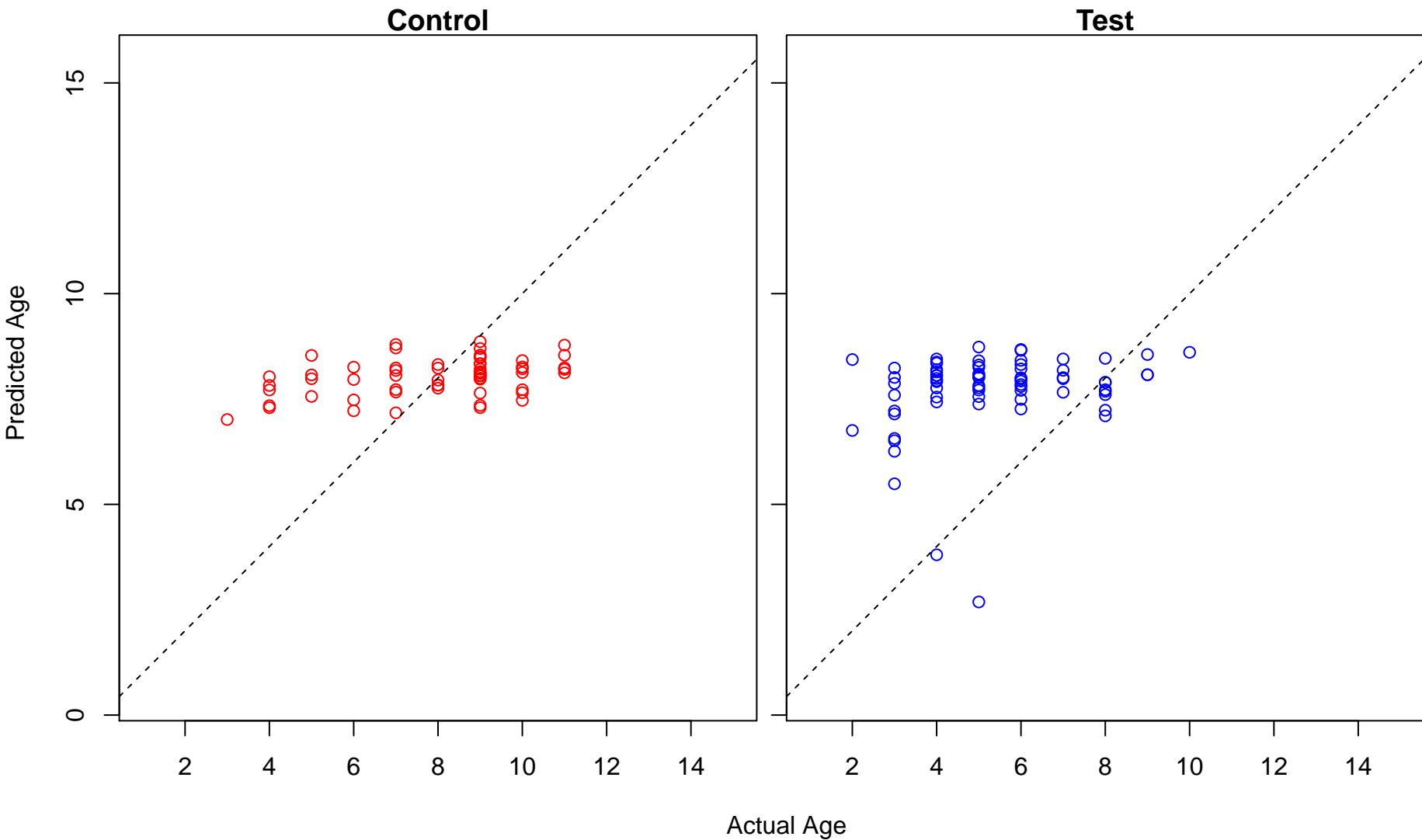
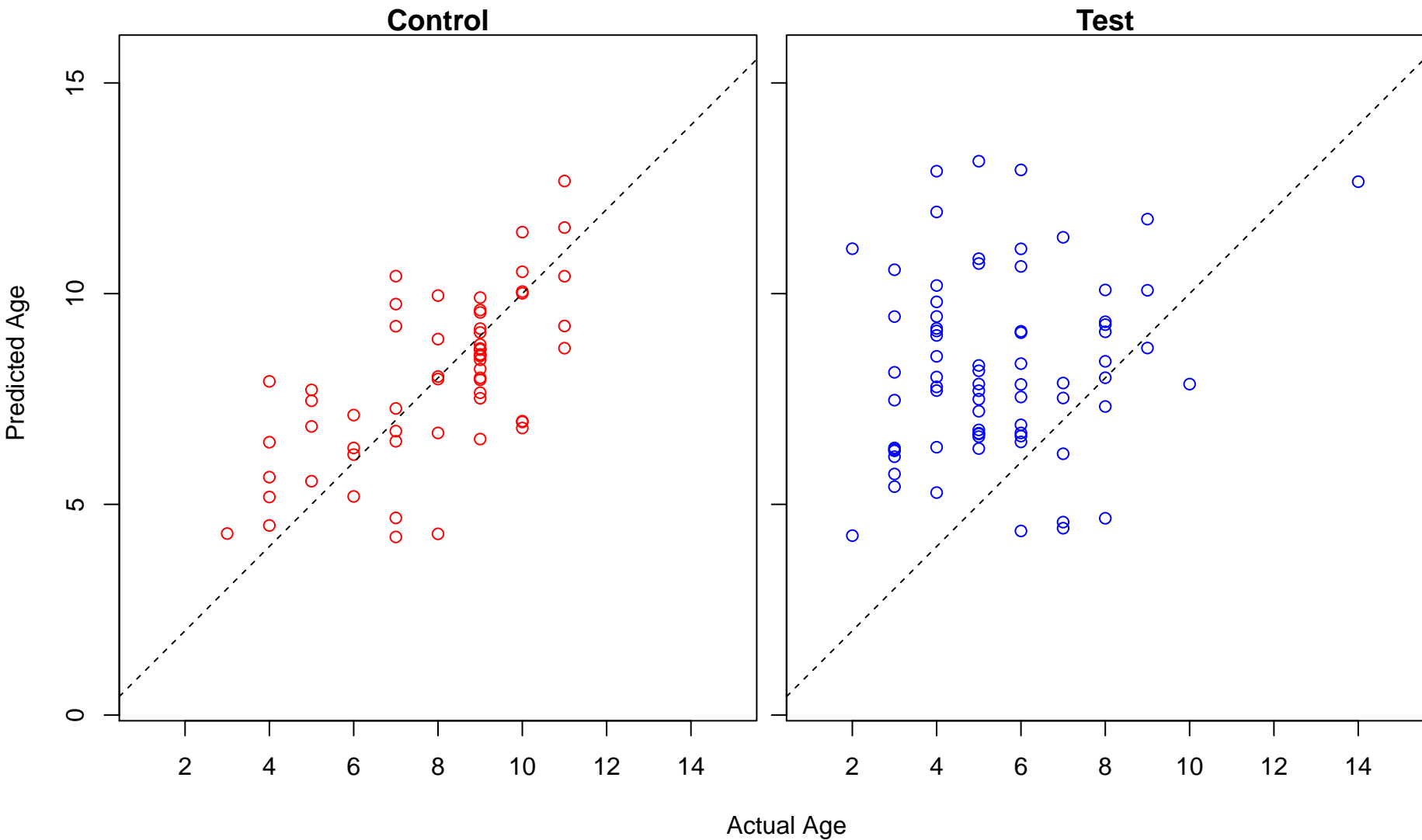


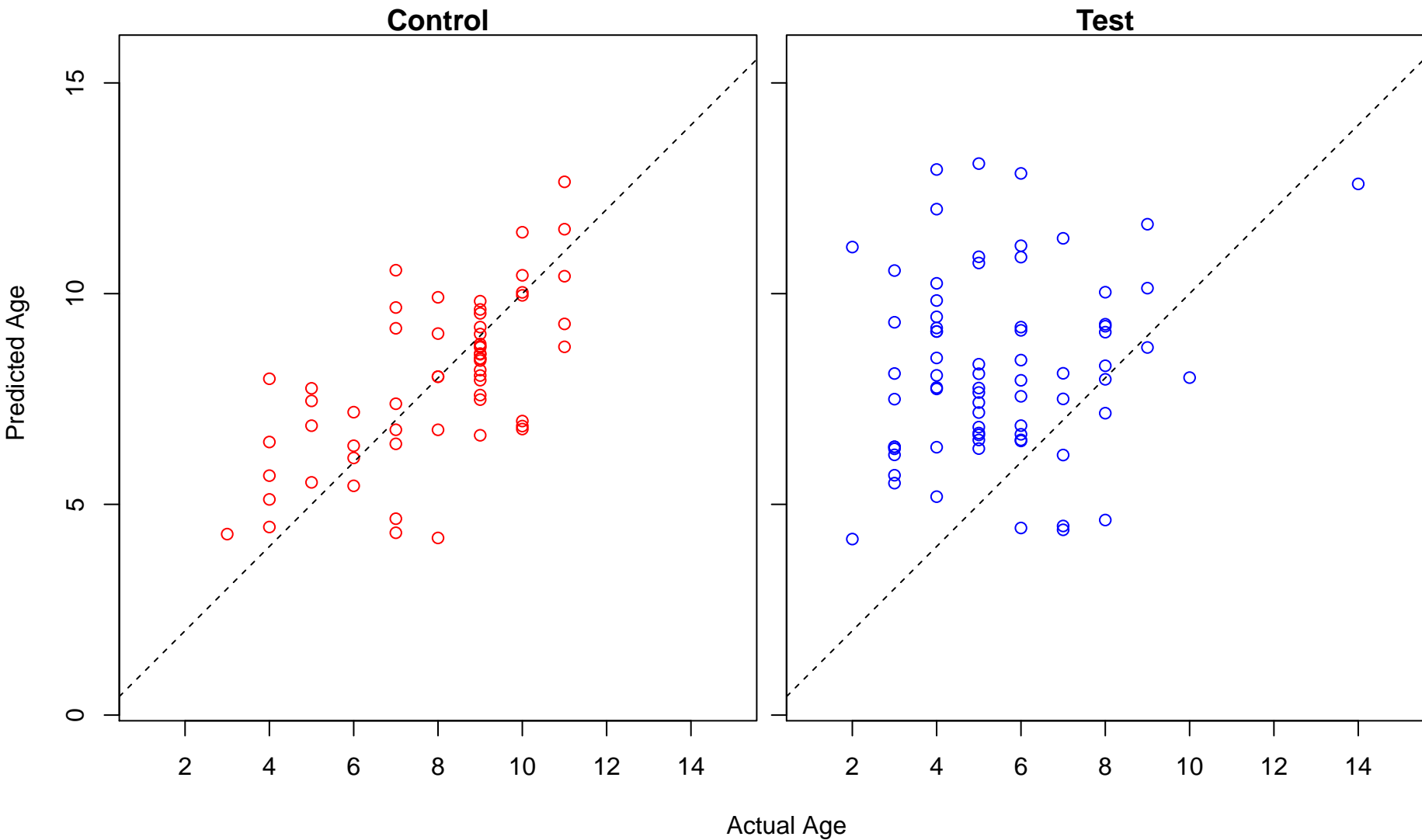
positive regulation of glomerulus development (Score: 3.899156)



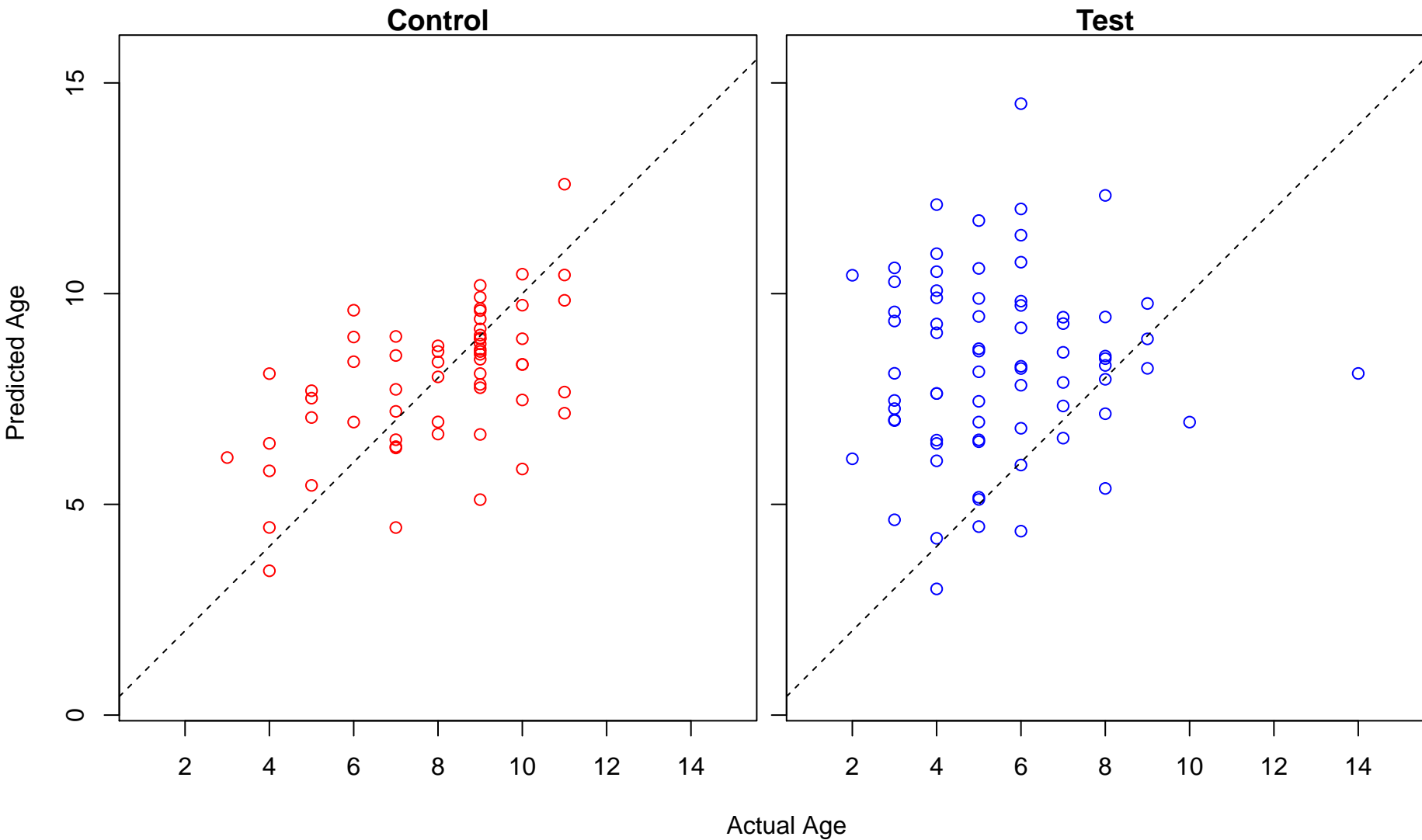
secretion by cell (Score: 2.581066)



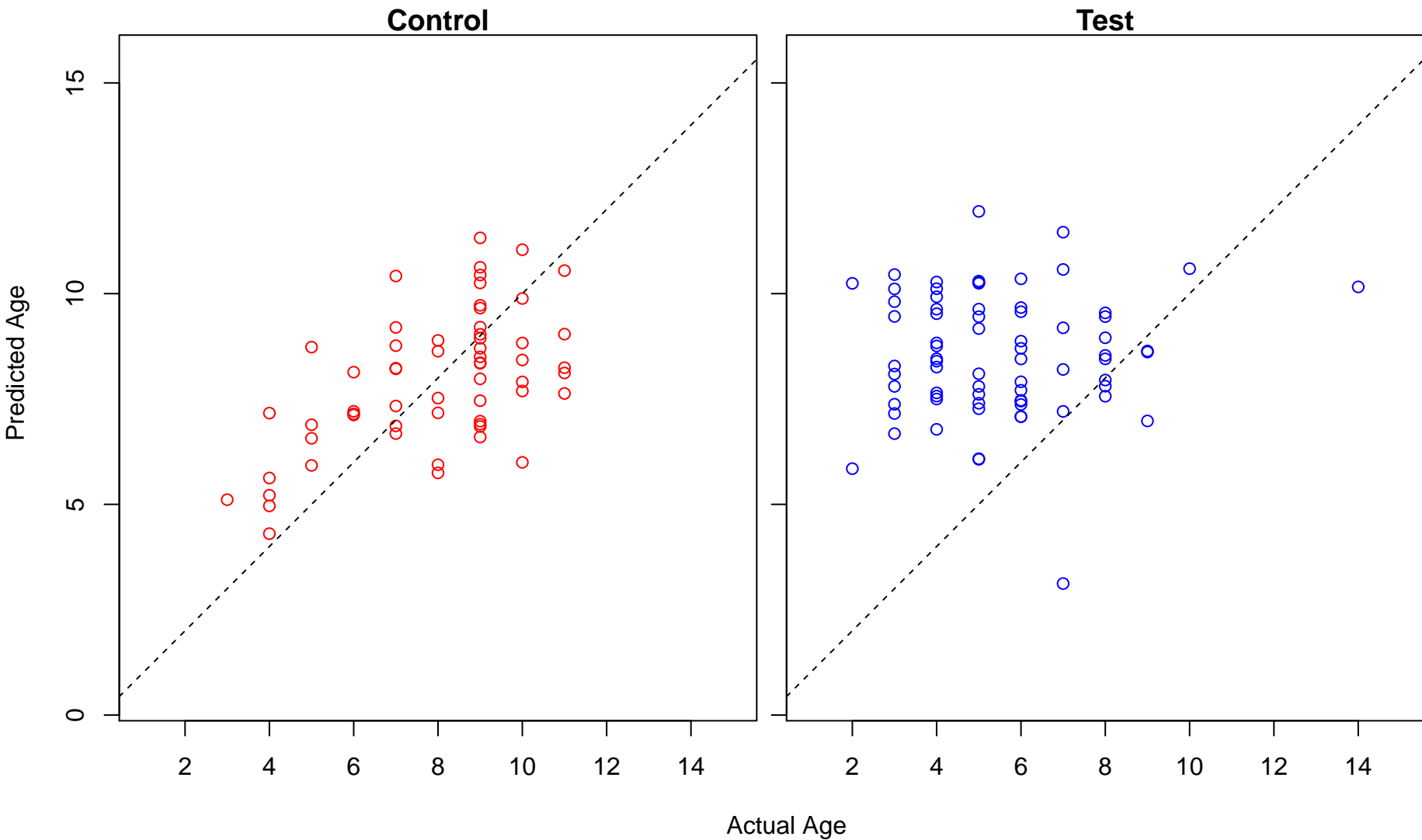
secretion (Score: 2.578287)



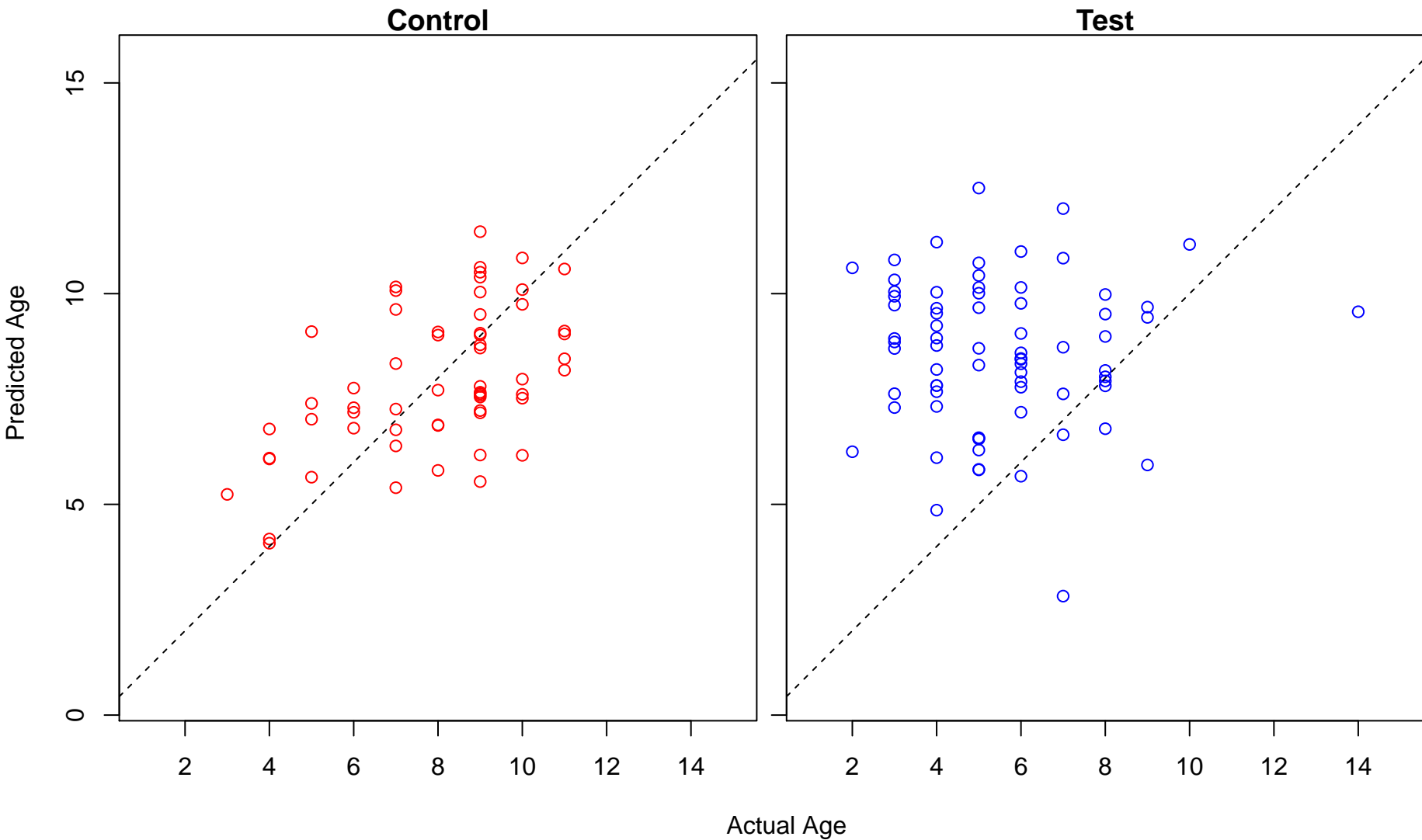
phosphatidylinositol biosynthetic process (Score: 2.455649)



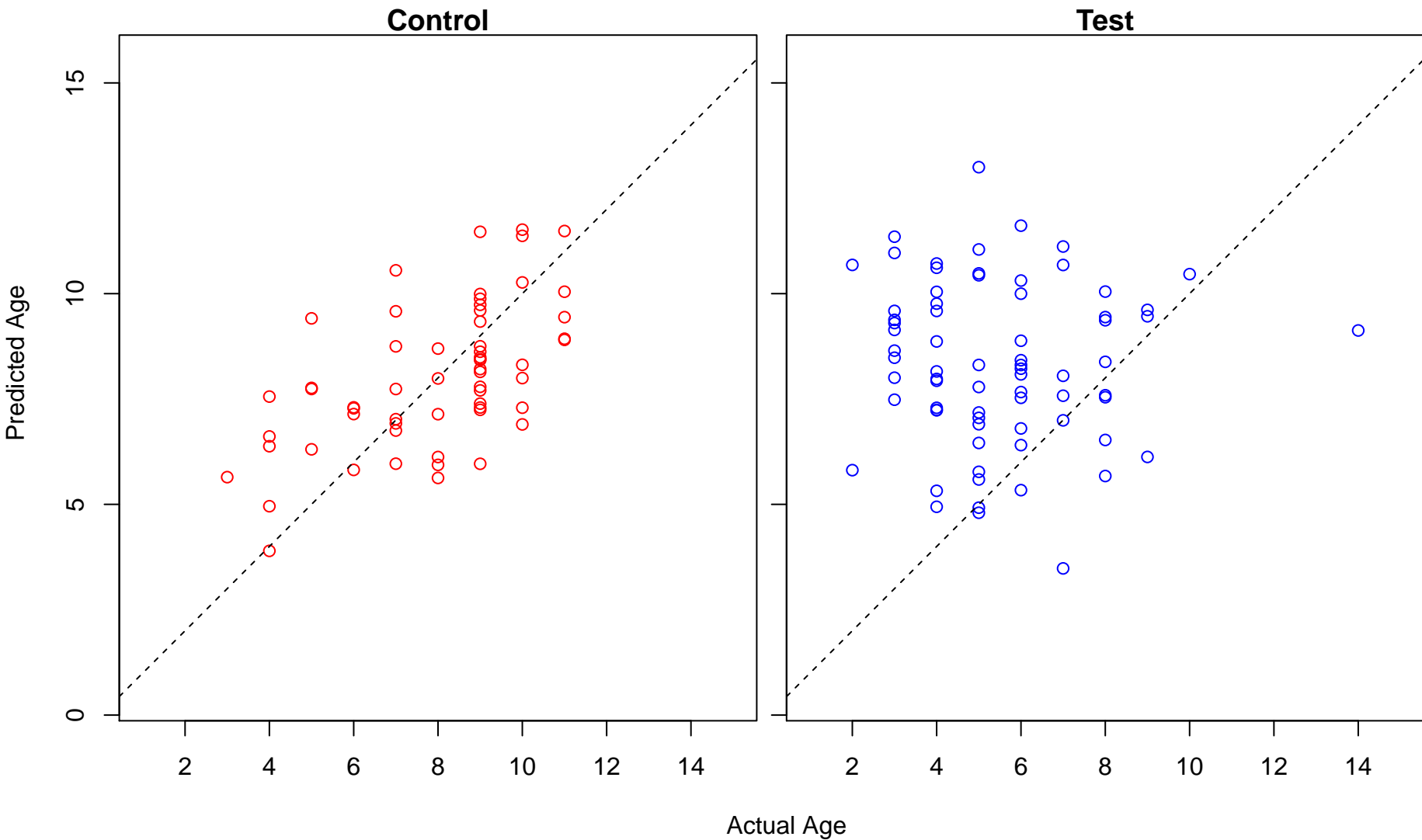
positive regulation of growth (Score: 2.405180)



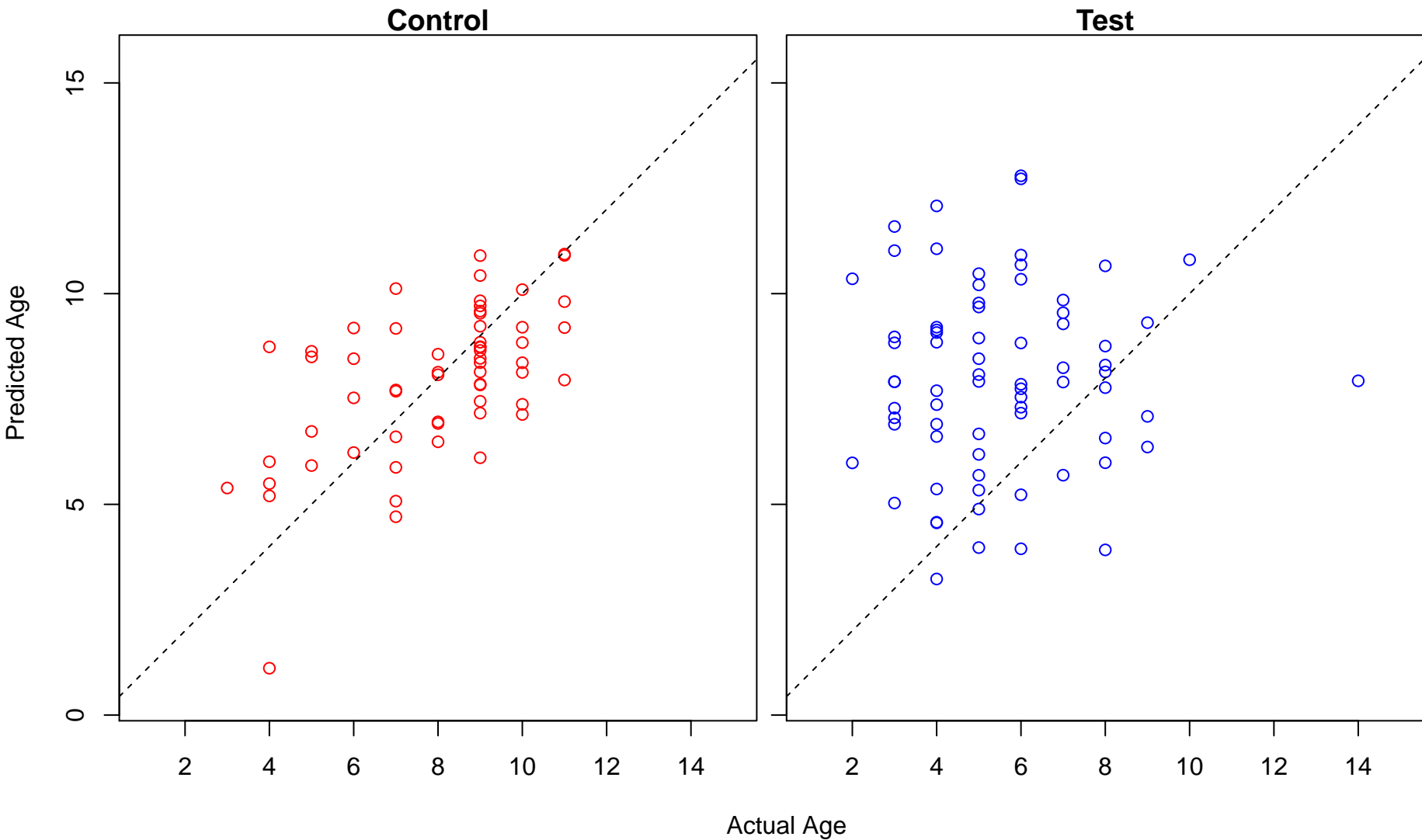
regulation of growth (Score: 2.397654)



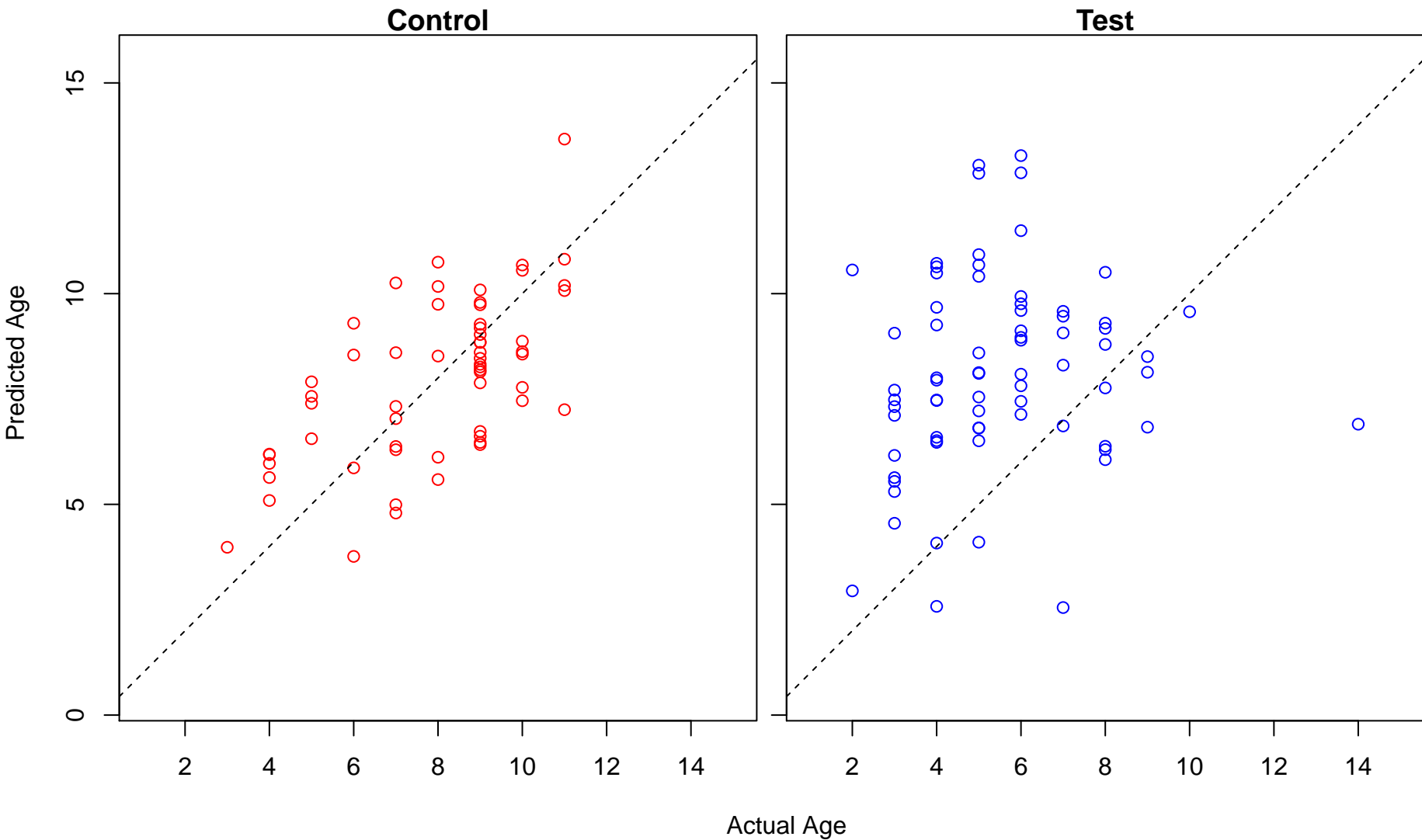
regulation of cell growth (Score: 2.397271)



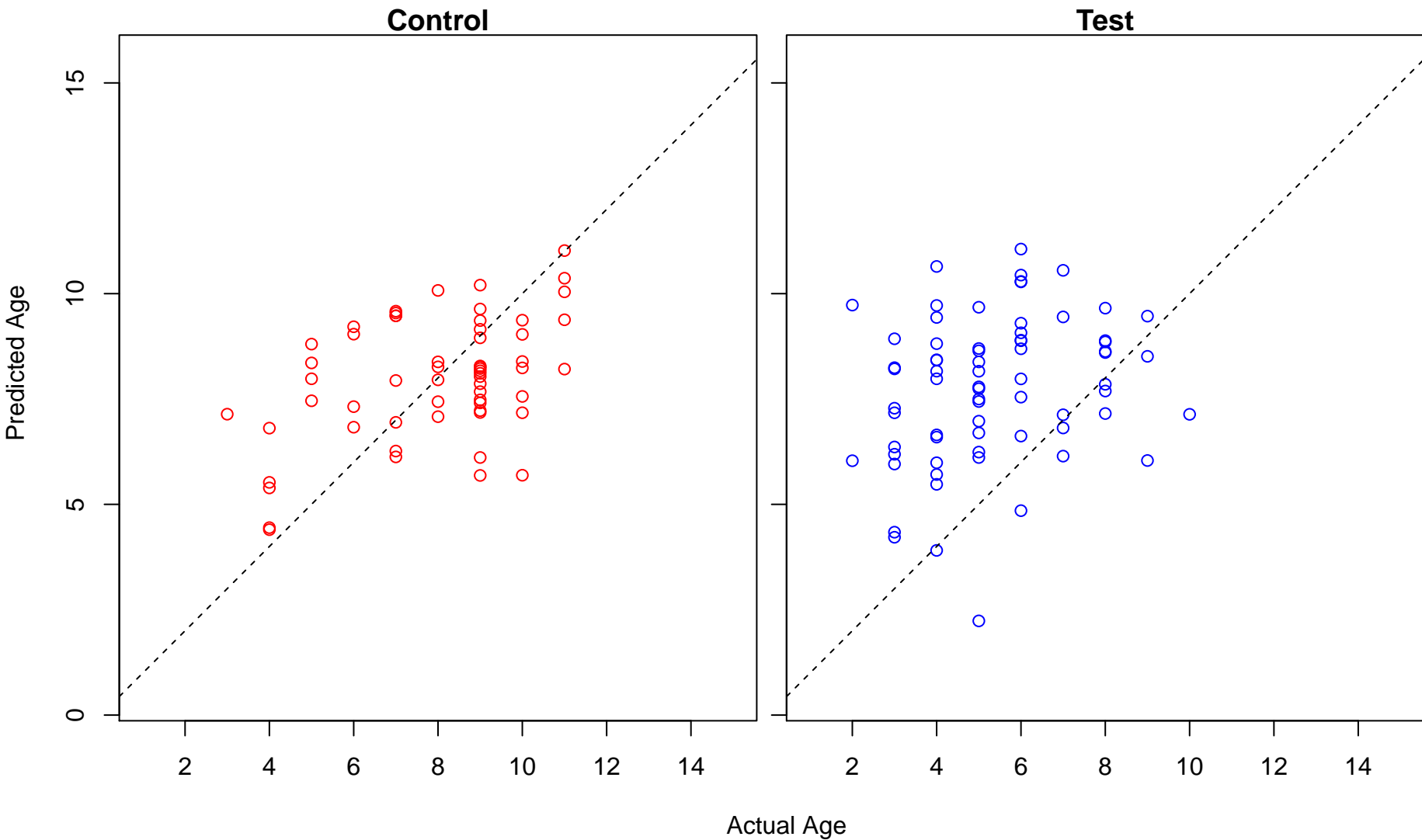
phospholipid metabolic process (Score: 2.343466)



myeloid leukocyte activation (Score: 2.343165)

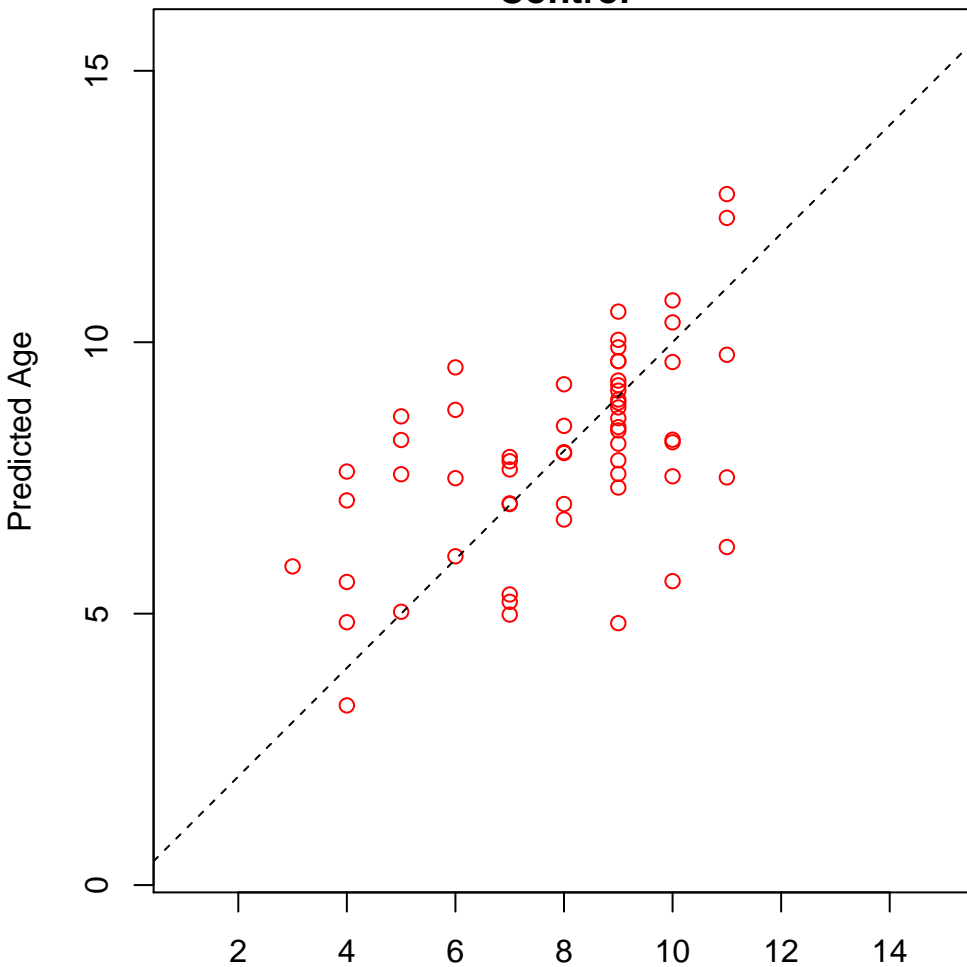


skeletal muscle cell differentiation (Score: 2.318438)

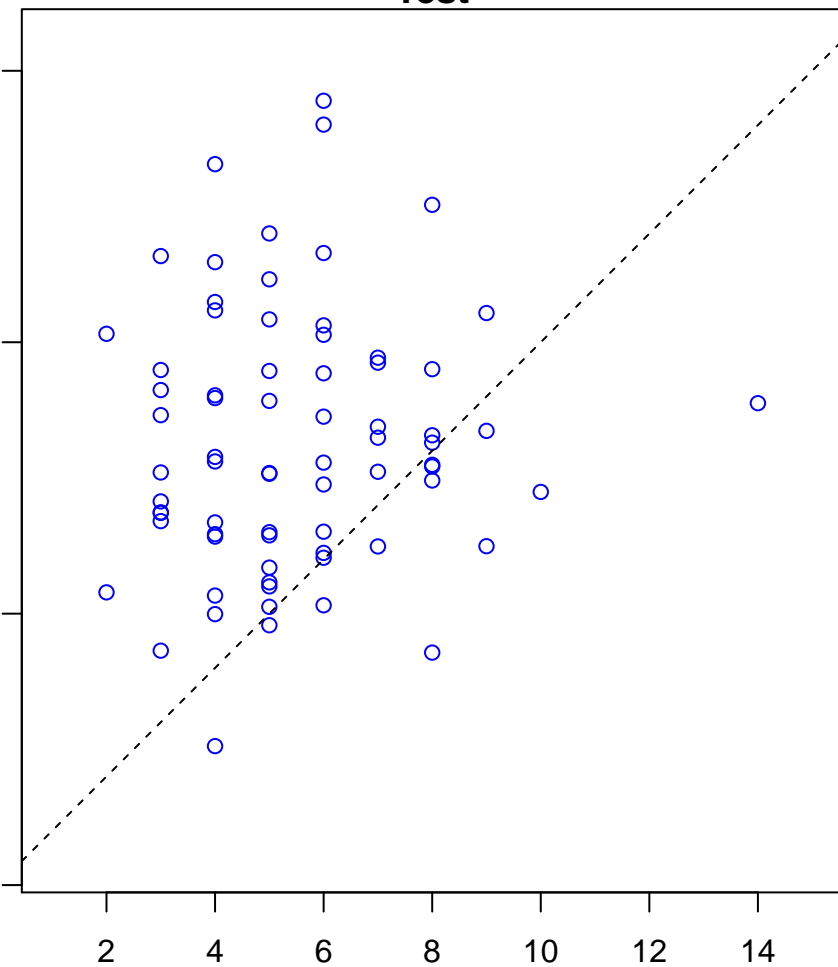


phosphatidylinositol metabolic process (Score: 2.309914)

Control



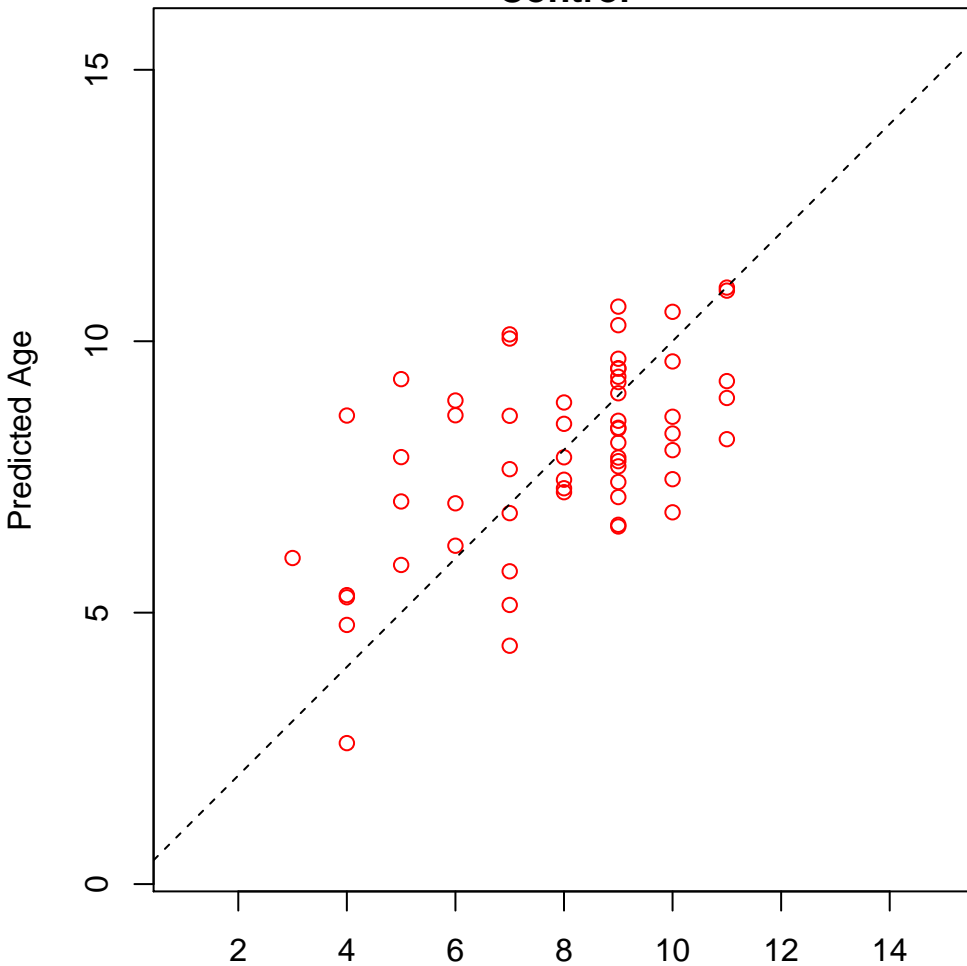
Test



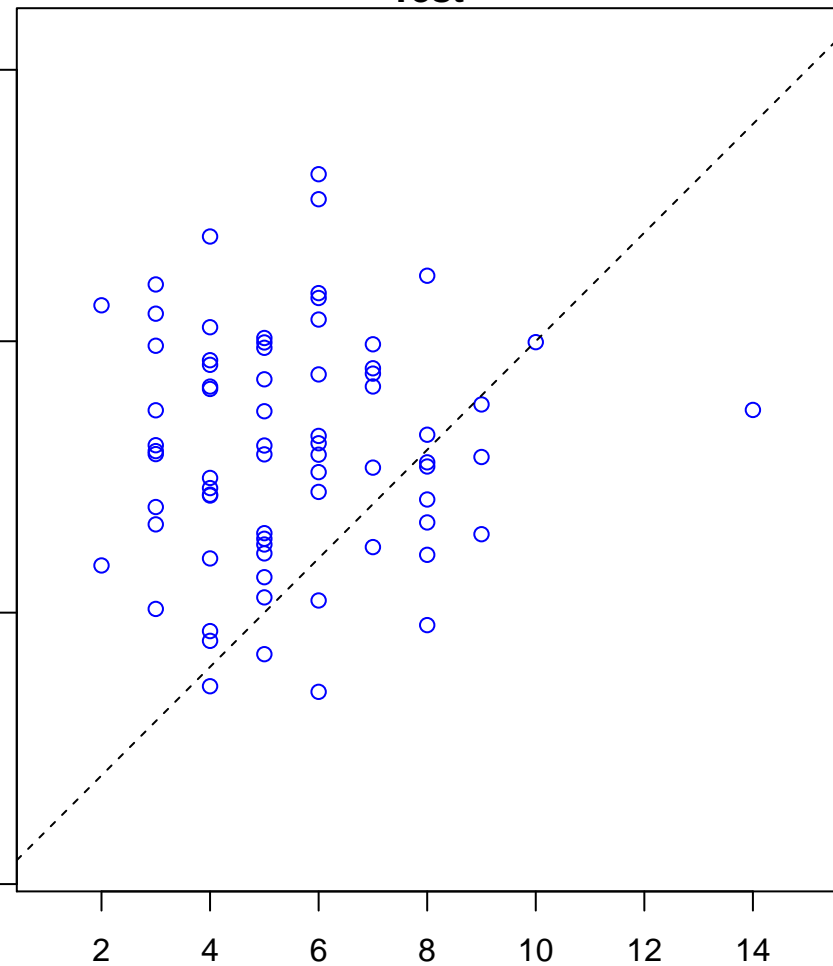
Actual Age

glycerophospholipid metabolic process (Score: 2.284586)

Control

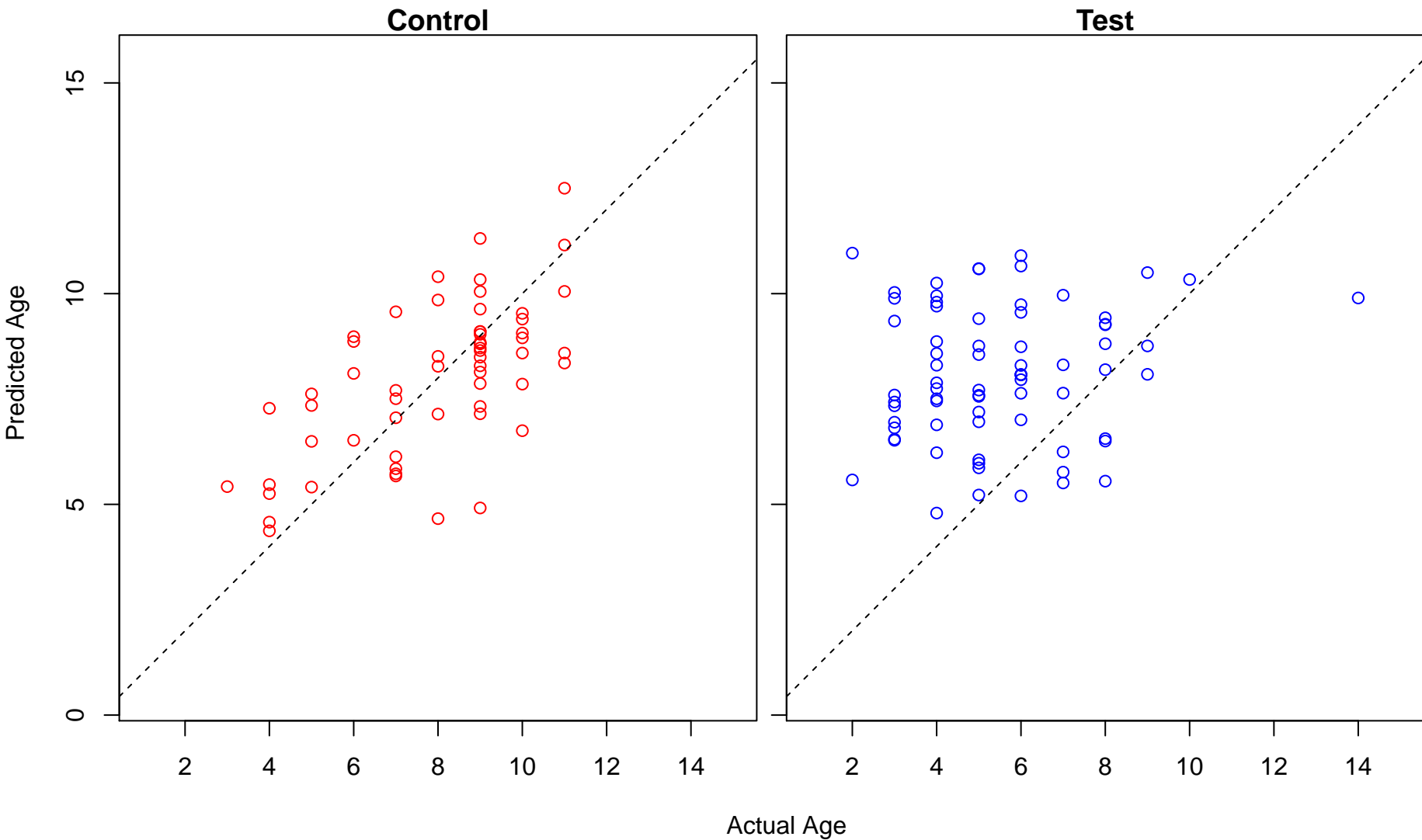


Test

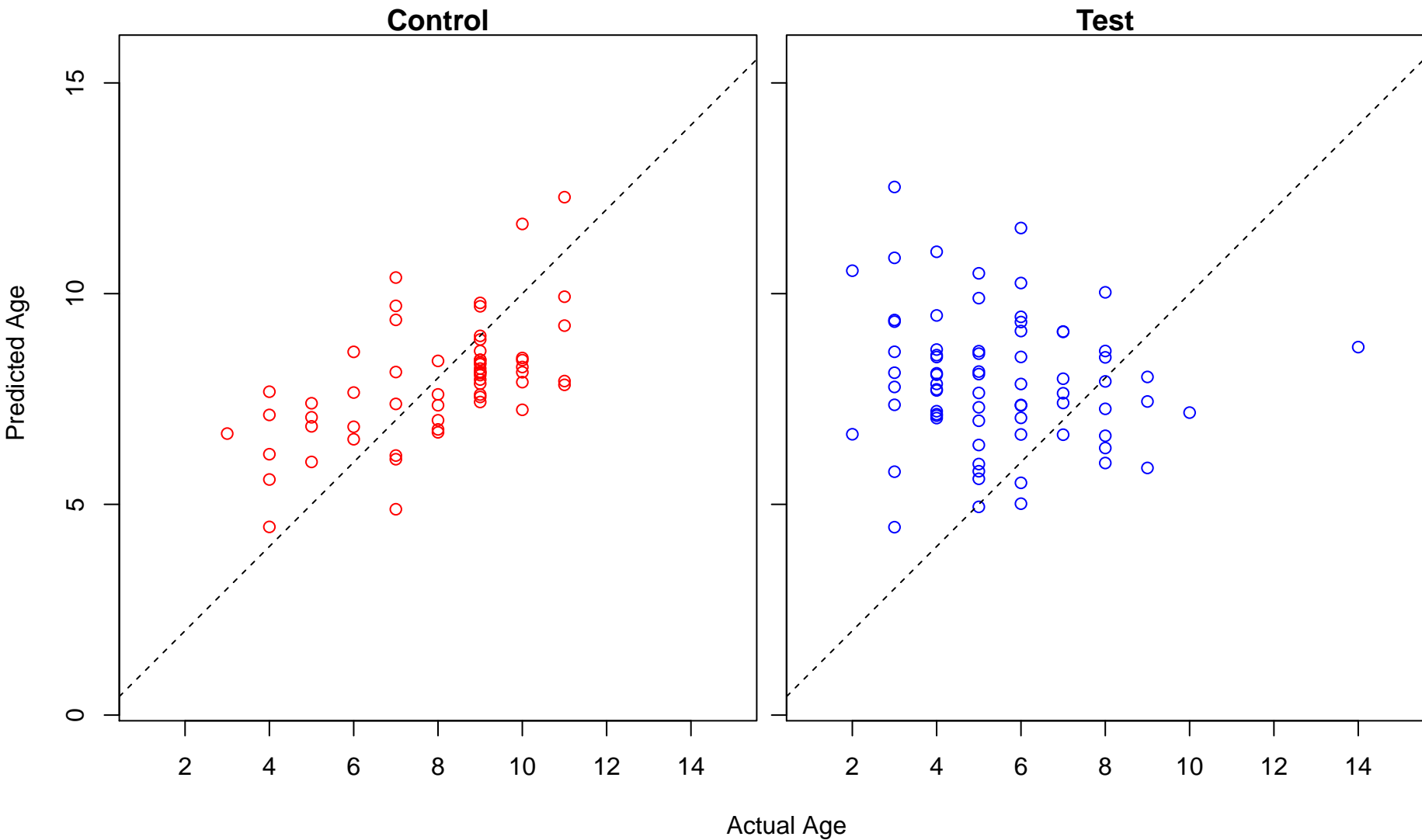


Actual Age

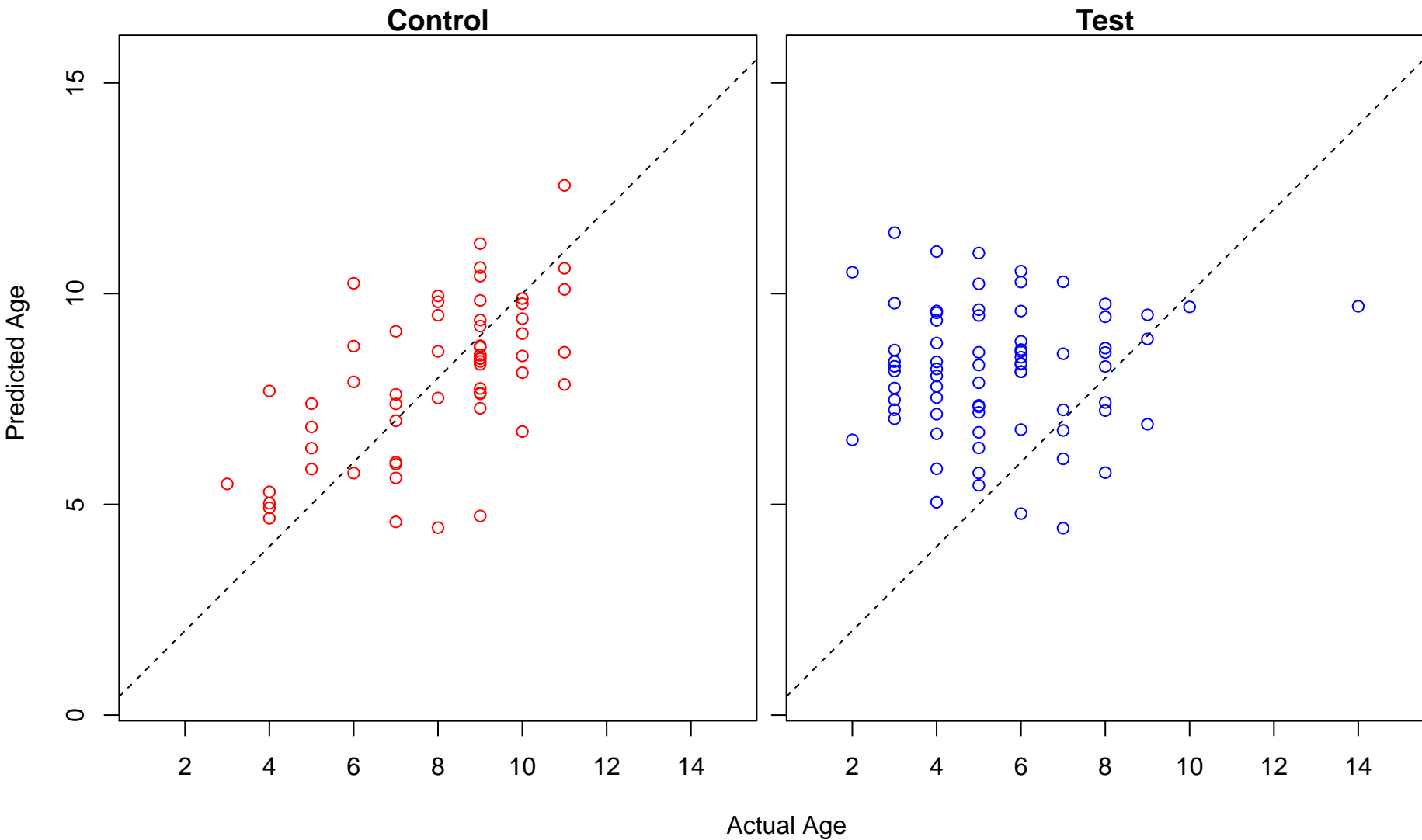
positive regulation of sequence-specific DNA binding transcription factor activity (Score: 2.283174)



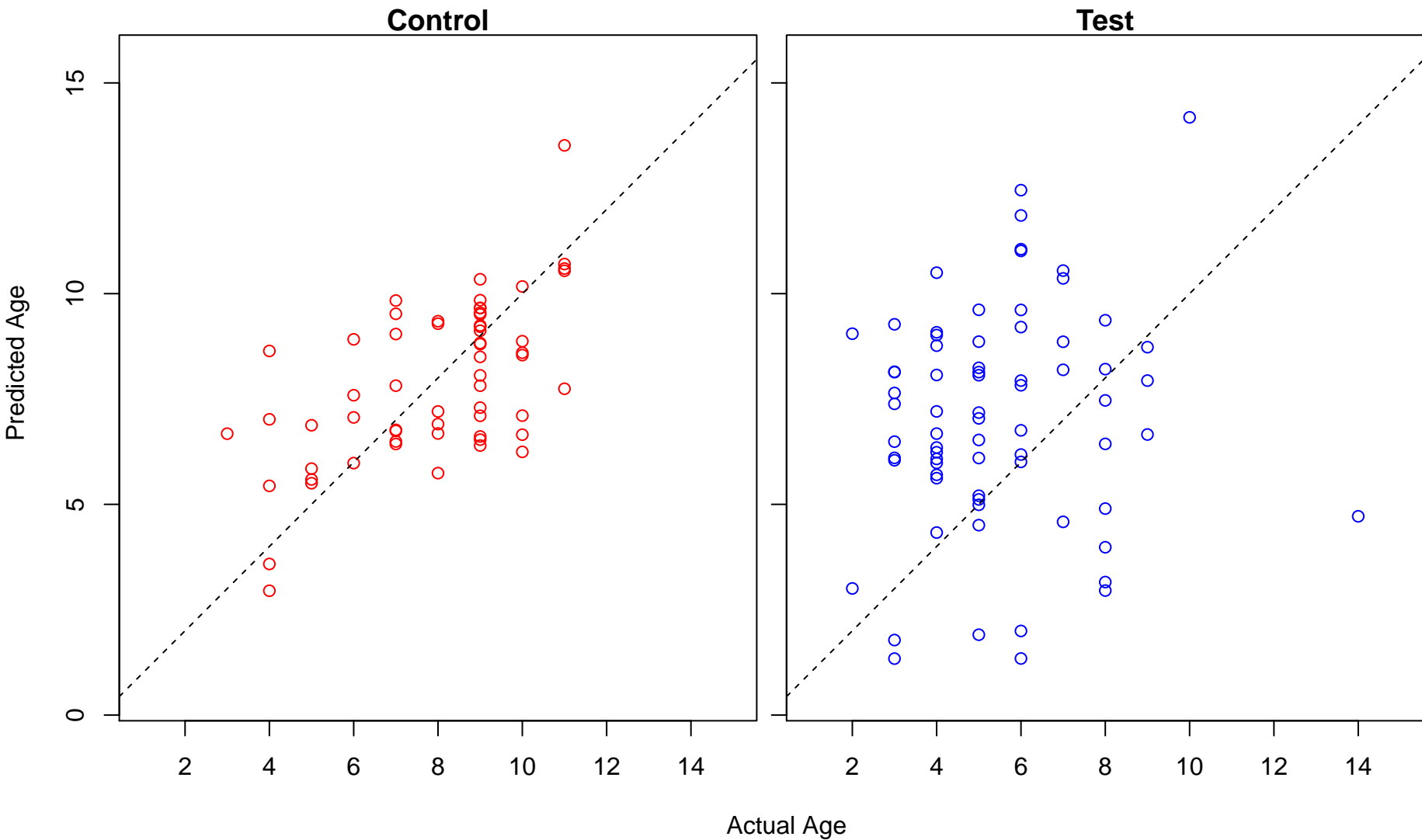
regulation of integrin-mediated signaling pathway (Score: 2.274229)



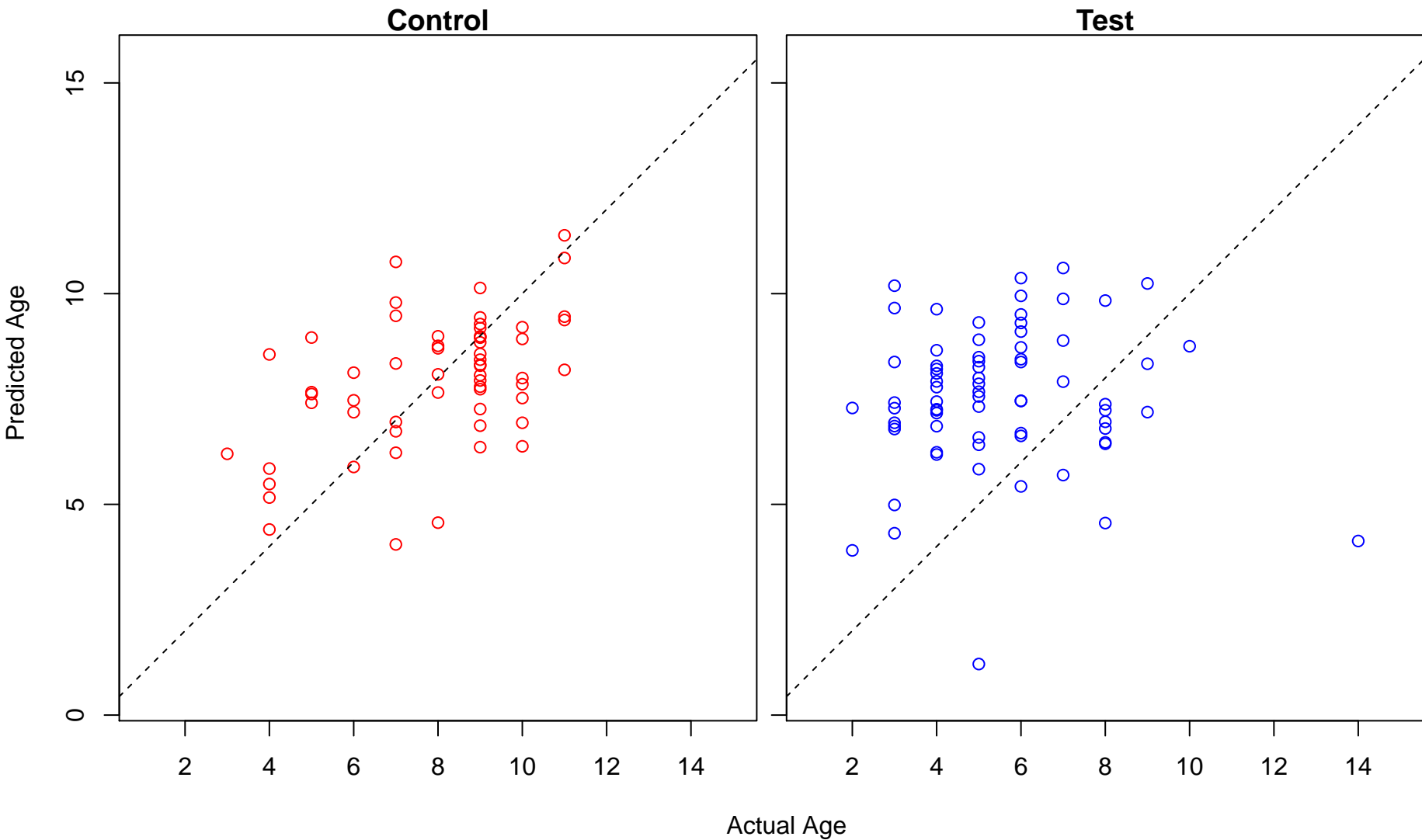
positive regulation of NF-kappaB transcription factor activity (Score: 2.249004)



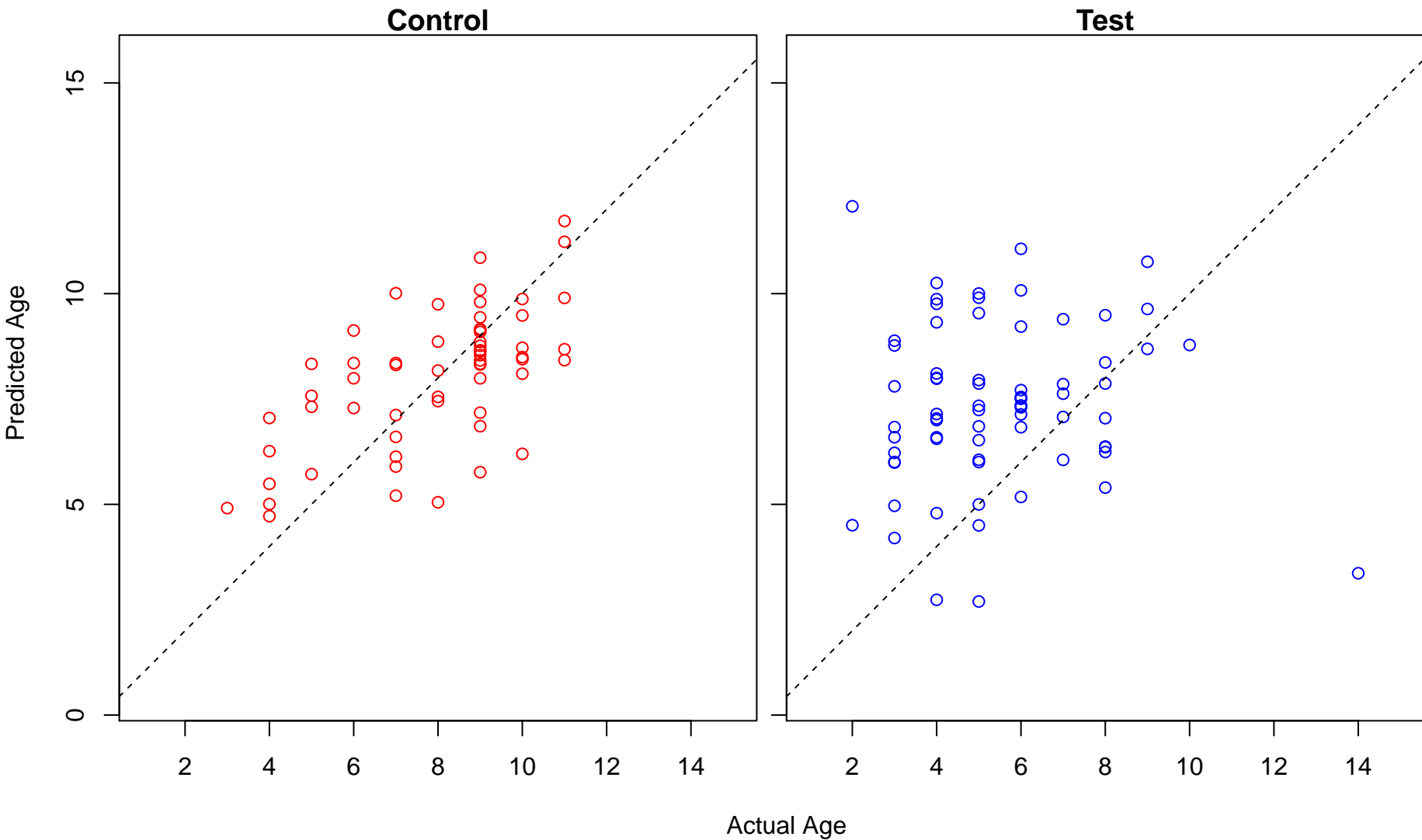
positive regulation of endothelial cell proliferation (Score: 2.240384)



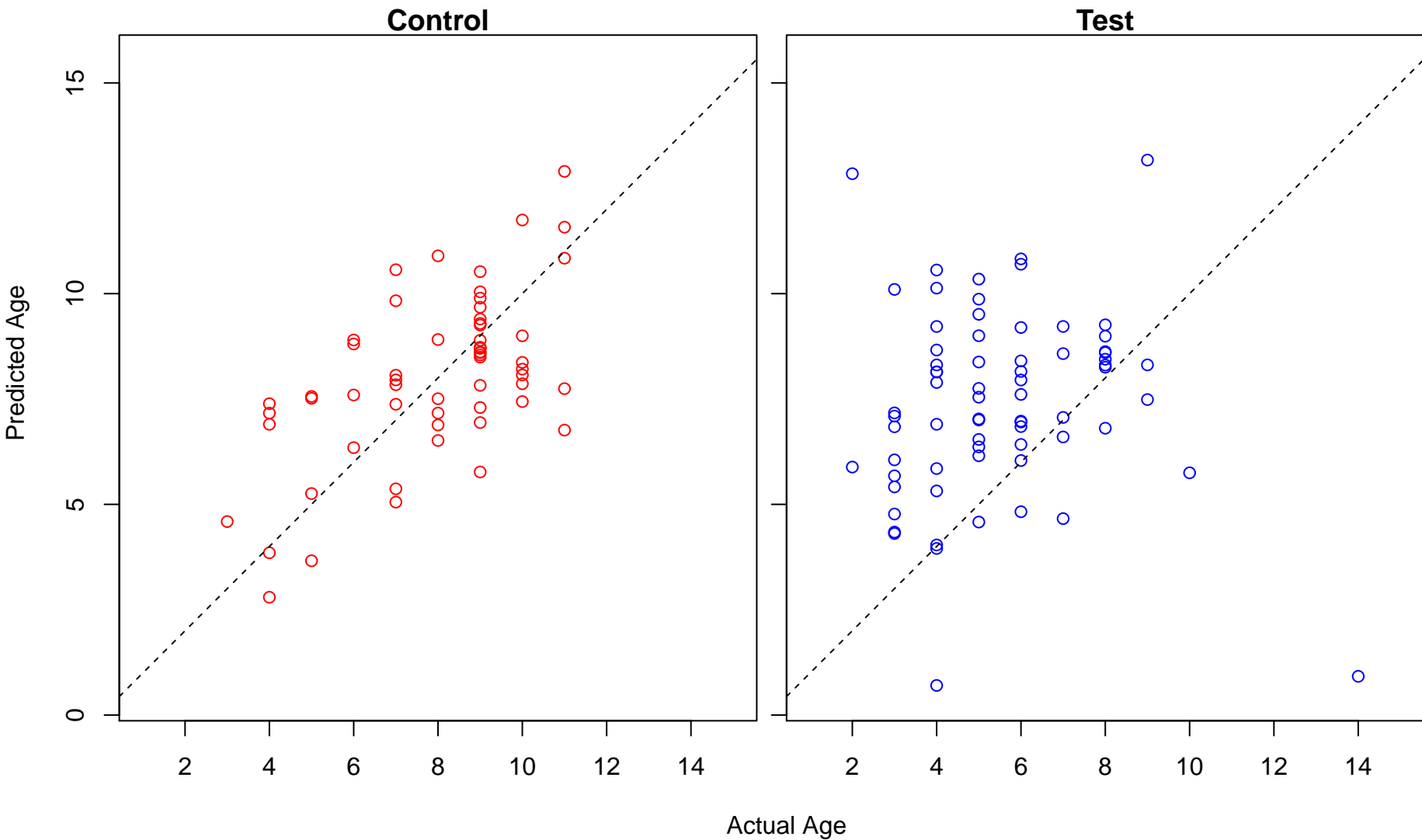
positive regulation of tyrosine phosphorylation of Stat3 protein (Score: 2.204379)



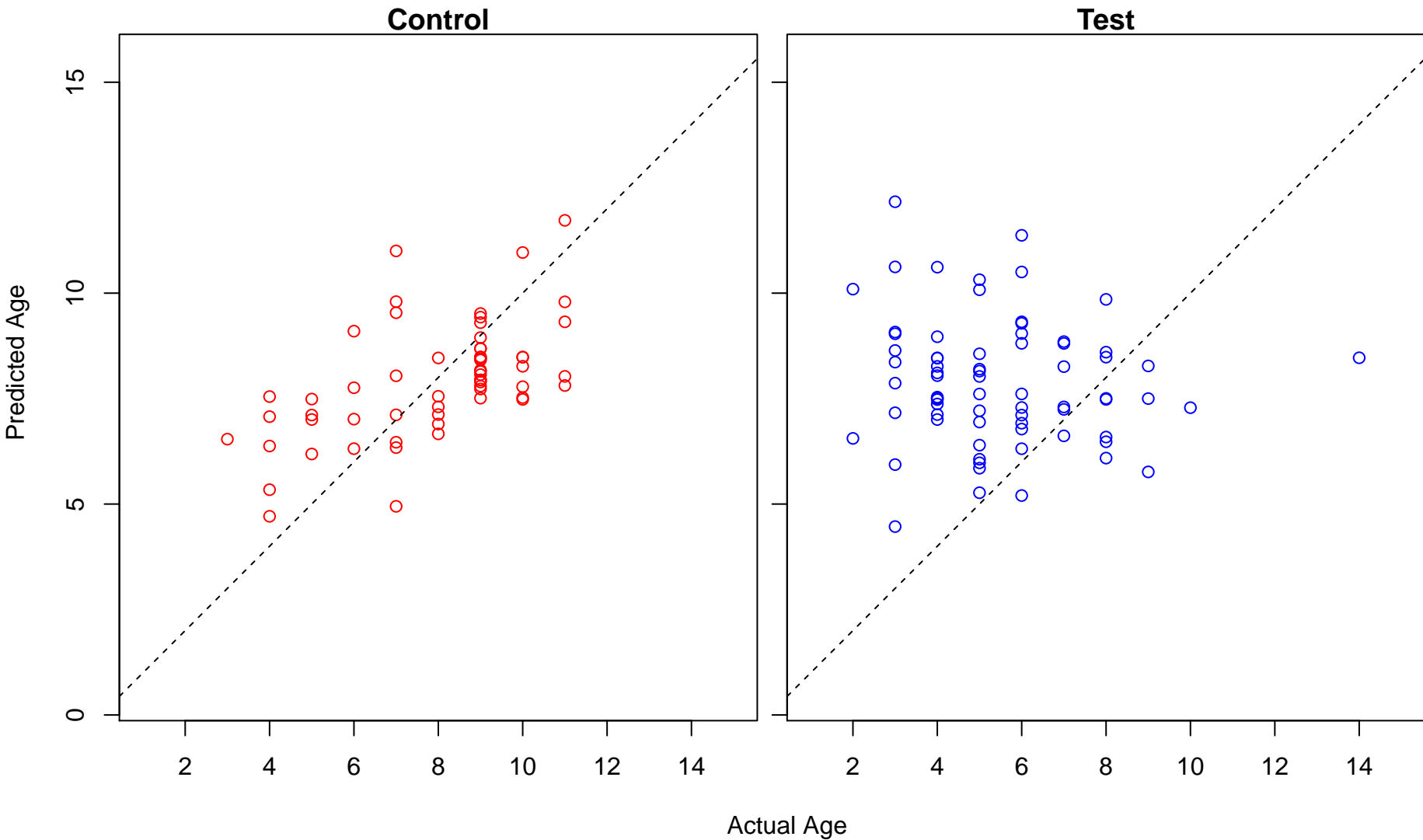
regulation of sequence-specific DNA binding transcription factor activity (Score: 2.192022)



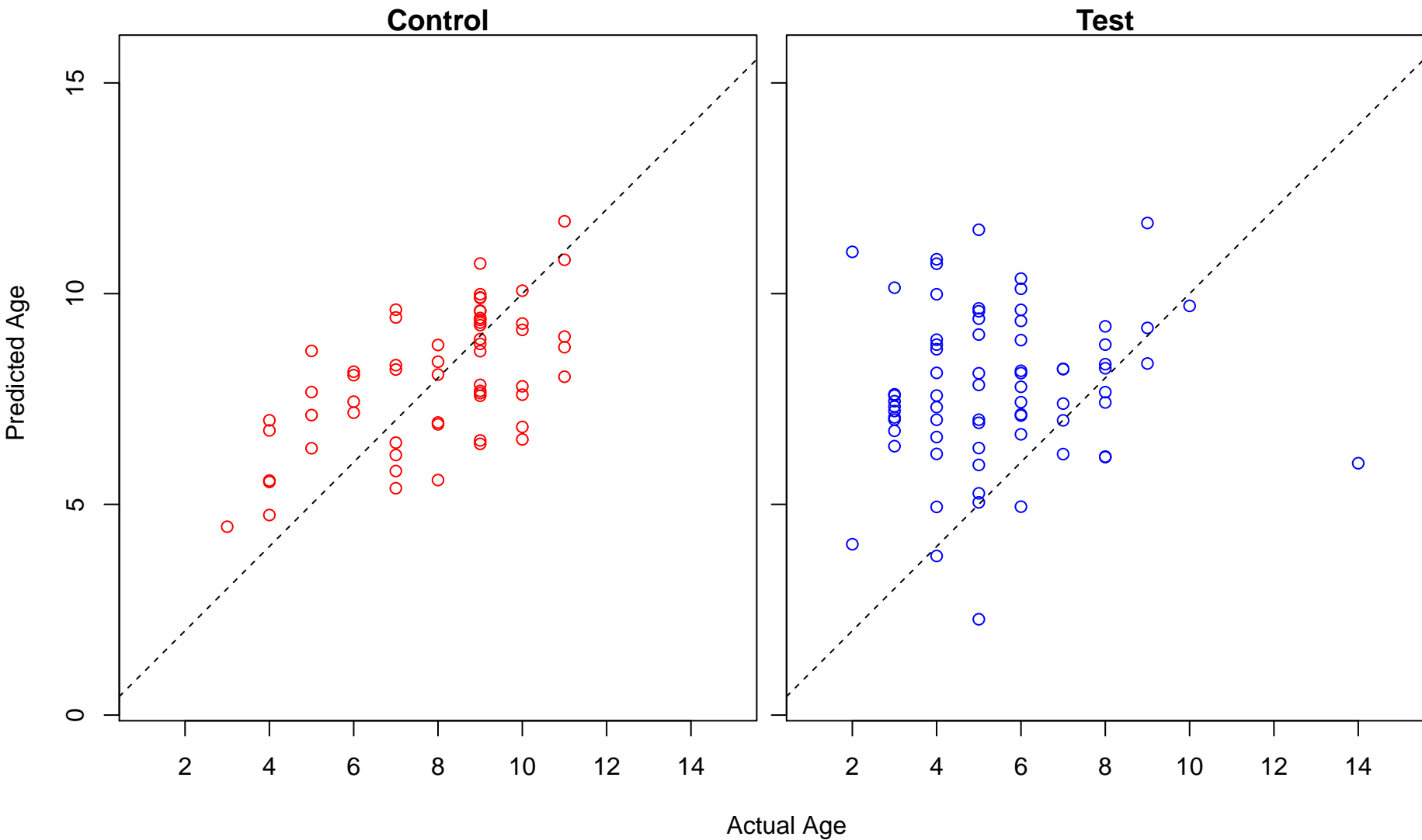
inflammatory response (Score: 2.189385)



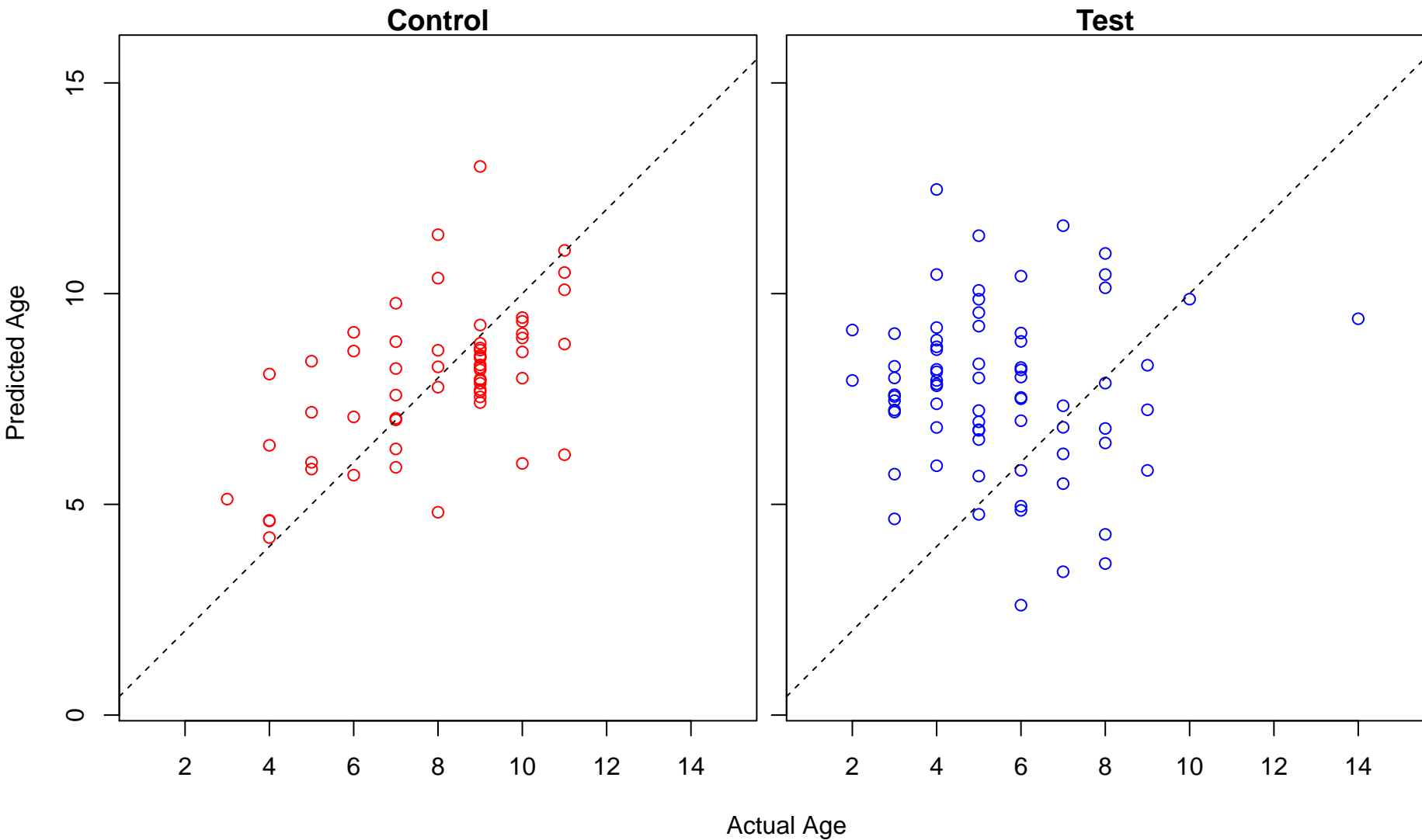
positive regulation of integrin-mediated signaling pathway (Score: 2.183181)



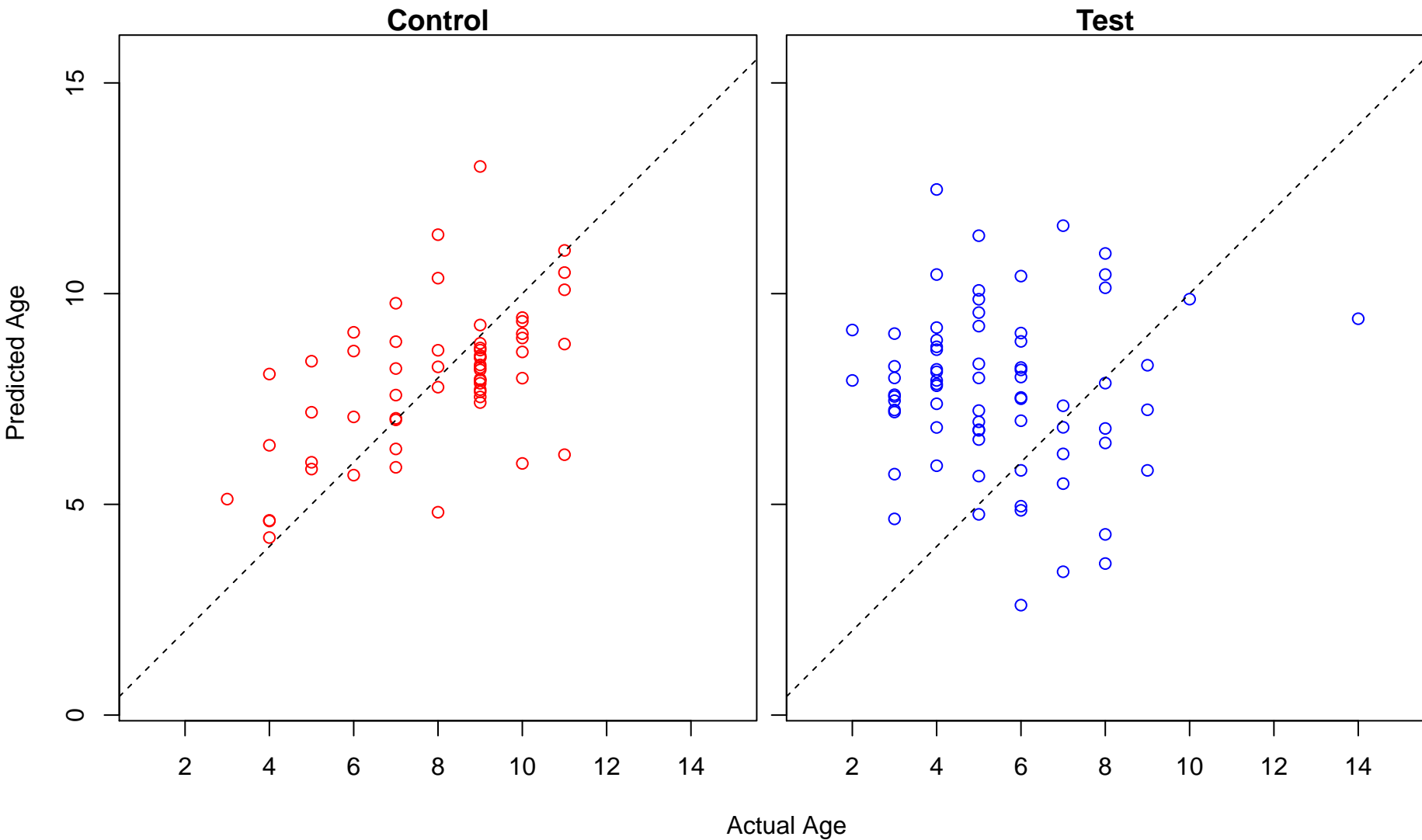
positive regulation of gene expression (Score: 2.171062)



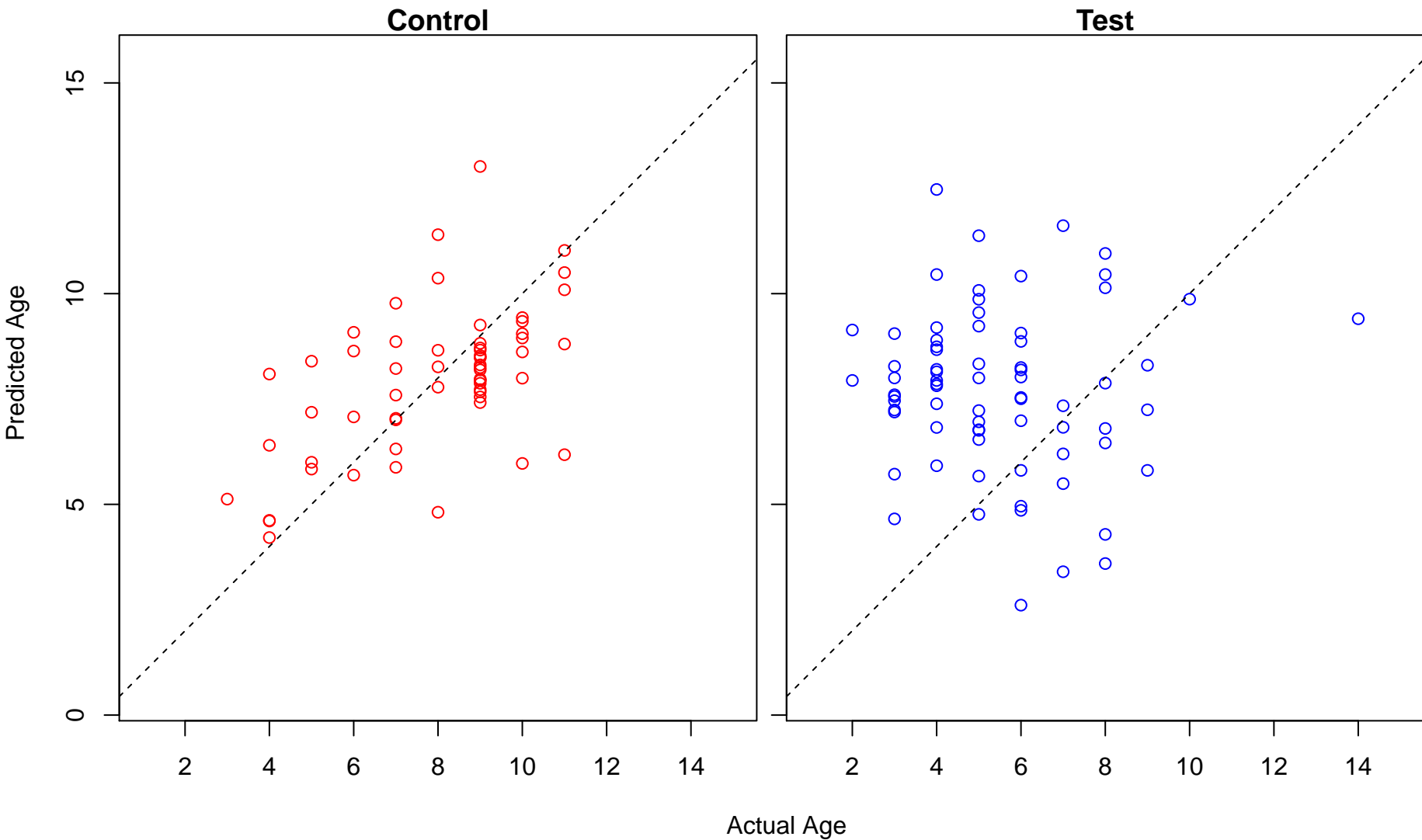
negative regulation of neurotransmitter uptake (Score: 2.168624)



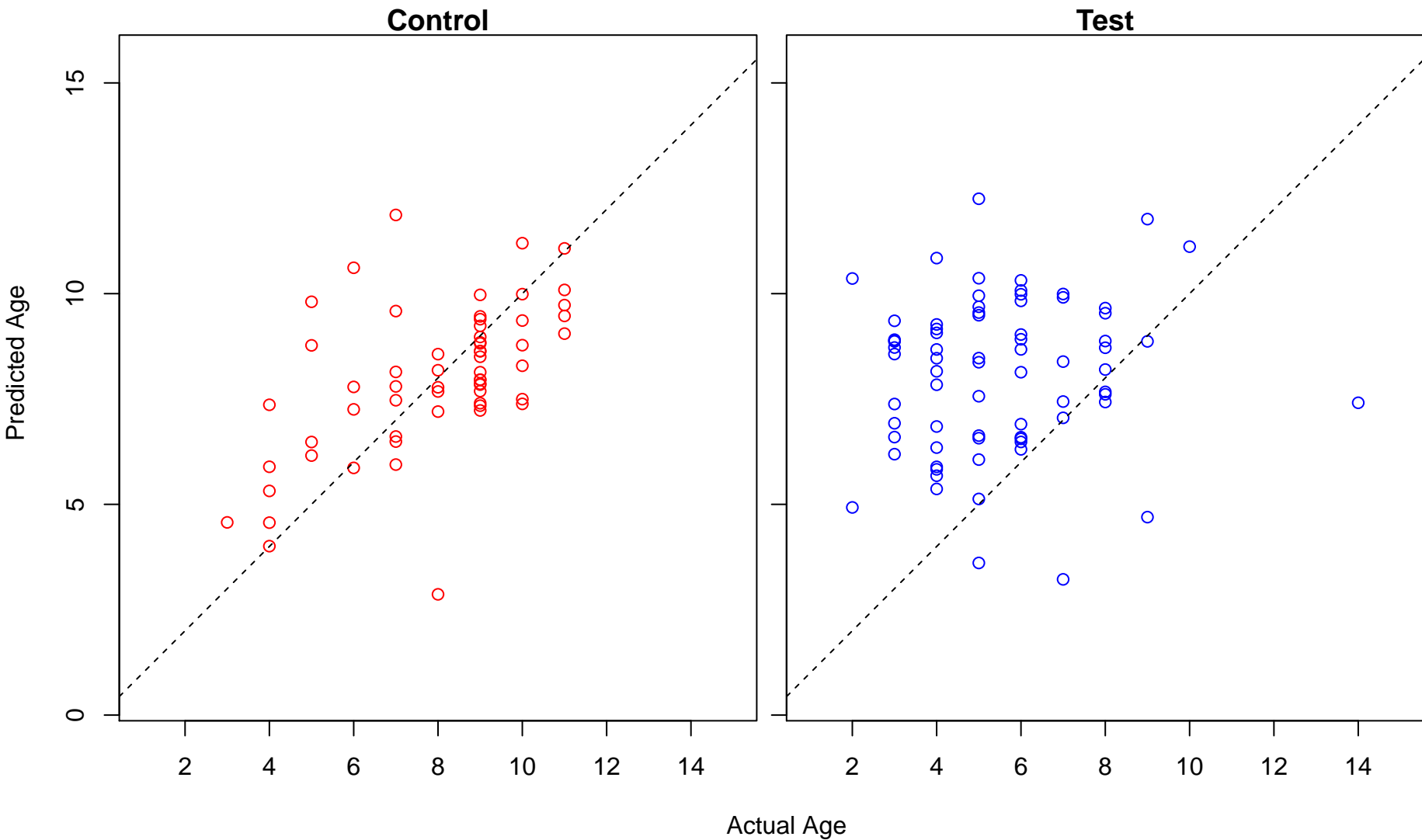
regulation of serotonin uptake (Score: 2.168624)



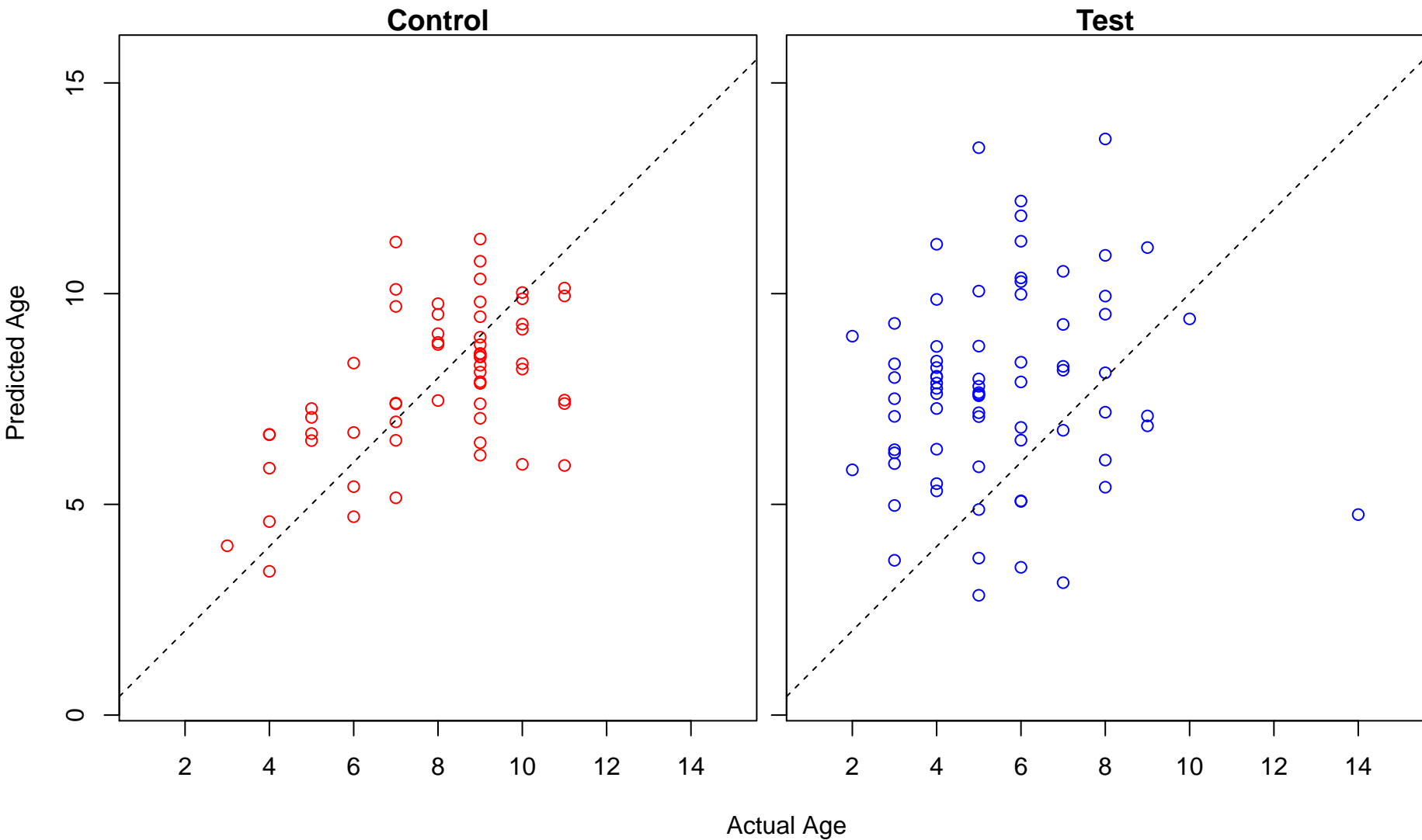
negative regulation of serotonin uptake (Score: 2.168624)



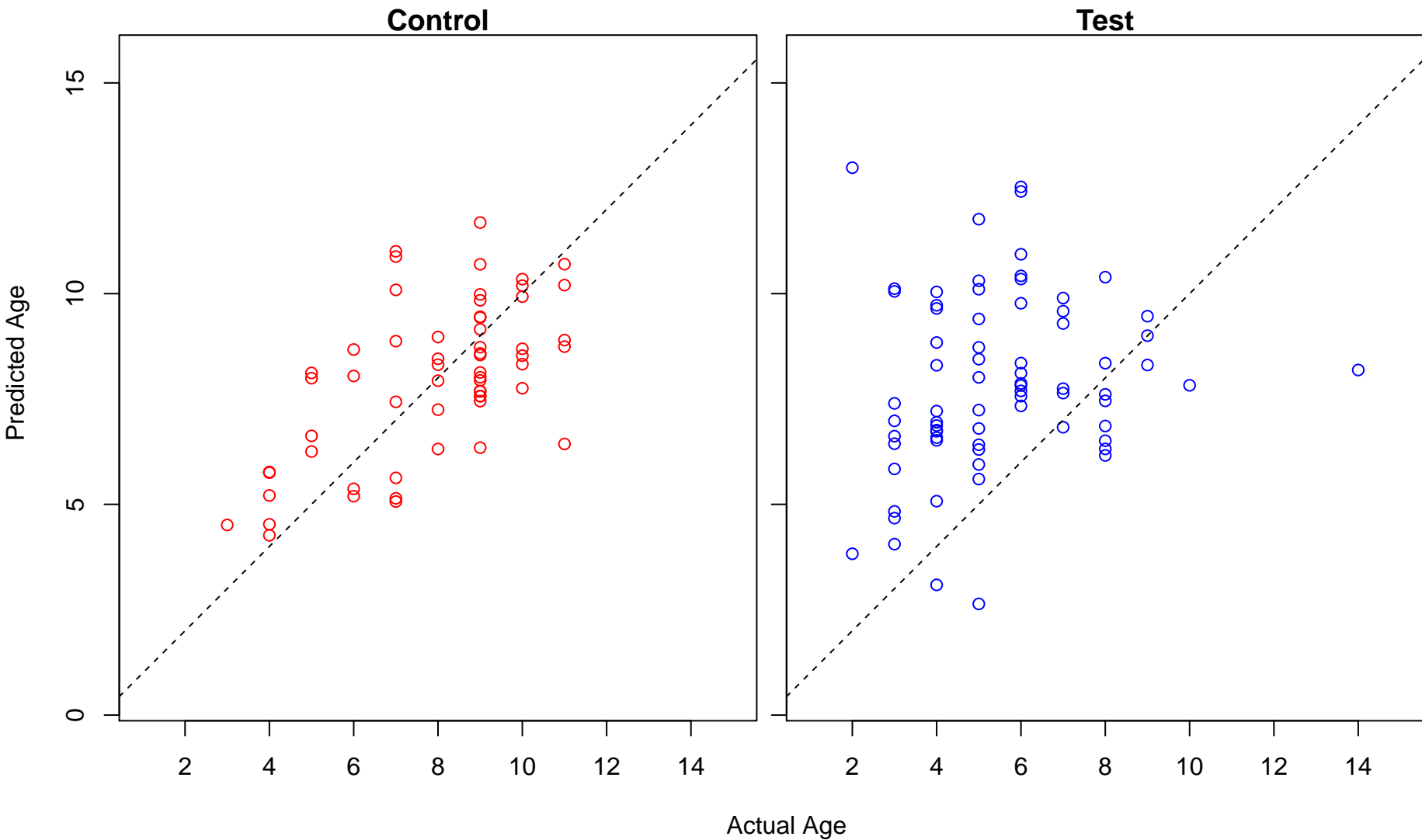
transition metal ion homeostasis (Score: 2.164906)



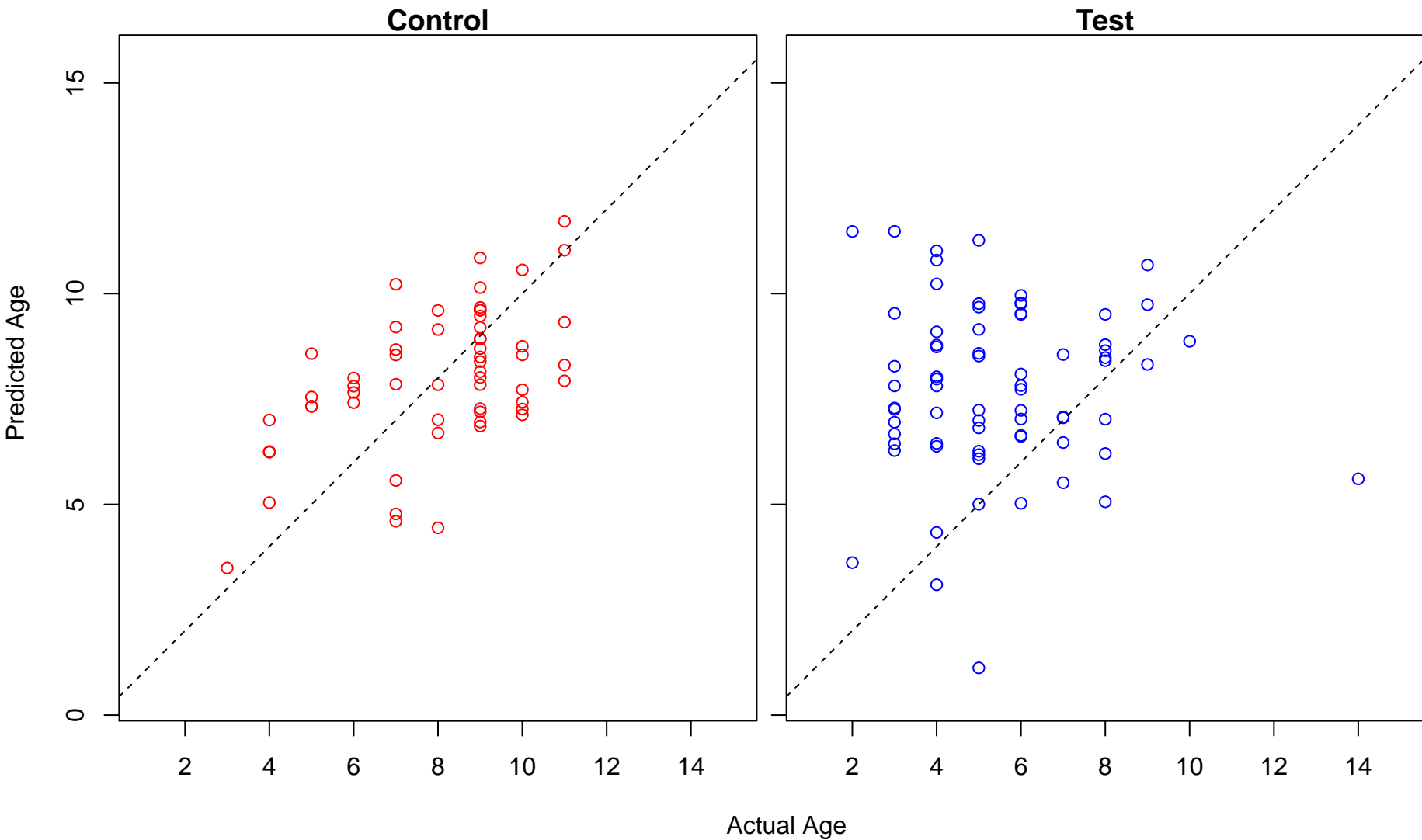
tissue homeostasis (Score: 2.141649)



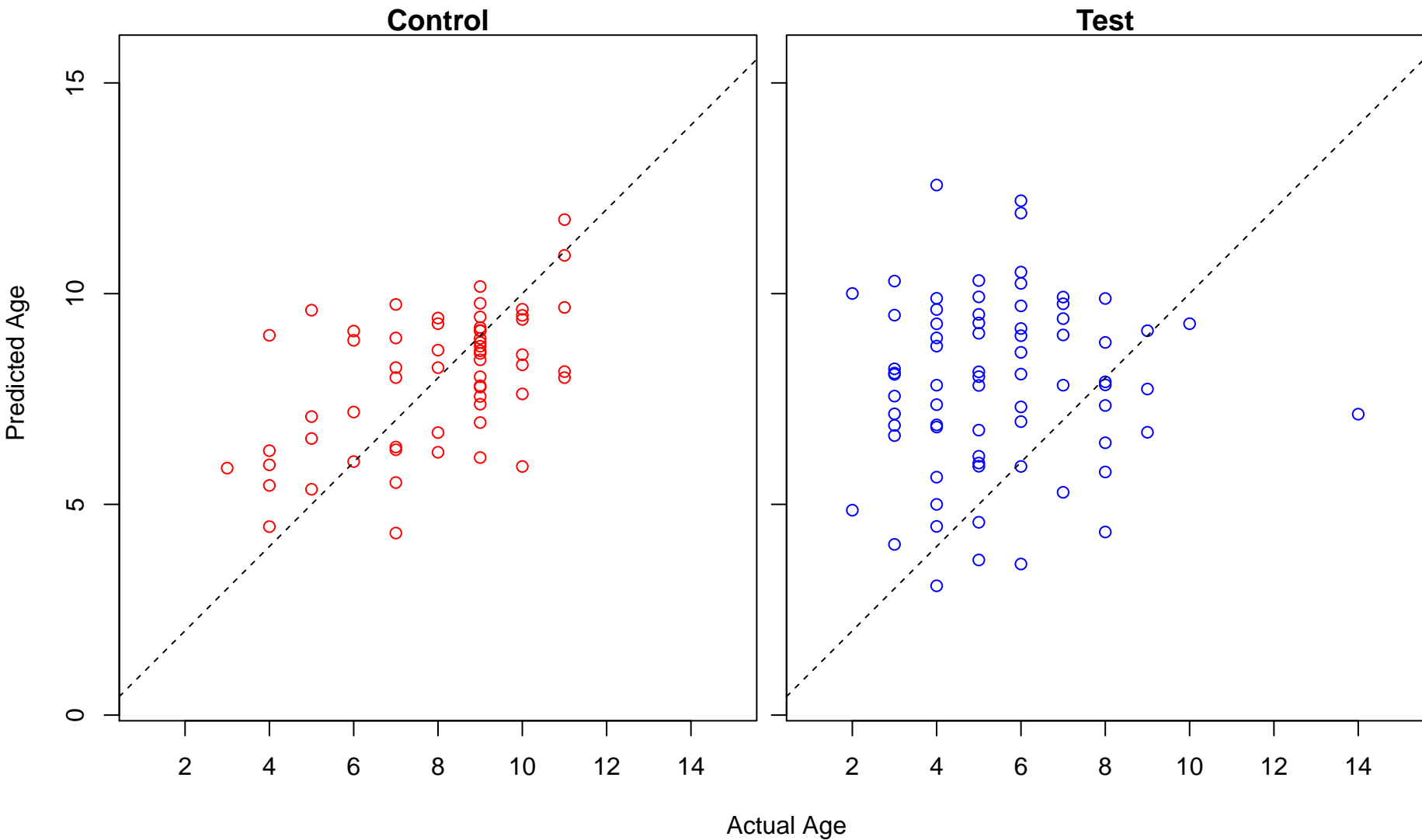
myeloid dendritic cell activation (Score: 2.138772)



