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

0.114

0.144

0.388

0.22

0.15

0.191

0.238

0.602

0.563

-0.023 -0.041 0.002 -0.132 -0.246

-0.138 -0.091 -0.151 -0.146 -0.281

-0.168 -0.103 -0.188 -0.227 -0.26

-0.113 -0.074 -0.096 -0.205 -0.256

-0.157 -0.099 -0.194 -0.204 -0.283

0.315 0.427 0.443

0.383

0.423

0.455 0.426

0.299 0.151

0.303 0.19

-0.072 -0.091 -0.205 -0.256

0.064

0.22

0.231

0.109

0.096

0.142

0.158

0.544

0.464

0.373 0.182

0.385

0.018 -0.005 0.025

0.383

0.398

NaN

0.276

0.268

0.093

0.161

0.134

0.209

0.495

0.458

"/e
10/1/V
0 1.0
12 0.294
.67 NaN
58 0.381
3

0.197

0.267

0.105

0.117

0.111

0.111

0.218

0.455 0.078

0.183

0.14

0.232

0.141

0.036

0.078

0.177

0.485

0.583

-0.1

0.273

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

Random (uniform, (0,1))

Kappa distance over gene traits

Jaccard 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 (go_type=BP, measure=Wang, combine=BMA)