

GeDiPNet Cluster 4 -- 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 15:48:06

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of transcription by RNA polymerase II	GO:0045944	347	IFNB1, MRTFB, ESR1, FGFR2, ABL1, ACVR1, AHR, AKT1, AR, ATM, BMP2, BMP4	1208	2396	2.24	1.430e-52	3.565e-48
negative regulation of apoptotic process	GO:0043066	197	AKT1, AKT2, ANGPTL4, ARAF, ARHGDIA, AURKA, BAG1, BARD1, BCL2, BCL2A1, BIRC2, BIRC5	524	2396	2.93	1.969e-48	3.820e-44
positive regulation of gene expression	GO:0010628	182	ACTA2, AGR2, AKT1, AR, ATM, BMP2, BMP4, BMPR2, BRCA1, CAV1, CD74, CDH5	504	2396	2.82	6.778e-42	7.888e-38
positive regulation of cell population proliferation	GO:0008284	183	FGFR2, ADAM10, AR, AREG, BCAR3, BCL2, BIRC5, BMP2, BMP4, CCND1, CDKN1B, CSF1	532	2396	2.68	8.827e-39	8.329e-35
apoptotic process	GO:0006915	225	CHEK2, FGFR2, ABL1, ADAR, AFP, AHR, AKT1, AKT2, AURKA, BAG1, BAX, BCL2	747	2396	2.35	3.438e-37	3.001e-33
positive regulation of DNA-templated transcription	GO:0045893	226	CHEK2, ESR1, ACVR1, AHR, AR, ARID1A, BIRC2, BMP2, BMP4, BRCA1, BRCA2, CD74	778	2396	2.27	1.103e-34	7.700e-31
negative regulation of transcription by RNA polymerase II	GO:0000122	266	ESR1, FGFR2, AR, BMP2, BMP4, C1QBP, CASP7, CAV1, CCND1, CCNE1, CDKN2A, CTNNB1	1002	2396	2.07	1.789e-33	1.201e-29
negative regulation of cell population proliferation	GO:0008285	151	ADAMTS1, AR, BAP1, BAX, BCHE, BCL2, BMP2, BMP4, BMPR2, CAV1, CDH5, CDKN1B	444	2396	2.65	1.808e-31	1.002e-27
positive regulation of cell migration	GO:0030335	116	ACVR1, ADAM10, AKT1, AKT2, ATM, BMP2, BMP4, CASP8, CAV1, CDH5, CLDN1, CLDN4	292	2396	3.10	2.352e-31	1.283e-27
response to xenobiotic stimulus	GO:0009410	105	HMGCS2, ABCB1, ABCC1, ABL1, ACACB, AHR, BCAR3, BCHE, BCL2, CAT, CCND1, CDH1	248	2396	3.30	2.750e-31	1.477e-27
positive regulation of apoptotic process	GO:0043065	124	ABL1, ATM, BARD1, BAX, BCL2, BCL2A1, BMP2, BMP4, C1QBP, CASP8, CDKN2A, CTNNB1	326	2396	2.97	2.816e-31	1.490e-27
response to hypoxia	GO:0001666	84	ABCB1, ANGPTL4, BIRC2, BMP2, CAT, CAV1, COMT, CPT1A, CXCL12, CXCR4, CYP1A1, DIO3	176	2396	3.72	8.848e-30	4.232e-26
positive regulation of MAPK cascade	GO:0043410	93	FGFR2, AR, BCAR3, BMP2, CD40, CD74, CDH2, CTNNB1, EFNA1, EGF, EGFR, ERBB2	224	2396	3.24	4.514e-27	1.771e-23
angiogenesis	GO:0001525	103	FGFR2, ANGPTL4, BMP4, CASP8, CAV1, CXCL8, CYP1B1, DLL4, EFNA1, EGF, ELK3, EPHB4	284	2396	2.83	2.913e-24	8.406e-21
regulation of cell population proliferation	GO:0042127	80	ABL1, ALK, BIRC2, BMPR2, CHEK1, CSF2, CTNNB1, CXCL9, DNMT1, EGFR, ERBB2, ERBB3	201	2396	3.10	4.590e-22	9.712e-19