	R-HSA-8982491	R-HSA-1474290	R-HSA-373755	R-HSA-422475	immune_only
Pairwise path length in reference tree	0.012	0.029	0.014	0.161	0.028
Jaccard distance over extended gene set	0.185	0.398	0.238	2.246	0.31
Dijkstra BMA PPI	107.92	943.024	302.419	61498.08	4836.394
WM distance over summary W2V	24.817	401.254	25.768	8212.347	NaN
WM distance over gene symbols W2V	0.814	16.67	2.325	328.283	9500.508
Cosine distance over over summary W2V	0.886	6.35	1.258	215.654	NaN
Cosine distance over over NCBI summary W2V	3.384	54.313	7.583	737.154	101.634
Cosine distance over gene symbols W2V	0.202	0.761	0.285	17.467	1.483
Cosine distance GO MF description W2V	9.172	27.654	24.075	2348.945	206.04
Cosine distance GO CC description W2V	5.542	52.808	28.758	2191.575	135.862
Cosine distance GO BP description W2V	11.603	154.268	124.624	20266.078	361.471
GO-distance (go_type=MF, measure=Wang, combine=BMA)	11.884	2588.84	301.245	2601.024	1954.441
GO-distance (go_type=CC, measure=Wang, combine=BMA)	5.406	72.14	502.832	3835.697	5870.326
GO-distance (go_type=BP, measure=Wang, combine=BMA)	24.084	826.678	1598.533	77040.866	48340.111
Overlap distance over genes	0.239	3.488	0.7	281.89	11.426
Overlap distance over gene traits	0.22	6.589	1.77	326.871	6.641
Minkowski distance (p=2) over genes	0.001	0.003	0.001	0.221	0.016
Minkowski distance (p=2) over gene traits	0.001	0.007	0.003	0.276	0.013
Minkowski distance (p=2) over gene trait frequency	0.001	0.018	0.006	0.327	0.192
Minkowski distance (p=1) over genes	0.0	0.003	0.001	0.161	0.016
Minkowski distance (p=1) over gene traits	0.0	0.007	0.003	0.204	0.014
Minkowski distance (p=1) over gene trait frequency	0.001	0.016	0.005	0.279	0.192
Kappa distance over genes	0.326	1.407	0.485	38.138	0.97
Kappa distance over gene traits	0.524	1.664	0.536	41.809	0.638
Jaccard distance over genes	0.0	0.001	0.001	0.053	0.008
Jaccard distance over gene traits	0.0	0.004	0.002	0.066	0.009
Cosine distance over gene trait frequency	0.001	0.013	0.004	0.115	0.197
Random (uniform, (0,1))	0.012	0.031	0.016	0.129	0.014