R-HSA-8982	45A-14>2	7-45A-3>3	"HSA-42	immune	07/ <sub>V</sub>
ence tree	1.0	1.0	1.0	1.0	1.0
	0.004	0.064	0.440	0.010	0.00

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

0.427

0.383

0.455

0.423

0.018

-0.168 -0.103 -0.188 -0.227

0.036

0.455

0.078

0.177

0.485

0.583

-0.1

-0.157

0.366

0.483

0.042

0.449

-0.008

-0.023 -0.041

0.111

0.078

0.111

0.218

0.142

0.151

0.158

0.19

0.544

0.464

0.002 -0.132 -0.246

0.443

0.373

0.426

0.385

-0.005

-0.072 -0.091 -0.205 -0.256

-0.099 -0.194 -0.204 -0.283

0.161

0.134

0.209

0.495

0.458

-0.26

0.182

0.383

0.398

0.025

·SA\89 <sub>82</sub>	'SA-14>	"SA-3>	"SA-42	MUNDO	
G.	2491 5491	115 <sub>4</sub> -3>	75 <sub>A-42</sub>	PAZS	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
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

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

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)