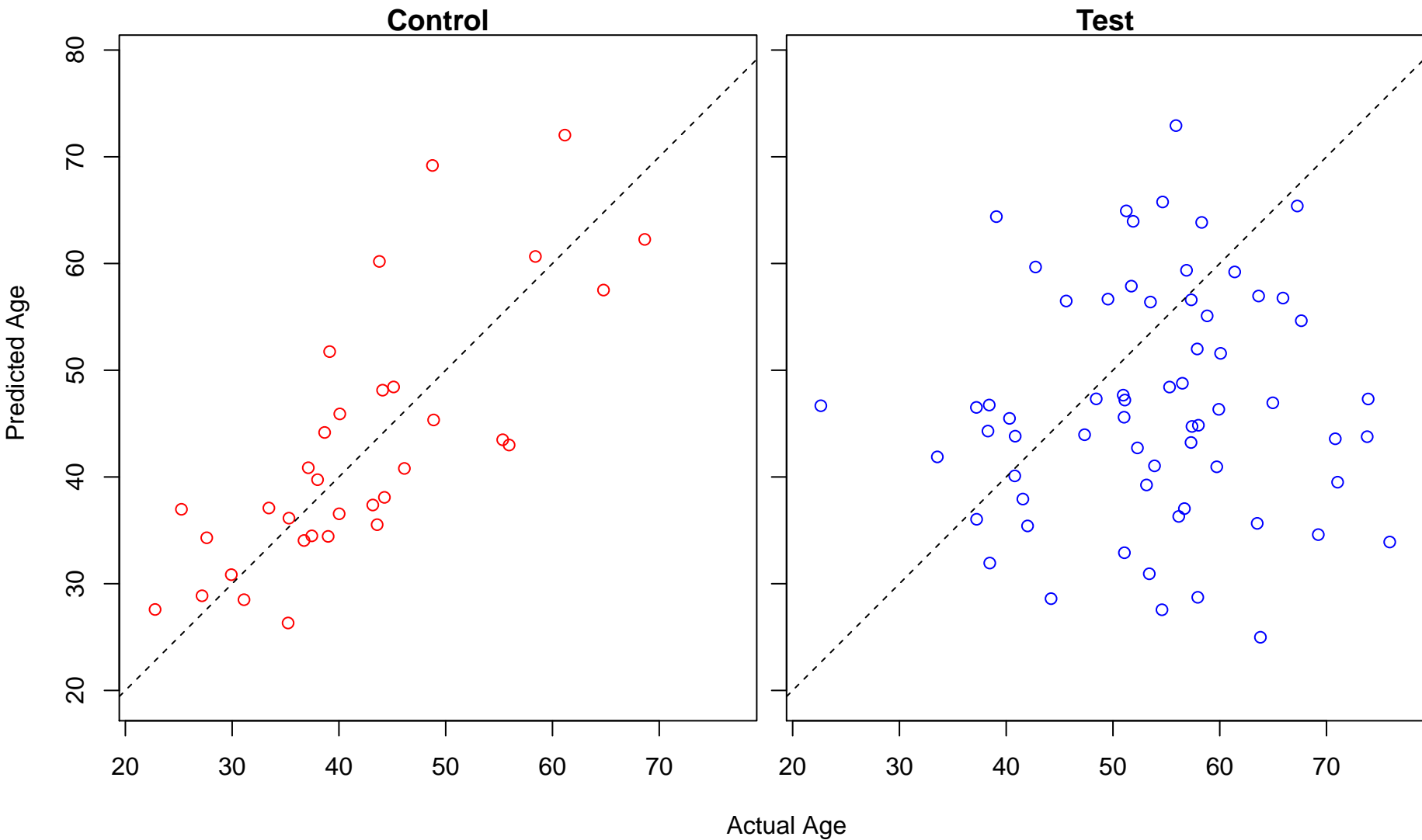
cellular aldehyde metabolic process (Score: 2.284997)



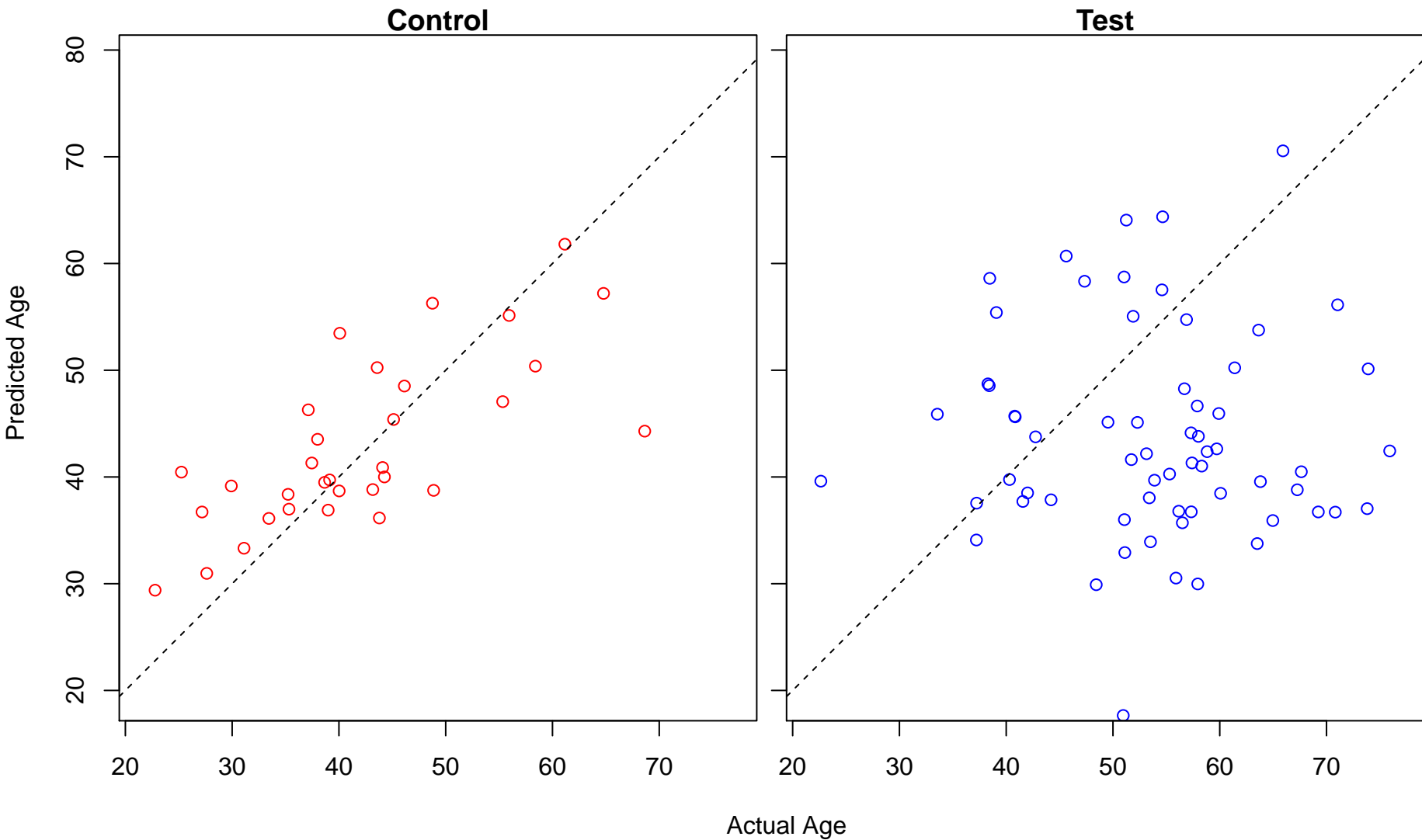
negative regulation of ERAD pathway (Score: 2.278894)



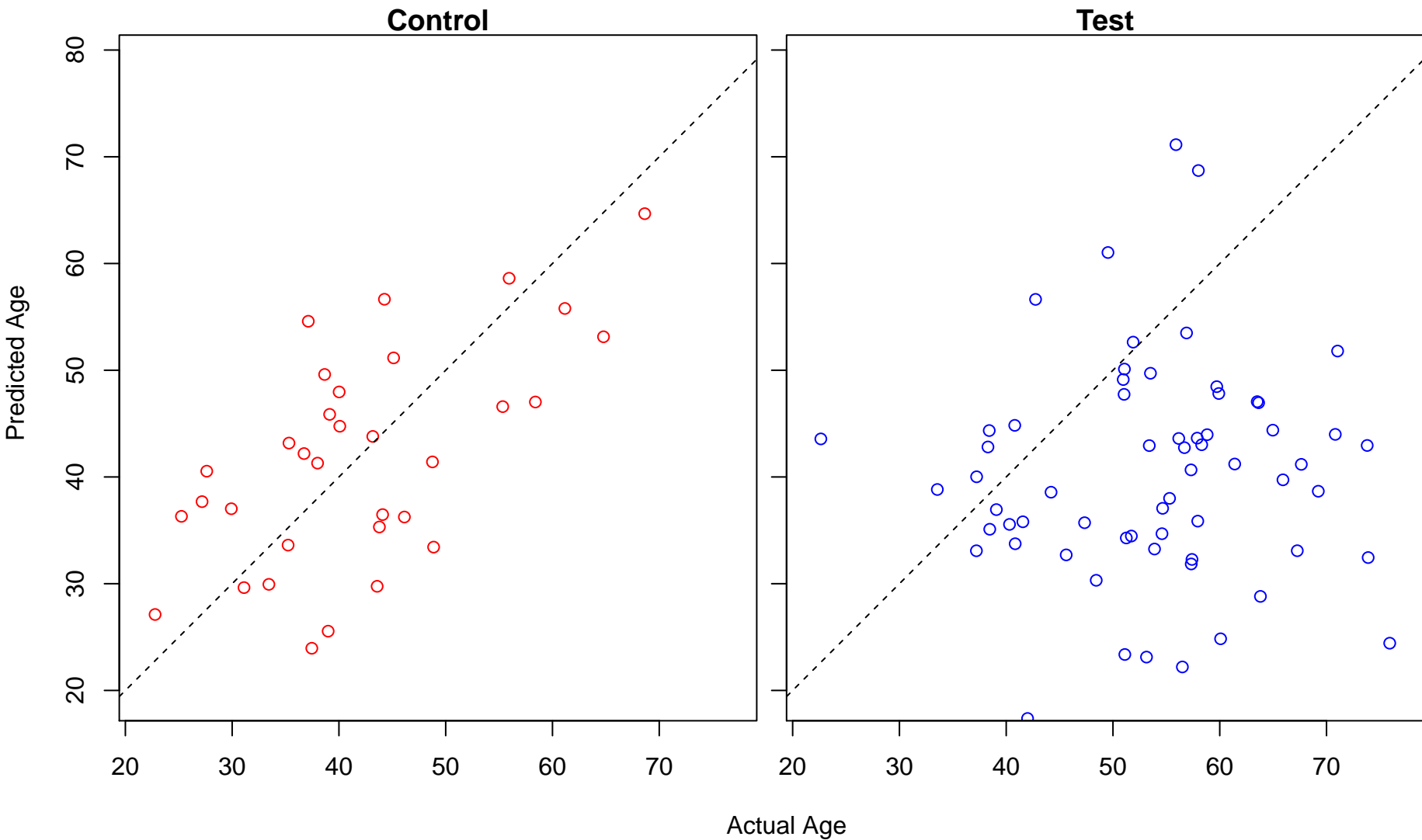
regulation of leukocyte degranulation (Score: 2.277556)



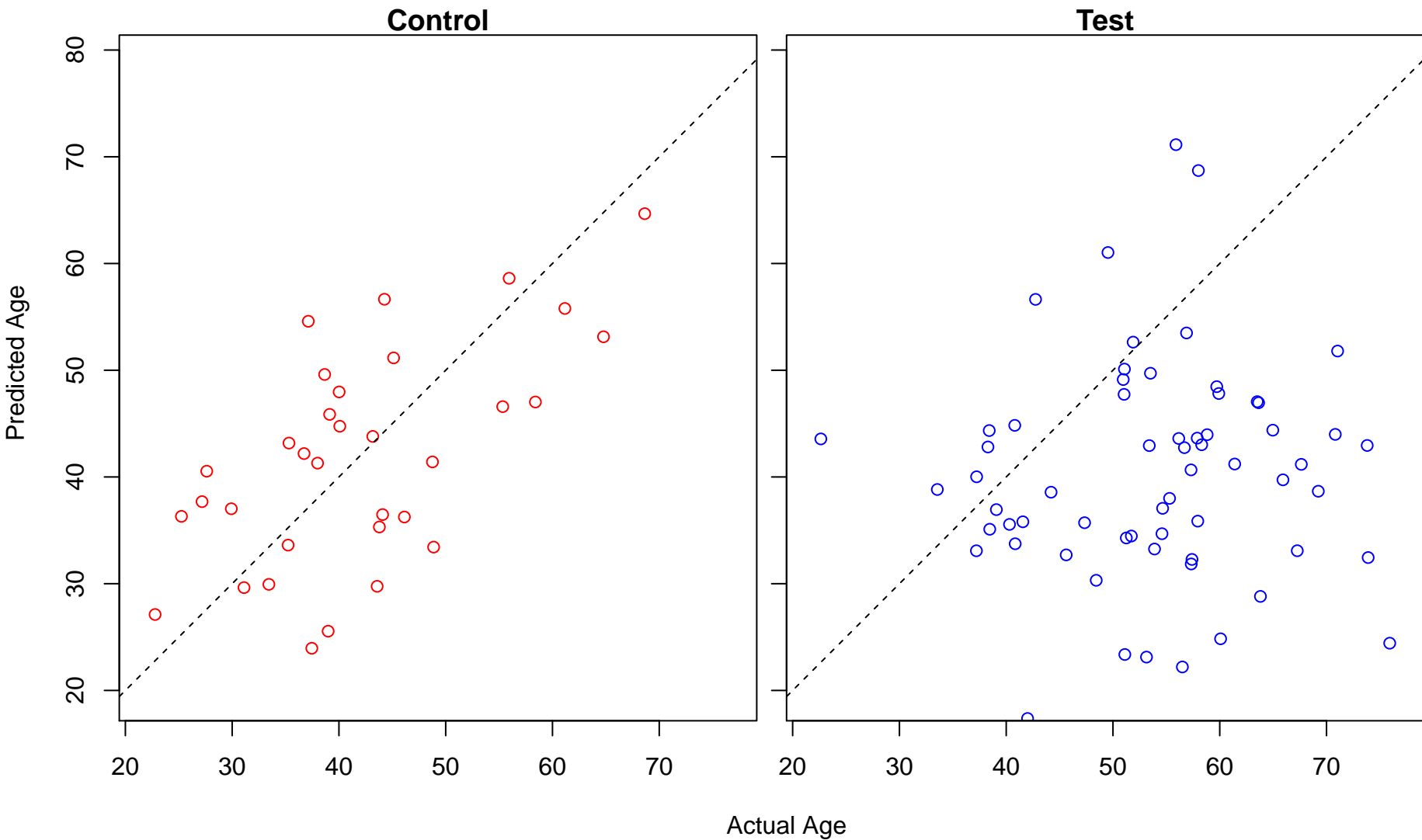
CDP-choline pathway (Score: 2.275862)



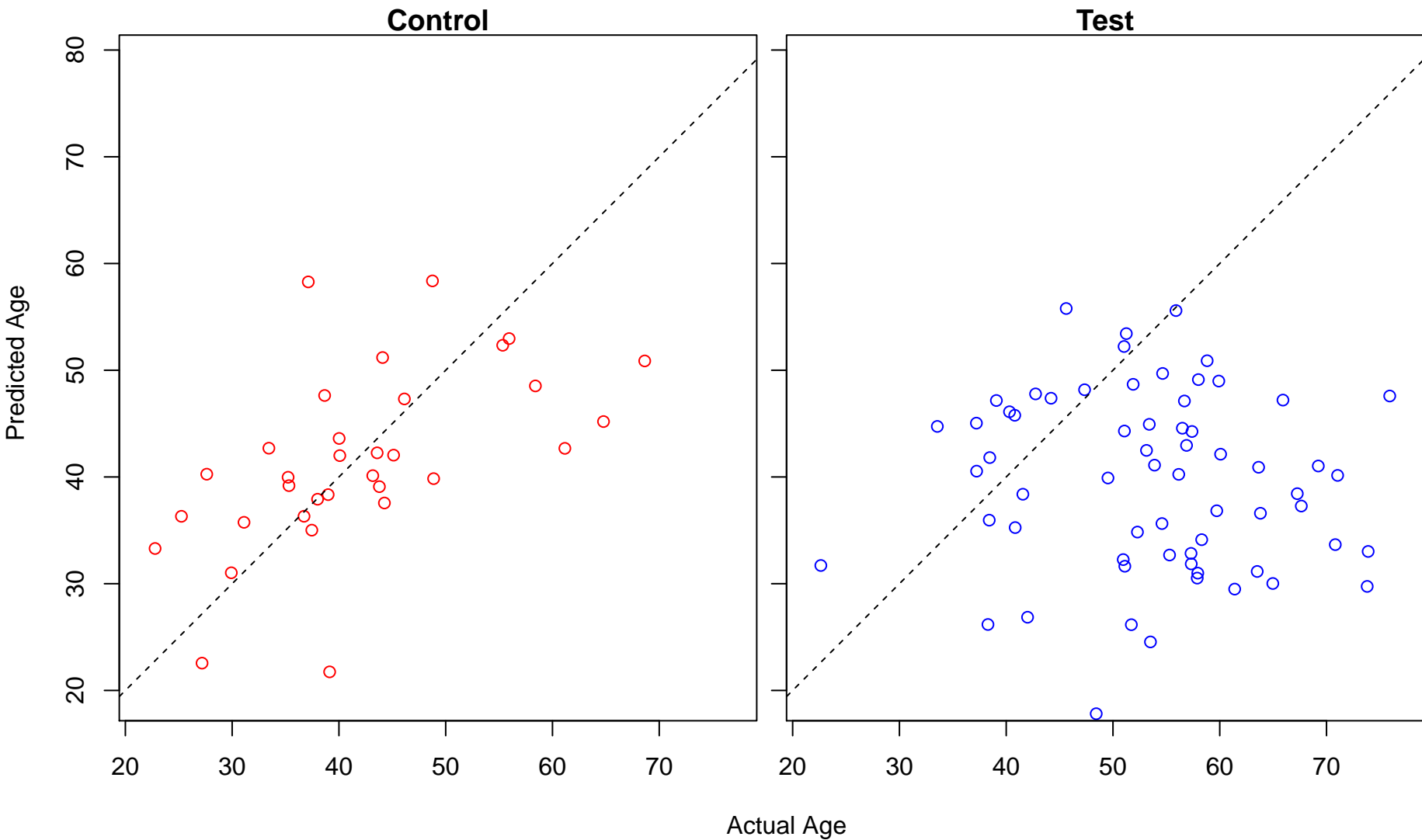
transferrin transport (Score: 2.268879)



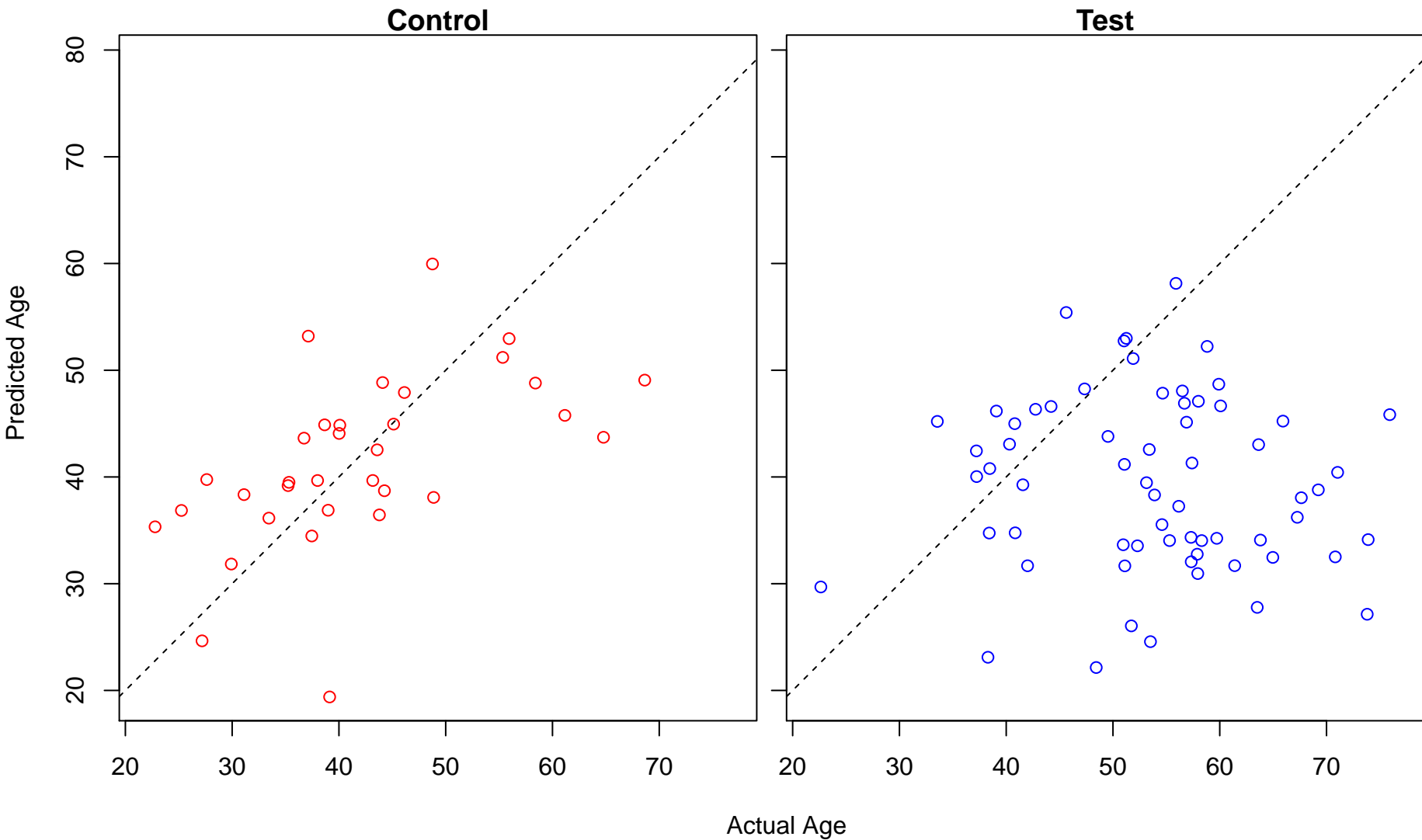
trivalent inorganic cation transport (Score: 2.268879)



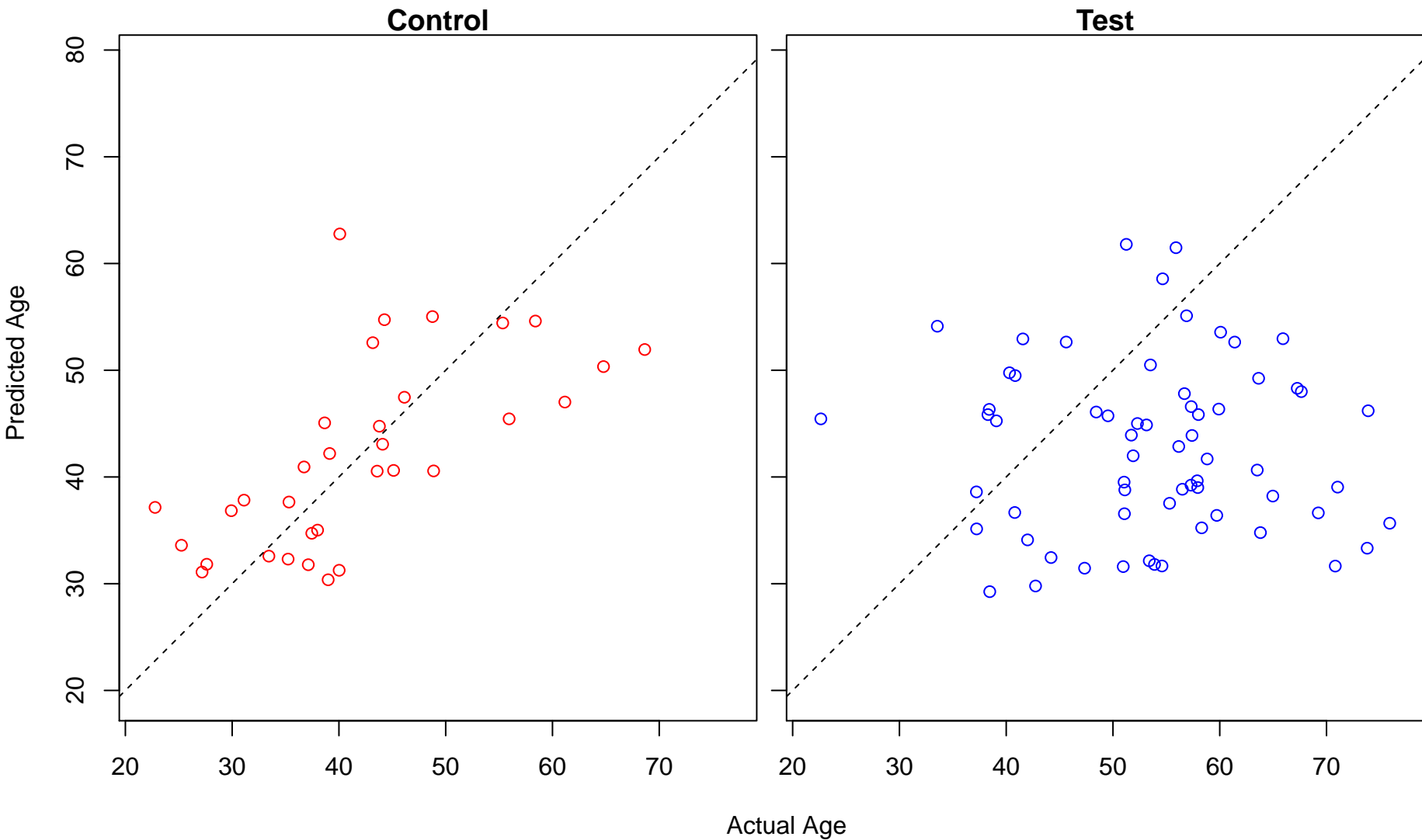
positive regulation of sodium ion transport (Score: 2.255220)



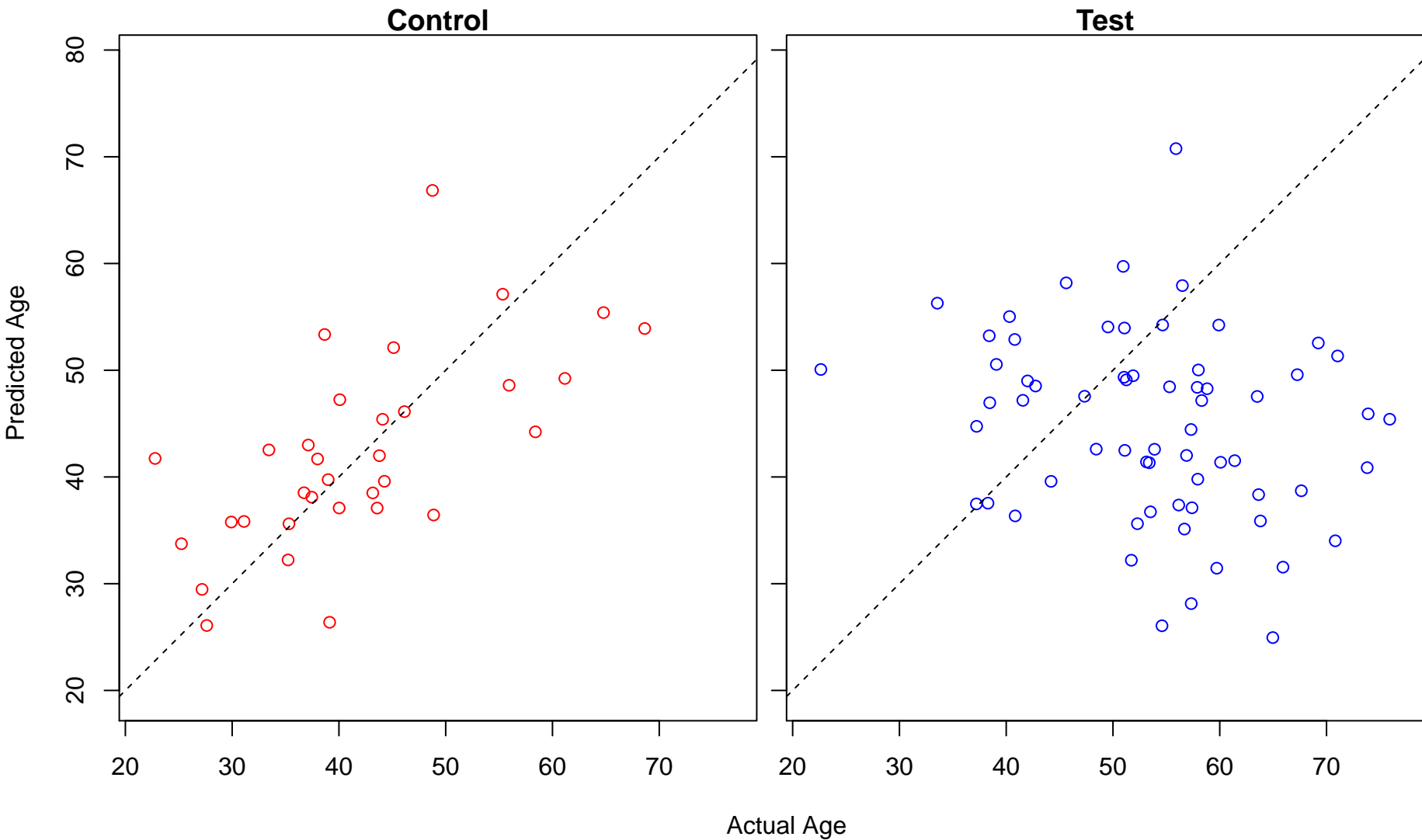
regulation of sodium ion transmembrane transport (Score: 2.235140)



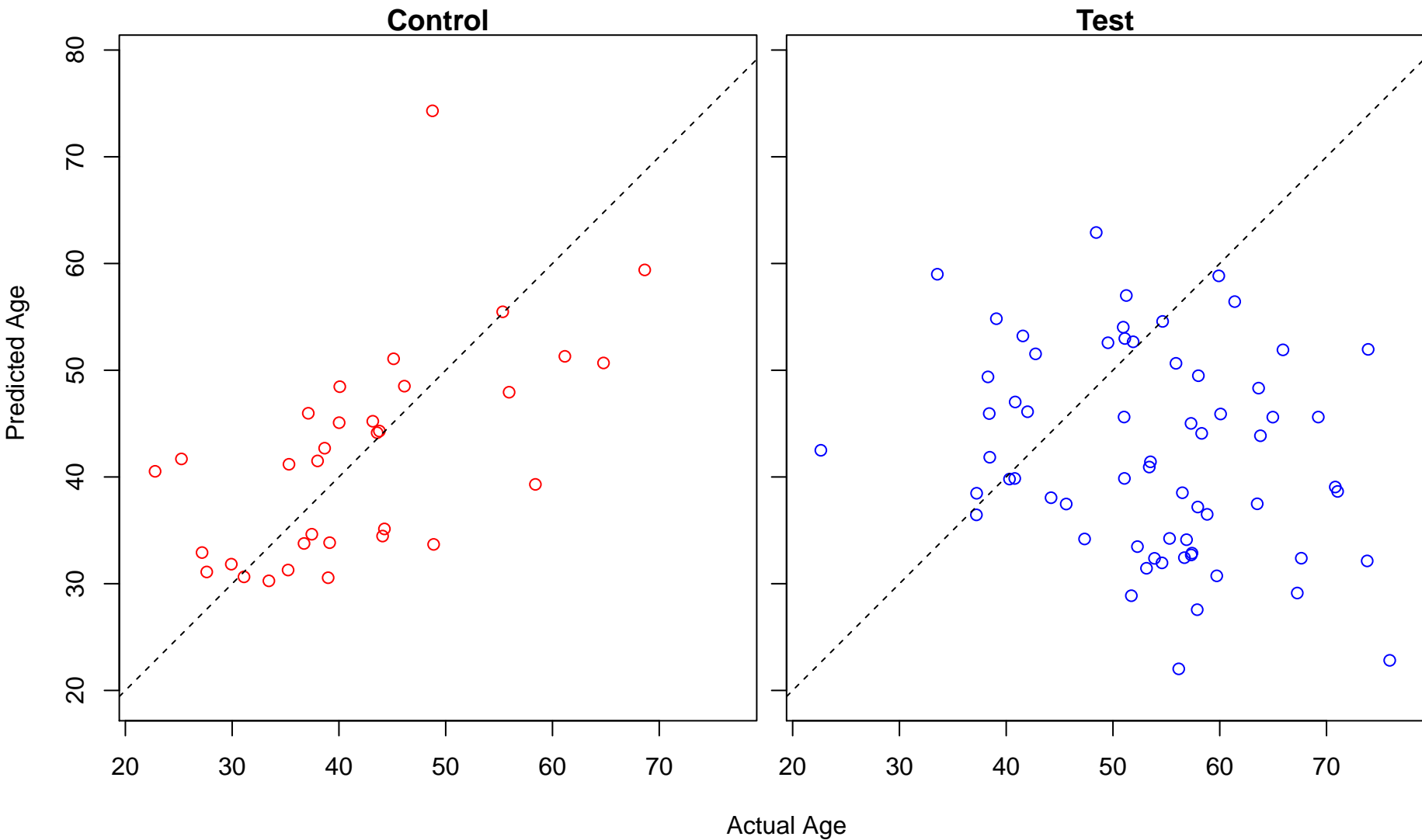
regulation of metalloendopeptidase activity (Score: 2.234738)



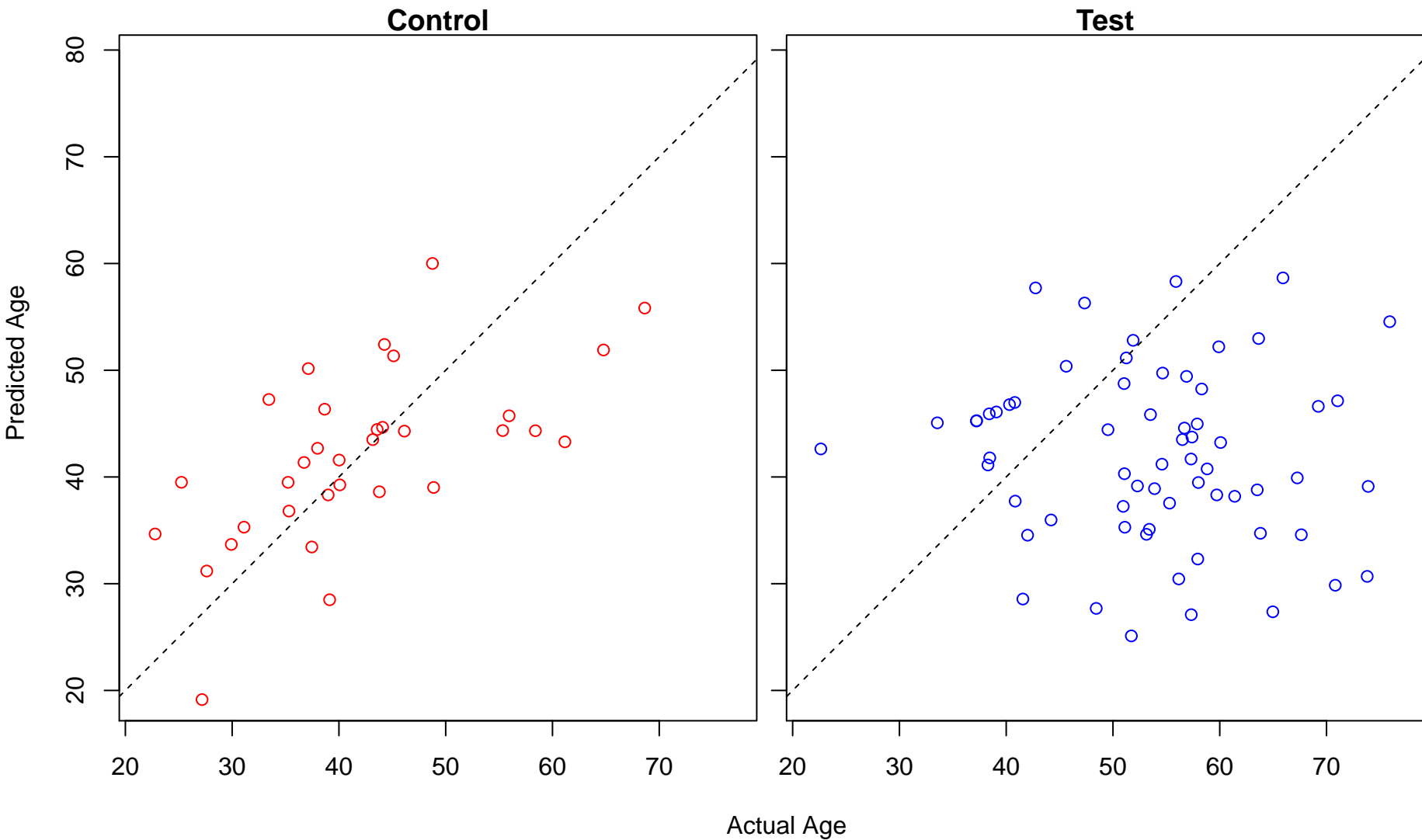
positive regulation of tumor necrosis factor production (Score: 2.233559)



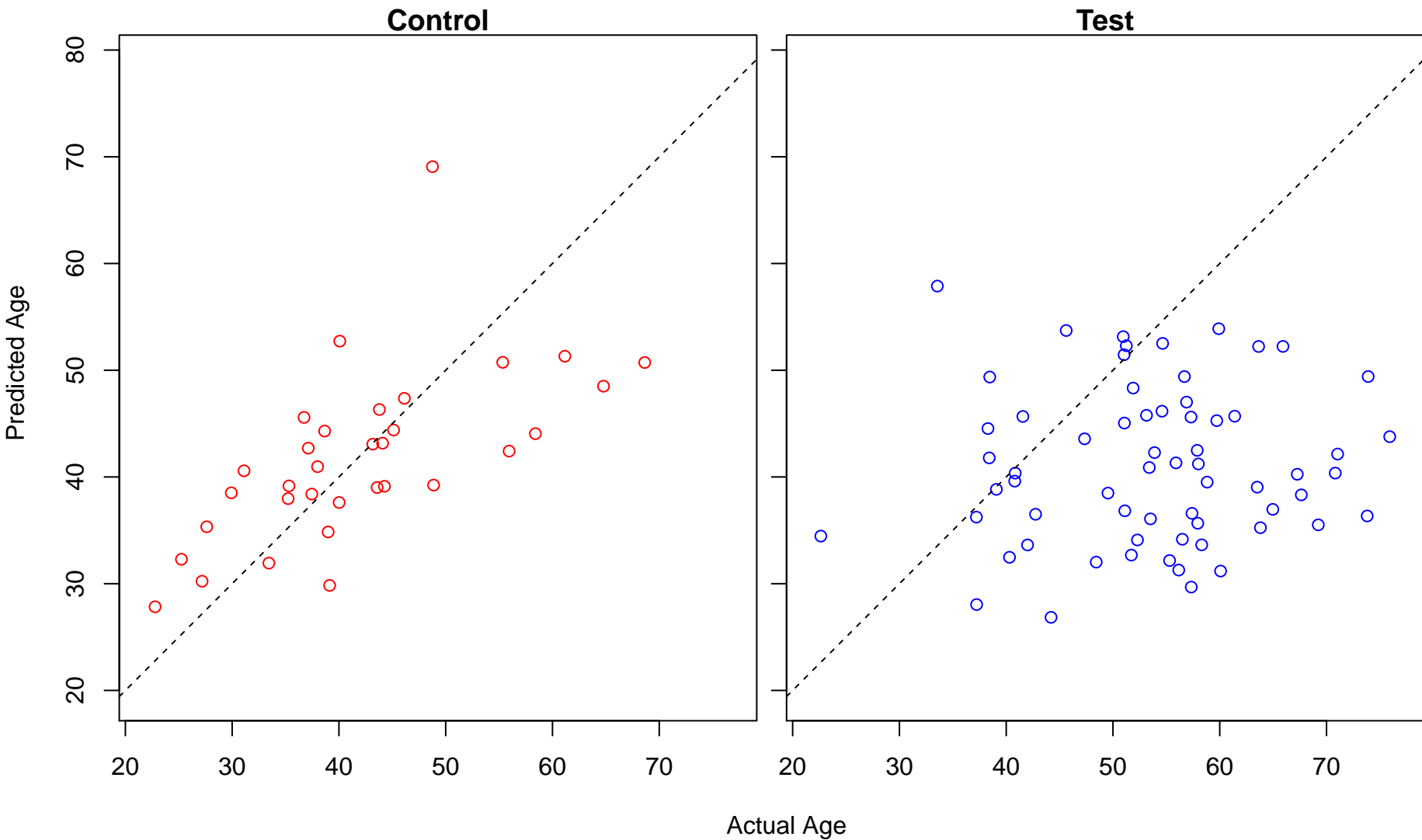
response to UV (Score: 2.224175)



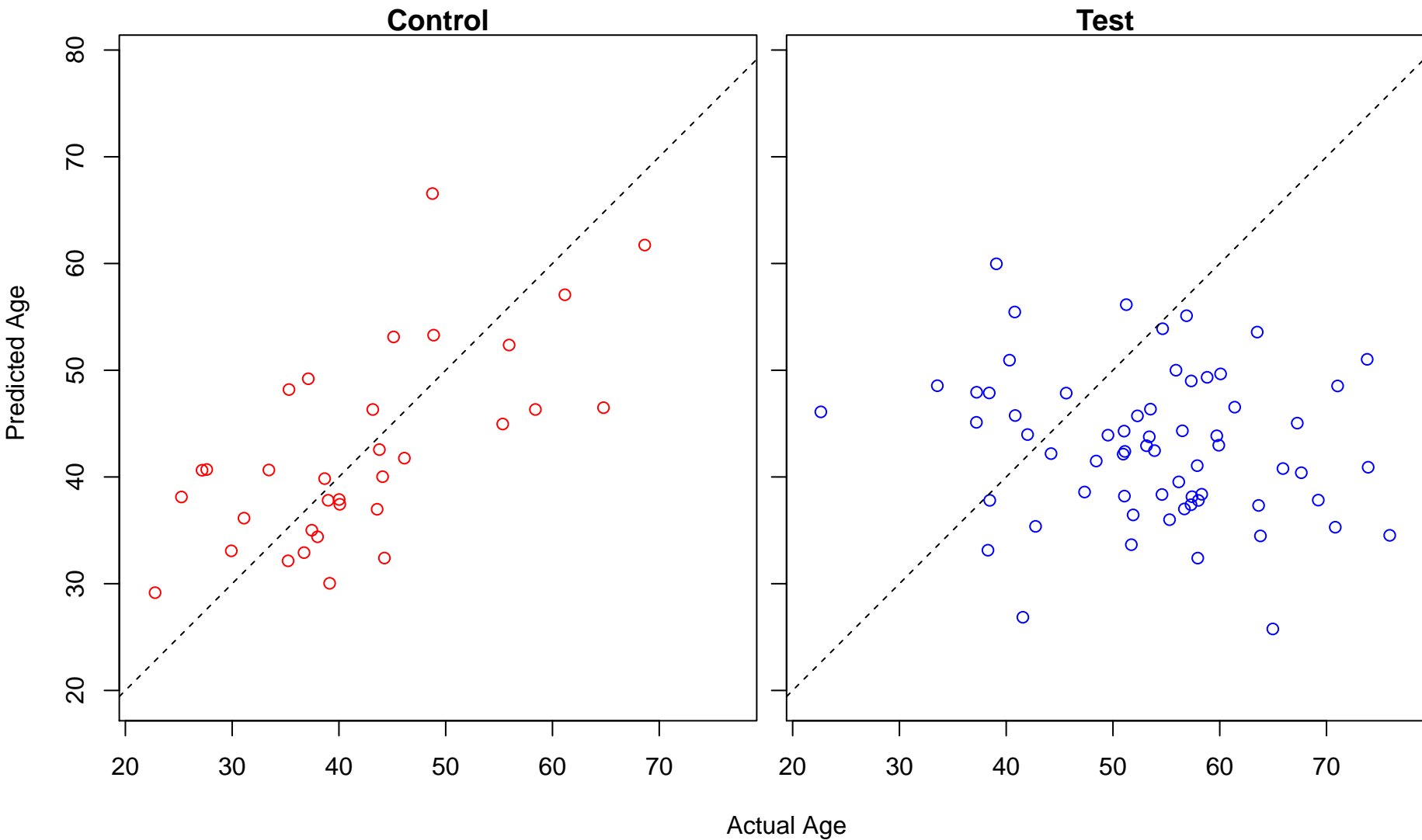
positive regulation of ATPase activity (Score: 2.198769)



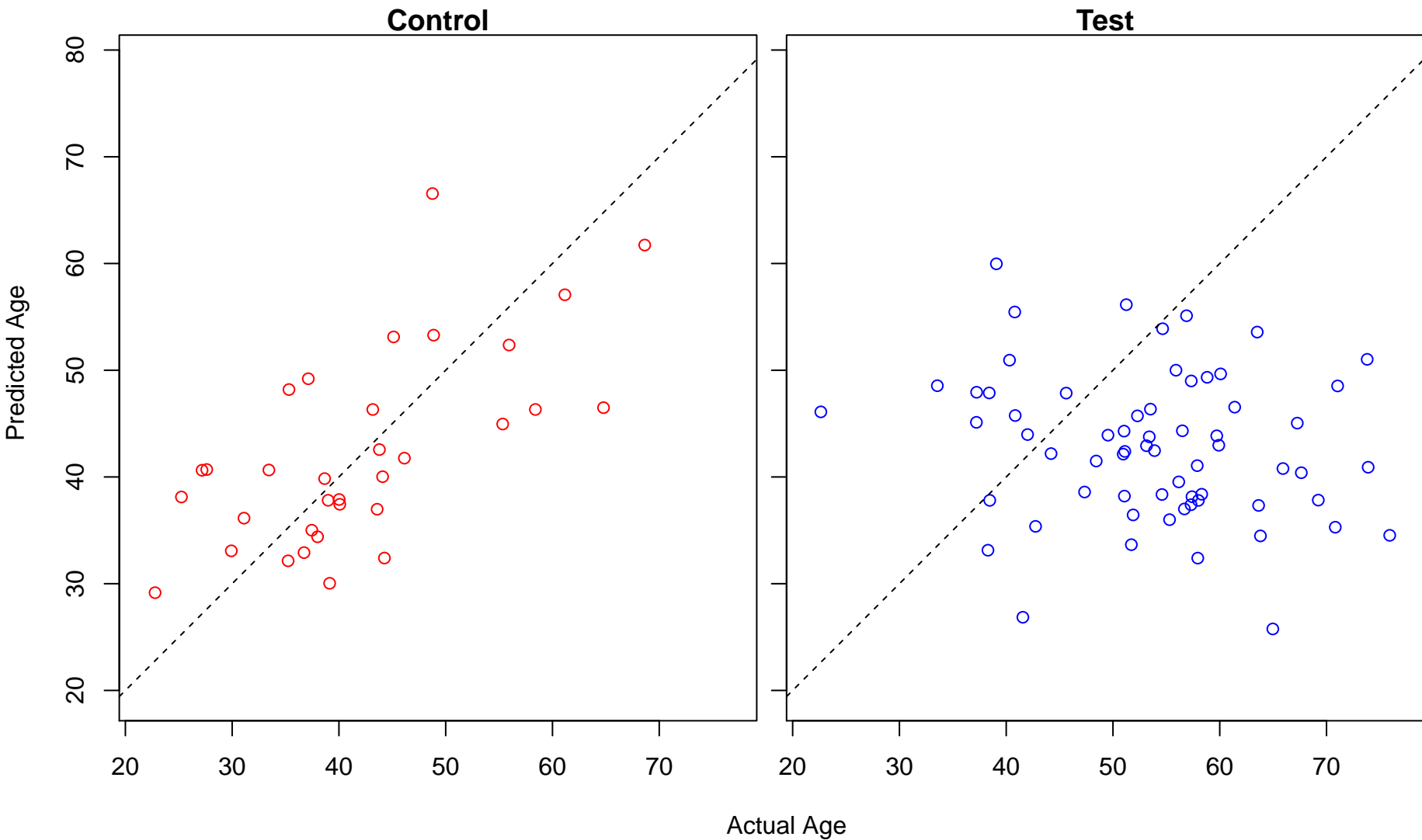
epidermal growth factor receptor signaling pathway (Score: 2.193274)



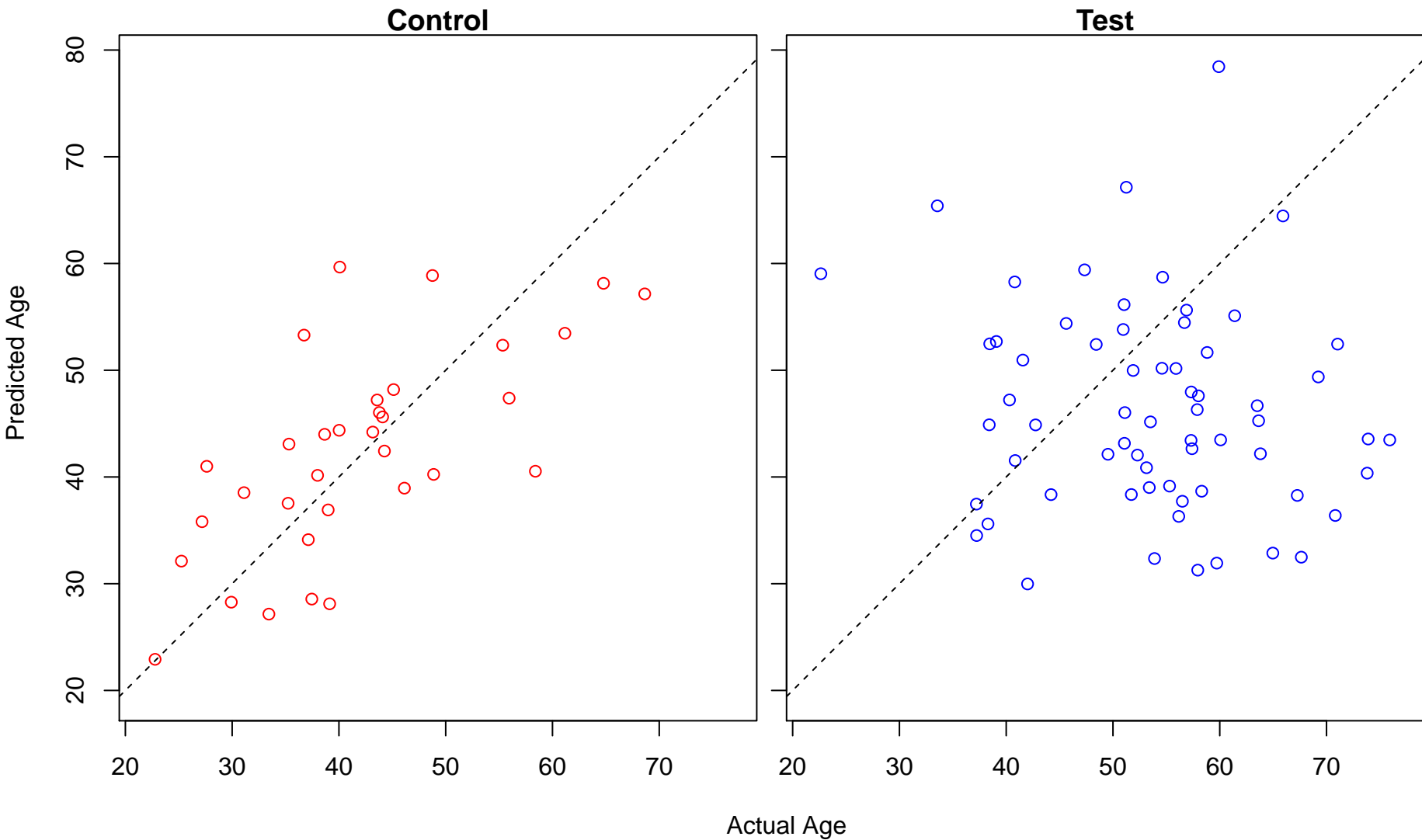
rhythmic behavior (Score: 2.193239)



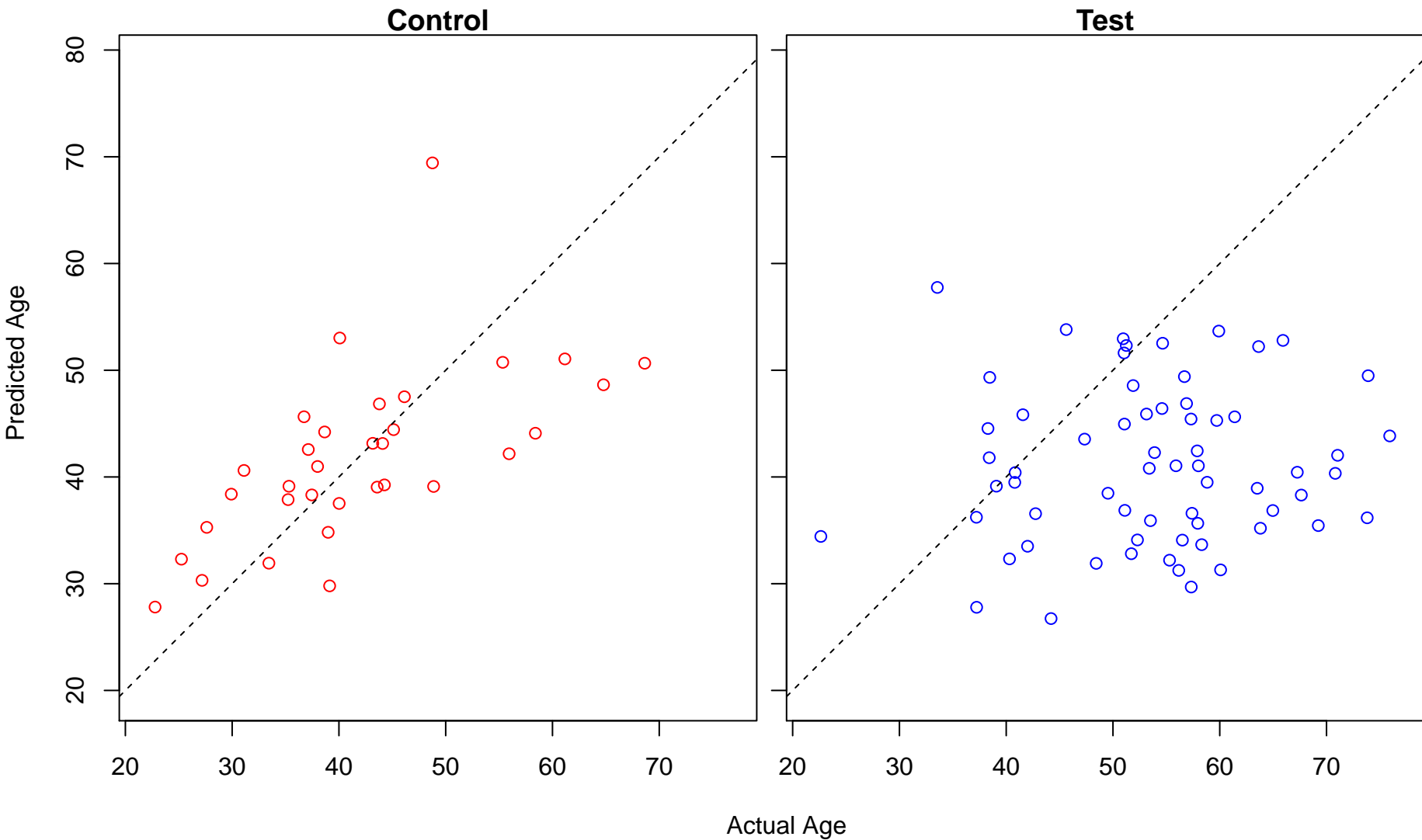
circadian behavior (Score: 2.193239)



