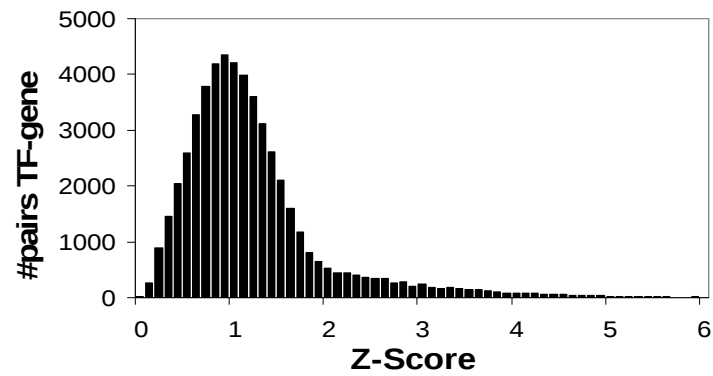
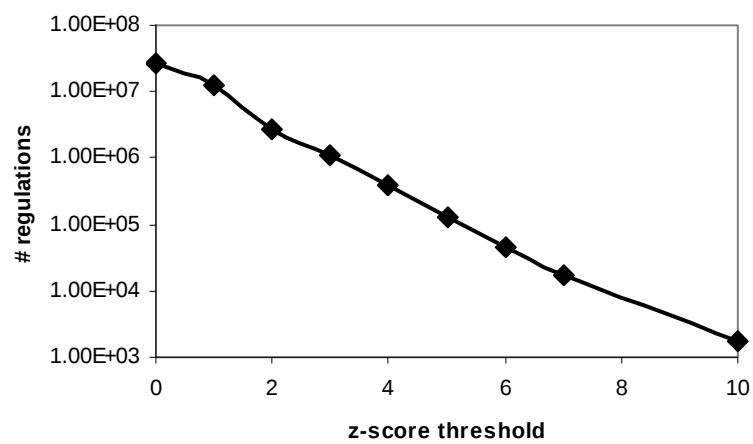
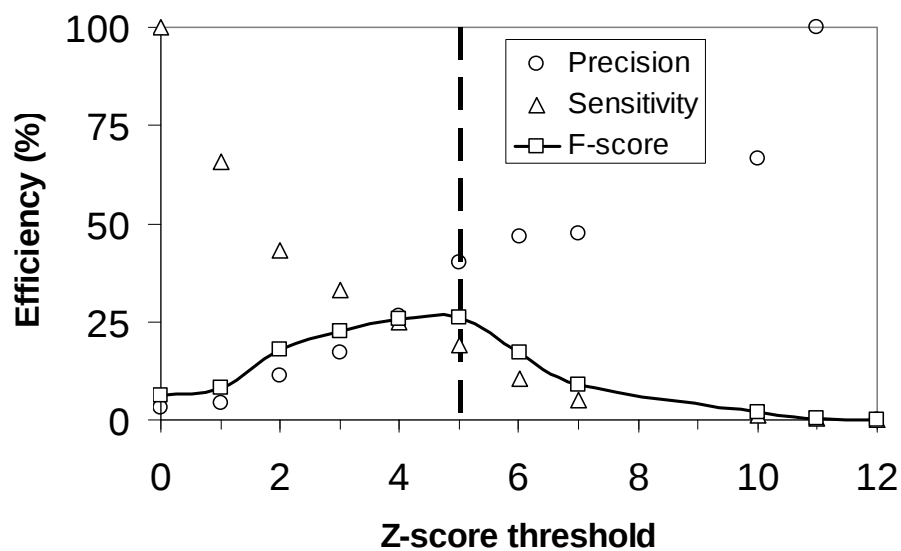




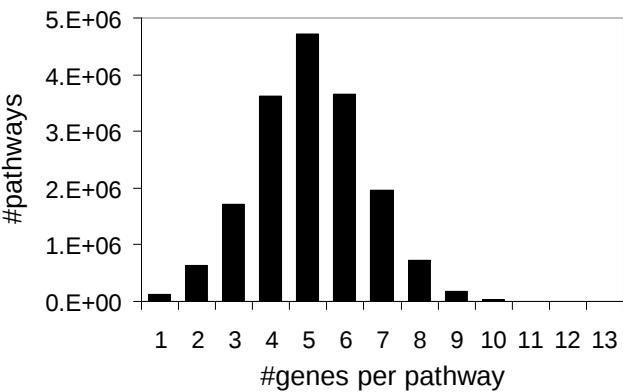
Supplementary Figure 1. z-score distribution from the mutual information calculation between all pairs gene-transcription factor.



