



Figure S3. Fold change in *RyhB1* sncRNA expression normalized to the mean of the corresponding iron free control of WT *S.Tm* (N=9, n=3) and the Δ entC strain (N=12, n=4) upon different iron sources. Expression data were normalized to their corresponding controls: WT (black circles) or Δ entC strain (grey bordered black circles). Gene expression was normalized using the $\Delta\Delta$ ct method using the *16S* ribosomal RNA (*16S rRNA*) and DNA-dependent RNA polymerase (*rpoB*) mRNA as reference transcripts. Graphs are depicted as mean \pm SD. For statistical analysis one-way ANOVA (a-d) corrected for multiple comparisons with the Holm-Sidak post hoc test was used (**: $p < 0.01$, numbers indicate a non-significant p -value > 0.05). N: number of biological replicates, n: number of experiments conducted. WT: wildtype *S.Tm*, Δ entC: *S.Tm* enterobactin/salmochelin knockout mutant strain.