he Set Enrichment Analysis

Gene set enrichment analysis heatmap. Rows (gene sets, top to bottom):

- cell cycle
- cell cycle checkpoints r−hsa−69620
- cell cycle r−hsa−1640170
- cell cycle, mitotic r−hsa−69278
- cellular macromolecule biosynthetic process (go:0034645)
- copi−dependent golgi−to−er retrograde traffic r−hsa−6811434
- cytoskeleton−dependent cytokinesis (go:0061640)
- dna metabolic process (go:0006259)
- dna replication (go:0006260)
- double−strand break repair via homologous recombination (go:0000724)
- eml4 and nudc in mitotic spindle formation r−hsa−9648025
- g1/s transition r−hsa−69206
- g2/m checkpoints r−hsa−69481
- g2/m transition r−hsa−69275
- m phase r−hsa−68886
- microtubule cytoskeleton organization involved in mitosis (go:1902850)
- mitotic anaphase r−hsa−68882
- mitotic g1 phase and g1/s transition r−hsa−453279
- mitotic g2−g2/m phases r−hsa−453274
- mitotic metaphase and anaphase r−hsa−2555396
- mitotic metaphase plate congression (go:0007080)
- mitotic nuclear division (go:0140014)
- mitotic prometaphase r−hsa−68877
- mitotic sister chromatid segregation (go:0000070)
- mitotic spindle checkpoint r−hsa−69618
- mitotic spindle organization (go:0007052)
- oocyte meiosis
- positive regulation of cell cycle process (go:0090068)
- progesterone−mediated oocyte maturation
- regulation of cell cycle process (go:0010564)
- regulation of cyclin−dependent protein serine/threonine kinase activity (go:0000079)
- regulation of cytokinesis (go:0032465)
- regulation of mitotic cell cycle phase transition (go:1901990)
- resolution of sister chromatid cohesion r−hsa−2500257
- rho gtpase effectors r−hsa−195258
- rho gtpases activate formins r−hsa−5663220
- separation of sister chromatids r−hsa−2467813
- signaling by rho gtpases r−hsa−194315
- sister chromatid segregation (go:0000819)
- unattached kinetochores signal amplification via a mad2 inhibitory signal r−hsa−141444

Columns (miRNAs): miR−323a−3p, miR−449b−5p, miR−491−3p, miR−892b, miR−1827, miR−4774−3p, miR−5681b

Legend:
Database: Gene Ontology BP, KEGG, Reactome
matrix_6: 4, 2, 0, −2, −4

Database