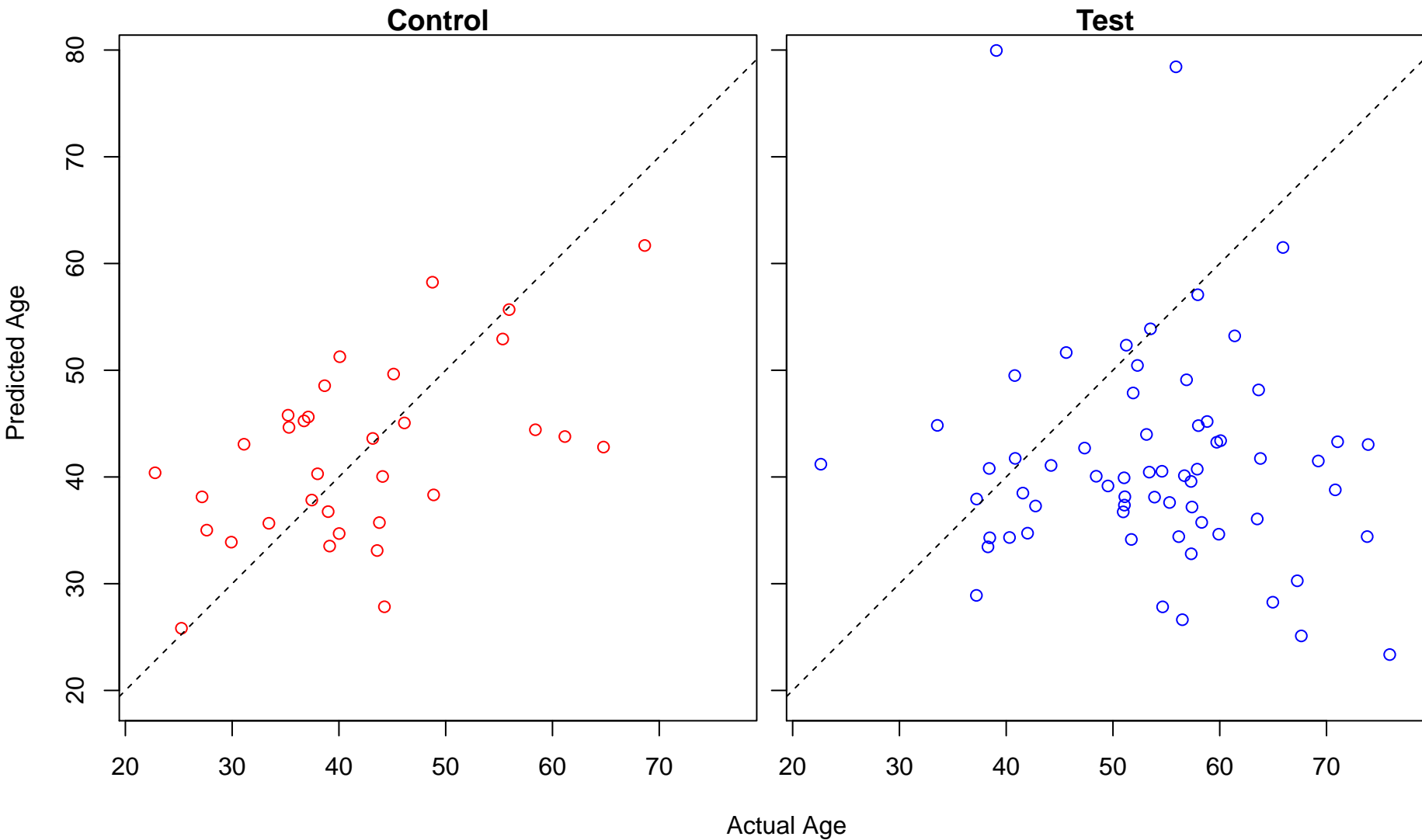
regulation of retrograde protein transport, ER to cytosol (Score: 2.180864)



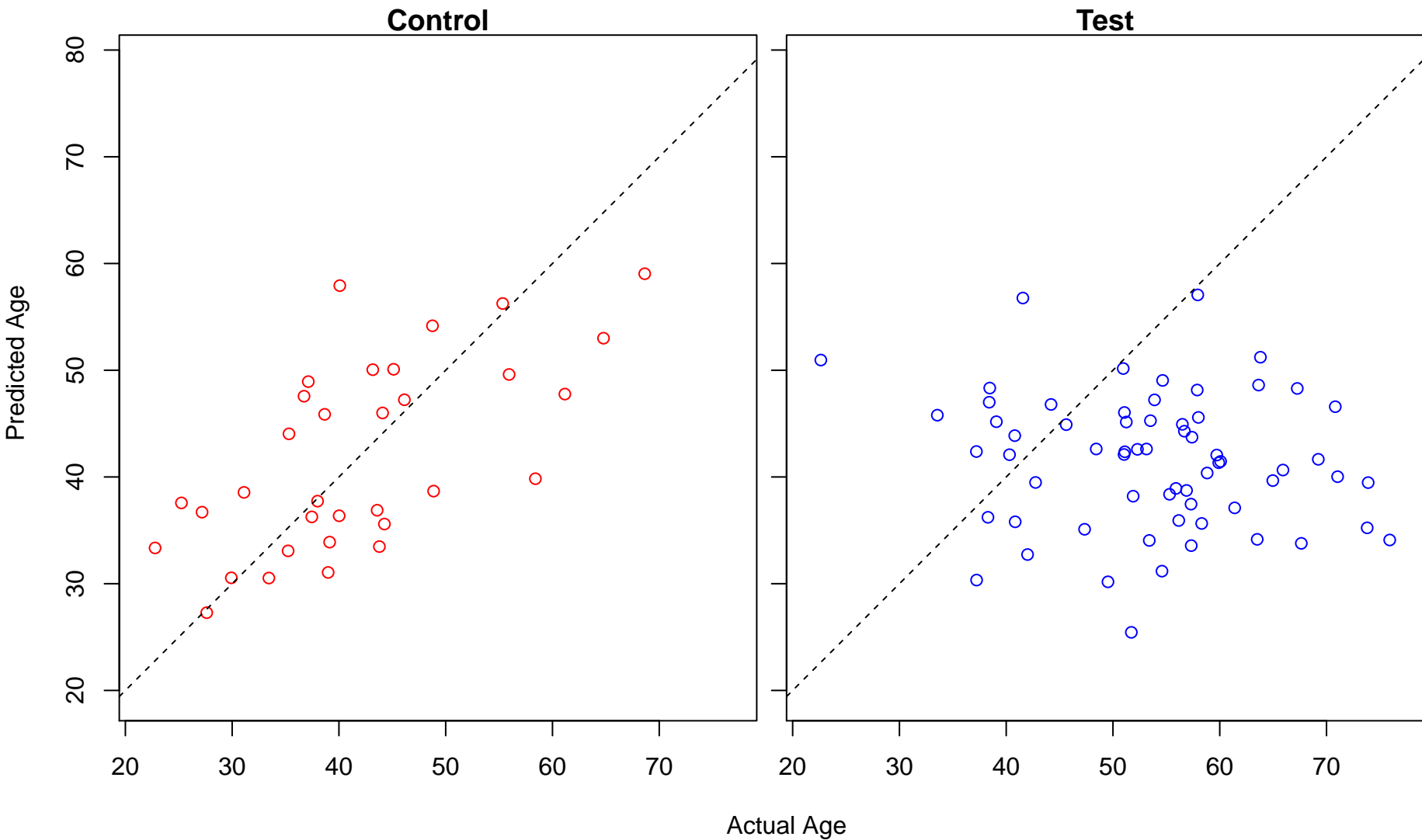
ERBB signaling pathway (Score: 2.179066)



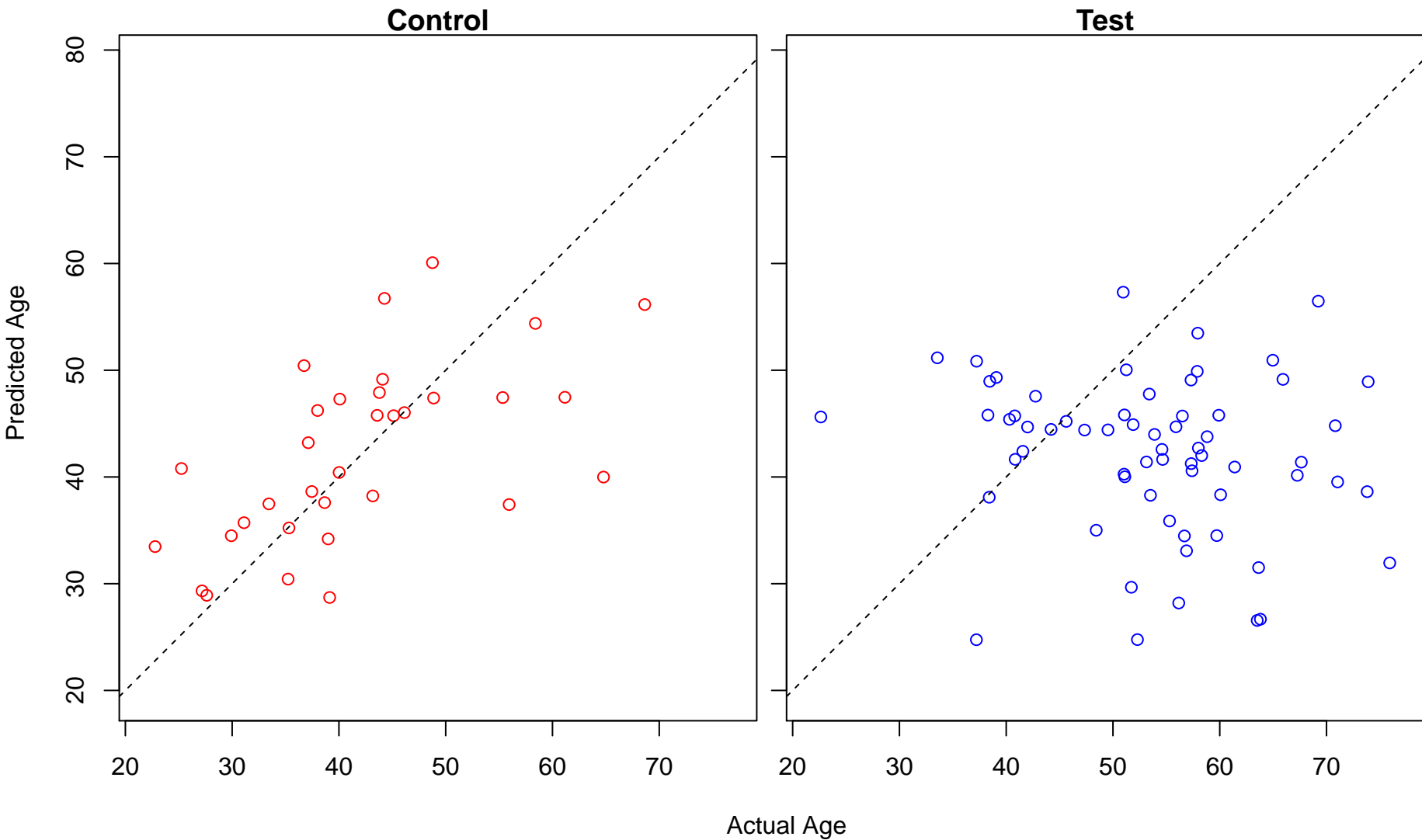
response to iron ion (Score: 2.178265)



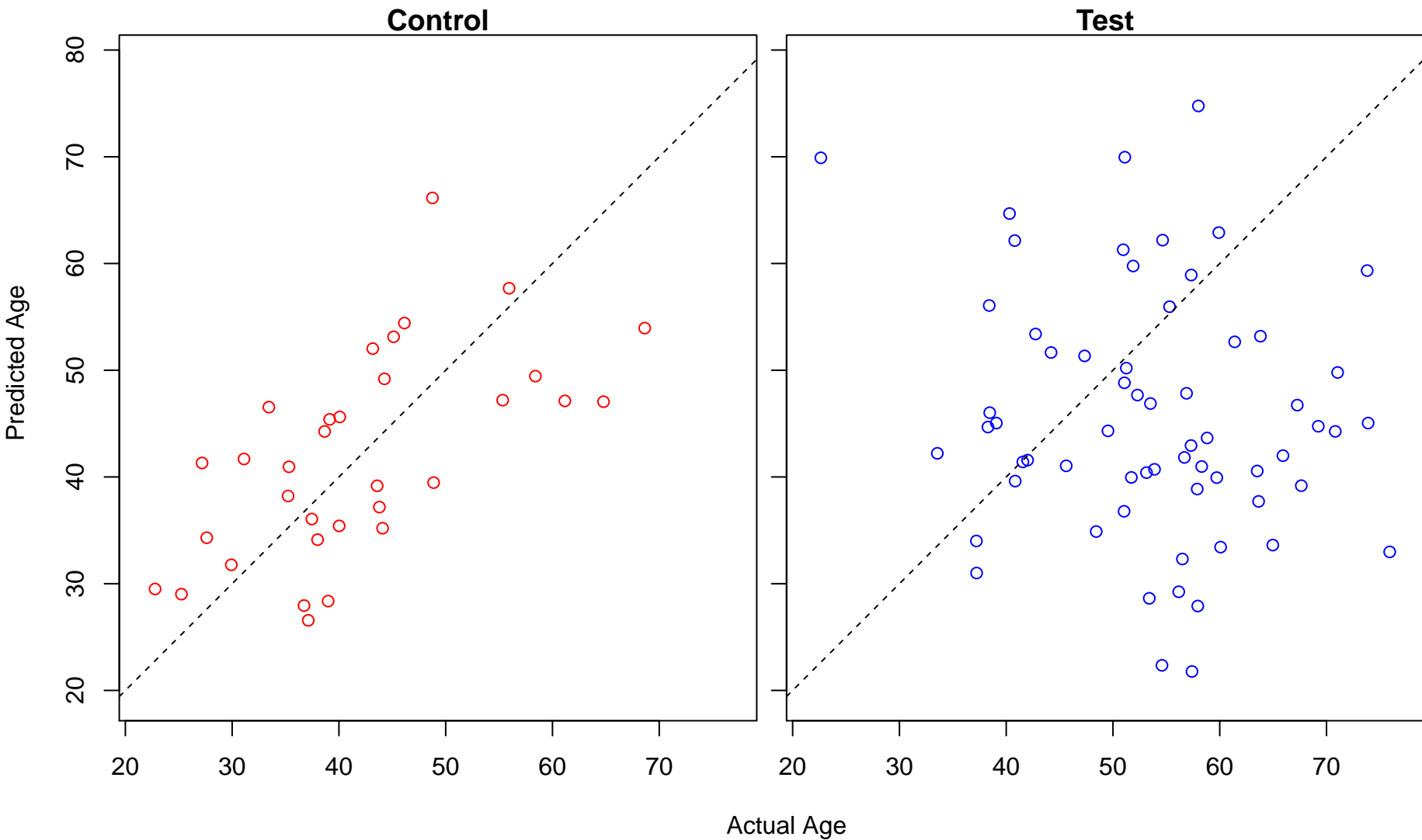
transmission of nerve impulse (Score: 2.177814)



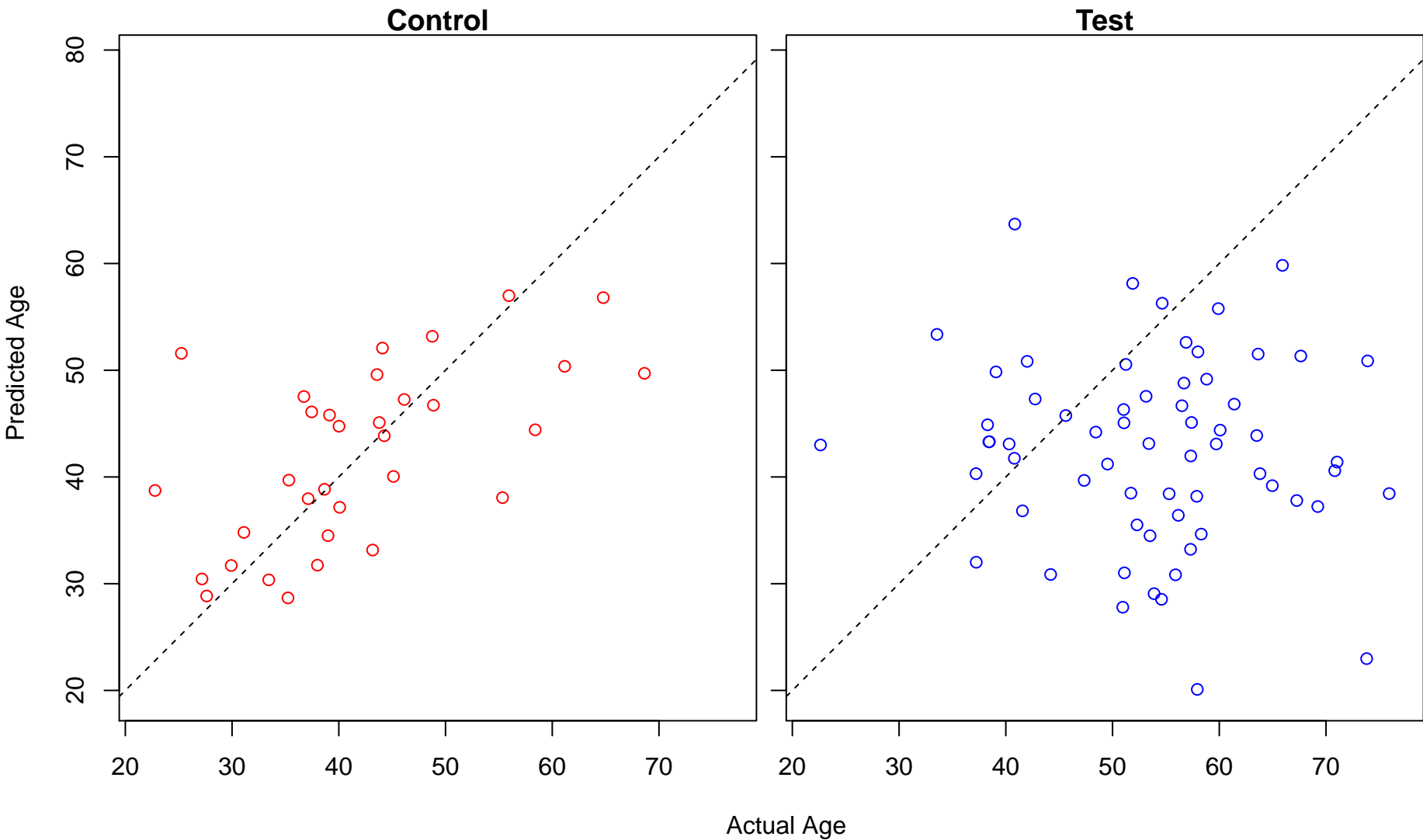
protein activation cascade (Score: 2.176364)



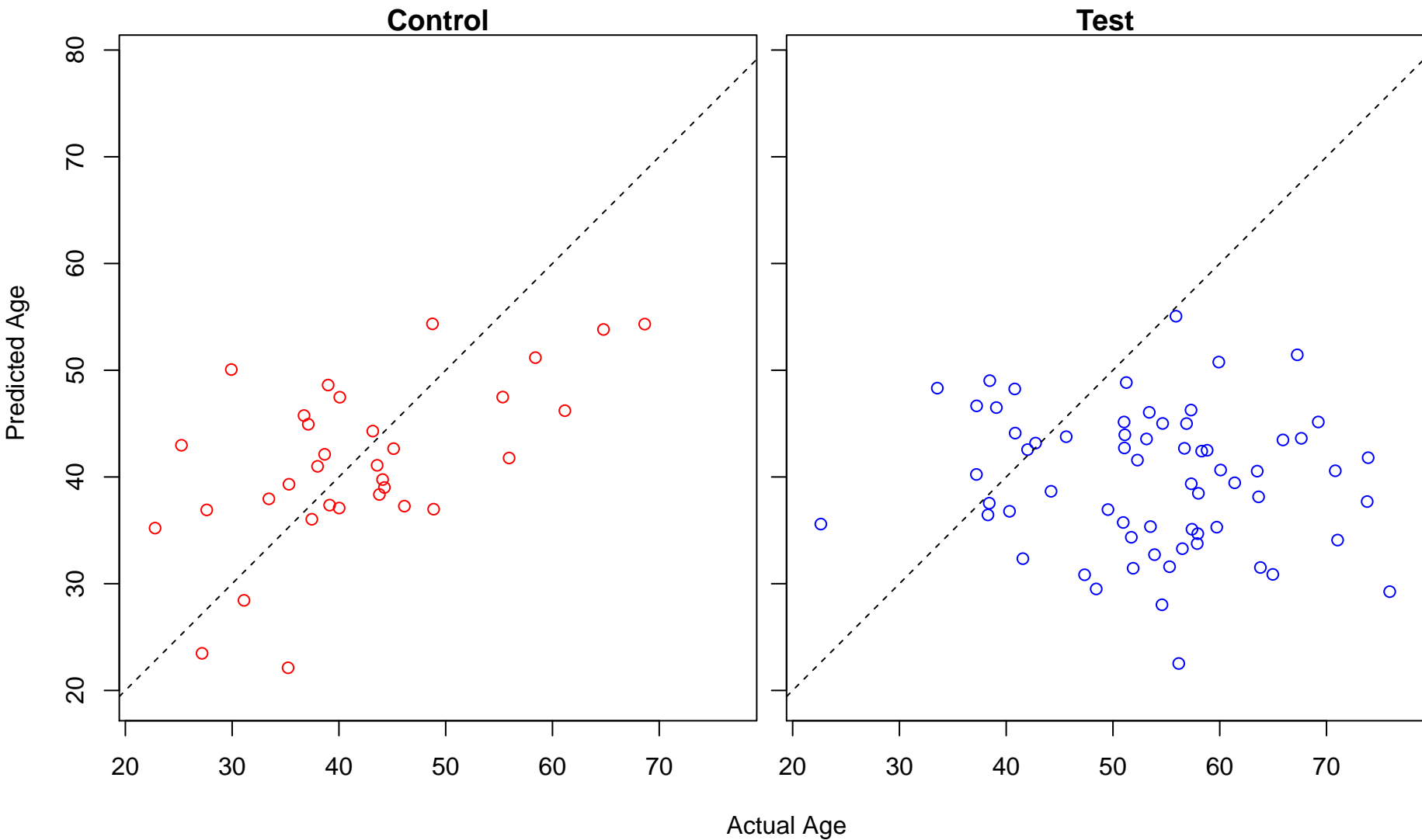
negative regulation of potassium ion transmembrane transporter activity (Score: 2.176362)



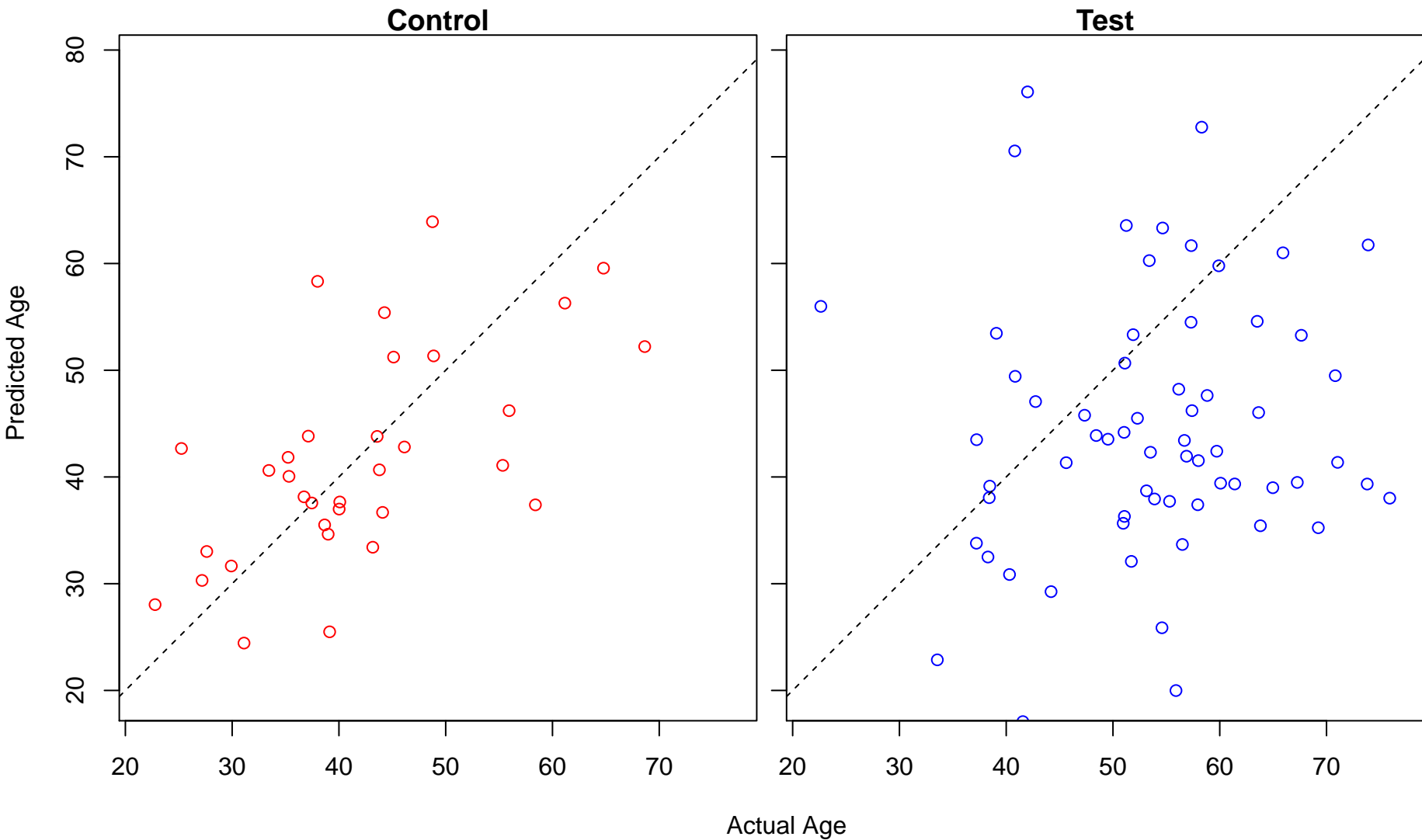
activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c (Score: 2)



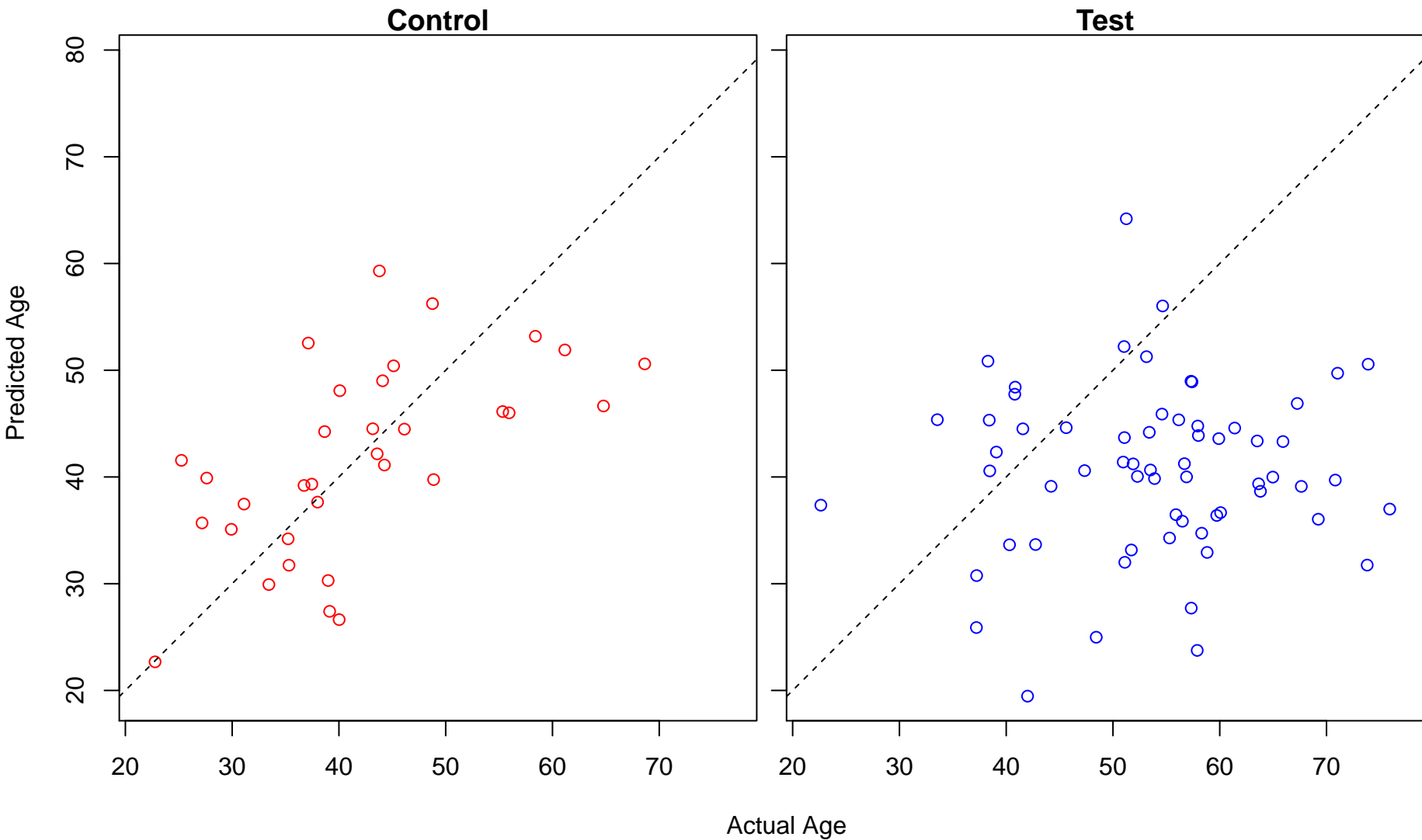
lipid homeostasis (Score: 2.174280)



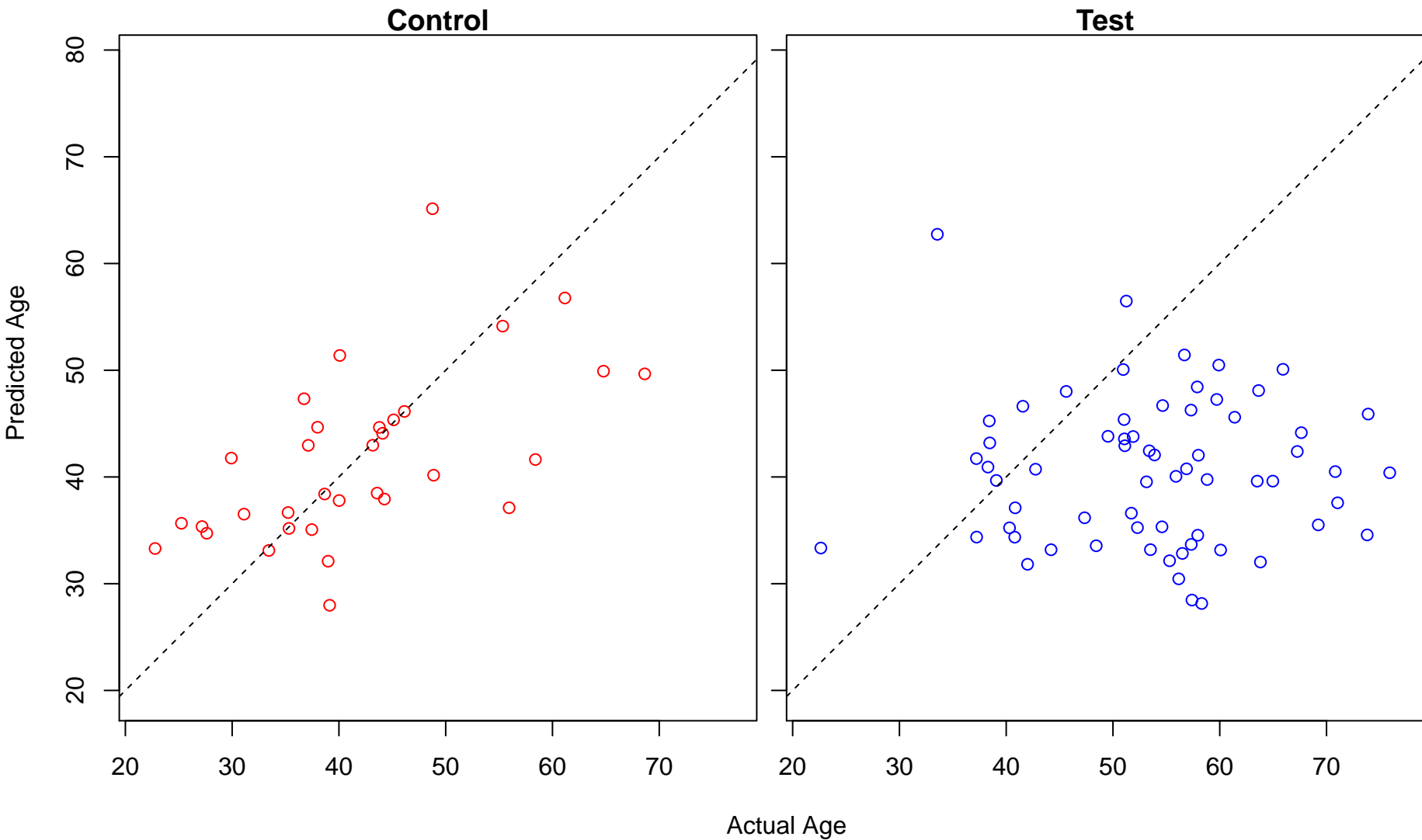
mitotic G2/M transition checkpoint (Score: 2.166363)



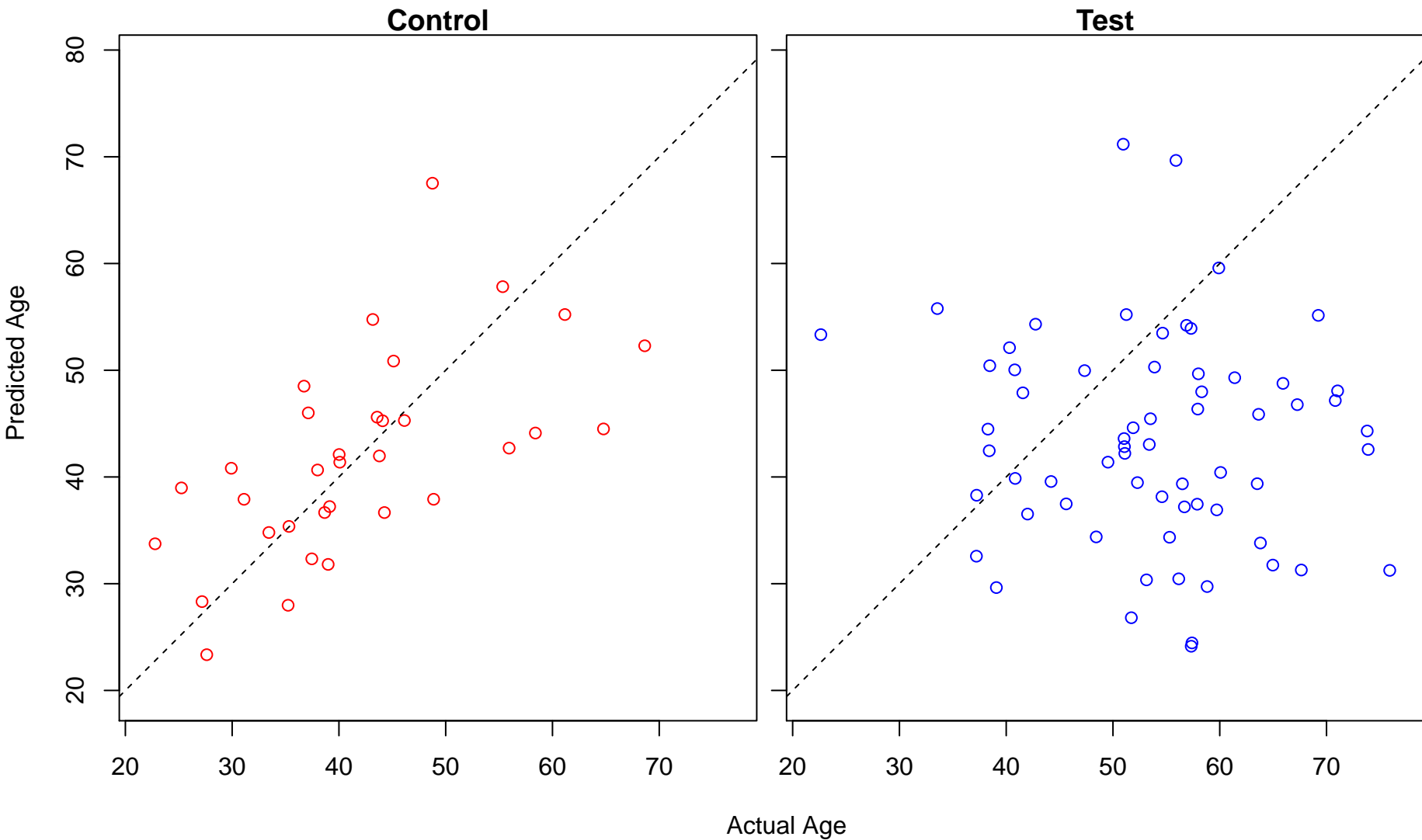
phosphatidylethanolamine metabolic process (Score: 2.166224)



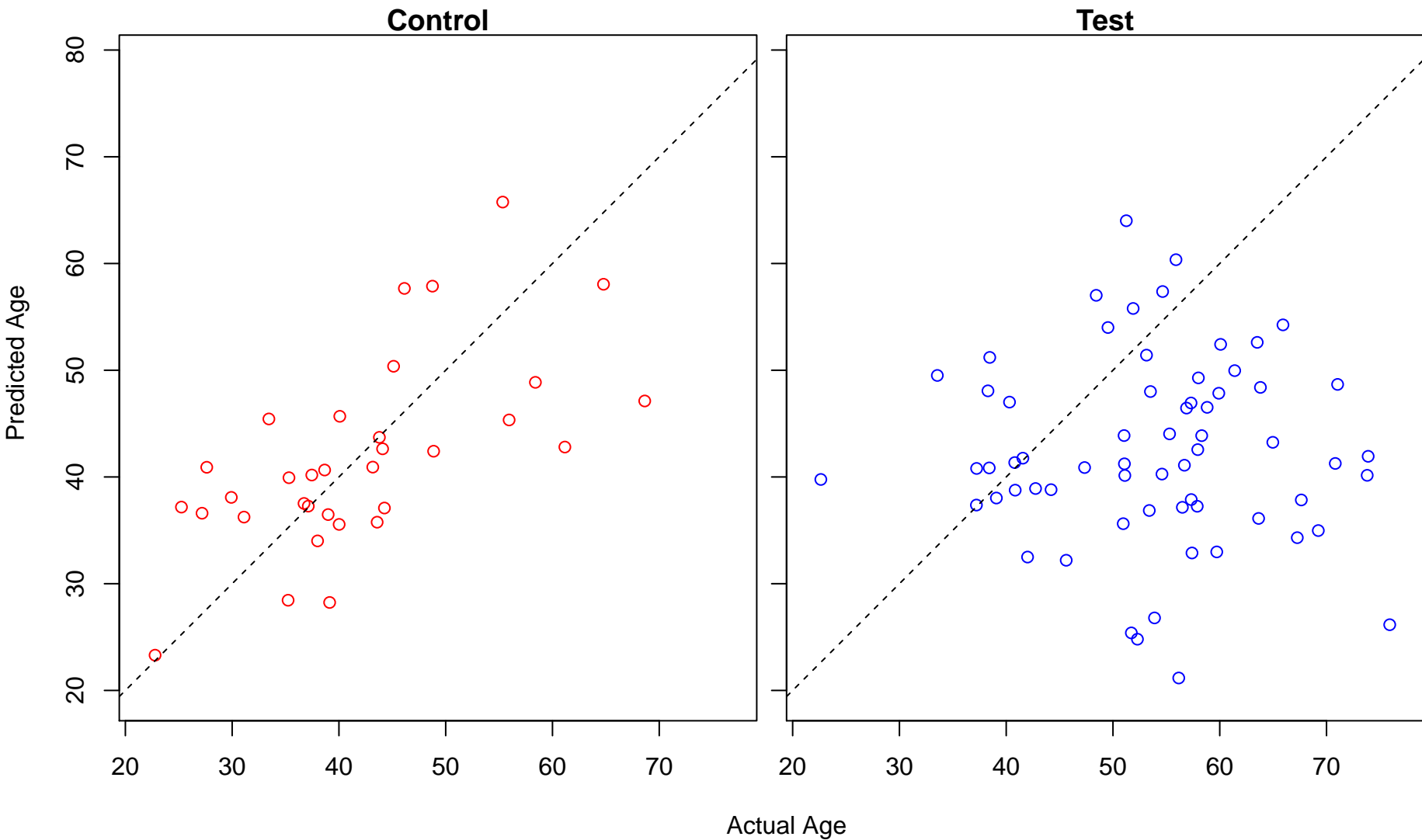
fibroblast growth factor receptor signaling pathway (Score: 2.165268)



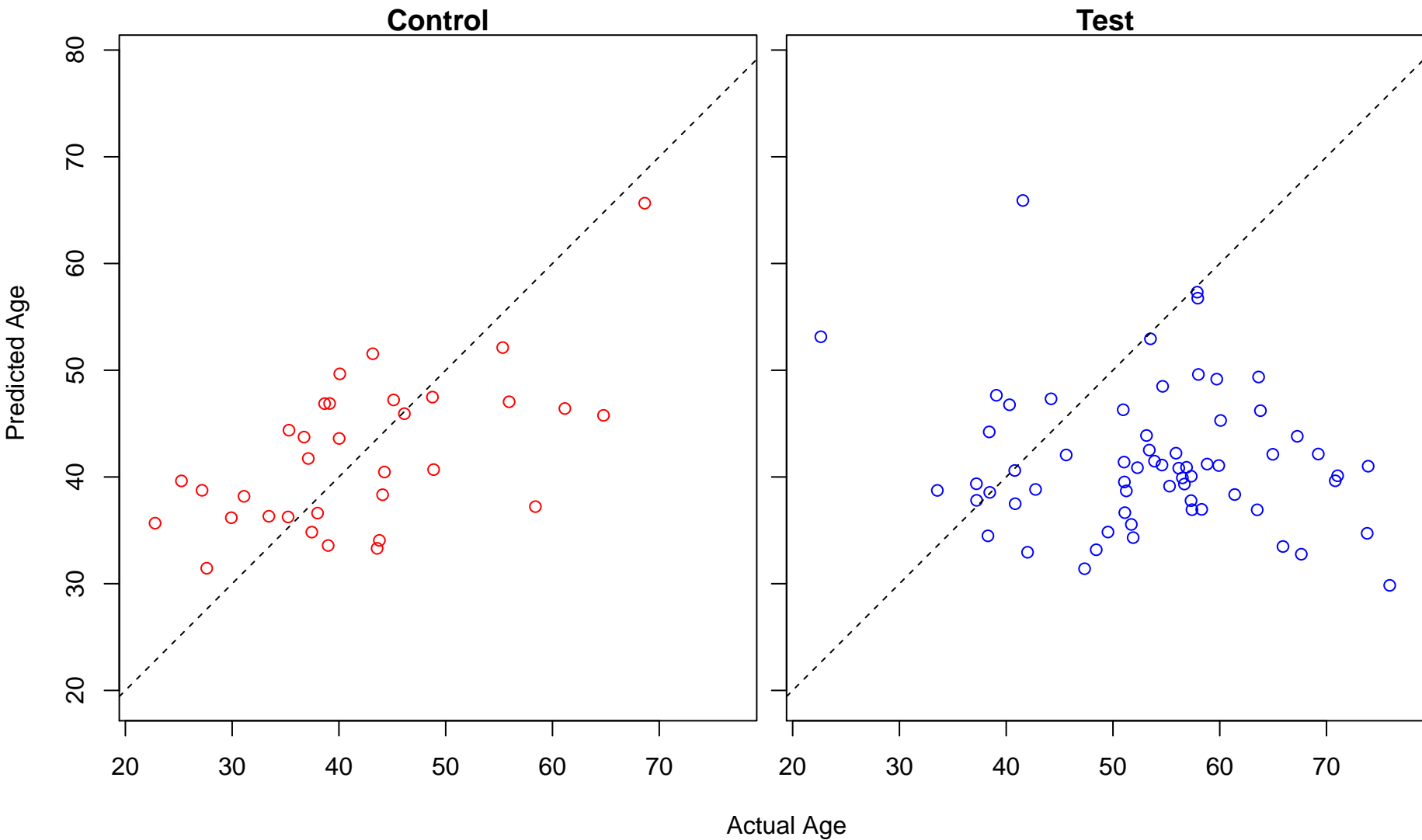
DNA damage response, detection of DNA damage (Score: 2.162150)



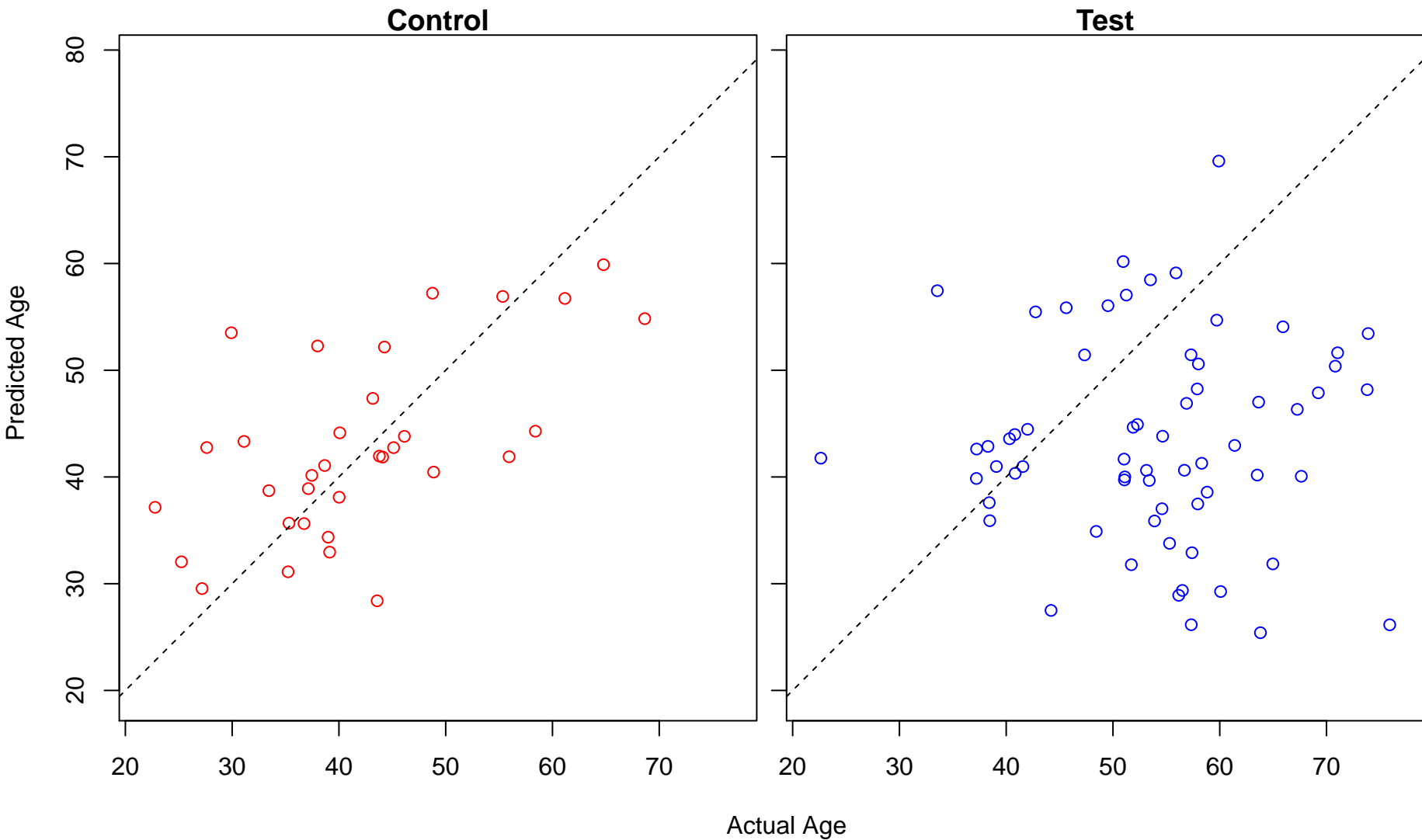
microtubule organizing center organization (Score: 2.153948)



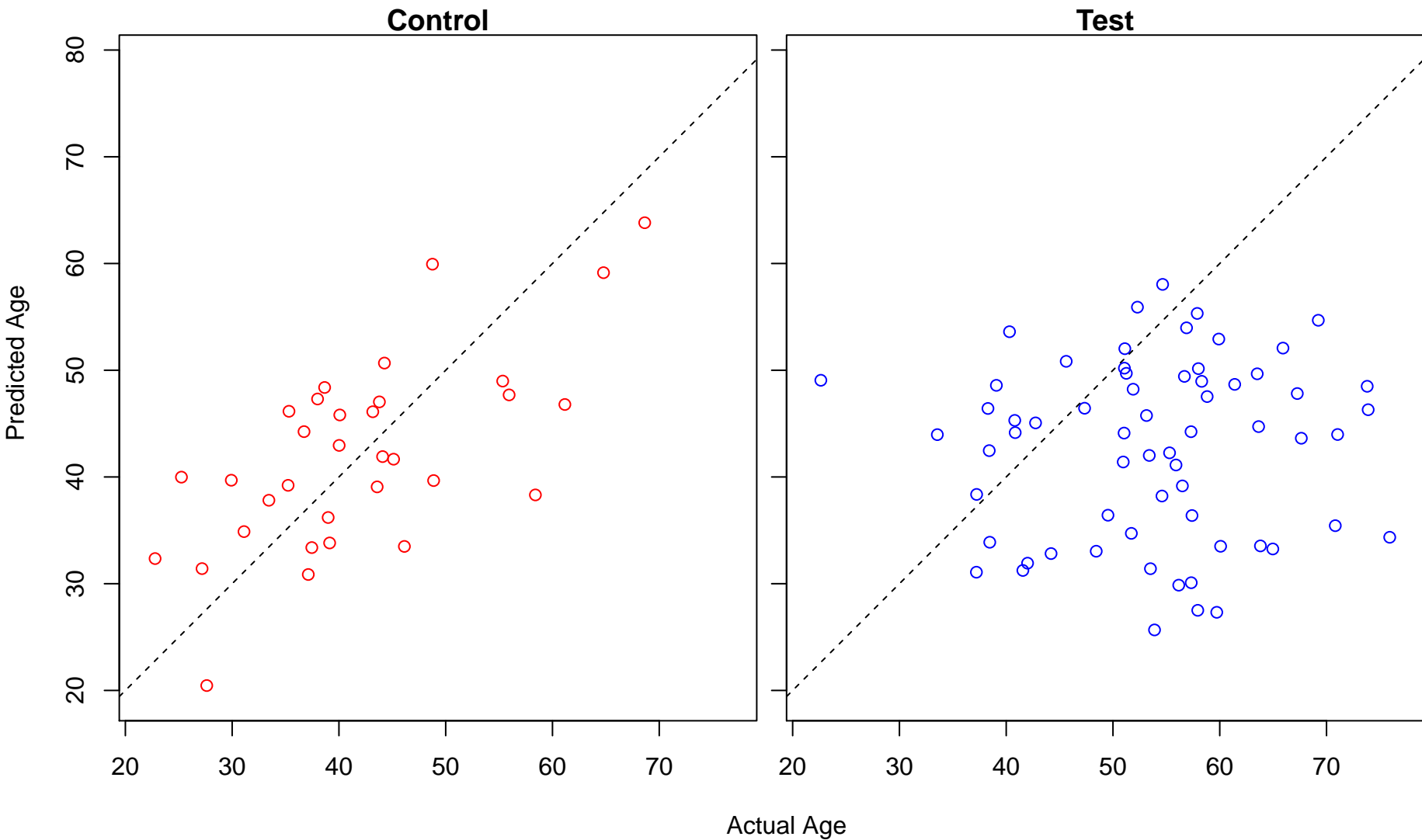
detection of calcium ion (Score: 2.150516)



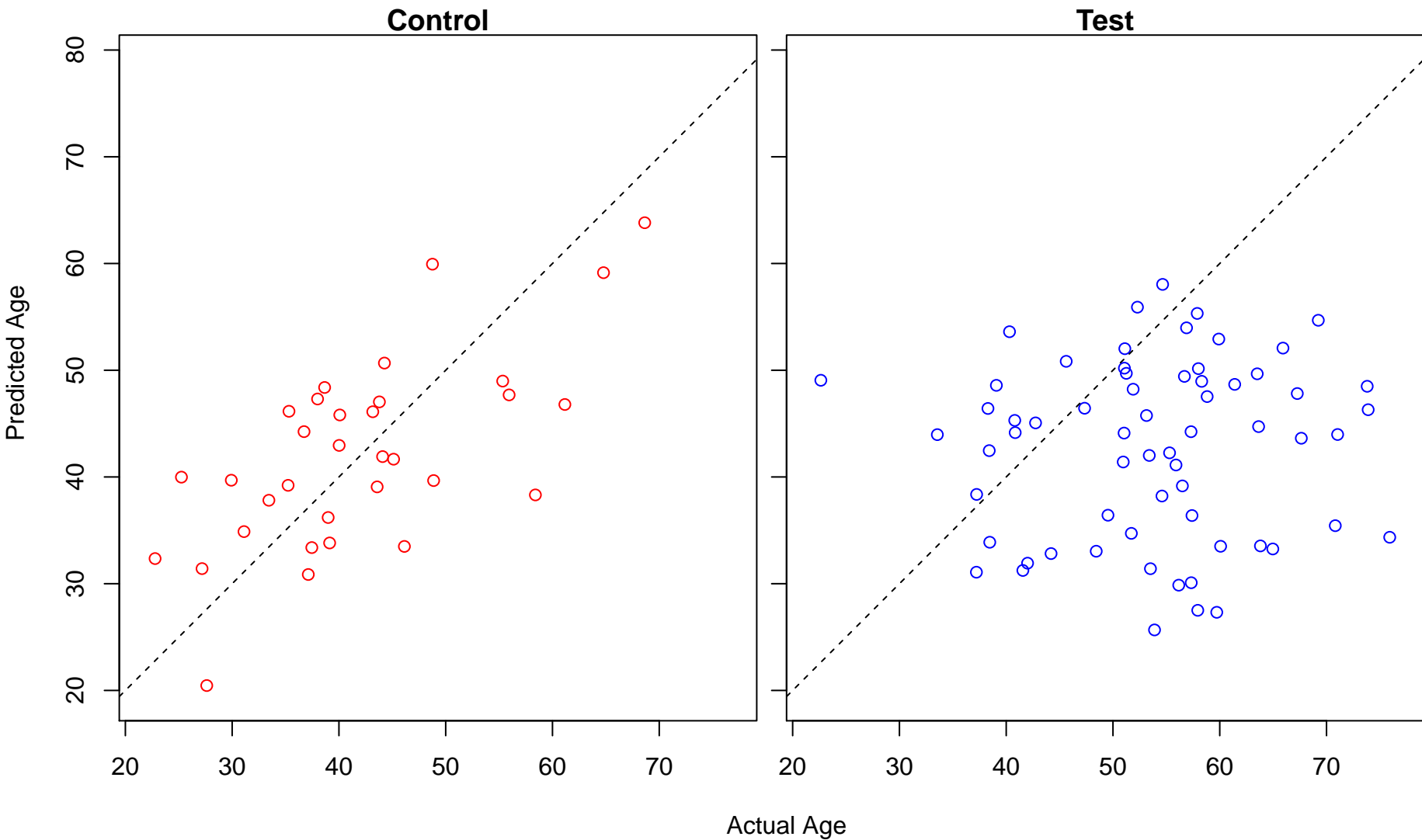
detection of external stimulus (Score: 2.149929)



