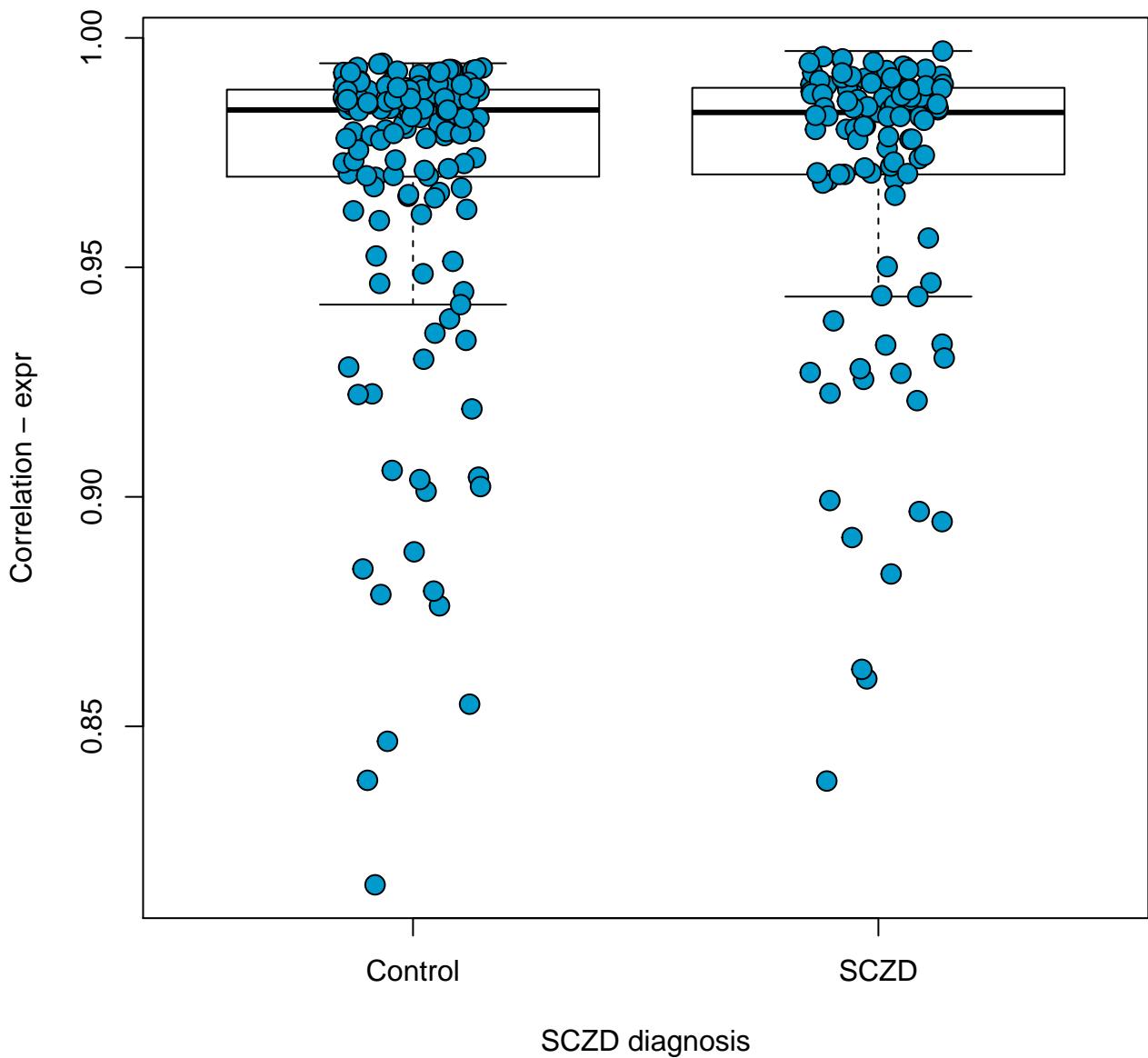
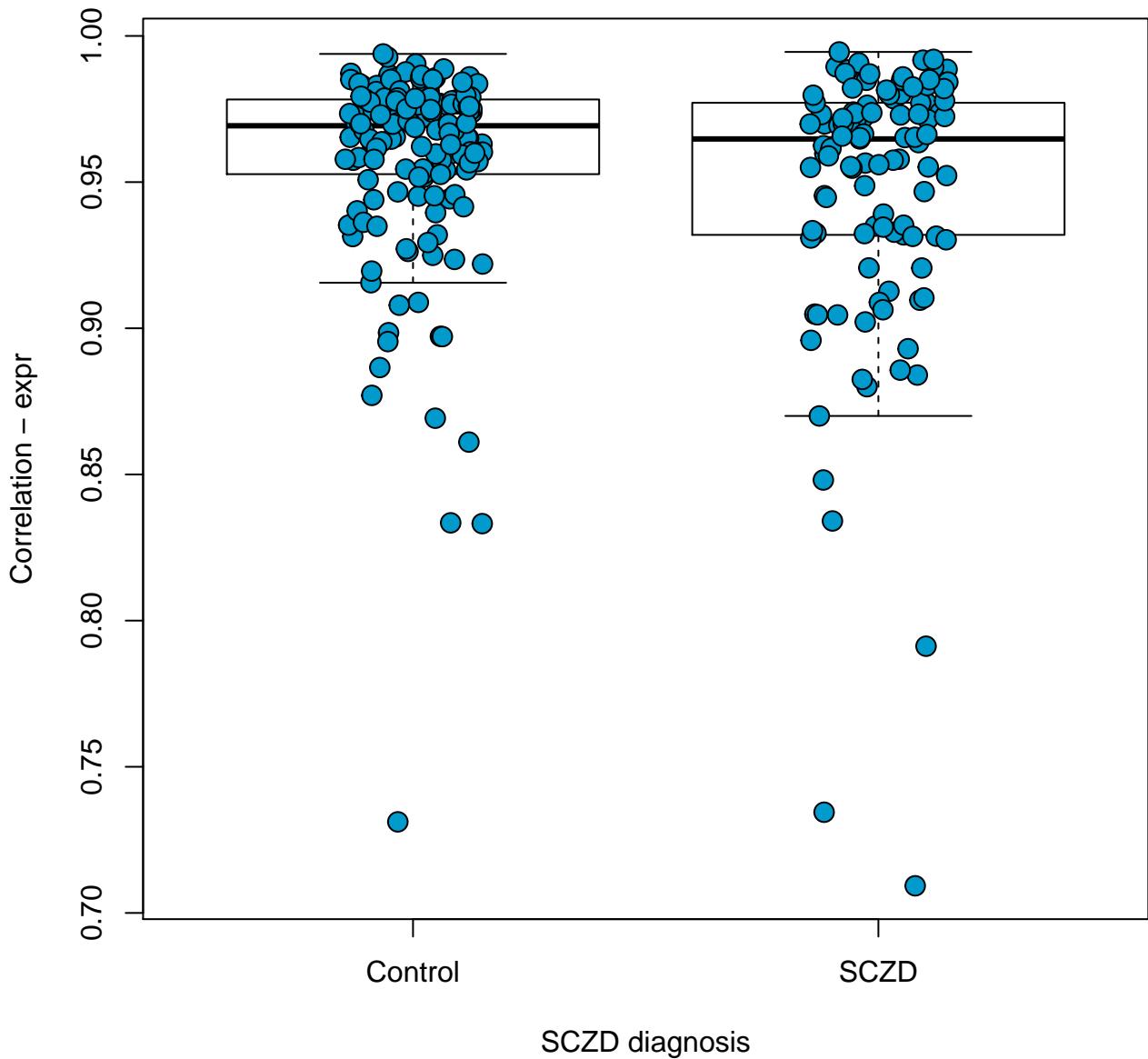


hsa00010: Glycolysis / Gluconeogenesis

p-value: 0.949

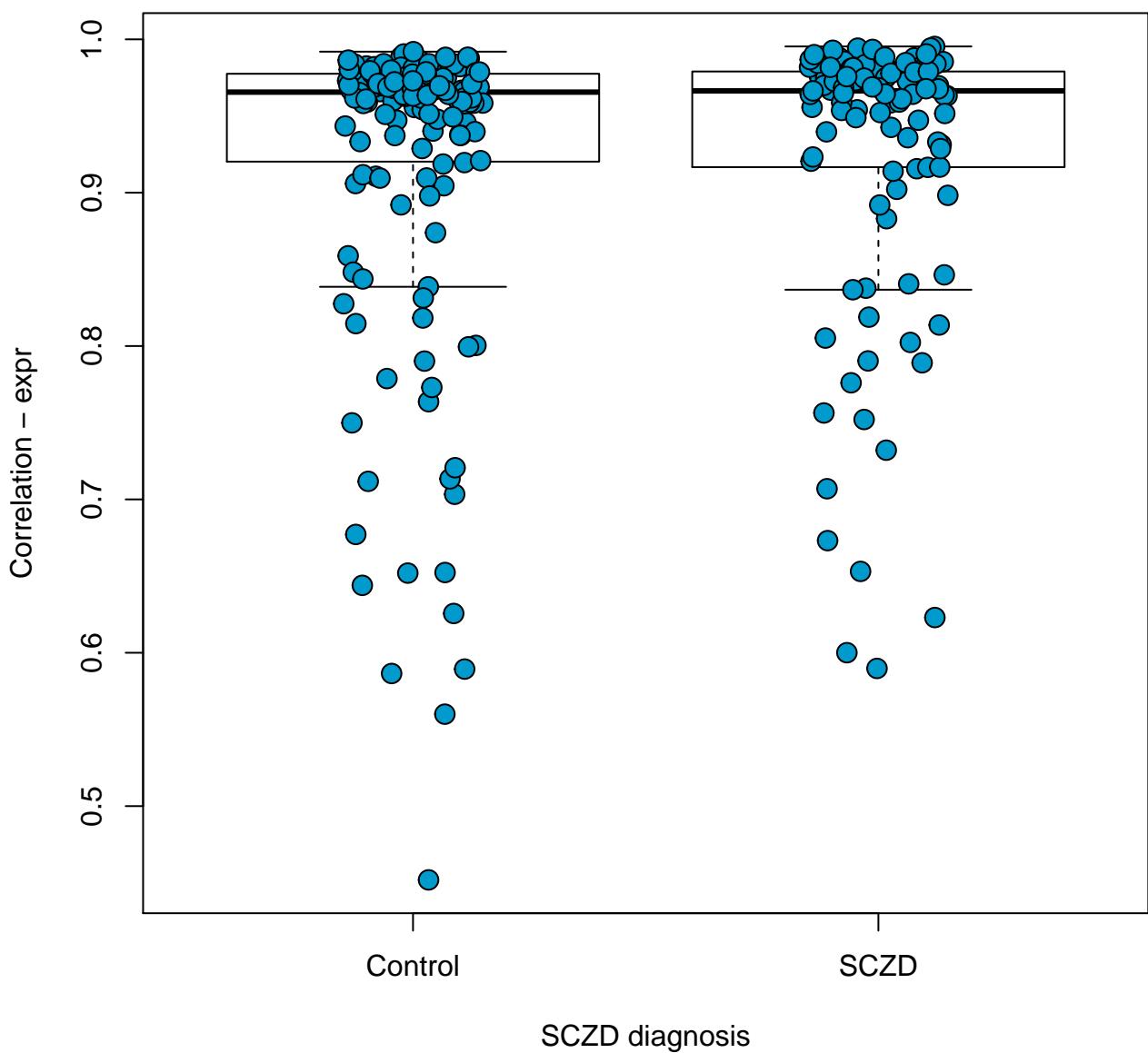


hsa00020: Citrate cycle (TCA cycle)
p-value: 0.027

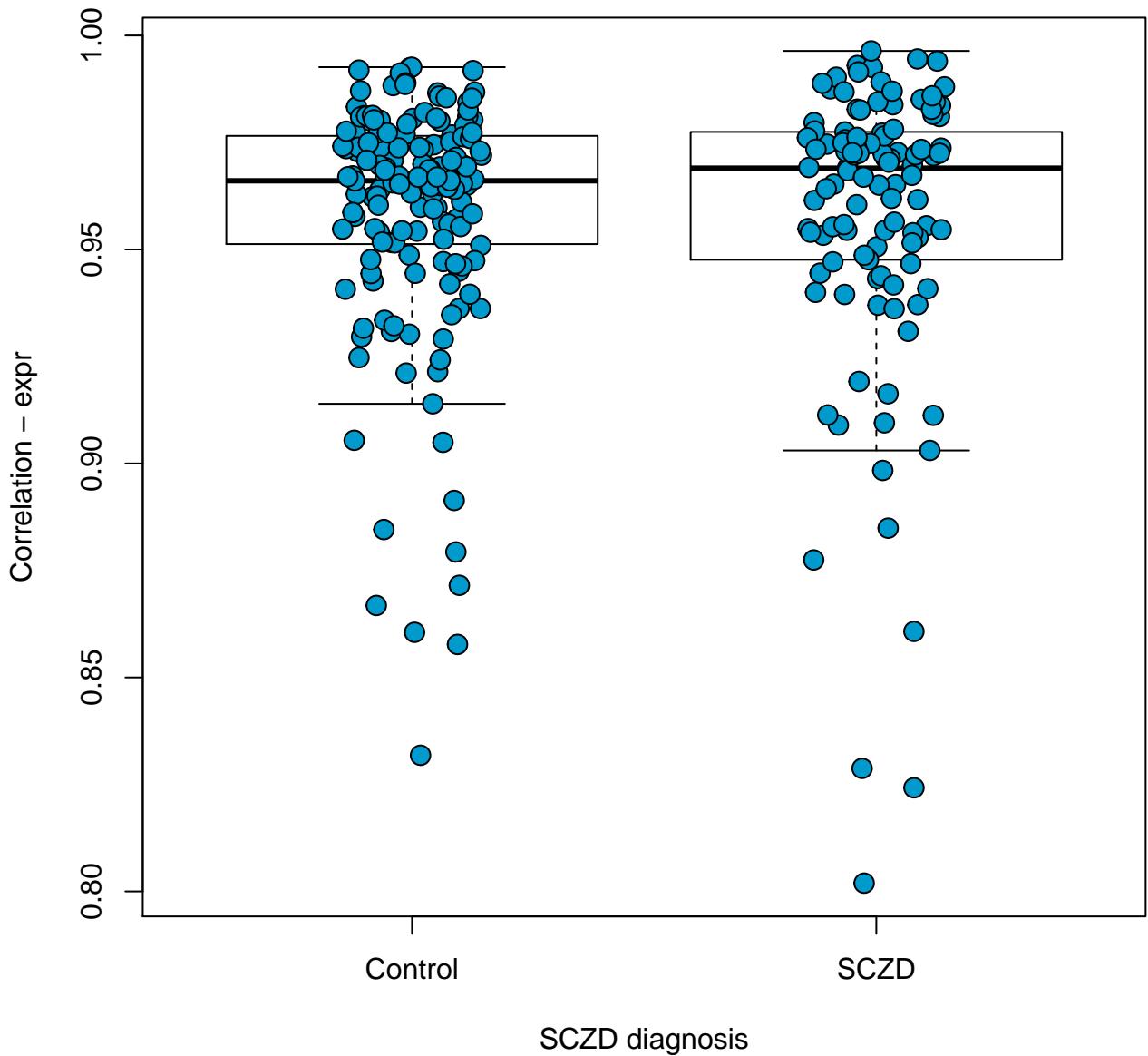


hsa00030: Pentose phosphate pathway

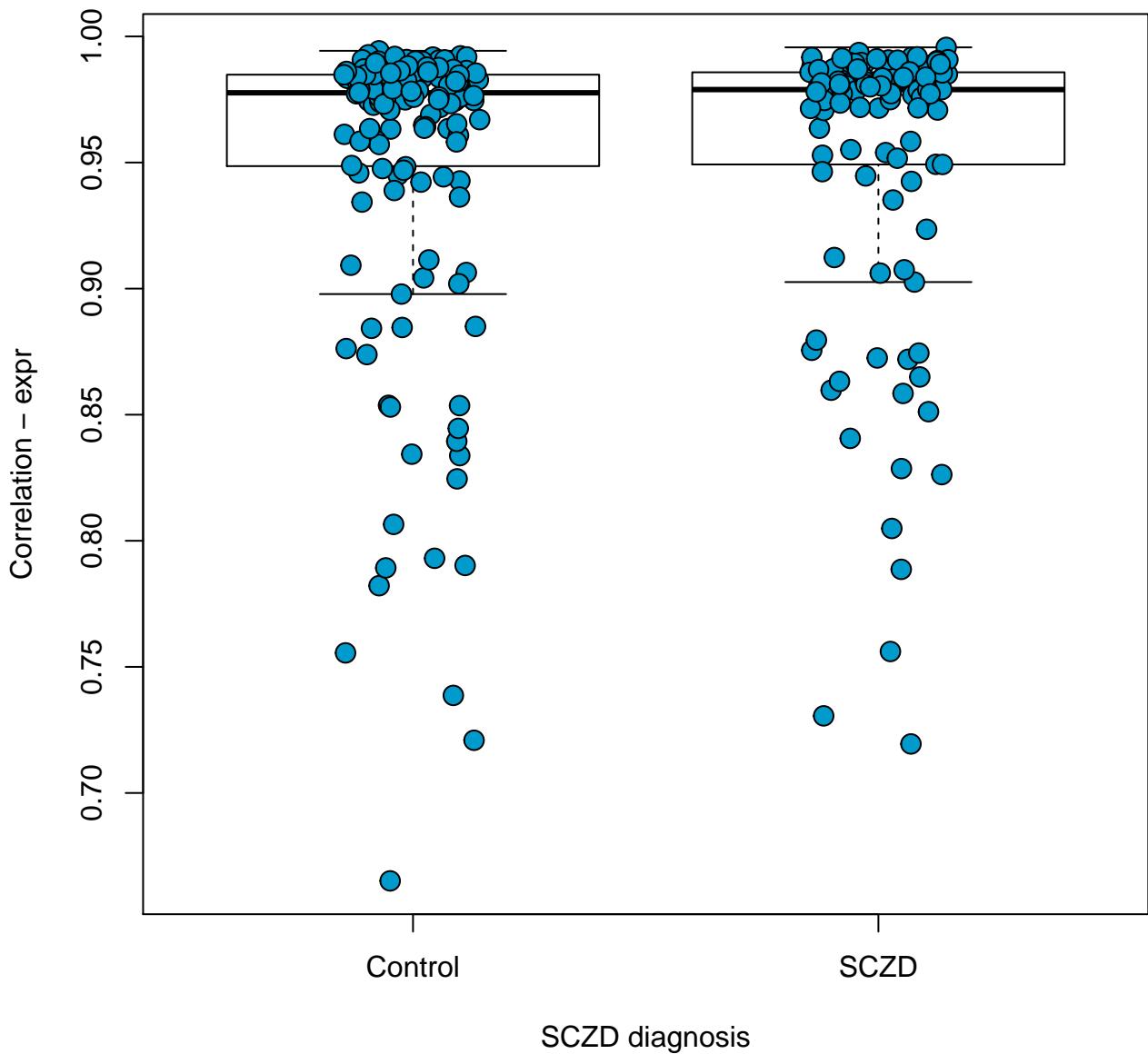
p-value: 0.748



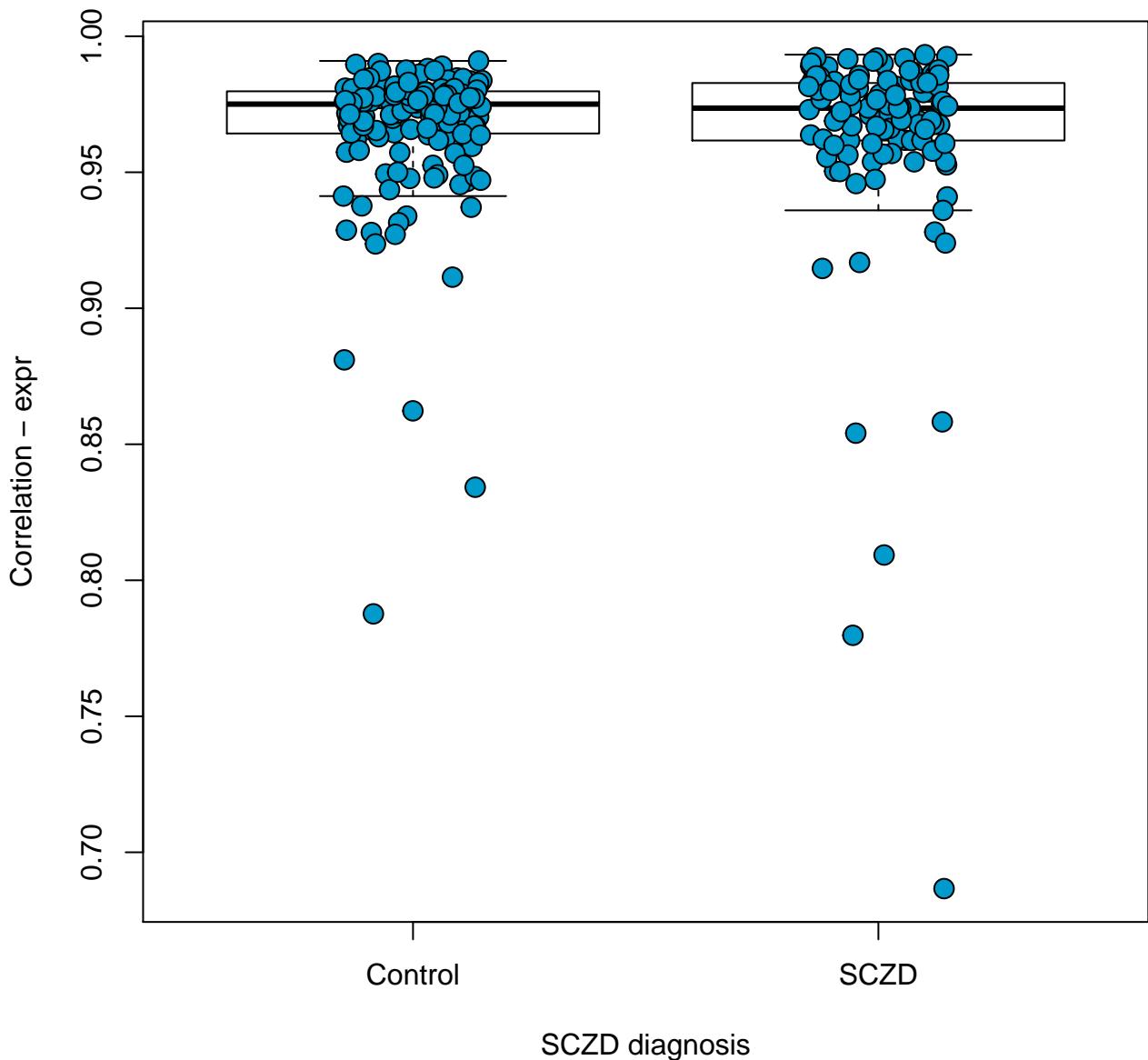
hsa00040: Pentose and glucuronate interconversions
p-value: 0.689



hsa00051: Fructose and mannose metabolism
p-value: 0.976

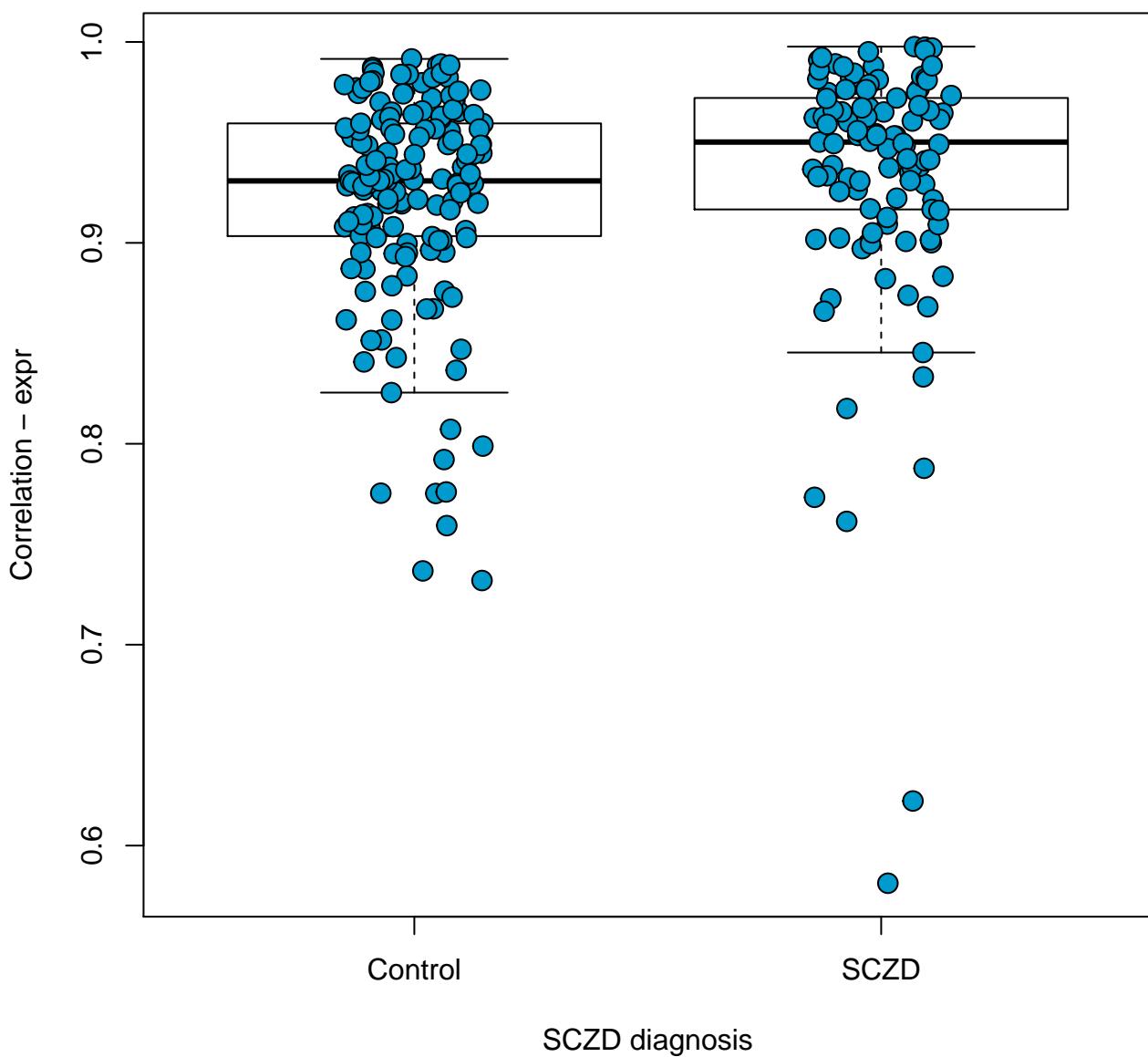


hsa00052: Galactose metabolism
p-value: 0.363

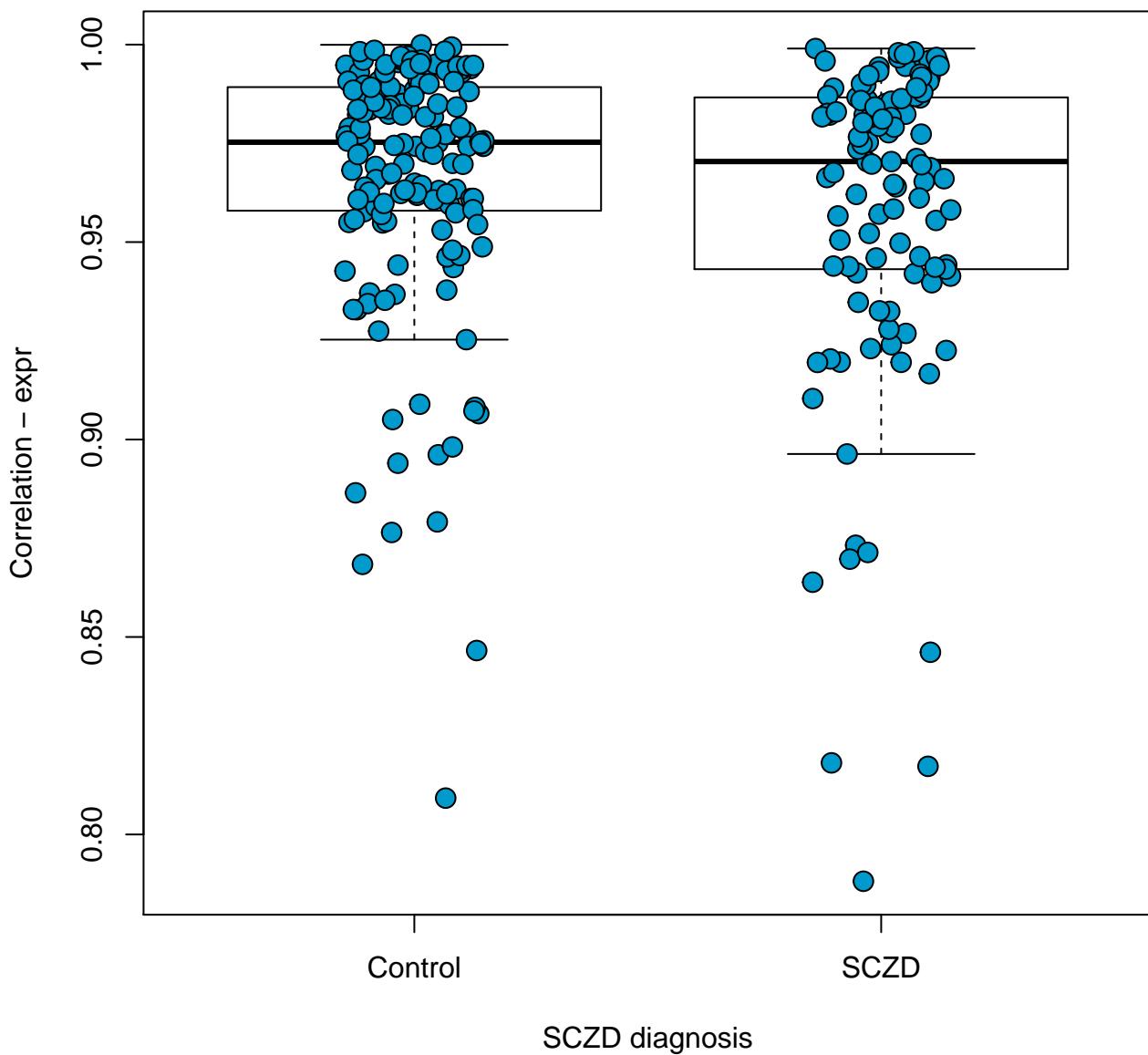


hsa00053: Ascorbate and aldarate metabolism

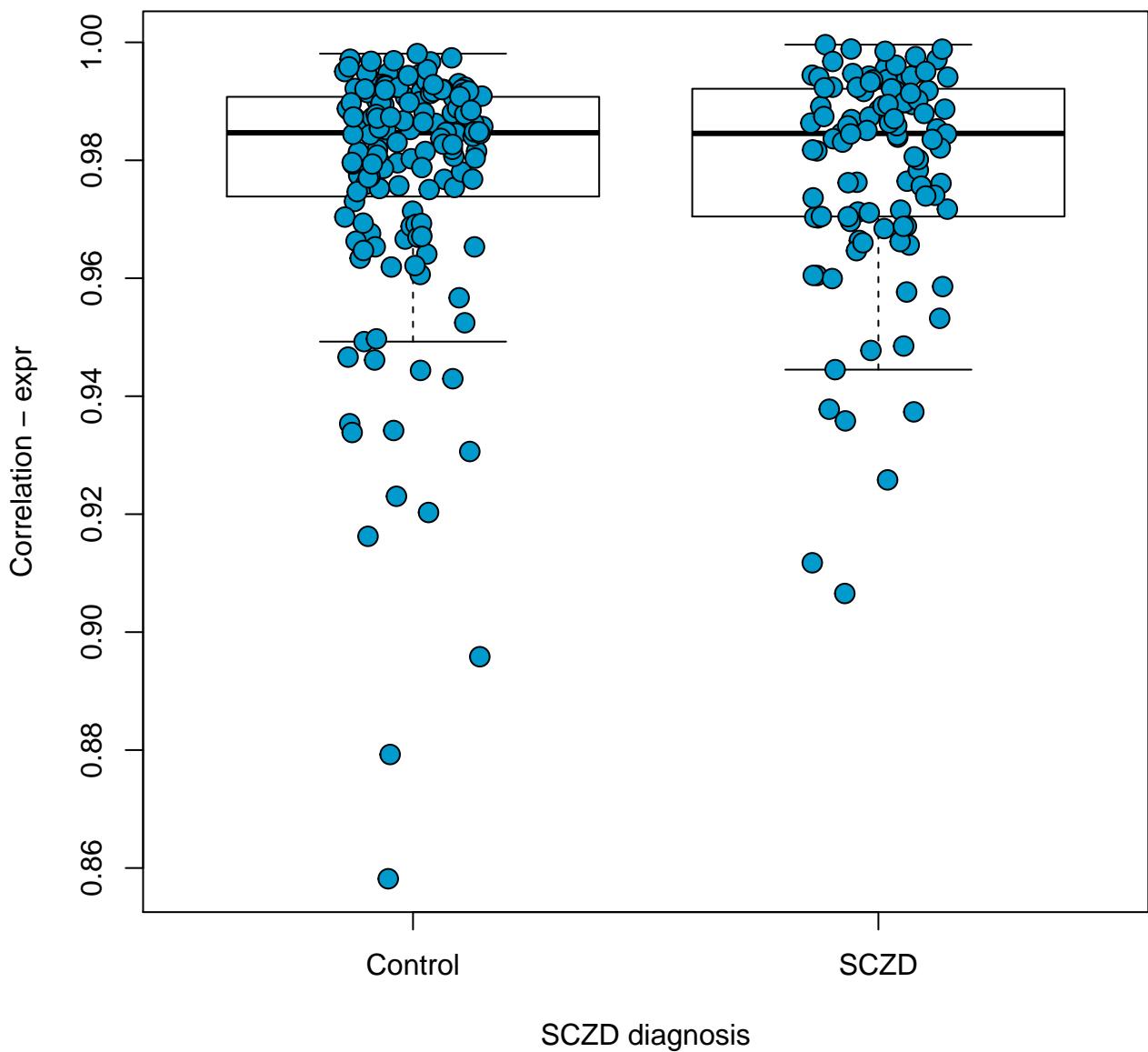
p-value: 0.157



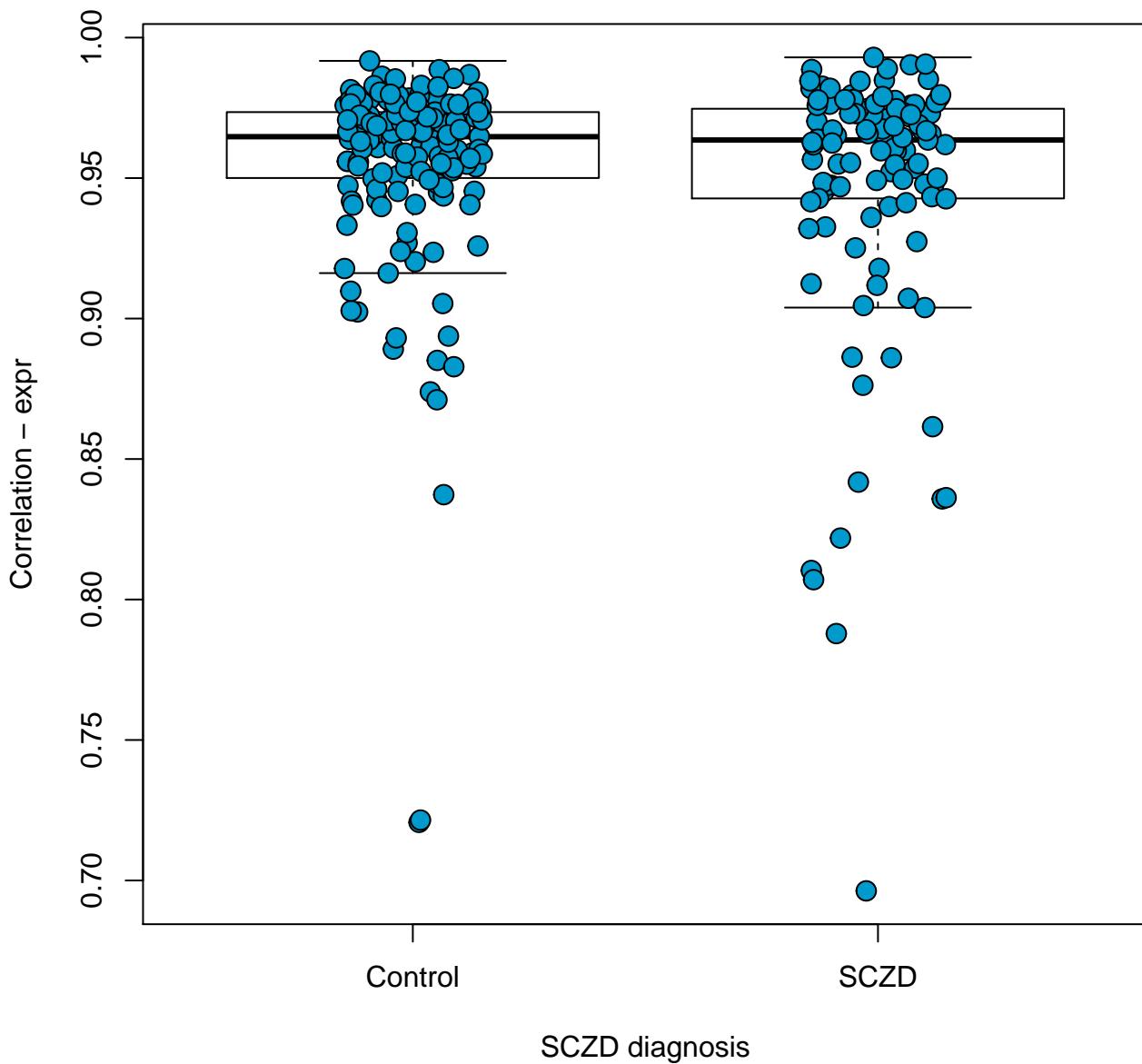
hsa00061: Fatty acid biosynthesis
p-value: 0.0622



hsa00062: Fatty acid elongation
p-value: 0.548

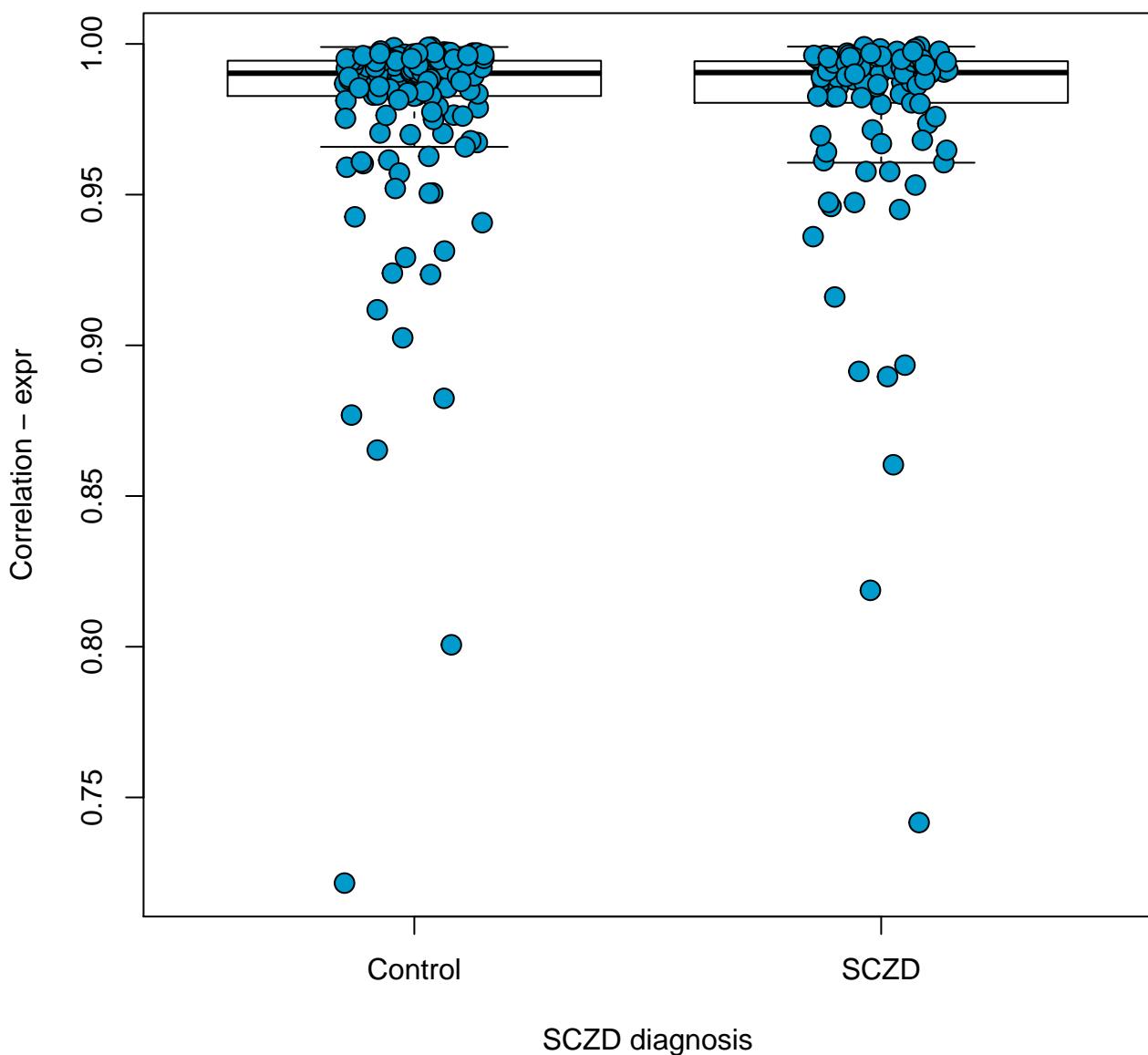


hsa00071: Fatty acid degradation
p-value: 0.15

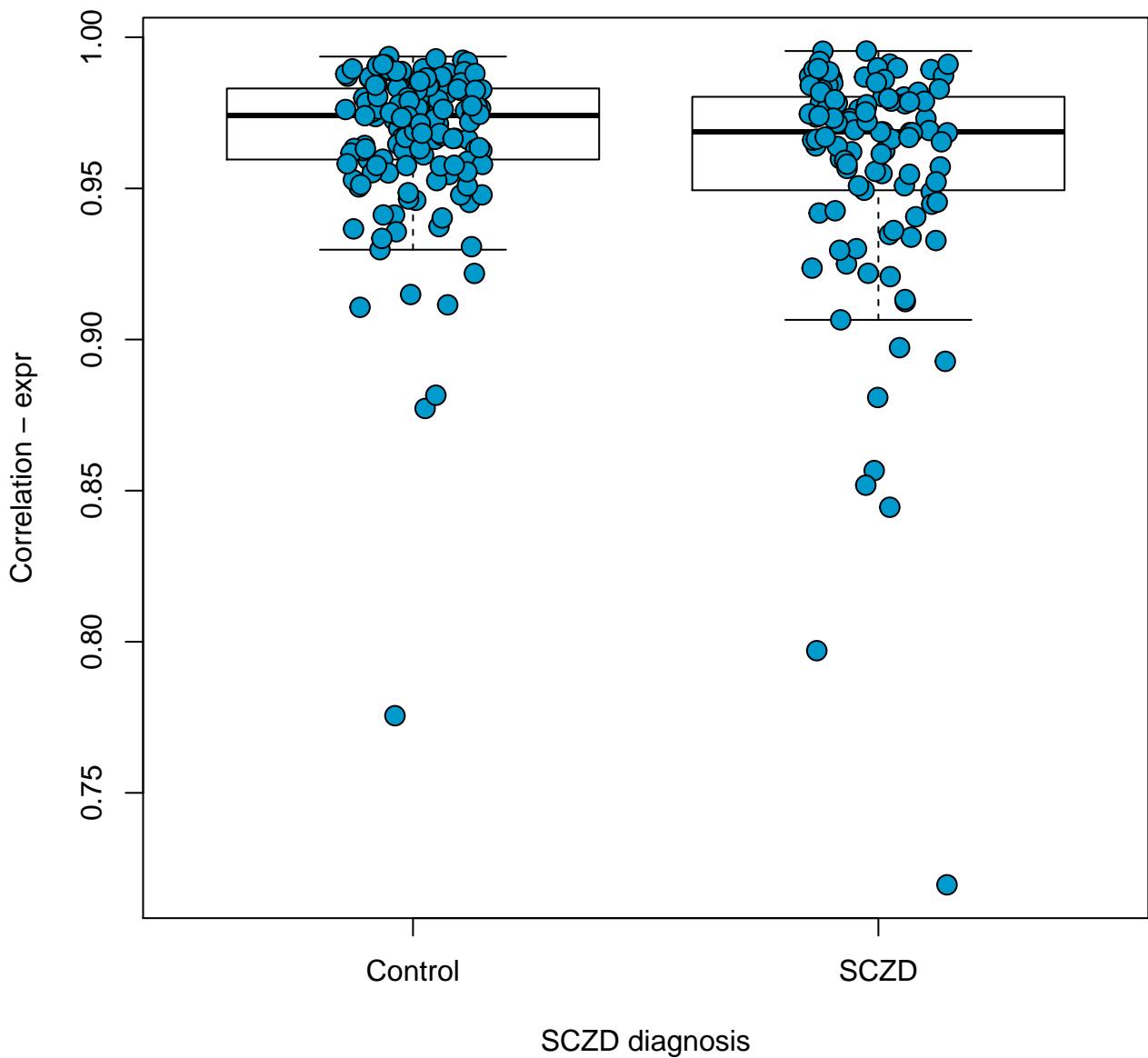


hsa00072: Synthesis and degradation of ketone bodies

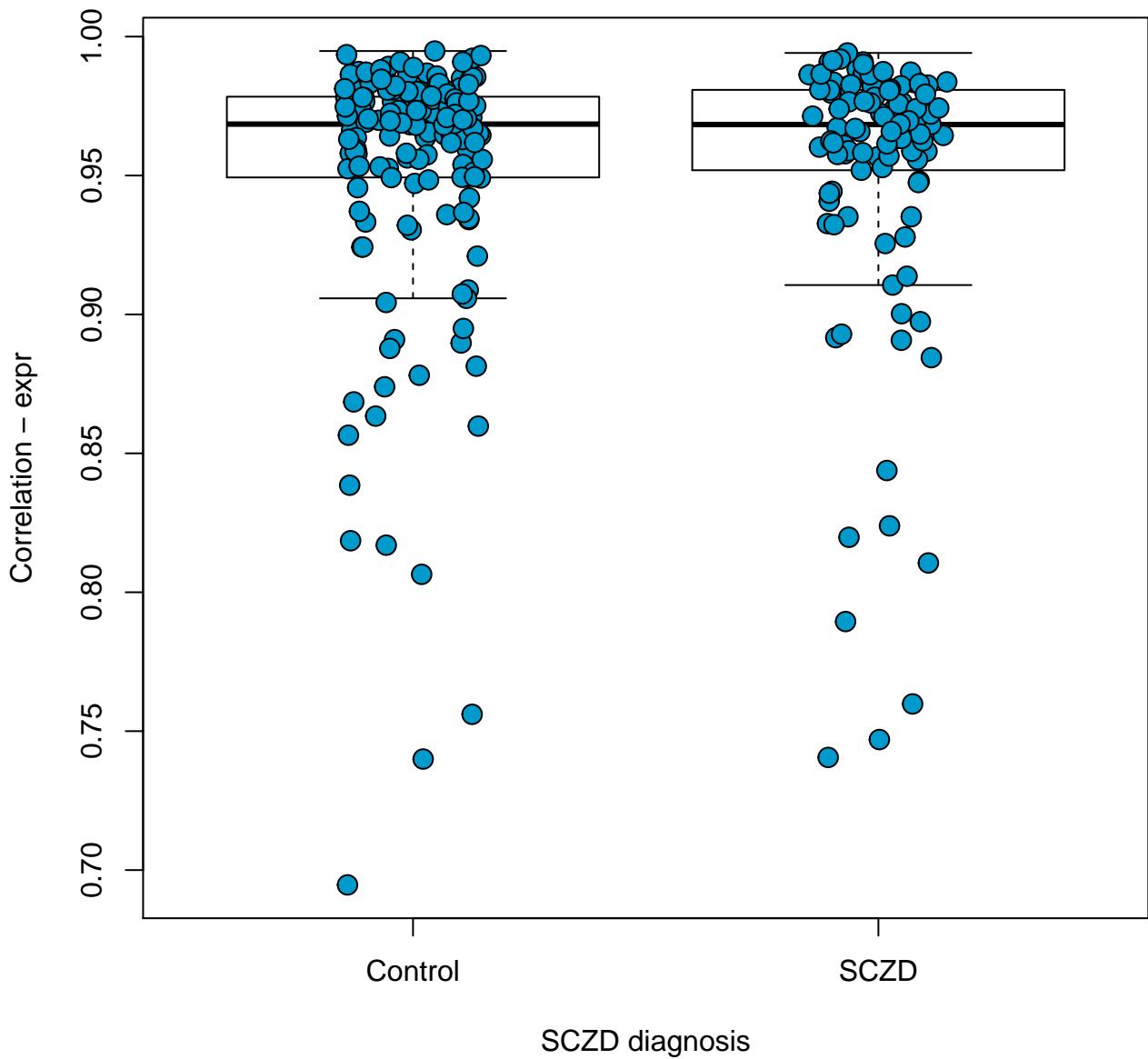
p-value: 0.698



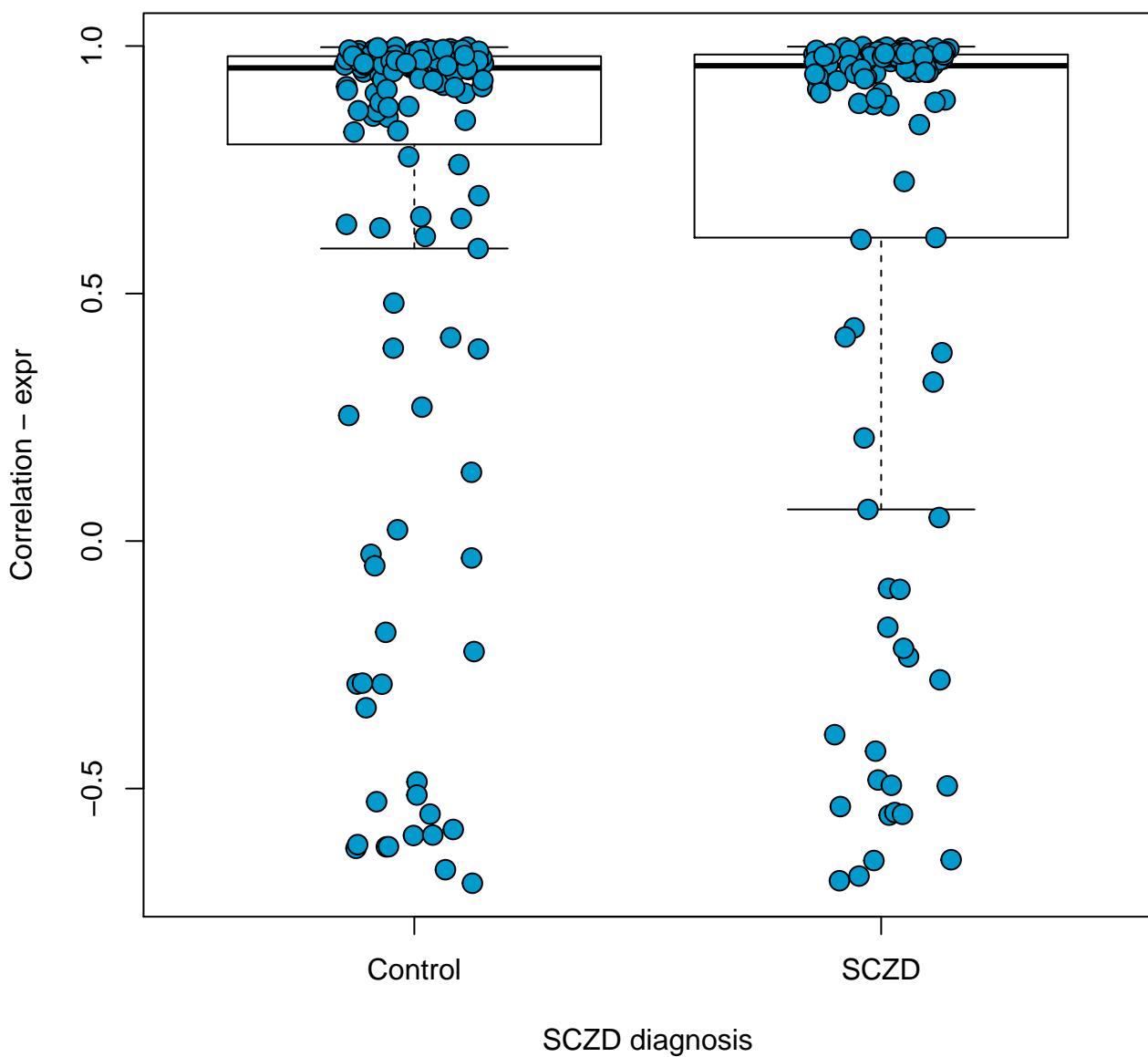
hsa00100: Steroid biosynthesis
p-value: 0.0117



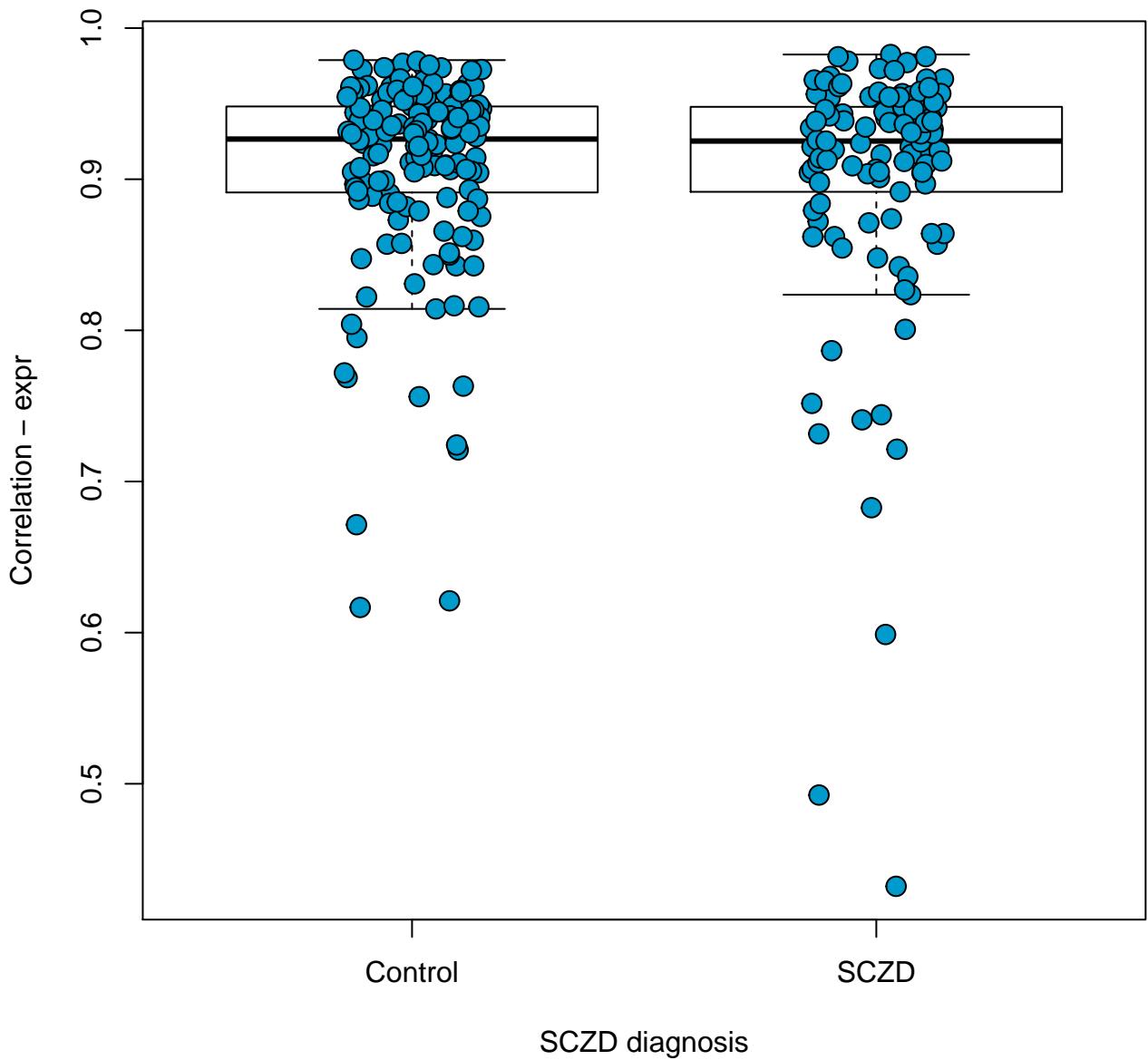
hsa00120: Primary bile acid biosynthesis
p-value: 0.936



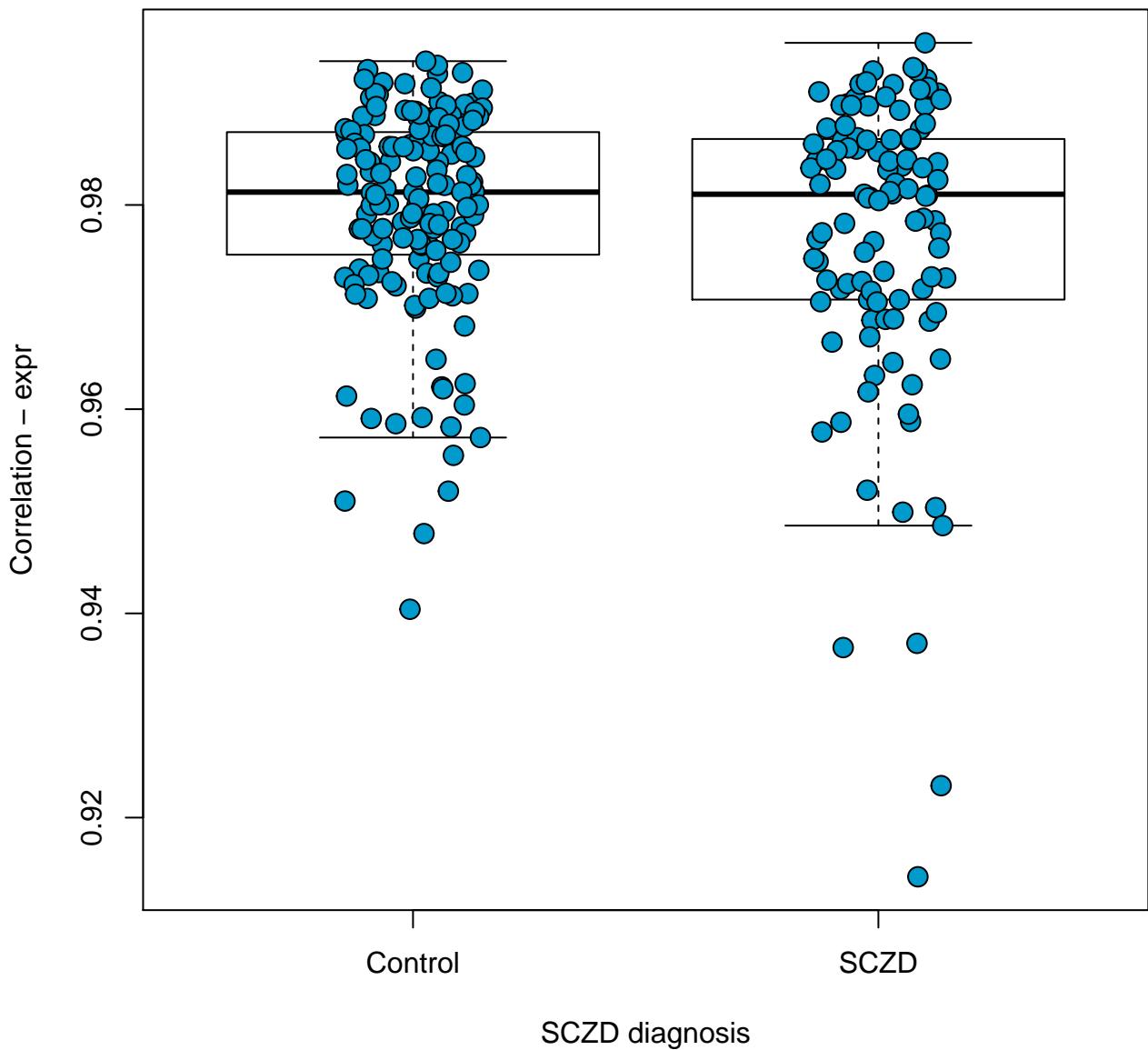
hsa00130: Ubiquinone and other terpenoid–quinone biosynthesis
p-value: 0.484



hsa00140: Steroid hormone biosynthesis
p-value: 0.366

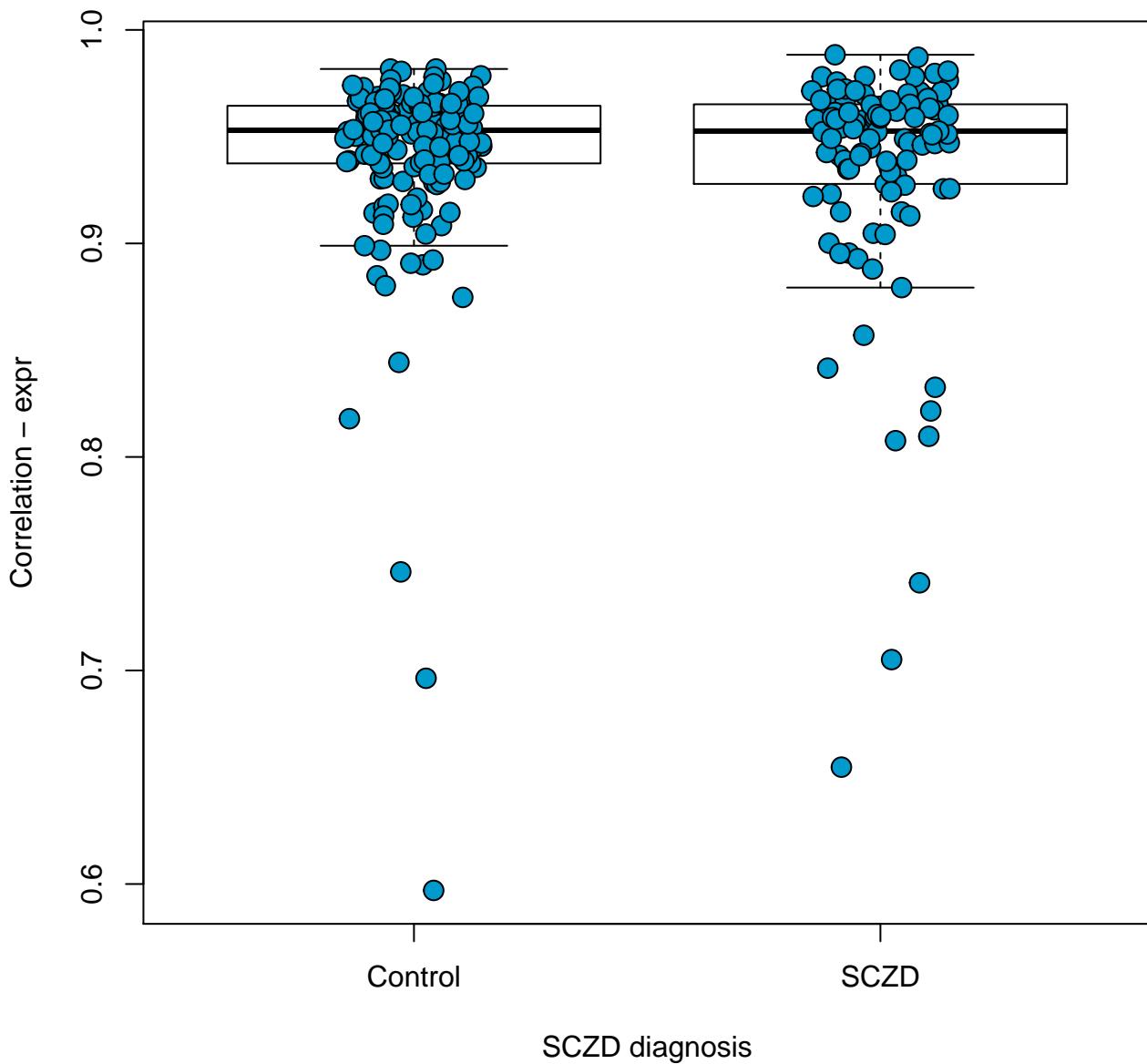


hsa00190: Oxidative phosphorylation
p-value: 0.0848

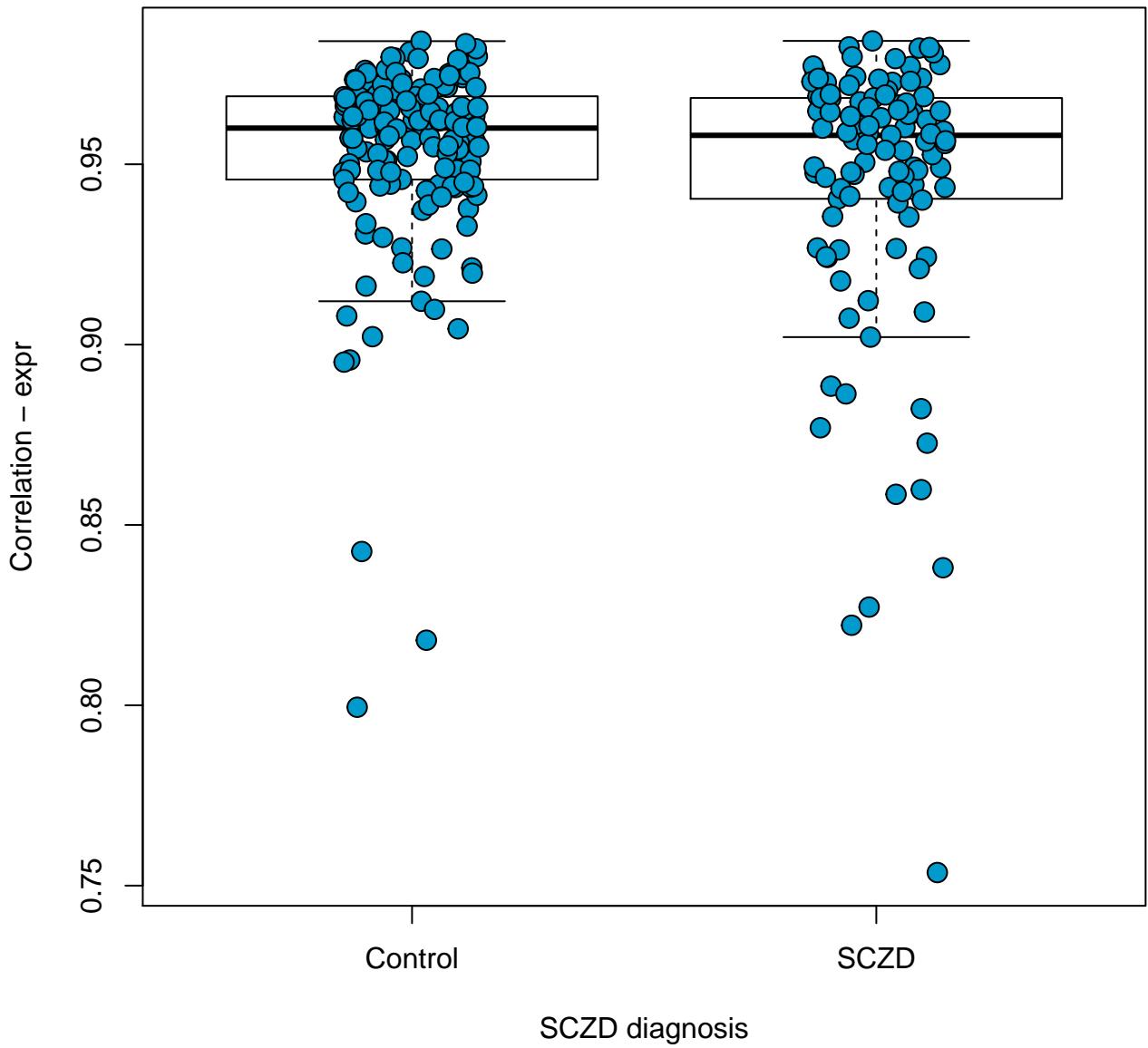


hsa00230: Purine metabolism

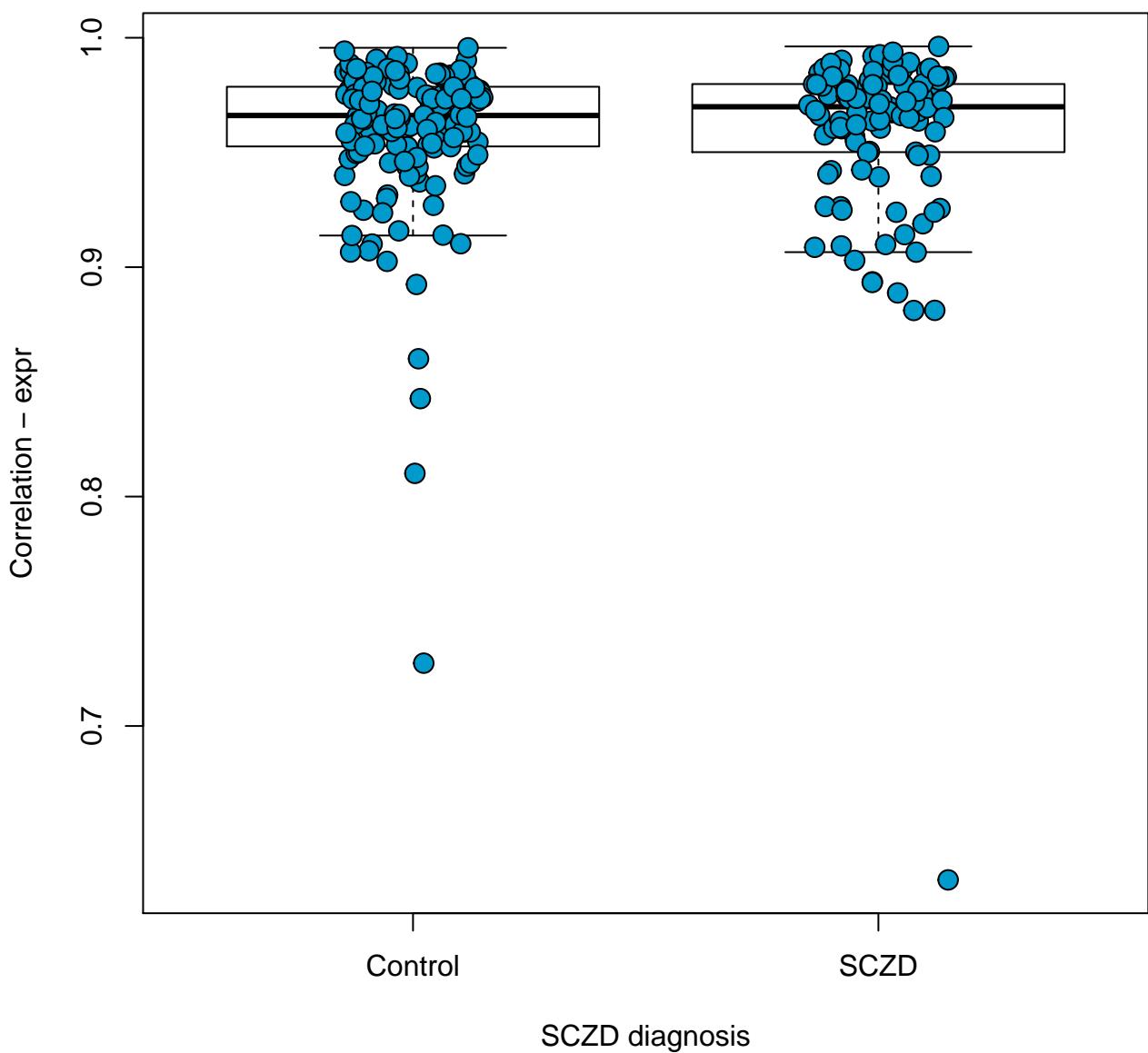
p-value: 0.381



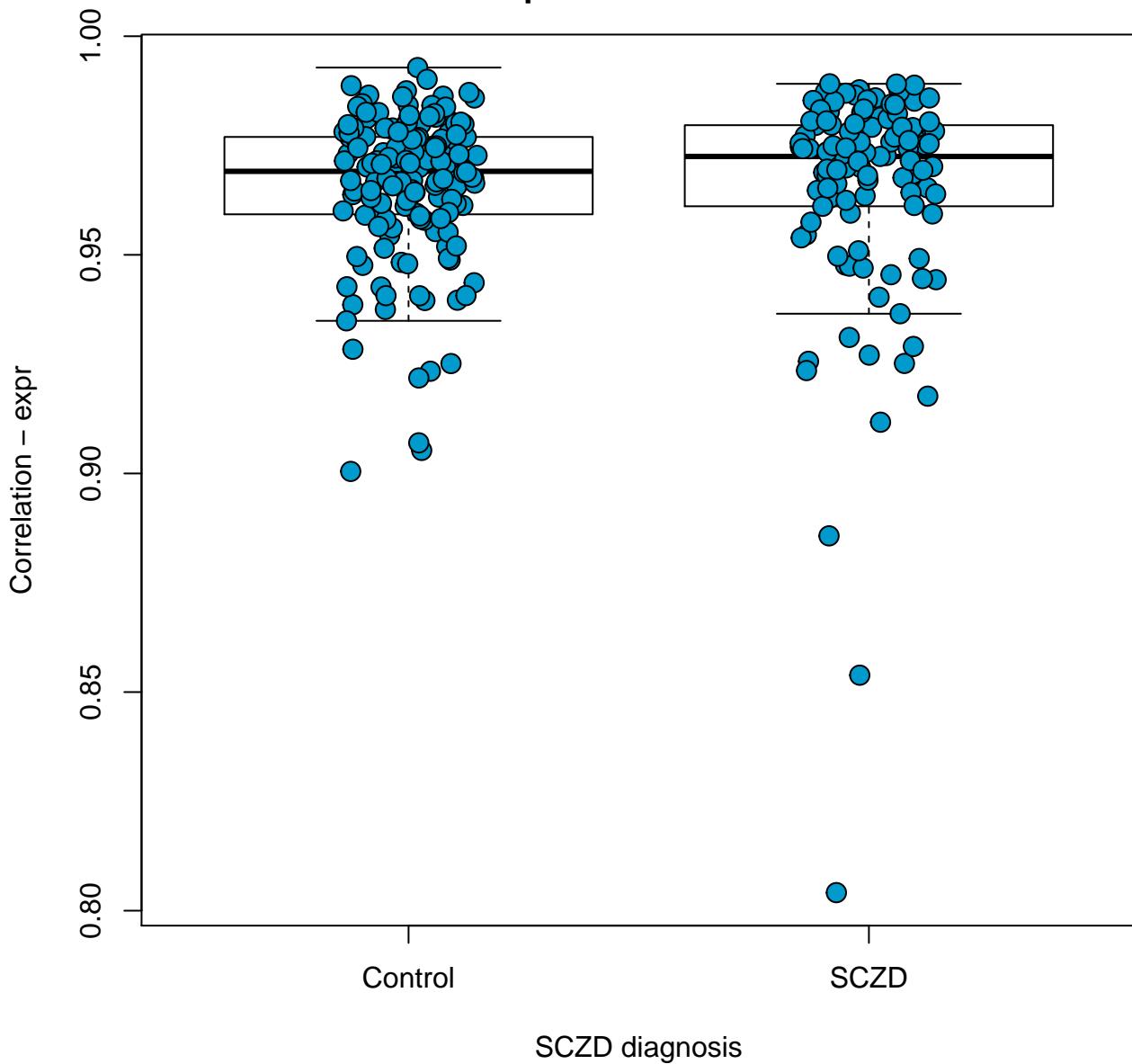
hsa00240: Pyrimidine metabolism
p-value: 0.0412



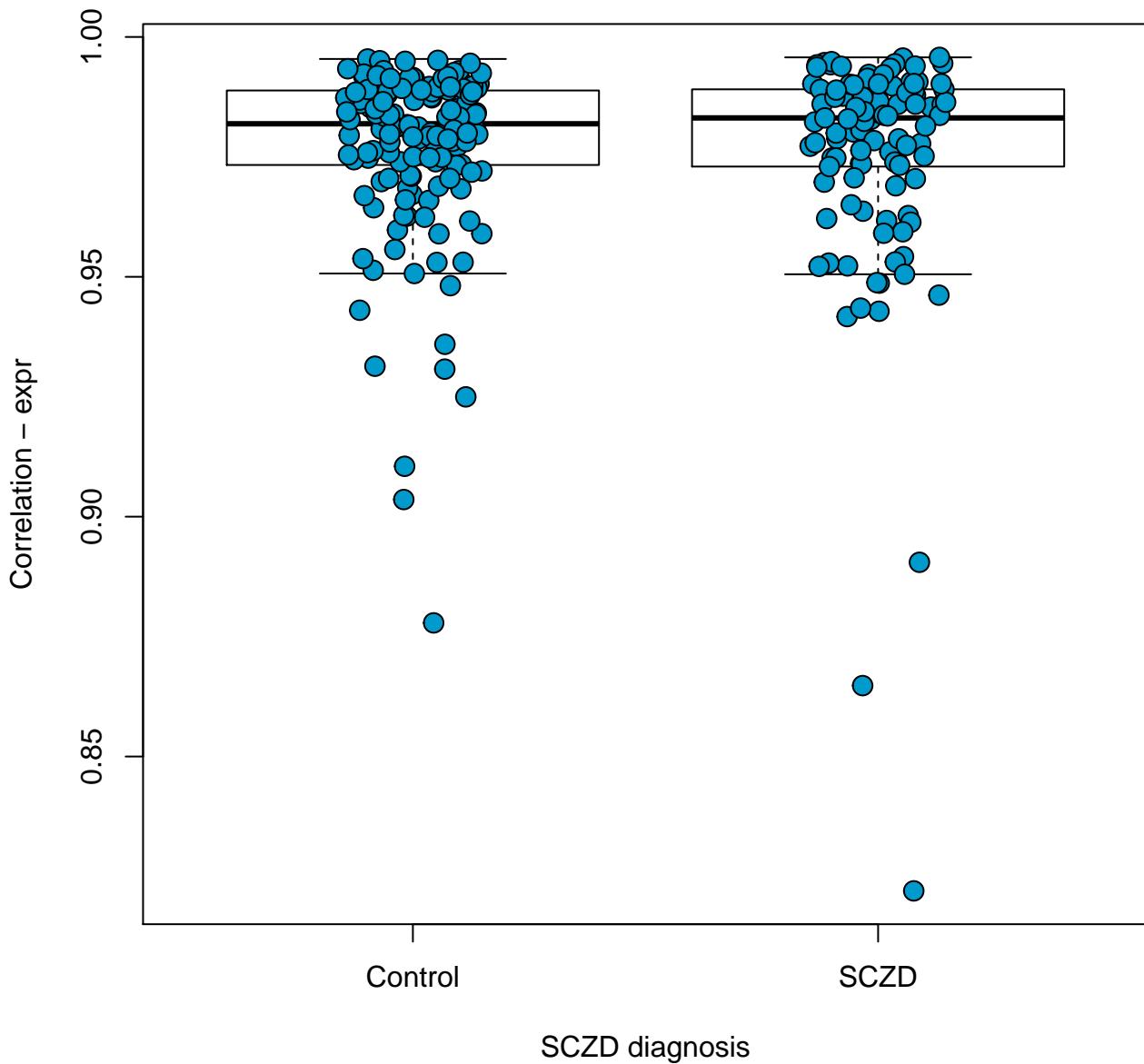
hsa00250: Alanine, aspartate and glutamate metabolism
p-value: 0.866



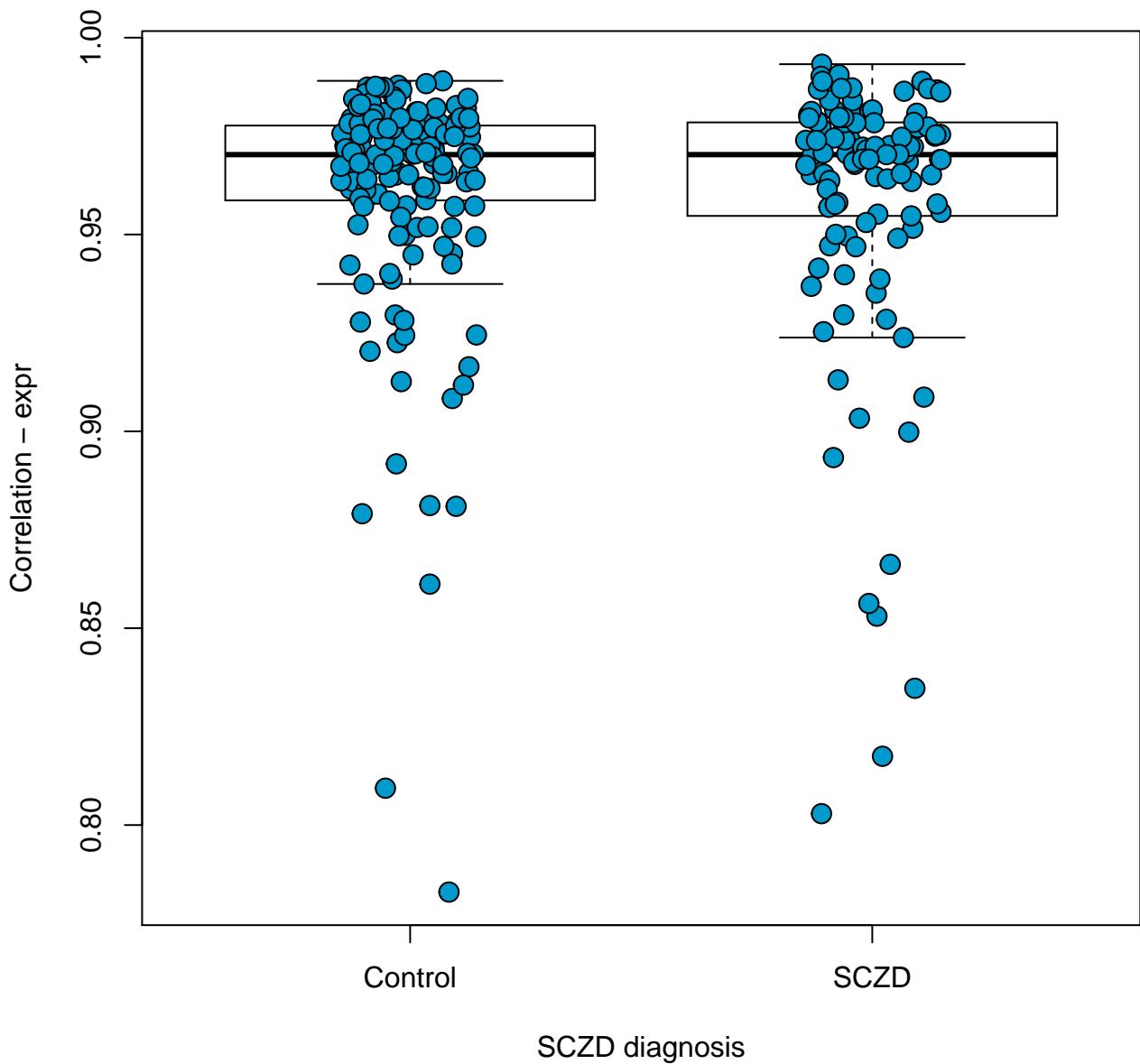
hsa00260: Glycine, serine and threonine metabolism
p-value: 0.623



hsa00270: Cysteine and methionine metabolism
p-value: 0.481

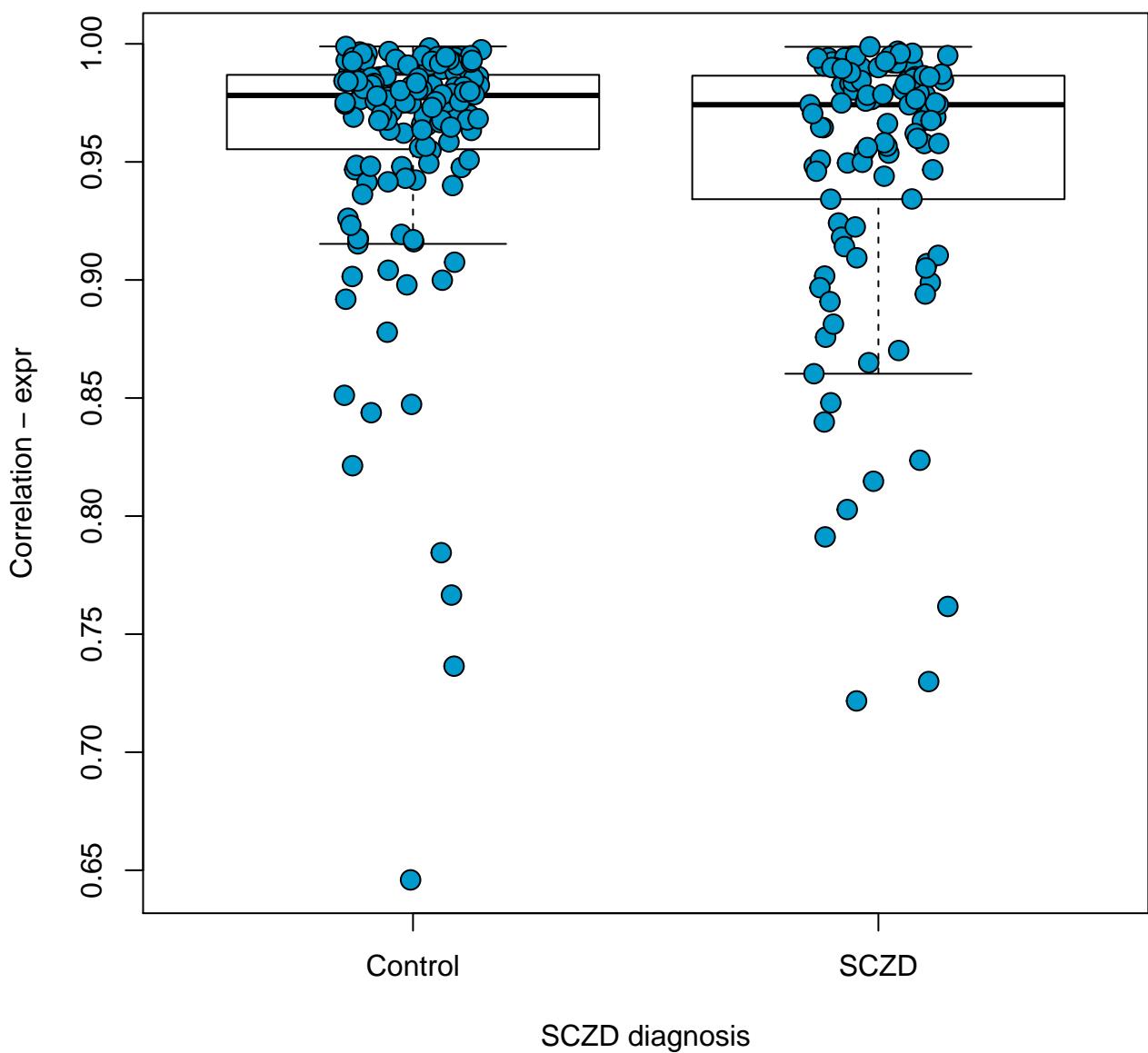


hsa00280: Valine, leucine and isoleucine degradation
p-value: 0.449

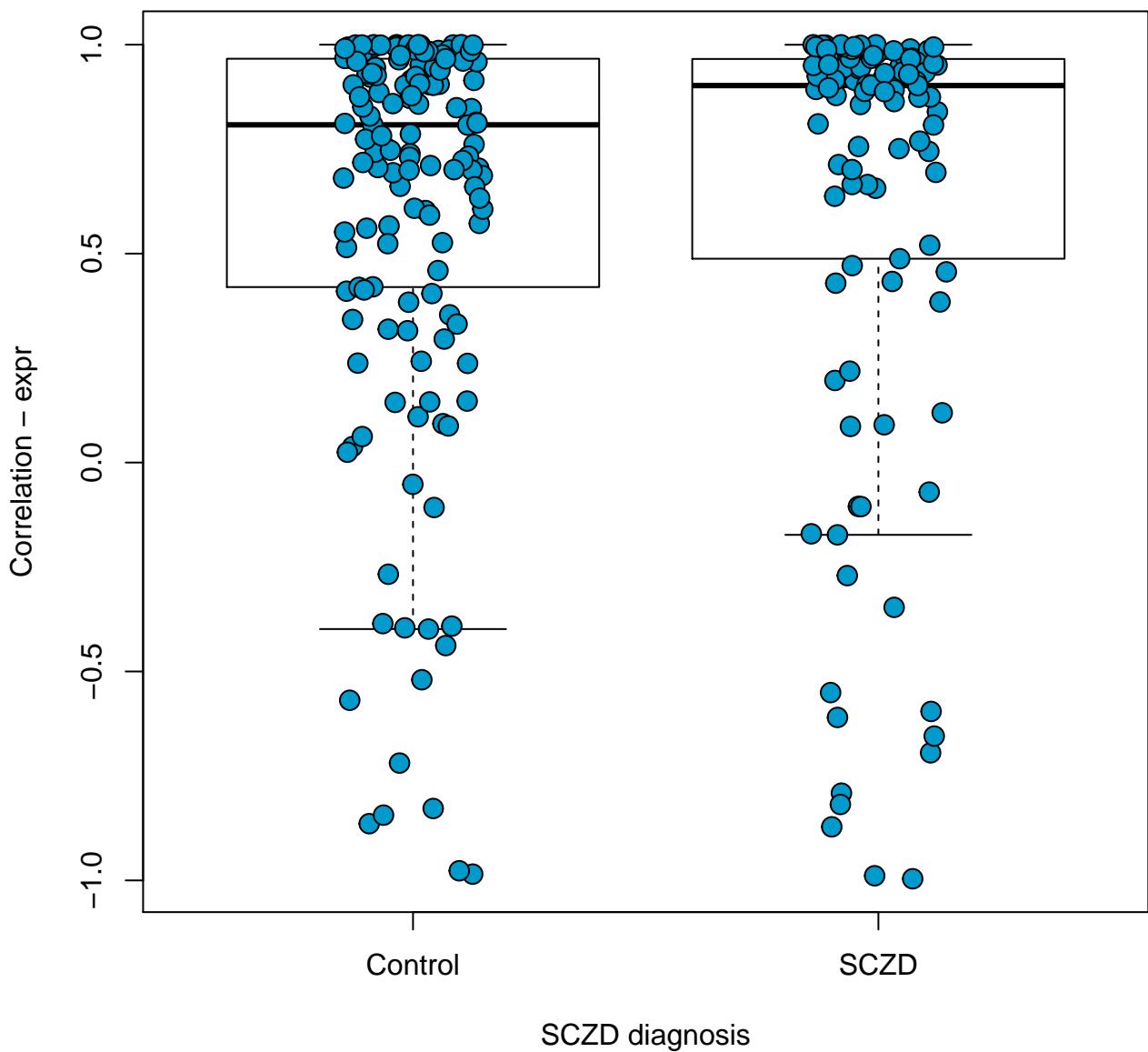


hsa00290: Valine, leucine and isoleucine biosynthesis

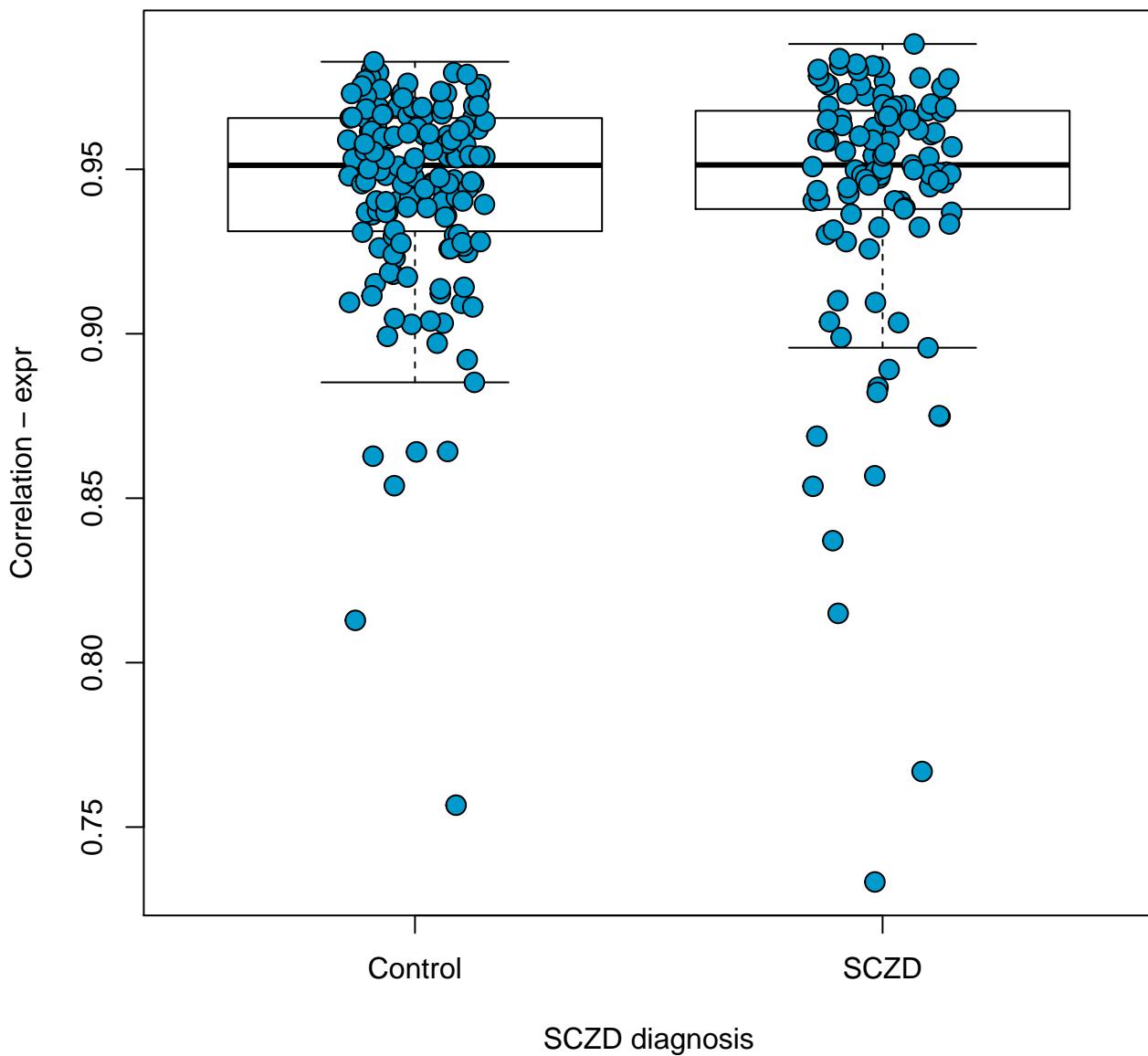
p-value: 0.0549



hsa00300: Lysine biosynthesis
p-value: 0.959

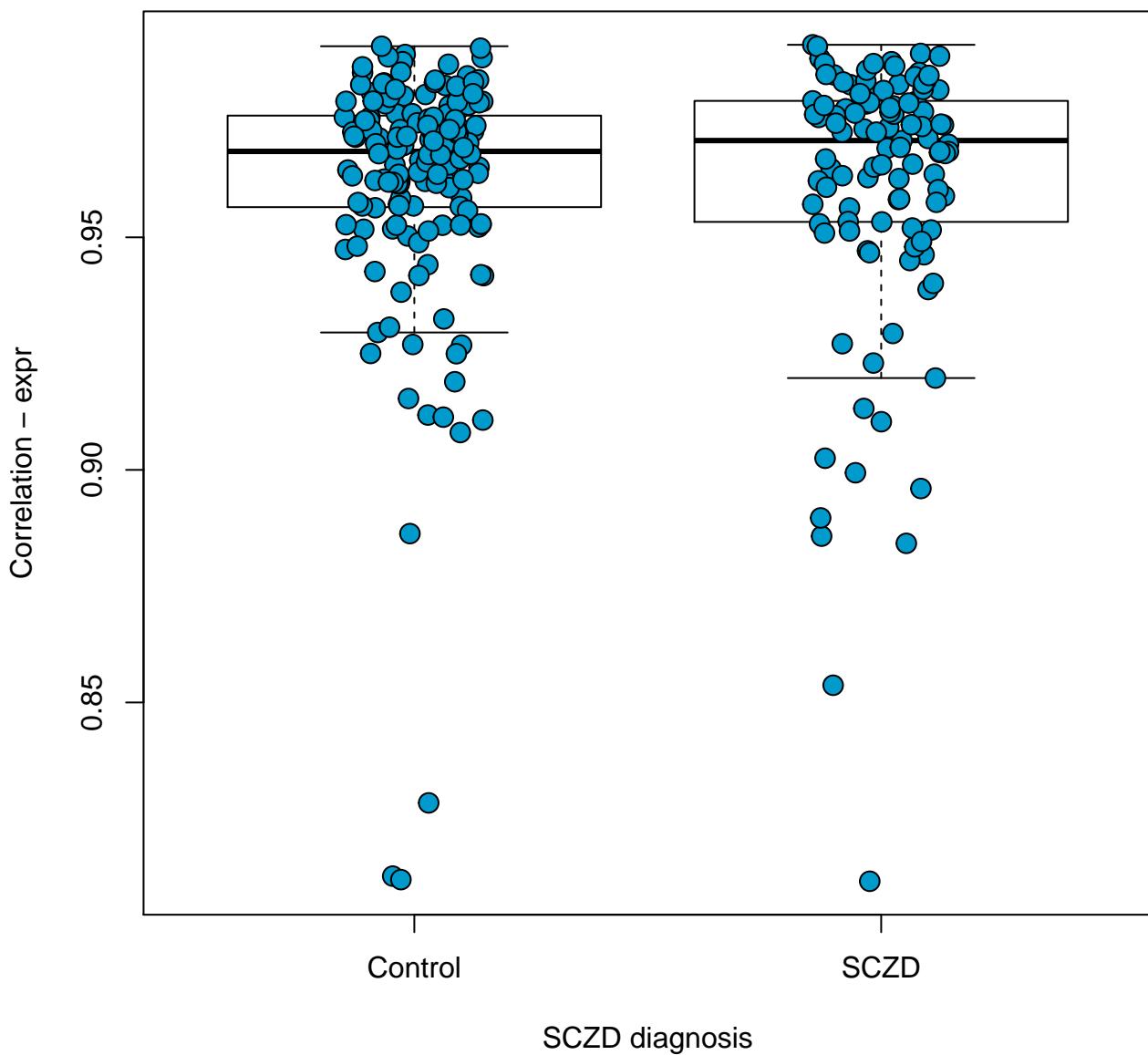


hsa00310: Lysine degradation
p-value: 0.712

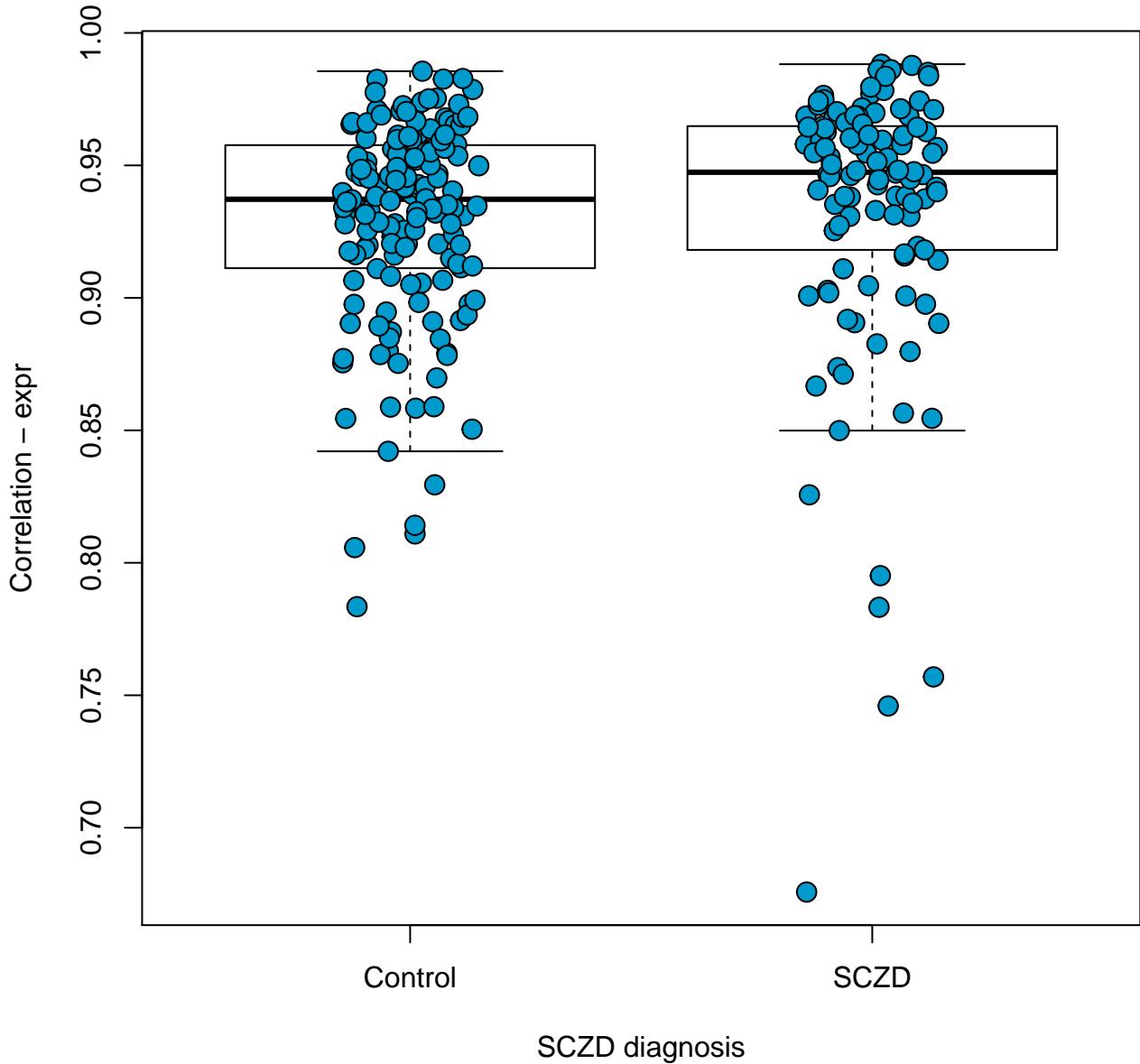


hsa00330: Arginine and proline metabolism

p-value: 0.973

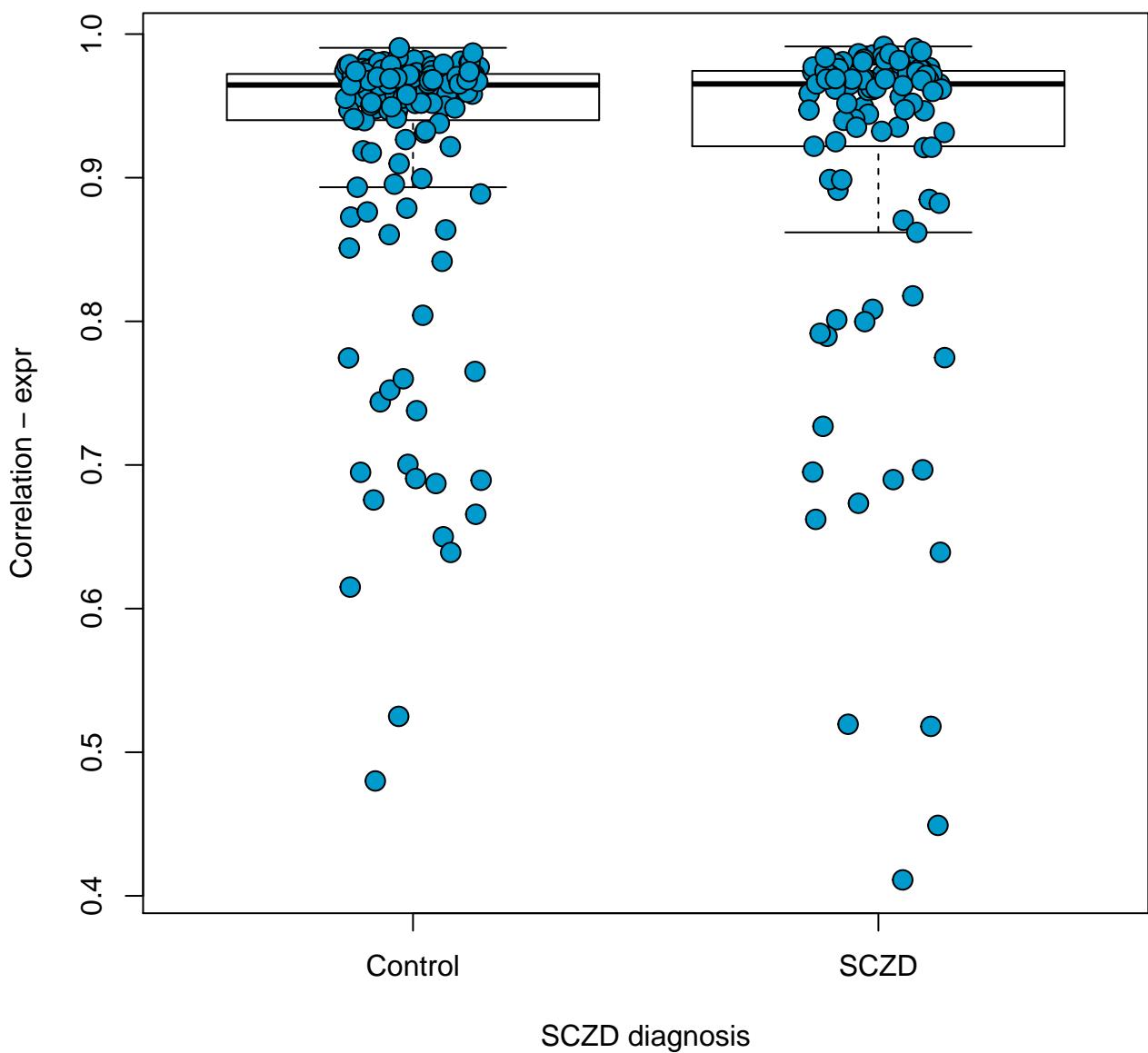


hsa00340: Histidine metabolism
p-value: 0.508

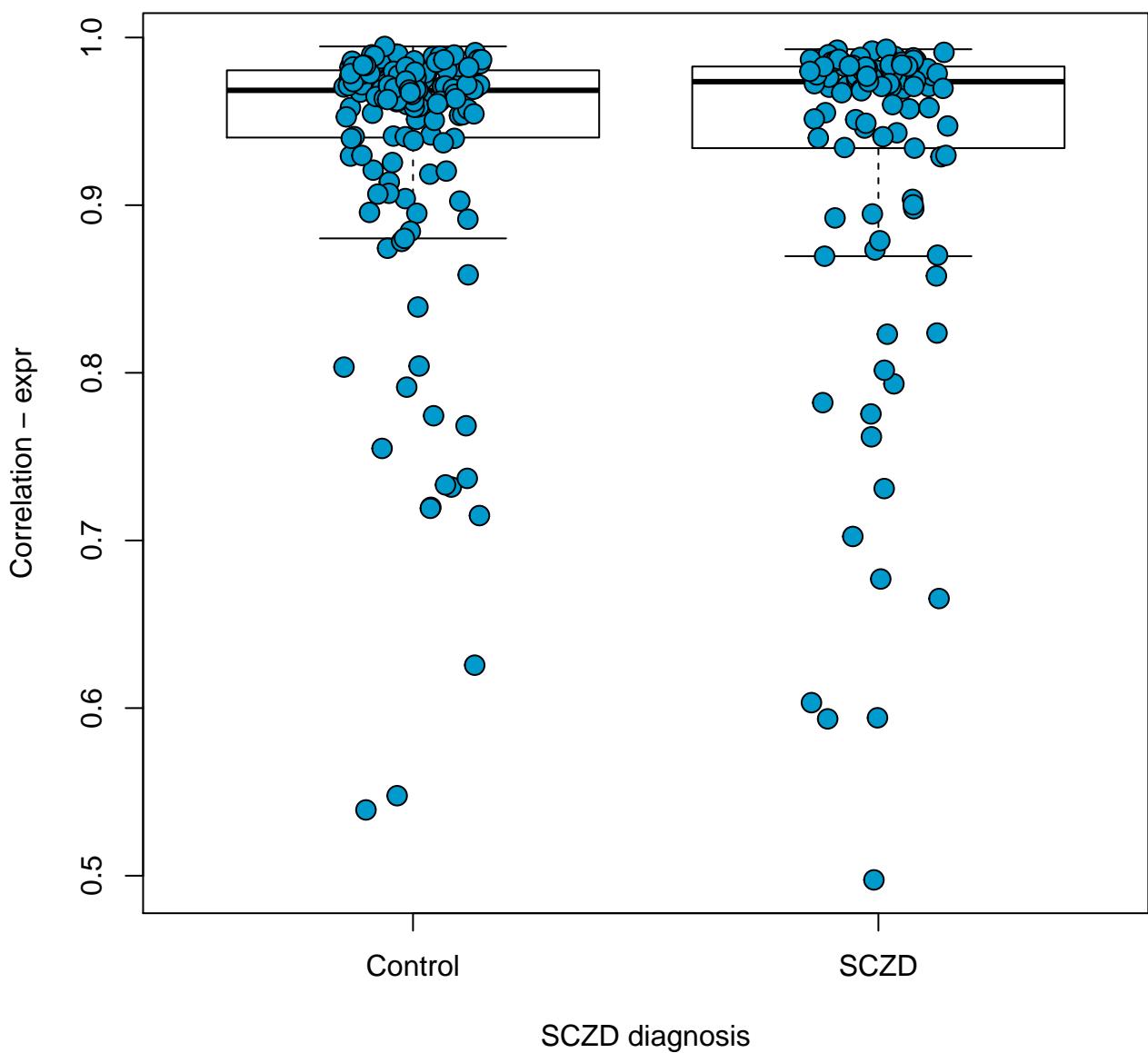


hsa00350: Tyrosine metabolism

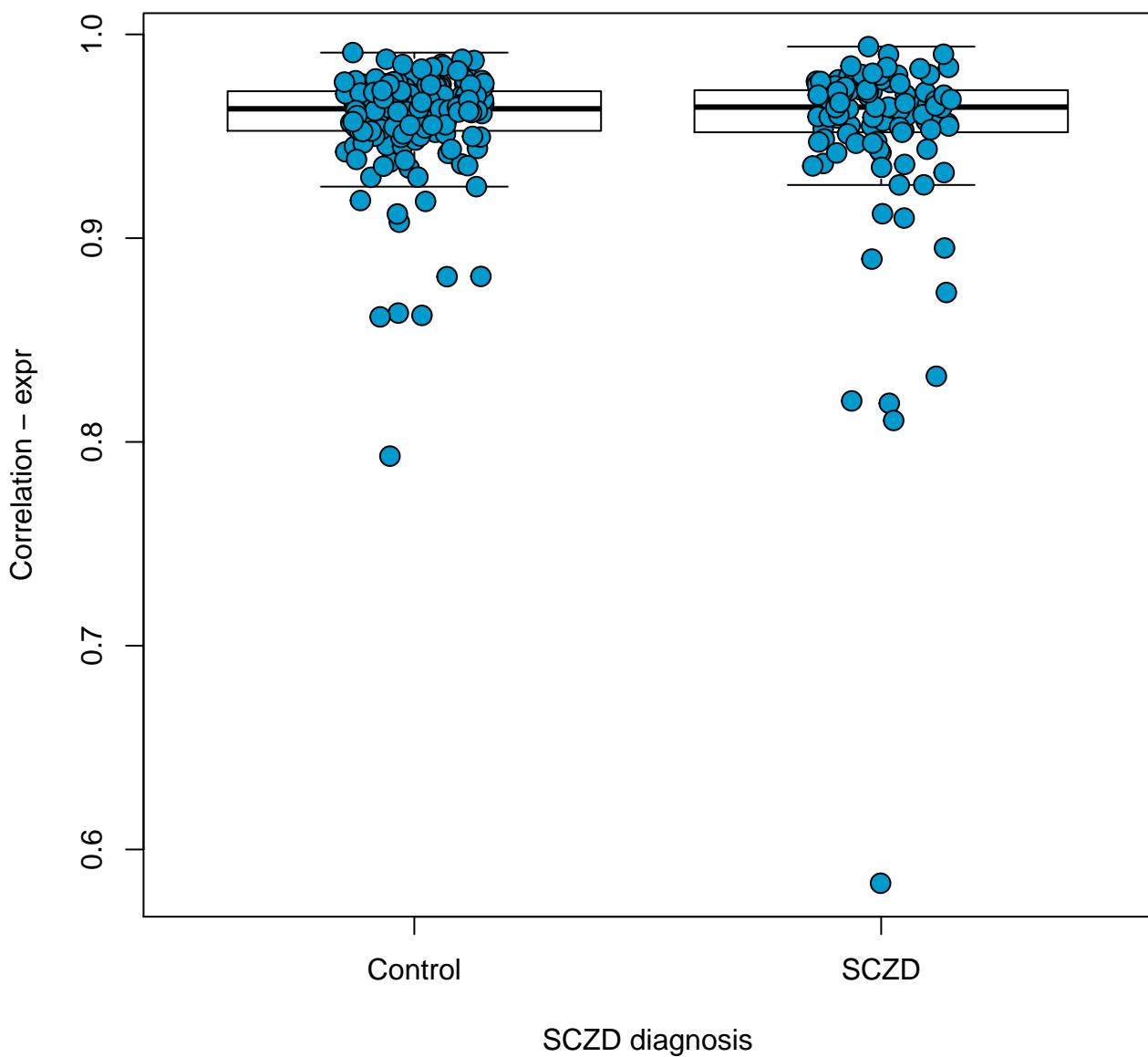
p-value: 0.438



hsa00360: Phenylalanine metabolism
p-value: 0.422

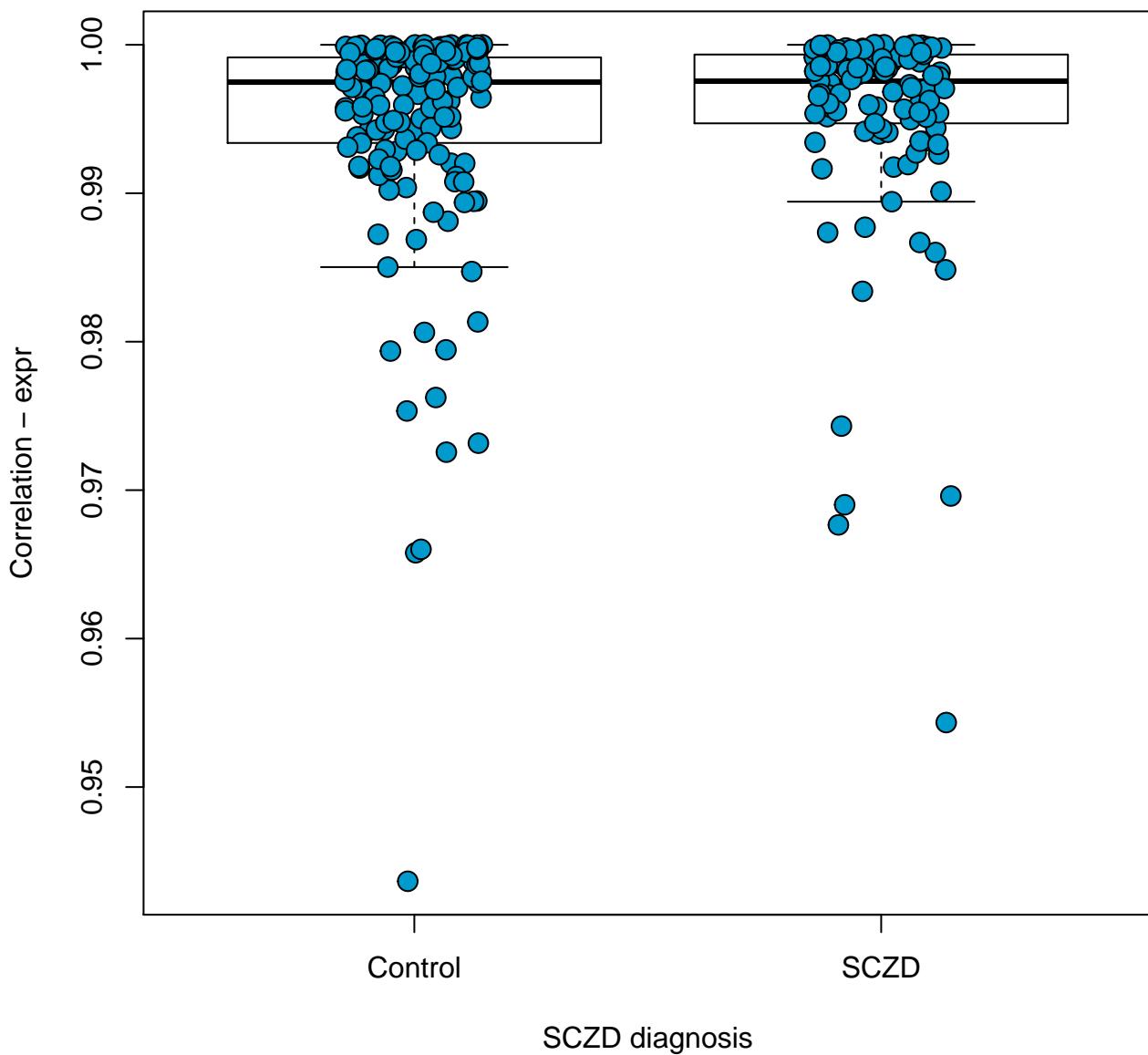


hsa00380: Tryptophan metabolism
p-value: 0.203

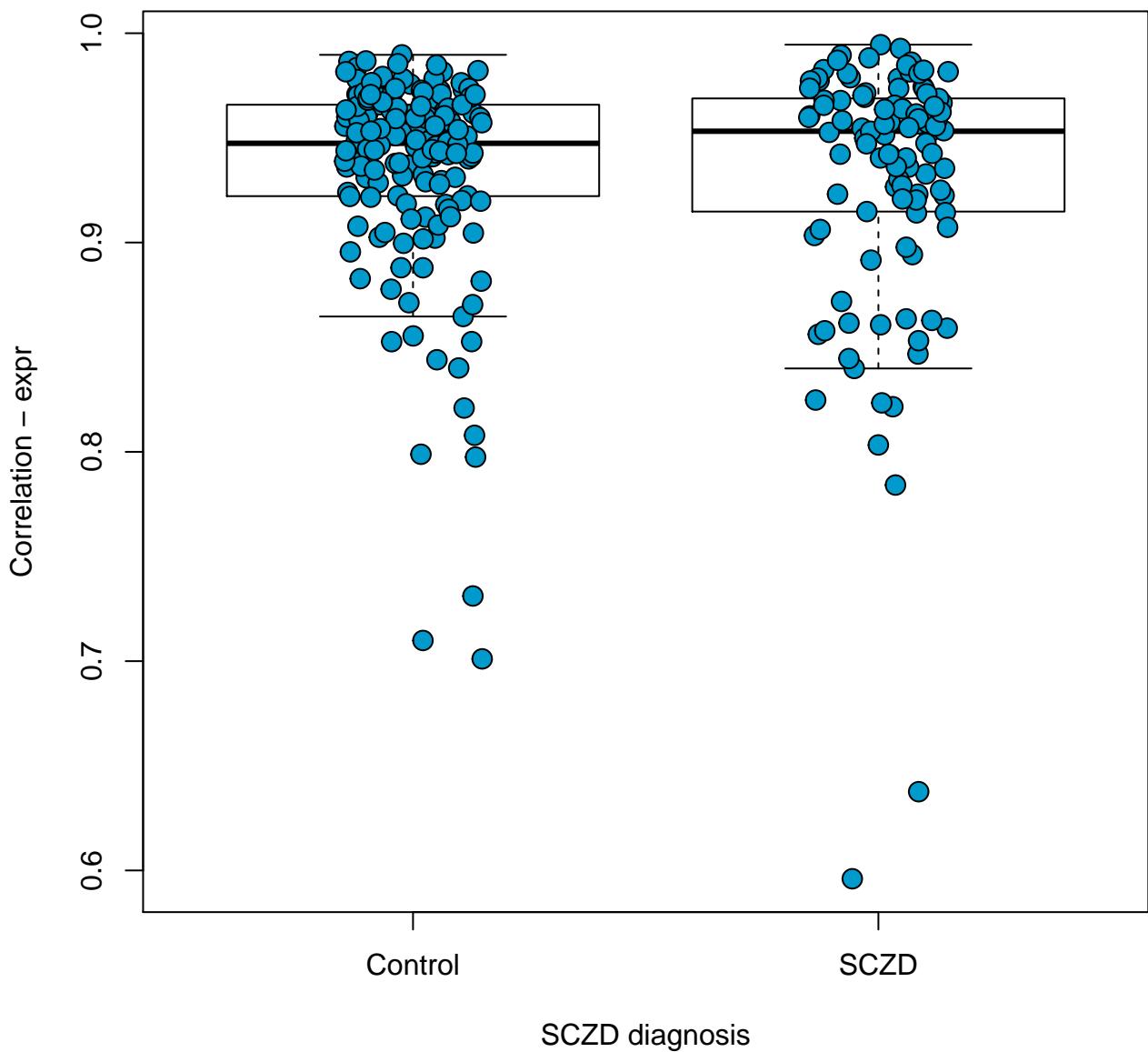


hsa00400: Phenylalanine, tyrosine and tryptophan biosynthesis

p-value: 0.642

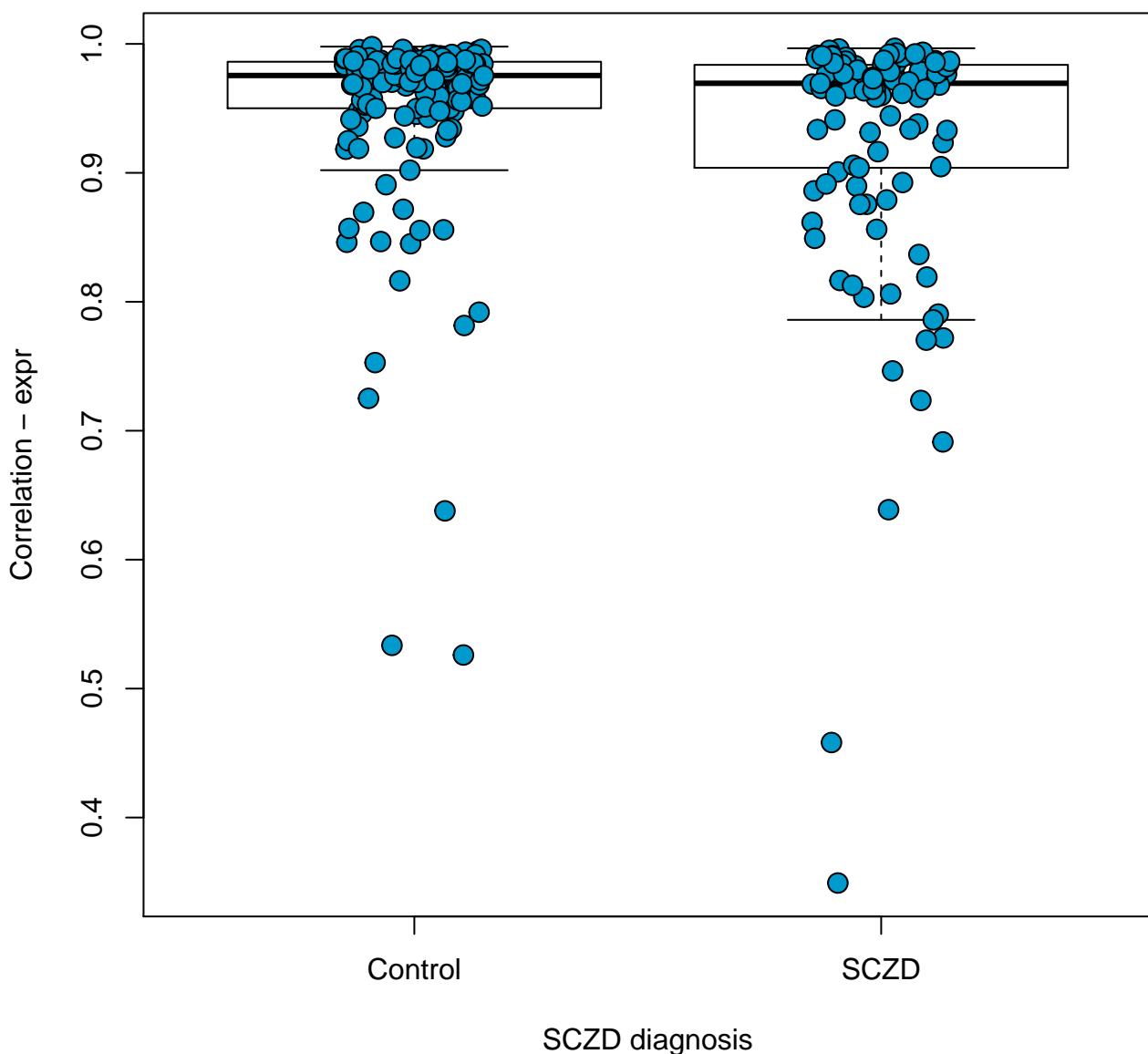


hsa00410: beta-Alanine metabolism
p-value: 0.505

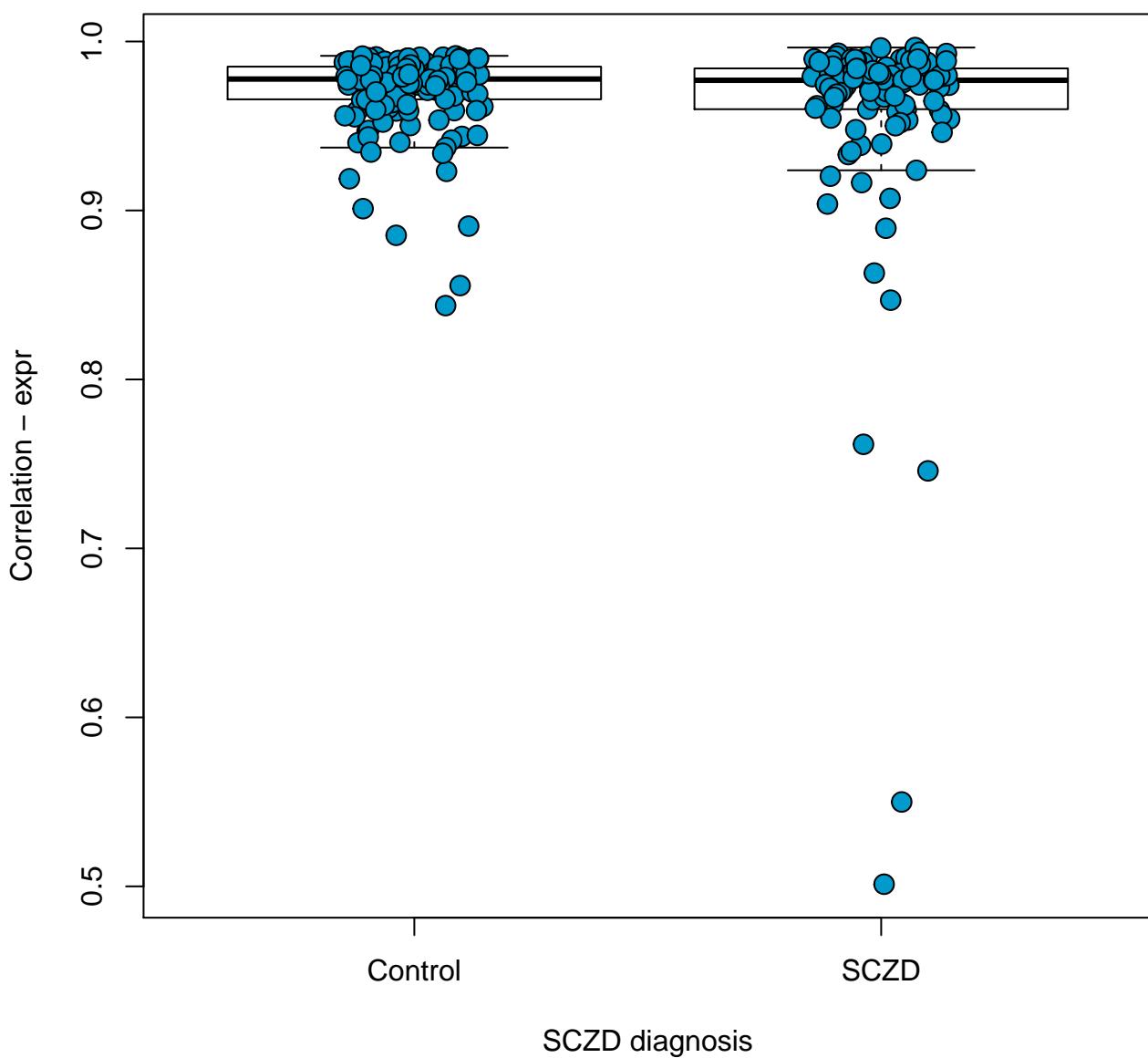


hsa00430: Taurine and hypotaurine metabolism

p-value: 0.0209

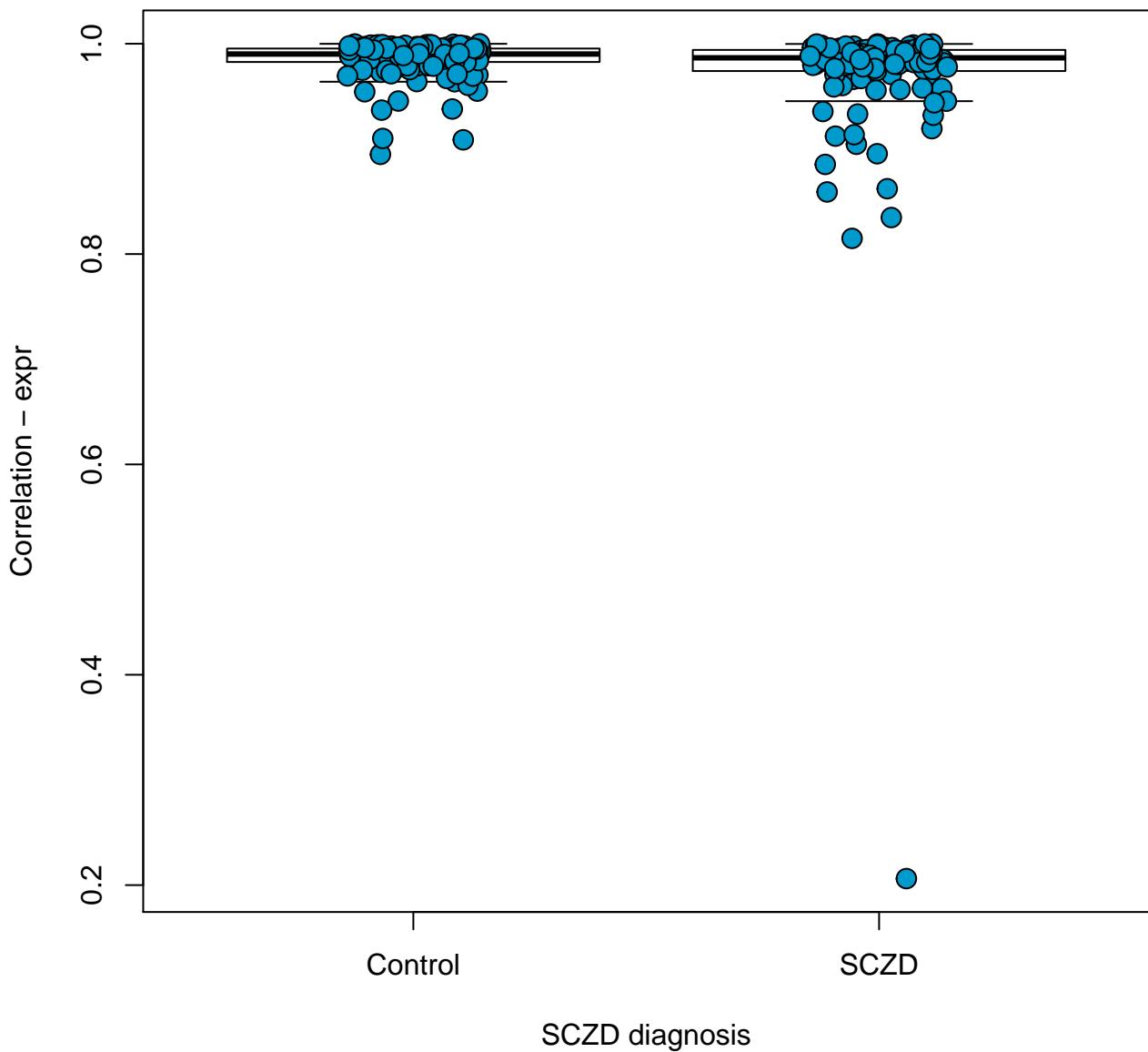


hsa00450: Selenocompound metabolism
p-value: 0.0207

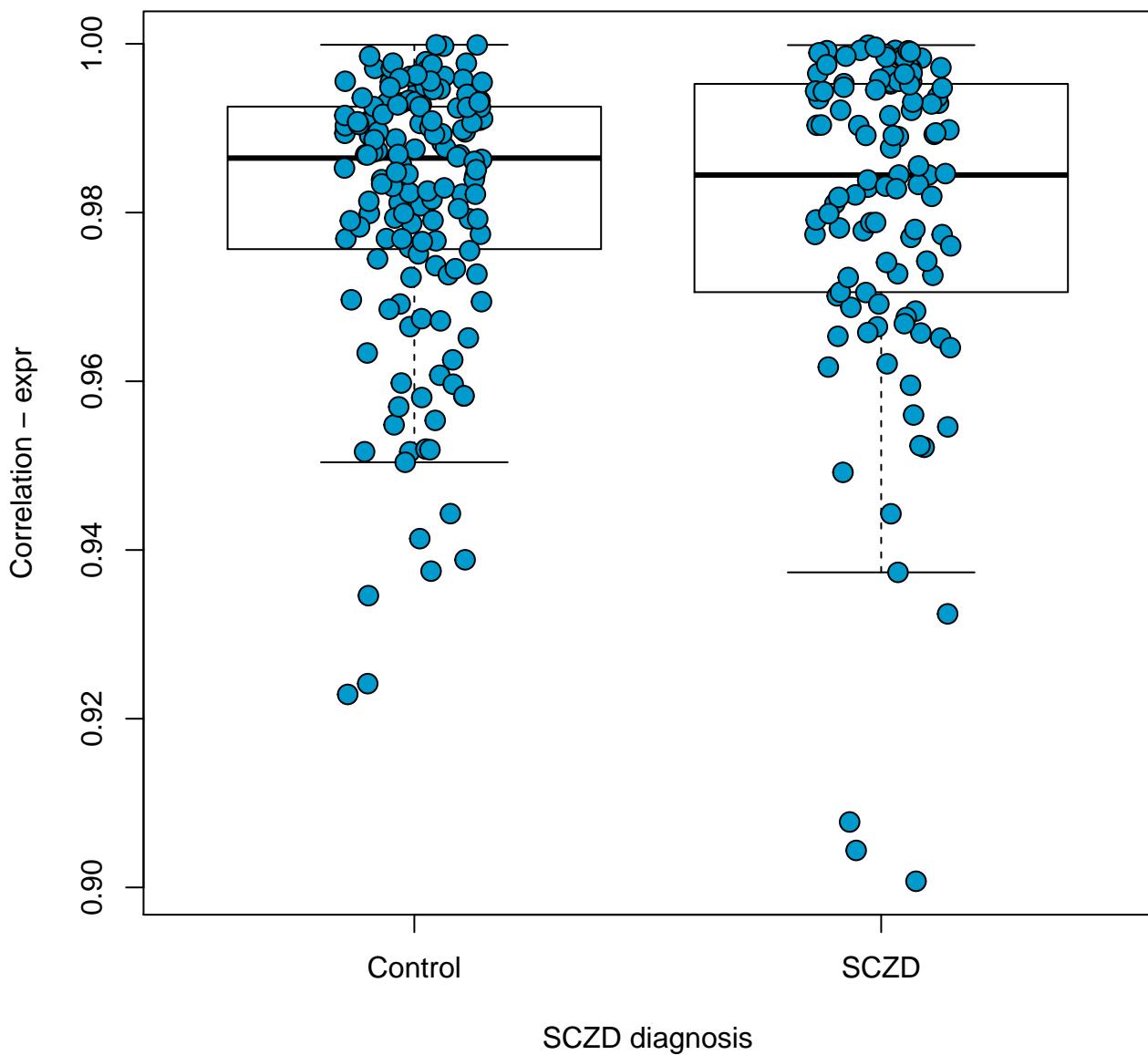


hsa00460: Cyanoamino acid metabolism

p-value: 0.00583

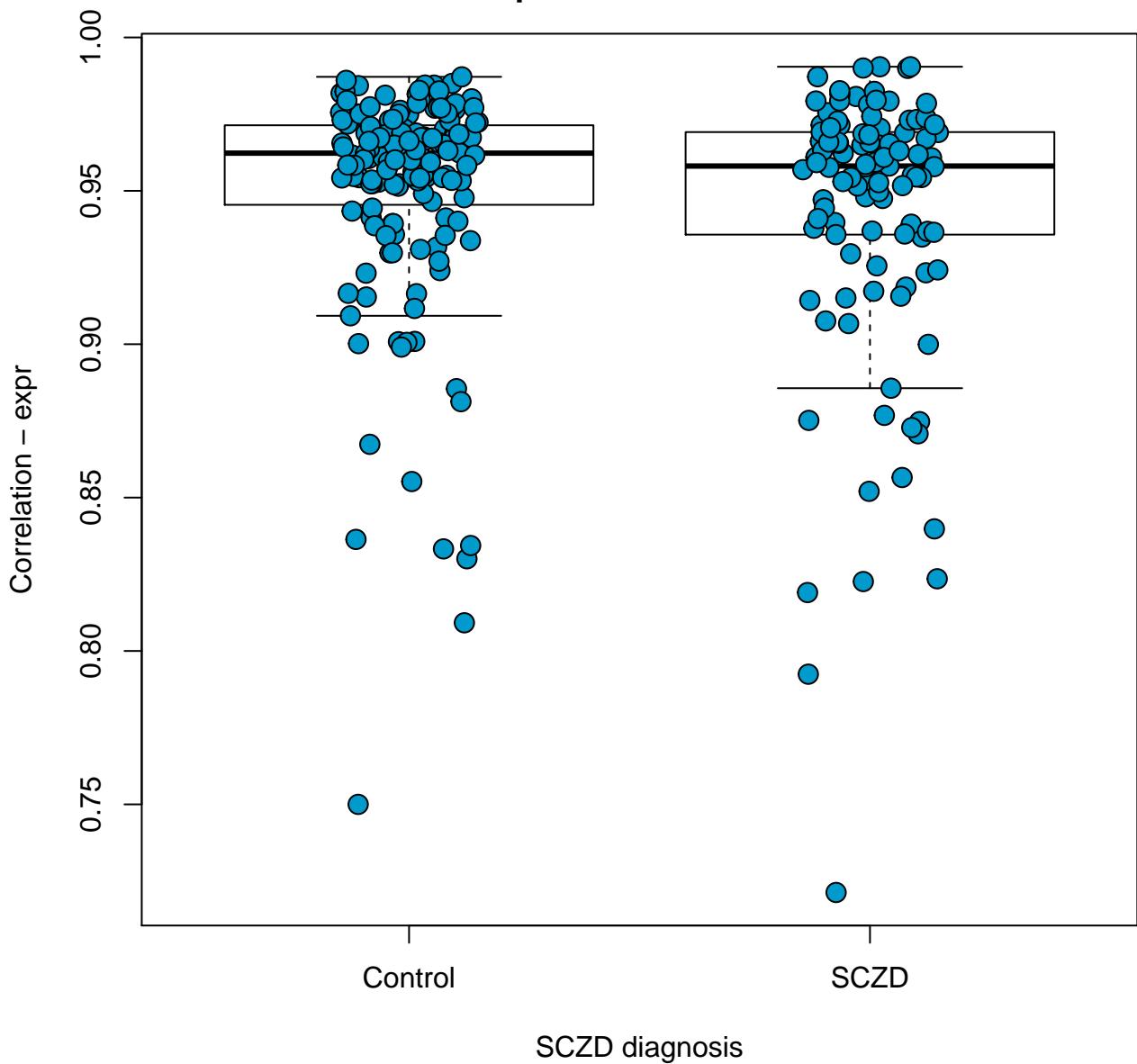


hsa00471: D-Glutamine and D-glutamate metabolism
p-value: 0.699

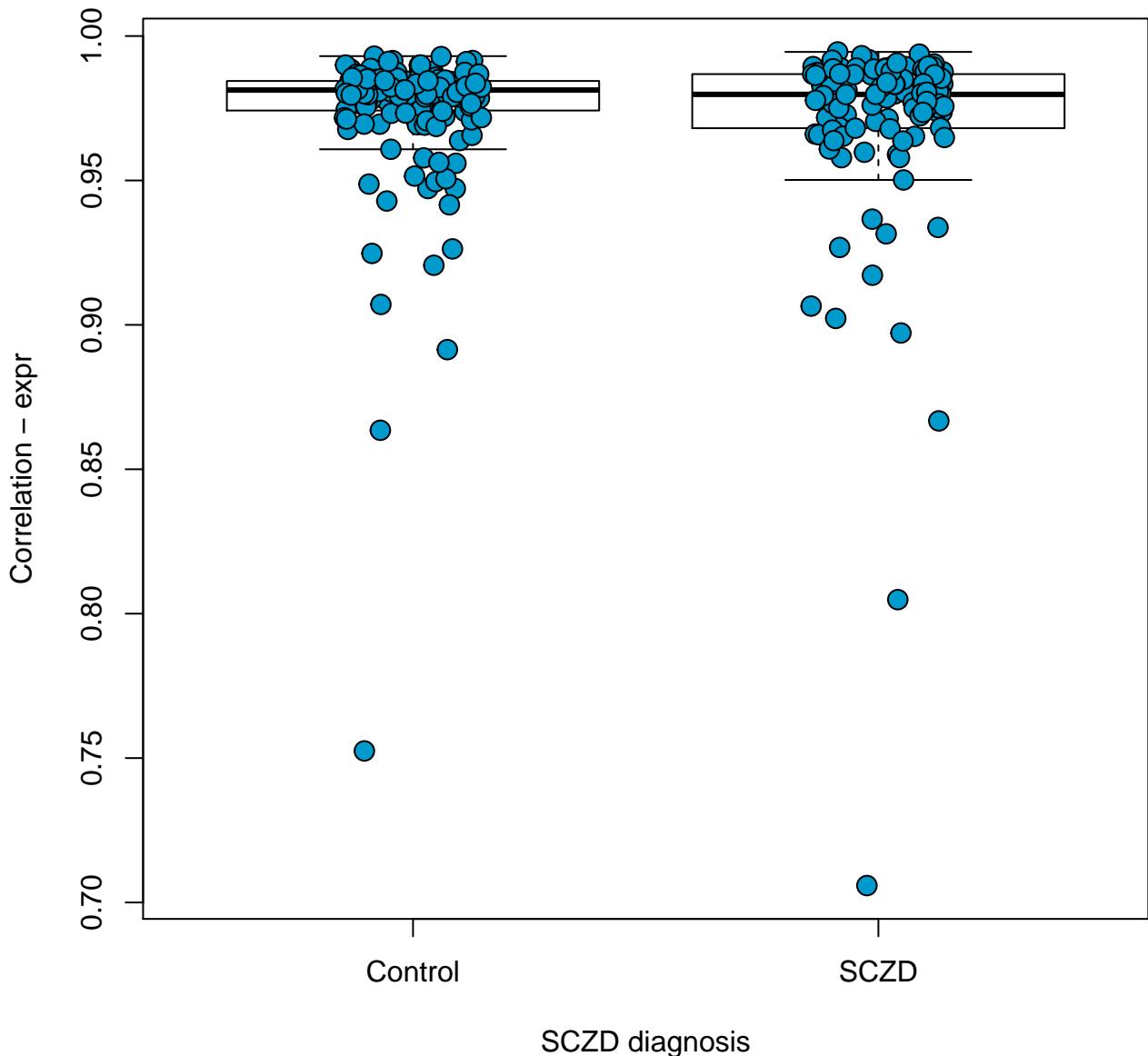


hsa00480: Glutathione metabolism

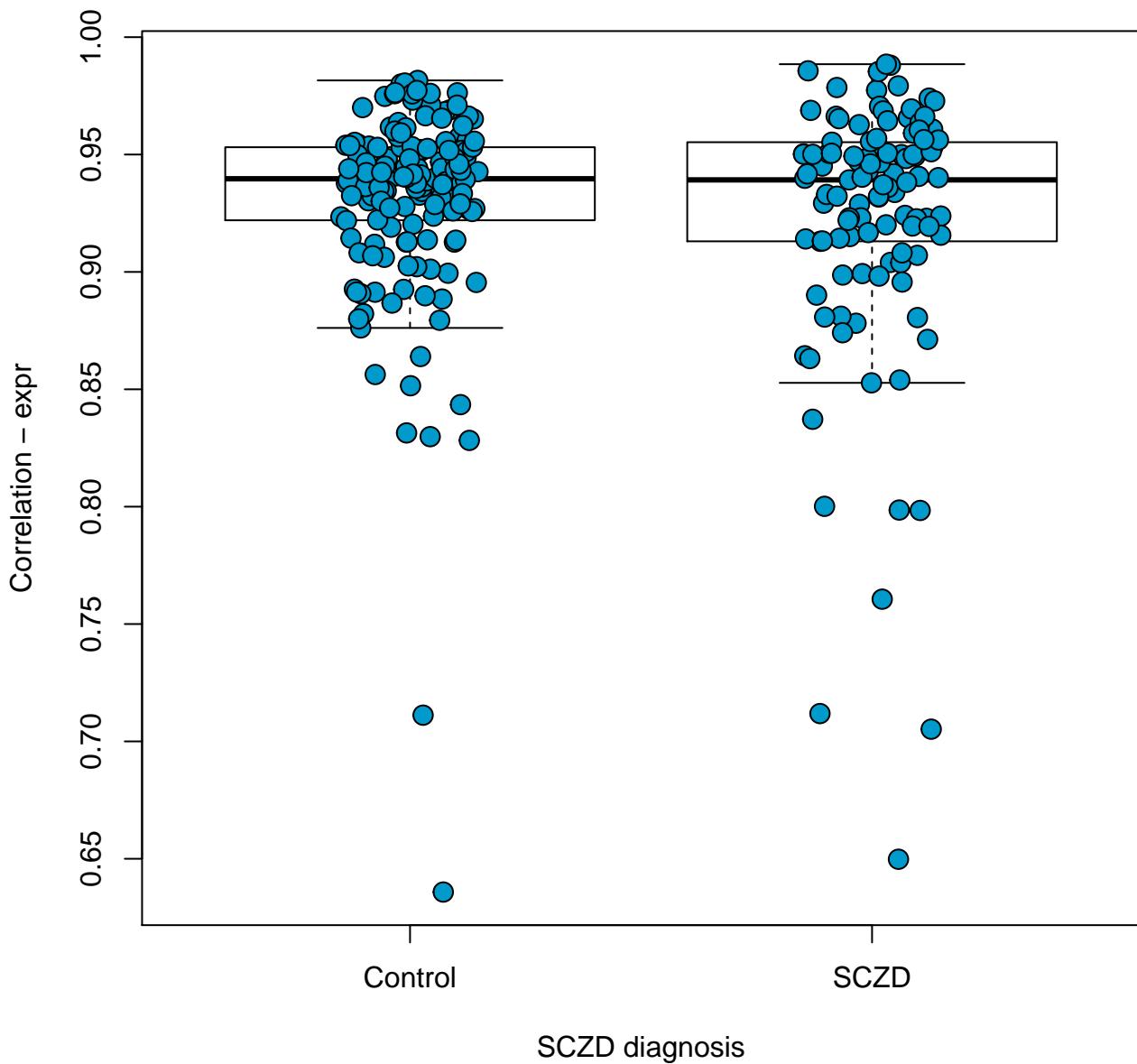
p-value: 0.0933



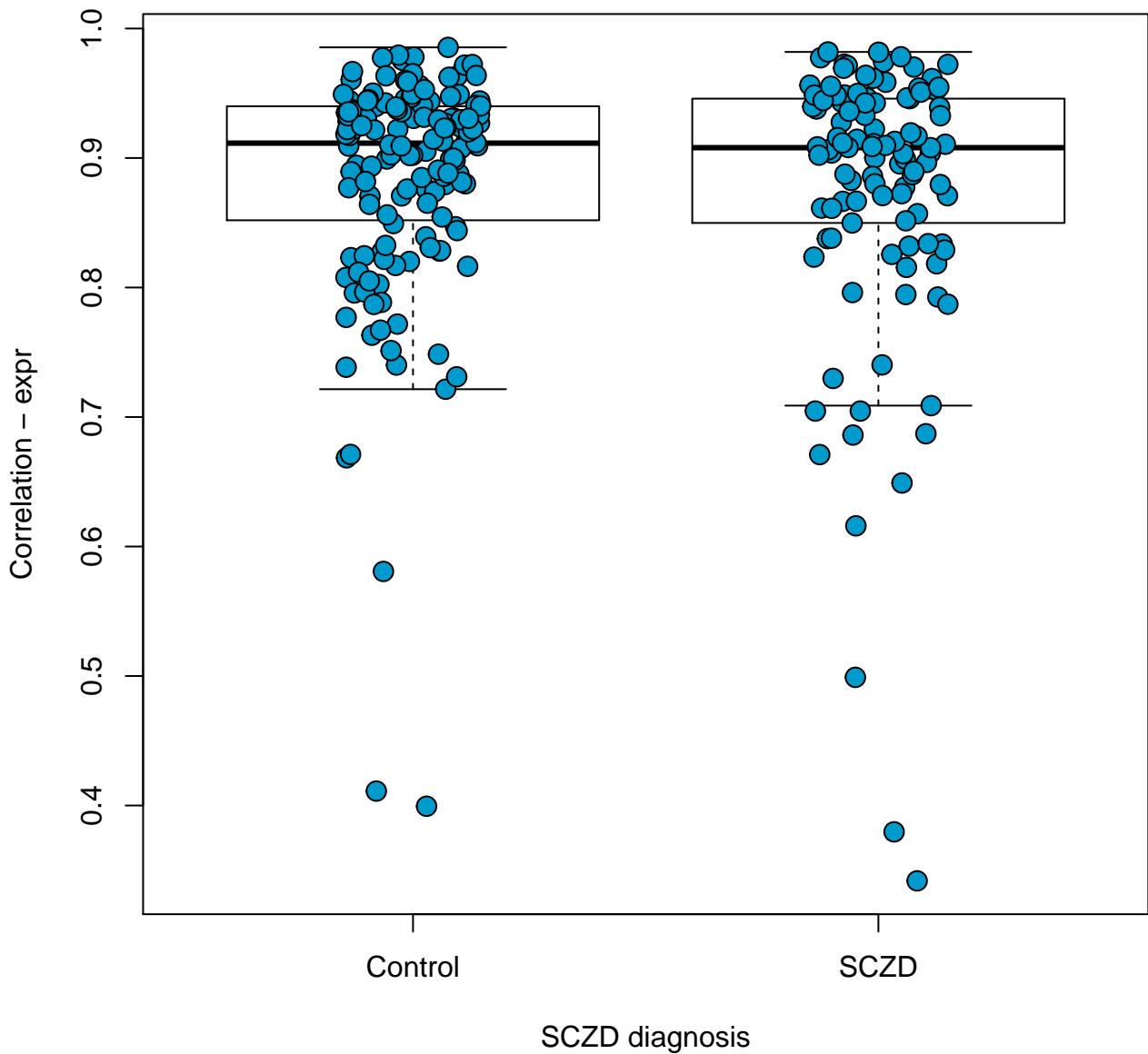
hsa00500: Starch and sucrose metabolism
p-value: 0.219



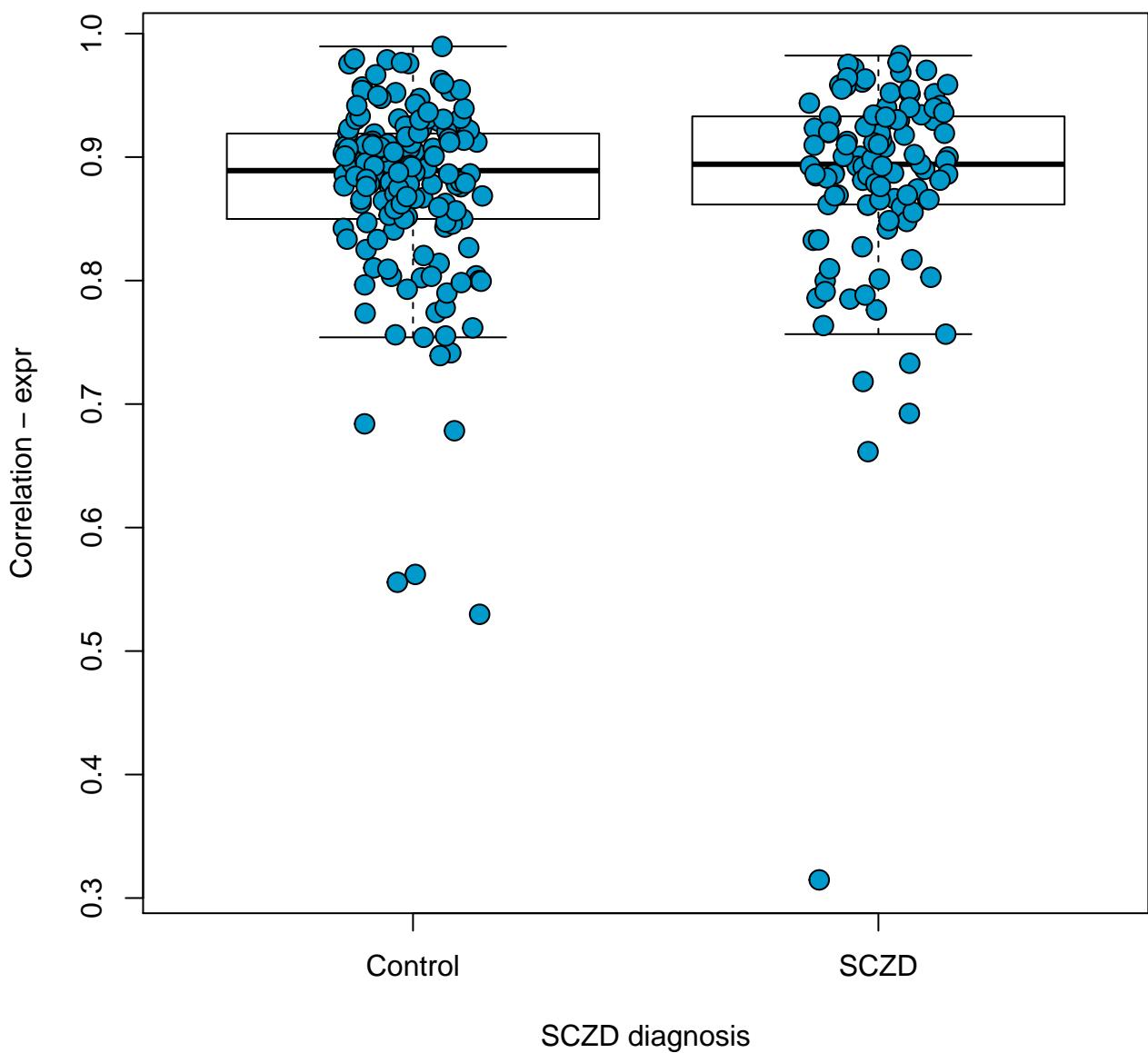
hsa00510: N-Glycan biosynthesis
p-value: 0.169



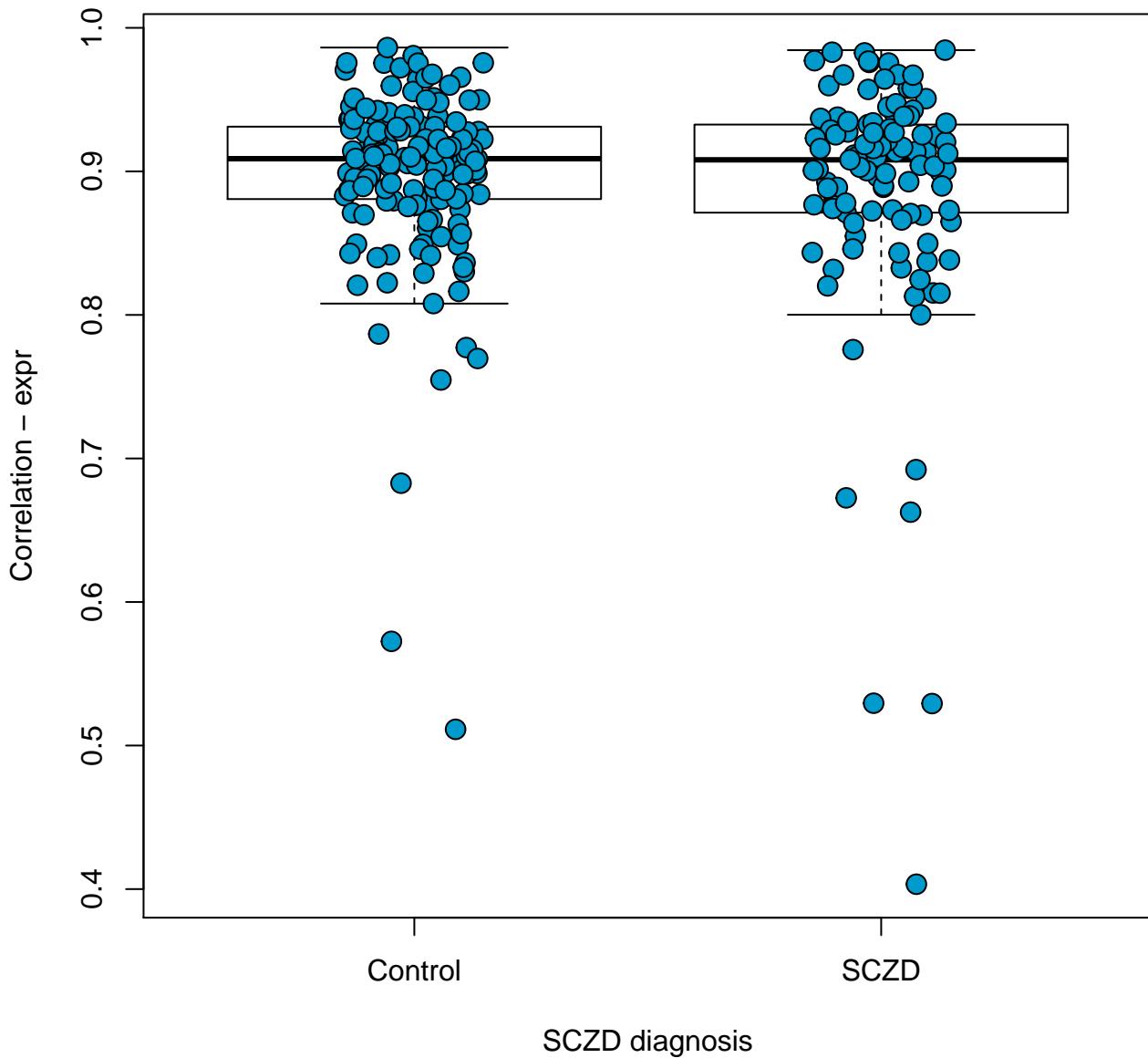
hsa00511: Other glycan degradation
p-value: 0.388



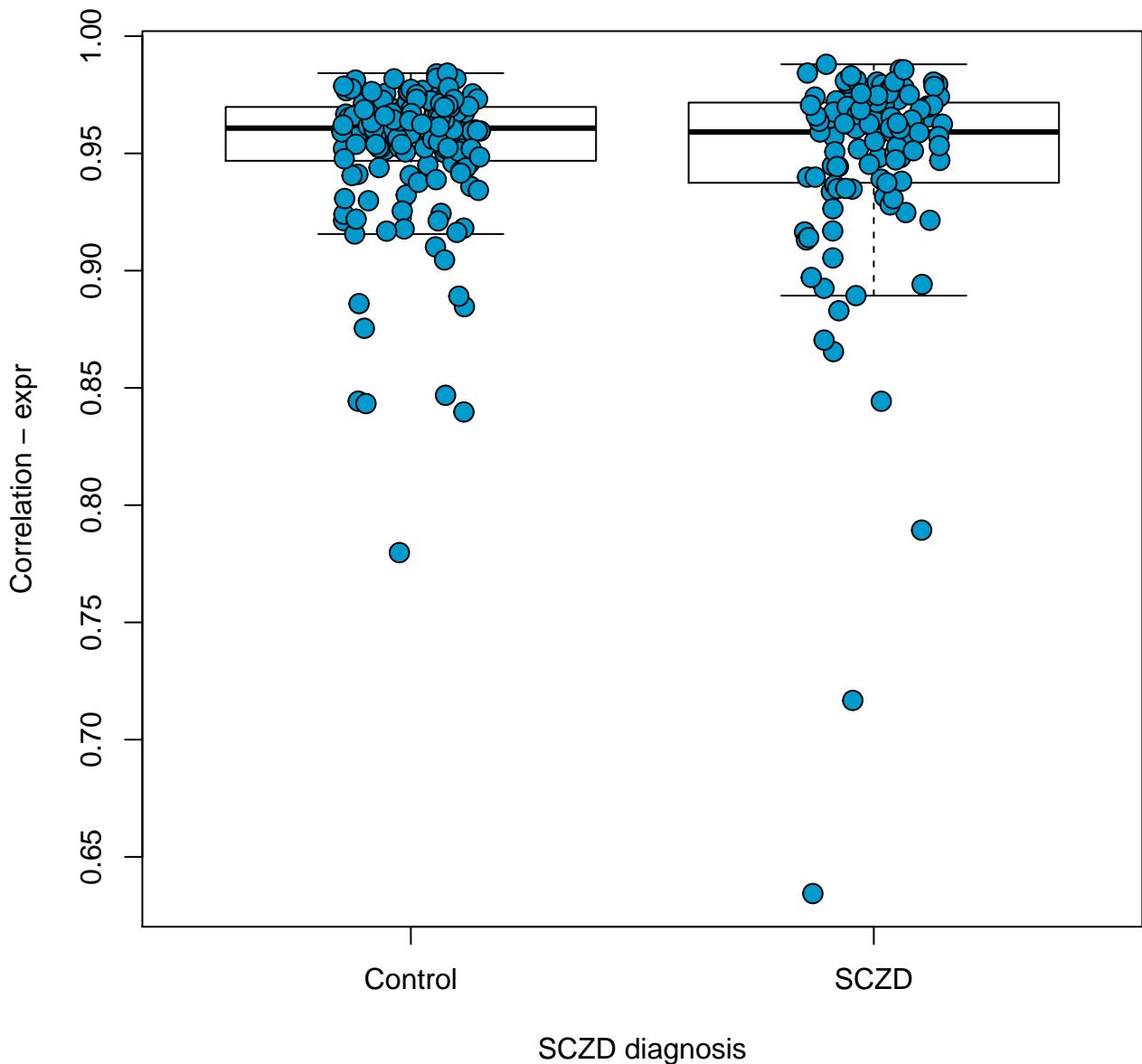
hsa00512: Mucin type O-Glycan biosynthesis
p-value: 0.399



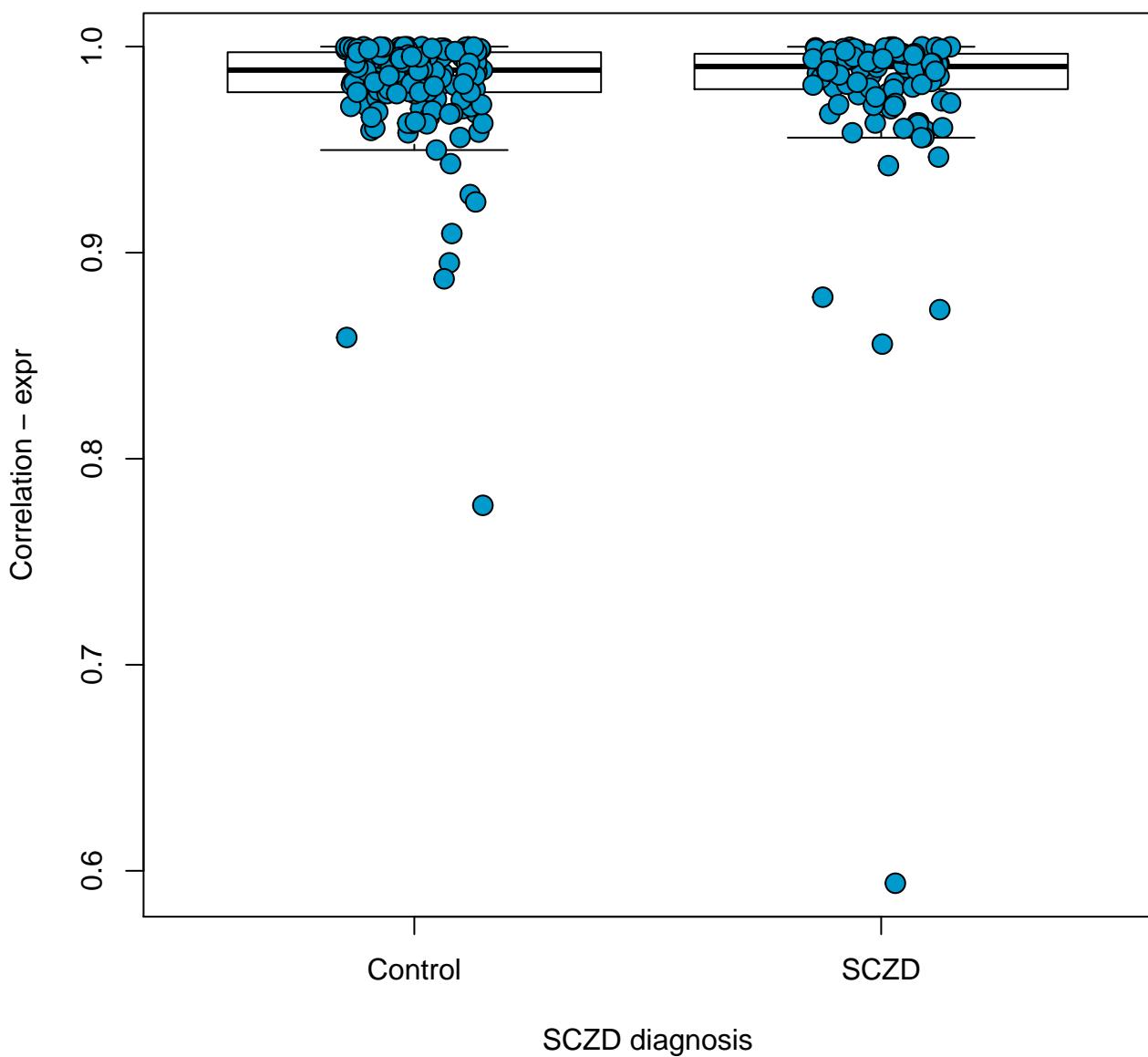
hsa00514: Other types of O-glycan biosynthesis
p-value: 0.248



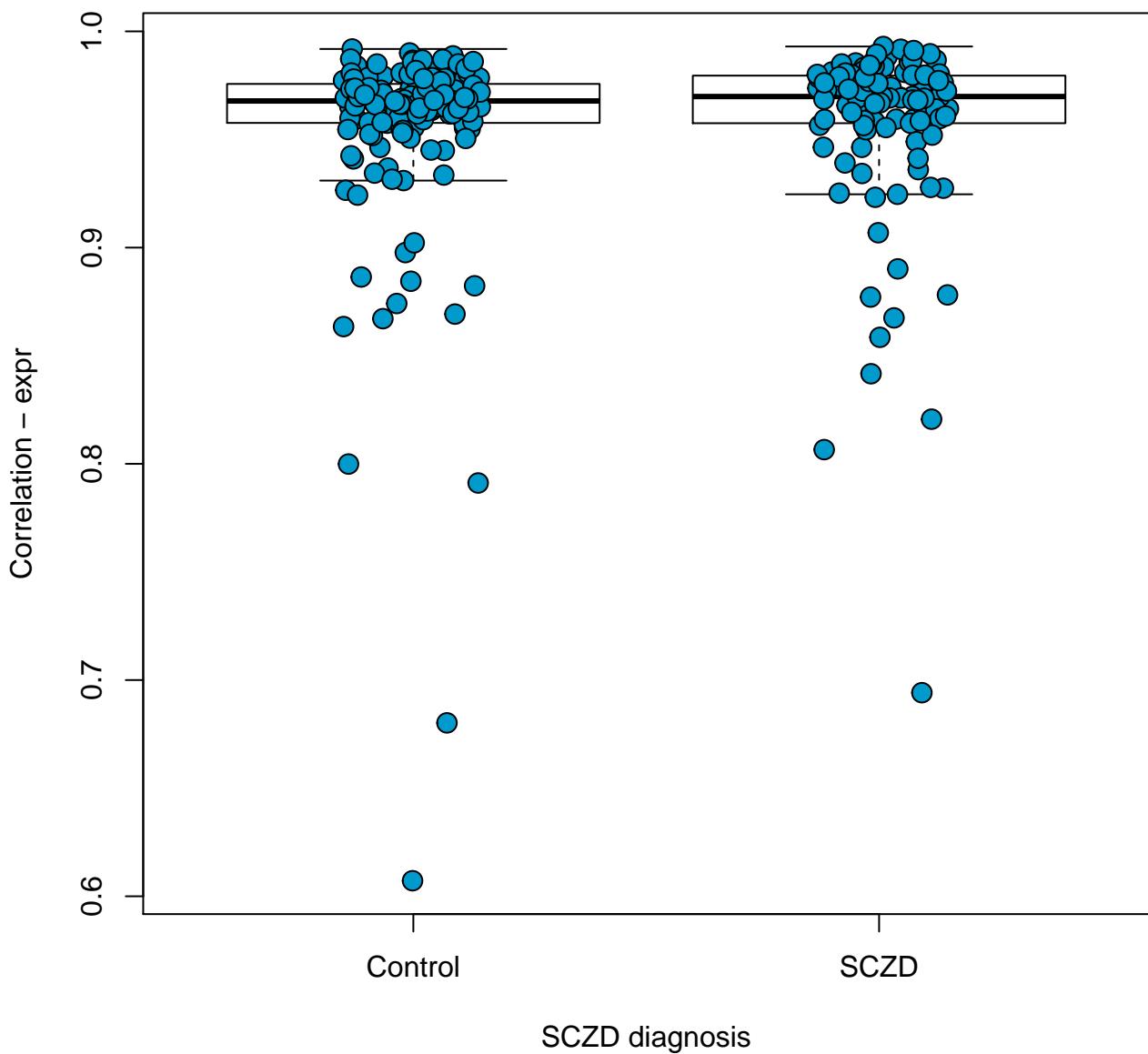
hsa00520: Amino sugar and nucleotide sugar metabolism
p-value: 0.17



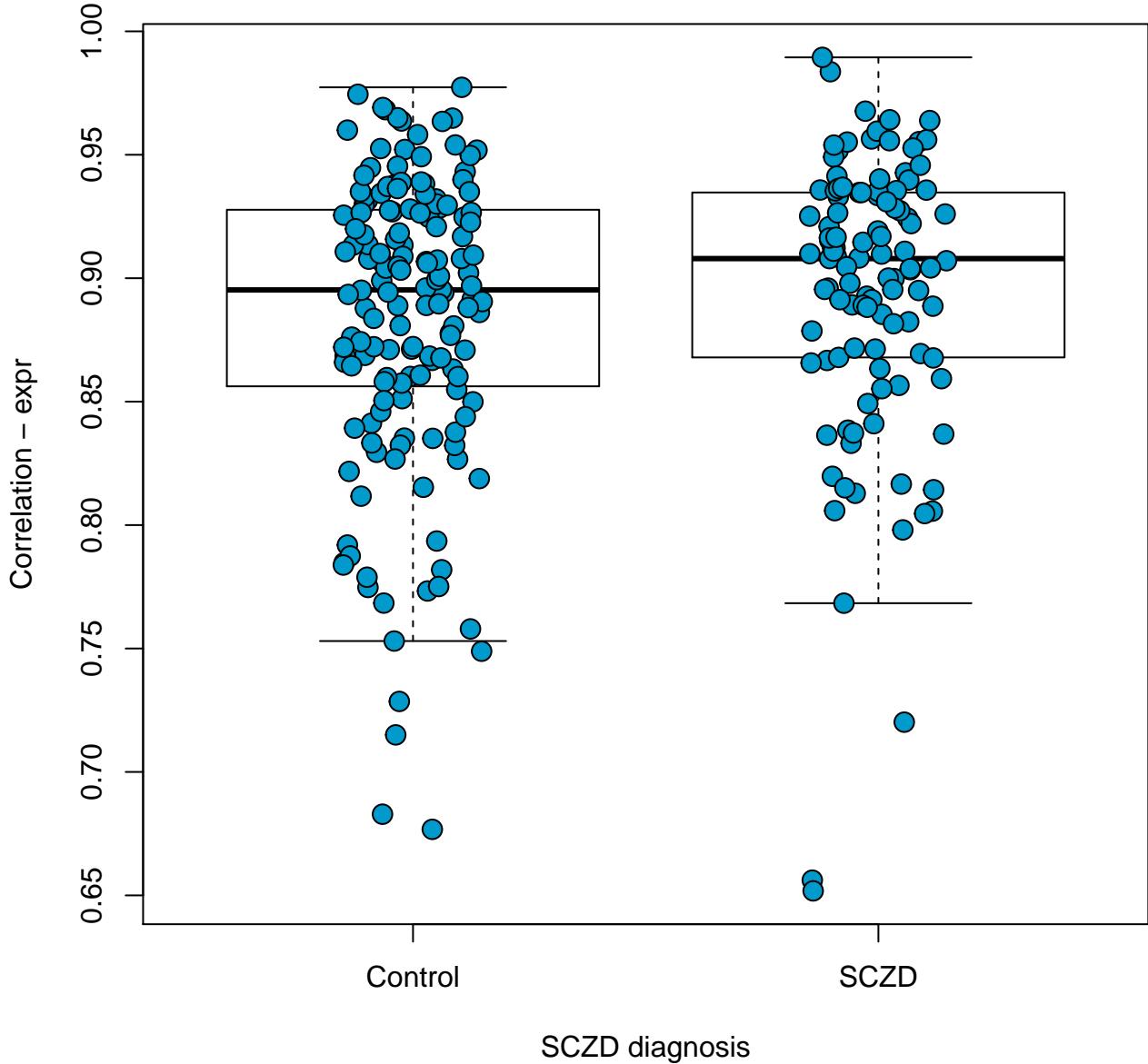
hsa00524: Butirosin and neomycin biosynthesis
p-value: 0.619



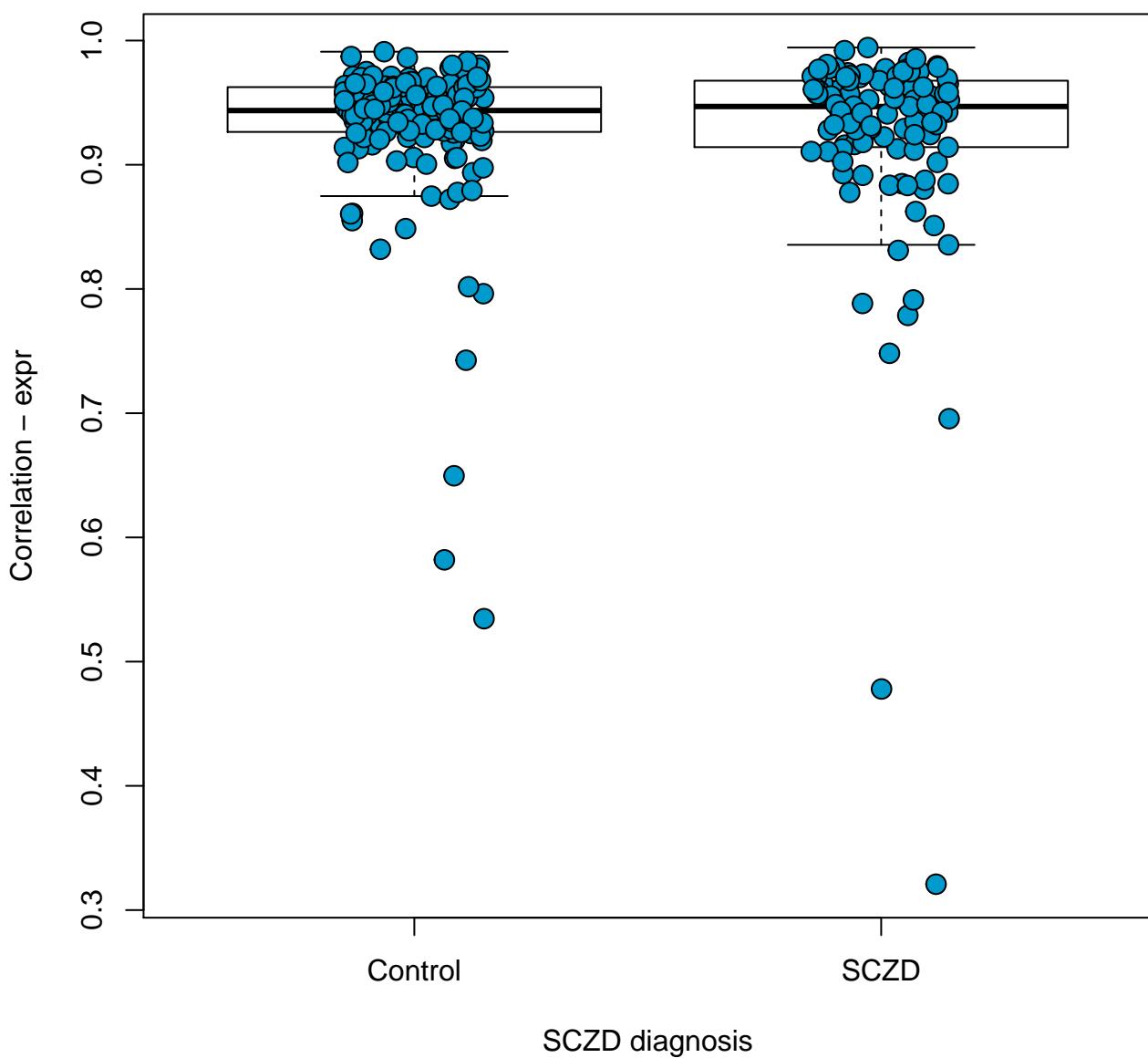
hsa00531: Glycosaminoglycan degradation
p-value: 0.816



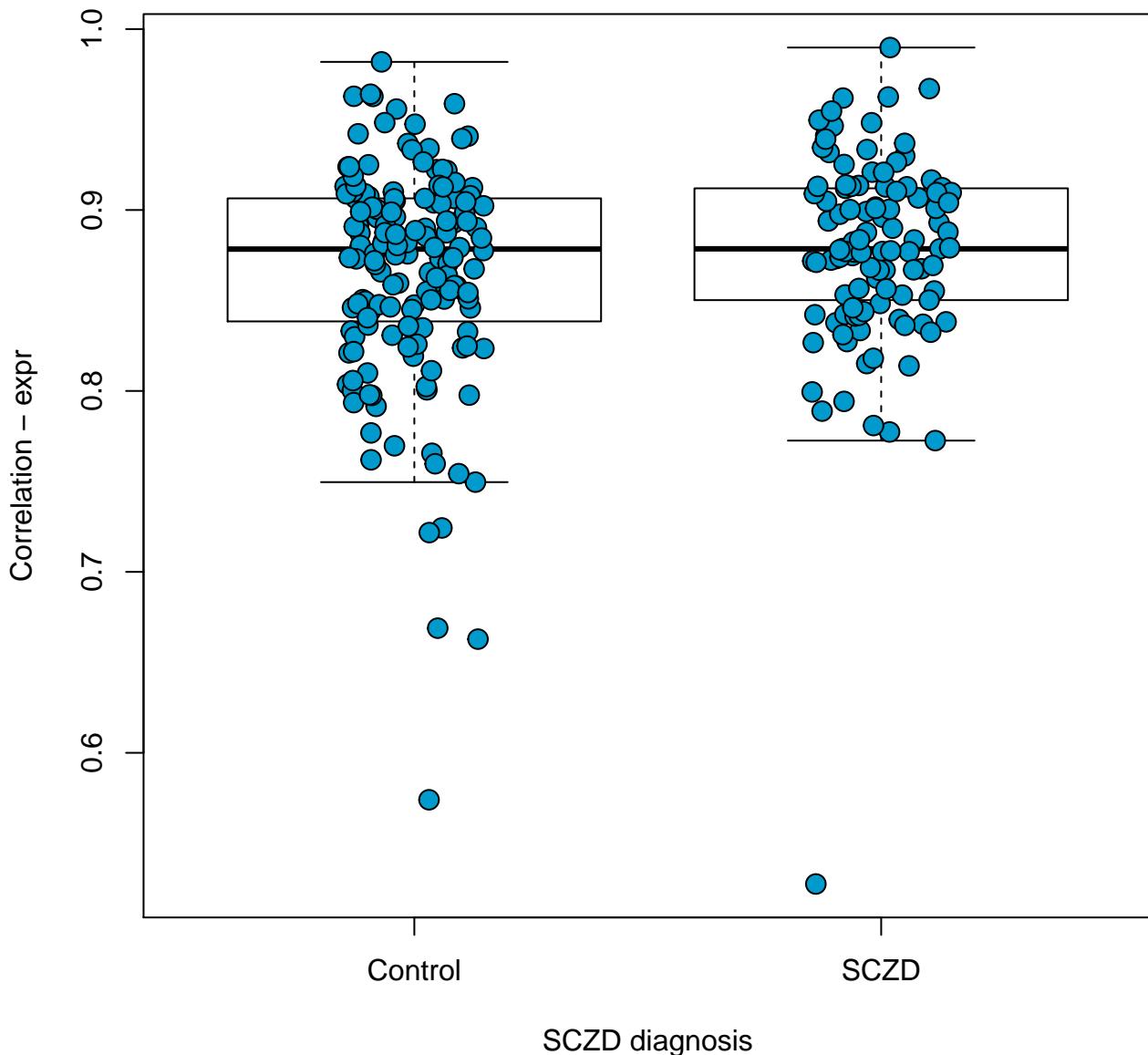
sa00532: Glycosaminoglycan biosynthesis – chondroitin sulfate / dermatan s
p-value: 0.152



hsa00533: Glycosaminoglycan biosynthesis – keratan sulfate
p-value: 0.358

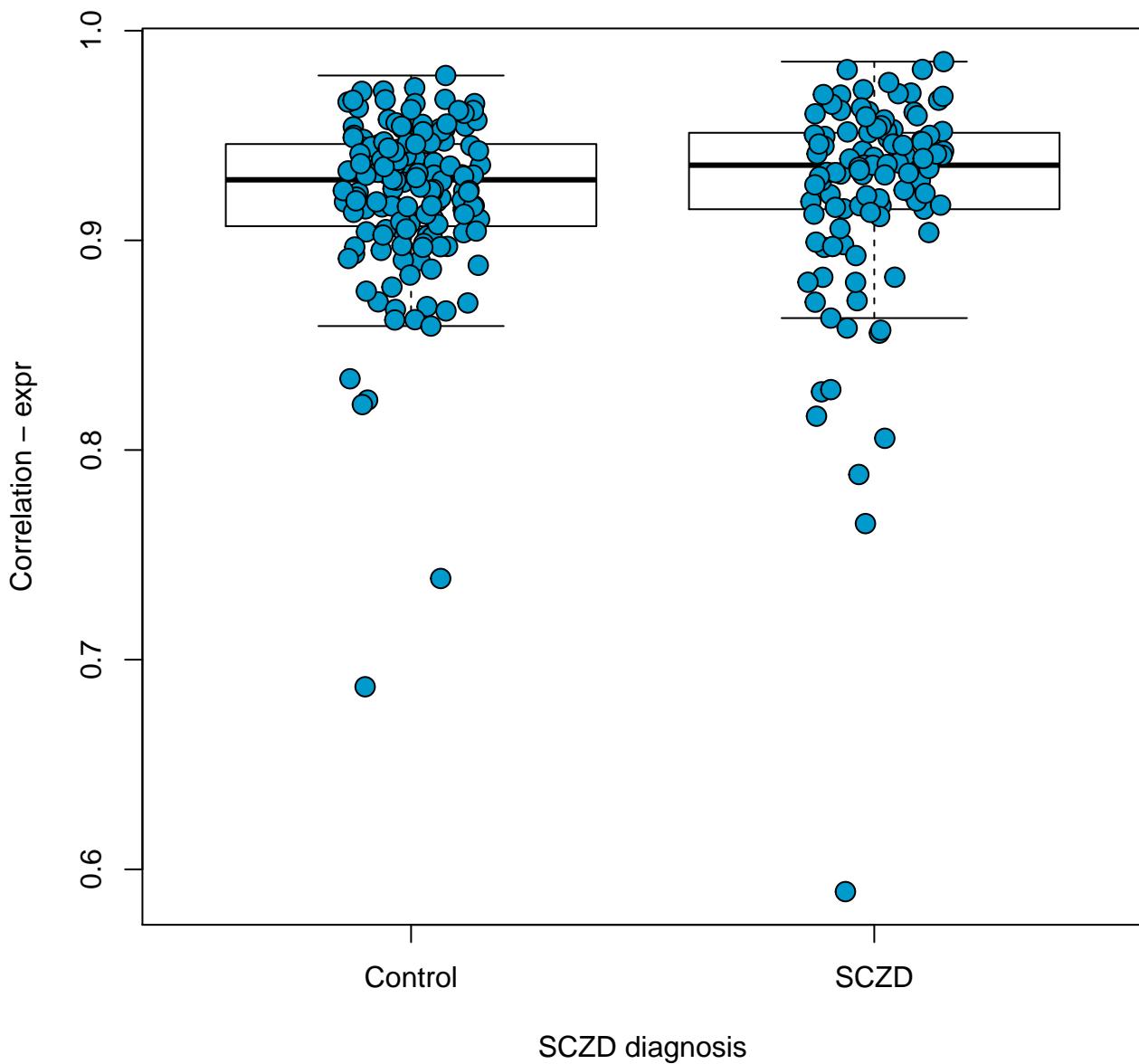


hsa00534: Glycosaminoglycan biosynthesis – heparan sulfate / heparin
p-value: 0.121

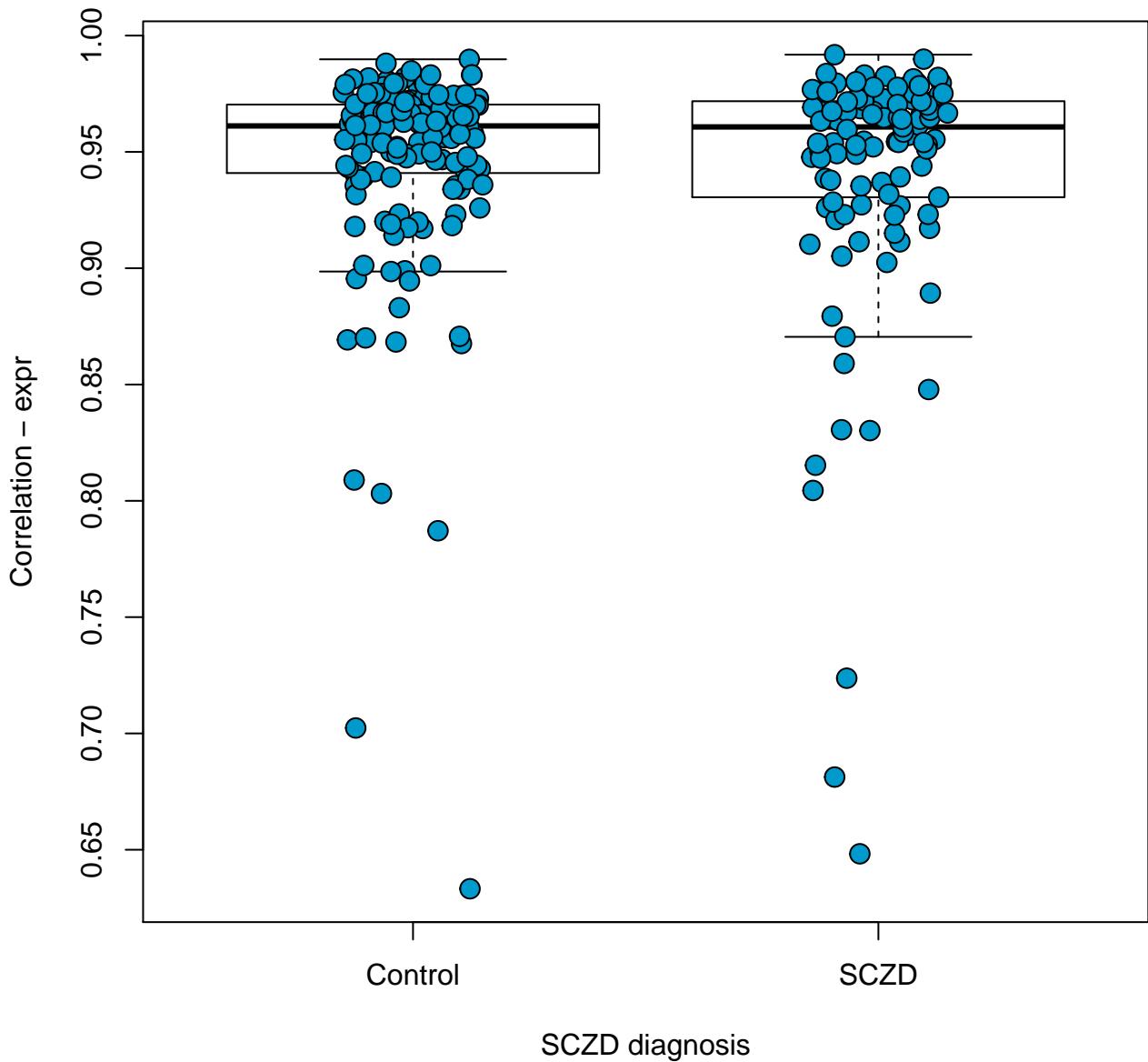


hsa00561: Glycerolipid metabolism

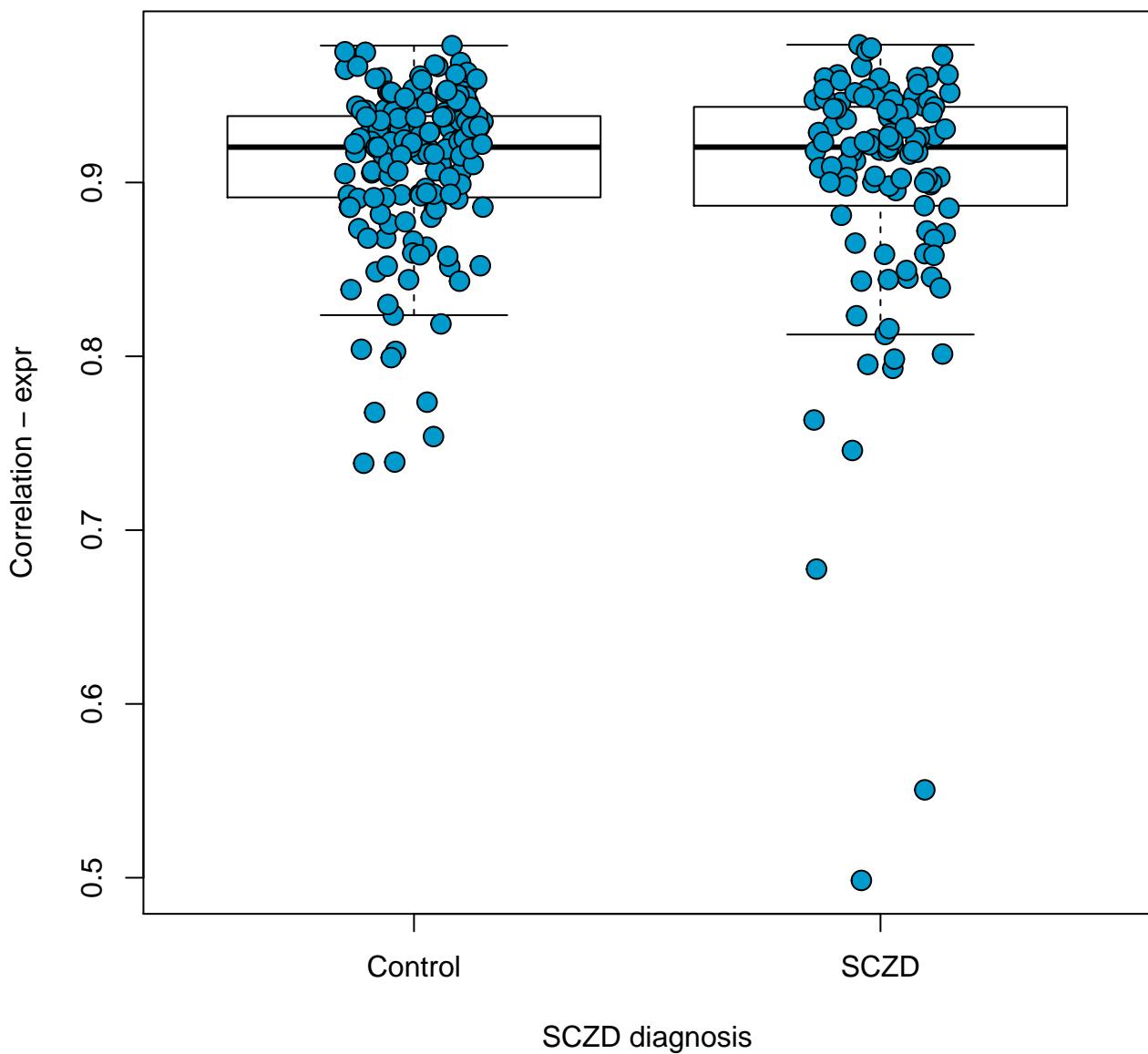
p-value: 0.947



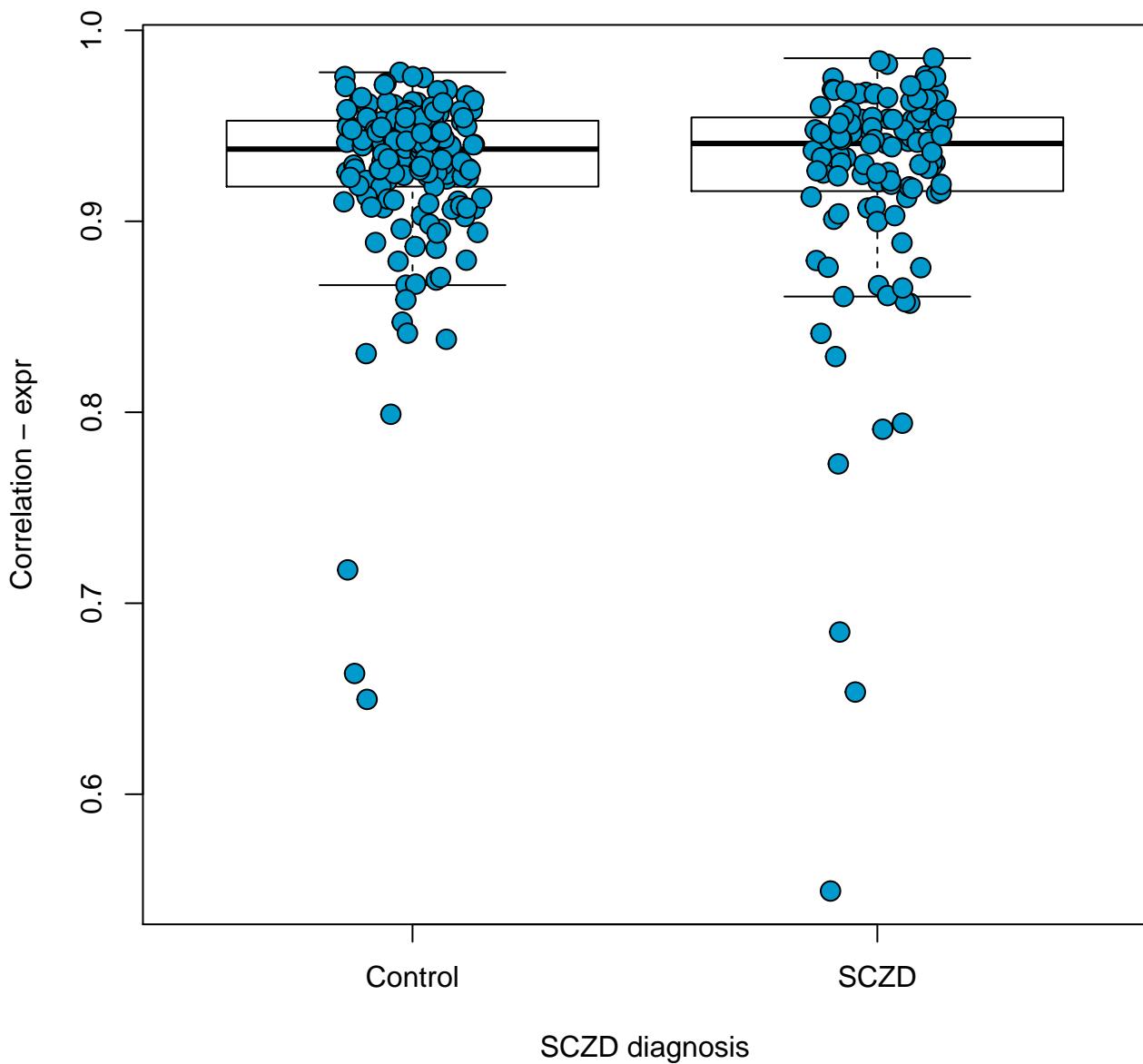
hsa00562: Inositol phosphate metabolism
p-value: 0.372



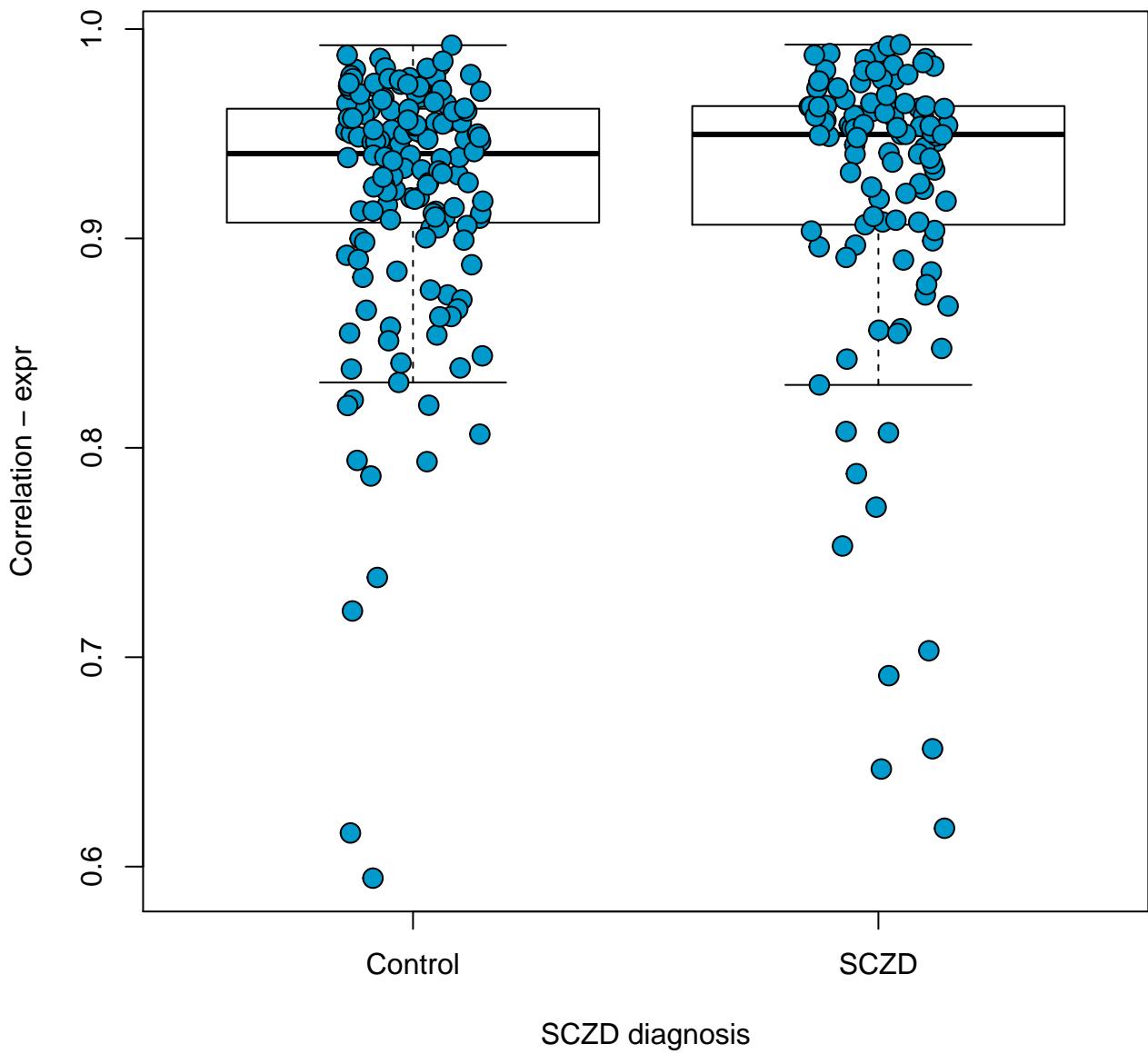
hsa00563: Glycosylphosphatidylinositol(GPI)-anchor biosynthesis
p-value: 0.247



hsa00564: Glycerophospholipid metabolism
p-value: 0.519

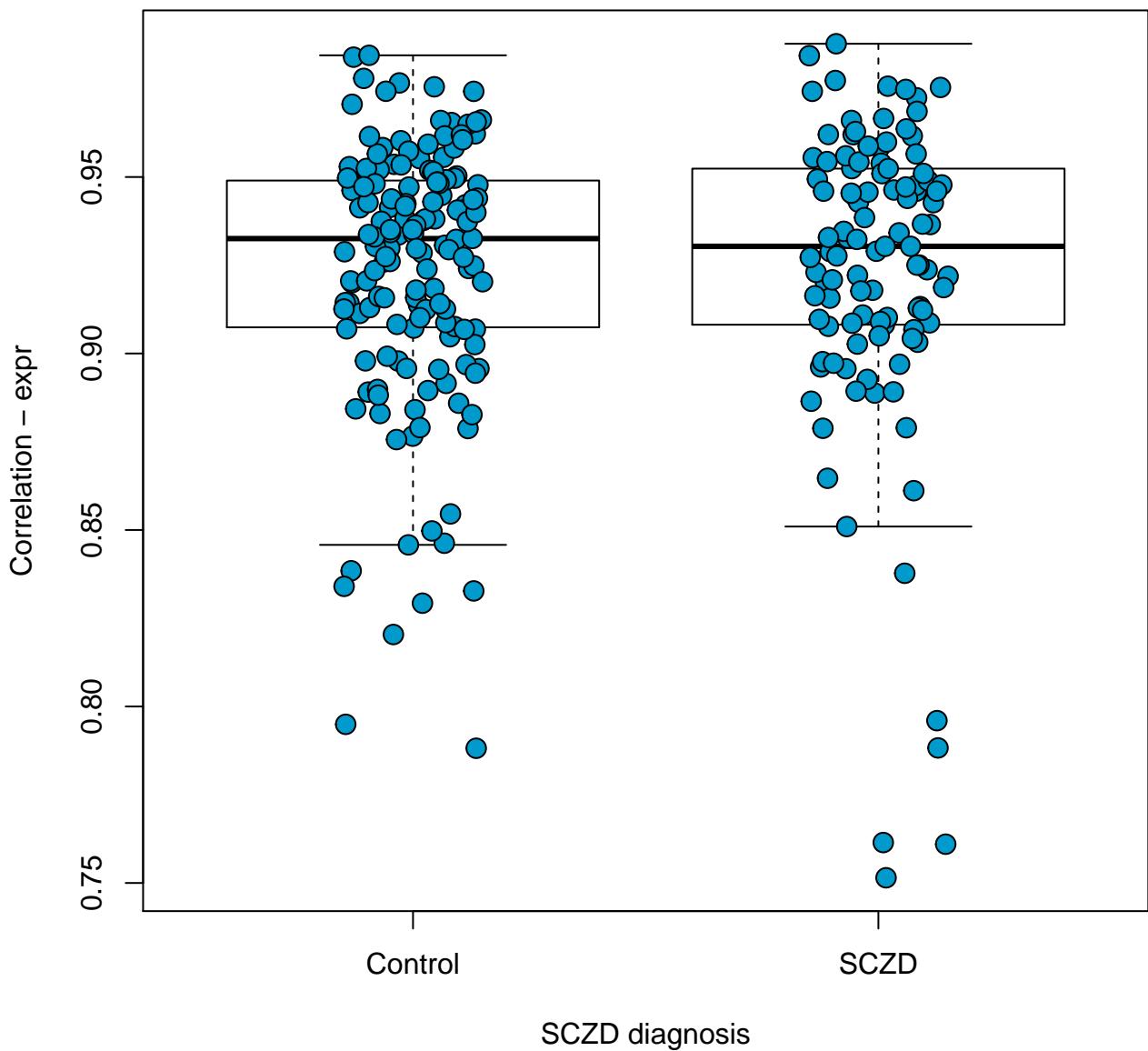


hsa00565: Ether lipid metabolism
p-value: 0.9



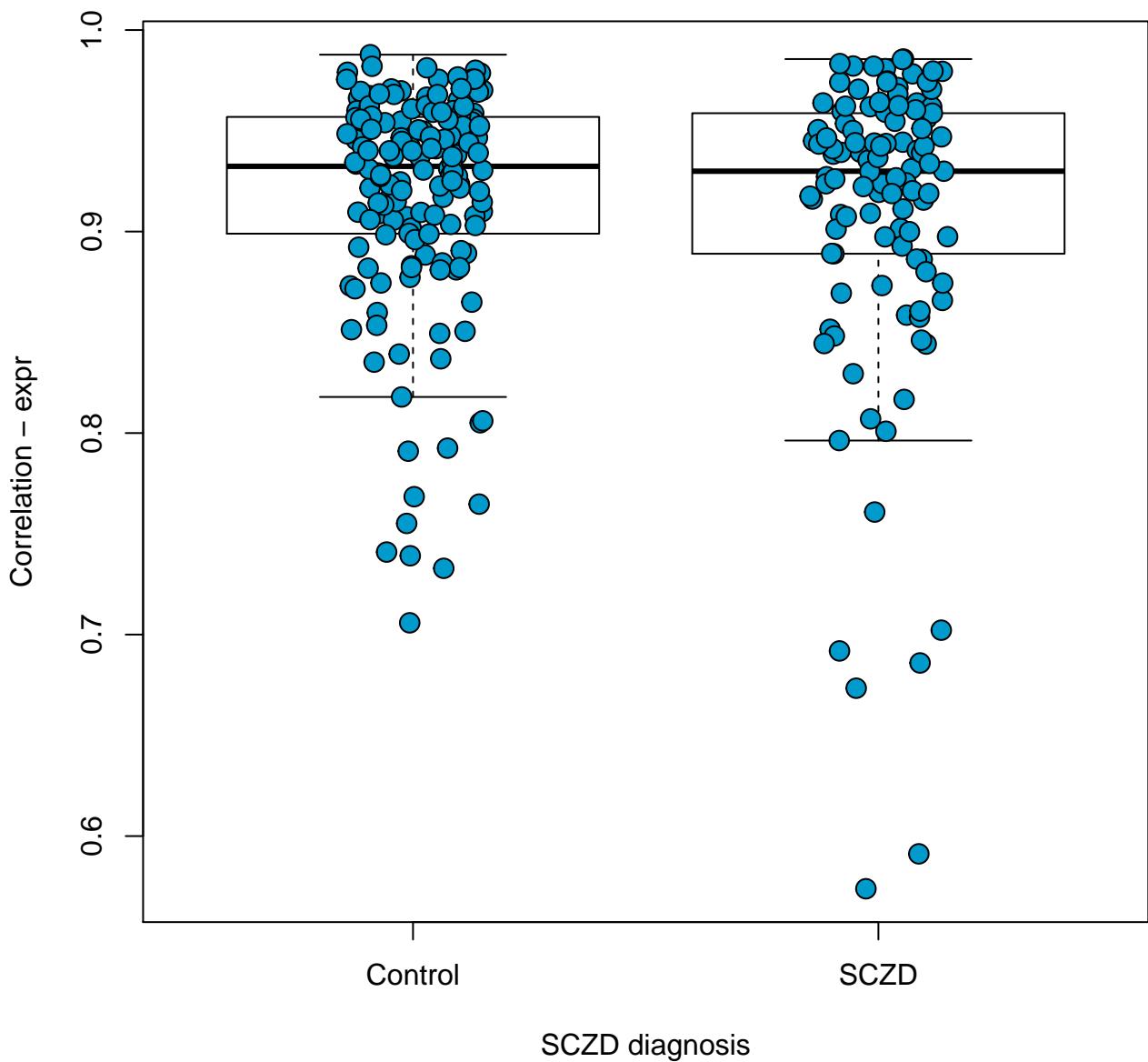
hsa00590: Arachidonic acid metabolism

p-value: 0.809

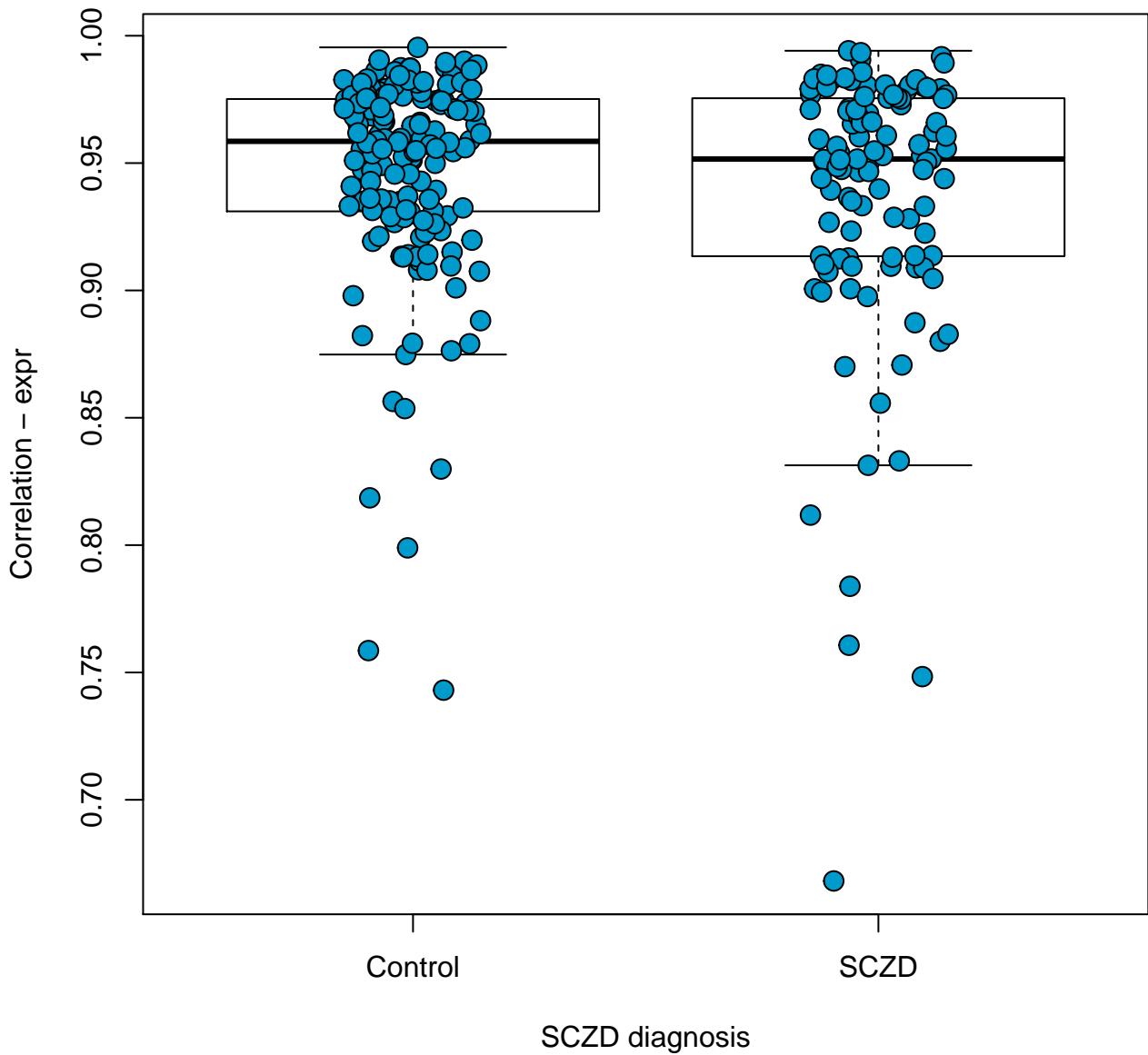


hsa00591: Linoleic acid metabolism

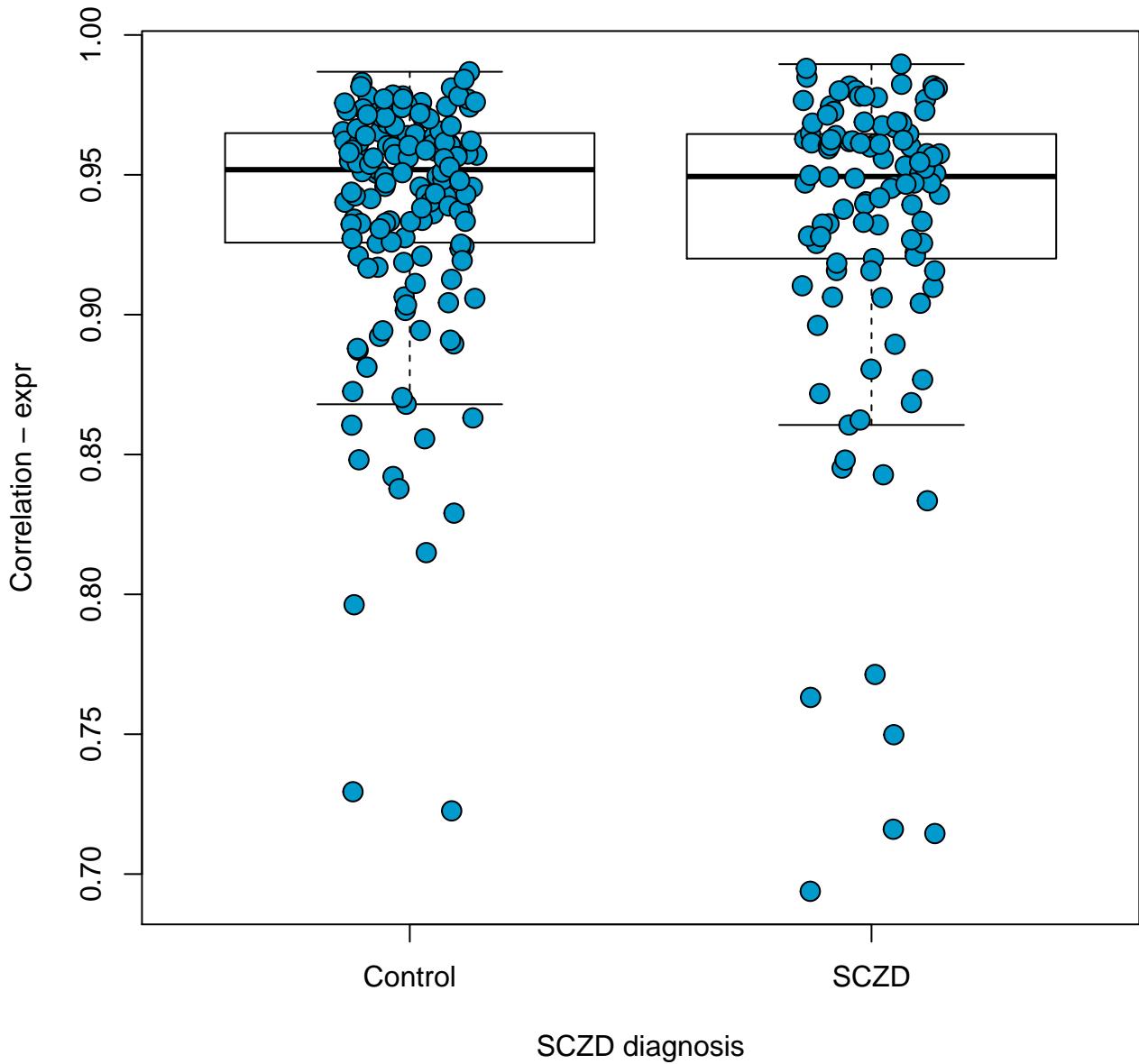
p-value: 0.214



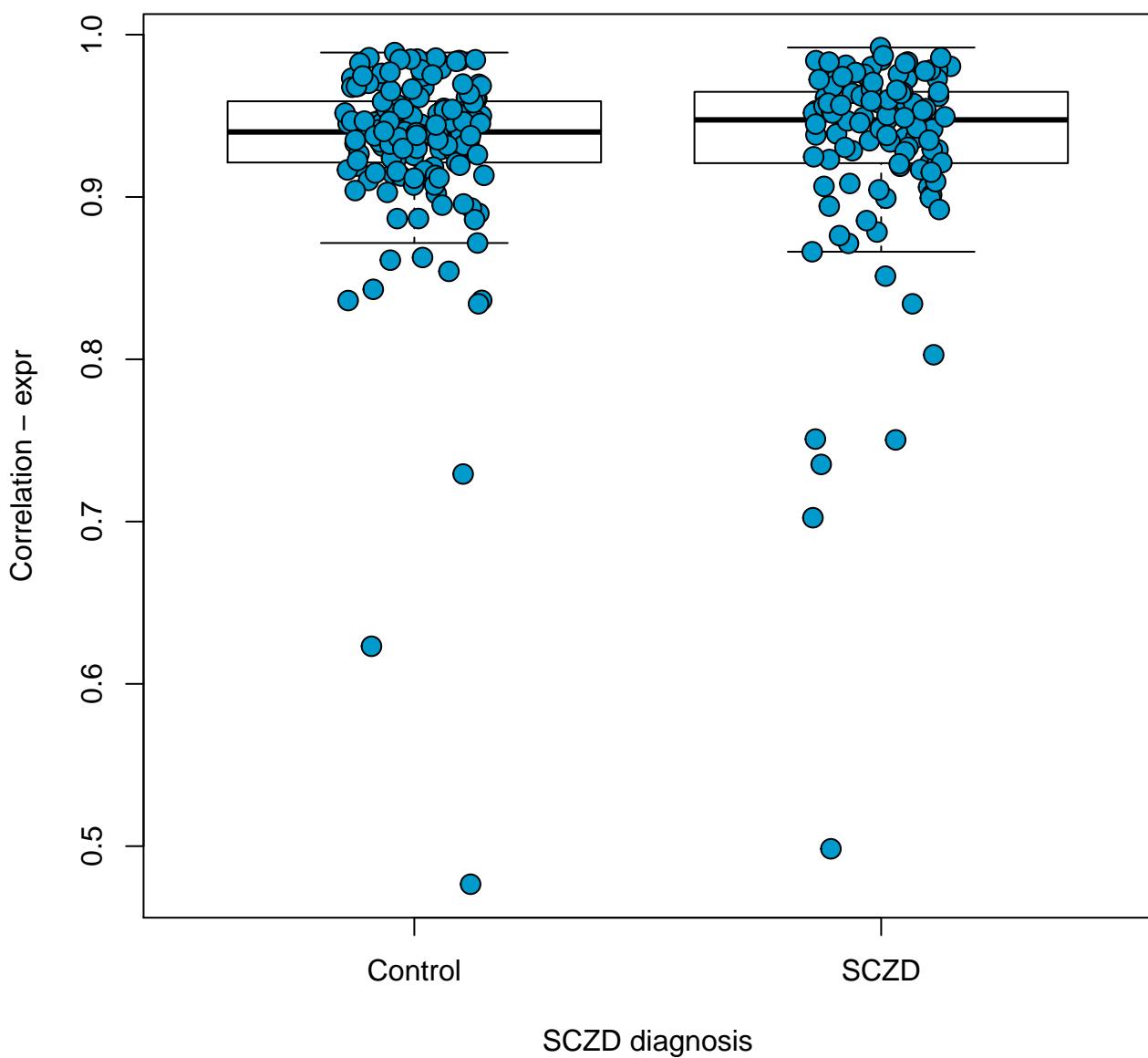
hsa00592: alpha-Linolenic acid metabolism
p-value: 0.115



