Operon Promoter Landscape

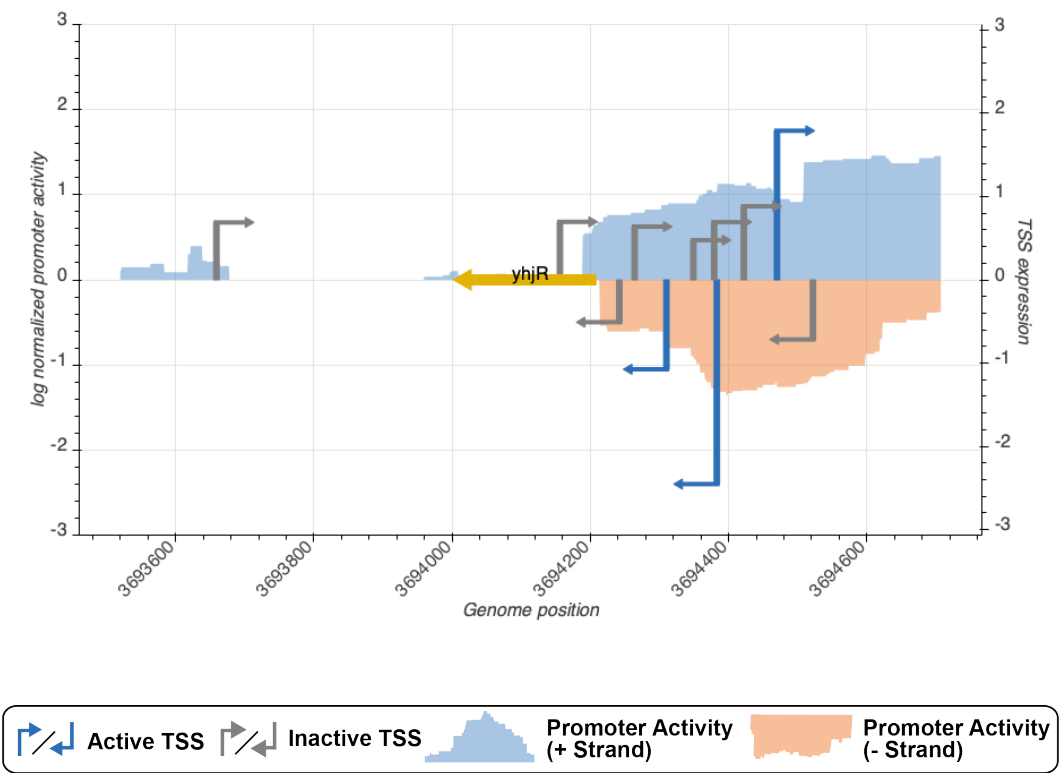| Operon	Strand	Operon start	Operon end
yhjR	-	3694208	3694020

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_14304_storz	3694260	+	0.6385152	inactive
TSS_14308_regulondb	3694379	-	2.4521378	active
TSS_14305_regulondb	3694306	-	1.0737537	active
TSS_14309_regulondb	3694418	+	0.8826286	inactive
TSS_14311_storz	3694518	-	0.7156143	inactive
TSS_14306_regulondb	3694345	+	0.4757168	inactive
TSS_14307_wanner	3694375	+	0.6924437	inactive
TSS_14310_regulondb	3694466	+	1.7894869	active
TSS_14303_regulondb	3694238	-	0.5087278	inactive

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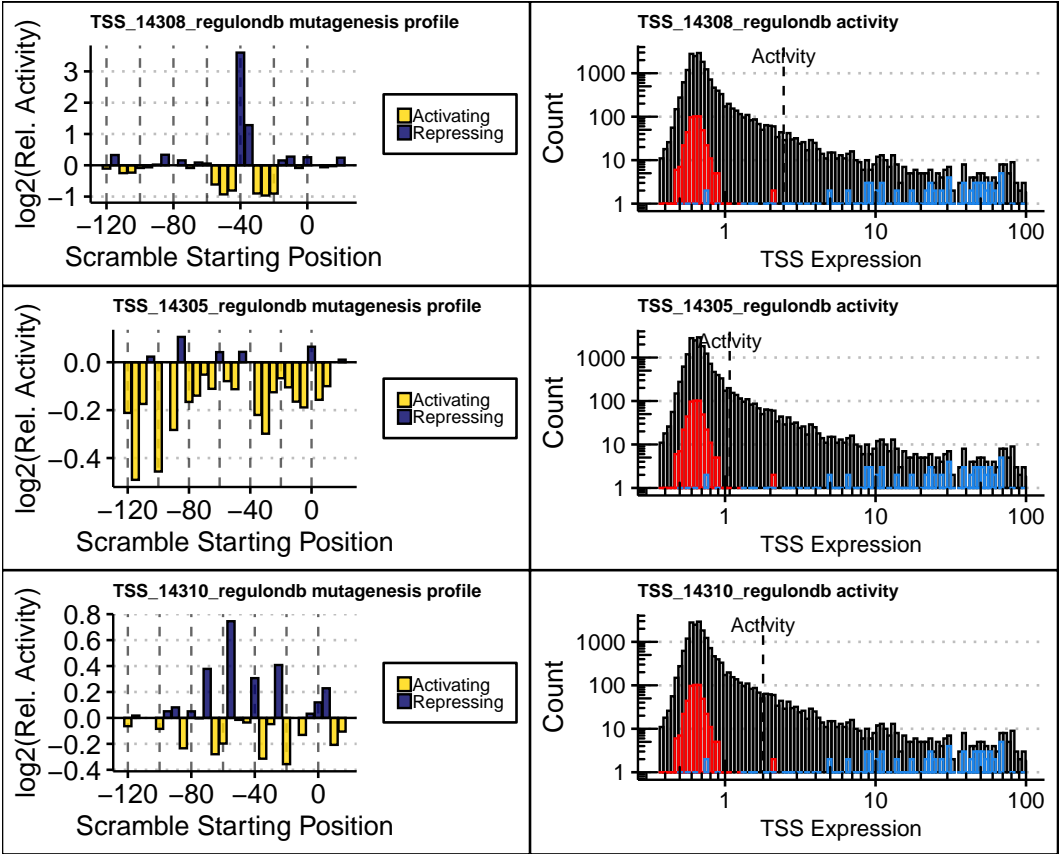
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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