

GeDiPNet Cluster 23 -- 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 16:43:51

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Packaging Of Telomere Ends	Reactome	7	H4C3, TINF2, H4C1, H4C11, H4C5, H2BC12, H4C9	52	114	14.18	5.423e-7	2.871e-5
Recognition and association of DNA glycosylase with site containing an affected purine	Reactome	7	H4C3, TINF2, H4C1, H4C11, H4C5, H2BC12, H4C9	56	114	13.17	9.112e-7	4.478e-5
Cleavage of the damaged purine	Reactome	7	H4C3, TINF2, H4C1, H4C11, H4C5, H2BC12, H4C9	56	114	13.17	9.112e-7	4.478e-5
DNA Damage/Telomere Stress Induced Senescence	Reactome	7	H4C3, TINF2, H4C1, H4C11, H4C5, H2BC12, H4C9	66	114	11.17	2.830e-6	1.200e-4
PRC2 methylates histones and DNA	Reactome	7	DNMT3A, H4C3, H4C1, H4C11, H4C5, H2BC12, H4C9	73	114	10.10	5.606e-6	2.128e-4
HDMs demethylate histones	Reactome	6	KDM5B, H4C3, H4C1, H4C11, H4C5, H4C9	50	114	12.64	7.247e-6	2.627e-4
NoRC negatively regulates rRNA expression	Reactome	6	H4C3, H4C1, H4C11, H4C5, H2BC12, H4C9	61	114	10.36	2.326e-5	6.915e-4
B-WICH complex positively regulates rRNA expression	Reactome	7	ERCC6, H4C3, H4C1, H4C11, H4C5, H2BC12, H4C9	91	114	8.10	2.420e-5	7.150e-4
HATs acetylate histones	Reactome	7	PAX3, H4C3, H4C1, H4C11, H4C5, H2BC12, H4C9	93	114	7.93	2.789e-5	8.010e-4
SIRT1 negatively regulates rRNA expression	Reactome	6	H4C3, H4C1, H4C11, H4C5, H2BC12, H4C9	63	114	10.03	2.803e-5	8.041e-4
RNA Polymerase I Promoter Opening	Reactome	6	H4C3, H4C1, H4C11, H4C5, H2BC12, H4C9	63	114	10.03	2.803e-5	8.041e-4
Hepatocellular carcinoma	KEGG	9	FZD5, WNT10A, WNT11, WNT3, WNT7A, HMOX1, IGF1R, IGF2, PIK3CA	170	114	5.58	3.352e-5	9.304e-4
Activated PKN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3	Reactome	6	H4C3, H4C1, H4C11, H4C5, H2BC12, H4C9	67	114	9.43	3.992e-5	1.079e-3
Nonhomologous End-Joining (NHEJ)	Reactome	6	H4C3, H4C1, H4C11, H4C5, H2BC12, H4C9	69	114	9.16	4.723e-5	1.236e-3
Signaling pathways regulating pluripotency of stem cells	KEGG	8	ISL1, FZD5, WNT10A, WNT11, WNT3, WNT7A, IGF1R, PIK3CA	144	114	5.85	6.633e-5	1.627e-3