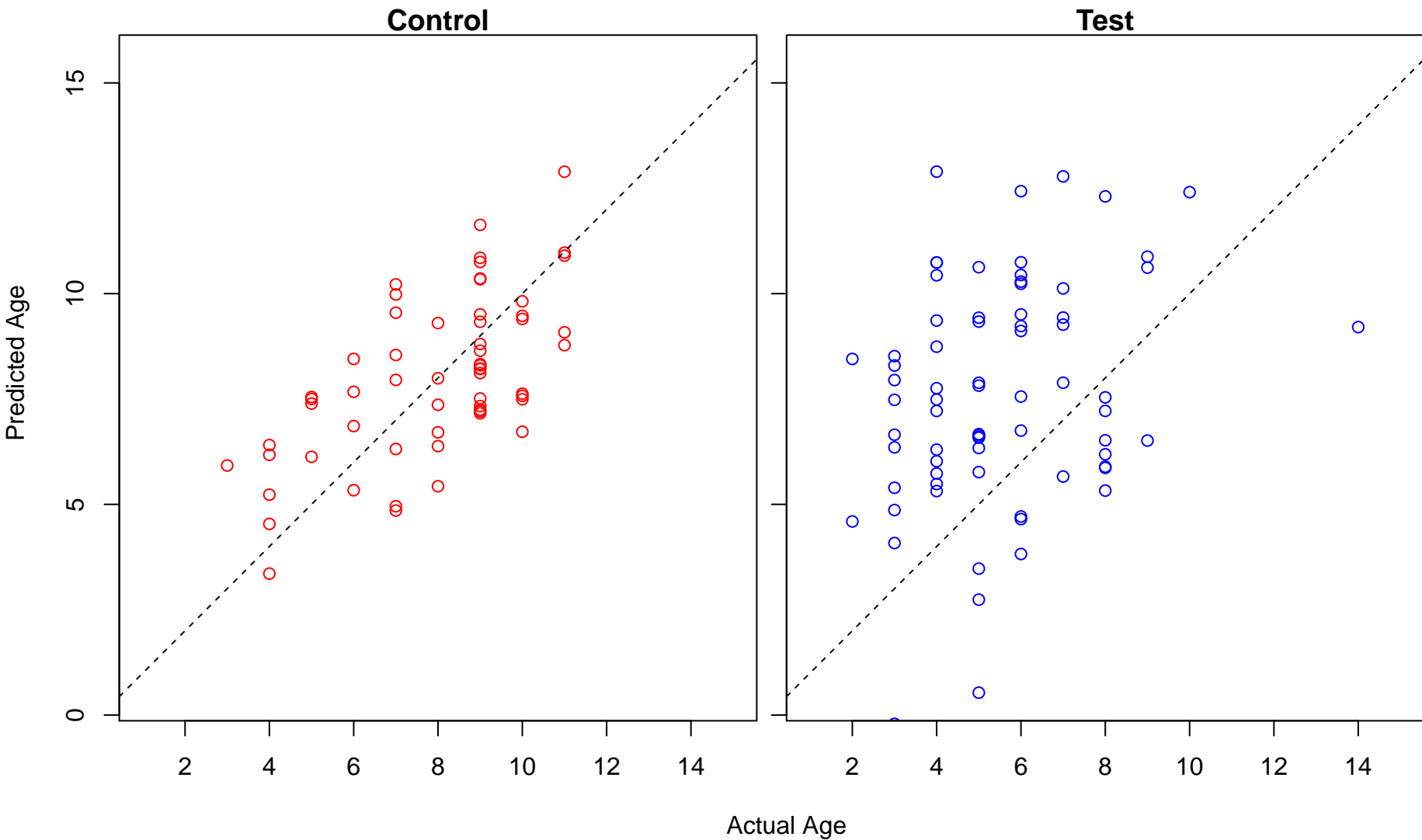
positive regulation of RNA metabolic process (Score: 2.134502)



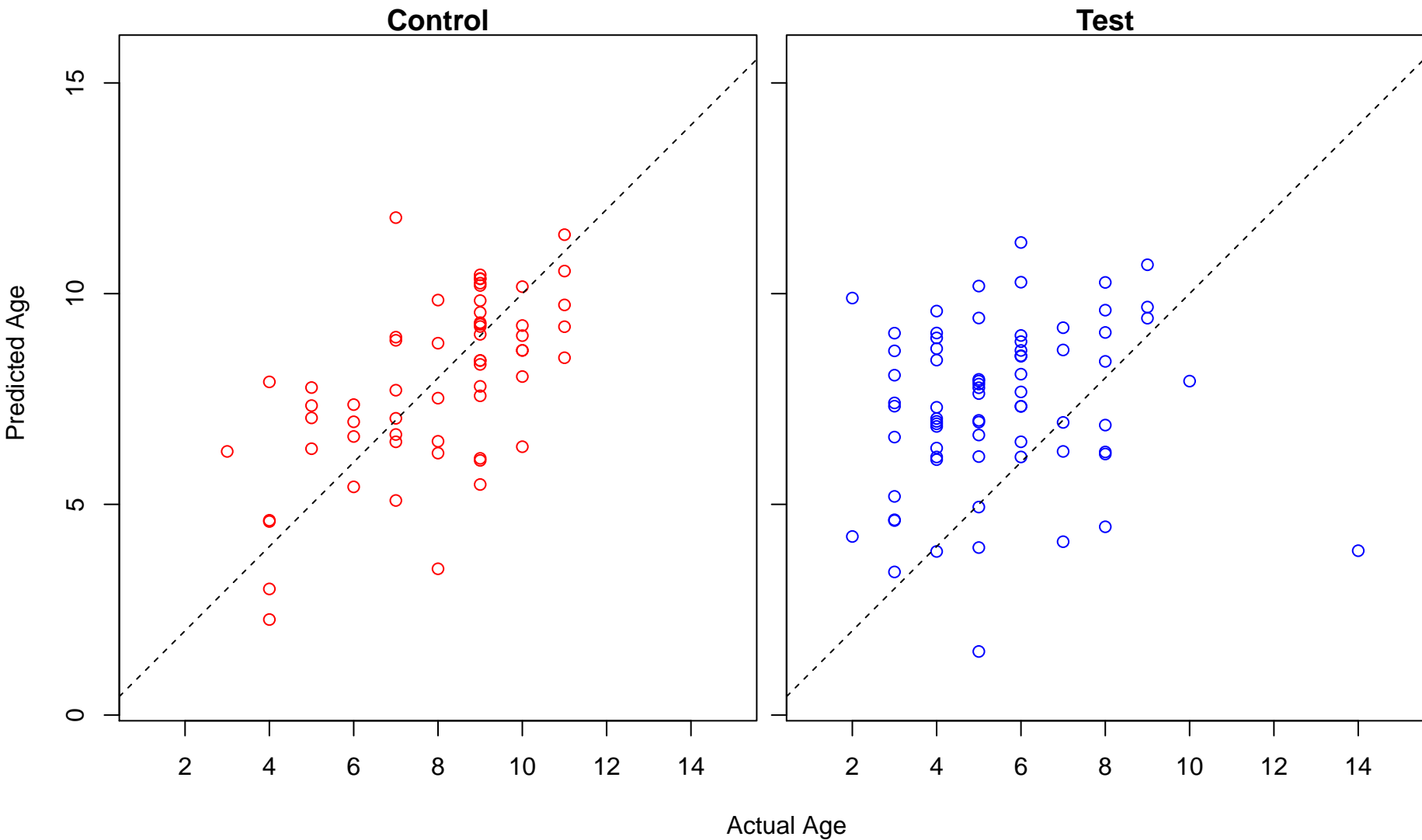
glycerophospholipid biosynthetic process (Score: 2.13152)



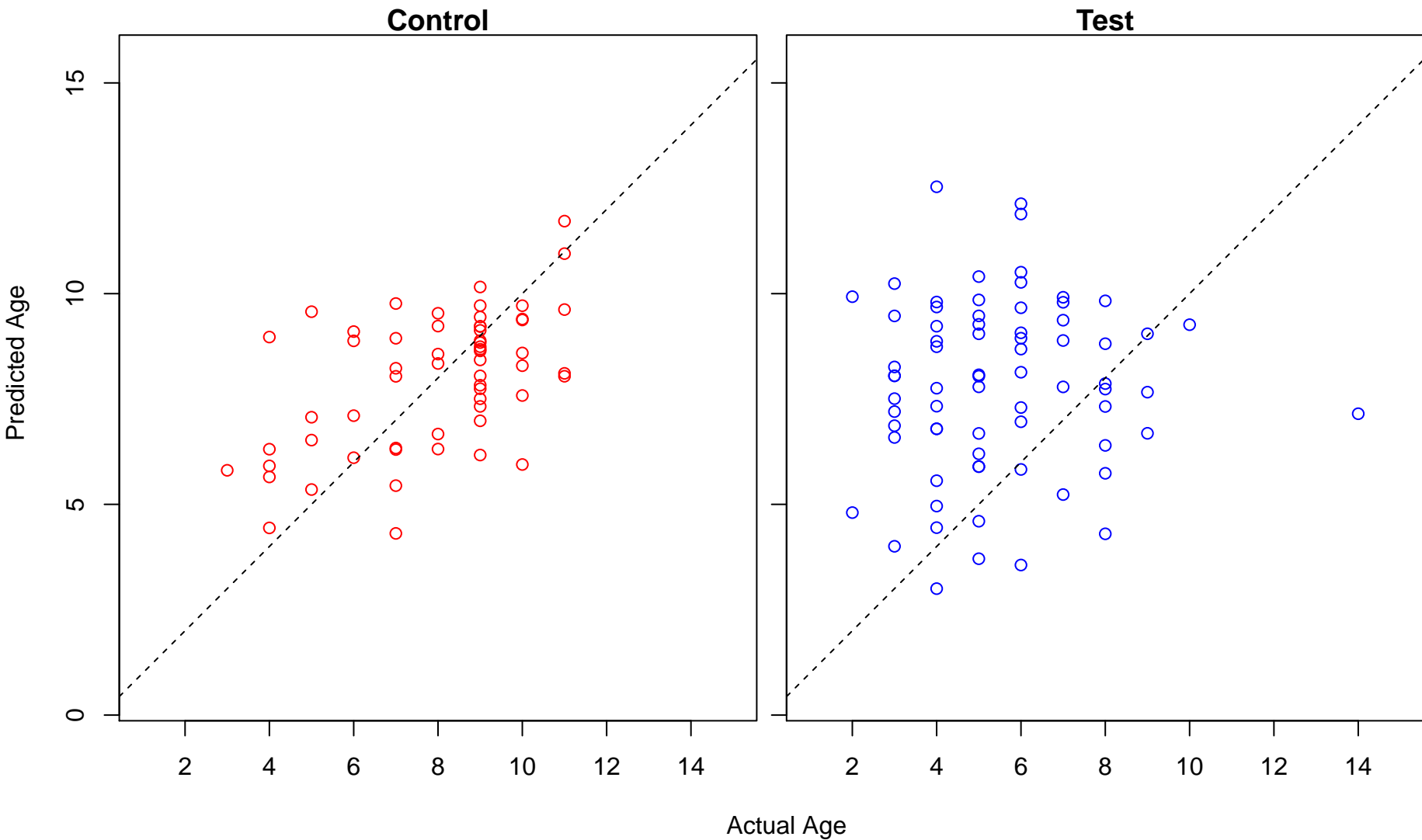
formation of primary germ layer (Score: 2.130959)



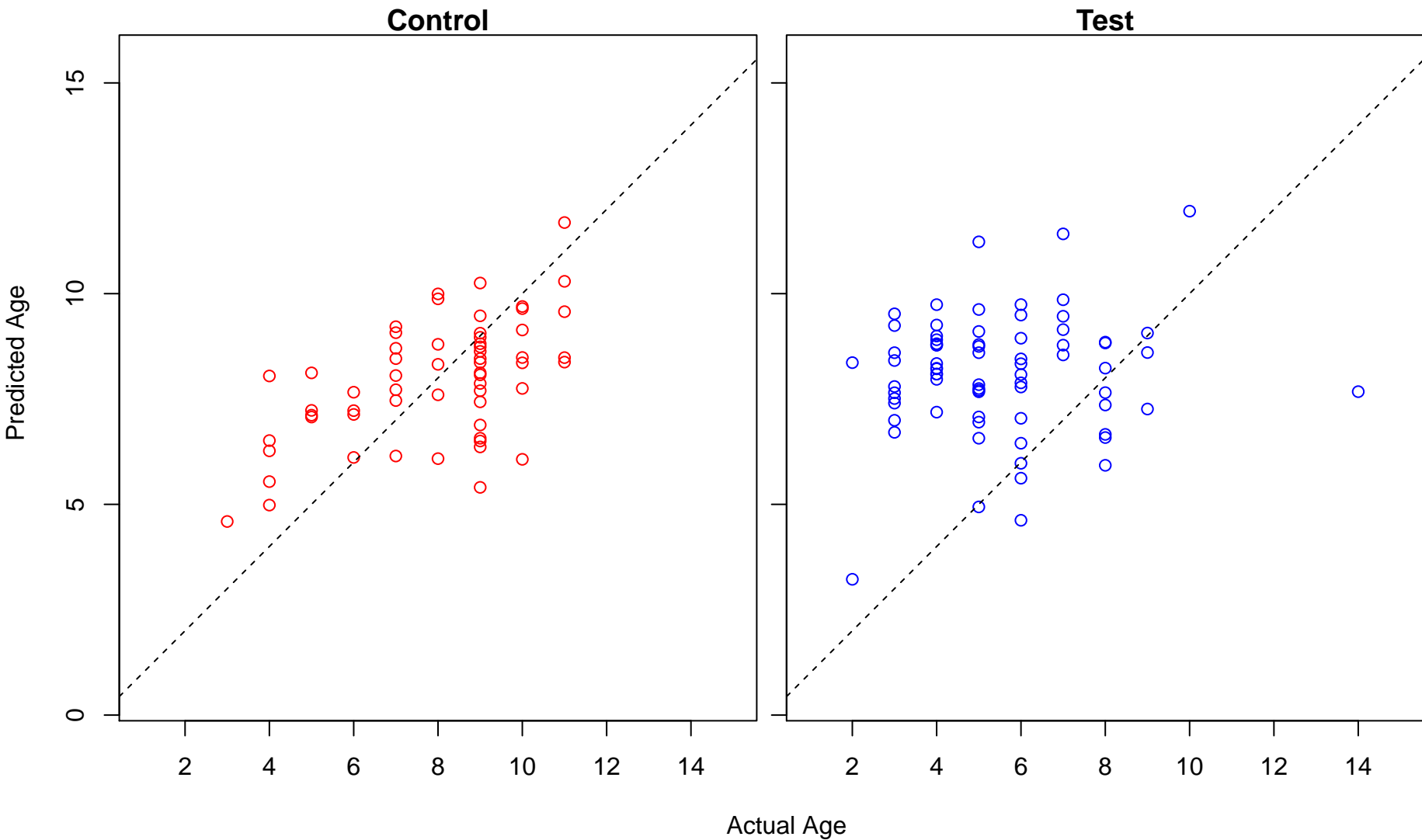
central nervous system neuron differentiation (Score: 2.122263)



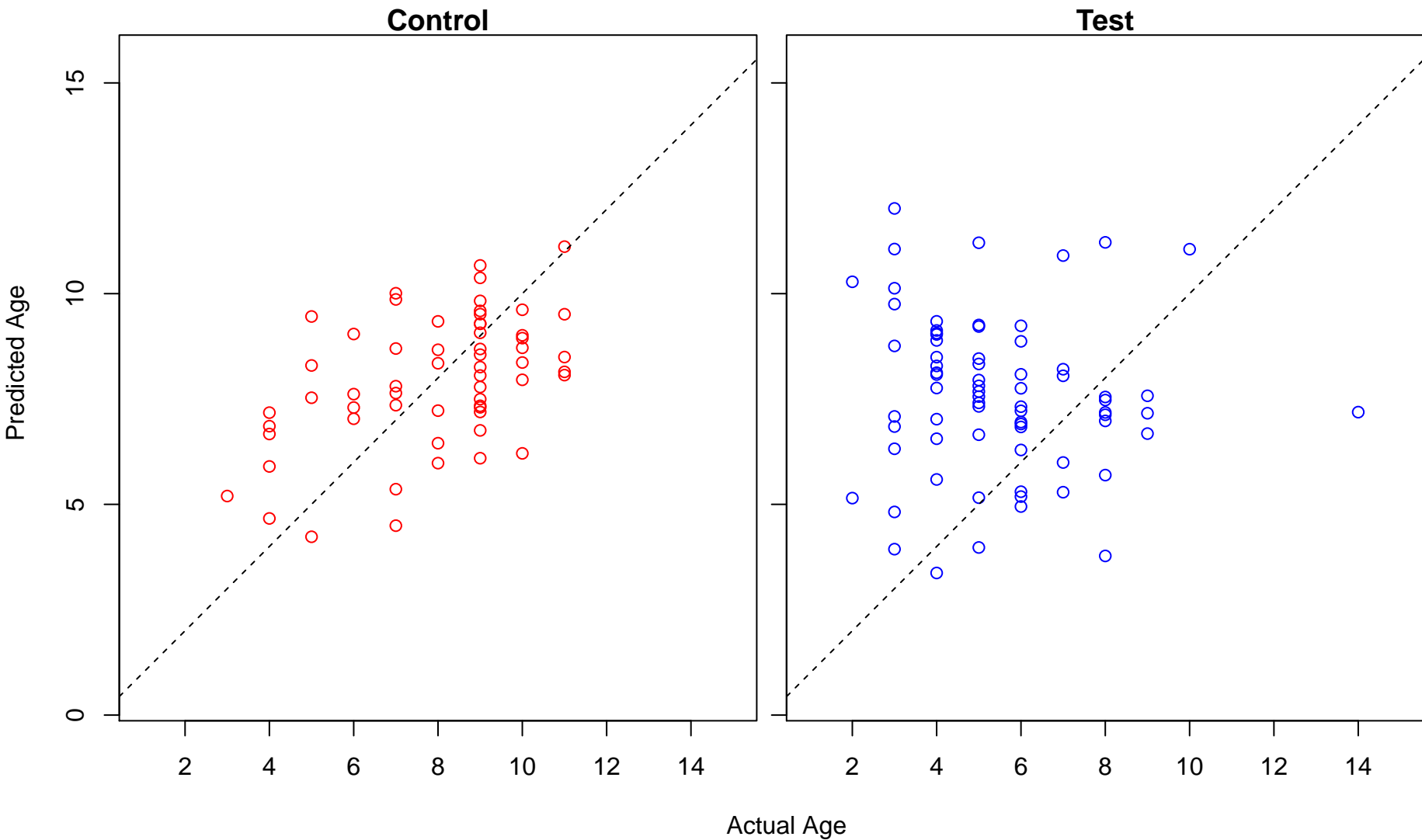
phospholipid biosynthetic process (Score: 2.12093)



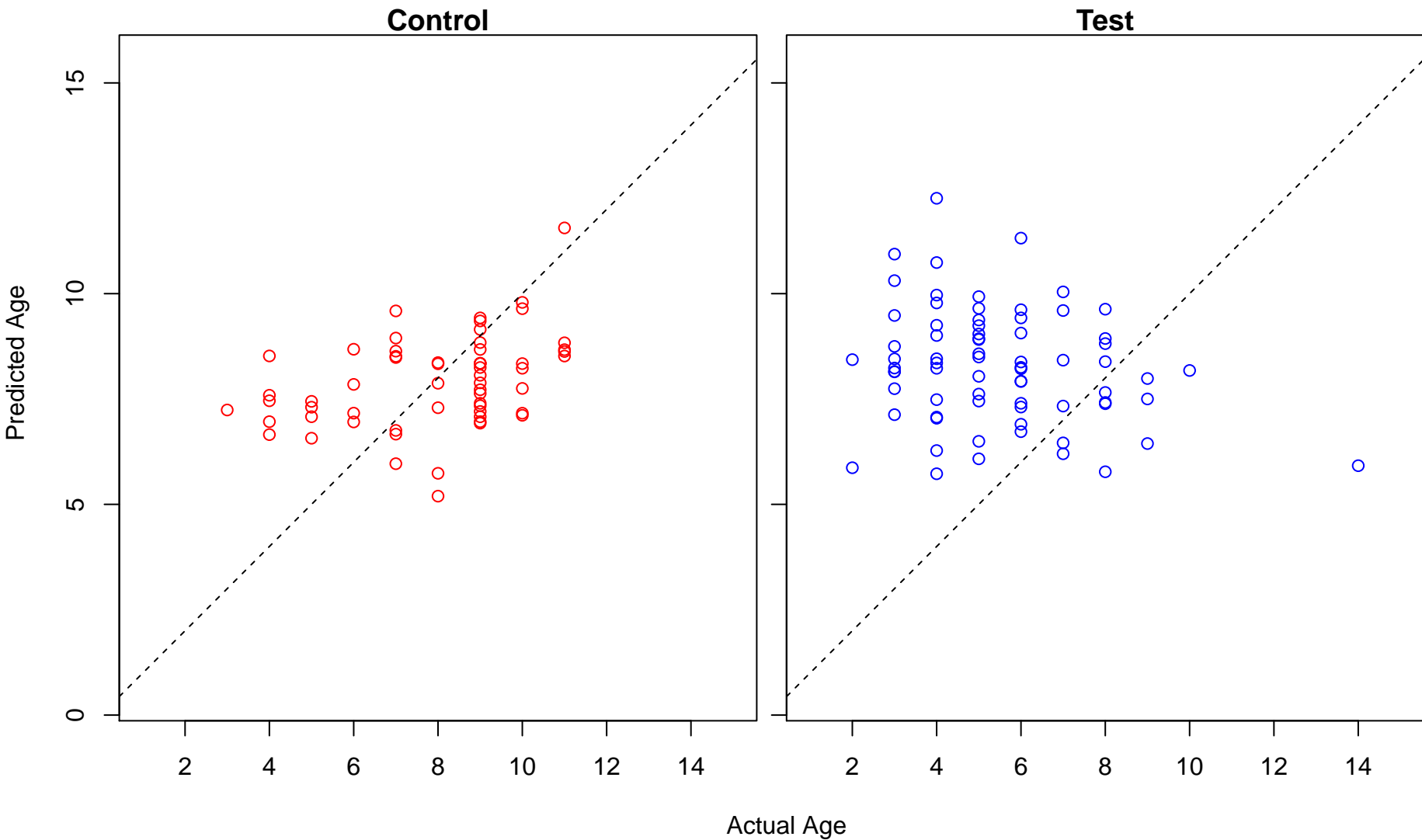
protein polyglutamylation (Score: 2.119333)



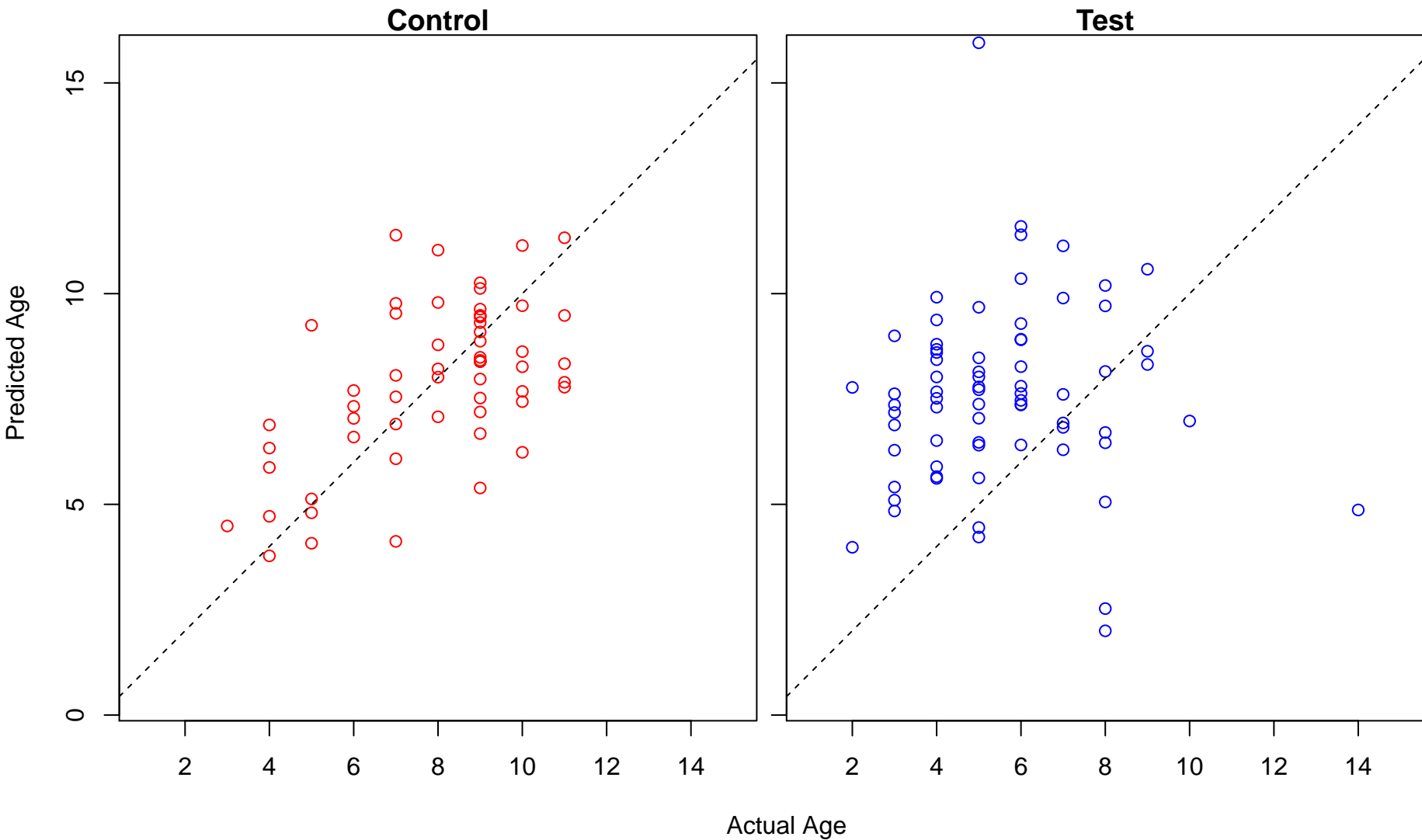
regulation of meiotic cell cycle (Score: 2.117780)



soft palate development (Score: 2.116172)

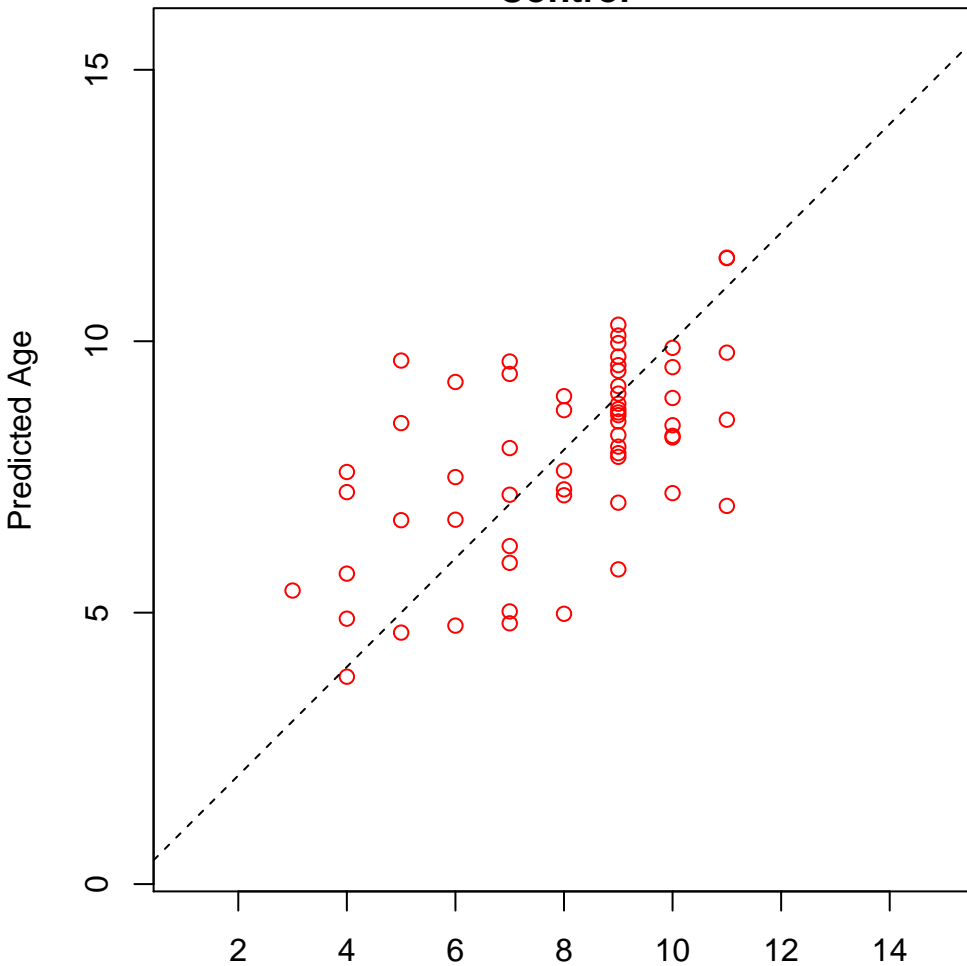


membrane fusion (Score: 2.111723)

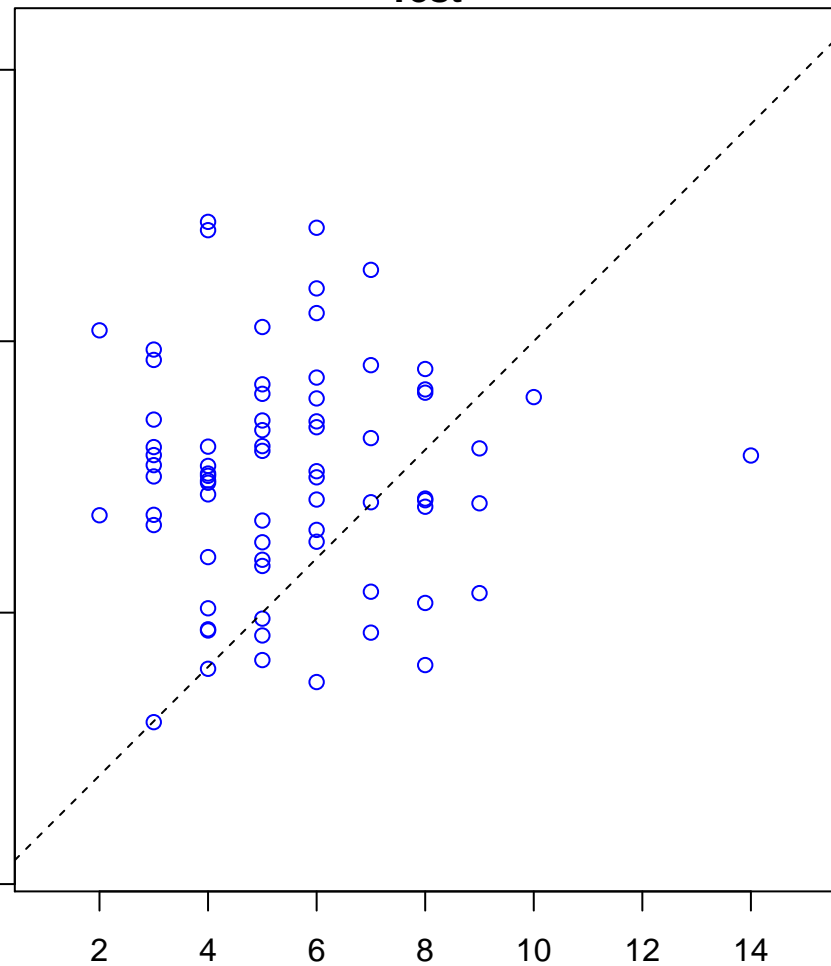


organophosphate biosynthetic process (Score: 2.108808)

Control

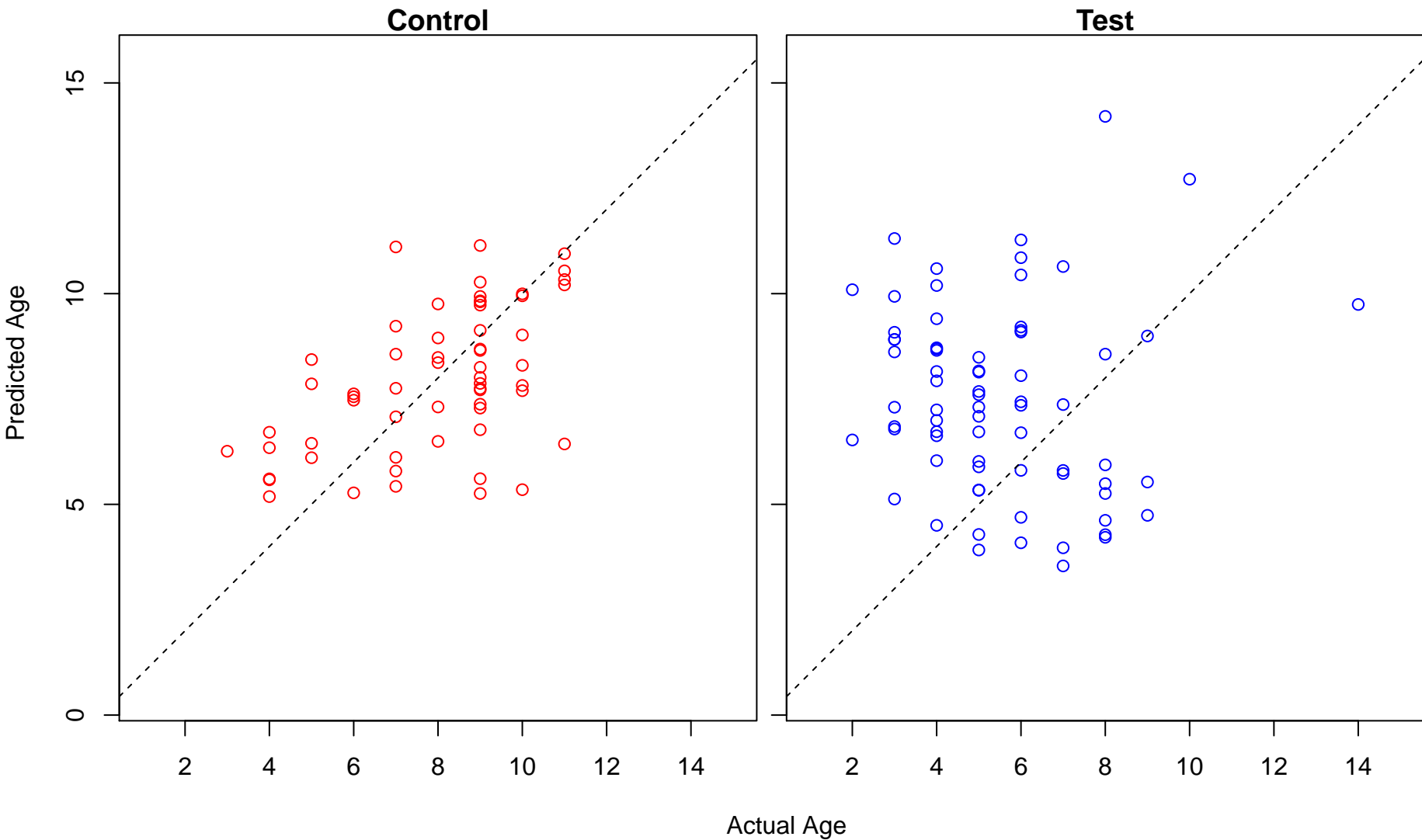


Test

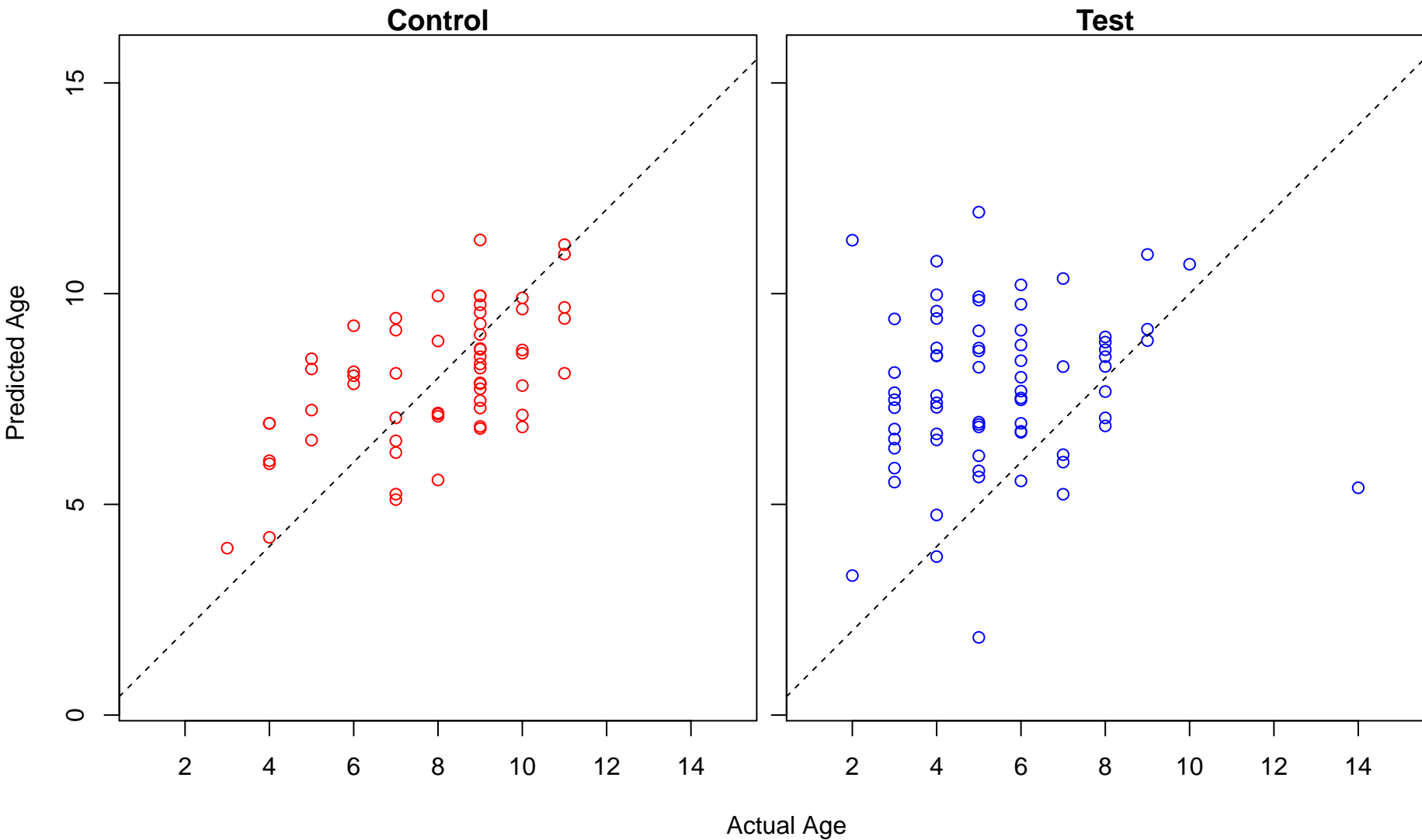


Actual Age

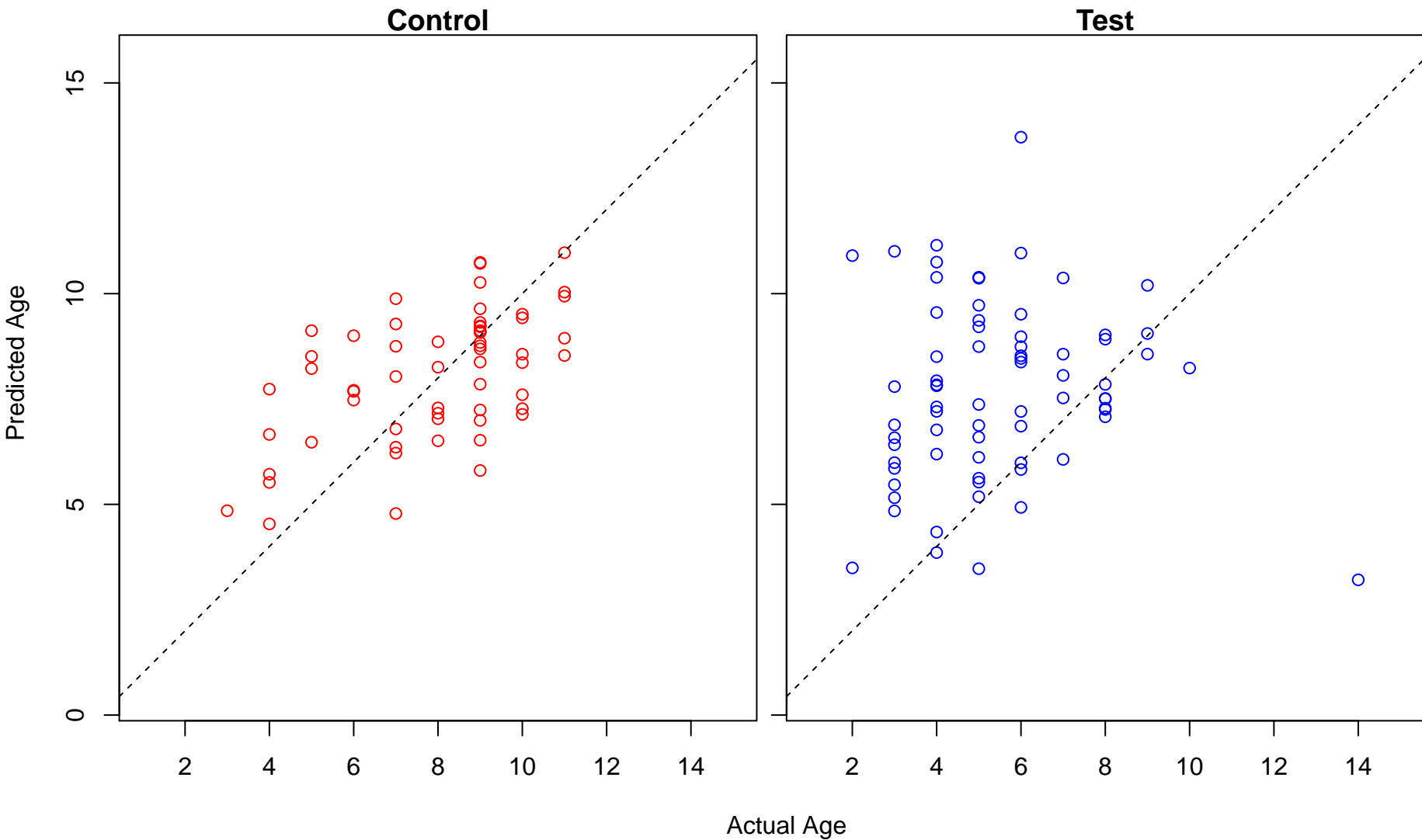
morphogenesis of a polarized epithelium (Score: 2.100017)



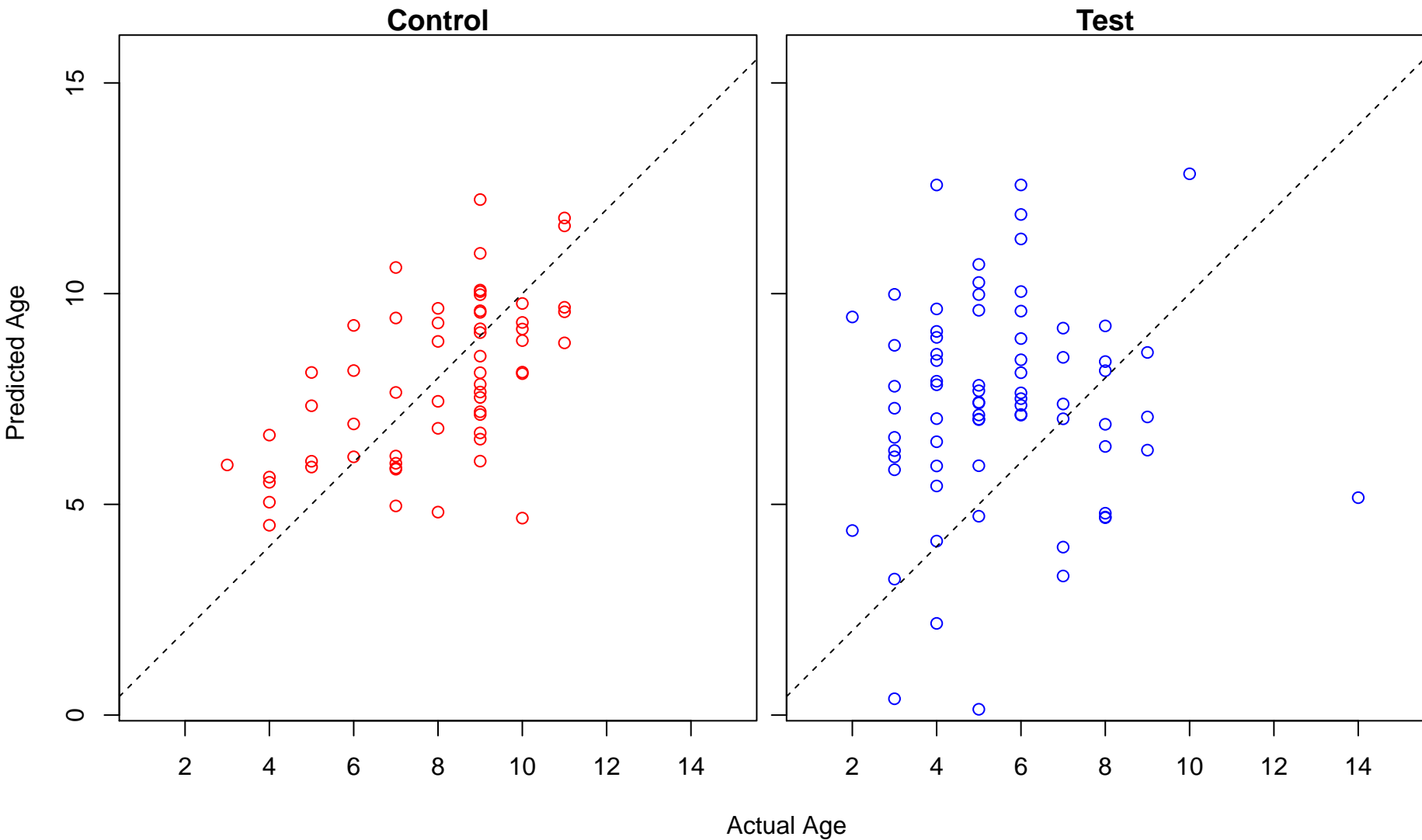
regulation of RNA biosynthetic process (Score: 2.099009)



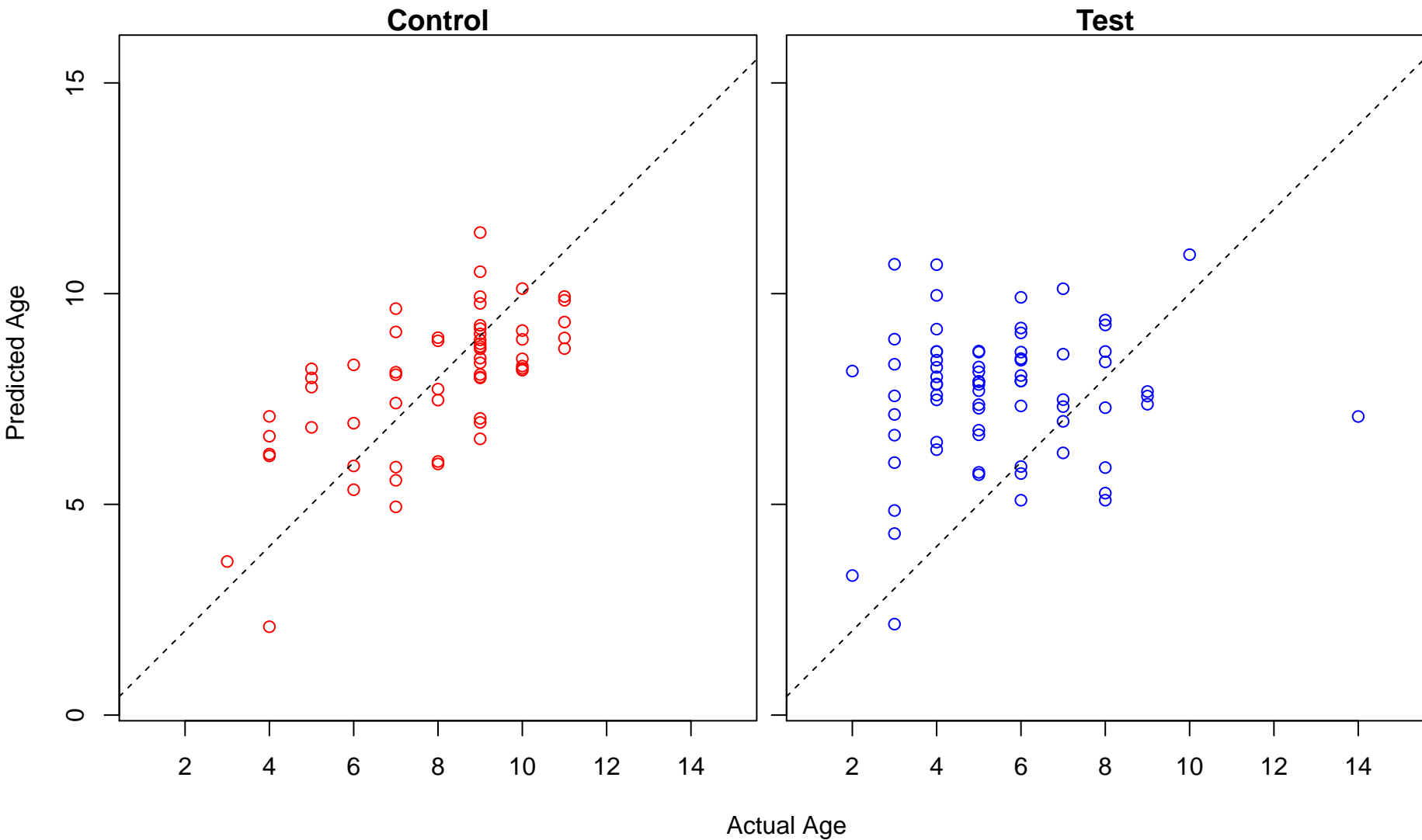
nervous system development (Score: 2.089575)



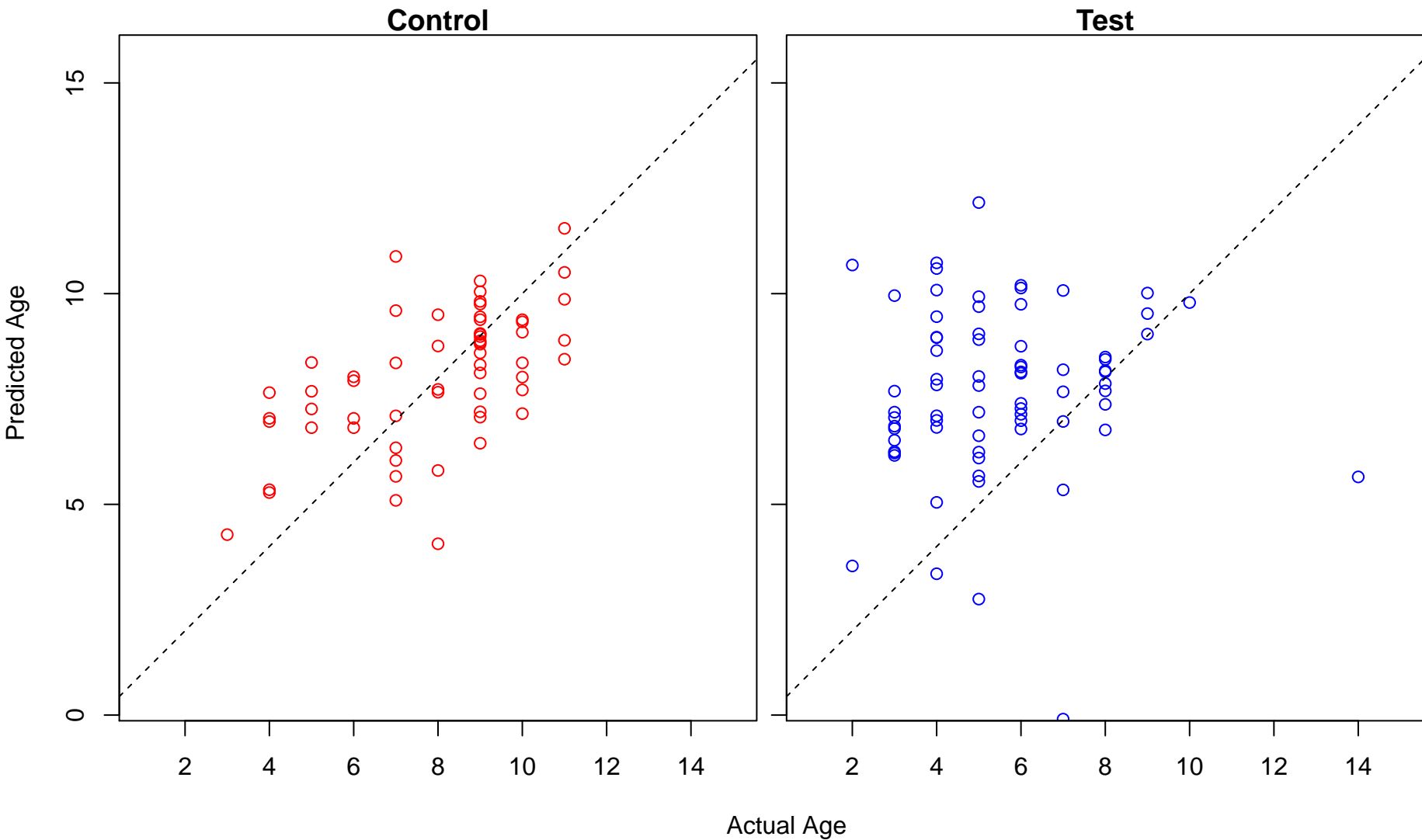
nuclear division (Score: 2.082128)



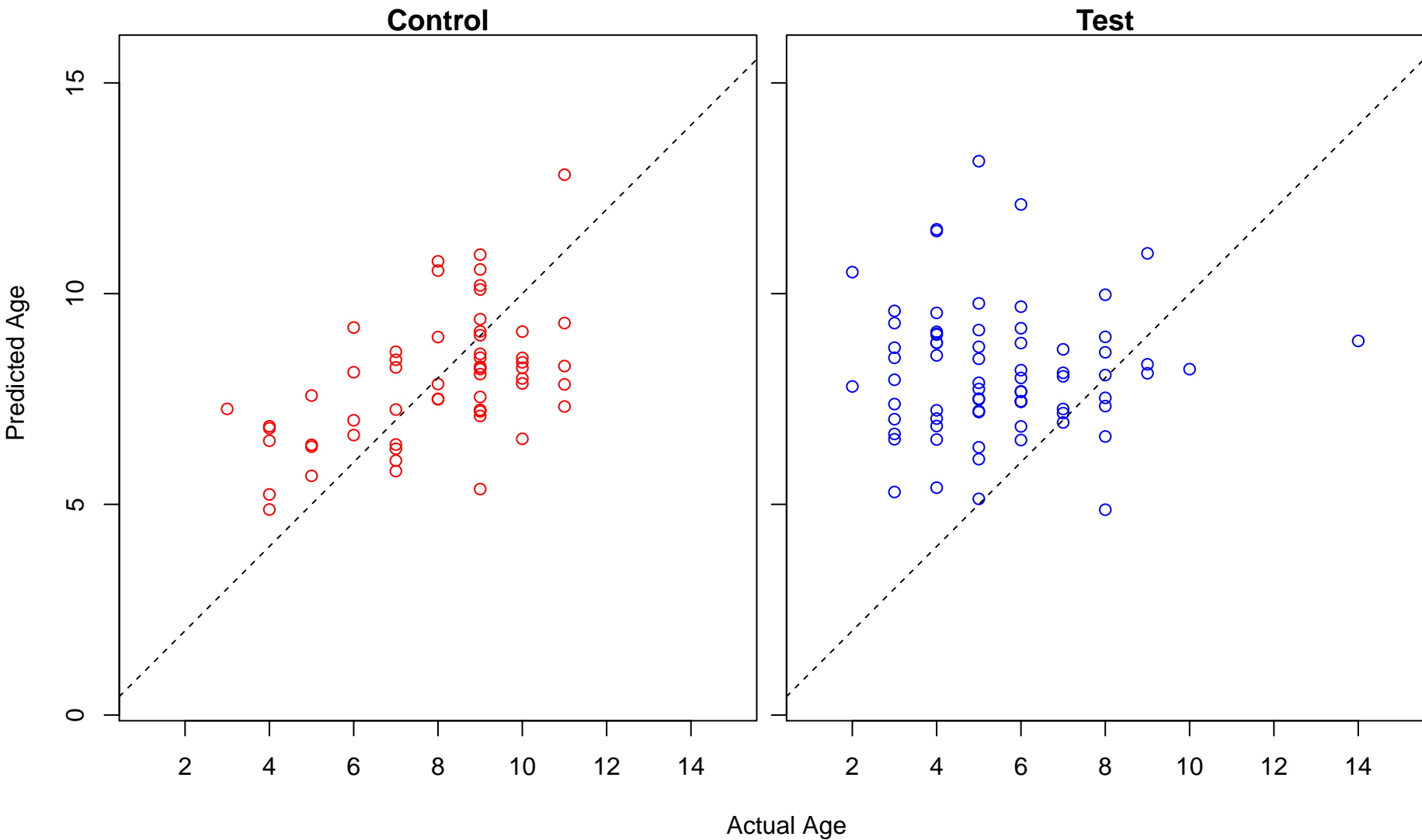
middle ear morphogenesis (Score: 2.072840)



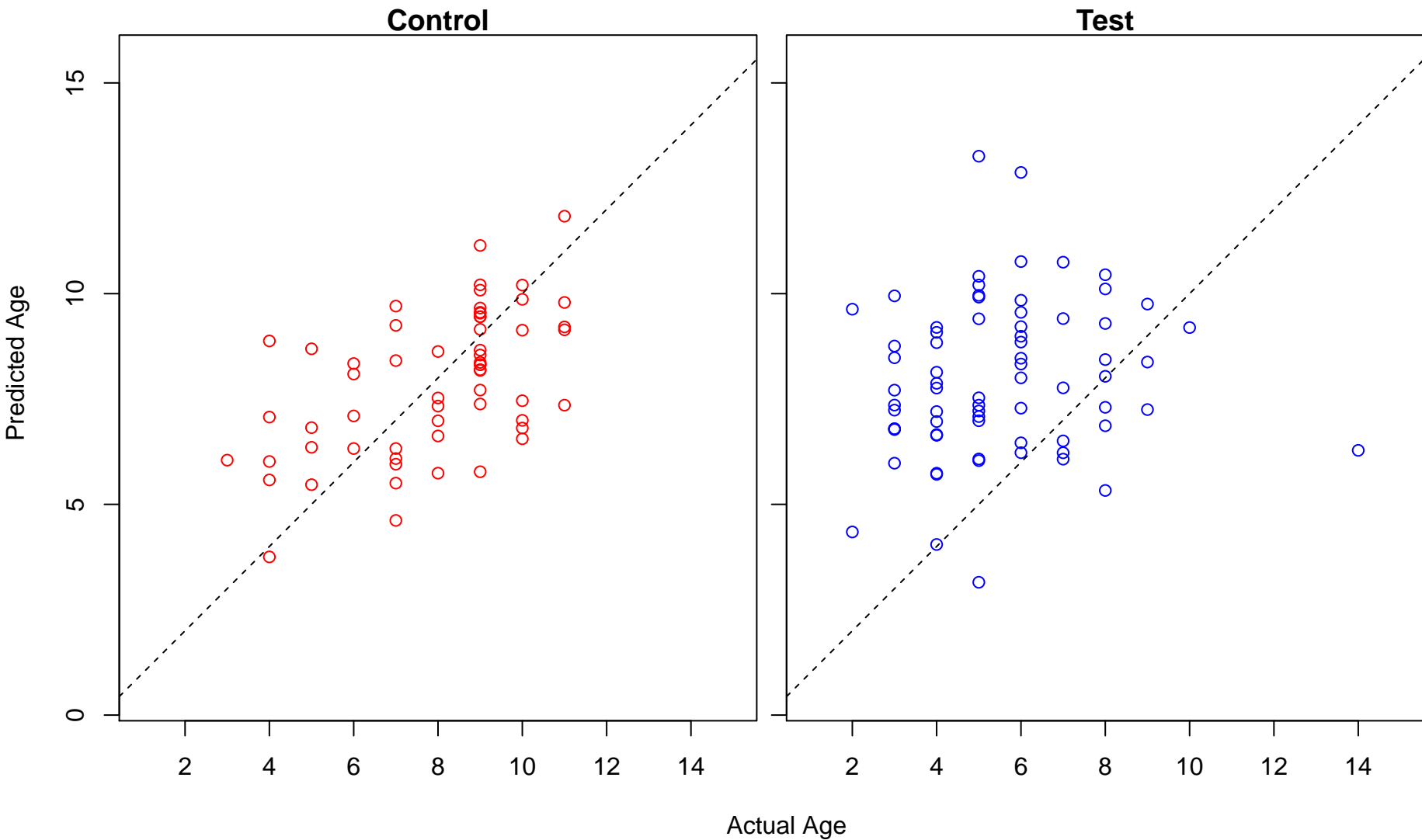
positive regulation of macromolecule metabolic process (Score: 2.058429)



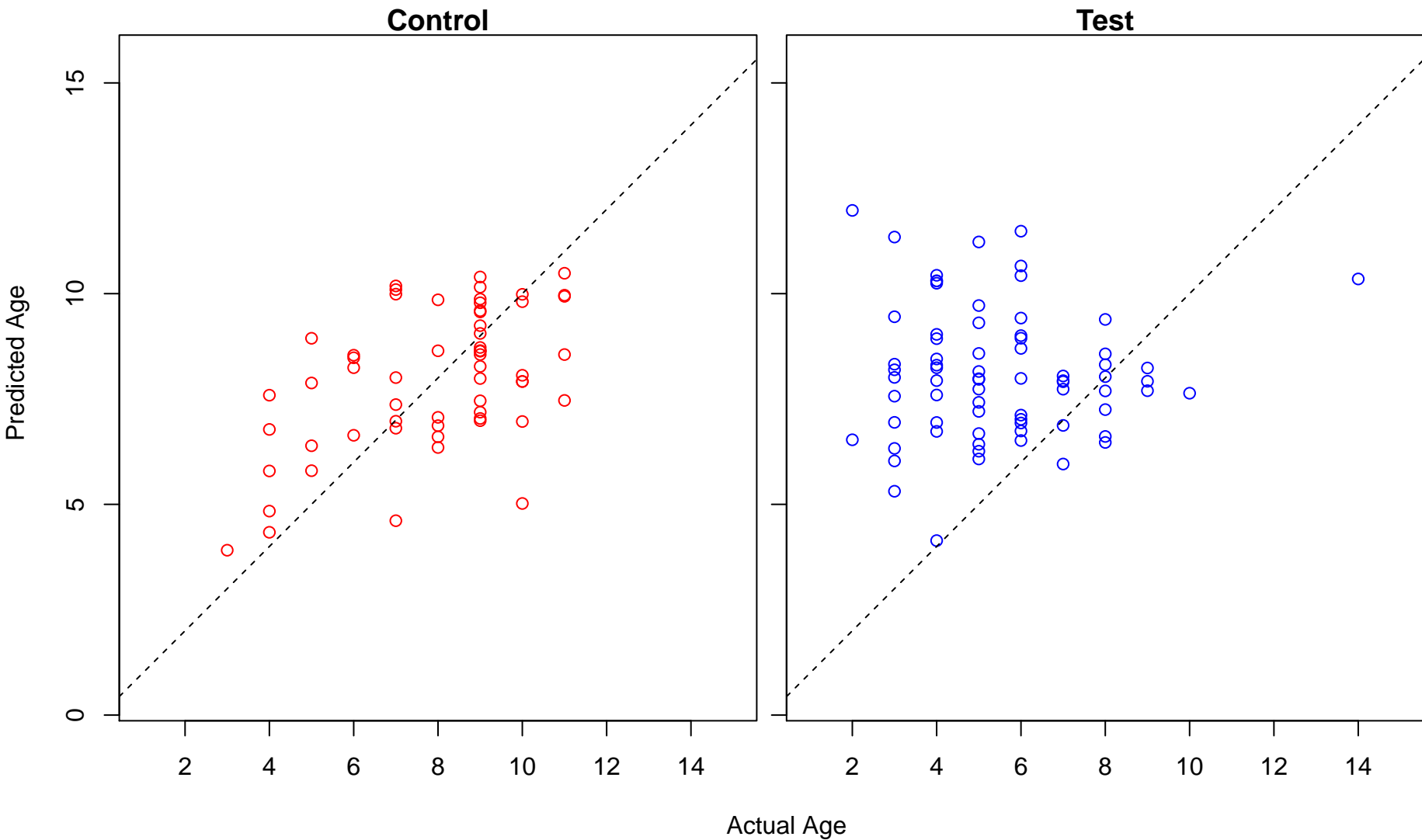
positive regulation of extrinsic apoptotic signaling pathway in absence of ligand (Score: 2.046433)



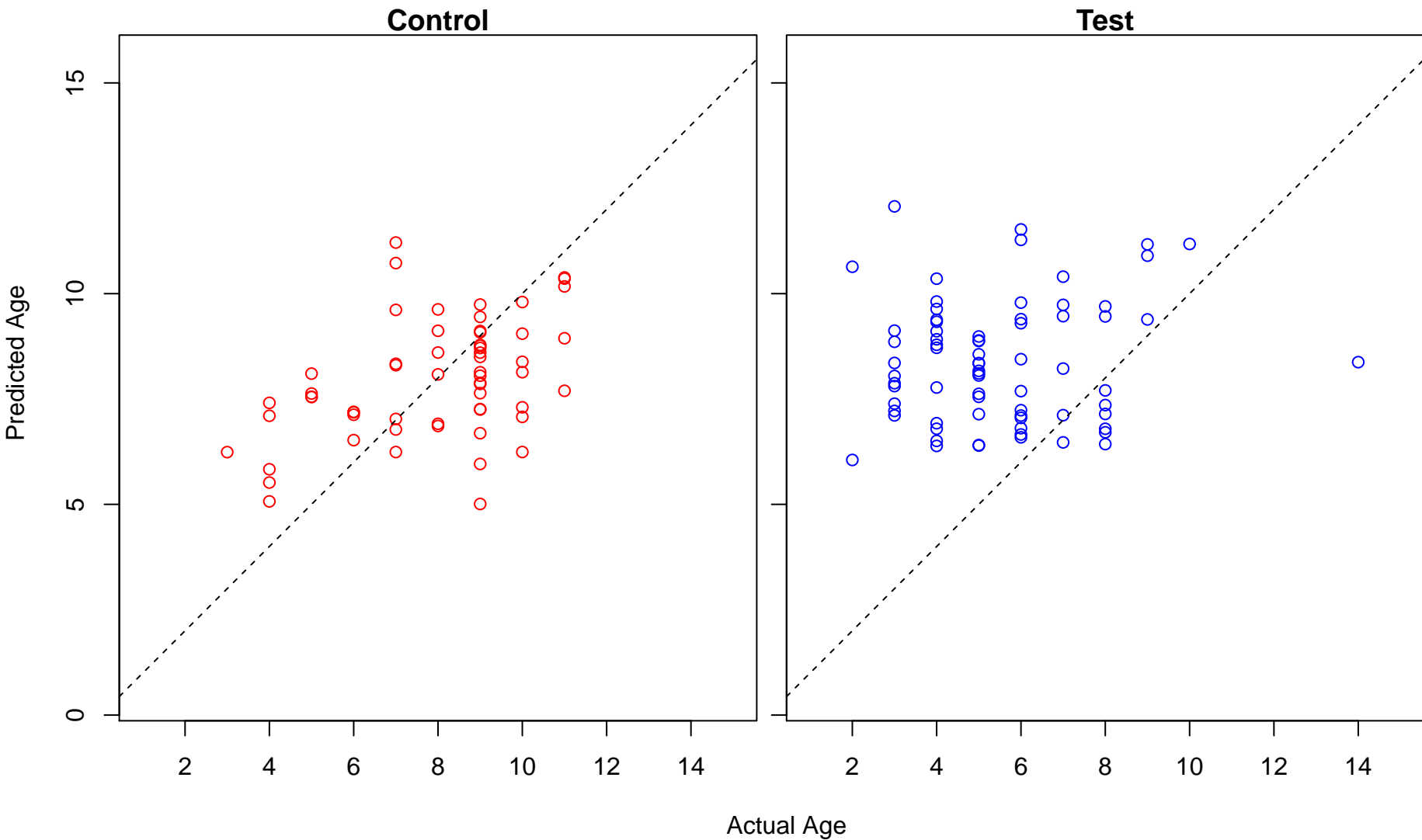
chondroitin sulfate catabolic process (Score: 2.046402)



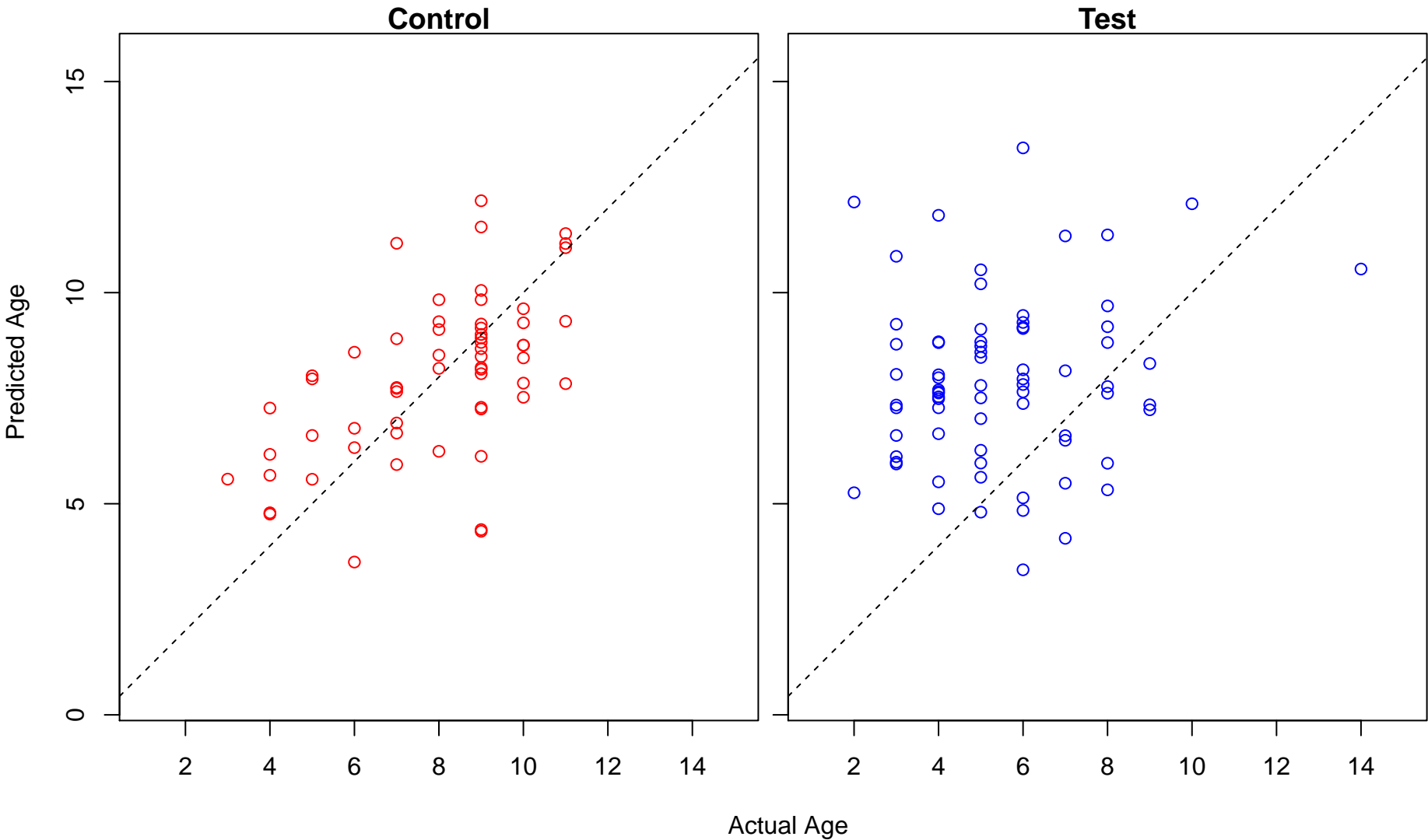
cytokine production (Score: 2.027923)



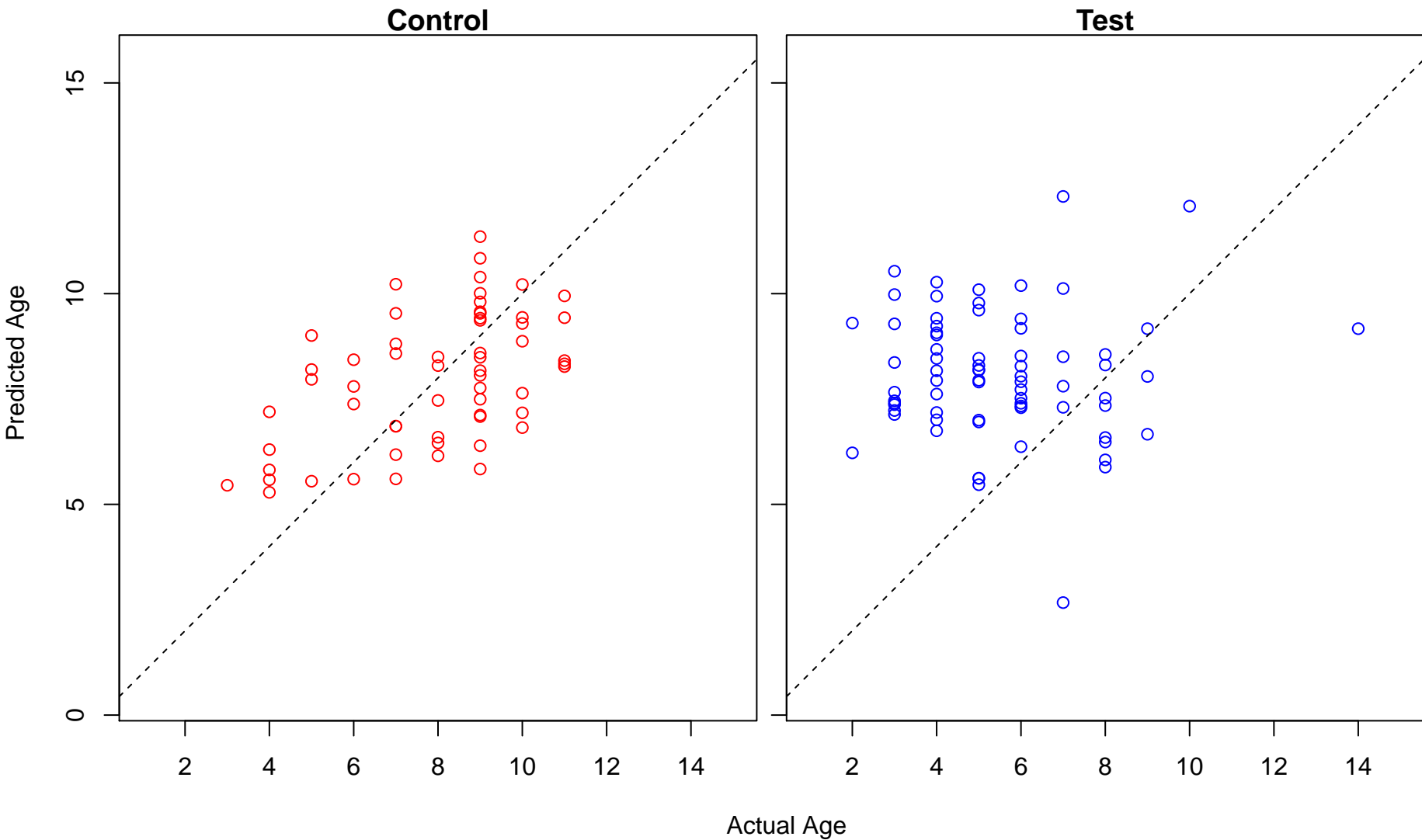
CRD-mediated mRNA stabilization (Score: 2.027406)



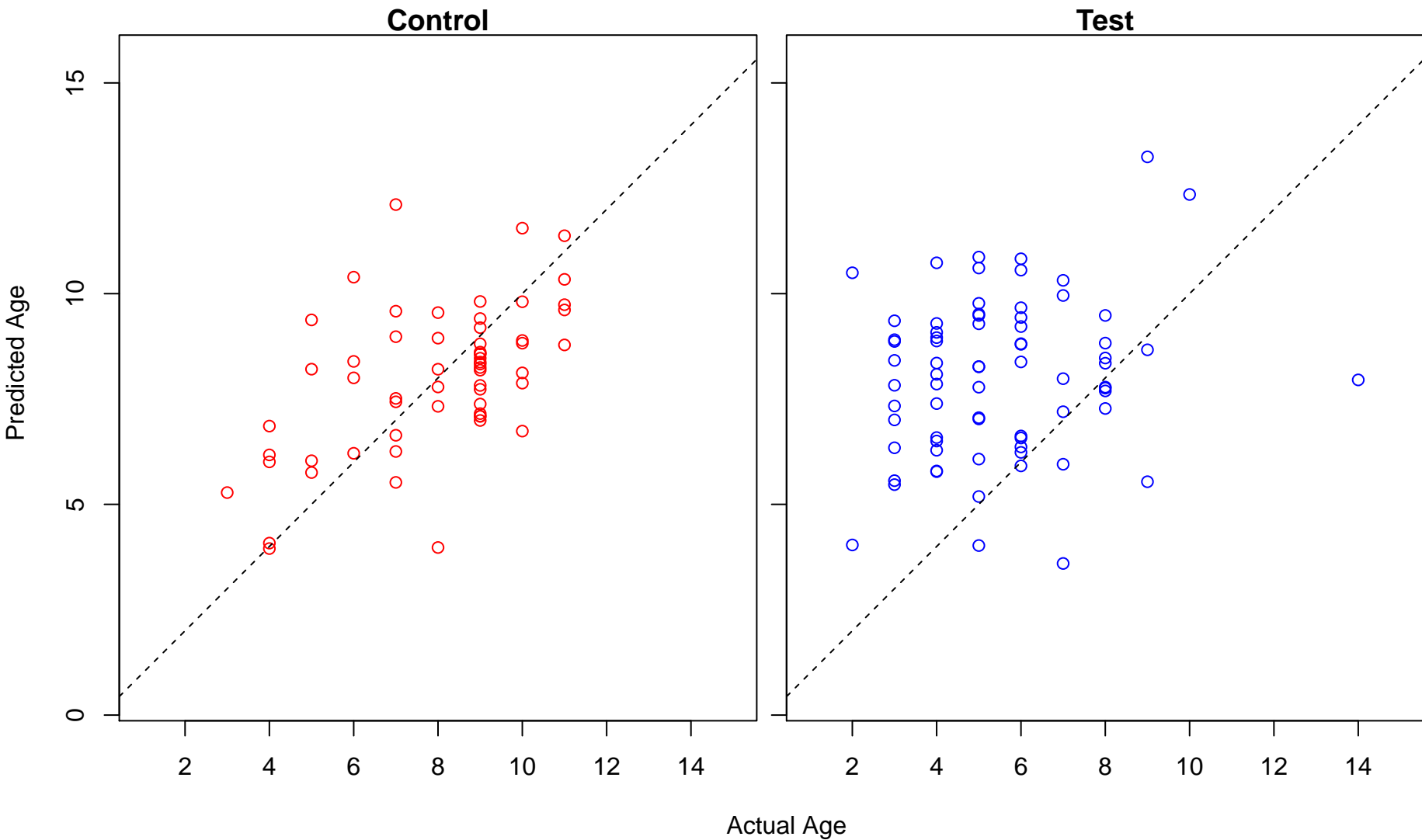
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (Score: 2.02)



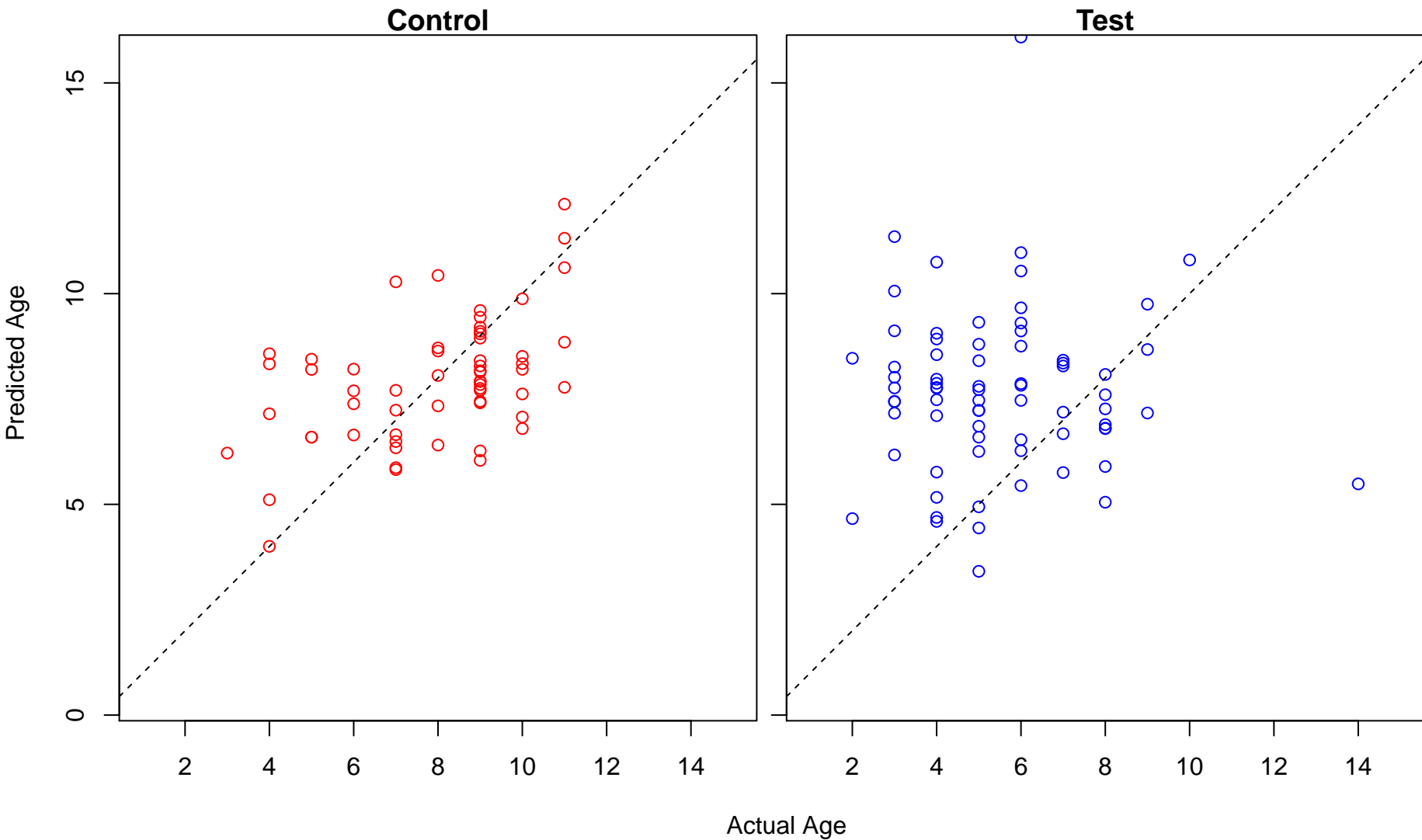
positive regulation of cell growth (Score: 2.016753)



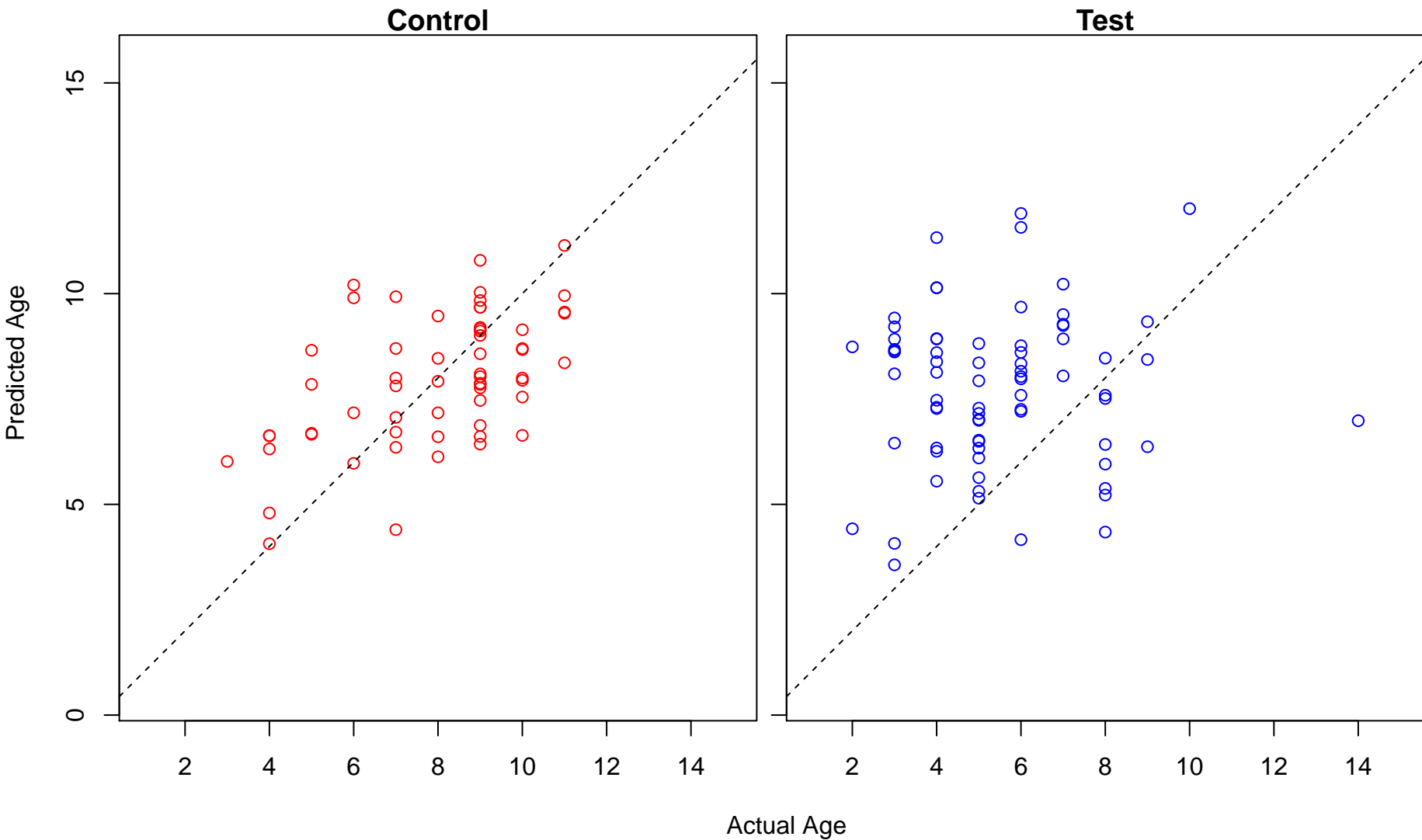
cellular transition metal ion homeostasis (Score: 2.016188)



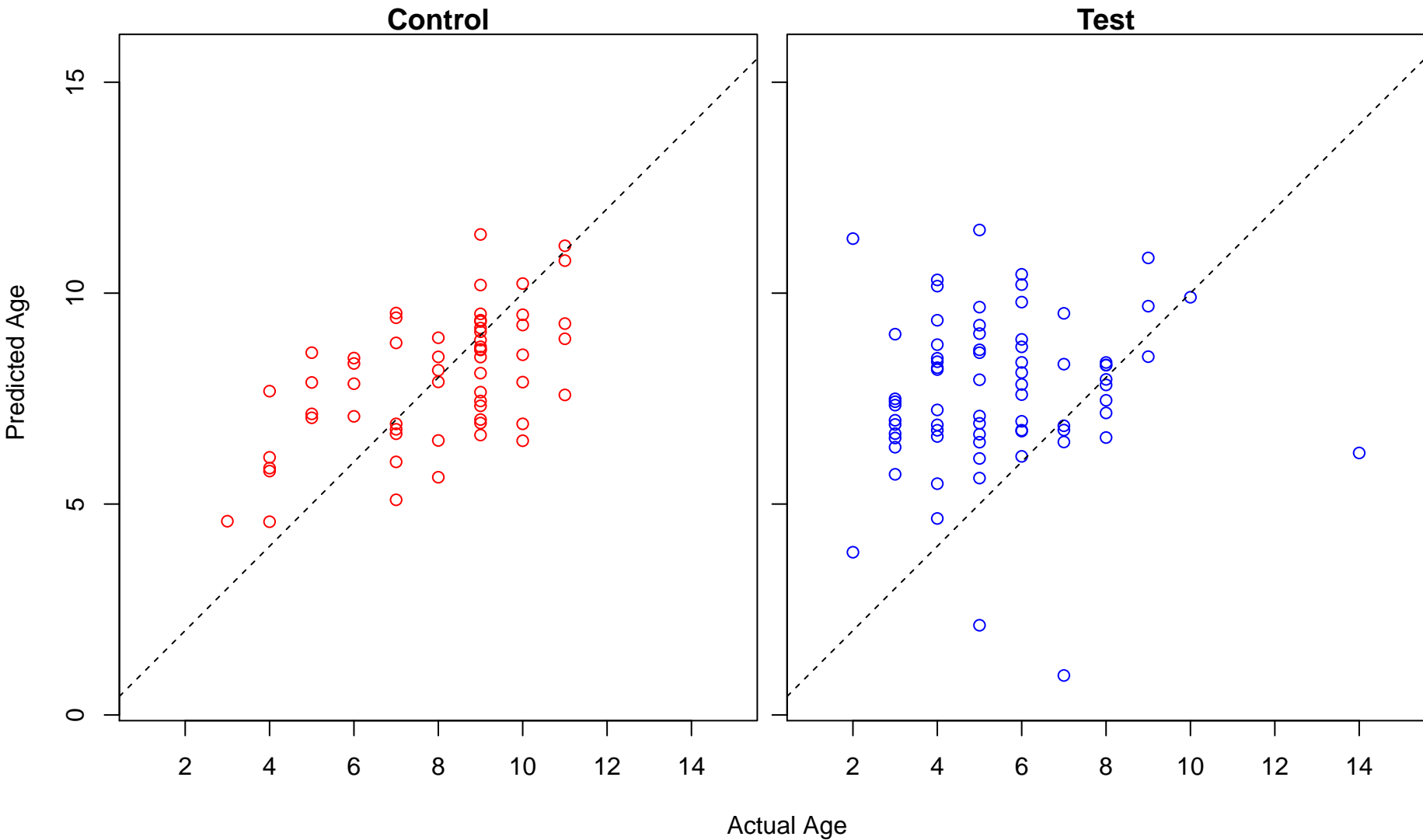
positive regulation of alpha-beta T cell differentiation (Score: 2.012015)



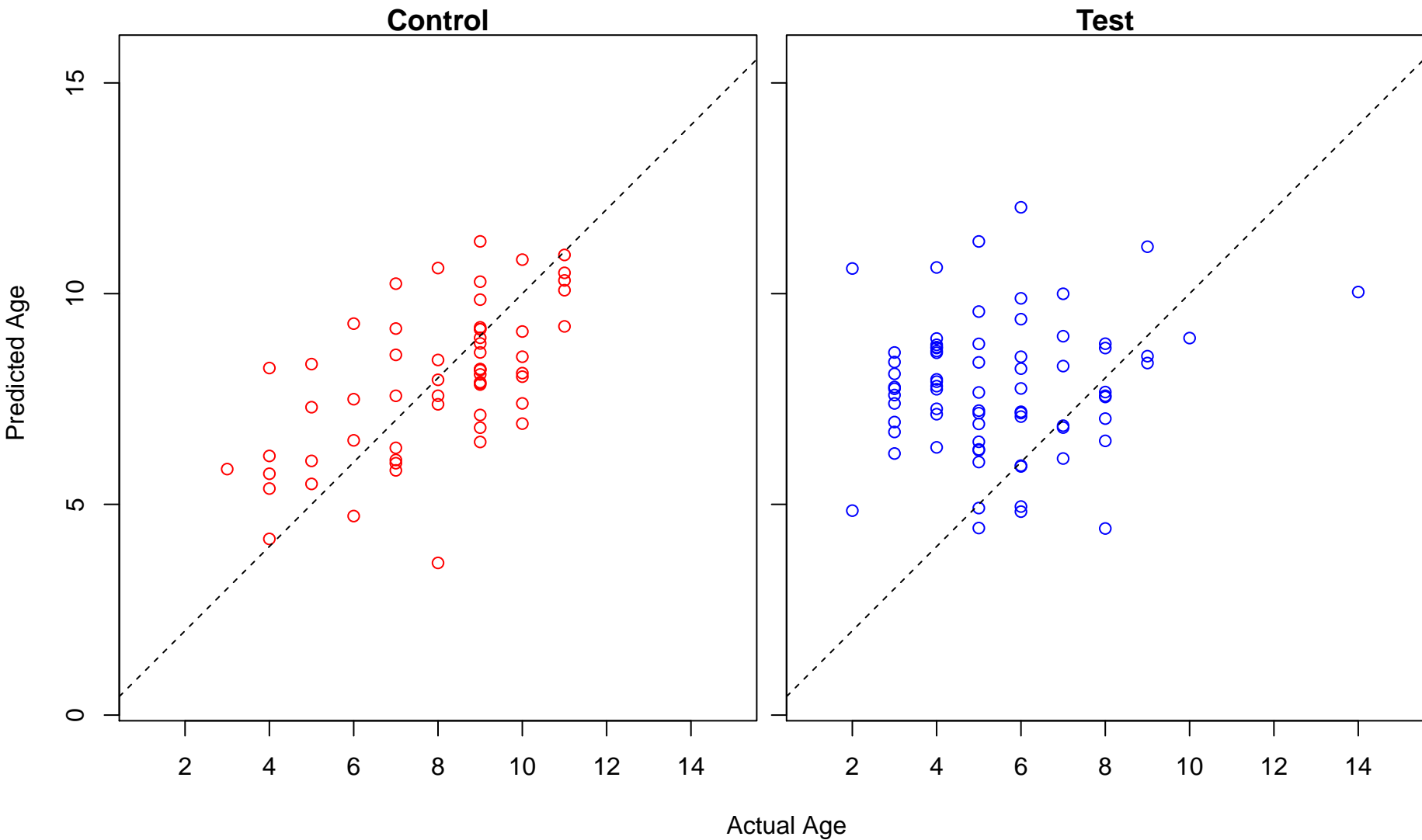
nucleus localization (Score: 2.006337)



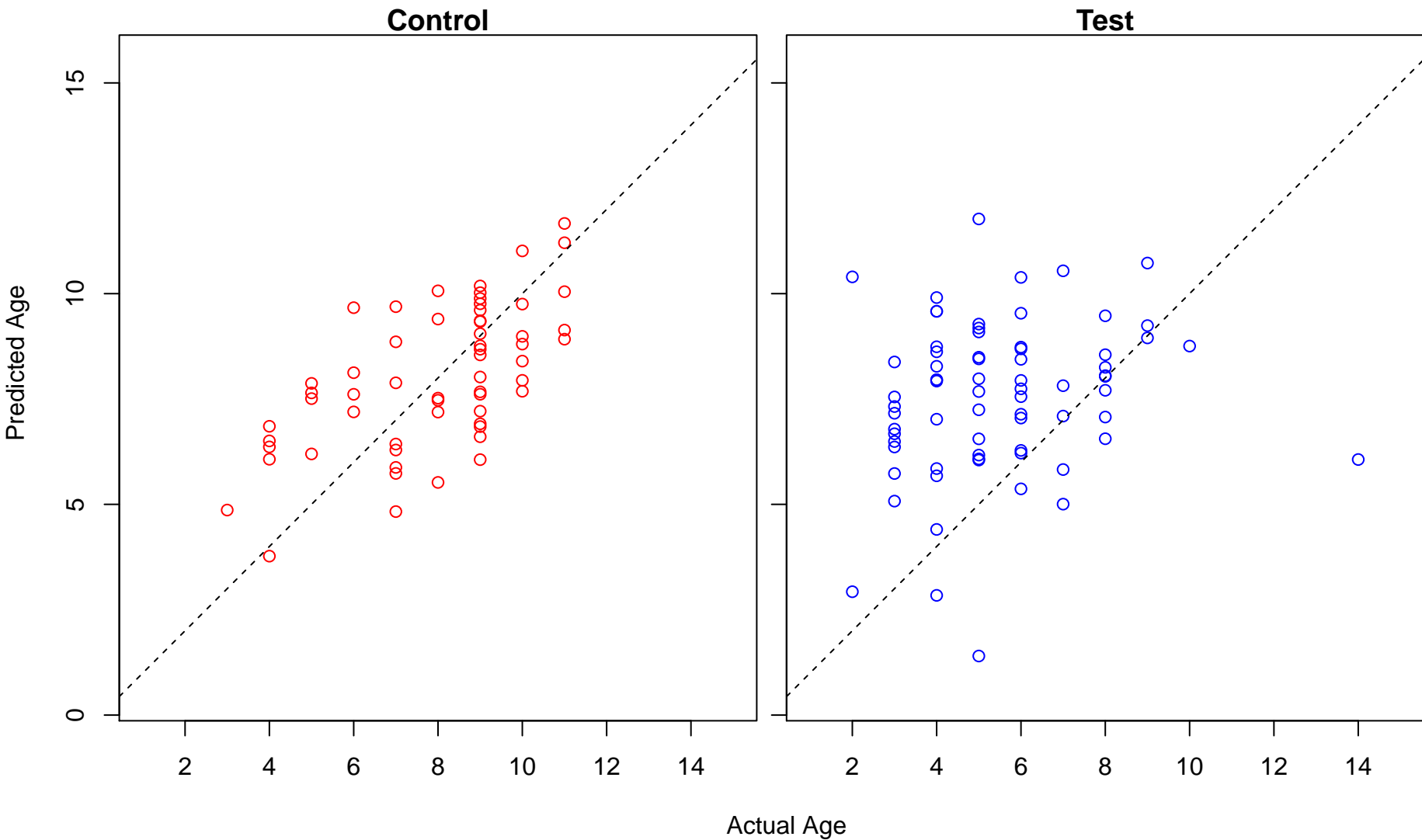
regulation of cellular macromolecule biosynthetic process (Score: 1.998632)



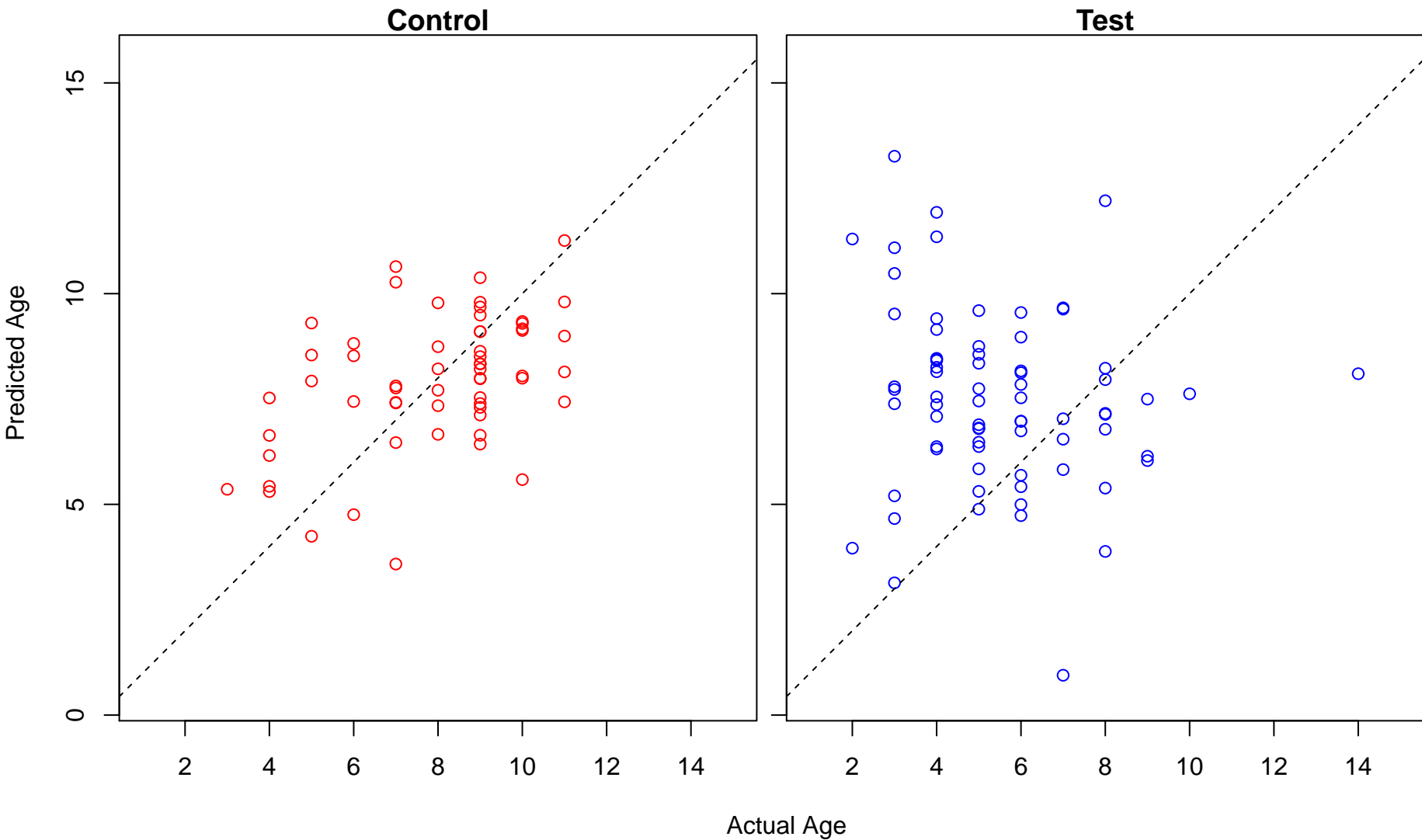
platelet degranulation (Score: 1.995507)



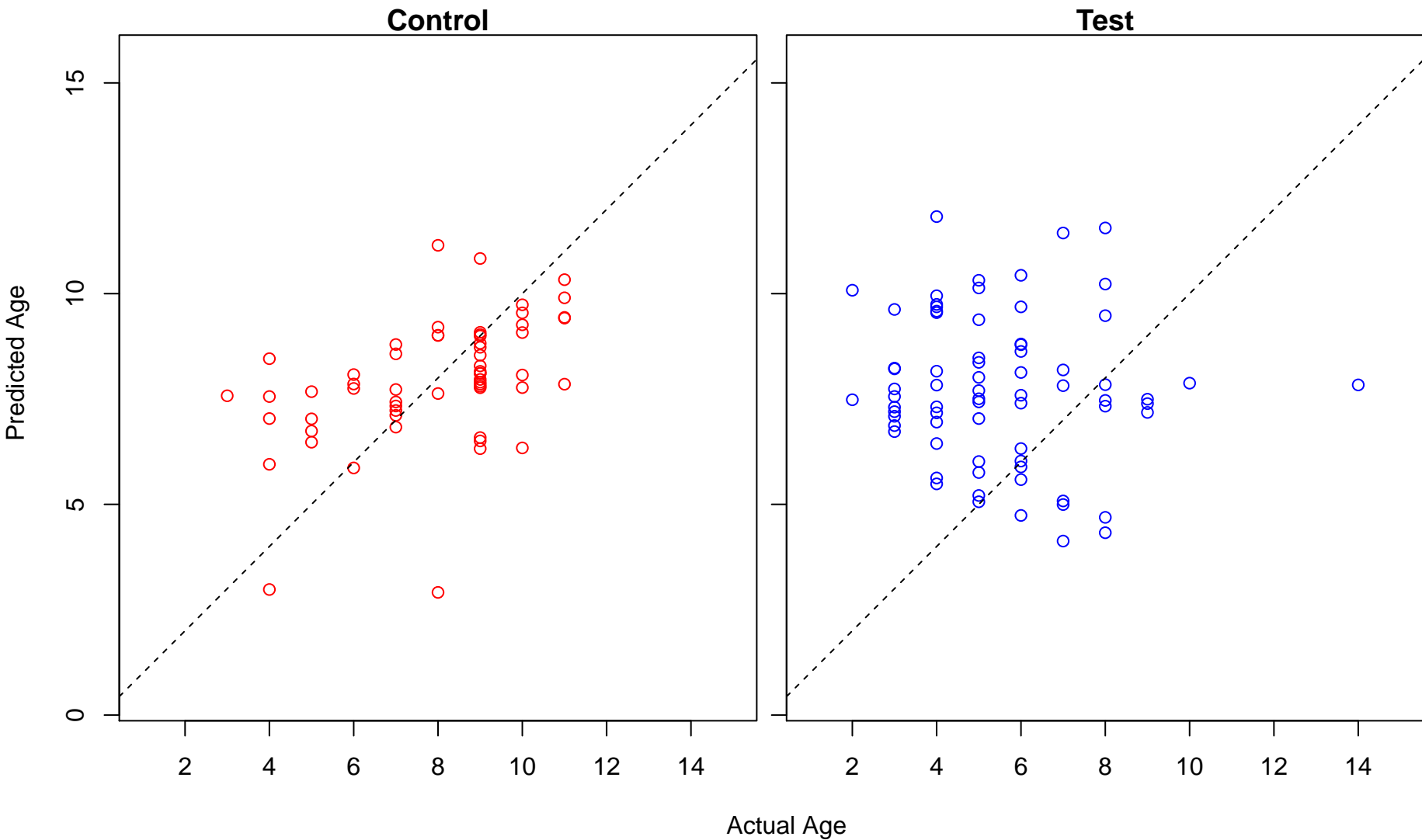
regulation of nucleobase-containing compound metabolic process (Score: 1.993934)



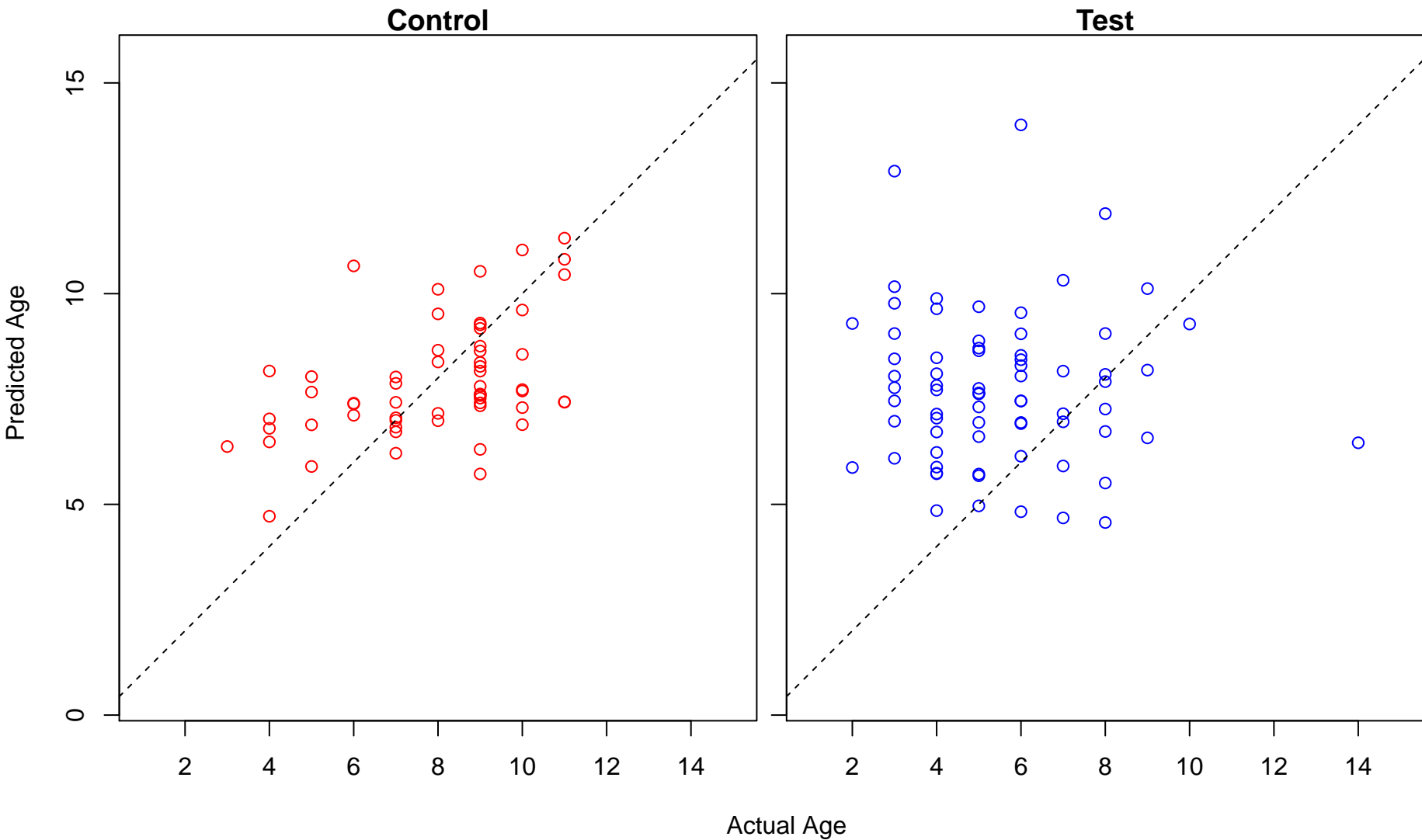
negative regulation of reproductive process (Score: 1.991862)



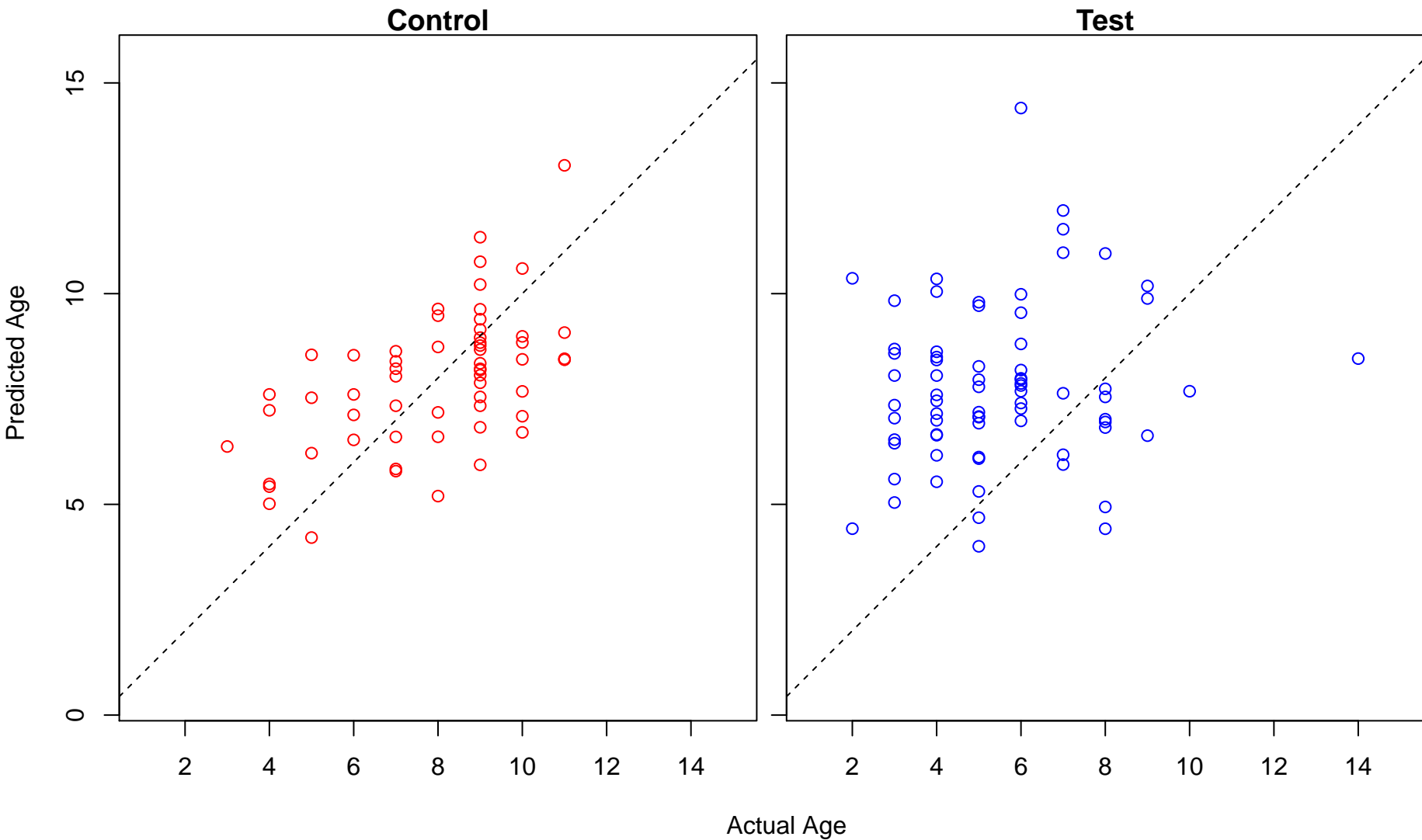
synaptic transmission, dopaminergic (Score: 1.988237)



