

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
dcuB-fumB	-	4346767	4343703

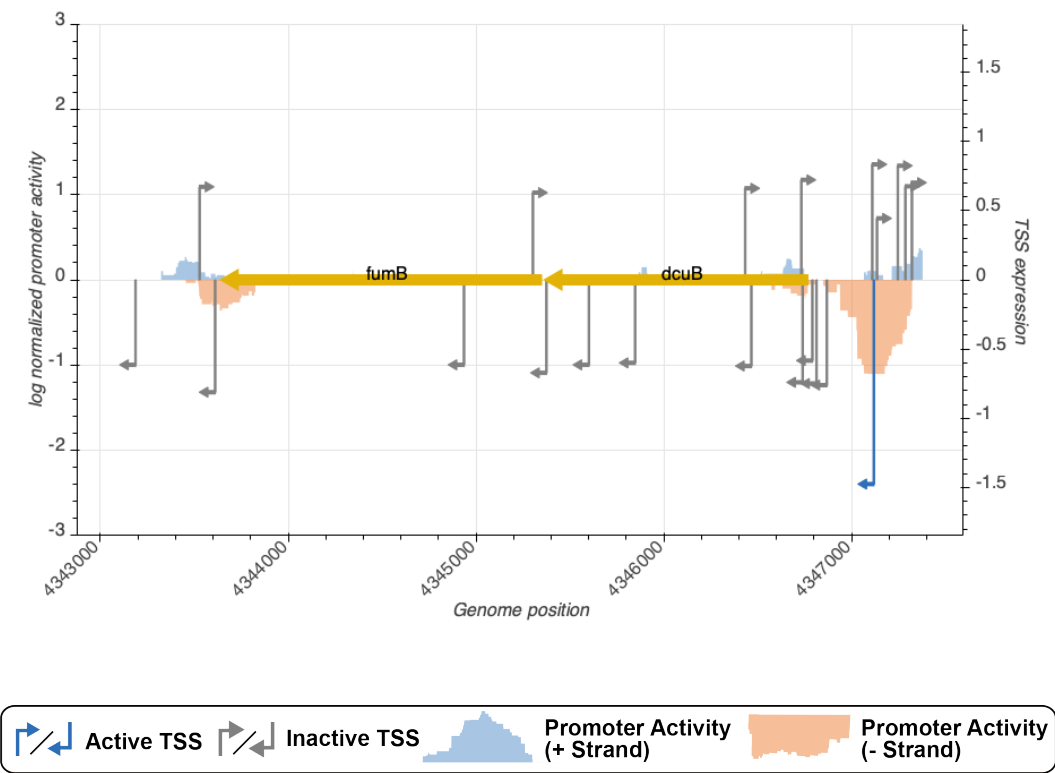


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_16950_regulondb	4346864	-	0.7603757	inactive
TSS_16948_regulondb	4346787	-	0.5830922	inactive
TSS_16949_regulondb	4346809	-	0.7487867	inactive
TSS_16952_storz_regulondb	4347114	-	1.4752823	active
TSS_16954_storz	4347242	+	0.8242517	inactive
TSS_16951_storz	4347106	+	0.8339857	inactive
TSS_16953_storz	4347131	+	0.4440802	inactive

TSS Scanning Mutagenesis

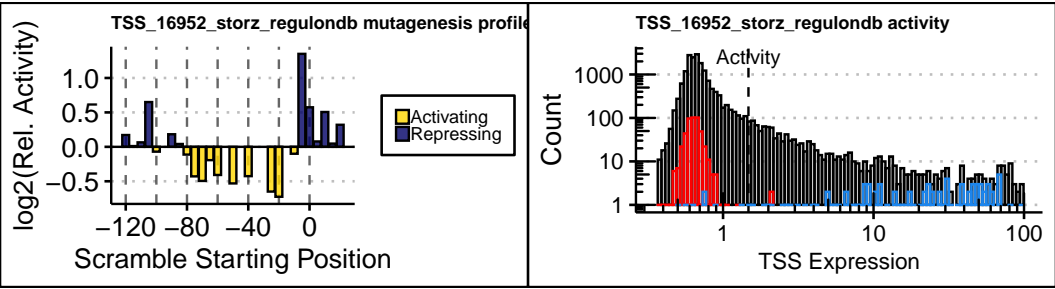


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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