Operon Promoter Landscape

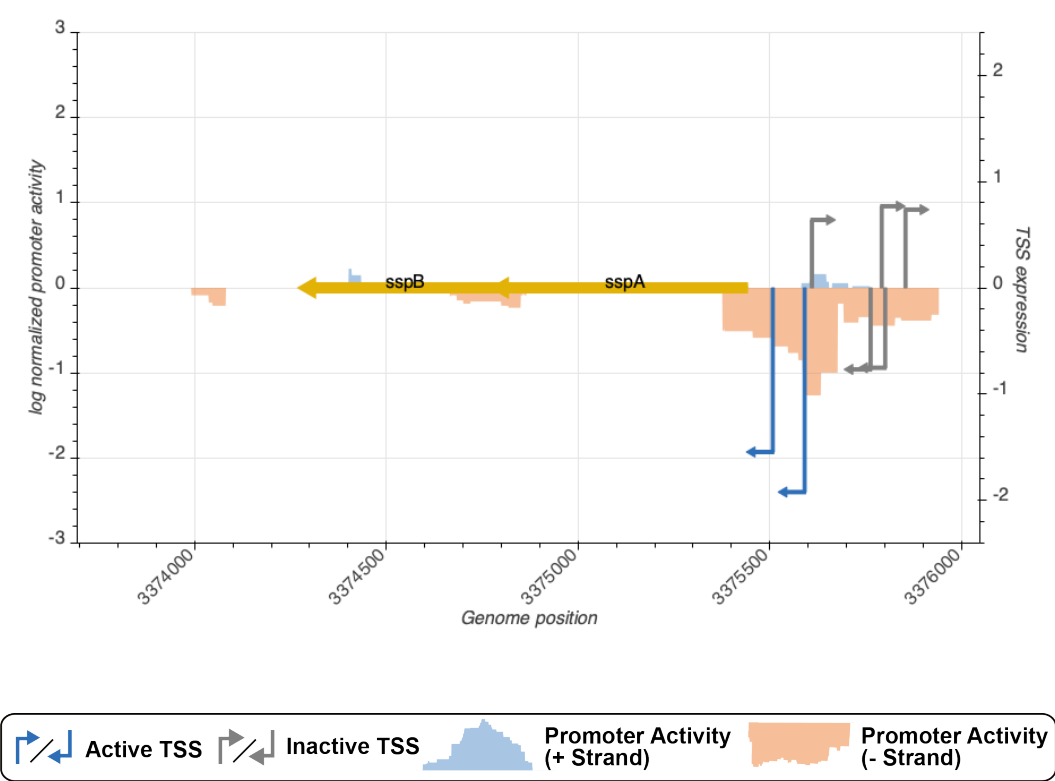| Operon	Strand	Operon start	Operon end
sspAB	-	3375442	3374301

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_12899_storz	3375788	+	0.7680428	inactive
TSS_12897_storz	3375606	+	0.6391195	inactive
TSS_12901_storz	3375850	+	0.7358152	inactive
TSS_12900_storz	3375797	-	0.7526635	inactive
TSS_12898_storz	3375759	-	0.7679535	inactive
TSS_12895_regulondb	3375504	-	1.5451355	active
TSS_12896_wanner	3375587	-	1.9223959	active

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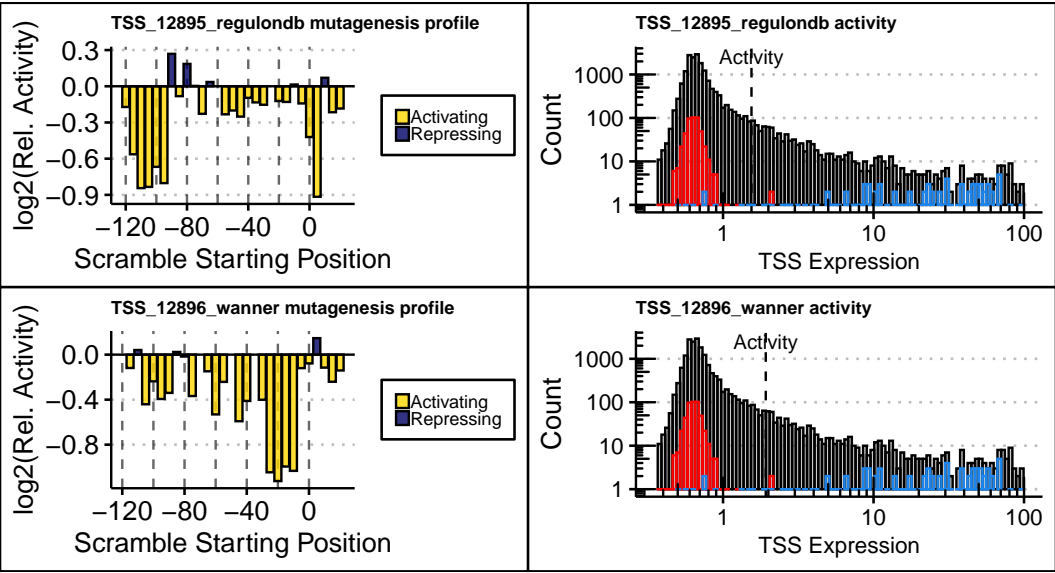
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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

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