

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
speAB	-	3083933	3080899

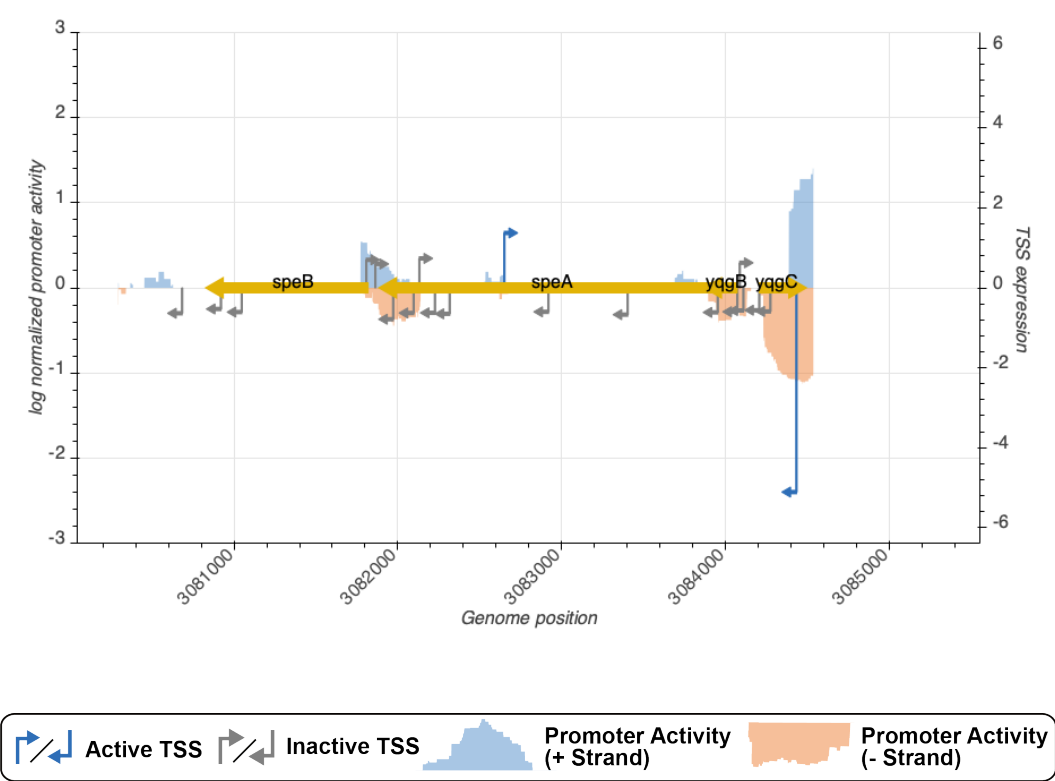


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_11657_storz_wanner	3084431	-	5.1089561	active
TSS_11651_storz	3083950	-	0.6139024	inactive
TSS_11655_regulondb	3084204	-	0.5599845	inactive
TSS_11653_storz	3084085	+	0.6261344	inactive
TSS_11654_storz	3084107	-	0.5669142	inactive
TSS_11652_regulondb	3084070	-	0.5984973	inactive
TSS_11656_regulondb	3084272	-	0.5909586	inactive

TSS Scanning Mutagenesis

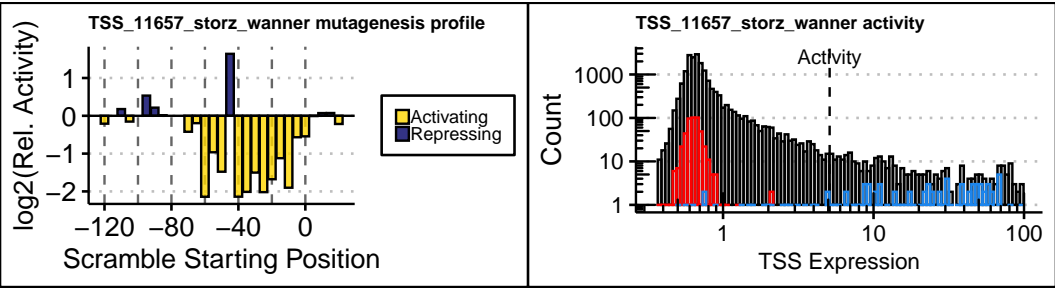


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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