

GeDiPNet Cluster 549 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:01:14

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	7	POU5F1, KMT2D, MAML2, CRT1C, CRT1C3, HRAS, CREB3L2	1208	17	6.37	5.071e-5	1.869e-3
regulation of cell cycle	GO:0051726	4	HRAS, MSH2, BAP1, BARD1	262	17	16.78	7.784e-5	2.568e-3
chromatin remodeling	GO:0006338	4	BAZ1A, CHD4, ARID1A, BARD1	320	17	13.74	1.684e-4	4.485e-3
tissue homeostasis	GO:0001894	2	BAP1, BARD1	27	17	81.42	2.698e-4	6.279e-3
chromatin organization	GO:0006325	4	KMT2D, CHD4, ARID1A, BAP1	449	17	9.79	6.104e-4	1.088e-2
cell fate commitment involved in formation of primary germ layer	GO:0060795	1	POU5F1	1	17	1099.24	9.097e-4	1.386e-2
beta-catenin-TCF complex assembly	GO:1904837	1	KMT2D	1	17	1099.24	9.097e-4	1.386e-2
thrombocyte differentiation	GO:0002574	1	BAP1	1	17	1099.24	9.097e-4	1.386e-2
nucleate erythrocyte differentiation	GO:0043363	1	BAP1	1	17	1099.24	9.097e-4	1.386e-2
negative regulation of mRNA 3'-end processing	GO:0031441	1	BARD1	1	17	1099.24	9.097e-4	1.386e-2
regulation of heterochromatin formation	GO:0031445	1	BAZ1A	1	17	1099.24	9.097e-4	1.386e-2
cellular response to cAMP	GO:0071320	2	CRT1C, CRT1C3	58	17	37.90	1.250e-3	1.661e-2
energy homeostasis	GO:0097009	2	CRT1C, CRT1C3	64	17	34.35	1.519e-3	1.840e-2
protein homotetramerization	GO:0051289	2	CRT1C, CRT1C3	66	17	33.31	1.615e-3	1.892e-2
endodermal-mesodermal cell signaling	GO:0003133	1	POU5F1	2	17	549.62	1.819e-3	2.024e-2