

Fig. S5: Overview of the protein level regulation mediated by HP1021 revealed by MS/LC-MS. **a** Volcano diagram of proteins differentially expressed in the wild-type strain after 60-min oxidative stress (WTS_60) compared to the non-stressed WT strain (WTS_60-WT). **b** Volcano diagram of proteins differentially expressed in the wild-type strain after 120 min of oxidative stress (WTS_120) compared to the non-stressed wild-type strain (WTS_120-WT). **c** Volcano diagram of proteins differentially expressed in the Δ HHP1021 mutant strain after 60 min of oxidative stress (Δ HHP1021S_60) compared to the non-stressed Δ HHP1021 mutant strain (Δ HHP1021- Δ HHP1021S_120). **d** Volcano diagram of proteins differentially expressed in the Δ HHP1021 mutant strain after 120 min of oxidative stress (Δ HHP1021S_120) compared to the non-stressed Δ HHP1021 mutant strain (Δ HHP1021S_120- Δ HHP1021). **a-d** Four independent biological replicates were analyzed. Green dots correspond to genes with $|\log_2 FC| \geq 1$ and $FDR \geq 0.05$; blue dots correspond to genes with $|\log_2 FC| \leq 1$ and $FDR \leq 0.05$; red dots correspond to genes with $|\log_2 FC| \geq 1$ and $FDR \leq 0.05$; grey dots correspond to genes that were not significantly changed. NS, non significant. FDR, false discovery rate.

