GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test (P(X>=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: 2026-10-20 03:00:20. Filters applied: disease name contains "Snyder-robinson syndrome" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 03:38:46

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Snyder-robinson syndrome	Syndromic X-linked intellectual disability Snyder type	1	1	SMS (2)	0.50000	1.00000	6.457e-5	1.985e-4	
Smith-magenis syndrome	Snyder-robinson syndrome	1	1	SMS (2)	0.25000	1.00000	1.937e-4	4.414e-4	
Snyder-robinson syndrome	X-linked intellectual disability	1	1	SMS (2)	0.01333	1.00000	4.778e-3	5.751e-3	
Intellectual developmental disorder, x-linked	Snyder-robinson syndrome	1	1	SMS (3)	0.01099	1.00000	5.811e-3	6.843e-3	
Developmental disability	Snyder-robinson syndrome	1	1	SMS (2)	0.00694	1.00000	9.233e-3	1.038e-2	