

Supplementary Figures

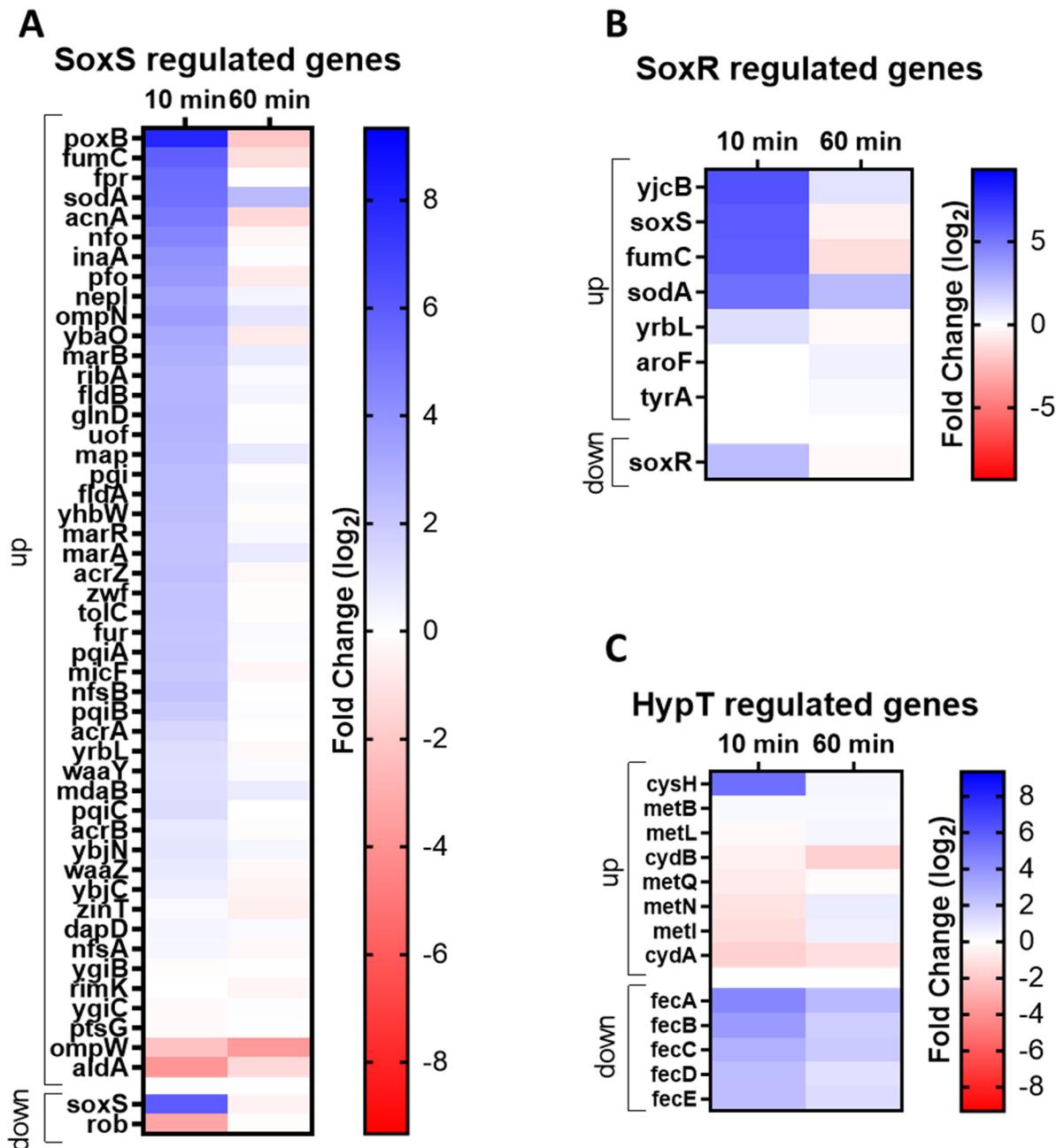


Figure S1. Heatmaps of genes regulated by the regulators SoxRS (A, B) and HypT (C) (involved in the response to oxidative stress). SoxRS were activated by H₂O₂, whereas the hypochlorite-sensitive transcription factor HypT did not display a pattern compatible with its activation. The color code corresponds to fold changes as compared to untreated cells at the respective time points (i.e. 10 and 60 min); n=4.

