

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: 2026-10-20 03:00:20. Filters applied: disease name contains "Urinary tract carcinoma" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 04:13:17

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Deafness, autosomal recessive 39	Urinary tract carcinoma	1	0	HGF (1)	0.50000	1.00000	6.457e-5	1.985e-4	
Ovarian angiosarcoma	Urinary tract carcinoma	1	0	HGF (1)	0.12500	1.00000	4.520e-4	8.260e-4	
Copper overload cirrhosis	Urinary tract carcinoma	1	1	HGF (3)	0.08333	1.00000	7.102e-4	1.174e-3	
Hyperbilirubinemia	Urinary tract carcinoma	1	1	HGF (2)	0.07143	1.00000	8.394e-4	1.336e-3	
Angle closure glaucoma	Urinary tract carcinoma	1	1	HGF (2)	0.06667	1.00000	9.039e-4	1.411e-3	