

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 "Sveinsson chorioretinal atrophy" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 16:23:00

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Aicardi syndrome	Sveinsson chorioretinal atrophy	1	1	TEAD1 (4)	0.25000	0.50000	2.598e-4	6.509e-4	
Lynch syndrome	Sveinsson chorioretinal atrophy	1	1	SEMA4A (2)	0.01961	0.50000	6.355e-3	7.624e-3	
Cone-rod dystrophy	Sveinsson chorioretinal atrophy	1	1	SEMA4A (6)	0.01316	0.50000	9.589e-3	1.090e-2	
Large artery stroke	Sveinsson chorioretinal atrophy	1	1	TEAD1 (4)	0.01250	0.50000	1.011e-2	1.146e-2	
Liver disease	Sveinsson chorioretinal atrophy	1	1	TEAD1 (4)	0.00629	0.50000	2.029e-2	2.206e-2	