

GeDiPNet Cluster 549 -- 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](scripts/build_cluster_enrichment.php) on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:02:46

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
SHC1 events in ERBB4 signaling	Reactome	2	ERBB4, HRAS	14	17	100.92	1.699e-4	2.893e-3
GRB2 events in ERBB2 signaling	Reactome	2	ERBB4, HRAS	14	17	100.92	1.699e-4	2.893e-3
Human T-cell leukemia virus 1 infection	KEGG	4	CRTC1, CRTC3, HRAS, CREB3L2	224	17	12.62	2.316e-4	3.683e-3
Signaling by ERBB2 TMD/JMD mutants	Reactome	2	ERBB4, HRAS	22	17	64.22	4.284e-4	5.929e-3
ATP-dependent chromatin remodeling	KEGG	3	BAZ1A, CHD4, ARID1A	117	17	18.11	5.546e-4	7.244e-3
Signaling by ERBB2 KD Mutants	Reactome	2	ERBB4, HRAS	25	17	56.52	5.550e-4	7.246e-3
Circadian Clock	Reactome	2	CRTC1, CRTC3	28	17	50.46	6.976e-4	8.619e-3
Human papillomavirus infection	KEGG	4	MAML2, CHD4, HRAS, CREB3L2	333	17	8.49	1.038e-3	1.166e-2
Transcriptional activation of mitochondrial biogenesis	Reactome	2	CRTC1, CRTC3	51	17	27.70	2.308e-3	2.119e-2
Viral carcinogenesis	KEGG	3	CHD4, HRAS, CREB3L2	205	17	10.34	2.793e-3	2.422e-2
Defective Mismatch Repair Associated With MSH6	Reactome	1	MSH2	2	17	353.24	2.829e-3	2.444e-2
Defective Mismatch Repair Associated With MSH3	Reactome	1	MSH2	2	17	353.24	2.829e-3	2.444e-2
Thermogenesis	KEGG	3	HRAS, CREB3L2, ARID1A	234	17	9.06	4.057e-3	3.162e-2
Defective Mismatch Repair Associated With MSH2	Reactome	1	MSH2	3	17	235.49	4.241e-3	3.256e-2
RAS GTPase cycle mutants	Reactome	1	HRAS	3	17	235.49	4.241e-3	3.256e-2