Supplemental Information for:

Escherichia coli SymE is a DNA-binding protein that can condense the nucleoid

Mary K. Thompson, Isabel Nocedal, Peter H. Culviner, Tong Zhang, Kevin R. Gozzi, Michael T. Laub

Supplemental Figures 1-4

Supplemental Tables (provided as .xls files)

Table S1. The most up- and down-regulated genes after *symE* induction

Table S2. Analysis of ChIP-seq replicates

Table S3. Strains

Table S4. Plasmids

Table S5. Oligonucleotides

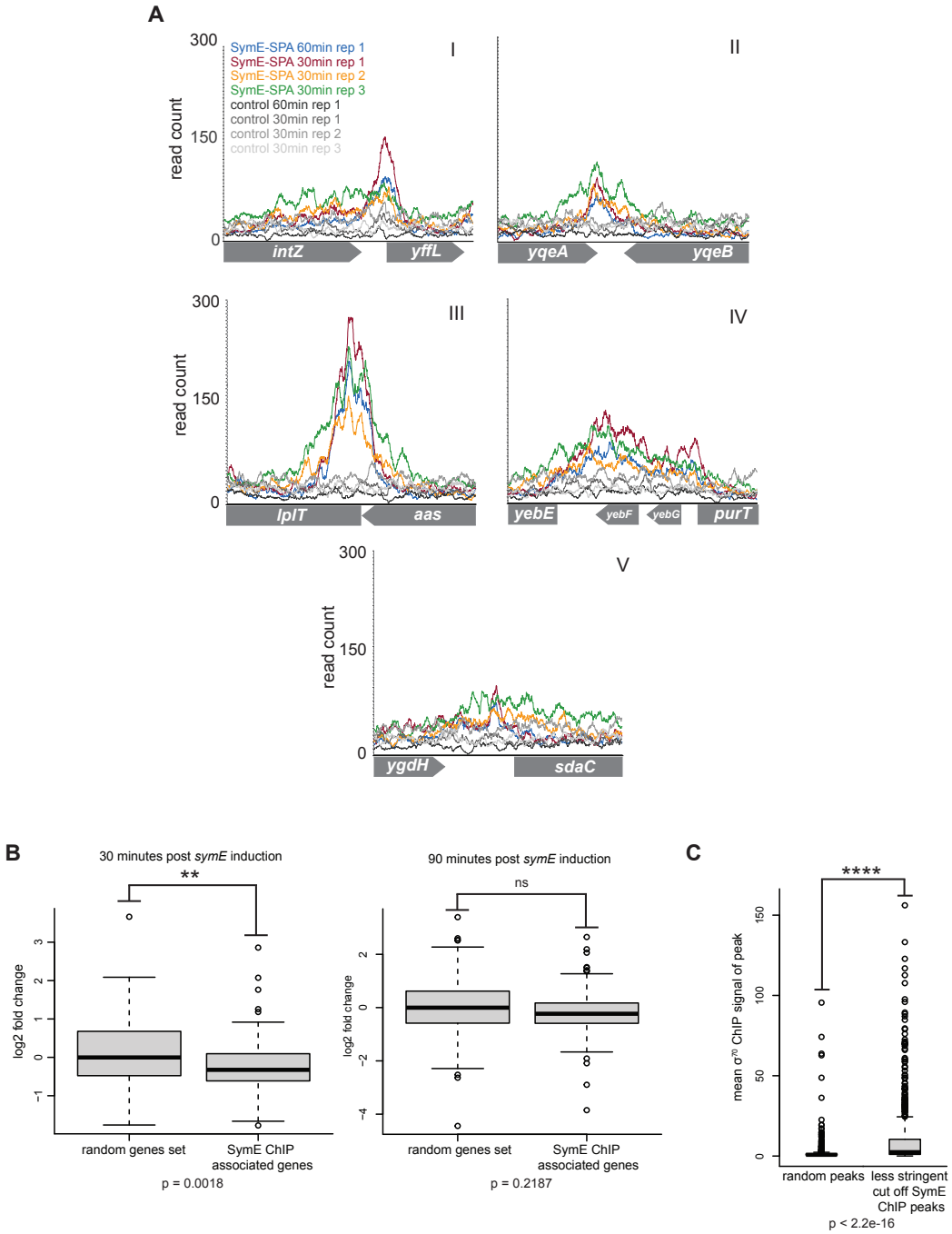

Figure S1. Additional ChIP-seq analysis.

