

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
feaR	-	1445307	1444402

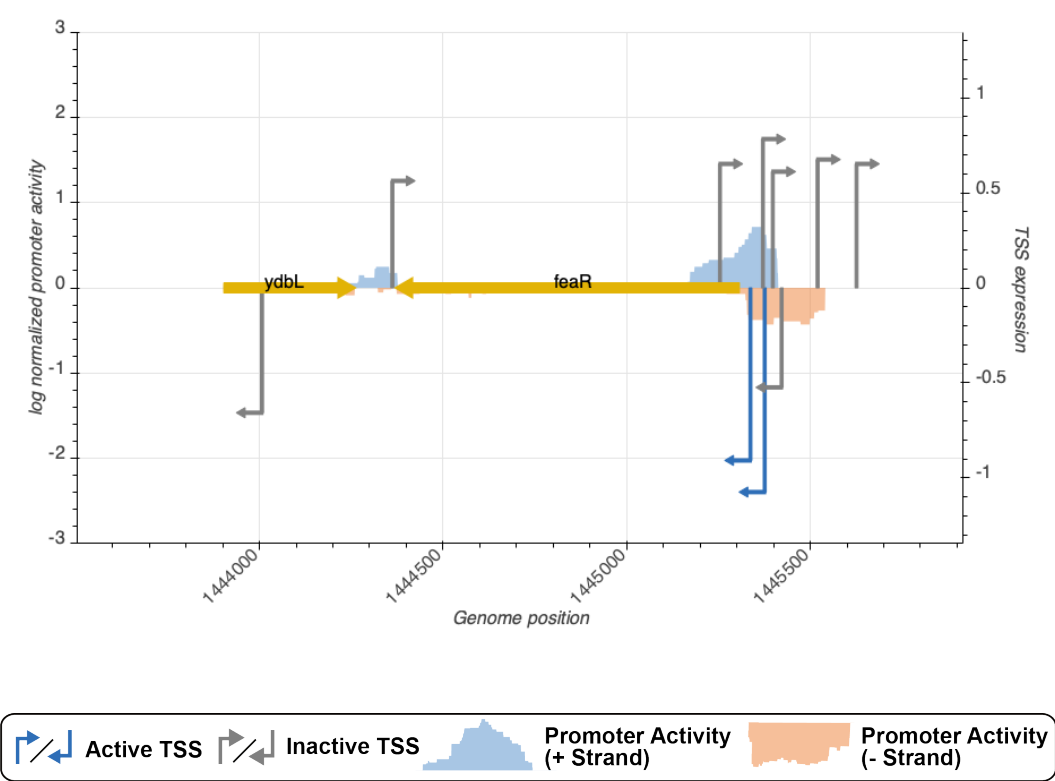


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_5652_regulondb	1445516	+	0.6755228	inactive
TSS_5653_storz	1445622	+	0.6524152	inactive
TSS_5649_wanner	1445372	-	1.0750818	active
TSS_5647_regulondb	1445333	-	0.9084563	active
TSS_5648_storz	1445367	+	0.7828982	inactive
TSS_5651_regulondb	1445418	-	0.5240393	inactive
TSS_5650_regulondb	1445394	+	0.6113981	inactive

TSS Scanning Mutagenesis

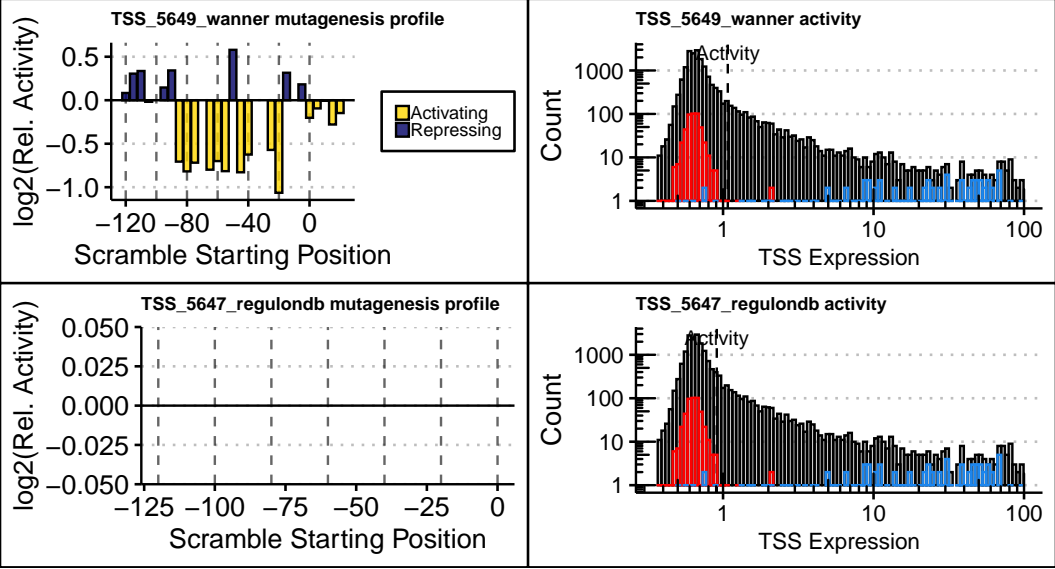


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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