

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 "Combined malonic and methylmalonic acidemia" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 15:10:21

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Combined malonic and methylmalonic acidemia	Combined malonic and methylmalonic aciduria	1	1	ACSF3 (7)	0.50000	1.00000	6.494e-5	2.331e-4	
Combined malonic and methylmalonic acidemia	Malonic aciduria	1	1	ACSF3 (6)	0.33333	1.00000	1.299e-4	3.931e-4	
Combined malonic and methylmalonic acidemia	Methylmalonic acidemia	1	1	ACSF3 (6)	0.03571	1.00000	1.753e-3	2.609e-3	
Combined malonic and methylmalonic acidemia	Non-melanoma skin carcinoma	1	1	ACSF3 (4)	0.00588	1.00000	1.098e-2	1.236e-2	
Combined malonic and methylmalonic acidemia	Global developmental delay	1	1	ACSF3 (5)	0.00270	1.00000	2.403e-2	2.575e-2	