Supplementary materials, Battle et al.

Supplementary Figure 1)

GFP-Sed5p localization defect in Δsgt2. GFP-Sed5p localization in WT, Δsgt2, Δmdy2 and Δget3 strains, showing a larger view than that in Figure 5.
Supplementary Figure 2)

Repeatability of Annealed Importance Sampling estimates: For five runs of APN learning using Annealed Importance Sampling, we estimated $P'(edge)$ for the edge potentially connecting each pair of genes. For every run $R$, we compared all estimates $P'(edge)$ to the corresponding estimates from every other run $Q$. In this figure, we plot every point $(P'(edge)$ from $R$, $P'(edge)$ from $Q)$ in a scatter plot. The maximum difference for any two runs, for any edge, was 0.15, and the standard deviation was less than .01, demonstrating highly repeatable estimates.
Sensitivity Analysis: To analyze the sensitivity of our method to reduced measurement precision, we introduced increasing levels of random noise to the data of Jonikas et al., and re-ran APN learning. For measurement in the dataset, we sampled from a Gaussian distribution with mean zero and standard deviation $s$, and added this value to the original measurement. We varied $s$, up to three times standard deviation of the repeat measurement error observed for the Jonikas et al. data. For each run, using a specific value for $s$, we compared all estimates of $P$(edge) to the original, noise-free estimates of $P$(edge). The plot shows the correlation between the estimates of a given run to the original estimates. The results suggest that network reconstruction is possible even with increased noise. Thus, our method may be appropriate even for data sets with somewhat less precise measurements than found in the Jonikas et al. (2009) data.