GENE ONTOLOGY (GO) ENRICHMENT ANALYSIS FOR TOP 37 GENES

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| Term\_name | Adjusted p\_value | Genes |
| transcription factor binding | 1.7463E-06 | CDKN2A, HES2, AGTR2, SIK1, SMAD2, NOTCH2, HEY1, HES6, ARID1A, GATA3, TAF4B |
| DNA-binding transcription factor binding | 0.00199832 | CDKN2A, SIK1, NOTCH2, HES6, ARID1A, TAF4B |
| NF-kappaB binding | 0.01103704 | CDKN2A, NOTCH2, TAF4B |
| protein serine/threonine kinase inhibitor activity | 0.01336124 | CDKN2A, SPRY2, CDKN2C |
| RNA polymerase II-specific DNA-binding transcription factor binding | 0.01355935 | CDKN2A, NOTCH2, HES6, ARID1A, TAF4B |
| steroid dehydrogenase activity | 0.01741588 | HSD3B7, SRD5A3, HSD17B13 |
| protein threonine kinase activity | 0.02311867 | RPS6KB1, PRKG1, MAP3K5, SIK1, MAPK3, CHEK2 |
| protein serine kinase activity | 0.02311867 | RPS6KB1, PRKG1, MAP3K5, SIK1, MAPK3, CHEK2 |
| cyclin-dependent protein serine/threonine kinase regulator activity | 0.03897986 | CDKN2A, CCND2, CDKN2C |
| kinase activity | 0.04146473 | CDKN2A, RPS6KB1, PRKG1, MAP3K5, SIK1, MAPK3,  CDKN2C, CHEK2 |
| heart development | 2.8414E-05 | MMP21, AGTR2, DNAH5, SIK1, SMAD2, MAPK3,  NOTCH2, HEY1, CASP7, ARID2, GATA3 |
| circulatory system development | 7.0175E-05 | MMP21, AGTR2, DNAH5, SIK1, NRARP, SMAD2, SPRY2,  MAPK3, NOTCH2, HEY1, PDGFA,  CASP7, ARID2, GATA3 |
| embryonic organ development | 0.0038325 | SMAD2, SPRY2, MAPK3, NOTCH2, HEY1, PDGFA, ARID2,  GATA3 |
| pattern specification process | 0.00453784 | HES2, MMP21, DNAH5, NRARP, SMAD2, NOTCH2,  HEY1, HES6 |
| regulation of cell population proliferation | 0.00728327 | CDKN2A, PRKG1, AGTR2, MAP3K5, CCND2,  NRARP, SMAD2, SPRY2, MAPK3, NOTCH2,  CDKN2C, PDGFA, ARID2, GATA3 |
| negative regulation of cellular process | 0.02202497 | BBC3, CDKN2A, WFDC2, HES2, E2F6, RPS6KB1,  PRKG1, AGTR2, CCND2, SIK1, NRARP, SMAD2,  SPRY2, MAPK3, NOTCH2, STMN2, CDKN2C,  HEY1, CHEK2, HES6, PDGFA, ARID2, GATA3 |
| G1/S transition of mitotic cell cycle | 0.02428497 | CDKN2A, E2F6, RPS6KB1, CCND2, CDKN2C, CHEK2 |
| cellular response to ionizing radiation | 0.02518894 | BBC3, CCND2, CHEK2, GATA3 |
| primary metabolic process | 0.02863732 | BBC3, CDKN2A, WFDC2, HES2, HSD3B7, E2F6,  RPS6KB1, SRD5A3, MMP25, MMP21, PRKG1,  AGTR2, HSD17B13, MAP3K5, CCND2, SIK1,  NRARP, SMAD2, MMP27, SPRY2, MAPK3,  NOTCH2, CDKN2C, HEY1, CHEK2, HES6,  PDGFA, CASP7, ARID1A, ARID2, SF3B1,  GATA3, TAF4B |
| developmental process | 0.03687792 | BBC3, CDKN2A, WFDC2, HES2, MMP25, MMP21,  PRKG1, AGTR2, DNAH5, SIK1, NRARP, SMAD2, SPRY2, MAPK3, NOTCH2, STMN2, CDKN2C,  HEY1, CHEK2, HES6, PDGFA, CASP7, ARID1A, ARID2,  GATA3, TAF4B |
