

GeDiPNet Cluster 459 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:02:41

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Breast cancer	KEGG	4	TP53, NOTCH2, KRAS, BRCA2	148	7	46.37	7.531e-7	3.258e-5
DNA Damage/Telomere Stress Induced Senescence	Reactome	3	ATM, TP53, POT1	66	7	77.99	5.462e-6	1.767e-4
Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	Reactome	3	ATM, TP53, NSD2	76	7	67.73	8.370e-6	2.516e-4
Pancreatic cancer	KEGG	3	TP53, KRAS, BRCA2	77	7	66.85	8.707e-6	2.602e-4
G2/M DNA damage checkpoint	Reactome	3	ATM, TP53, NSD2	84	7	61.28	1.132e-5	3.226e-4
MicroRNAs in cancer	KEGG	4	ATM, TP53, NOTCH2, KRAS	311	7	22.07	1.452e-5	3.977e-4
Stabilization of p53	Reactome	2	ATM, TP53	11	7	311.95	1.598e-5	4.315e-4
Endocrine resistance	KEGG	3	TP53, NOTCH2, KRAS	99	7	51.99	1.857e-5	4.899e-4
Human papillomavirus infection	KEGG	4	ATM, TP53, NOTCH2, KRAS	333	7	20.61	1.902e-5	5.000e-4
TP53 Regulates Transcription of Caspase Activators and Caspases	Reactome	2	ATM, TP53	12	7	285.95	1.917e-5	5.023e-4
Thyroid hormone signaling pathway	KEGG	3	TP53, NOTCH2, KRAS	122	7	42.19	3.475e-5	8.177e-4
Apoptosis	KEGG	3	ATM, TP53, KRAS	137	7	37.57	4.915e-5	1.077e-3
Regulation of TP53 Activity through Methylation	Reactome	2	ATM, TP53	19	7	180.60	4.956e-5	1.083e-3
TP53 Regulates Transcription of Genes Involved in Cytochrome C Release	Reactome	2	ATM, TP53	20	7	171.57	5.505e-5	1.177e-3
Cellular senescence	KEGG	3	ATM, TP53, KRAS	157	7	32.78	7.381e-5	1.490e-3