GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test (P(X>=k)), Benjamini-Hochberg FDR-corrected across all tested pairs. Corroborated Shared Genes: count of shared genes backed by >=2 distinct disease_gdp.main_source values combined across both diseases (e.g. GWAS-backed for one, ClinVar-backed for the other still counts); Shared Gene Names lists each gene's own source count in parentheses. Overlap Coefficient: shared genes / MIN(each disease's own total gene count) -- complements the Jaccard-based Similarity Score by showing how much of the SMALLER disease's entire known gene-set is covered by this pair, which Jaccard (dividing by the union) can understate. Shared Cluster: cluster id if both diseases fall in the same label-propagation cluster (scripts/build_disease_clusters.php), blank otherwise. See scripts/build_related.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-09 03:00:13. Filters applied: disease name contains "fanconi anemia complementation group d1" (6 matching pairs). · Rows: 6 · Generated: 2026-10-09 20:04:05

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
BRCA2-related cancer predisposition	fanconi anemia complementation group d1	1	0	BRCA2 (1)	0.50000	1.00000	6.494e-5	2.329e-4	
Bronchus cancer	fanconi anemia complementation group d1	1	1	BRCA2 (2)	0.16667	1.00000	3.247e-4	7.705e-4	
fanconi anemia complementation group d1	Hereditary breast-ovarian cancer syndrome	1	1	BRCA2 (4)	0.16667	1.00000	3.247e-4	7.705e-4	
Chordoma	fanconi anemia complementation group d1	1	1	BRCA2 (2)	0.16667	1.00000	3.247e-4	7.705e-4	
fanconi anemia complementation group d1	Respiratory system cancer	1	1	BRCA2 (2)	0.16667	1.00000	3.247e-4	7.705e-4	
fanconi anemia complementation group d1	Tumor predisposition syndrome	1	1	BRCA2 (2)	0.14286	1.00000	3.897e-4	8.660e-4	