

Supporting Information Captions

Supplementary Figures

Figure S1. The absolute (abs) coefficient of variation (CV) in % of the differentially expressed genes among 11 strains.

The absolute CV of each gene is plotted on semi-log₁₀ scale.

Figure S2. Merging of modules on the basis of correlation coefficient between module eigengenes.

(A) Cluster dendrogram showing the modules before and after merging. (B) Dendrogram of module eigengenes. The modules with module eigengenes (MEs) below the red line were merged. (C) & (D) Heatmap colouring corresponding to correlation coefficient values between the module eigengenes before and after the merger.

Figure S3. Pearson's correlation coefficient (PCC) of all co-expressed connections with edge weight (Topological Overlap) > 0.08.

The PCCs points are coloured in green and the weights are coloured in light orange.

Figure S4. Altered fluxes of reactions on *in-silico* knock down of 9 reactions associated with highly connected genes.

The left panel shows proportional decrease with changing slopes whereas other types of behaviours were shown in right panel.

Figure S5. Boxplot of gene expression data of 48 samples used for network construction.

boxplot of normalized log₂ ratio data of 48 samples using 'boxplot' function in R. The boxplot shows that all the samples are in same scale. The median of log₂ ratio is centred at zero for all the samples.

Figure S6. Average hierarchical clustering of samples of gene expression data (GSE3201).

The samples, which have been strikedthrough with yellow line were removed from the dataset because they were either outliers or did not group together with other replicates.

Figure S7. Calculating soft threshold by fitting network to scale free topology.

The highlighted row in the Table below the plots shows the power used for fitting scale free topology at $R^2 = 0.86$.

Supplementary Tables

Table S1. Enriched biological processes in constructed co-expression network obtained from DAVID.

Table S2. Numbers and identities of genes under common transcriptional regulation in different modules of co-expression network.

Table S3. Proportion of differentially expressed target genes of known regulators

Table S4. One tailed Fisher's Exact test for number of differentially expressed genes regulated by major transcriptional regulators in the co-expressed modules taken together.

Table S5. Random sampling of genes of sample size same as the 5 co-expressed modules with common connections to STRING data at high confidence score > 0.8.

The common connections with STRING in all the modules are significantly higher than the mean+3*SD of random samples of same gene size as the co-expressed modules.

Table S6. Co-expressed connections in agreement with the STRING database

Table S7. Total connections in extracted (TR network supported, common with STRING and high topological overlap weight > 0.8) co-expression network along with their topological overlap.

Table S8. List of hub genes in the co-expressed modules sorted in descending order of linear of sum of modified z-scores of three criteria.

We included three different criteria for hub genes identification (1) Connectivity of genes (2) Intra modular connectivity, which is sum of adjacencies with all connected genes (2) PCC with module eigengene (ME). The list contains 89 genes common in top 250 genes all modules taken together from each three criteria.

Table S9. List of known drug targets mapped on the co-expressed modules.