

GeDiPNet Cluster 9 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 16:20:32

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cell population proliferation	GO:0008283	33	CTNNB1, KRAS, TP53, CCND1, JUN, MYC, VEGFA, VEGFC, BAP1, ERBB2, ERCC1, BTC	263	270	8.68	1.463e-21	2.870e-18
positive regulation of transcription by RNA polymerase II	GO:0045944	66	CDKN2A, CTNNB1, PTEN, TP53, NRF1, PPARGC1A, GLI1, CSF3, HRAS, JUN, MYC, VEGFA	1208	270	3.78	1.522e-21	2.969e-18
positive regulation of DNA-templated transcription	GO:0045893	49	CDKN1C, CDKN2A, CTNNB1, TP53, PPARGC1A, GLI1, JUN, MYC, ARID1A, NFKBIA, TP63, BLM	778	270	4.36	1.905e-18	2.375e-15
positive regulation of cell population proliferation	GO:0008284	40	CTNNB1, PTEN, CCND1, GLI1, CSF3, FLT1, HRAS, KDR, MYC, VEGFA, VEGFC, IGF2	532	270	5.20	8.843e-18	9.991e-15
negative regulation of transcription by RNA polymerase II	GO:0000122	54	CDKN1C, CDKN2A, CTNNB1, TP53, CCND1, JUN, MYC, VEGFA, IGF2, PCNA, NFKBIA, TP63	1002	270	3.73	2.634e-17	2.673e-14
positive regulation of gene expression	GO:0010628	37	CDKN2A, CTNNB1, KRAS, TP53, PPARGC1A, IL32, BRAF, HRAS, MYC, VEGFA, ERBB2, ERBB3	504	270	5.08	3.643e-16	3.006e-13
heart development	GO:0007507	27	CTNNB1, PTEN, TP53, CCDC39, TEK, PCNA, ERBB2, ERBB3, MMP2, SOD2, ADAMTS6, BCOR	273	270	6.85	3.513e-15	2.419e-12
regulation of gene expression	GO:0010468	32	CDKN2A, CTNNB1, GLI1, MYC, BAP1, NFKBIA, PIK3CA, BMI1, EZH2, LOX, MET, PHLDA2	402	270	5.51	4.413e-15	2.963e-12
negative regulation of apoptotic process	GO:0043066	35	CTNNB1, TP53, BRAF, JUN, KDR, MYC, TEK, VEGFA, AKT2, ERBB2, ERBB3, SOD2	524	270	4.62	4.176e-14	2.402e-11
negative regulation of DNA-templated transcription	GO:0045892	38	CDKN1C, CDKN2A, CTNNB1, TP53, JUN, BAP1, TP63, BCOR, EZH2, HDAC6, MECOM, NR1I2	631	270	4.17	8.126e-14	4.454e-11
positive regulation of epithelial cell proliferation	GO:0050679	15	HRAS, KDR, MYC, VEGFA, VEGFC, TGFA, ERBB2, ERBB3, EGFR, RUNX2, BMP6, NOTCH1	73	270	14.22	1.164e-13	6.241e-11
neuron differentiation	GO:0030182	23	CTNNB1, CCND1, ERBB2, ERBB3, EGFR, HDAC6, MET, RB1, RUNX2, SOX2, DNMT3A, ALDH1A2	222	270	7.17	1.578e-13	8.246e-11
regulation of cell population proliferation	GO:0042127	21	CTNNB1, TP53, BRAF, COL18A1, FLT1, HRAS, JUN, ERBB2, ERBB3, NFKBIA, EGFR, EZH2	201	270	7.23	1.583e-12	6.822e-10
kidney development	GO:0001822	18	CDKN1C, CTNNB1, TRAF3IP1, VEGFA, AMER1, ADAMTS6, COMT, WT1, TP73, ALDH1A2, BAG6, BMP6	146	270	8.53	3.893e-12	1.562e-9
negative regulation of cell population proliferation	GO:0008285	29	APC, CDKN2A, CTNNB1, PTEN, TP53, COL18A1, HRAS, JUN, BAP1, SOD2, TNFRSF8, RB1	444	270	4.52	1.280e-11	4.531e-9