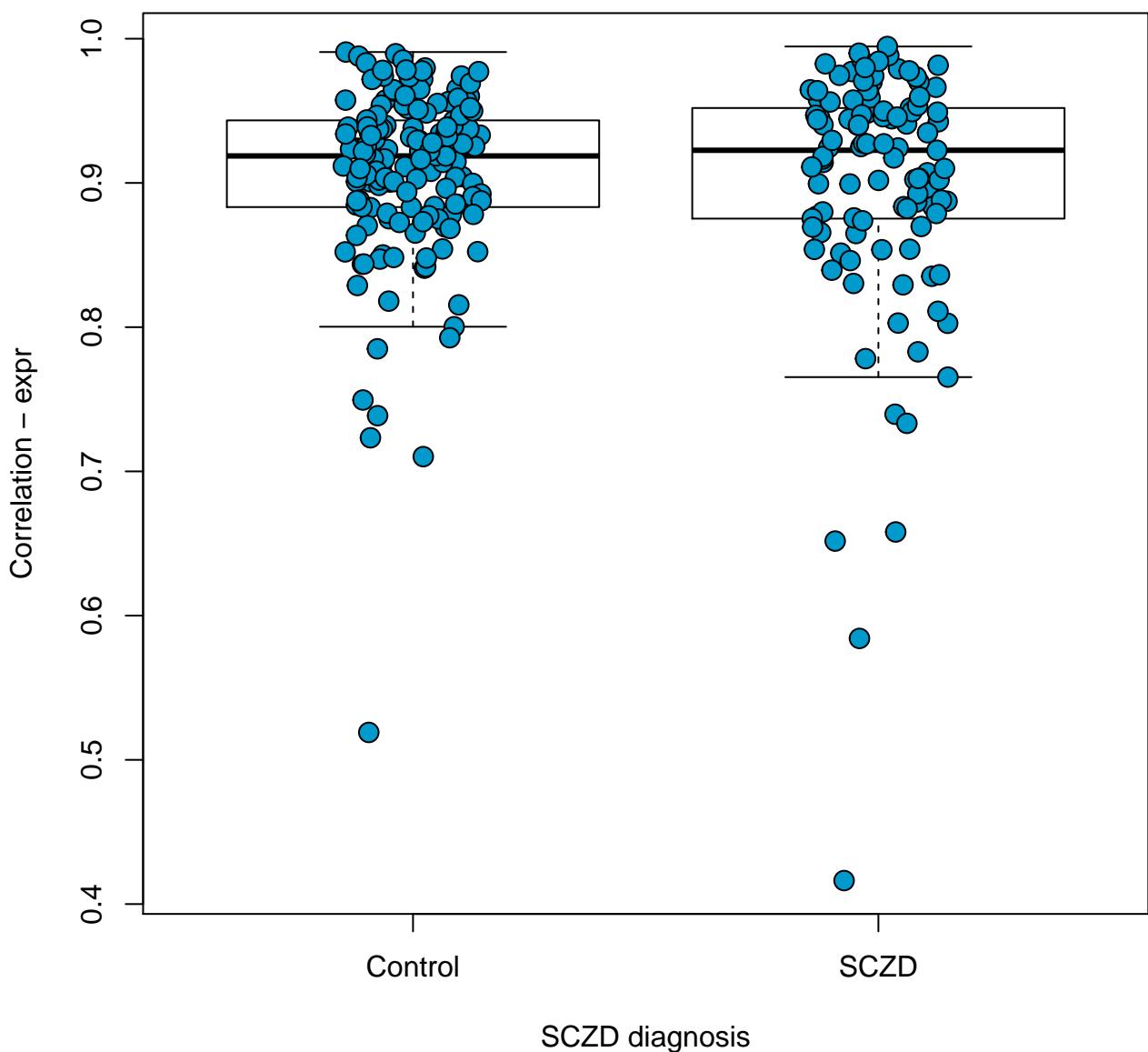
hsa00600: Sphingolipid metabolism
p-value: 0.24



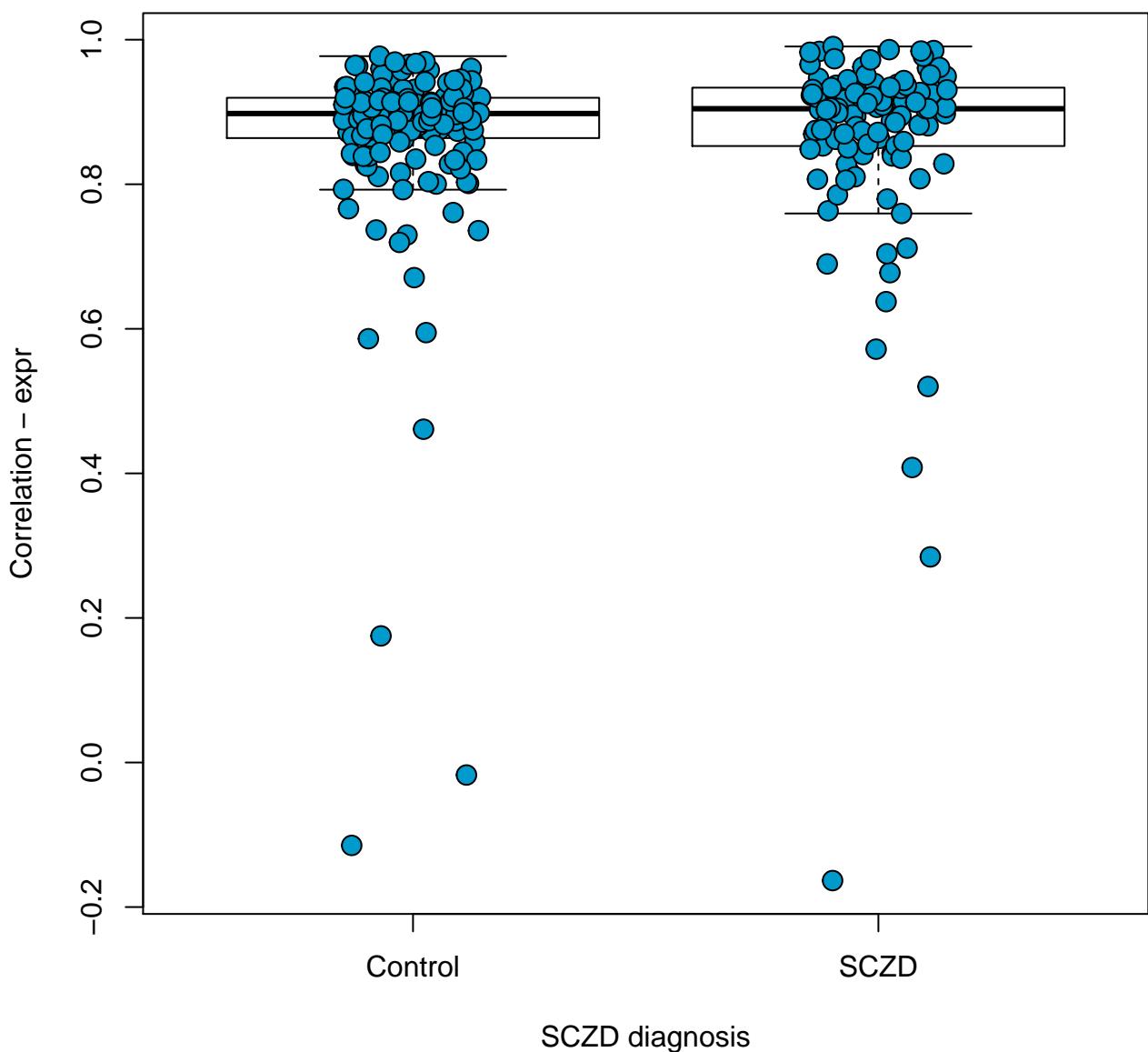
hsa00601: Glycosphingolipid biosynthesis – lacto and neolacto series
p-value: 0.807



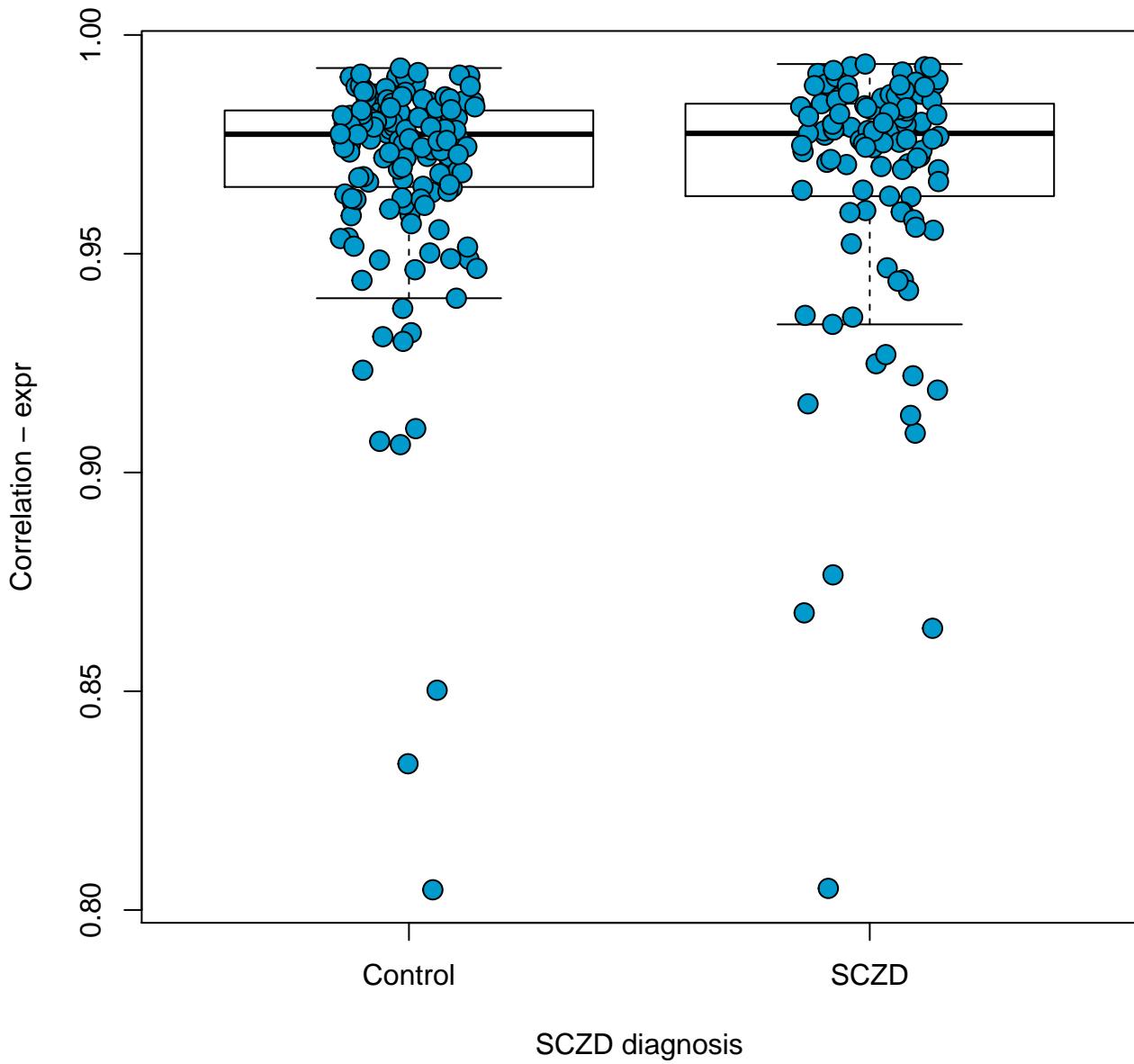
hsa00603: Glycosphingolipid biosynthesis – globo series
p-value: 0.404



hsa00604: Glycosphingolipid biosynthesis – ganglio series
p-value: 0.944

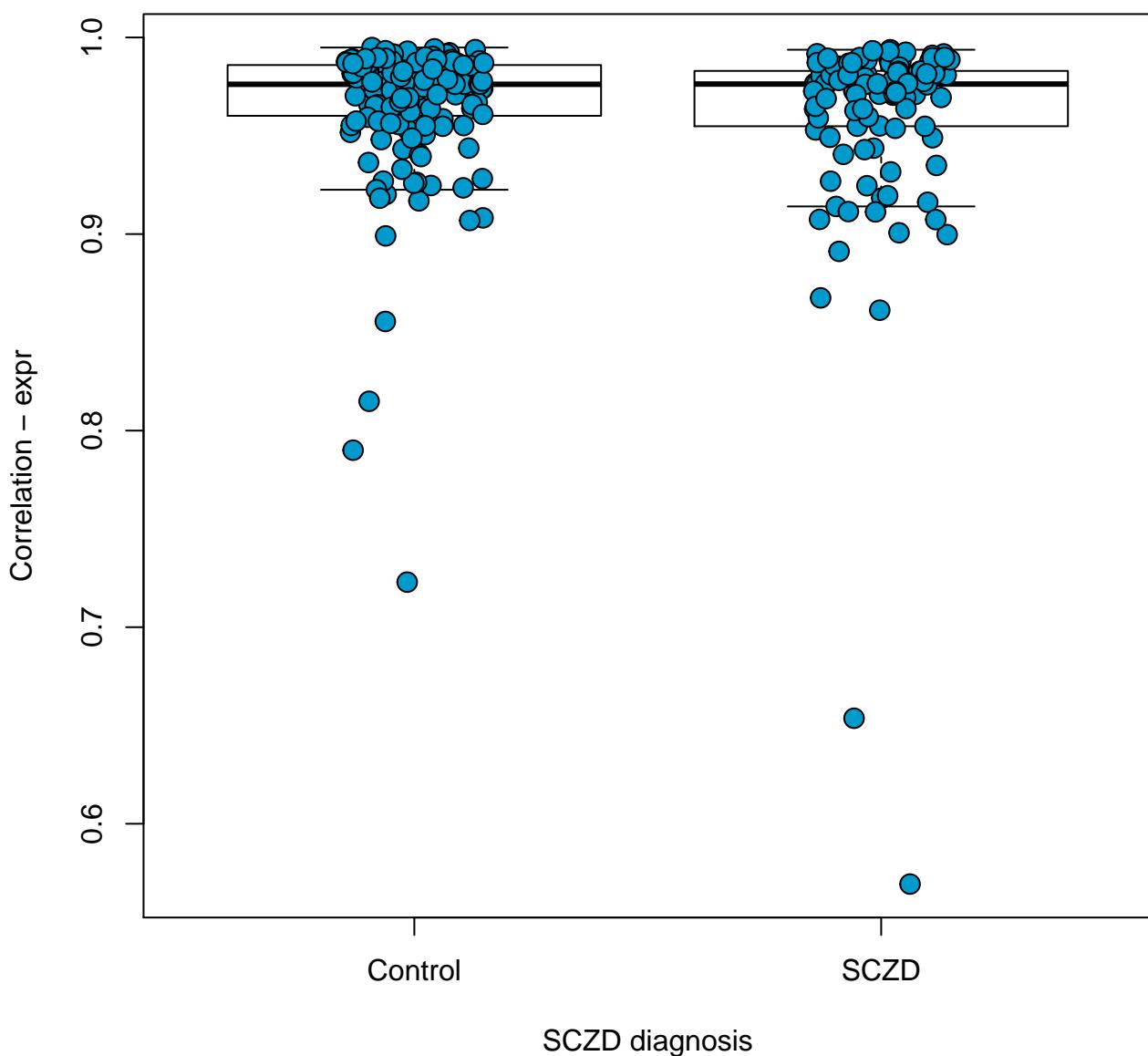


hsa00620: Pyruvate metabolism
p-value: 0.534



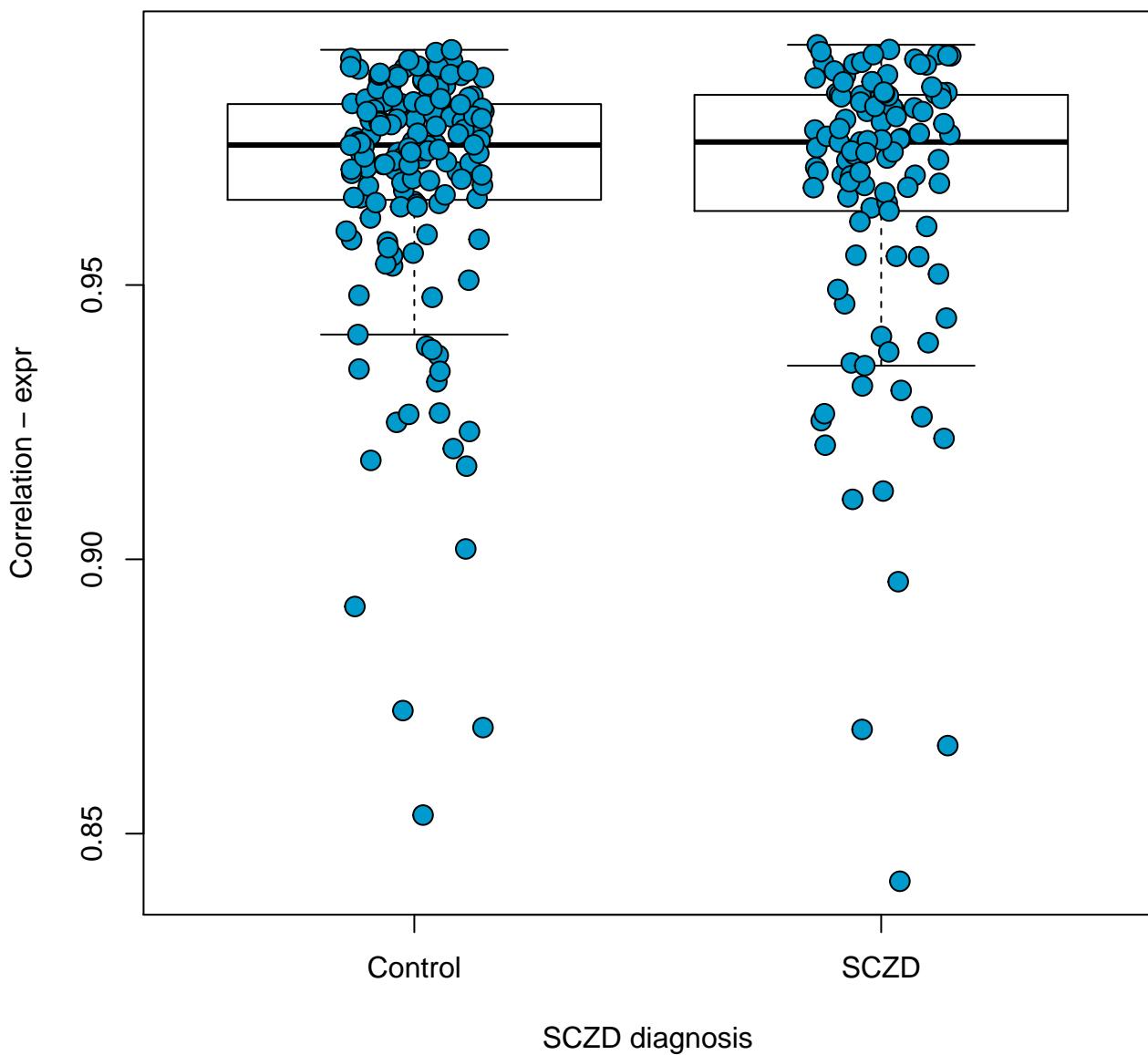
hsa00630: Glyoxylate and dicarboxylate metabolism

p-value: 0.205



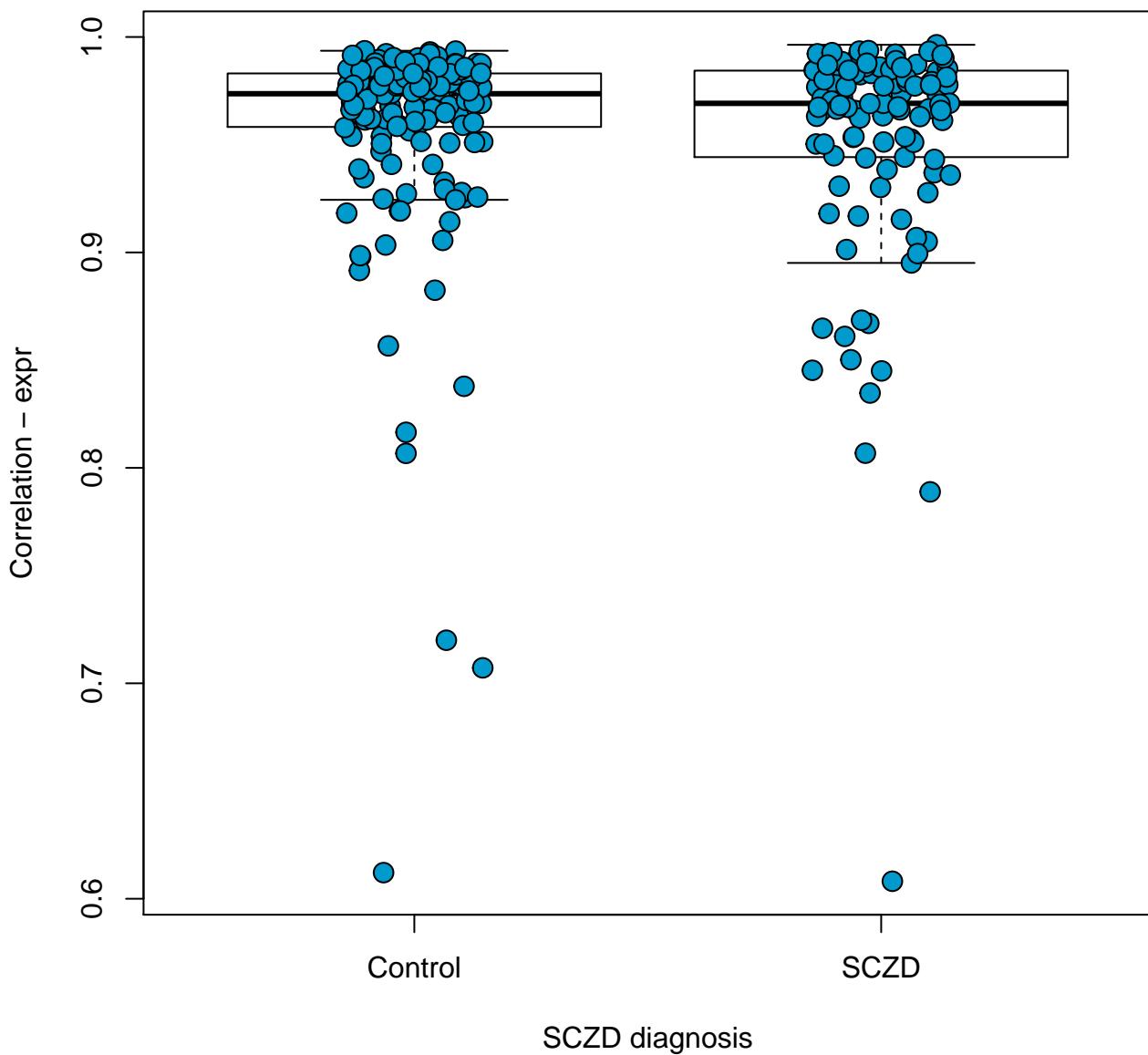
hsa00640: Propanoate metabolism

p-value: 0.532

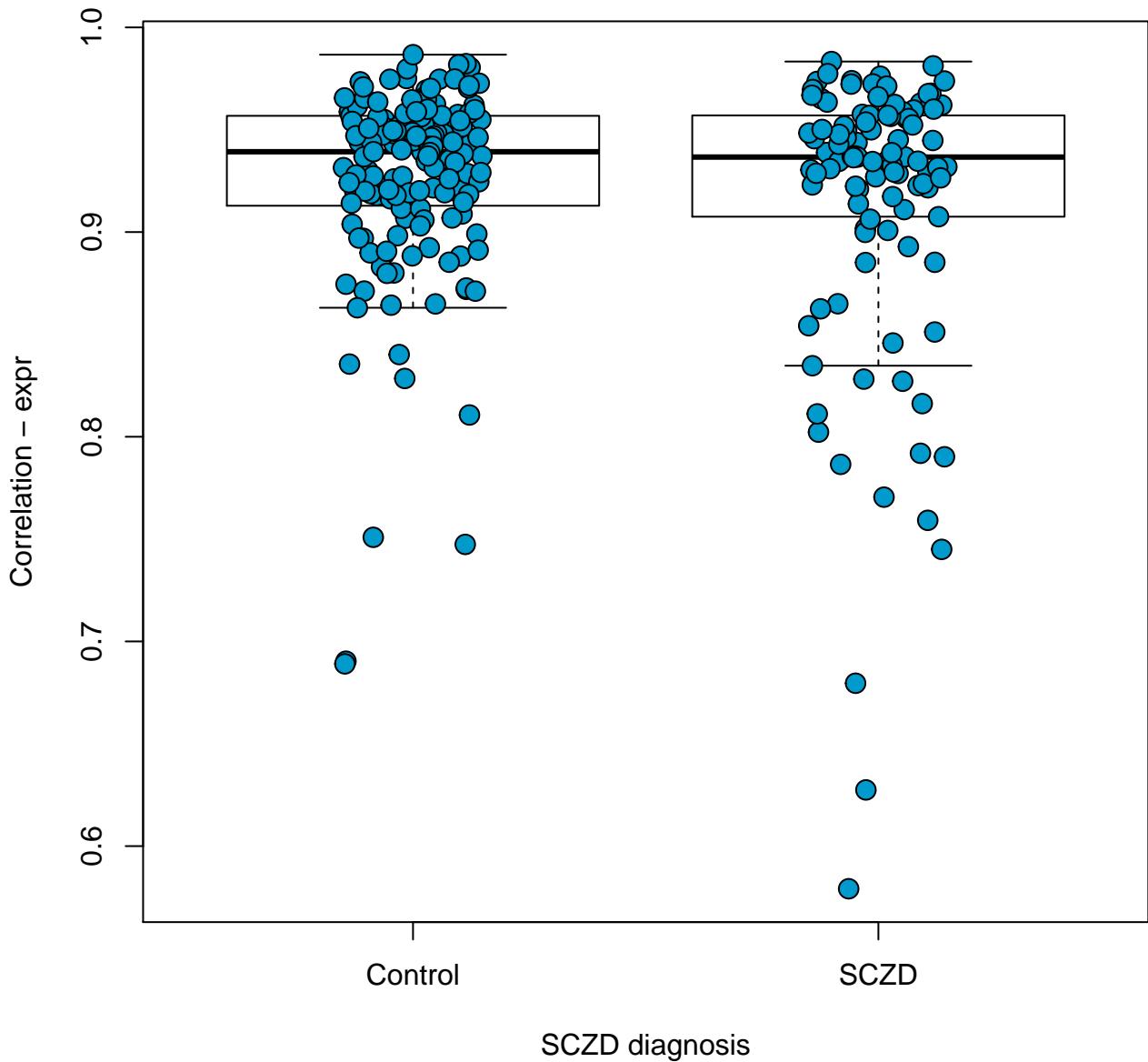


hsa00650: Butanoate metabolism

p-value: 0.372

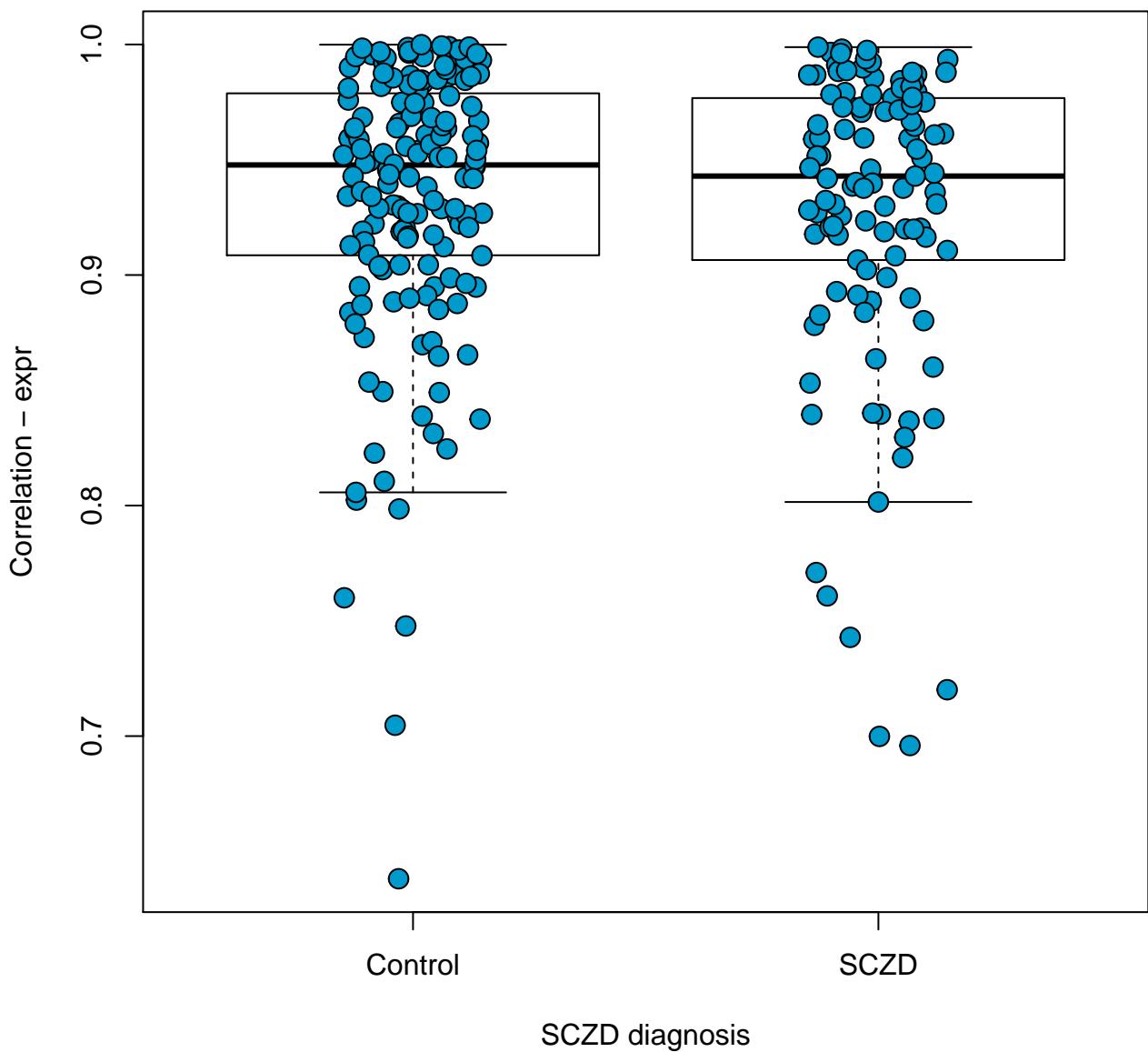


hsa00670: One carbon pool by folate
p-value: 0.0919

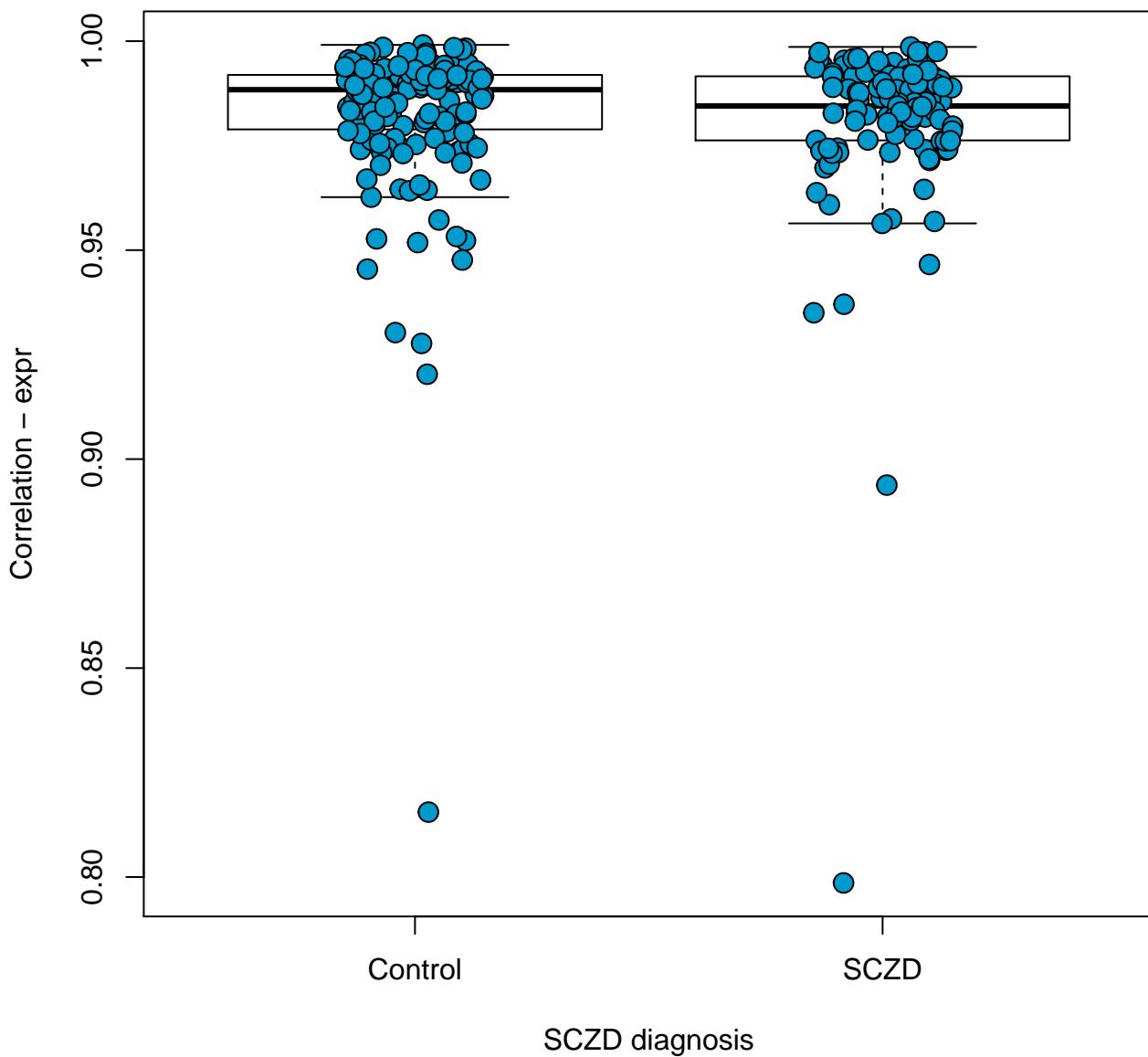


hsa00730: Thiamine metabolism

p-value: 0.488

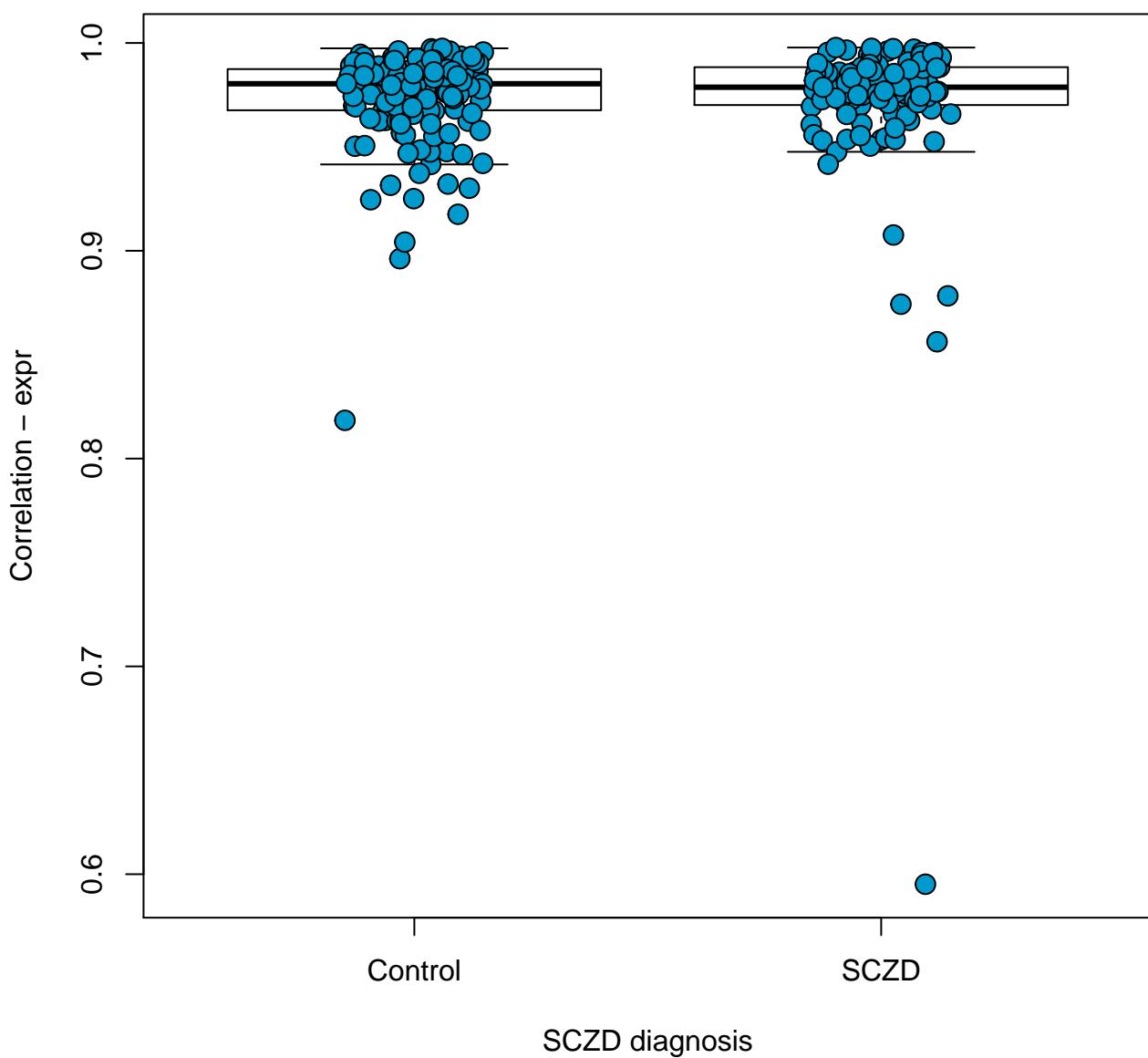


hsa00740: Riboflavin metabolism
p-value: 0.422

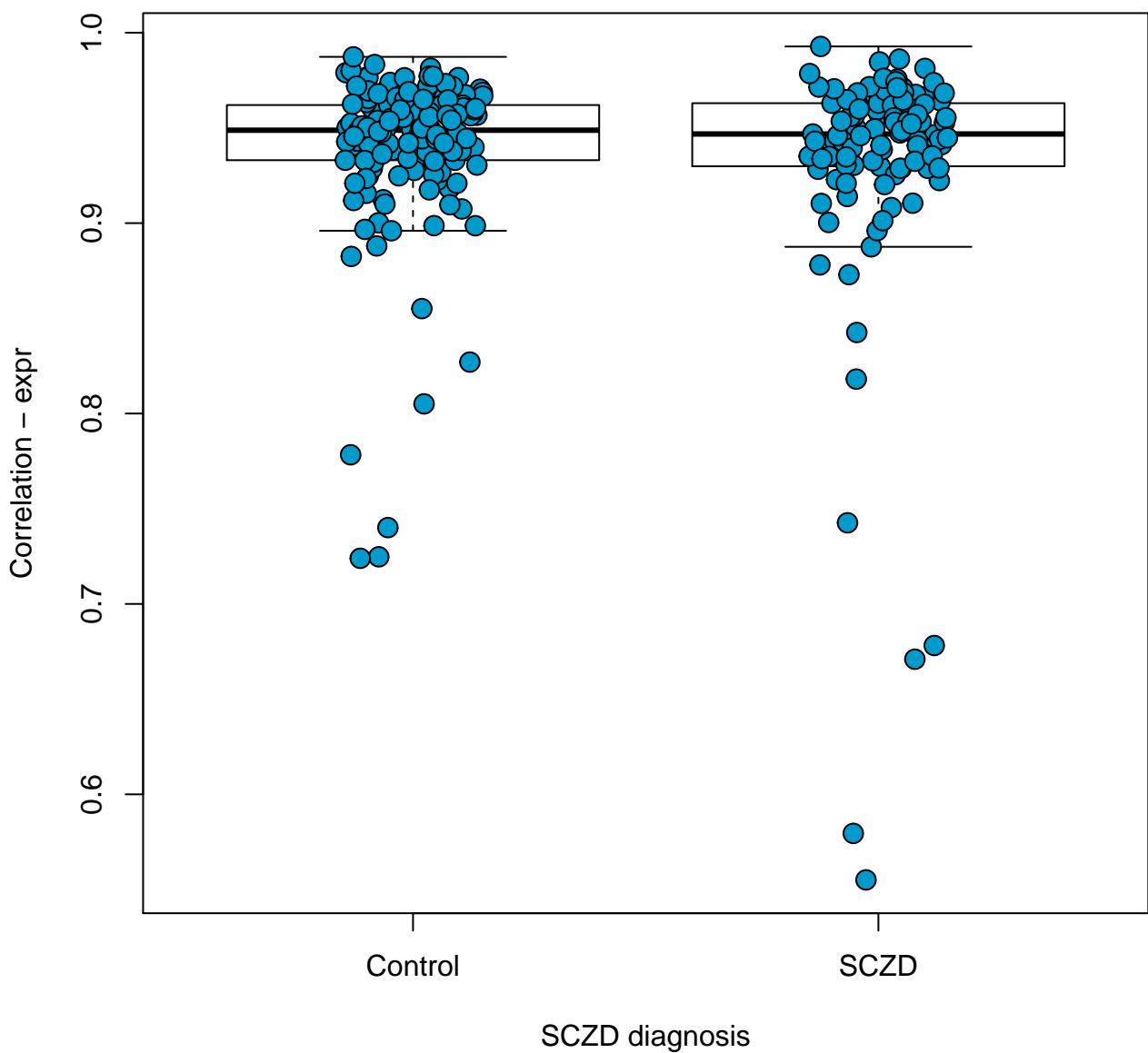


hsa00750: Vitamin B6 metabolism

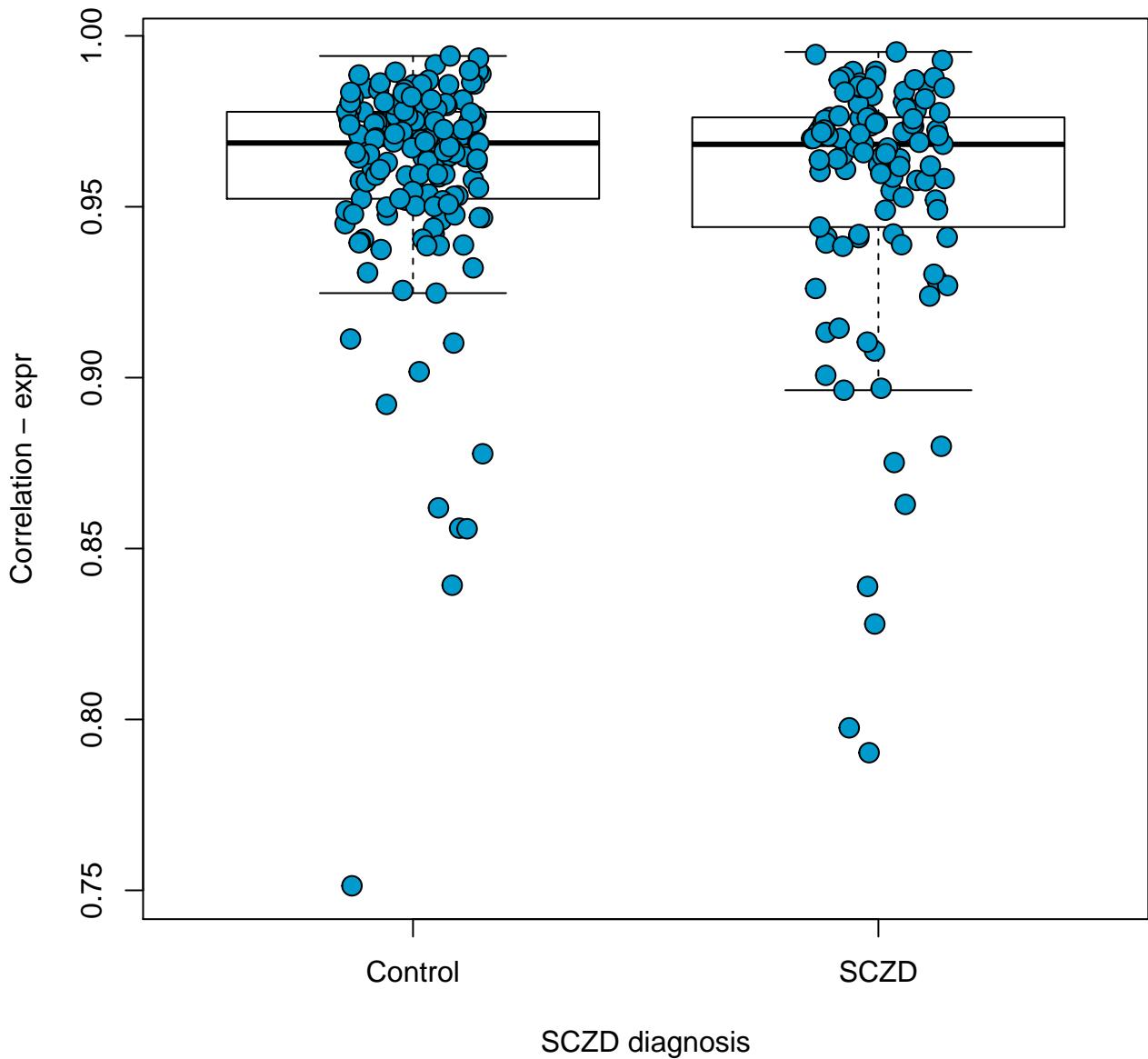
p-value: 0.47



hsa00760: Nicotinate and nicotinamide metabolism
p-value: 0.168

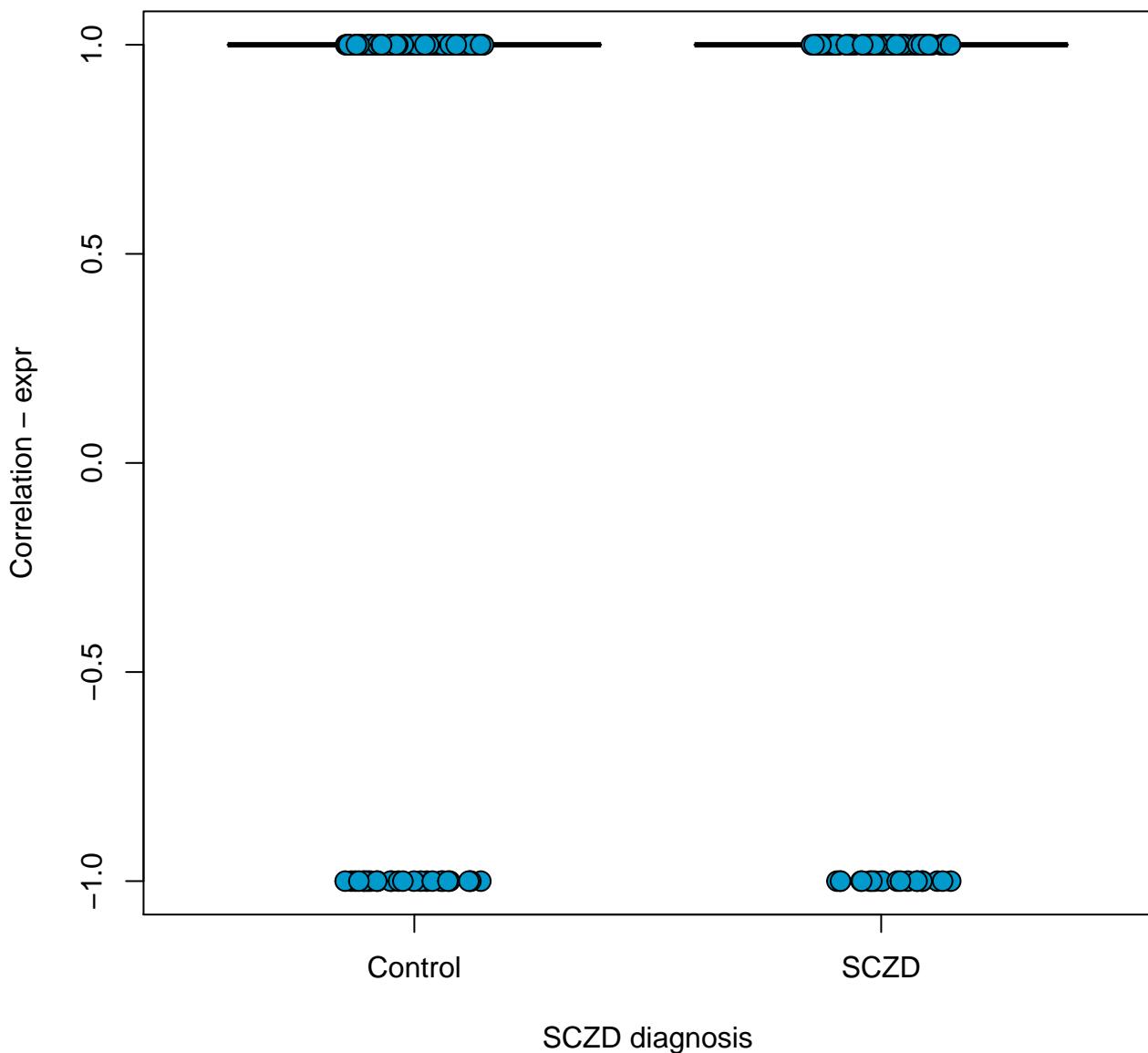


hsa00770: Pantothenate and CoA biosynthesis
p-value: 0.233



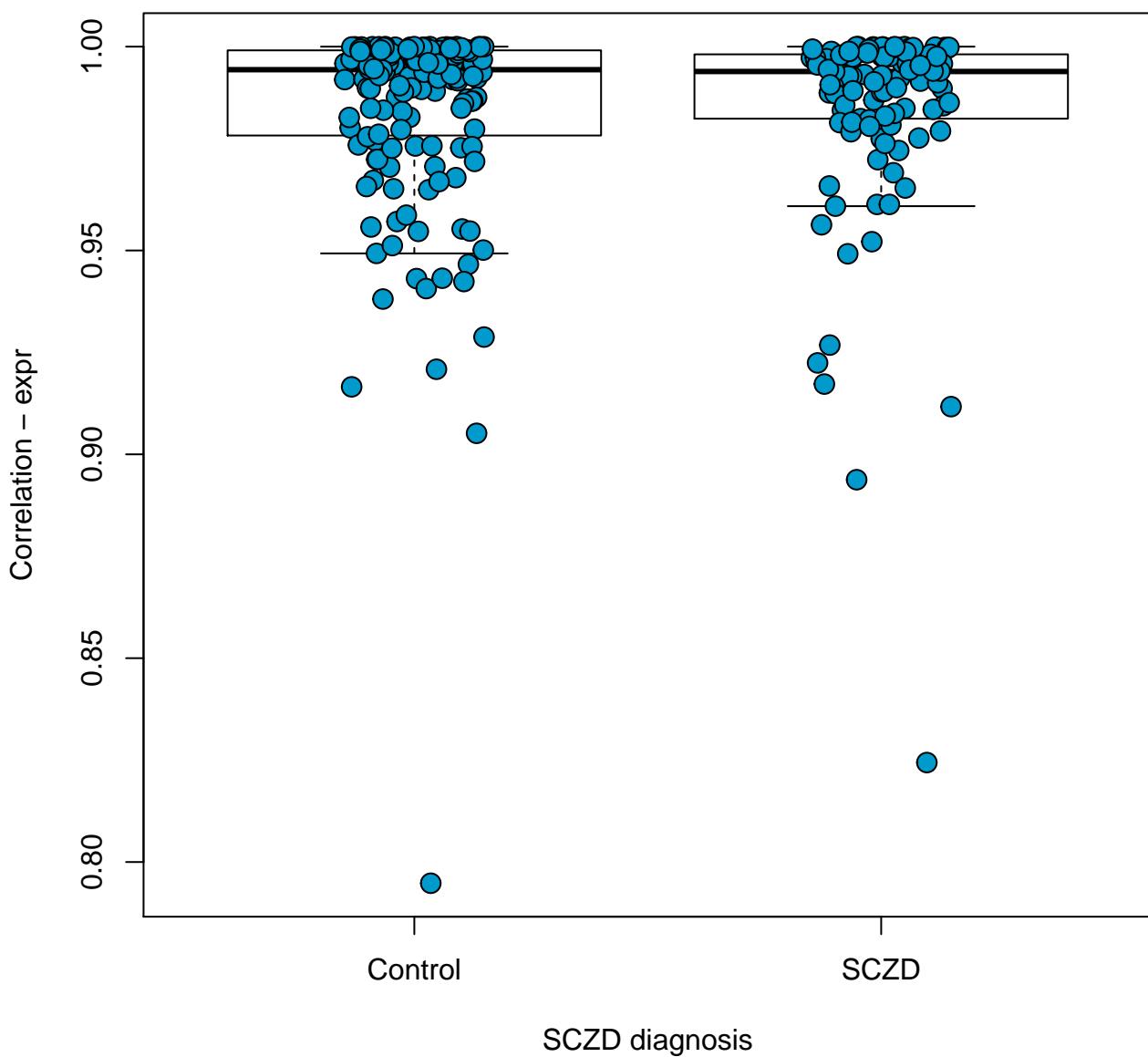
hsa00780: Biotin metabolism

p-value: 0.871

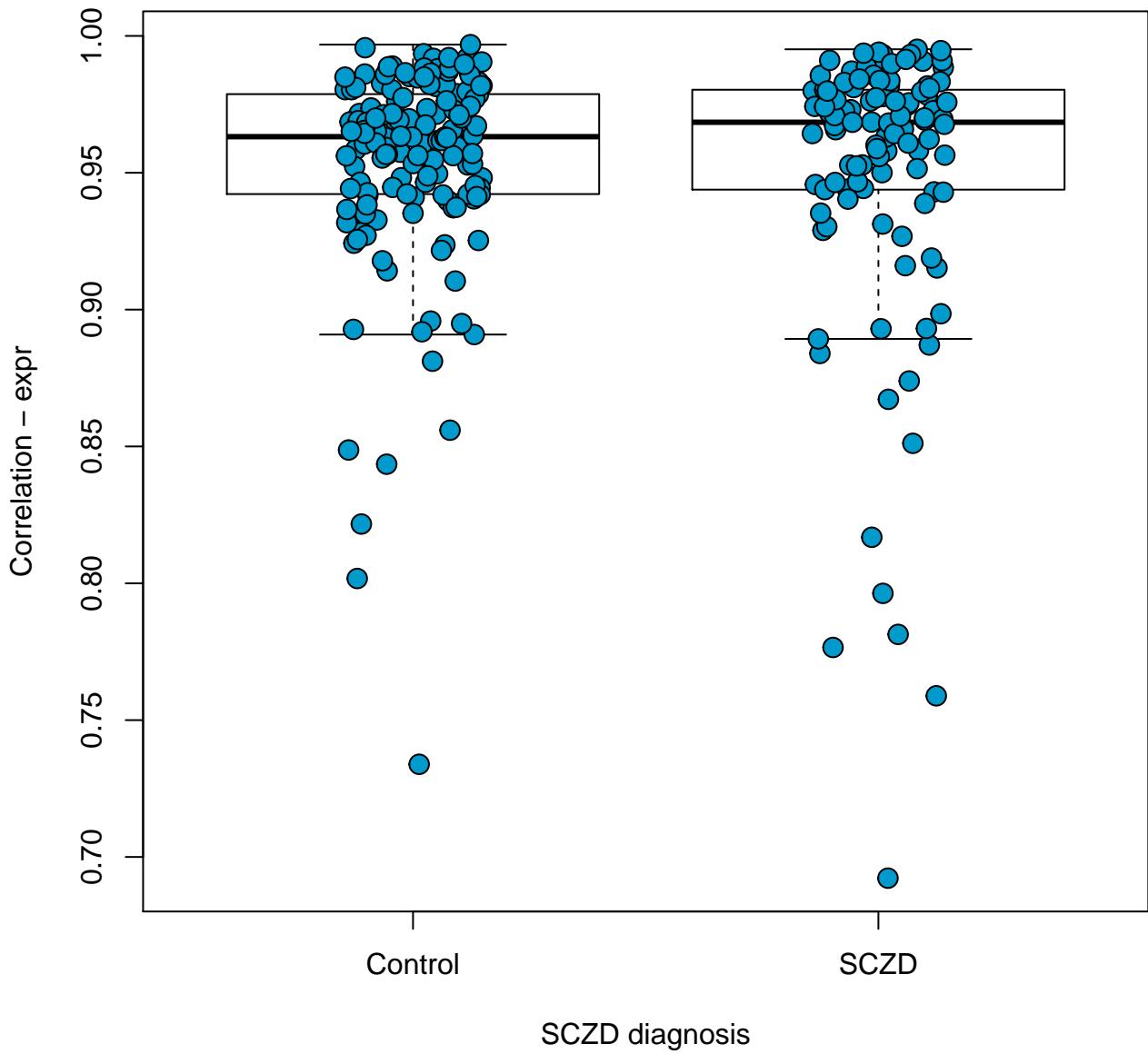


hsa00785: Lipoic acid metabolism

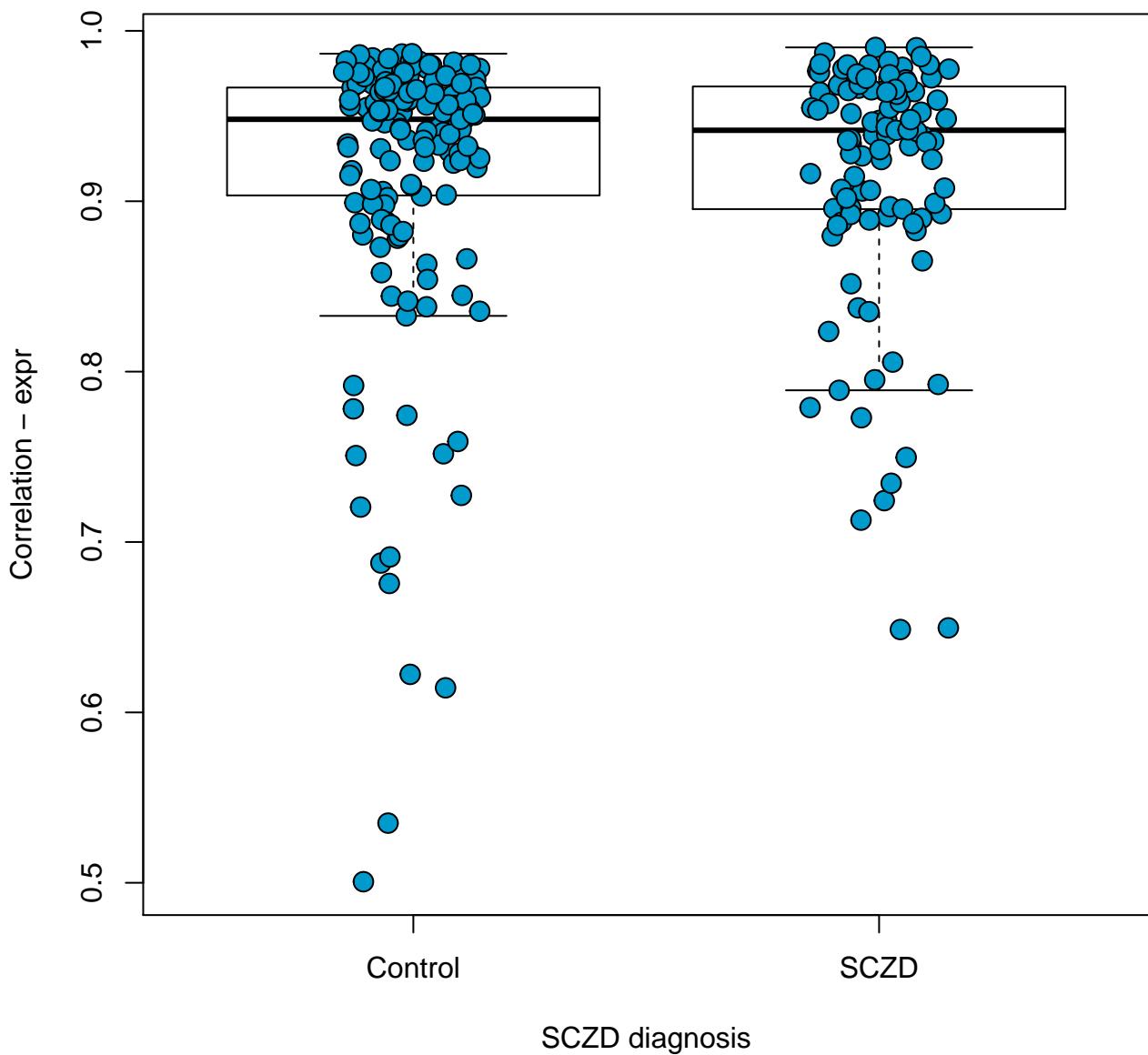
p-value: 0.909



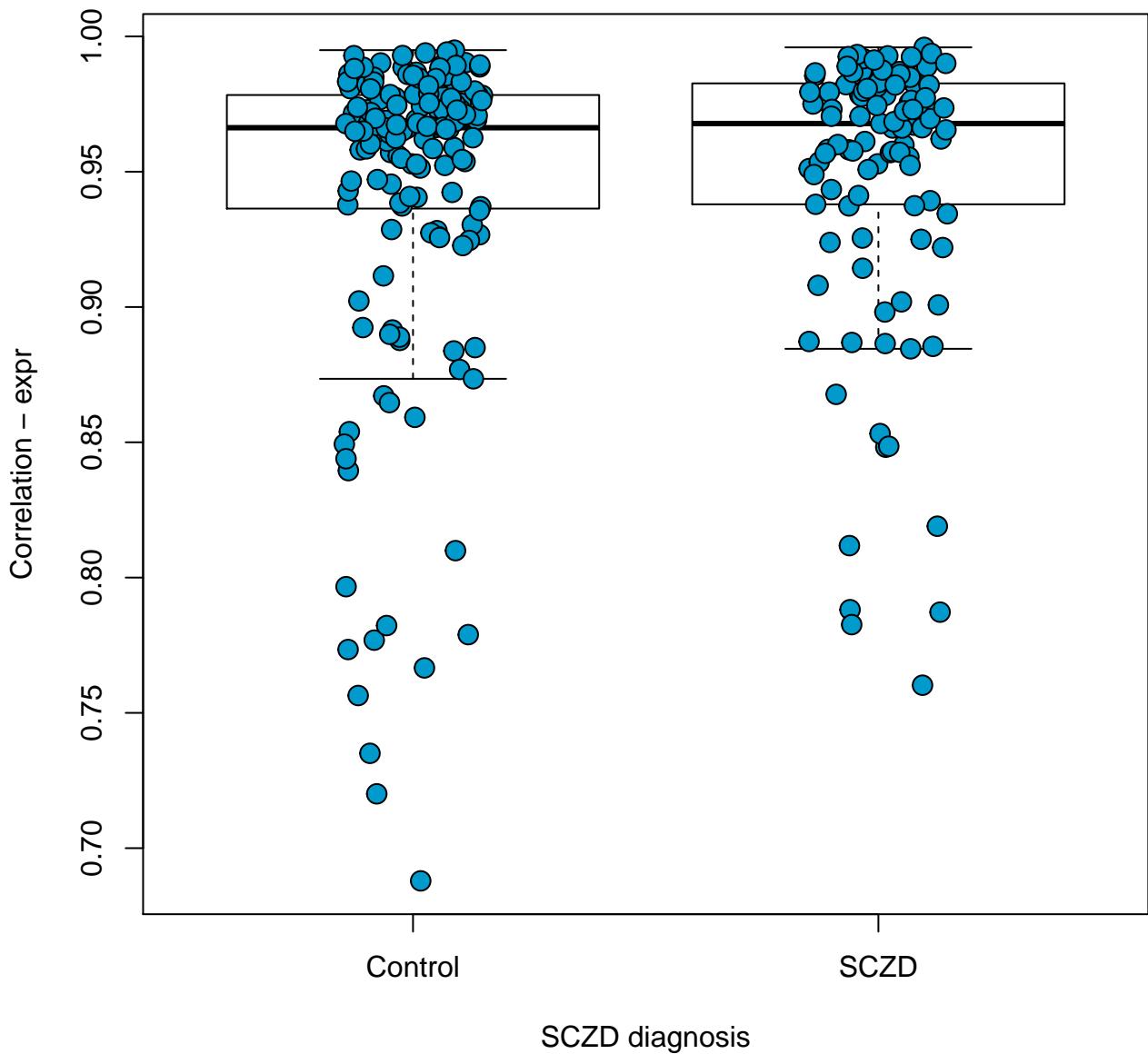
hsa00790: Folate biosynthesis
p-value: 0.362



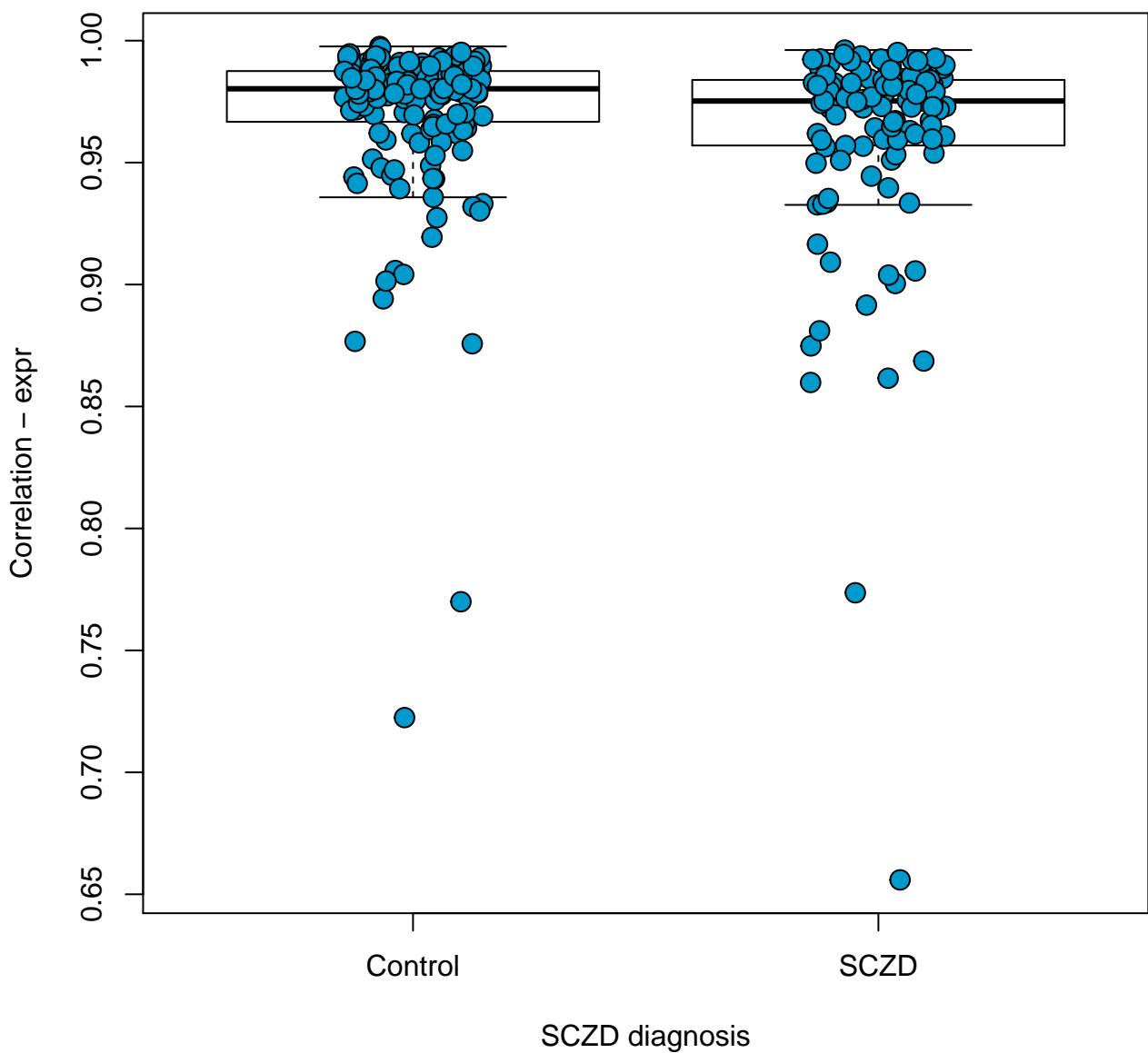
hsa00830: Retinol metabolism
p-value: 0.922



hsa00860: Porphyrin and chlorophyll metabolism
p-value: 0.341

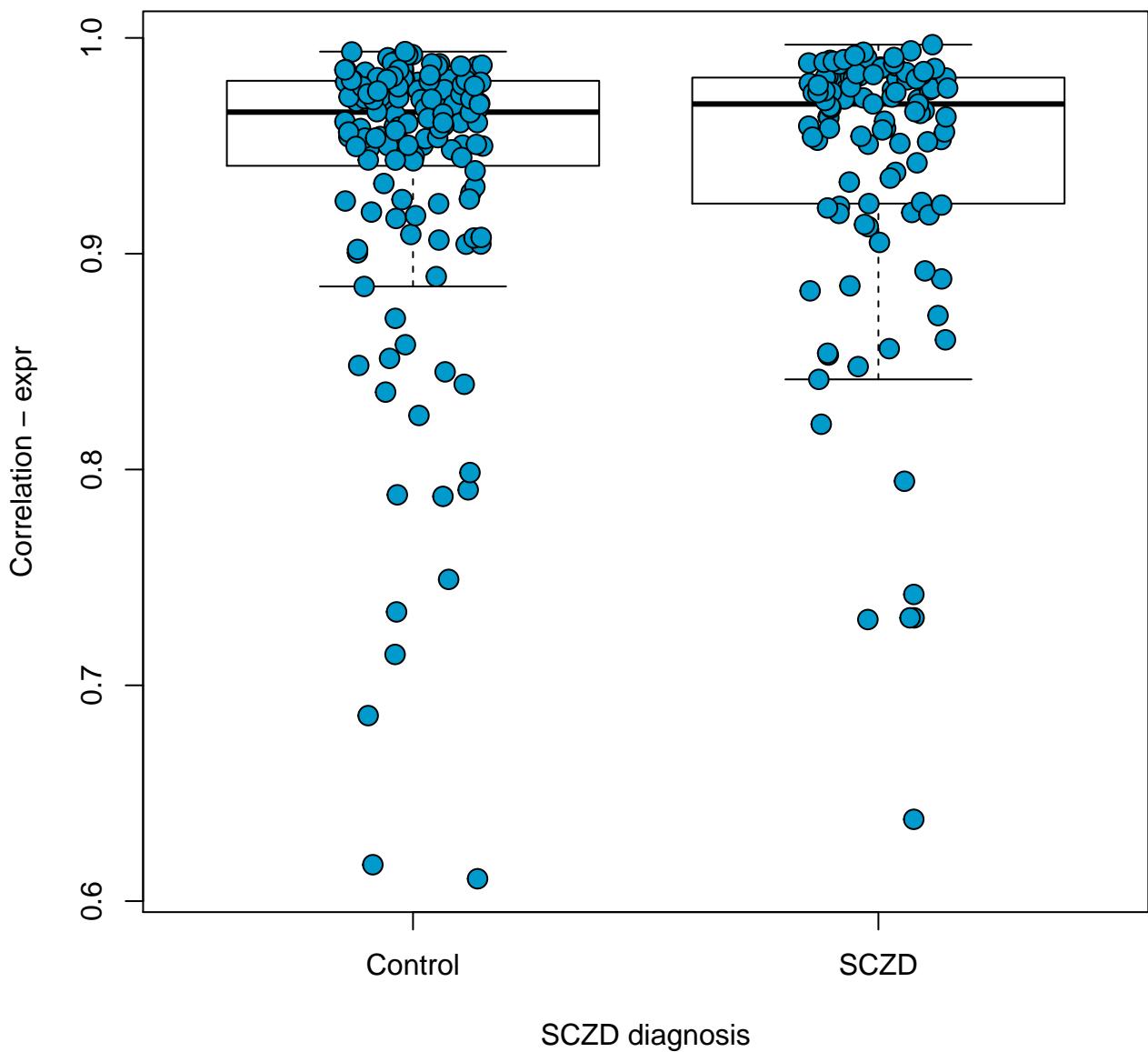


hsa00900: Terpenoid backbone biosynthesis
p-value: 0.0436

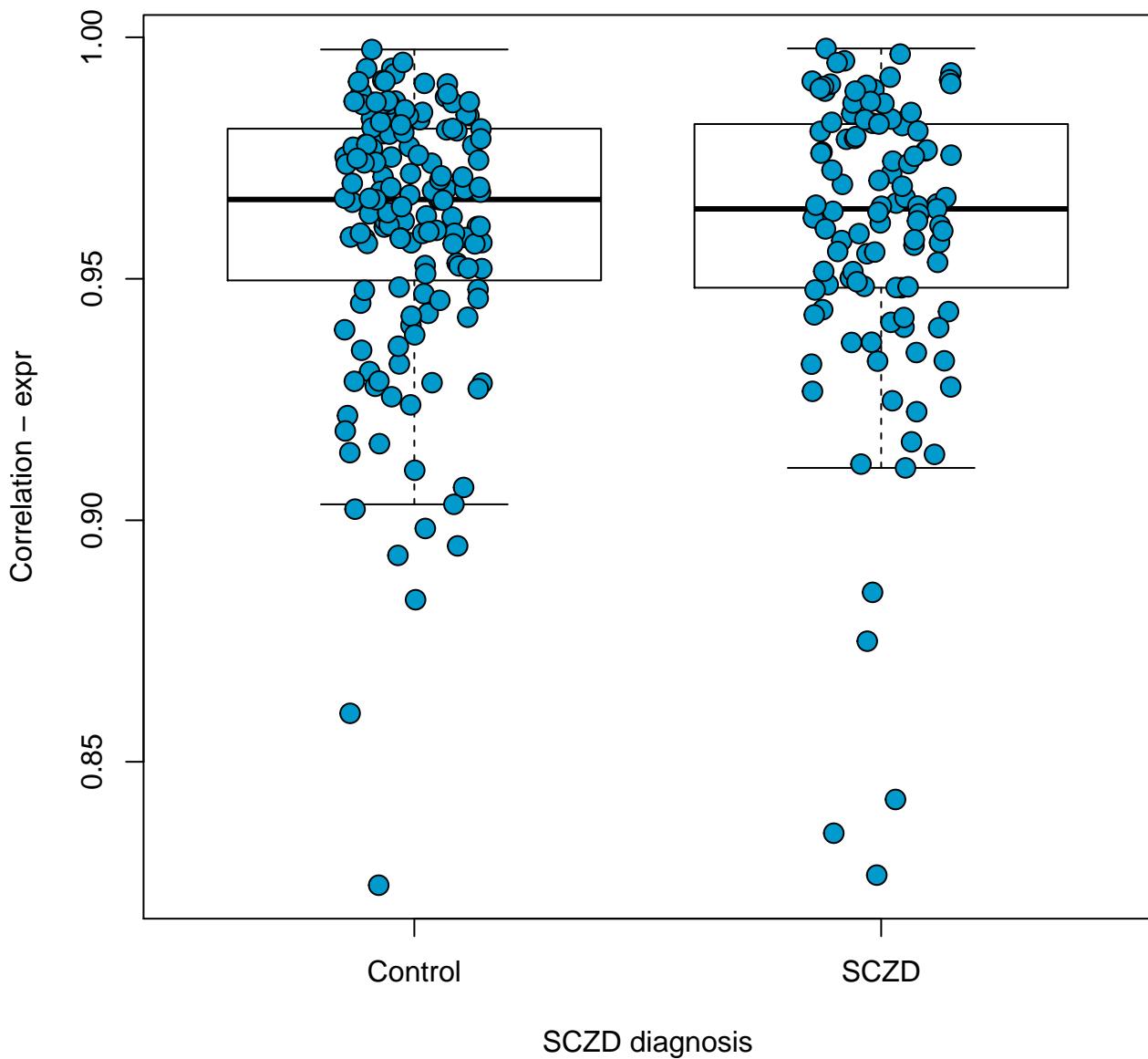


hsa00910: Nitrogen metabolism

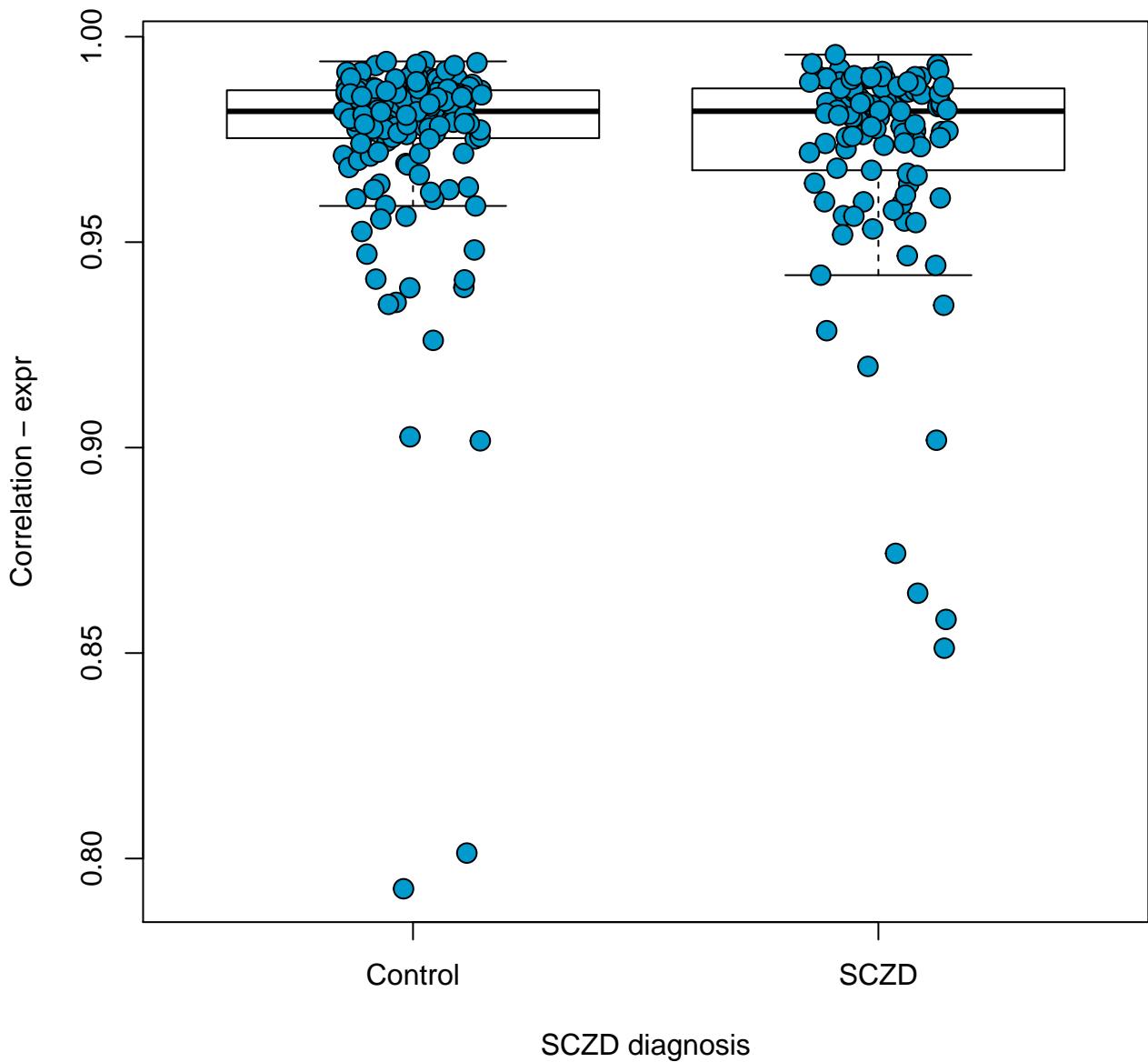
p-value: 0.924



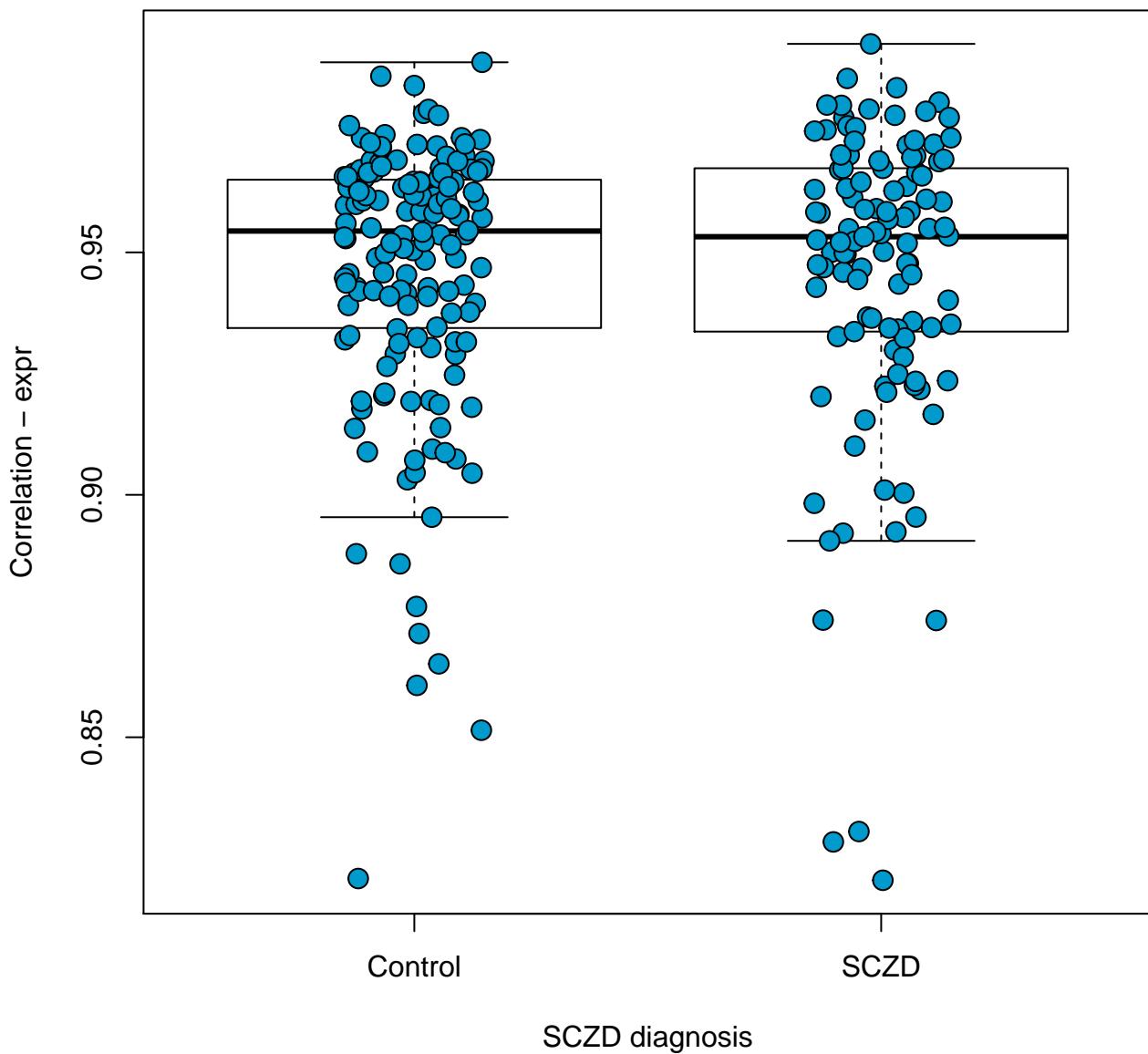
hsa00920: Sulfur metabolism
p-value: 0.628



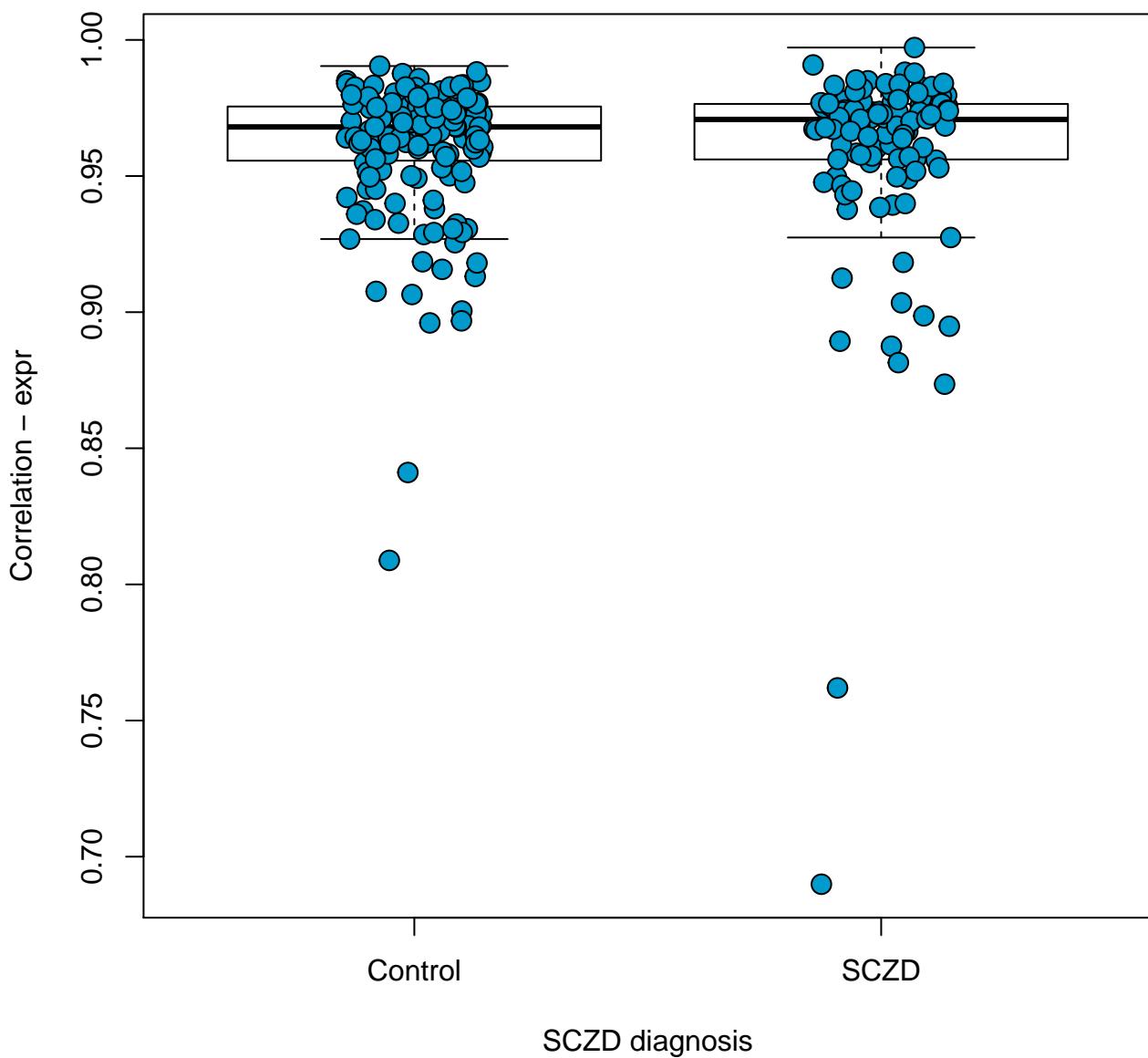
hsa00970: Aminoacyl-tRNA biosynthesis
p-value: 0.356



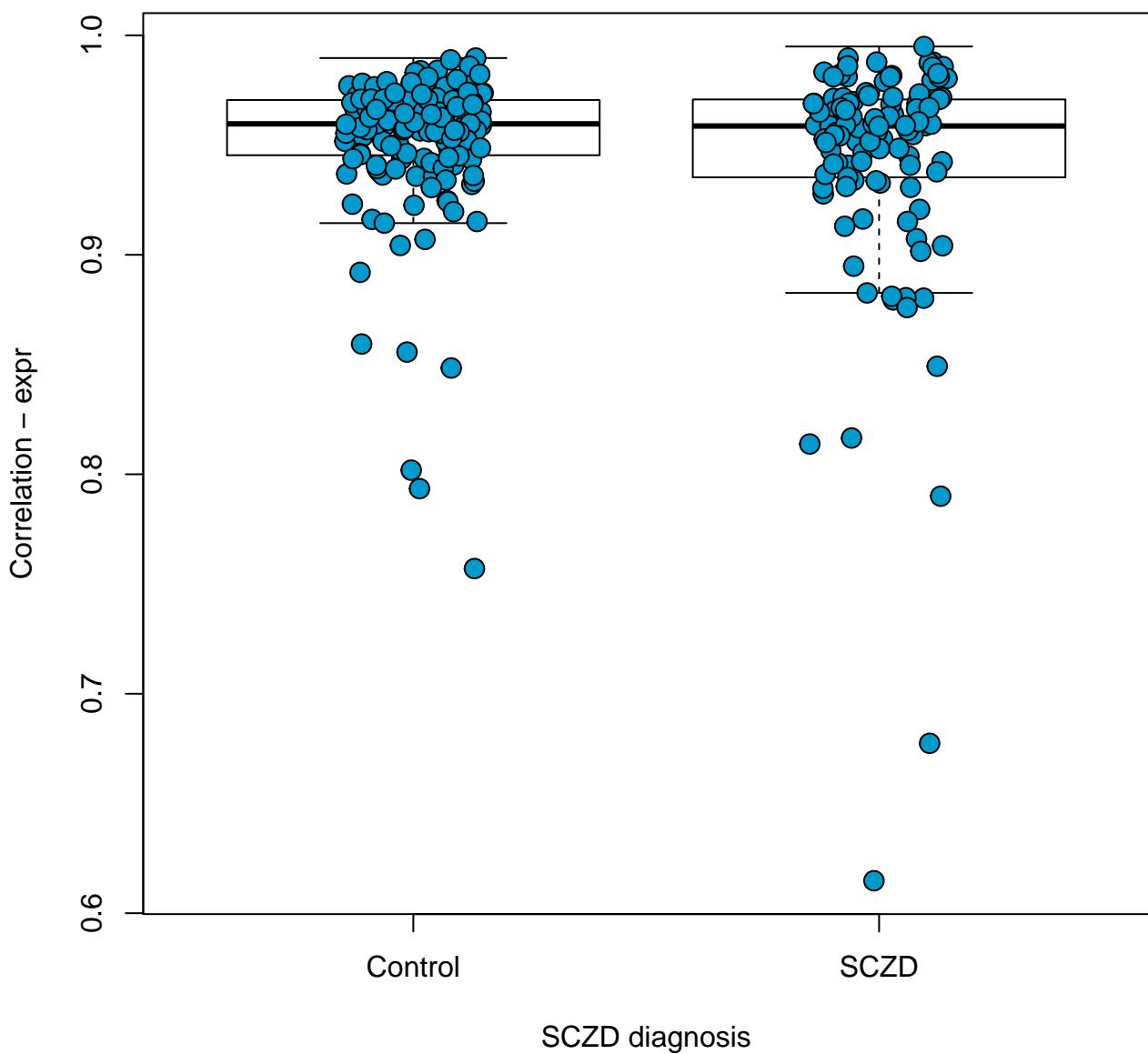
hsa00980: Metabolism of xenobiotics by cytochrome P450
p-value: 0.767



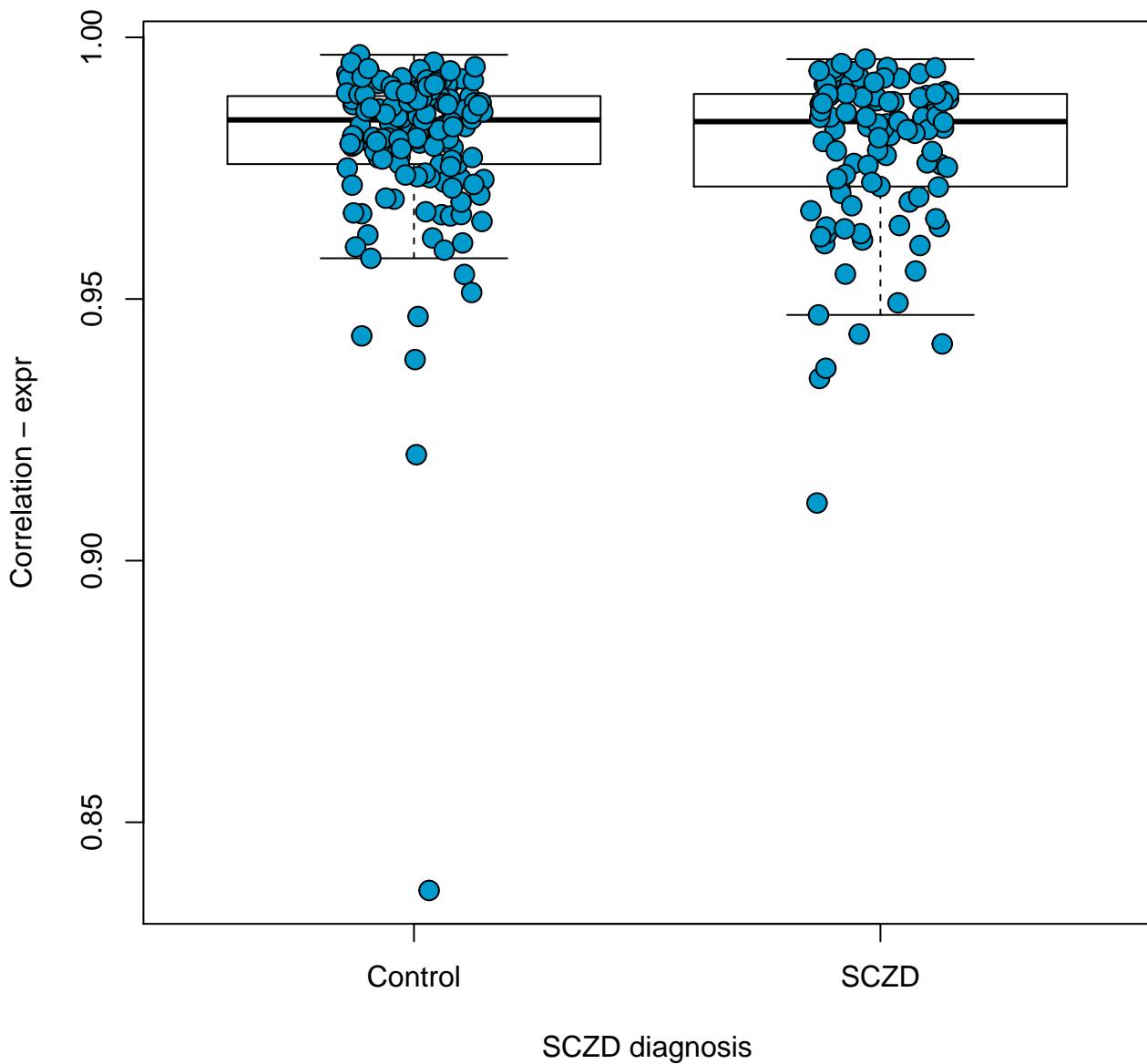
hsa00982: Drug metabolism – cytochrome P450
p-value: 0.534



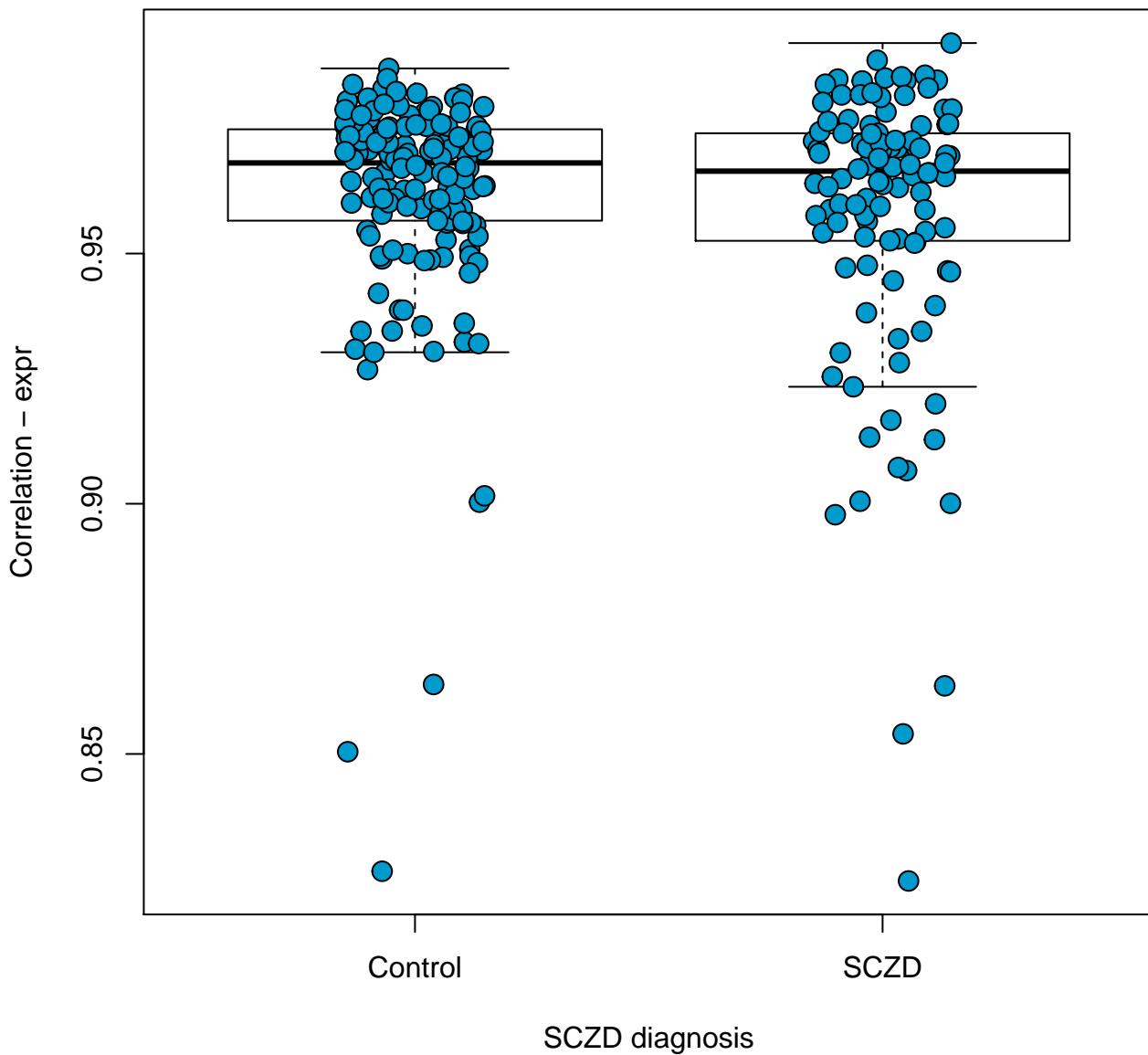
hsa00983: Drug metabolism – other enzymes
p-value: 0.0649



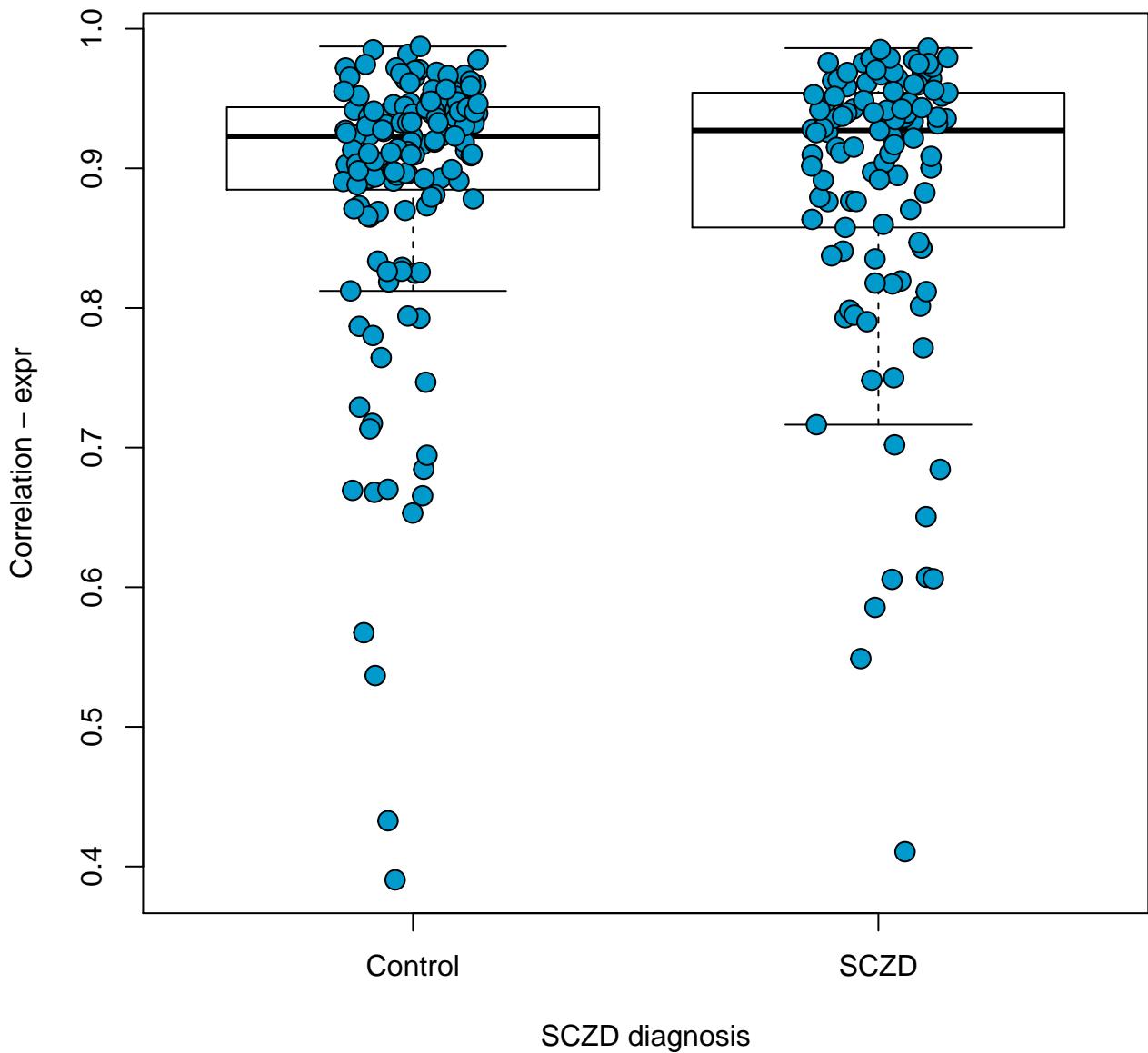
hsa01040: Biosynthesis of unsaturated fatty acids
p-value: 0.611



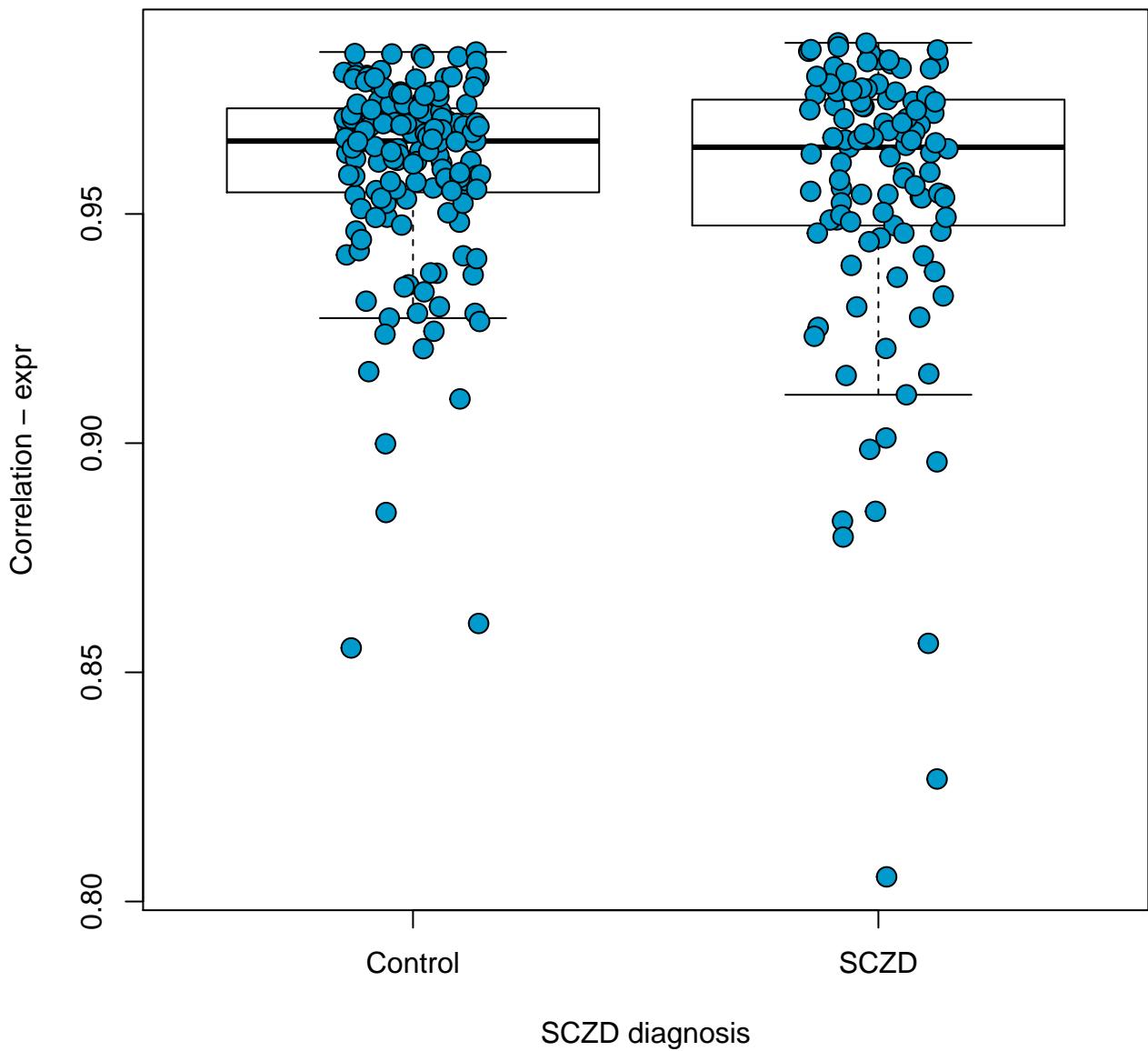
hsa01100: Metabolic pathways
p-value: 0.173



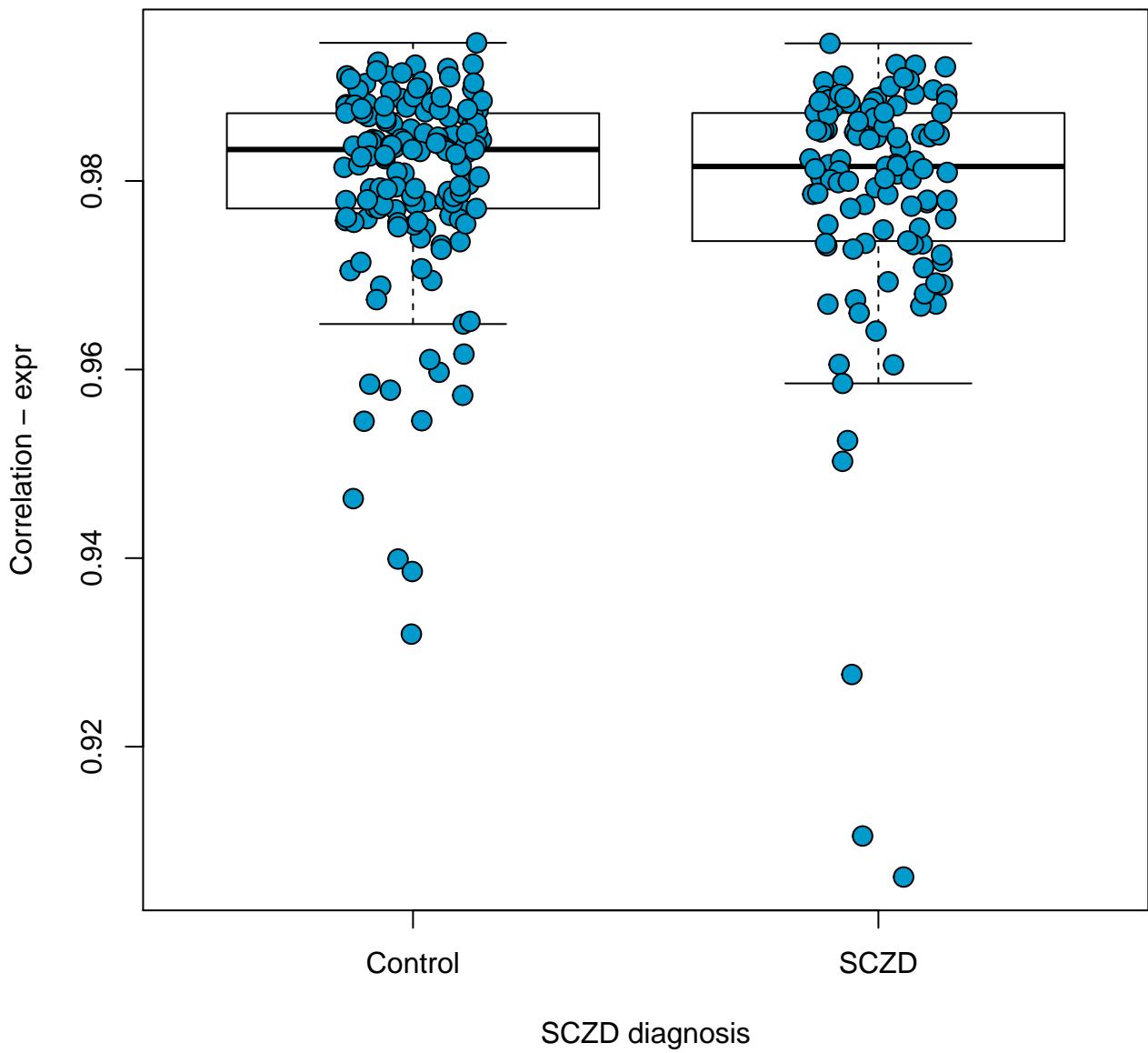
hsa02010: ABC transporters
p-value: 0.763



hsa03008: Ribosome biogenesis in eukaryotes
p-value: 0.0819

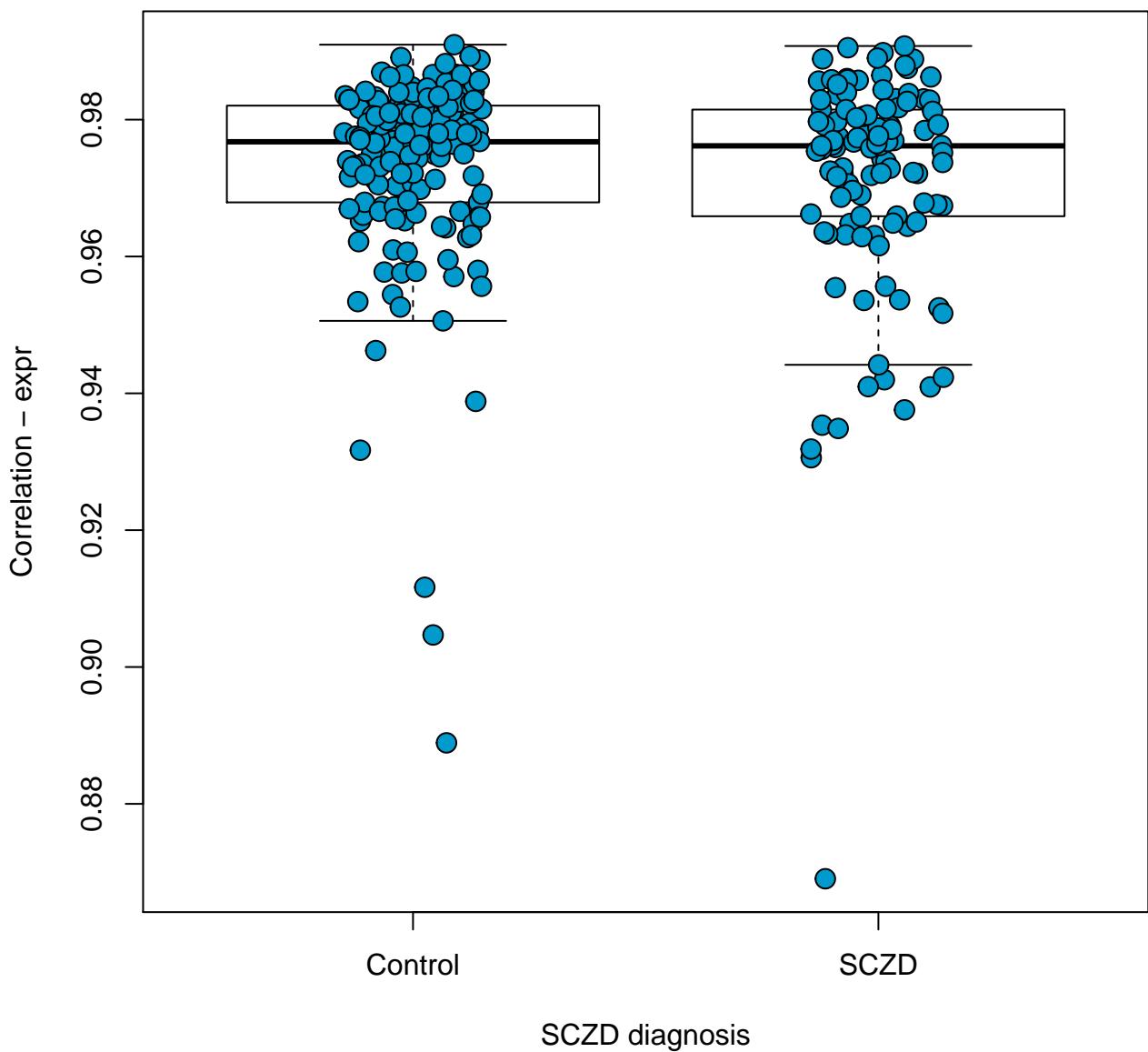


hsa03010: Ribosome
p-value: 0.212

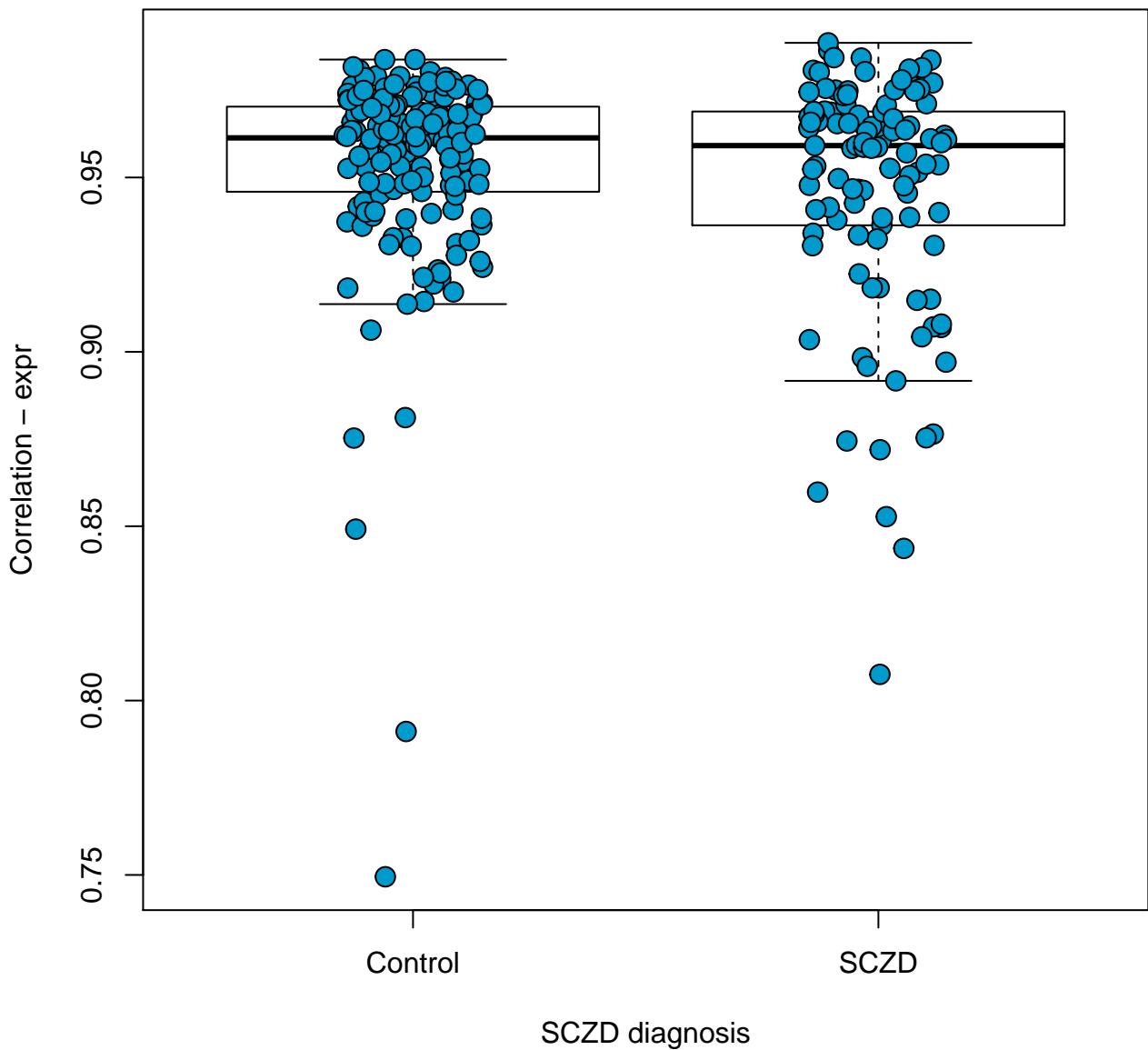


hsa03013: RNA transport

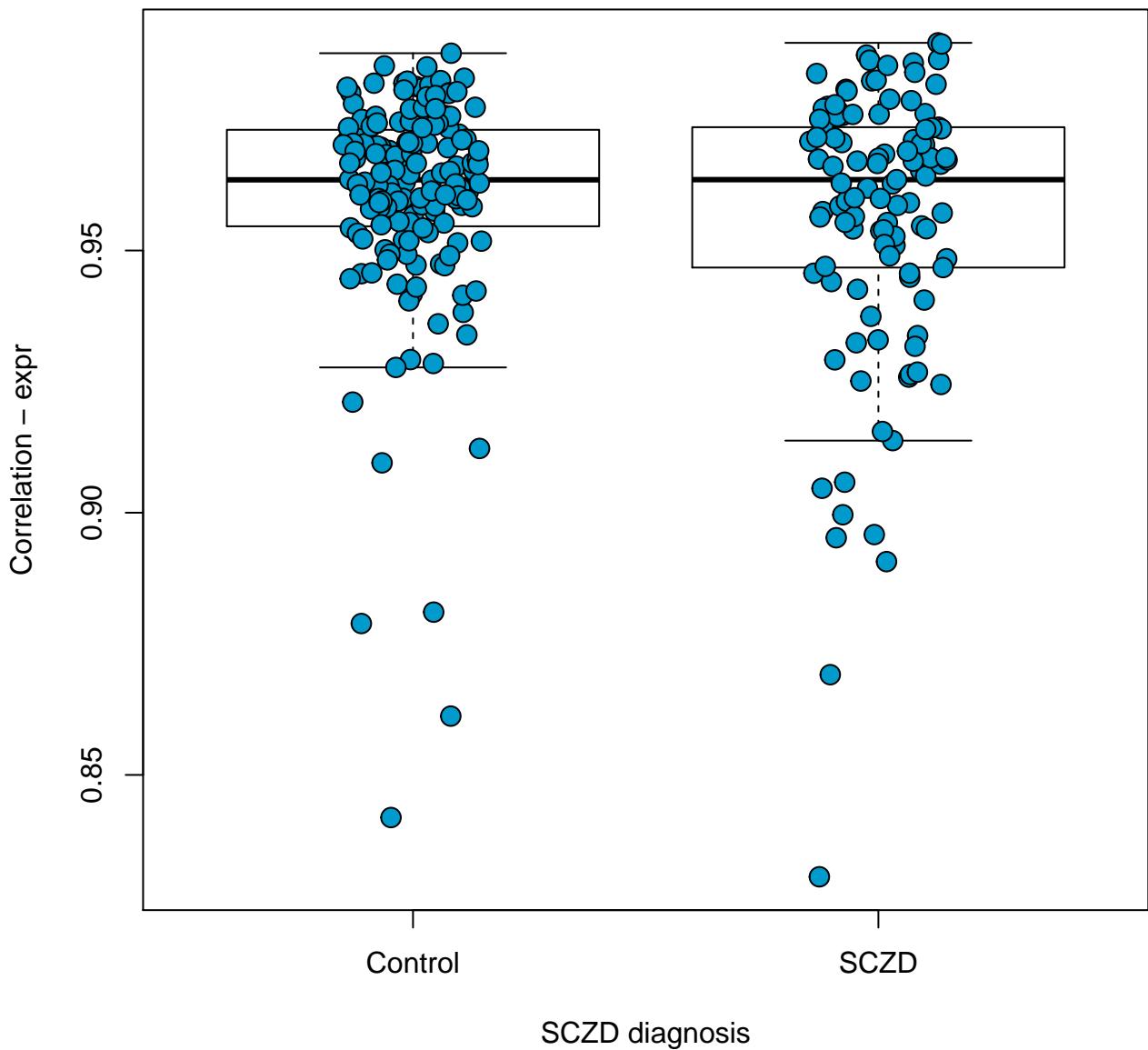
p-value: 0.269



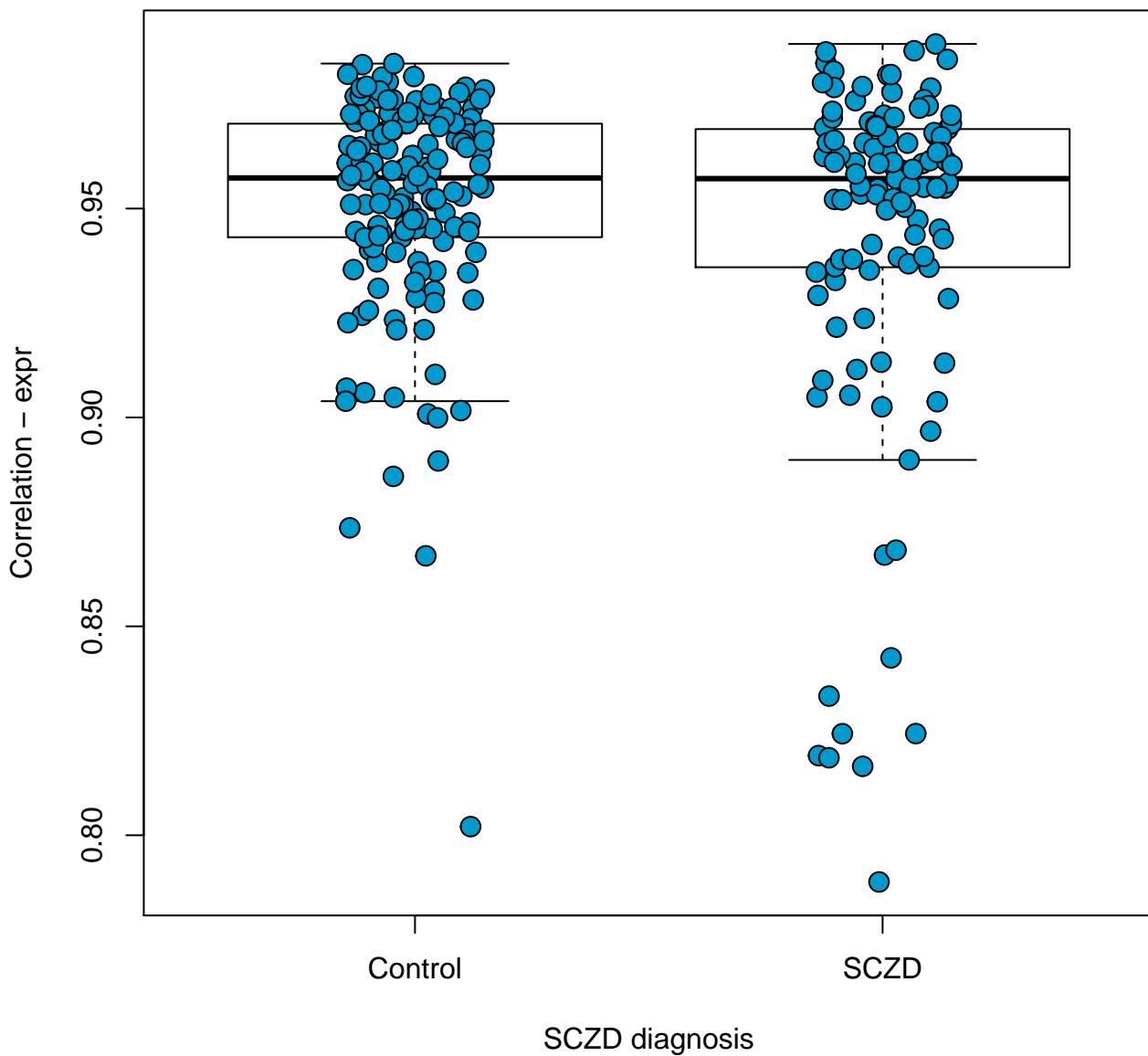
hsa03015: mRNA surveillance pathway
p-value: 0.117



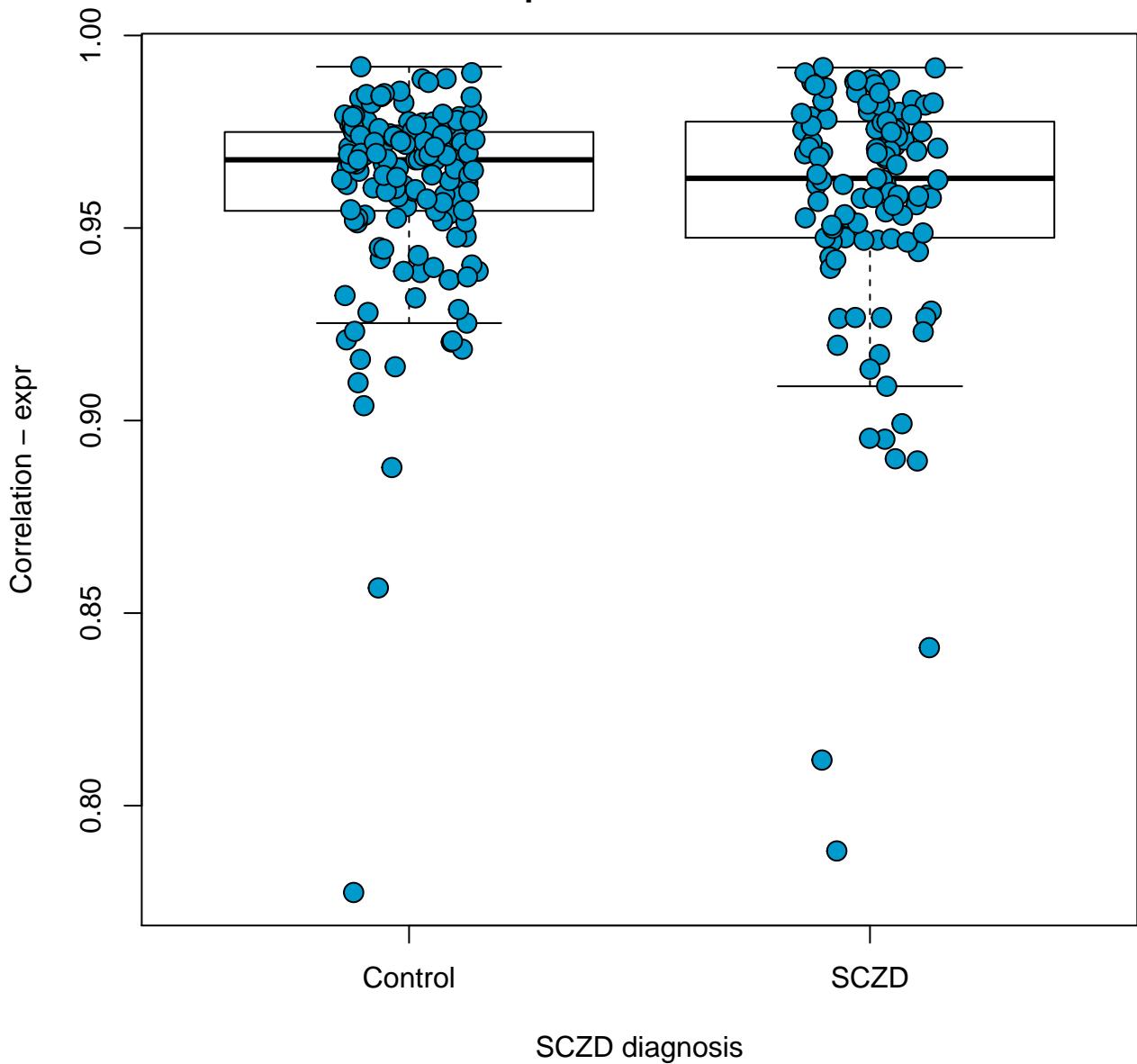
hsa03018: RNA degradation
p-value: 0.162



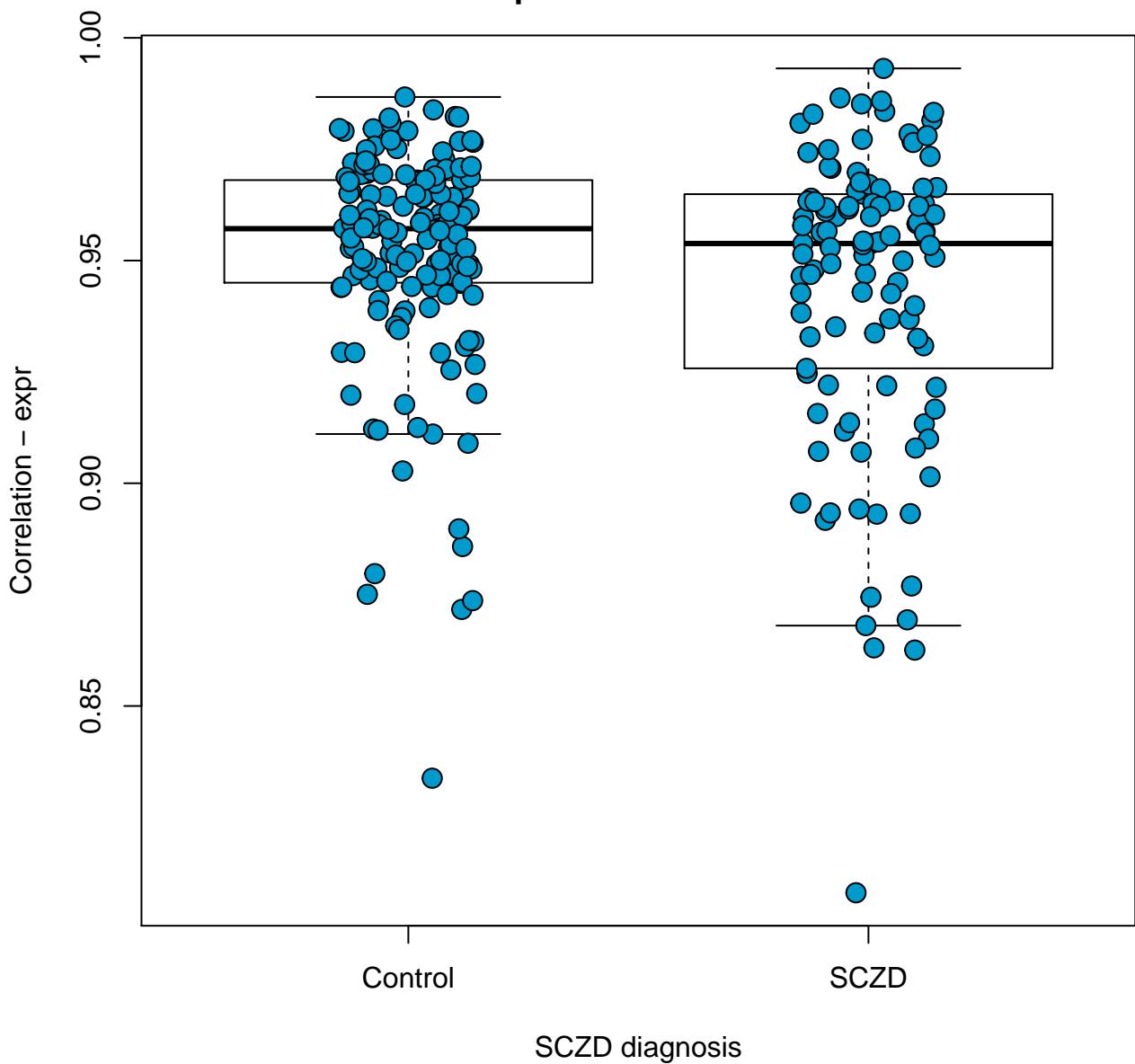
hsa03020: RNA polymerase
p-value: 0.032



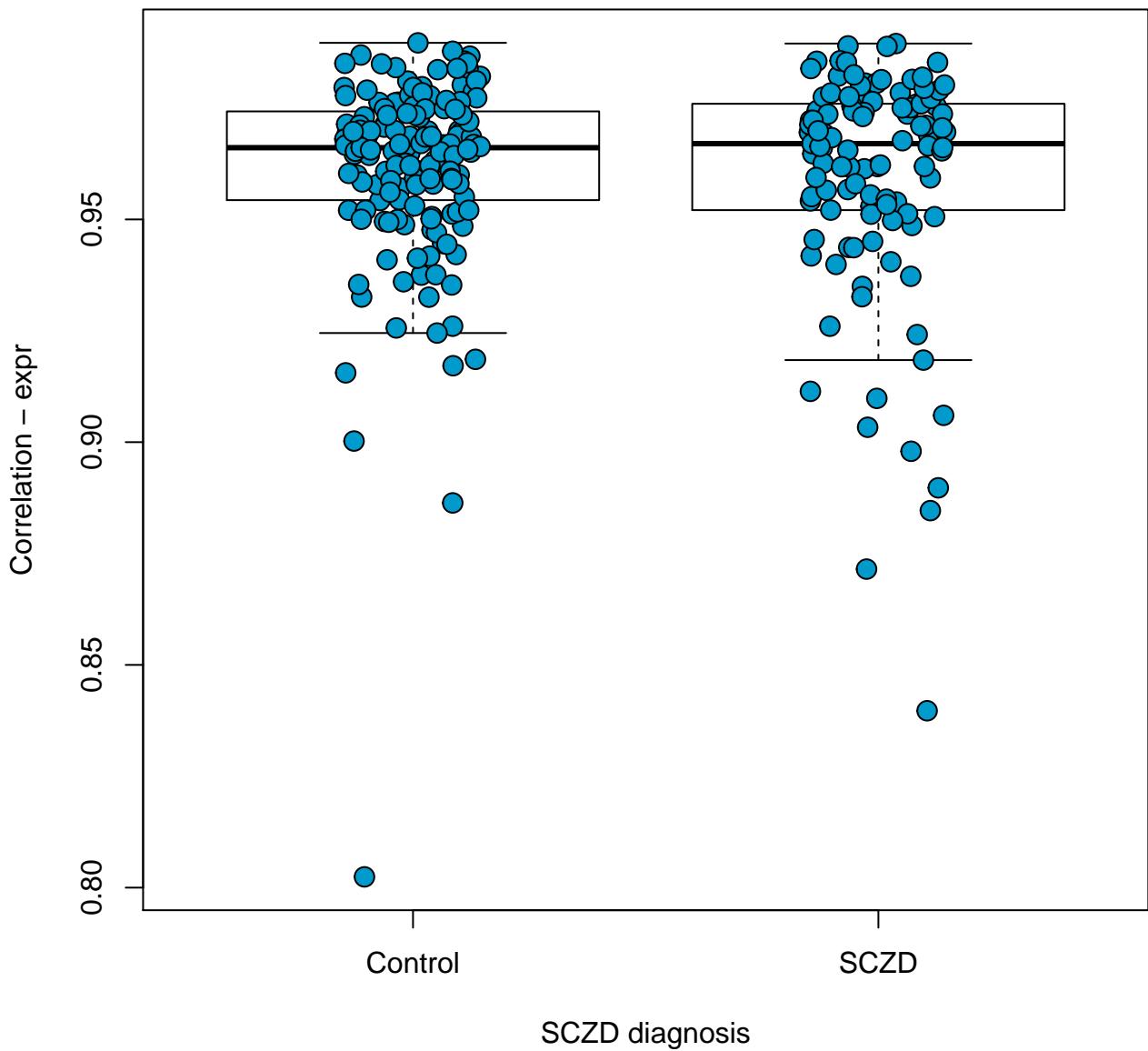
hsa03022: Basal transcription factors
p-value: 0.206



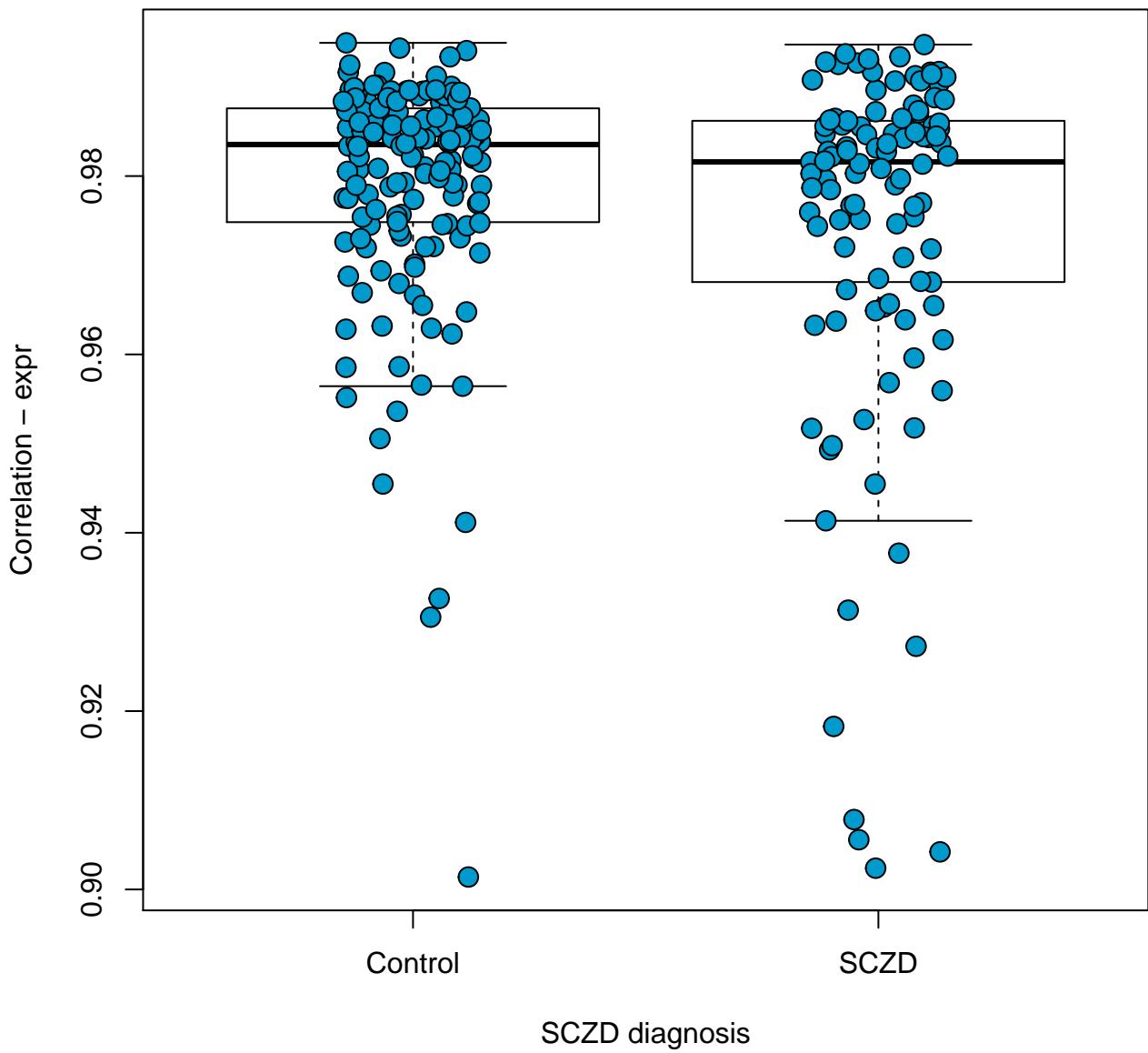
hsa03030: DNA replication
p-value: 0.0275



hsa03040: Spliceosome
p-value: 0.474

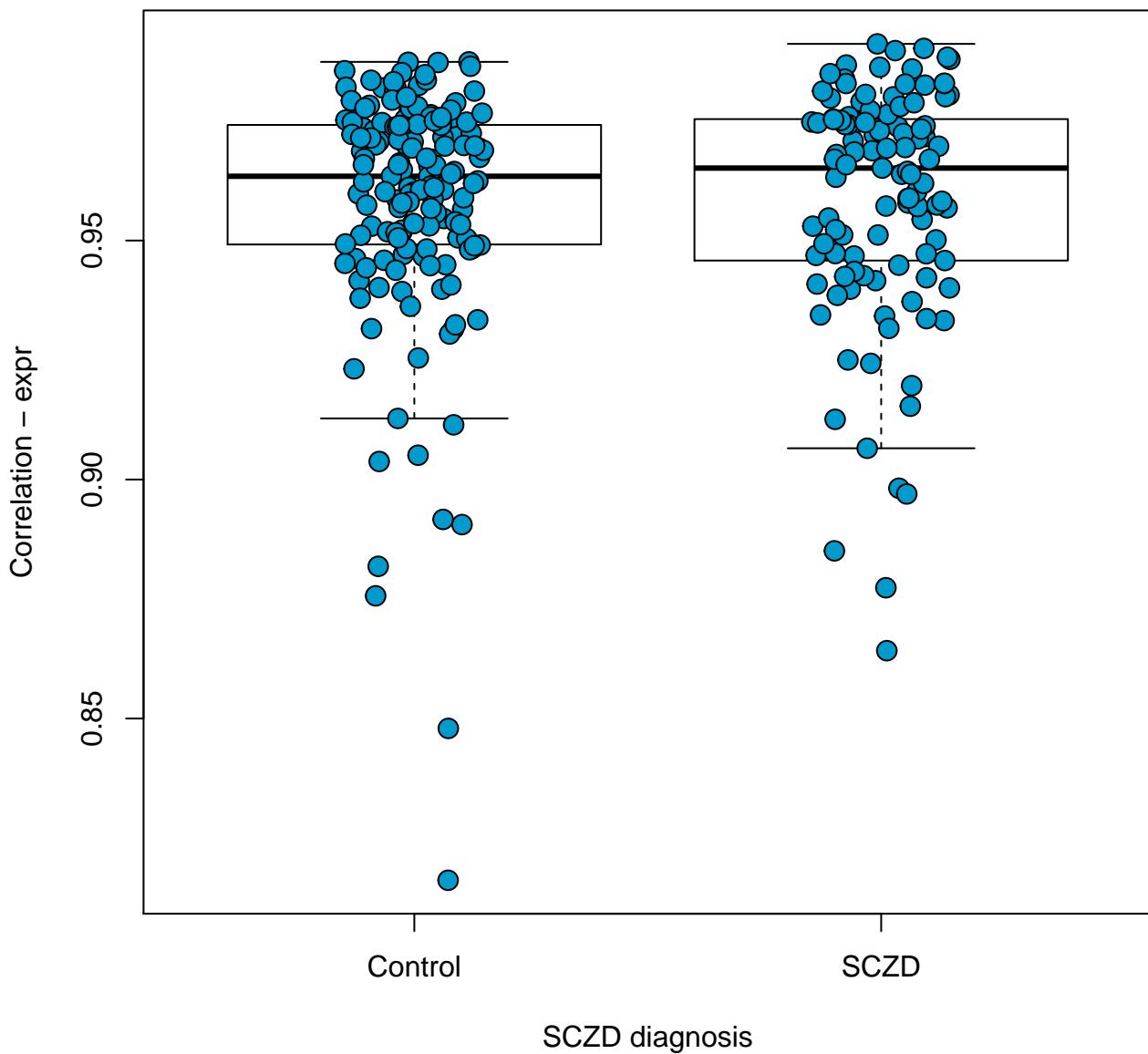


hsa03050: Proteasome
p-value: 0.0132

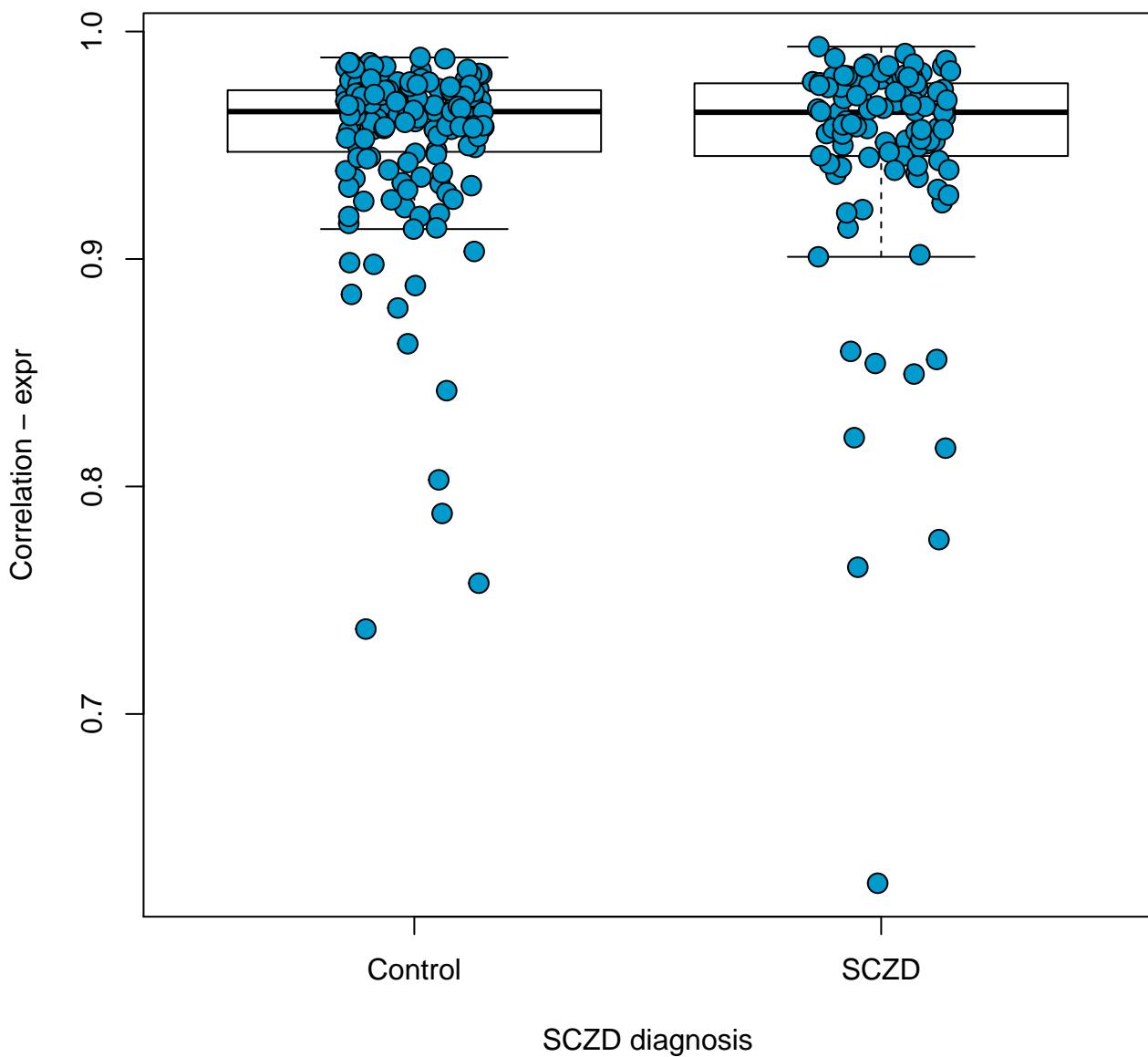


hsa03060: Protein export

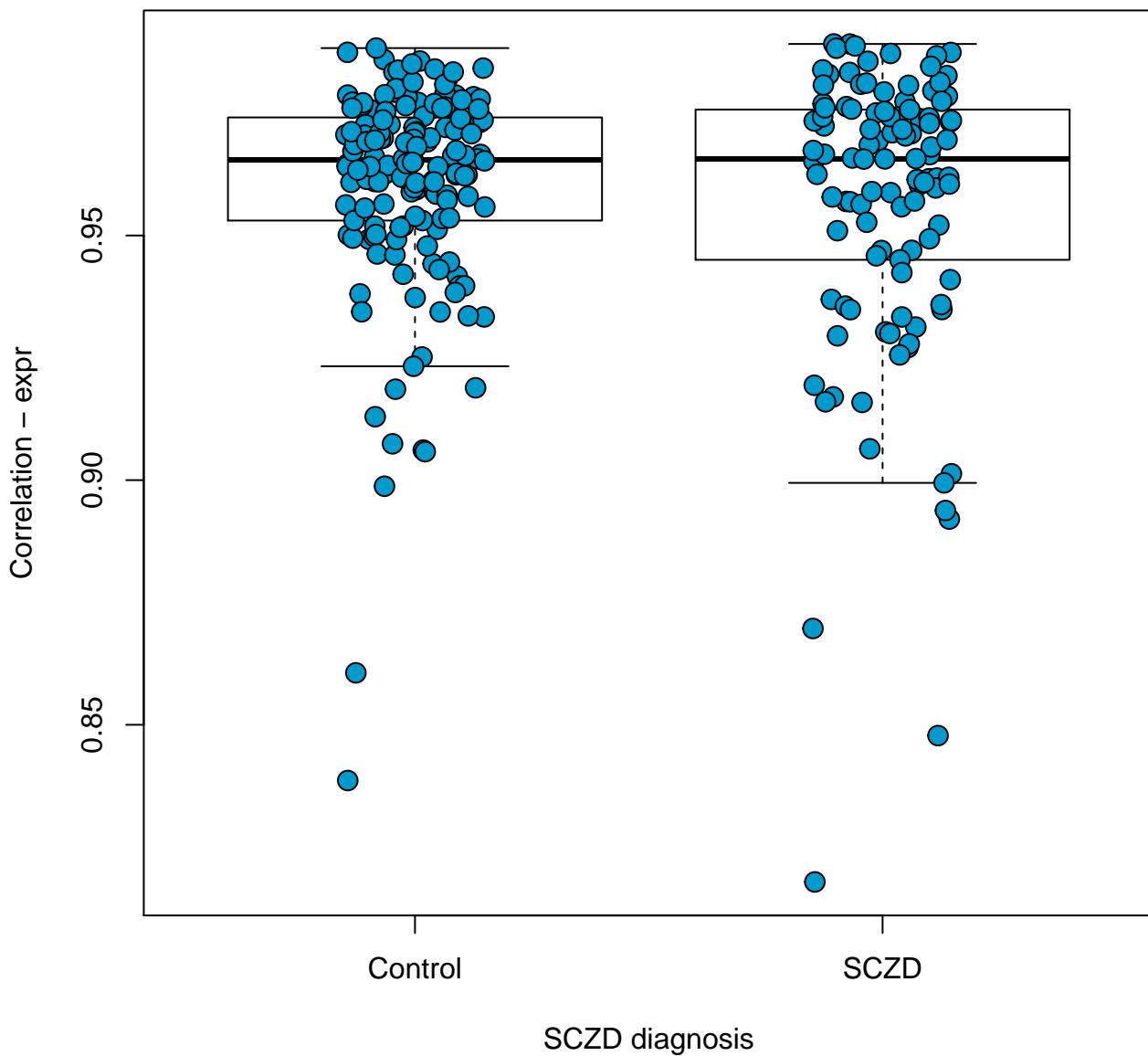
p-value: 0.869



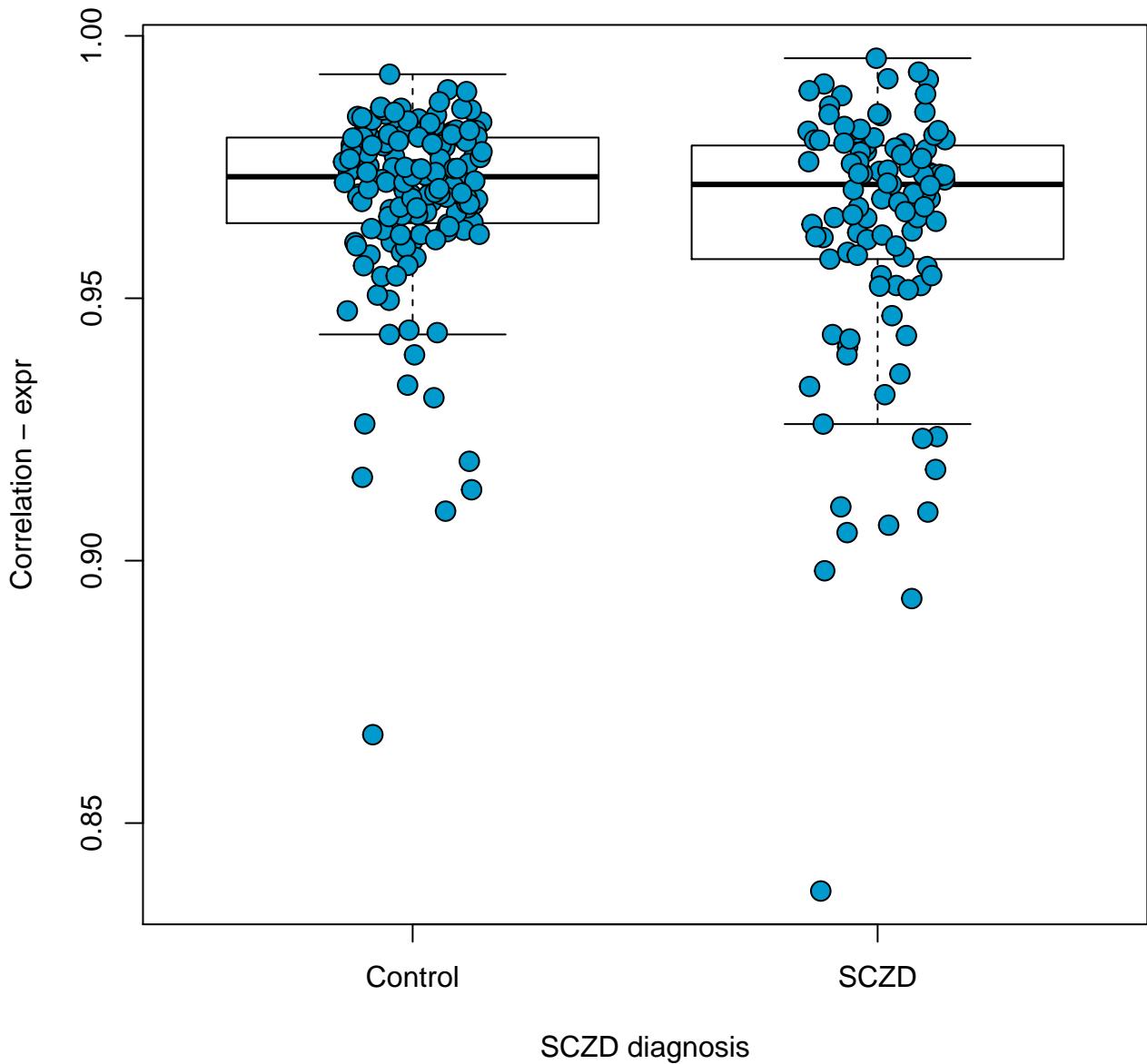
hsa03320: PPAR signaling pathway
p-value: 0.458



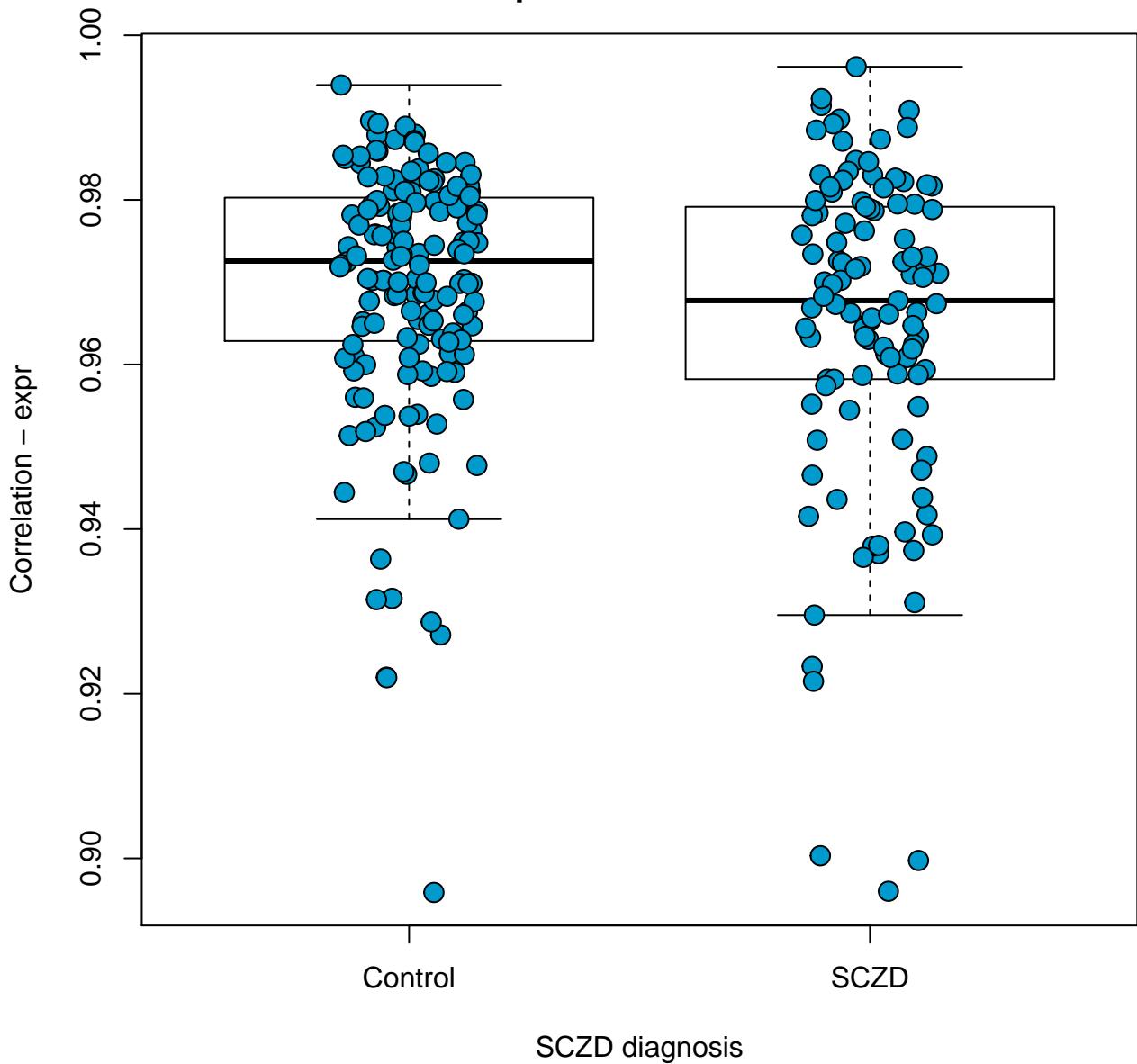
hsa03410: Base excision repair
p-value: 0.181



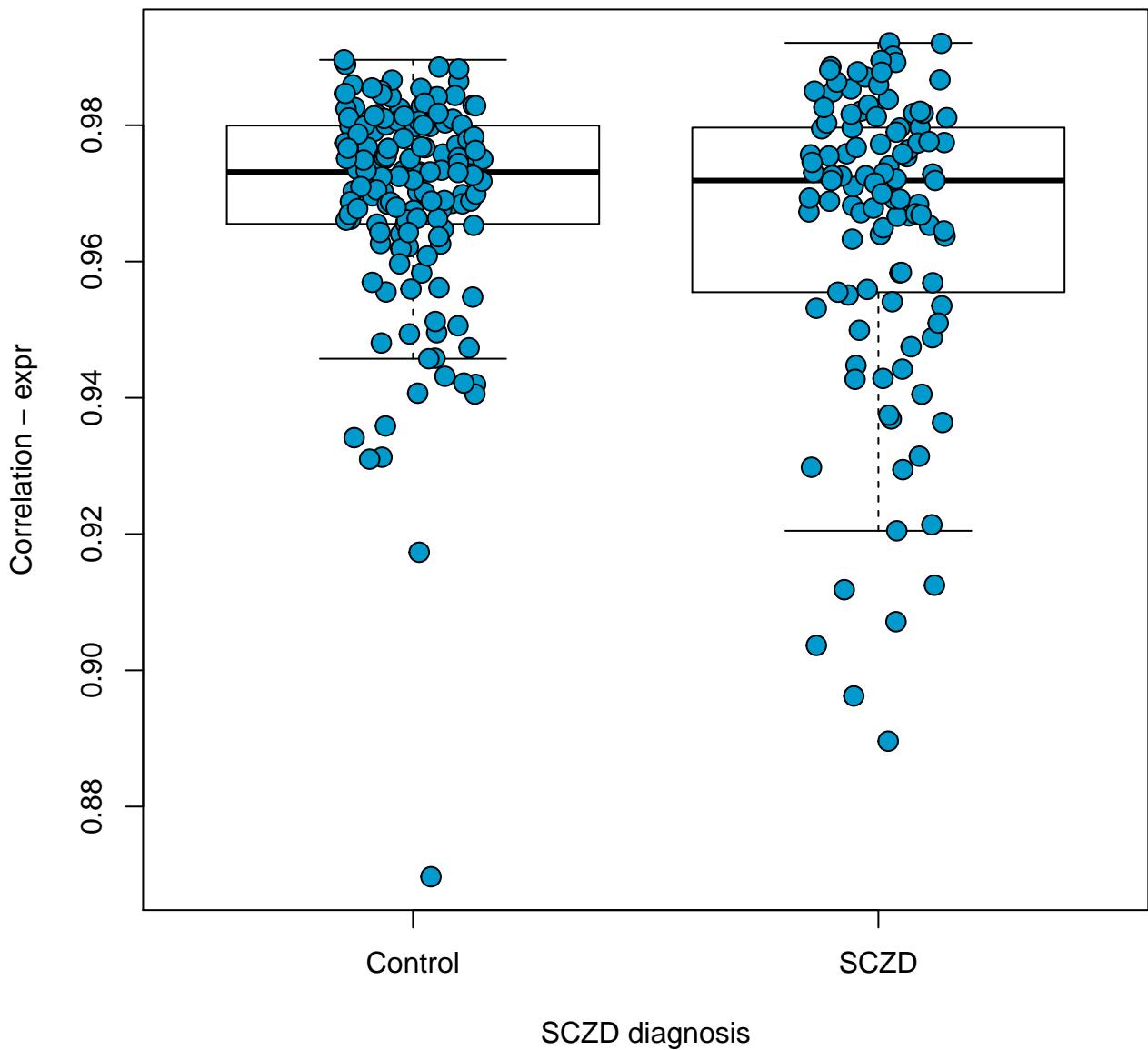
hsa03420: Nucleotide excision repair
p-value: 0.0178



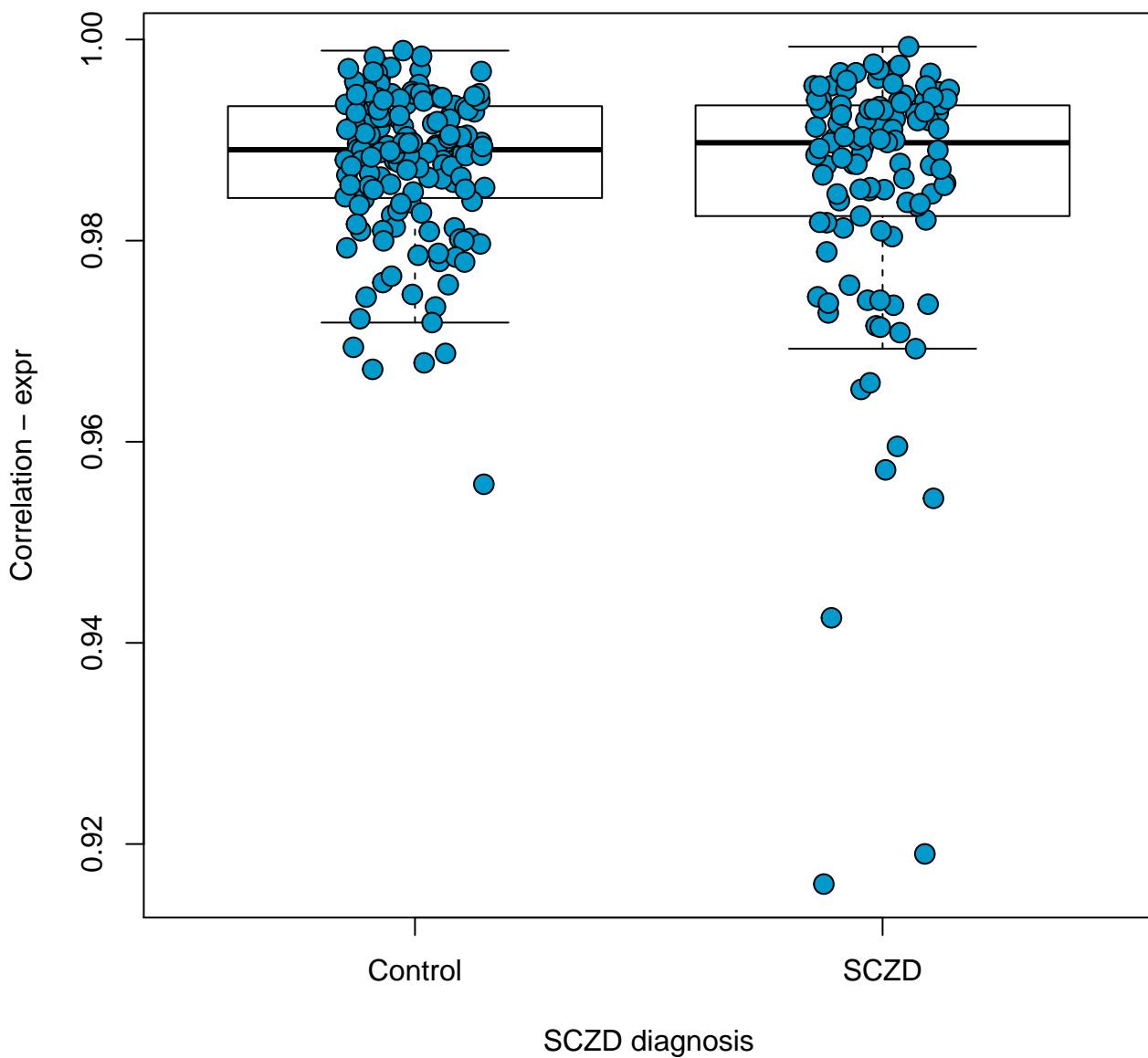
hsa03430: Mismatch repair
p-value: 0.0303



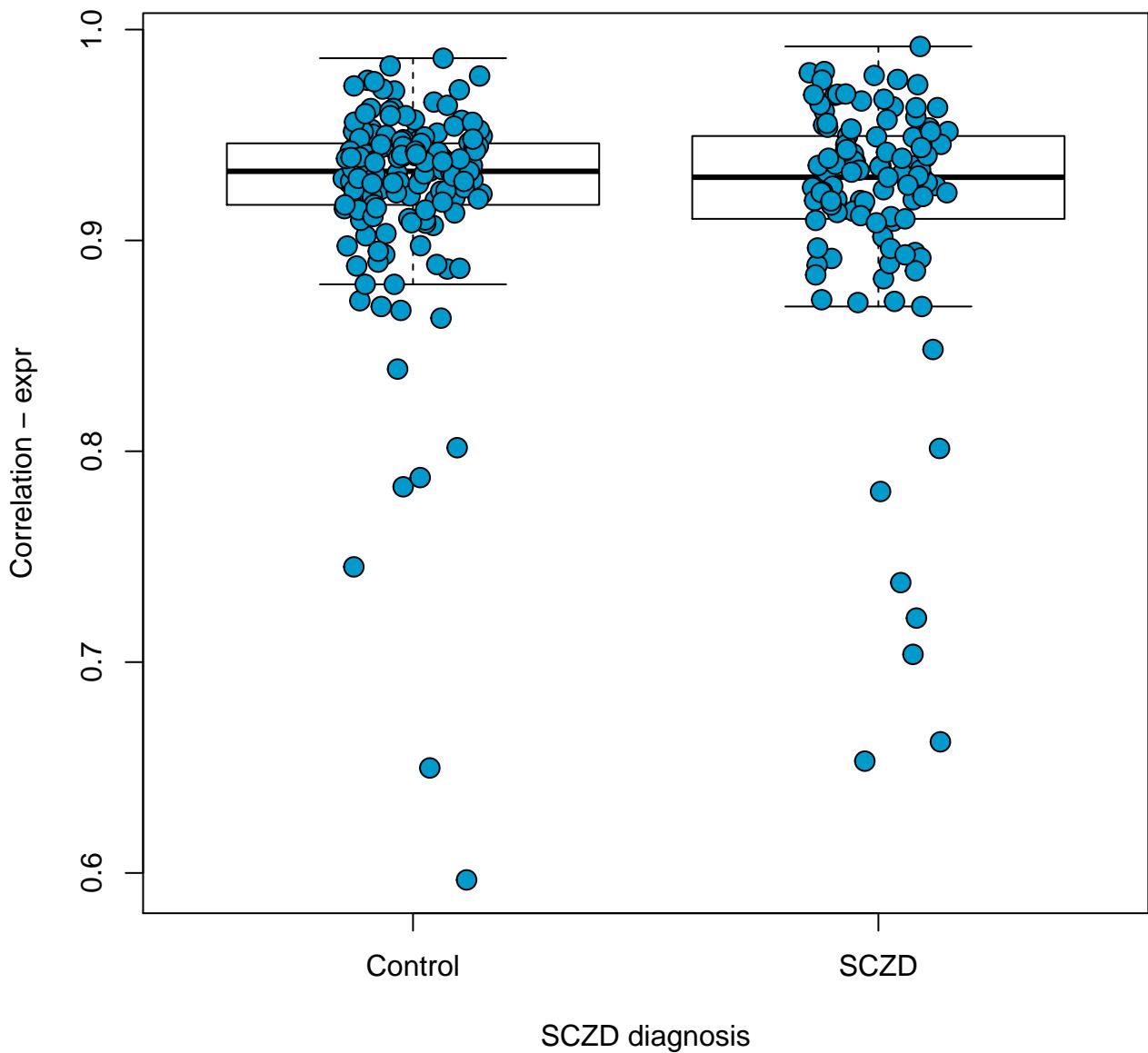
hsa03440: Homologous recombination
p-value: 0.0405



hsa03450: Non-homologous end-joining
p-value: 0.0491

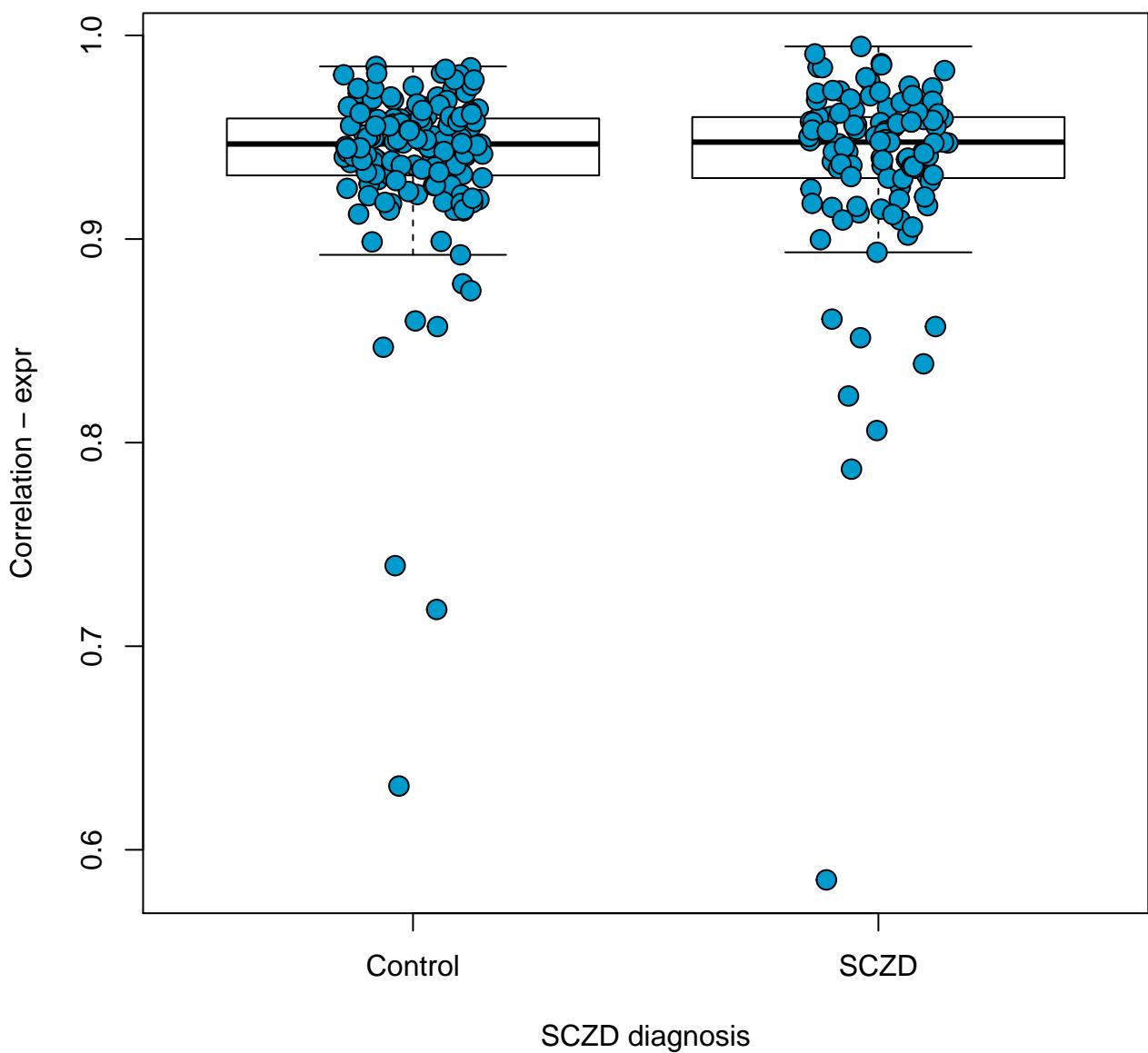


hsa04010: MAPK signaling pathway
p-value: 0.365

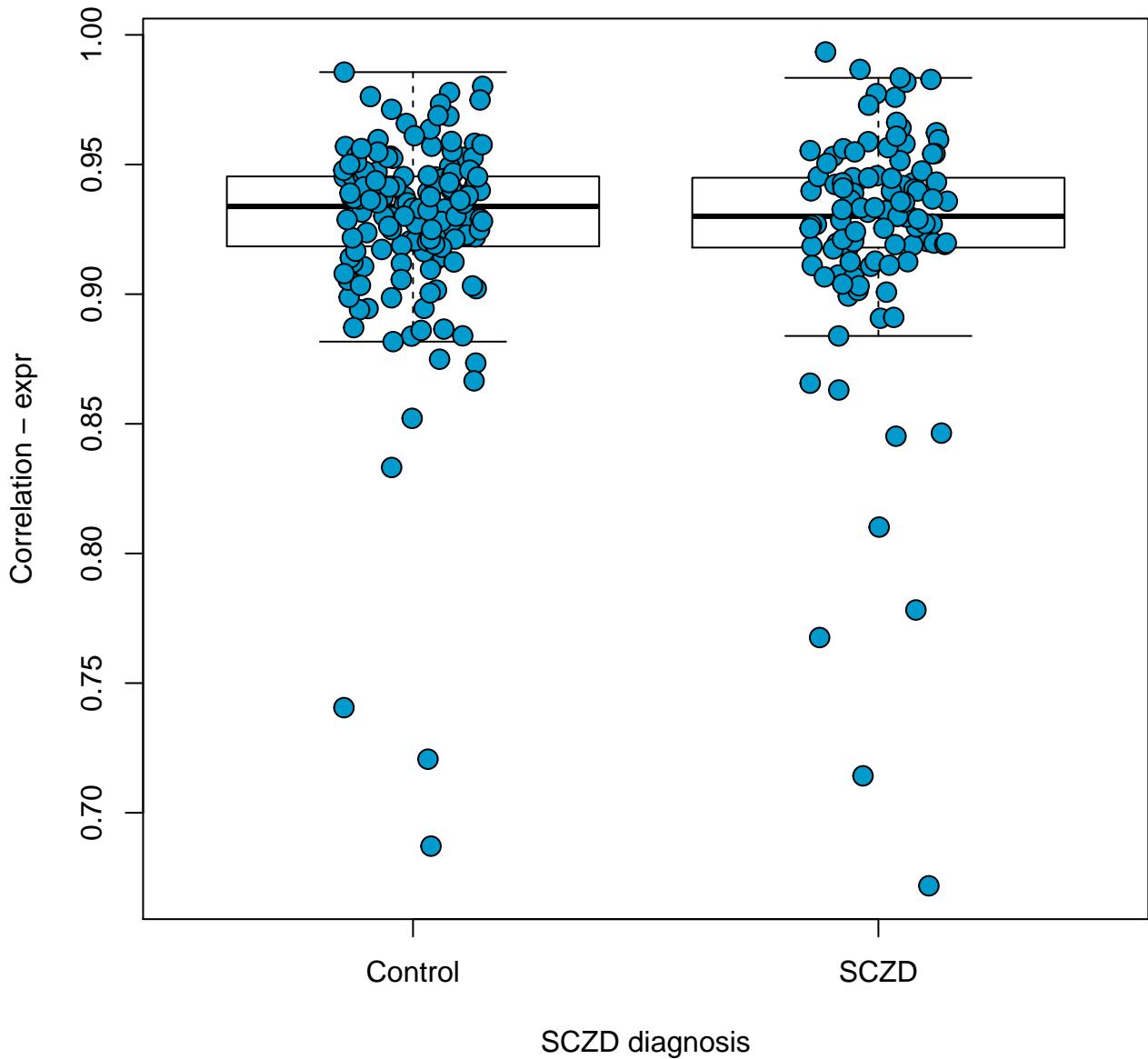


hsa04012: ErbB signaling pathway

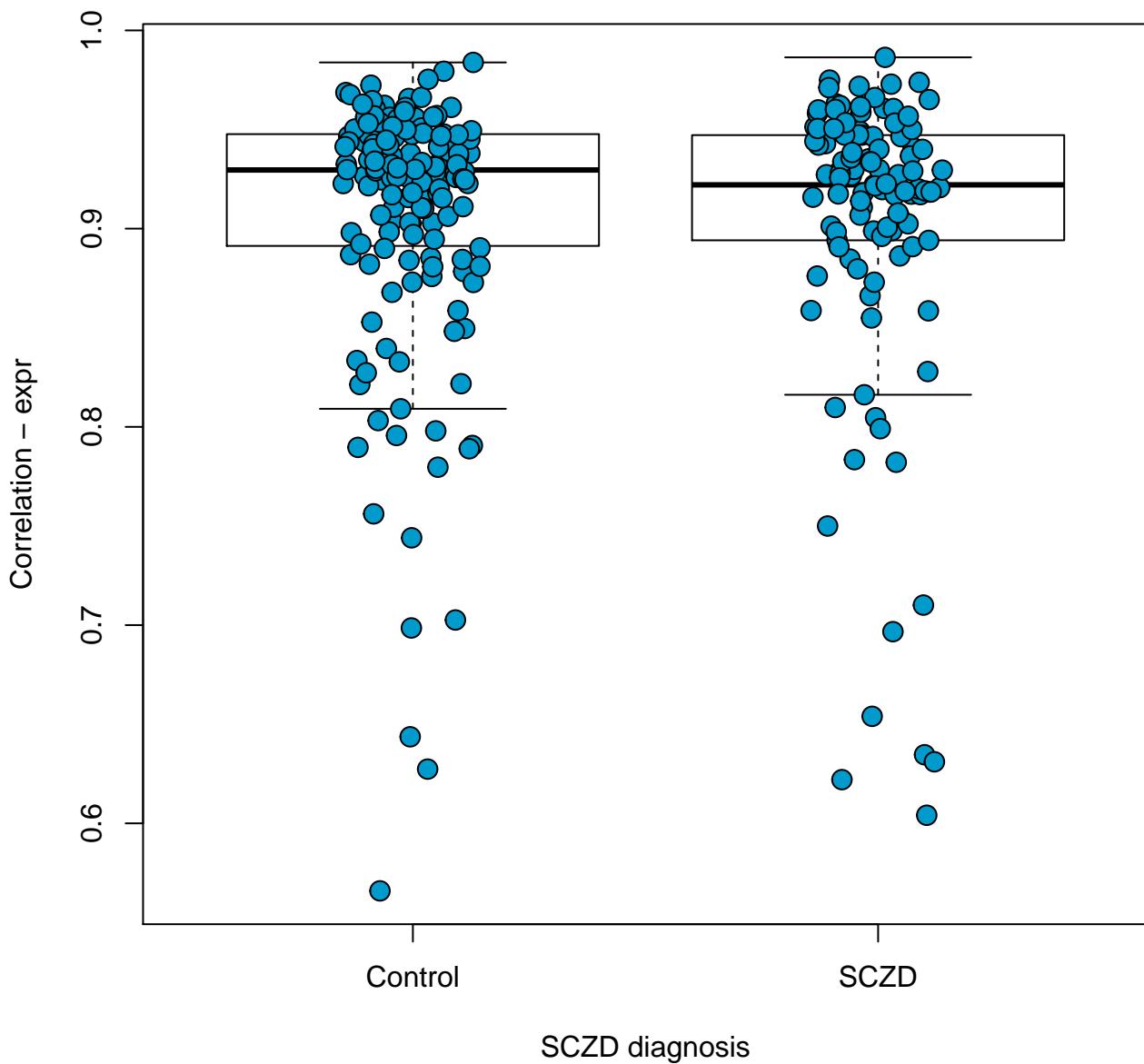
p-value: 0.692



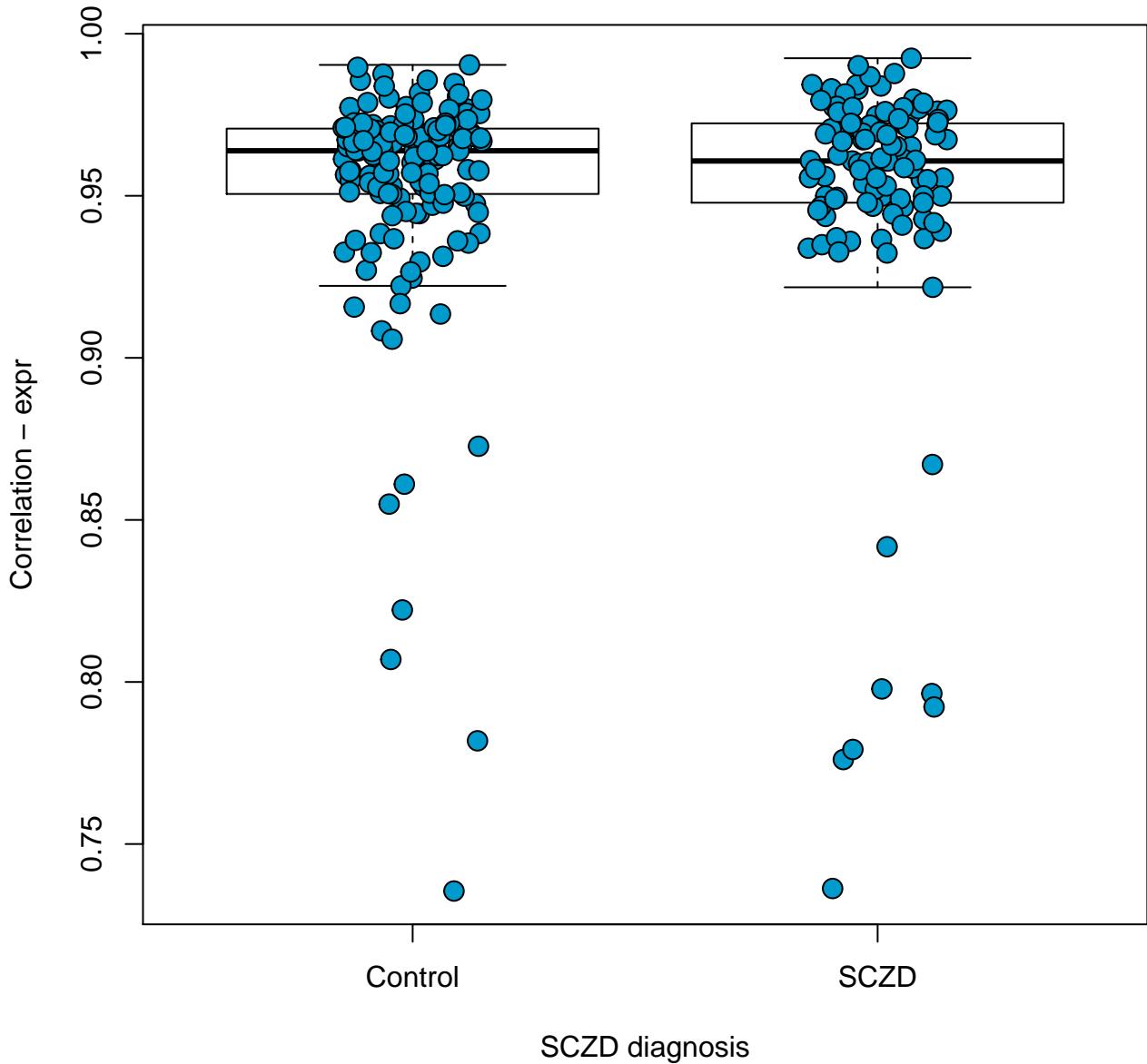
hsa04020: Calcium signaling pathway
p-value: 0.537



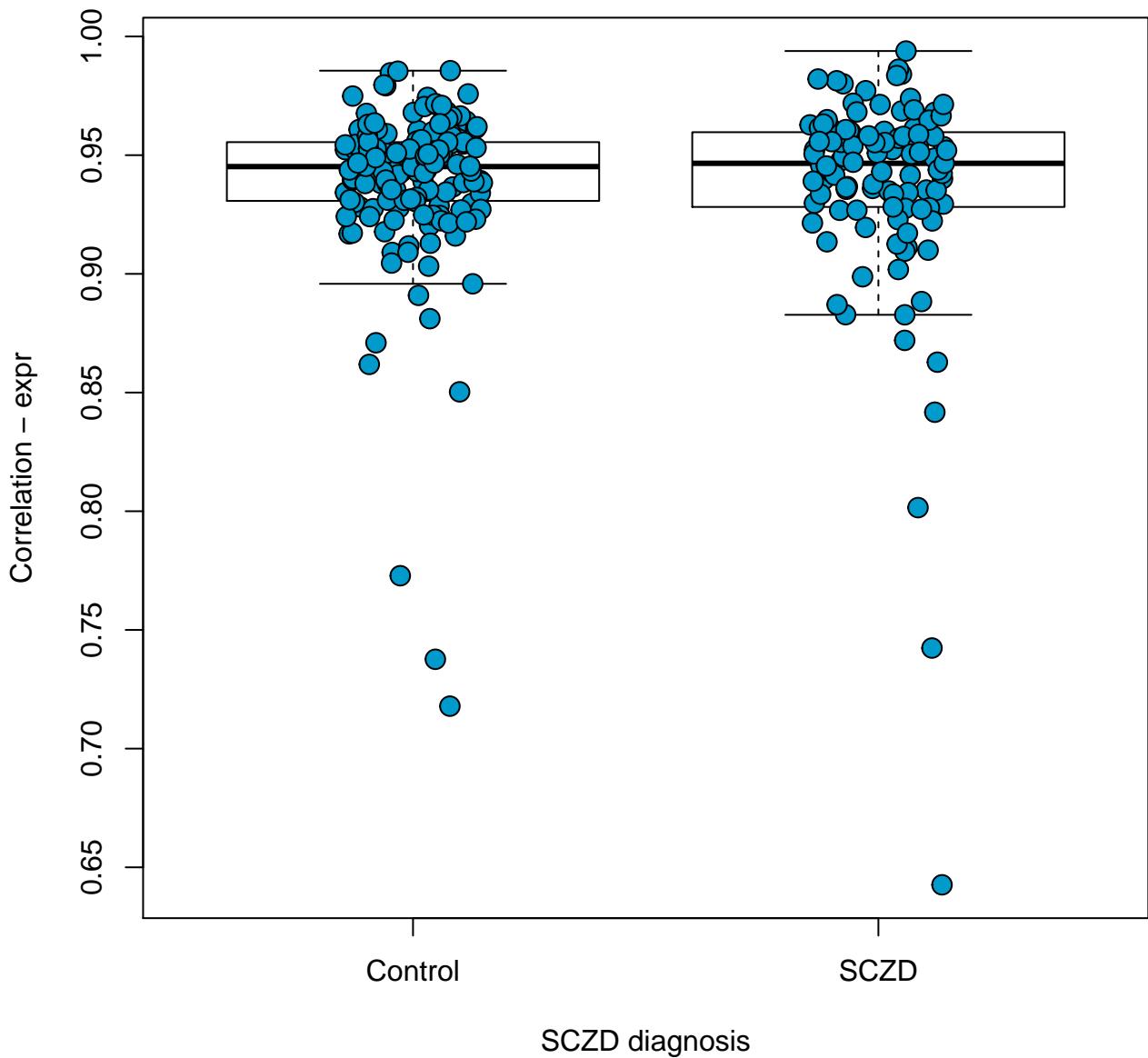
hsa04060: Cytokine–cytokine receptor interaction
p-value: 0.447



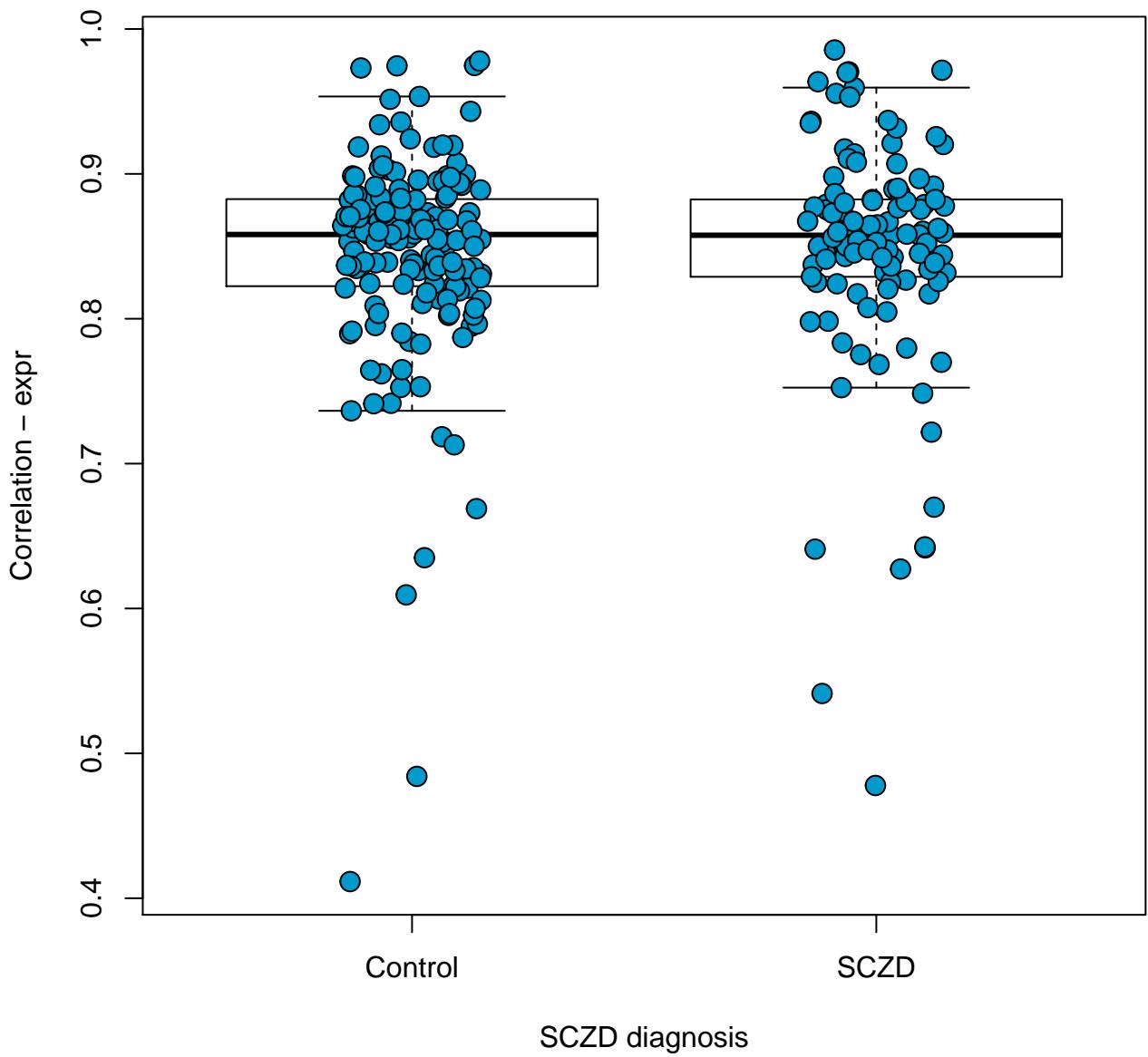
hsa04062: Chemokine signaling pathway
p-value: 0.413



hsa04070: Phosphatidylinositol signaling system
p-value: 0.673

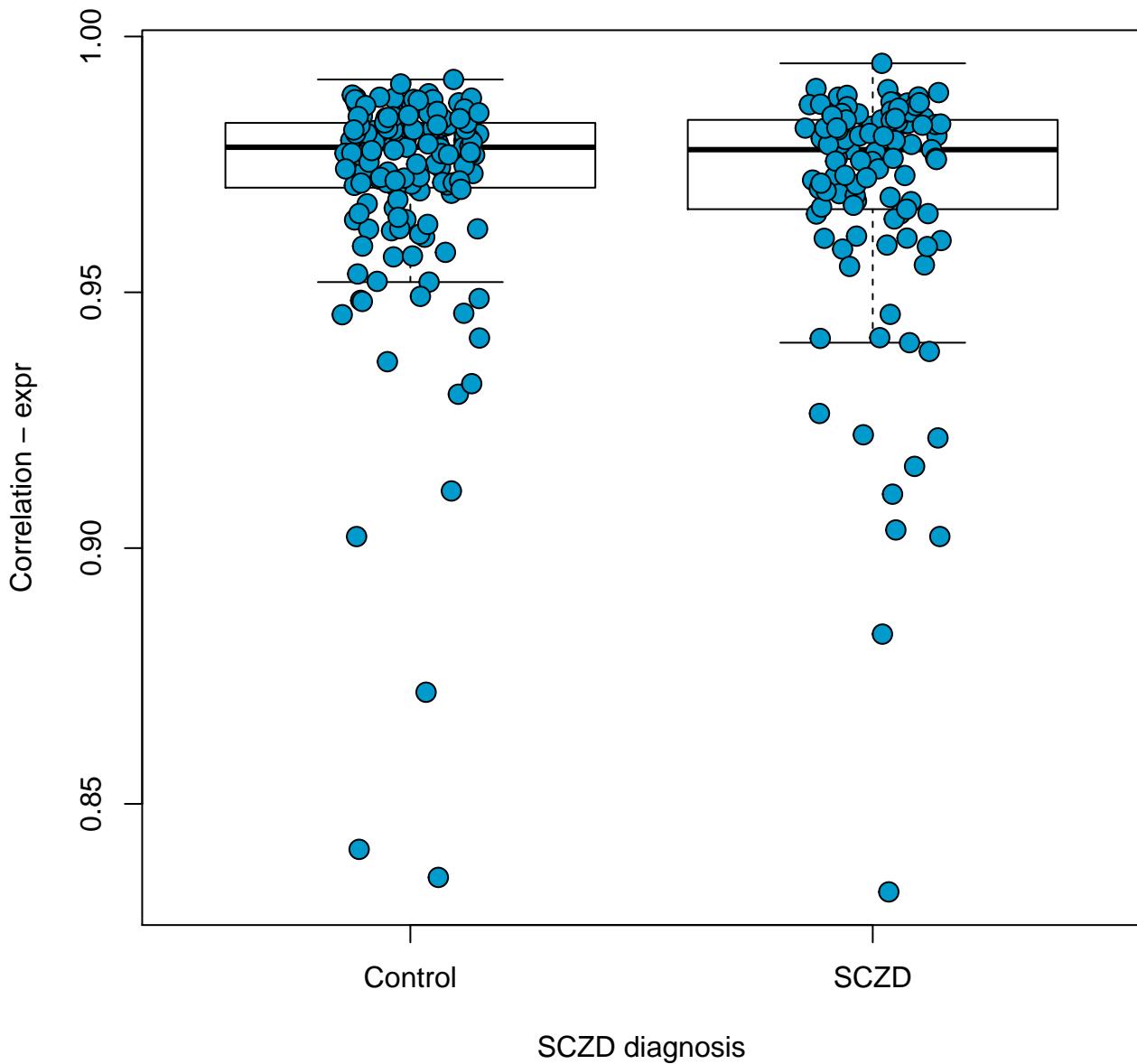


hsa04080: Neuroactive ligand–receptor interaction
p-value: 0.823

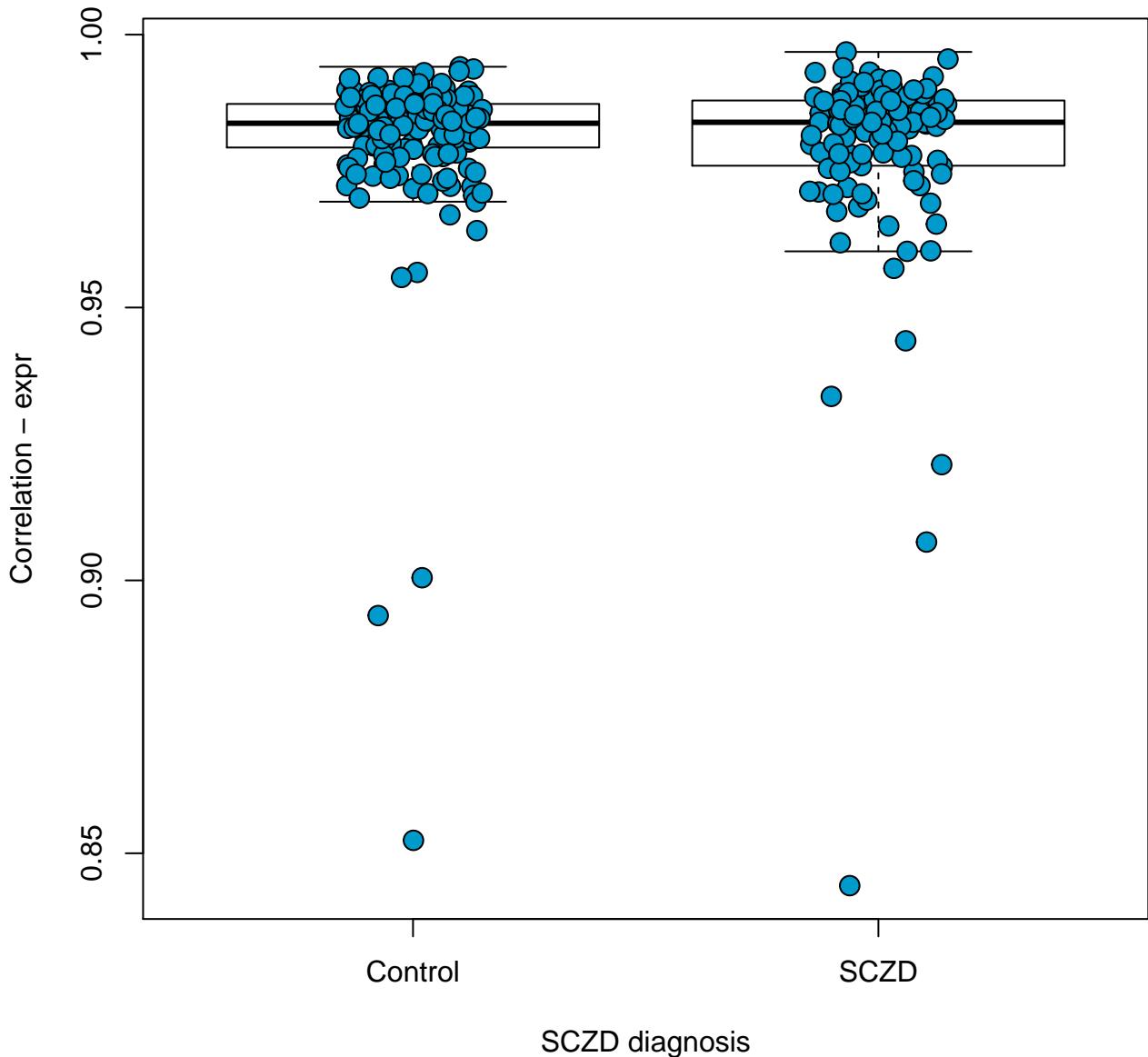


hsa04110: Cell cycle

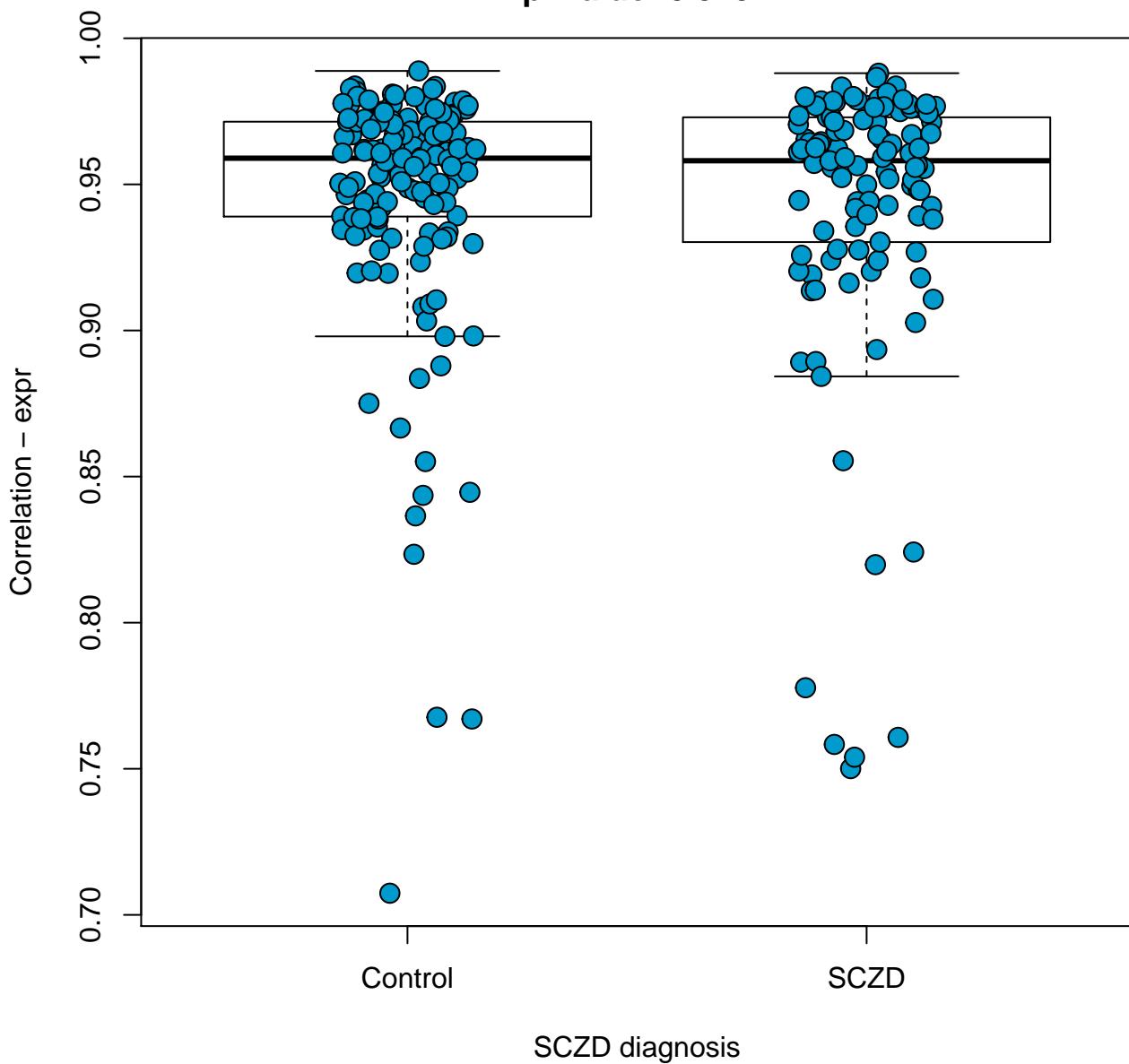
p-value: 0.443



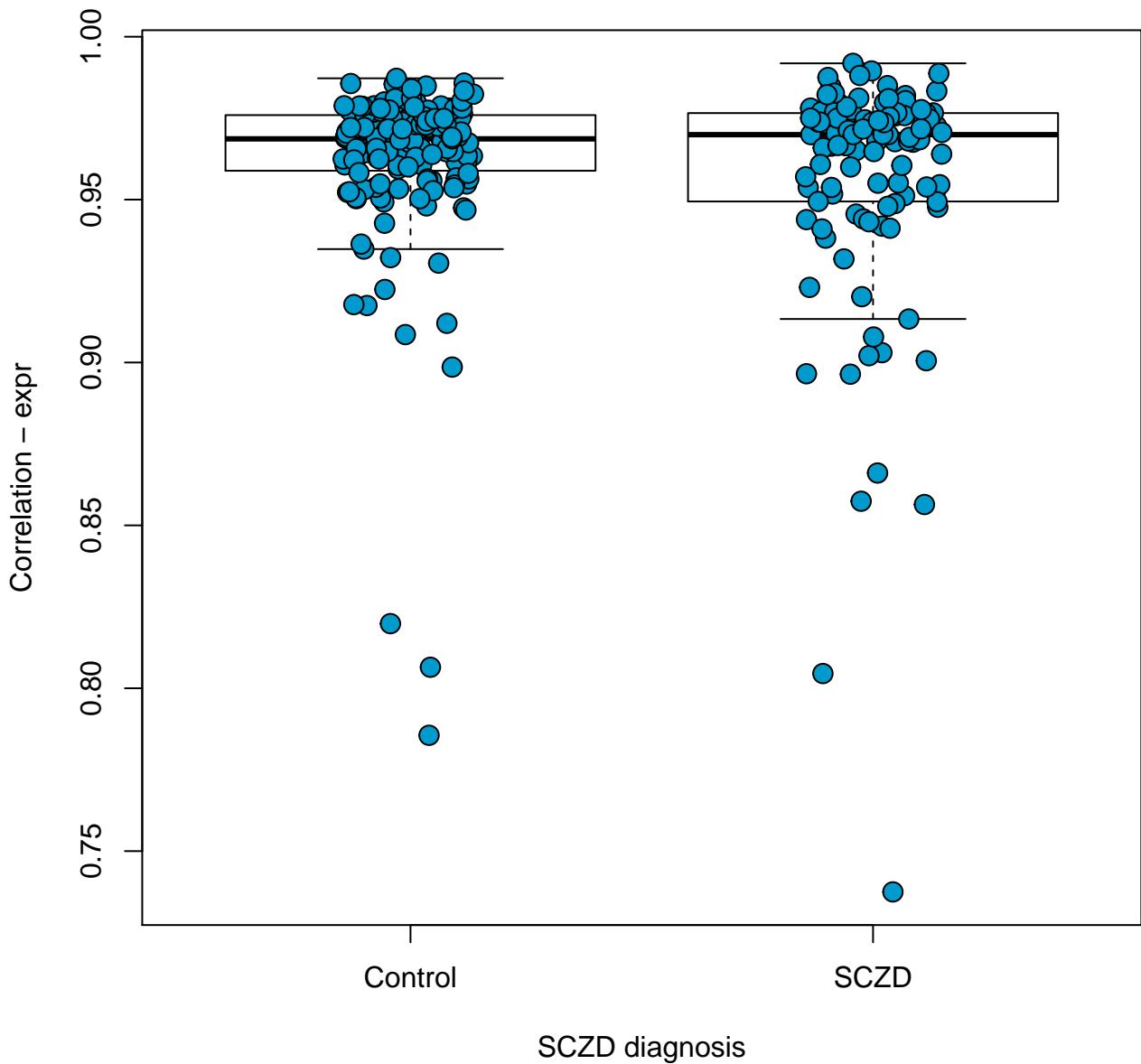
hsa04114: Oocyte meiosis
p-value: 0.37



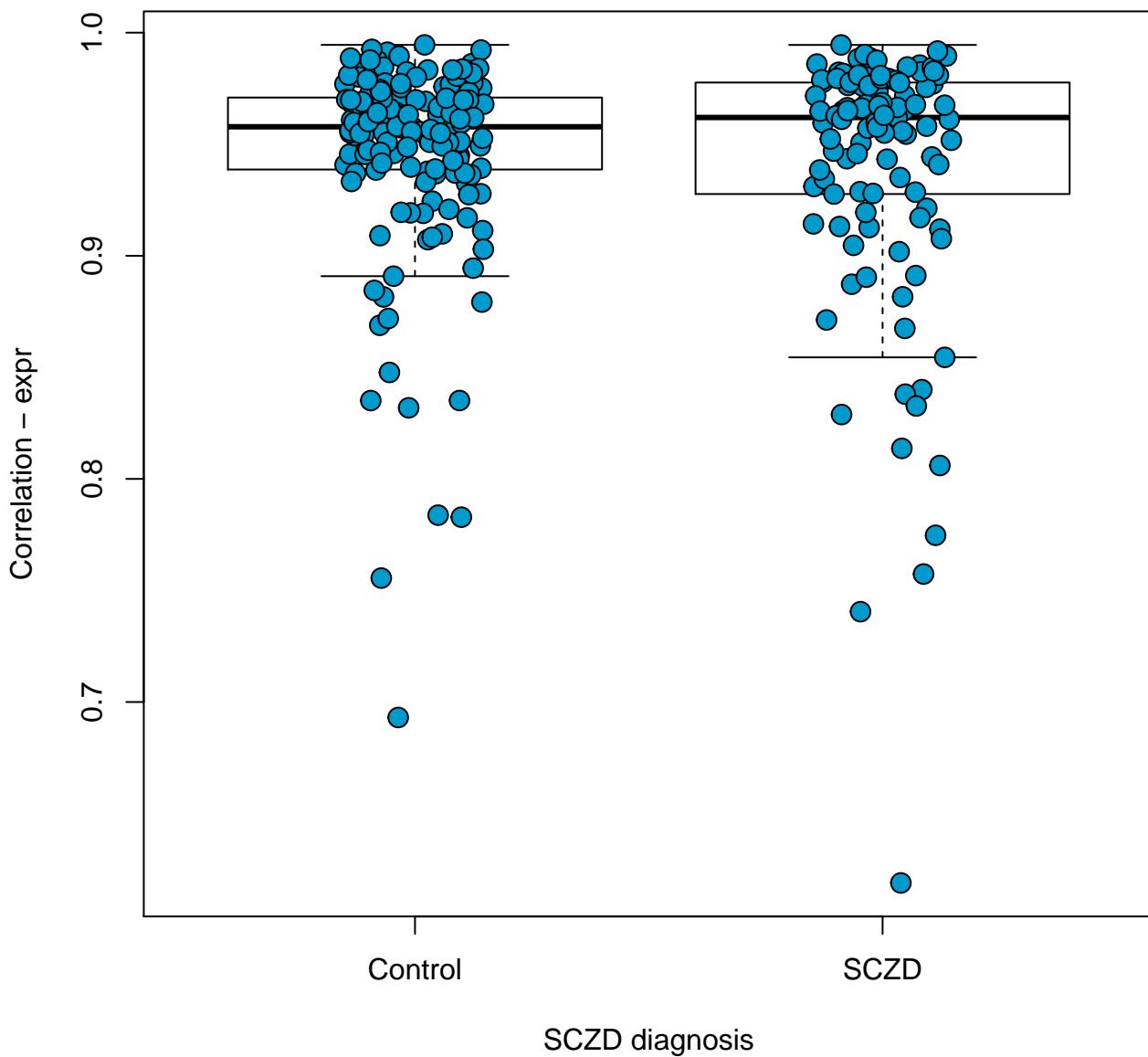
hsa04115: p53 signaling pathway
p-value: 0.375



