



**Figure S2: Scale Free Distribution of Networks.** We calculated the degree of every node in the largest connected component of the genomwide network for both fission yeast (**A**) and budding yeast (**B**). We then calculated a histogram for frequency of degree (with number of bins equal to the maximum degree observed in the network) and plotted  $\log(\text{frequency})$  vs  $\log(\text{degree})$ . Best fits to  $\log(P(k)) \sim \log(ck^{-\gamma})$  were calculated using a least square minimization algorithm from scipy (<http://www.scipy.org/>).