

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
sokB	+	1490143	1490198

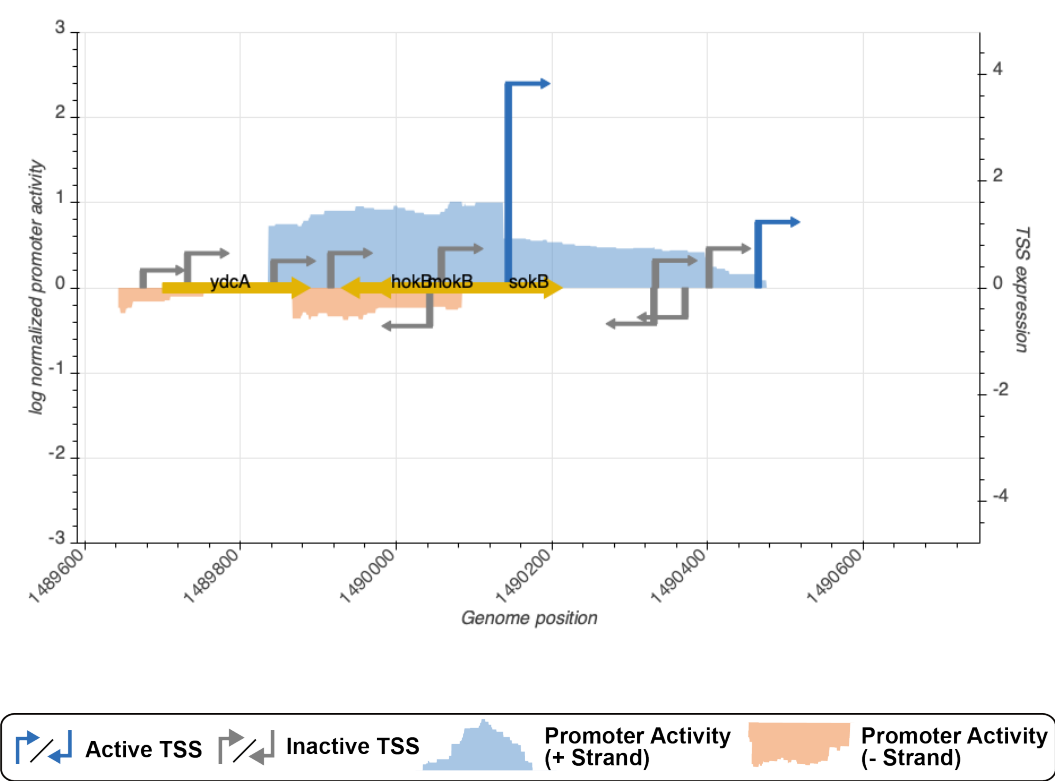


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_5781_storz	1489728	+	0.6472356	inactive
TSS_5785_storz	1490054	+	0.7337487	inactive
TSS_5784_storz	1490039	-	0.7158358	inactive
TSS_5782_storz	1489839	+	0.5022838	inactive
TSS_5786_regulondb	1490140	+	3.8308939	active
TSS_5783_regulondb	1489912	+	0.6513581	inactive
TSS_5780_regulondb	1489671	+	0.3287941	inactive

TSS Scanning Mutagenesis

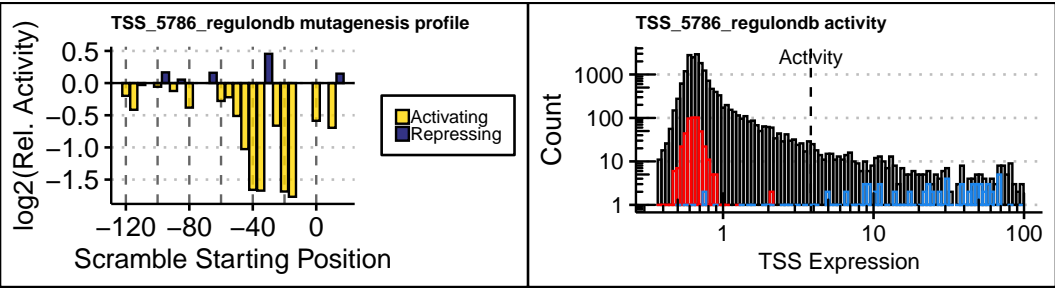


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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