

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yijO	-	4146340	4145489

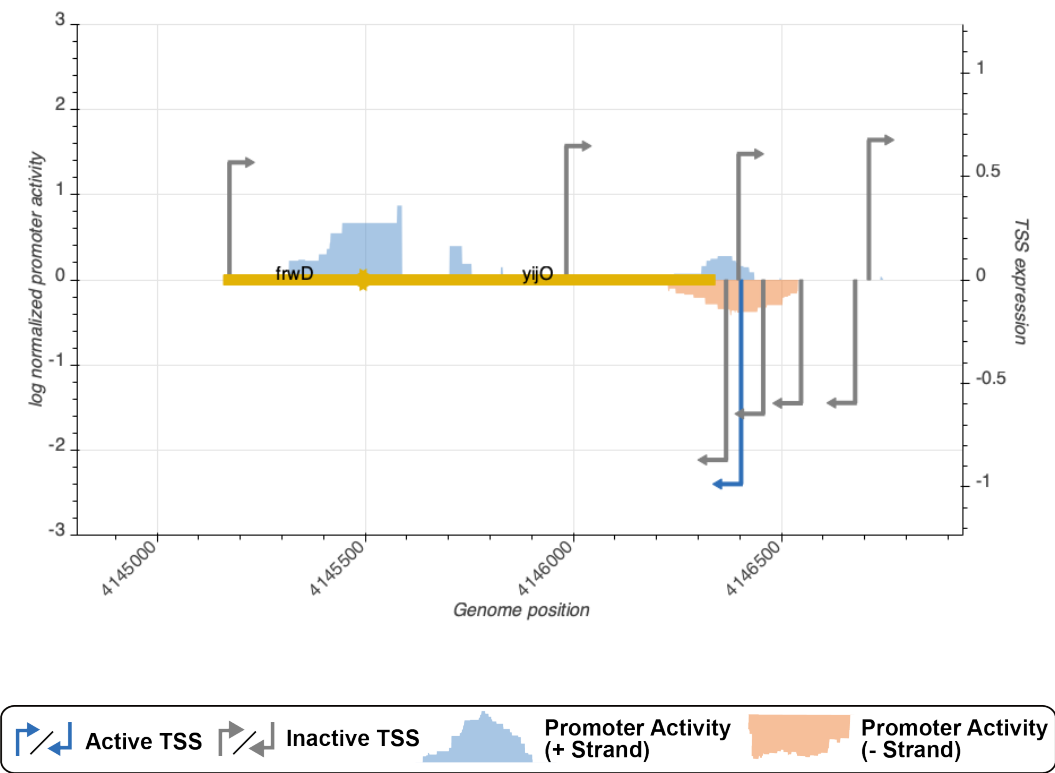


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_16166_storz	4146393	+	0.6078586	inactive
TSS_16171_storz	4146706	+	0.6755228	inactive
TSS_16168_regulondb	4146452	-	0.6471634	inactive
TSS_16170_storz	4146673	-	0.5946460	inactive
TSS_16169_storz	4146543	-	0.5961556	inactive
TSS_16165_storz	4146363	-	0.8698869	inactive
TSS_16167_storz	4146399	-	0.9863822	active

TSS Scanning Mutagenesis

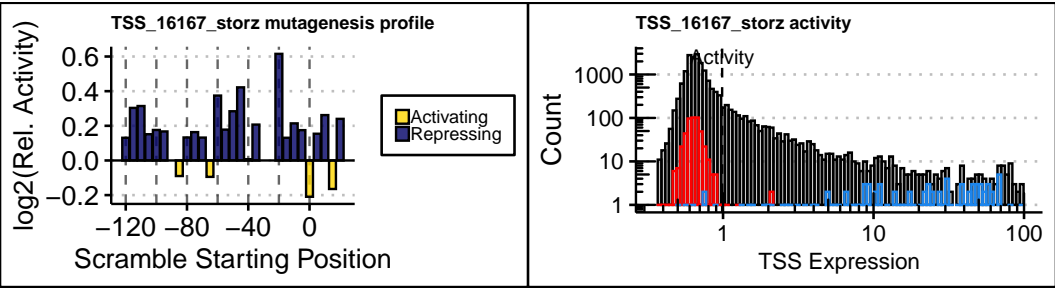


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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