(A) Comparison of ChIP-seq peaks from replicate data sets indicated at the top left. Peaks shown are the same as those in Figure 4C.

(B) Comparison of the expression change of SymE-SPA ChIP-associated genes to the same number of randomly chosen genes 30- and 90- minutes post-induction of *symE*. Asterisks indicate statistical significance (*t*-test) with the p-value listed below in each case.

(C) Analysis of the overlap between all SymE-SPA ChIP-peak locations called by MACS without any additional thresholding and signal from σ^{70} ChIP-seq studies. When compared to a random set of locations, SymE-SPA ChIP locations had significantly higher overlap with mean signal from σ^{70} ChIP-seq. Asterisks indicate statistical significance (*t*-test) with the p-value listed below.

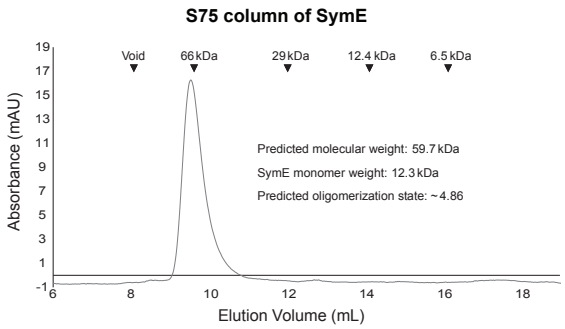

Figure S2. Size exclusion chromatography of SymE indicates multimerization.

When run on an S75 size exclusion column, SymE eluted at approximately 9.8 mL, corresponding to a molecular weight of 59.7 kDa based on a standard curve calculated from known standards. A SymE monomer is approximately 12.3 kDa, which predicts SymE to be either a tetramer or a pentamer.