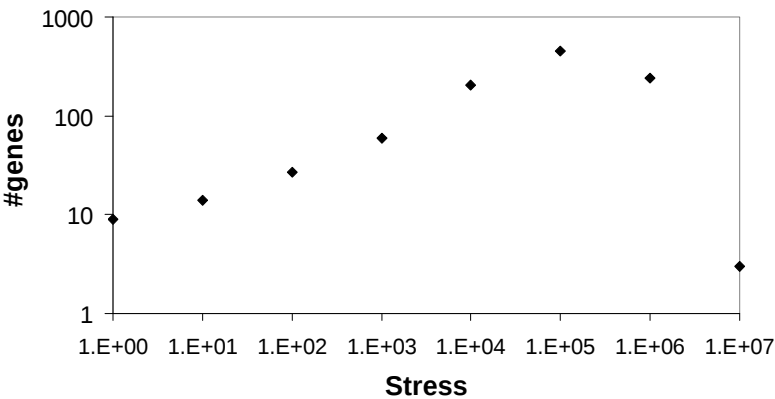
Supplementary Figure 2. Number of regulations of model depending on the cut-off threshold selection.



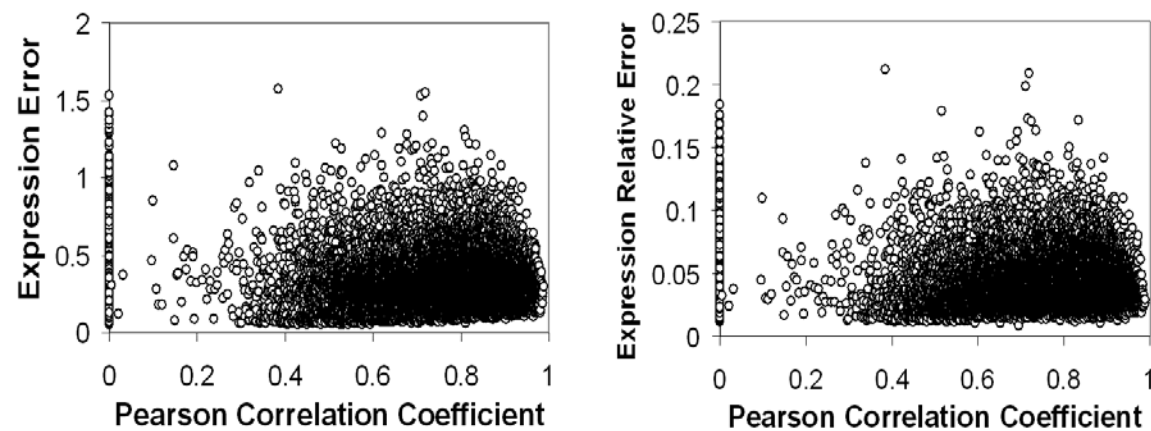
Supplementary Figure 3. Efficiency (precision, sensitivity and absolute efficiency or *F*-score) of the transcriptional model with respect to reference set. Vertical dashed line indicates the optimum value for the z-score threshold ($= 5$) according to the *F* value.