| cell population proliferation | 0.0409935 | CDKN2A, PRKG1, AGTR2, MAP3K5, CCND2, NRARP,  SMAD2, SPRY2, MAPK3, NOTCH2, CDKN2C,  PDGFA, ARID2, GATA3 |
| cell cycle G1/S phase transition | 0.04250565 | CDKN2A, E2F6, RPS6KB1, CCND2, CDKN2C, CHEK2 |
| negative regulation of neurotrophin TRK receptor signaling pathway | 0.0499161 | AGTR2, SPRY2 |
| Pathways in cancer | 0.00043514 | BBC3, CDKN2A, RPS6KB1, CCND2, SMAD2, MAPK3,  NOTCH2, HEY1, PDGFA, CASP7 |
| Endocrine resistance | 0.00112564 | CDKN2A, RPS6KB1, MAPK3, NOTCH2, CDKN2C |
| Hepatocellular carcinoma | 0.00125909 | CDKN2A, RPS6KB1, SMAD2, MAPK3, ARID1A, ARID2 |
| Cell cycle | 0.00407894 | CDKN2A, CCND2, SMAD2, CDKN2C, CHEK2 |
| Human T-cell leukemia virus 1 infection | 0.00554072 | CDKN2A, CCND2, SMAD2, MAPK3, CDKN2C, CHEK2 |
| Platinum drug resistance | 0.00702061 | BBC3, CDKN2A, MAP3K5, MAPK3 |
| Human papillomavirus infection | 0.0072762 | HES2, RPS6KB1, CCND2, MAPK3, NOTCH2, HEY1, HES6 |
| p53 signaling pathway | 0.00740976 | BBC3, CDKN2A, CCND2, CHEK2 |
| Pancreatic cancer | 0.00867141 | CDKN2A, RPS6KB1, SMAD2, MAPK3 |
| Cellular senescence | 0.01210297 | CDKN2A, CCND2, SMAD2, MAPK3, CHEK2 |
| Colorectal cancer | 0.01401179 | BBC3, RPS6KB1, SMAD2, MAPK3 |
| MicroRNAs in cancer | 0.03948985 | CDKN2A, CCND2, SPRY2, MAPK3, NOTCH2, PDGFA |
| Generic Transcription Pathway | 0.00071347 | BBC3, CDKN2A, E2F6, CCND2, SMAD2, MAPK3,  NOTCH2, HEY1, CHEK2, ARID1A, ARID2, GATA3,  TAF4B |
| Gene expression (Transcription) | 0.0009357 | BBC3, CDKN2A, E2F6, CCND2, SMAD2, MAPK3,  NOTCH2, HEY1, CHEK2, ARID1A, ARID2, SF3B1,  GATA3, TAF4B |
| RNA Polymerase II Transcription | 0.00207795 | BBC3, CDKN2A, E2F6, CCND2, SMAD2, MAPK3,  NOTCH2, HEY1, CHEK2, ARID1A, ARID2, GATA3,  TAF4B |
| Intrinsic Pathway for Apoptosis | 0.0024113 | BBC3, CDKN2A, MAPK3, CASP7 |
| Apoptotic factor-mediated response | 0.00284414 | CDKN2A, MAPK3, CASP7 |
| Oncogene Induced Senescence | 0.02220946 | CDKN2A, MAPK3, CDKN2C |
| Signaling Pathways in Glioblastoma | 0.00192932 | CDKN2A, CCND2, SPRY2, MAPK3, CDKN2C |
| Integrated Cancer Pathway | 0.00318909 | BBC3, MAP3K5, SMAD2, CHEK2 |
| Apoptosis Modulation and Signaling | 0.00335919 | BBC3, CDKN2A, MAP3K5, MAPK3, CASP7 |
| Osteoblast differentiation | 0.01098478 | HES2, MAPK3, NOTCH2, HEY1, HES6 |
| Notch Signaling Pathway Netpath | 0.01213282 | NOTCH2, HEY1, HES6, GATA3 |
| Cell Cycle | 0.01236421 | CDKN2A, CCND2, SMAD2, CDKN2C, CHEK2 |
| Matrix Metalloproteinases | 0.02533739 | MMP25, MMP21, MMP27 |
| Pancreatic adenocarcinoma pathway | 0.04433688 | CDKN2A, RPS6KB1, SMAD2, MAPK3 |
| p16-cyclin D2-CDK4 complex | 0.01001842 | CDKN2A, CCND2 |
| Adrenocortical carcinoma | 0.02561608 | CDKN2A, CDKN2C, CHEK2 |