Operon Promoter Landscape

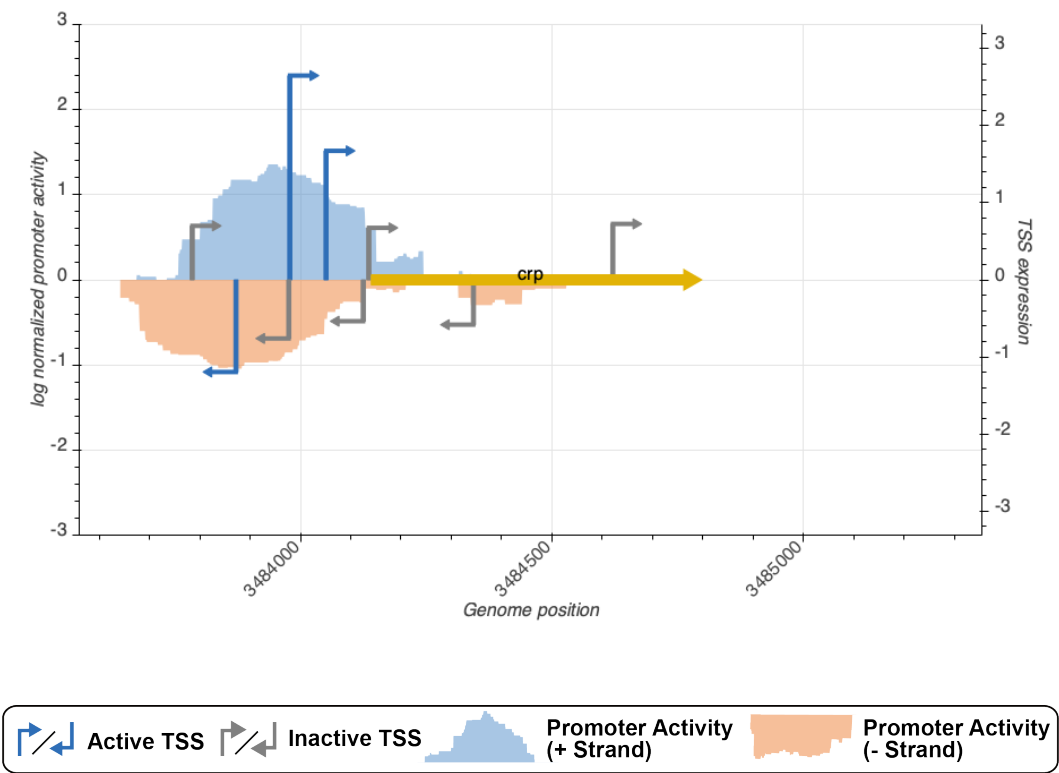| Operon	Strand	Operon start	Operon end
crp	+	3484142	3484774

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_13487_regulondb	3483868	-	1.1957108	active
TSS_13489_storz_regulondb	3483975	+	2.6504341	active
TSS_13488_wanner_regulondb	3483973	-	0.7607206	inactive
TSS_13492_regulondb	3484132	+	0.6745553	inactive
TSS_13486_storz	3483781	+	0.7002389	inactive
TSS_13491_storz	3484121	-	0.5368769	inactive
TSS_13490_regulondb	3484047	+	1.6736112	active

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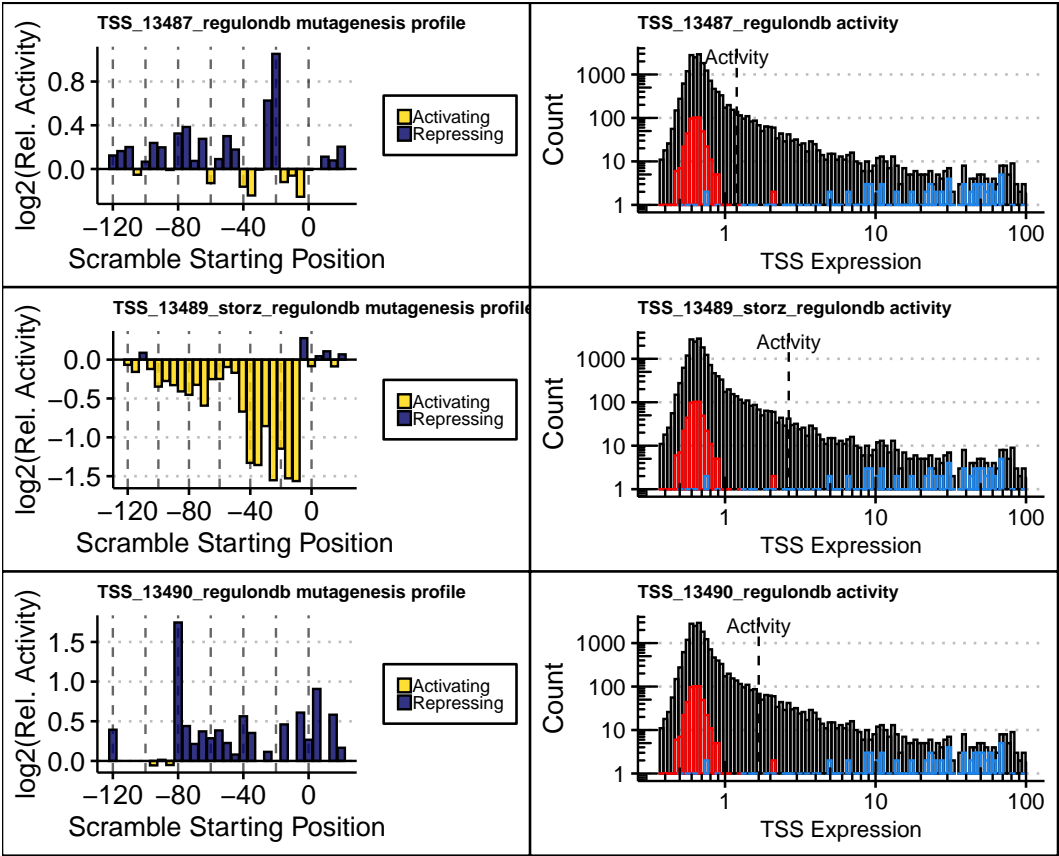
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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