Operon Promoter Landscape
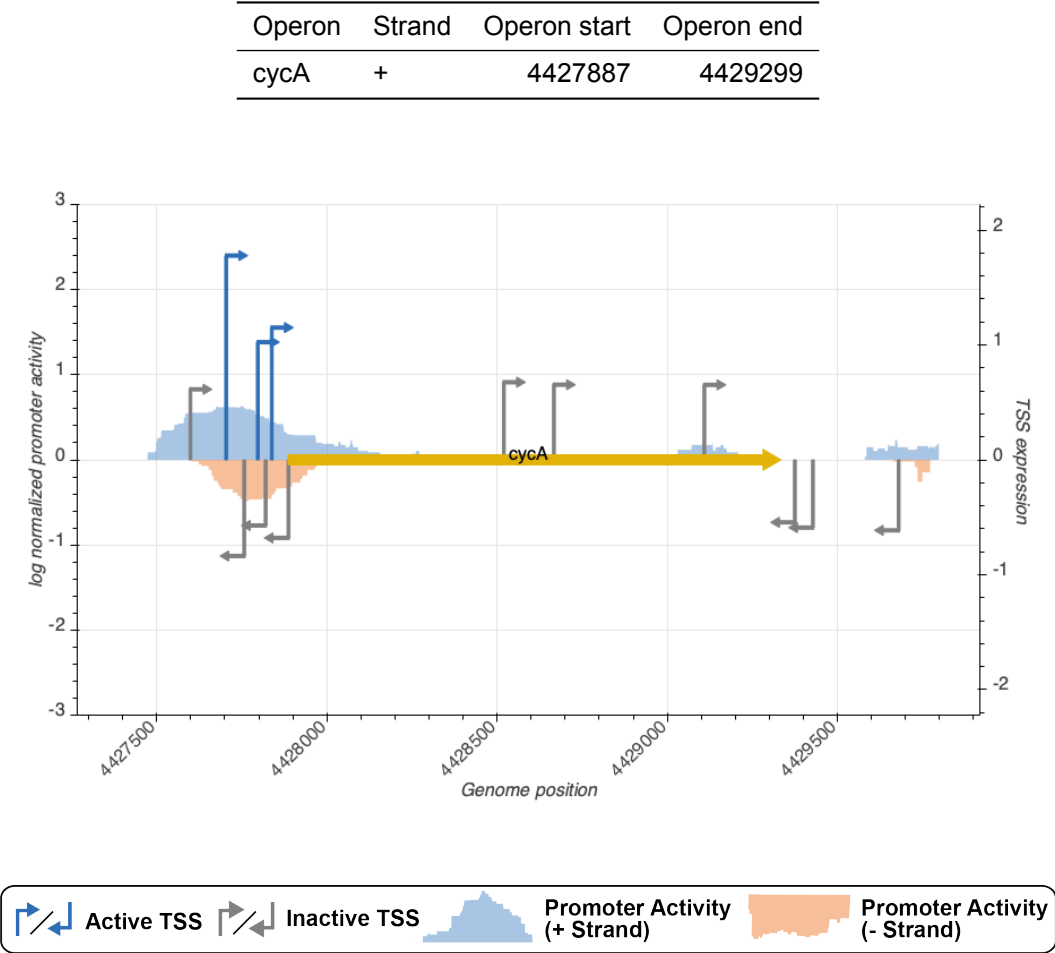
Operon	Strand	Operon start	Operon end
cycA	+	4427887	4429299

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_17318_storz	4427700	+	1.7777111	active
TSS_17317_storz	4427595	+	0.6139024	inactive
TSS_17322_regulondb	4427834	+	1.1507793	active
TSS_17323_storz	4427883	-	0.6795955	inactive
TSS_17321_storz	4427816	-	0.5714301	inactive
TSS_17319_wanner	4427753	-	0.8369482	inactive
TSS_17320_storz_regulondb	4427793	+	1.0242057	active

TSS Scanning Mutagenesis
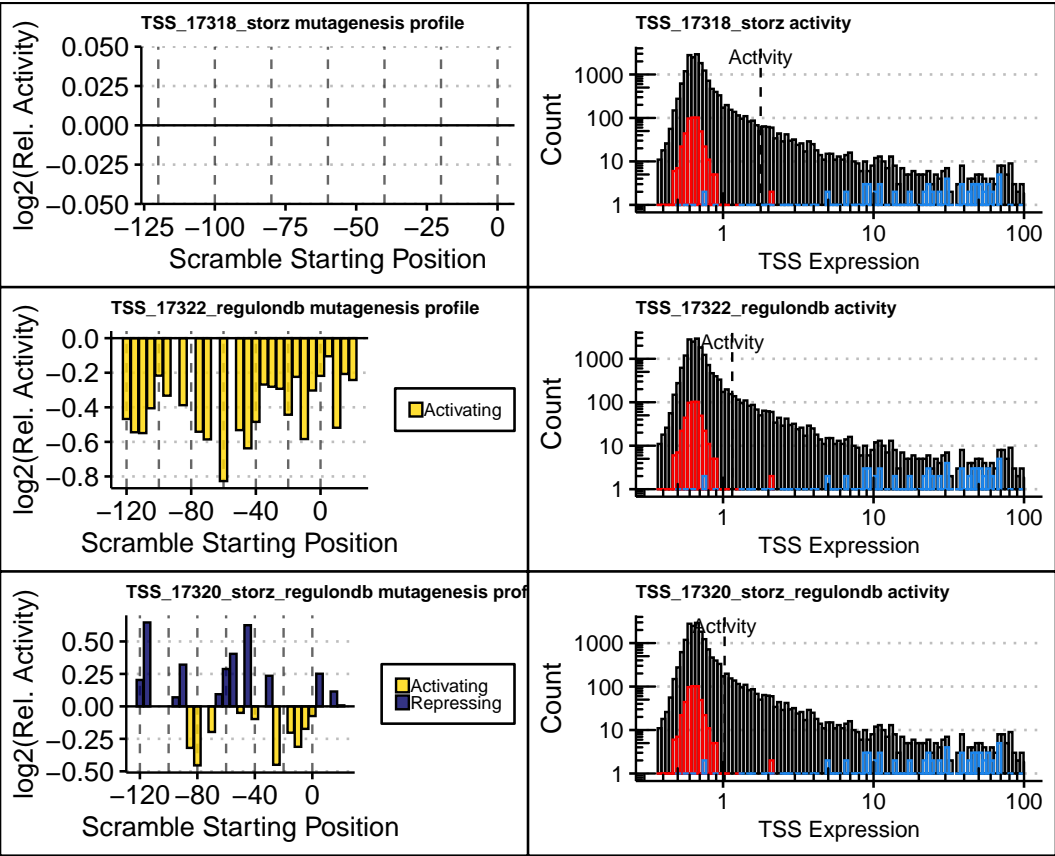
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals 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).