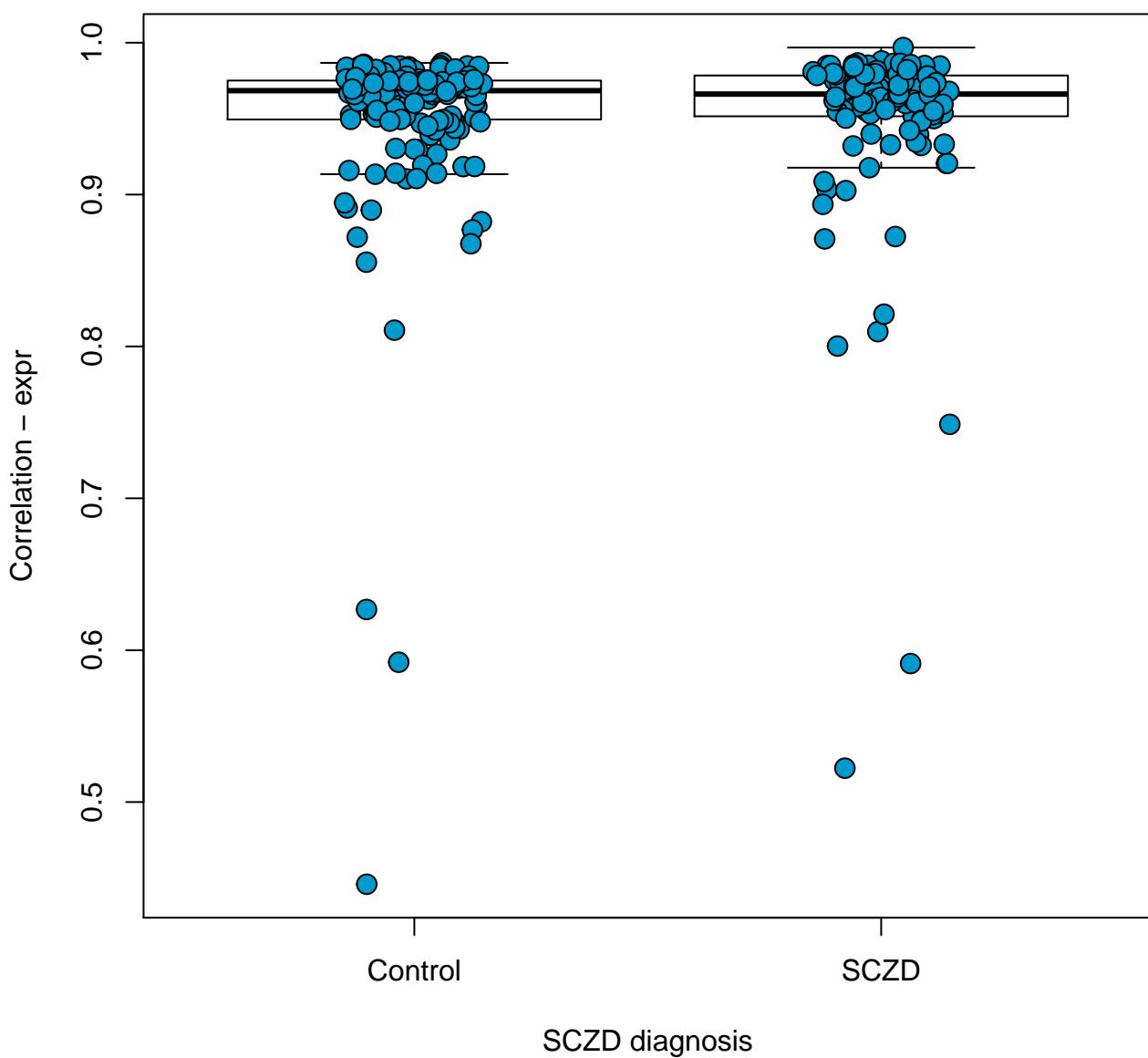
hsa04120: Ubiquitin mediated proteolysis
p-value: 0.117



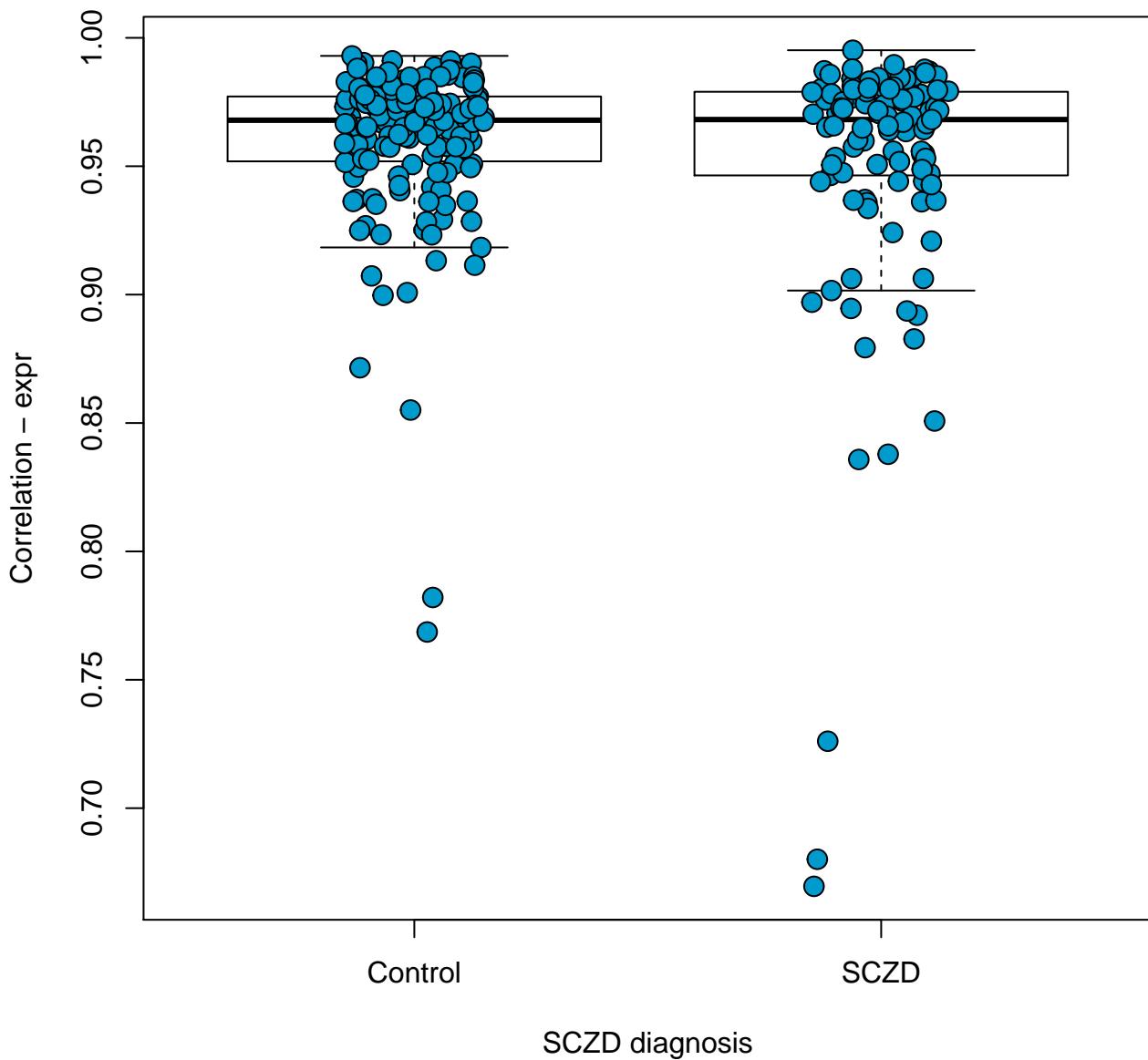
hsa04122: Sulfur relay system
p-value: 0.253



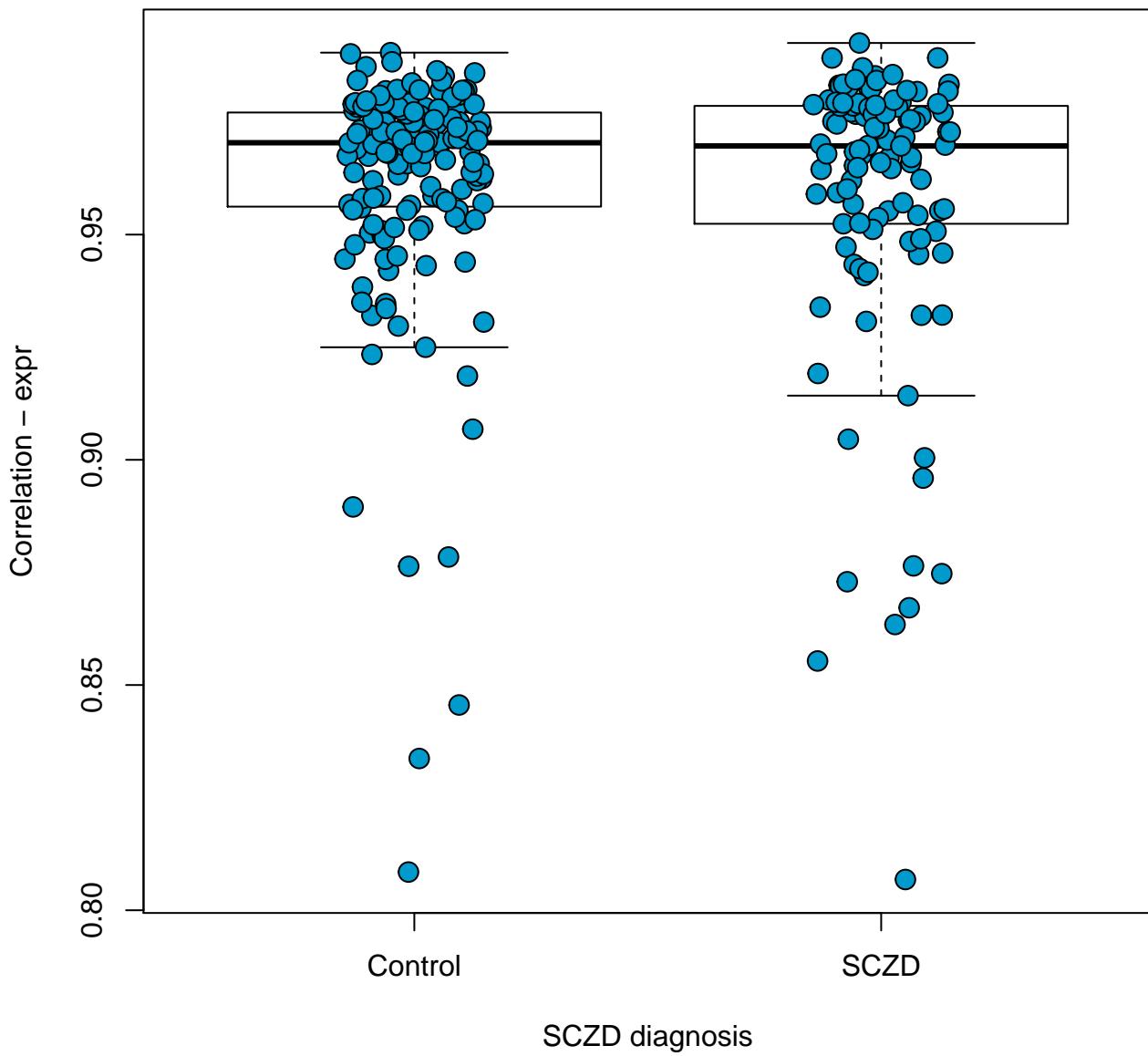
hsa04130: SNARE interactions in vesicular transport **p-value: 0.761**



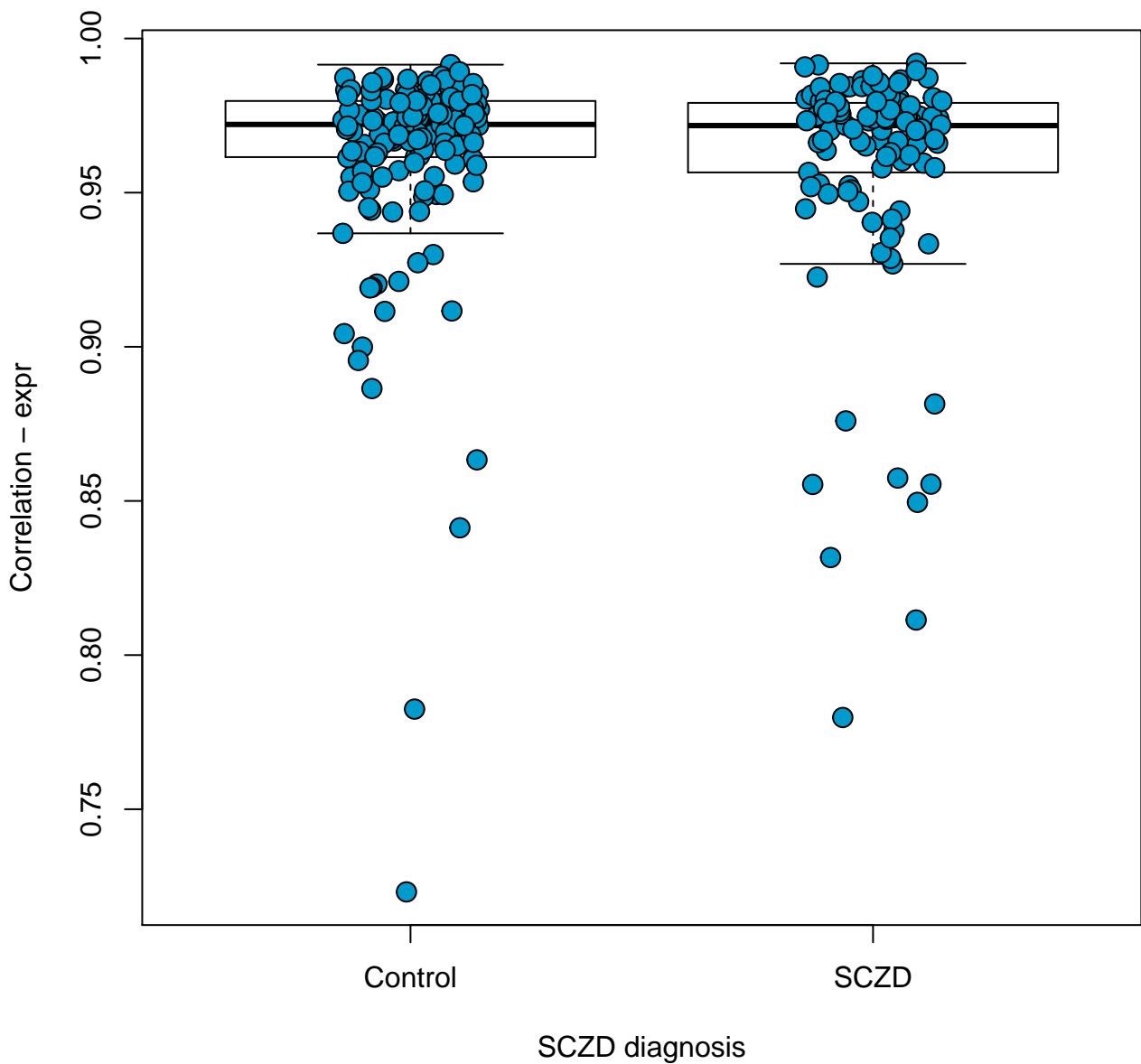
hsa04140: Regulation of autophagy
p-value: 0.0604



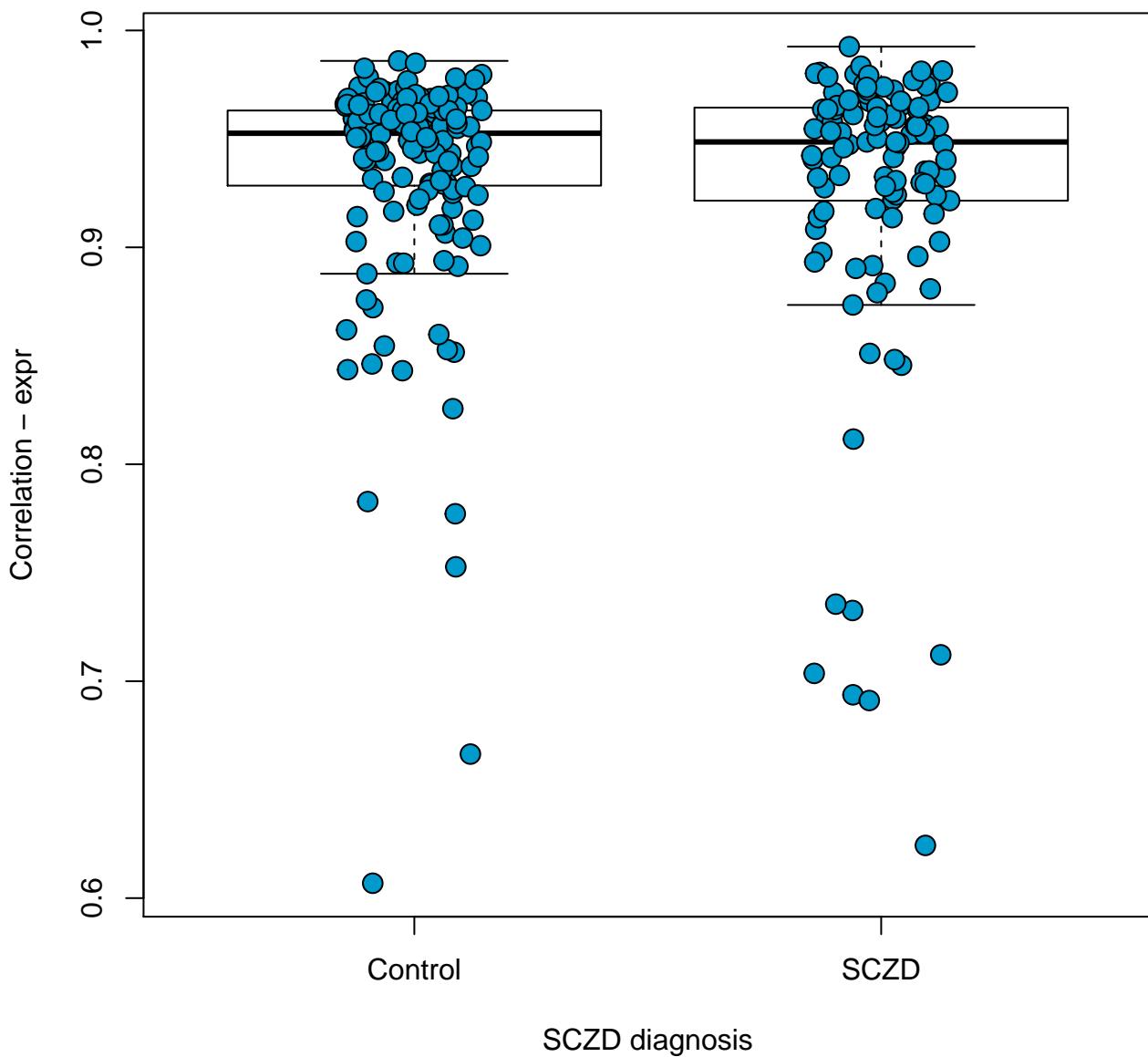
hsa04141: Protein processing in endoplasmic reticulum
p-value: 0.336



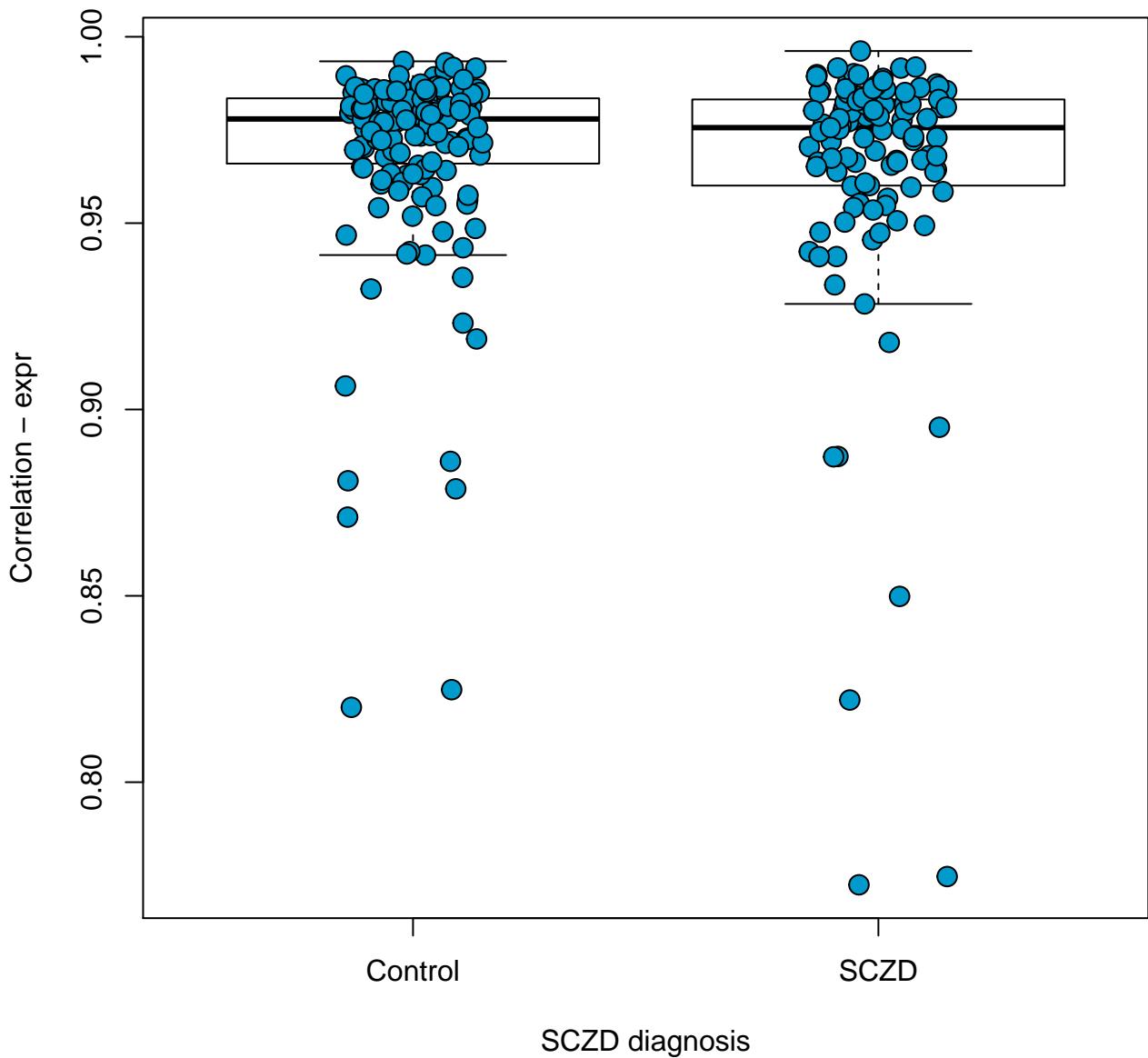
hsa04142: Lysosome
p-value: 0.343



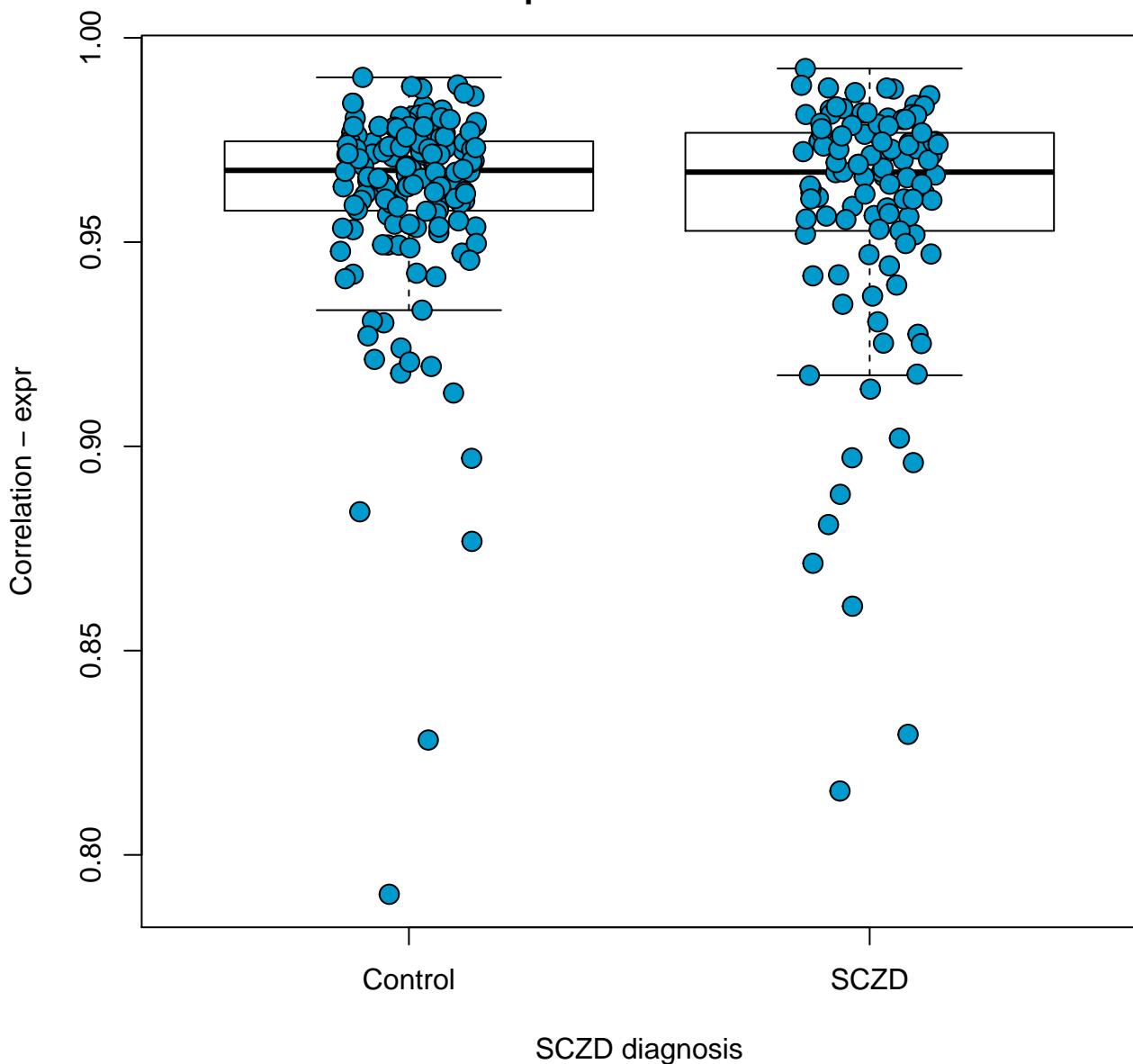
hsa04144: Endocytosis
p-value: 0.246



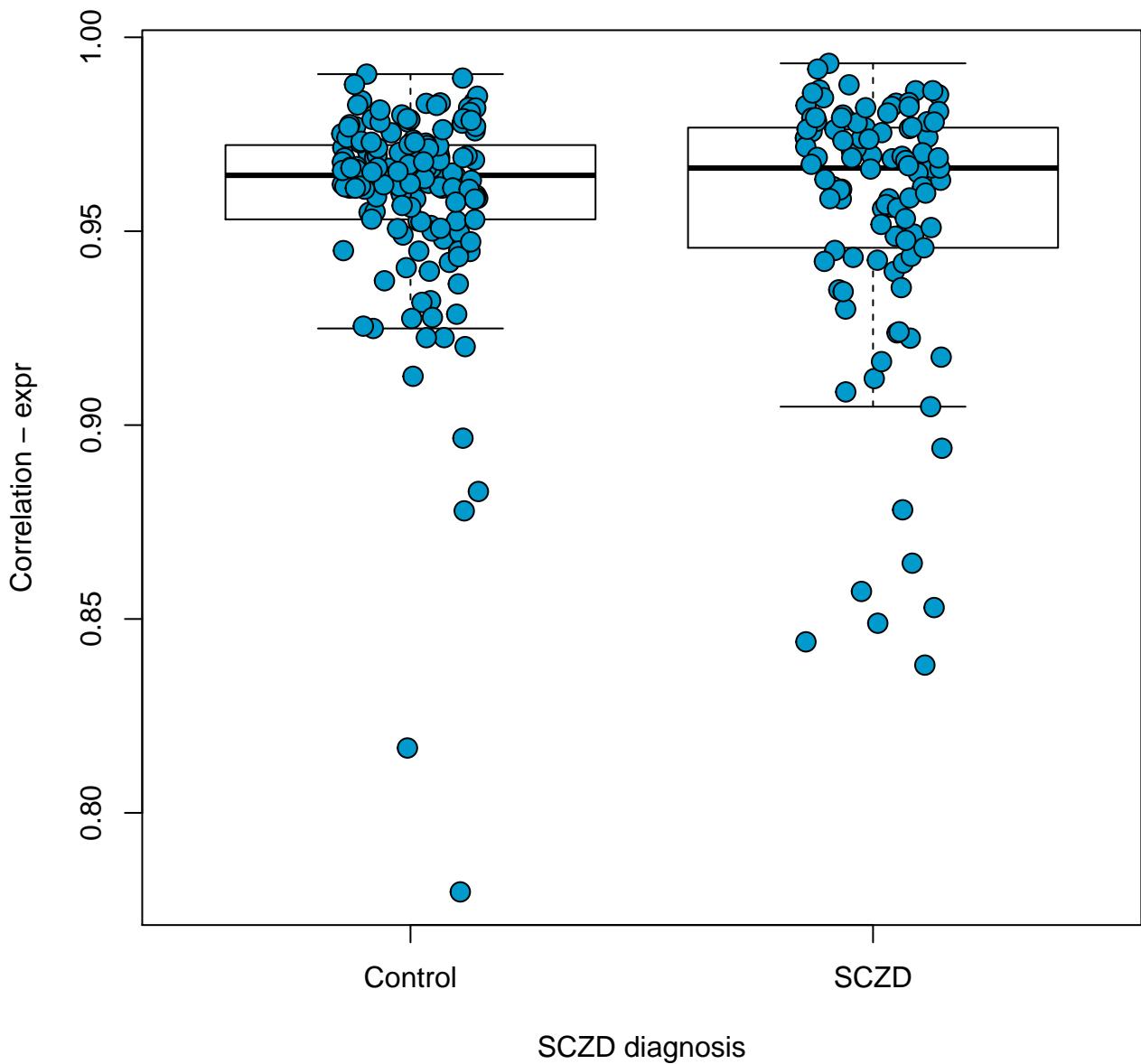
hsa04145: Phagosome
p-value: 0.176



hsa04146: Peroxisome
p-value: 0.278

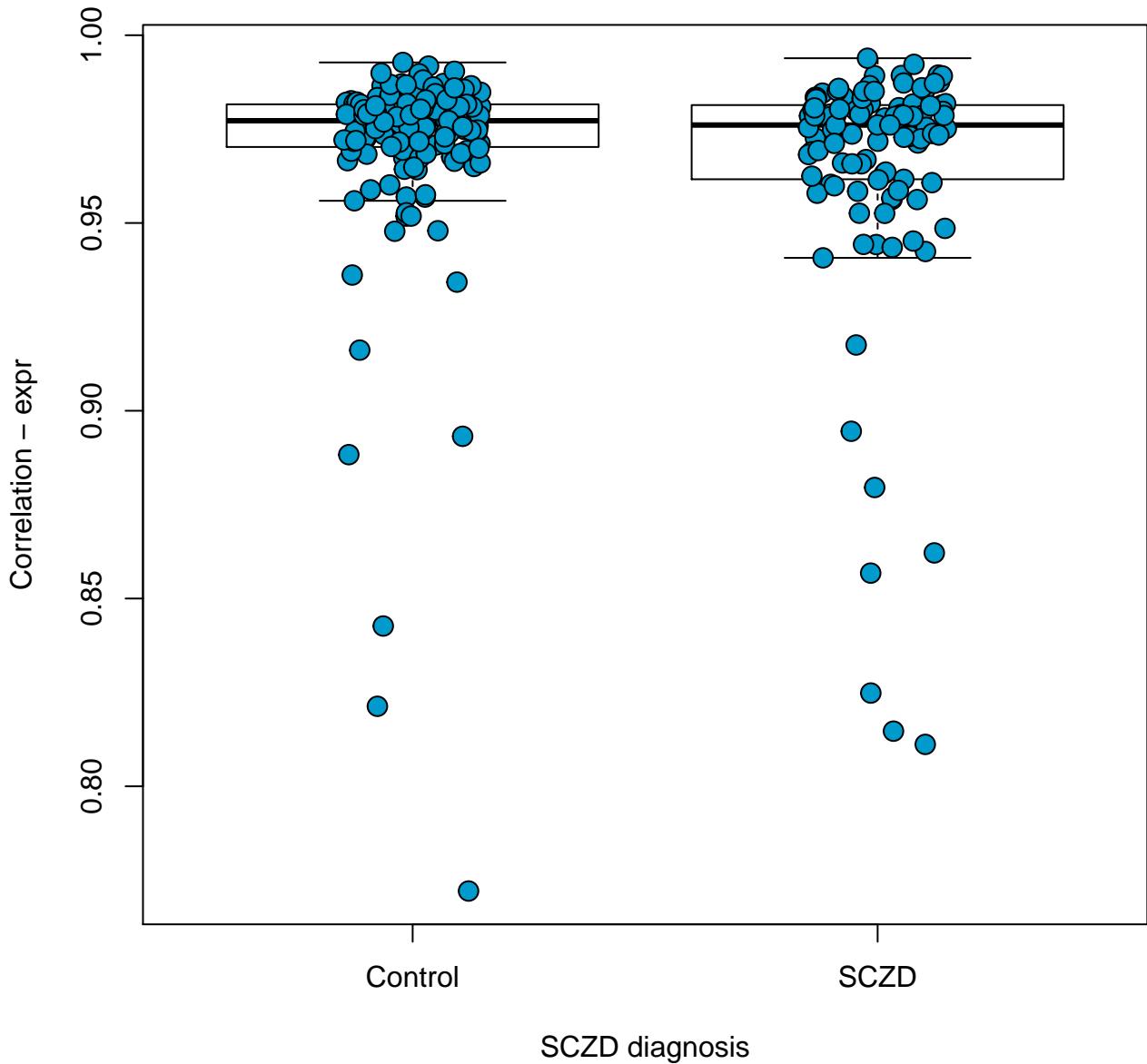


hsa04150: mTOR signaling pathway
p-value: 0.277



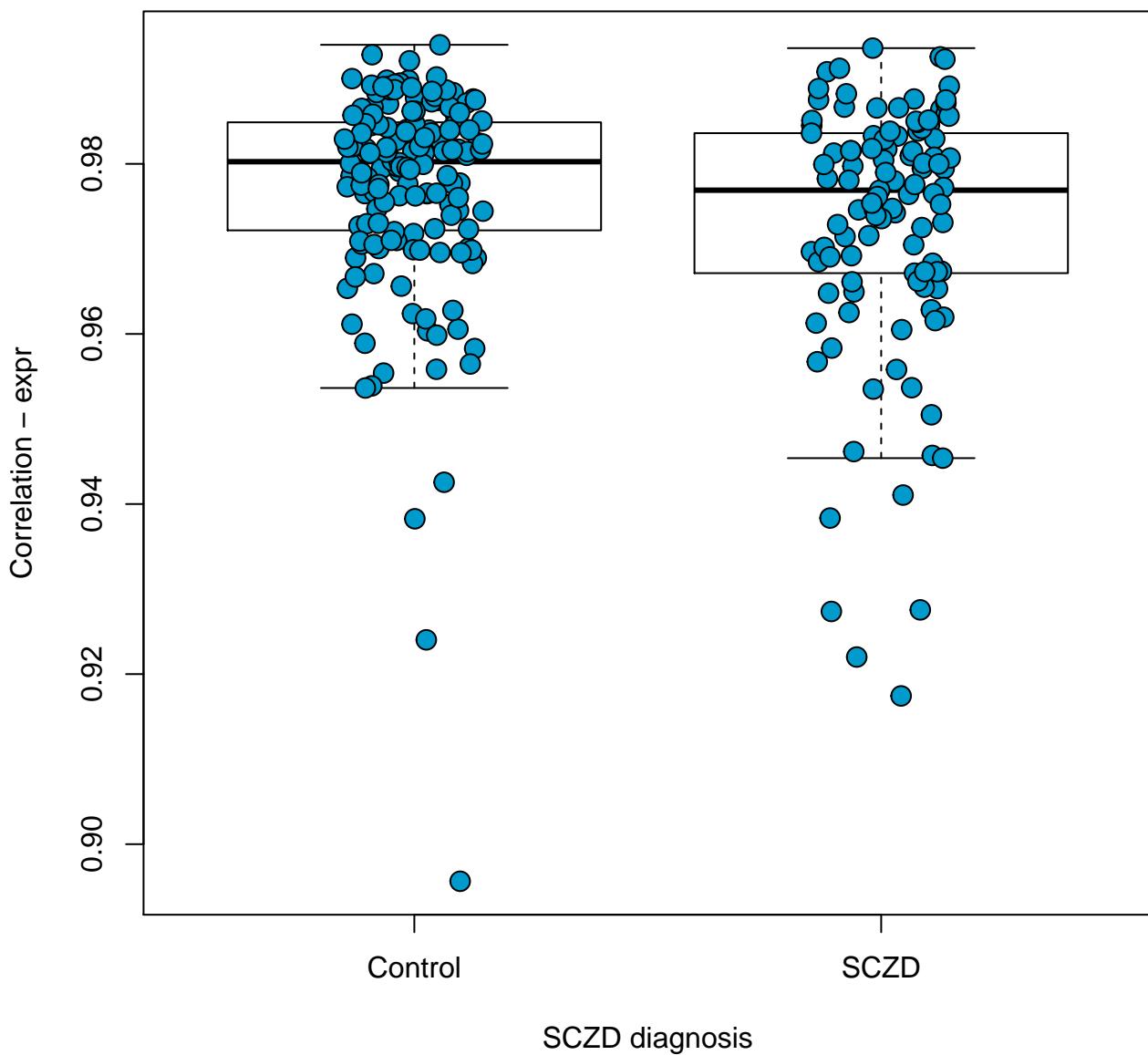
hsa04210: Apoptosis

p-value: 0.116

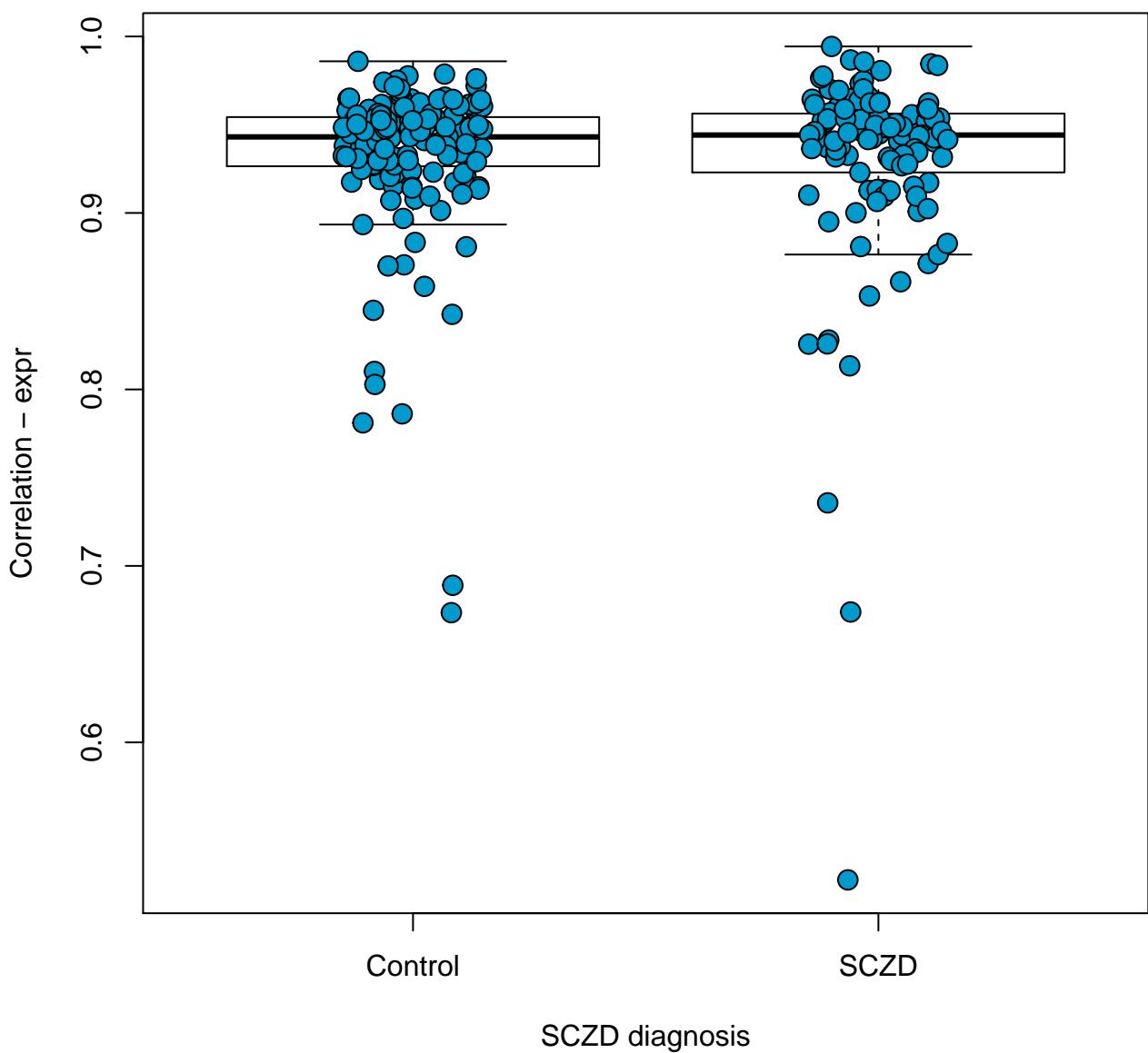


hsa04260: Cardiac muscle contraction

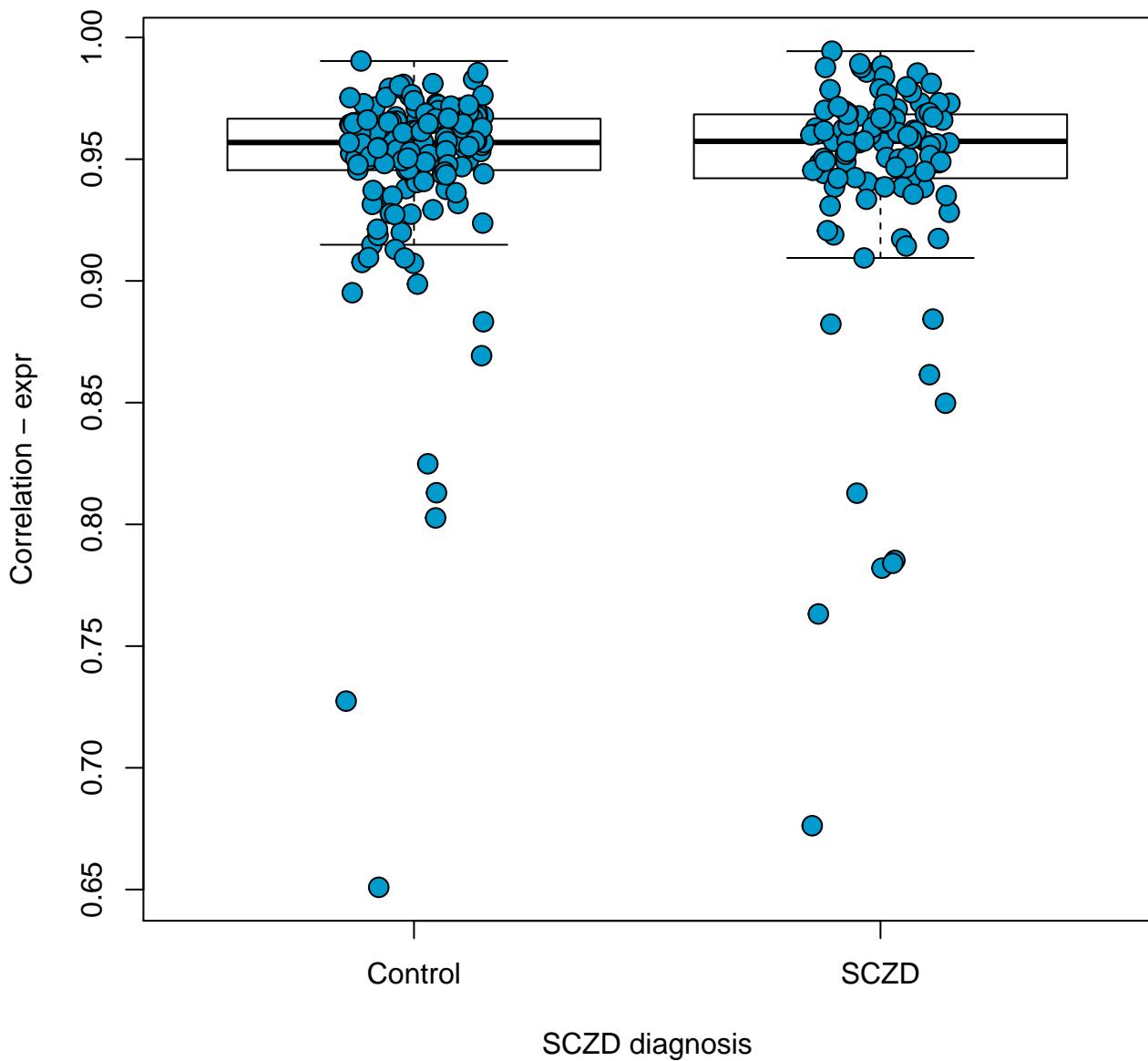
p-value: 0.0145



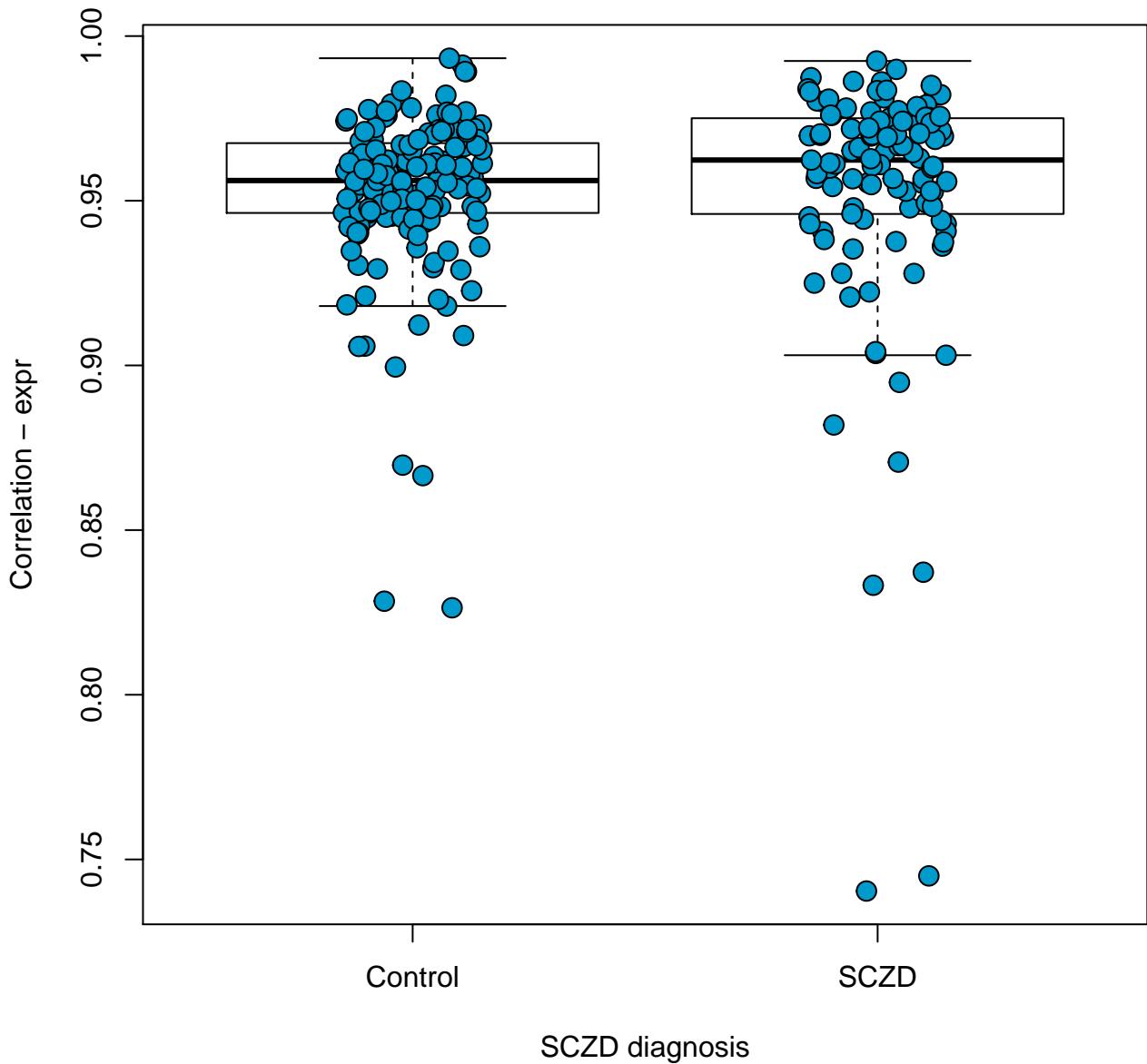
hsa04270: Vascular smooth muscle contraction
p-value: 0.583



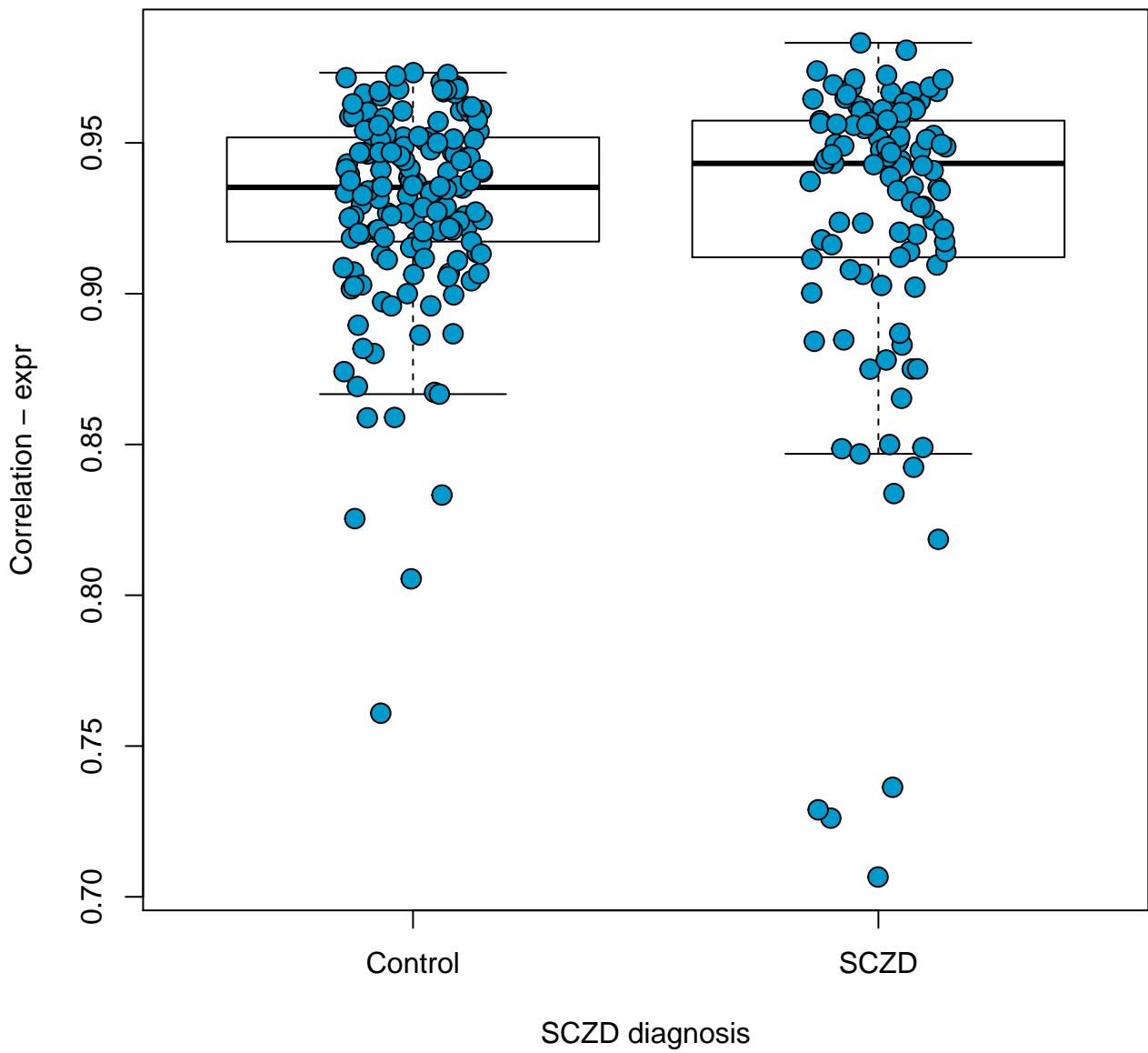
hsa04310: Wnt signaling pathway
p-value: 0.514



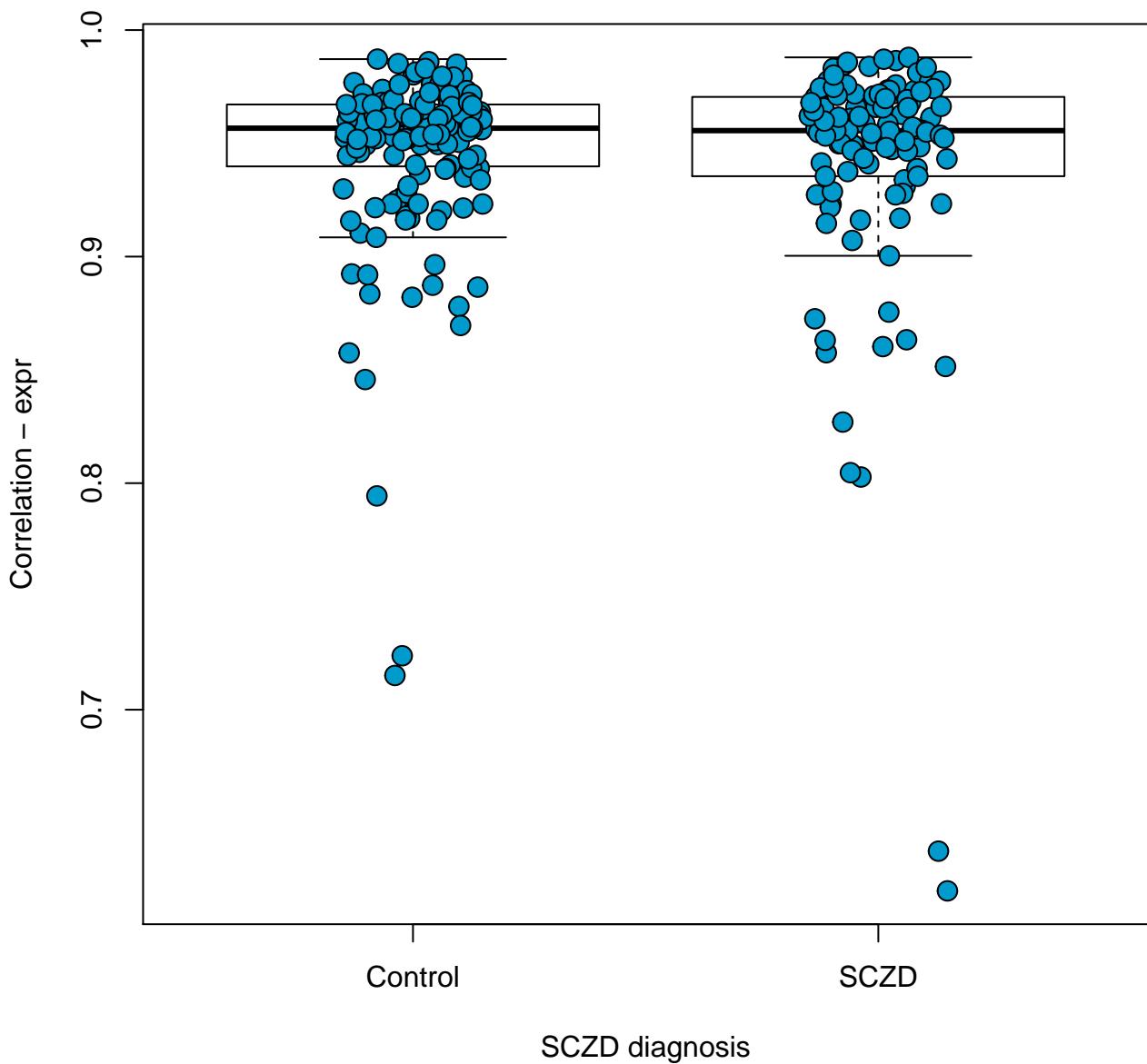
hsa04320: Dorso–ventral axis formation
p-value: 0.993



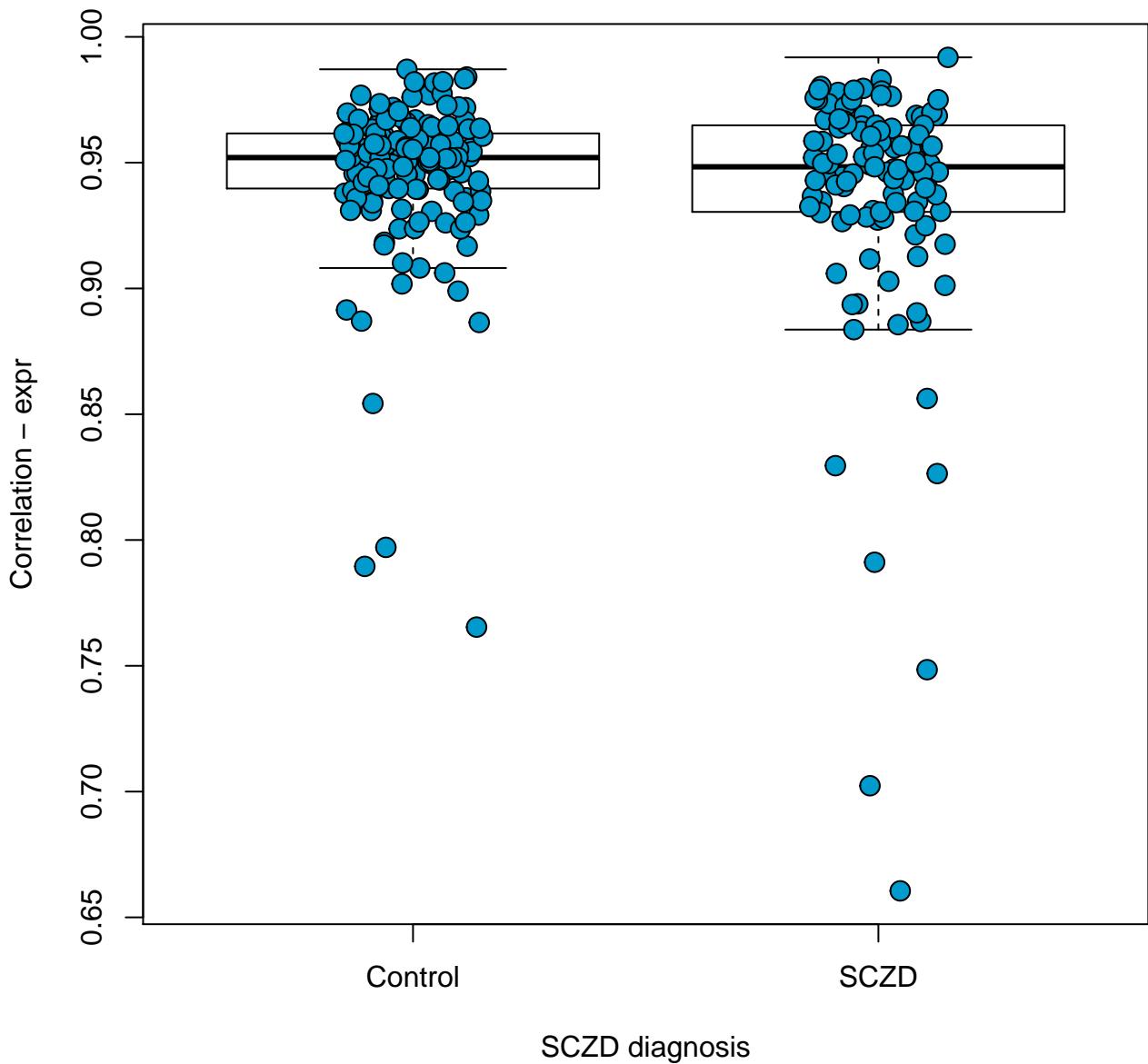
hsa04330: Notch signaling pathway
p-value: 0.324



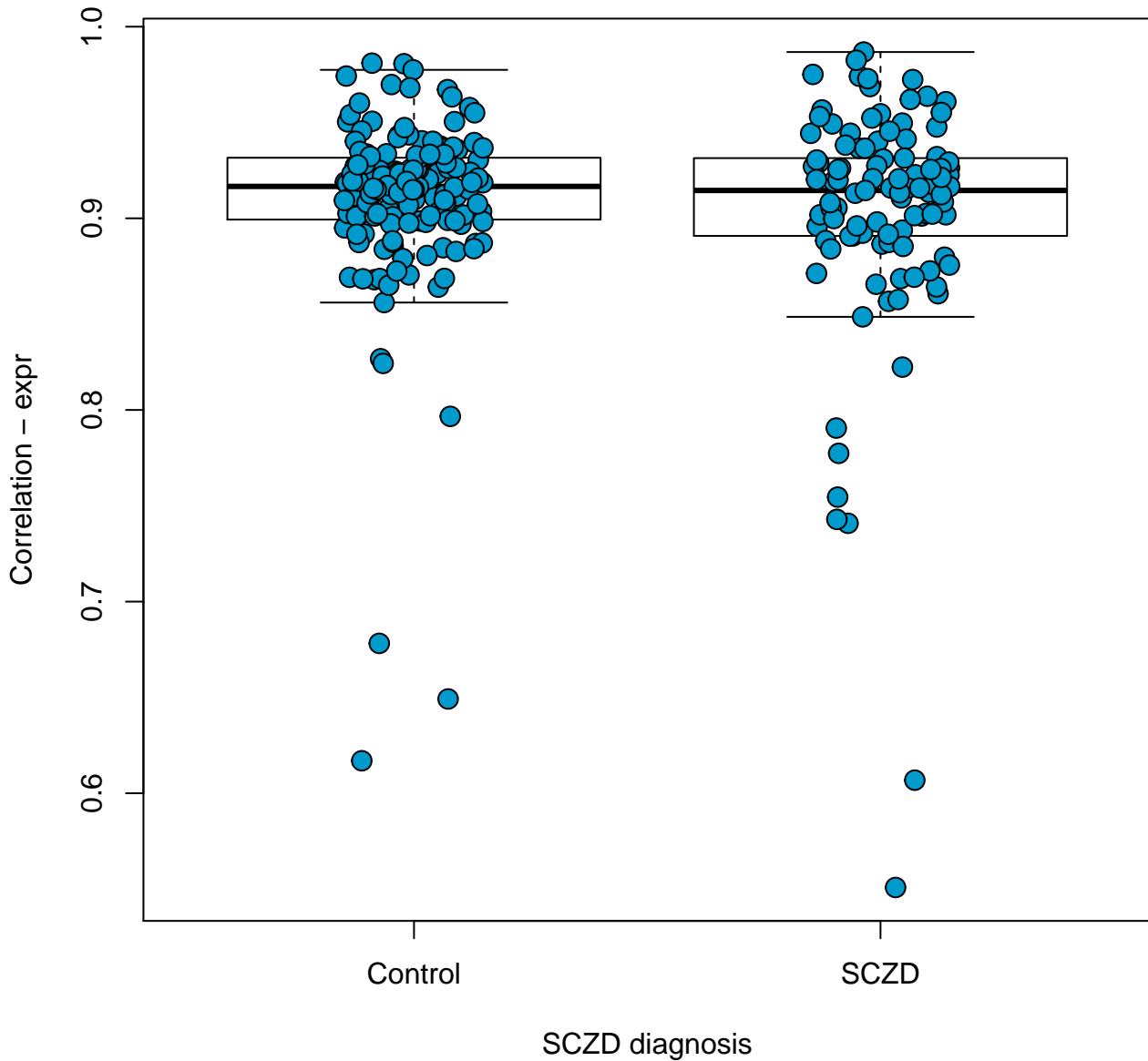
hsa04340: Hedgehog signaling pathway
p-value: 0.335



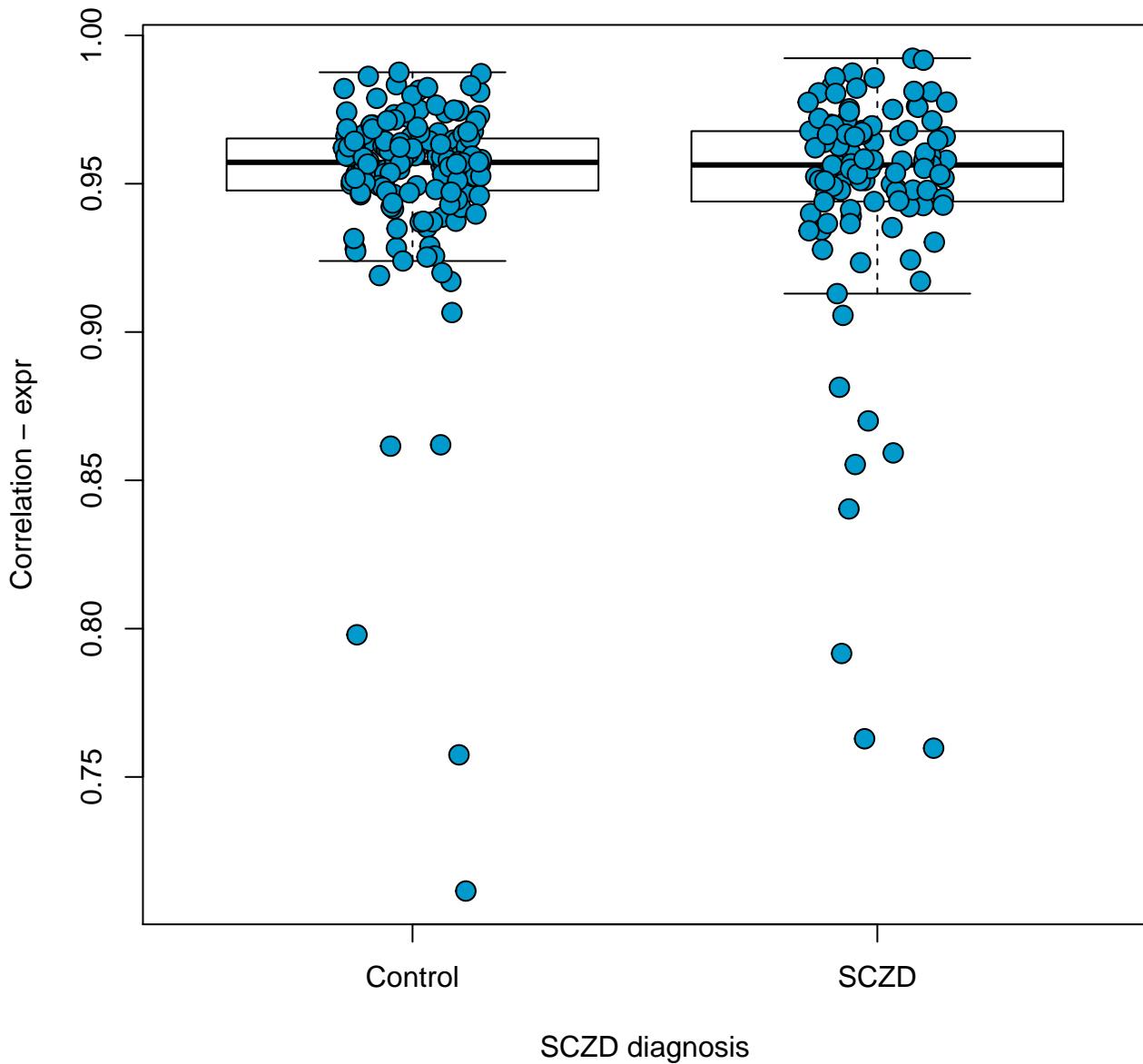
hsa04350: TGF–beta signaling pathway
p-value: 0.0465



hsa04360: Axon guidance
p-value: 0.302

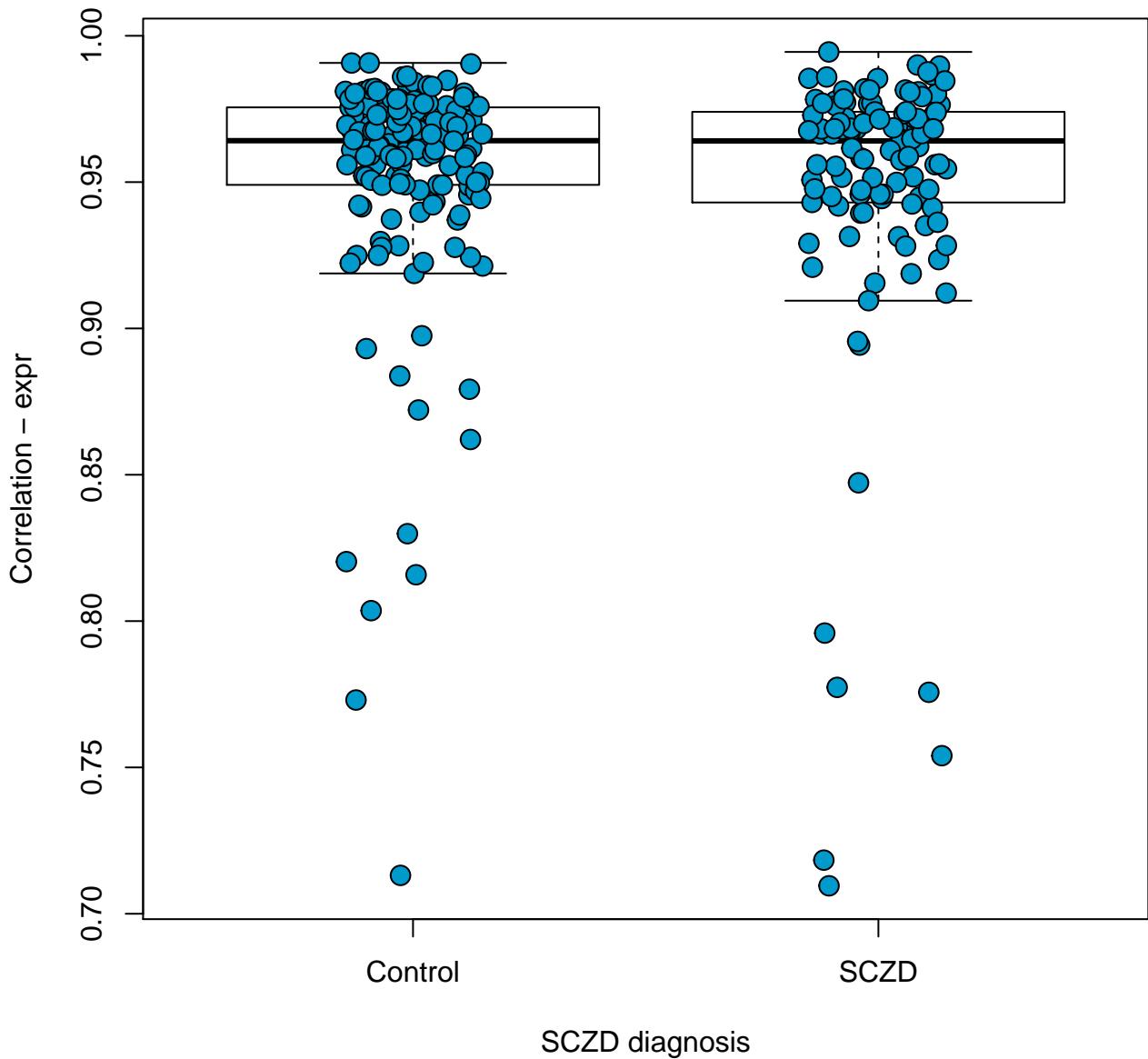


hsa04370: VEGF signaling pathway
p-value: 0.434

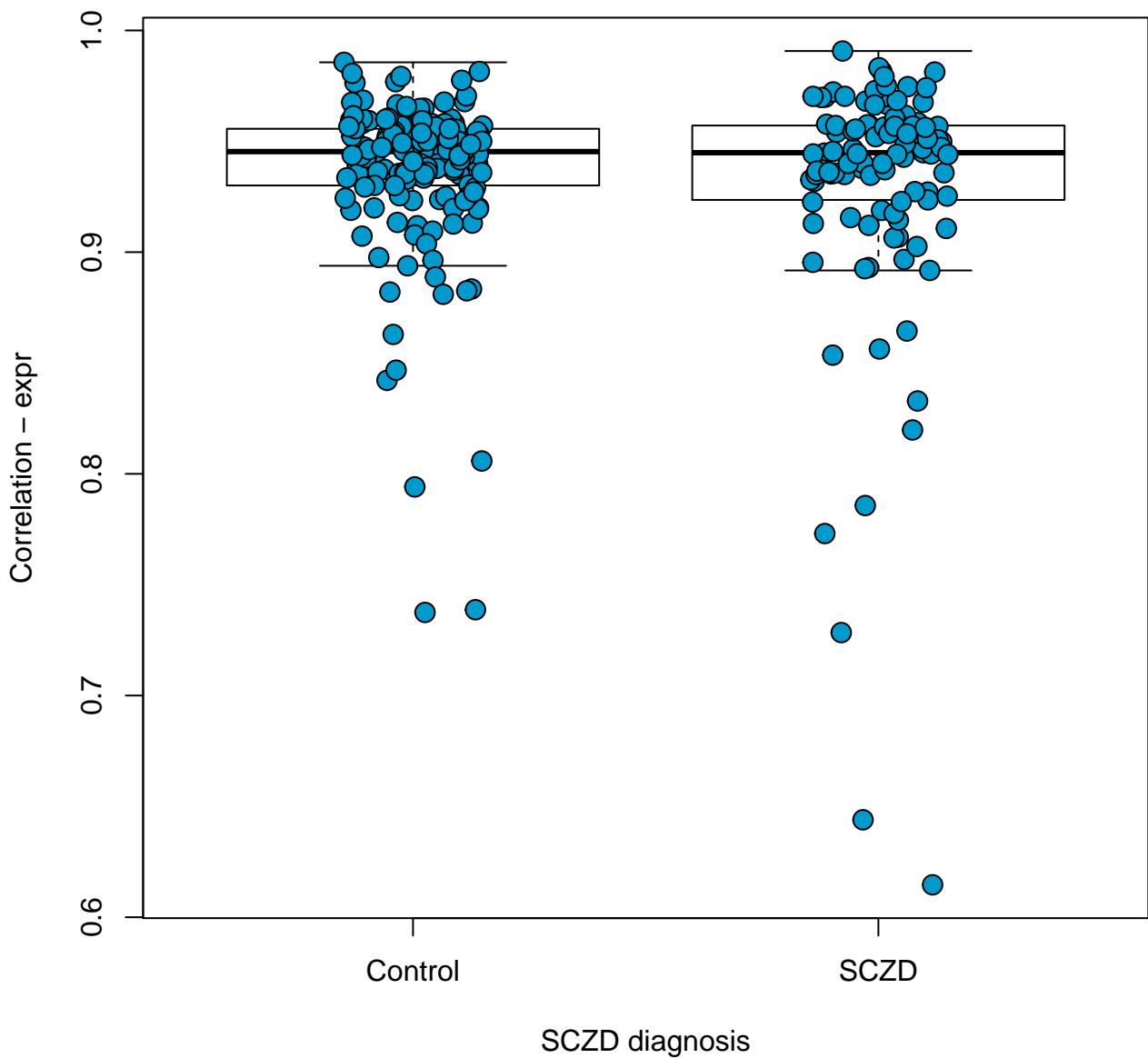


hsa04380: Osteoclast differentiation

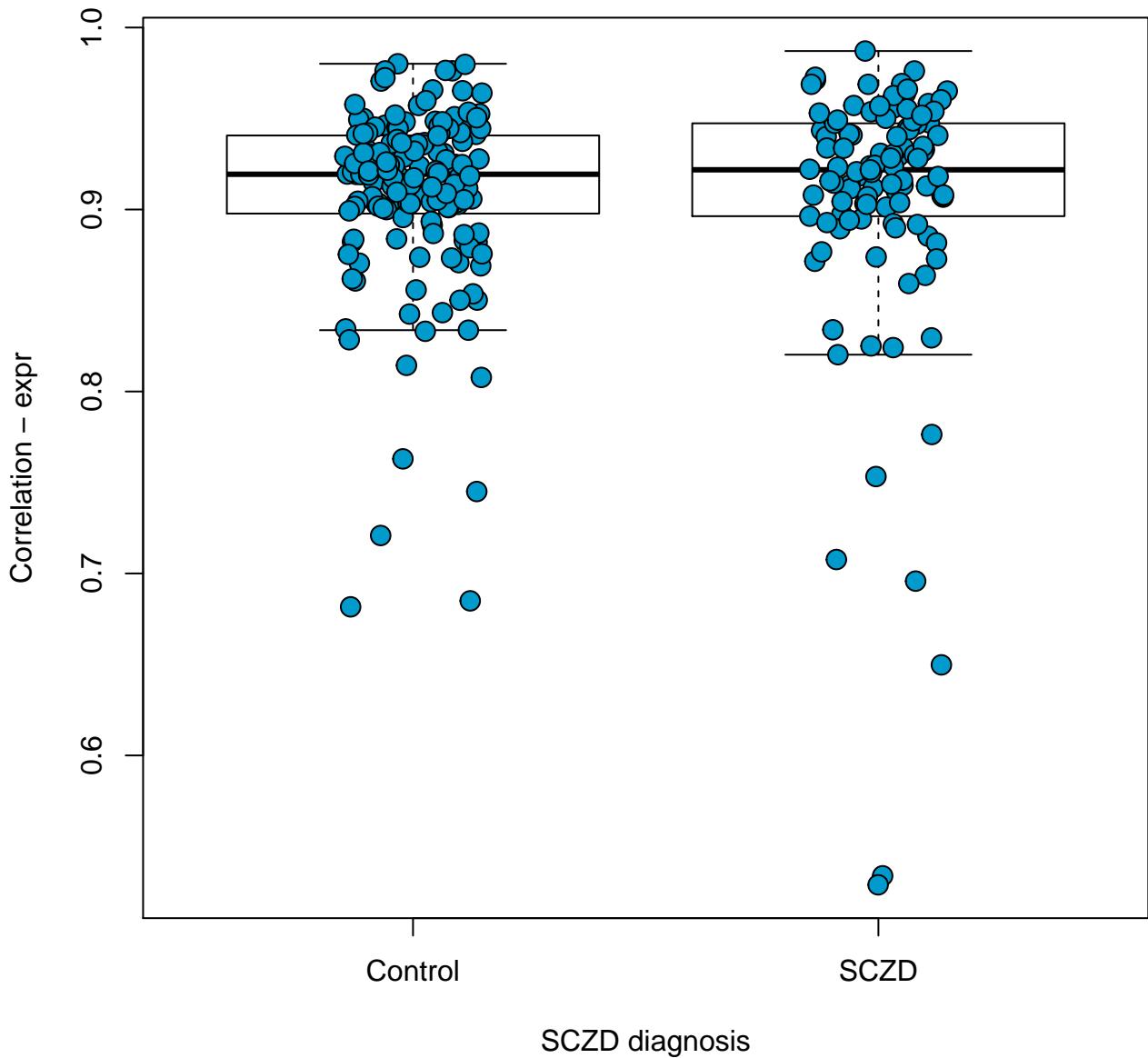
p-value: 0.293



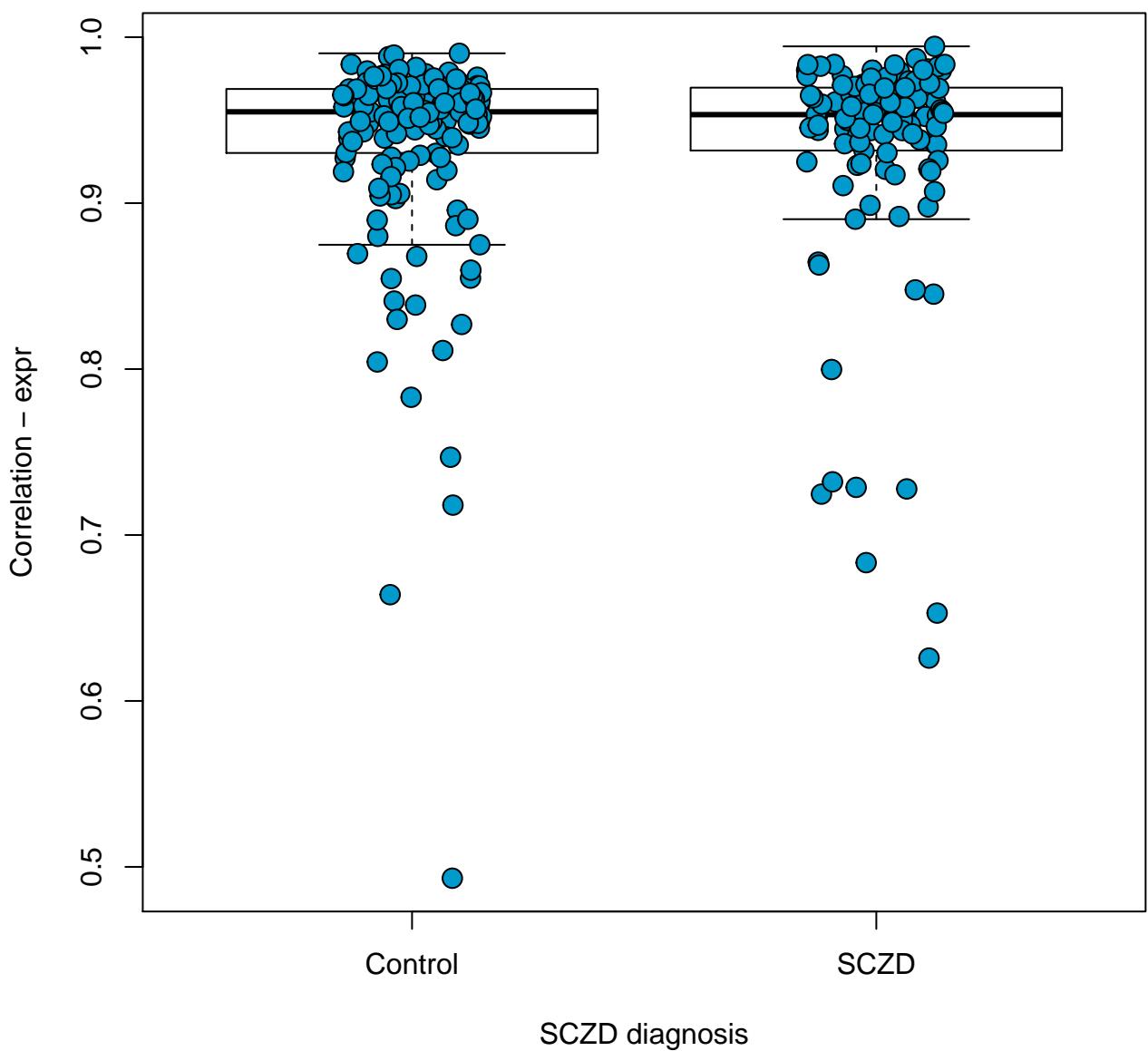
hsa04510: Focal adhesion
p-value: 0.263



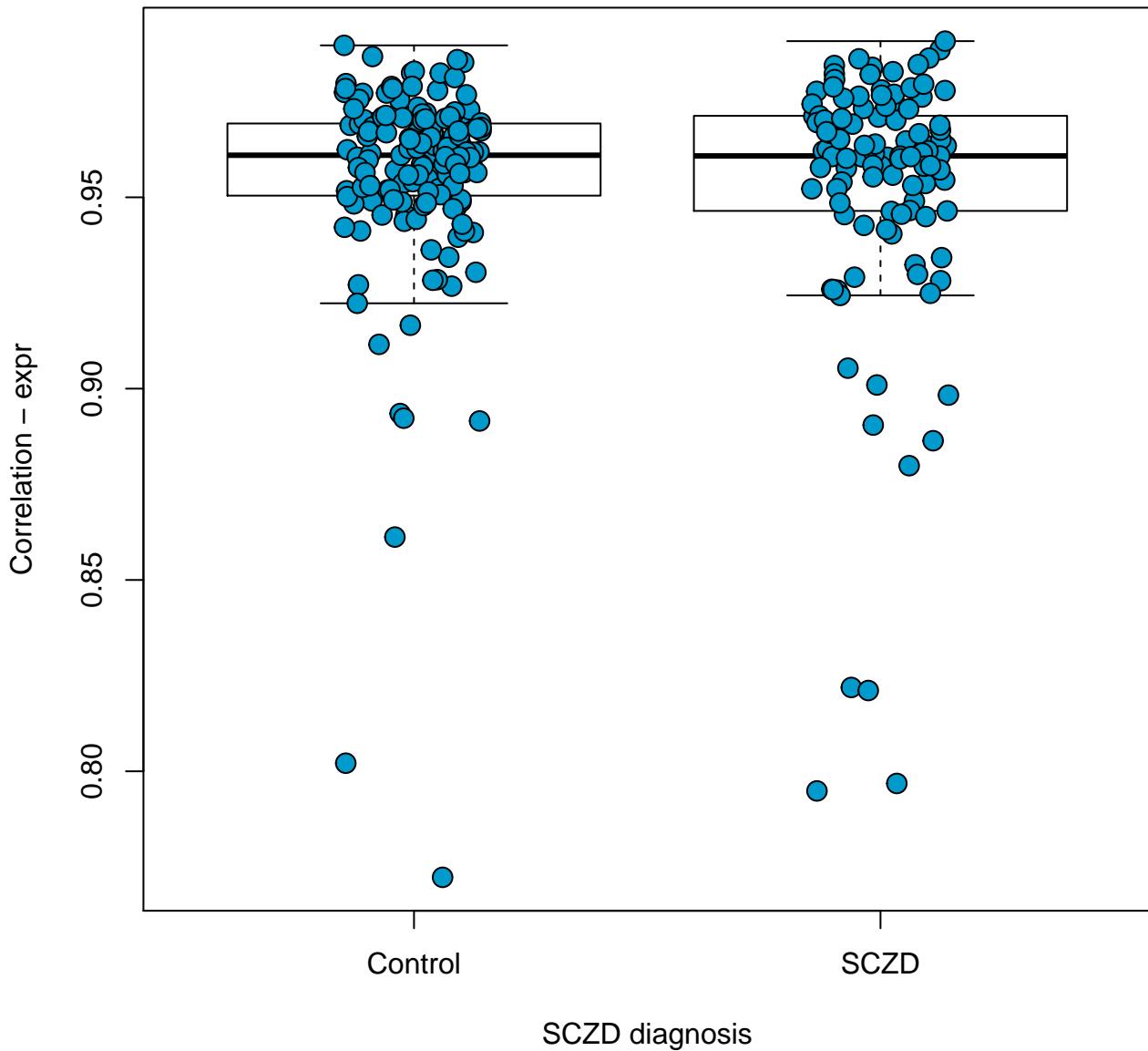
hsa04512: ECM–receptor interaction
p-value: 0.567



hsa04514: Cell adhesion molecules (CAMs)
p-value: 0.649

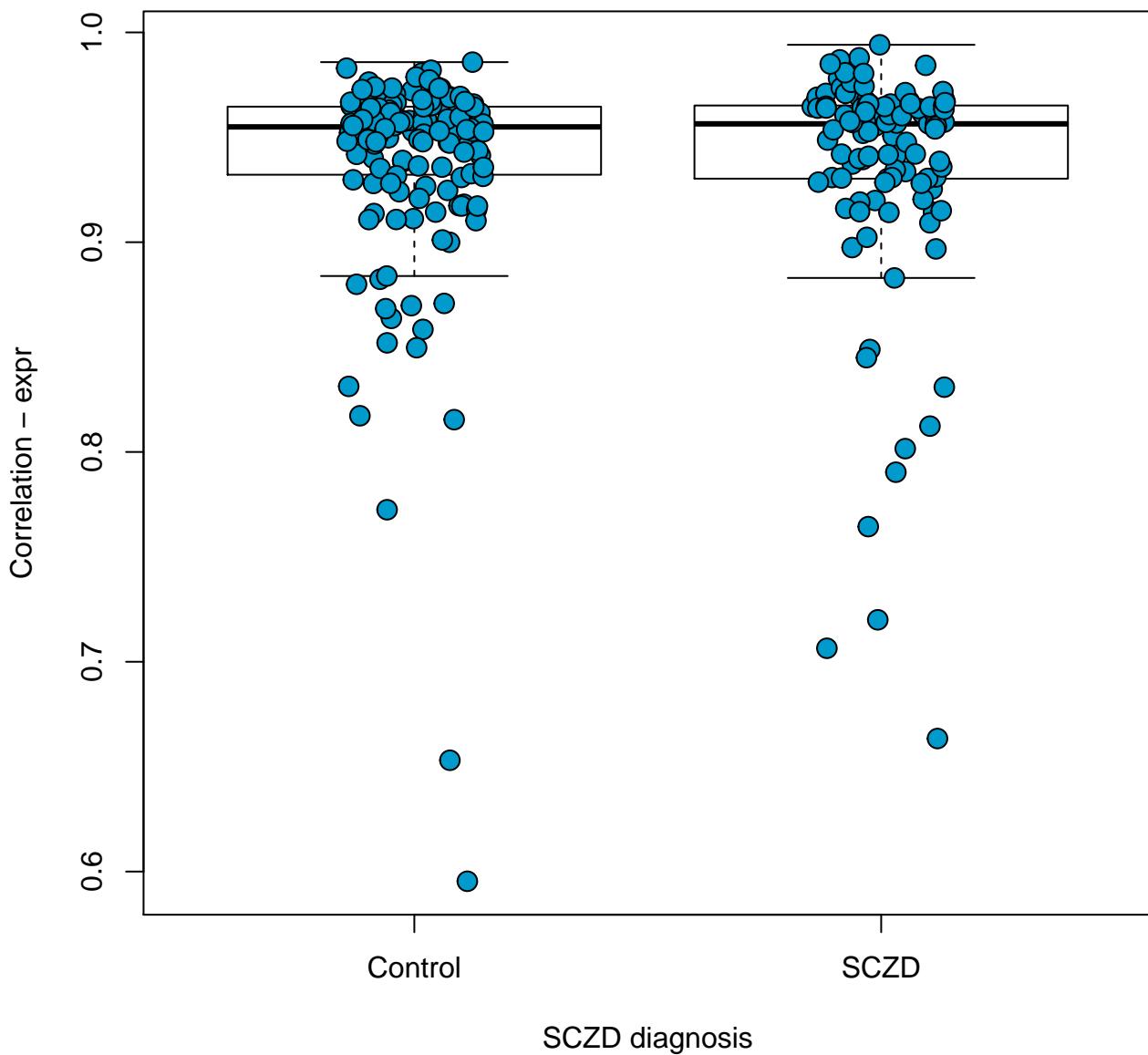


hsa04520: Adherens junction
p-value: 0.341

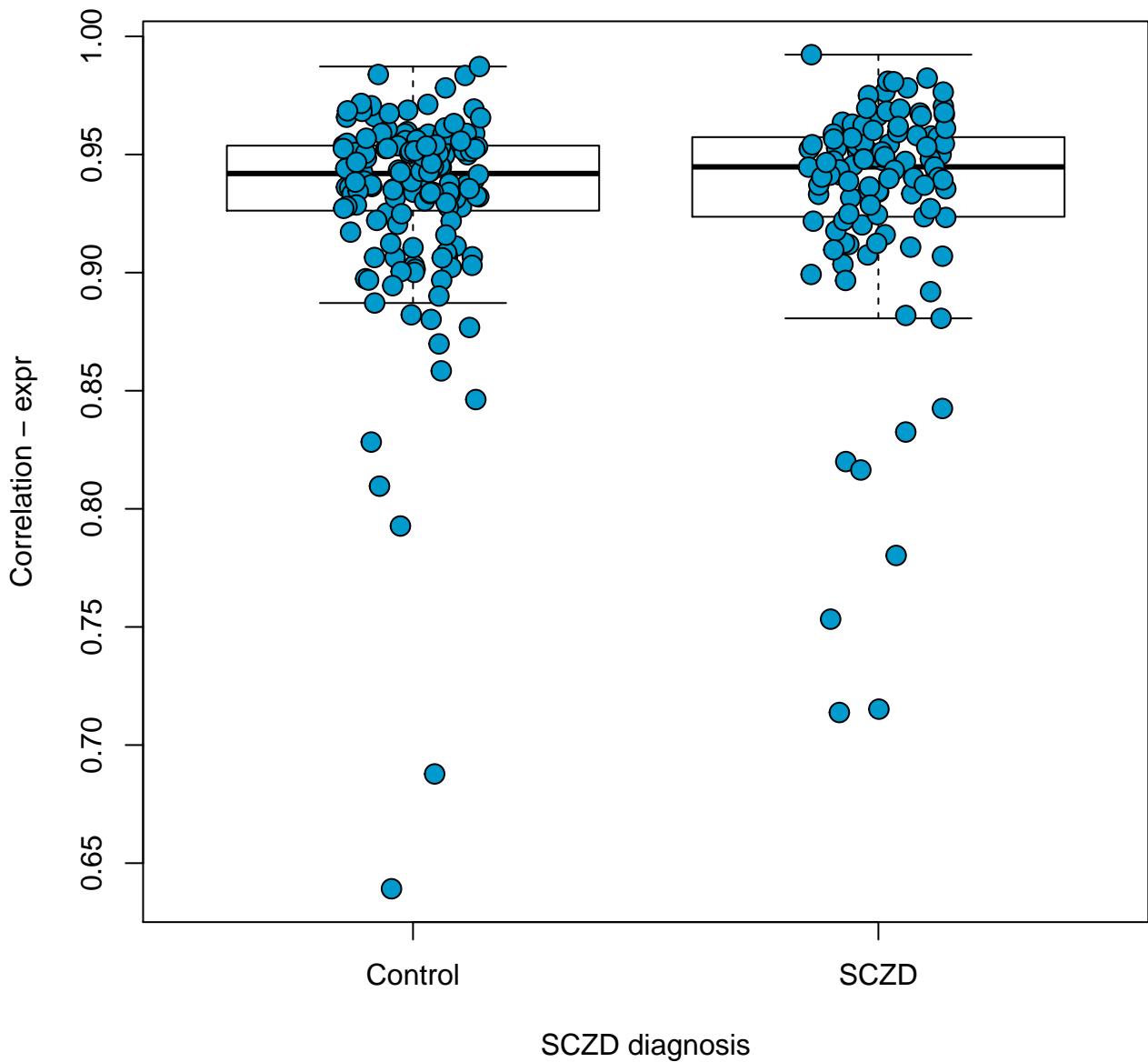


hsa04530: Tight junction

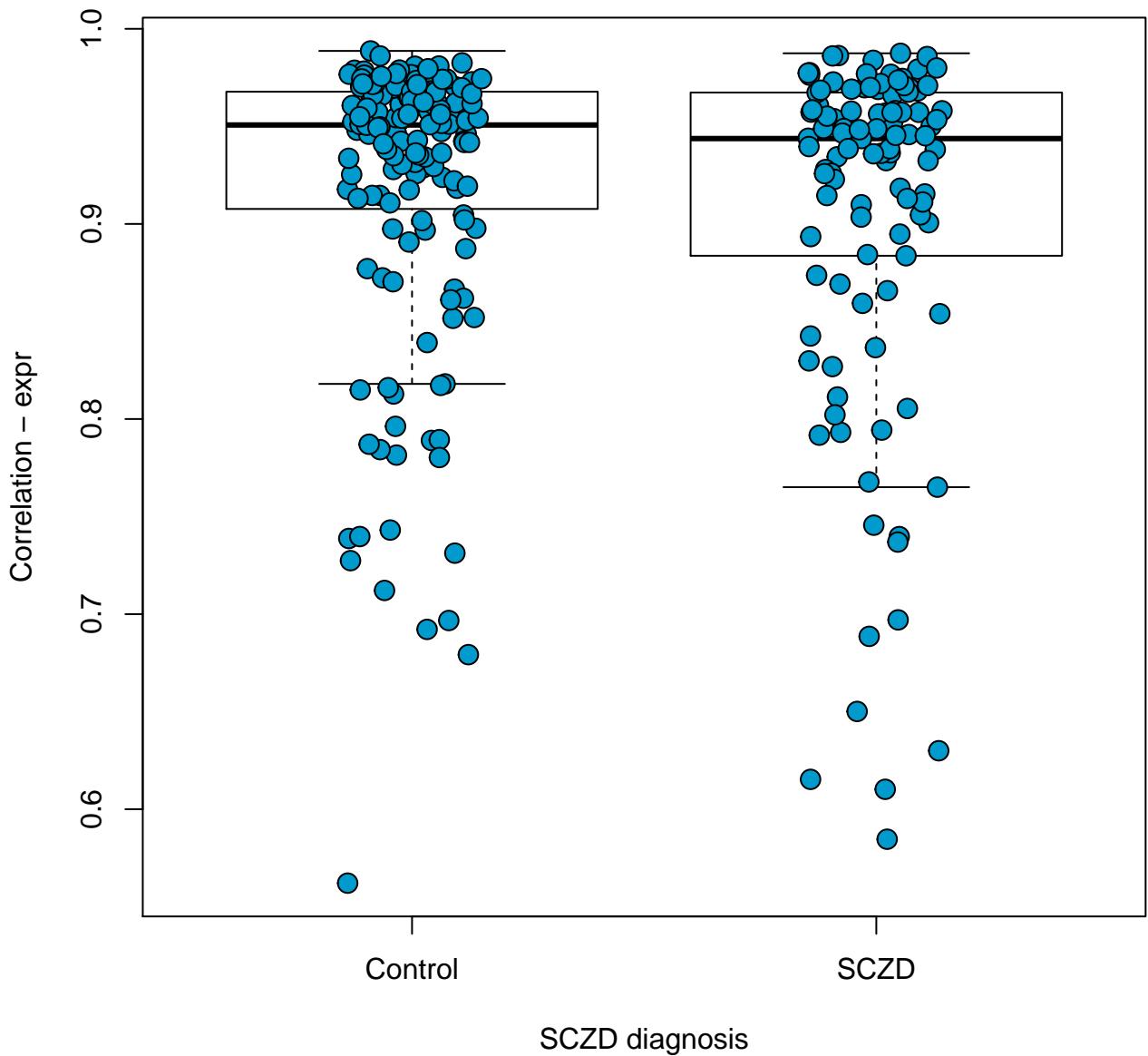
p-value: 0.535



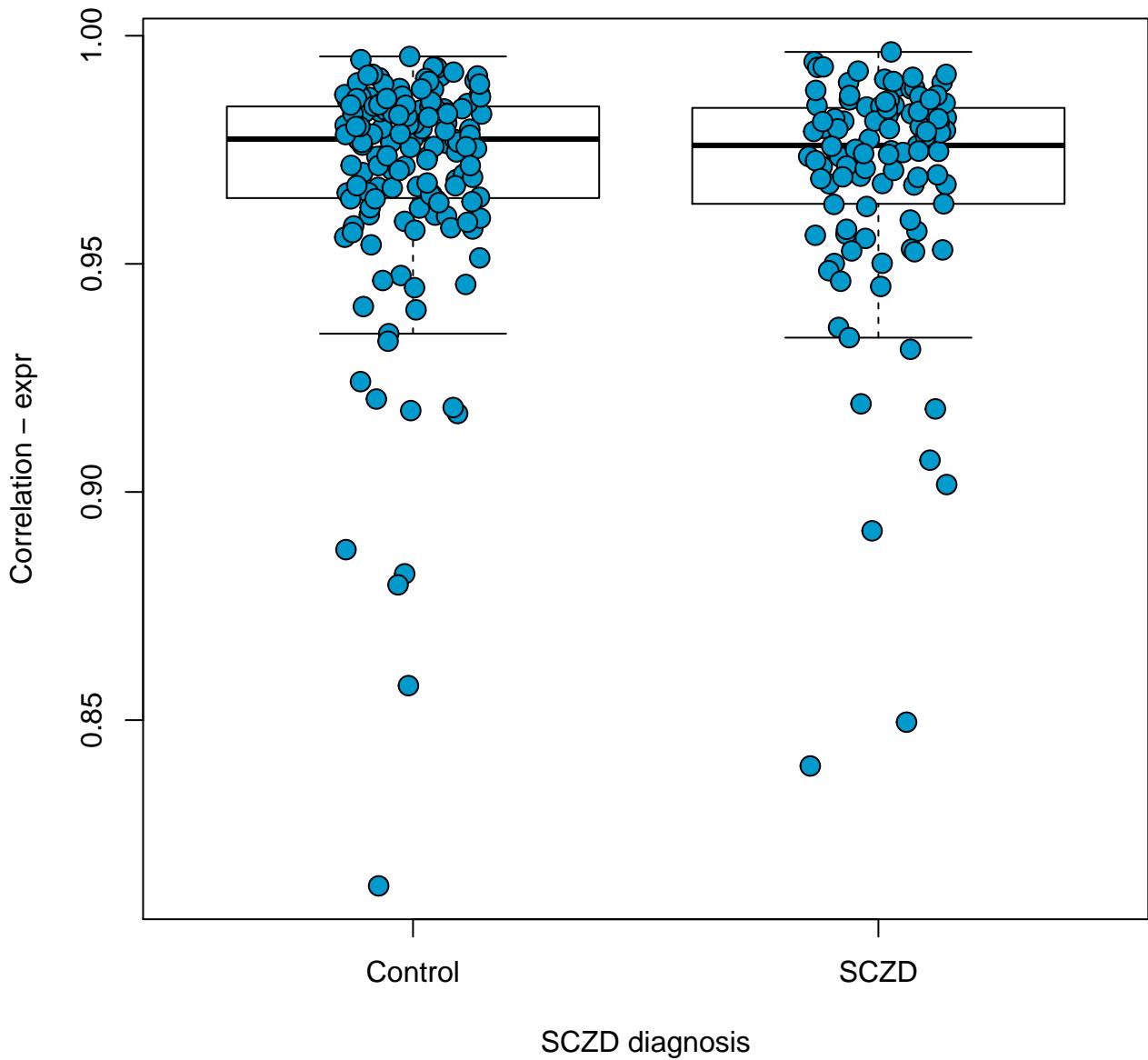
hsa04540: Gap junction
p-value: 0.983



hsa04610: Complement and coagulation cascades
p-value: 0.154

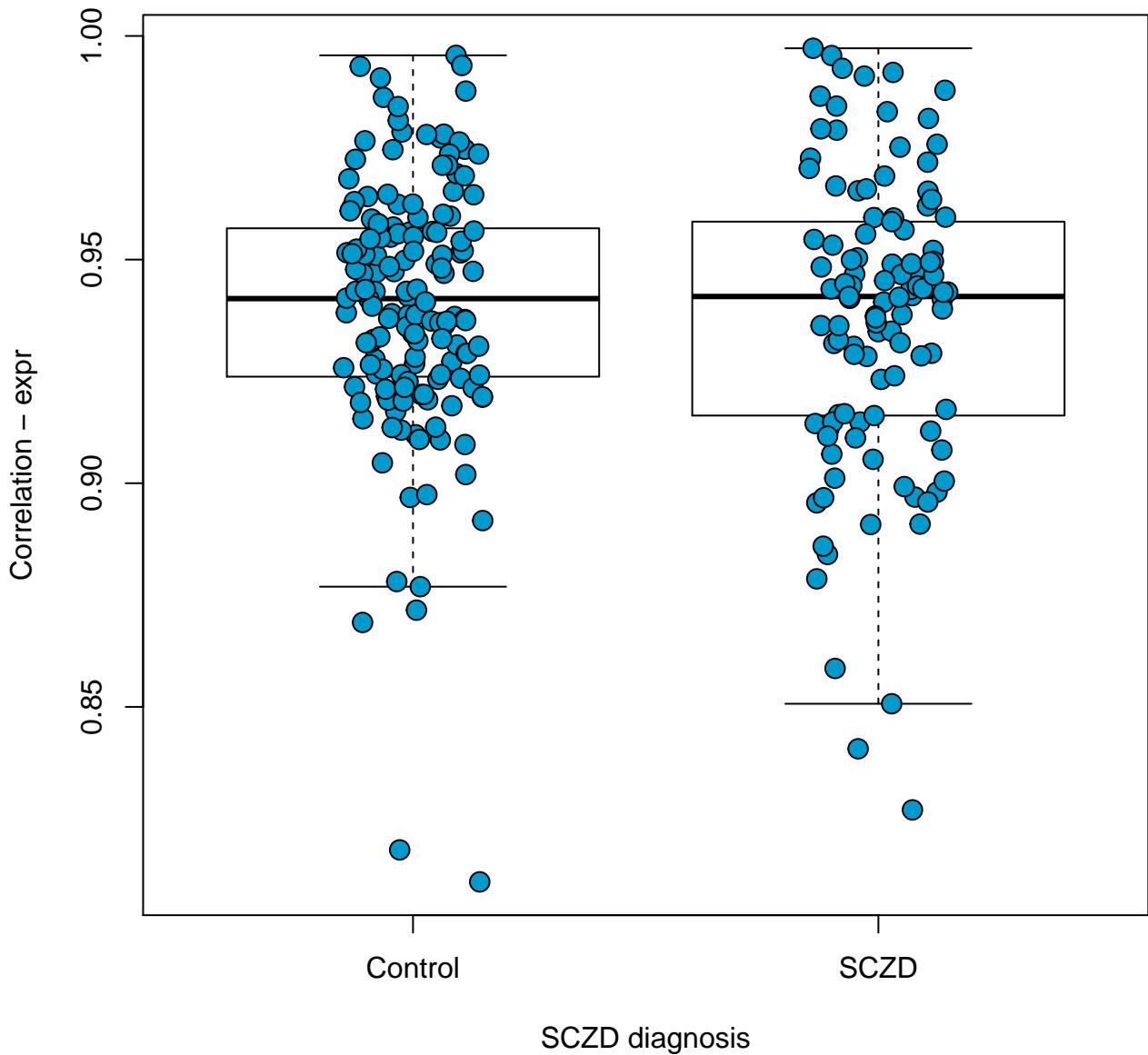


hsa04612: Antigen processing and presentation
p-value: 0.819

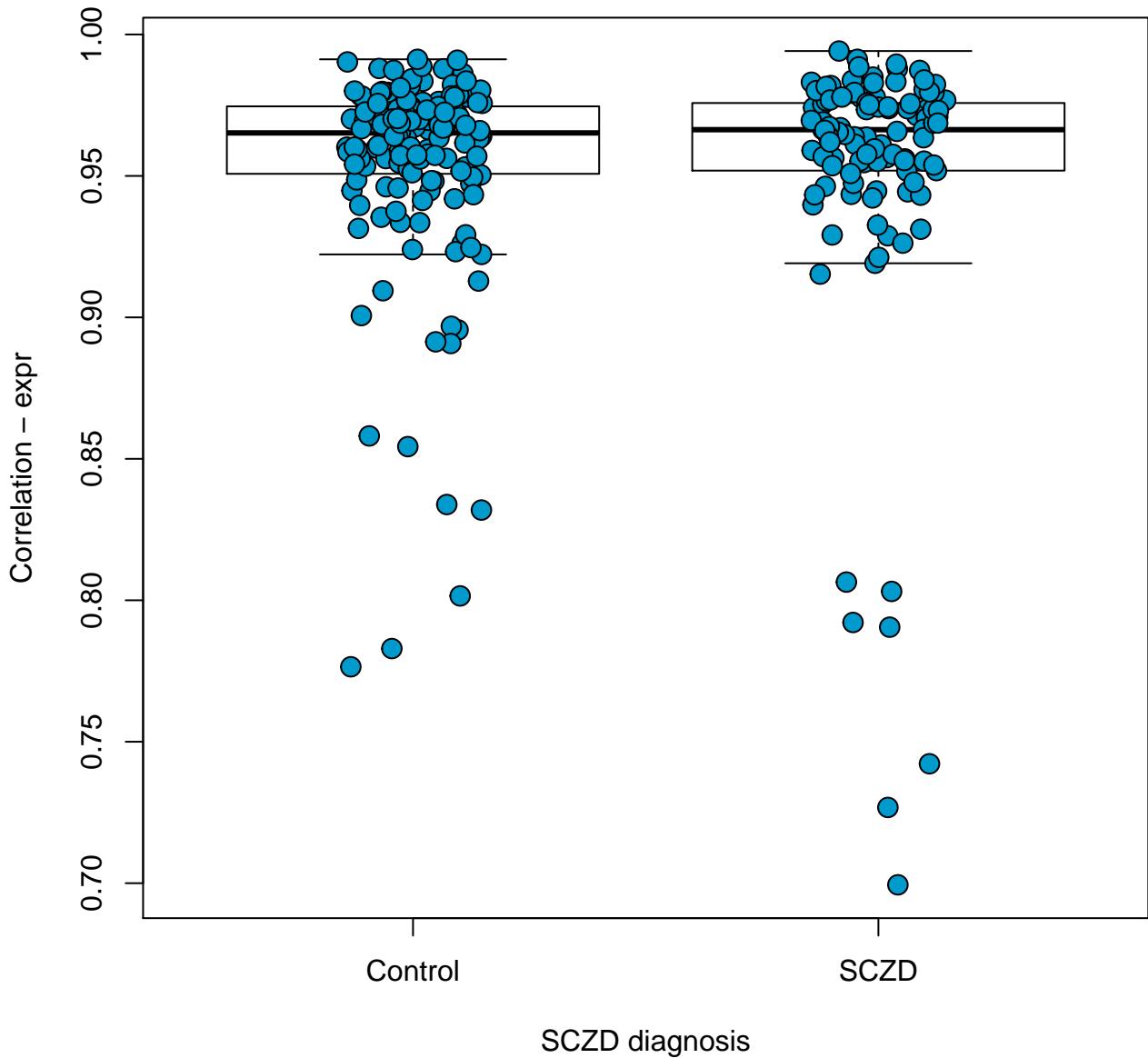


hsa04614: Renin–angiotensin system

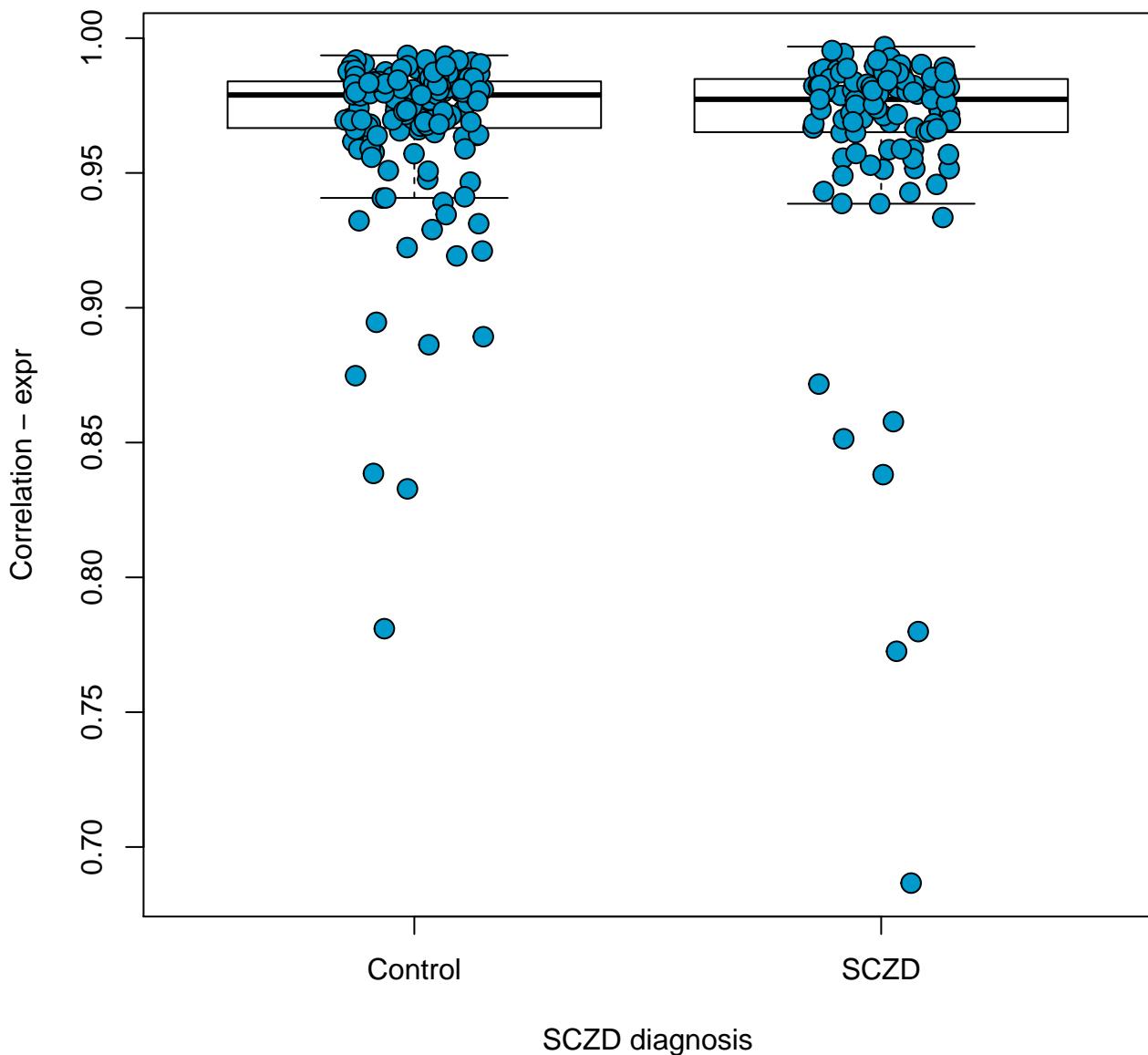
p-value: 0.426



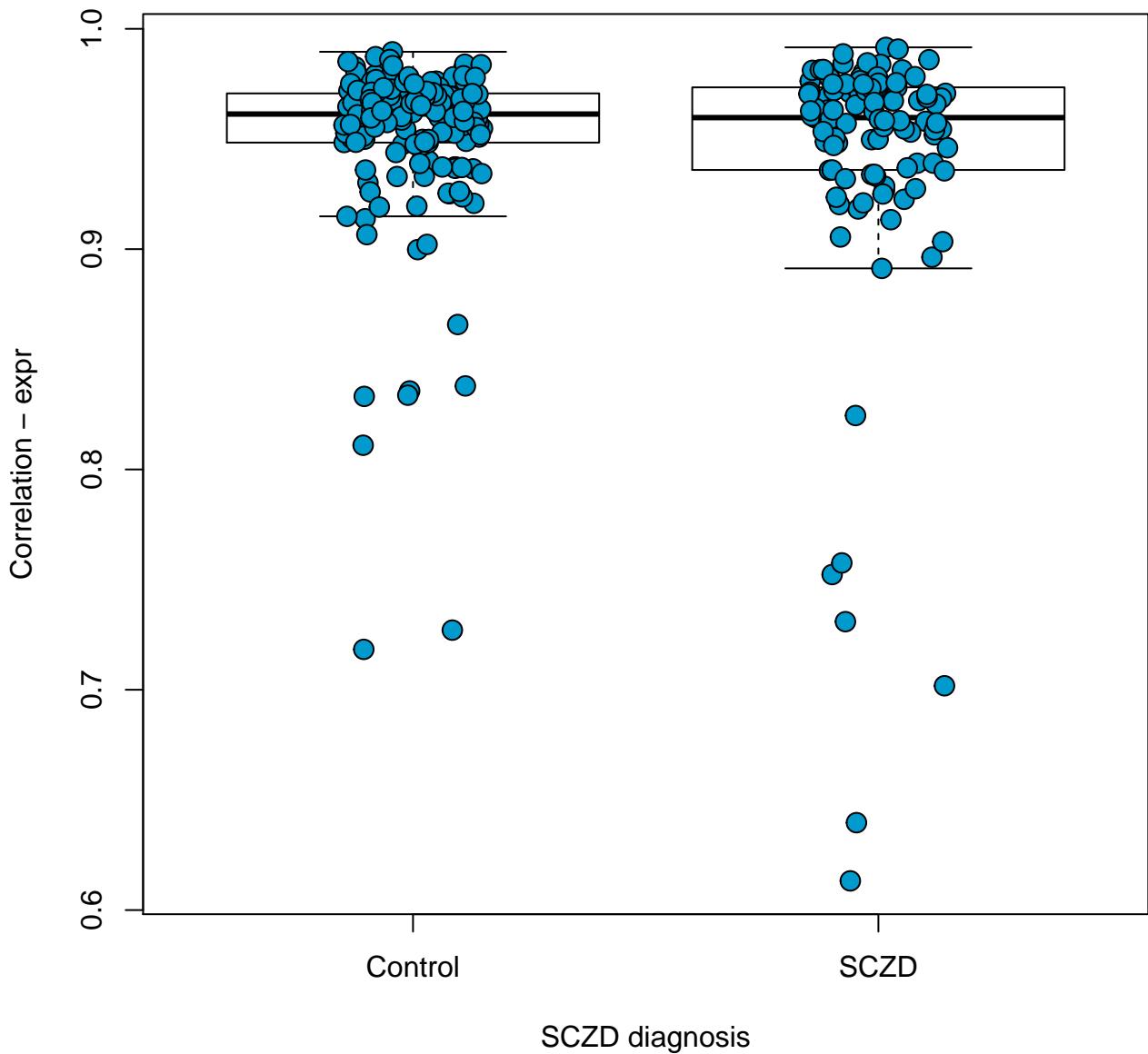
hsa04620: Toll-like receptor signaling pathway
p-value: 0.577



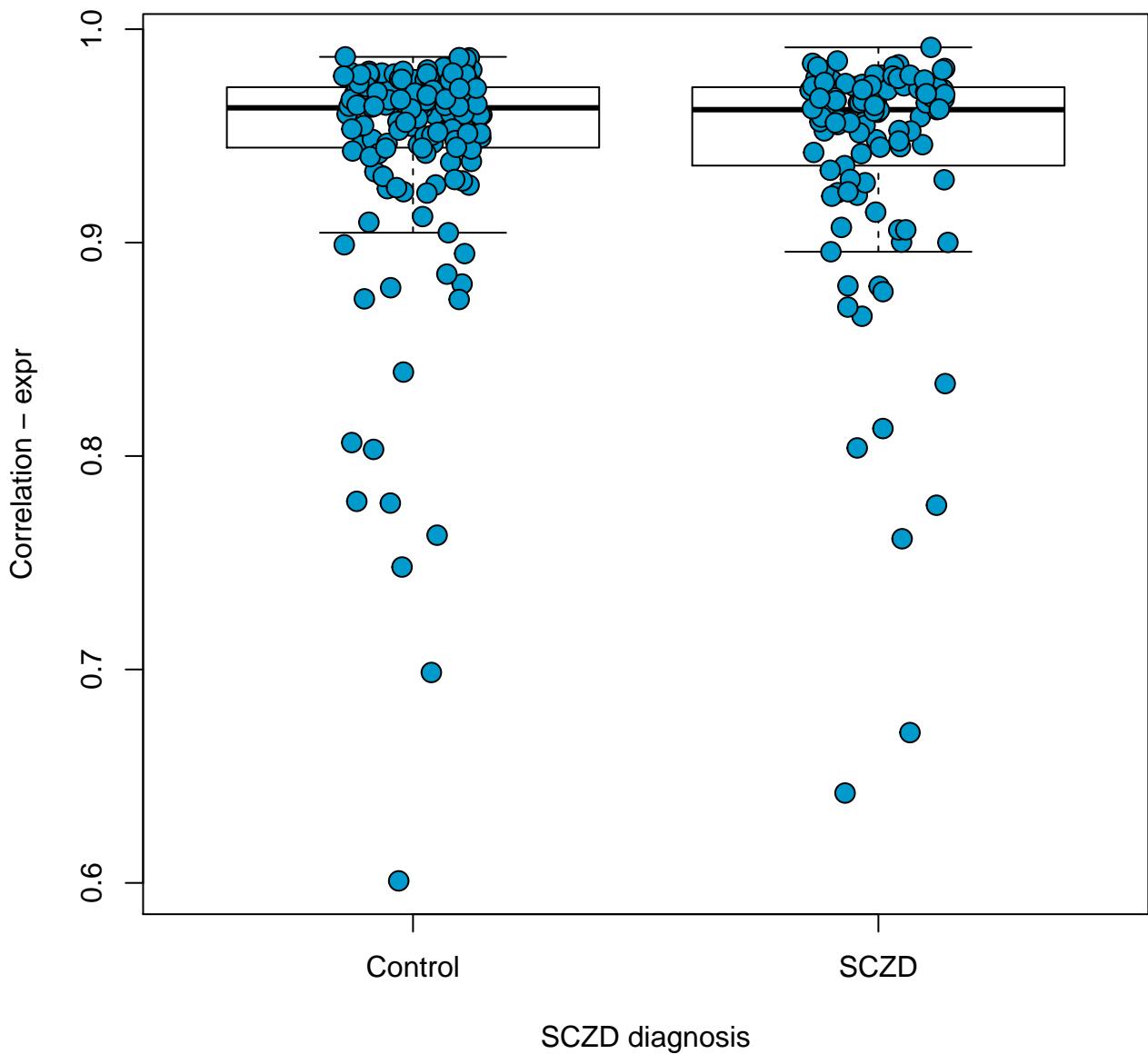
hsa04621: NOD-like receptor signaling pathway
p-value: 0.319



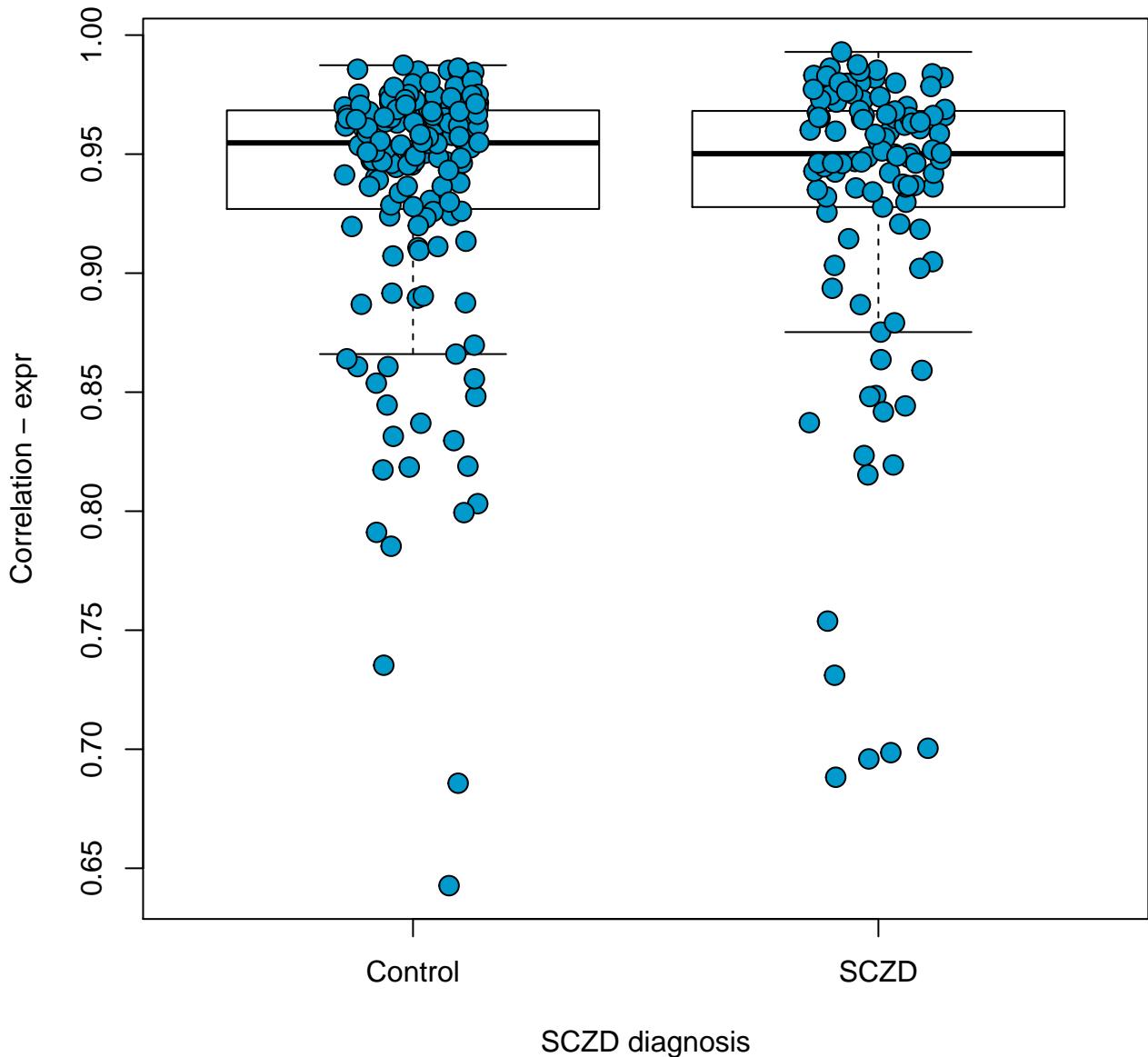
hsa04622: RIG-I-like receptor signaling pathway
p-value: 0.176



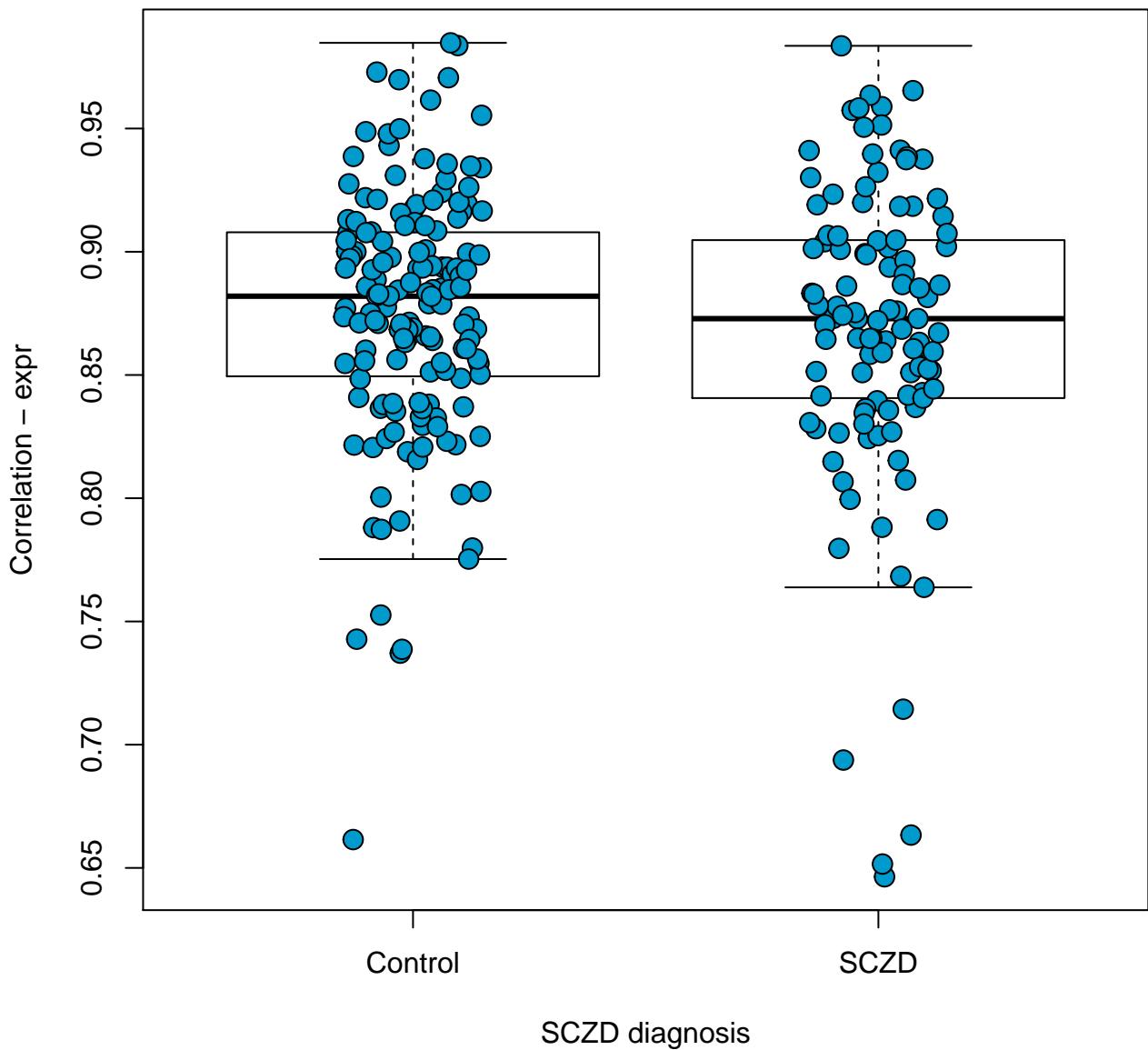
hsa04623: Cytosolic DNA–sensing pathway
p-value: 0.572



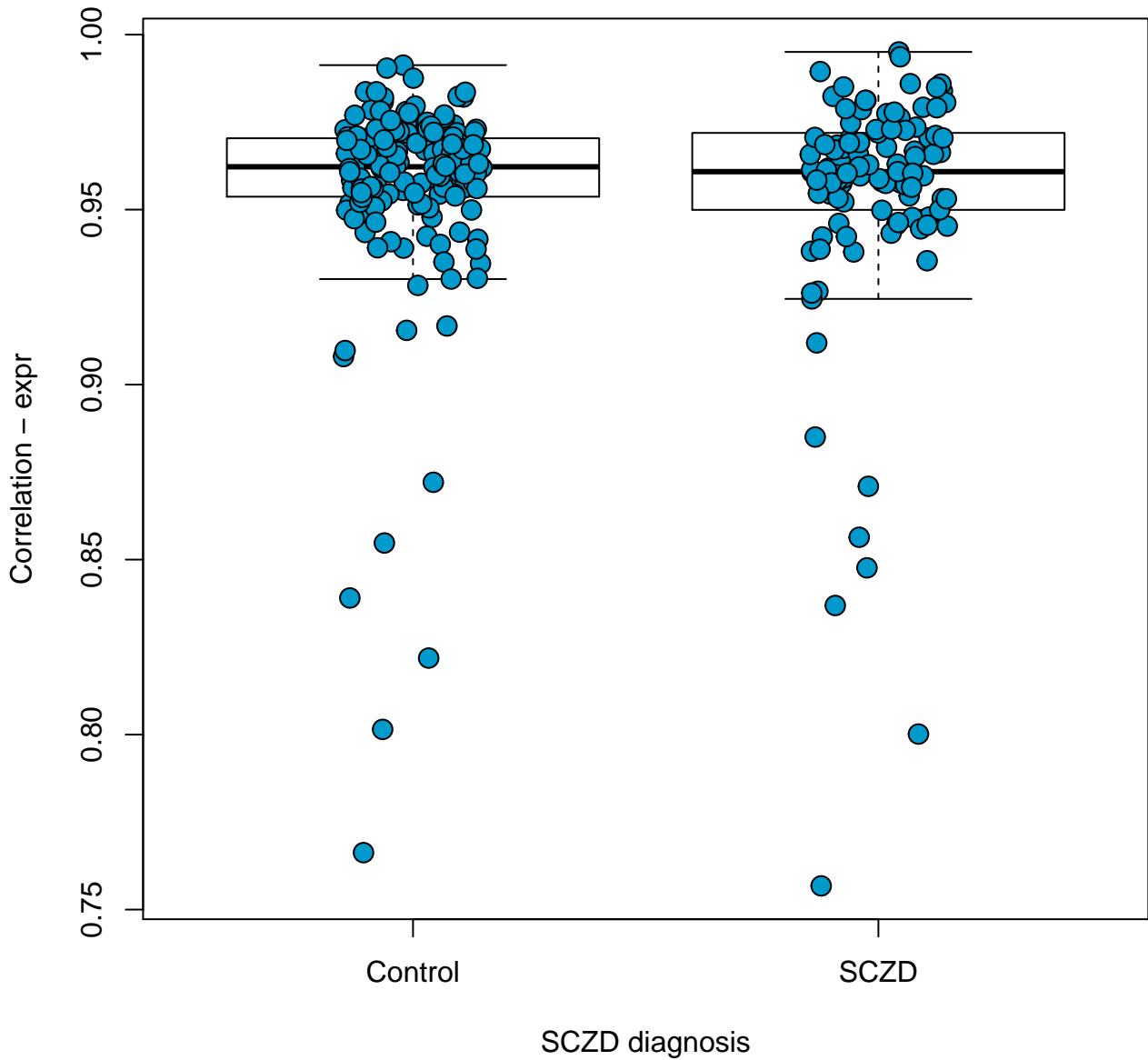
hsa04630: Jak–STAT signaling pathway
p-value: 0.536



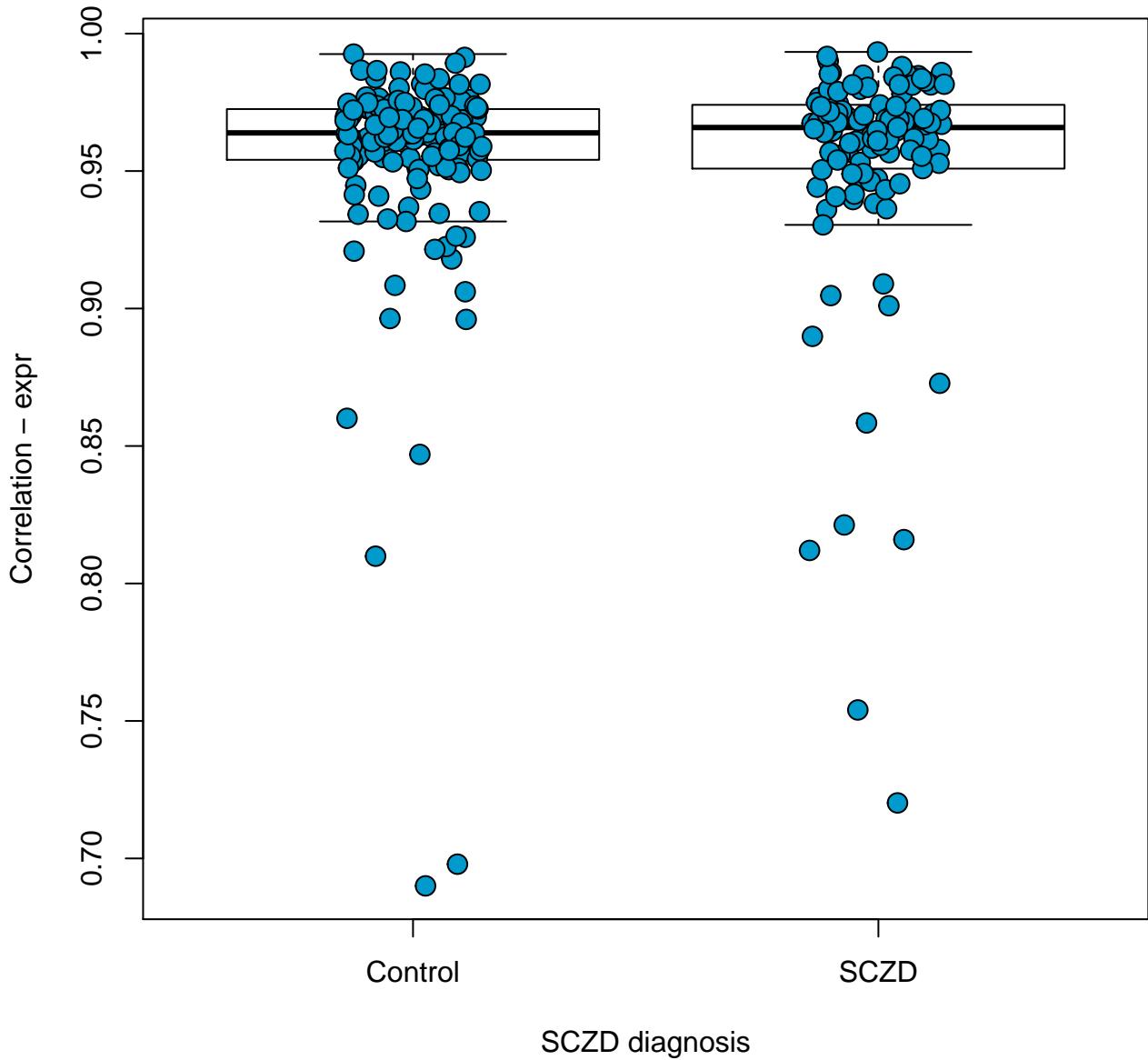
hsa04640: Hematopoietic cell lineage
p-value: 0.252



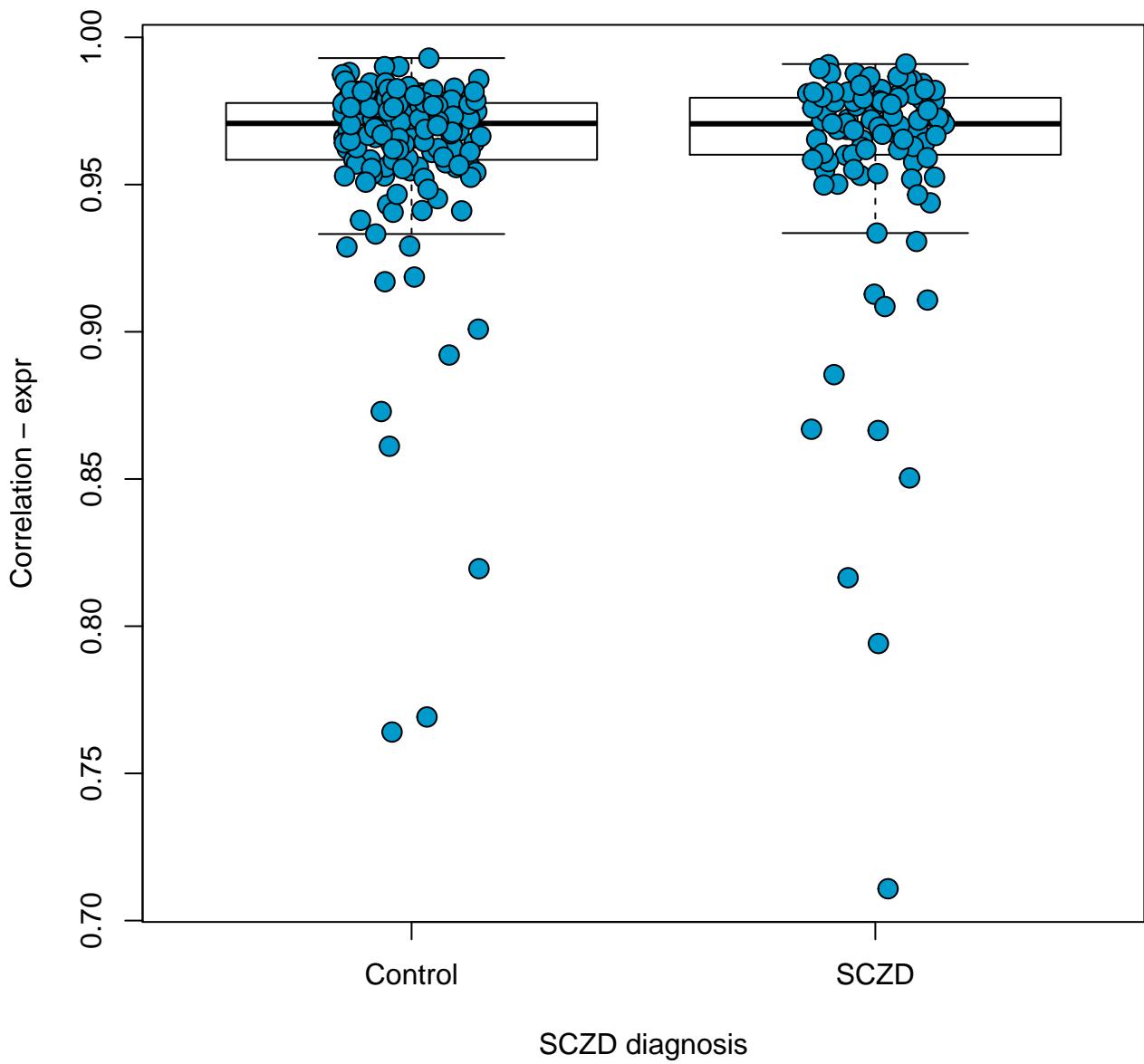
hsa04650: Natural killer cell mediated cytotoxicity
p-value: 0.646



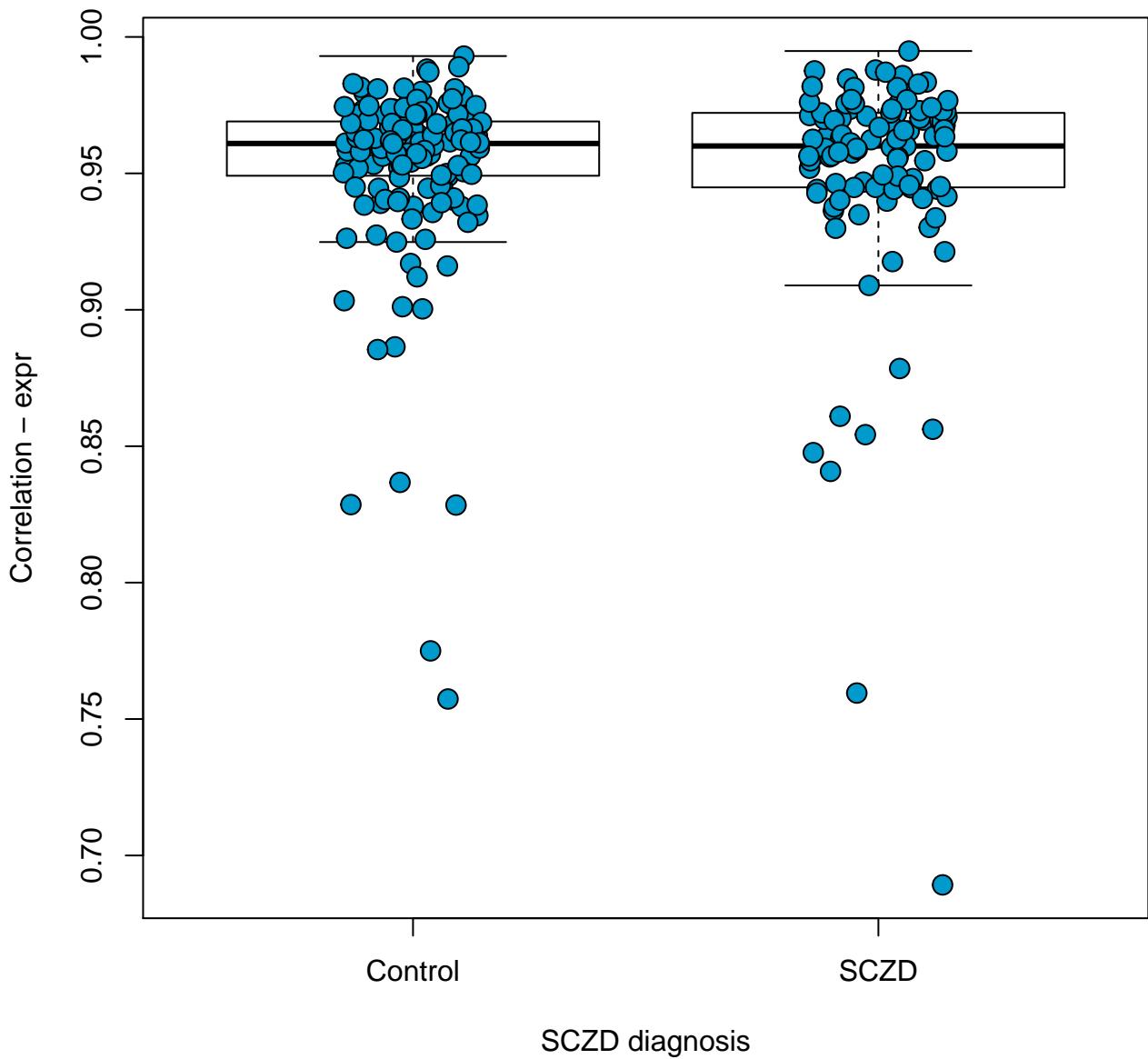
hsa04660: T cell receptor signaling pathway
p-value: 0.655



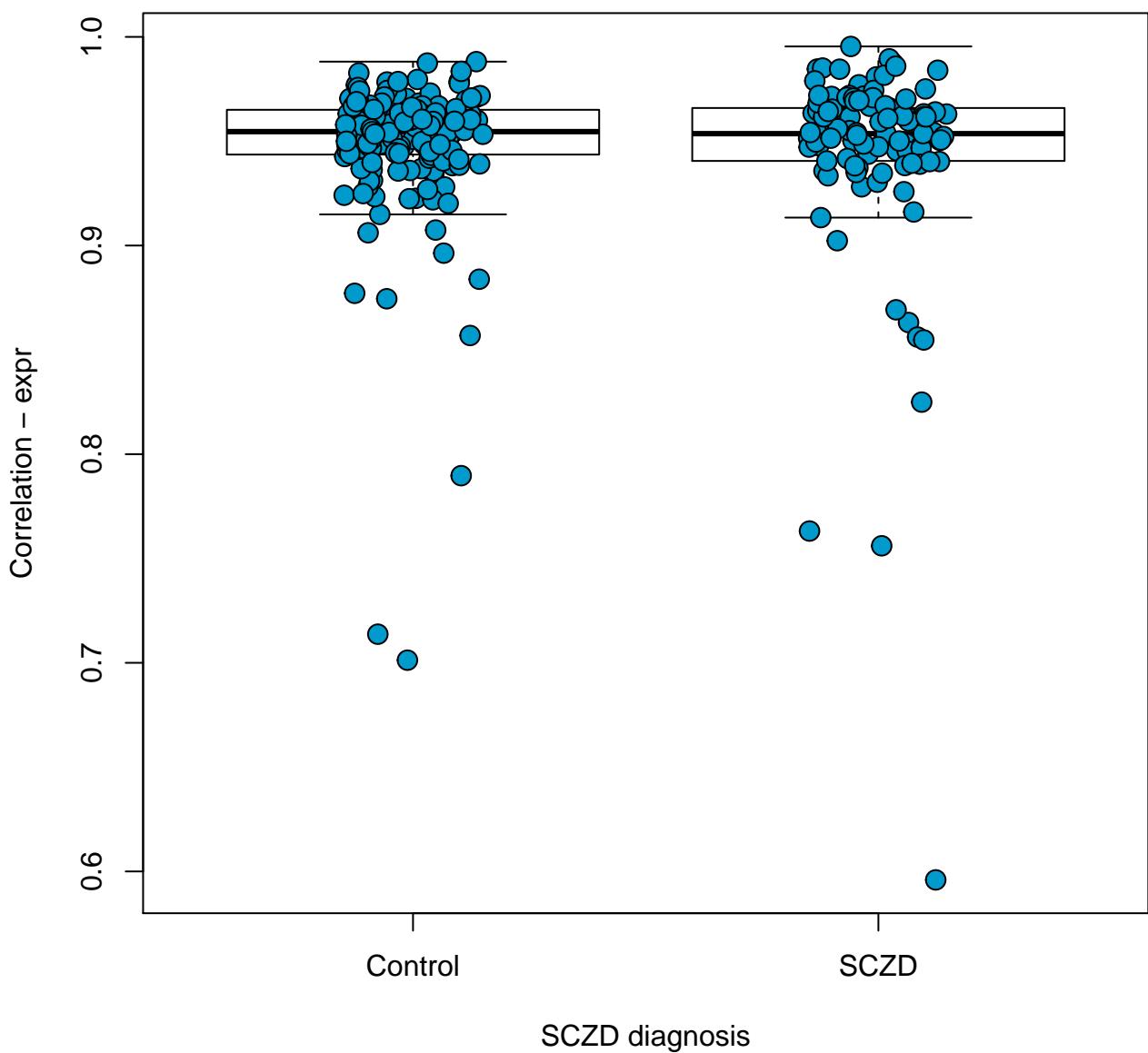
hsa04662: B cell receptor signaling pathway
p-value: 0.592



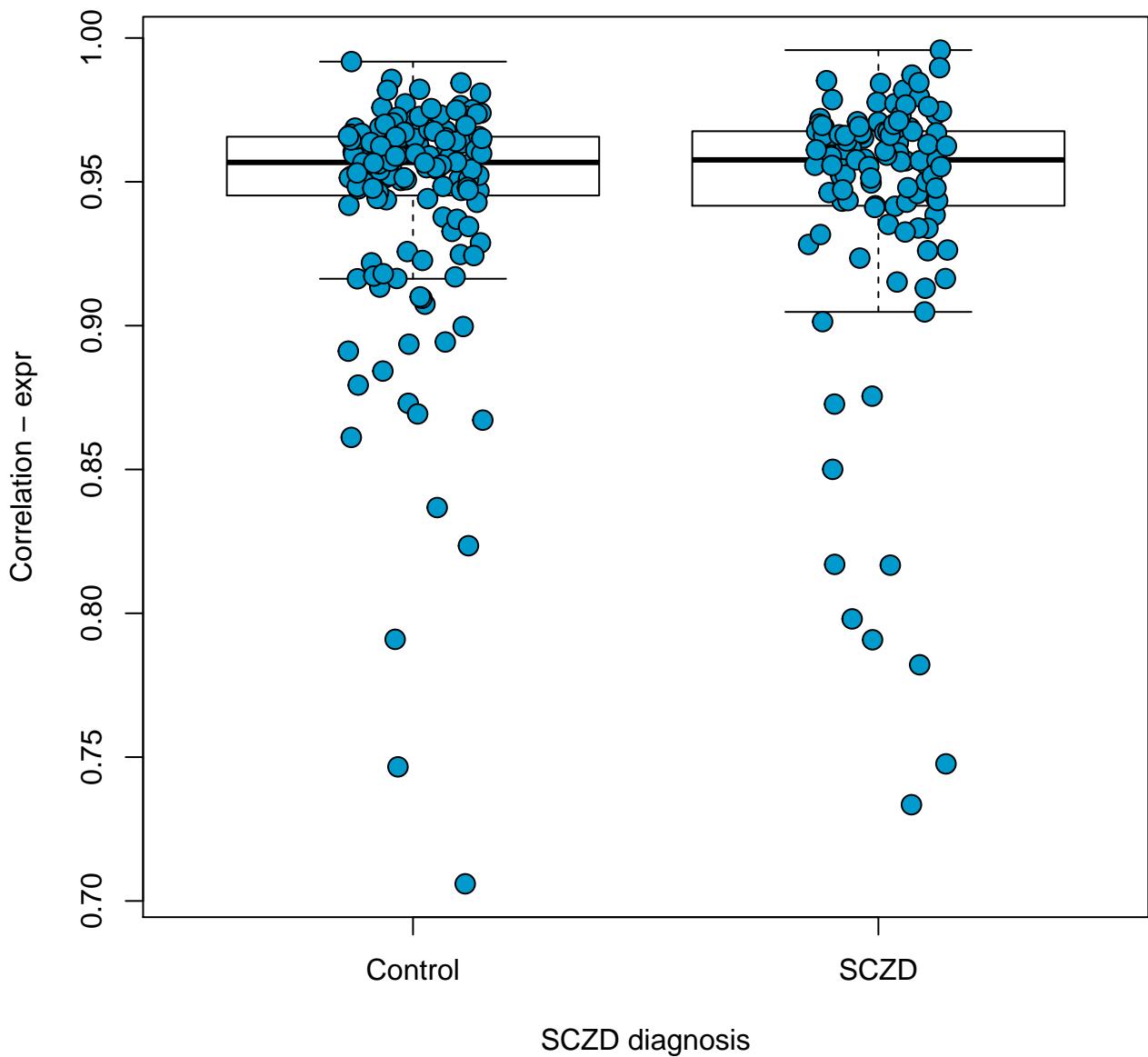
hsa04664: Fc epsilon RI signaling pathway
p-value: 0.641



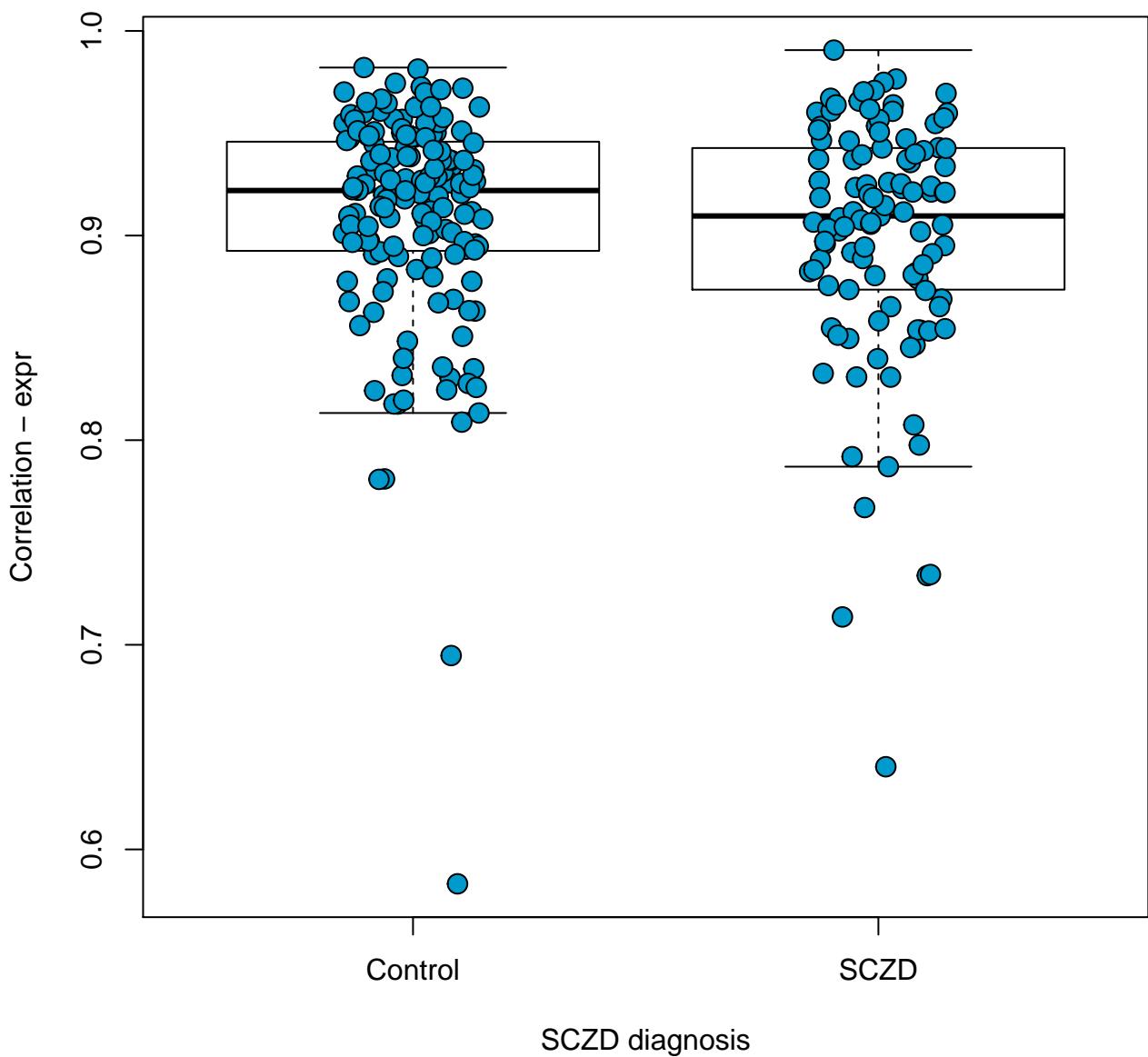
hsa04666: Fc gamma R-mediated phagocytosis
p-value: 0.545



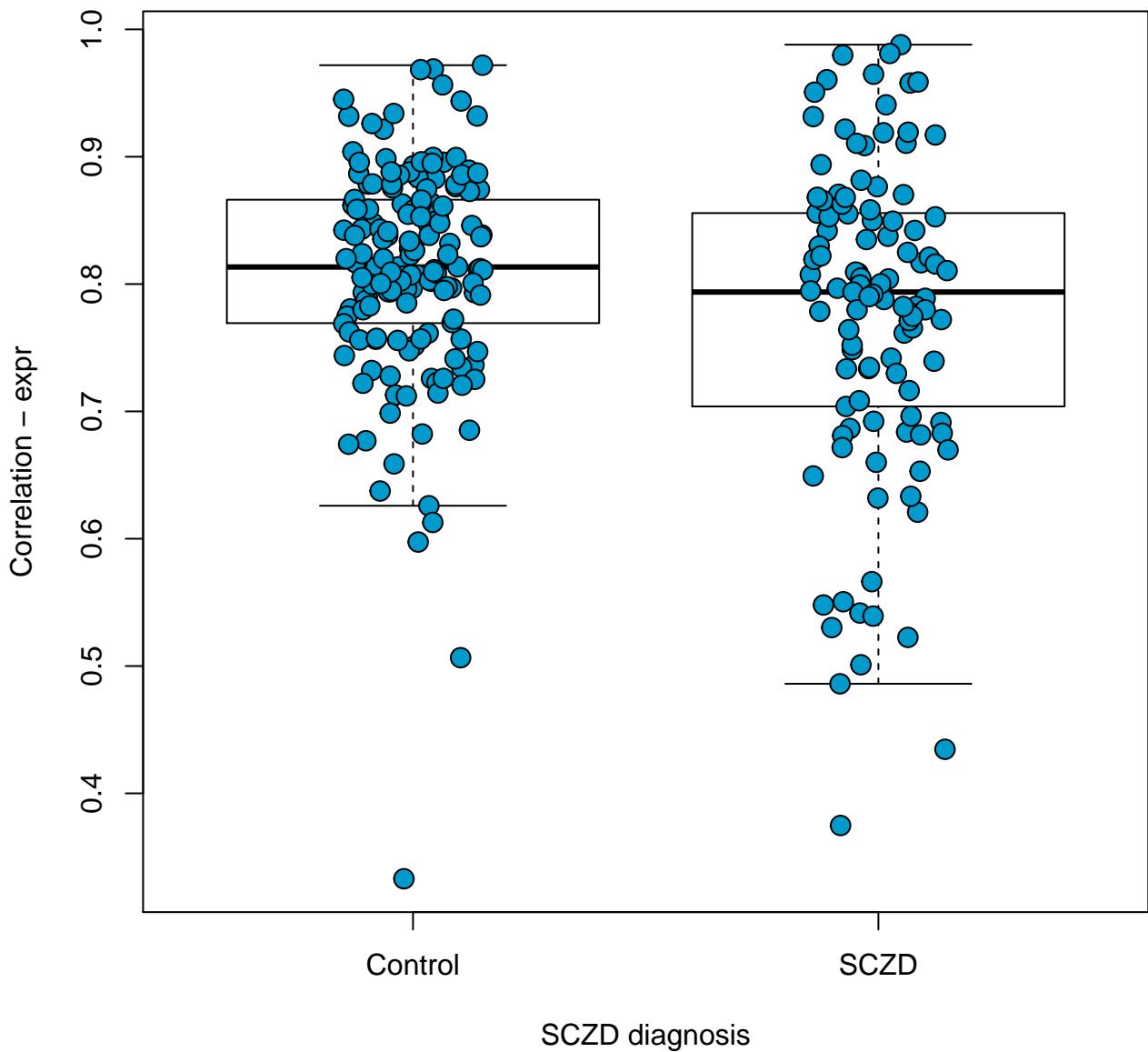
hsa04670: Leukocyte transendothelial migration
p-value: 0.672



hsa04672: Intestinal immune network for IgA production
p-value: 0.183

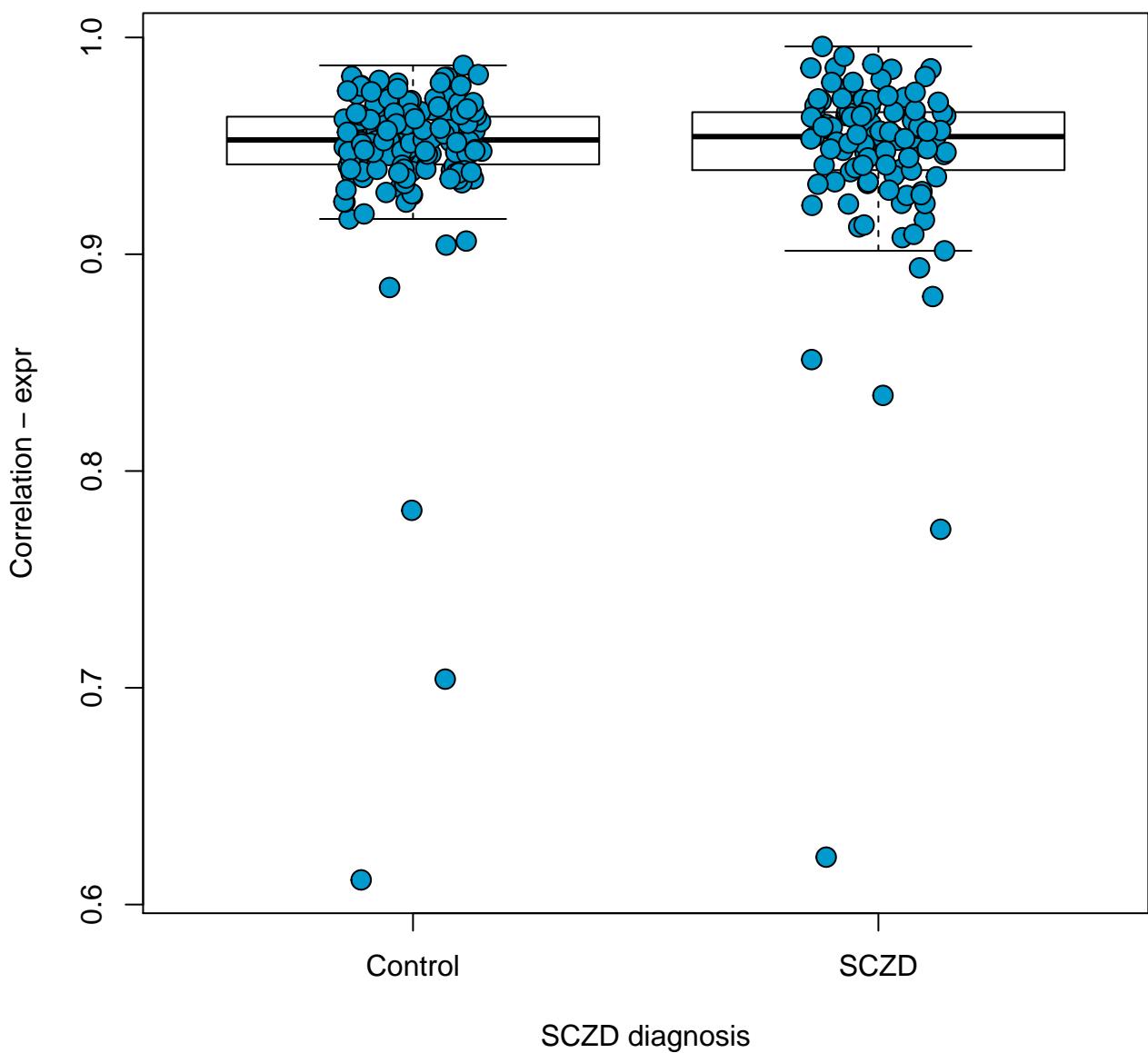


hsa04710: Circadian rhythm
p-value: 0.00755

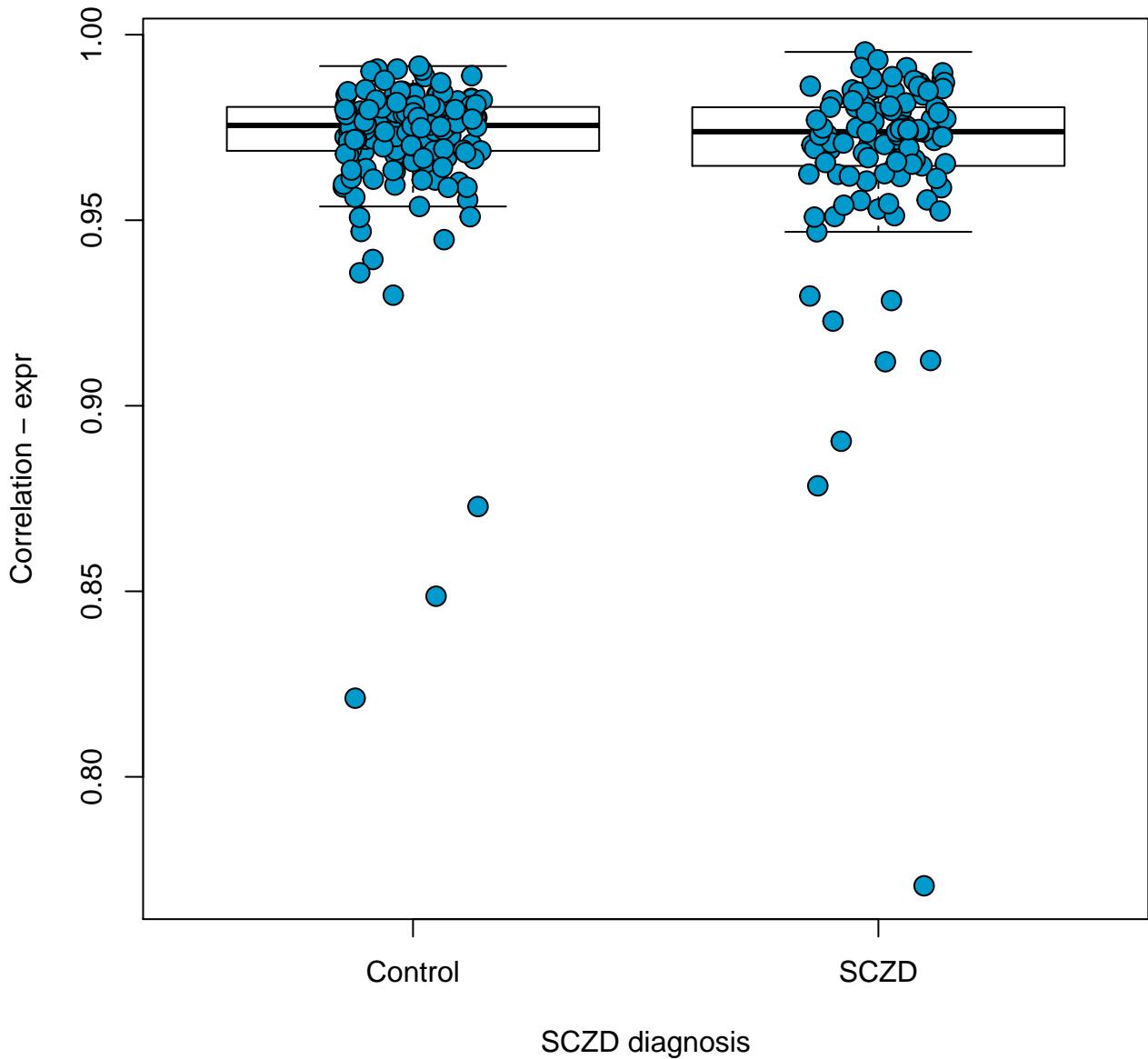


hsa04720: Long-term potentiation

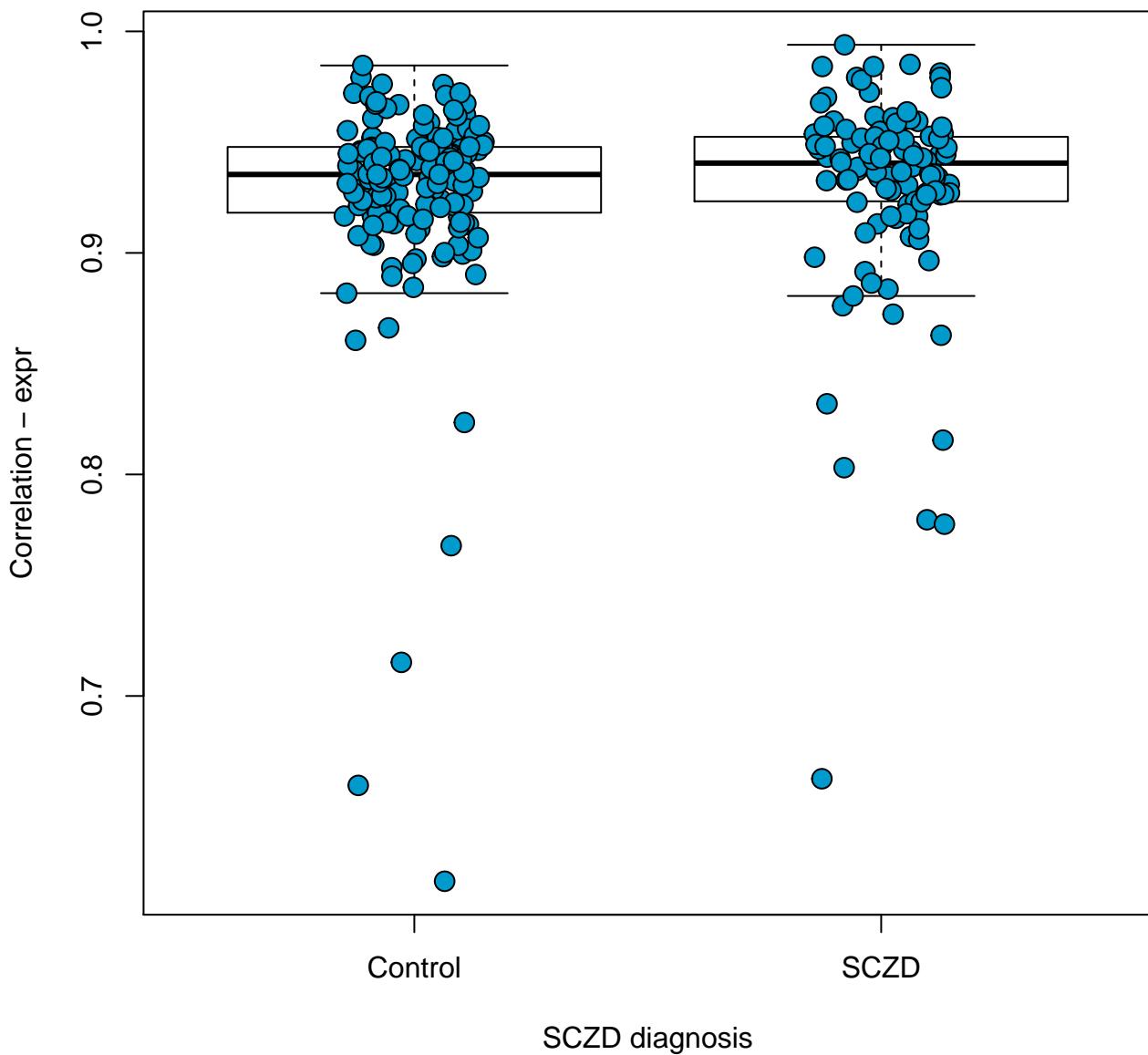
p-value: 0.671



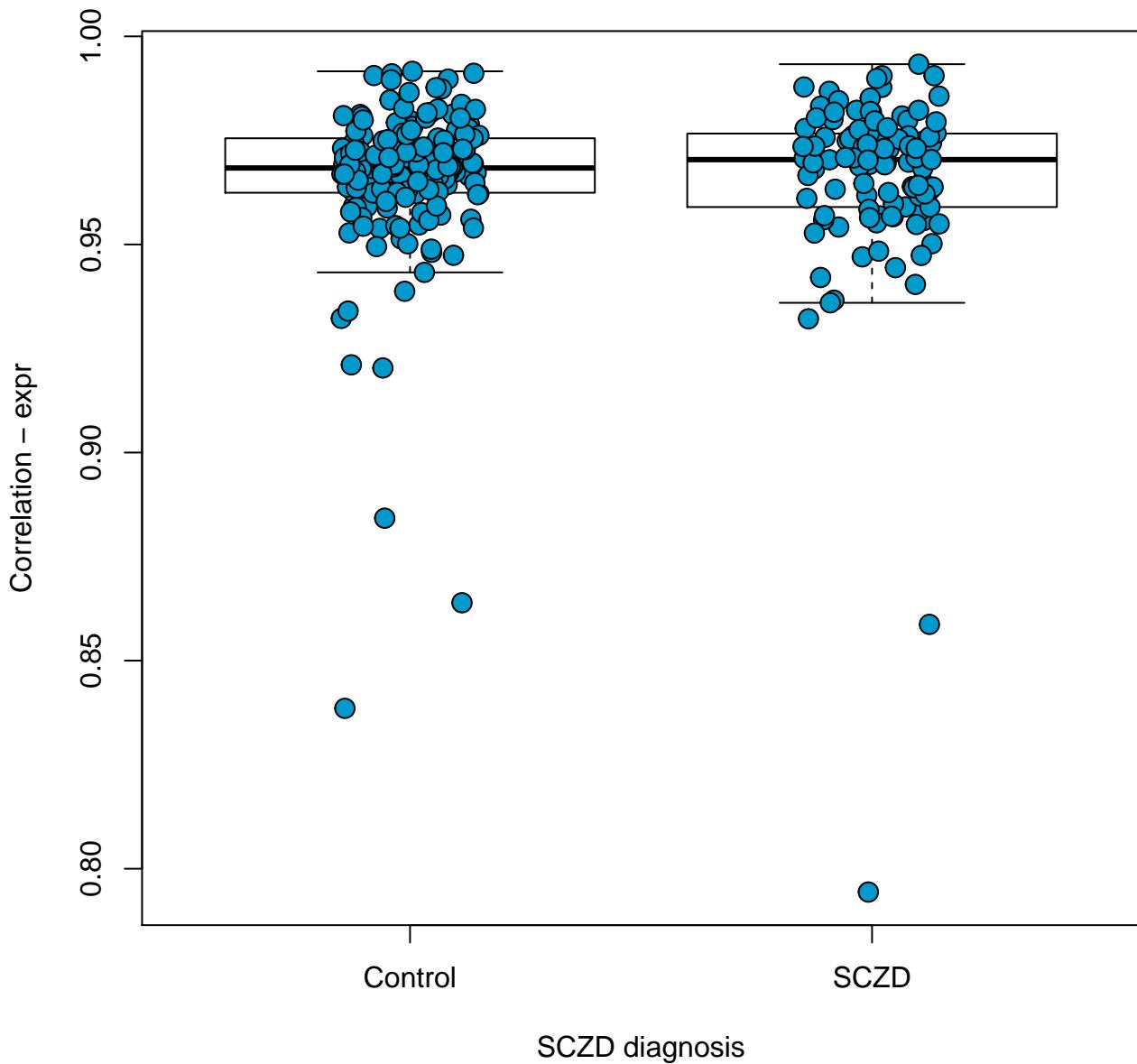
hsa04722: Neurotrophin signaling pathway
p-value: 0.222



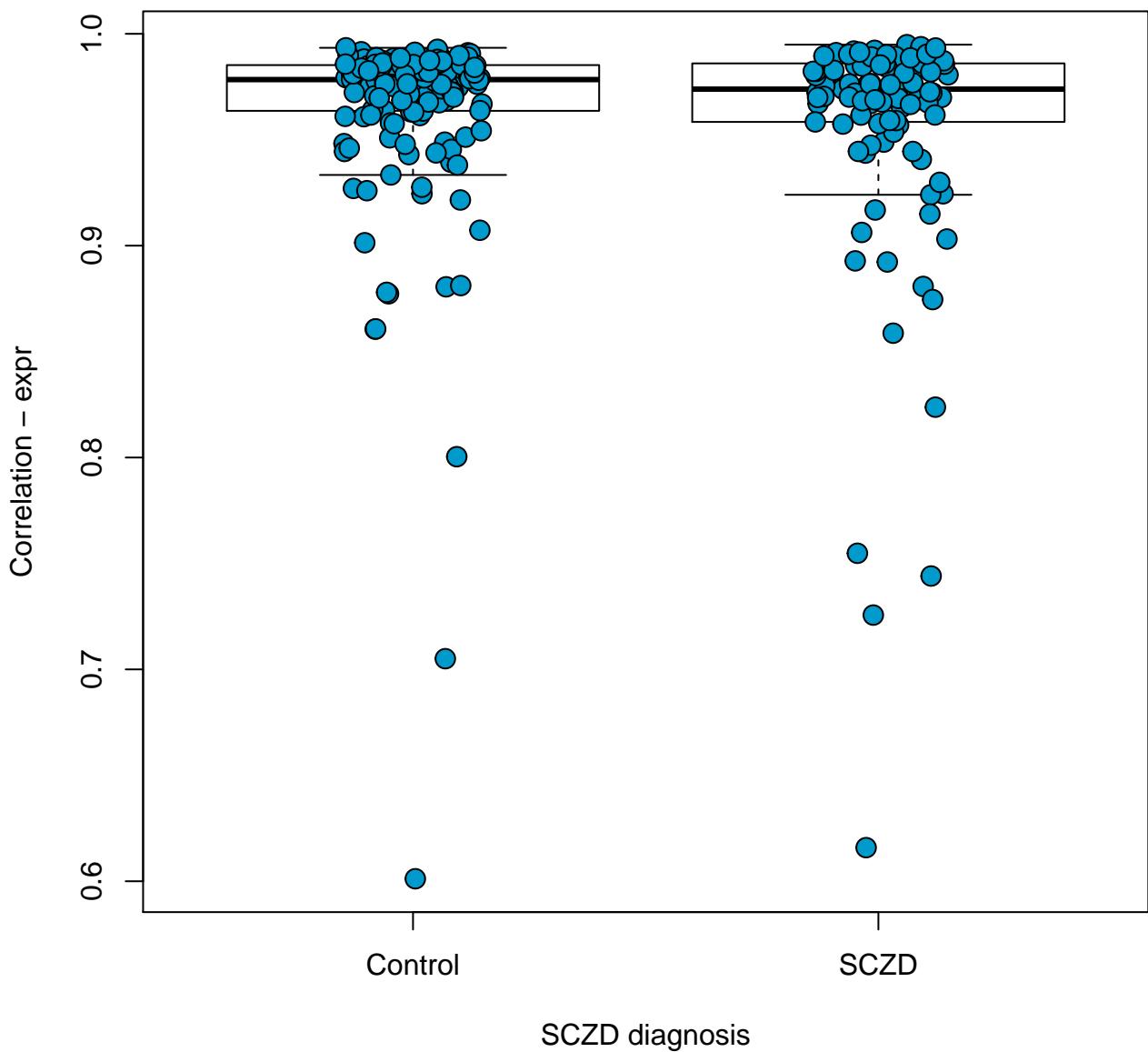
hsa04730: Long-term depression
p-value: 0.656



hsa04740: Olfactory transduction
p-value: 0.992

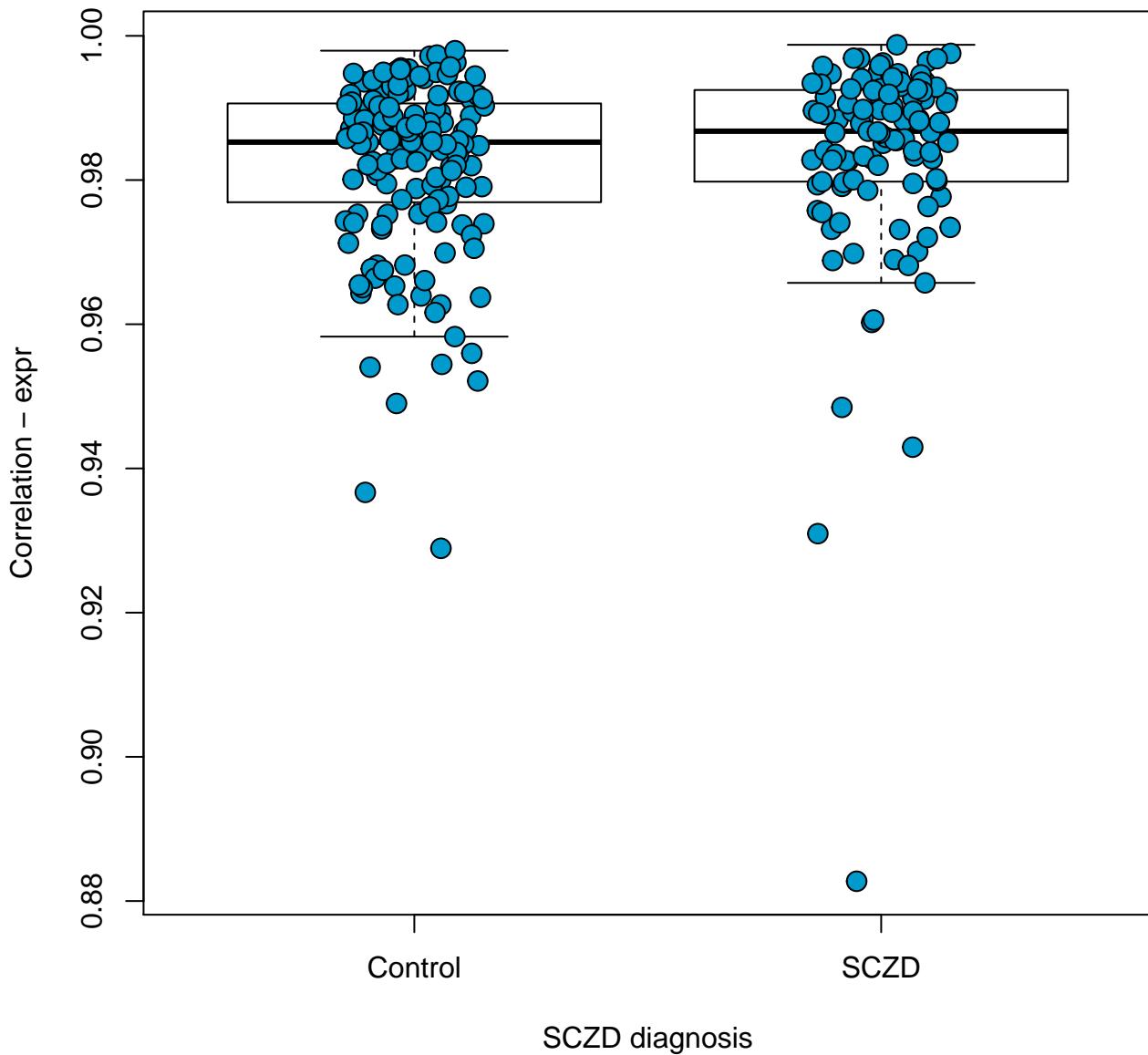


hsa04742: Taste transduction
p-value: 0.256

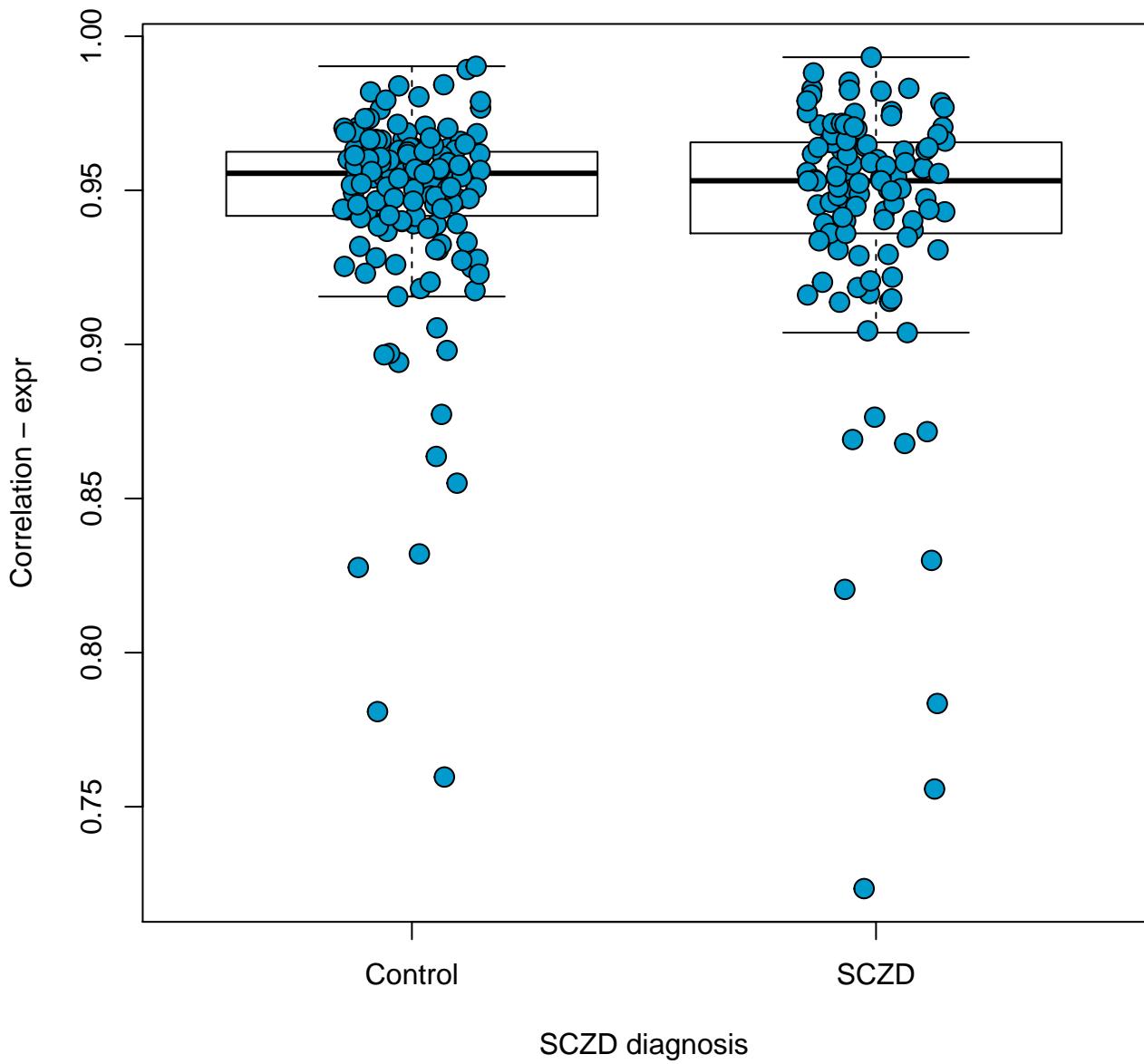


hsa04744: Phototransduction

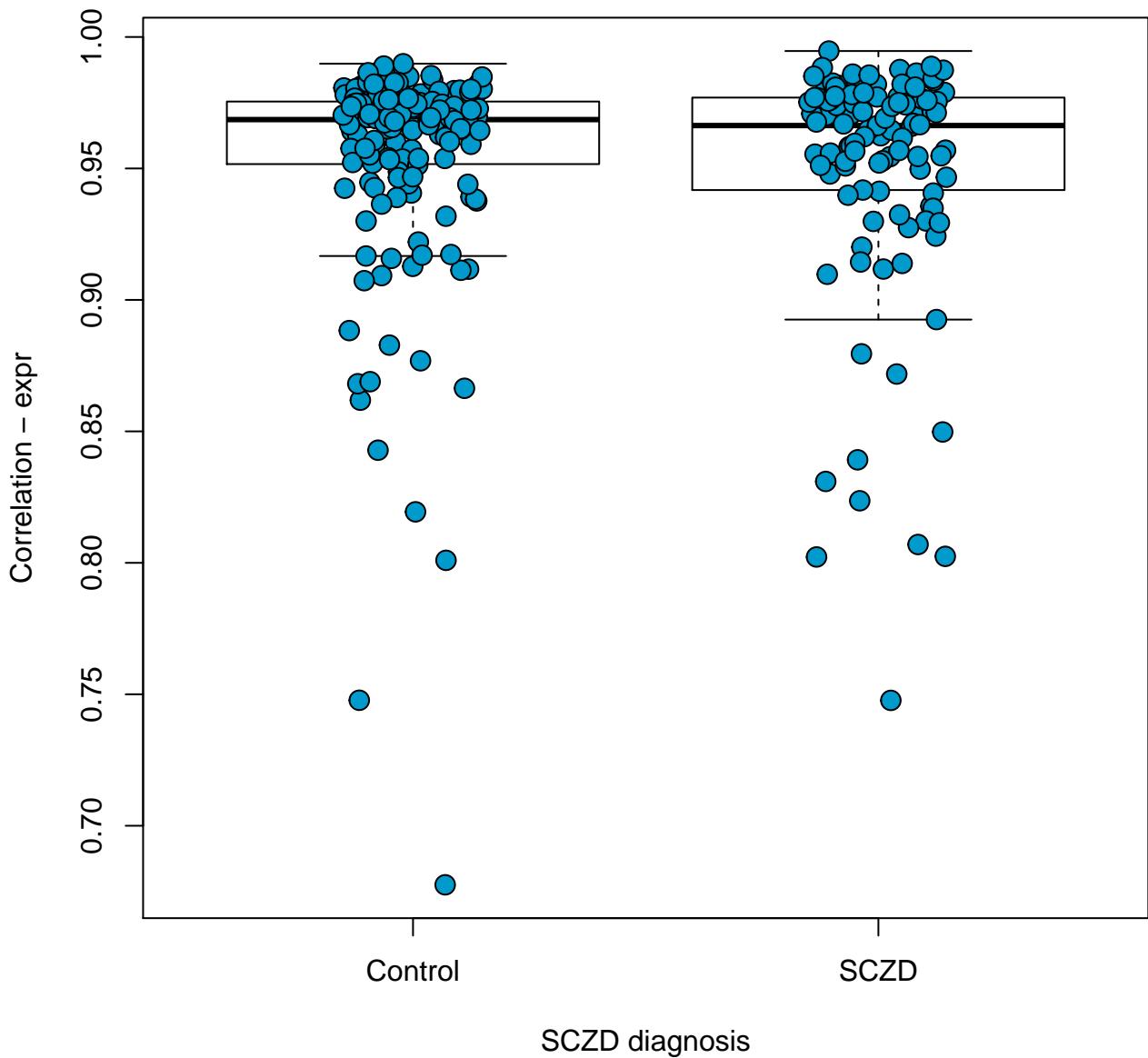
p-value: 0.365



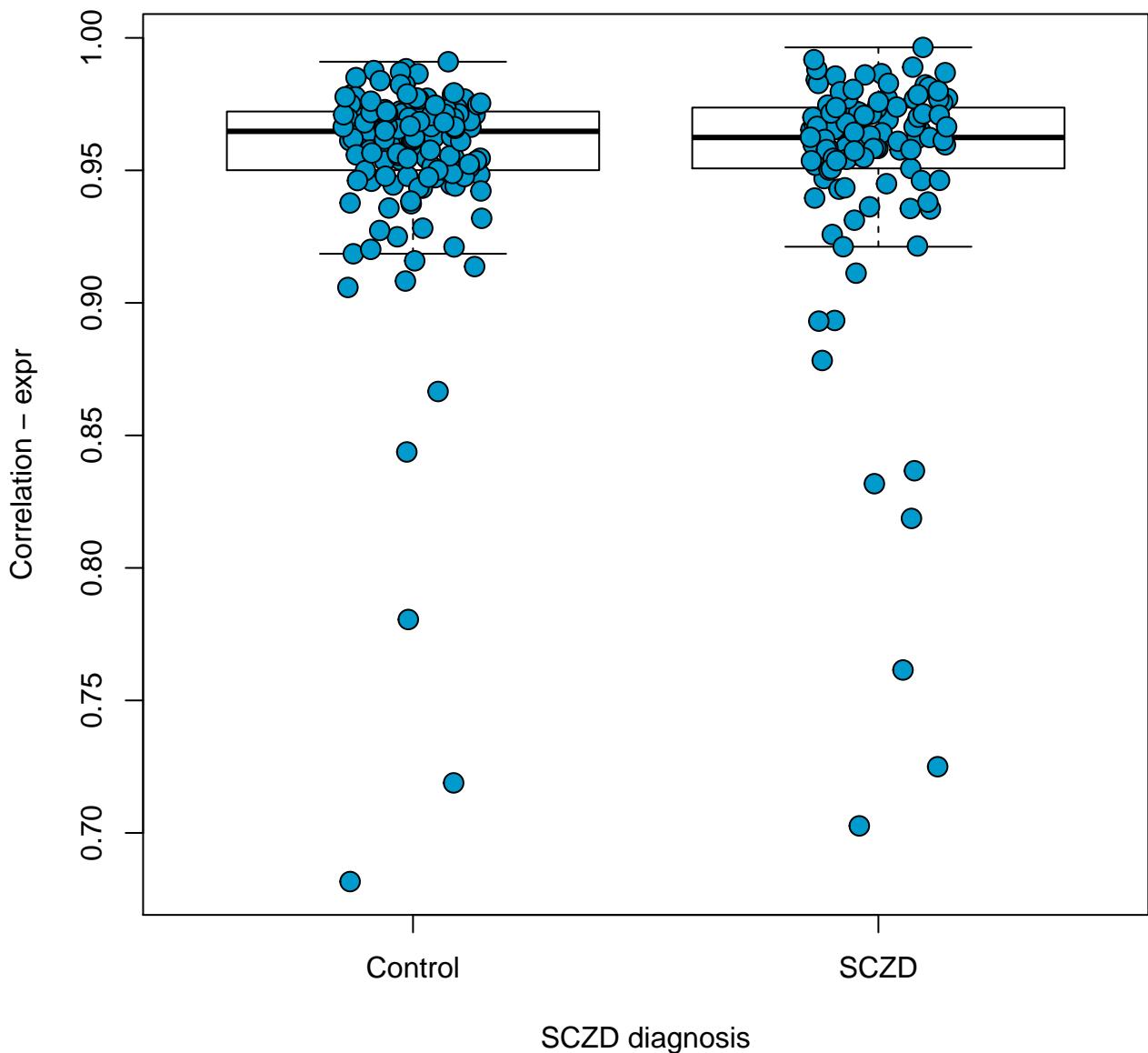
hsa04810: Regulation of actin cytoskeleton
p-value: 0.374



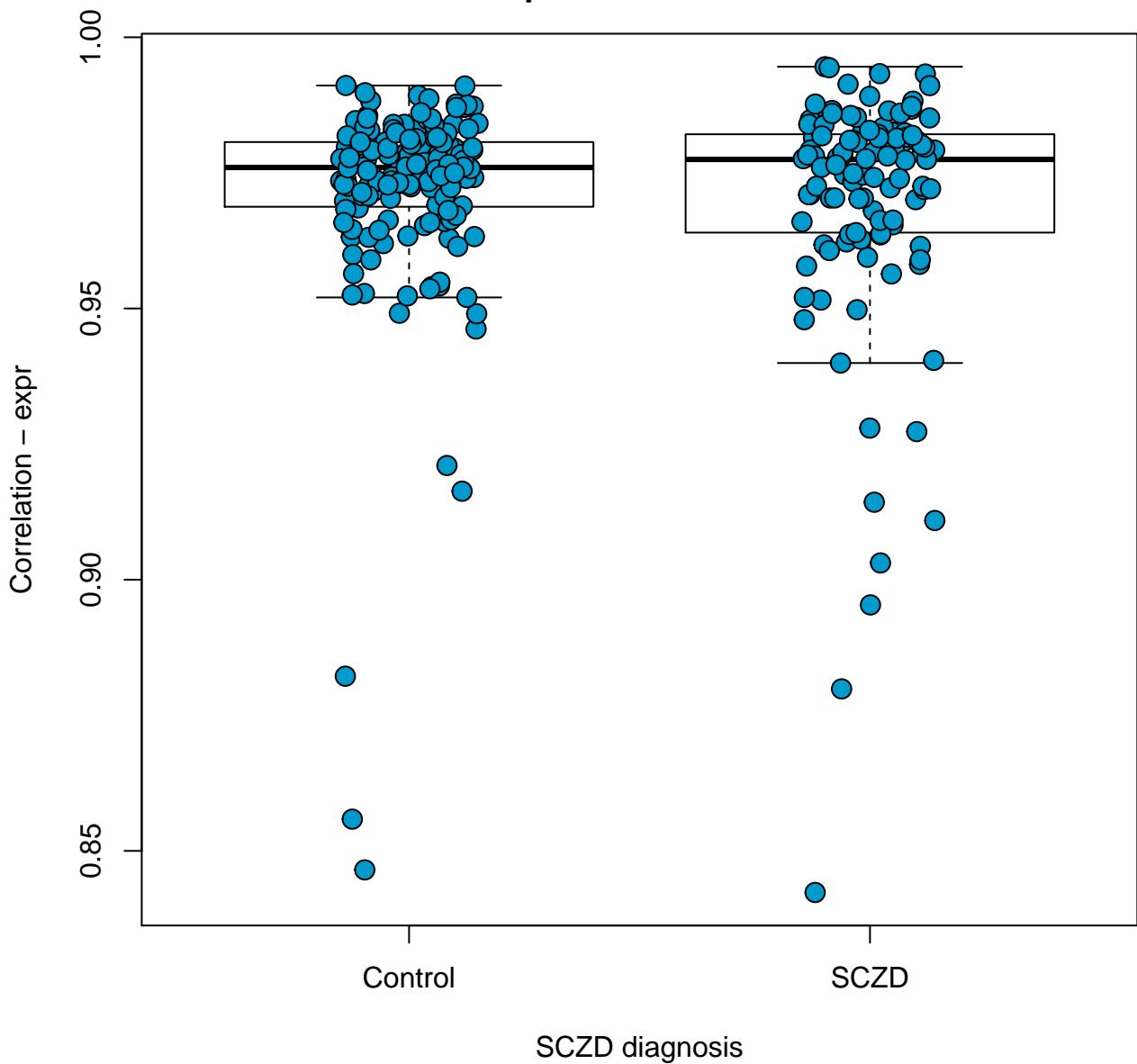
hsa04910: Insulin signaling pathway
p-value: 0.485



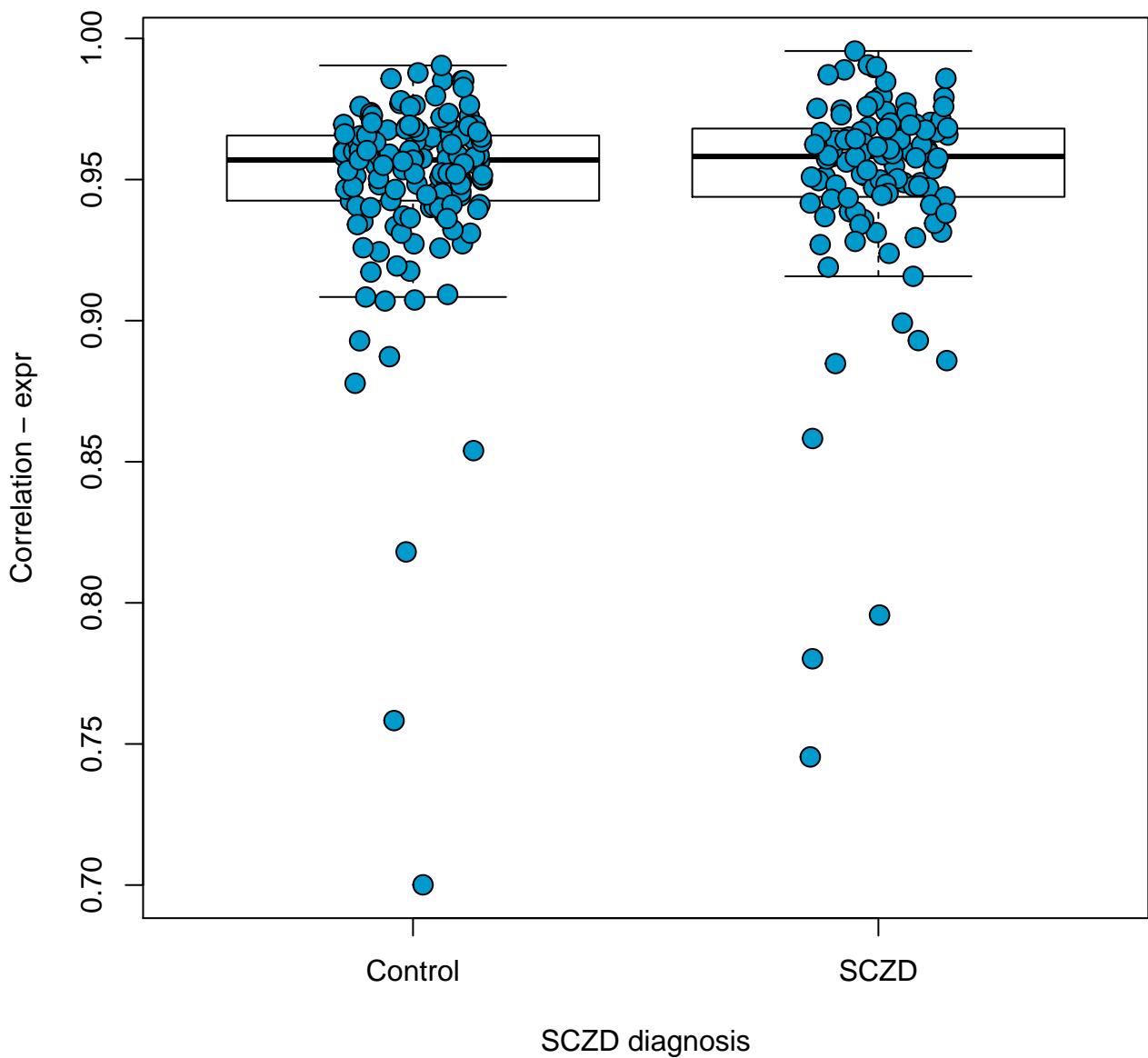
hsa04912: GnRH signaling pathway
p-value: 0.433



hsa04914: Progesterone–mediated oocyte maturation
p-value: 0.429

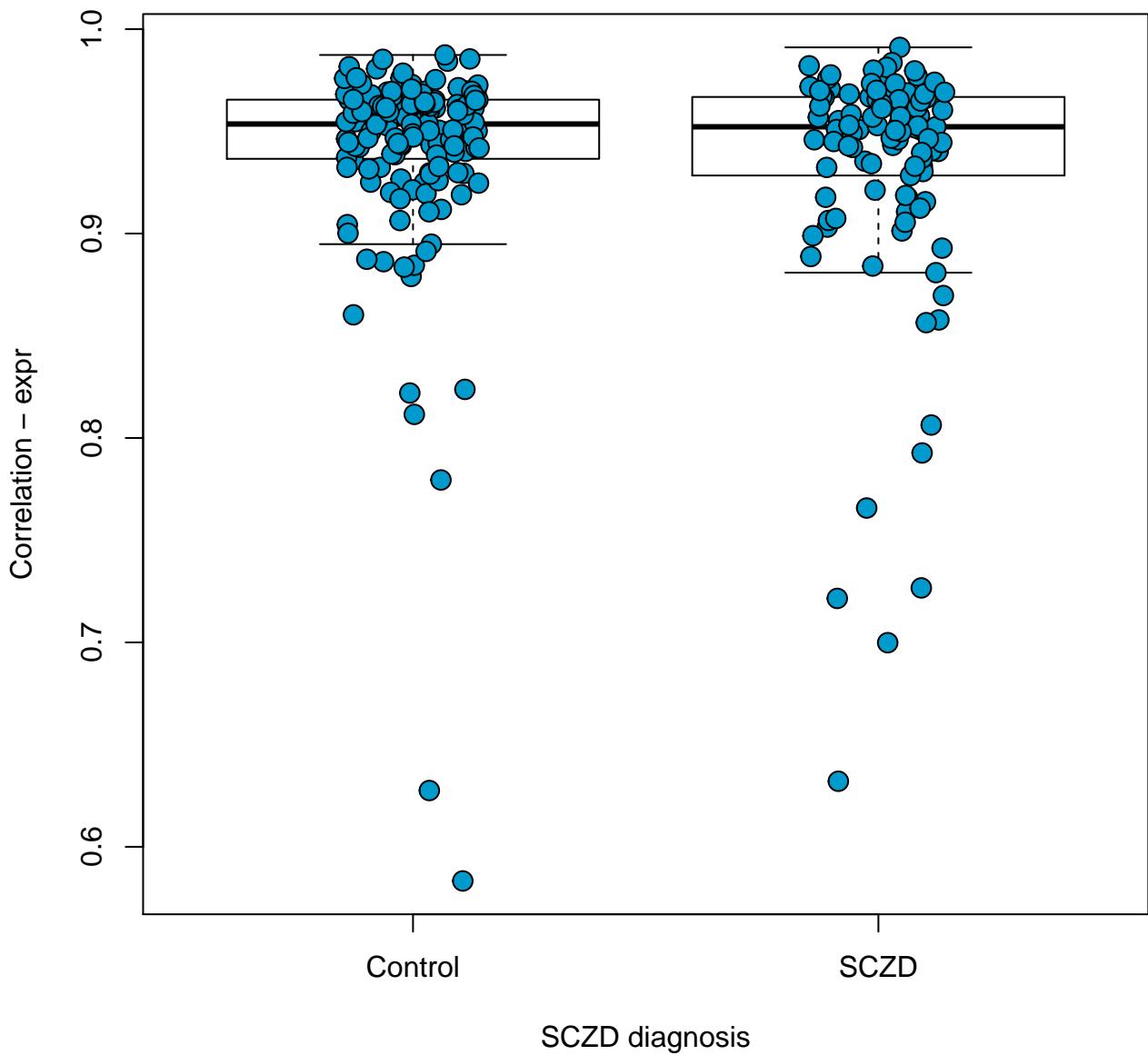


hsa04916: Melanogenesis
p-value: 0.928



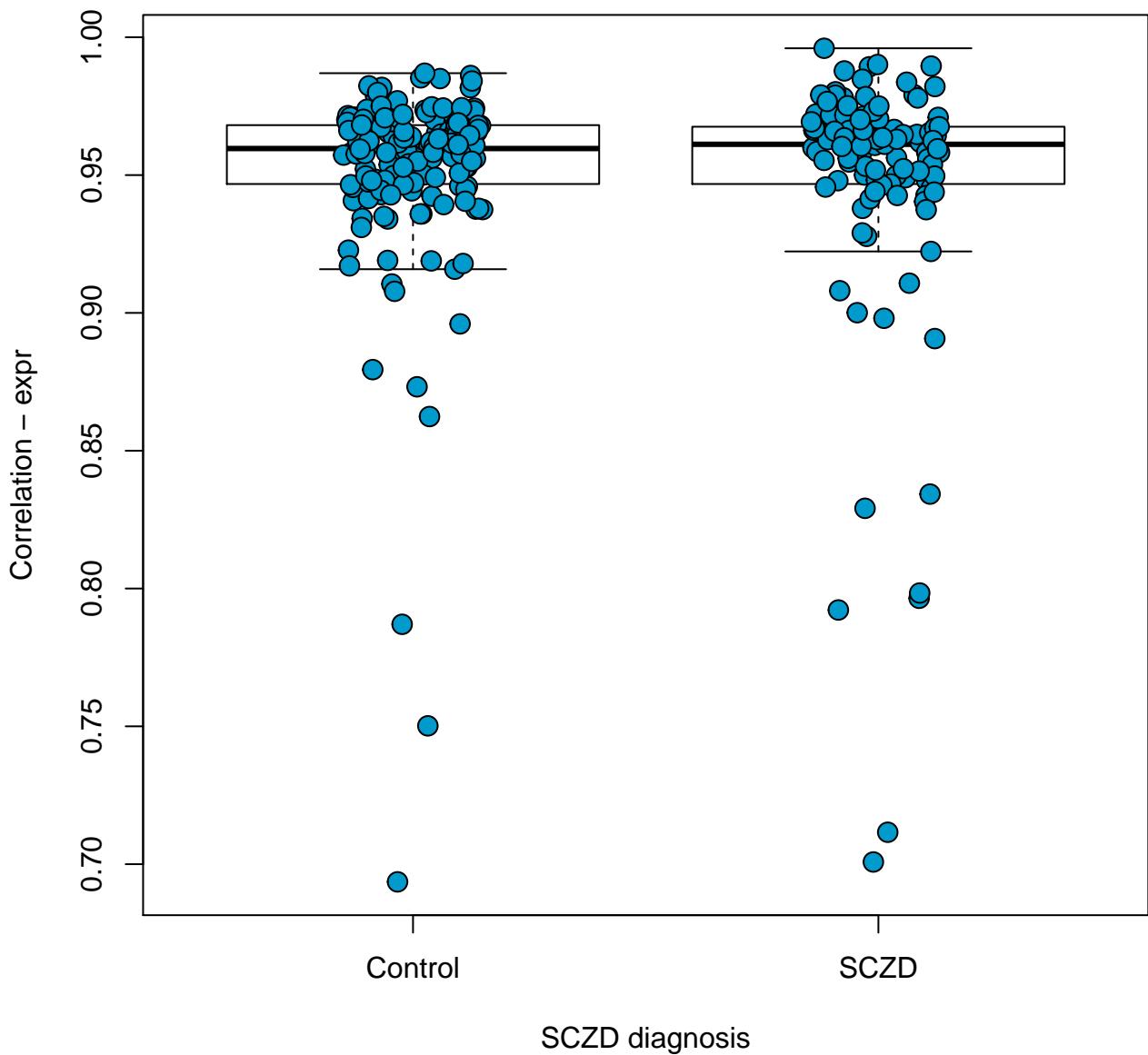
hsa04920: Adipocytokine signaling pathway

p-value: 0.236



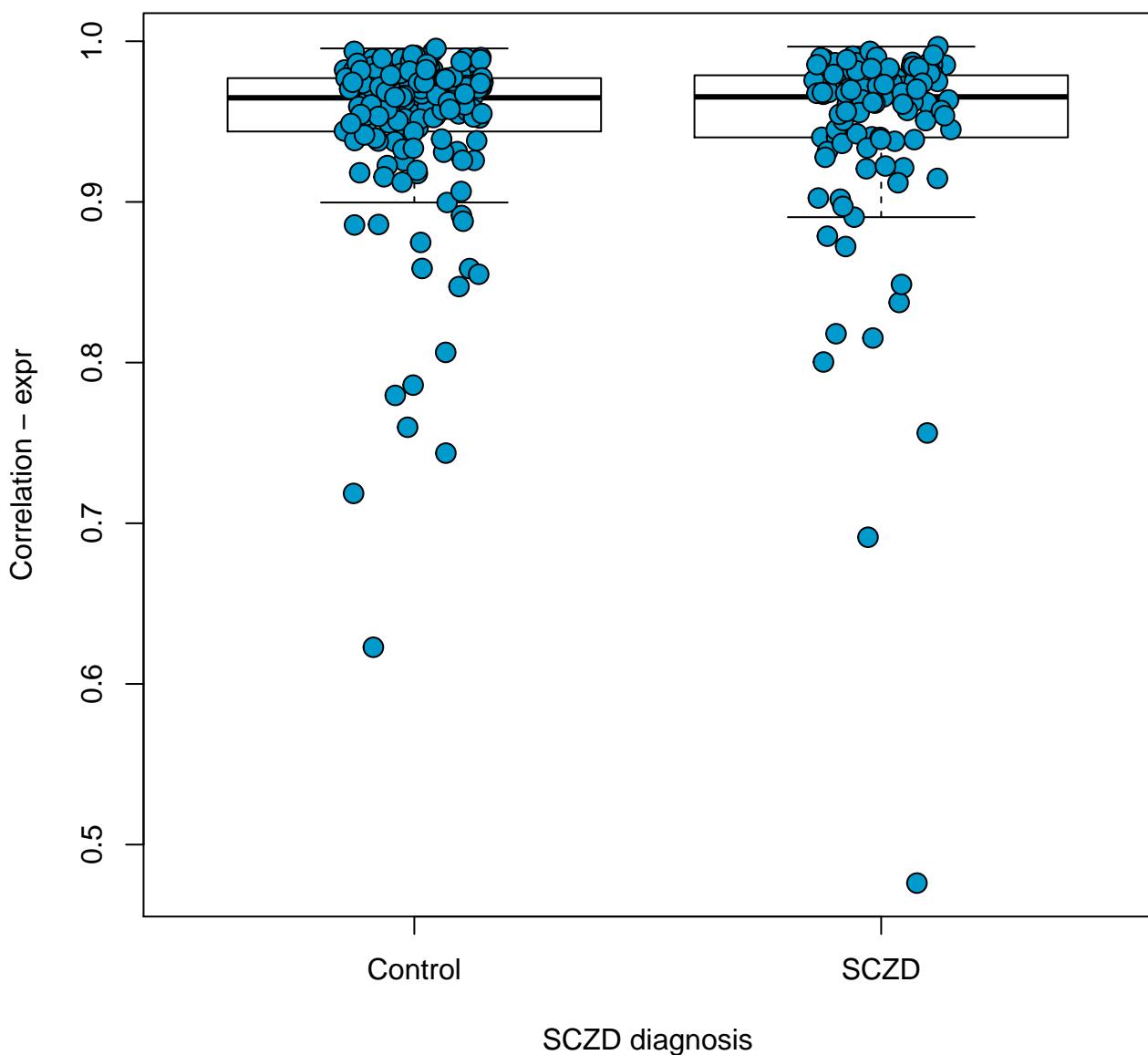
hsa04930: Type II diabetes mellitus

p-value: 0.415

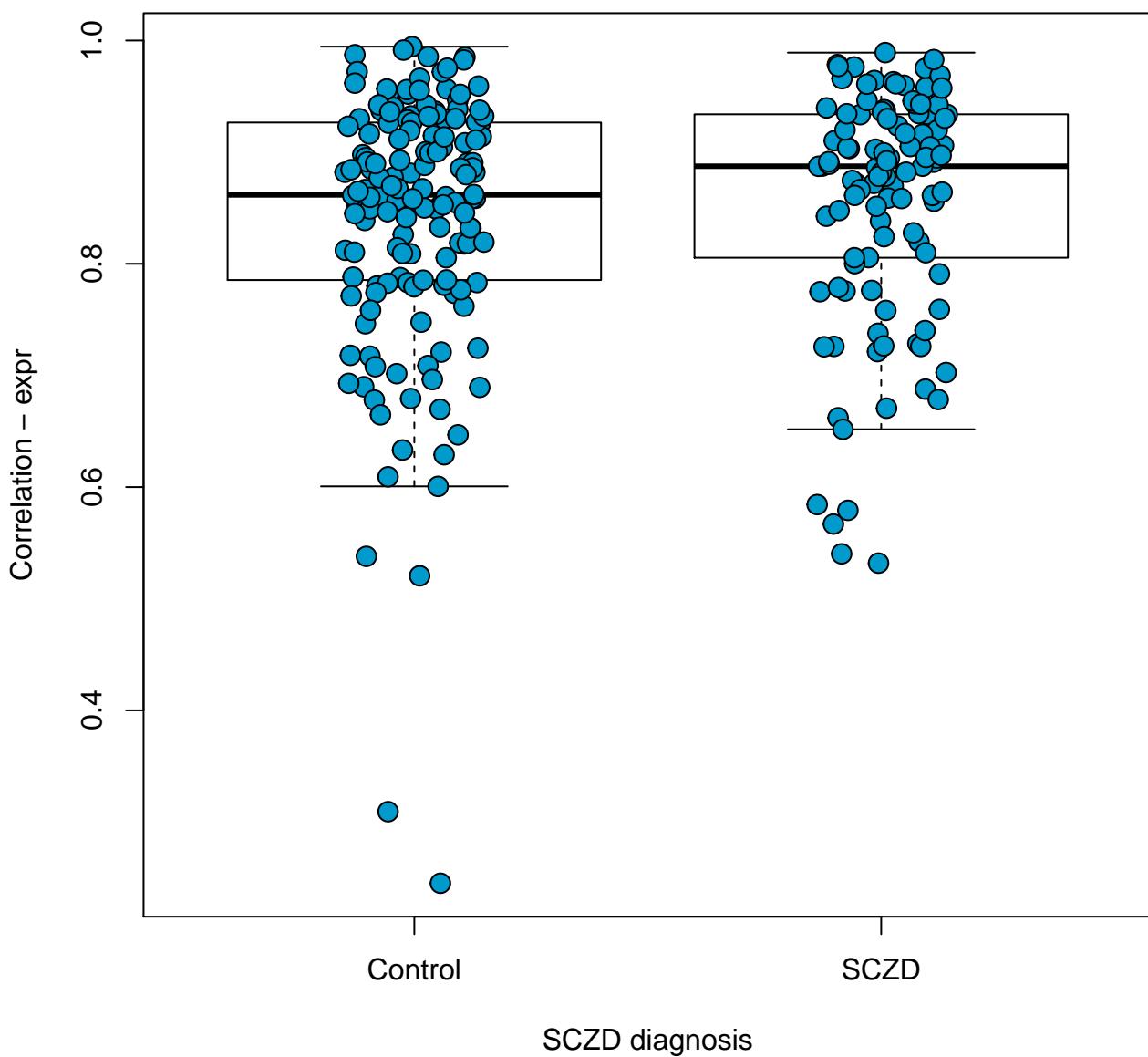


hsa04940: Type I diabetes mellitus

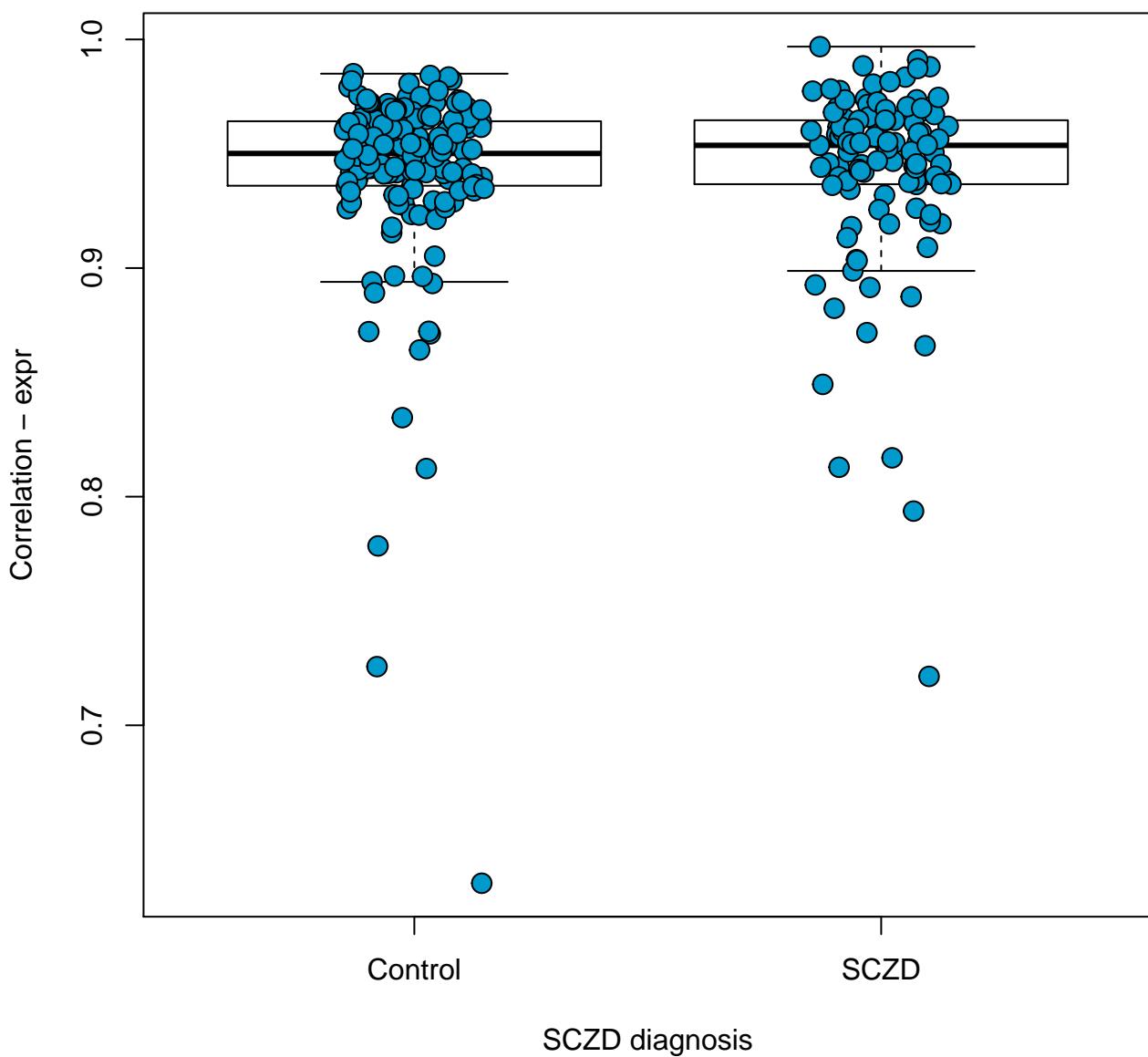
p-value: 0.689



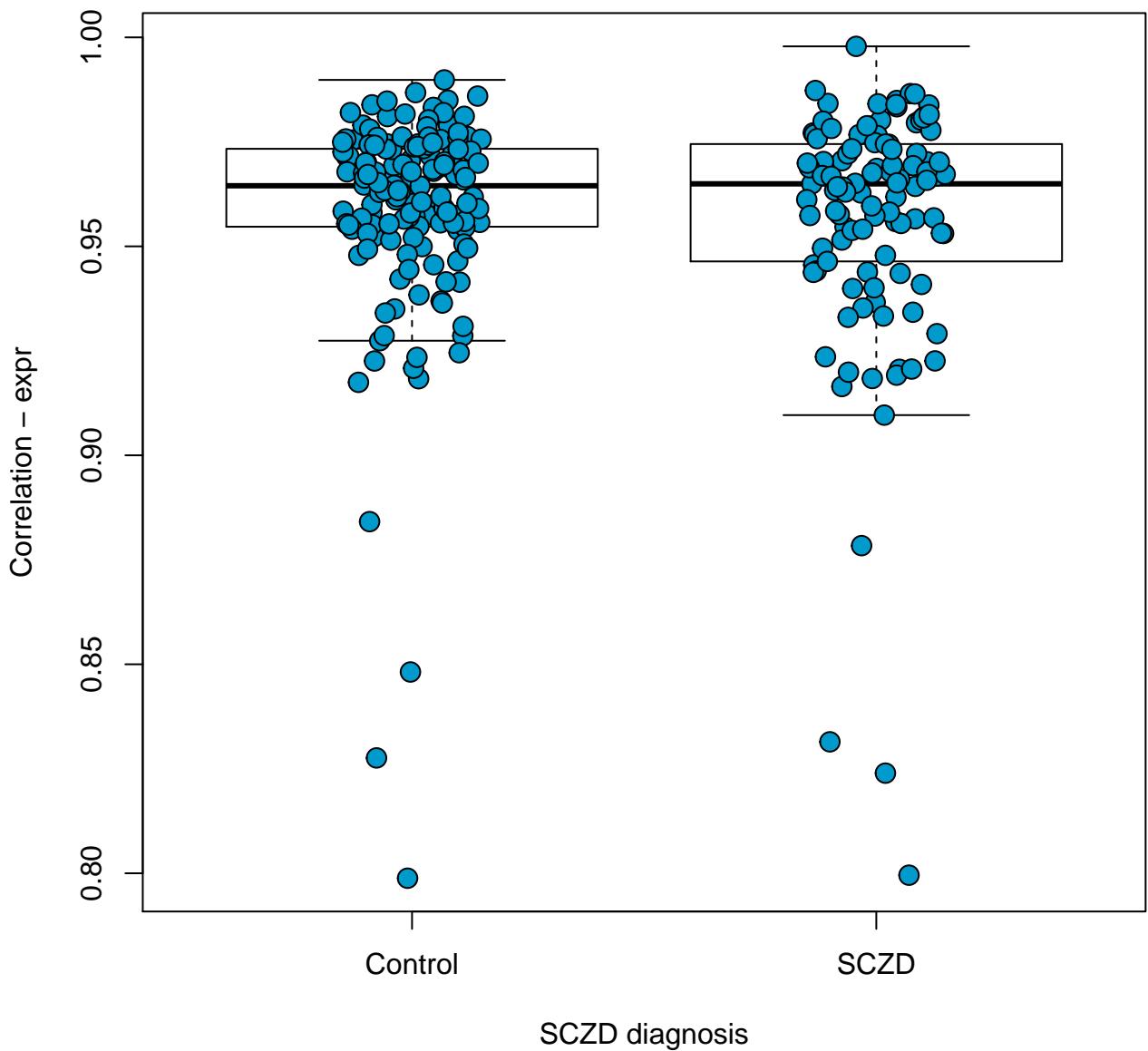
hsa04950: Maturity onset diabetes of the young
p-value: 0.327



