BP: regulation of cytokinesis (GO:0032465)
MF: Unclassified (UNCLASSIFIED)
CC: spindle midzone (GO:0051233)
Pathway: Unclassified (UNCLASSIFIED)
ABCA1,AURKA,AURKB,CDCA8,CENPU,DMD,INCENP,KIF11,NCAPH,PLK1,PLK2,PTEN,SPAG5,TPX2,SMC2,PRC1,USP13
BP: intracellular signal transduction (GO:0035556)
MF: kinase binding (GO:0019900)
CC: perinuclear region of cytoplasm (GO:0048471)
Pathway: Histamine H2 receptor mediated signaling pathway (P04386)
ABL1,ABL2,CAV1,CAV2,HBA1,HBB,HSPA1A,MYRIP,NOS3,PRKAR2A,PRKAR2B,RAB27B,RIN1,PTGS2,SH2D3C,TRPC1,VAV2,ERN1,AKAP13,MAP2,PRKACA
BP: positive regulation of cellular component organization (GO:0051130)
MF: Unclassified (UNCLASSIFIED)
CC: Unclassified (UNCLASSIFIED)
Pathway: Unclassified (UNCLASSIFIED)
ACTA1,BAIAP2,GSN,HIP1R,MTSS1,SPIRE1,GC,VCL
BP: positive regulation of mitotic nuclear division (GO:0045840)
MF: transmembrane receptor protein tyrosine kinase activity (GO:0004714)
CC: Unclassified (UNCLASSIFIED)
Pathway: EGF receptor signaling pathway (P00018)
AGER,BTC,EGF,EGFR,ERBB3,ERRFI1,HGFAC,LINGO1,MET,NKD2,NRG1,SPINT1,TGFA,AREG,GPNMB,HGF
BP: dendritic spine organization (GO:0097061)
MF: signaling adaptor activity (GO:0035591)
CC: dendritic spine (GO:0043197)
Pathway: Ionotropic glutamate receptor pathway (P00037)
AHR,BAIAP2L1,DDB1,EPS8,SHANK1,SHANK2,SHANK3,WDTC1,DCAF4,FBXW5
BP: hippo signaling (GO:0035329)
MF: RNA polymerase II cis-regulatory region sequence-specific DNA binding (GO:0000978)
CC: transcription regulator complex (GO:0005667)
Pathway: Apoptosis signaling pathway (P00006)
AMOT,FOS,FOSL1,JUN,MBD3,MECOM,PTPN14,RUNX2,SOX2,SOX9,TEAD1,TEAD3,TLE1,YAP1,ATF3,KLF4,POU5F1,FOSB,JUNB,AMOTL2,TEAD4
BP: negative regulation of mitotic sister chromatid segregation (GO:0033048)
MF: Unclassified (UNCLASSIFIED)
CC: Not Significant
Pathway: Unclassified (UNCLASSIFIED)
AP4B1,BUB1B,CDC20,CDC27,PTTG1,BUB1
BP: Unclassified (UNCLASSIFIED)
MF: phosphotransferase activity, alcohol group as acceptor (GO:0016773)
CC: RNA polymerase II, holoenzyme (GO:0016591)
Pathway: VEGF signaling pathway (P00056)
AR,BAG1,CDK7,POLR2A,PRKCB,PRKCD,RIPK4,RPRD1B,TGFB1I1,FOXA1,TMF1,CCNK,SMN1,PIK3CG
BP: transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)
MF: transmembrane signaling receptor activity (GO:0004888)
CC: Unclassified (UNCLASSIFIED)
Pathway: Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway (P00026)
ARRB2,CNR1,GRM2,HTR2A,INSR,IRS1,MAP1A,NDUFB10,NTF3,NTRK3,PTPN1,PTPN3,SORT1,ADRB1,EDNRA,NKS1B,GLUL,PON2,GRB14,BDNF