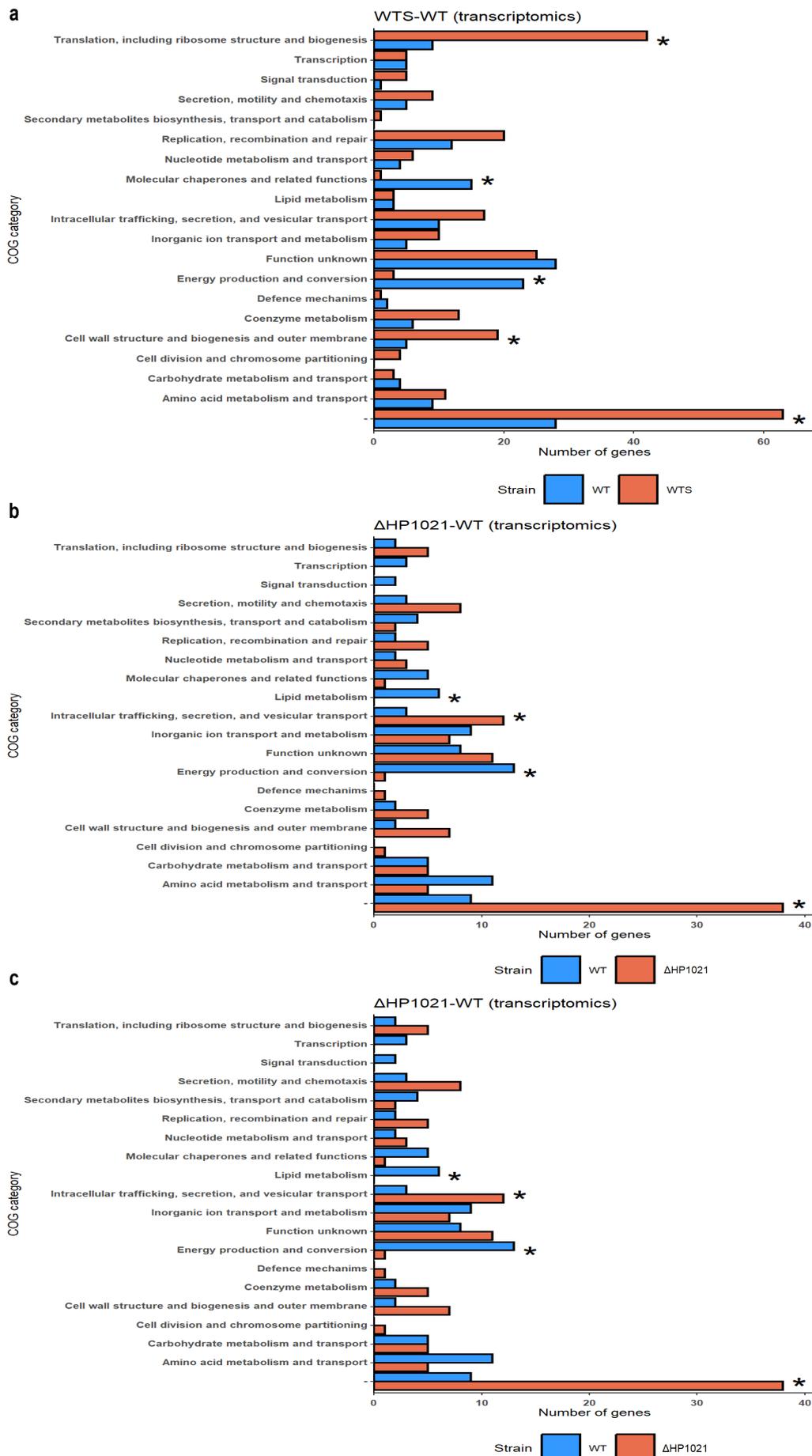
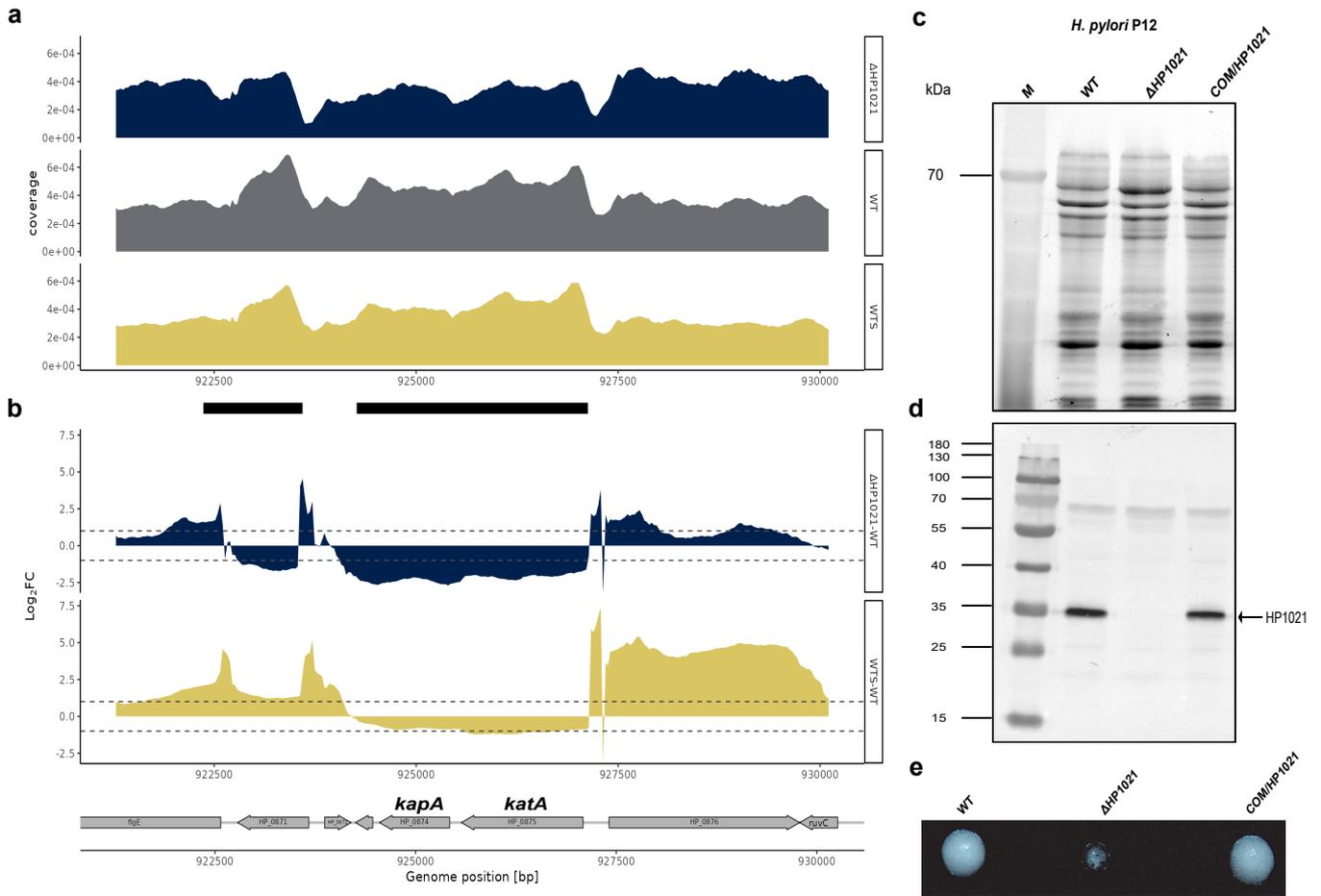


