

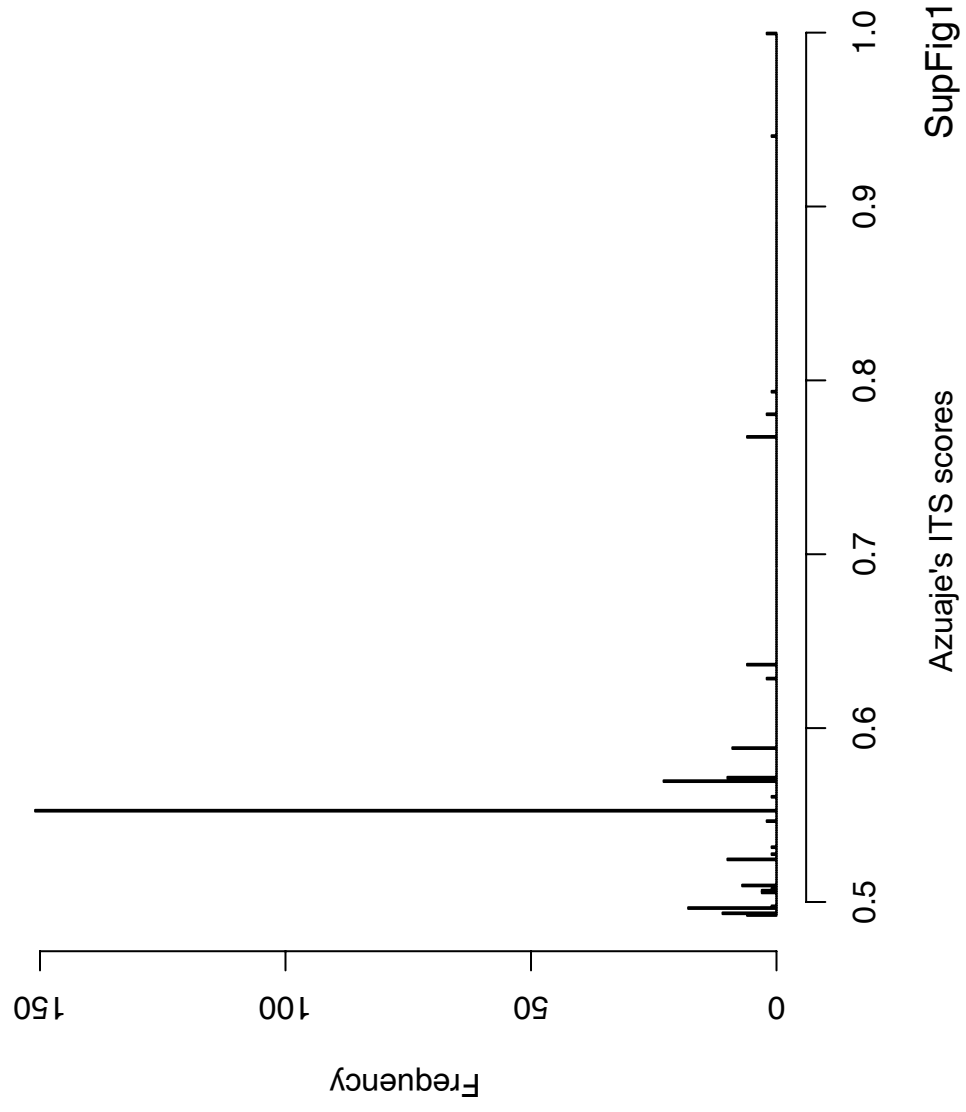
Supplementary materials for: Developing a similarity measure in biological function space

