

GeDiPNet Cluster 218 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See [scripts/build_cluster_enrichment.php](#) on [gedipnet.bicnirrh.res.in](#). Data as of: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 10:36:46

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Regulation of TP53 Activity through Acetylation	Reactome	3	EP300, KAT6A, CHD4	23	44	35.60	7.720e-5	1.838e-3
Polycomb repressive complex	KEGG	4	EP300, AUTS2, ASXL2, ASXL3	83	44	13.15	2.333e-4	4.454e-3
RUNX1 interacts with co-factors whose precise effect on RUNX1 targets is not known	Reactome	3	EP300, AUTS2, CSNK2A1	38	44	21.55	3.539e-4	6.210e-3
DCC mediated attractive signaling	Reactome	2	RAC1, TRIO	11	44	49.63	7.065e-4	1.066e-2
HDMs demethylate histones	Reactome	3	KDM6A, KDM3B, KDM6B	50	44	16.38	7.974e-4	1.171e-2
Lysine degradation	KEGG	3	KMT2D, KMT2C, NSD2	63	44	13.00	1.563e-3	1.950e-2
Transcriptional regulation of white adipocyte differentiation	Reactome	3	EP300, MED13L, MED23	67	44	12.22	1.866e-3	2.215e-2
PKMTs methylate histone lysines	Reactome	3	KMT2D, KMT2C, NSD2	71	44	11.53	2.204e-3	2.504e-2
Signal transduction by L1	Reactome	2	CSNK2A1, RAC1	21	44	26.00	2.636e-3	2.859e-2
Adherens junction	KEGG	3	EP300, CSNK2A1, RAC1	93	44	8.80	4.732e-3	4.290e-2
RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	Reactome	3	EP300, KMT2D, KMT2C	97	44	8.44	5.322e-3	4.650e-2
NGF-stimulated transcription	Reactome	2	EP300, CHD4	35	44	15.60	7.229e-3	5.699e-2
Processing of Capped Intron-Containing Pre-mRNA	Reactome	2	HNRNPR, HNRNPH1	37	44	14.75	8.054e-3	6.112e-2
PPARA activates gene expression	Reactome	3	EP300, MED13L, MED23	115	44	7.12	8.516e-3	6.334e-2
NRAGE signals death through JNK	Reactome	2	RAC1, TRIO	55	44	9.93	1.723e-2	9.752e-2