

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 "HAND2 related congenital heart defect" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 07:47:59

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
HAND2 related congenital heart defect	Neuroblastoma	1	1	HAND2 (2)	0.00658	1.00000	9.806e-3	1.113e-2	
HAND2 related congenital heart defect	Tetralogy of fallot	1	1	HAND2 (3)	0.00870	1.00000	7.404e-3	8.700e-3	
Cardiomegaly	HAND2 related congenital heart defect	1	1	HAND2 (2)	0.01176	1.00000	5.455e-3	6.632e-3	
Congenital heart defects	HAND2 related congenital heart defect	1	1	HAND2 (3)	0.01408	1.00000	4.546e-3	5.668e-3	
HAND2 related congenital heart defect	Ventricular remodeling	1	1	HAND2 (2)	0.03846	1.00000	1.624e-3	2.461e-3	