

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ackA-pta	+	2411492	2414913

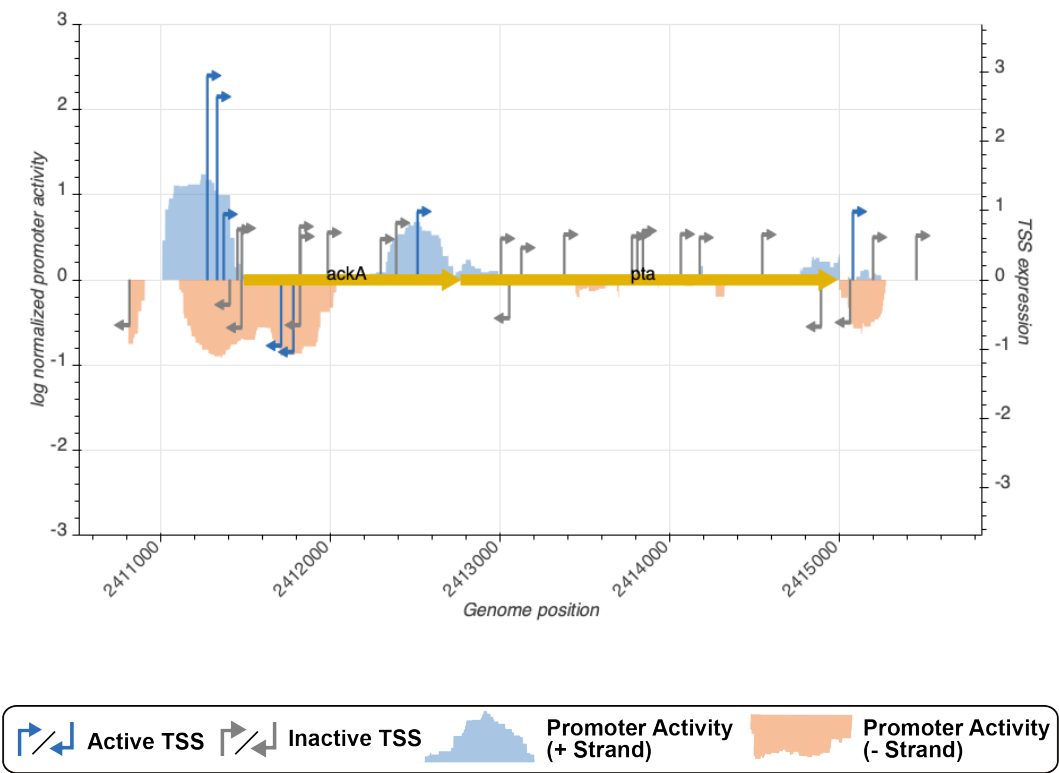


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_9105_regulondb	2411447	+	0.7265392	inactive
TSS_9101_storz	2411269	+	2.9423874	active
TSS_9102_regulondb	2411327	+	2.6385453	active
TSS_9104_storz	2411401	-	0.3579179	inactive
TSS_9107_regulondb	2411473	+	0.7434784	inactive
TSS_9106_storz	2411470	-	0.6896306	inactive
TSS_9103_storz_regulondb	2411366	+	0.9446381	active

TSS Scanning Mutagenesis

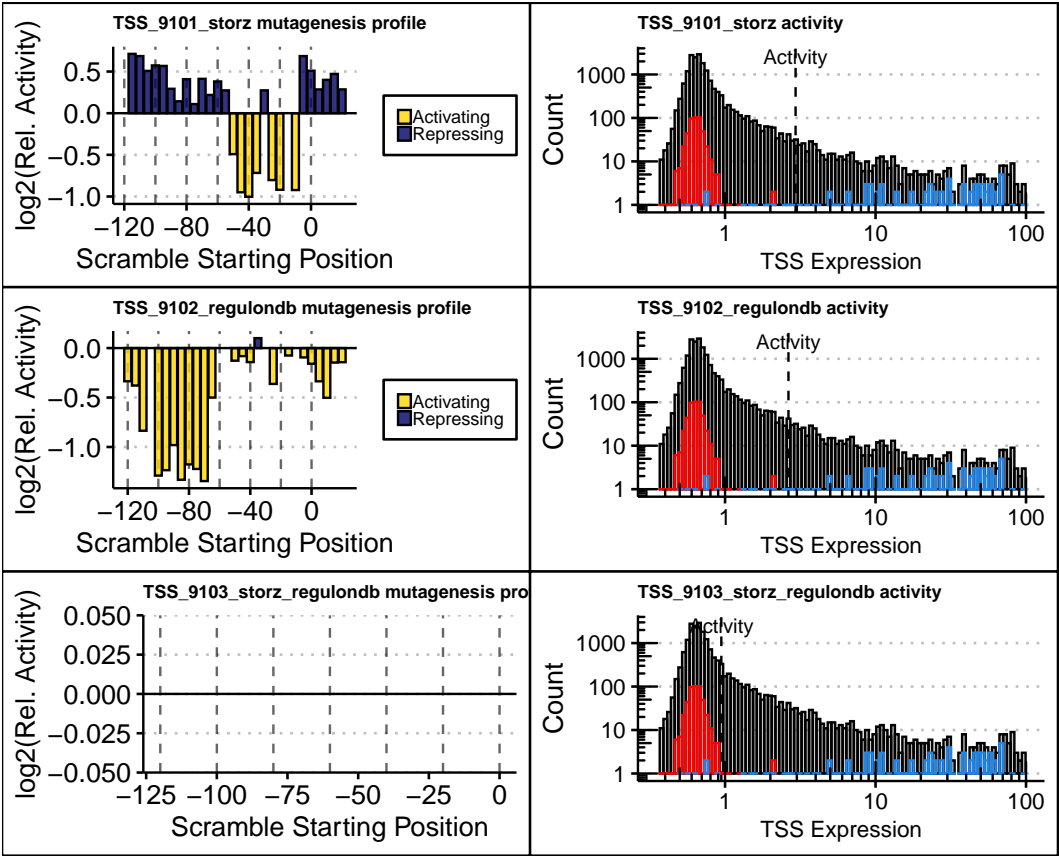


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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