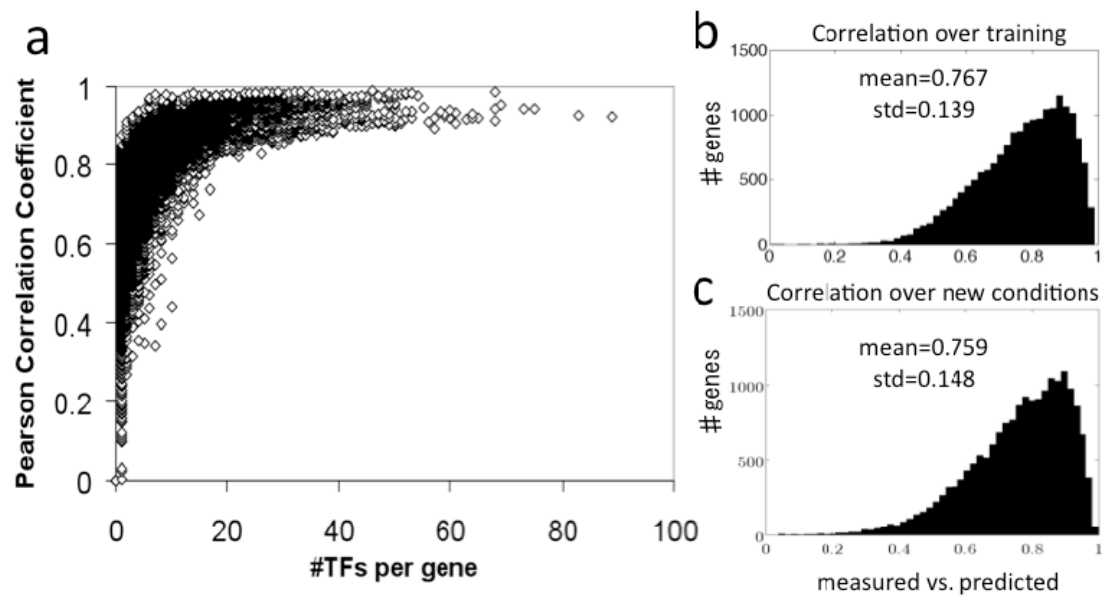
Supplementary Figure 4. Gene distribution in the pathways (clusters) found in the transcriptional network.



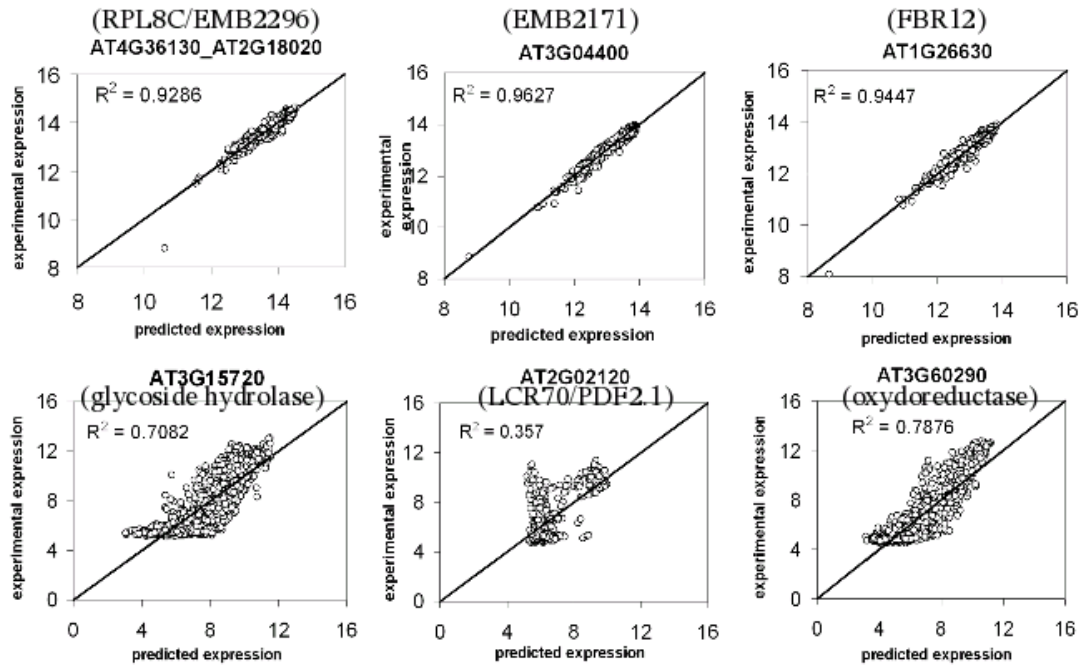
Supplementary Figure 5. Stress distribution of the transcriptional network.



Supplementary Figure 6. Absolute and relative gene expression errors versus the correlation coefficient between the experimental and predicted gene expressions for all conditions from the training set.



Supplementary Figure 7. (a) Correlation coefficient between the experimental and predicted gene expressions for all conditions versus the number of transcription factors regulating that gene. (b, c) Prediction in different environments using the transcriptional regulatory network. Histogram of Pearson correlations of measured and predicted gene expressions over 1292 experiments in the training set (b) and 144 conditions in the test set (c) are shown.



Supplementary Figure 8. Predictive power on gene expression of the effective model (including the transcriptional and non-transcriptional layers). We show the regression coefficient (R^2) between the model inferred using the whole data (1436 experiments) both as training and as tester sets for the best (top) and worst (bottom) predicted genes.