R-HSA-898	45A-14>2	1290 R	-HSA-42.	immune	
٥٥	SADI	1290	3>55 (<	A>5 .G	ONLY
ance tree	1.0	1.0	1.0	1.0	1.0

982 <sub>491</sub> 18A-3>3>55 17NUNE ONLY							
Ů,	491	1590	3>55 \	475	07/2		
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		

0.197

0.267

0.105

0.117

0.111

0.111

0.218

0.455 0.078

-0.023 -0.041

0.114

0.144

0.388

0.22

0.15

0.191

0.238

0.602

0.563

-0.138 -0.091 -0.151 -0.146 -0.281

-0.113 -0.074 -0.096 -0.205 -0.256

-0.157 -0.099 -0.194 -0.204 -0.283

0.383

0.455

0.423

-0.168 -0.103 -0.188 -0.227

0.299 0.151

-0.072 -0.091 -0.205 -0.256

0.427 0.443

0.064

0.22

0.231

0.109

0.096

0.142

0.158

0.19

0.544

0.464

0.002 -0.132 -0.246

0.373

0.426

0.385

0.018 -0.005 0.025

NaN

0.268

0.274

0.093

0.161

0.134

0.209

0.495 0.458

-0.26

0.182

0.383

0.398

0.183

0.14

0.232

0.141

0.036

0.078

0.177

0.485

0.583

-0.1

0.366

0.483

0.449

0.042 -0.008

Cosine distance over over summary W2V

Cosine distance over gene symbols W2V

Cosine distance GO MF description W2V

Cosine distance GO CC description W2V

Cosine distance GO BP description W2V

Overlap distance over genes

Kappa distance over genes

Jaccard distance over genes Jaccard distance over gene traits

Random (uniform, (0,1))

Kappa distance over gene traits

Overlap distance over gene traits

Minkowski distance (p=2) over genes

Minkowski distance (p=1) over genes

Minkowski distance (p=2) over gene traits

Minkowski distance (p=1) over gene traits

Cosine distance over gene trait frequency

Minkowski distance (p=2) over gene trait frequency

Minkowski distance (p=1) over gene trait frequency

Cosine distance over over NCBI summary W2V

GO-distance (go\_type=MF, measure=Wang, combine=BMA)

GO-distance (go\_type=CC, measure=Wang, combine=BMA)

GO-distance (qo\_type=BP, measure=Wang, combine=BMA)