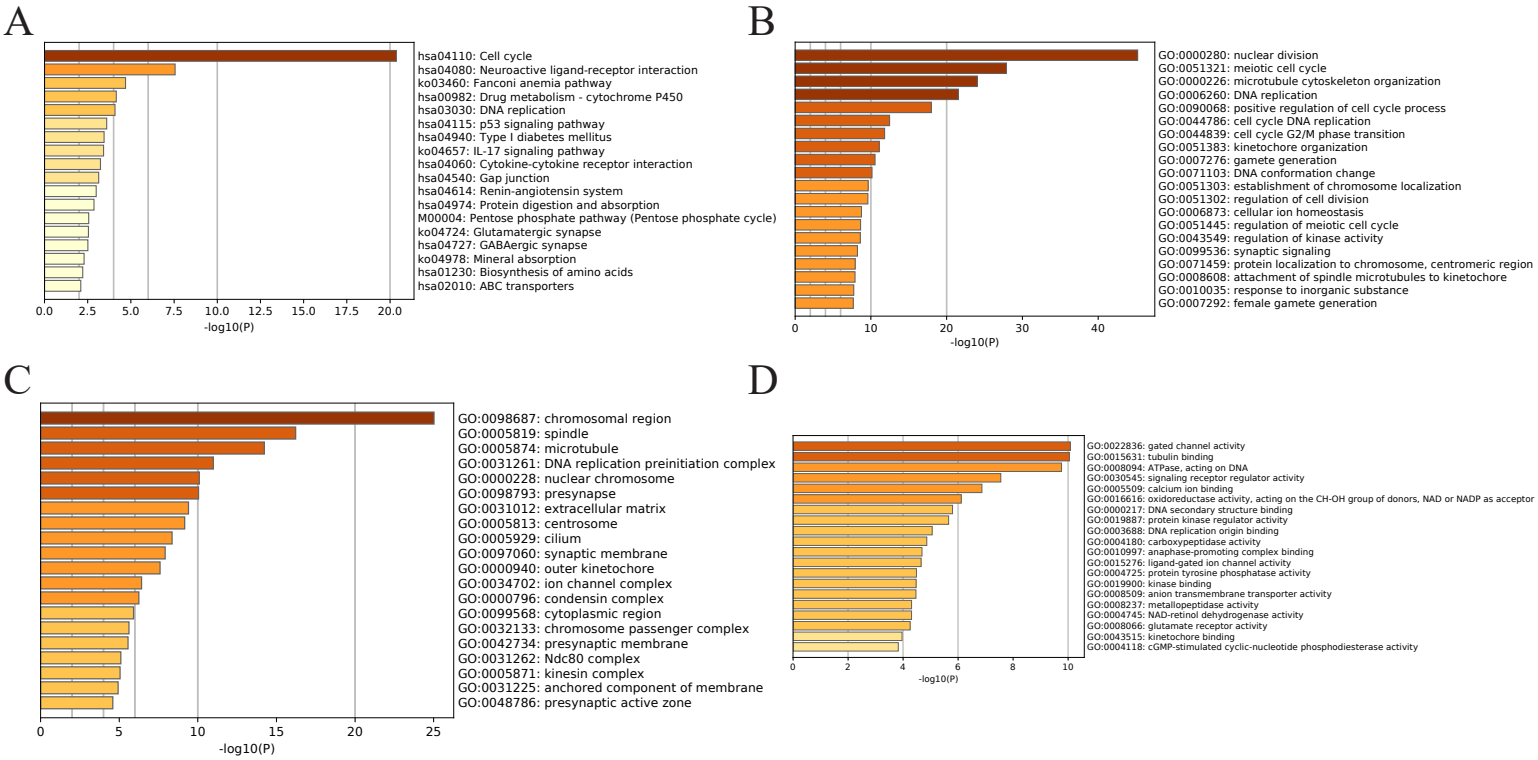
A
hsa04110: Cell cycle
hsa04080: Neuroactive ligand-receptor interaction
ko03460: Fanconi anemia pathway
hsa00982: Drug metabolism - cytochrome P450
hsa03030: DNA replication
hsa04115: p53 signaling pathway
hsa04940: Type I diabetes mellitus
ko04657: IL-17 signaling pathway
hsa04060: Cytokine-cytokine receptor interaction
hsa04540: Gap junction
hsa04614: Renin-angiotensin system
hsa04974: Protein digestion and absorption
M00004: Pentose phosphate pathway (Pentose phosphate cycle)
ko04724: Glutamatergic synapse
hsa04727: GABAergic synapse
ko04978: Mineral absorption
hsa01230: Biosynthesis of amino acids
hsa02010: ABC transporters
0.0 2.5 5.0 7.5 10.0 12.5 15.0 17.5 20.0
-log10(P)
B
GO:0000280: nuclear division
GO:0051321: meiotic cell cycle
GO:0000226: microtubule cytoskeleton organization
GO:0006260: DNA replication
GO:0090068: positive regulation of cell cycle process
GO:0044786: cell cycle DNA replication
GO:0044839: cell cycle G2/M phase transition
GO:0051383: kinetochore organization
GO:0007276: gamete generation
GO:0071103: DNA conformation change
GO:0051303: establishment of chromosome localization
GO:0051302: regulation of cell division
GO:0006873: cellular ion homeostasis
GO:0051445: regulation of meiotic cell cycle
GO:0043549: regulation of kinase activity
GO:0099536: synaptic signaling
GO:0071459: protein localization to chromosome, centromeric region
GO:0008608: attachment of spindle microtubules to kinetochore
GO:0010035: response to inorganic substance
GO:0007292: female gamete generation
0 10 20 30 40
-log10(P)
C
GO:0098687: chromosomal region
GO:0005819: spindle
GO:0005874: microtubule
GO:0031261: DNA replication preinitiation complex
GO:0000228: nuclear chromosome
GO:0098793: presynapse
GO:0031012: extracellular matrix
GO:0005813: centrosome
GO:0005929: cilium
GO:0097060: synaptic membrane
GO:0000940: outer kinetochore
GO:0034702: ion channel complex
GO:0000796: condensin complex
GO:0099568: cytoplasmic region
GO:0032133: chromosome passenger complex
GO:0042734: presynaptic membrane
GO:0031262: Ndc80 complex
GO:0005871: kinesin complex
GO:0031225: anchored component of membrane
GO:0048786: presynaptic active zone
0 5 10 15 20 25
-log10(P)
D
GO:0022836: gated channel activity
GO:0015631: tubulin binding
