Supporting Information

Peters et al. 10.1073/pnas.0903846106

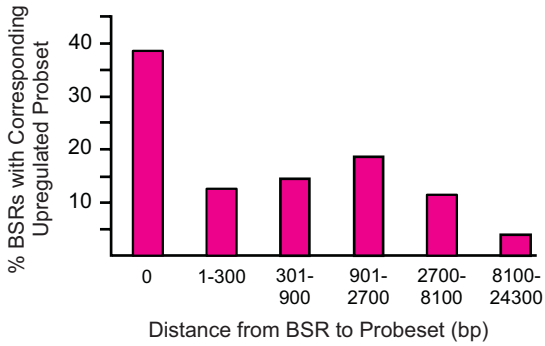

Fig. S1. Comparison of BSR positions to genes reported to be affected by BCM in expression-profiling experiments [Cardinale CJ, et al. (2008) Termination factor Rho and its cofactors NusA and NusG silence foreign DNA in E. coli. *Science* 320(5878):935–938.]. Bars represent the percentage of BSRs that are within the indicated distance of a gene reported to be at least 2-fold upregulated by BCM treatment. Distance indicates overlap between BSRs and BCM upregulated genes.

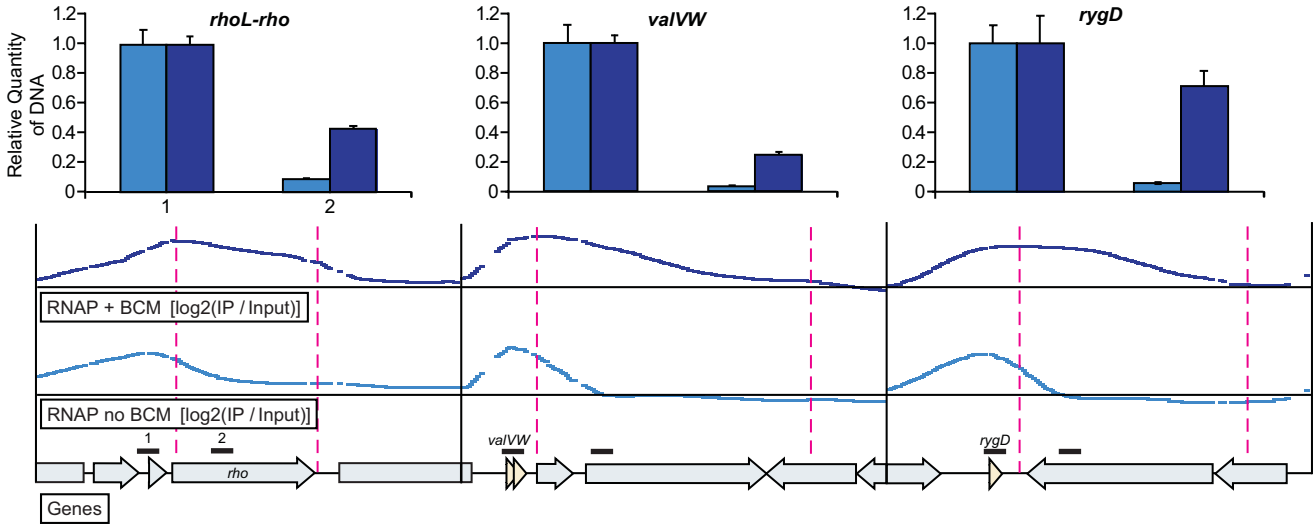

Fig. S2. Quantitative PCR confirmation of ChIP-chip results. Bar graphs indicate the relative quantity of DNA as determined by quantitative PCR normalized to the primer set before the BSR. Each primer set is designated by a horizontal black bar above its priming position. Colors, labels, and data smoothing are as described in Fig. 1*B*, except that noncoding RNA genes are colored yellow.

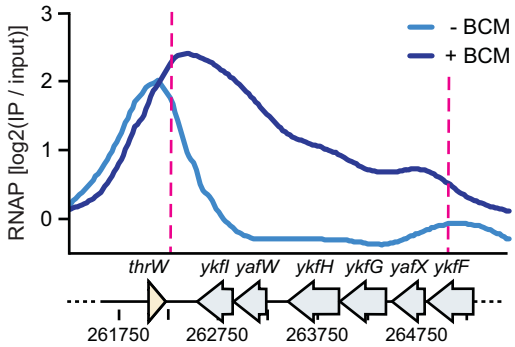

Fig. S3. BCM effect on the distribution of RNAP at the *thrW* tRNA. Colors, labels, and data smoothing are as described in Fig. 1*B*, except that noncoding RNA genes are colored yellow.

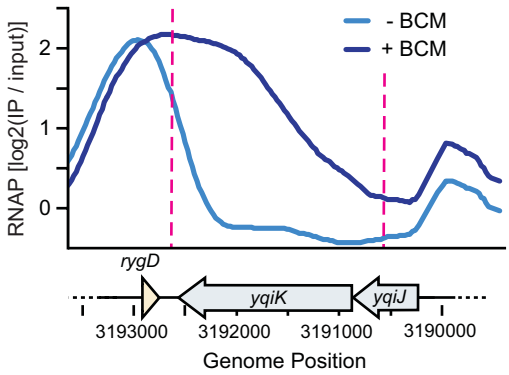

Fig. S4. BCM effect on the distribution of RNAP at the *rygD* sRNA. Colors, labels, and data smoothing are as described in Fig. 1*B*, except that noncoding RNA genes are colored yellow.

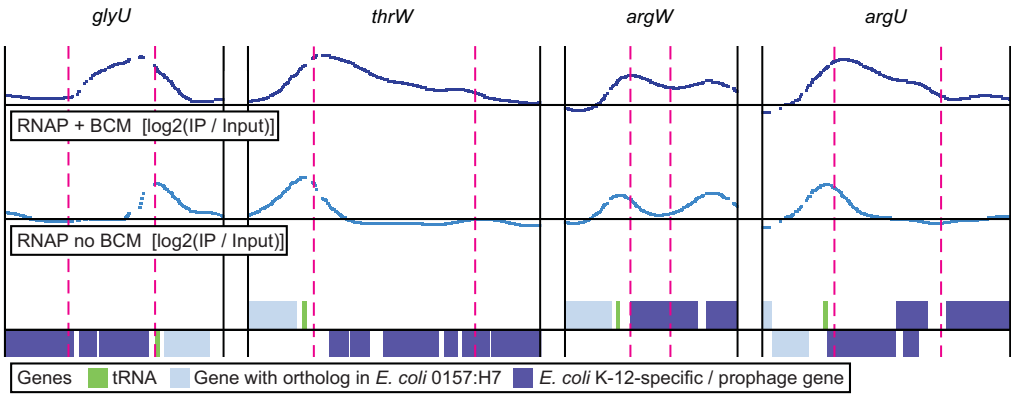

Fig. S5. Transcriptional readthough from tRNA operons onto K-12-specific genes and prophage elements. Genes above the black line are transcribed to the right, and genes below the line are transcribed to the left. Colors, labels, and data smoothing are as described in Fig. 1*B*, except that tRNA genes are colored green, and *E. coli* K-12-specific genes and prophage genes are colored violet.

Other Supporting Information Files

Table S1
Table S2
Table S3
Table S4