Operon Promoter Landscape

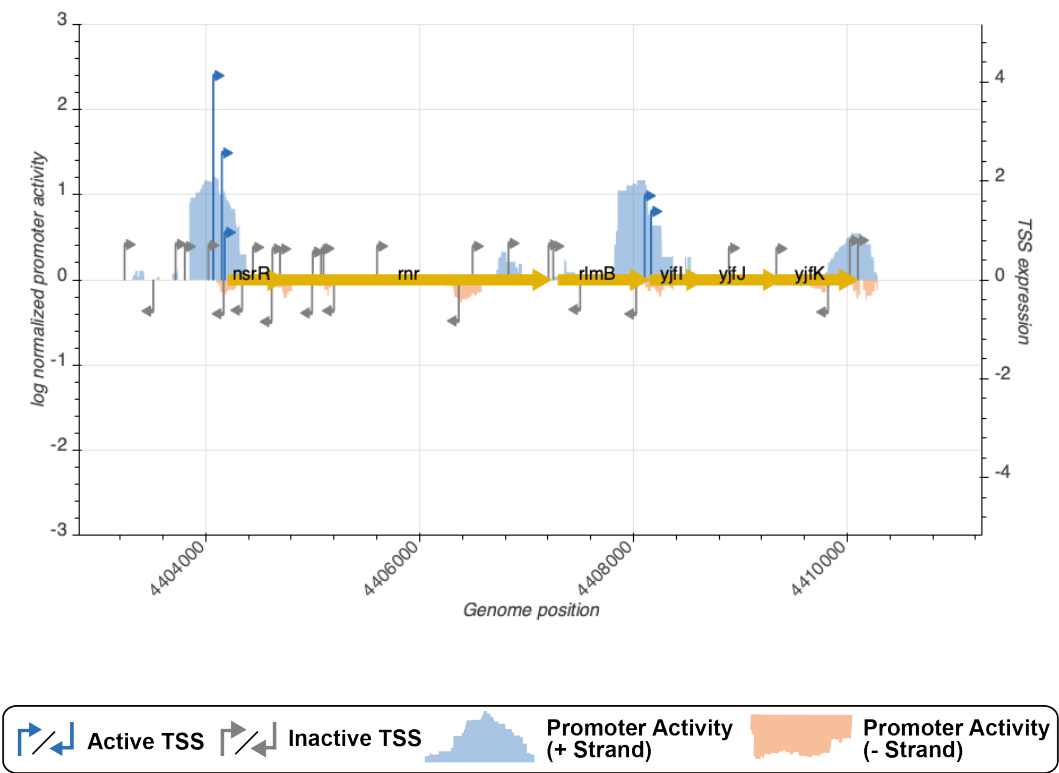| Operon	Strand	Operon start	Operon end
nsrR-rnr-rlmB-yjfIJ	+	4404213	4409274

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_17224_storz	4403714	+	0.7194000	inactive
TSS_17230_storz	4404174	+	0.9580455	active
TSS_17229_storz	4404164	-	0.6852524	inactive
TSS_17227_regulondb	4404067	+	4.1261203	active
TSS_17228_storz	4404147	+	2.5634454	active
TSS_17225_regulondb	4403800	+	0.6718212	inactive
TSS_17226_storz	4404020	+	0.6959095	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).

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