

GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test ($P(X \geq k)$), 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 A" (5 matching pairs). · Rows: 5 · Generated: 2026-10-09 14:04:52

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Fanconi anemia complementation group A	Salivary gland neoplasms	1	1	FANCA (2)	0.02222	1.00000	2.858e-3	3.805e-3	
Fanconi anemia complementation group A	Hyperinsulinism	1	1	FANCA (3)	0.02326	1.00000	2.728e-3	3.664e-3	
Fanconi anemia	Fanconi anemia complementation group A	1	1	FANCA (7)	0.02500	1.00000	2.533e-3	3.445e-3	
Fanconi anemia complementation group A	Pituitary stalk interruption syndrome	1	1	FANCA (2)	0.03125	1.00000	2.013e-3	2.900e-3	
Fanconi anemia complementation group A	Renal pelvis neoplasms	1	1	FANCA (2)	0.14286	1.00000	3.897e-4	8.660e-4	