	R-HSA-8982491	R-HSA-1474290	R-HSA-373755	R-HSA-422475	immune_only
Pairwise path length in reference tree	1.0	1.0	1.0	1.0	1.0
Jaccard distance over extended gene set	0.231	0.264	0.413	0.312	0.294
Dijkstra BMA PPI	0.247	0.133	0.302	0.333	0.206
WM distance over summary W2V	0.227	0.446	0.196	0.267	NaN
WM distance over gene symbols W2V	0.279	0.372	0.434	0.358	0.381
Cosine distance over over summary W2V	0.183	0.332	0.114	0.064	NaN
Cosine distance over over NCBI summary W2V	0.14	0.197	0.144	0.22	0.276
Cosine distance over gene symbols W2V	0.34	0.267	0.388	0.231	0.268
Cosine distance GO MF description W2V	0.232	0.105	0.22	0.109	0.274
Cosine distance GO CC description W2V	0.141	0.117	0.15	0.096	0.093
Cosine distance GO BP description W2V	0.036	0.111	0.191	0.142	0.3
GO-distance (go_type=MF, measure=Wang, combine=BMA)	0.455	0.078	0.299	0.151	0.161
GO-distance (go_type=CC, measure=Wang, combine=BMA)	0.078	0.111	0.238	0.158	0.134
GO-distance (go_type=BP, measure=Wang, combine=BMA)	0.177	0.218	0.303	0.19	0.209
Overlap distance over genes	0.485	0.319	0.602	0.544	0.495
Overlap distance over gene traits	0.583	0.348	0.563	0.464	0.458
Minkowski distance (p=2) over genes	-0.1	-0.072	-0.091	-0.205	-0.256
Minkowski distance (p=2) over gene traits	-0.023	-0.041	0.002	-0.132	-0.246
Minkowski distance (p=2) over gene trait frequency	-0.138	-0.091	-0.151	-0.146	-0.281
Minkowski distance (p=1) over genes	-0.168	-0.103	-0.188	-0.227	-0.26
Minkowski distance (p=1) over gene traits	-0.113	-0.074	-0.096	-0.205	-0.256
Minkowski distance (p=1) over gene trait frequency	-0.157	-0.099	-0.194	-0.204	-0.283
Kappa distance over genes	0.273	0.315	0.427	0.443	0.306
Kappa distance over gene traits	0.366	0.317	0.383	0.373	0.182
Jaccard distance over genes	0.307	0.332	0.455	0.426	0.383
Jaccard distance over gene traits	0.348	0.334	0.423	0.385	0.296
Cosine distance over gene trait frequency	0.483	0.449	0.323	0.334	0.398
Random (uniform, (0,1))	0.042	-0.008	0.018	-0.005	0.025