

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yecR	+	1986246	1986569

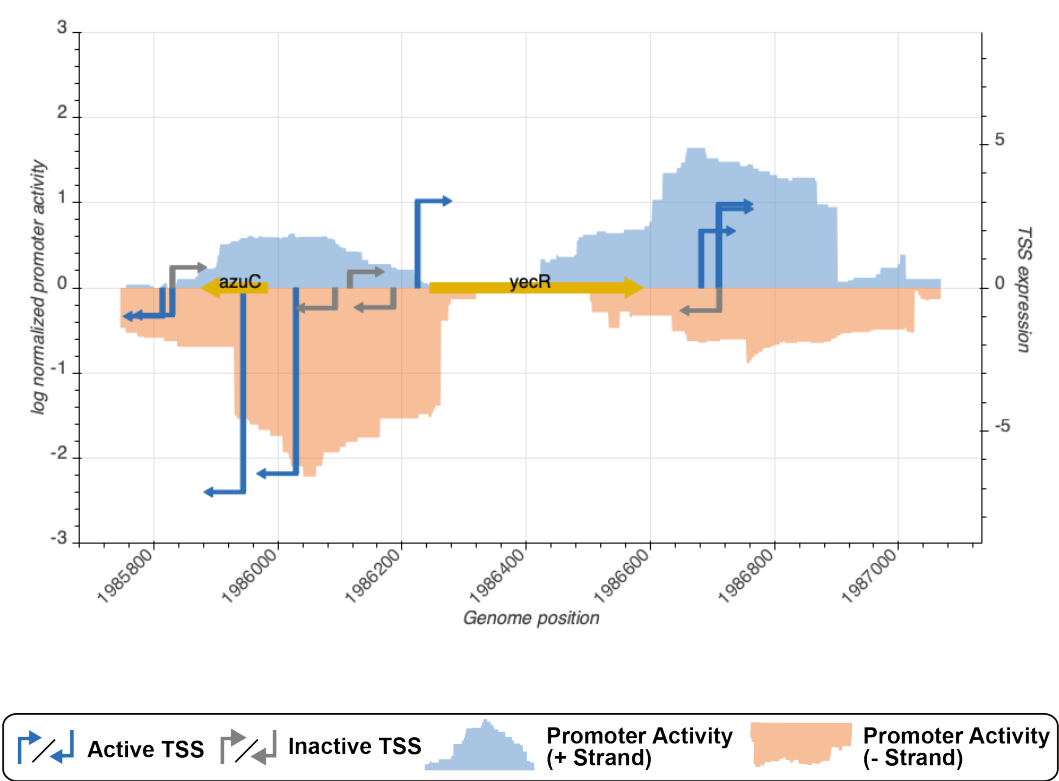


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_7619_storz	1985826	+	0.7126064	inactive
TSS_7625_storz	1986182	-	0.6839150	inactive
TSS_7623_storz	1986088	-	0.7047030	inactive
TSS_7620_regulondb	1985826	-	0.9496643	active
TSS_7618_regulondb	1985810	-	0.9956048	active
TSS_7622_wanner_regulondb	1986025	-	6.4791981	active
TSS_7621_storz	1985940	-	7.1221474	active
TSS_7626_storz	1986221	+	3.0273212	active
TSS_7624_storz	1986112	+	0.5592391	inactive

TSS Scanning Mutagenesis

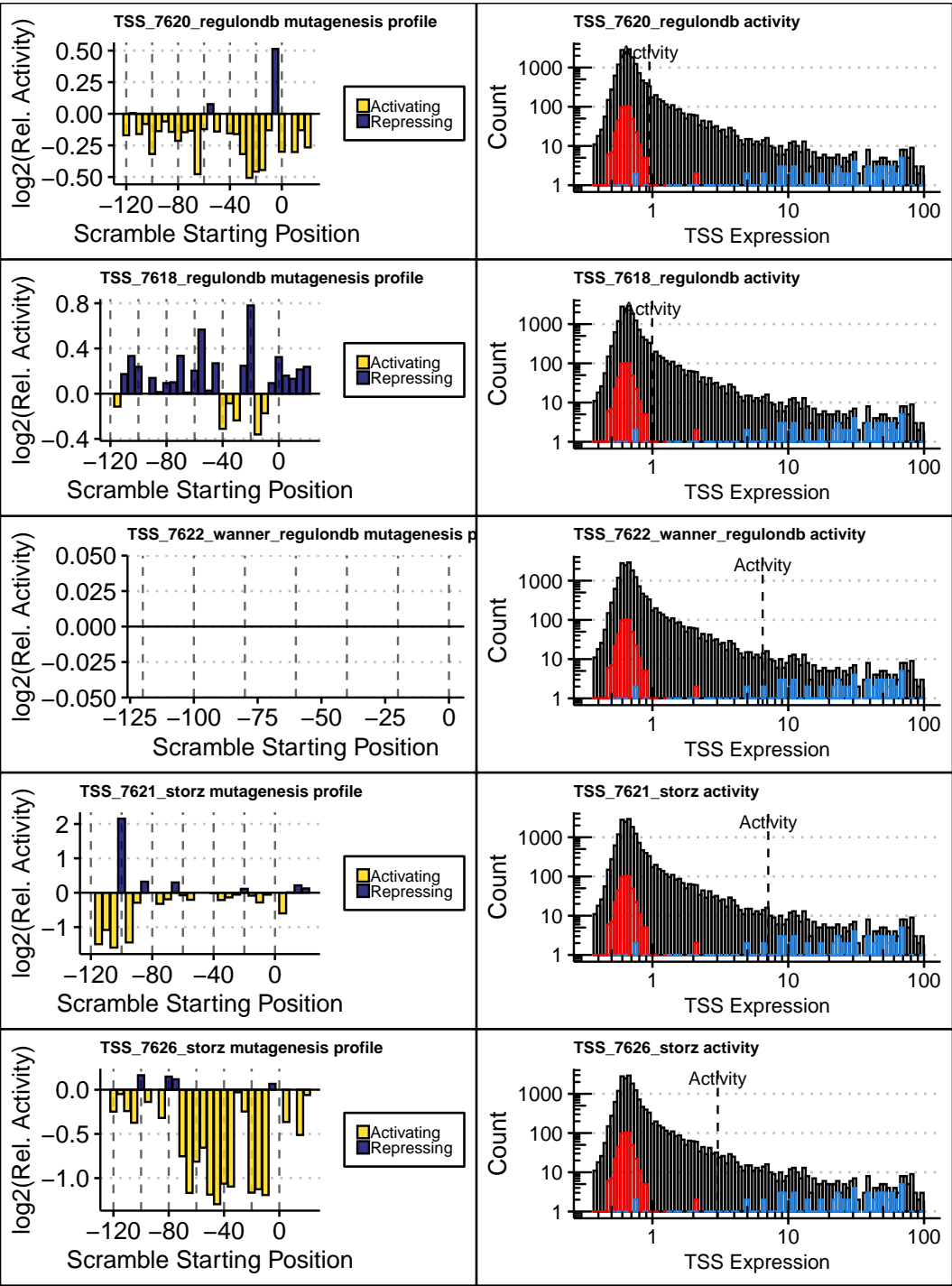


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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