

Fig. 1. Gene expression profiles in a set of stress treatments clustered into 12 DC clusters. Each subfigure contains the genes within one cluster, and each row is the profile of one of the genes. The rightmost column shows the class of the gene: whether it is up- or down-regulated in the acid treatment in the mutant strain lacking *Msn2/4p*. Continued in **Figs. 2–3**.

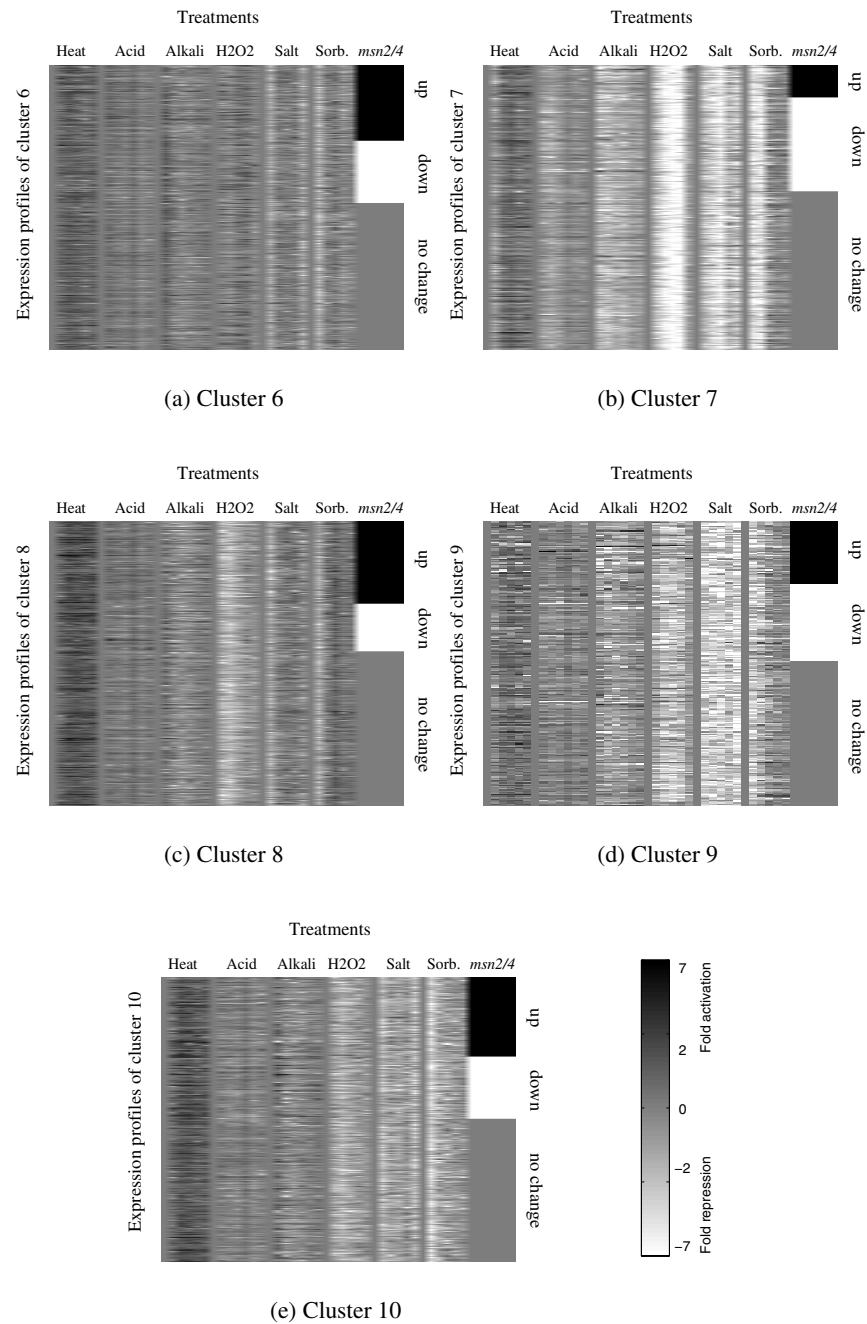


Fig. 2. Gene expression profiles in a set of stress treatments clustered into 12 DC clusters. Each subfigure contains the genes within one cluster, and each row is the profile of one of the genes. The rightmost column shows the class of the gene: whether it is up- or down-regulated in the acid treatment in the mutant strain lacking *Msn2/4p*. Continued in **Figs. 1.** and **3.**

