

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ybjM	+	889312	889689

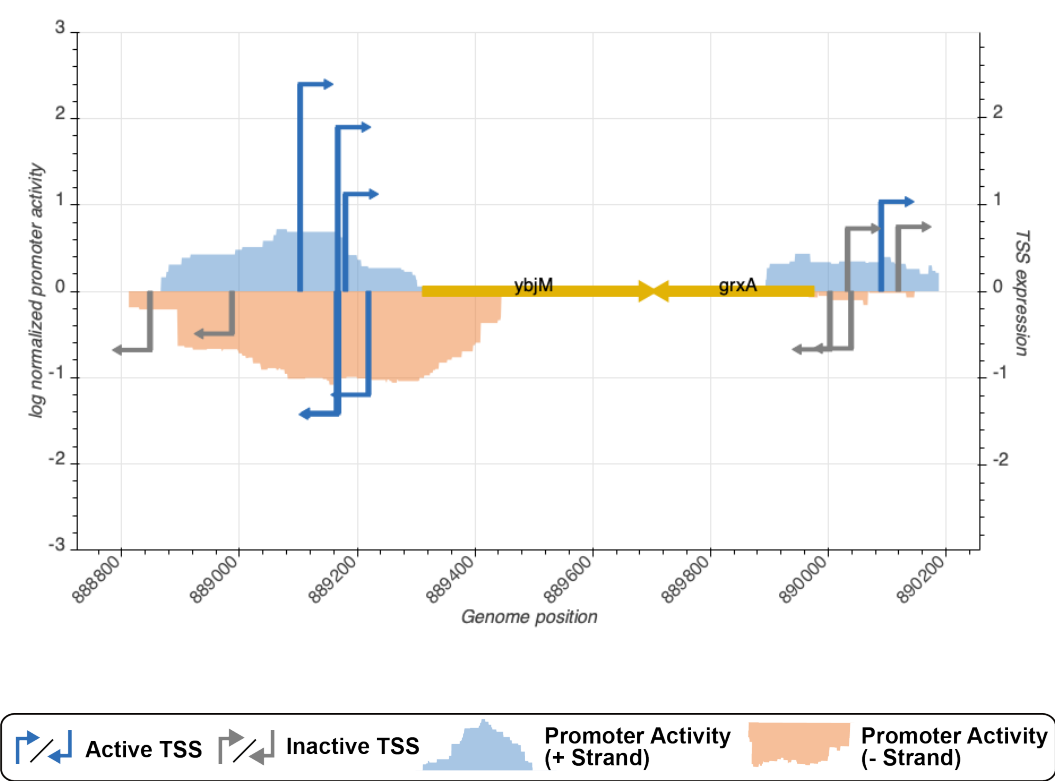


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_3397_storz	889099	+	2.3785841	active
TSS_3402_wanner	889215	-	1.1898100	active
TSS_3398_regulondb	889161	-	1.4161375	active
TSS_3395_storz	888844	-	0.6759383	inactive
TSS_3400_regulondb	889164	-	1.3981530	active
TSS_3396_storz	888983	-	0.4885926	inactive
TSS_3399_regulondb	889163	+	1.8853930	active
TSS_3401_wanner	889176	+	1.1164884	active

TSS Scanning Mutagenesis

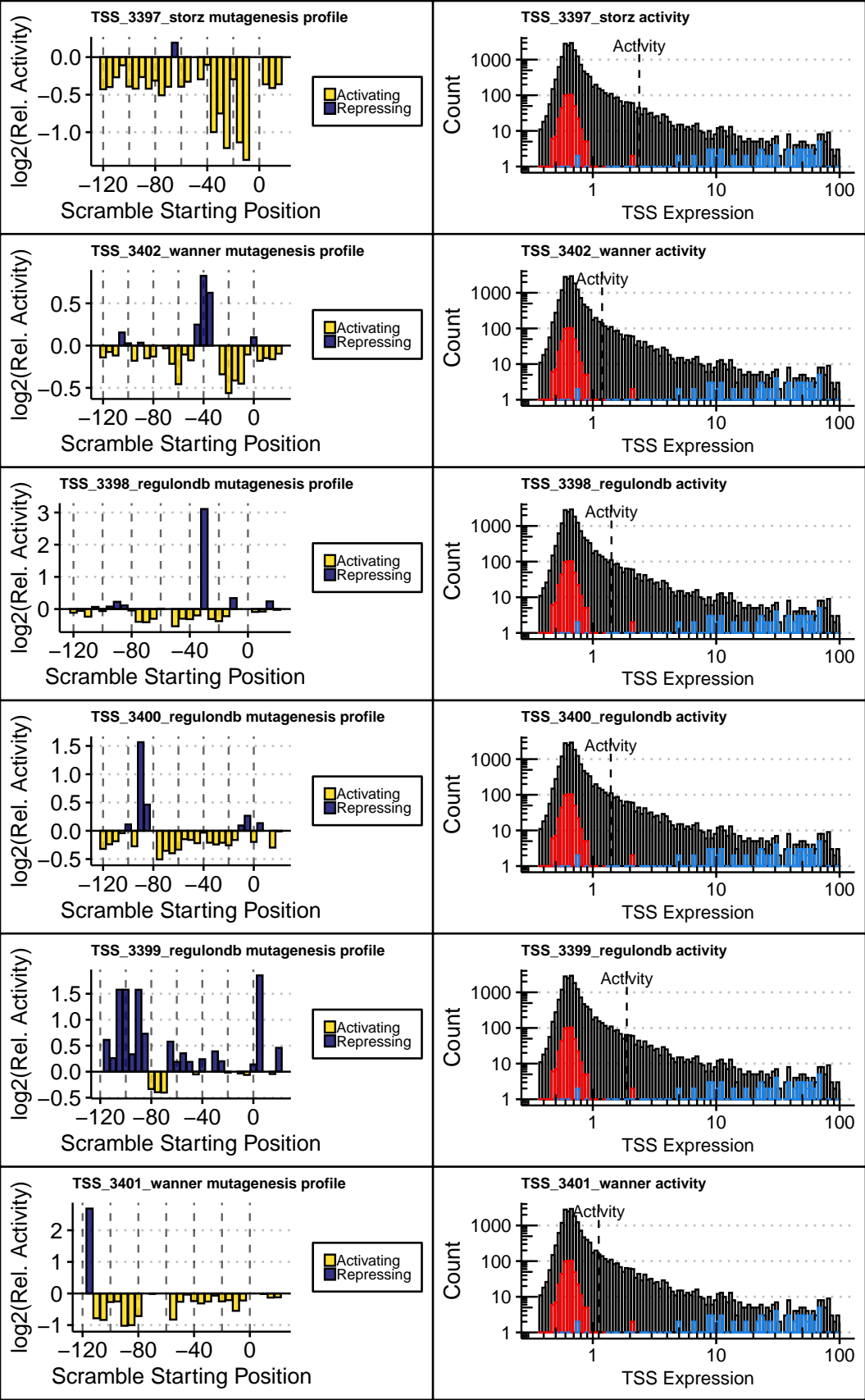


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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