

GeDiPNet Cluster 37 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 06:31:26

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of cell population proliferation	GO:0042127	12	TNF, CTNNB1, BCL6, CSF2, ERBB2, JUN, PTGS1, PTGS2, CDK6, DNMT1, PTCH1, STAT3	201	70	15.94	1.063e-11	3.902e-9
cell population proliferation	GO:0008283	13	CTNNB1, BCL6, CSF2, ERBB2, CCND1, JUN, BRCA2, CDK9, IRS2, MYC, MYCN, SMO	263	70	13.20	1.470e-11	5.198e-9
negative regulation of apoptotic process	GO:0043066	14	TERT, TNF, CTNNB1, AVP, BCL6, LTF, ERBB2, GNRH1, JUN, PTGS2, DDX3X, MYC	524	70	7.13	7.154e-9	1.280e-6
negative regulation of DNA-templated transcription	GO:0045892	15	TNF, CTNNB1, BCL6, CSF2, JUN, DNMT1, EHMT1, KAT6A, L3MBTL2, L3MBTL3, PRAME, PRMT5	631	70	6.35	9.257e-9	1.601e-6
positive regulation of mesenchymal cell proliferation	GO:0002053	5	CTNNB1, IRS2, MYC, MYCN, SMO	26	70	51.34	3.947e-8	5.552e-6
positive regulation of gene expression	GO:0010628	13	TNF, CTNNB1, AVP, CSF2, ERBB2, CDK6, DDX3X, DNMT1, KAT6A, MYC, MYCN, SMO	504	70	6.89	3.996e-8	5.607e-6
positive regulation of miRNA transcription	GO:1902895	6	TERT, TNF, JUN, MYC, MYCN, STAT3	56	70	28.60	6.219e-8	8.144e-6
positive regulation of DNA-templated transcription	GO:0045893	15	TNF, CTNNB1, IRF4, JUN, BRCA2, BRD4, ESR2, FLI1, KAT6A, MYC, MYCN, OTX2	778	70	5.15	1.456e-7	1.662e-5
regulation of DNA-templated transcription	GO:0006355	20	SUFU, IRF4, HIC1, JUN, BRCA2, BRD2, BRD3, BRD4, ESR2, FLI1, KAT6A, L3MBTL2	1454	70	3.67	2.156e-7	2.311e-5
regulation of gene expression	GO:0010468	11	CTNNB1, CSF2, GNRH1, BRD2, CDK6, DNMT1, KDM4B, KDM4C, MYC, PRMT5, SMO	402	70	7.30	2.760e-7	2.842e-5
positive regulation of transcription by RNA polymerase II	GO:0045944	18	TNF, CTNNB1, IRF4, JUN, ATOH1, BRD3, BRD4, CDK9, DDX3X, ESR2, FLI1, KDM4C	1208	70	3.98	3.177e-7	3.189e-5
response to xenobiotic stimulus	GO:0009410	9	TNF, LTA, CTNNB1, AVP, CCND1, JUN, MYC, PTCH1, VAV1	248	70	9.69	3.550e-7	3.503e-5
negative regulation of transcription by RNA polymerase II	GO:0000122	16	TNF, CTNNB1, SUFU, BCL6, HIC1, CCND1, JUN, CCNE1, CDK6, DNMT1, EHMT1, ESR2	1002	70	4.26	6.661e-7	5.951e-5
chromatin organization	GO:0006325	11	BRD2, BRD3, BRD4, DNMT1, EHMT1, KAT6A, KDM4B, KDM4C, L3MBTL2, L3MBTL3, PRMT5	449	70	6.54	8.235e-7	7.086e-5
positive regulation of fibroblast proliferation	GO:0048146	5	JUN, CDK6, MYC, PDGFRA, S100A6	55	70	24.27	1.919e-6	1.391e-4