

GeDiPNet Cluster 273 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 16:51:37

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Deactivation of the beta-catenin transactivating complex	Reactome	3	TCF7L1, SOX2, SOX3	42	20	42.89	4.350e-5	1.141e-3
Basal cell carcinoma	KEGG	3	GLI2, TCF7L1, SHH	63	20	28.60	1.472e-4	3.065e-3
Pathways in cancer	KEGG	5	GLI2, TCF7L1, ARNT2, FGFR1, SHH	533	20	5.63	1.504e-3	1.849e-2
Signaling pathways regulating pluripotency of stem cells	KEGG	3	HESX1, FGFR1, SOX2	144	20	12.51	1.657e-3	1.992e-2
Signaling by FGFR1 amplification mutants	Reactome	1	FGFR1	1	20	600.50	1.665e-3	1.998e-2
Hippo signaling pathway	KEGG	3	GLI2, TCF7L1, SOX2	157	20	11.47	2.122e-3	2.383e-2
Hedgehog signaling pathway	KEGG	2	GLI2, SHH	56	20	21.45	3.845e-3	3.666e-2
Signaling by plasma membrane FGFR1 fusions	Reactome	1	FGFR1	3	20	200.17	4.988e-3	4.365e-2
FGFR1c and Klotho ligand binding and activation	Reactome	1	FGFR1	3	20	200.17	4.988e-3	4.365e-2
GLI proteins bind promoters of Hh responsive genes to promote transcription	Reactome	1	GLI2	3	20	200.17	4.988e-3	4.365e-2
POU5F1 (OCT4), SOX2, NANOG repress genes related to differentiation	Reactome	1	SOX2	3	20	200.17	4.988e-3	4.365e-2
Regulation of commissural axon pathfinding by SLIT and ROBO	Reactome	1	ROBO1	3	20	200.17	4.988e-3	4.365e-2
Role of ABL in ROBO-SLIT signaling	Reactome	1	ROBO1	4	20	150.13	6.645e-3	5.278e-2
HHAT G278V abrogates palmitoylation of Hh-Np	Reactome	1	SHH	4	20	150.13	6.645e-3	5.278e-2
SLIT2:ROBO1 increases RHOA activity	Reactome	1	ROBO1	4	20	150.13	6.645e-3	5.278e-2