

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yaeP-rof	-	214125	213678

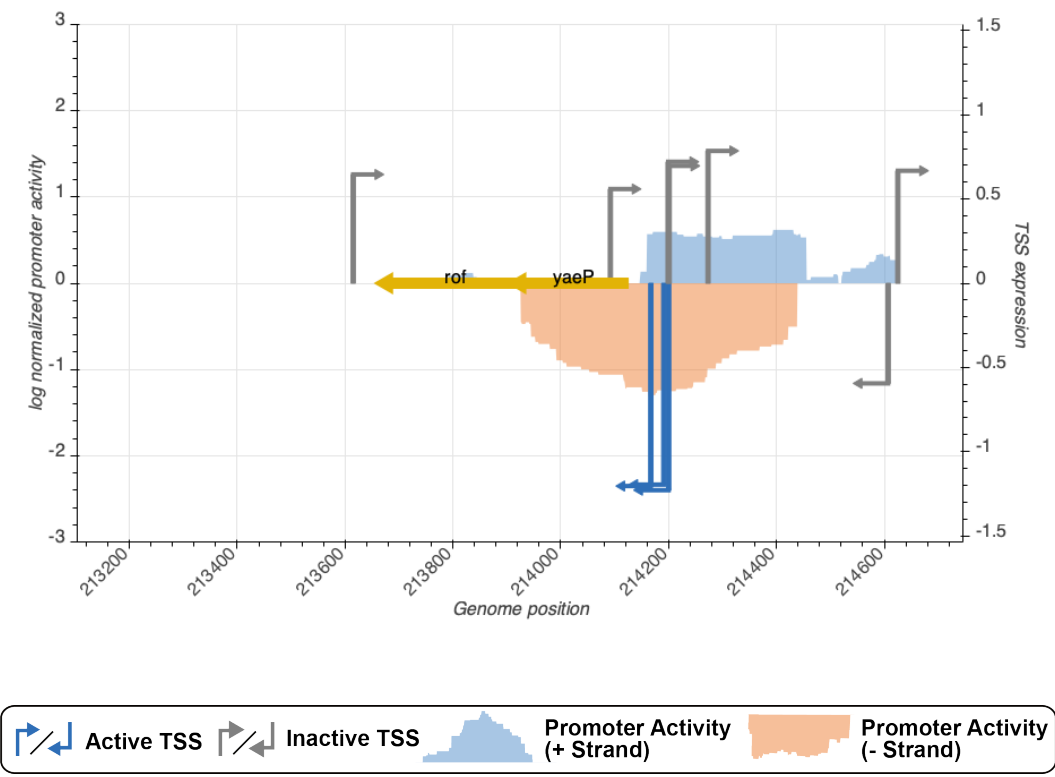


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_924_storz_regulondb	214269	+	0.7858590	inactive
TSS_921_regulondb	214195	+	0.7210740	inactive
TSS_919_regulondb	214163	-	1.2044076	active
TSS_920_regulondb	214187	-	1.1957164	active
TSS_925_storz	214603	-	0.5946460	inactive
TSS_926_storz	214621	+	0.6678672	inactive
TSS_922_wanner	214196	-	1.2289558	active
TSS_923_wanner	214197	+	0.6968530	inactive

TSS Scanning Mutagenesis

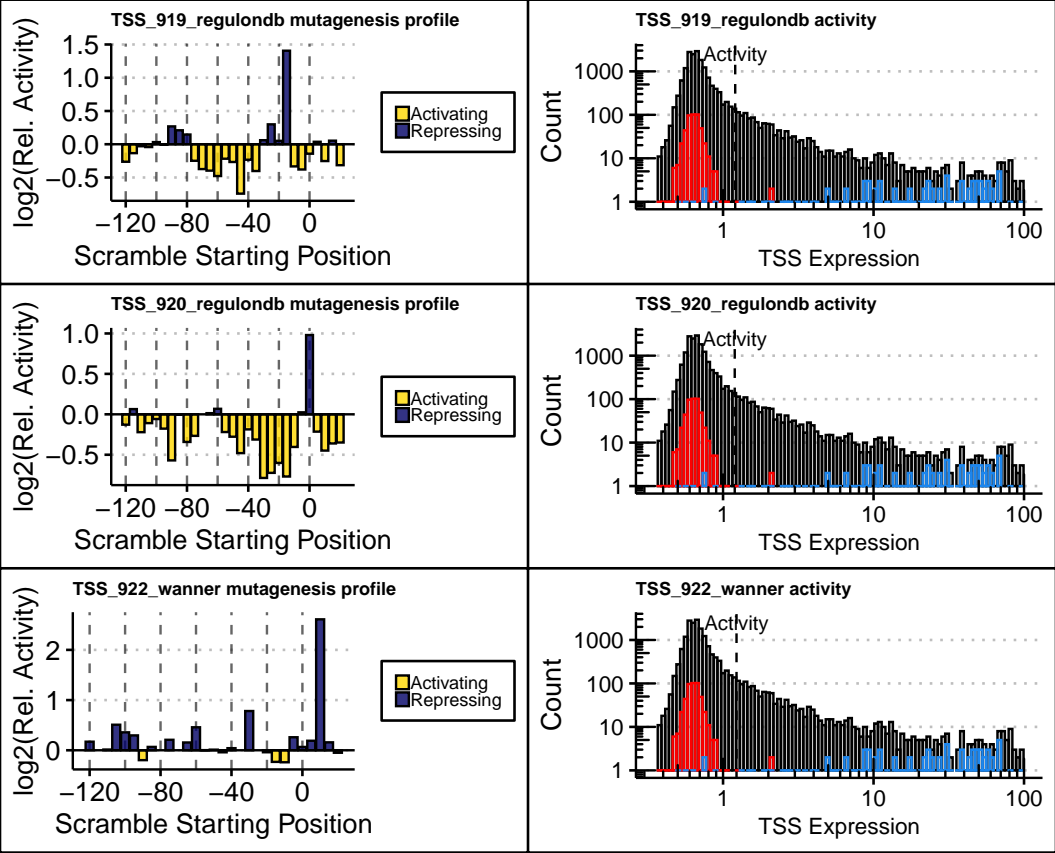


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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