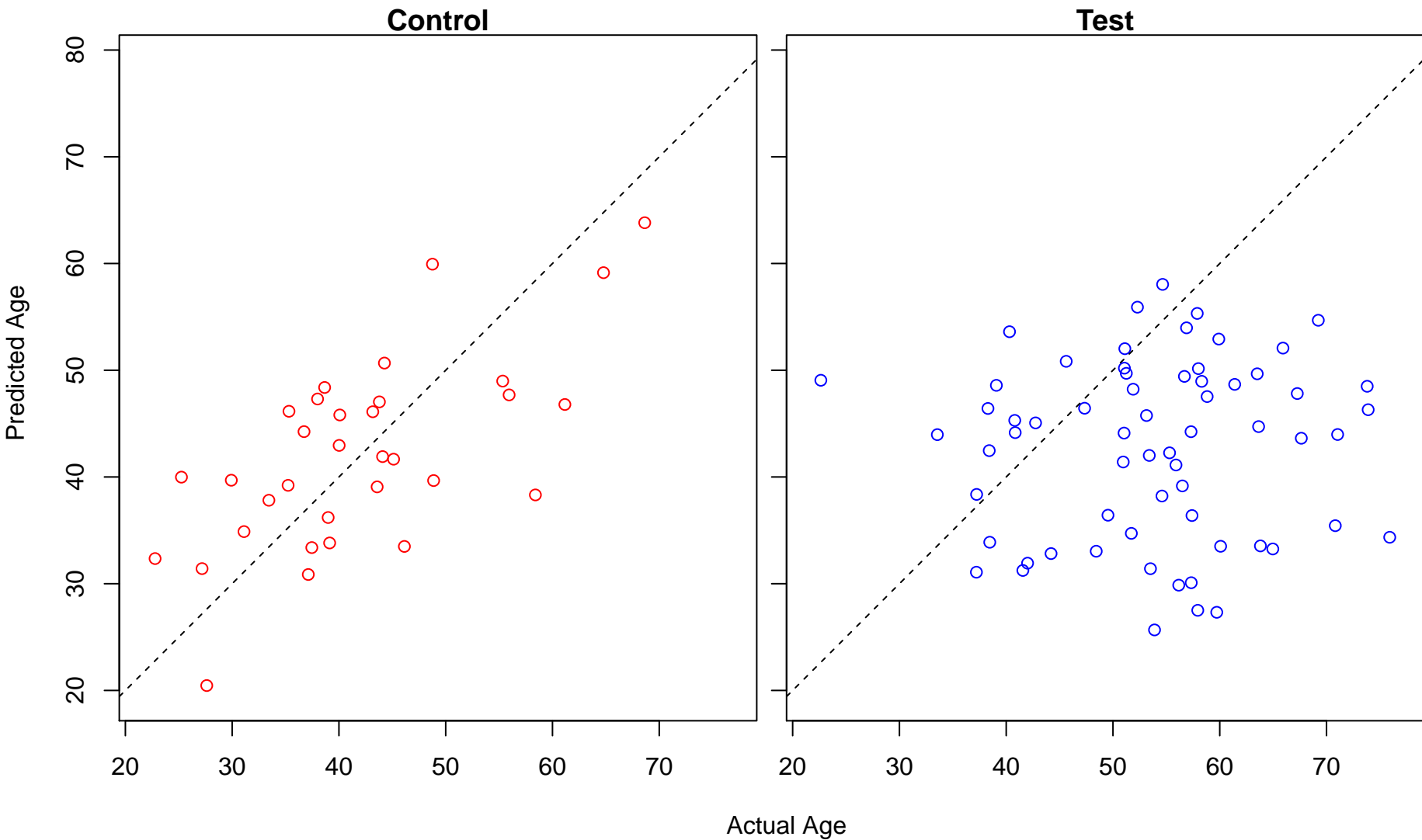
protein targeting to peroxisome (Score: 2.148769)



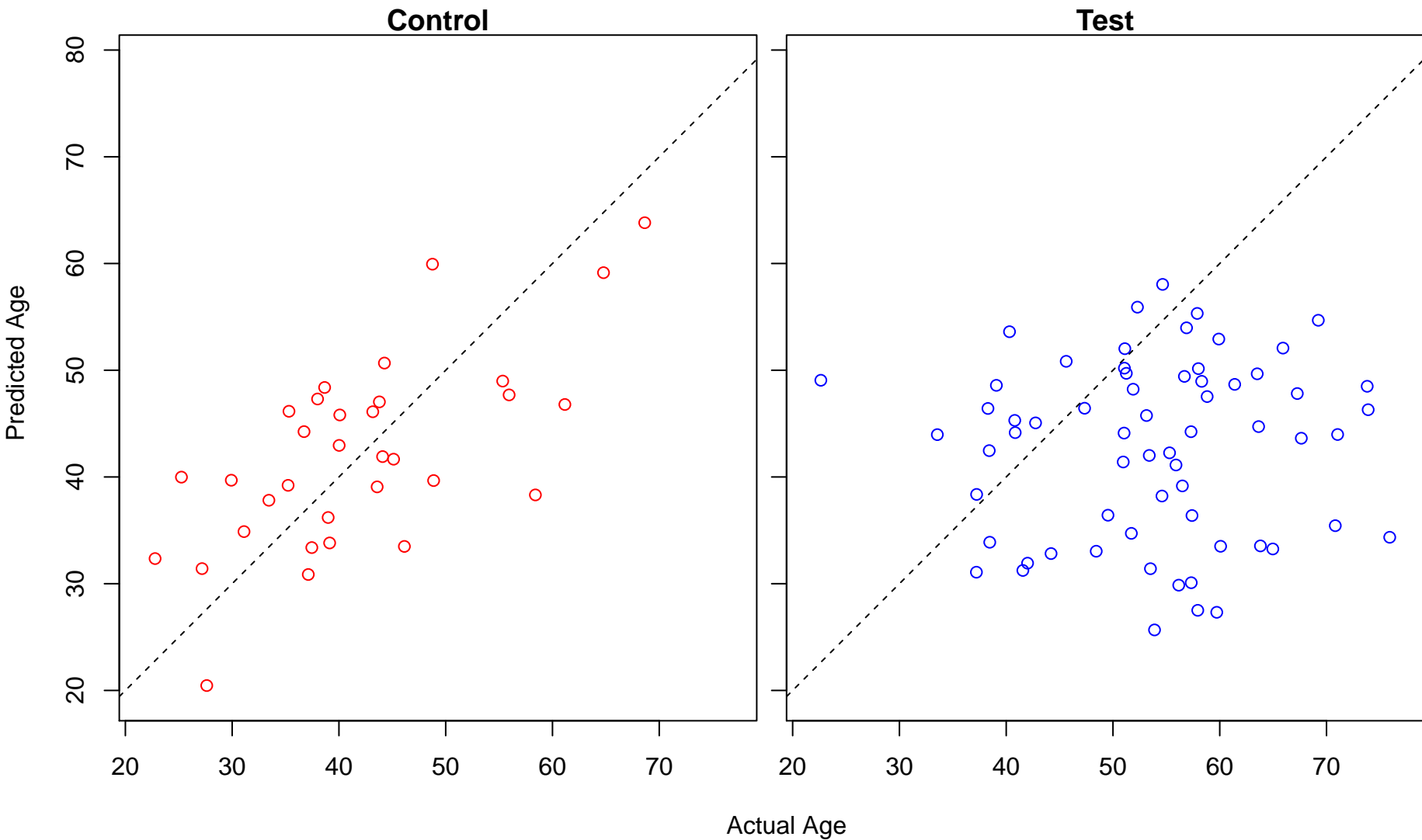
peroxisomal transport (Score: 2.148769)



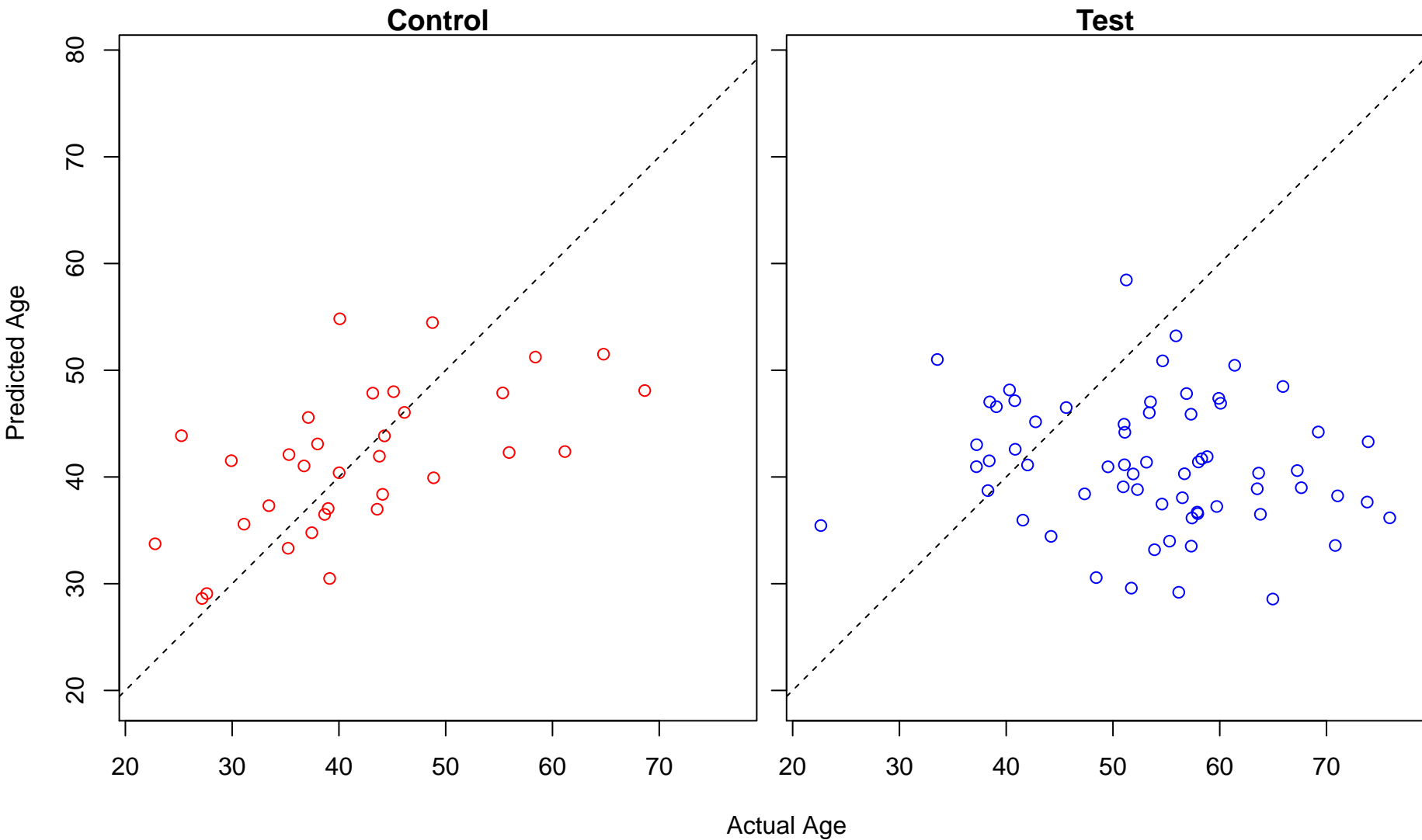
protein localization to peroxisome (Score: 2.148769)



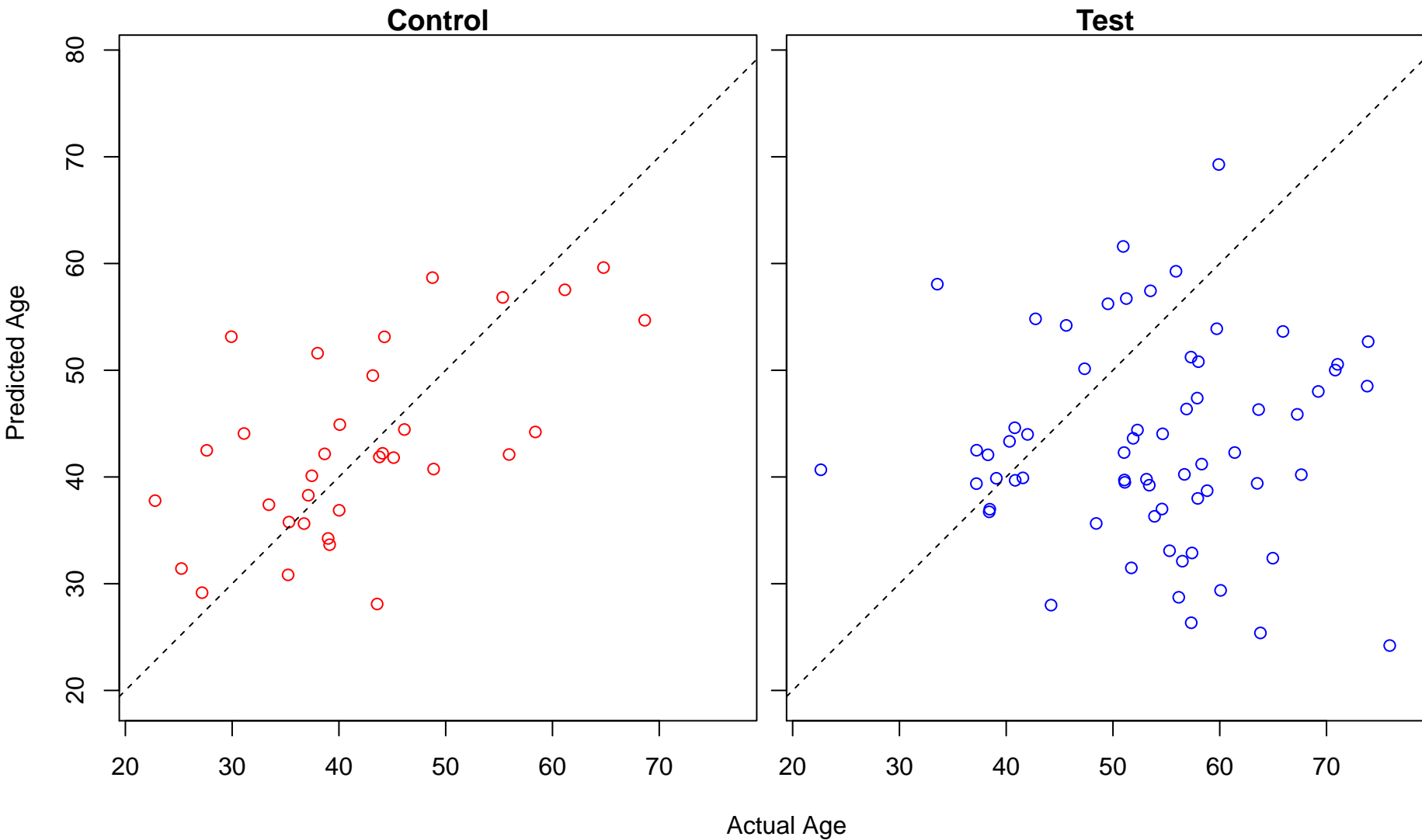
establishment of protein localization to peroxisome (Score: 2.148769)



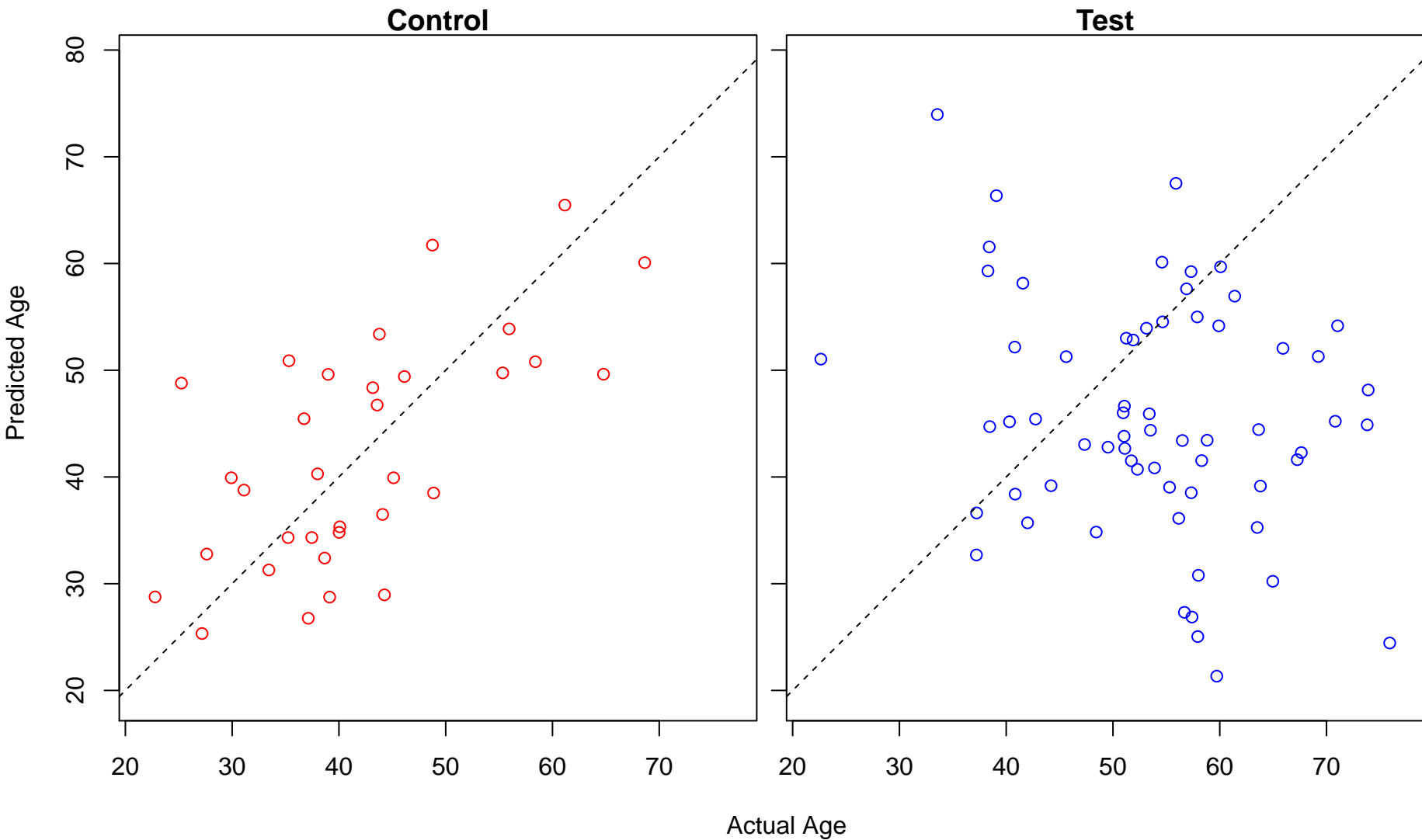
organic hydroxy compound transport (Score: 2.145796)



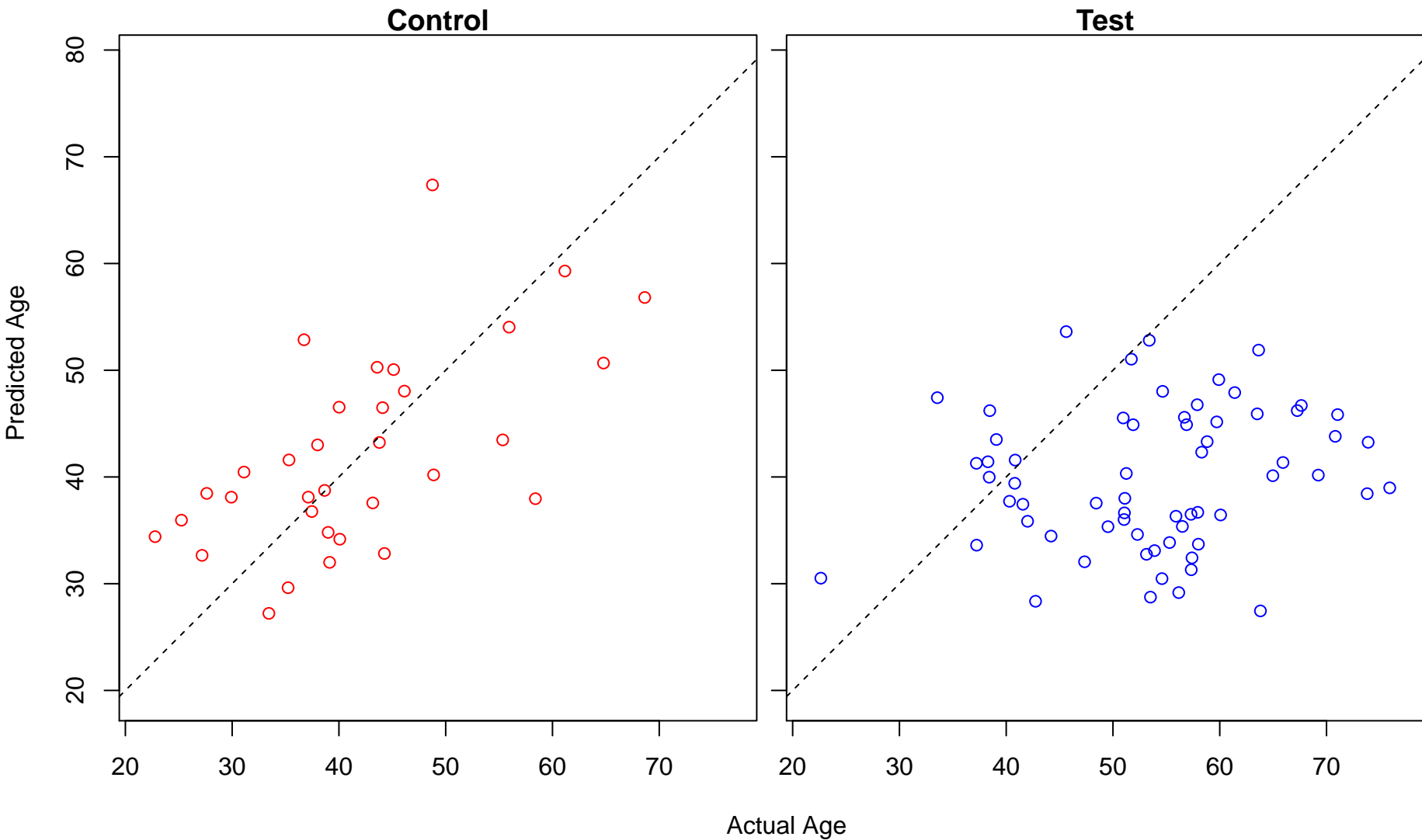
detection of abiotic stimulus (Score: 2.140861)



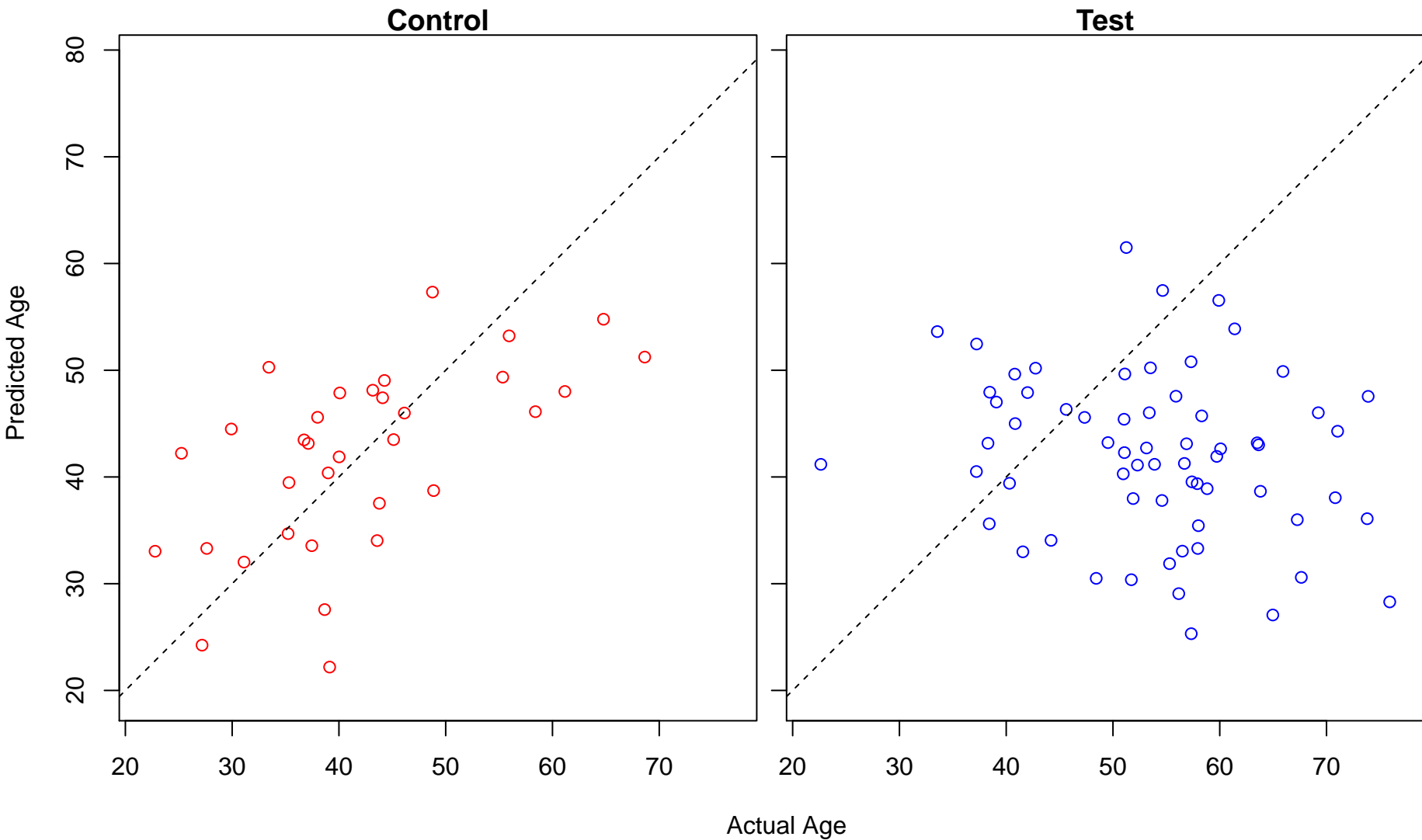
spermatid development (Score: 2.139050)



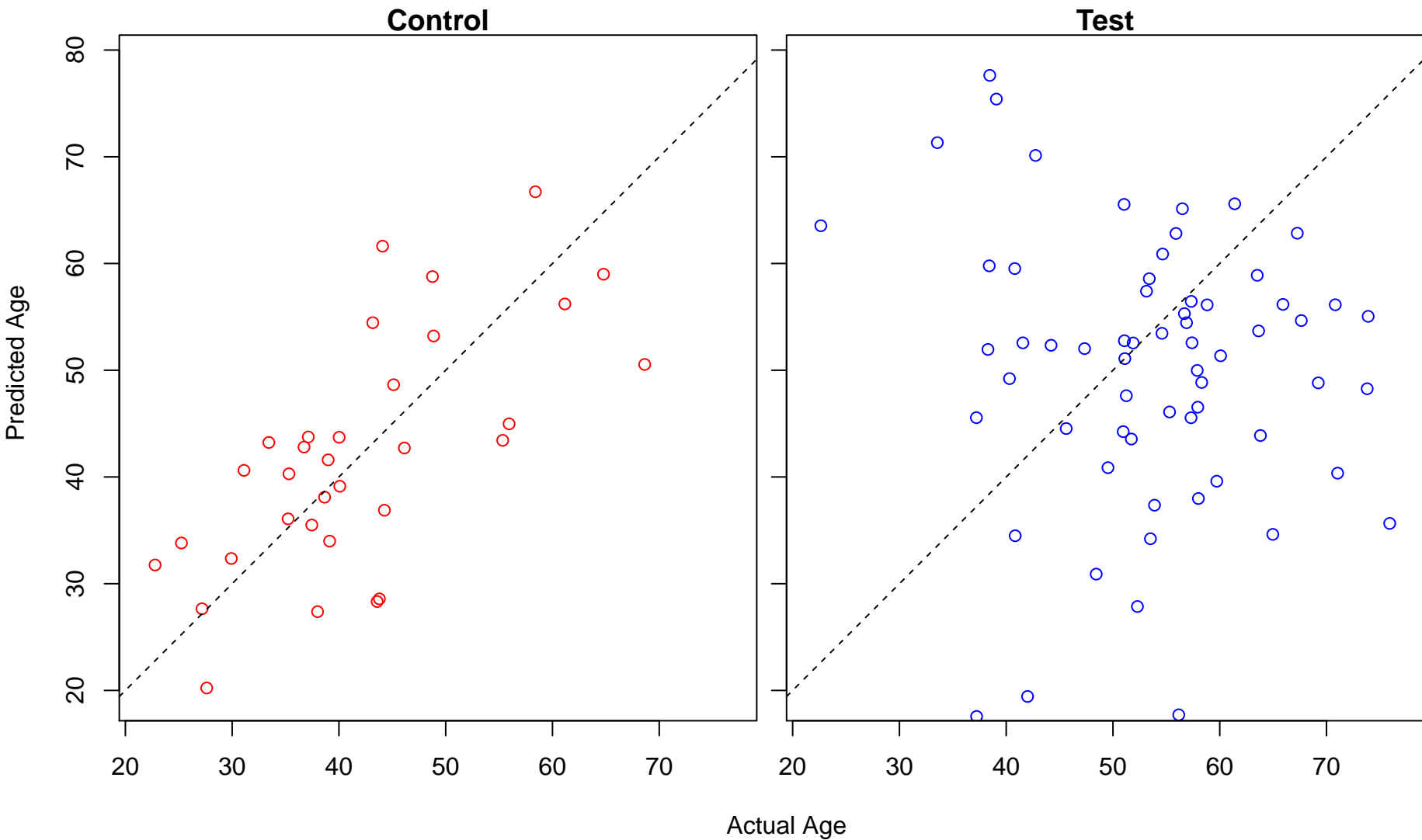
positive regulation of adherens junction organization (Score: 2.136614)



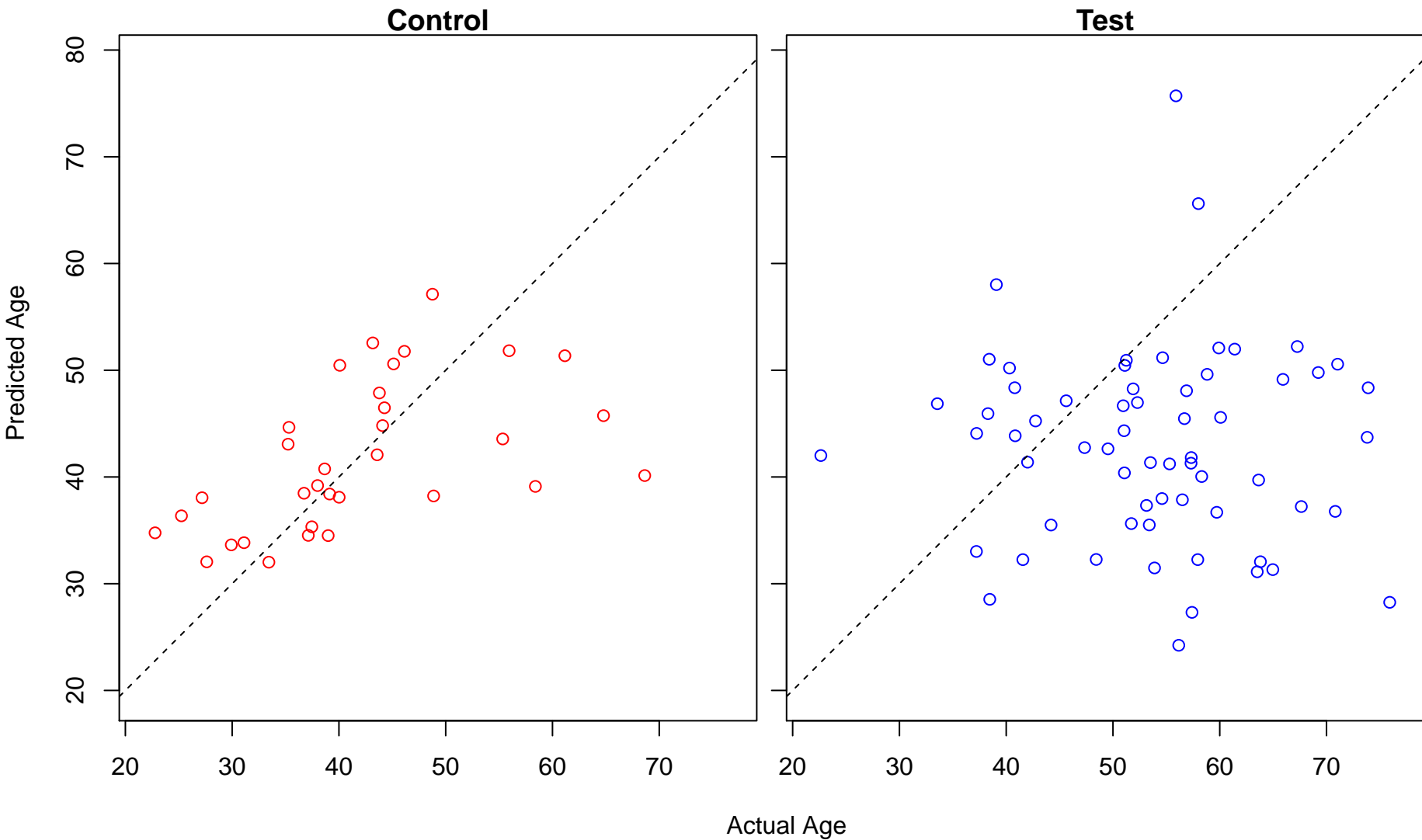
response to organophosphorus (Score: 2.135644)



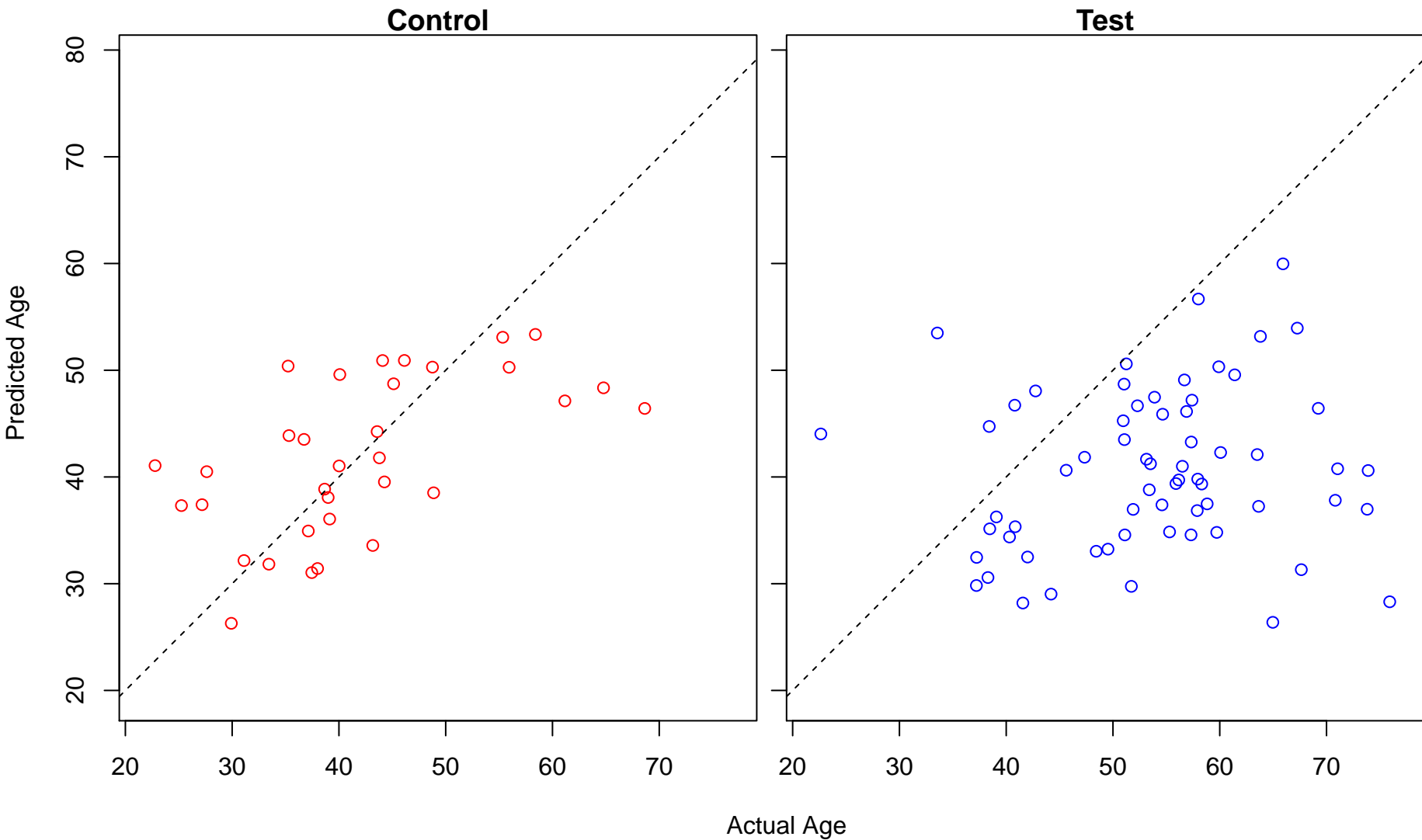
acute inflammatory response (Score: 2.133554)



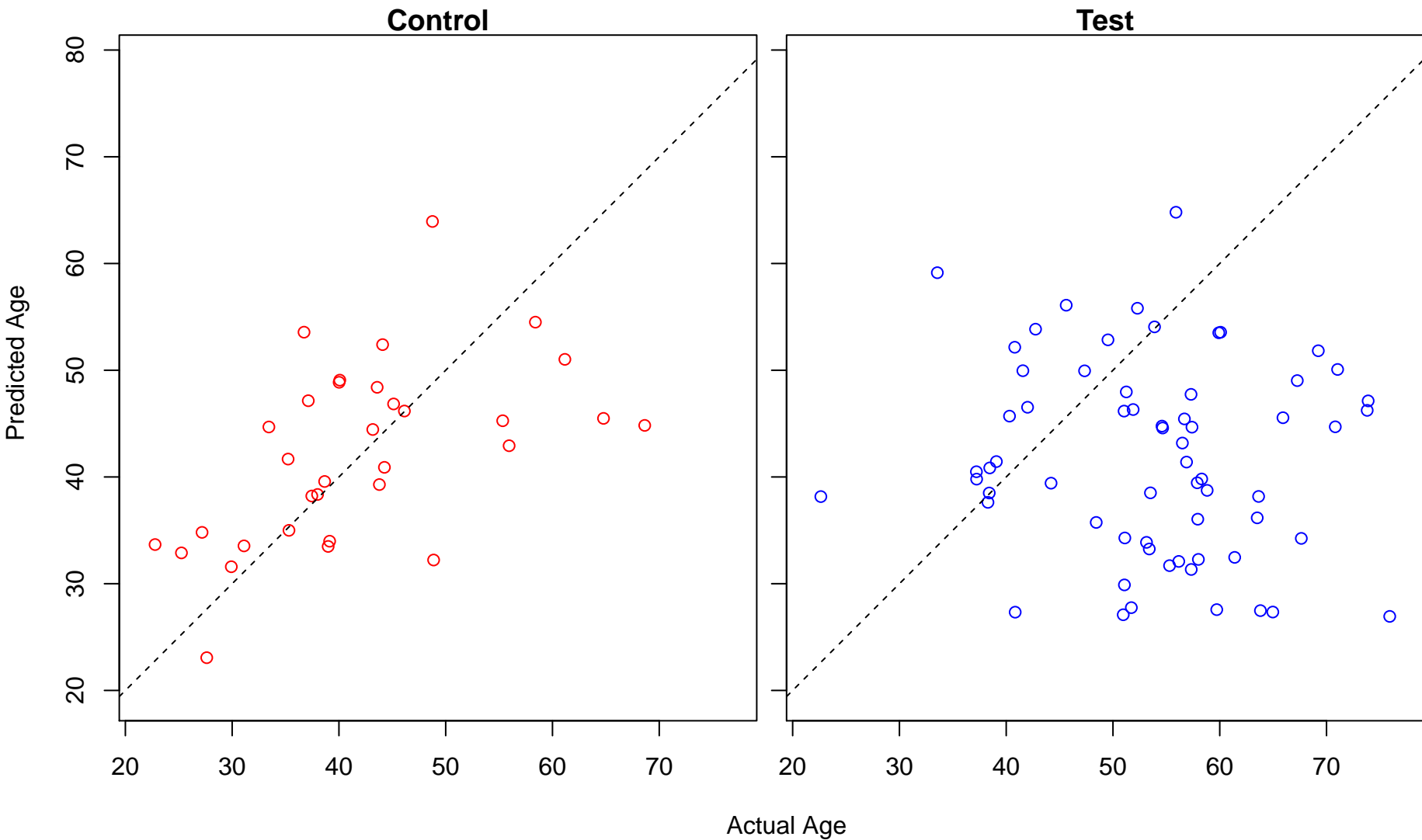
negative regulation of potassium ion transport (Score: 2.121302)



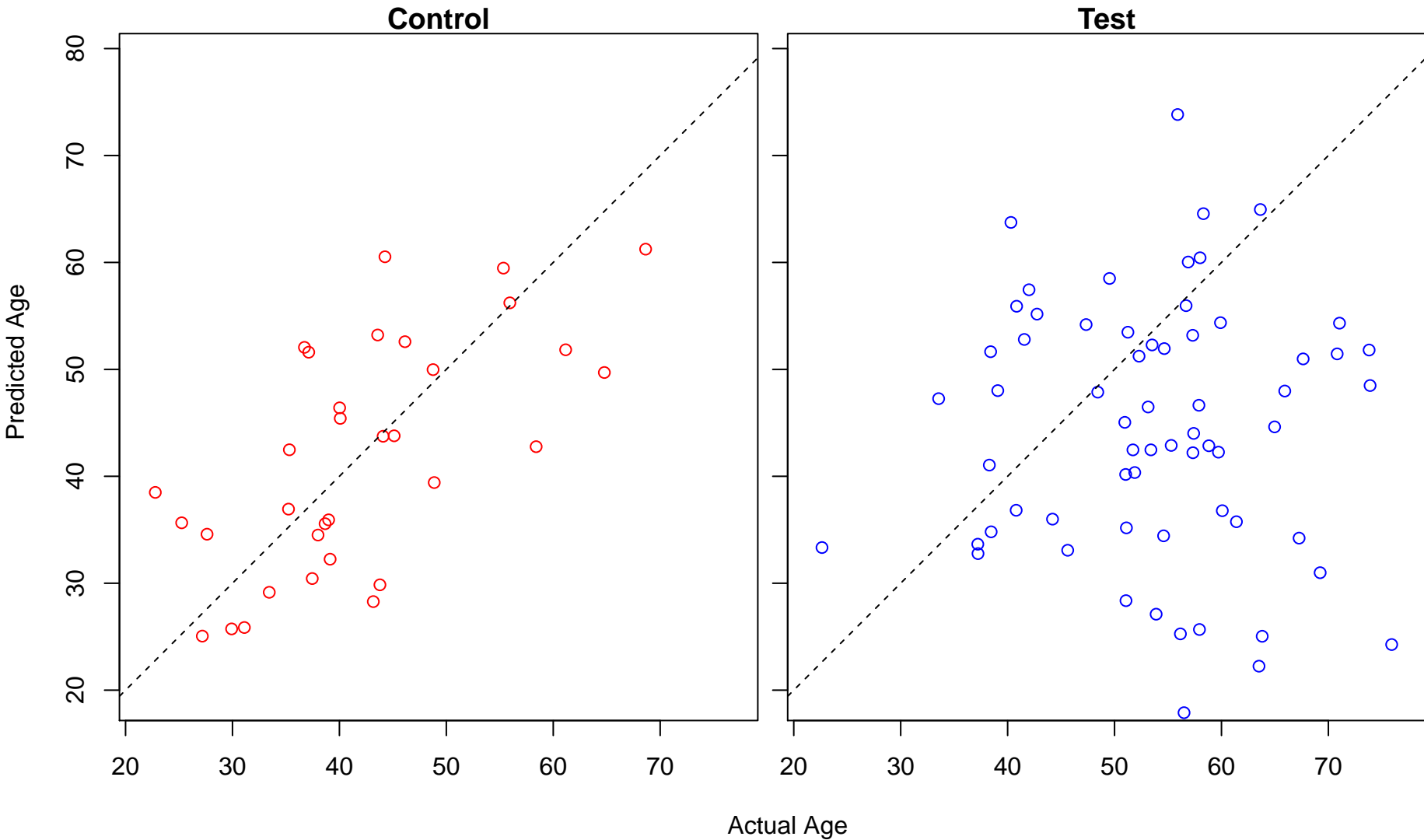
cell-cell signaling involved in cardiac conduction (Score: 2.119317)



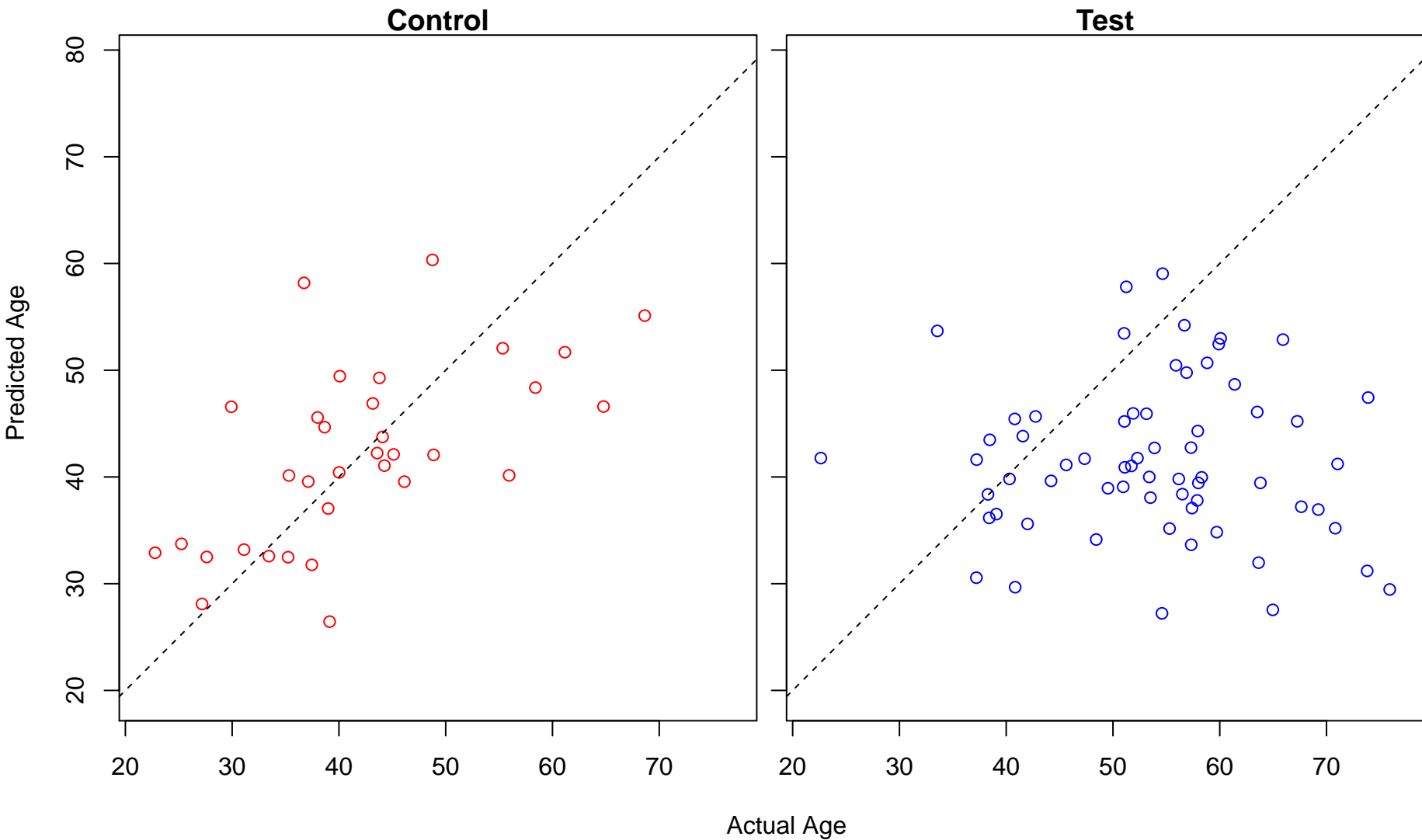
membrane depolarization (Score: 2.114795)



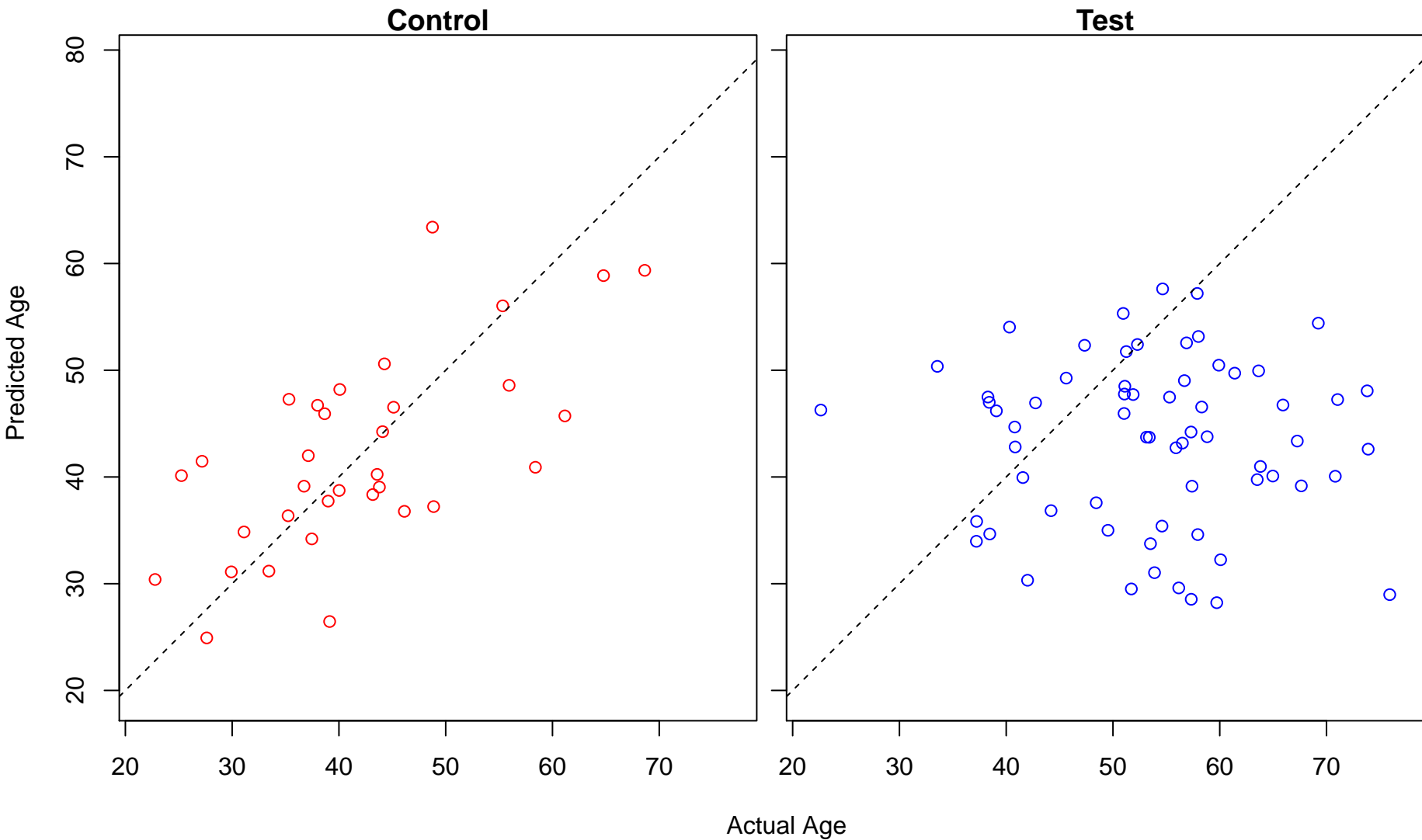
regulation of nitric oxide biosynthetic process (Score: 2.109653)



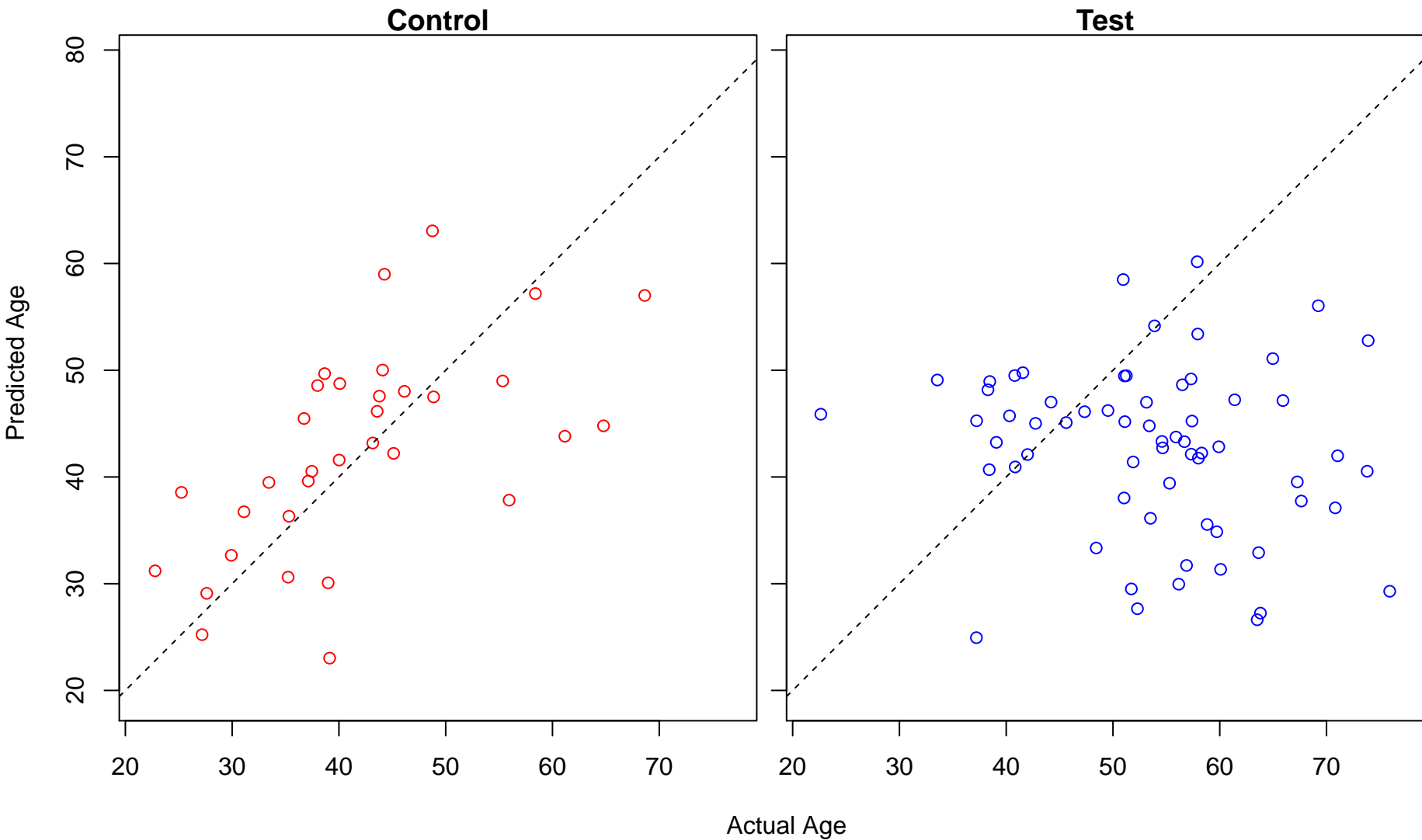
cellular response to tumor necrosis factor (Score: 2.109328)