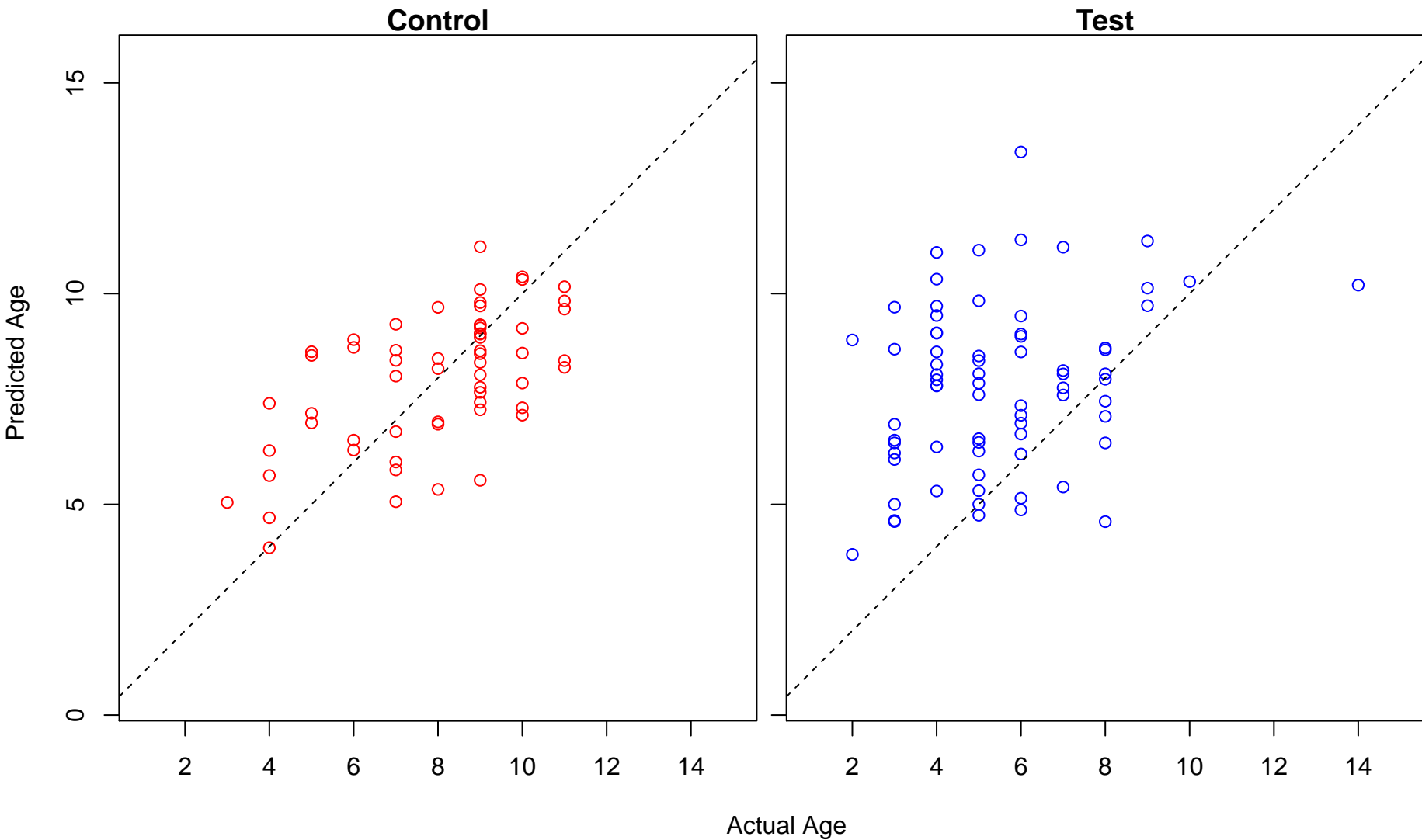
actin filament reorganization (Score: 1.98359)



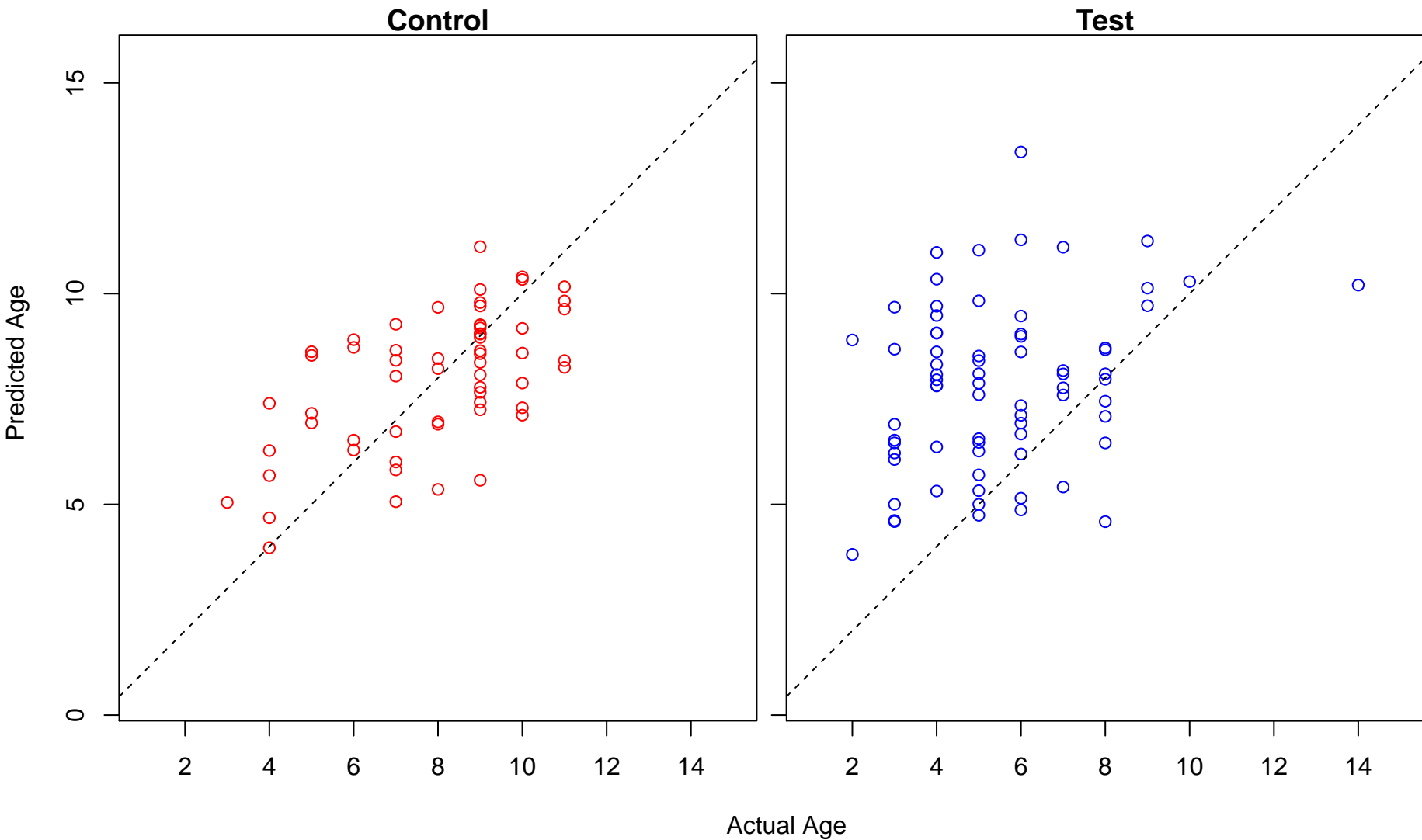
regulation of activated T cell proliferation (Score: 1.978984)



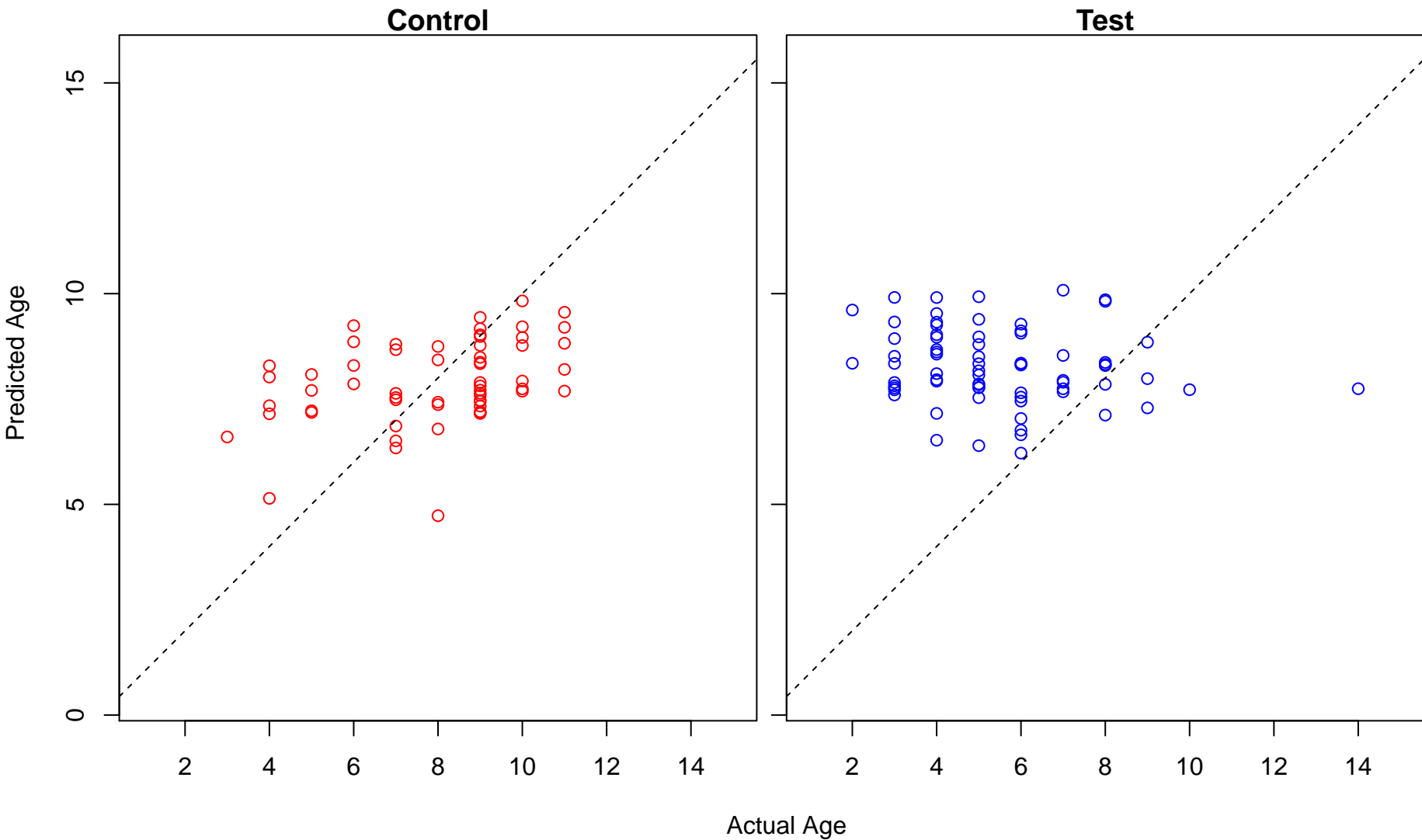
chemotaxis (Score: 1.974711)



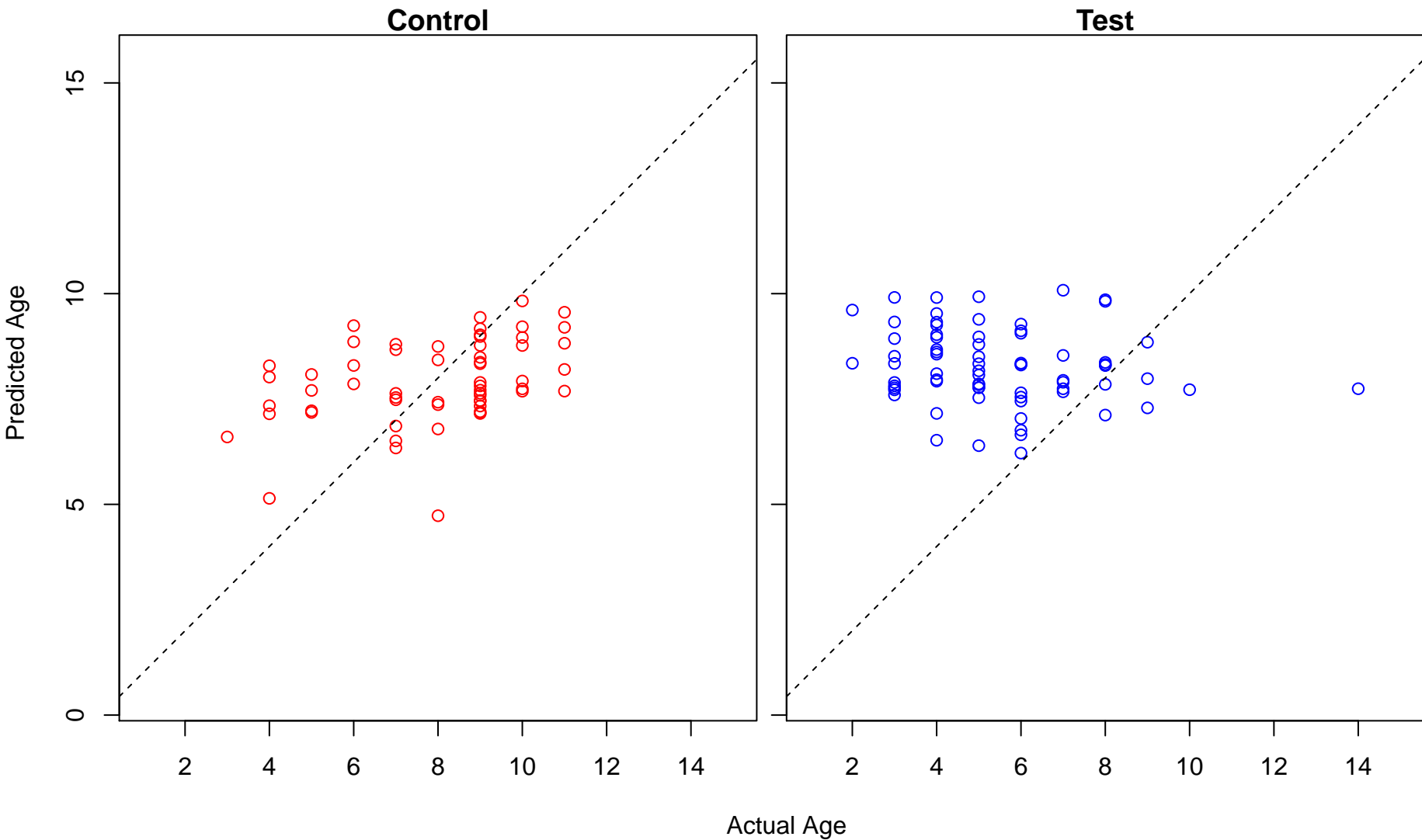
taxis (Score: 1.974711)



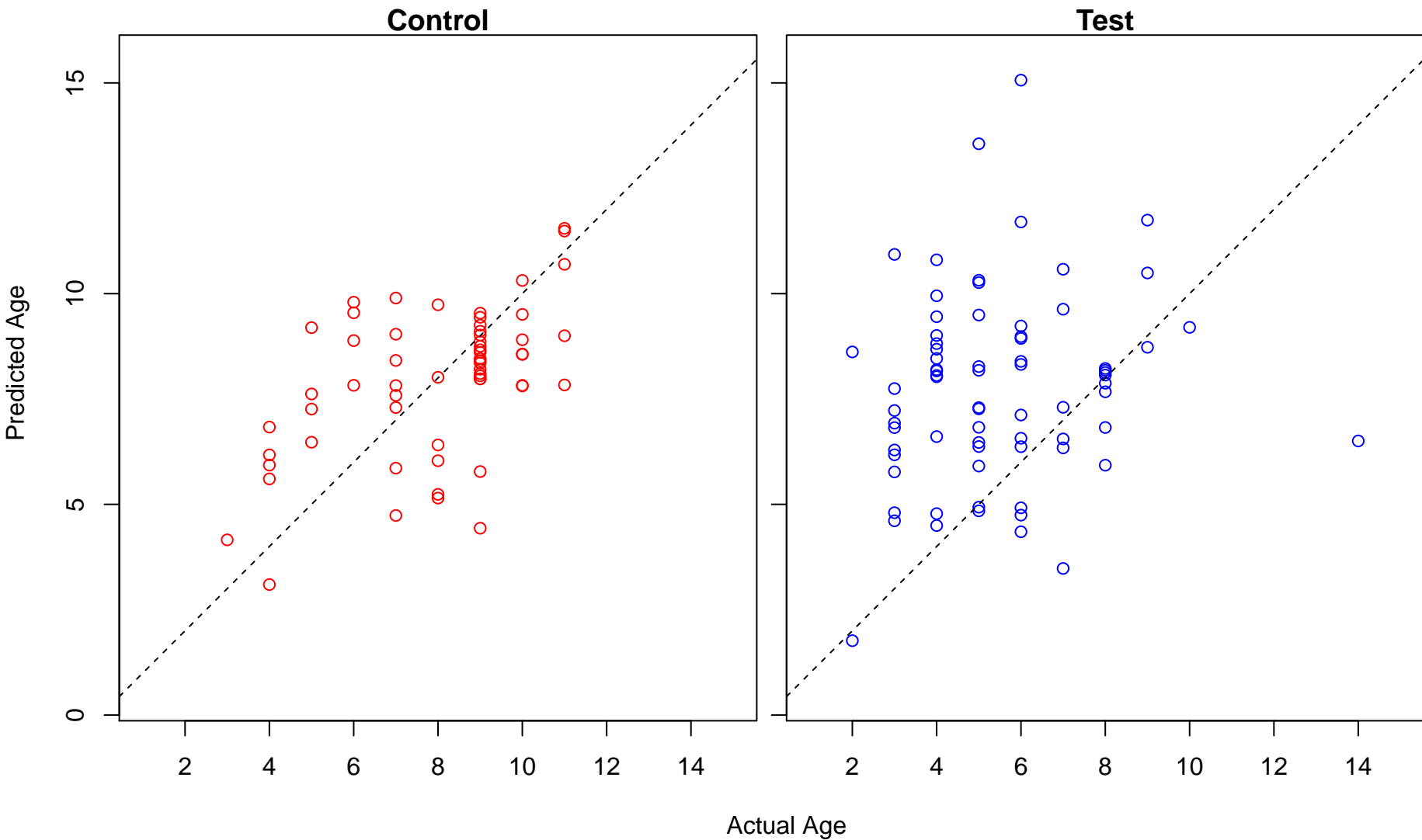
hemoglobin metabolic process (Score: 1.972210)



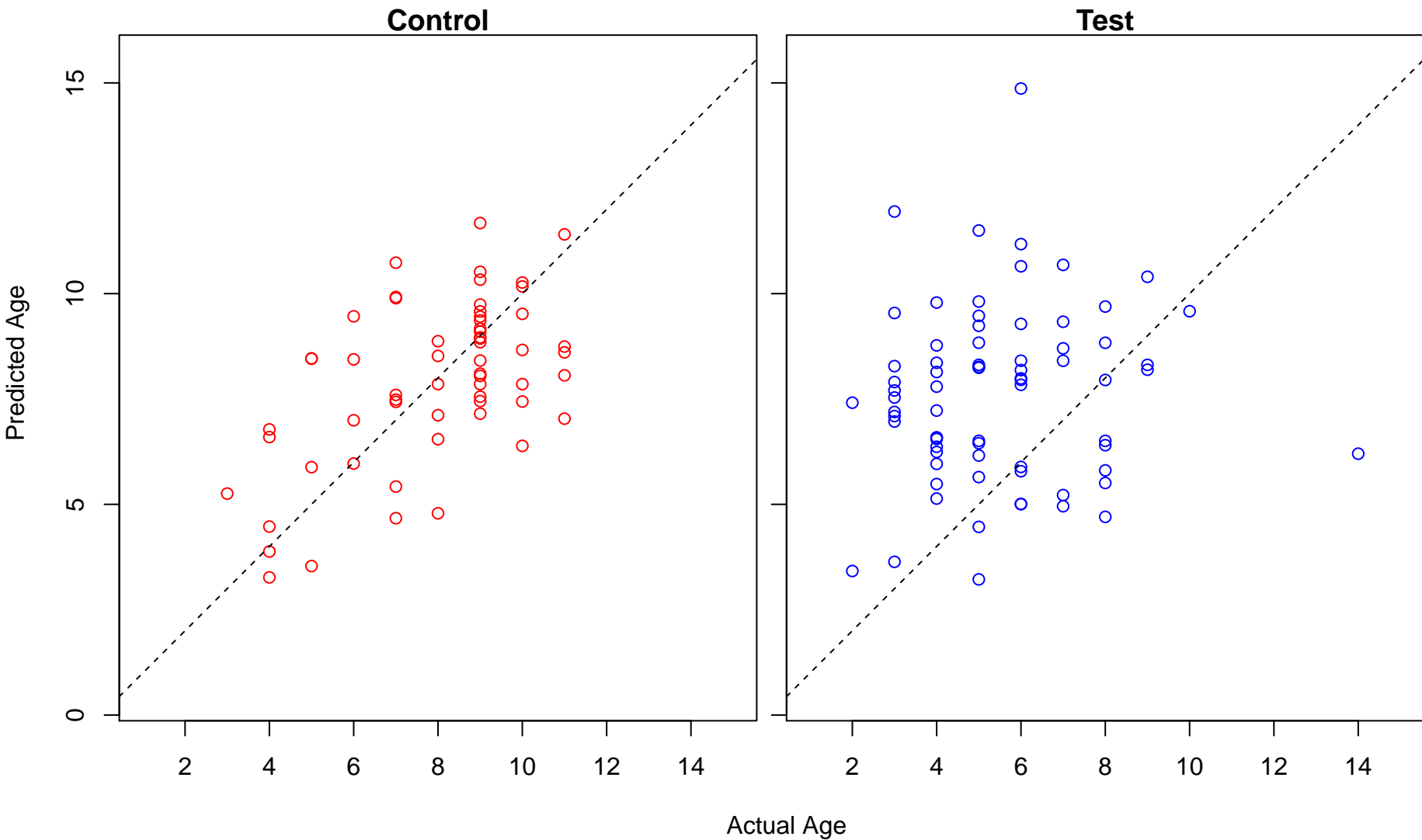
hemoglobin biosynthetic process (Score: 1.972210)



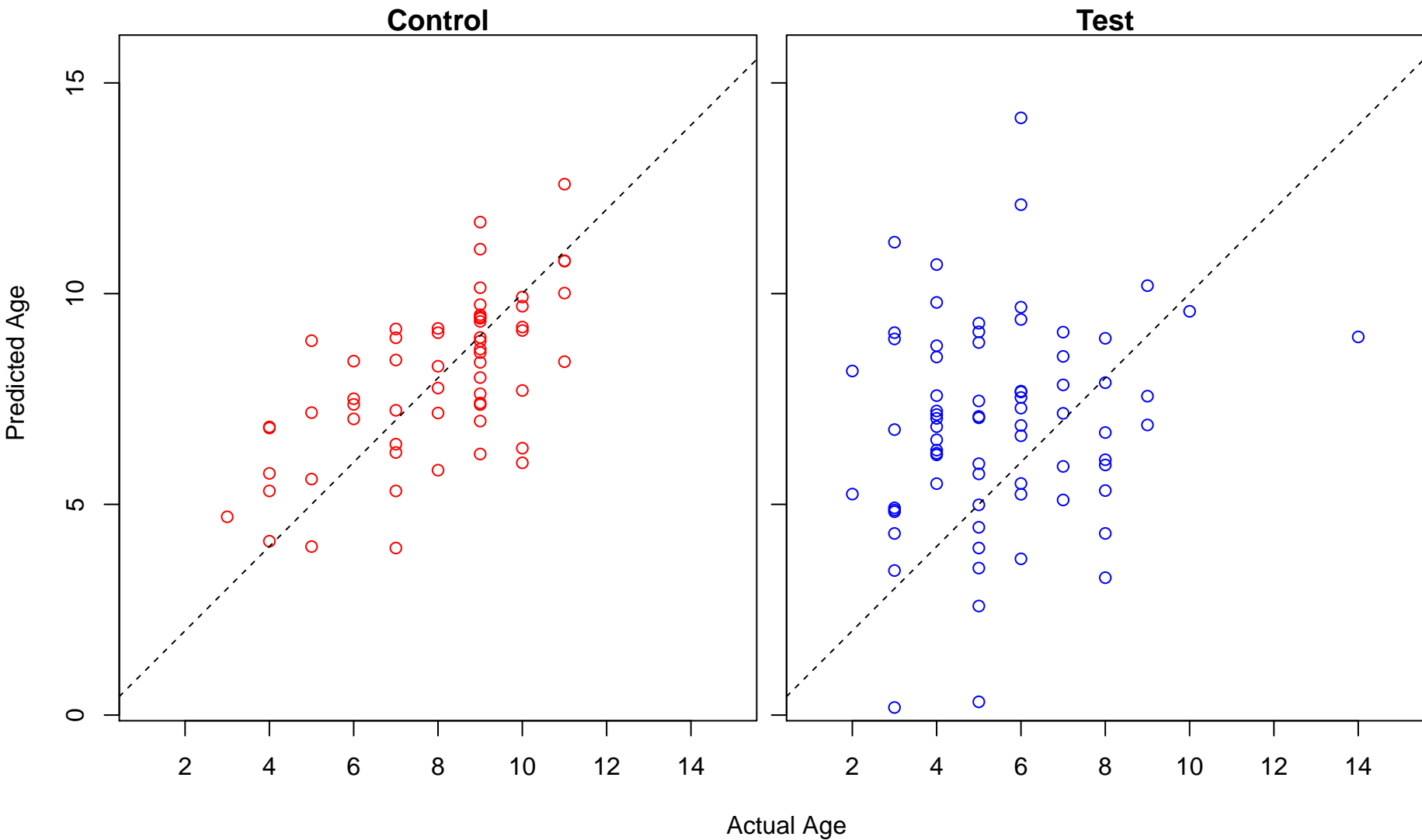
insulin receptor signaling pathway (Score: 1.968942)



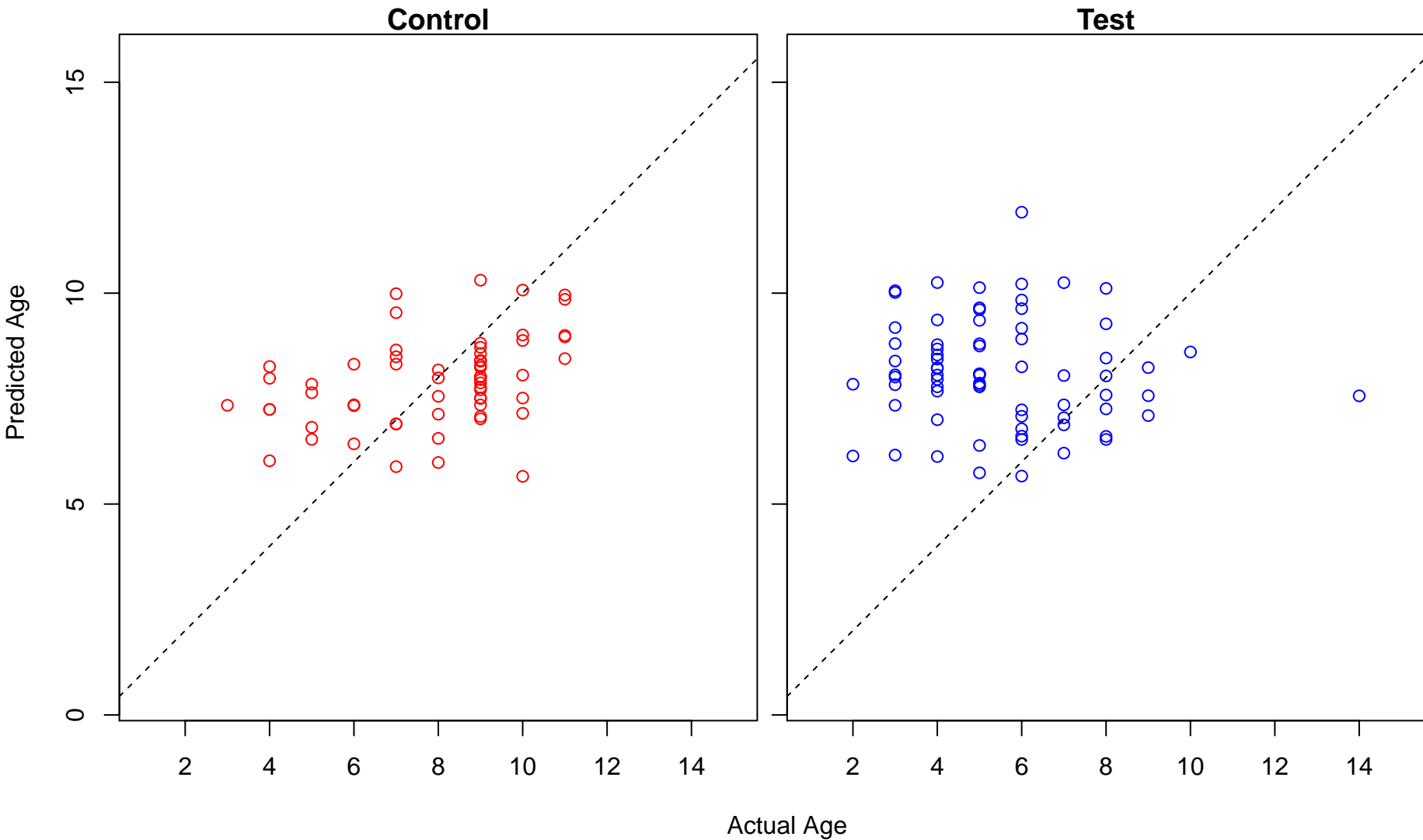
sulfur compound catabolic process (Score: 1.964168)



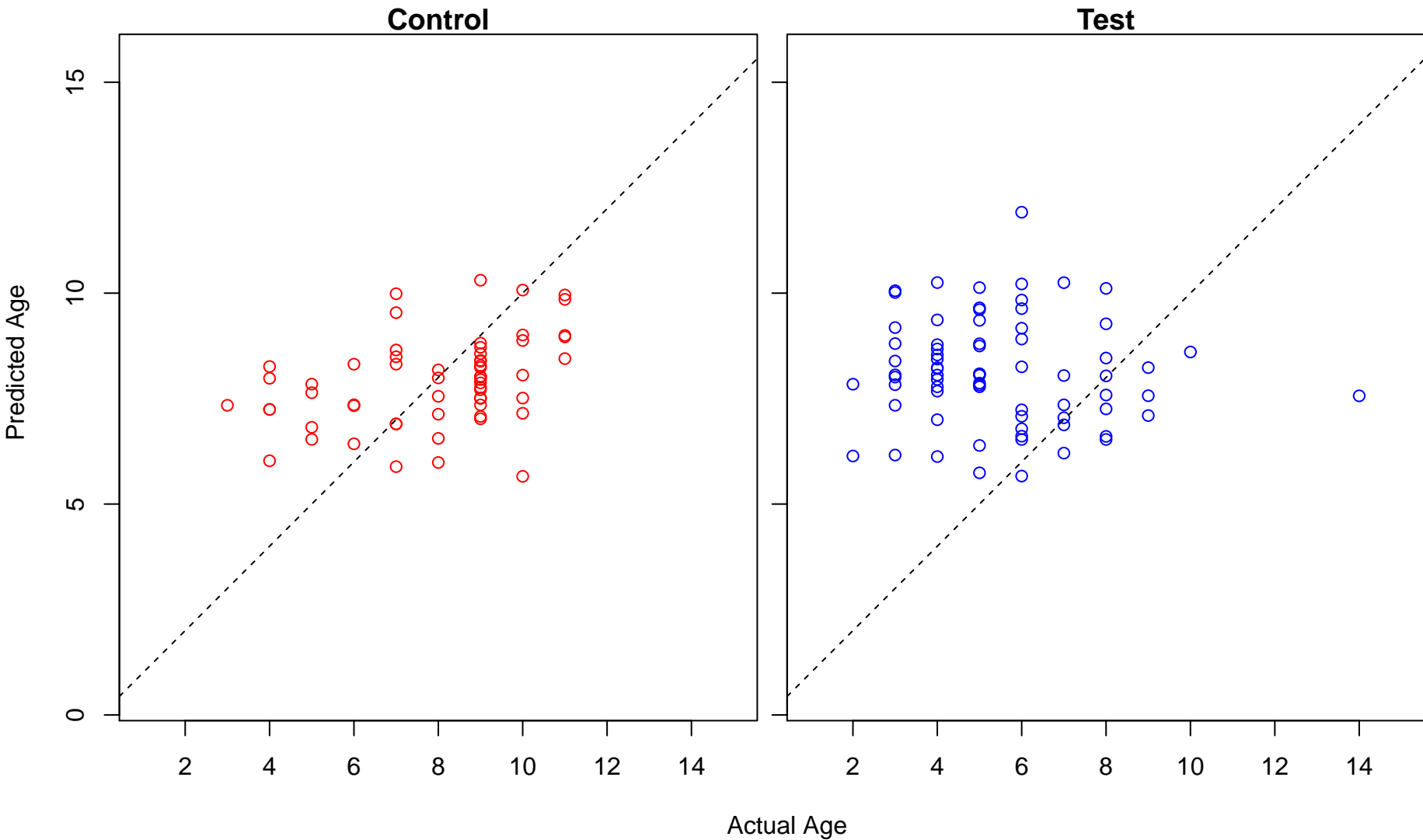
morphogenesis of an epithelial bud (Score: 1.962387)



protein insertion into ER membrane (Score: 1.956970)

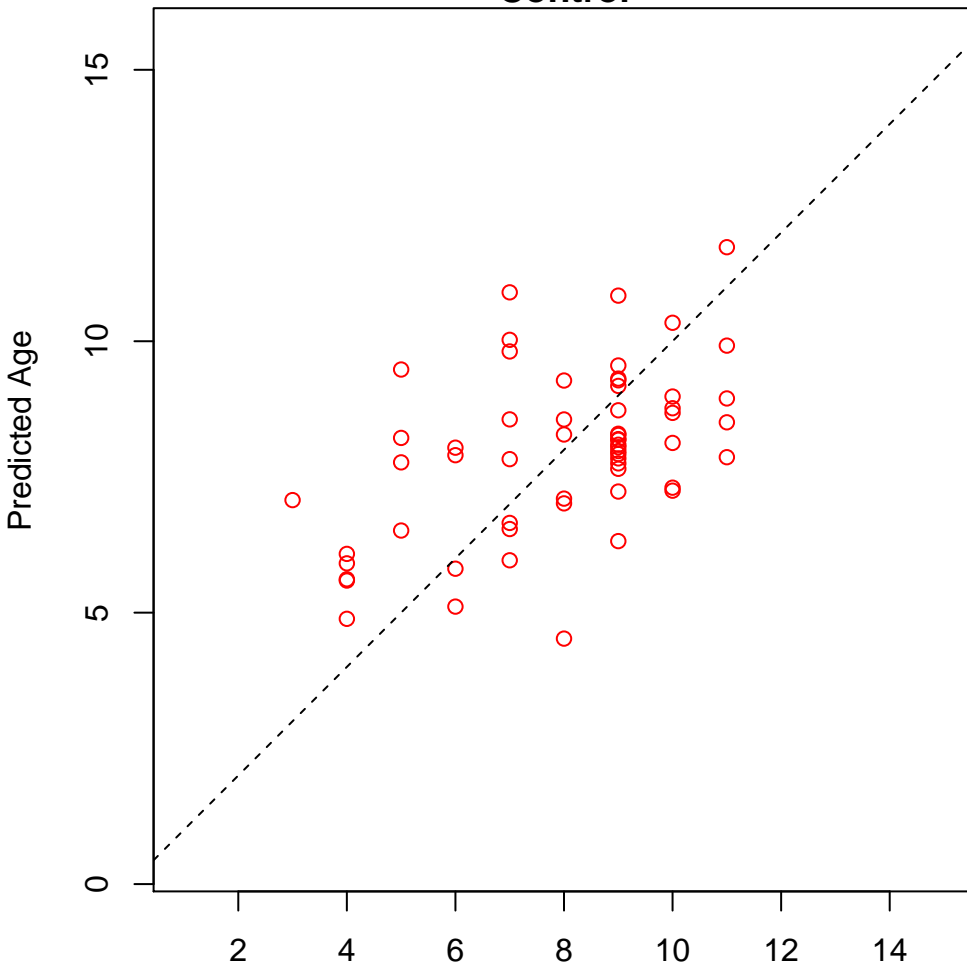


tail-anchored membrane protein insertion into ER membrane (Score: 1.956970)

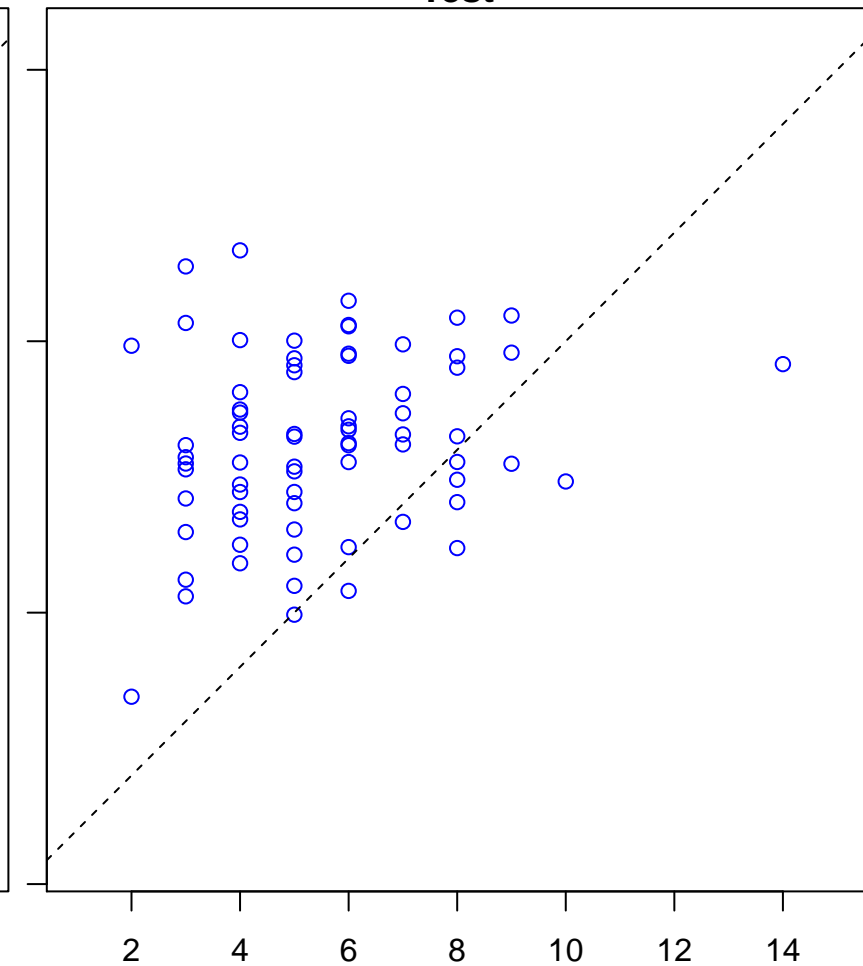


morphogenesis of an epithelial sheet (Score: 1.947765)

Control

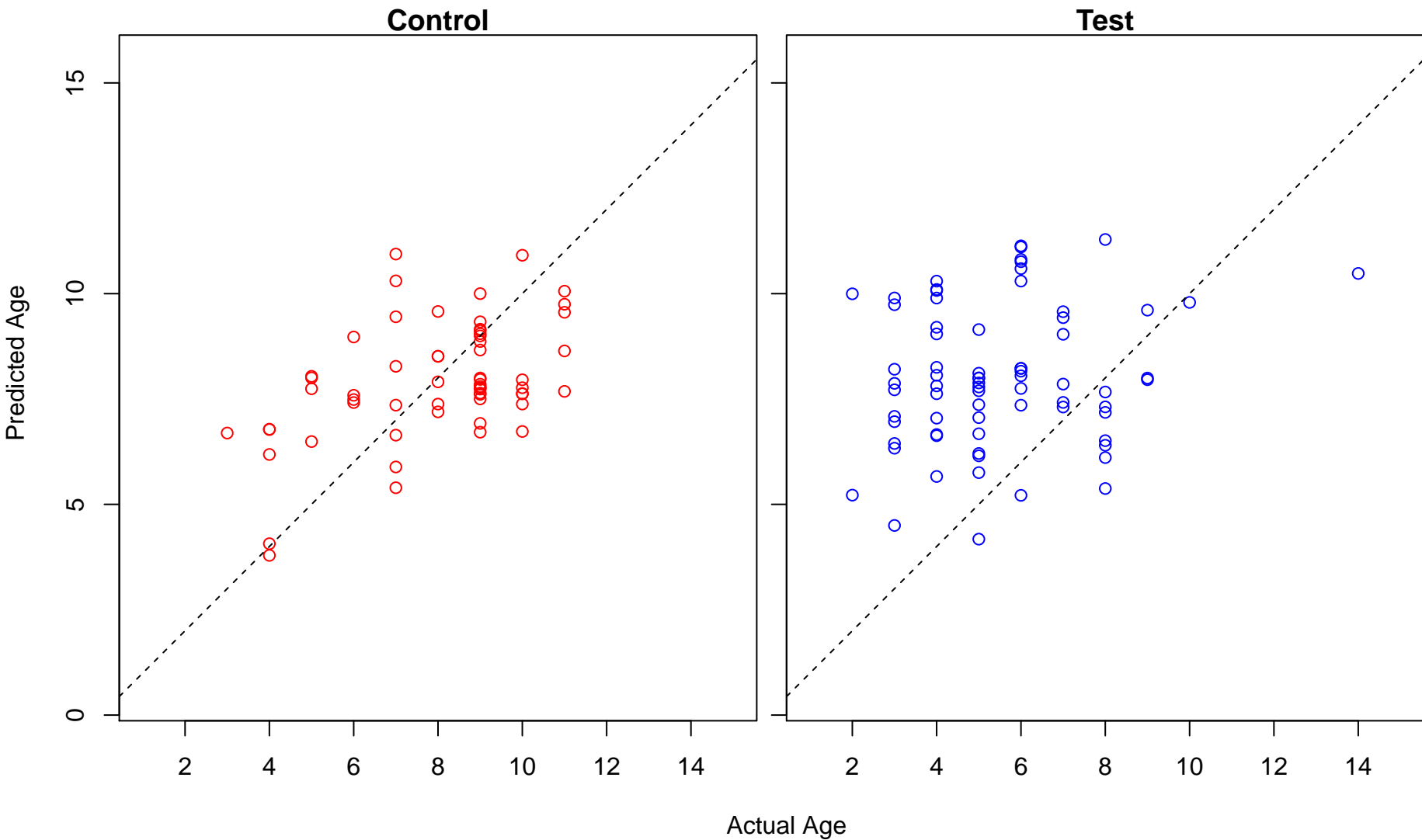


Test

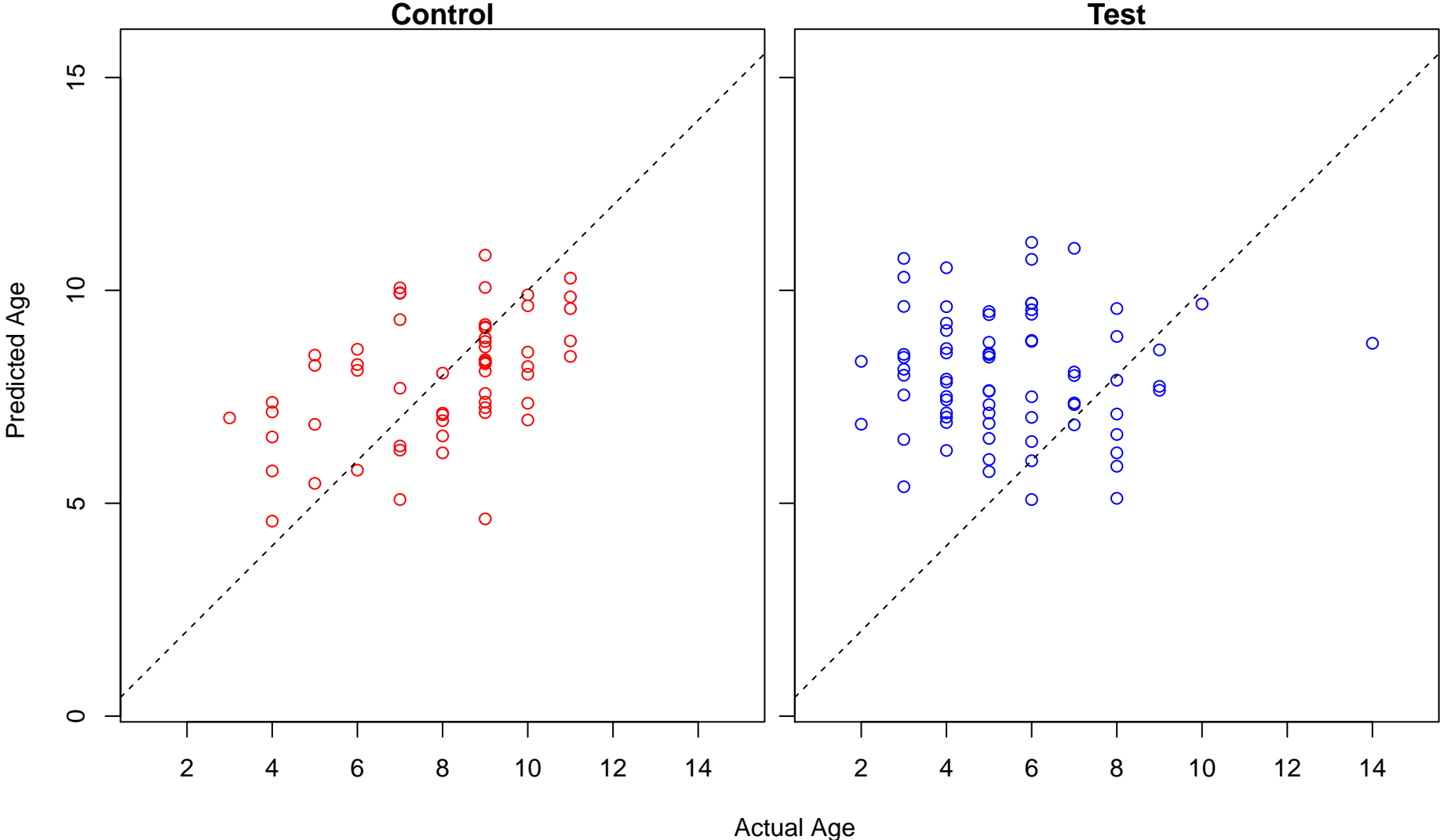


Actual Age

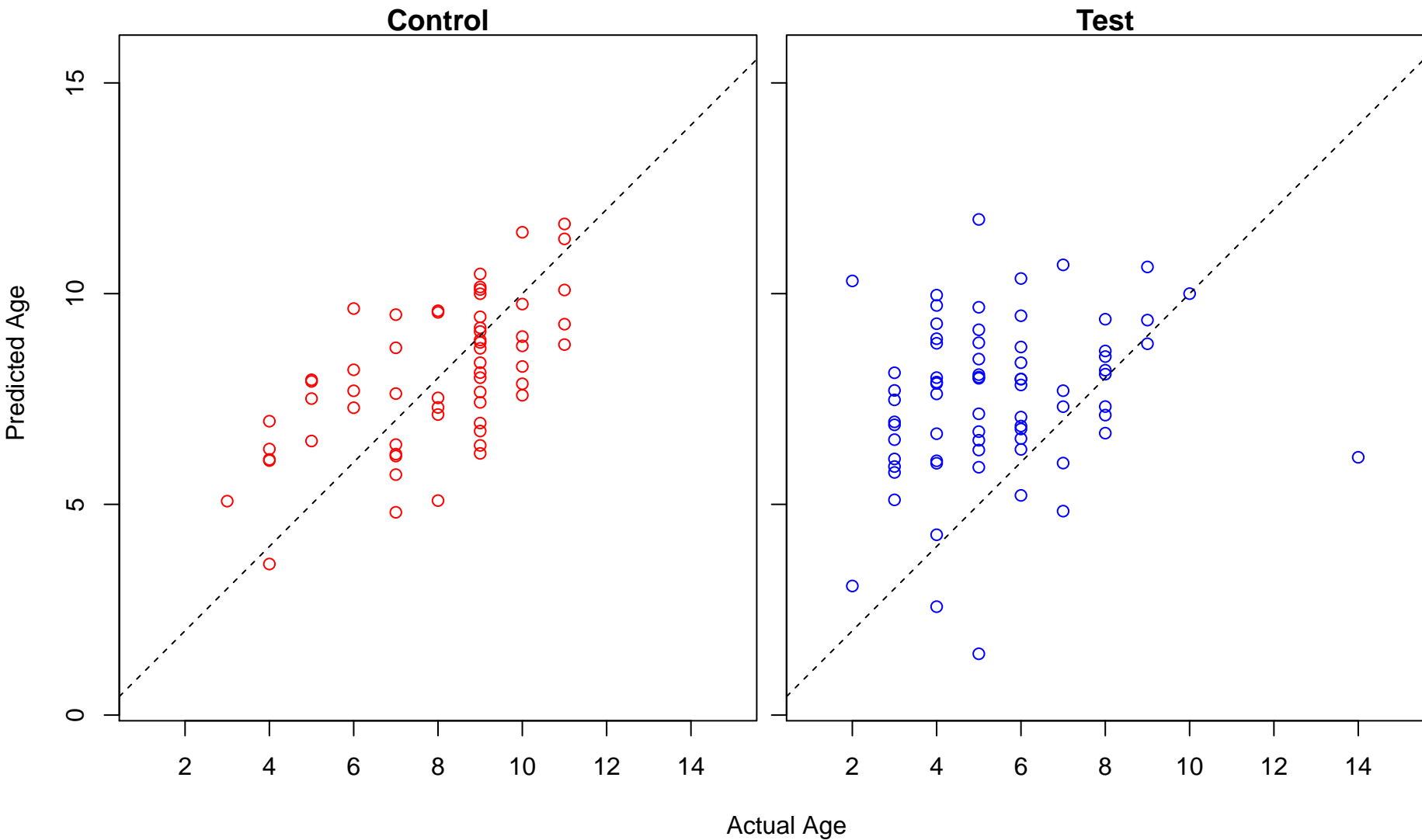
regulation of Ras protein signal transduction (Score: 1.947529)



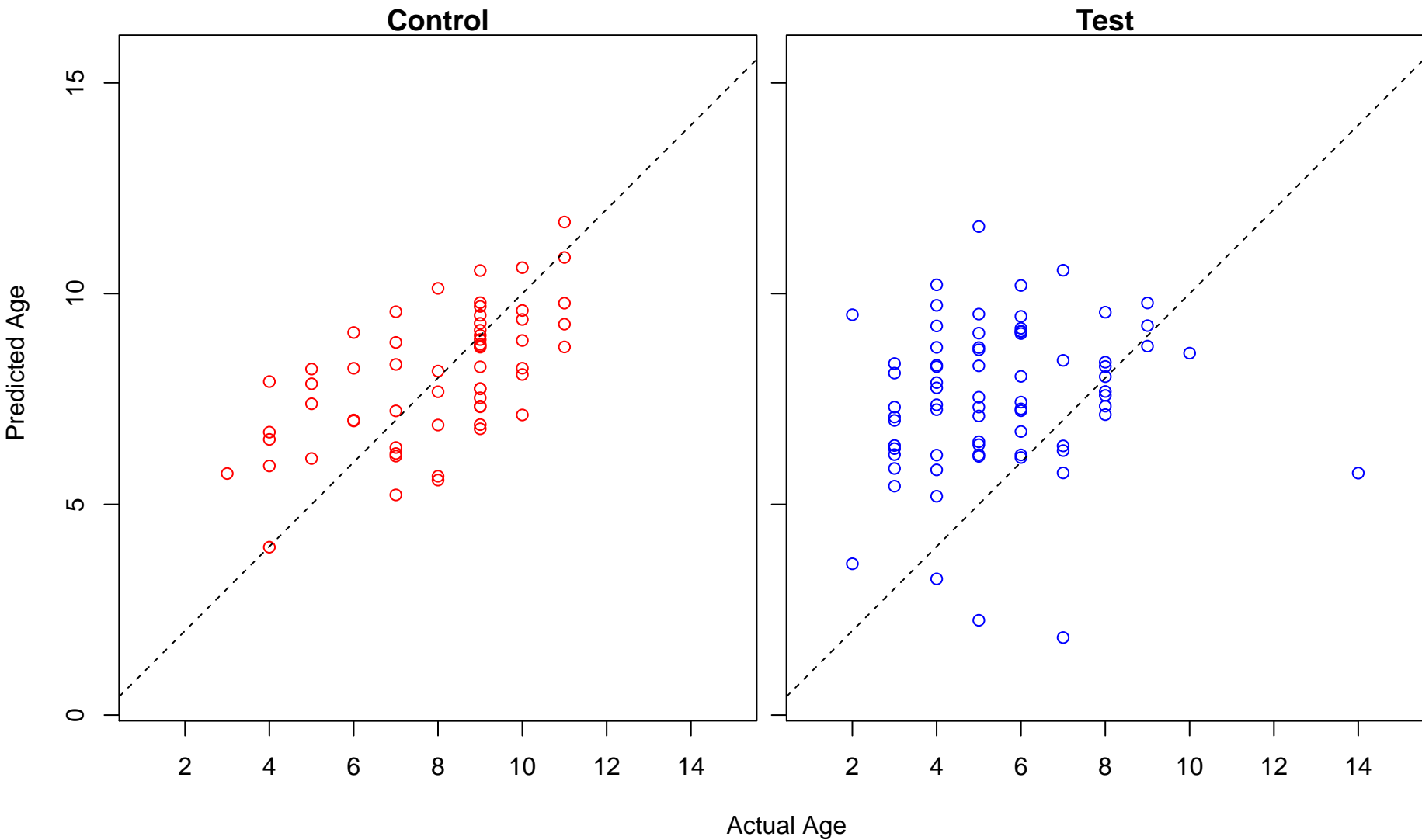
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (Score: 1.943)



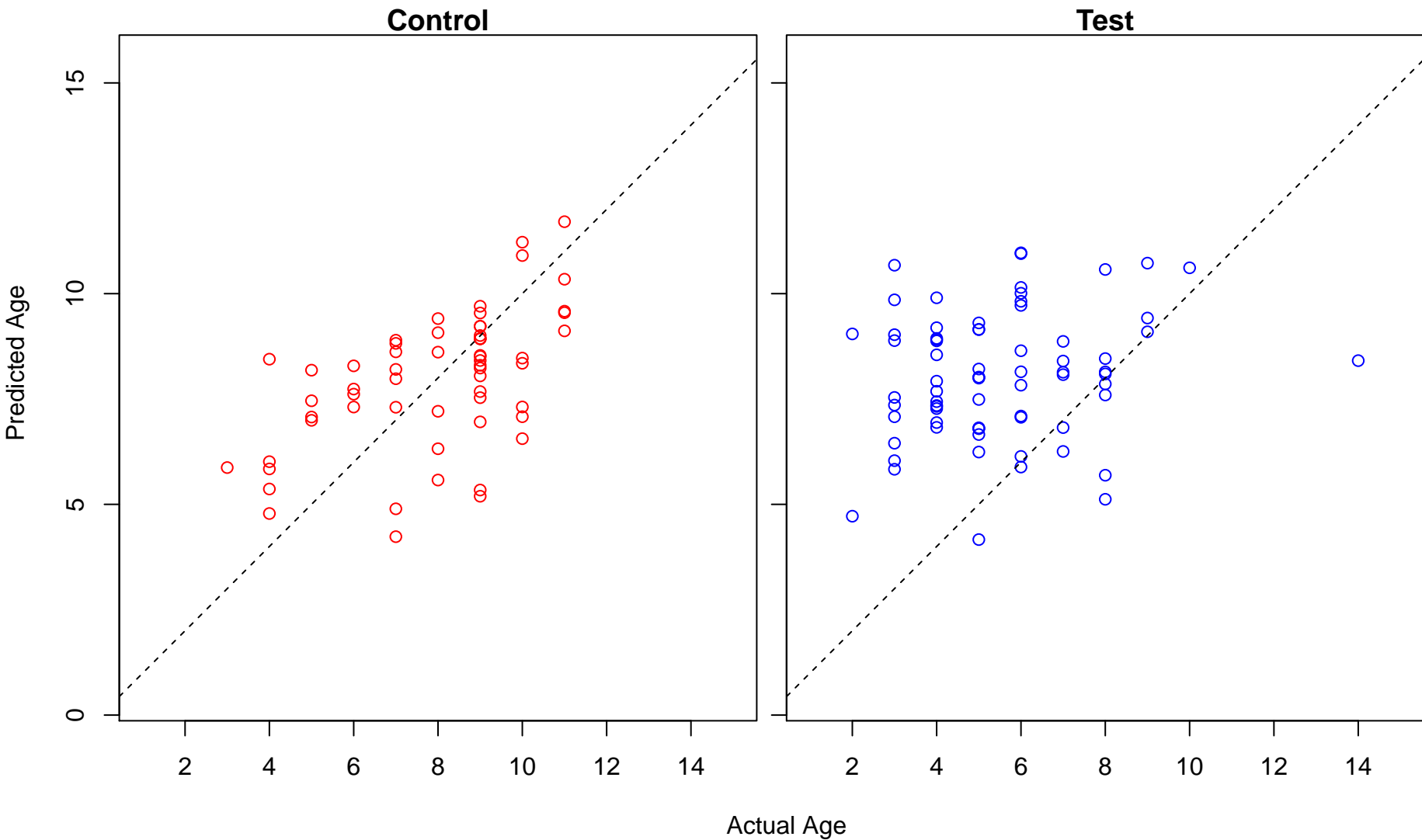
regulation of RNA metabolic process (Score: 1.943862)



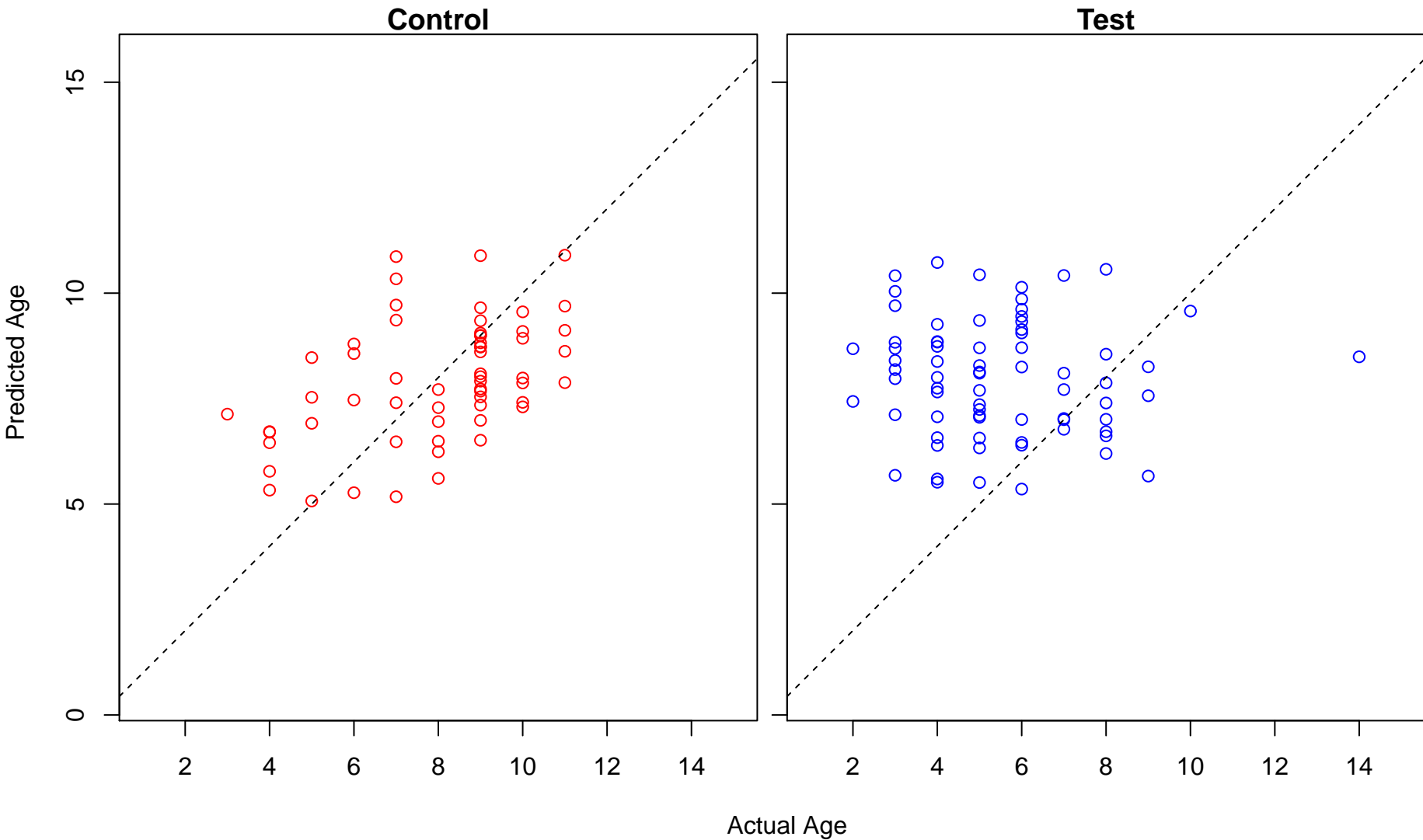
regulation of macromolecule metabolic process (Score: 1.943820)



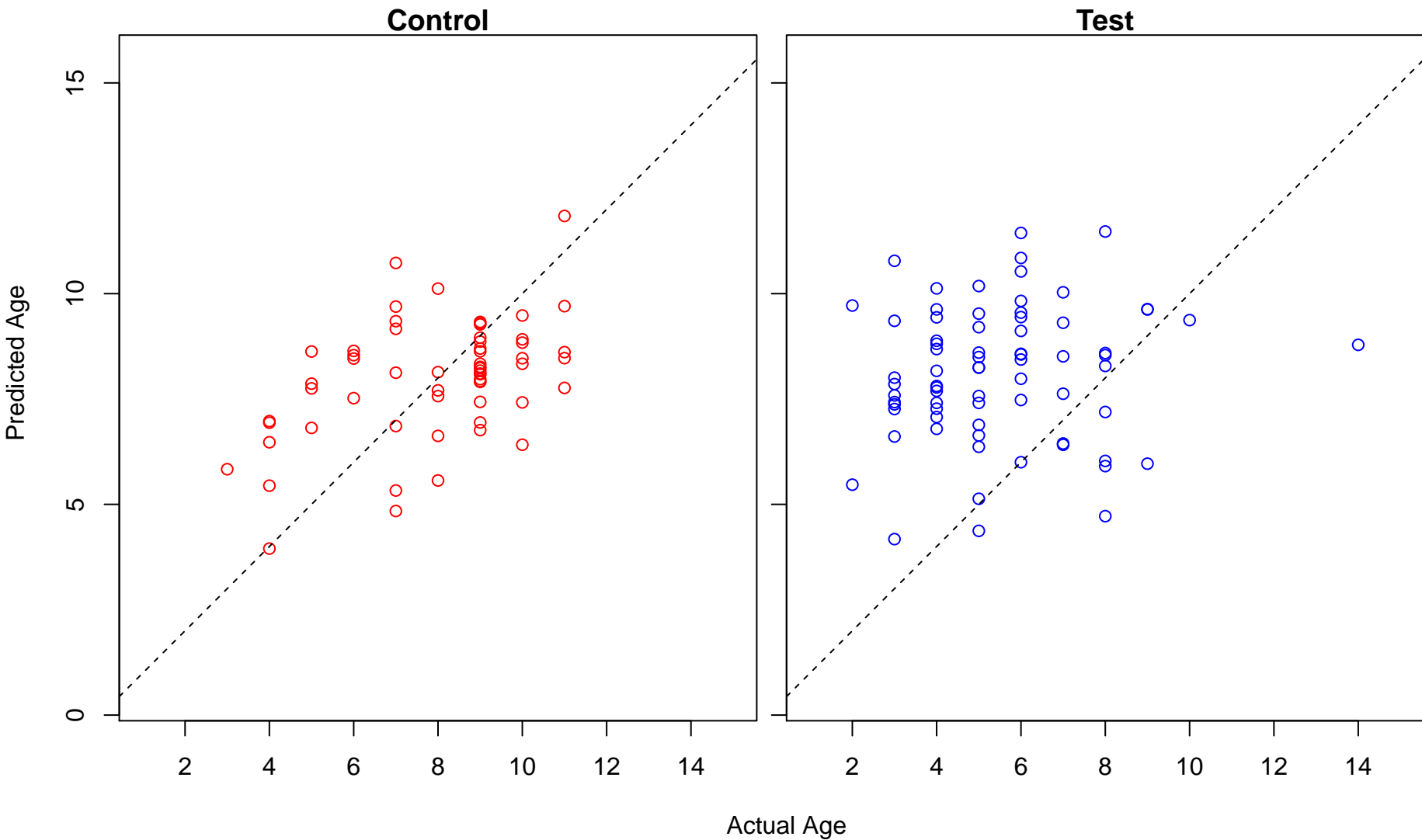
thymus development (Score: 1.943178)



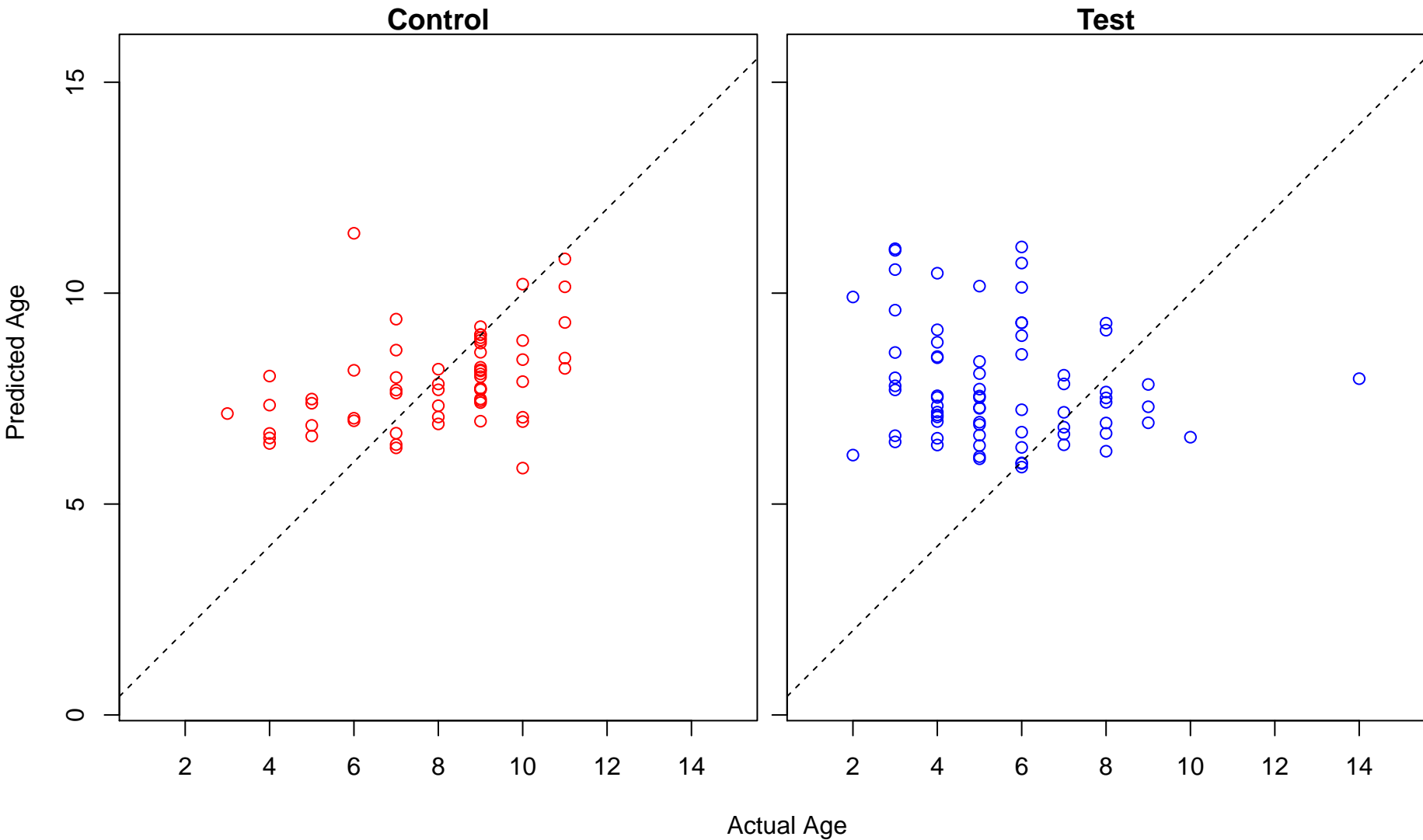
intrinsic apoptotic signaling pathway in response to DNA damage (Score: 1.939683)



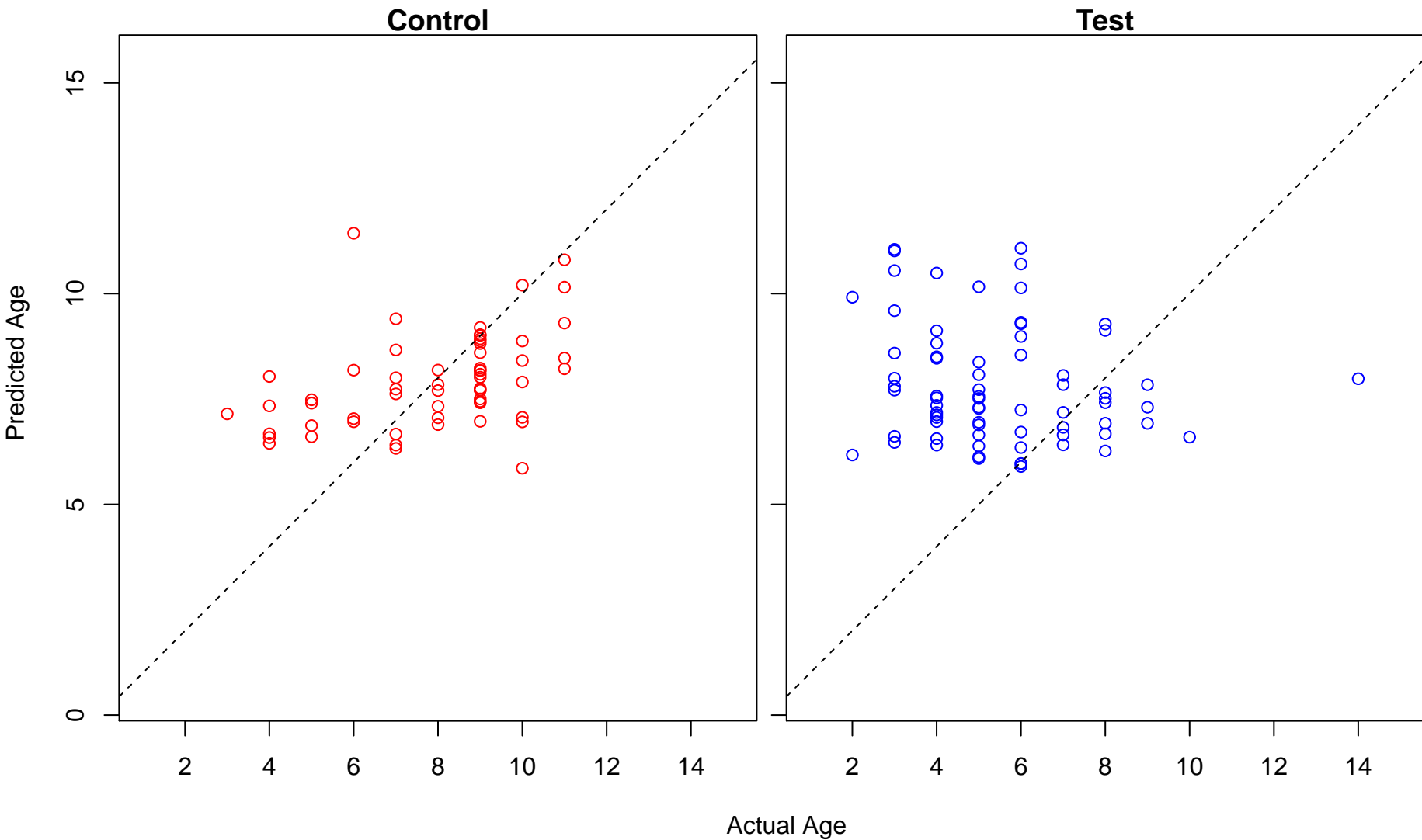
palate development (Score: 1.938116)



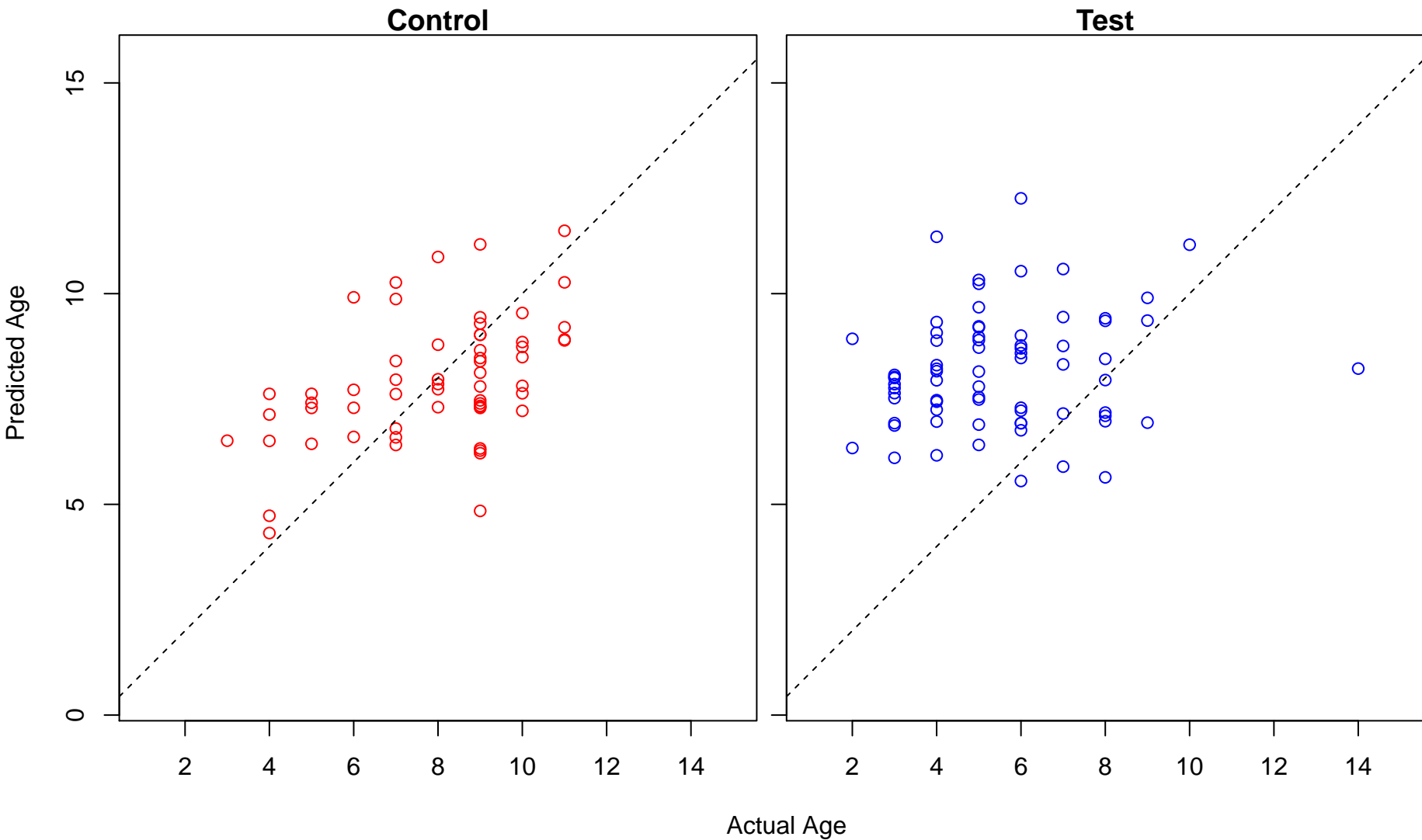
adenylate cyclase-inhibiting dopamine receptor signaling pathway (Score: 1.936302)



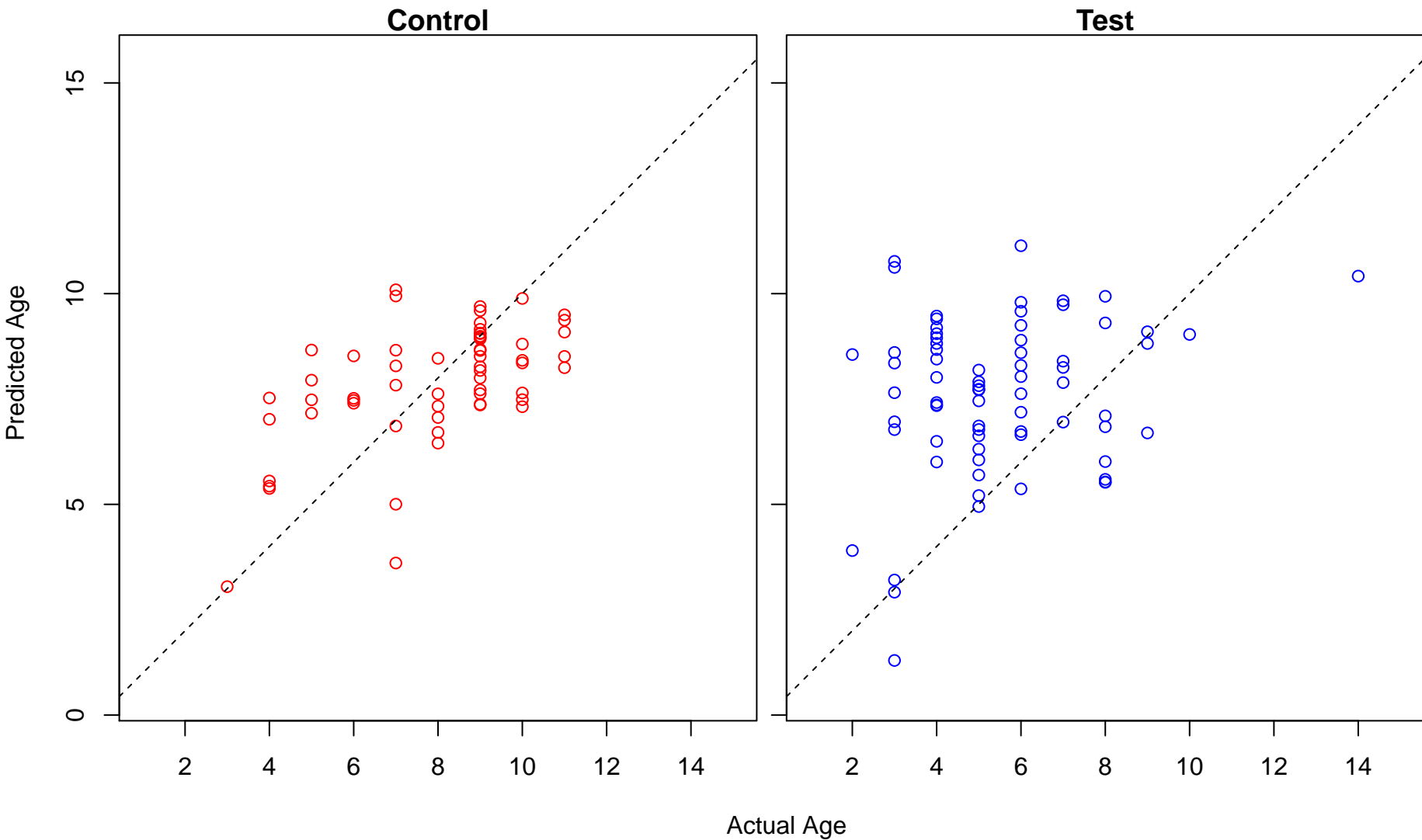
actin crosslink formation (Score: 1.933298)



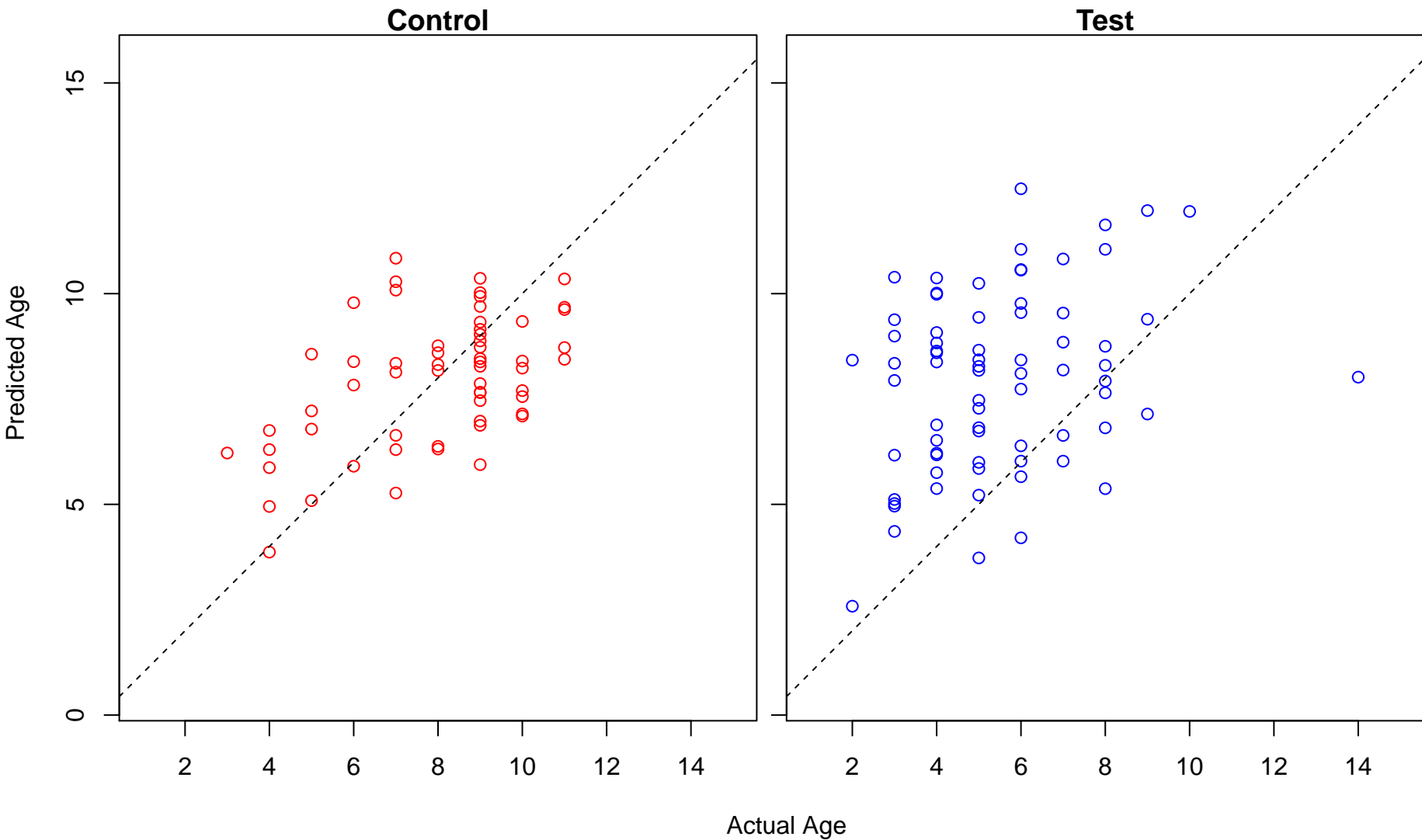
histone H4 deacetylation (Score: 1.930827)



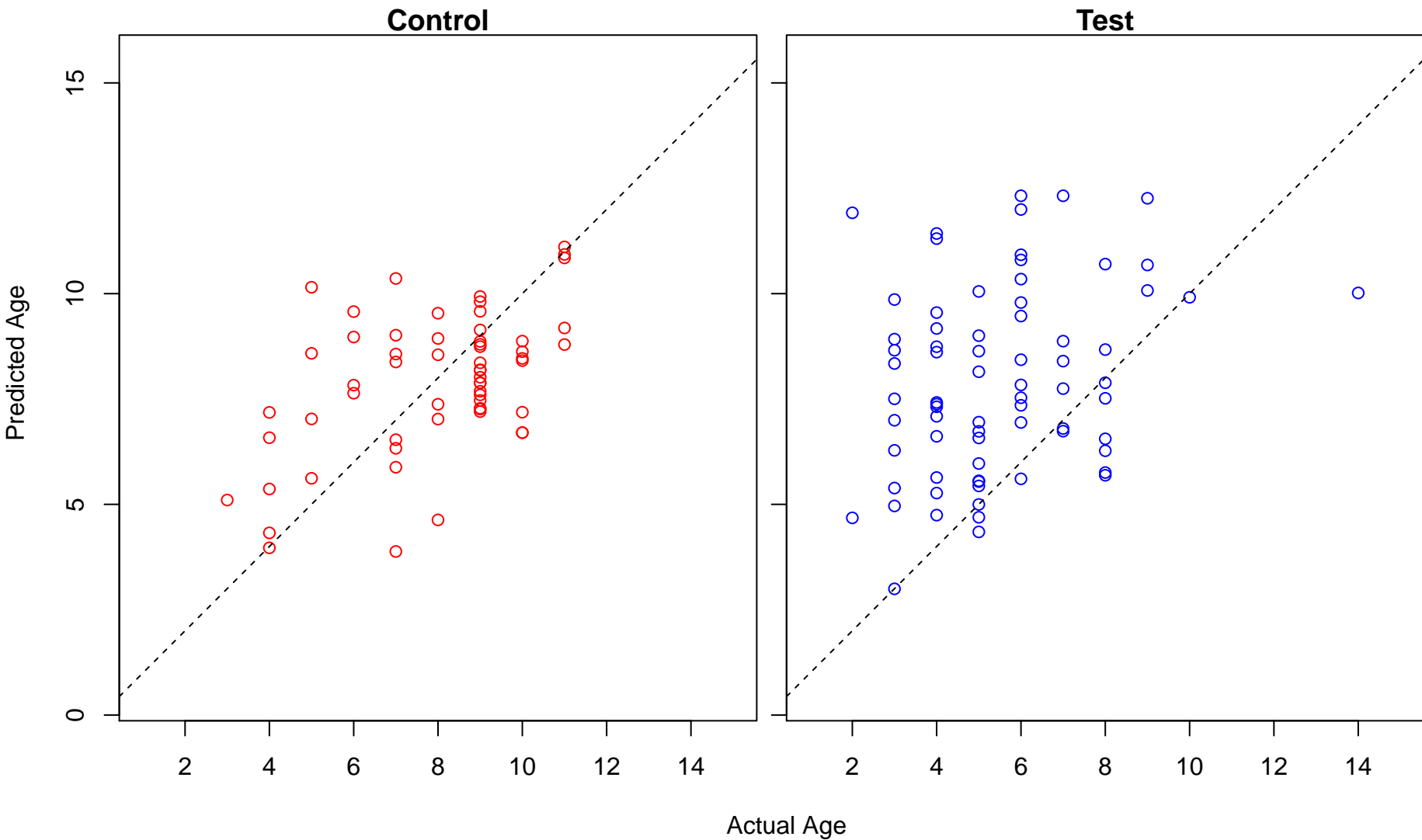
neural plate pattern specification (Score: 1.927696)



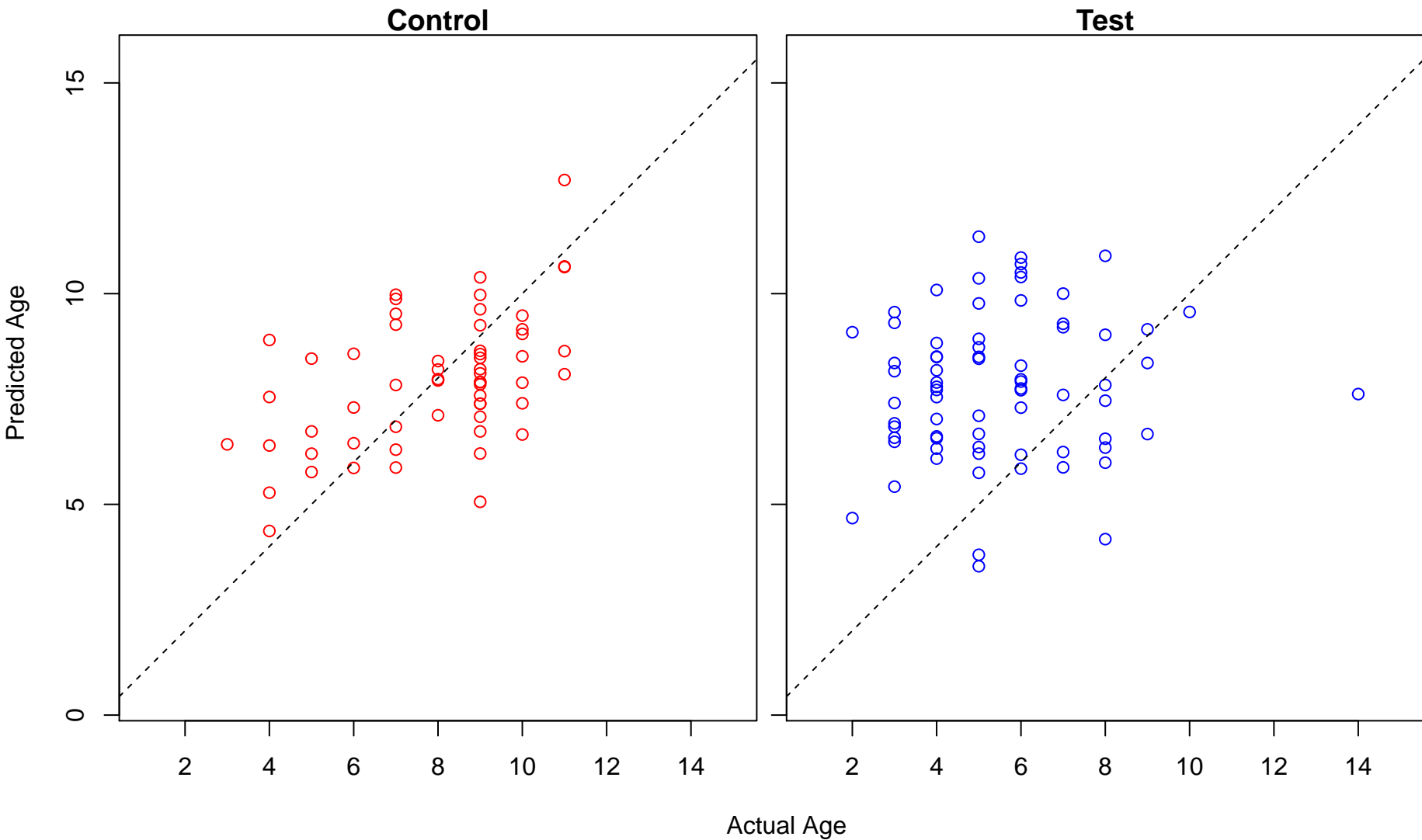
cerebral cortex neuron differentiation (Score: 1.925122)



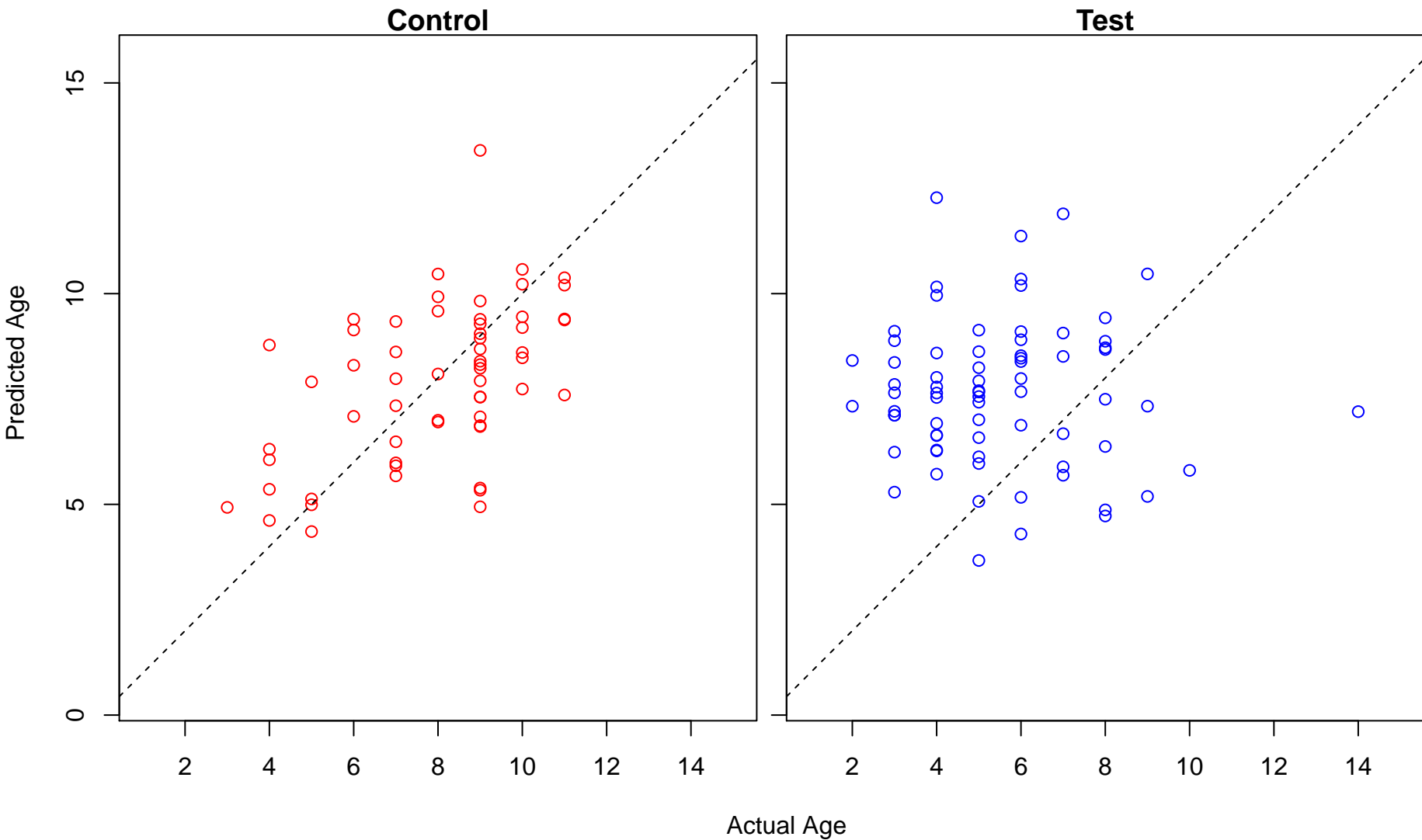
blastocyst development (Score: 1.924257)



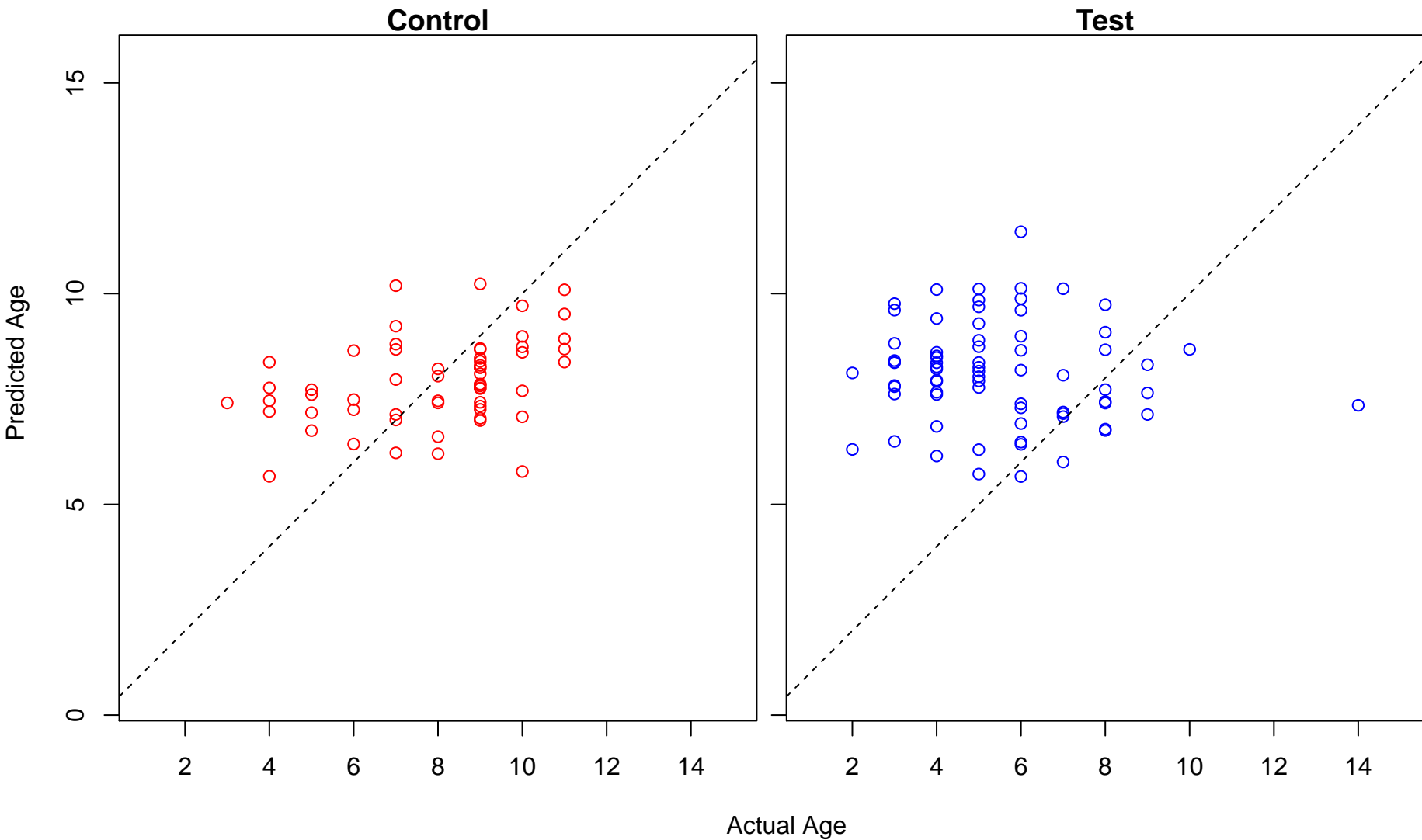
ribonucleoprotein complex disassembly (Score: 1.922323)



ovarian follicle development (Score: 1.922036)

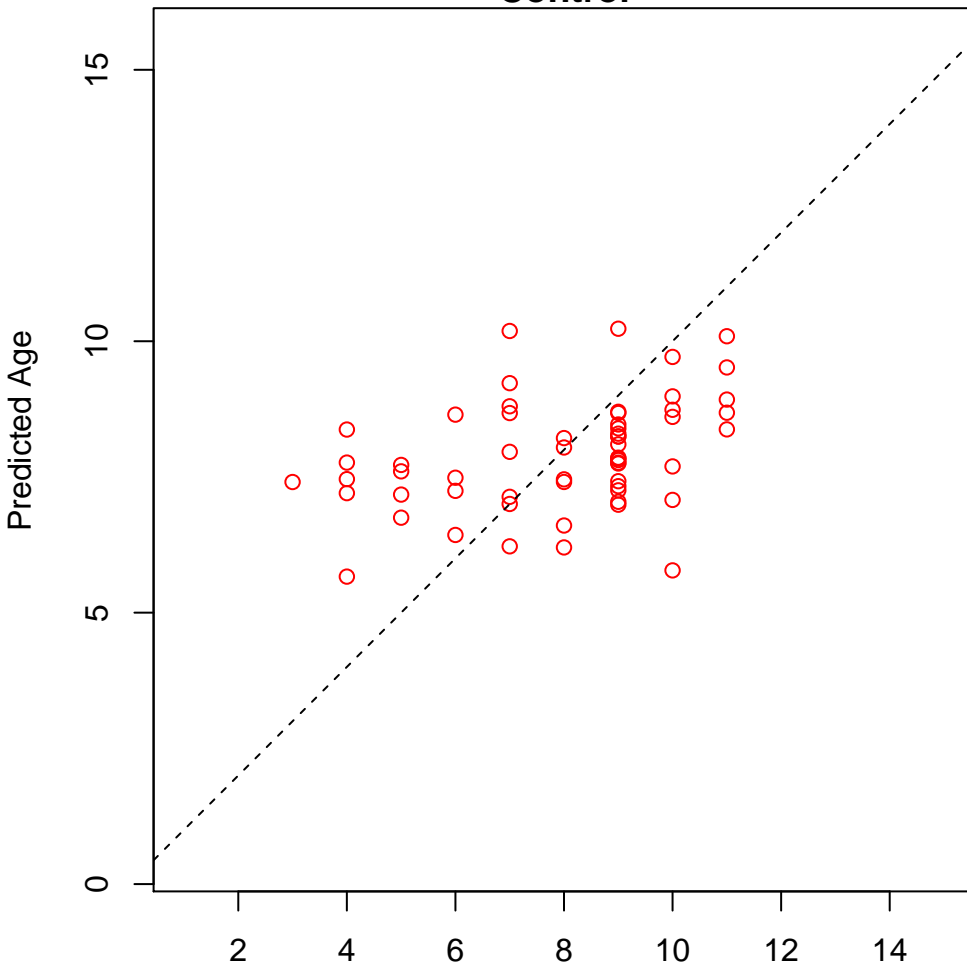


synaptonemal complex assembly (Score: 1.916501)

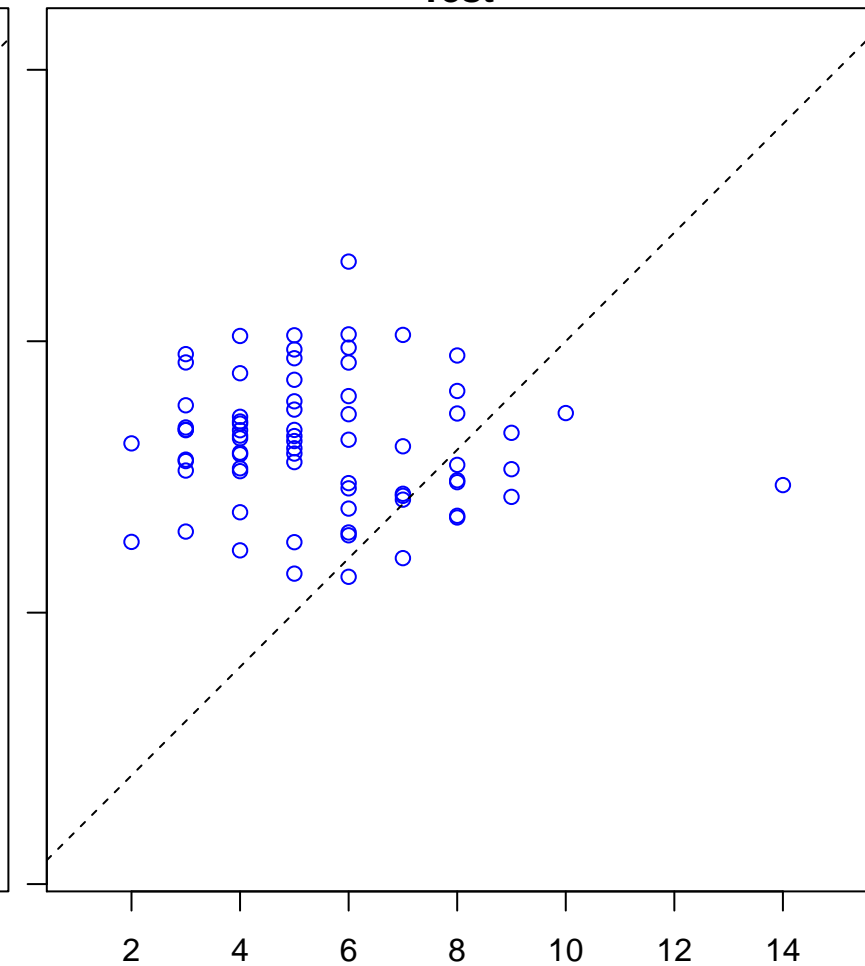


synaptonemal complex organization (Score: 1.916501)

Control



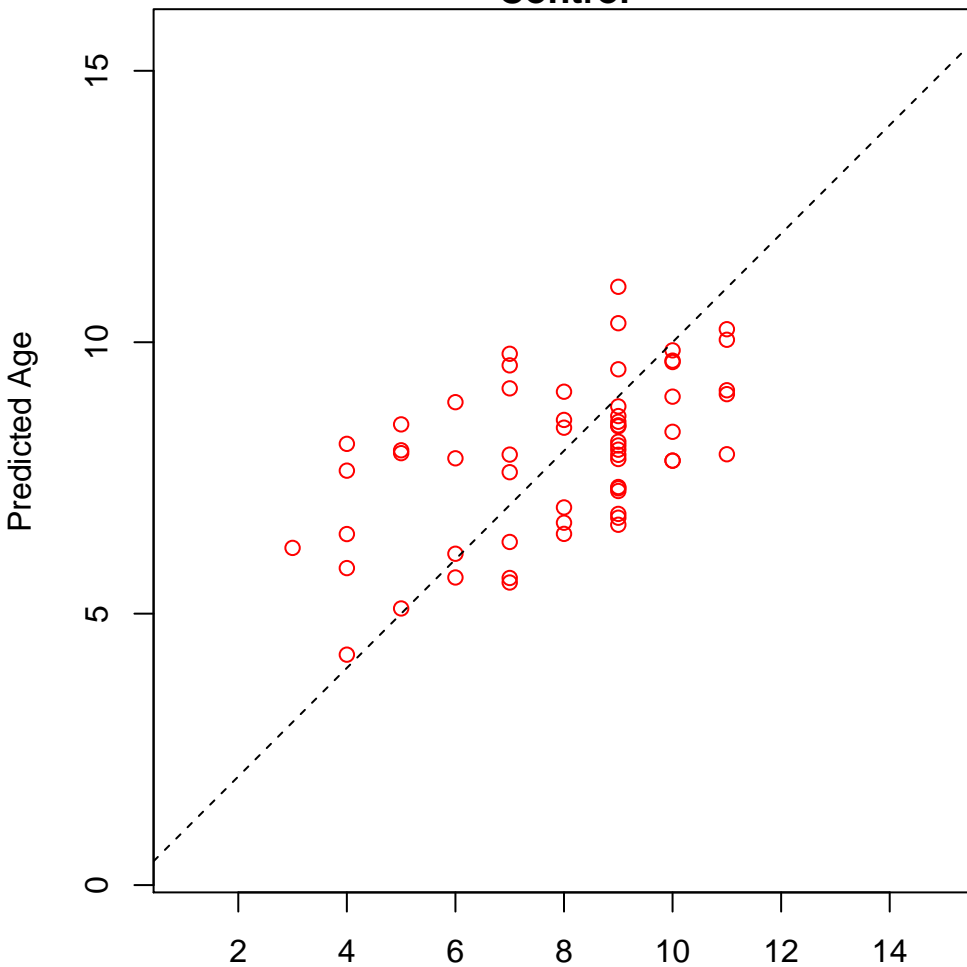
Test



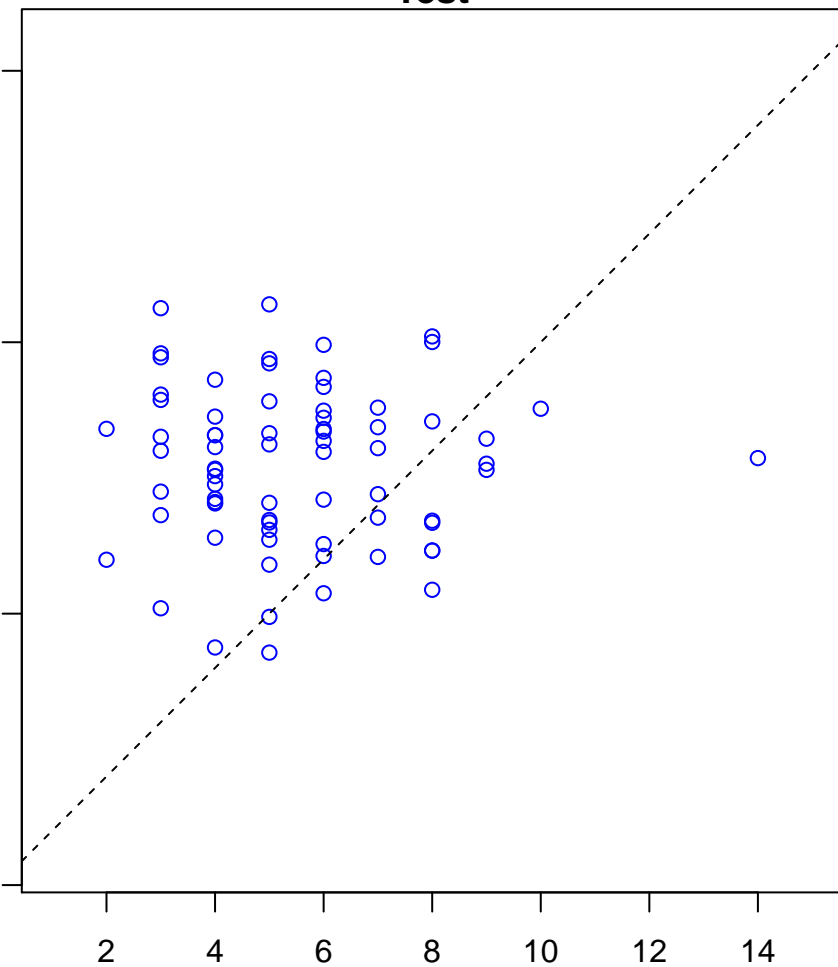
Actual Age

endosome to melanosome transport (Score: 1.914384)

