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 "Abnormal brain morphology" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 08:43:15

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Abnormal brain morphology	Neuroblastoma	1	1	LRRC45 (2)	0.00375	0.50000	3.393e-2	3.559e-2	
Abnormal brain morphology	Ciliopathy	1	1	LRRC45 (3)	0.01205	0.50000	1.043e-2	1.162e-2	
Abnormal brain morphology	Hydrocephalus	1	0	WDR91 (1)	0.02941	0.50000	4.128e-3	5.056e-3	
Abnormal brain morphology	Neurodevelopmental delay	1	0	WDR91 (1)	0.12500	0.50000	7.747e-4	1.247e-3	
Abnormal brain morphology	Hygroma	1	0	WDR91 (1)	0.33333	1.00000	1.291e-4	3.269e-4	