

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ybjQ-amiD	+	903816	904966

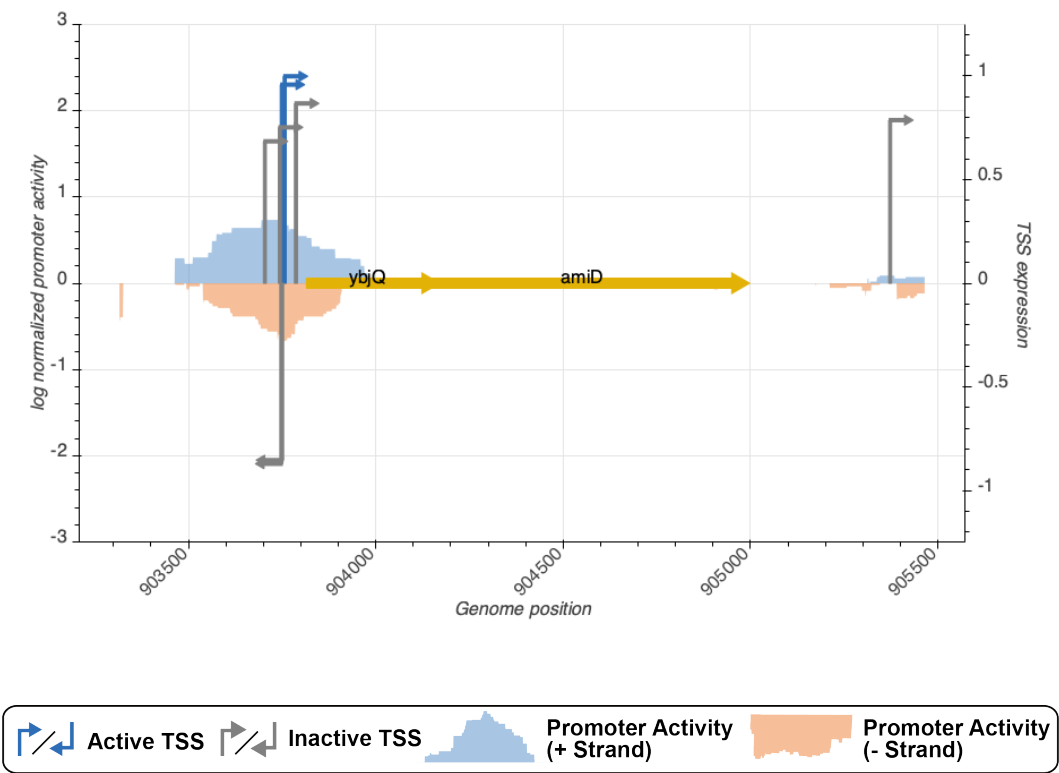


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_3455_regulondb	903700	+	0.6839256	inactive
TSS_3460_regulondb	903753	+	0.9973037	active
TSS_3458_regulondb	903745	+	0.9567799	active
TSS_3457_wanner	903744	-	0.8698869	inactive
TSS_3459_regulondb	903746	-	0.8524655	inactive
TSS_3456_storz_regulondb	903740	+	0.7512542	inactive
TSS_3461_wanner	903783	+	0.8664875	inactive

TSS Scanning Mutagenesis

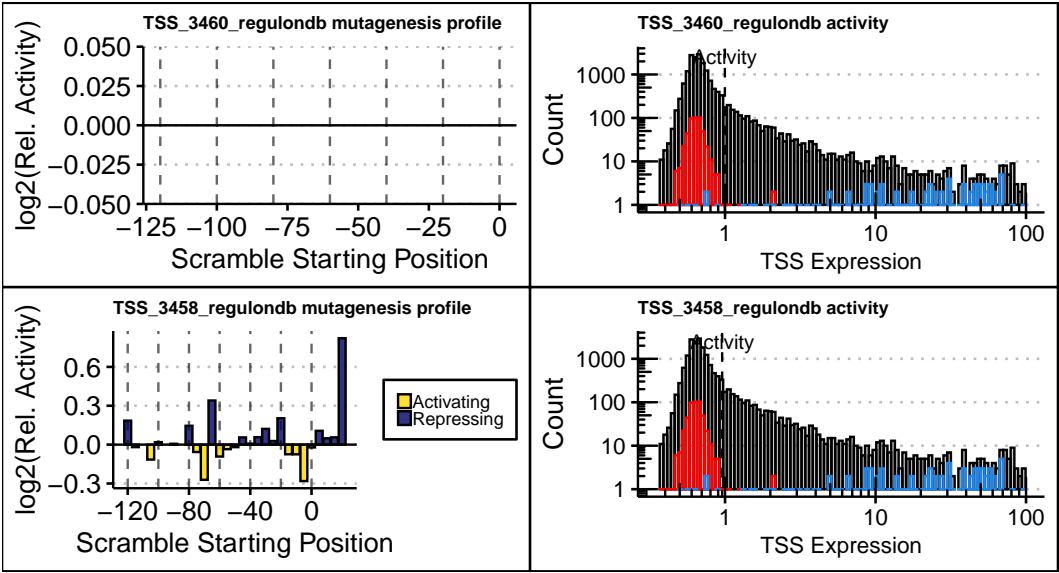


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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