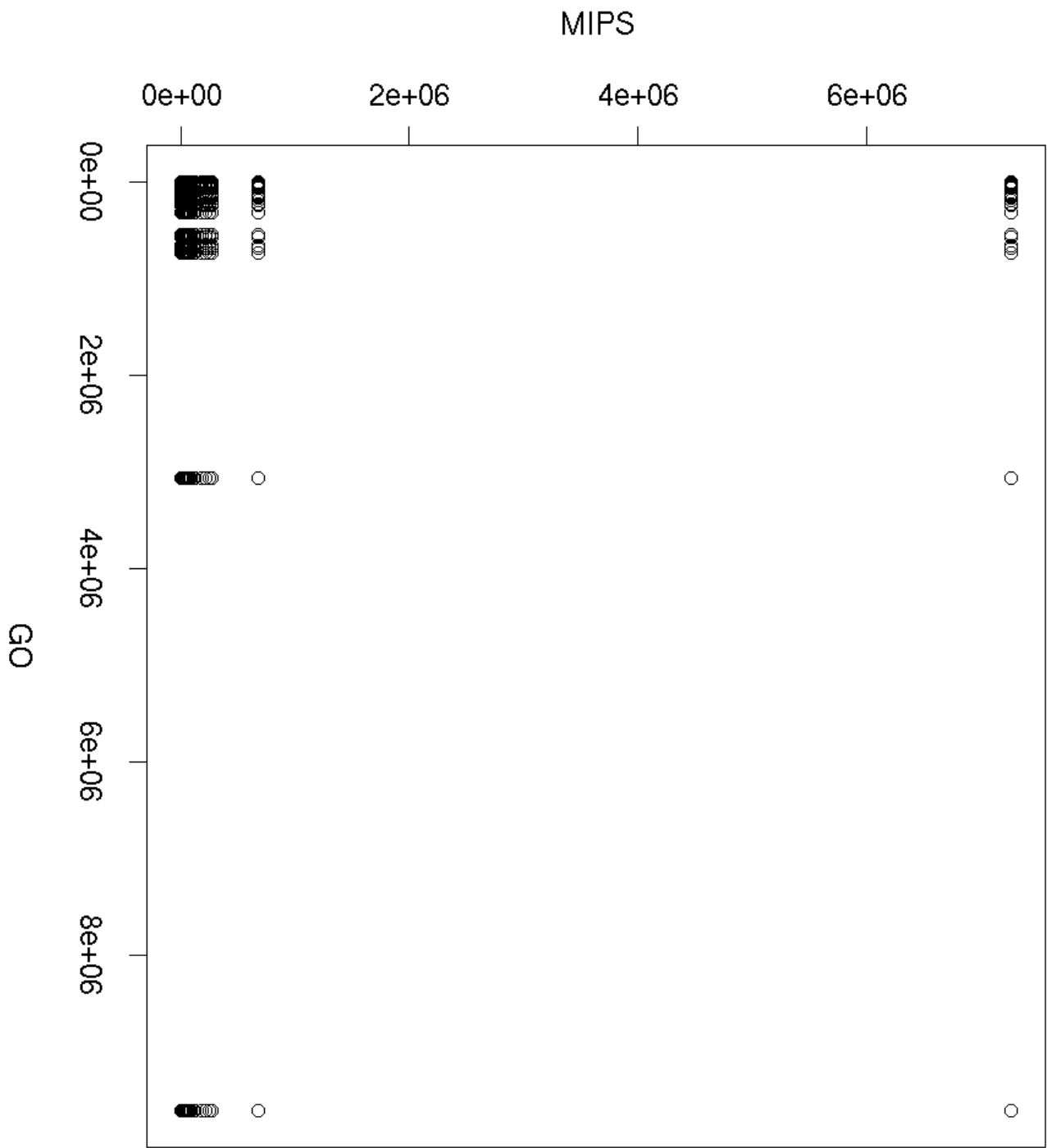
Supplementary Figure 1. The distribution of Azuaje's ITS scores for the protein pairs that have significant ITS scores (top 5%), but have non-significant total ancestry scores (below 50%).

