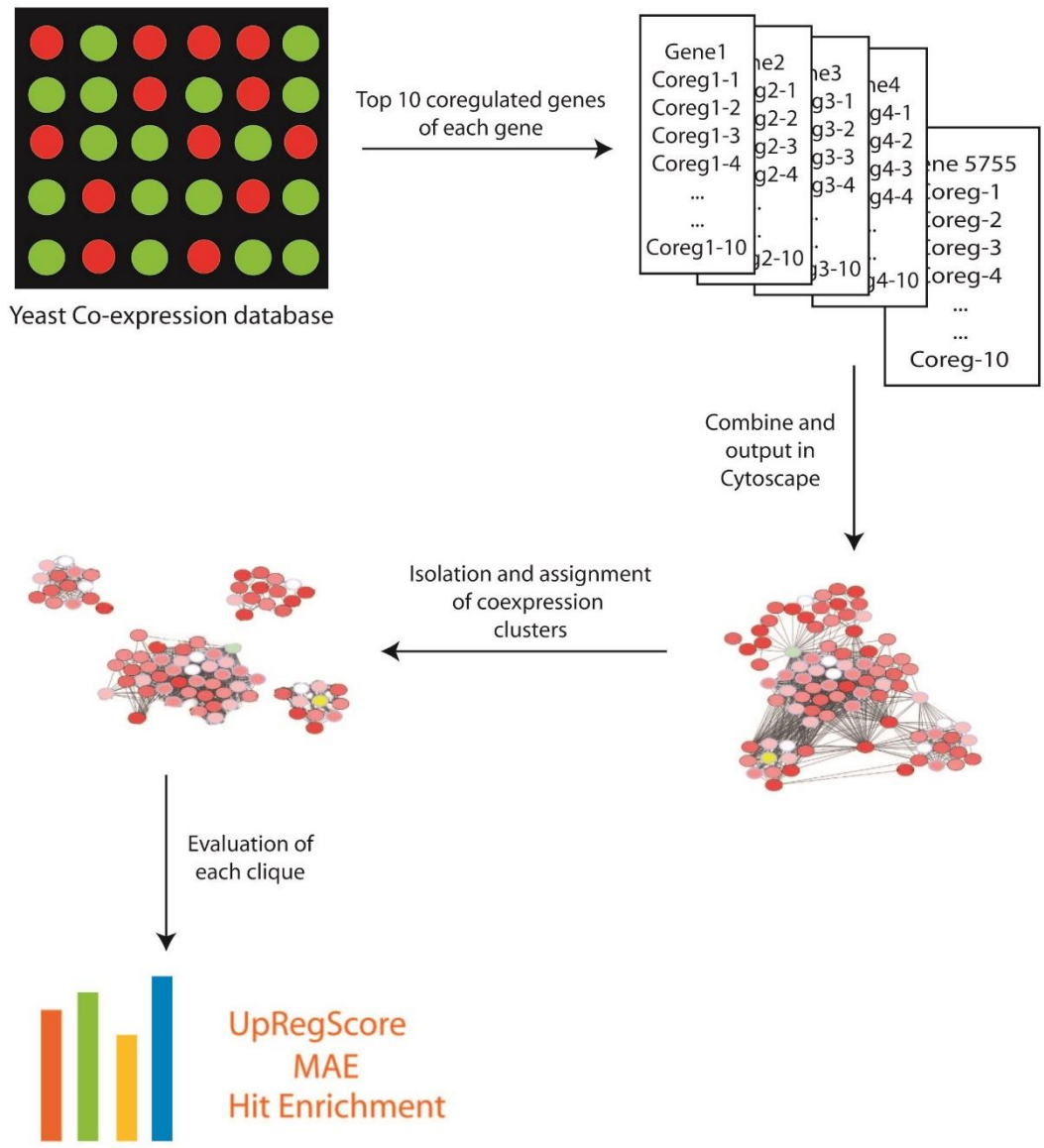
