R-HSA.	R-4.	SA-12	R-HSA-3 4290	R-HSA-5 3>3>55	immun 122475	
	-385 ⁴	19 ₁	4290 S	⁷³ >55	122475 1011111111111111111111111111111111111	e only
		4 6	4.0		4.6	

0.175

0.192

0.174

0.124

0.217

0.253

0.012

0.023

0.012

0.023

0.434

-0.008

-0.054 -0.001

0.438 0.122

0.255

0.239

0.25

0.234

0.222

0.554

0.501

-0.042

0.111

0.114

0.183

0.136

0.143

0.144

0.408

0.259

-0.09

-0.033 -0.084 -0.192

-0.033 -0.084 -0.192

-0.08 -0.074 -0.228

0.133

0.4

0.209

-0.004 0.022

-0.011 -0.106 -0.038 -0.241

-0.042 -0.09

0.442 0.201

0.359 0.162

0.371

0.503

0.264

0.019

0.28

0.079

0.291

0.14

0.118

0.172

0.614

0.449

-0.201

-0.201

0.458

0.099

0.604

0.213

0.388

	491	⁷²⁹⁰	155	475	ONLY
Pairwise path length in reference tree	1.0	1.0	1.0	1.0	1.0
Jaccard distance over extended gene set	0.244	0.195	0.3	0.178	0.215
Dijkstra BMA PPI	0.226	0.084	0.332	0.216	0.143
WM distance over summary W2V	0.182	0.362	0.162	0.203	NaN
WM distance over gene symbols W2V	0.266	0.349	0.367	0.21	0.335
Cosine distance over over summary W2V	0.174	0.351	0.102	0.06	NaN
Cosine distance over over NCBI summary W2V	0.161	0.251	0.318	0.228	0.267
Cosine distance over gene symbols W2V	0.39	0.277	0.382	0.196	0.278

0.263

0.135

0.105

0.078

0.144

0.428

0.583

-0.09

-0.019

-0.08

-0.09

-0.019

0.27

0.418

0.468

0.555

0.04

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

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)