Supplementary Figures and Tables

**Supplemental Figure S1.** Receiver operating characteristic curves illustrating the performance of TINGe on the five different DREAM4 test networks.

**Supplemental Figure S2.** Cumulative node degree distribution in the reconstructed *Arabidopsis* whole-genome network.

**Supplemental Figure S3.** Probability distribution of the number of connected components observed in 102,400 random networks for each biological process. Vertical line indicates the number of connected components in the input network.

**Supplemental Table S1.** List of various microarray experiments obtained from different public repositories.

**Supplemental Table S2.** Comparison of performance and run-time of three network reconstruction methods on synthetic data from SynTReN.

**Supplemental Table S3.** TINGe runtime in seconds for different numbers of genes $n$, and different number of expression observations $m$.

**Supplemental Table S4.** List of genes included in the network. Information about the node degree, betweenness centrality, clustering coefficient and annotation is provided for all genes in the network.

**Supplemental Table S5.** List of genes used for biological verification of gene-gene interactions in the *Arabidopsis* whole-genome network. Each sheet in the file contains genes for a particular cellular process. Genes for each process were downloaded from the Arabidopsis TAIR website (http://www.arabidopsis.org).

**Supplemental Table S6.** Functional enrichment analysis of genes in GeNA extracted subnetworks using GOMiner. For each GO term, the total number of genes with that functional category in the *Arabidopsis* whole-genome network and the GeNA extracted subnetwork, respectively, are shown. The number of “in subnetwork” genes does not include seed genes.

**Supplemental Table S7.** List of genes used to generate subnetworks in Figures 4, 5 and 6. Information on GeneRank and functional classification is provided for each gene.