

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: 2026-10-11 03:00:14. Filters applied: disease name contains "Laryngeal carcinoma" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 19:24:06

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Laryngeal carcinoma	Male reproductive system disease	1	0	WNT7B (1)	0.07143	0.25000	2.595e-3	3.514e-3	
Bilateral generalized polymicrogyria	Laryngeal carcinoma	1	1	RTTN (3)	0.08333	0.50000	1.298e-3	2.063e-3	
Laryngeal carcinoma	Wagner syndrome	1	1	VCAN (5)	0.09091	1.00000	6.494e-4	1.241e-3	
Laryngeal carcinoma	microcephalic primordial dwarfism due to RTTN deficiency	1	1	RTTN (2)	0.09091	1.00000	6.494e-4	1.241e-3	
Laryngeal carcinoma	Laryngeal neoplasms	4	0	ATXN10 (1), PRKG1 (1), WNT7B (1), SH3BP4 (1)	0.30769	0.66667	1.345e-12	1.607e-11	