GO:0008094: ATPase, acting on DNA
GO:0030545: signaling receptor regulator activity
GO:0005509: calcium ion binding
GO:0016616: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
GO:0000217: DNA secondary structure binding
GO:0019887: protein kinase regulator activity
GO:0003688: DNA replication origin binding
GO:0004180: carboxypeptidase activity
GO:0010997: anaphase-promoting complex binding
GO:0015276: ligand-gated ion channel activity
GO:0004725: protein tyrosine phosphatase activity
GO:0019900: kinase binding
GO:0008509: anion transmembrane transporter activity
GO:0008237: metallopeptidase activity
GO:0004745: NAD-retinol dehydrogenase activity
GO:0008066: glutamate receptor activity
GO:0043515: kinetochore binding
GO:0004118: cGMP-stimulated cyclic-nucleotide phosphodiesterase activity
0 2 4 6 8 10
-log10(P)
E
Biological pathway for DEmiRs
Signaling events mediated by Hepatocyte Growth Factor Receptor (c-Met) (32.4%)
Syndecan-1-mediated signaling events (32.5%)
ErbB receptor signaling network (32.7%)
IFN-gamma pathway (32.4%)
Alpha9 beta1 integrin signaling events (32.5%)
Plasma membrane estrogen receptor signaling (32.4%)
IGF1 pathway (32.2%)
Glypican 1 network (32.3%)
EGFR-dependent Endothelin signaling events (32.1%)
LKB1 signaling events (32.4%)
F
Biological process for DEmiRs
Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism (19.8%)
Signal transduction (24.9%)
Cell communication (23.2%)
Regulation of cell growth (0.3%)
Organogenesis (0.2%)
Cell differentiation (0.3%)
Regulation of metabolism (0.1%)
Regulation of exocytosis (0.1%)
Regulation of translation (0.2%)
Regulation of gene expression, epigenetic (0.6%)
G
Cellular component for DEmiRs
Nucleus (50%)
Cytoplasm (46.7%)
Golgi aparatus (8.3%)
Endosome (3.3%)
Cyclin-dependent protein kinase holoenzyme complex (0.2%)
Cytosol (9.8%)
Cytoplasmic vesicle (1.7%)
Perinuclear region (1.4%)
ESC/E(Z) complex (0.2%)
Caveola (0.4%)
H
Molecular function for DEmiRs
Transcription factor activity (8.5%)
Protein serine/threonine kinase activity (3%)
Ubiquitin-specific protease activity (3.1%)
GTPase activity (2%)
Receptor binding (1.3%)
Transcription regulator activity (5.9%)
GTPase activator activity (1.4%)
Transferase activity (1.4%)
Cytoskeletal protein binding (1.9%)
Receptor signaling protein serine/threonine kinase activity (0.3%)