Supplementary Material (ESI) for Molecular BioSystems

Meta-analysis of genome regulation and expression variability across hundreds of environmental and genetic perturbations in fission yeast

Vera Pancaldi, Falk Schubert, Jürg Bähler

Supplementary figures

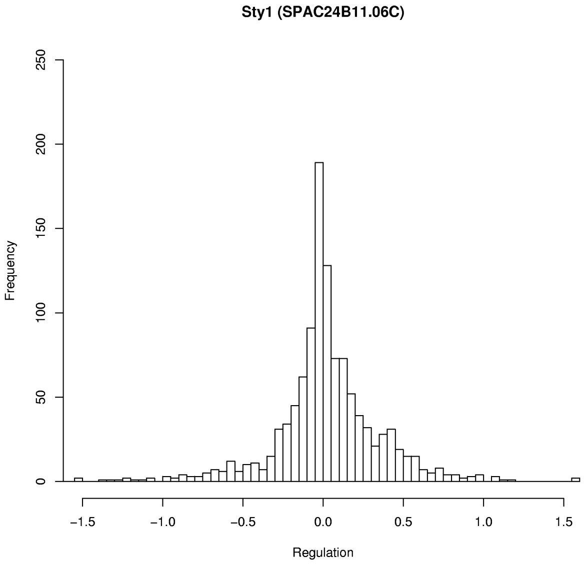


Figure 1: Distribution of relative expression of a single gene over all conditions. Notice that the distribution is approximately normal and uni-modal. For this reason we can take the standard deviation of the regulation to measure the variability in gene expression for a particular set of conditions.

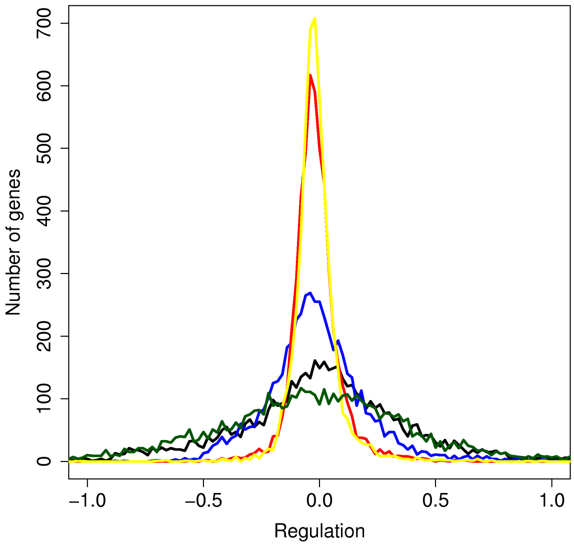
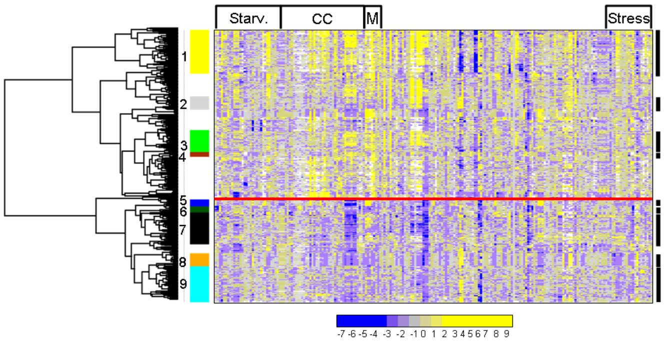
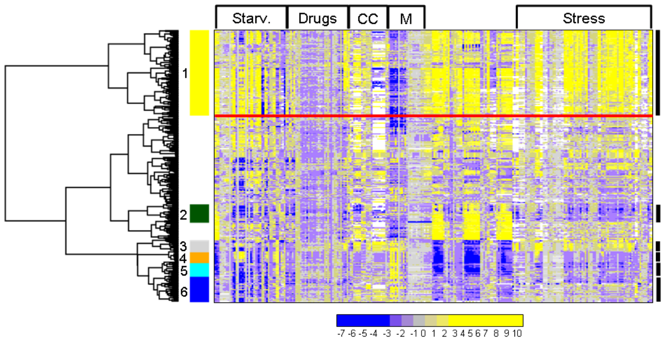


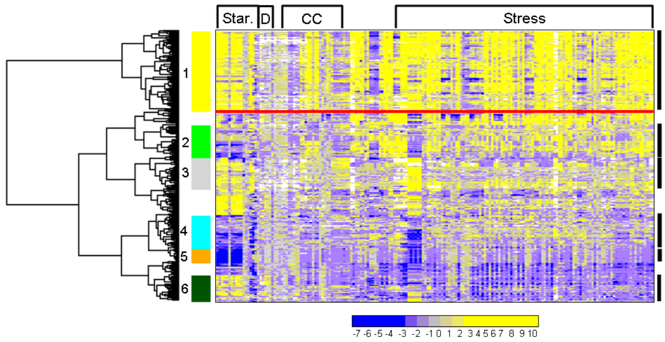
Figure 2: Control for Figure 3a in the main text, using same colour scheme. The analysis of gene regulation was repeated eliminating conditions where the environmental perturbation was combined with genetic modification of one of the 11 genes for which an only genetic condition is available. The main effect is to lower the number of genes that have little or no average regulation over conditions.



