

miRPathDB Enrichment Summary: KI67_>20

miRPathDB Enriched: KI67_>20

GO Biological
process
(miRPathDB)

GO Molecular
function
(miRPathDB)

macroautophagy
morphogenesis of a polarized epithelium
Wnt signaling pathway planar cell
polarity pathway
cytosolic transport
establishment of planar polarity
protein depolymerization
regulation of establishment of planar
polarity
regulation of macroautophagy
innate immune response-activating signal
transduction
lens fiber cell apoptotic process
protein dephosphorylation
trachea morphogenesis

SMAD binding
molecular adaptor activity
histone deacetylase regulator activity
protein binding bridging
protein serinethreoninetyrosine kinase
activity
unfolded protein binding
C3HC4-type RING finger domain binding
G protein-coupled receptor binding
MAP kinase kinase activity
RNA polymerase binding
basal RNA polymerase II transcription
machinery binding
beta-catenin binding

KEGG
(miRPathDB)

Reactome
(miRPathDB)

Endocytosis
Alzheimers disease
MicroRNAs in cancer
VEGF signaling pathway
Fc gamma R-mediated phagocytosis
Natural killer cell mediated
cytotoxicity
Bacterial invasion of epithelial cells
Chemokine signaling pathway
Protein processing in endoplasmic
reticulum
Thyroid cancer
Notch signaling pathway
Pathways in cancer

Constitutive Signaling by NOTCH1 HD
Domain Mutants
Signaling by NOTCH1 HD Domain Mutants in
Cancer
Vesicle-mediated transport
Transport to the Golgi and subsequent
modification
Membrane Trafficking
Ca2+ pathway
Cellular response to hypoxia
Clathrin-mediated endocytosis
Competing endogenous RNAs ceRNAs
regulate PTEN translation
Downregulation of TGF-beta receptor
signaling
Regulation of RUNX3 expression and
activity
SUMOylation of transcription cofactors

miRPathDB Depleted: KI67_>20

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positive regulation of leukocyte
adhesion to vascular endothelial cell
regulation of erythrocyte
differentiation
female meiotic nuclear division
mRNA transport
negative regulation of myeloid leukocyte
differentiation
response to antibiotic
response to osmotic stress
response to water-immersion restraint
stress
telomere maintenance
telomere organization
dendritic spine morphogenesis
double-strand break repair via
homologous recombination

p53 binding
RNA polymerase II-specific DNA-binding
transcription factor binding
DNA polymerase binding
damaged DNA binding
heat shock protein binding
nitric-oxide synthase regulator activity
protein serinethreonine kinase inhibitor
activity
transcription factor binding
oxidoreductase activity
extracellular matrix binding
RNA-directed DNA polymerase activity
RNA binding

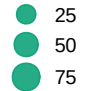
KEGG
(miRPathDB)

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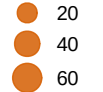
Legionellosis
mRNA surveillance pathway
Basal cell carcinoma
Cell cycle
Arrhythmogenic right ventricular
cardiomyopathy ARVC
Dopaminergic synapse
Inflammatory bowel disease IBD
Jak-STAT signaling pathway
Malaria
Melanoma
NF-kappa B signaling pathway
PI3K-Akt signaling pathway

FOXO-mediated transcription of cell
death genes
Interleukin-10 signaling
KSRP KHSRP binds and destabilizes mRNA
TFAP2 AP-2 family regulates
transcription of growth factors and
their receptors
ERBB2 Regulates Cell Motility
Transcription of E2F targets under
negative control by p107 RBL1 and p130
RBL2 in complex with HDAC1
Activated NTRK3 signals through RAS
Activation of PUMA and translocation to
mitochondria
Apoptosis induced DNA fragmentation
CDC6 association with the ORCorigin
complex
ERBB2 Activates PTK6 Signaling
Erythropoietin activates RAS

Observed



Observed



-log10(P-adjusted)

-log10(P-adjusted)