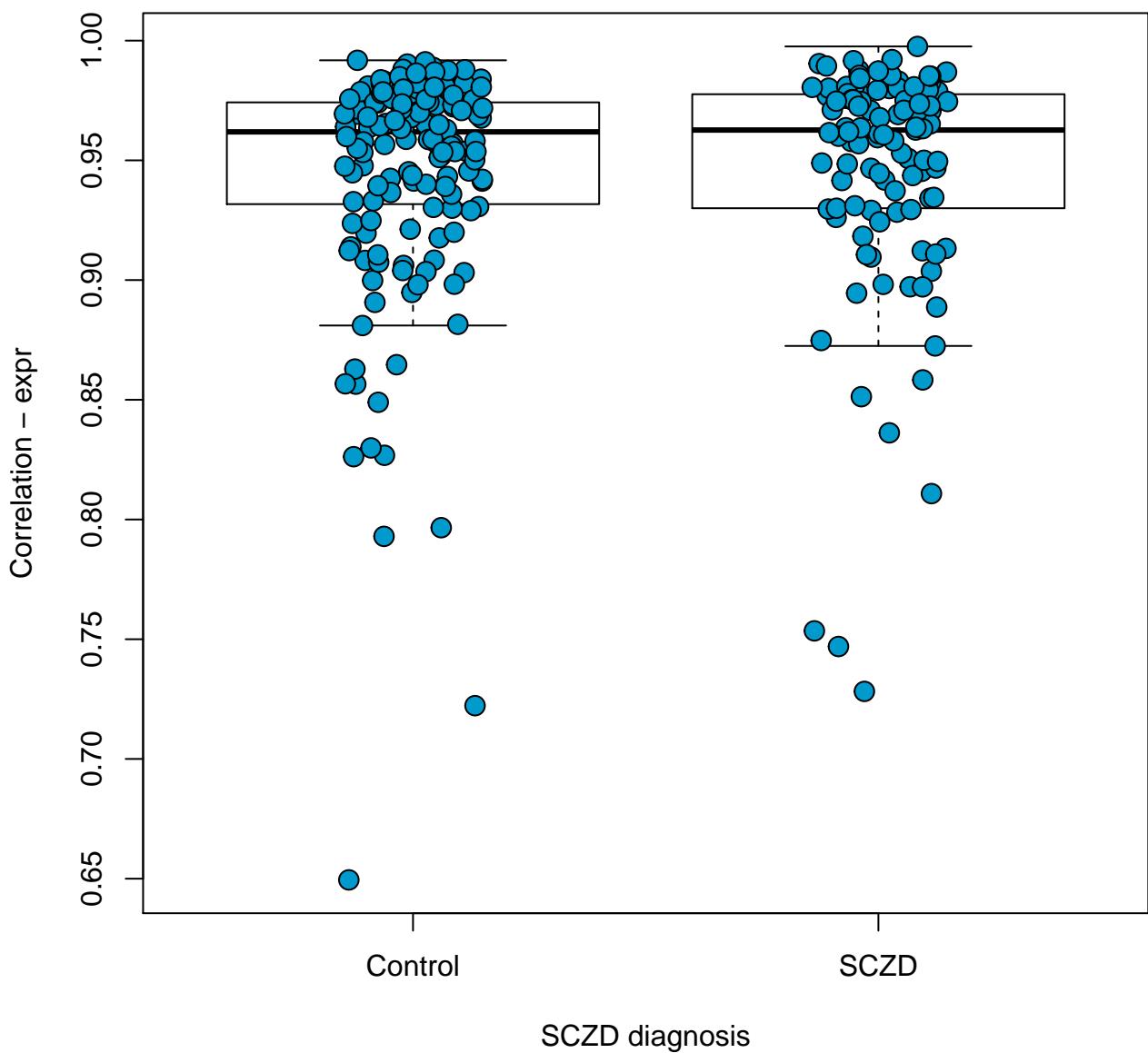
hsa04960: Aldosterone-regulated sodium reabsorption
p-value: 0.959



hsa04962: Vasopressin-regulated water reabsorption
p-value: 0.4

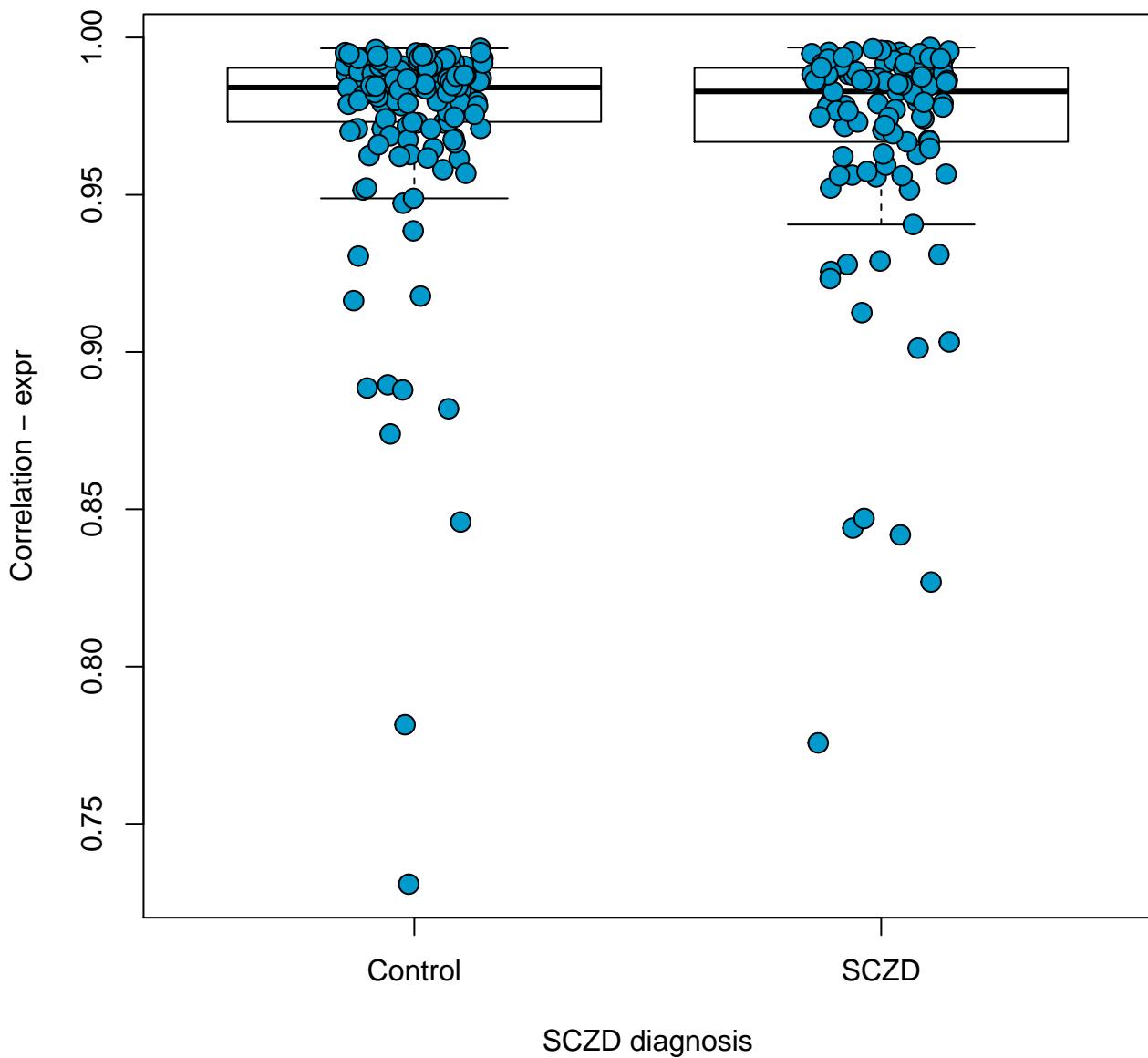


hsa04964: Proximal tubule bicarbonate reclamation
p-value: 0.829

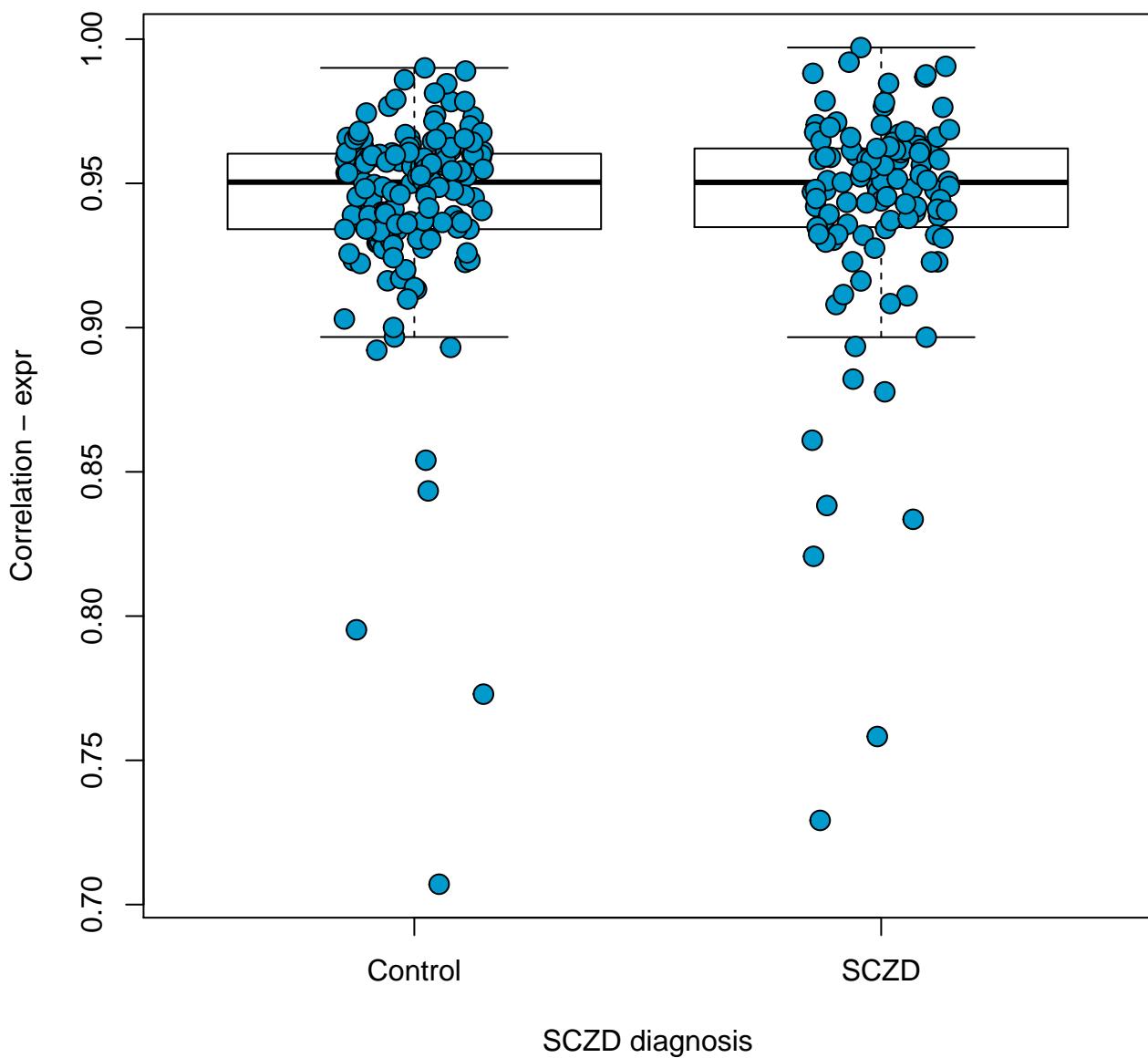


hsa04966: Collecting duct acid secretion

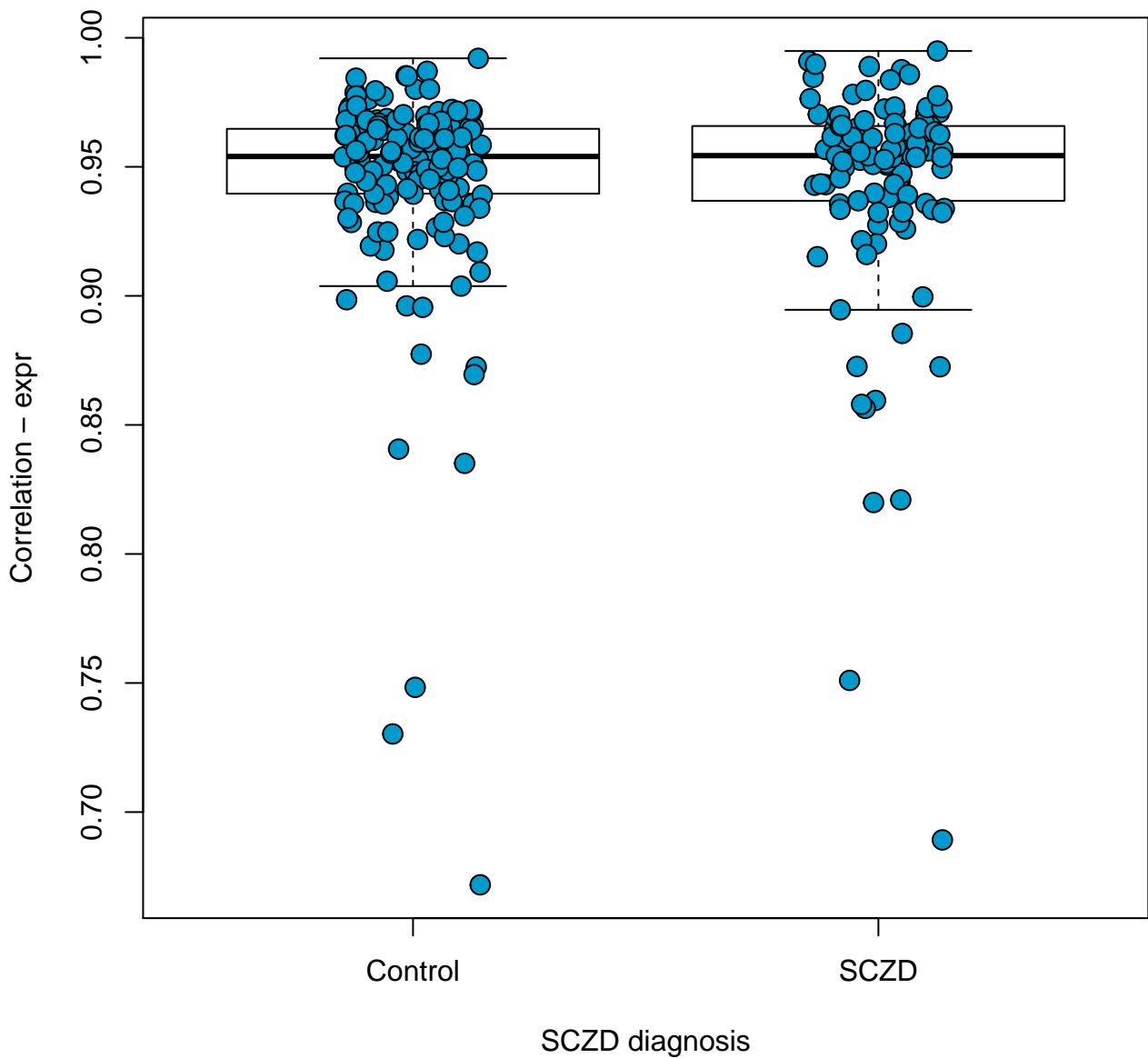
p-value: 0.314



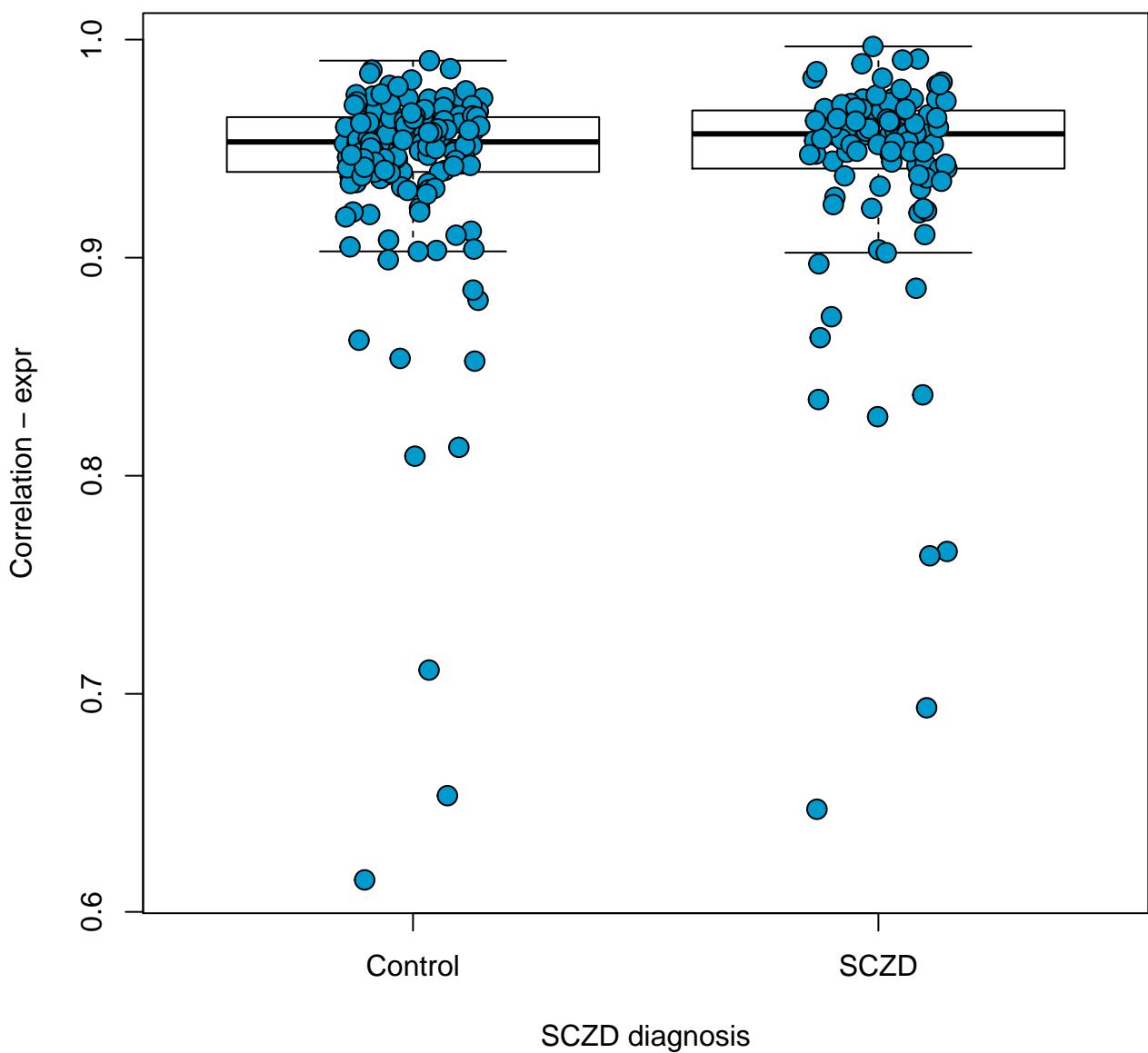
hsa04970: Salivary secretion
p-value: 0.765



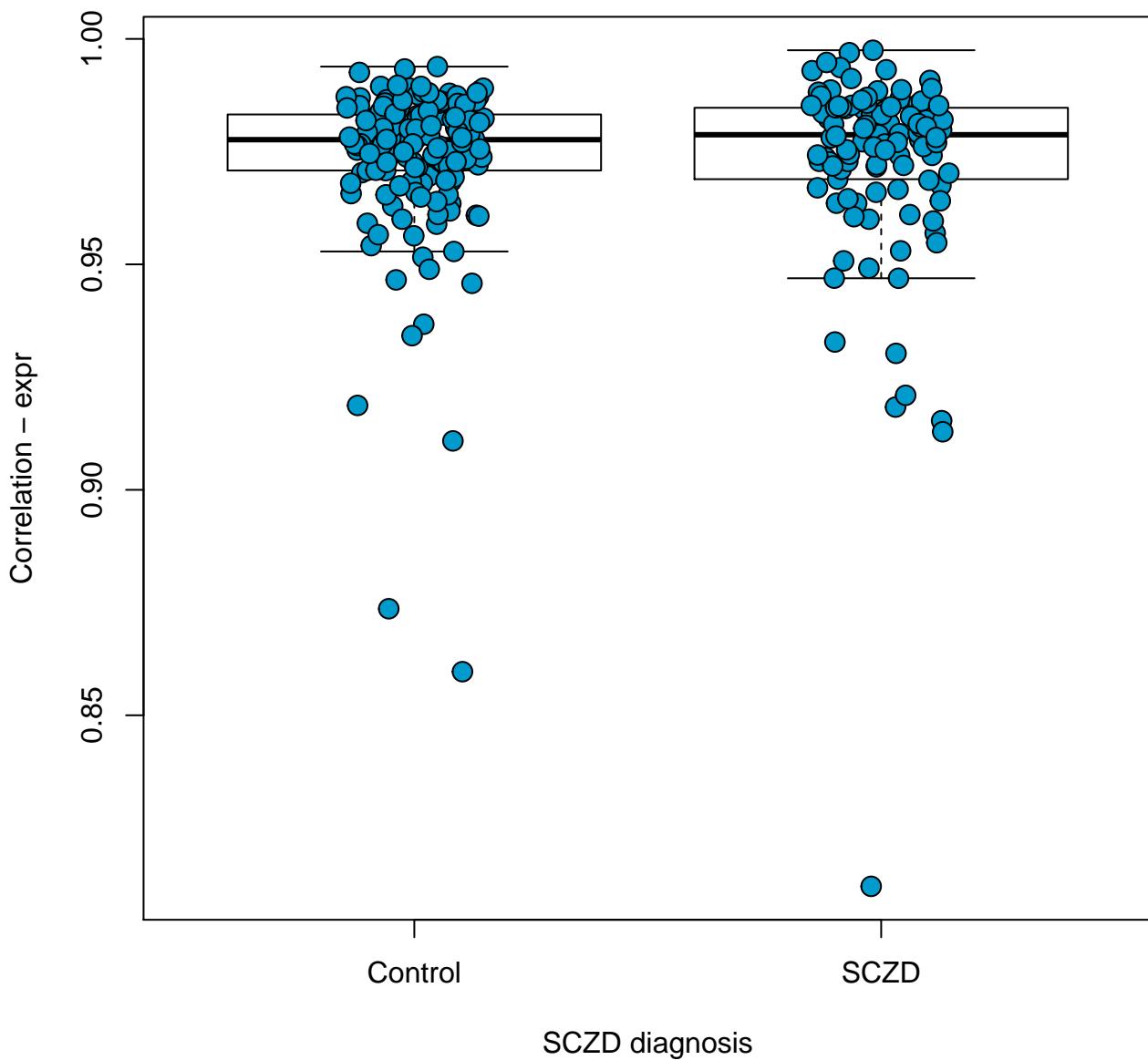
hsa04971: Gastric acid secretion
p-value: 0.752



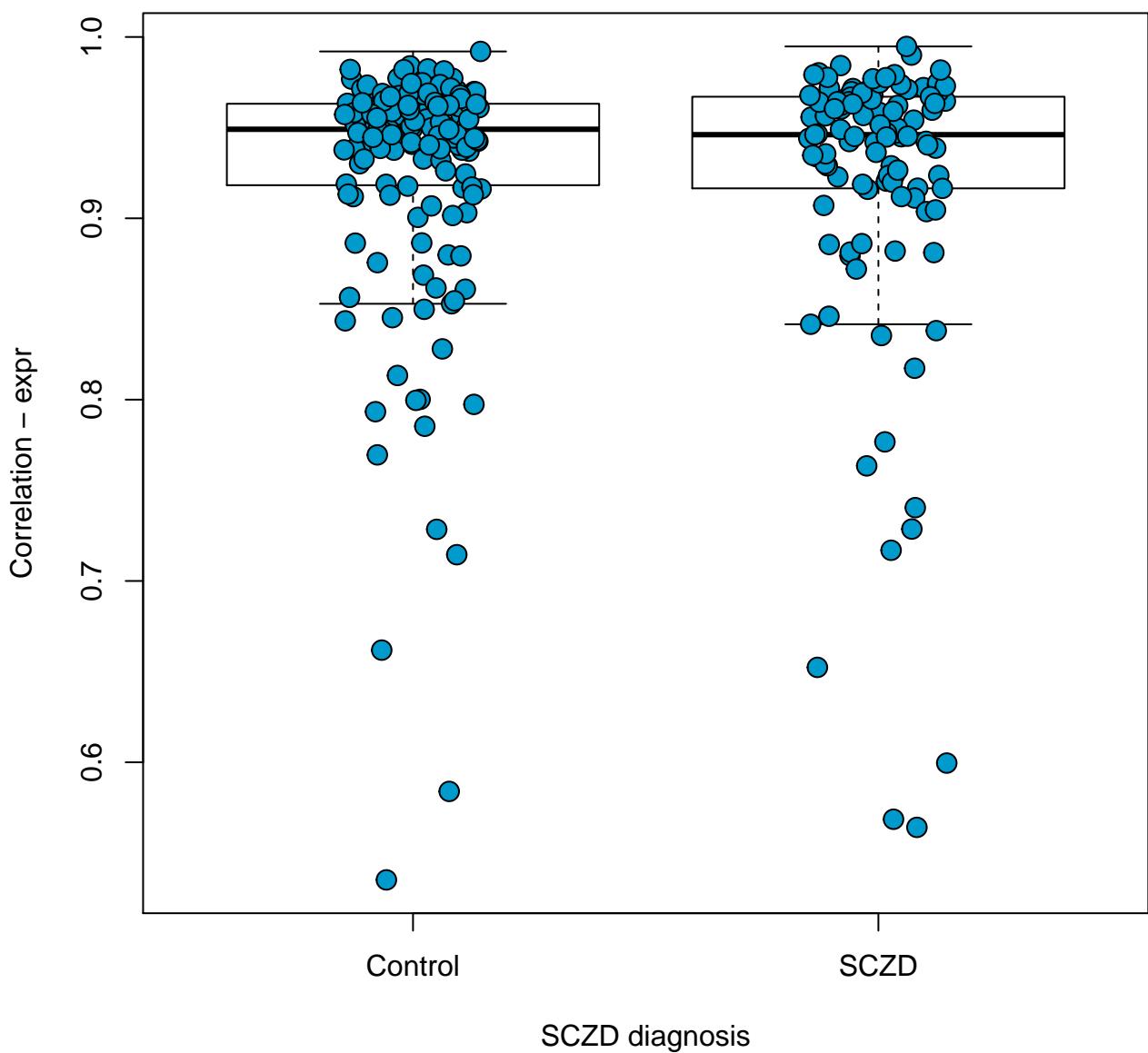
hsa04972: Pancreatic secretion
p-value: 0.913



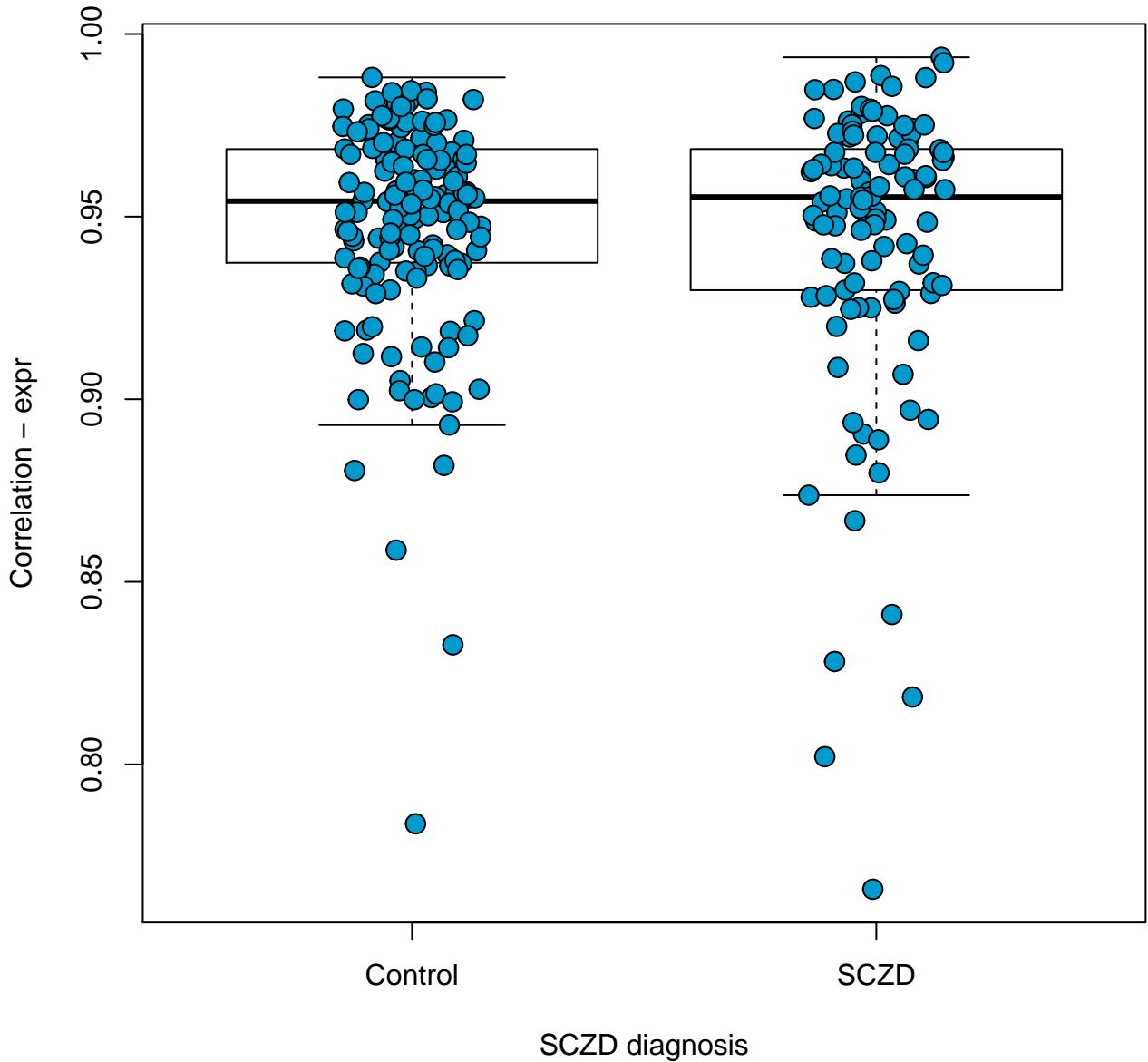
hsa04973: Carbohydrate digestion and absorption
p-value: 0.679



hsa04974: Protein digestion and absorption
p-value: 0.486

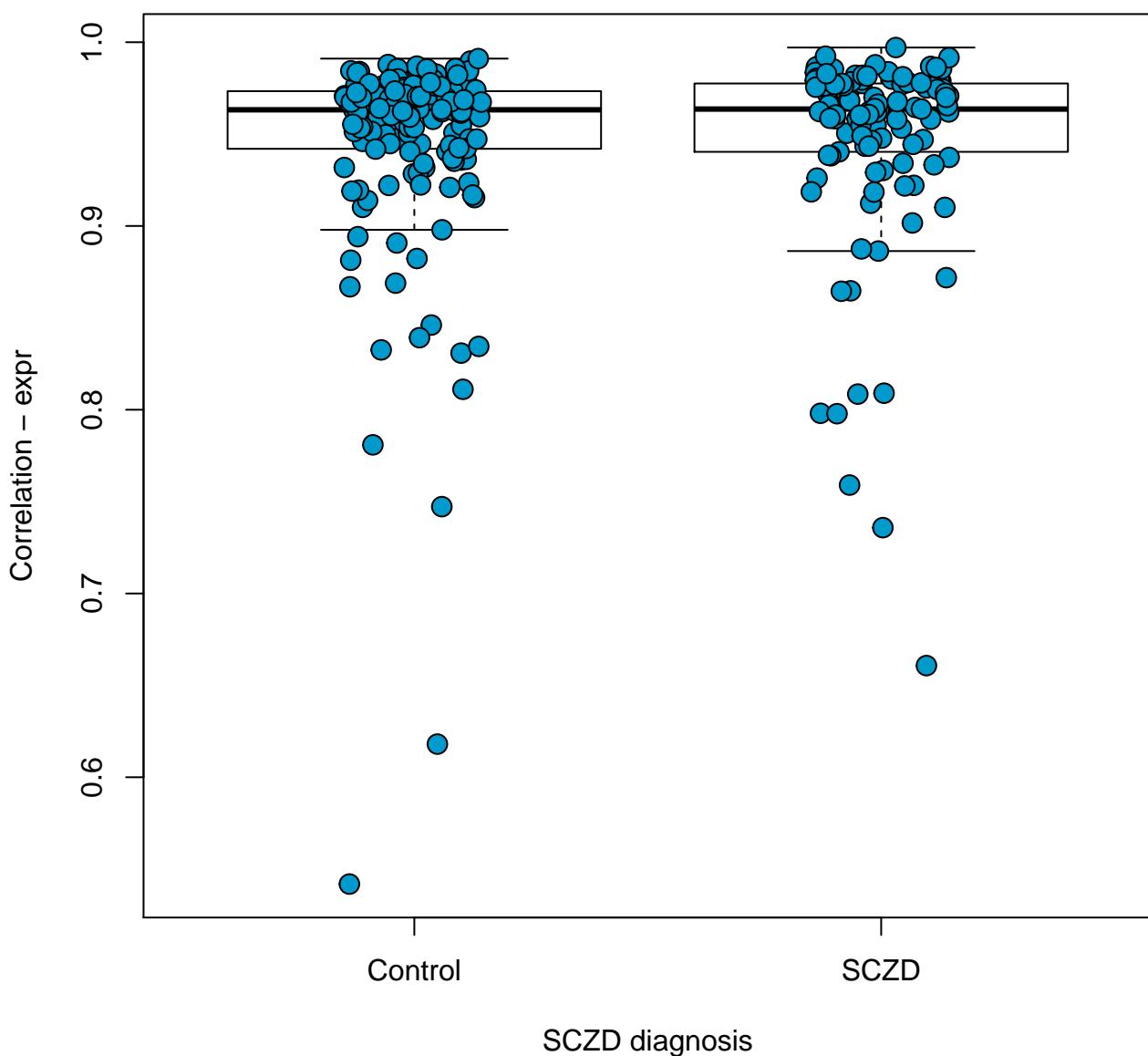


hsa04975: Fat digestion and absorption
p-value: 0.334

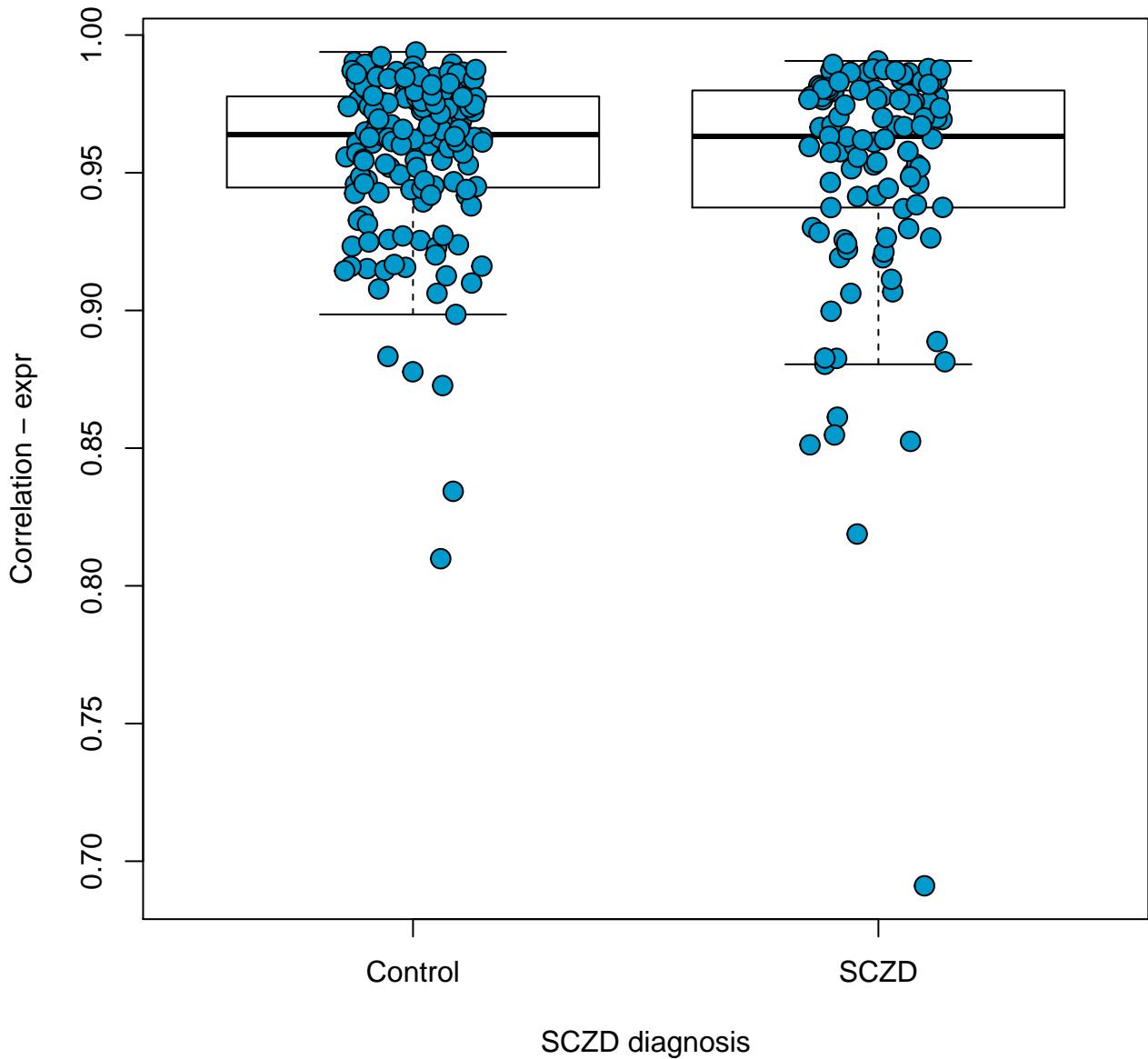


hsa04976: Bile secretion

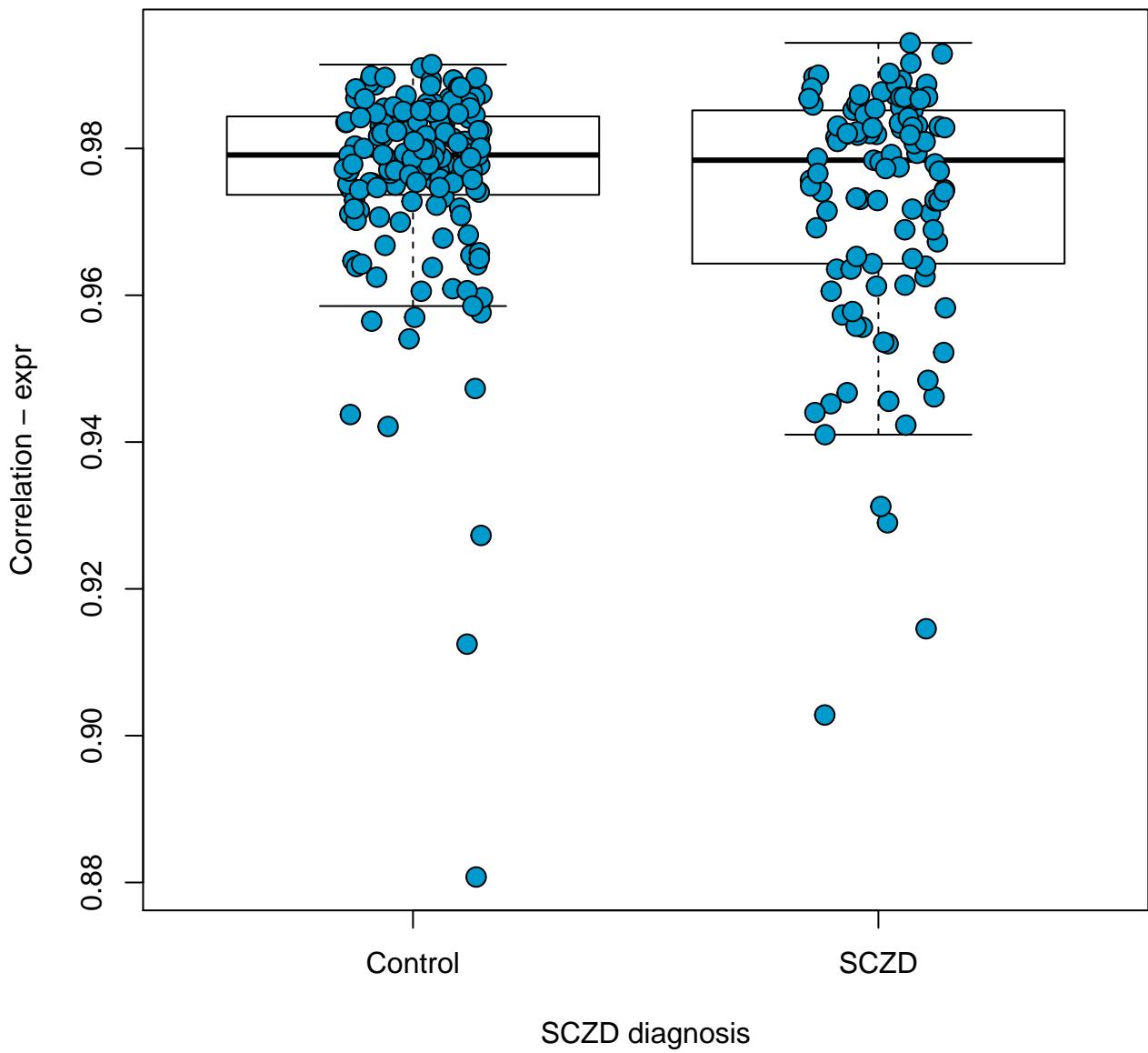
p-value: 0.896



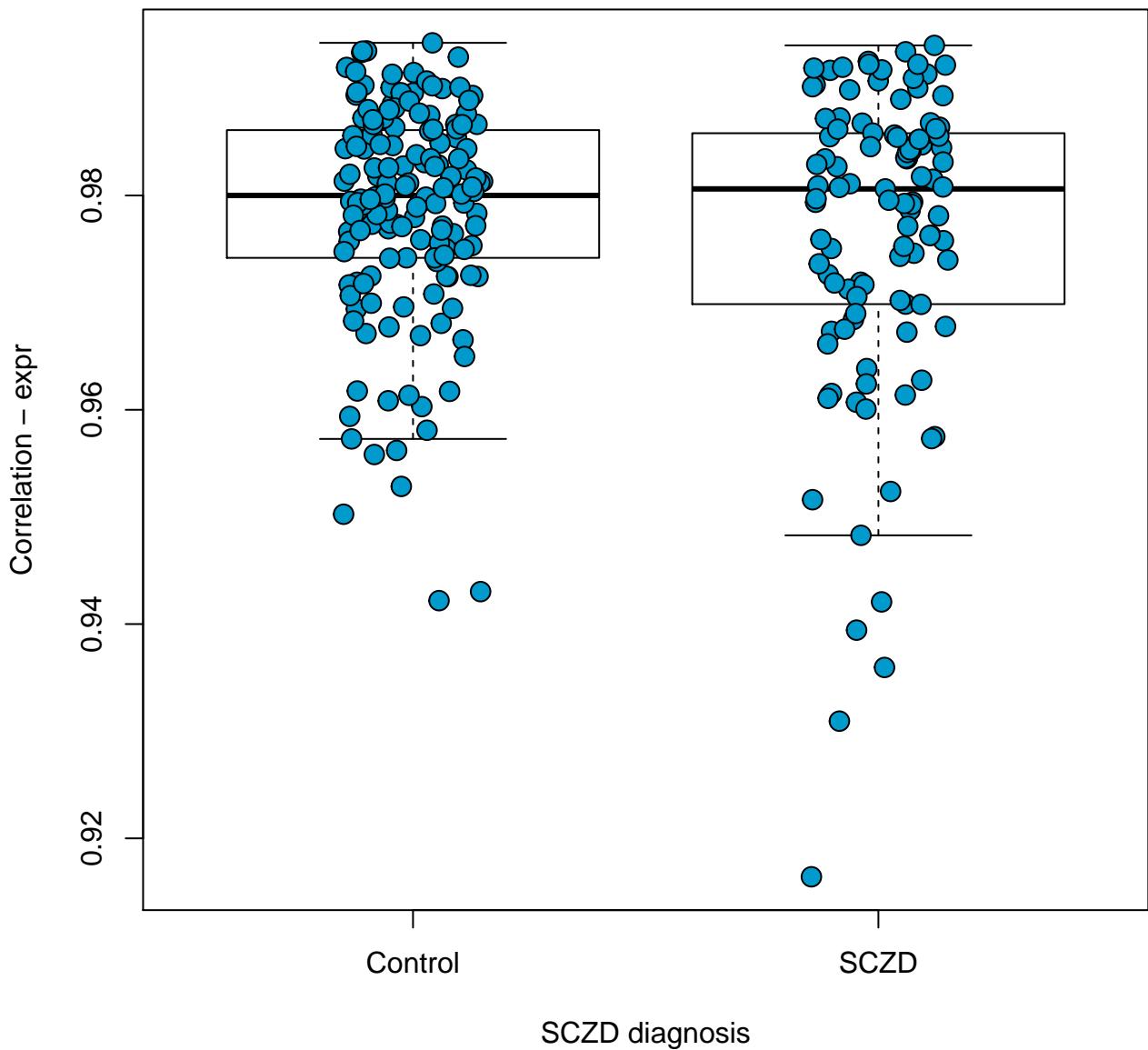
hsa04977: Vitamin digestion and absorption
p-value: 0.145



hsa05010: Alzheimer's disease
p-value: 0.0834

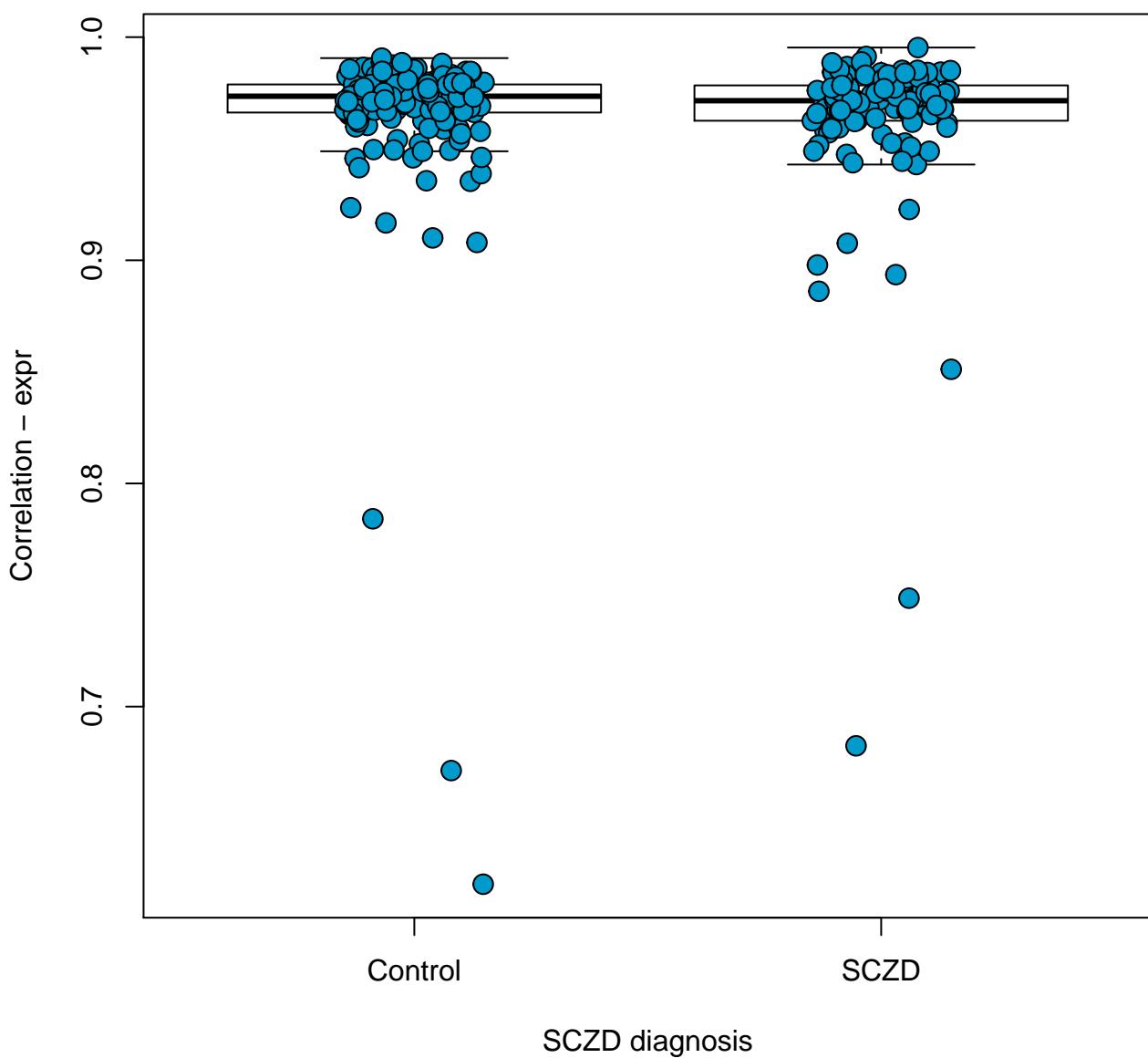


hsa05012: Parkinson's disease
p-value: 0.132

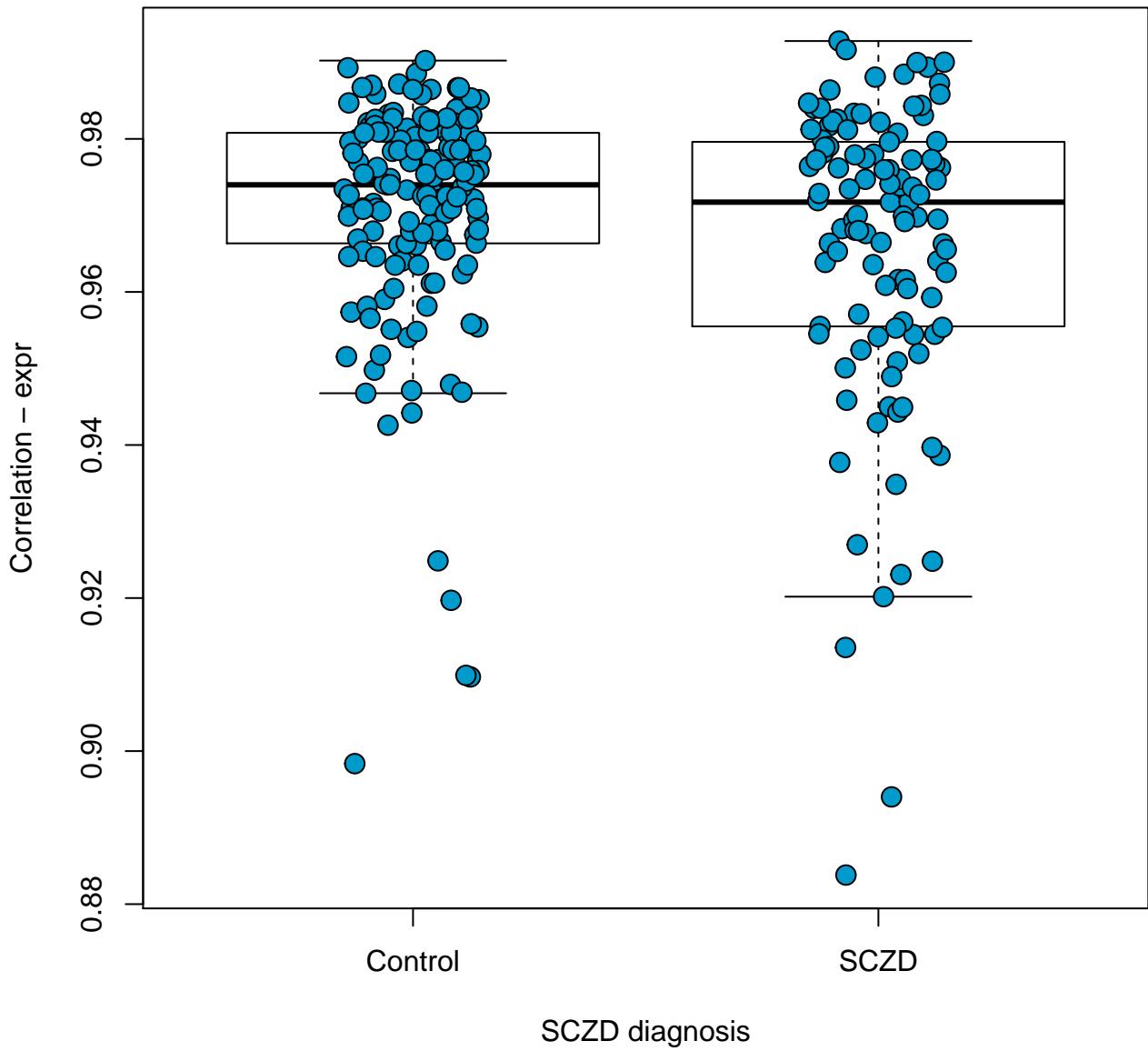


hsa05014: Amyotrophic lateral sclerosis (ALS)

p-value: 0.639

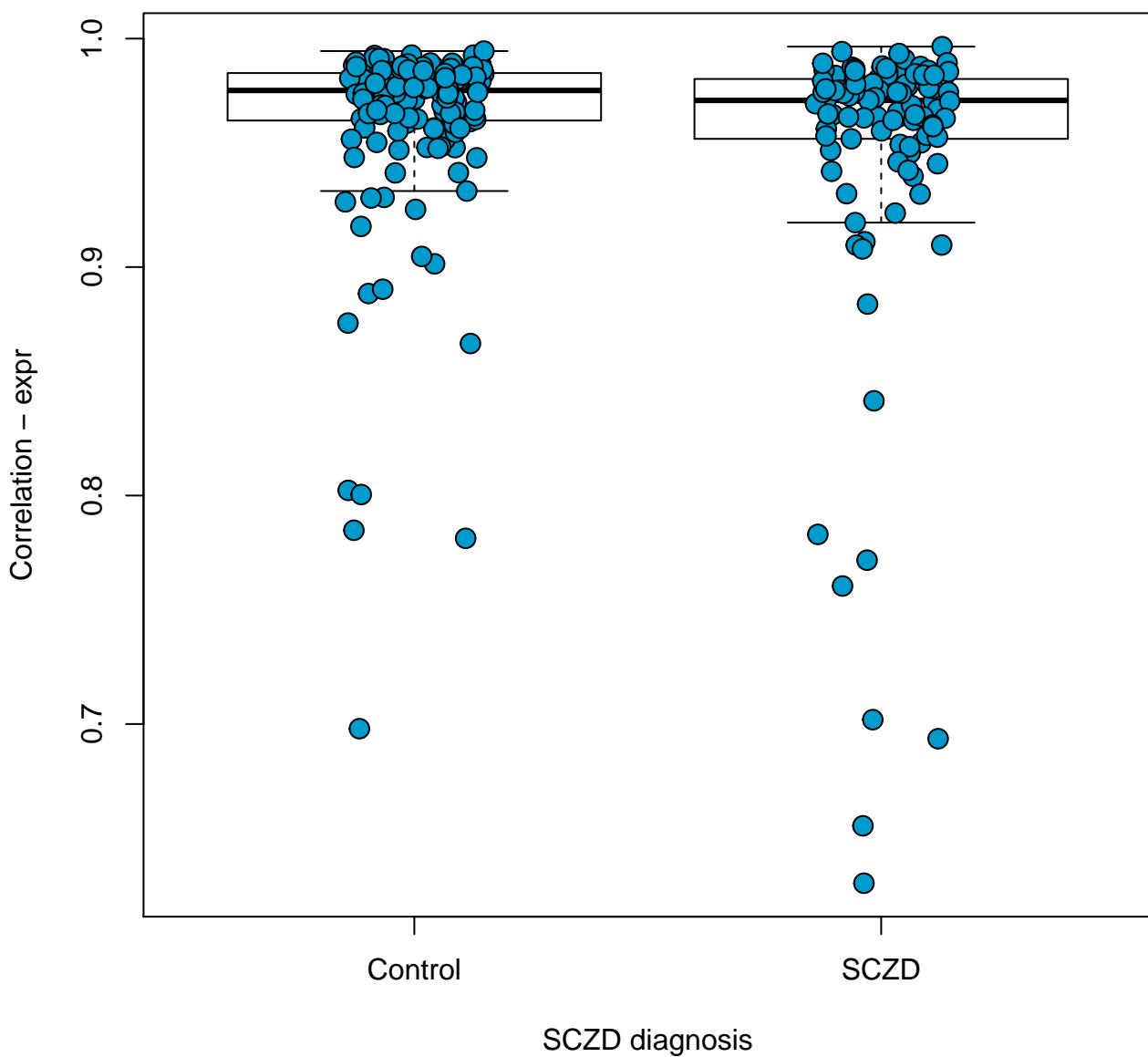


hsa05016: Huntington's disease
p-value: 0.0241

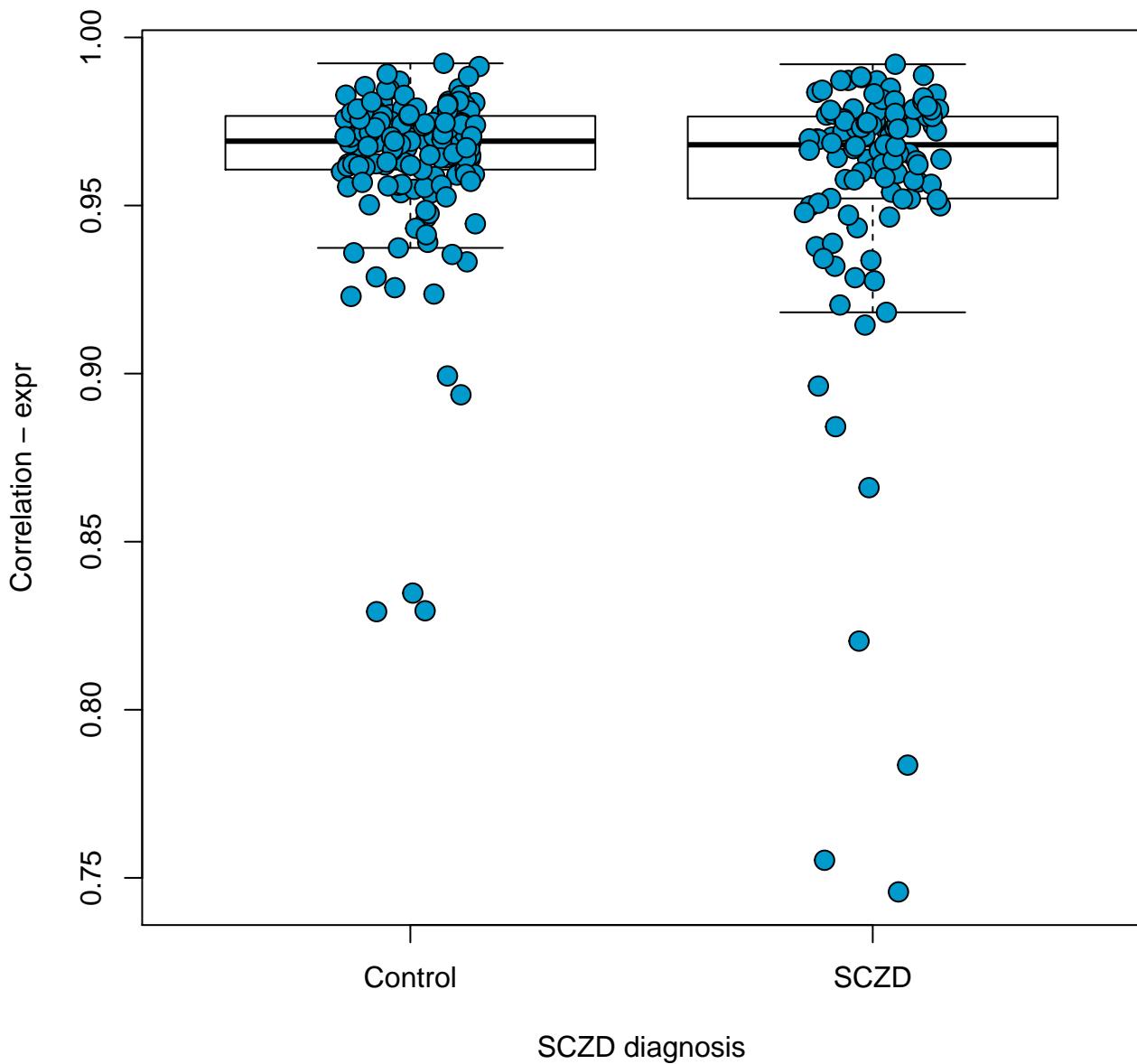


hsa05020: Prion diseases

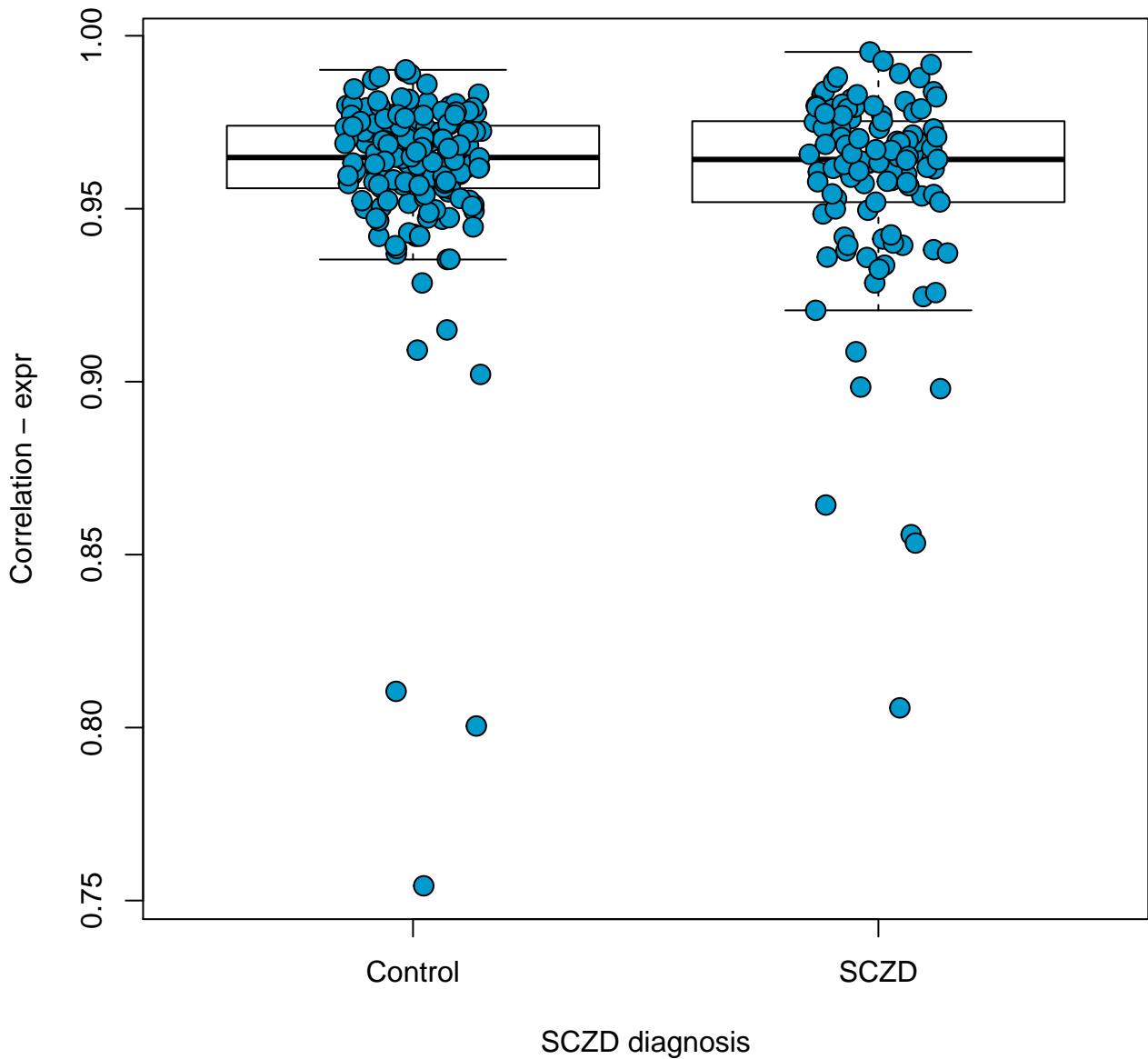
p-value: 0.0419



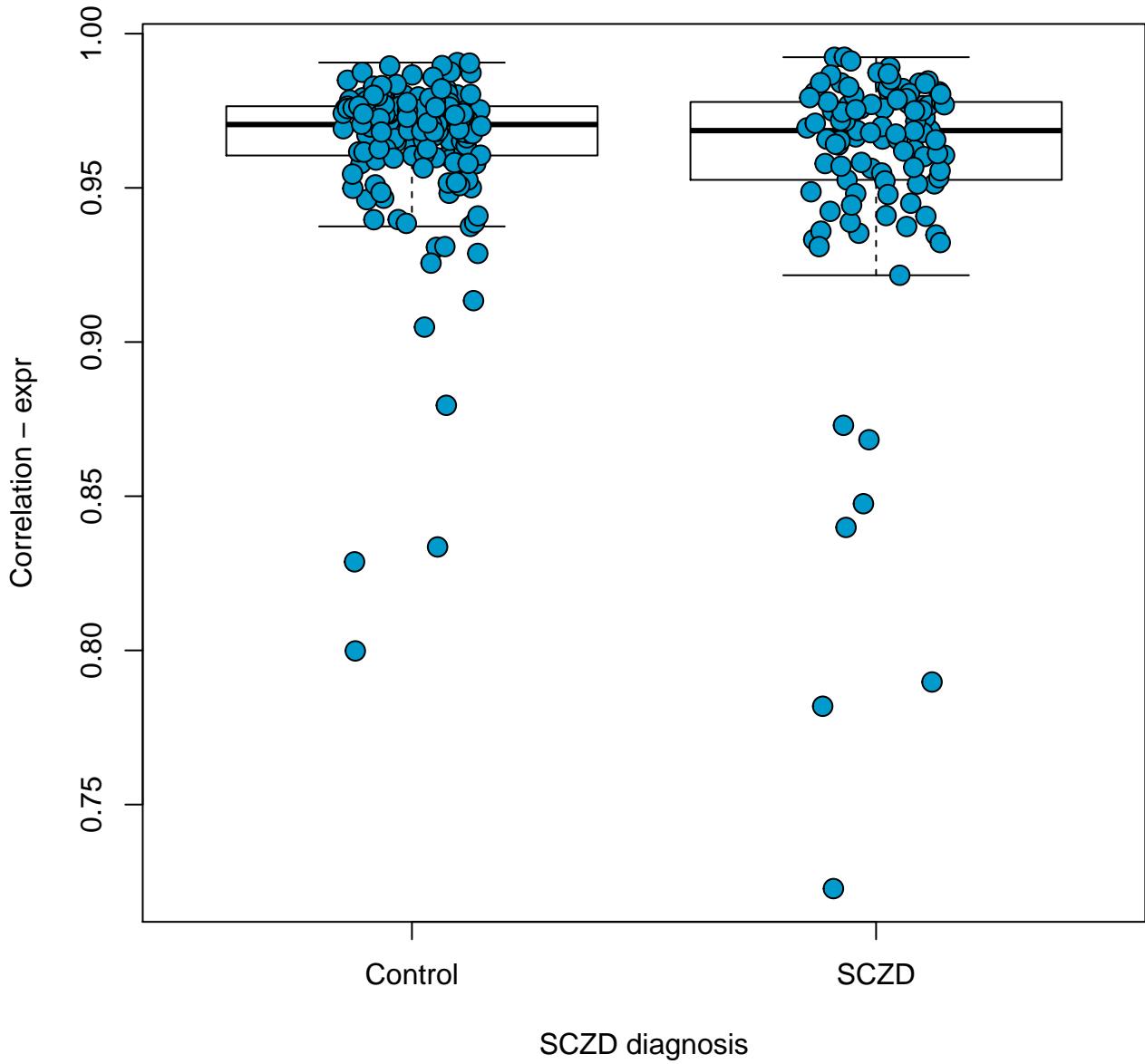
hsa05100: Bacterial invasion of epithelial cells
p-value: 0.0707



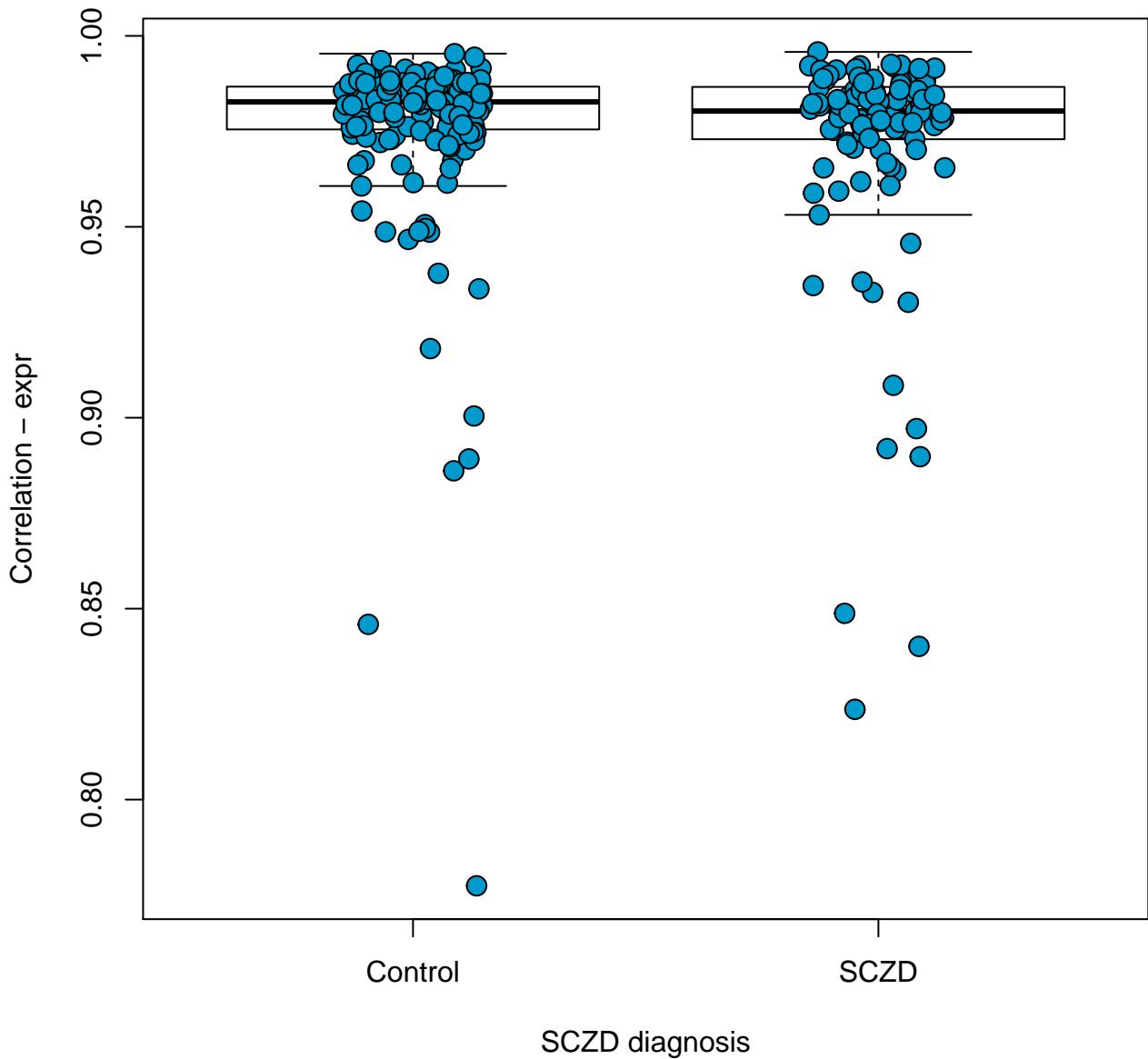
hsa05110: Vibrio cholerae infection
p-value: 0.454



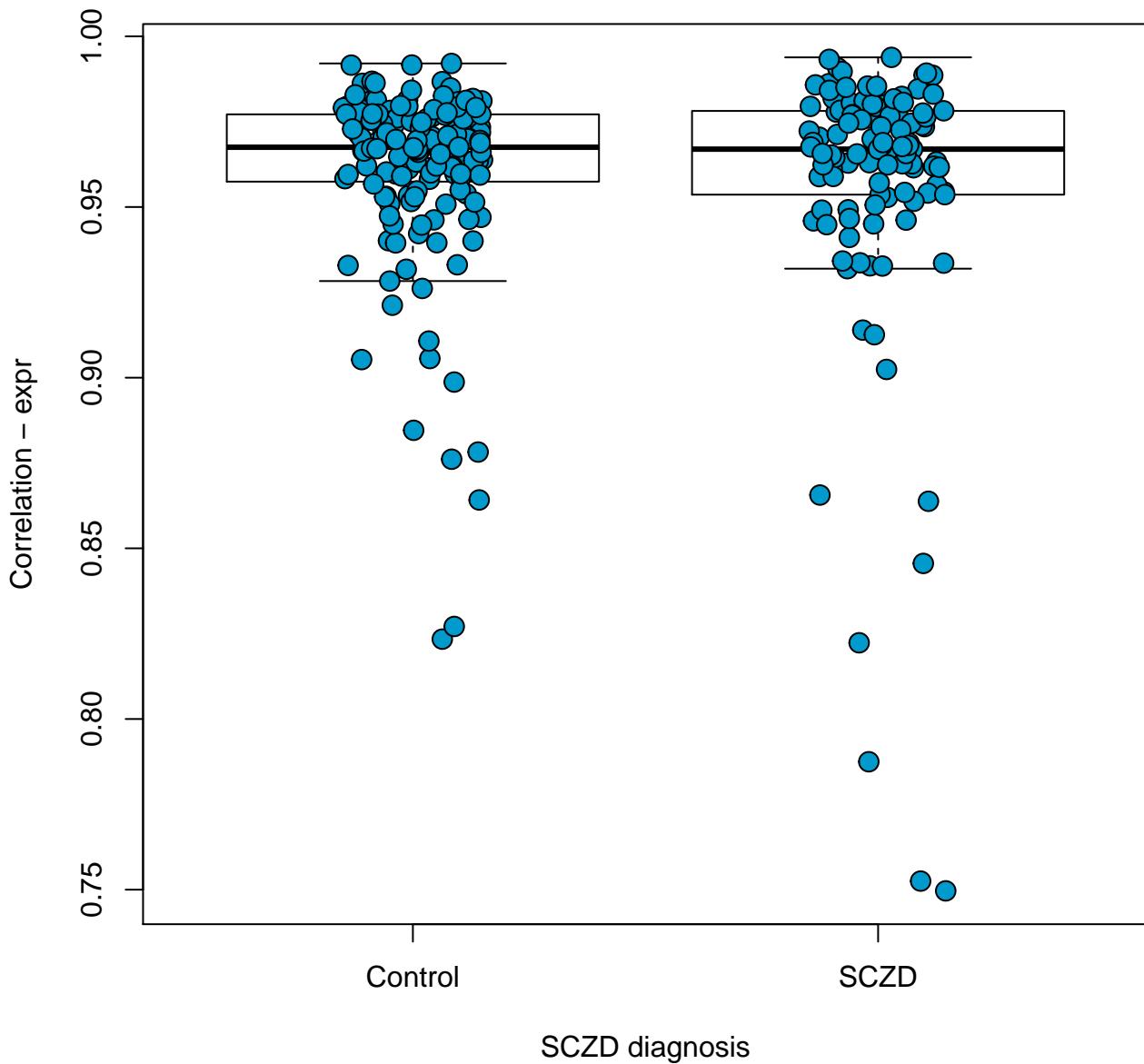
hsa05120: Epithelial cell signaling in Helicobacter pylori infection
p-value: 0.104



hsa05130: Pathogenic Escherichia coli infection
p-value: 0.247

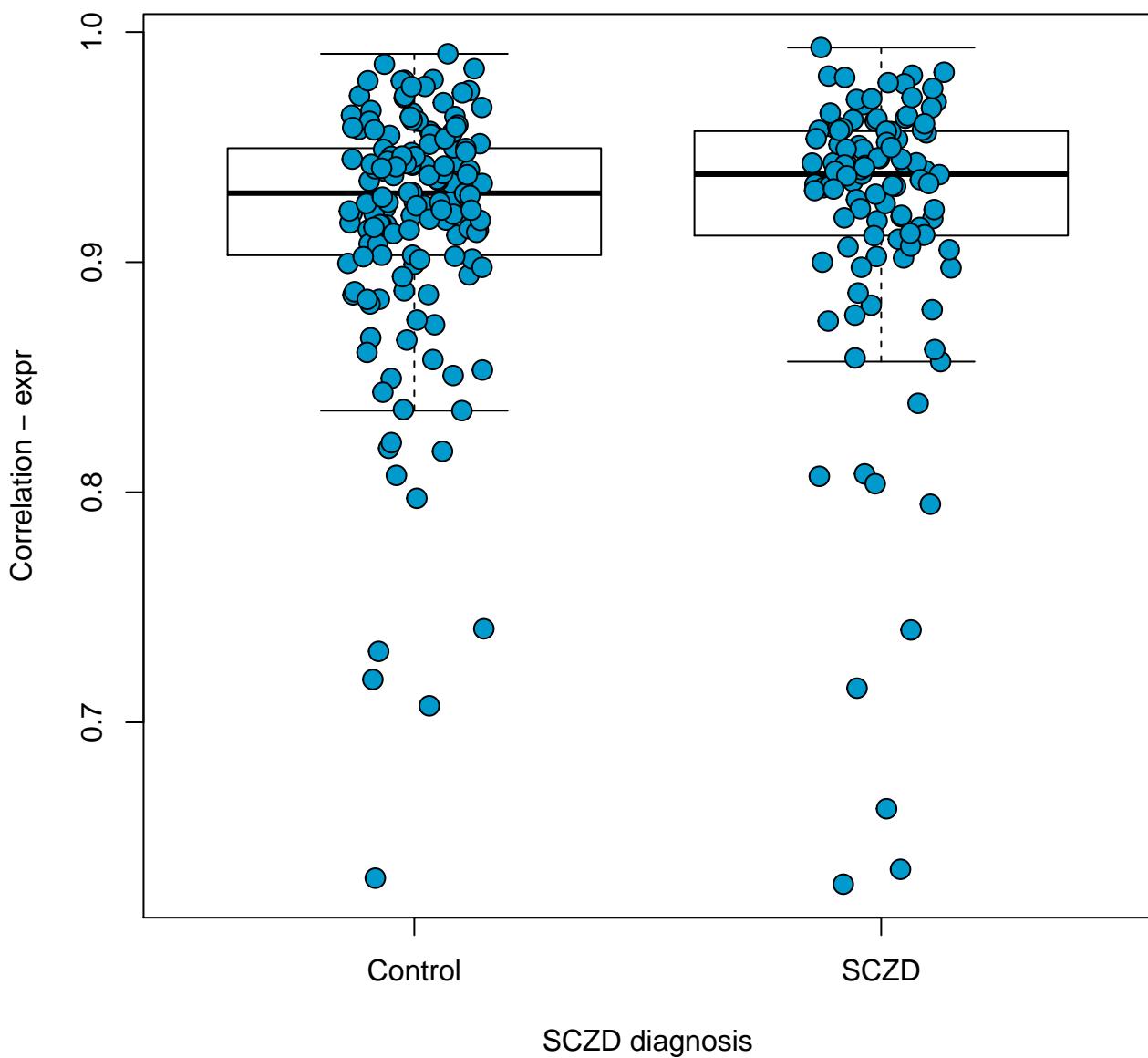


hsa05131: Shigellosis
p-value: 0.226

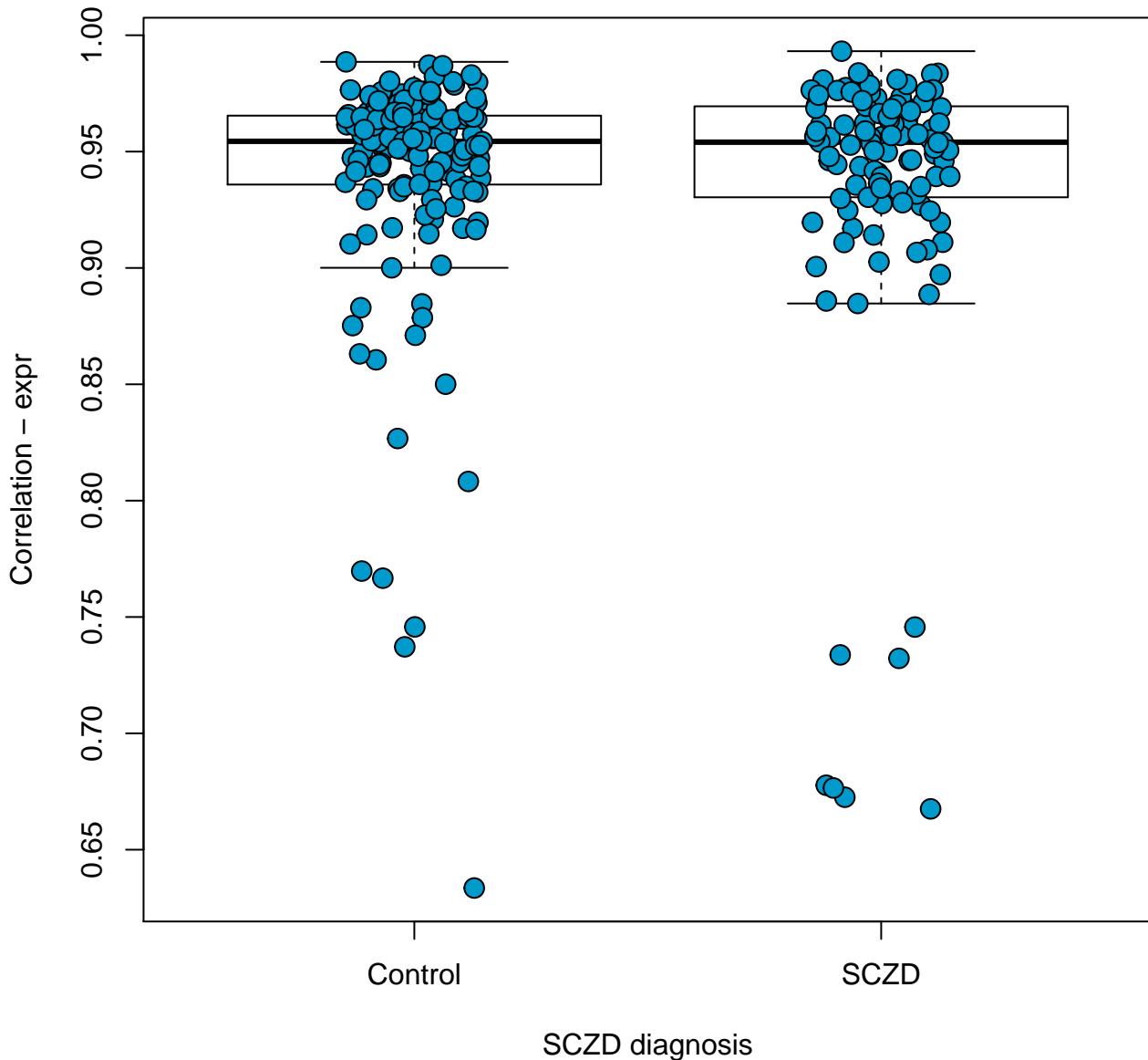


hsa05140: Leishmaniasis

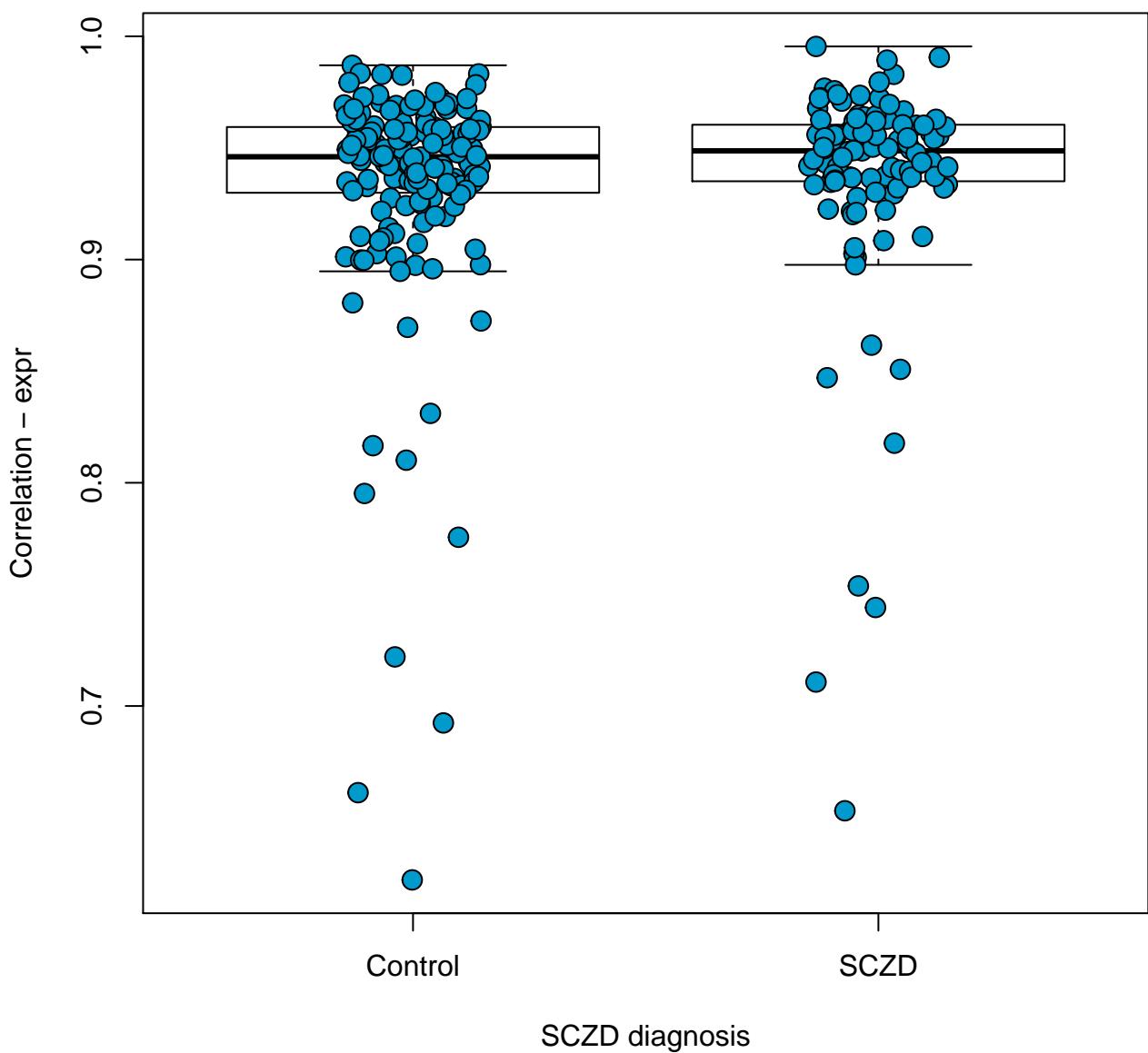
p-value: 0.917



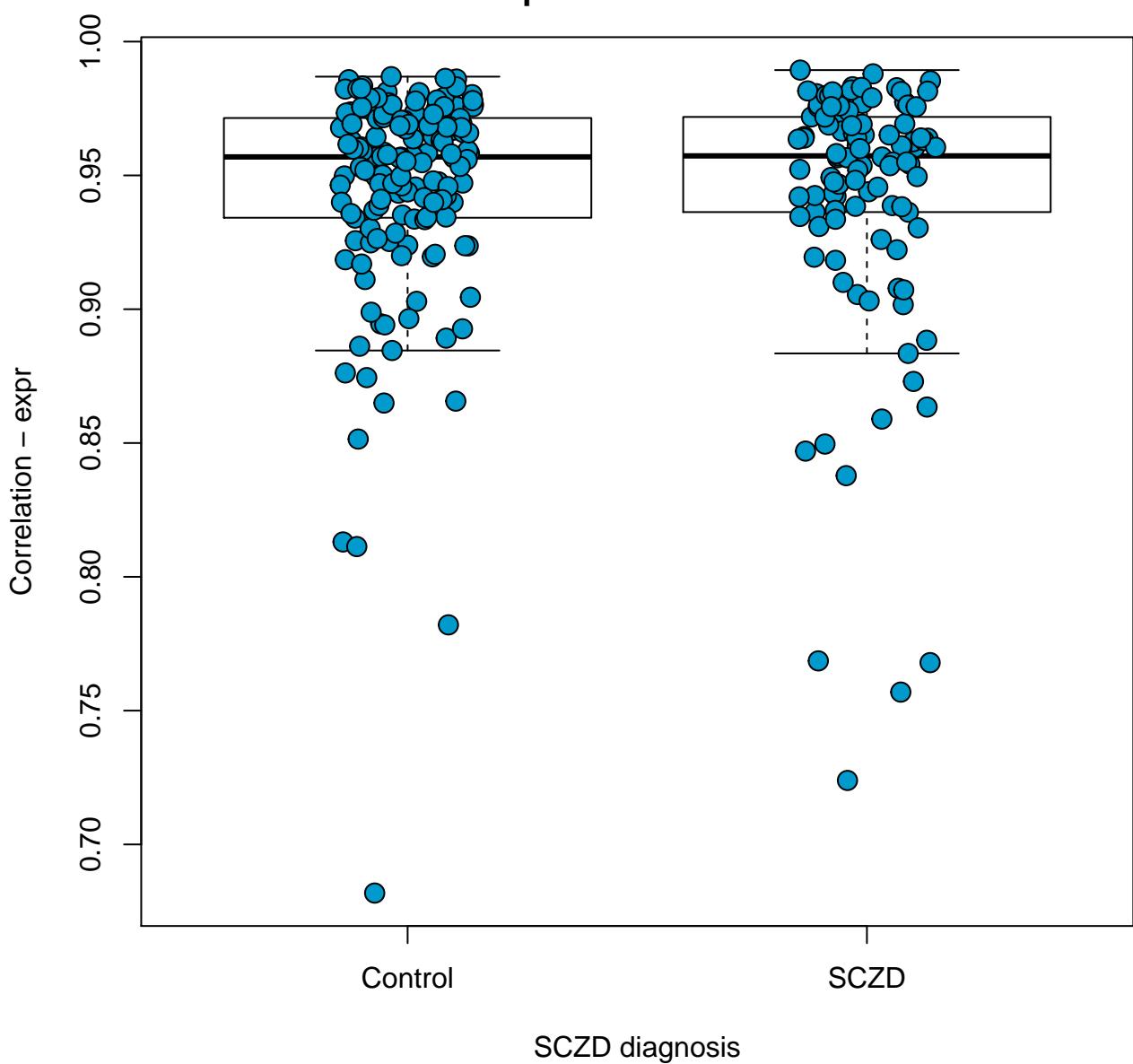
hsa05142: Chagas disease (American trypanosomiasis)
p-value: 0.403



hsa05143: African trypanosomiasis
p-value: 0.593

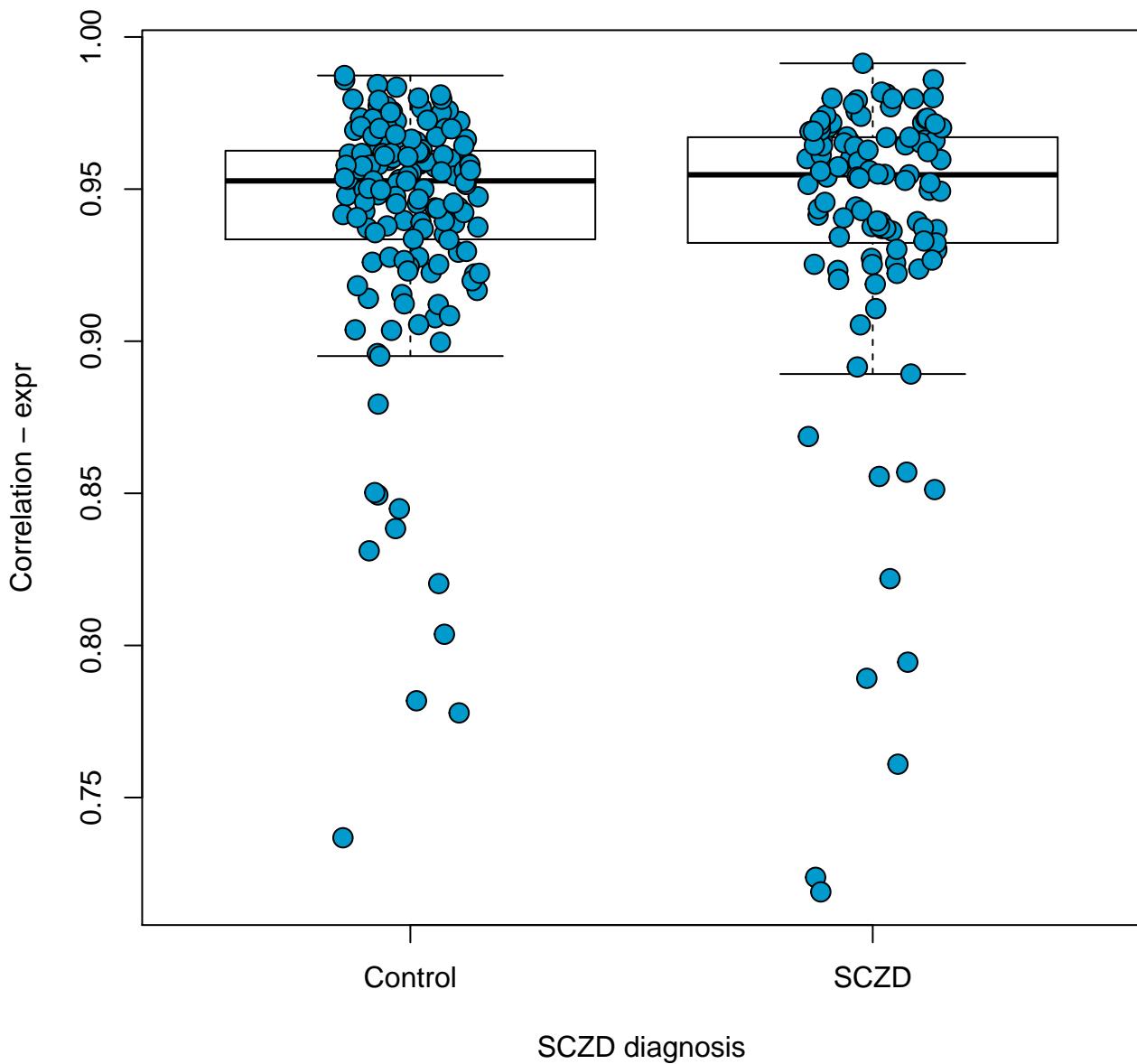


hsa05144: Malaria
p-value: 0.603

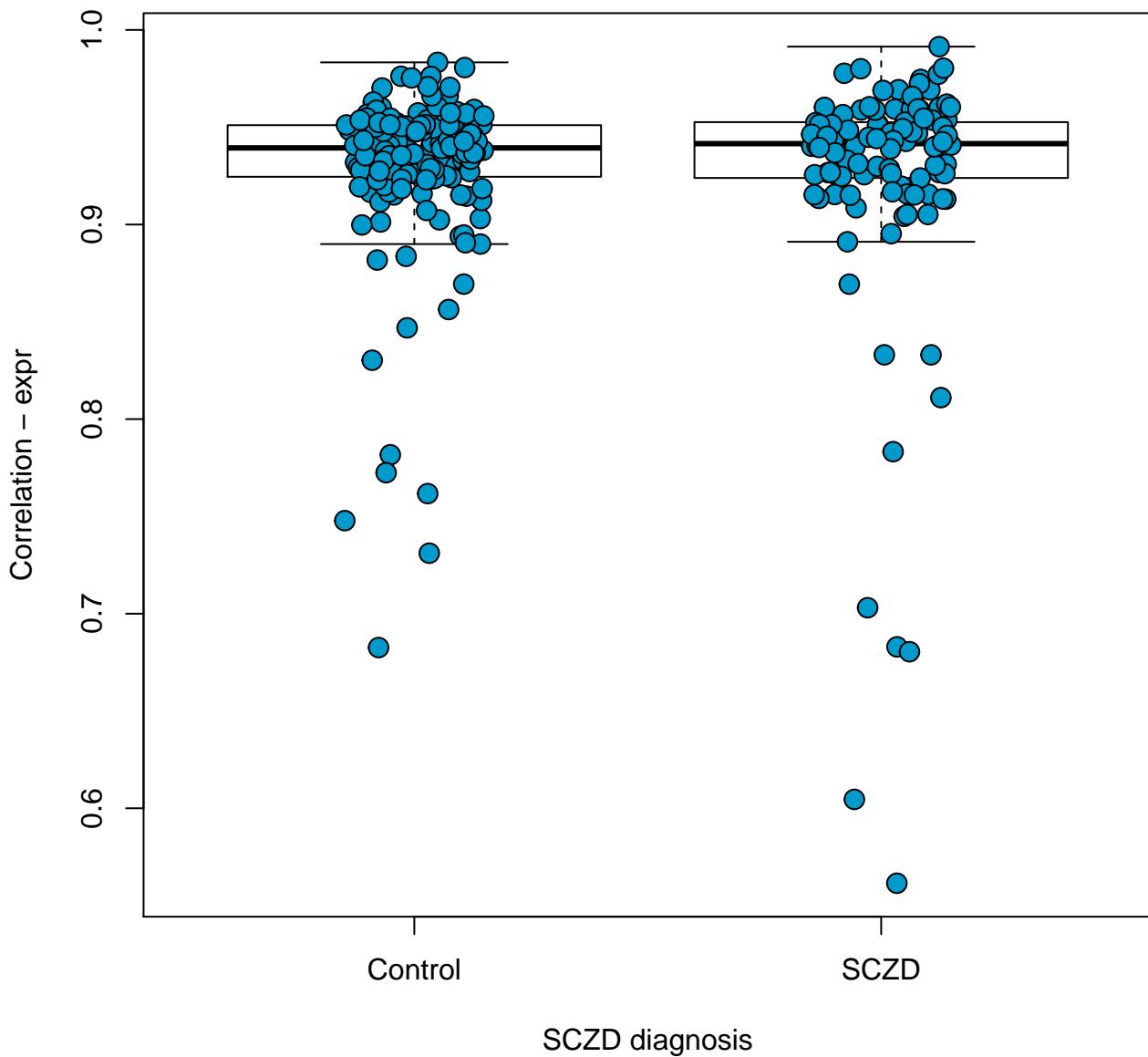


hsa05145: Toxoplasmosis

p-value: 0.718

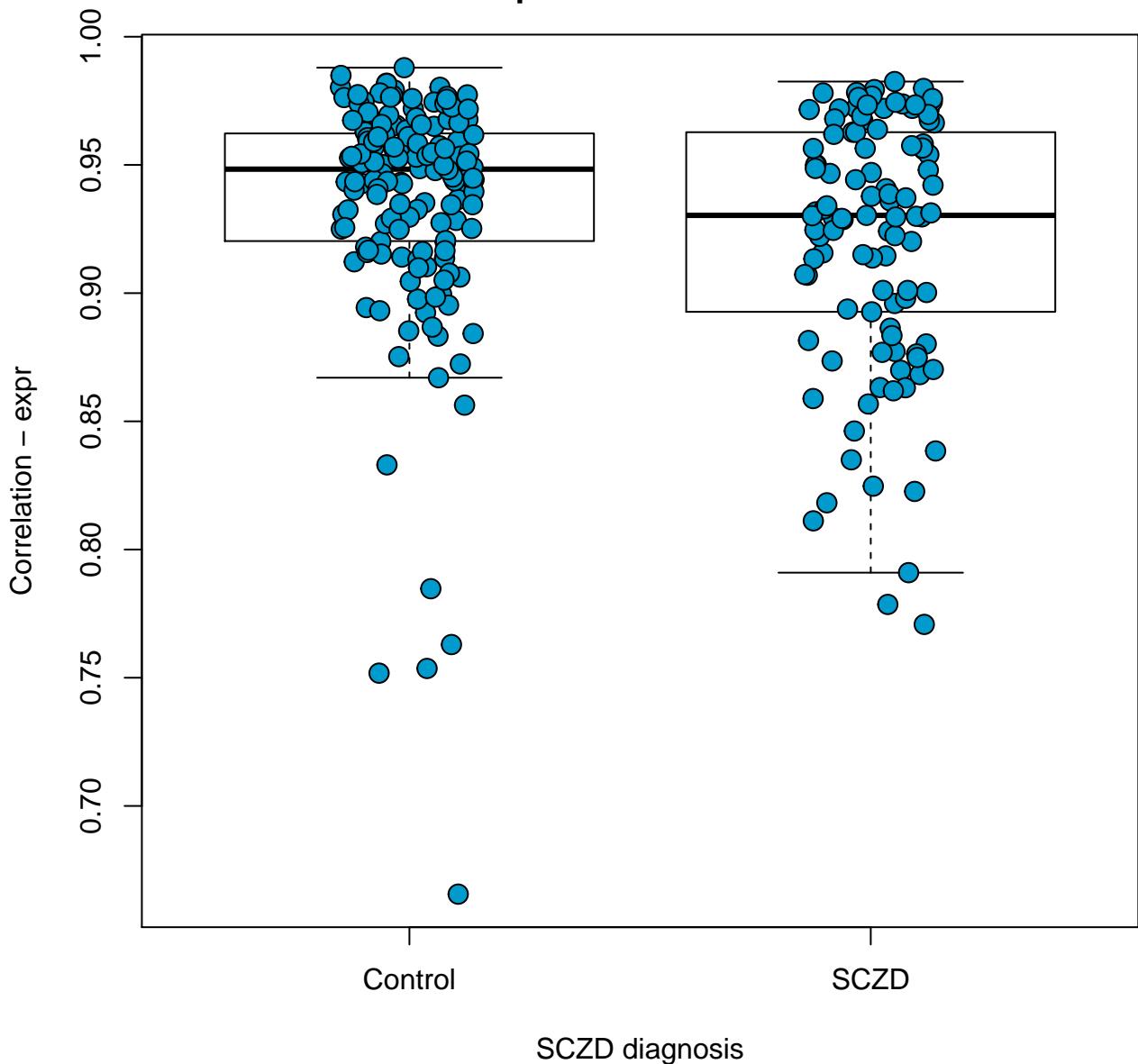


hsa05146: Amoebiasis
p-value: 0.393

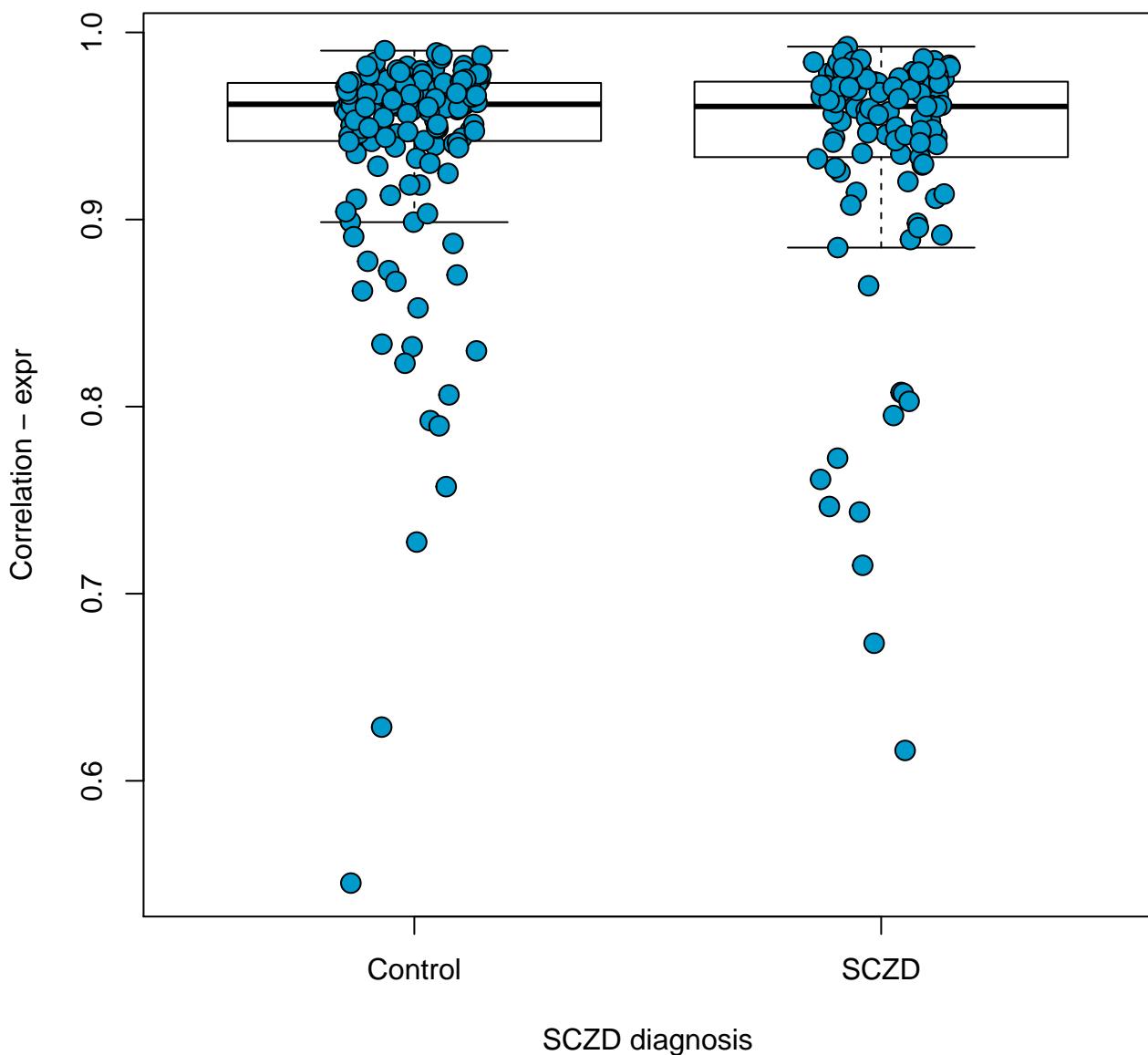


hsa05150: Staphylococcus aureus infection

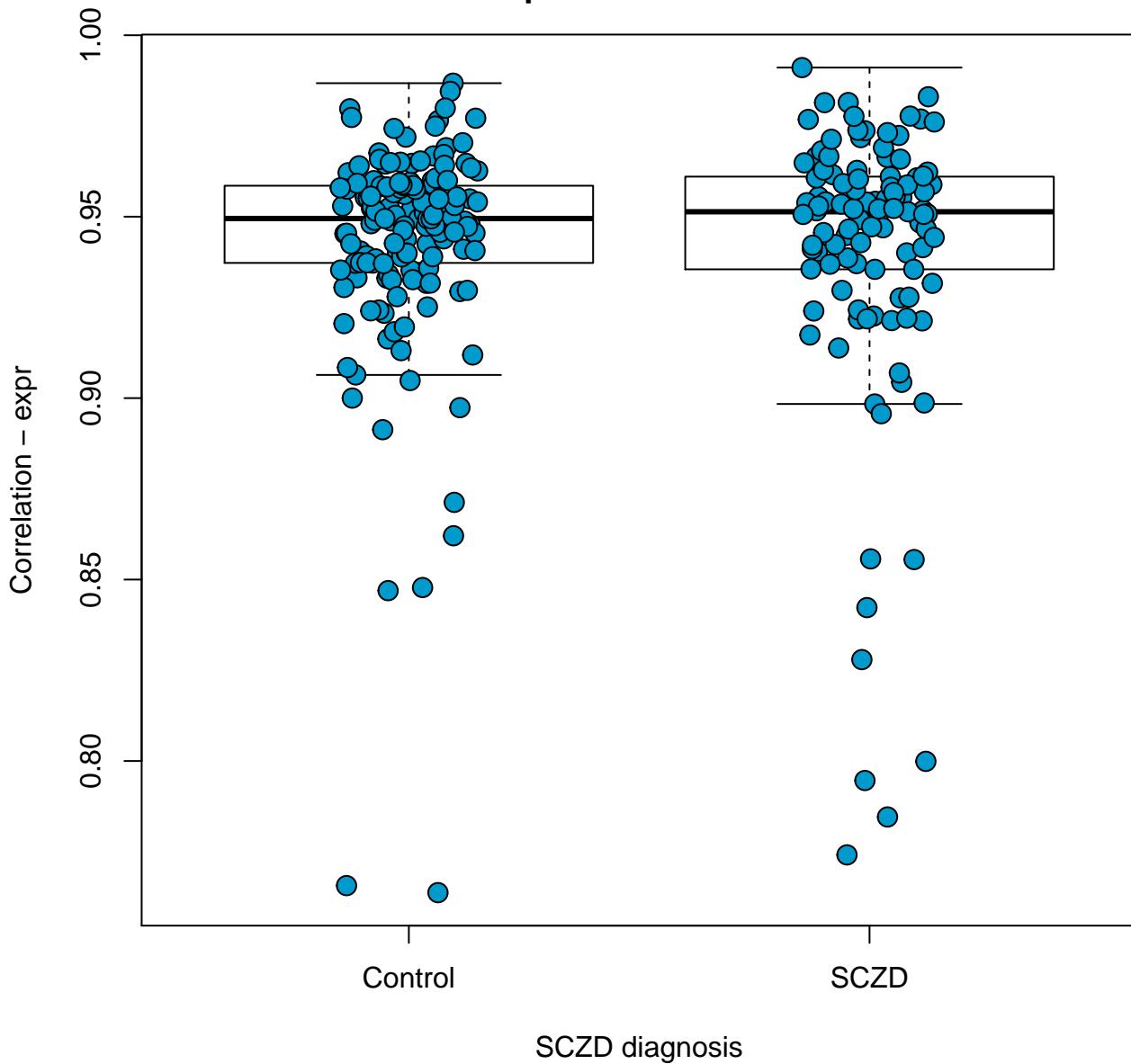
p-value: 0.0161



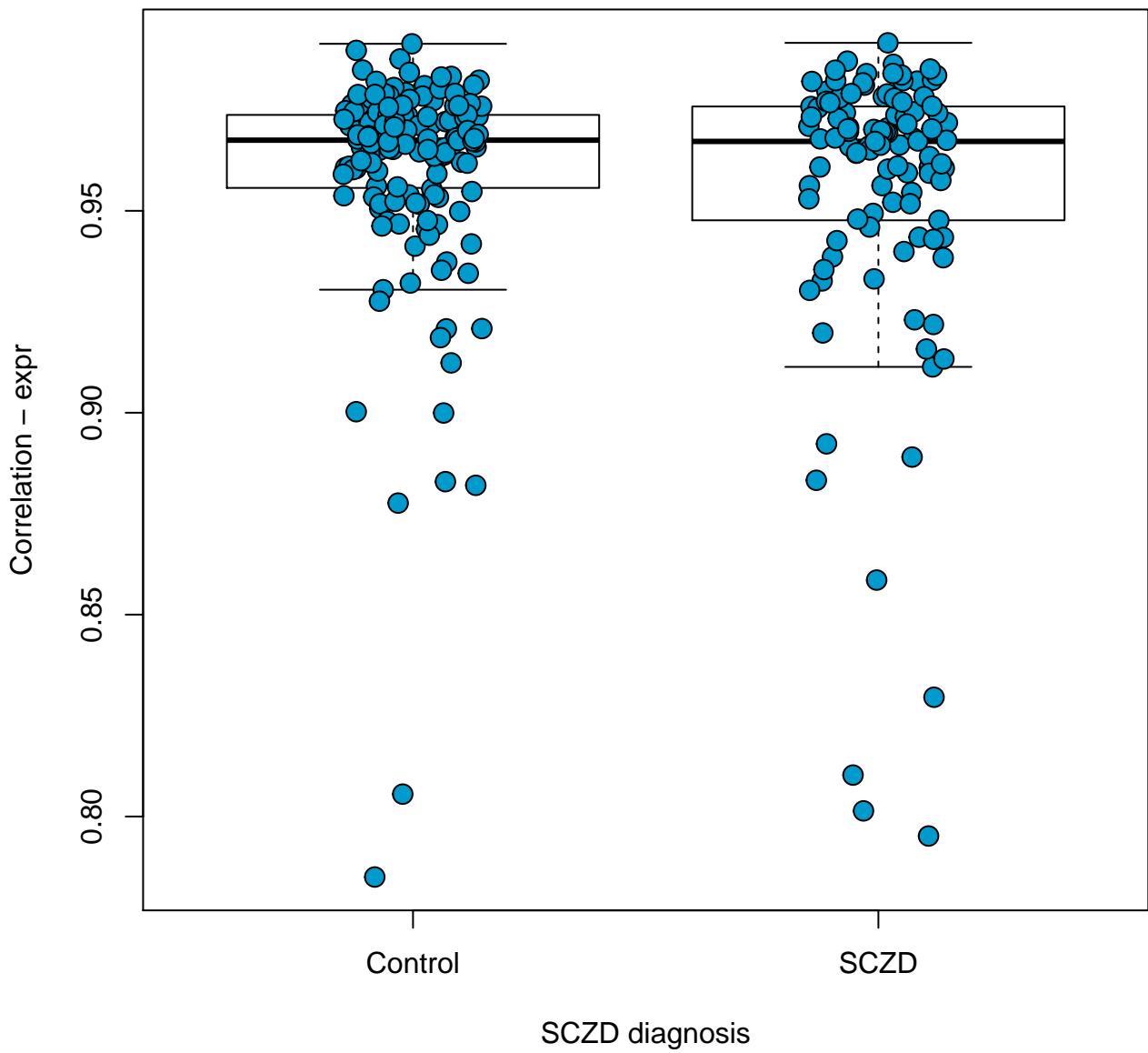
hsa05160: Hepatitis C
p-value: 0.438



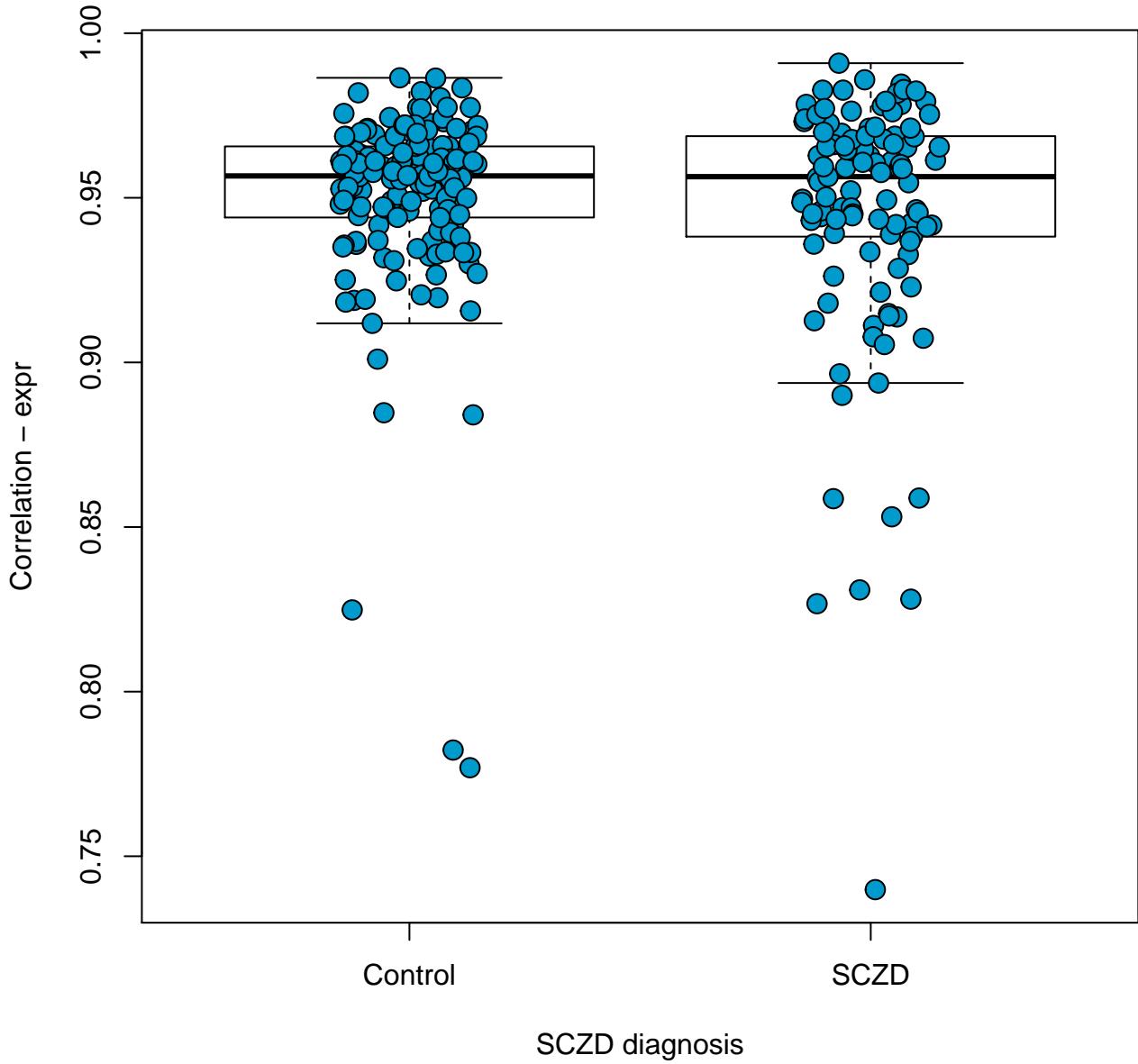
hsa05200: Pathways in cancer
p-value: 0.403



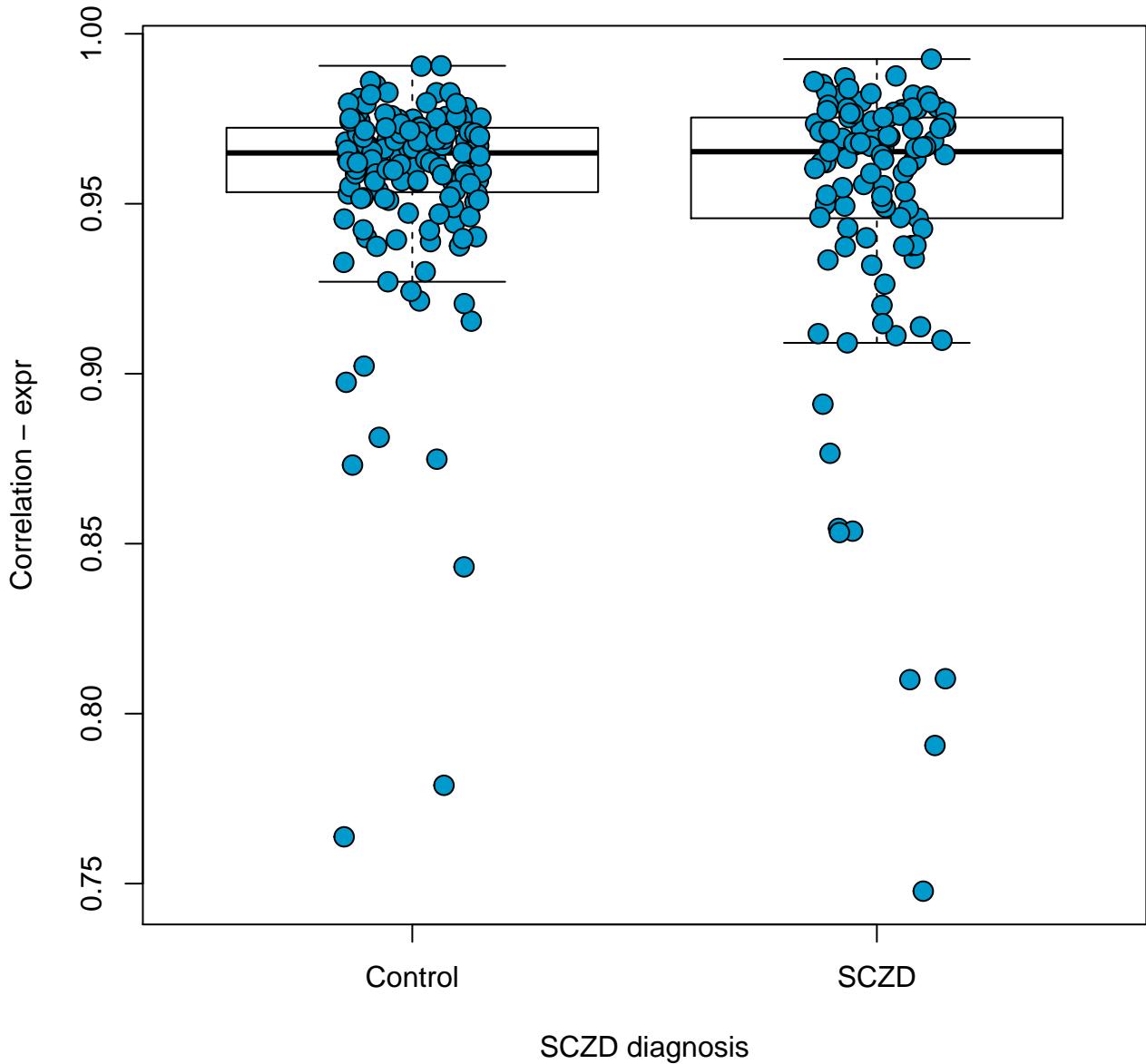
hsa05210: Colorectal cancer
p-value: 0.15



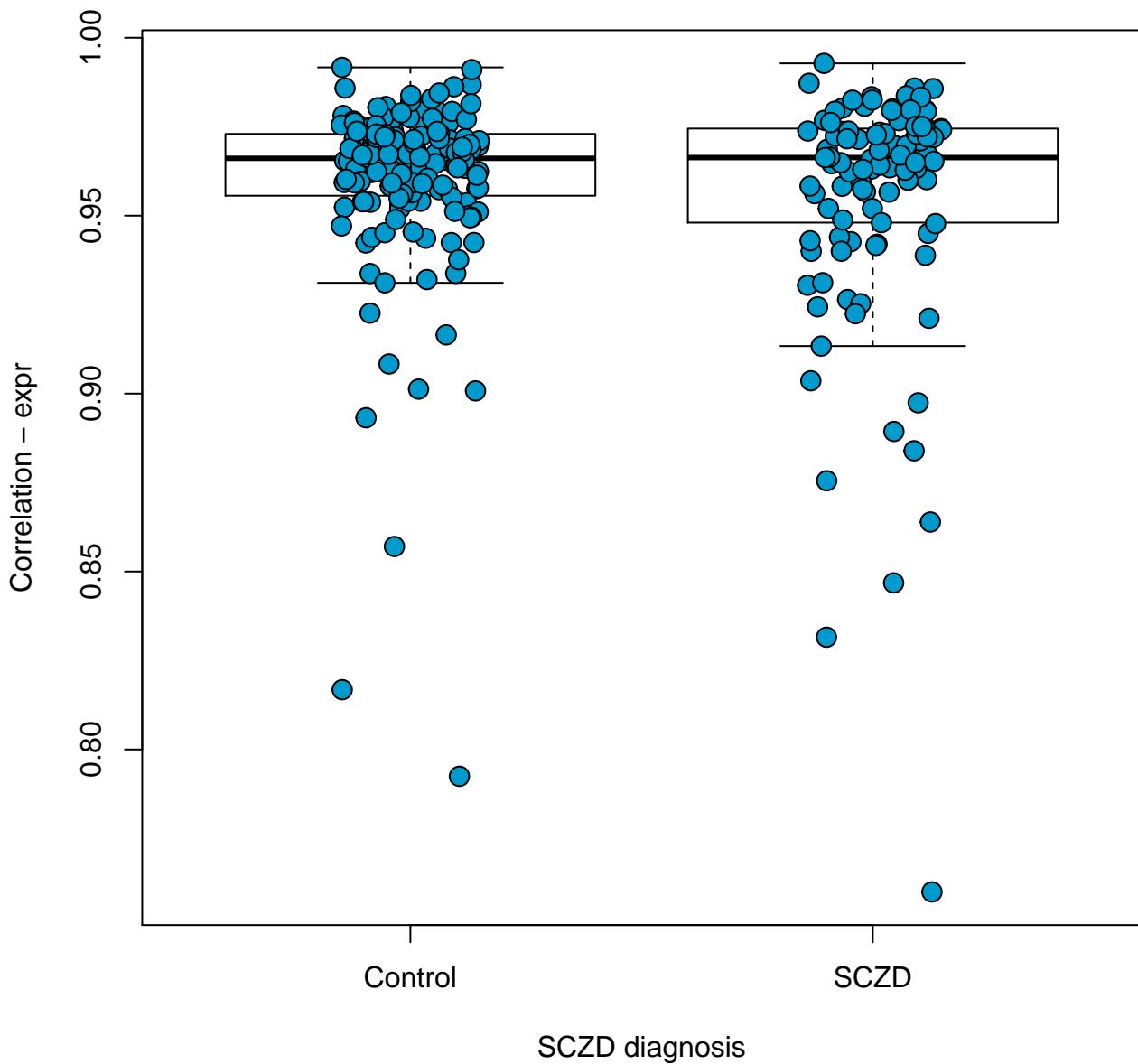
hsa05211: Renal cell carcinoma
p-value: 0.202



hsa05212: Pancreatic cancer
p-value: 0.149

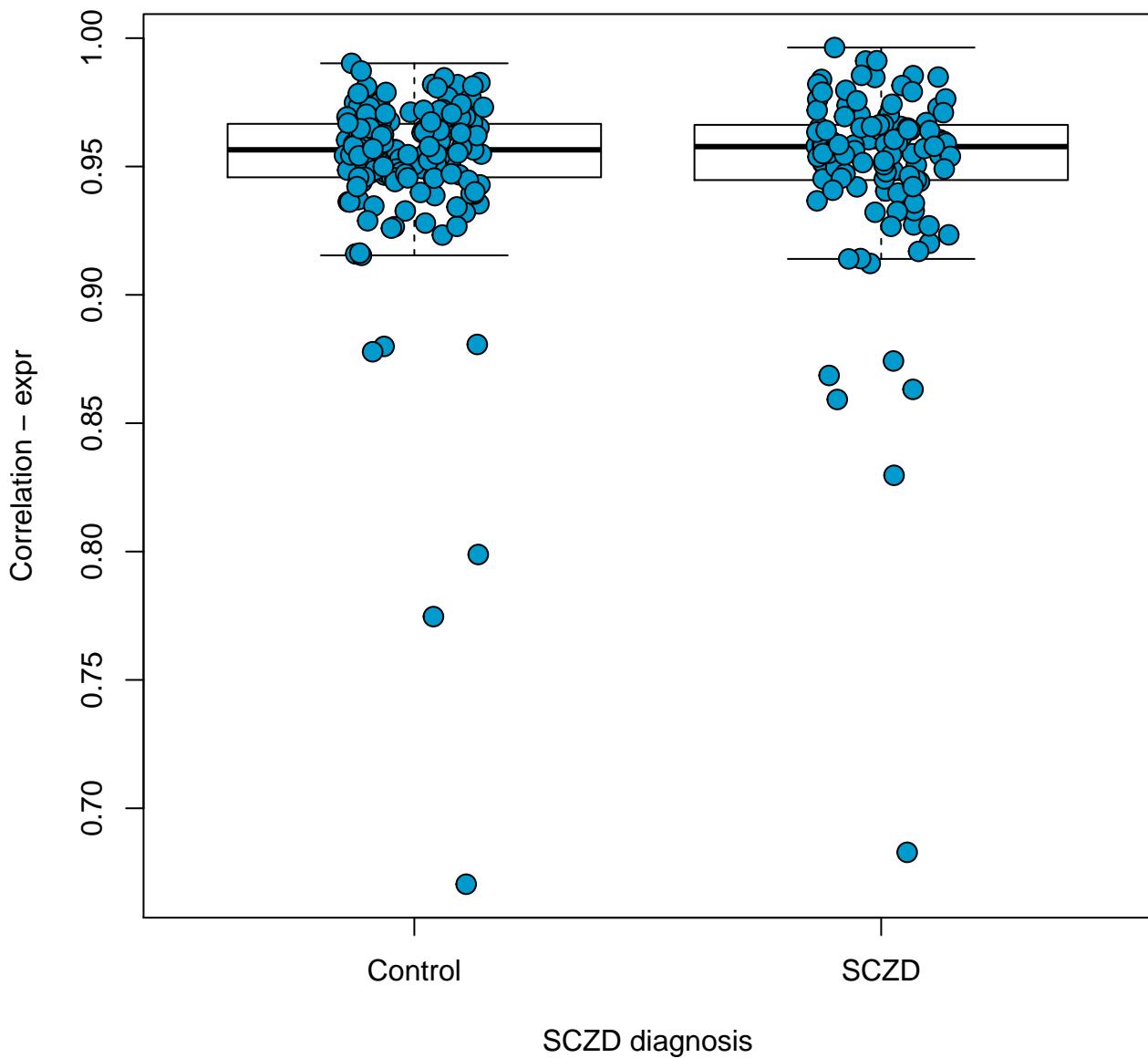


hsa05213: Endometrial cancer
p-value: 0.202

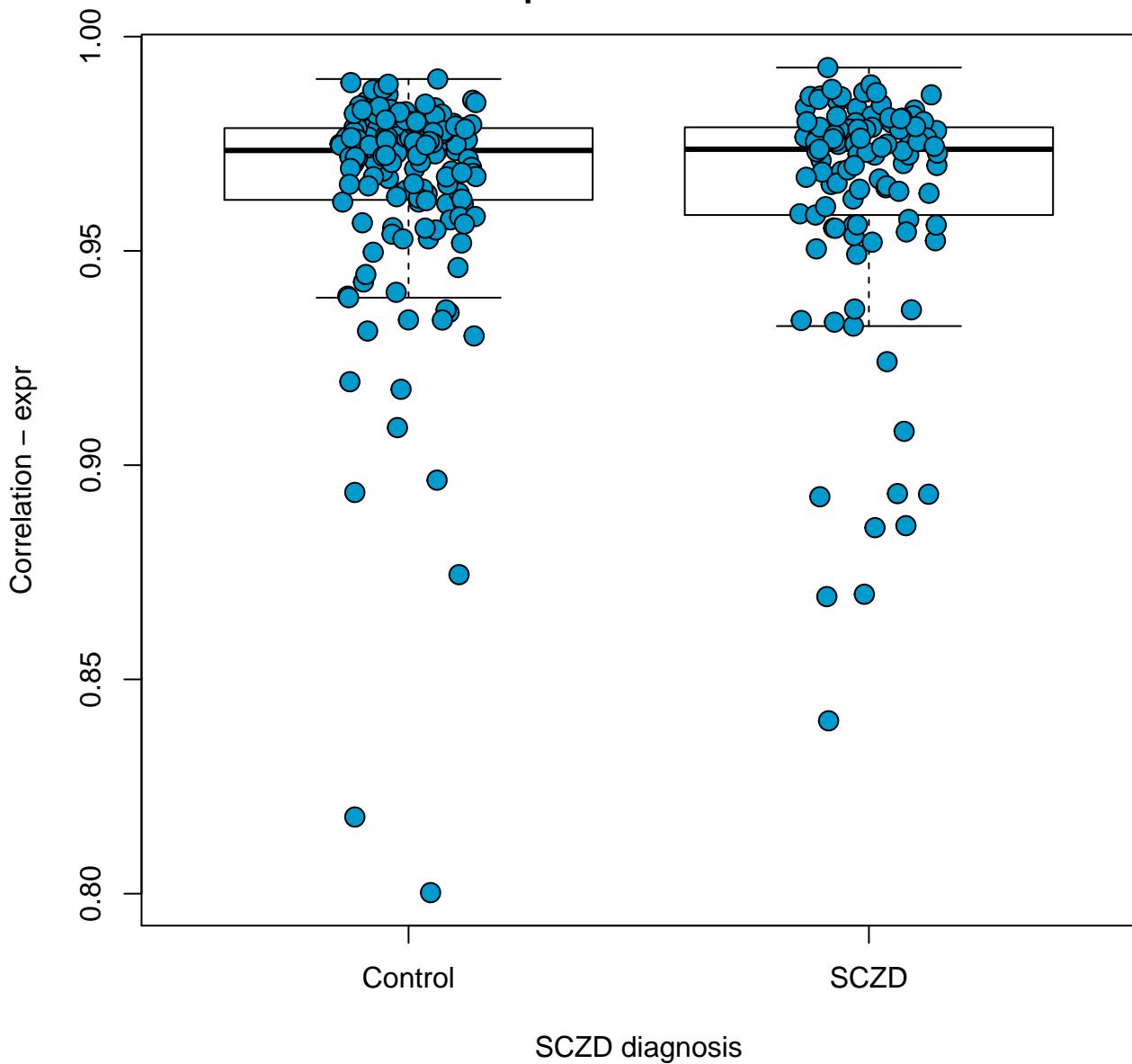


hsa05214: Glioma

p-value: 0.819

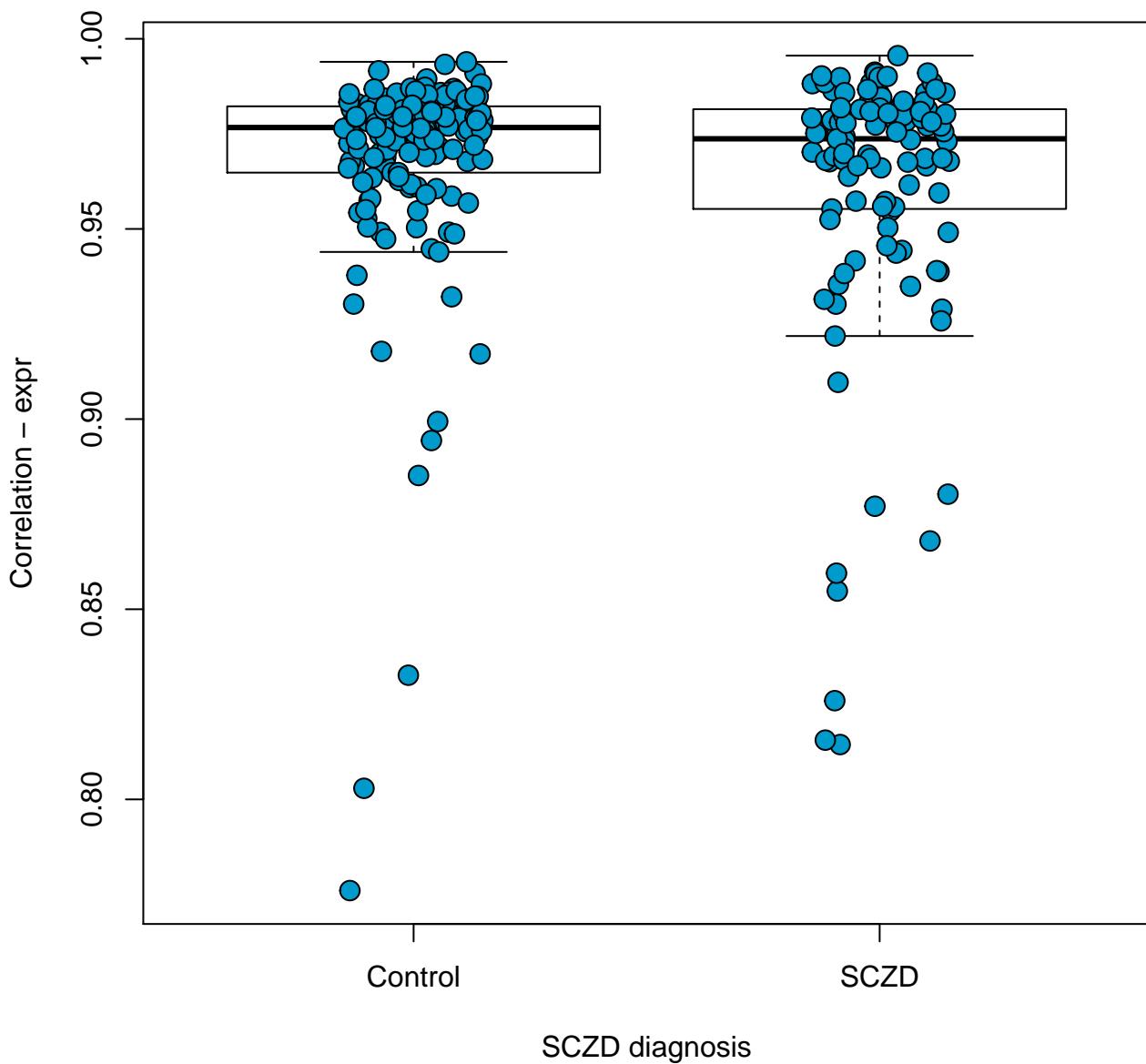


hsa05215: Prostate cancer
p-value: 0.509

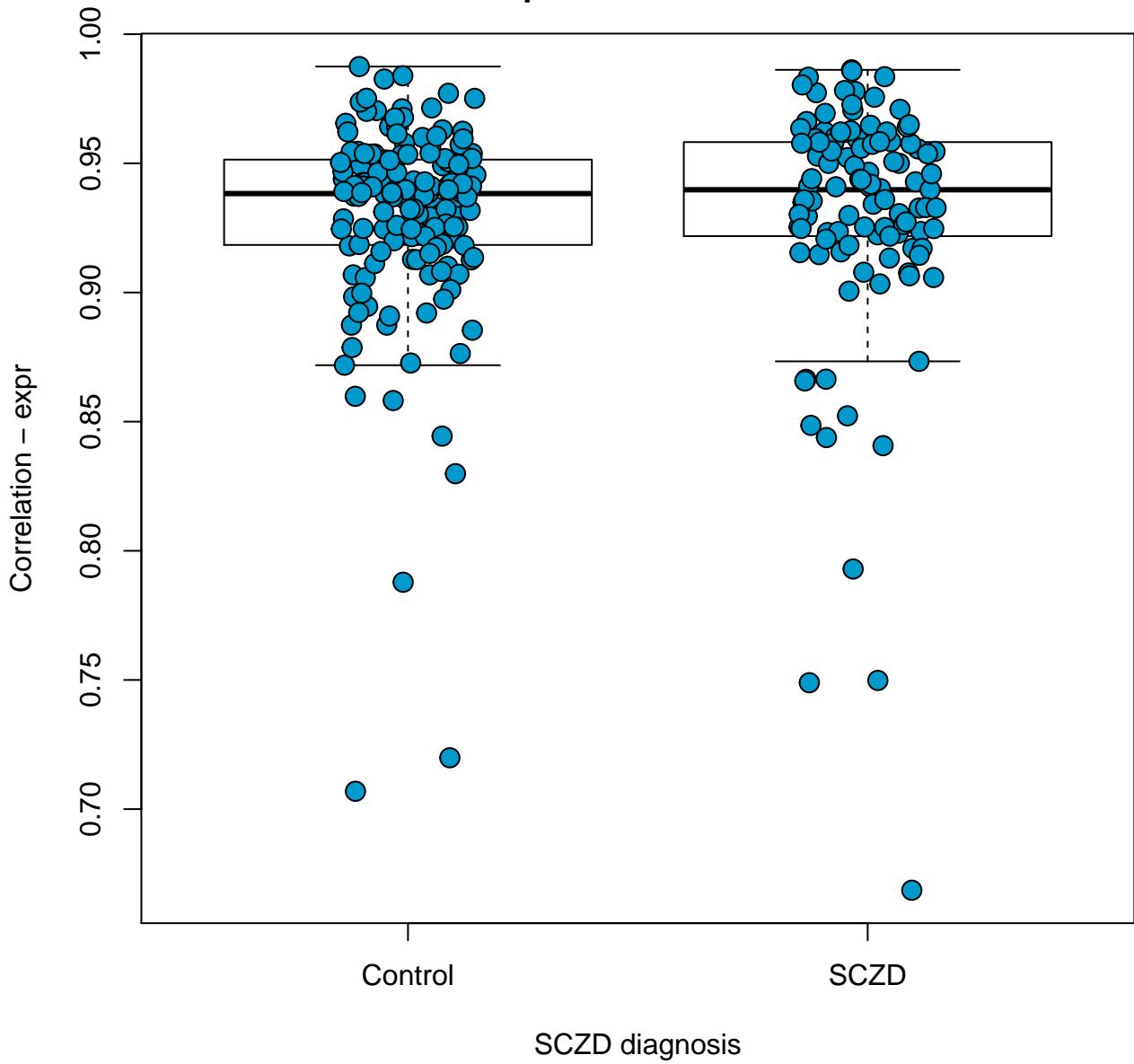


hsa05216: Thyroid cancer

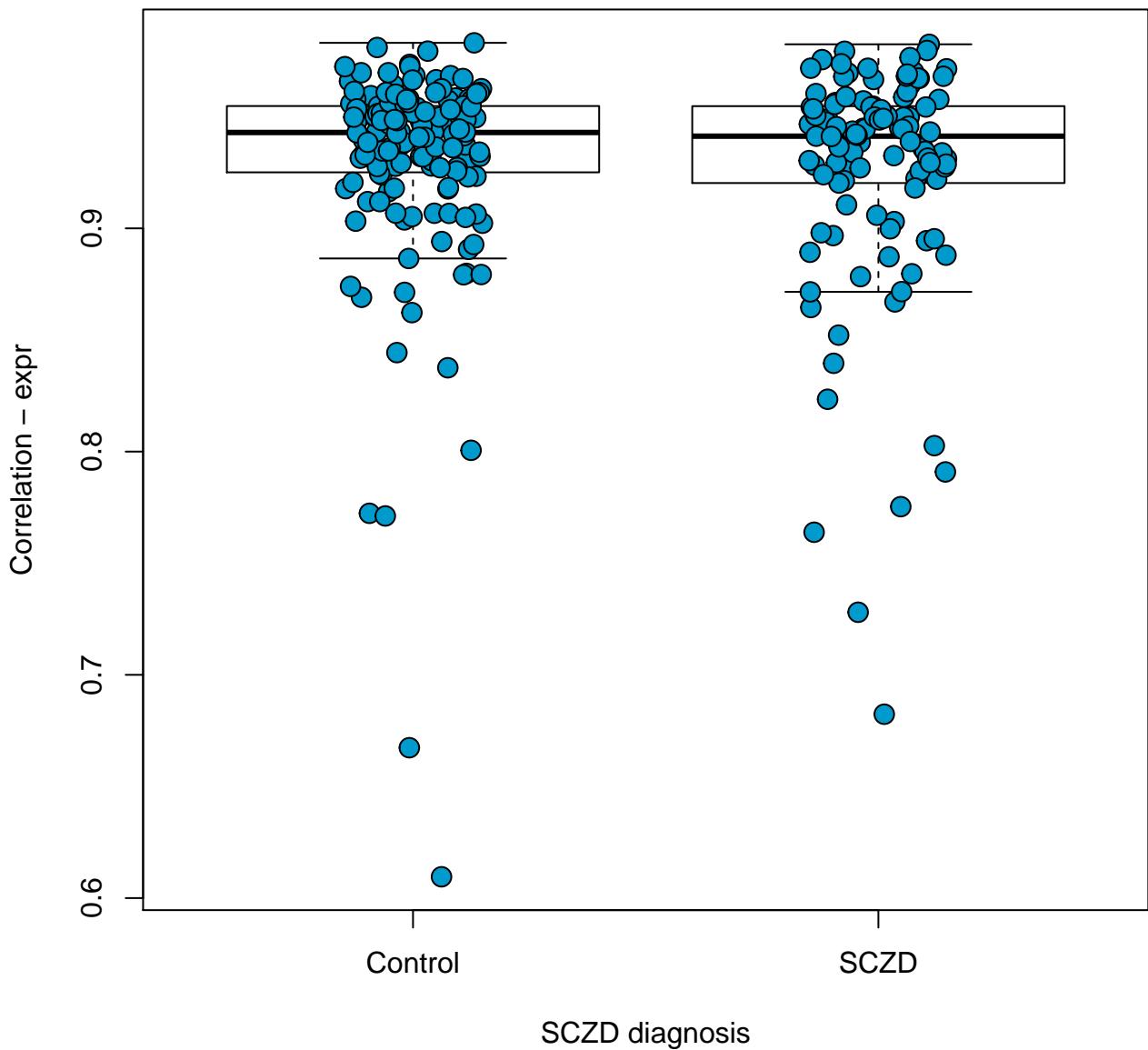
p-value: 0.0703



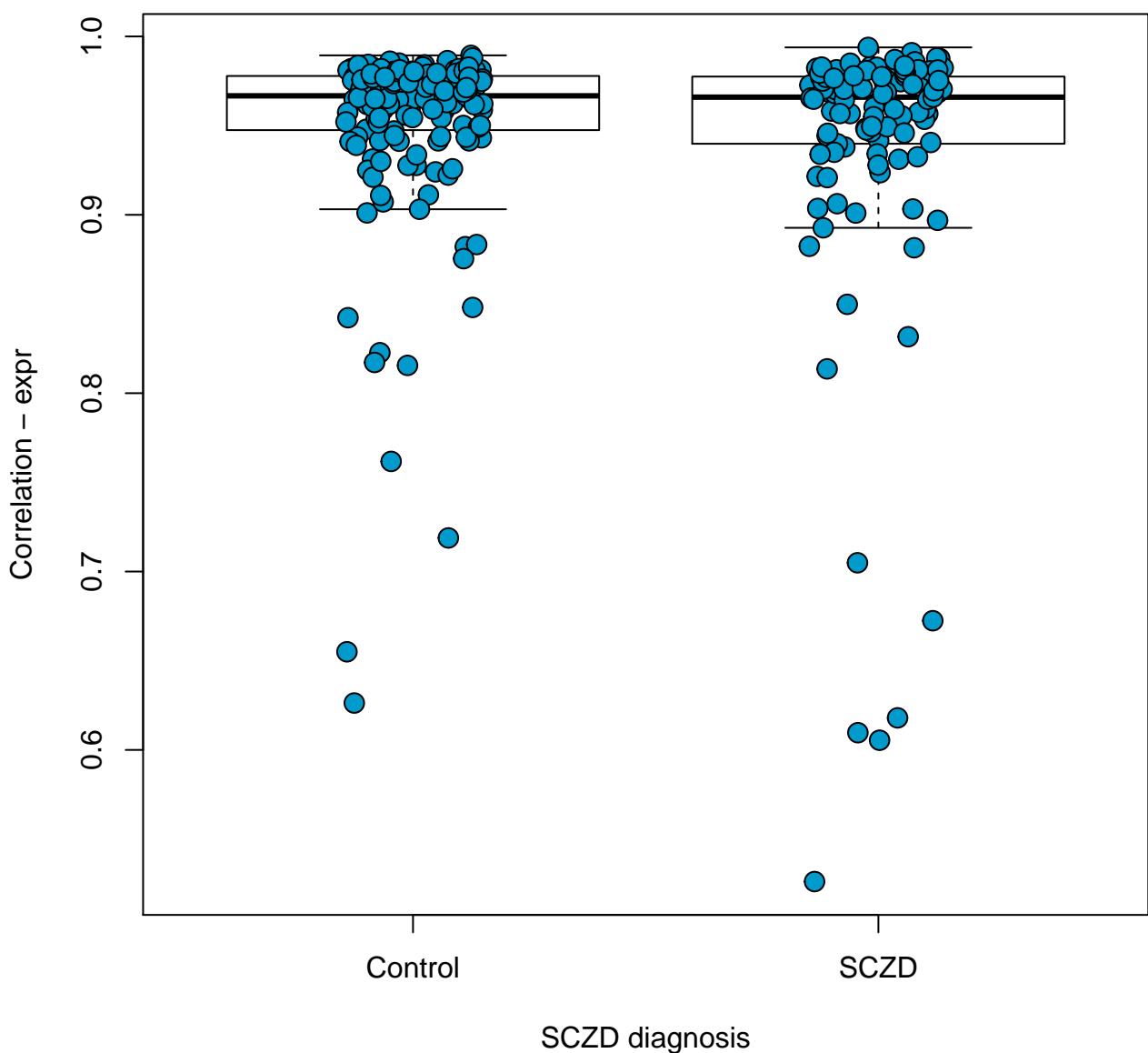
hsa05217: Basal cell carcinoma
p-value: 0.985



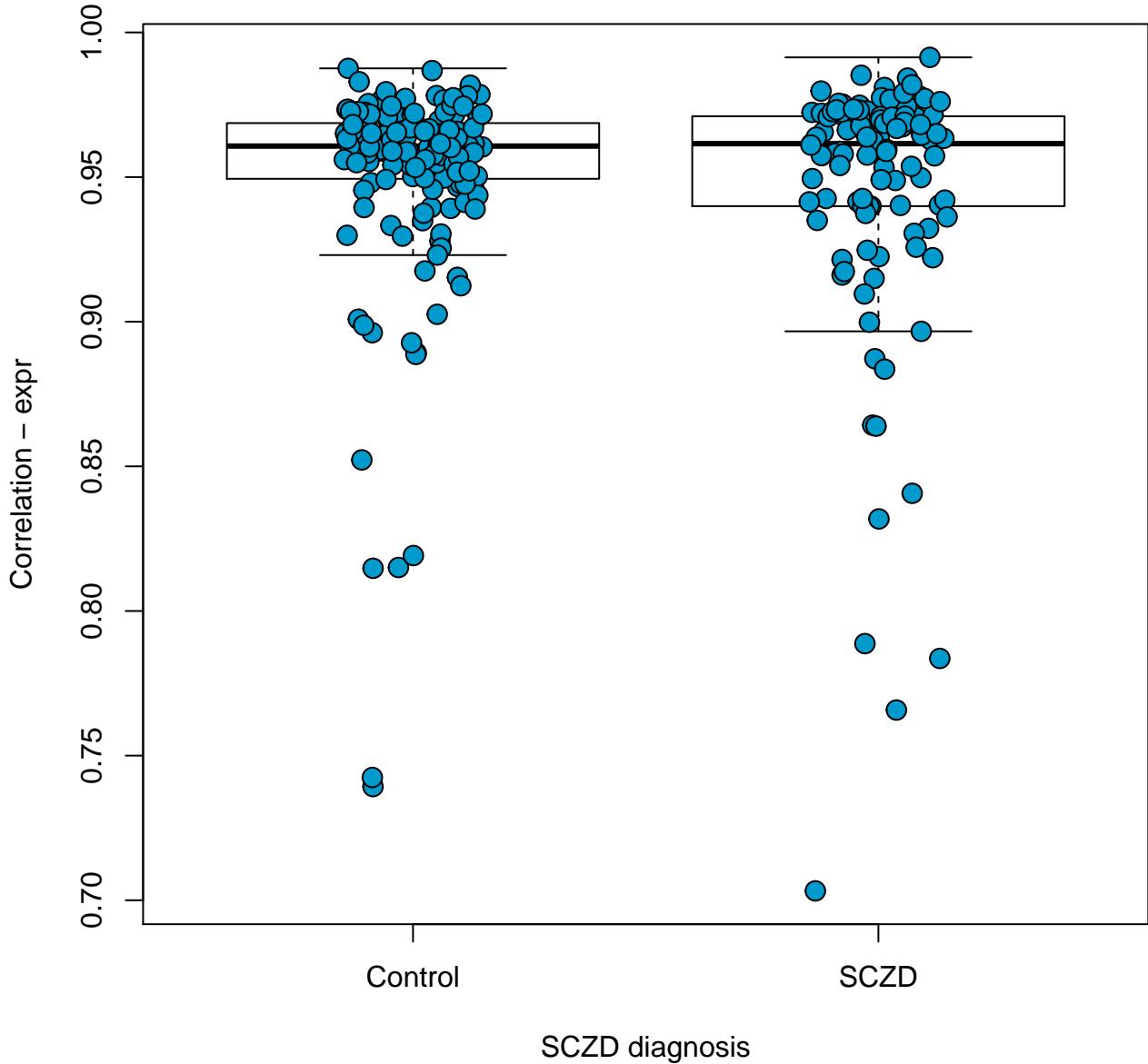
hsa05218: Melanoma
p-value: 0.399



hsa05219: Bladder cancer
p-value: 0.123

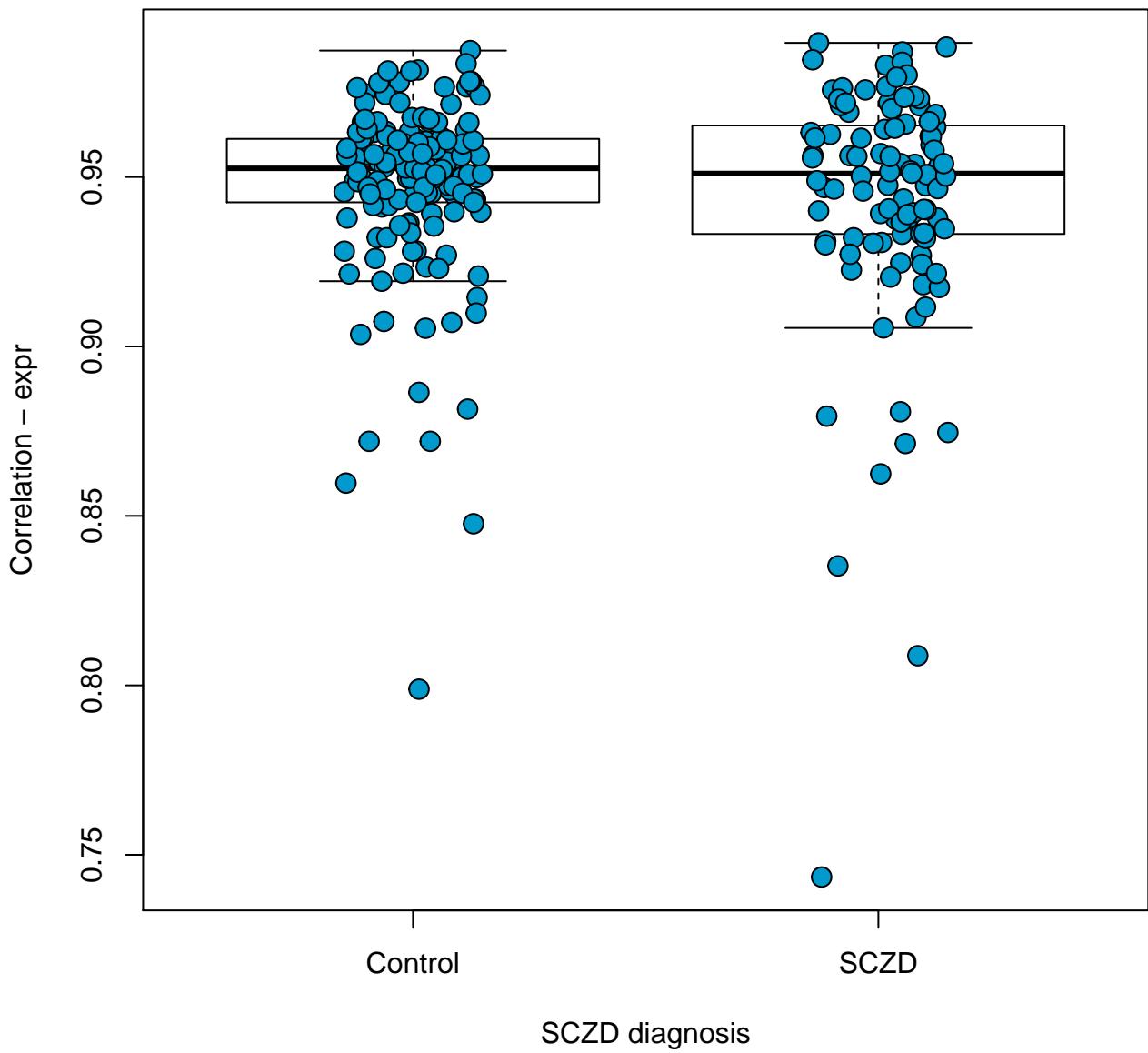


hsa05220: Chronic myeloid leukemia
p-value: 0.255

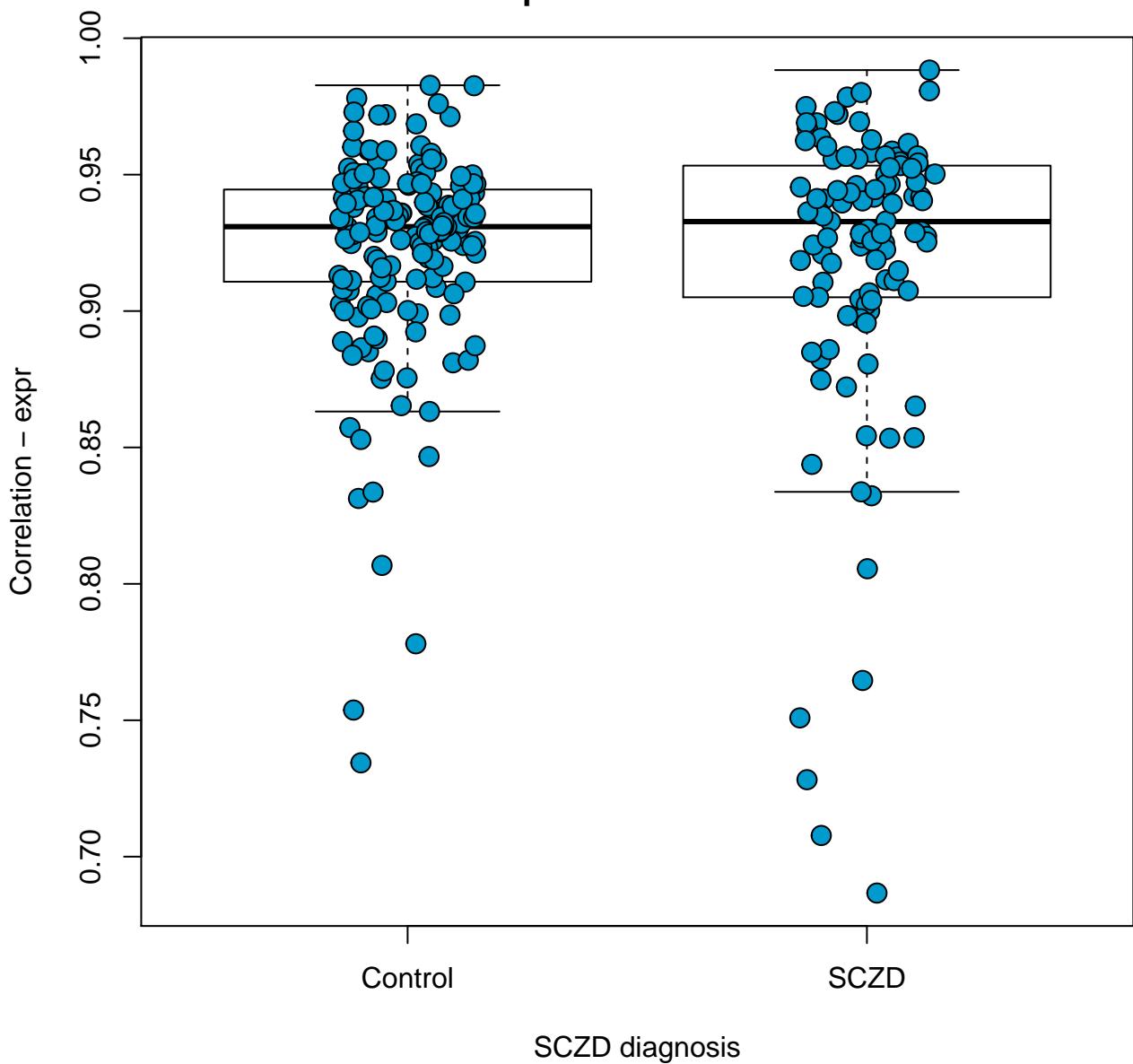


hsa05221: Acute myeloid leukemia

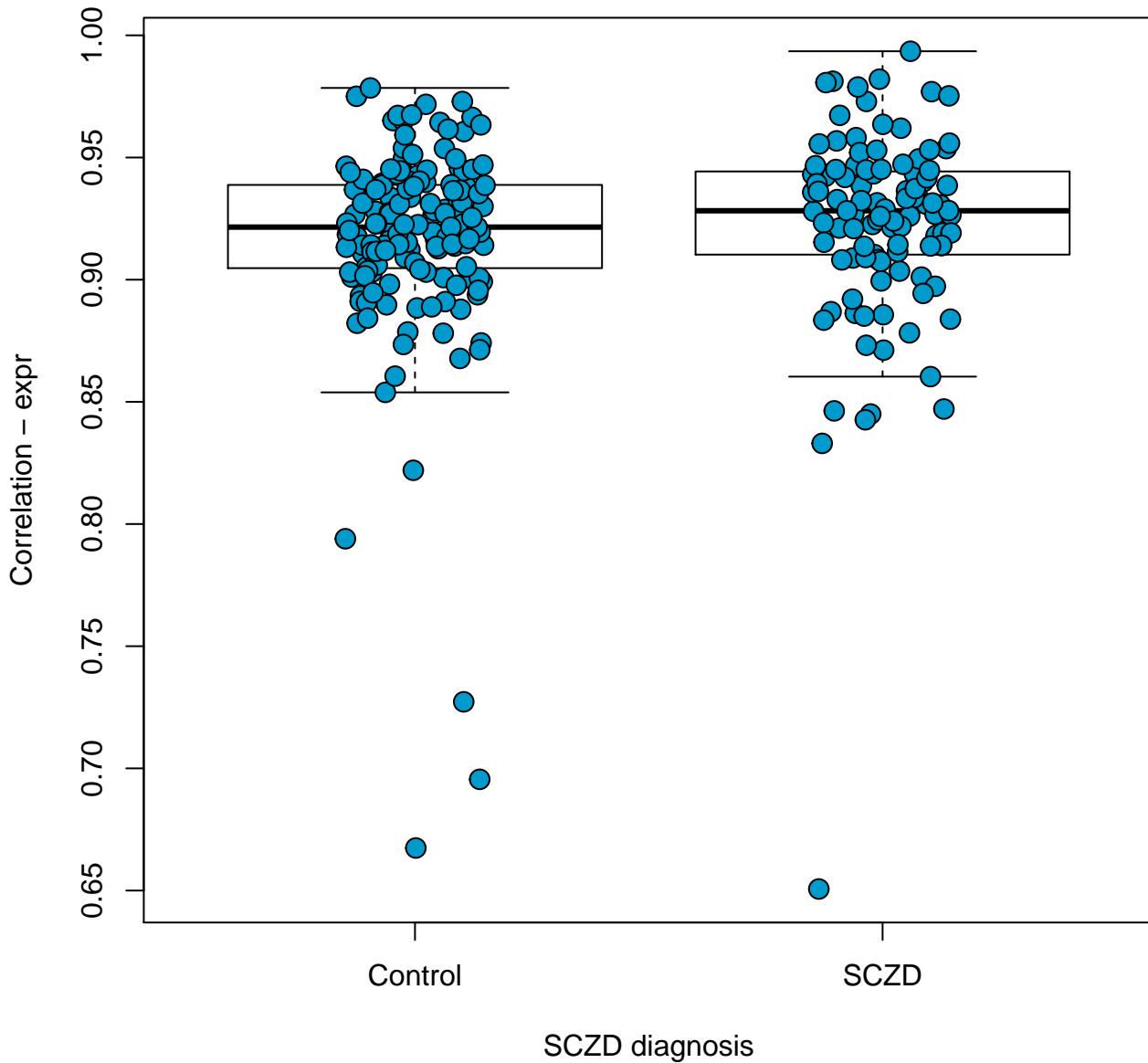
p-value: 0.326



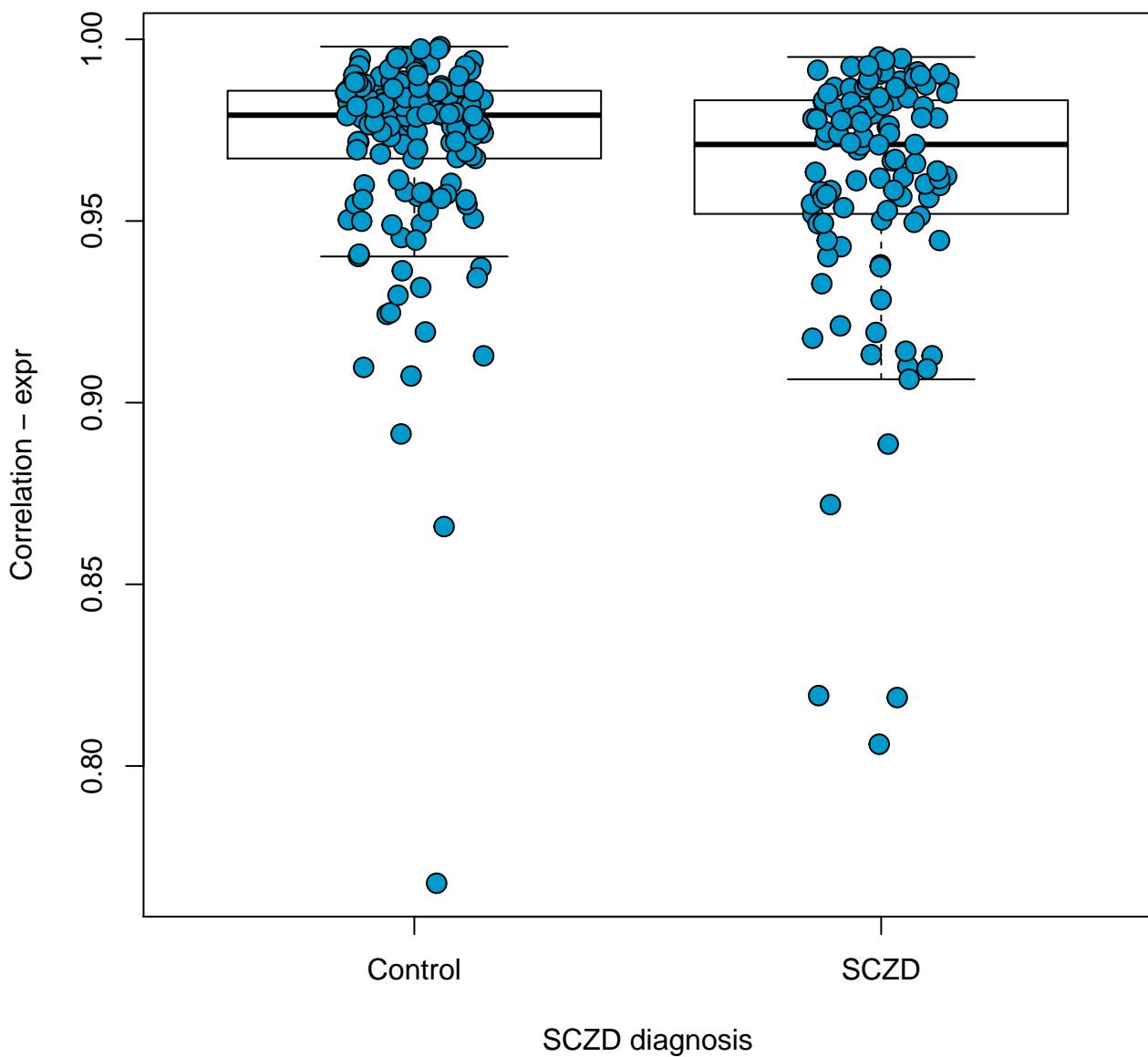
hsa05222: Small cell lung cancer
p-value: 0.555



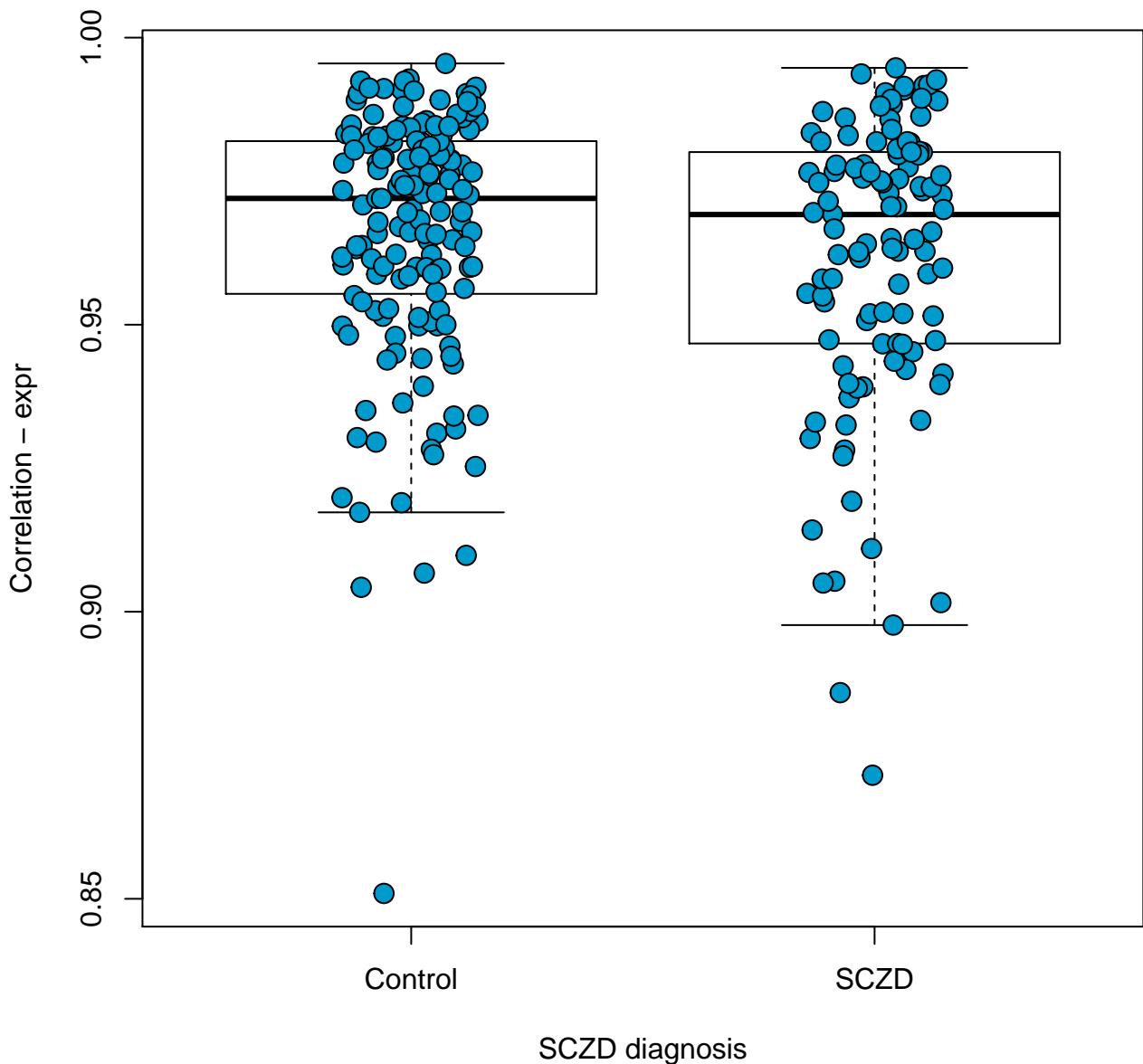
hsa05223: Non–small cell lung cancer
p-value: 0.253



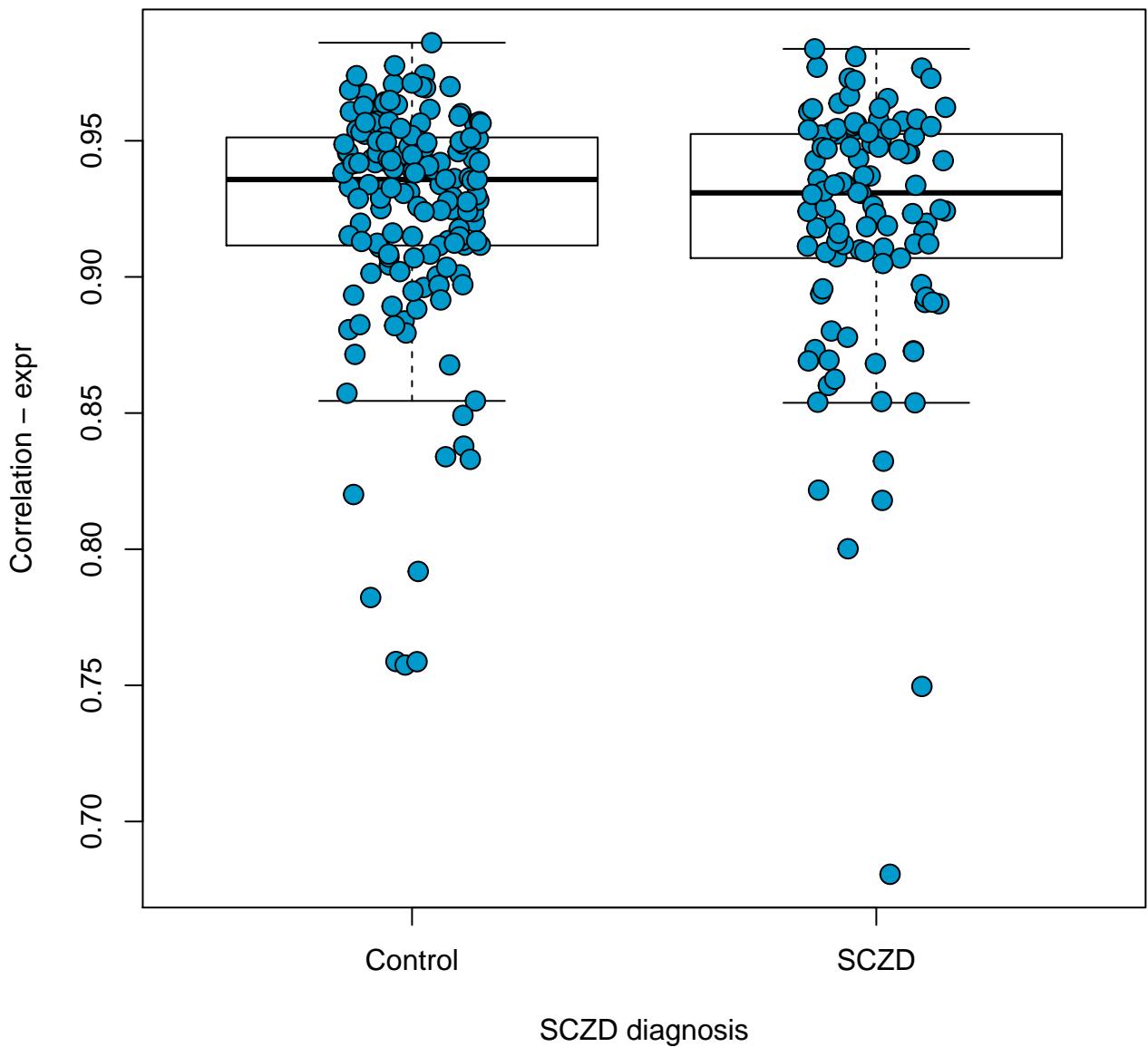
hsa05310: Asthma
p-value: 0.00983



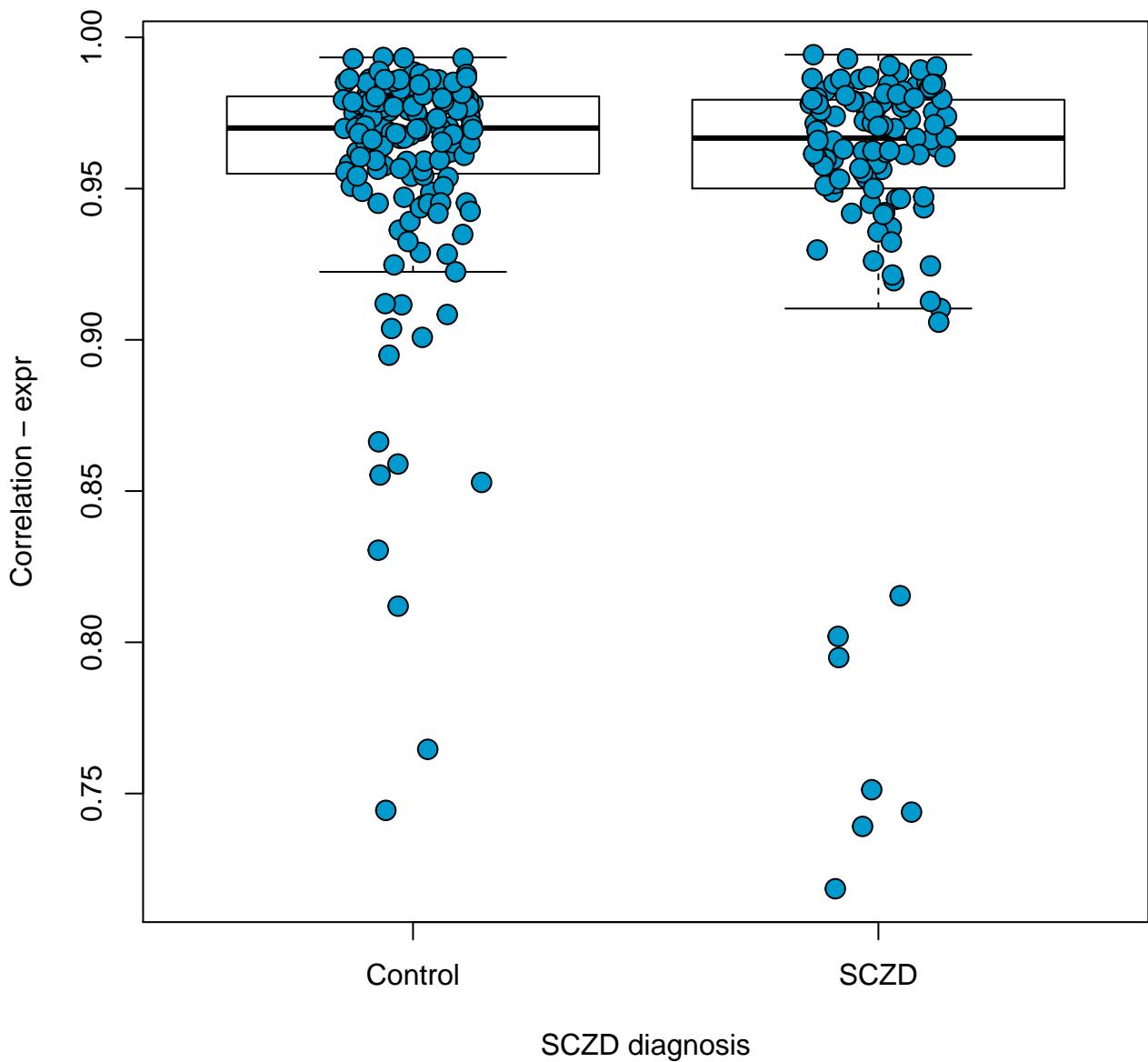
hsa05320: Autoimmune thyroid disease
p-value: 0.135



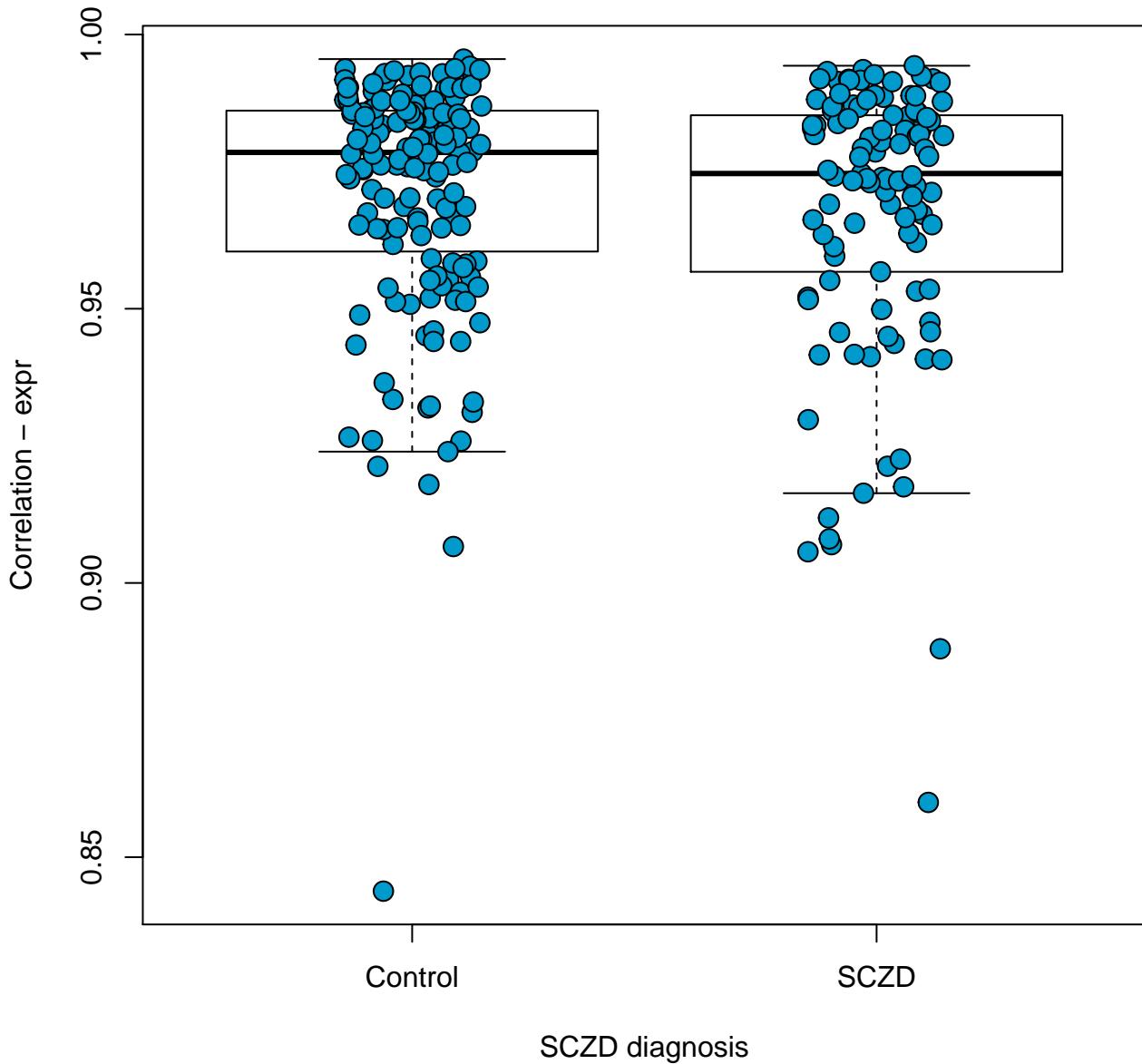
hsa05322: Systemic lupus erythematosus
p-value: 0.384



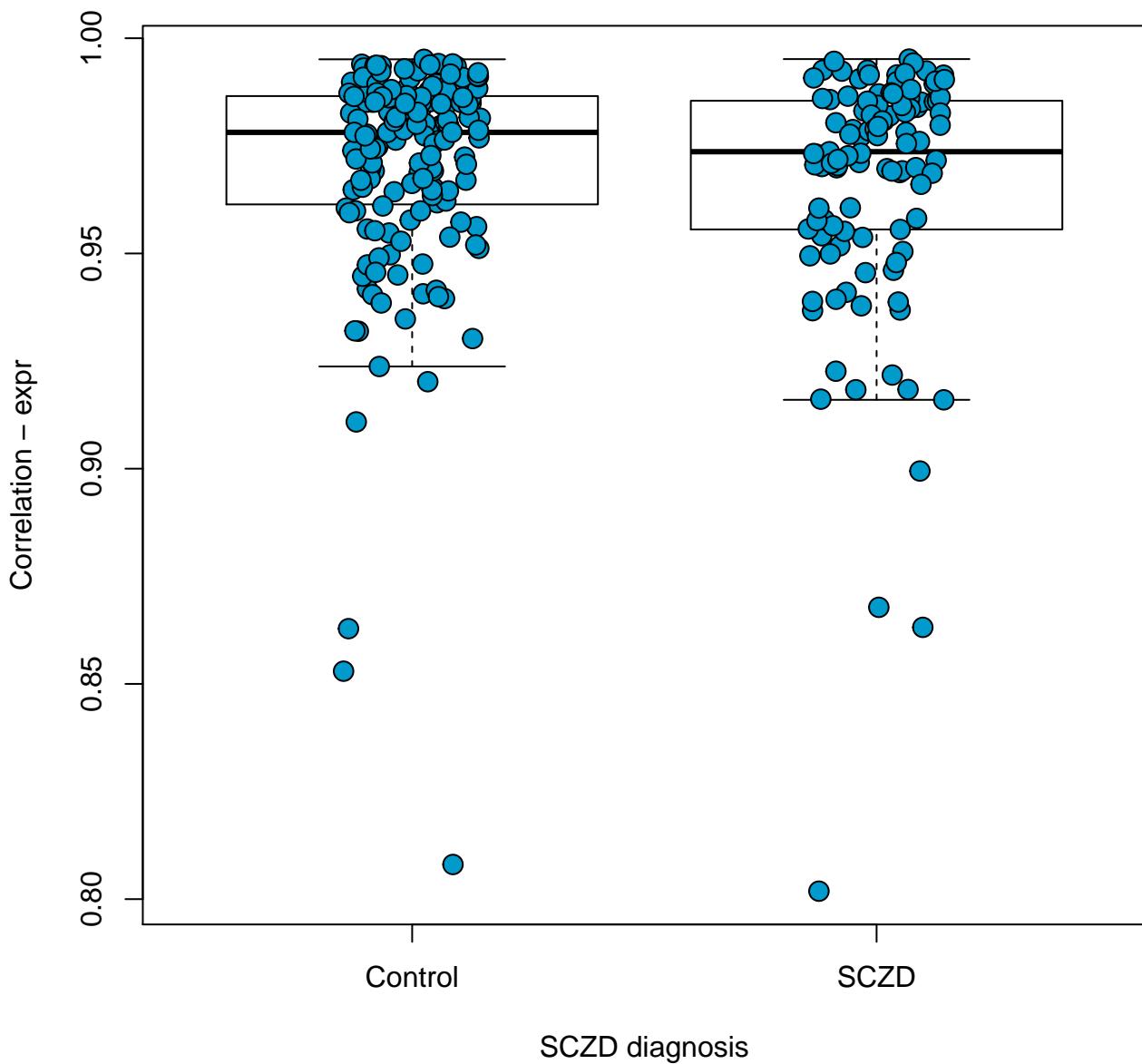
hsa05323: Rheumatoid arthritis
p-value: 0.209



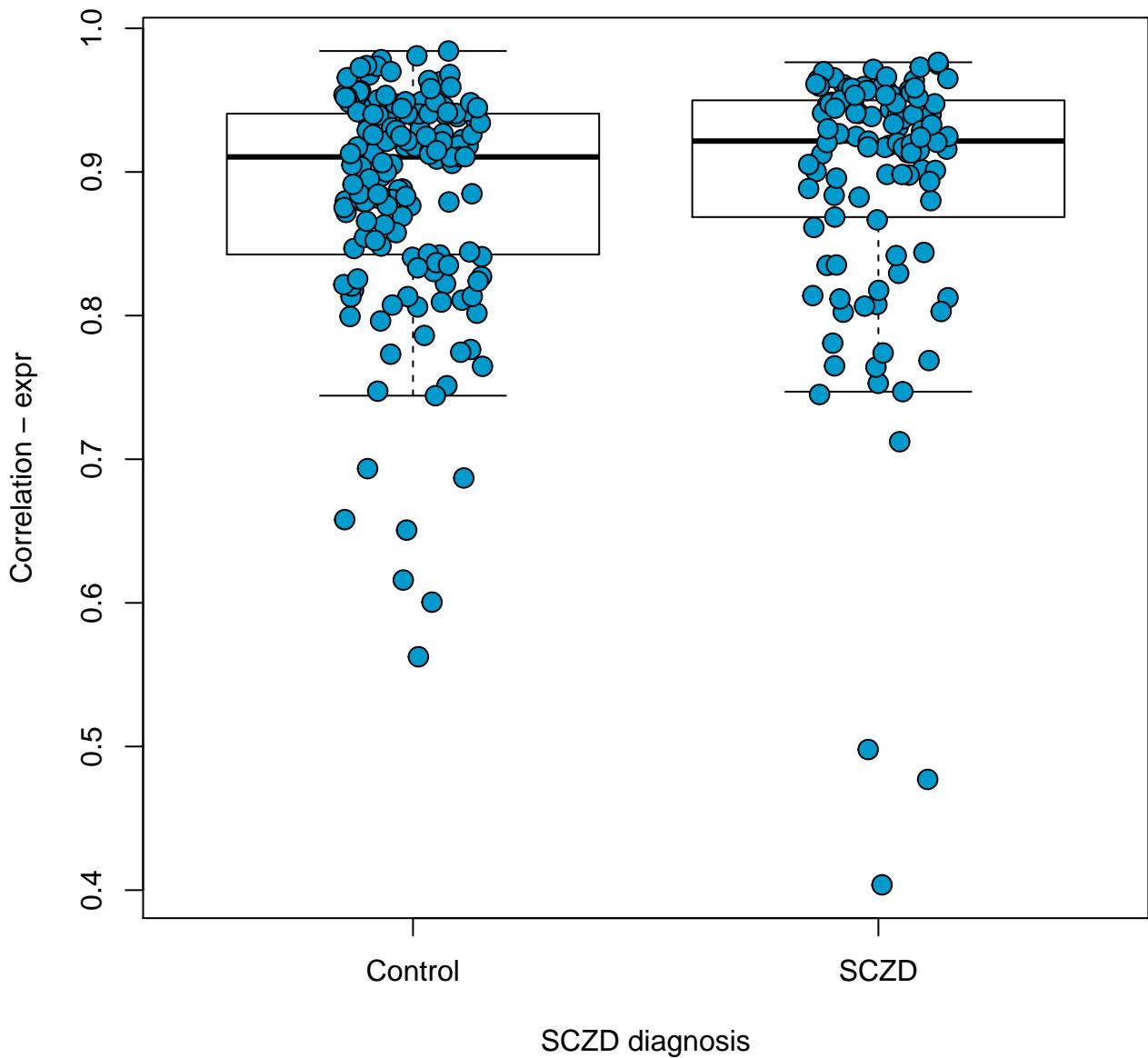
hsa05330: Allograft rejection
p-value: 0.234



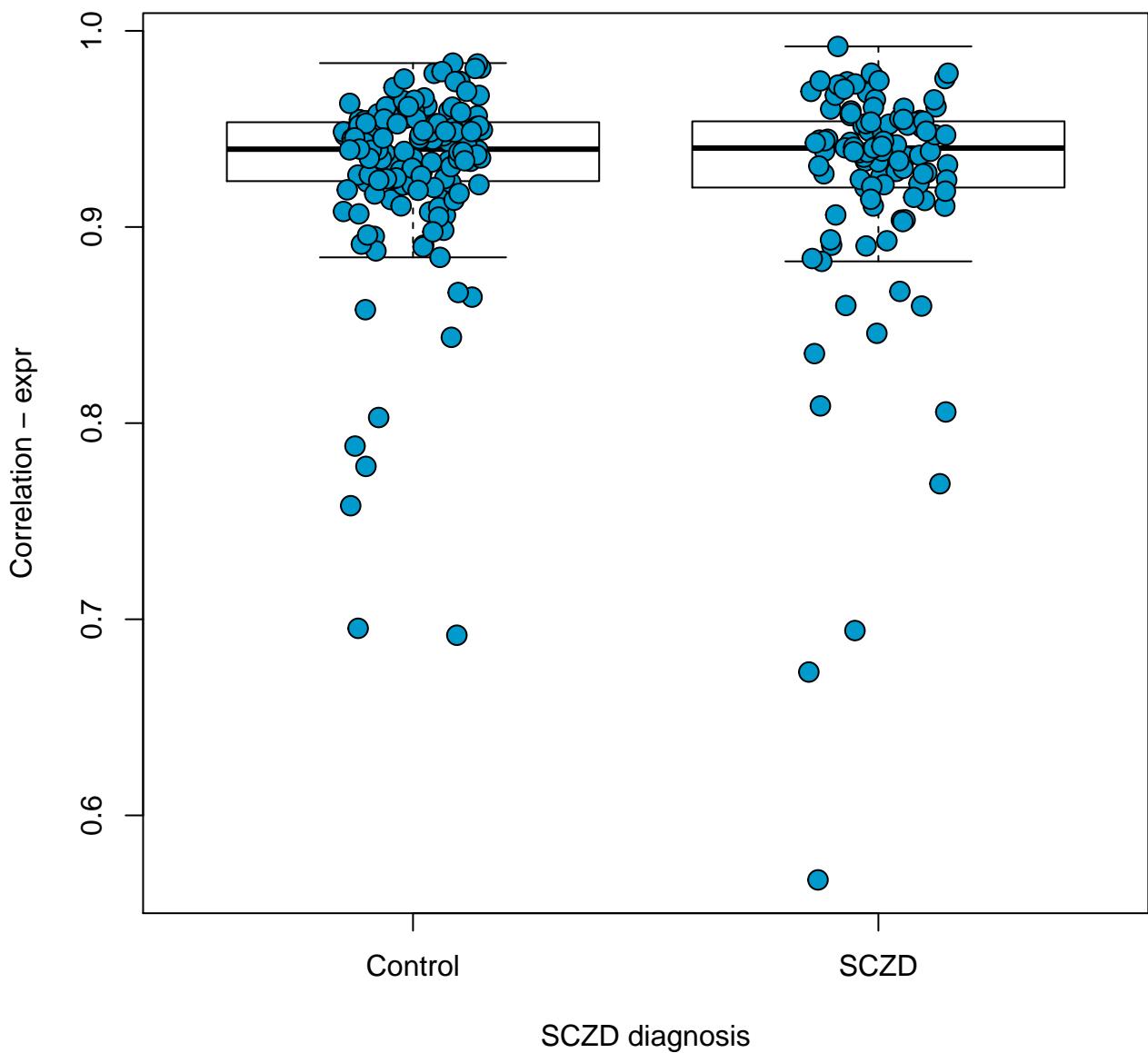
hsa05332: Graft-versus-host disease
p-value: 0.212