(a) Genetic conditions

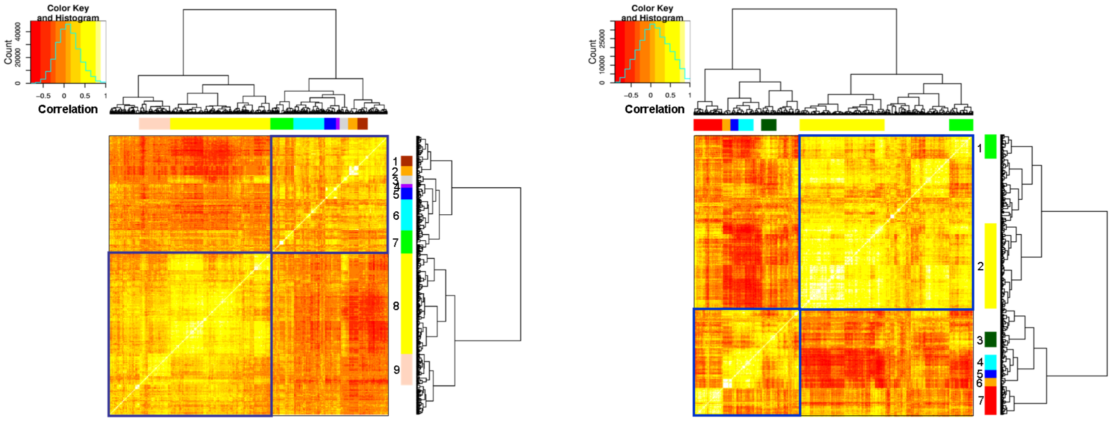


(b) Environmental conditions



(c) Both genetic and environmental conditions

Figure 3: Hierarchical clustering of the top-500 most variable genes using only selected experimental categories. The colour legends show the entire range of regulation (log2 of expression ratios). Selected GO categories that were enriched in clusters are highlighted as indicated below. Conditions are grouped as in Figure ??. (a) Experiments based on genetic perturbations. Cluster 1 (yellow): stress response, cluster 2 (grey): protein folding, cluster 3 (green): conjugation, cluster 4 (brown): respiration, cluster 5 (blue): vitamins and thiamine, cluster 6 (dark green): cytokinesis, cluster 7 (black): transmembrane transport, cluster 8 (orange): translation, and cluster 9 (cyan): metabolism. (b) Experiments based on environmental perturbations. Cluster 1 (yellow): stress response, cluster 2 (dark green): cytokinesis, cluster 3 (grey): protein folding, cluster 4 (orange): translation, cluster 5 (cyan): metabolism, and cluster 6 (blue): vitamins and thiamine. (c) Experiments based on combined genetic and environmental perturbations. Cluster 1 (yellow): stress response, cluster 2 (green): conjugation, cluster 3 (grey): protein folding, cluster 4 (cyan): metabolism, cluster 5 (orange): translation, cluster 6 (dark green): cytokinesis. The blue squares highlight the two major clusters. The colour legend shows the correlation values from inverse (dark red) to positive (bright yellow) along with the distribution of the matrix values (green line).



(a)

(b)

Figure 4: Hierarchical clustering of the top-500 most variable genes using only selected experimental categories. Colour legends as in Figure 6. Selected GO categories that were enriched in clusters are highlighted as indicated below. (a) Experiments based on genetic perturbations. Cluster 1 (brown): organic acid metabolism, cluster 2 (orange): translation, cluster 3 (grey): protein folding, cluster 4 (magenta): iron-related functions, cluster 5 (blue): vitamins and thiamine, cluster 6 (cyan): metabolism, cluster 7 (gree): conjugation, cluster 8 (yellow): stress response, and cluster 9 (pink): cell differentiation and meiosis. (b) Experiments based on environmental perturbations. Cluster 1 (green): conjugation, cluster 2 (yellow): stress response, cluster 3 (dark-green): cytokinesis, cluster 4 (cyan): metabolism, cluster 5 (blue): vitamins and thiamine, cluster 6 (orange): translation, and cluster 7 (red): meiosis. The blue squares highlight the two major clusters. The colour legend shows the correlation values from inverse (dark red) to positive (bright yellow) along with the distribution of the matrix values (green line)