

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yoaE	-	1899609	1898053

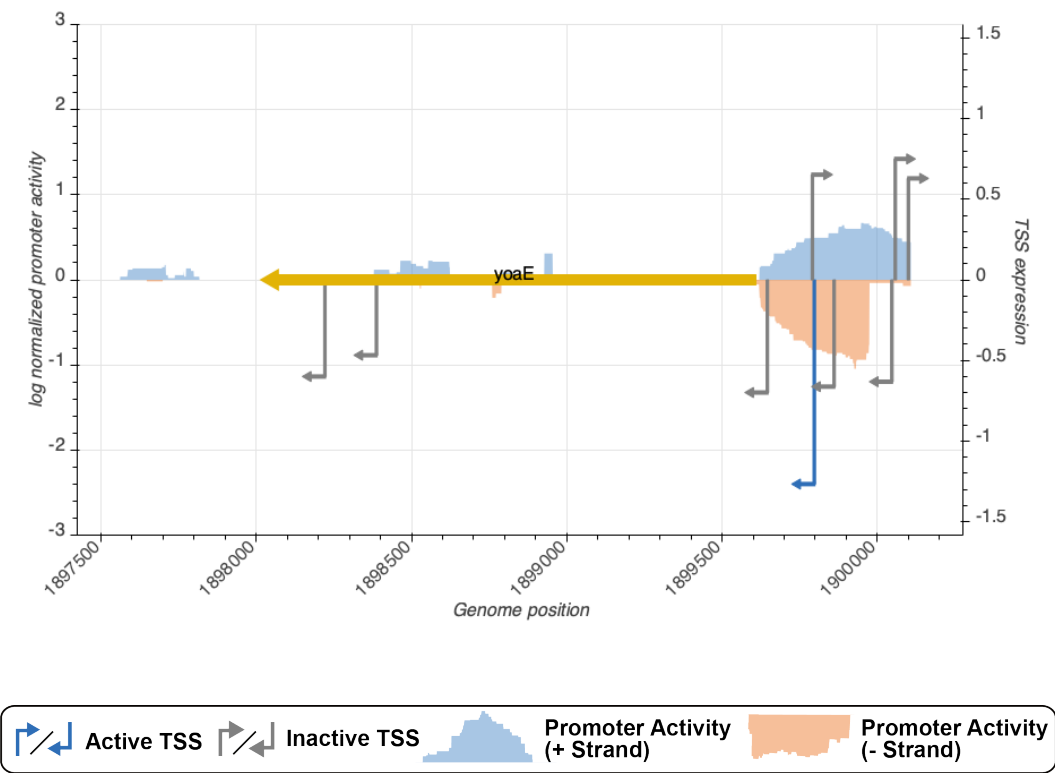


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_7256_storz	1899787	+	0.6524152	inactive
TSS_7260_storz	1900043	-	0.6320261	inactive
TSS_7258_storz	1899857	-	0.6627327	inactive
TSS_7261_regulondb	1900054	+	0.7499652	inactive
TSS_7257_regulondb	1899793	-	1.2670590	active
TSS_7255_storz	1899642	-	0.6991027	inactive
TSS_7262_storz_regulondb	1900096	+	0.6293075	inactive

TSS Scanning Mutagenesis

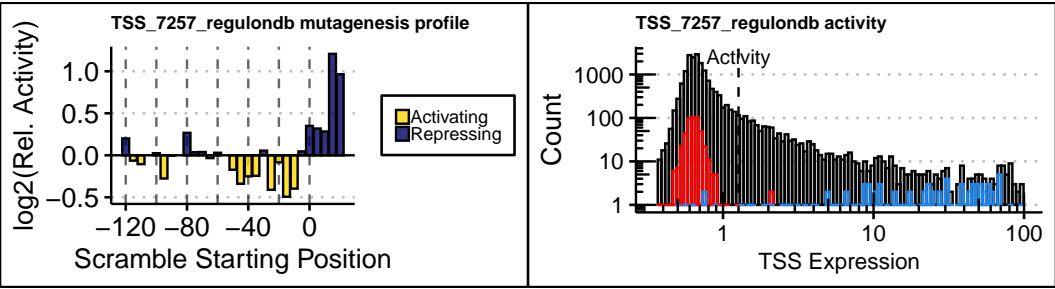


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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