

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
djlA	+	57364	58179

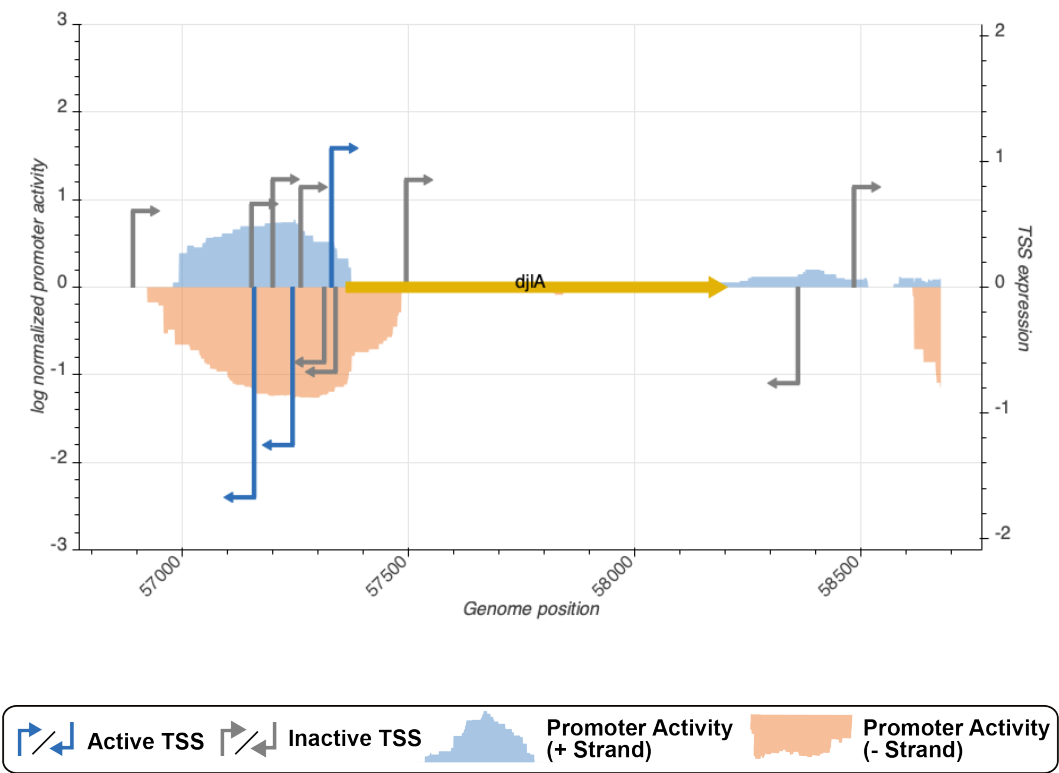


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_249_storz	57311	-	0.5962989	inactive
TSS_248_storz	57259	+	0.7957535	inactive
TSS_250_wanner	57327	+	1.1054847	active
TSS_245_storz_regulondb	57156	-	1.6714832	active
TSS_251_regulondb	57336	-	0.6733660	inactive
TSS_243_storz	56888	+	0.6061999	inactive
TSS_247_storz_regulondb	57241	-	1.2556048	active
TSS_244_storz	57150	+	0.6622984	inactive
TSS_246_storz	57197	+	0.8578889	inactive

TSS Scanning Mutagenesis

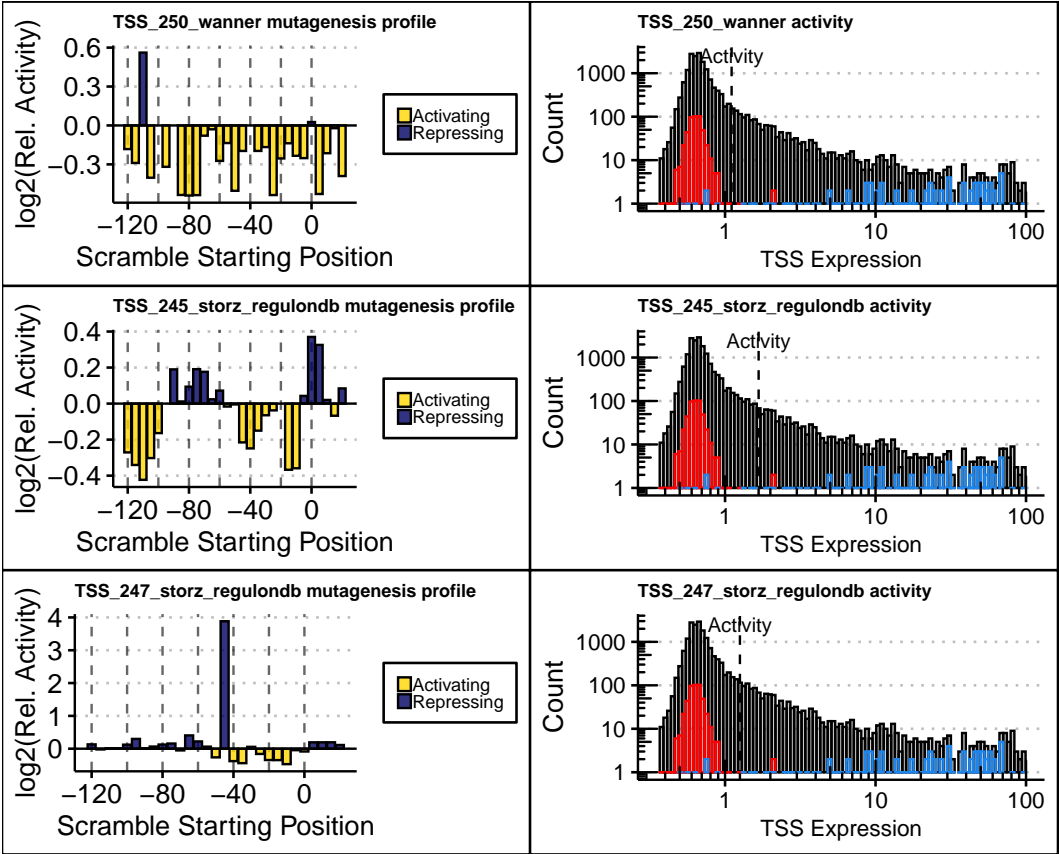


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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