regulation of nuclear cell cycle DNA replication (SLIP)
positive regulation of oligodendrocyte progenitor proliferation (LRP2)
mitotic spindle midzone assembly (KIF23)
epithelial cell proliferation involved in renal tubule morphogenesis (MTSS1)
actomyosin contractile ring assembly (KIF23)
cell cycle and proliferation
telomeric 3' overhang formation (MRE11)
regulation of telomere maintenance (YLPM1; SMG1)
regulation of cell morphogenesis (ZMYM1; SH319; CAMP1; STRP1)
oocyte karyosome formation (LOK)
mRNA 5'−splice site recognition (RU1C; PSIP1)
microtubule cytoskeleton organization (TBCD; TBA1; CK5P2; CAMP1; PARD3; TBB4B)
histone exchange (SRCAP; TRA1)
endothelial cell morphogenesis (HEG1; NOTC4; MET)
endosomal vesicle fusion (VPS8; VPS4A; VPS11; VPS41)
cell wall organization (TAGD; DAC)
bicellular tight junction assembly (MPP5; TBCD; PARD3)
cell organization and biogenesis
negative regulation of synaptic vesicle exocytosis (RAP1B)
membrane depolarization during Purkinje myocyte cell action potential (TRPM4)
membrane depolarization during bundle of His cell action potential (TRPM4)
membrane depolarization during AV node cell action potential (TRPM4)
cell−cell signaling
negative regulation of hydrogen peroxide−mediated programmed cell death (MET)
death
developmental processes
pyrimidine dimer repair by nucleotide−excision repair (XPC; SIR1)
DNA demethylation (ALKB1; ALKB4)
DNA metabolism
other biological processes
other metabolic processes
protein metabolism
rescue of stalled ribosome (ZN598; NEMF)
regulation of complement activation, lectin pathway (FUCL6; FUCL7)
protein−pyridoxal−5−phosphate linkage via peptidyl−N6−pyridoxal phosphate−L−lysine (CGL)
protein transport to vacuole involved in ubiquitin−dependent protein catabolic process via the multivesicular body sorting pathway (DDI1)
protein sulfhydration (CGL)
protein lipoylation (LIPT2)
protein demethylation (ALKB4; KDM1A)
positive regulation of protein sumoylation (TRAF7; HDAC4)
positive regulation of peptidyl−lysine acetylation (AAPK2)
positive regulation of histone H3−K9 methylation (SIR1; JARD2)
negative regulation of peptidyl−threonine phosphorylation (MET; PARD3)
negative regulation of histone H3−K9 methylation (DNM3B; KDM1A)
miRNA mediated inhibition of translation (AGO2; NOTC4)
histone H2A acetylation (TRRAP; EPC1)
dermatan sulfate proteoglycan biosynthetic process (B3GA3)
activation of MAPKKK activity (TAB1; TRAF7; KSR1)
tRNA wobble cytosine modification (ALKB1)
transcription, DNA−templated (RFX3; TRA1; ILF2; DIDO1; INO80)
snoRNA polyadenylation (PAPD5)
snoRNA guided rRNA pseudouridine synthesis (GAR1)
RNA repair (ALKB1)
RNA 3' uridylation (PAPD5)
oxidative RNA demethylation (ALKB1)
negative regulation of termination of RNA polymerase II transcription, poly(A)−coupled (SCAF8)
negative regulation of nuclear−transcribed mRNA poly(A) tail shortening (PAPD5)
ncRNA polyadenylation involved in polyadenylation−dependent ncRNA catabolic process (PAPD5)
ncRNA polyadenylation (PAPD5)
RNA metabolism
Wnt signaling pathway, calcium modulating pathway (WNT5A; AGO2)
Wnt signaling pathway (WNT7B; NXN; WNT5A; LRP4; APLP; TNKS1; NPHP3; KC1G3; AAPK2; LRP6; GSK3B; CSK2B)
TRIF−dependent toll−like receptor signaling pathway (TBK1; BIRC2)
positive regulation of transcription of Notch receptor target (NOTC1; NOTC4)
positive regulation of ephrin receptor signaling pathway (NOTC1)
positive regulation of cGMP−mediated signaling (ANPRA)
positive regulation of calcineurin−NFAT signaling cascade (SL9A1; AKAP5)
