

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
nuoABCEFGHIJKLMN	-	2403094	2388070

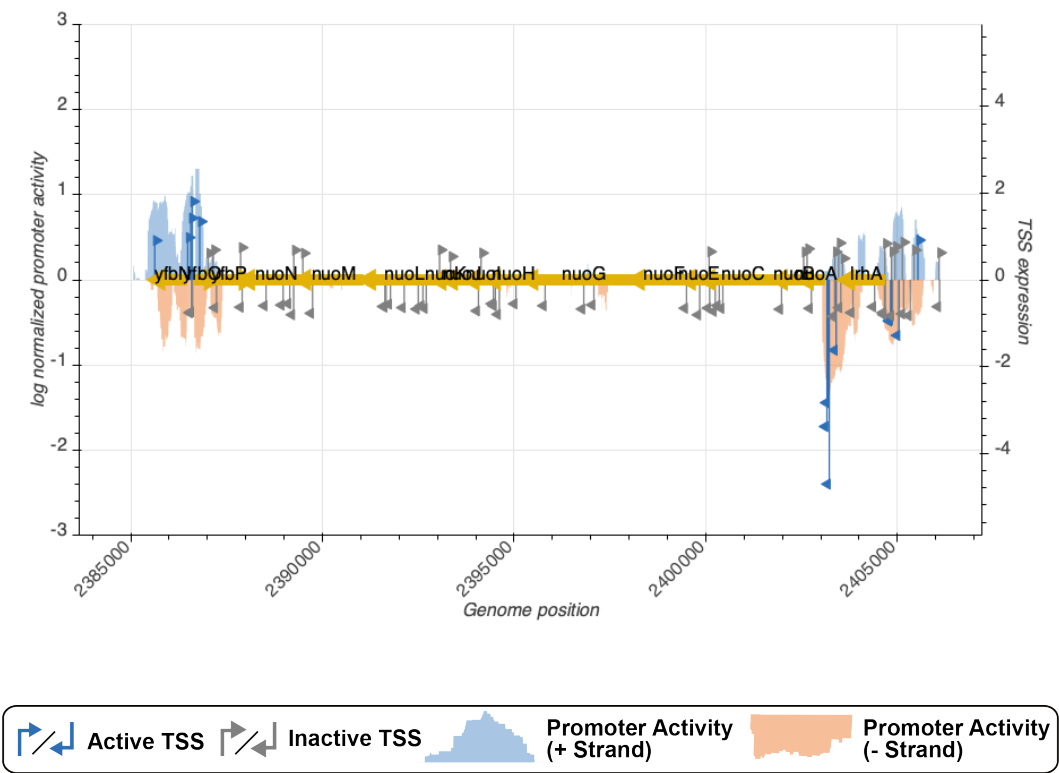


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_9053_storz	2403564	+	0.4934919	inactive
TSS_9052_storz	2403520	-	0.6417024	inactive
TSS_9051_storz_wanner	2403463	+	0.8495002	inactive
TSS_9047_storz	2403219	-	4.7149350	active
TSS_9045_regulondb	2403158	-	3.3866083	active
TSS_9048_regulondb	2403357	-	0.8449008	inactive
TSS_9050_storz_wanner	2403399	-	1.6242355	active
TSS_9049_storz	2403362	+	0.6444824	inactive
TSS_9046_regulondb	2403184	-	2.8367090	active

TSS Scanning Mutagenesis

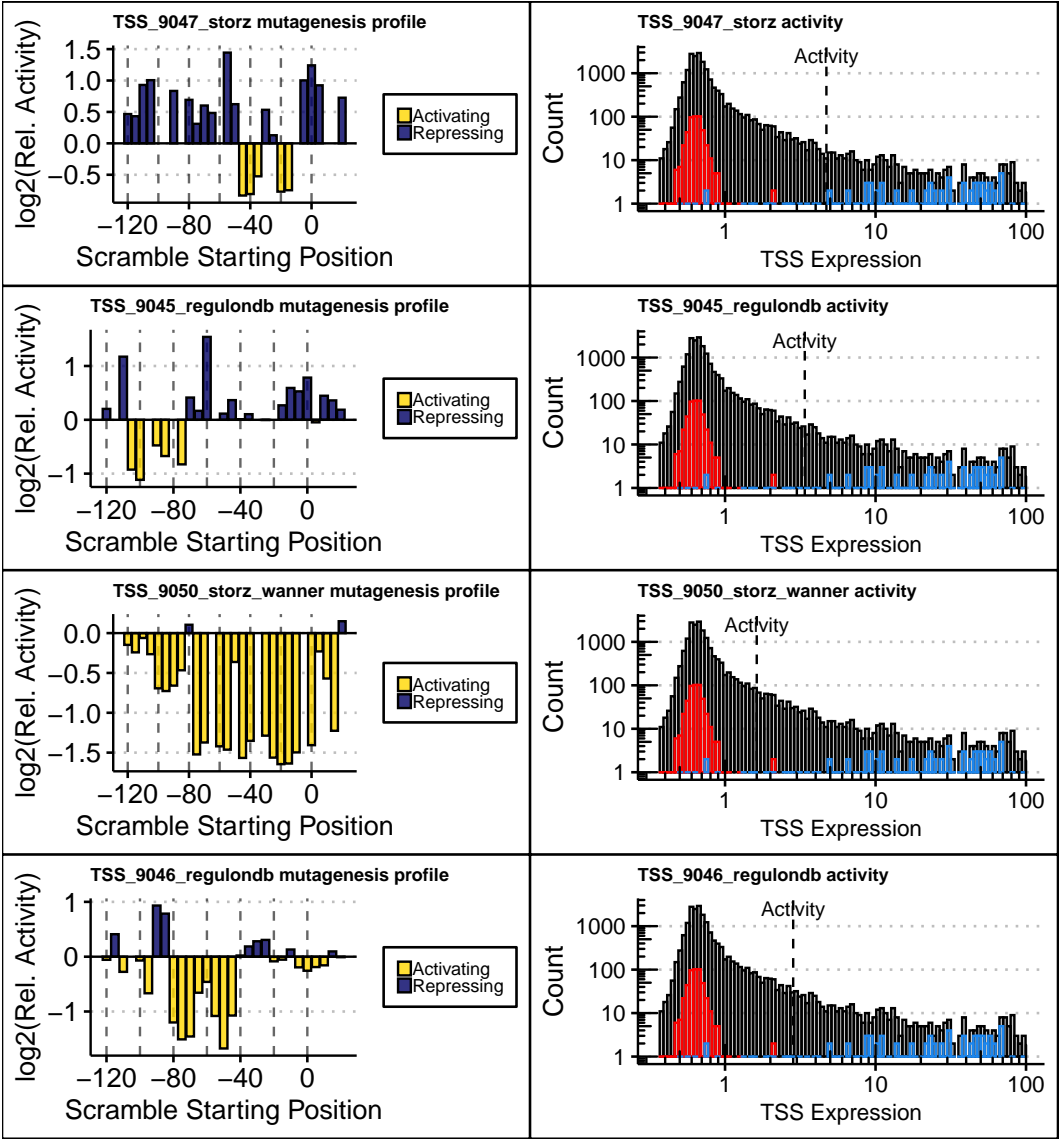


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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