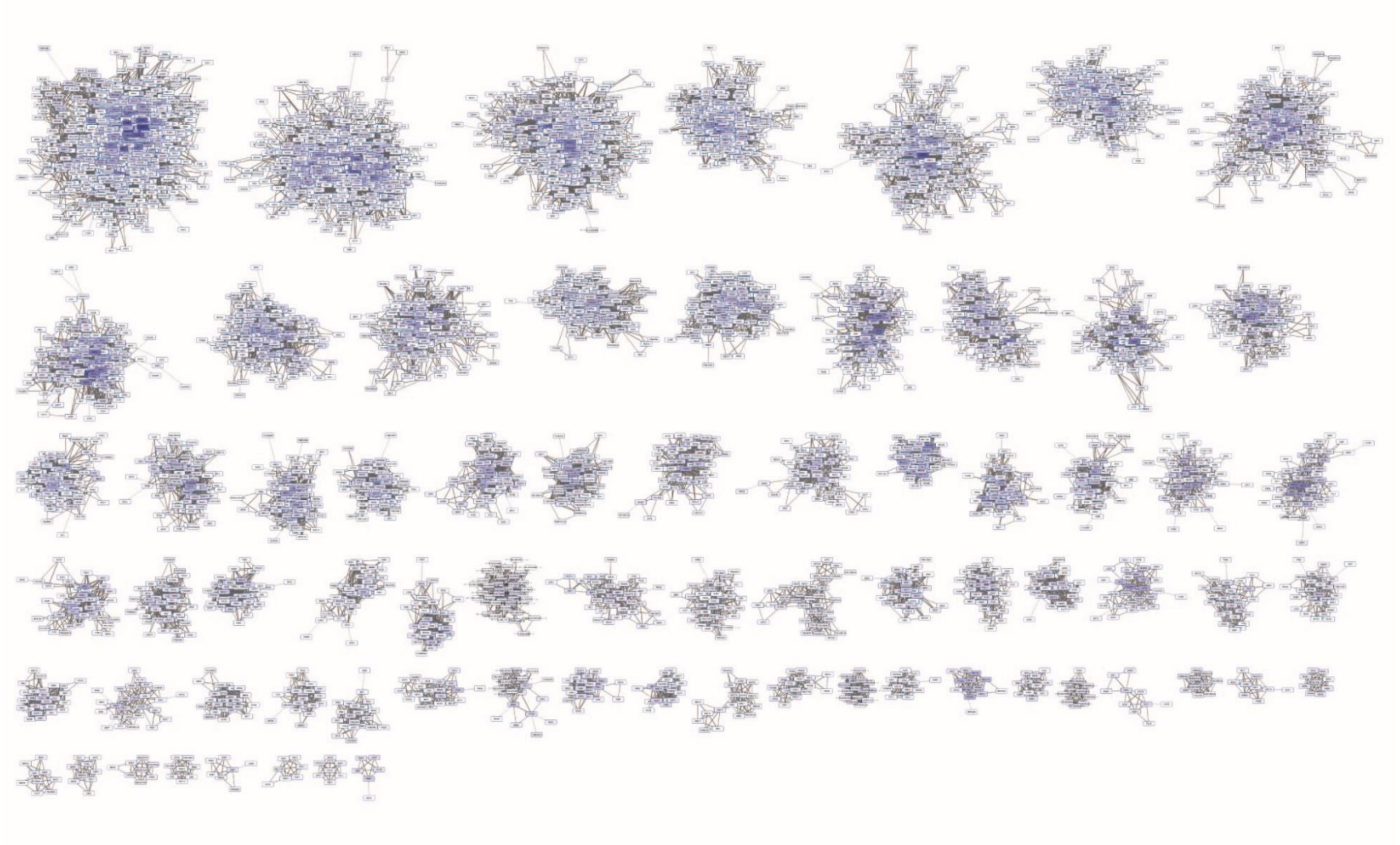
