

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
argG	+	3316659	3318002

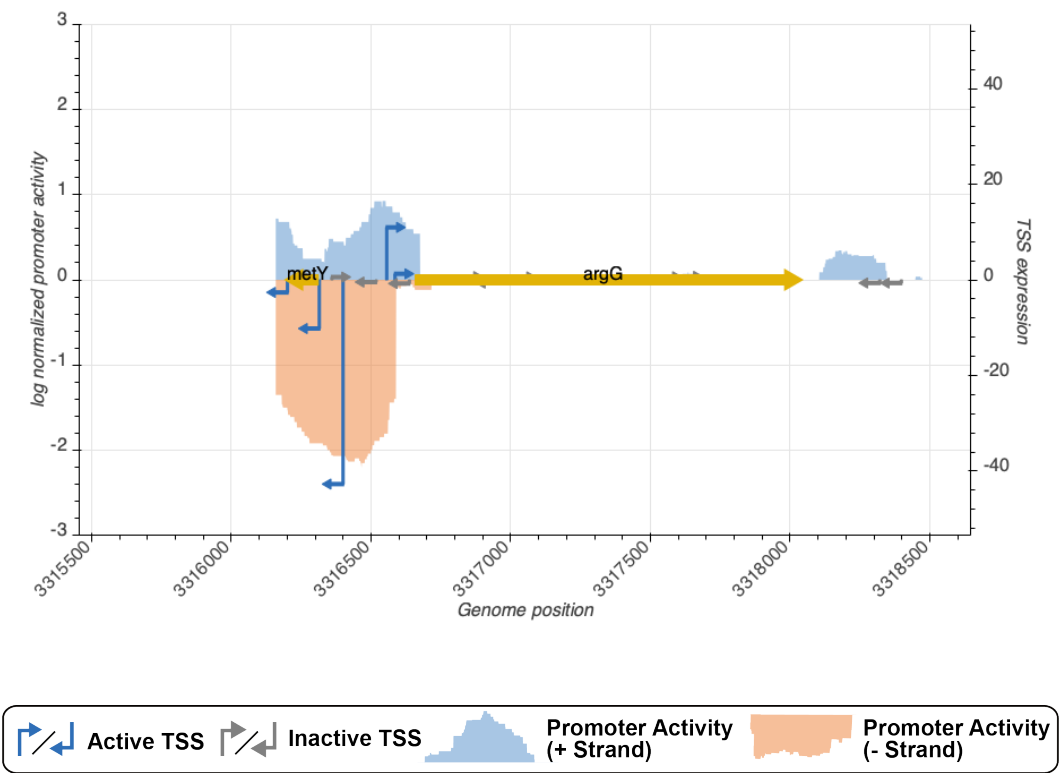


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_12599_storz	3316633	-	0.7791145	inactive
TSS_12592_storz	3316218	+	0.6472422	inactive
TSS_12593_storz	3316311	-	10.1888852	active
TSS_12595_wanner	3316396	-	42.7213746	active
TSS_12591_storz_wanner_regulondb	3316197	-	2.6293515	active
TSS_12594_storz	3316356	+	0.5802280	inactive
TSS_12598_storz	3316582	+	1.2560855	active
TSS_12596_storz	3316514	-	0.4674785	inactive
TSS_12597_storz	3316552	+	10.9689491	active

TSS Scanning Mutagenesis

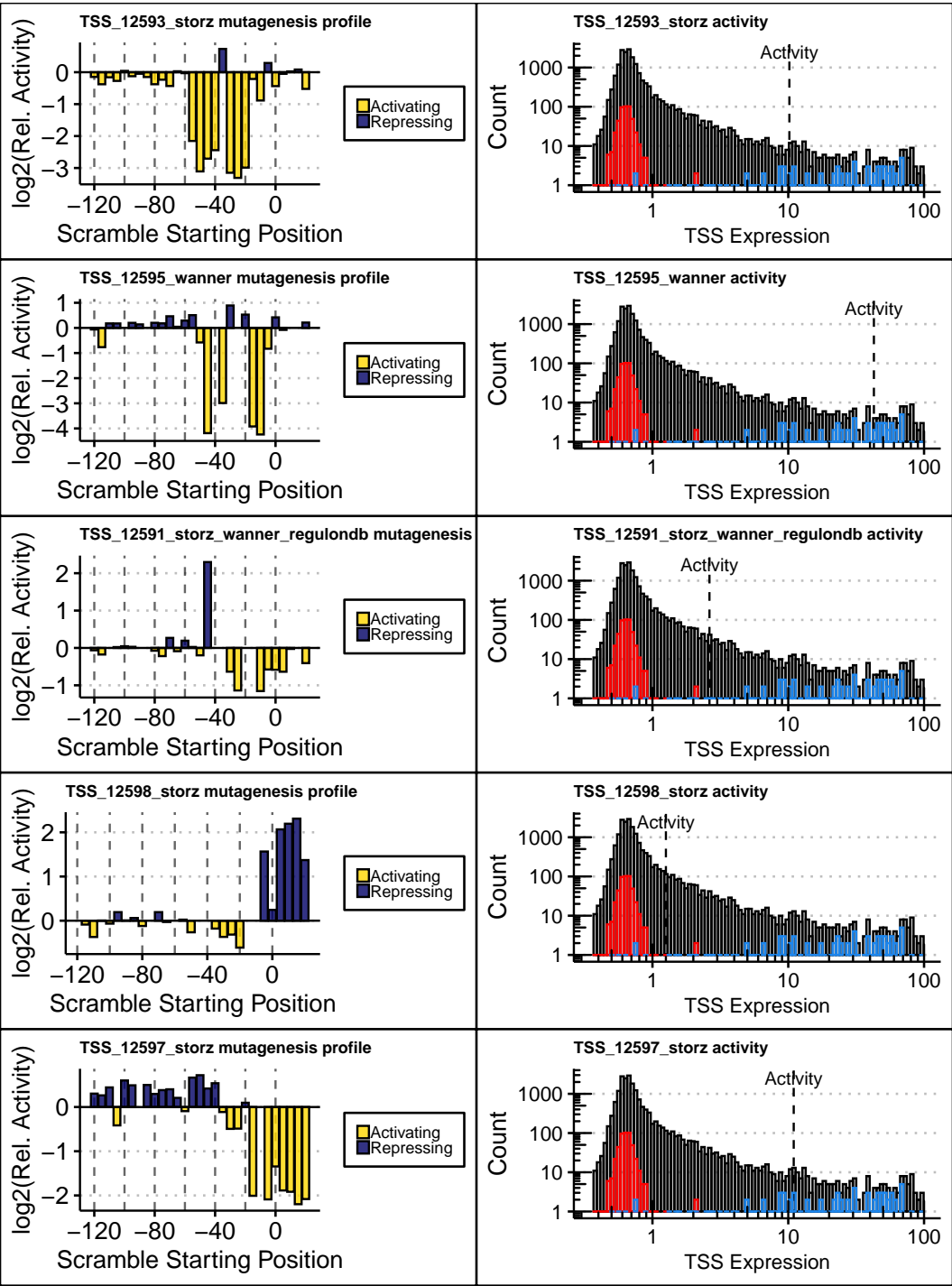


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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