

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: 2026-10-10 03:00:13. Filters applied: disease name contains "Digeorge syndrome" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 16:37:06

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
22q11 deletion syndrome	Digeorge syndrome	1	1	FGF8 (2)	0.05000	1.00000	1.234e-3	1.986e-3	
Digeorge syndrome	Intermittent explosive disorder	1	1	COMT (2)	0.05000	1.00000	1.234e-3	1.986e-3	
Chromosome 22q11.2 microduplication syndrome	Digeorge syndrome	1	1	TBX1 (5)	0.05000	1.00000	1.234e-3	1.986e-3	
Digeorge syndrome	Velocardiofacial syndrome	5	5	TBX1 (6), DGCR8 (4), DGCR2 (4), DGCR6 (4), ESS2 (4)	0.25000	1.00000	1.613e-15	2.379e-14	
22q11.2 deletion syndrome	Digeorge syndrome	9	9	ARVCF (2), COMT (3), GP1BB (2), HIRA (2), JMJD1C (3), RREB1 (3), SEC24C (3), TBX1 (6), UFD1 (2)	0.45000	1.00000	6.905e-28	1.945e-26	