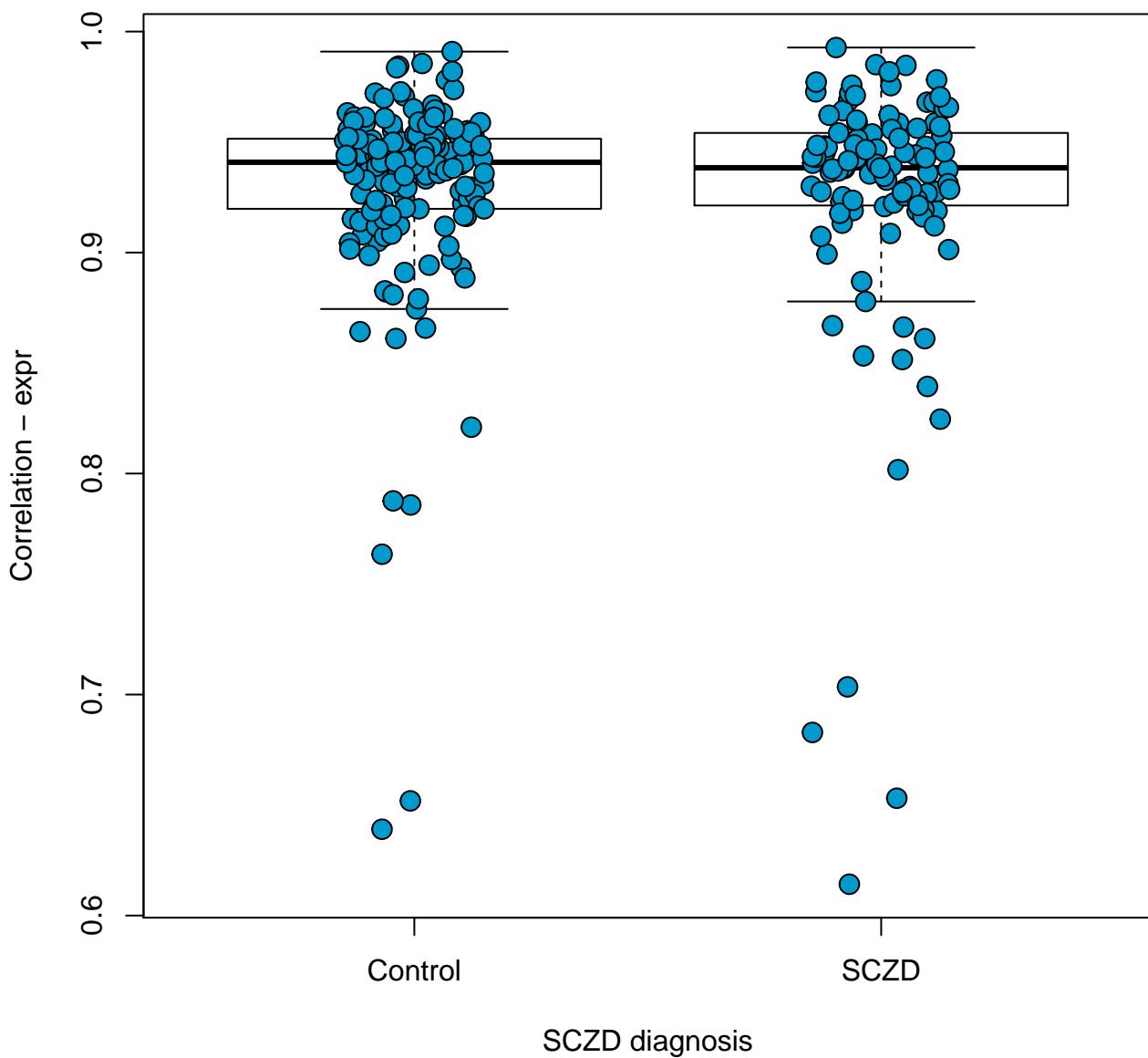
hsa05340: Primary immunodeficiency
p-value: 0.518



hsa05410: Hypertrophic cardiomyopathy (HCM)
p-value: 0.315

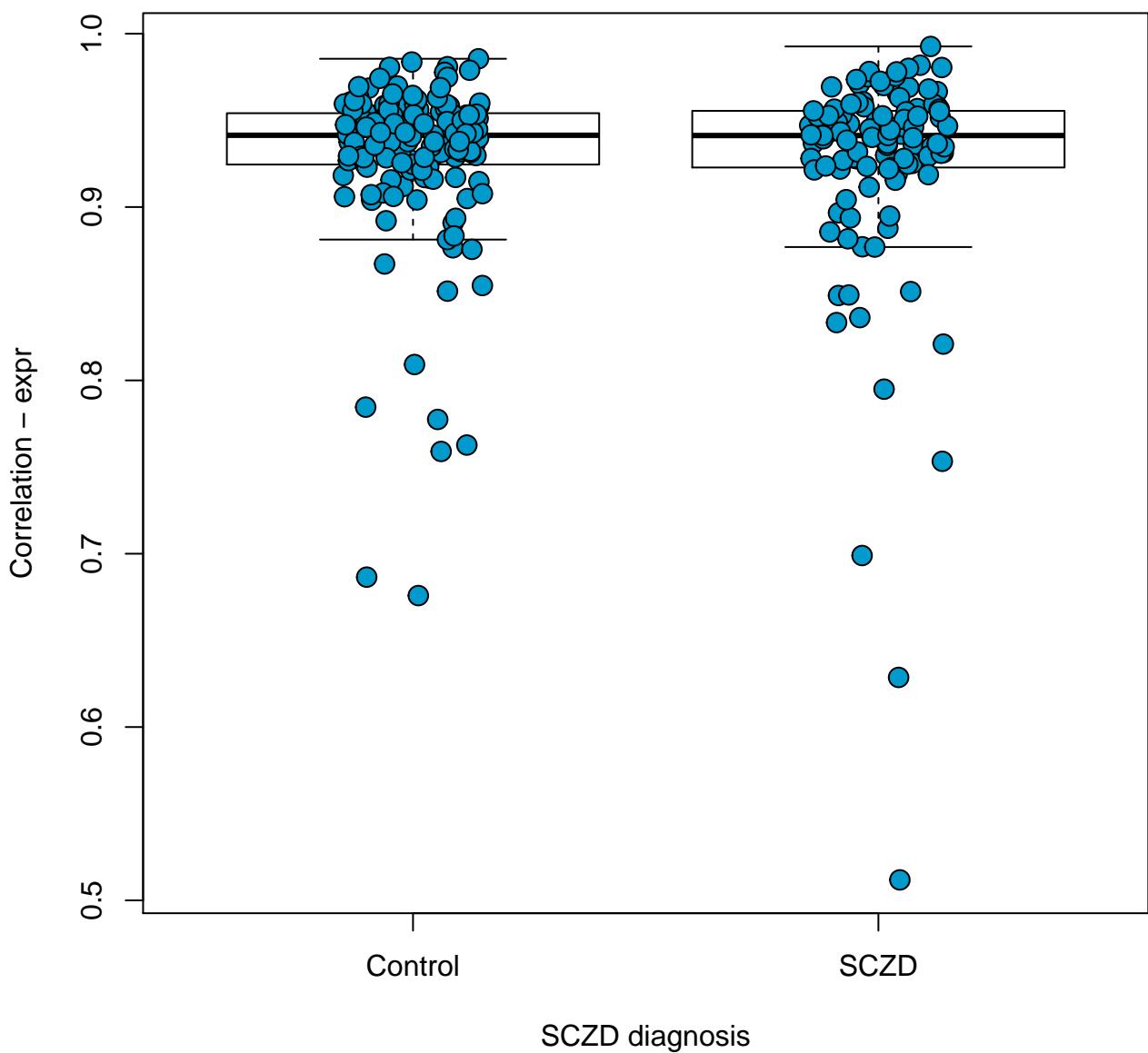


hsa05412: Arrhythmogenic right ventricular cardiomyopathy (ARVC)
p-value: 0.532

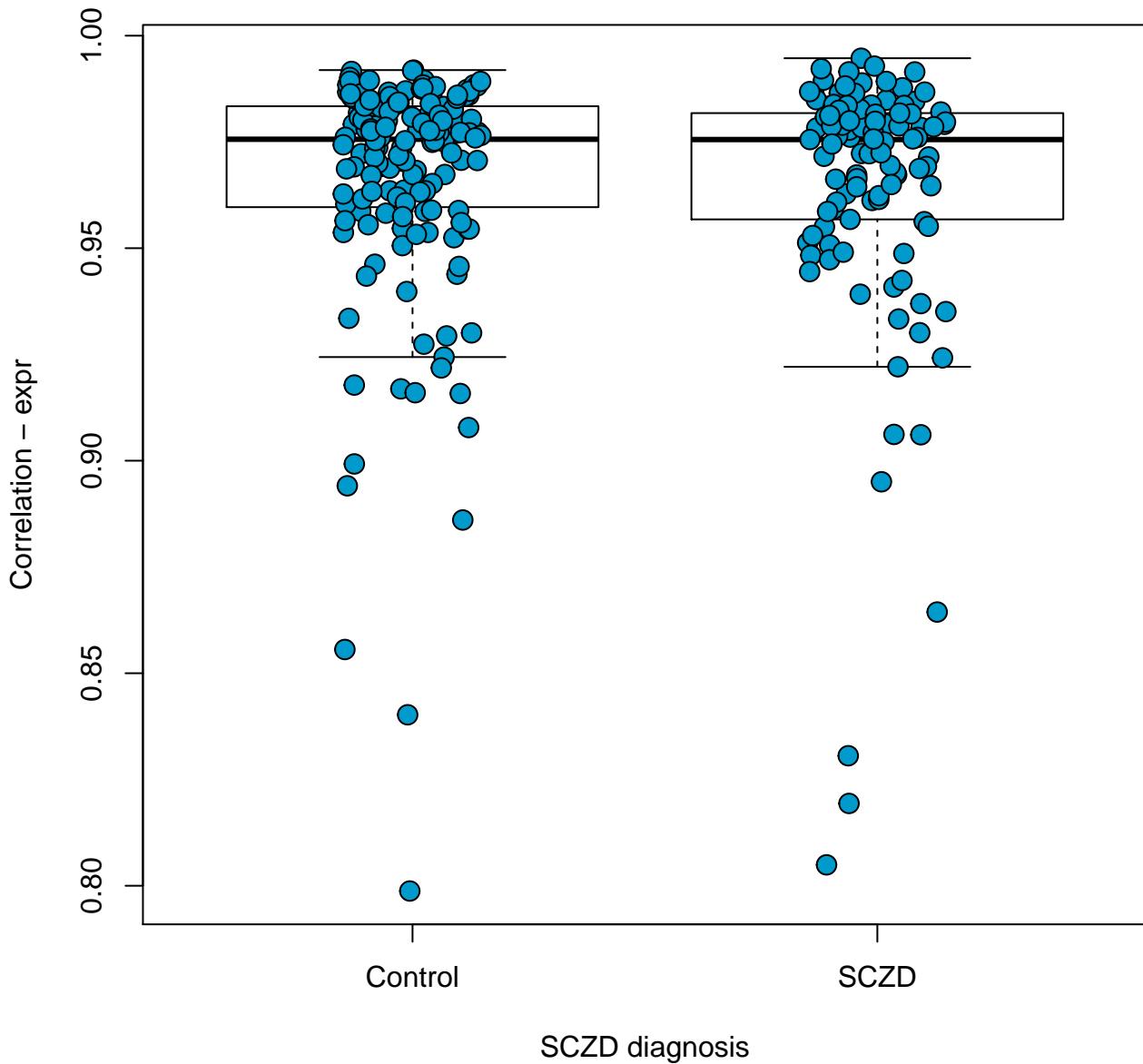


hsa05414: Dilated cardiomyopathy

p-value: 0.36

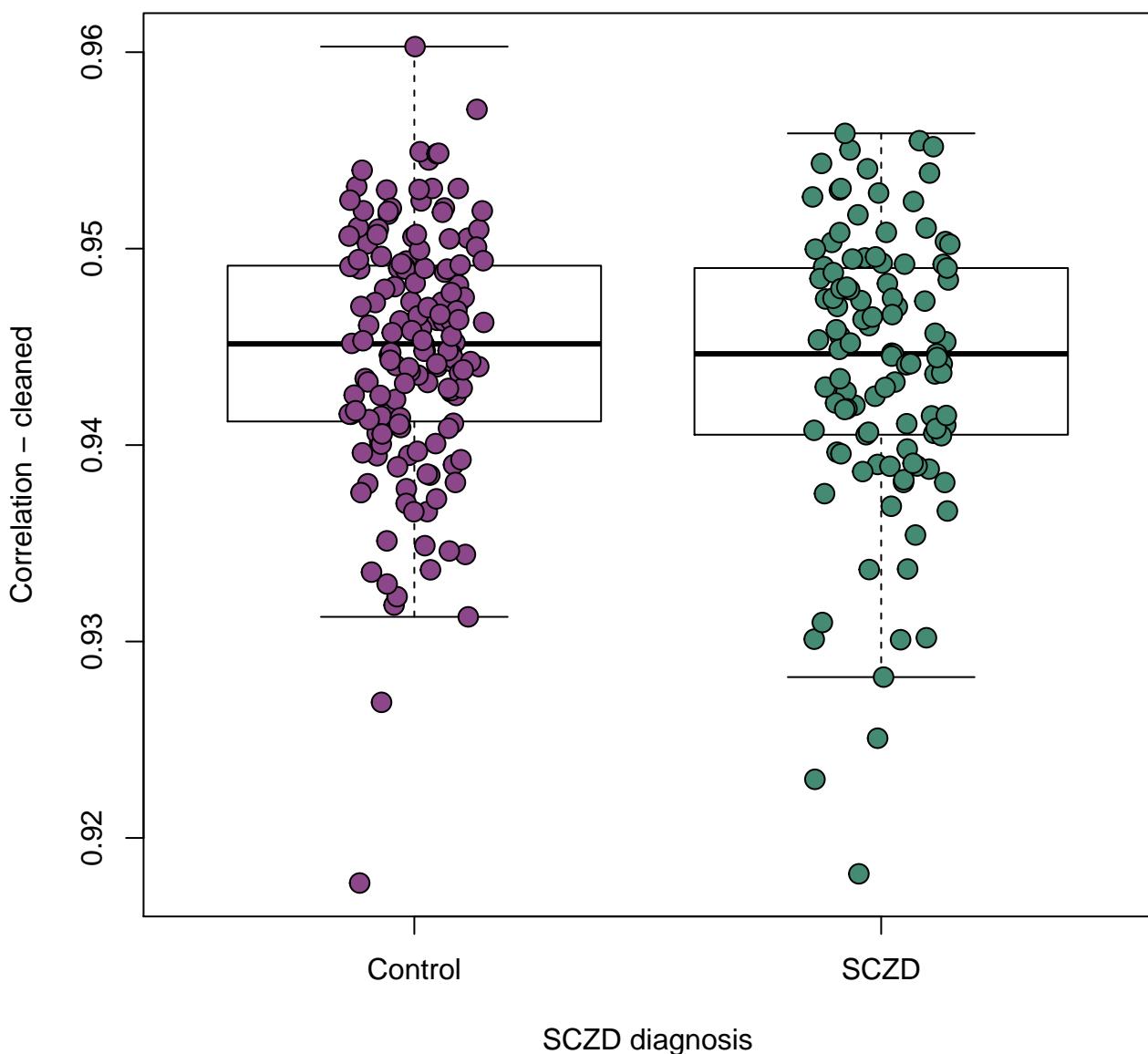


hsa05416: Viral myocarditis
p-value: 0.491

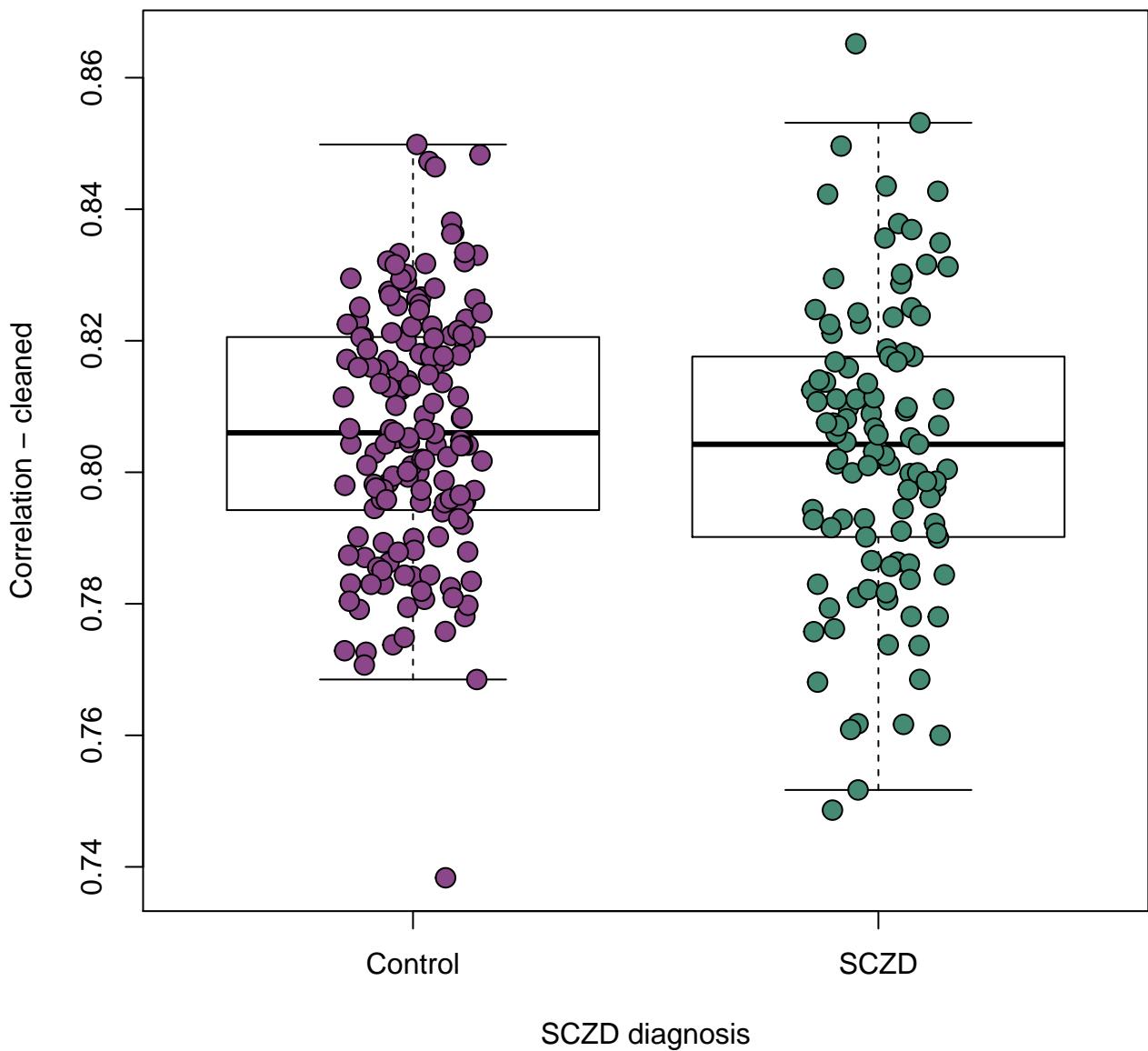


hsa00010: Glycolysis / Gluconeogenesis

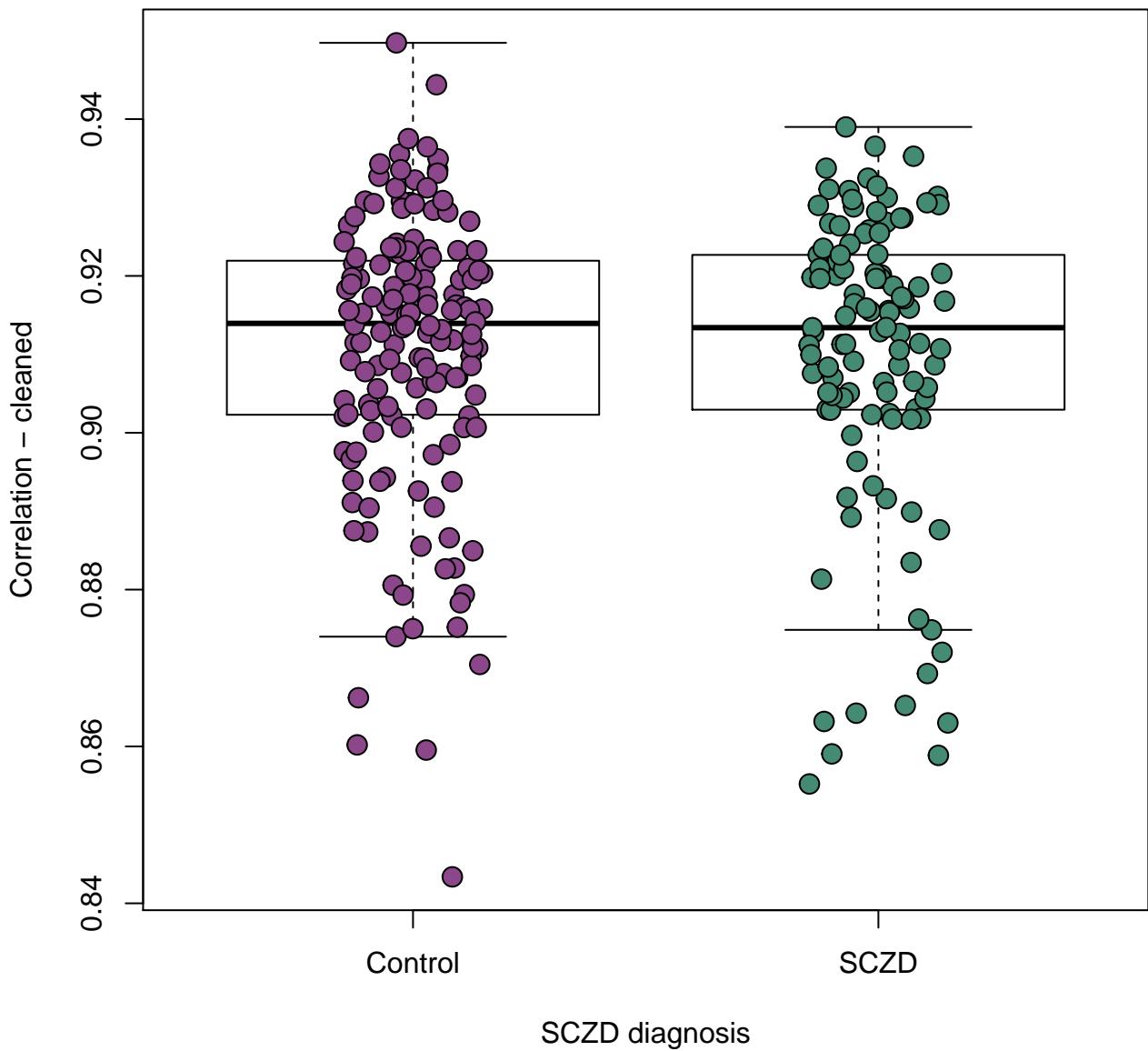
p-value: 0.304



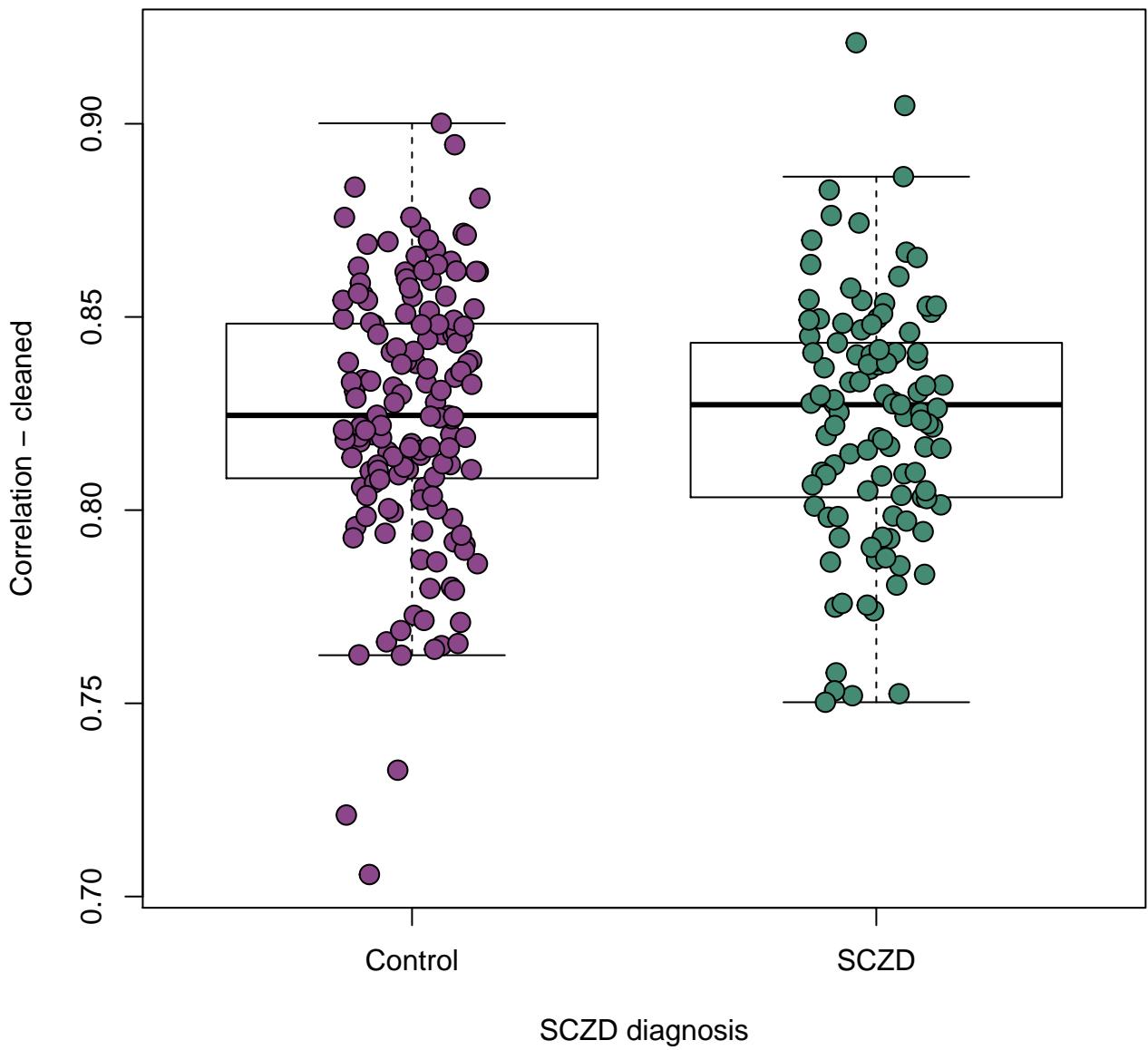
hsa00020: Citrate cycle (TCA cycle)
p-value: 0.282



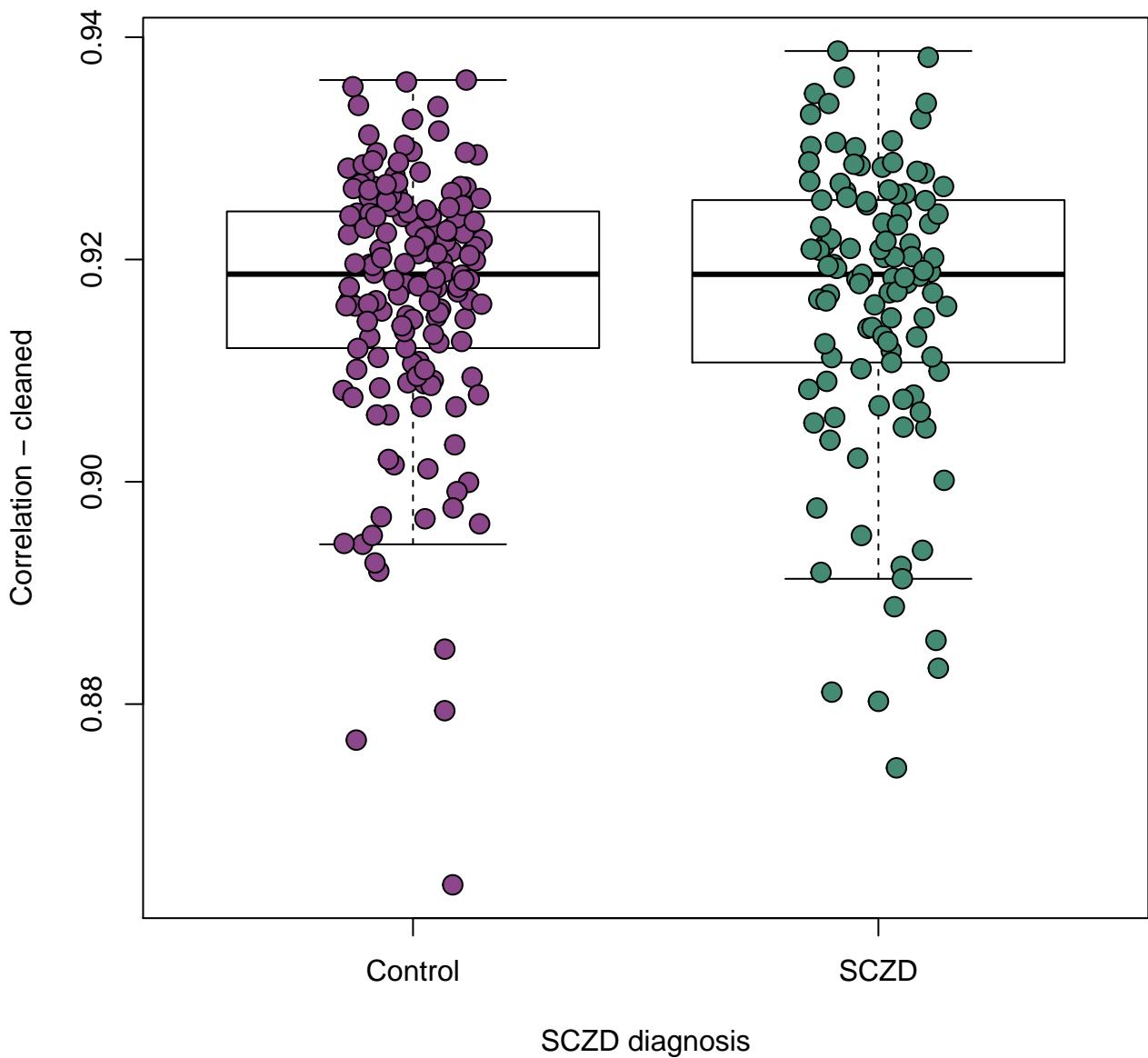
hsa00030: Pentose phosphate pathway
p-value: 0.652



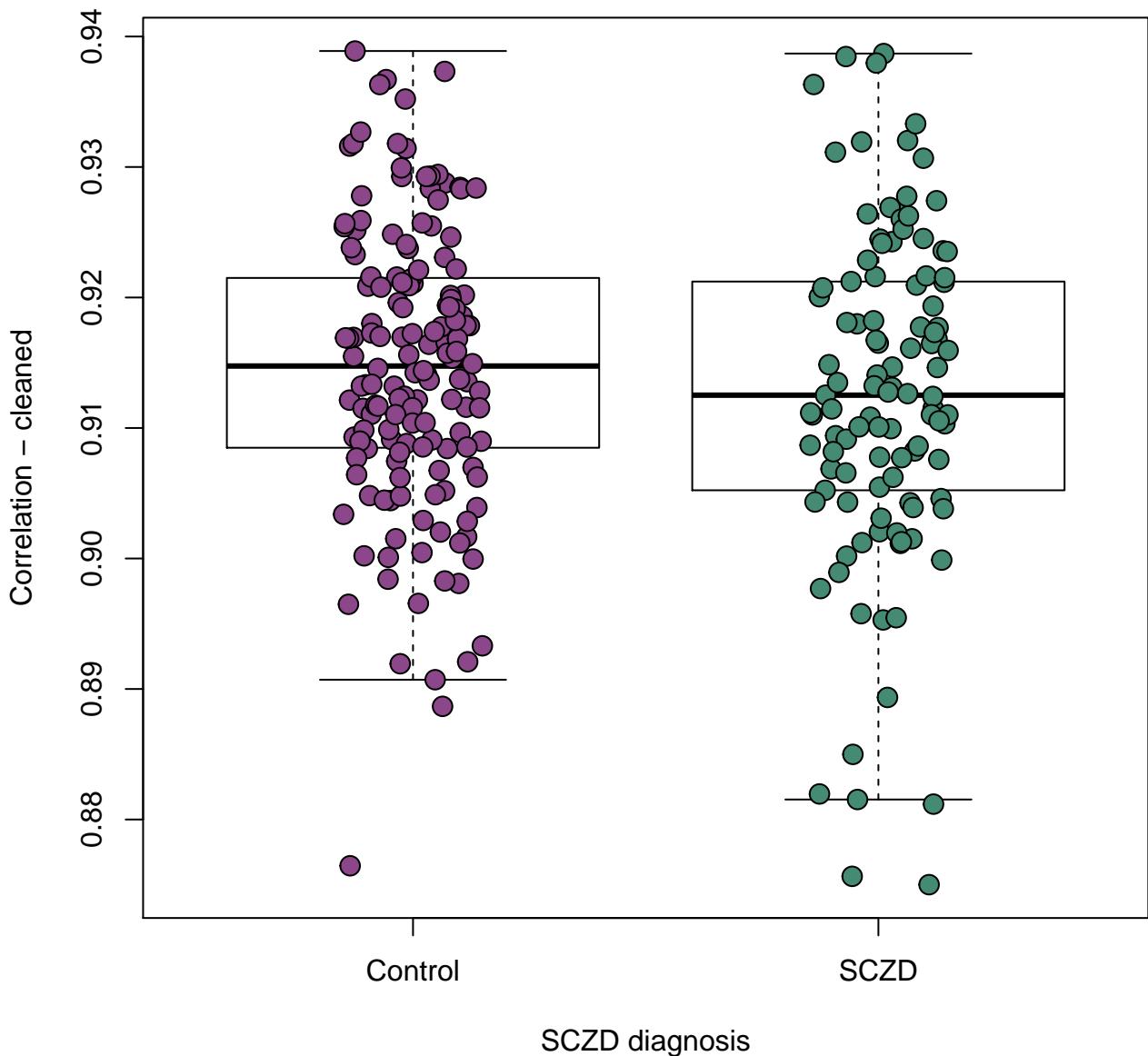
hsa00040: Pentose and glucuronate interconversions
p-value: 0.77



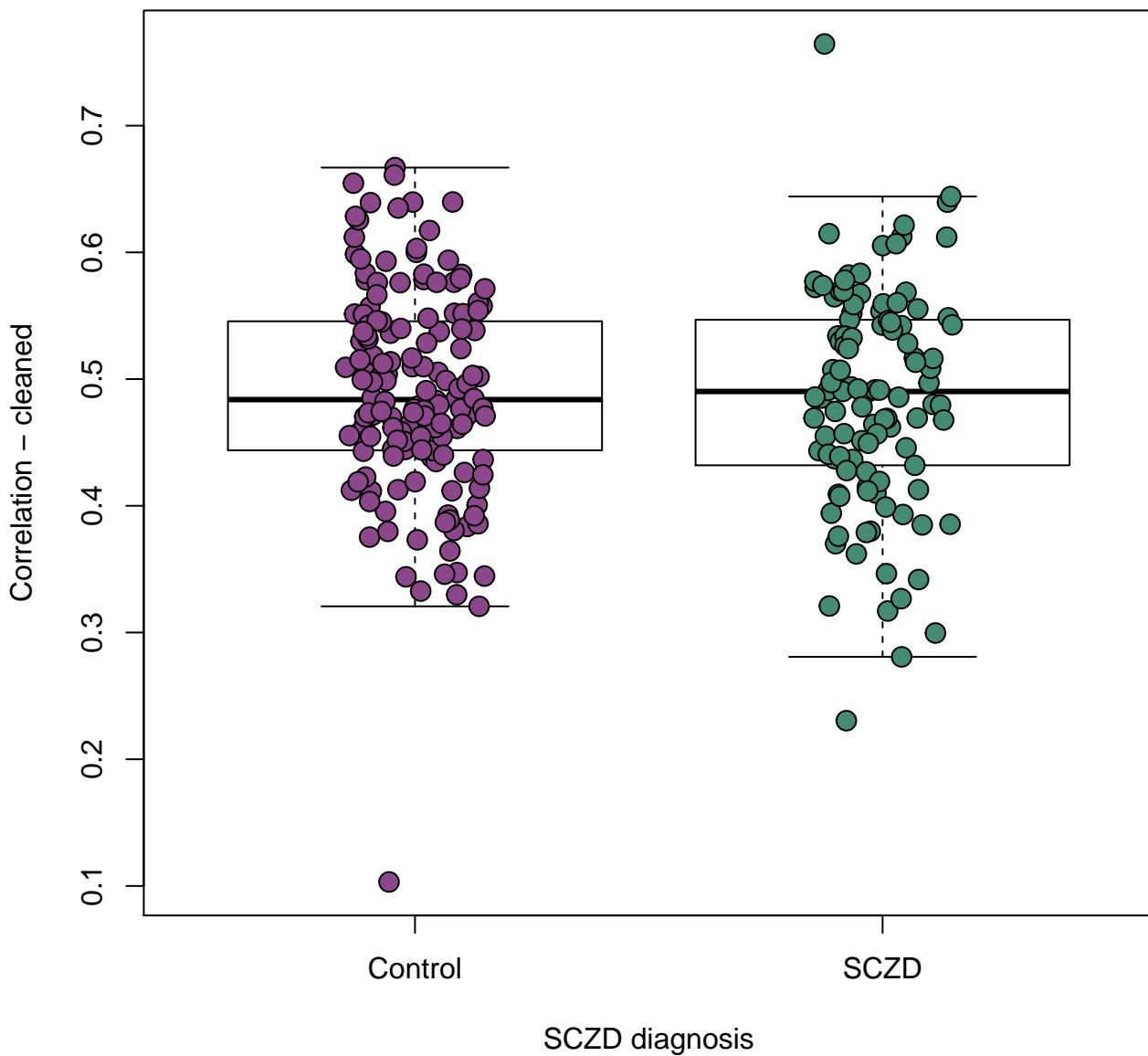
hsa00051: Fructose and mannose metabolism
p-value: 0.756



hsa00052: Galactose metabolism
p-value: 0.126

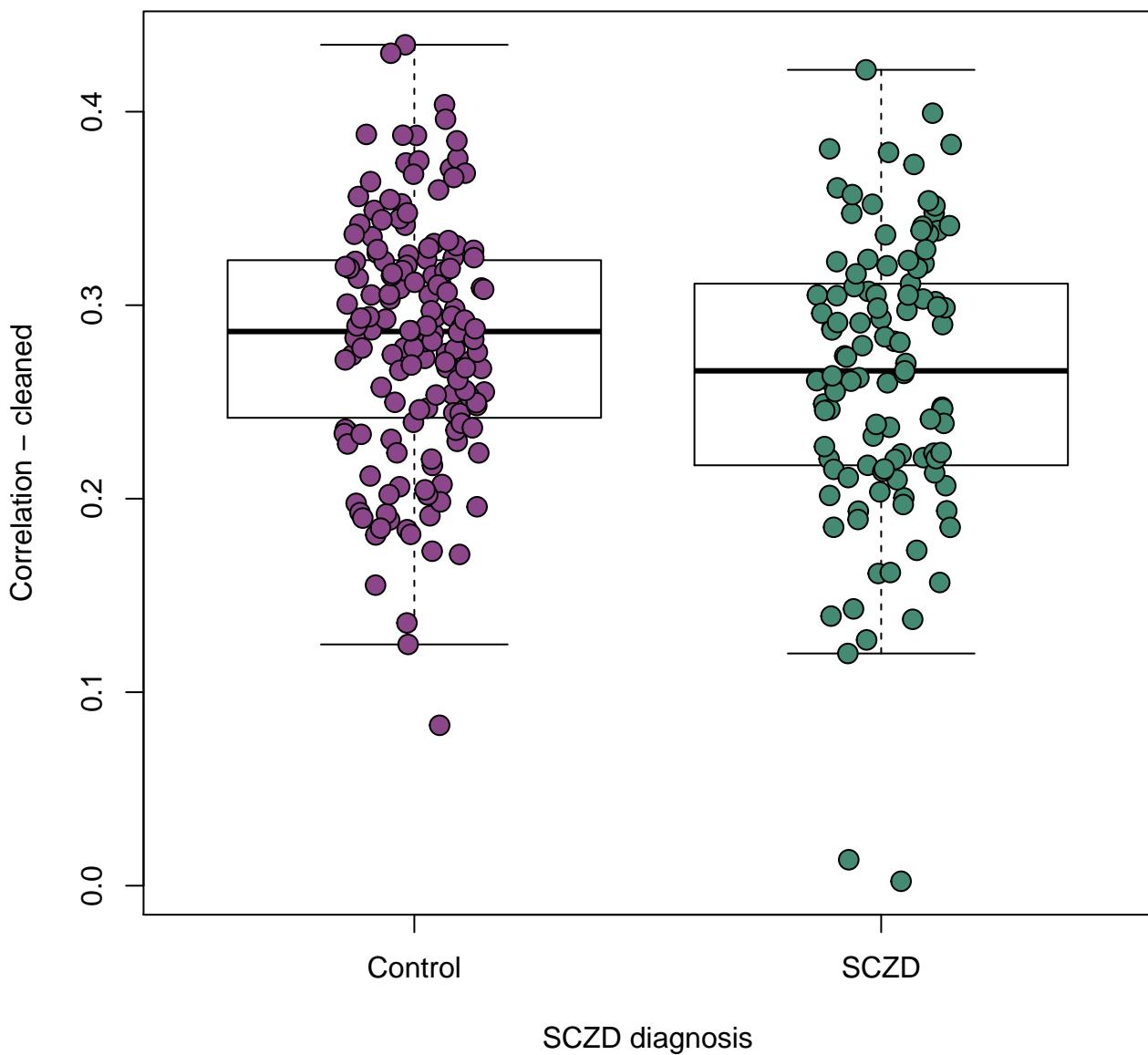


hsa00053: Ascorbate and aldarate metabolism
p-value: 0.714

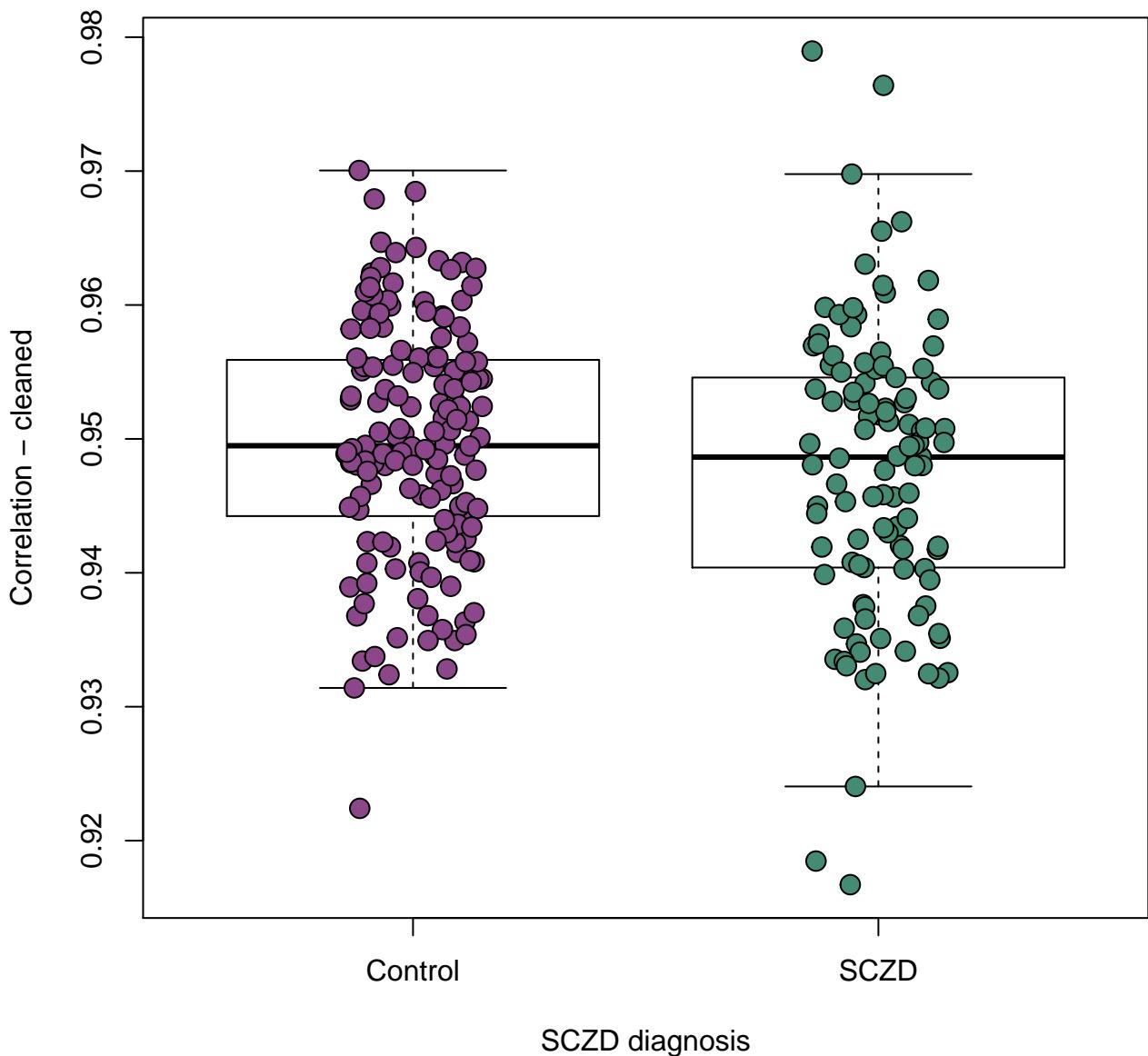


hsa00061: Fatty acid biosynthesis

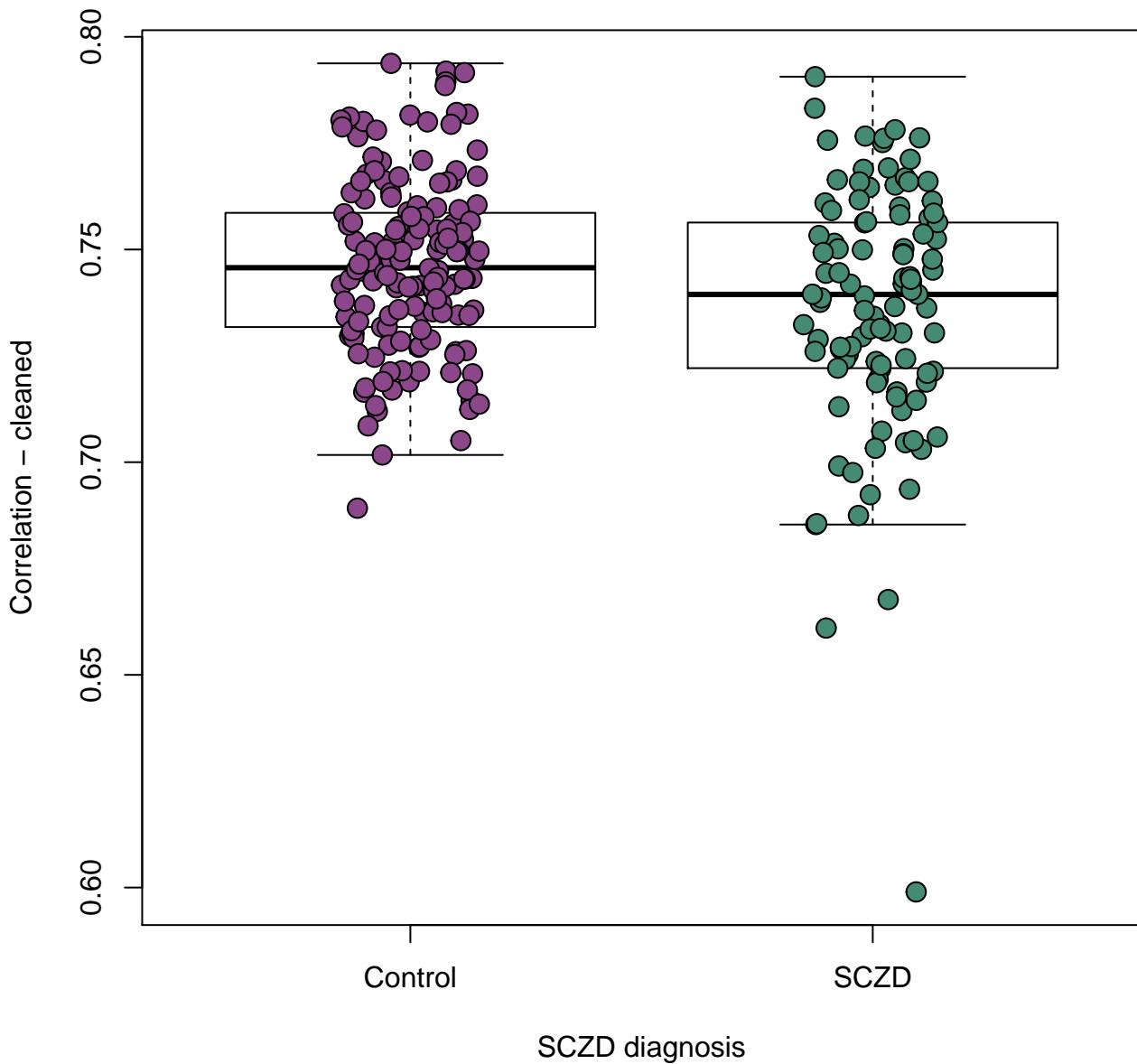
p-value: 0.0225



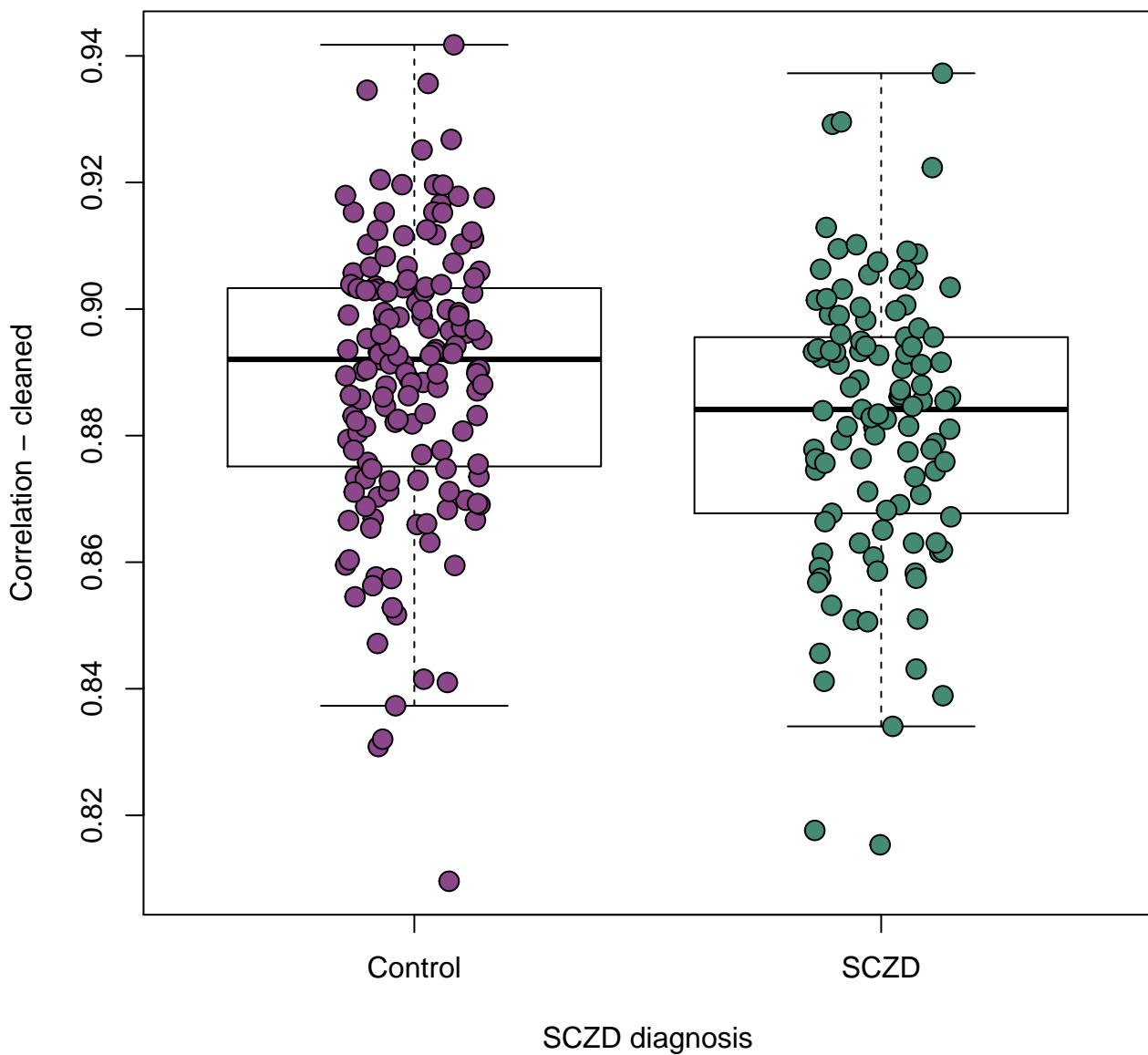
hsa00062: Fatty acid elongation
p-value: 0.0622



hsa00071: Fatty acid degradation
p-value: 0.000806

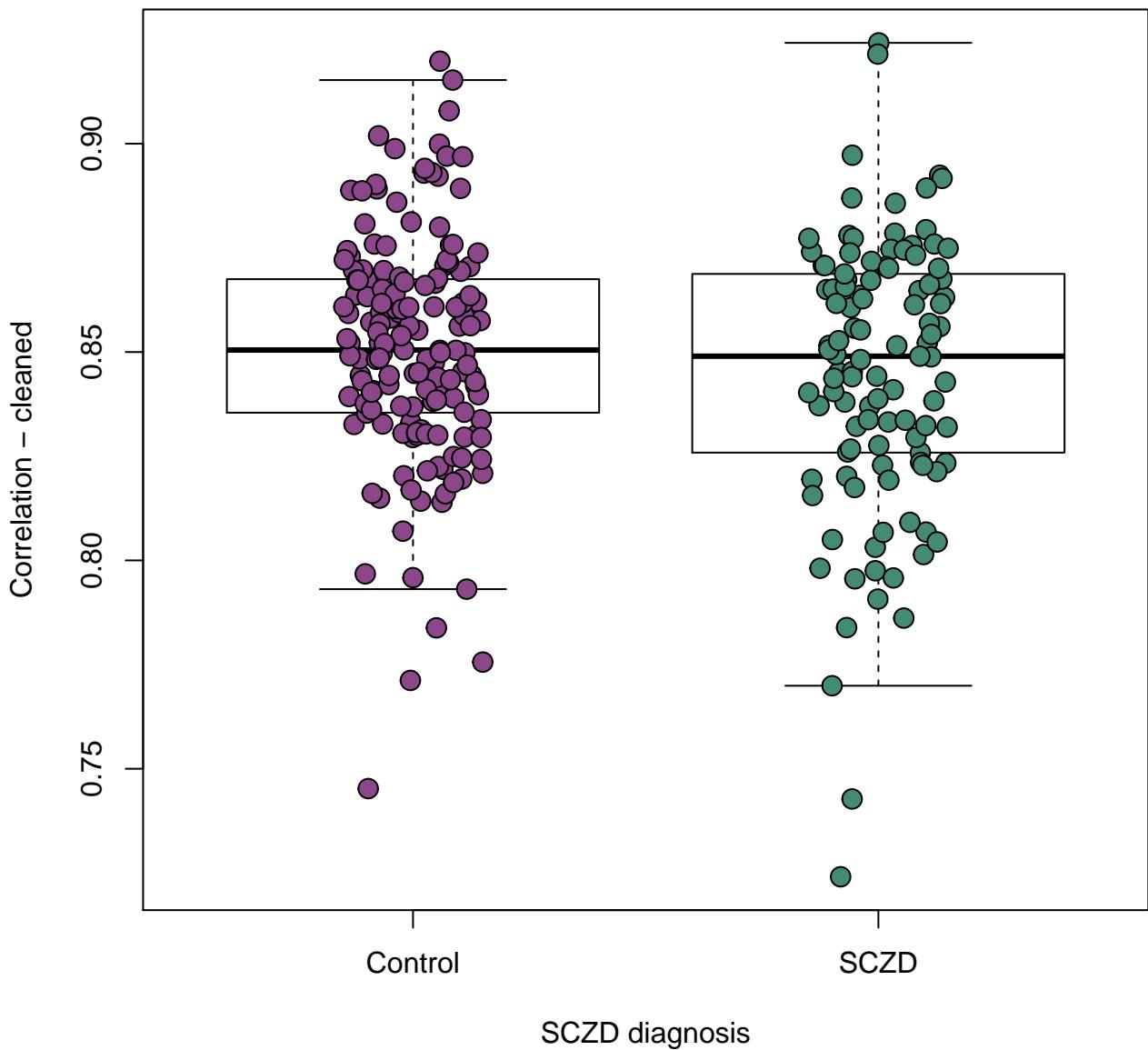


hsa00072: Synthesis and degradation of ketone bodies
p-value: 0.00932

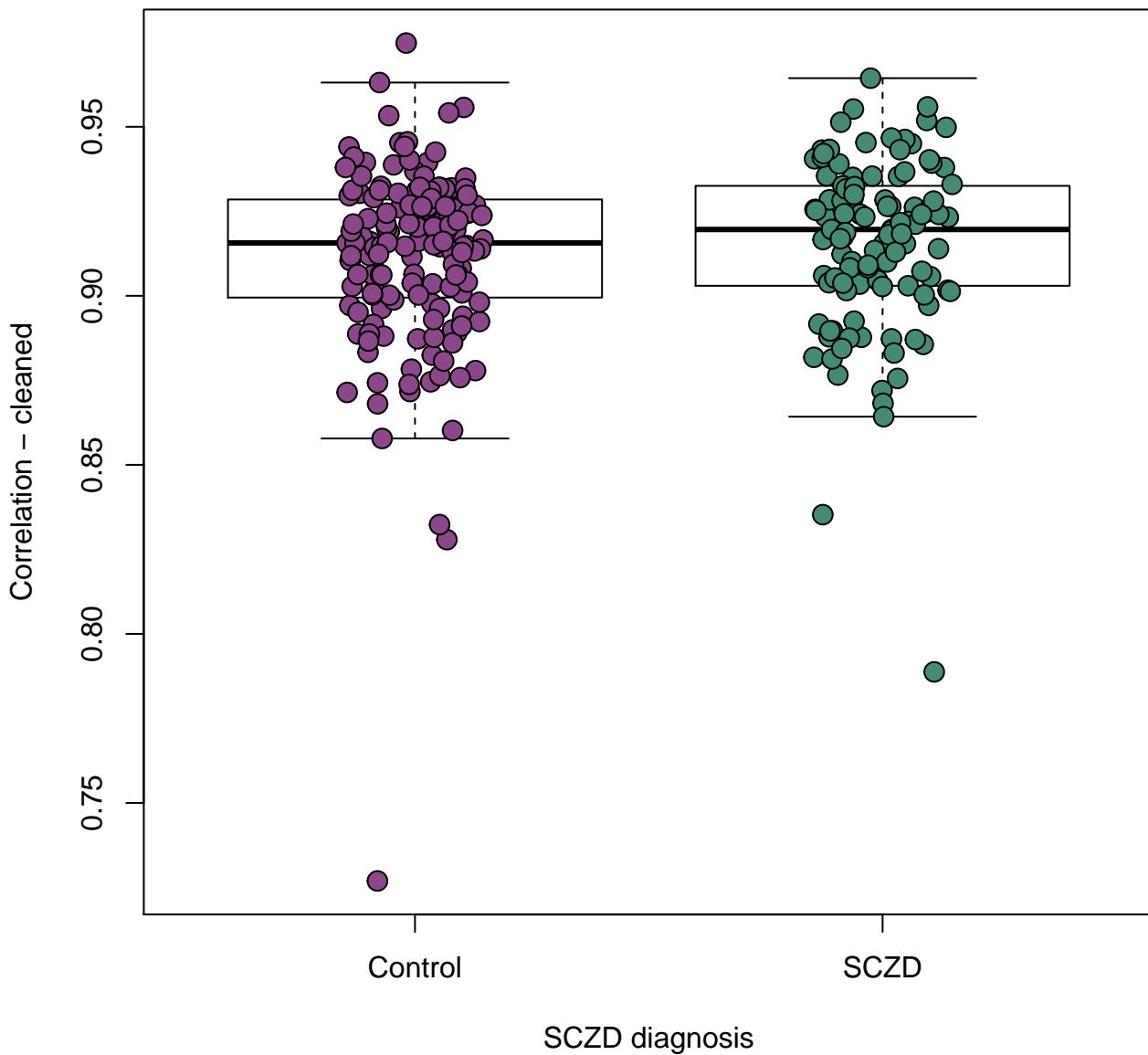


hsa00100: Steroid biosynthesis

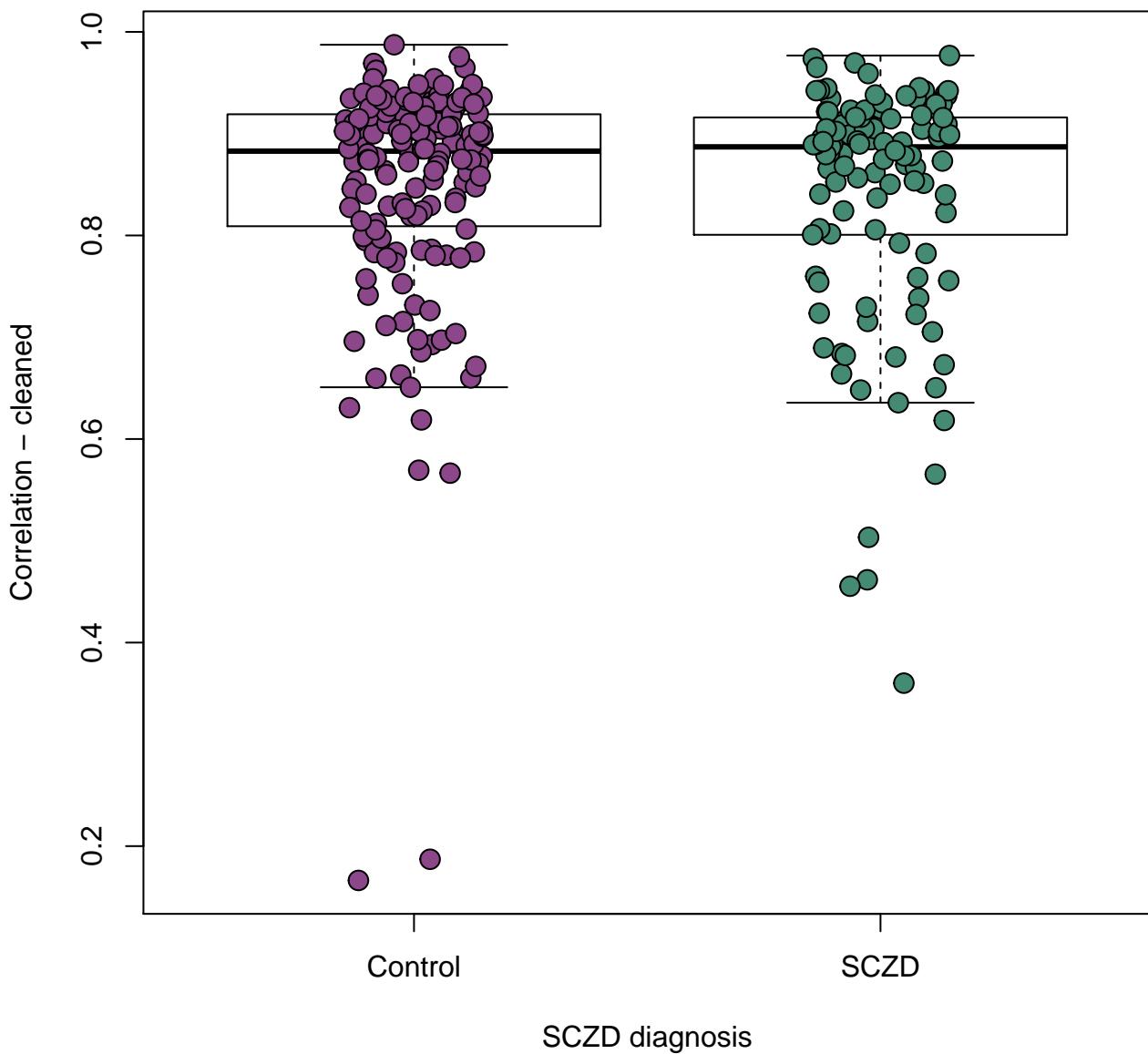
p-value: 0.106



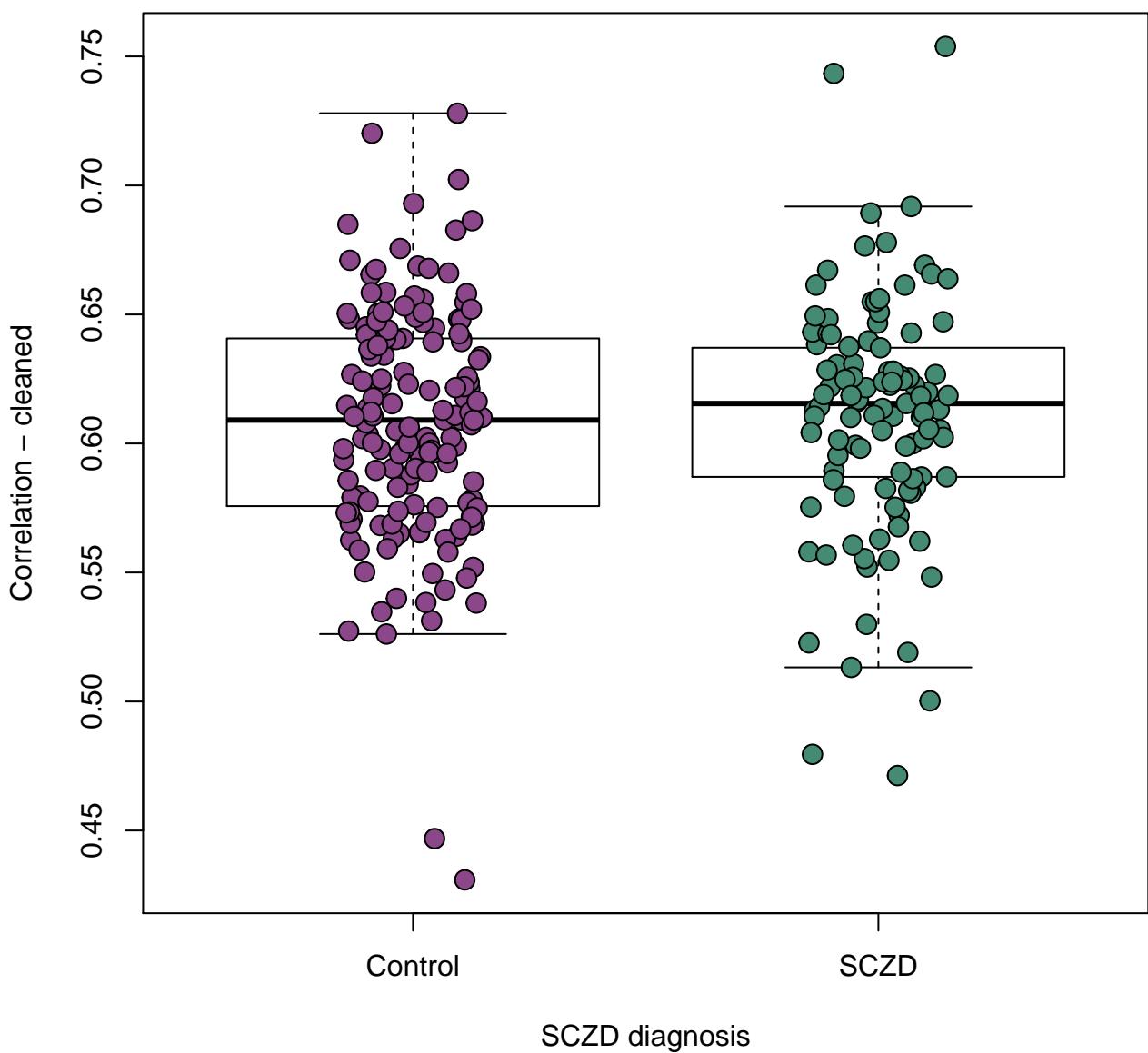
hsa00120: Primary bile acid biosynthesis
p-value: 0.237



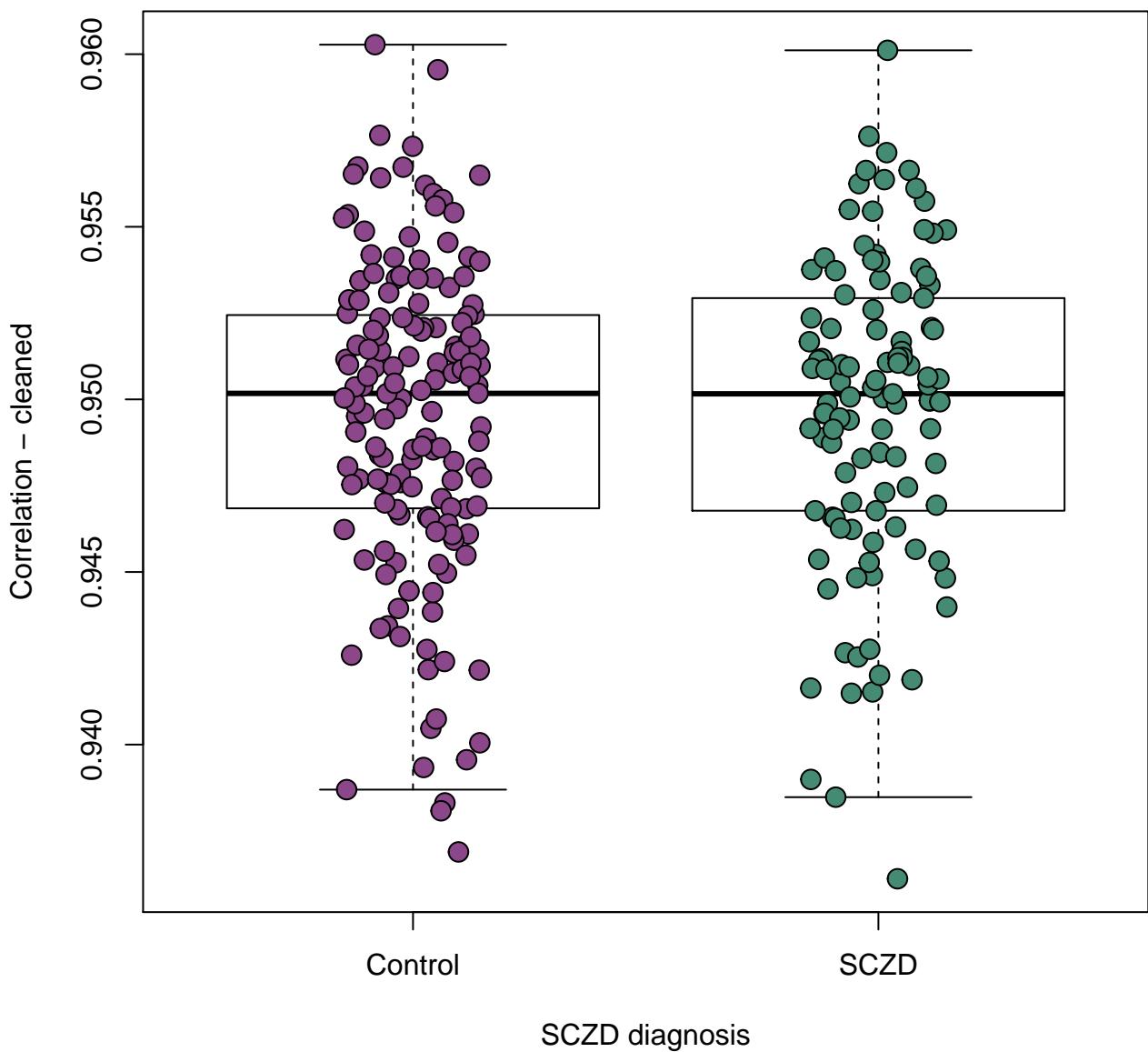
hsa00130: Ubiquinone and other terpenoid–quinone biosynthesis
p-value: 0.562



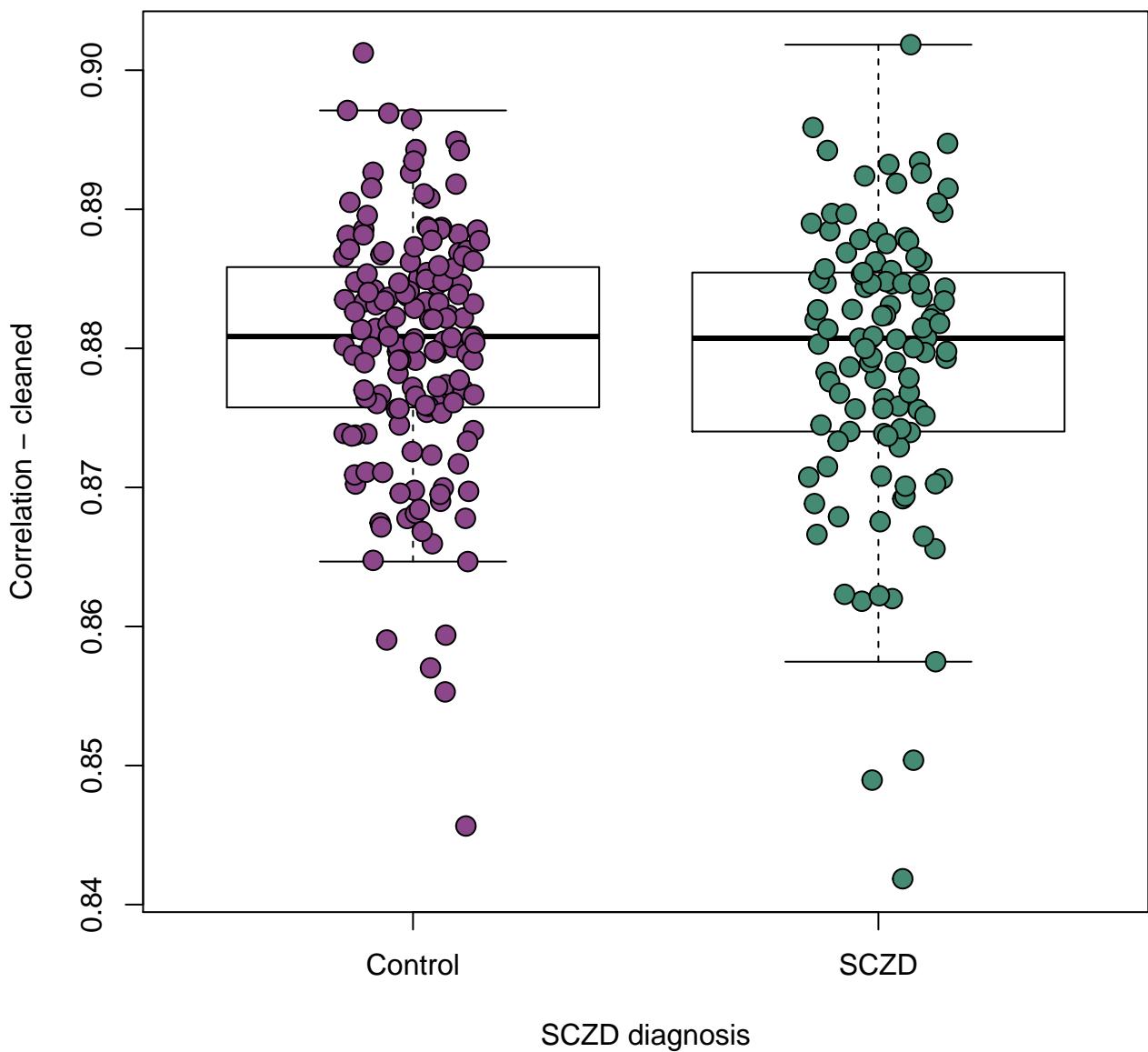
hsa00140: Steroid hormone biosynthesis
p-value: 0.593



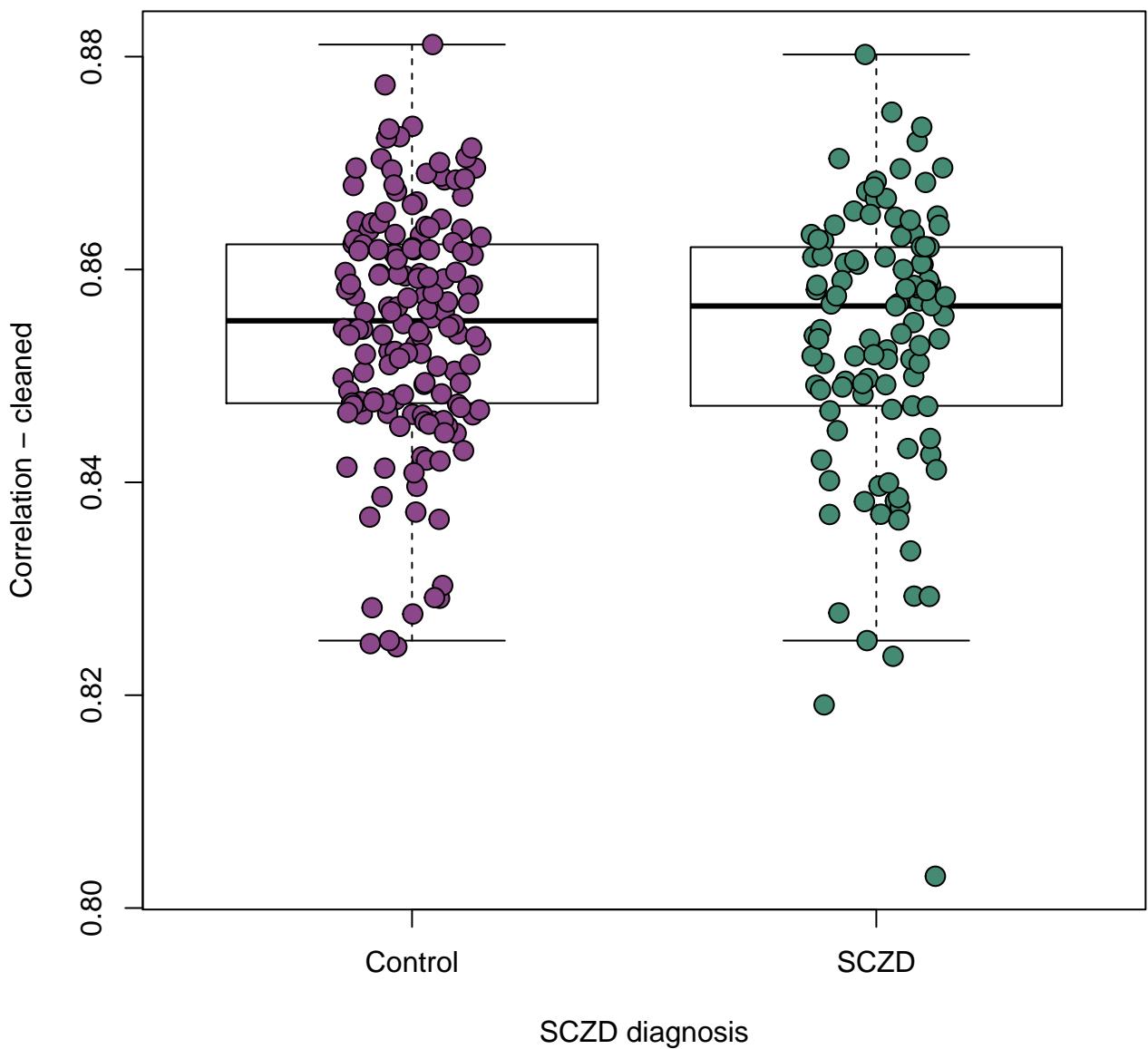
hsa00190: Oxidative phosphorylation
p-value: 0.734



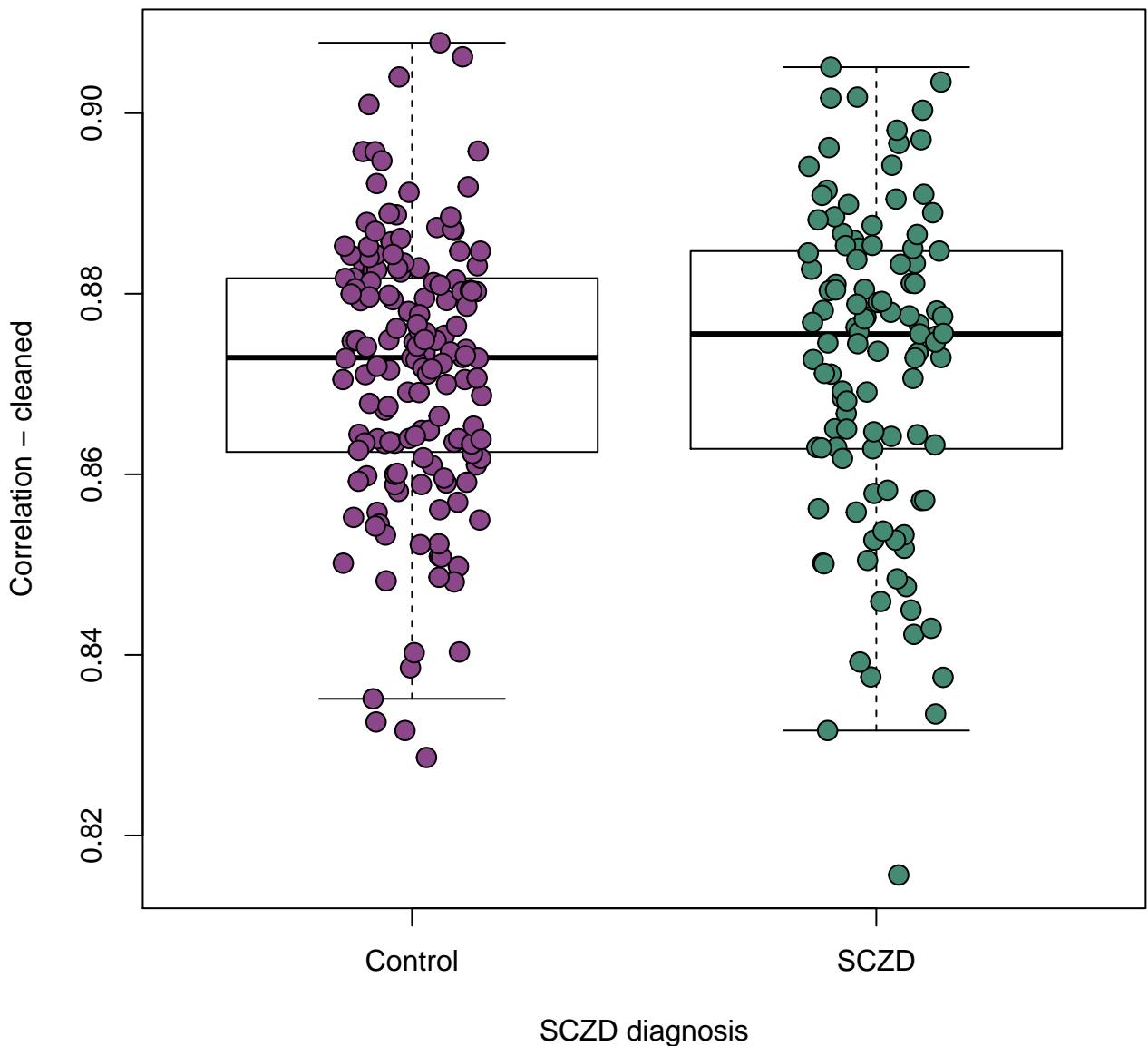
hsa00230: Purine metabolism
p-value: 0.415



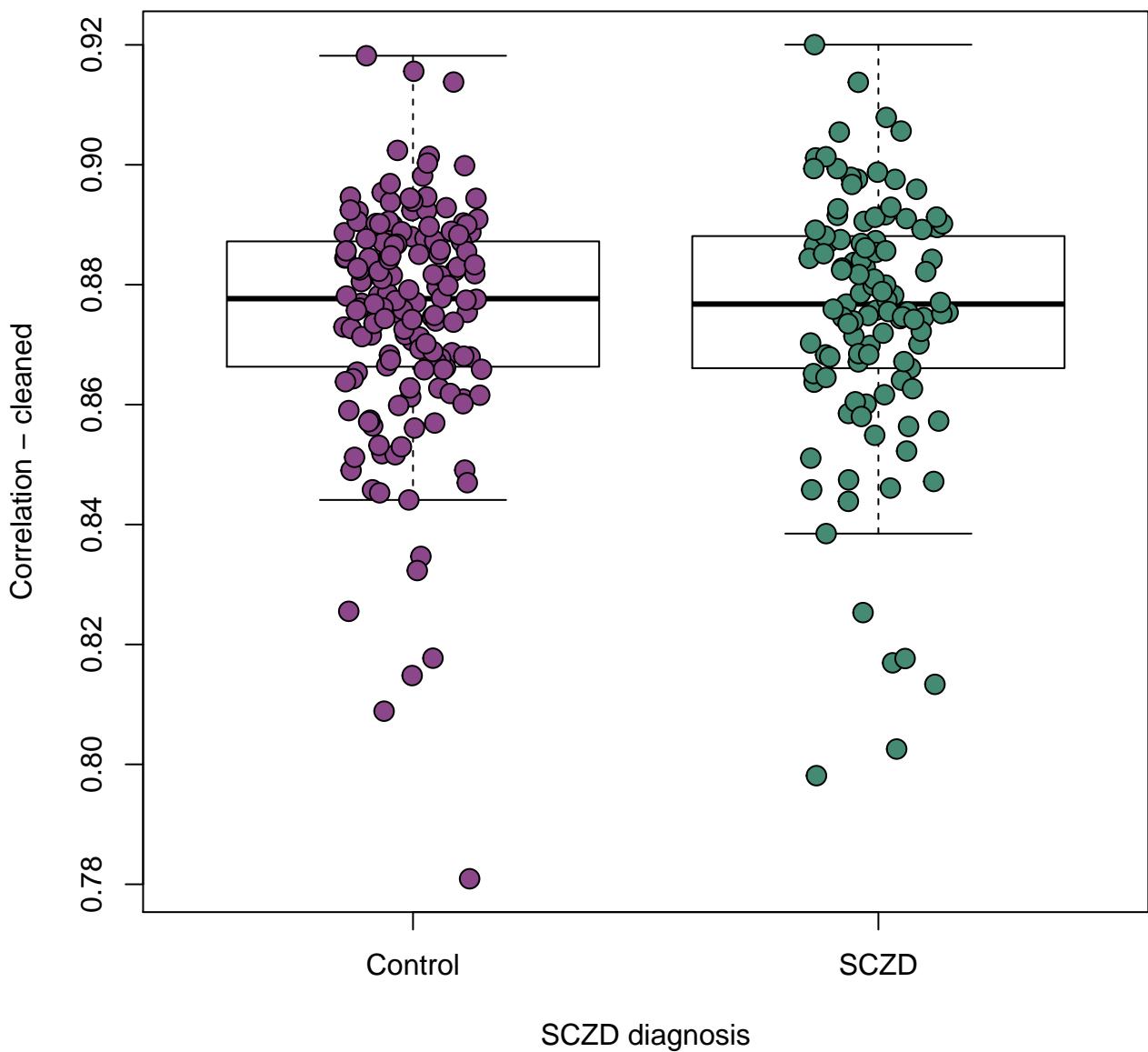
hsa00240: Pyrimidine metabolism
p-value: 0.386



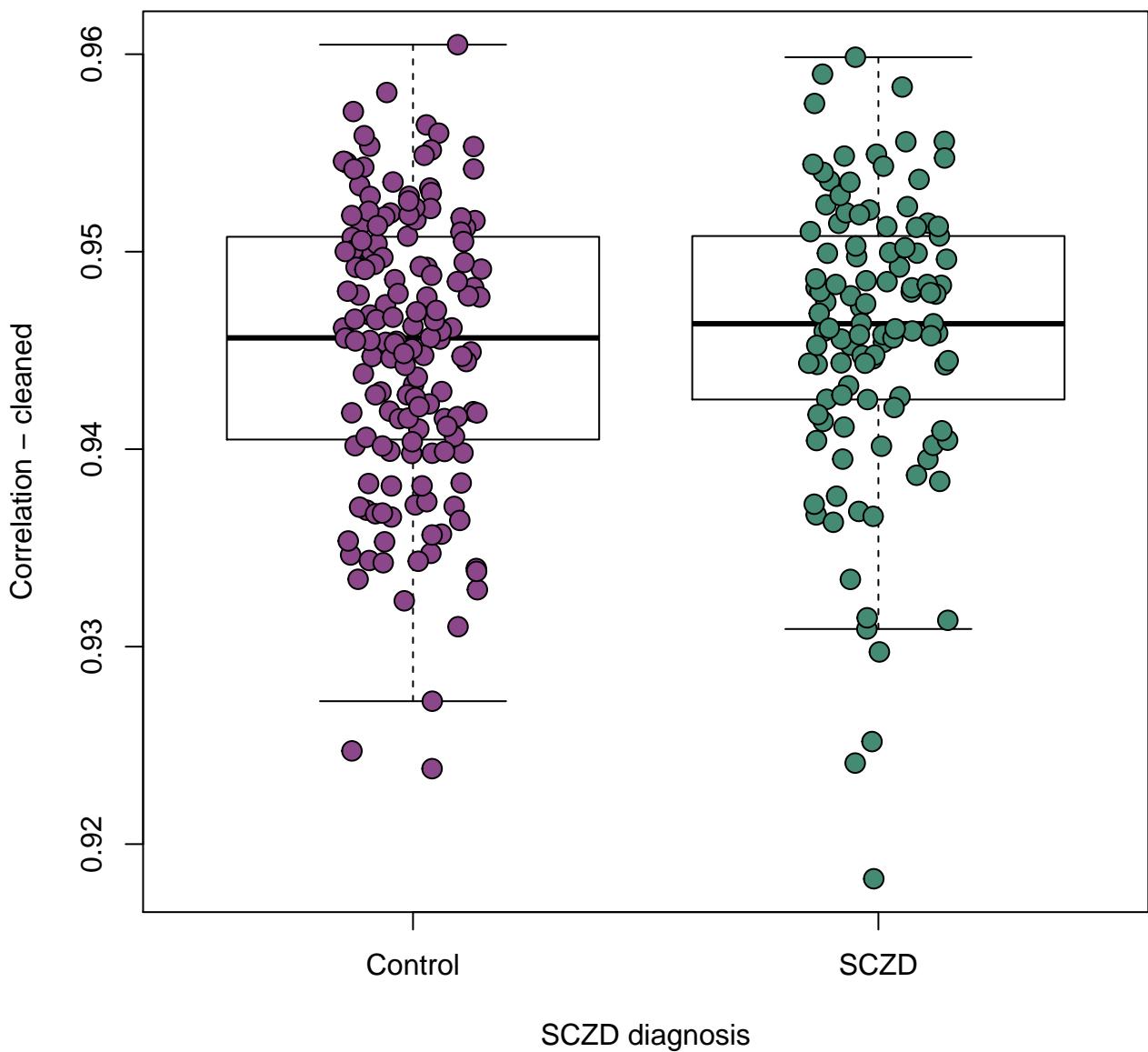
hsa00250: Alanine, aspartate and glutamate metabolism
p-value: 0.745



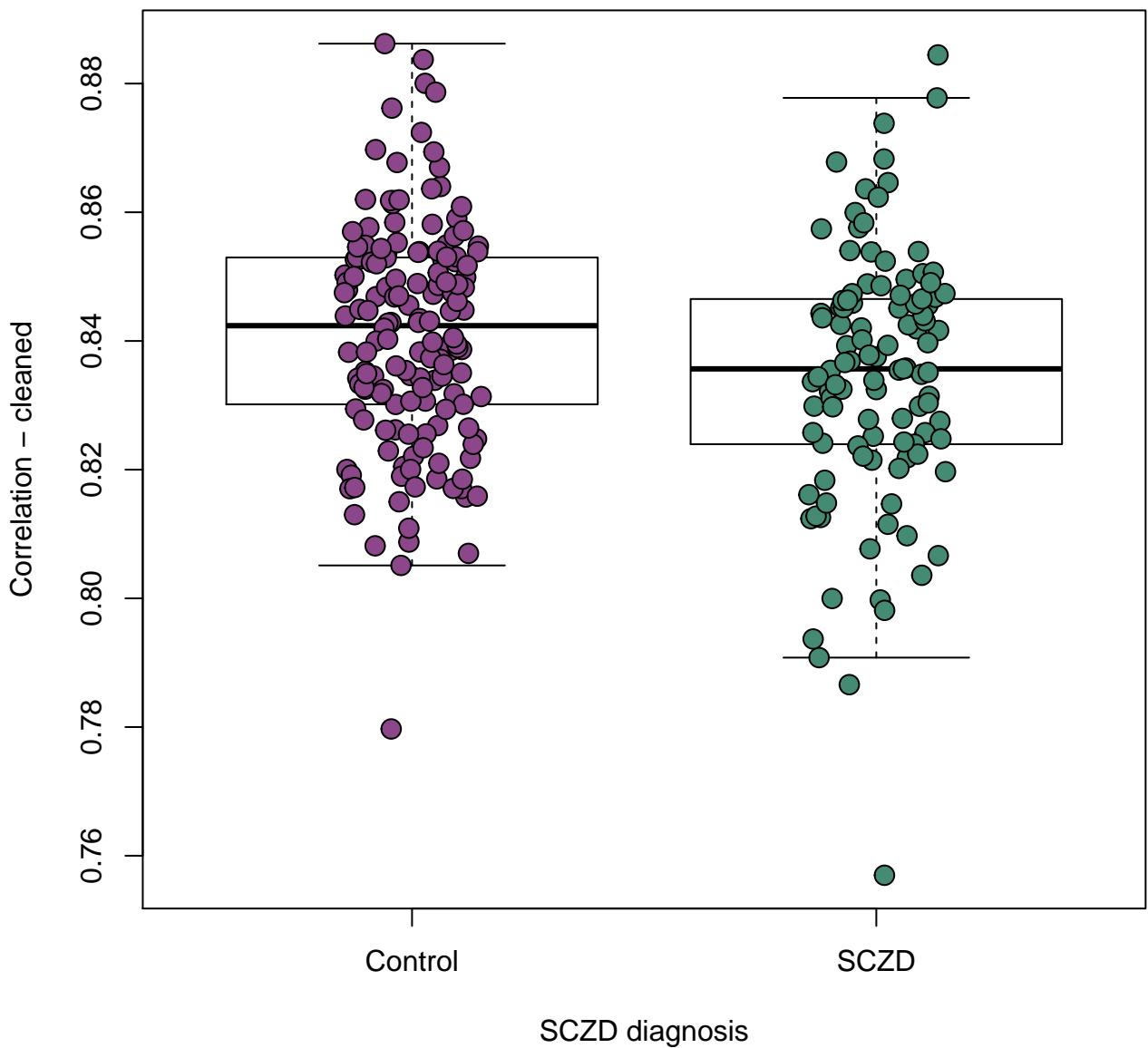
hsa00260: Glycine, serine and threonine metabolism
p-value: 0.909



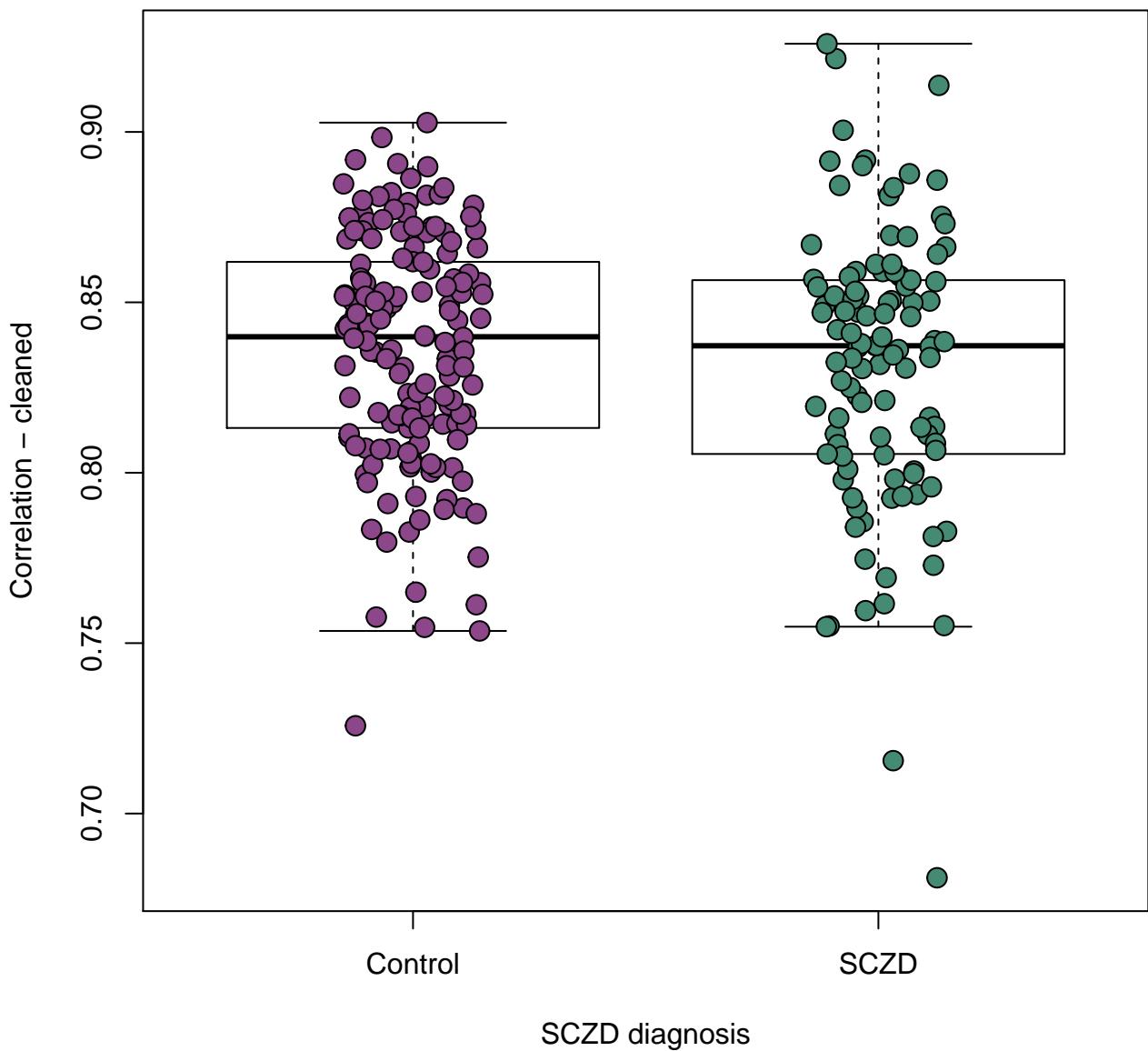
hsa00270: Cysteine and methionine metabolism
p-value: 0.521



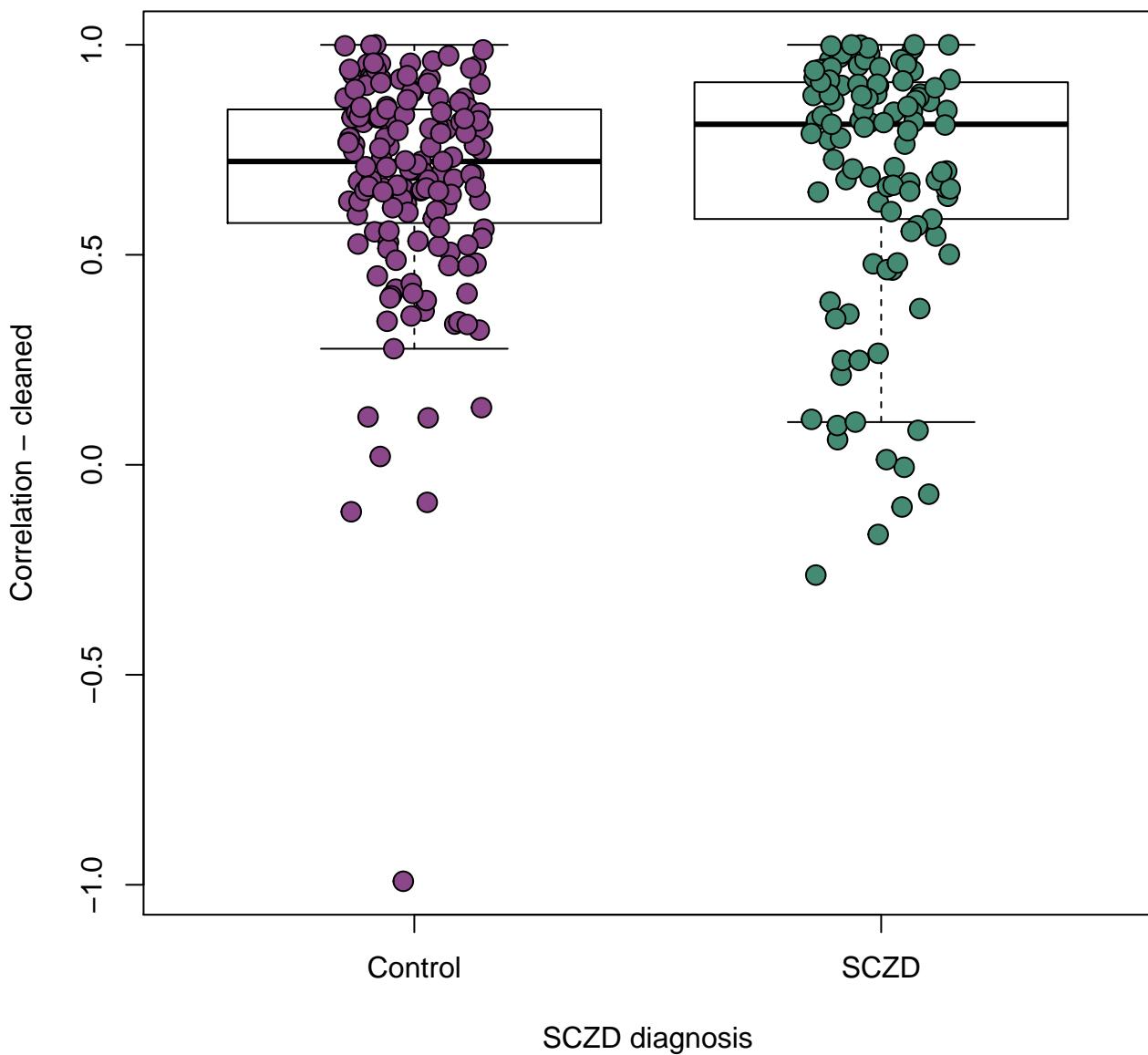
hsa00280: Valine, leucine and isoleucine degradation
p-value: 0.0054



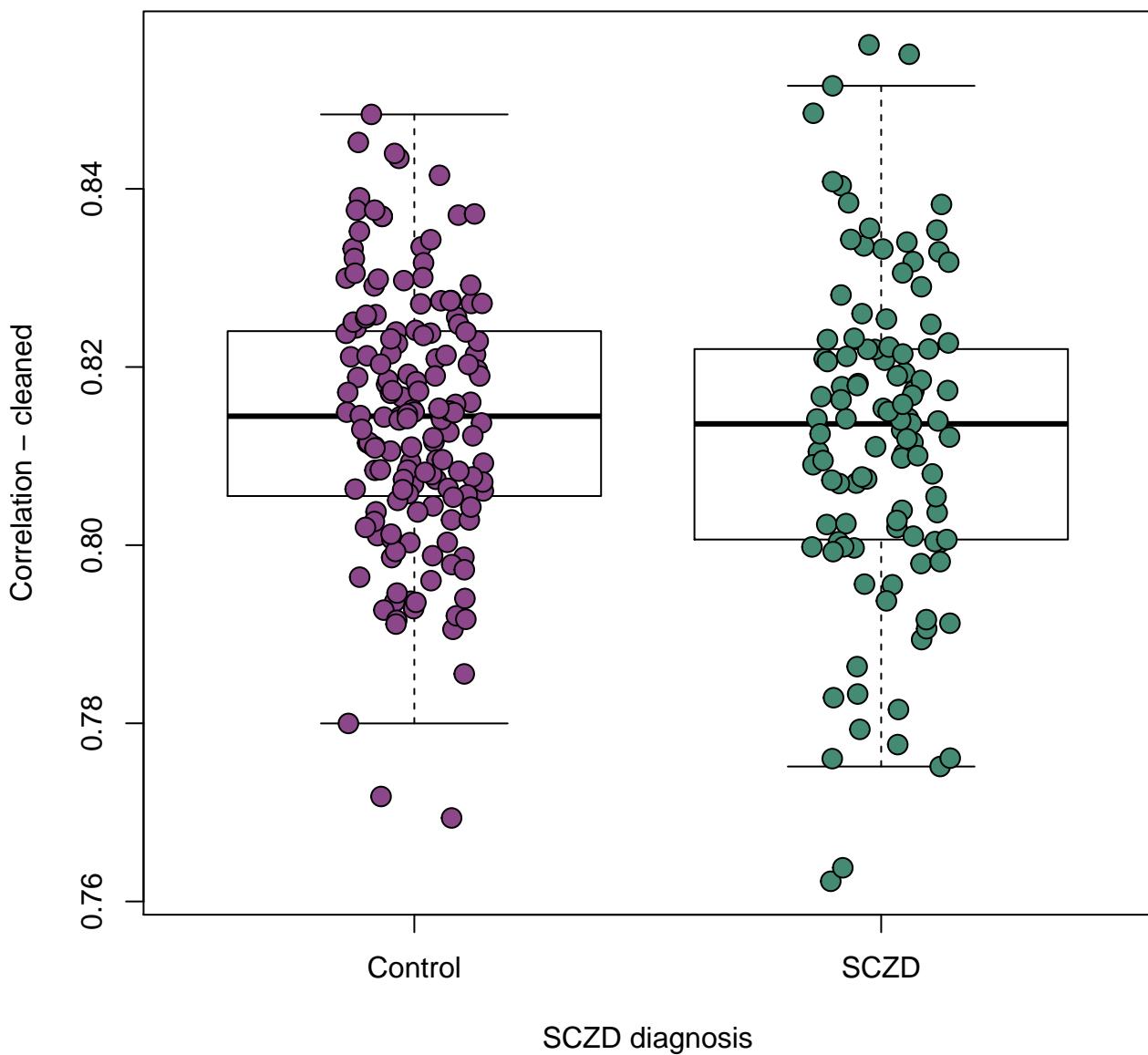
hsa00290: Valine, leucine and isoleucine biosynthesis
p-value: 0.339



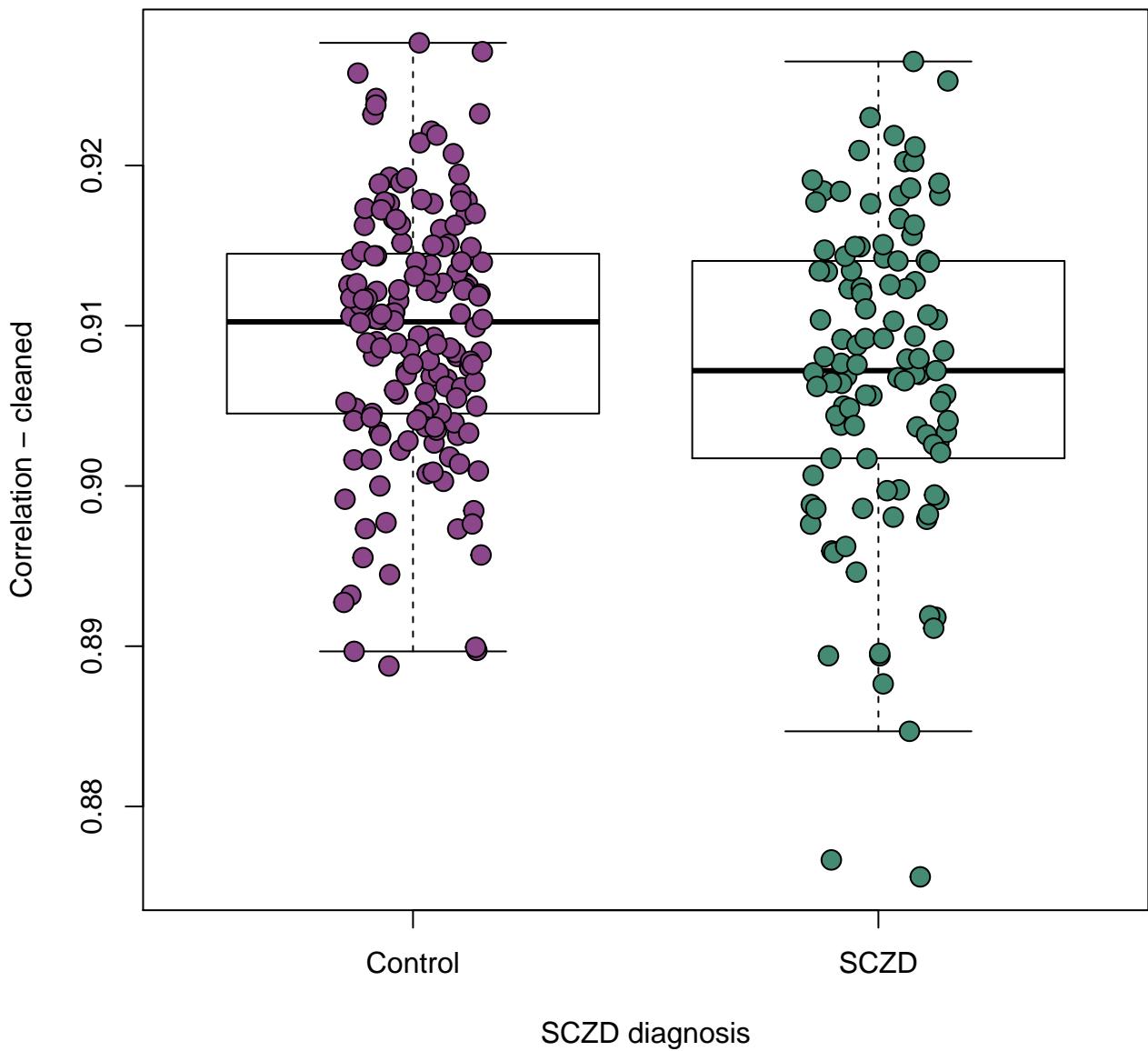
hsa00300: Lysine biosynthesis
p-value: 0.747



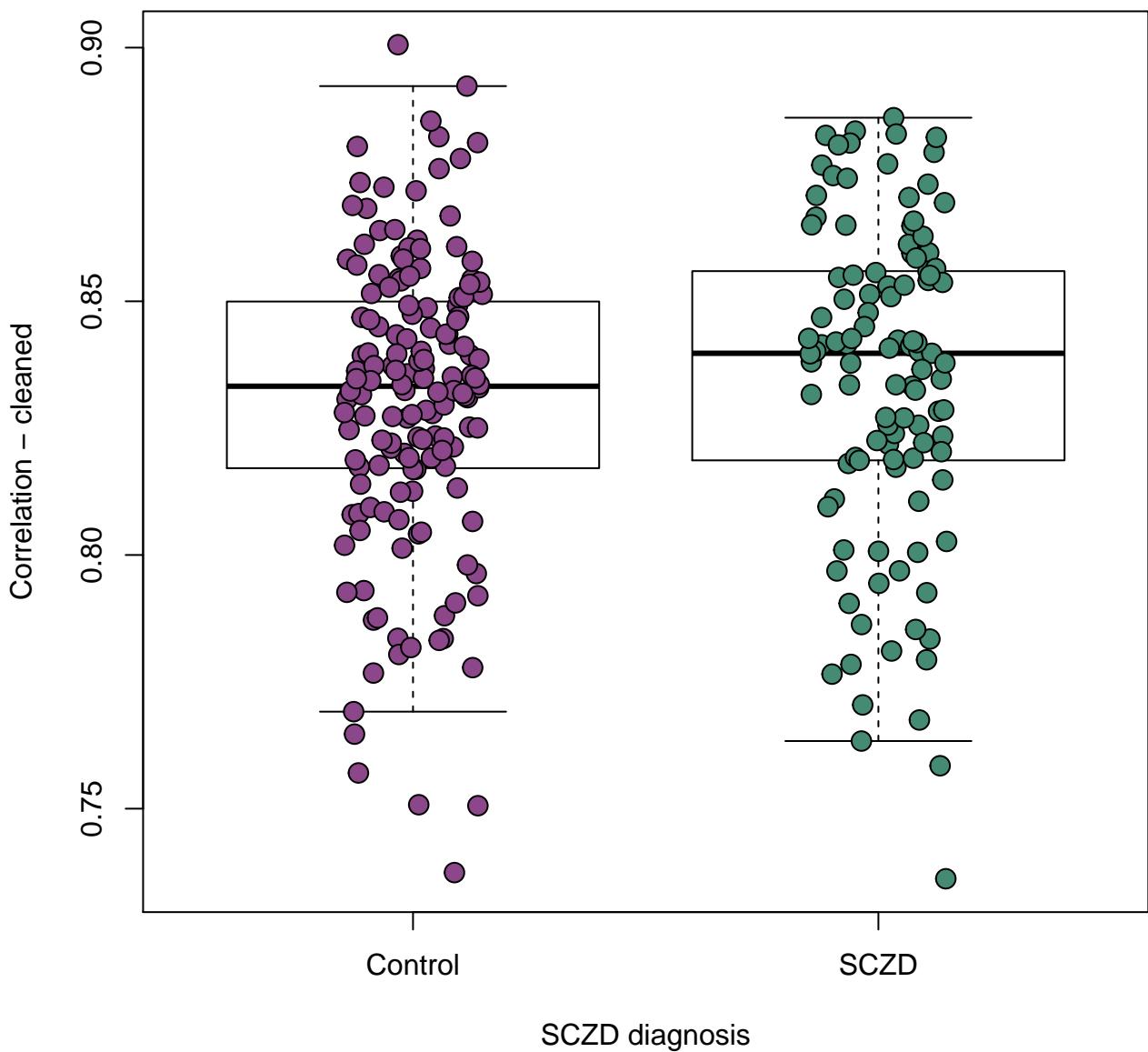
hsa00310: Lysine degradation
p-value: 0.264



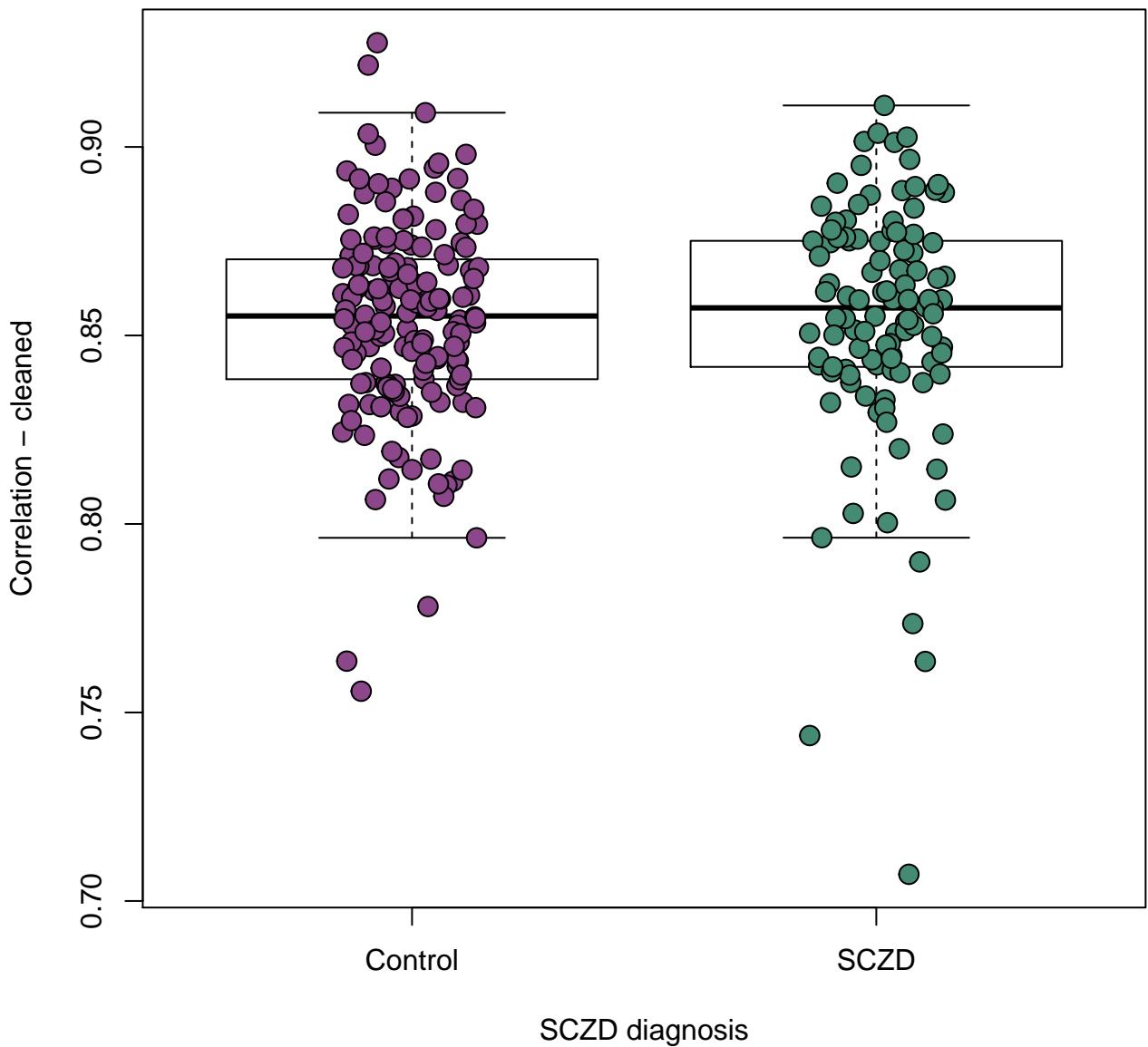
hsa00330: Arginine and proline metabolism
p-value: 0.0246



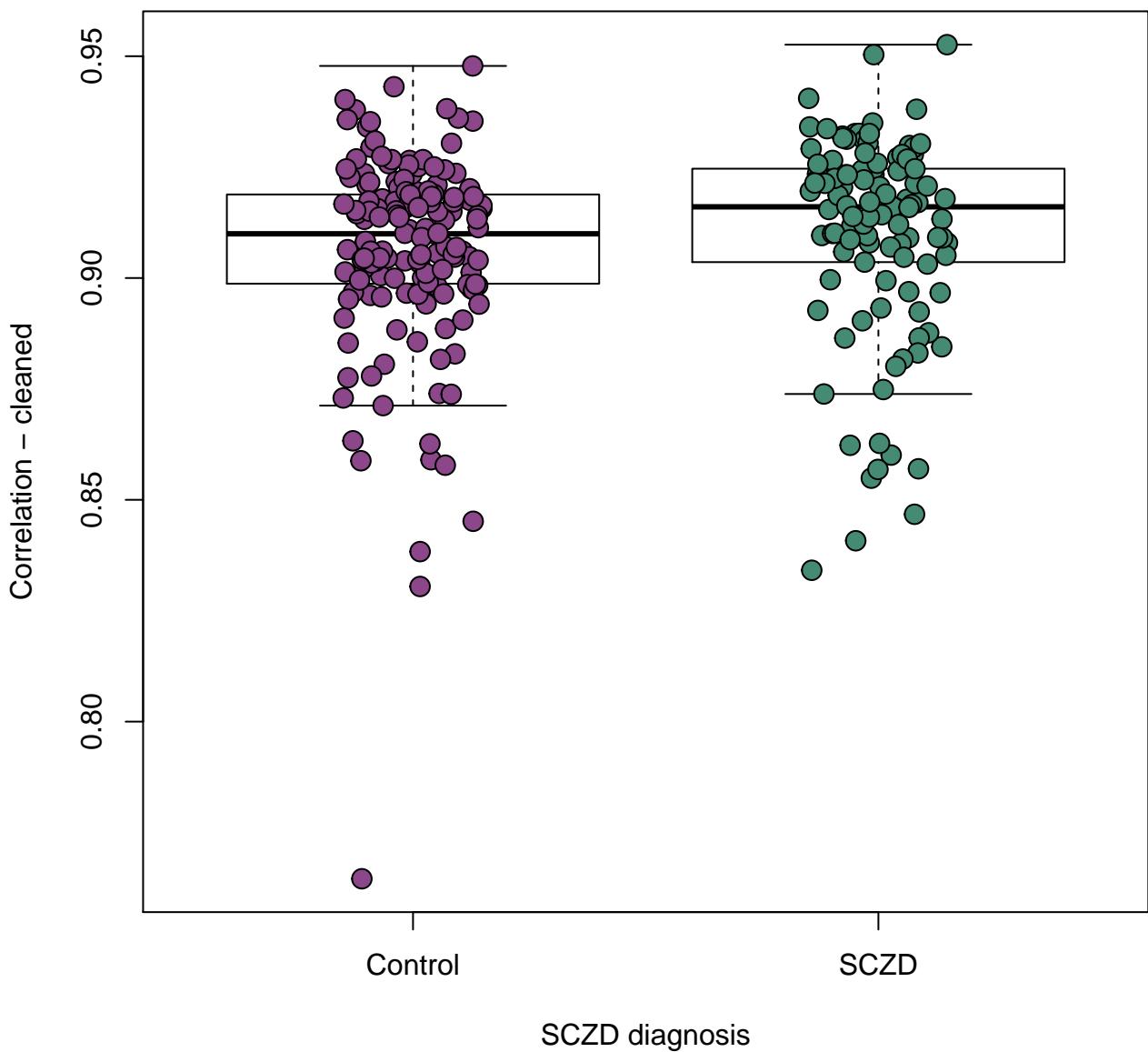
hsa00340: Histidine metabolism
p-value: 0.327



hsa00350: Tyrosine metabolism
p-value: 0.874

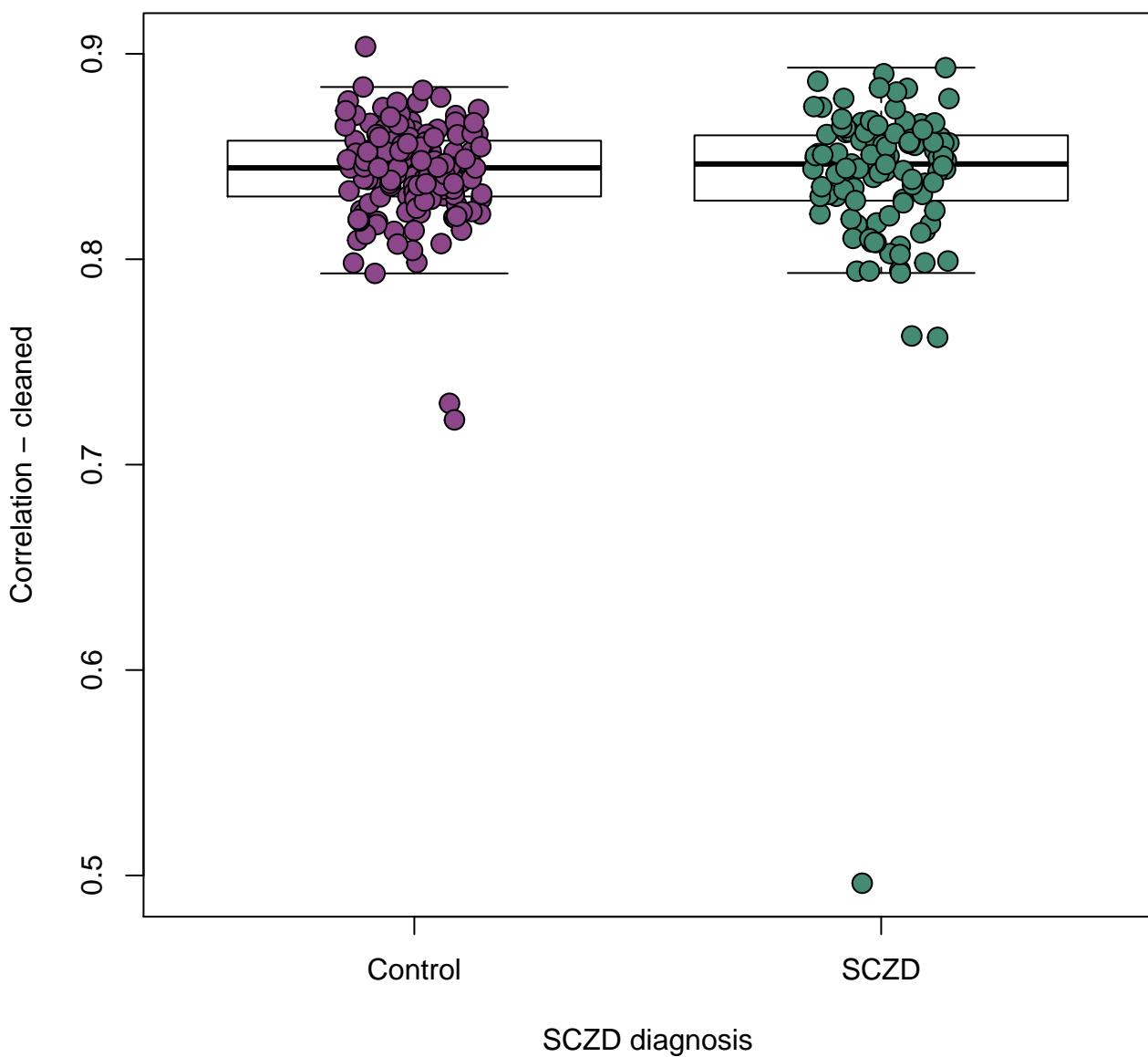


hsa00360: Phenylalanine metabolism
p-value: 0.17

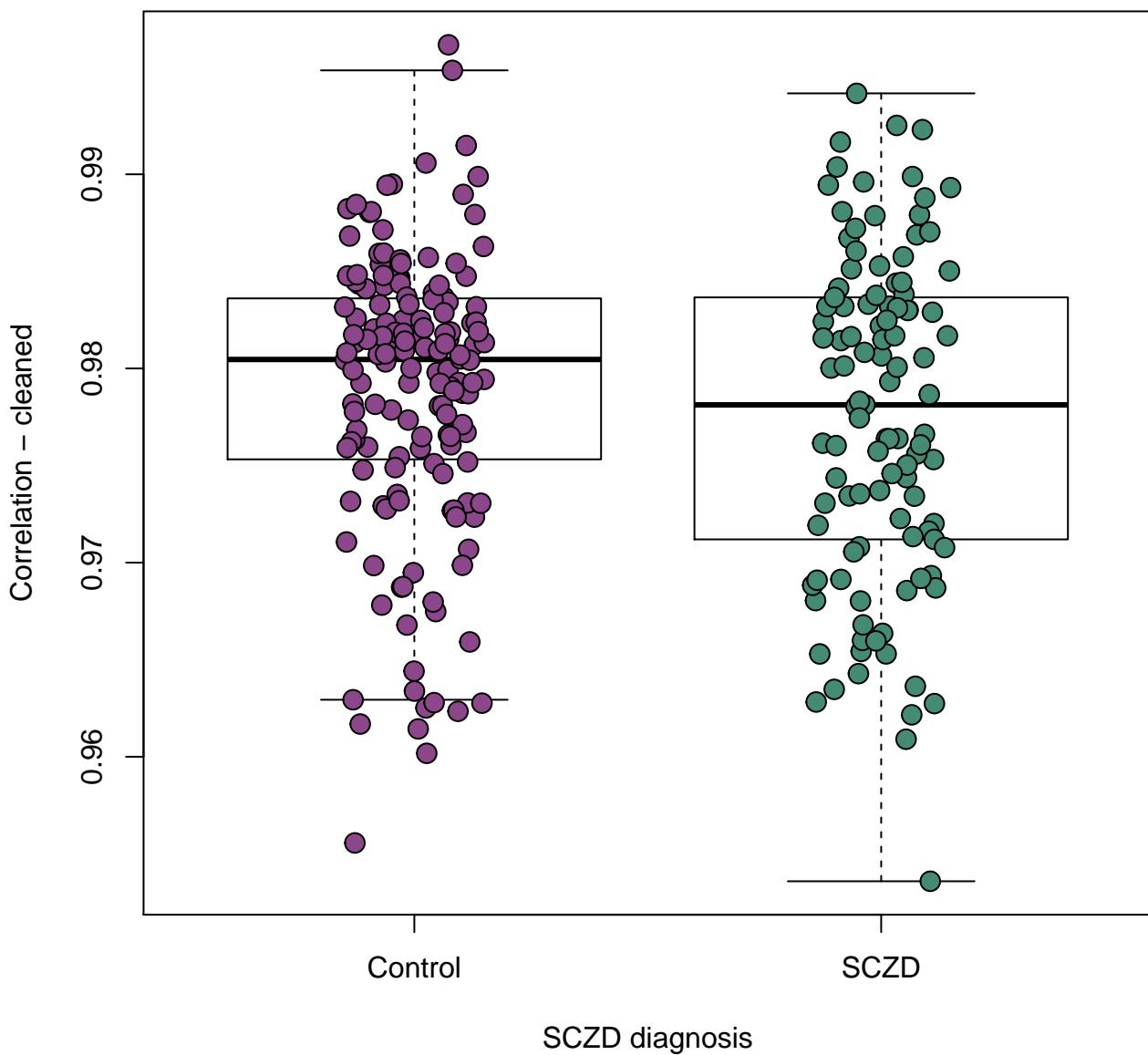


hsa00380: Tryptophan metabolism

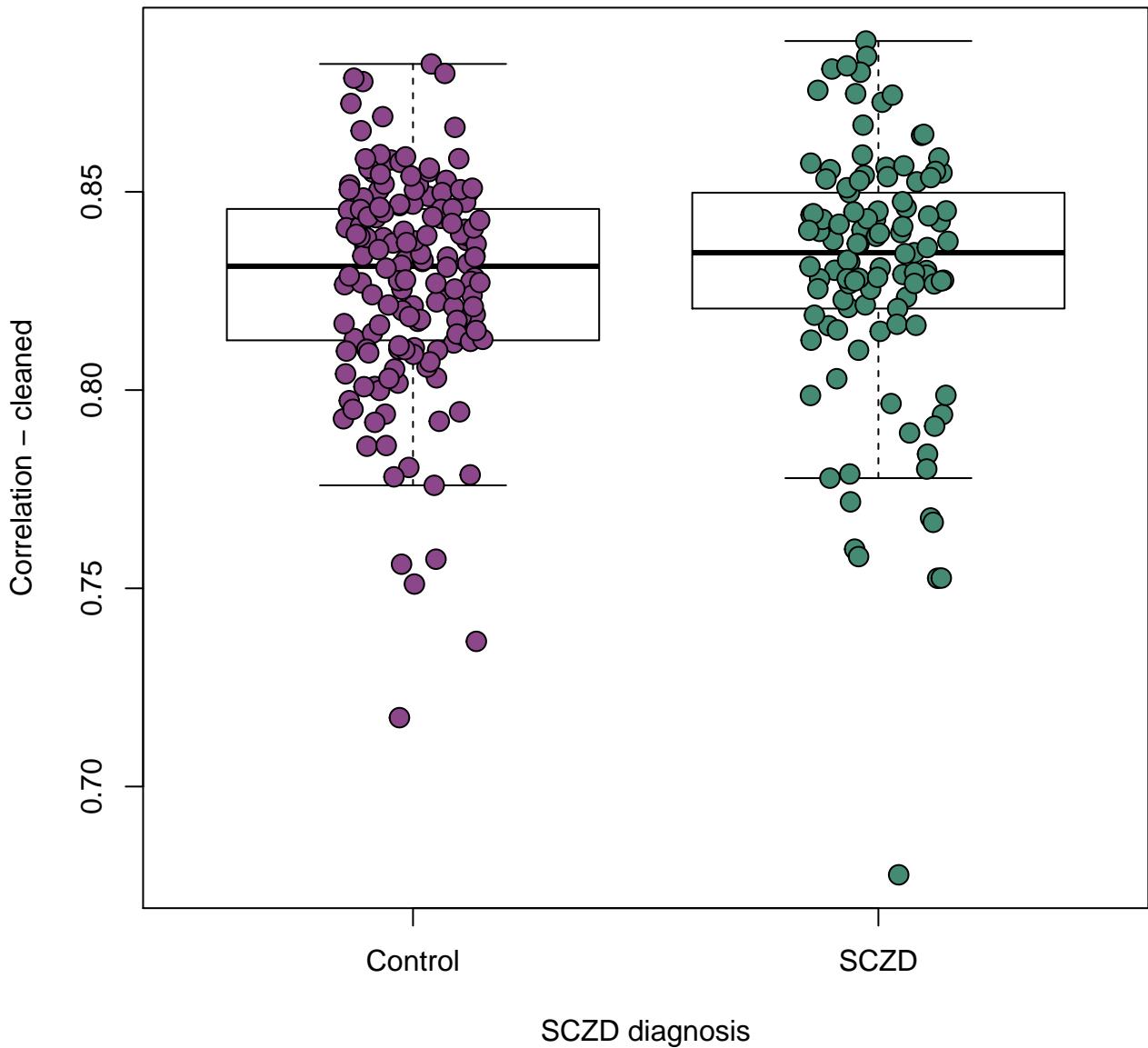
p-value: 0.492



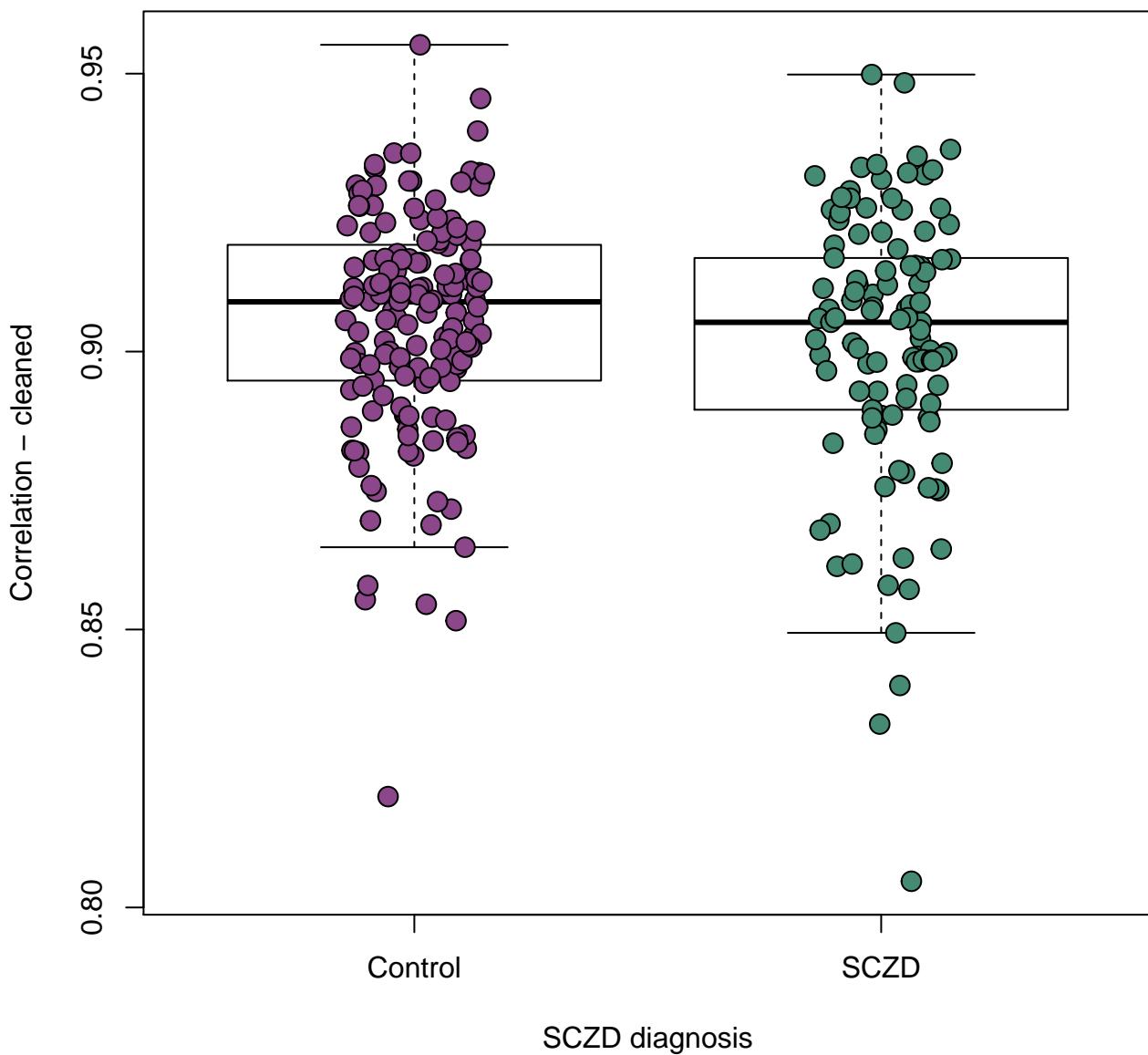
hsa00400: Phenylalanine, tyrosine and tryptophan biosynthesis
p-value: 0.161



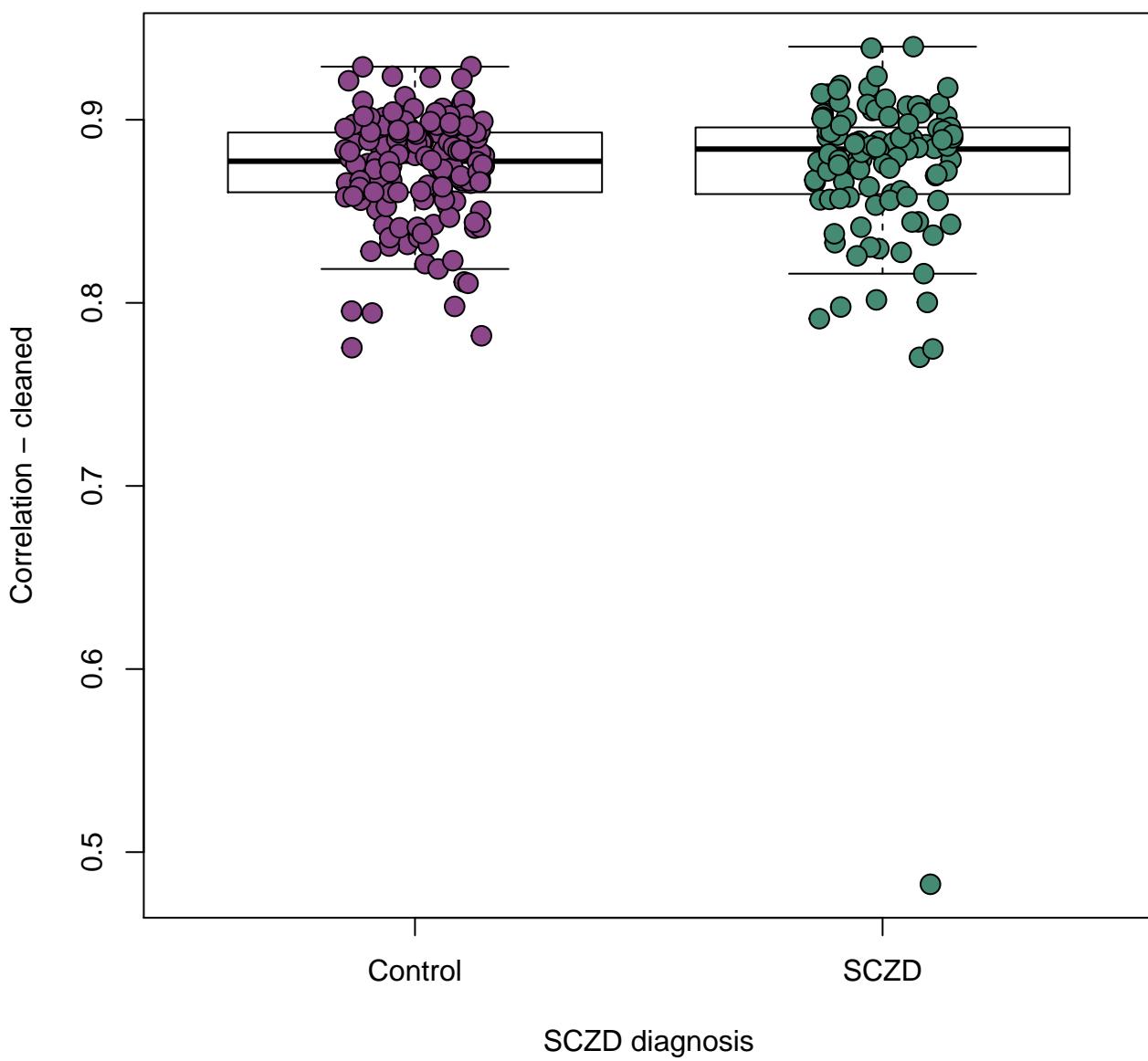
hsa00410: beta-Alanine metabolism
p-value: 0.499



hsa00430: Taurine and hypotaurine metabolism
p-value: 0.173

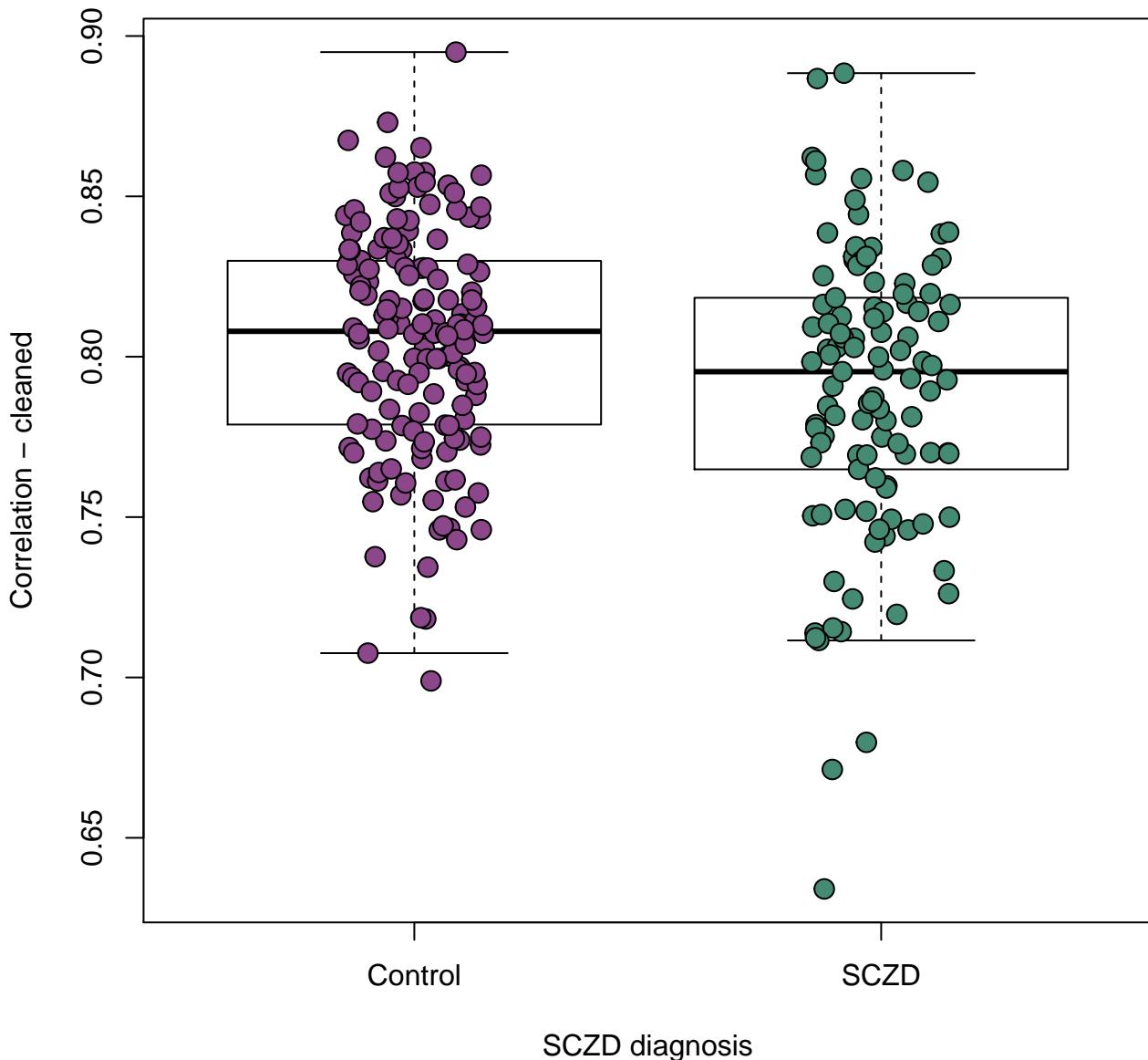


hsa00450: Selenocompound metabolism
p-value: 0.892

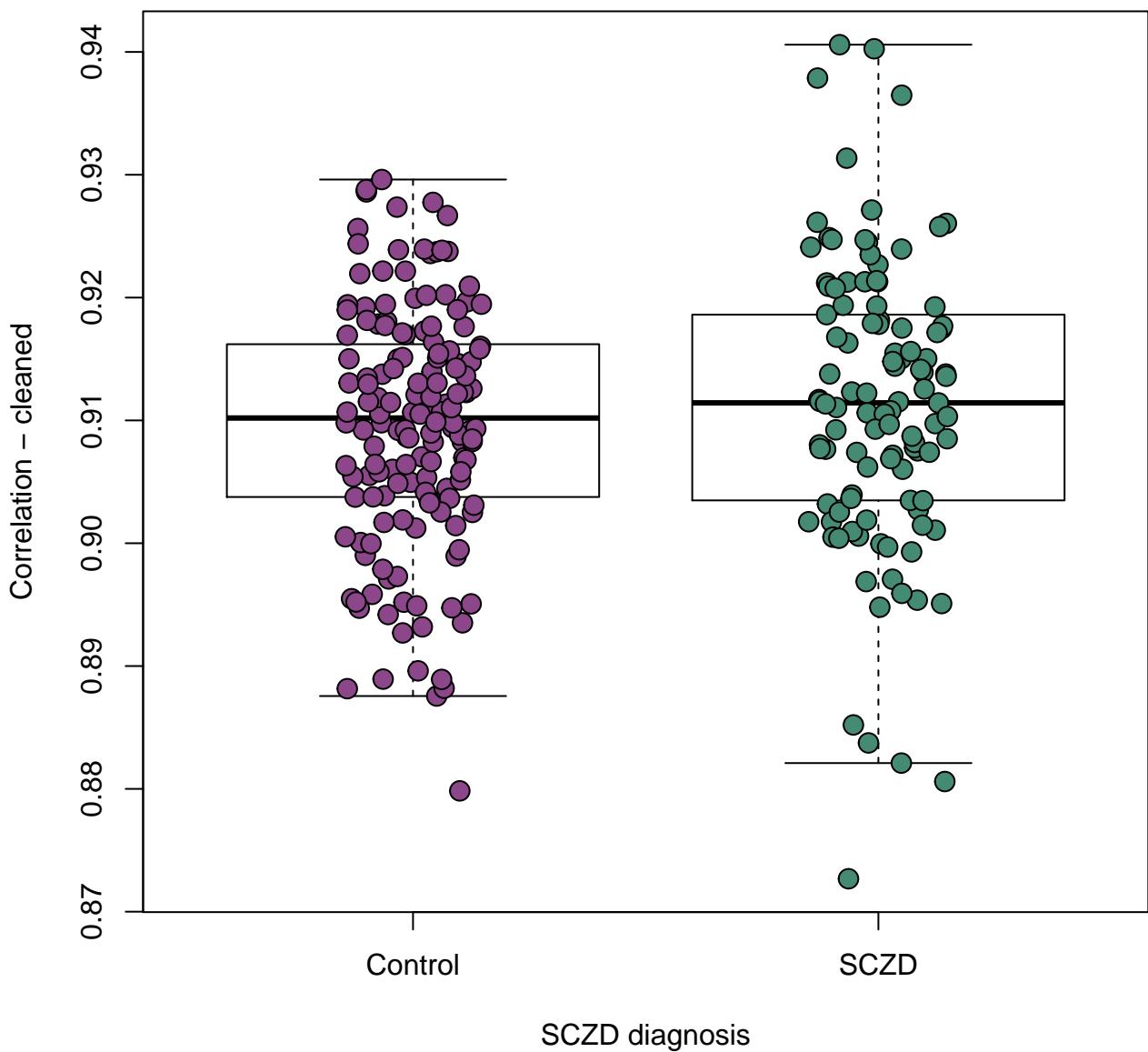


hsa00460: Cyanoamino acid metabolism

p-value: 0.00178

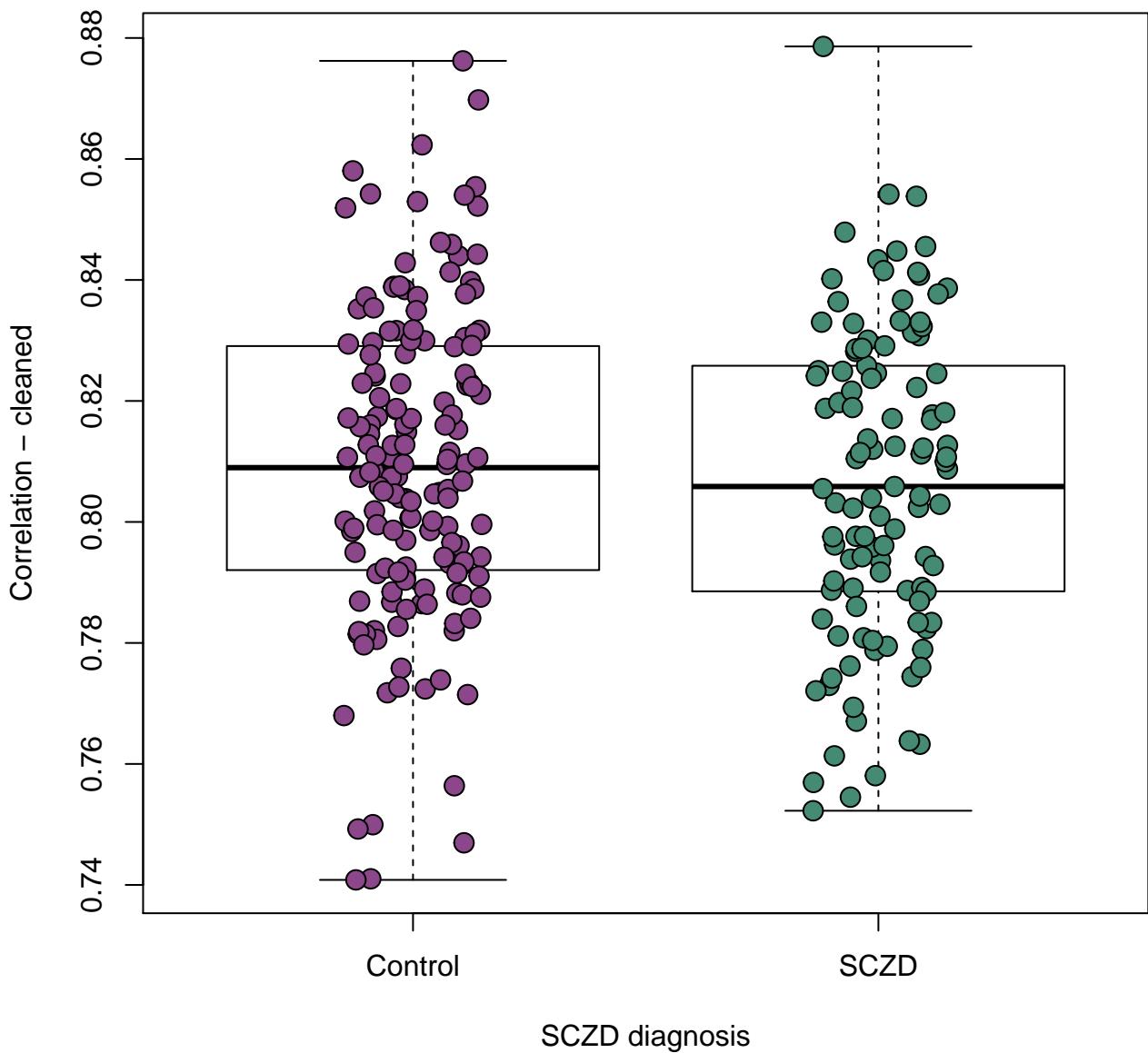


hsa00471: D-Glutamine and D-glutamate metabolism
p-value: 0.202

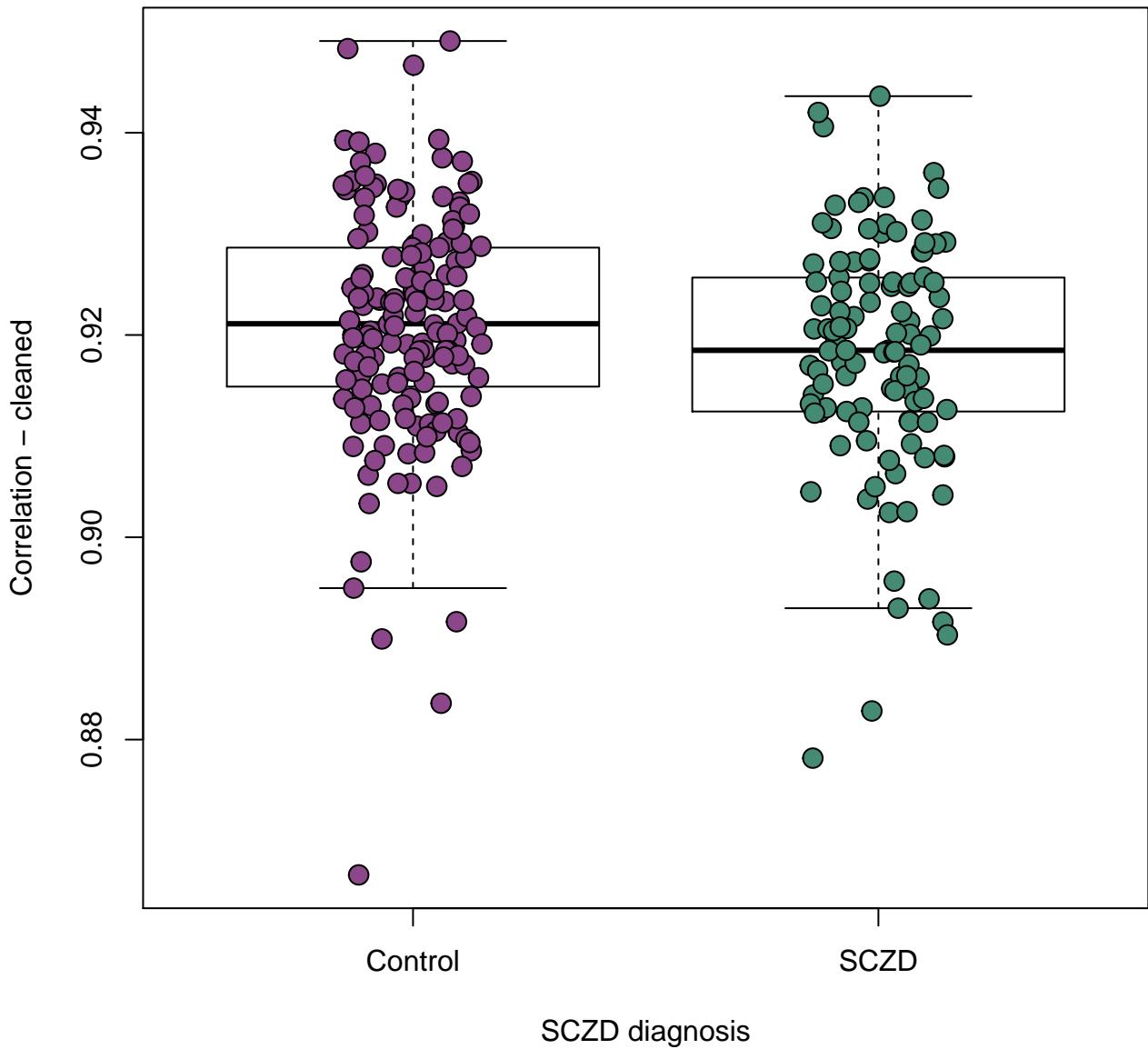


hsa00480: Glutathione metabolism

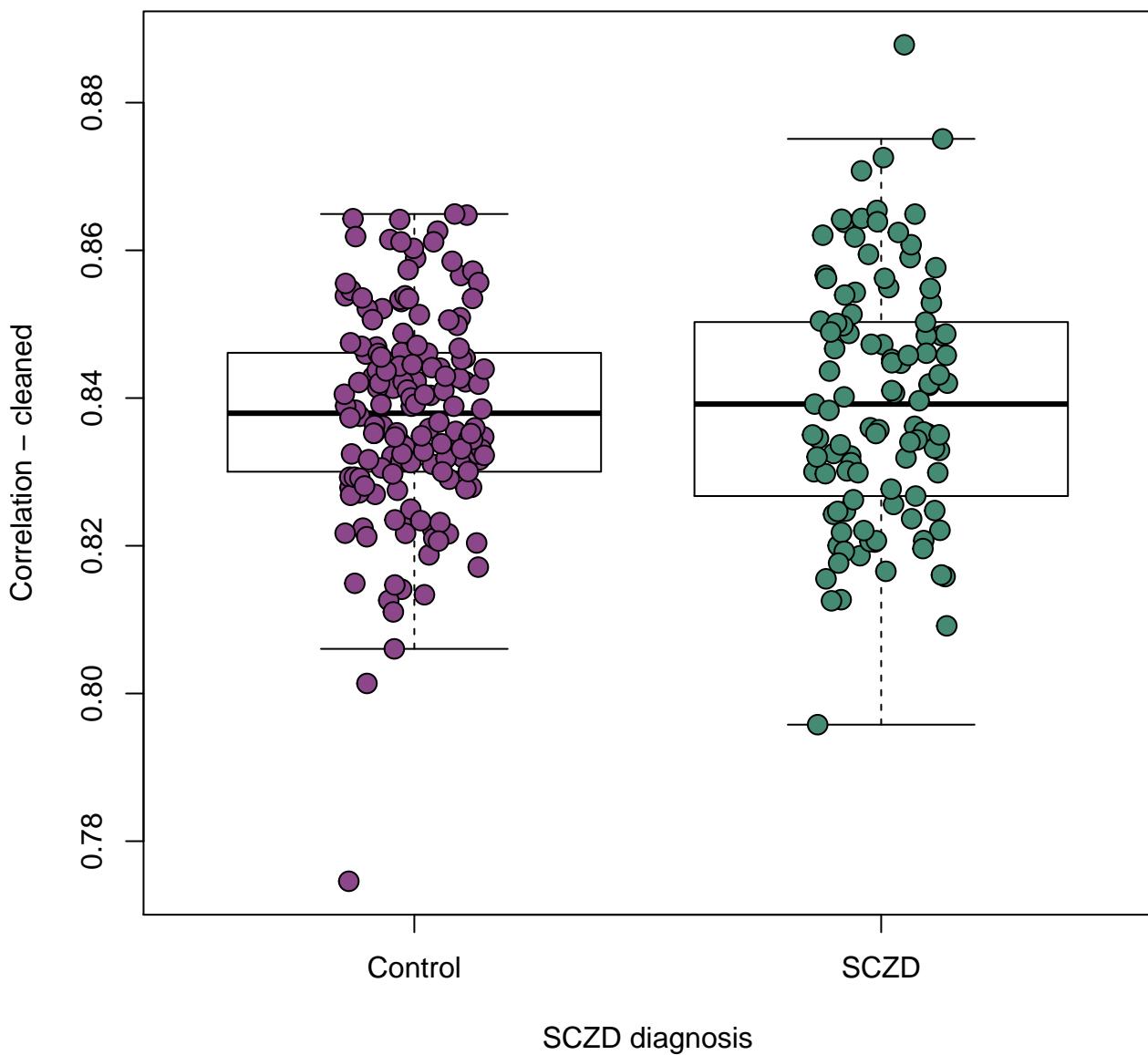
p-value: 0.355



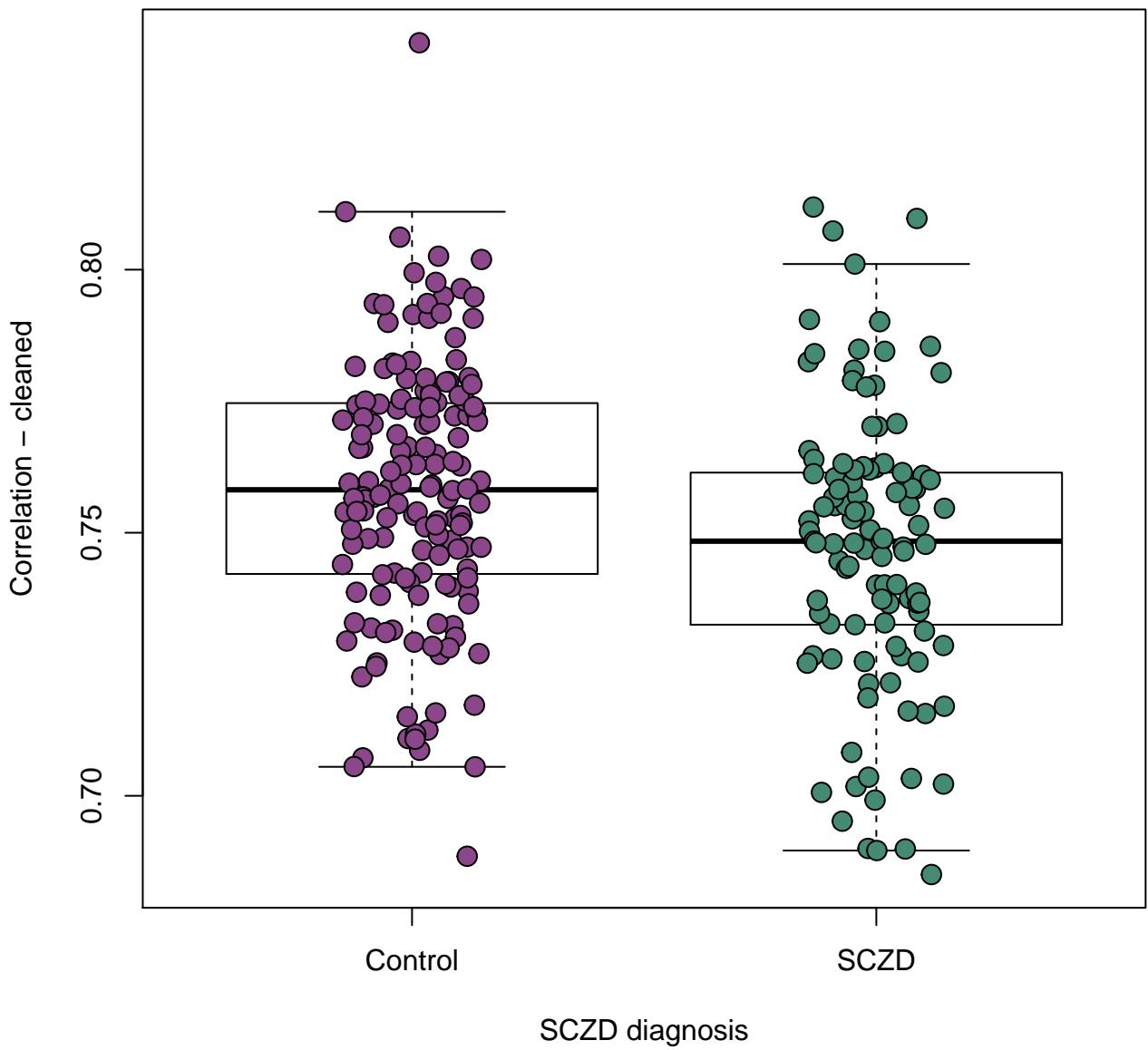
hsa00500: Starch and sucrose metabolism
p-value: 0.0489



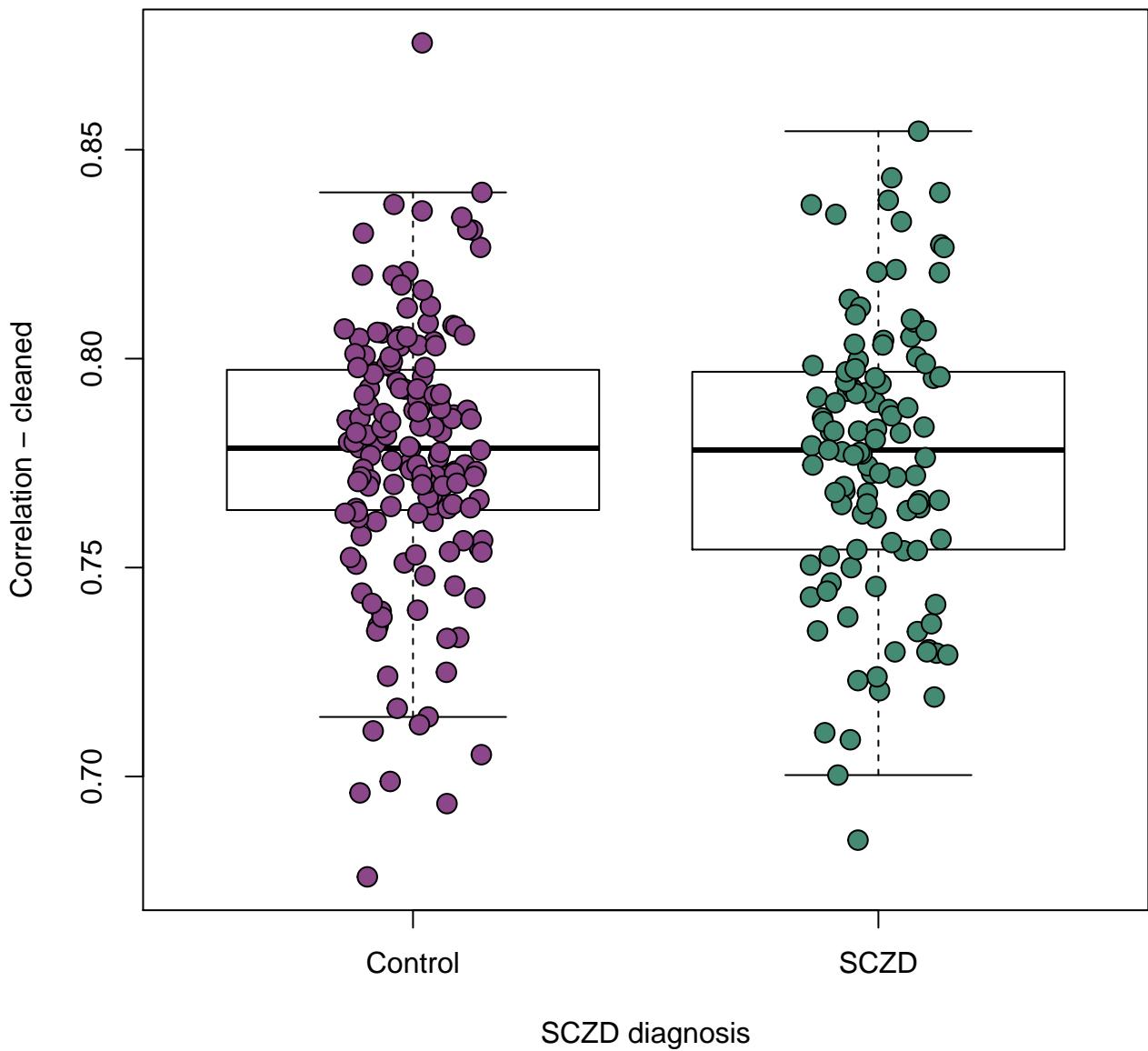
hsa00510: N-Glycan biosynthesis
p-value: 0.349



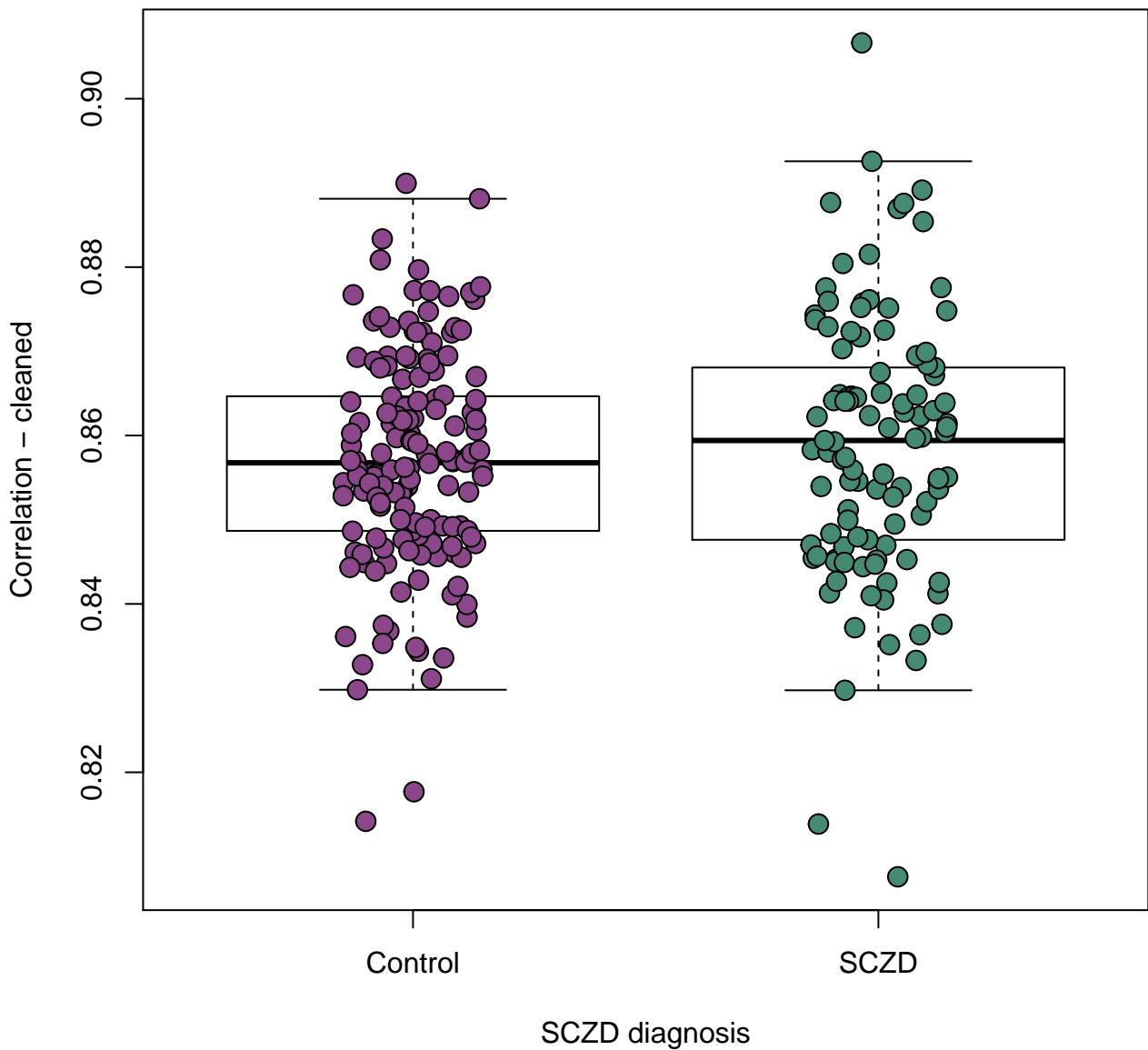
hsa00511: Other glycan degradation
p-value: 0.000565



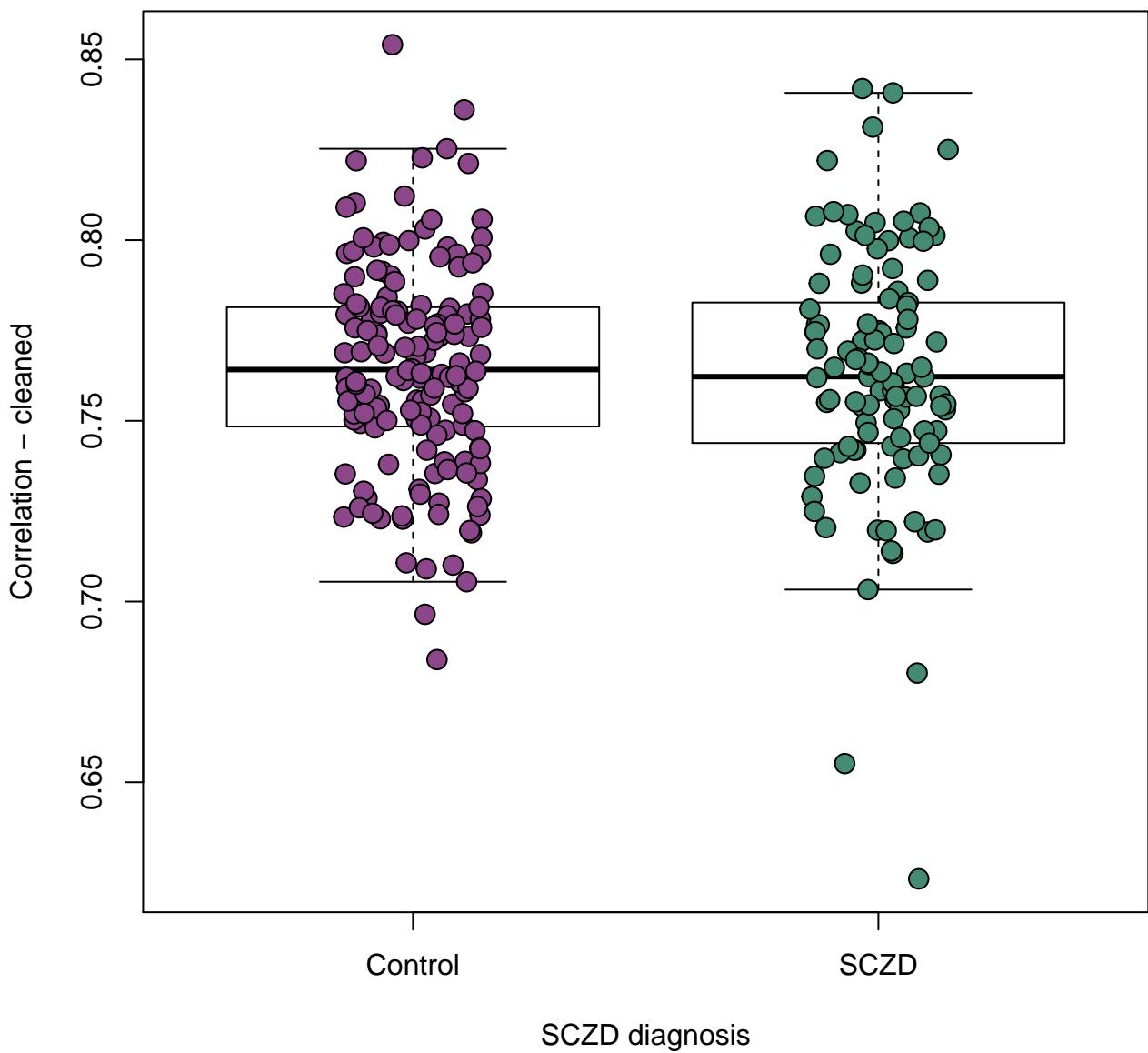
hsa00512: Mucin type O-Glycan biosynthesis
p-value: 0.858



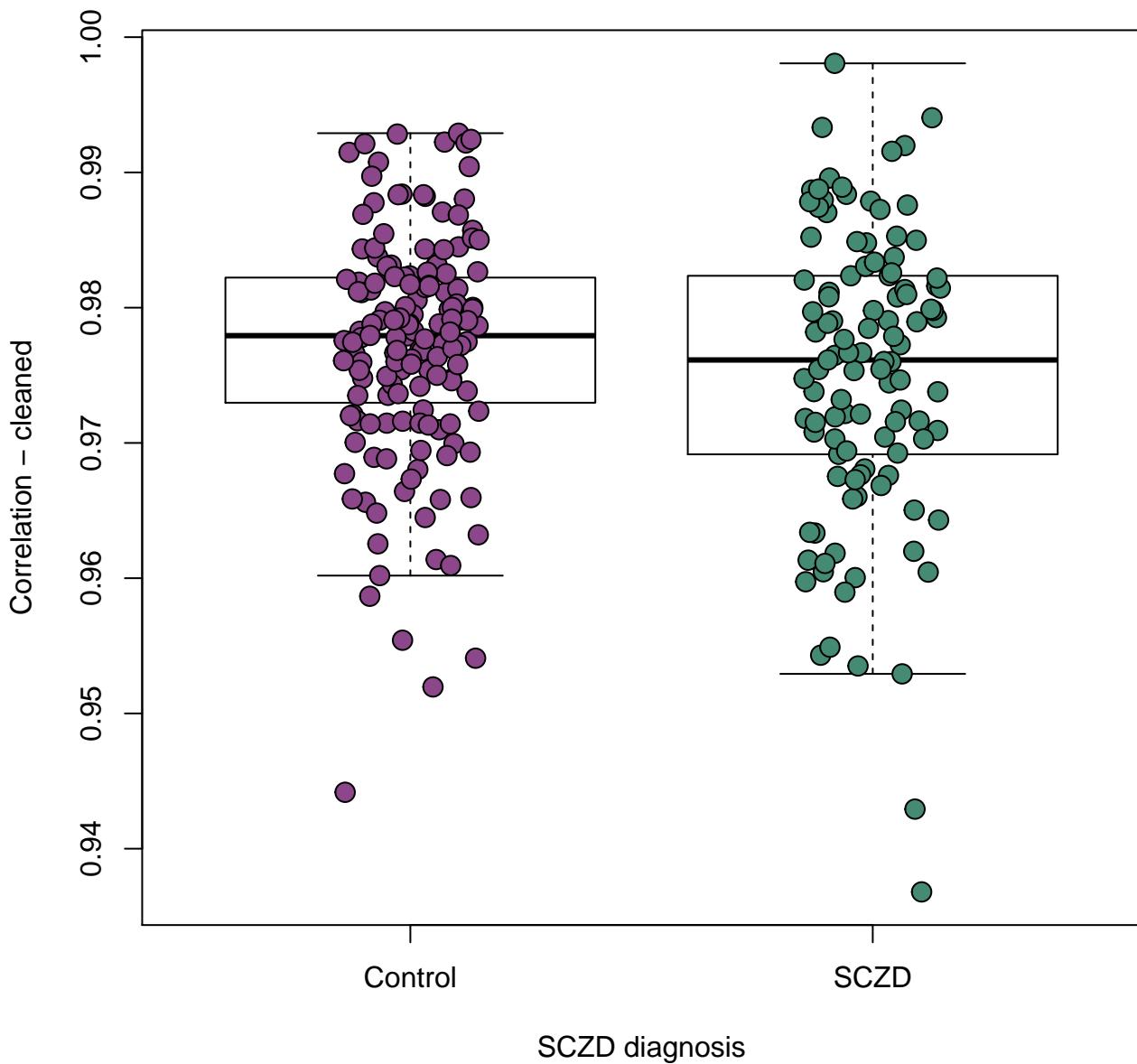
hsa00514: Other types of O-glycan biosynthesis
p-value: 0.257



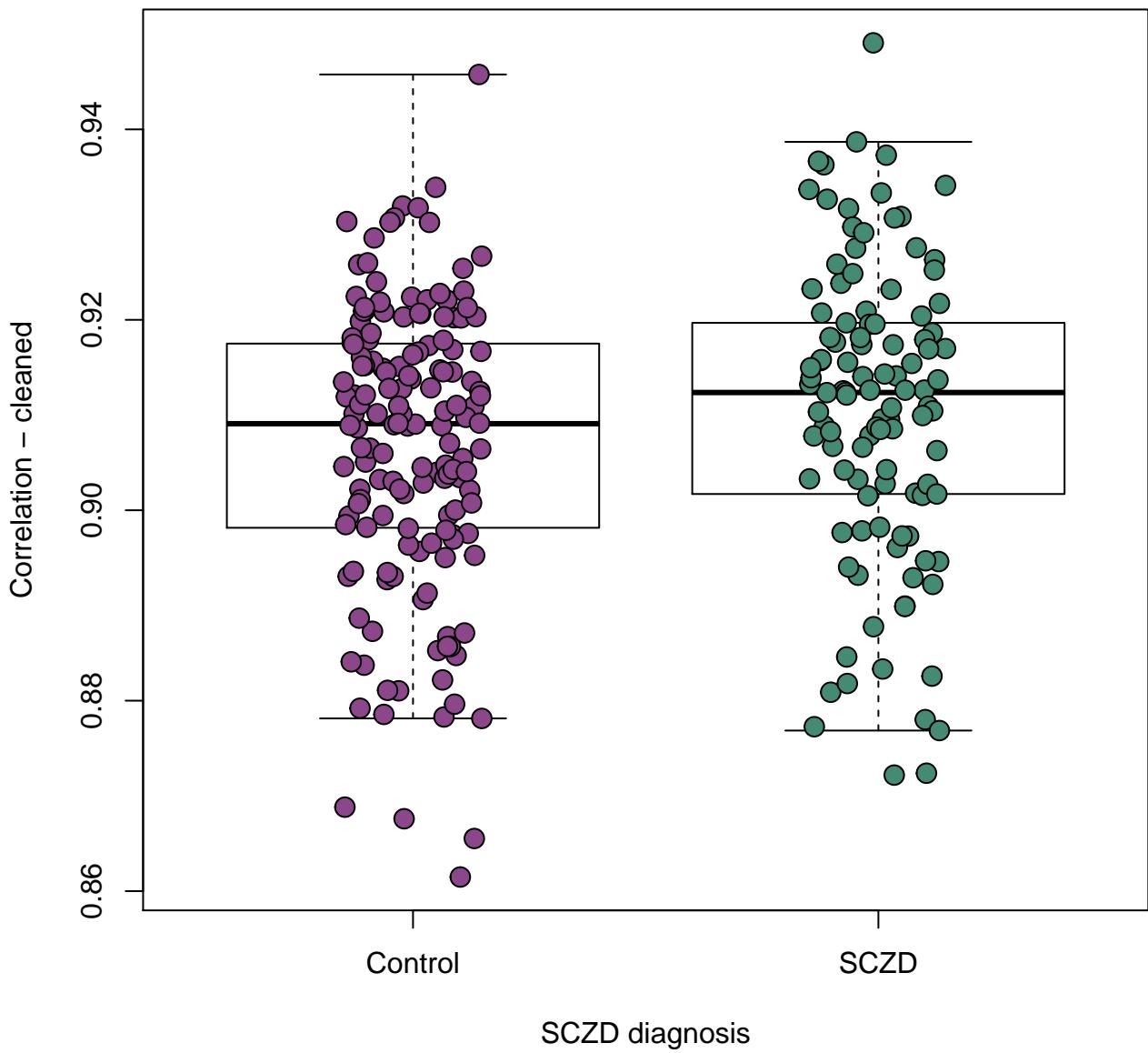
hsa00520: Amino sugar and nucleotide sugar metabolism
p-value: 0.615



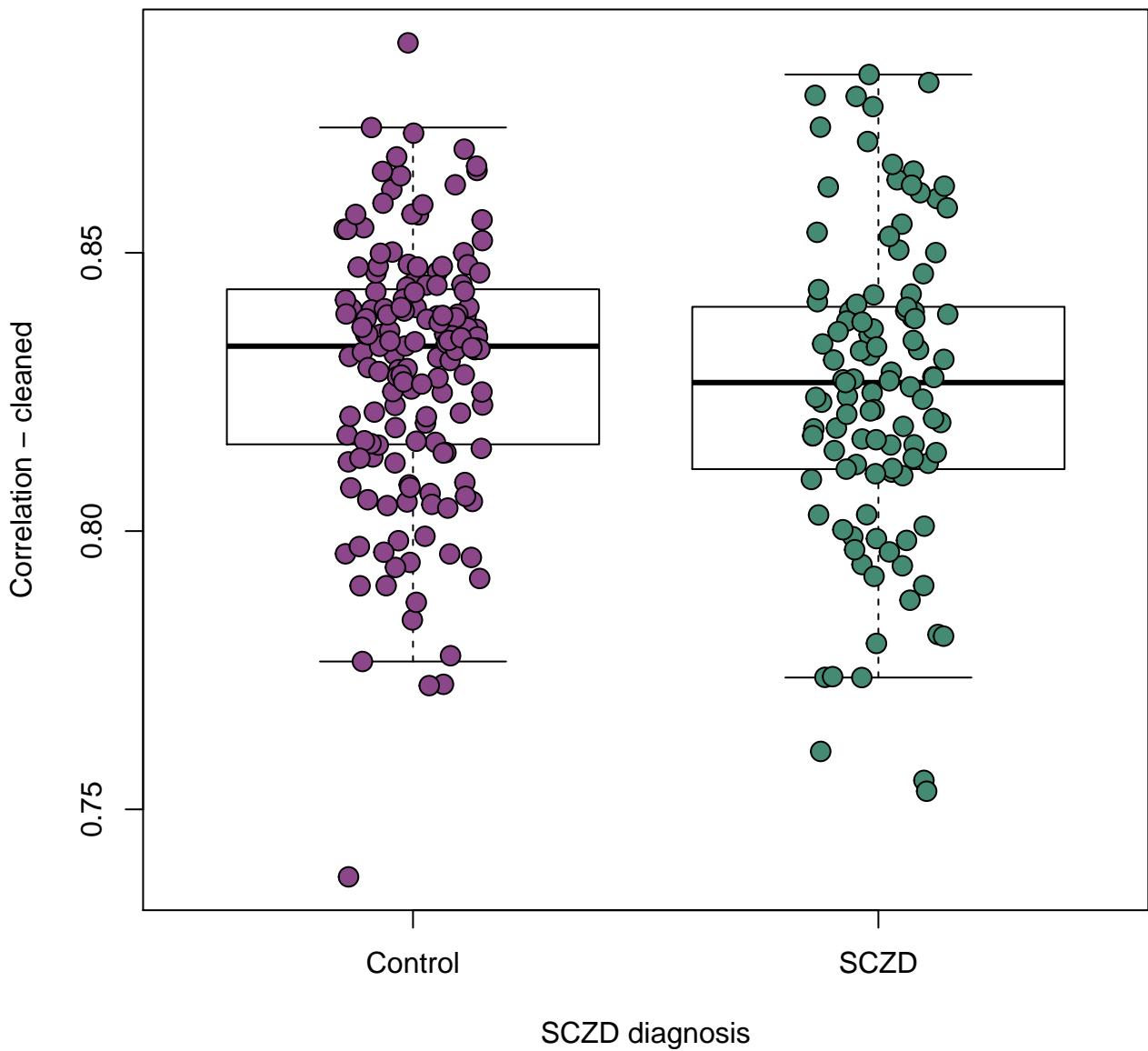
hsa00524: Butirosin and neomycin biosynthesis
p-value: 0.0736



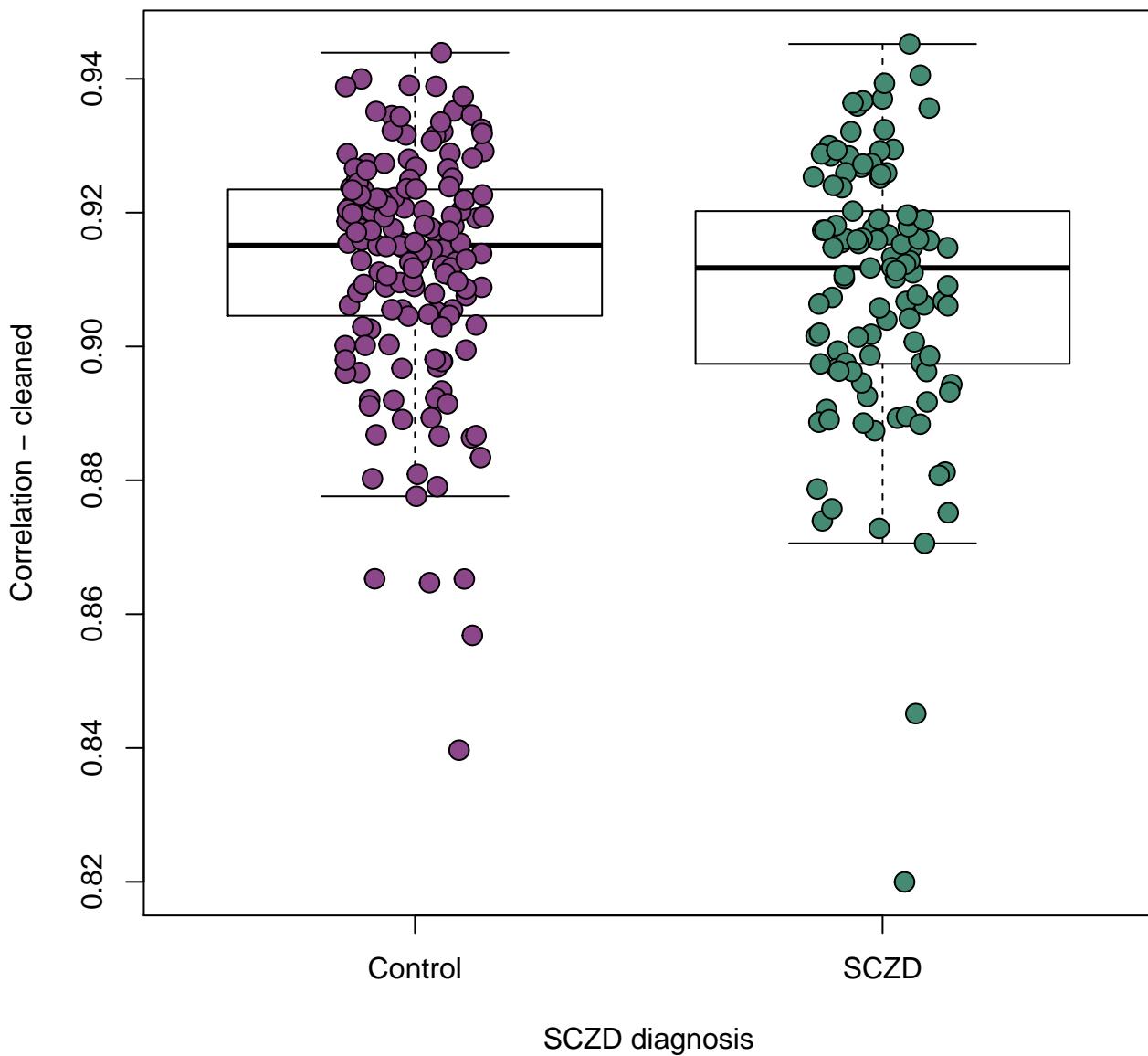
hsa00531: Glycosaminoglycan degradation
p-value: 0.0652



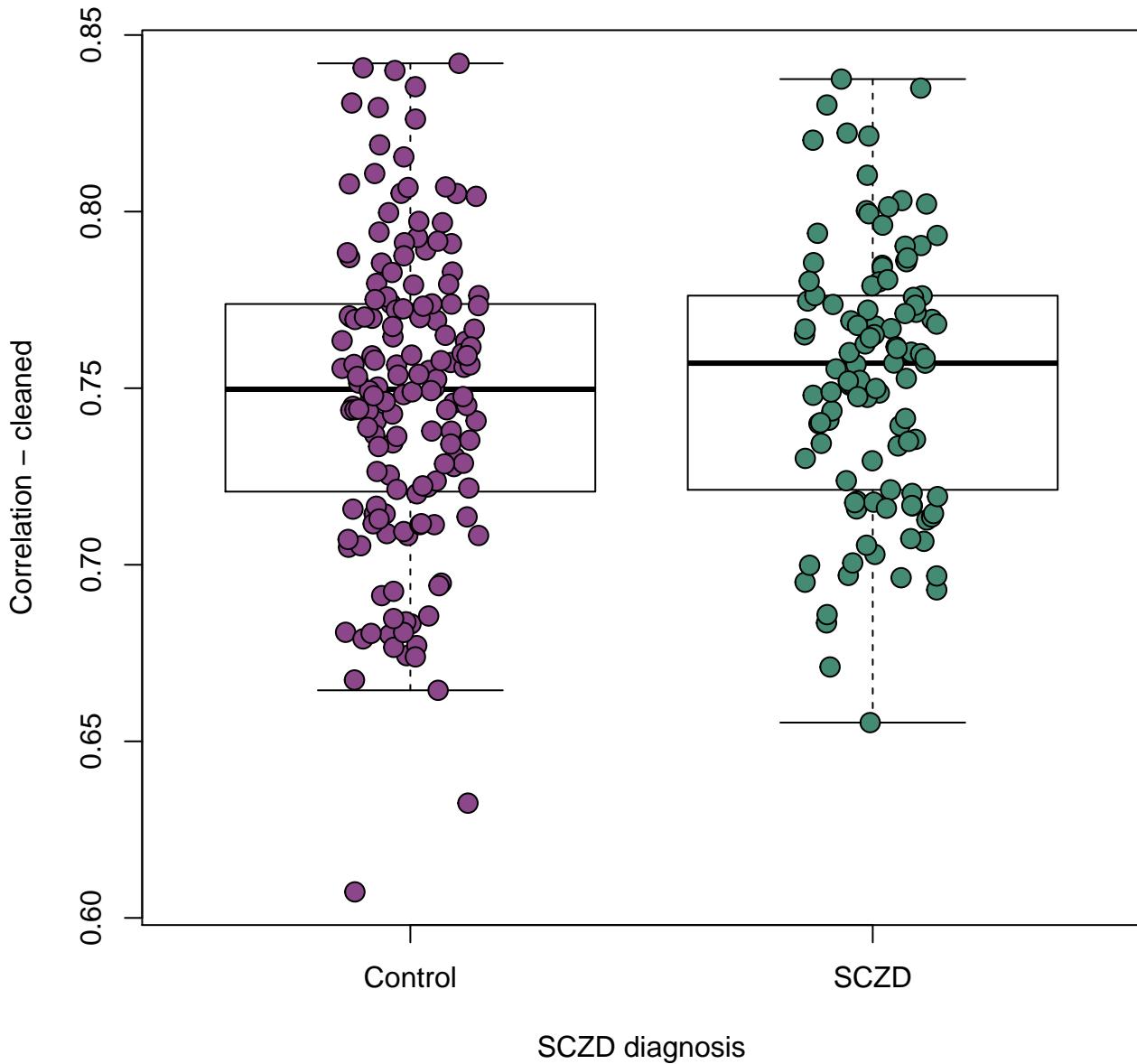
sa00532: Glycosaminoglycan biosynthesis – chondroitin sulfate / dermatan s
p-value: 0.231



hsa00533: Glycosaminoglycan biosynthesis – keratan sulfate
p-value: 0.122

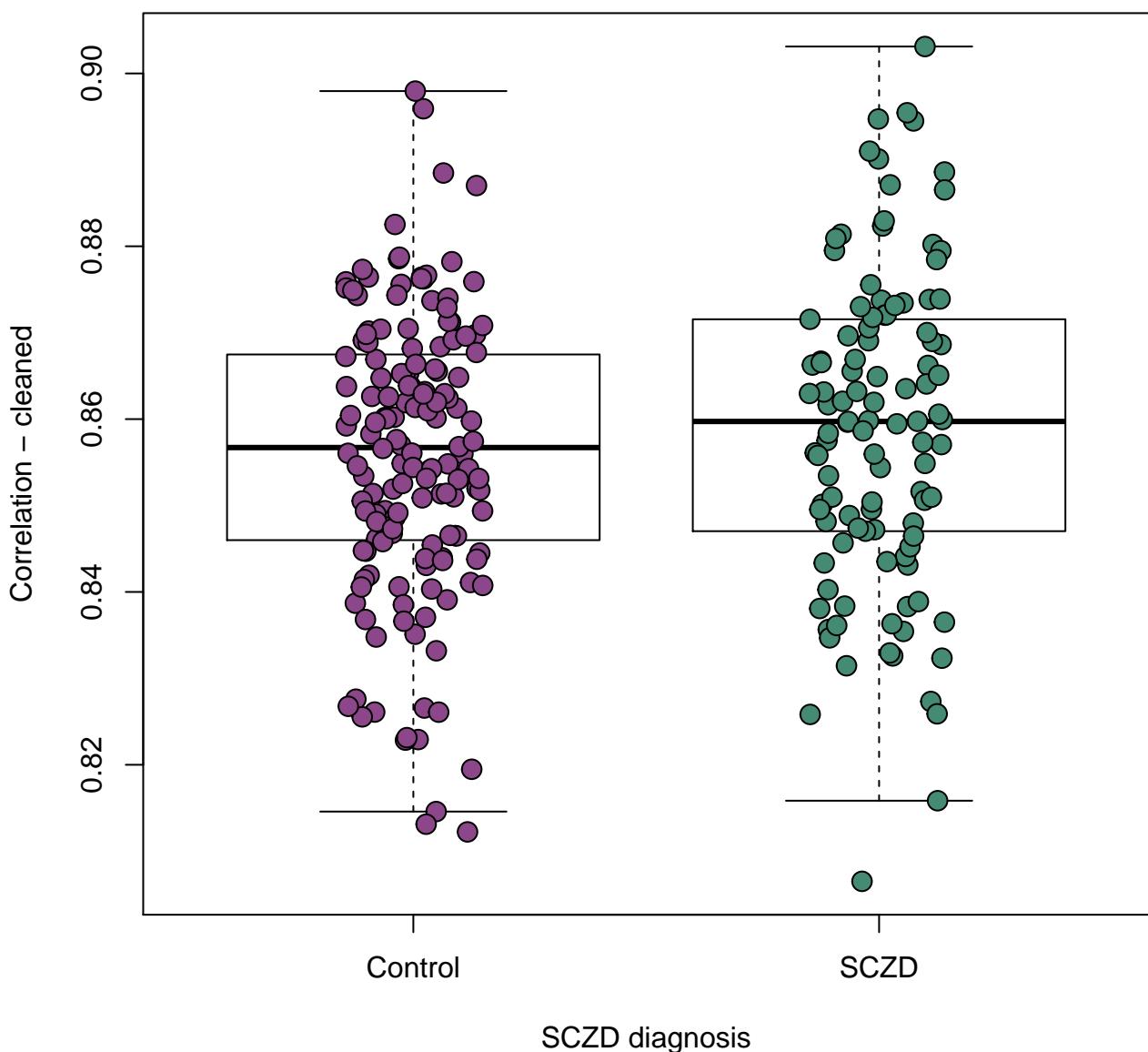


hsa00534: Glycosaminoglycan biosynthesis – heparan sulfate / heparin
p-value: 0.296

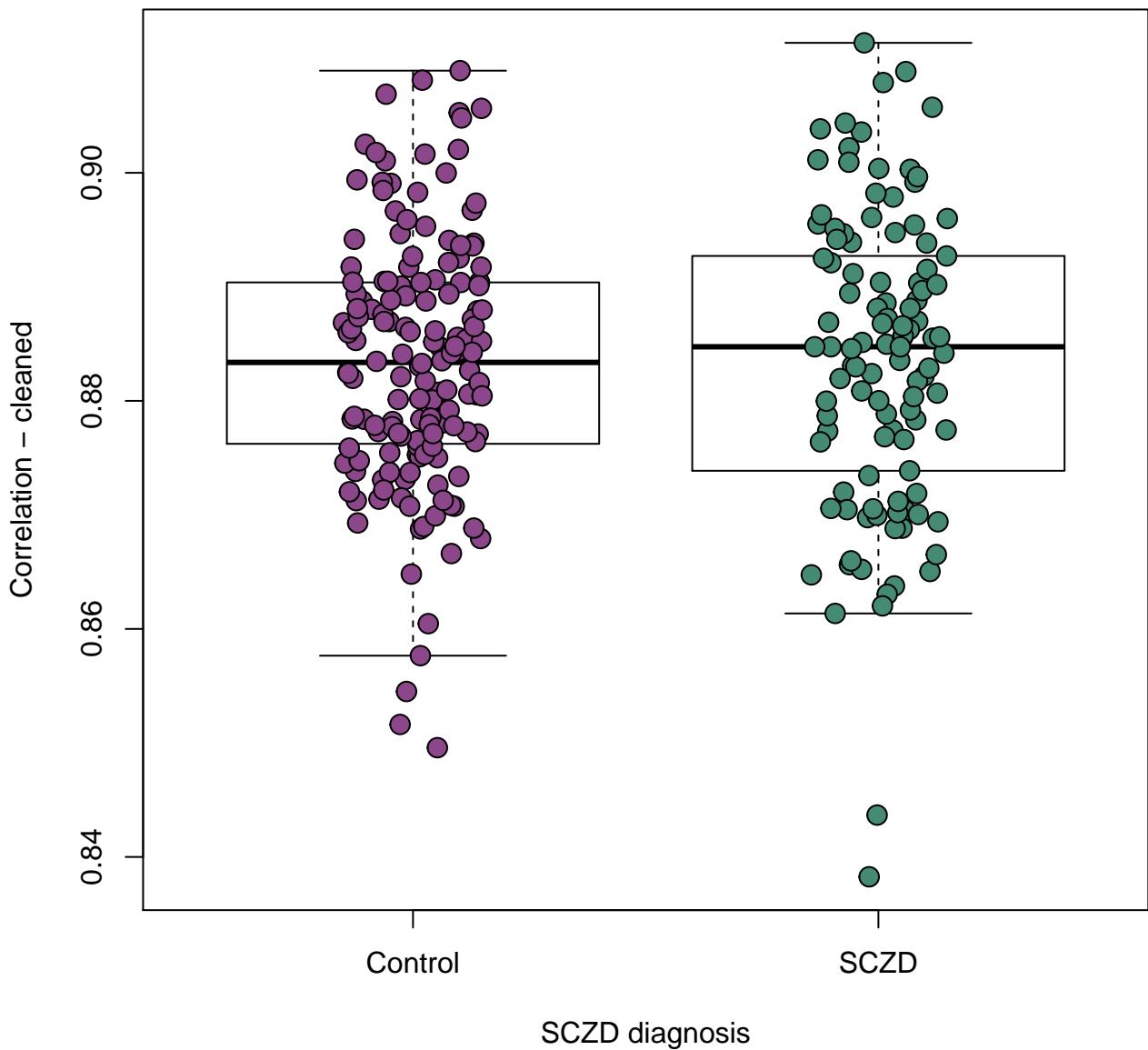


hsa00561: Glycerolipid metabolism

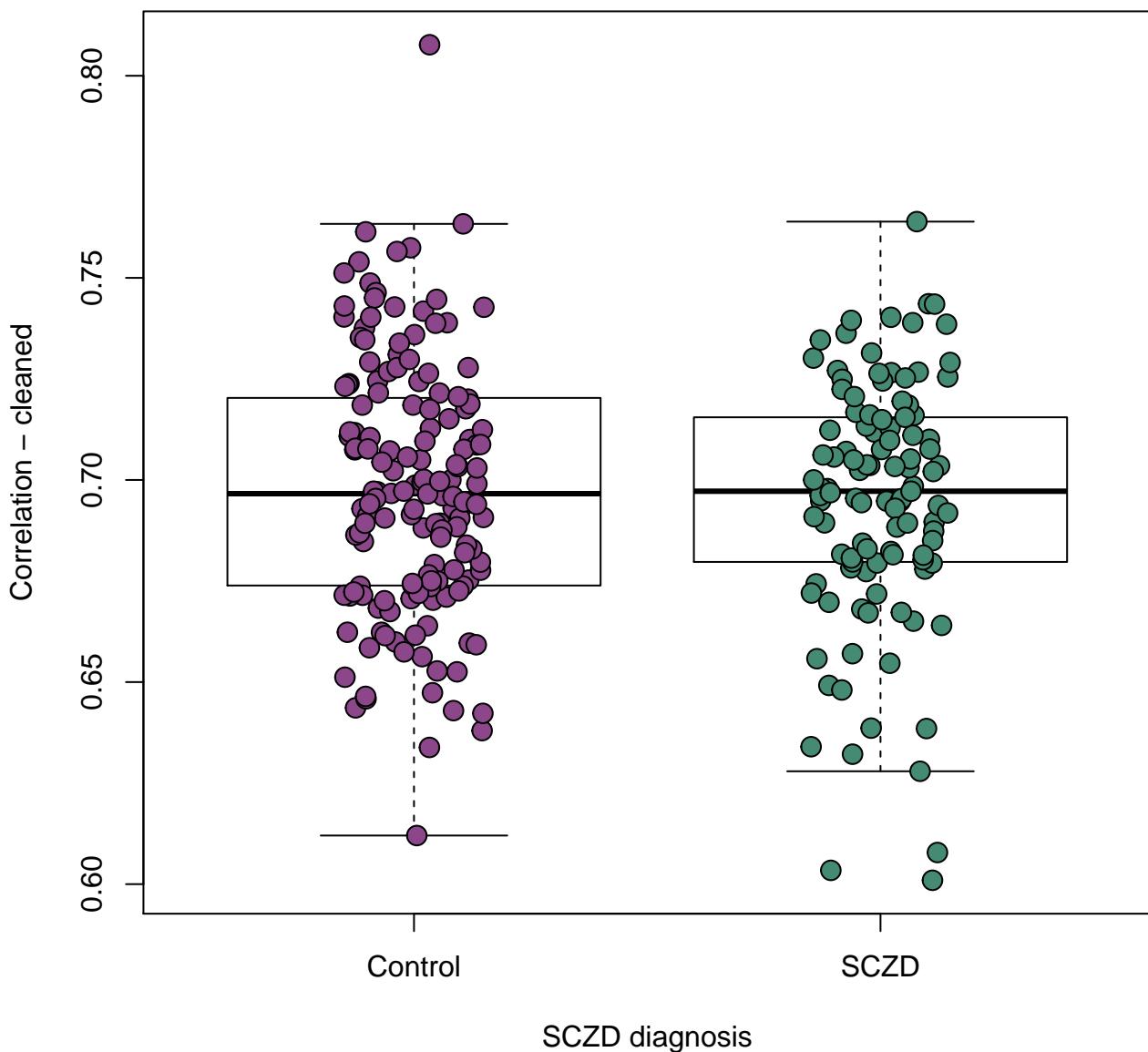
p-value: 0.172



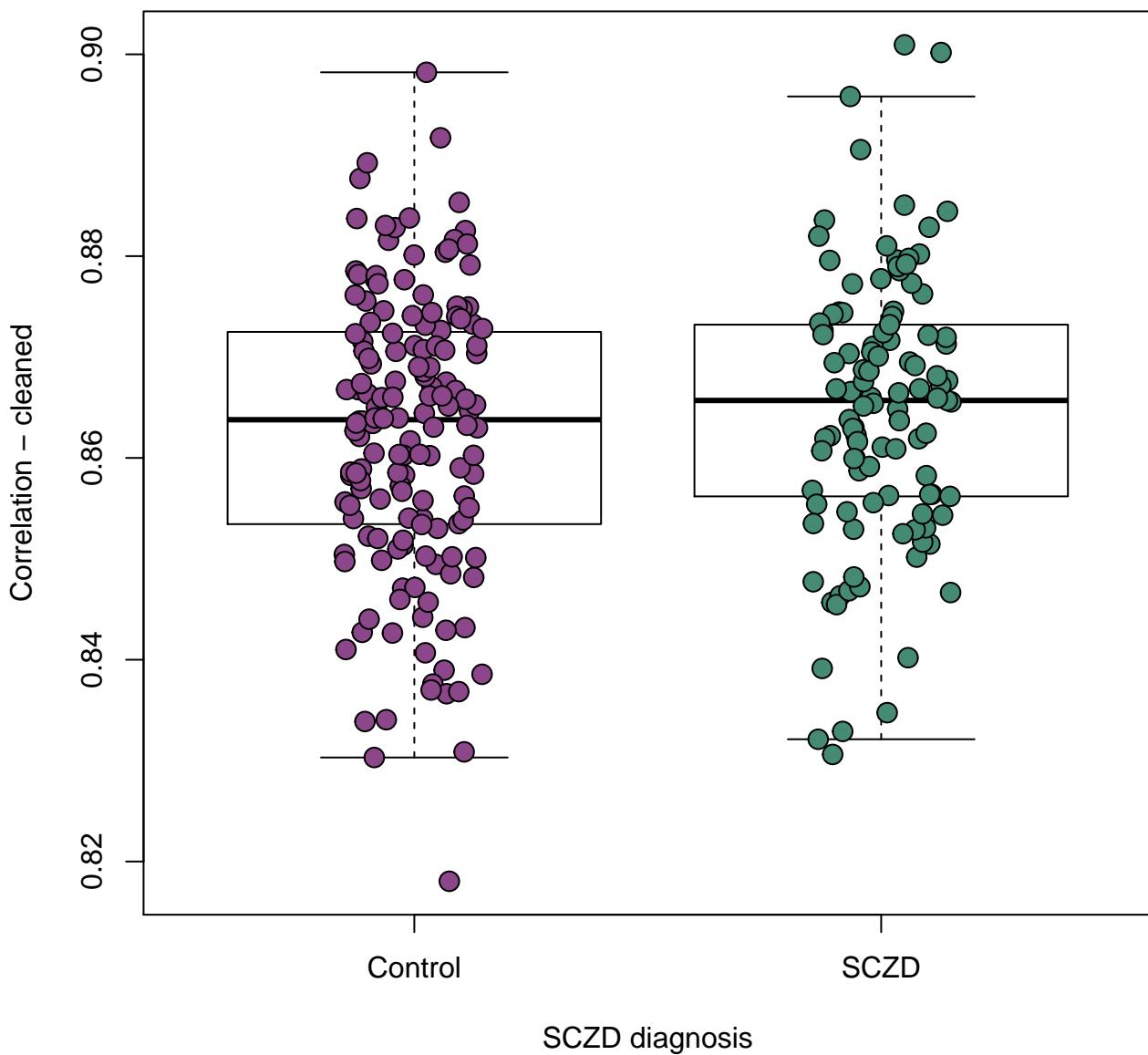
hsa00562: Inositol phosphate metabolism
p-value: 0.914



