Operon Promoter Landscape
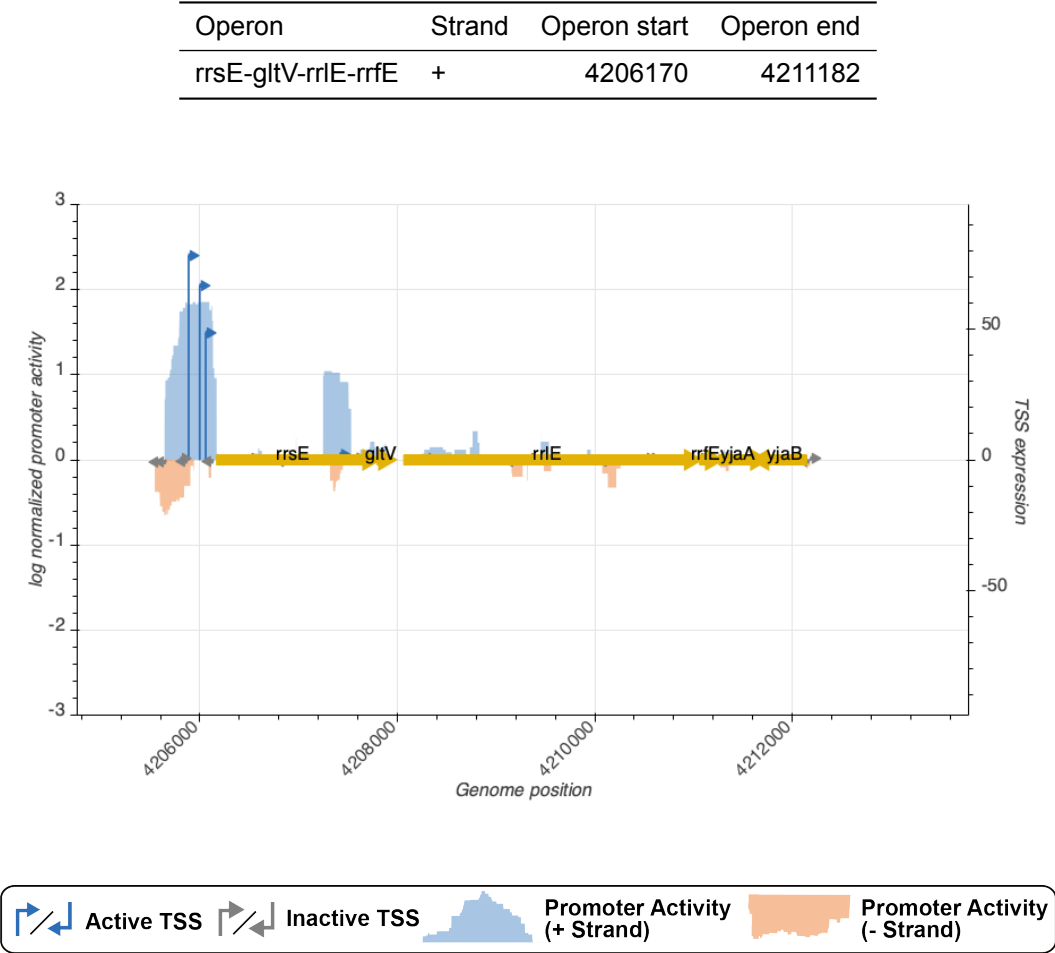
Operon	Strand	Operon start	Operon end
rrsE-gltV-rrlE-rrfE	+	4206170	4211182

Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 pre-viously 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 corre-sponds to *E. coli* genome version U00096.2.

TSS Summary

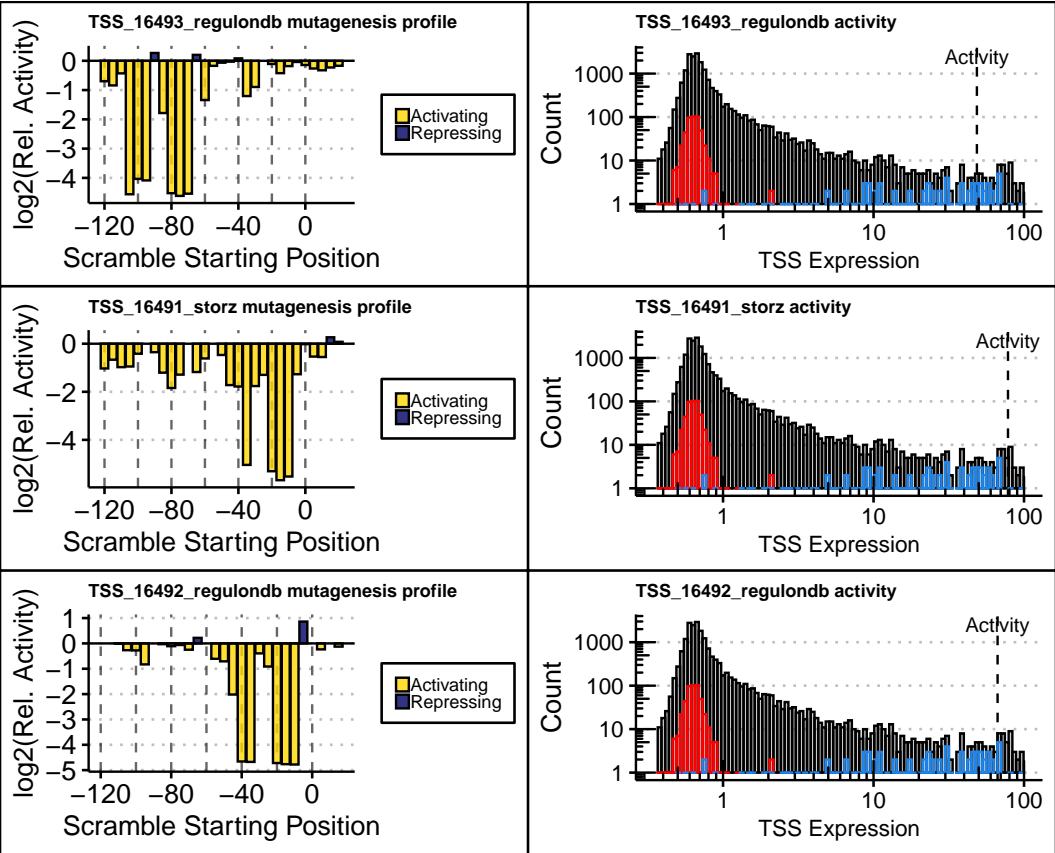| TSS name	TSS position	Strand	TSS activity	Category
TSS_16493_regulondb	4206055	+	48.6181118	active
TSS_16490_storz	4205865	-	0.5822669	inactive
TSS_16491_storz	4205882	+	78.2308593	active
TSS_16492_regulondb	4205994	+	66.7272458	active
TSS_16494_storz	4206129	-	0.5957855	inactive
TSS_16489_storz	4205803	+	0.5500832	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 in-dicates 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 ex-pression 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).