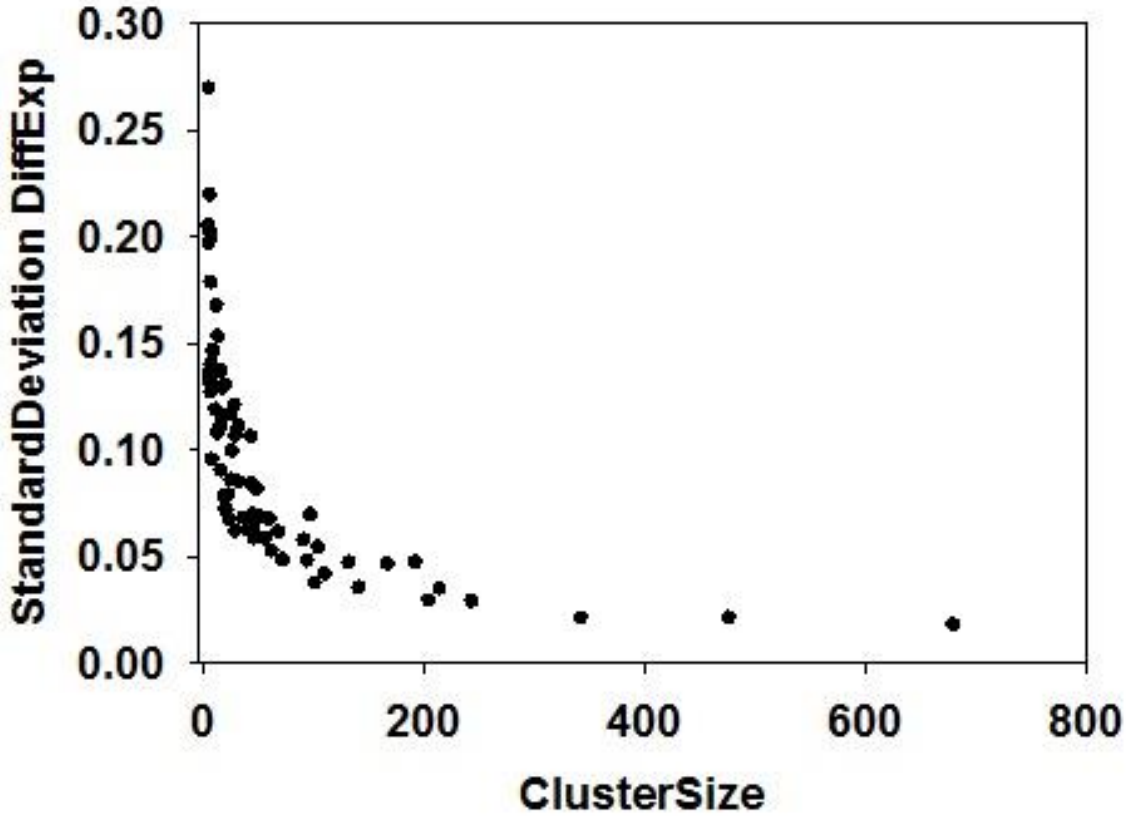