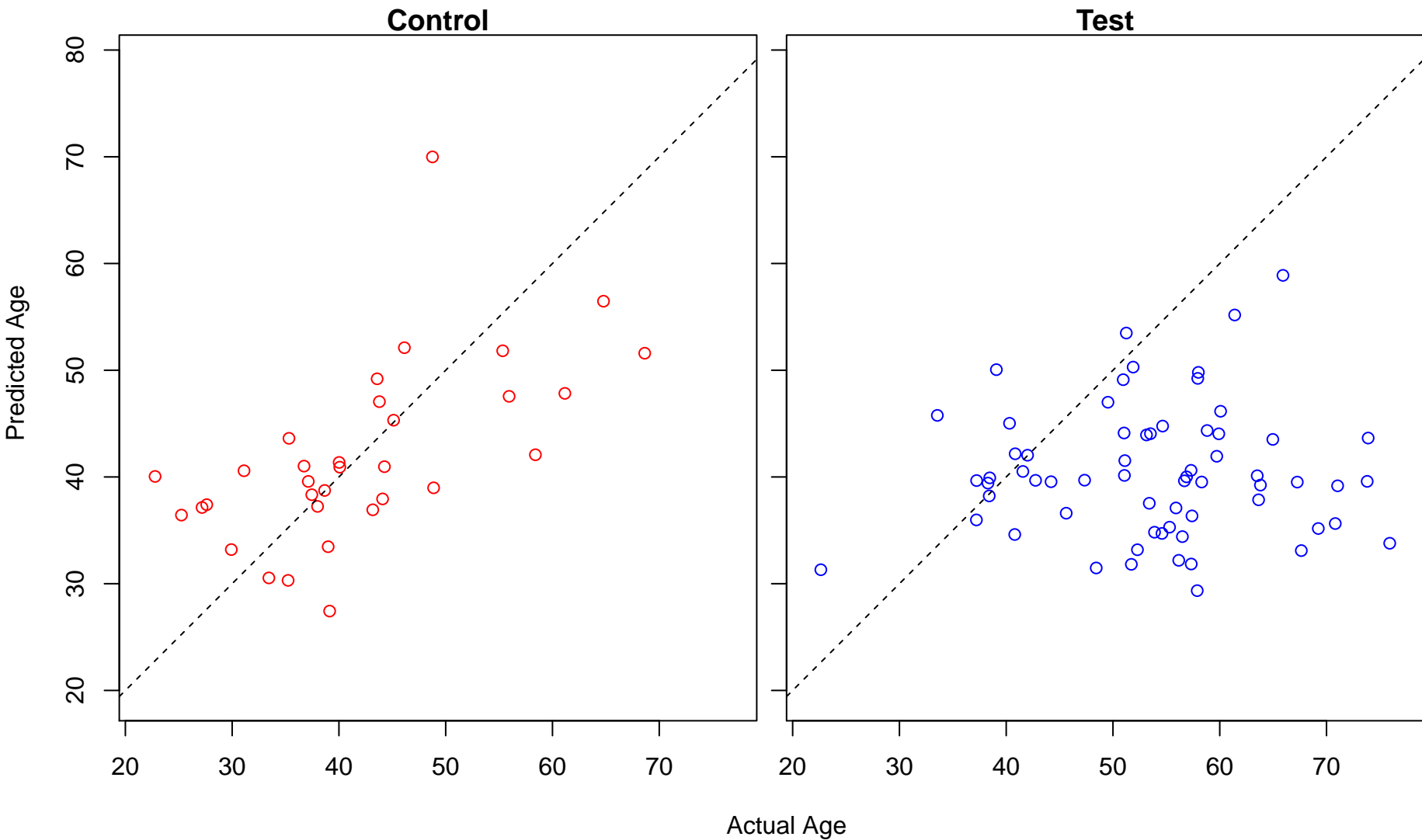
intracellular protein transmembrane import (Score: 2.106189)



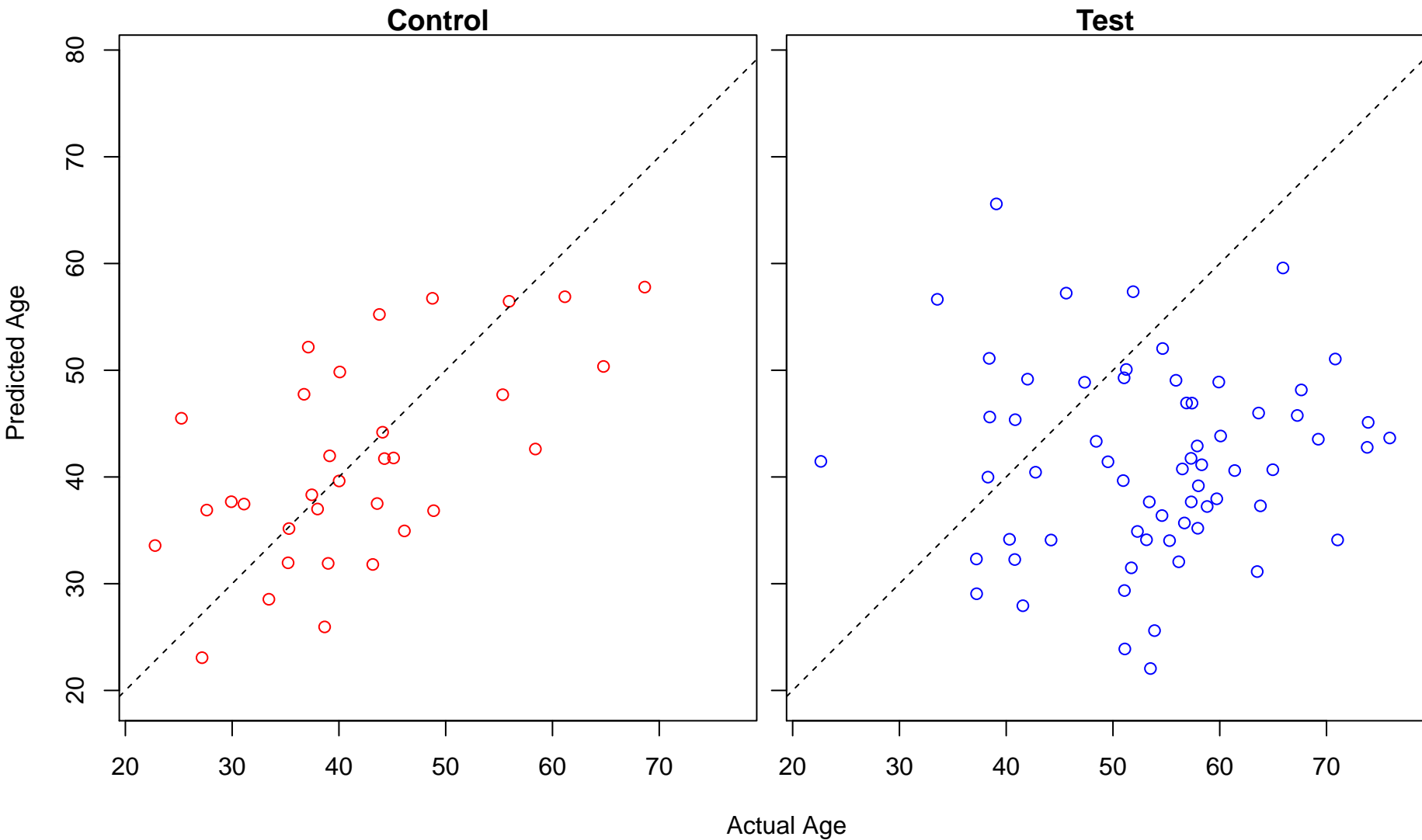
complement activation (Score: 2.105137)



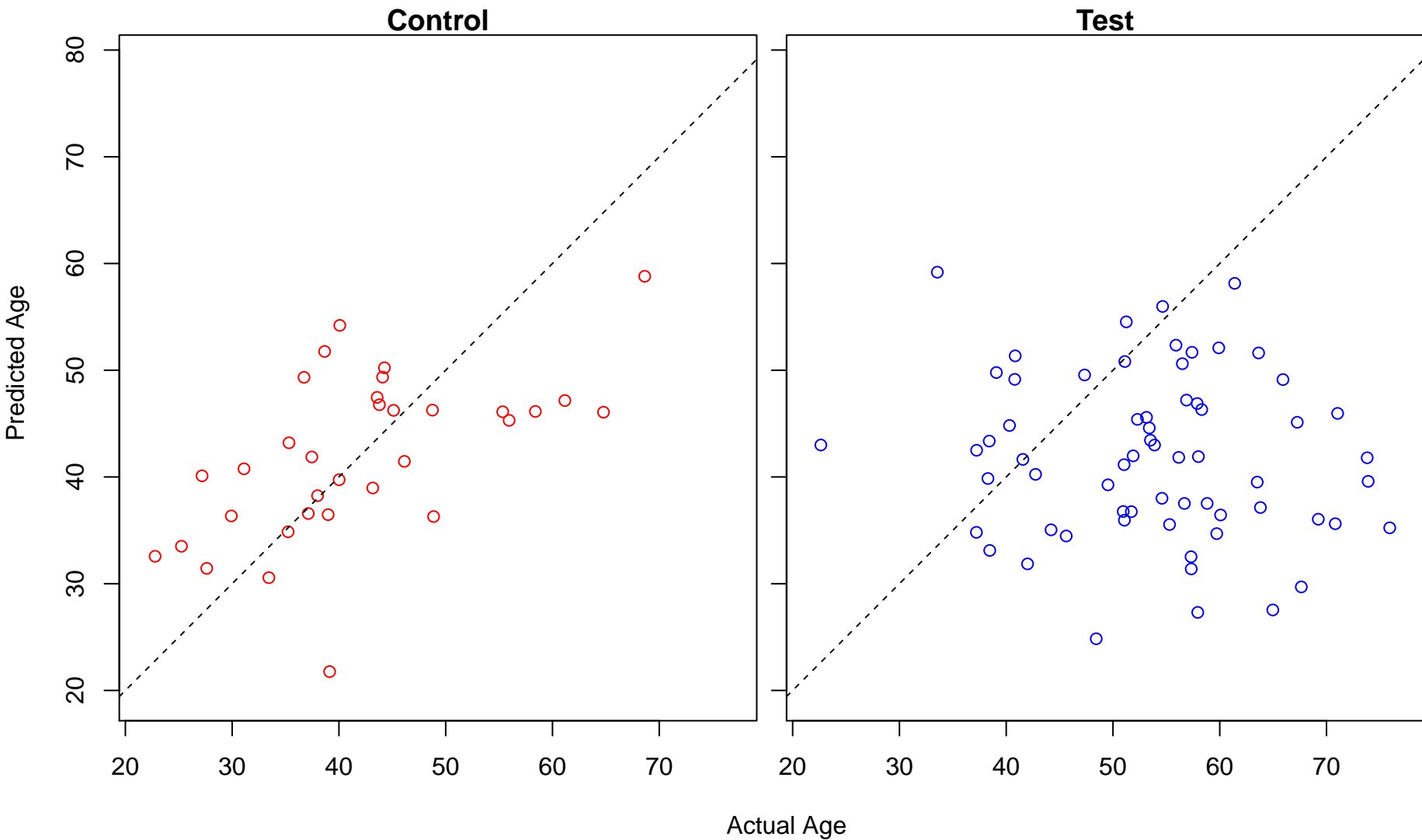
G2 DNA damage checkpoint (Score: 2.104443)



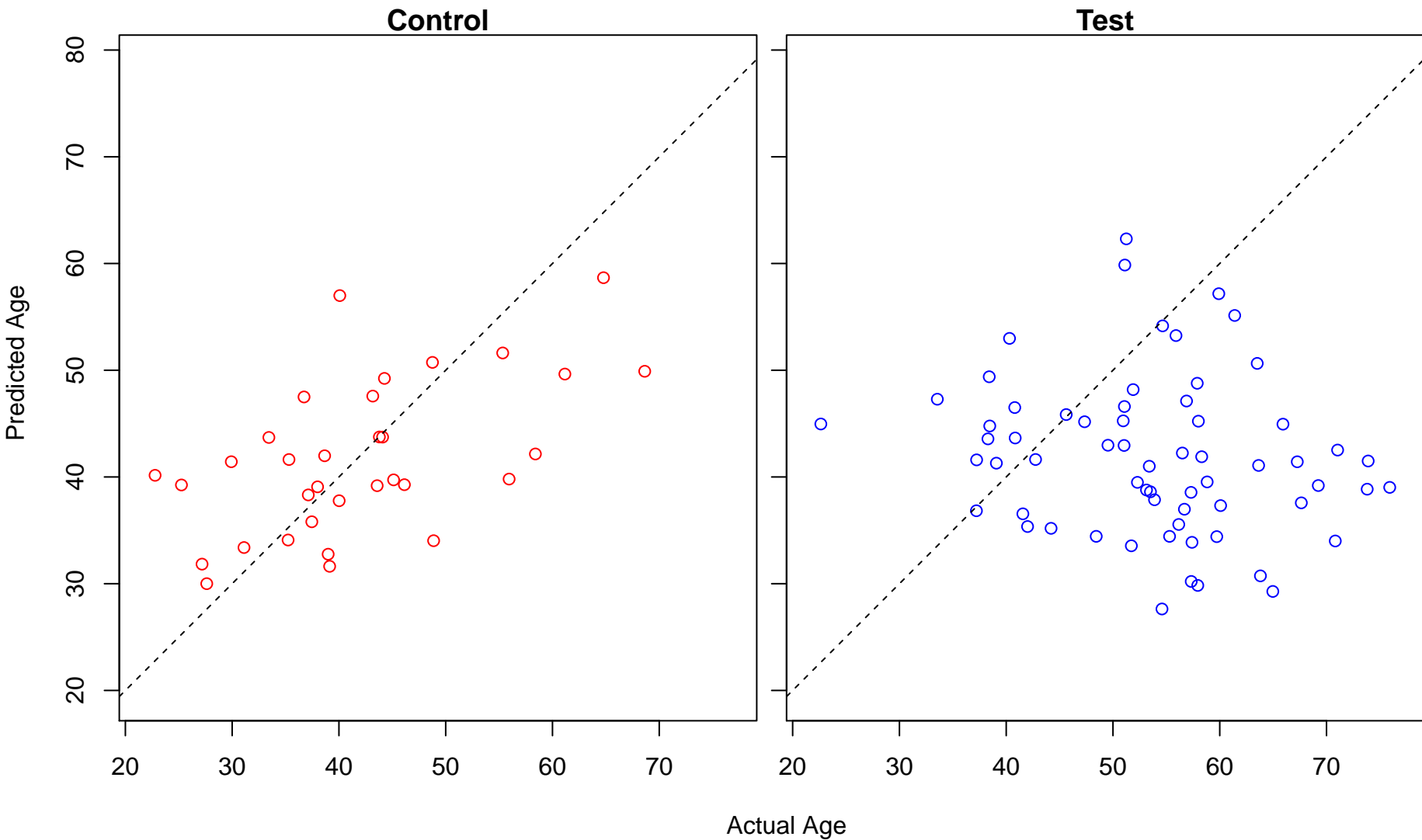
blood coagulation, fibrin clot formation (Score: 2.102637)



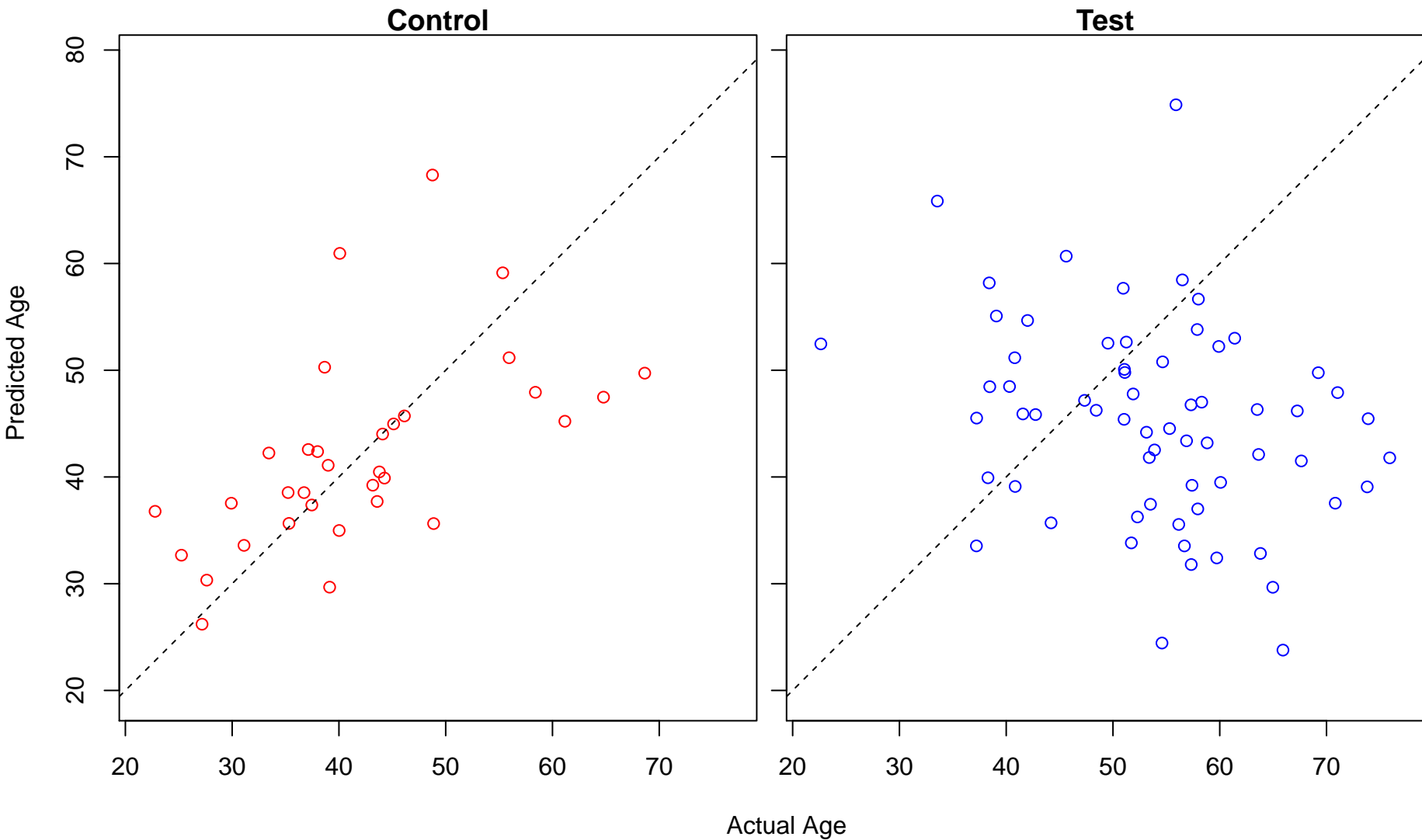
developmental process involved in reproduction (Score: 2.097542)



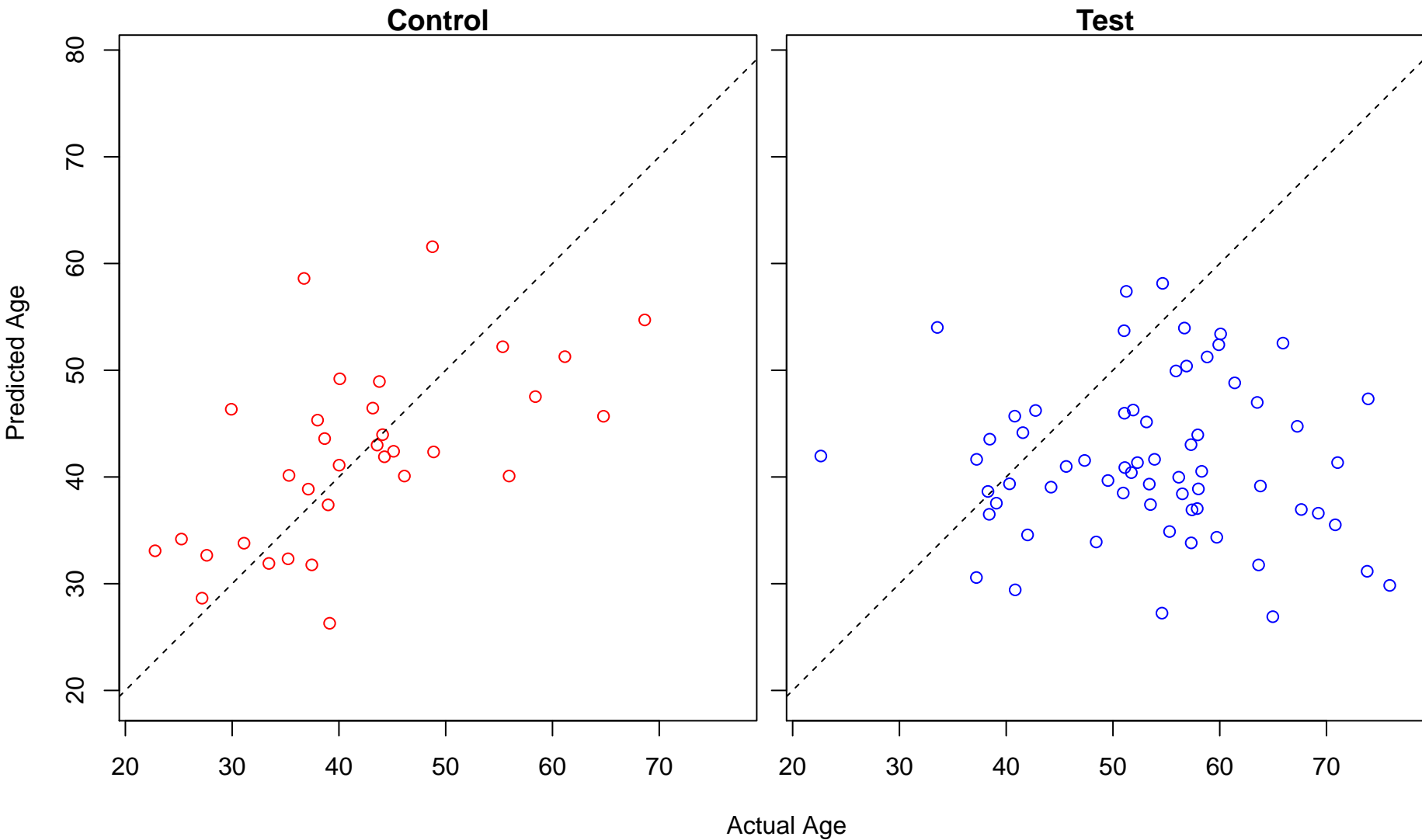
viral mRNA export from host cell nucleus (Score: 2.094031)



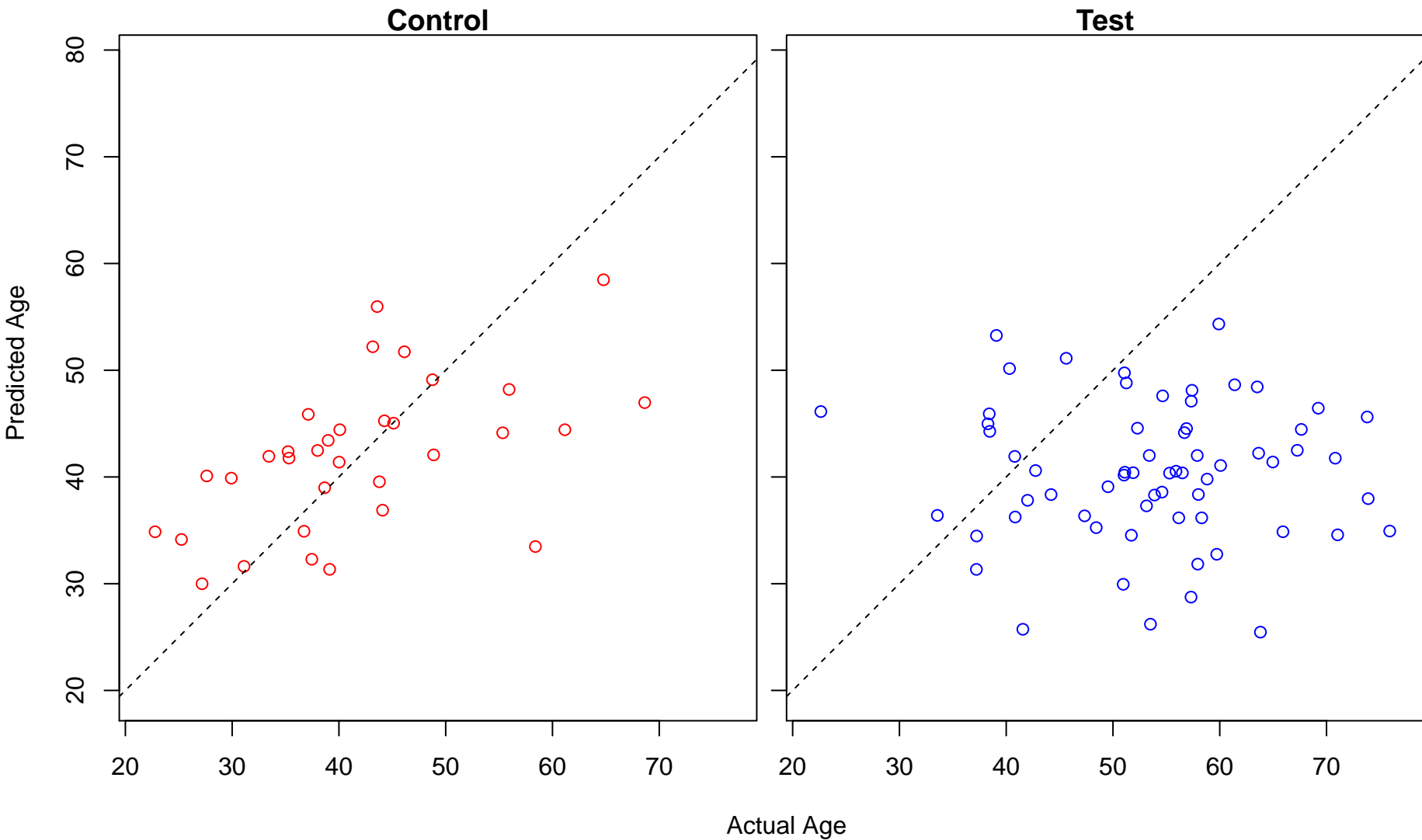
regulation of tumor necrosis factor production (Score: 2.091921)



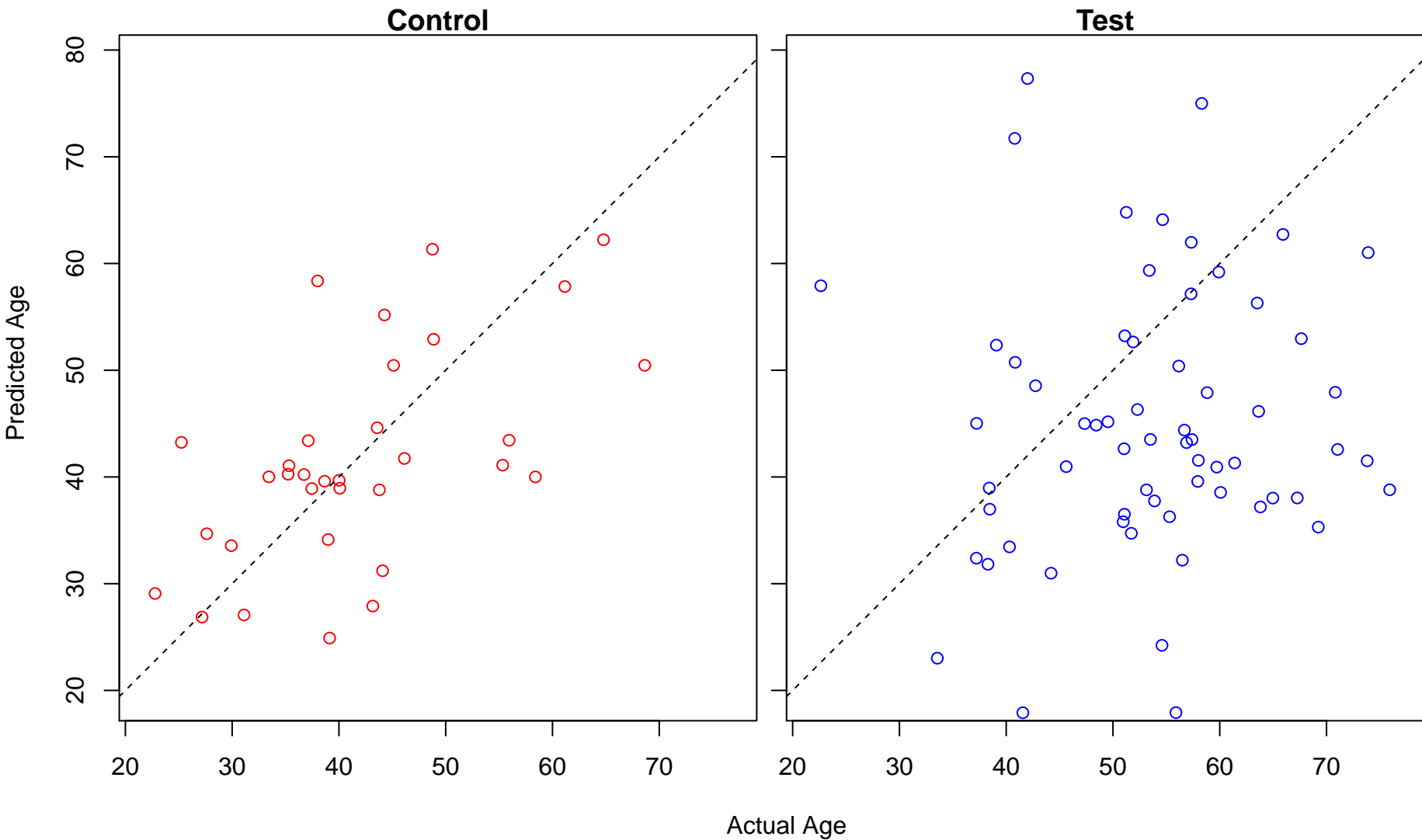
response to tumor necrosis factor (Score: 2.090946)



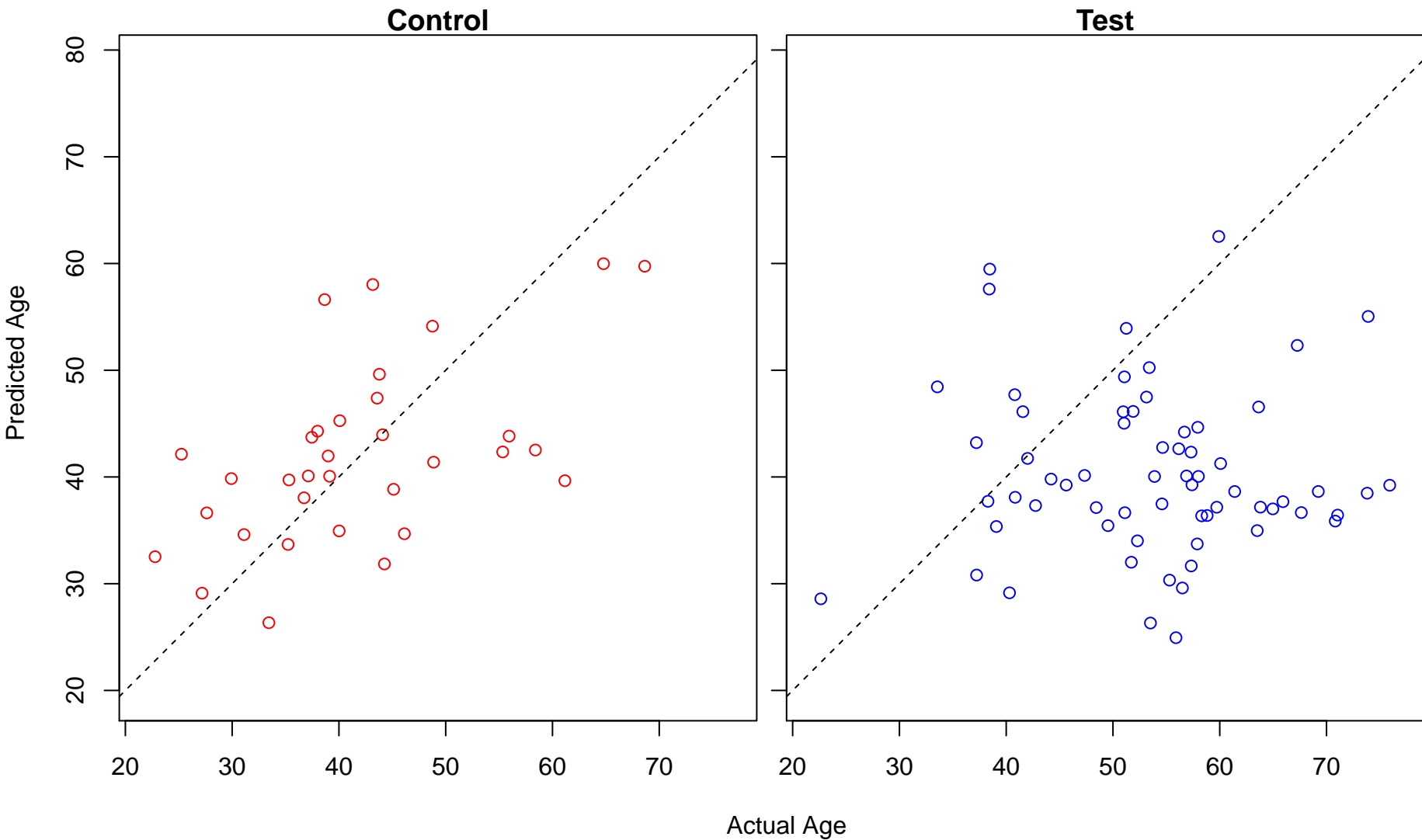
receptor guanylyl cyclase signaling pathway (Score: 2.090194)



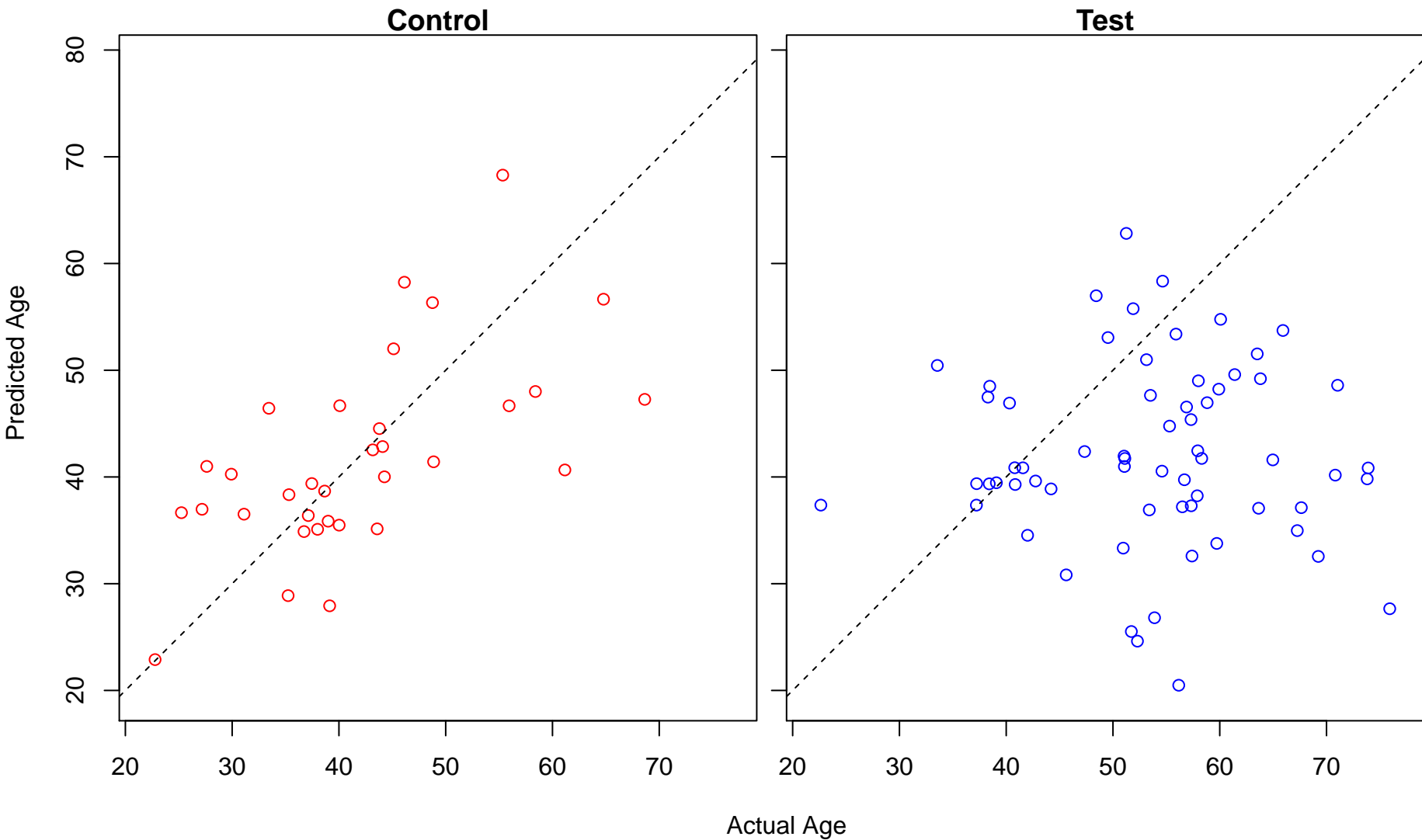
negative regulation of G2/M transition of mitotic cell cycle (Score: 2.088121)



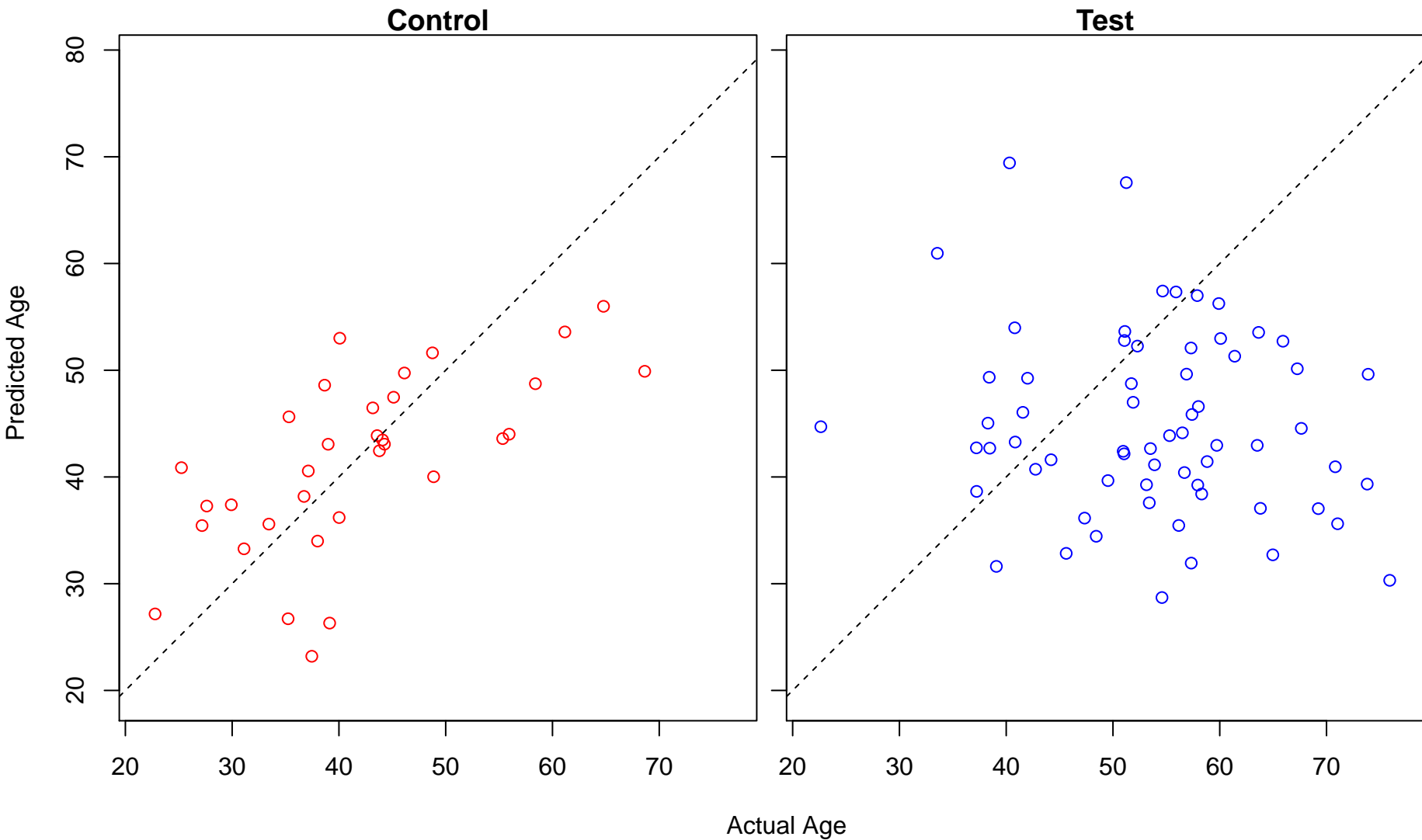
phospholipid catabolic process (Score: 2.082779)



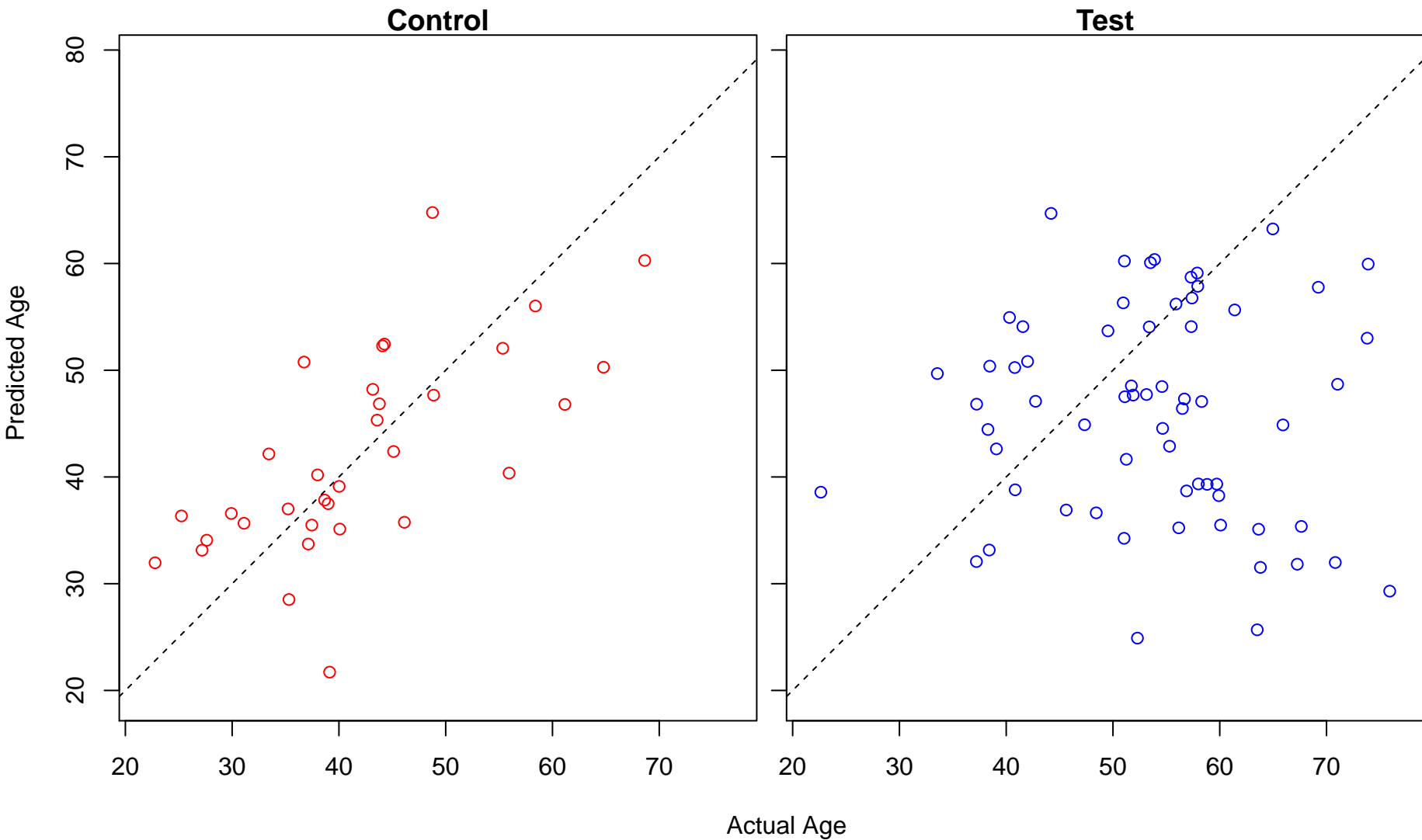
centrosome organization (Score: 2.073131)



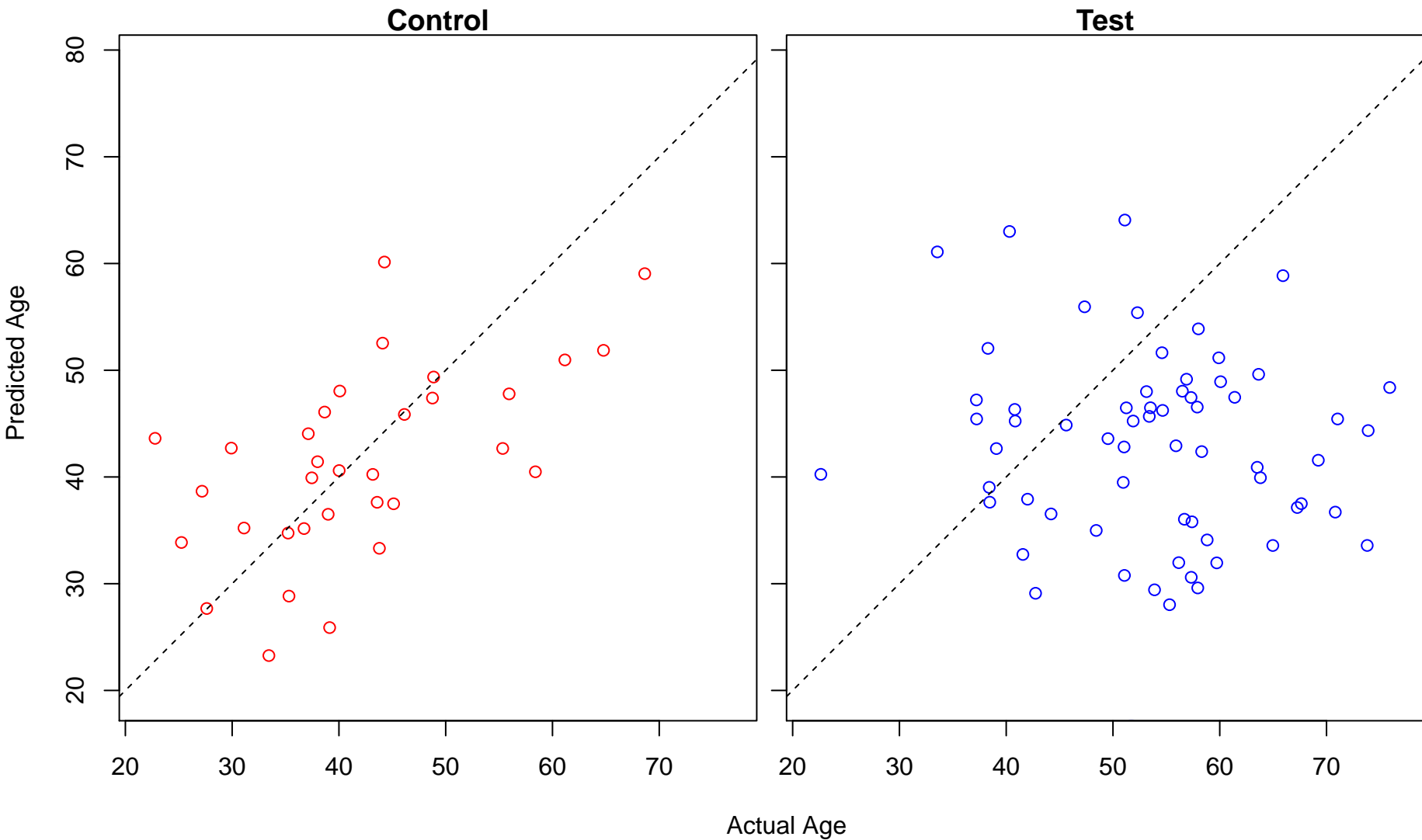
temperature homeostasis (Score: 2.056333)



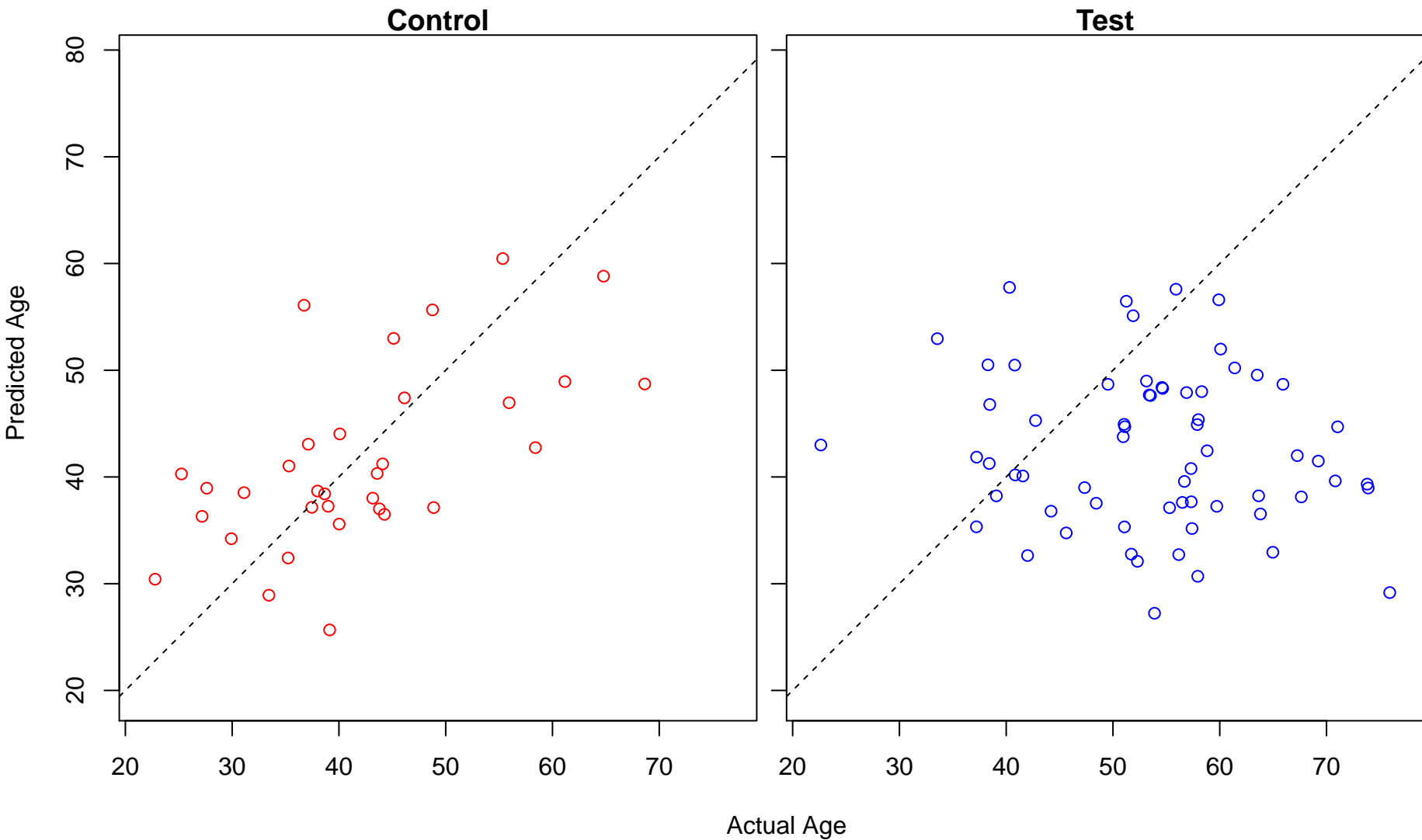
humoral immune response mediated by circulating immunoglobulin (Score: 2.055793)



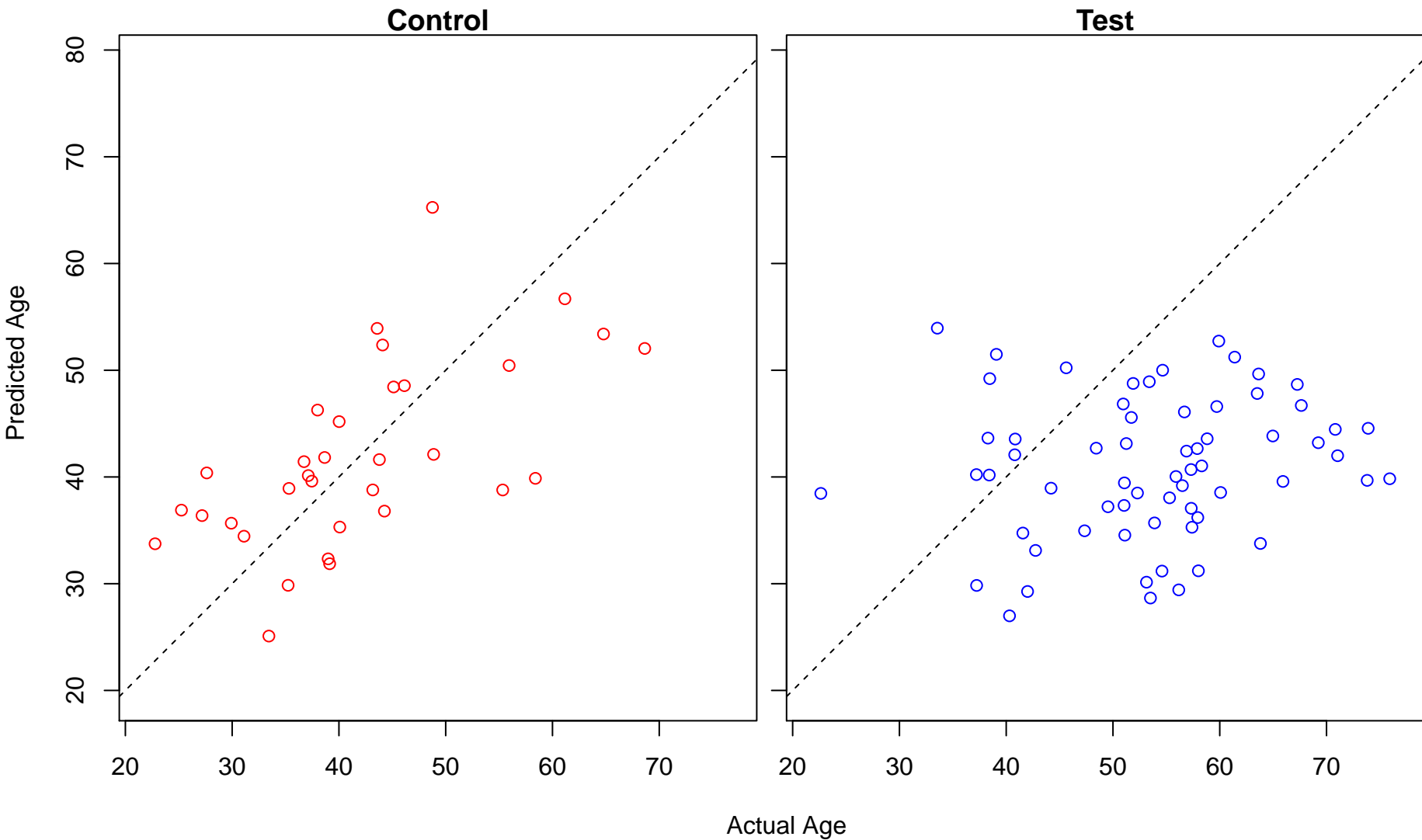
peptidyl-arginine N-methylation (Score: 2.042938)



