

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yeeX	-	2077385	2077056

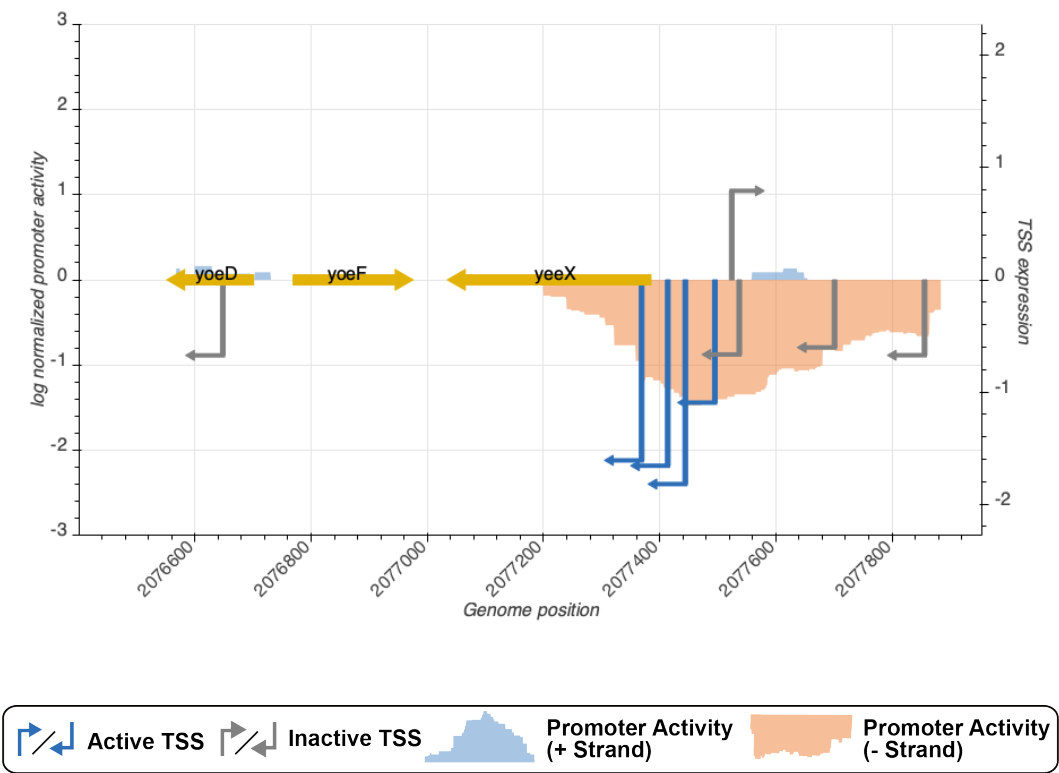


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_7971_wanner	2077697	-	0.6028988	inactive
TSS_7969_storz	2077520	+	0.7931196	inactive
TSS_7966_regulondb	2077410	-	1.6570761	active
TSS_7970_storz	2077533	-	0.6657108	inactive
TSS_7972_wanner	2077852	-	0.6724312	inactive
TSS_7968_storz	2077491	-	1.0945200	active
TSS_7967_regulondb	2077440	-	1.8206838	active

TSS Scanning Mutagenesis

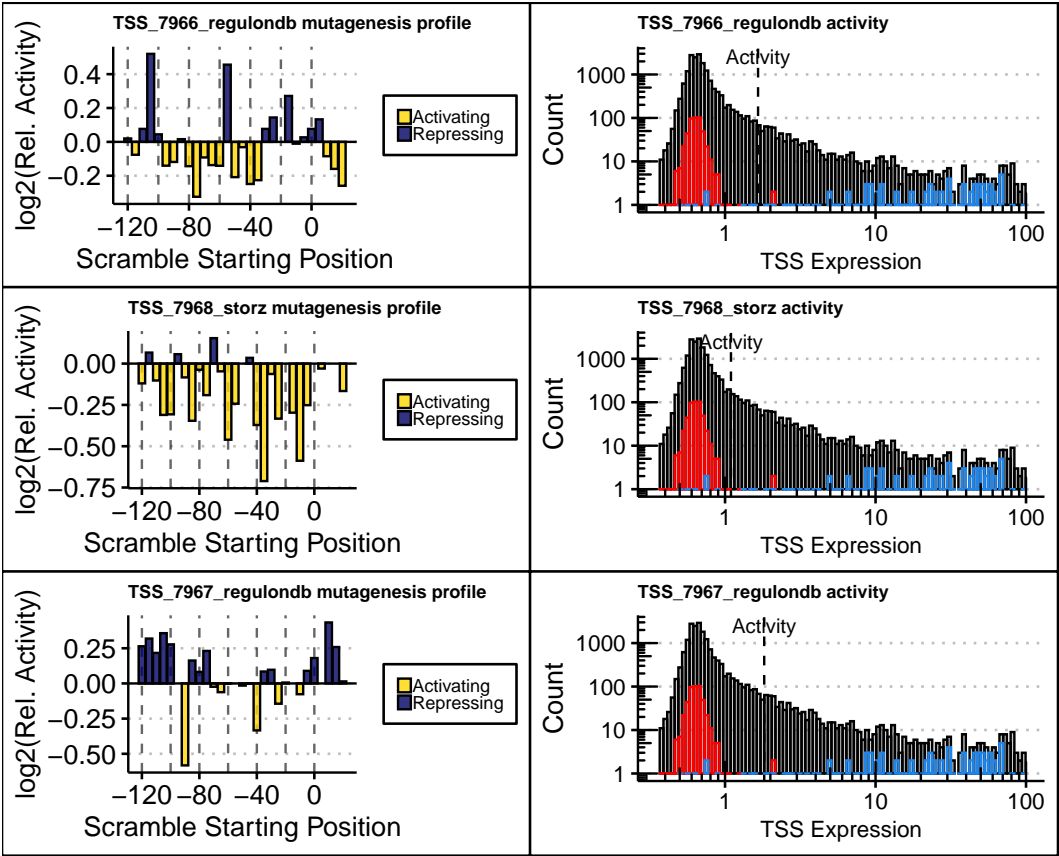


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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