Supplementary Figure 2. A scatter plot to show the correlation between MIPS and GO functional scores calculated by the total ancestry method.

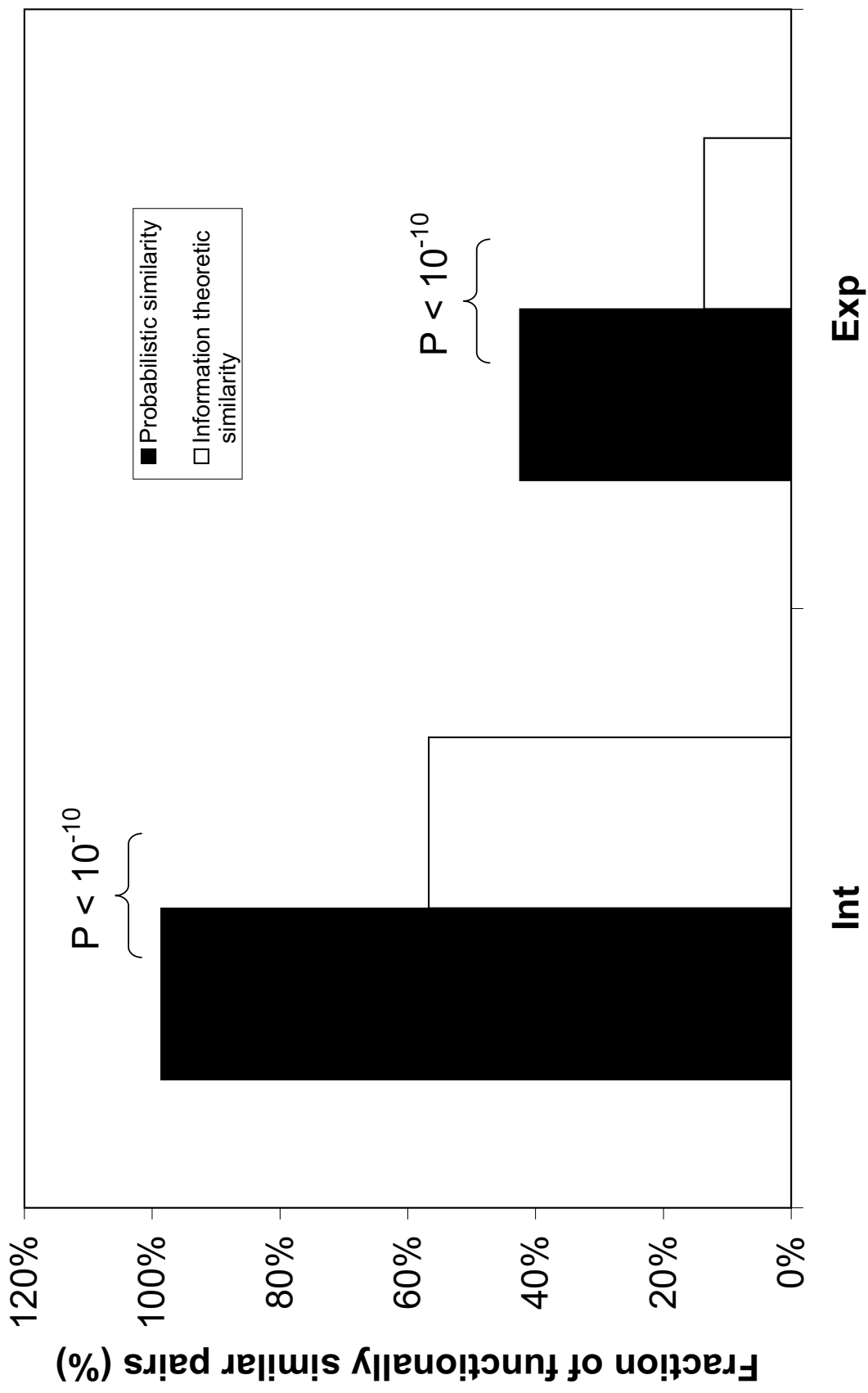
Supplementary Figure 3. Comparison of the enrichment of the functionally similar protein pairs between interacting and co-expressed pairs using Azuaje's ITS method and our total ancestry method.

