Operon Promoter Landscape
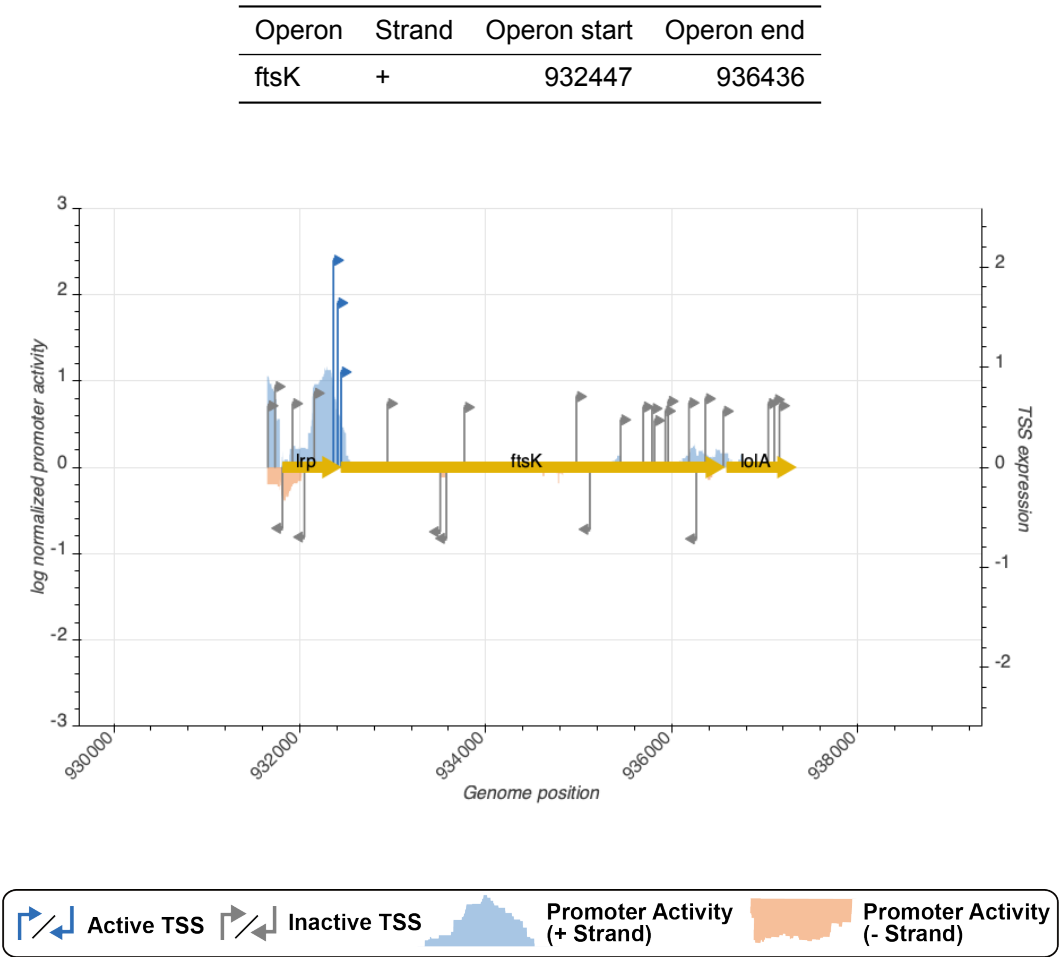
Operon	Strand	Operon start	Operon end
ftsK	+	932447	936436

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

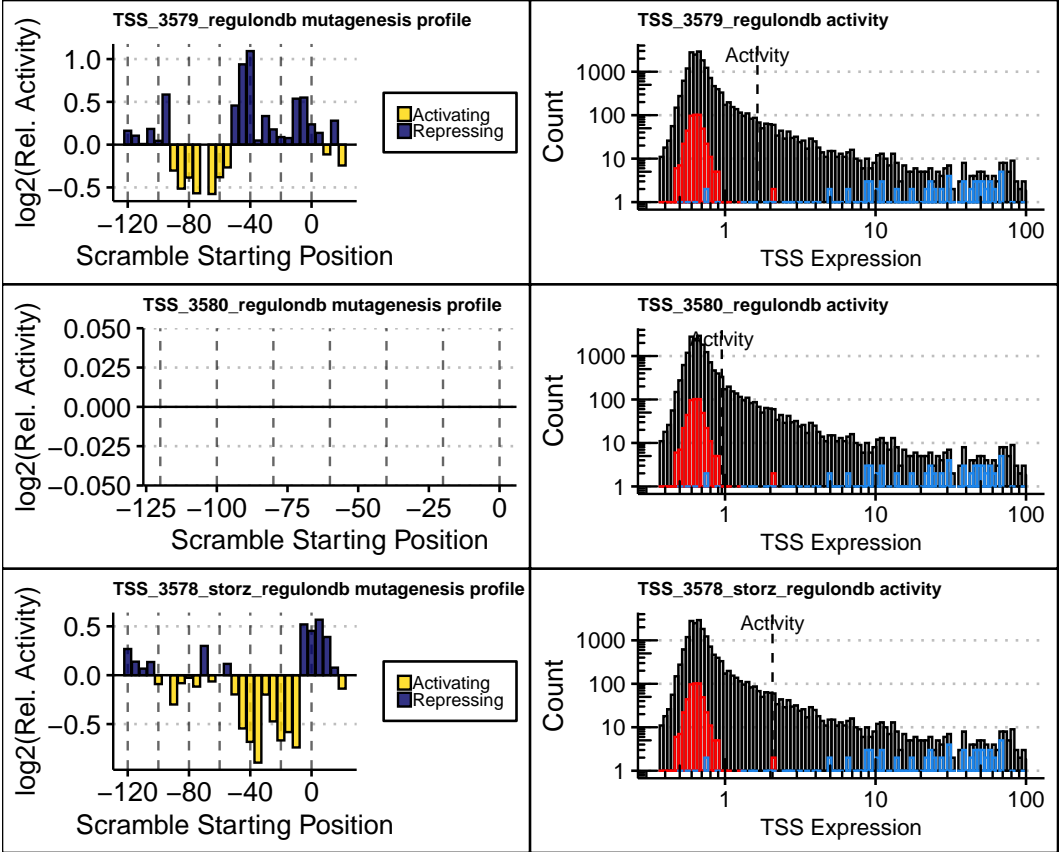| TSS name	TSS position	Strand	TSS activity	Category
TSS_3577_storz_regulondb	932152	+	0.7393094	inactive
TSS_3579_regulondb	932404	+	1.6416293	active
TSS_3580_regulondb	932441	+	0.9511231	active
TSS_3576_storz	932046	-	0.6973548	inactive
TSS_3578_storz_regulondb	932358	+	2.0676906	active

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).