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2 **Figure S1. Additional translationally activated genes with σ^B transcript inside σ^A**
3 **polycistron.**
4 Rend-seq and ribosome profiling data from conditions with inactive/active σ^B for the operons
5 containing (A) *yhdF*, (B) *yocK*, (C) *ydbD*, (D) *yflH*, and (E) *ymxB*, (F) *csbX*. Orange and blue
6 bars represent 5'- and 3'-mapped read counts, respectively, and the black scale bars correspond
7 to 0.5 kb. Rend-seq data indicating the σ^B transcription start sites are marked by red arrows. Fold
8 changes (FC) between σ^B active and σ^B inactive conditions are shown. Putative σ^B -dependent
9 promoter sequences are indicated for each gene (+1 corresponds to the 5' end of the σ^B -
10 dependent isoform mapped by Rend-seq). The *yocK* σ^A polycistron includes multiple upstream
11 genes not shown for clarity. A likely post-lysis RNase A 5'/3' doublet in *ydbD* is marked by *.
12 PnpA and Rho dependent 3' ends (Lalanne et al., 2018) in *csbX* are indicated with #. See also
13 Figure 2.