Supplementary Figure 4. The cumulative density distribution (F) of the total ancestry similarity scores (P) from different DAG structures all follow power law distributions. We randomly generated these four DAG structures with three parameters: L: the number of layers; M: the number of items in each leaf node; N: the number of daughter nodes from one parent node.



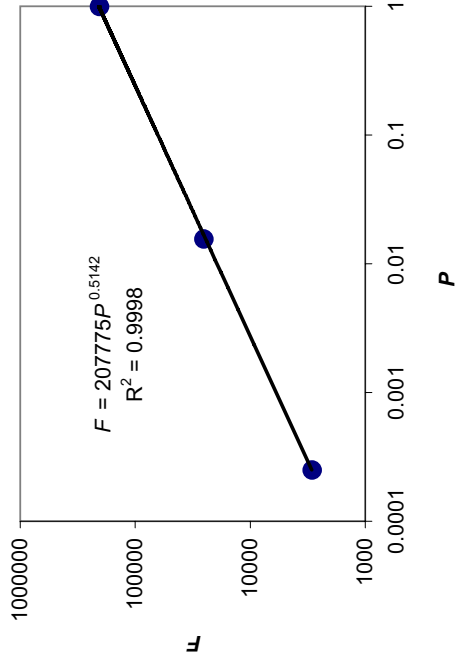


SupFig2

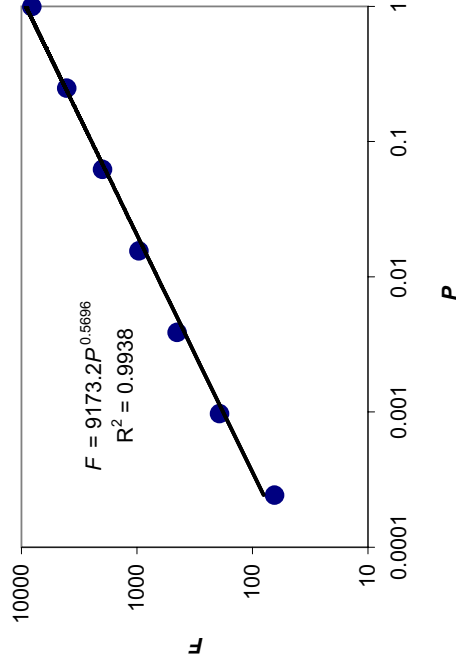


SupFig3

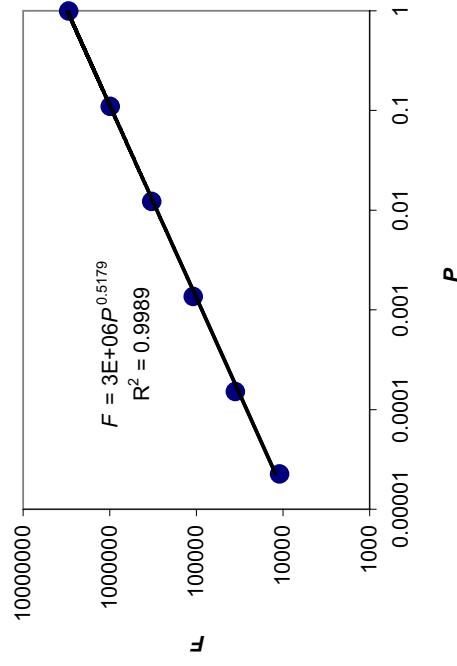
A. L = 3, M = 10, N = 8



B. L = 7, M = 2, N = 2



C. L = 6, M = 10, N = 3



D. L = 4, M = 6, N = 8

