

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yefM-yoeB	-	2087737	2087235

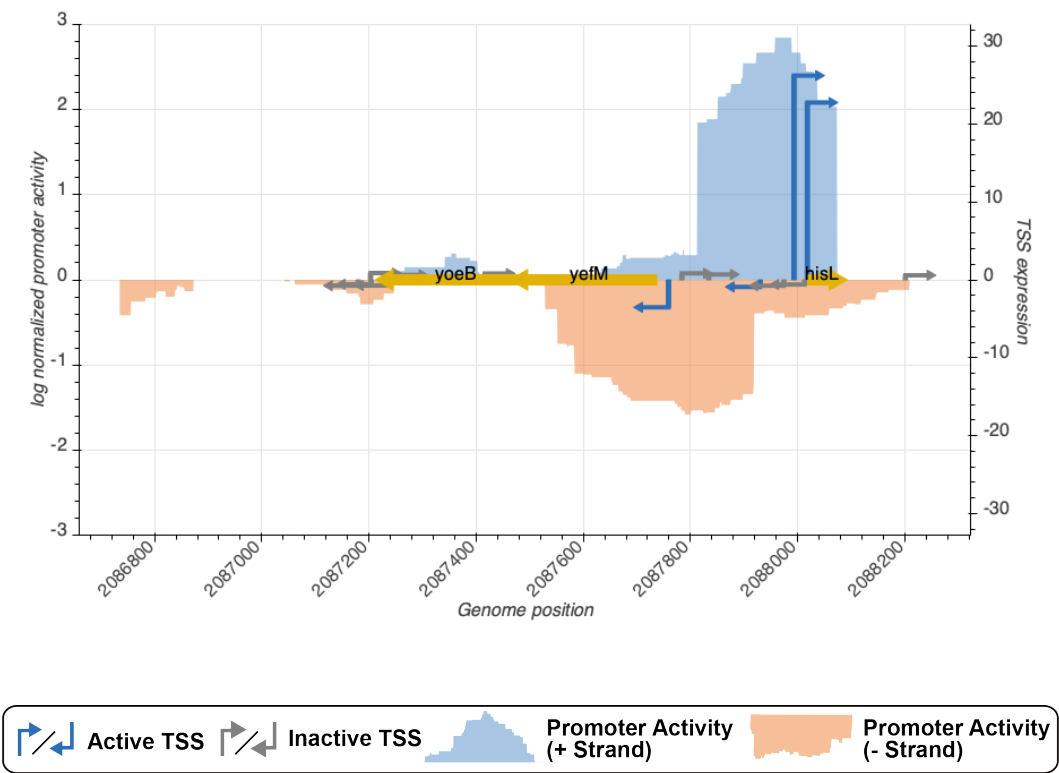


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_8025_storz	2087970	-	0.7566357	inactive
TSS_8021_storz_regulondb	2087755	-	3.5295178	active
TSS_8023_storz	2087830	+	0.6887272	inactive
TSS_8029_regulondb	2088197	+	0.5861024	inactive
TSS_8022_storz	2087780	+	0.8291135	inactive
TSS_8027_storz	2088009	-	0.5980369	inactive
TSS_8024_regulondb	2087926	-	0.9079999	active
TSS_8028_regulondb	2088014	+	22.7532297	active
TSS_8026_storz_regulondb	2087989	+	26.2169528	active

TSS Scanning Mutagenesis

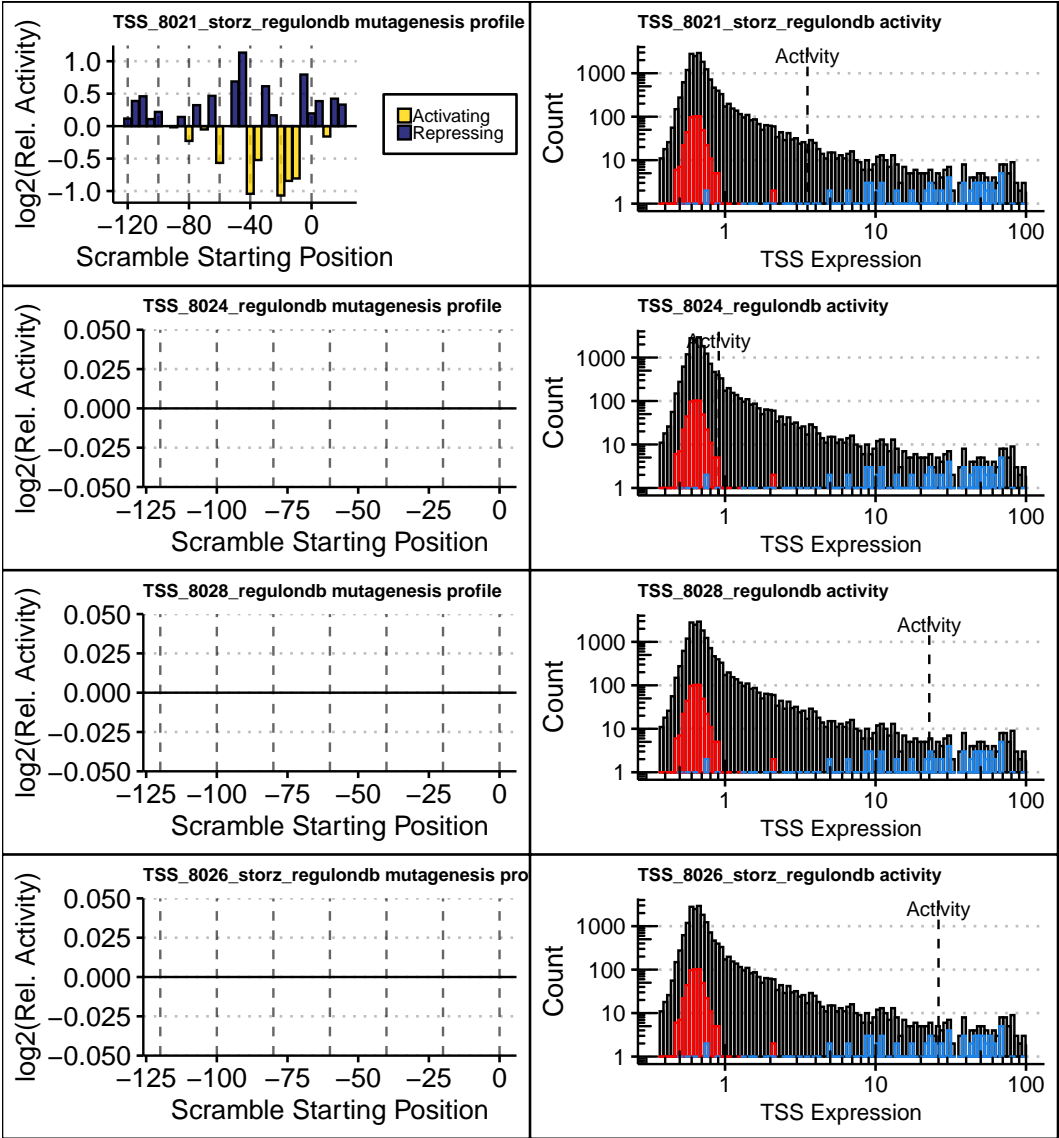


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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