Control



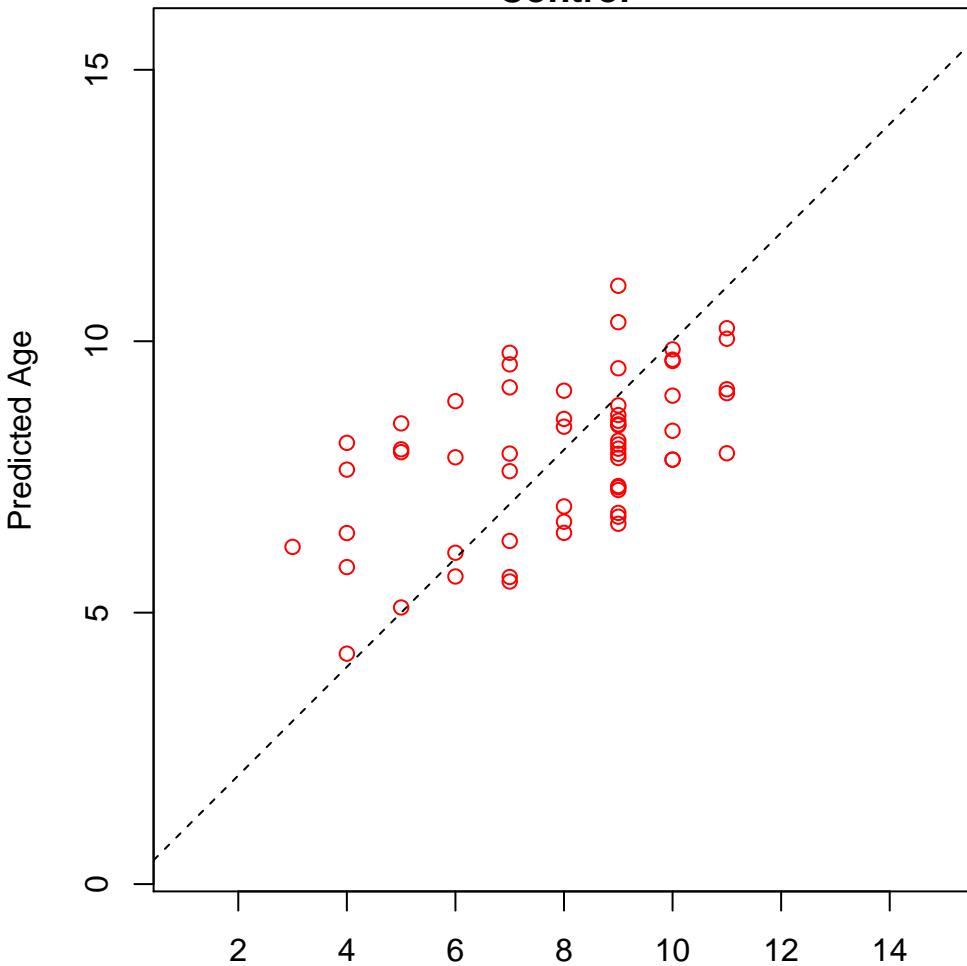
Test



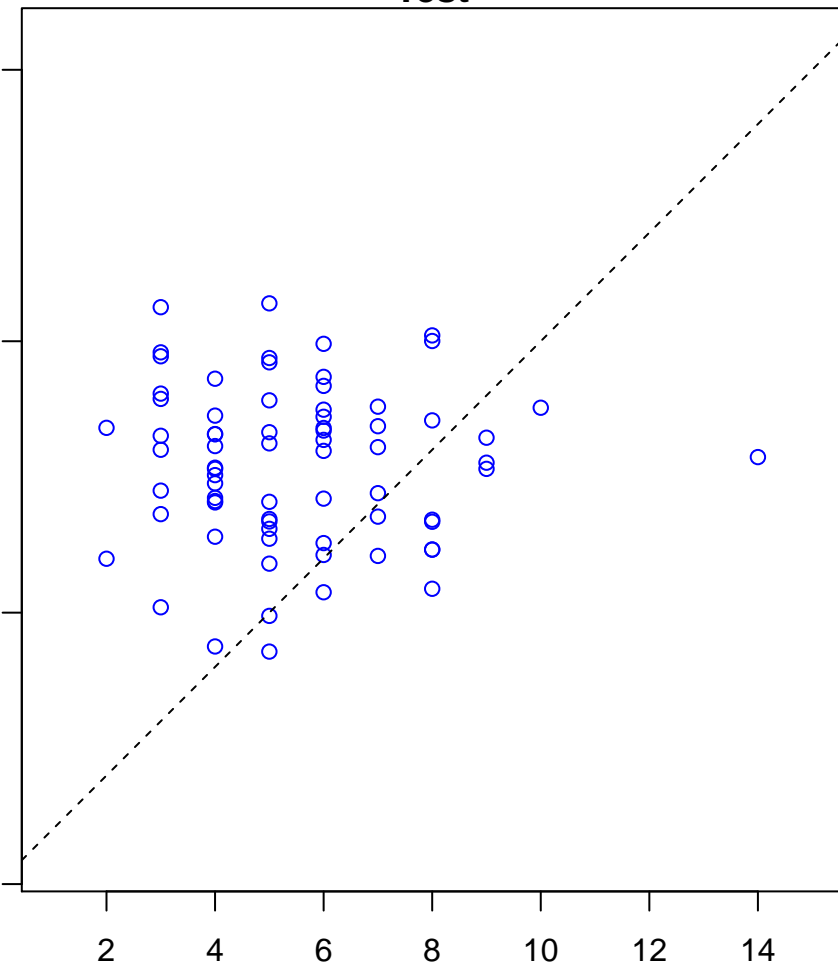
Actual Age

endosome to pigment granule transport (Score: 1.914384)

Control

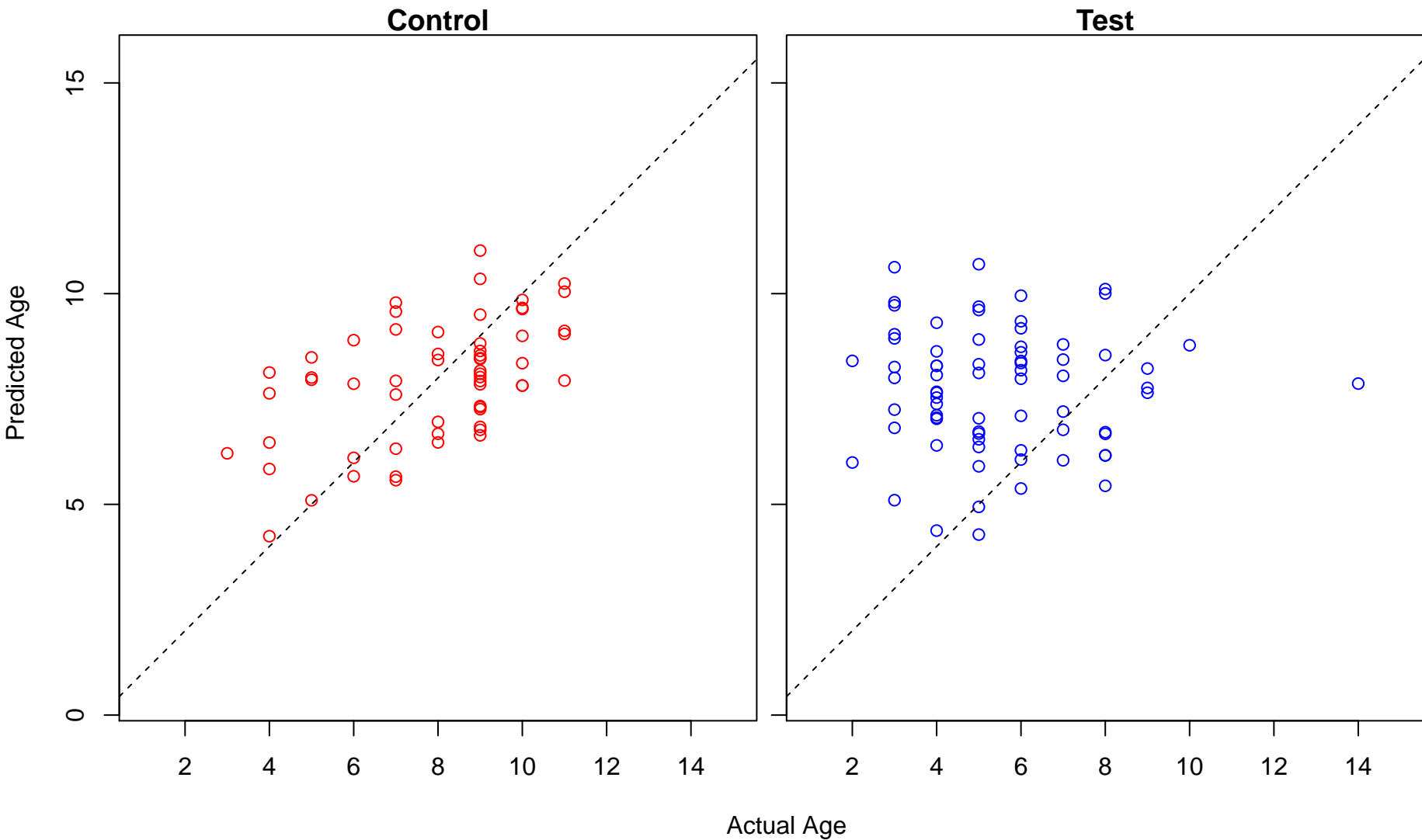


Test

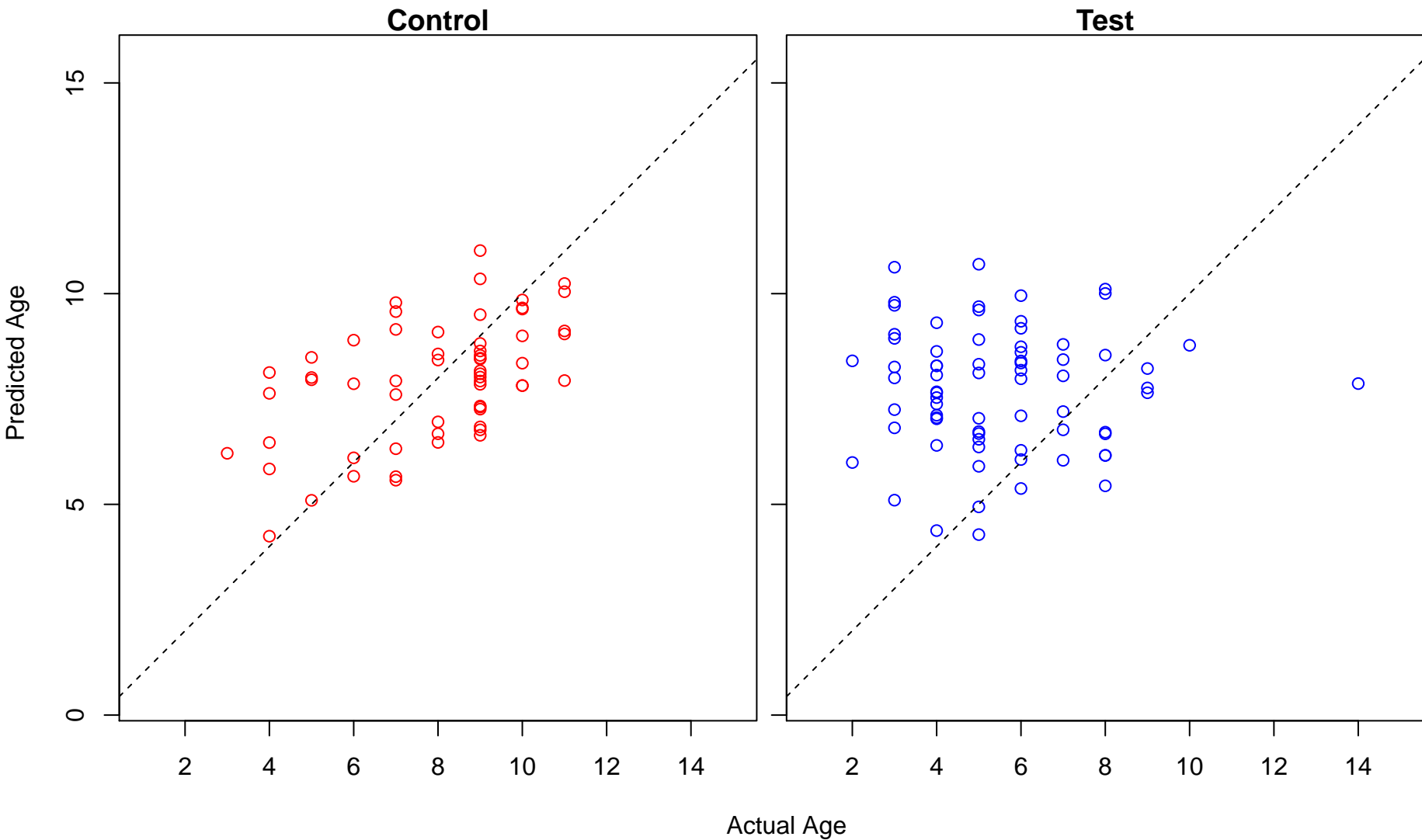


Actual Age

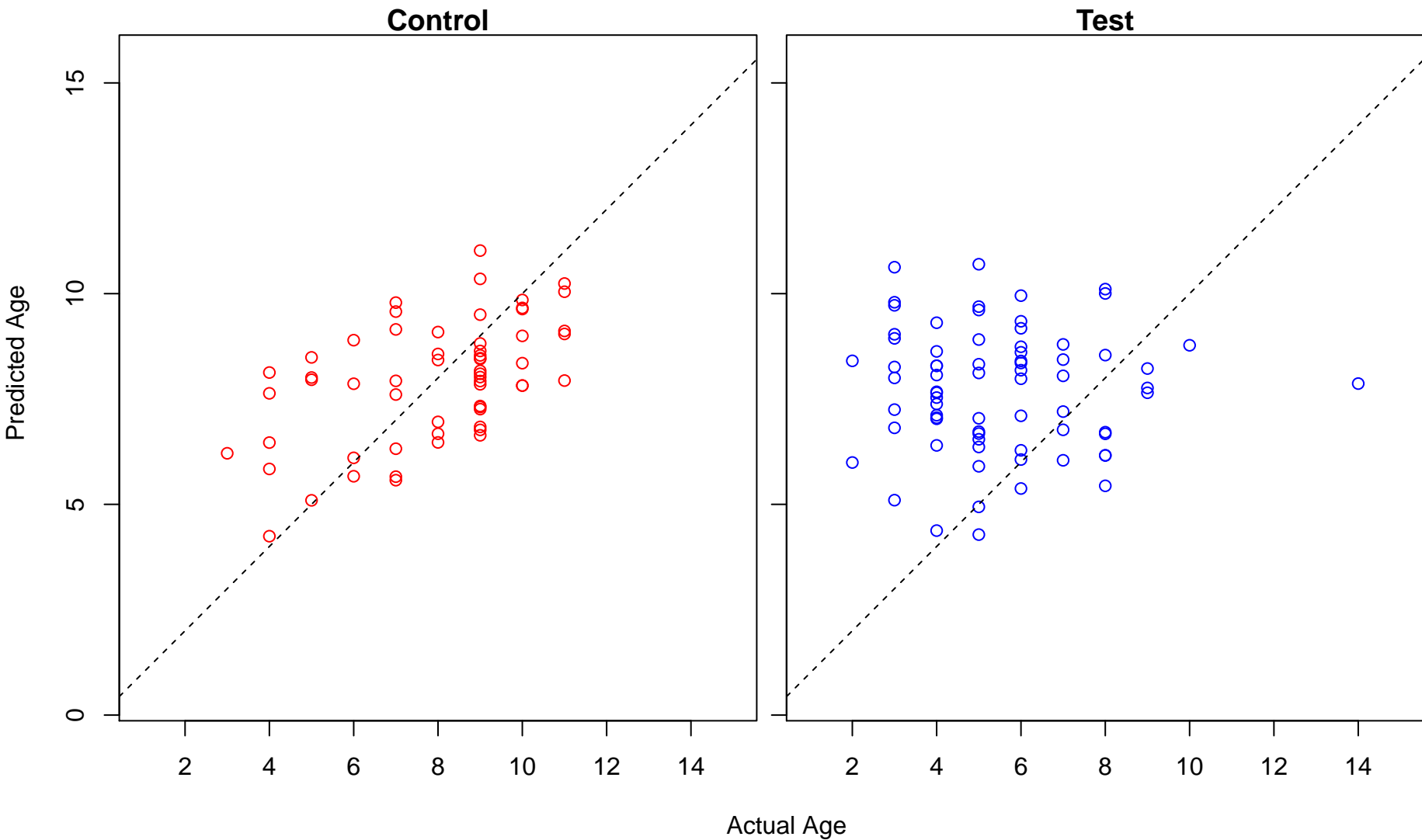
pigment granule maturation (Score: 1.914384)



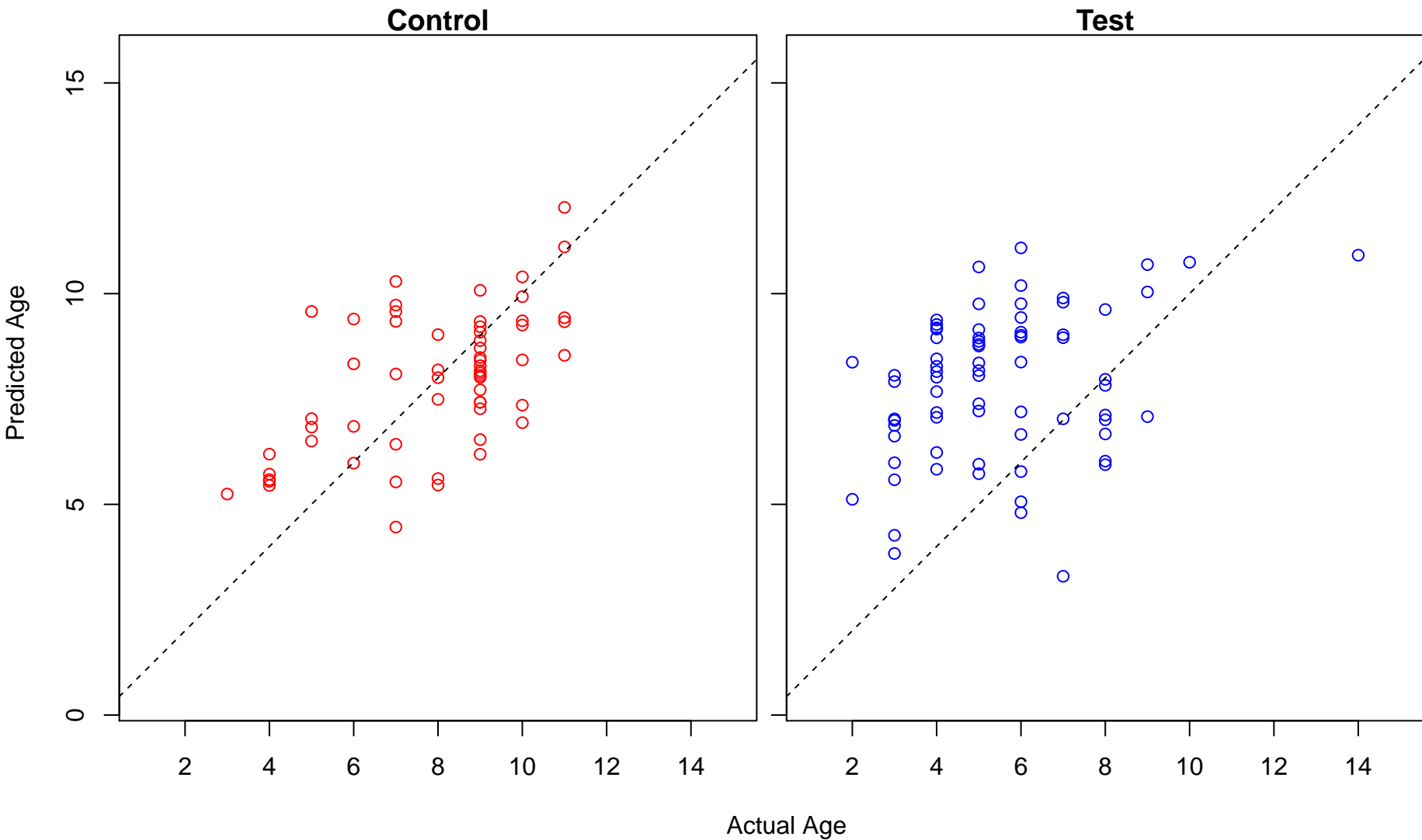
pigment accumulation (Score: 1.914366)



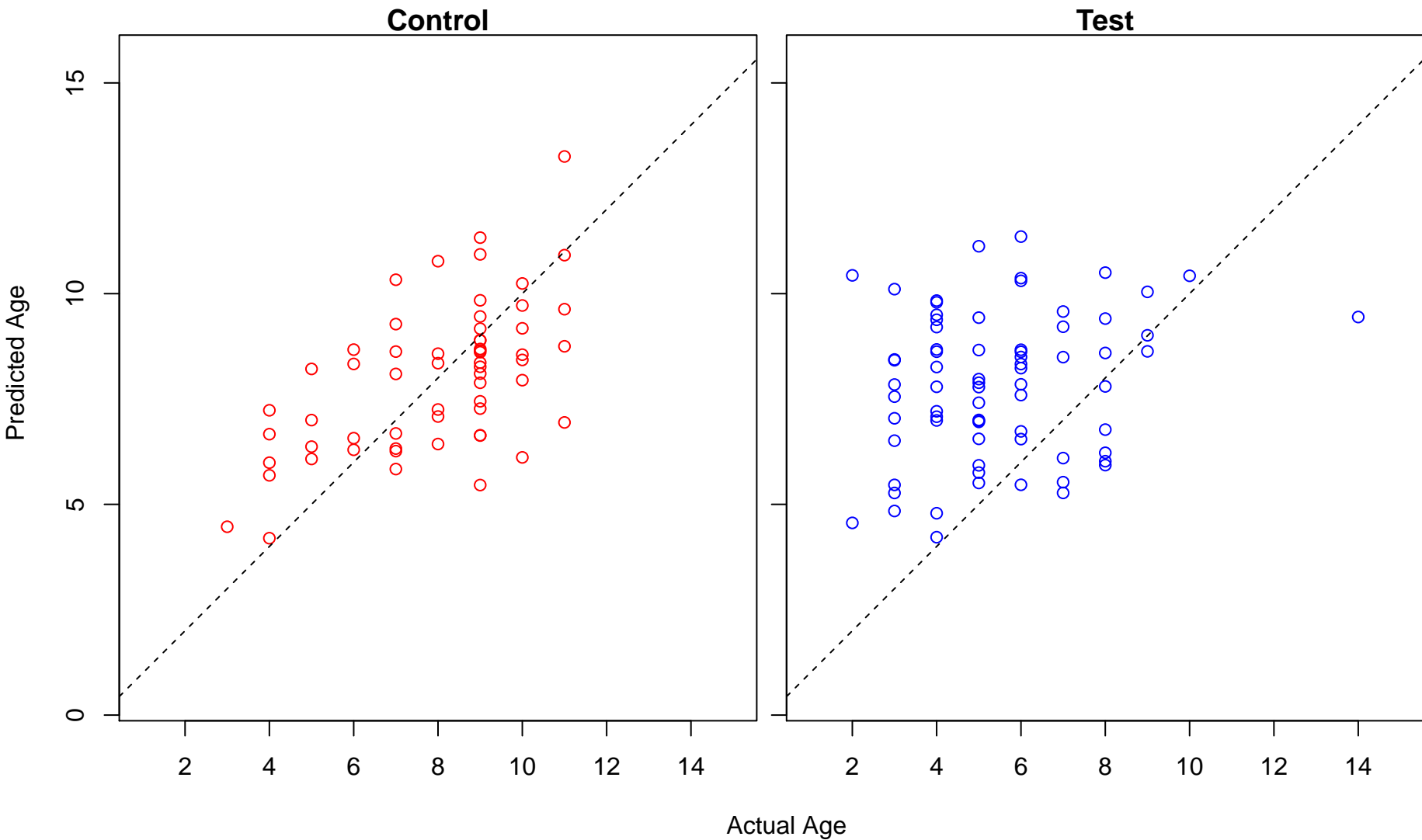
cellular pigment accumulation (Score: 1.914366)



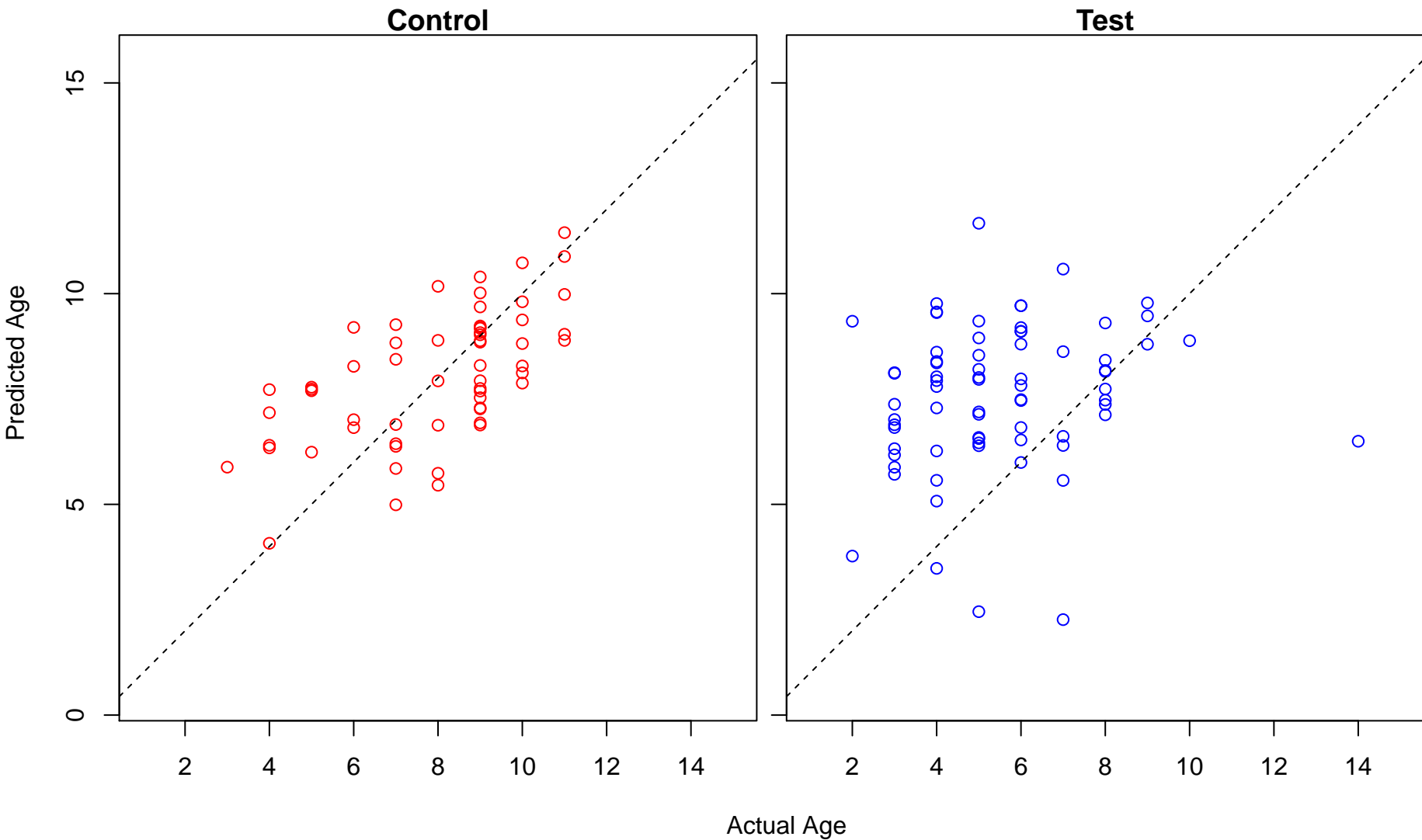
internal peptidyl-lysine acetylation (Score: 1.911700)



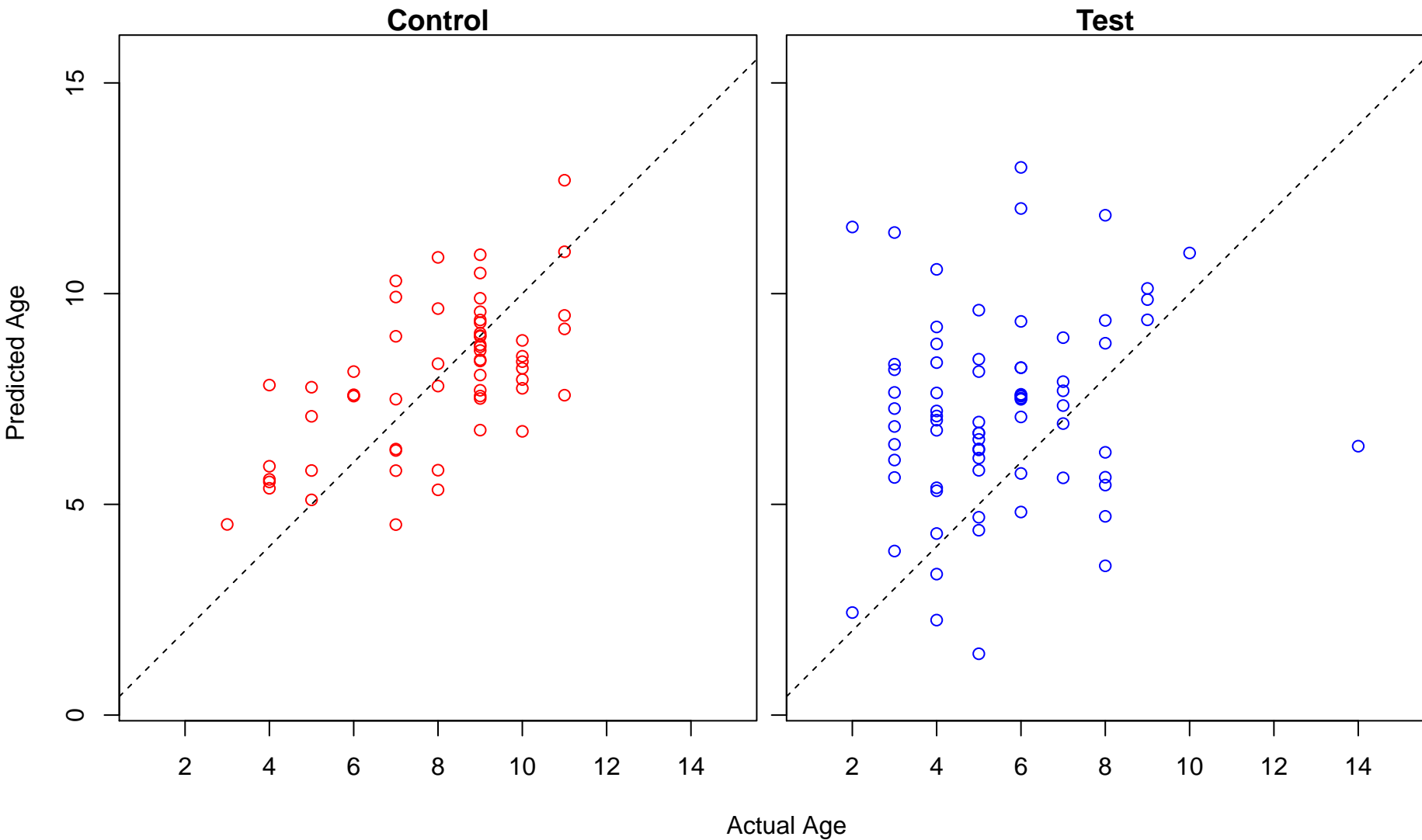
positive regulation of response to external stimulus (Score: 1.909306)



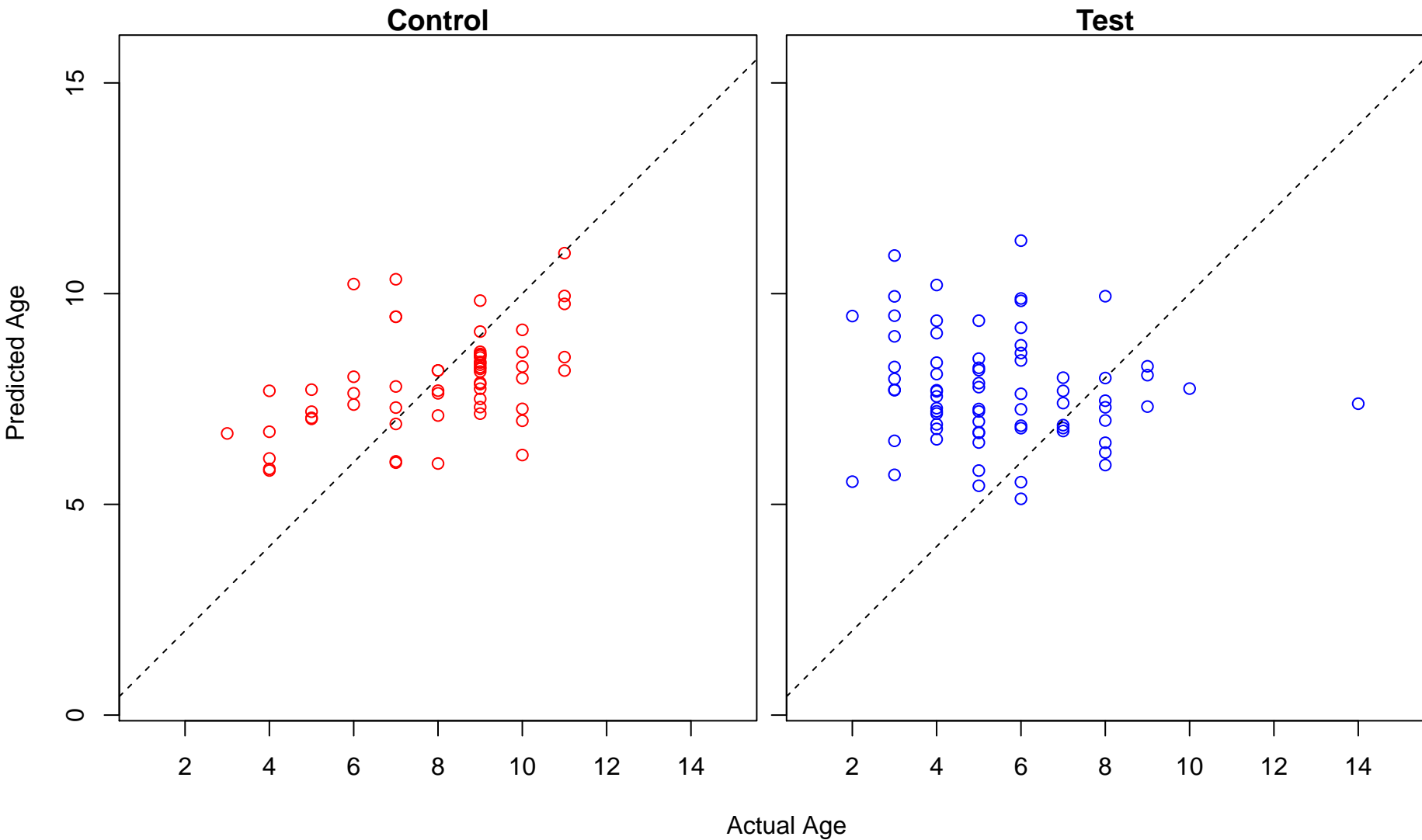
regulation of cellular metabolic process (Score: 1.906175)



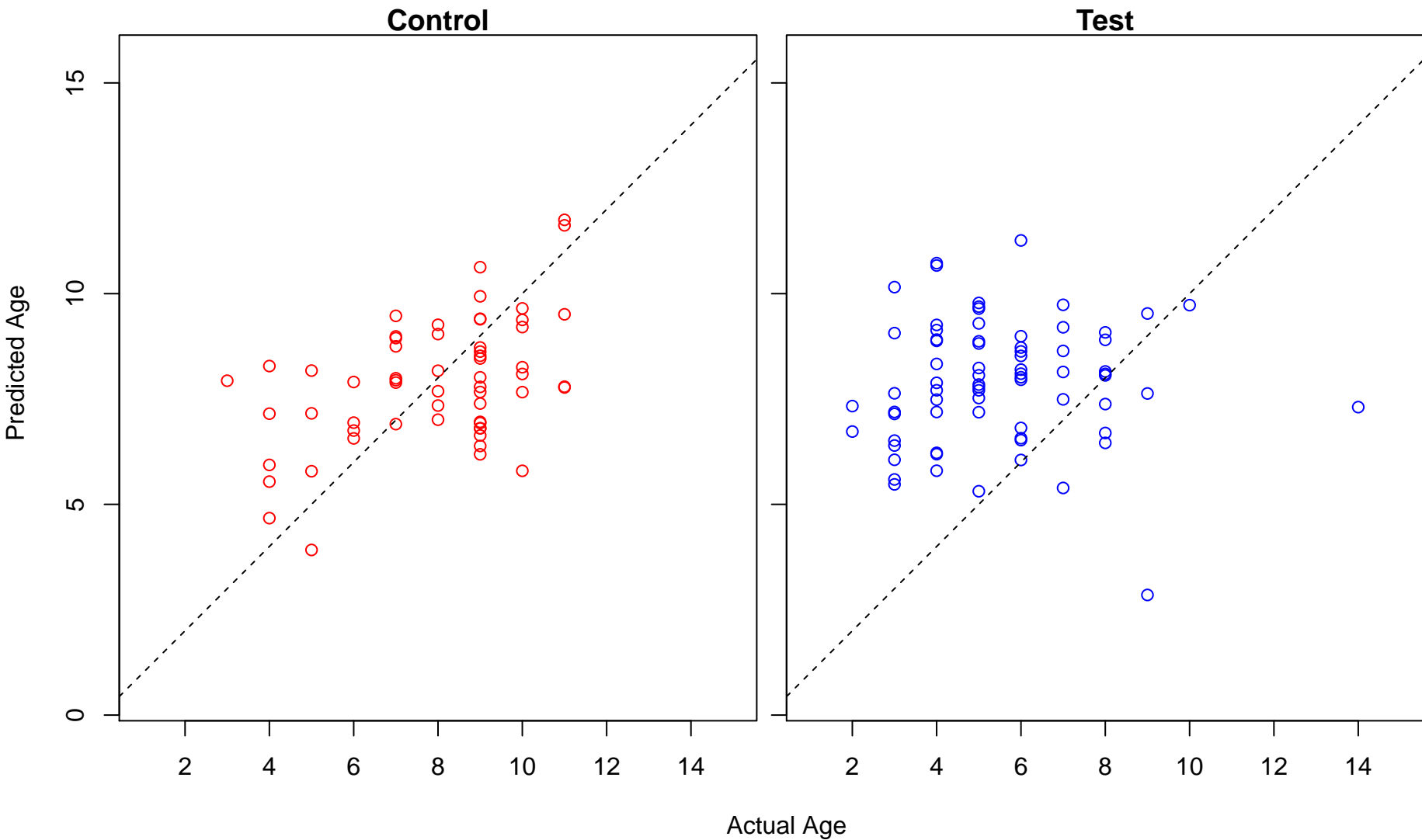
positive regulation of secretion (Score: 1.904390)



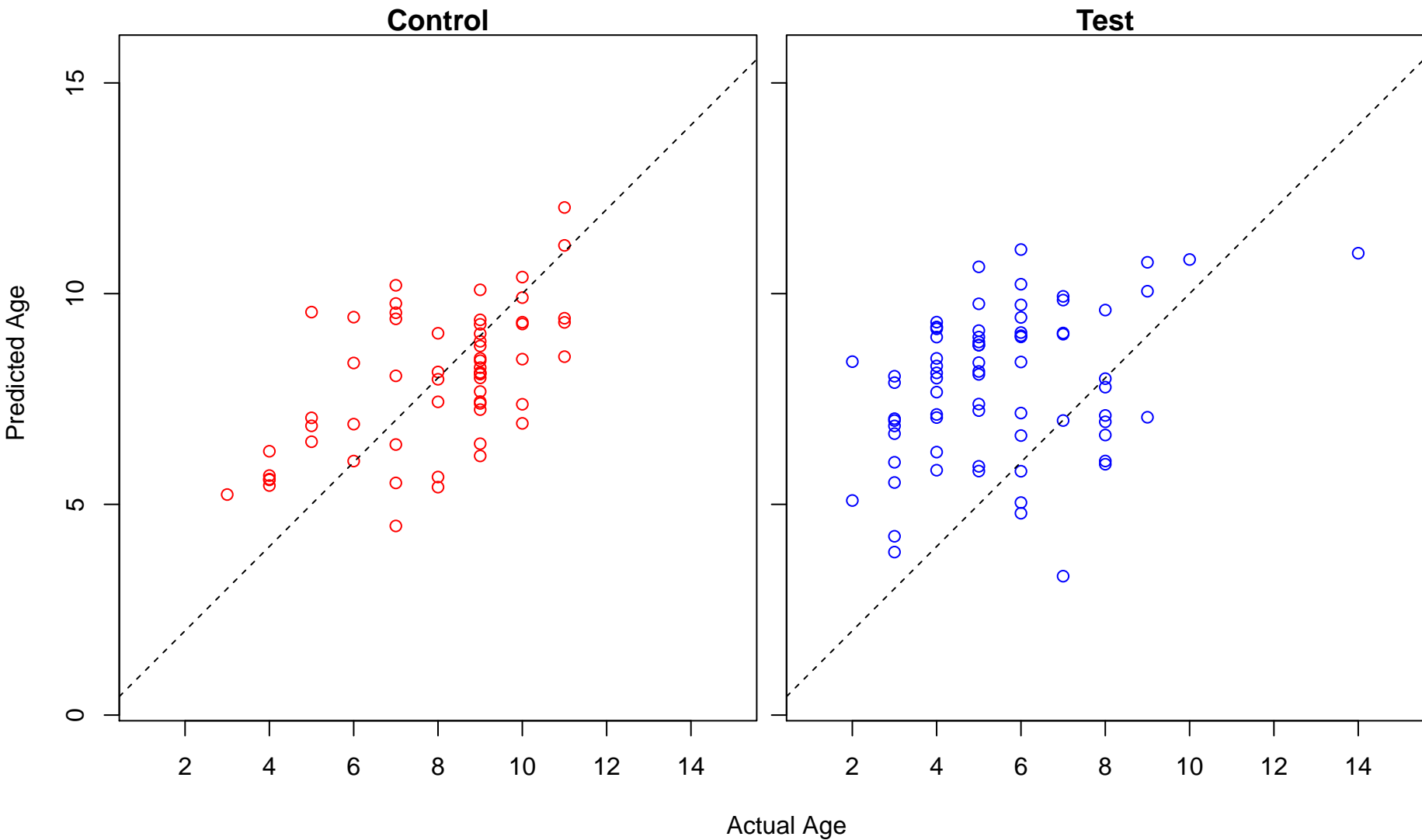
actin cytoskeleton reorganization (Score: 1.903866)



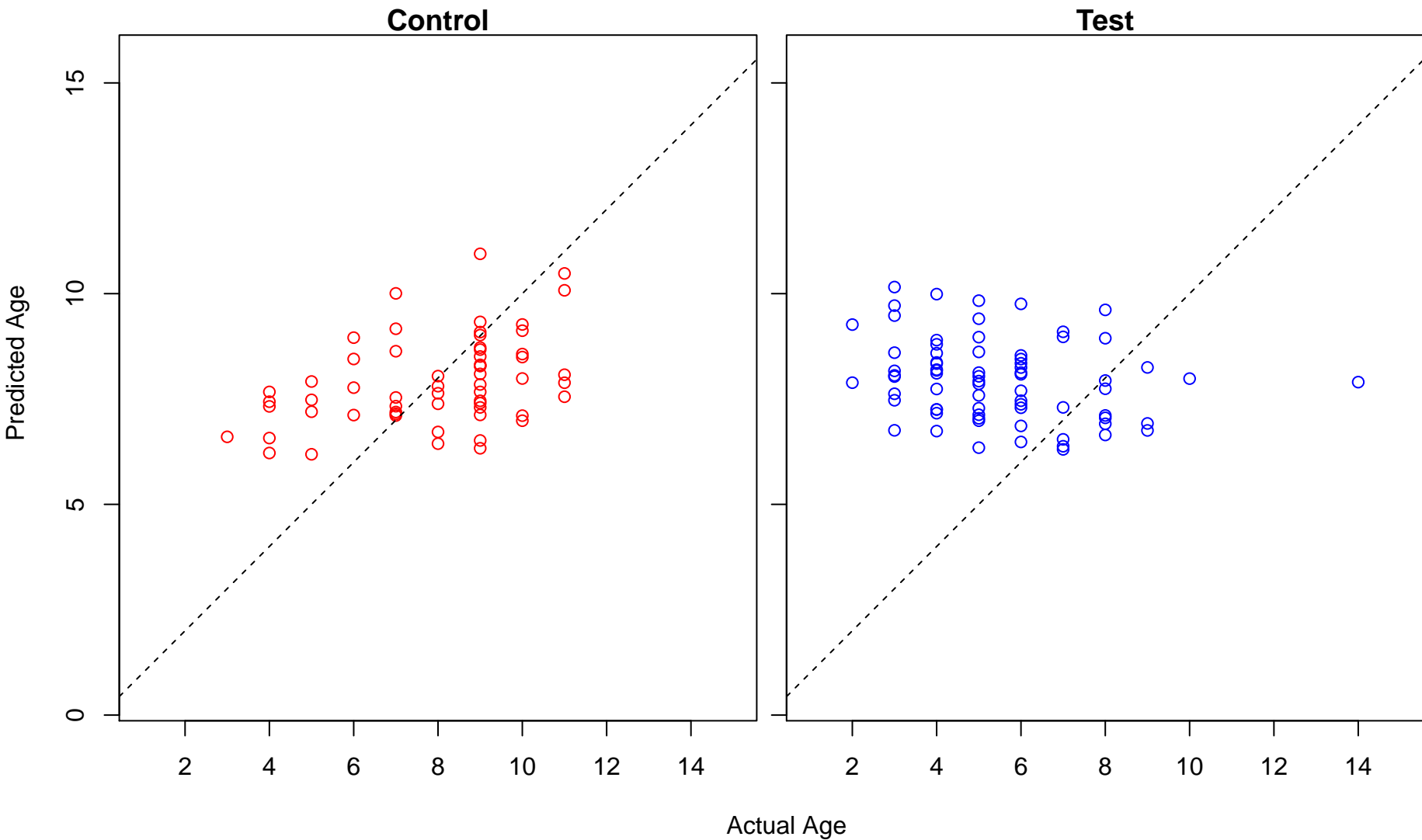
serotonin receptor signaling pathway (Score: 1.899840)



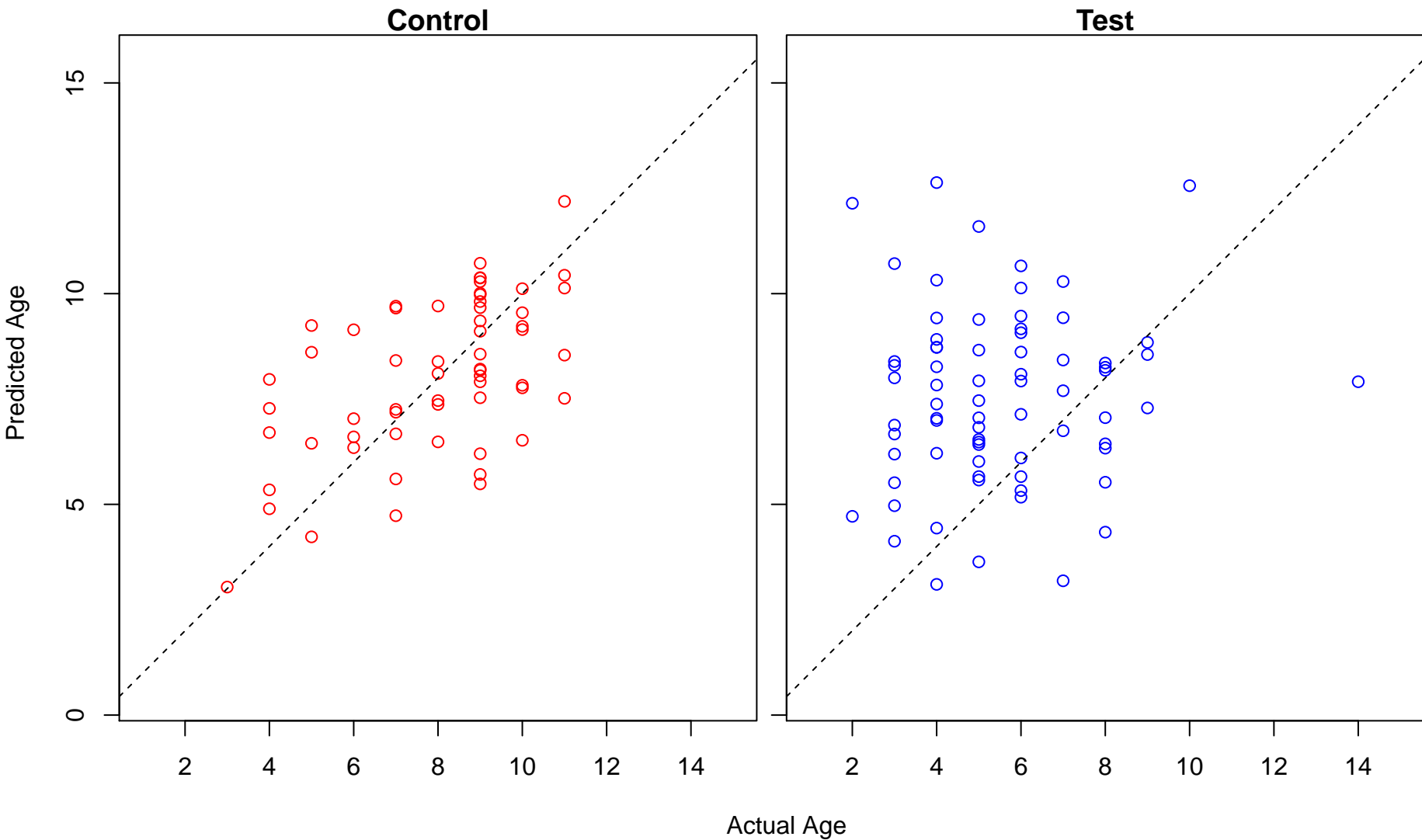
internal protein amino acid acetylation (Score: 1.899192)



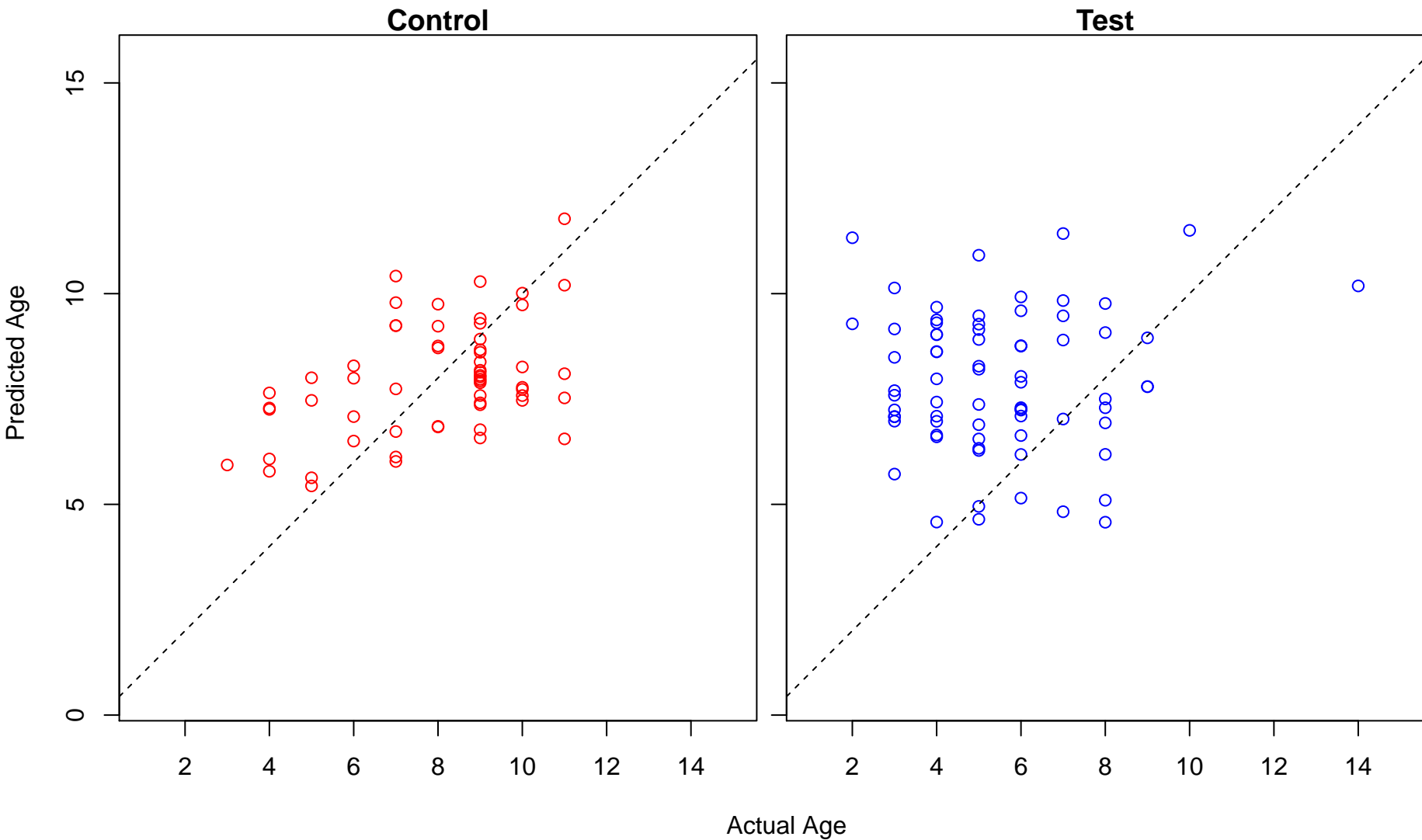
aldehyde catabolic process (Score: 1.895627)



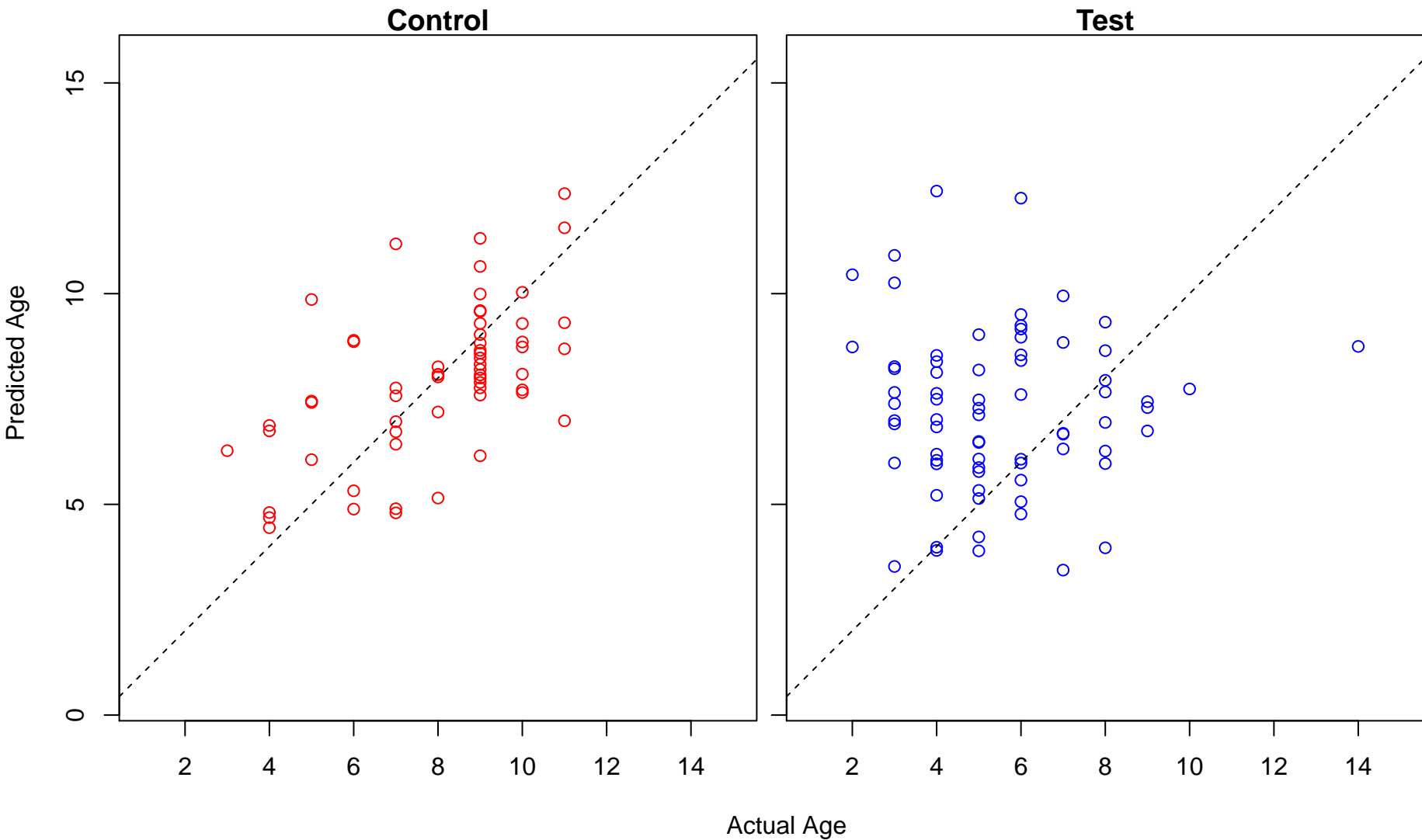
positive regulation of apoptotic signaling pathway (Score: 1.895584)



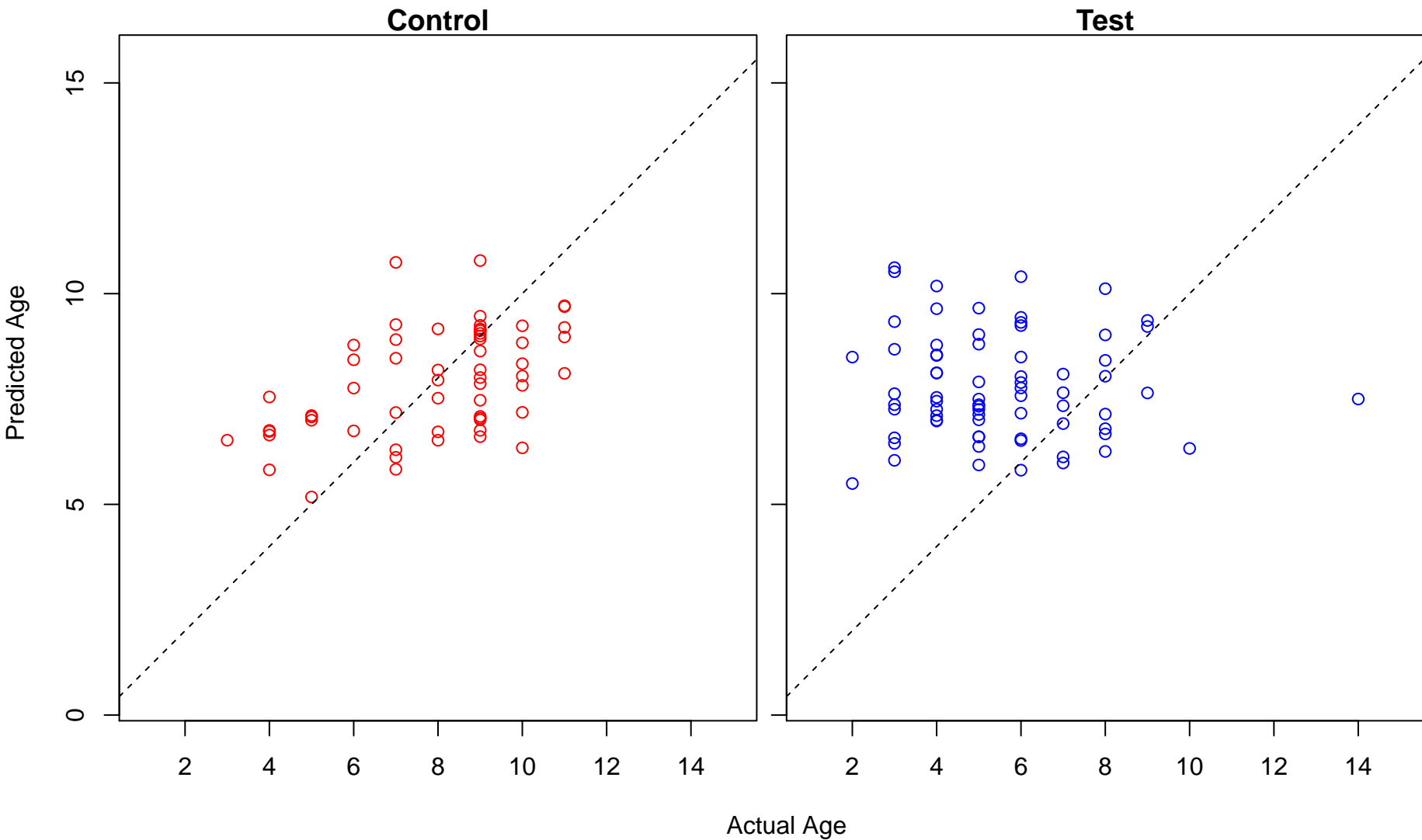
transcription from RNA polymerase III promoter (Score: 1.893442)



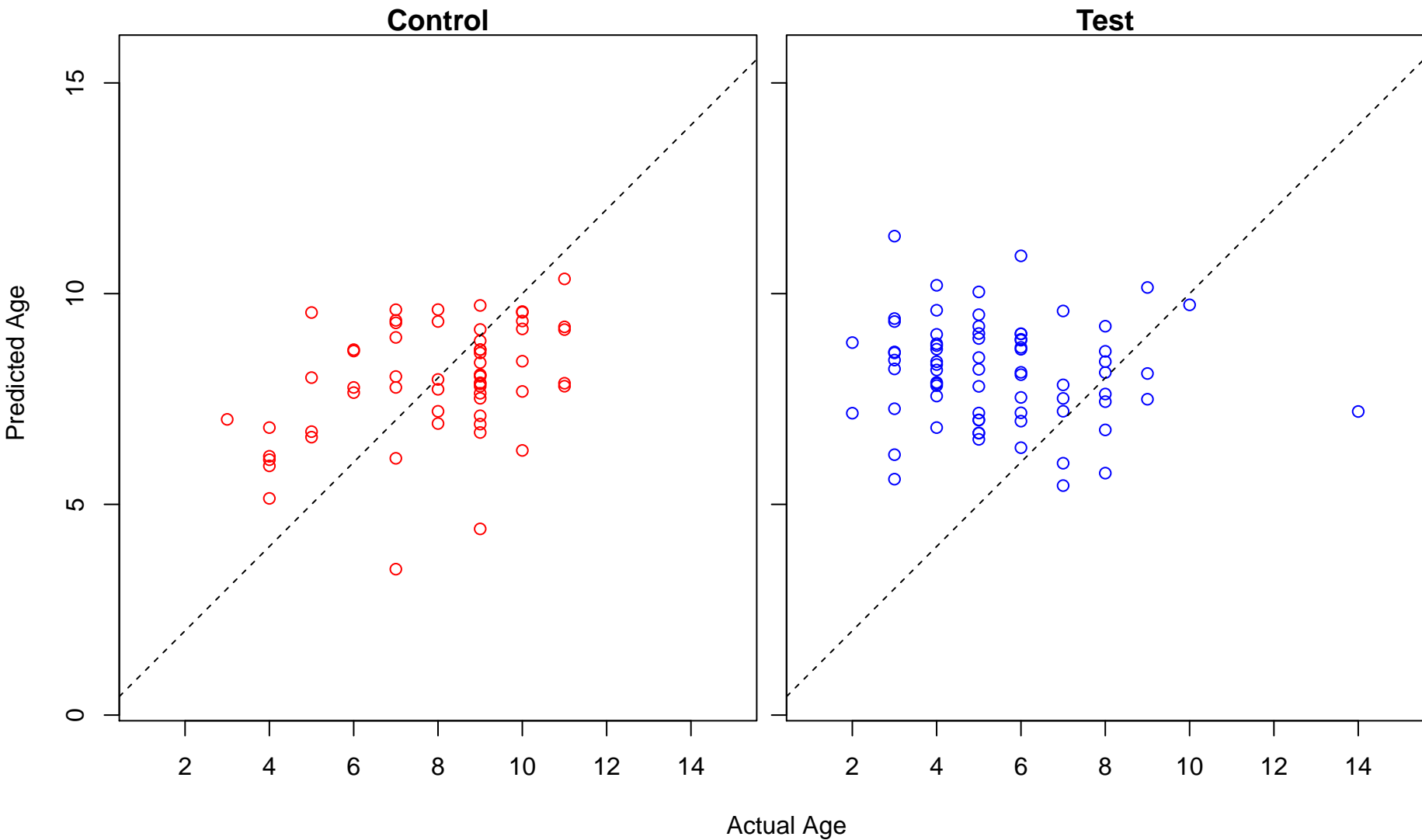
nucleotide biosynthetic process (Score: 1.887544)



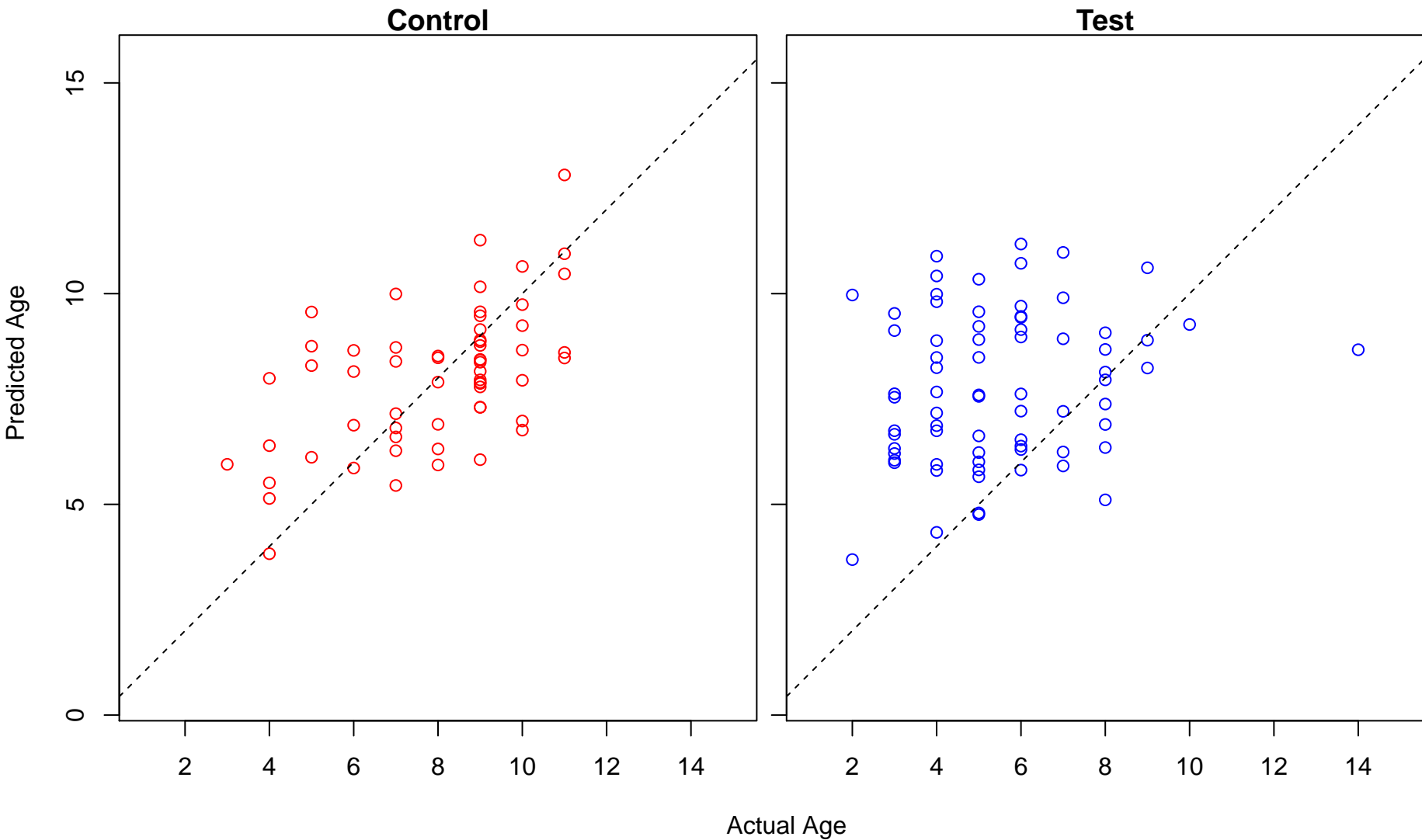
JAK-STAT cascade (Score: 1.886628)



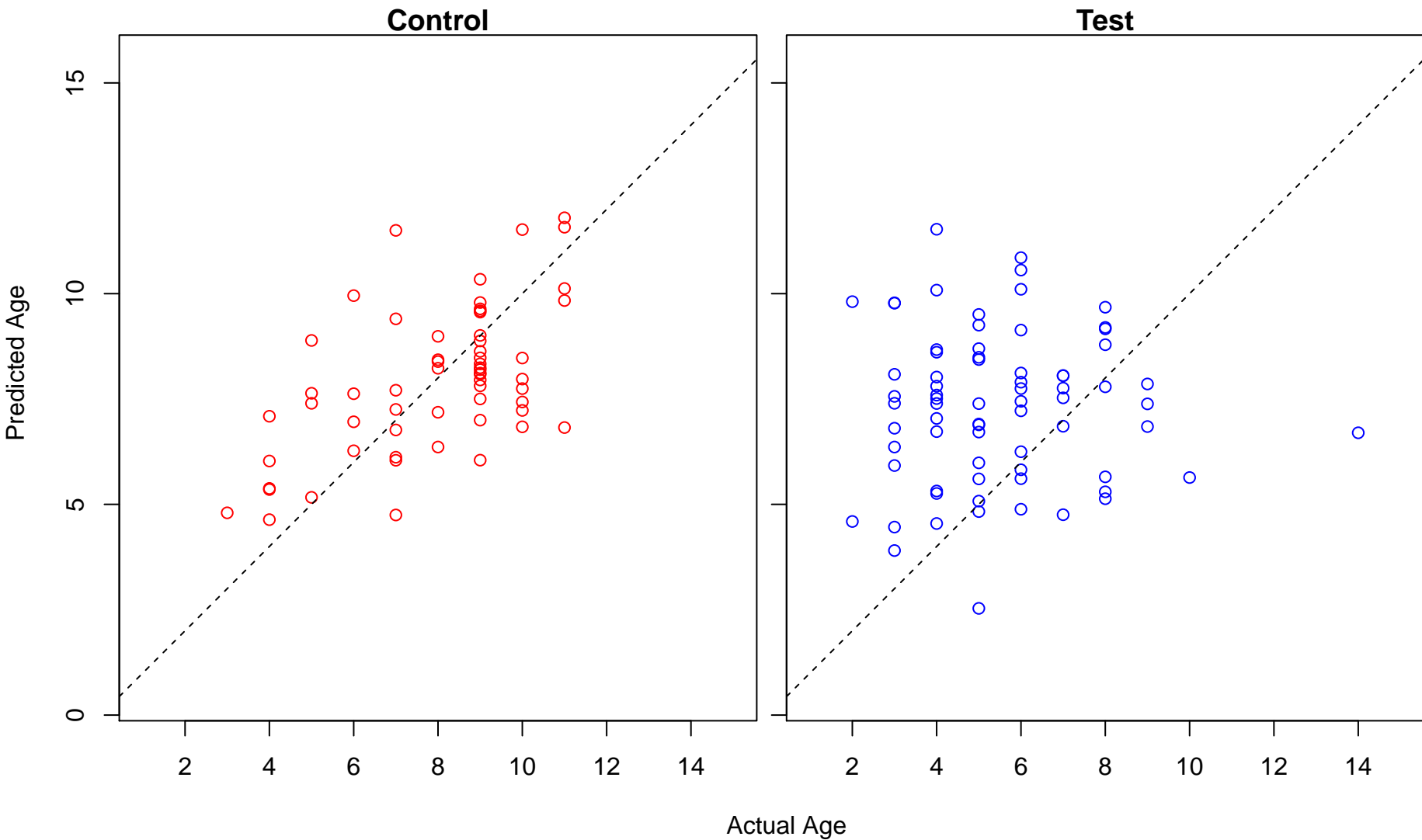
SCF complex assembly (Score: 1.885482)



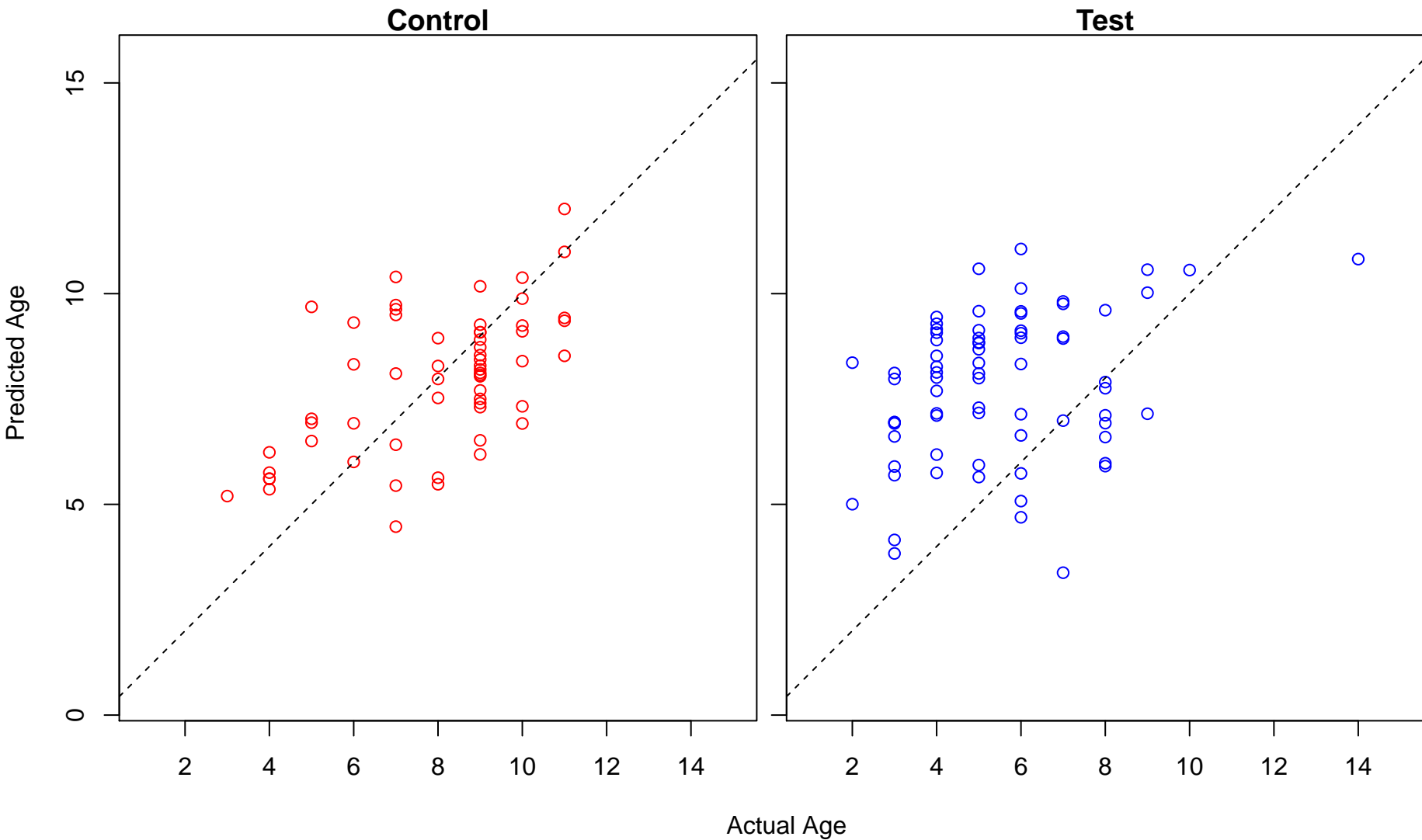
programmed cell death (Score: 1.884441)



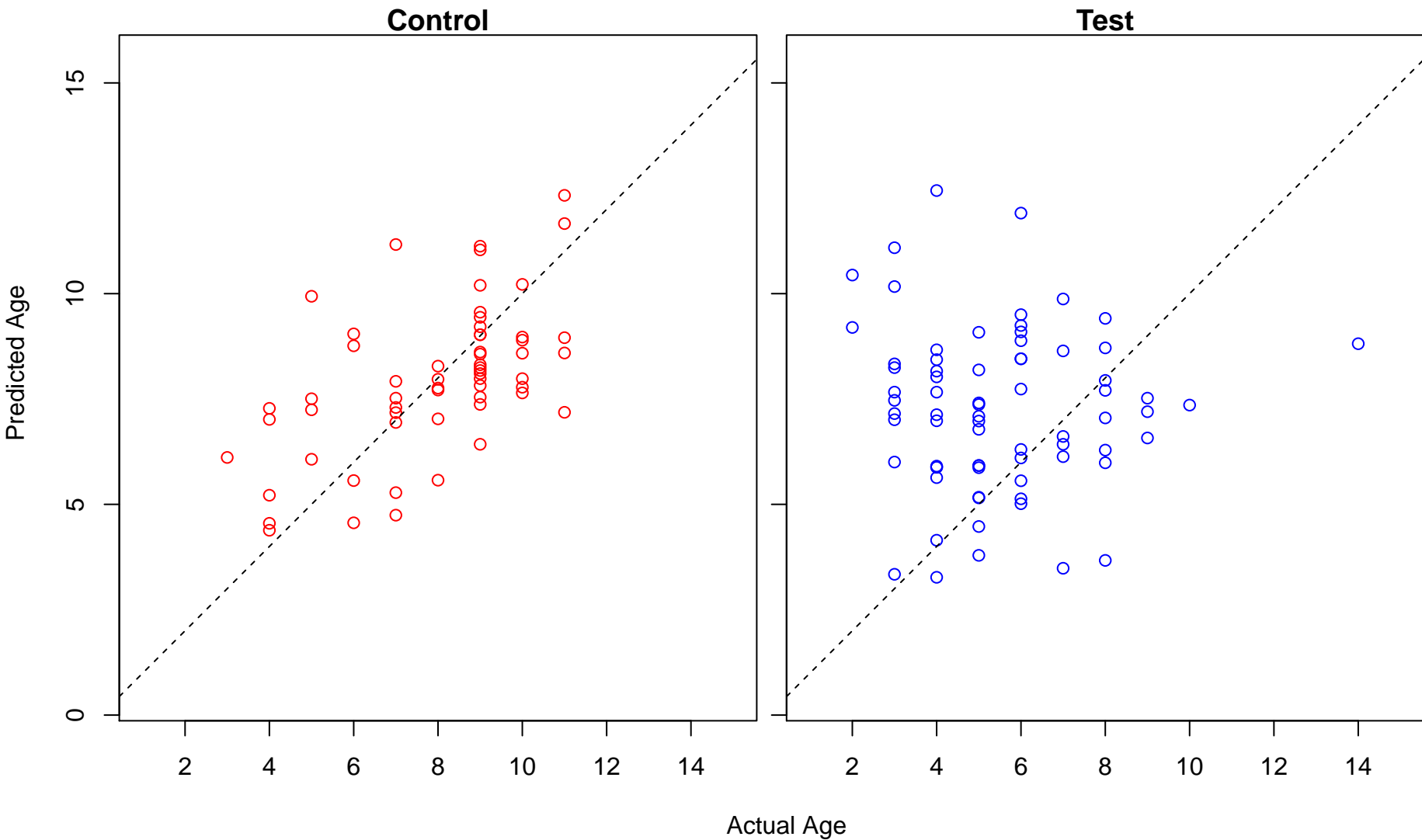
negative regulation of catabolic process (Score: 1.881069)



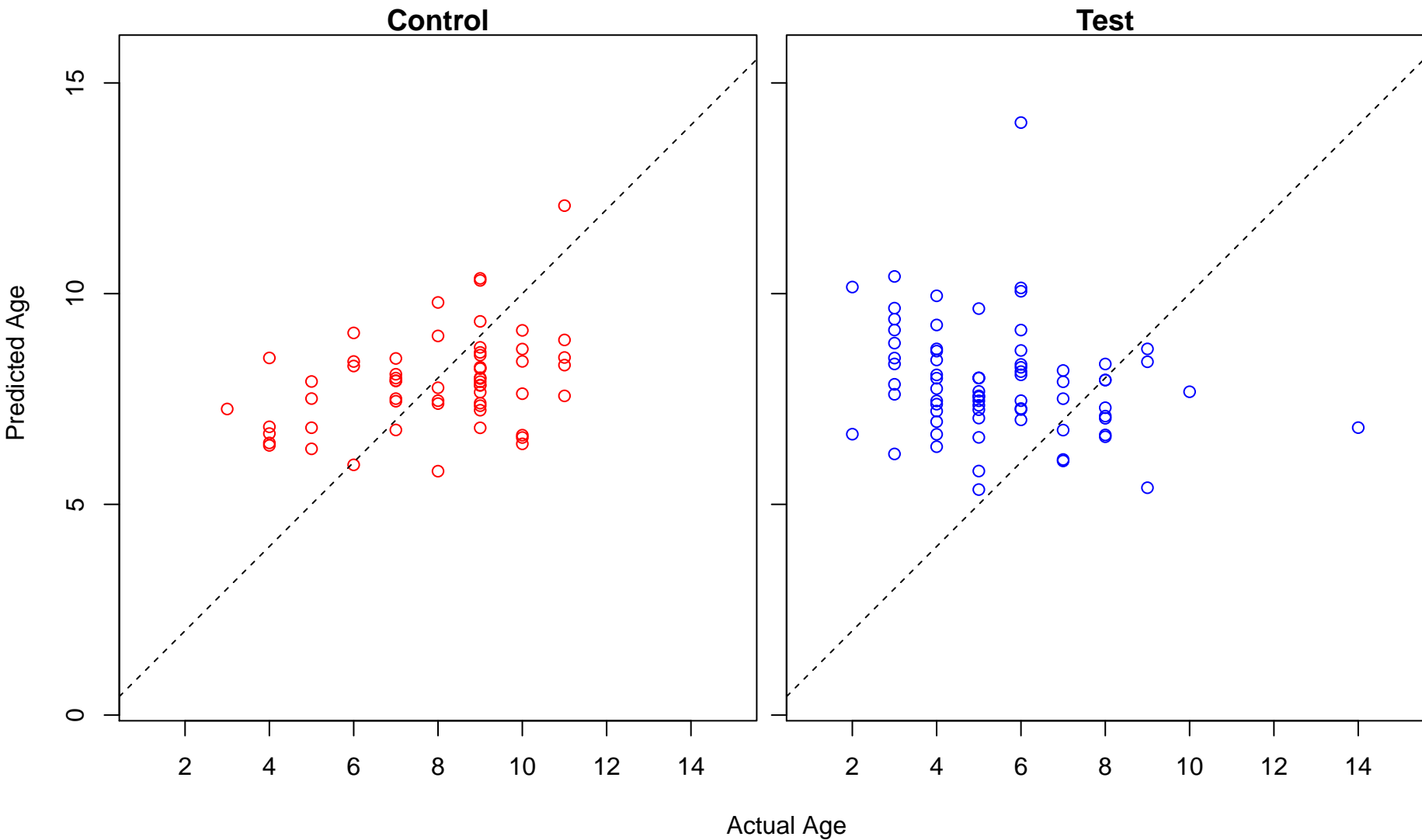
peptidyl-lysine acetylation (Score: 1.880998)



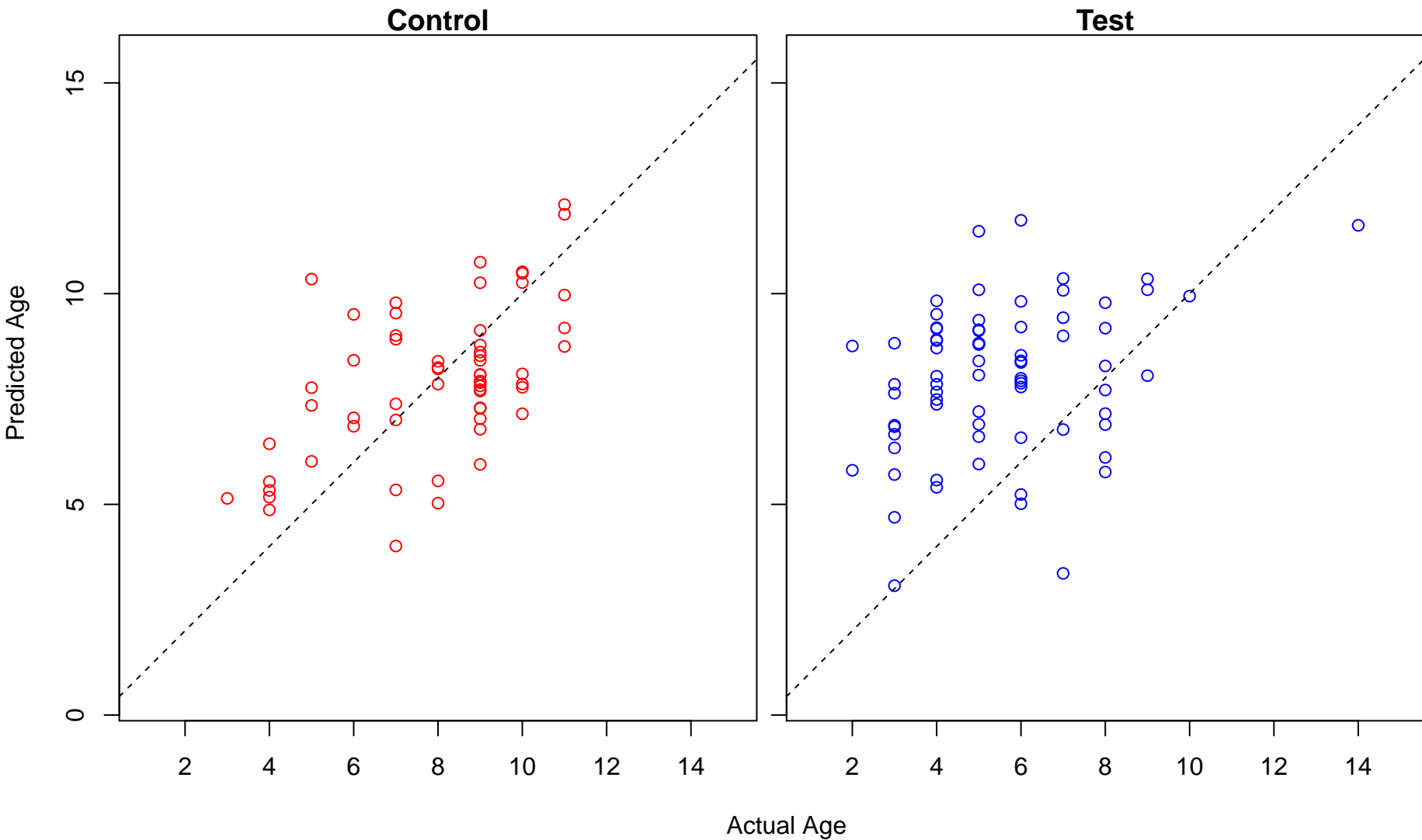
purine nucleotide biosynthetic process (Score: 1.880273)



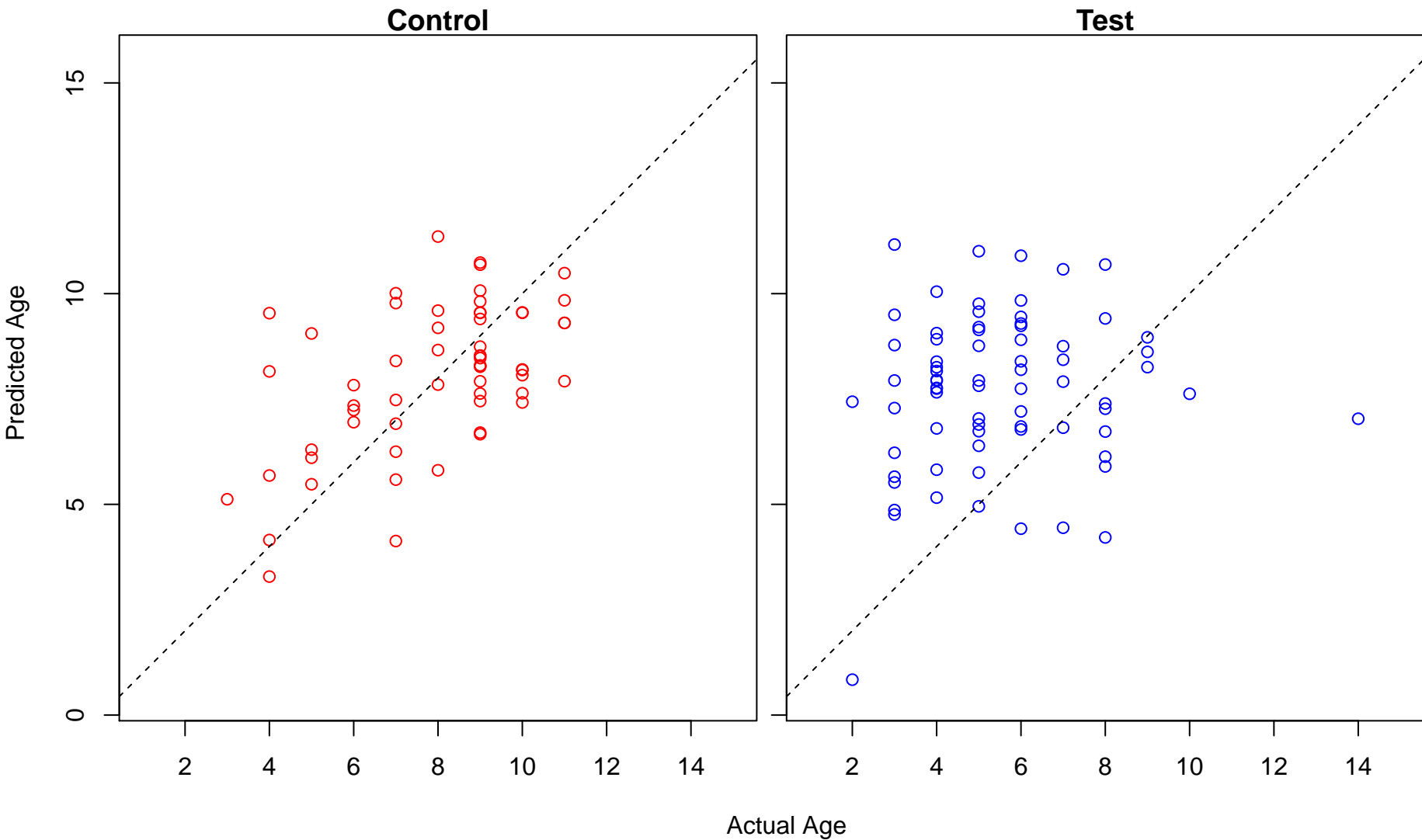
negative regulation of activated T cell proliferation (Score: 1.879818)



protein acylation (Score: 1.876242)

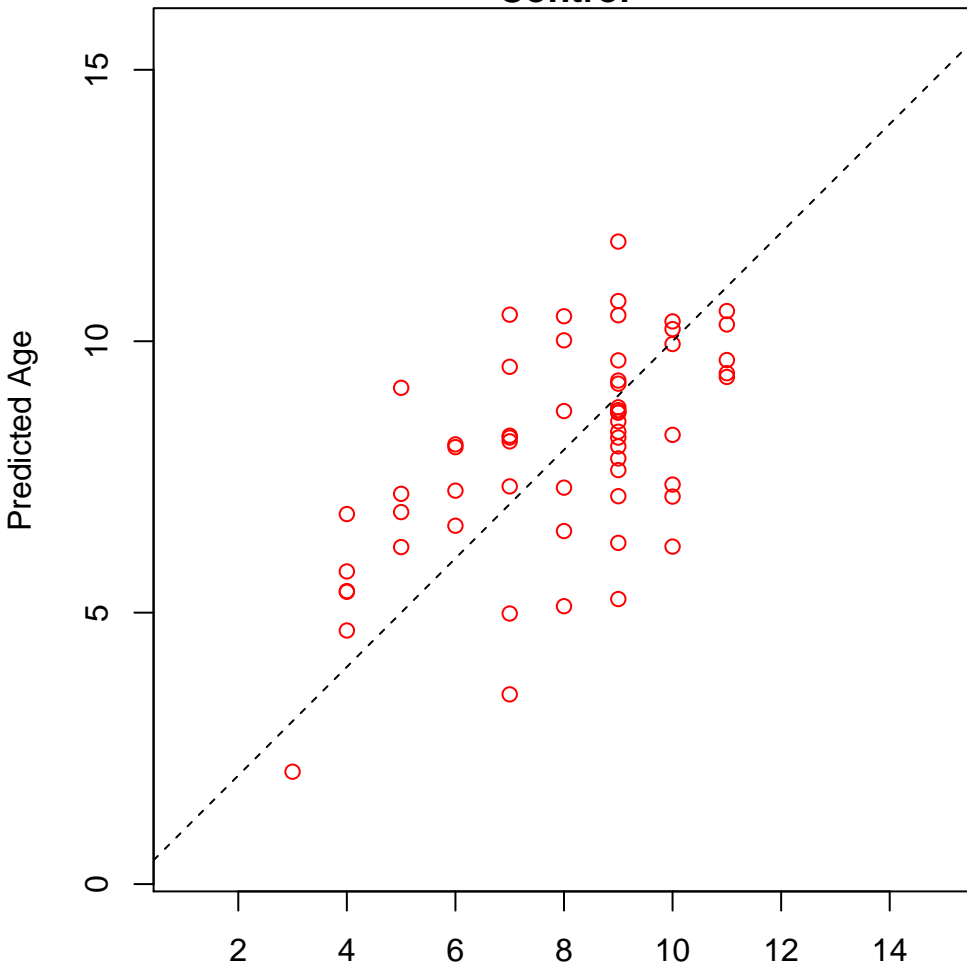


regulation of tyrosine phosphorylation of STAT protein (Score: 1.876073)

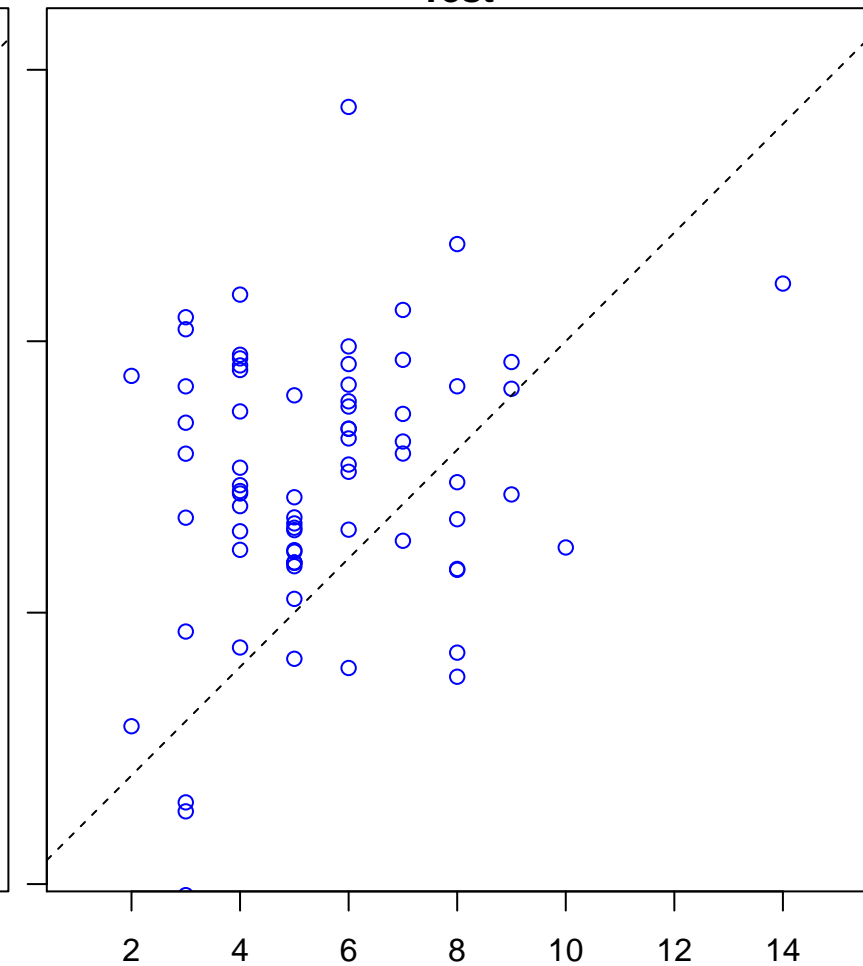


mesonephric epithelium development (Score: 1.874966)

Control

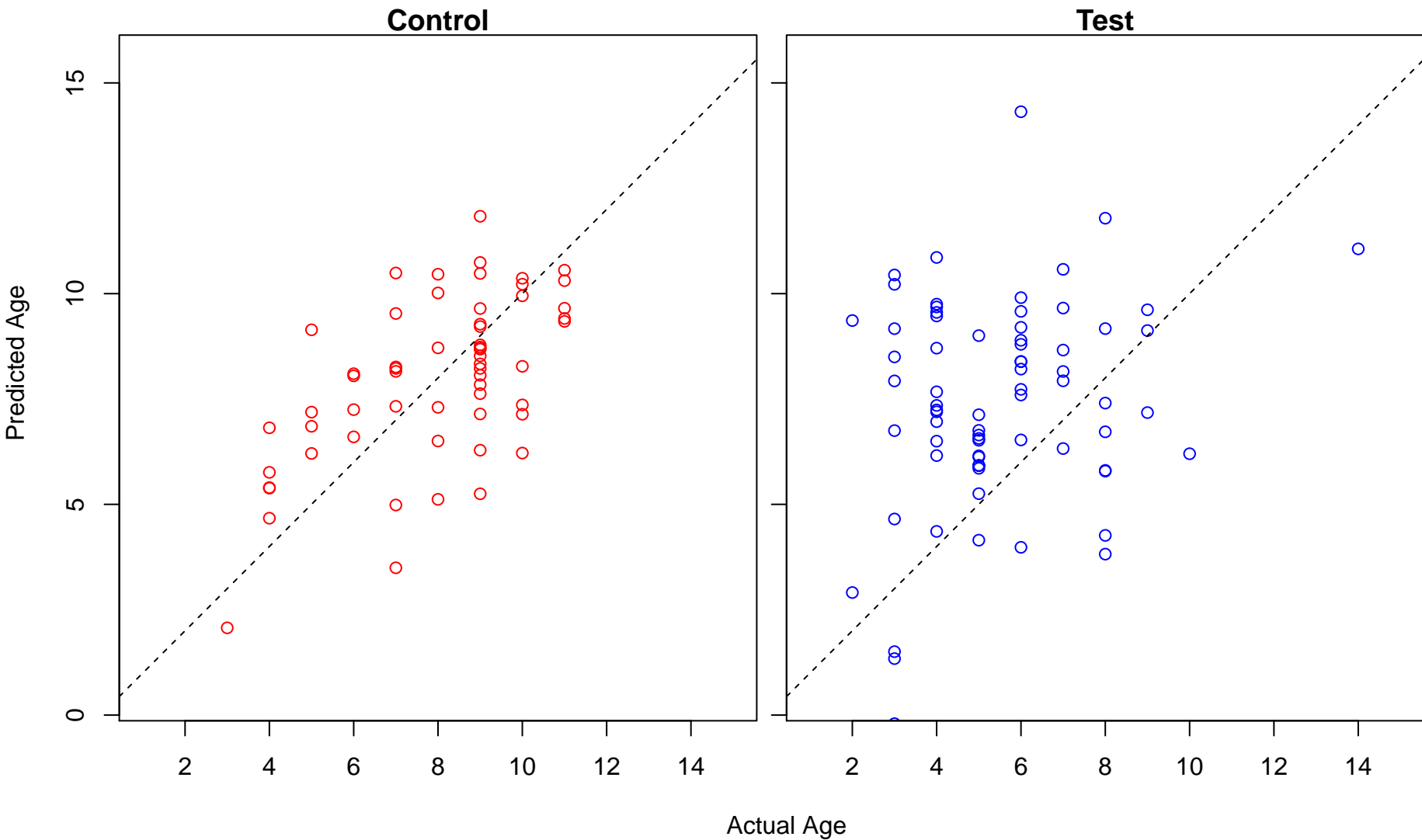


Test

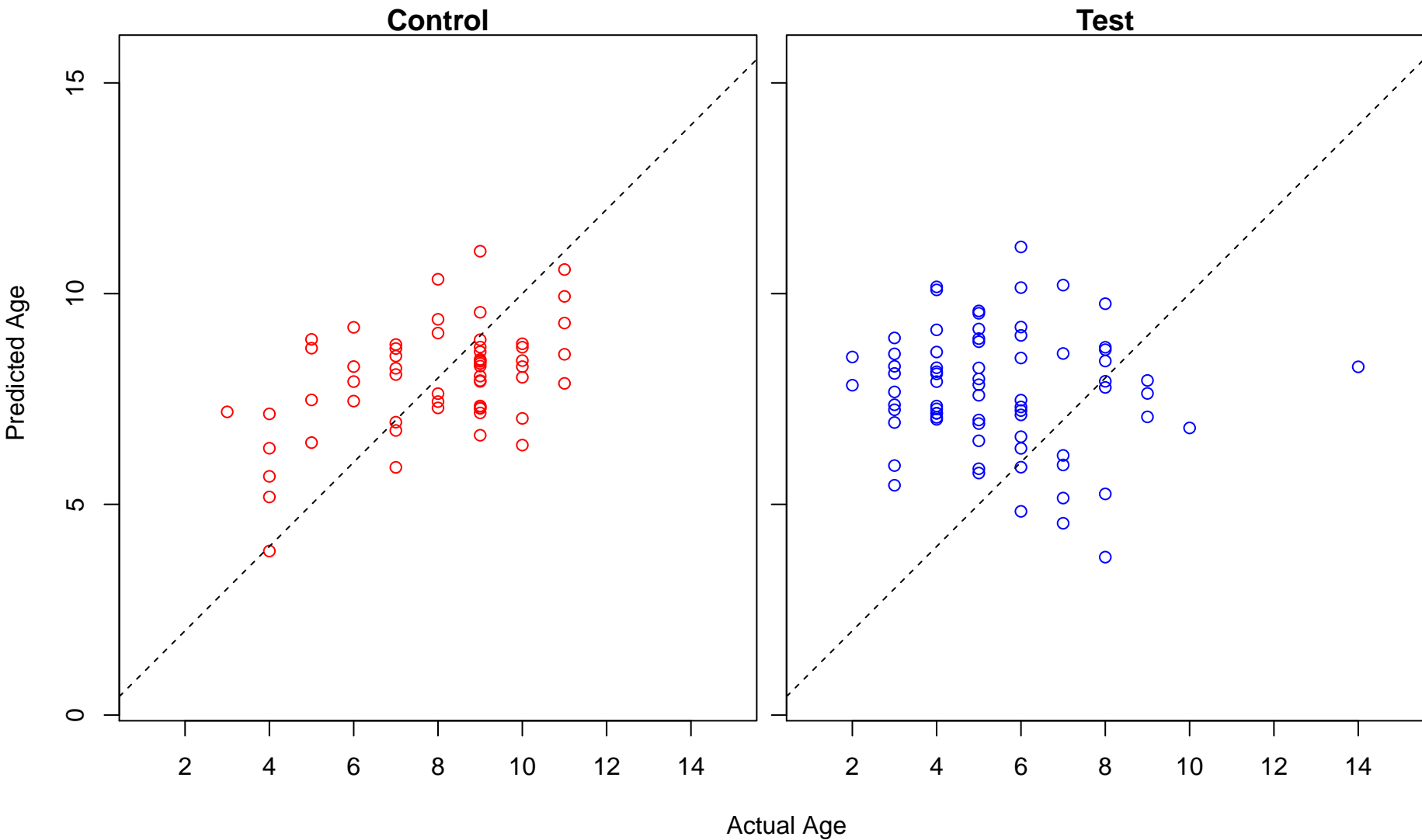


Actual Age

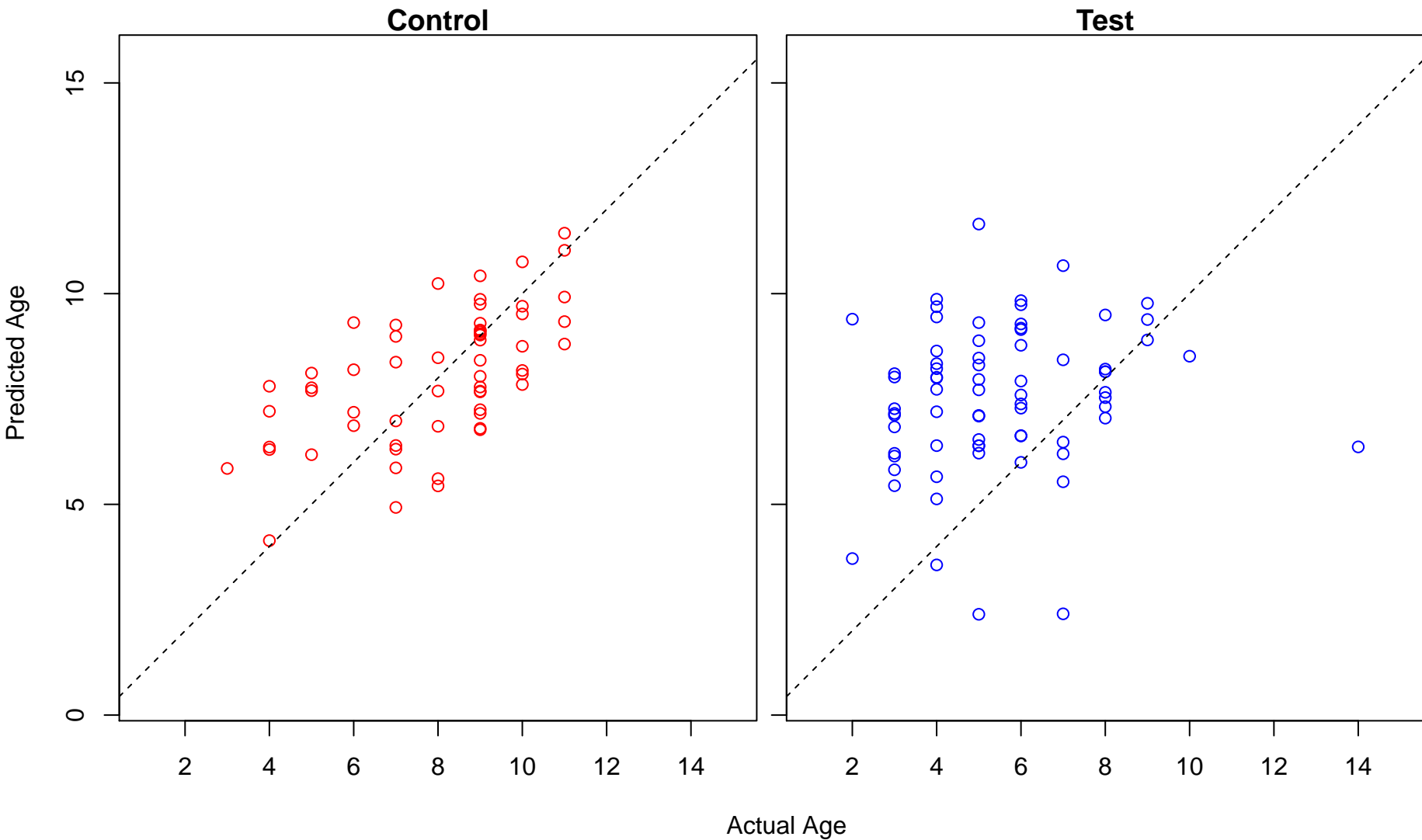
mesonephric tubule development (Score: 1.874966)



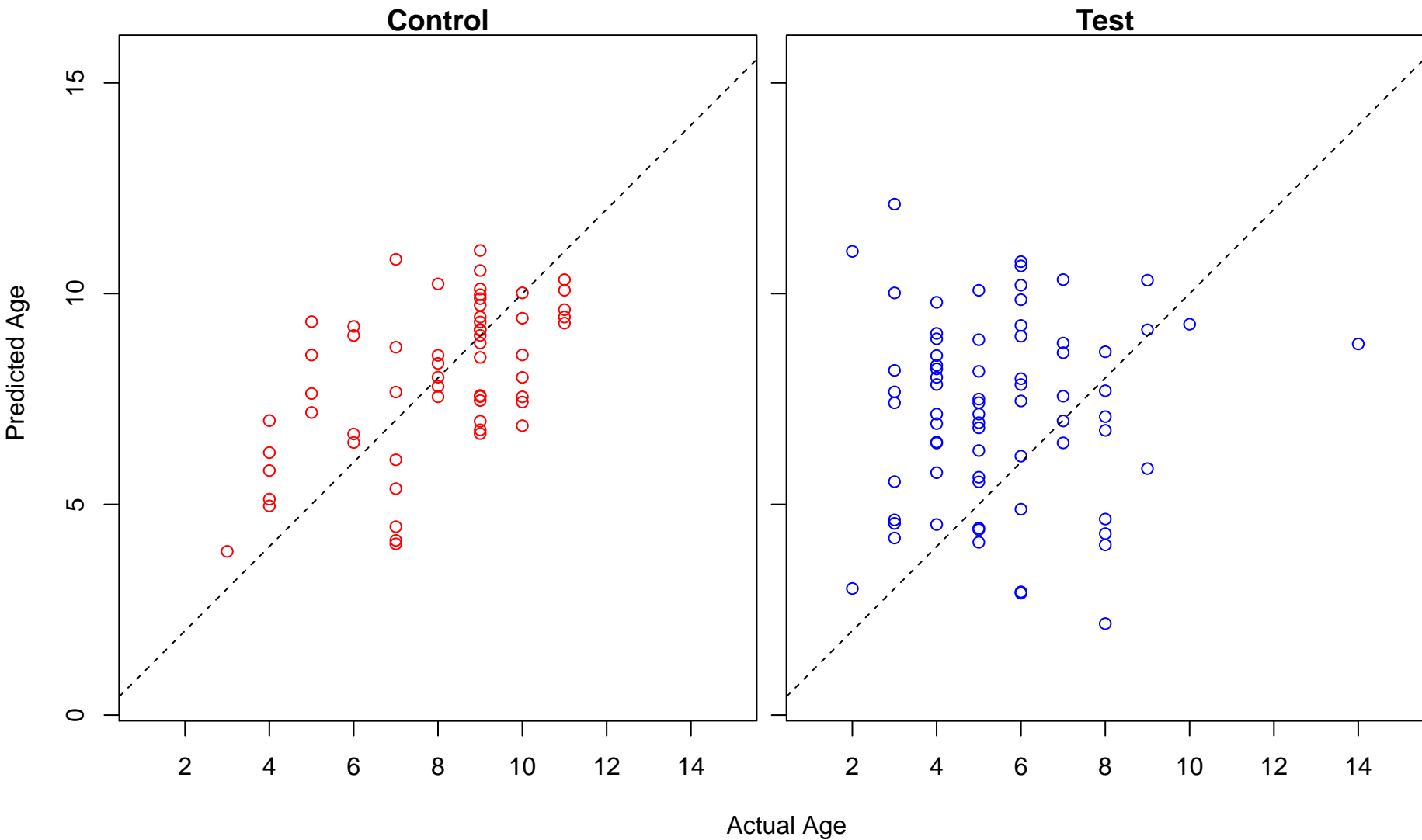
negative regulation of neurotransmitter transport (Score: 1.873387)



