Operon Promoter Landscape
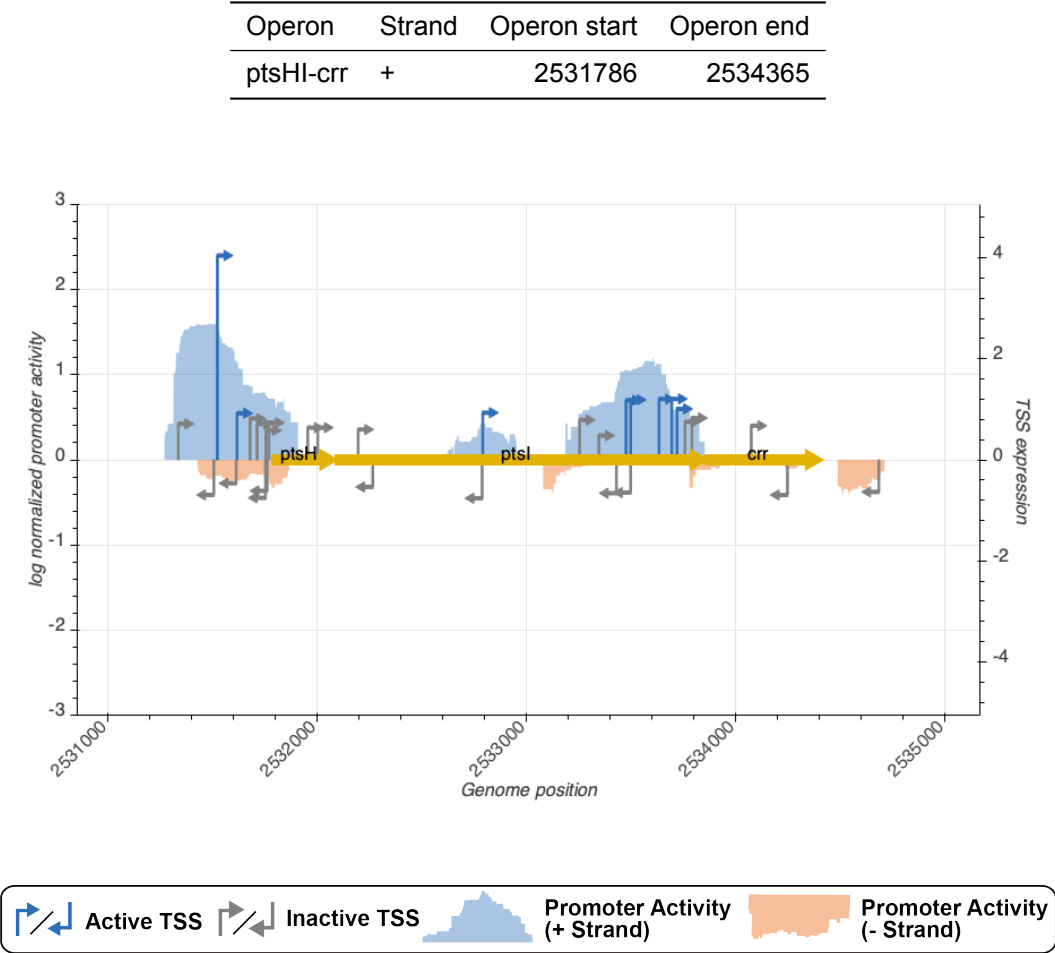
Operon	Strand	Operon start	Operon end
ptsHI-crr	+	2531786	2534365

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_9559_storz	2531758	-	0.6139024	inactive
TSS_9553_storz	2531610	-	0.4640673	inactive
TSS_9549_storz_regulondb	2531333	+	0.7111711	inactive
TSS_9556_regulondb	2531710	+	0.7114681	inactive
TSS_9558_storz	2531752	+	0.5830922	inactive
TSS_9552_regulondb	2531520	+	4.0430187	active
TSS_9560_regulondb	2531766	+	0.7348253	inactive
TSS_9554_regulondb	2531614	+	0.9223981	active
TSS_9555_regulondb	2531676	+	0.8181293	inactive
TSS_9557_storz	2531750	-	0.7534344	inactive
TSS_9551_storz	2531503	-	0.6952474	inactive

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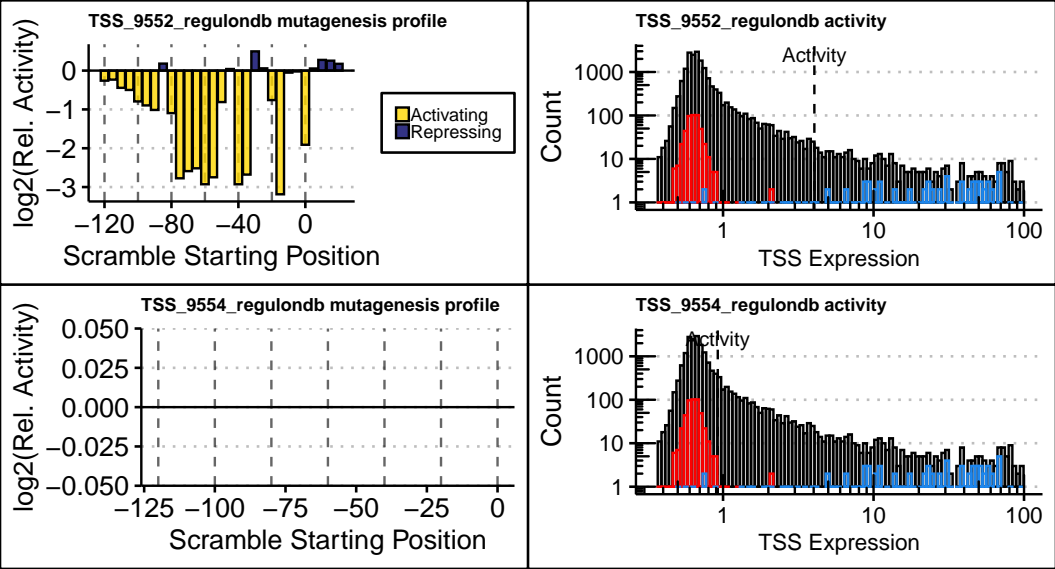
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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