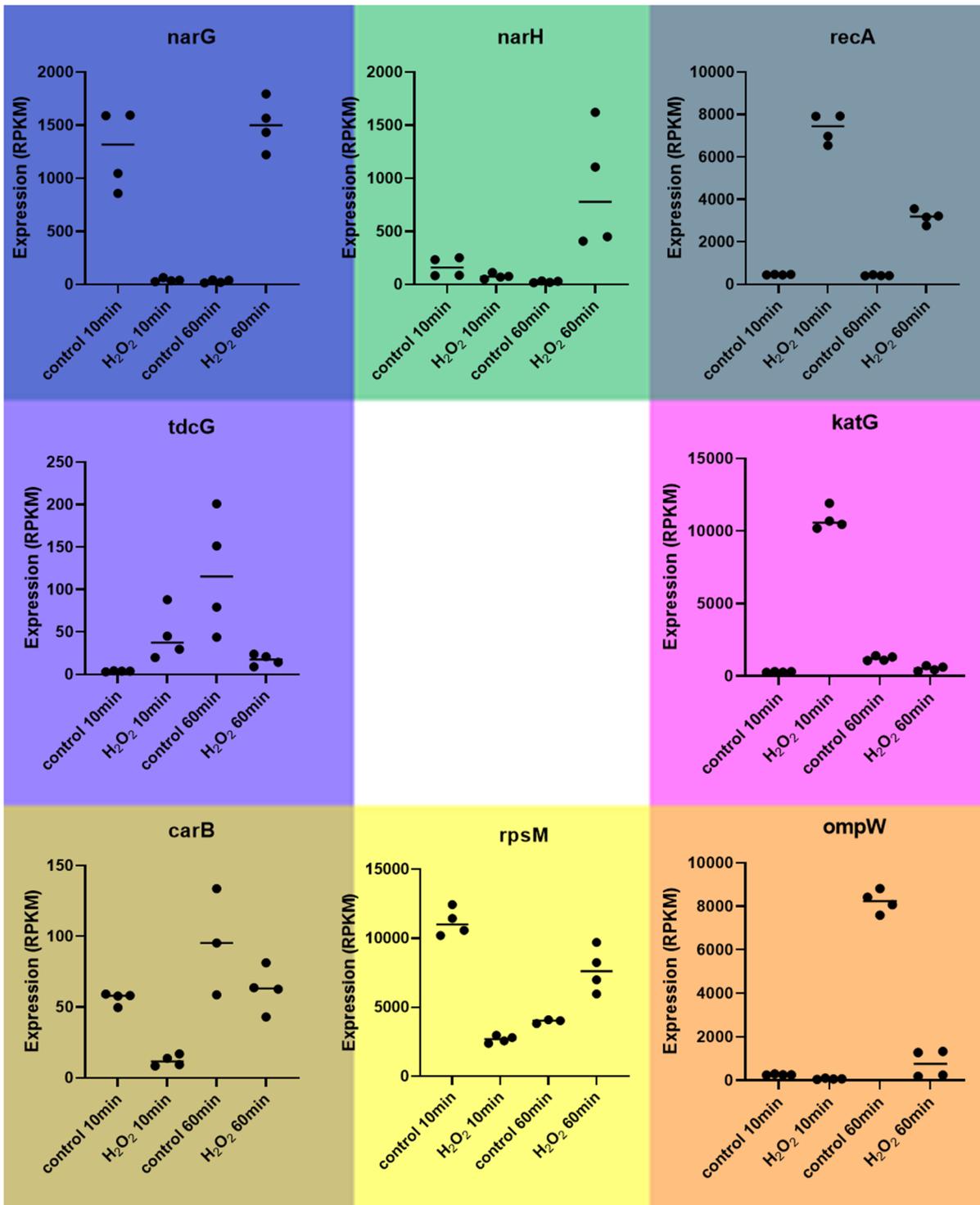


Figure S2. Expression levels of genes representative of the expression pattern represented in Figure 3; mean and individual values, n=4. Data are shown as reads per kilobase million (RPKM).