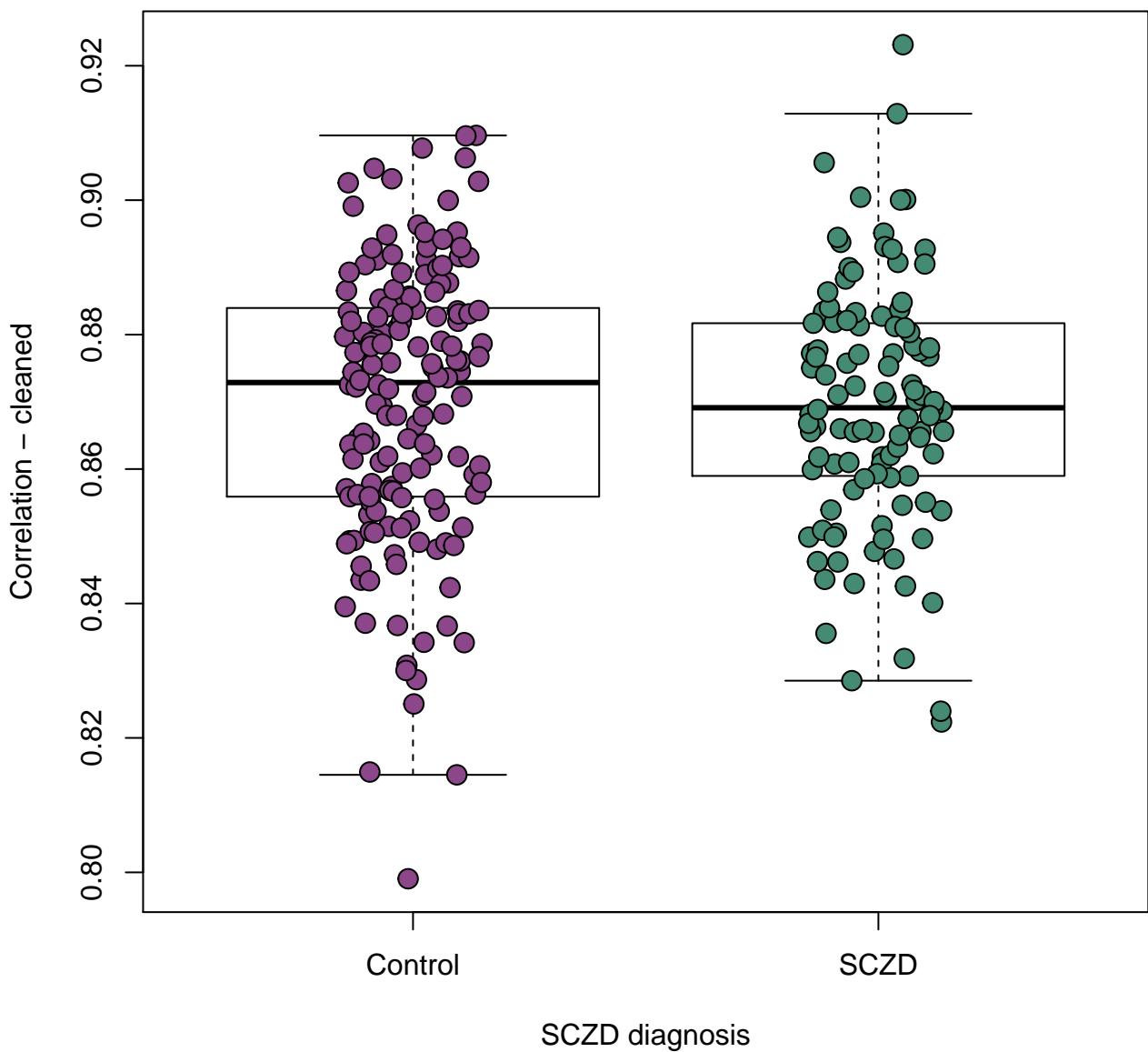
hsa00563: Glycosylphosphatidylinositol(GPI)-anchor biosynthesis
p-value: 0.393



hsa00564: Glycerophospholipid metabolism
p-value: 0.175

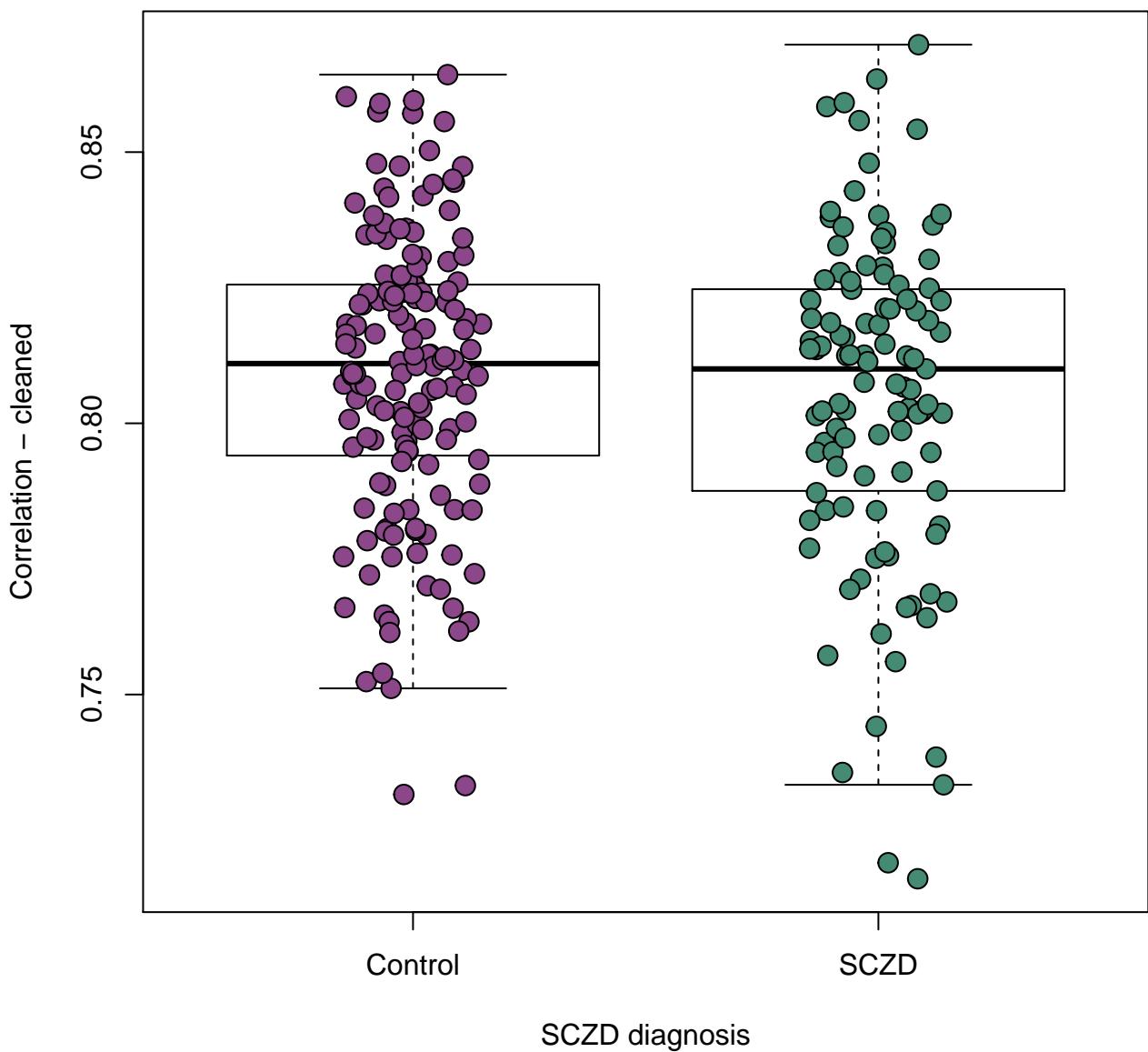


hsa00565: Ether lipid metabolism
p-value: 0.907



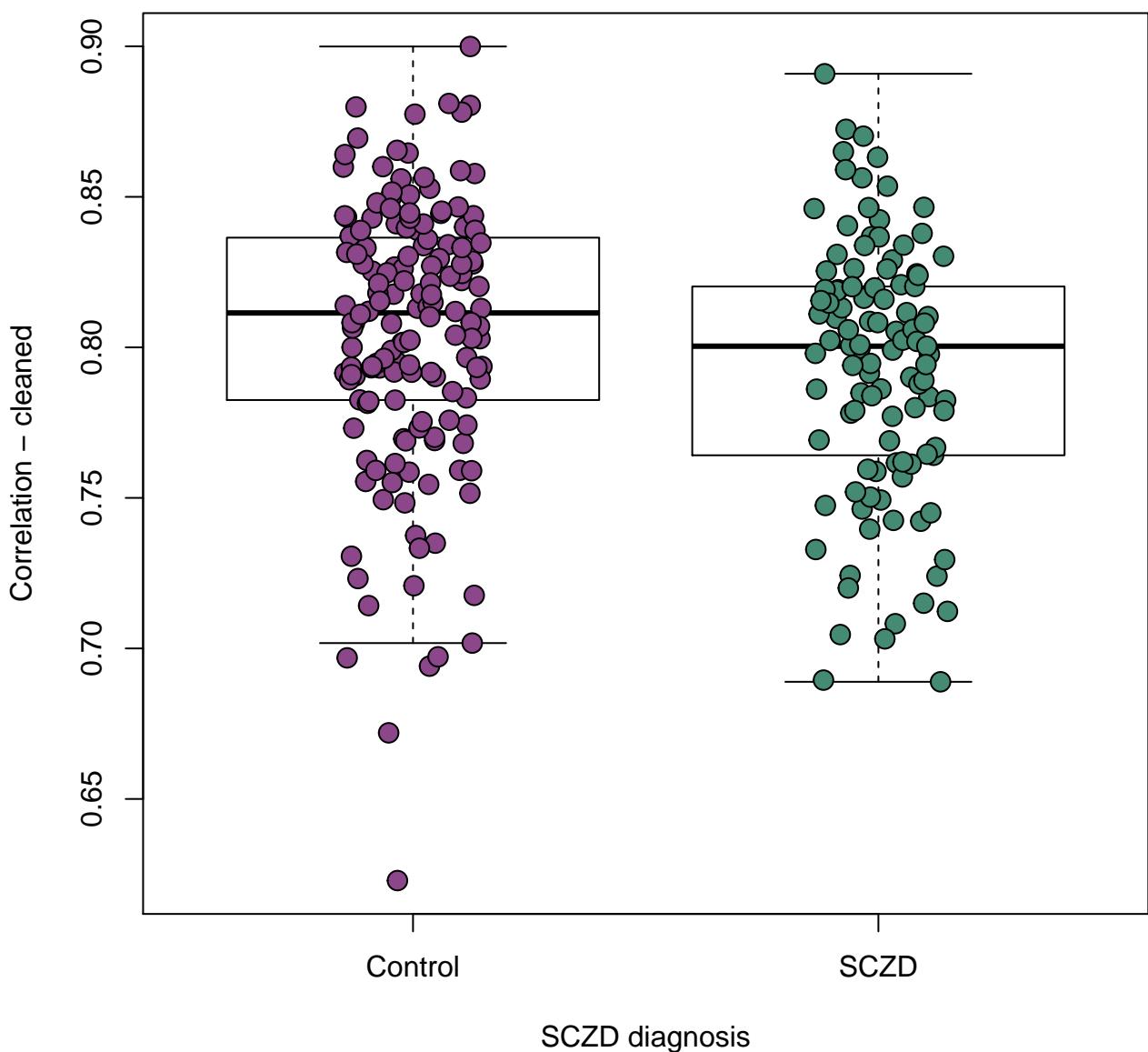
hsa00590: Arachidonic acid metabolism

p-value: 0.24

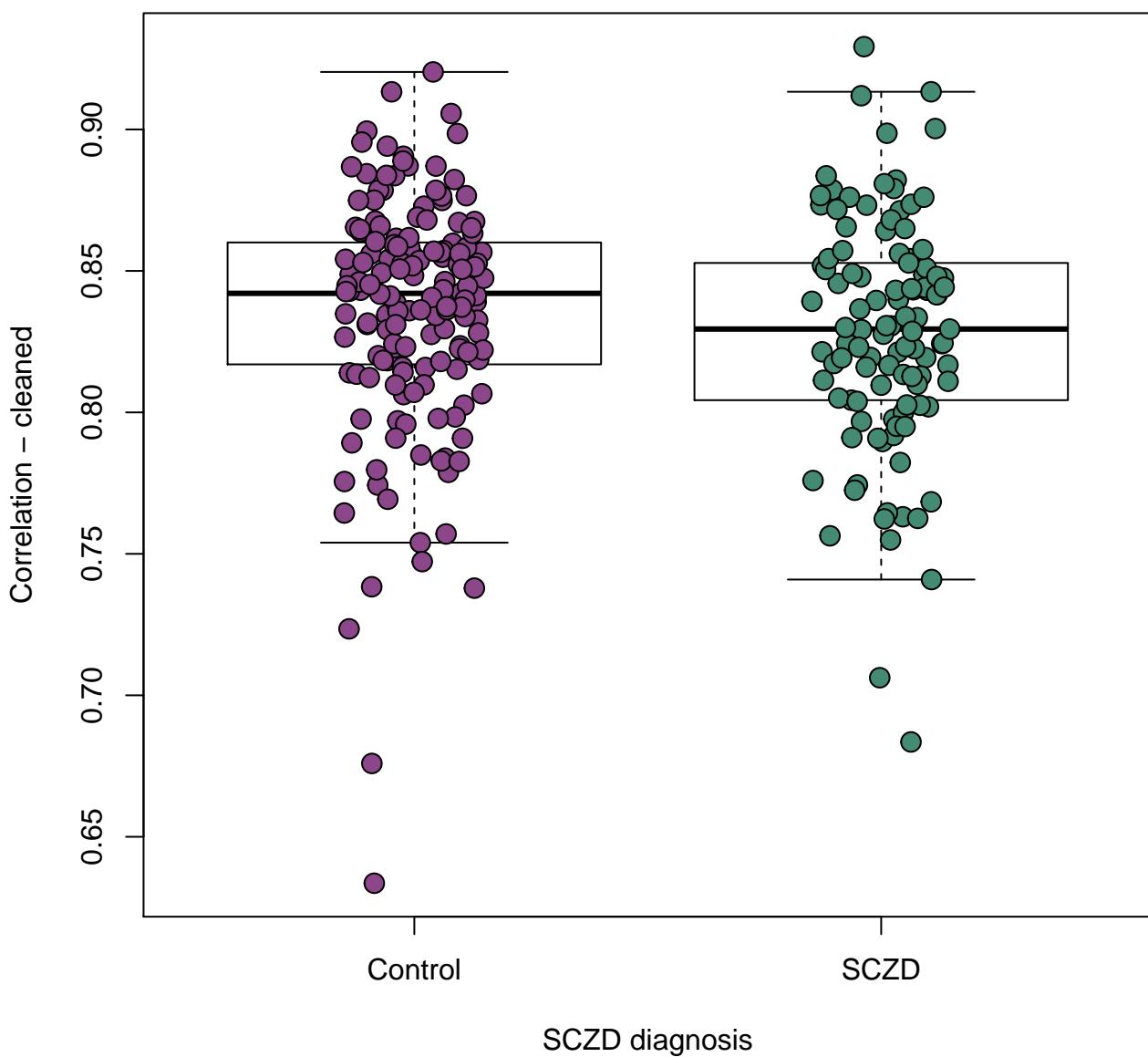


hsa00591: Linoleic acid metabolism

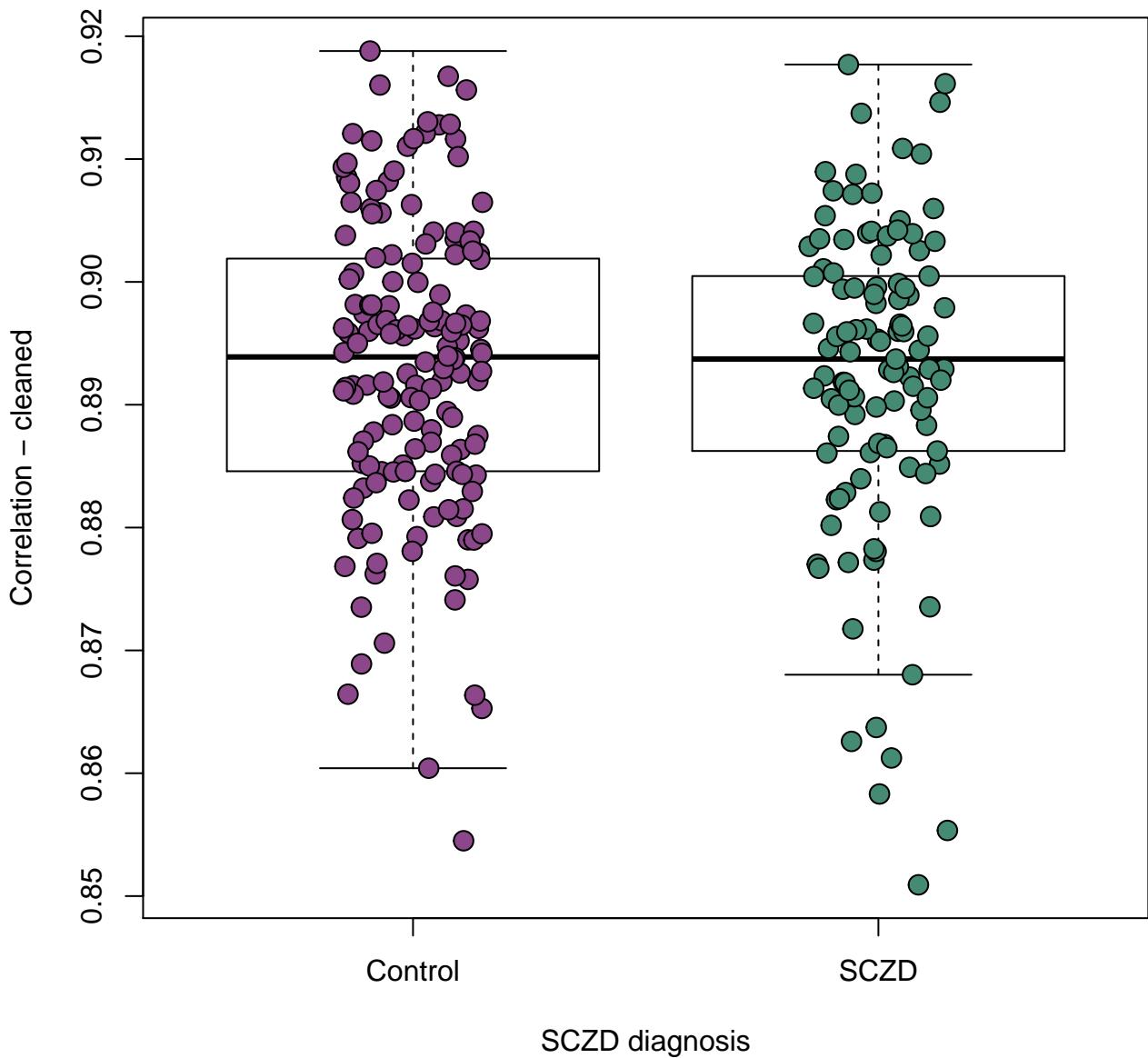
p-value: 0.0365



hsa00592: alpha-Linolenic acid metabolism
p-value: 0.162

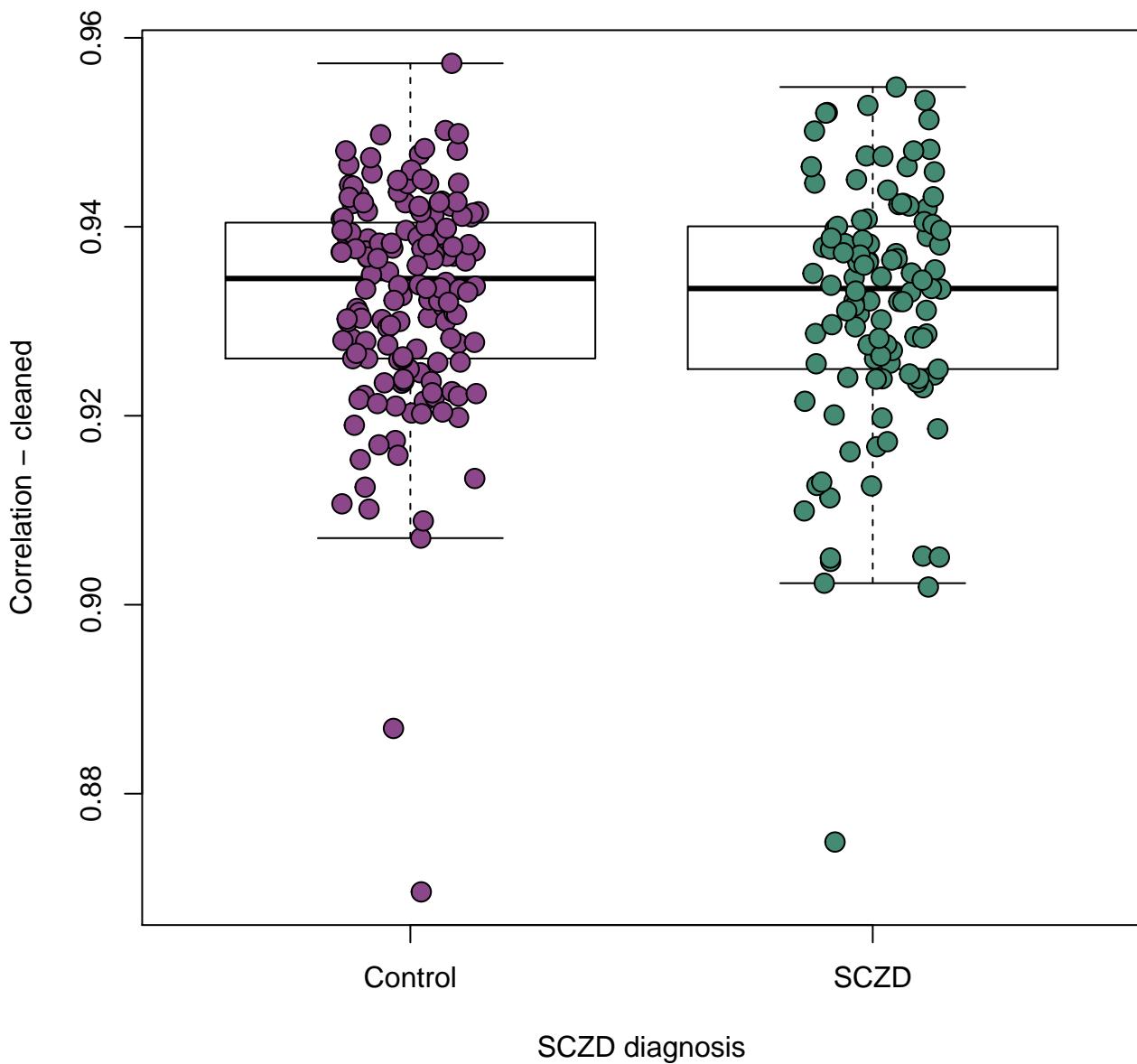


hsa00600: Sphingolipid metabolism
p-value: 0.636

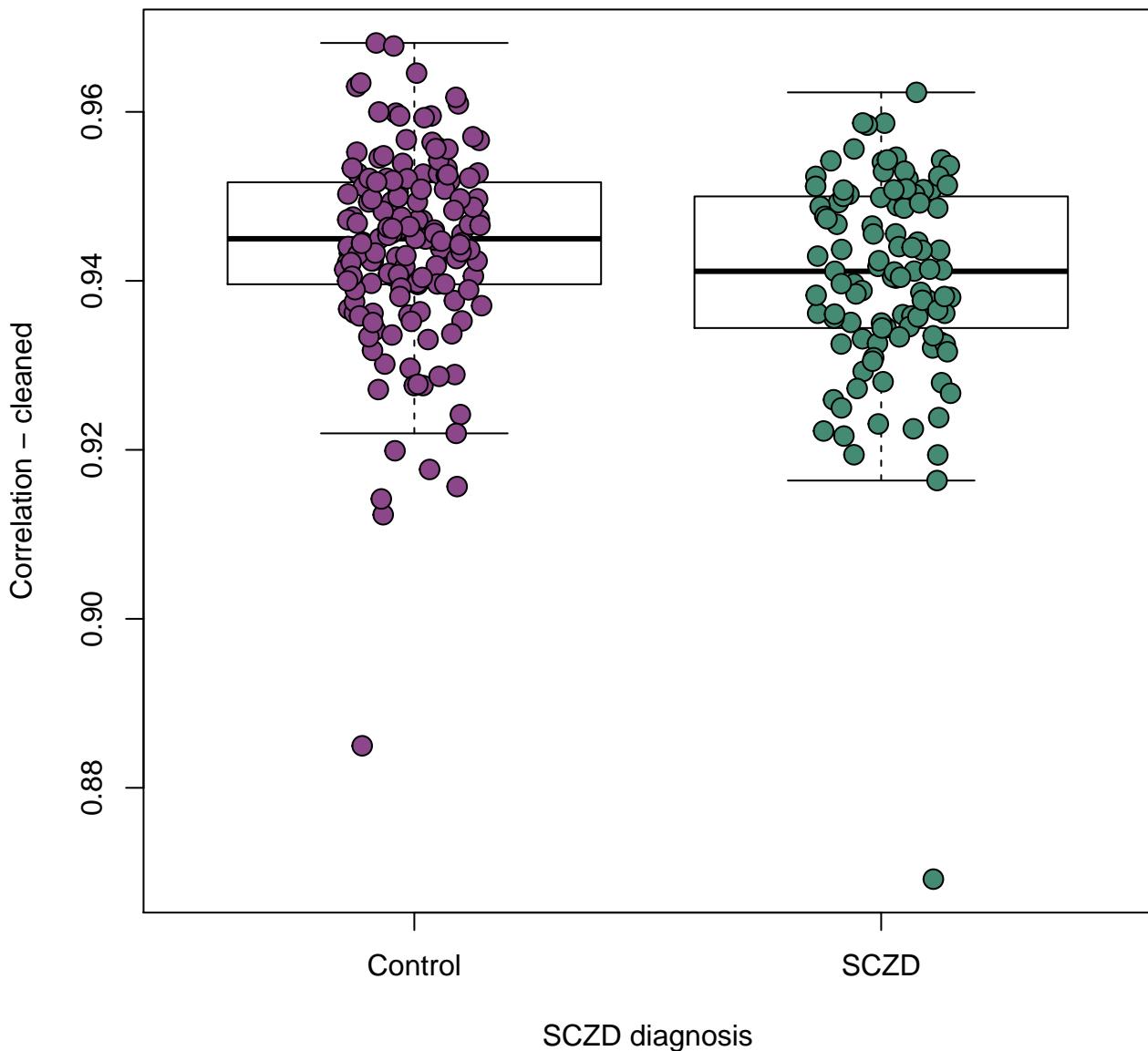


hsa00601: Glycosphingolipid biosynthesis – lacto and neolacto series

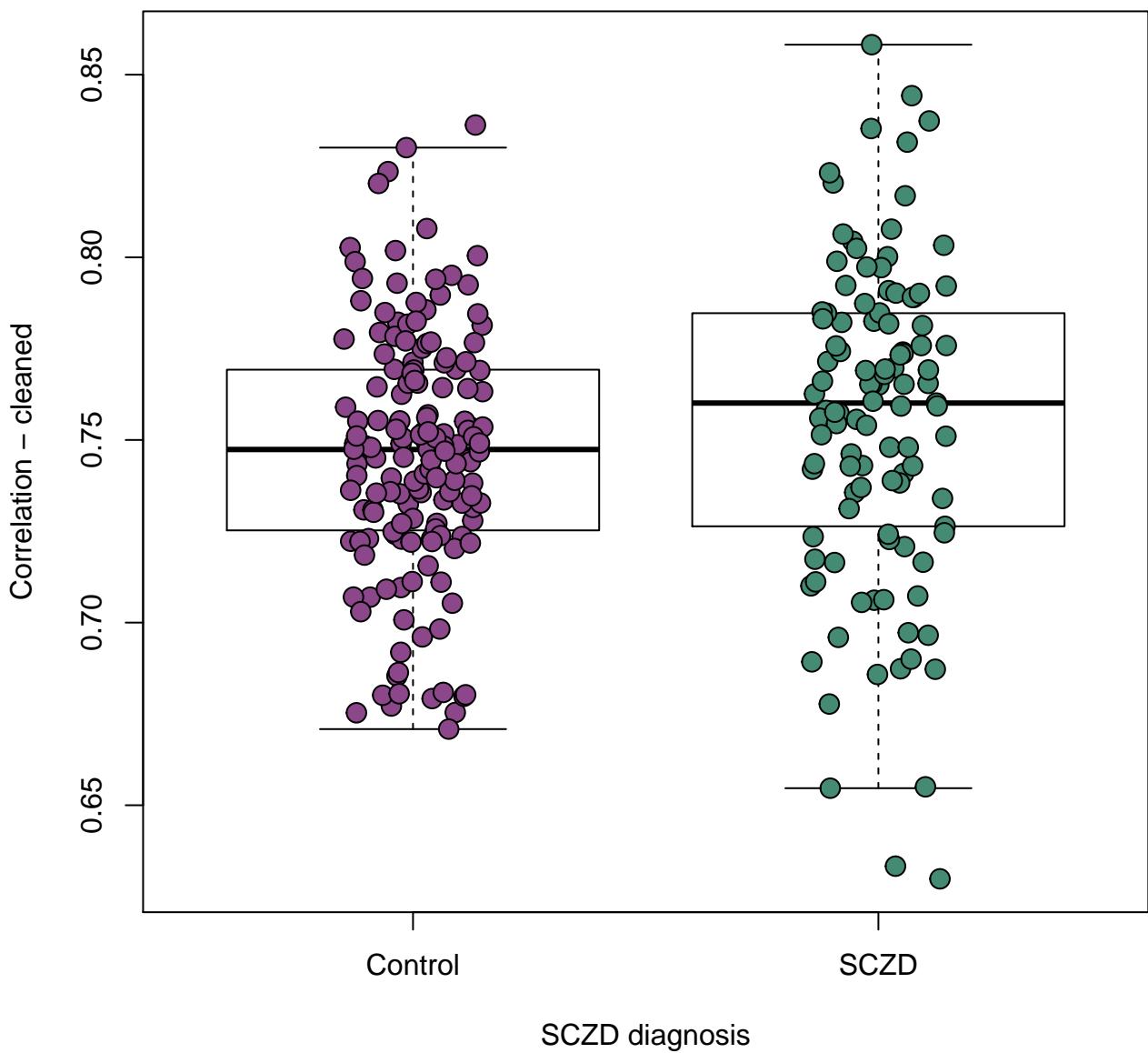
p-value: 0.51



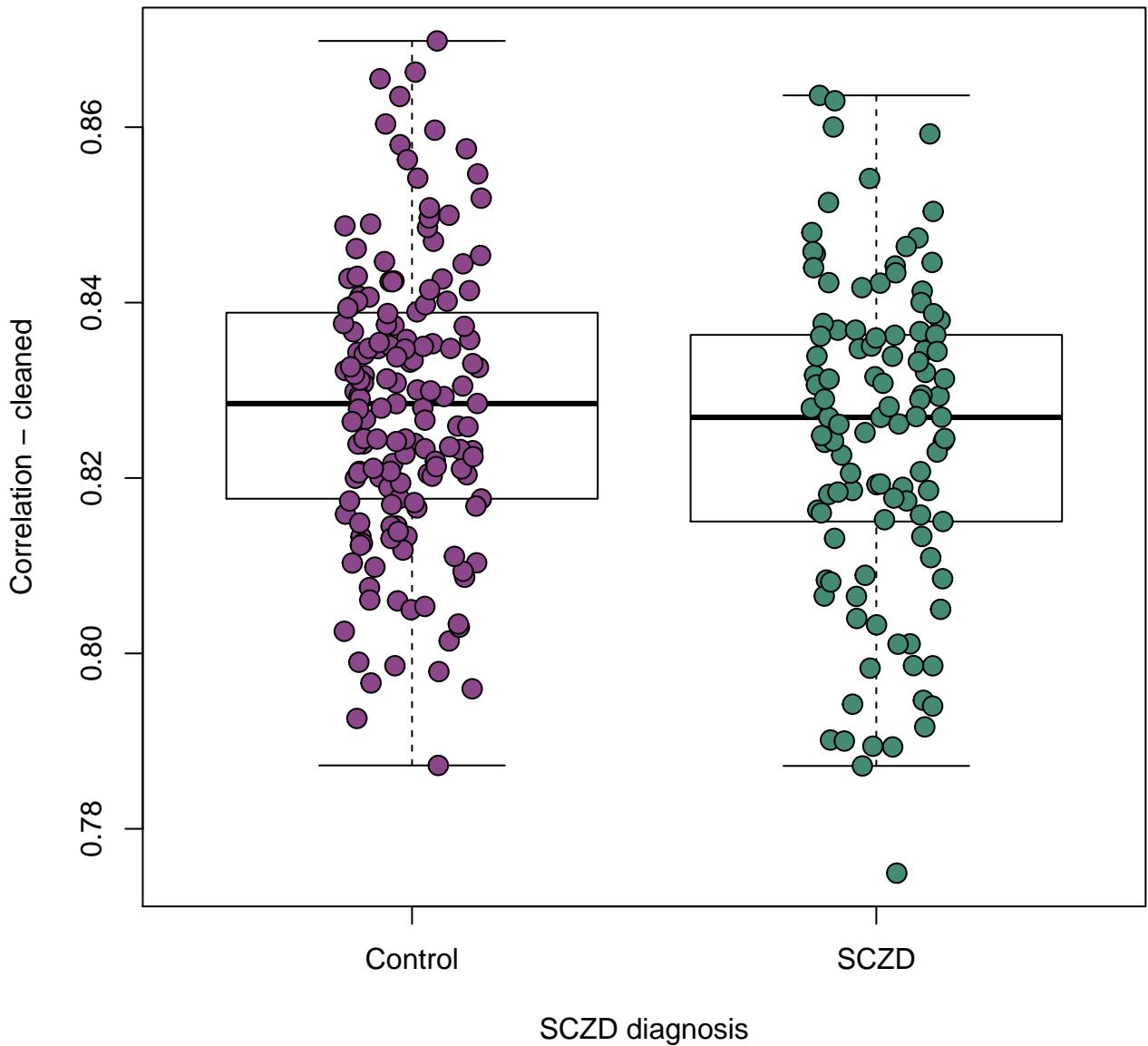
hsa00603: Glycosphingolipid biosynthesis – globo series
p-value: 0.0123



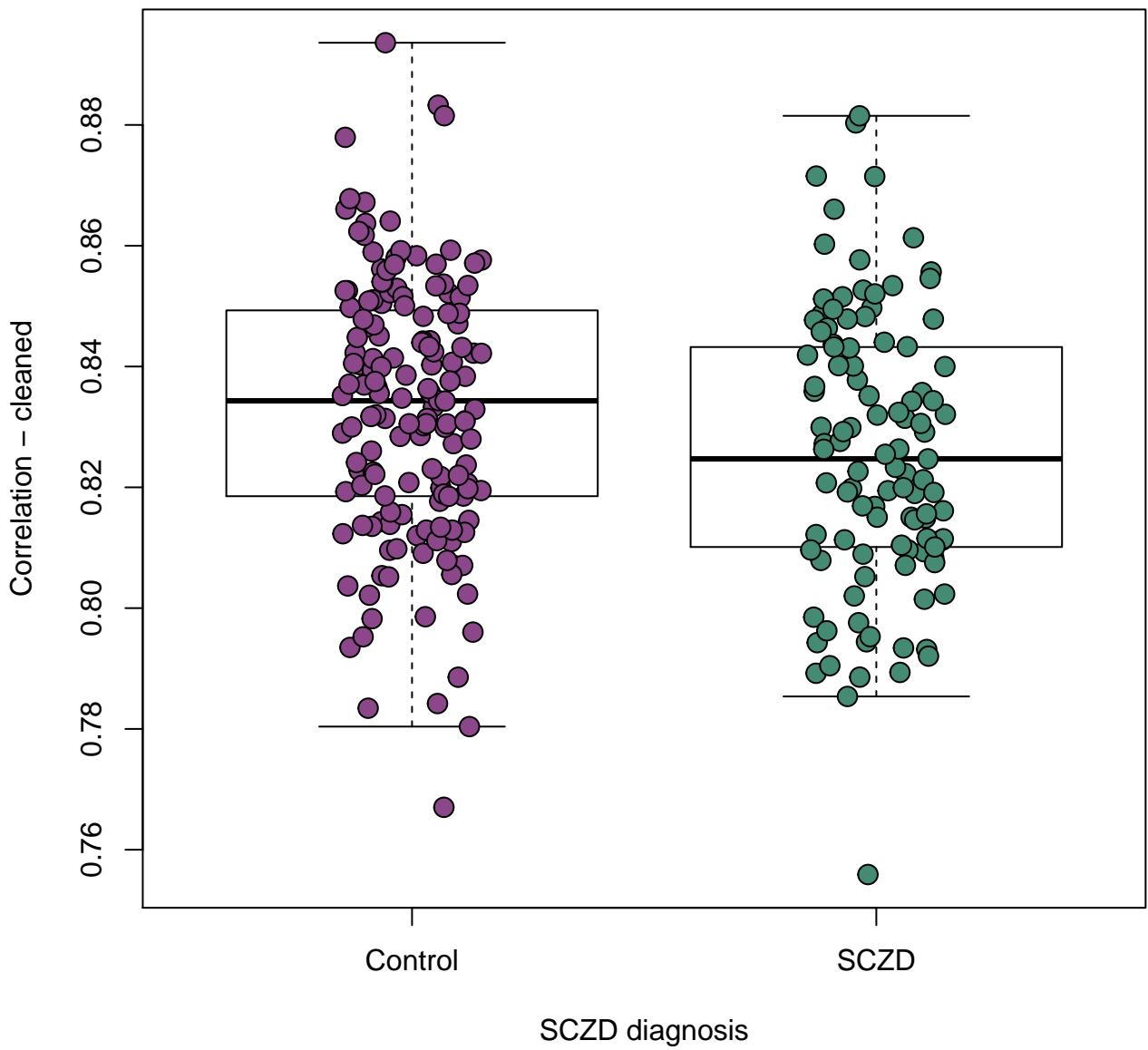
hsa00604: Glycosphingolipid biosynthesis – ganglio series
p-value: 0.0564



hsa00620: Pyruvate metabolism
p-value: 0.0728

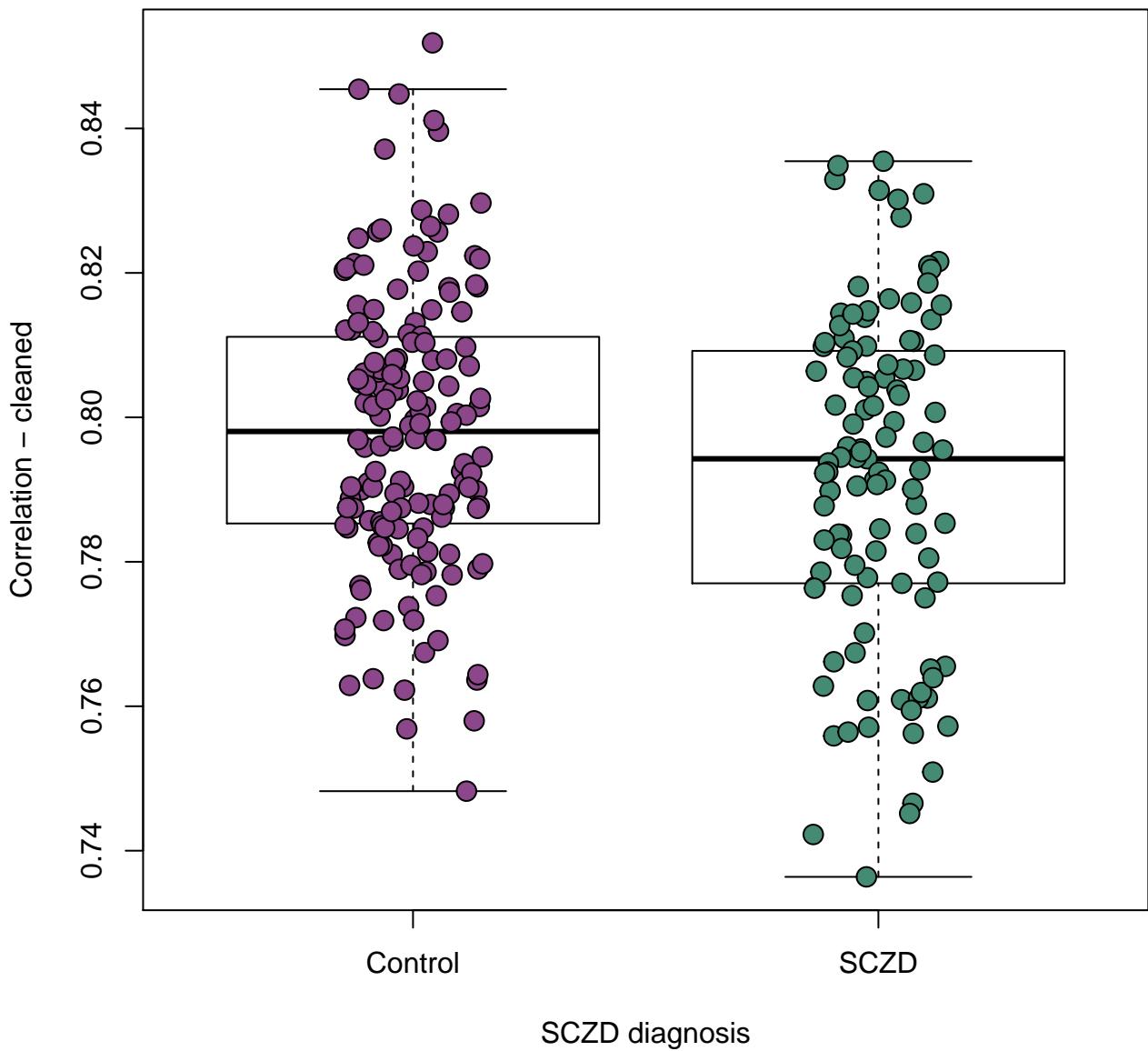


hsa00630: Glyoxylate and dicarboxylate metabolism
p-value: 0.00872

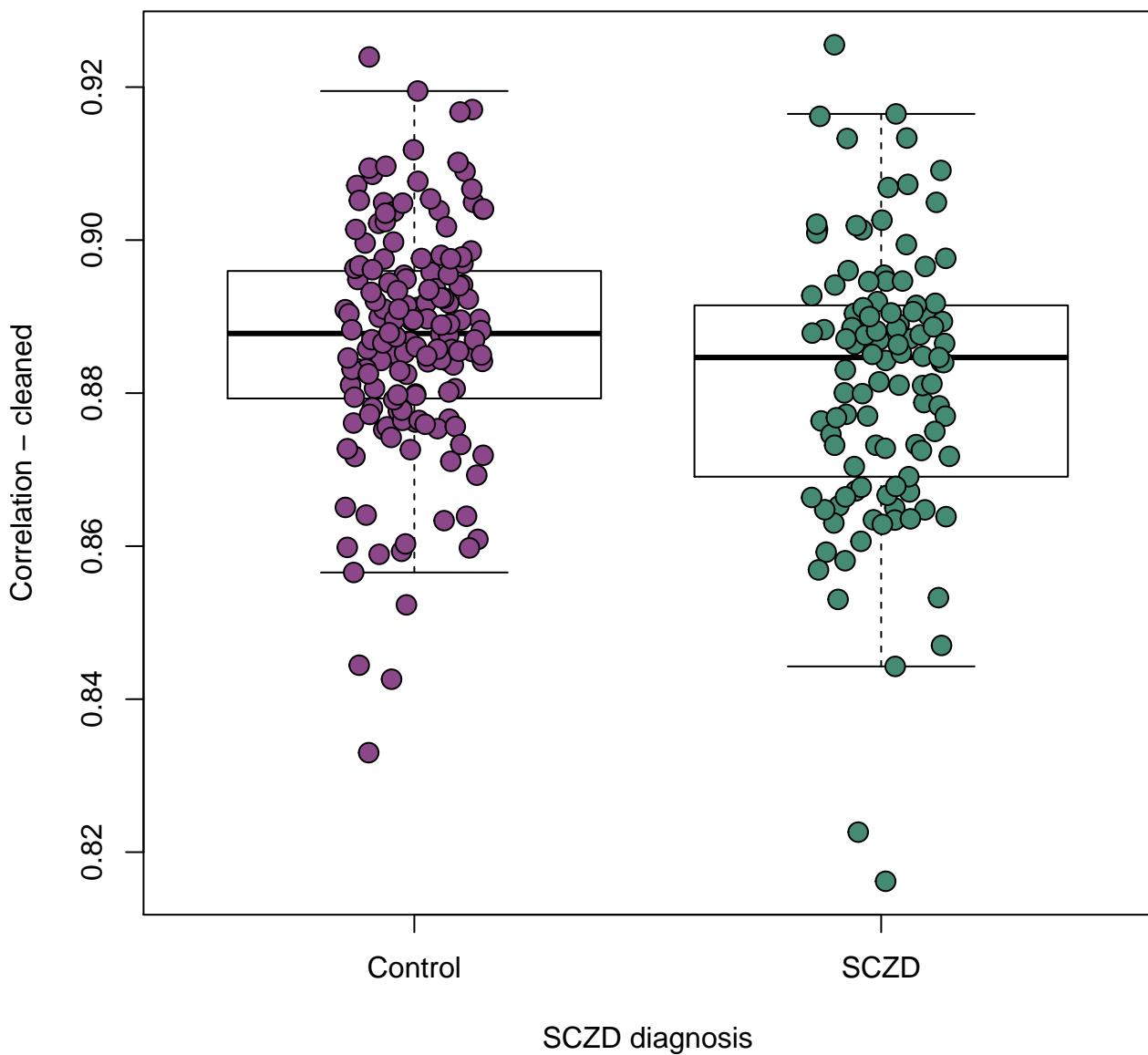


hsa00640: Propanoate metabolism

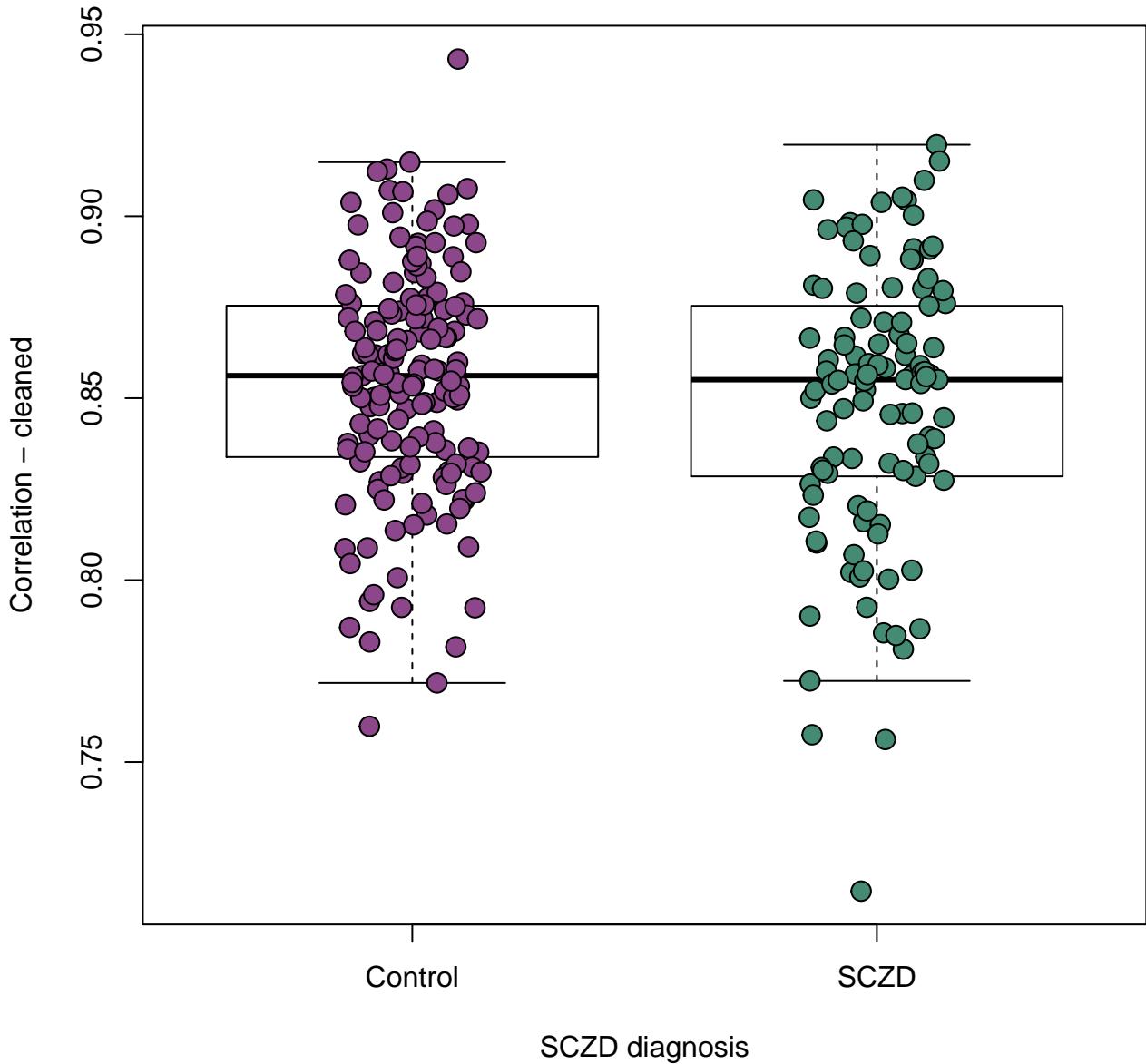
p-value: 0.0147



hsa00650: Butanoate metabolism
p-value: 0.00732

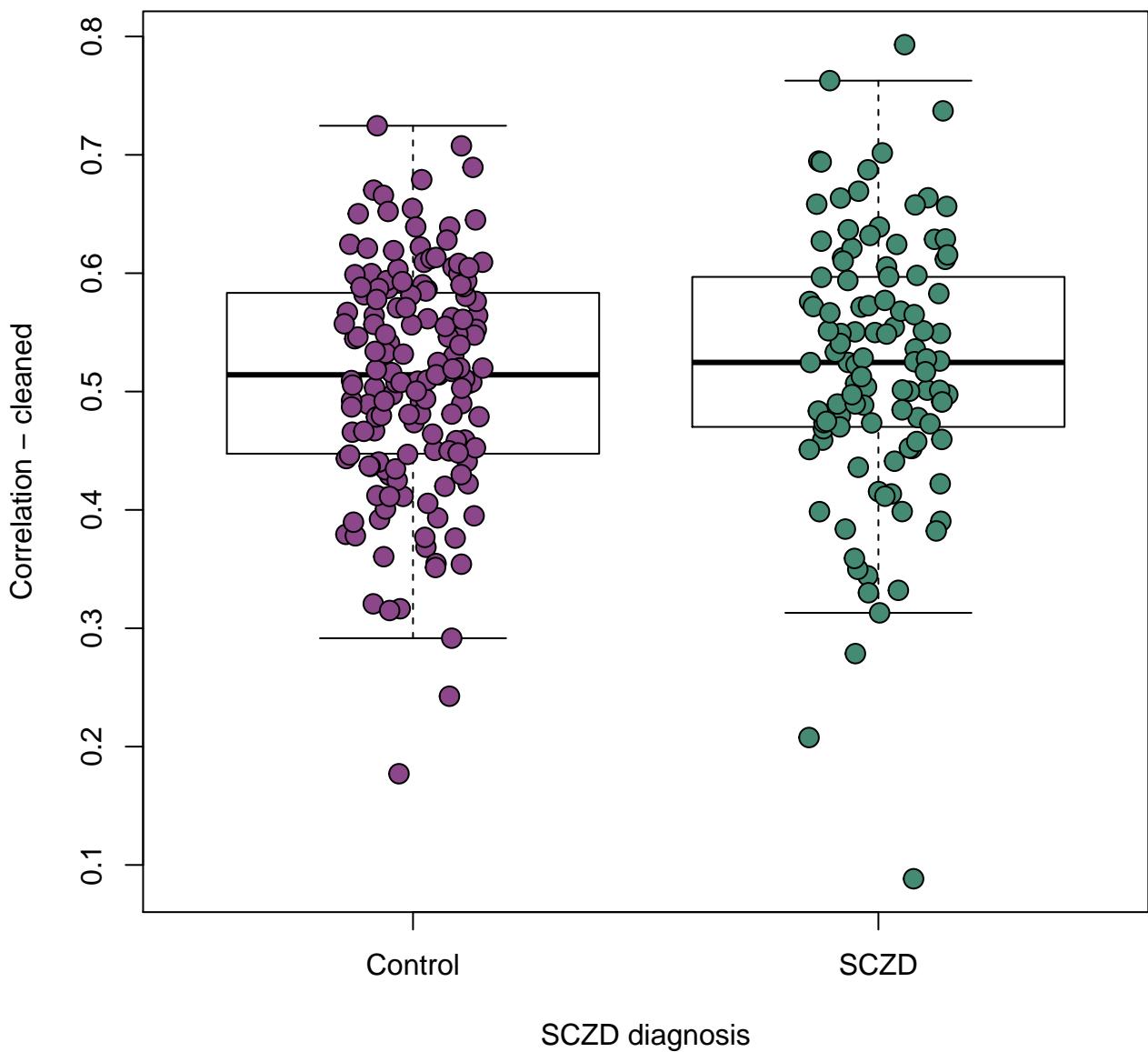


hsa00670: One carbon pool by folate
p-value: 0.183

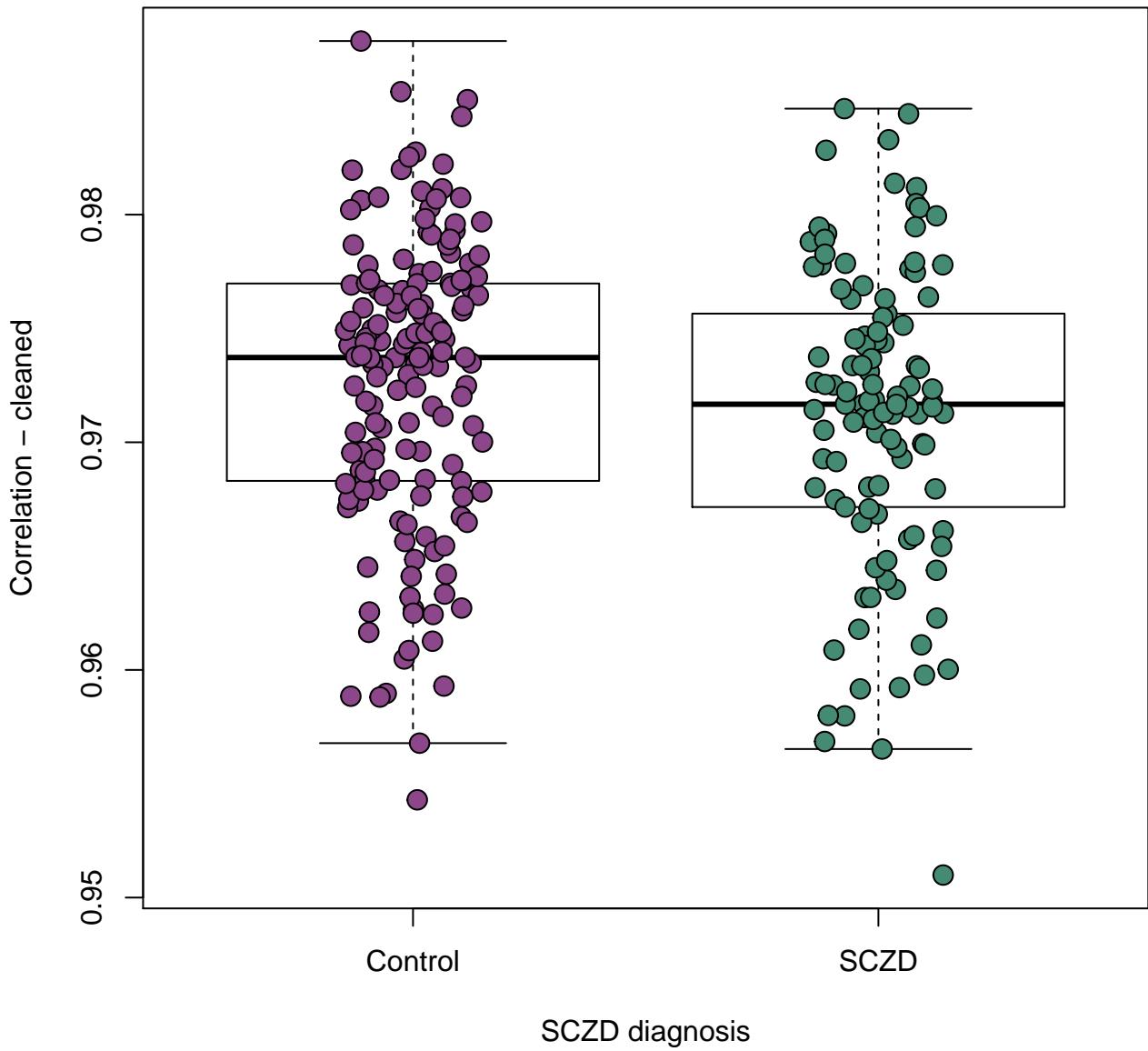


hsa00730: Thiamine metabolism

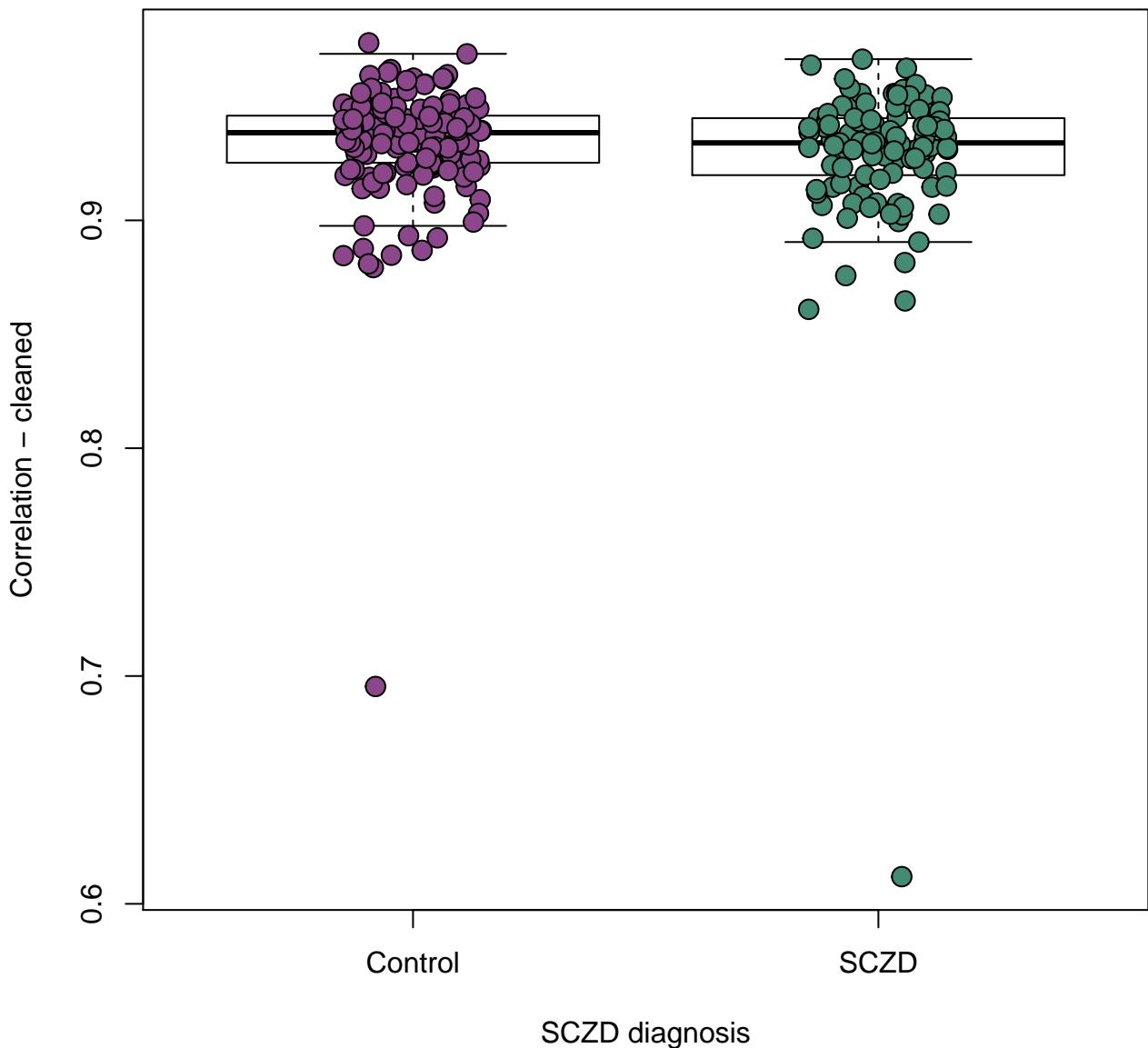
p-value: 0.373



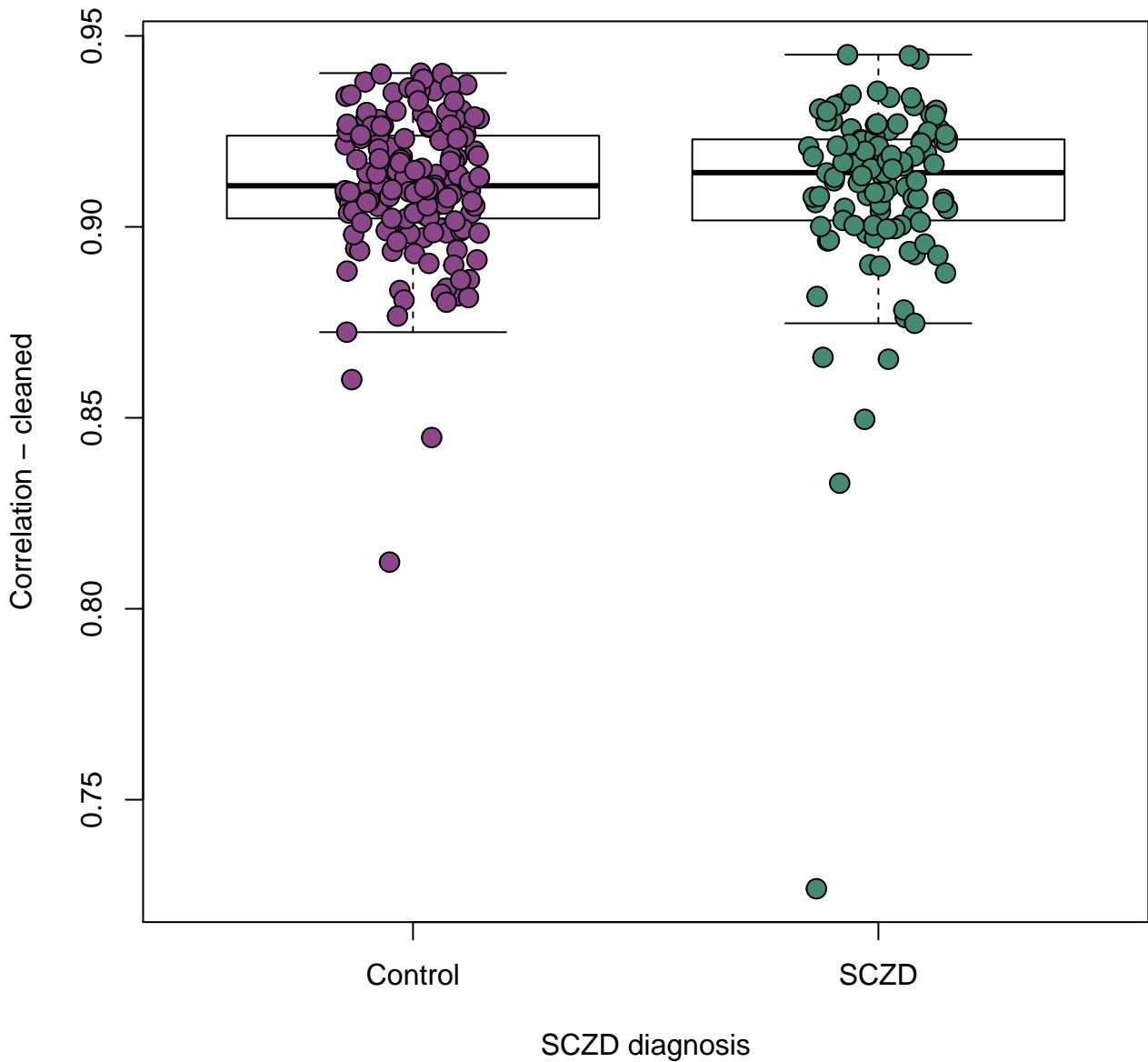
hsa00740: Riboflavin metabolism
p-value: 0.0733



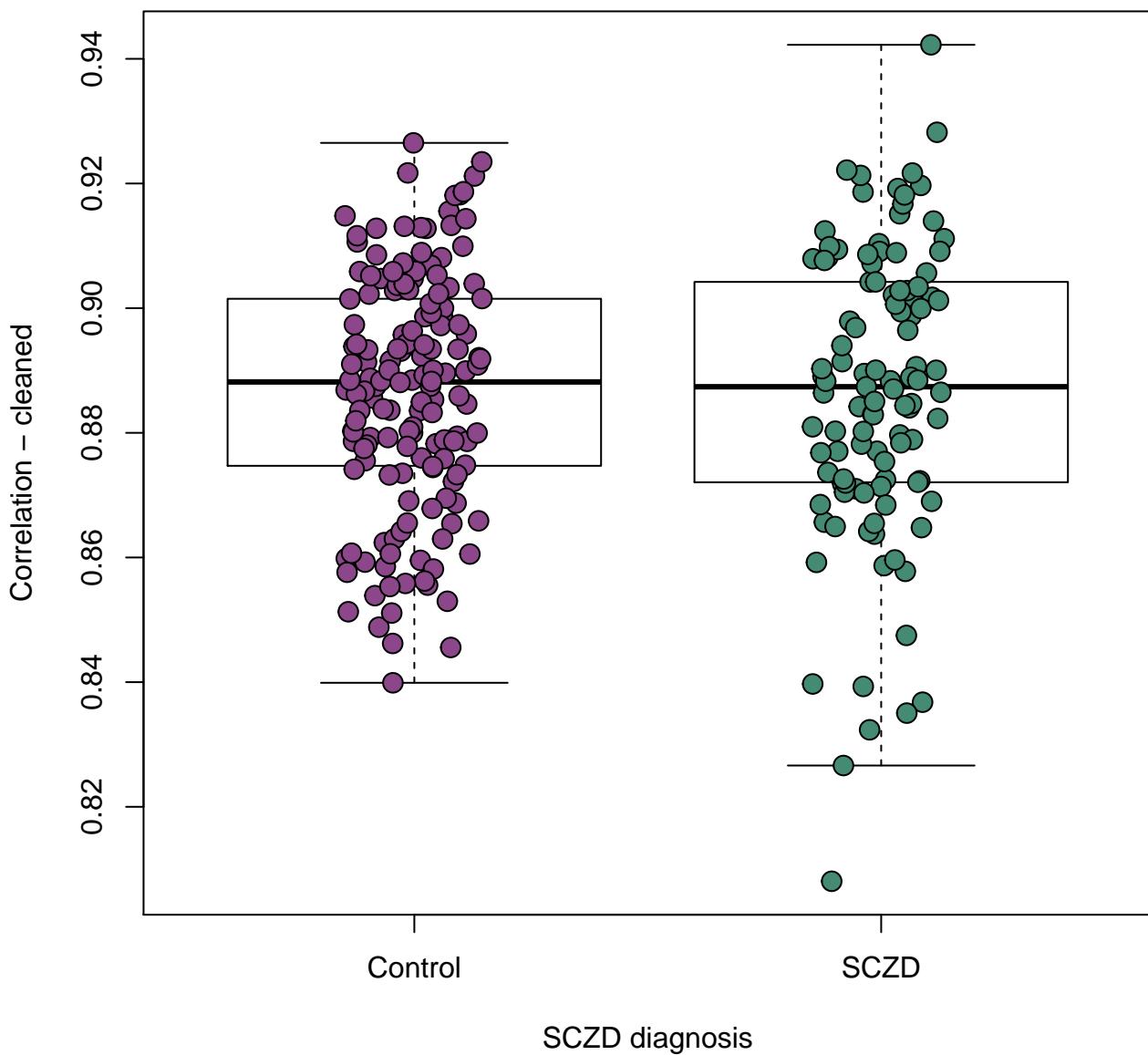
hsa00750: Vitamin B6 metabolism
p-value: 0.195



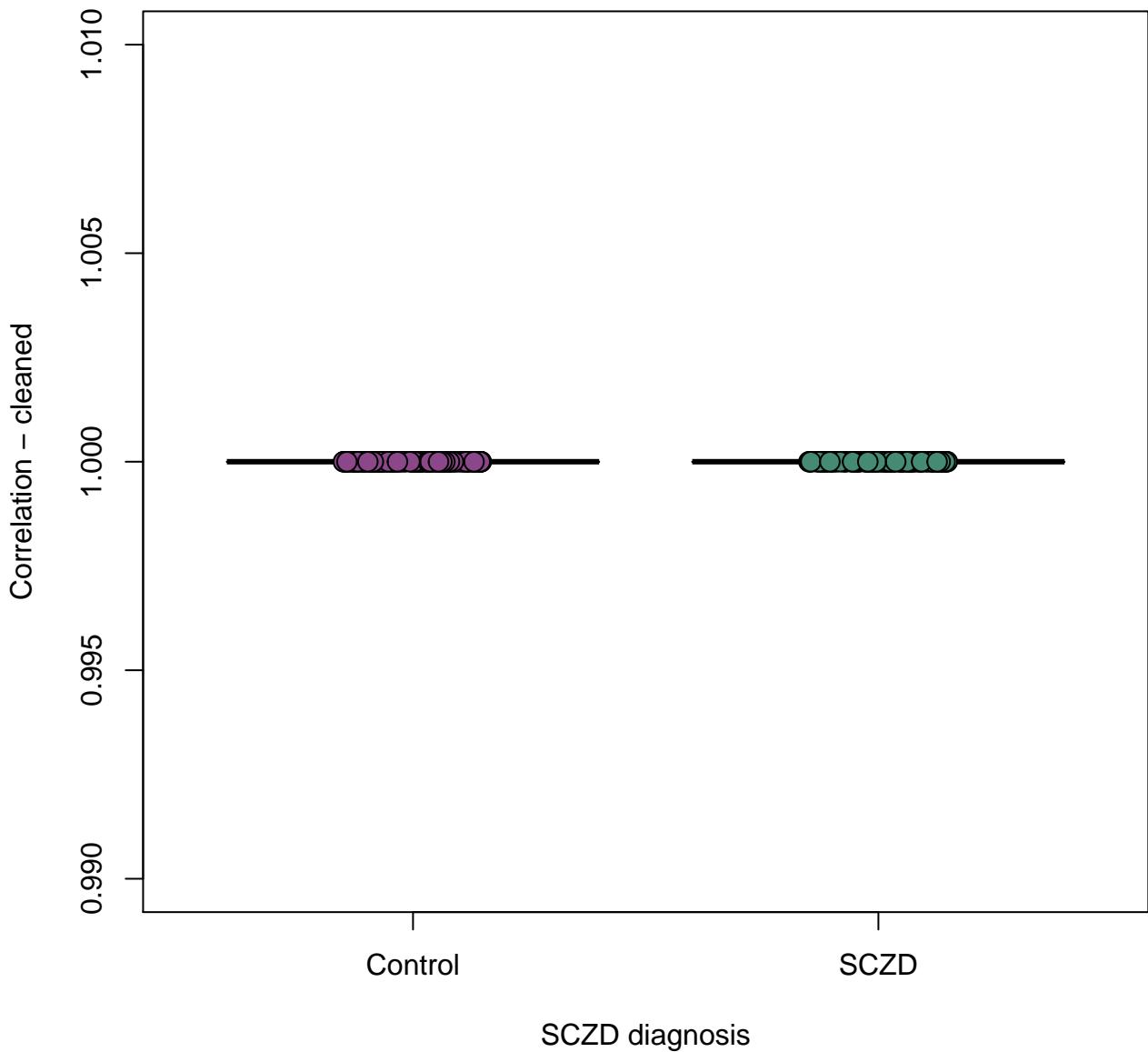
hsa00760: Nicotinate and nicotinamide metabolism
p-value: 0.754



hsa00770: Pantothenate and CoA biosynthesis
p-value: 0.997

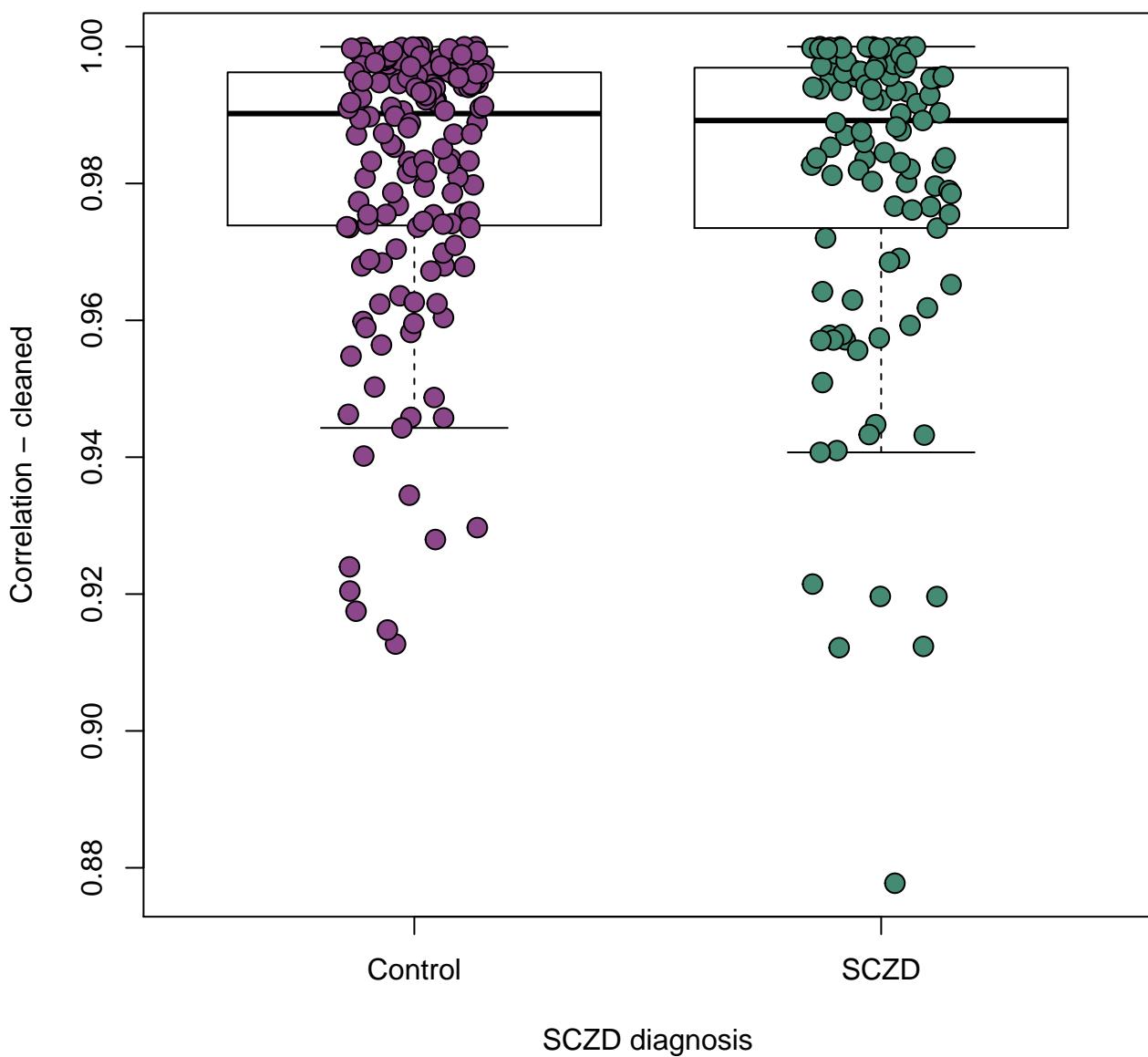


hsa00780: Biotin metabolism
p-value: 0.392

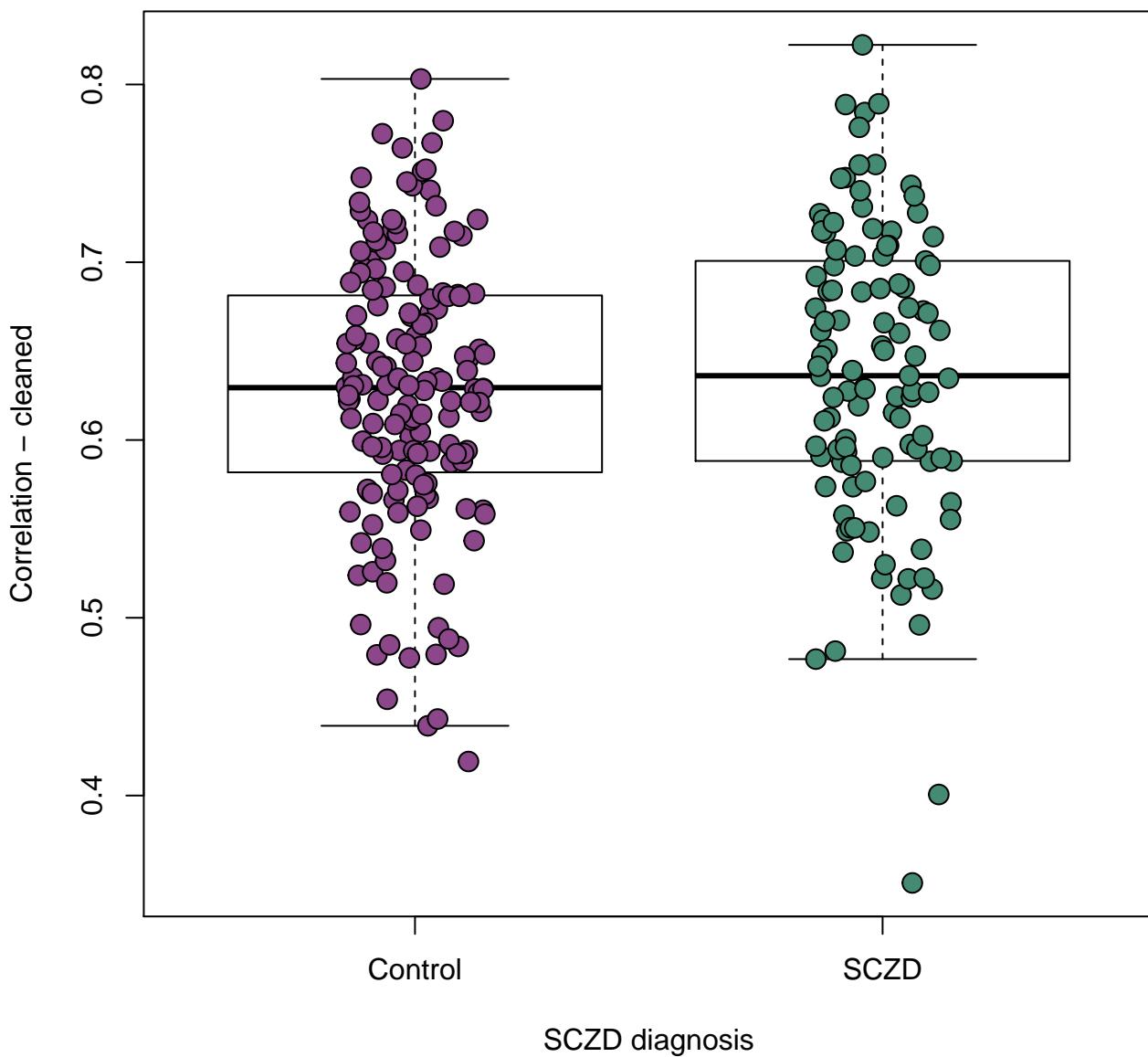


hsa00785: Lipoic acid metabolism

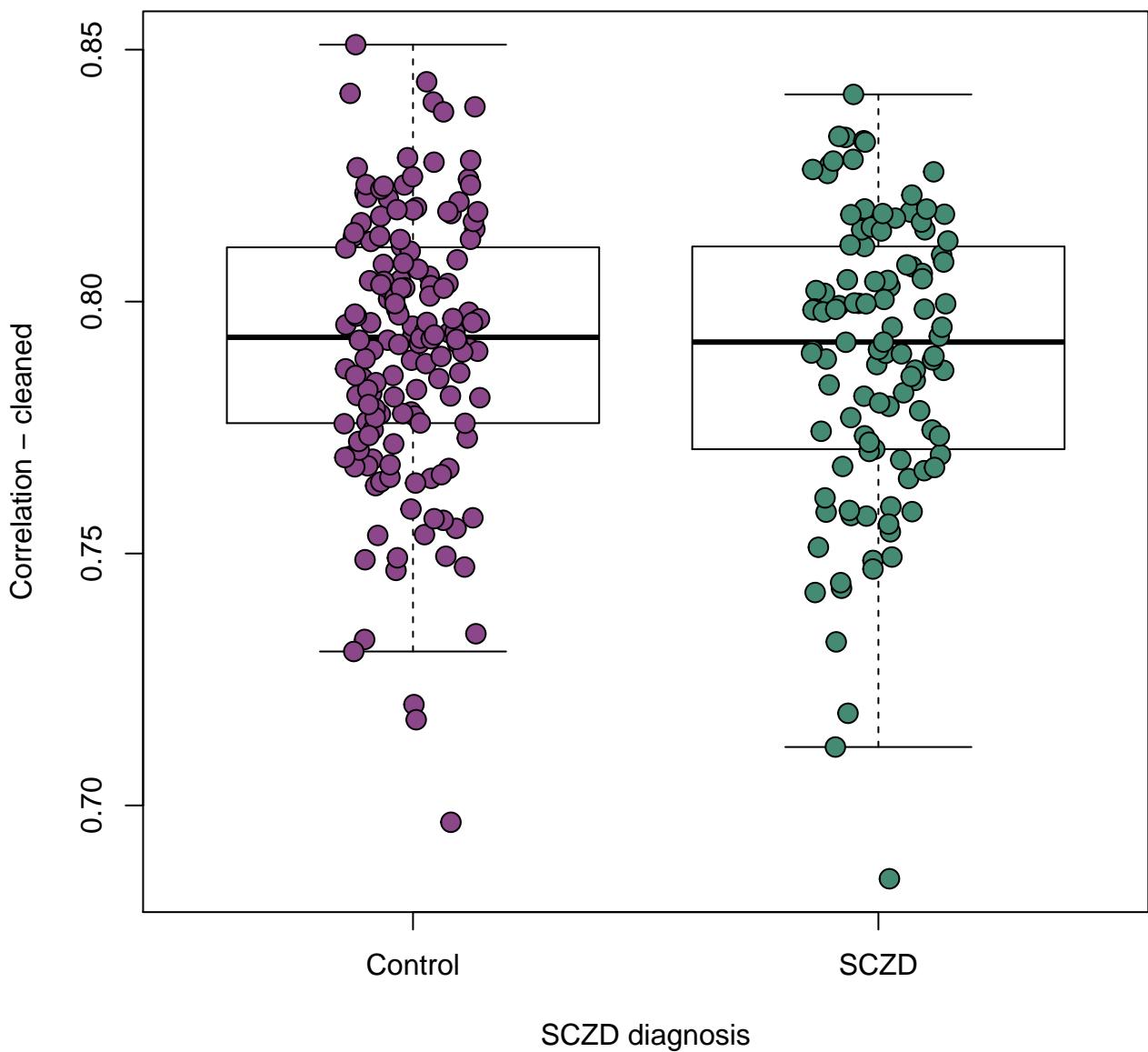
p-value: 0.637



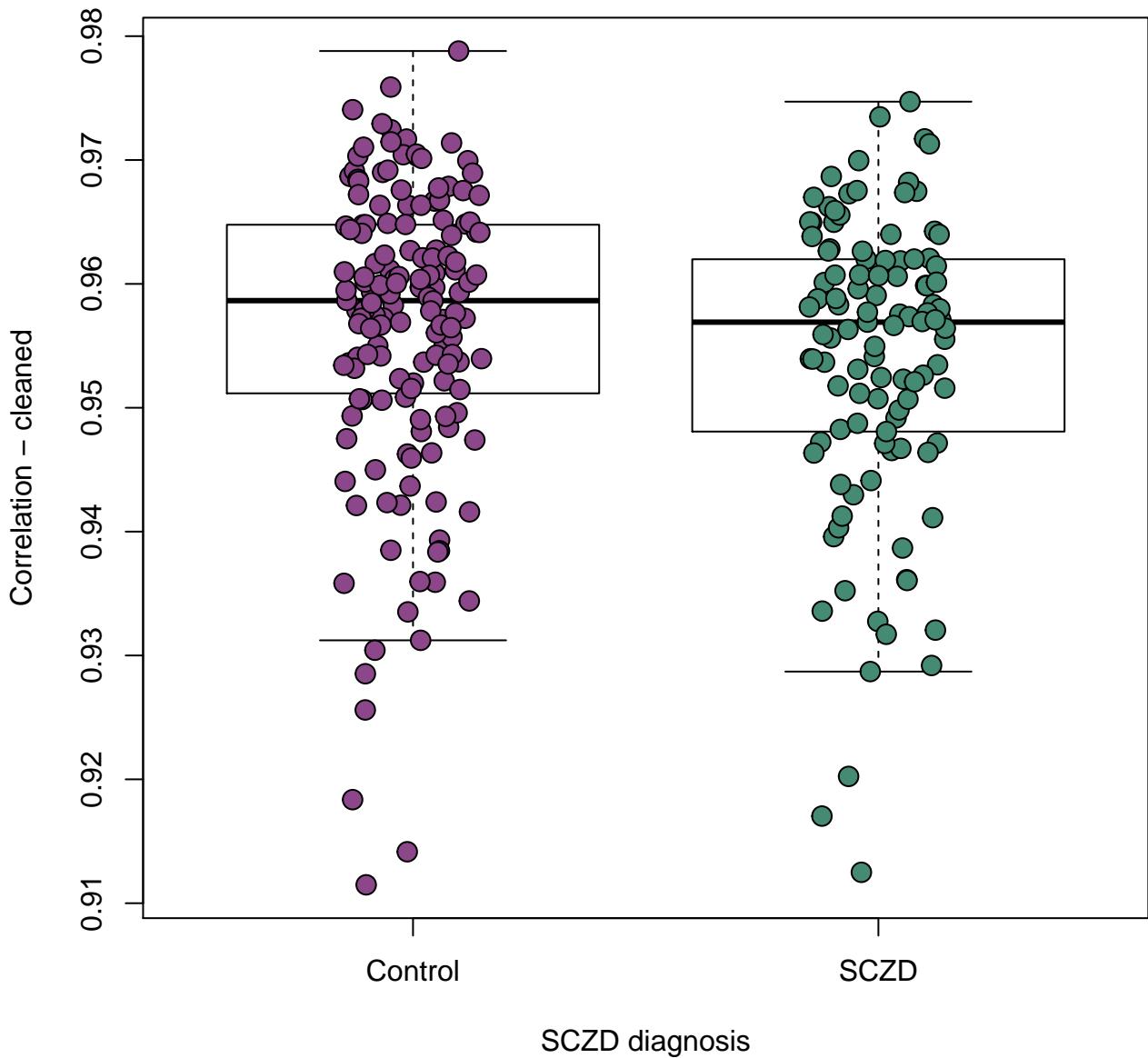
hsa00790: Folate biosynthesis
p-value: 0.323



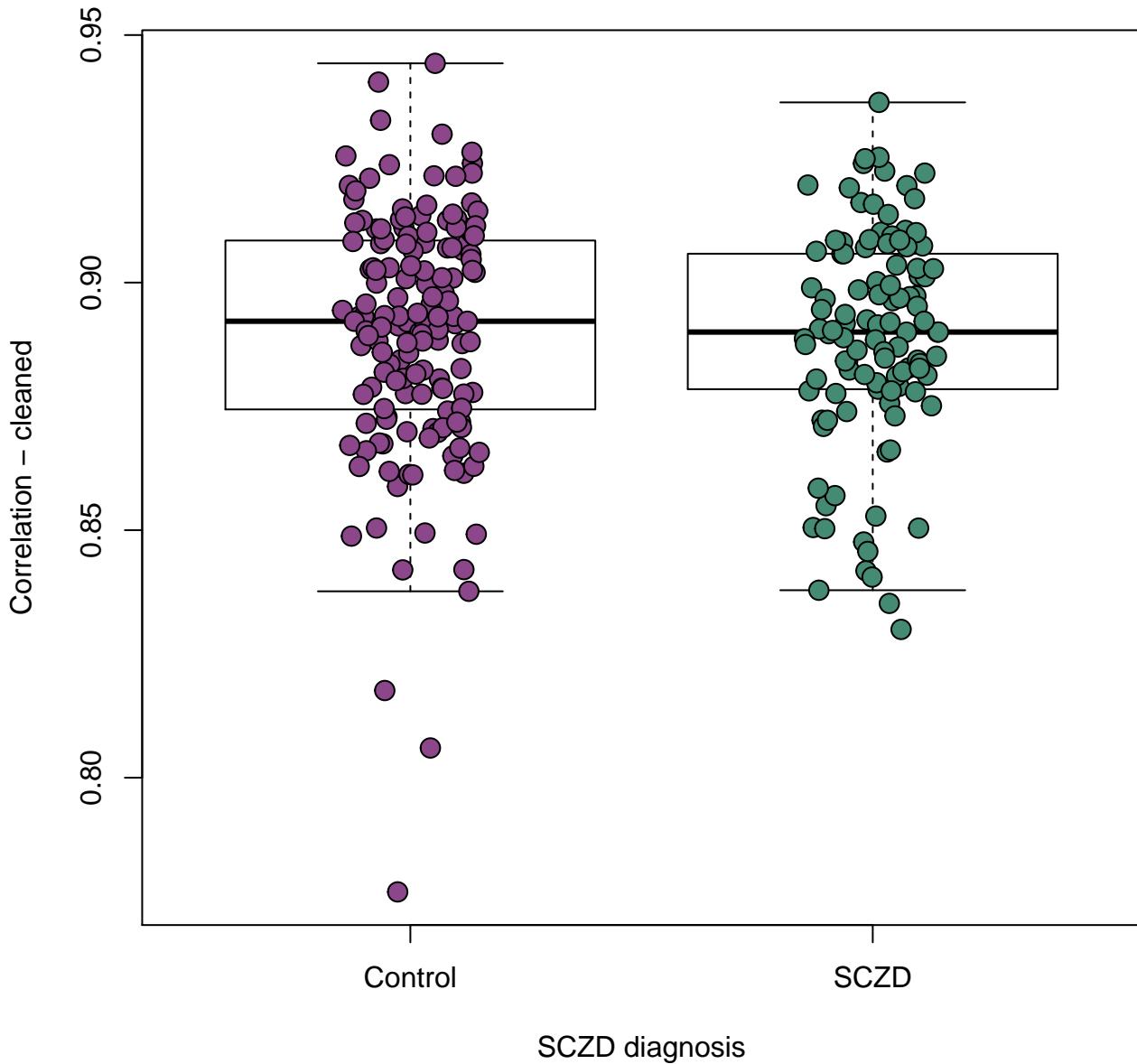
hsa00830: Retinol metabolism
p-value: 0.565



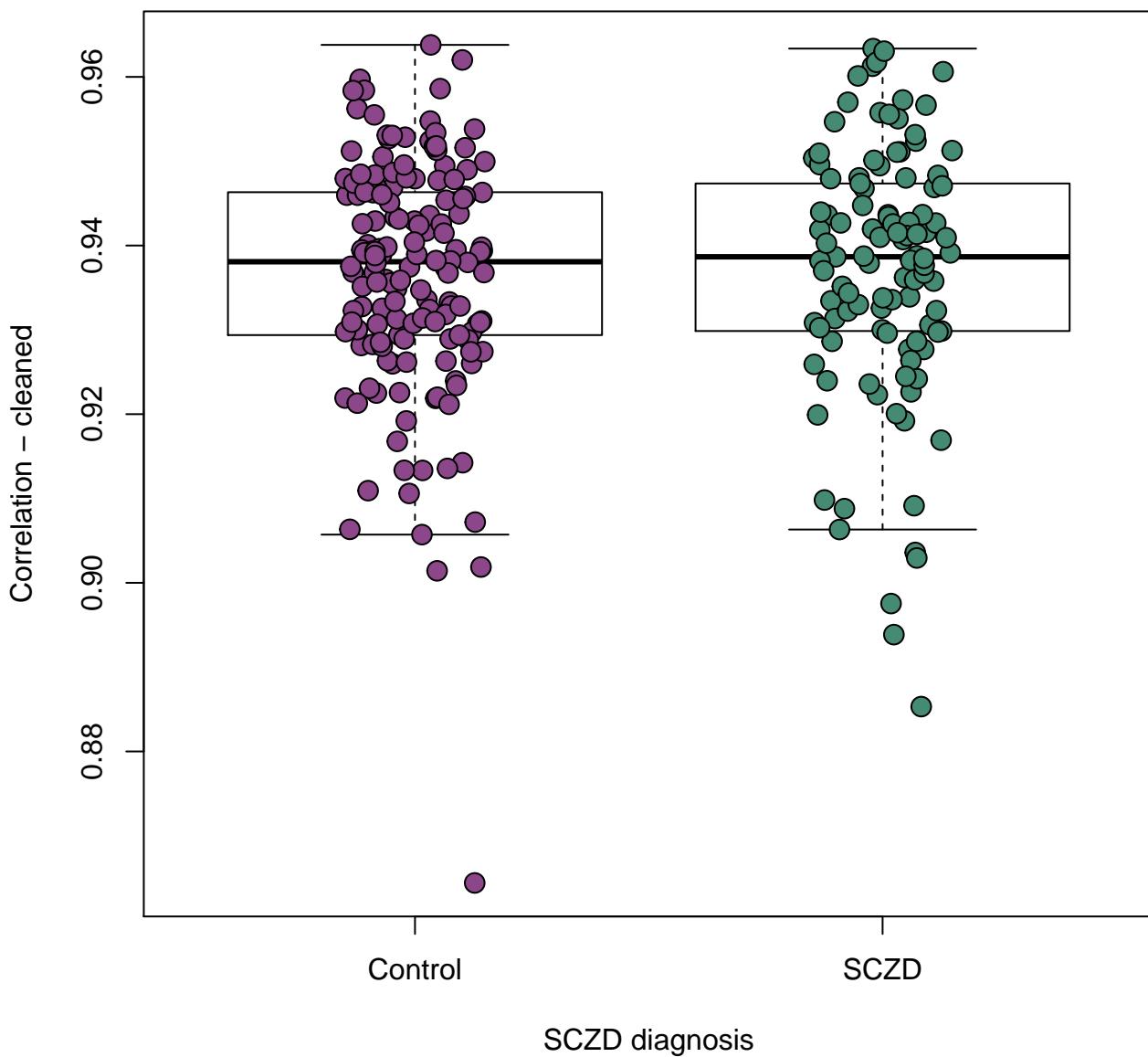
hsa00860: Porphyrin and chlorophyll metabolism
p-value: 0.0979



hsa00900: Terpenoid backbone biosynthesis
p-value: 0.681

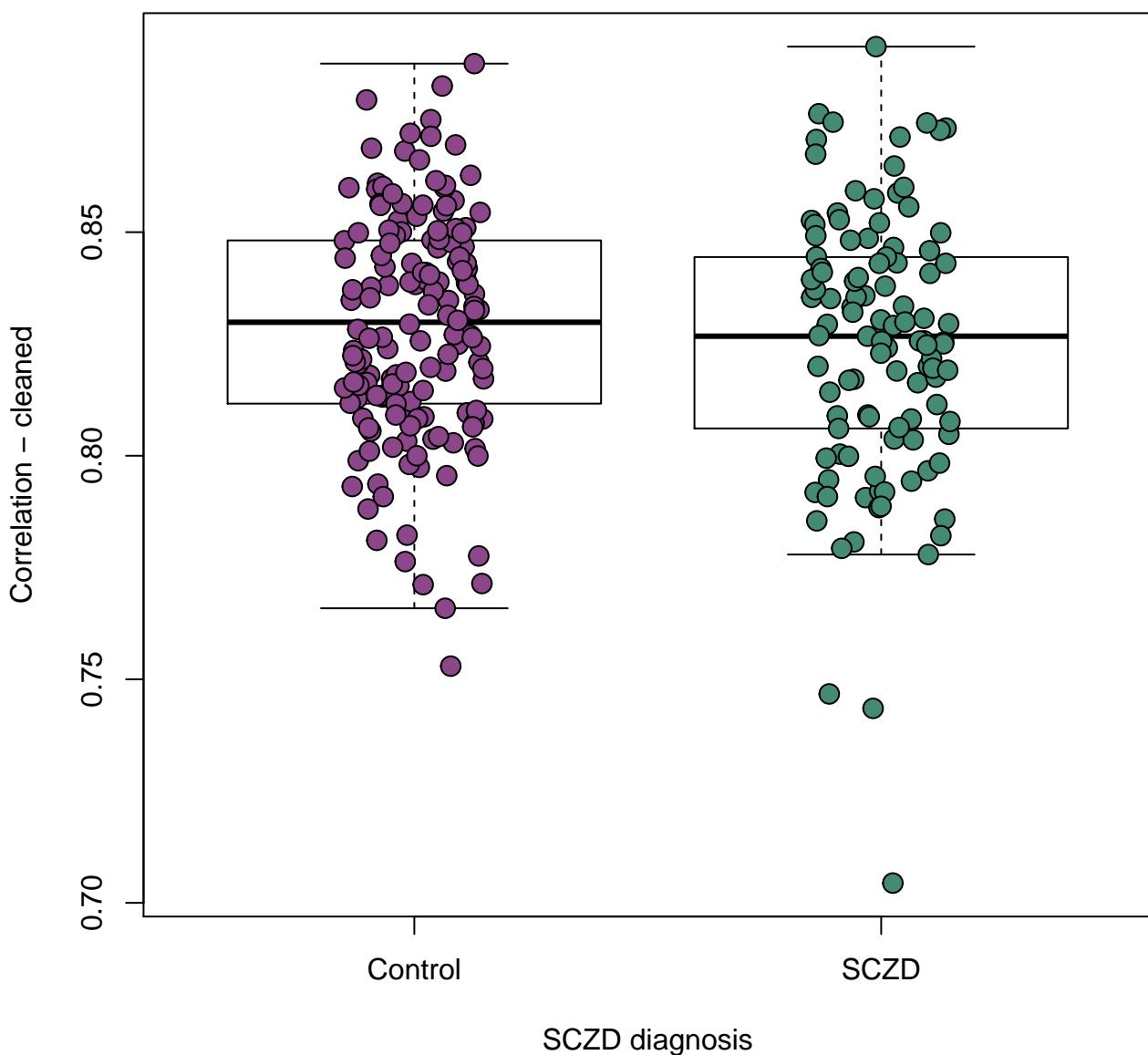


hsa00910: Nitrogen metabolism
p-value: 0.772

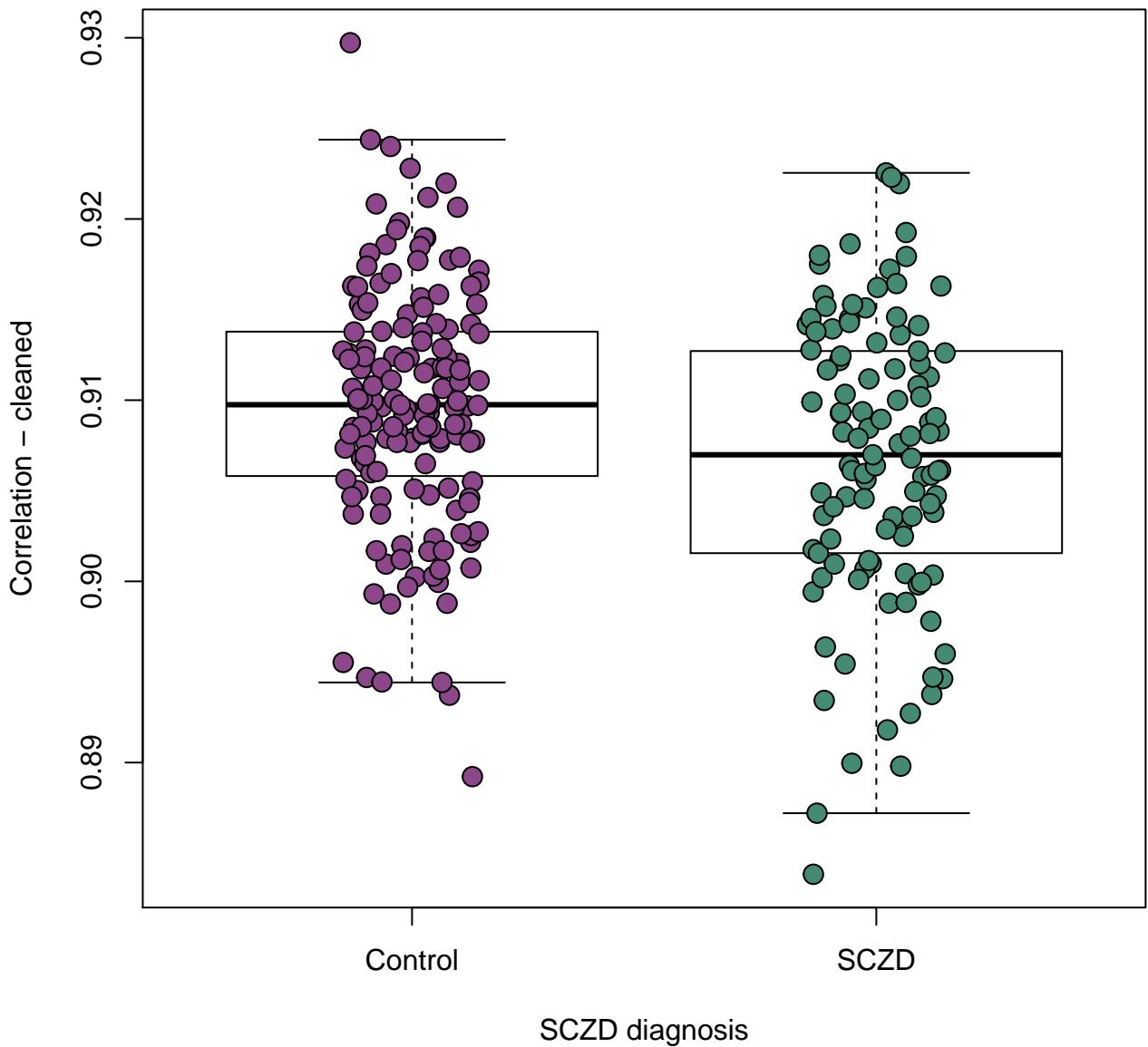


hsa00920: Sulfur metabolism

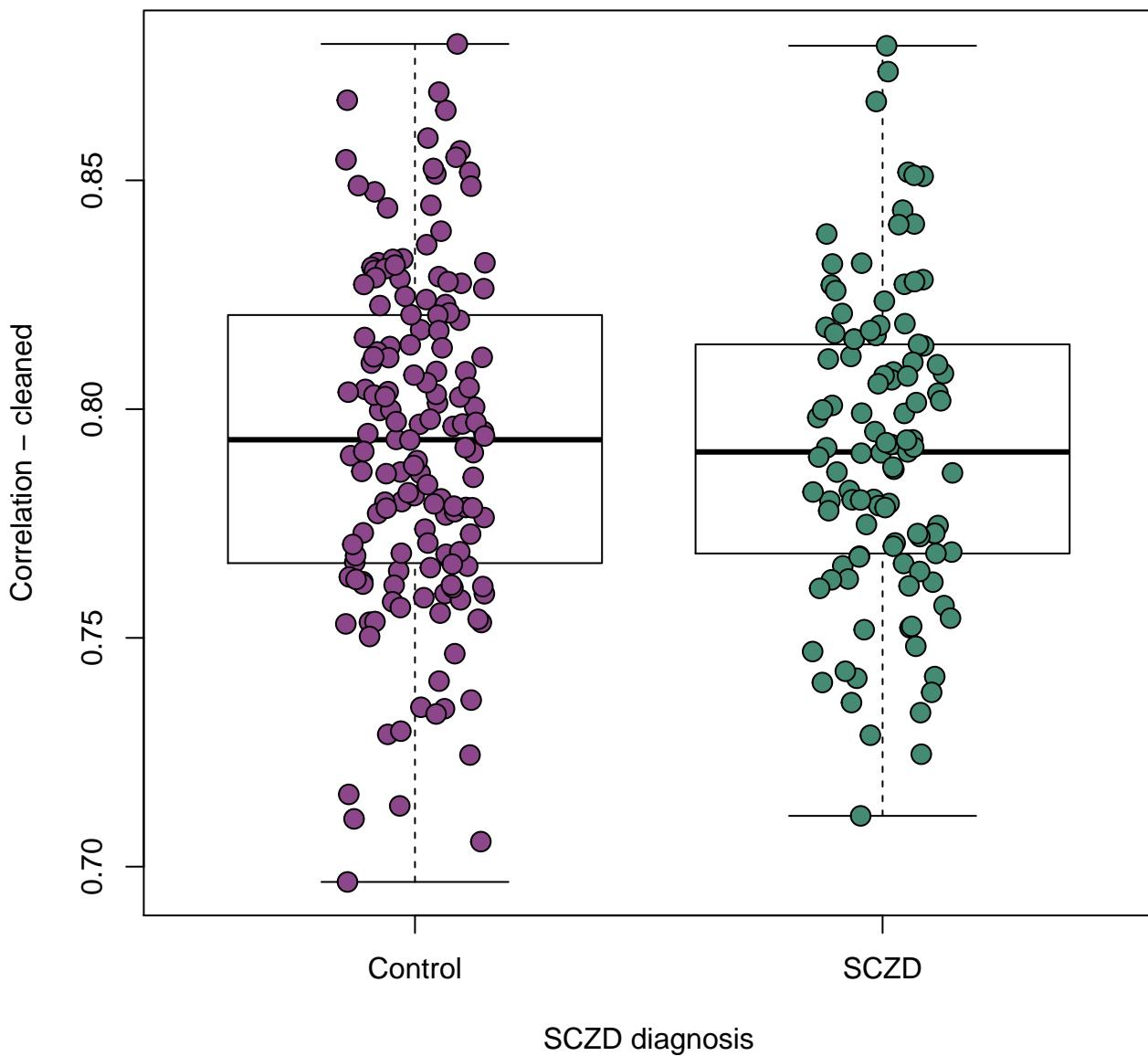
p-value: 0.209



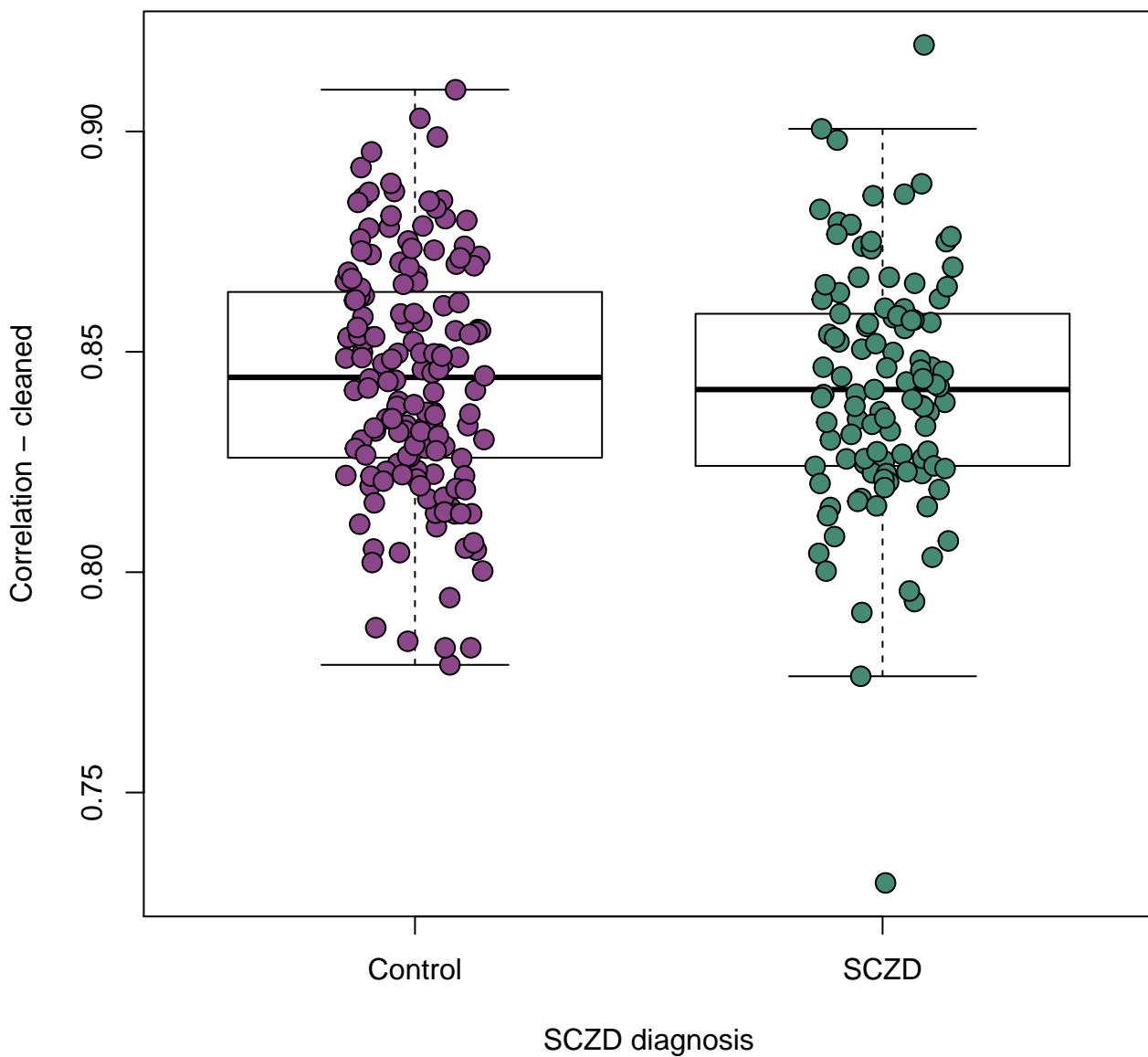
hsa00970: Aminoacyl-tRNA biosynthesis
p-value: 0.00124



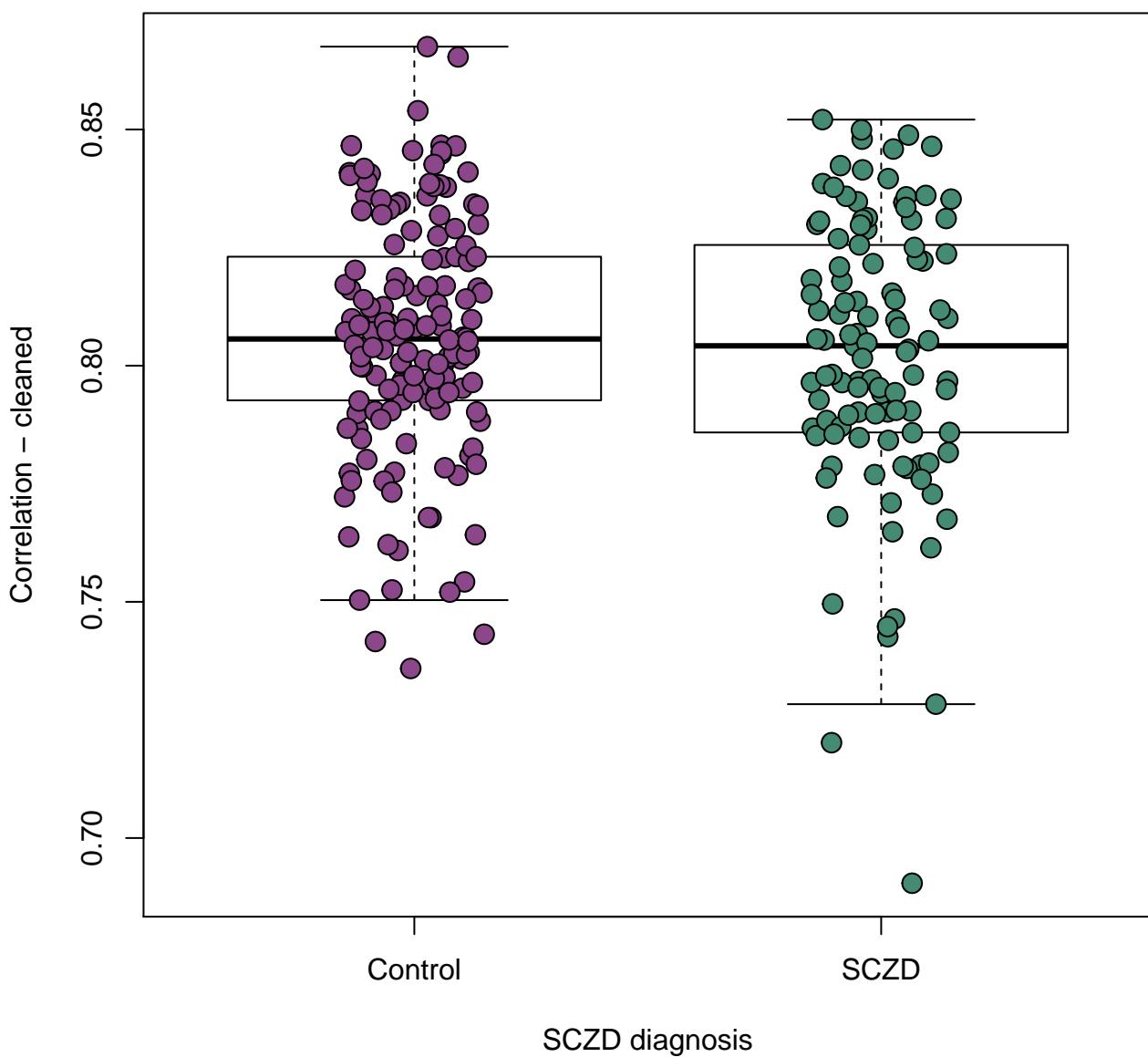
hsa00980: Metabolism of xenobiotics by cytochrome P450
p-value: 0.73



hsa00982: Drug metabolism – cytochrome P450
p-value: 0.558

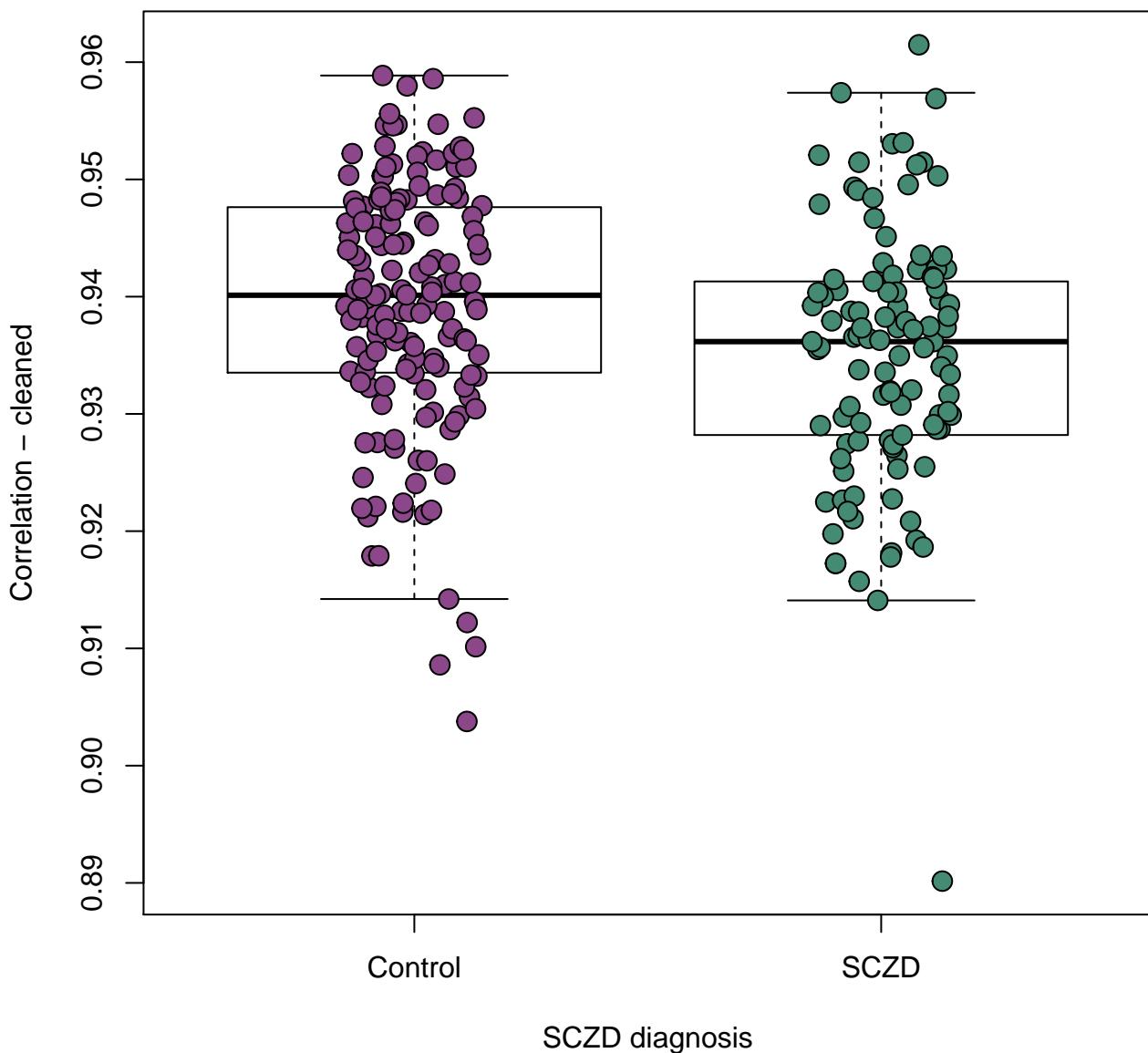


hsa00983: Drug metabolism – other enzymes
p-value: 0.3

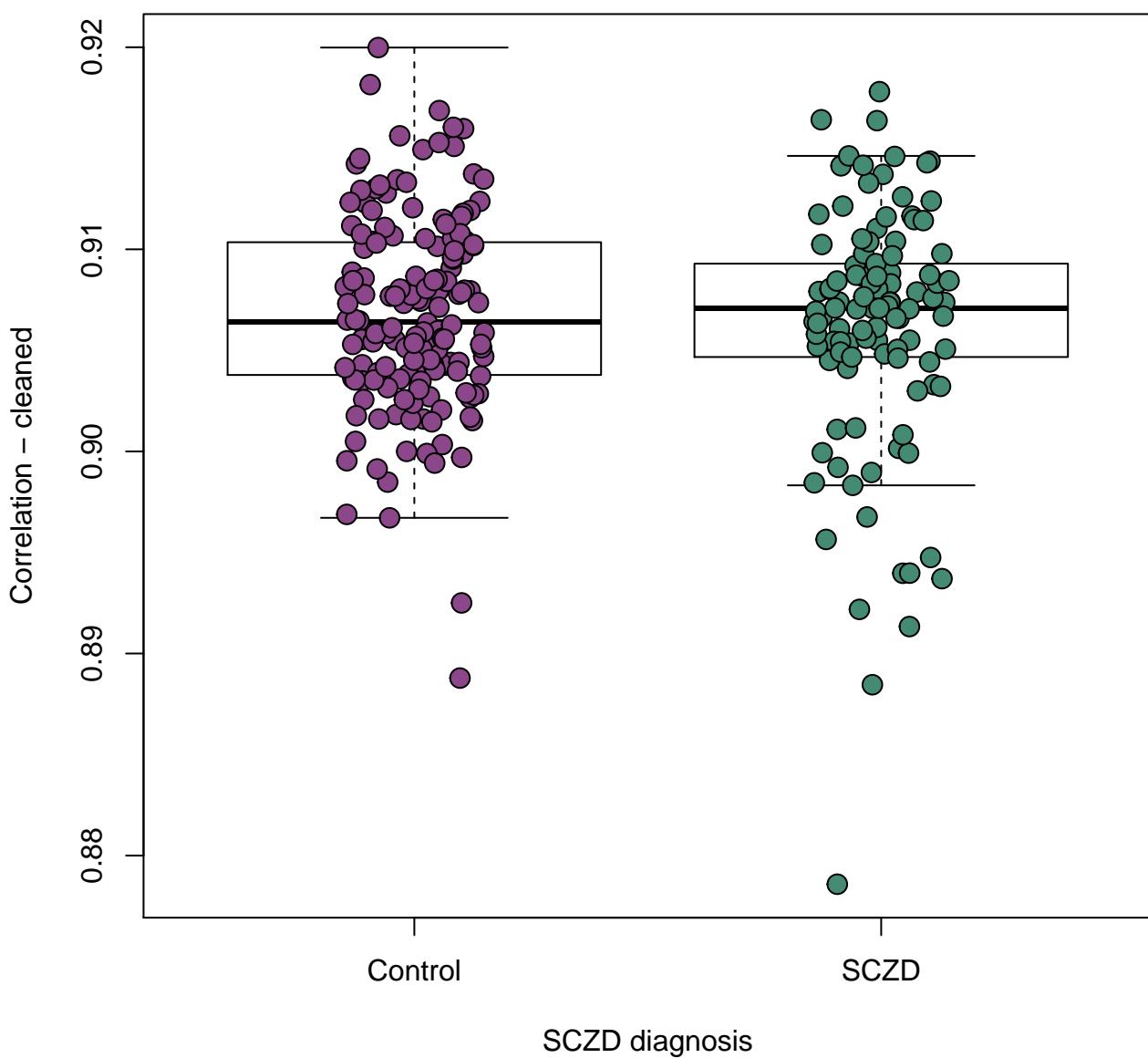


hsa01040: Biosynthesis of unsaturated fatty acids

p-value: 0.00126

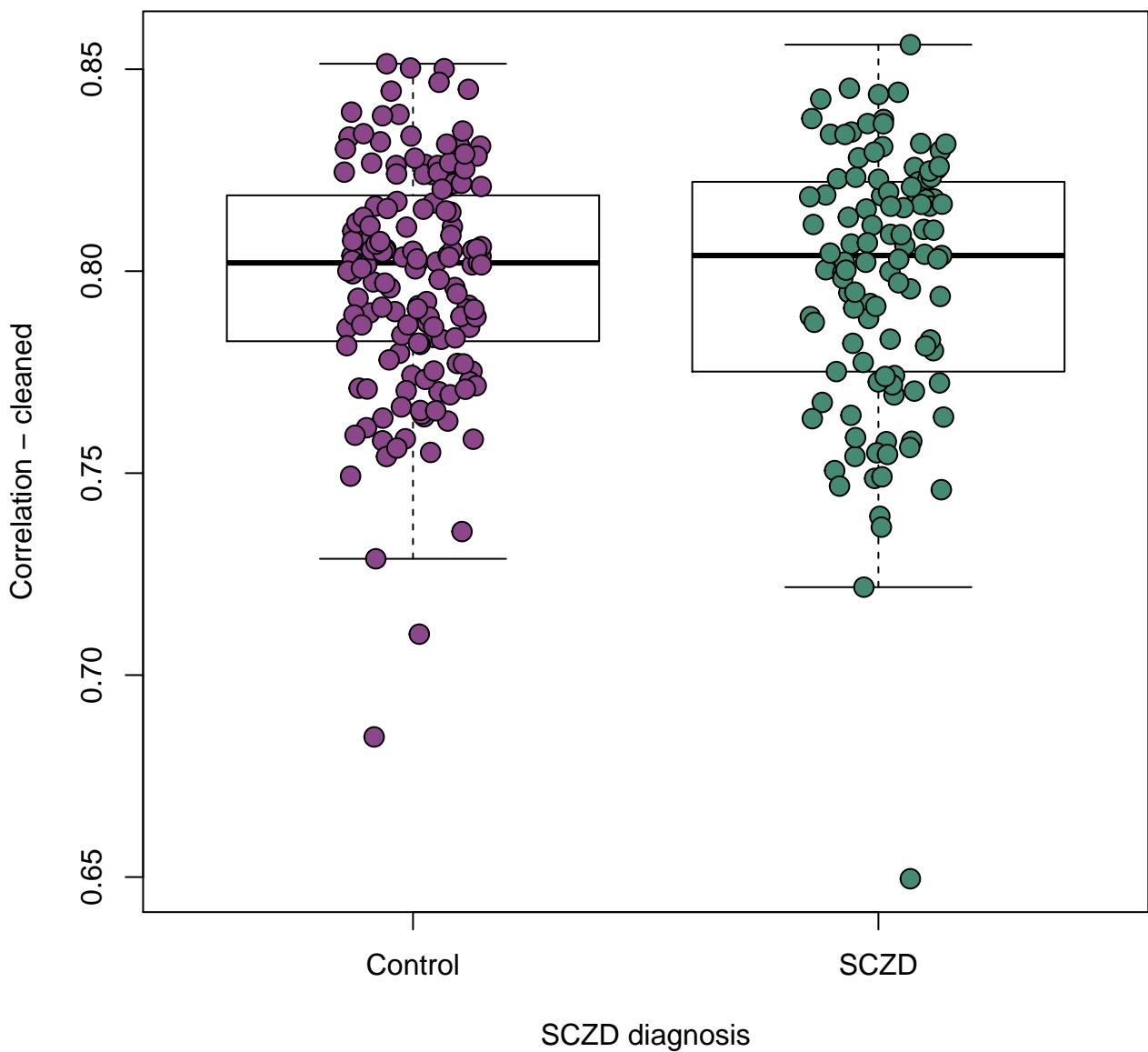


hsa01100: Metabolic pathways
p-value: 0.272

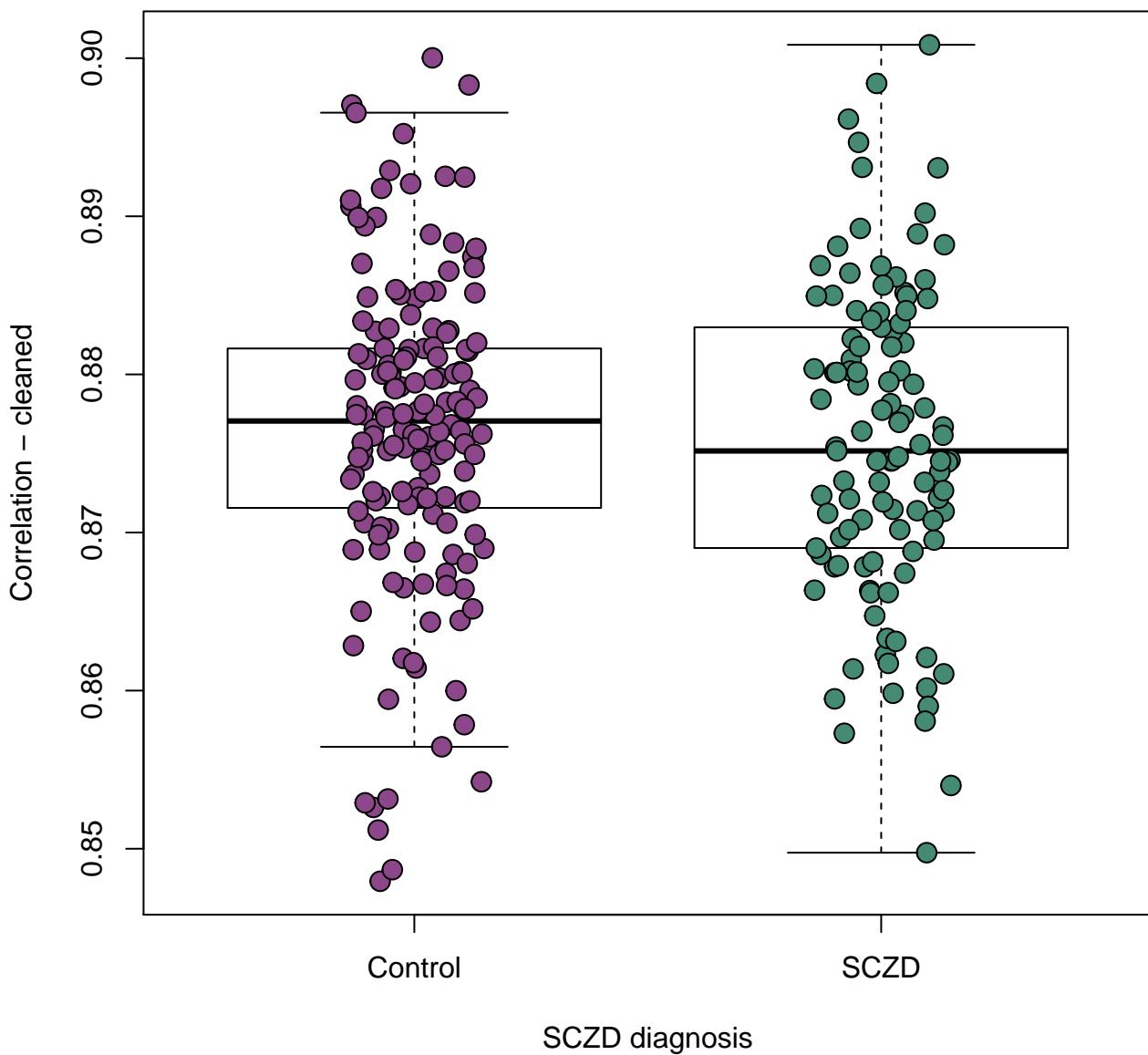


hsa02010: ABC transporters

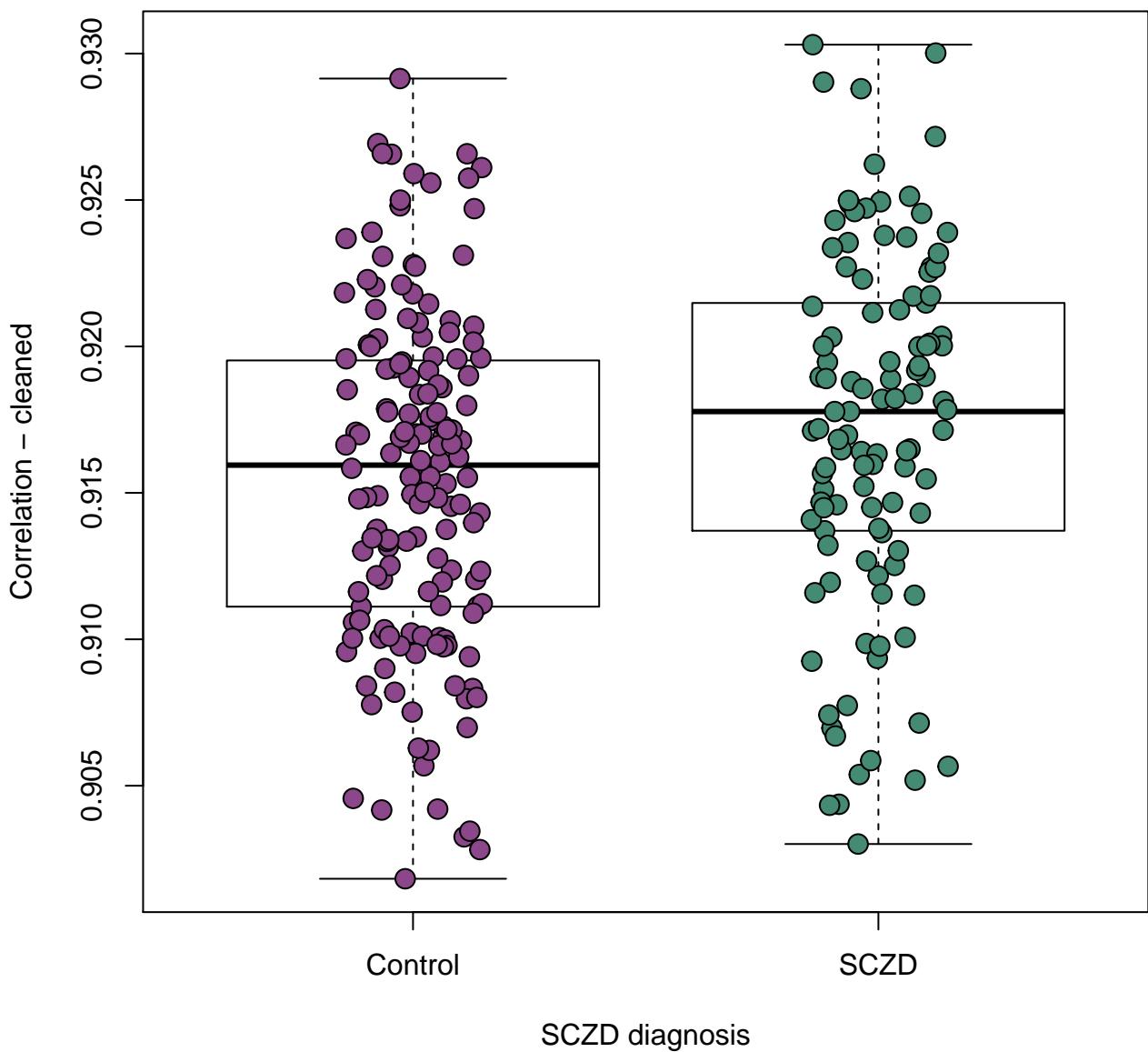
p-value: 0.887



hsa03008: Ribosome biogenesis in eukaryotes
p-value: 0.575

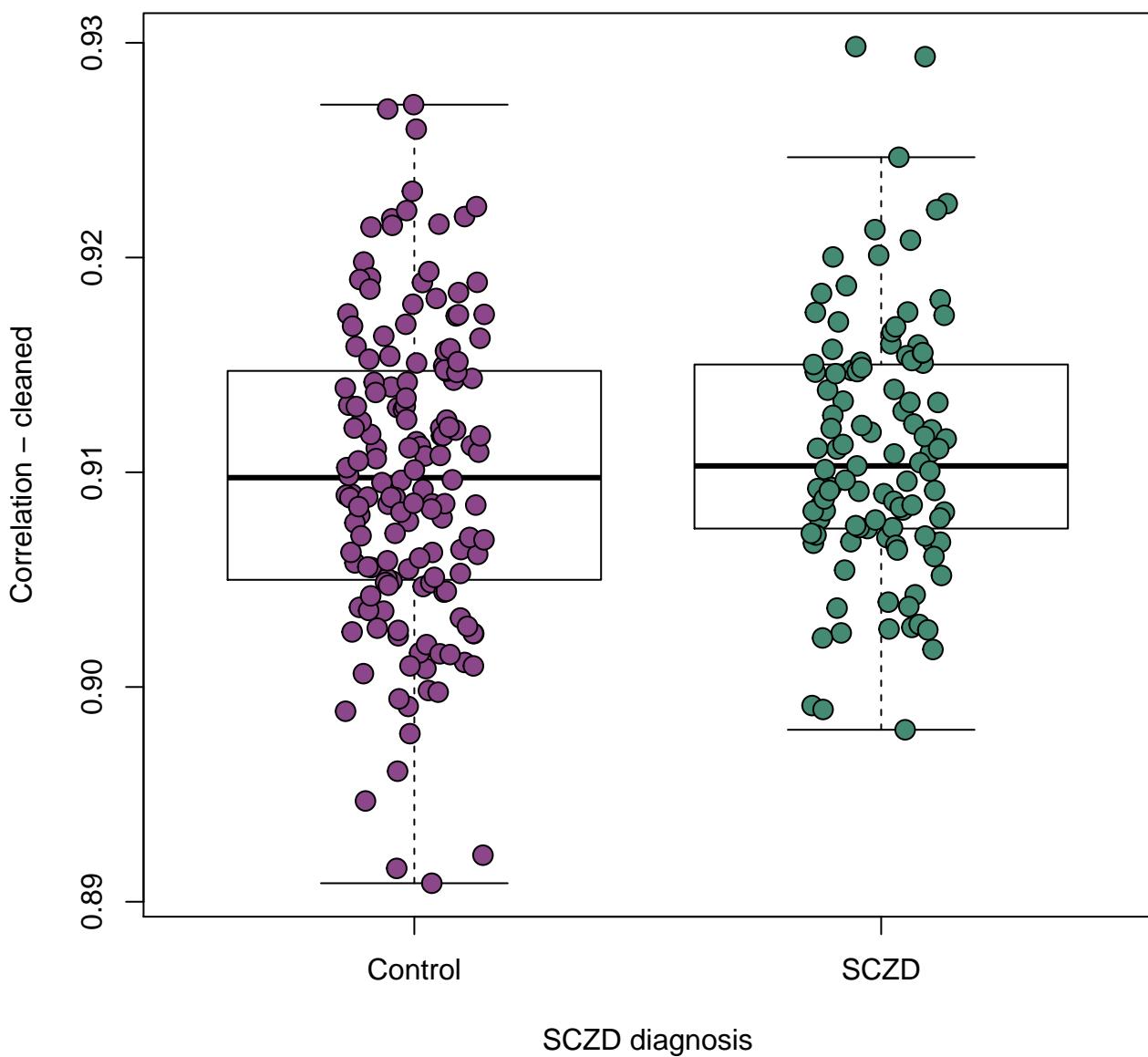


hsa03010: Ribosome
p-value: 0.0245

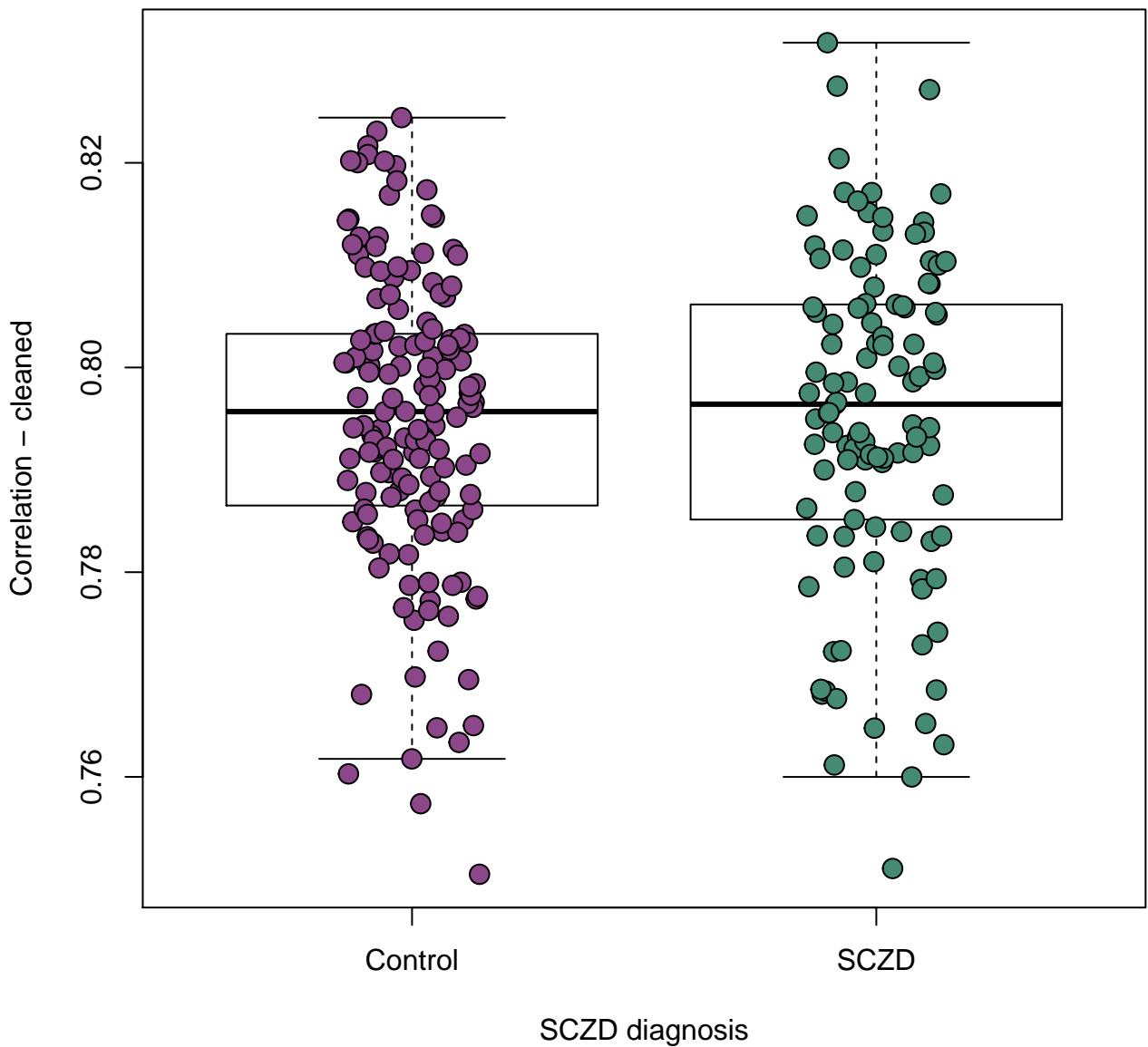


hsa03013: RNA transport

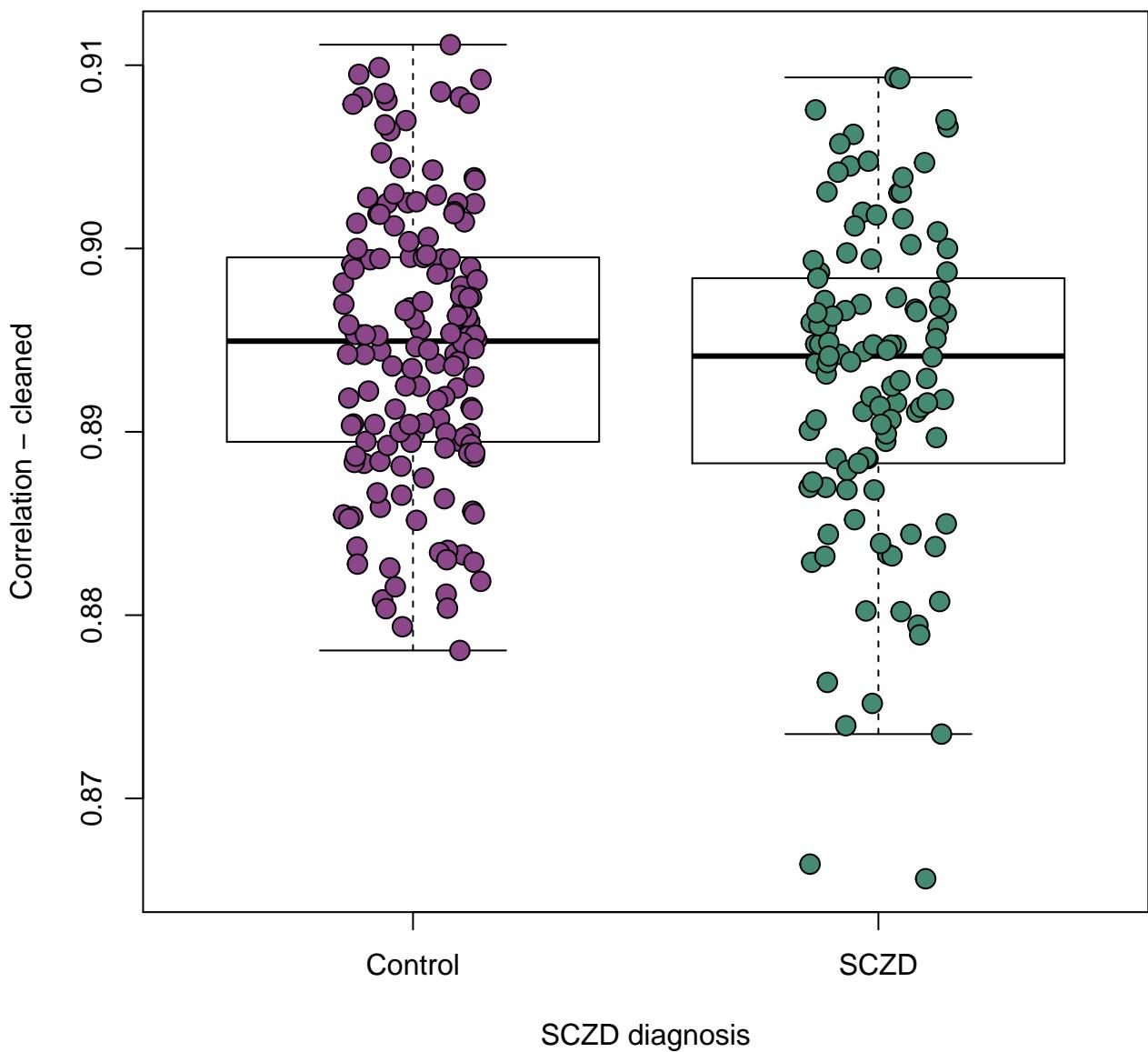
p-value: 0.156



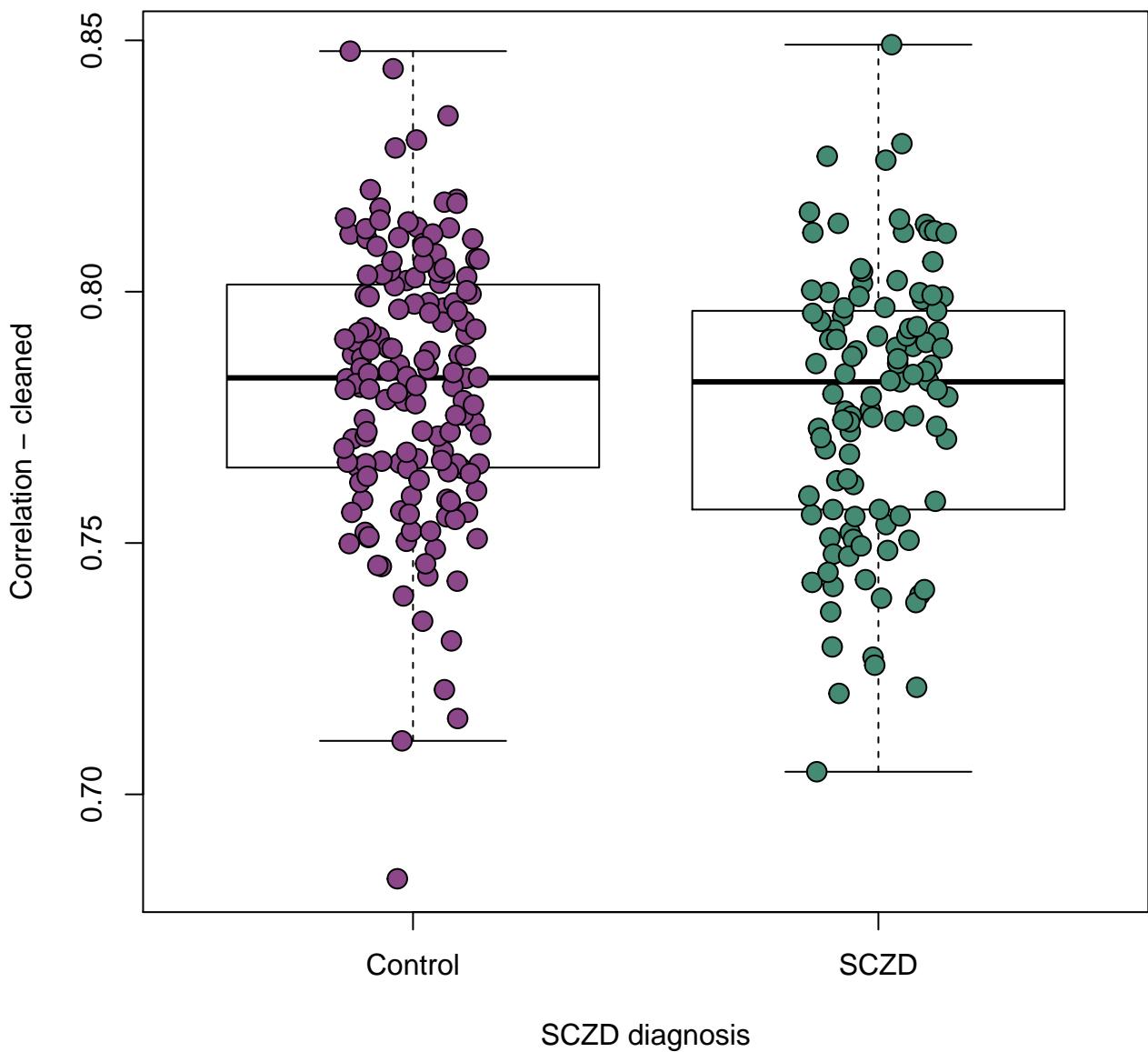
hsa03015: mRNA surveillance pathway
p-value: 0.859



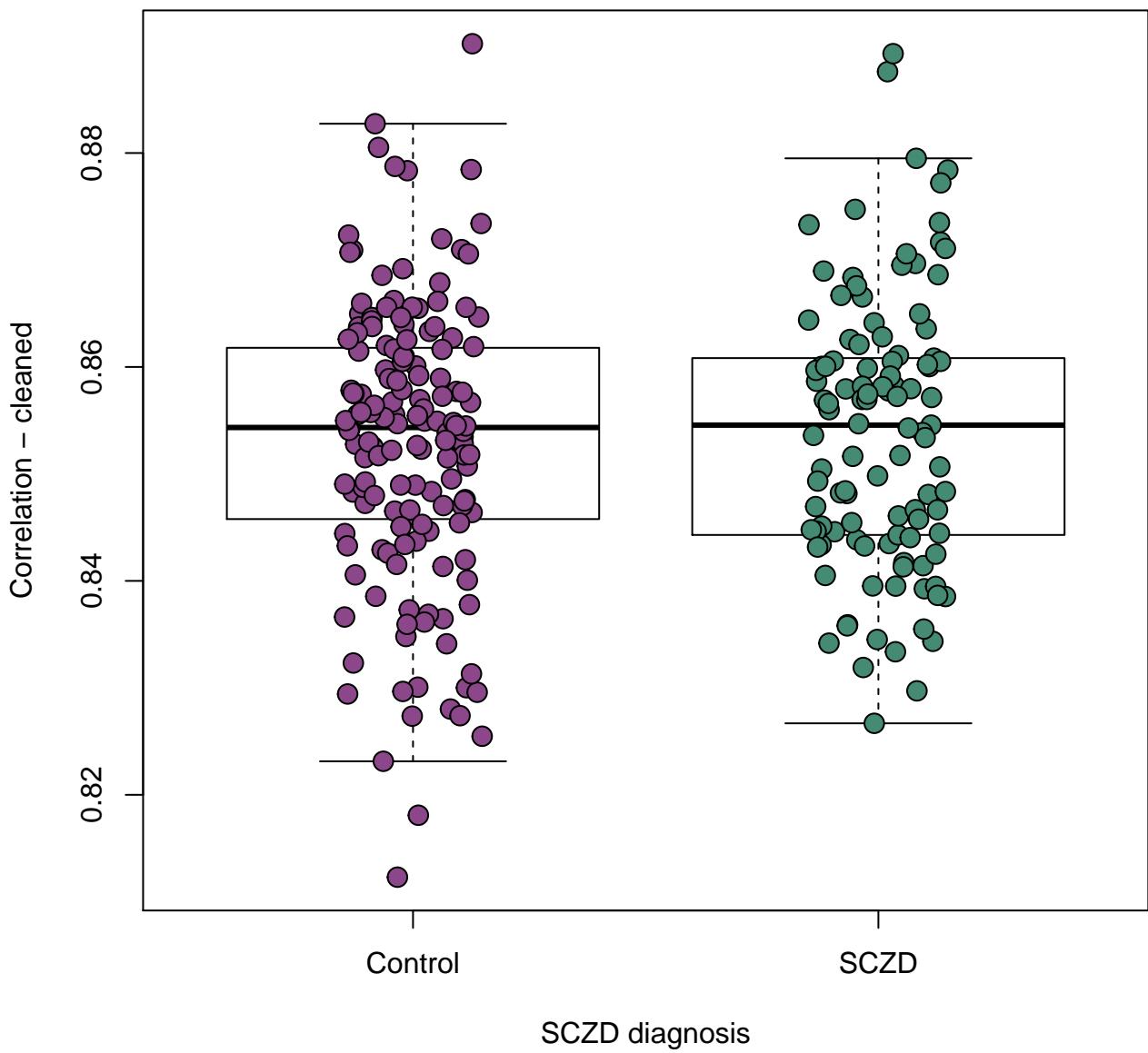
hsa03018: RNA degradation
p-value: 0.0783



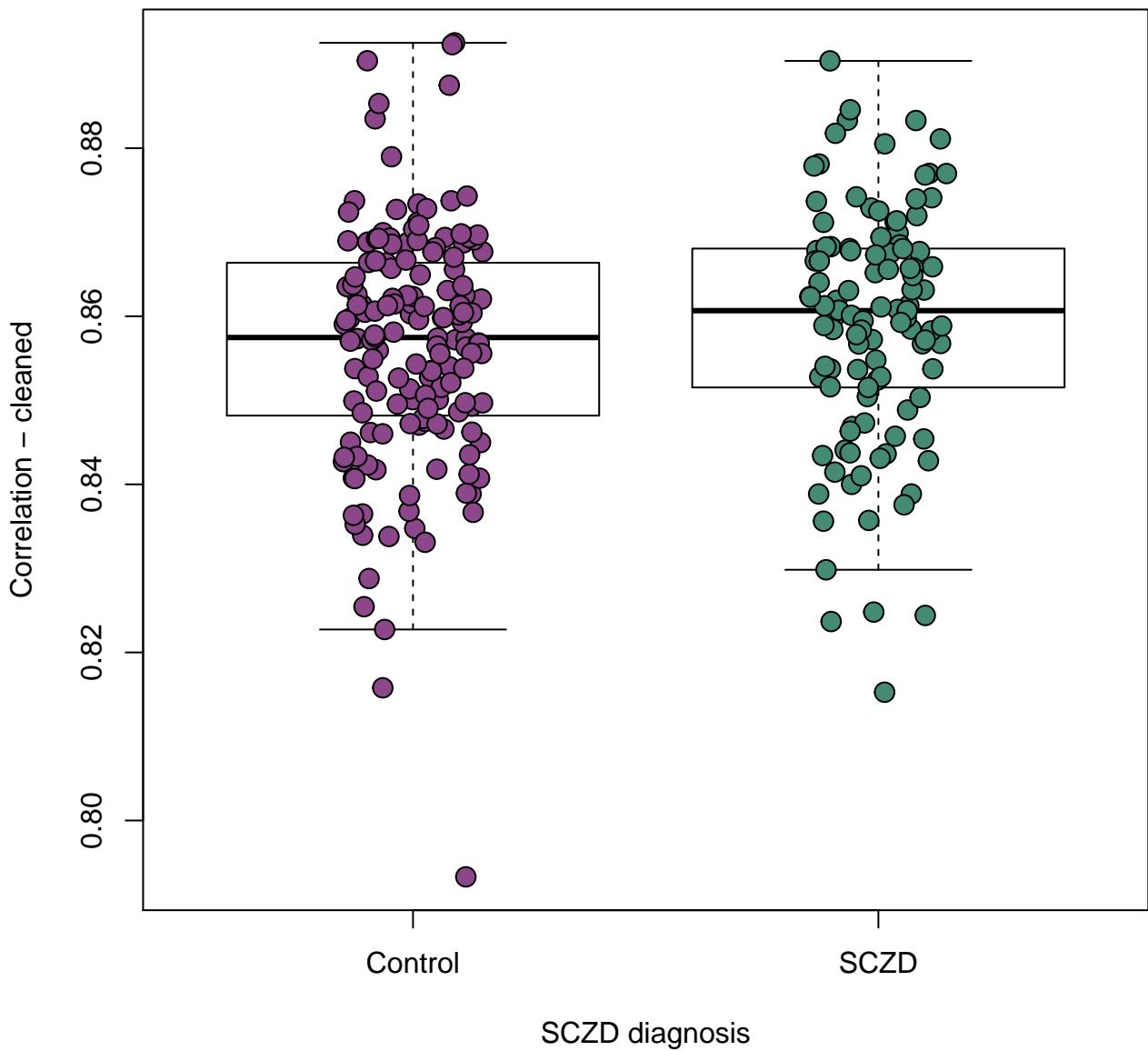
hsa03020: RNA polymerase
p-value: 0.235



hsa03022: Basal transcription factors
p-value: 0.572

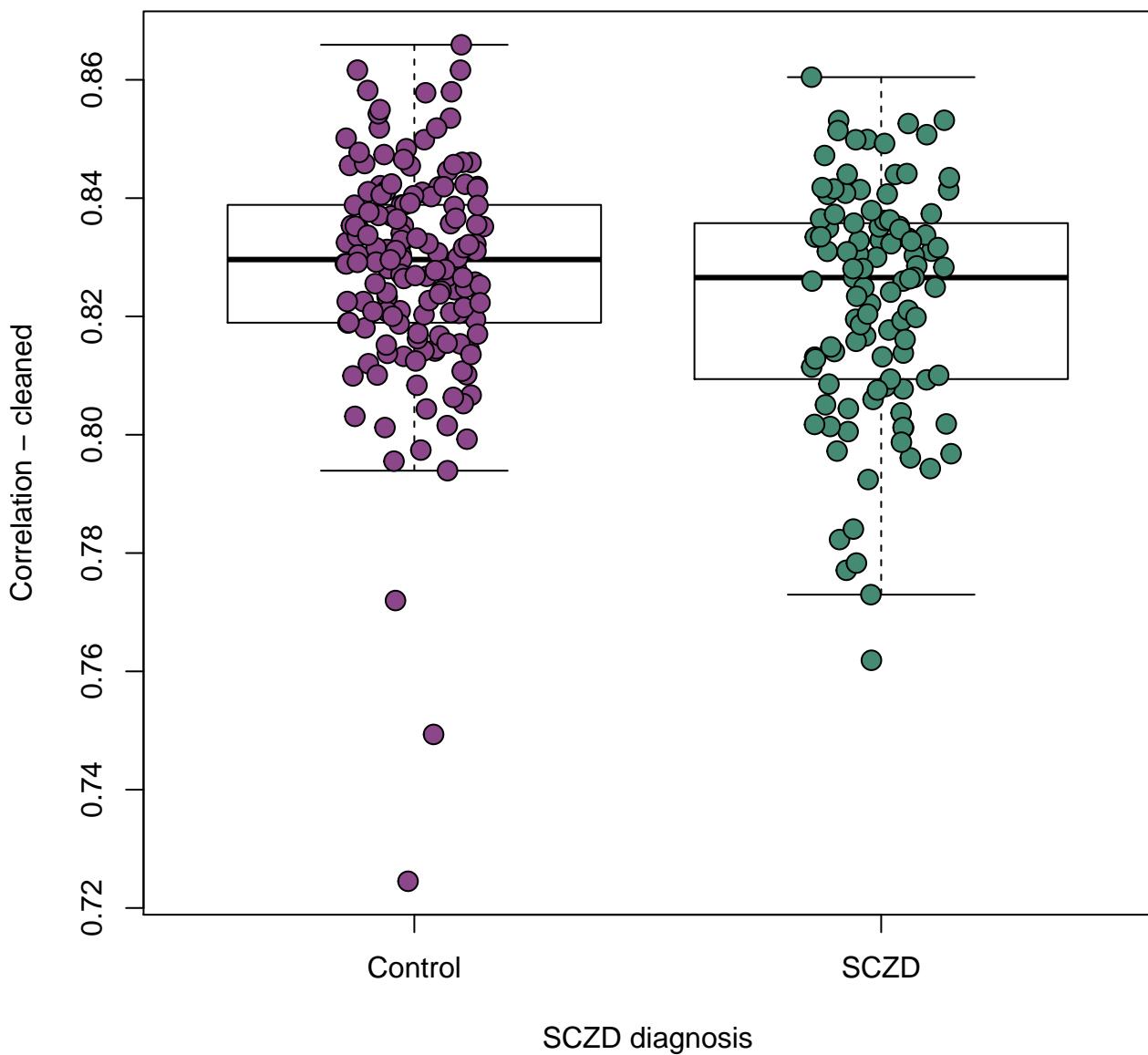


hsa03030: DNA replication
p-value: 0.148

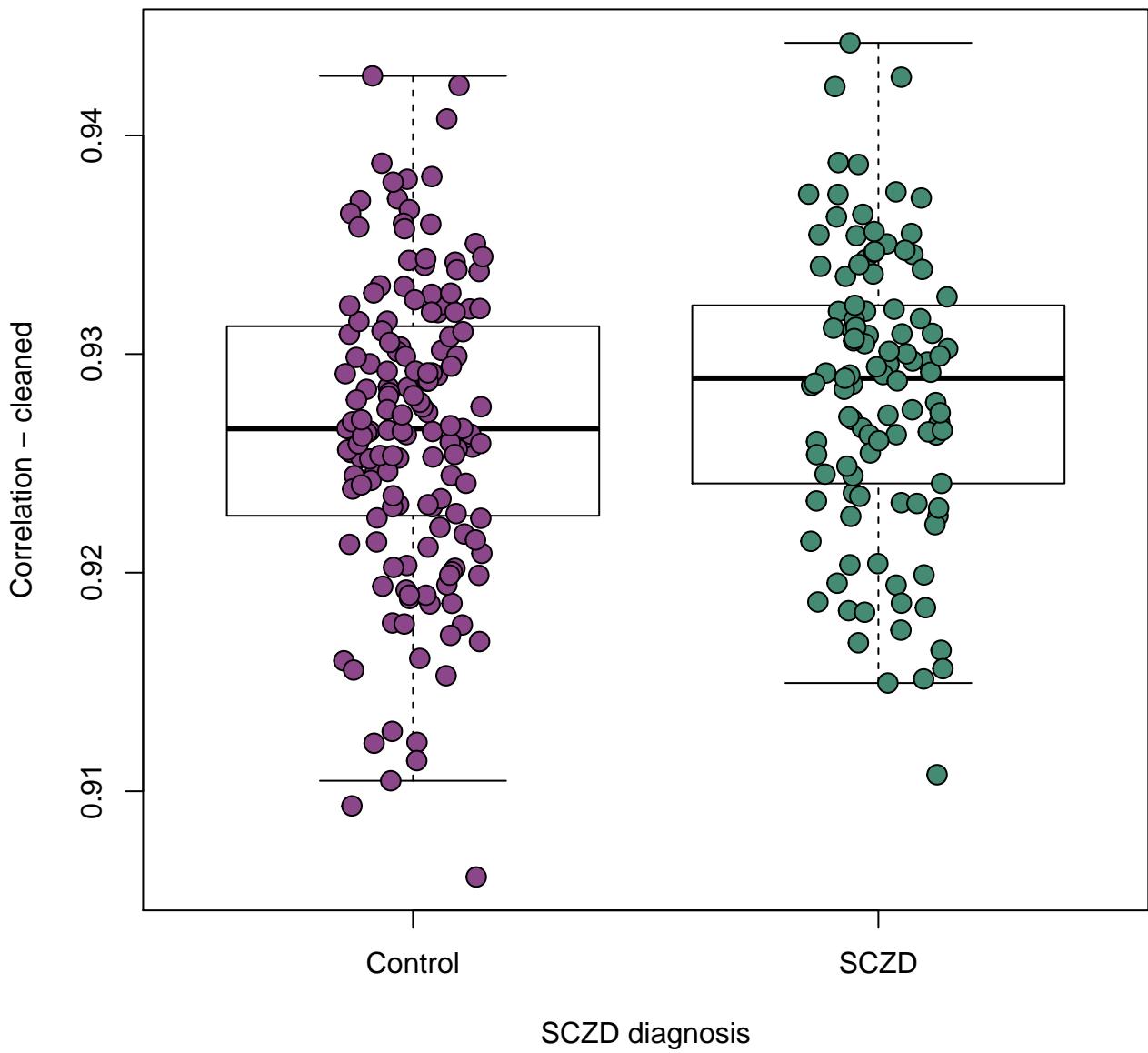


hsa03040: Spliceosome

p-value: 0.0326

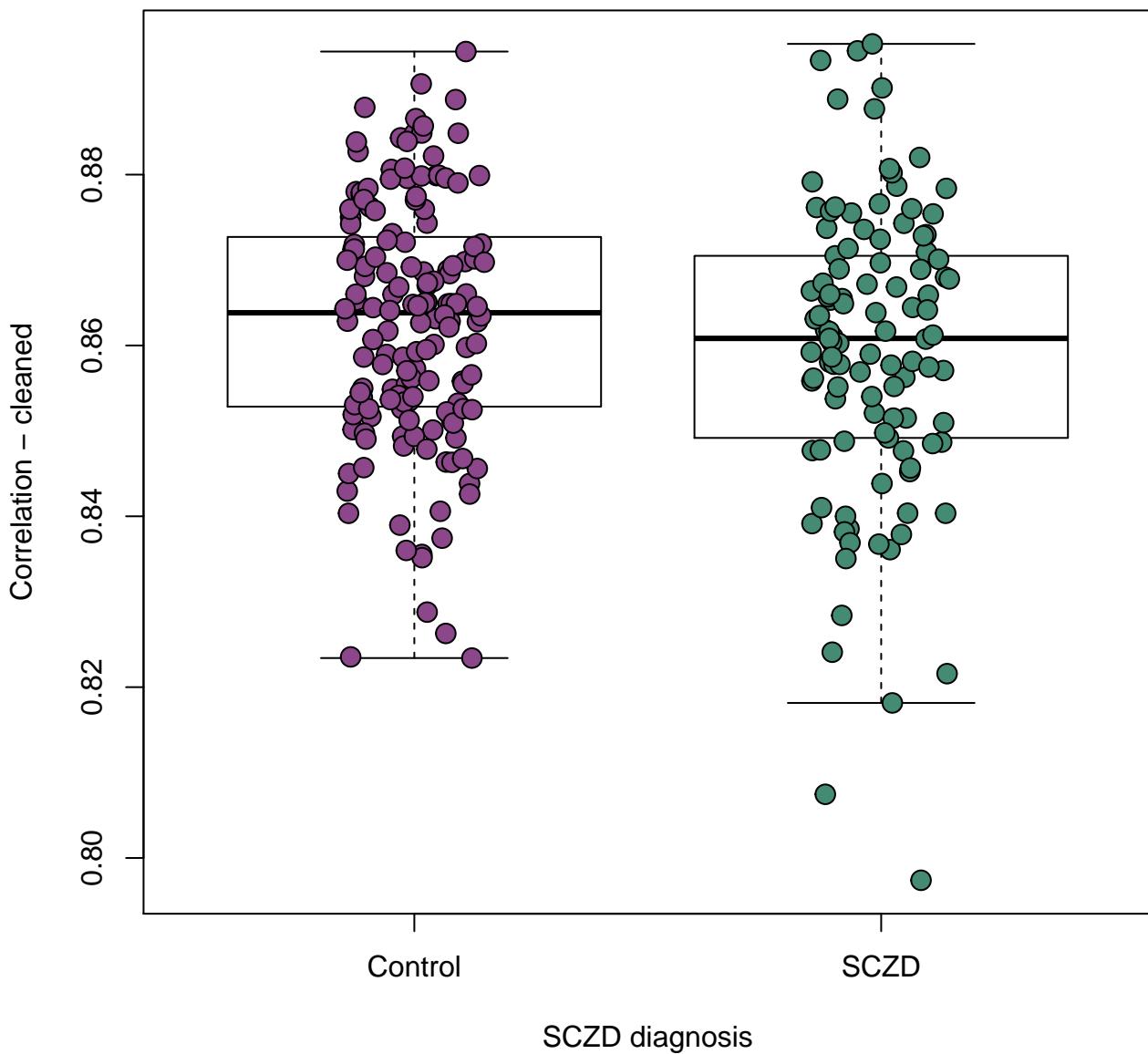


hsa03050: Proteasome
p-value: 0.048



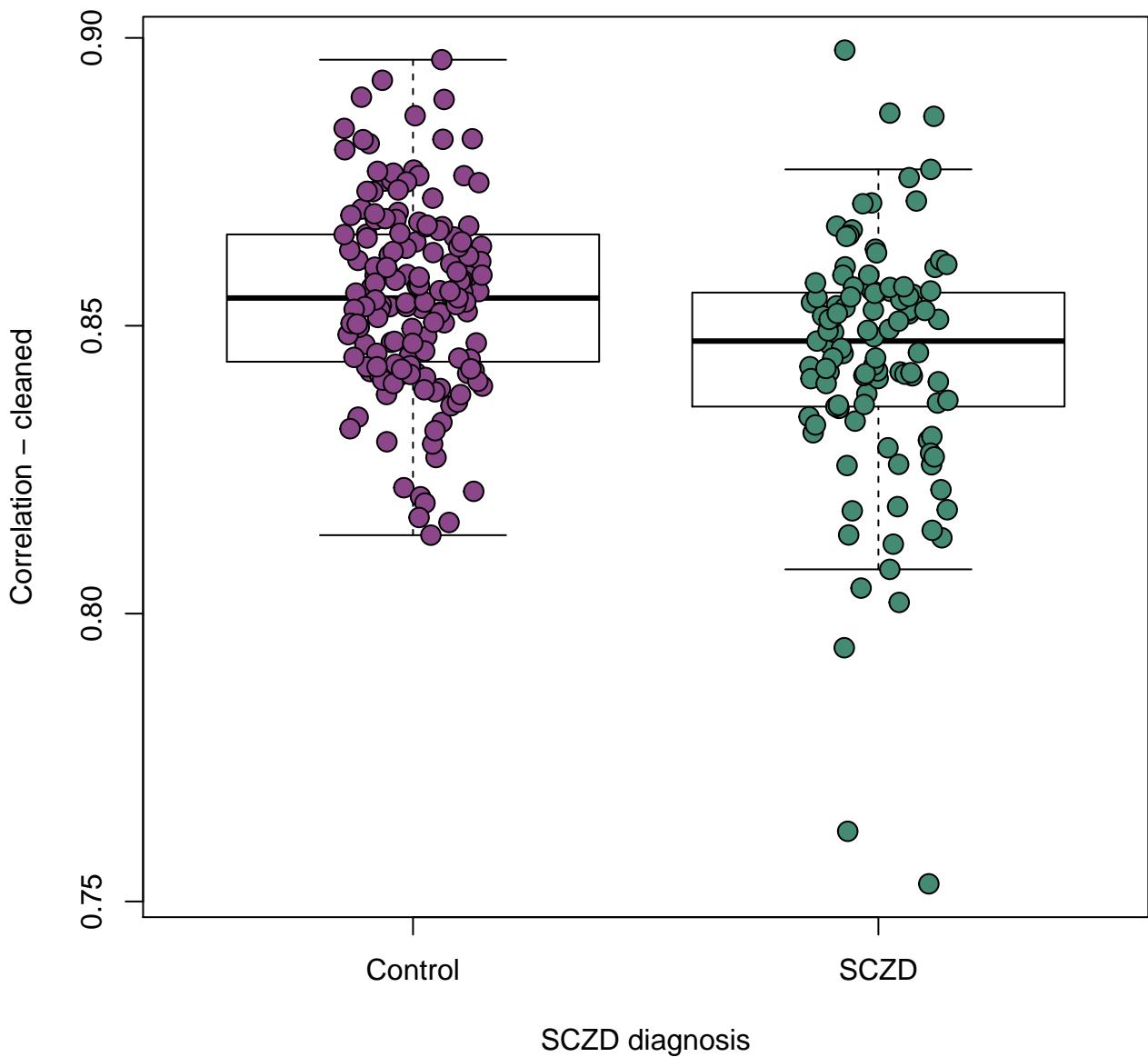
hsa03060: Protein export

p-value: 0.0841

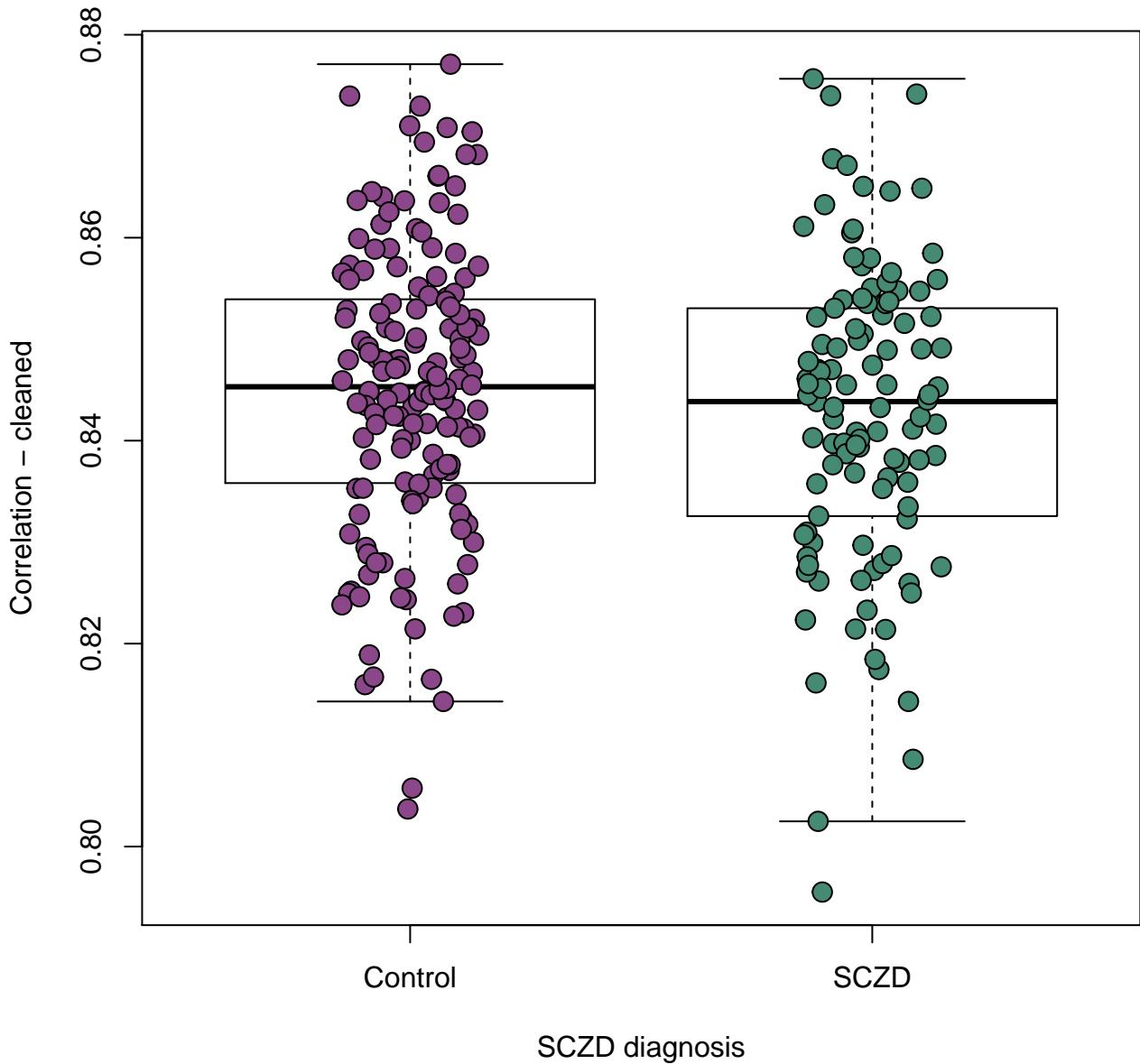


hsa03320: PPAR signaling pathway

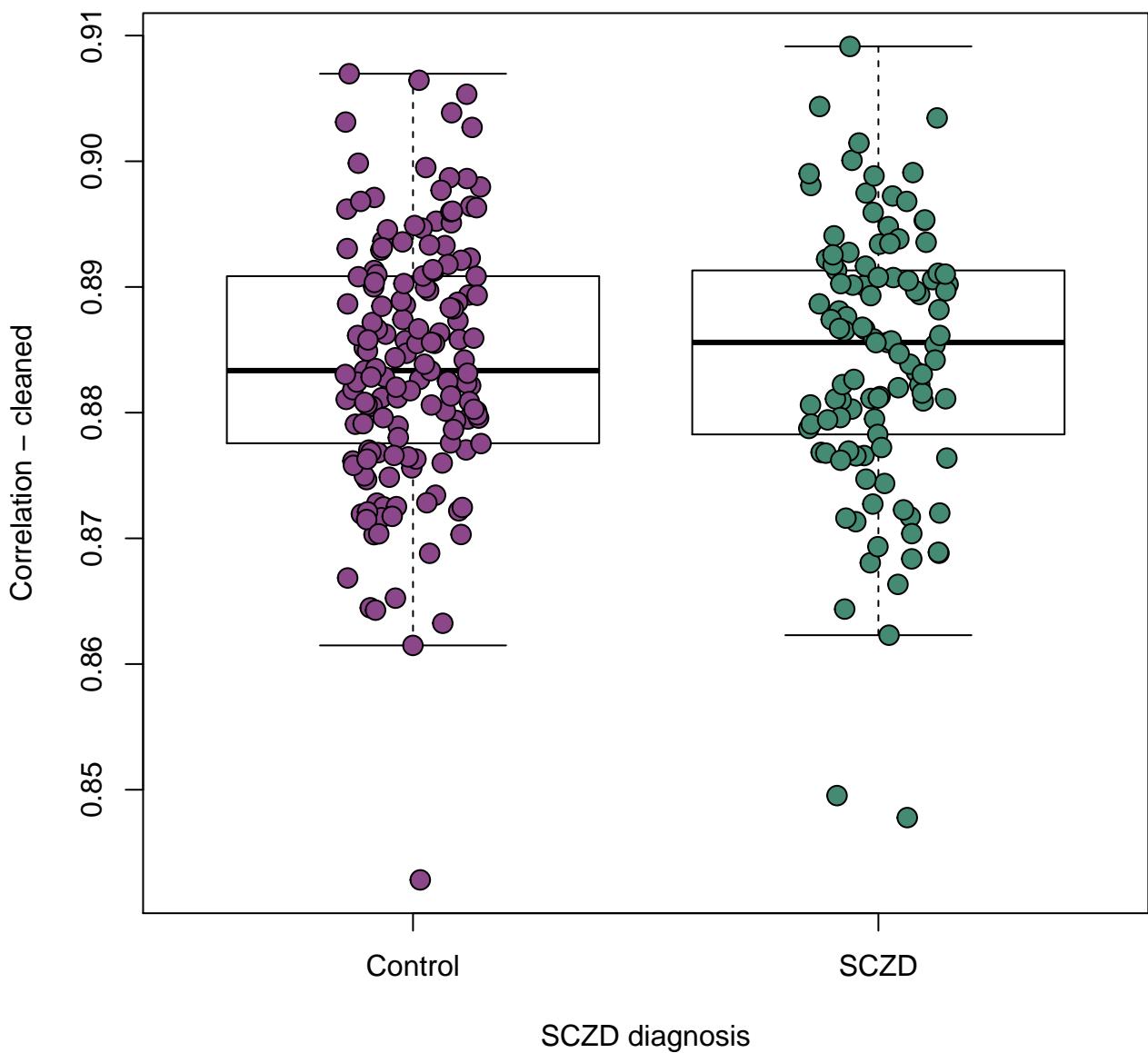
p-value: 2.57e-06



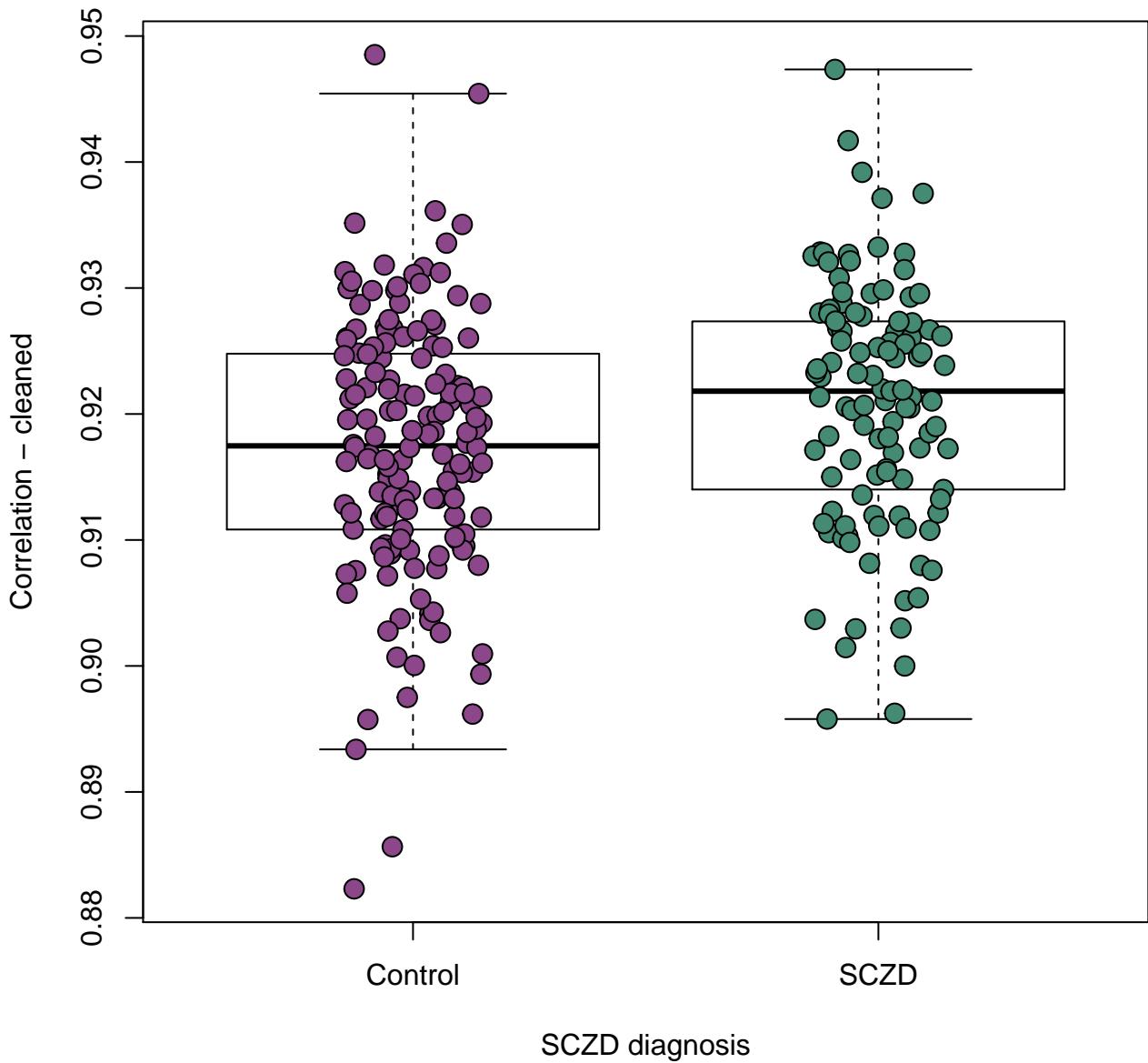
hsa03410: Base excision repair
p-value: 0.186



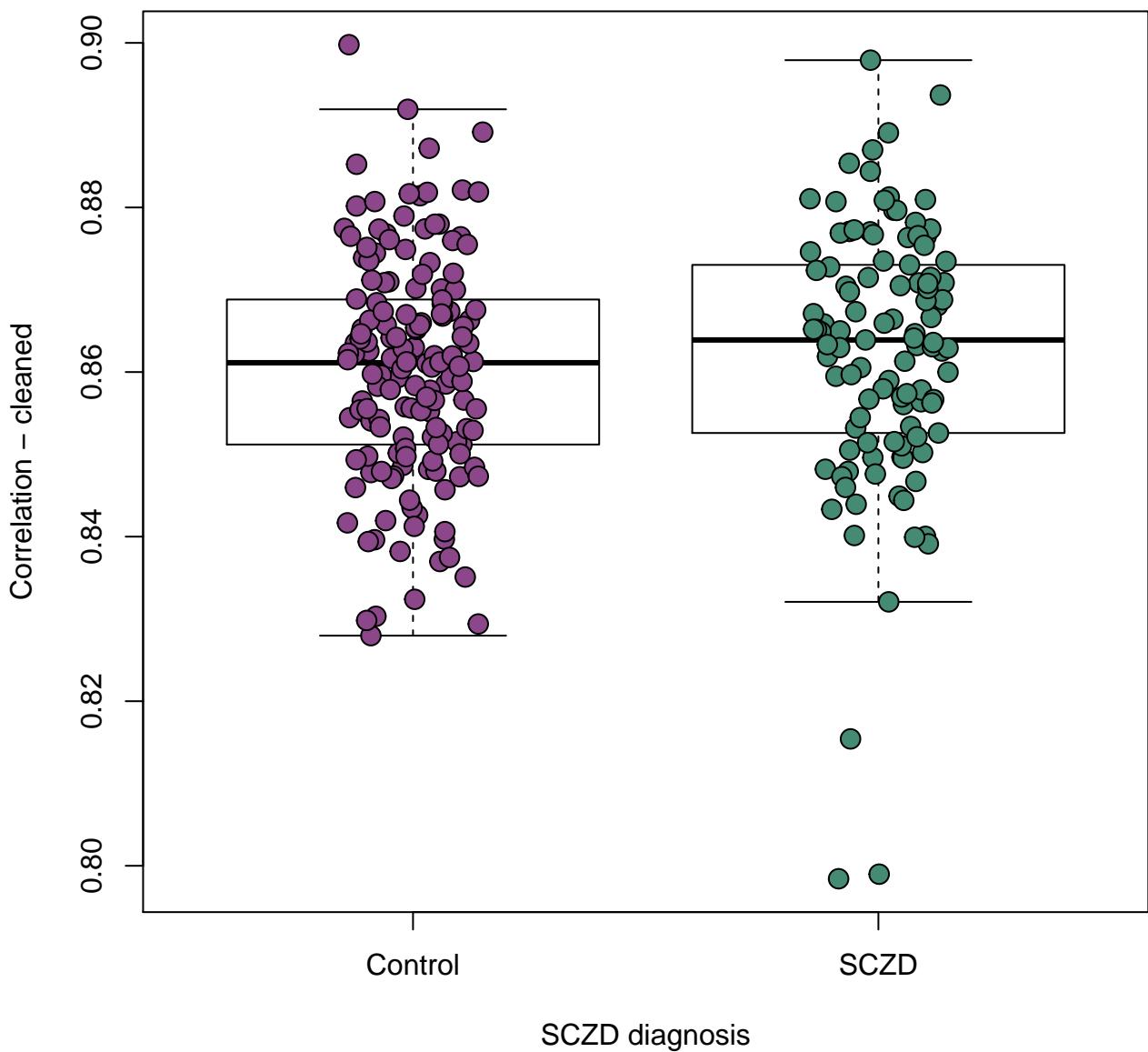
hsa03420: Nucleotide excision repair
p-value: 0.761



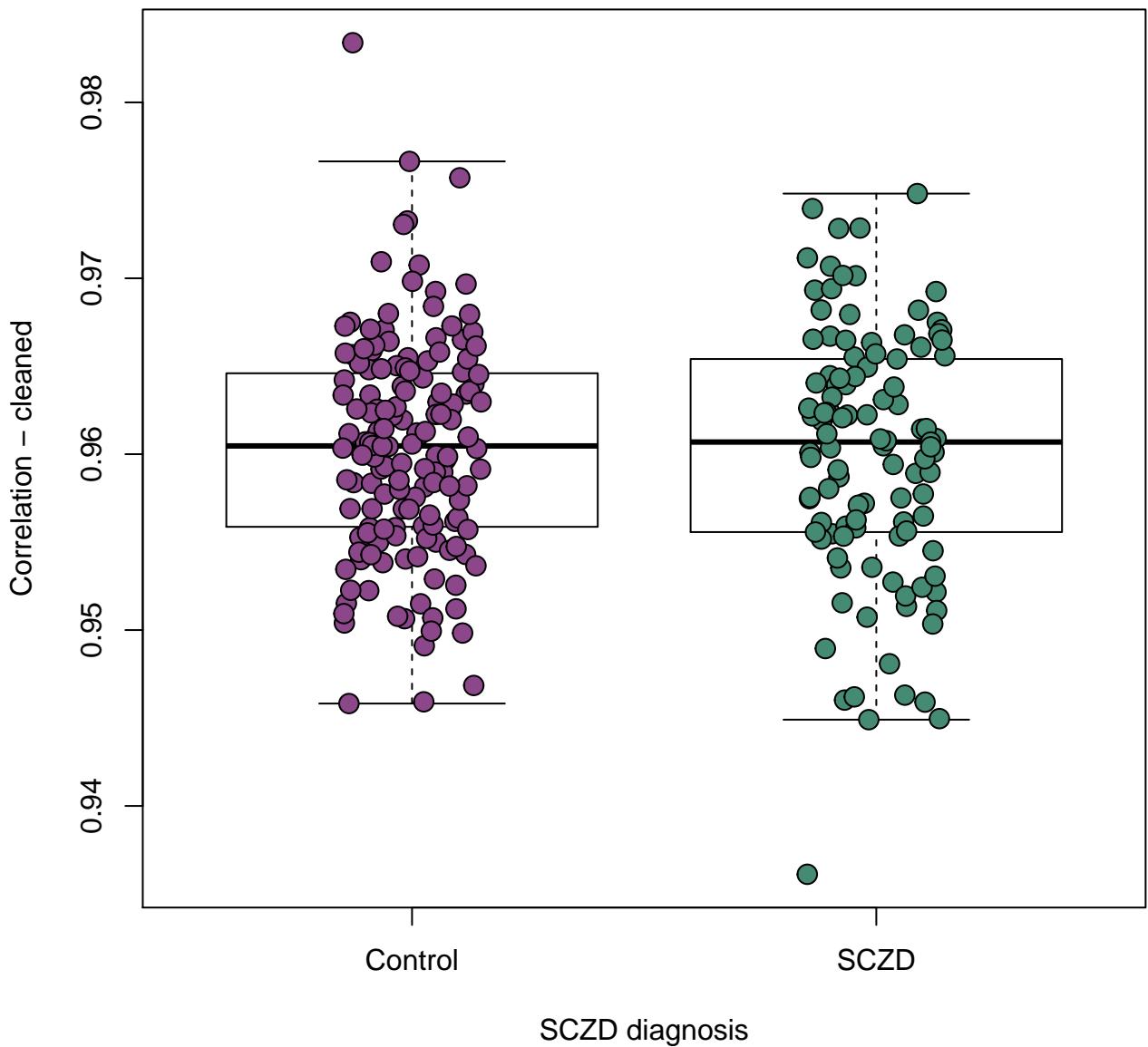
hsa03430: Mismatch repair
p-value: 0.0071



hsa03440: Homologous recombination
p-value: 0.309

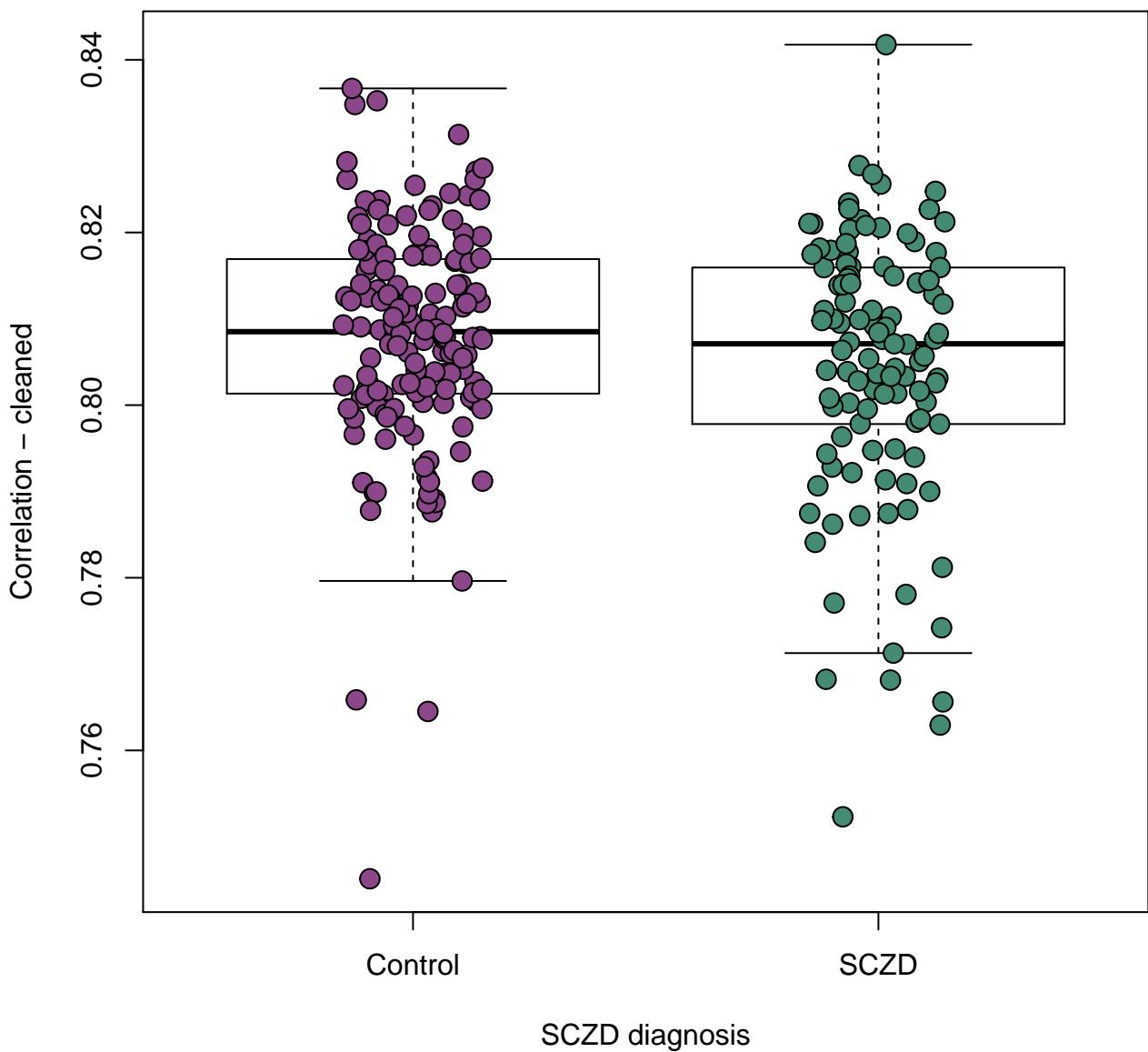


hsa03450: Non-homologous end-joining
p-value: 0.617



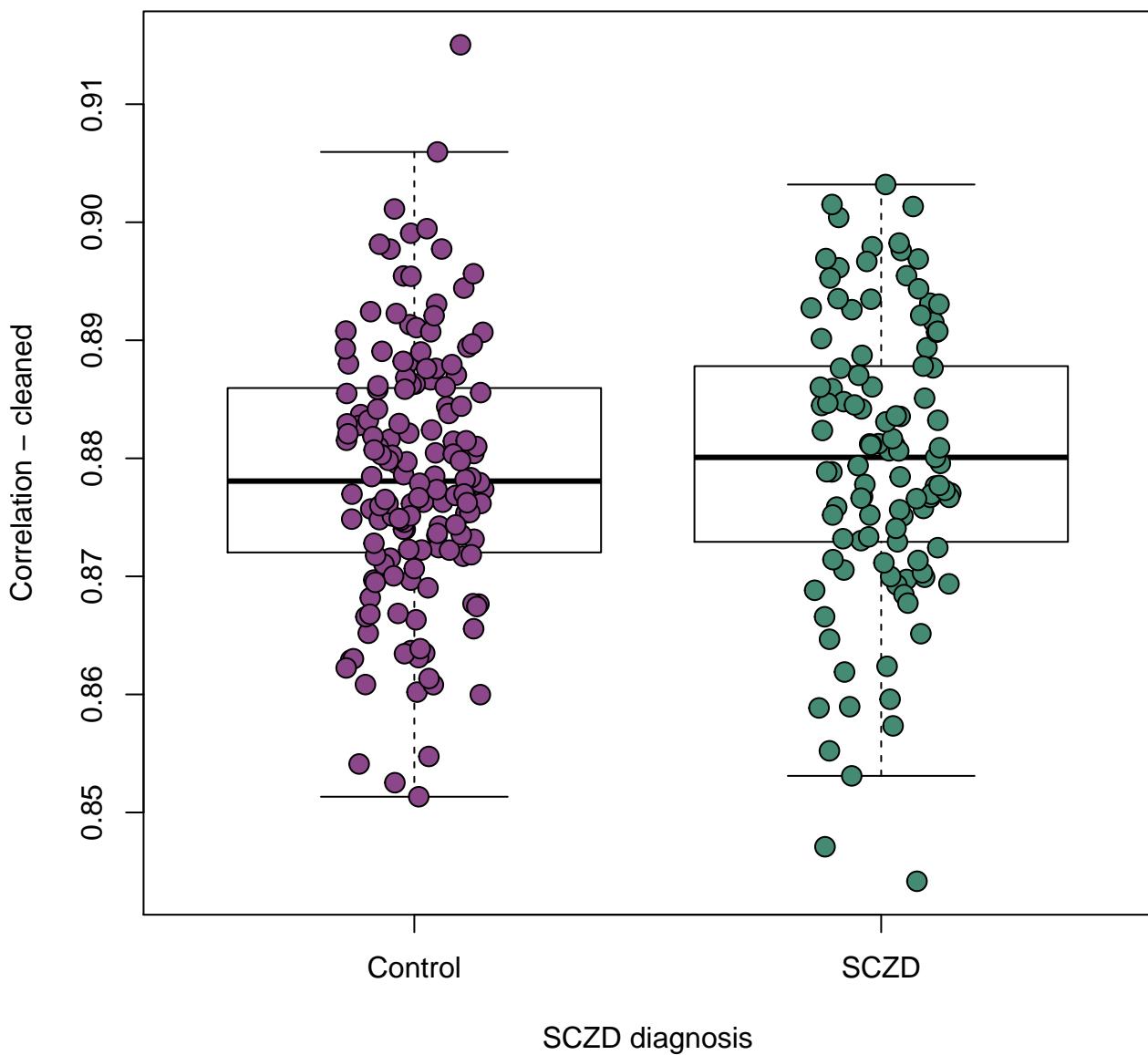
hsa04010: MAPK signaling pathway

p-value: 0.0469

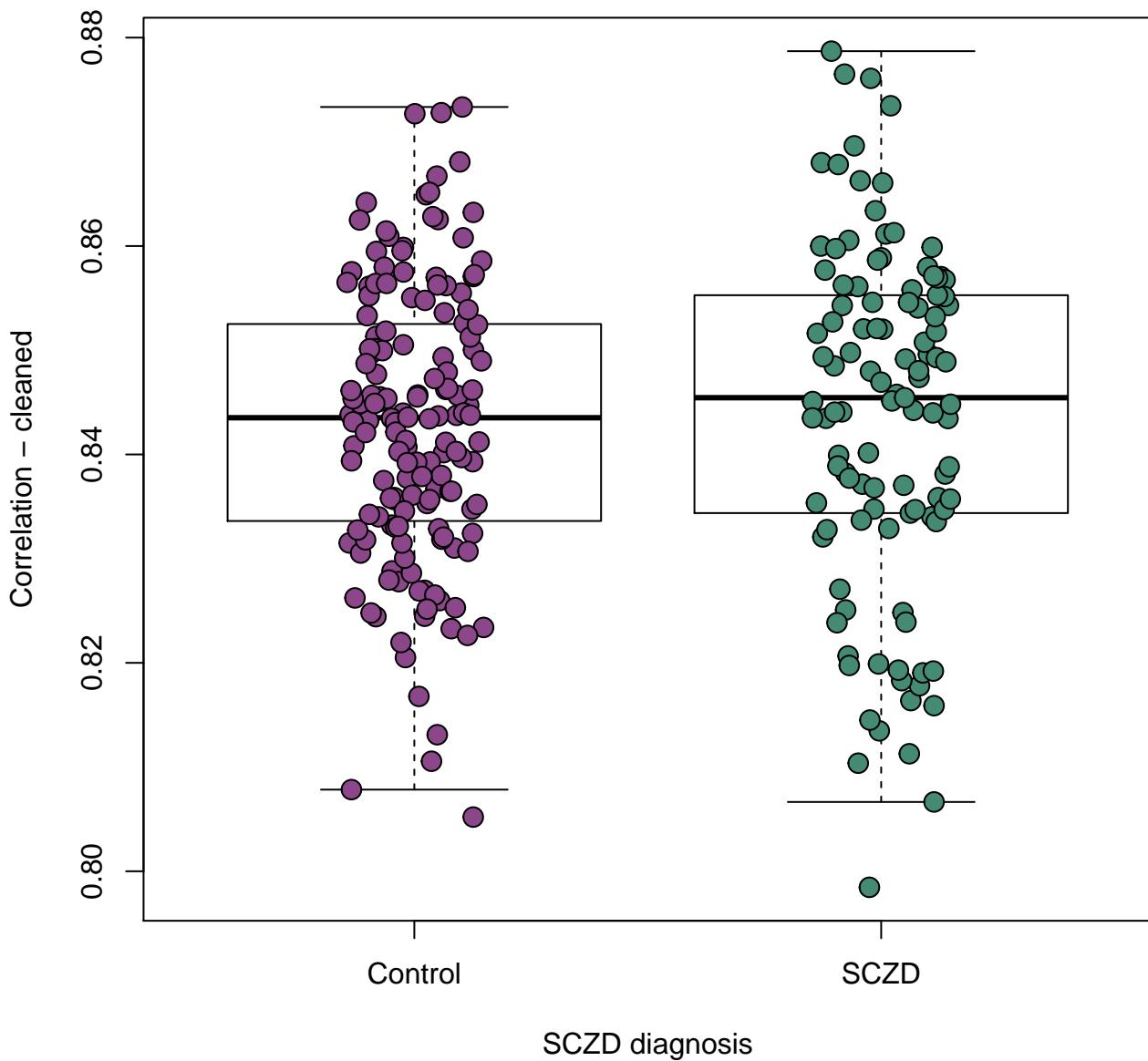


hsa04012: ErbB signaling pathway

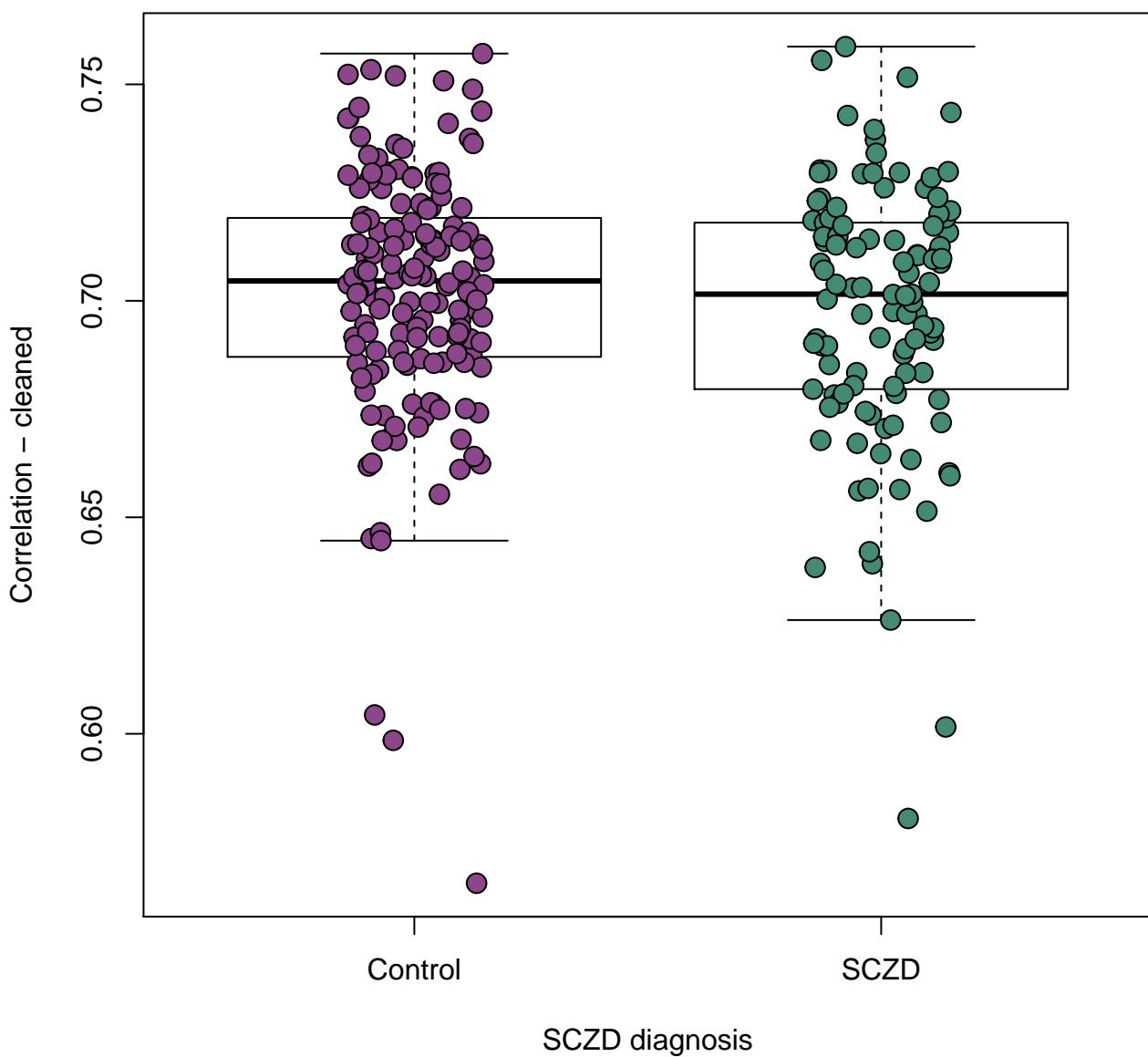
p-value: 0.355



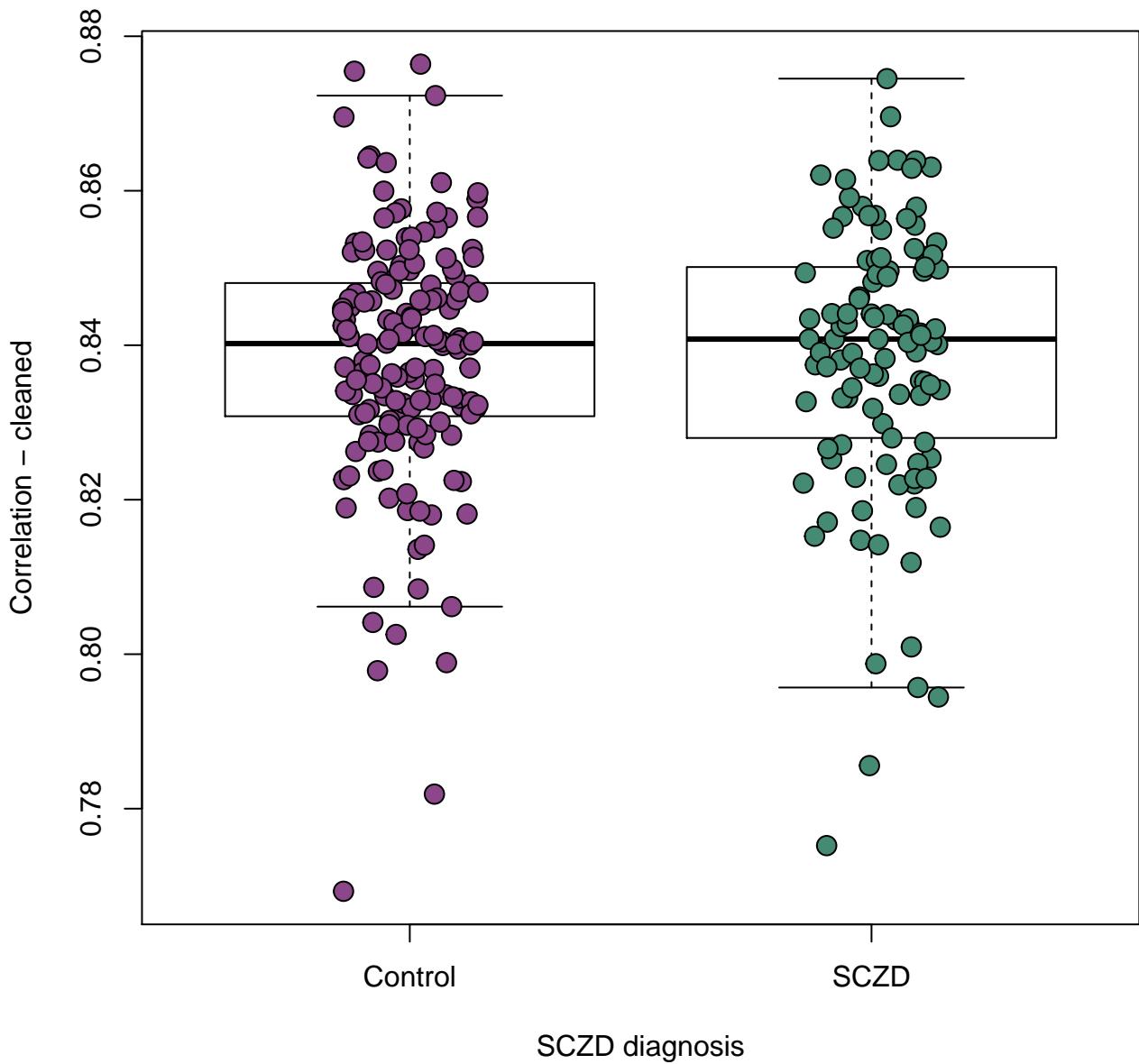
hsa04020: Calcium signaling pathway
p-value: 0.684



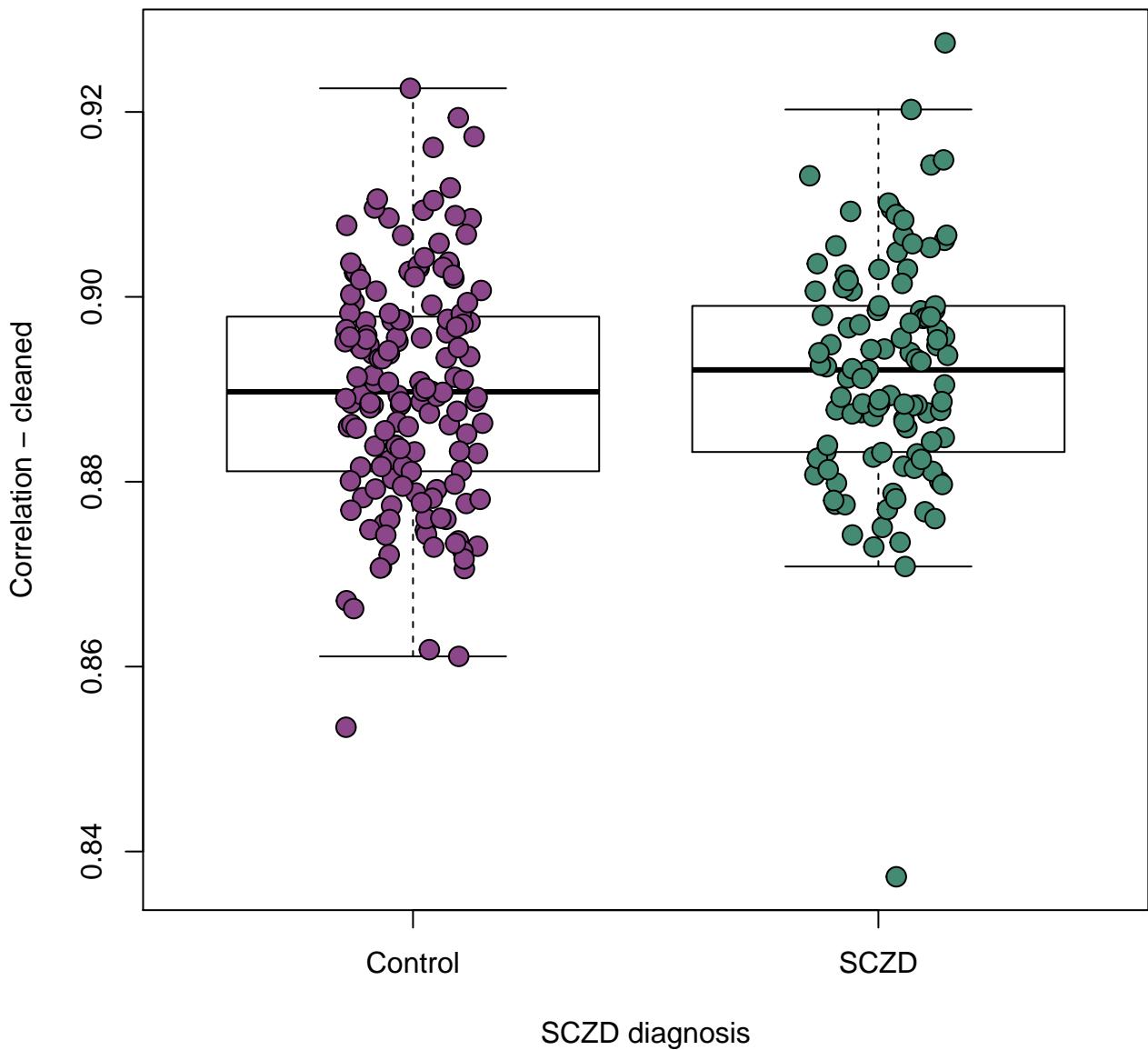
hsa04060: Cytokine–cytokine receptor interaction
p-value: 0.249



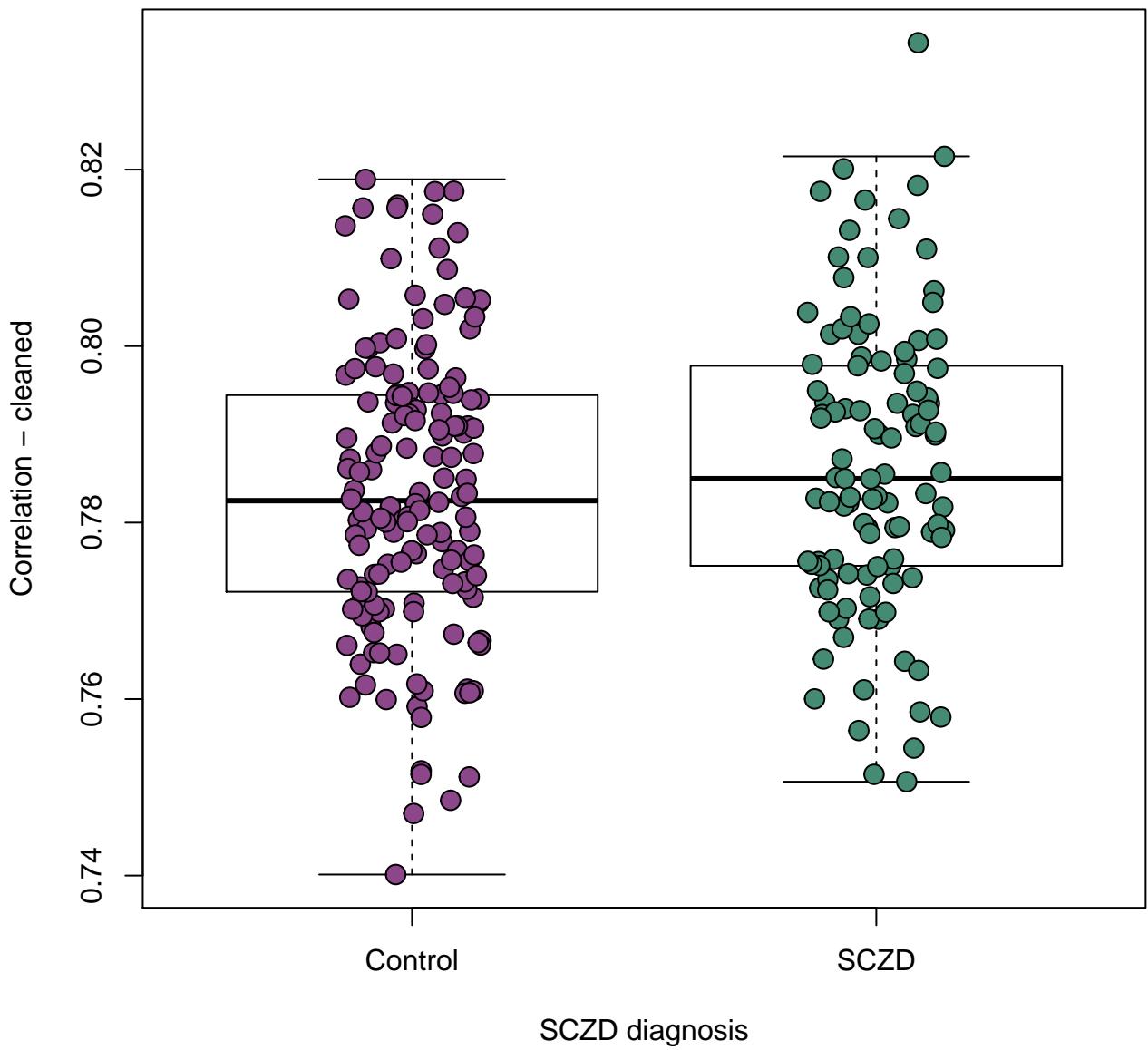
hsa04062: Chemokine signaling pathway
p-value: 0.986



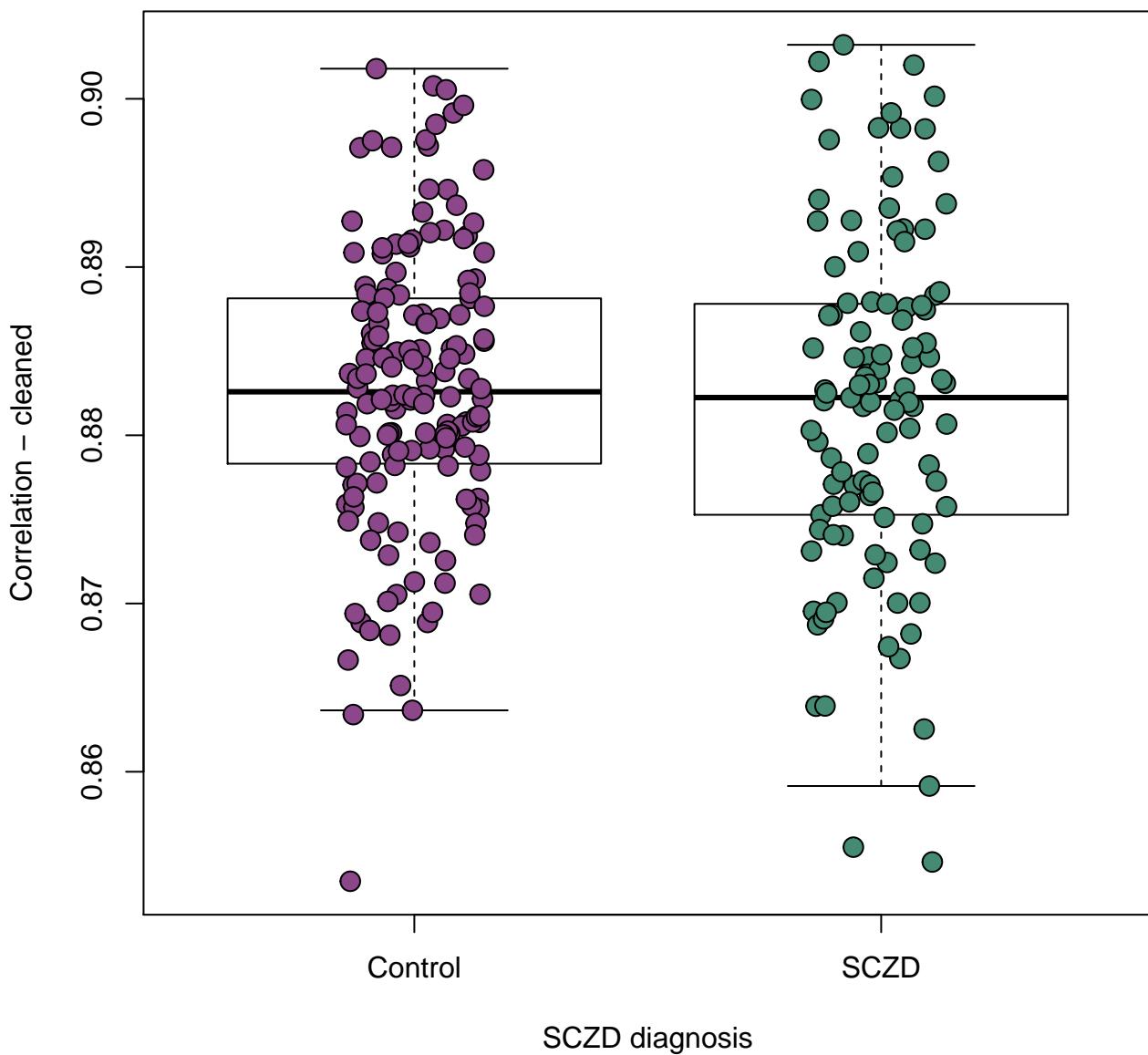
hsa04070: Phosphatidylinositol signaling system
p-value: 0.205



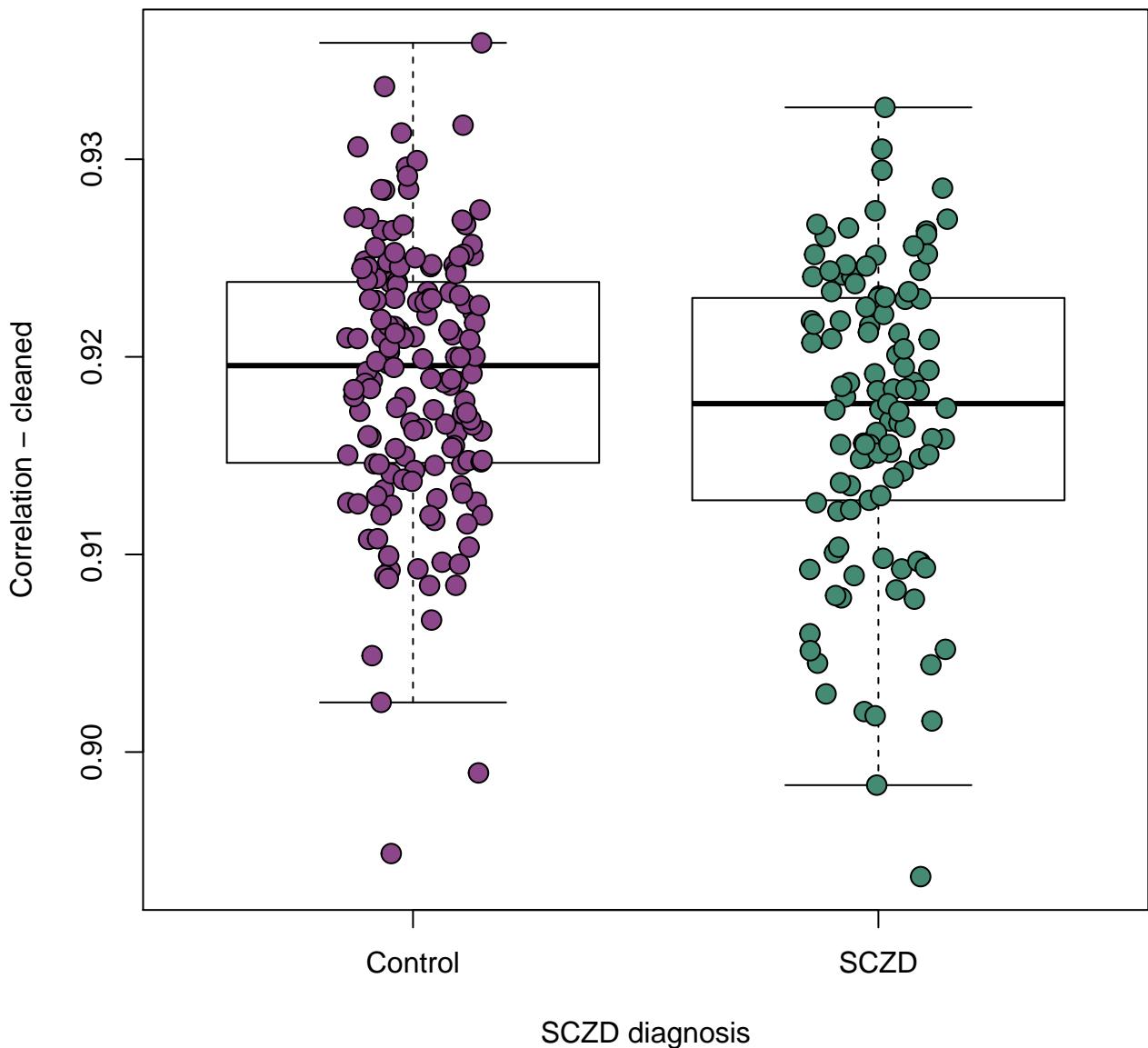
hsa04080: Neuroactive ligand–receptor interaction
p-value: 0.156



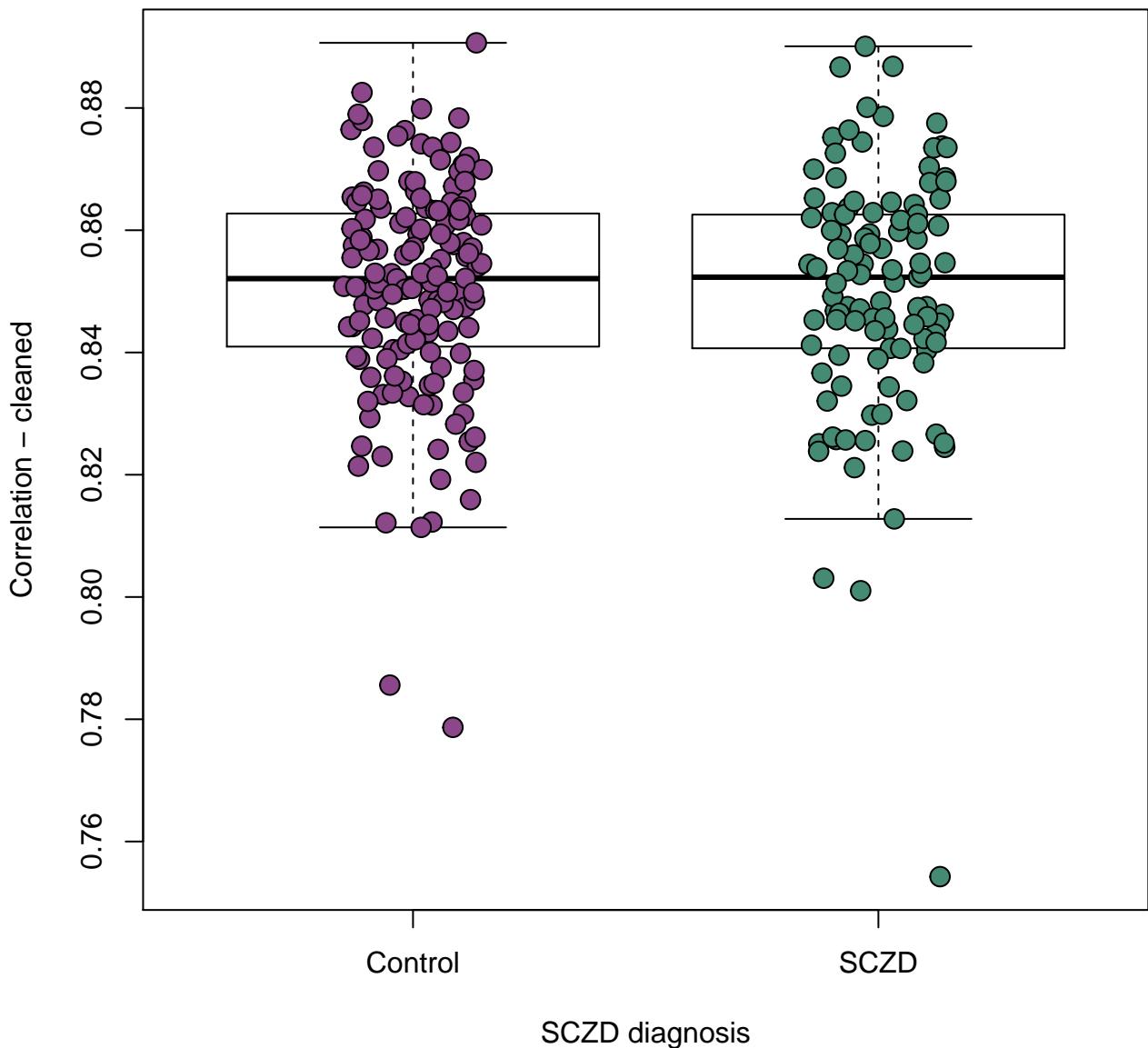
hsa04110: Cell cycle
p-value: 0.339



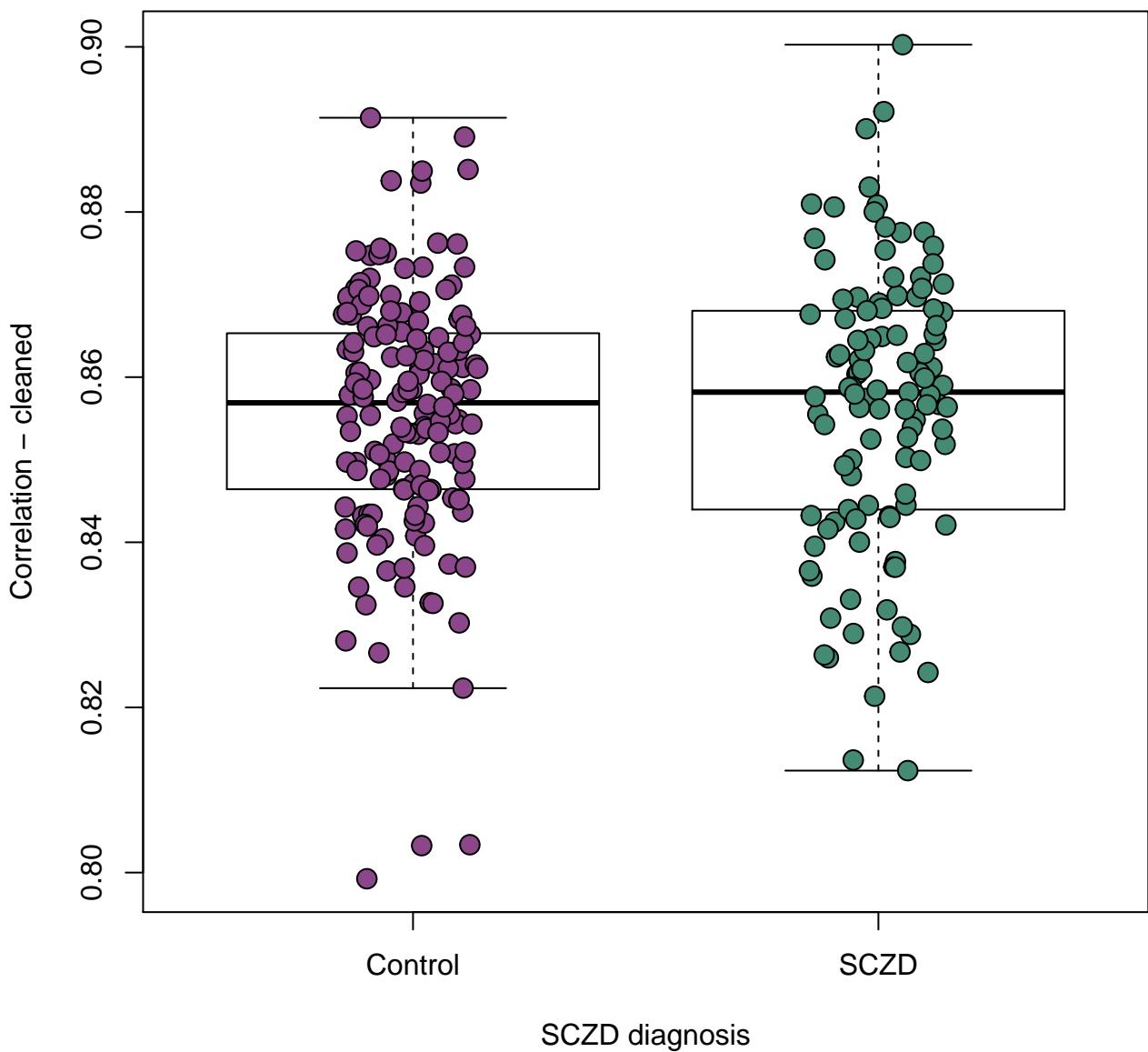
hsa04114: Oocyte meiosis
p-value: 0.0249



