

Dynamics of the yeast transcriptome during wine fermentation reveals the Fermentation Stress Response

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Supplementary Tables

[Supplementary Table 1](#): Position weight matrix models for transcription factor binding sites used in the regulatory analysis.

[Supplementary Table 2](#): Probe-set-summarized, normalized expression measures and data analysis for RNA hybridized to Affymetrix S98 arrays. Cells were harvested during fermentations at 0.5 %, 2 %, 3.5 %, 7 %, and 10 % (v/v) ethanol, corresponding to approximately 24 h, 48 h, 60 h, 120 h, and 340h time points, respectively.

[Supplementary Table 3](#): (A) Forty most highly glucose repressed genes (derived from Young *et al.*, 2003). (B) Induced genes involved in mitochondrial respiration/oxidative phosphorylation. (C) Induced genes involved in sterol biosynthesis. (D) Induced genes involved in oxidative stress. (E) Induced genes annotated to carbohydrate metabolism.

[Supplementary Table 4](#): Identification of over-represented transcription factor binding site motifs in each gene cluster. Scores are also shown for genes in larger groupings of the clusters.

Supplementary Figures

[Supplementary Figure 1](#): Venn diagram showing the number of induced or repressed genes in fermentation that are associated with transcriptionally characterized stress responses. Environmental Stress Response (ESR), Common Environmental Response (CER), Fermentation Stress Response (FSR).