

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ycgR	-	1243750	1243016

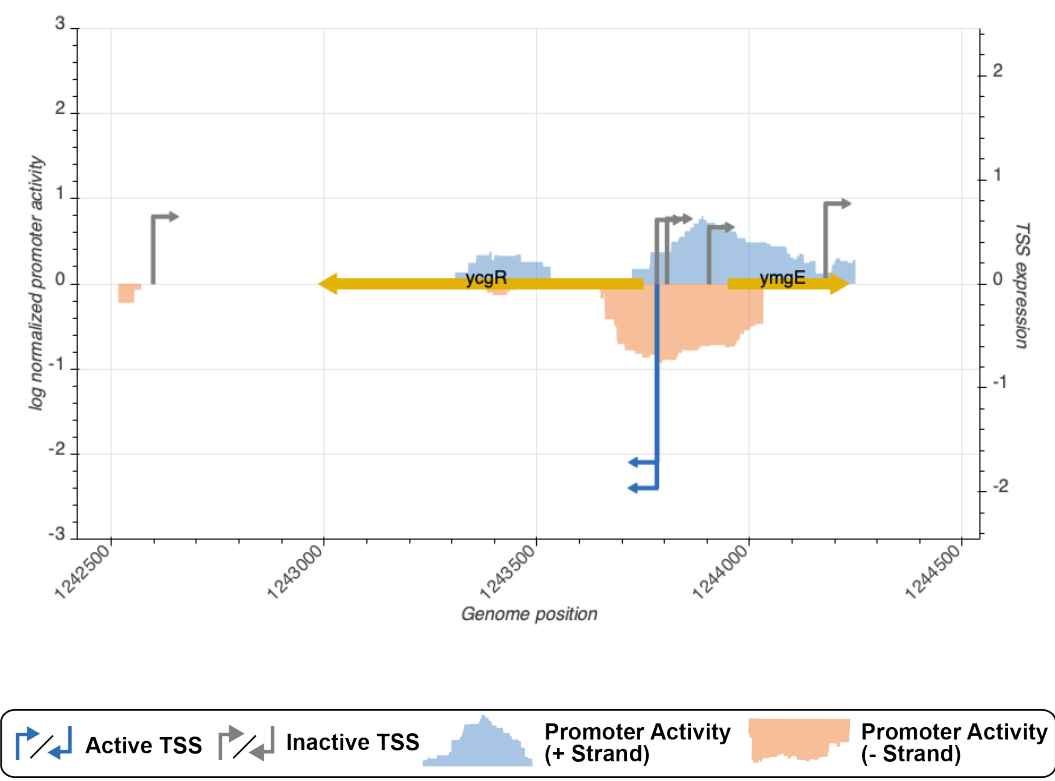


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_4817_storz	1243901	+	0.5432052	inactive
TSS_4815_regulondb	1243779	-	1.7142904	active
TSS_4818_storz	1244175	+	0.7704274	inactive
TSS_4814_regulondb	1243778	+	0.6139024	inactive
TSS_4816_regulondb	1243802	+	0.6249061	inactive
TSS_4813_storz	1243778	-	1.9616750	active

TSS Scanning Mutagenesis

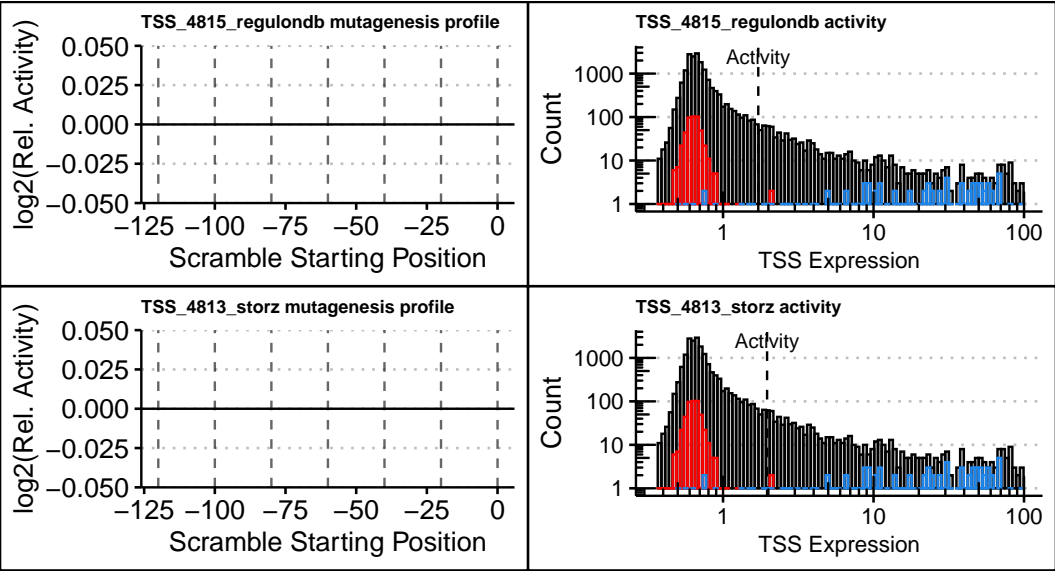


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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