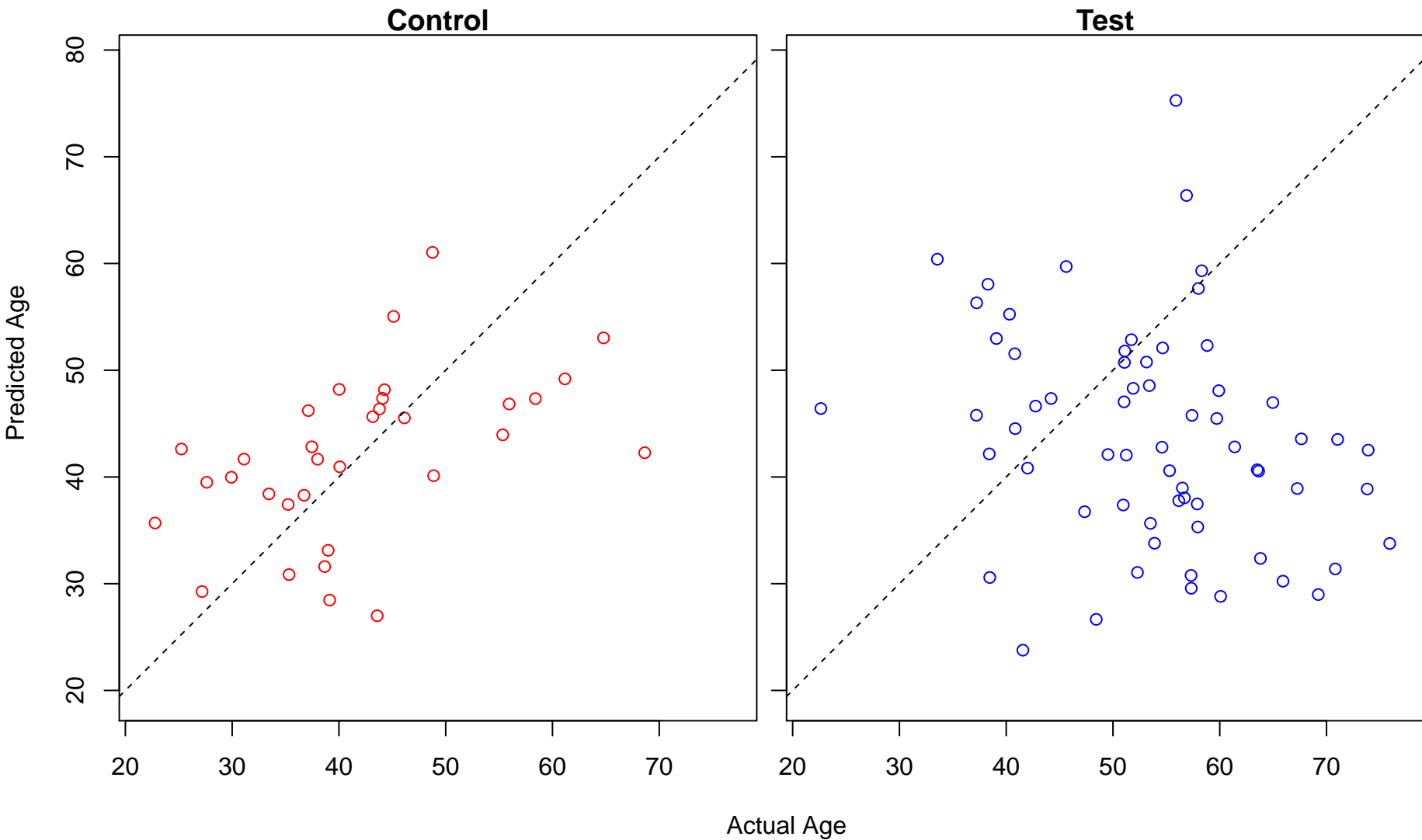
microtubule cytoskeleton organization (Score: 2.033371)



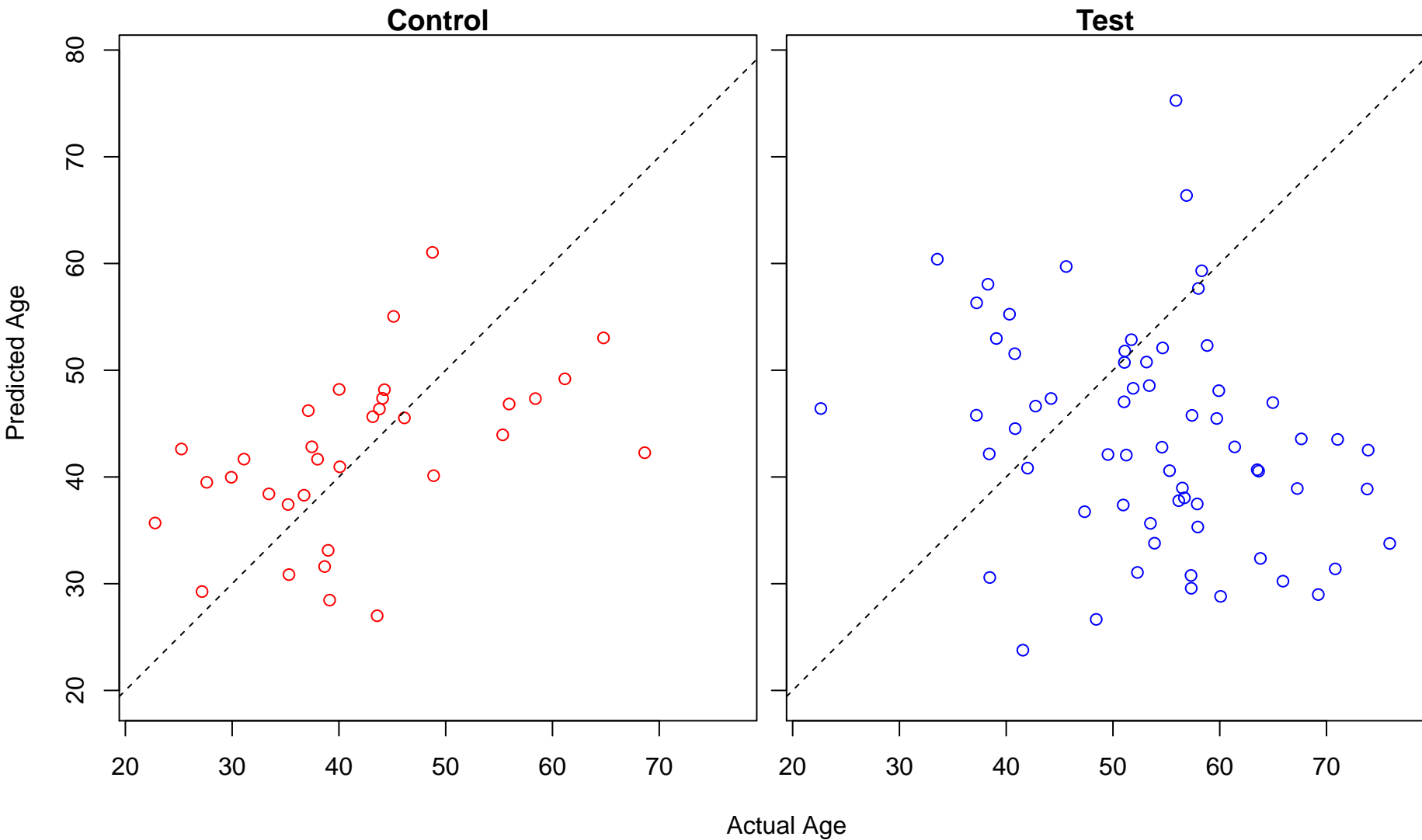
positive regulation of focal adhesion assembly (Score: 2.029282)



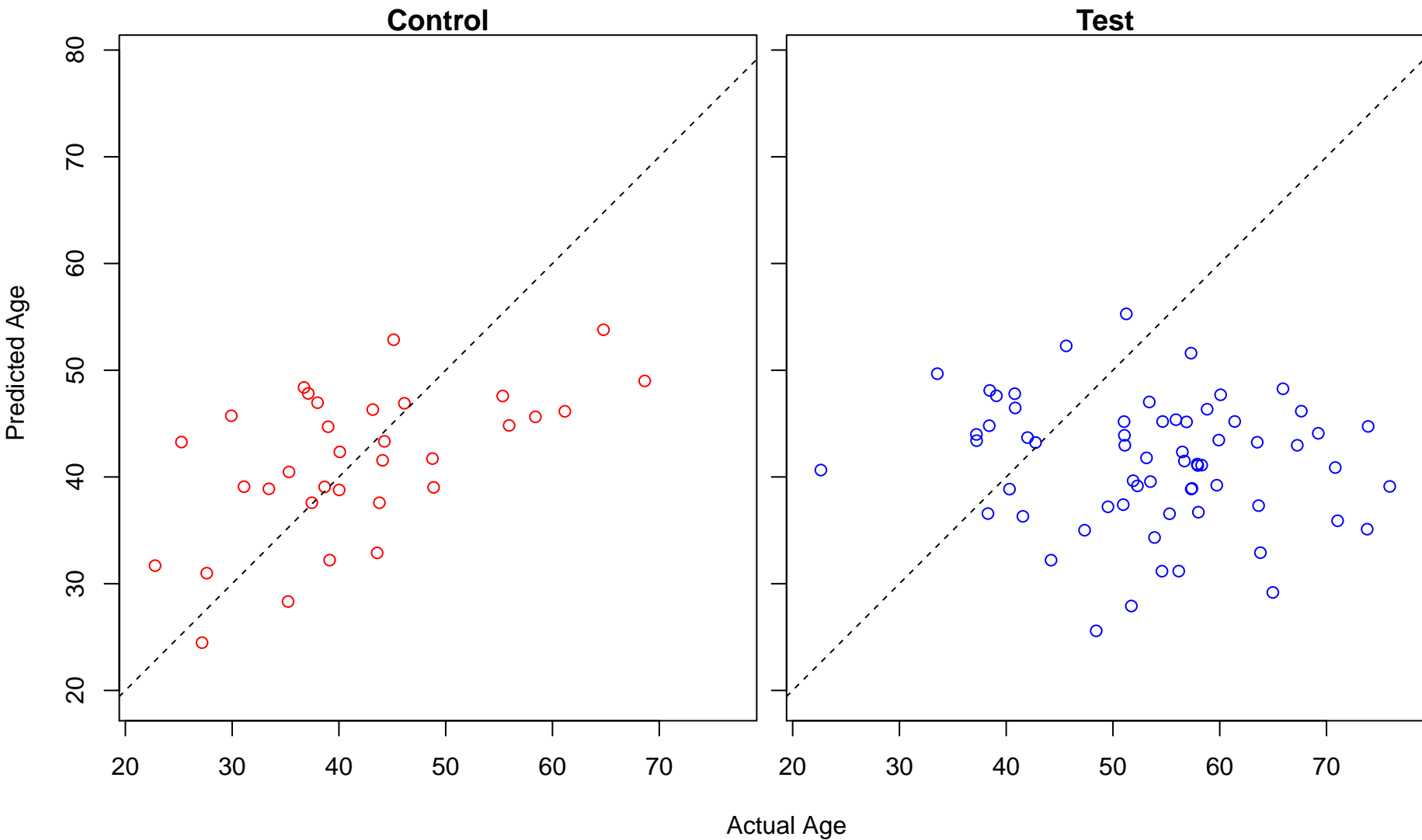
regulation of immature T cell proliferation (Score: 2.029048)



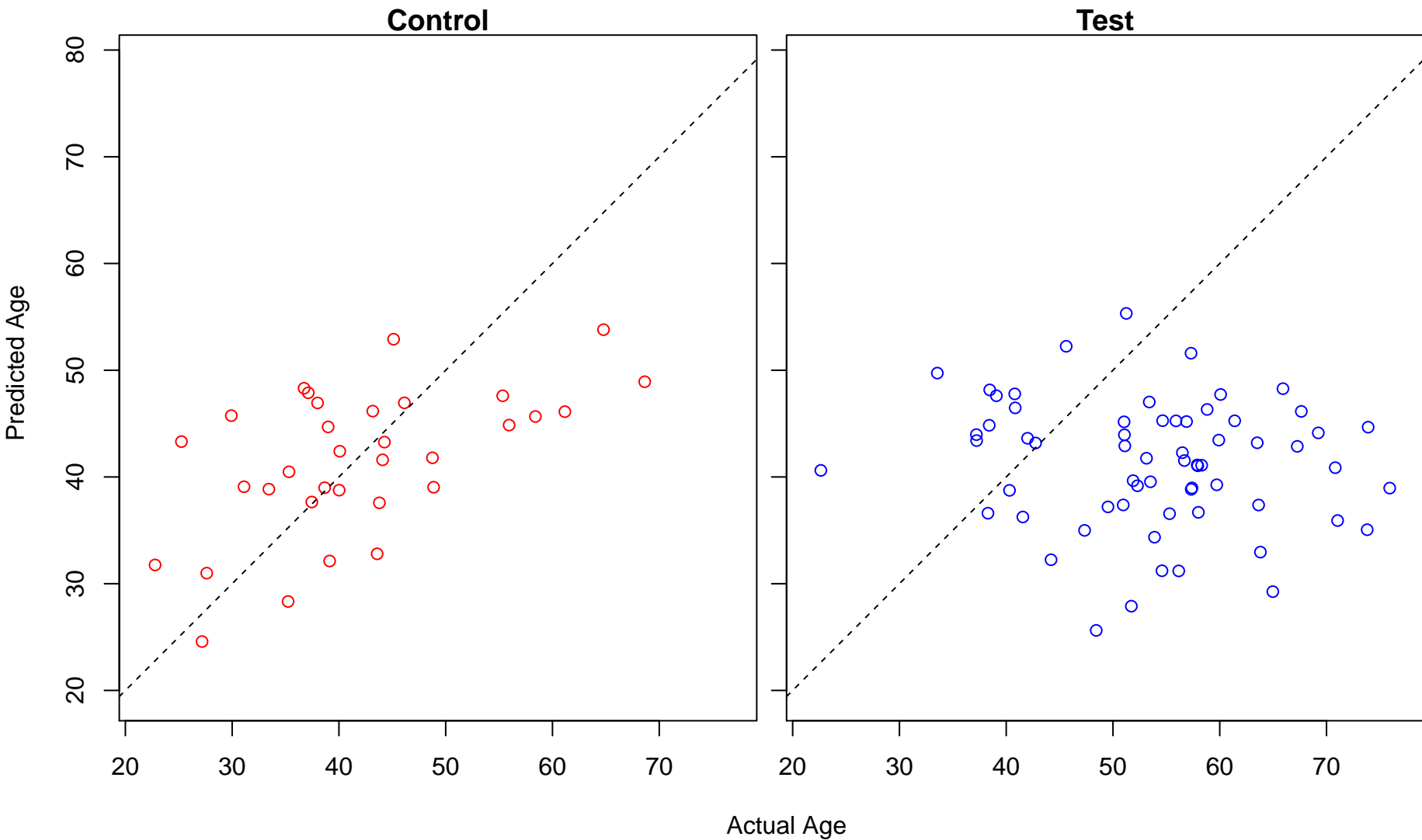
regulation of immature T cell proliferation in thymus (Score: 2.029048)



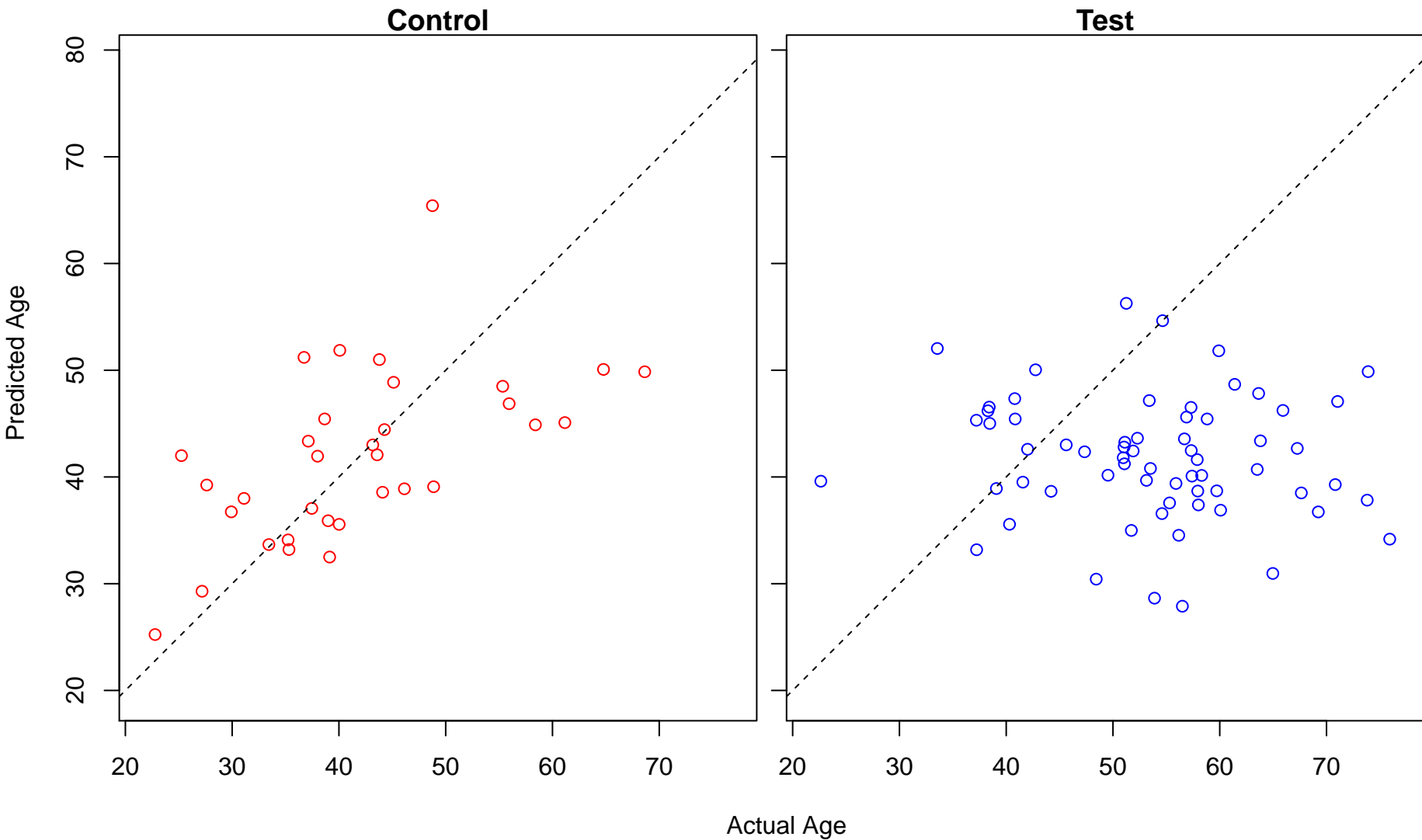
cholesterol transport (Score: 2.022350)



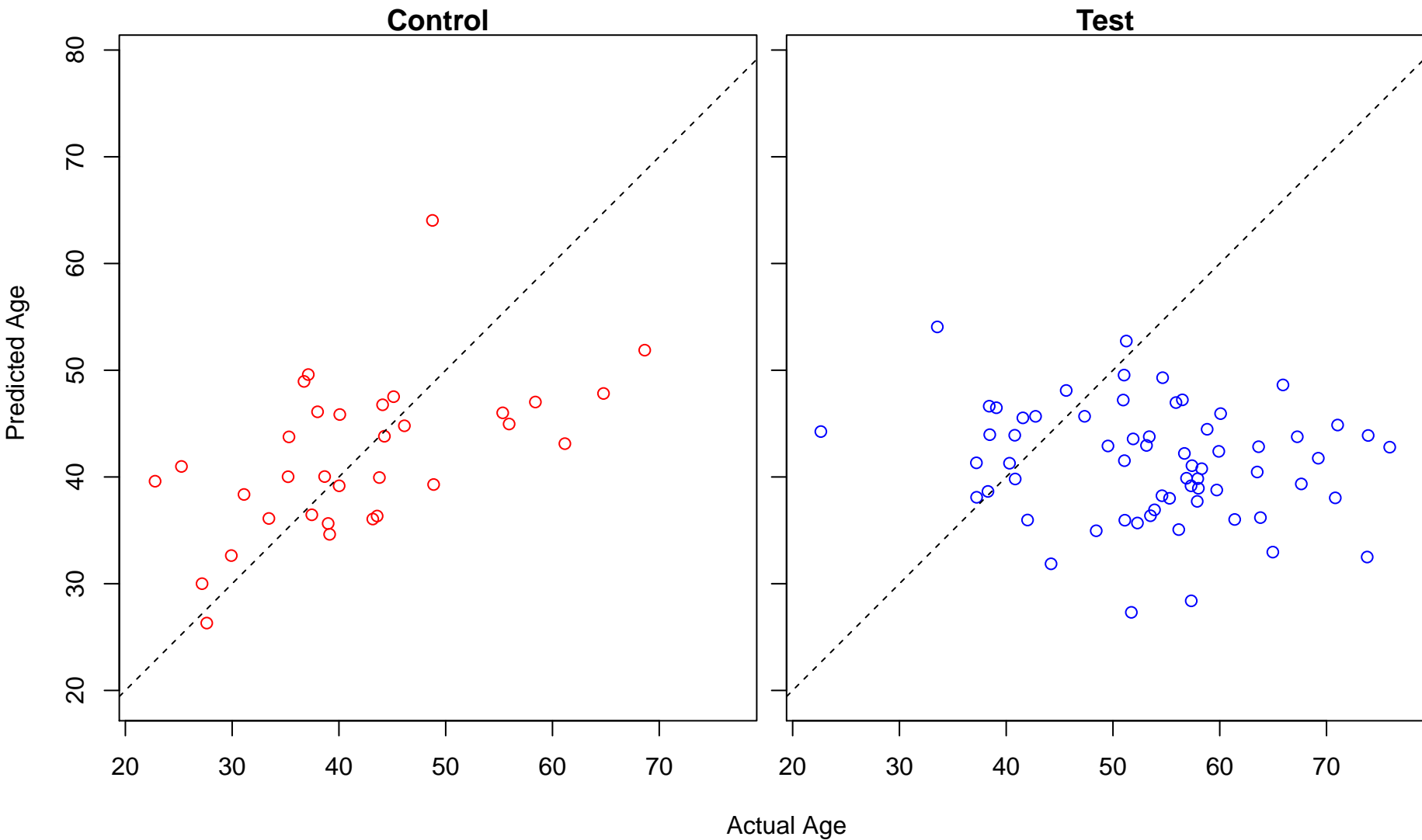
sterol transport (Score: 2.021118)



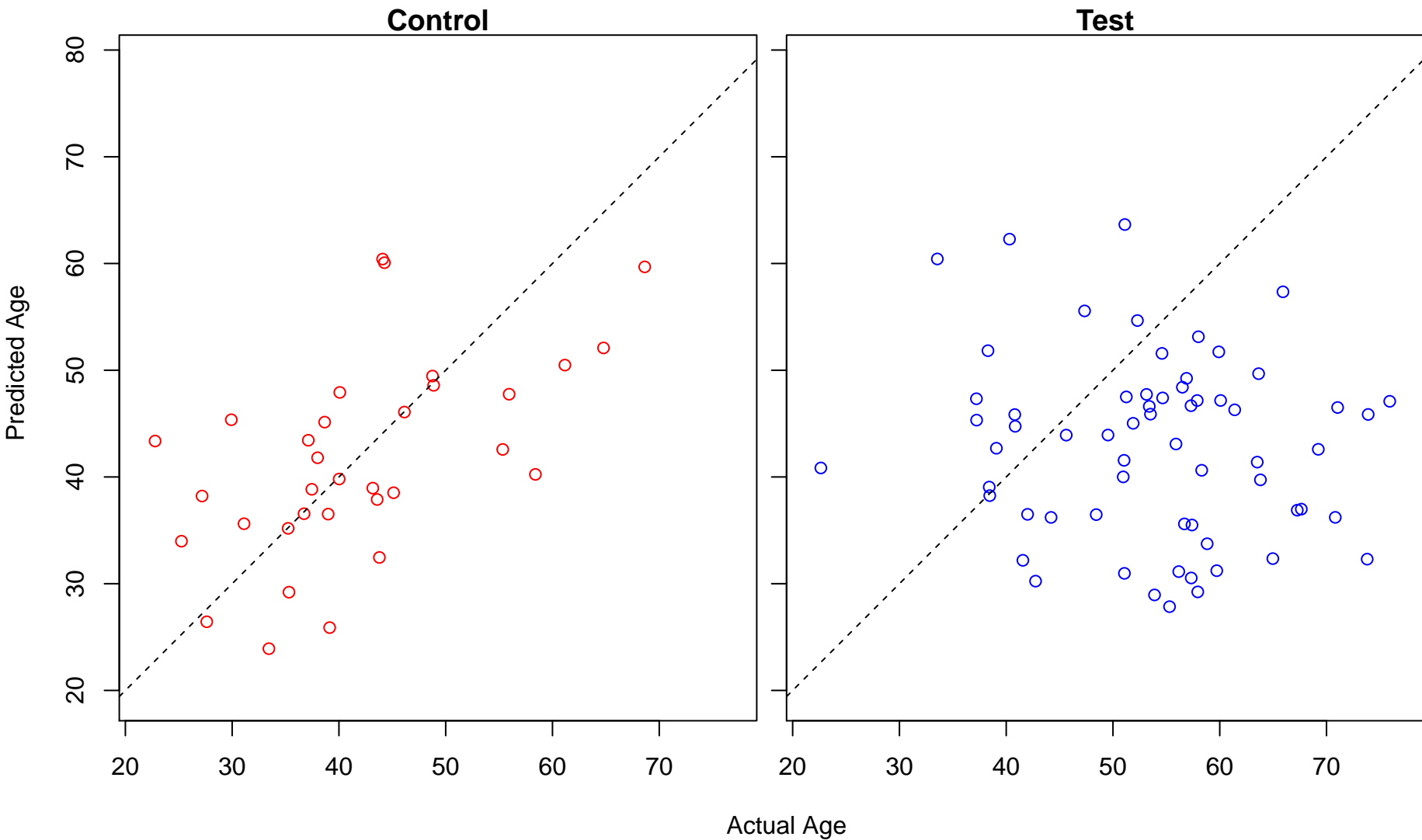
organic hydroxy compound metabolic process (Score: 2.006990)



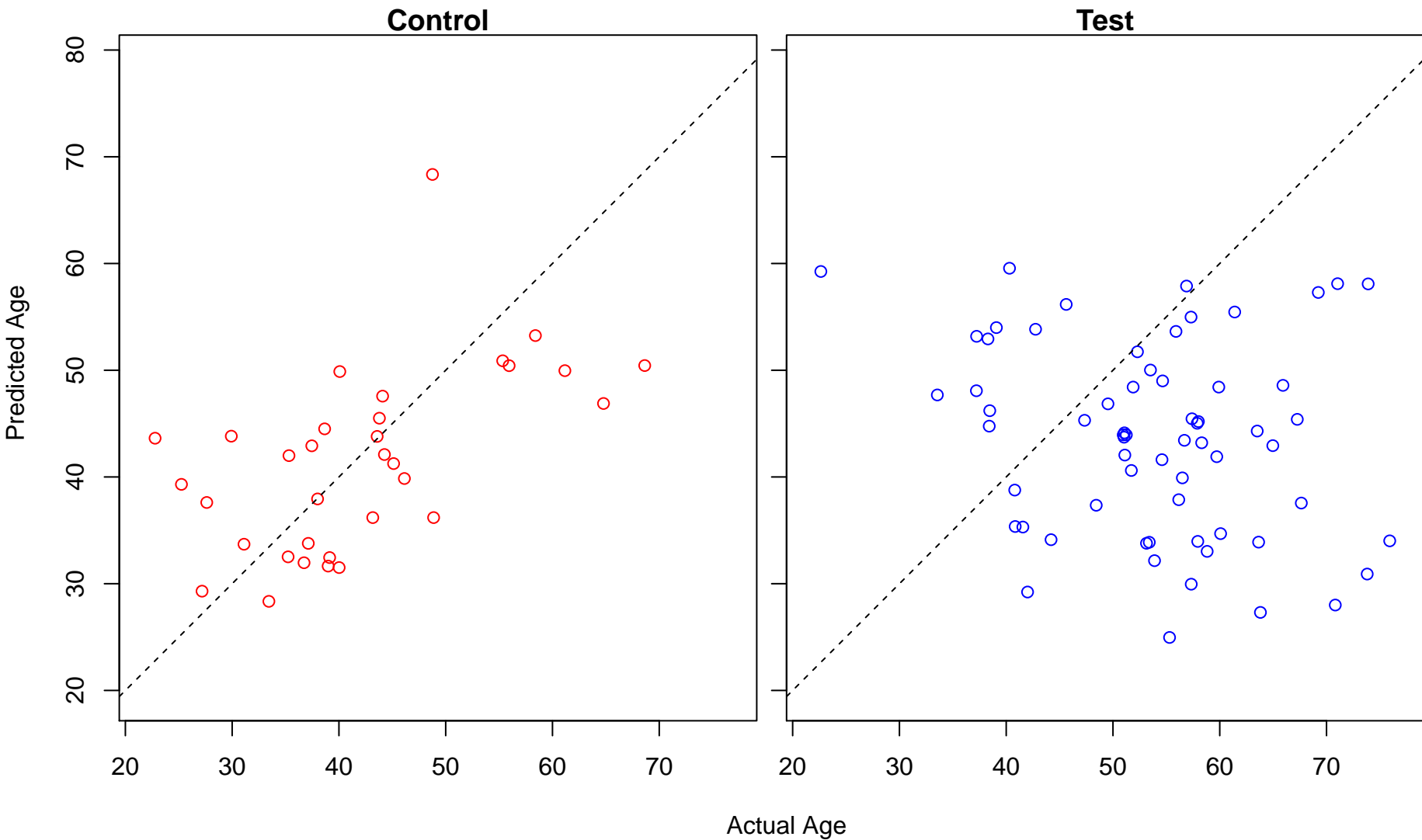
negative regulation of protein oligomerization (Score: 2.000312)



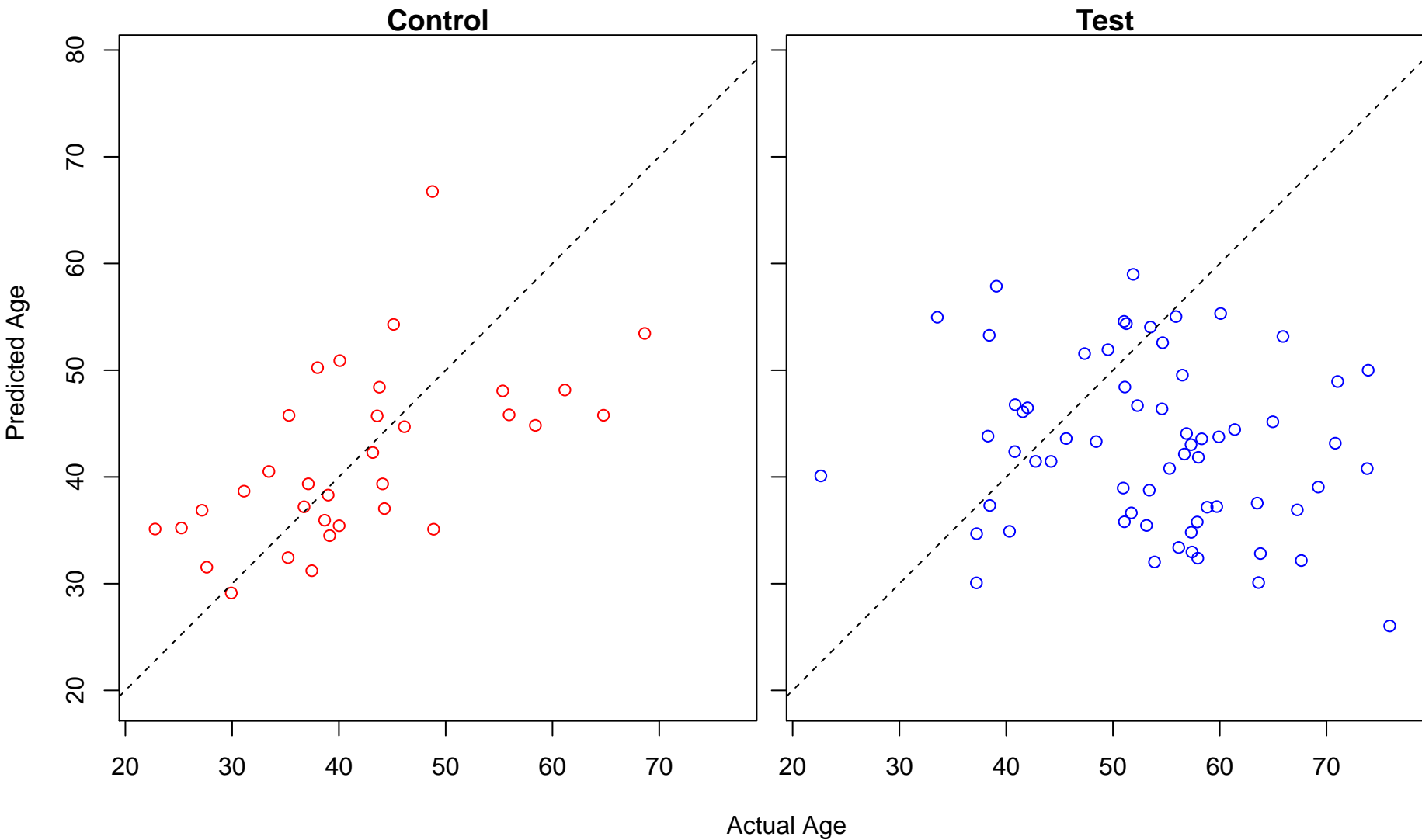
peptidyl-arginine methylation (Score: 2.000167)



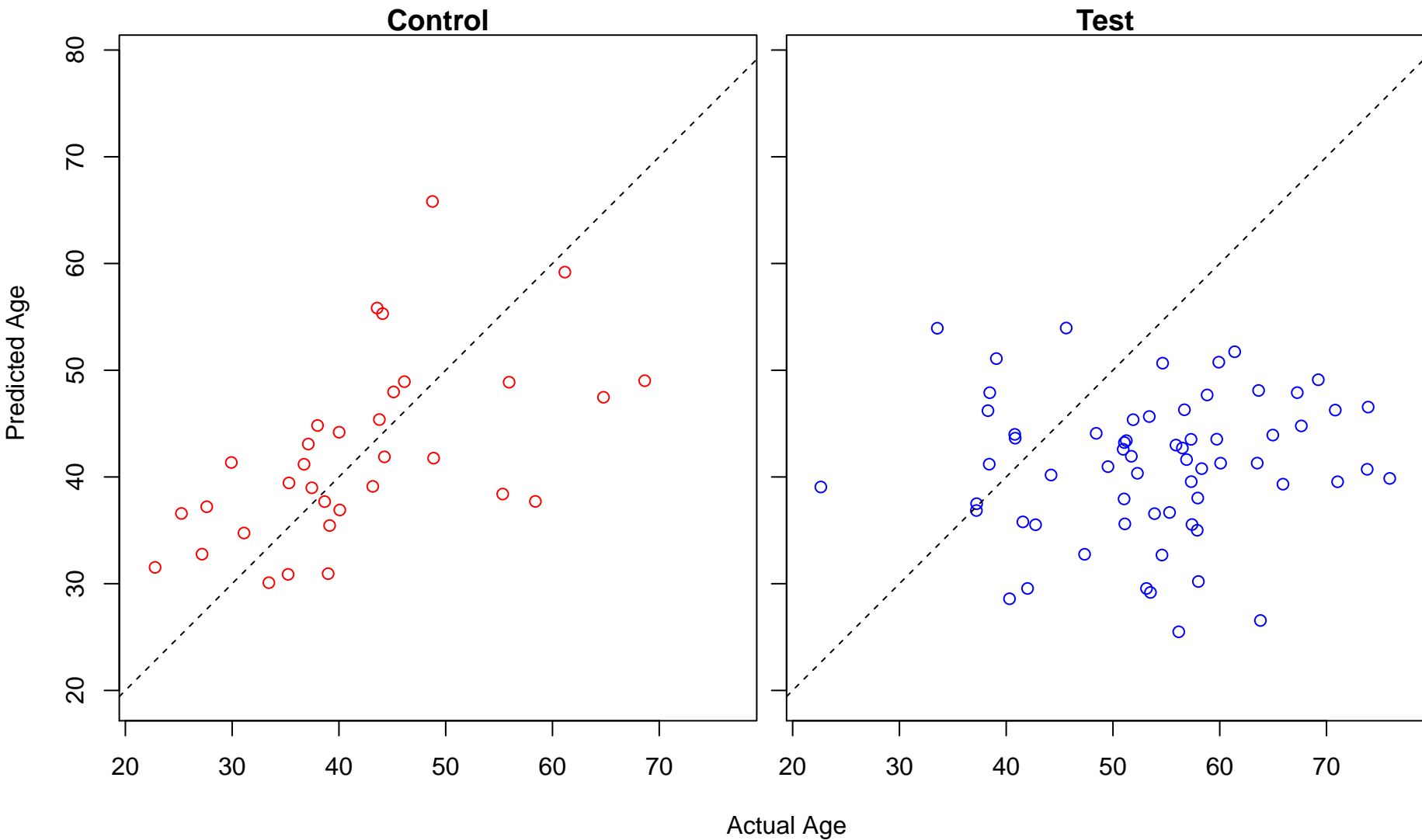
receptor clustering (Score: 1.998568)



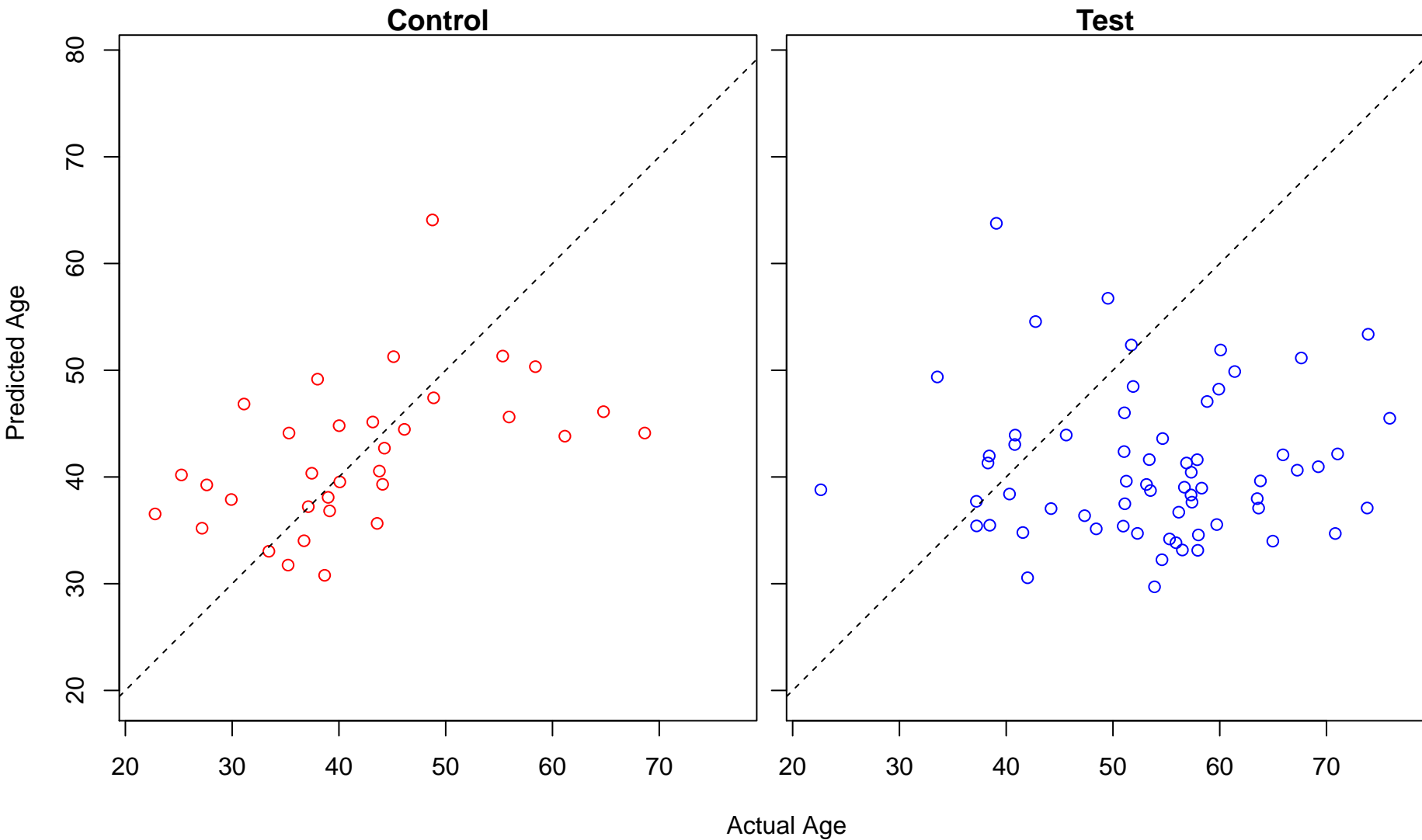
snRNA transcription from RNA polymerase II promoter (Score: 1.997185)



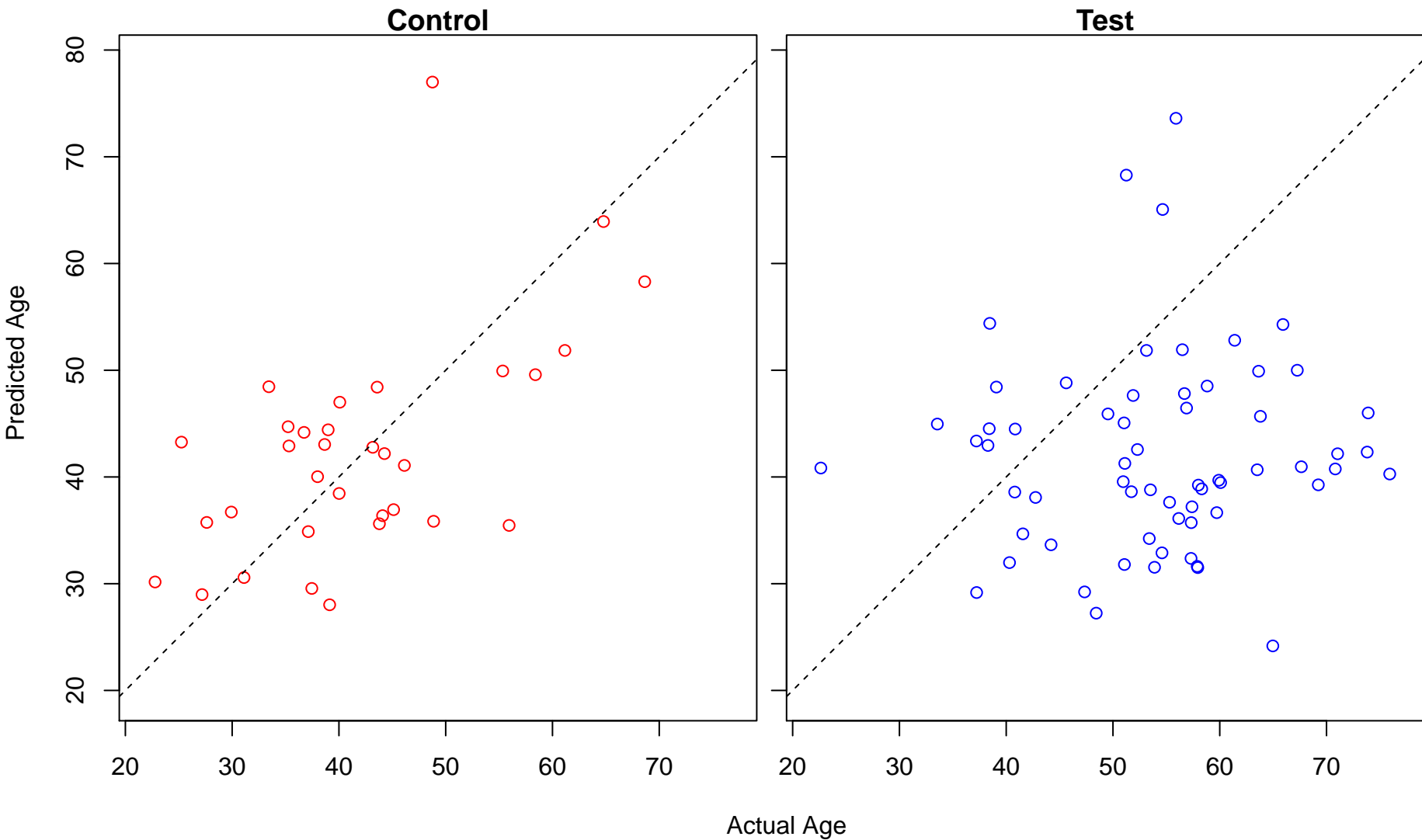
positive regulation of cell junction assembly (Score: 1.996848)



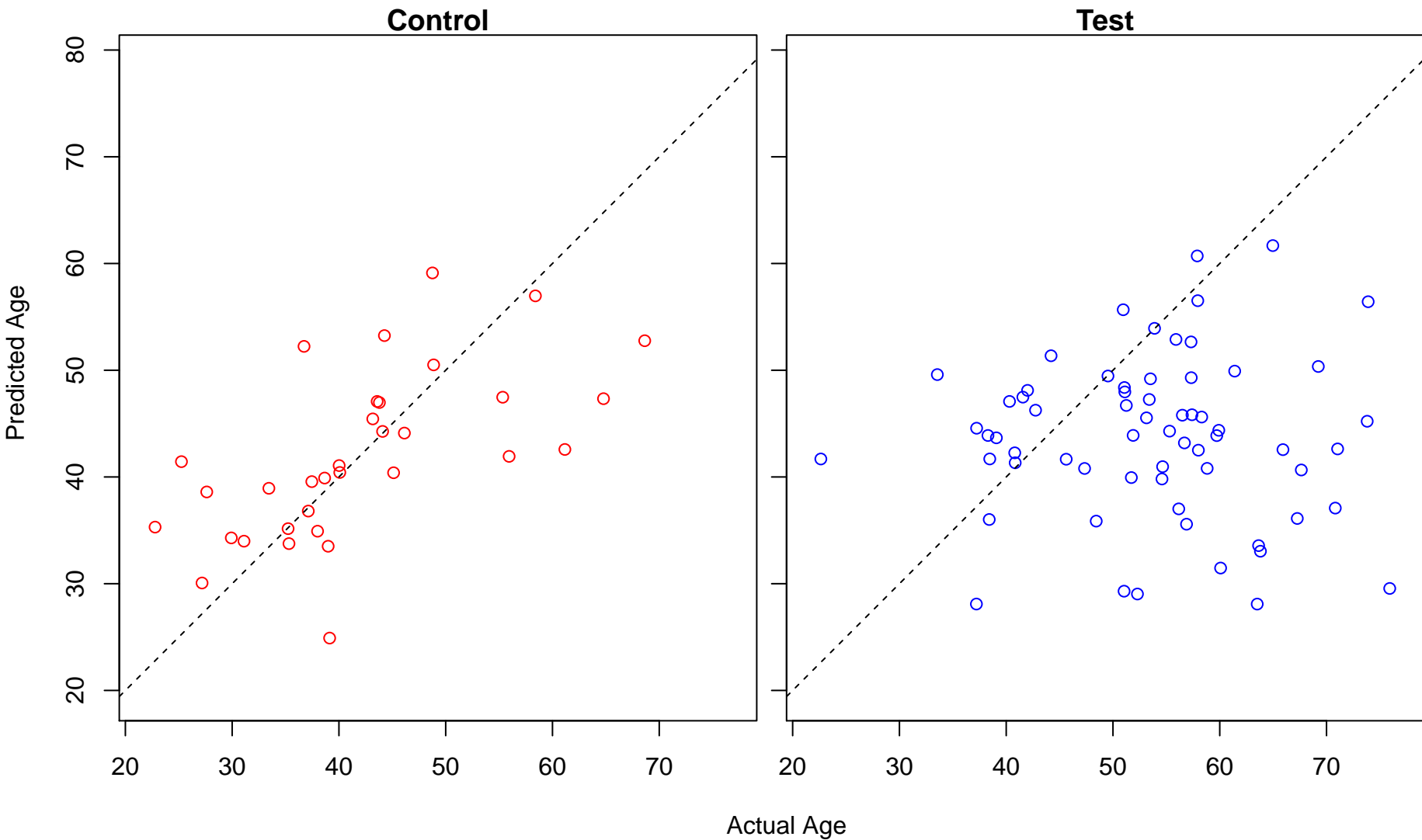
negative regulation of DNA damage response, signal transduction by p53 class mediator (Score: 1.987)



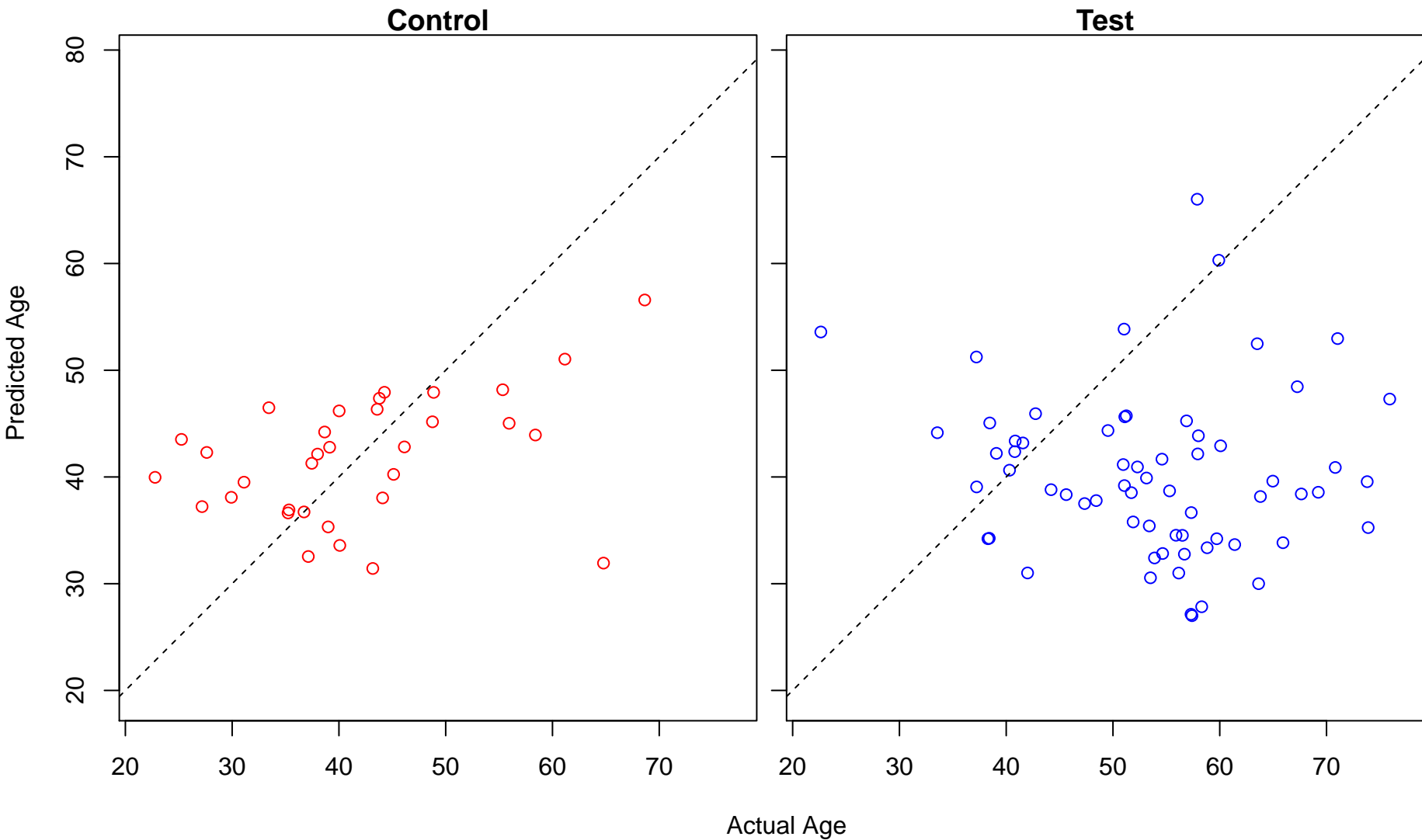
protein localization to Golgi apparatus (Score: 1.987629)



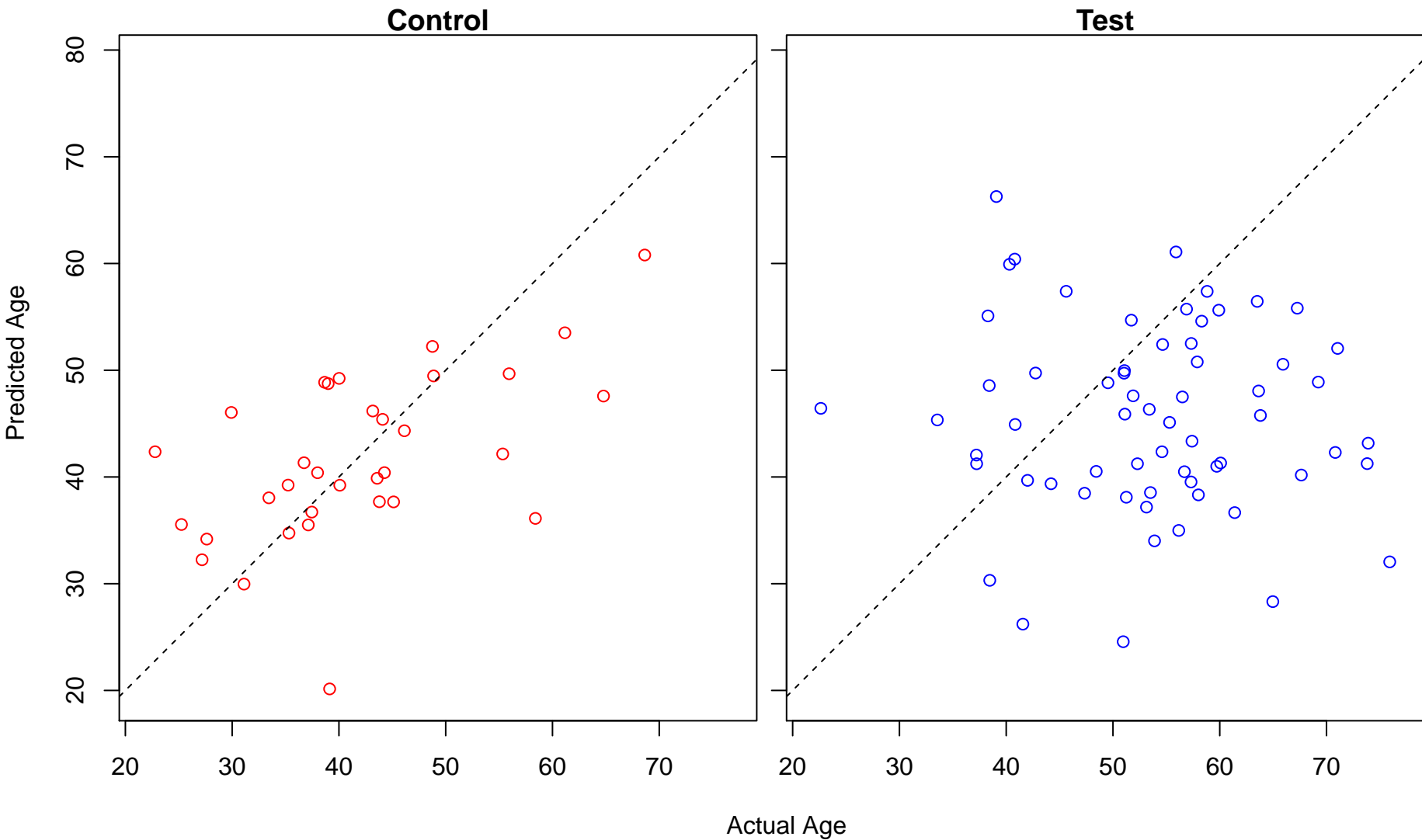
complement activation, classical pathway (Score: 1.980318)



