

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ispB	+	3331732	3332703

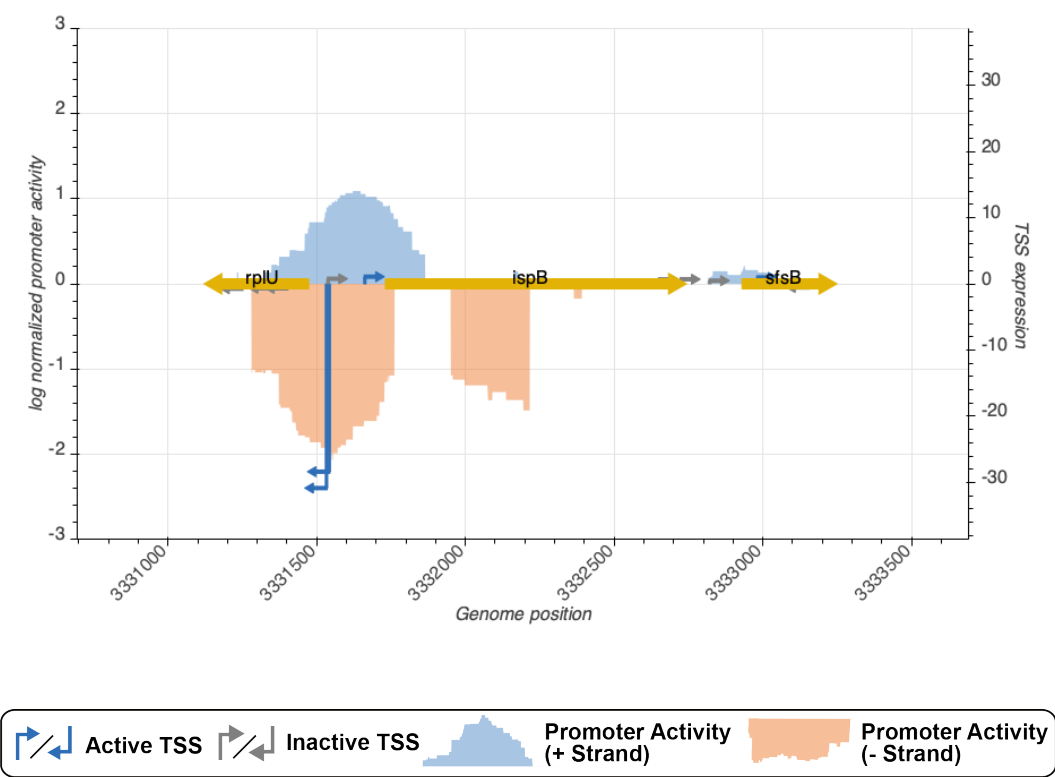


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_12681_regulondb	3331529	-	30.8560770	active
TSS_12680_regulondb	3331397	-	0.6861138	inactive
TSS_12682_storz	3331534	+	0.7642519	inactive
TSS_12684_storz	3331658	+	1.0775171	active
TSS_12679_regulondb	3331342	-	0.6722217	inactive
TSS_12683_storz_wanner	3331538	-	28.3797497	active
TSS_12678_regulondb	3331246	-	0.7460959	inactive

TSS Scanning Mutagenesis

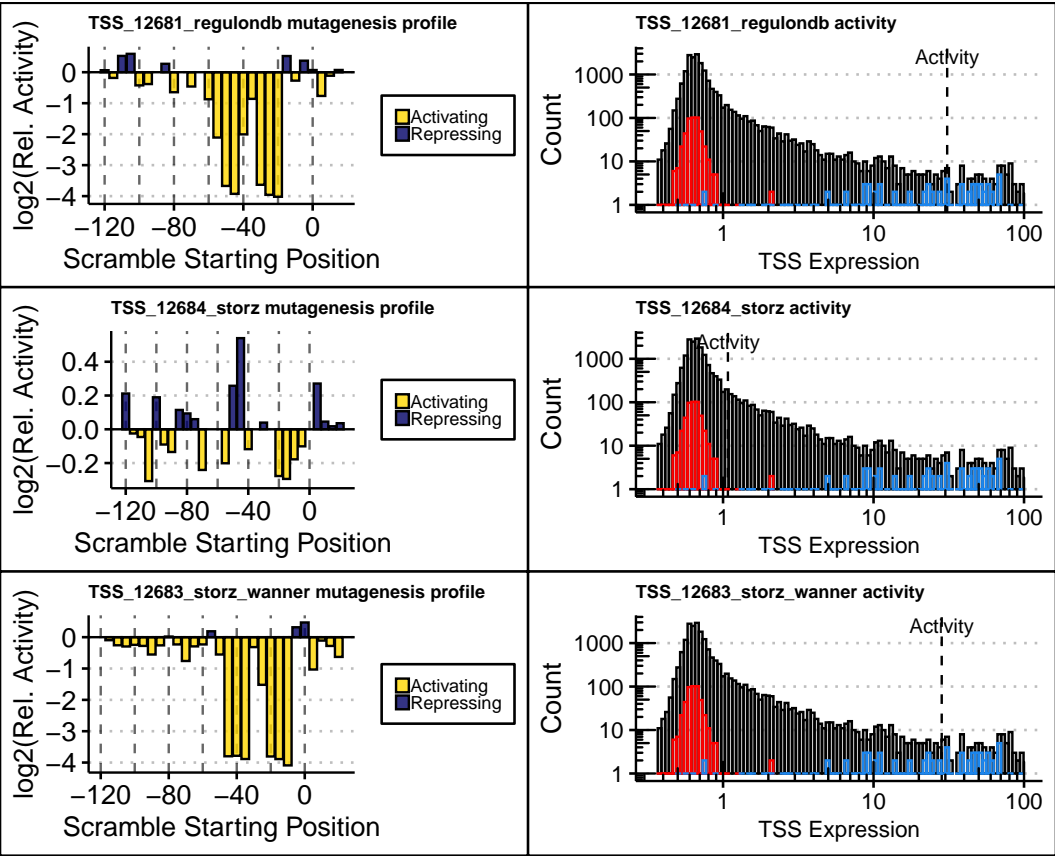


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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