

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
rlmG	-	3233897	3232761

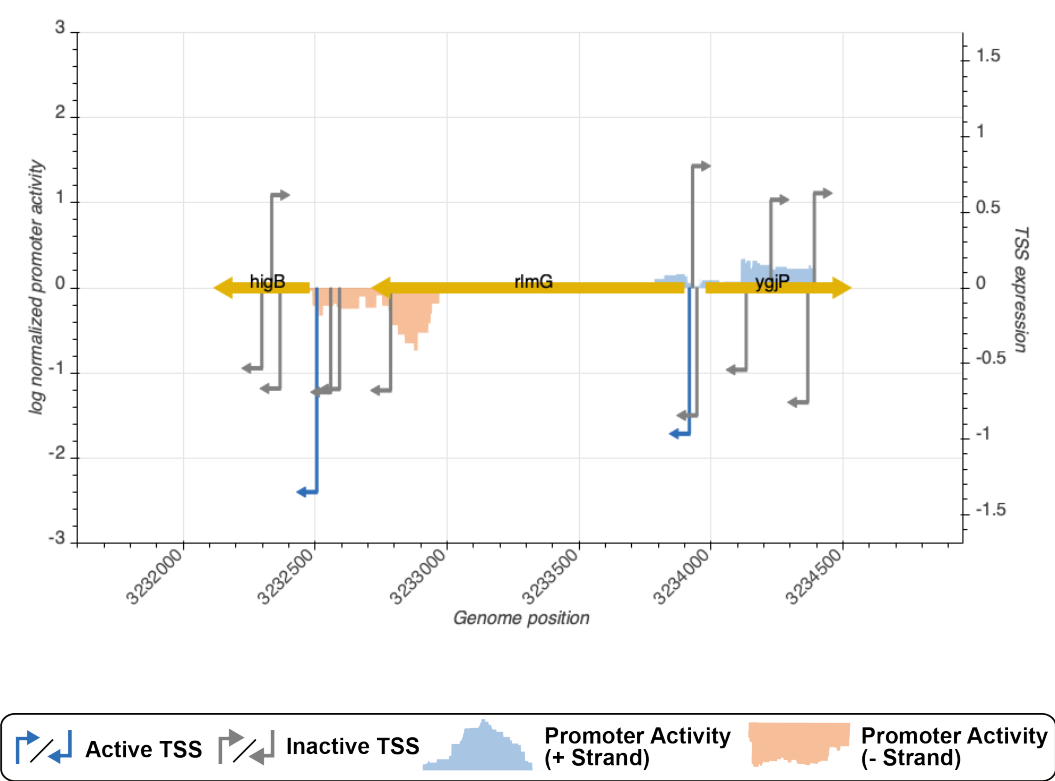


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_12252_wanner	3233942	-	0.8444035	inactive
TSS_12254_storz	3234223	+	0.5830922	inactive
TSS_12253_storz	3234129	-	0.5425398	inactive
TSS_12251_storz	3233926	+	0.8060580	inactive
TSS_12250_regulondb	3233914	-	0.9658242	active
TSS_12256_regulondb	3234387	+	0.6264219	inactive
TSS_12255_storz	3234362	-	0.7580130	inactive

TSS Scanning Mutagenesis

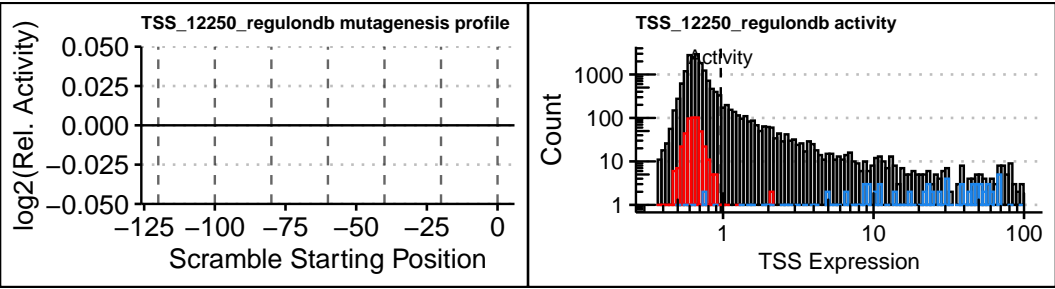


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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