

Figure S5: Robustness analysis of linkerity of proteins in the fission yeast polarity network.

We systematically analysed the robustness of linkerity in the presence of imperfect network interaction data. We added 10% edges preferentially to nodes with high degree (\mathbf{A}) or removed 10% edges at random (\mathbf{B}) to the core network. In the preferential attachment model, the probability P that a given node N had of gaining an edge was directly proportional to its degree $P(N) \sim Degree(N)$. In the random model $P(N) \sim k$ where k is a constant. Probabilities were normalized to increase or decrease the total edges of the network by 10%. We calculated the mean and standard deviation for the betweenness centrality of every protein belonging to the polarity subnetwork after repeating the procedure 1000 times. We plotted the top 20% of nodes and their mean and standard deviation. The blue dotted line represents the cutoff for top 10% nodes, and the red dotted line represents the cutoff for top 20% of nodes.