Operon Promoter Landscape

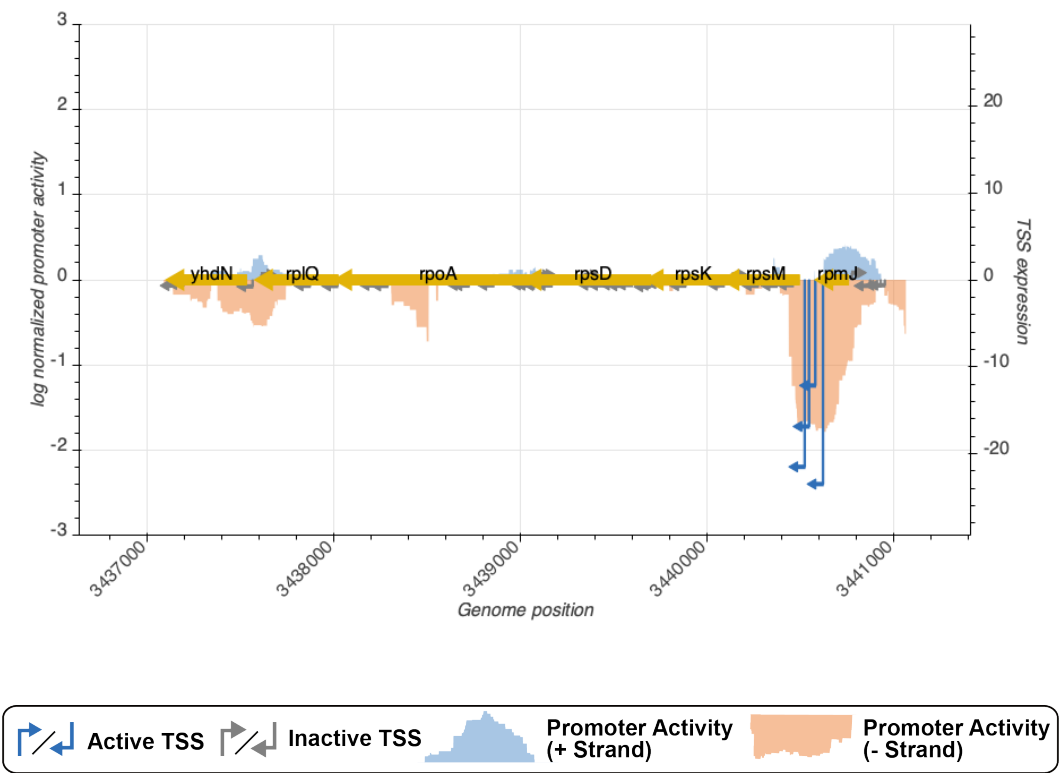| Operon	Strand	Operon start	Operon end
rpsMKD-rpoA-rplQ	-	3440493	3437638

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_13219_regulondb	3440540	-	16.8718100	active
TSS_13222_storz	3440770	+	0.8189202	inactive
TSS_13223_regulondb	3440867	-	0.6951803	inactive
TSS_13224_regulondb	3440924	-	0.6301172	inactive
TSS_13220_regulondb	3440574	-	12.1610610	active
TSS_13225_regulondb	3440946	-	0.6220556	inactive
TSS_13218_regulondb	3440517	-	21.5181191	active
TSS_13221_regulondb	3440615	-	23.5014388	active

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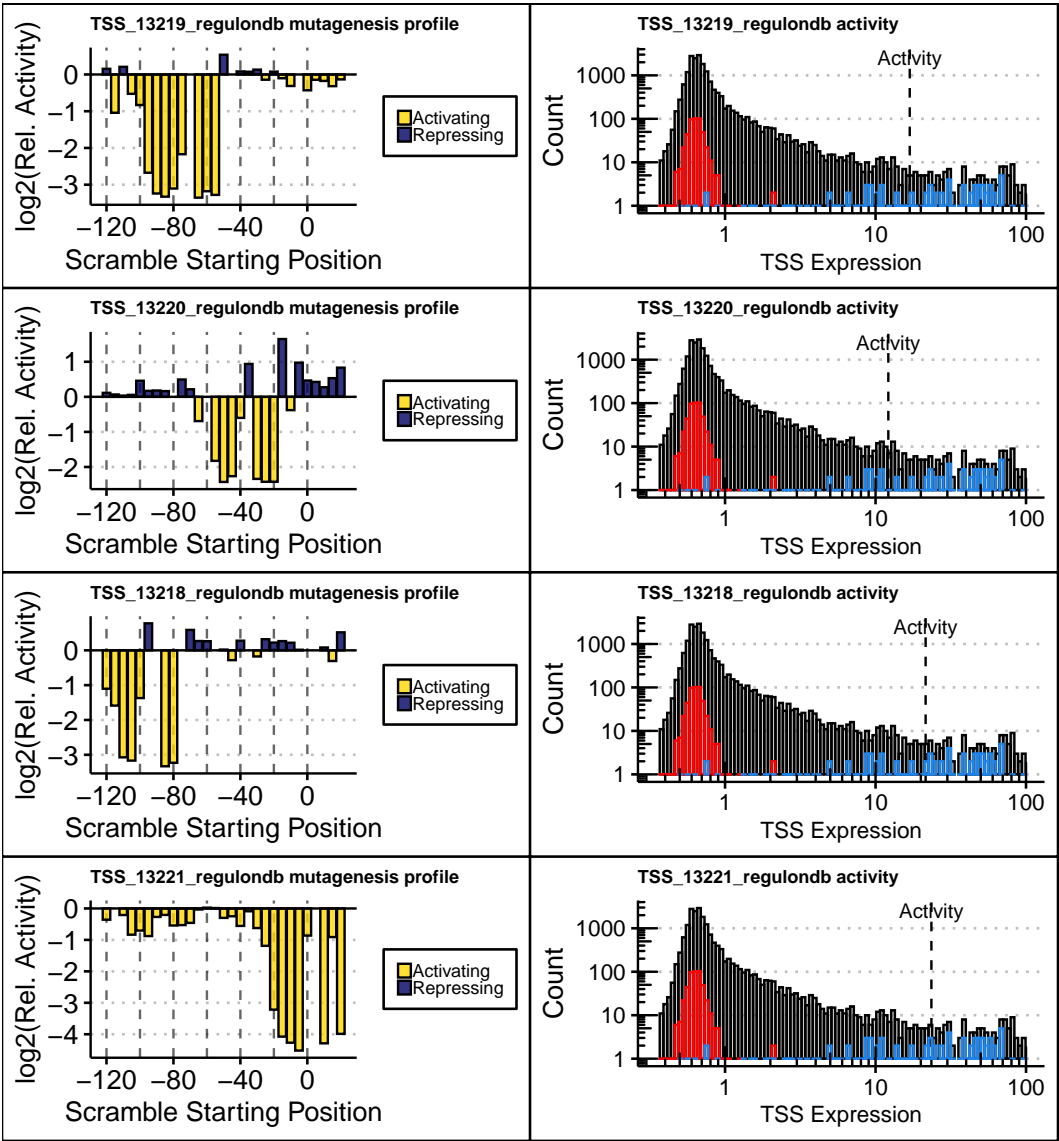
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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

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