



1

2

3 **Figure S2. Additional σ^B translationally activated genes with changes in RNA isoform.**

4 Rend-seq and ribosome profiling data from conditions with inactive/active σ^B for the operons

5 containing (A) *yjbc*, (B) *yjzE*, (C) *ygxB*, (D) *aldY*. Orange and blue bars represent 5'- and 3'-

6 mapped read counts, respectively, and the black scale bars correspond to 0.5 kb. Rend-seq data

7 indicating the σ^B transcription start sites are marked by red arrows. Fold changes (FC) between

8 σ^B active and σ^B inactive conditions are shown. Putative σ^B -dependent promoter sequences are

9 indicated for each gene (+1 corresponds to the 5' end of the σ^B -dependent isoform mapped by

10 Rend-seq). *yjbc*'s mRNA is part of a polycistronic transcript including *spxA*, which is not shown

11 for clarity. Due to low sequencing coverage, Rend-seq data from (Lalanne et al., 2018) was used
12 to annotate some transcript isoforms in the σ^B inactive condition. We note that the annotation for
13 *ygxB* is likely incorrect based on our ribosome profiling data.