

## LEGENDS FOR SUPPLEMENTAL FIGURES AND TABLES

### **Figure S1: Distribution of P-values for randomly selected non-CCo datasets**

1000 sets of non-CCOs having the same size as the CCo set were randomly selected from the GI network, and the different centrality scores were calculated. Subsequently, the P-values (using Wilcoxon–Mann–Whitney test) with respect to the CCo dataset were obtained and plotted as histograms and boxplots as shown for (A) degree, (B) eigenvector, (C) betweenness and (D) closeness centrality. The mean, median, and other parameters of the P-value distributions are given in the tables. The line colored in red within the box is the median value. The diamond colored in teal represents the mean and the upper and lower 95% confidence limits of the mean. The ends of the box correspond to the 25th and 75th quantiles, also called 1st and 3rd quartiles, respectively. The difference between the 1st and 3rd quartiles is called the interquartile range (IQR). The bottom whisker extends to zero (in this case) from the bottom of the box. The top whisker extends 1.5xIQR from the top of the box. Dots represent outliers which are data points that fall outside the whiskers.

### **Table S1. Sec63 membrane yeast two-hybrid (MYTH) prey proteins**

The table lists prey proteins obtained from MYTH screens for Sec63. CYC2014 complexes enriched for Sec63 interaction (Figure 7A) are given next to their respective subunits. See methods for details.

**Table S2. Enrichment analysis of *SEC63* interacting complexes present in the CYC2014 catalog**

This file contains the significantly enriched ( $P < 0.03$ ) CYC2014 complexes interacting with *SEC63* in the negative GIs, positive GIs and GIPC datasets. Complexes that are also identified in the MYTH assays are highlighted in green. See methods for details.