

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
rpmH-rnpA	+	3882359	3882875

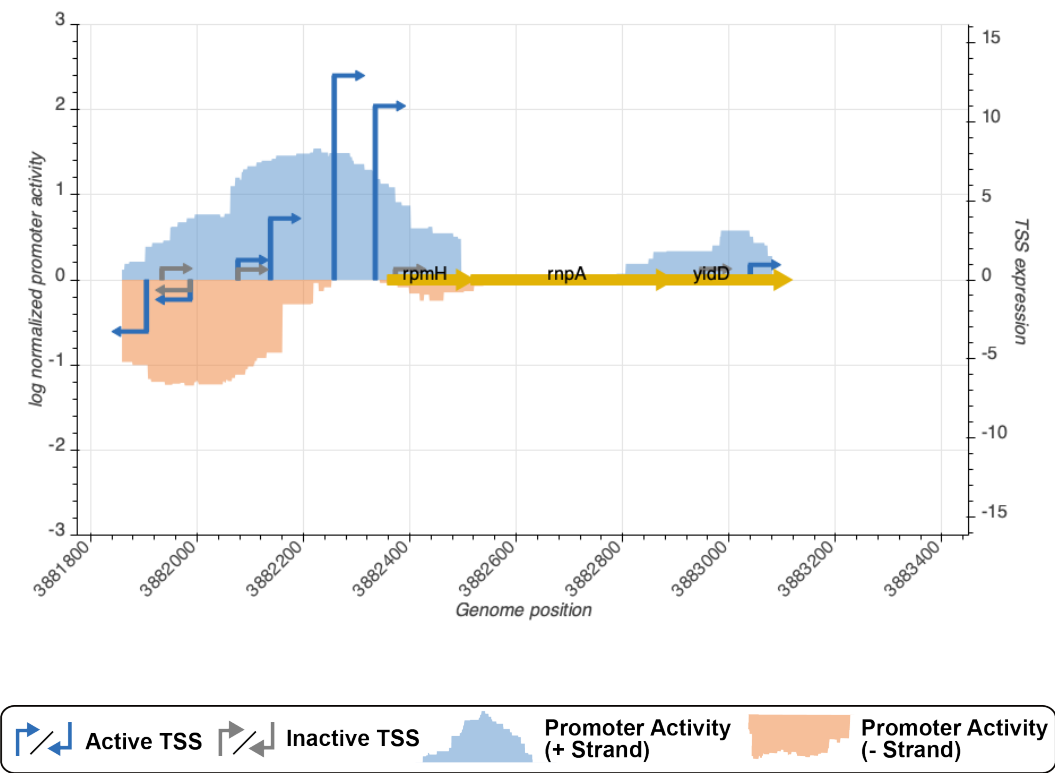


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_15044_storz	3882073	+	1.2504521	active
TSS_15043_wanner	3881983	-	1.2504521	active
TSS_15042_storz	3881930	+	0.7155458	inactive
TSS_15041_regulondb	3881901	-	3.2690491	active
TSS_15044_storz	3882073	+	0.6524152	inactive
TSS_15043_wanner	3881983	-	0.6524152	inactive
TSS_15045_regulondb	3882134	+	3.8831791	active
TSS_15046_storz	3882254	+	12.9213519	active
TSS_15047_regulondb	3882331	+	10.9985871	active

TSS Scanning Mutagenesis

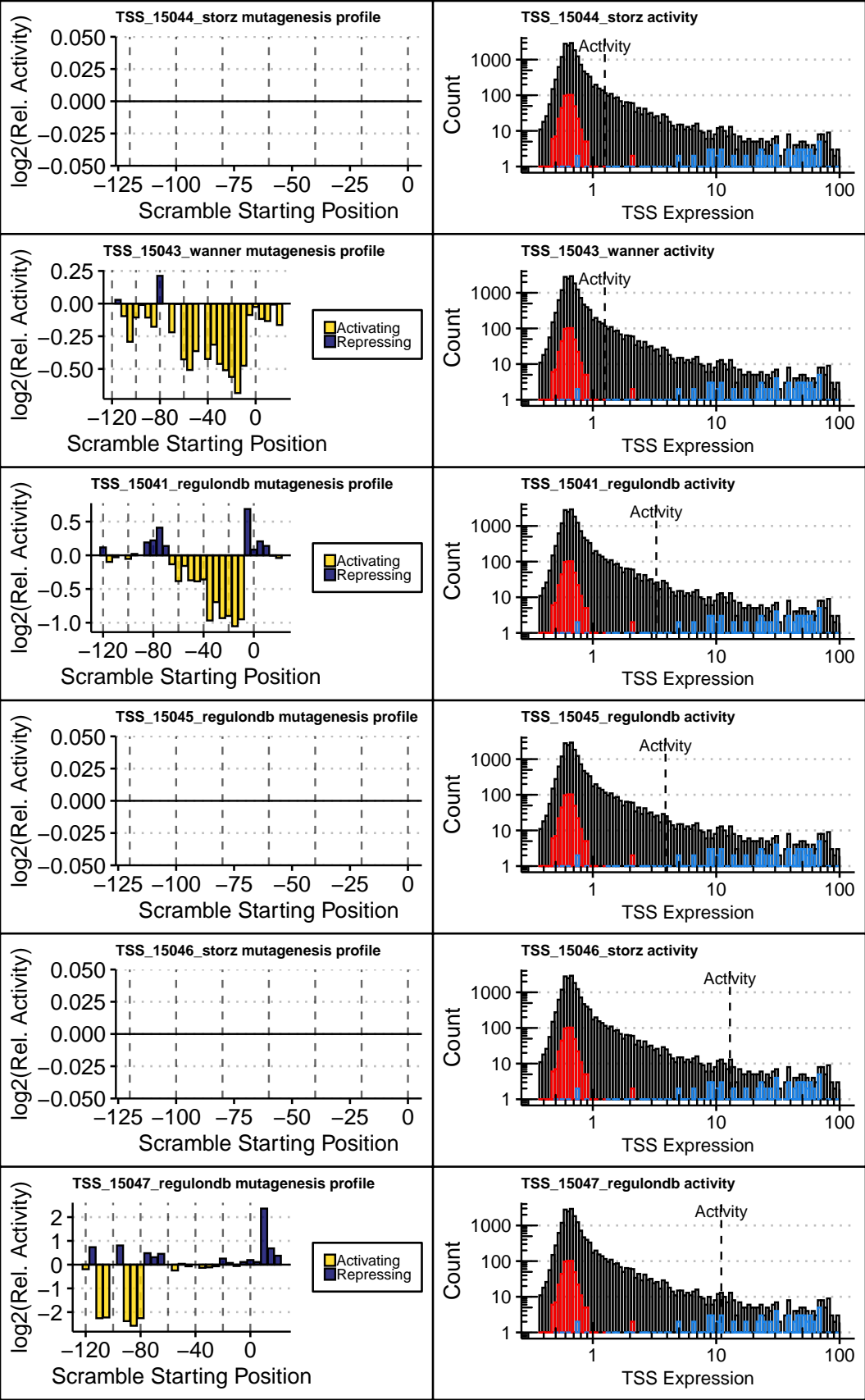


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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