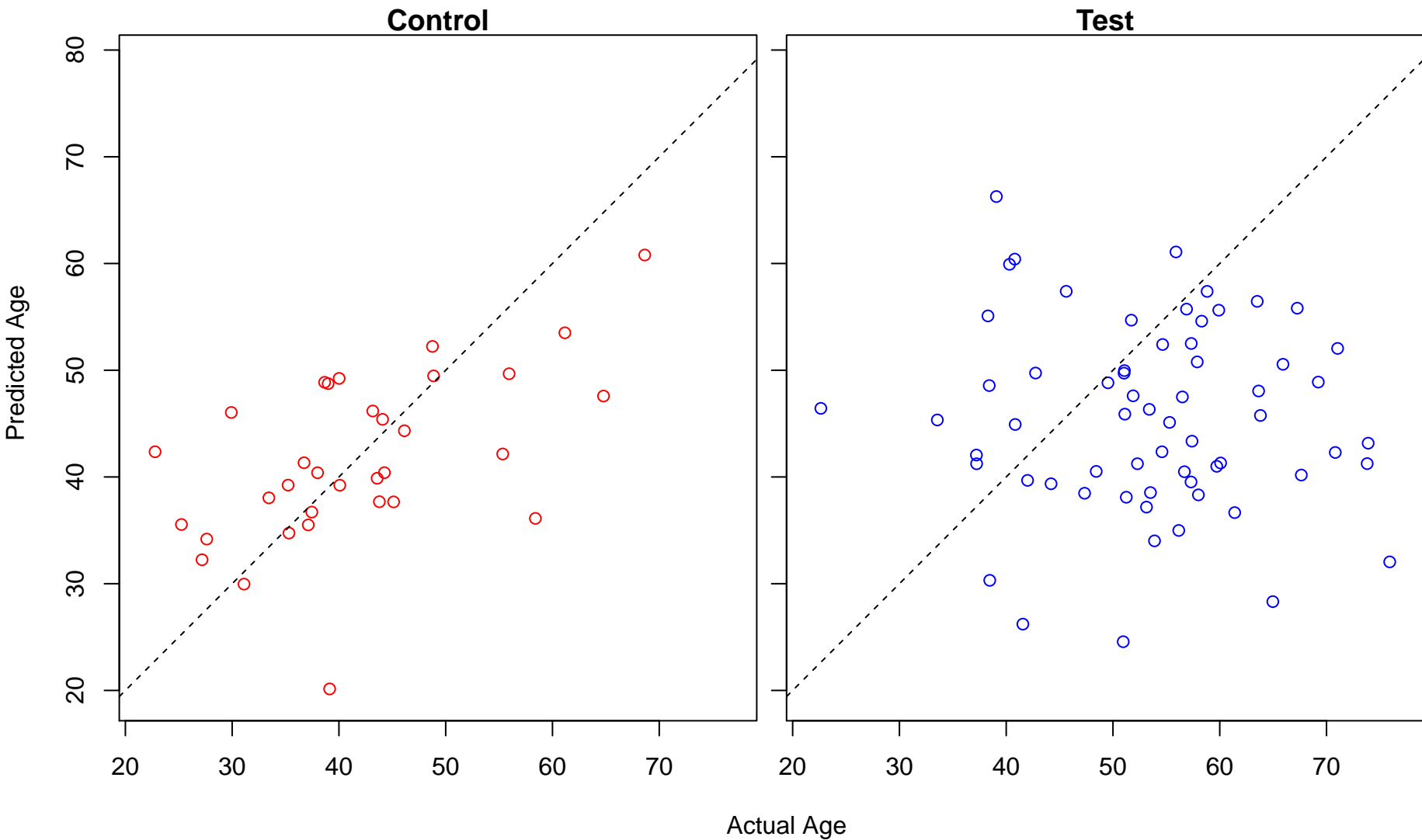
regulation of myoblast proliferation (Score: 1.968676)



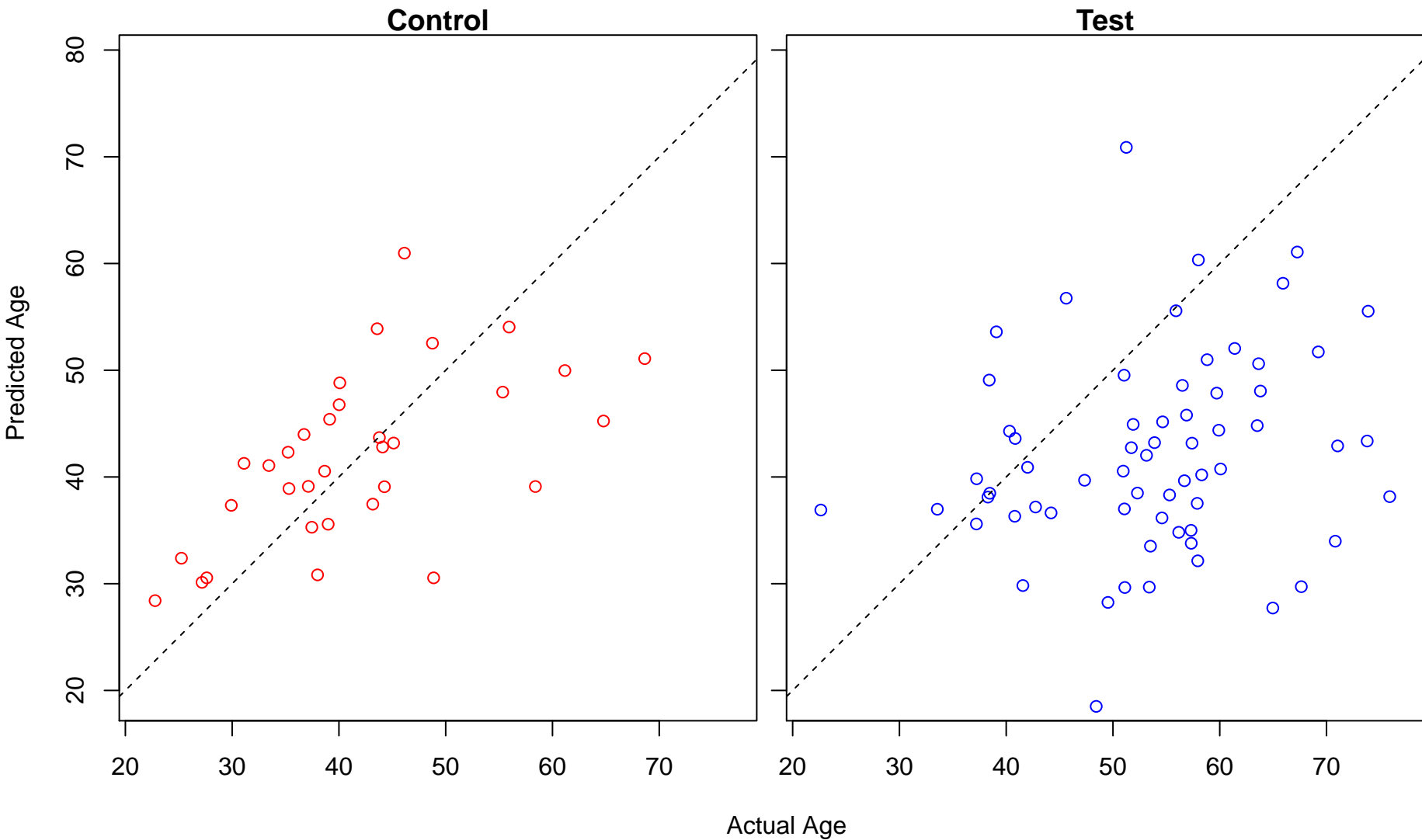
subpallium development (Score: 1.967144)



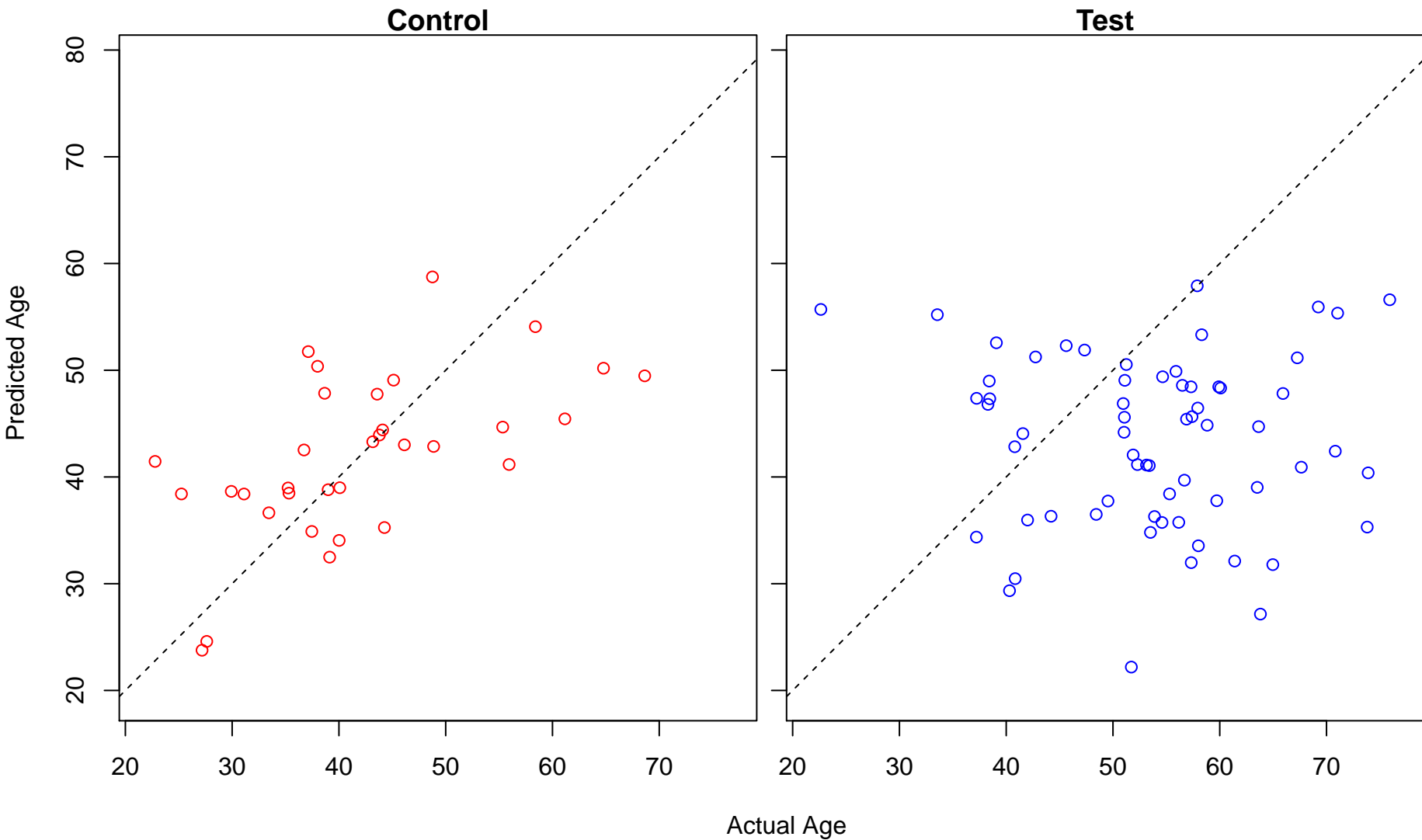
striatum development (Score: 1.967144)



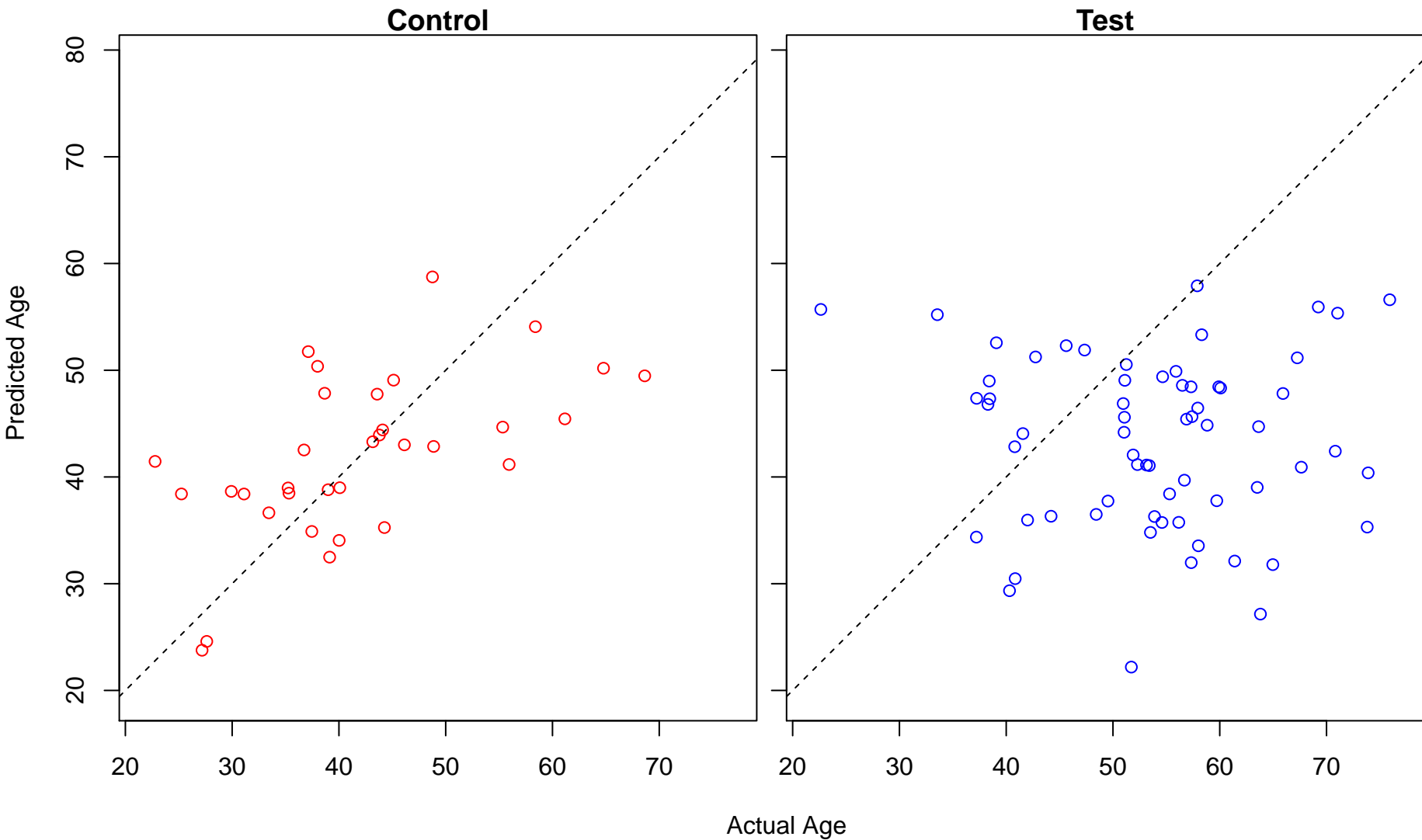
positive regulation of potassium ion transmembrane transport (Score: 1.965751)



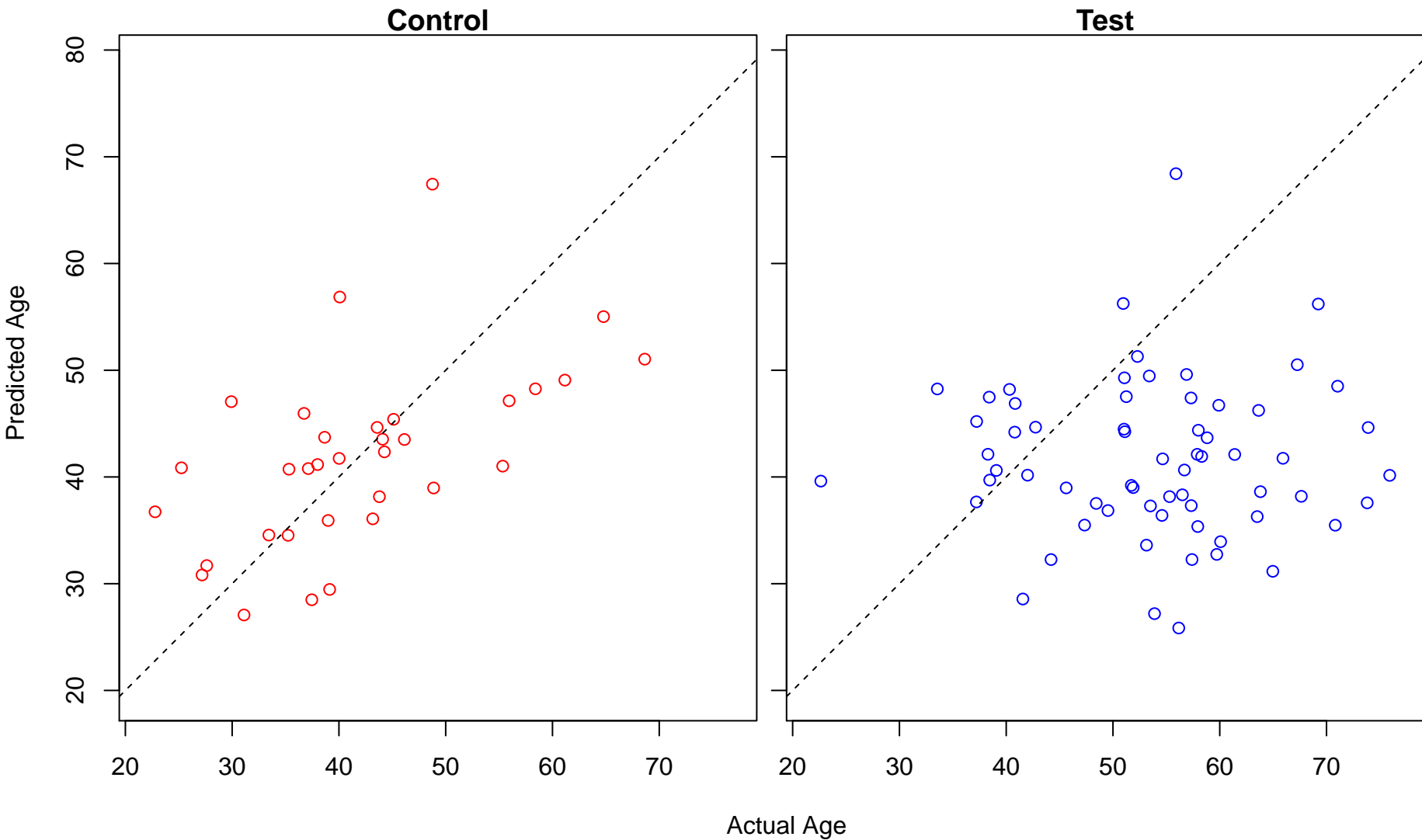
central nervous system myelination (Score: 1.962543)



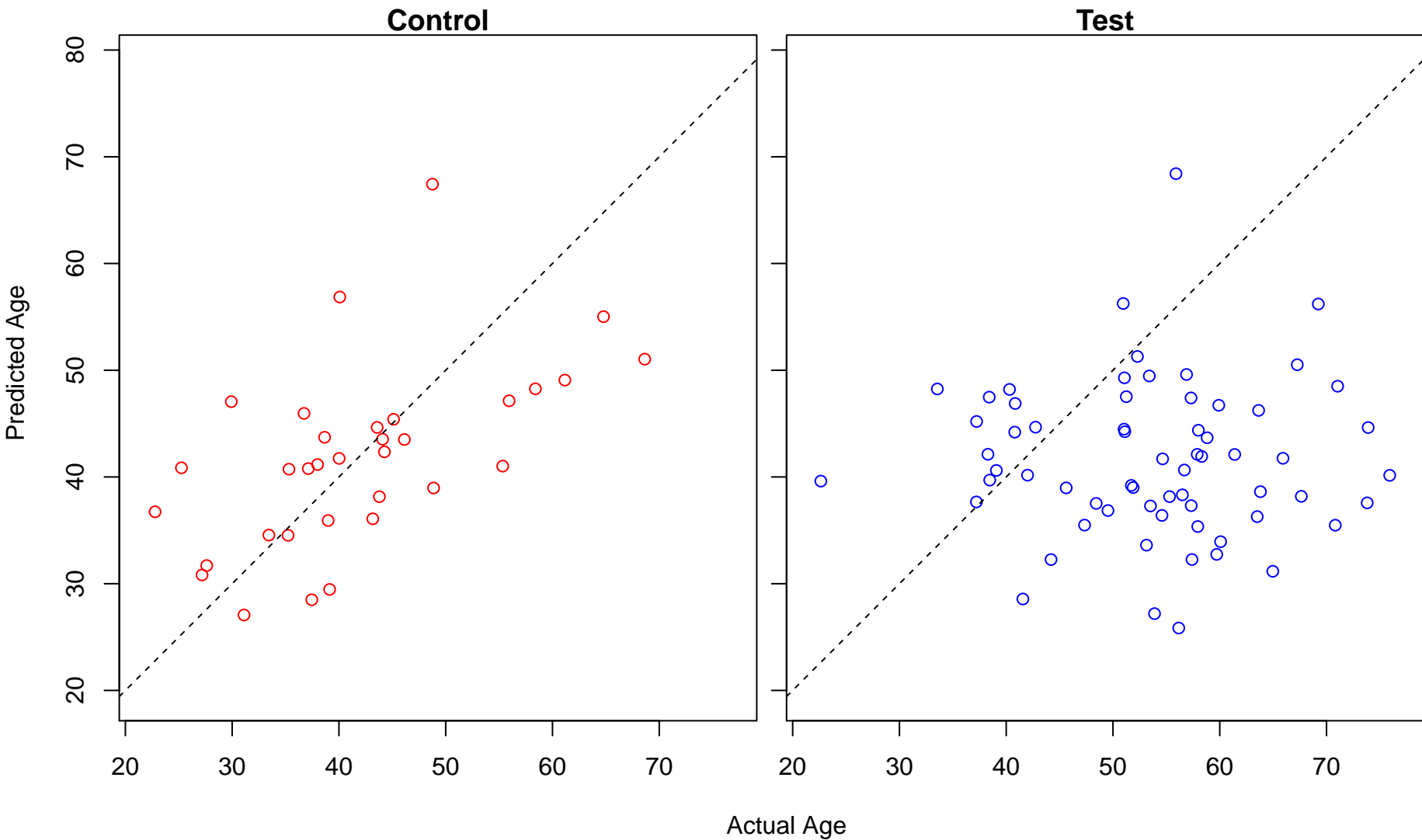
axon ensheathment in central nervous system (Score: 1.962543)



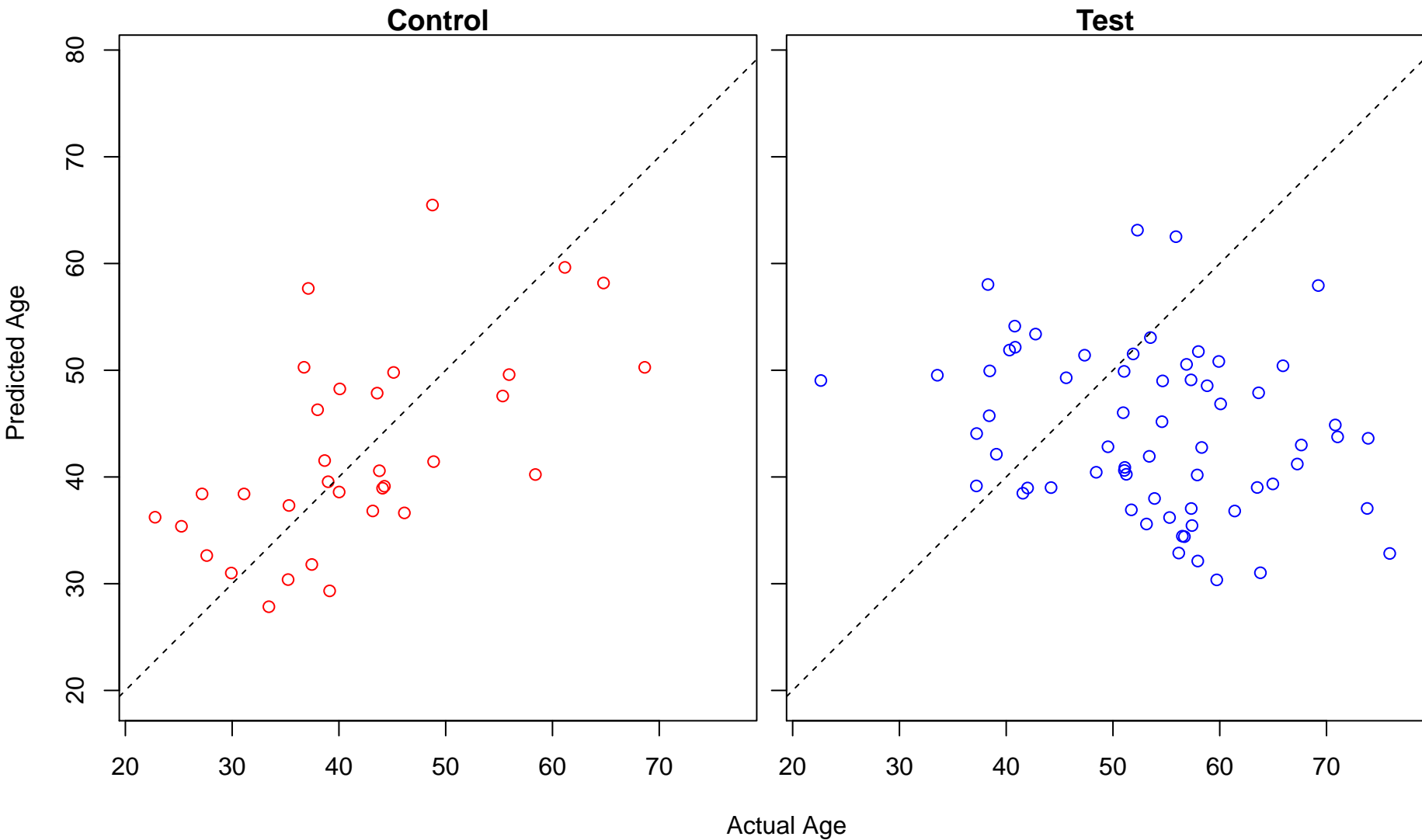
regulation of sterol transport (Score: 1.960805)



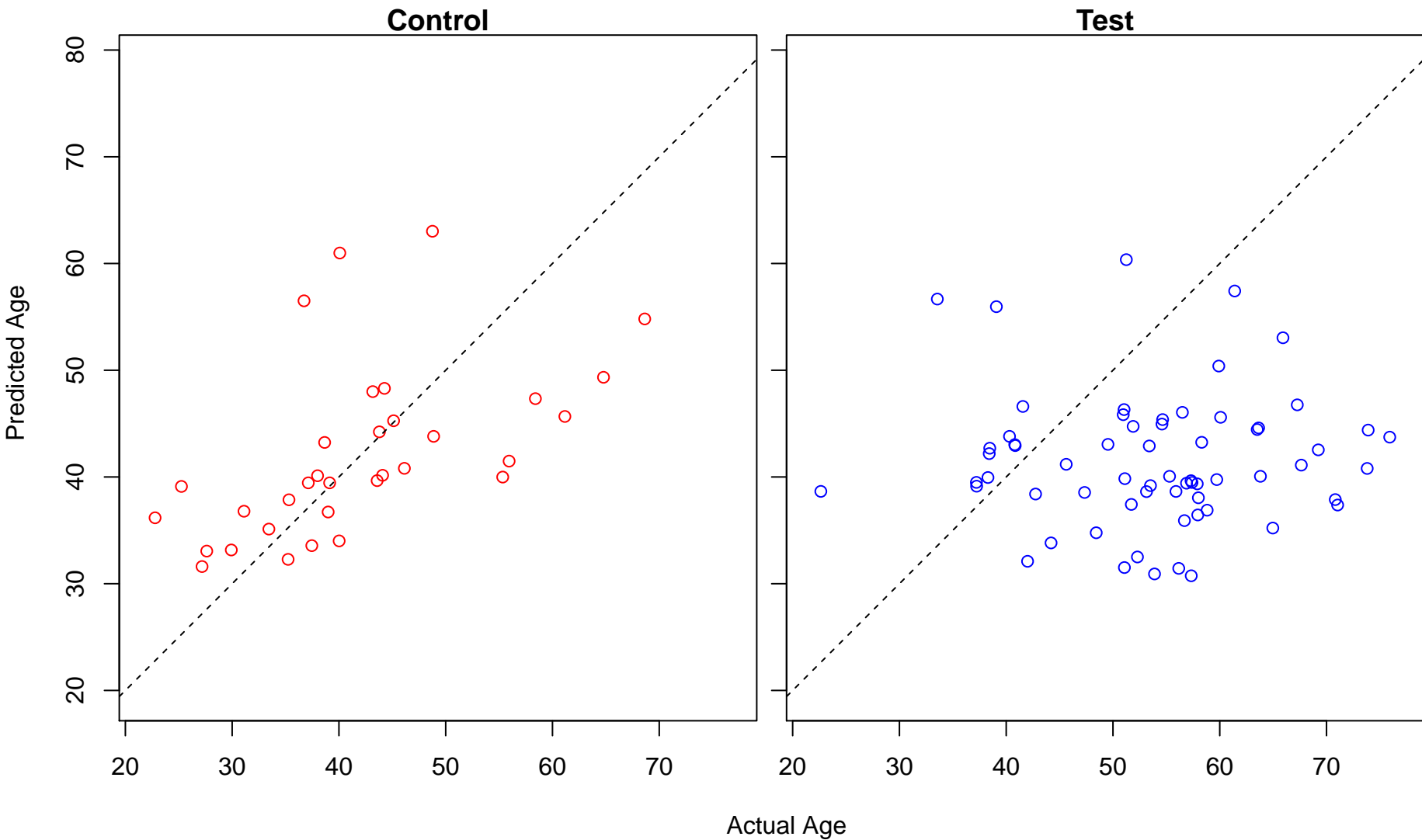
regulation of cholesterol transport (Score: 1.960805)



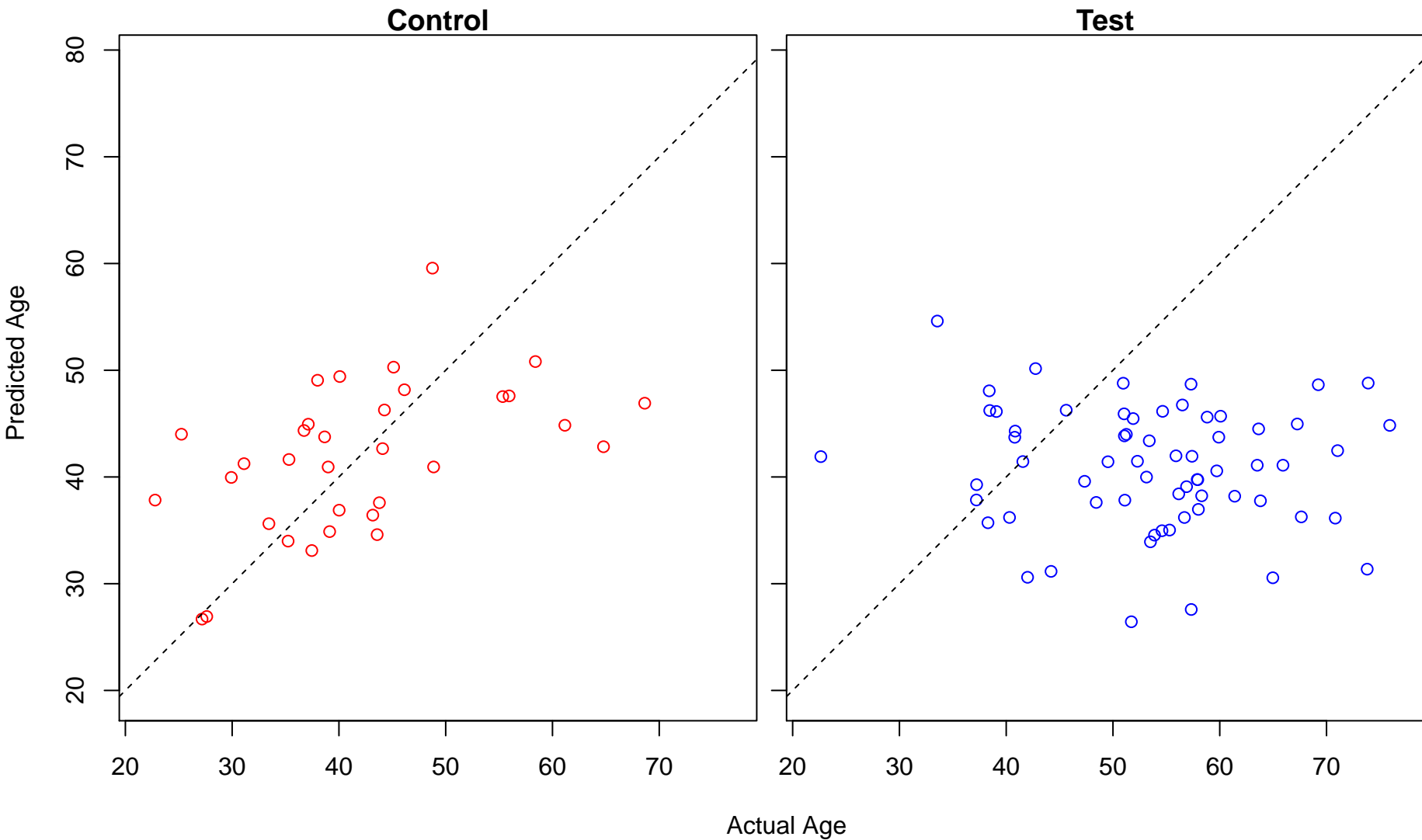
negative regulation of telomere capping (Score: 1.953586)



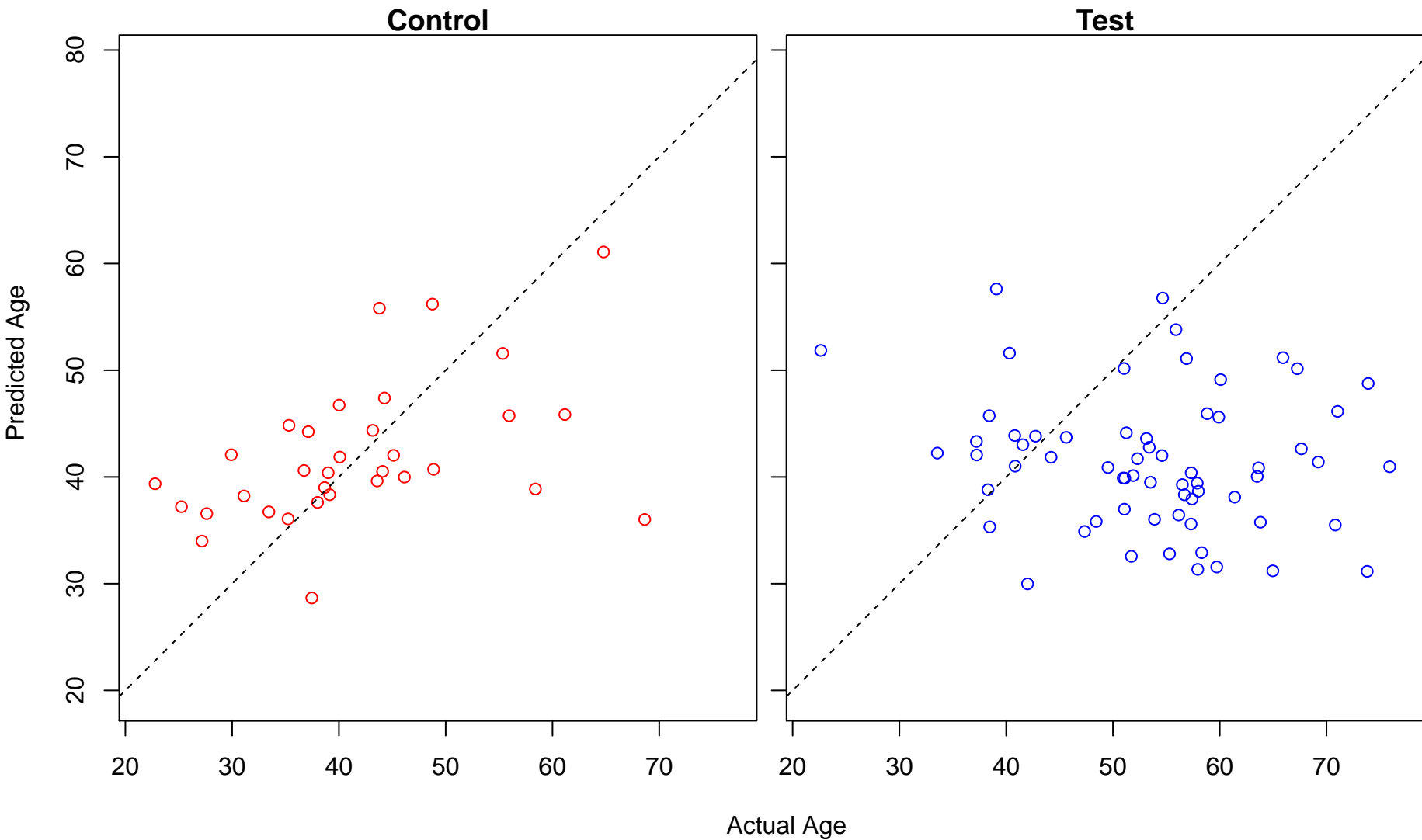
negative regulation of skeletal muscle tissue development (Score: 1.950253)



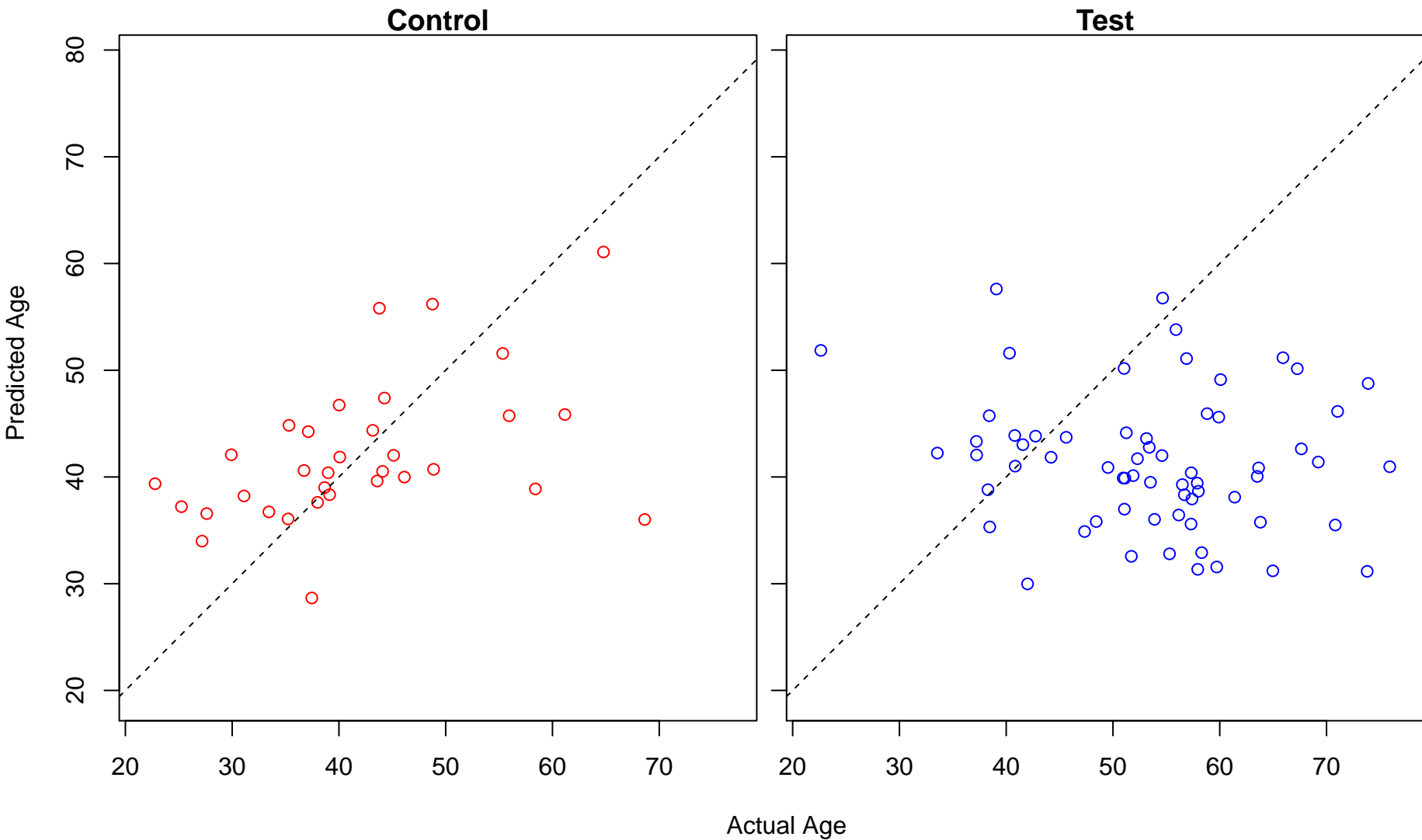
regulation of inclusion body assembly (Score: 1.946439)



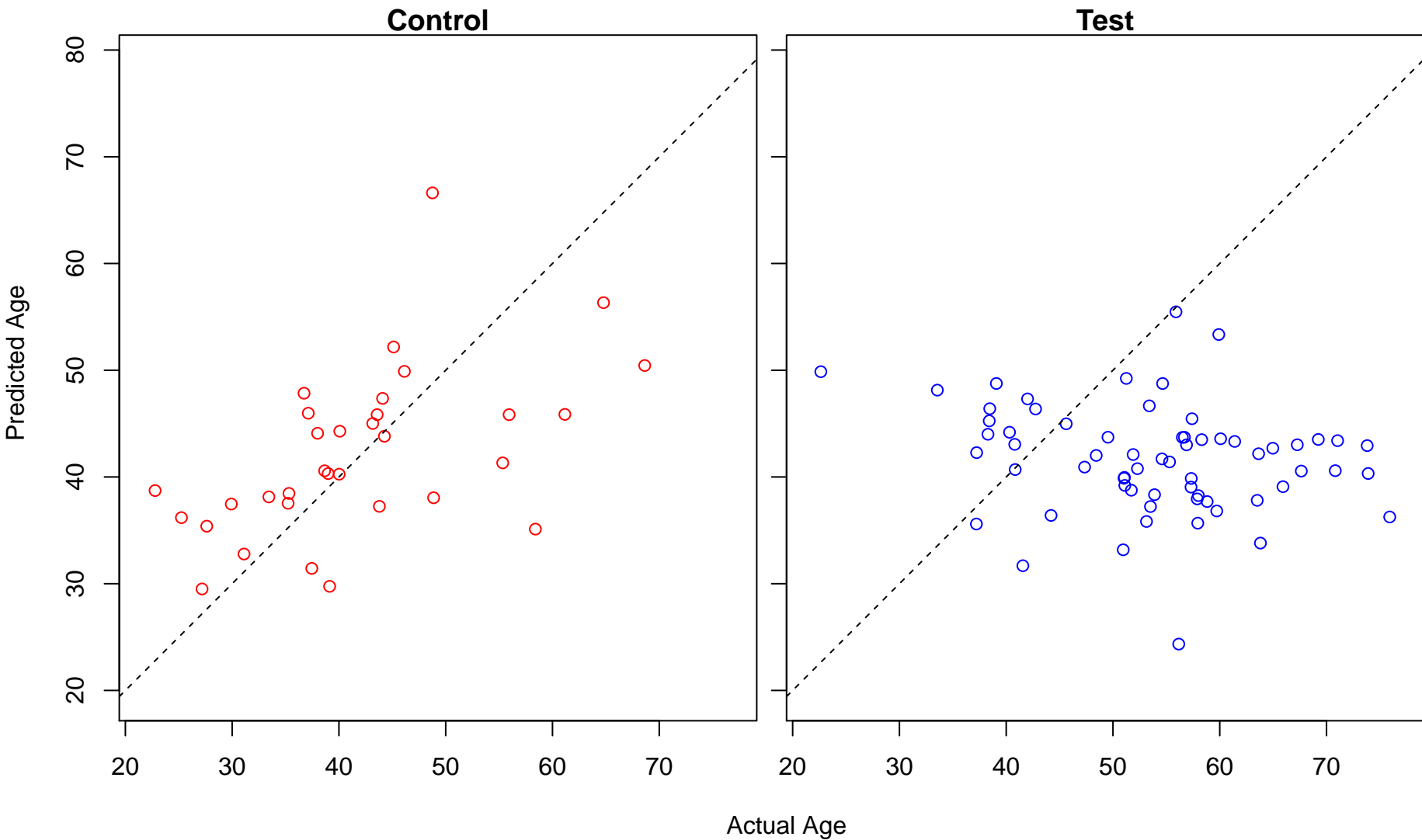
cartilage condensation (Score: 1.943537)



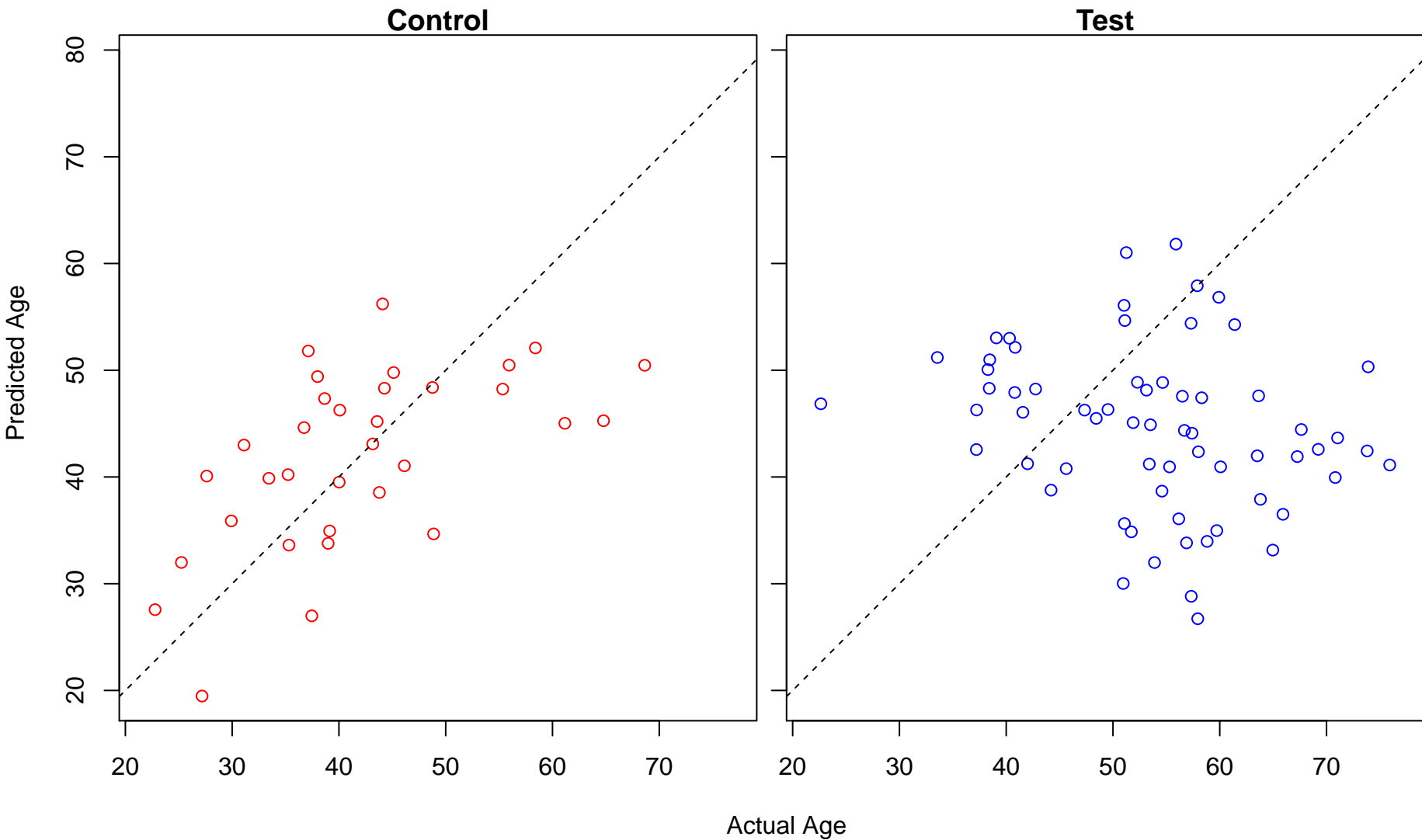
cell aggregation (Score: 1.943537)



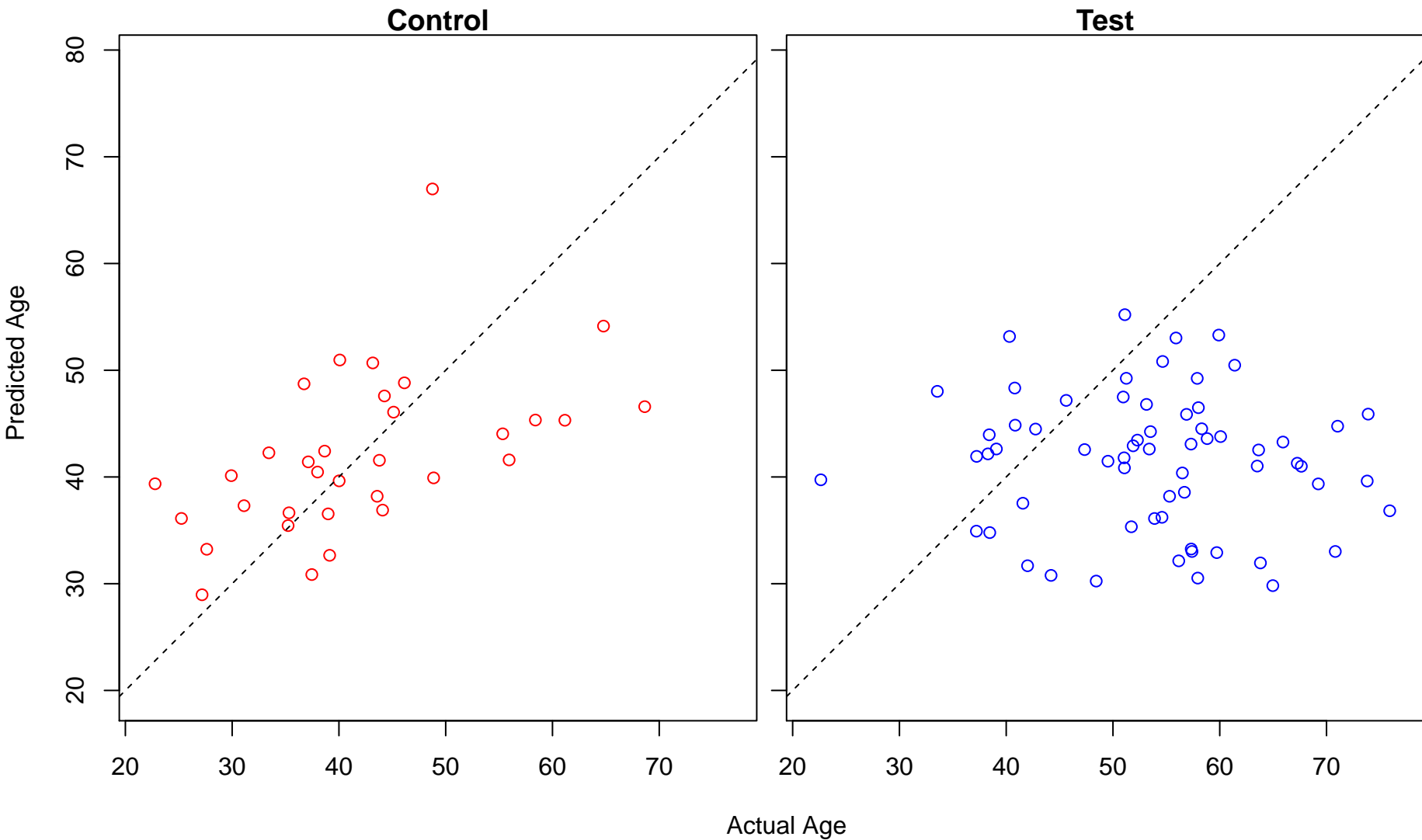
cGMP biosynthetic process (Score: 1.938124)



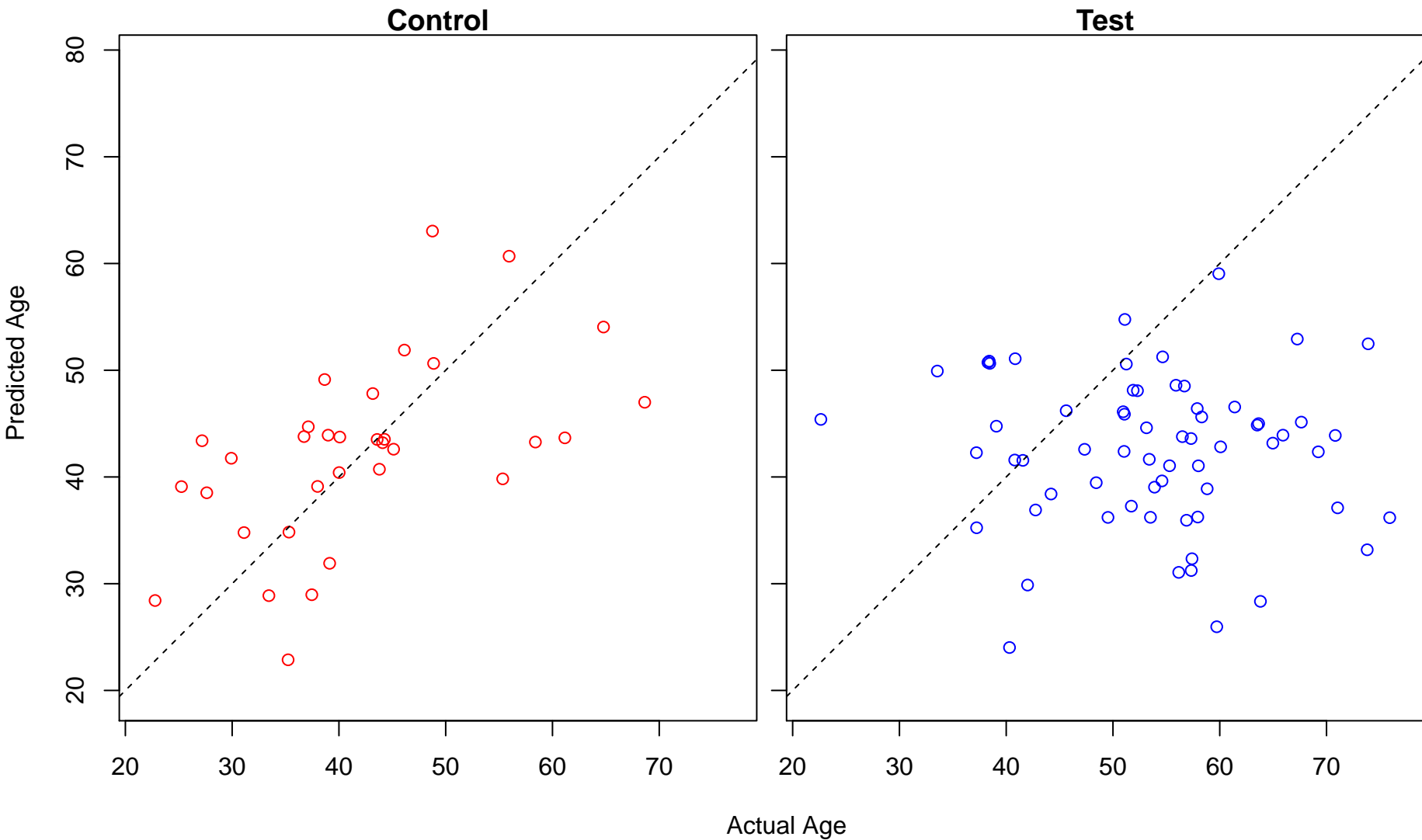
vasoconstriction (Score: 1.929679)