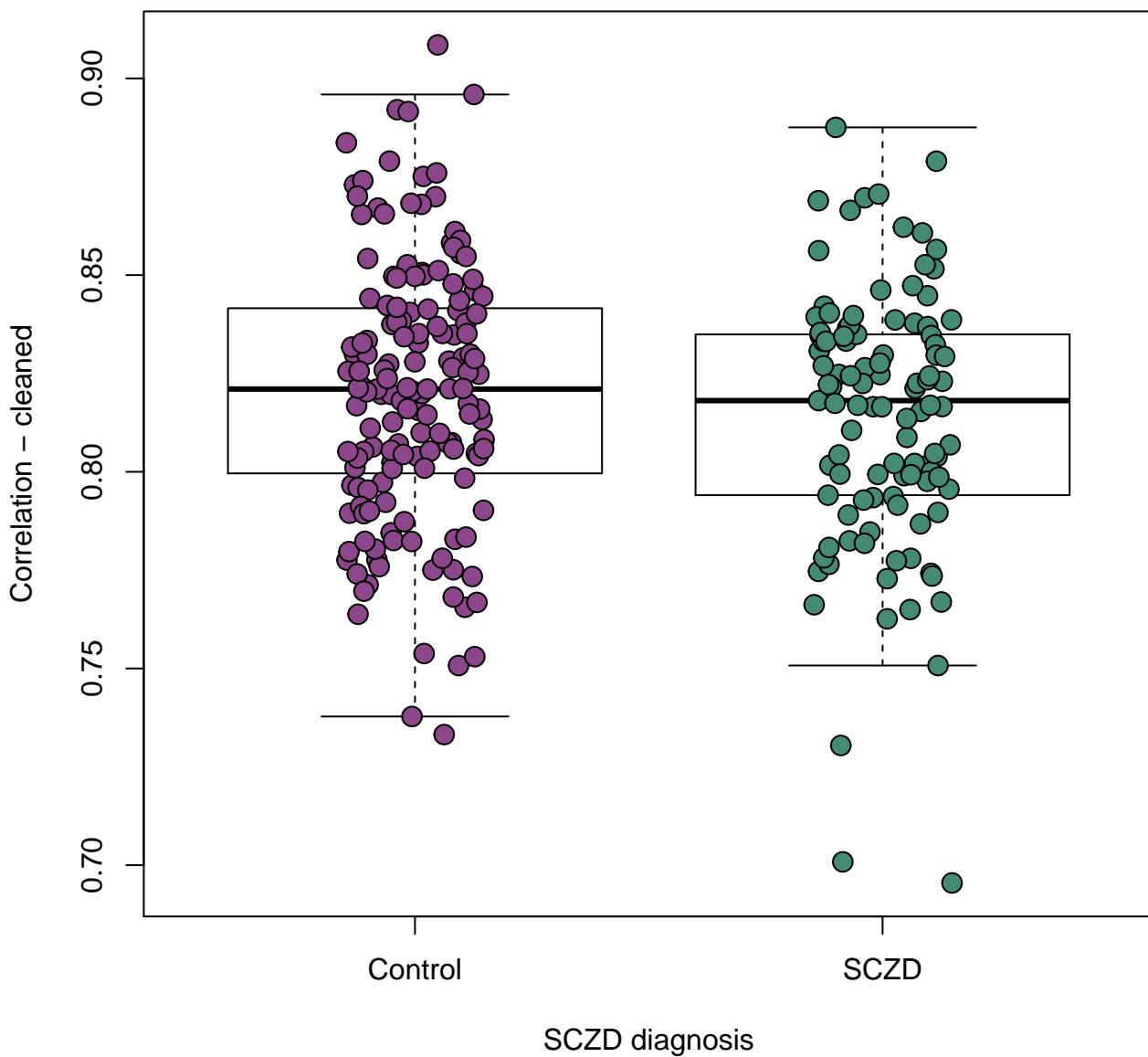
hsa04115: p53 signaling pathway
p-value: 0.769



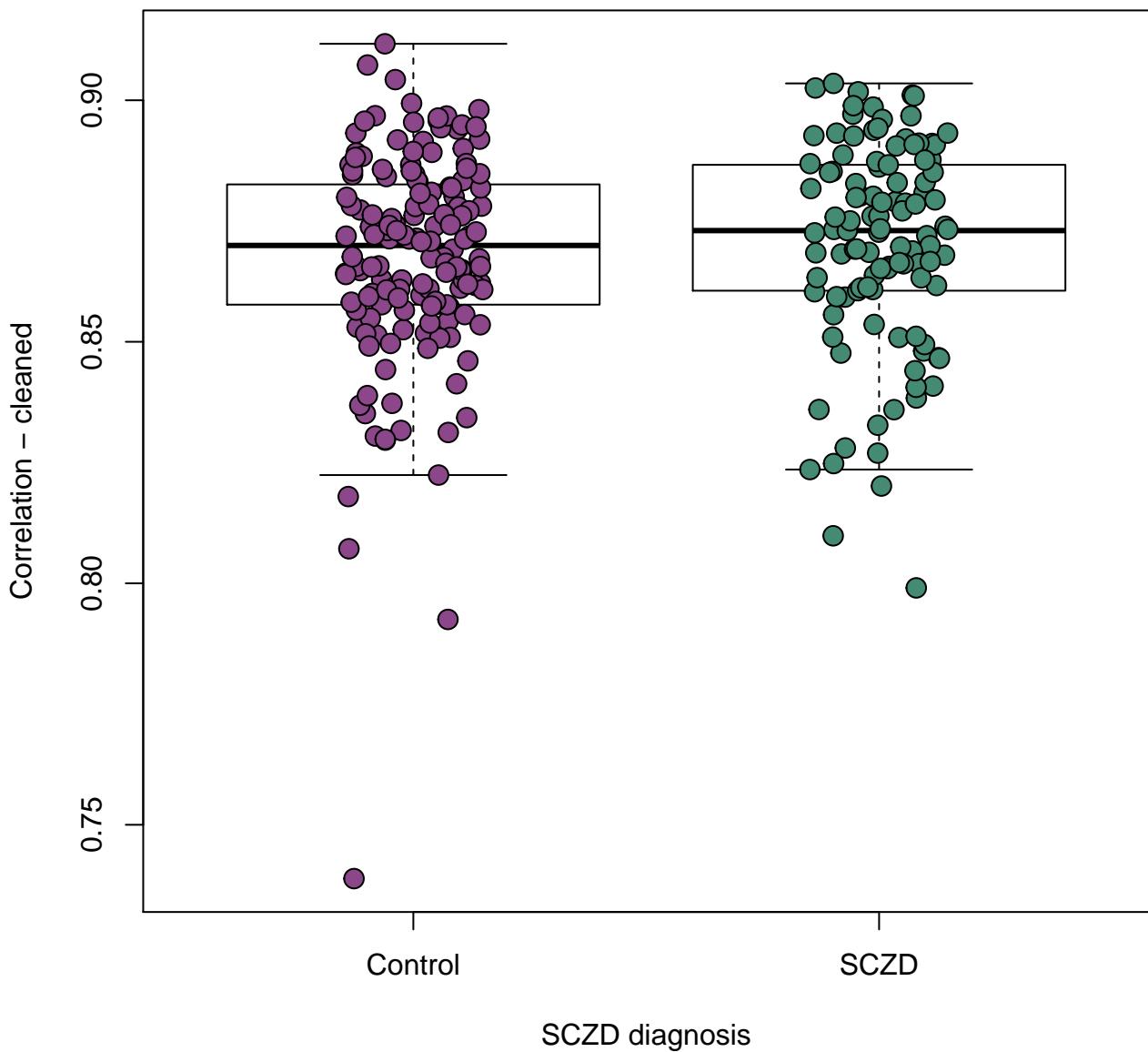
hsa04120: Ubiquitin mediated proteolysis
p-value: 0.676



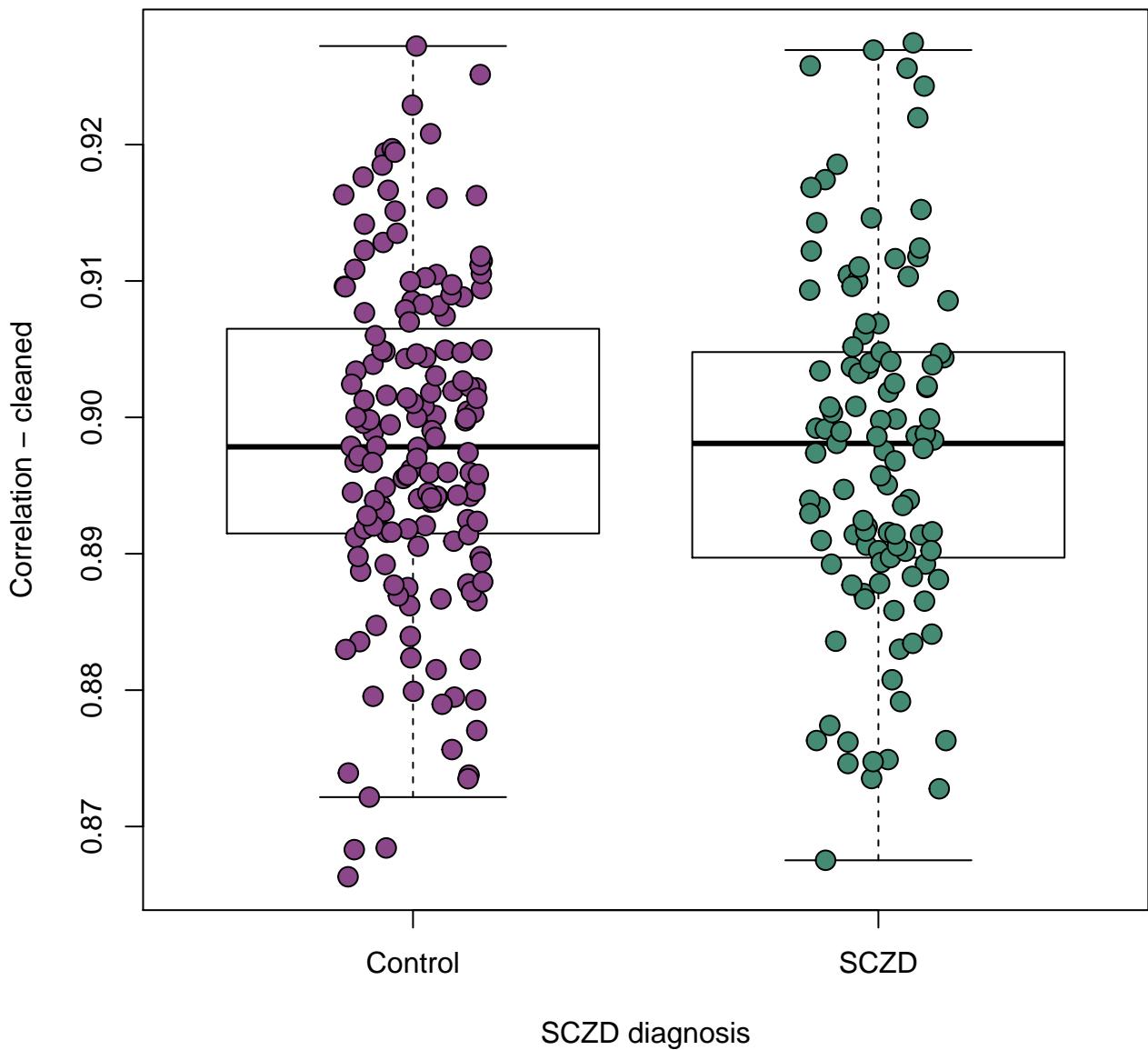
hsa04122: Sulfur relay system
p-value: 0.137



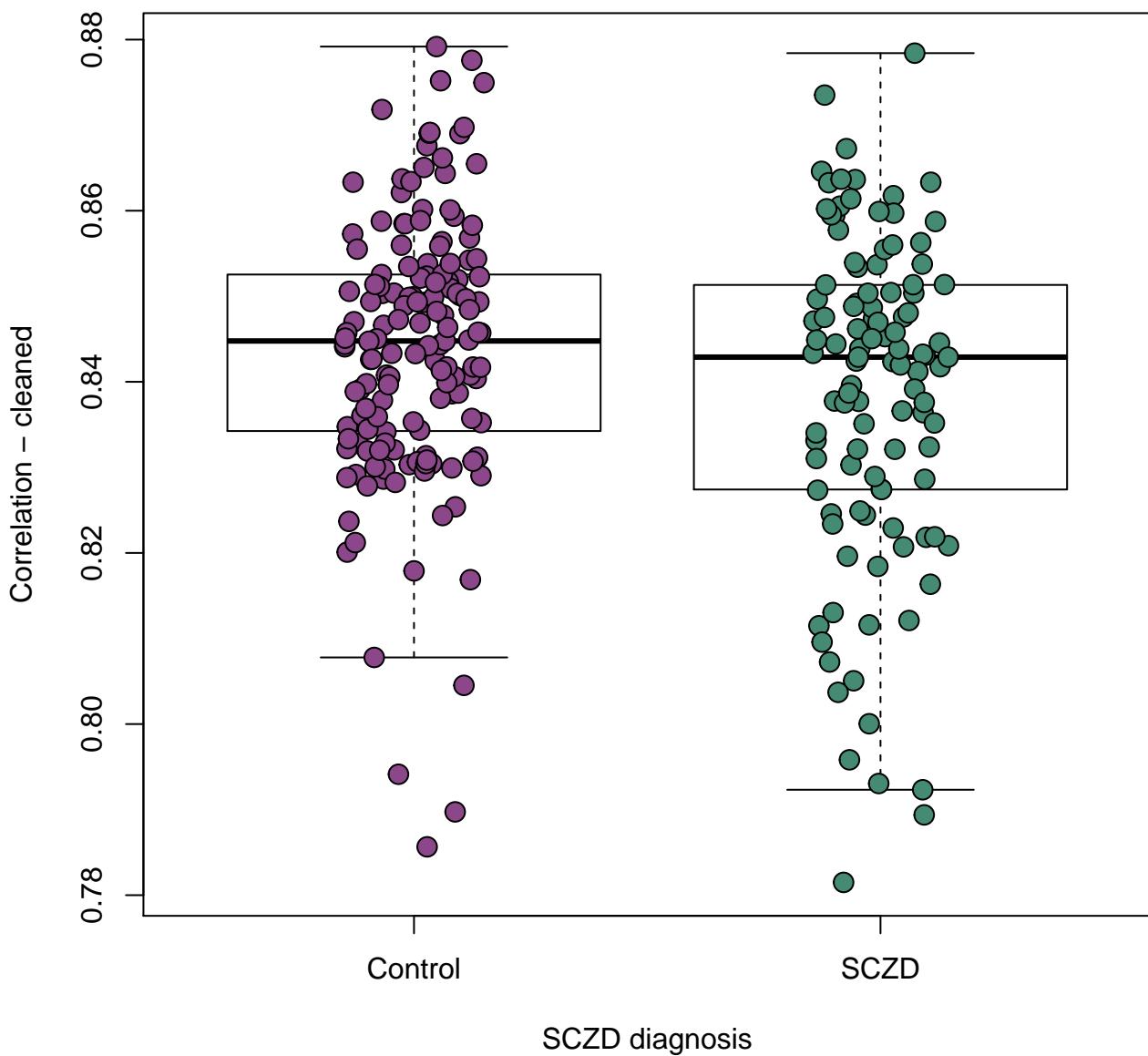
hsa04130: SNARE interactions in vesicular transport
p-value: 0.375



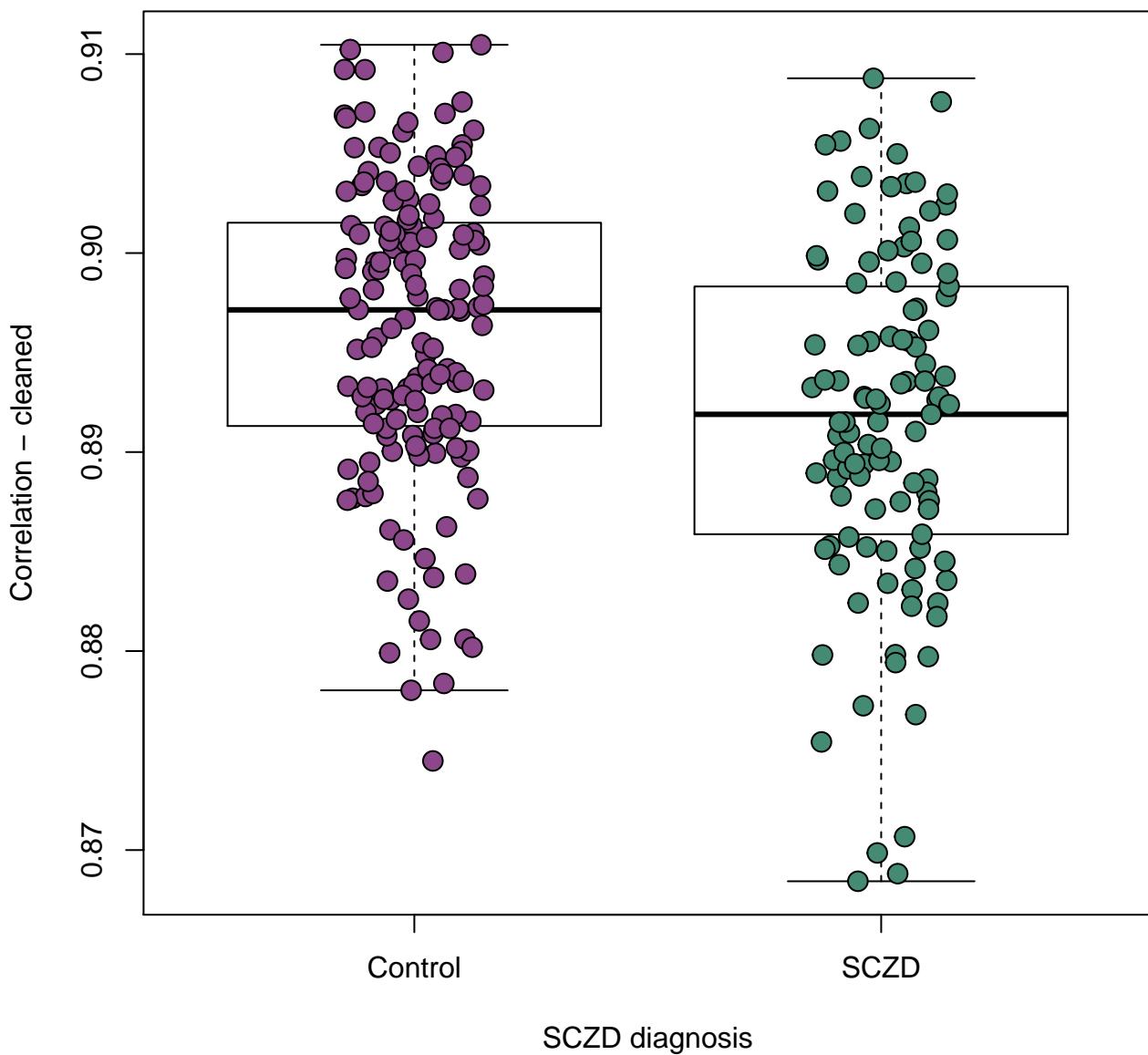
hsa04140: Regulation of autophagy
p-value: 0.799



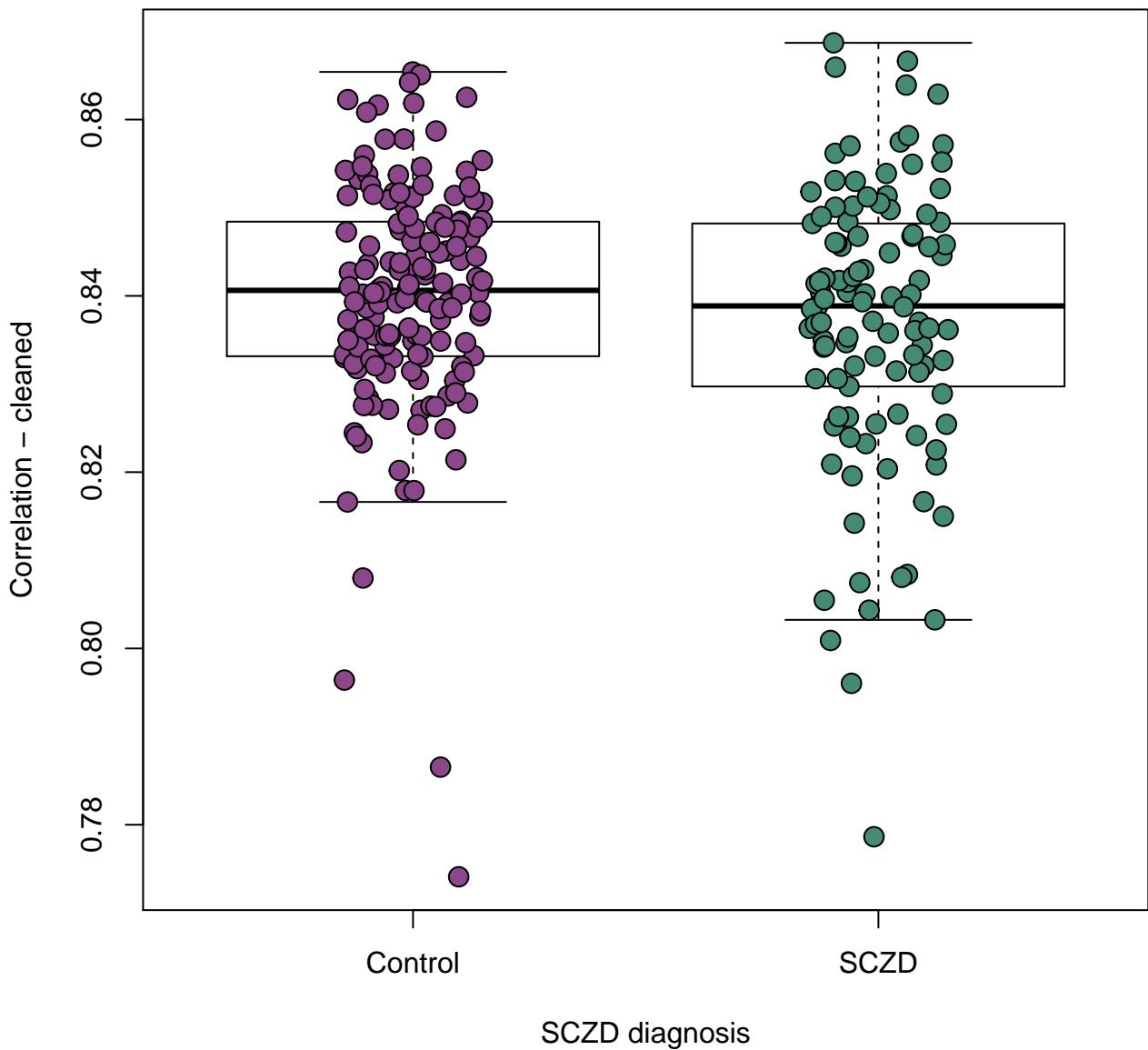
hsa04141: Protein processing in endoplasmic reticulum
p-value: 0.0114



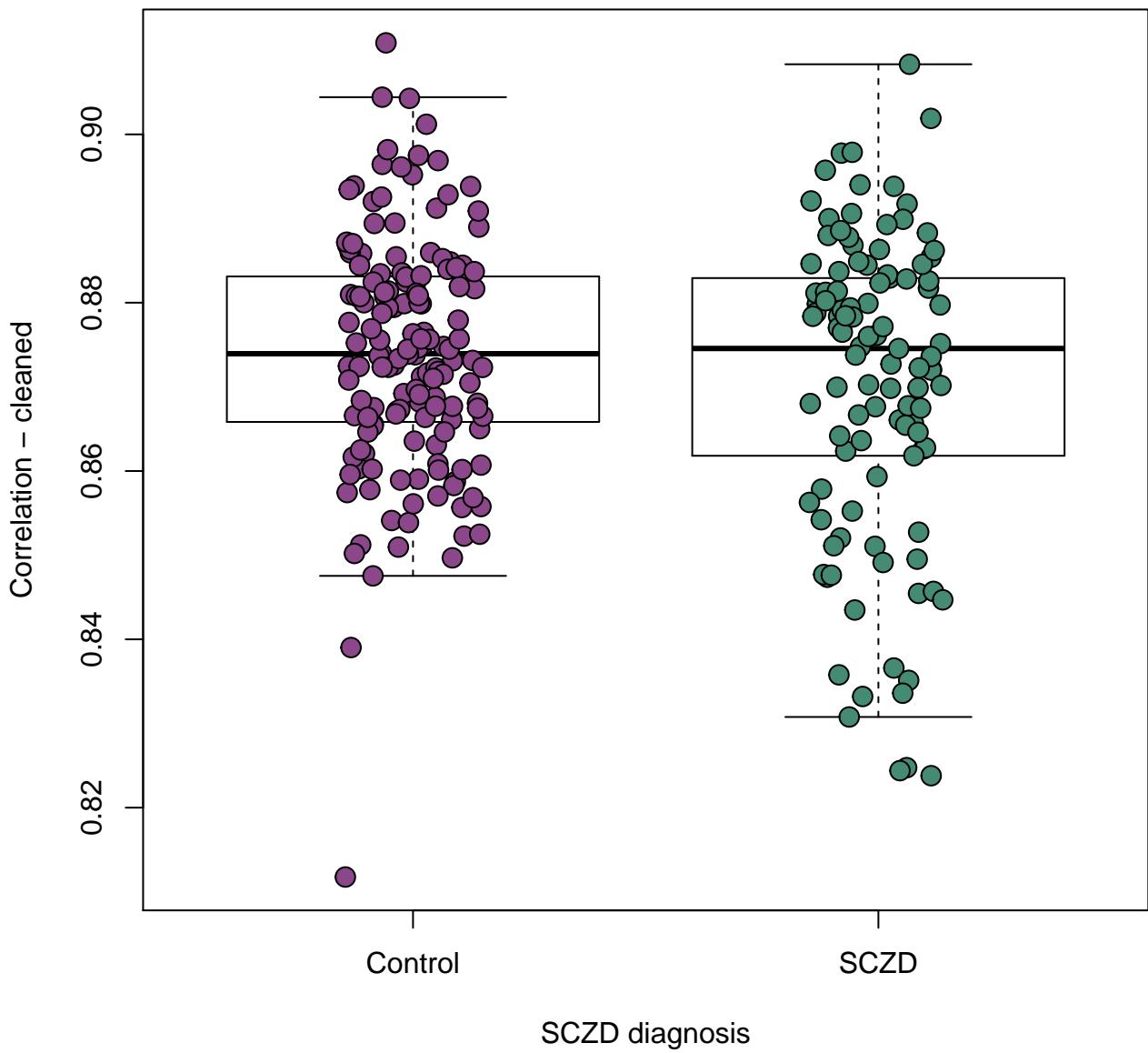
hsa04142: Lysosome
p-value: 6.44e-06



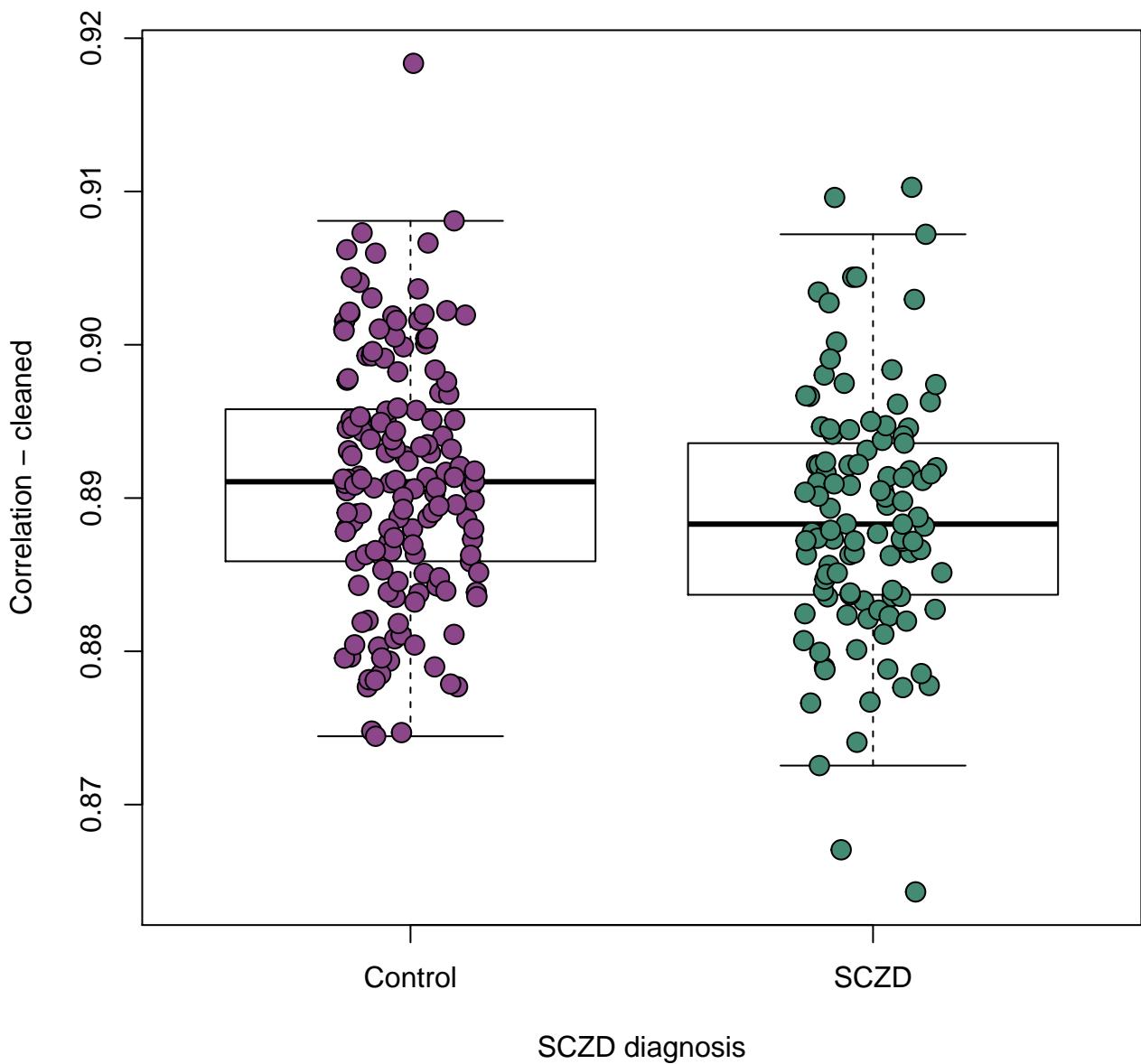
hsa04144: Endocytosis
p-value: 0.0964



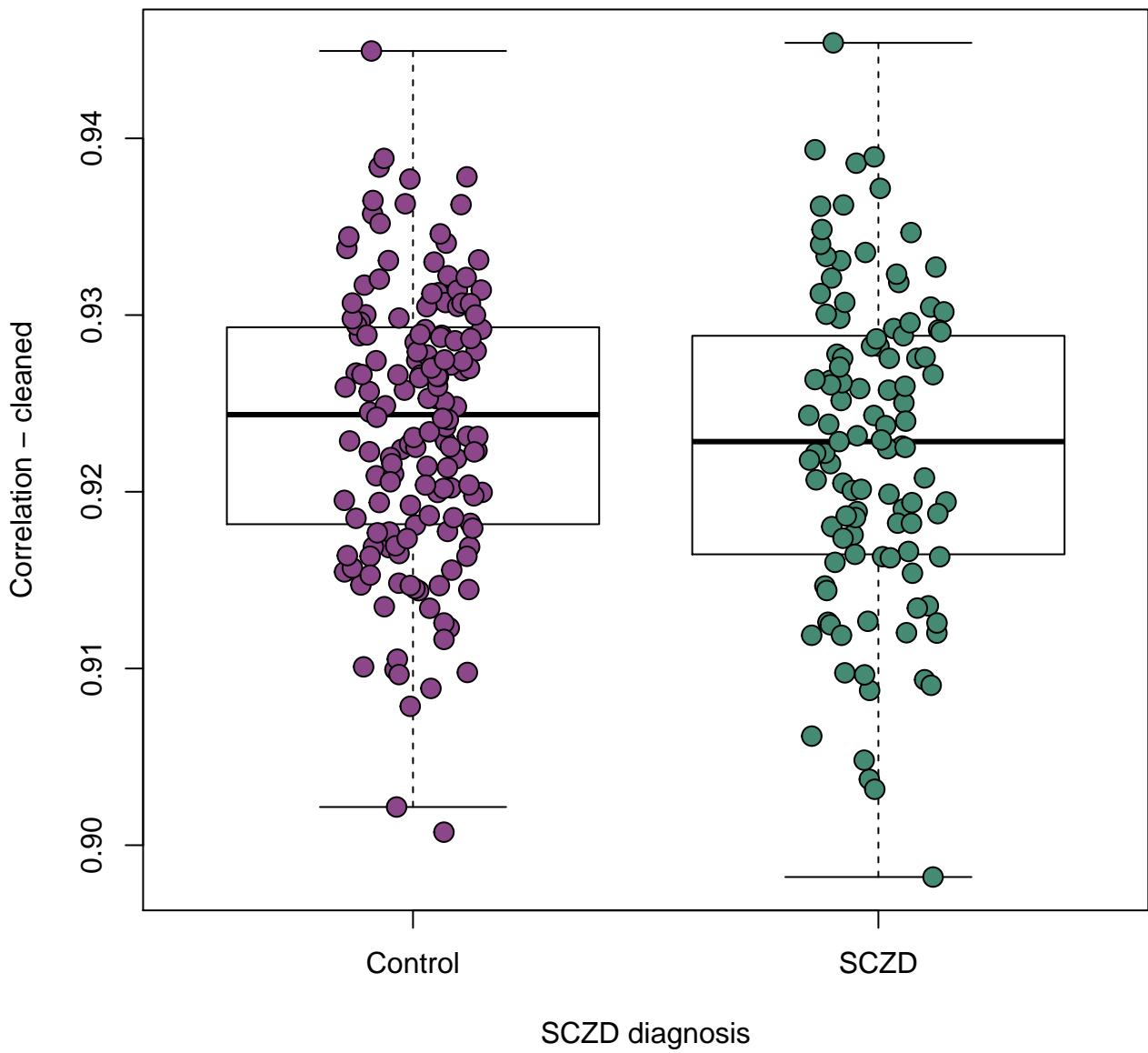
hsa04145: Phagosome
p-value: 0.0639



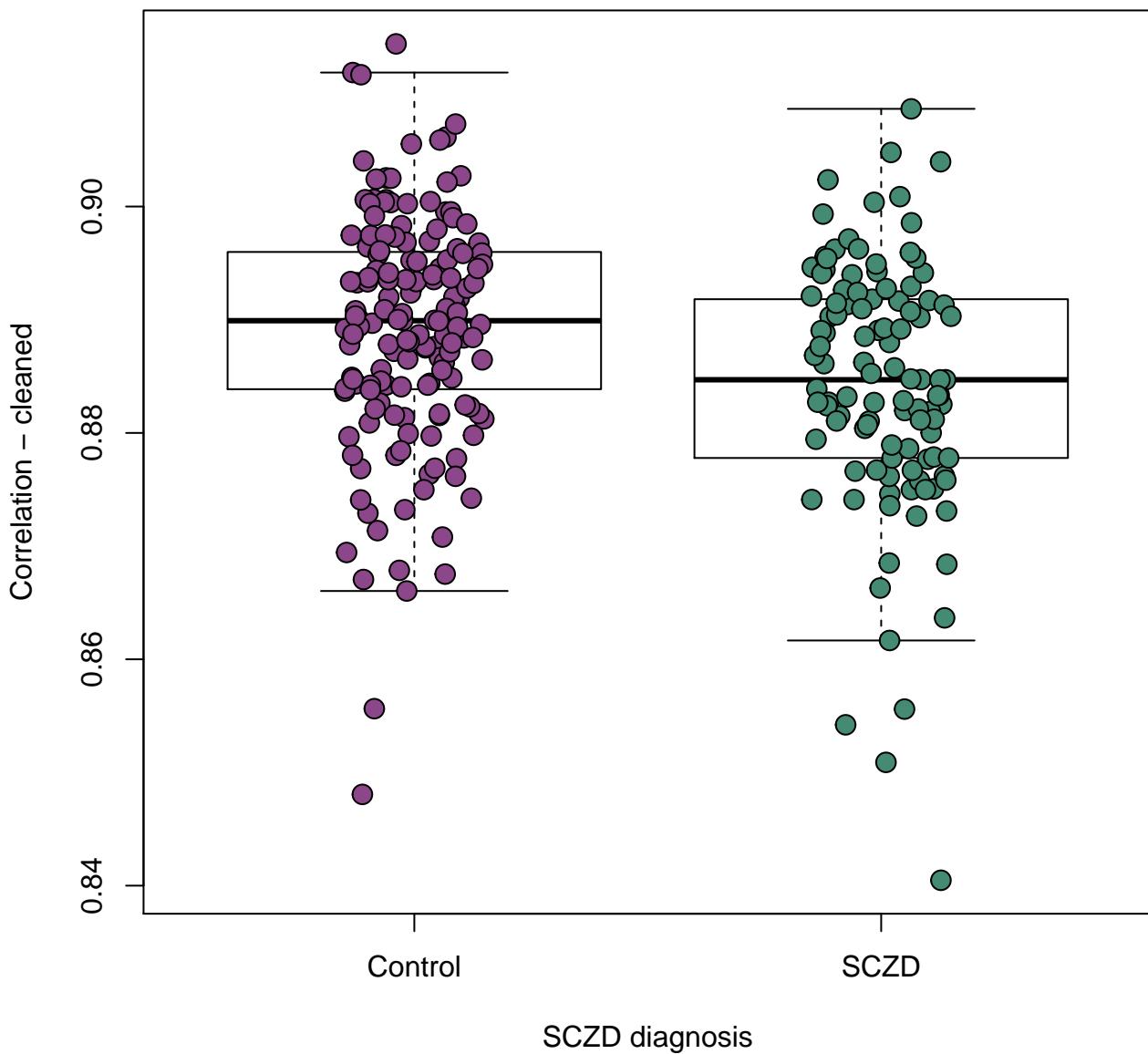
hsa04146: Peroxisome
p-value: 0.0175



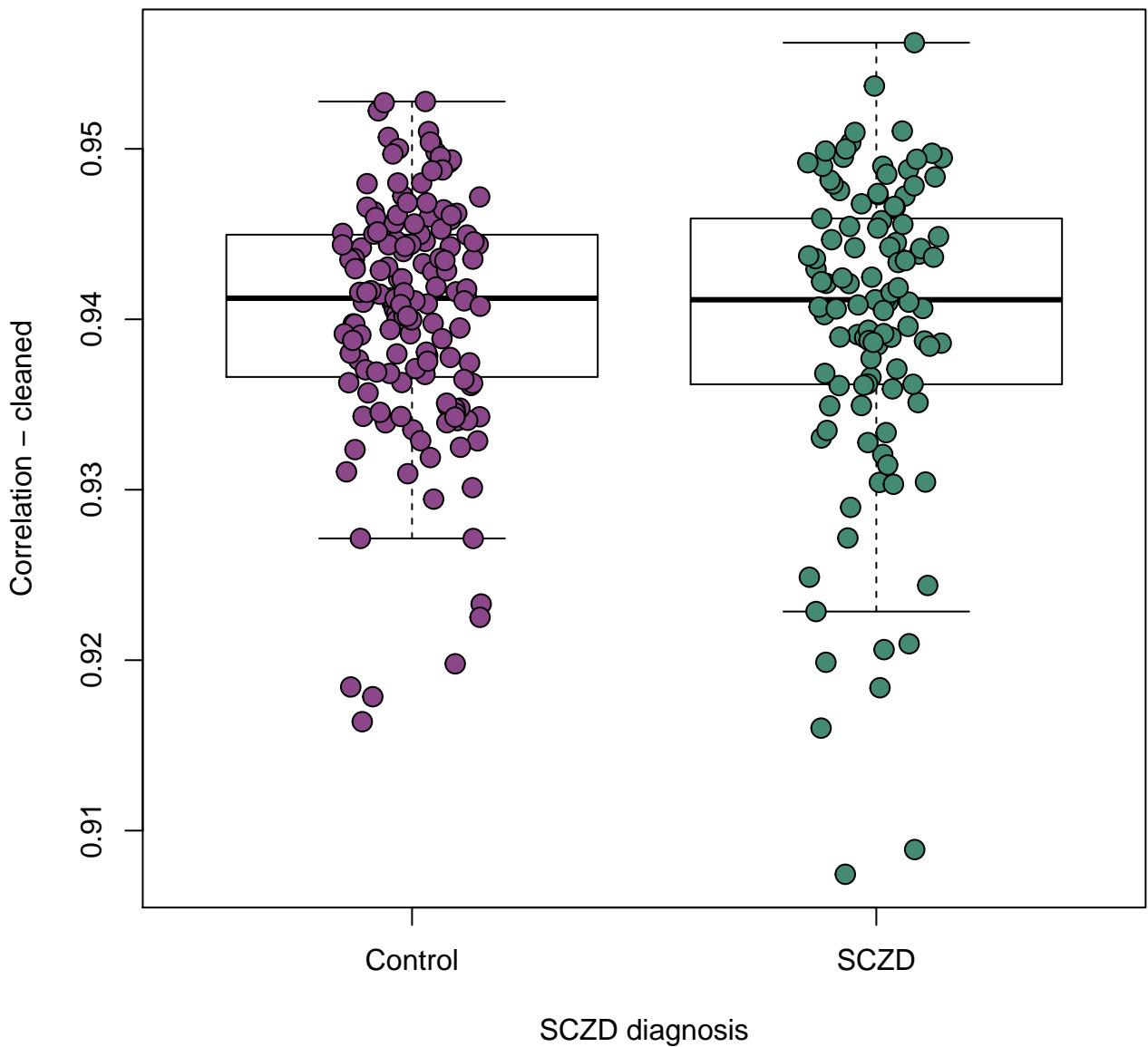
hsa04150: mTOR signaling pathway
p-value: 0.217



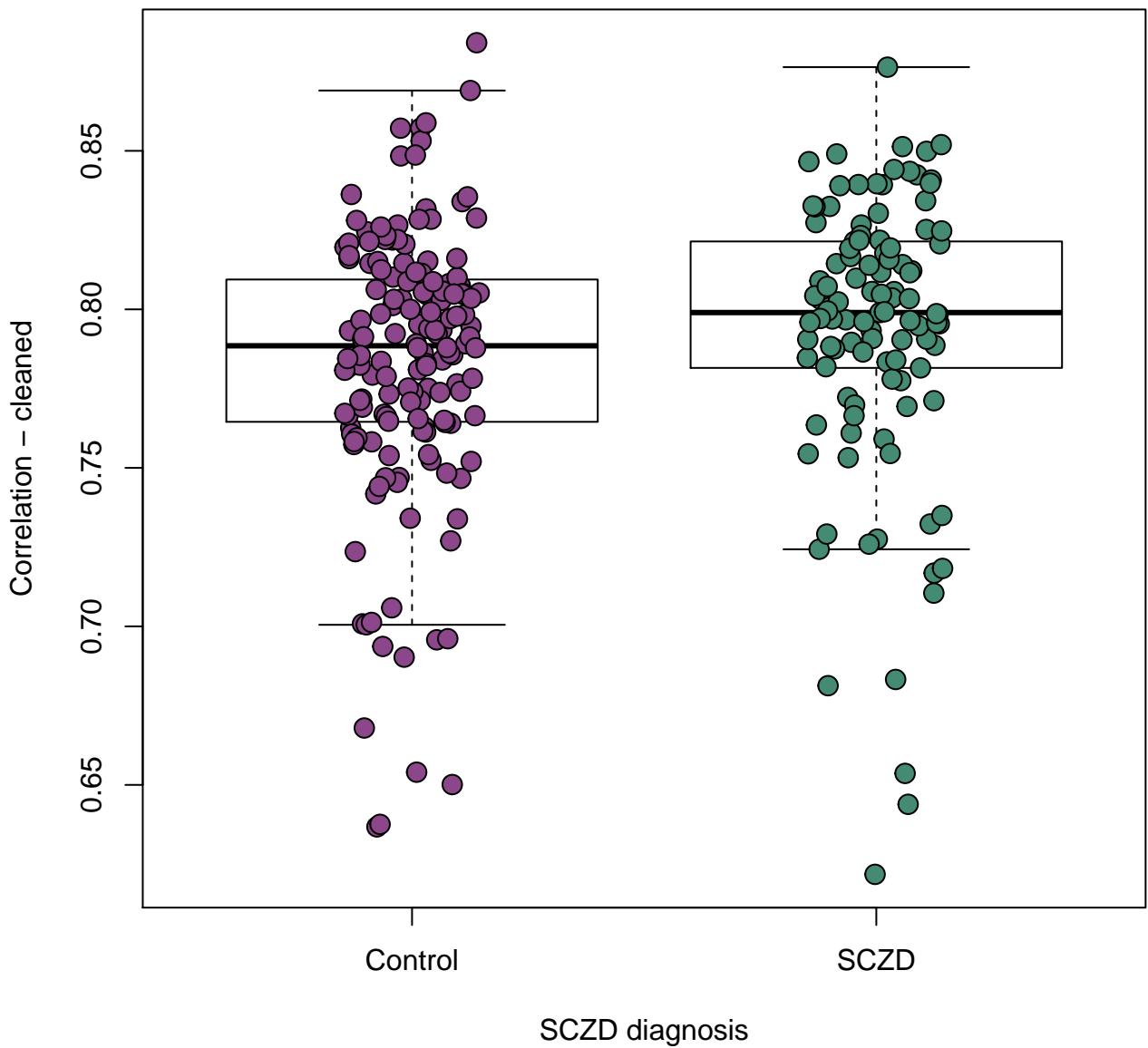
hsa04210: Apoptosis
p-value: 0.000293



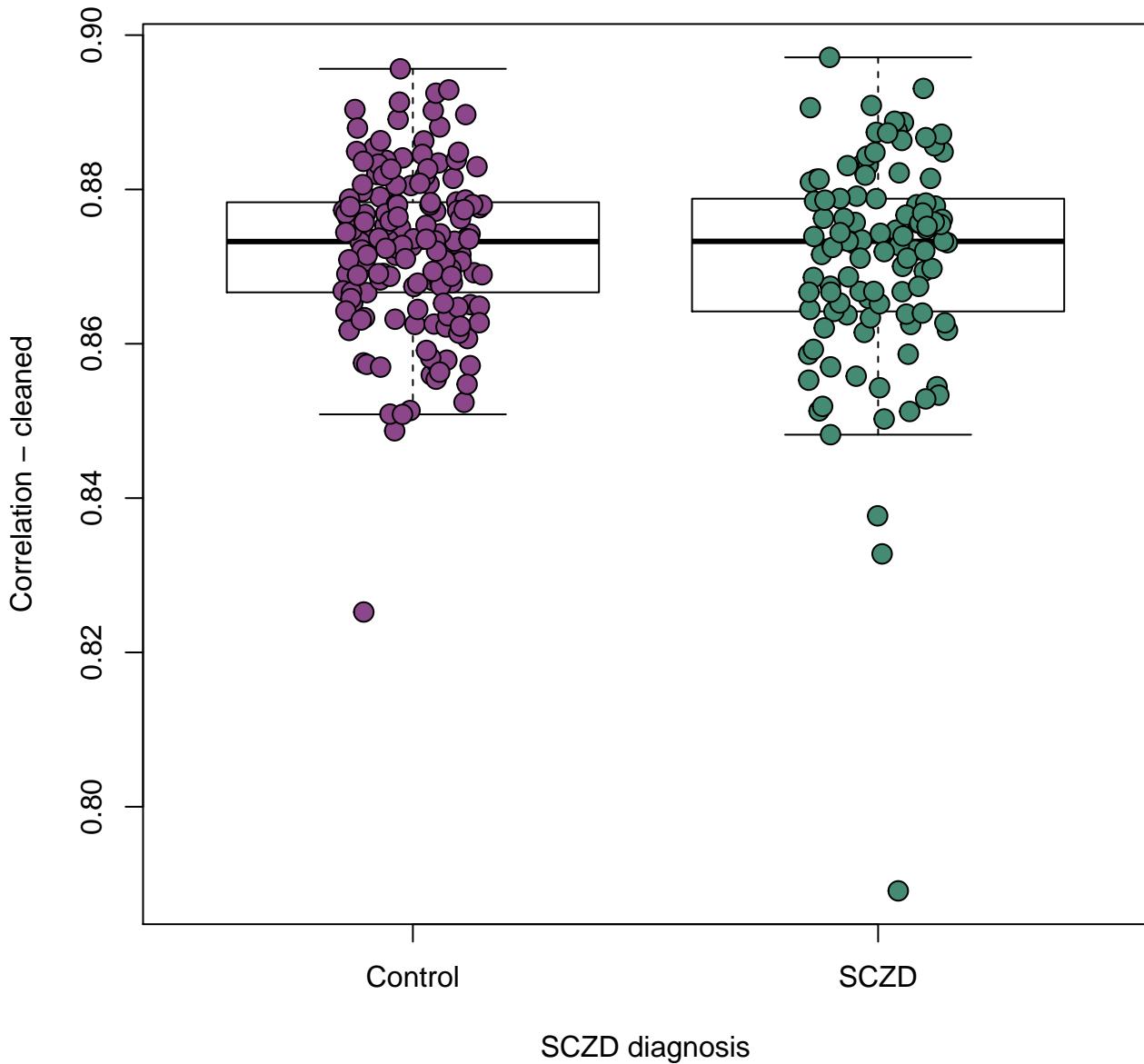
hsa04260: Cardiac muscle contraction
p-value: 0.551



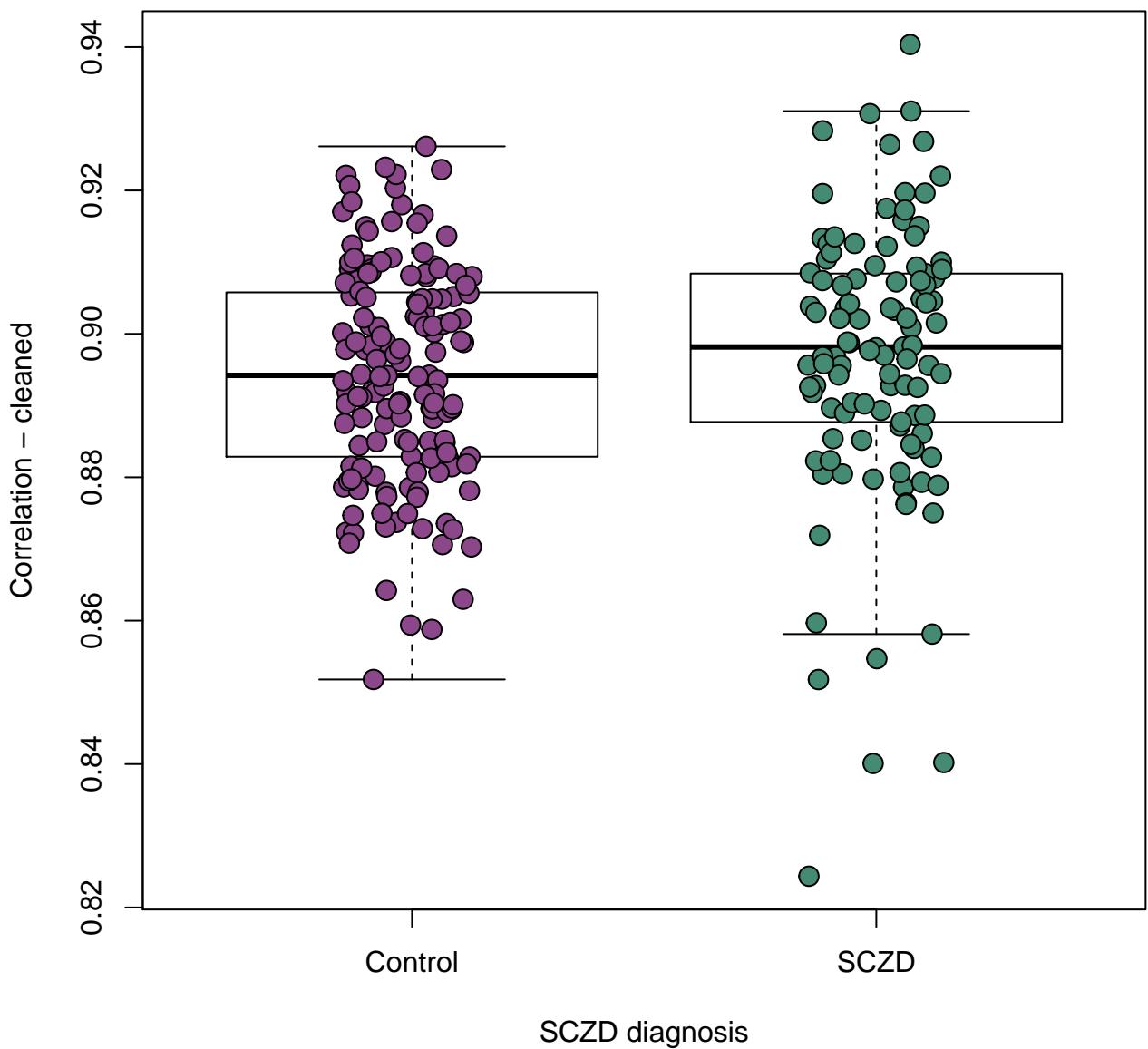
hsa04270: Vascular smooth muscle contraction
p-value: 0.0755



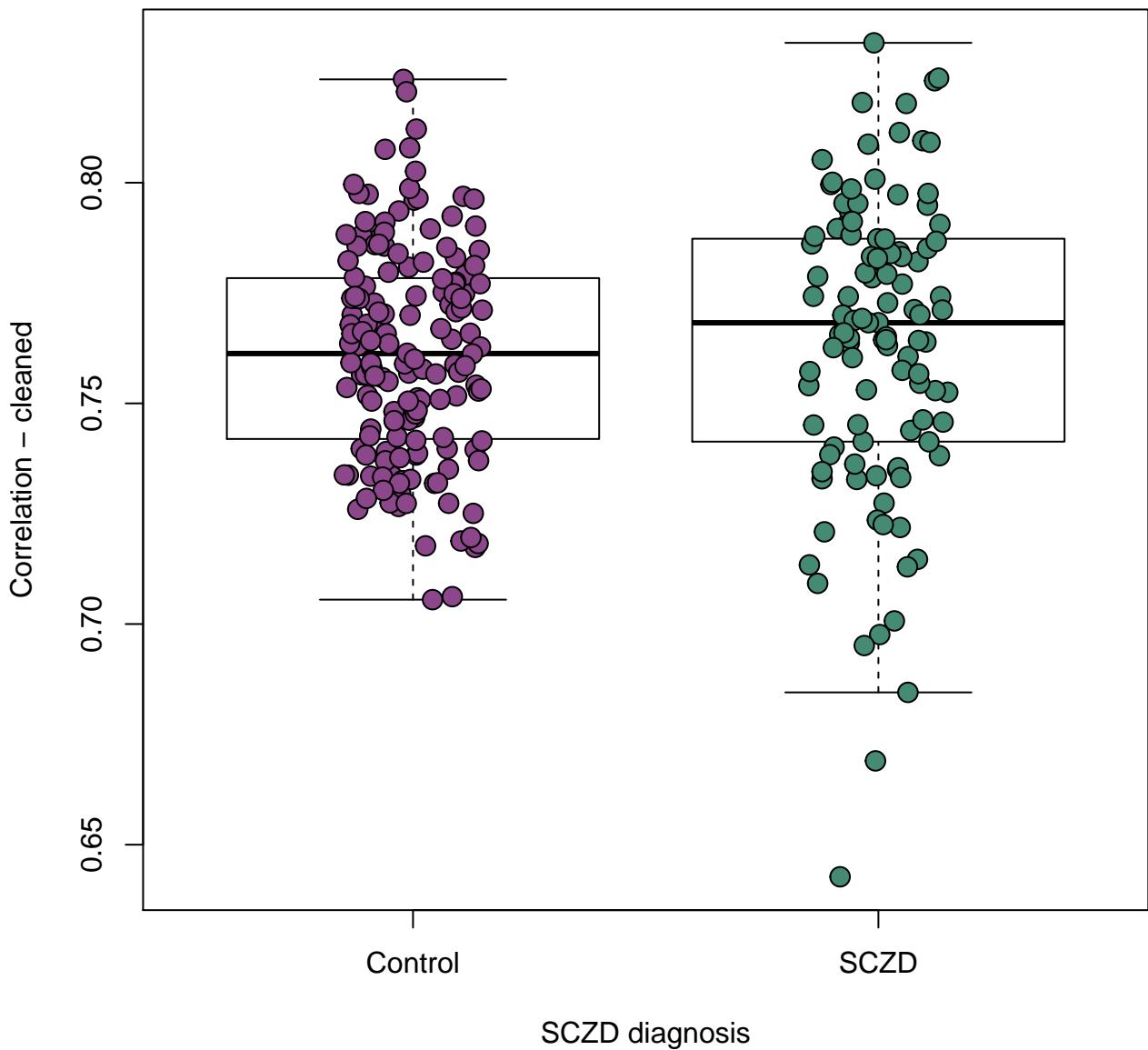
hsa04310: Wnt signaling pathway
p-value: 0.366



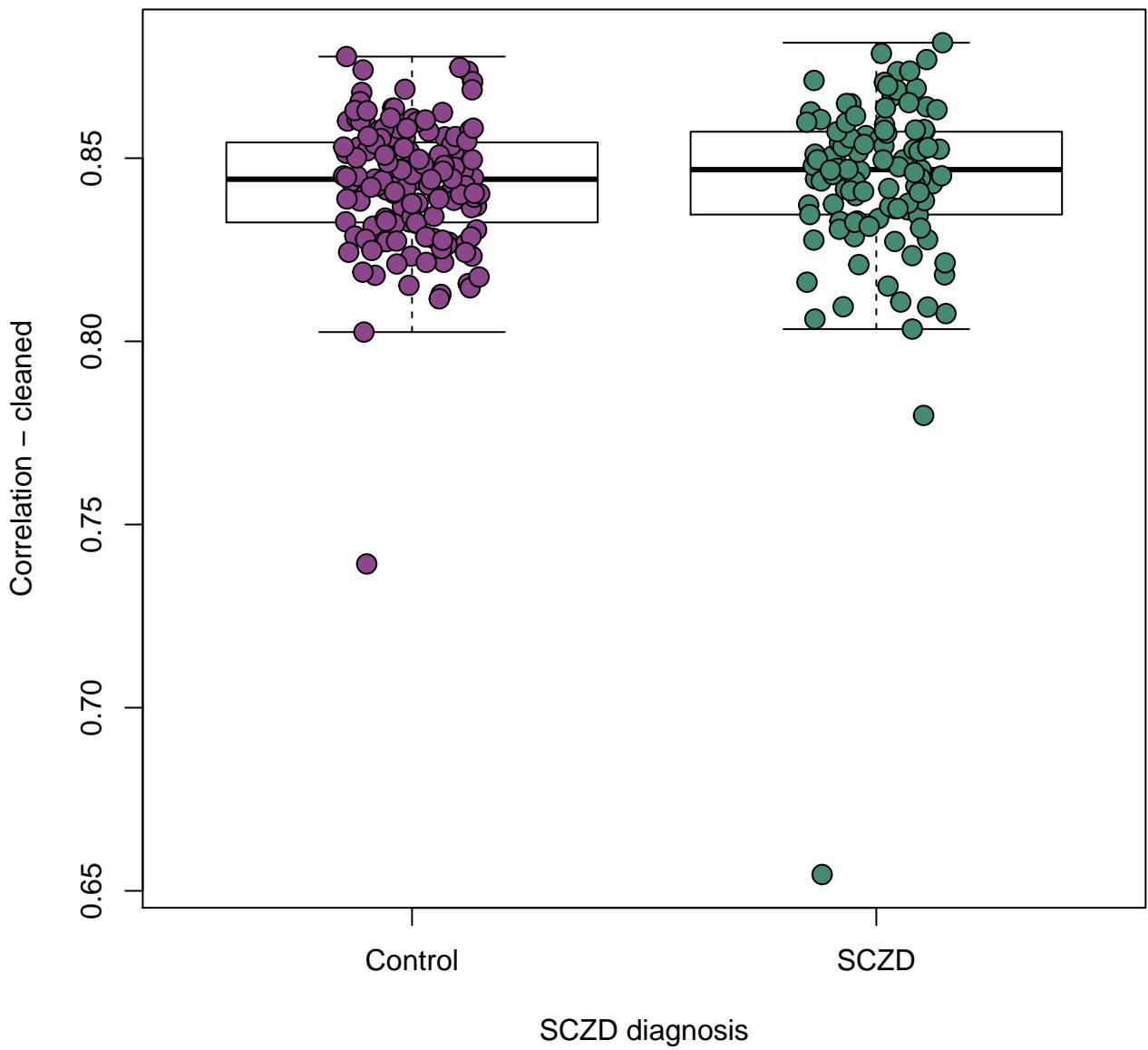
hsa04320: Dorso–ventral axis formation
p-value: 0.282



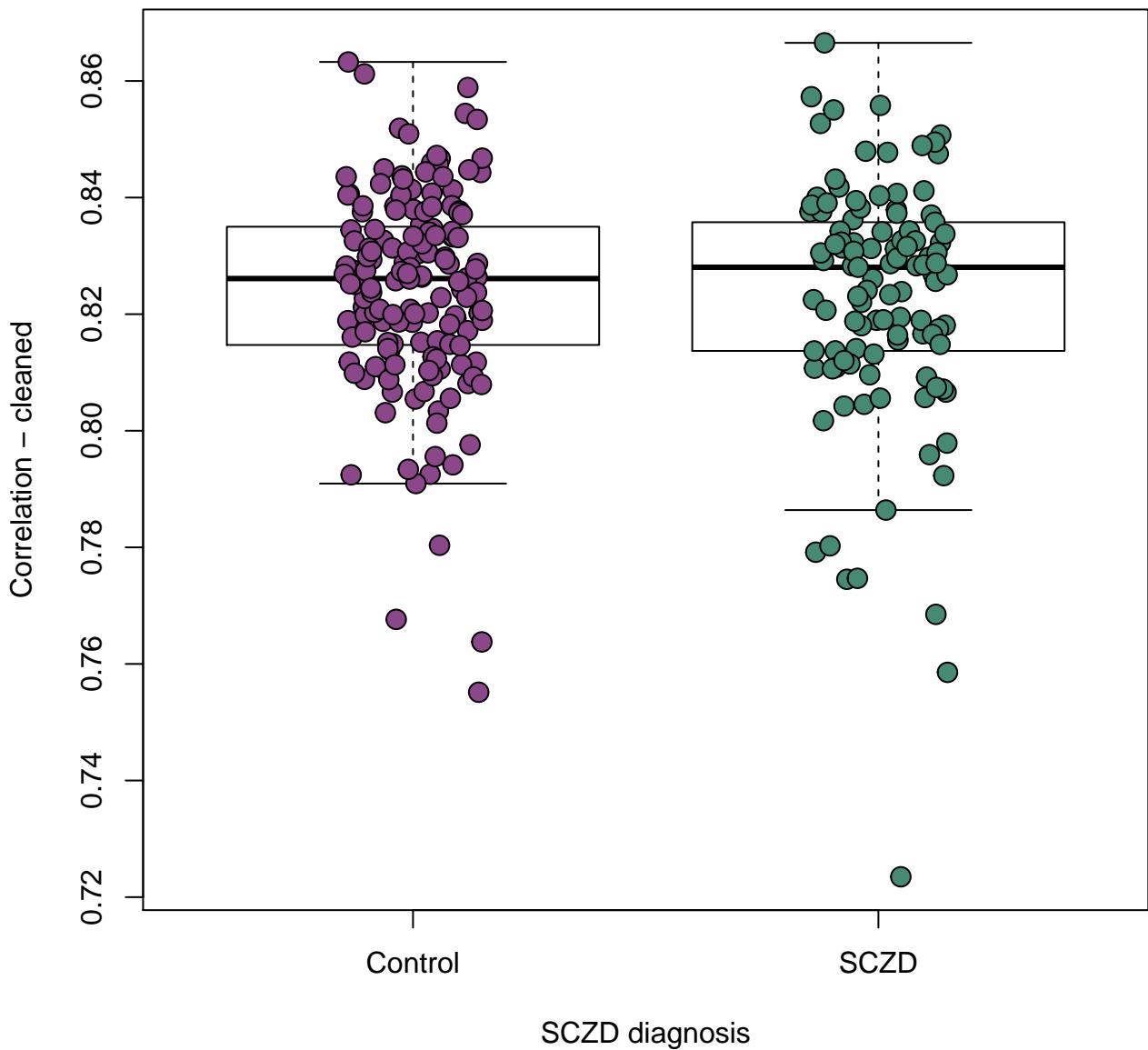
hsa04330: Notch signaling pathway
p-value: 0.486



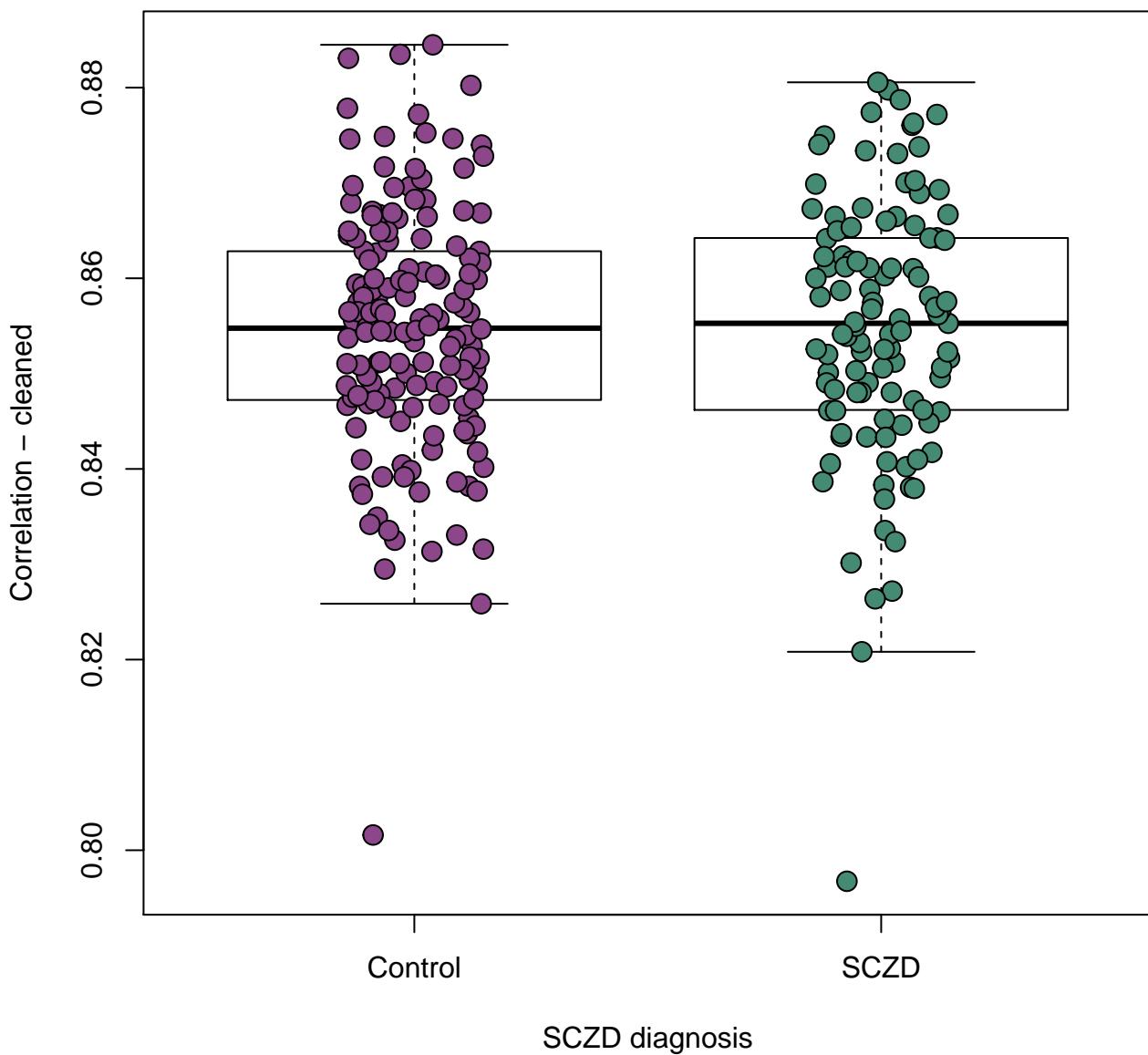
hsa04340: Hedgehog signaling pathway
p-value: 0.842



hsa04350: TGF–beta signaling pathway
p-value: 0.528

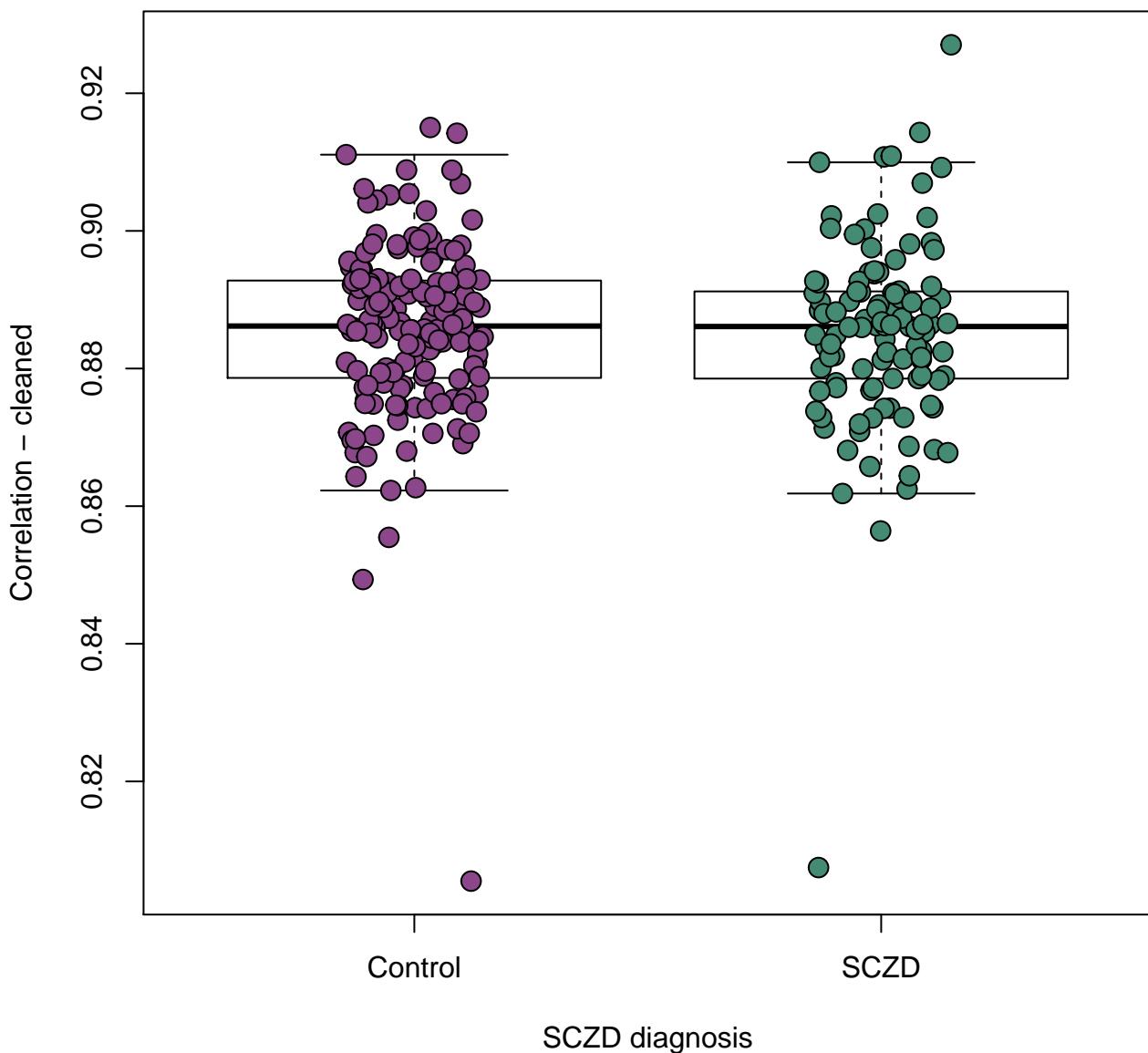


hsa04360: Axon guidance
p-value: 0.96



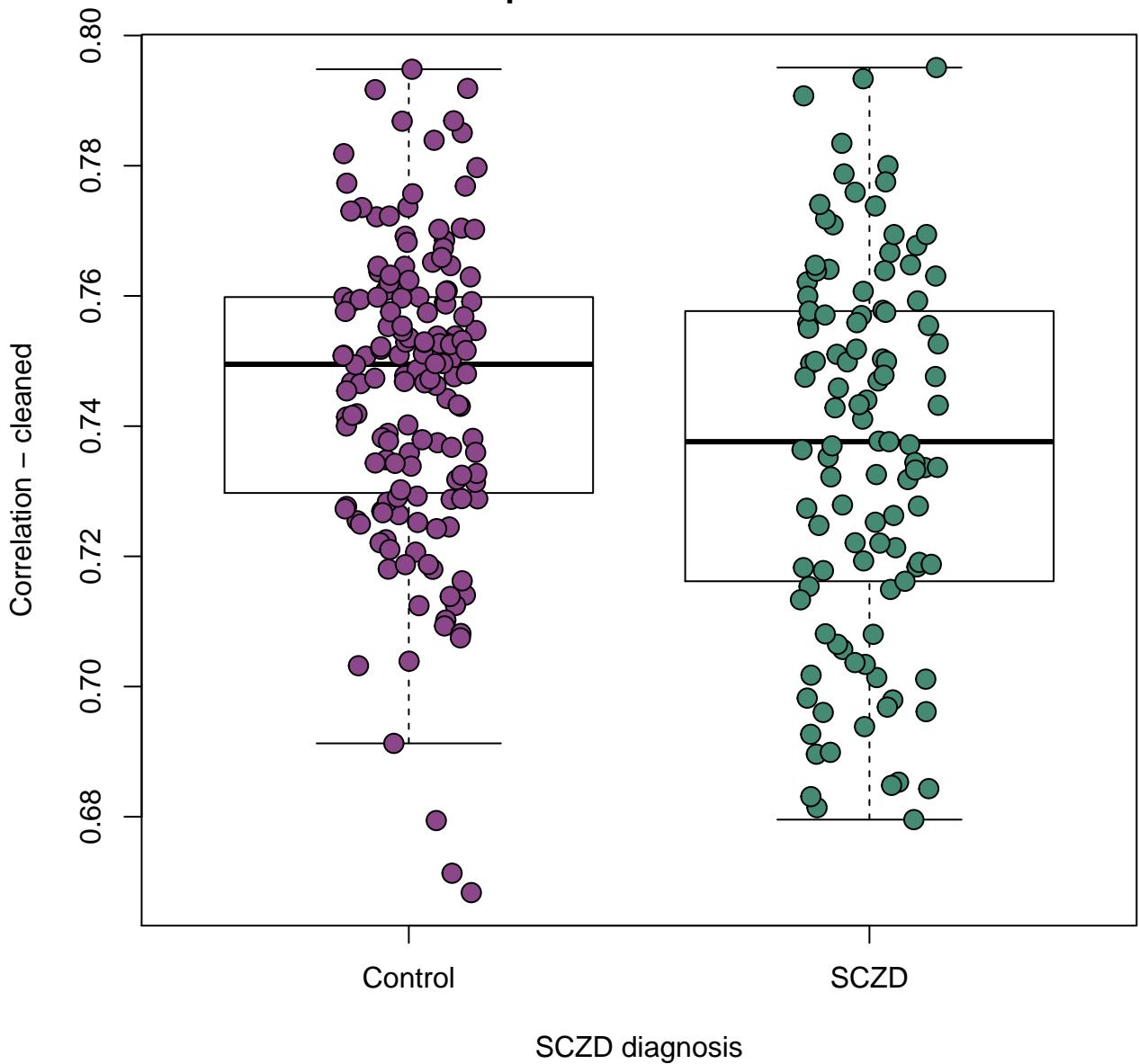
hsa04370: VEGF signaling pathway

p-value: 0.771

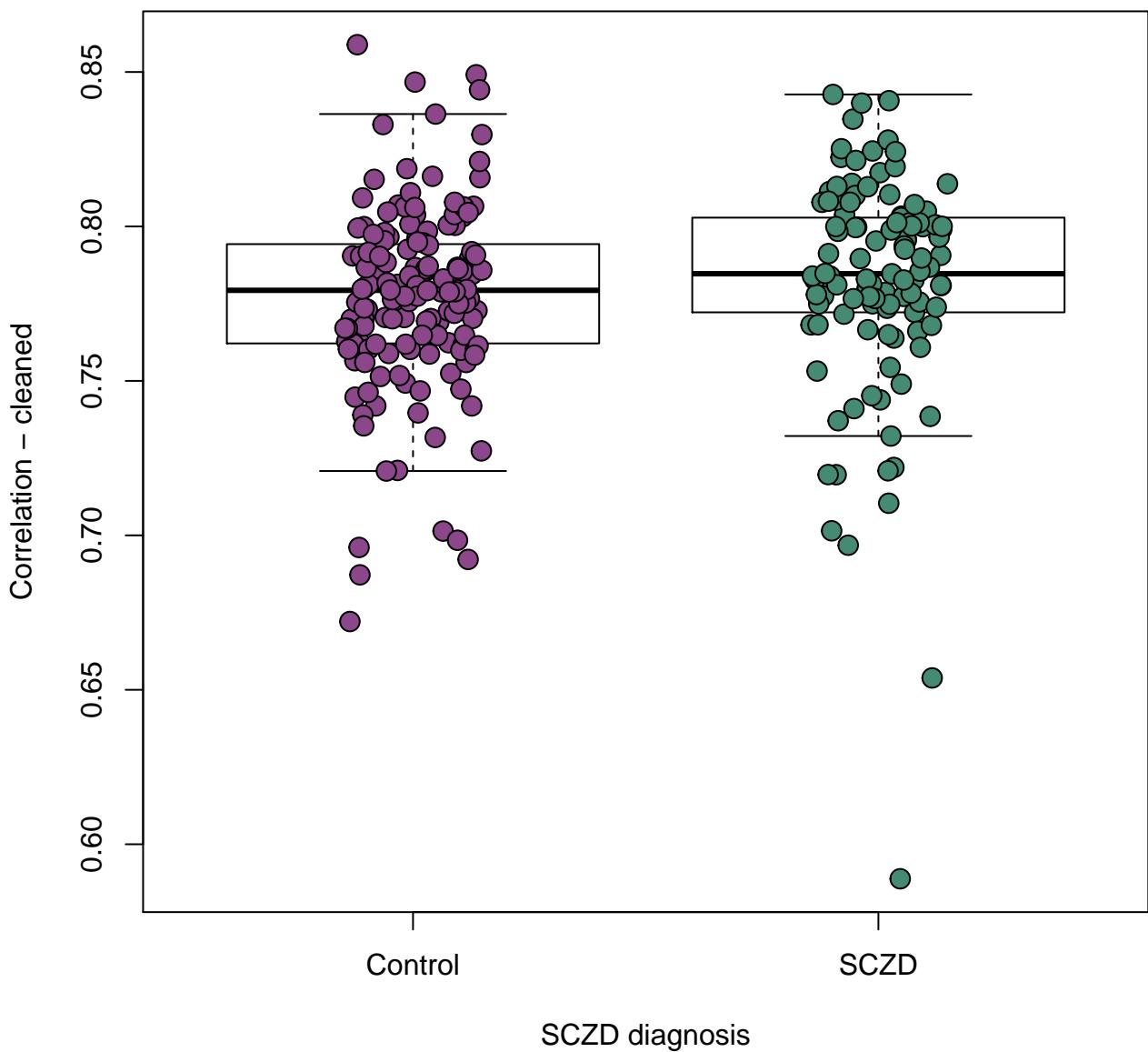


hsa04380: Osteoclast differentiation

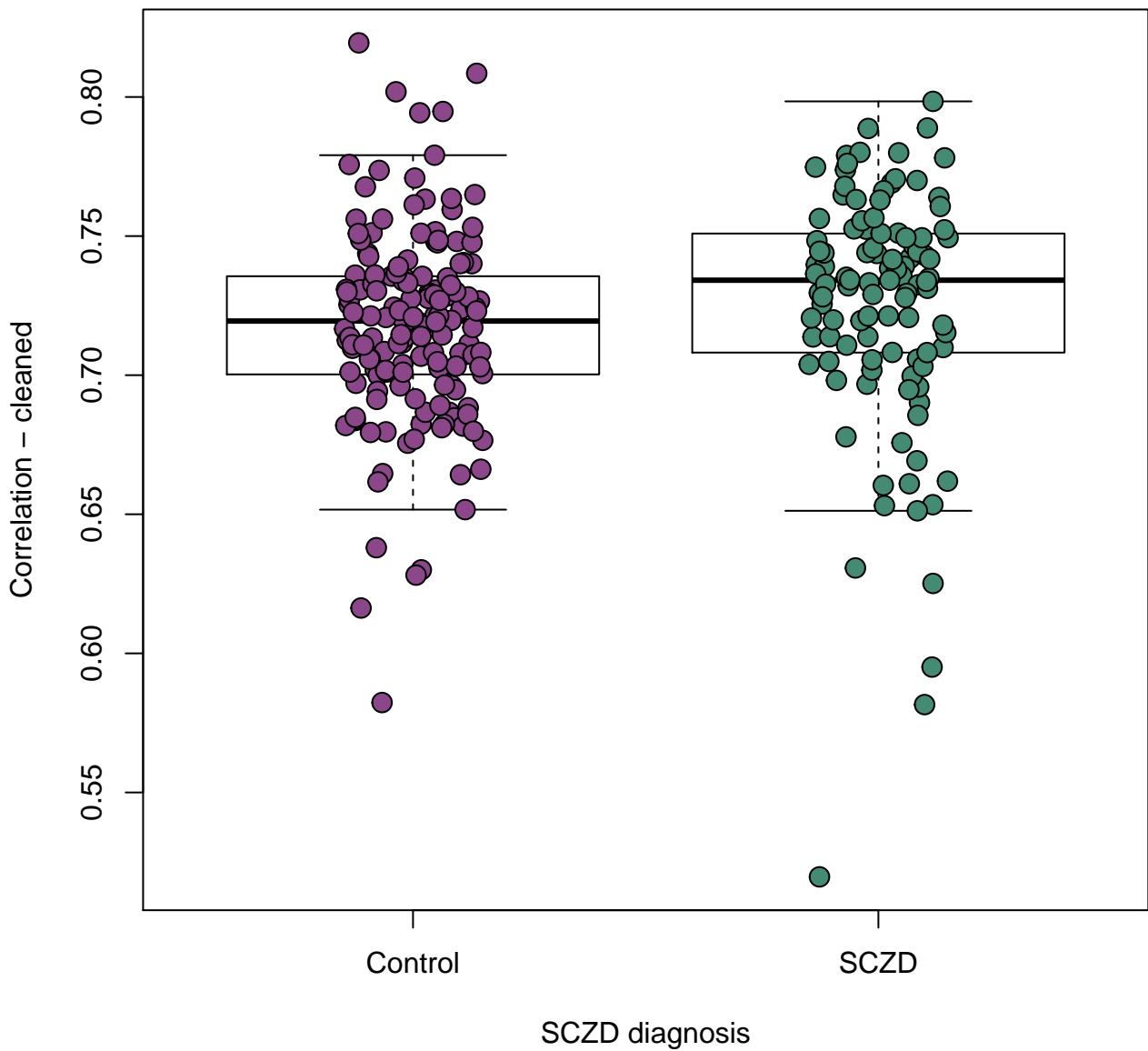
p-value: 0.00365



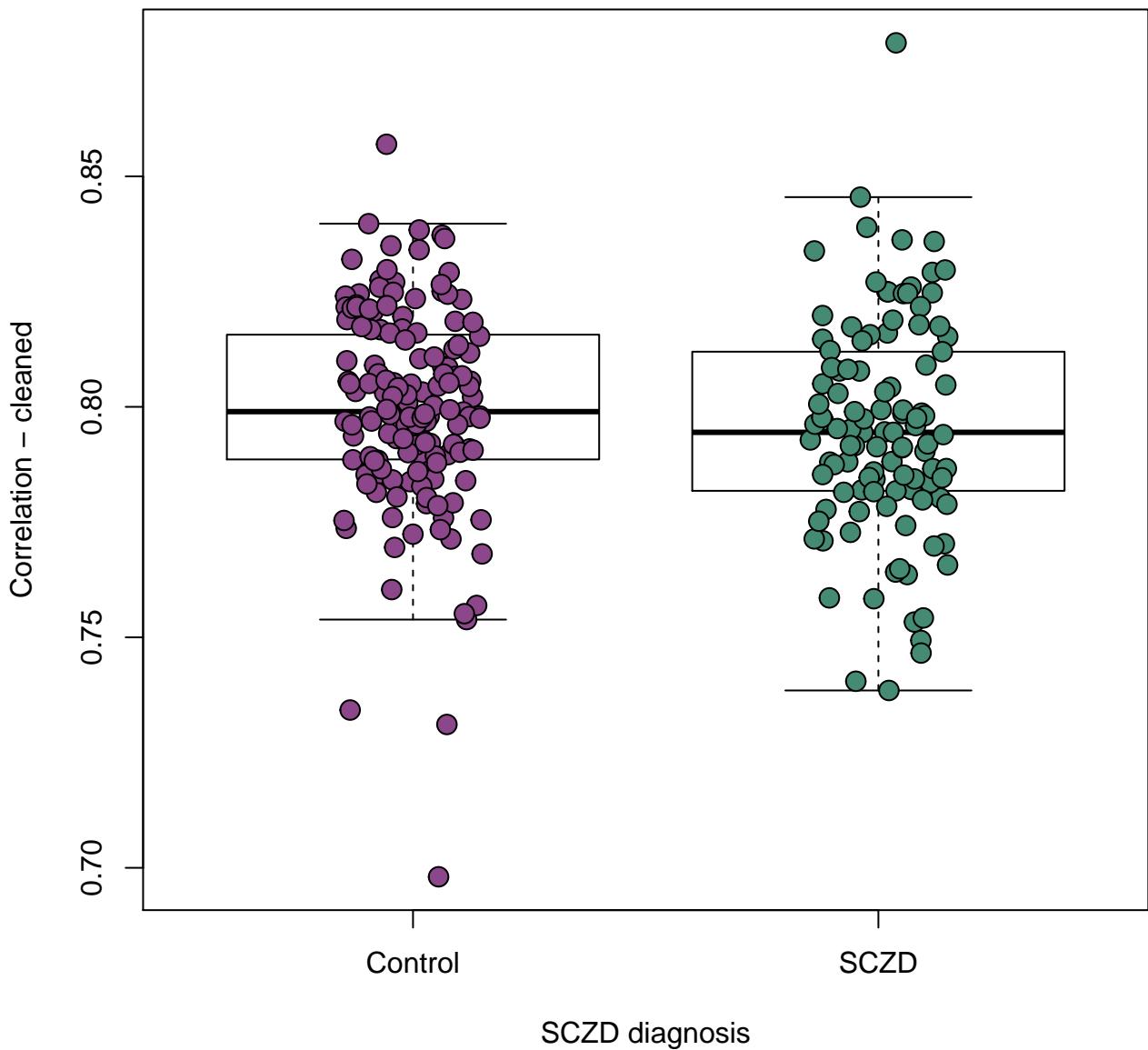
hsa04510: Focal adhesion
p-value: 0.287



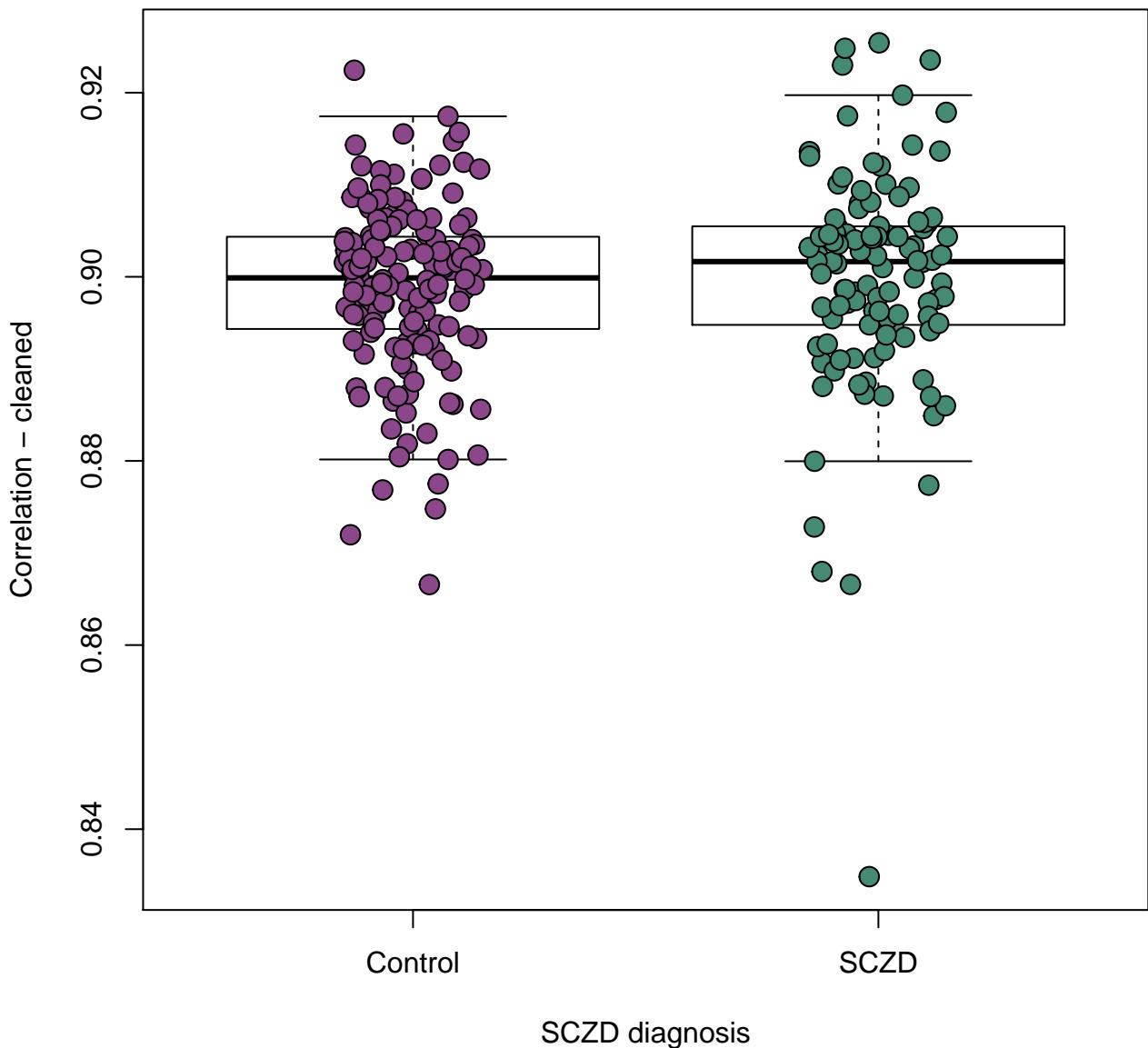
hsa04512: ECM–receptor interaction
p-value: 0.125



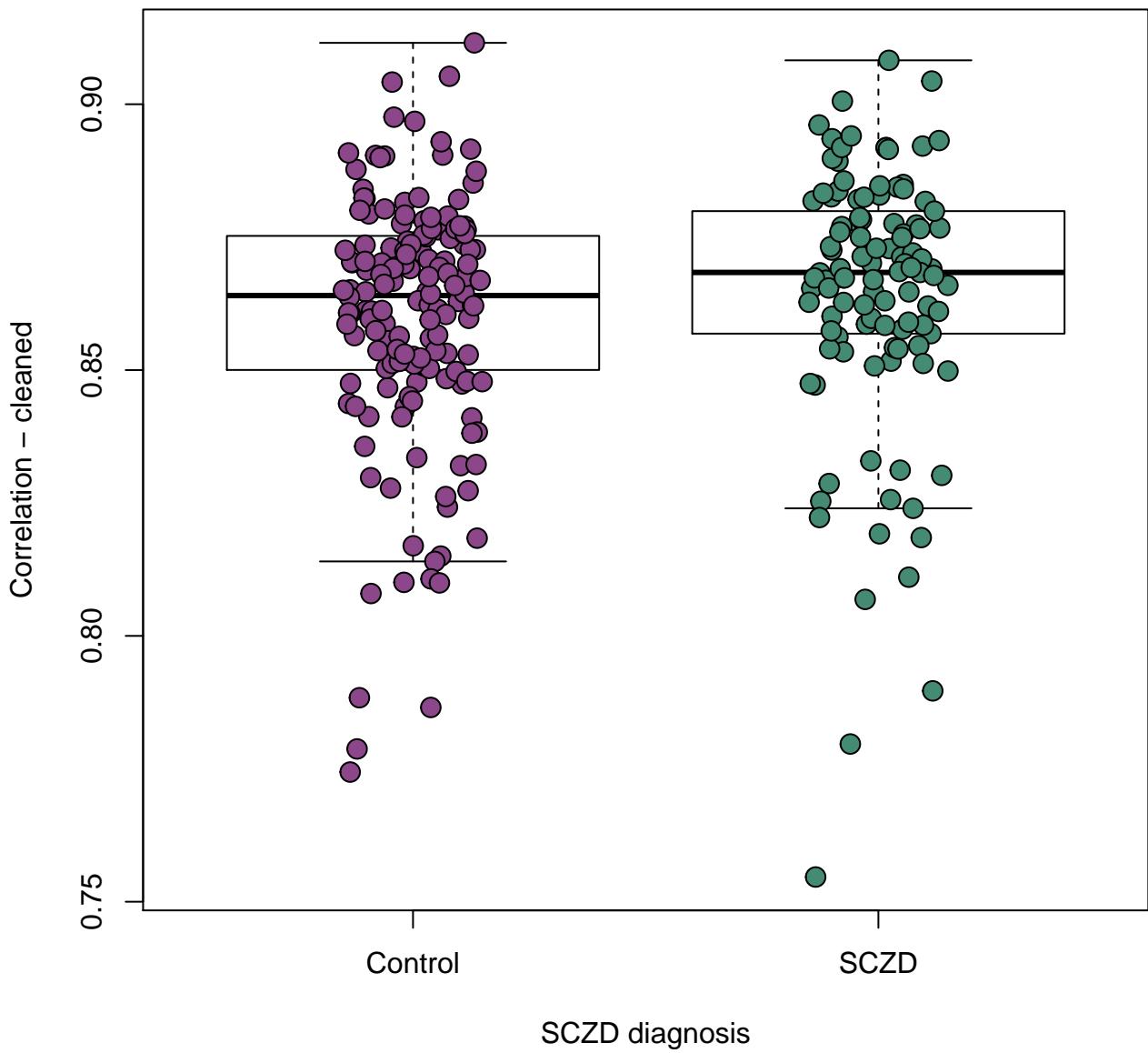
hsa04514: Cell adhesion molecules (CAMs)
p-value: 0.115



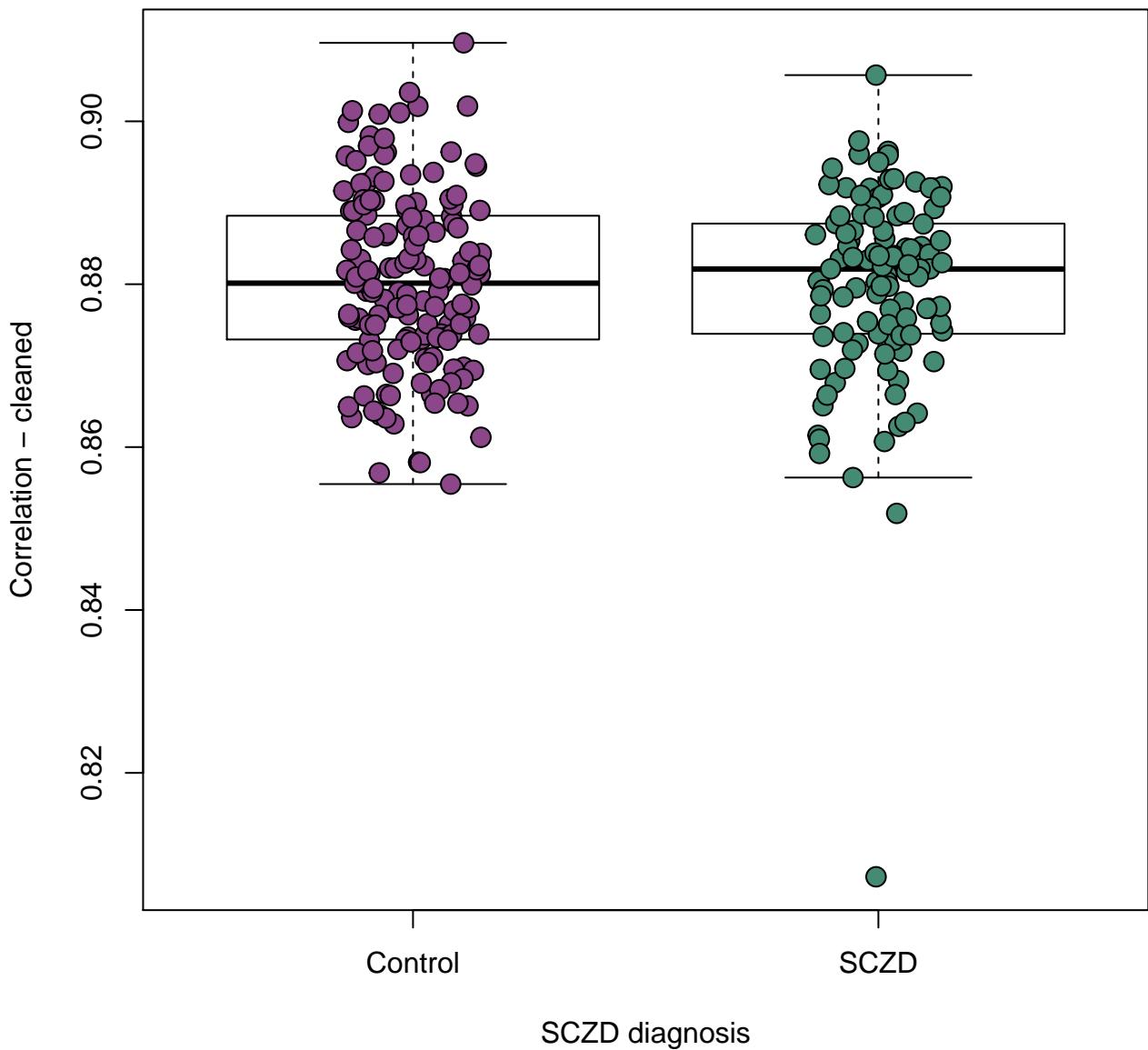
hsa04520: Adherens junction
p-value: 0.49



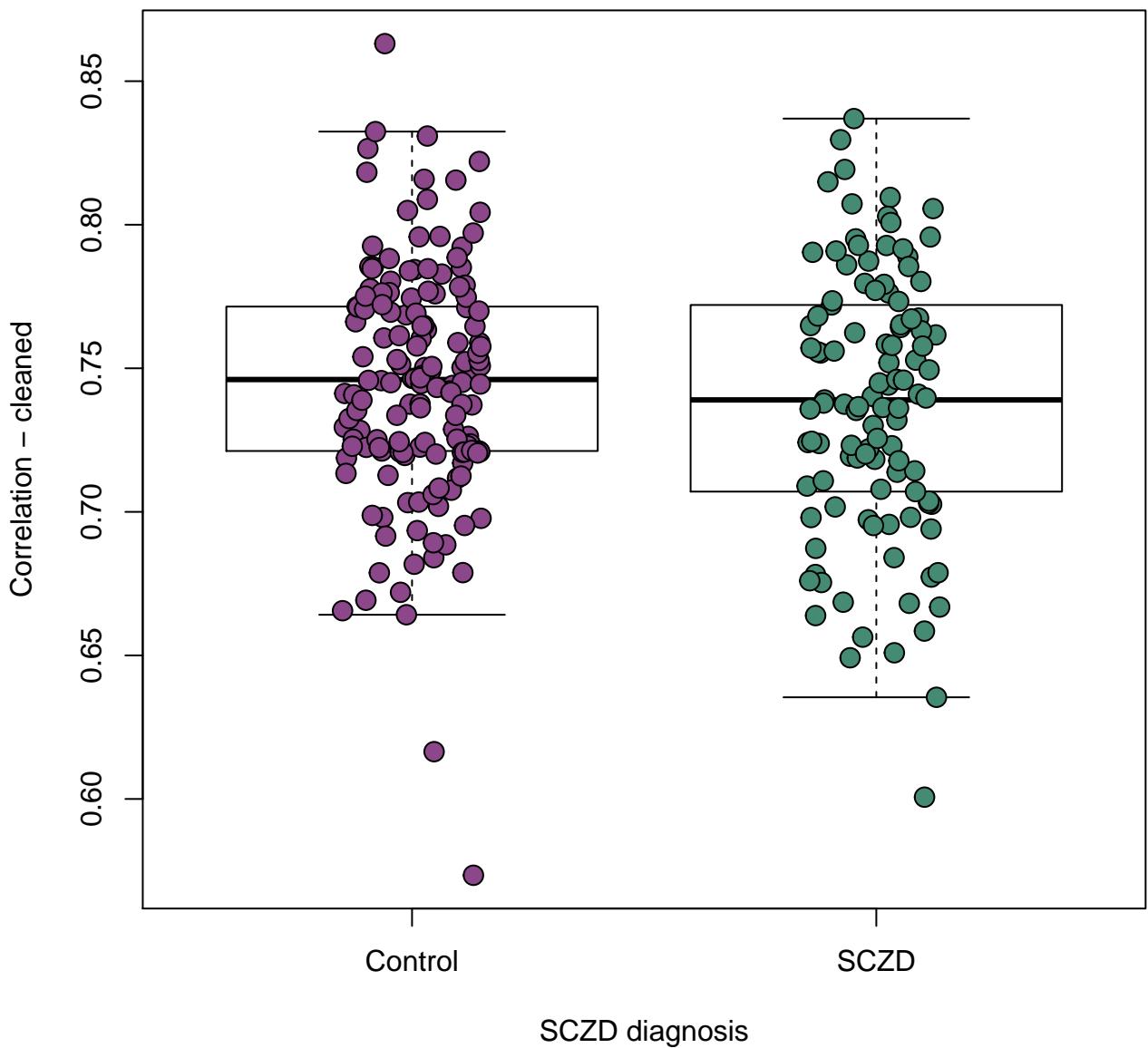
hsa04530: Tight junction
p-value: 0.156



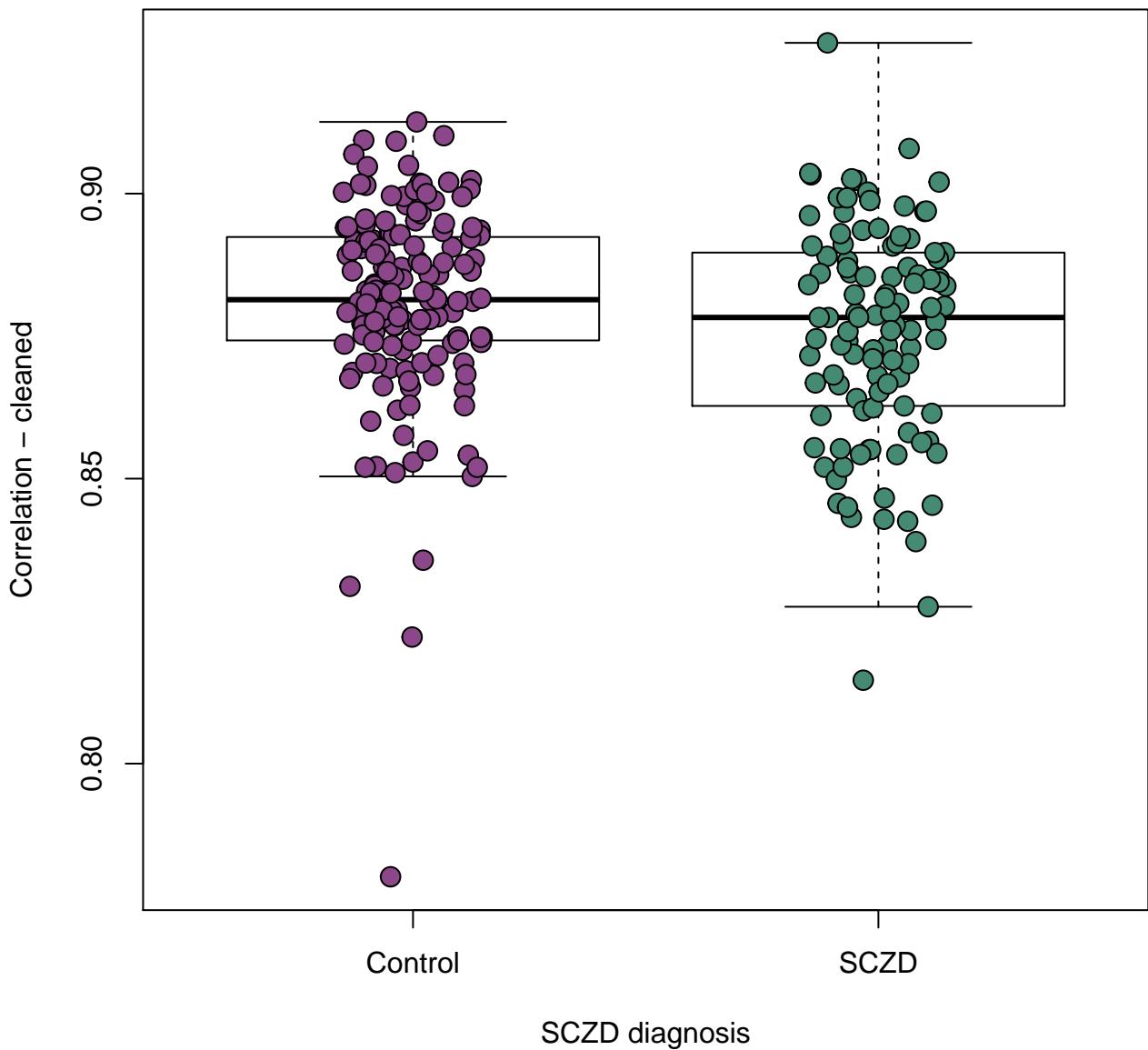
hsa04540: Gap junction
p-value: 0.655



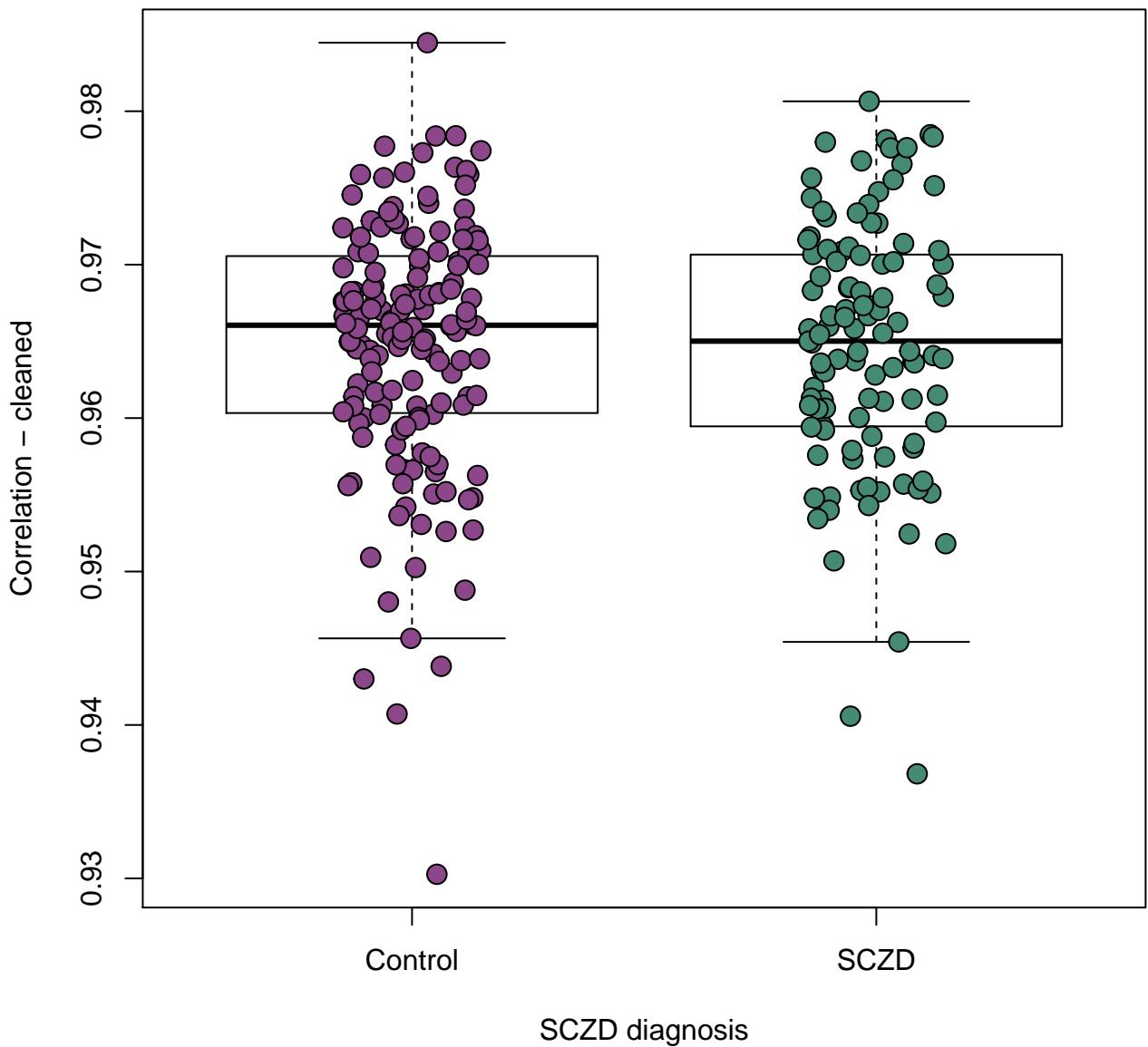
hsa04610: Complement and coagulation cascades
p-value: 0.168



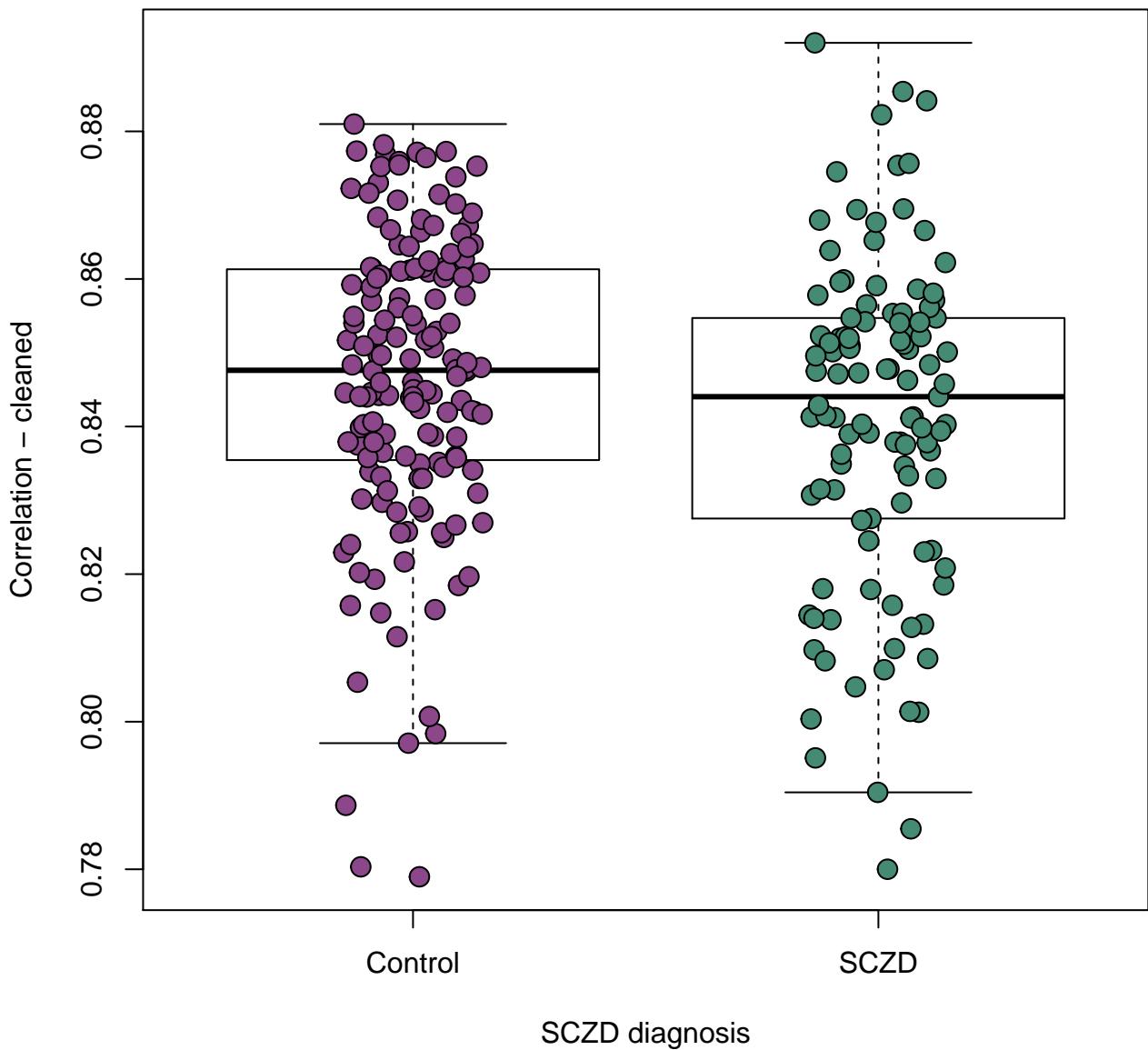
hsa04612: Antigen processing and presentation
p-value: 0.0197



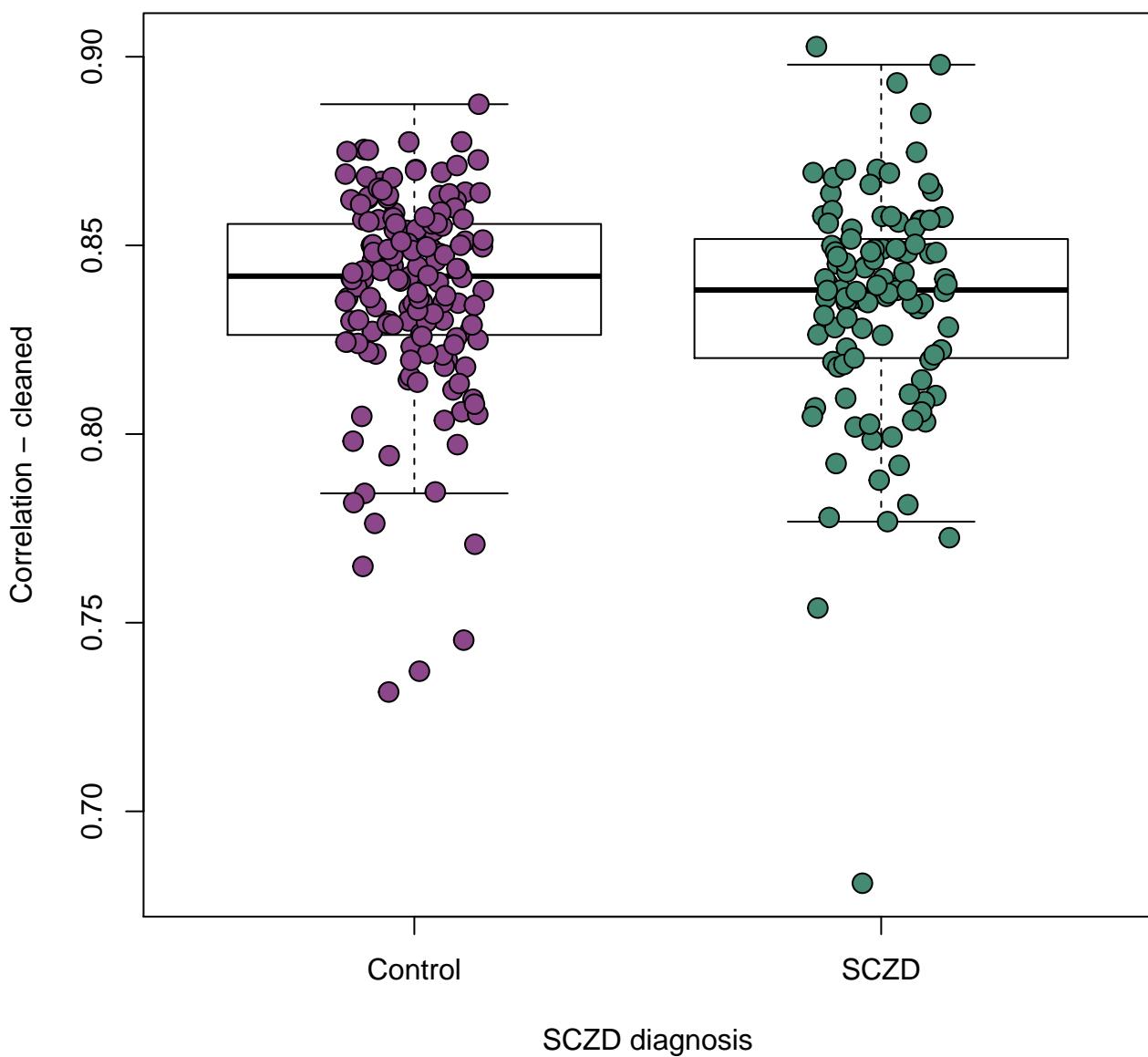
hsa04614: Renin–angiotensin system
p-value: 0.898



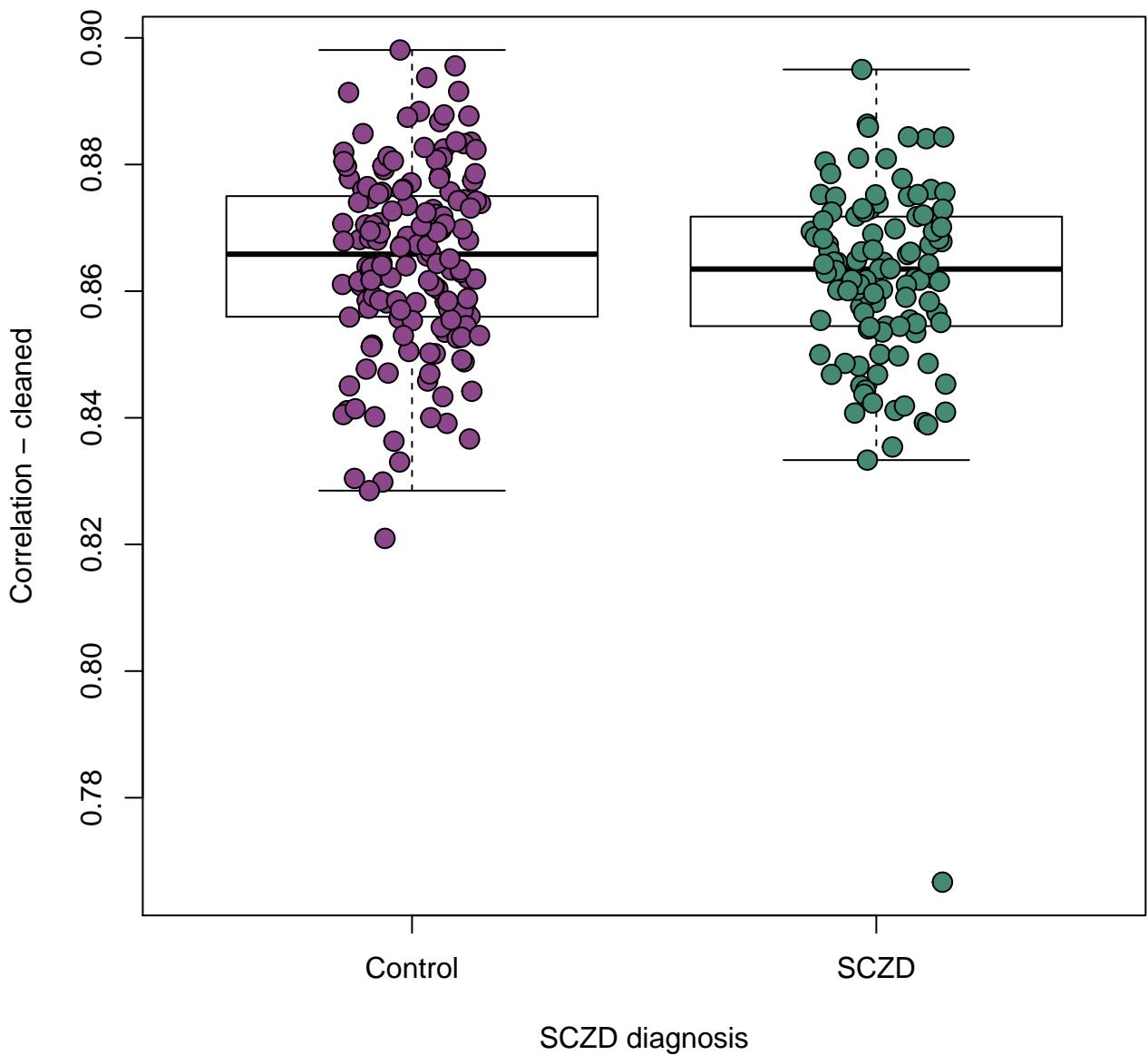
hsa04620: Toll-like receptor signaling pathway
p-value: 0.0327



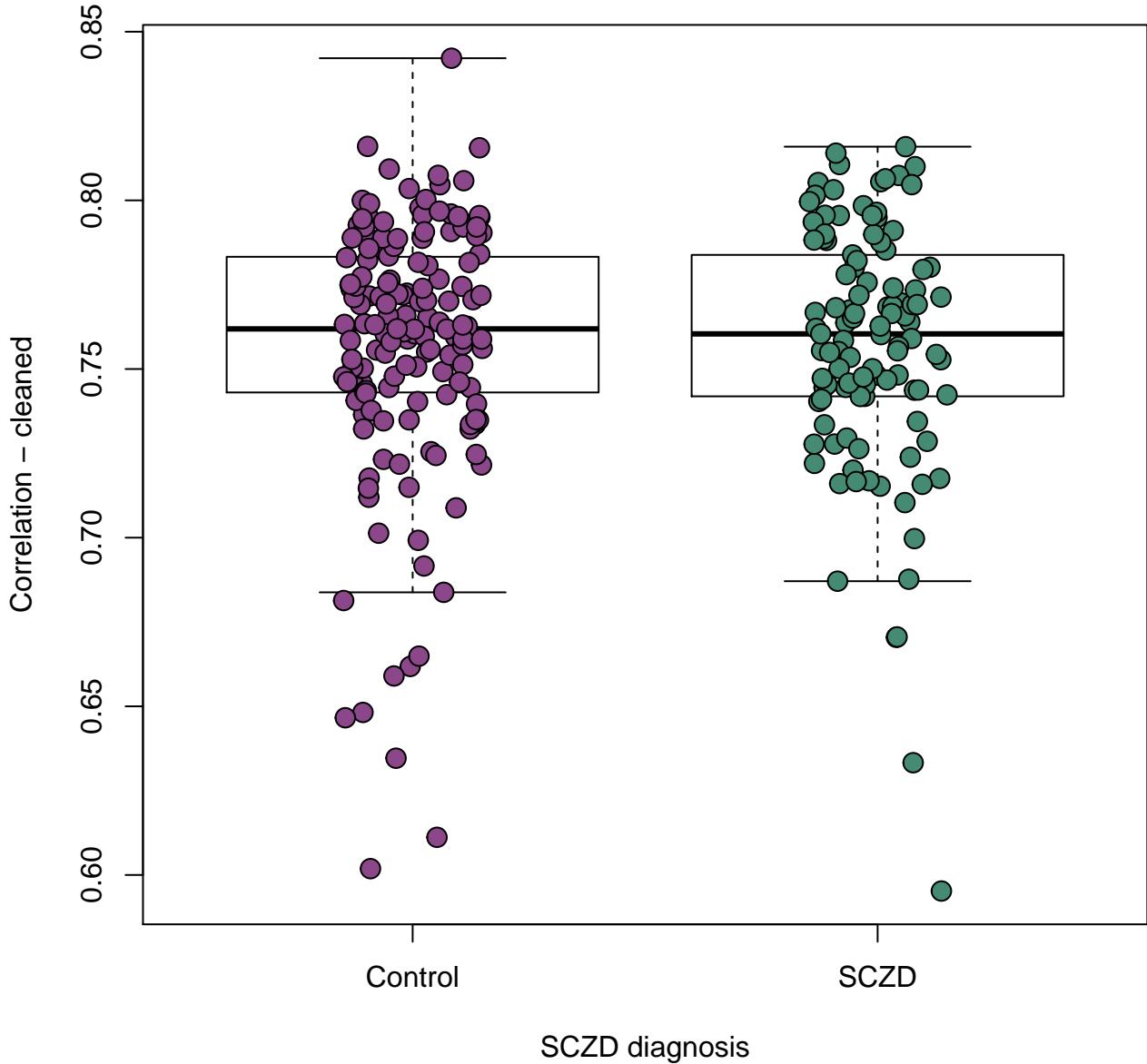
hsa04621: NOD-like receptor signaling pathway
p-value: 0.368



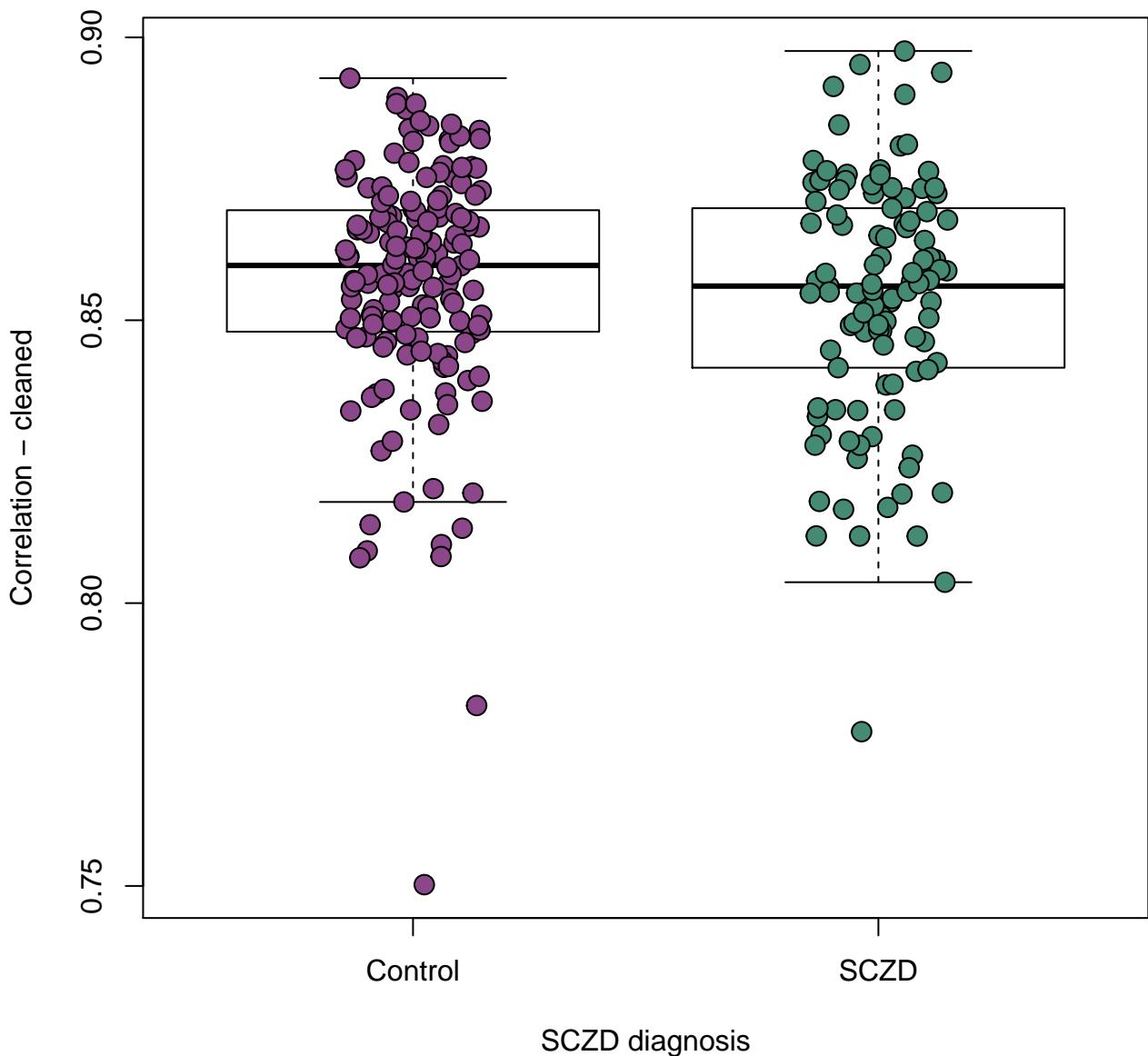
hsa04622: RIG-I-like receptor signaling pathway
p-value: 0.0957



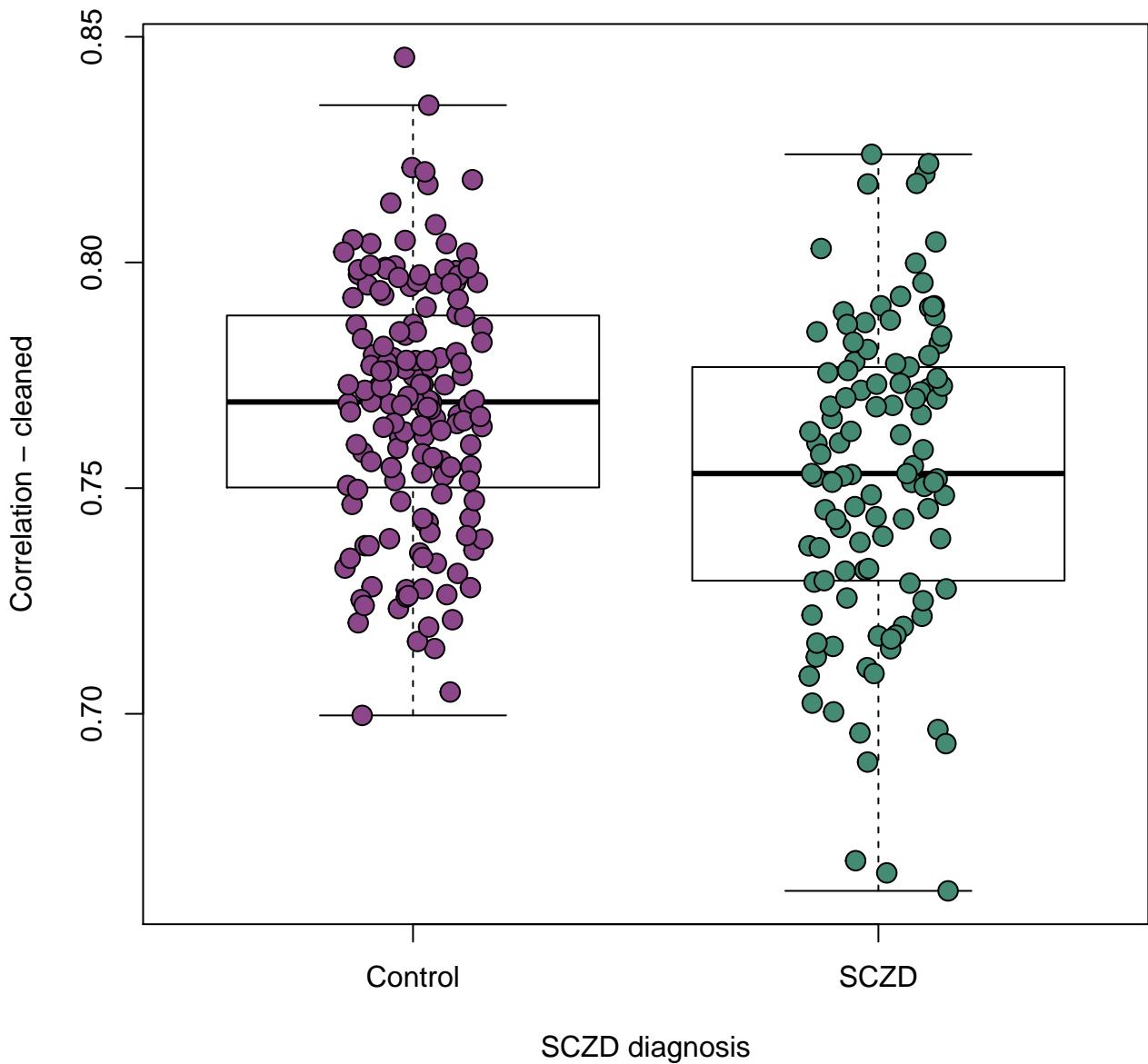
hsa04623: Cytosolic DNA–sensing pathway
p-value: 0.958



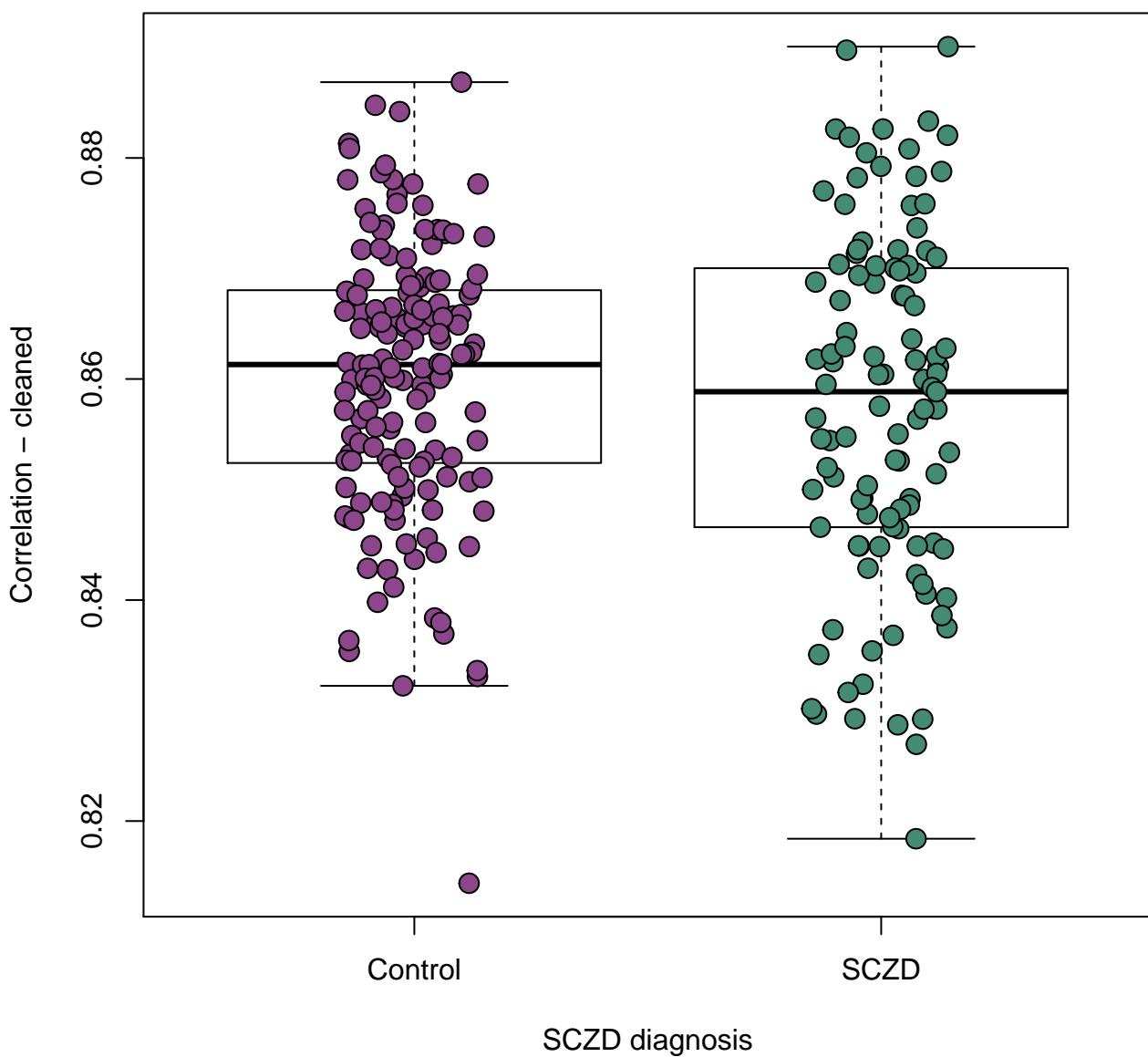
hsa04630: Jak–STAT signaling pathway
p-value: 0.259



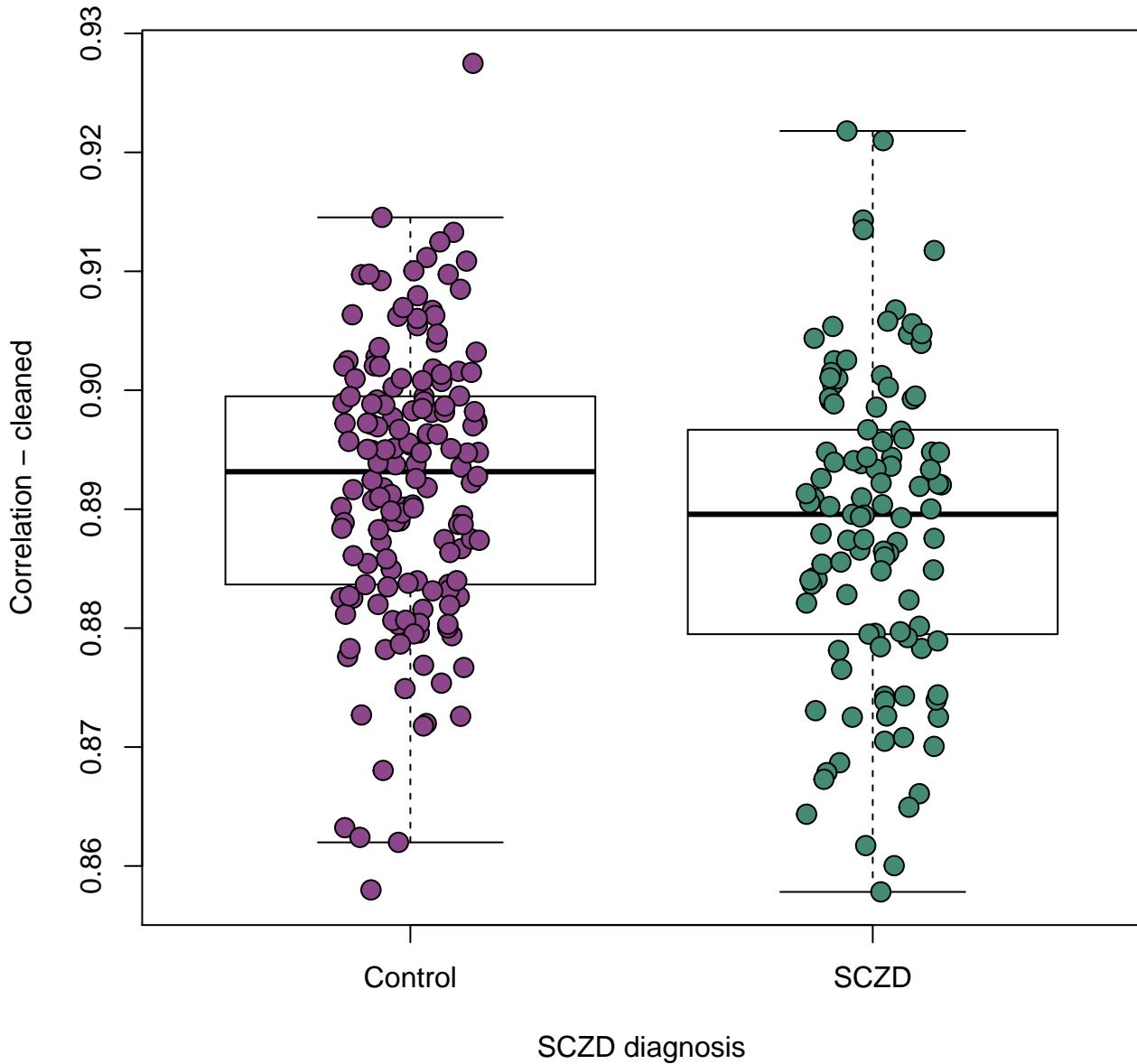
hsa04640: Hematopoietic cell lineage
p-value: 0.000123



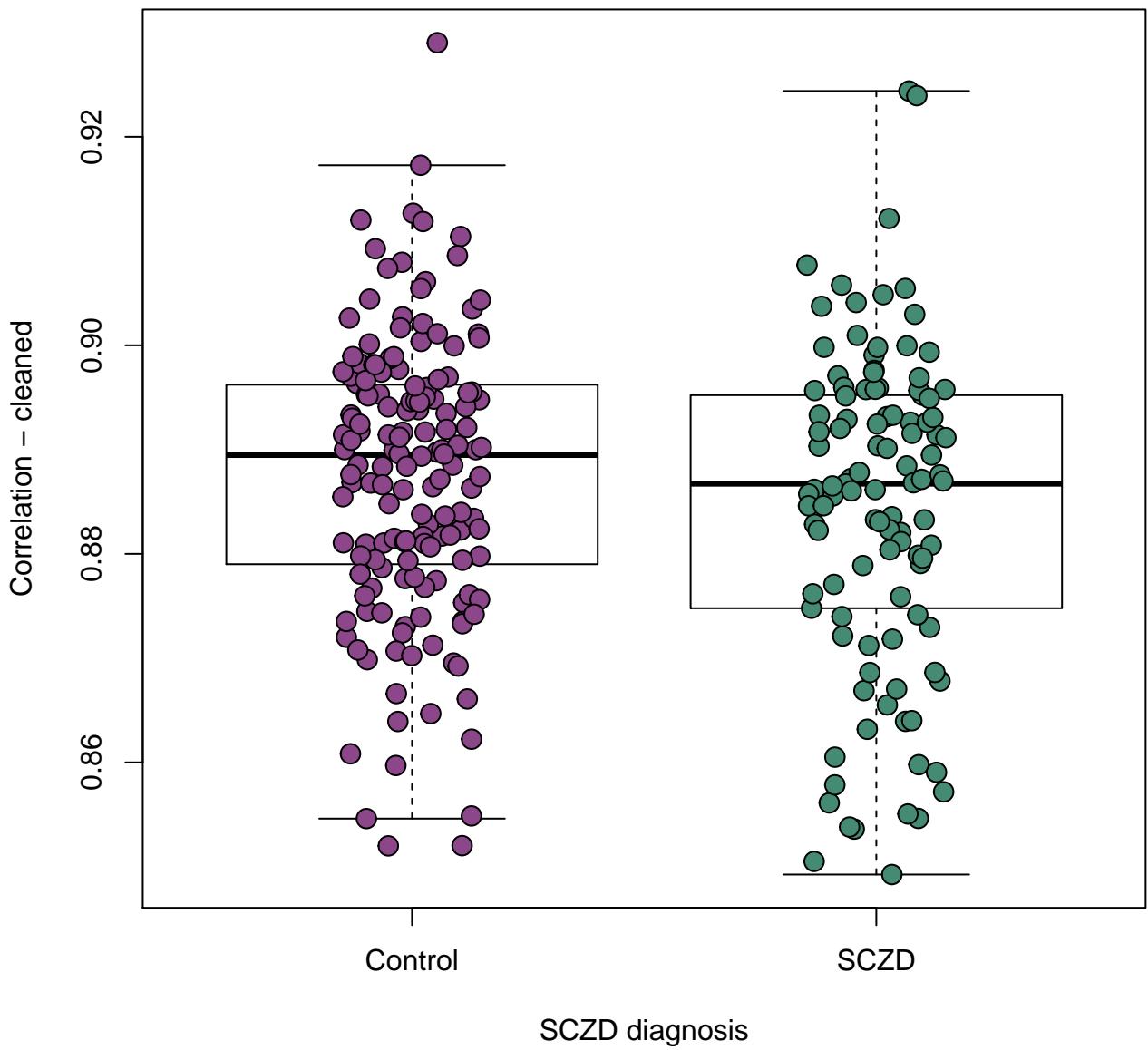
hsa04650: Natural killer cell mediated cytotoxicity
p-value: 0.152



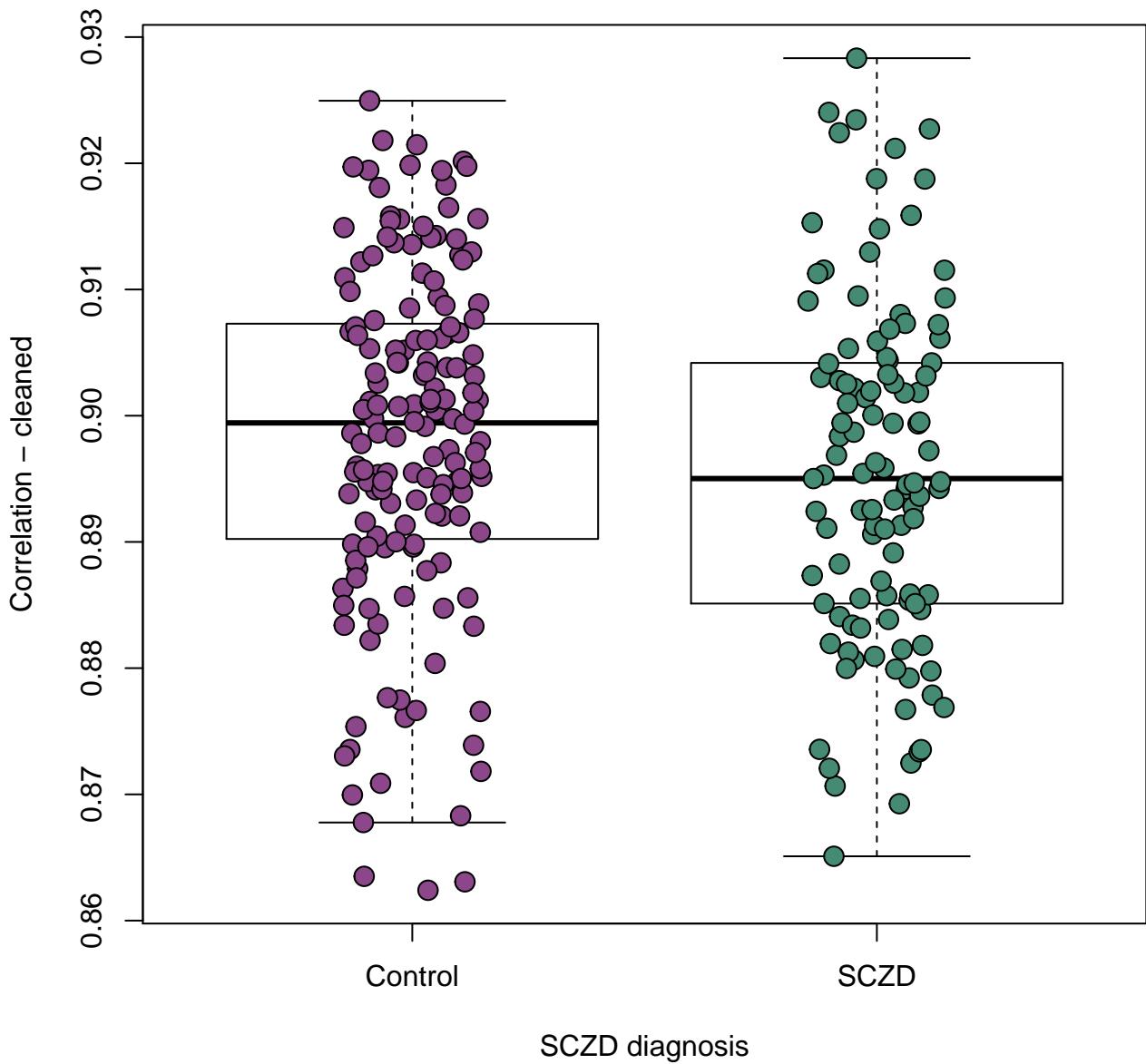
hsa04660: T cell receptor signaling pathway
p-value: 0.0179



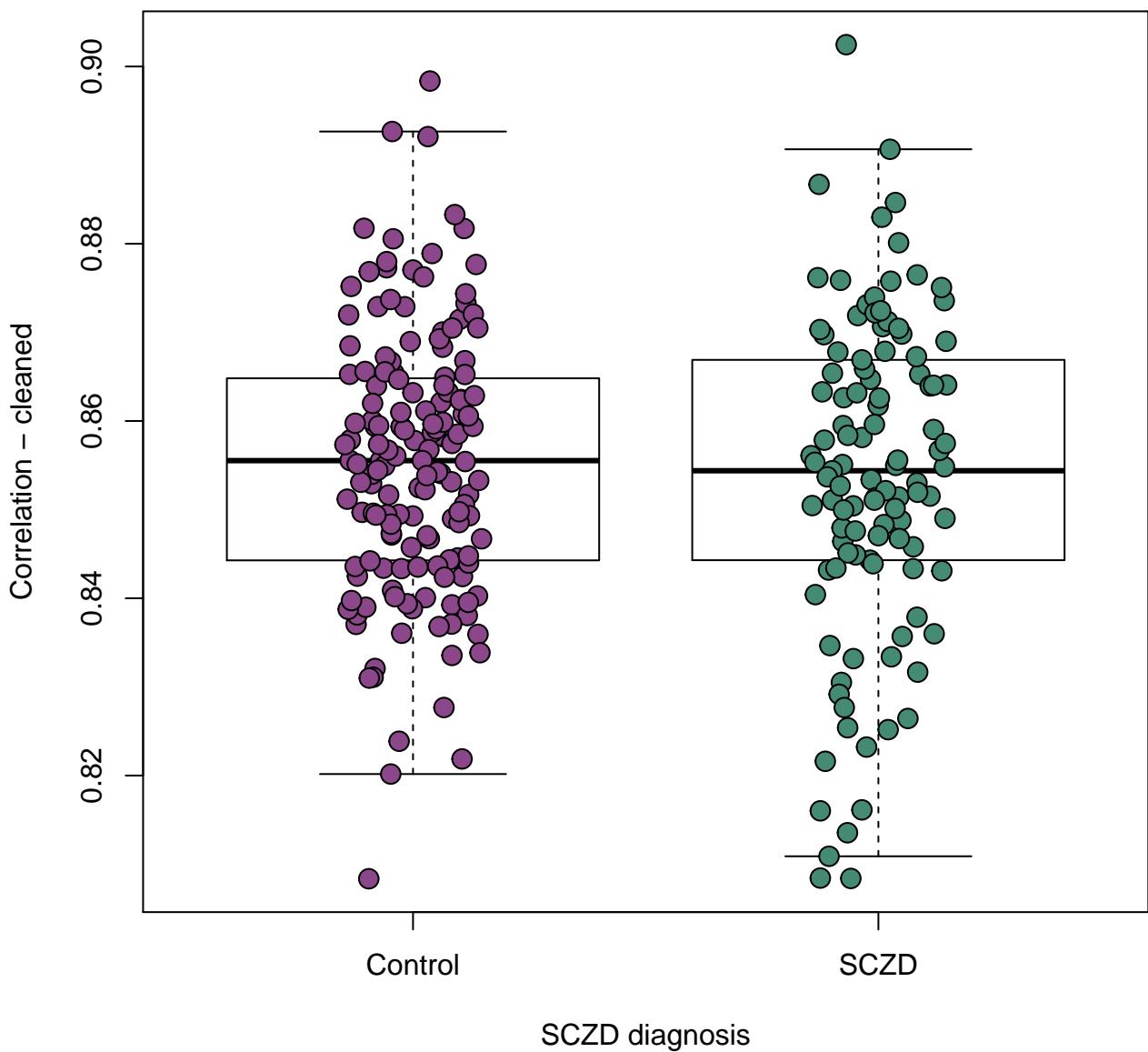
hsa04662: B cell receptor signaling pathway
p-value: 0.0945



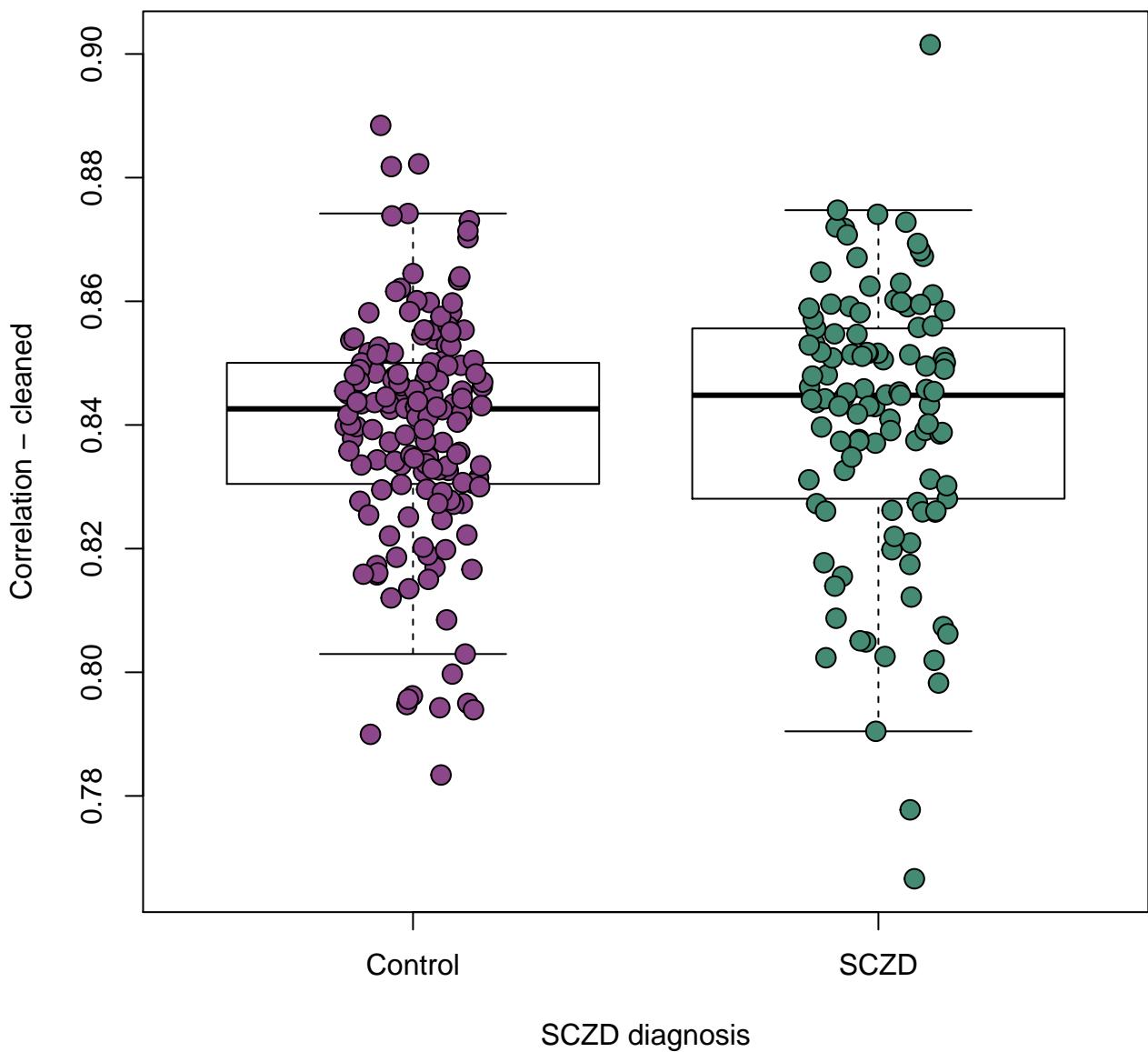
hsa04664: Fc epsilon RI signaling pathway
p-value: 0.112



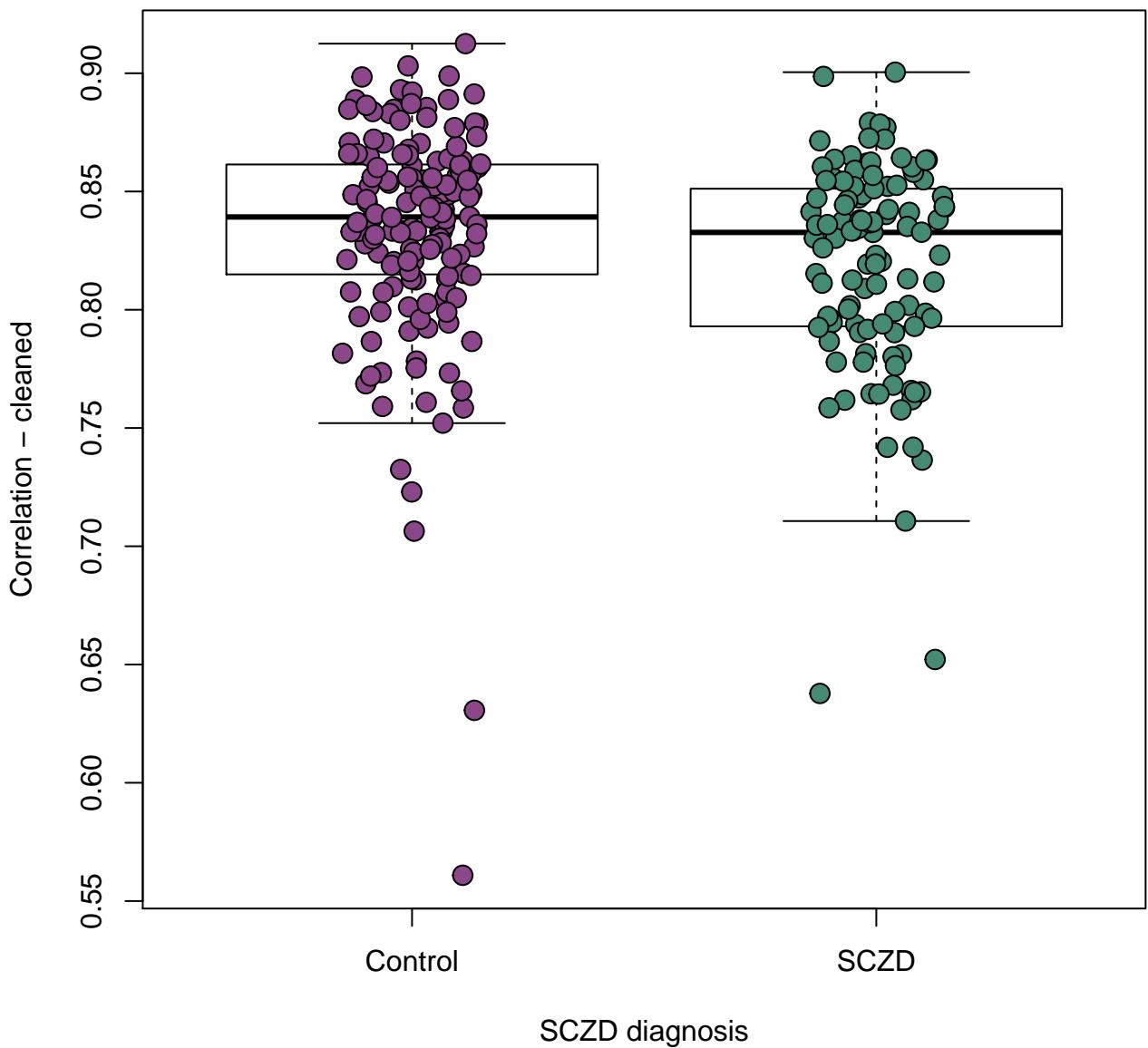
hsa04666: Fc gamma R-mediated phagocytosis
p-value: 0.413



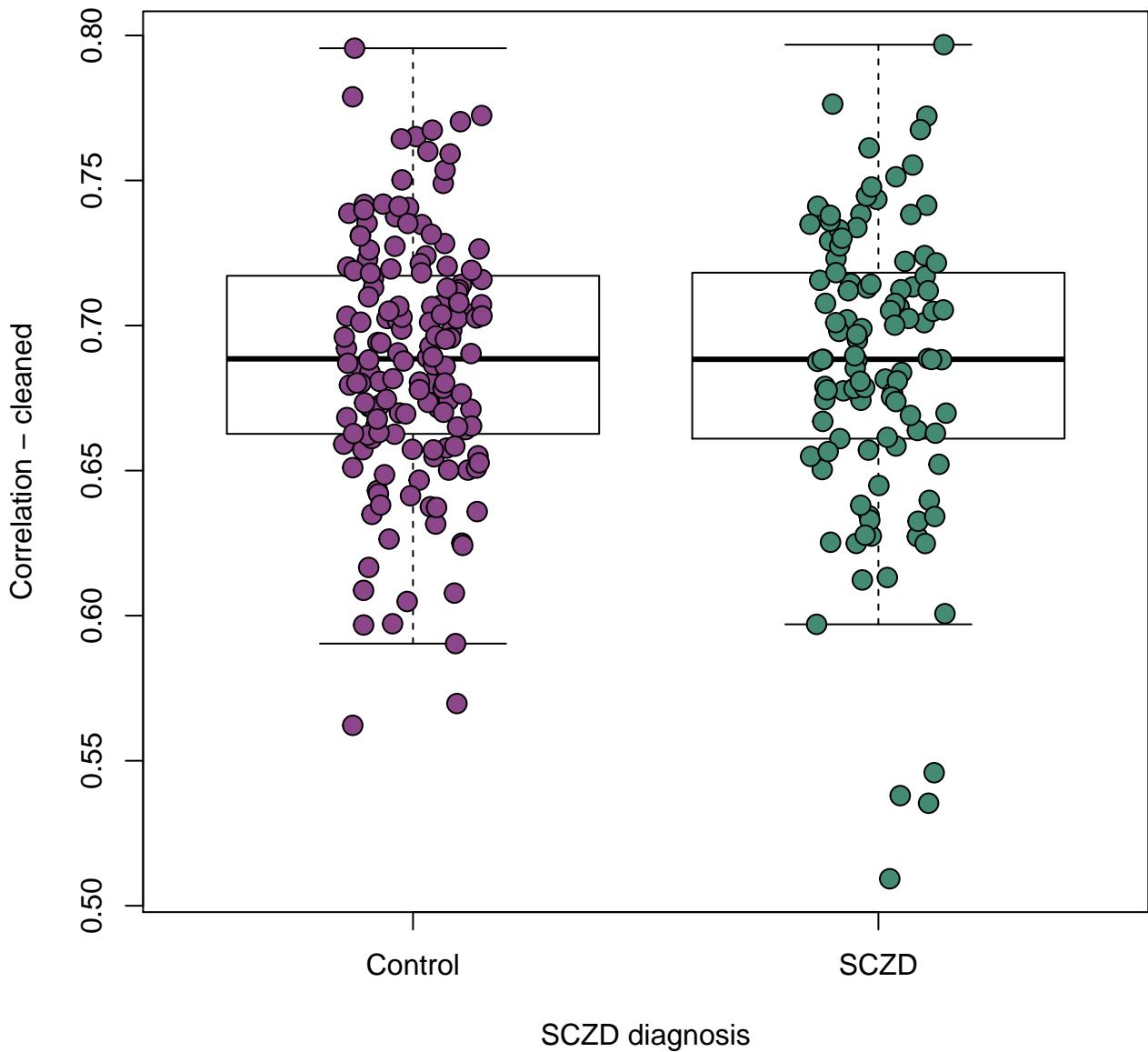
hsa04670: Leukocyte transendothelial migration
p-value: 0.482



hsa04672: Intestinal immune network for IgA production
p-value: 0.00786

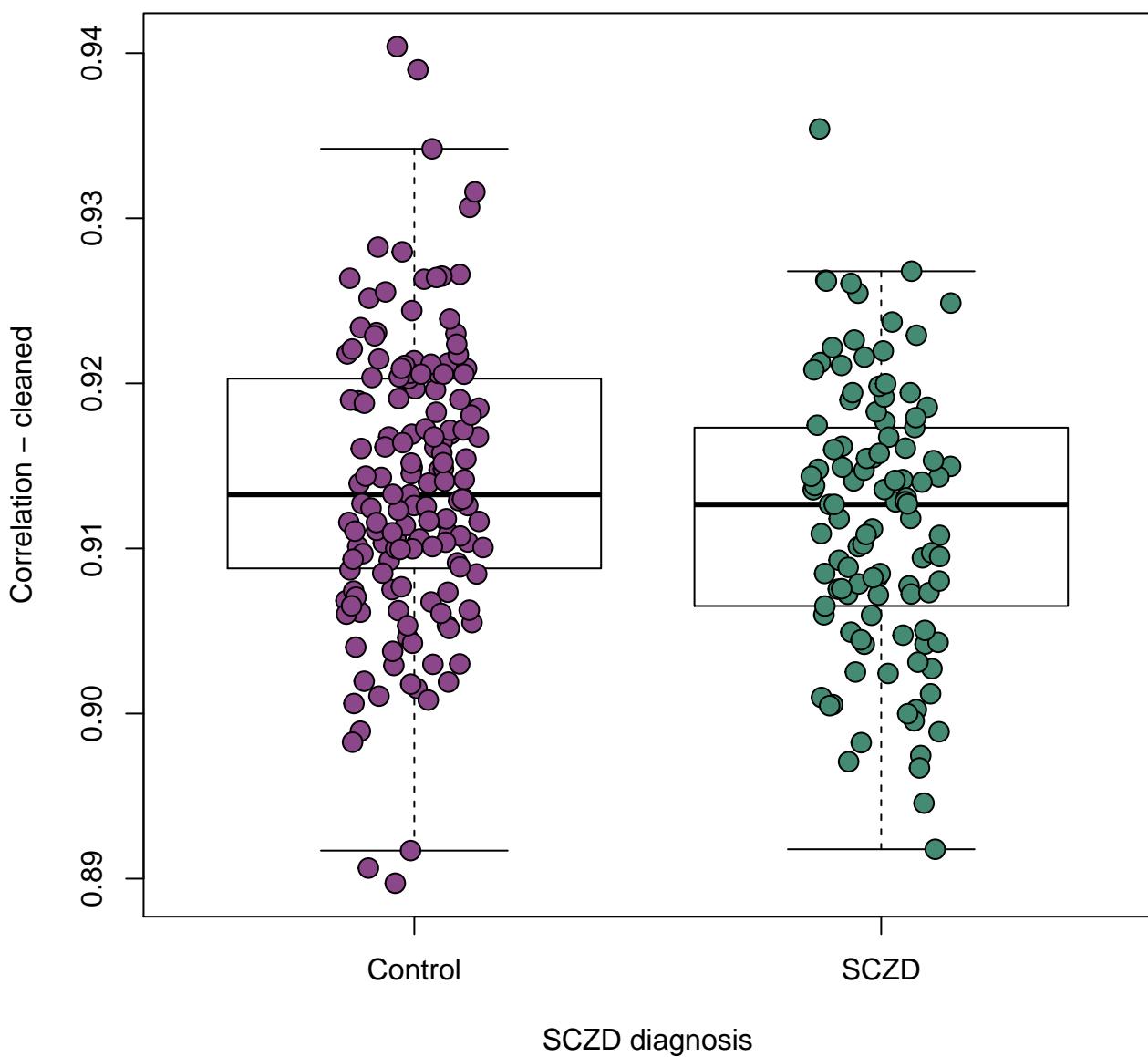


hsa04710: Circadian rhythm
p-value: 0.697

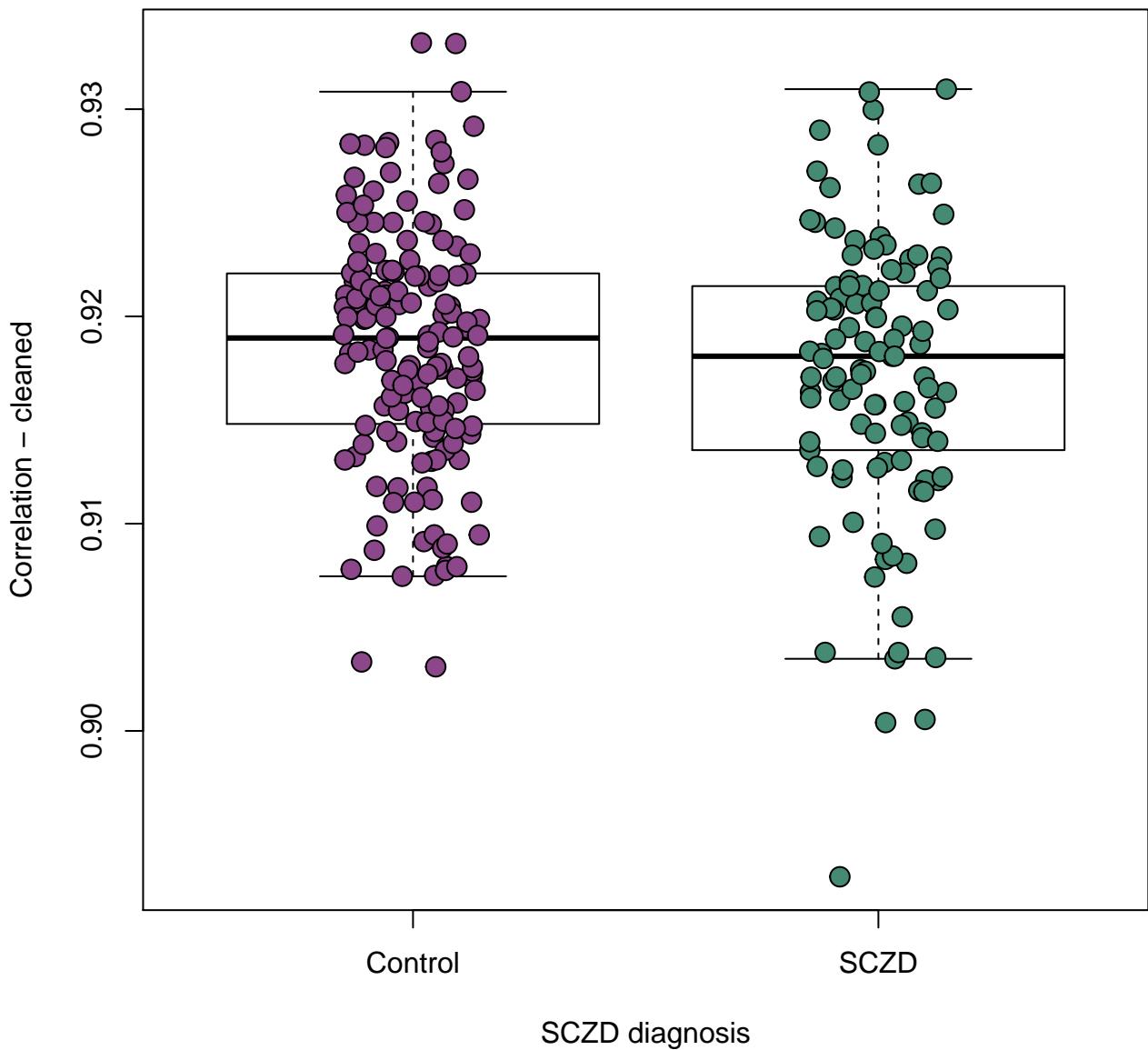


hsa04720: Long-term potentiation

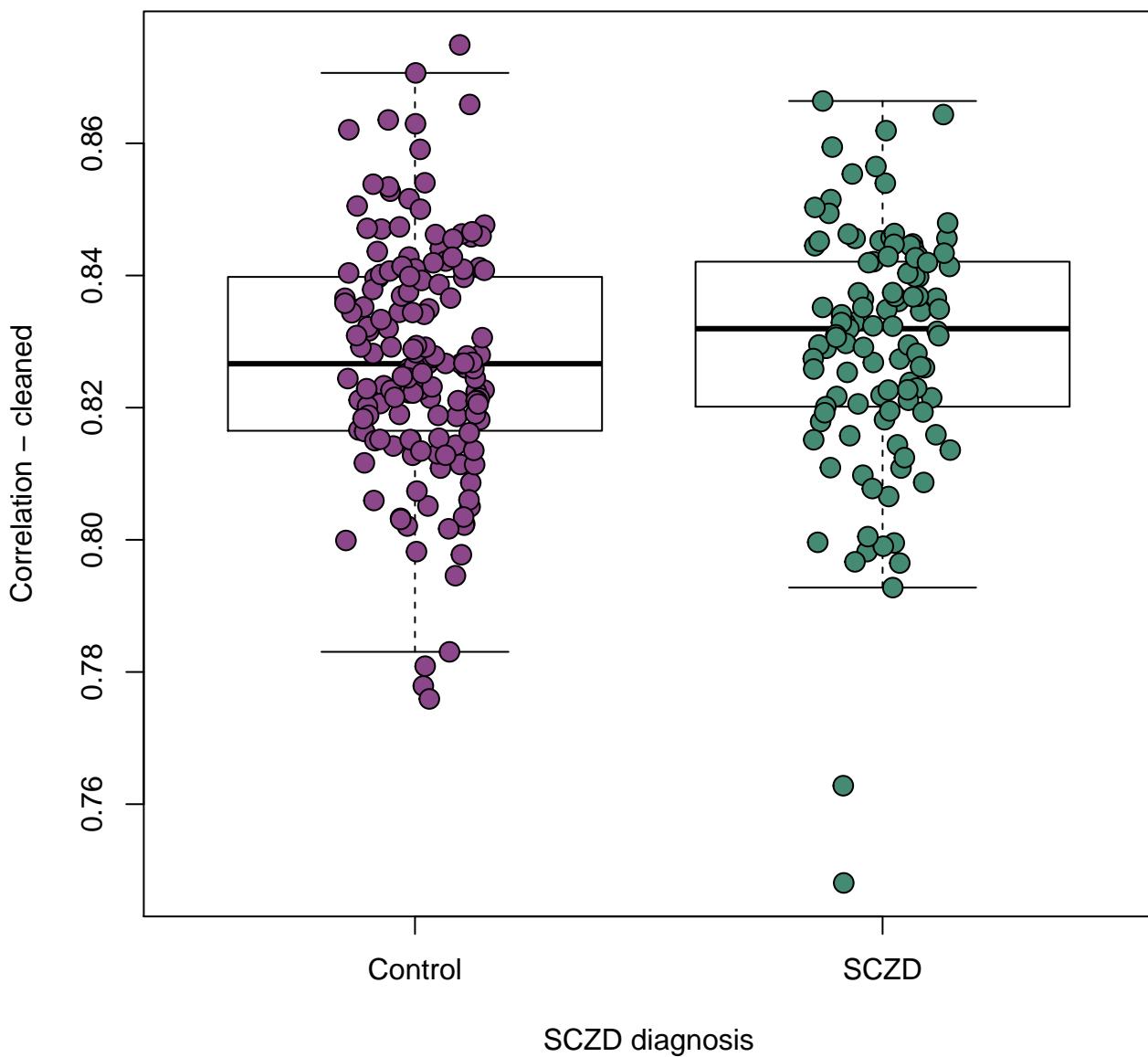
p-value: 0.0343



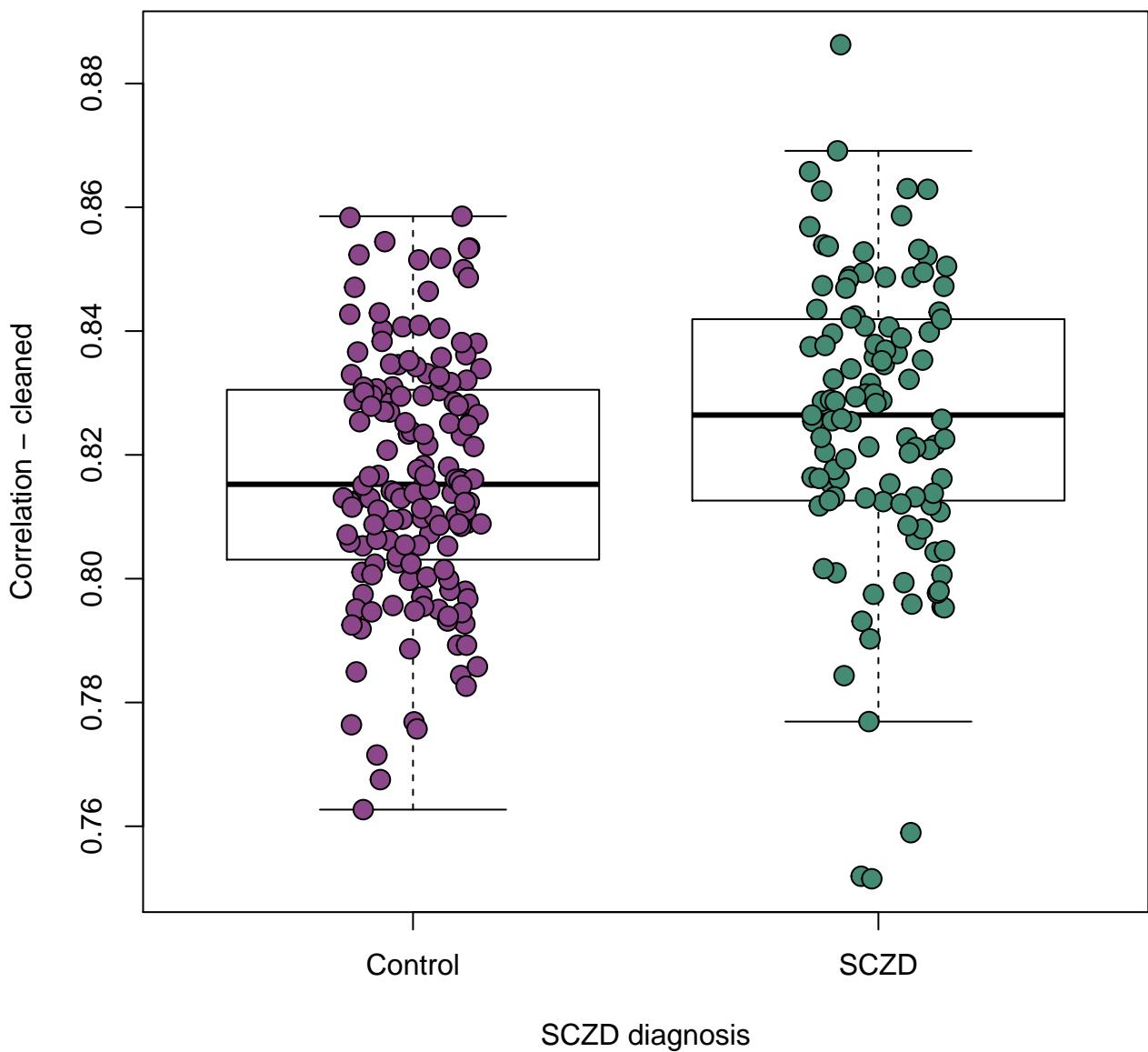
hsa04722: Neurotrophin signaling pathway
p-value: 0.0763



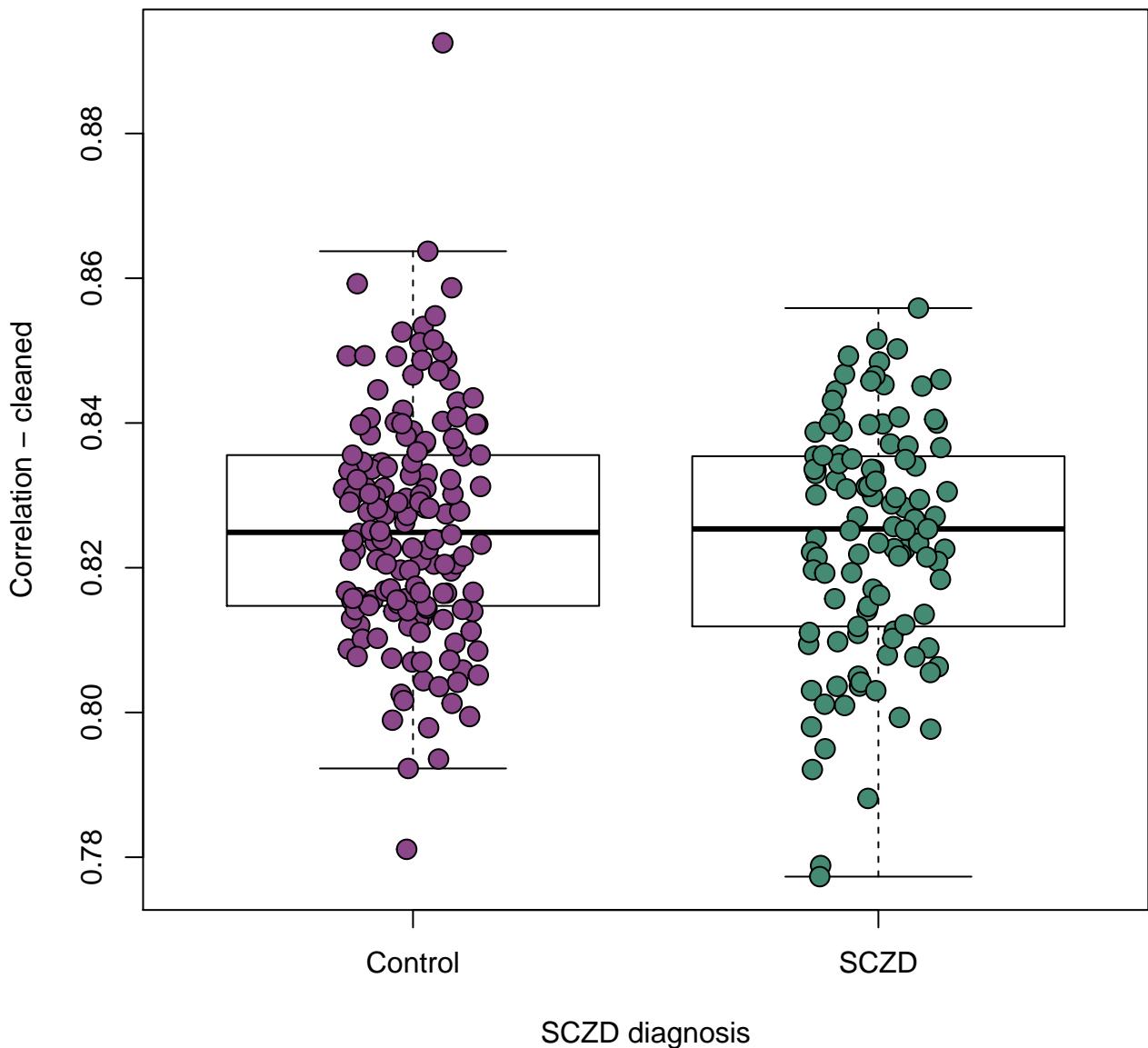
hsa04730: Long-term depression
p-value: 0.388



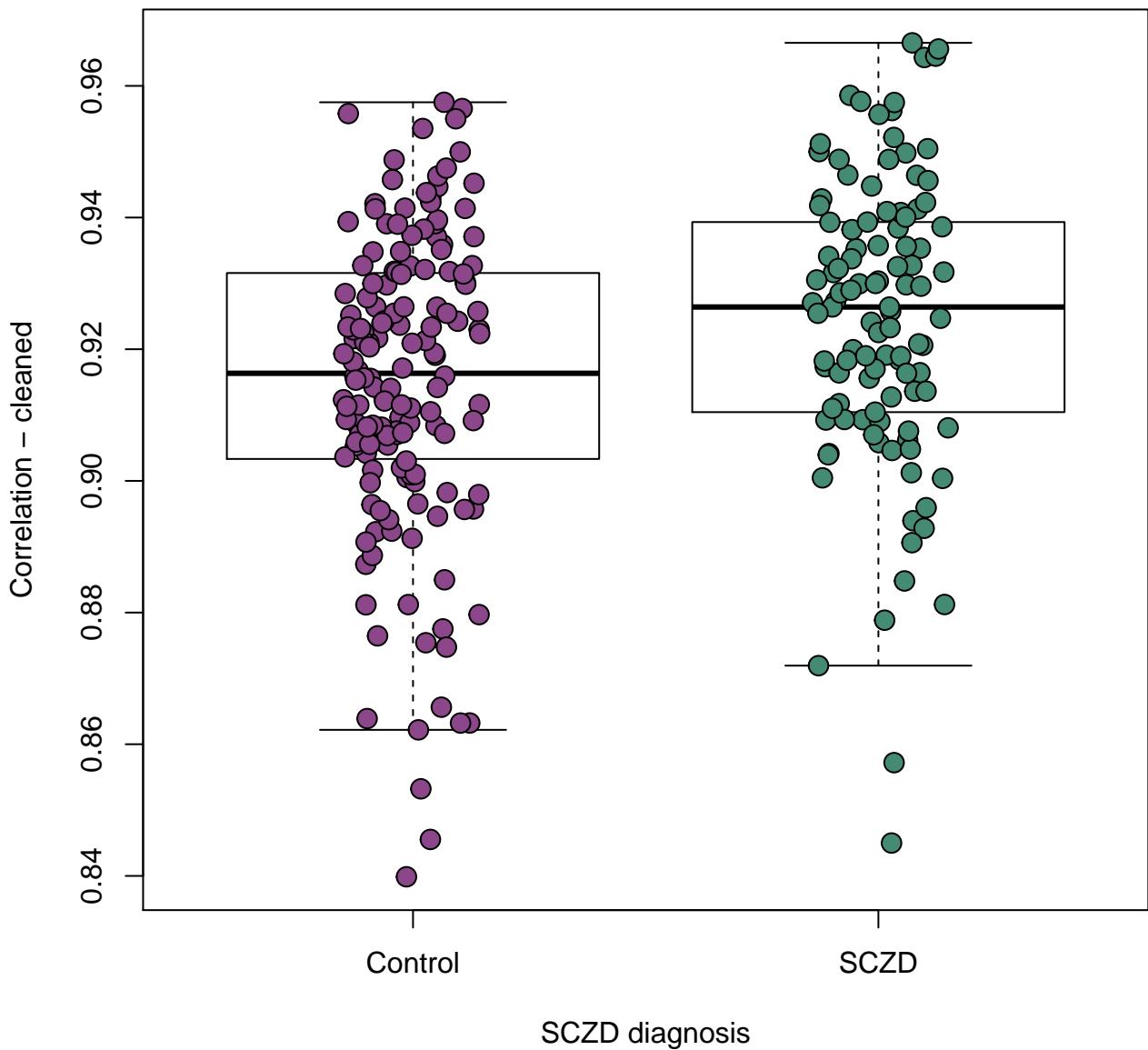
hsa04740: Olfactory transduction
p-value: 0.000541



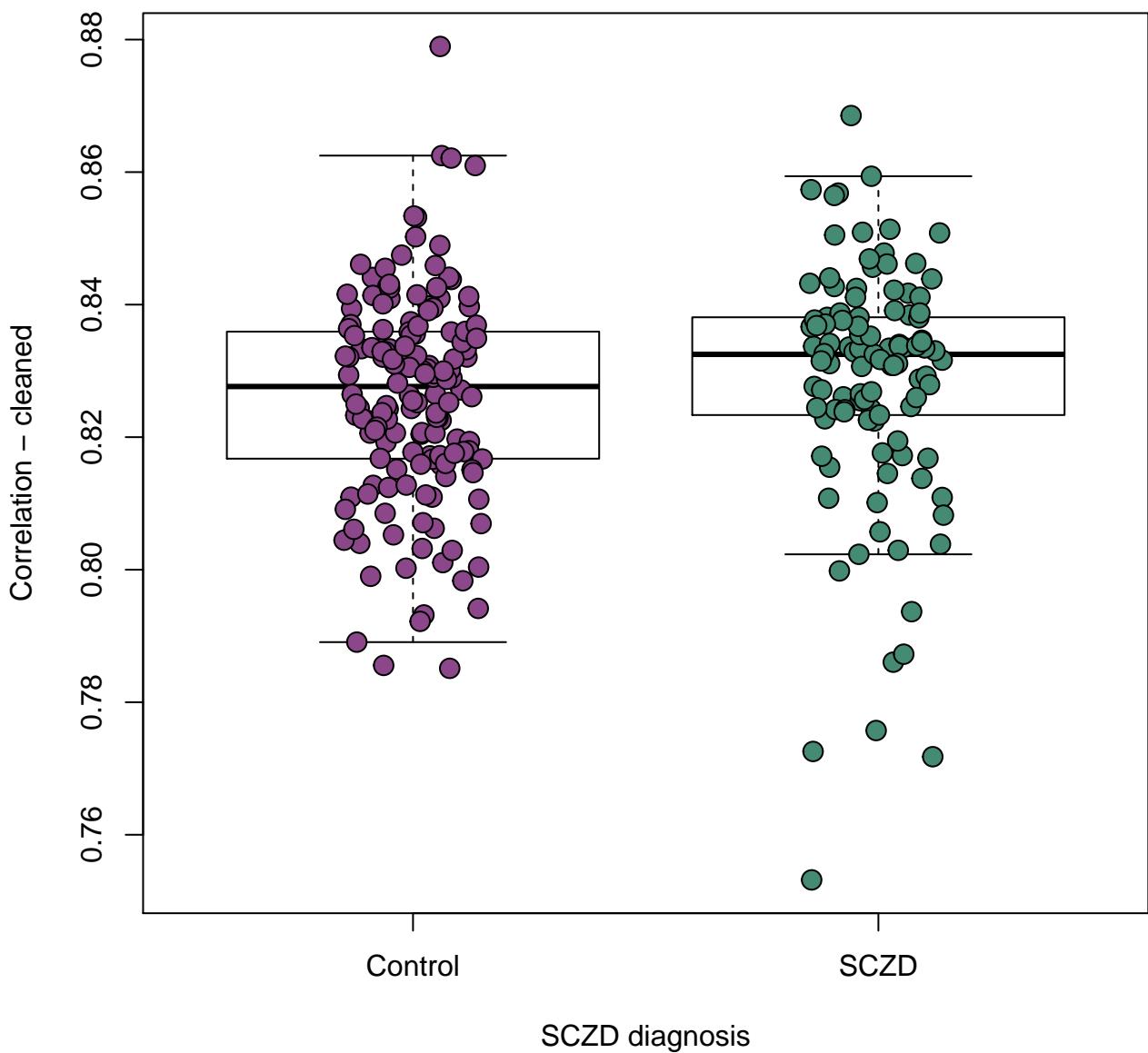
hsa04742: Taste transduction
p-value: 0.355



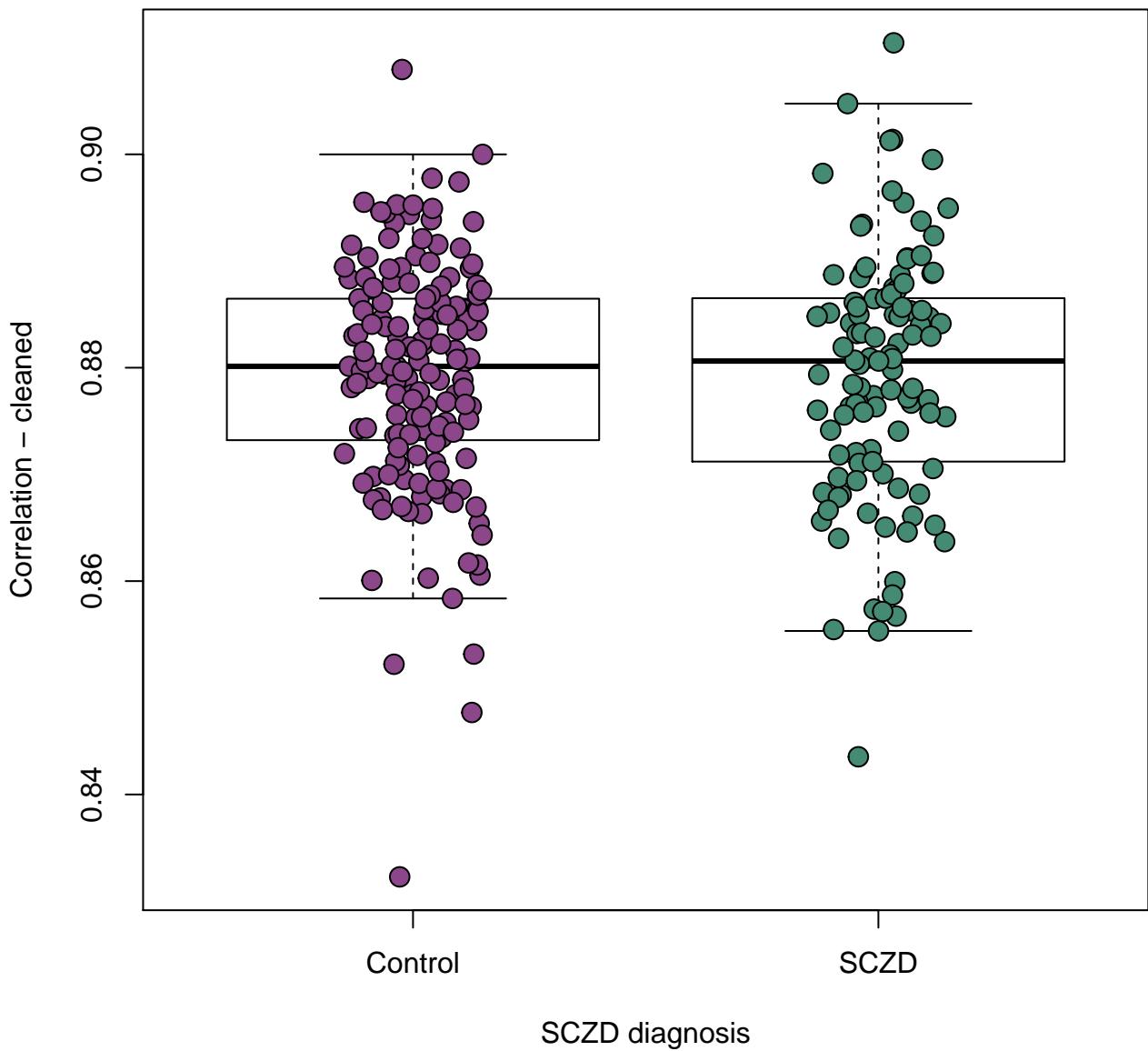
hsa04744: Phototransduction
p-value: 0.000908



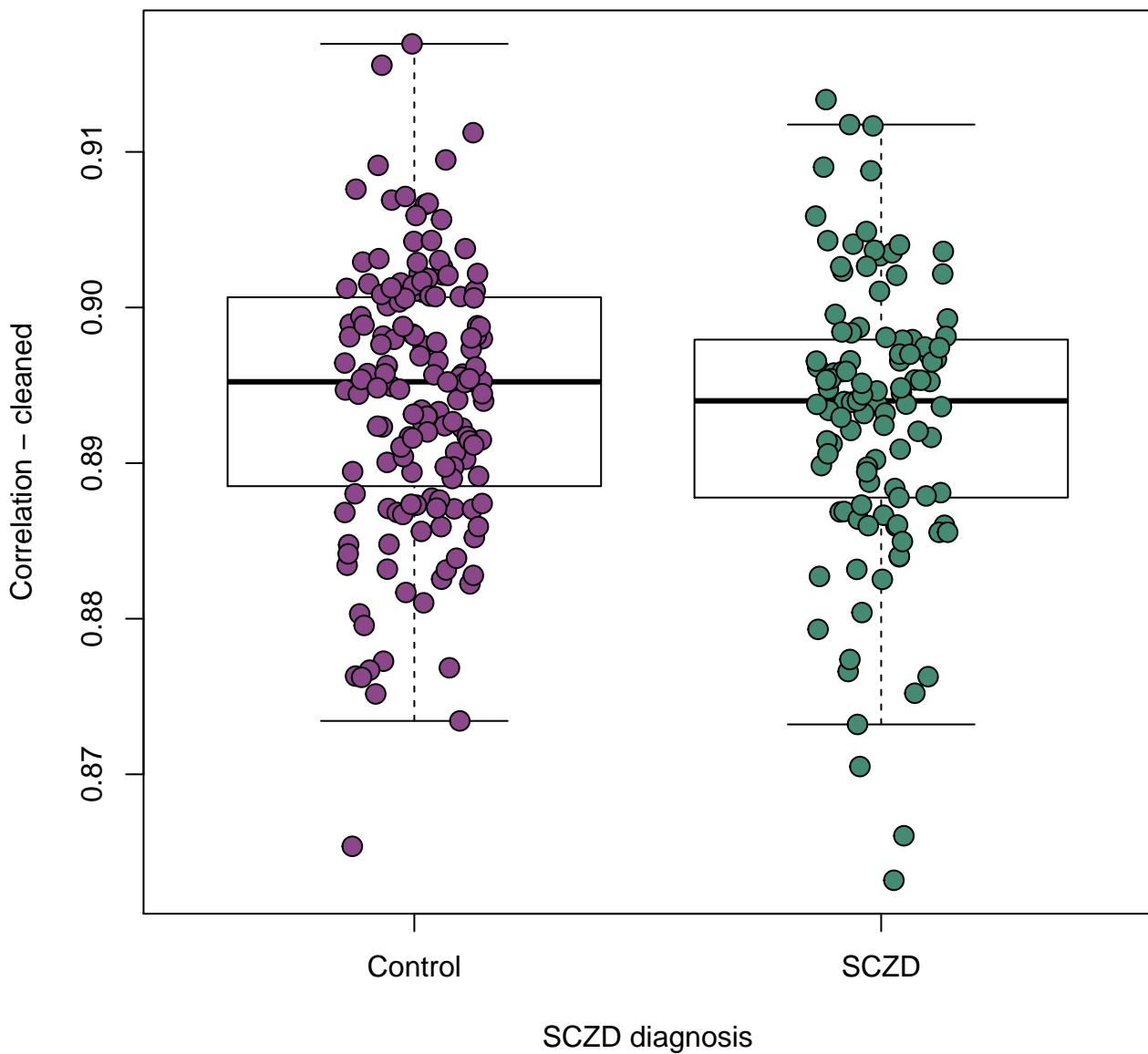
hsa04810: Regulation of actin cytoskeleton
p-value: 0.302



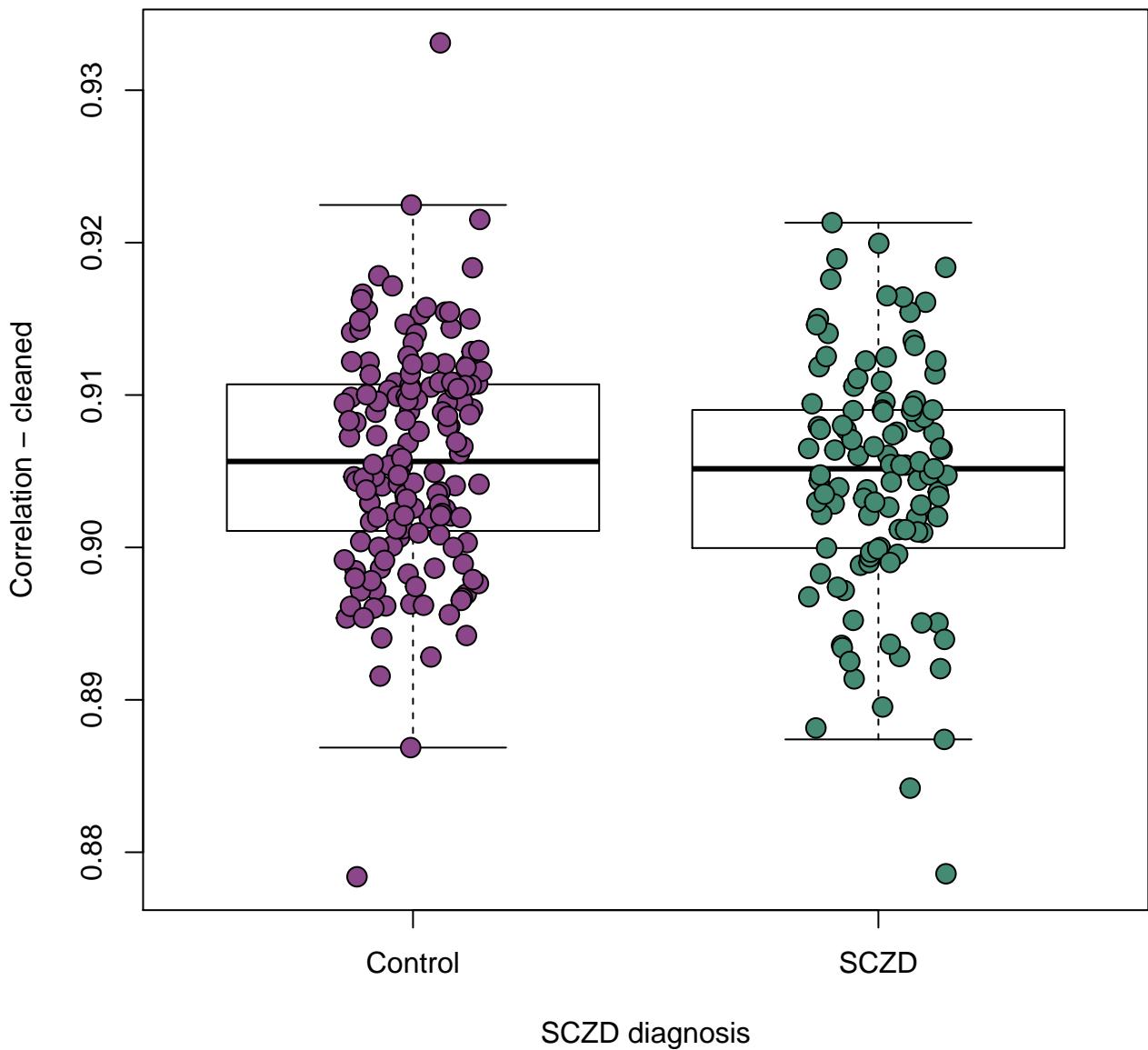
hsa04910: Insulin signaling pathway
p-value: 0.994



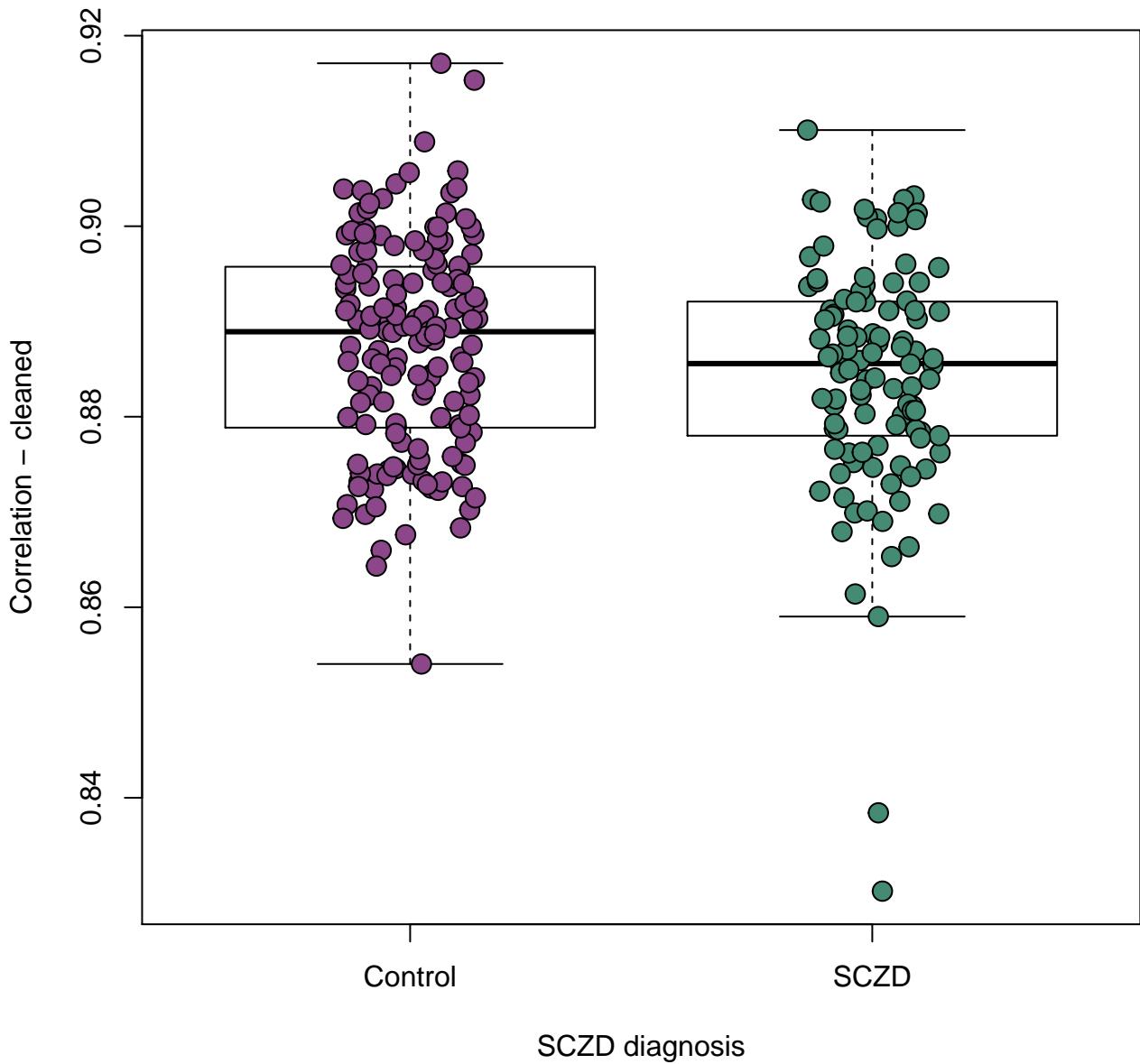
hsa04912: GnRH signaling pathway
p-value: 0.274



