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: 2026-10-22 03:00:19. Filters applied: disease name contains "Mental retardation, autosomal dominant 50" (5 matching pairs). · Rows: 5 · Generated: 2026-10-21 23:06:40

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Congenital heart disease	Mental retardation, autosomal dominant 50	1	0	NAA15 (1)	0.00559	1.00000	1.149e-2	1.272e-2	
Developmental disability	Mental retardation, autosomal dominant 50	1	1	NAA15 (2)	0.00694	1.00000	9.233e-3	1.038e-2	
Mental retardation, autosomal dominant 50	Tetralogy of fallot	1	1	NAA15 (2)	0.00885	1.00000	7.231e-3	8.372e-3	
Mental retardation, autosomal dominant 50	Syndromic intellectual disability	1	1	NAA15 (2)	0.01852	1.00000	3.422e-3	4.286e-3	
Intellectual developmental disorder, autosomal dominant 50, with behavioral abnormalities	Mental retardation, autosomal dominant 50	1	0	NAA15 (1)	0.50000	1.00000	6.457e-5	1.985e-4	