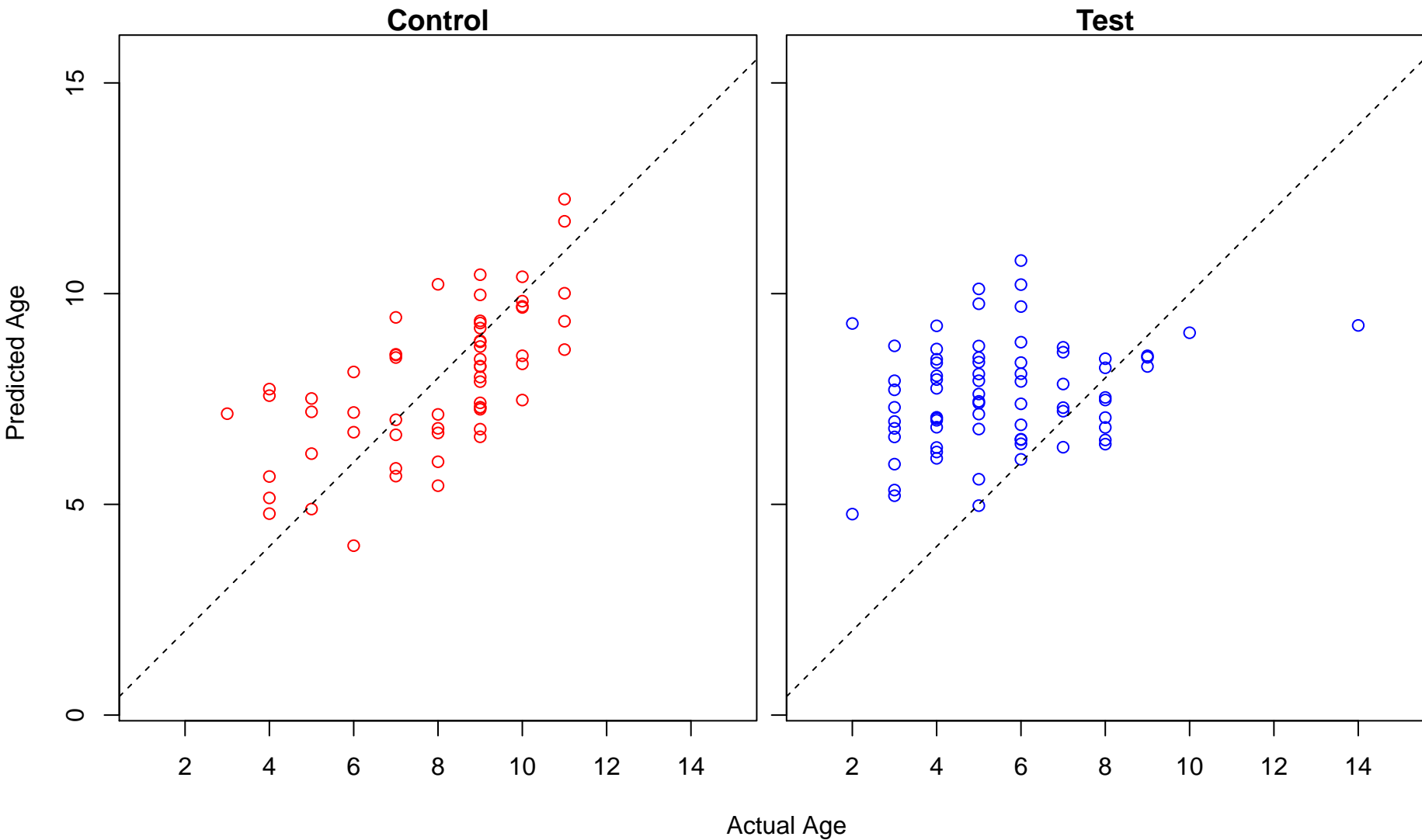
regulation of primary metabolic process (Score: 1.873300)



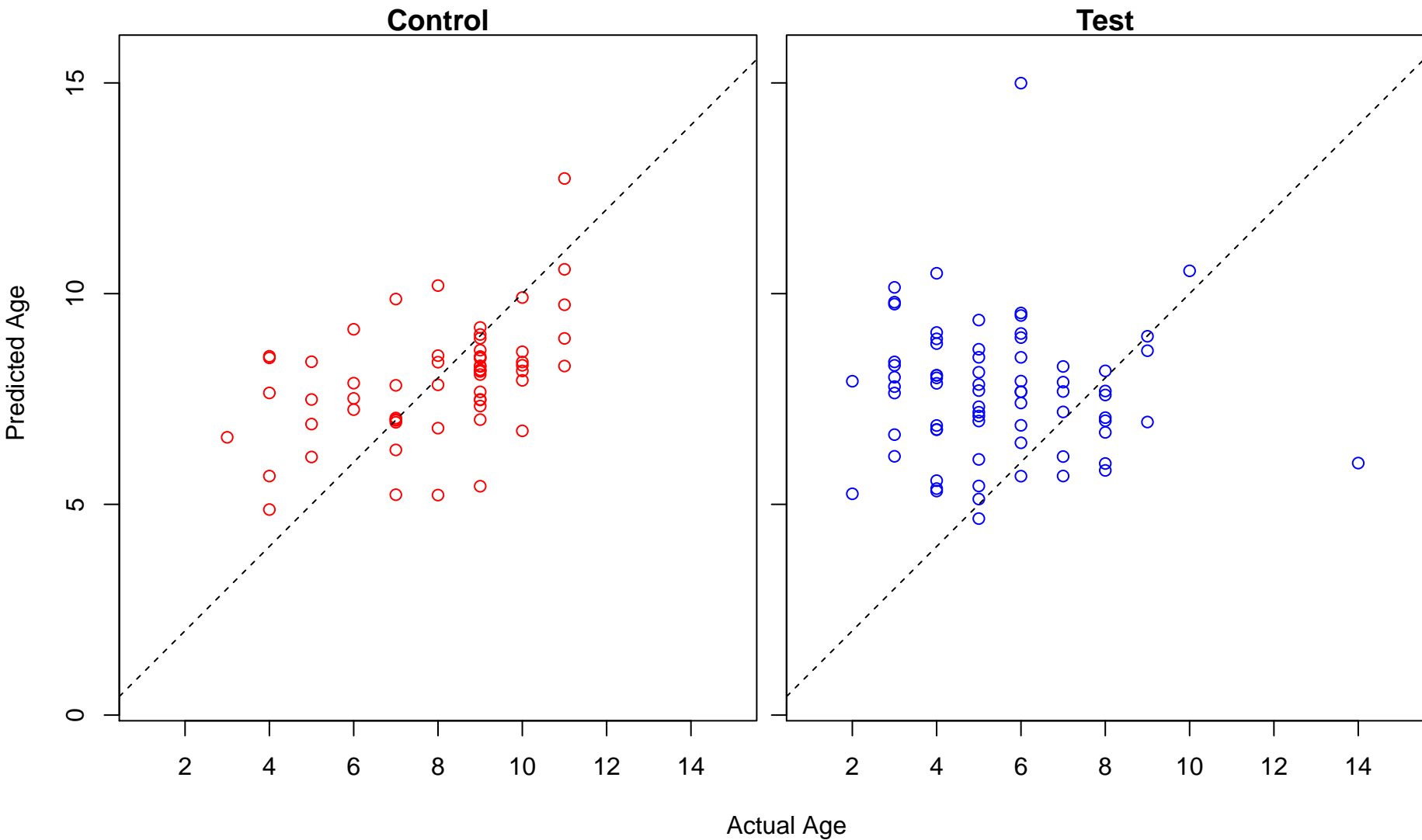
spinal cord development (Score: 1.873234)



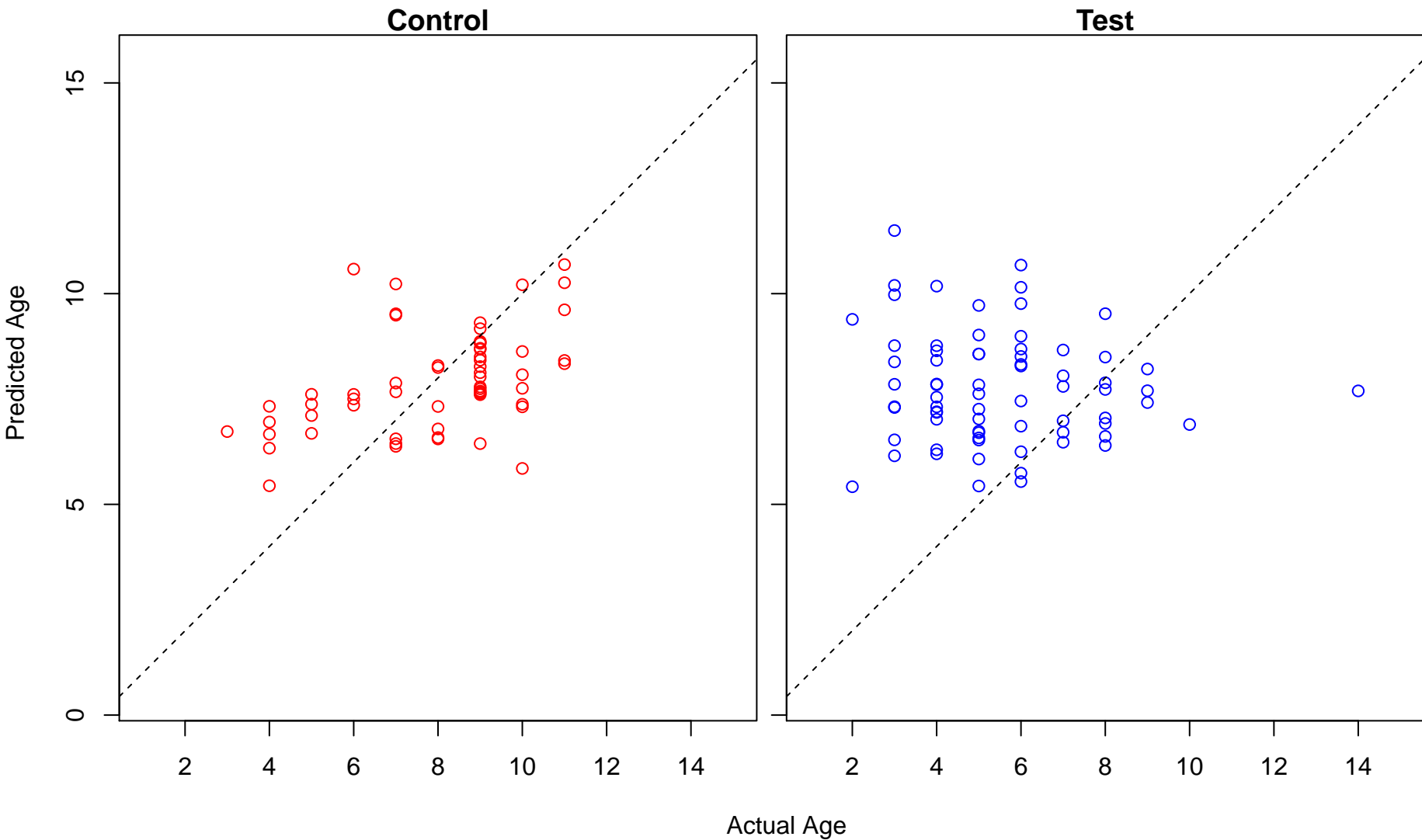
macromolecule localization (Score: 1.871290)



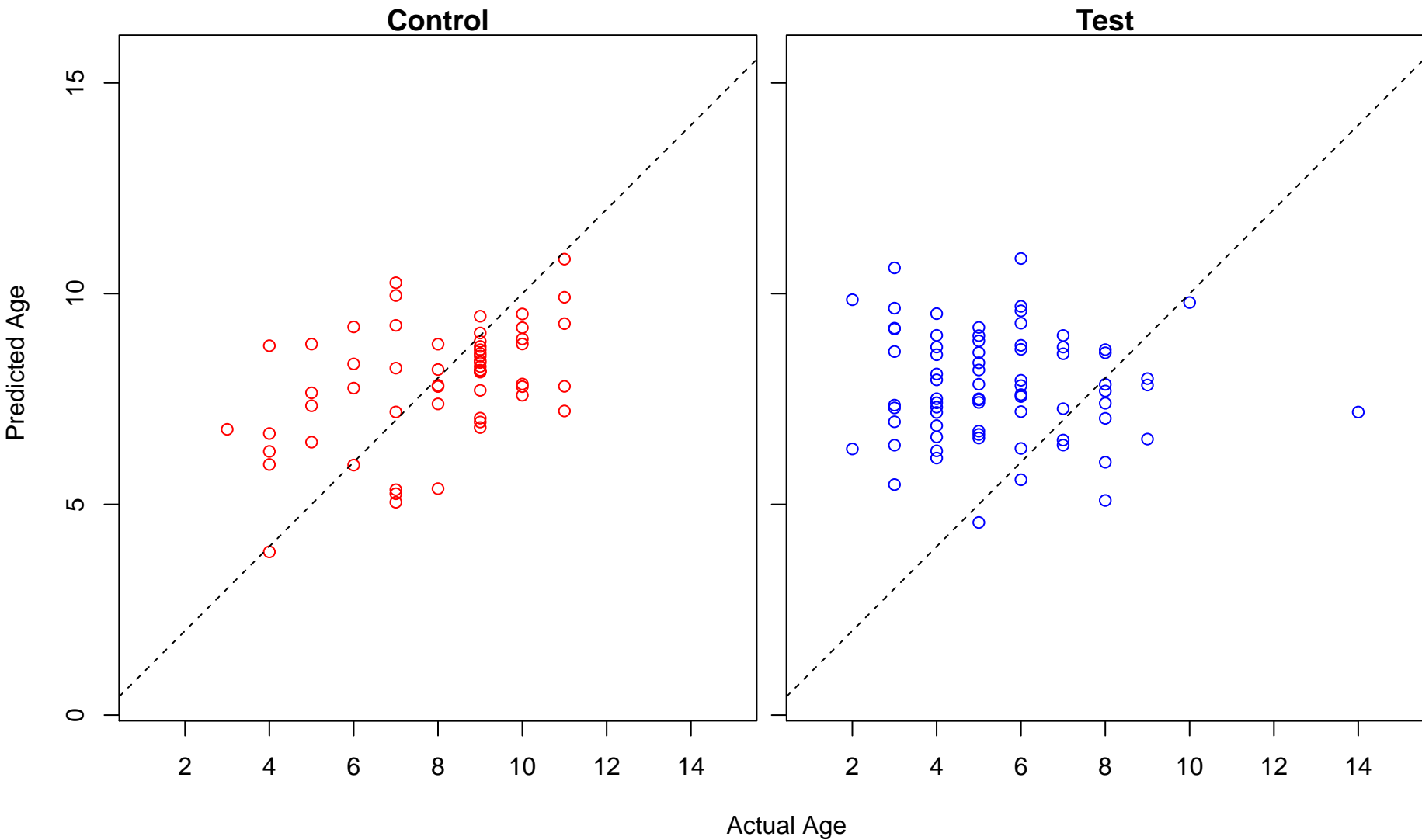
positive regulation of CD4-positive, alpha-beta T cell differentiation (Score: 1.870825)



receptor clustering (Score: 1.869070)

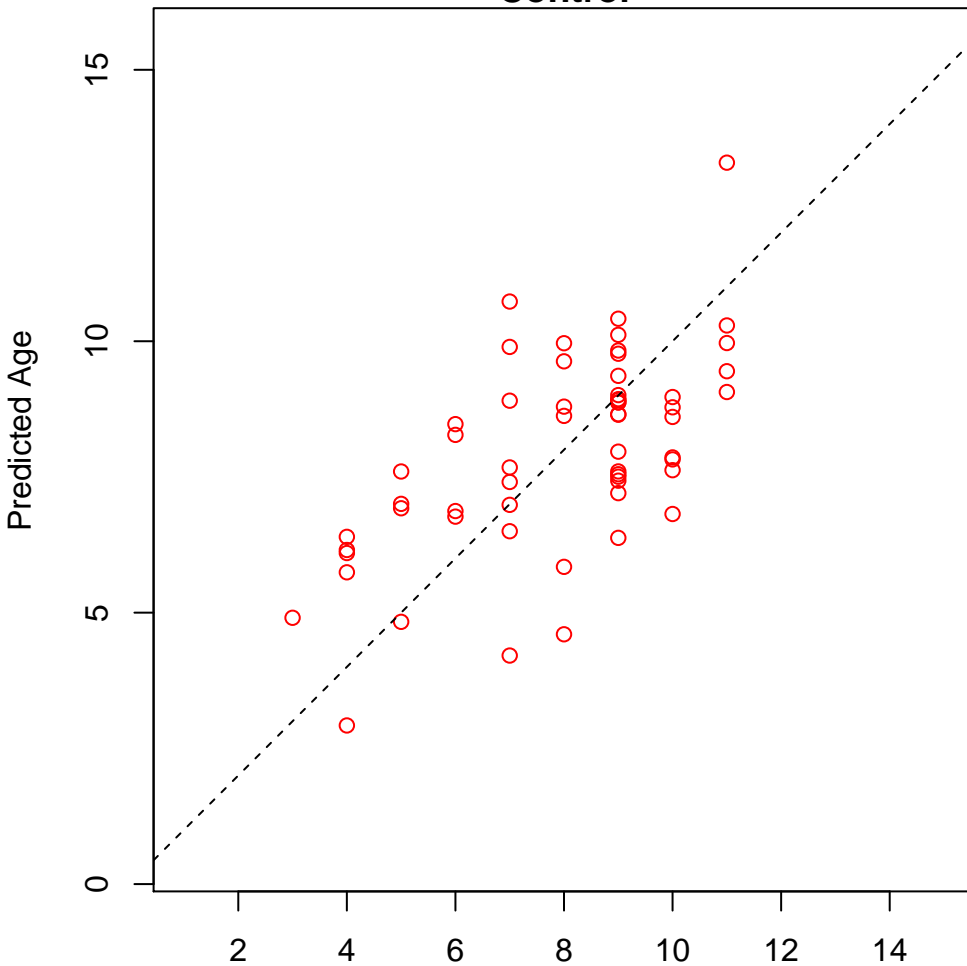


mRNA splice site selection (Score: 1.867010)

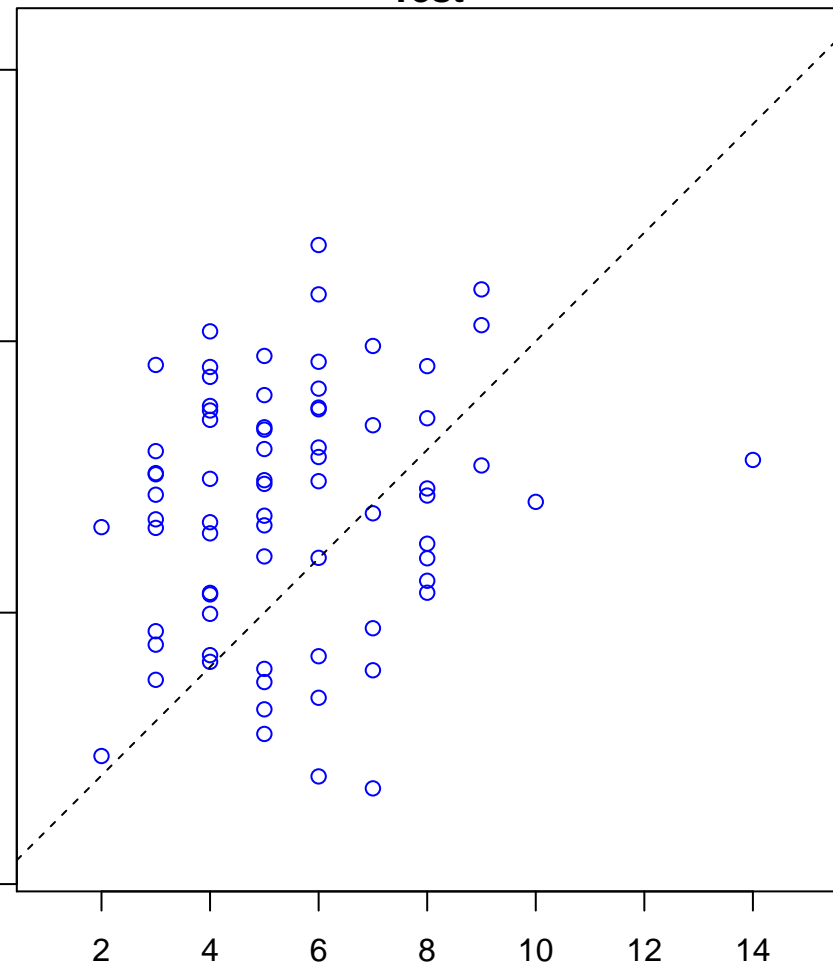


regulation of glucose metabolic process (Score: 1.865743)

Control

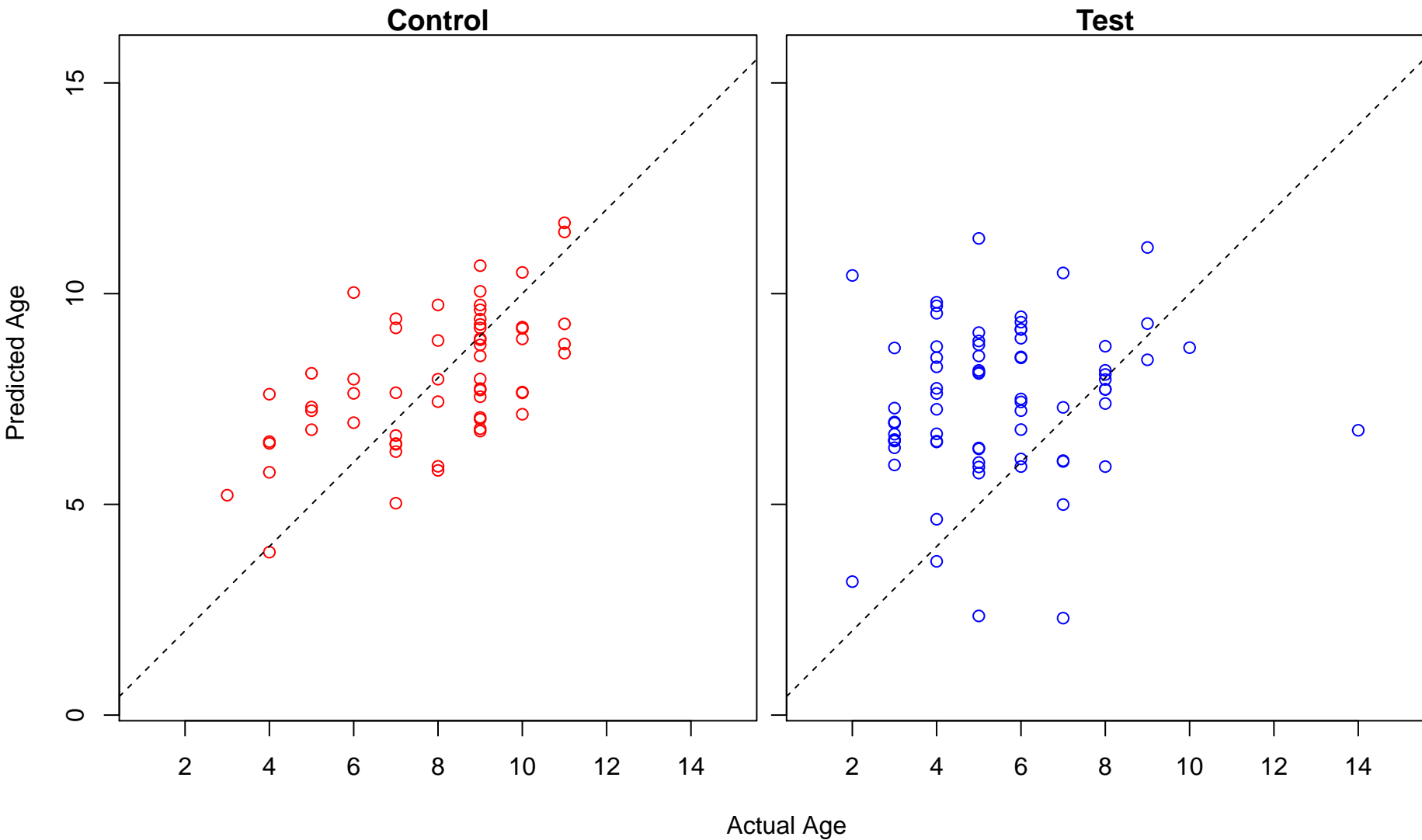


Test

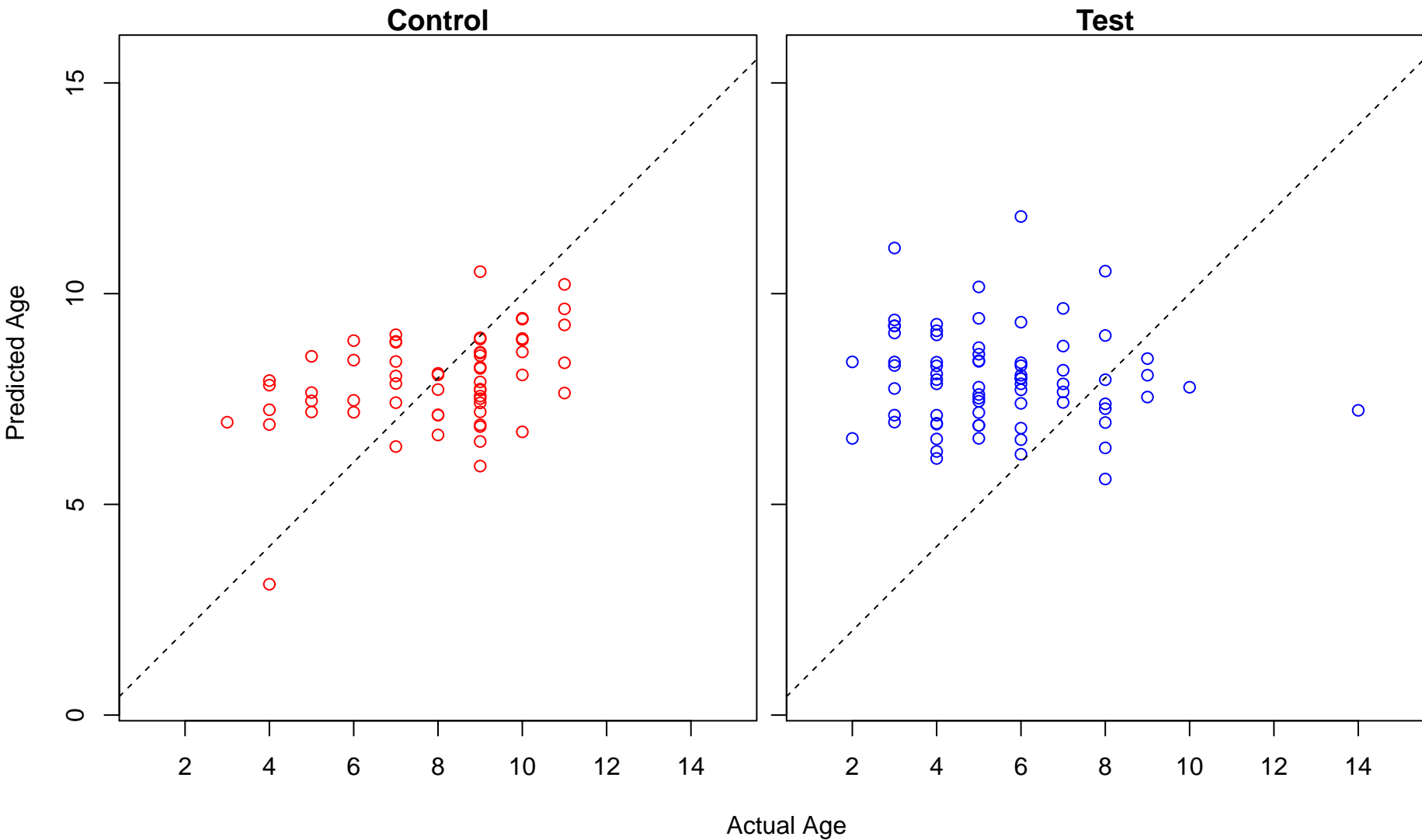


Actual Age

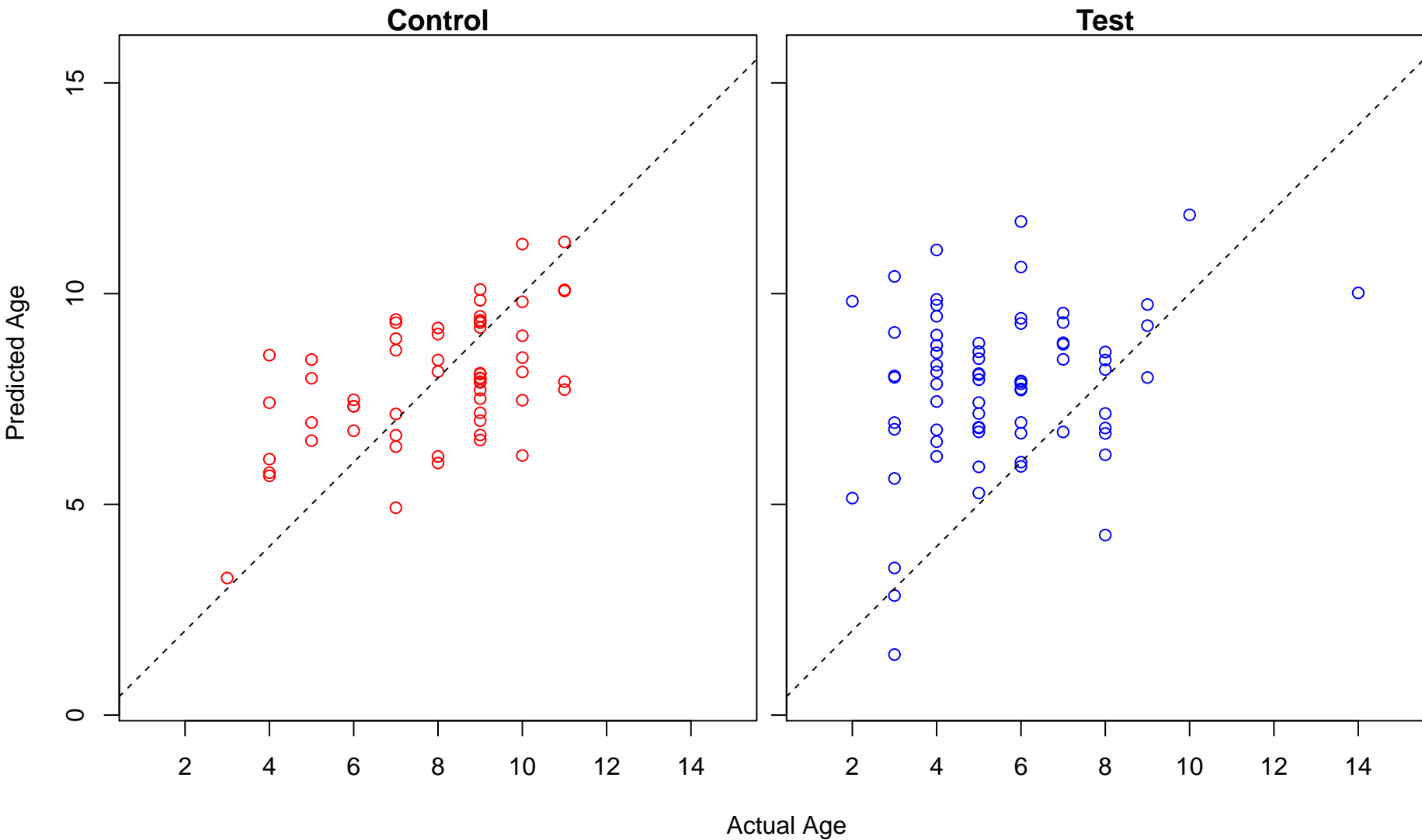
regulation of gene expression (Score: 1.865056)



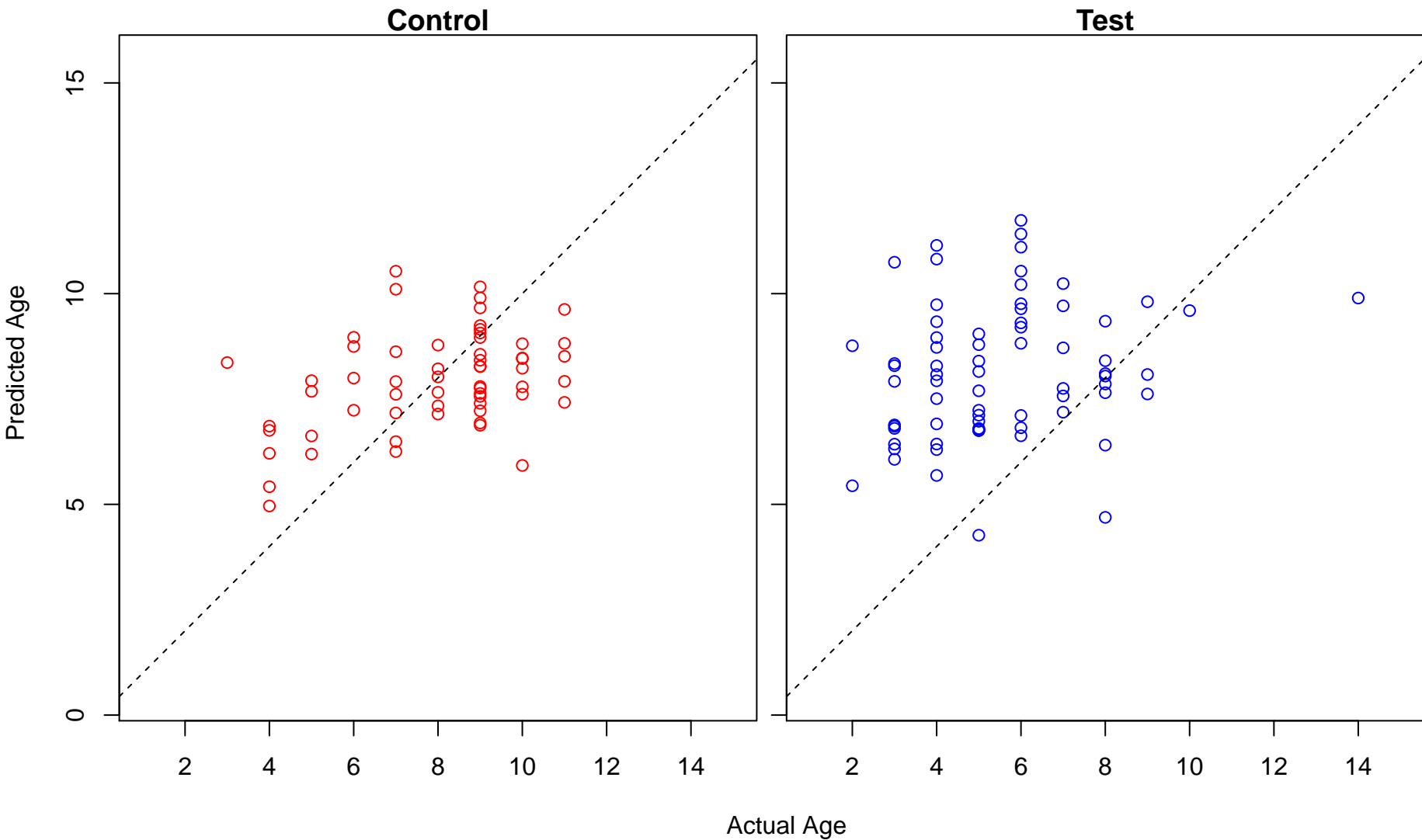
medulla oblongata development (Score: 1.864677)



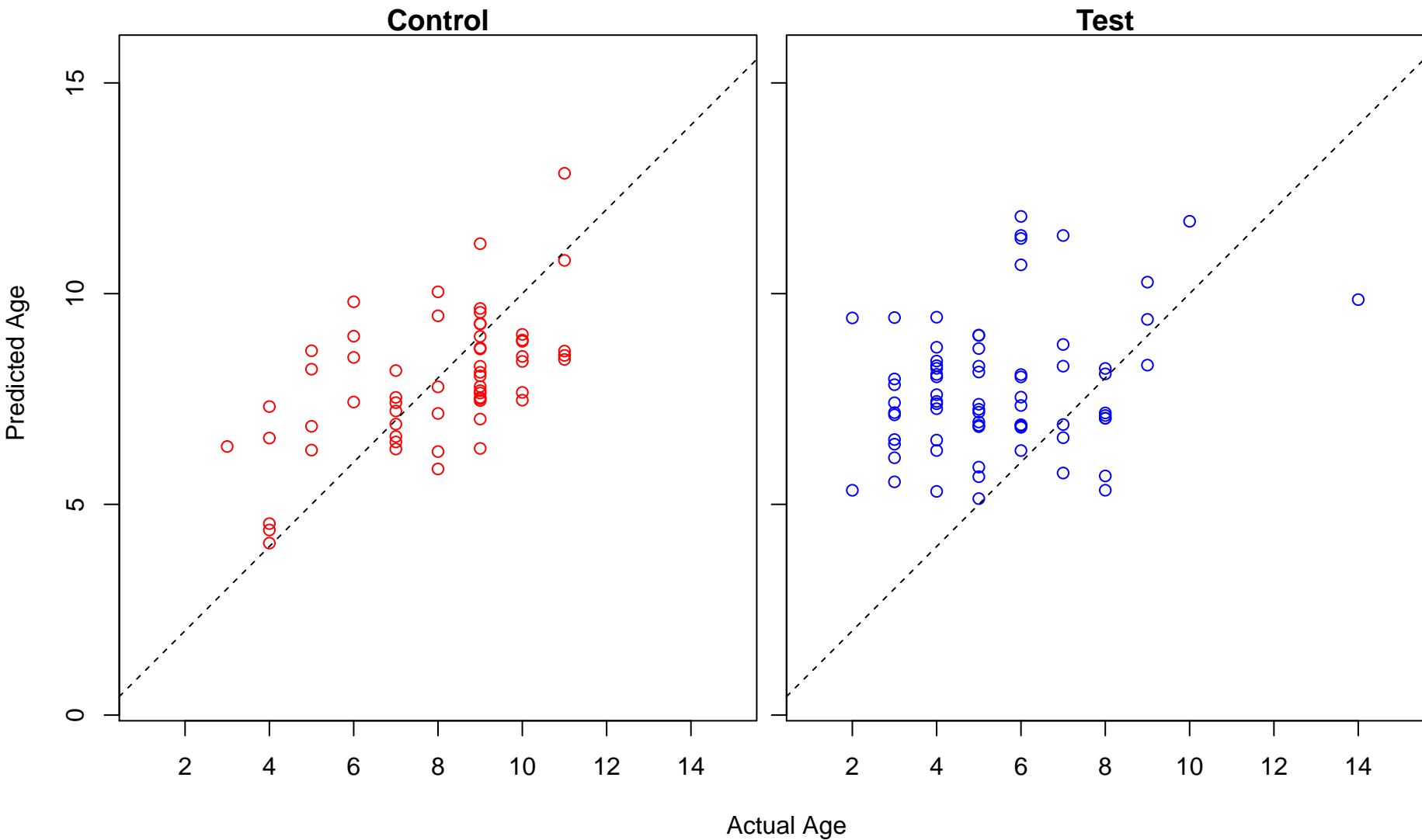
regulation of mesonephros development (Score: 1.864043)



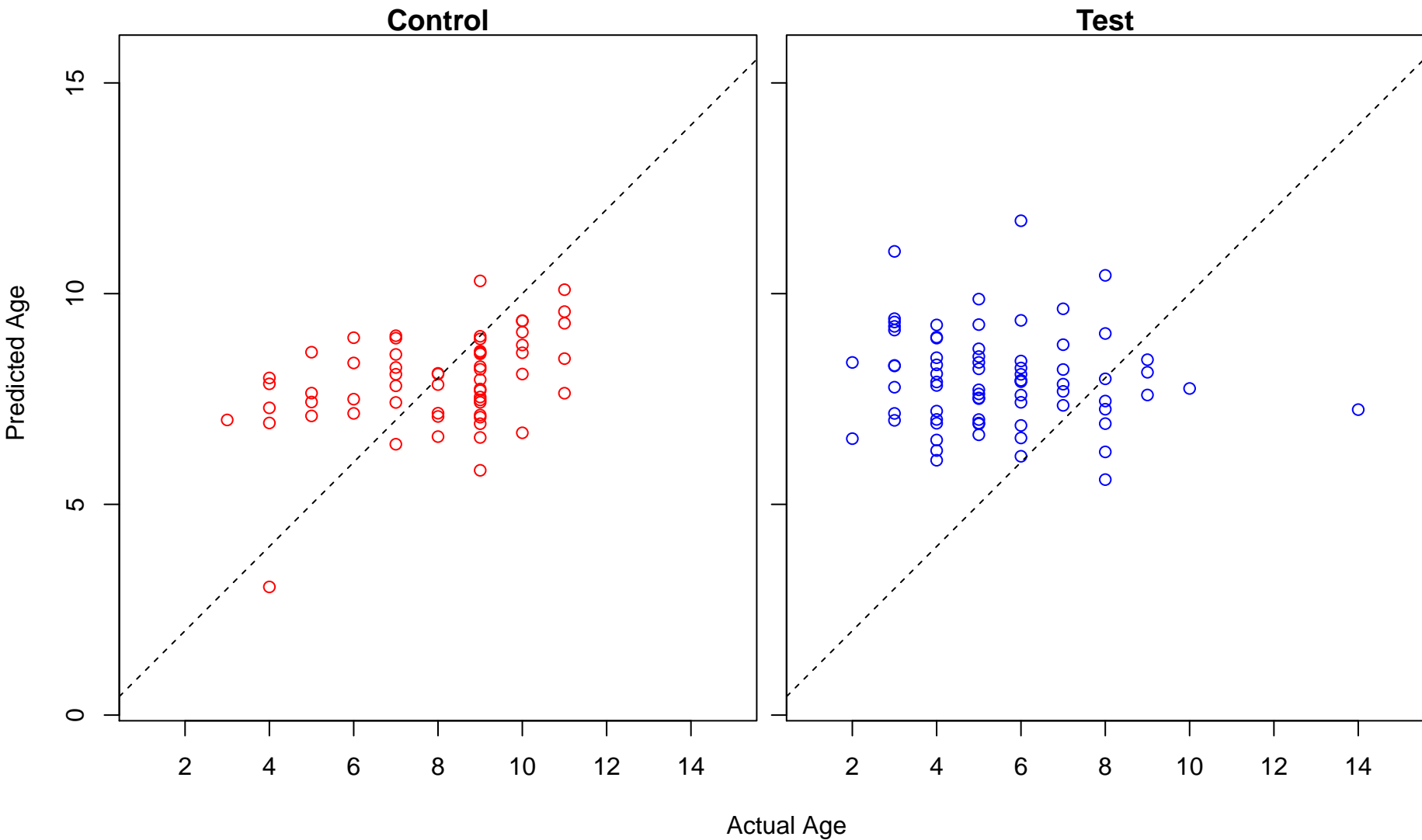
positive regulation of Rho protein signal transduction (Score: 1.863494)



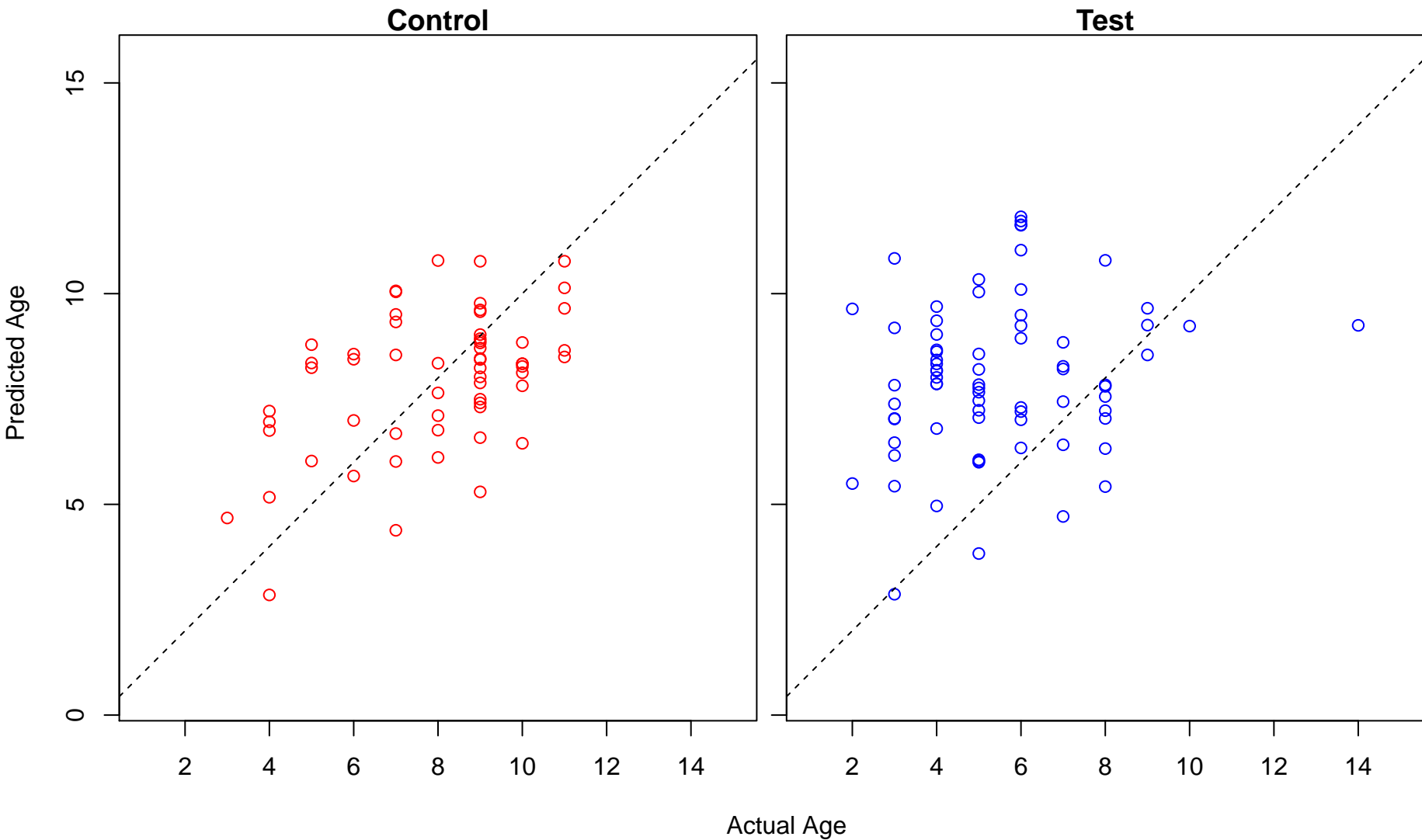
positive regulation of phagocytosis (Score: 1.862176)



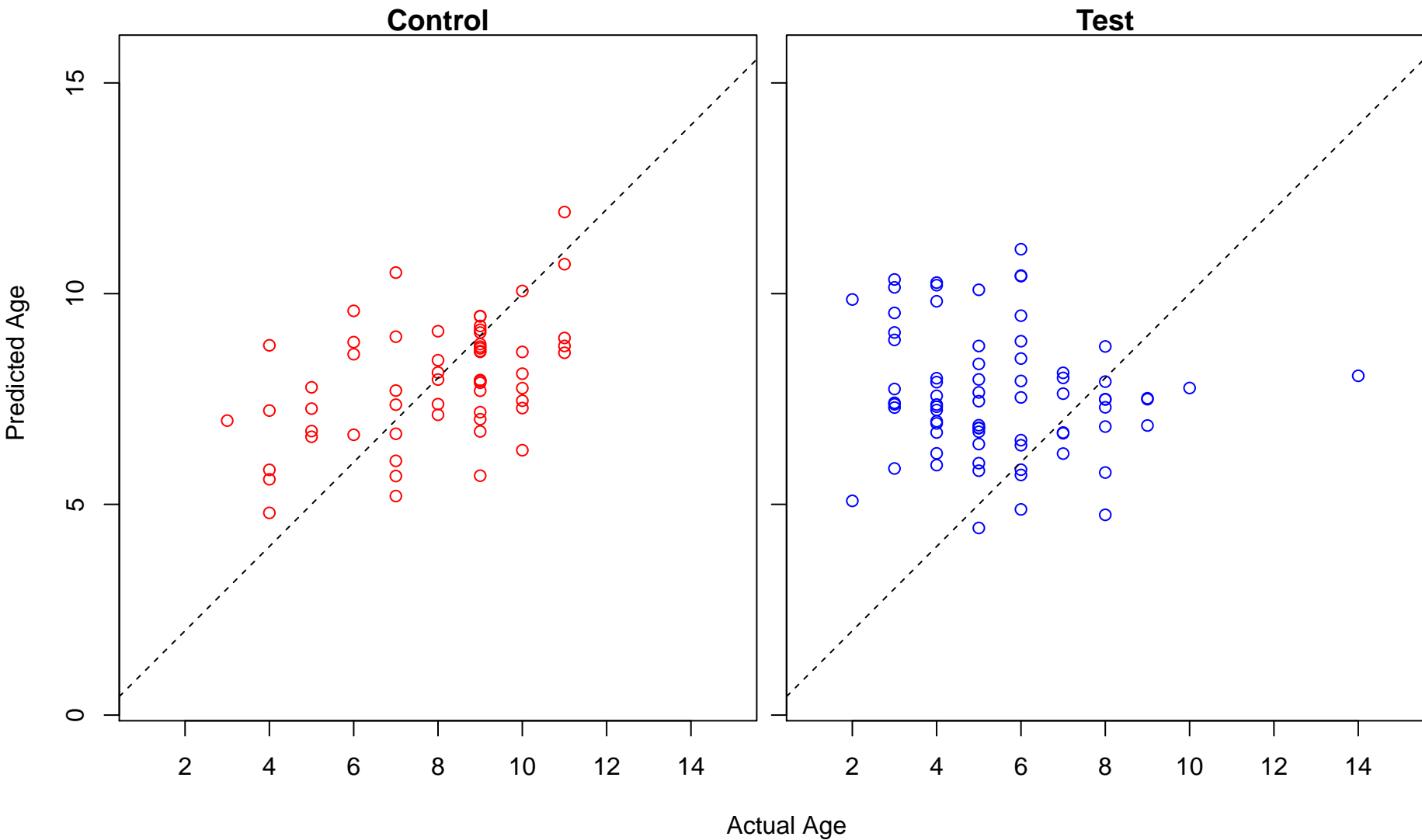
vestibular nucleus development (Score: 1.862077)



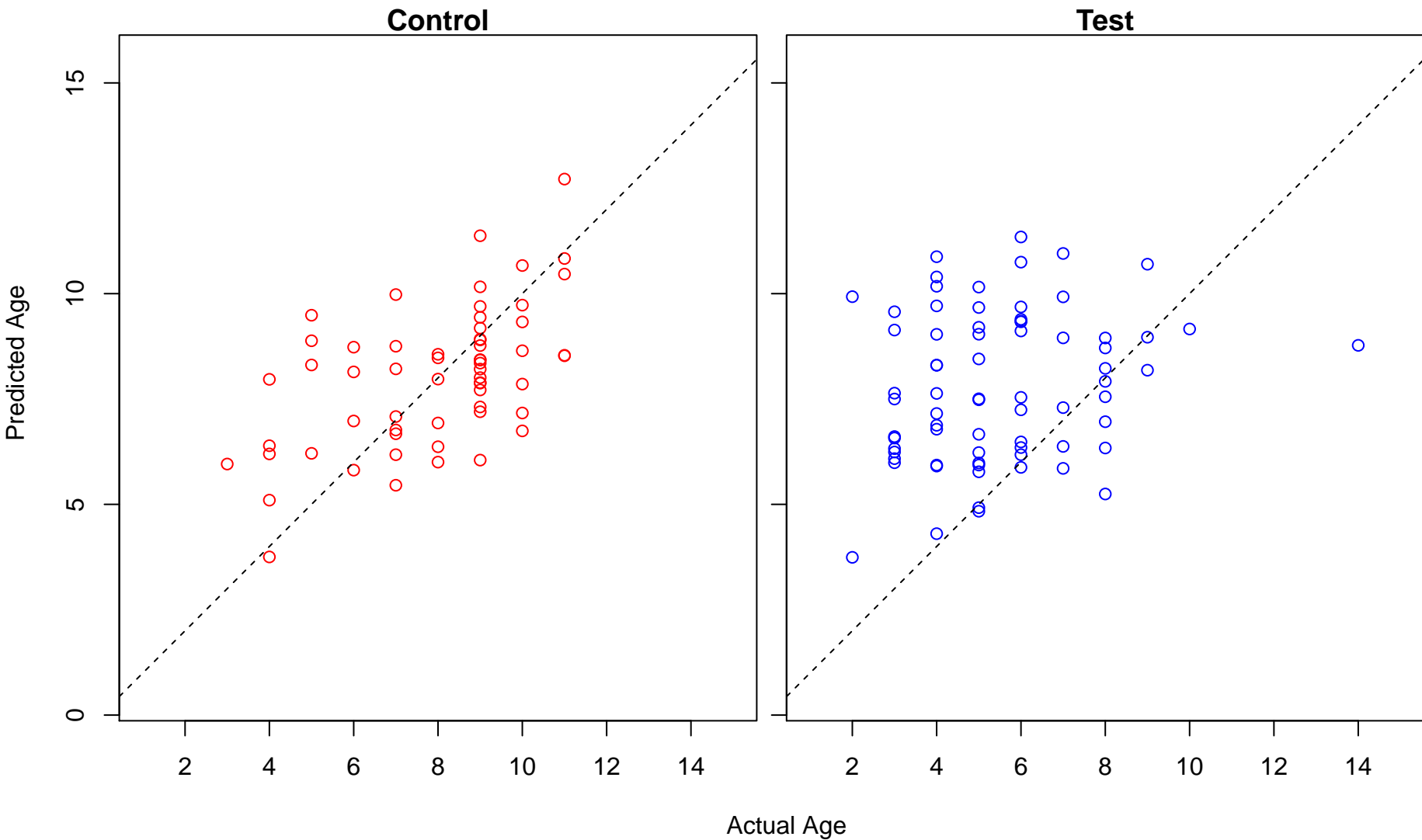
dendritic cell differentiation (Score: 1.861989)



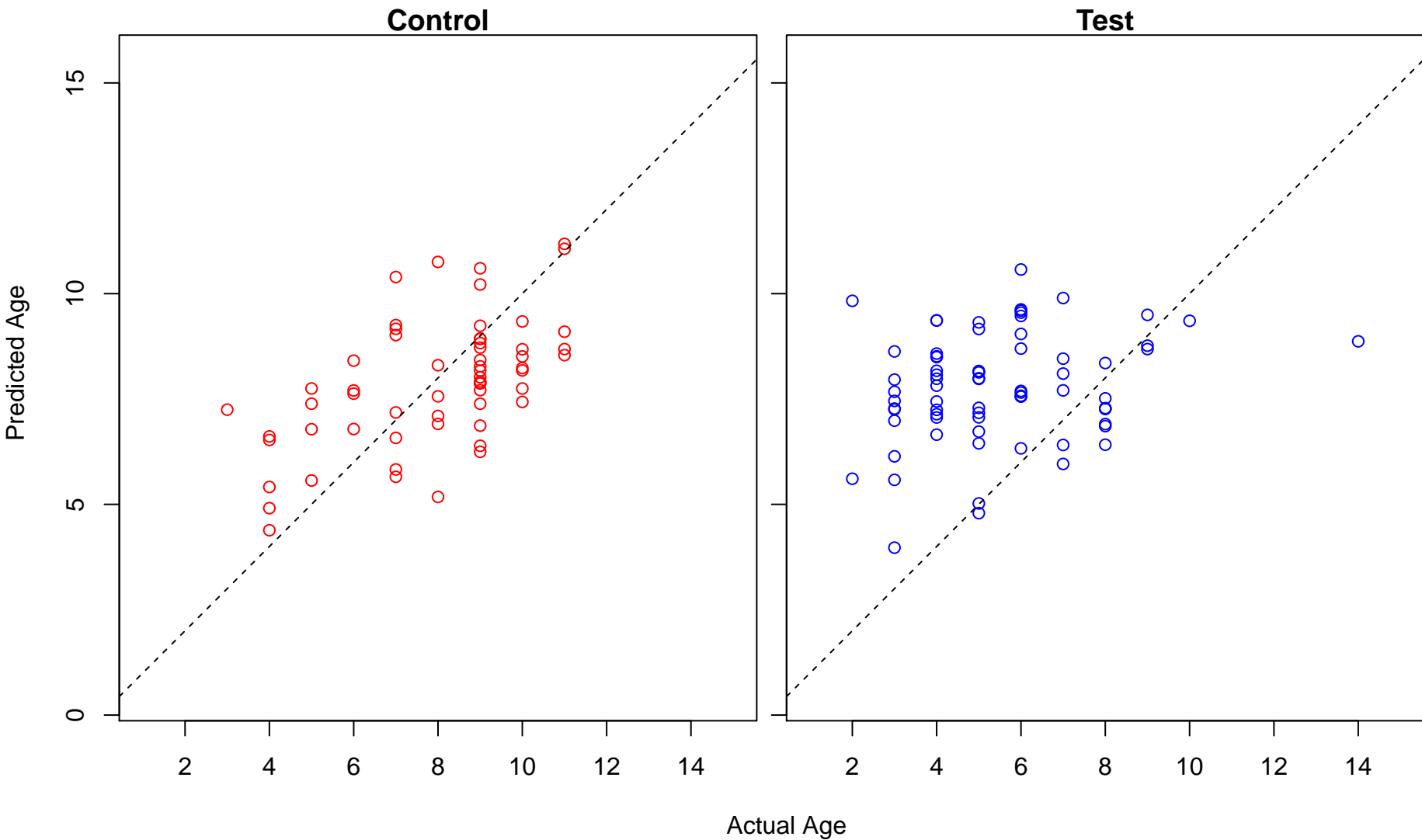
adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway (Score: 1.858175)



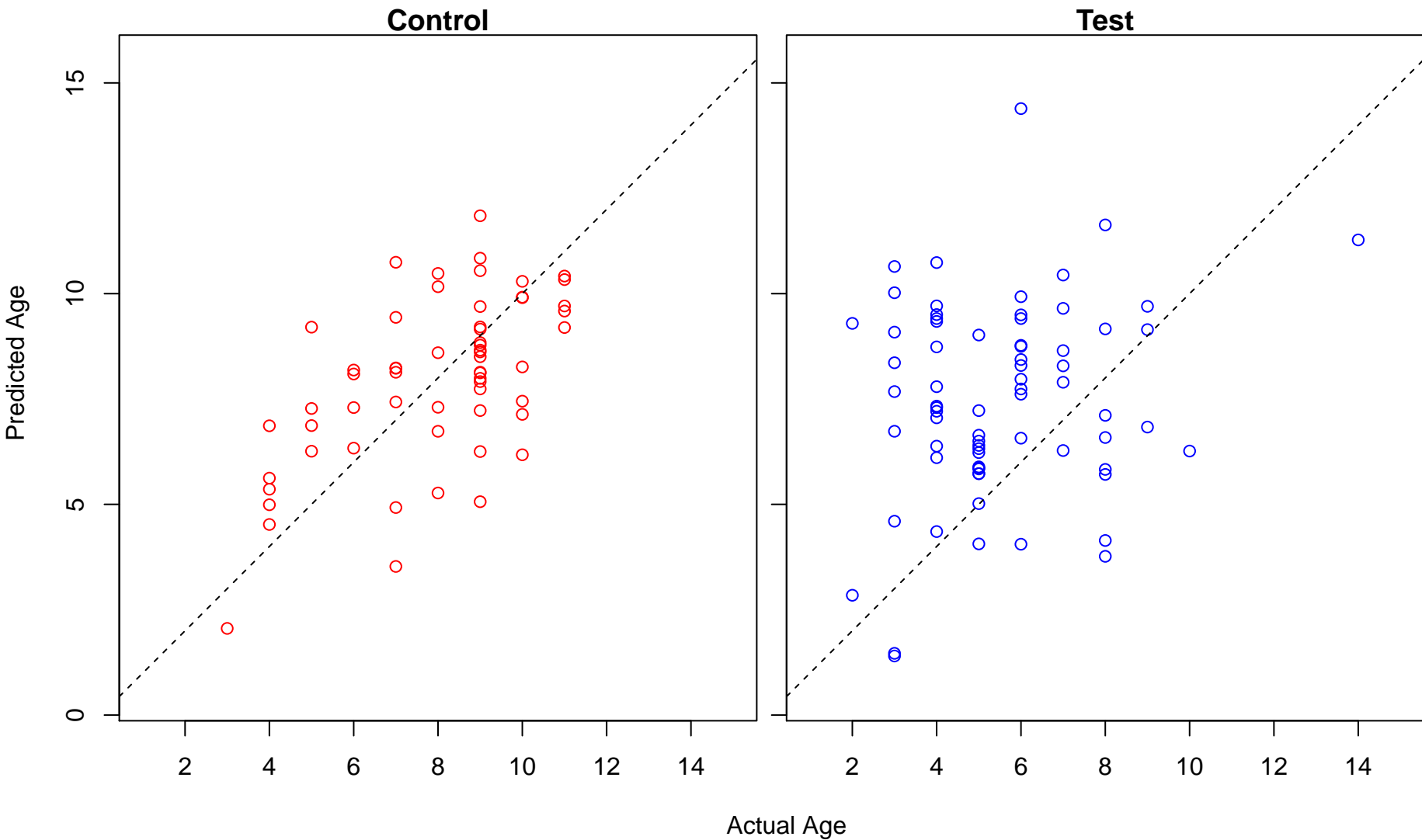
apoptotic process (Score: 1.855612)



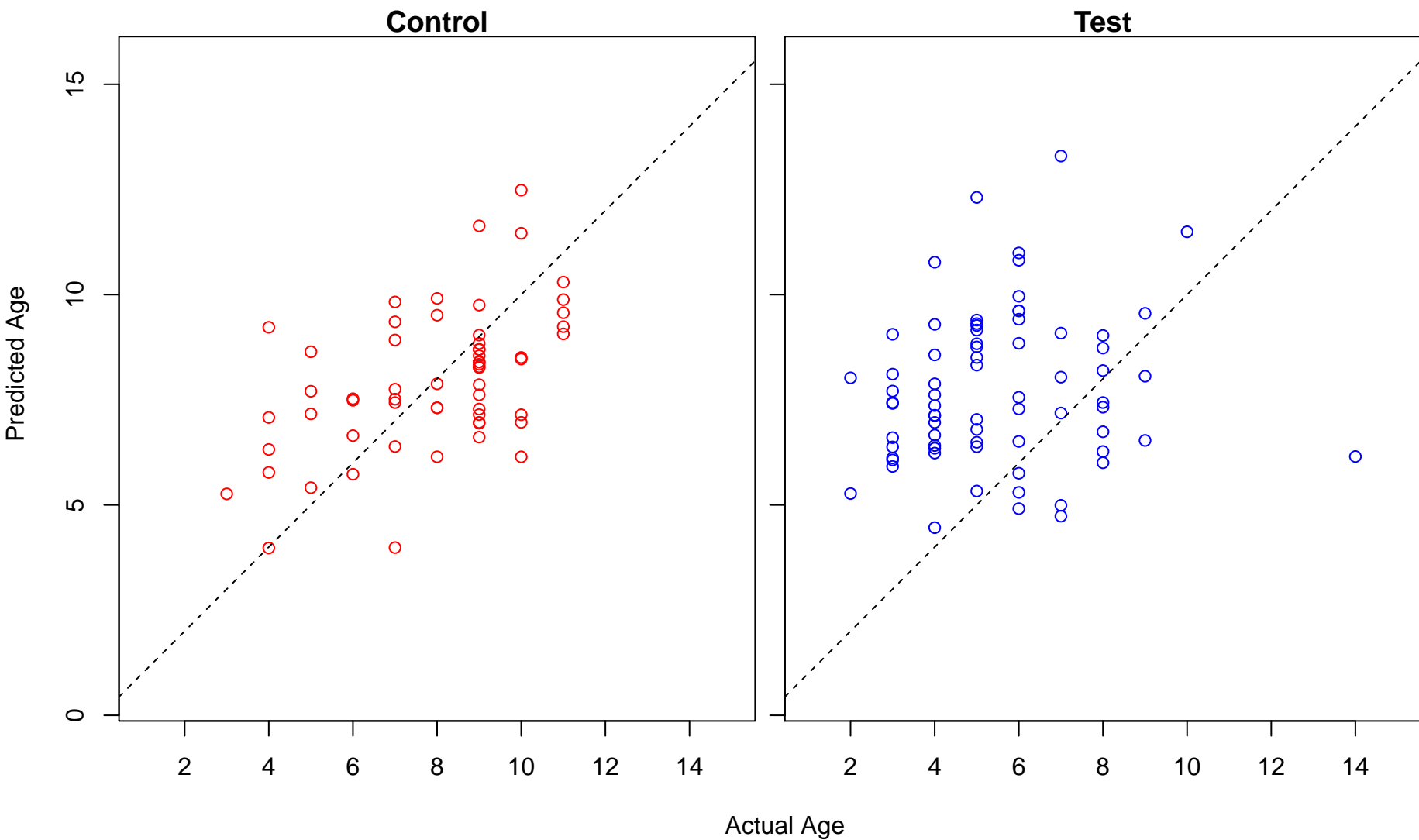
cellular metabolic process (Score: 1.855416)



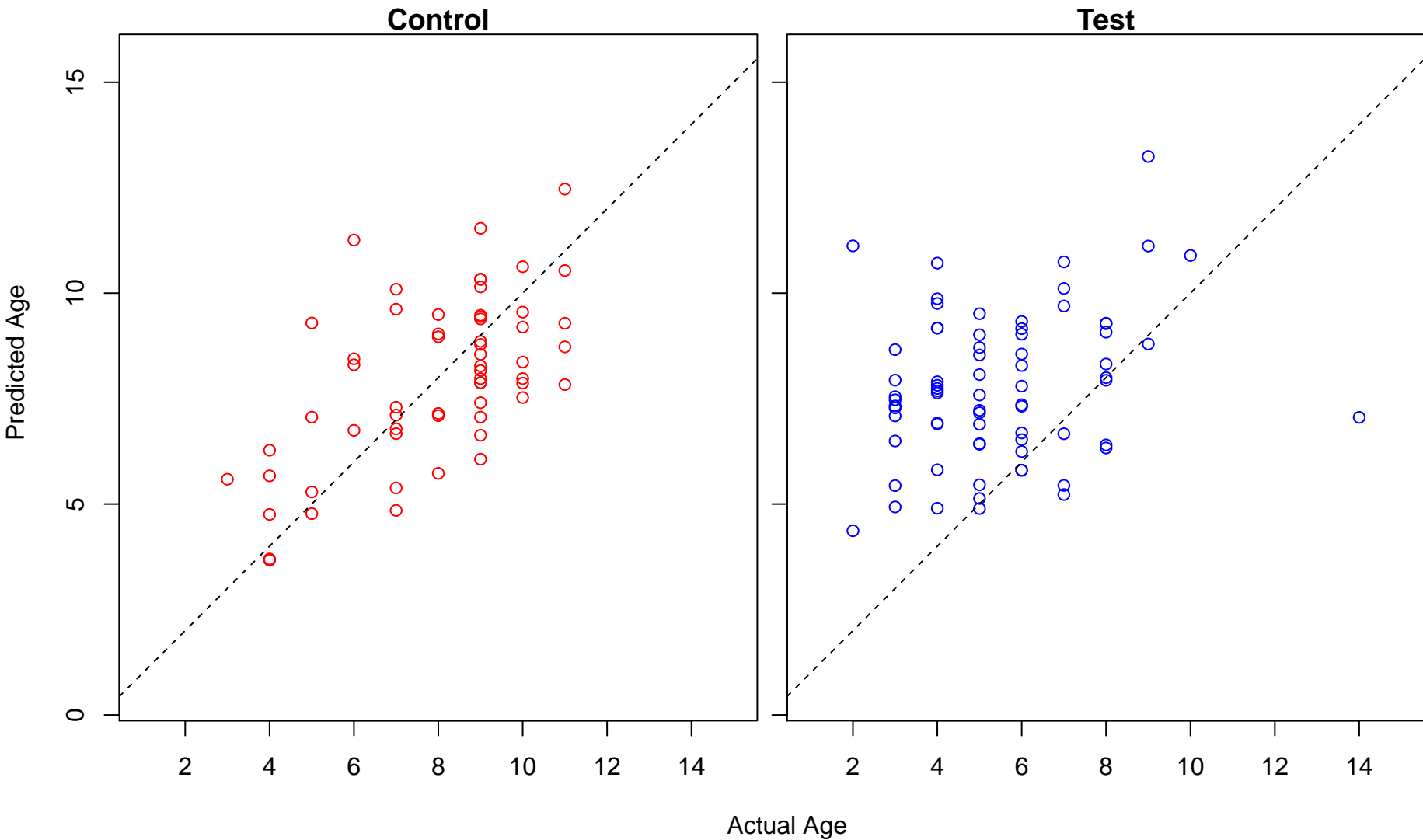
ureteric bud development (Score: 1.851900)



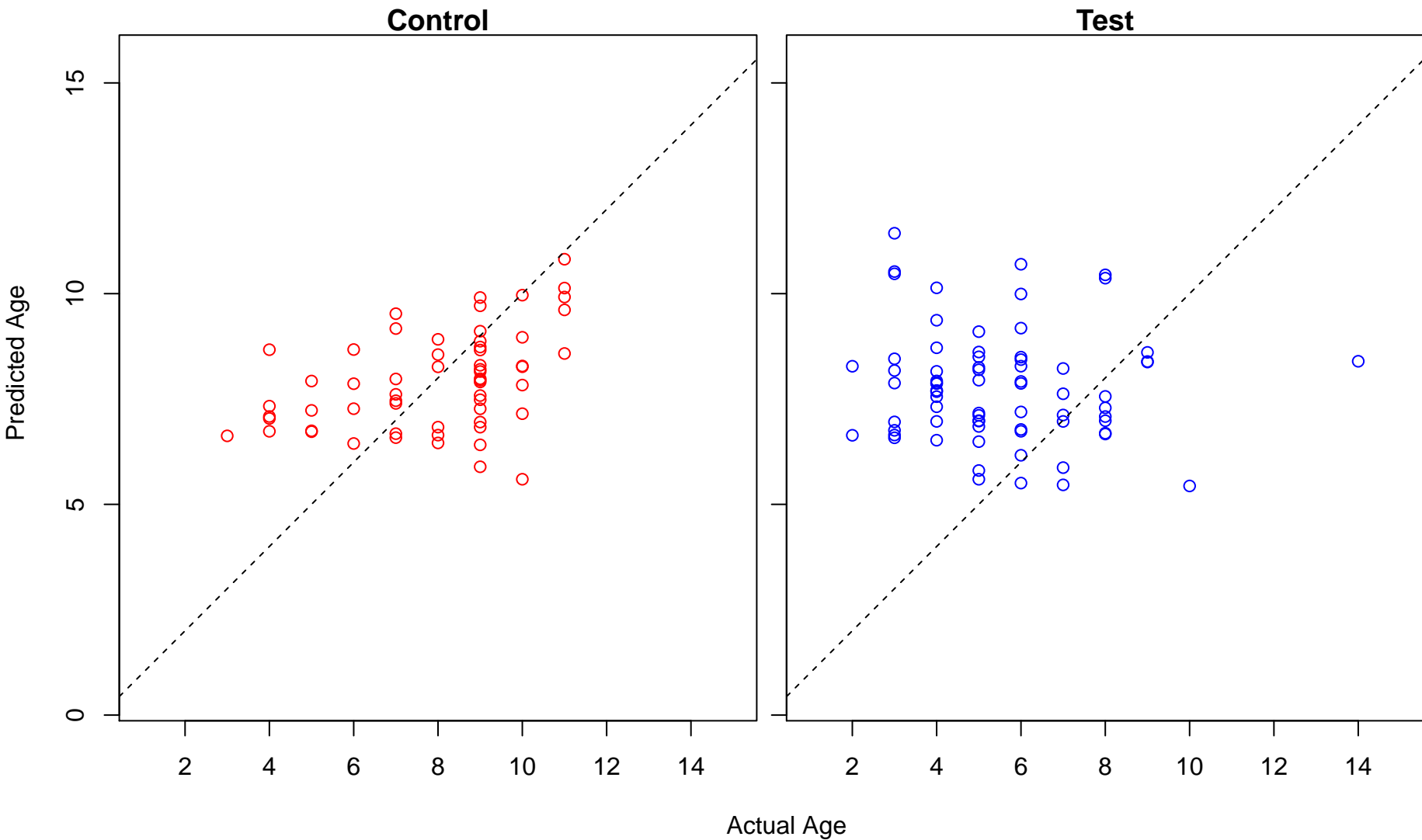
intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress (Score: 1.85119)



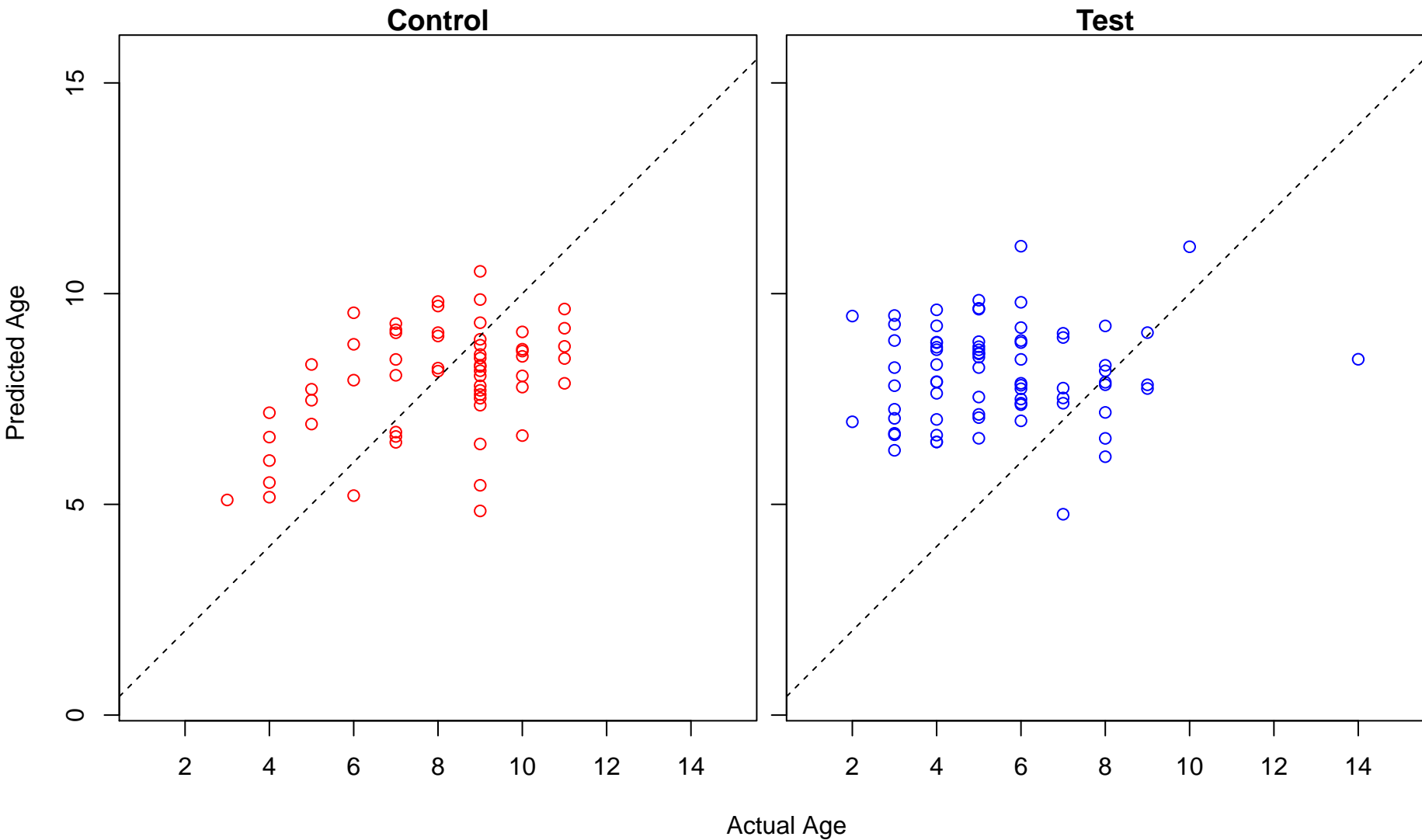
positive regulation of neuron differentiation (Score: 1.850721)



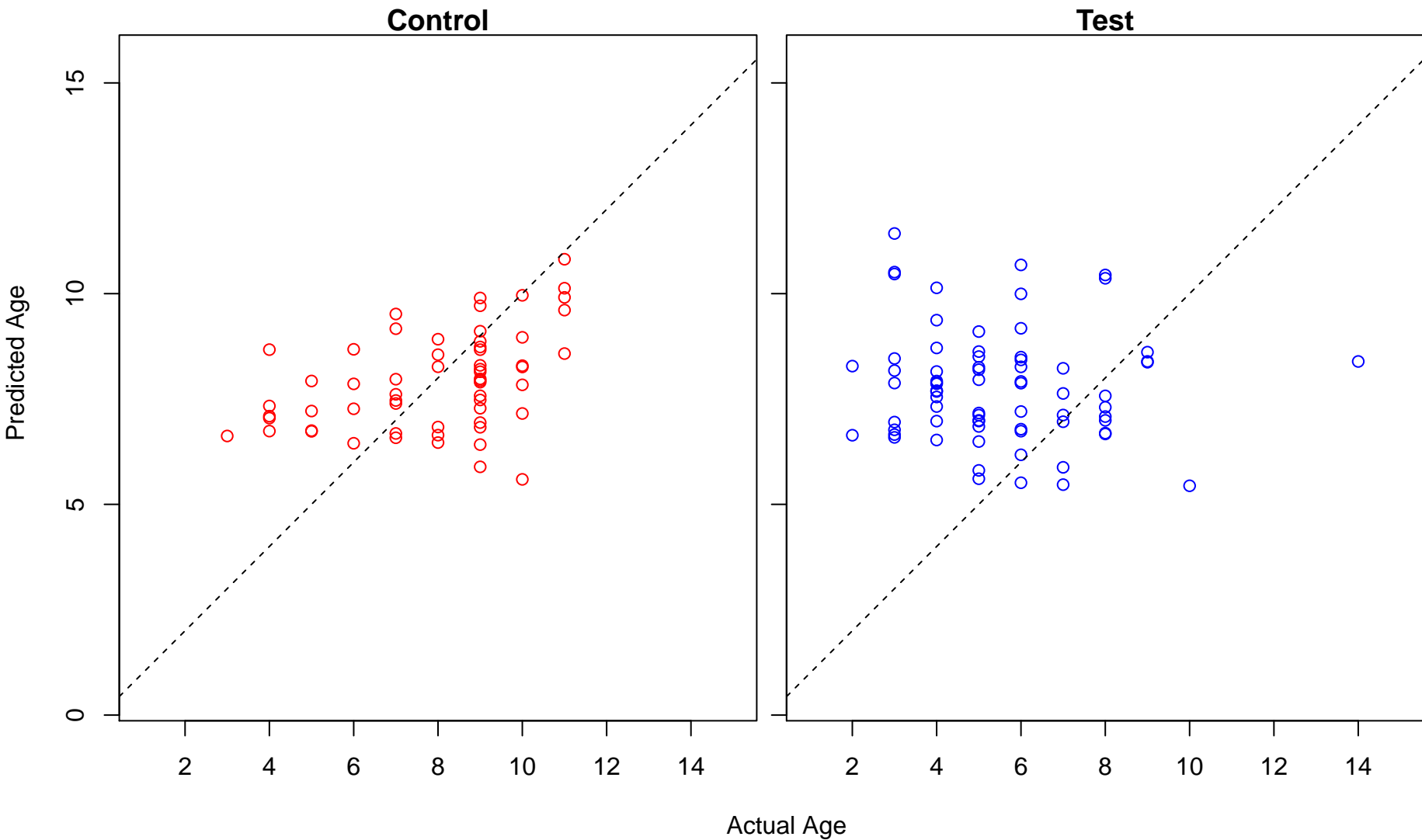
platelet morphogenesis (Score: 1.848582)



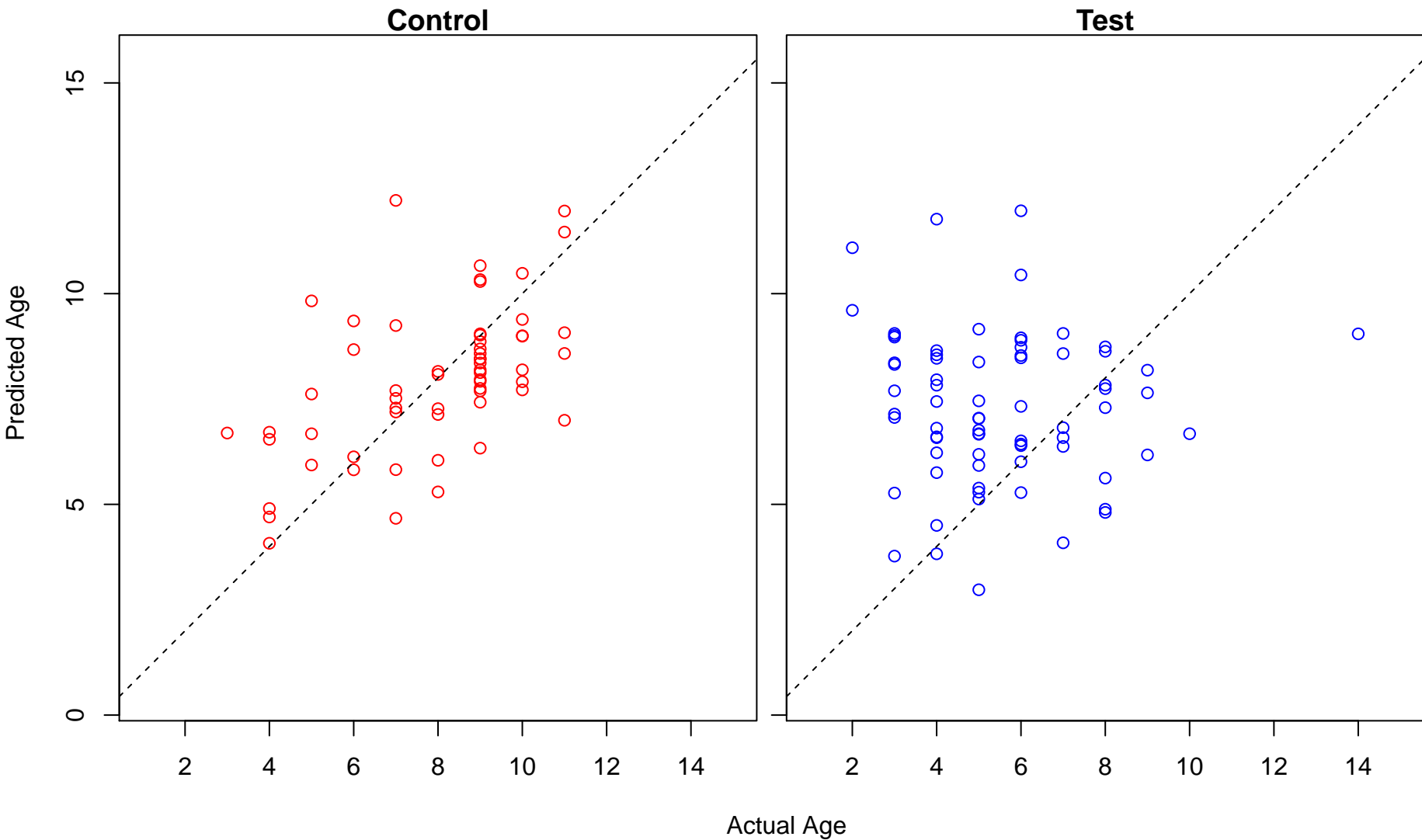
very-low-density lipoprotein particle assembly (Score: 1.848220)



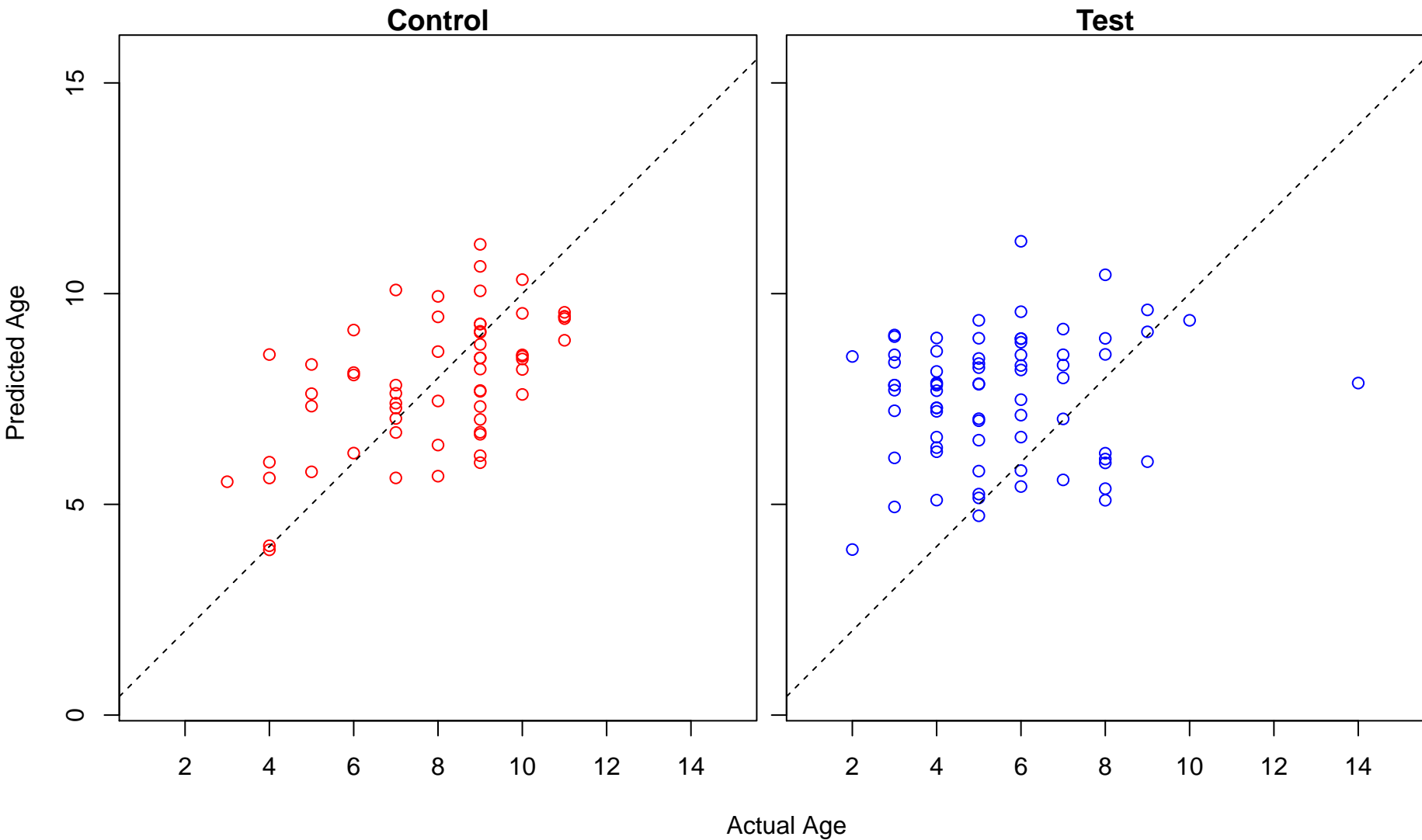
platelet formation (Score: 1.848004)



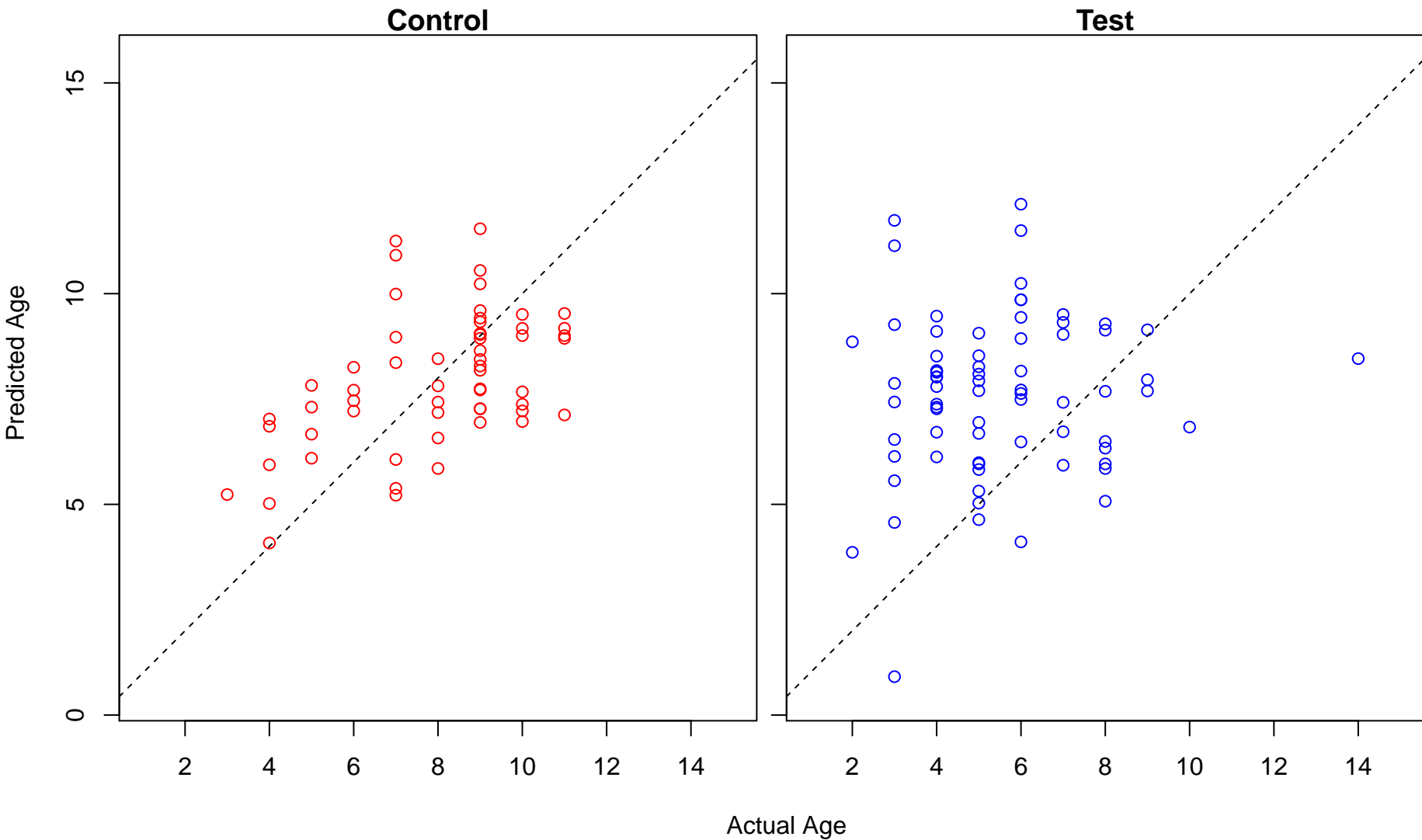
ribose phosphate biosynthetic process (Score: 1.847853)



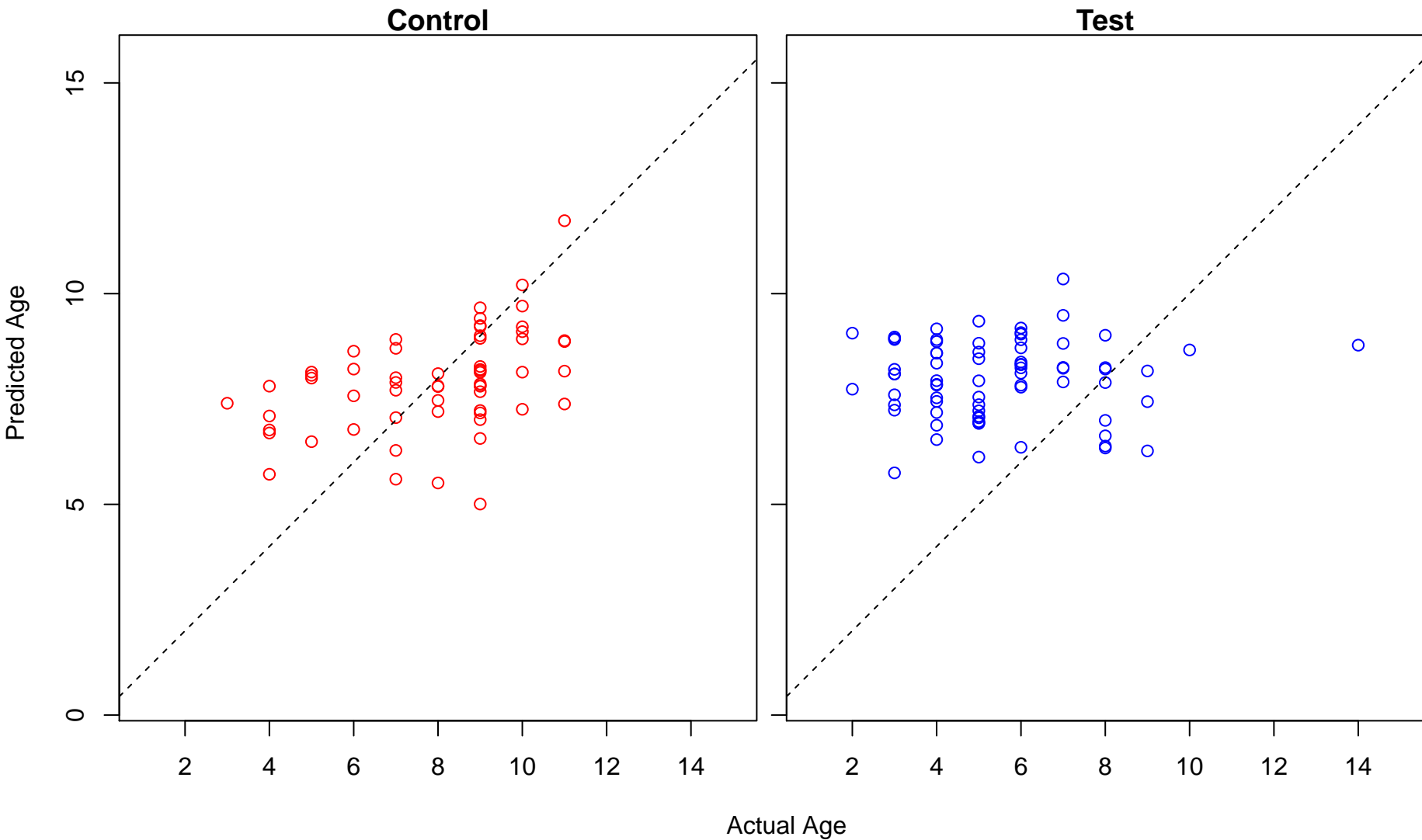
pigment cell differentiation (Score: 1.846188)



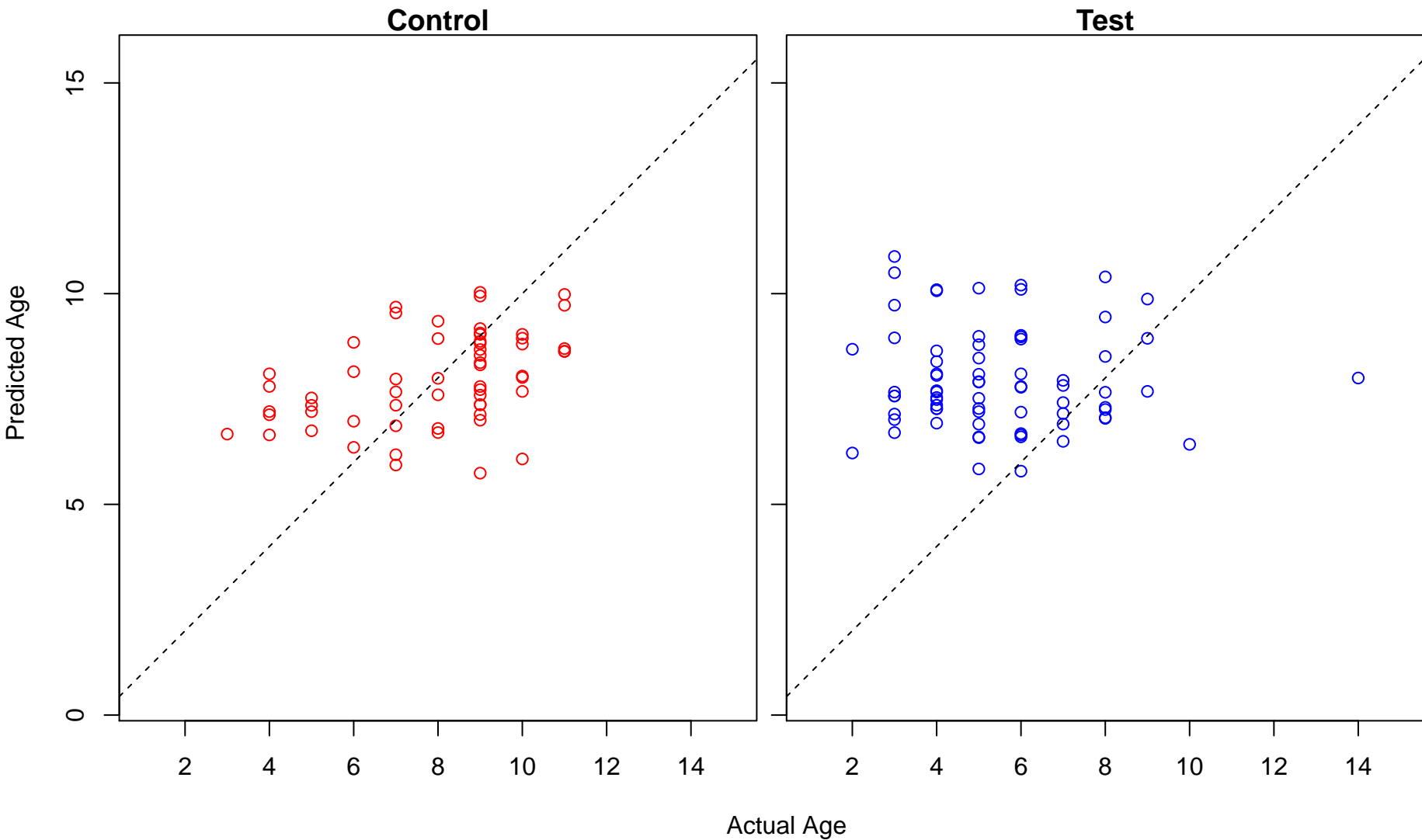
regulation of pathway-restricted SMAD protein phosphorylation (Score: 1.845599)



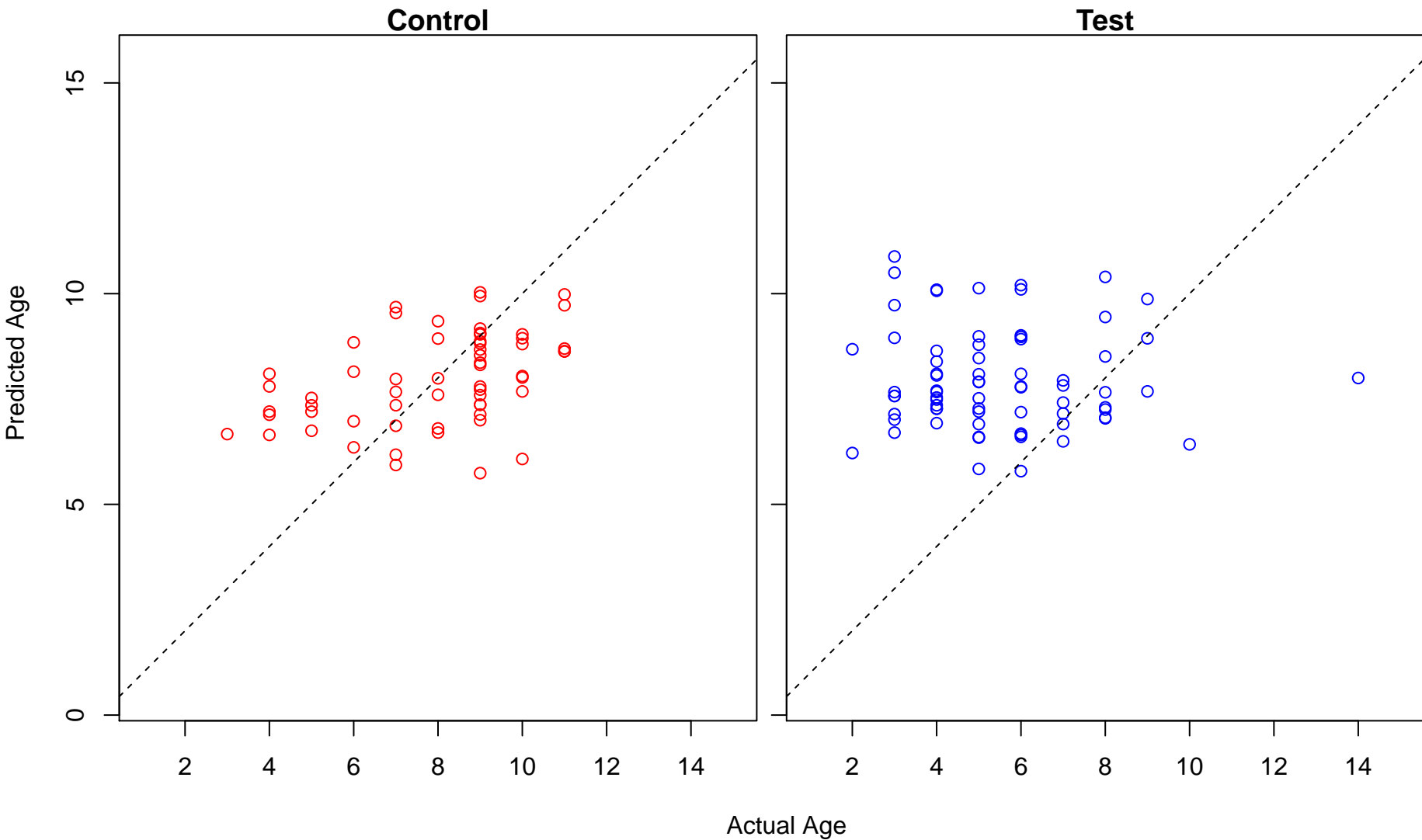
smoothened signaling pathway involved in dorsal/ventral neural tube patterning (Score: 1.845509)



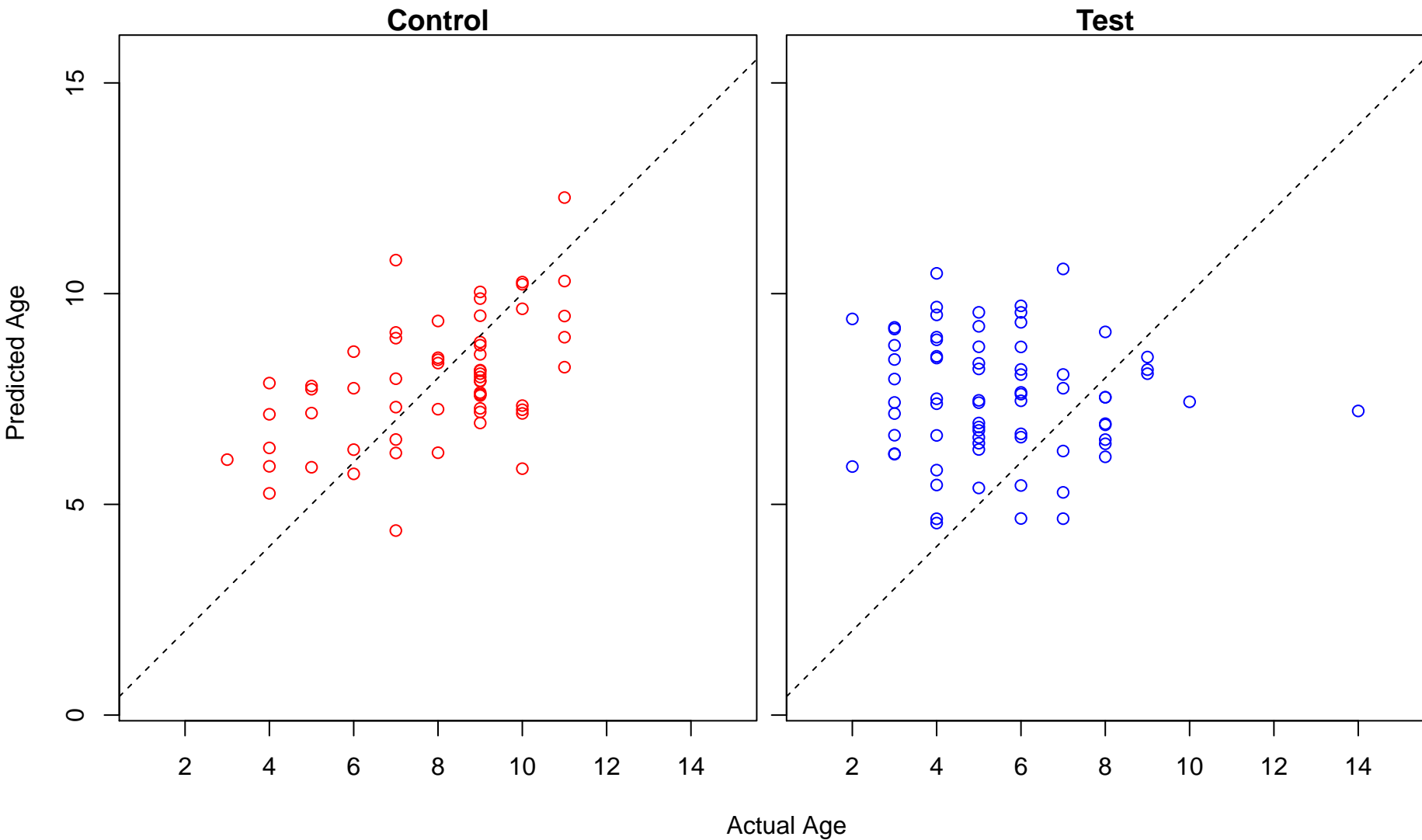
growth hormone receptor signaling pathway (Score: 1.844237)



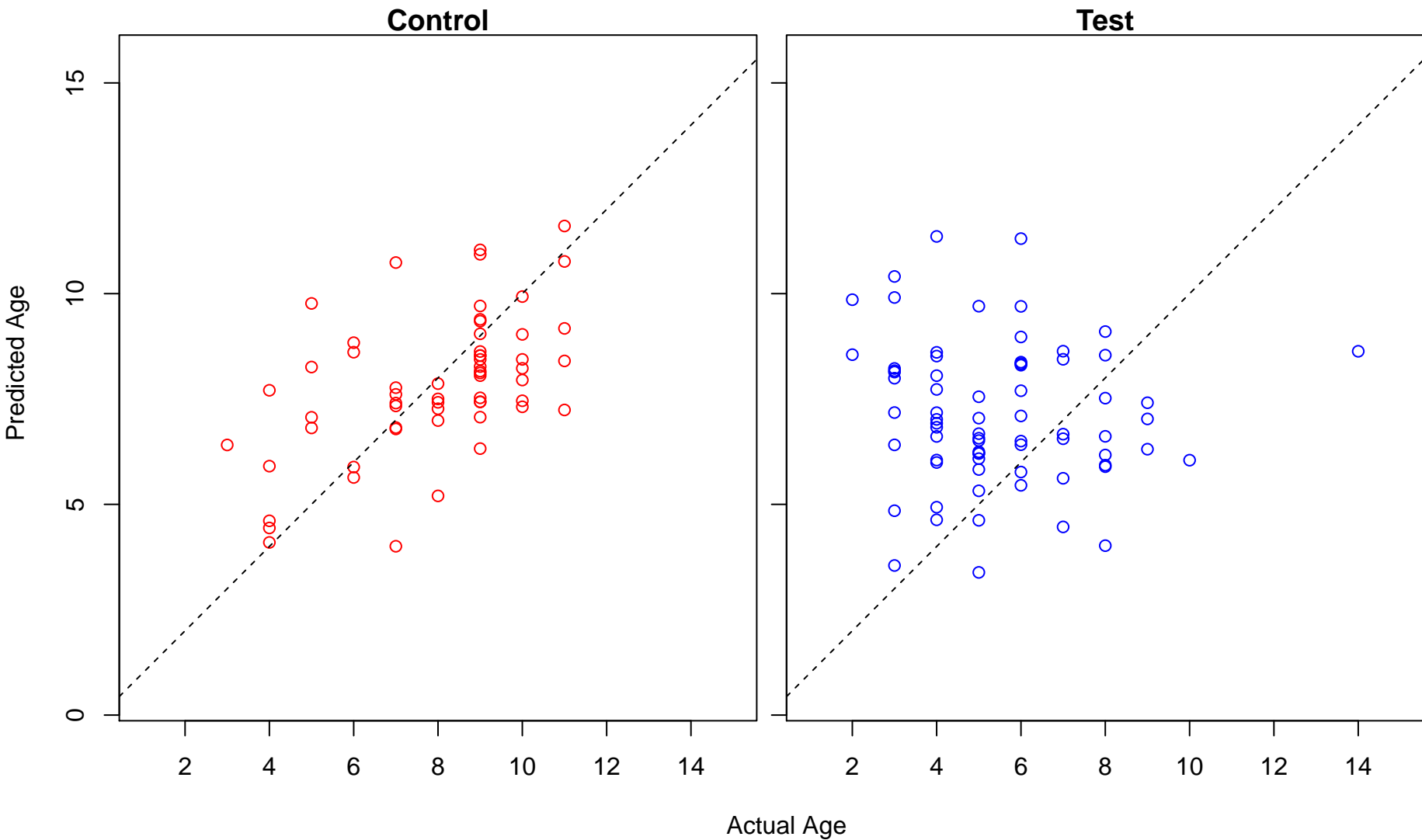
cellular response to growth hormone stimulus (Score: 1.844237)



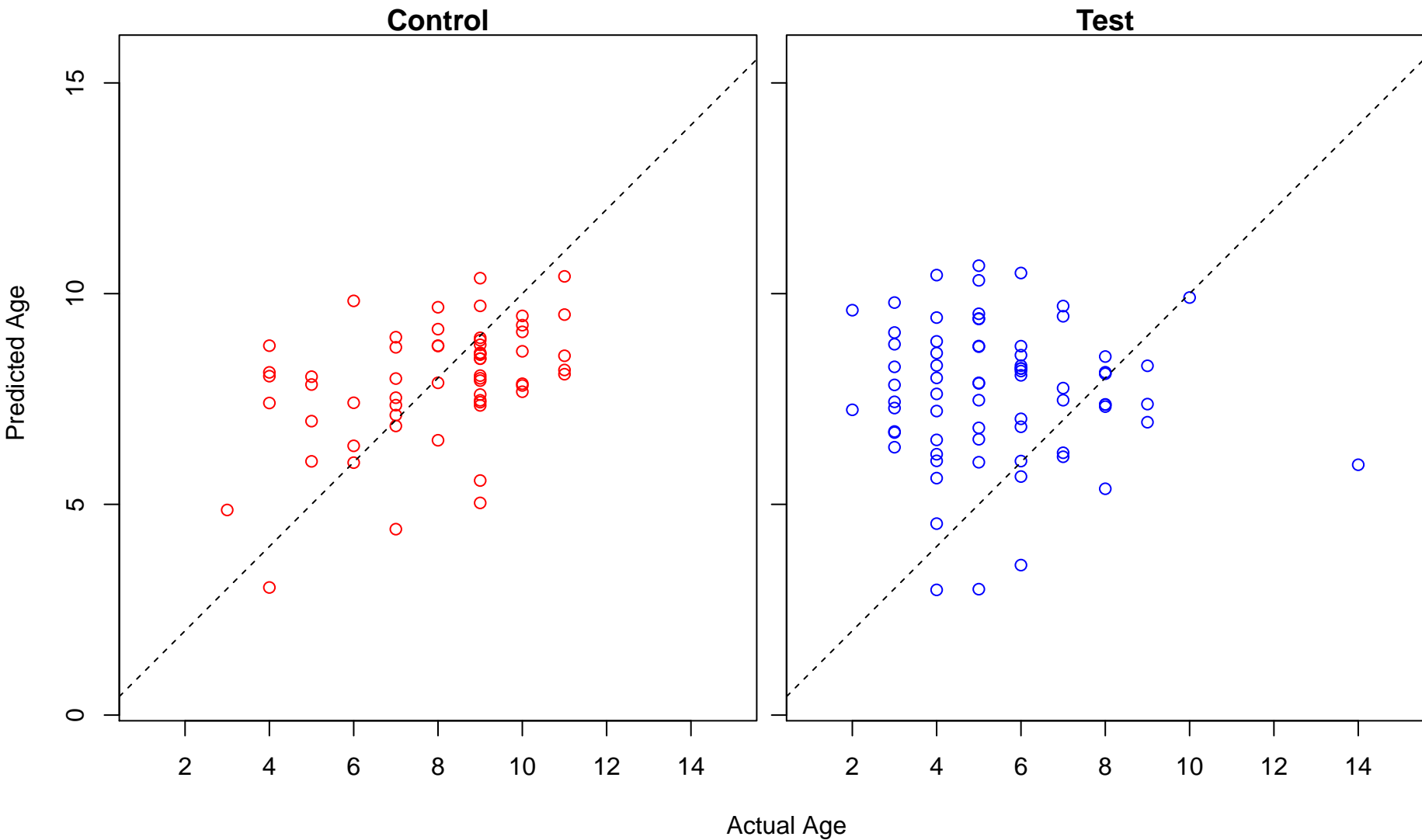
establishment of epithelial cell apical/basal polarity (Score: 1.844048)



