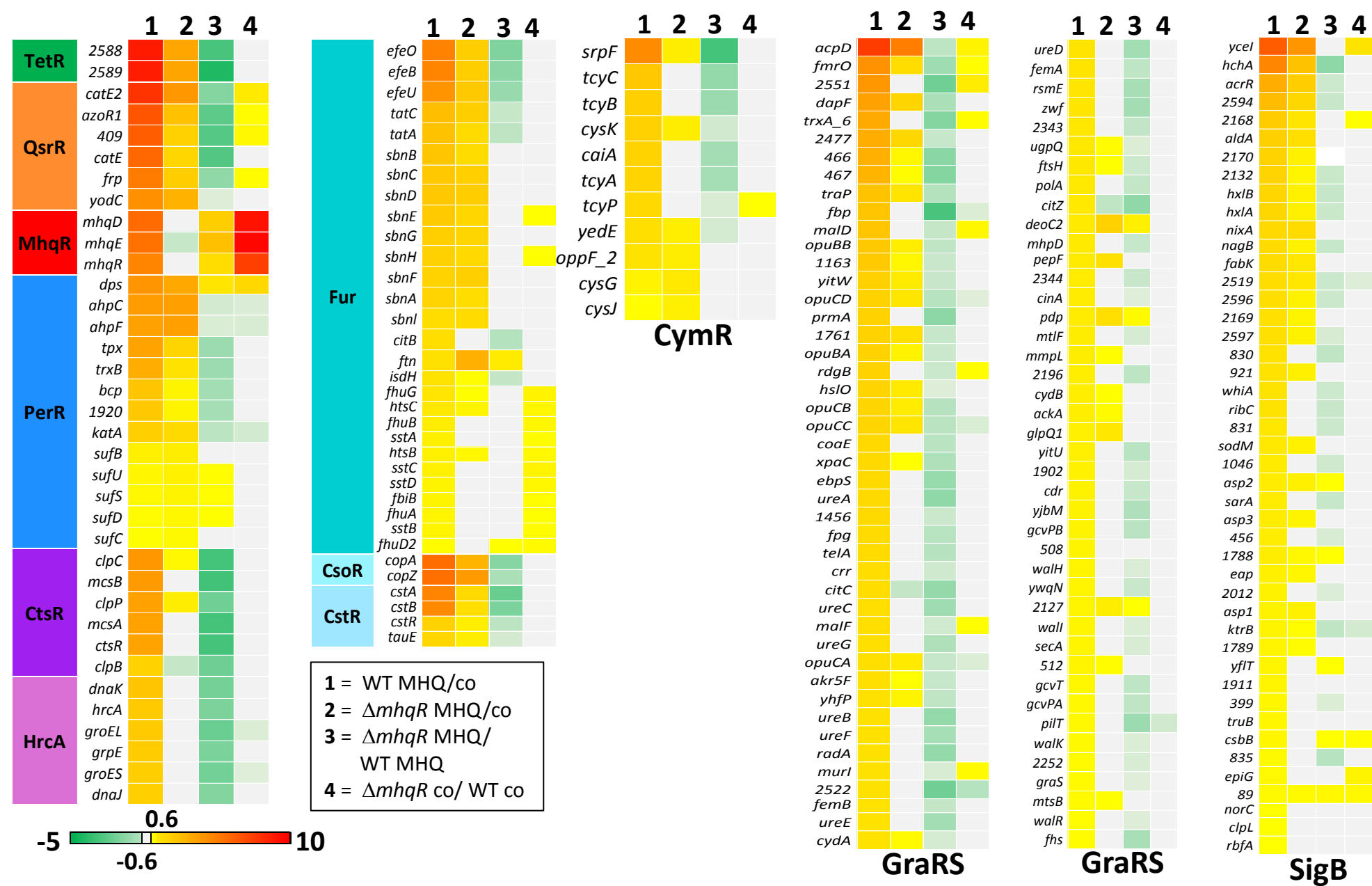


**Figure S2**



**Fig. S2. RNA-seq transcriptomics of *S. aureus* COL wild type and the *mhqR* mutant under MHQ stress.** For RNA-seq transcriptomics, *S. aureus* COL and the *mhqR* mutant were grown in RPMI1640 medium and treated with 45  $\mu$ M MHQ stress for 30 min. The gene expression profile of highly induced or repressed genes under MHQ stress is shown in a colour-coded heatmap. Red and green indicate significantly induced and repressed transcripts, respectively (M-value  $\geq 0.6$   $\leq -0.6$ ; p-value  $\leq 0.05$ ). The heatmap displays log<sub>2</sub> fold-changes of gene transcription between the wild type and the *mhqR* mutant under control and MHQ stress obtained from three biological replicates. The RNA-seq expression data are listed in Tables S1-S2.