Fig. S6: *H. pylori* N6 Clusters of Orthologous Groups (COG). **a** COG groups of genes differently transcribed in the wild-type strain under oxidative stress (WTS) compared to the non-stressed wild-type strain (WTS-WT). **b** COG groups of genes differently transcribed in the Δ HP1021 mutant strain compared to the wild-type (WT) strain (Δ HP1021-WT). **c** COG groups of proteins expressed differently transcribed in the Δ HP1021 mutant strain compared to the wild-type (WT) strain (Δ HP1021-WT). **a-b** Chi-squared test determined the P value; significantly affected COGs ($P \leq 0.05$) are marked with black stars.



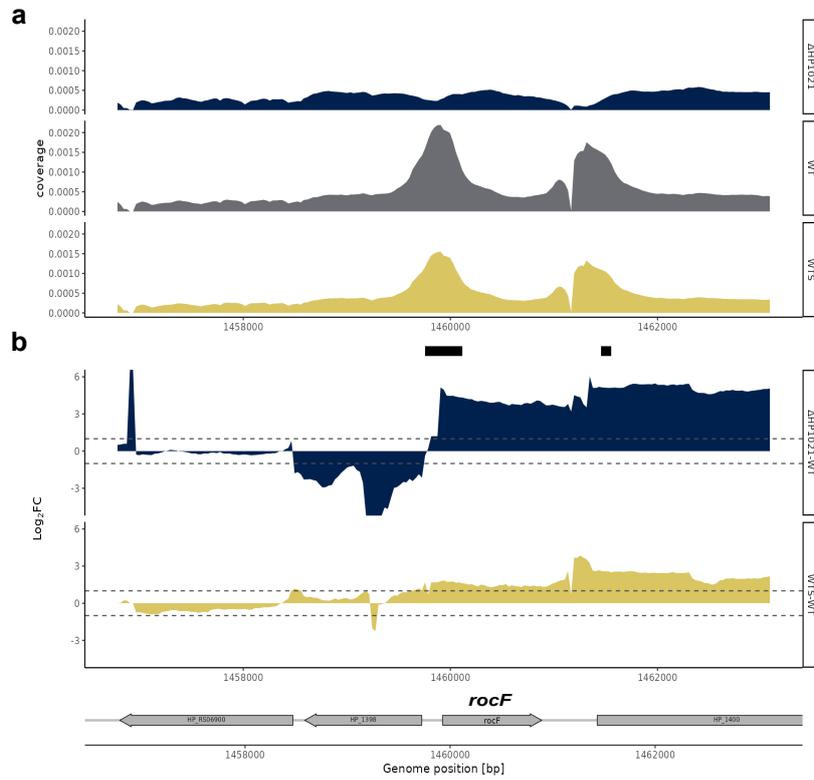


Fig. S8: HP1021 controls *rocF* expression. **a** ChIP-seq data profile of the *rocF* gene. Read counts were determined for *H. pylori* N6 WT, WTS and Δ HP1021 strains. The y-axis represents the coverage of the DNA reads, while the x-axis represents the position of the genome (in bps). The main peak of the binding site is marked with a thick black line under the x-axis. **b** RNA-seq data profile of *rocF* gene. The genomic locus for *H. pylori* N6 WT, WTS and Δ HP1021 strains with the WTS-WT and Δ HP1021-WT expression comparison; values above the black dashed lines indicate a change in the expression of $|\log_2FC| \geq 1$; $FDR \leq 0.05$.