

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yjgN	+	4477753	4478949

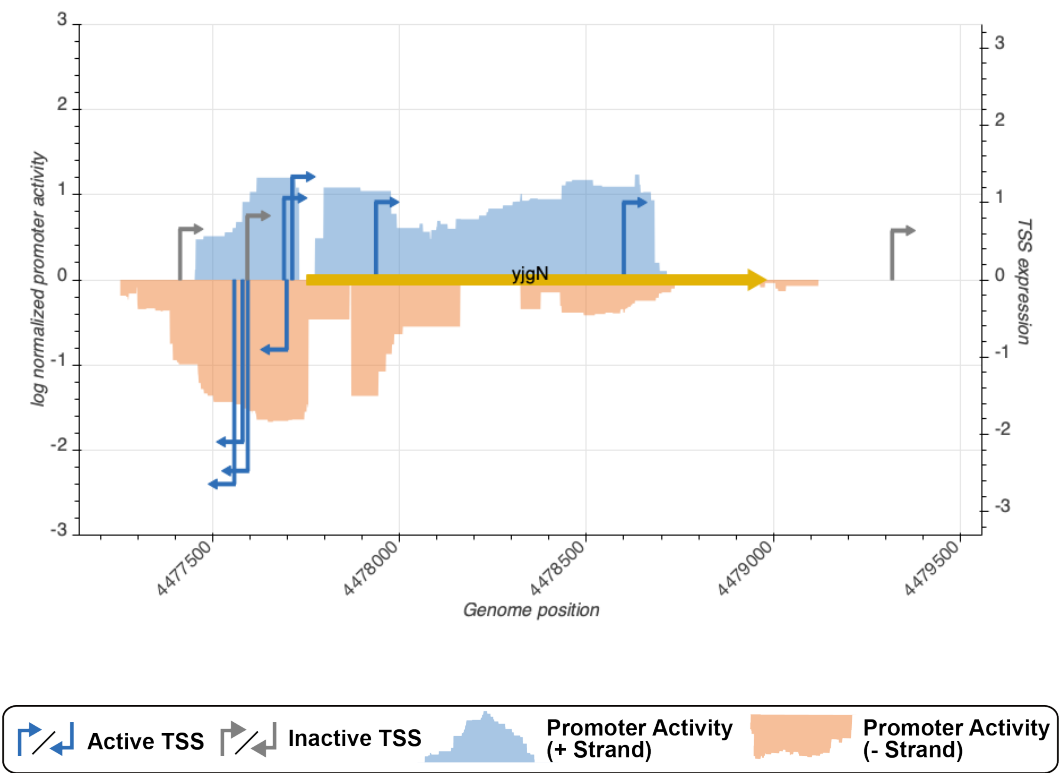


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_17511_storz	4477409	+	0.6569998	inactive
TSS_17512_storz	4477554	-	2.6436385	active
TSS_17517_regulondb	4477694	-	0.9026351	active
TSS_17513_regulondb	4477576	-	2.0976159	active
TSS_17514_regulondb	4477589	+	0.8291135	inactive
TSS_17516_regulondb	4477687	+	1.0589553	active
TSS_17518_regulondb	4477709	+	1.3344327	active
TSS_17515_regulondb	4477590	-	2.4729642	active

TSS Scanning Mutagenesis

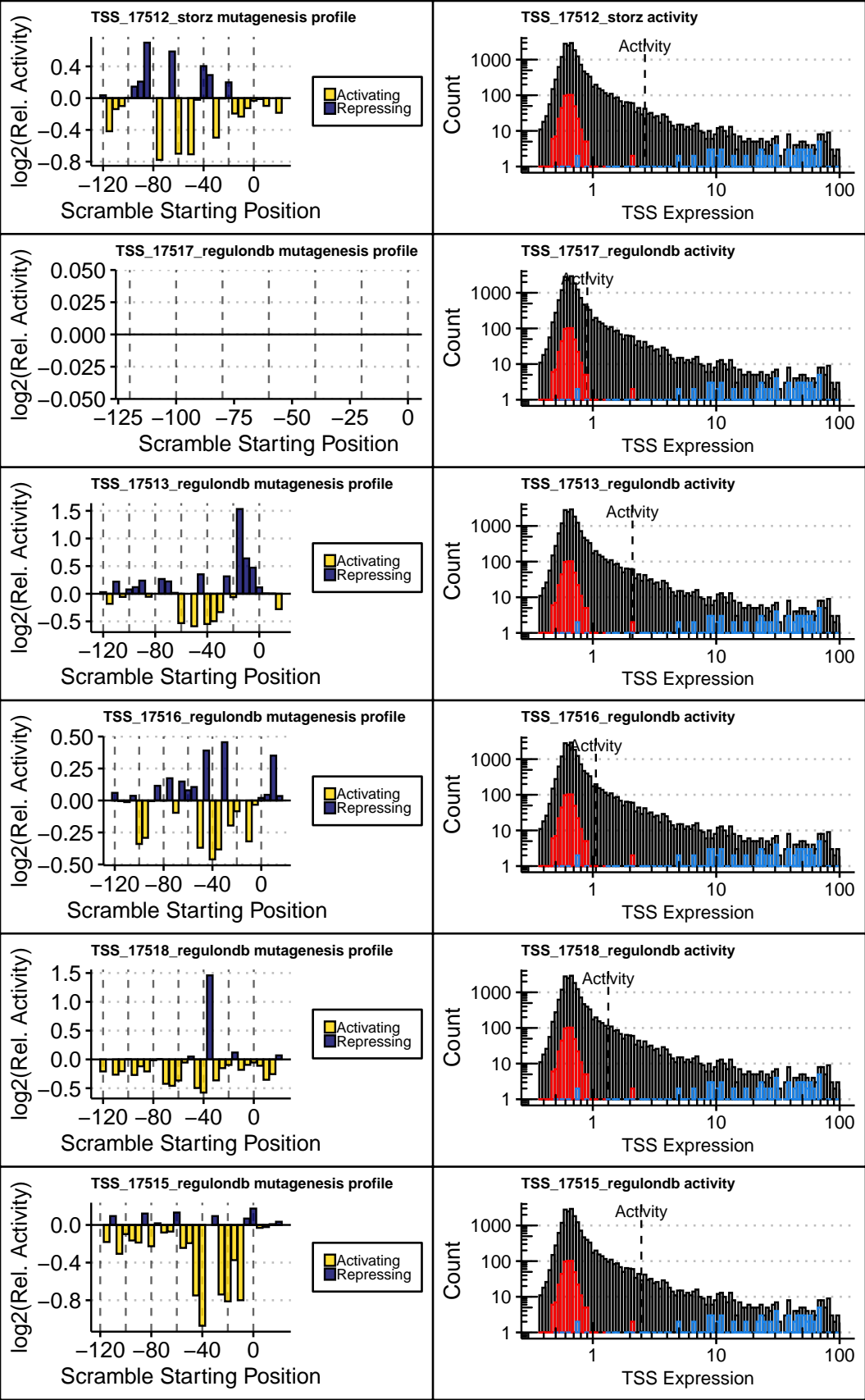


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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