GO slim gene networks were created using the igraph module in R version 2.14.1 (cran.r-project.org). The script is included as Supplementary file xxx. In brief, a table of enriched, differentially expressed genes, including the GO domains and GO slim terms, was read into R. To make the network nodes (circles), the number of genes per GO slim terms was counted. To make the network edges (lines), the number of genes shared between two GO slim terms was counted. These numbers were put into an igraph network and visualized with the help of tkplot.

Network statistics were obtained through a program written in Python version 2.7.2 ([www.python.org](http://www.python.org)) using the NetworkX module. The input to the igraph network was also written as a csv file and the headers removed before it was read into Python. A NetworkX network was created from these files, and NetworkX functions were used to gain basic statistics: average and variance in degree (number of edges per node); density (proportion of observed edges to all possible edges); average, variance, and maximum length of shortest paths (shortest distance from one node to another, traversing the edges); and average and variance in clustering (proportion of triangles).