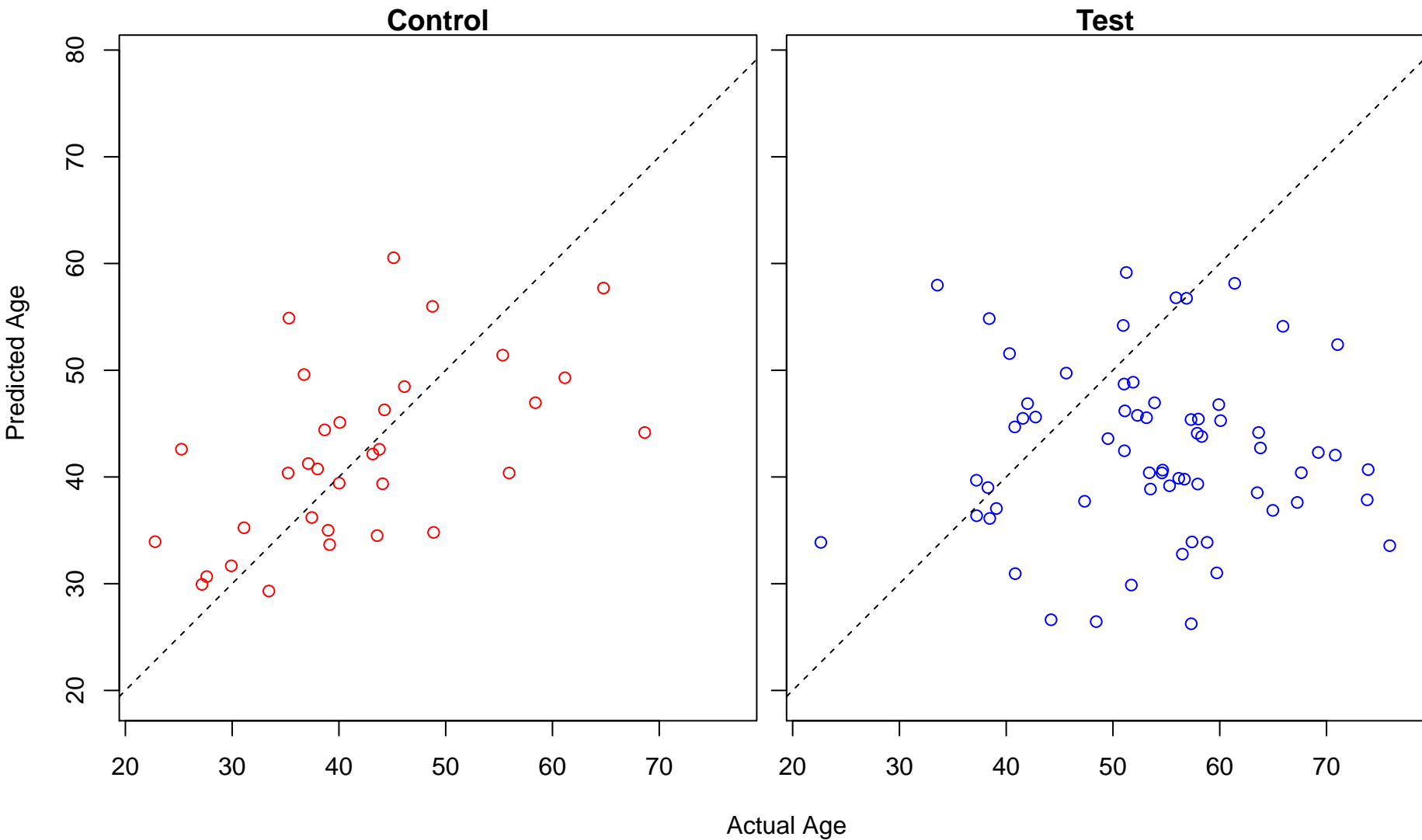
purine deoxyribonucleotide catabolic process (Score: 1.916069)



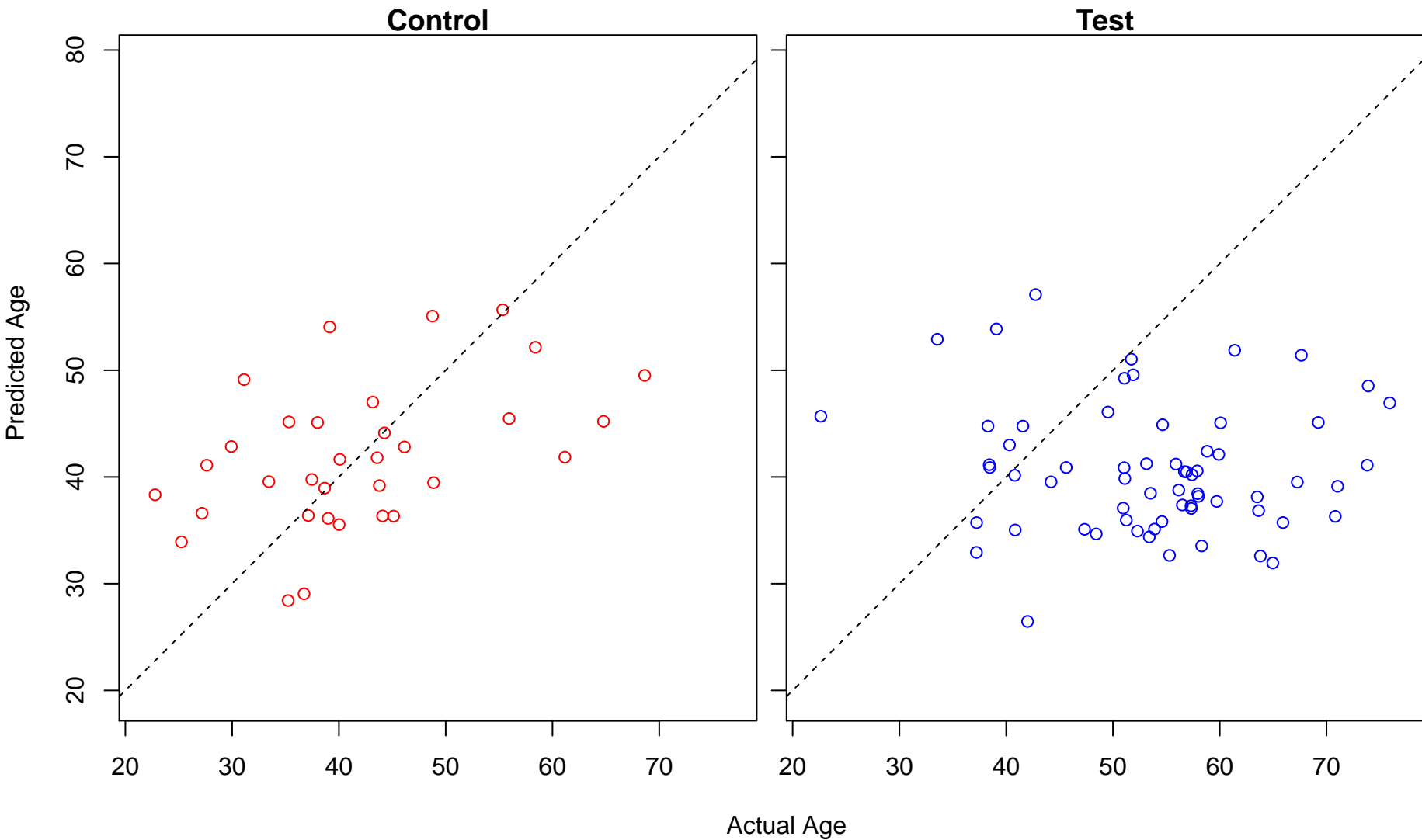
regulation of macrophage cytokine production (Score: 1.915377)



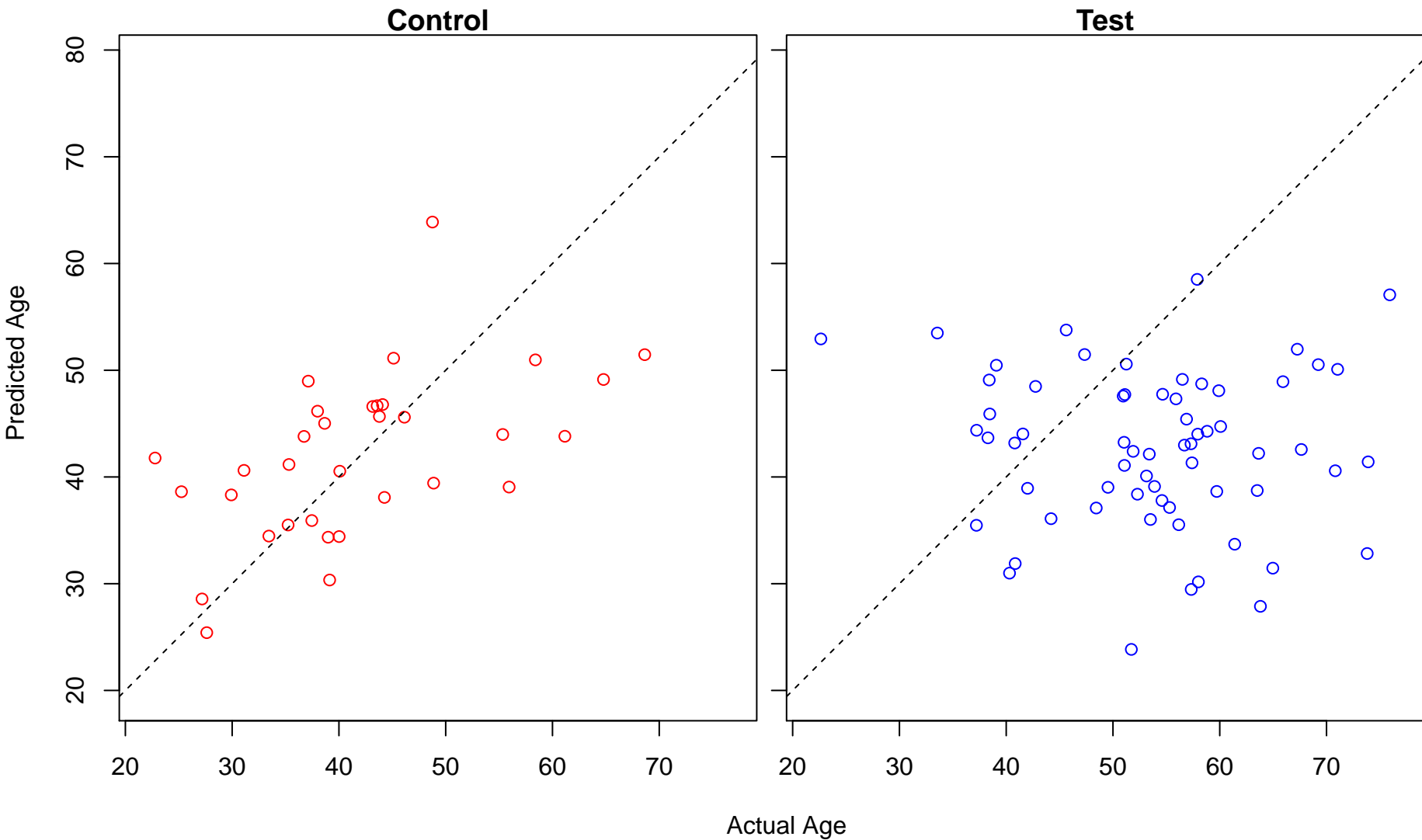
spinal cord development (Score: 1.914189)



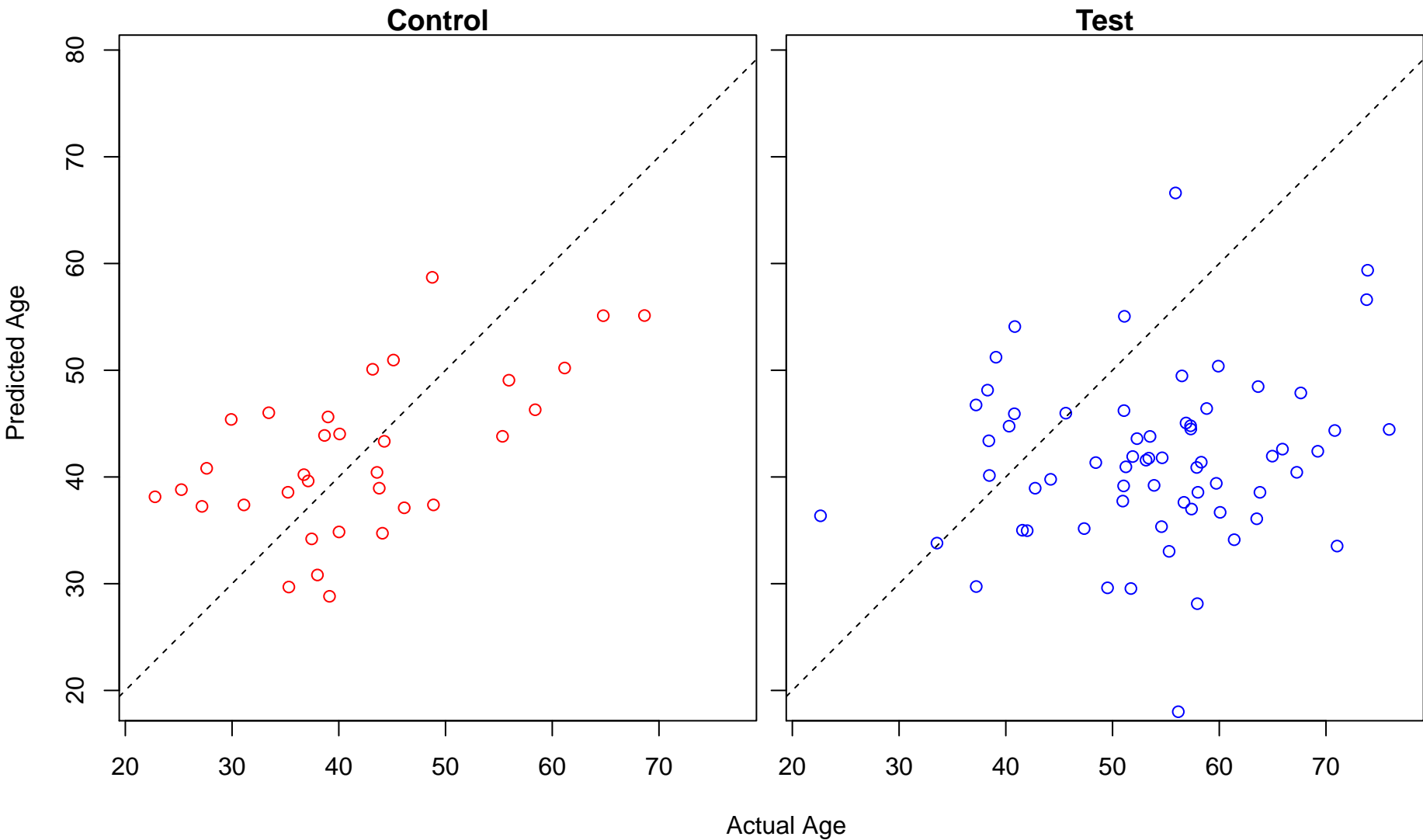
Notch signaling involved in heart development (Score: 1.911713)



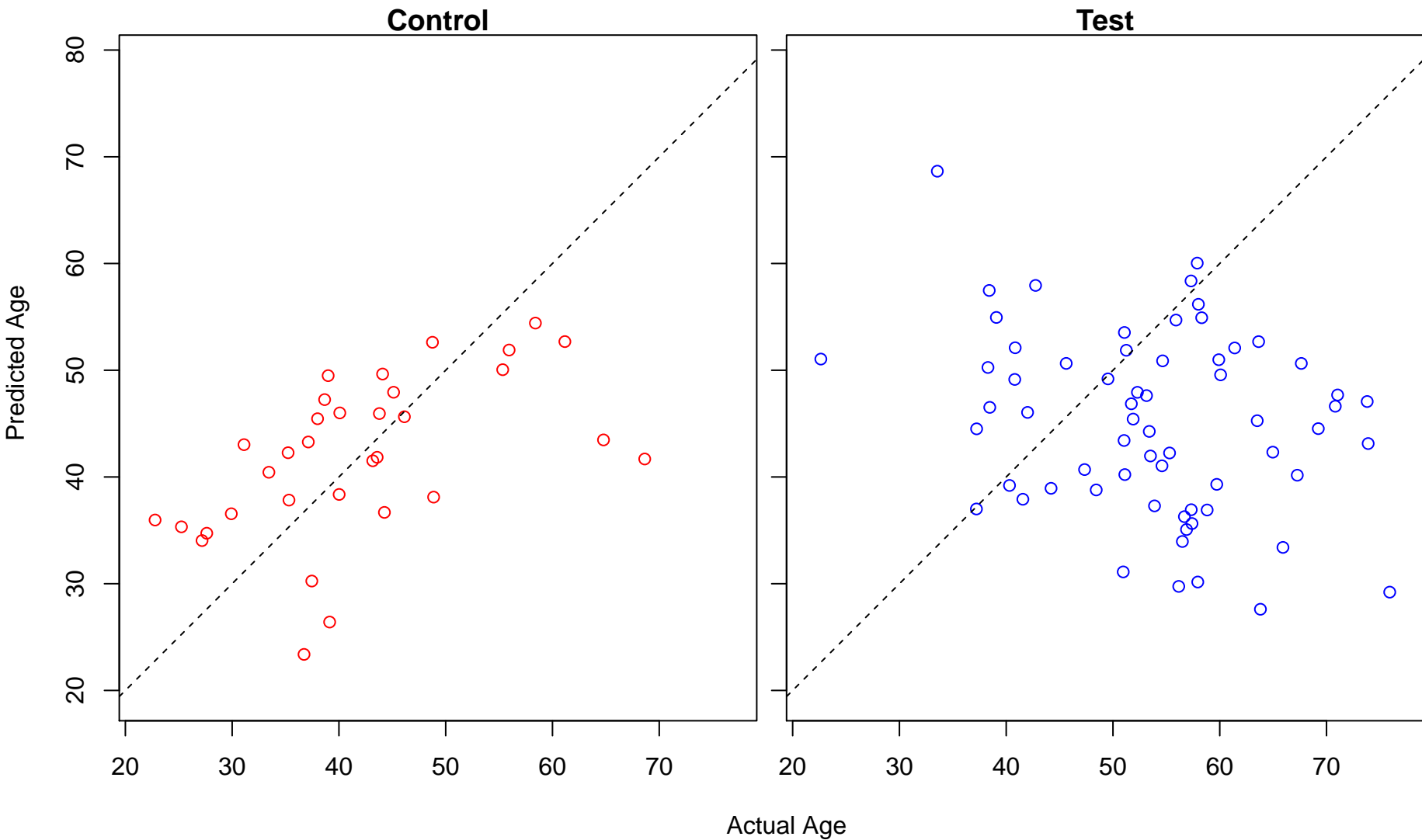
myelin maintenance (Score: 1.911417)



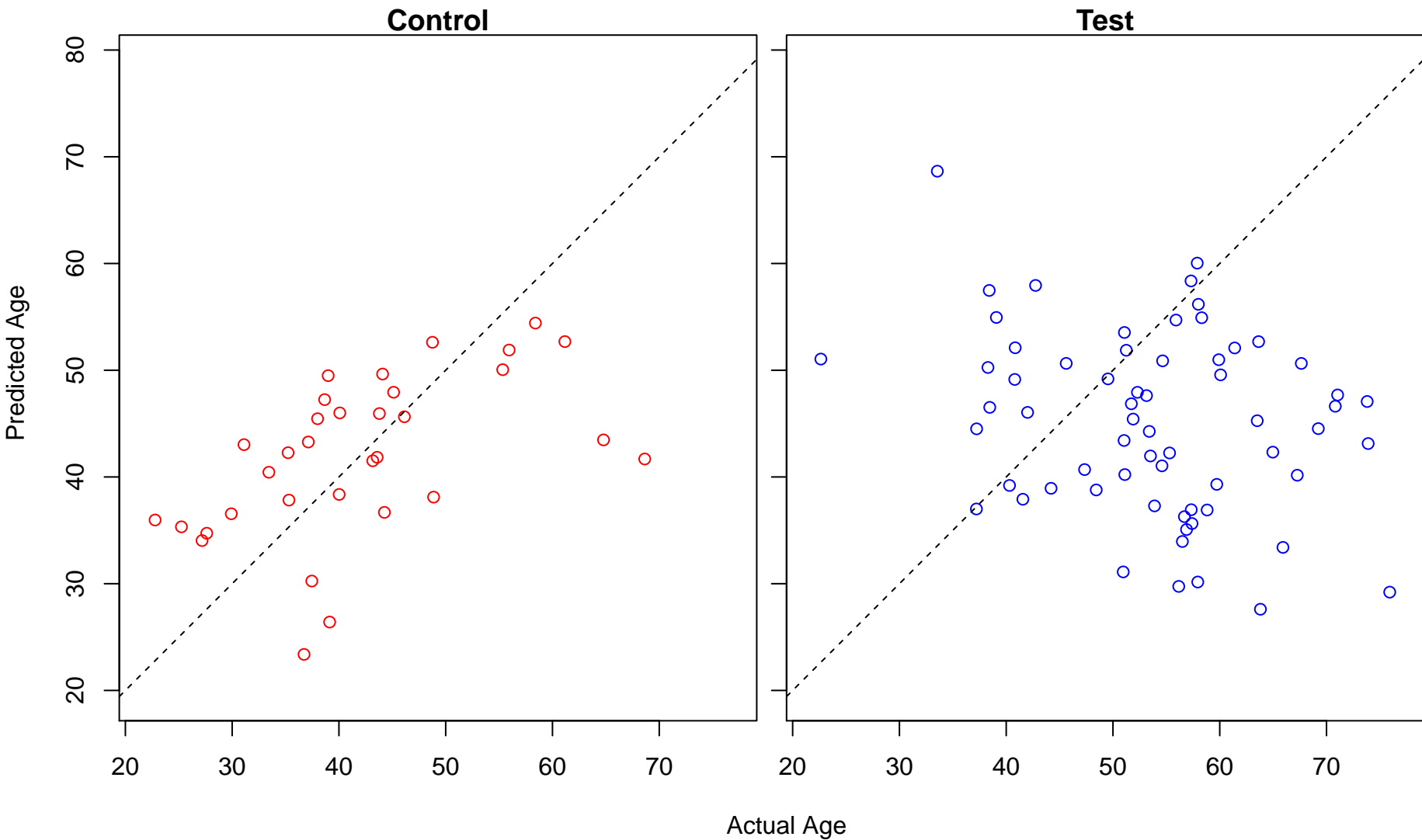
vitamin transport (Score: 1.905324)



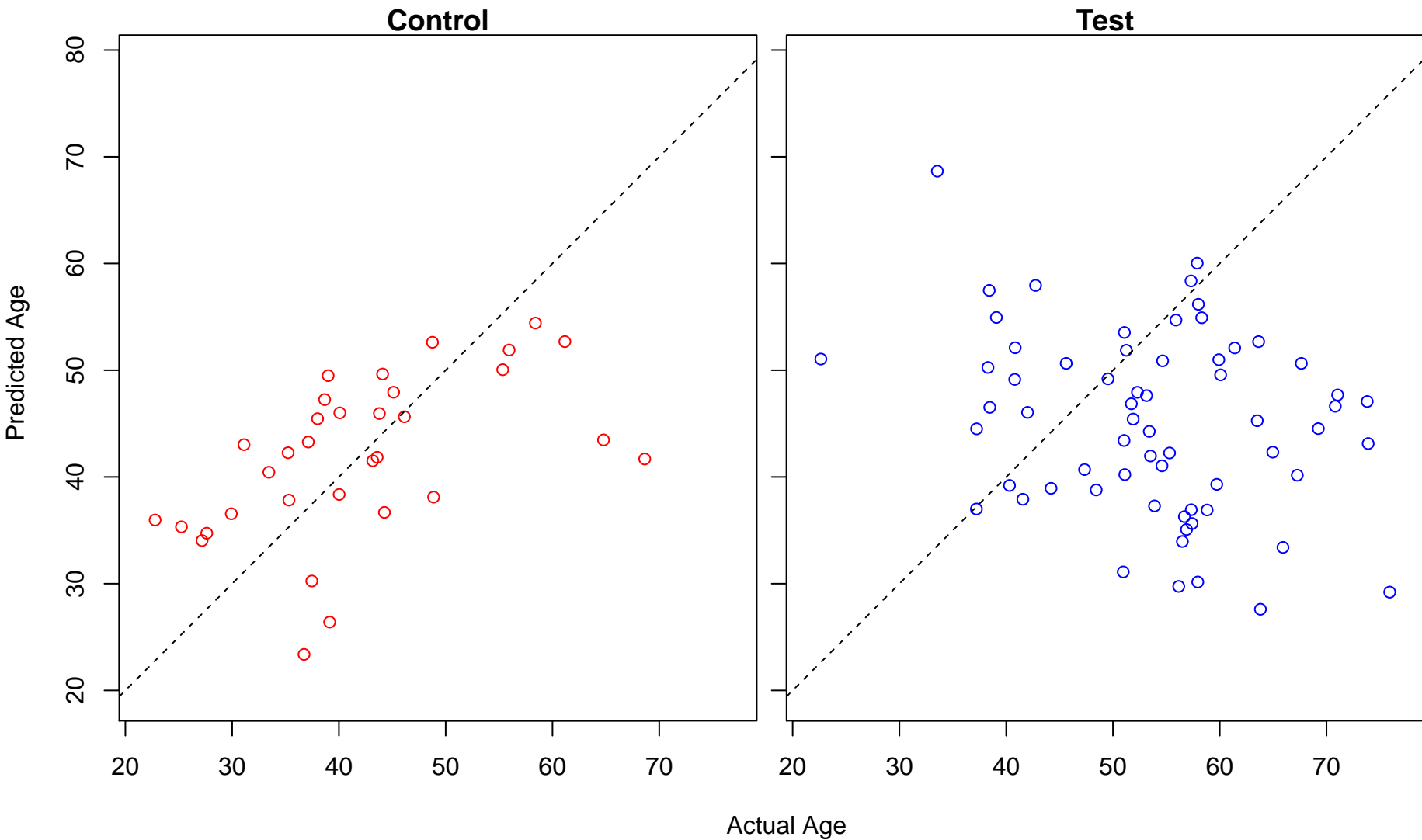
response to caffeine (Score: 1.895626)



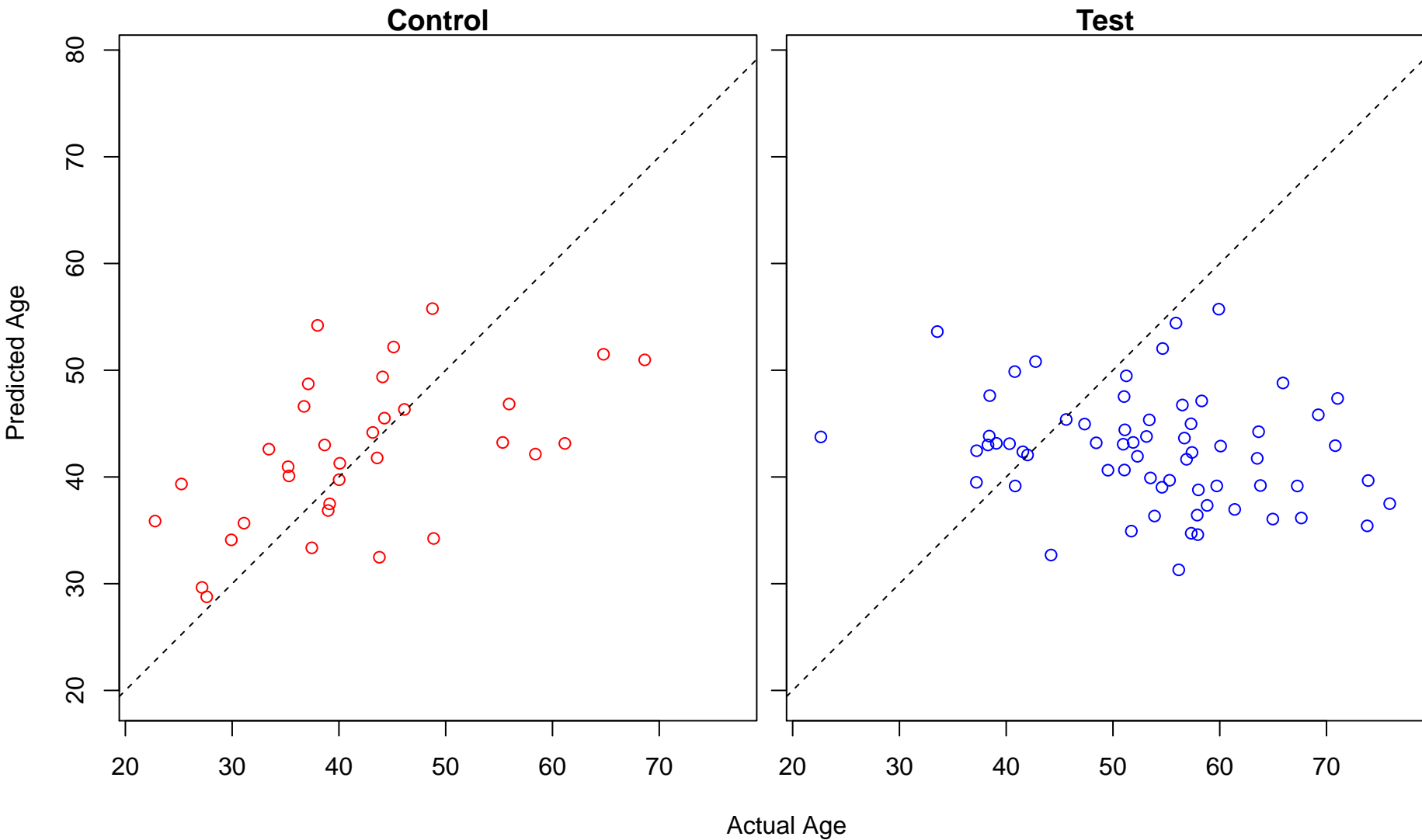
cellular response to caffeine (Score: 1.895626)



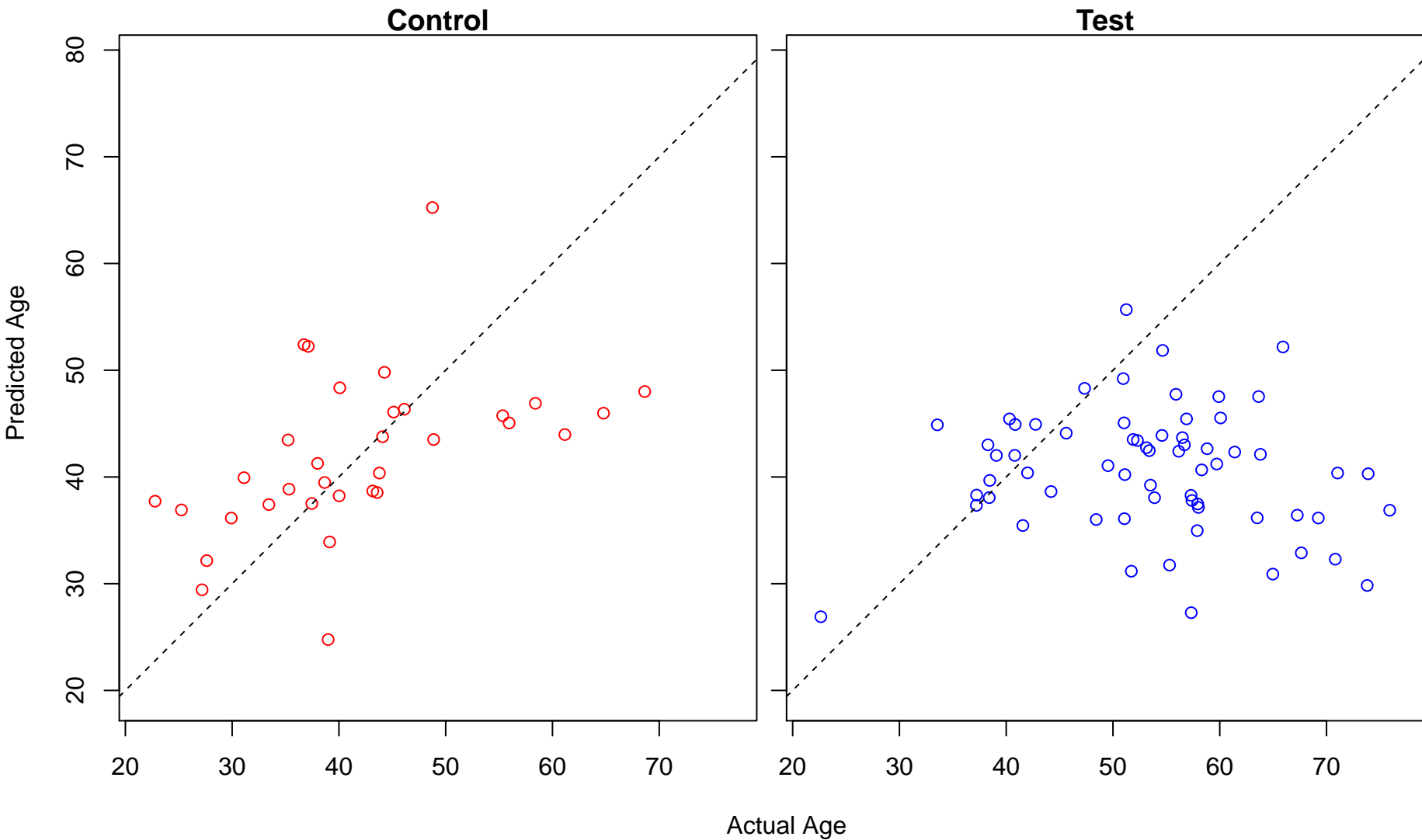
cellular response to purine-containing compound (Score: 1.895626)



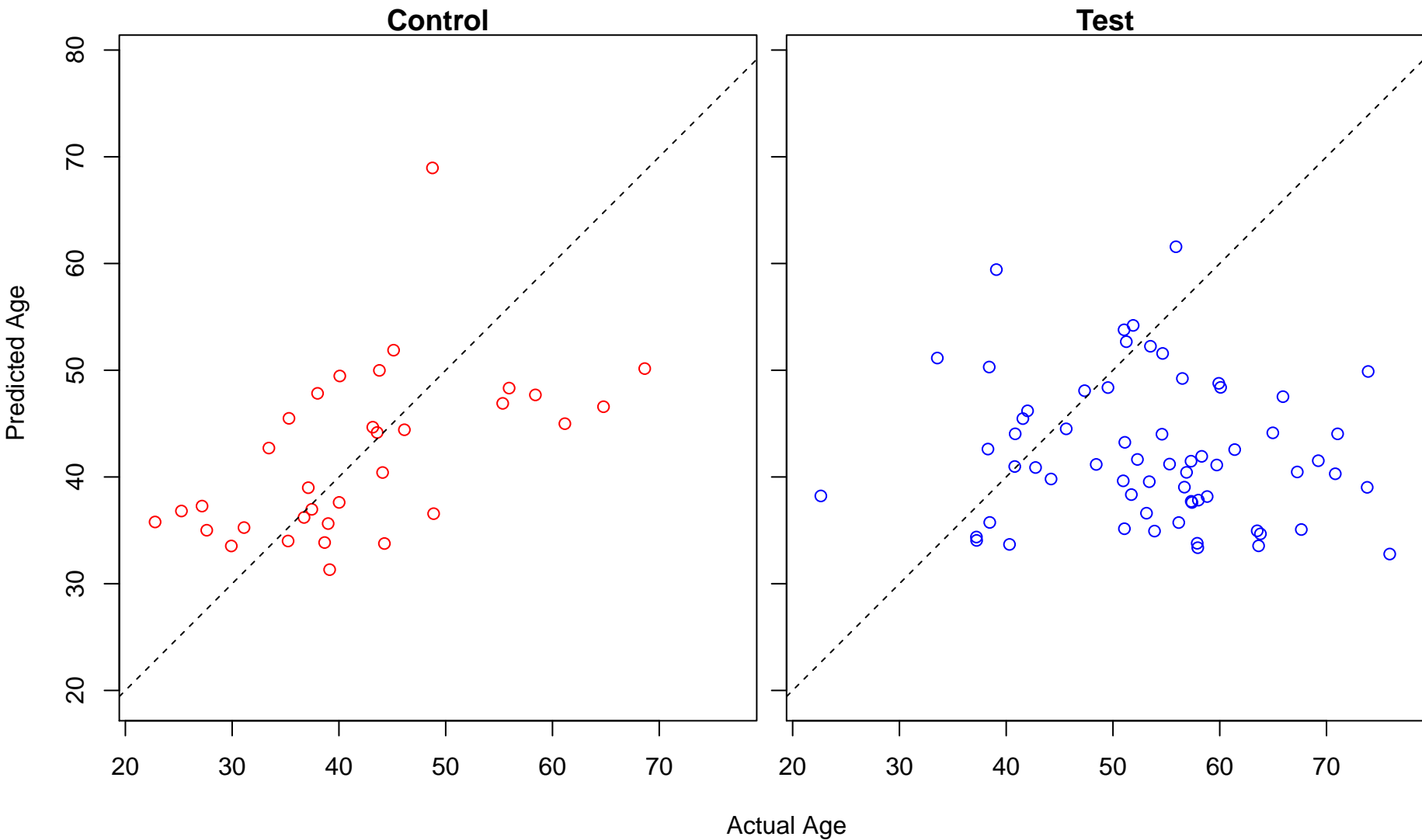
cGMP metabolic process (Score: 1.889046)



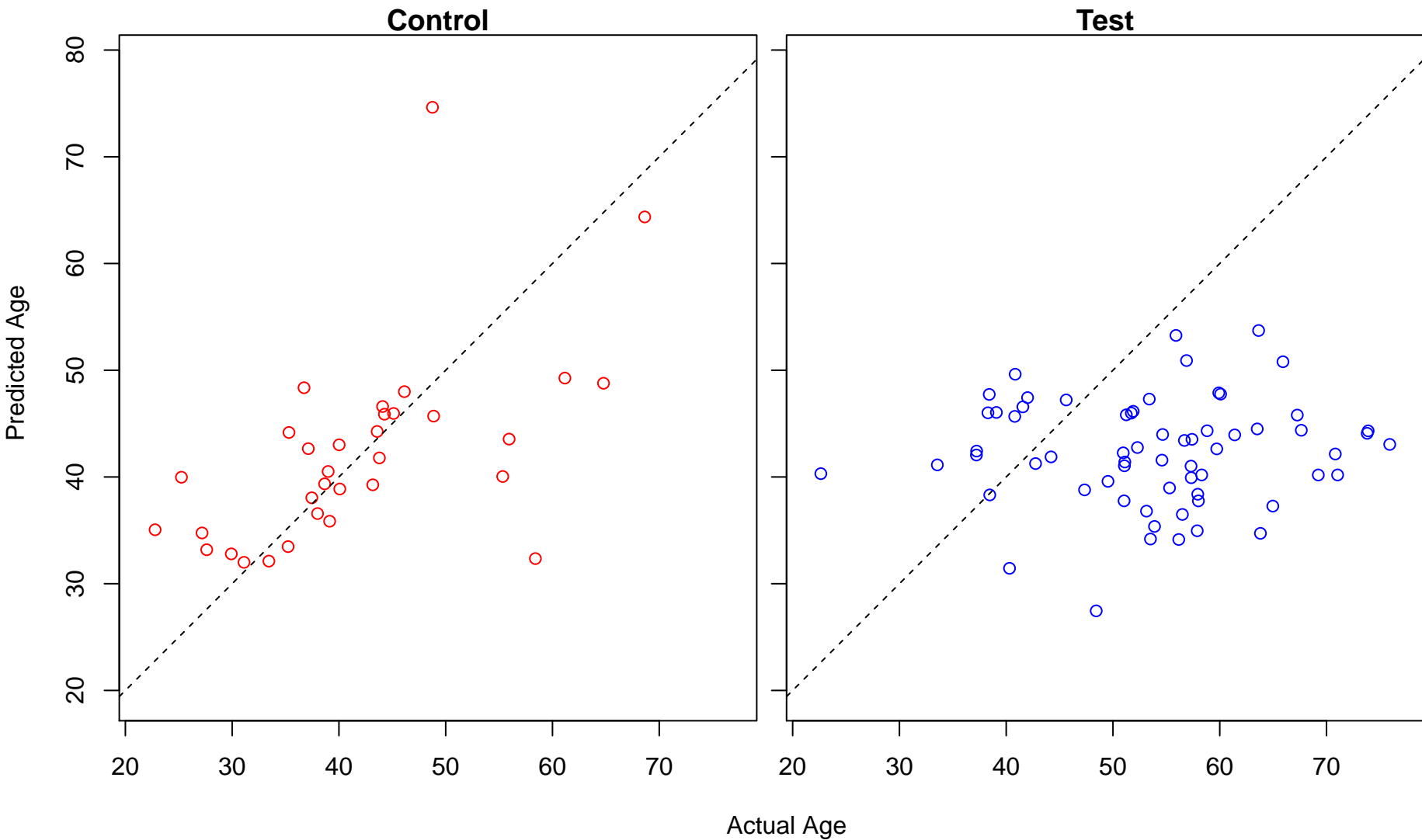
erythrocyte development (Score: 1.889016)



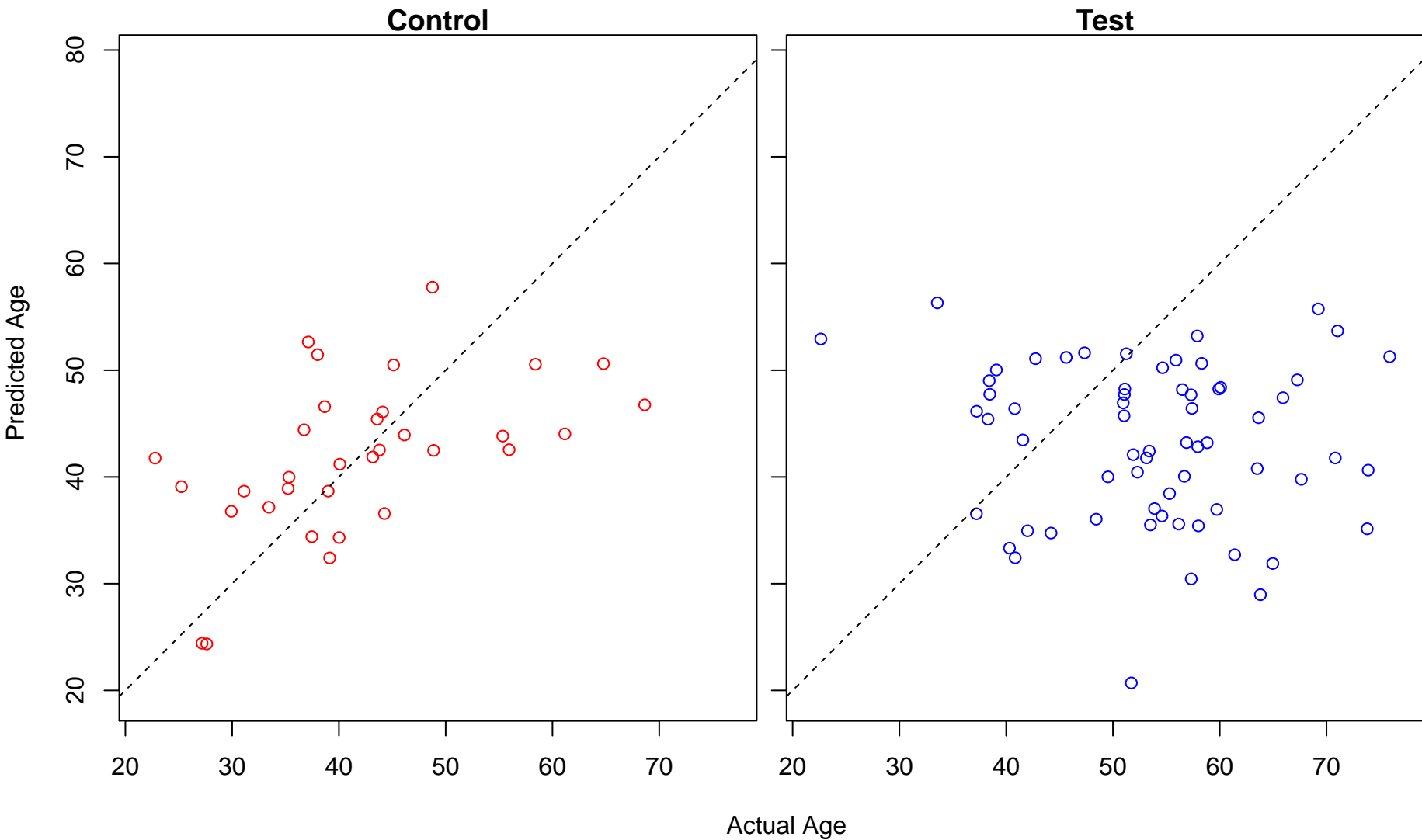
snRNA transcription from RNA polymerase III promoter (Score: 1.886558)



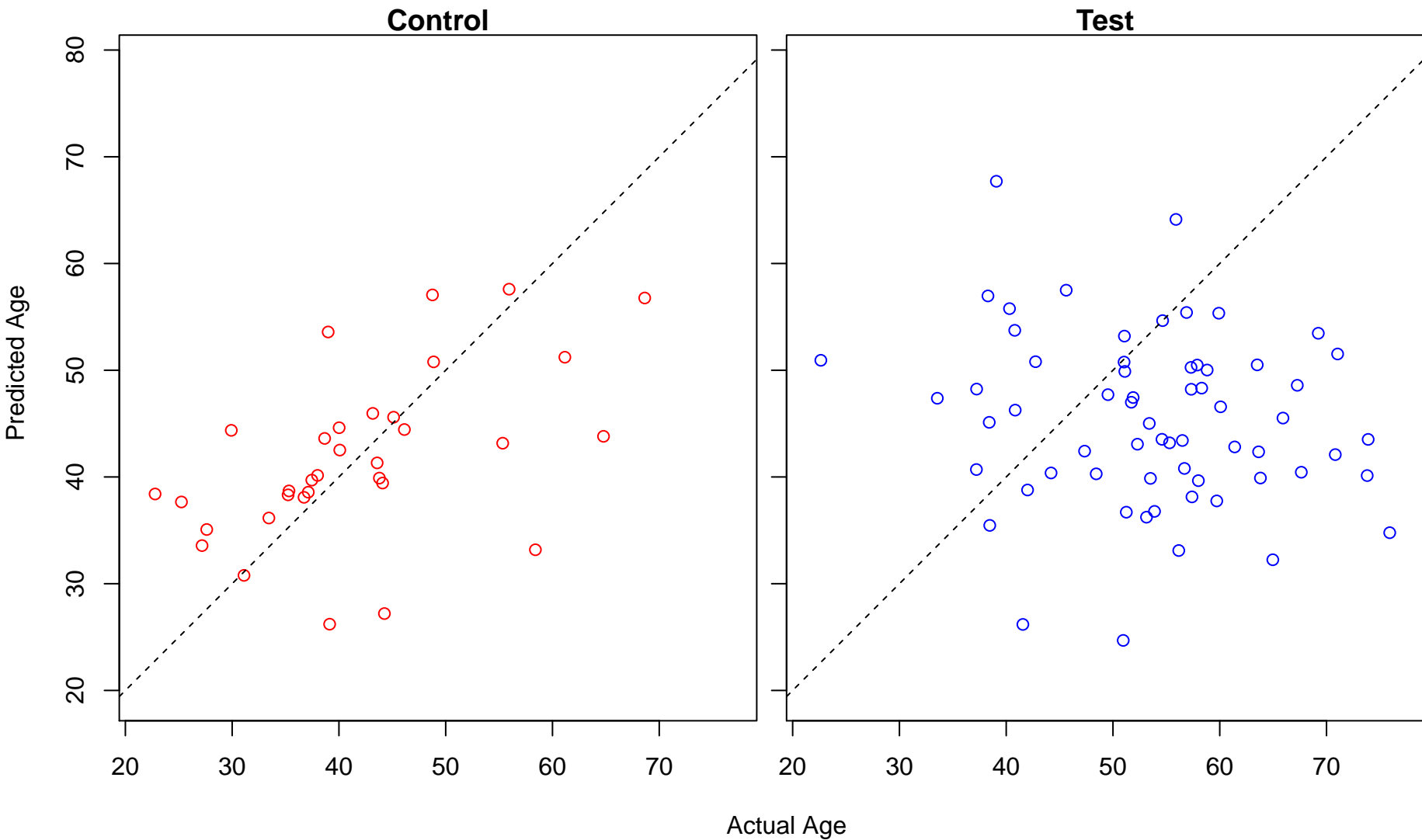
DNA replication initiation (Score: 1.879183)



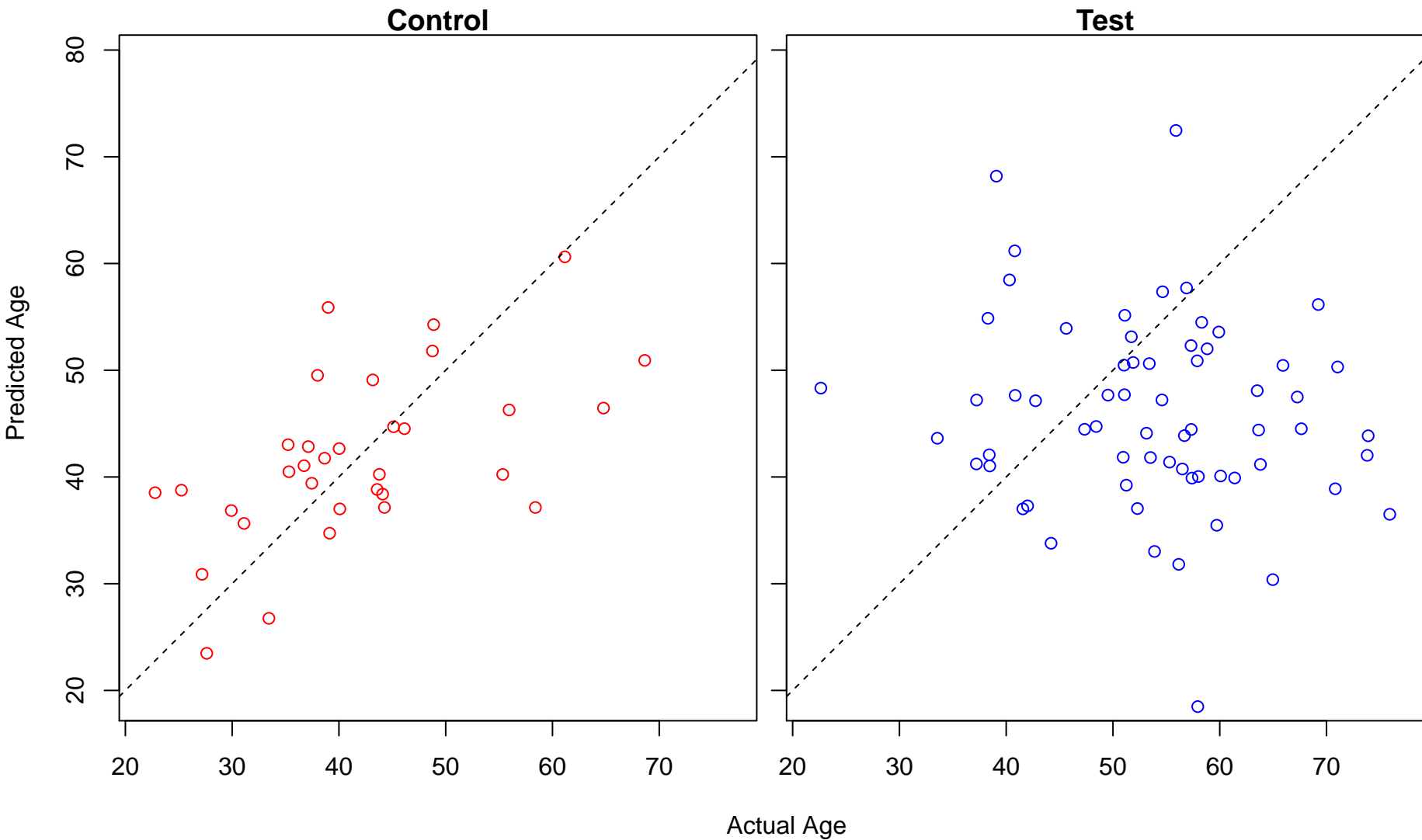
oligodendrocyte development (Score: 1.869238)



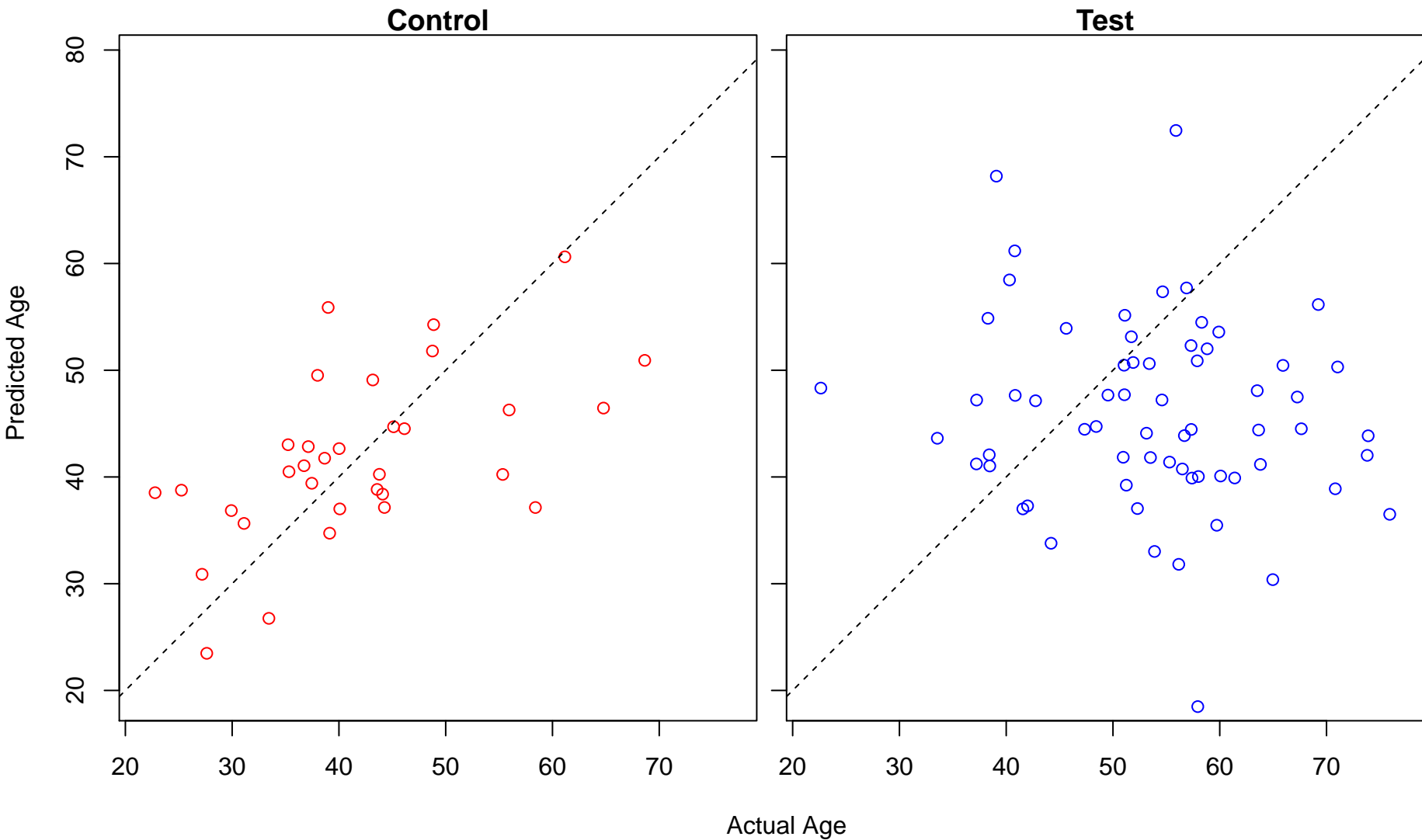
leptin-mediated signaling pathway (Score: 1.867724)