Supplemental Figure S1: Flow diagram of clusterEx. Edges in the network are generated by connections within the co-expression database. For each gene the Top10 co-regulated genes from the database are used to generate 121 edges and 11 nodes. Edges are summed up and the resulting matrix file is used to draw the network. It further is used to cut the network in the more dense modules by preferentially maintaining the edges, which have higher numbers of occurrence as described in Material and Methods.

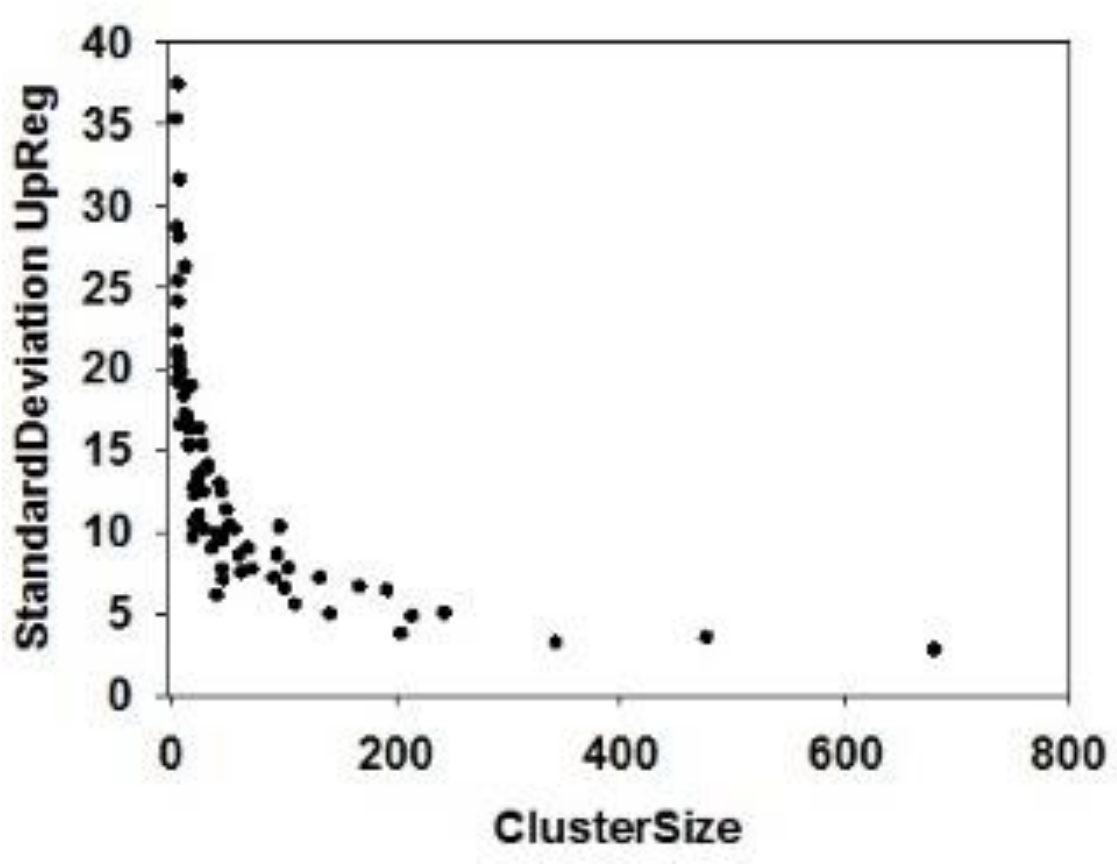
Supplemental Figure S2: Cluster of the entire yeast genome as represented on GeneChip Yeast 2.0 arrays based on 3120 microarray experiments and the observed co-expression relationships.



