

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 "Coronary syndrome" (7 matching pairs). · Rows: 7 · Generated: 2026-10-10 16:37:07

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Coronary syndrome	Endometrial hyperplasia	1	1	CELSR2 (3)	0.07143	0.25000	2.595e-3	3.514e-3	
Common migraine	Coronary syndrome	1	1	PHACTR1 (2)	0.07143	0.25000	2.595e-3	3.514e-3	
Connective tissue neoplasm	Coronary syndrome	1	0	LPL (1)	0.08333	0.25000	2.077e-3	2.969e-3	
Coronary syndrome	Paralytic strabismus	1	0	PHACTR1 (1)	0.10000	0.25000	1.558e-3	2.376e-3	
Cerebrovascular trauma	Coronary syndrome	1	1	PHACTR1 (2)	0.20000	1.00000	2.598e-4	6.509e-4	
Aneurysm	Coronary syndrome	2	0	CELSR2 (1), LPA (1)	0.06667	0.50000	1.773e-5	8.460e-5	
Aortic stenosis	Coronary syndrome	3	0	LPL (1), CELSR2 (1), LPA (1)	0.04839	0.75000	2.244e-7	1.483e-6	