

GeDiPNet Cluster 214 -- 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 20:39:28

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
negative regulation of cell population proliferation	GO:0008285	18	BAP1, CDKN1B, NDRG1, RAF1, SOD2, TNFRSF9, TSC2, VHL, CDKN2A, PTEN, RB1, TP53	444	148	5.12	1.497e-8	2.427e-6
heart development	GO:0007507	14	BCOR, CDKN1B, MAPK1, SOD2, TSC2, PRKG1, PTEN, TP53, ASCL1, BMP6, DYNC2H1, EP300	273	148	6.48	3.713e-8	5.266e-6
chromatin organization	GO:0006325	17	BAP1, BCOR, HLTF, ARID1A, BRD9, CHD3, DNMT3A, KMT2C, KMT2D, RB1, SMARCA4, TET2	449	148	4.78	1.037e-7	1.245e-5
positive regulation of cell differentiation	GO:0045597	8	VHL, ARID1A, RPS6KA1, SMARCA4, TP73, FGFR1, INSM1, SOX2	83	148	12.17	3.058e-7	3.096e-5
regulation of G1/S transition of mitotic cell cycle	GO:2000045	7	CCND1, CDKN1B, ARID1A, CDKN2A, RB1, SMARCA4, ID2	57	148	15.51	3.218e-7	3.224e-5
face development	GO:0060324	5	BRAF, MAPK1, MAPK3, RAF1, ALDH1A2	22	148	28.70	6.879e-7	6.123e-5
regulation of gene expression	GO:0010468	15	BAP1, MAPK3, VHL, CDKN2A, DNMT3A, IL2RG, TET2, TP73, ASCL1, FGFR1, ID2, INSM1	402	148	4.71	7.344e-7	6.463e-5
positive regulation of transcription by RNA polymerase II	GO:0045944	27	HLTF, IL2, MAPK3, RAF1, CD28, CDKN2A, CREBBP, KMT2C, KMT2D, PTEN, RB1, RPS6KA1	1208	148	2.82	8.485e-7	7.253e-5
negative regulation of apoptotic process	GO:0043066	17	AURKA, AXL, BRAF, FIGNL1, IL2, PTGS2, RAF1, SOD2, TPT1, VHL, CD28, RPS6KA1	524	148	4.10	9.040e-7	7.632e-5
cell population proliferation	GO:0008283	12	BAP1, CCND1, RB1, TP53, ZEB1, ALDH1A2, BRCA2, CNTNAP2, EGFR, FGFR1, INSM1, KIT	263	148	5.76	1.259e-6	9.980e-5
neuron differentiation	GO:0030182	11	CCND1, DNMT3A, RB1, ALDH1A2, ASCL1, BMP6, DYNC2H1, EGFR, ID2, INSM1, SOX2	222	148	6.26	1.596e-6	1.205e-4
chromatin remodeling	GO:0006338	13	AURKA, BCOR, ARID1A, BRD9, CHD3, CREBBP, KMT2C, RB1, SMARCA4, BRCA2, EP300, PHC1	320	148	5.13	1.642e-6	1.233e-4
mammary gland epithelial cell proliferation	GO:0033598	4	CCND1, MAPK1, CDKN2A, ID2	12	148	42.09	1.780e-6	1.314e-4
apoptotic process	GO:0006915	20	AURKA, AXL, CDKN1B, MAPK1, MAPK3, RAF1, RASSF5, TNFRSF9, TNFSF10, TNFRSF1B, CDKN2A, PTEN	747	148	3.38	1.861e-6	1.359e-4
response to epidermal growth factor	GO:0070849	3	MAPK1, MAPK3, ASCL1	5	148	75.76	4.812e-6	2.911e-4