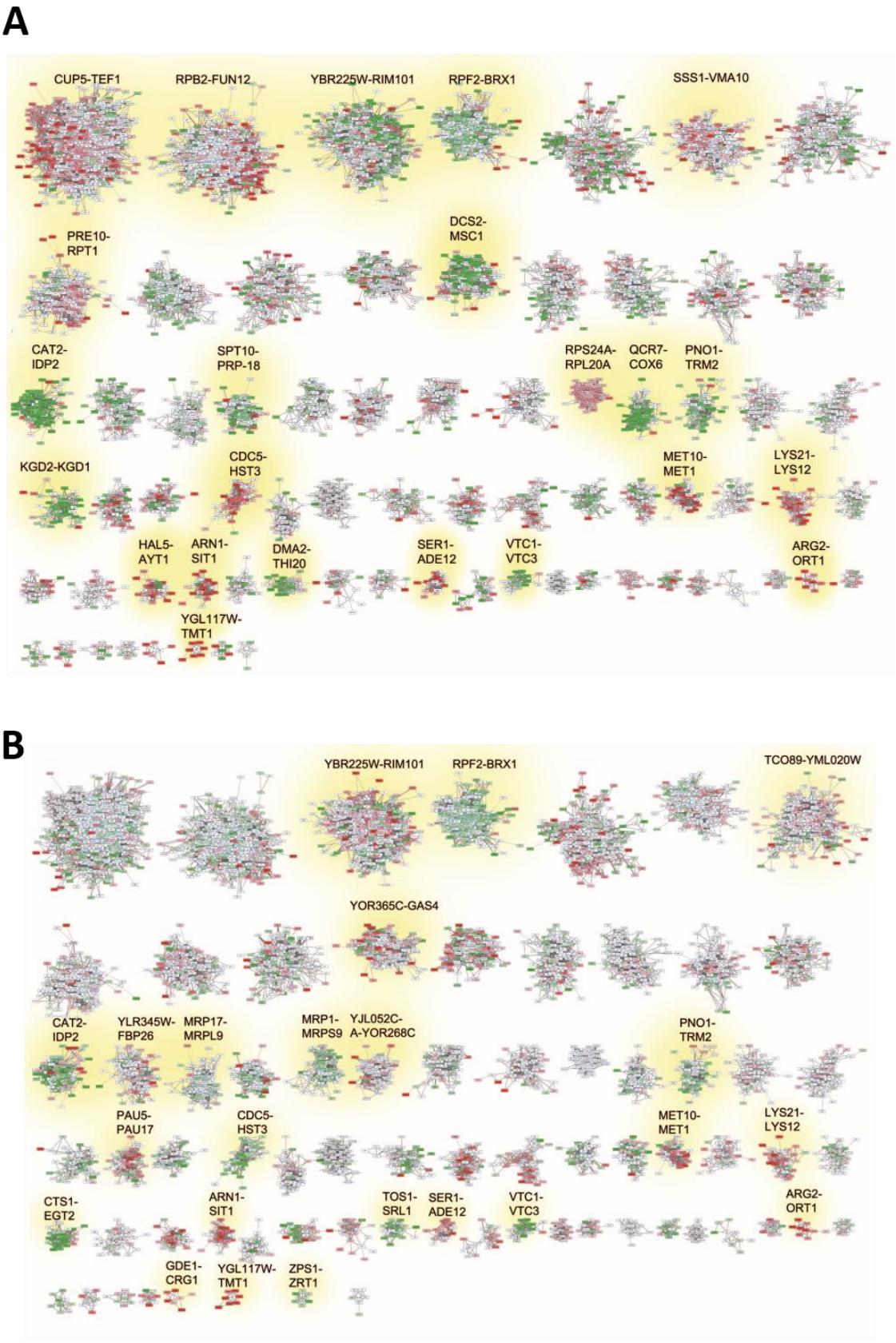
Supplemental Figure S3: Clusters separated from the network in supplemental figure 2. The bluish color shows the number of connections within the genome-wide cluster for the respective gene. This value varies between 8 for the Affymetrix Probe RPTR-Sc-A00196-1_s_at (white) and 3328 for TEF1 (blue). Clusters are arranged according to size and numbers will be assigned to them as 1 to 7 (first row), 8 to 16 (second row), 17 to 29 (third row), 30 to 44 (fourth row), 45 to 64 (fifth row) and 65 to 72 (last row).



