miRPathDB Enrichment Summary: SINAPTOFISINA_1_vs_0
miRPathDB Enriched: SINAPTOFISINA_1_vs_0
miRPathDB Depleted: SINAPTOFISINA_1_vs_0
GO Biological process (miRPathDB)
keratinocyte migration
trachea formation
receptor-mediated endocytosis
thymus development
microtubule polymerization or depolymerization
mRNA cleavage involved in gene silencing by miRNA
artery morphogenesis
negative regulation of stem cell differentiation
positive regulation of vasoconstriction
regulation of RNA polymerase II transcriptional preinitiation complex assembly
calcium ion import into sarcoplasmic reticulum
vesicle cargo loading
GO Molecular function (miRPathDB)
protein N-terminus binding
endoribonuclease activity cleaving miRNA-paired mRNA
insulin-like growth factor receptor binding
cyclin-dependent protein serinethreonine kinase inhibitor activity
structural molecule activity
MAP kinase kinase activity
endoribonuclease activity producing 5-phosphomonoesters
histone deacetylase regulator activity
signaling receptor activity
single-stranded DNA binding
BH3 domain binding
BH domain binding
KEGG (miRPathDB)
Protein processing in endoplasmic reticulum
Aldosterone-regulated sodium reabsorption
Fc gamma R-mediated phagocytosis
Arrhythmogenic right ventricular cardiomyopathy ARVC
Viral myocarditis
Alcoholism
Amyotrophic lateral sclerosis ALS
Prion diseases
Dorso-ventral axis formation
B cell receptor signaling pathway
DNA replication
Natural killer cell mediated cytotoxicity
0.4
0.5
0.6
0.7
Reactome (miRPathDB)
Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimers disease models
Neurodegenerative Diseases
Transport to the Golgi and subsequent modification
E3 ubiquitin ligases ubiquitinate target proteins
Protein ubiquitination
Asparagine N-linked glycosylation
CaMK IV-mediated phosphorylation of CREB
NOTCH2 intracellular domain regulates transcription
NOTCH4 Intracellular Domain Regulates Transcription
Phosphate bond hydrolysis by NTPDase proteins
Negative regulation of FGFR3 signaling
Neddylation
0.4
0.5
0.6
0.7
-log10(P-adjusted)
GO Biological process (miRPathDB)
positive regulation of protein localization to nucleus
cell cycle phase transition
regulation of cellular response to oxidative stress
regulation of ubiquitin-protein transferase activity
regulation of translation
regulation of cellular response to stress
regulation of metabolic process
regulation of protein localization to nucleus
mitotic cell cycle phase transition
regulation of mitotic cell cycle phase transition
cellular response to DNA damage stimulus
apoptotic signaling pathway
GO Molecular function (miRPathDB)
protein kinase binding
proximal promoter sequence-specific DNA binding
ubiquitin-like protein ligase binding
enzyme binding
nucleic acid binding
phosphatase binding
organic cyclic compound binding
DNA binding
kinase binding
nucleoside-triphosphatase activity
DNA-binding transcription factor activity
GTPase activity
Observed
5
10
15
20
KEGG (miRPathDB)
Small cell lung cancer
Melanoma
Hepatitis B
Focal adhesion
Pancreatic cancer
Prostate cancer
Amphetamine addiction
Salmonella infection
Measles
Colorectal cancer
mTOR signaling pathway
Long-term potentiation
1.0
1.5
2.0
Reactome (miRPathDB)
Circadian Clock
EPH-Ephrin signaling
Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation
HSP90 chaperone cycle for steroid hormone receptors SHR
Interleukin-12 family signaling
PTK6 Regulates RHO GTPases RAS GTPase and MAP kinases
Protein folding
RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function
Signaling by NOTCH
Signaling by TGF-beta family members
Signaling by VEGF
TP53 Regulates Transcription of Cell Cycle Genes
1.0
1.5
2.0
-log10(P-adjusted)
Observed
25
50
75
100