

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yhbY	+	3325812	3326105

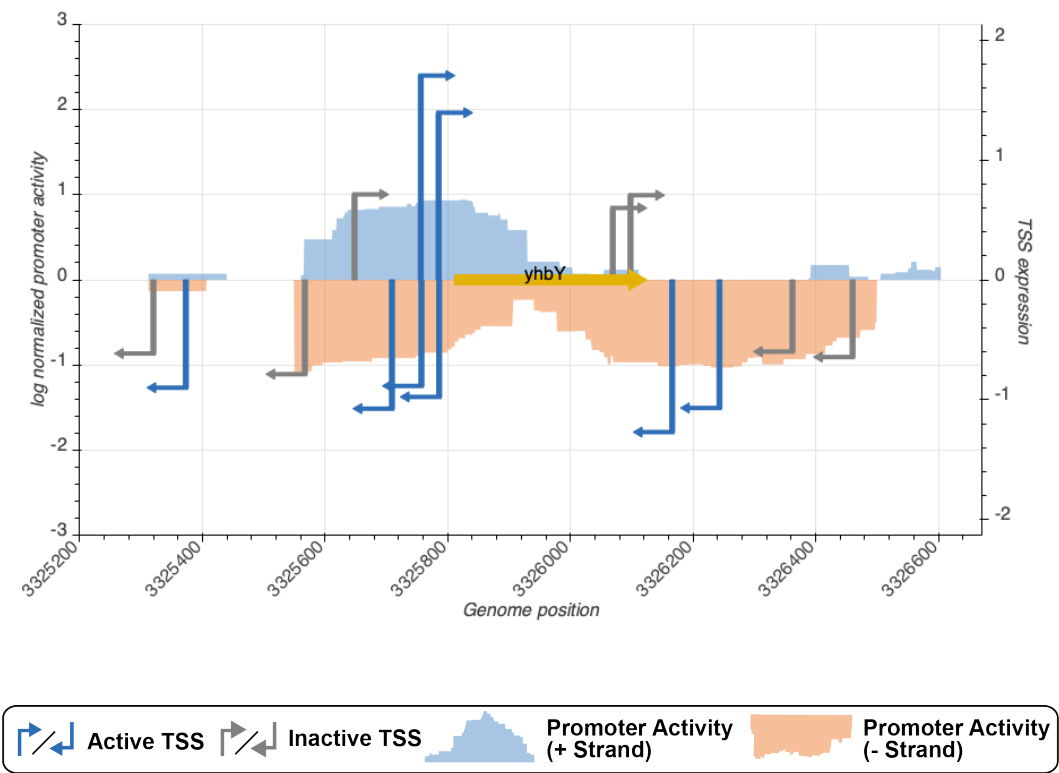


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_12641_storz_regulondb	3325369	-	0.8990107	active
TSS_12649_storz_regulondb	3325781	+	1.3928221	active
TSS_12647_storz	3325752	+	1.7025033	active
TSS_12644_storz	3325563	-	0.7862891	inactive
TSS_12645_storz	3325644	+	0.7122189	inactive
TSS_12648_storz_regulondb	3325753	-	0.8844488	active
TSS_12640_regulondb	3325316	-	0.6139024	inactive
TSS_12650_regulondb	3325782	-	0.9758977	active
TSS_12646_storz	3325705	-	1.0737537	active

TSS Scanning Mutagenesis

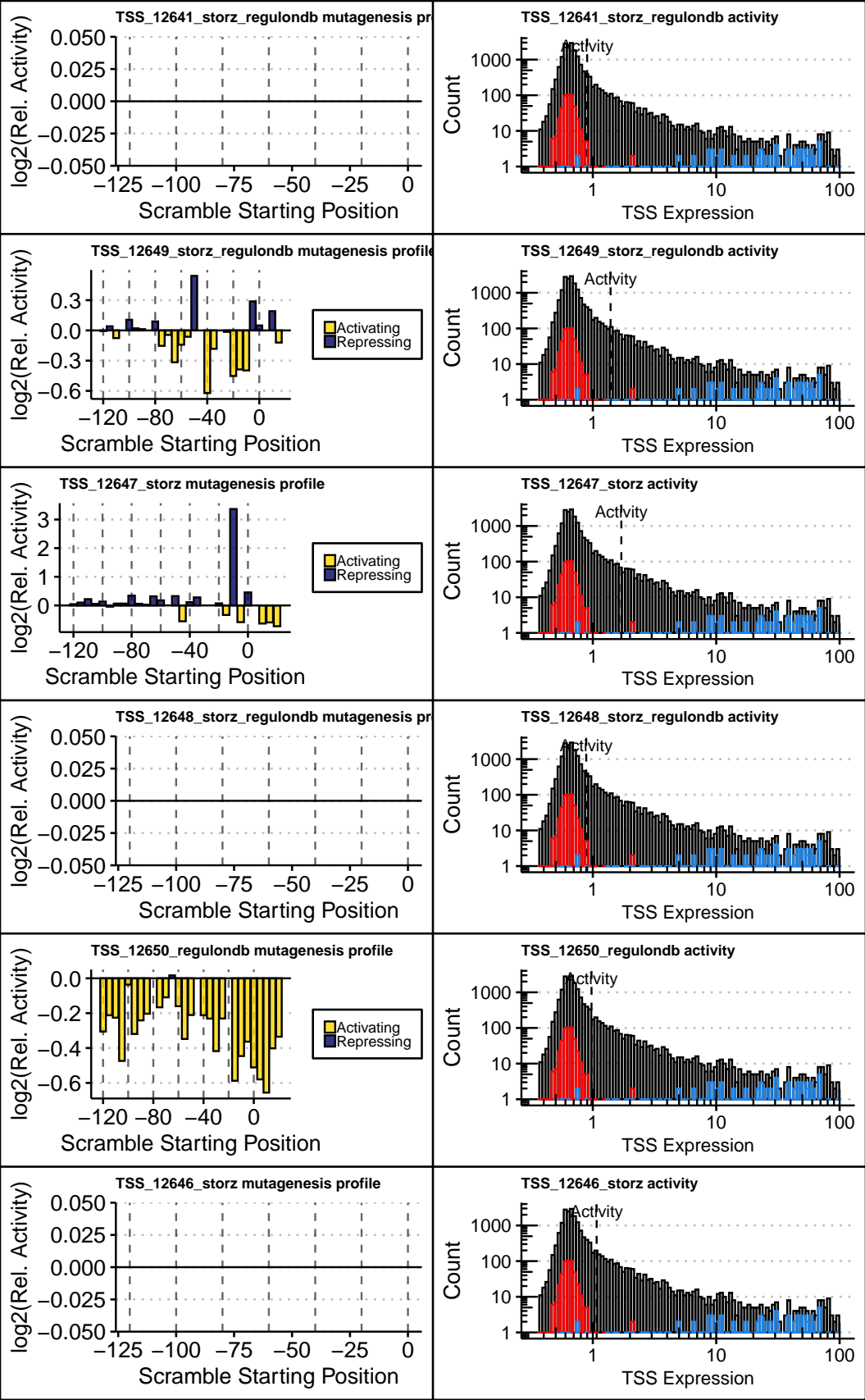


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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