miRPathDB Enrichment Summary: GENERO_1_vs_0
miRPathDB Enriched: GENERO_1_vs_0
GO Biological process (miRPathDB)
axon guidance
cellular response to hydrogen peroxide
endoplasmic reticulum unfolded protein response
extracellular matrix organization
extracellular structure organization
negative regulation of endothelial cell apoptotic process
negative regulation of epithelial cell apoptotic process
neuron projection guidance
nucleobase-containing small molecule interconversion
platelet-derived growth factor receptor signaling pathway
positive regulation of osteoblast differentiation
prostate gland growth
GO Molecular function (miRPathDB)
growth factor binding
steroid hormone receptor binding
RNA polymerase II complex binding
collagen binding
enhancer binding
DNA cytosine-5--methyltransferase activity
endoribonuclease activity
enhancer sequence-specific DNA binding
integrin binding
platelet-derived growth factor receptor binding
structural molecule activity
ATP-dependent RNA helicase activity
KEGG (miRPathDB)
Axon guidance
Dopaminergic synapse
Amoebiasis
Non-small cell lung cancer
Gap junction
Estrogen signaling pathway
Acute myeloid leukemia
Aldosterone-regulated sodium reabsorption
Chagas disease American trypanosomiasis
Chemokine signaling pathway
Cholinergic synapse
ErbB signaling pathway
0.35
0.40
Reactome (miRPathDB)
Collagen formation
Interconversion of nucleotide di- and triphosphates
MET activates PTK2 signaling
Signaling by PDGF
Degradation of the extracellular matrix
Extracellular matrix organization
Signaling by EGFR
Signaling by MET
rRNA processing in the mitochondrion
Cell-Cell communication
Downstream signaling of activated FGFR1
Insulin-like Growth Factor-2 mRNA Binding Proteins IGF2BPsIMPsVICKZs bind RNA
0.35
0.40
-log10(P-adjusted)
miRPathDB Depleted: GENERO_1_vs_0
GO Biological process (miRPathDB)
RNA export from nucleus
RNA localization
RNA processing
Schwann cell proliferation
cytosolic transport
dosage compensation by inactivation of X chromosome
glial cell proliferation
intracellular transport of virus
mRNA export from nucleus
maintenance of location in cell
positive regulation of IRE1-mediated unfolded protein response
positive regulation of telomerase activity
GO Molecular function (miRPathDB)
protein binding
enzyme regulator activity
oxidoreductase activity
protein serinethreoninetyrosine kinase activity
cyclin-dependent protein serinethreonine kinase inhibitor activity
transcription cofactor binding
ribonucleoprotein complex binding
histone deacetylase regulator activity
insulin receptor substrate binding
RNA-directed DNA polymerase activity
cyclin-dependent protein serinethreonine kinase regulator activity
telomerase activity
Observed
10
20
30
40
KEGG (miRPathDB)
Amyotrophic lateral sclerosis ALS
Prion diseases
Prostate cancer
Adherens junction
Adipocytokine signaling pathway
Alcoholism
Apoptosis
Basal cell carcinoma
Bladder cancer
Cell cycle
Colorectal cancer
Epithelial cell signaling in Helicobacter pylori infection
0.35
0.40
Reactome (miRPathDB)
Cell Cycle Mitotic
Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimers disease models
Mitophagy
Mitotic Prophase
Negative regulators of DDX58IFIH1 signaling
Neurodegenerative Diseases
PIP3 activates AKT signaling
Pre-NOTCH Expression and Processing
Pre-NOTCH Transcription and Translation
RHO GTPases activate PKNs
RNA Polymerase I Transcription
RUNX3 regulates BCL2L11 BIM transcription
0.35
0.40
-log10(P-adjusted)
Observed
20
40
60
80