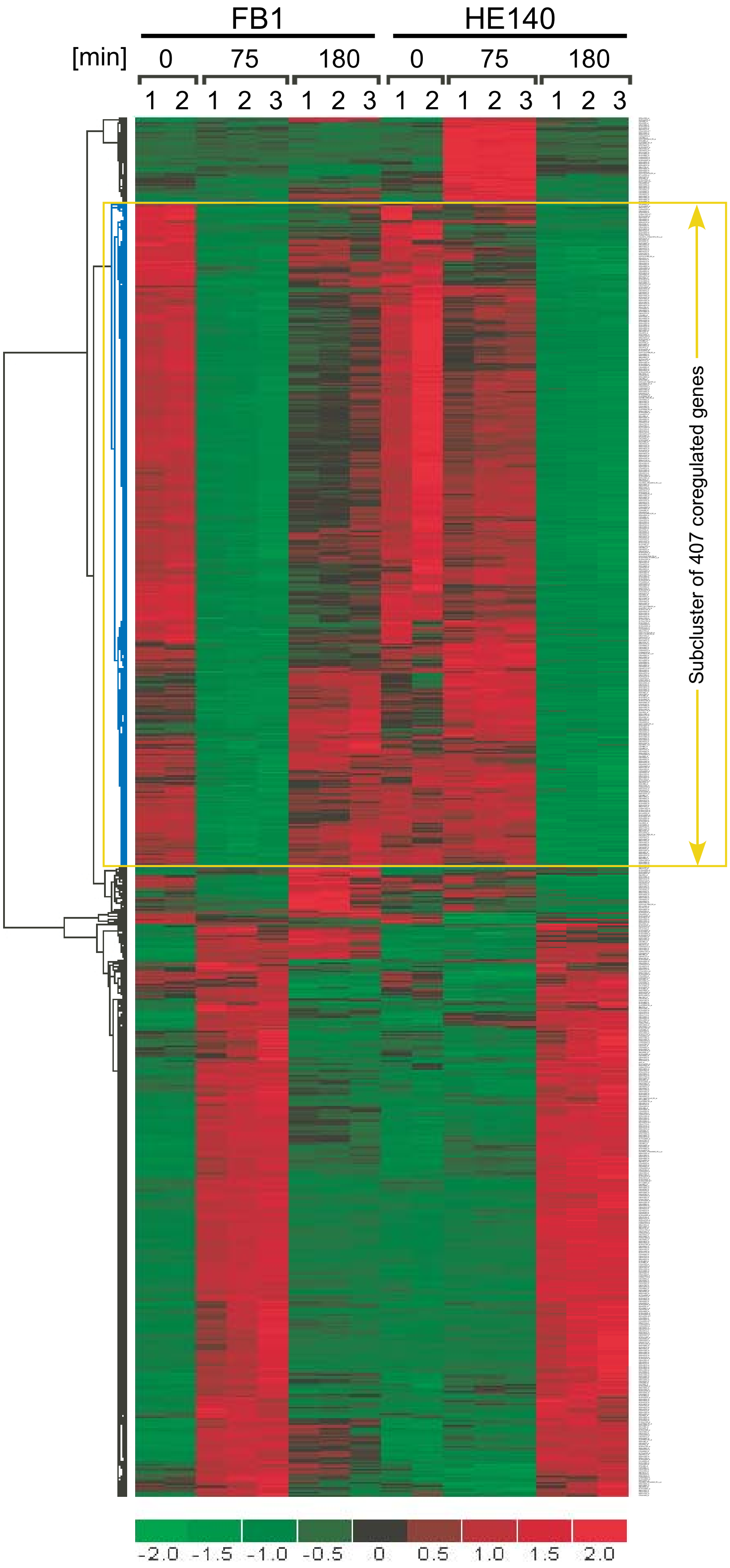

Supplemental Figure 1. Hierarchical cluster analysis of Adr1-regulated genes. A hierarchical cluster analysis of expression profiles of 847 differentially regulated genes is shown. Transcription profiles were compared of wild type strain FB1 and strain HE140 (FB1 Pcrg1:adr1) grown in CM containing glucose (0 min) and 75 as well as 180 min after induction of adr1 with arabinose. Statistical analysis of the data points was performed as described in Materials and Methods. In case of two probesets for the same gene, the one showing lower adjusted p-values was used. The probesets were clustered using the dChip 1.2 software package (Li and Hung Wong, 2001a, b; http://biosun1.harvard.edu/complab/dchip/) on gene lists generated by means of Bioconductor and the expression values calculated by MAS5.0. The single experiments are represented in temporal order from left to right. Arabic numerals indicate biological replicates. The colors represent the relative expression levels of the individual genes according to the color code on the bottom of the figure. Expression levels that are higher than the mean expression value are represented in red, those that are lower are represented in green (Eisen et al., 1998). The cluster of 407 coregulated genes is boxed. On the right side, each individual gene is identified by the probeset. Individual probesets as well as gene identifiers, annotation, fold changes and experimental means can be found in Supplemental Table 1.

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