

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
mdh	-	3382290	3381352

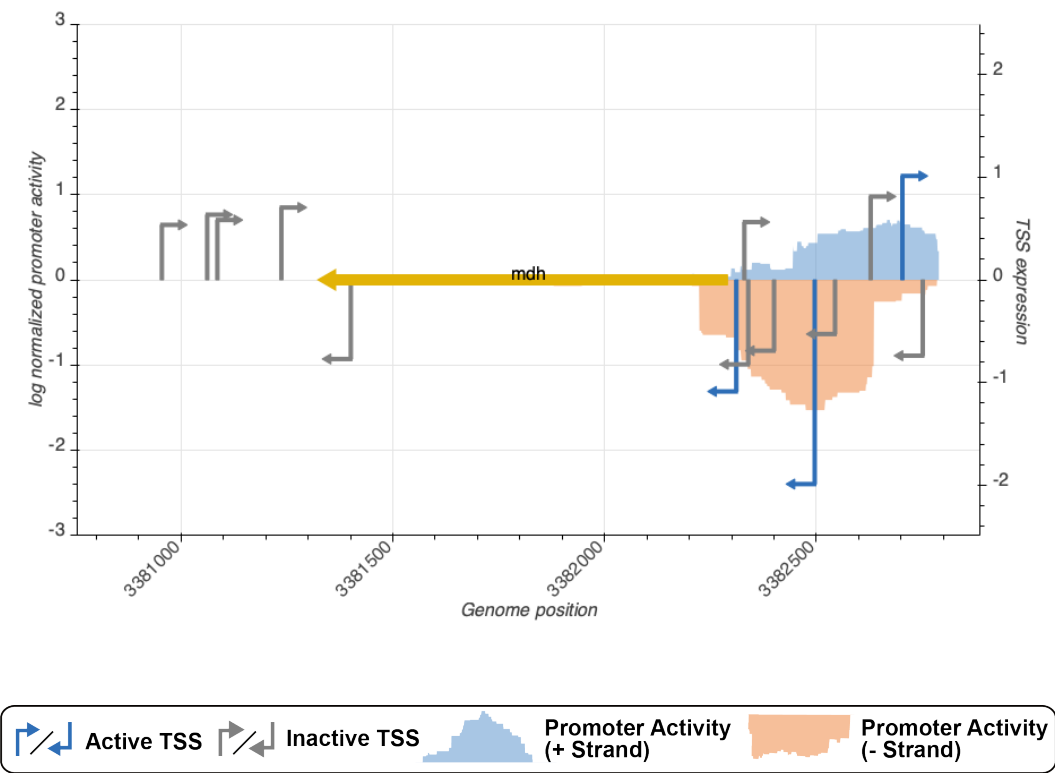


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_12945_storz_regulondb	3382699	+	1.0121456	active
TSS_12941_storz	3382396	-	0.6909279	inactive
TSS_12939_storz	3382326	+	0.5625141	inactive
TSS_12943_storz	3382540	-	0.5282783	inactive
TSS_12946_storz	3382747	-	0.7390689	inactive
TSS_12944_regulondb	3382624	+	0.8116392	inactive
TSS_12942_regulondb	3382492	-	1.9903872	active
TSS_12940_regulondb	3382335	-	0.8240169	inactive
TSS_12938_regulondb	3382307	-	1.0876461	active

TSS Scanning Mutagenesis

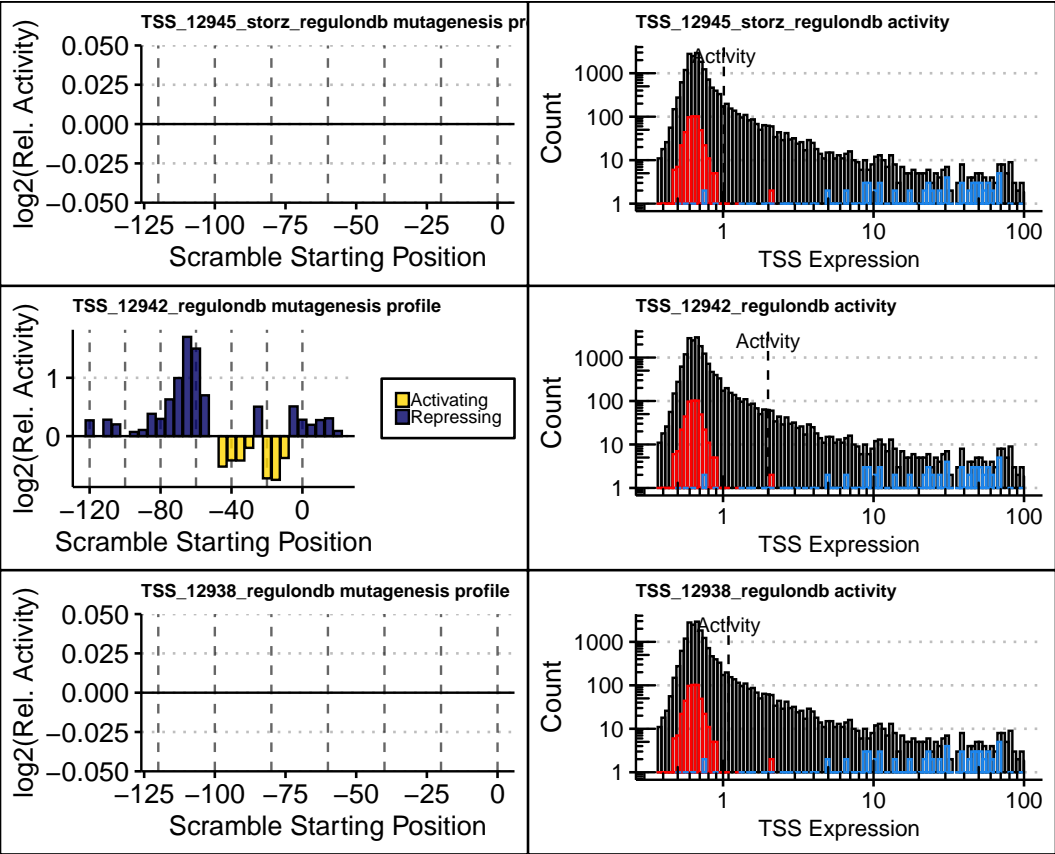


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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