

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
uspC	+	1977777	1978205

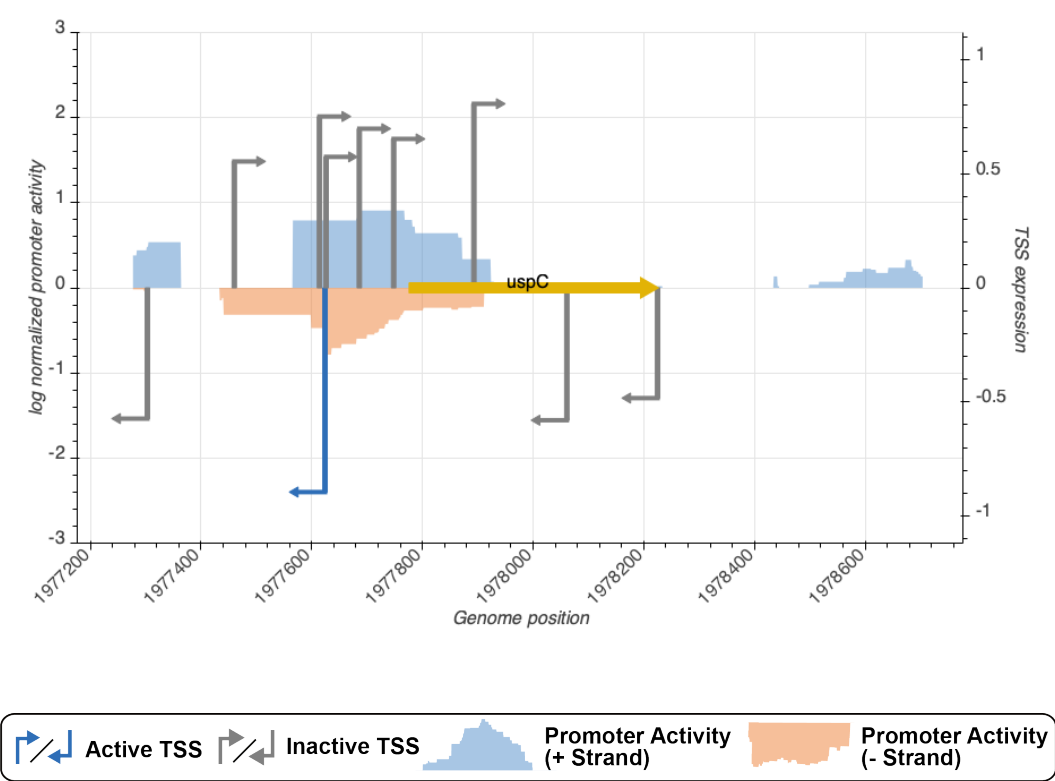


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_7583_storz	1977744	+	0.6521274	inactive
TSS_7576_storz	1977299	-	0.5728221	inactive
TSS_7577_storz	1977456	+	0.5535861	inactive
TSS_7580_regulondb	1977622	+	0.5735894	inactive
TSS_7582_regulondb	1977682	+	0.6970698	inactive
TSS_7578_regulondb	1977610	+	0.7504974	inactive
TSS_7579_storz	1977620	-	0.8946118	active

TSS Scanning Mutagenesis

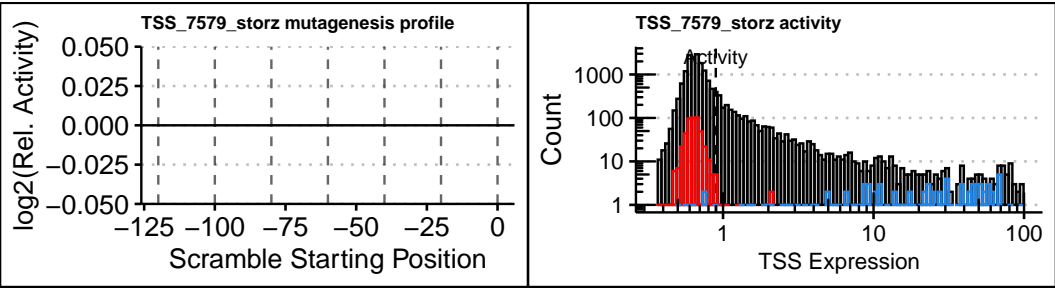


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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