Operon Promoter Landscape
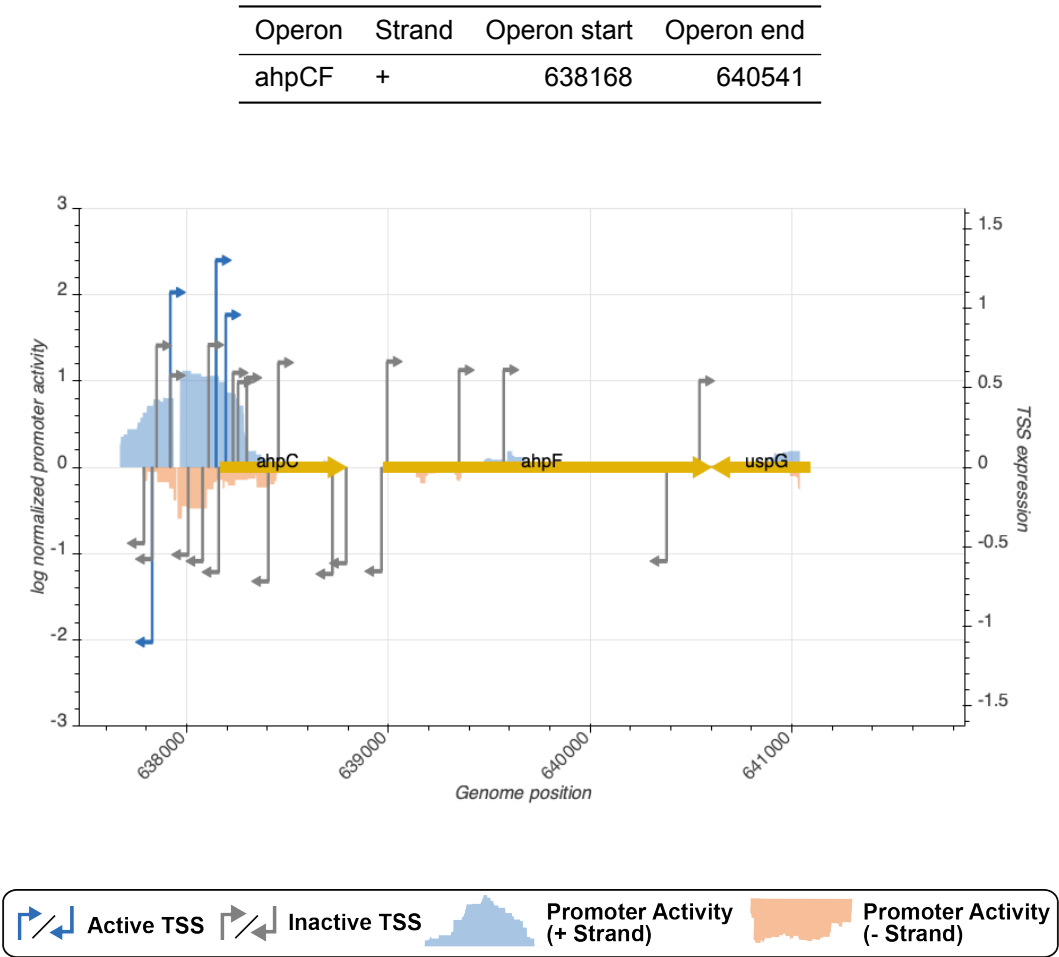
Operon	Strand	Operon start	Operon end
ahpCF	+	638168	640541

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_2429_wanner	638003	-	0.5514577	inactive
TSS_2427_wanner	637914	+	0.5789055	inactive
TSS_2424_regulondb	637824	-	0.5789055	inactive
TSS_2433_regulondb	638141	+	1.3048303	active
TSS_2425_storz	637846	+	0.7670903	inactive
TSS_2434_storz	638154	-	0.6610911	inactive
TSS_2432_storz	638104	+	0.7711211	inactive
TSS_2431_storz	638074	-	0.5921228	inactive
TSS_2427_wanner	637914	+	1.1026383	active
TSS_2424_regulondb	637824	-	1.1026383	active
TSS_2423_storz	637783	-	0.4794247	inactive

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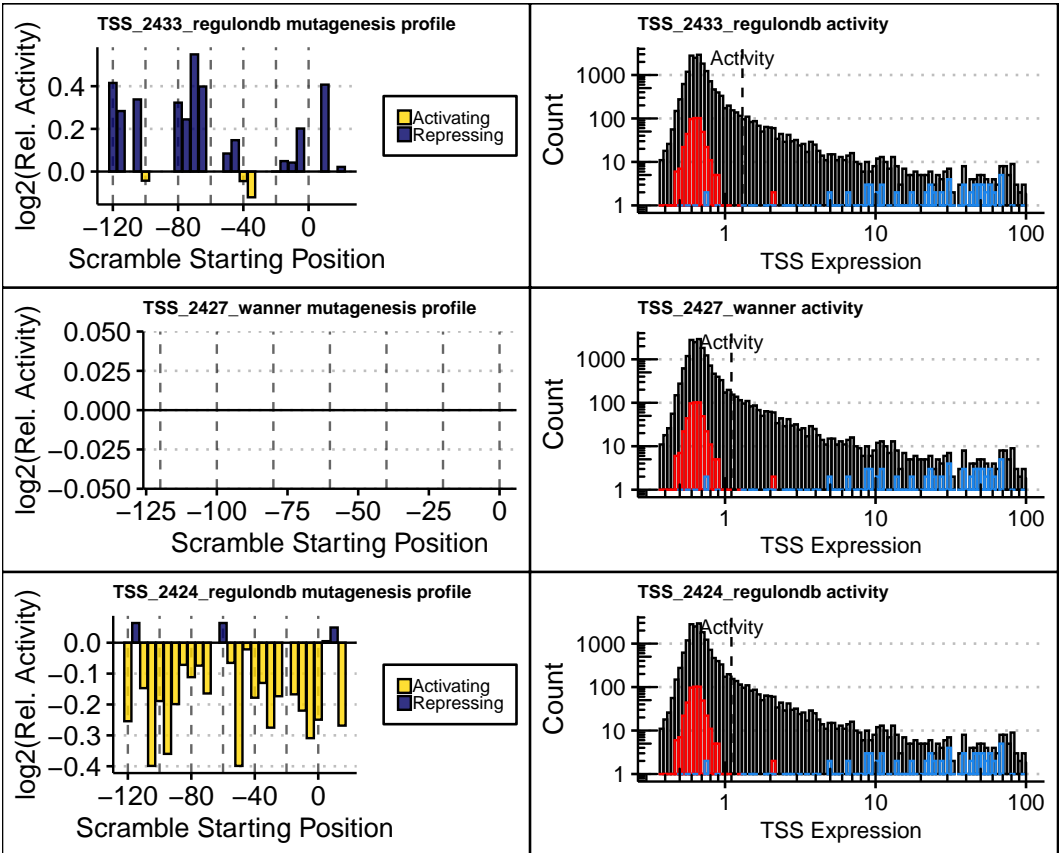
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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

1