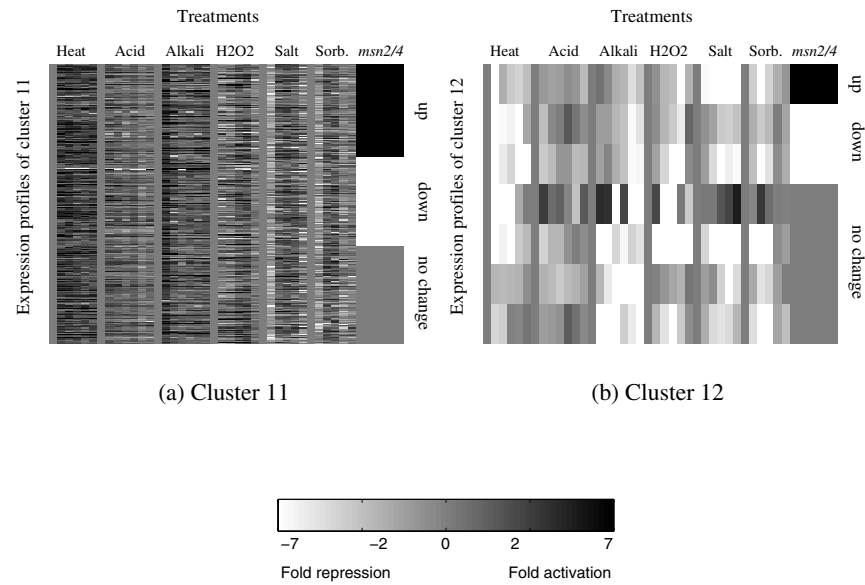


Fig. 3. Gene expression profiles in a set of stress treatments clustered into 12 DC clusters. Each subfigure contains the genes within one cluster, and each row is the profile of one of the genes. The rightmost column shows the class of the gene: whether it is up- or down-regulated in the acid treatment in the mutant strain lacking *Msn2/4p*. Continued from **Figs. 1.–2.**

Table 1. Unexpectedness of the enriched contingency table cells. The table shows P-values for those cells where the number of samples exceeded the expected amount. For instance, in cluster 5 the number of downregulated genes is significantly higher than expected, whereas the number of upregulated and not changed genes is smaller than expected (marked by “–” and treated in **Table 2.**)

	upregulated	downregulated	no change
Cluster 1	0.02	–	0.31
Cluster 2	–	0.41	0.46
Cluster 3	0.40	0.07	–
Cluster 4	–	0.17	0.23
Cluster 5	–	< 0.01	–
Cluster 6	0.22	–	0.31
Cluster 7	–	< 0.01	0.11
Cluster 8	0.06	–	0.13
Cluster 9	–	0.30	0.43
Cluster 10	0.15	–	0.47
Cluster 11	0.01	0.03	–
Cluster 12	–	0.44	0.45

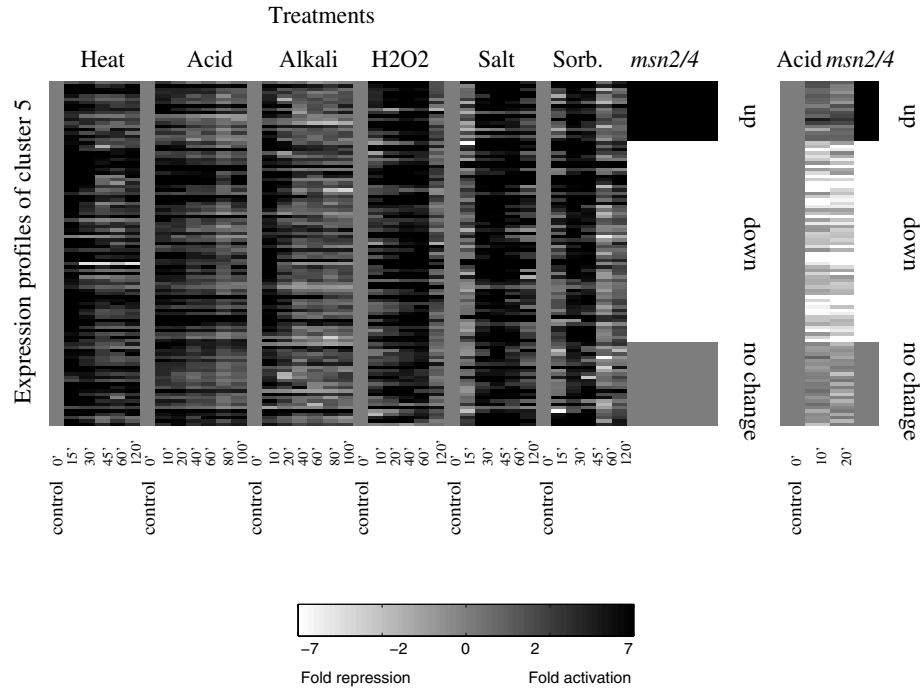


Fig. 4. Left: Enlarged gene expression profiles in a set of stress treatments for genes in cluster 5. Each row represents the expression profile and the class (rightmost column) of one of the genes. The genes have been ordered according to their classification. Right: Expression profiles of the same genes in the mutant strain lacking *Msn2/4p*. These profiles have been used for defining the classes of the genes (shown in the rightmost columns). The classes tell whether the genes are up- or down-regulated in the acid treatment in the mutant. The order of the genes is the same as in left picture

We cannot verify quantitatively how closely our findings match those of Causton *et al.* [1] since they do not report the full list of gene names. We will, however, compare our list with the list of another study [3] in Sect. 4.2.

Other Findings

We tried to see if the clustering would find a group of stress response genes, the expression of which is independent of the *Msn2/4p* regulation. Cluster 7 (**Fig. 1 (b)**) contains many down-regulated genes, especially in the peroxide and osmotic shock experiments. Since *Msn2/4p* are primarily transcription activator factors (and not repressors) [10] these down-regulated genes are probably not under the direct control of *Msn2/4p*. However, these genes could be under an indirect control of *Msn2/4p* if one considers that *Msn2/4p* could activate some secondary repressing regulators. Therefore, the relatively high abundance of down-regulated genes in cluster 7 is not



<http://www.springer.com/978-3-540-22901-8>

Bioinformatics Using Computational Intelligence
Paradigms

Seiffert, U.; Schweizer, P. (Eds.)

2005, VII, 211 p., Hardcover

ISBN: 978-3-540-22901-8