

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ybjD	+	915696	917354

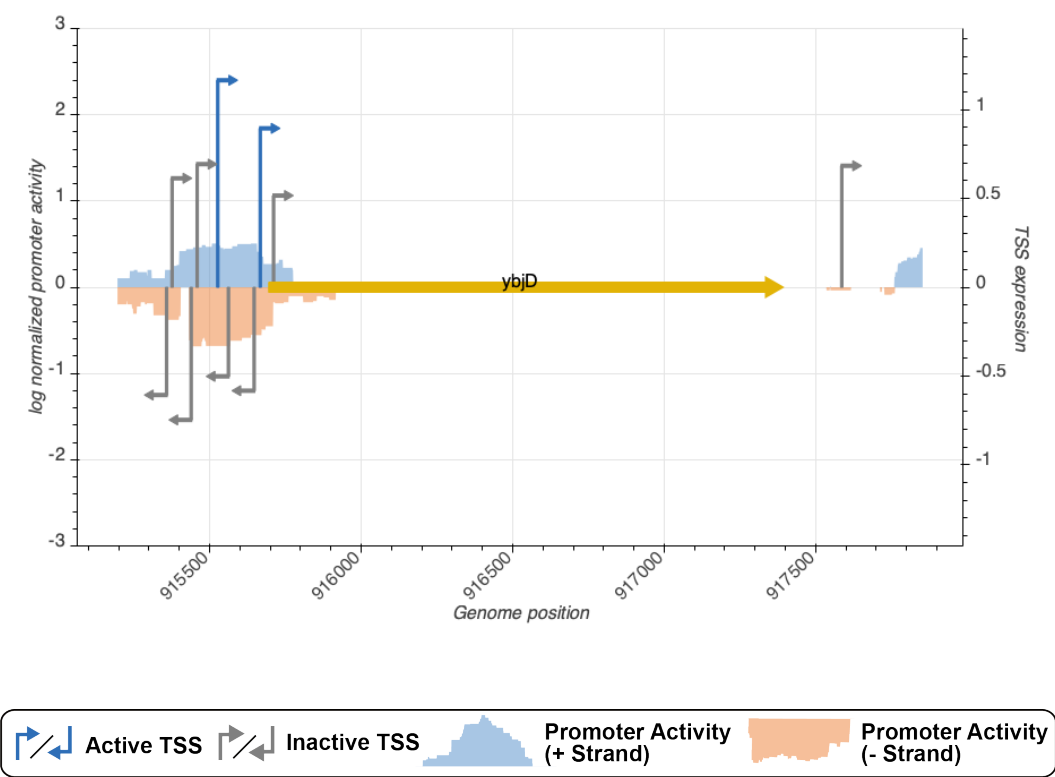


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_3495_wanner	915455	+	0.6935111	inactive
TSS_3492_storz	915354	-	0.6074358	inactive
TSS_3498_storz	915643	-	0.5830922	inactive
TSS_3496_storz	915523	+	1.1661844	active
TSS_3499_storz	915663	+	0.8953703	active
TSS_3493_storz	915372	+	0.6139024	inactive
TSS_3497_storz	915558	-	0.5021014	inactive
TSS_3494_regulondb	915435	-	0.7475668	inactive

TSS Scanning Mutagenesis

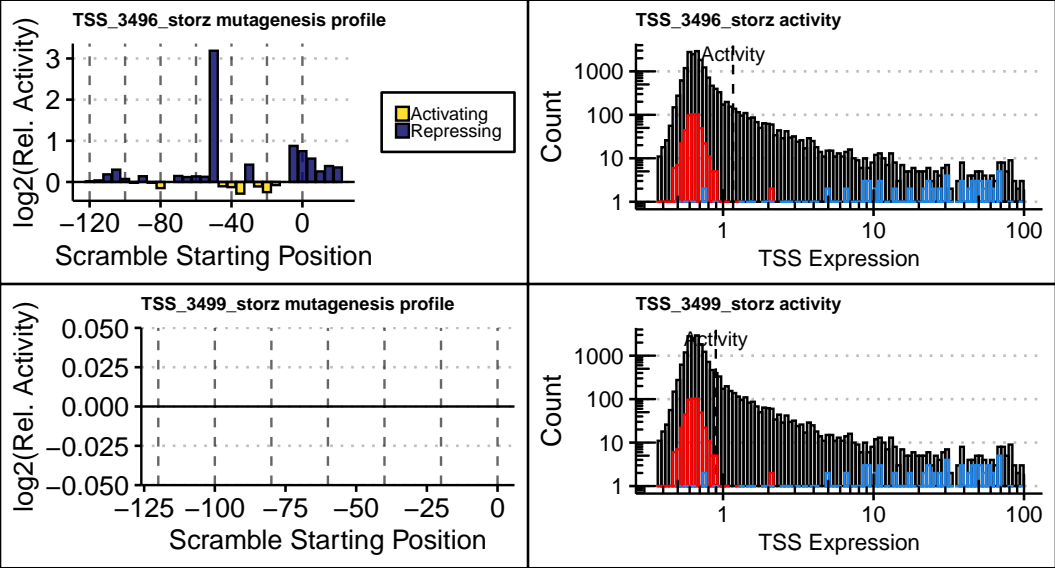


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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