Supplementary Figure S4. Plot of the standard deviation of averaged expression changes in random experiments against the size of the clusters. The relationship is as expected and fits to STD_0/sqrt(ClusterSize) are reasonably good for ClusterSize > 10.

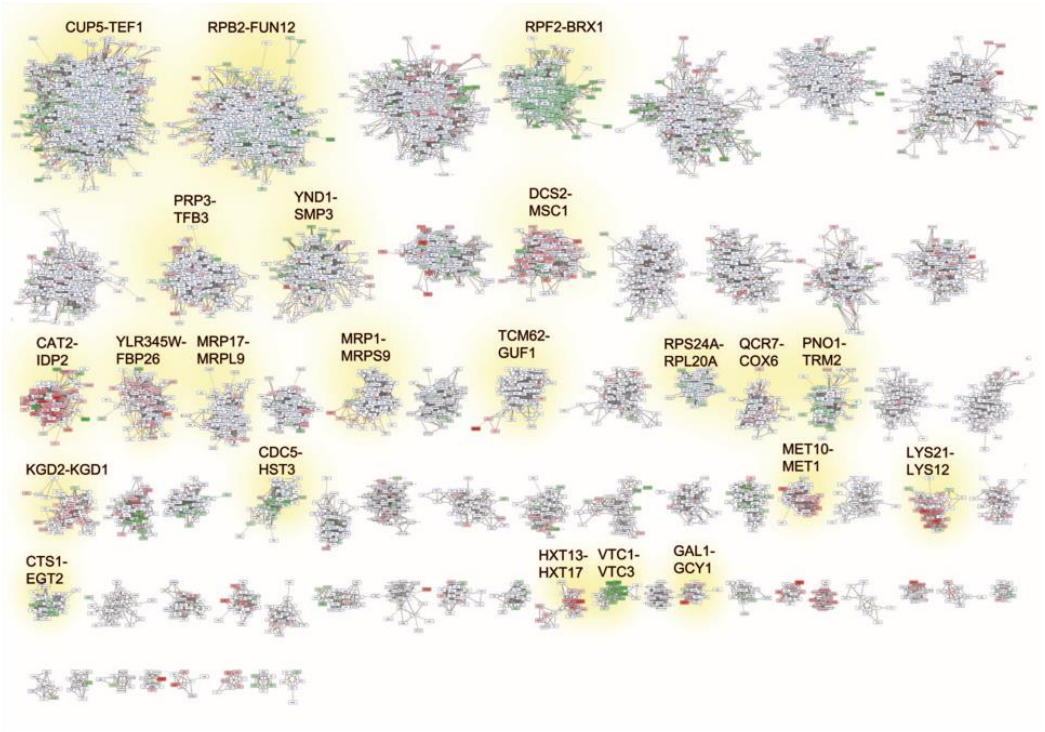


Supplementary Figure S5: Plot of the standard deviation of UpRegScores in random experiments against the size of the clusters. The relationship is as expected and fits to STD_0/sqrt(ClusterSize) are reasonably good for ClusterSize > 10.

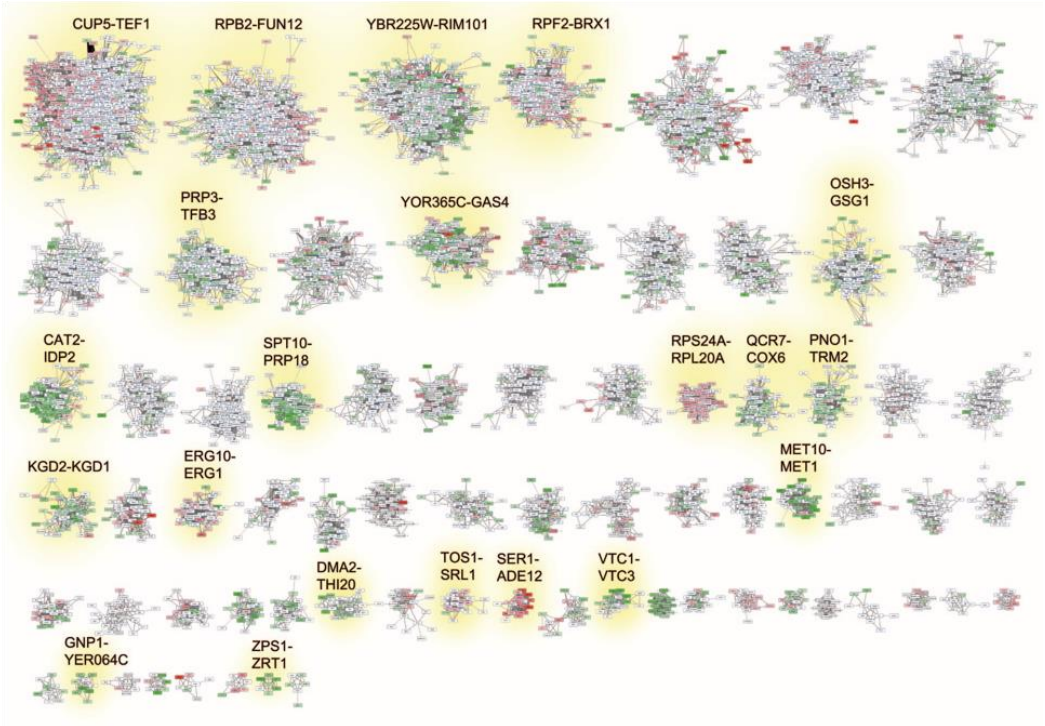


Supplementary Figure S6: Expression of the first (A) and second (B) replicate of Q56/Q0-experiments and shading of the genes according to their expression values.

A



B



Supplementary Figure S7: Expression differences visualized for the first (A) and second (B) experiments of Q30/Q0 comparisons.