

Description of Additional Supplementary Files

Supplementary Data 1:

Identification of HP1021 binding sites on *H. pylori* N6 genome by ChIP-seq. Chromosome position defined according to *H. pylori* 26695 strain (NC_000915.1).

Supplementary Data 2:

Analysis of HP1021 dependent gene expression in *H. pylori* N6 WT and Δ HP0121 strains under microaerobic and aerobic conditions. RNA-seq, ChIP-seq and LC-MS/MS data are presented. Genes annotation according to *H. pylori* 26695 strain (NC_000915.1).

Supplementary Data 3:

Comprehensive ChIP-seq, RNA-seq and MS data results for genes of selected processes or pathways in *H. pylori* N6. Genes annotation according to *H. pylori* 26695 strain (NC_000915.1). ComB uptake system according to Fisher et al., 2020 and Damke et al., 2022. The glucose metabolism pathway is based on the KEGG database, Kather et al. 2000, Corthesy-Theulaz et al. 1997 and Steiner et al. 2021. ROS and RNS response according to Flint et. al 2016. Transcriptomic and proteomic data are presented as log₂-fold changes. Legends specific to each pathway/process were added below particular tables. For more data, see Supplementary Data 1.