

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
tsr	+	4589680	4591335

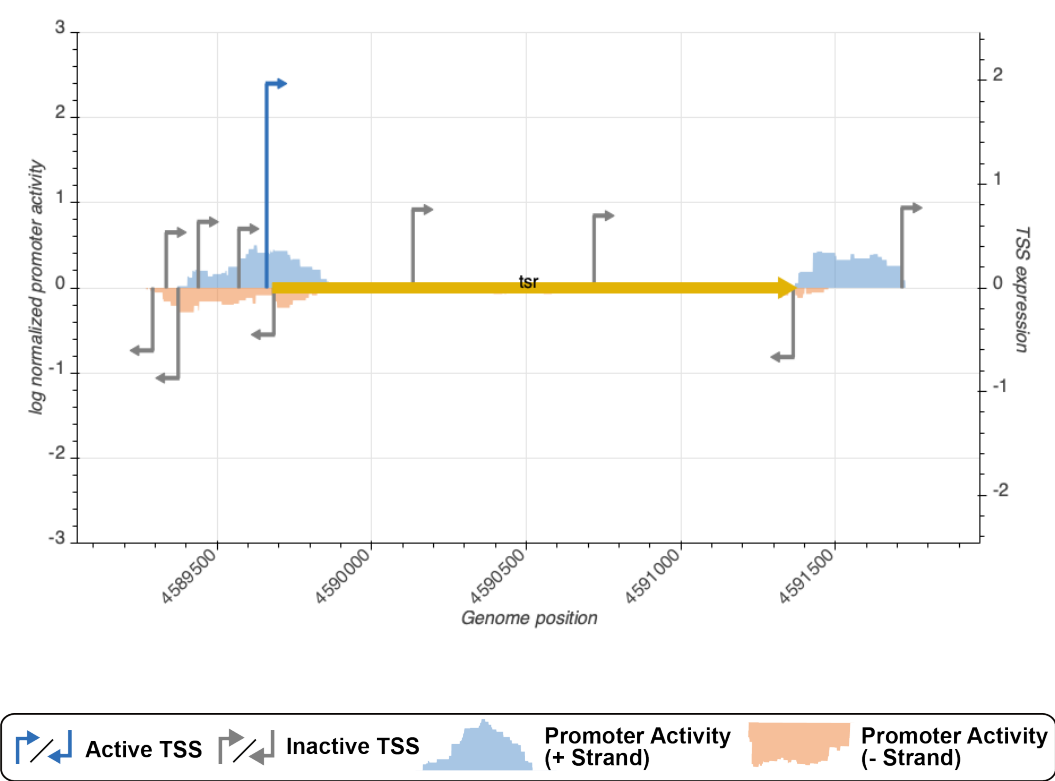


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_17937_storz	4589331	+	0.5343607	inactive
TSS_17938_regulondb	4589370	-	0.8698869	inactive
TSS_17939_regulondb	4589435	+	0.6357453	inactive
TSS_17940_storz	4589566	+	0.5689010	inactive
TSS_17941_regulondb	4589656	+	1.9694769	active
TSS_17936_storz	4589287	-	0.6042151	inactive
TSS_17942_storz	4589679	-	0.4512528	inactive

TSS Scanning Mutagenesis

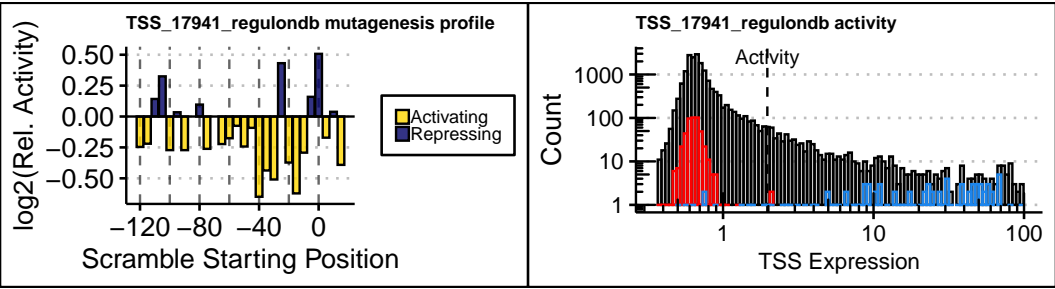


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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