

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yobB-exoX	+	1923464	1924806

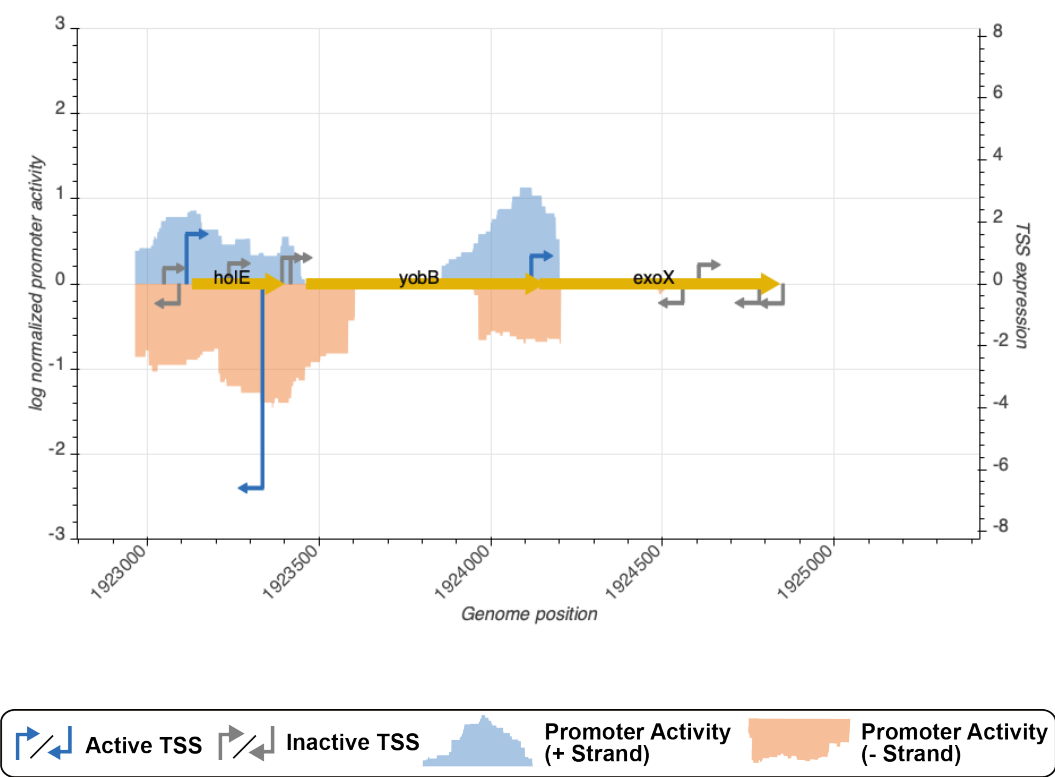


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_7366_regulondb	1923233	+	0.6588203	inactive
TSS_7368_regulondb	1923388	+	0.8418098	inactive
TSS_7369_storz_regulondb	1923413	+	0.8440583	inactive
TSS_7367_storz_regulondb	1923331	-	6.5985623	active
TSS_7364_wanner	1923088	-	0.6342891	inactive
TSS_7365_storz_regulondb	1923110	+	1.6101702	active
TSS_7363_regulondb	1923044	+	0.5038659	inactive

TSS Scanning Mutagenesis

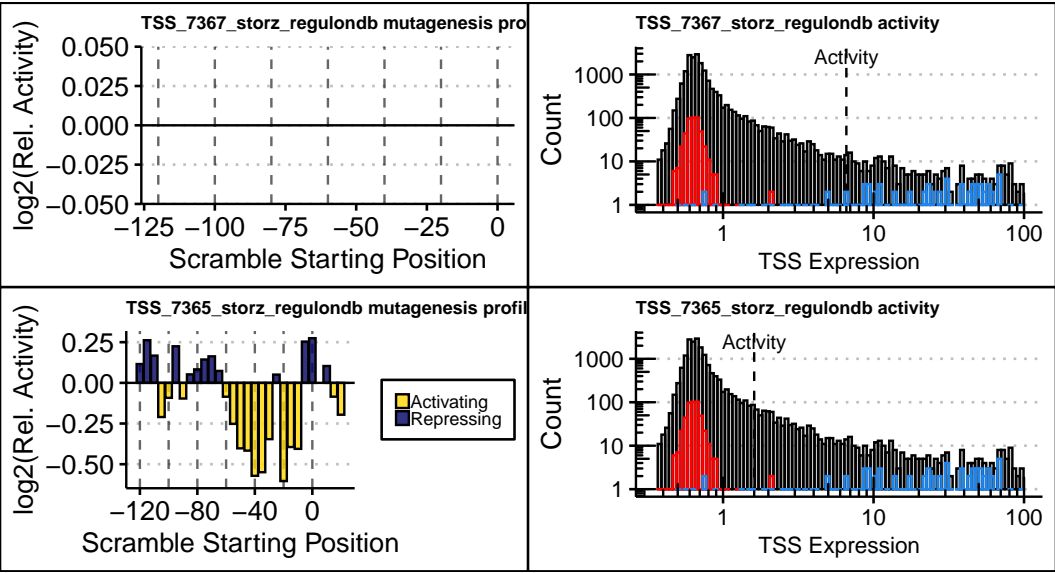


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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