Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
pheLA	+	2735621	2736927

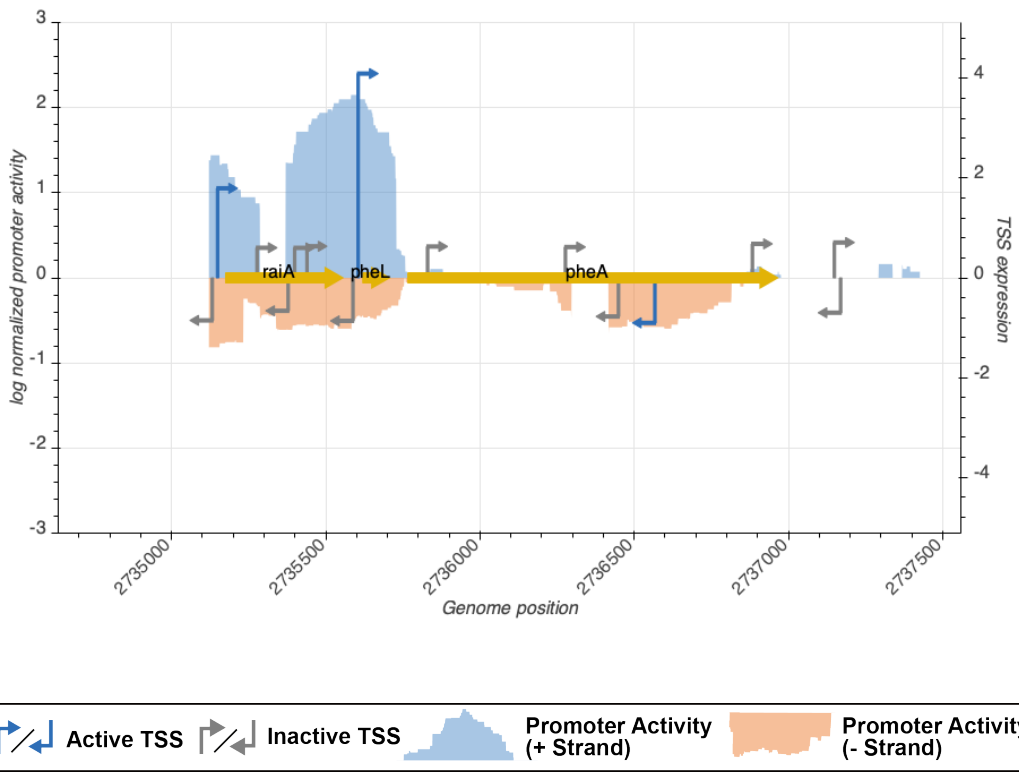

Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_10327_storz	2735584	-	0.8628182	inactive
TSS_10321_storz	2735128	-	0.8533393	inactive
TSS_10325_regulondb	2735395	+	0.6004467	inactive
TSS_10322_regulondb	2735145	+	1.7944341	active
TSS_10324_storz	2735374	-	0.6610578	inactive
TSS_10328_regulondb	2735601	+	4.0956141	active
TSS_10323_regulondb	2735273	+	0.6028988	inactive
TSS_10326_regulondb	2735435	+	0.6328142	inactive

TSS Scanning Mutagenesis

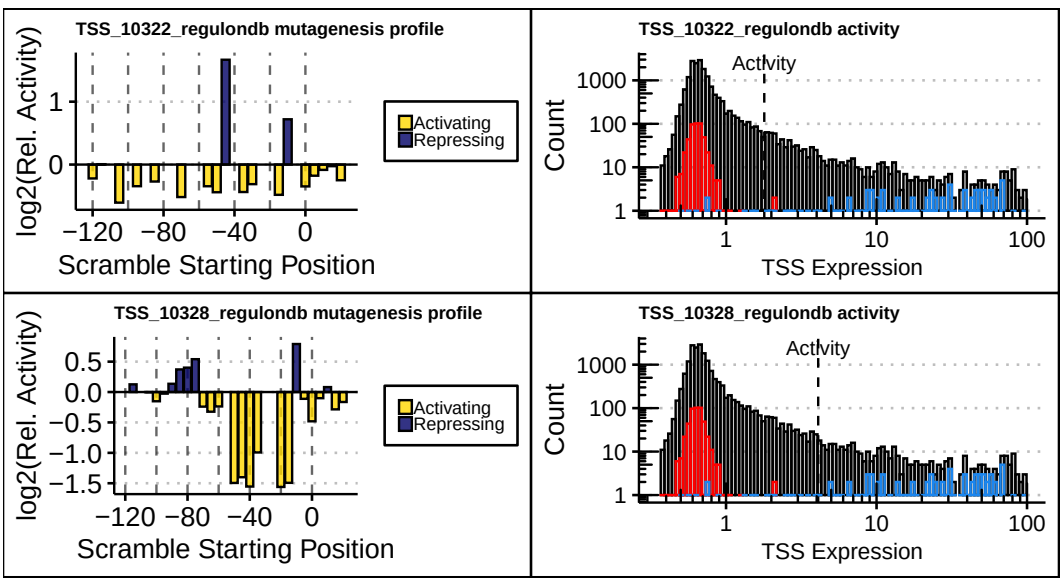

Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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