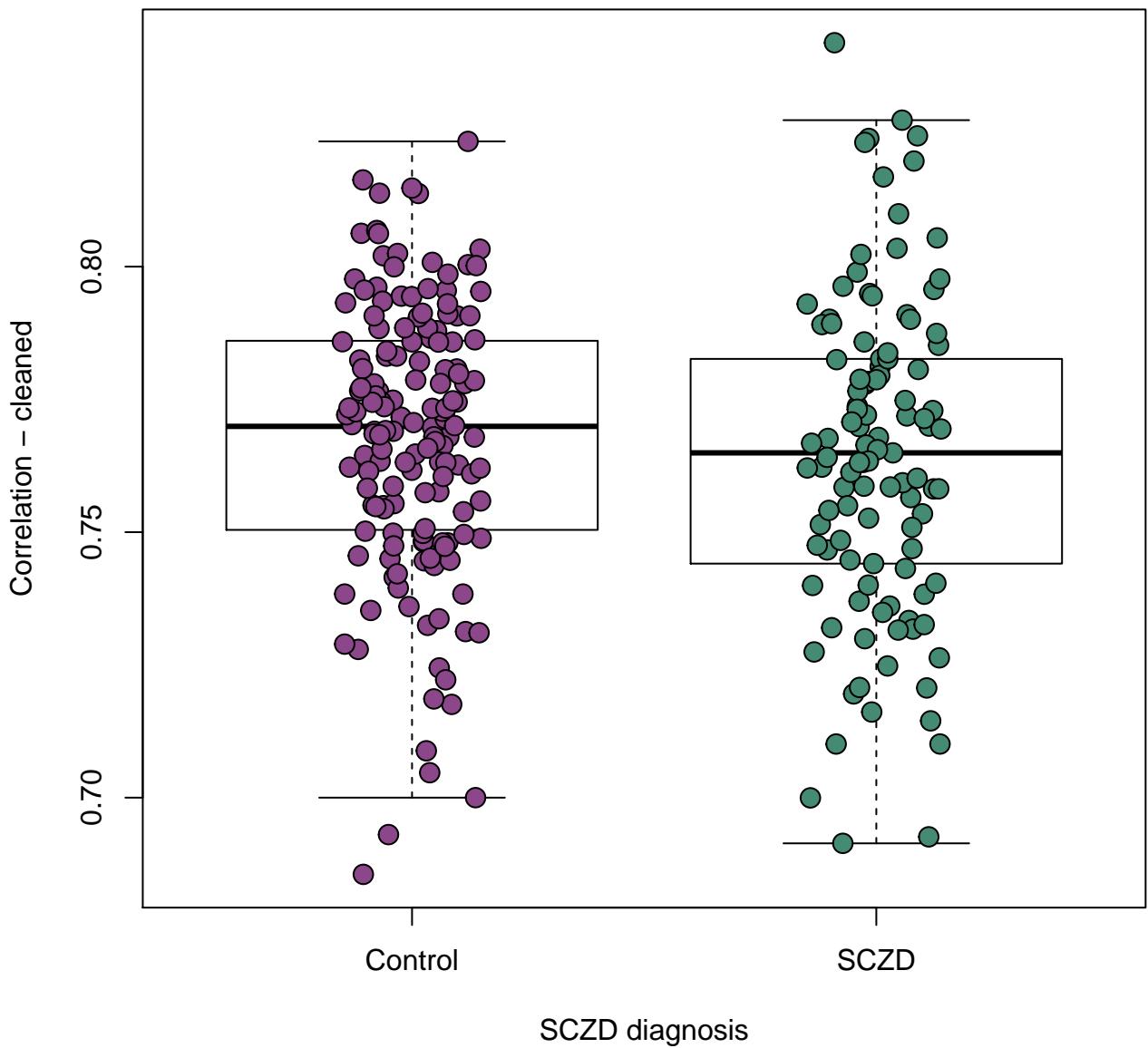
hsa04914: Progesterone–mediated oocyte maturation
p-value: 0.145



hsa04916: Melanogenesis
p-value: 0.0382

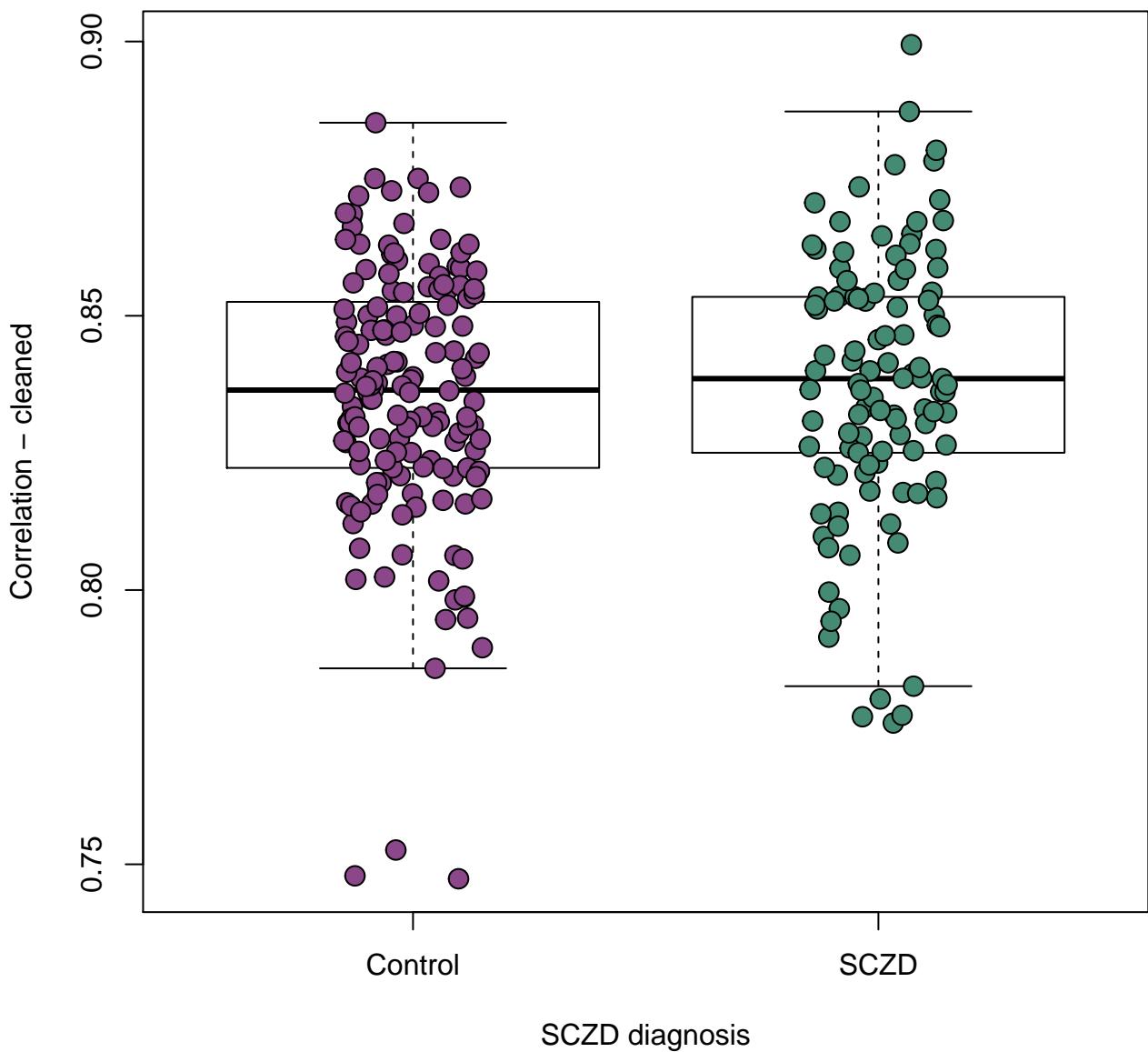


hsa04920: Adipocytokine signaling pathway
p-value: 0.285

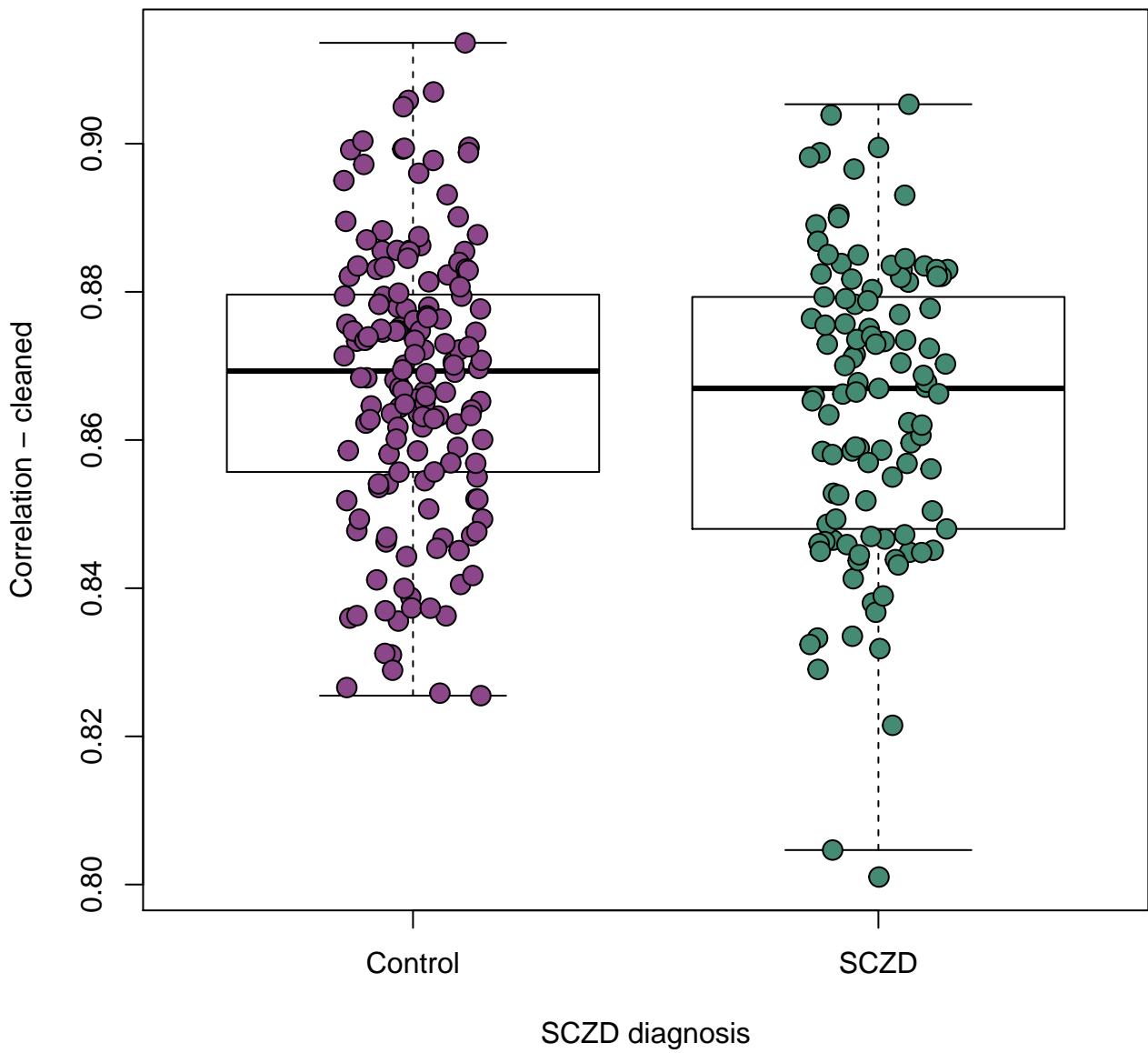


hsa04930: Type II diabetes mellitus

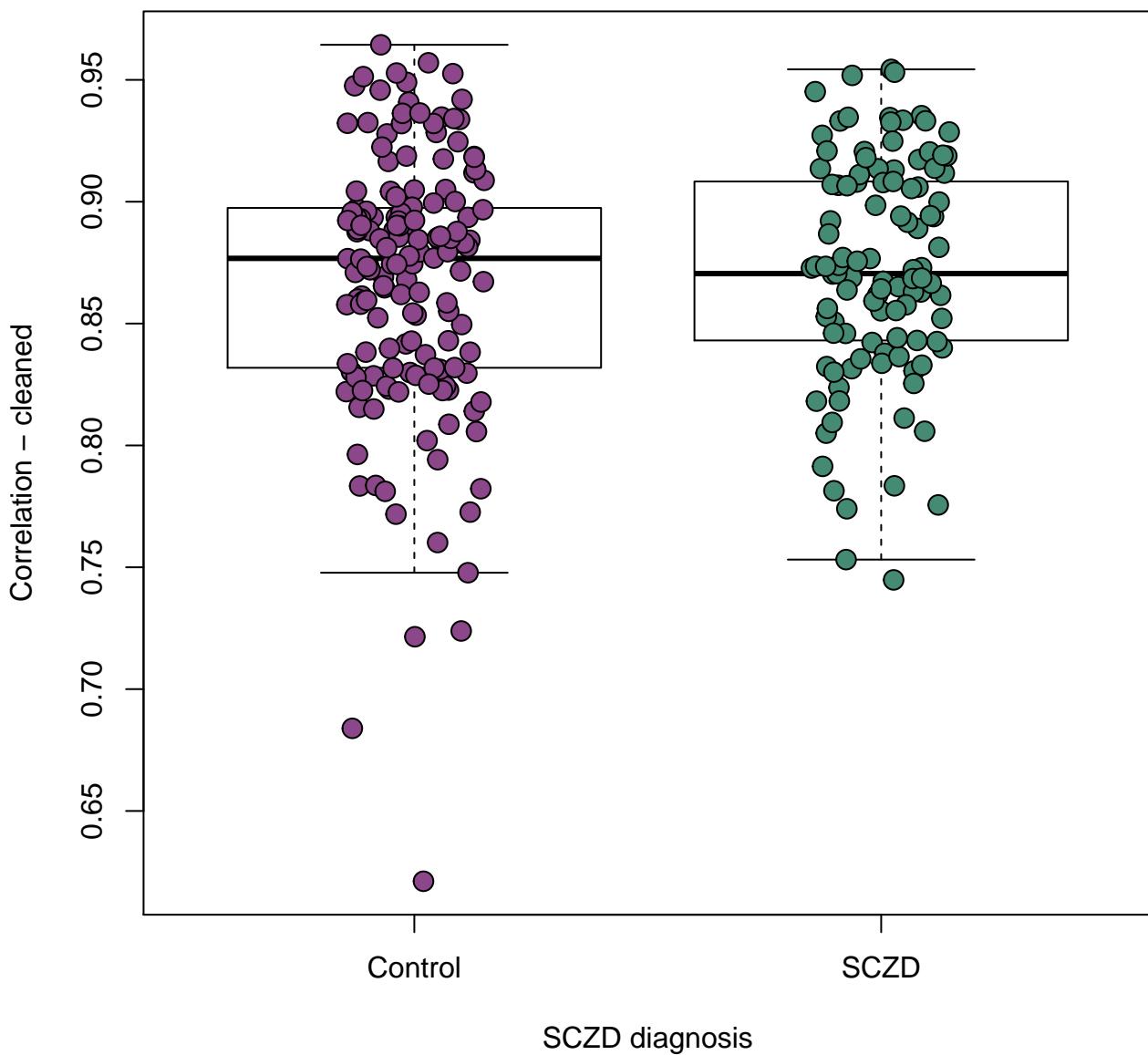
p-value: 0.471



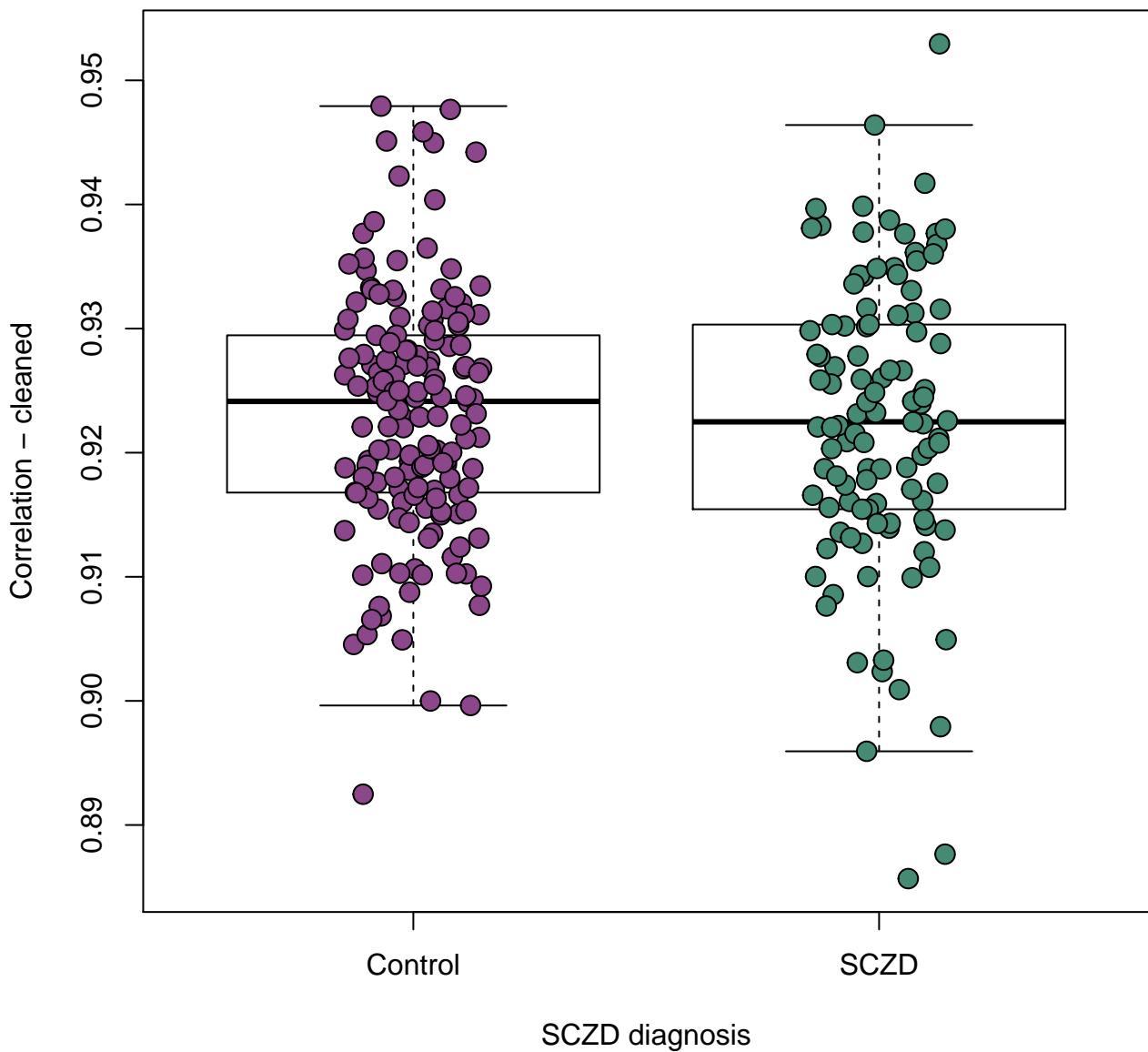
hsa04940: Type I diabetes mellitus
p-value: 0.143



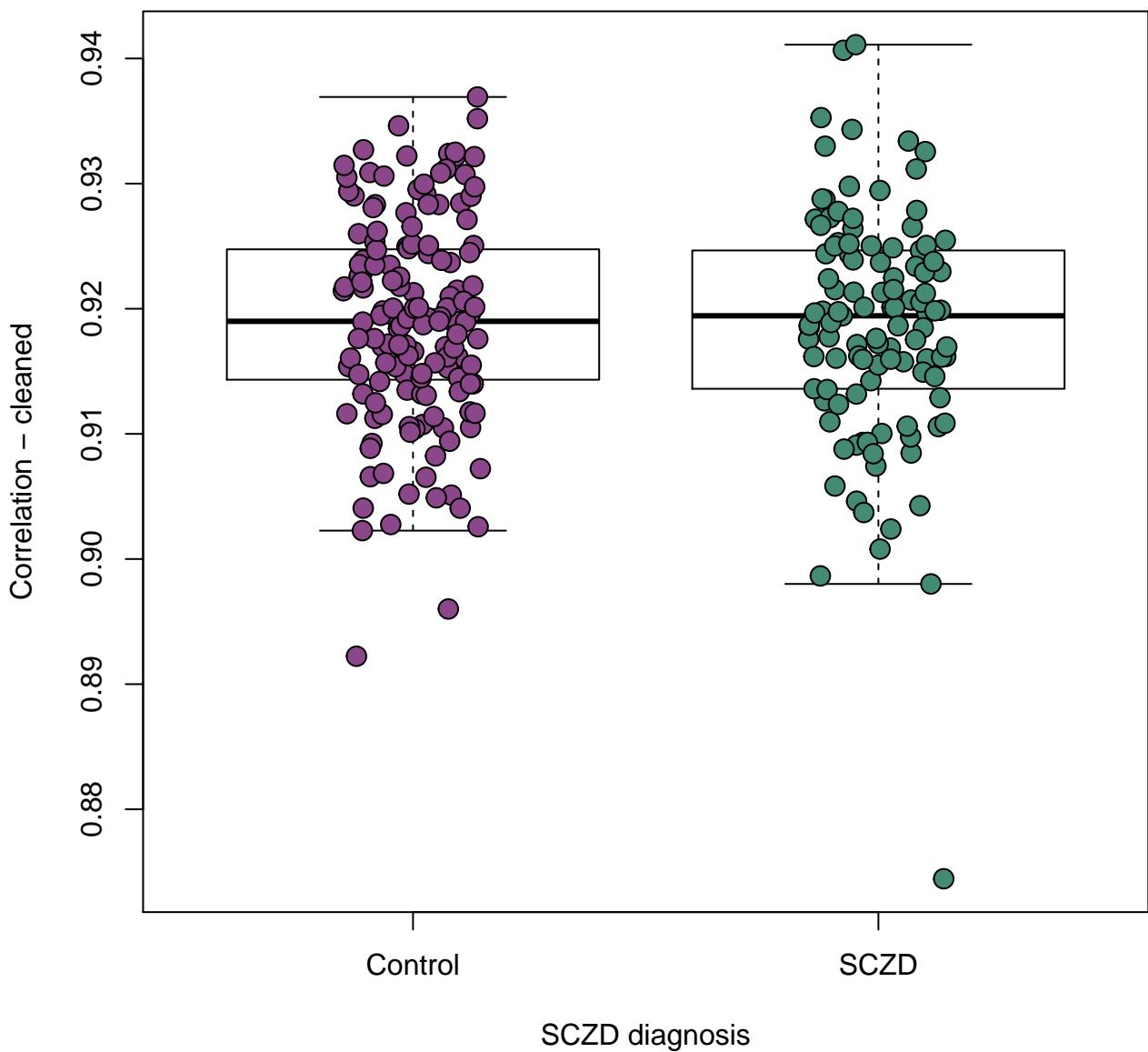
hsa04950: Maturity onset diabetes of the young
p-value: 0.457



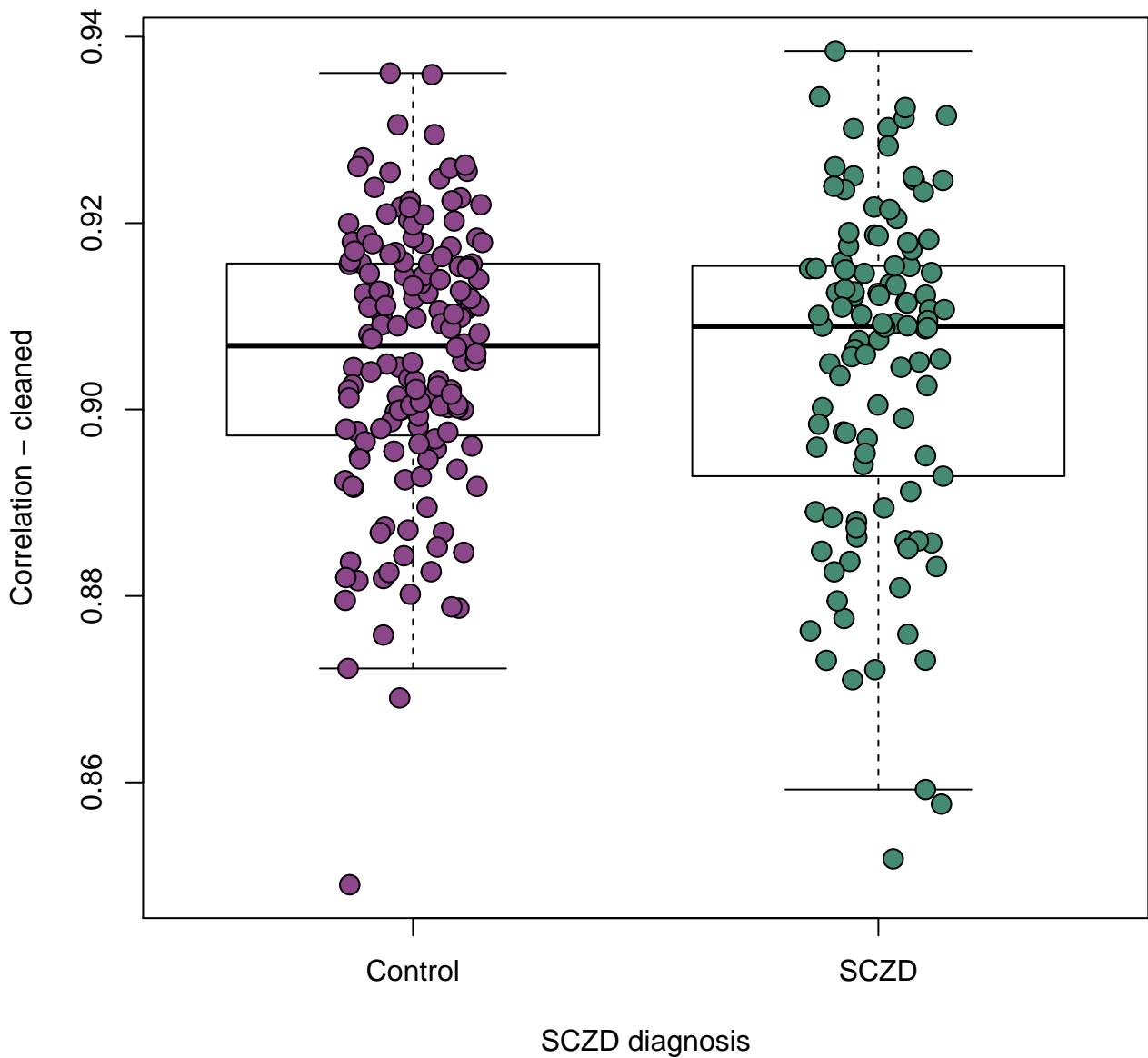
hsa04960: Aldosterone-regulated sodium reabsorption
p-value: 0.623



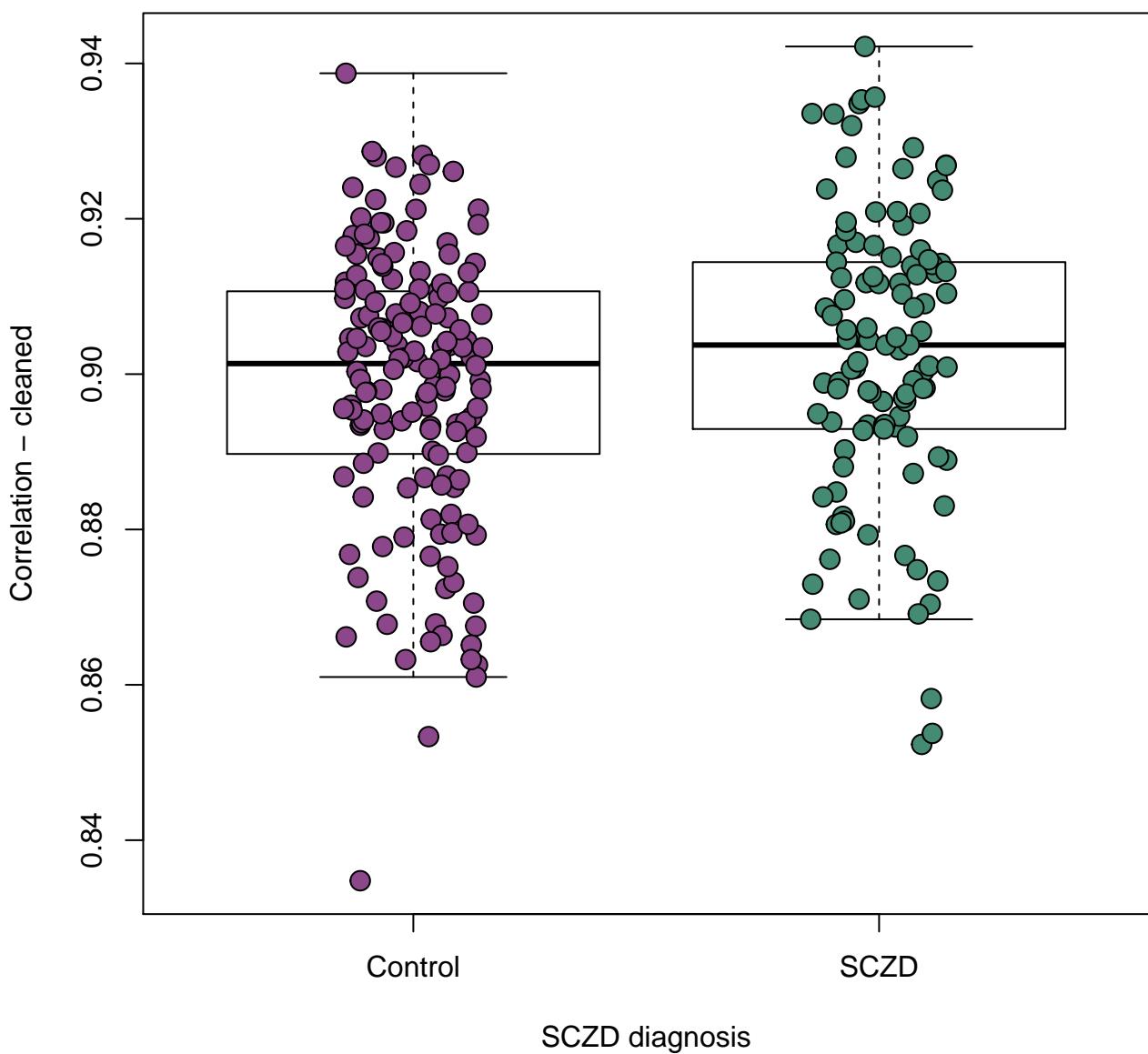
hsa04962: Vasopressin-regulated water reabsorption
p-value: 0.654



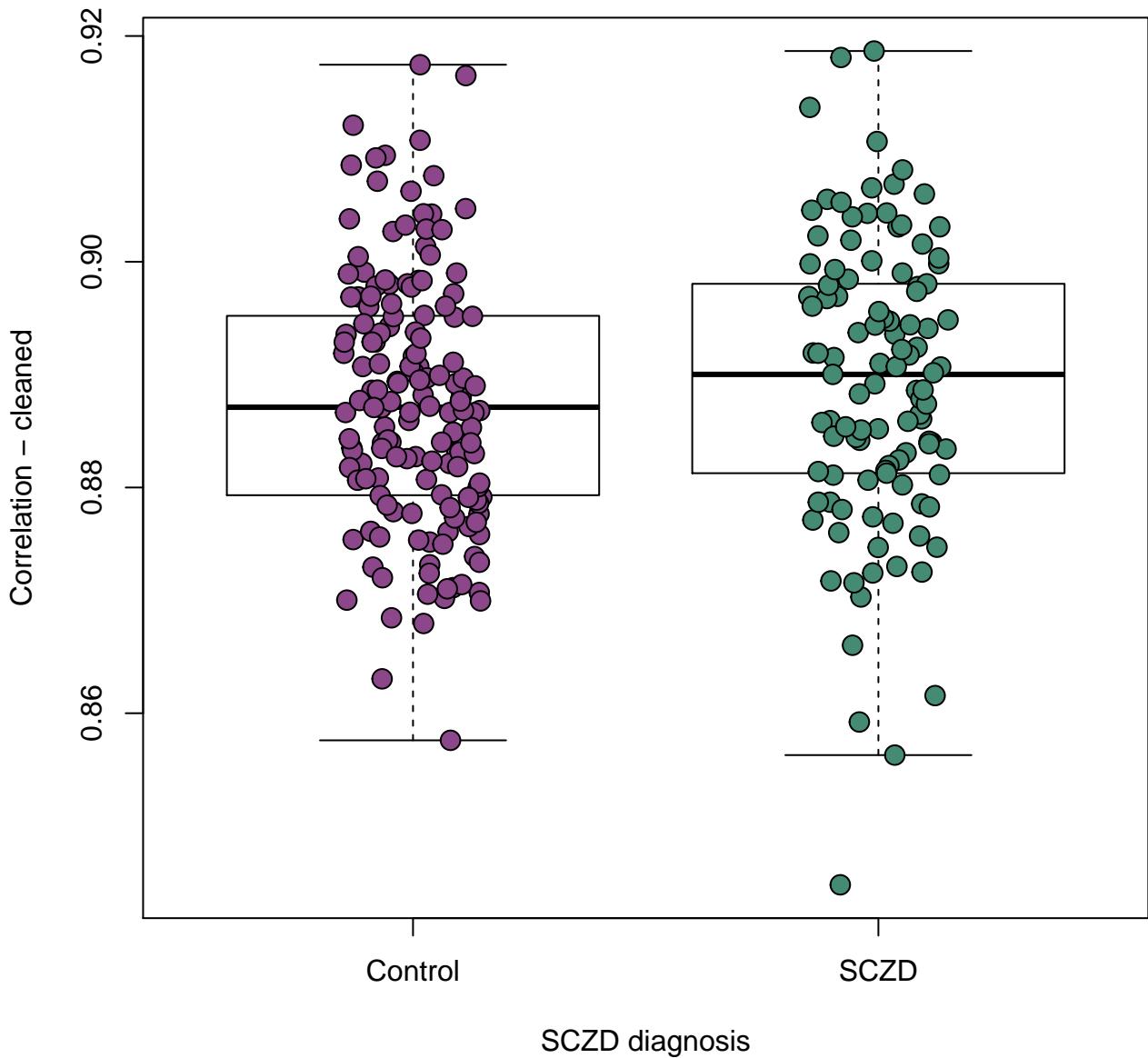
hsa04964: Proximal tubule bicarbonate reclamation
p-value: 0.658



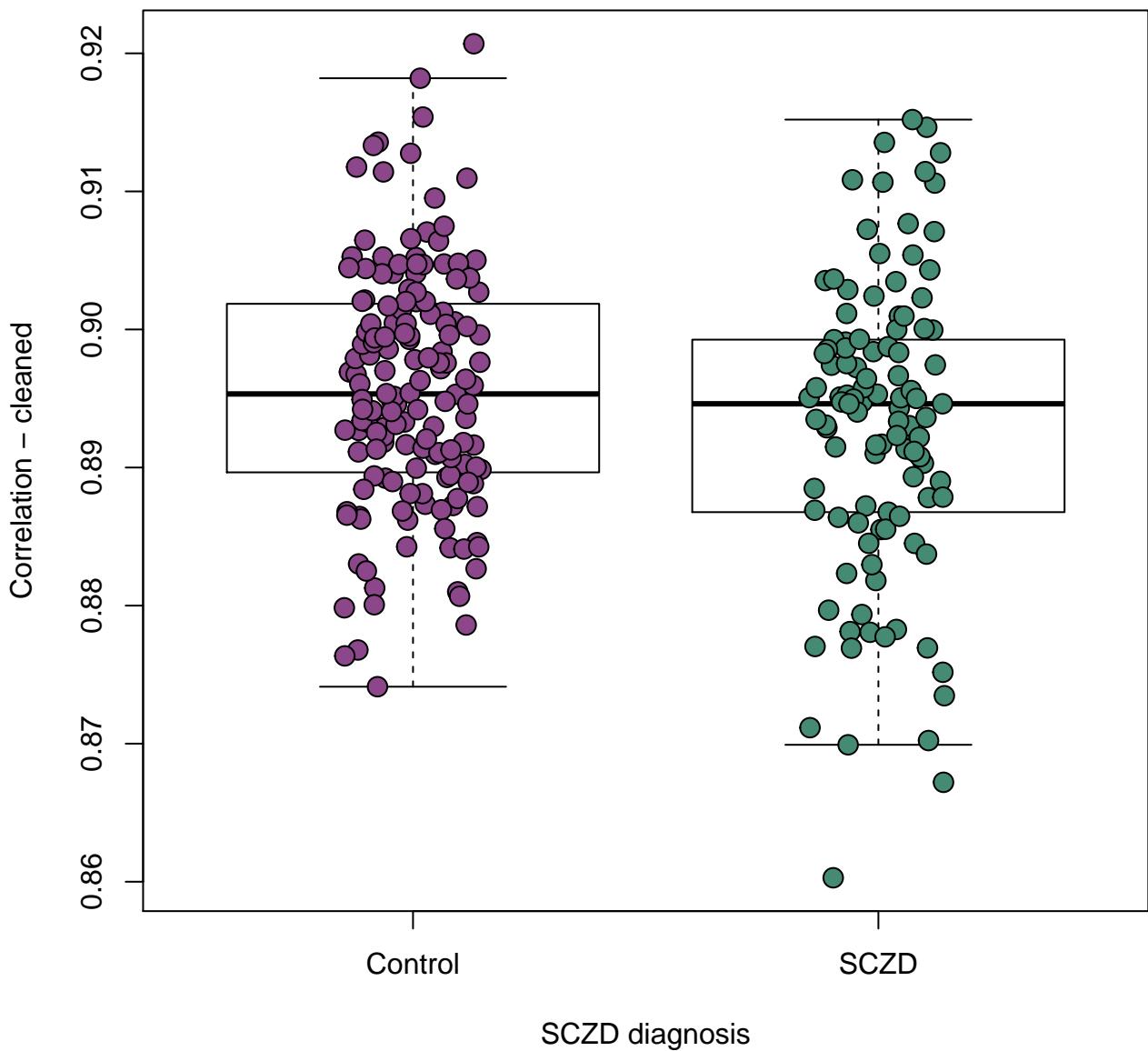
hsa04966: Collecting duct acid secretion
p-value: 0.0884



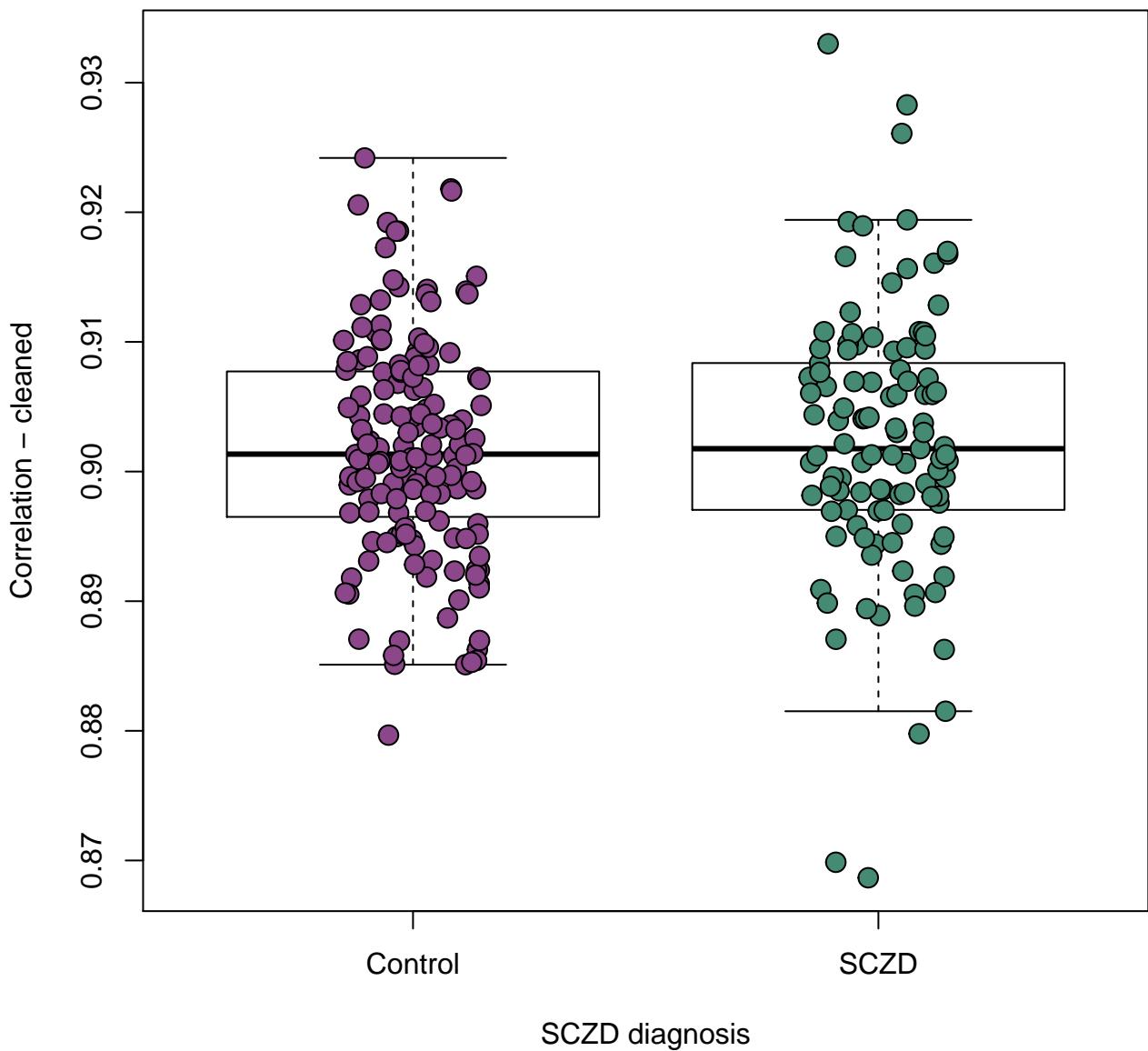
hsa04970: Salivary secretion
p-value: 0.303



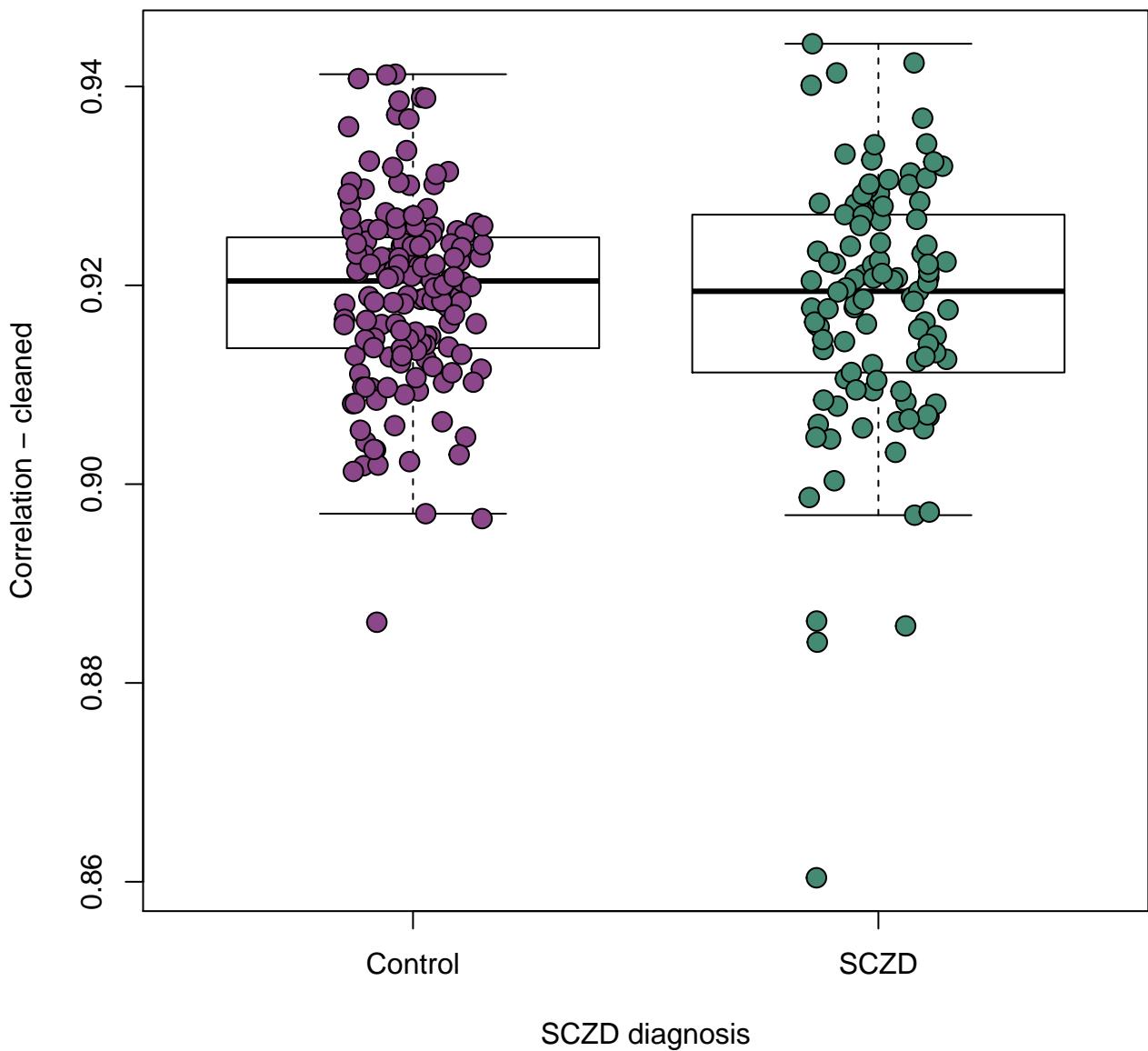
hsa04971: Gastric acid secretion
p-value: 0.0247



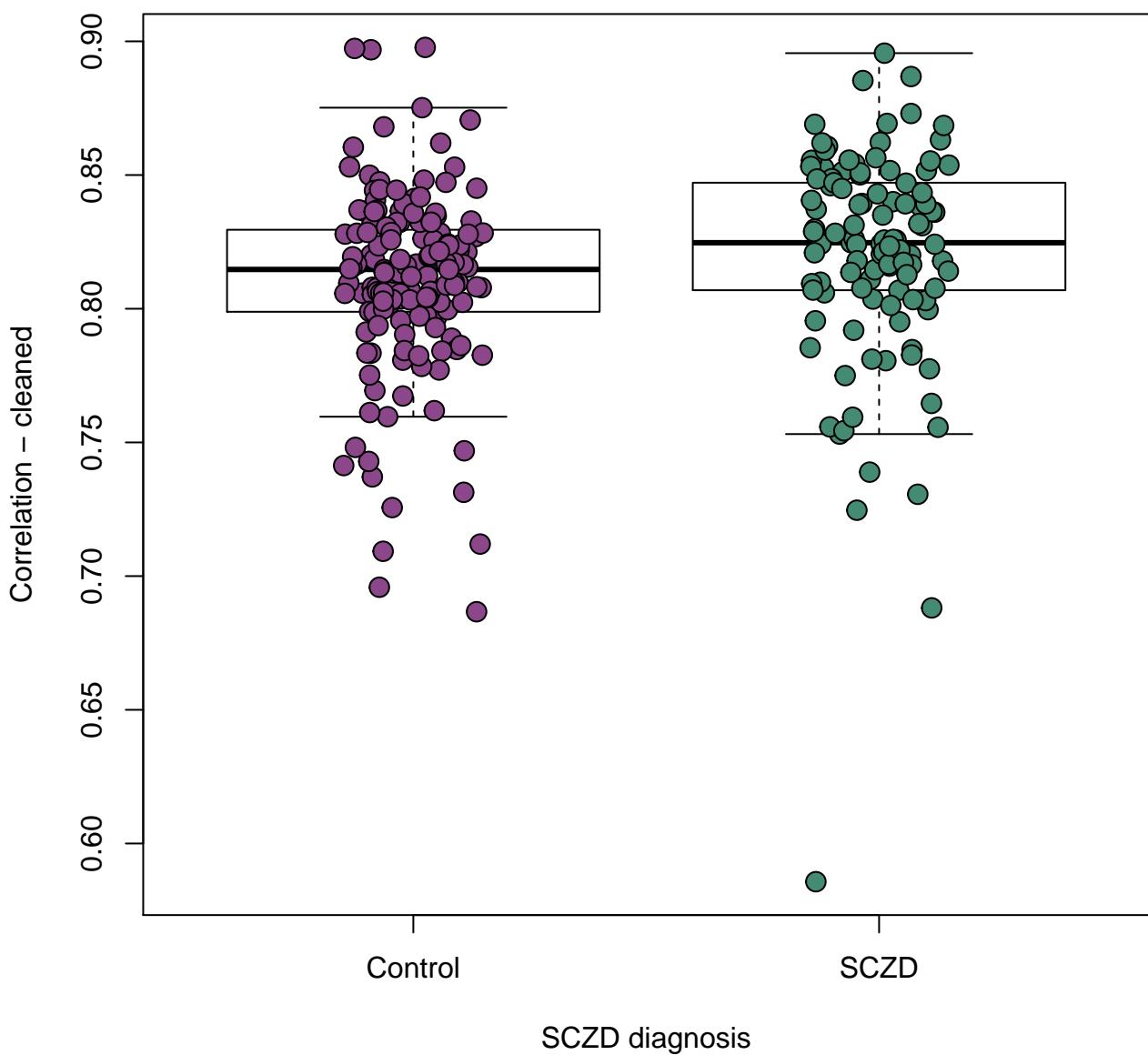
hsa04972: Pancreatic secretion
p-value: 0.698



hsa04973: Carbohydrate digestion and absorption
p-value: 0.346

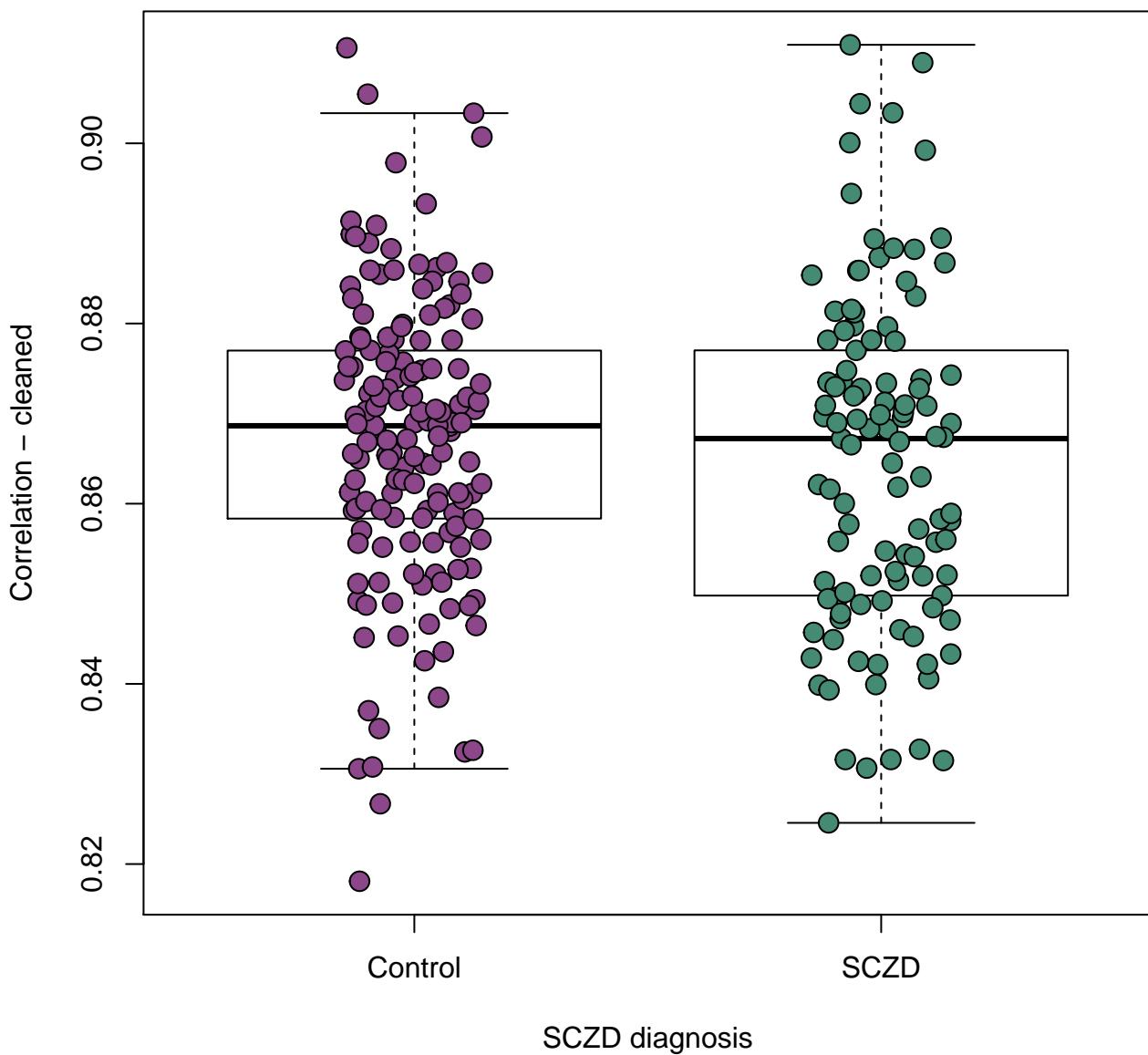


hsa04974: Protein digestion and absorption
p-value: 0.0538



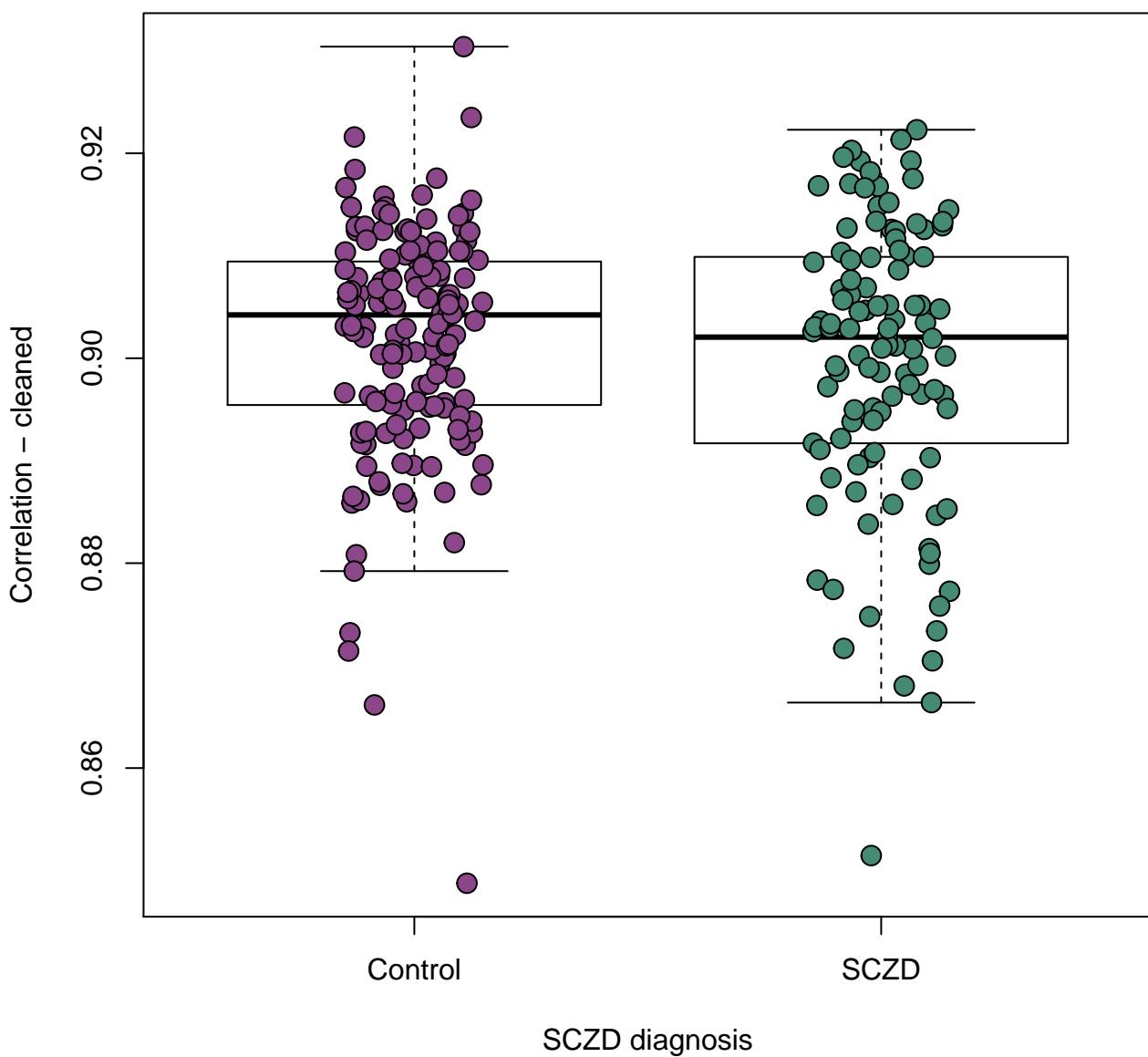
hsa04975: Fat digestion and absorption

p-value: 0.249

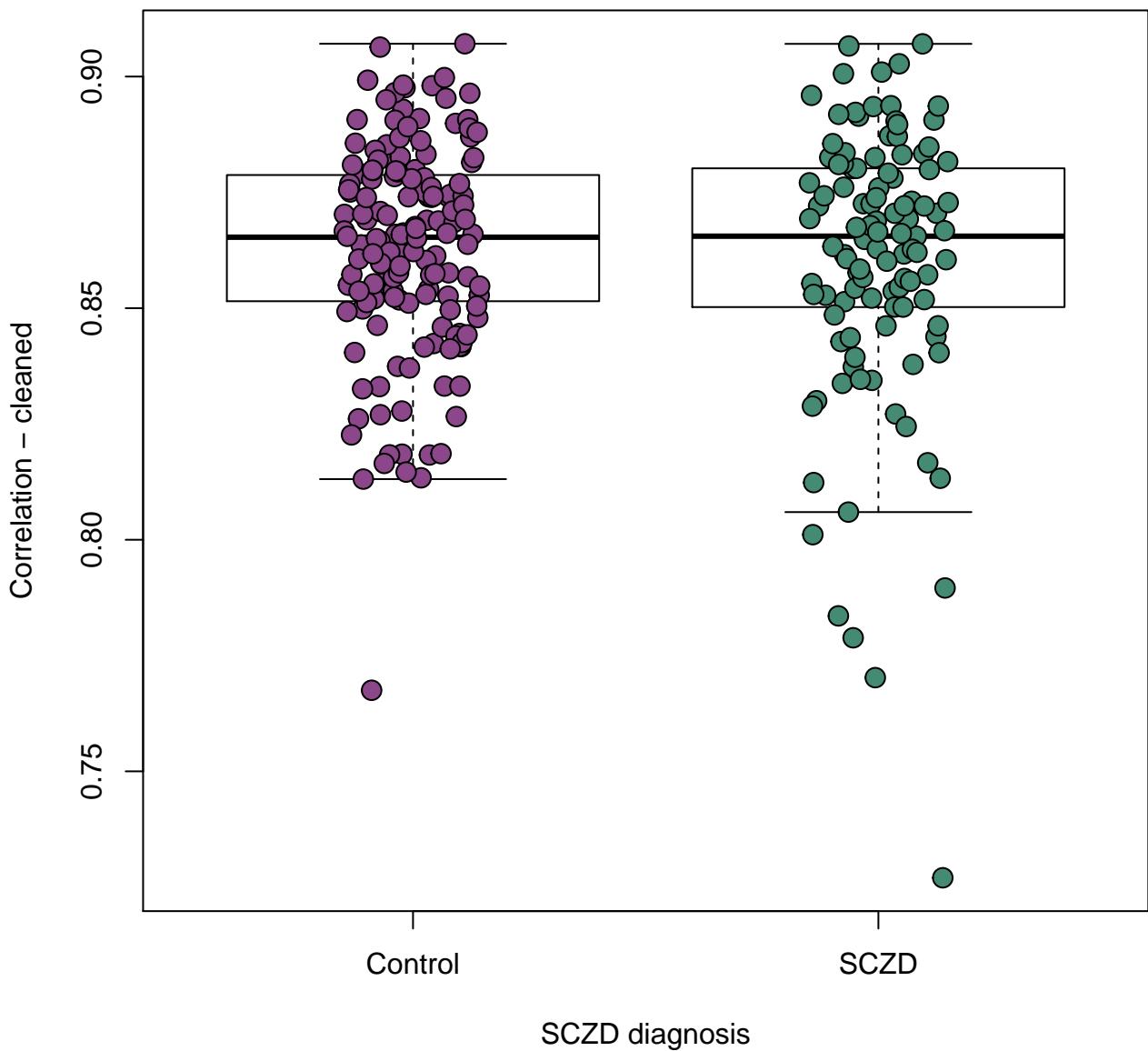


hsa04976: Bile secretion

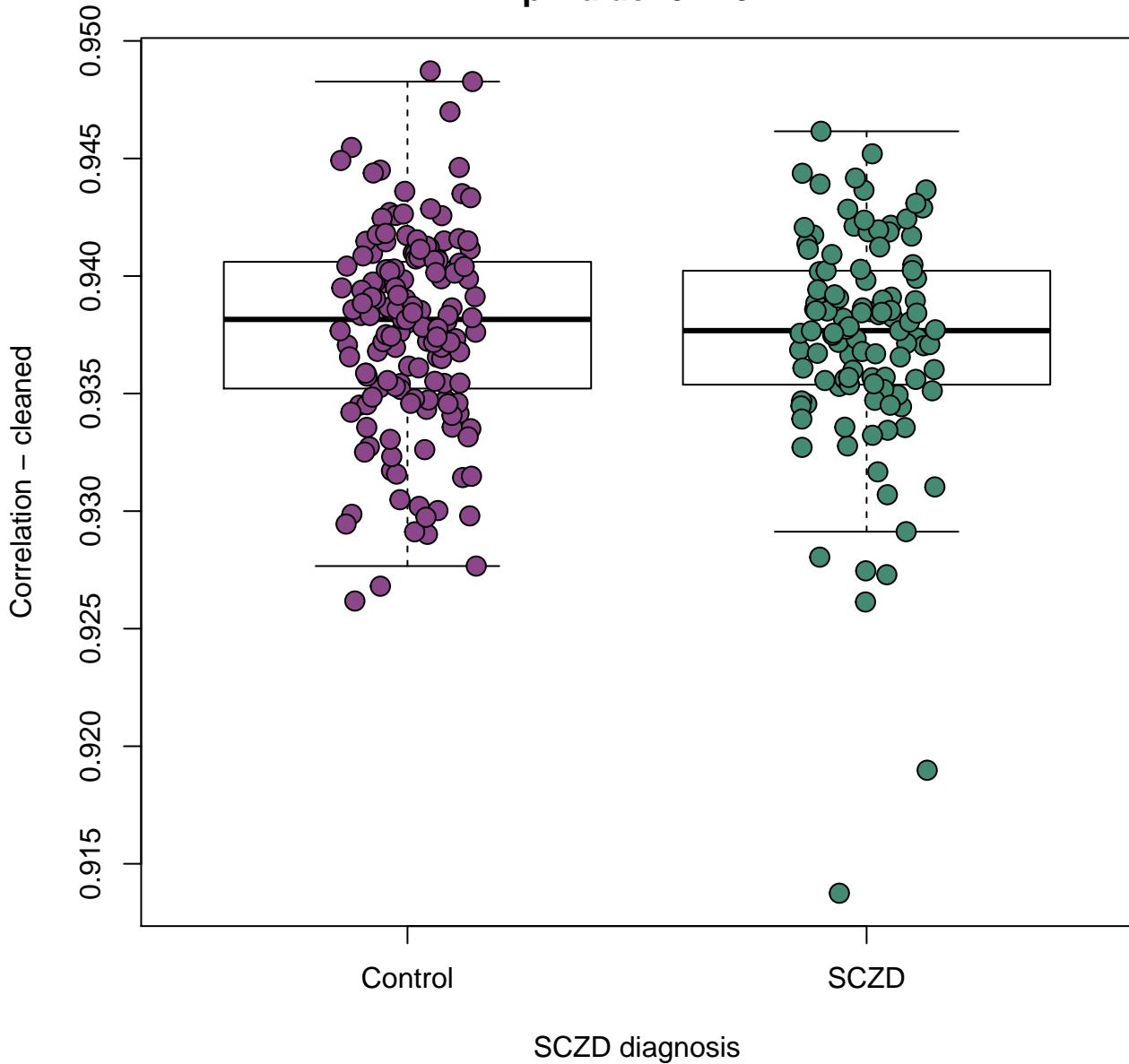
p-value: 0.141



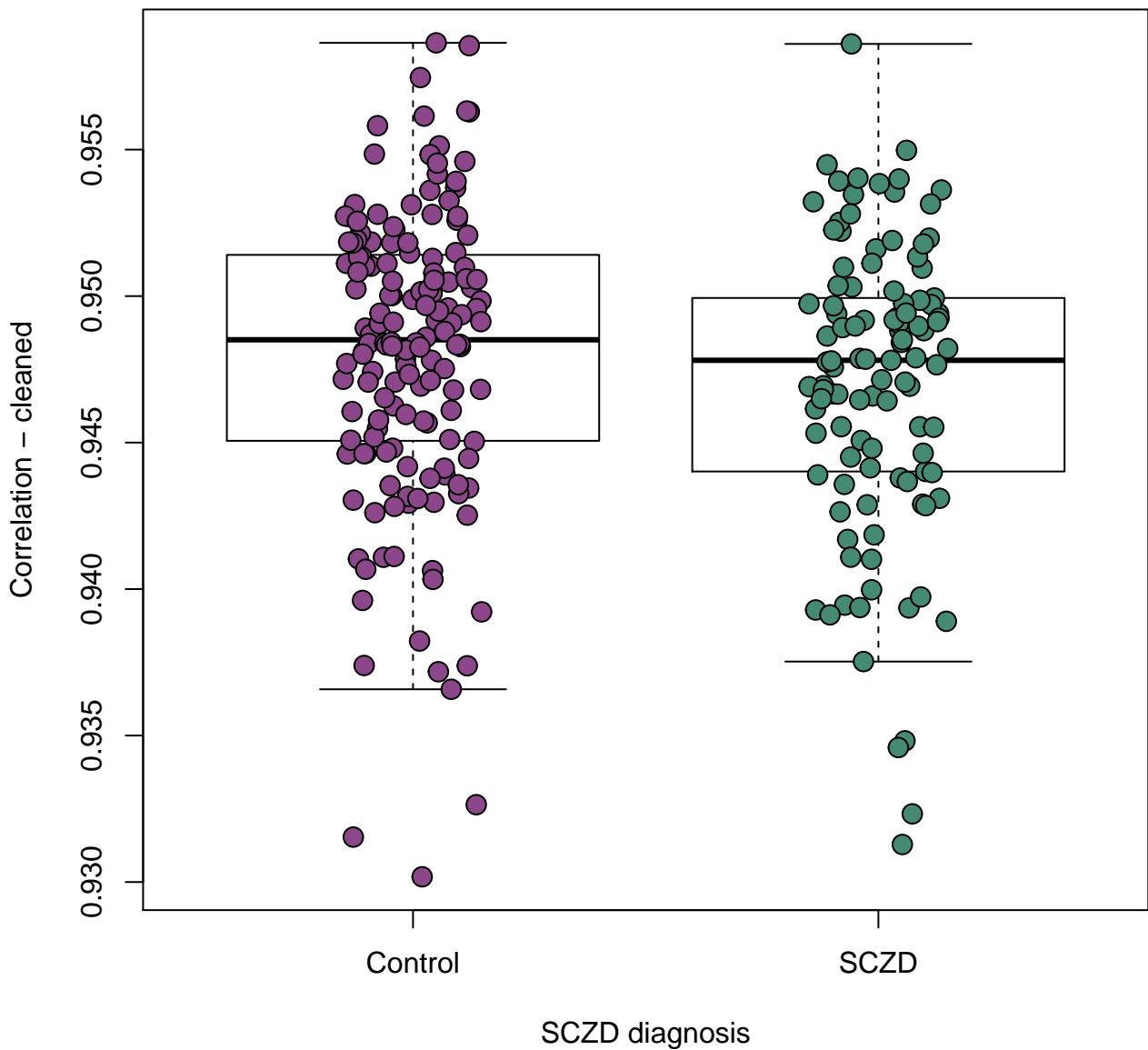
hsa04977: Vitamin digestion and absorption
p-value: 0.372



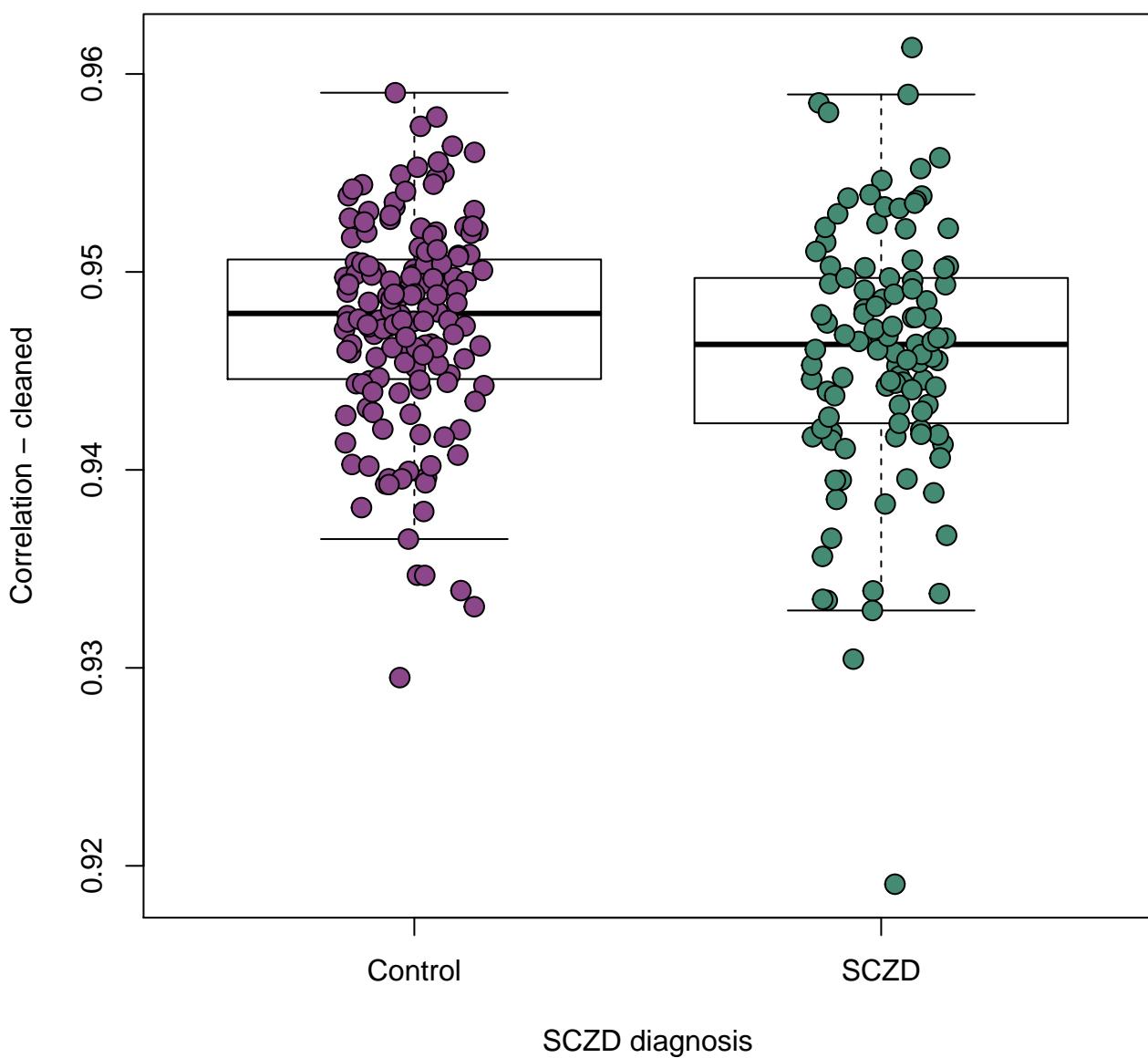
hsa05010: Alzheimer's disease
p-value: 0.425



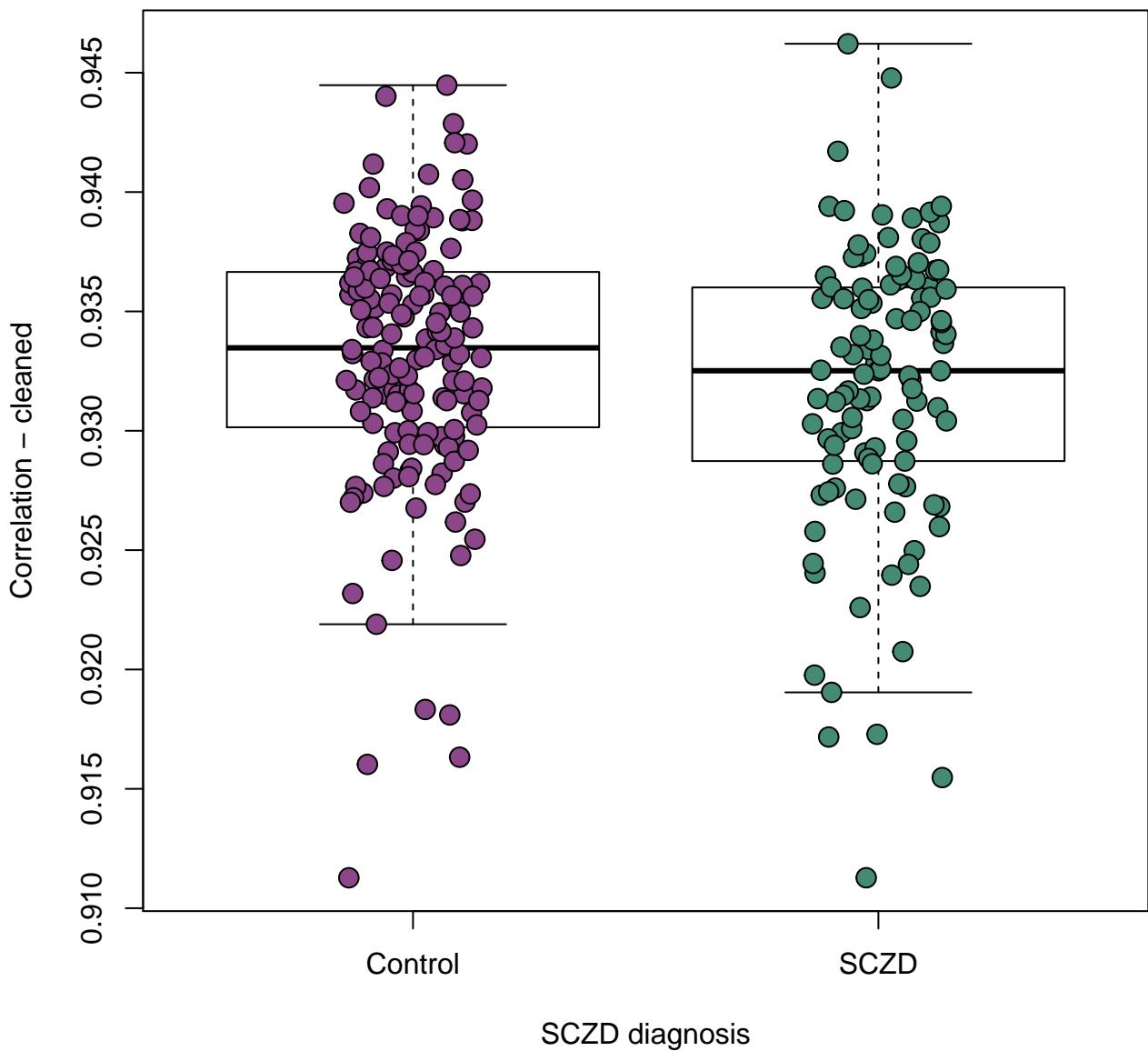
hsa05012: Parkinson's disease
p-value: 0.112



hsa05014: Amyotrophic lateral sclerosis (ALS)
p-value: 0.0251

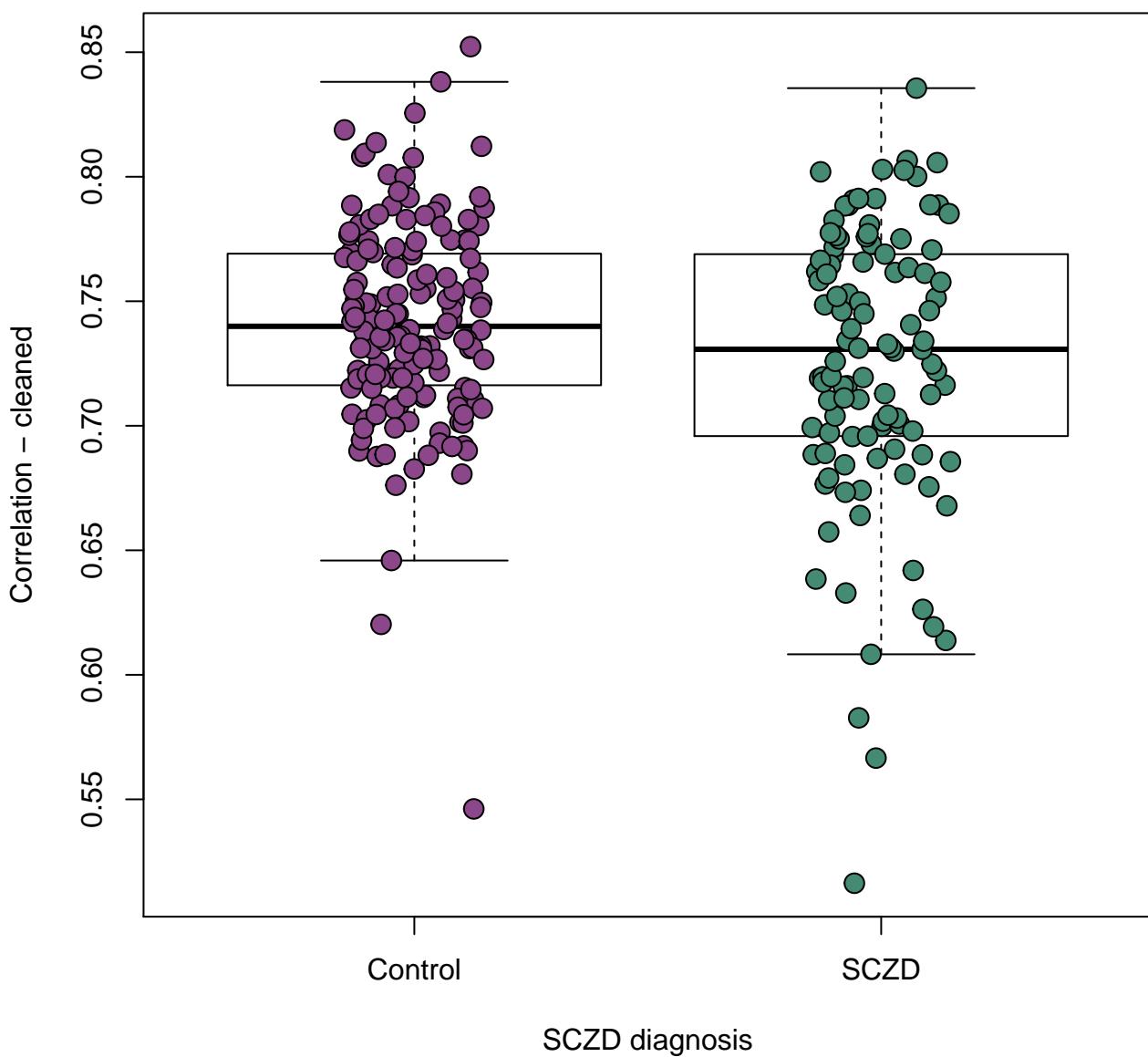


hsa05016: Huntington's disease
p-value: 0.0686

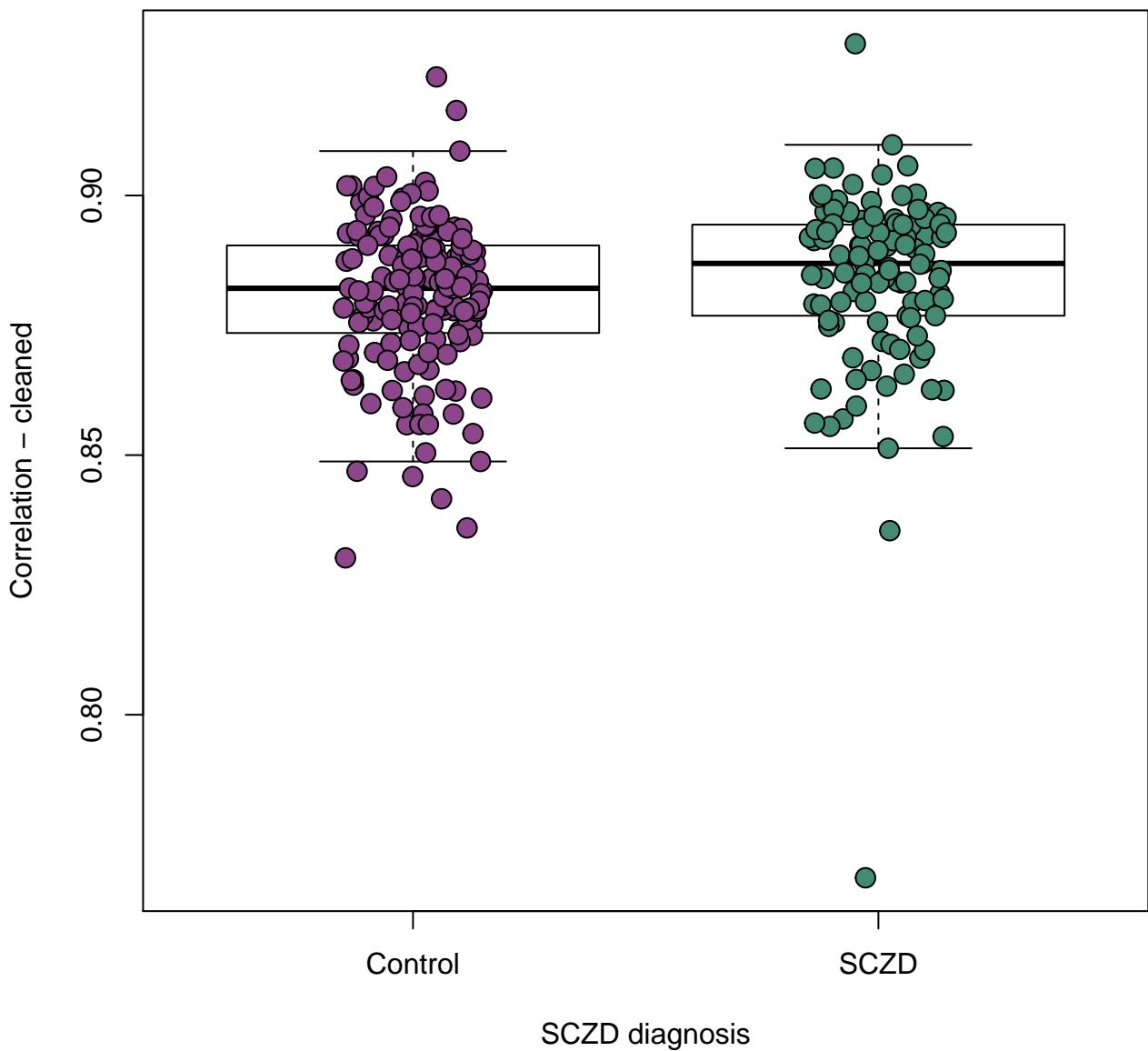


hsa05020: Prion diseases

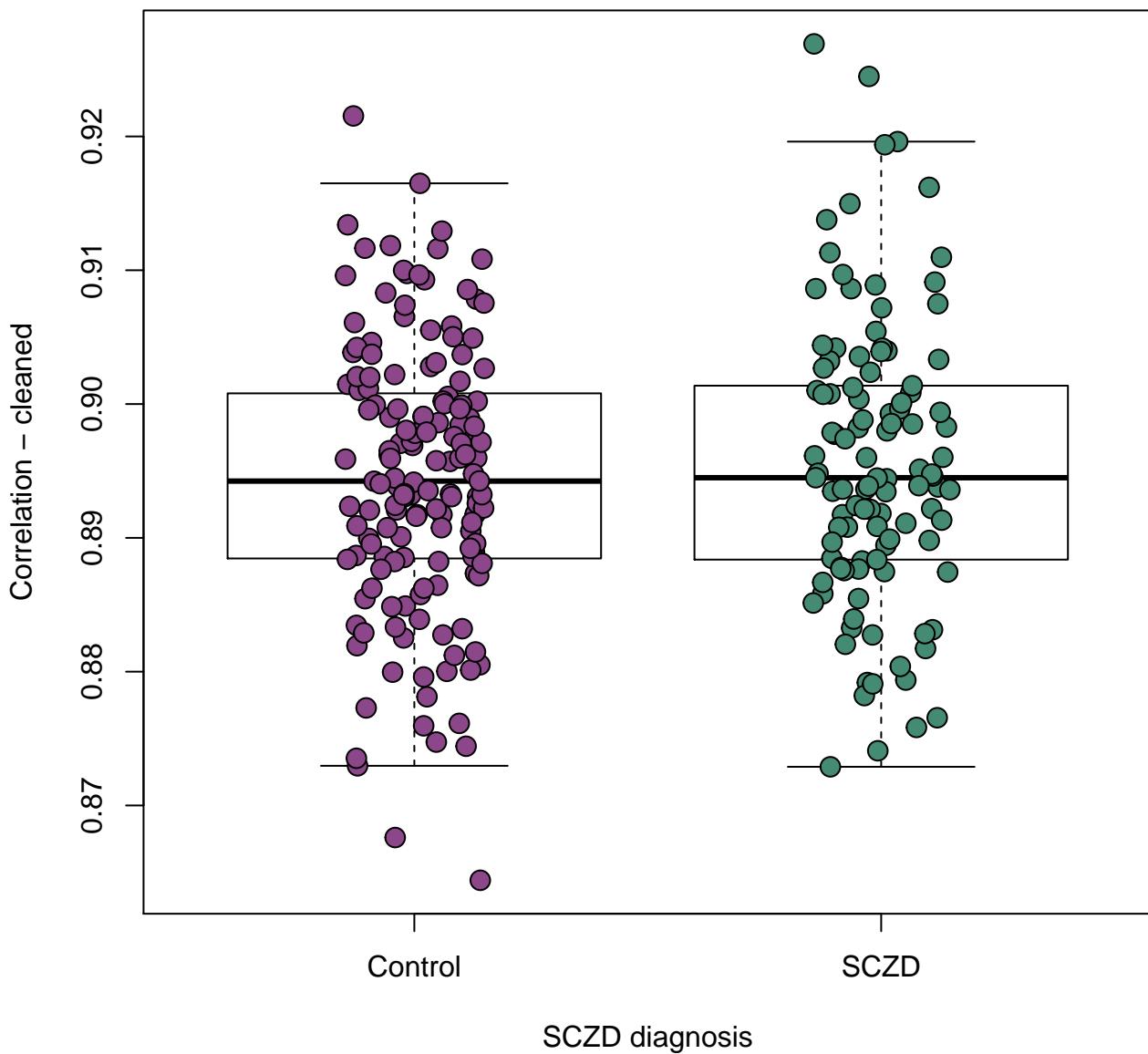
p-value: 0.00933



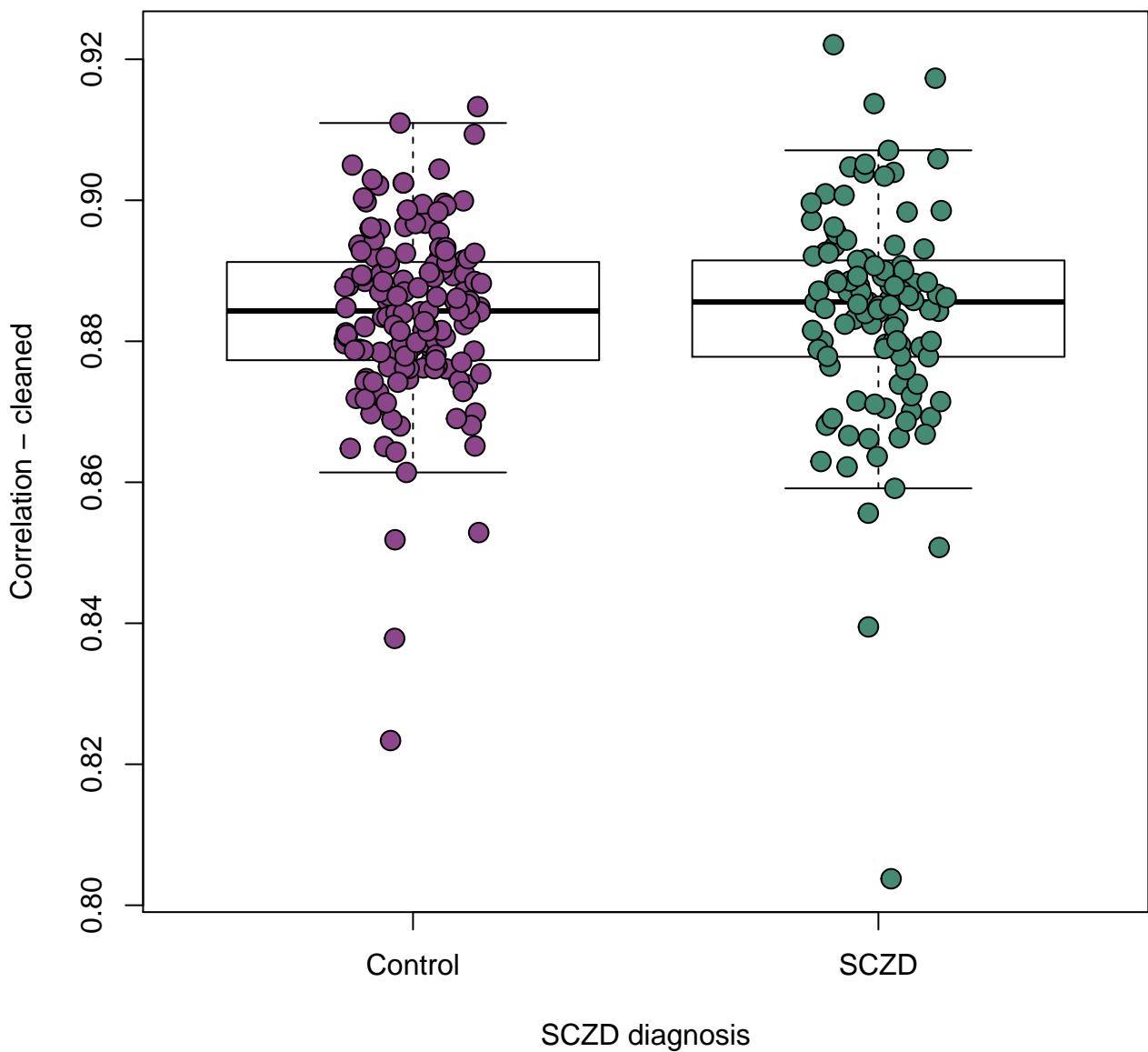
hsa05100: Bacterial invasion of epithelial cells
p-value: 0.113



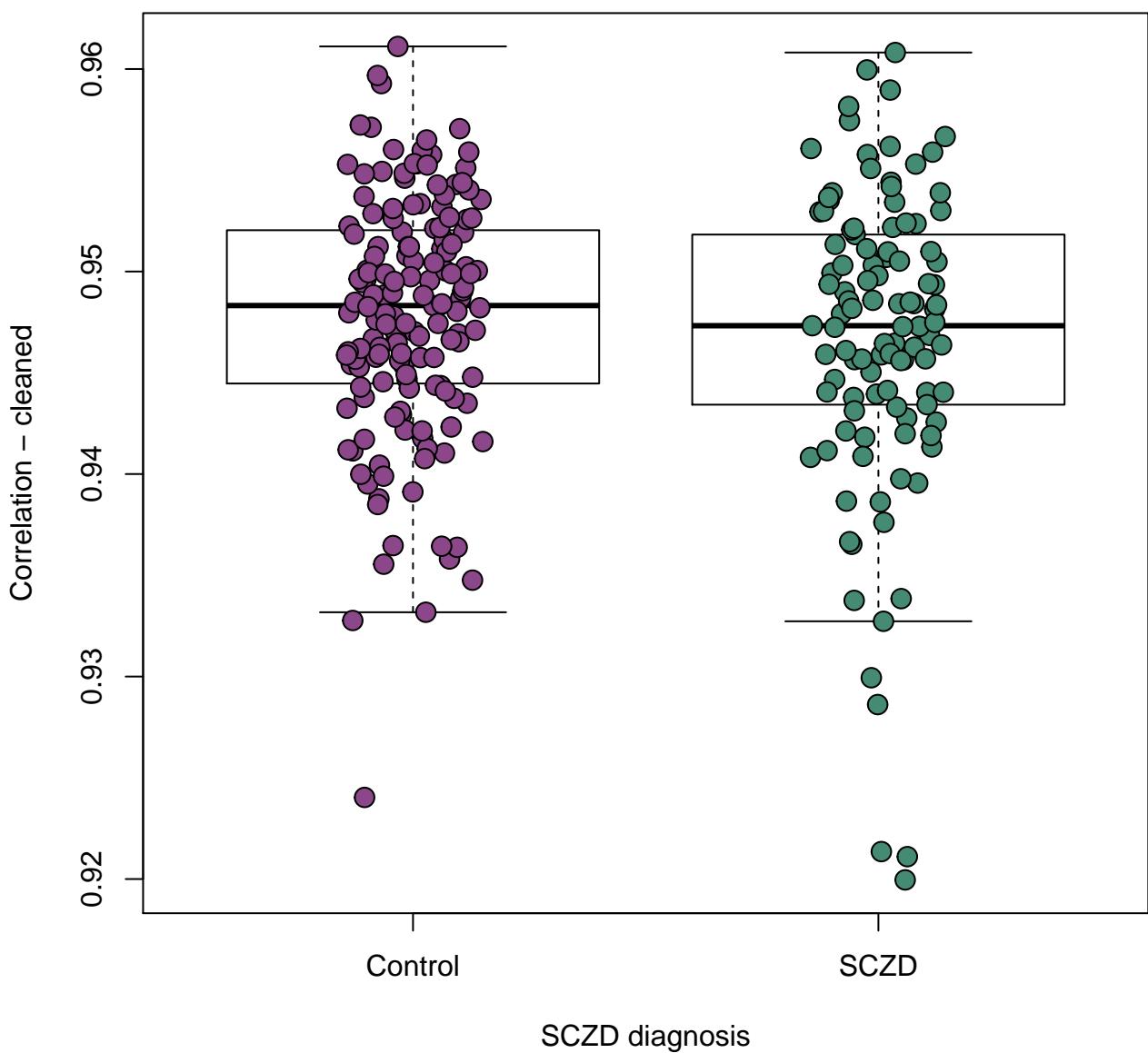
hsa05110: Vibrio cholerae infection
p-value: 0.374



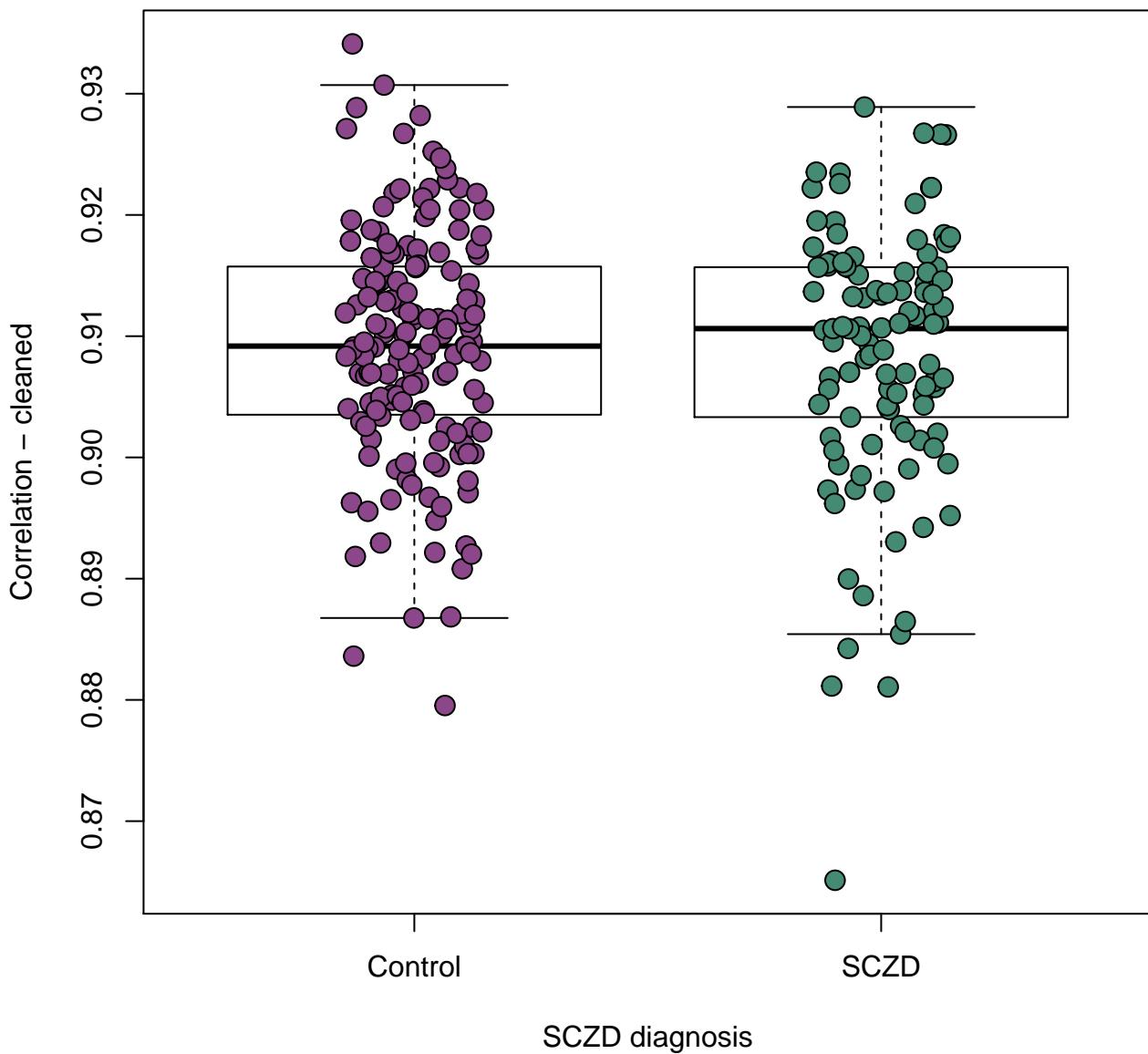
hsa05120: Epithelial cell signaling in Helicobacter pylori infection
p-value: 0.91



hsa05130: Pathogenic Escherichia coli infection
p-value: 0.162

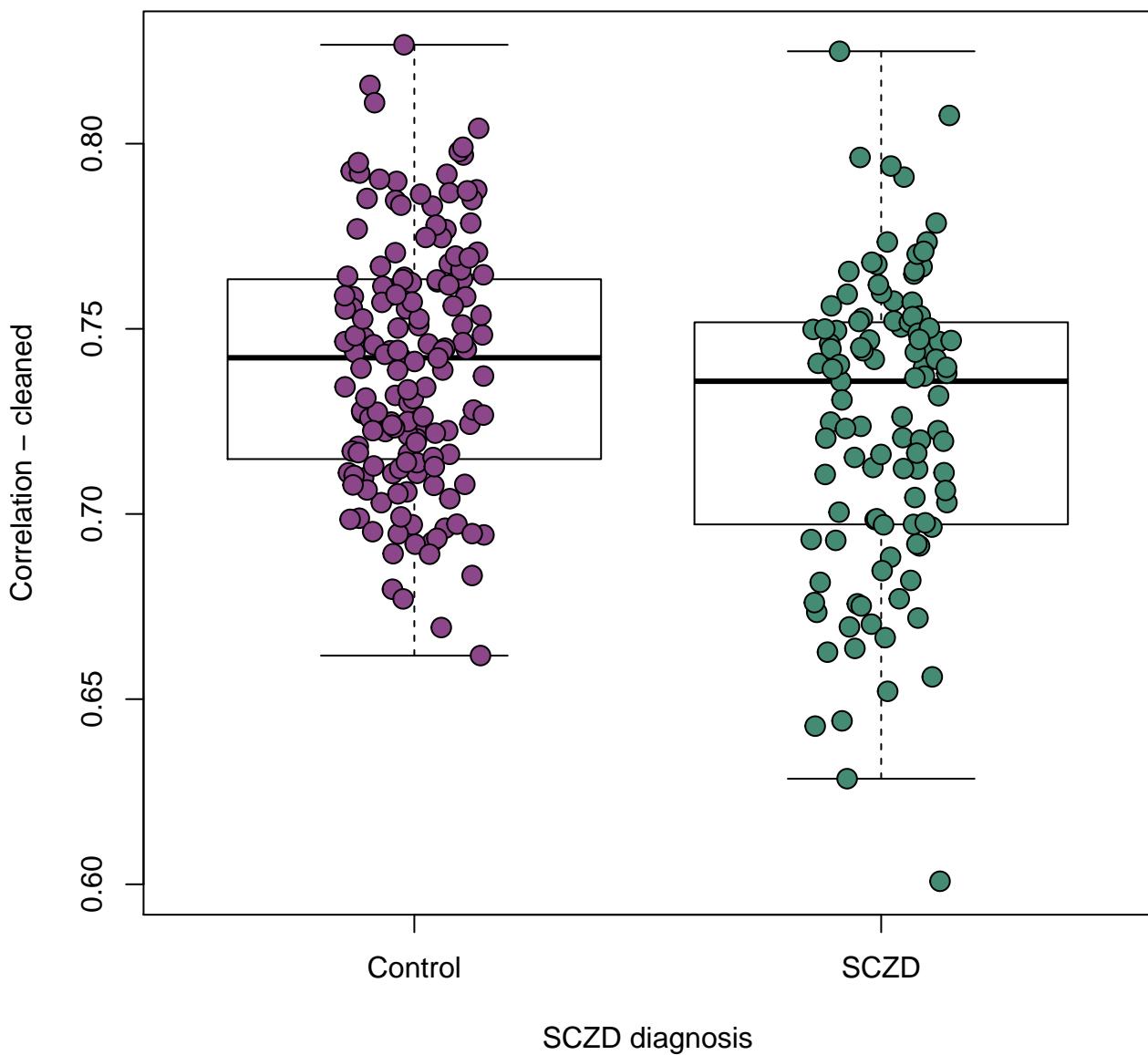


hsa05131: Shigellosis
p-value: 0.617

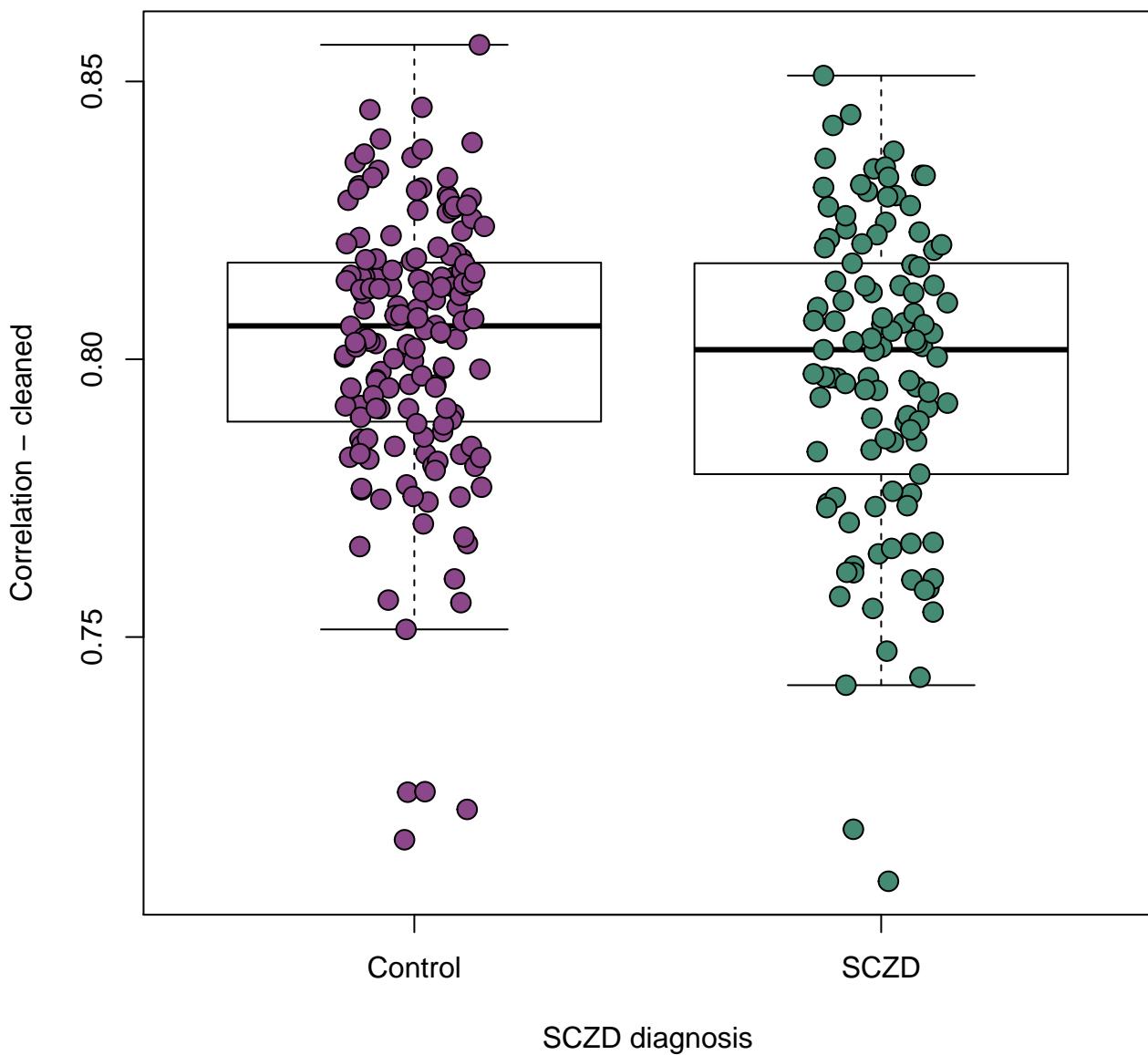


hsa05140: Leishmaniasis

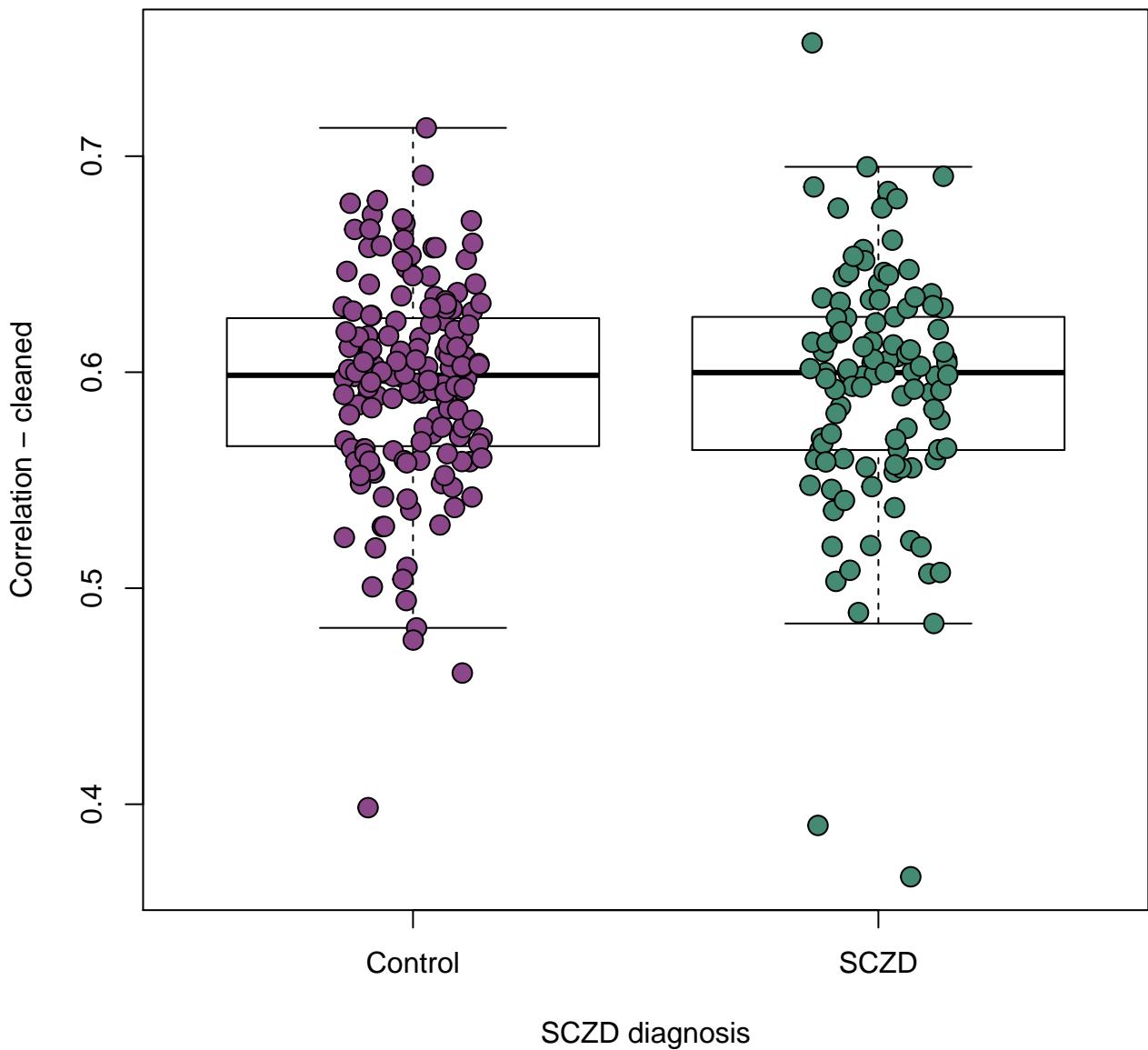
p-value: 0.000597



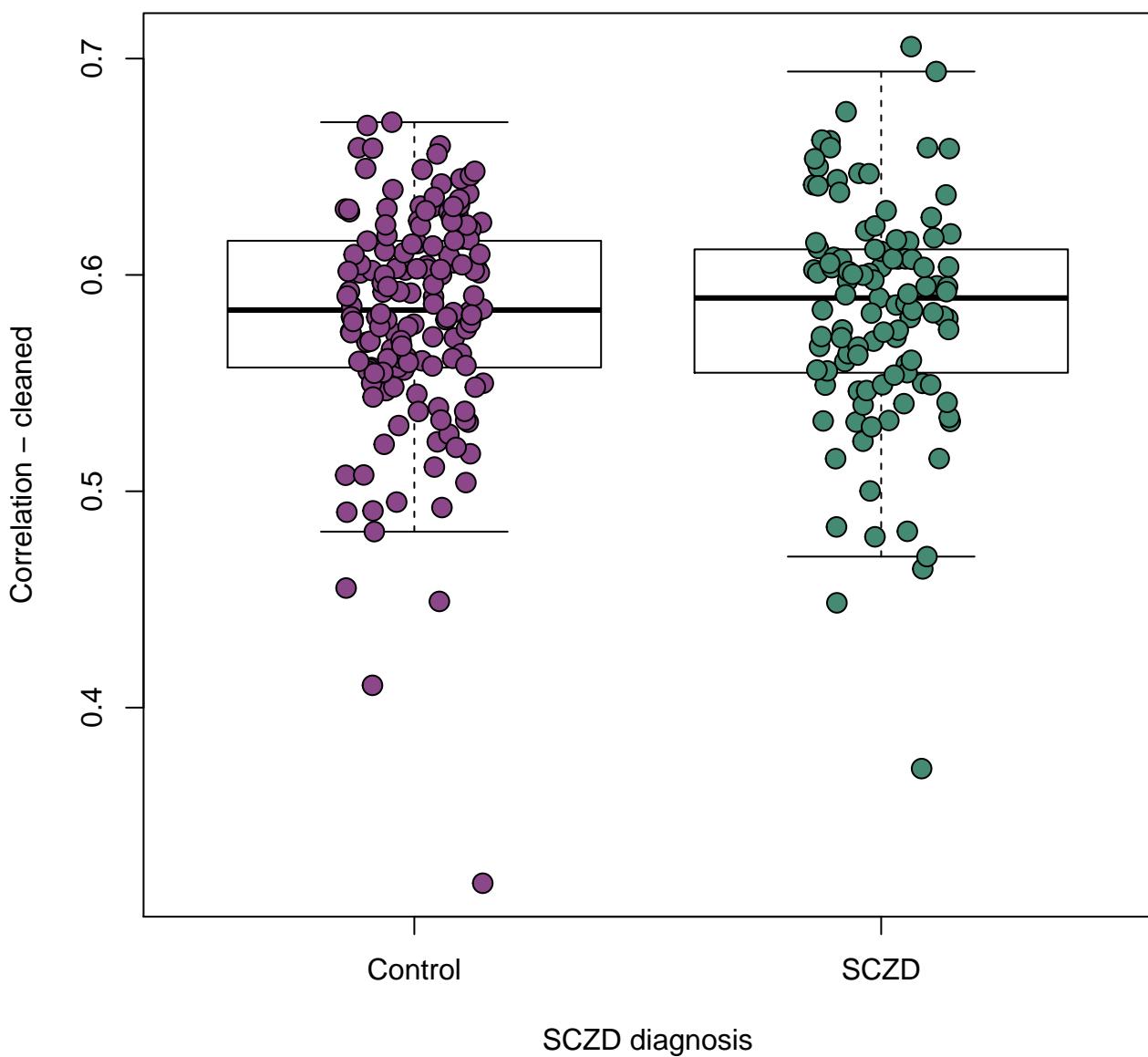
hsa05142: Chagas disease (American trypanosomiasis)
p-value: 0.113



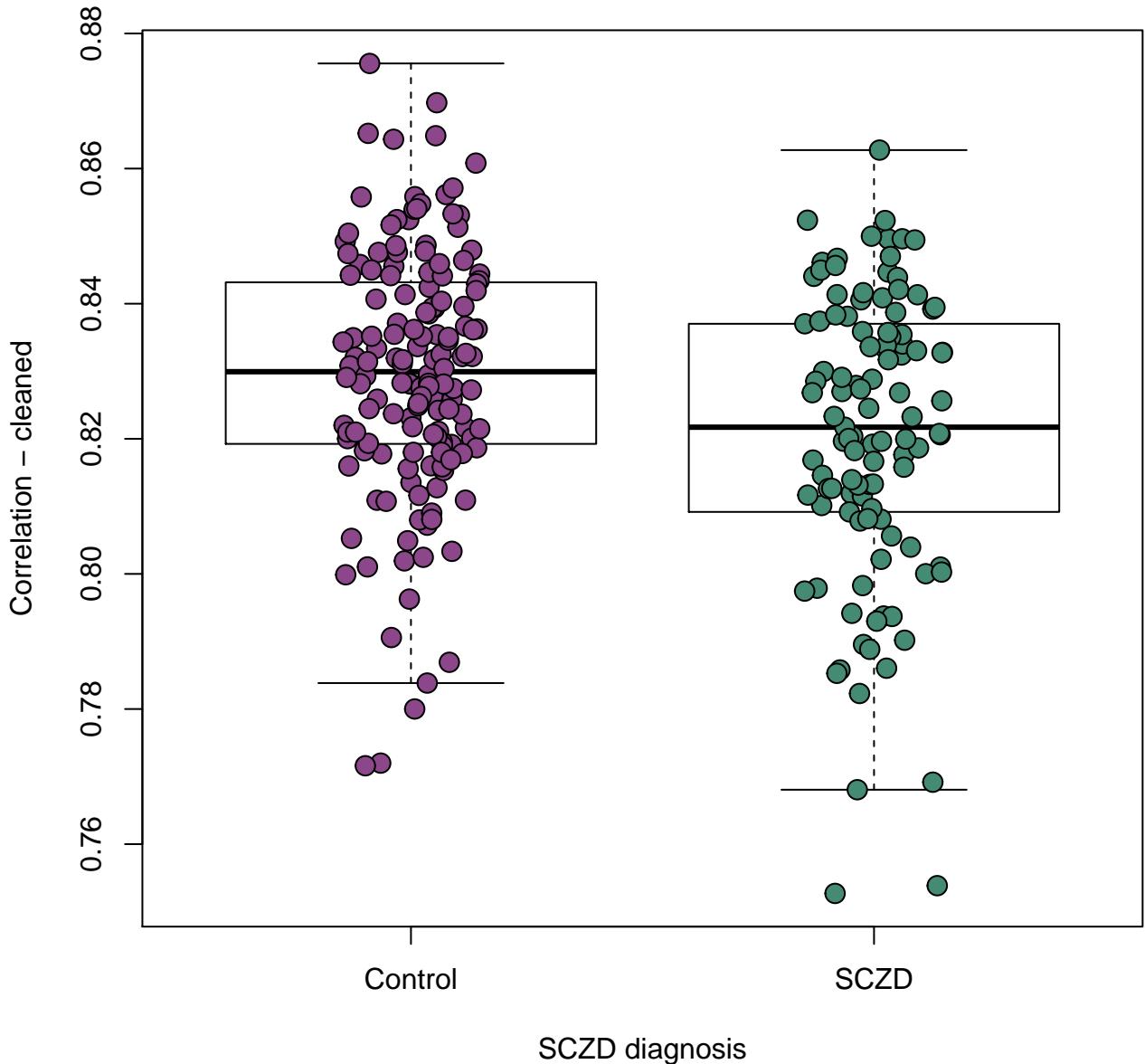
hsa05143: African trypanosomiasis
p-value: 0.795



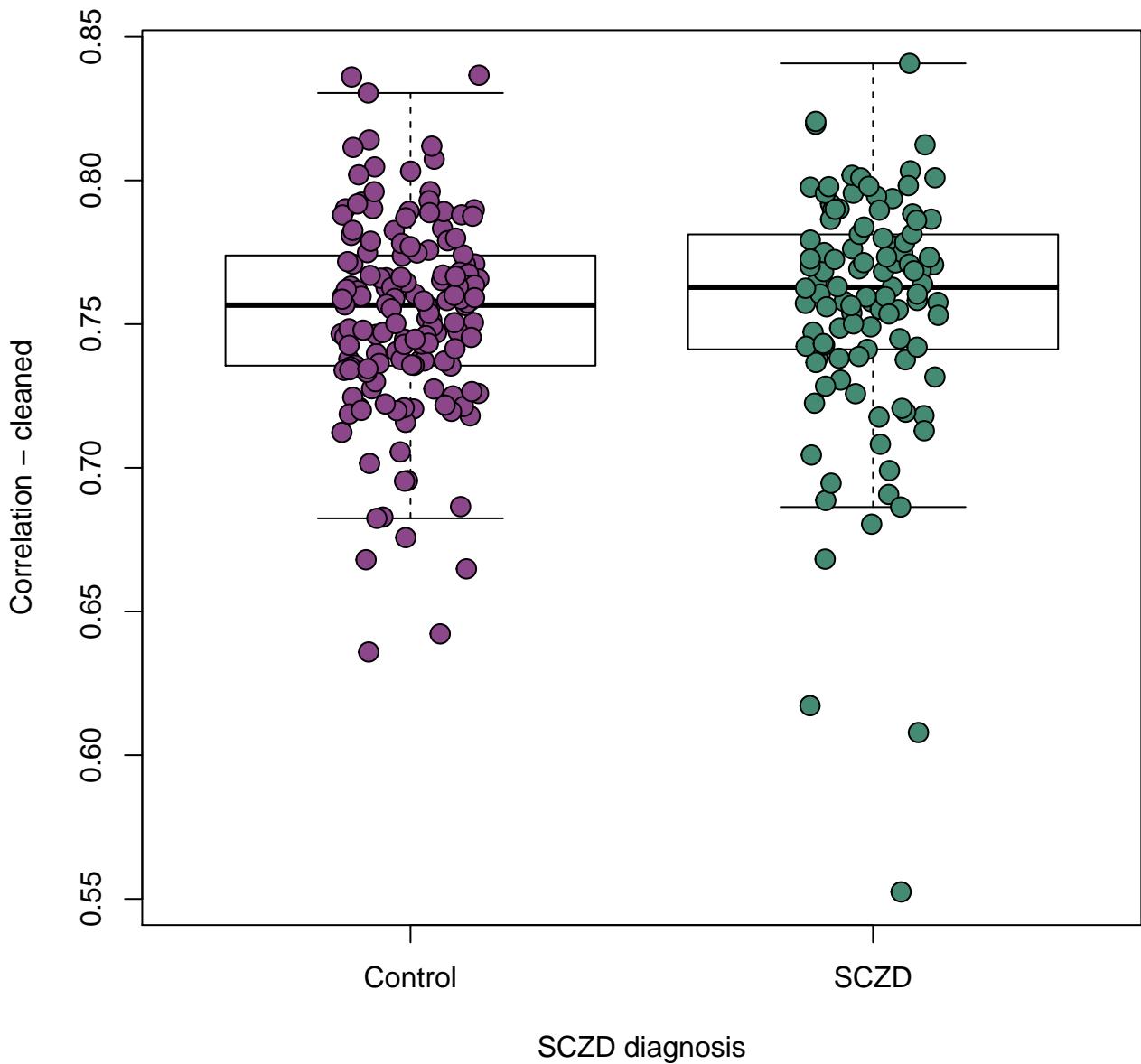
hsa05144: Malaria
p-value: 0.805



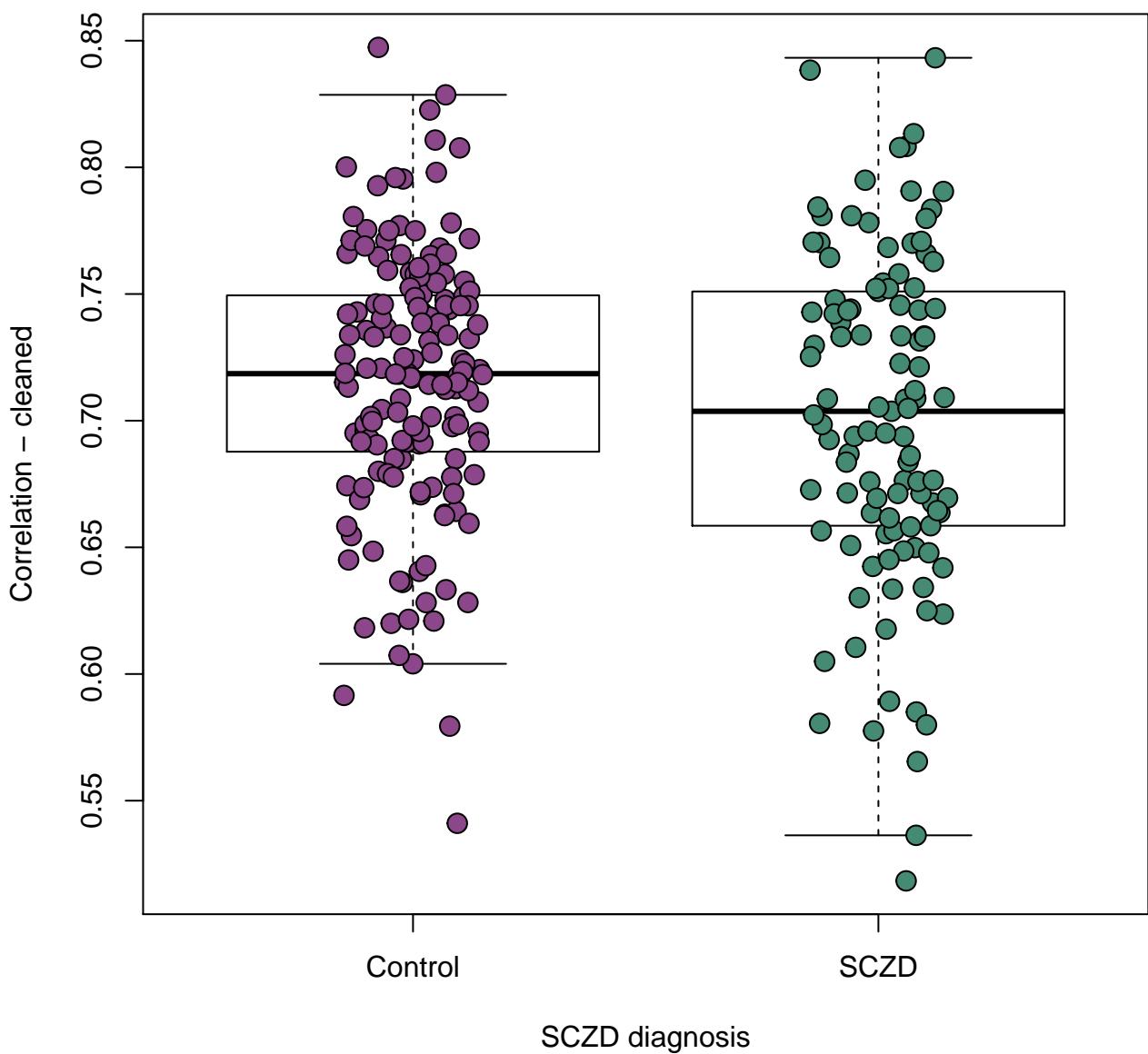
hsa05145: Toxoplasmosis
p-value: 0.000207



hsa05146: Amoebiasis
p-value: 0.535

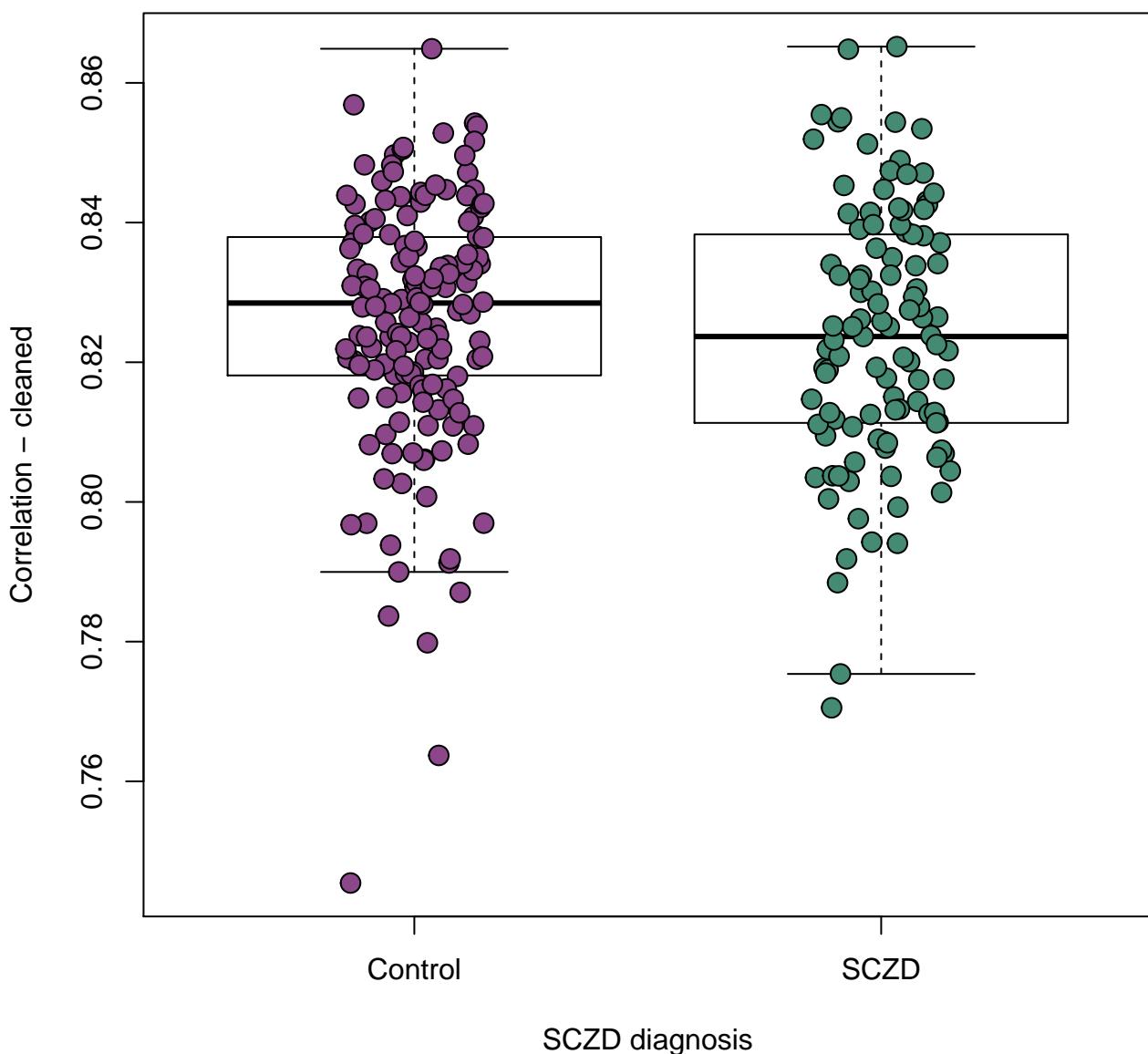


hsa05150: Staphylococcus aureus infection
p-value: 0.0507

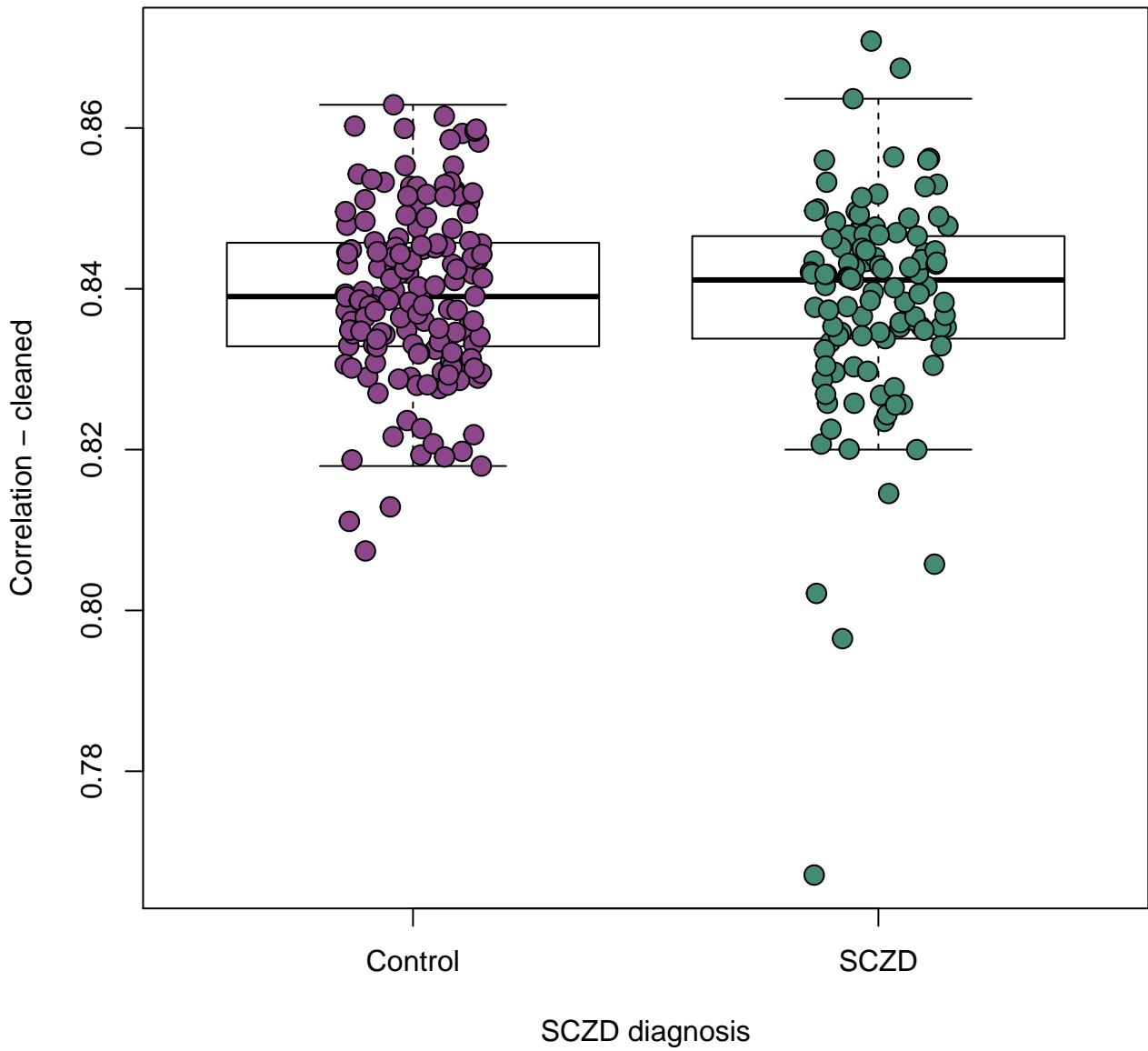


hsa05160: Hepatitis C

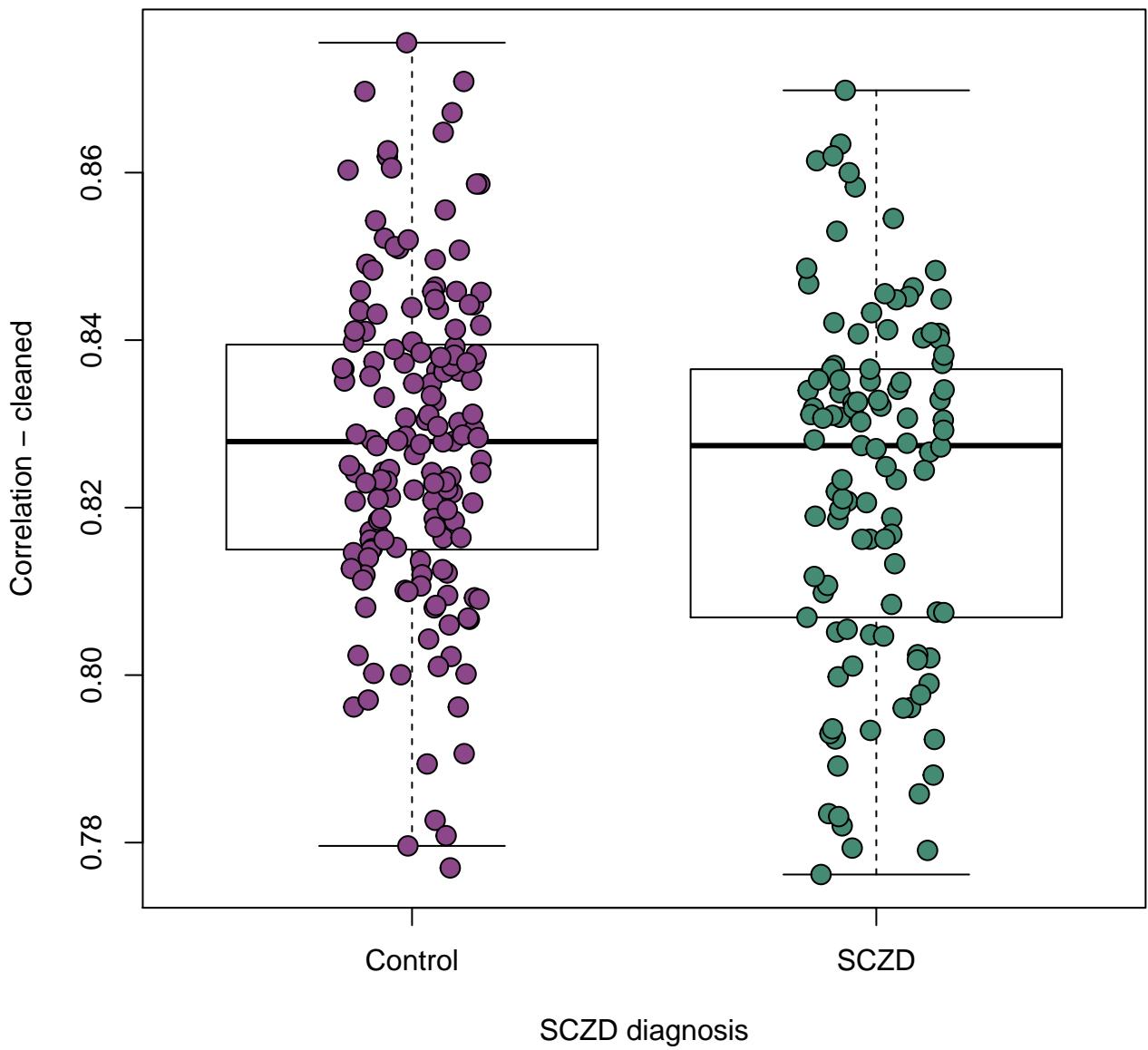
p-value: 0.35



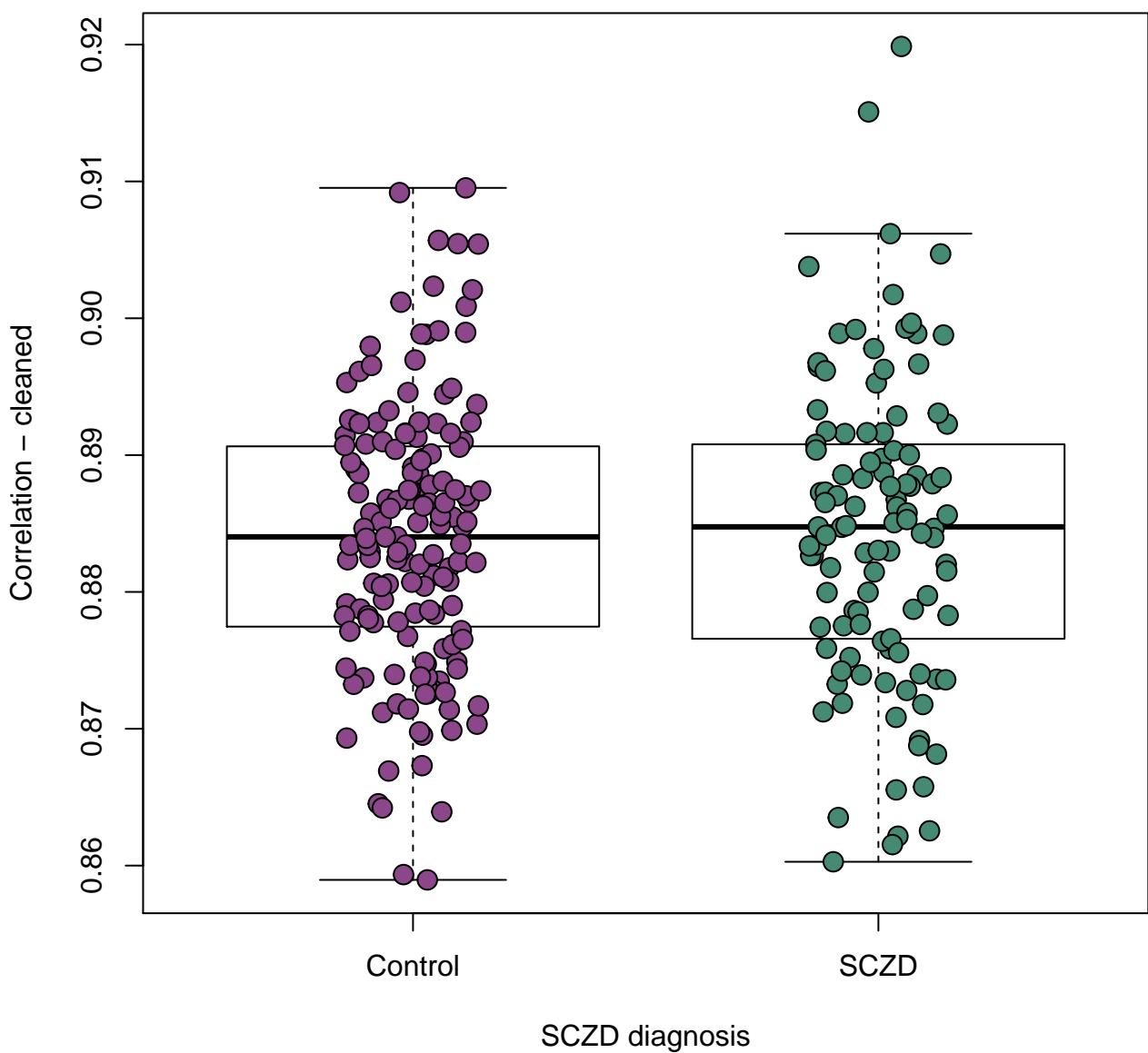
hsa05200: Pathways in cancer
p-value: 0.505



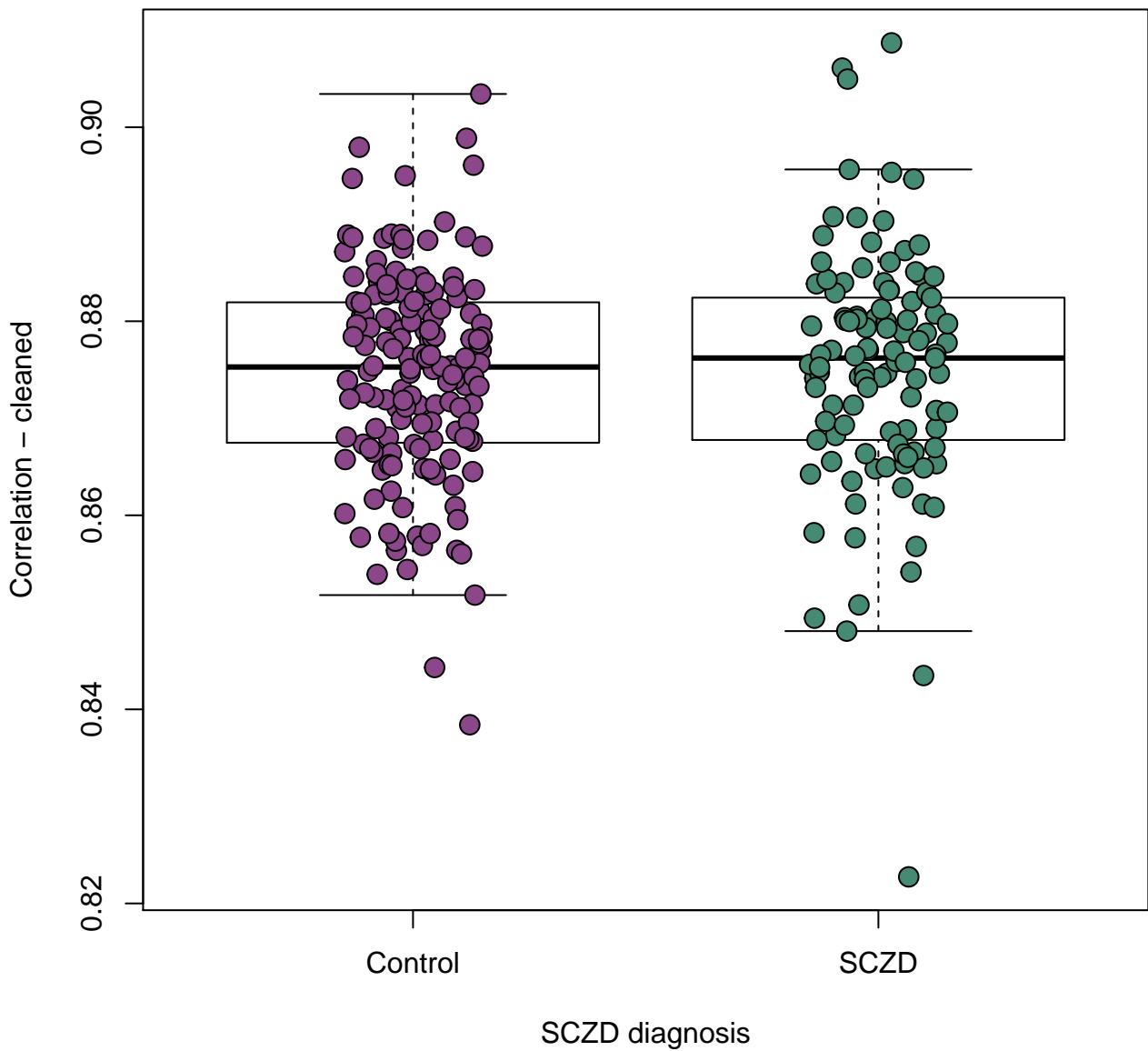
hsa05210: Colorectal cancer
p-value: 0.0648



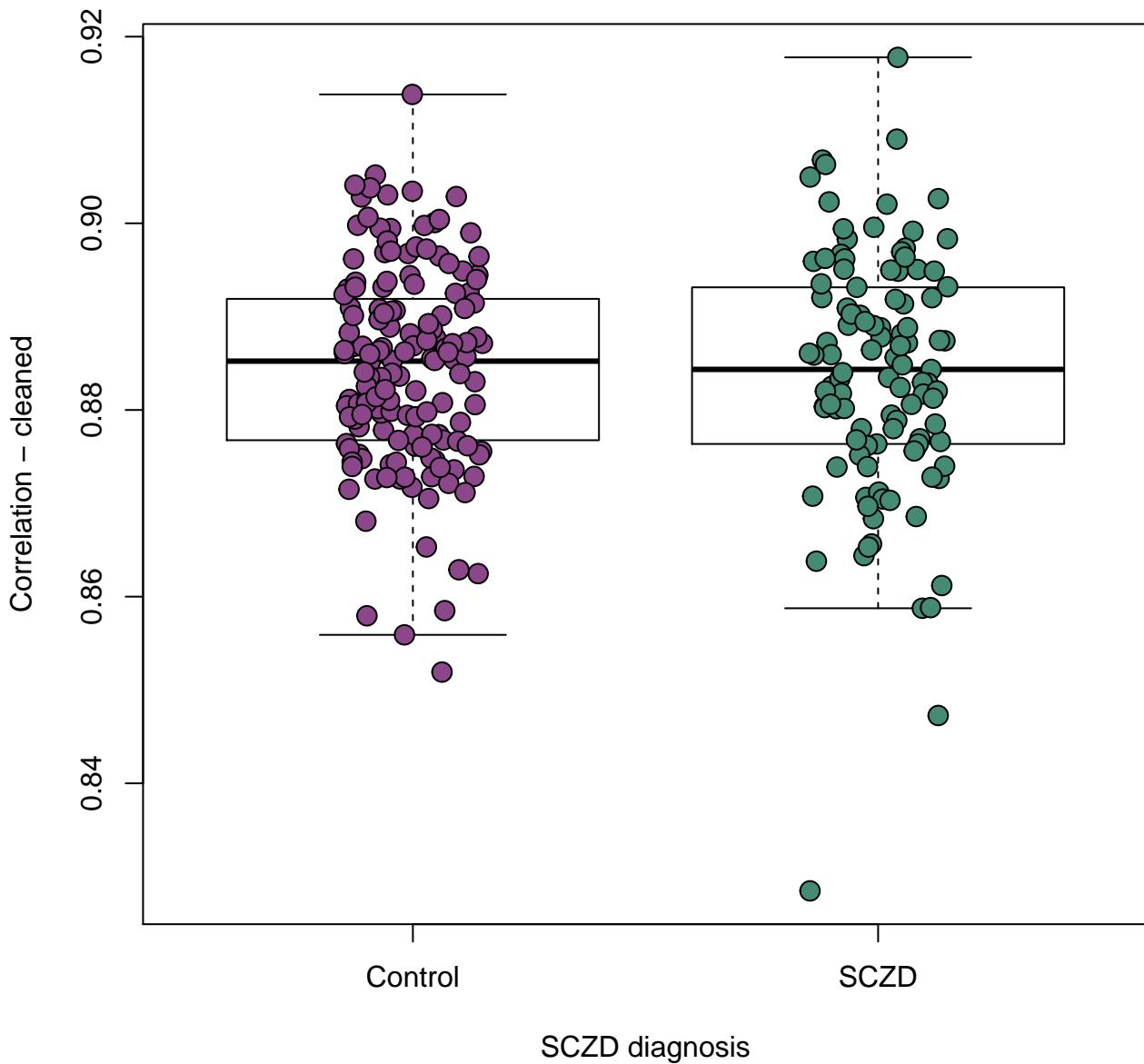
hsa05211: Renal cell carcinoma
p-value: 0.764



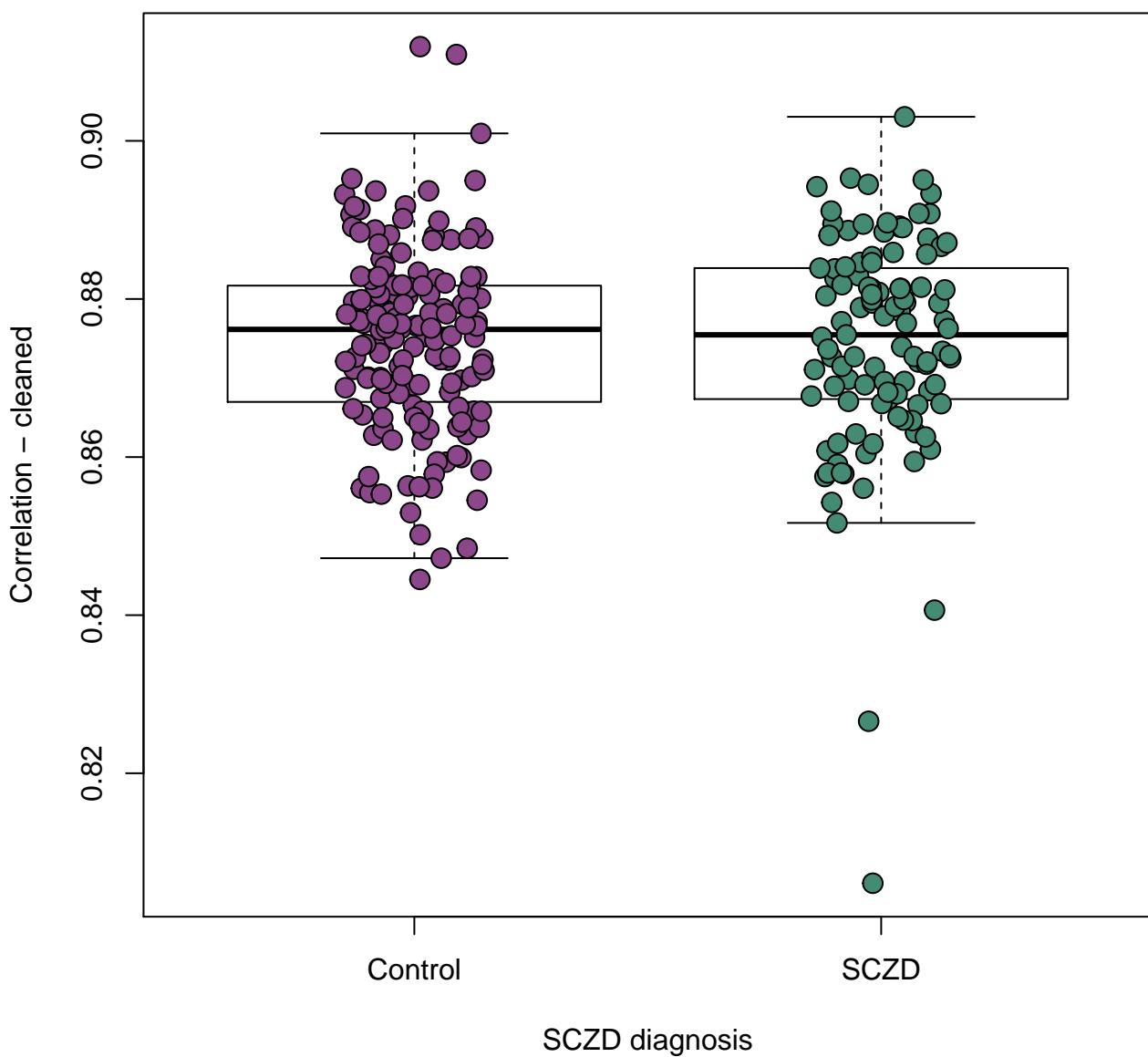
hsa05212: Pancreatic cancer
p-value: 0.694



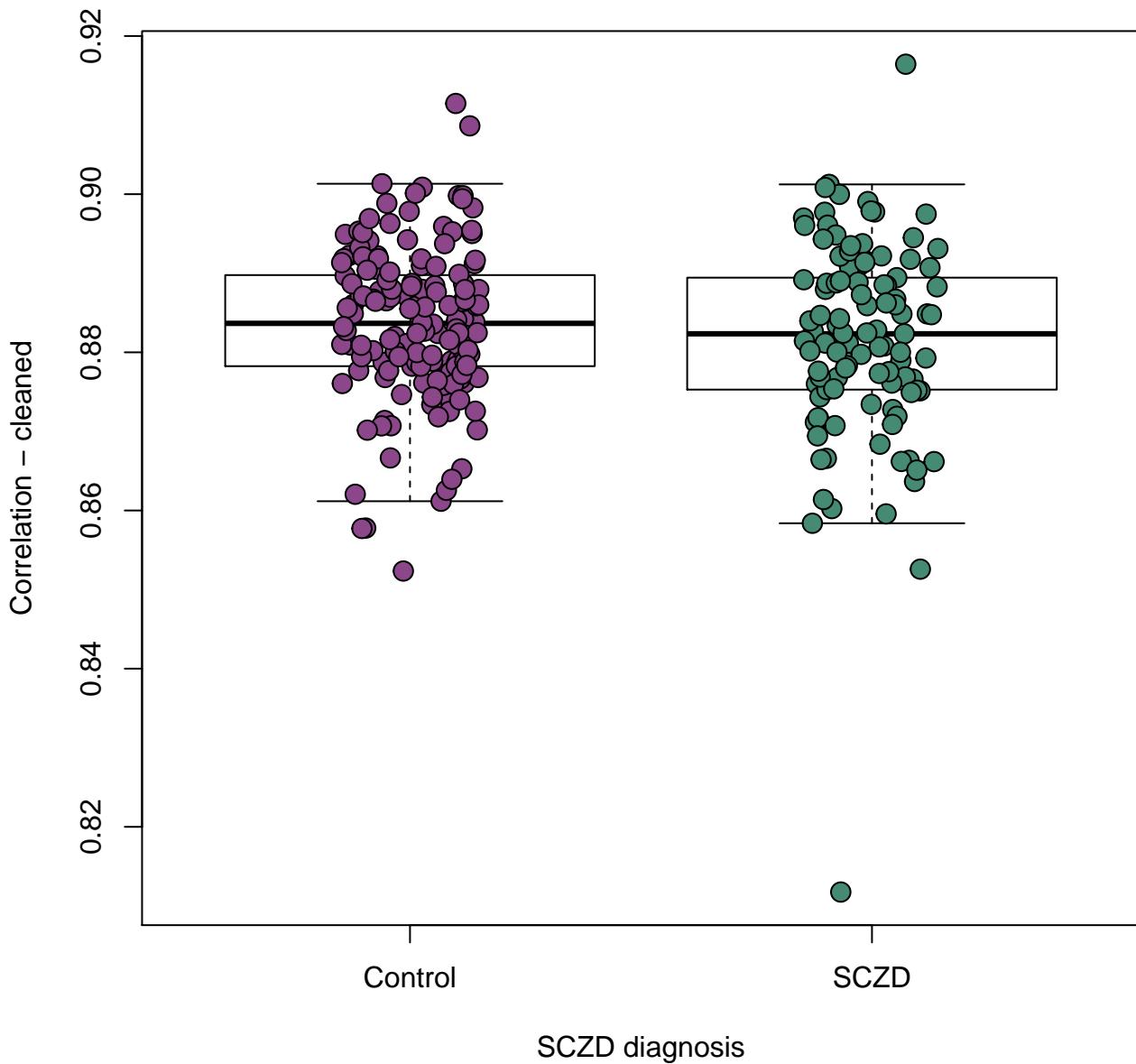
hsa05213: Endometrial cancer
p-value: 0.706



hsa05214: Glioma
p-value: 0.826

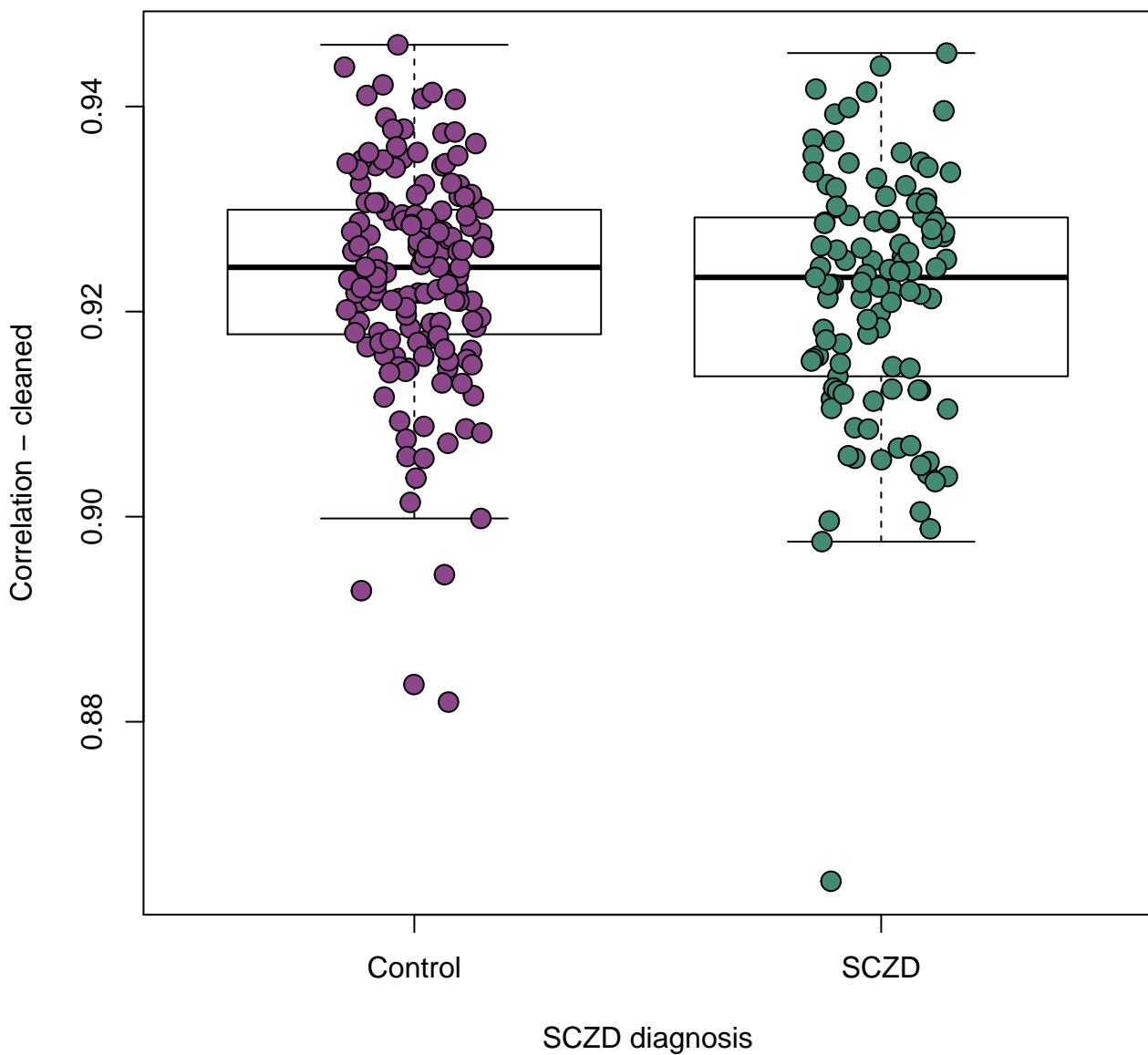


hsa05215: Prostate cancer
p-value: 0.145

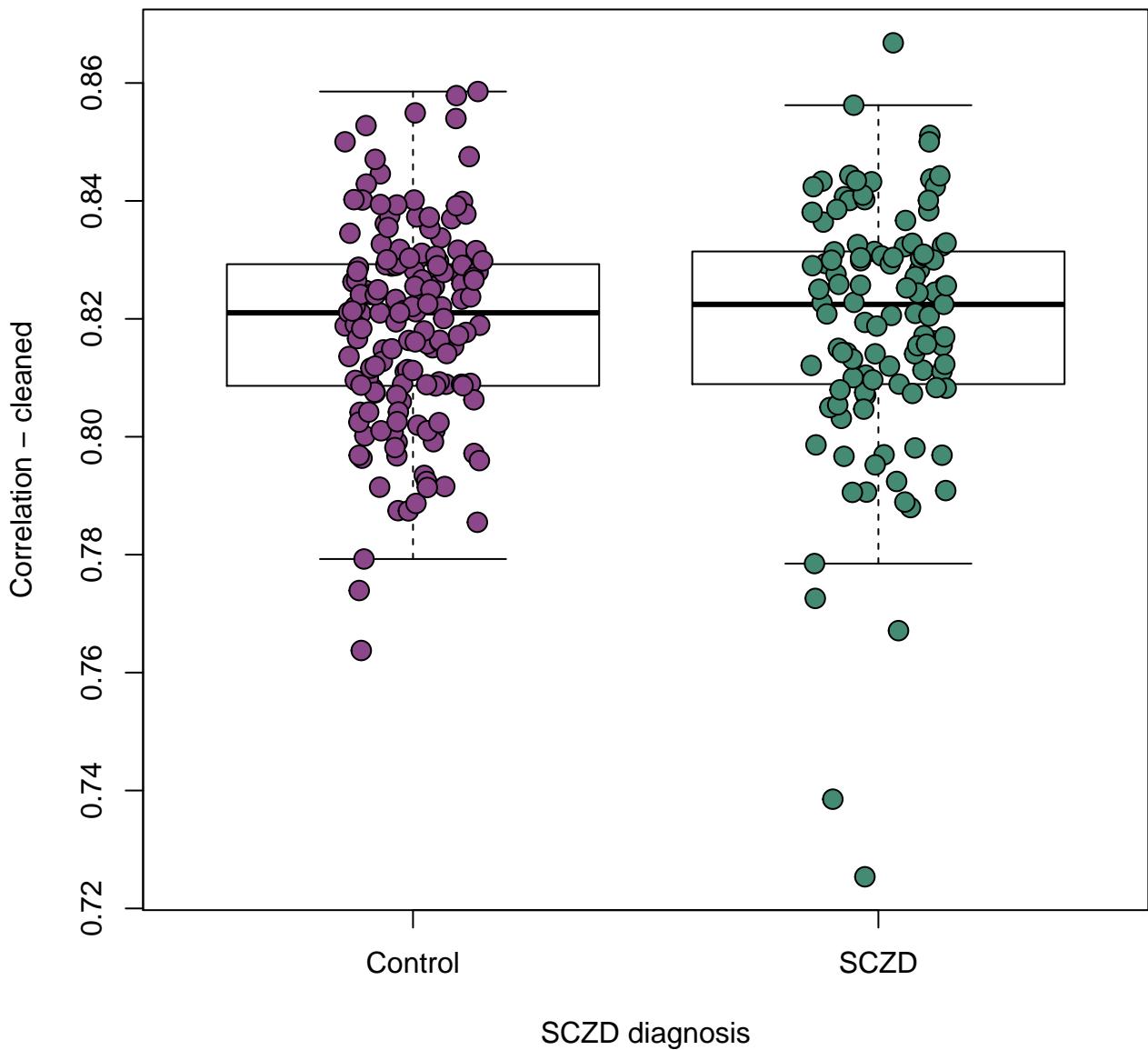


hsa05216: Thyroid cancer

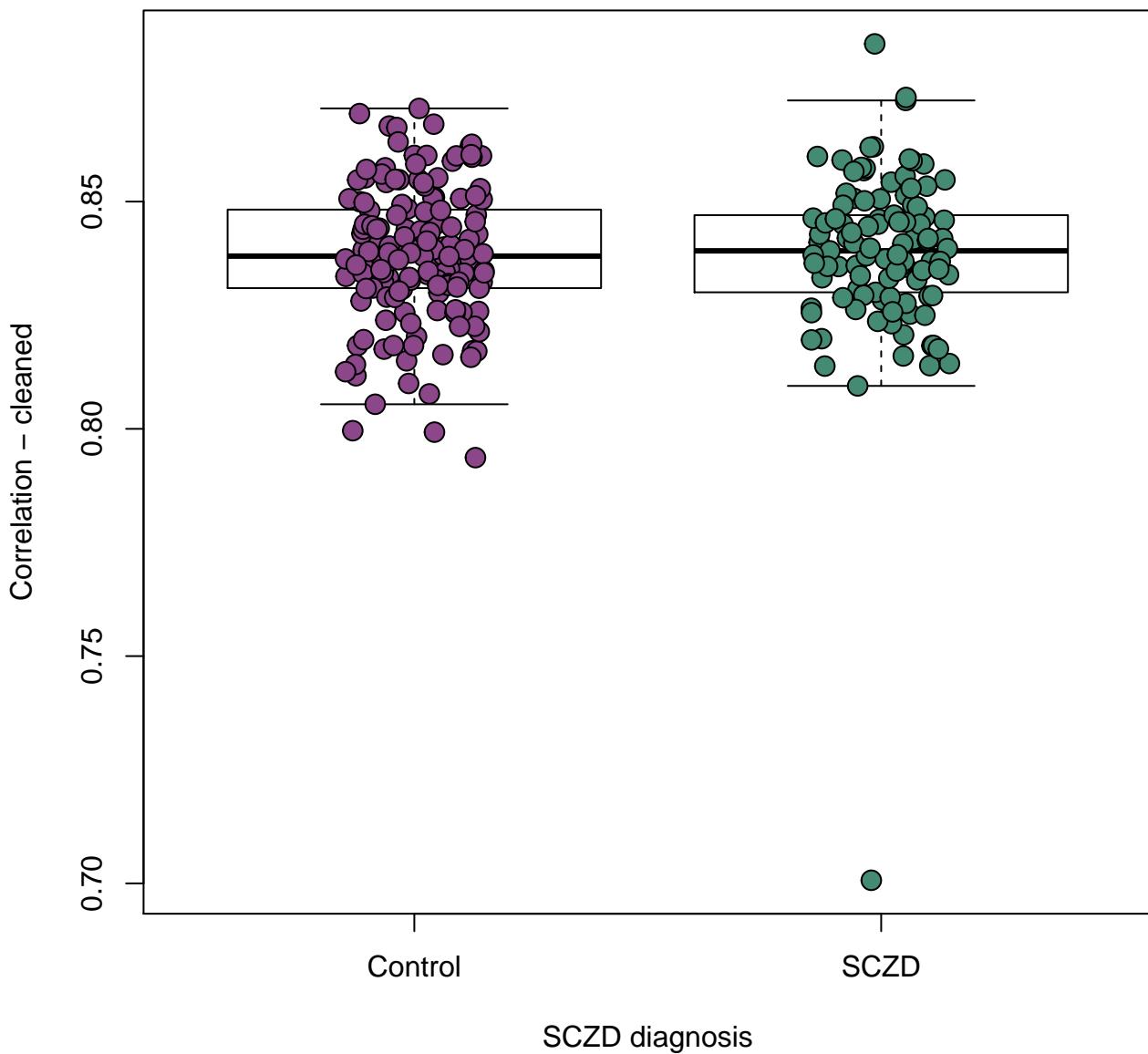
p-value: 0.185



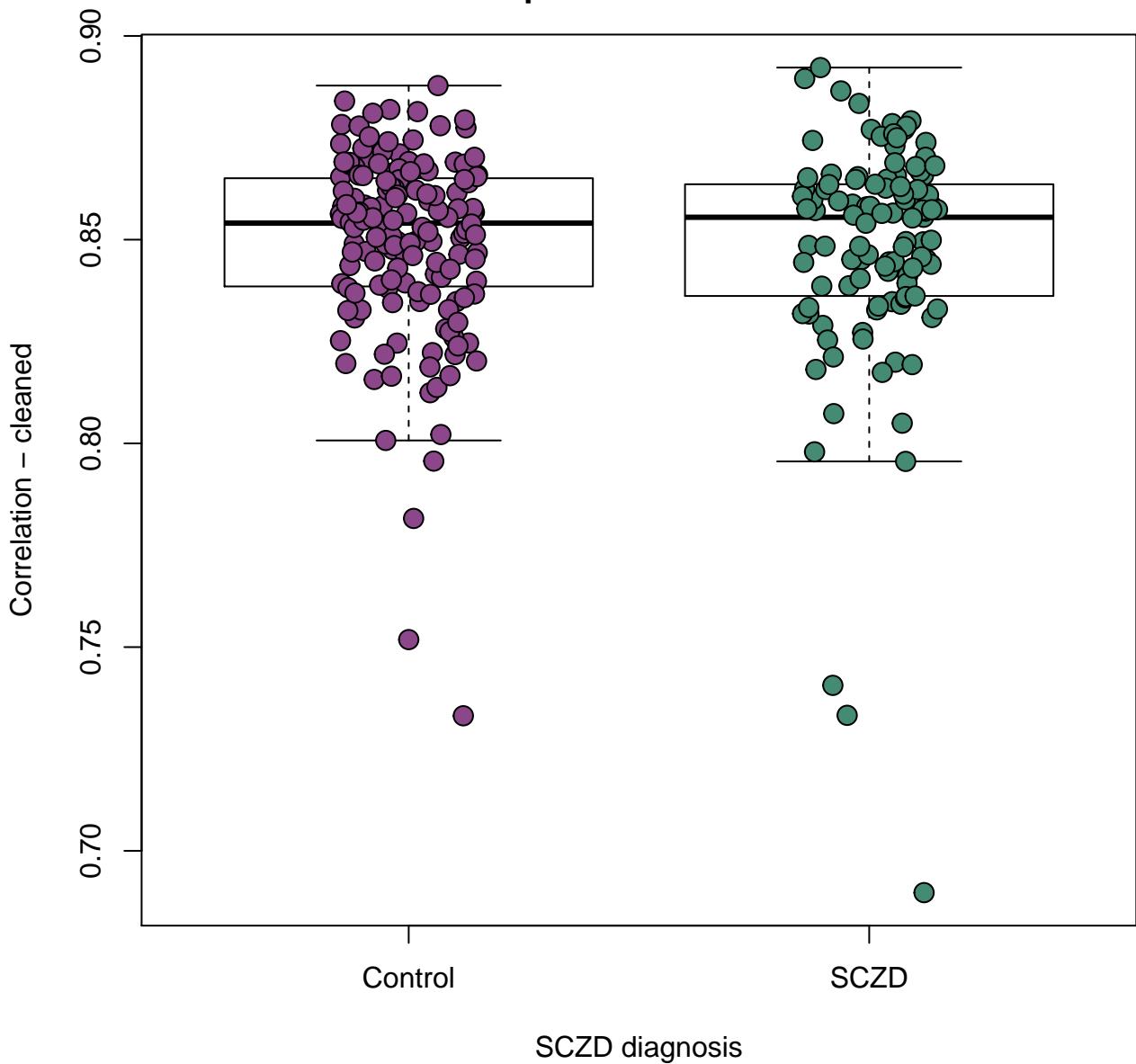
hsa05217: Basal cell carcinoma
p-value: 0.948



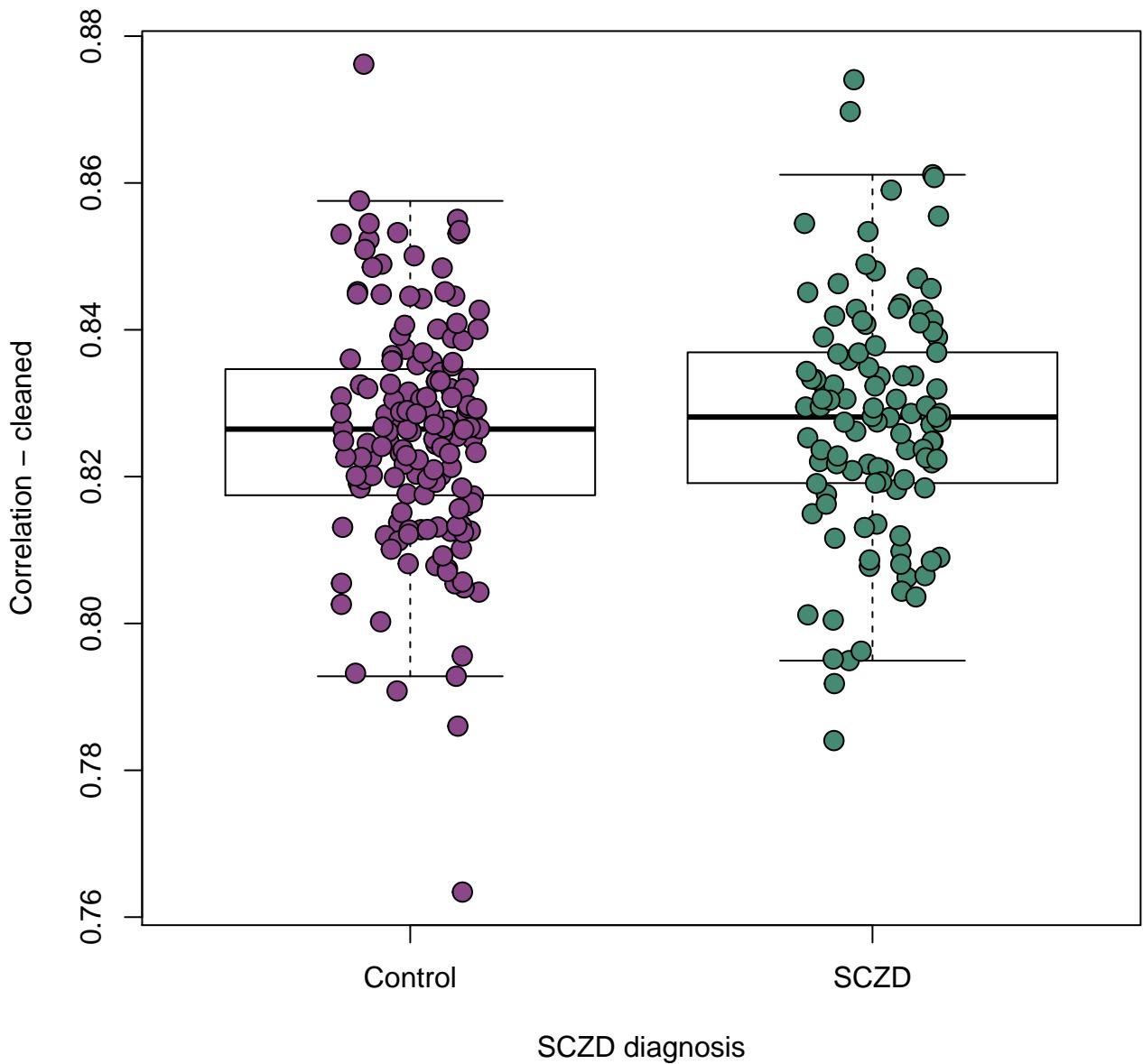
hsa05218: Melanoma
p-value: 0.904



hsa05219: Bladder cancer
p-value: 0.613

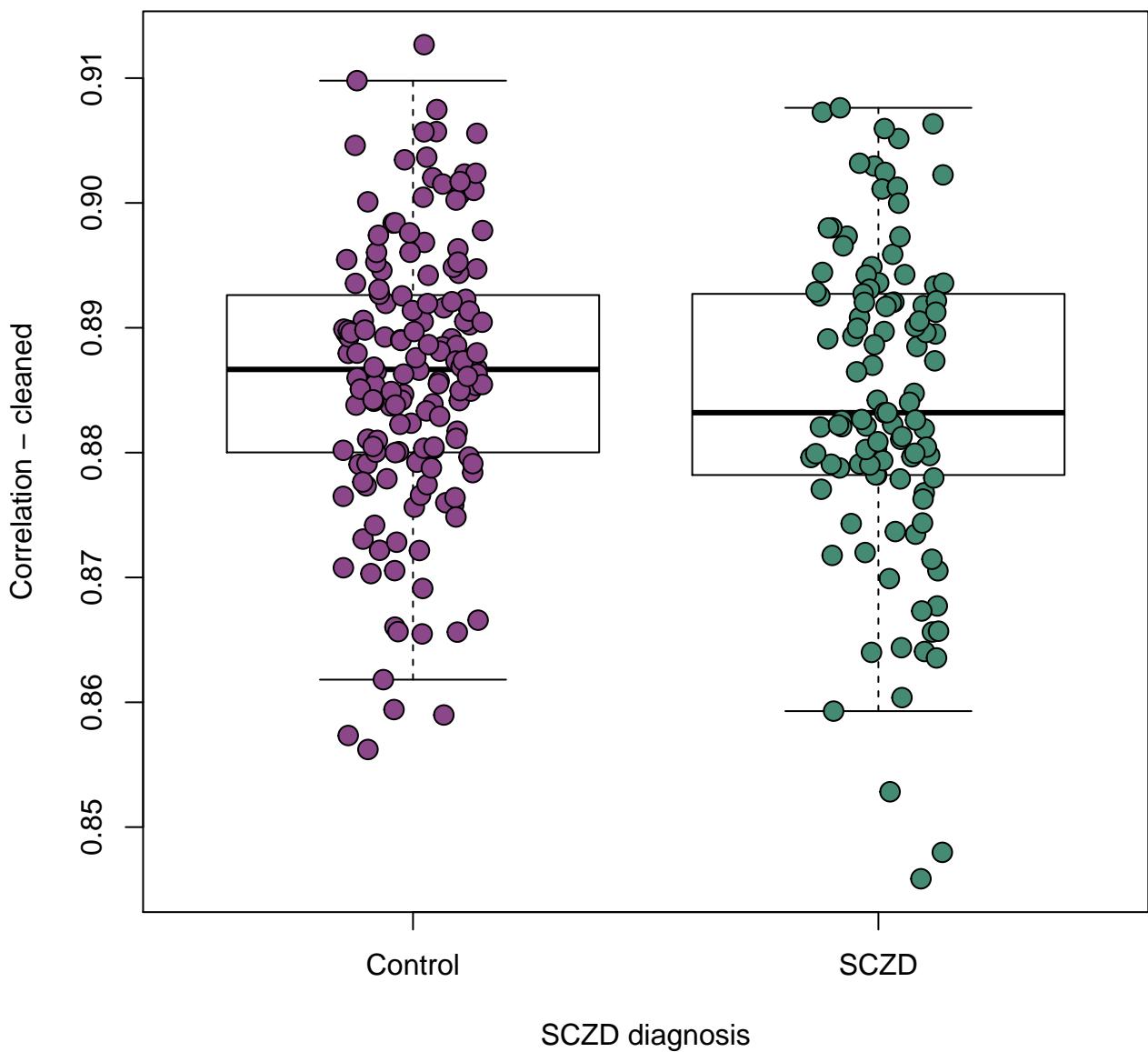


hsa05220: Chronic myeloid leukemia
p-value: 0.371

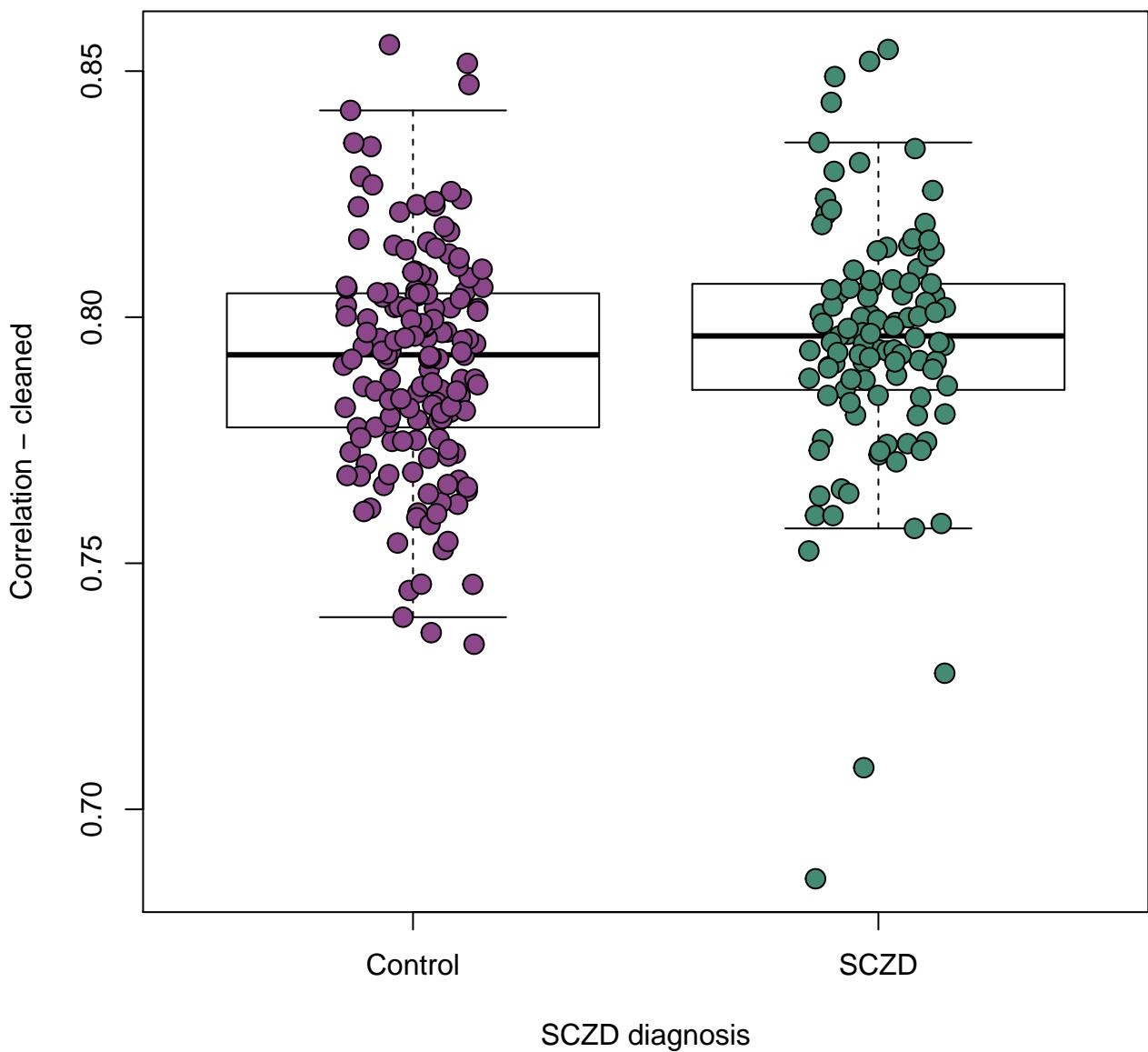


hsa05221: Acute myeloid leukemia

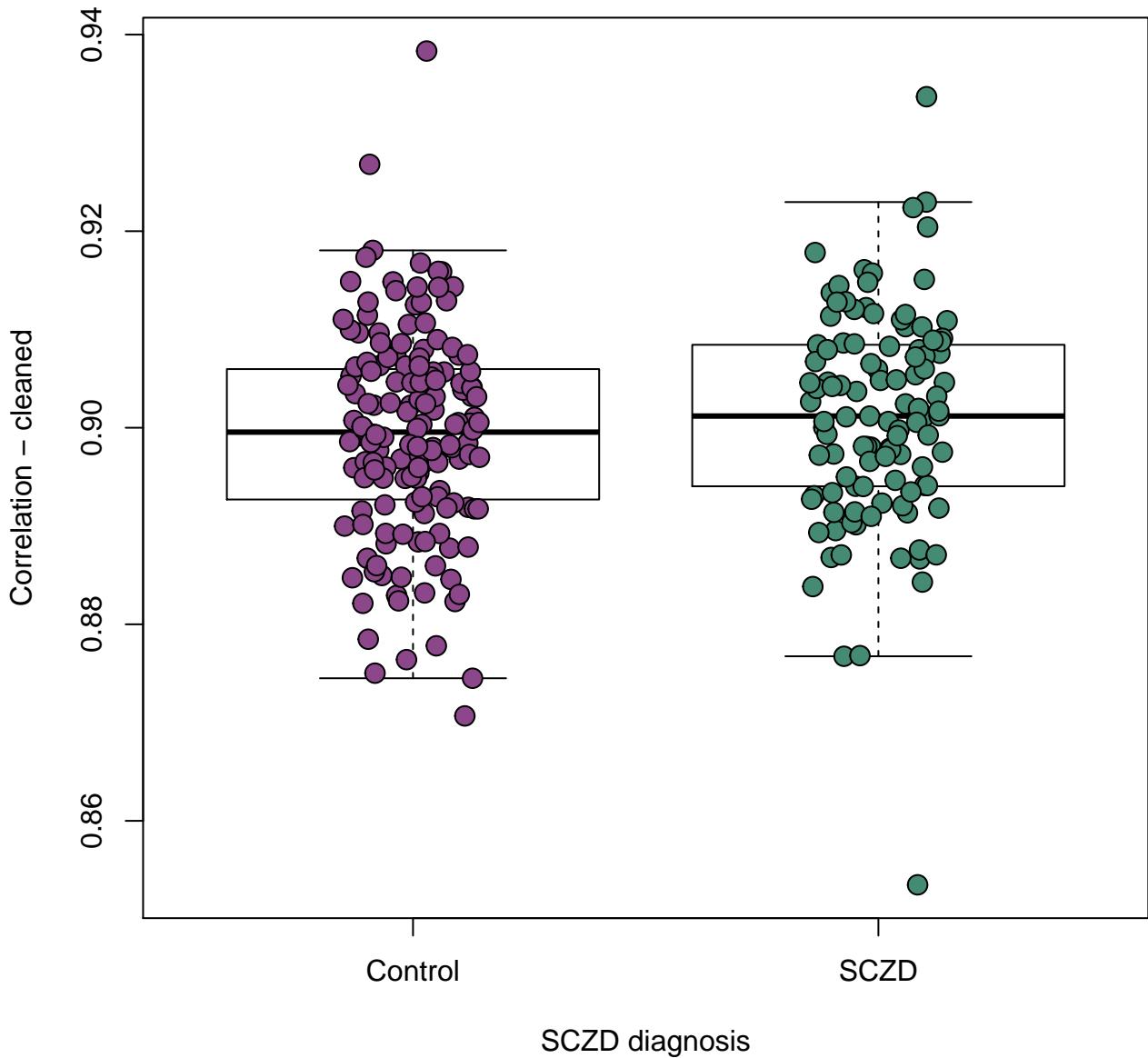
p-value: 0.143



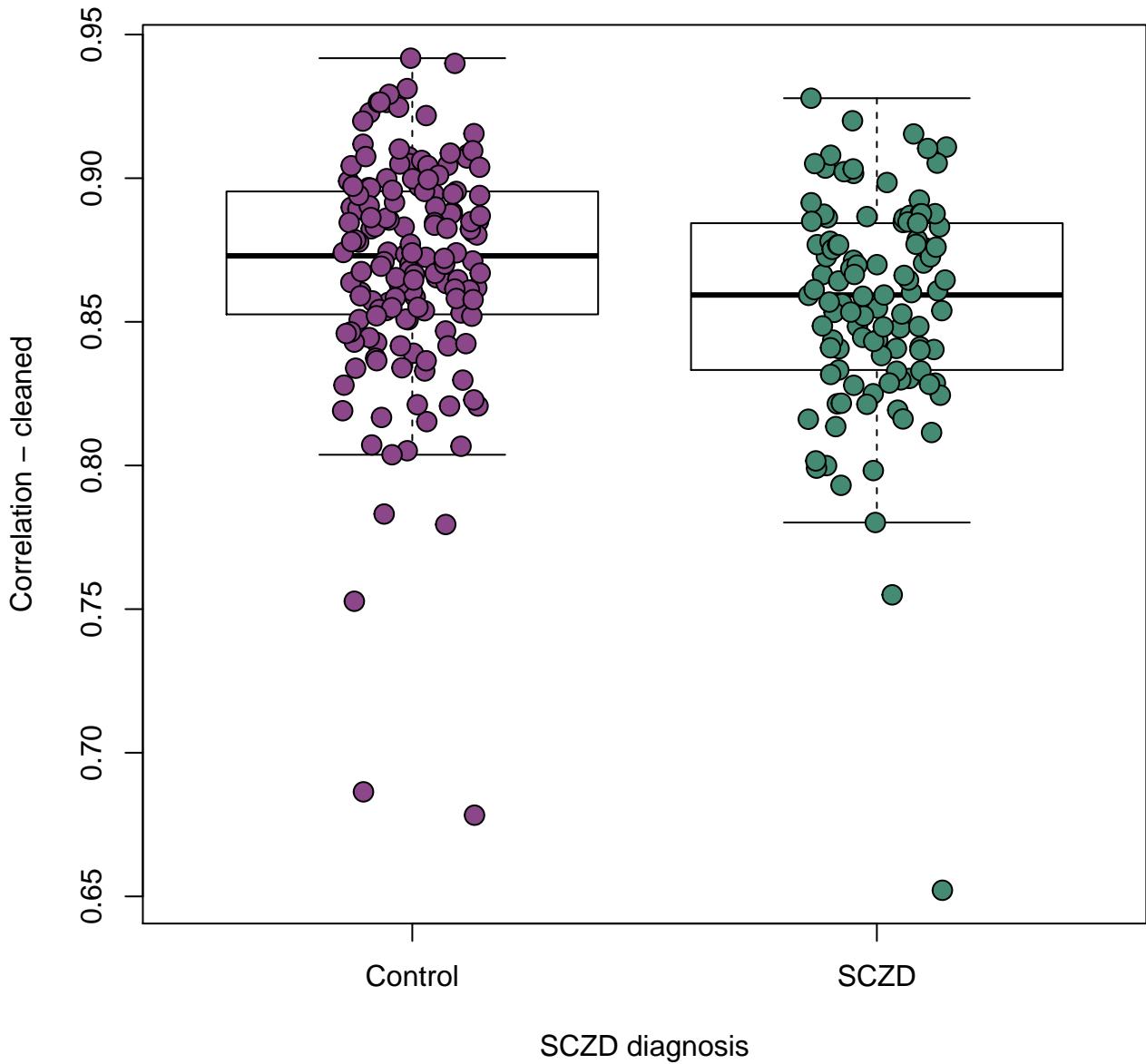
hsa05222: Small cell lung cancer
p-value: 0.207



hsa05223: Non–small cell lung cancer
p-value: 0.189

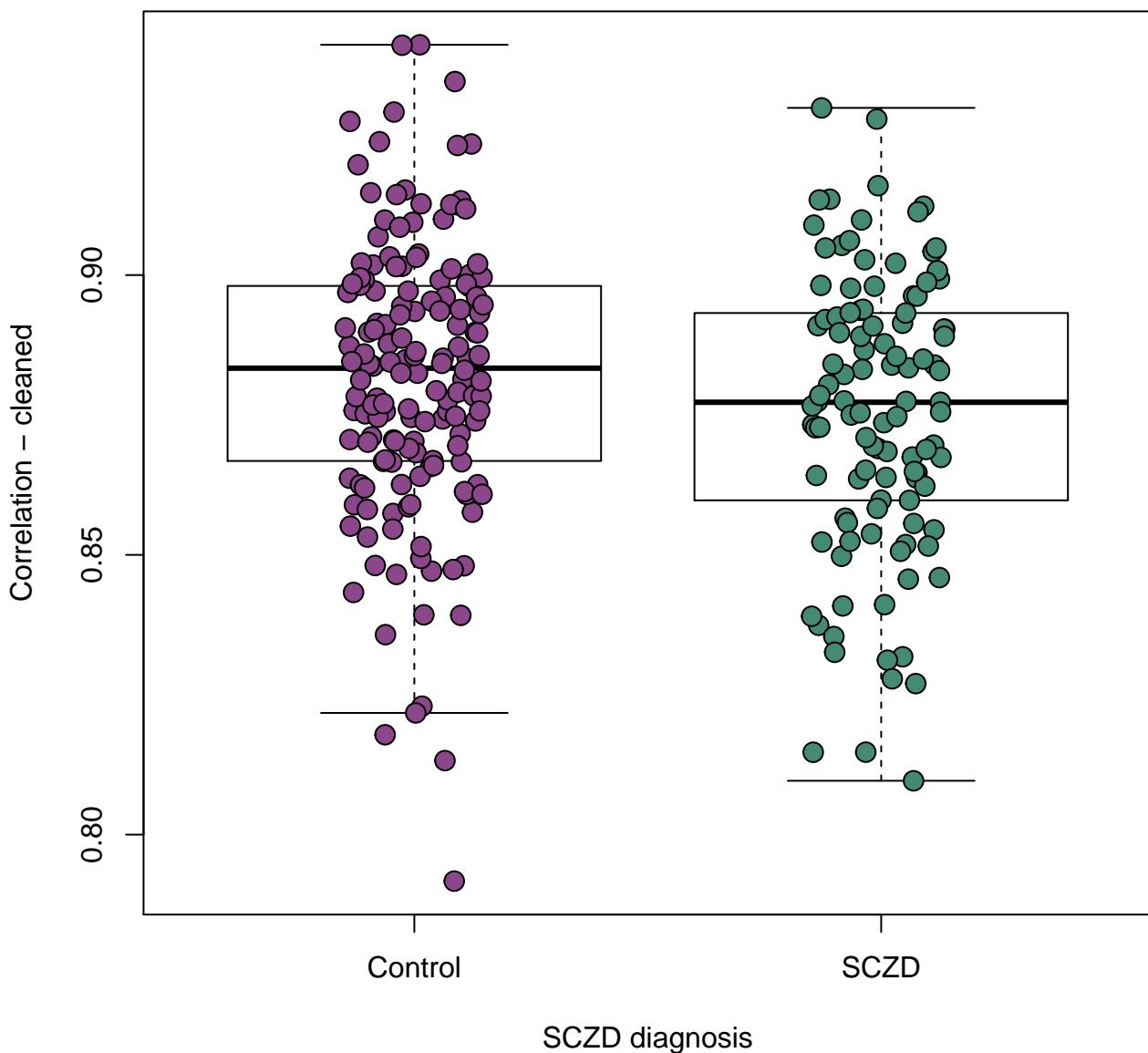


hsa05310: Asthma
p-value: 0.00652

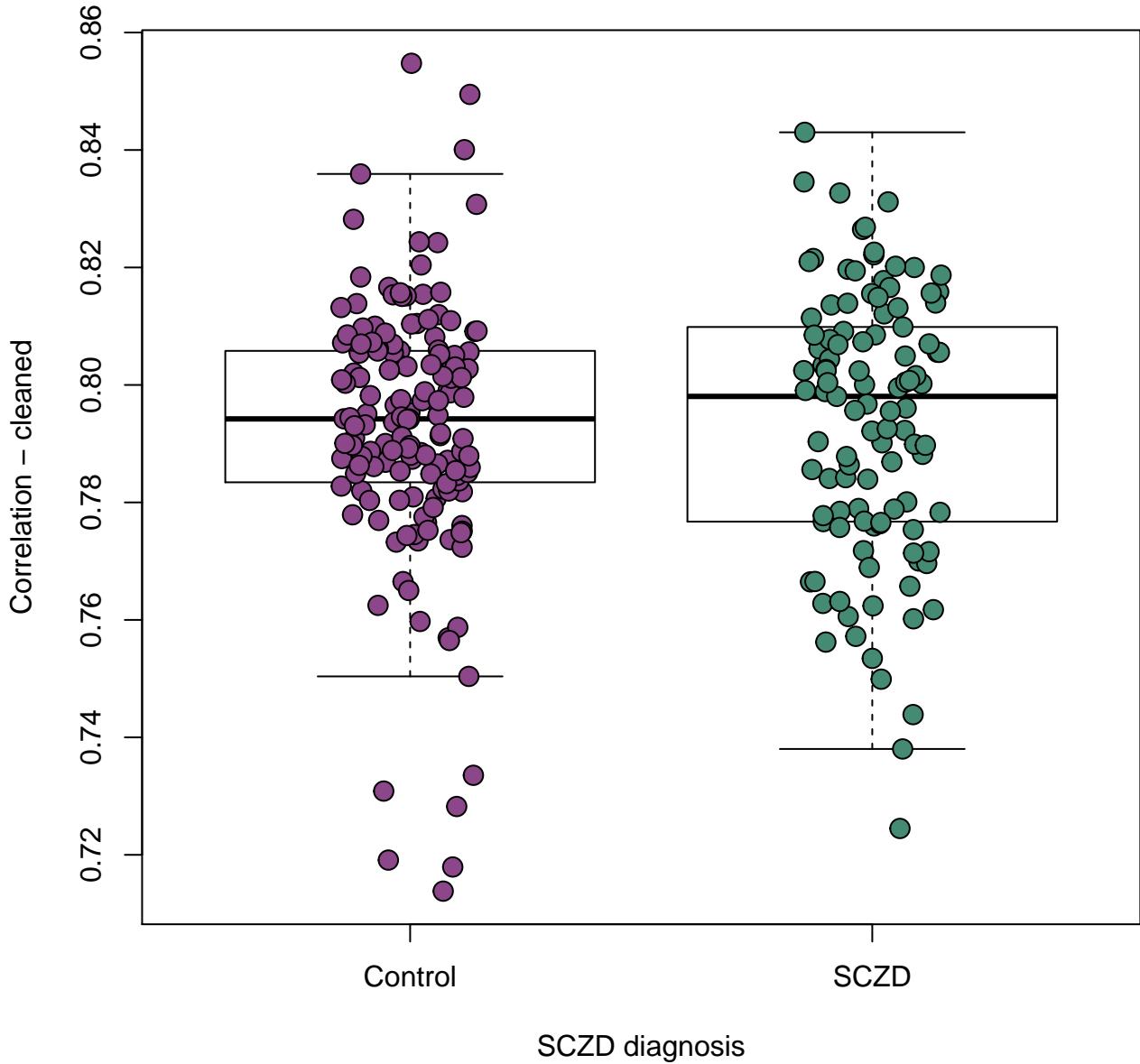


hsa05320: Autoimmune thyroid disease

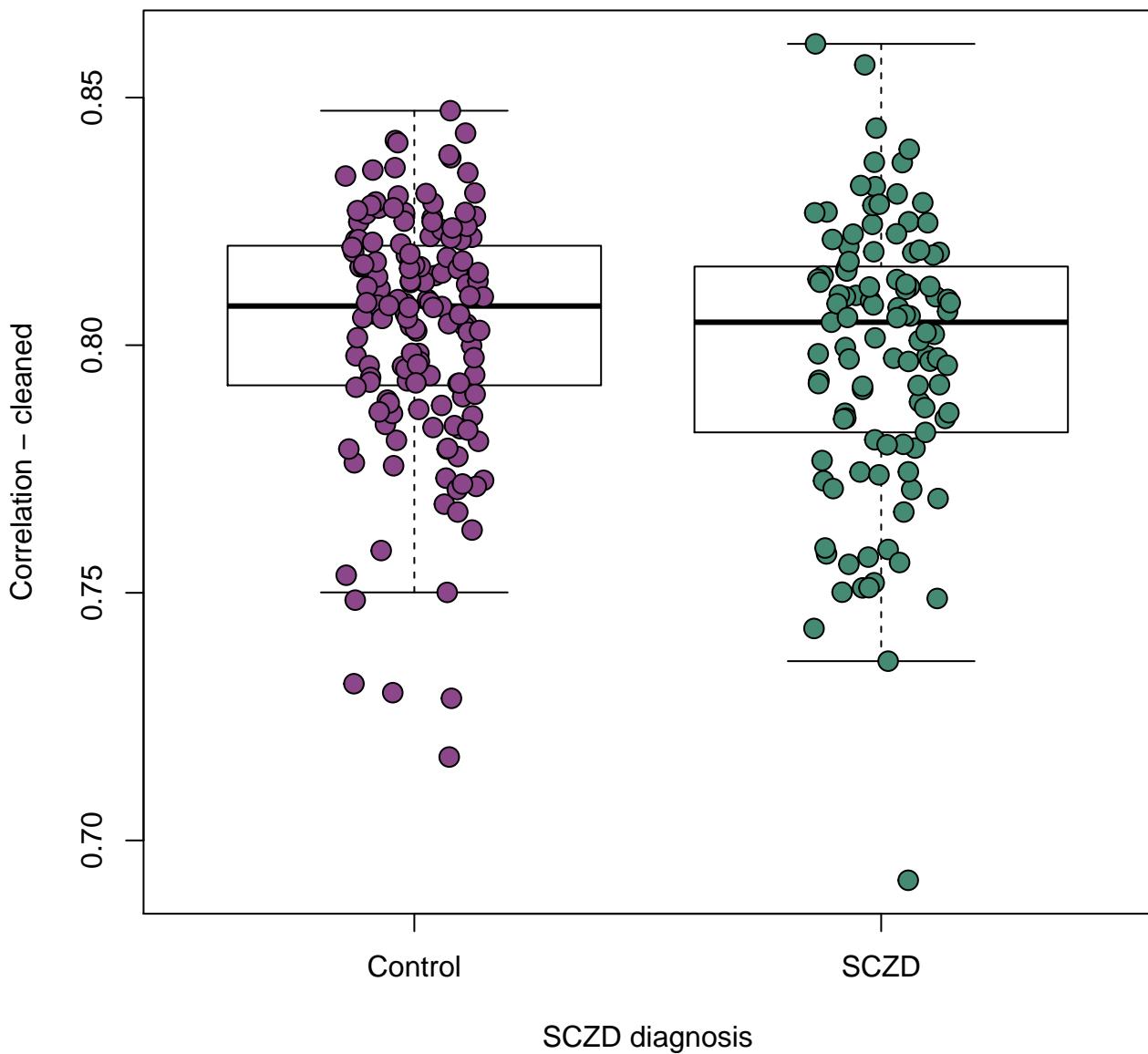
p-value: 0.041



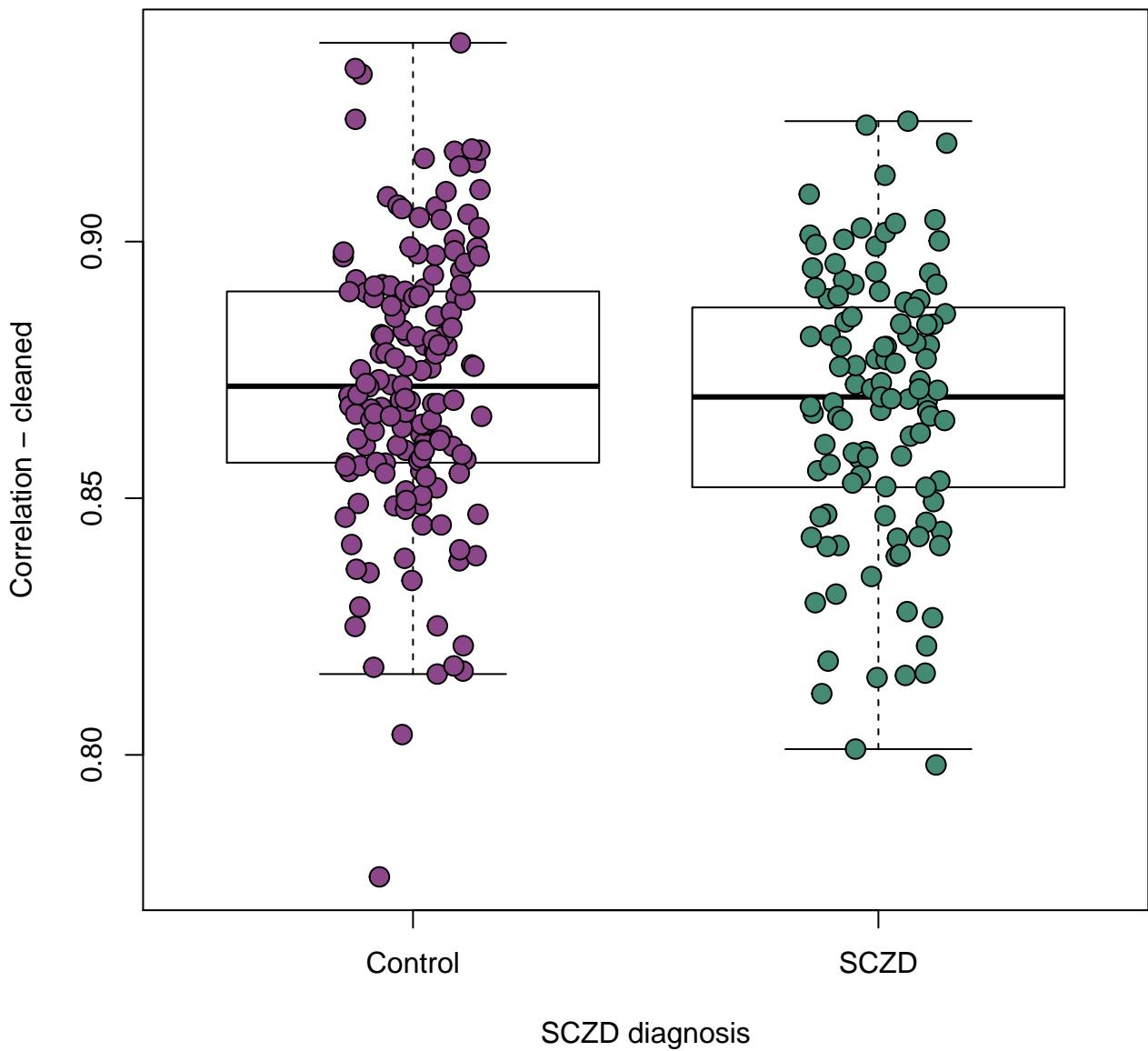
hsa05322: Systemic lupus erythematosus
p-value: 0.805



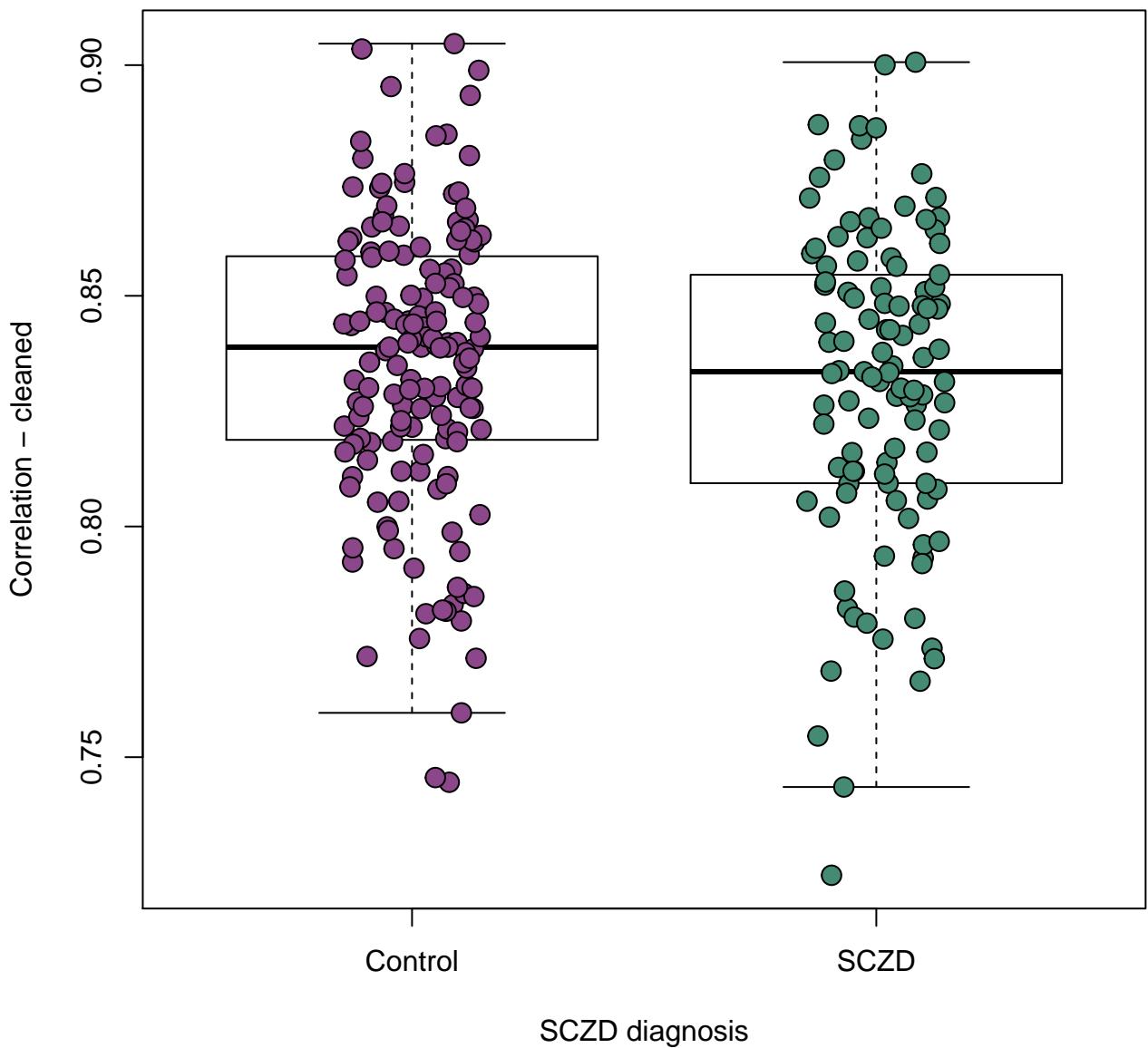
hsa05323: Rheumatoid arthritis
p-value: 0.0994



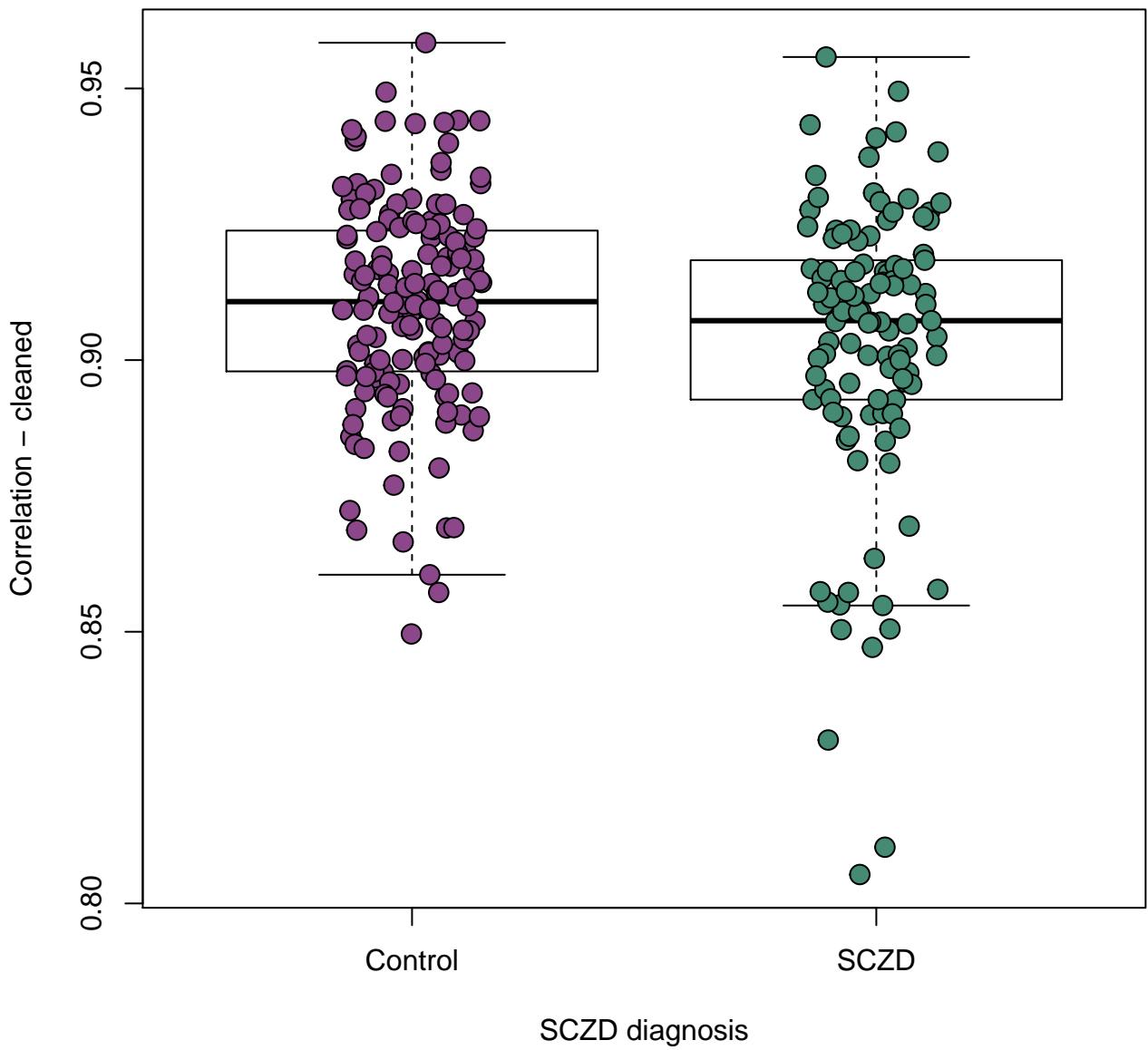
hsa05330: Allograft rejection
p-value: 0.172



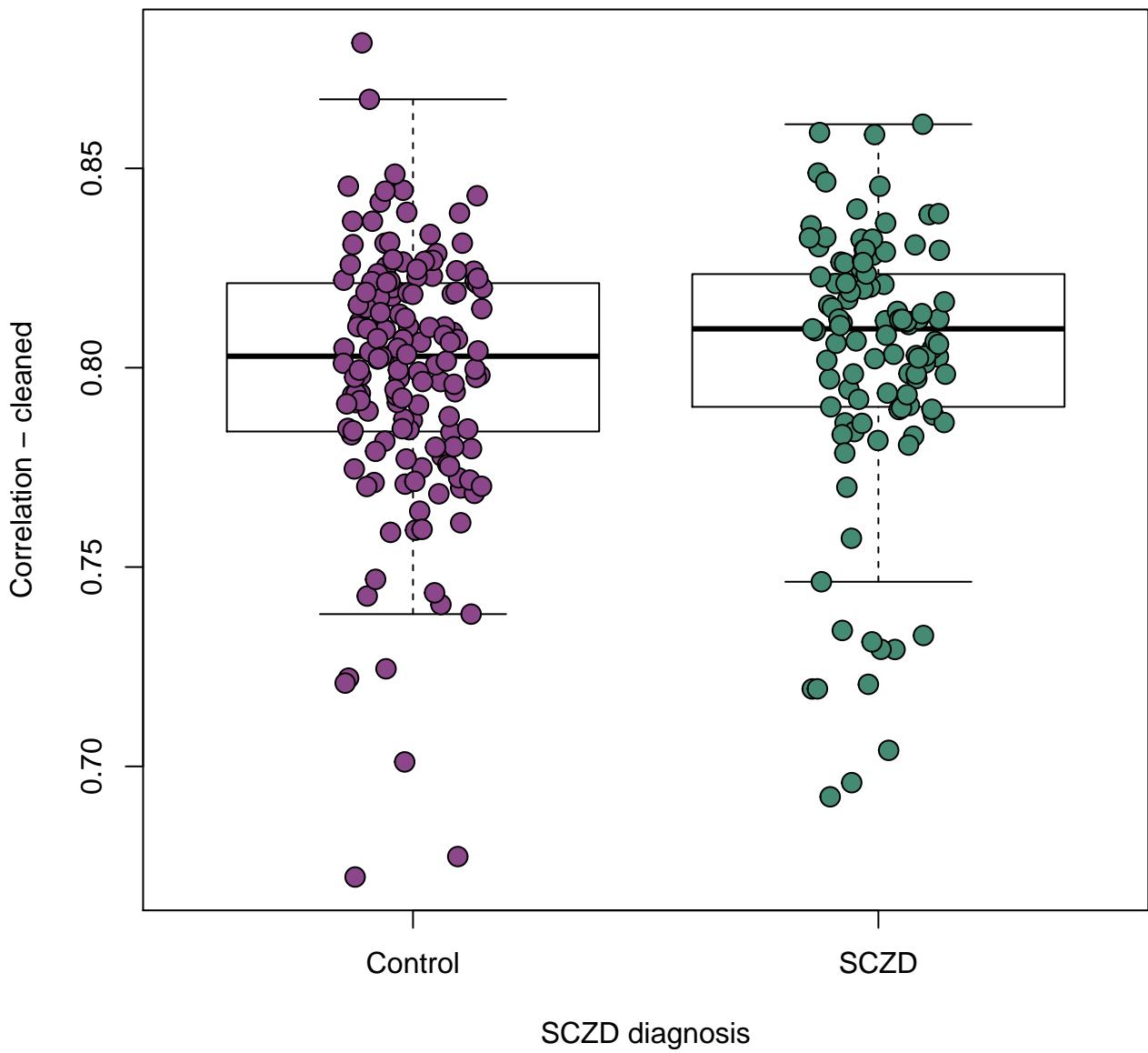
hsa05332: Graft-versus-host disease
p-value: 0.267



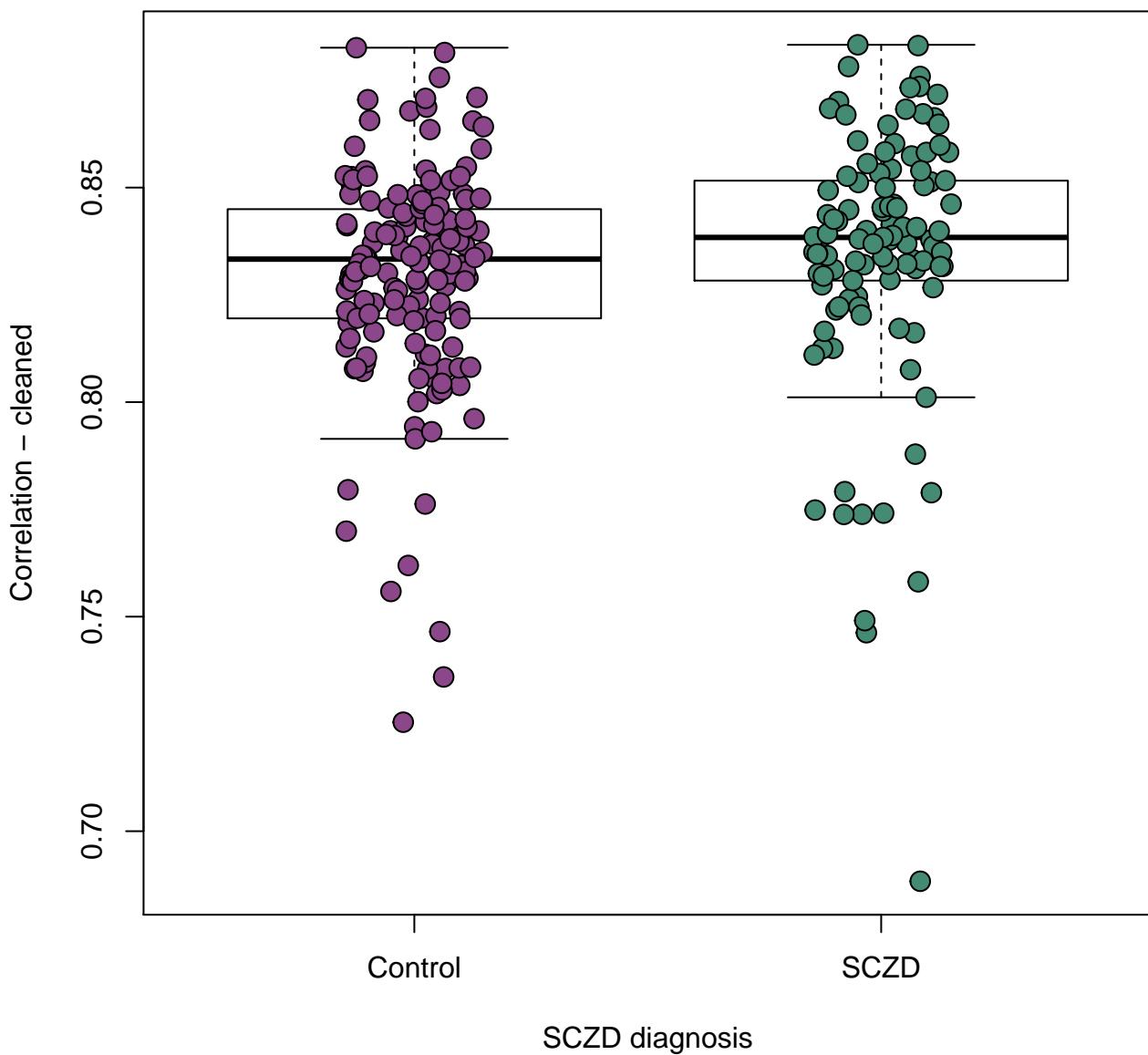
hsa05340: Primary immunodeficiency
p-value: 0.0118



hsa05410: Hypertrophic cardiomyopathy (HCM)
p-value: 0.464

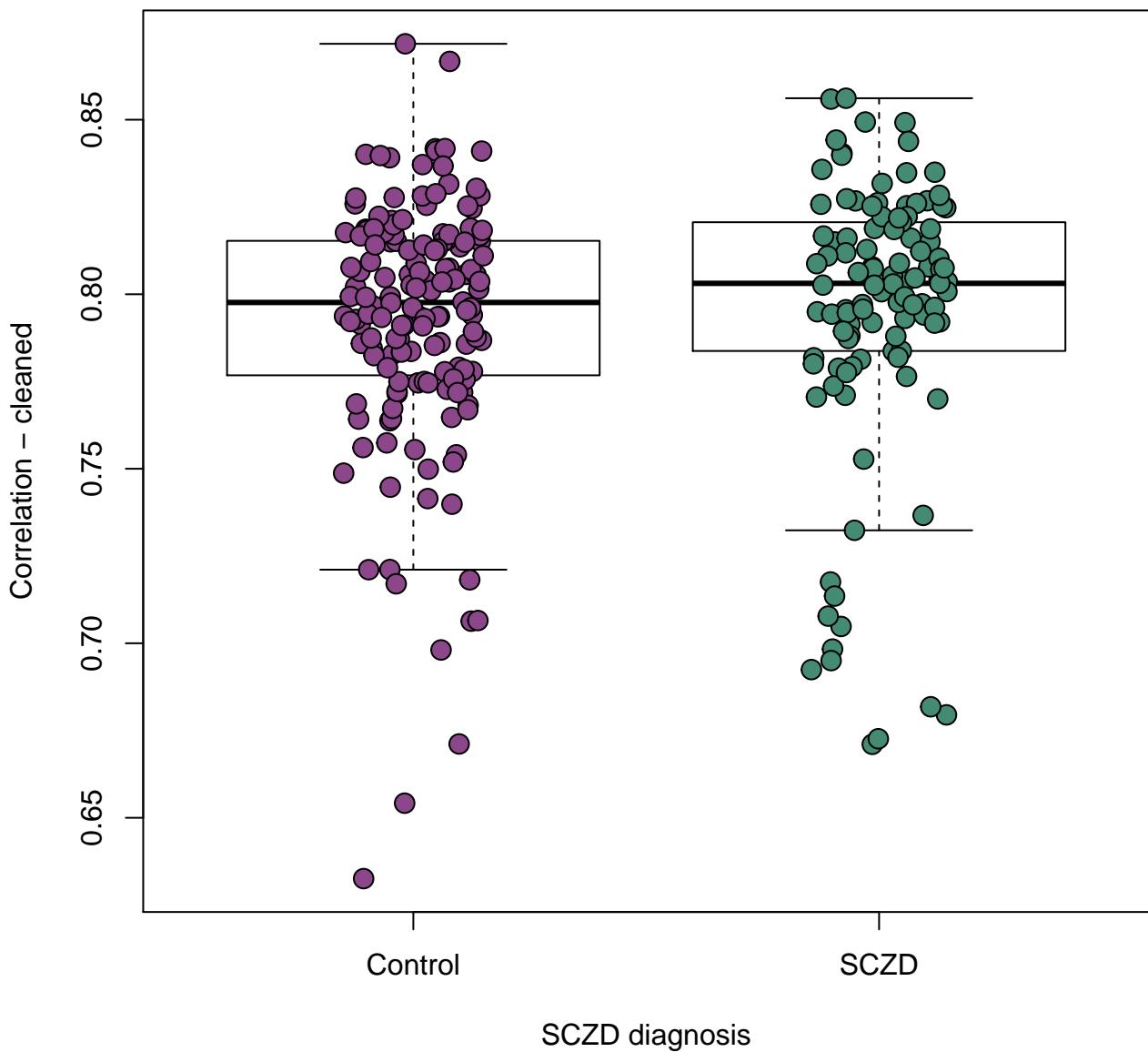


hsa05412: Arrhythmogenic right ventricular cardiomyopathy (ARVC)
p-value: 0.186



hsa05414: Dilated cardiomyopathy

p-value: 0.66



hsa05416: Viral myocarditis
p-value: 0.779