negative regulation of thrombin−activated receptor signaling pathway (MET)
negative regulation of SMAD protein signal transduction (PBLD; CILP1)
negative regulation of Rho protein signal transduction (HEG1; MET; RIPR1)
negative regulation of G protein−coupled receptor signaling pathway (RGS12; FTM)
negative regulation of canonical Wnt signaling pathway (WNT5A; VNG2B; NOTC1; LATS1; LRP4; LRP6)
negative regulation of calcineurin−NFAT signaling cascade (CMYA5; FHL2; GSK3B)
negative regulation of BMP signaling pathway (WNT5A; SORL; TRI33; NOTC1)
cAMP−mediated signaling (RPGF4; PDE4D; PDE2A; AGRG6)
signal transduction
regulation of innate immune response (FUCL6; BIRC2; FUCL7; SAMH1)
regulation of cellular defense response (FUCL6; FUCL7)
positive regulation of inflammatory response (WNT5A; STA5A; TLR2; PDE2A)
negative regulation of DNA damage response, signal transduction by p53 class mediator (KDM1A; SIR1)
heat acclimation (DAF12)
cellular response to fluid shear stress (MTSS1)
cellular response to cold (SL9A1; DNJC3)
base−excision repair, DNA ligation (XRCC1)
stress response
sodium−independent organic anion transport (SO4C1)
regulation of gastric acid secretion (KCNQ1)
positive regulation of renal sodium excretion (ANPRA)
positive regulation of receptor−mediated endocytosis (TLN1; DRK)
plus−end−directed vesicle transport along microtubule (KIF23)
pinocytosis (SNX5; CLN3)
organic anion transport (SO4C1)
neurotransmitter transport (ICA69; VGLU1; EAA2)
negative regulation of ion transport (AKAP5; SLOB)
membrane repolarization (KCNQ1)
L−glutamate transmembrane transport (CMC2; EAA2; EAA3)
hormone secretion (LRP2)
D−aspartate import across plasma membrane (EAA2; EAA3)
cytoplasmic transport, nurse cell to oocyte (ABL; FLNA)
body fluid secretion (ANPRA; RAB14)
aspartate transmembrane transport (CMC2; S13A3)
transport
tRNA demethylation (ALKB1)
sodium ion import across plasma membrane (SL9A1; TRPM4)
regulation of stress granule assembly (AAPK2)
regulation of postsynapse organization (WNT5A; RGS4)
regulation of cardiac conduction (ANPRA; NAC3)
prostaglandin catabolic process (ABHGA)
positive regulation of translation initiation in response to endoplasmic reticulum stress (DNJC3)
positive regulation of regulation of vascular associated smooth muscle cell membrane depolarization (TRPM4)
positive regulation of protein localization to synapse (WNT5A; NLGN3)
positive regulation of neuronal action potential (RPGF4)
positive regulation of lipoprotein transport (LRP2)
positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage (HAPB3)
positive regulation of cardioblast proliferation (NEDD4)
positive regulation of cardiac myofibril assembly (NEDD4)
positive regulation of atrial cardiac muscle cell action potential (TRPM4)
positive regulation of adipose tissue development (TRPM4; SORL)
negative regulation of neuron projection arborization (ARL2)
negative regulation of ubiquitin protein ligase activity (WBP11)
negative regulation of telomere DNA binding (TNKS1)
negative regulation of calcium ion transmembrane transport via high voltage−gated calcium channel (KCNS1)
mitochondrial double−strand break repair via homologous recombination (MRE11)
endothelial tube lumen extension (SLIT3)
DNA strand resection involved in replication fork processing (MRE11; ATM)
chemoattraction of axon (SLIT3; ANO4)
calcium activated phosphatidylserine scrambling (ANO6; ANO4)
calcium activated phosphatidylcholine scrambling (ANO7; ANO4)
calcium activated galactosylceramide scrambling (ANO7; ANO4)
NA
over_represented_pvalue
0.04
0.03
0.02
0.01