Supplementary Data

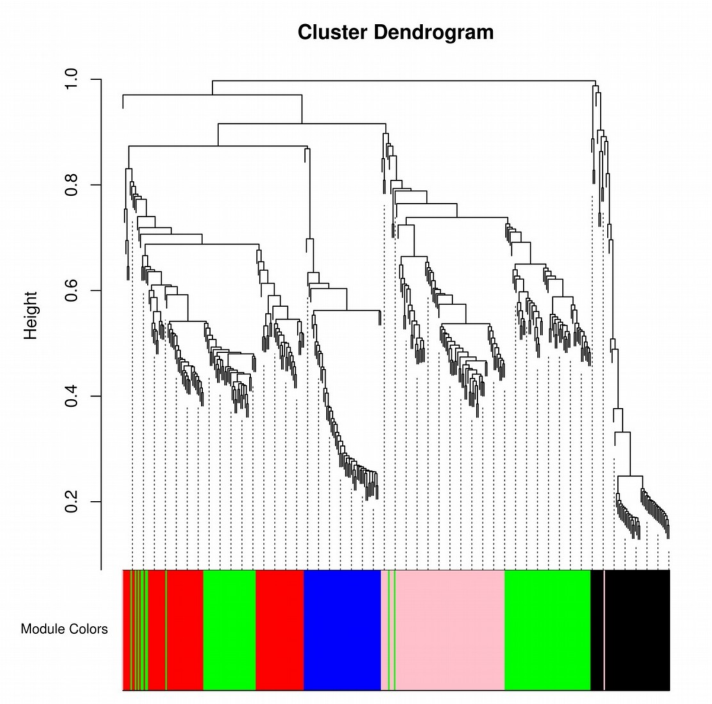

Figure S1. Hierarchical clustering of co-expression network. Gene dendrogram constructed by average linkage hierarchical clustering (upper panel), while the color-coded row underneath the cluster tree (lower panel) indicating module assignment

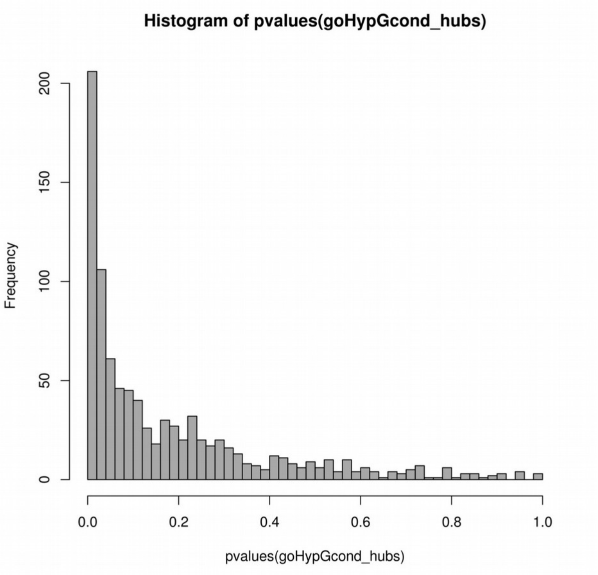

Figure S2. Over-representation analysis of gene ontology terms. Histogram of p-values for over-representation of genes in all gene ontology terms

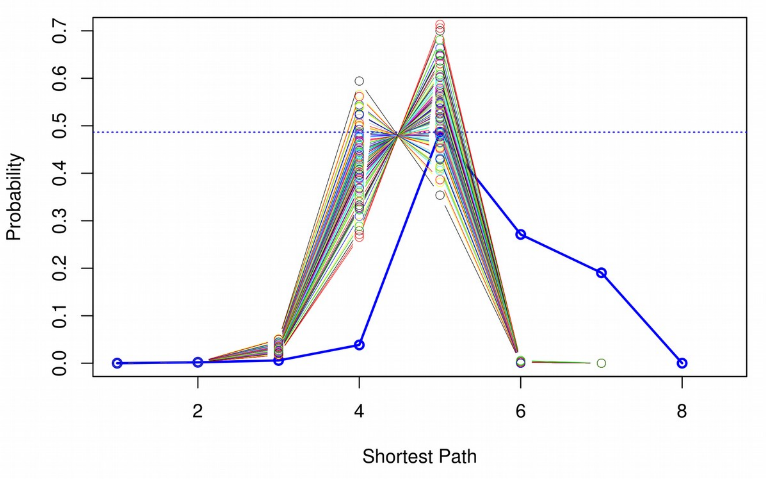

Figure S3. Comparison between shortest path (sp) length distributions of native networks (blue color) and their corresponding random networks (multiple-colors).