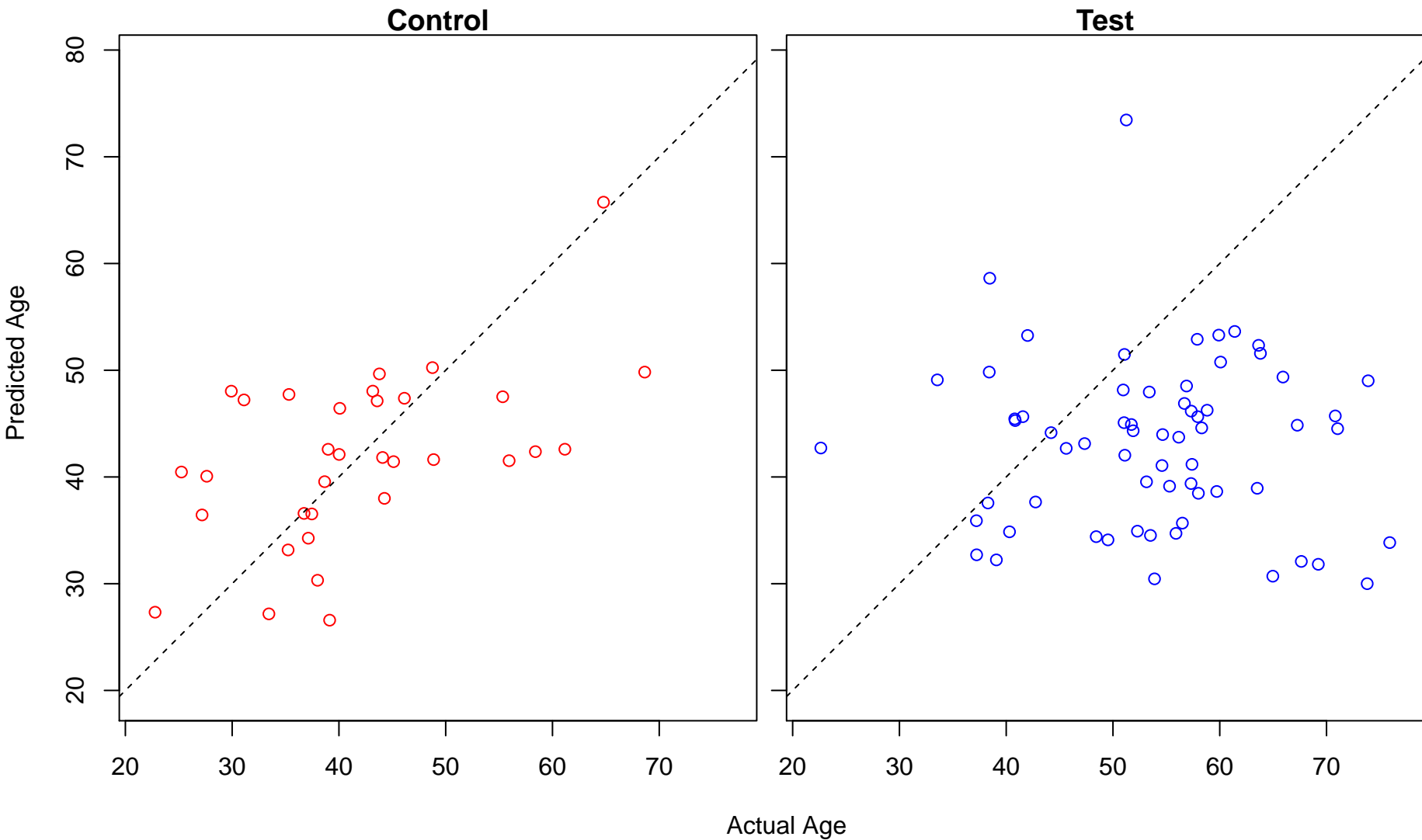
negative regulation of response to food (Score: 1.852769)



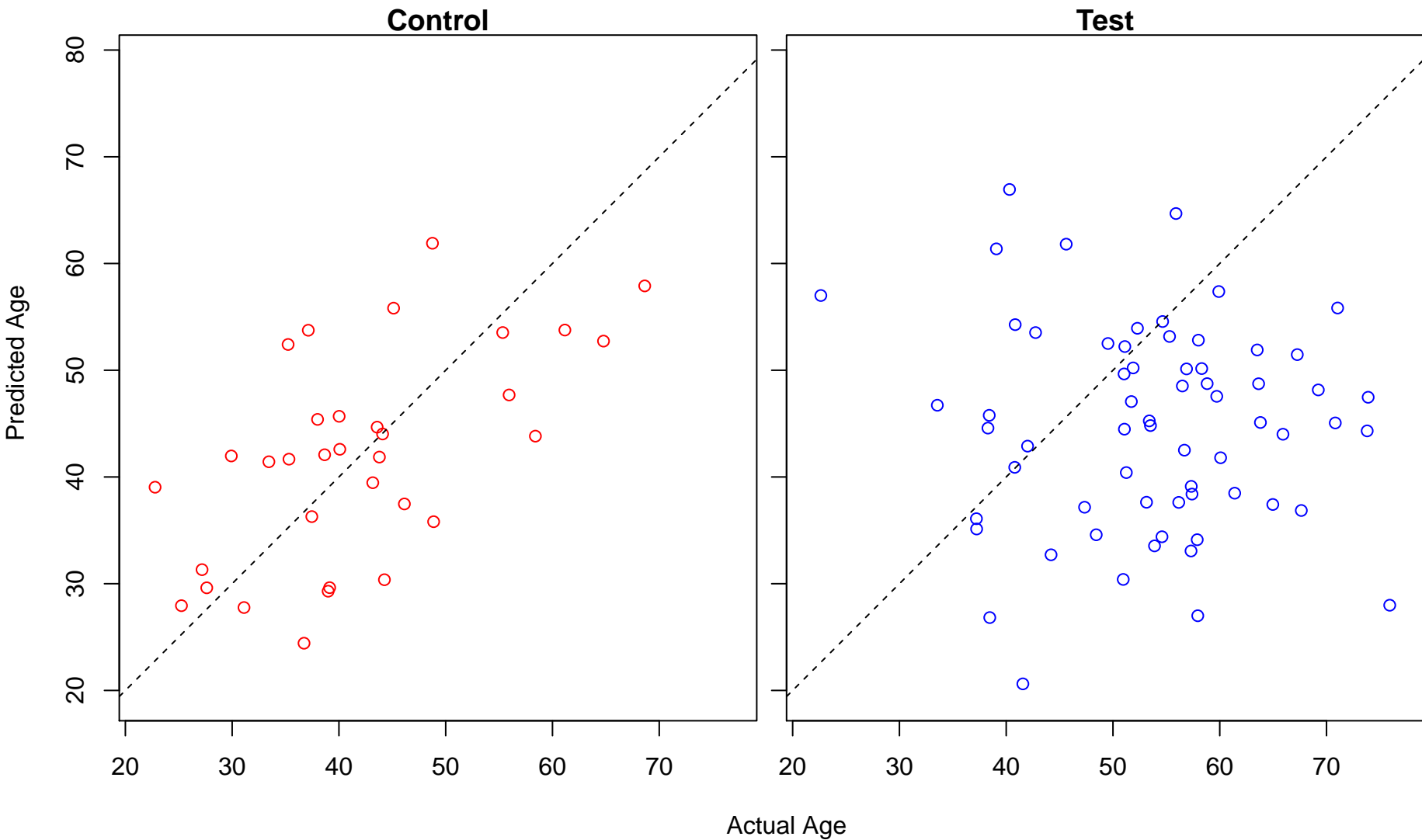
negative regulation of appetite (Score: 1.852769)



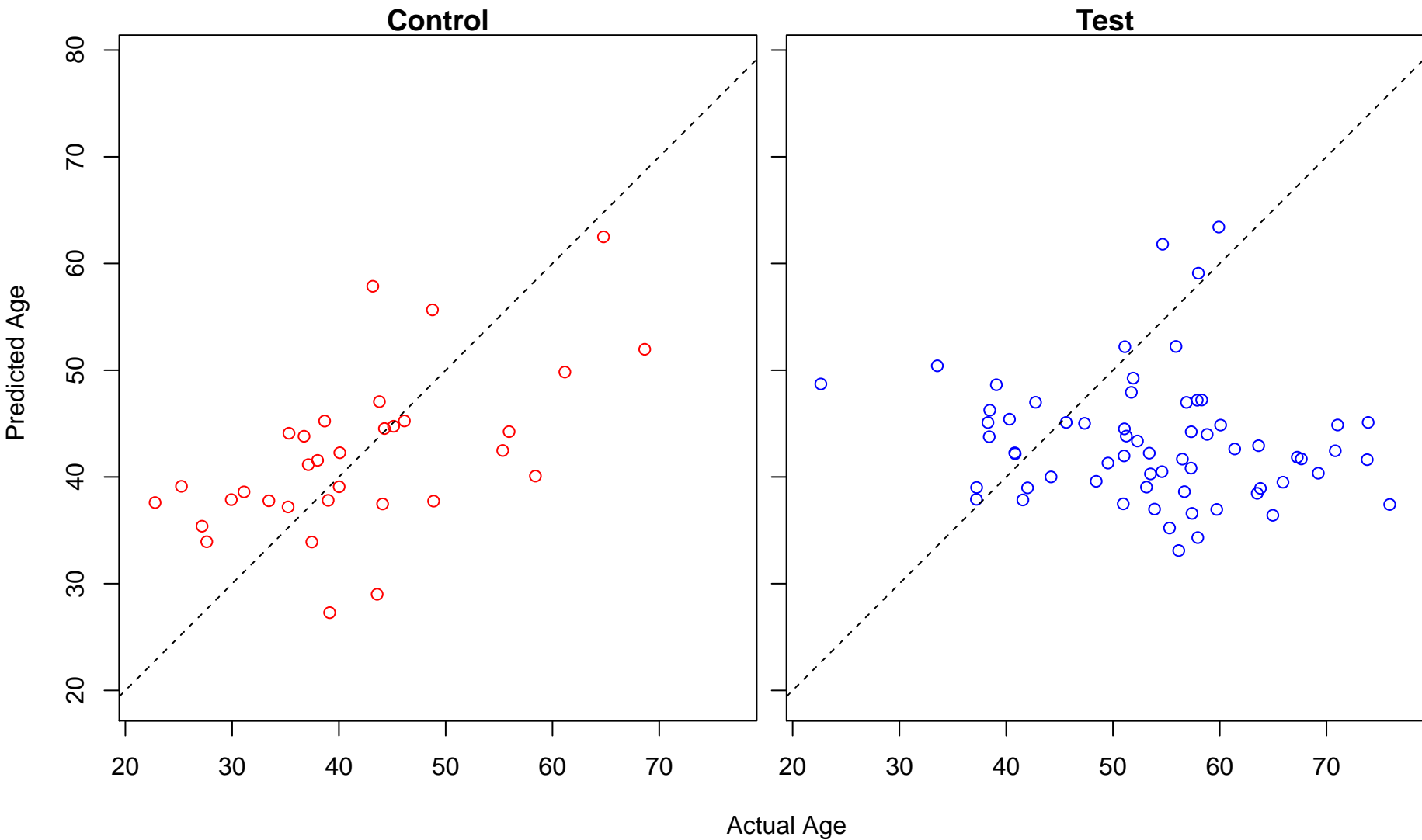
phosphatidylserine acyl-chain remodeling (Score: 1.849620)



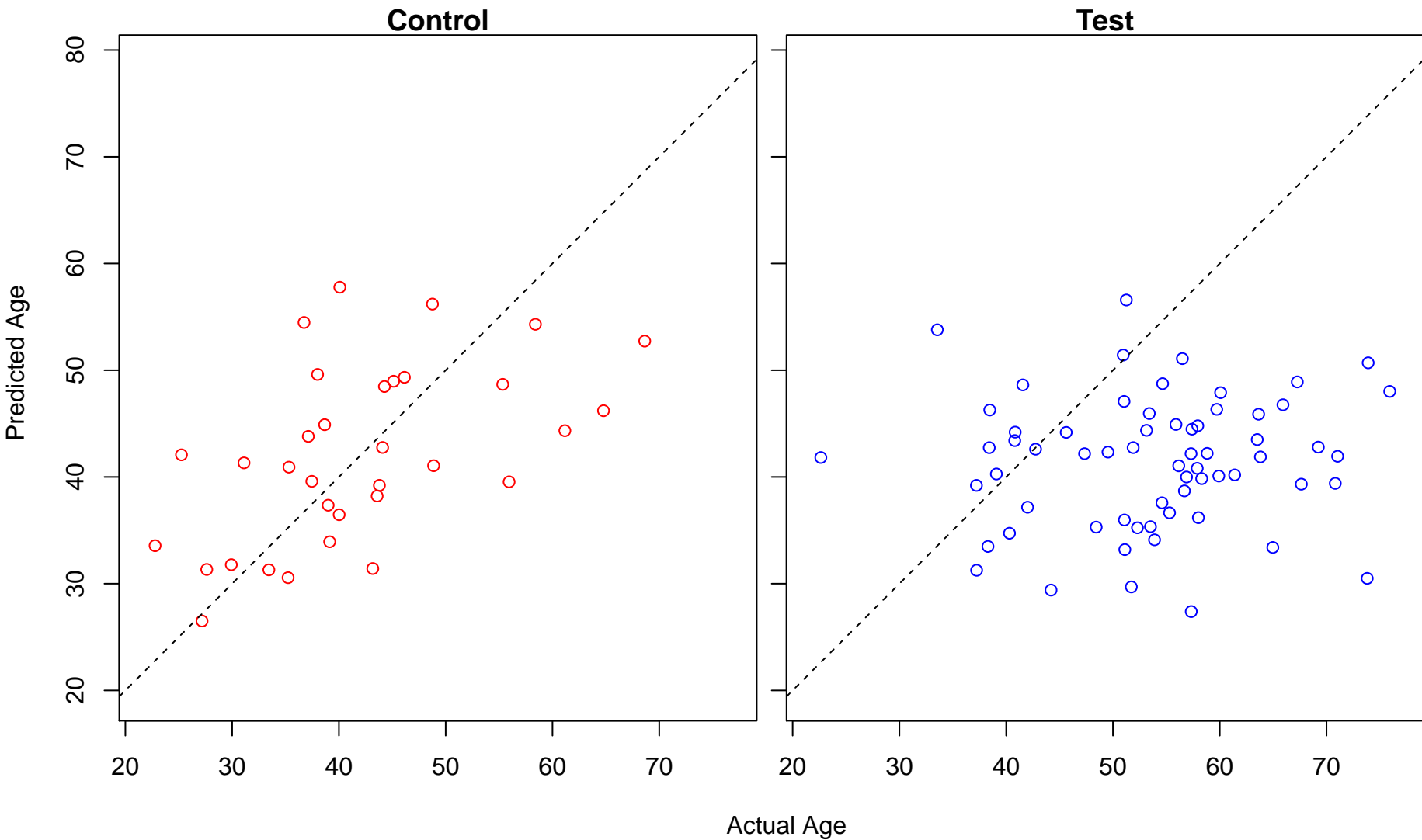
detection of mechanical stimulus (Score: 1.839243)



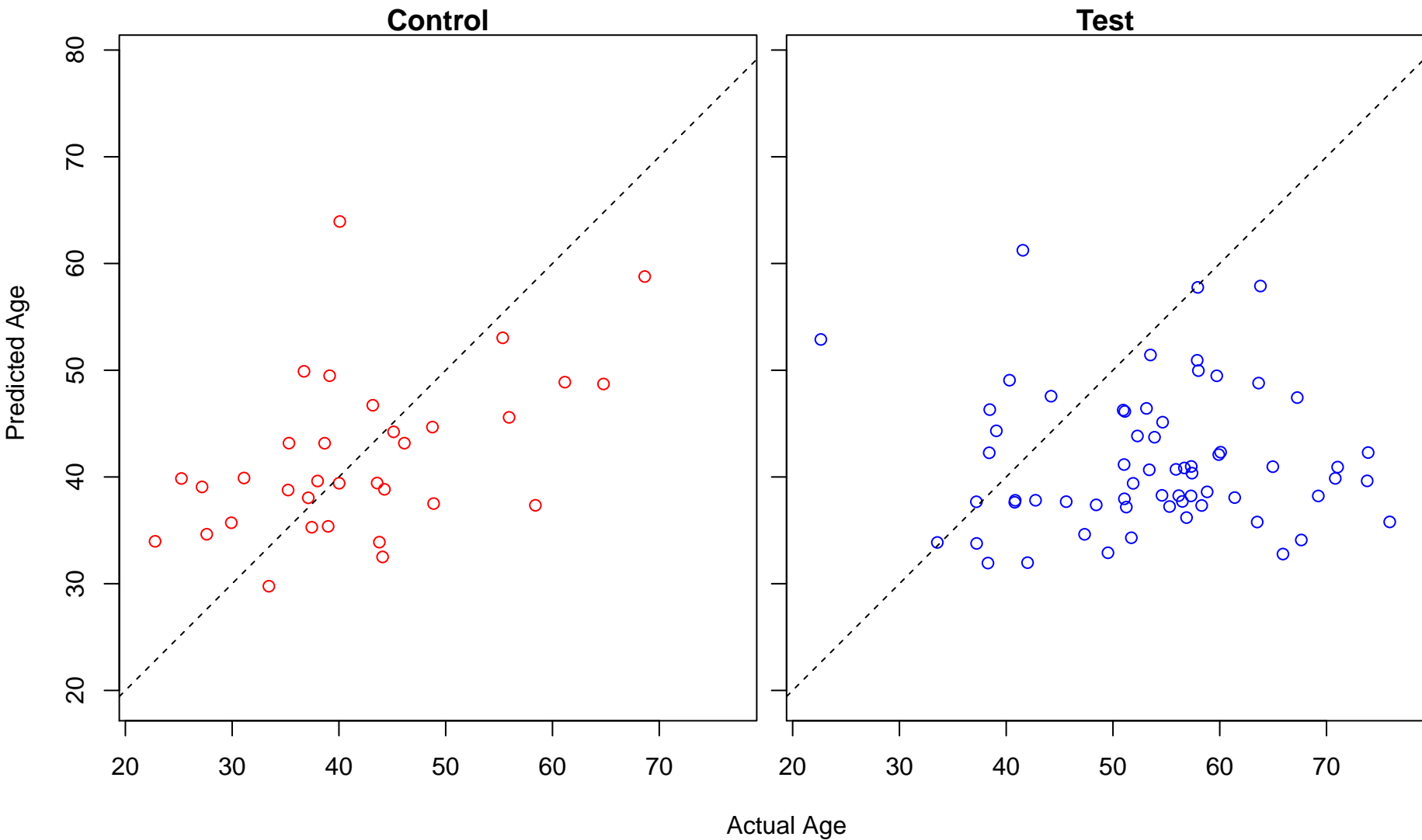
positive regulation of nuclear cell cycle DNA replication (Score: 1.838873)



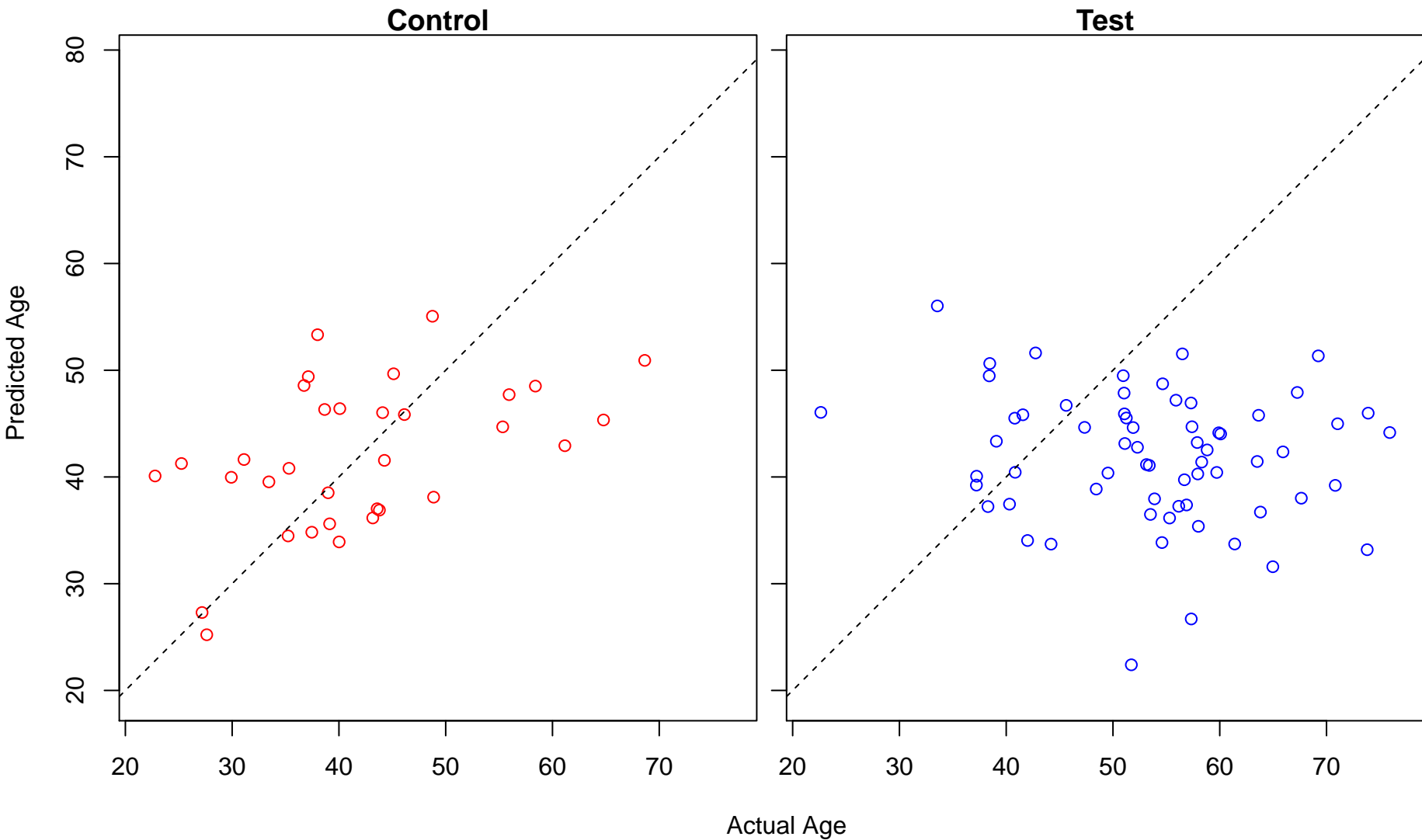
negative regulation of beta-amyloid formation (Score: 1.836703)



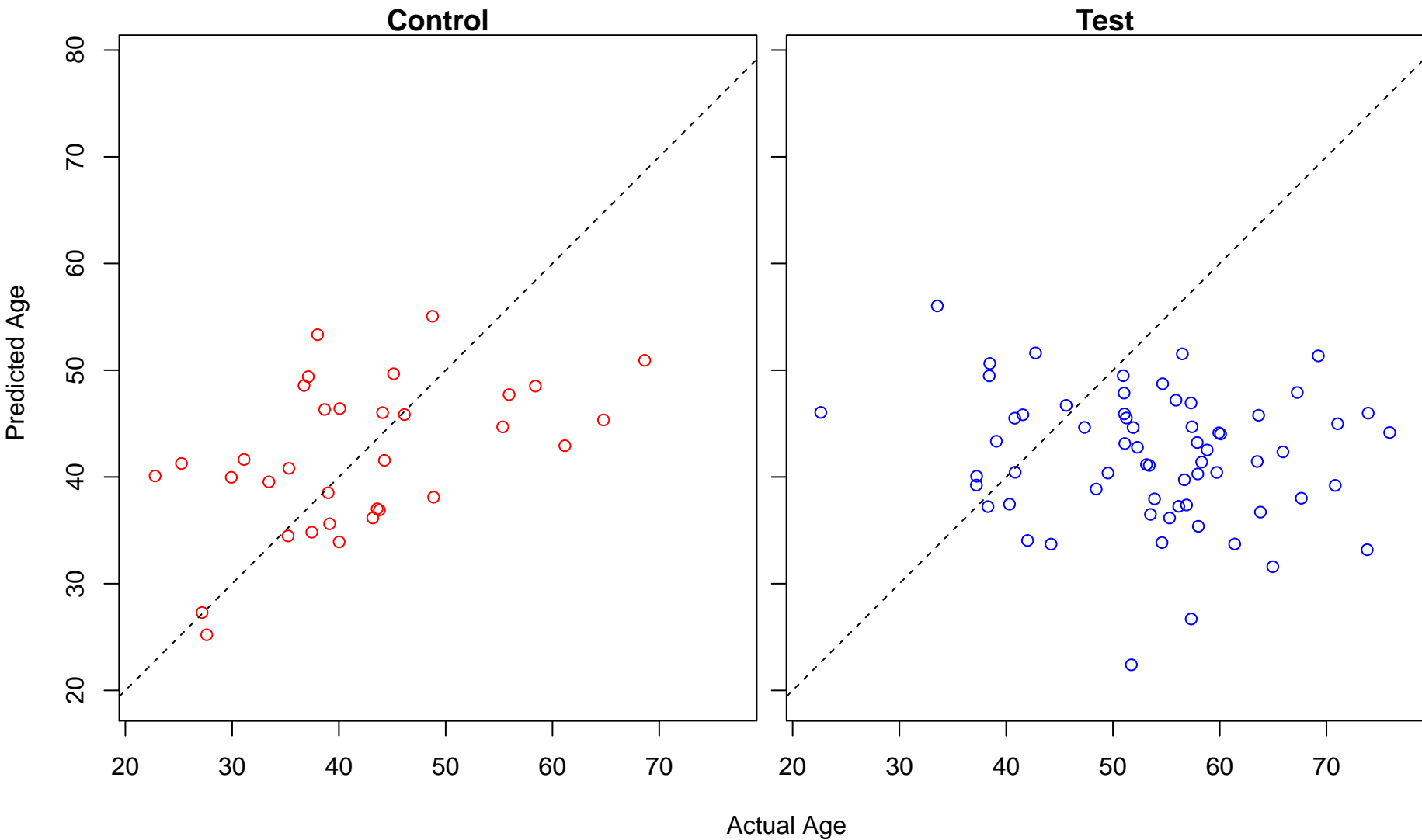
neuronal action potential (Score: 1.833595)



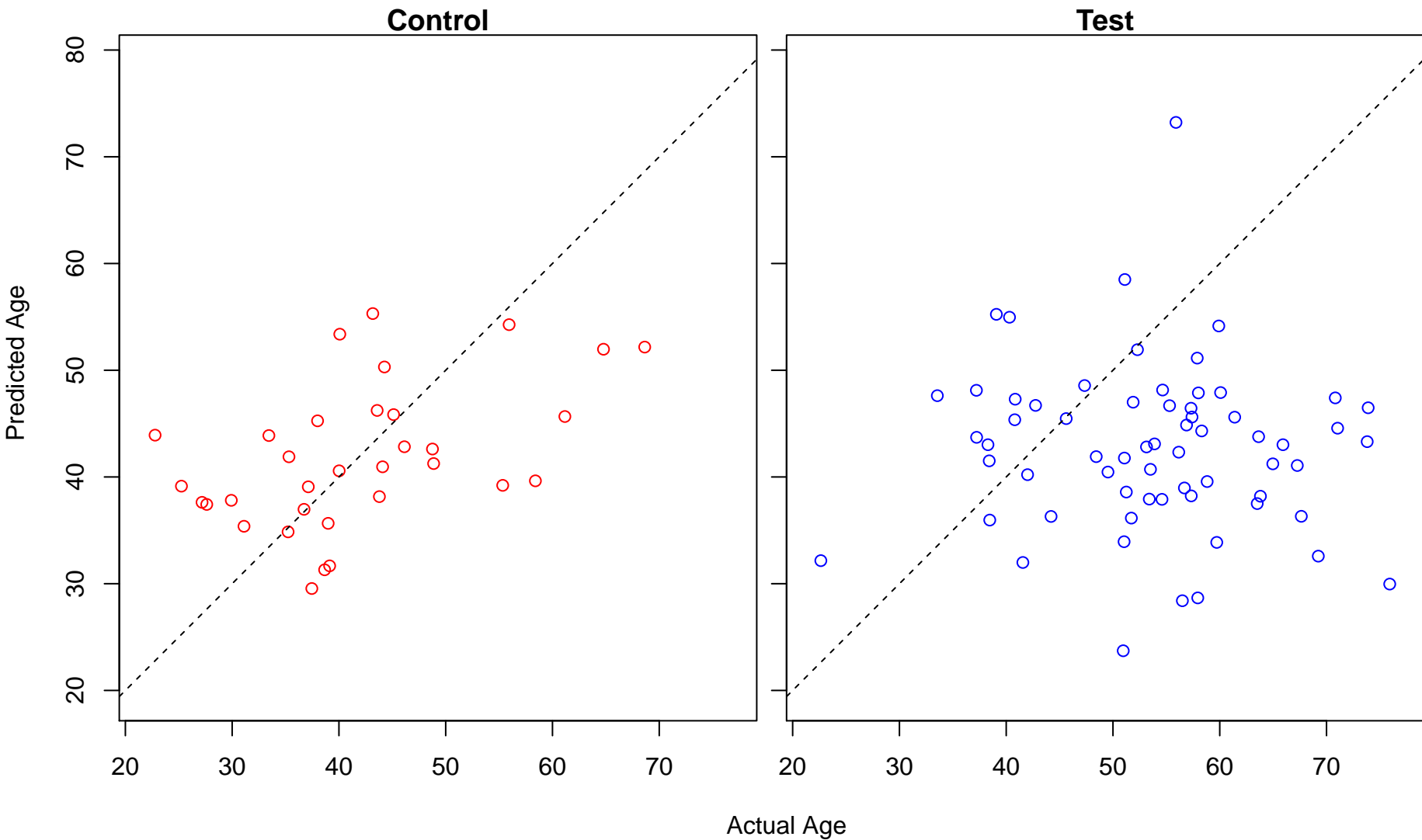
positive regulation of beta-amyloid formation (Score: 1.831933)



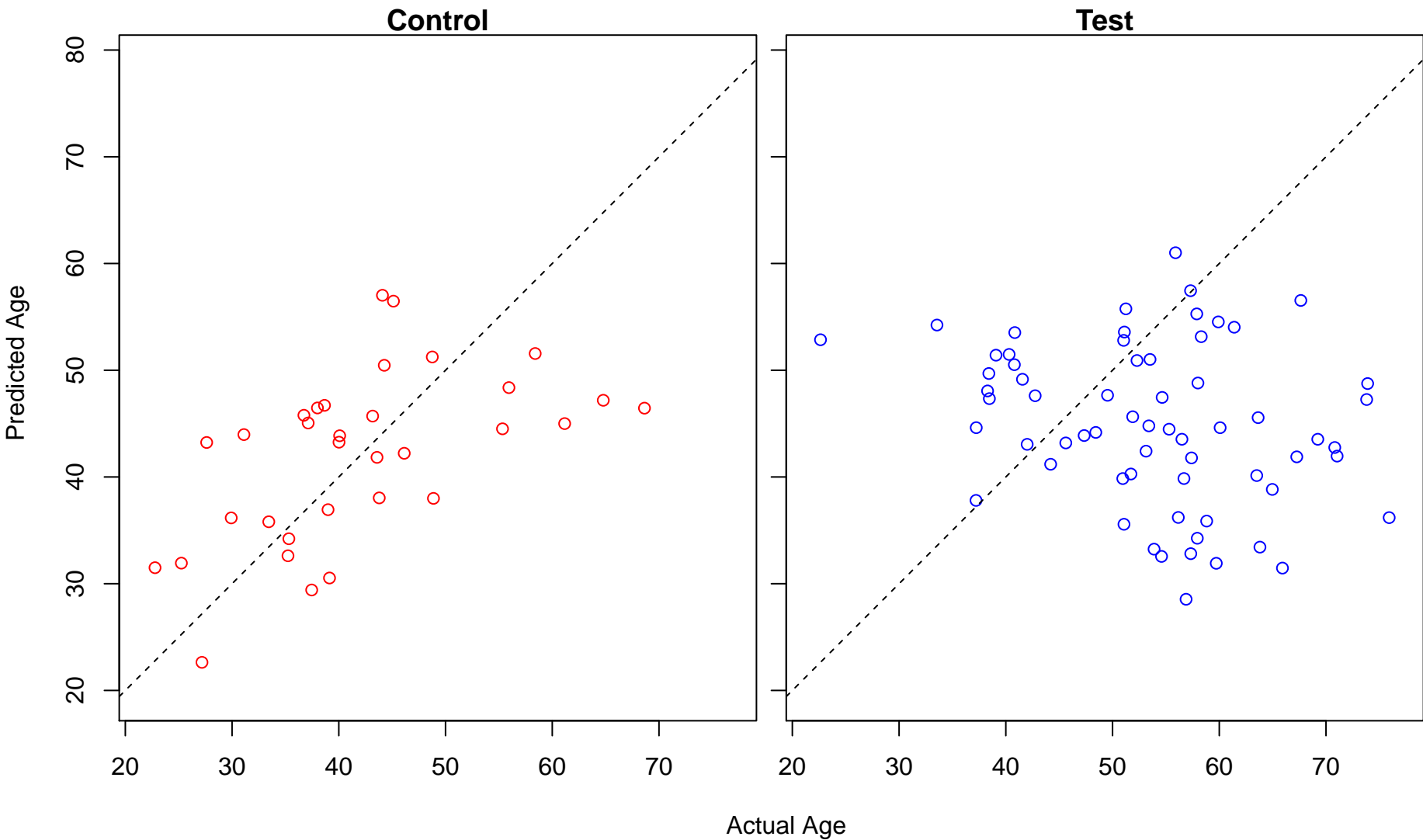
positive regulation of amyloid precursor protein catabolic process (Score: 1.831933)



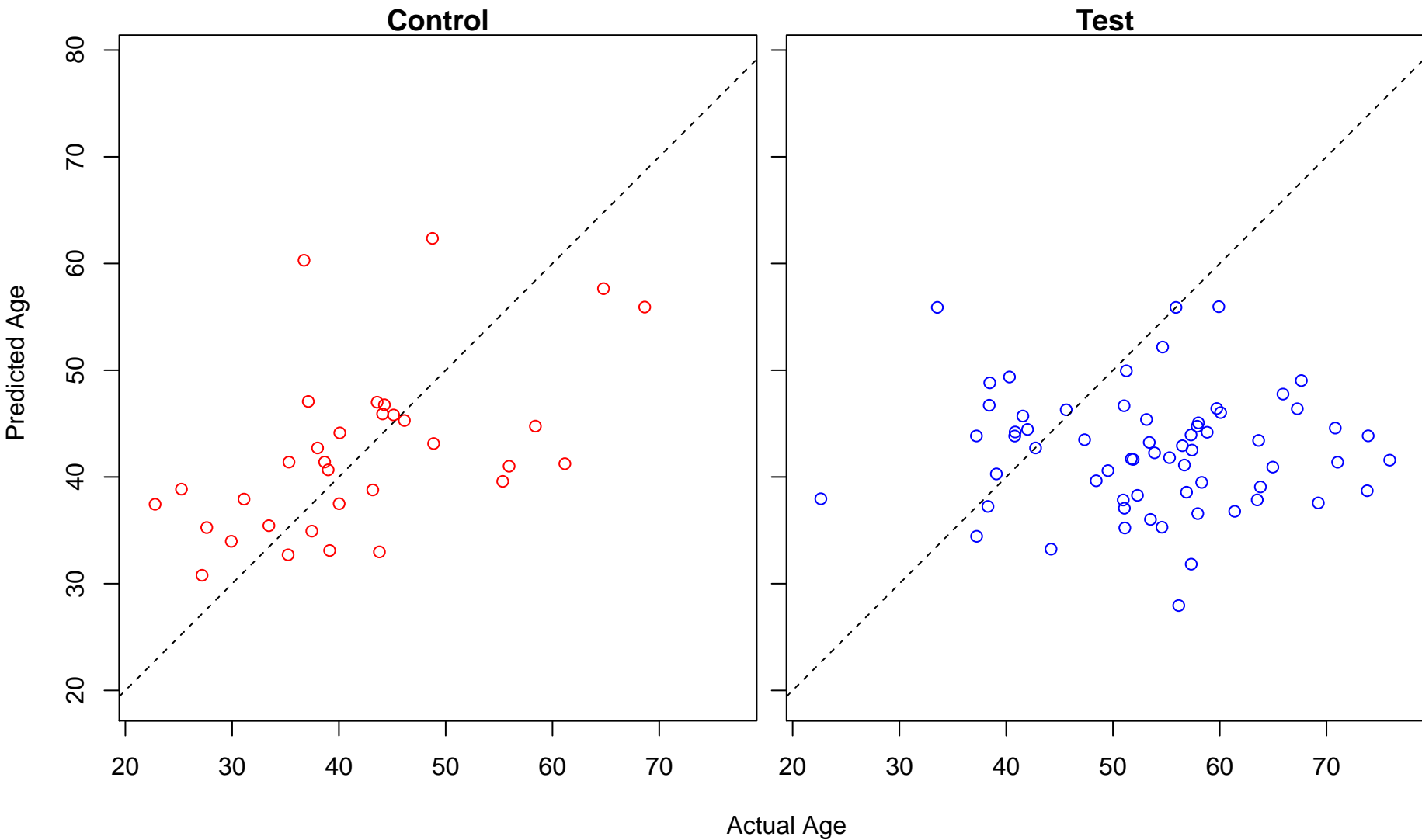
heterochromatin assembly (Score: 1.828030)



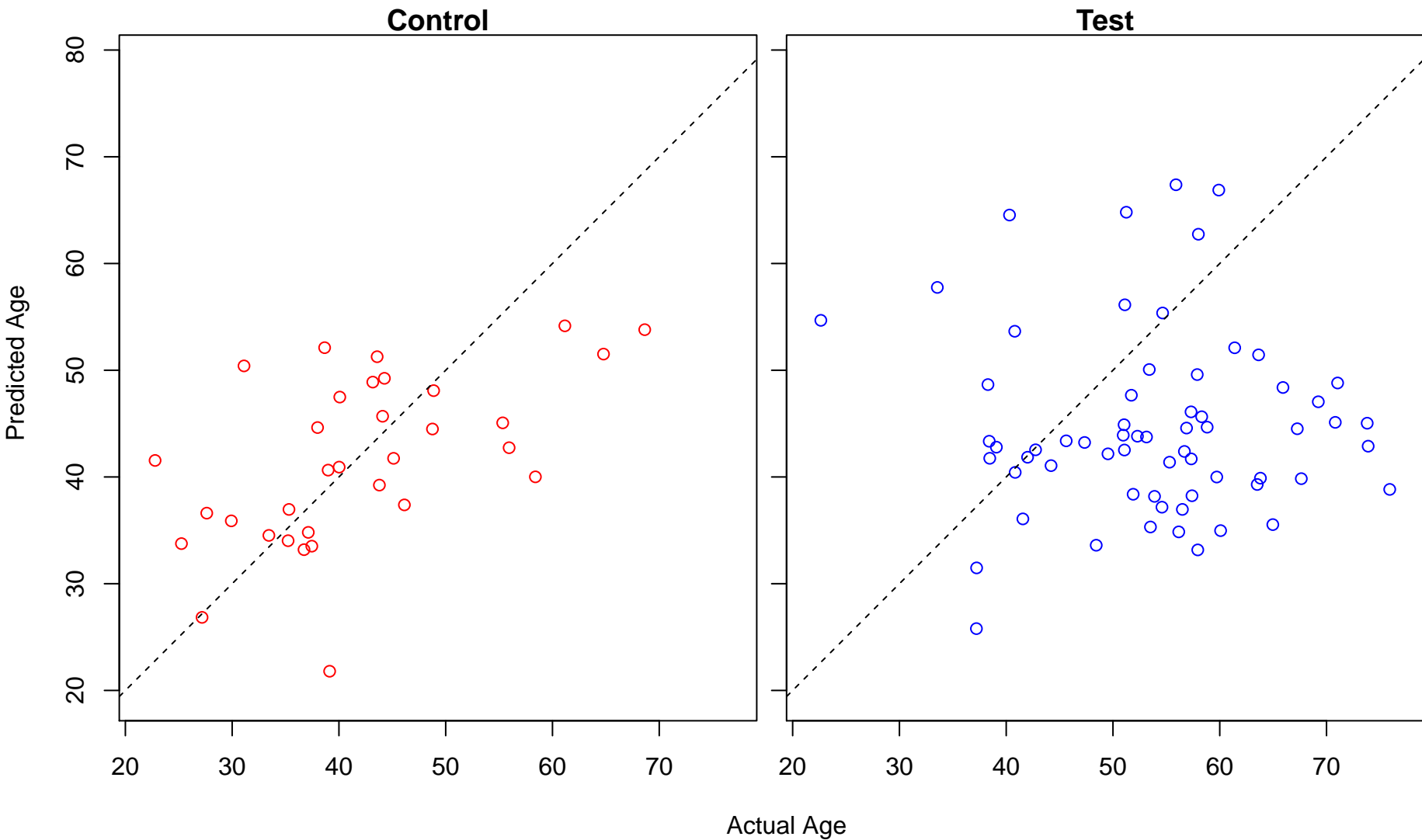
vascular smooth muscle contraction (Score: 1.825465)



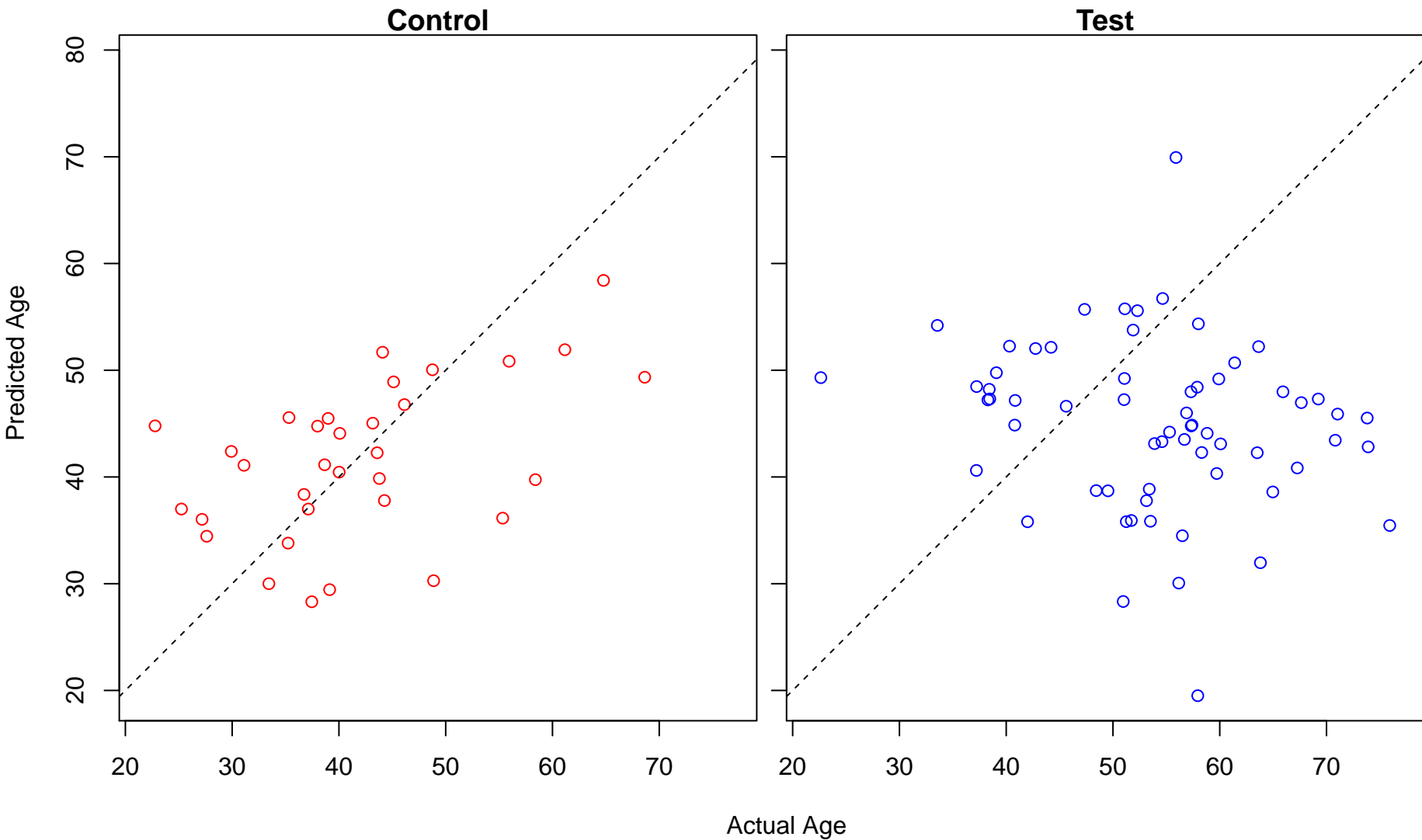
cellular response to nitric oxide (Score: 1.818678)



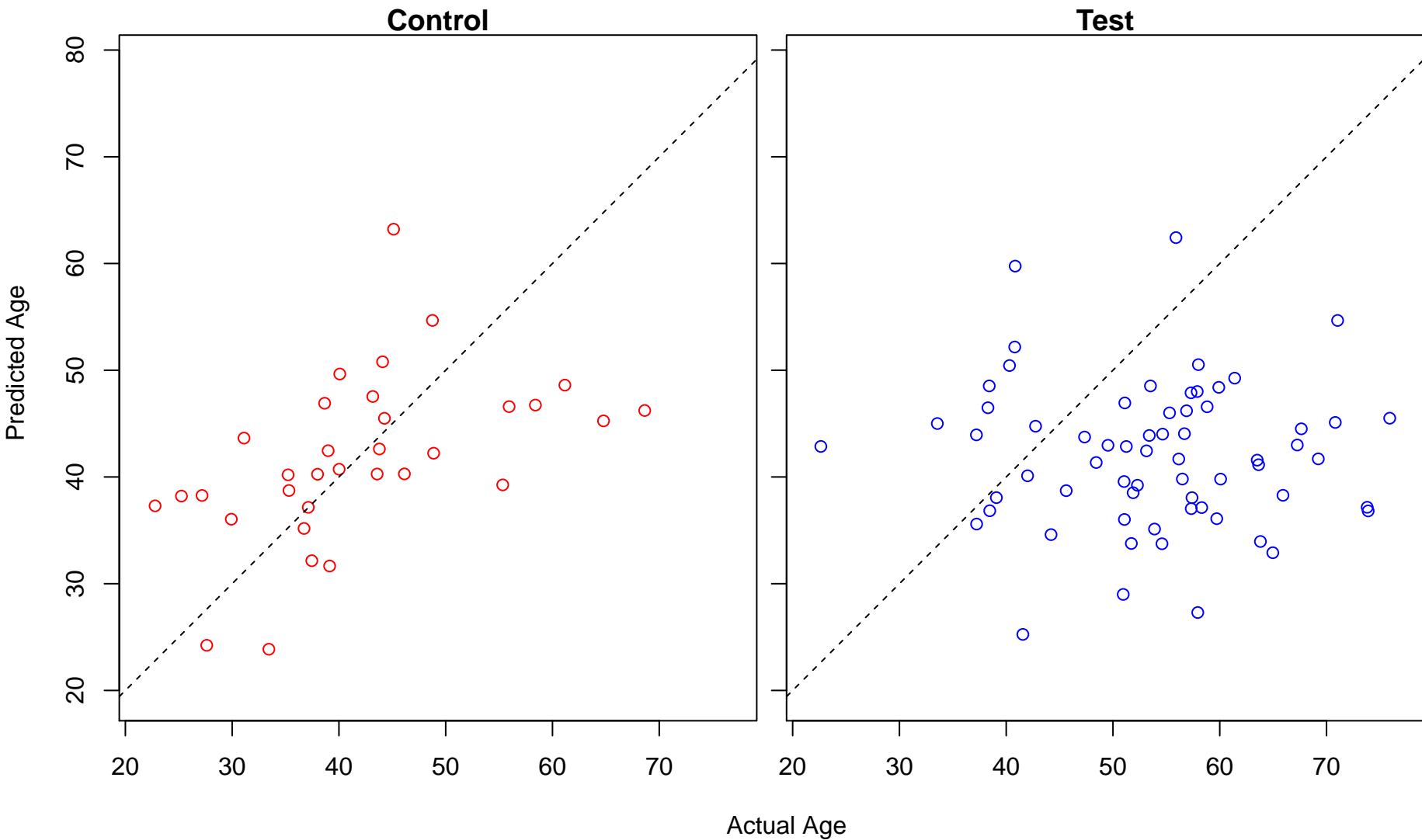
negative regulation of histone H3-K9 methylation (Score: 1.809628)



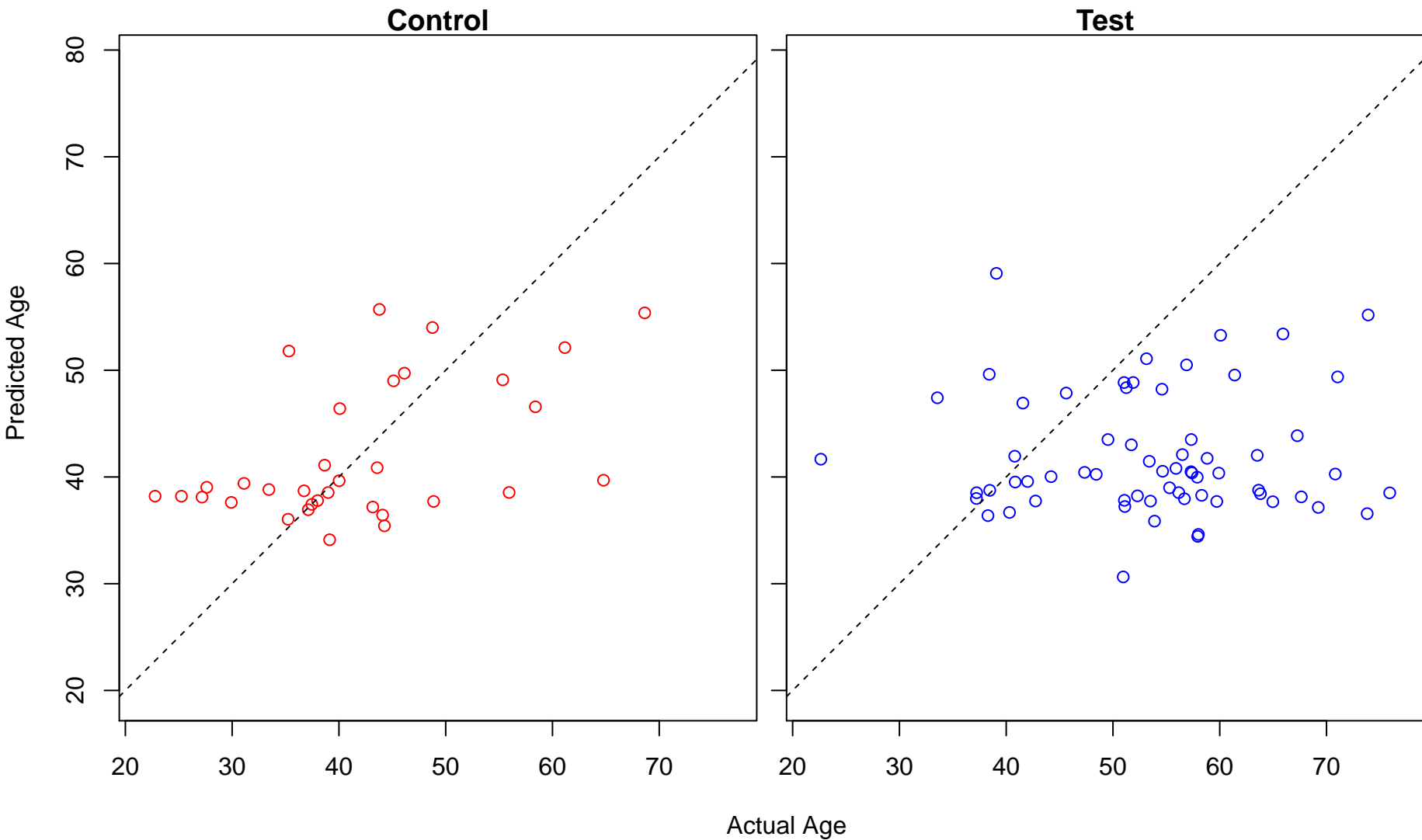
mitochondrial outer membrane permeabilization (Score: 1.808995)



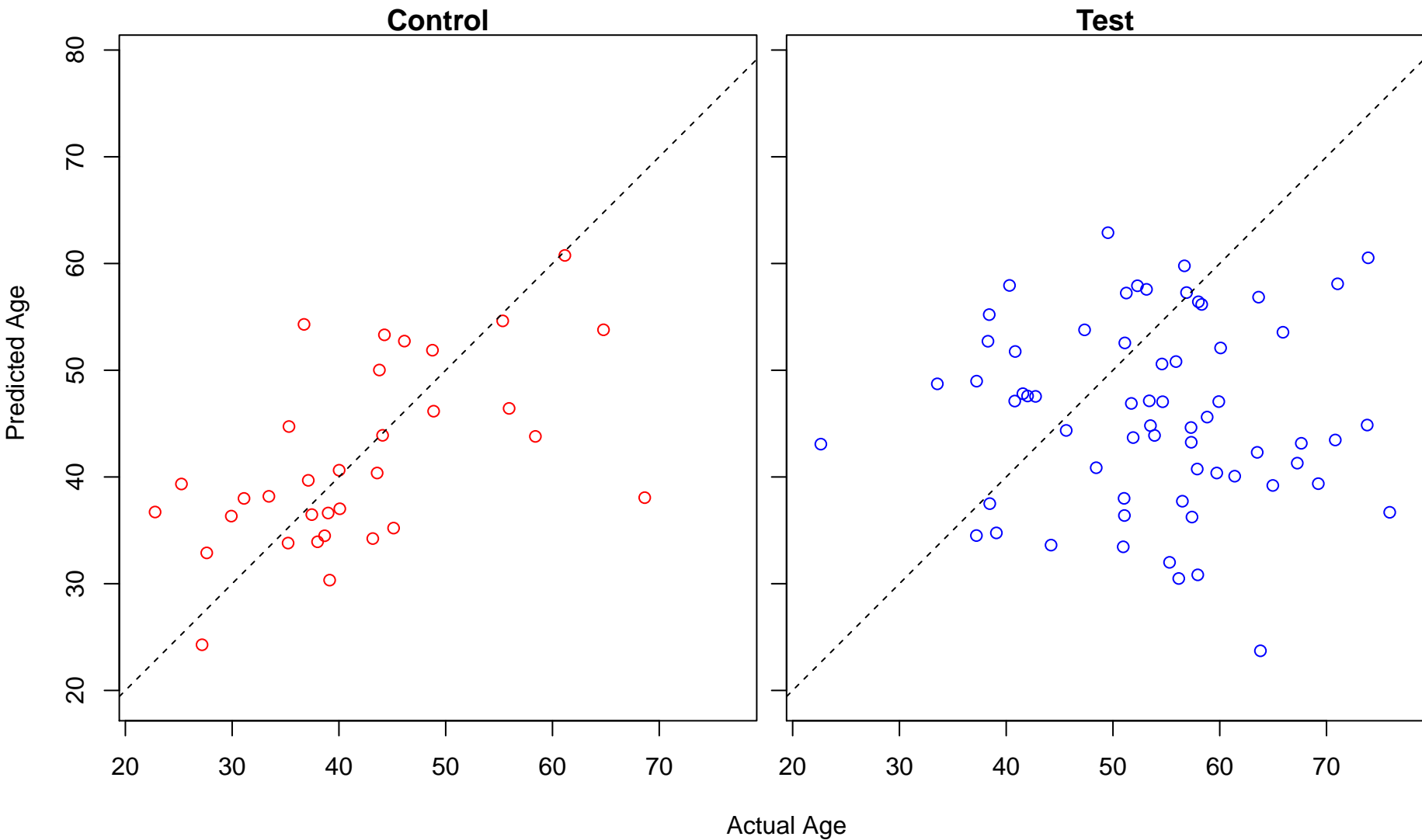
protein K29-linked ubiquitination (Score: 1.800503)



regulation of cytoplasmic mRNA processing body assembly (Score: 1.797659)



negative regulation of reactive oxygen species biosynthetic process (Score: 1.787434)



regulation of atrial cardiac muscle cell membrane depolarization (Score: 1.704459)

