

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
amiC	-	2947032	2945779

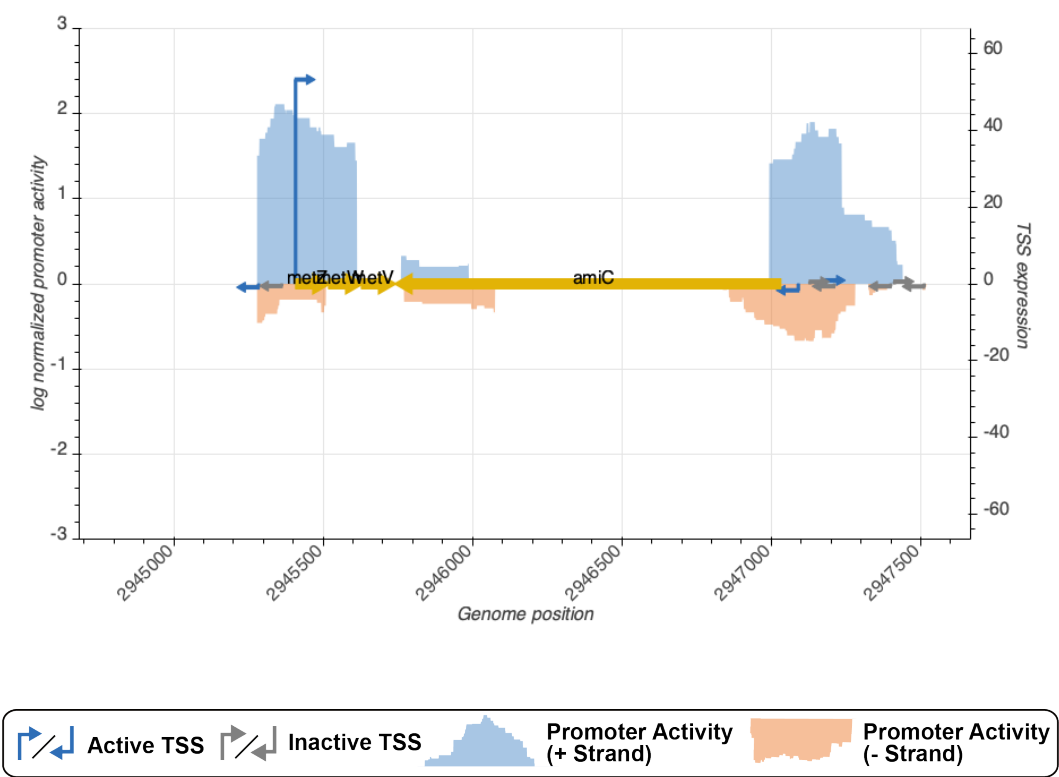


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_11137_storz	2947507	-	0.6880224	inactive
TSS_11132_storz	2947125	+	0.5588842	inactive
TSS_11131_regulondb	2947086	-	1.6841737	active
TSS_11135_storz	2947395	-	0.6359097	inactive
TSS_11134_wanner	2947206	-	0.6263604	inactive
TSS_11136_storz	2947408	+	0.5986308	inactive
TSS_11133_regulondb	2947178	+	0.9106603	active

TSS Scanning Mutagenesis

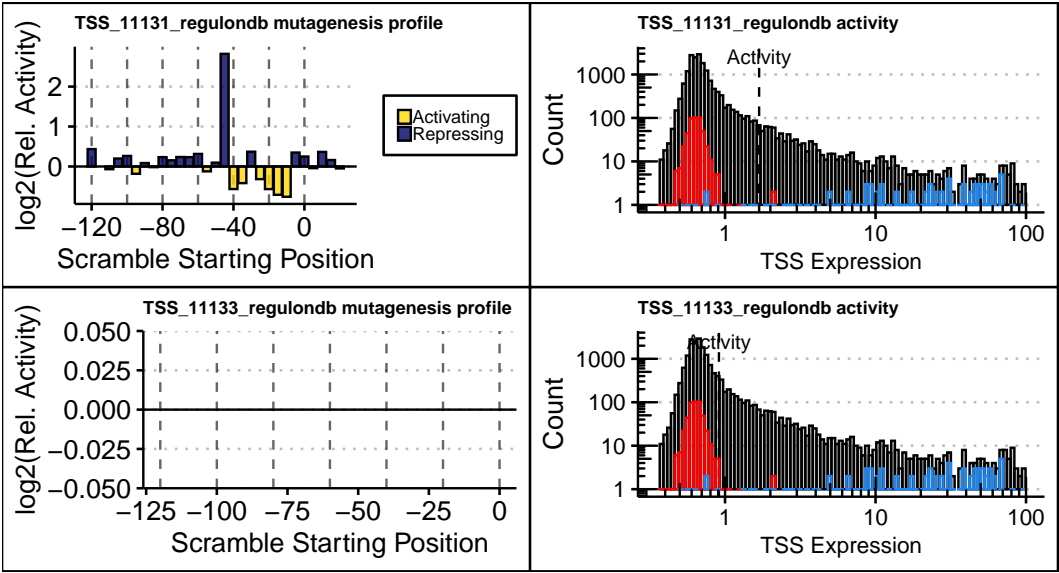


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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