

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: 2026-10-22 03:00:19. Filters applied: disease name contains "Kufs disease" (5 matching pairs). · Rows: 5 · Generated: 2026-10-21 23:44:21

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Kufs disease	Metabolic syndrome	1	1	DNAJC5 (2)	0.00077	1.00000	8.419e-2	8.509e-2	
Hypertension	Kufs disease	1	1	DNAJC5 (2)	0.00087	1.00000	7.412e-2	7.519e-2	
Kufs disease	Neuronal ceroid lipofuscinosis	1	1	DNAJC5 (6)	0.03125	1.00000	2.002e-3	2.719e-3	
Adult neuronal ceroid lipofuscinosis	Kufs disease	1	1	DNAJC5 (2)	0.33333	1.00000	1.291e-4	3.269e-4	
Ceroid lipofuscinosis, neuronal, 4b (kufs type), autosomal dominant	Kufs disease	1	0	DNAJC5 (1)	0.50000	1.00000	6.457e-5	1.985e-4	