

	R-HSA-8982491	R-HSA-1474290	R-HSA-373755	R-HSA-422475	immune_only
Pairwise path length in reference tree	0.0	0.0	0.0	0.0	0.0
Jaccard distance over extended gene set	0.0	0.0	0.0	0.0	0.0
Dijkstra BMA PPI	0.0007	0.0	0.0	0.0	0.0
WM distance over summary W2V	0.0052	0.0	0.0	0.0	NaN
WM distance over gene symbols W2V	0.0	0.0	0.0	0.0	0.0
Cosine distance over over summary W2V	0.0027	0.0	0.0005	0.0	NaN
Cosine distance over over NCBI summary W2V	0.0005	0.0	0.0	0.0	0.0
Cosine distance over gene symbols W2V	0.0	0.0	0.0	0.0	0.0
Cosine distance GO MF description W2V	0.0	0.0	0.0	0.0	0.0
Cosine distance GO CC description W2V	0.0	0.0	0.0	0.0	0.0476
Cosine distance GO BP description W2V	0.2682	0.0	0.0	0.0	0.0
GO-distance (go_type=MF, measure=Wang, combine=BMA)	0.0	0.0	0.0	0.0	0.0004
GO-distance (go_type=CC, measure=Wang, combine=BMA)	0.0004	0.0	0.0	0.0	0.0029
GO-distance (go_type=BP, measure=Wang, combine=BMA)	0.0223	0.0	0.0	0.0	0.0
Overlap distance over genes	0.0	0.0	0.0	0.0	0.0
Overlap distance over gene traits	0.0	0.0	0.0	0.0	0.0
Minkowski distance (p=2) over genes	0.0061	0.2457	0.2867	0.0	0.0
Minkowski distance (p=2) over gene traits	0.9516	0.0009	0.6076	0.0	0.0
Minkowski distance (p=2) over gene trait frequency	0.1526	0.5101	0.0015	0.0	0.0
Minkowski distance (p=1) over genes	0.0061	0.2457	0.2867	0.0	0.0
Minkowski distance (p=1) over gene traits	0.9516	0.0009	0.6076	0.0	0.0
Minkowski distance (p=1) over gene trait frequency	0.408	0.1588	0.024	0.0	0.0
Kappa distance over genes	0.0	0.0	0.0	0.0	0.0
Kappa distance over gene traits	0.0	0.0	0.0	0.0	0.0133
Jaccard distance over genes	0.0	0.0	0.0	0.0	0.0
Jaccard distance over gene traits	0.0	0.0	0.0	0.0	0.0
Cosine distance over gene trait frequency	0.0	0.0	0.0	0.0	0.0
Random (uniform, (0,1))	0.7903	0.555	0.4201	0.3821	0.5835