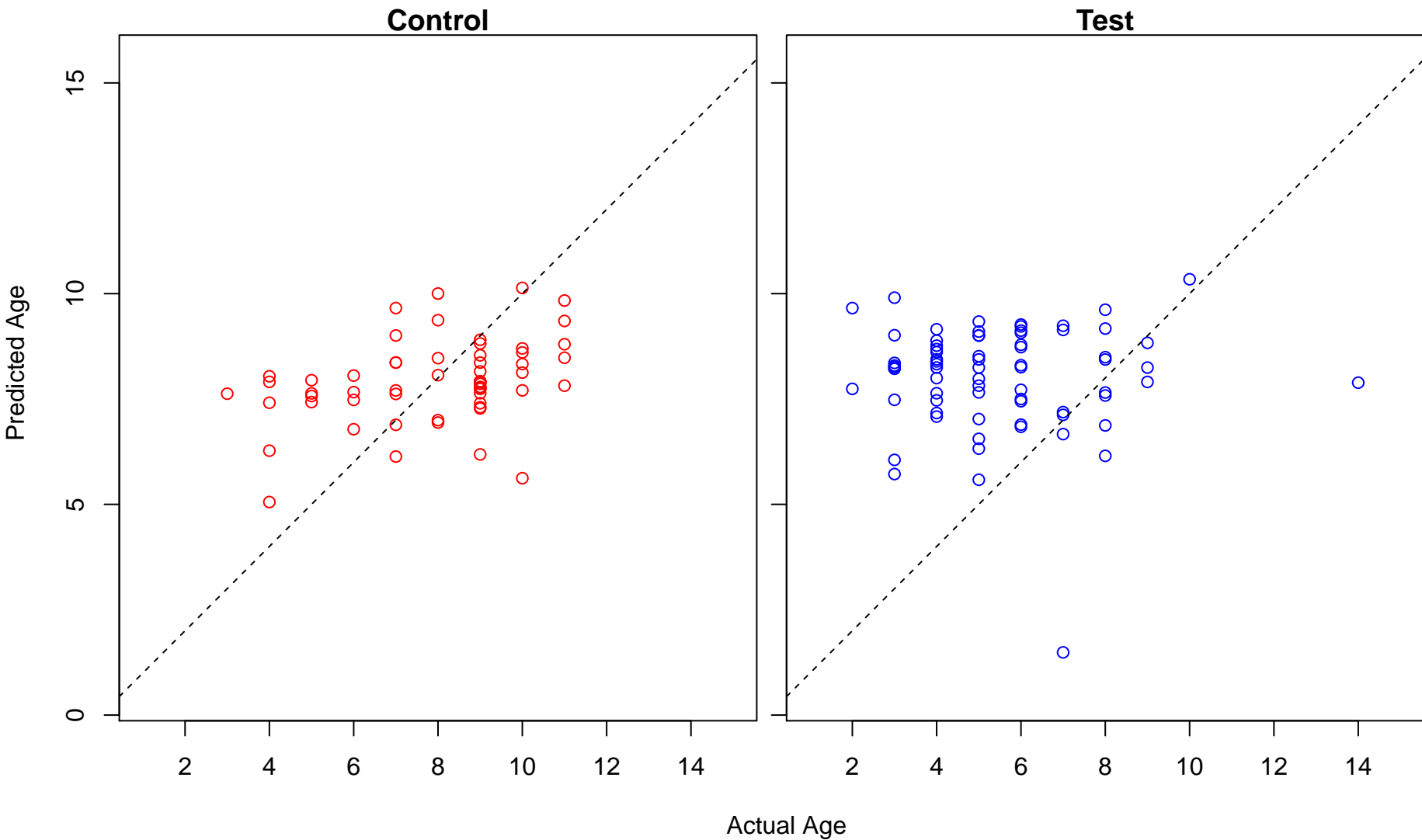
purine-containing compound biosynthetic process (Score: 1.837131)



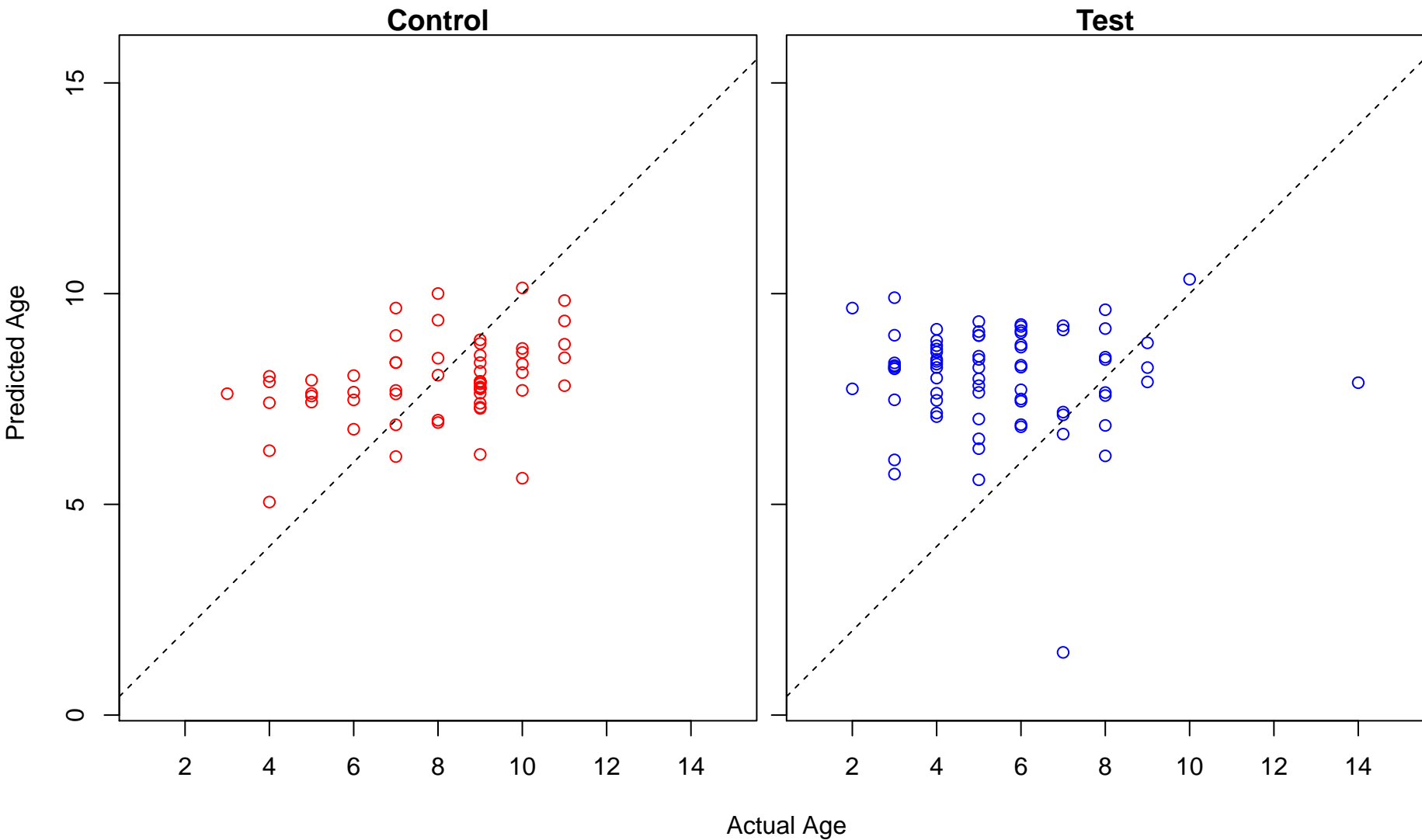
oxidative DNA demethylation (Score: 1.836608)



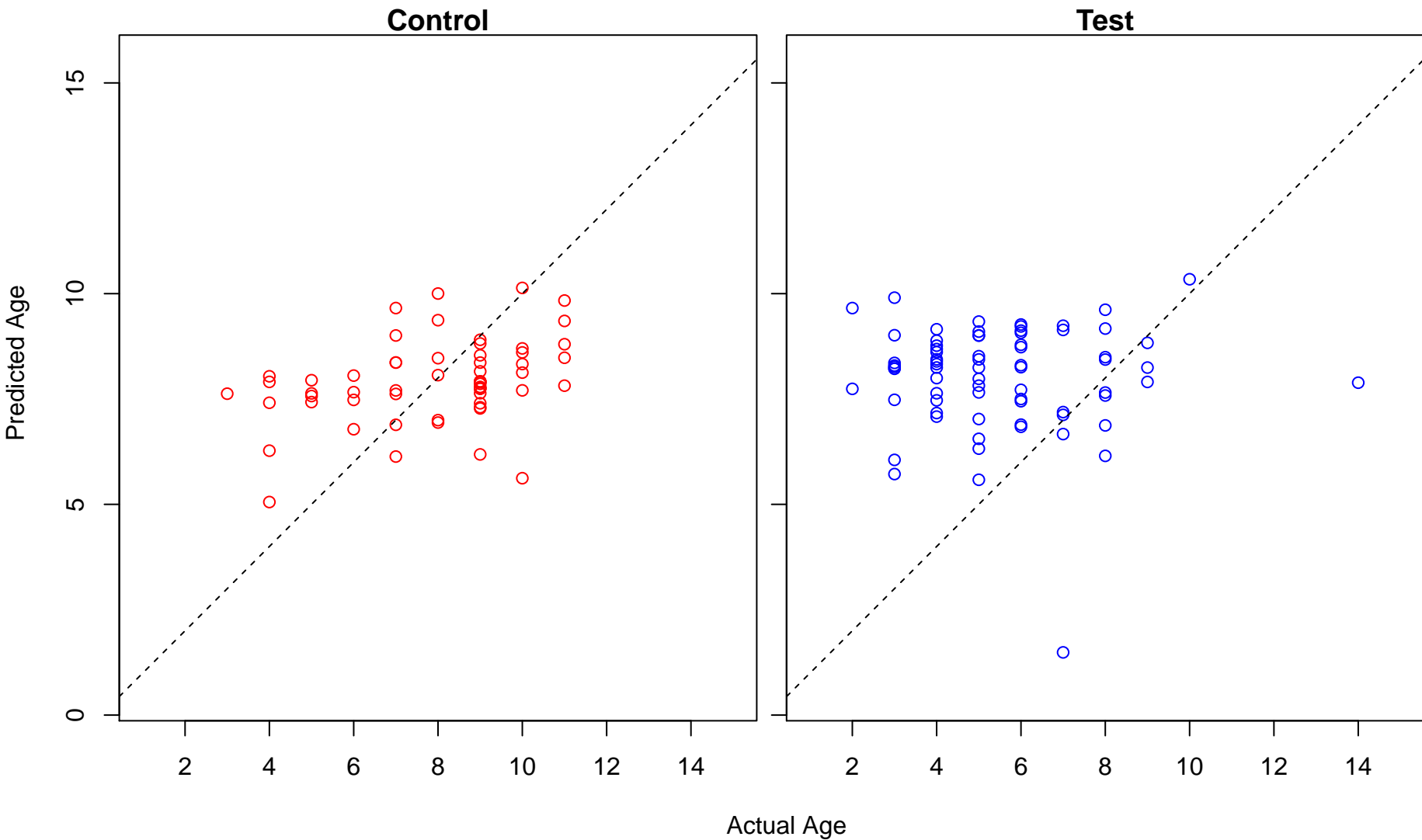
peptidyl-lysine hydroxylation (Score: 1.834489)



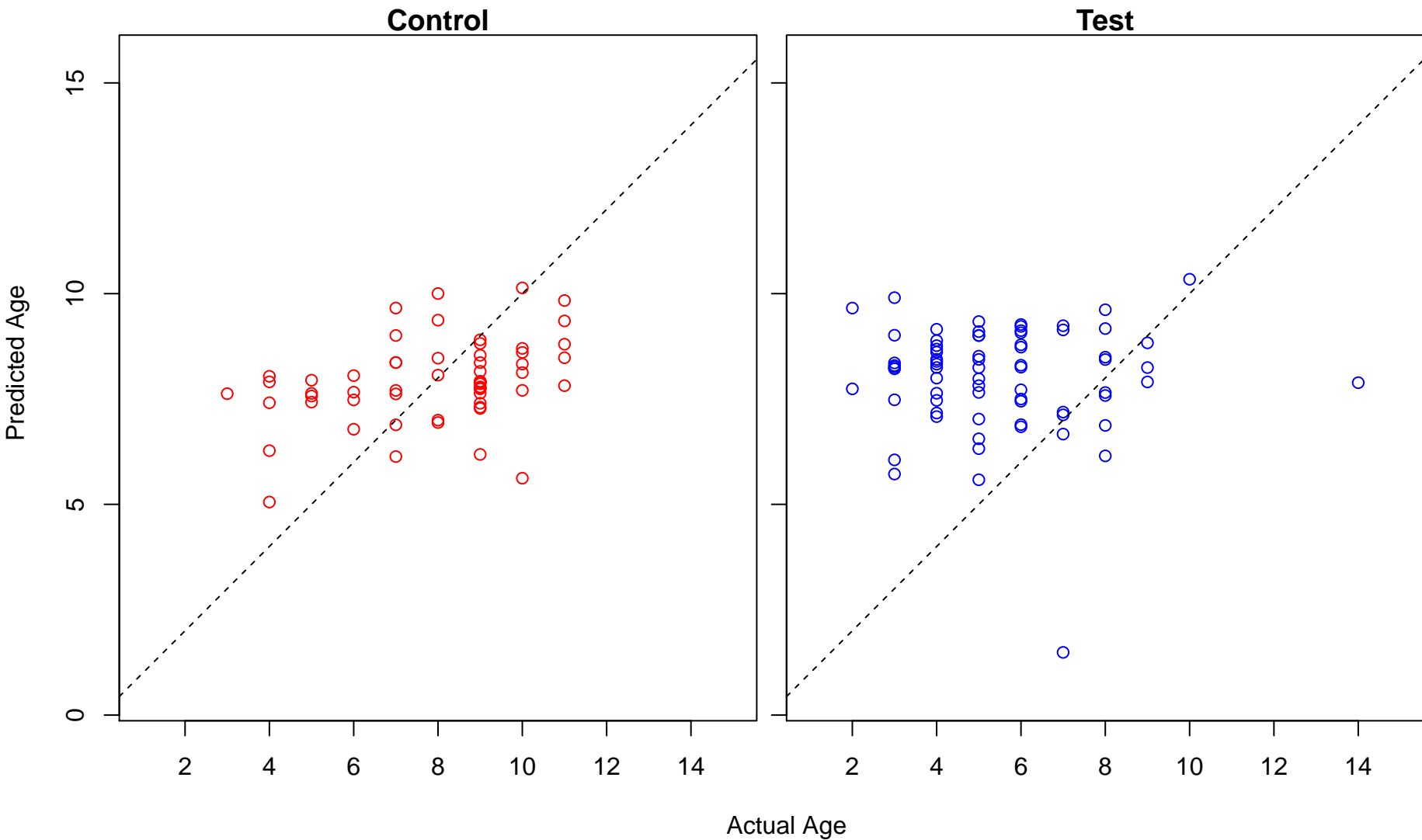
peptidyl-lysine hydroxylation to 5-hydroxy-L-lysine (Score: 1.834489)



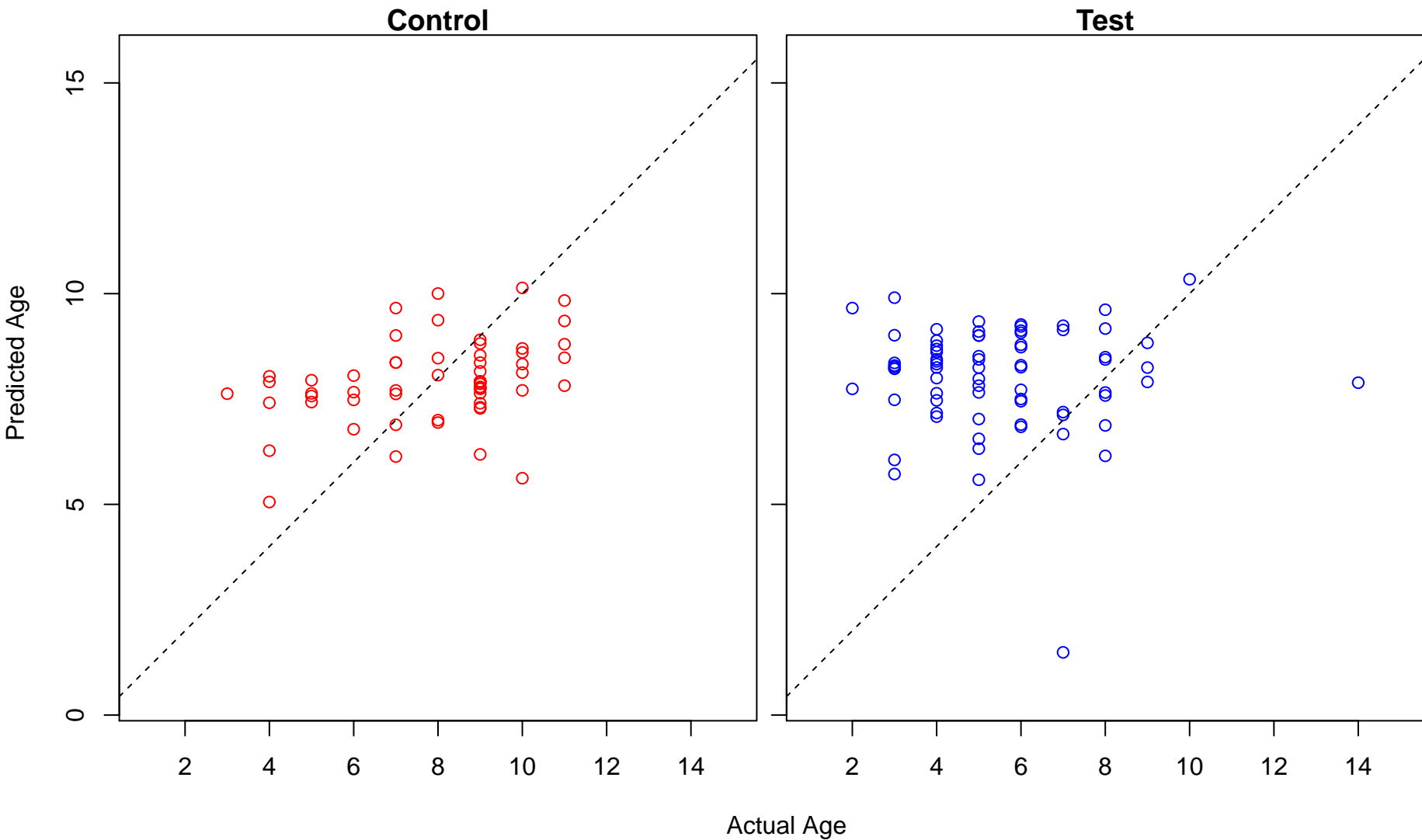
histone arginine demethylation (Score: 1.834489)



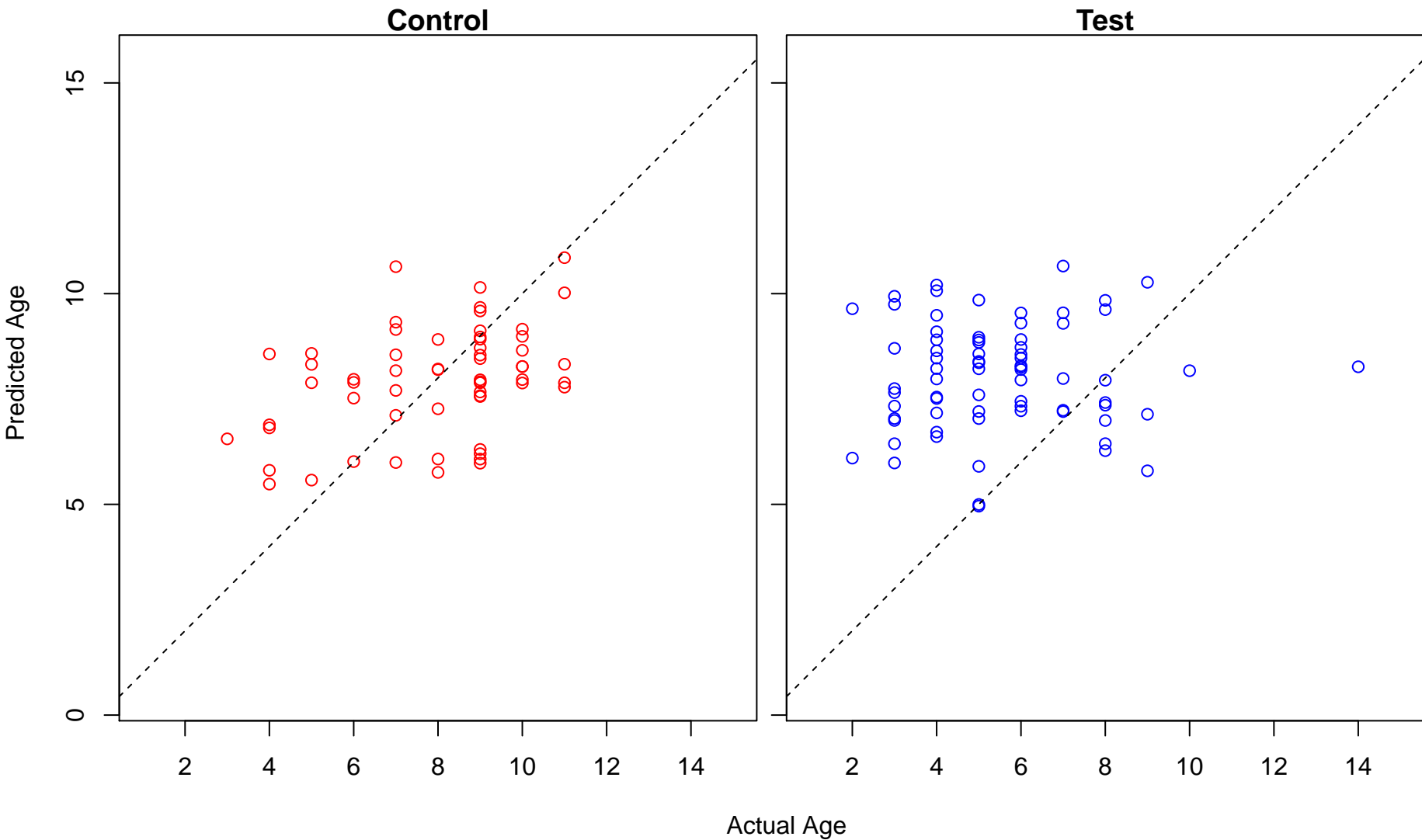
histone H3-R2 demethylation (Score: 1.834489)



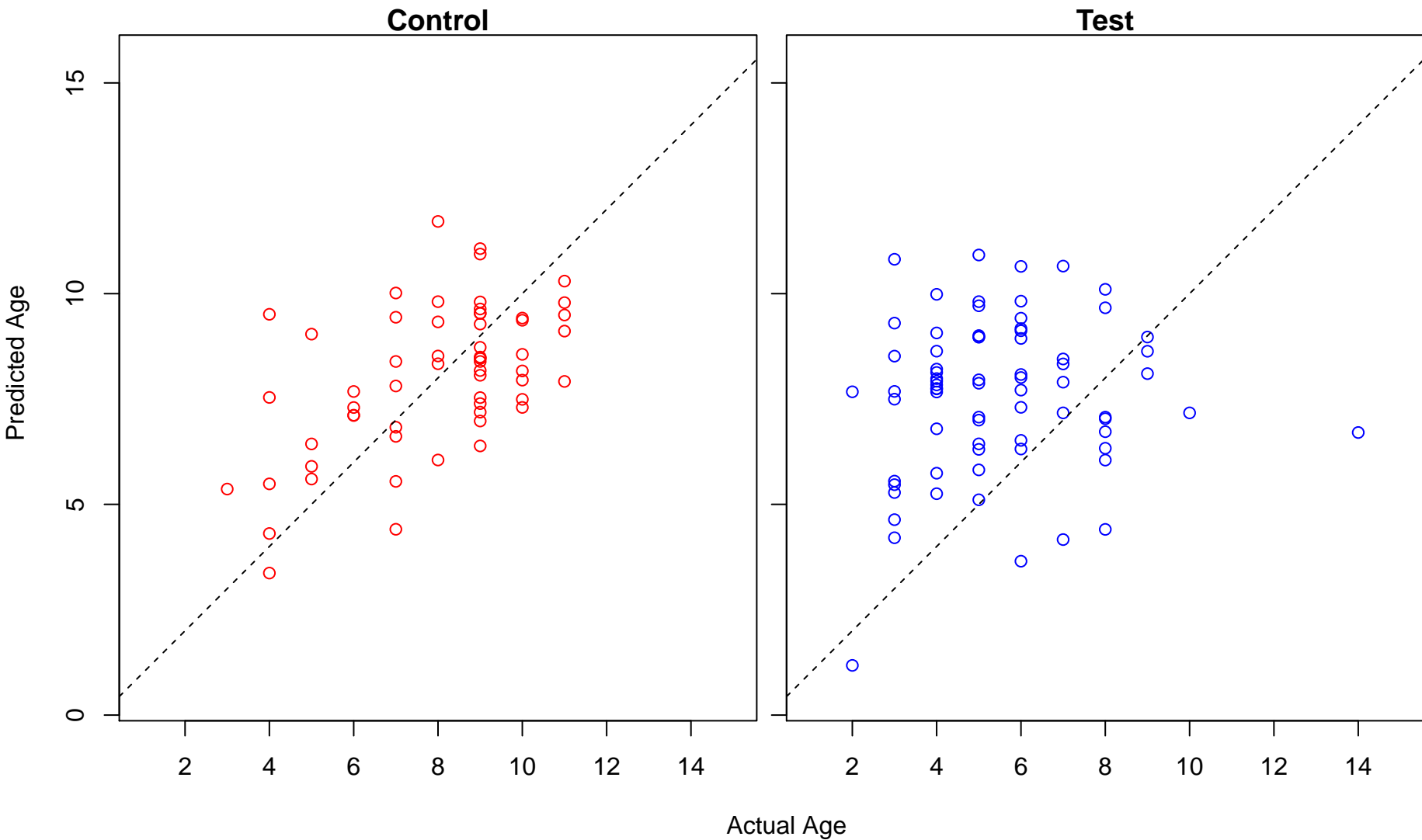
histone H4-R3 demethylation (Score: 1.834489)



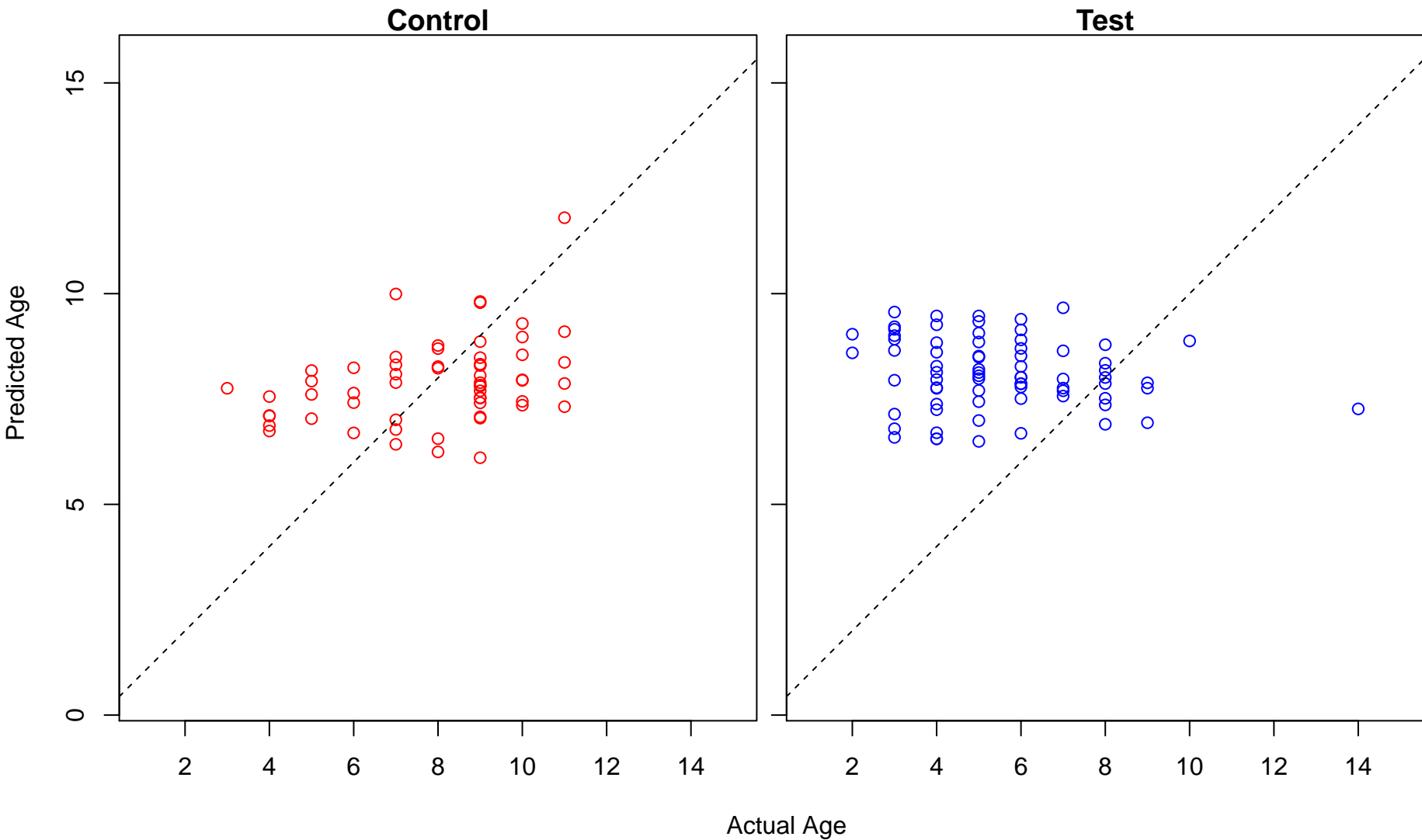
ribosome disassembly (Score: 1.832773)



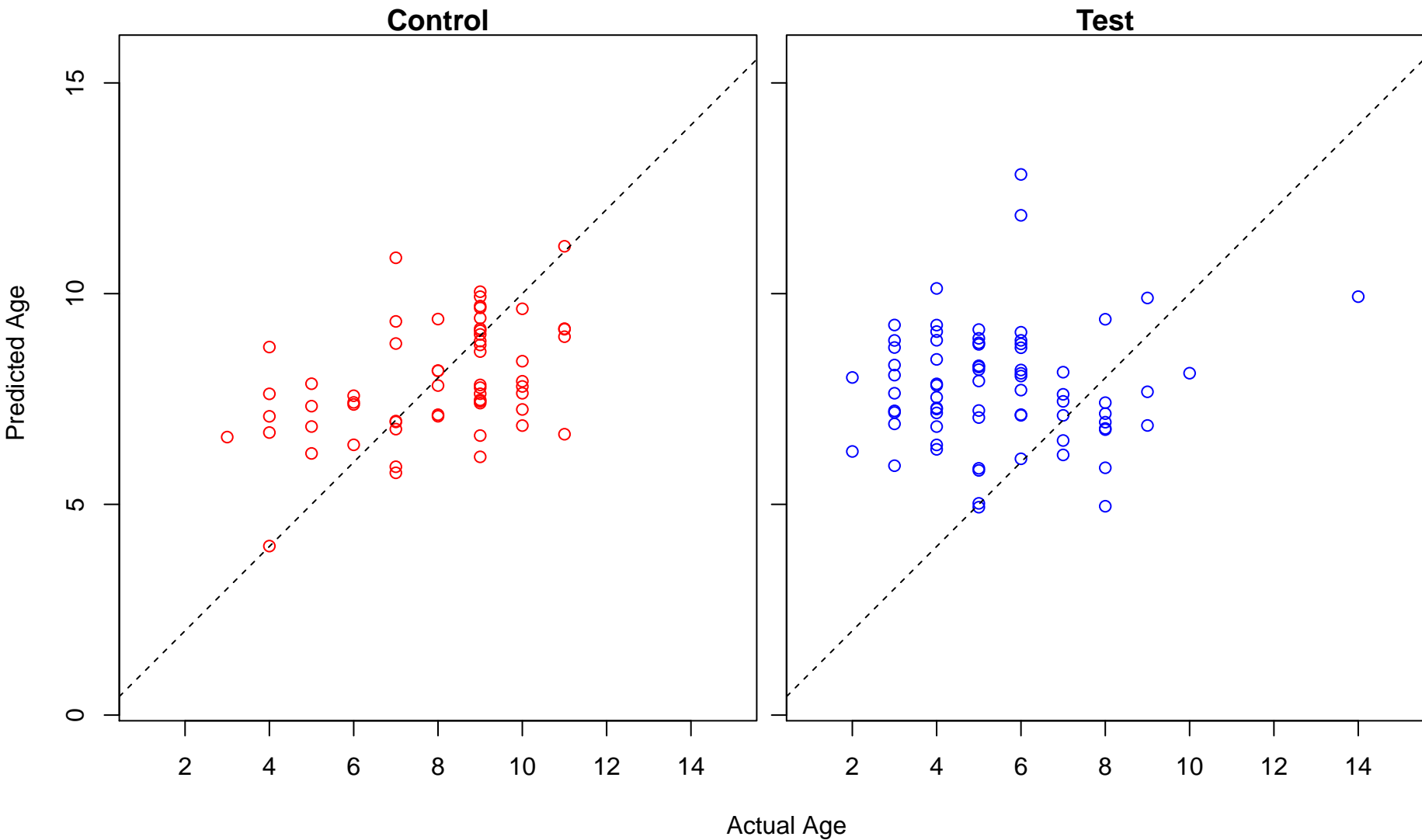
positive regulation of tyrosine phosphorylation of STAT protein (Score: 1.830671)



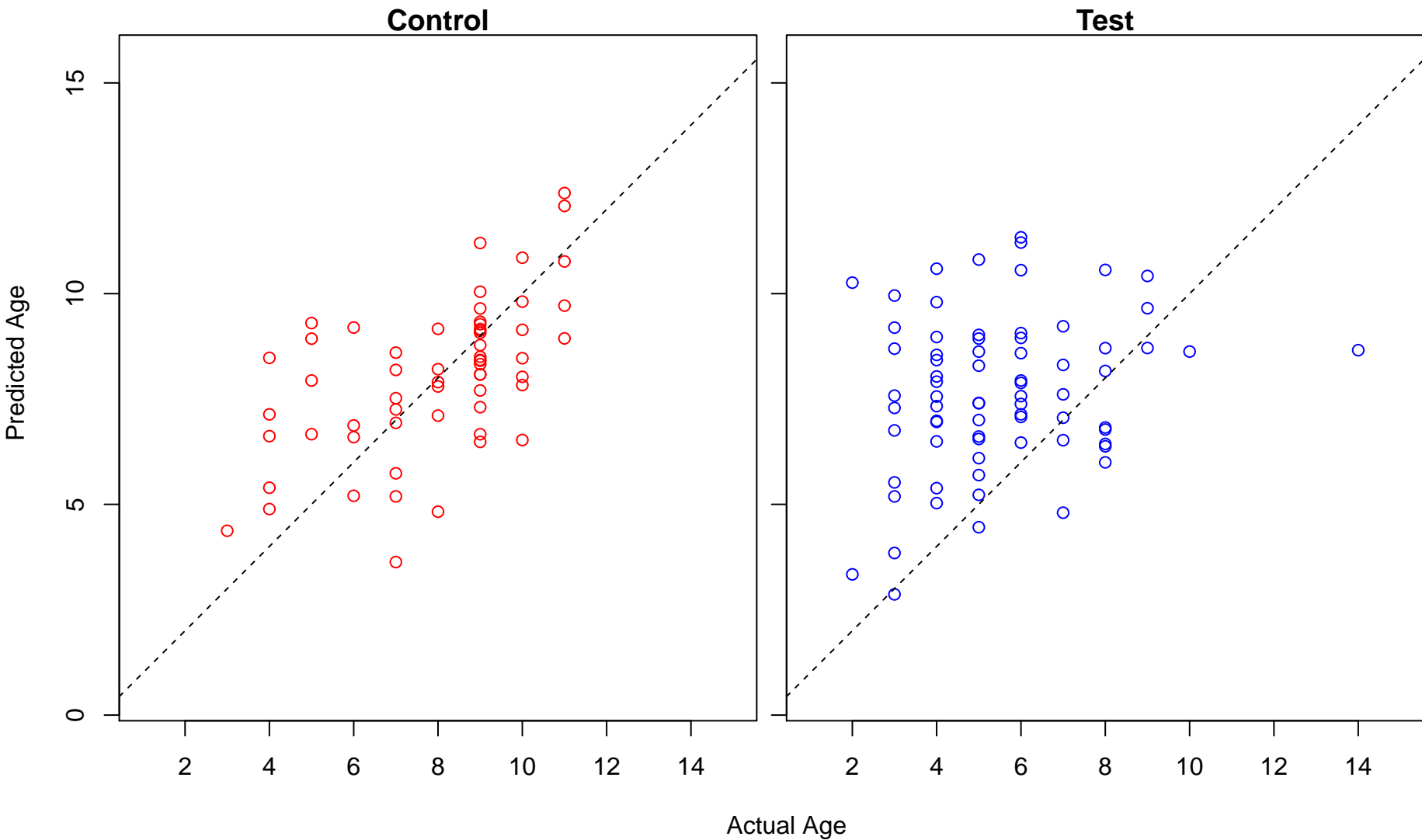
negative regulation of smoothened signaling pathway involved in ventral spinal cord patterning (Score: 1)



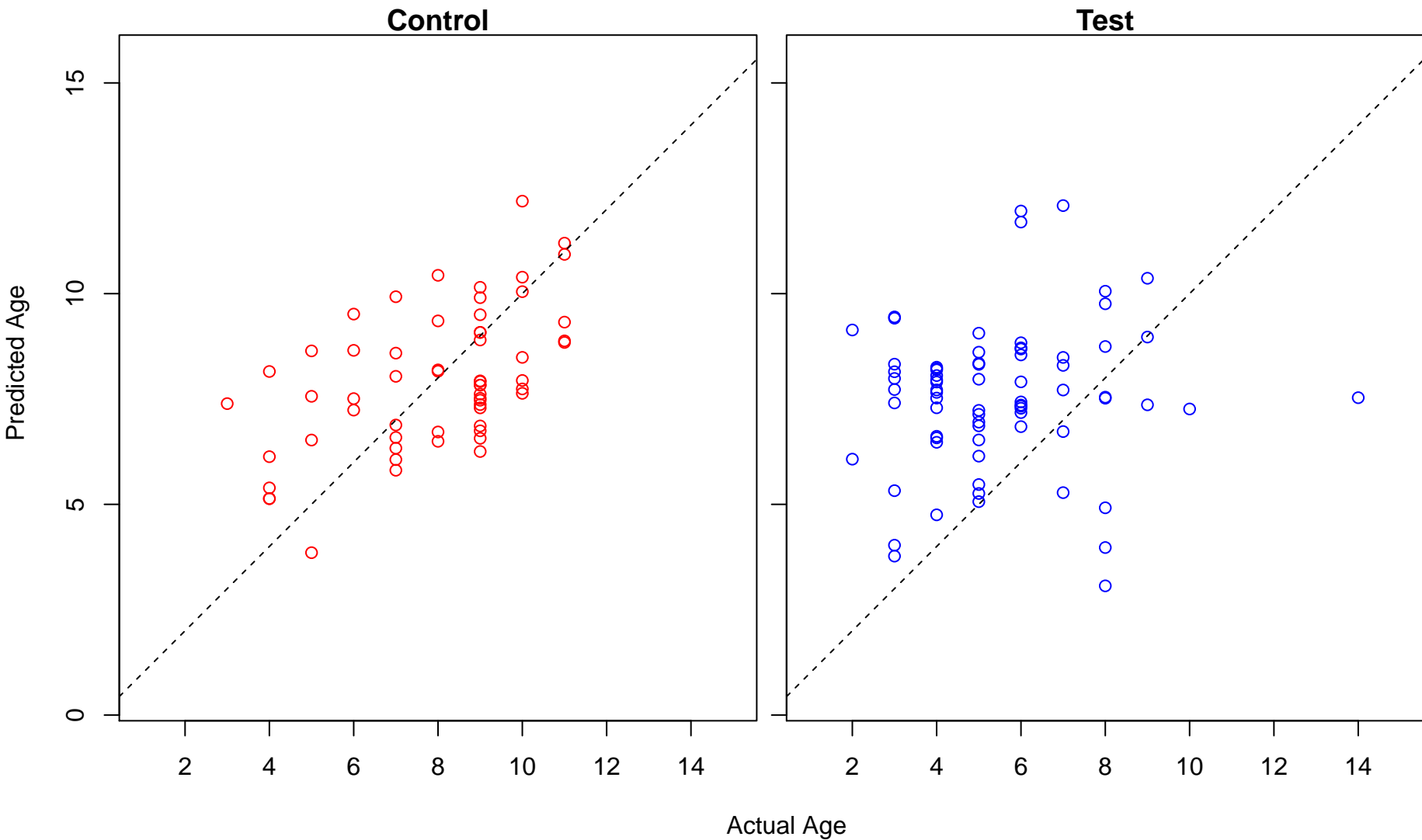
regulation of lipid kinase activity (Score: 1.820356)



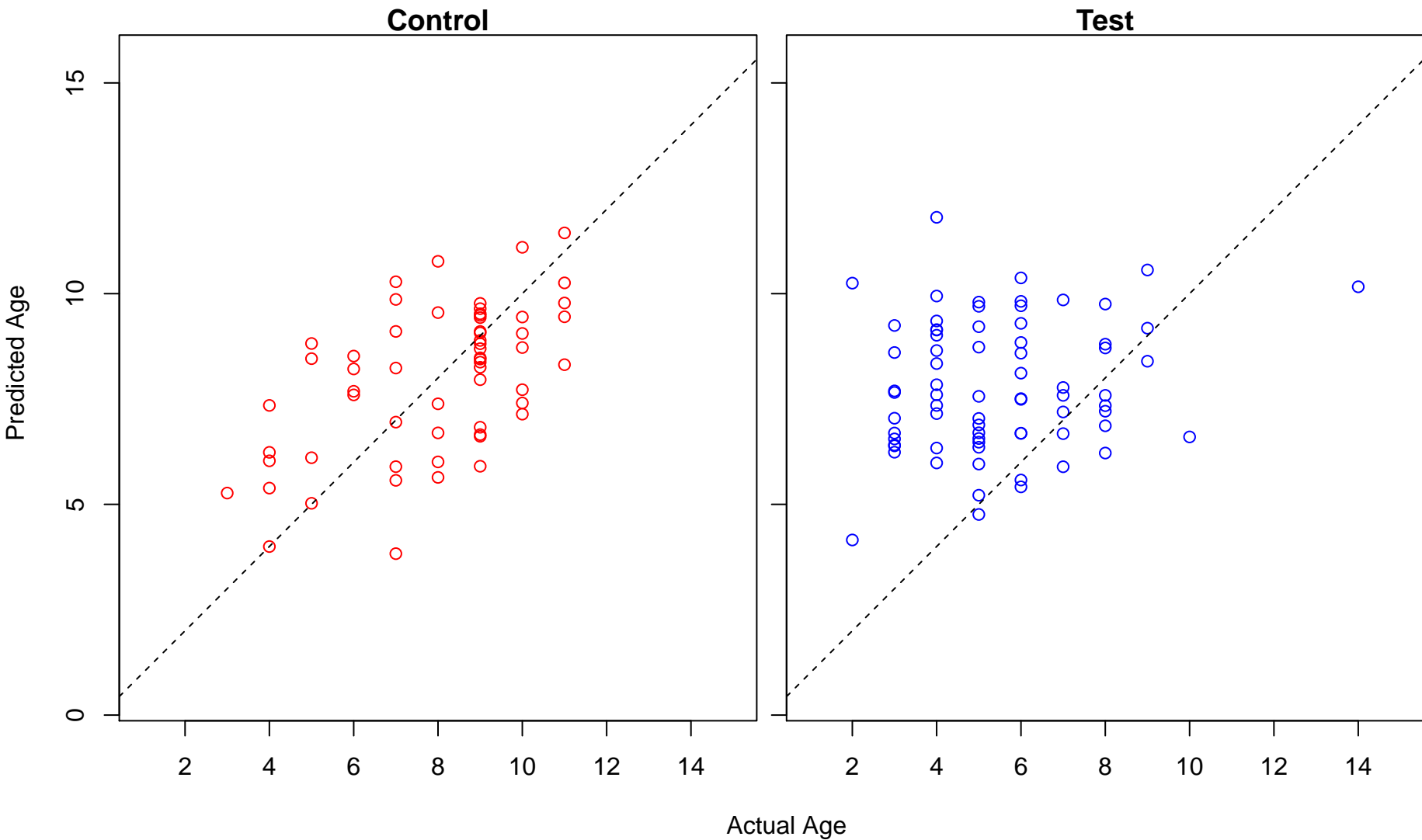
myeloid cell differentiation (Score: 1.820229)



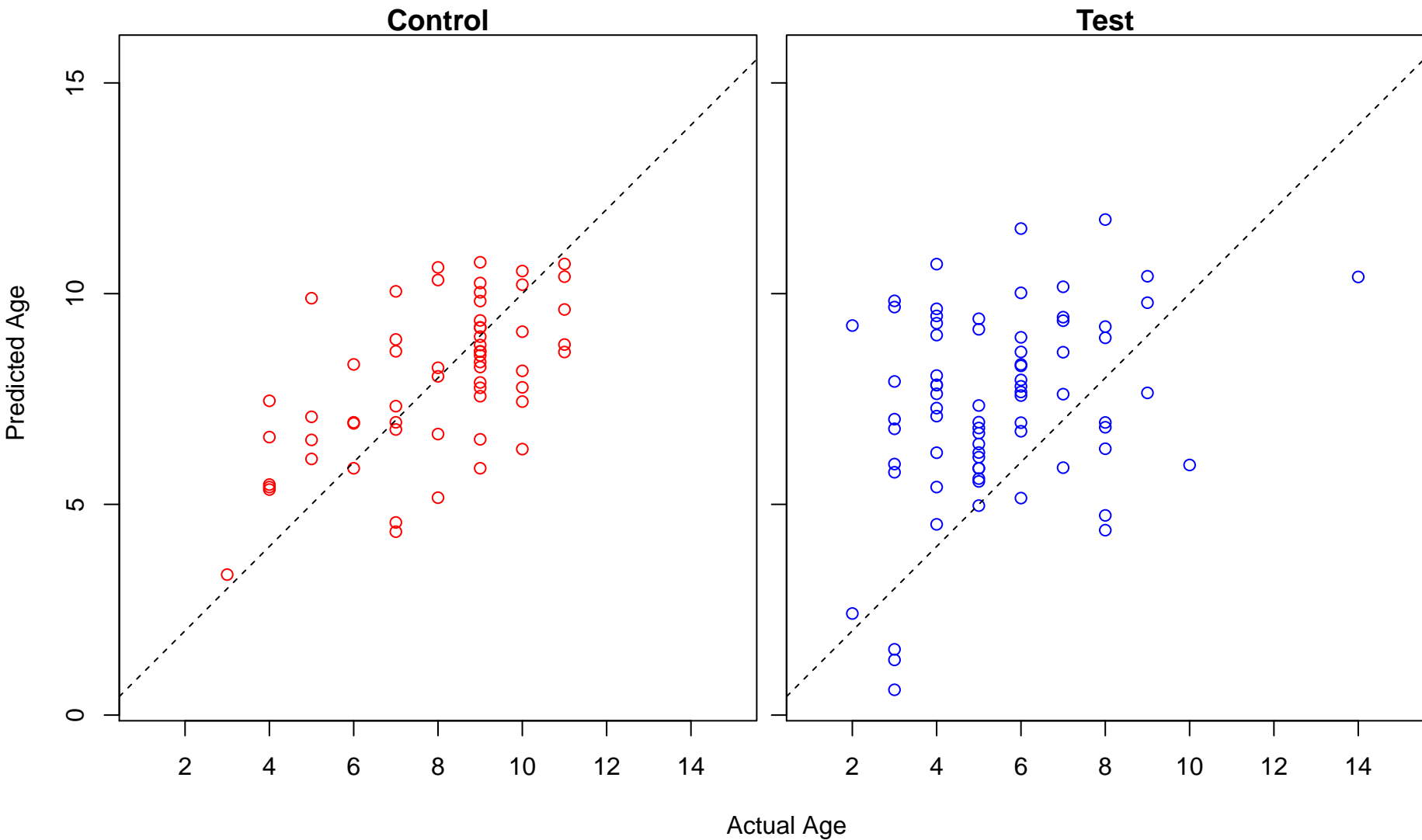
positive regulation of blood vessel endothelial cell migration (Score: 1.818630)



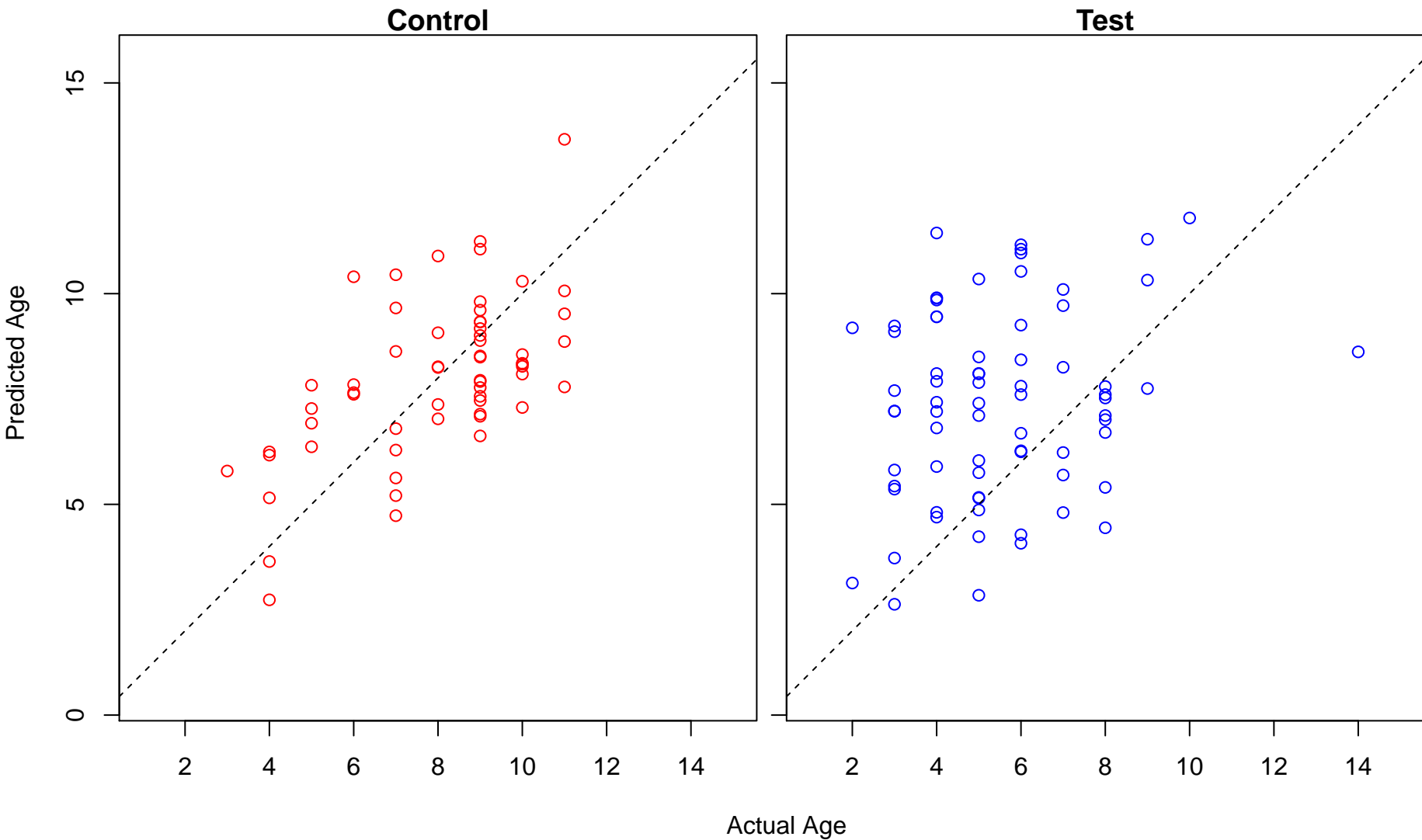
leukocyte migration (Score: 1.814978)



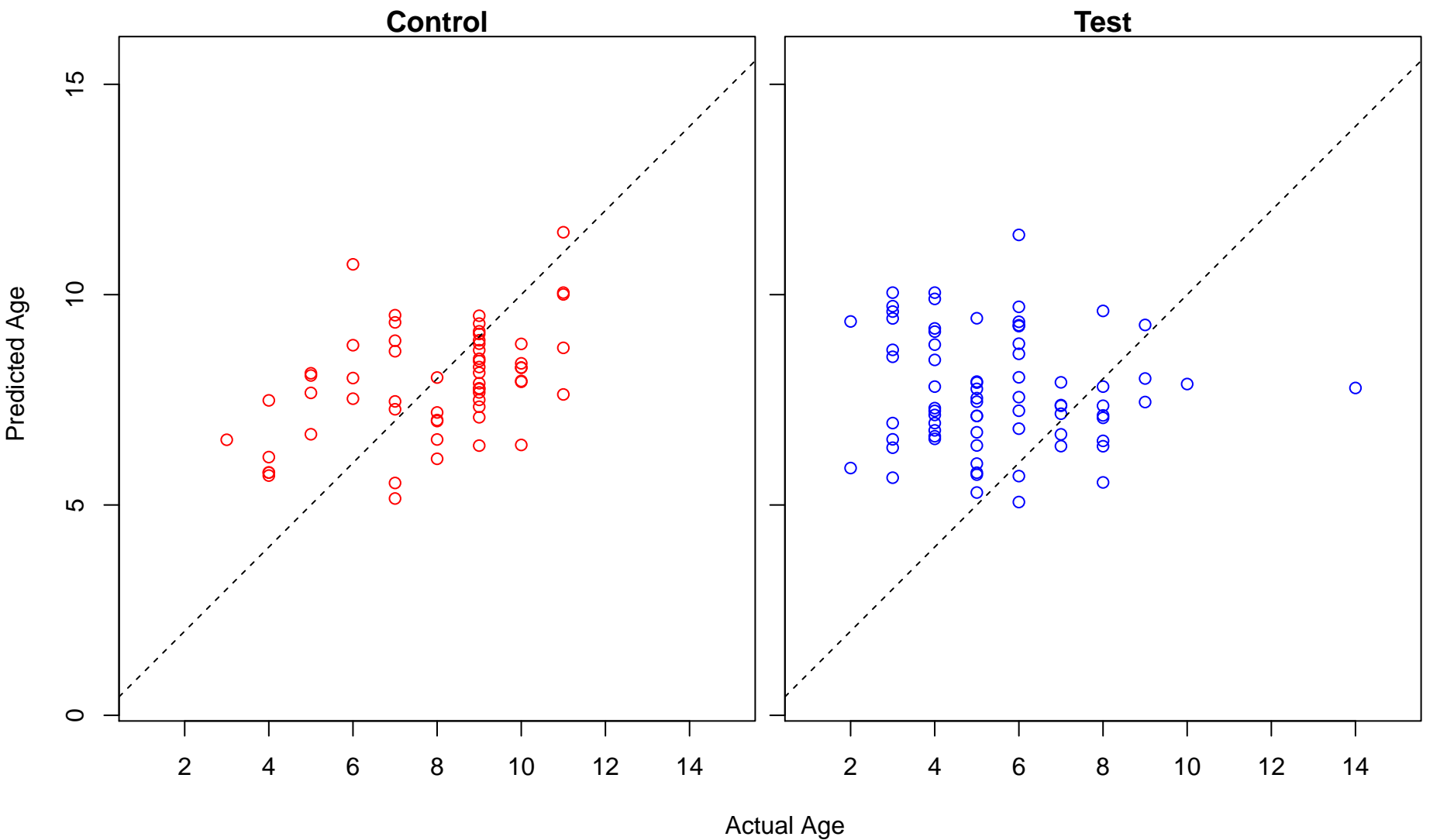
nephron tubule morphogenesis (Score: 1.813996)



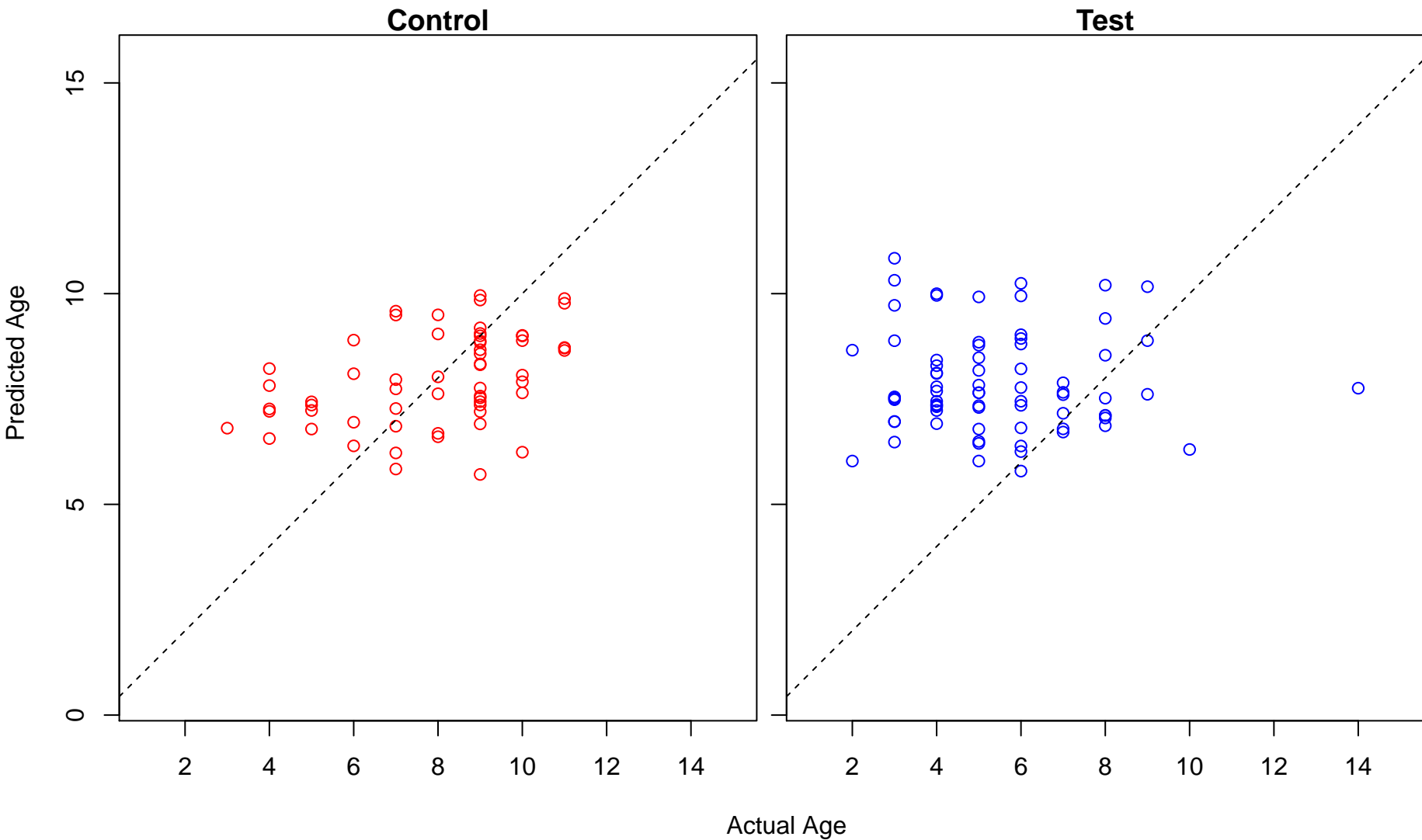
positive regulation of axonogenesis (Score: 1.813376)



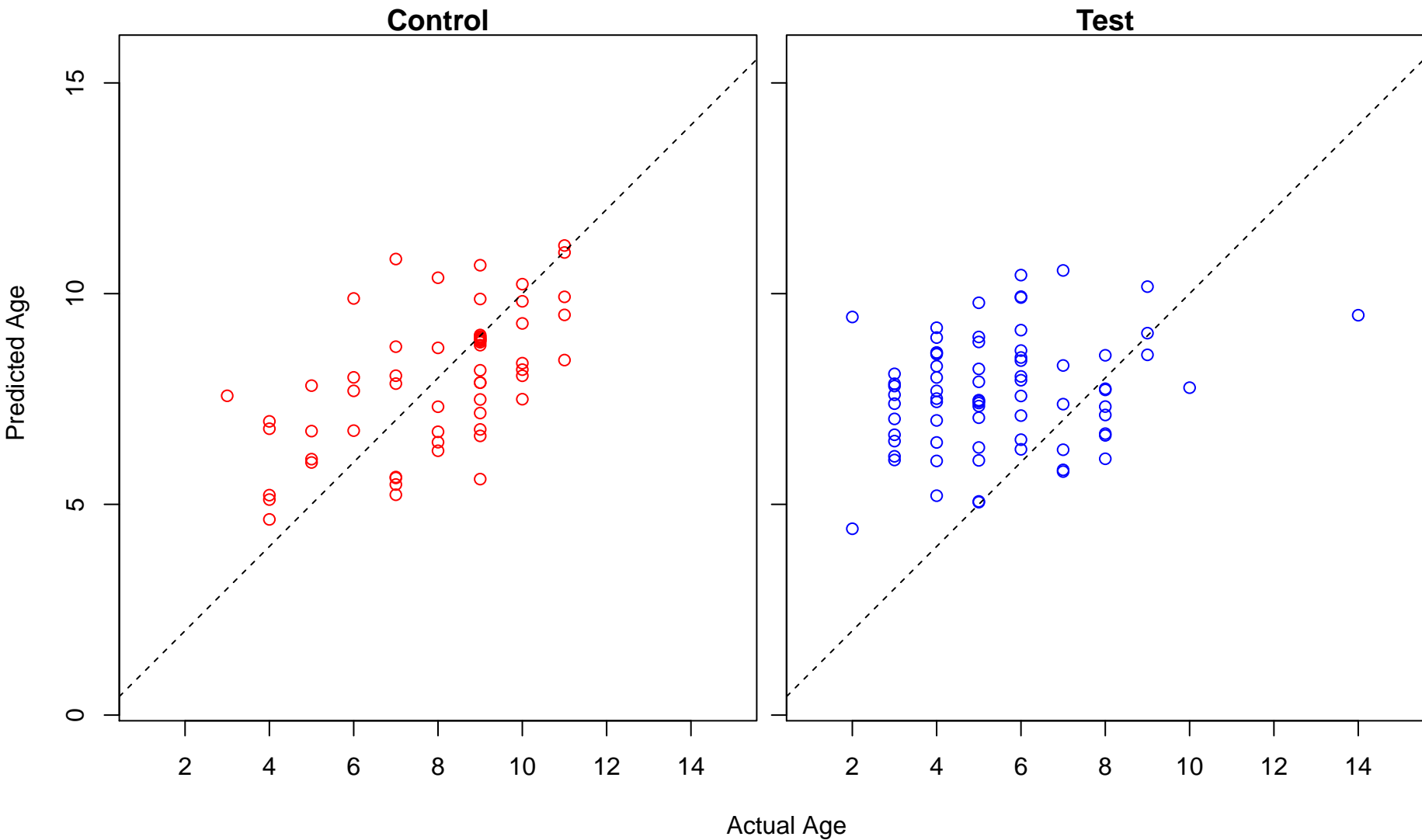
G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (Score: 1)



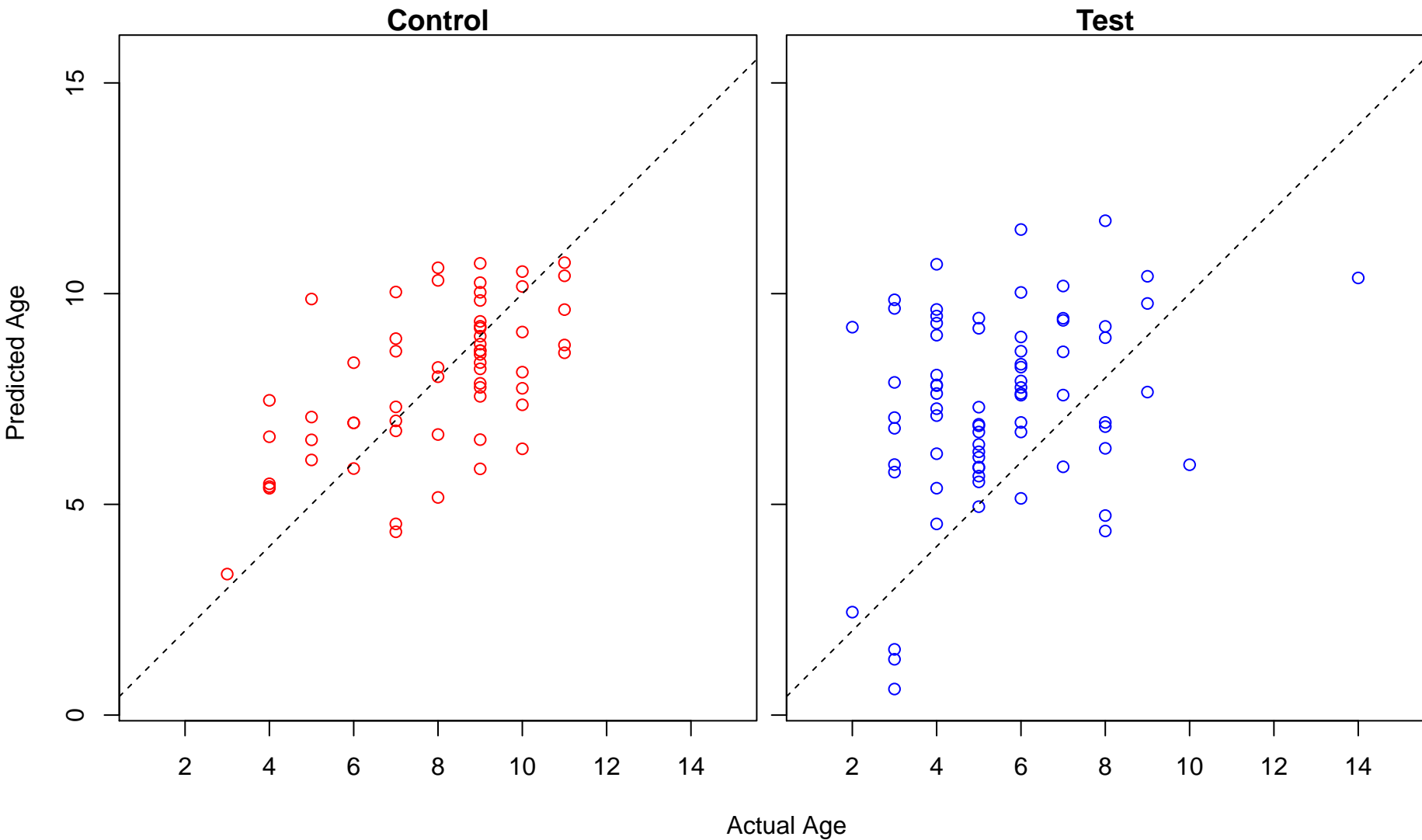
JAK-STAT cascade involved in growth hormone signaling pathway (Score: 1.808742)



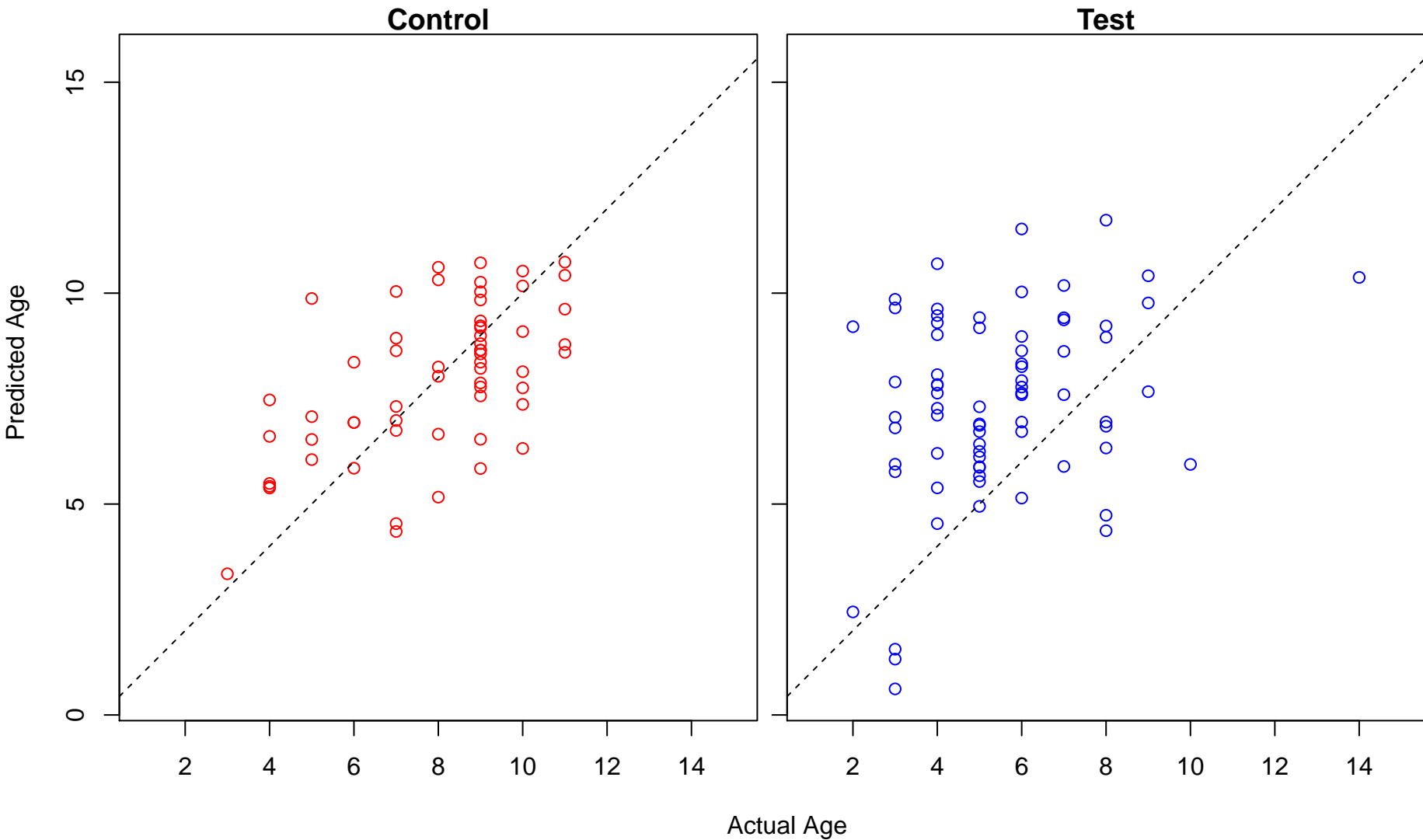
regulation of nitrogen compound metabolic process (Score: 1.808372)



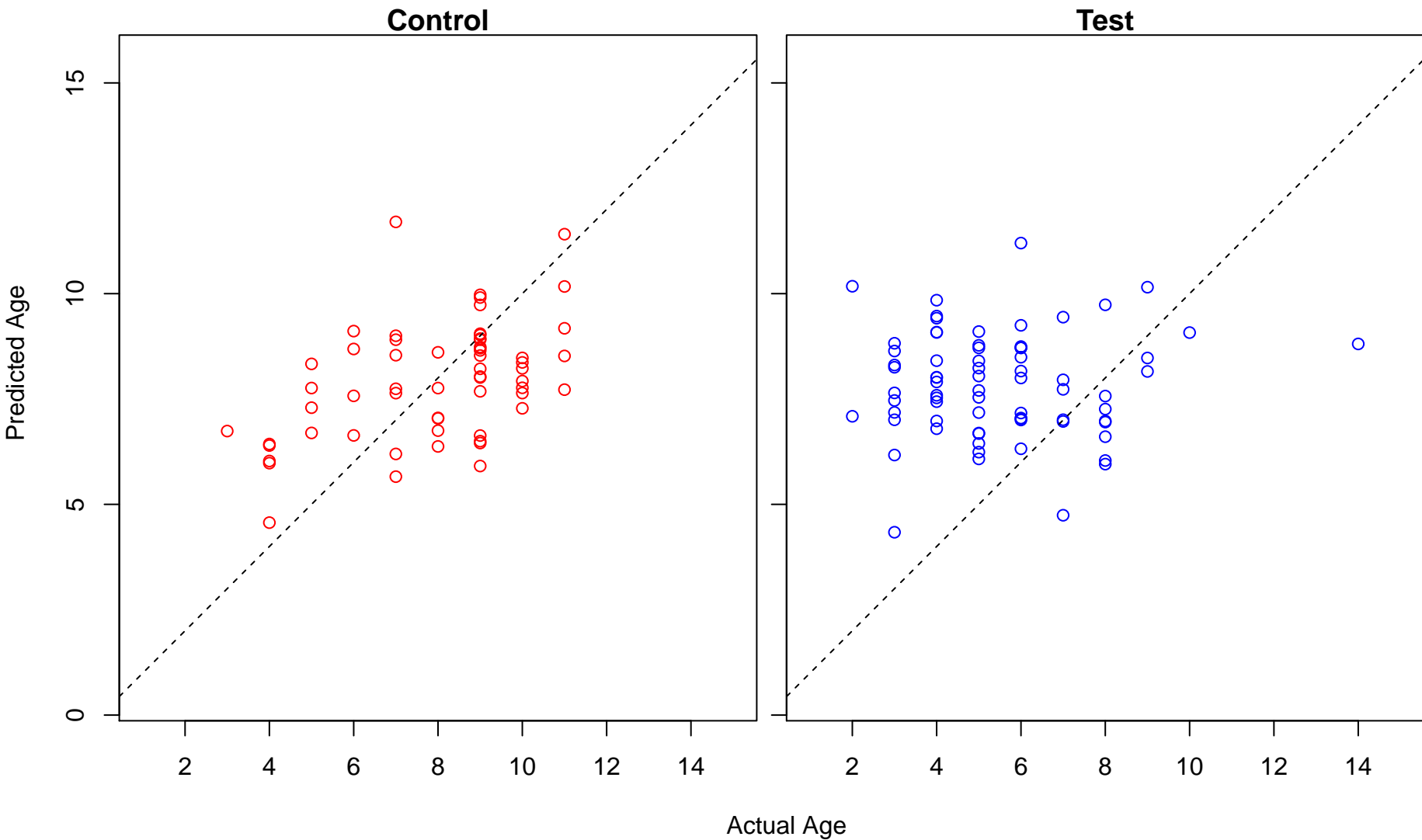
nephron morphogenesis (Score: 1.808123)



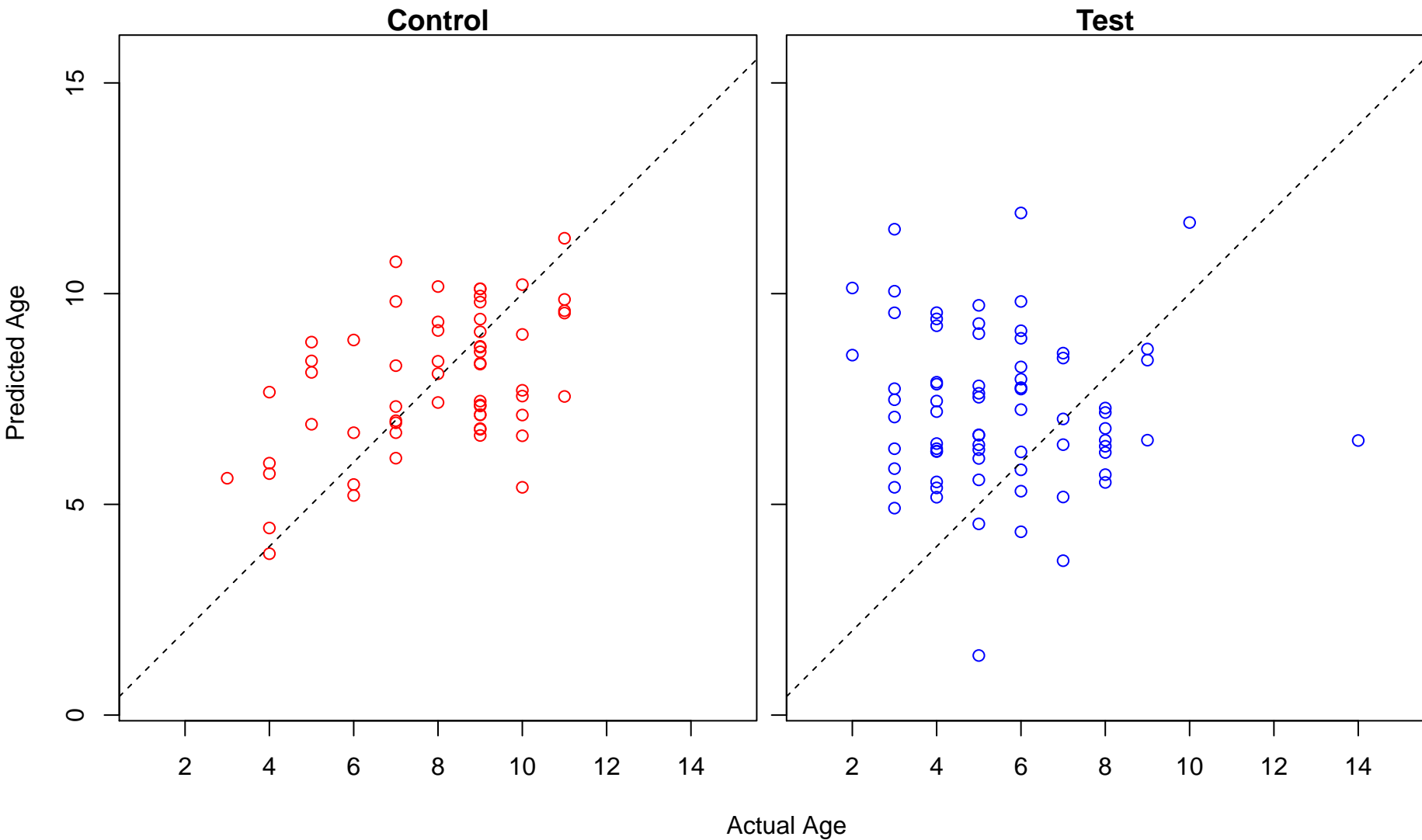
nephron epithelium morphogenesis (Score: 1.808123)



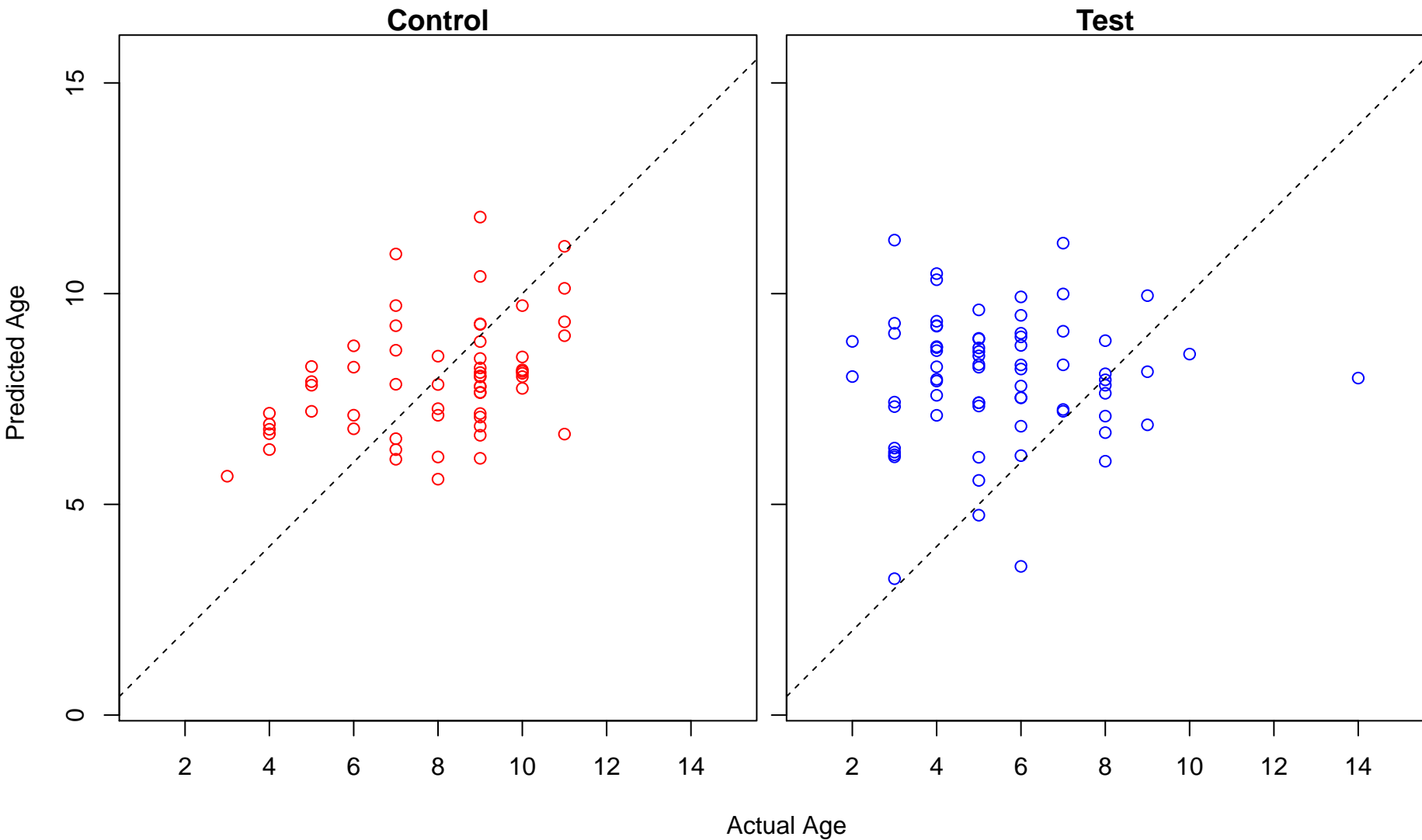
alpha-beta T cell differentiation (Score: 1.802597)



telomere capping (Score: 1.802258)

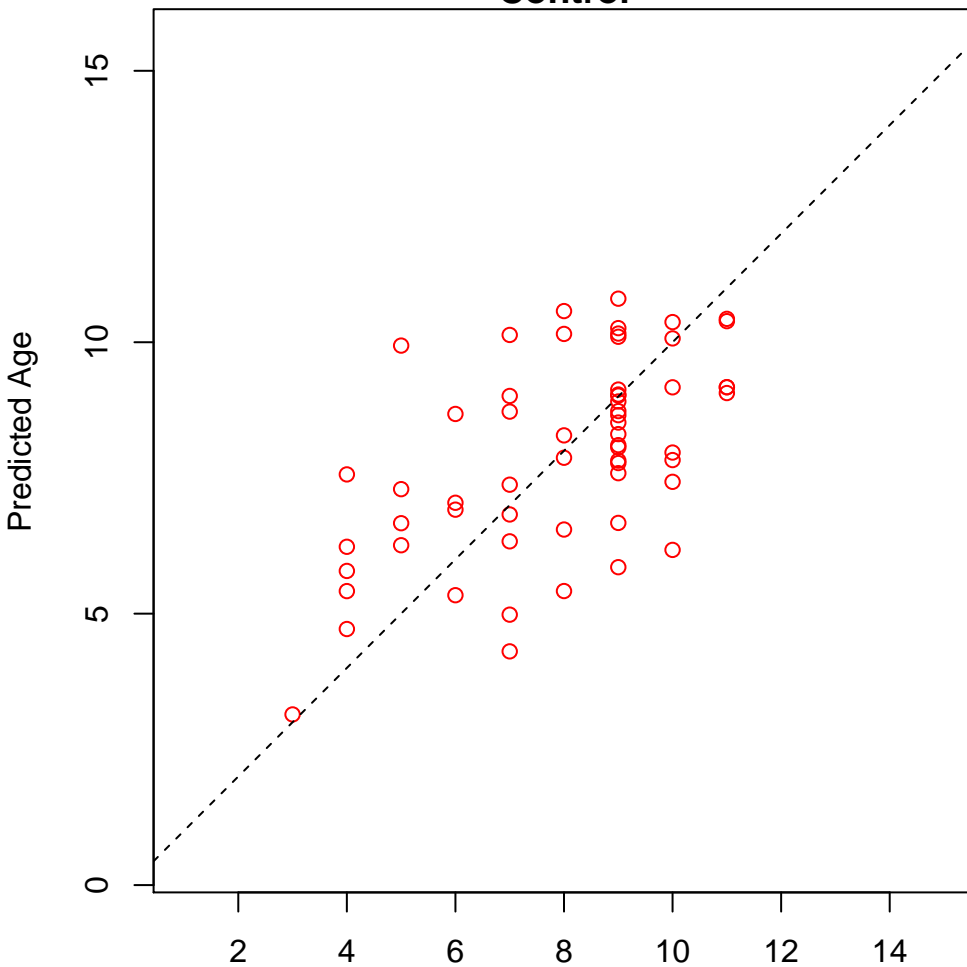


negative regulation of mitochondrial fusion (Score: 1.801199)

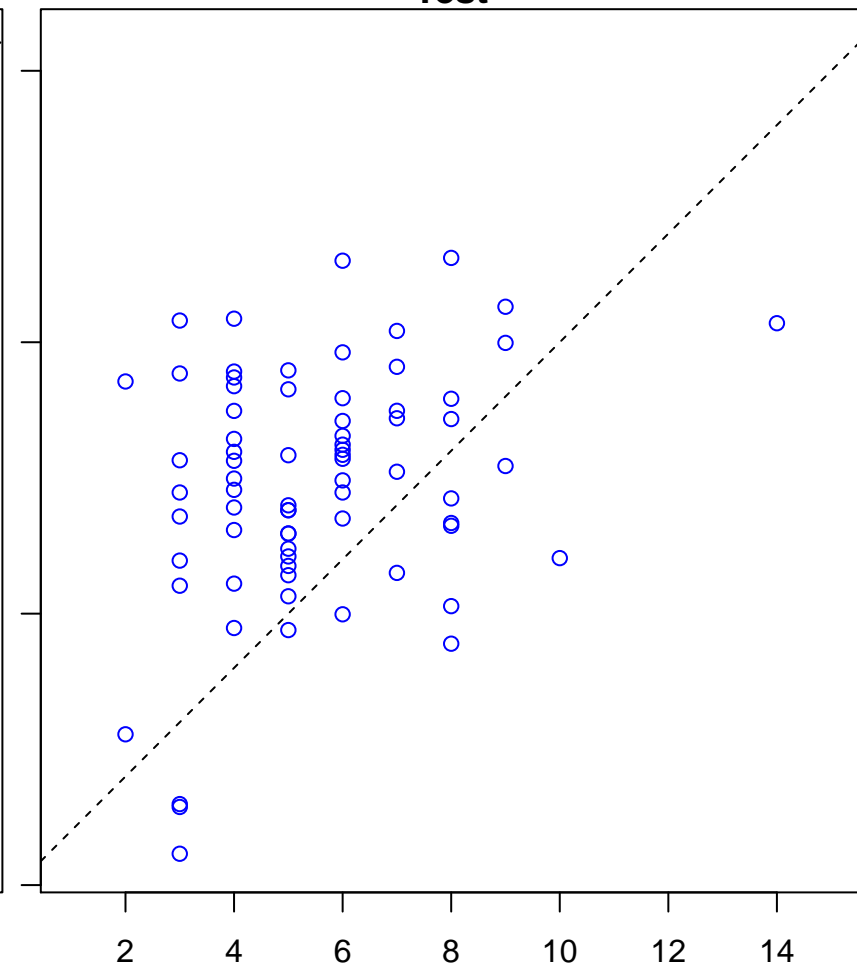


mesonephric tubule morphogenesis (Score: 1.800135)

Control

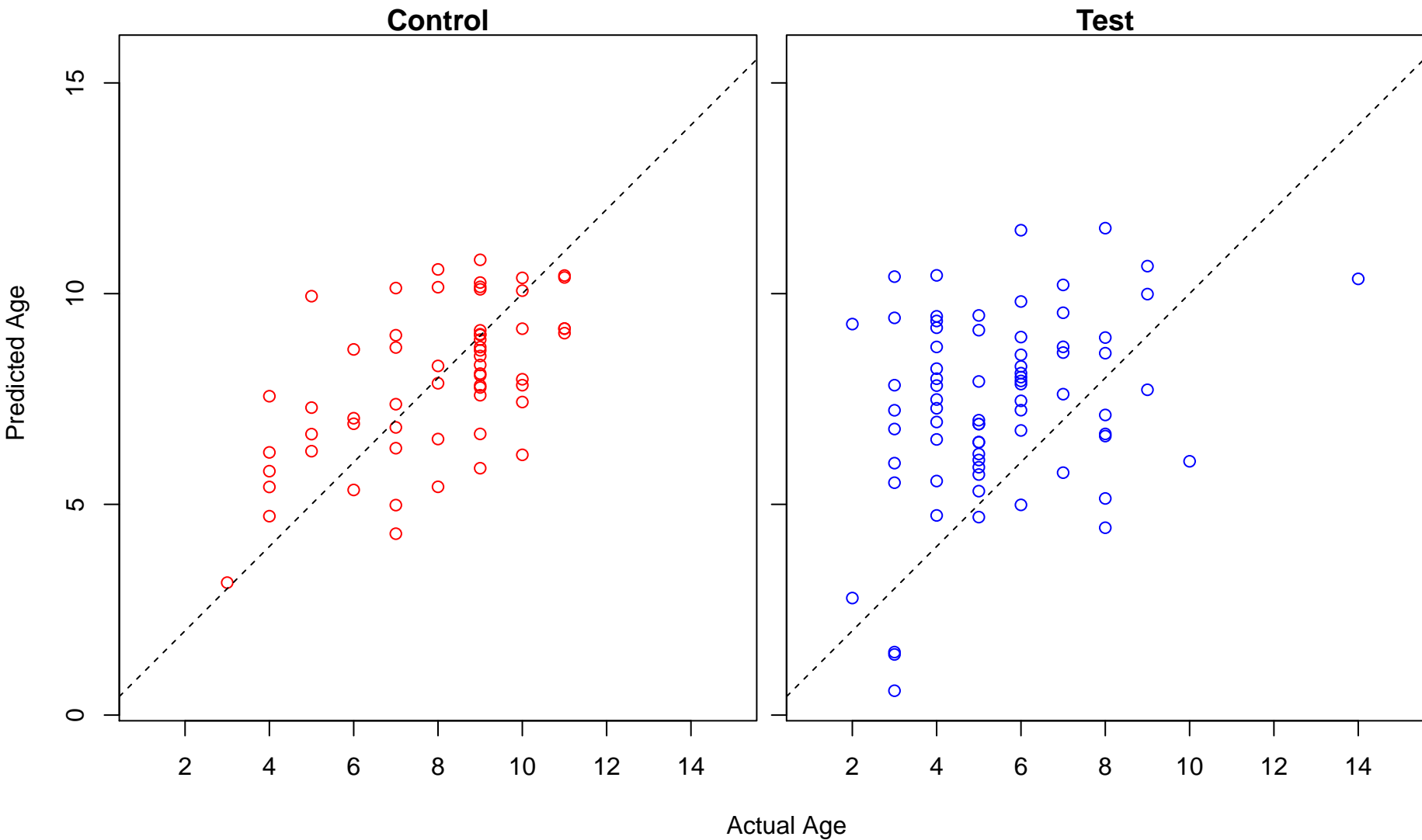


Test

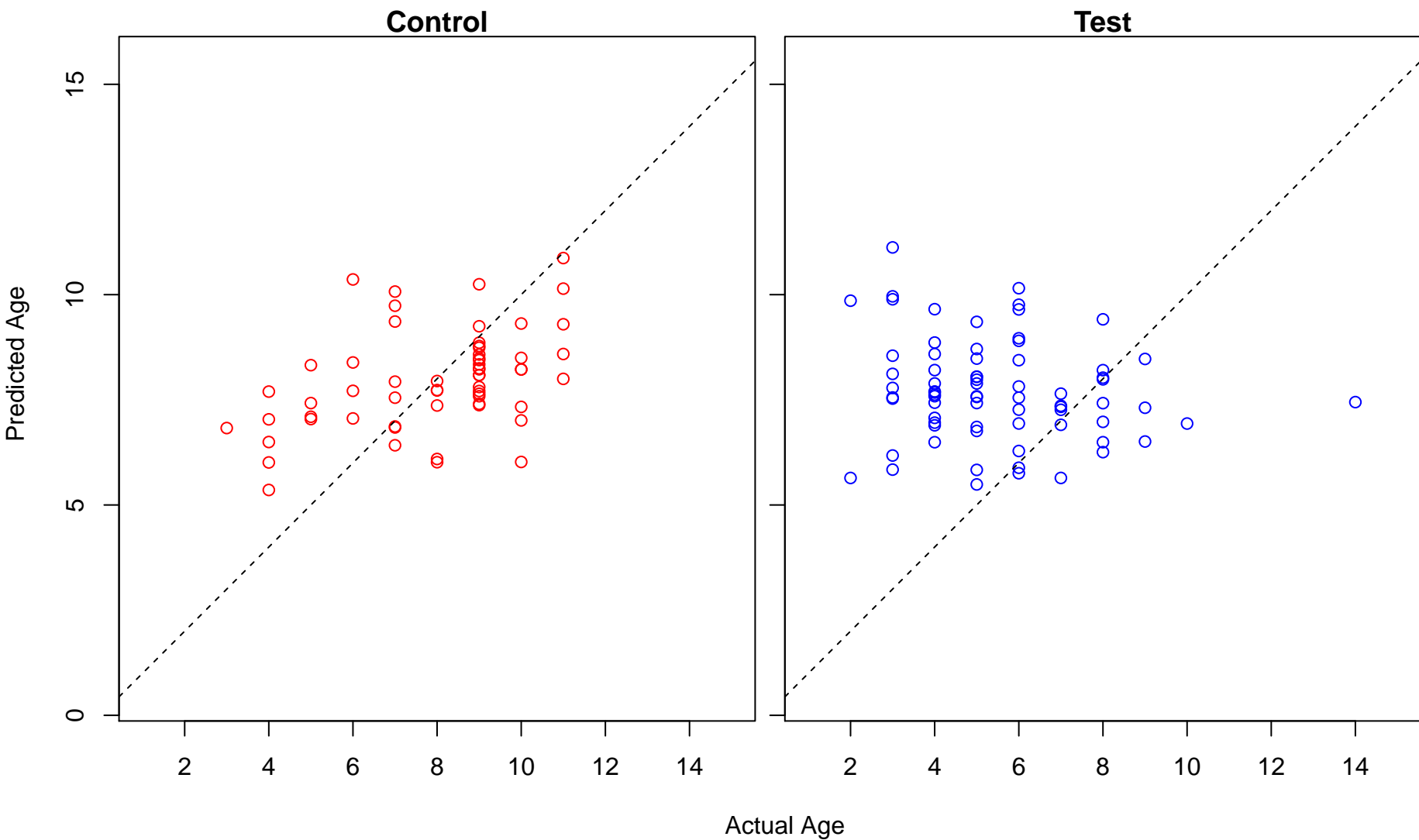


Actual Age

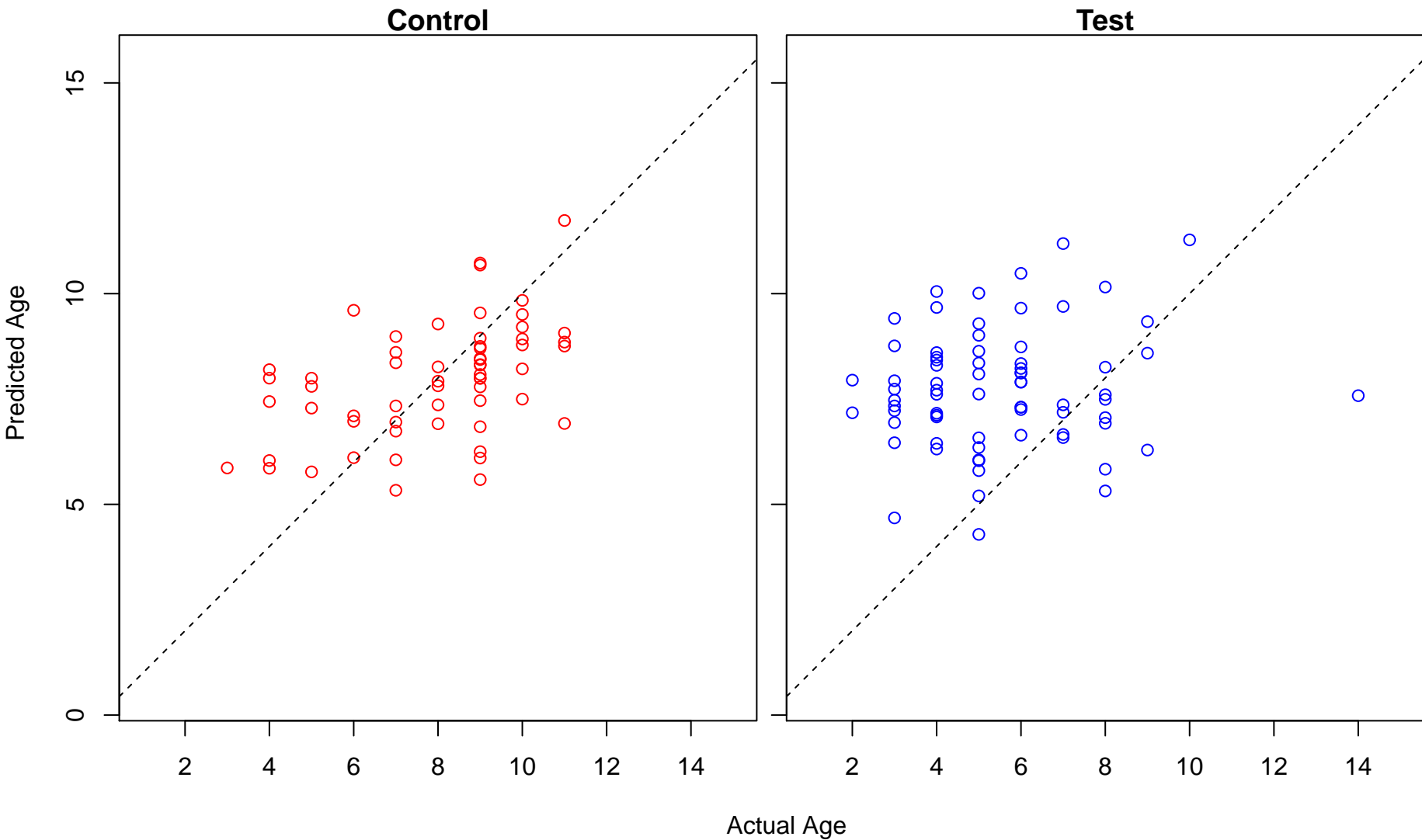
ureteric bud morphogenesis (Score: 1.799930)



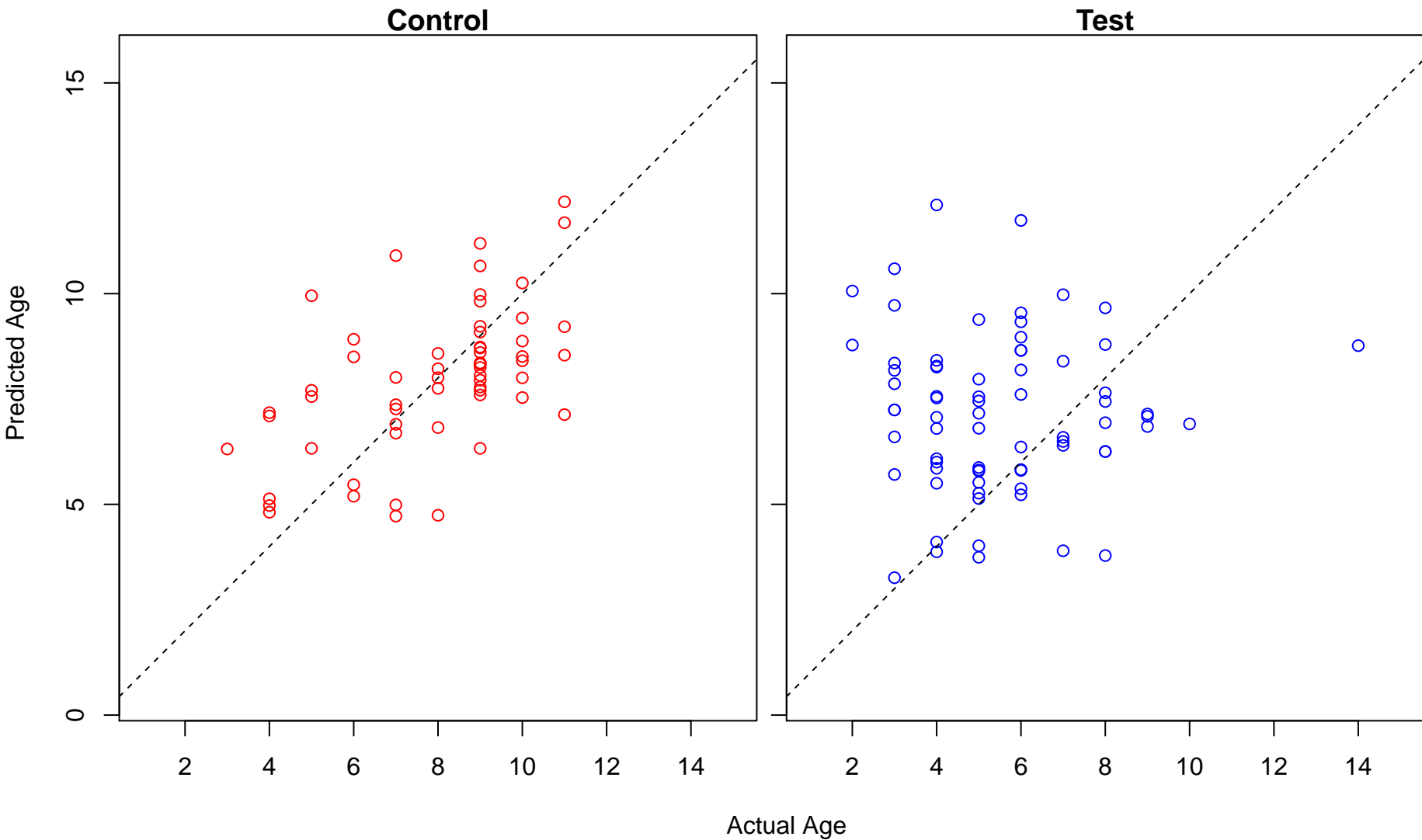
positive regulation of transcription factor import into nucleus (Score: 1.793533)



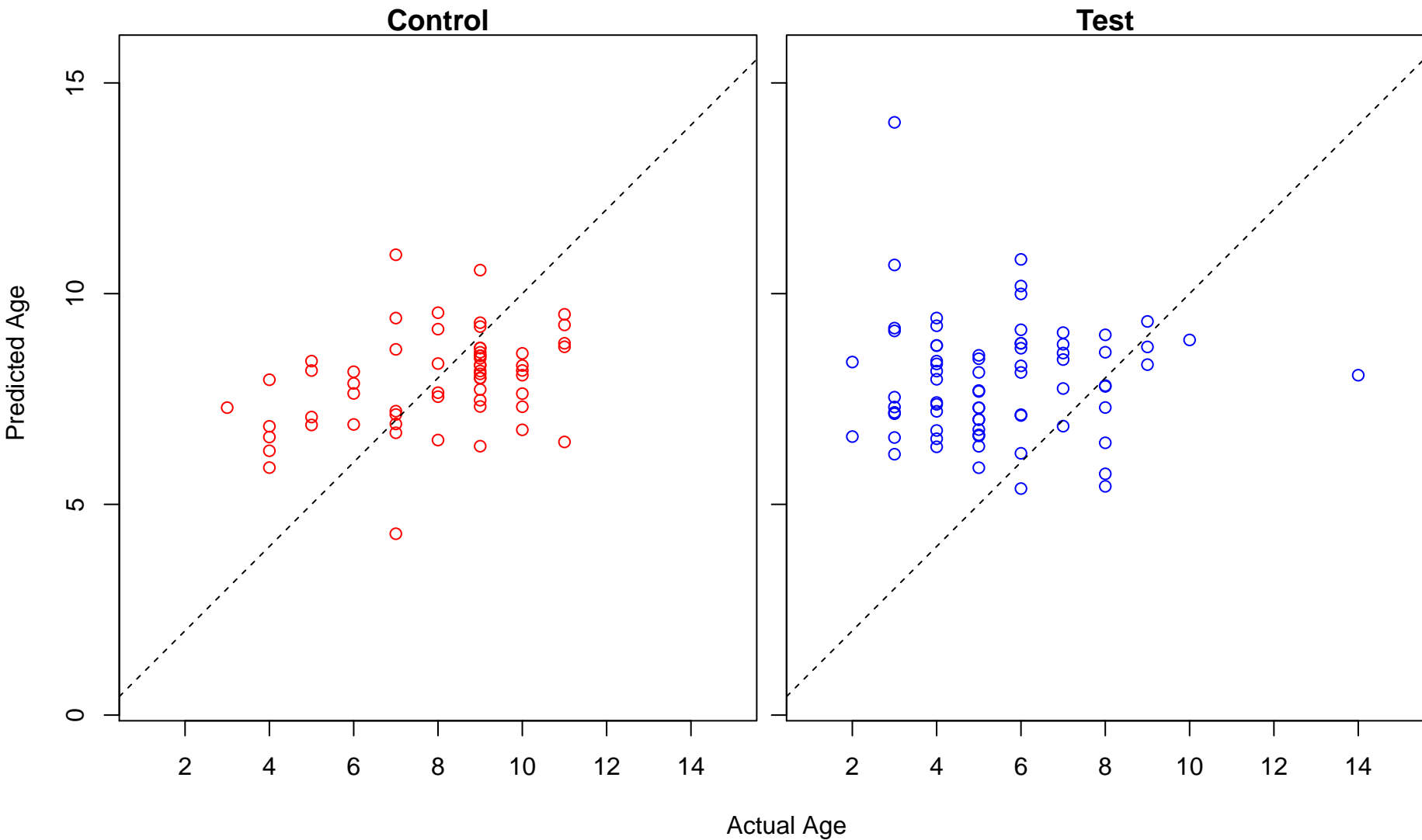
response to calcium ion (Score: 1.792266)



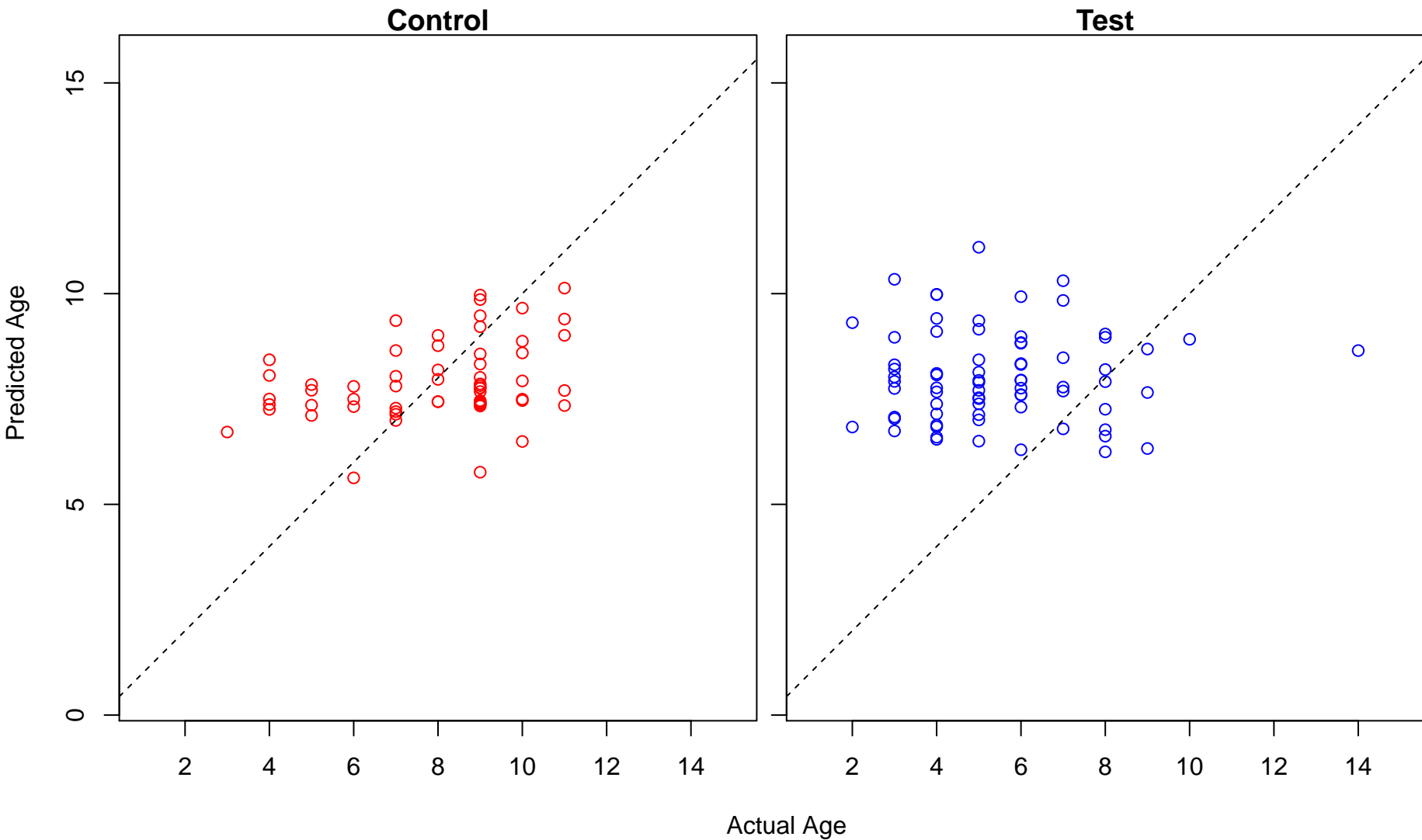
nucleoside phosphate biosynthetic process (Score: 1.792051)



