

GeDiPNet Cluster 39 -- 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 04:48:02

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Fanconi anemia pathway	KEGG	24	MLH1, PALB2, PMS2, FANCM, BRCA1, BRCA2, BRIP1, ERCC4, FAAP100, FANCA, FANCB, FANCC	54	126	42.36	3.413e-34	1.396e-30
Fanconi Anemia Pathway	Reactome	17	FANCM, ERCC4, FAAP100, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL	40	126	40.51	5.373e-24	8.798e-21
Resolution of D-loop Structures through Holliday Junction Intermediates	Reactome	16	ATM, PALB2, RAD51D, BRCA1, BRCA2, BRIP1, RAD51, RAD51C, SLX4, XRCC2, BARD1, MRE11	33	126	46.21	8.107e-24	1.227e-20
Homologous DNA Pairing and Strand Exchange	Reactome	14	ATM, PALB2, RAD51D, BRCA1, BRCA2, BRIP1, RAD51, RAD51C, XRCC2, BARD1, MRE11, NBN	25	126	53.38	3.773e-22	4.433e-19
Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA)	Reactome	14	ATM, PALB2, RAD51D, BRCA1, BRCA2, BRIP1, RAD51, RAD51C, XRCC2, BARD1, MRE11, NBN	26	126	51.32	8.103e-22	8.773e-19
HDR through Homologous Recombination (HRR)	Reactome	15	ATM, PALB2, RAD51D, POLE, BRCA1, BRCA2, BRIP1, RAD51, RAD51C, XRCC2, BARD1, MRE11	48	126	29.79	7.134e-19	4.863e-16
Presynaptic phase of homologous DNA pairing and strand exchange	Reactome	14	ATM, RAD51D, BRCA1, BRCA2, BRIP1, RAD51, RAD51C, XRCC2, BARD1, MRE11, NBN, RAD50	39	126	34.22	1.129e-18	7.514e-16
Homologous recombination	KEGG	14	ATM, PALB2, RAD51D, BRCA1, BRCA2, BRIP1, RAD51, RAD51C, XRCC2, BARD1, MRE11, NBN	41	126	32.55	2.593e-18	1.600e-15
HDR through Single Strand Annealing (SSA)	Reactome	11	ATM, BRCA1, BRIP1, ERCC4, RAD51, BARD1, MRE11, NBN, RAD50, ATRIP, EXO1	37	126	28.34	7.385e-14	1.928e-11
Colorectal cancer	KEGG	14	MLH1, MSH2, MSH6, TGFBR2, APC, TP53, PIK3CA, KRAS, MSH3, SMAD2, SMAD3, SMAD4	87	126	15.34	2.658e-13	6.300e-11
Cellular senescence	KEGG	17	ATM, CHEK2, RB1, TGFBR2, TP53, MRE11, NBN, PTEN, RAD50, PIK3CA, E2F4, KRAS	157	126	10.32	5.388e-13	1.227e-10
Hepatocellular carcinoma	KEGG	17	RB1, TGFBR2, APC, TP53, GSTM1, GSTT1, PTEN, PIK3CA, SMARCA4, KRAS, SMAD2, SMAD3	170	126	9.53	1.998e-12	4.132e-10
Pathways in cancer	KEGG	27	MLH1, MSH2, MSH6, RB1, TGFBR2, APC, TP53, BRCA2, GSTM1, GSTT1, RAD51, VHL	533	126	4.83	5.954e-12	1.113e-9
Pancreatic cancer	KEGG	12	RB1, TGFBR2, TP53, BRCA2, RAD51, PIK3CA, KRAS, SMAD2, SMAD3, SMAD4, TGFBR1, VEGFA	77	126	14.85	2.158e-11	3.583e-9
TP53 Regulates Transcription of DNA Repair Genes	Reactome	11	ATM, MLH1, MSH2, PMS2, RAD51D, TP53, BRCA1, FANCC, FANCD2, FANCI, CDK9	65	126	16.13	6.038e-11	9.097e-9