Operon Promoter Landscape
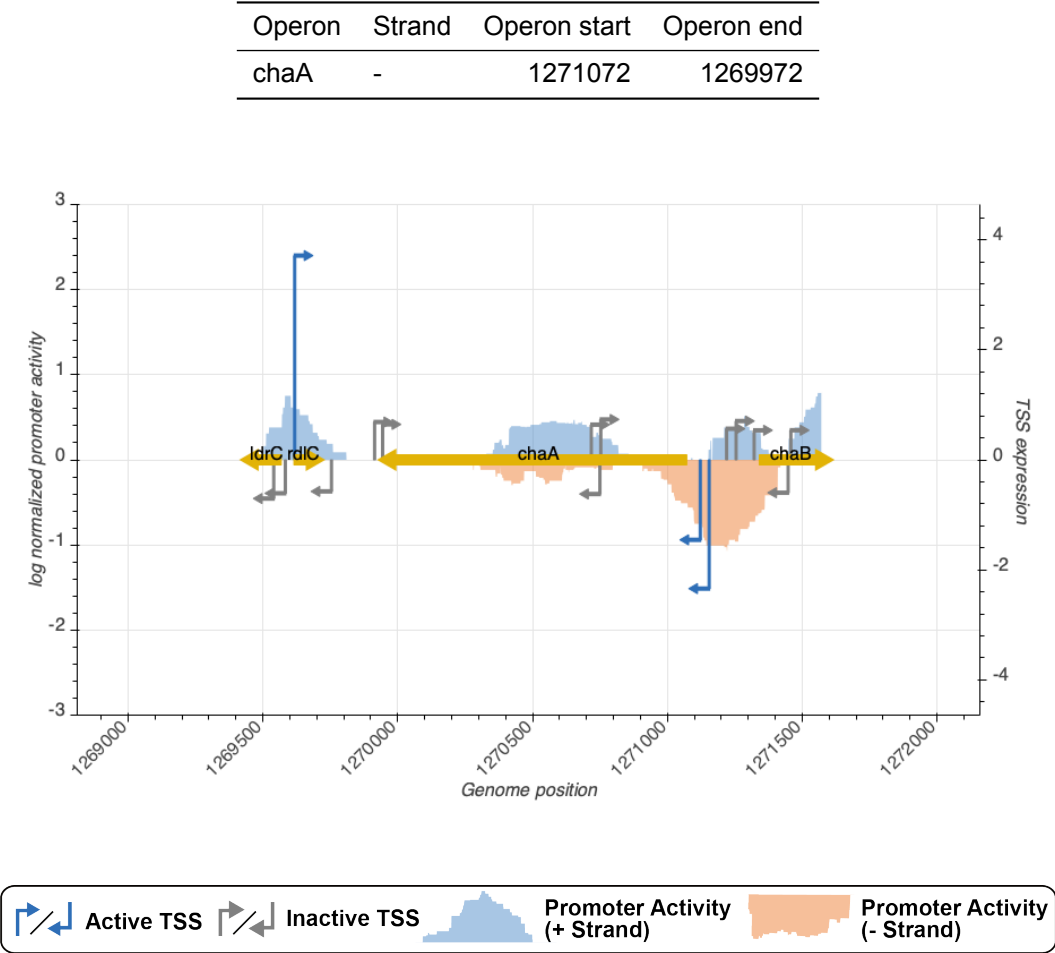
Operon	Strand	Operon start	Operon end
chaA	-	1271072	1269972

Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left Y-axis) was determined by measuring expression of over 300,000 genomic fragments spanning the *E. coli* genome and averaging promoter activity at all nucleotide positions in a strand-specific fashion. Genome coordinates corresponds to *E. coli* genome version U00096.2.

TSS Summary

| TSS name	TSS position	Strand	TSS activity	Category
TSS_4938_storz_regulondb	1271318	+	0.5368317	inactive
TSS_4940_regulondb	1271454	+	0.5371504	inactive
TSS_4937_regulondb	1271251	+	0.7052432	inactive
TSS_4936_storz_regulondb	1271216	+	0.5647513	inactive
TSS_4939_storz	1271444	-	0.5978077	inactive
TSS_4935_storz	1271151	-	2.3404971	active
TSS_4934_wanner	1271118	-	1.4543874	active

TSS Scanning Mutagenesis
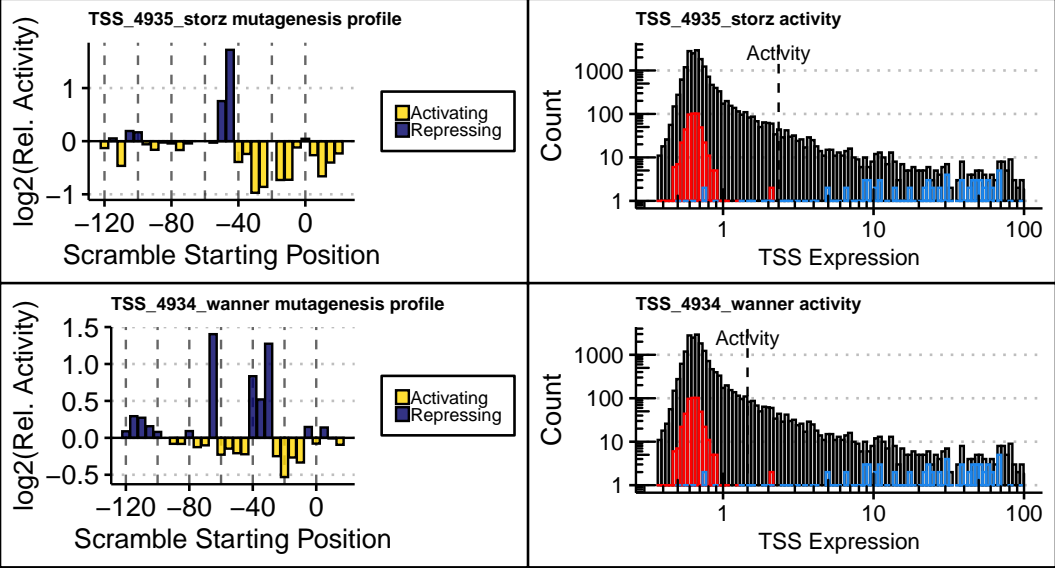
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals spanning the promoter. Bar color identifies the region as a putative activator (yellow) or repressor (purple). **(Right)** Dashed line indicates the expression of the indicated TSS relative to all tested TSS sequences. The distributions of expression is shown for all tested TSSs (black), 500 negative controls (red), and a set of constitutive promoters from the BioBrick registry (blue).