Operon Promoter Landscape

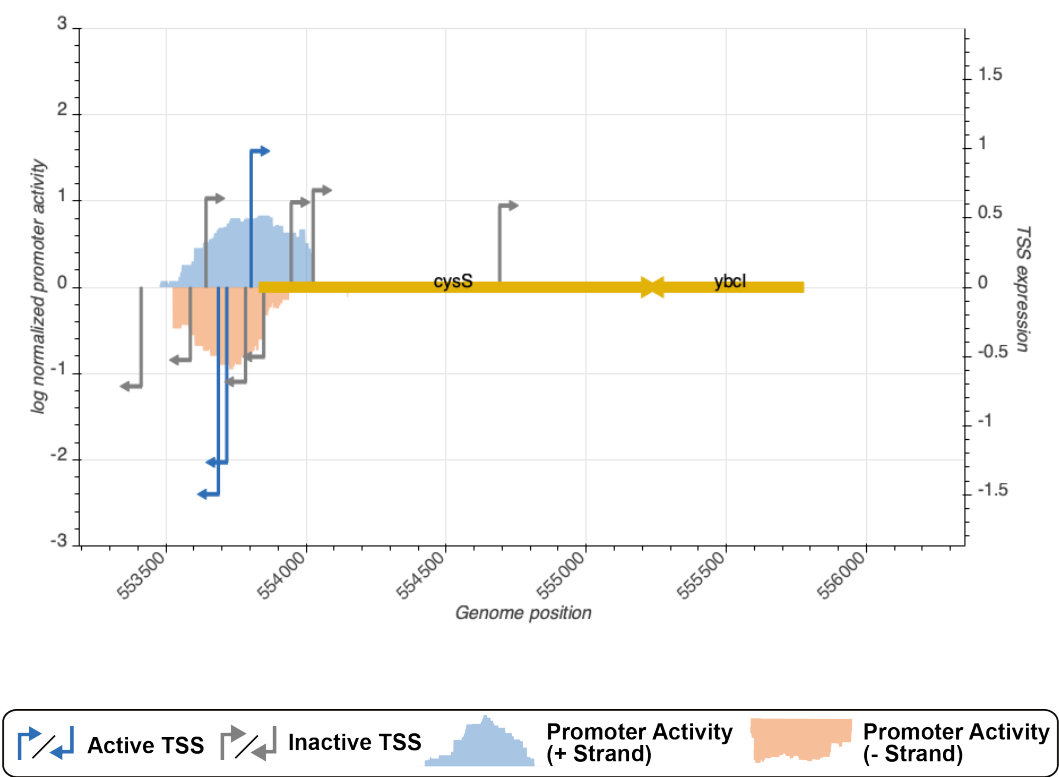| Operon	Strand	Operon start	Operon end
cysS	+	553834	555219

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_2120_storz	553639	+	0.6418270	inactive
TSS_2122_storz_regulondb	553713	-	1.2657421	active
TSS_2123_wanner	553780	-	0.6834017	inactive
TSS_2121_regulondb	553683	-	1.4960465	active
TSS_2124_storz_regulondb	553800	+	0.9844446	active
TSS_2118_storz	553407	-	0.7163261	inactive
TSS_2119_regulondb	553583	-	0.5262021	inactive

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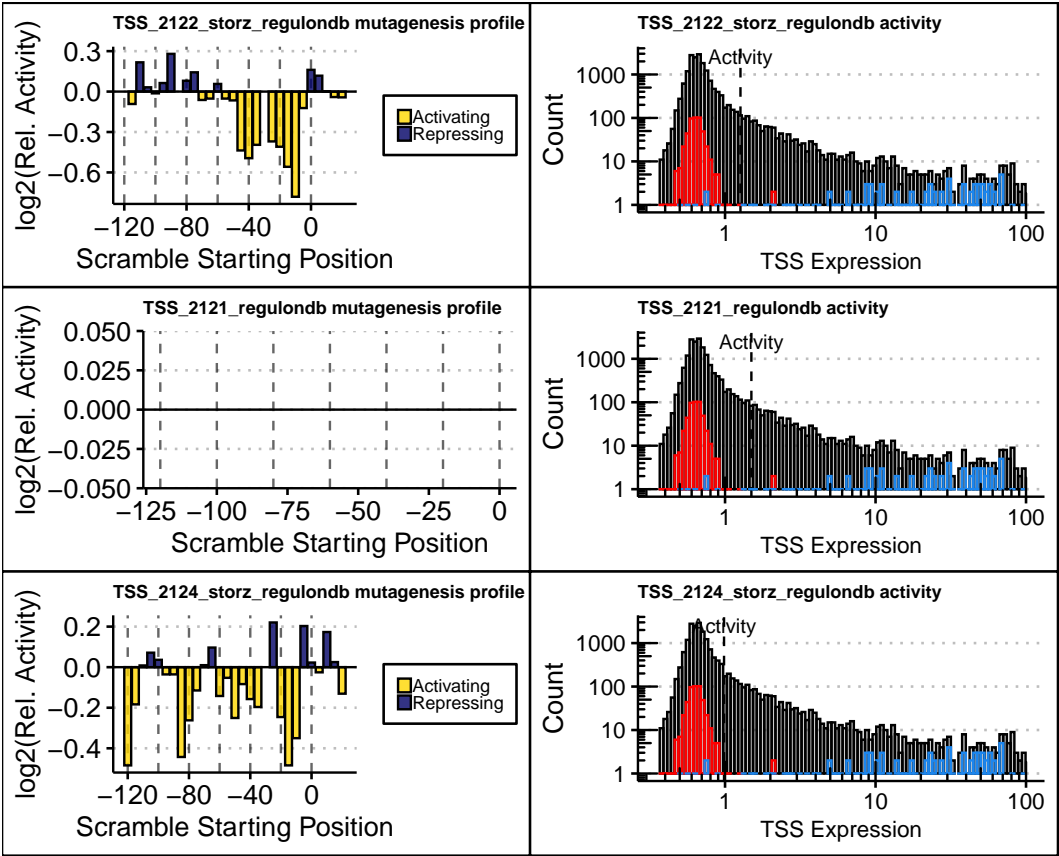
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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

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