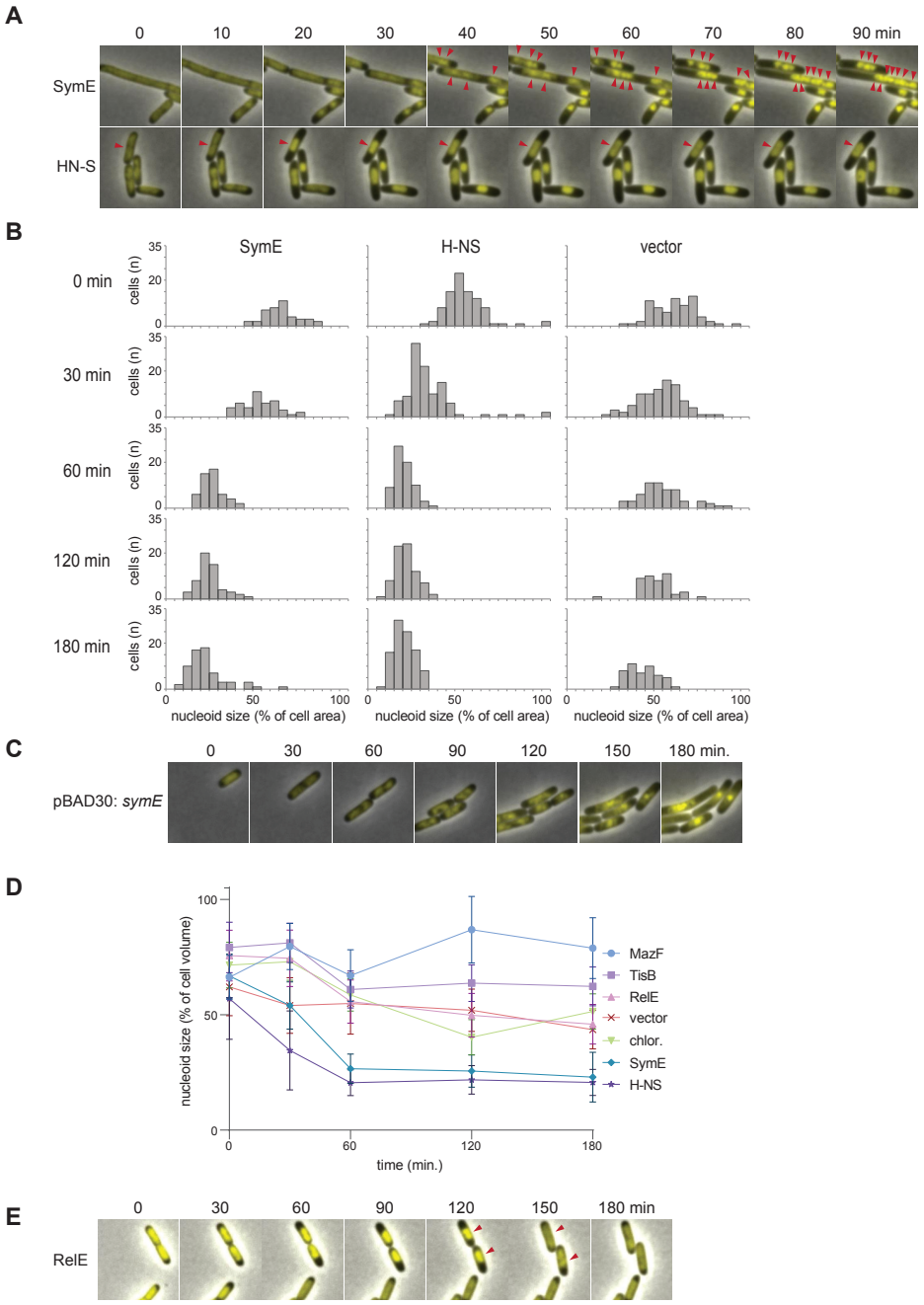

Figure S3. Additional data and analysis of time-lapse microscopy studies.

(A) Additional time-lapse imaging of cells overexpressing *symE* or *hns* and HU-GFP to stain the nucleoids.

(B) Histograms of the cell area taken up by the nucleoid, based on fluorescence measurements, for cells induced to express *symE*, *hns*, or an empty vector.

(C) Additional time-lapse imaging of cells overexpressing *symE* from pBAD30 (which has a lower copy number/ weaker promoter than pBAD24, the vector used in panel (A) and Figure 6).

(D) Quantification of nucleoid size for all conditions shown in Figure 6A.

(E) Cells from a population expressing *relE* illustrating their capacity to fully decondense their nucleoids after initial condensation.

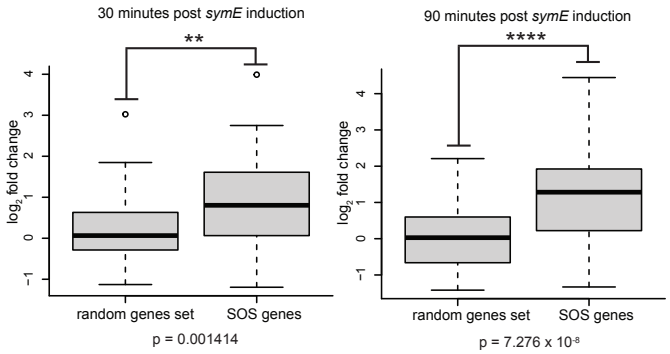

Figure S4. Statistical analysis of SOS gene induction following *symE* expression.

Comparison of the expression change of SOS regulon genes to the same number of randomly chosen genes 30- and 90- minutes post *symE* induction. Asterisks indicate statistical significance (*t*-test) with the p-value listed below in each case.