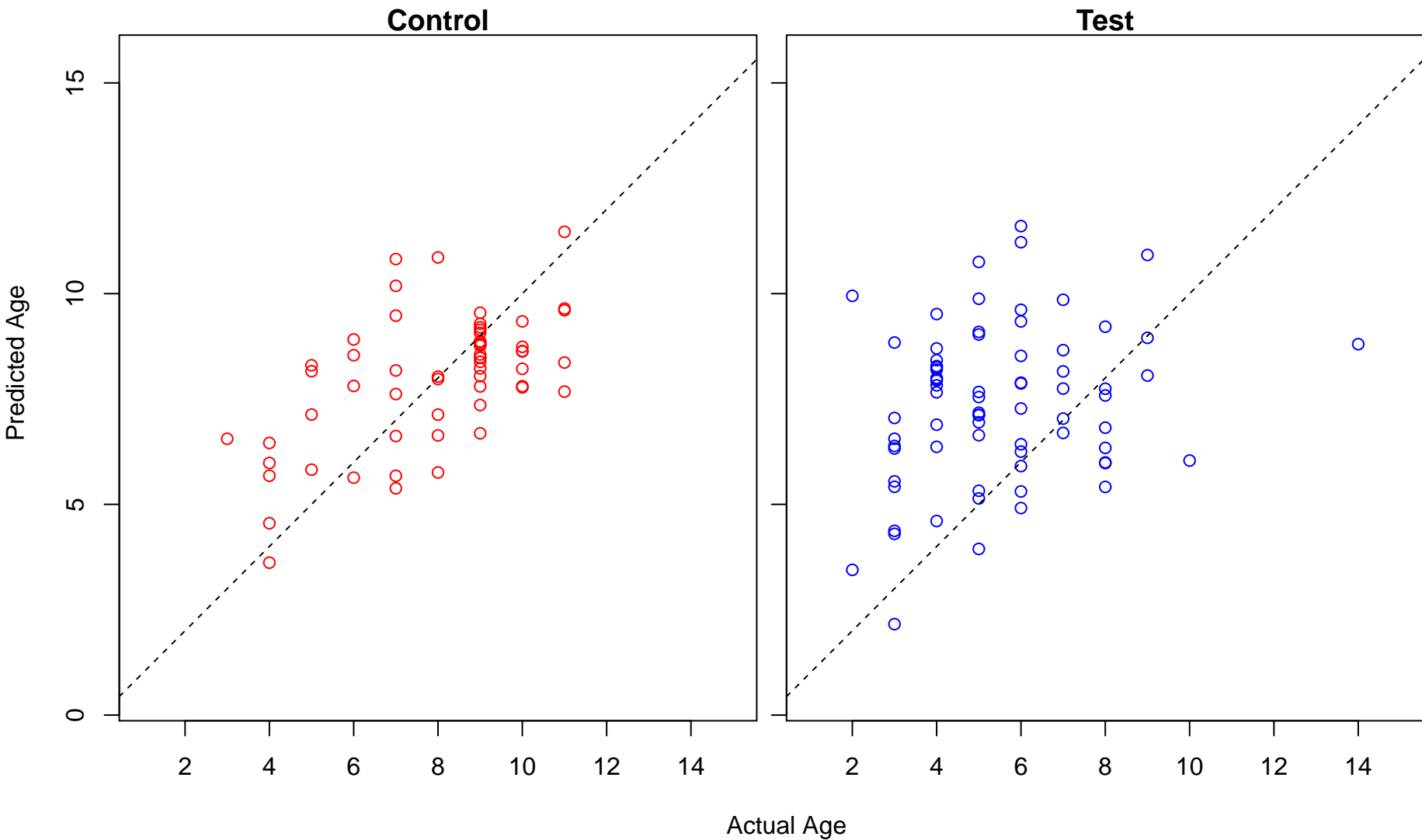
cell migration involved in vasculogenesis (Score: 1.791511)



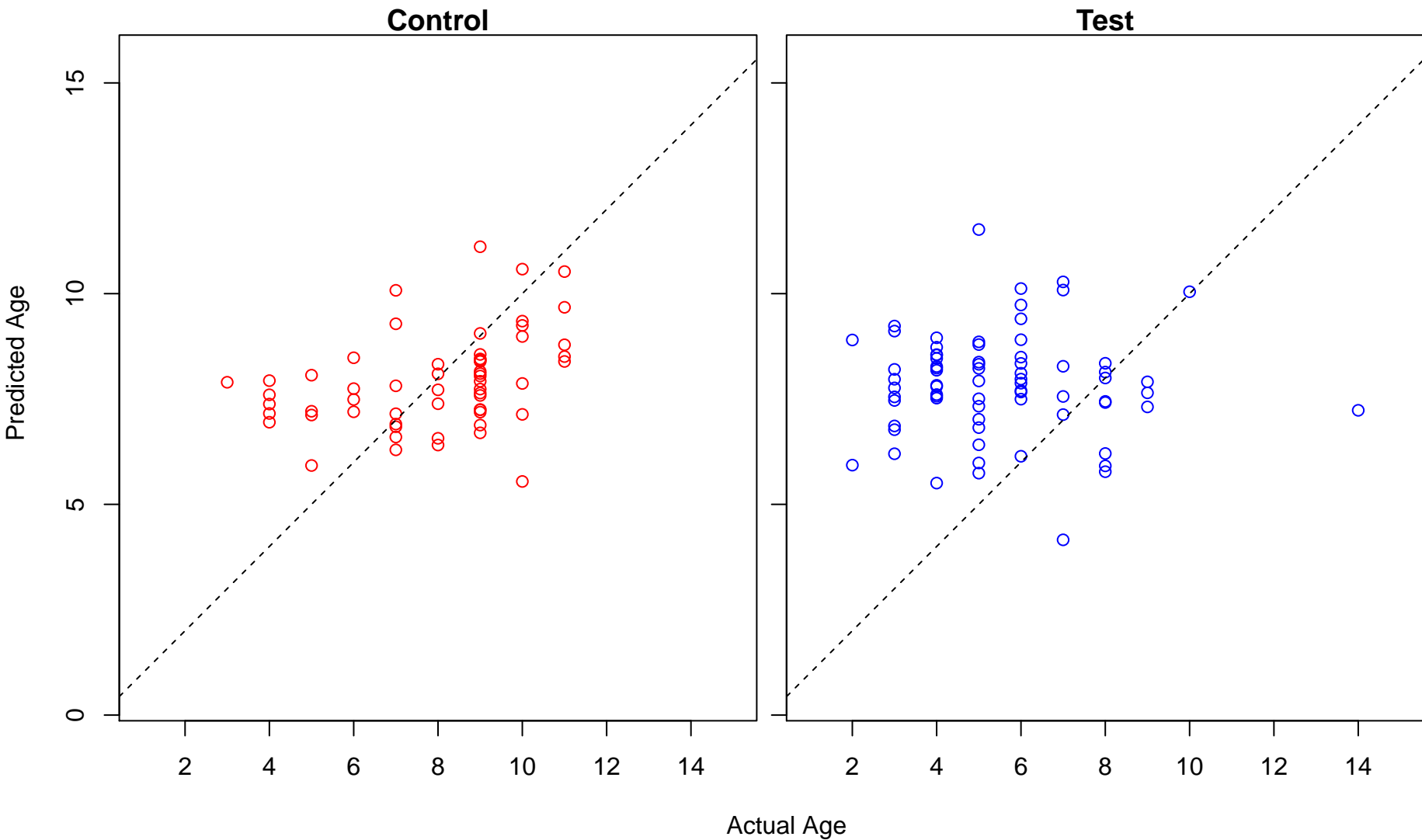
posterior midgut development (Score: 1.790387)



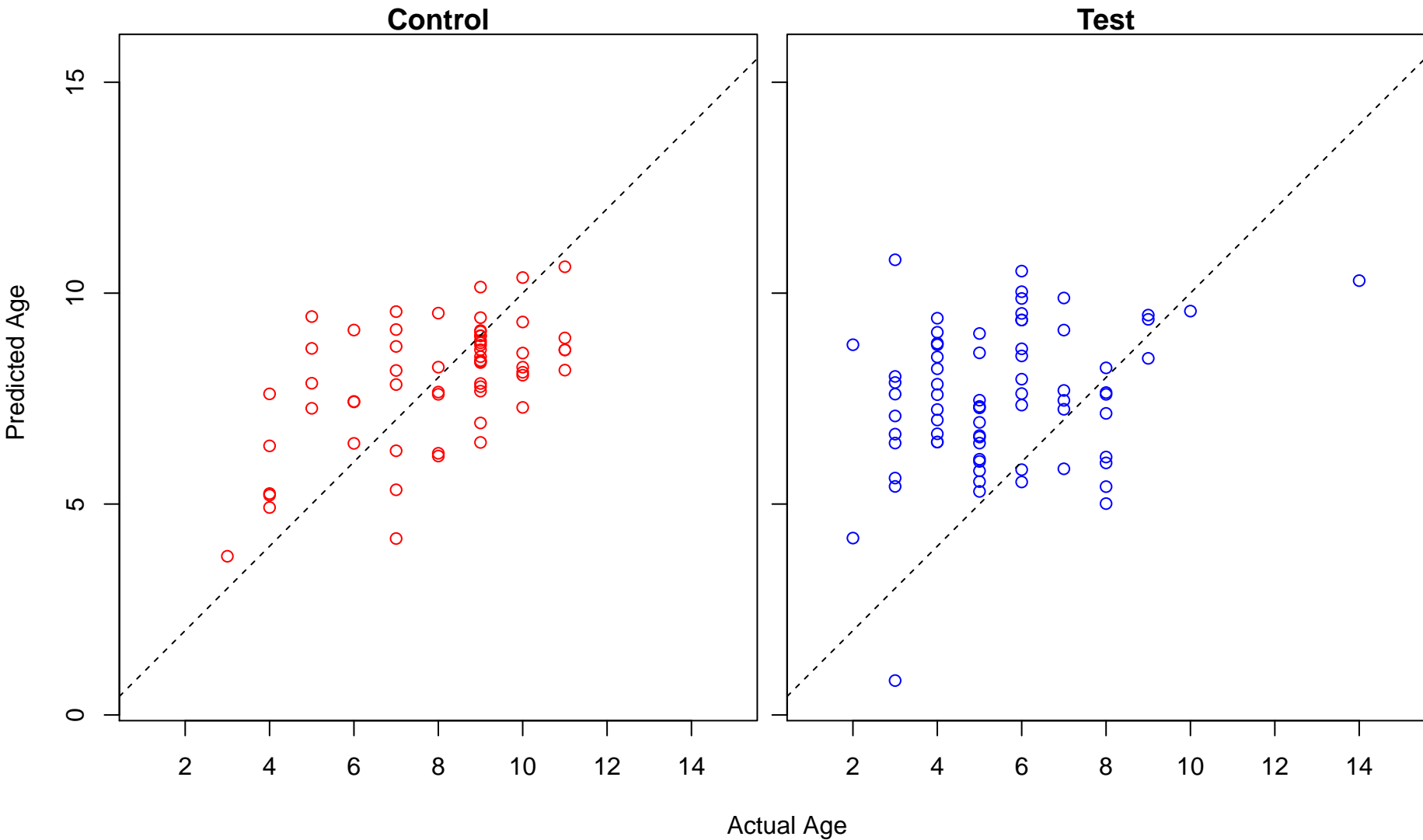
lymphocyte migration (Score: 1.788739)



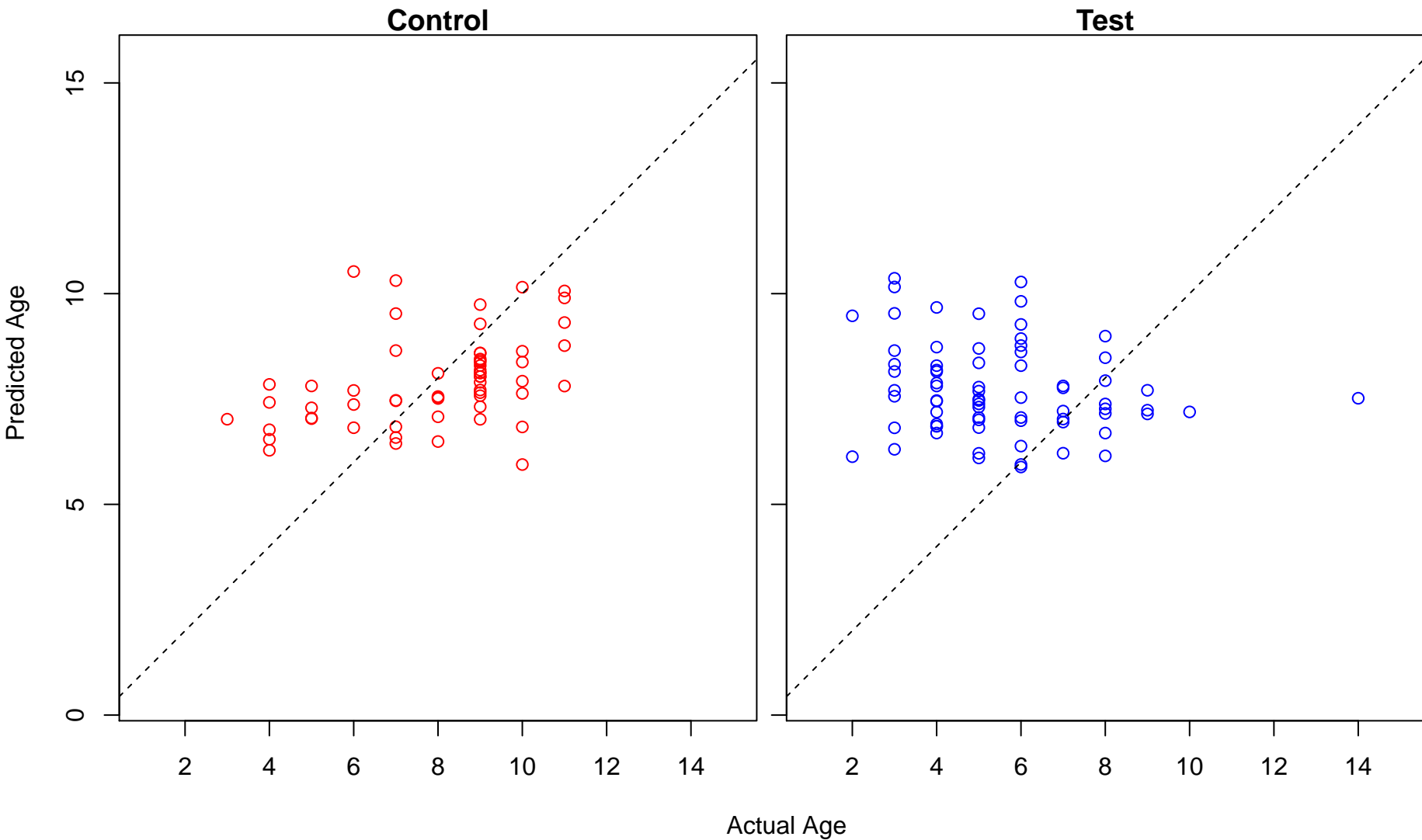
trachea cartilage morphogenesis (Score: 1.787709)



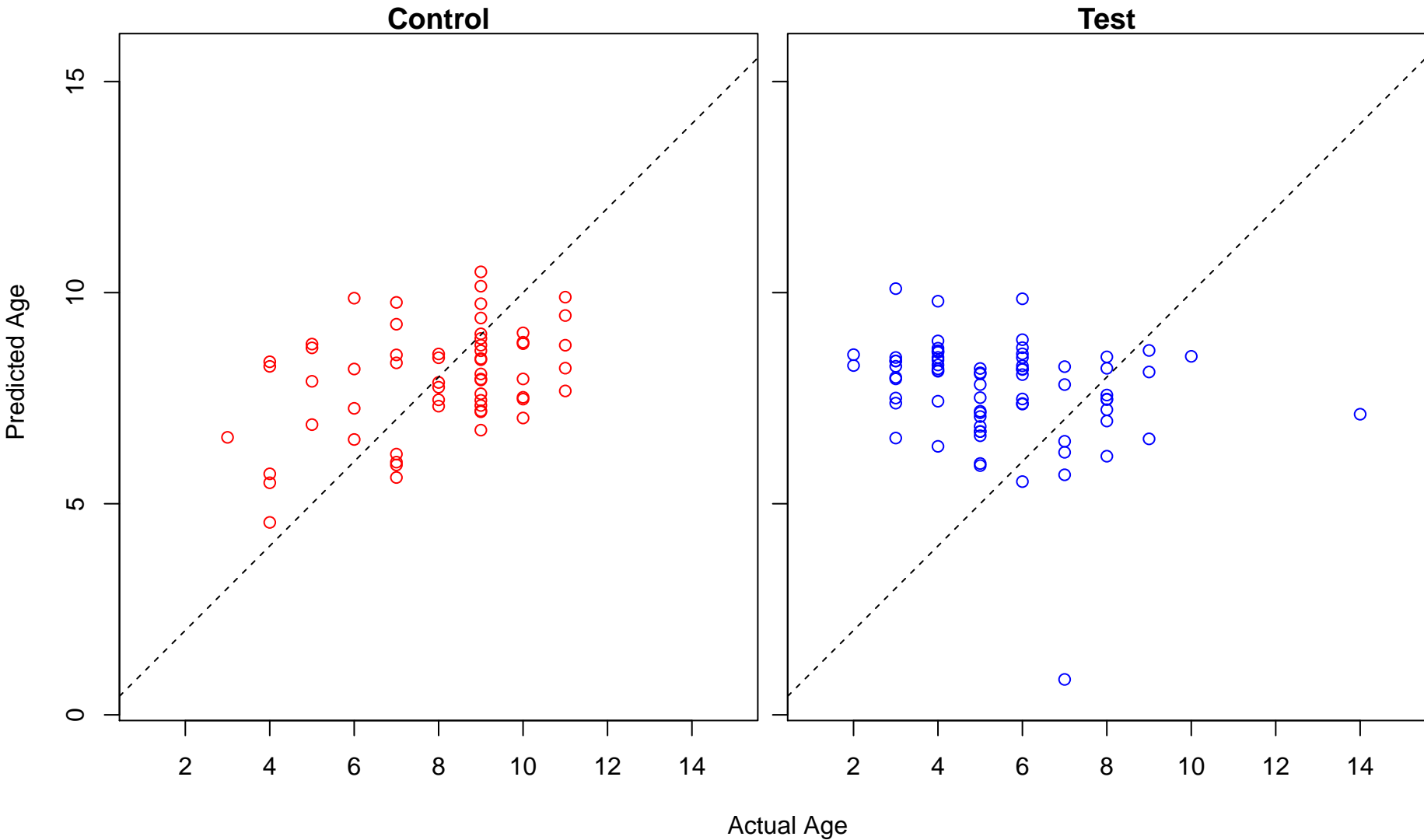
negative regulation of pathway-restricted SMAD protein phosphorylation (Score: 1.787280)



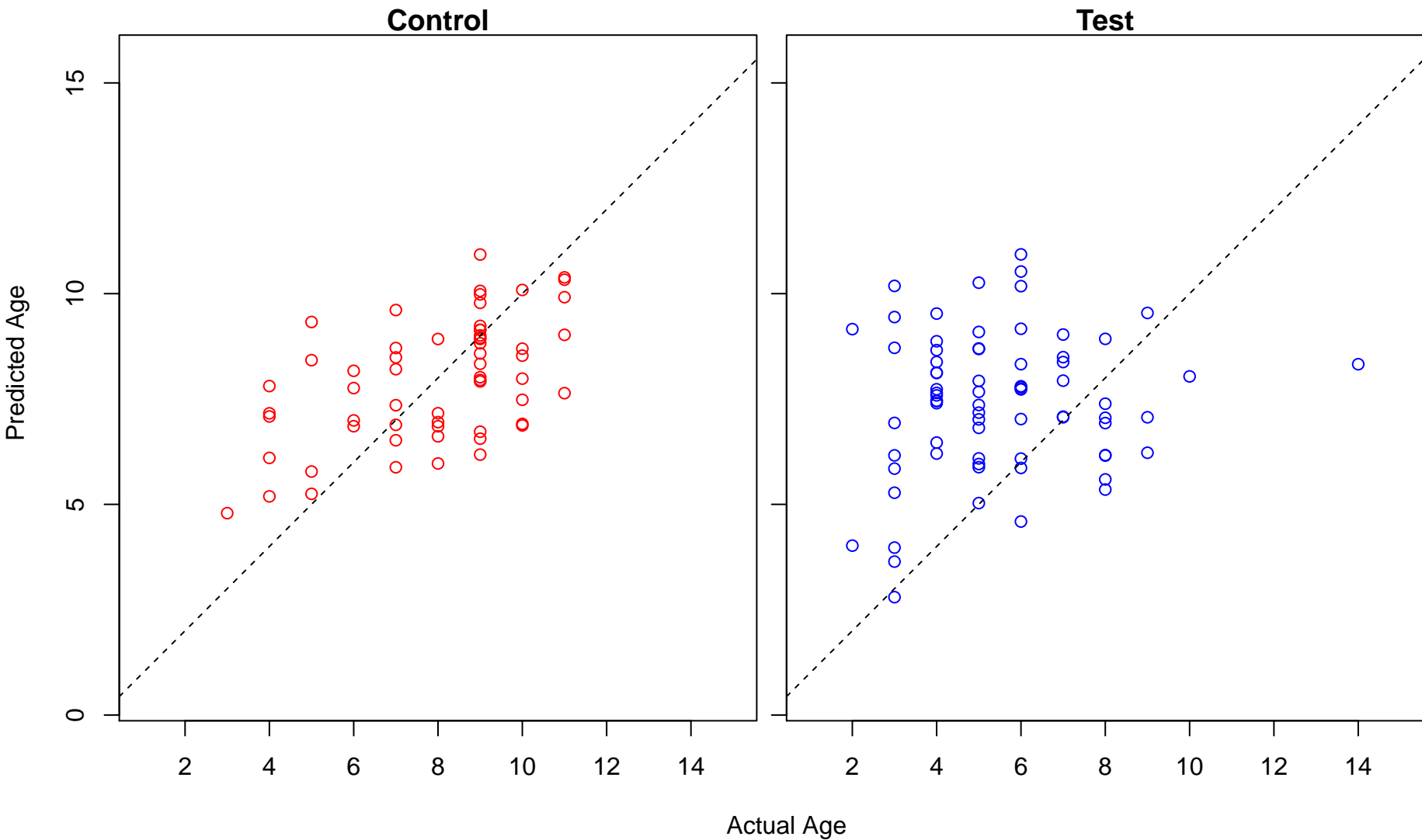
regulation of transcription from RNA polymerase I promoter (Score: 1.783582)



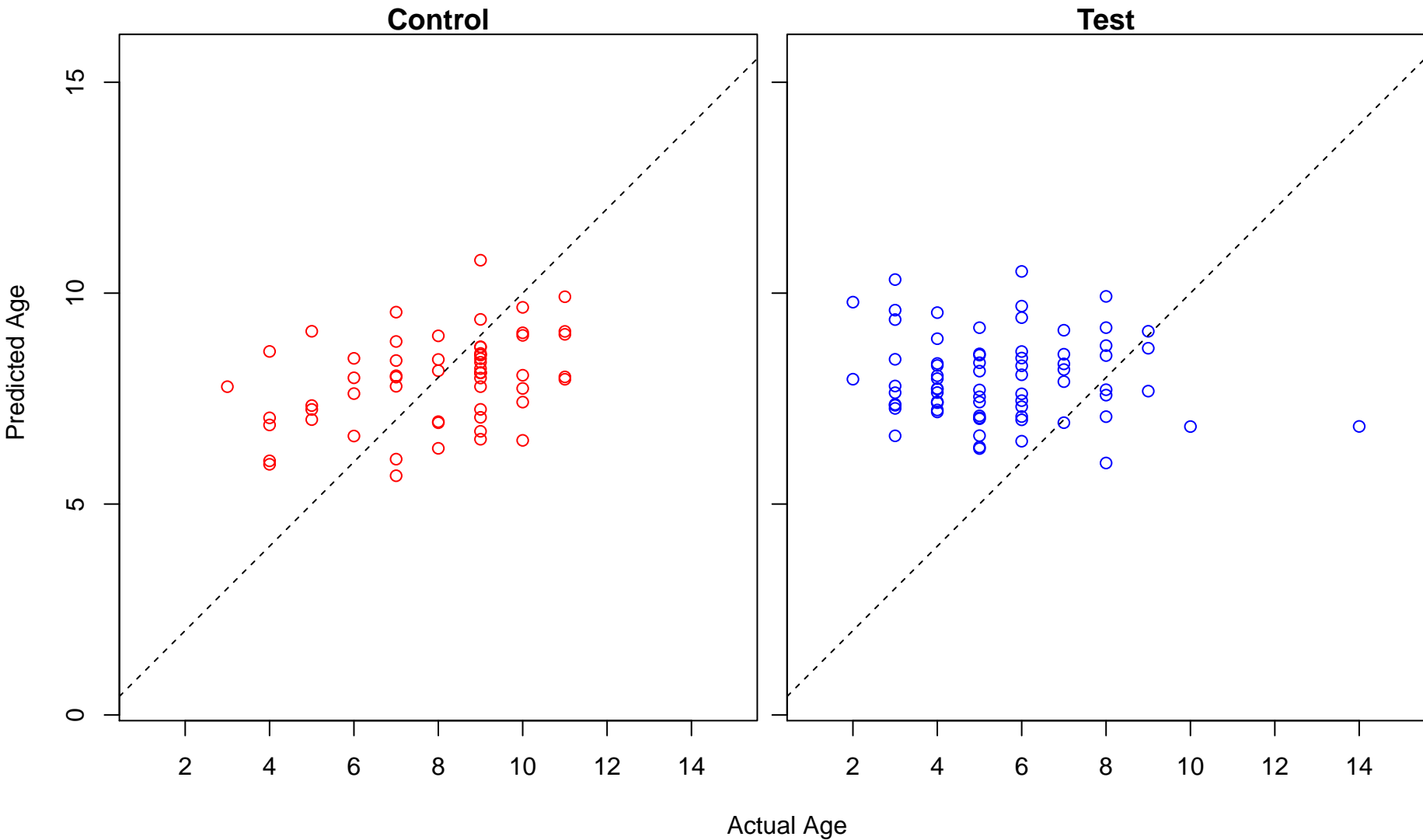
negative regulation of bone mineralization (Score: 1.782467)



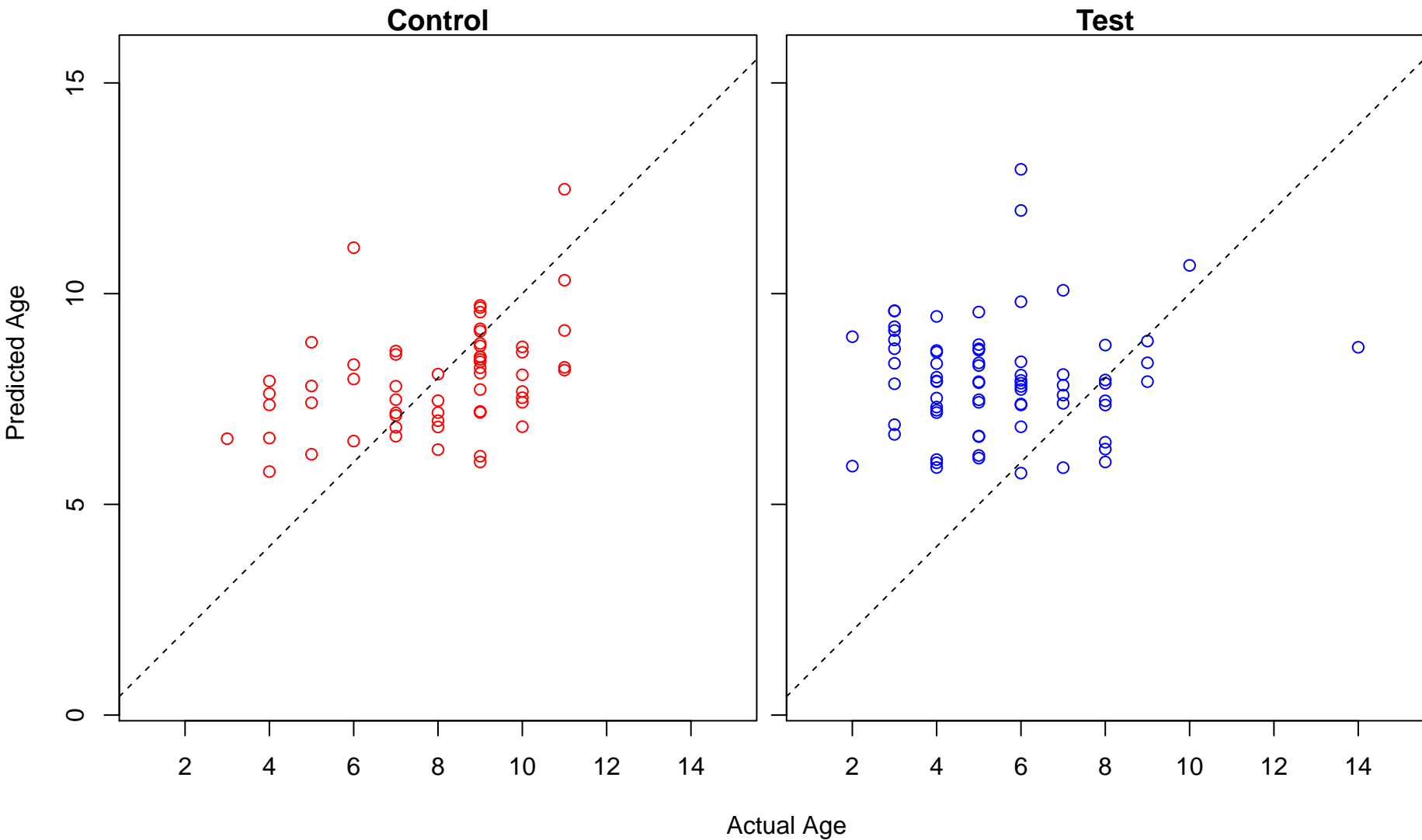
prostatic bud formation (Score: 1.781780)



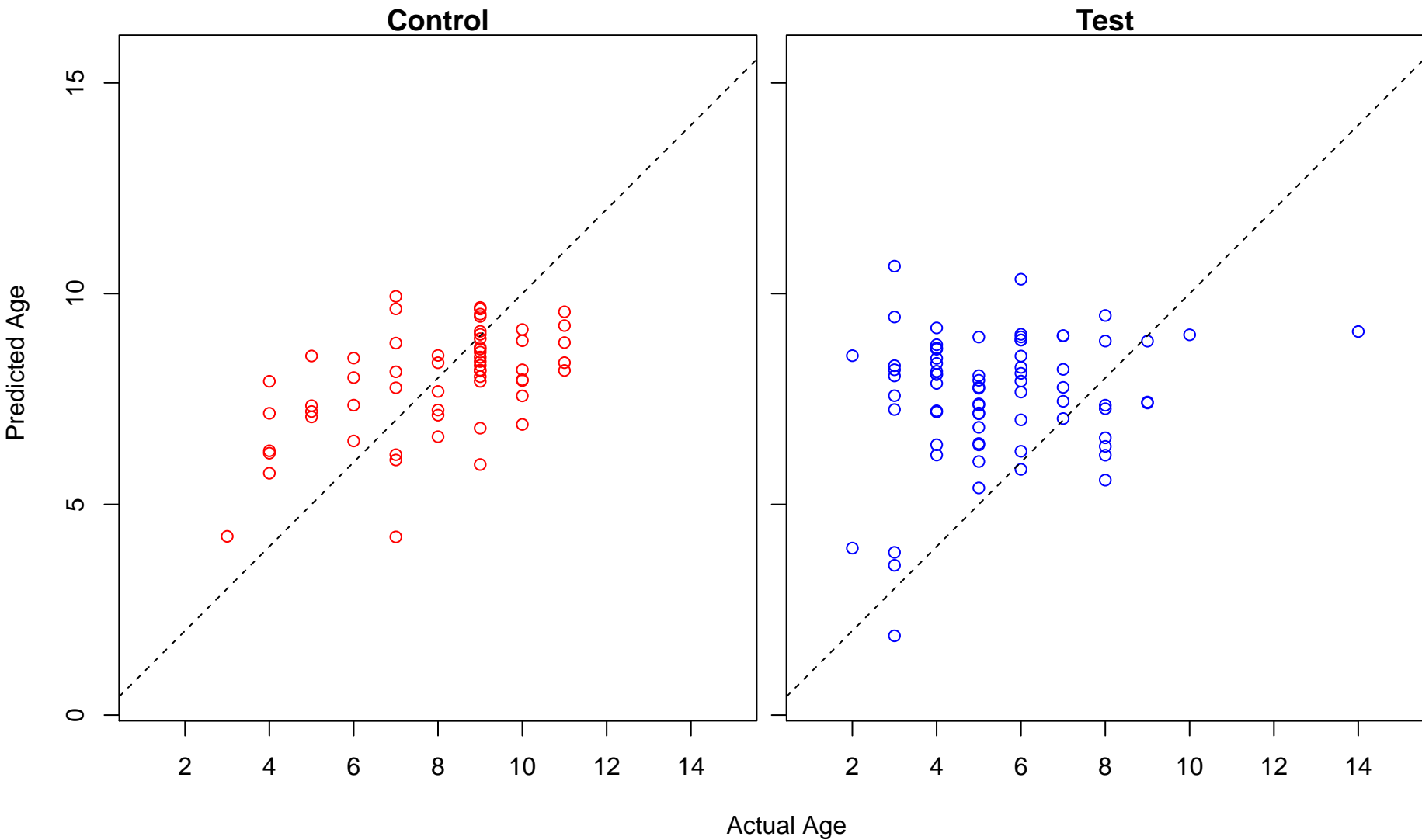
lamellipodium assembly involved in ameboidal cell migration (Score: 1.780986)



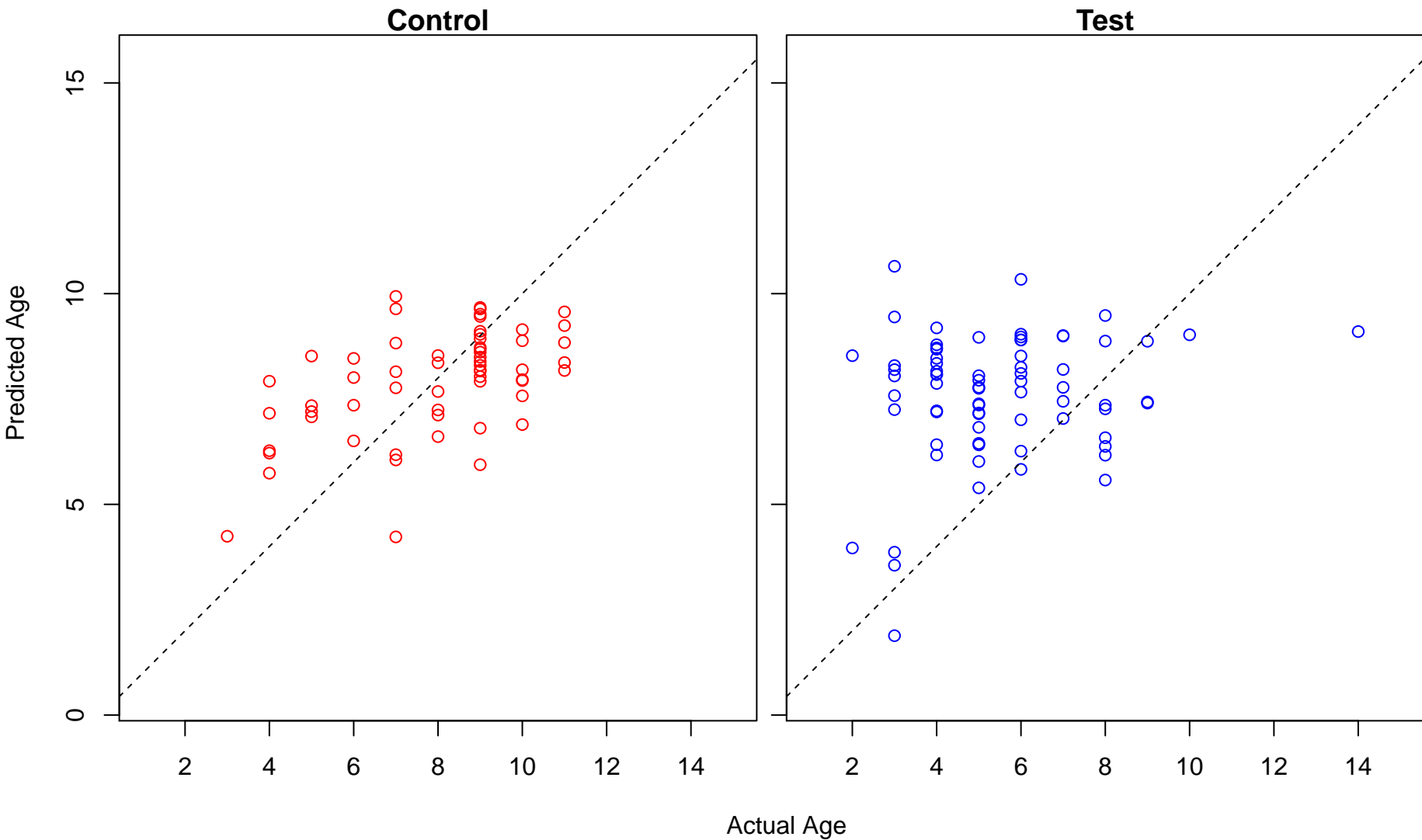
negative regulation of interferon-beta production (Score: 1.780118)



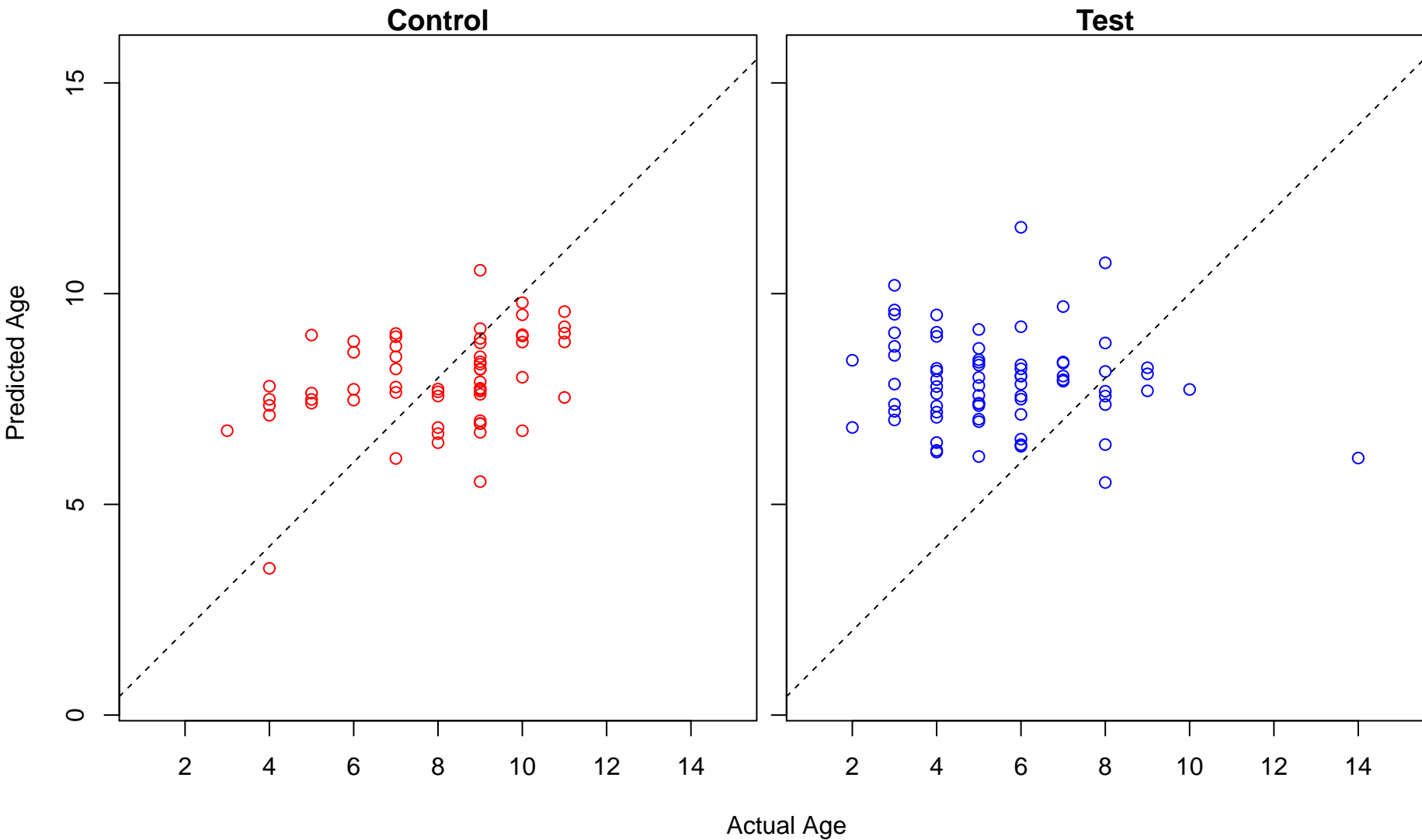
neural plate regionalization (Score: 1.779152)



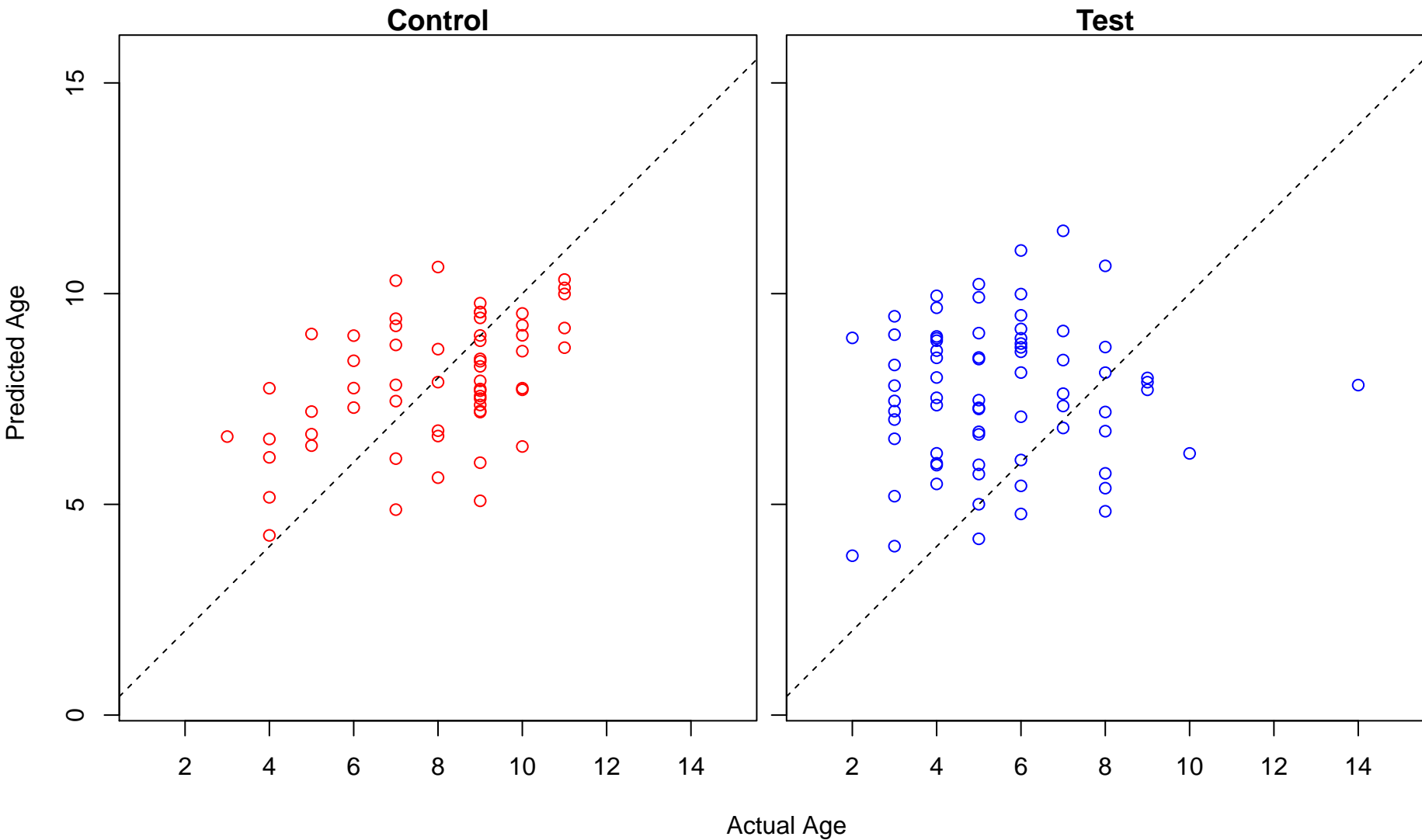
neural plate anterior/posterior regionalization (Score: 1.779082)



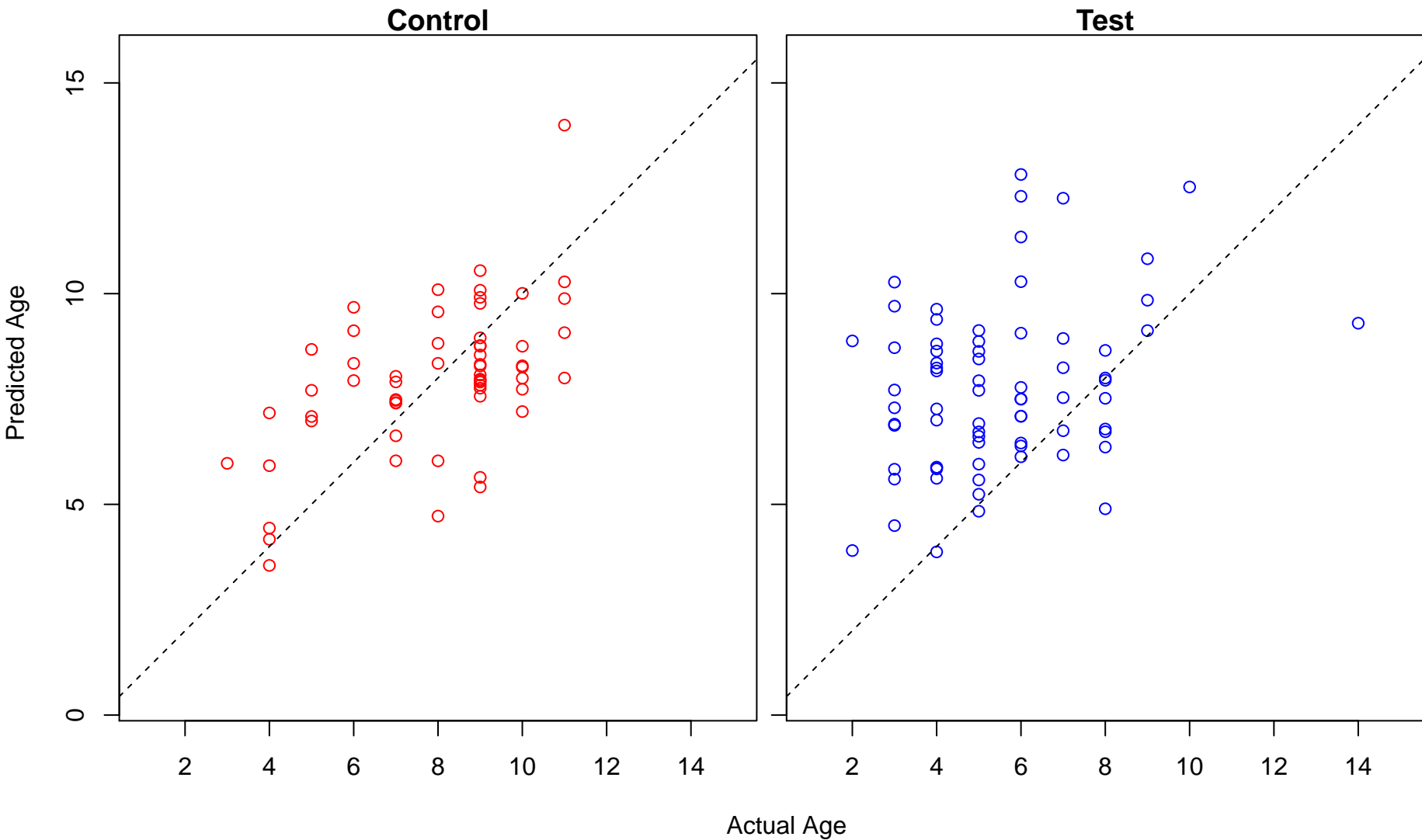
cerebellar molecular layer development (Score: 1.777849)



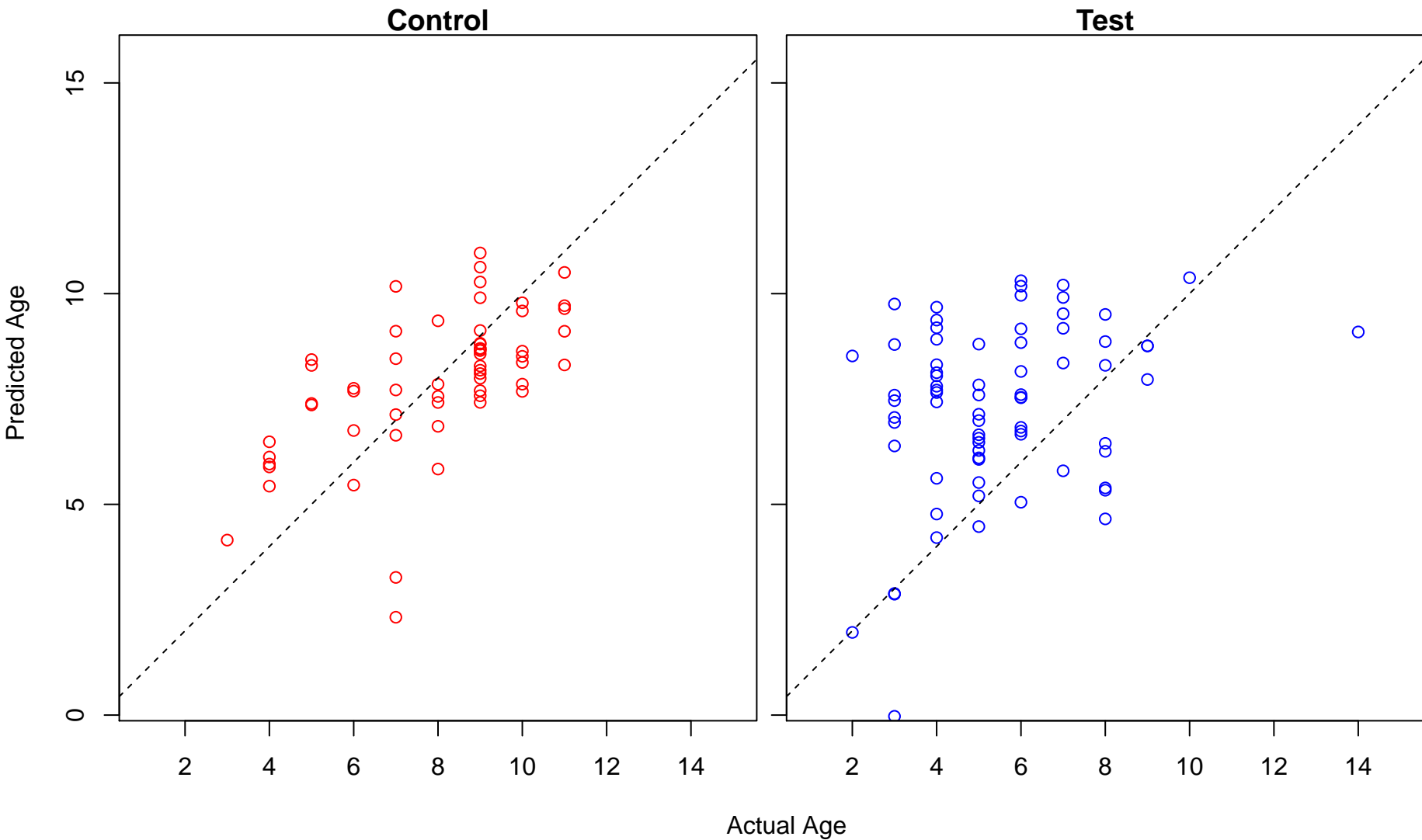
positive regulation of cyclin–dependent protein kinase activity (Score: 1.775357)



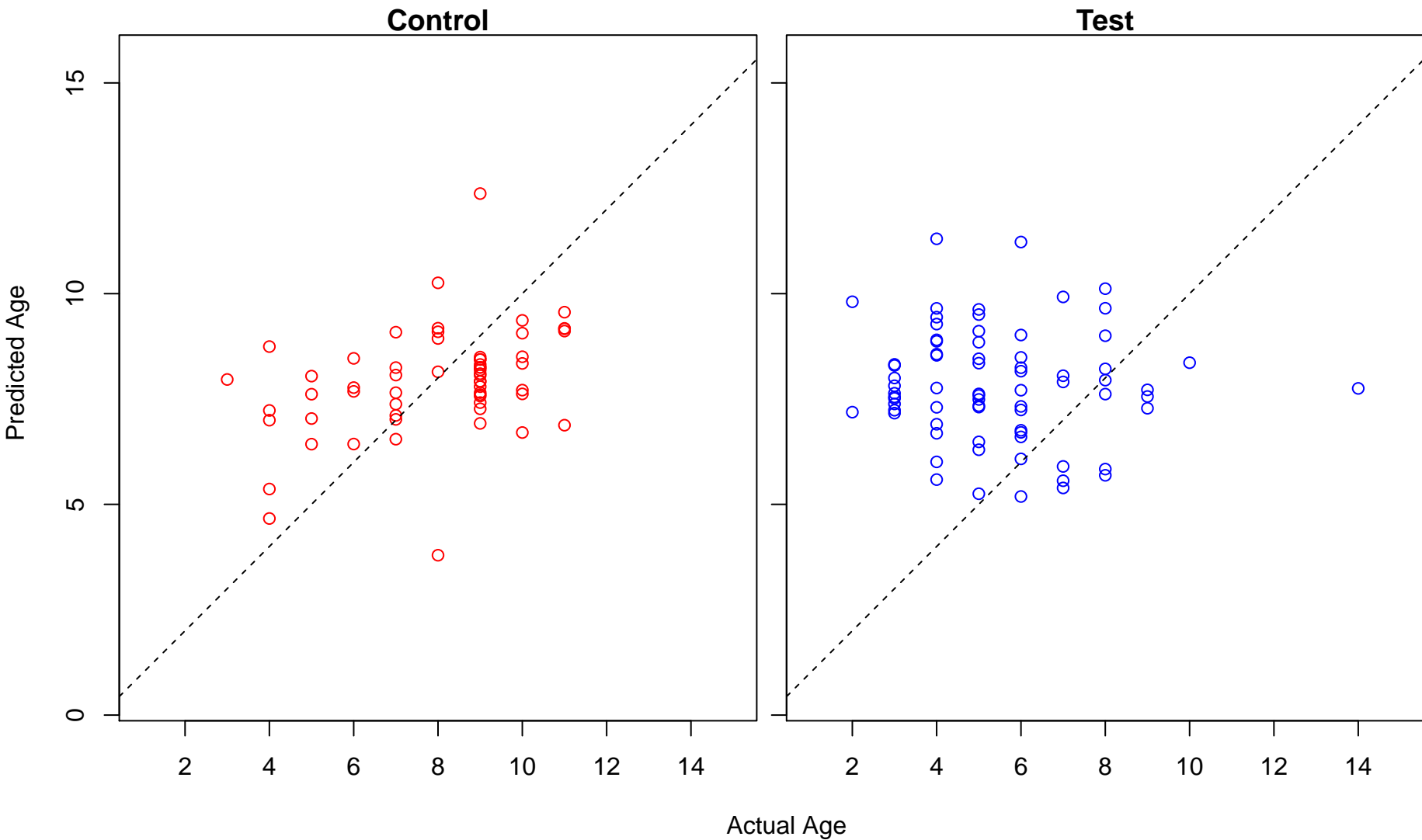
regulation of phagocytosis (Score: 1.774691)



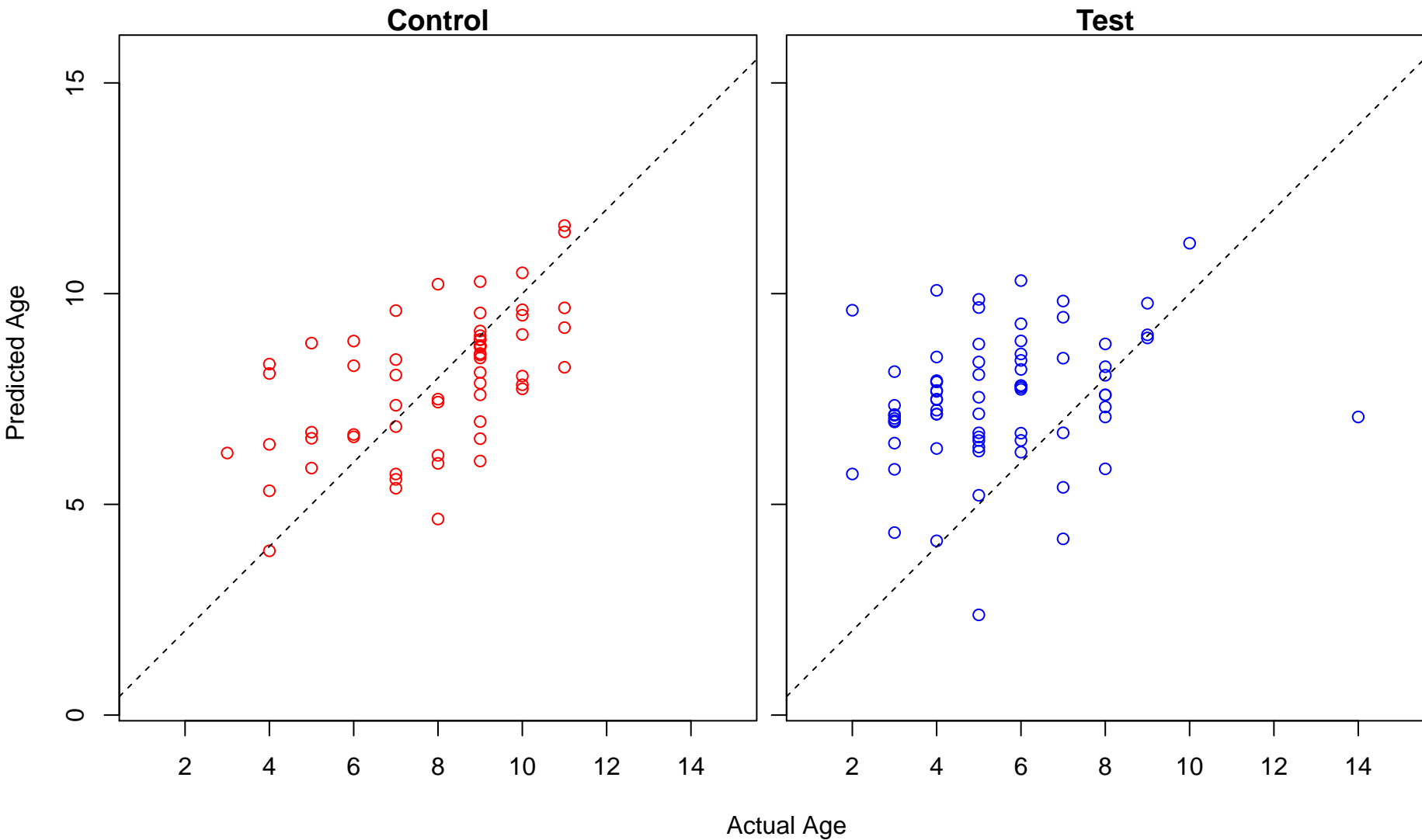
negative regulation of osteoblast differentiation (Score: 1.773848)



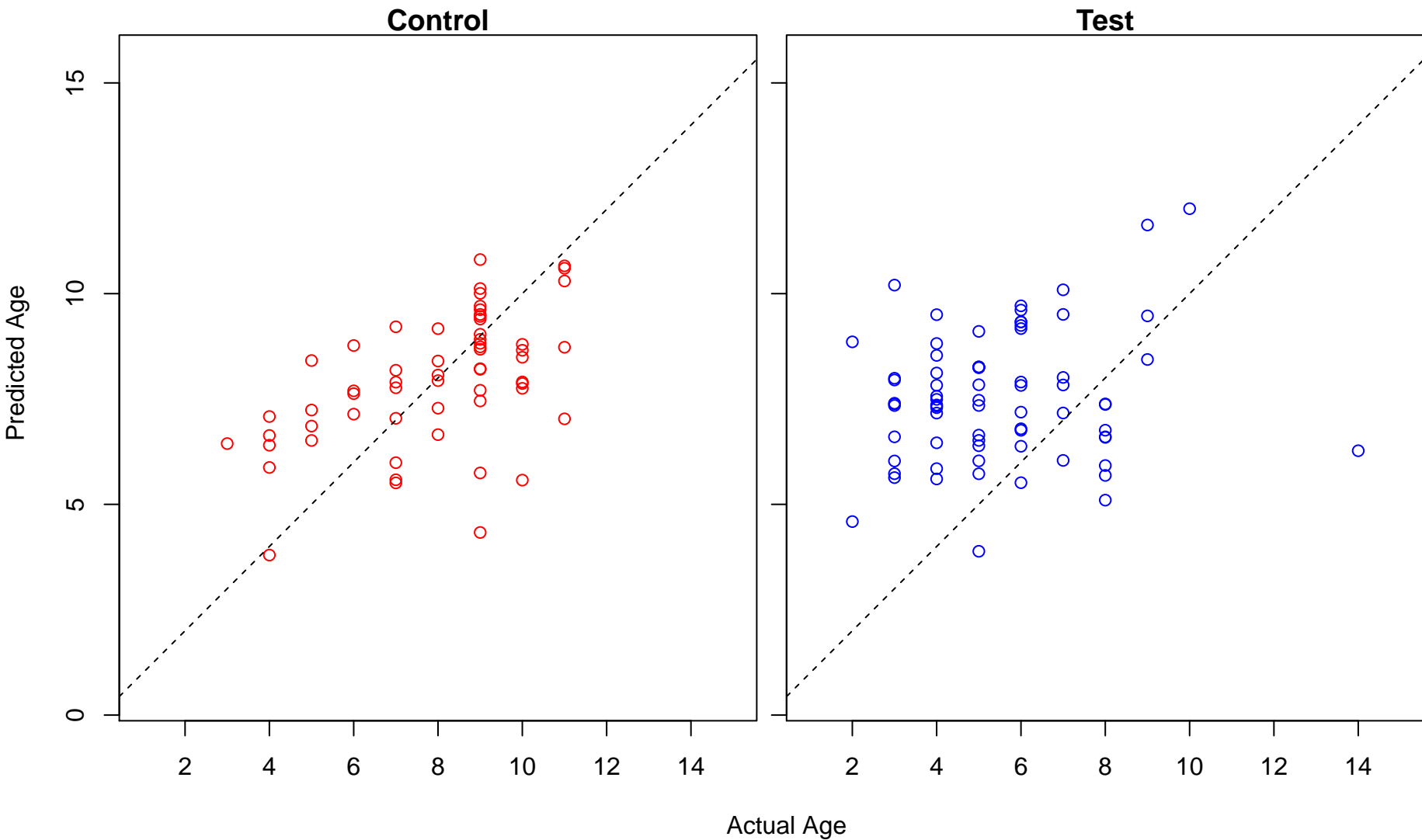
response to iron(II) ion (Score: 1.773409)



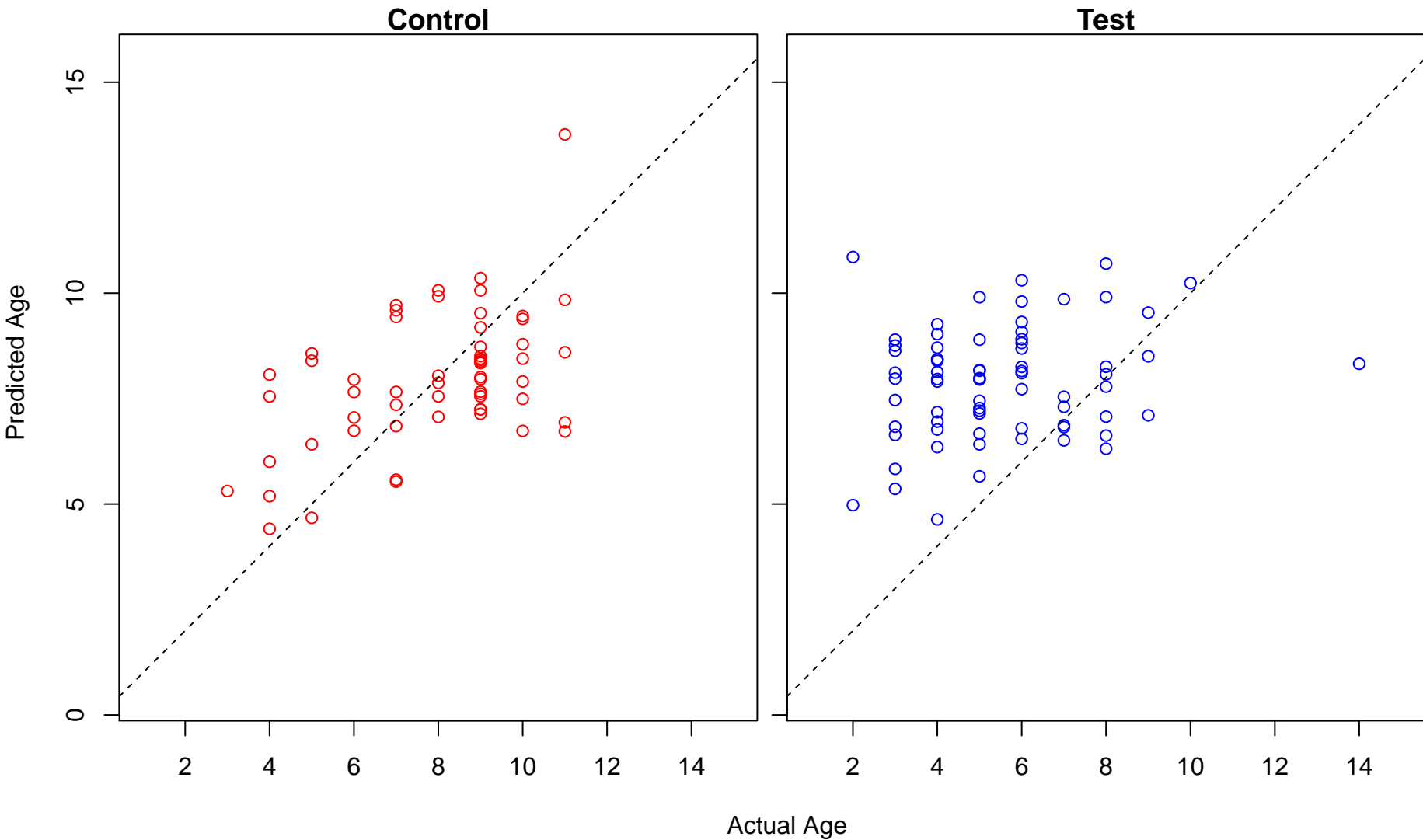
organic substance metabolic process (Score: 1.771362)



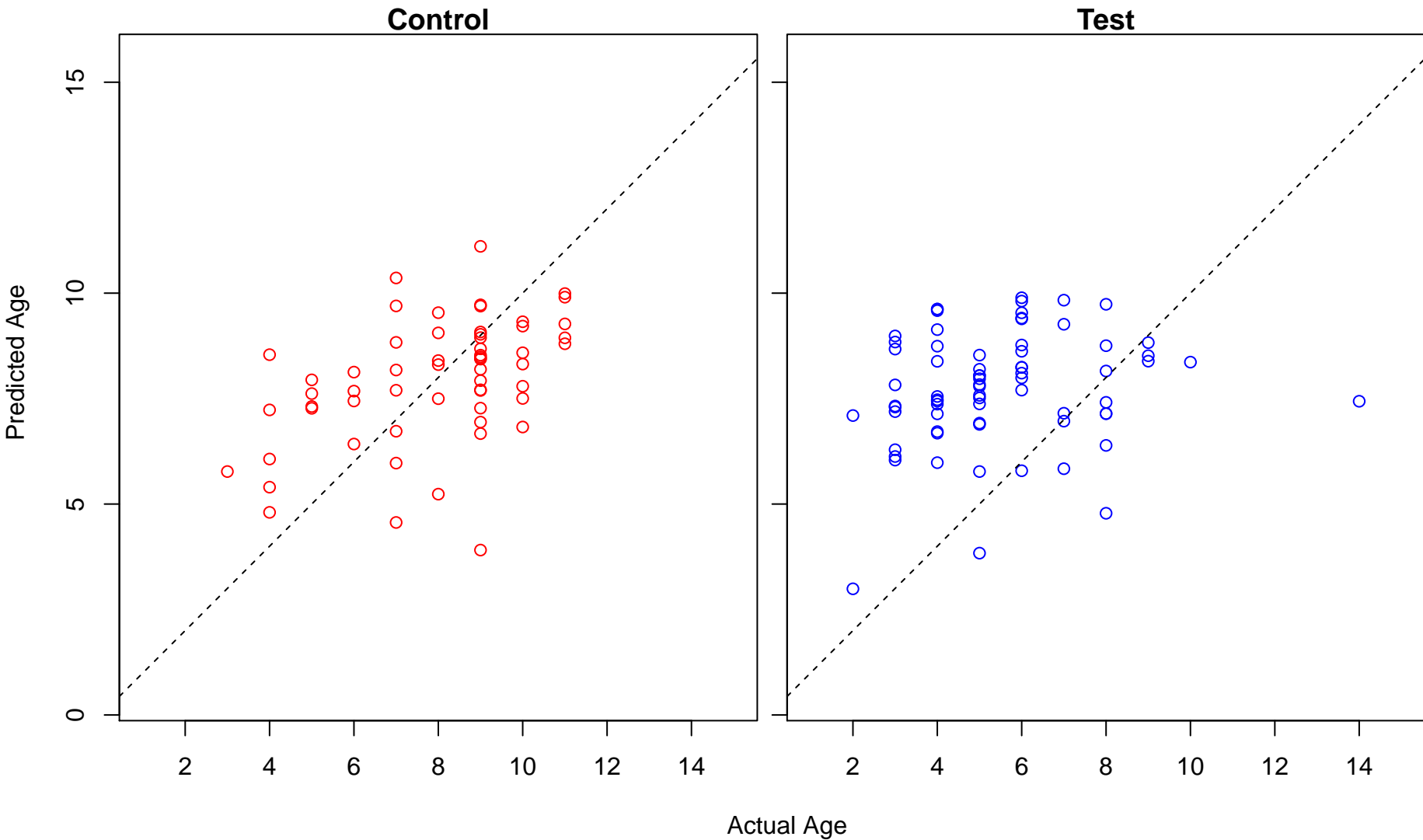
regulation of spindle assembly (Score: 1.769771)



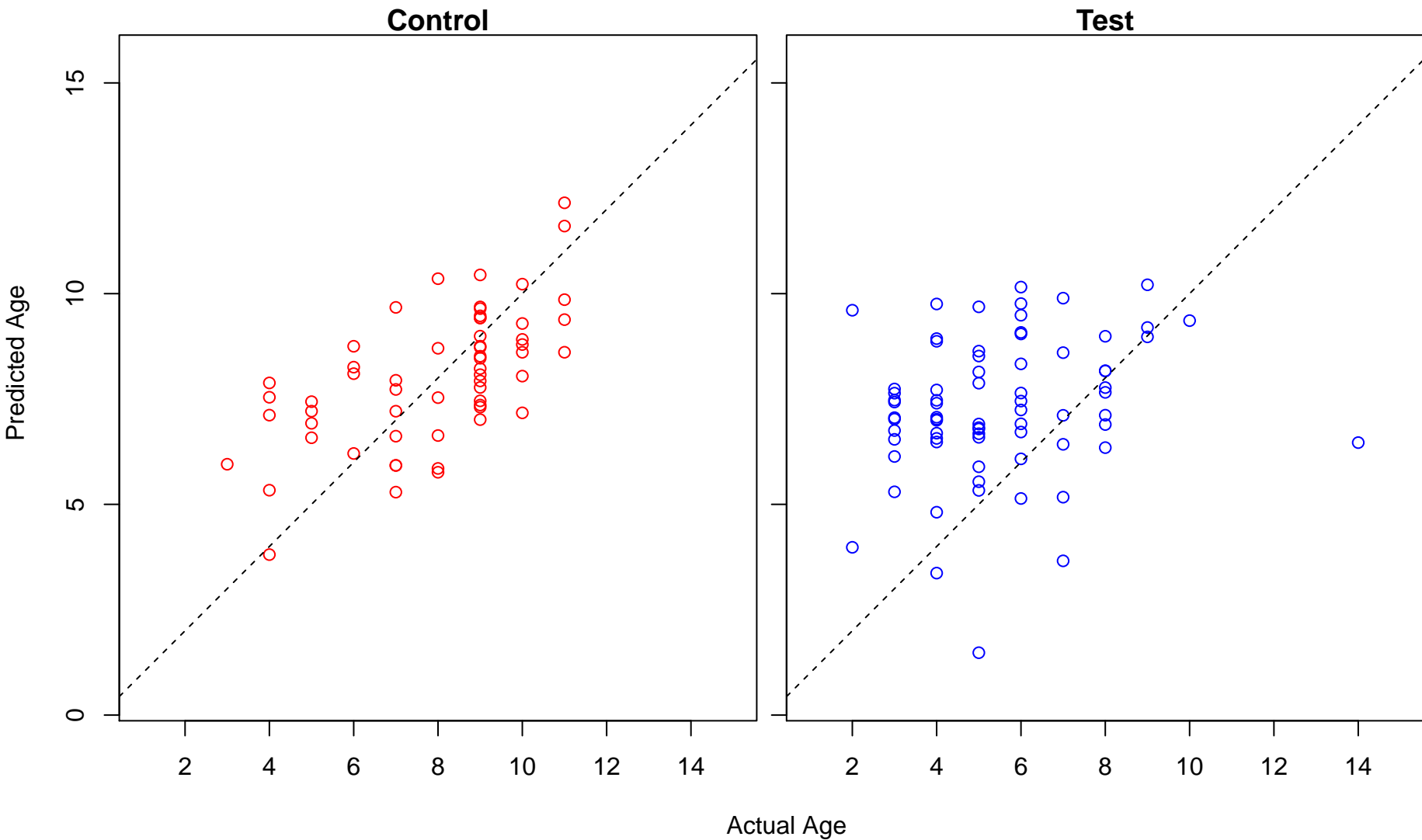
positive regulation of antigen receptor-mediated signaling pathway (Score: 1.768944)



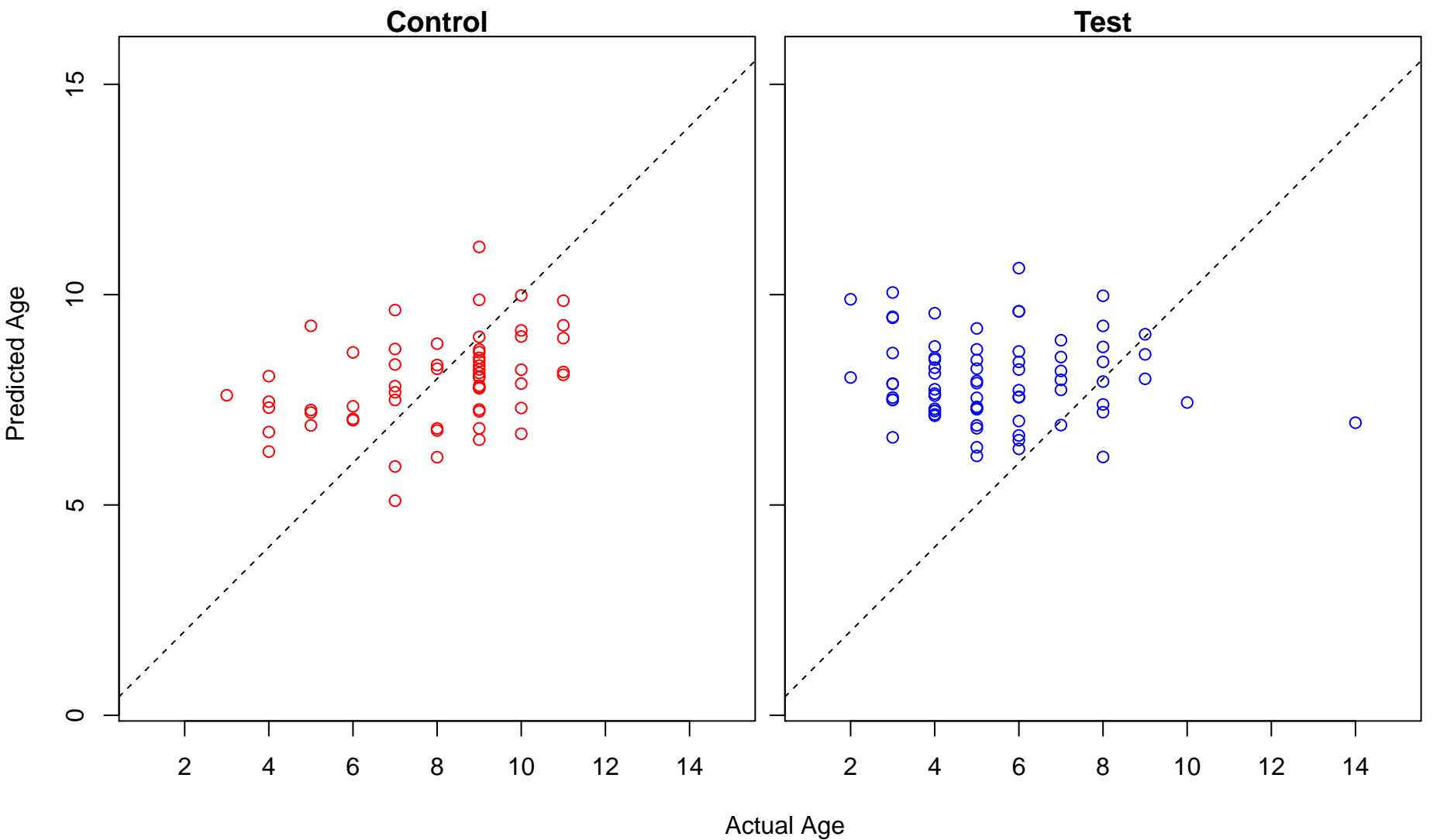
regulation of tyrosine phosphorylation of Stat3 protein (Score: 1.768339)



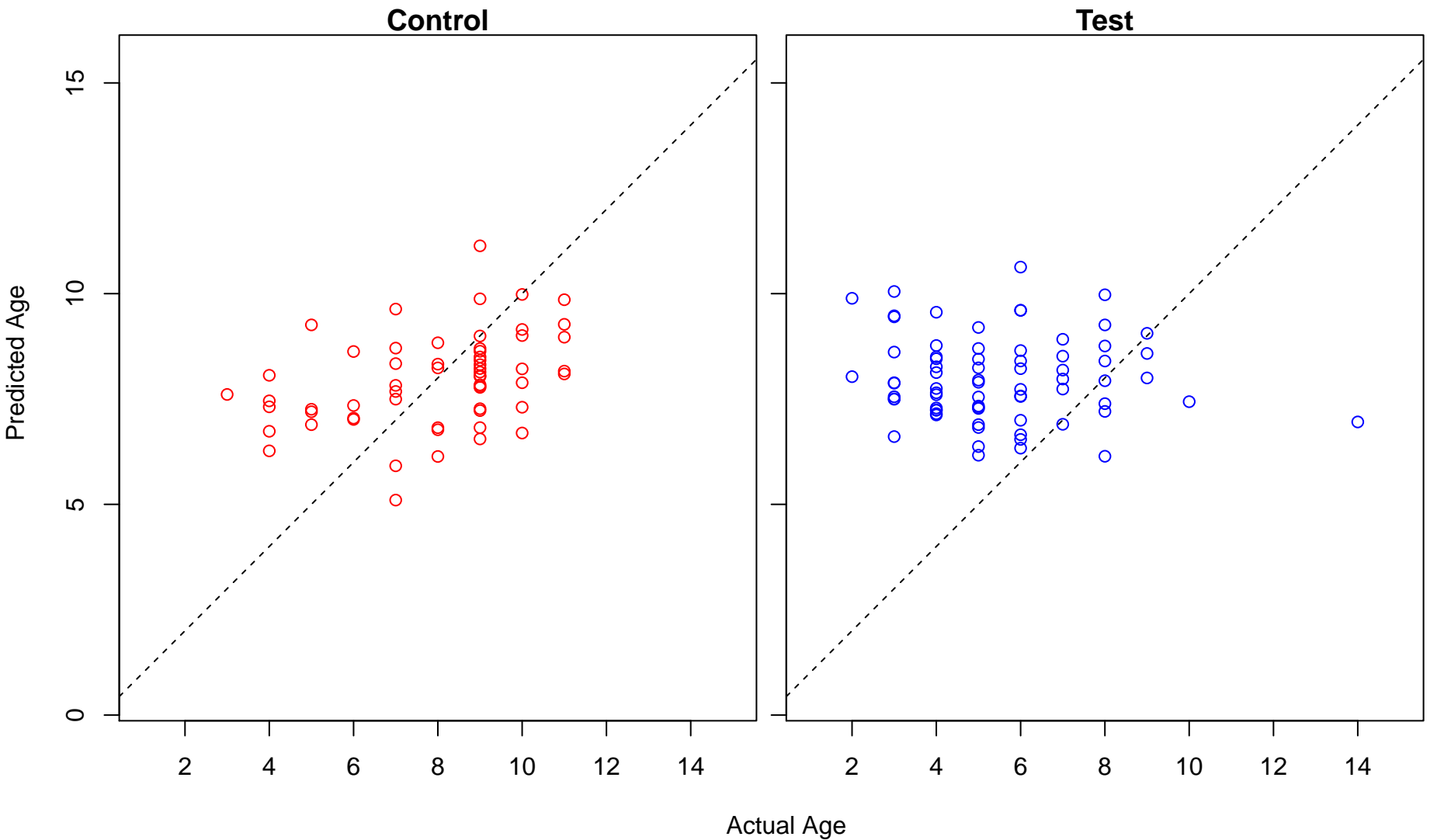
regulation of metabolic process (Score: 1.767941)



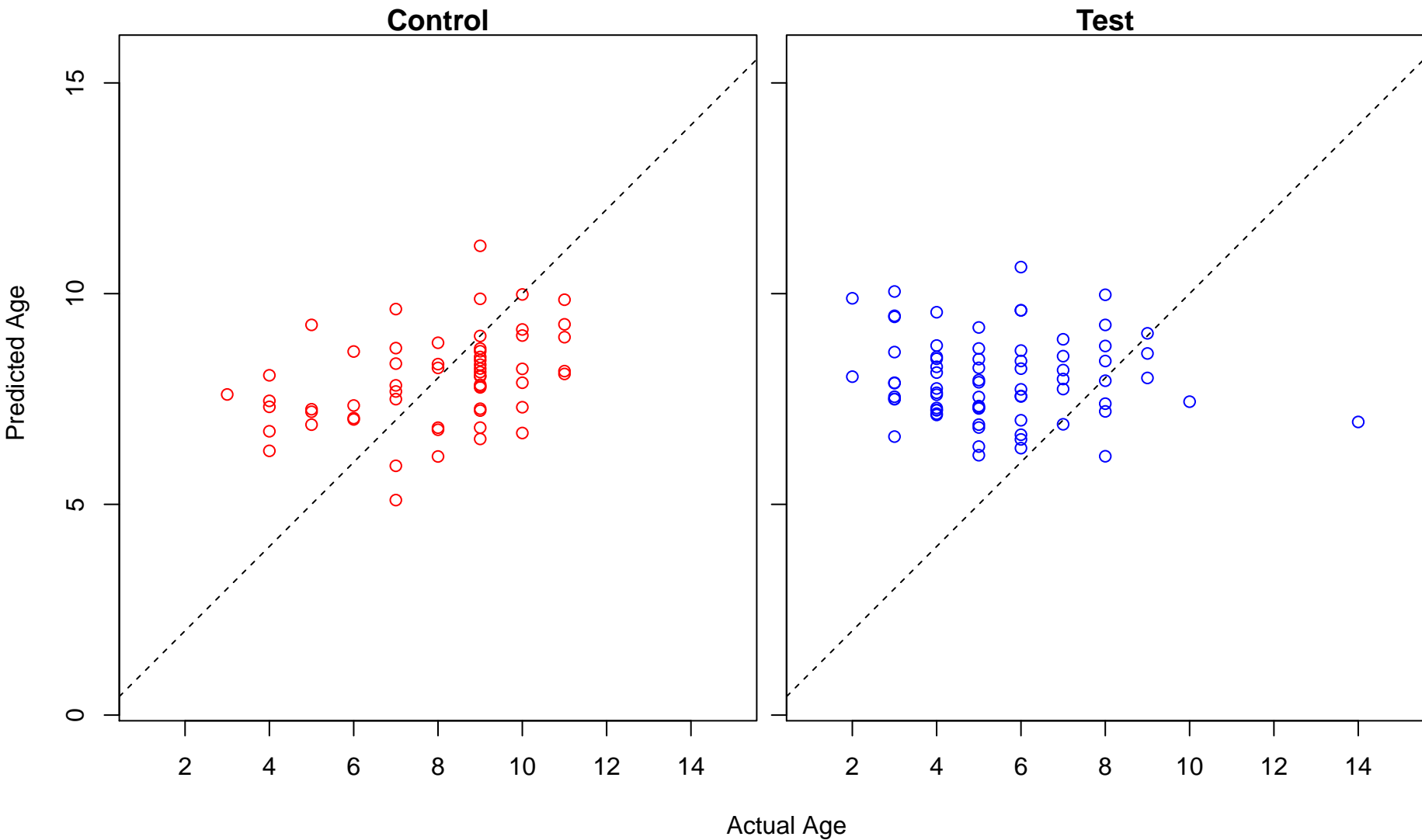
modulation of microtubule cytoskeleton involved in cerebral cortex radial glia guided migration (Score: 1)



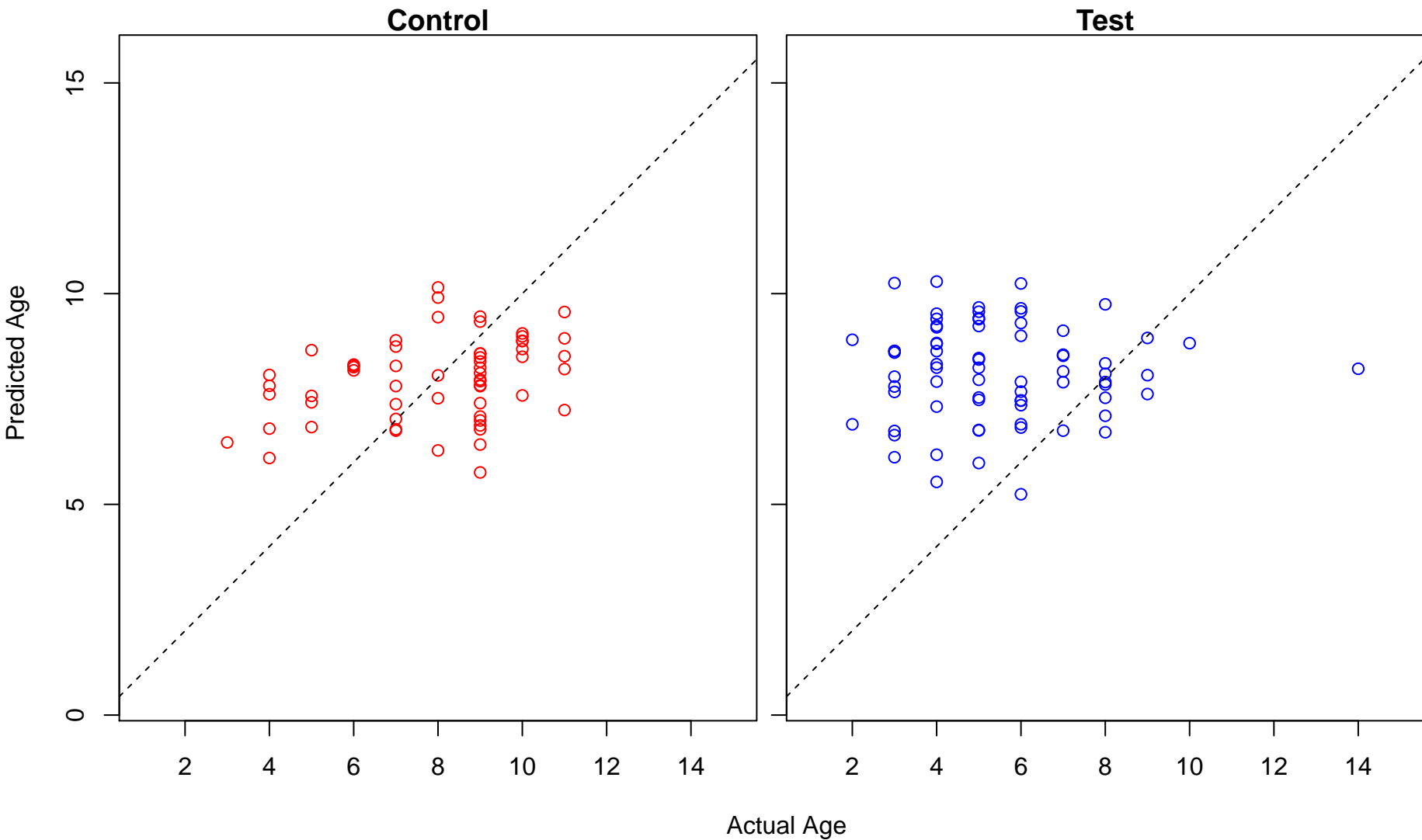
tension of a leading process involved in cell motility in cerebral cortex radial glia guided migration (Score



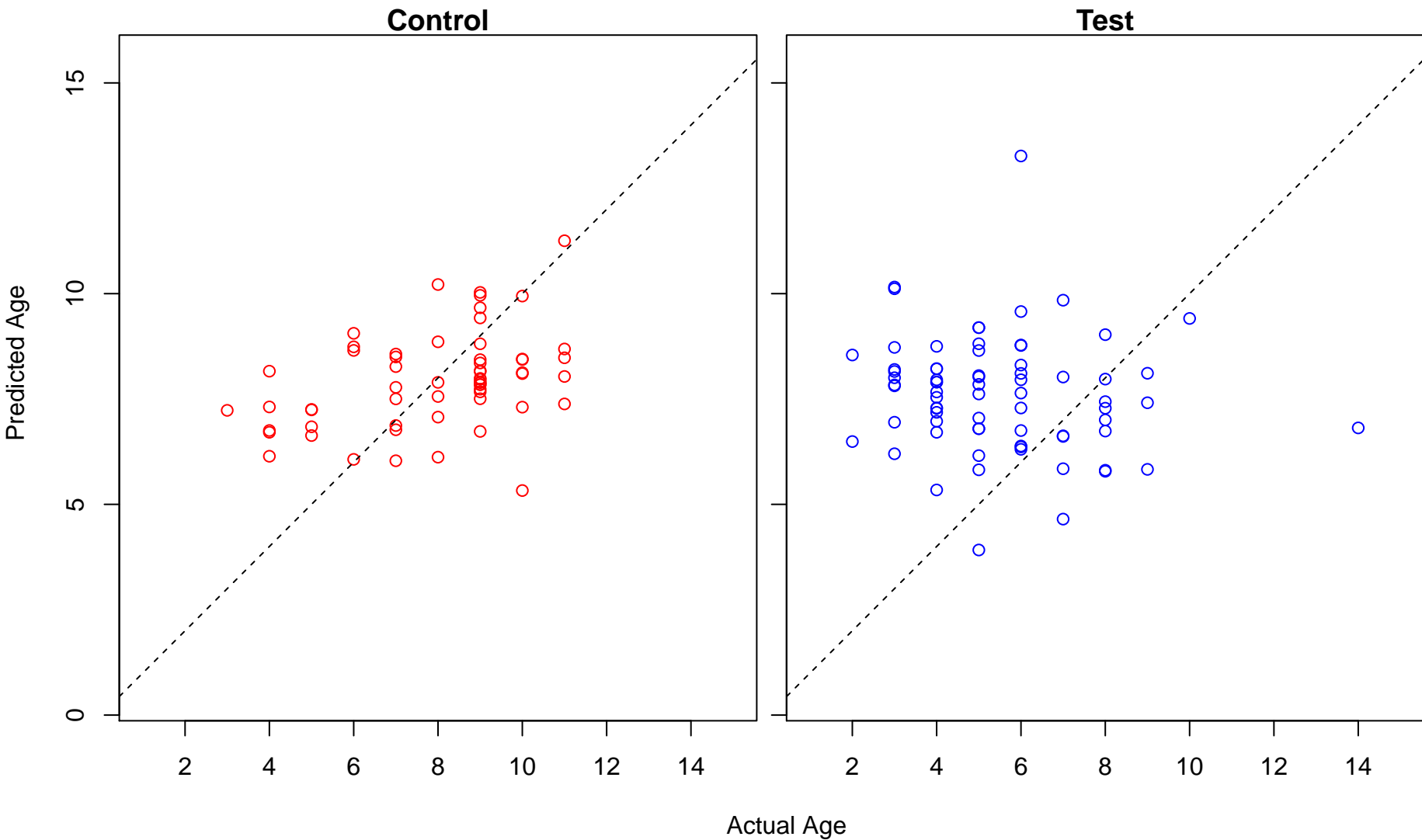
pseudopodium assembly (Score: 1.765798)



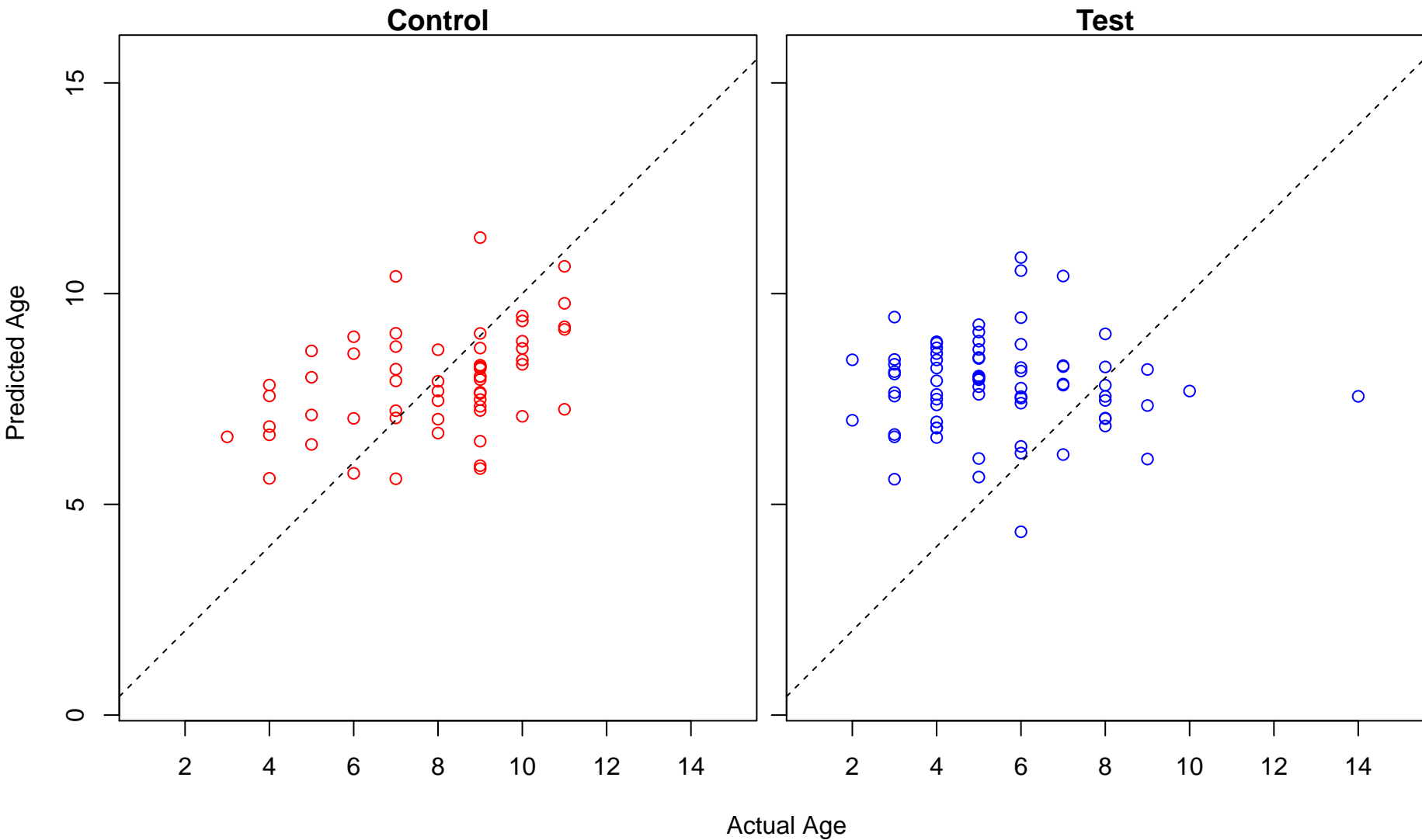
resolution of meiotic recombination intermediates (Score: 1.765022)



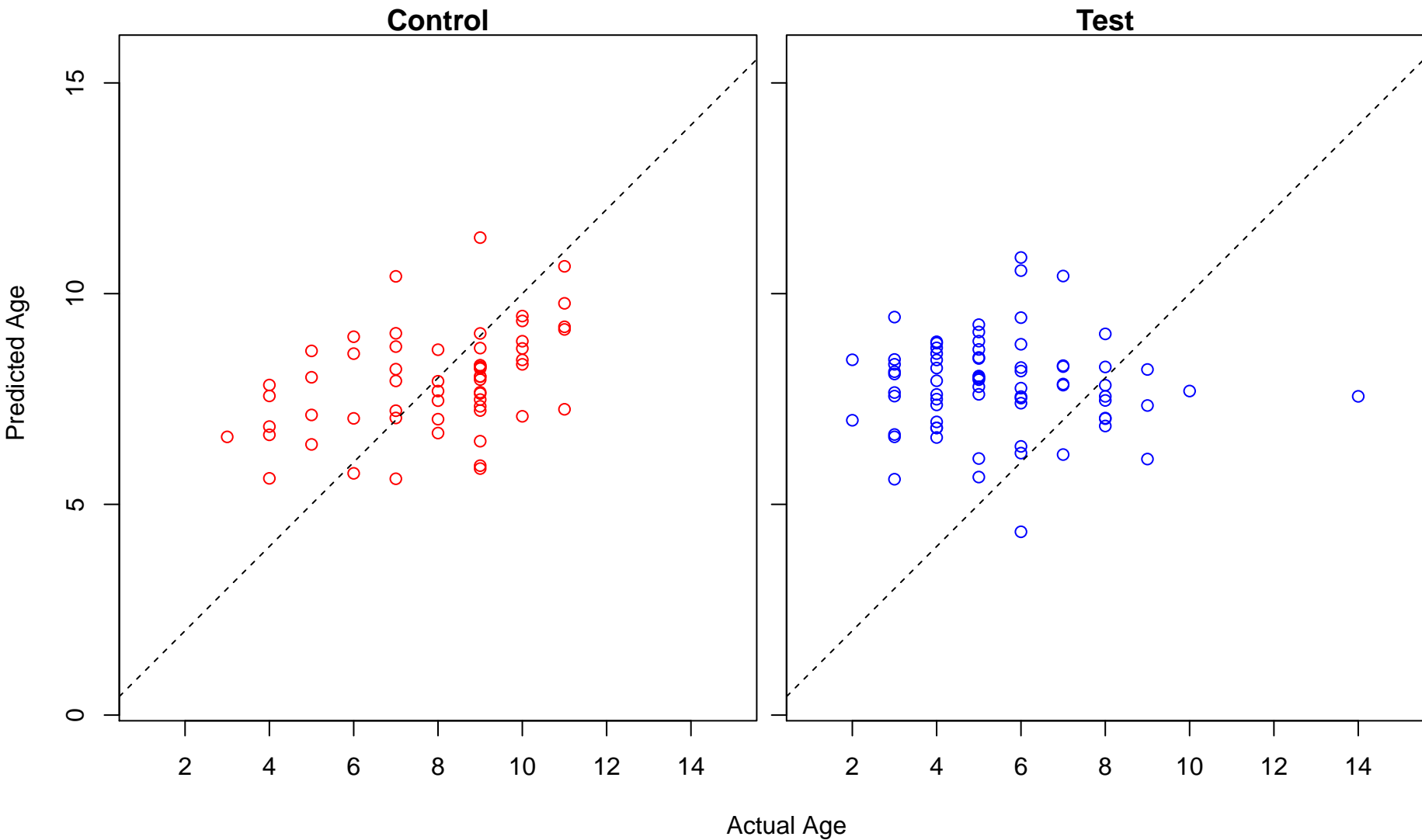
regulation of monocyte chemotactic protein-1 production (Score: 1.764703)



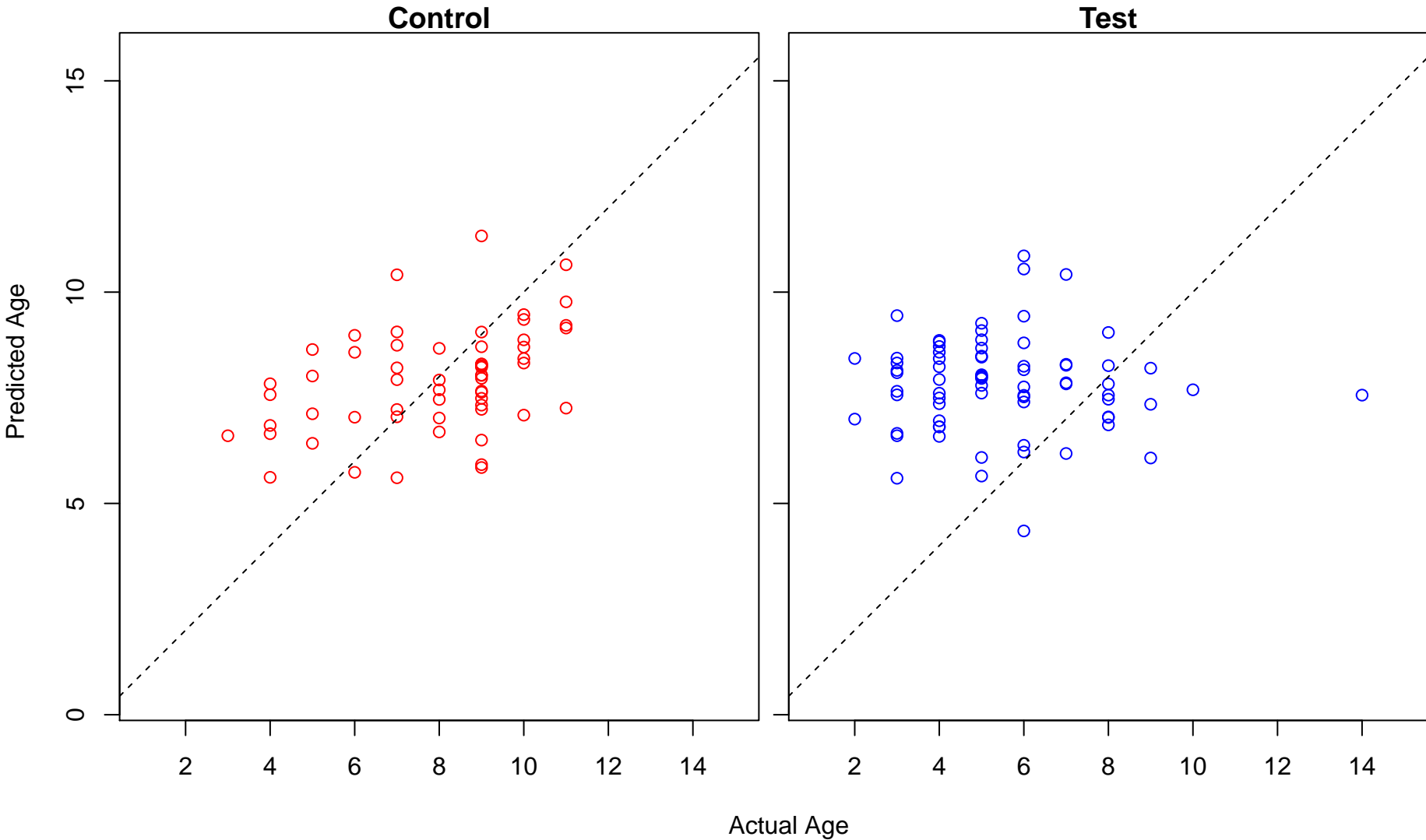
muscle hypertrophy in response to stress (Score: 1.763740)



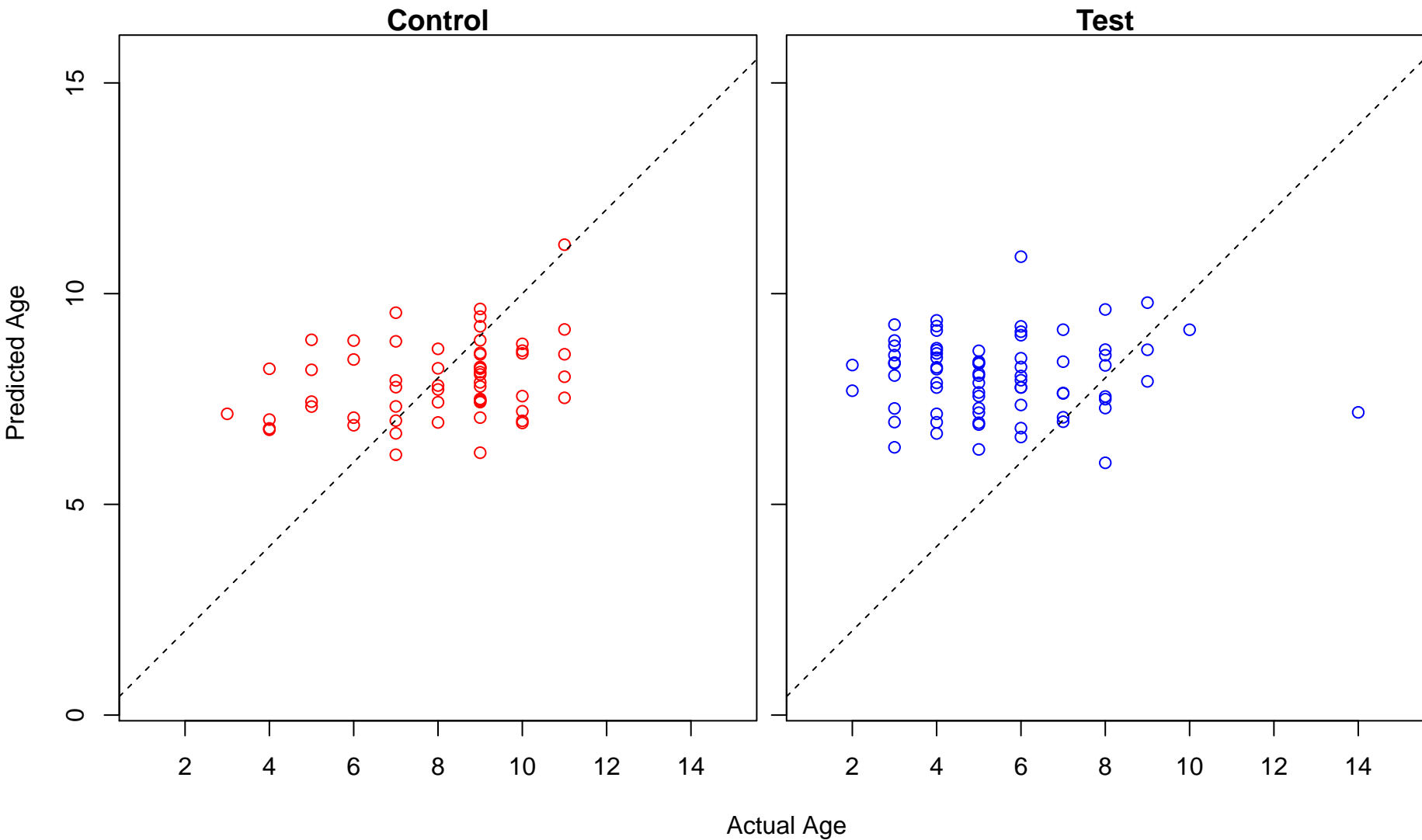
cardiac muscle adaptation (Score: 1.763740)



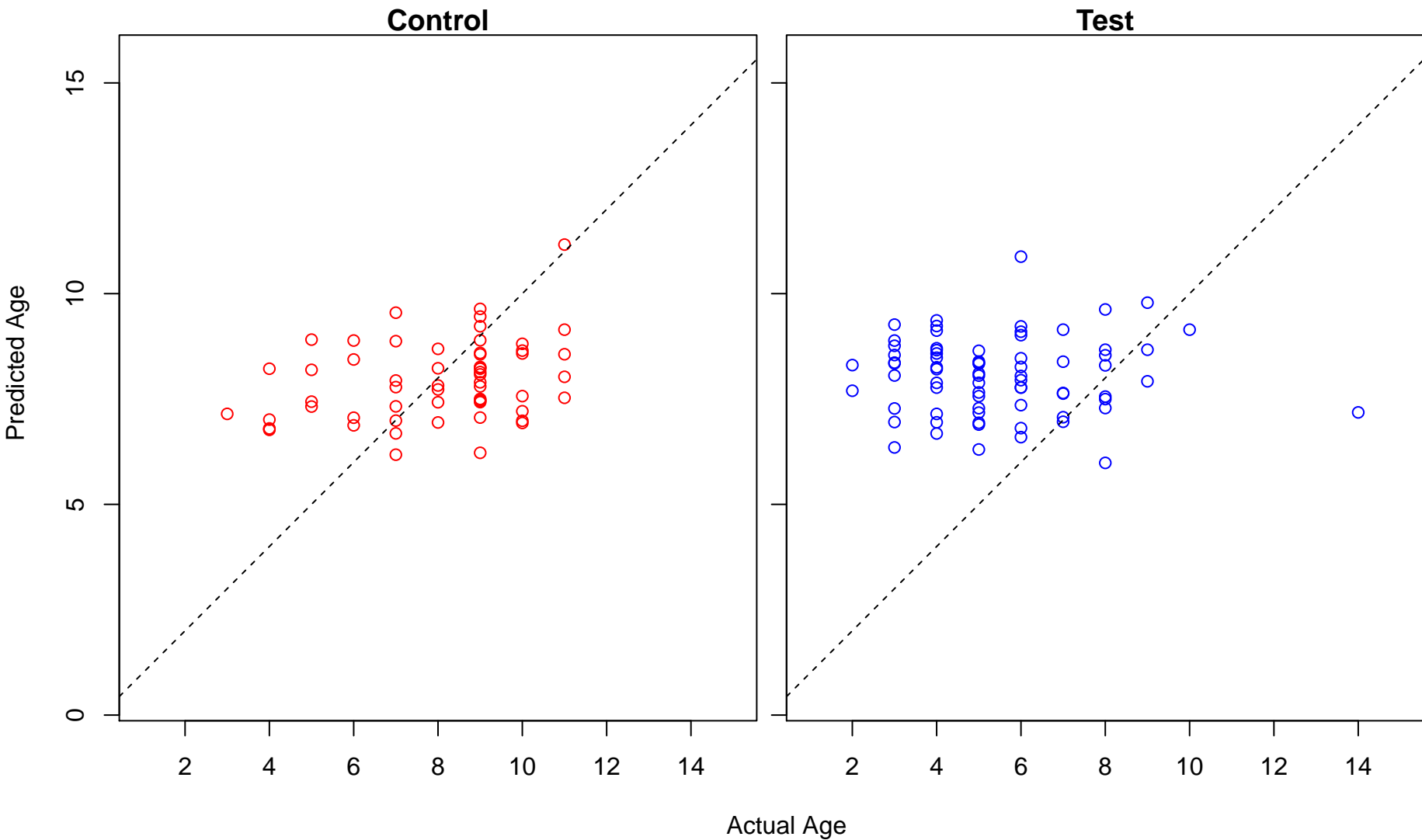
cardiac muscle hypertrophy in response to stress (Score: 1.763740)



negative regulation of T-helper 2 cell differentiation (Score: 1.761541)

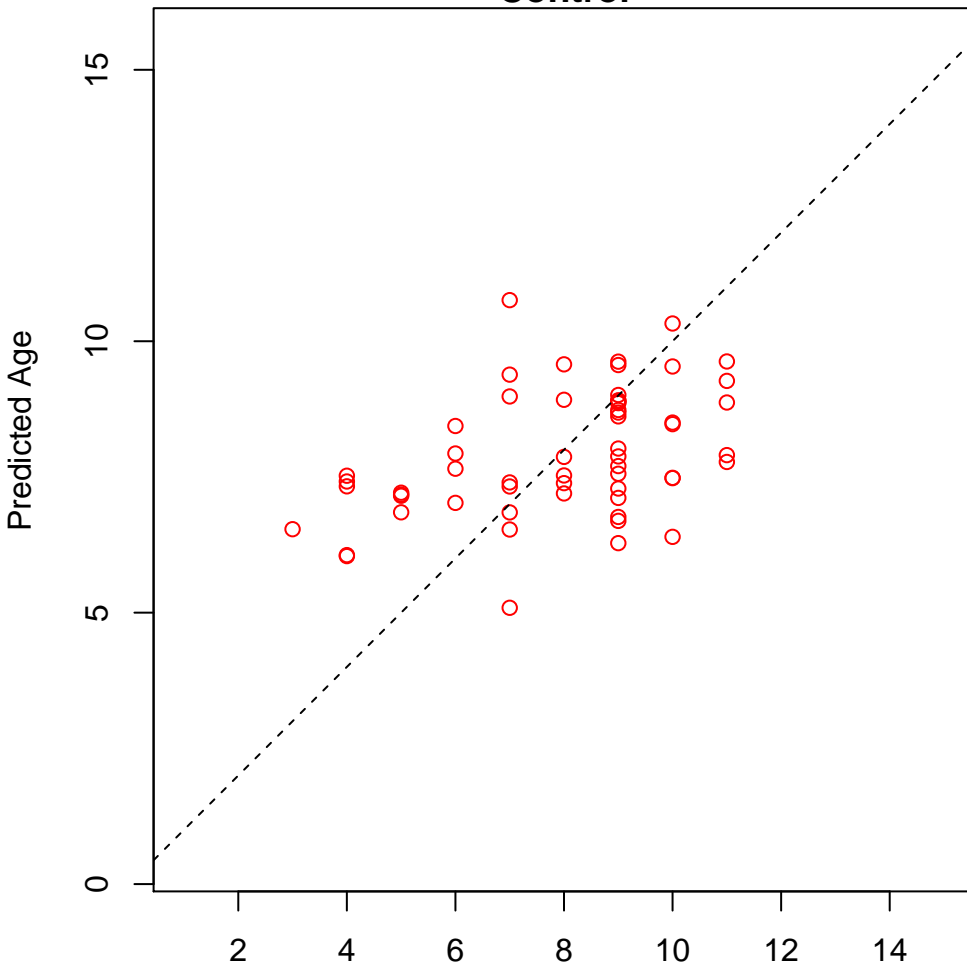


positive regulation of T-helper 1 cell differentiation (Score: 1.761173)

