Operon Promoter Landscape

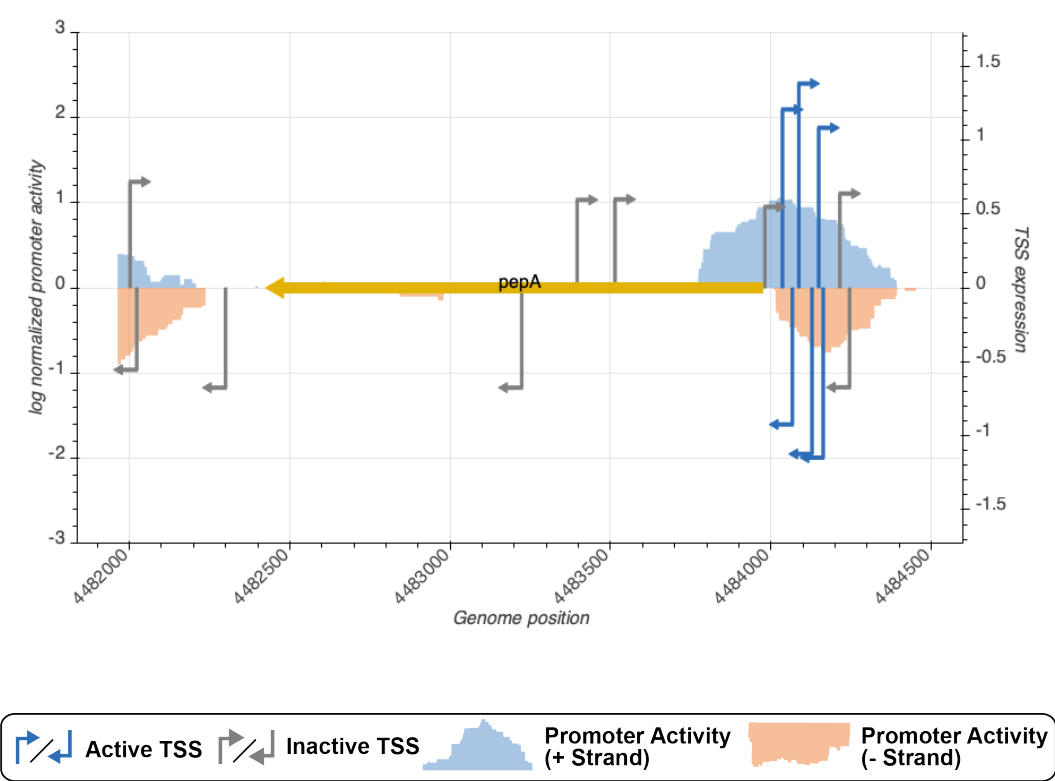| Operon	Strand	Operon start	Operon end
pepA	-	4483974	4482463

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_17540_regulondb	4484145	+	1.0817341	active
TSS_17536_storz	4484032	+	1.2057975	active
TSS_17538_storz	4484083	+	1.3809351	active
TSS_17543_storz	4484241	-	0.6728019	inactive
TSS_17541_storz	4484159	-	1.1481961	active
TSS_17539_regulondb	4484124	-	1.1234121	active
TSS_17535_storz	4483977	+	0.5468420	inactive
TSS_17542_regulondb	4484211	+	0.6373126	inactive
TSS_17537_regulondb	4484063	-	0.9237764	active

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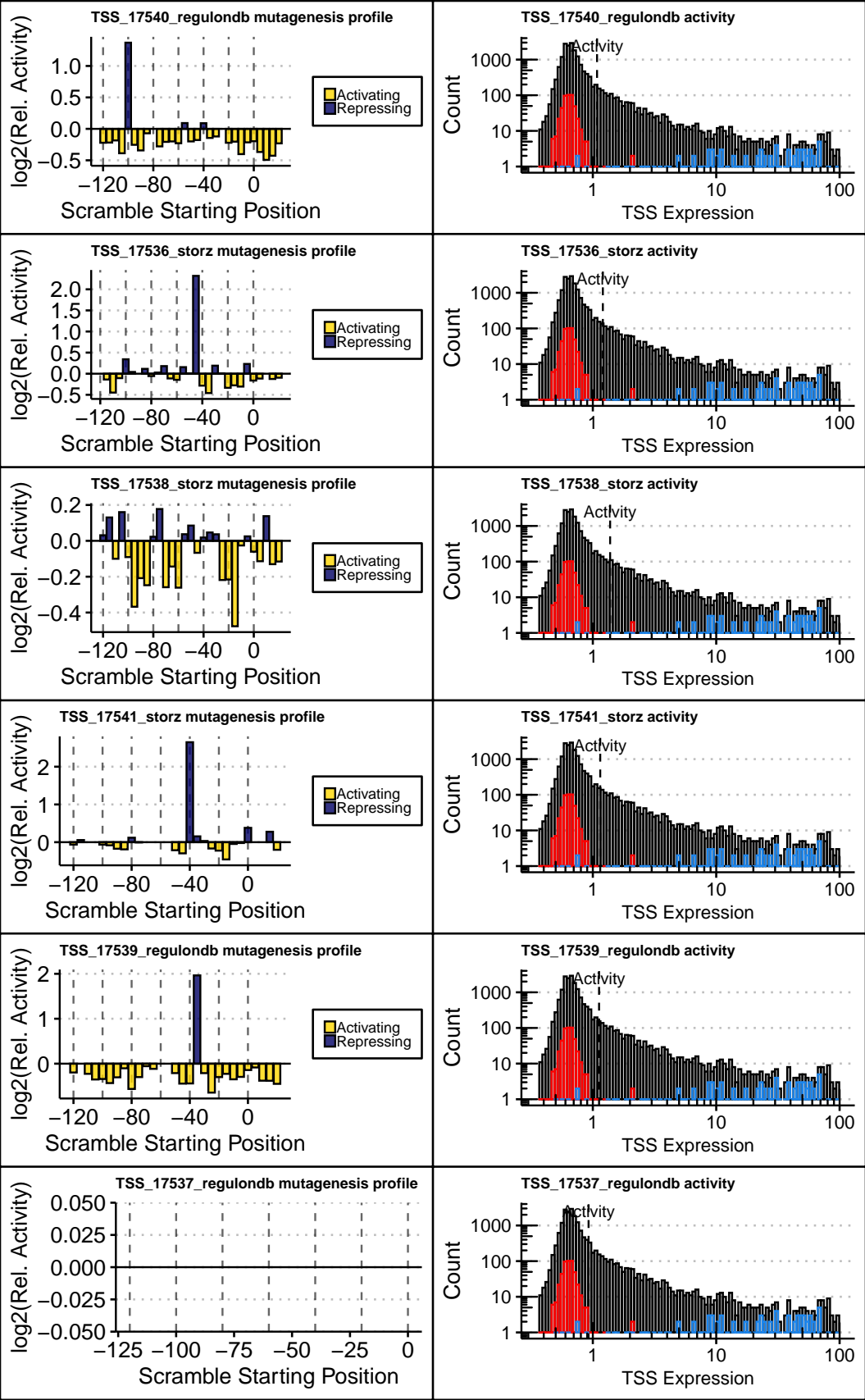
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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