BP: regulation of transcription by RNA polymerase II (GO:0006357)
MF: RNA polymerase II cis-regulatory region sequence-specific DNA binding (GO:0000978)
CC: Unclassified (UNCLASSIFIED)
Pathway: Unclassified (UNCLASSIFIED)
ATAD2,CSF2RB,ESR1,PBXIP1,PGR,PIK3CA,PIK3R1,THRB,ZBTB17,NR2F1,GFI1
BP: protein autophosphorylation (GO:0046777)
MF: cytokine binding (GO:0019955)
CC: extrinsic component of cytoplasmic side of plasma membrane (GO:0031234)
Pathway: Interleukin signaling pathway (P00036)
BTK,CDCP1,GP6,HCK,IL6,IL6R,IL6ST,LIFR,LYN,OSM,PLAUR,SYK,TYK2,YES1,FAS,LIF,FGR,PLAU,RPS6KA2
BP: regulation of cyclin-dependent protein kinase activity (GO:1904029)
MF: cyclin-dependent protein serine/threonine kinase regulator activity (GO:0016538)
CC: cyclin-dependent protein kinase holoenzyme complex (GO:0000307)
Pathway: Cell cycle (P00013)
CCNA2,CCNB1,CCND1,CCNE1,CCP110,CDK1,CDK6,CDKN1A,CDKN1B,CDKN3,DDB2,GADD45G,MXD1,RPS6KA1,SCML2,AKT3,FBXO31,CCNF,GADD45A,CDKN2D
BP: microtubule cytoskeleton organization involved in mitosis (GO:1902850)
MF: Unclassified (UNCLASSIFIED)
CC: spindle (GO:0005819)
Pathway: Unclassified (UNCLASSIFIED)
CDH1,CDK5RAP2,CEP135,CEP152,CTNNA1,ECT2,KCNQ1,LIMA1,PLK4,RACGAP1,WDR62,PTPRM,AKAP9,CEP170,TUBG1,KIF23
BP: axon guidance (GO:0007411)
MF: cadherin binding (GO:0045296)
CC: adherens junction (GO:0005912)
Pathway: Alzheimer disease-presenilin pathway (P00004)
CDH2,CTNNA2,CTNNB1,EFNB3,EPHA2,EPHA3,EPHA4,ID2,JUP,PDLIM5,PPARGC1A,PRKAA2,TCF4,TCF7L2,IQGAP1,FHIT,NR5A2,SATB1,EFNA1,EFNA5,ID1
BP: regulation of phosphatidylinositol 3-kinase signaling (GO:0014066)
MF: growth factor receptor binding (GO:0070851)
CC: Unclassified (UNCLASSIFIED)
Pathway: Angiogenesis (P00005)
COL1A1,FN1,IL1R1,IRAK1,KDR,KRT19,PDGFA,PDGFB,PDGFRA,PDGFRB,PELI1,PELI2,RASA1,TGM2,MBP,PELI3,PDGFC
BP: cellular response to hypoxia (GO:0071456)
MF: nucleic acid binding (GO:0003676)
CC: Not Significant
Pathway: Unclassified (UNCLASSIFIED)
EGLN1,EIF4A1,EIF4G1,EPAS1,FOXO3,HIF1A,MUC1,PABPC1,PDCD4,FBP1,ESRRA
BP: pre-replicative complex assembly involved in nuclear cell cycle DNA replication (GO:0006267)
MF: DNA replication origin binding (GO:0003688)
CC: MCM core complex (GO:0097373)
Pathway: Toll receptor signaling pathway (P00054)
GRK5,MCM4,MCM5,MCM7,NFKBIA,REL,MAP3K8
BP: nucleotide biosynthetic process (GO:0009165)
MF: ubiquitin protein ligase activity (GO:0061630)
CC: Not Significant
Pathway: P53 pathway feedback loops 1 (P04392)
MDM2,RBBP6,RNF144B,RRM1,RRM2B,TP63,TP73,RRM2,PPP1R13L,SIAH1