

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
fabR-yijD	+	4159090	4160153

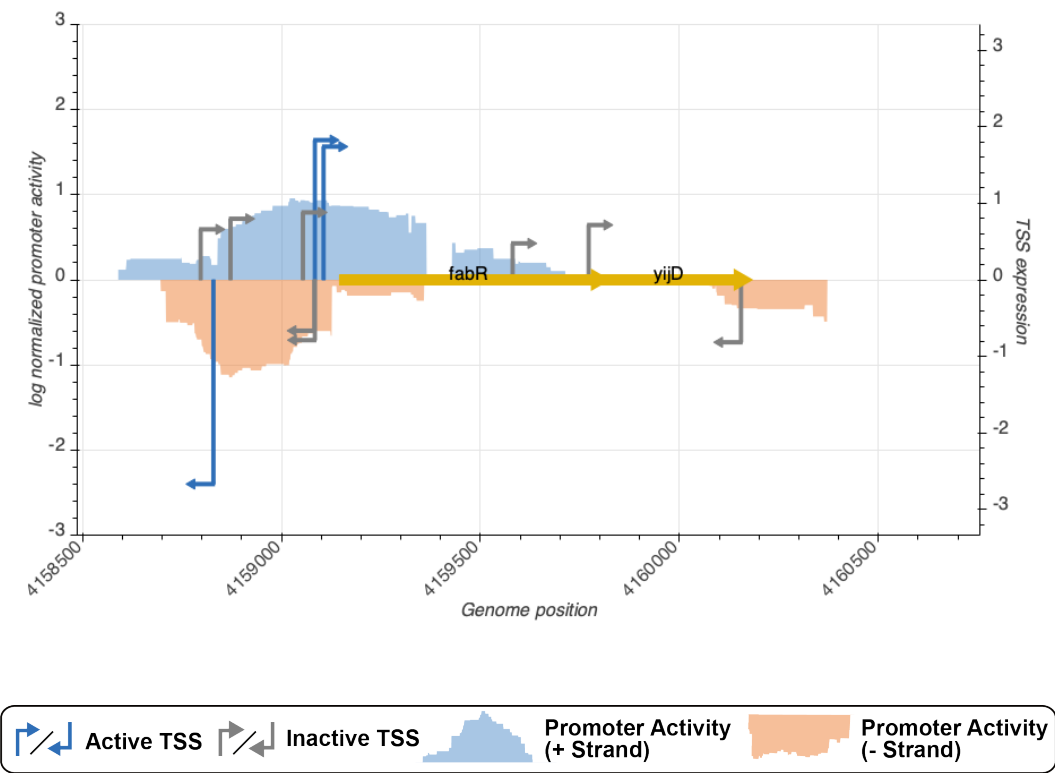


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_16226_storz	4158793	+	0.6592115	inactive
TSS_16229_storz	4159050	+	0.8800802	inactive
TSS_16231_storz	4159080	+	1.8250272	active
TSS_16227_regulondb	4158825	-	2.6674298	active
TSS_16232_wanner	4159080	-	0.7875289	inactive
TSS_16230_storz	4159079	-	0.6645269	inactive
TSS_16228_storz	4158868	+	0.7976127	inactive

TSS Scanning Mutagenesis

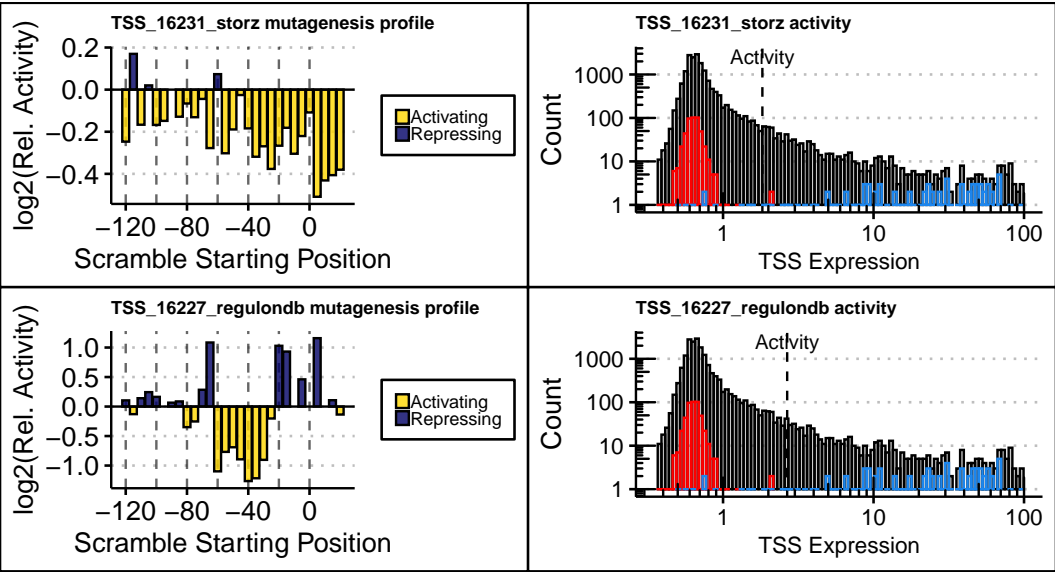


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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