

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
zapB	+	4116538	4116783

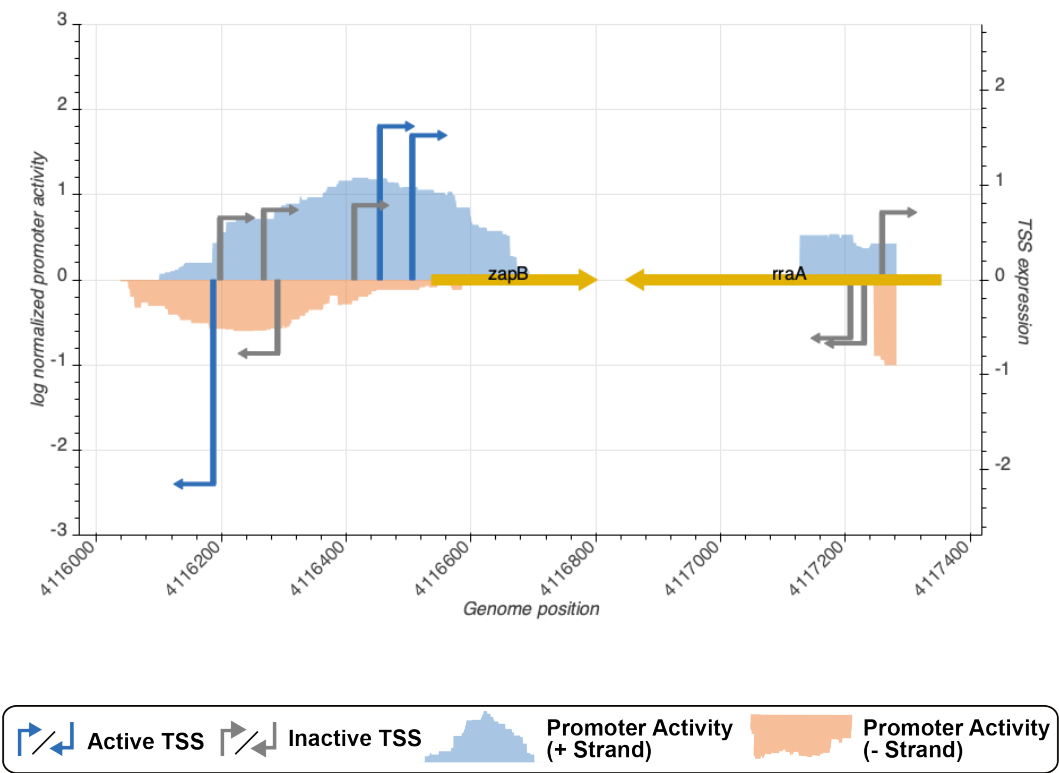


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_16057_regulondb	4116502	+	1.5207514	active
TSS_16056_regulondb	4116450	+	1.6153479	active
TSS_16055_regulondb	4116409	+	0.7838271	inactive
TSS_16051_wanner	4116183	-	2.1498094	active
TSS_16054_storz	4116286	-	0.7747412	inactive
TSS_16053_storz	4116264	+	0.7359923	inactive
TSS_16052_storz	4116194	+	0.6524152	inactive

TSS Scanning Mutagenesis

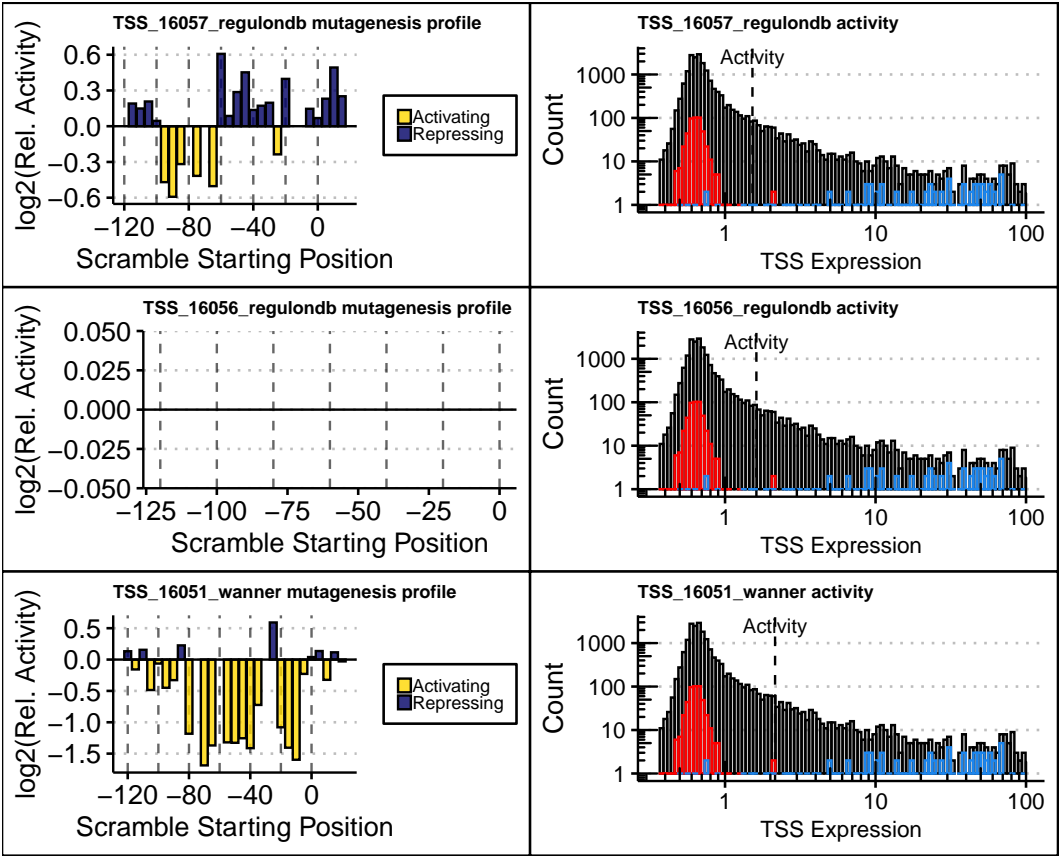


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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