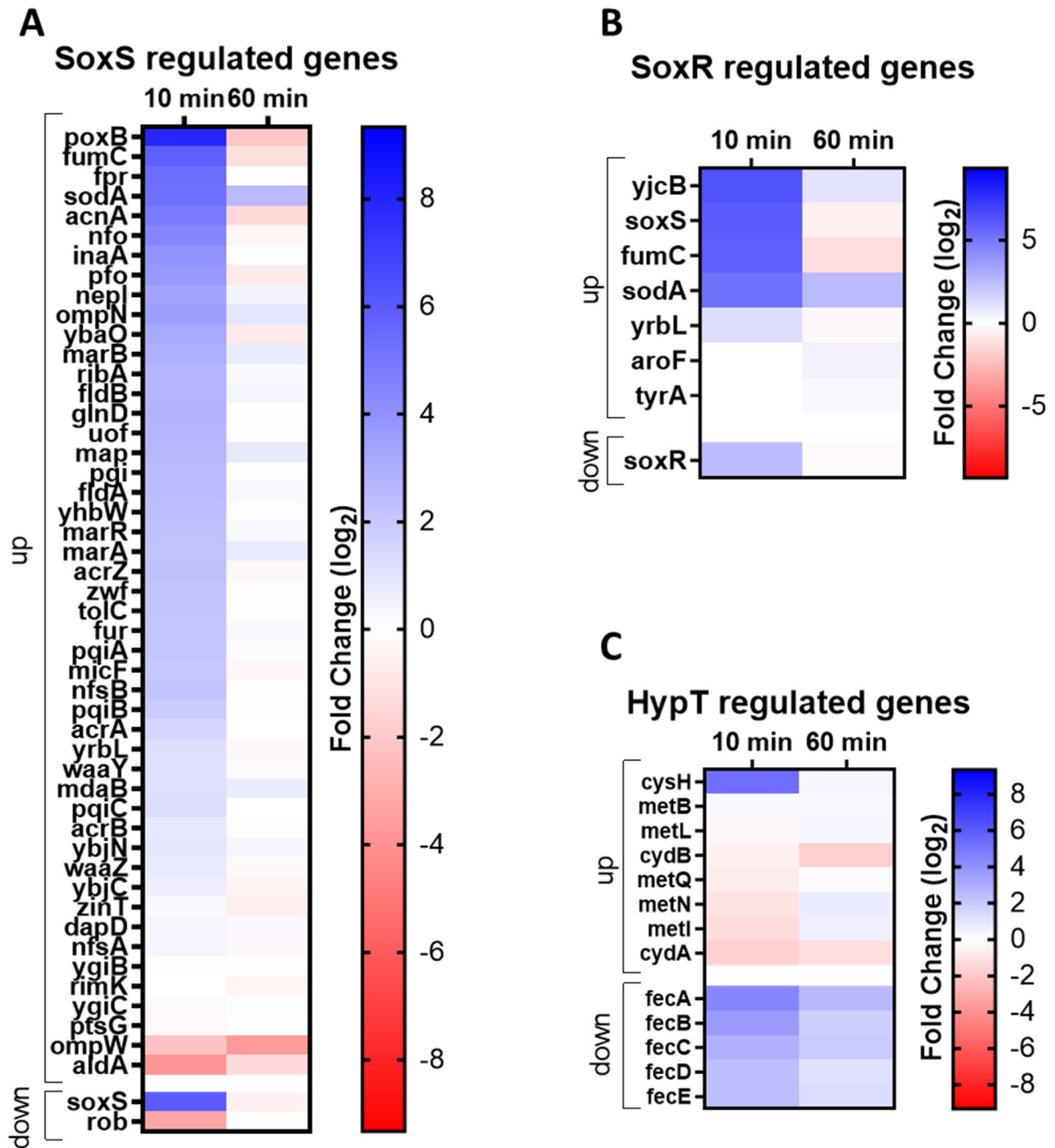
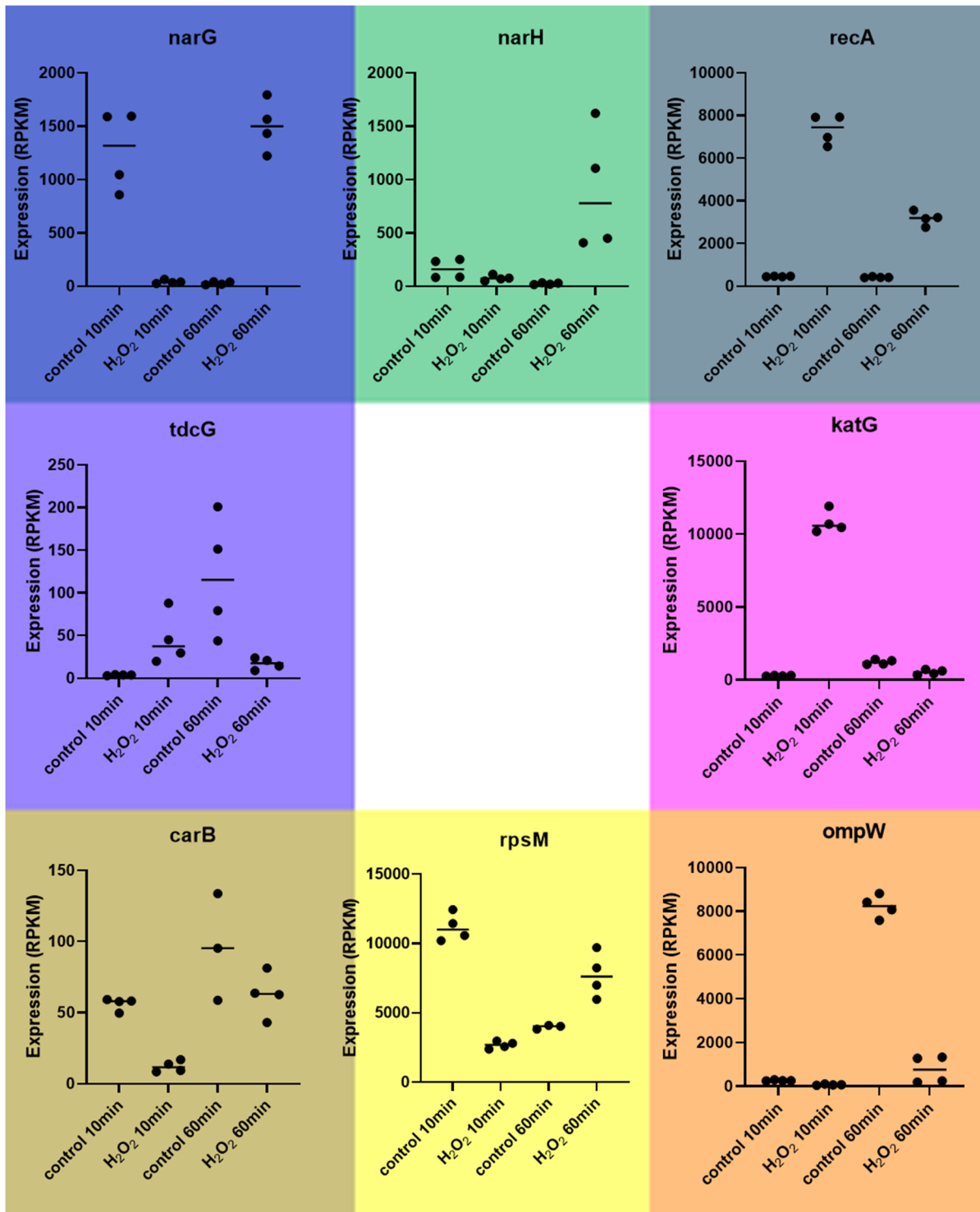


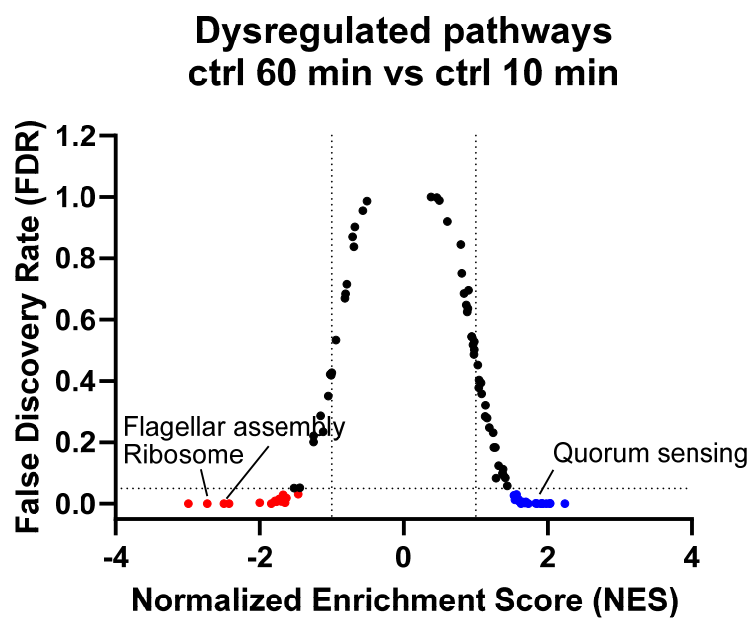
## Supplementary Figures



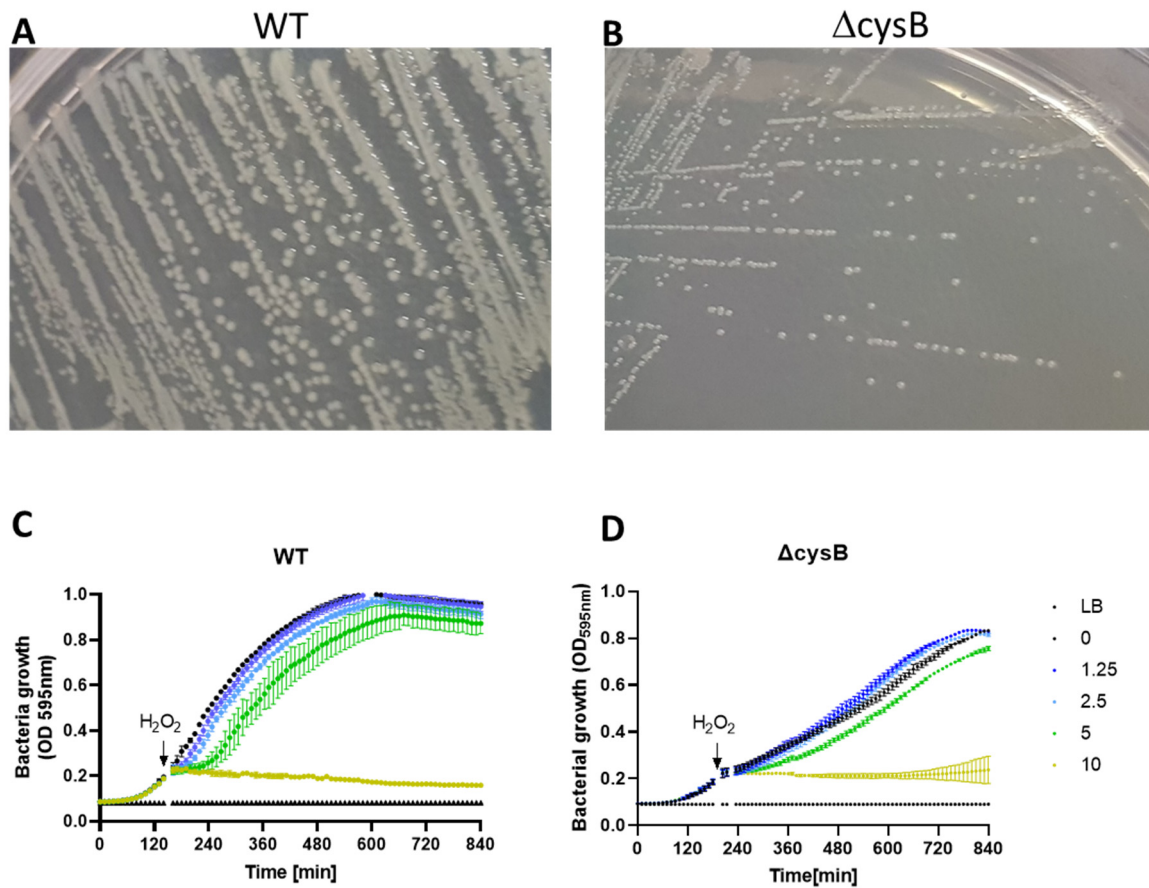
**Figure S1.** Heatmaps of genes regulated by the regulators SoxRS (A, B) and HypT (C) (involved in the response to oxidative stress). SoxRS were activated by  $H_2O_2$ , whereas the hypochlorite-sensitive transcription factor HypT did not display a pattern compatible with its activation. The color code 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).



**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 H<sub>2</sub>O<sub>2</sub>, added during the exponential phase (OD<sub>595nm</sub>=0.2). *cysB* deleted mutant showed a slower growth but an identical sensitivity to H<sub>2</sub>O<sub>2</sub>. One representative experiment.

