Operon Promoter Landscape

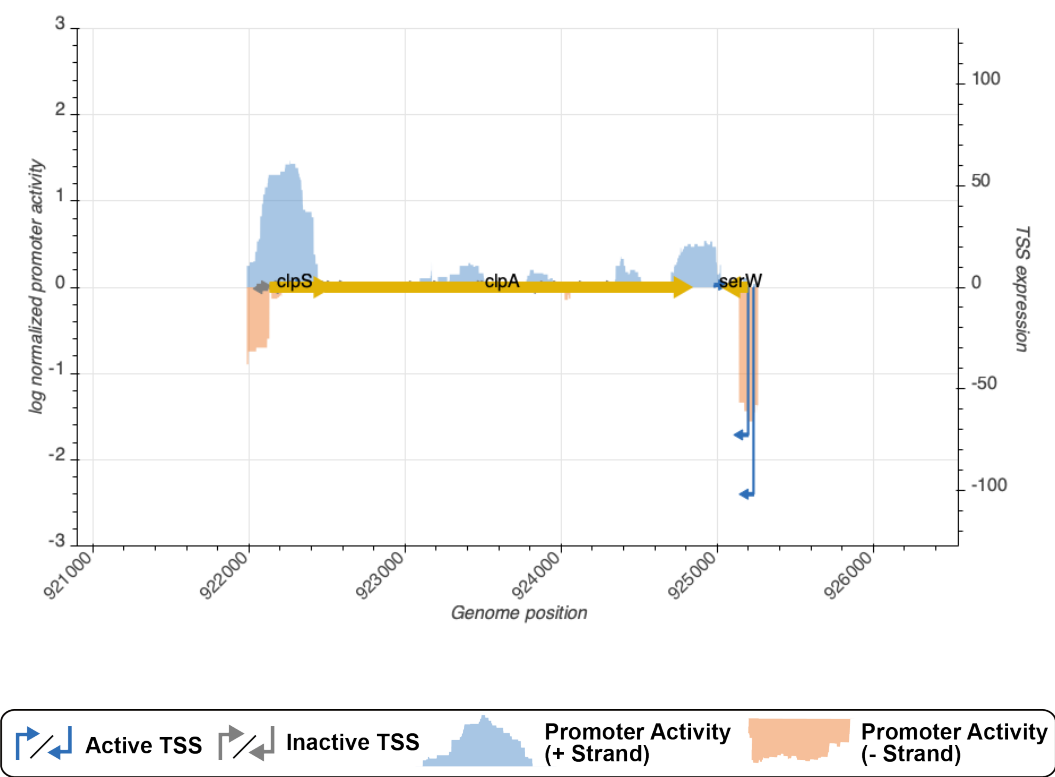| Operon	Strand	Operon start	Operon end
clpA	+	922487	924763

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_3526_storz	922271	+	1.3560922	active
TSS_3525_storz	922231	+	0.6798726	inactive
TSS_3527_regulondb	922433	+	0.6447126	inactive
TSS_3521_regulondb	922050	+	0.6472958	inactive
TSS_3522_storz	922115	-	0.7088335	inactive
TSS_3523_regulondb	922135	+	0.7358169	inactive
TSS_3524_storz	922219	-	0.6689206	inactive
TSS_3528_regulondb	922471	+	0.6812997	inactive

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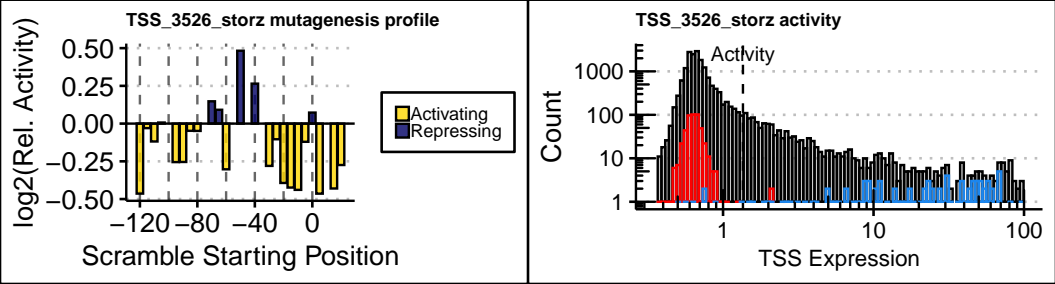
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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