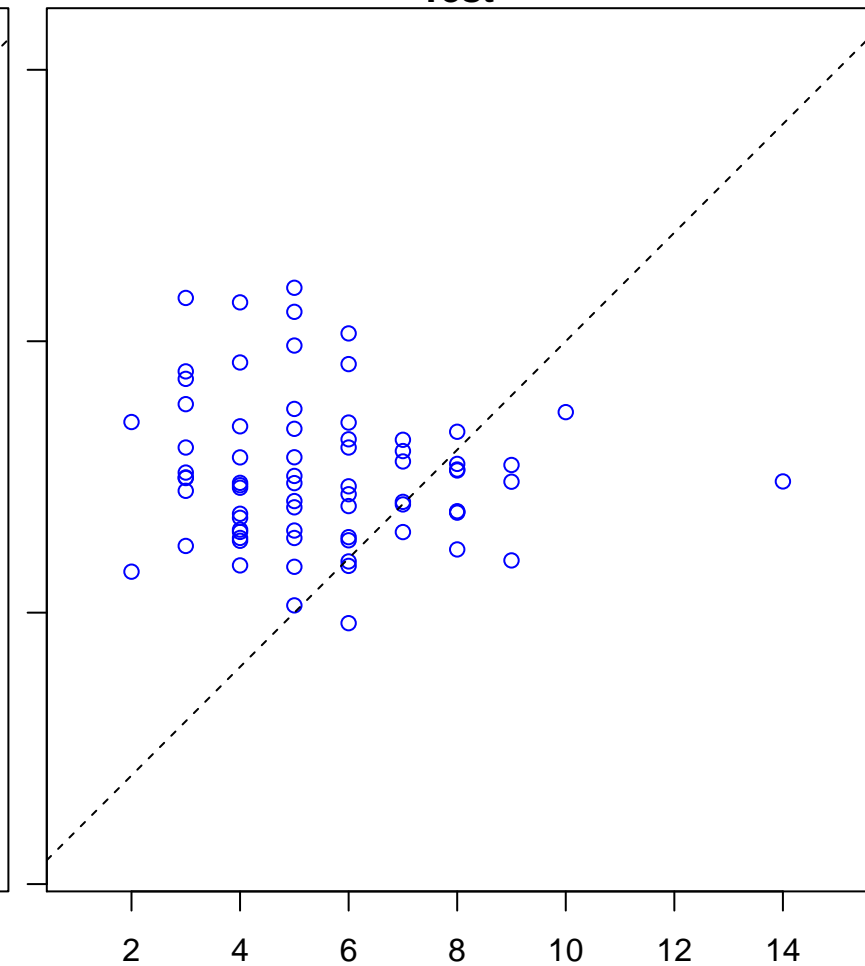


protein import into mitochondrial matrix (Score: 1.760675)

Control

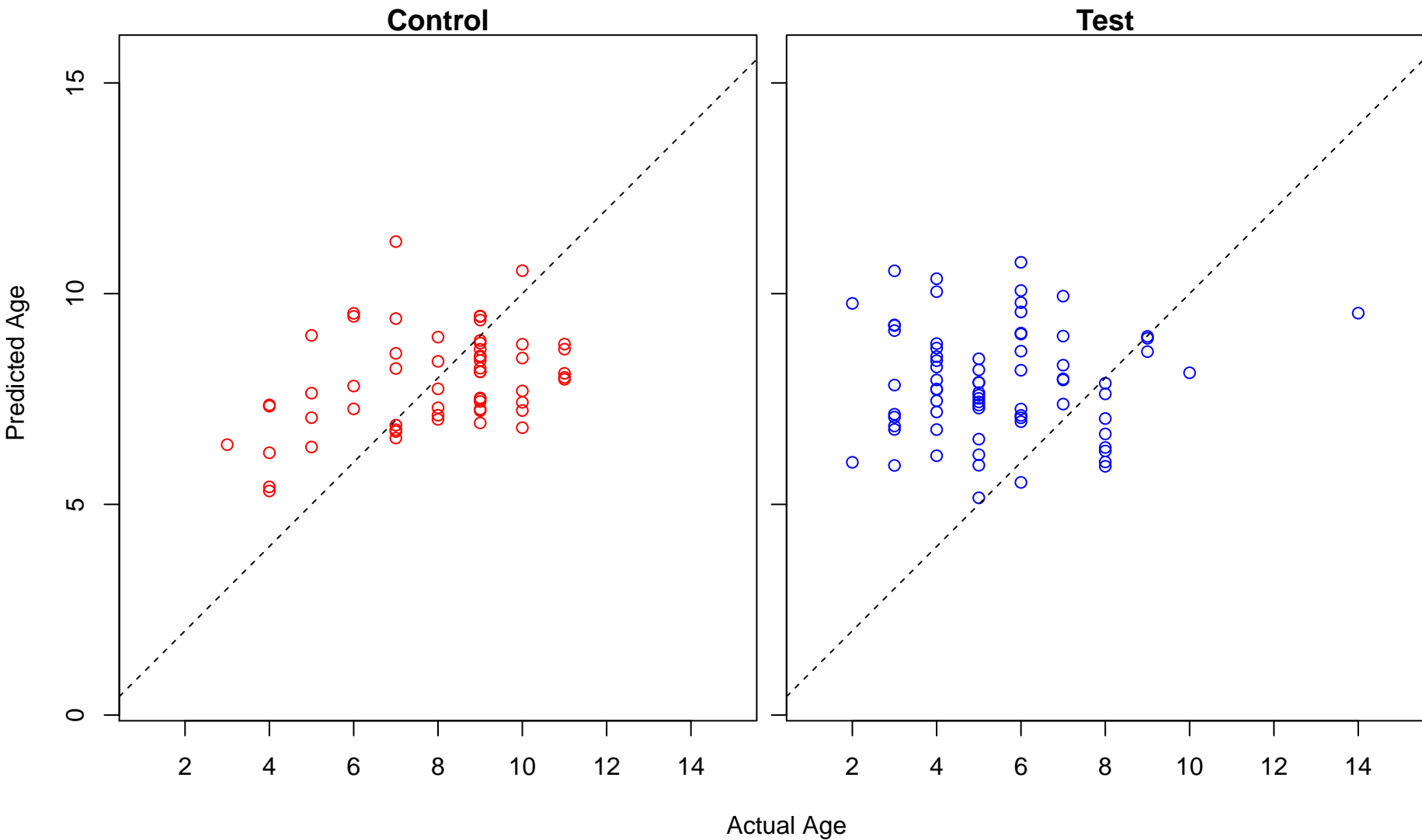


Test



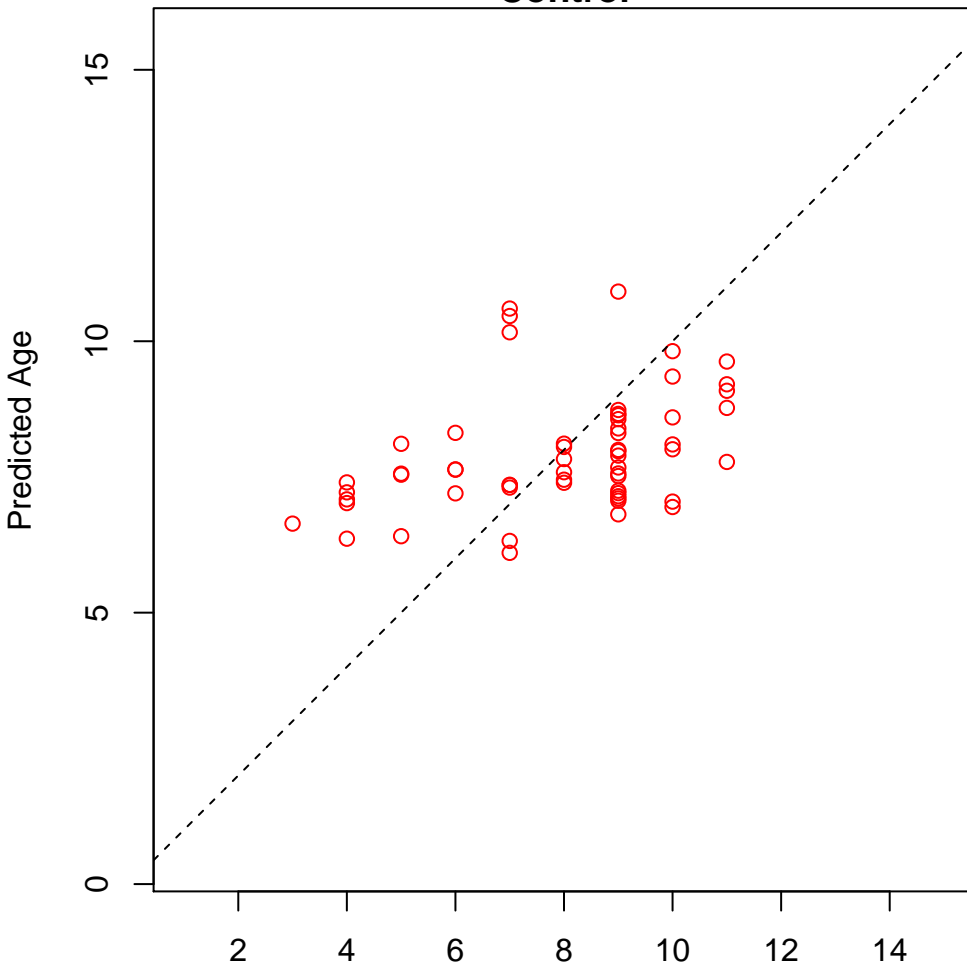
Actual Age

cell killing (Score: 1.757152)

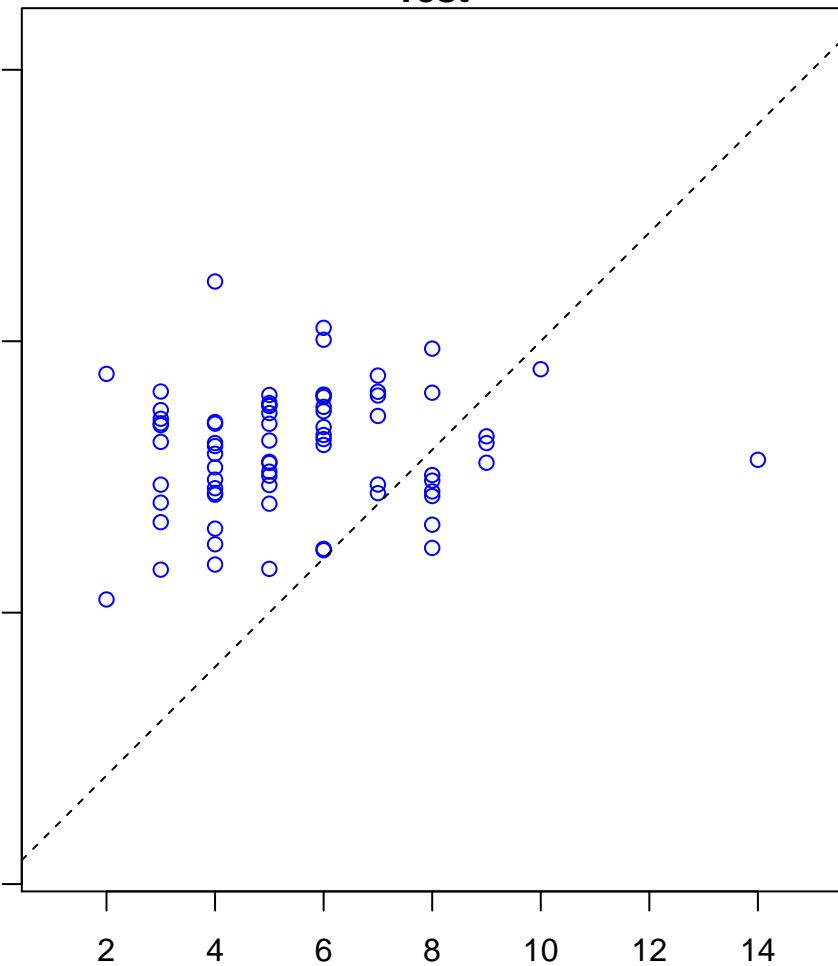


phosphatidic acid metabolic process (Score: 1.755894)

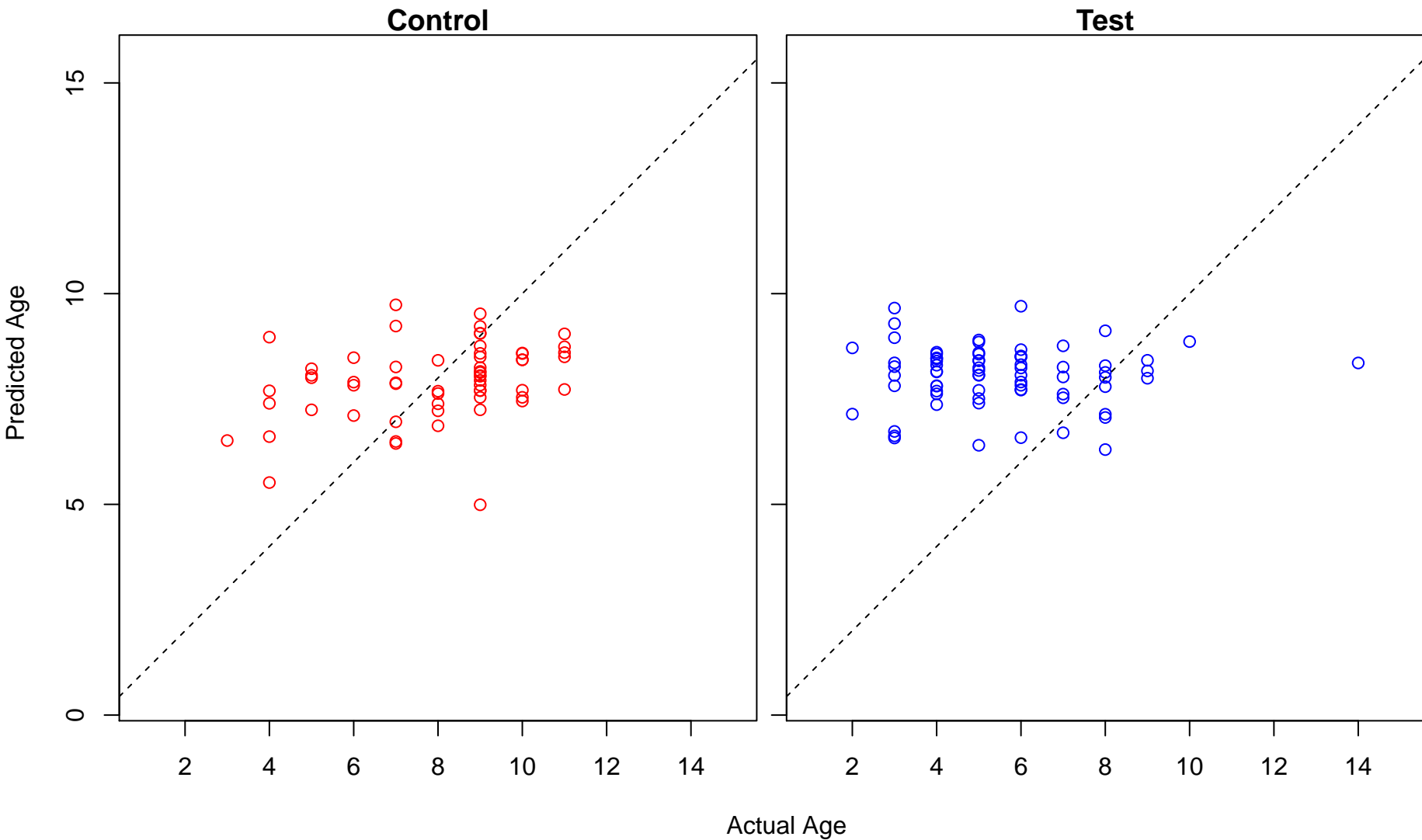
Control



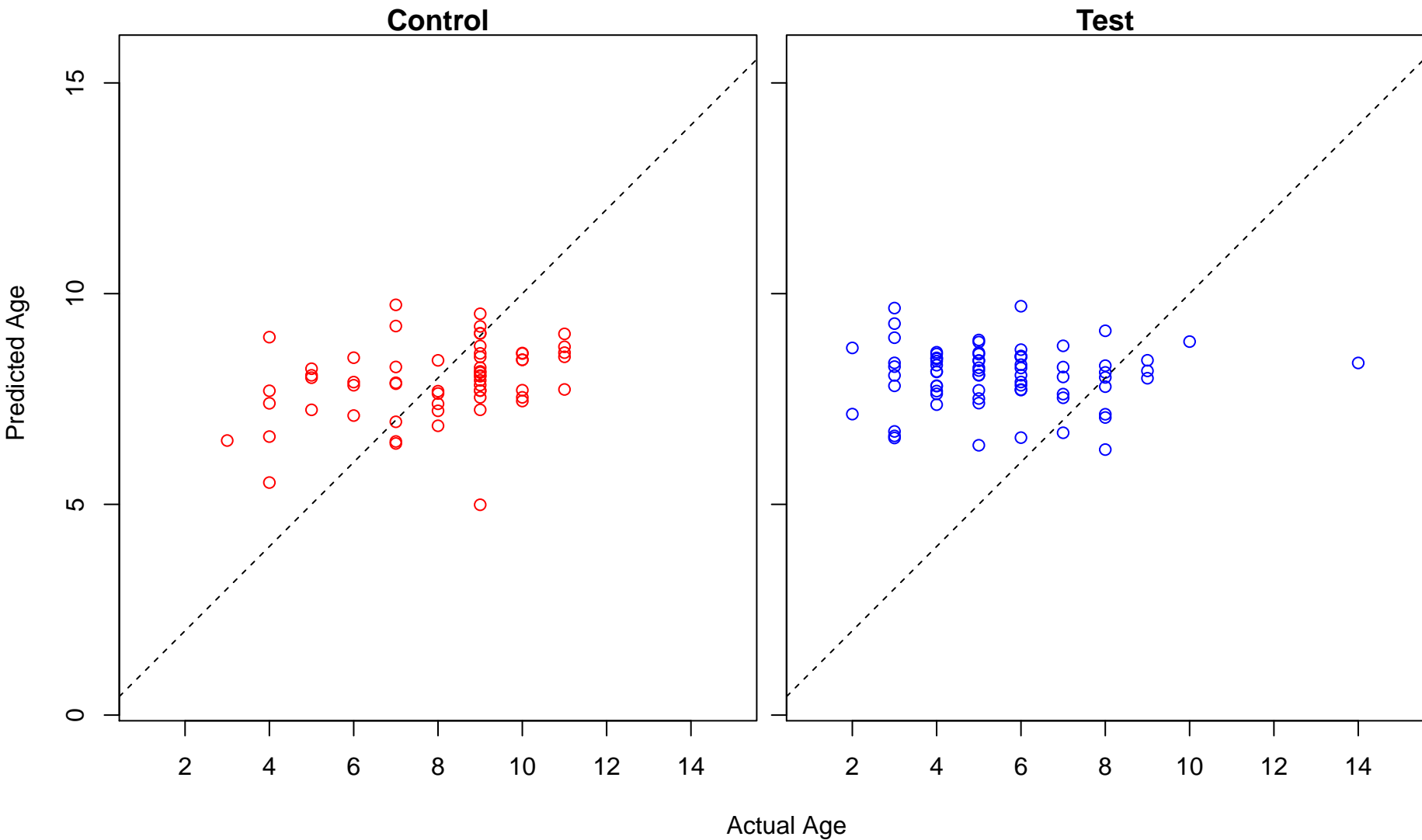
Test



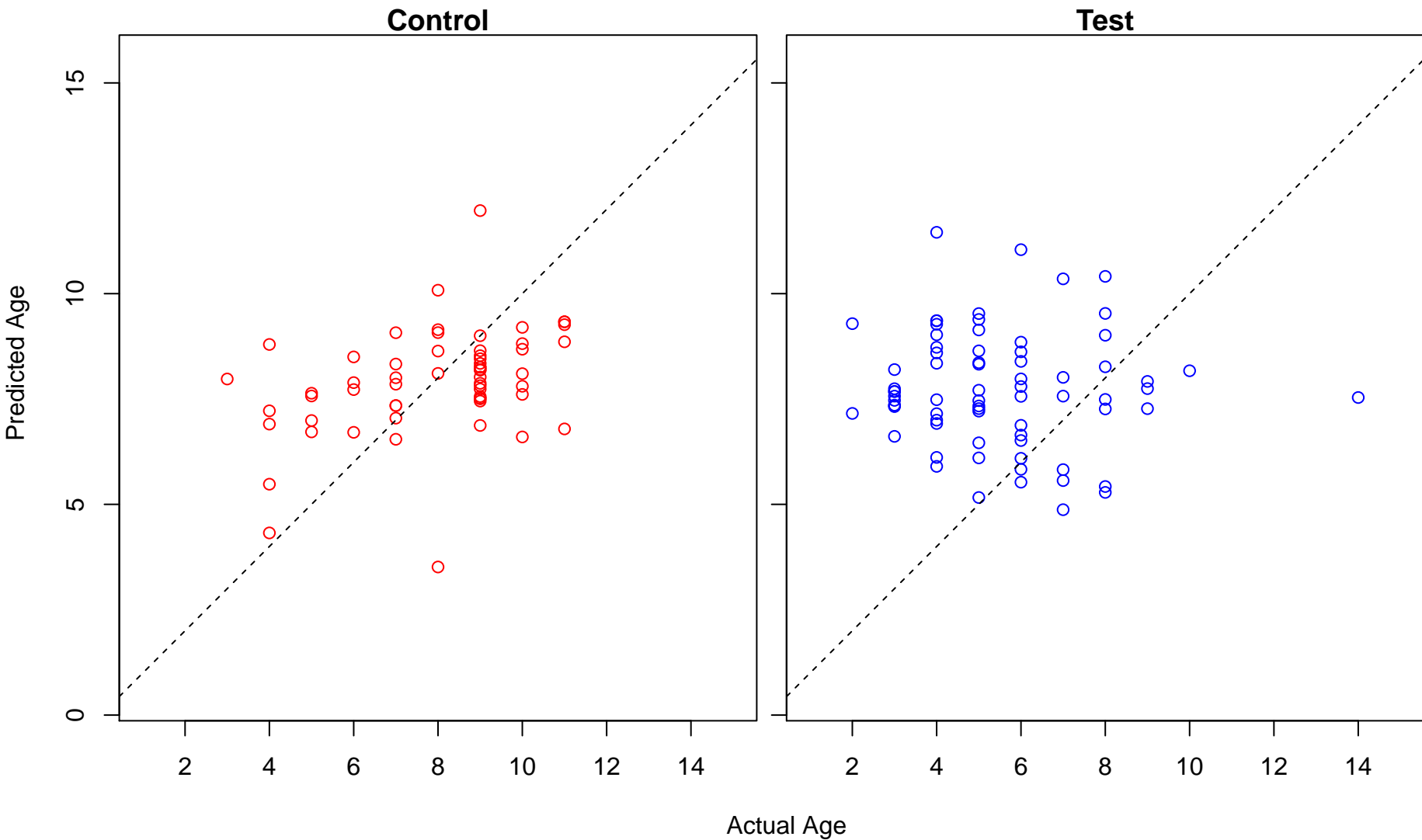
striatal medium spiny neuron differentiation (Score: 1.753962)



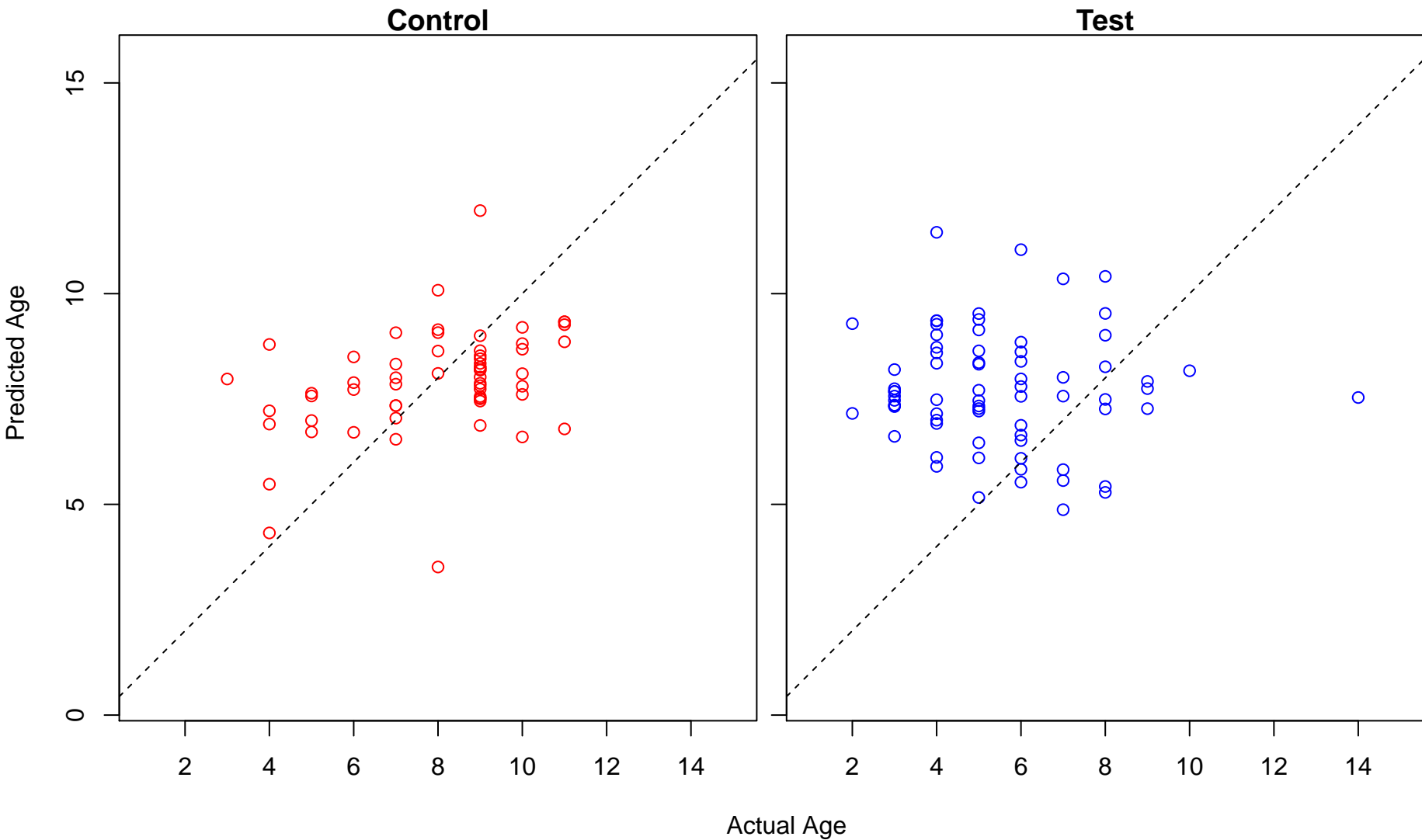
olfactory bulb axon guidance (Score: 1.753884)



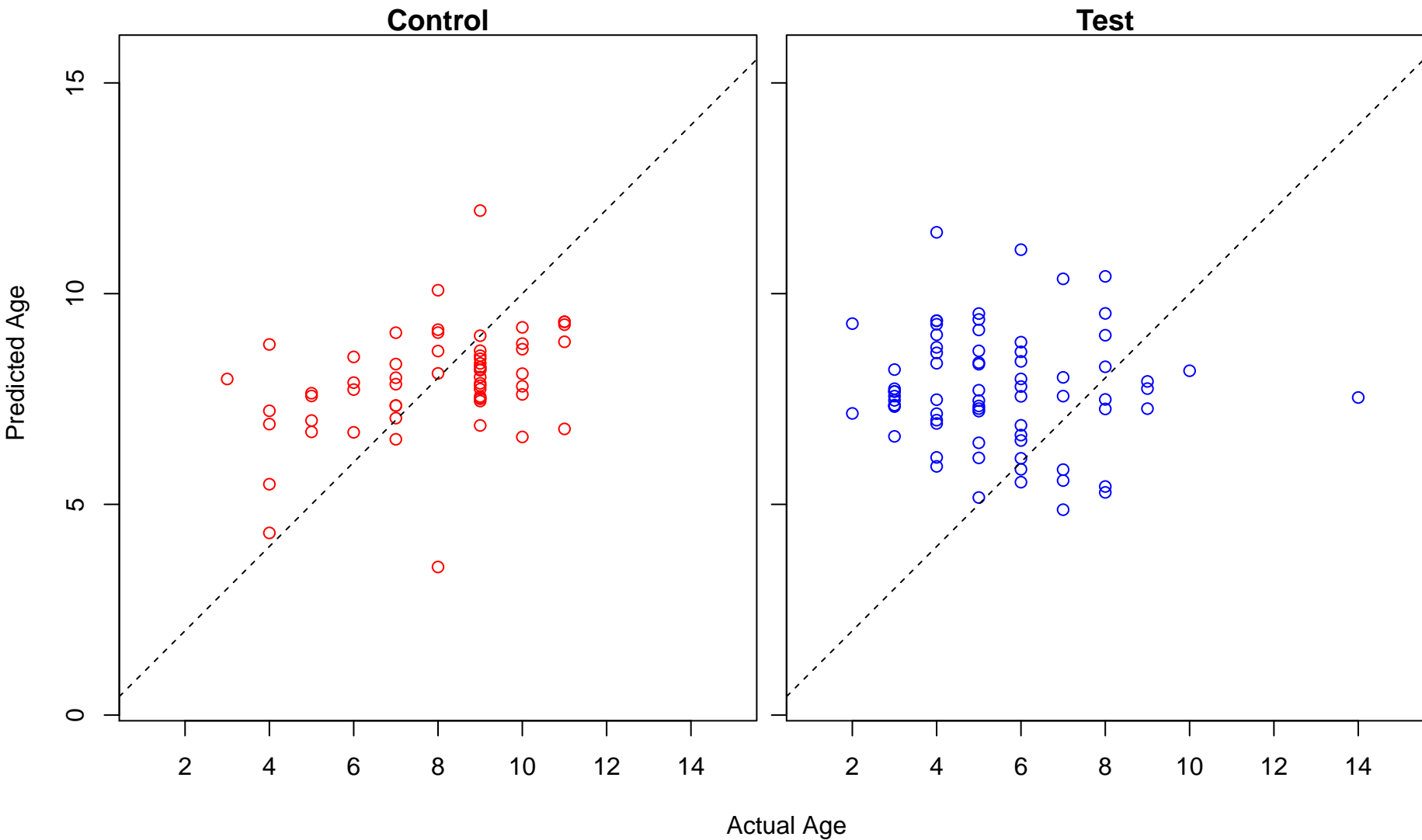
dopamine uptake involved in synaptic transmission (Score: 1.752577)



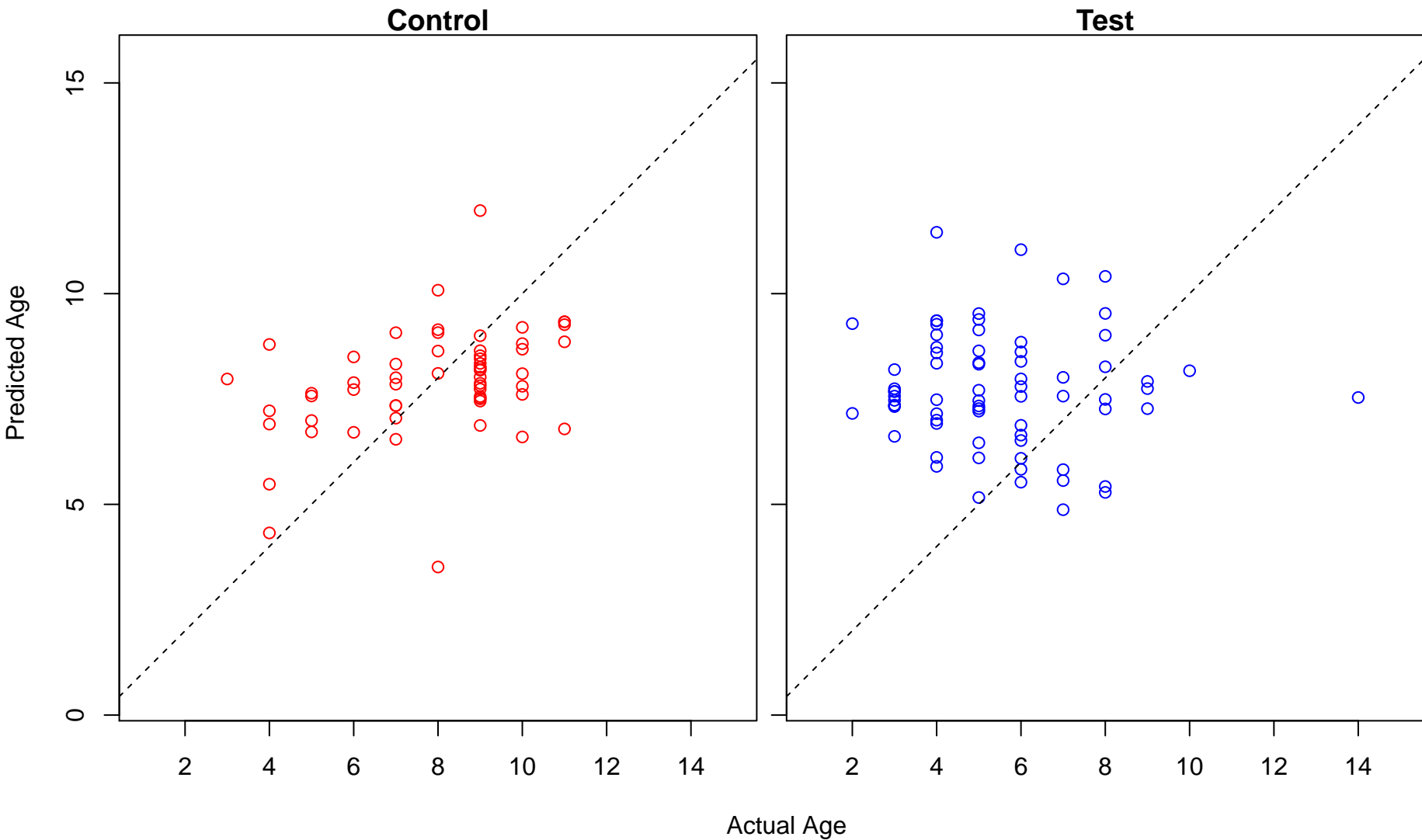
negative regulation of dopamine uptake involved in synaptic transmission (Score: 1.752577)



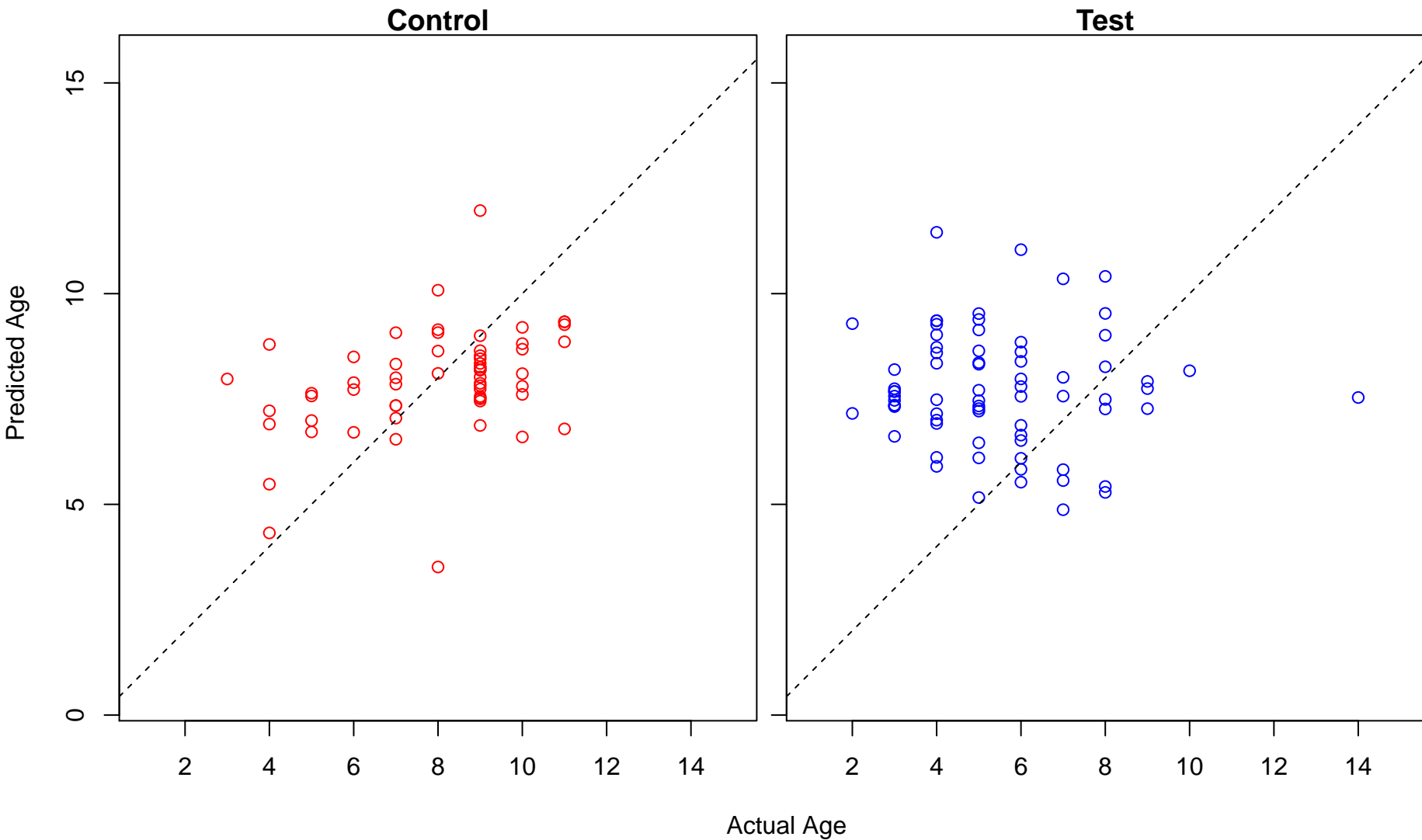
regulation of norepinephrine uptake (Score: 1.752577)



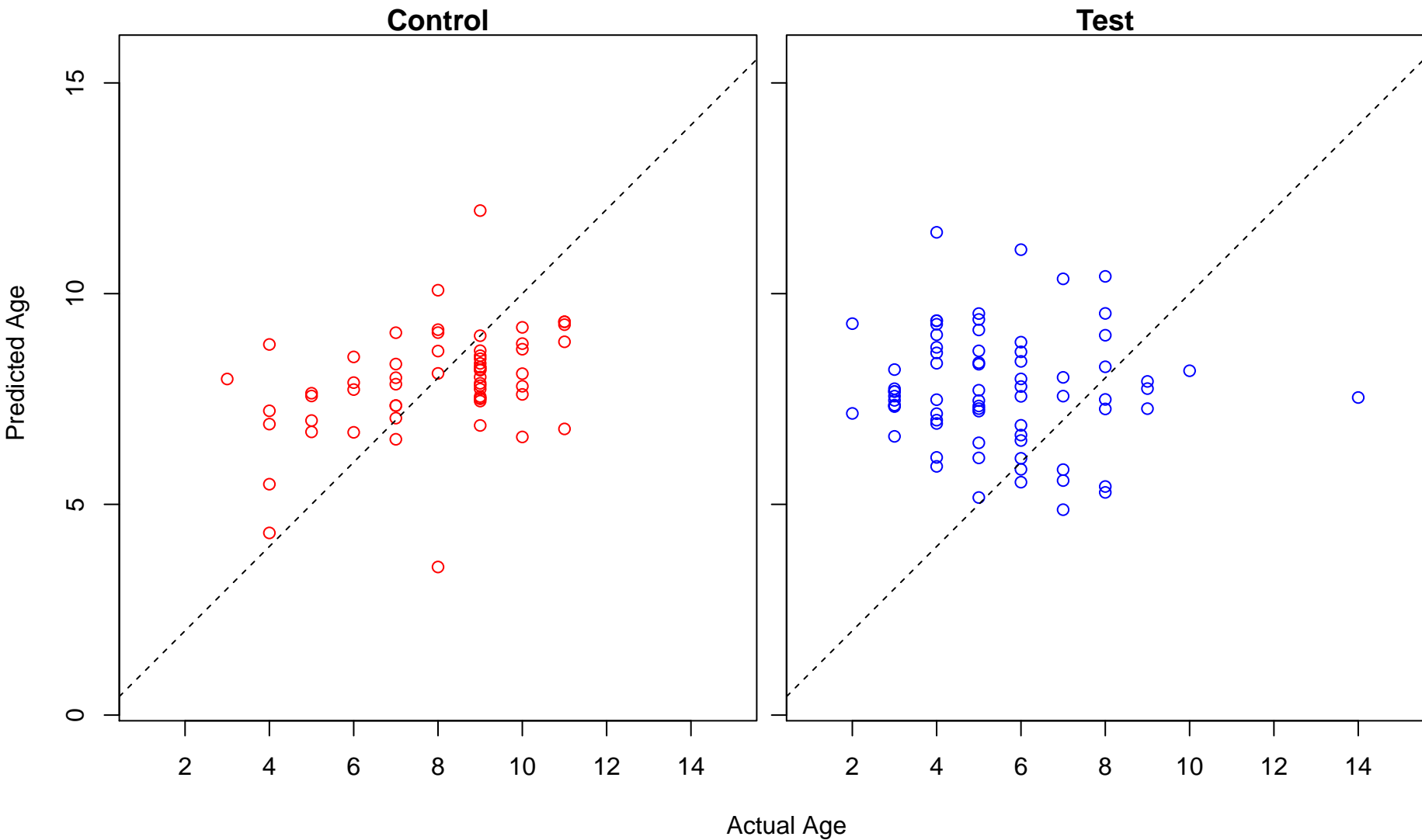
negative regulation of norepinephrine uptake (Score: 1.752577)



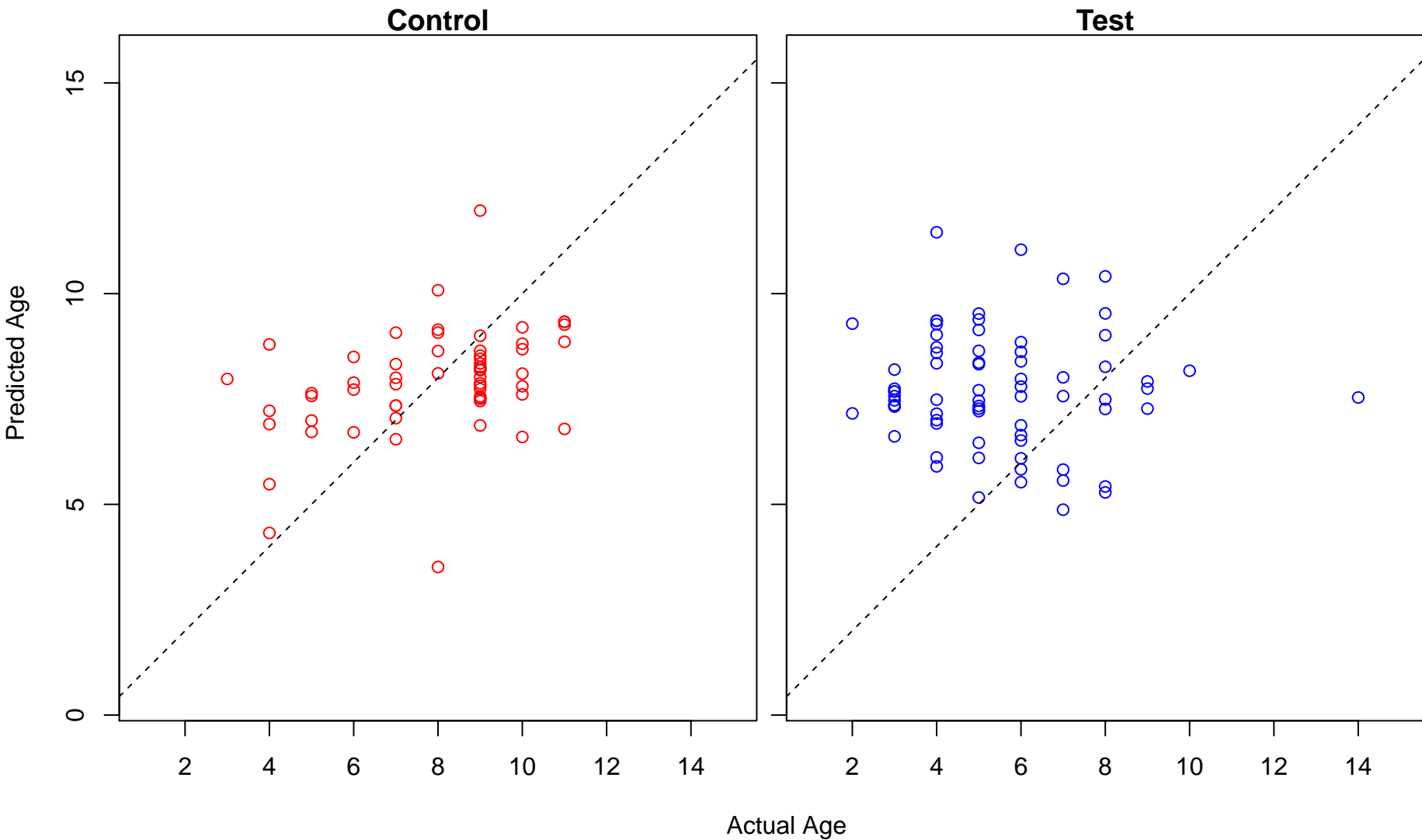
catecholamine uptake involved in synaptic transmission (Score: 1.752577)



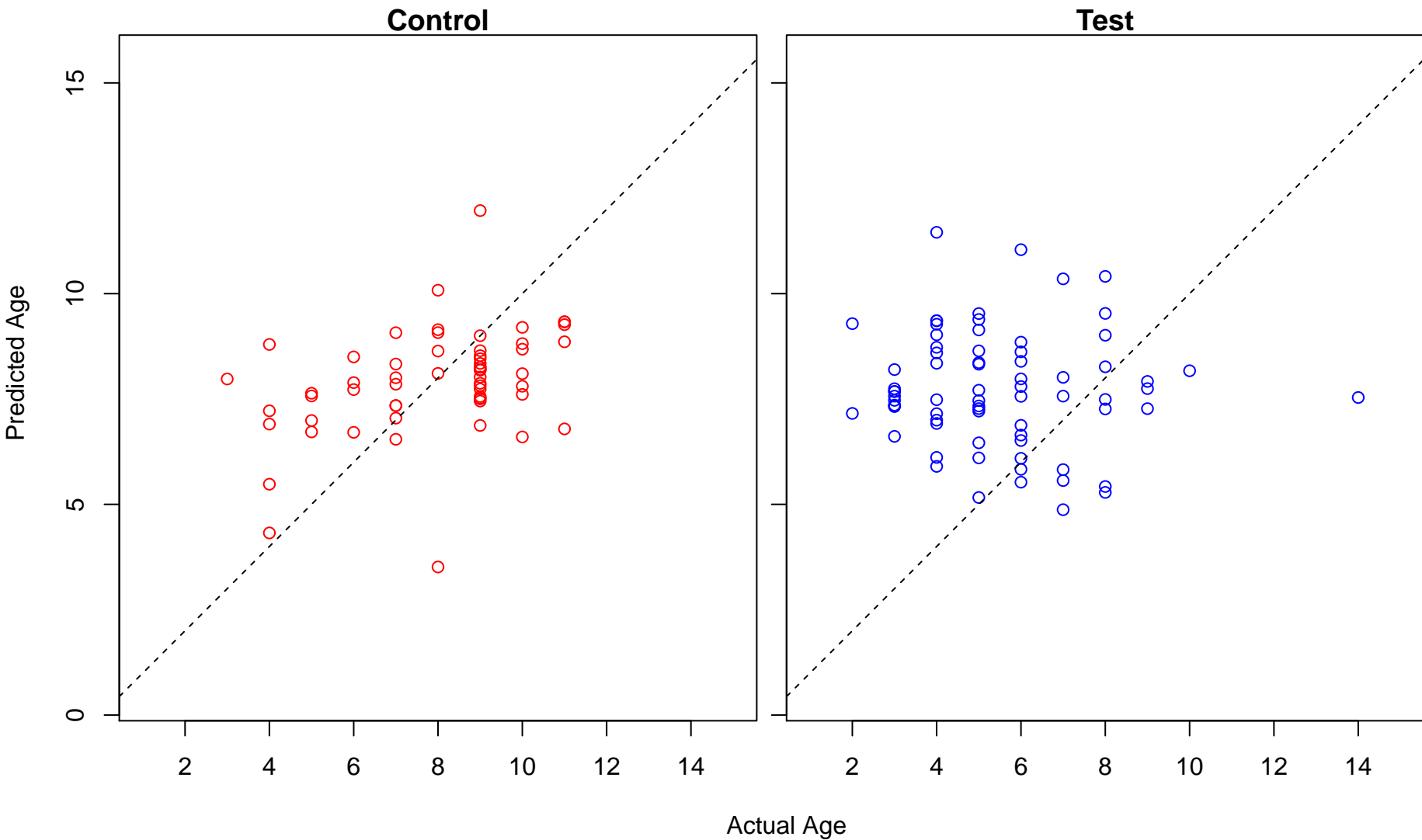
negative regulation of catecholamine uptake involved in synaptic transmission (Score: 1.752577)



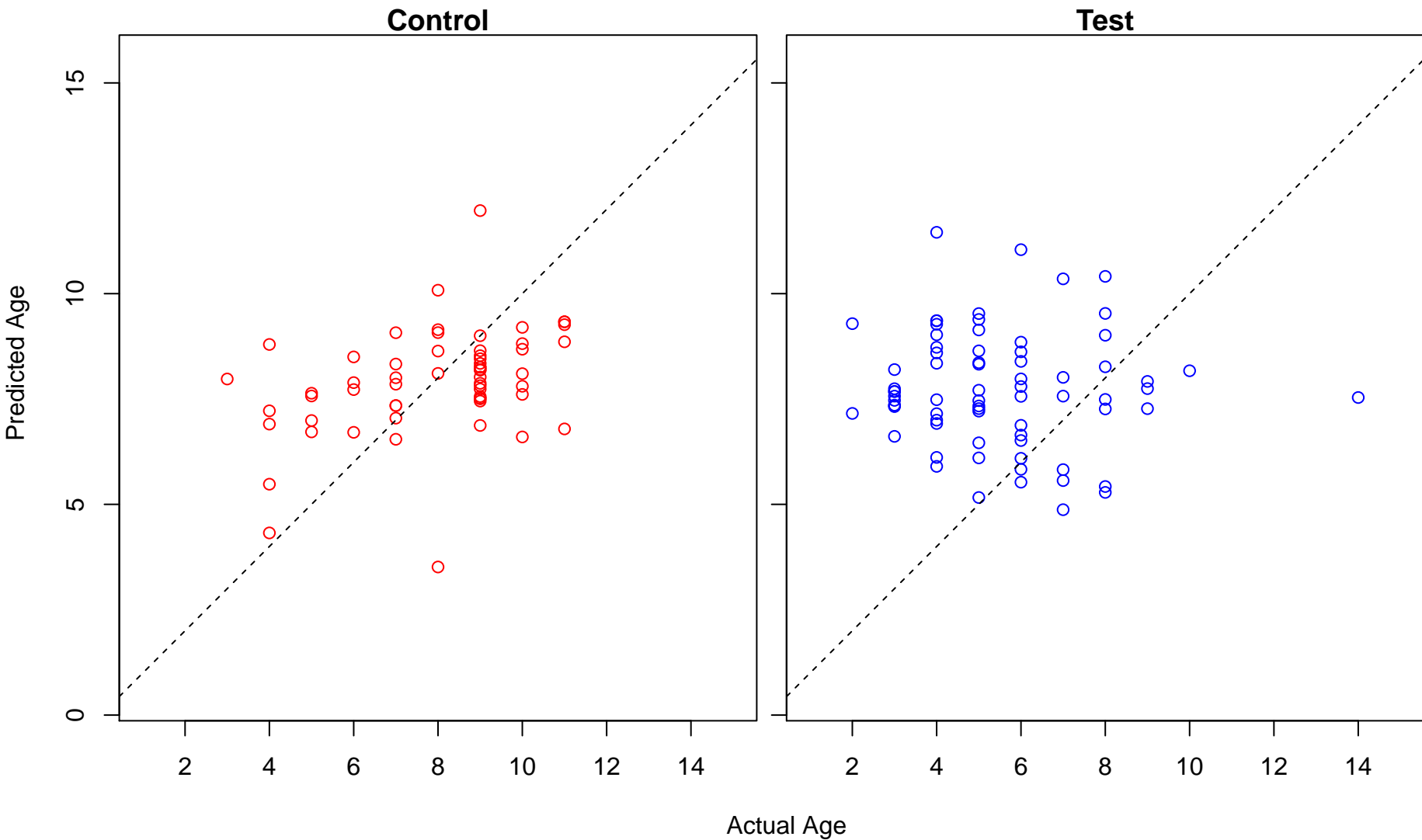
regulation of thrombin receptor signaling pathway (Score: 1.752577)



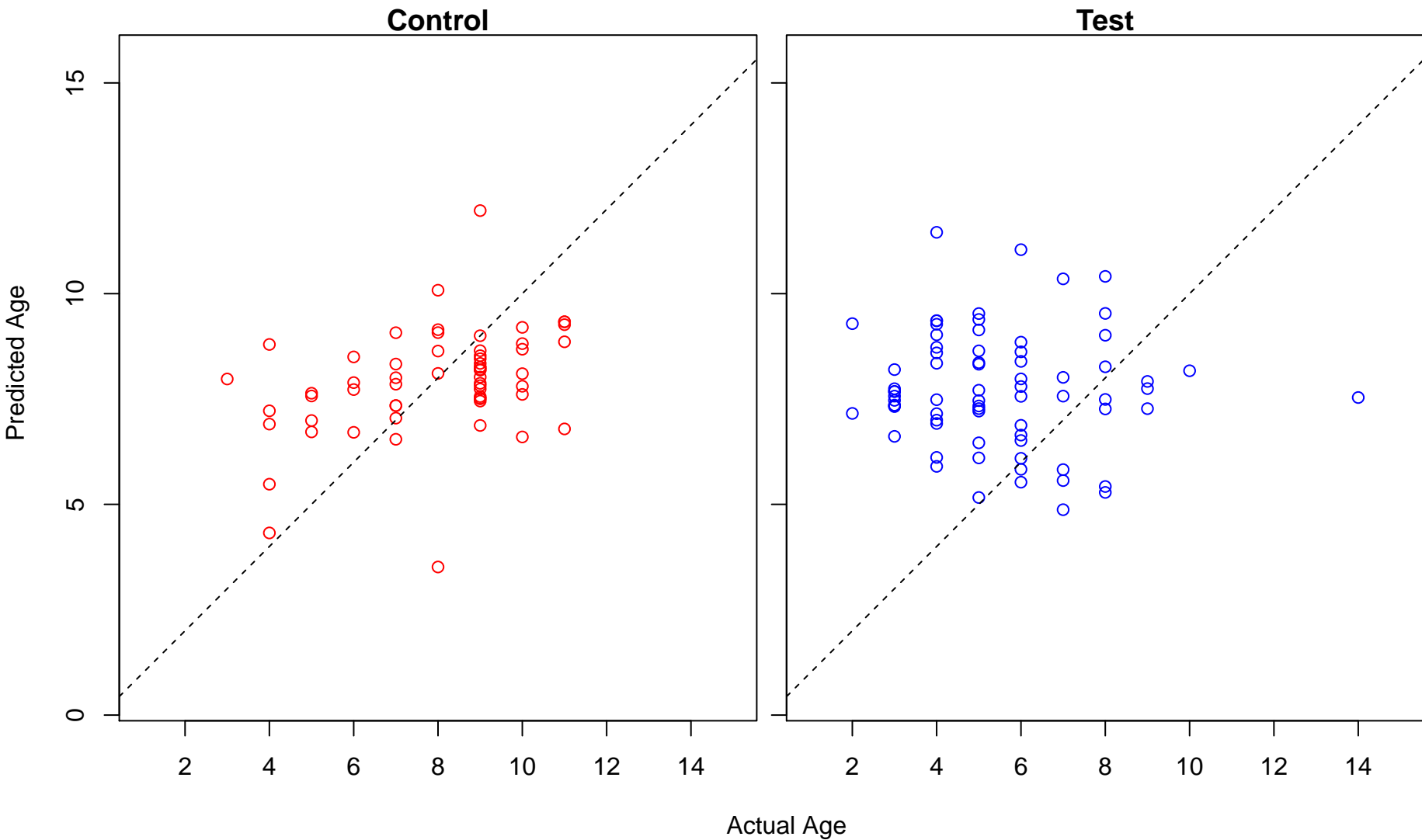
negative regulation of thrombin receptor signaling pathway (Score: 1.752577)



catecholamine uptake (Score: 1.752577)

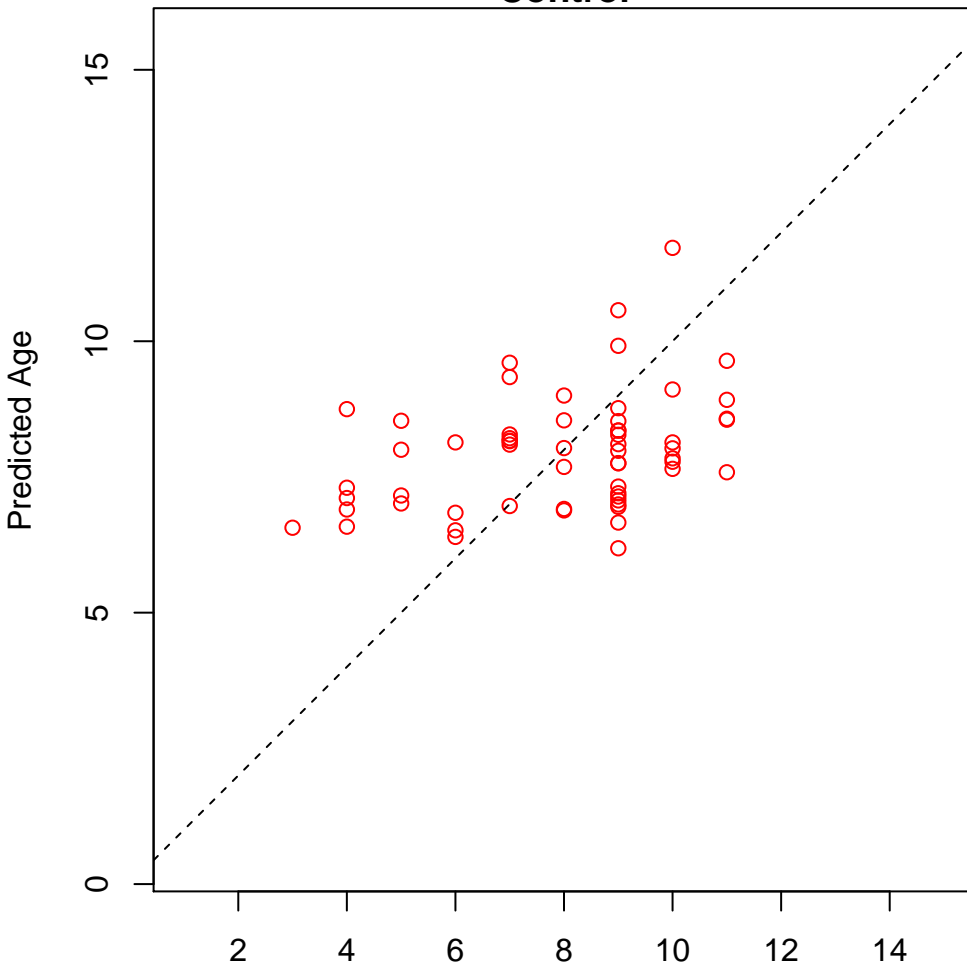


dopamine uptake (Score: 1.752577)

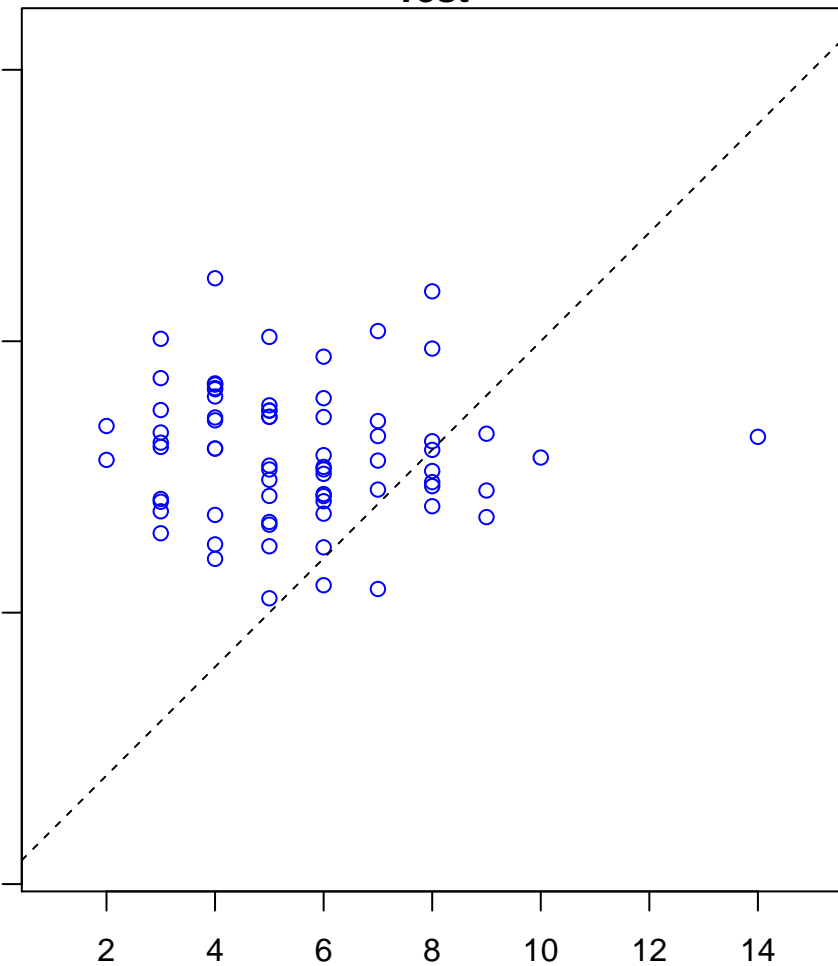


cell migration involved in heart formation (Score: 1.750893)

Control

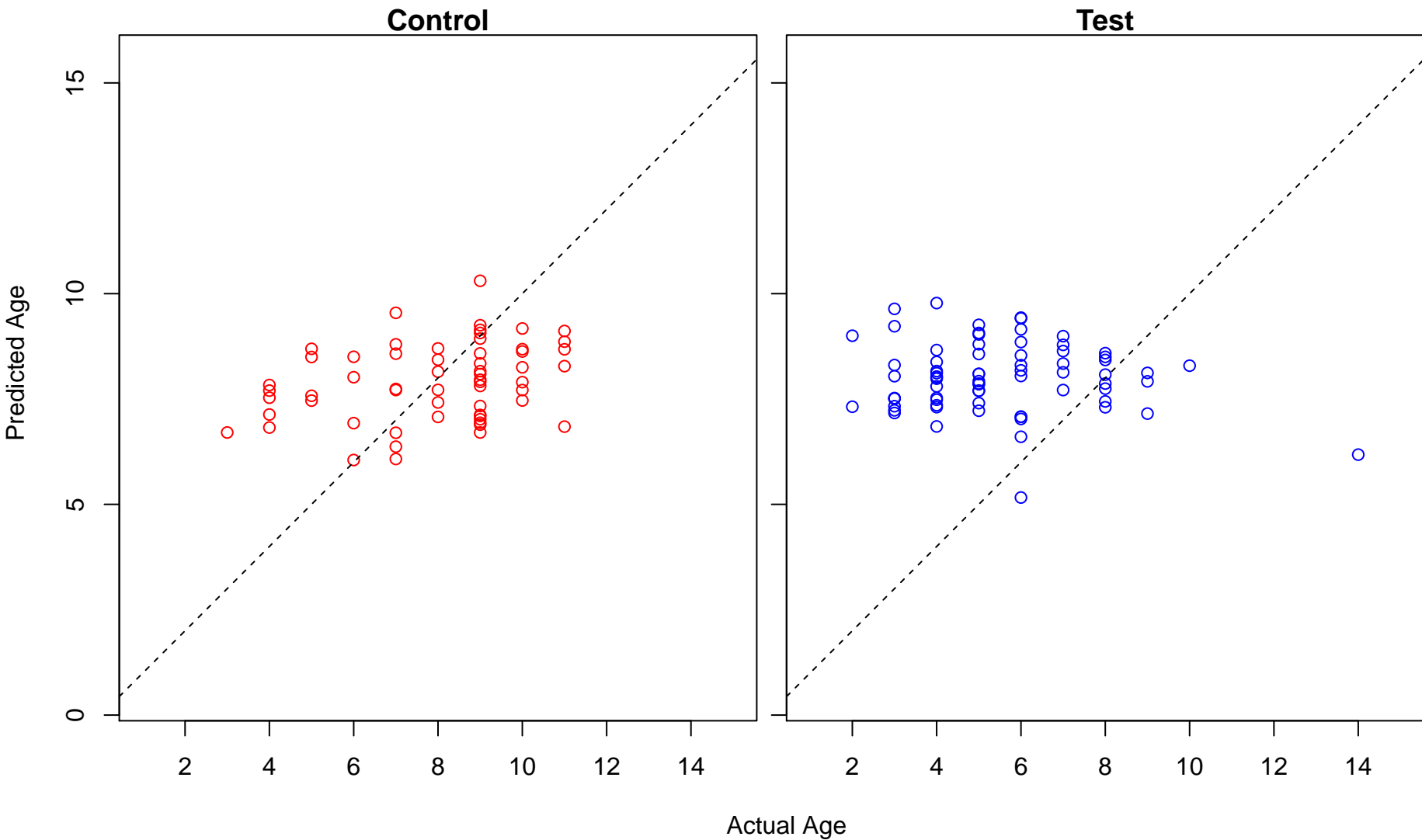


Test

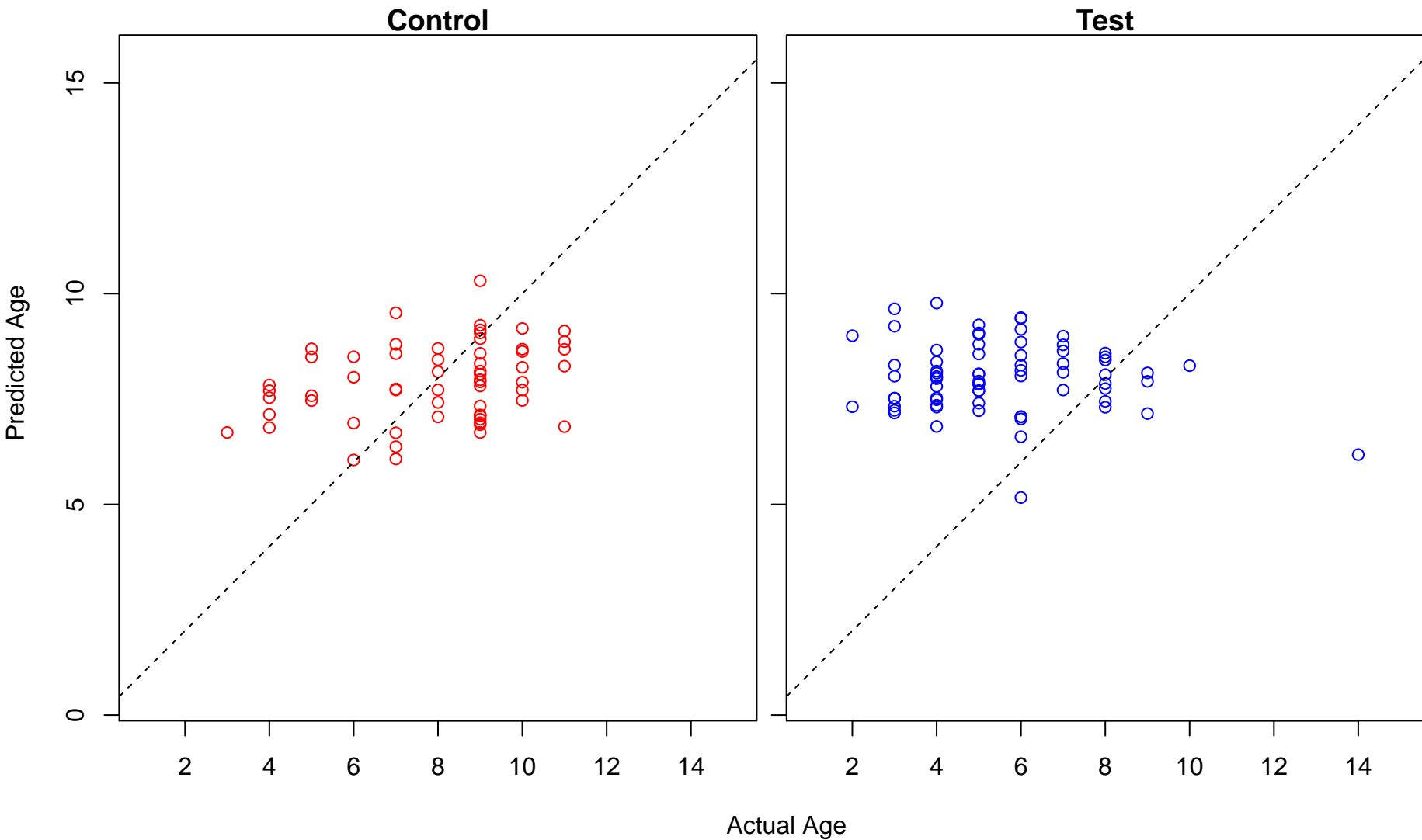


Actual Age

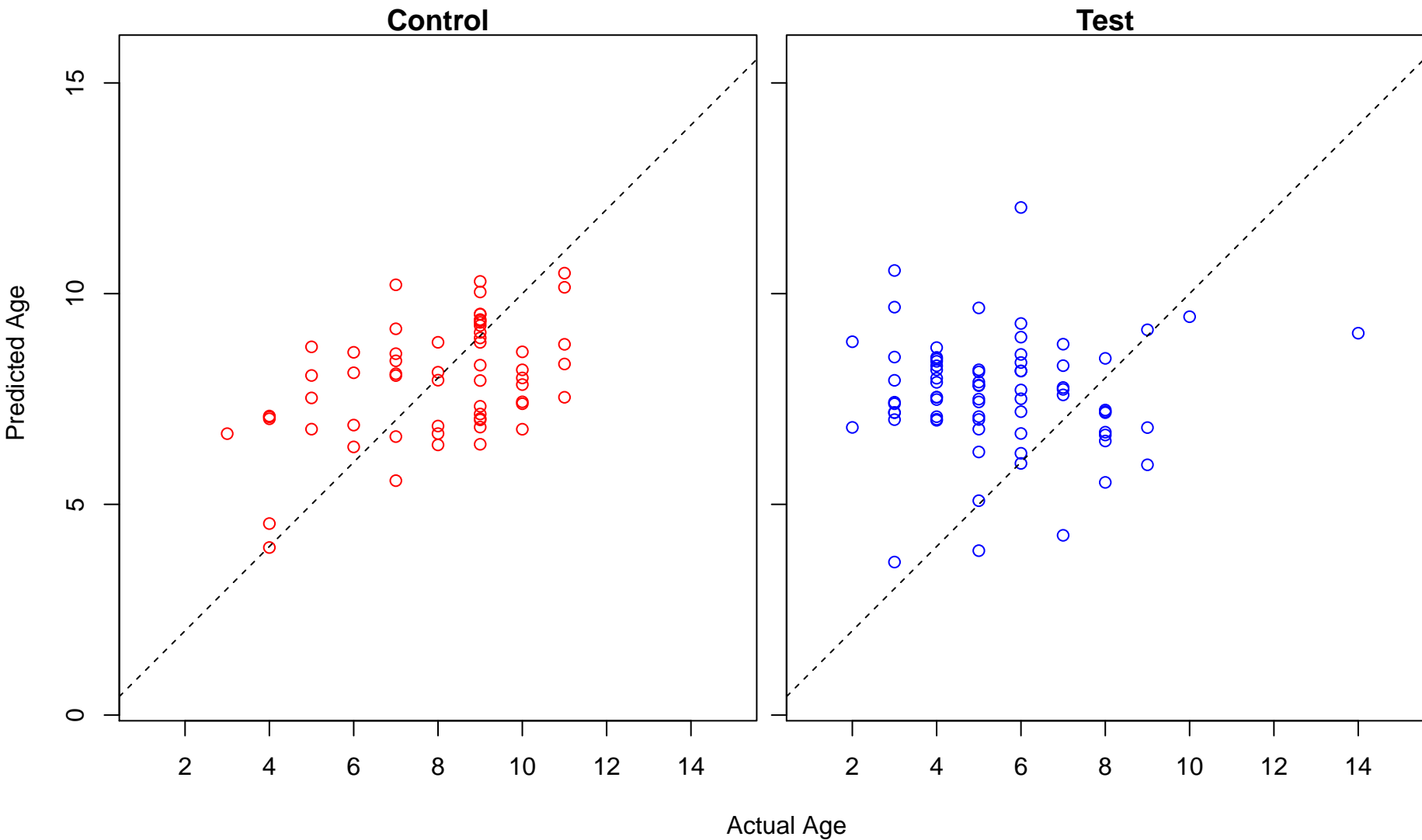
cellular manganese ion homeostasis (Score: 1.744943)



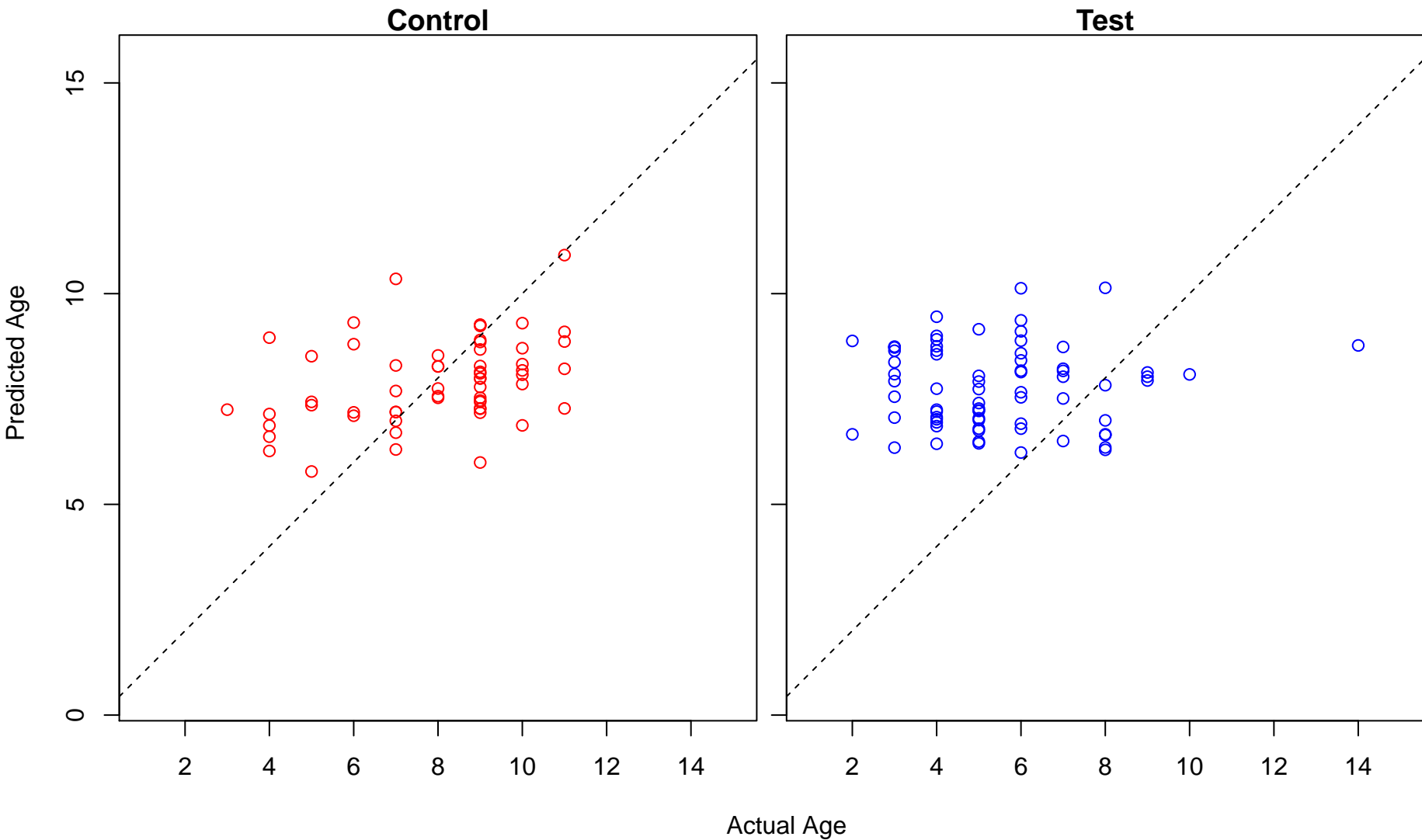
manganese ion homeostasis (Score: 1.744943)



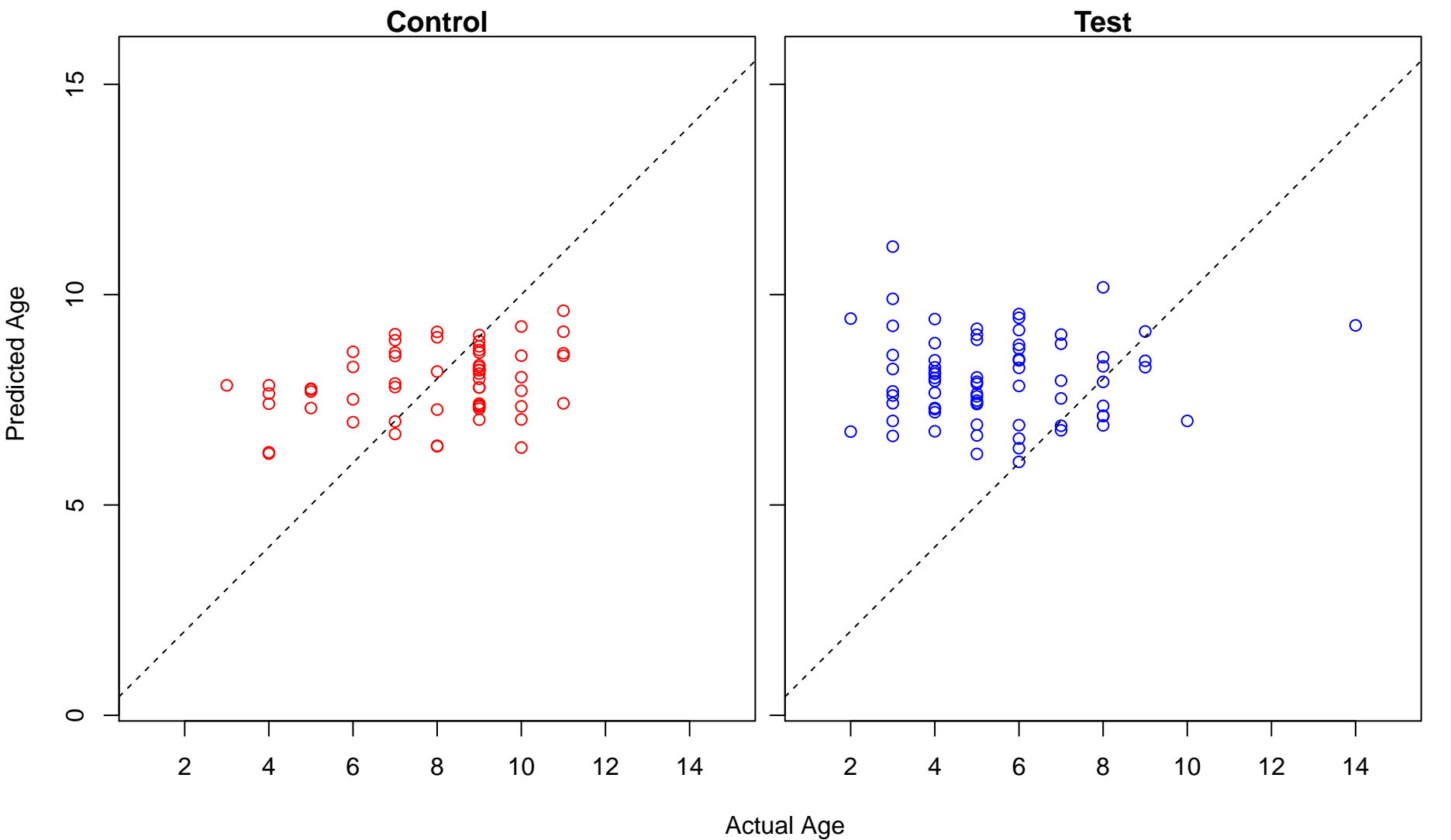
positive regulation of dendritic cell chemotaxis (Score: 1.743531)



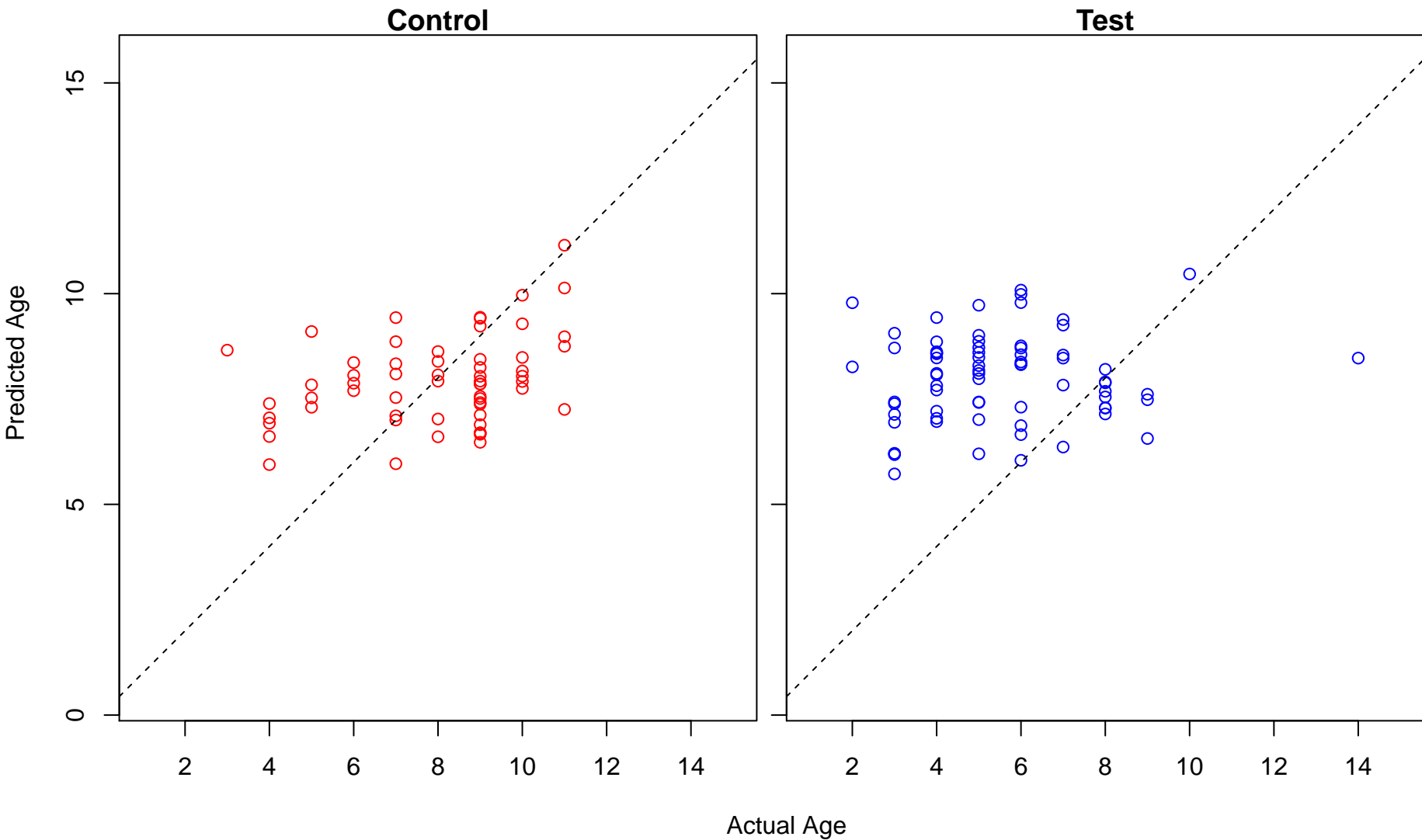
establishment or maintenance of apical/basal cell polarity (Score: 1.726932)



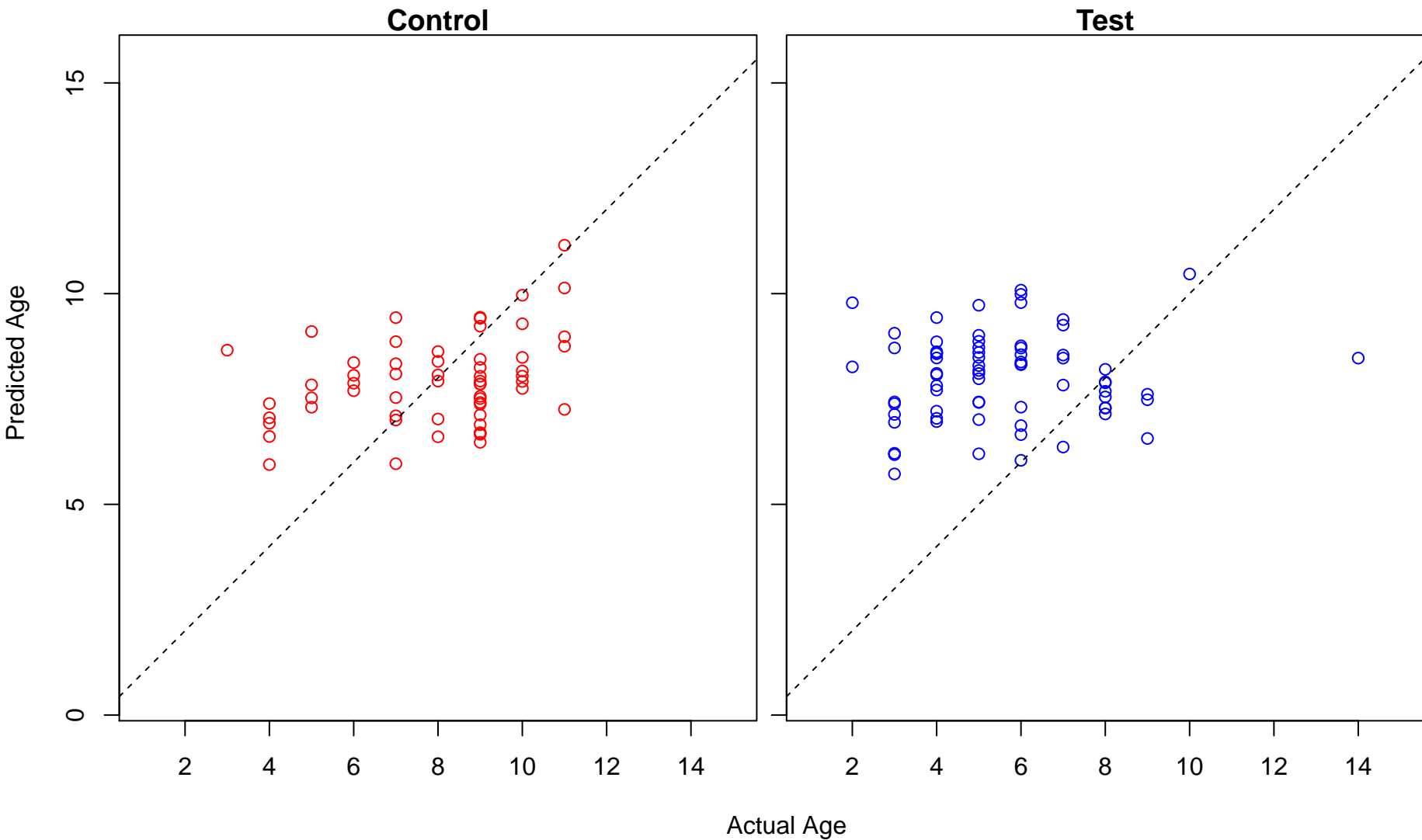
activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell (Sc



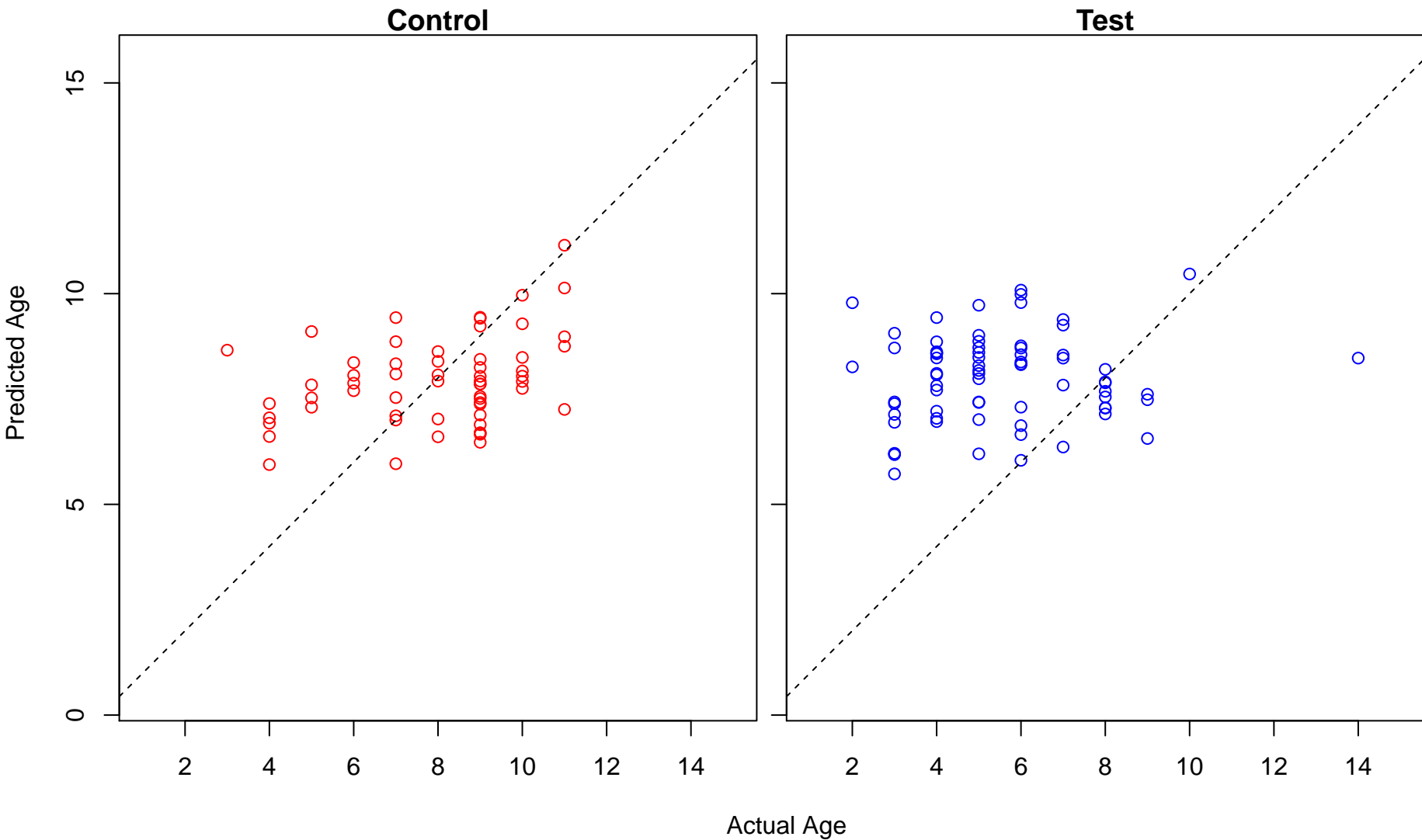
nickel cation transport (Score: 1.718013)



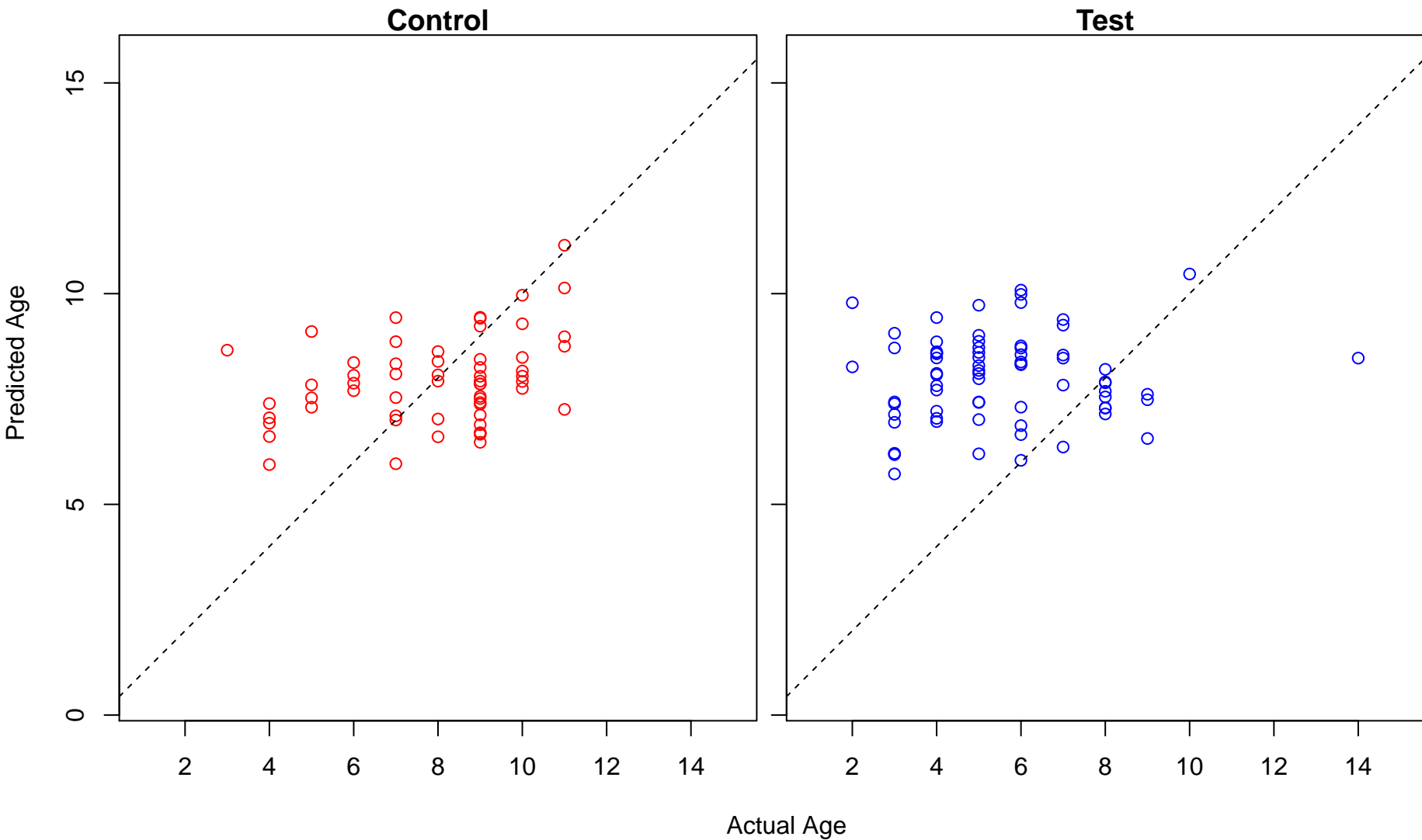
vanadium ion transport (Score: 1.718013)



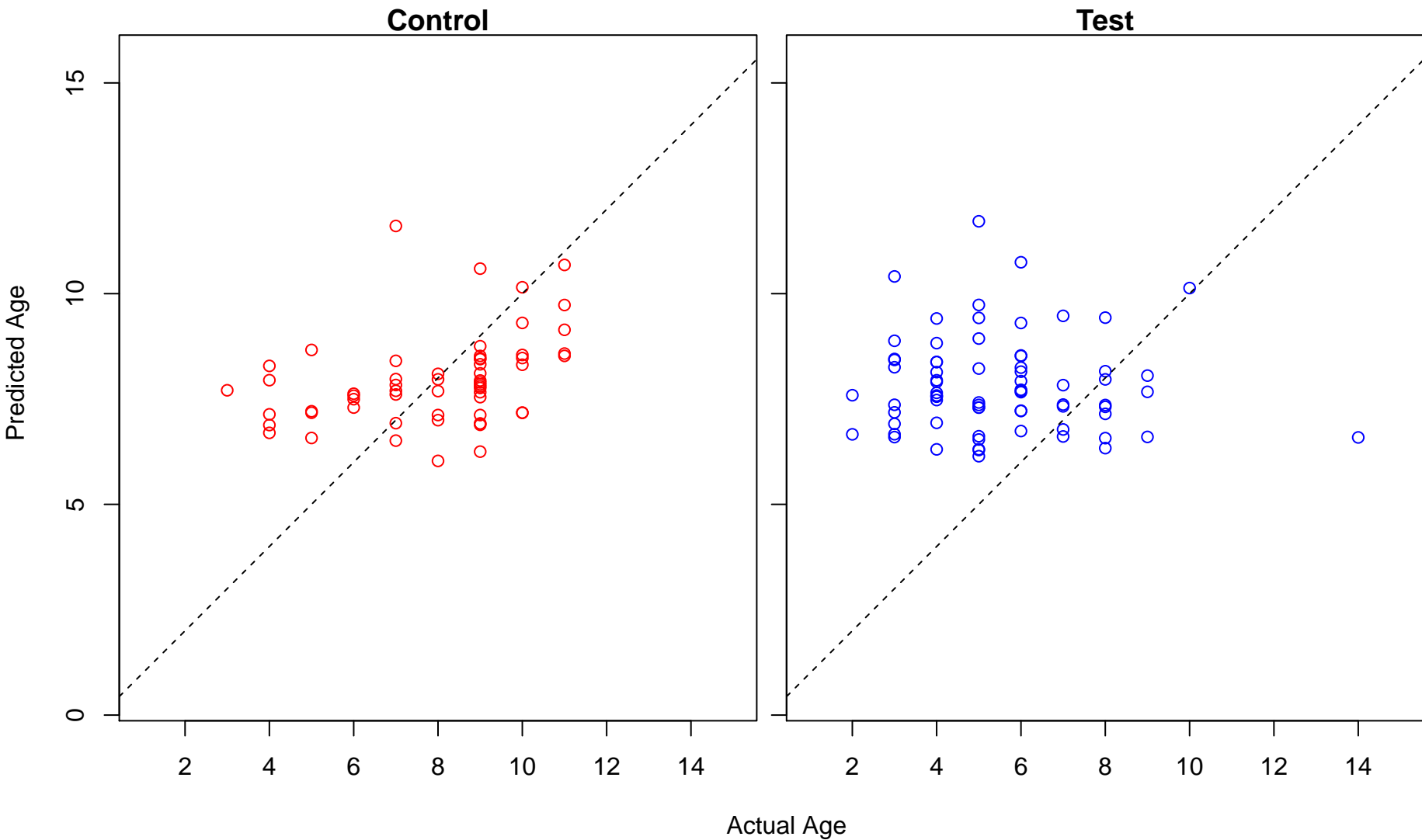
lead ion transport (Score: 1.718013)



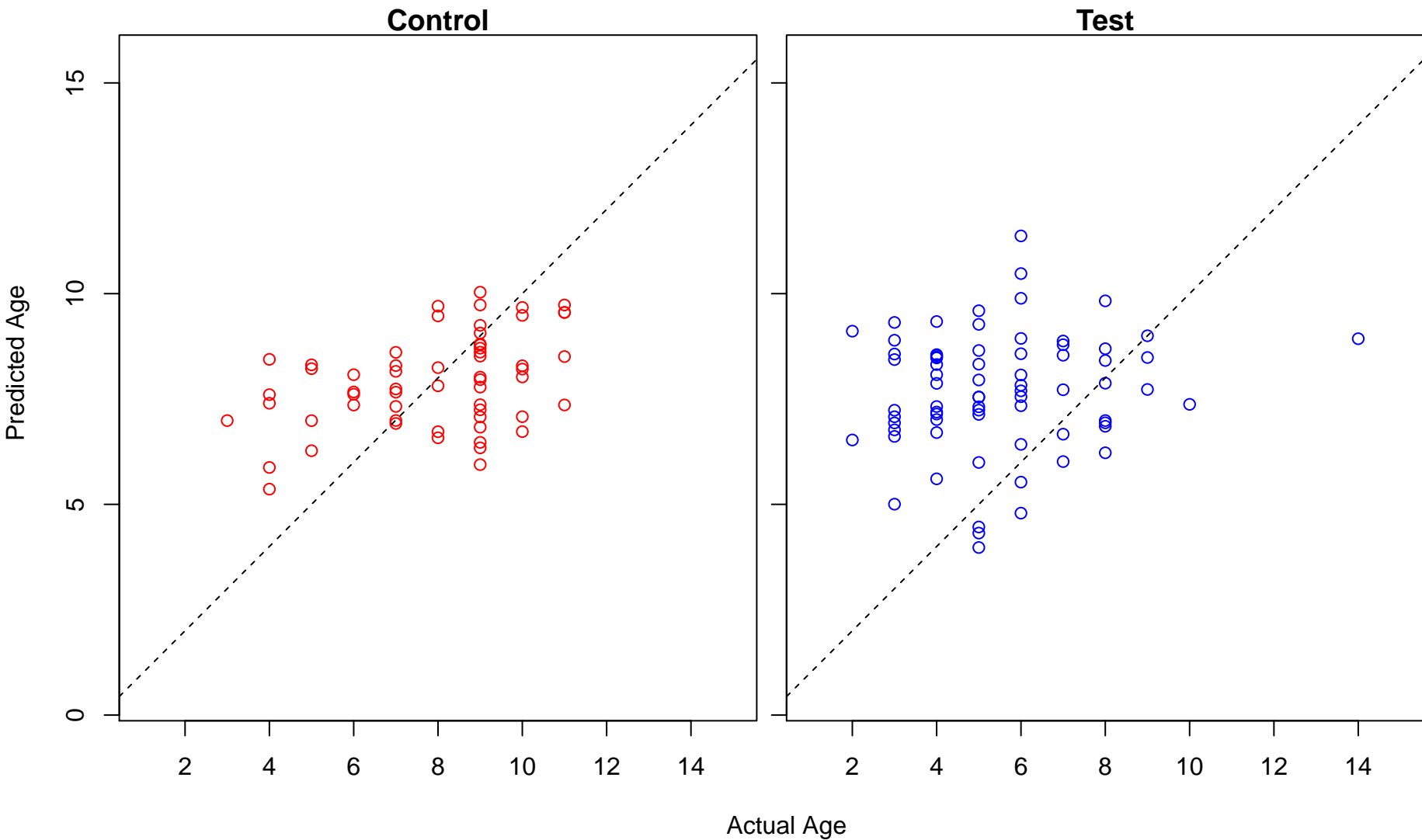
nickel cation transmembrane transport (Score: 1.718013)



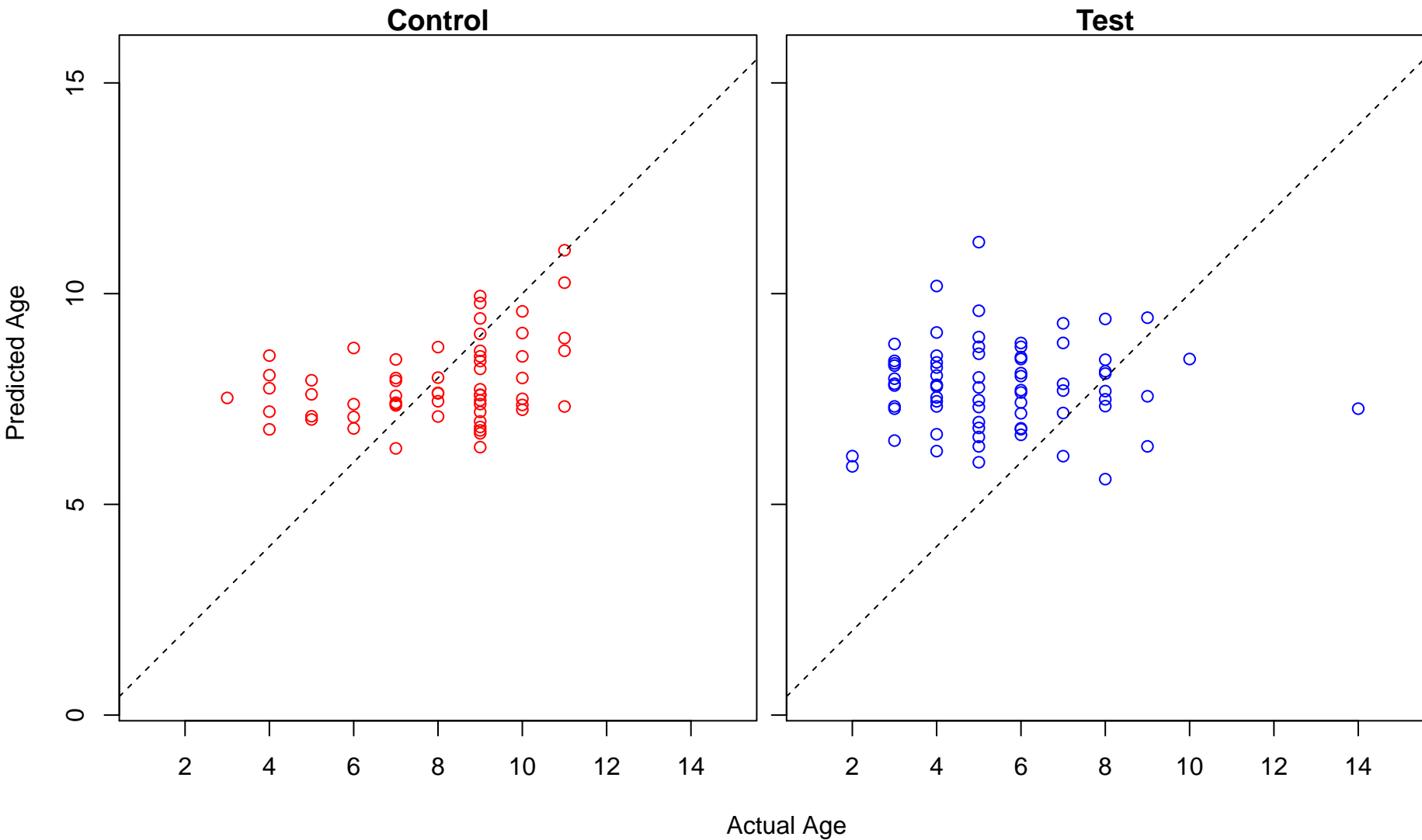
inner medullary collecting duct development (Score: 1.715128)



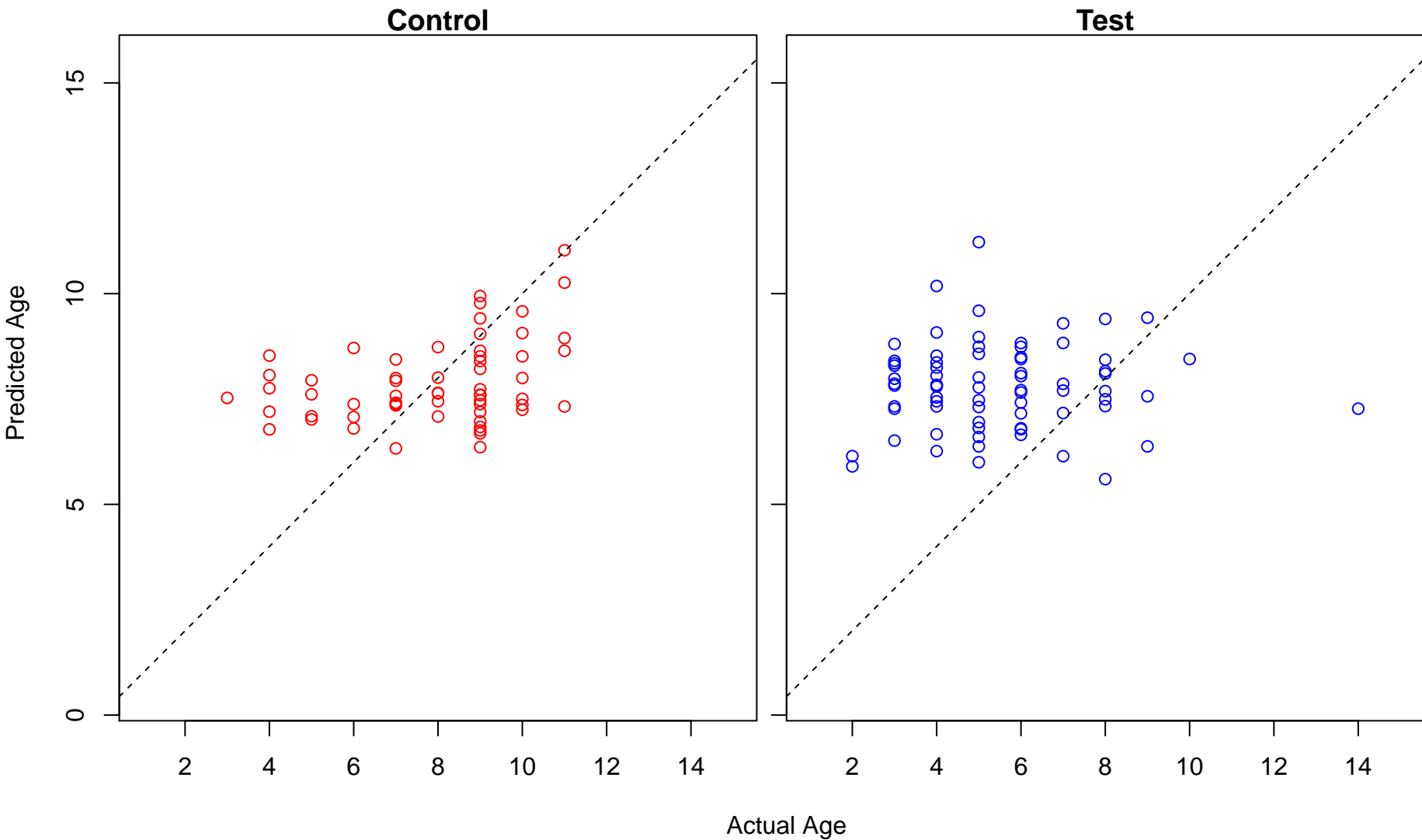
notochord formation (Score: 1.696927)



regulation of calcium ion binding (Score: 1.690790)



negative regulation of calcium ion binding (Score: 1.690790)



UDP-glucuronic acid transport (Score: 1.682944)

