Signatures from each combination of pooled datasets

Enrichment p-values, Bonferroni corrected per signature, for each gene set at least 1 enrichment p<0.05

C2: ptc1Pathway
C2: srcRPTPPathway
C2: cdc25Pathway
C2: SA_G2_AND_M_PHASES
C2: mprPathway
GO:0008283: cell proliferation
KEGG – hsa03050 – Proteasome
C2: proteasomePathway
C2: GLUT_DOWN
GO:0007052: mitotic spindle organization and biogenesis
Reactome: DNA Replication
GO:0004674: protein serine/threonine kinase activity
GO:0005515: protein binding
C2: cellcyclePathway
C2: radiation_sensitivity
GO:0000704: regulation of progression through cell cycle
GO:0006260: DNA replication
GO:0000709: regulation of cyclin–dependent protein kinase activity
GO:0000166: nucleotide binding
GO:0005524: ATP binding
GO:0003777: microtubule motor activity
GO:0007018: microtubule–based movement
GO:0007049: cell cycle
C2: CR_CELL_CYCLE
GO:0007067: mitosis
KEGG – hsa04110 – Cell cycle
C2: Cell_Cycle
GO:0051301: cell division
Reactome: Cell Cycle, Mitotic
C2: LEU_DOWN
GO:0007051: spindle organization and biogenesis
GO:0048015: phosphoinositide–mediated signaling
Reactome: Cell Cycle Checkpoints
C2: g2Pathway