



Figure S4. Accuracy of network recovery as a function of S-gene knowledge and number of microarray replicates, and E-gene inhibition. A. Influence of incomplete pathway knowledge on network recovery. Expression data for a subset of S-genes was made available for network recovery. AUC (y-axis) plotted as a function of the percent of S-genes having available data (x-axis). 40% inhibition and four replicates were used. Solid lines indicate AUC of S-graph connectivity. Dashed lines indicate AUC using both S-graph connectivity and sign. **B. Influence of replicates in network recovery.** AUC (y-axis) plotted as a function of varying numbers of microarray hybridization replicates (x-axis). Artificial networks contained 40% inhibitory interactions. **C. Influence of inhibitory E-gene connections in network recovery.** Networks with only activating S-gene interactions were reconstructed with varying amount of E-gene inhibition. At each inhibition level, 100 networks were used.