Dysregulated pathways ctrl 60 min vs ctrl 10 min

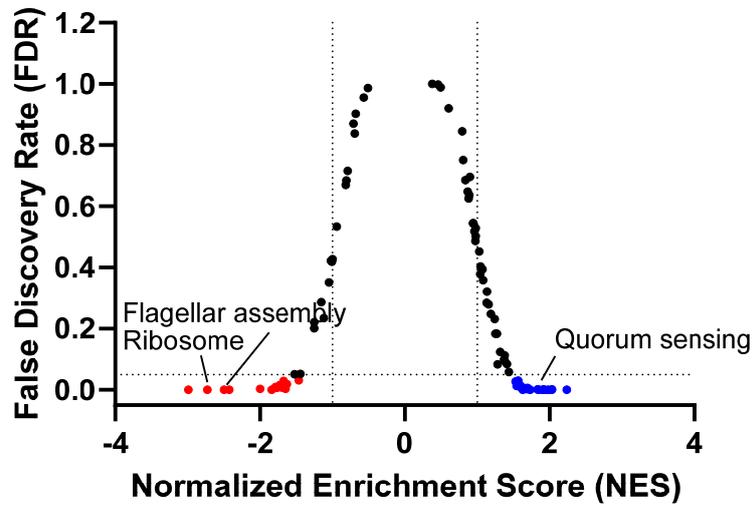


Figure S3. Dysregulated pathway comparing the untreated conditions at 60 min vs 10 min, using gene set enrichment analysis. Each dot represent a pathway from the KEGG database; thresholds: FDR=0.05, NES (normalized enrichment score) >1 and < -1.

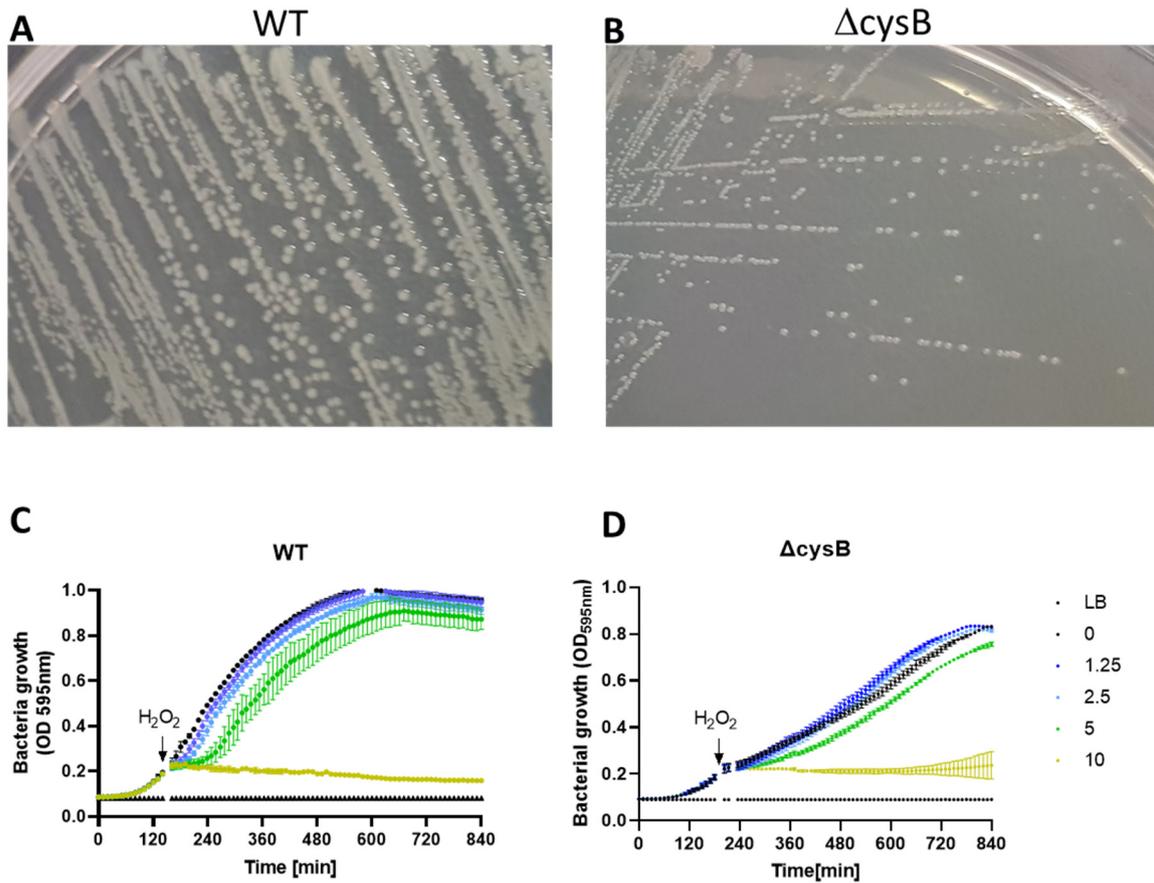


Figure S4. Impaired fitness of *cysB* deleted mutant. (A-B) *CysB* deleted mutant displayed smaller and paler colonies on agar plate at the same magnification. (C-D) Growth in LB under increasing H₂O₂, added during the exponential phase (OD_{595nm}=0.2). *cysB* deleted mutant showed a slower growth but an identical sensitivity to H₂O₂. One representative experiment.

