Operon Promoter Landscape

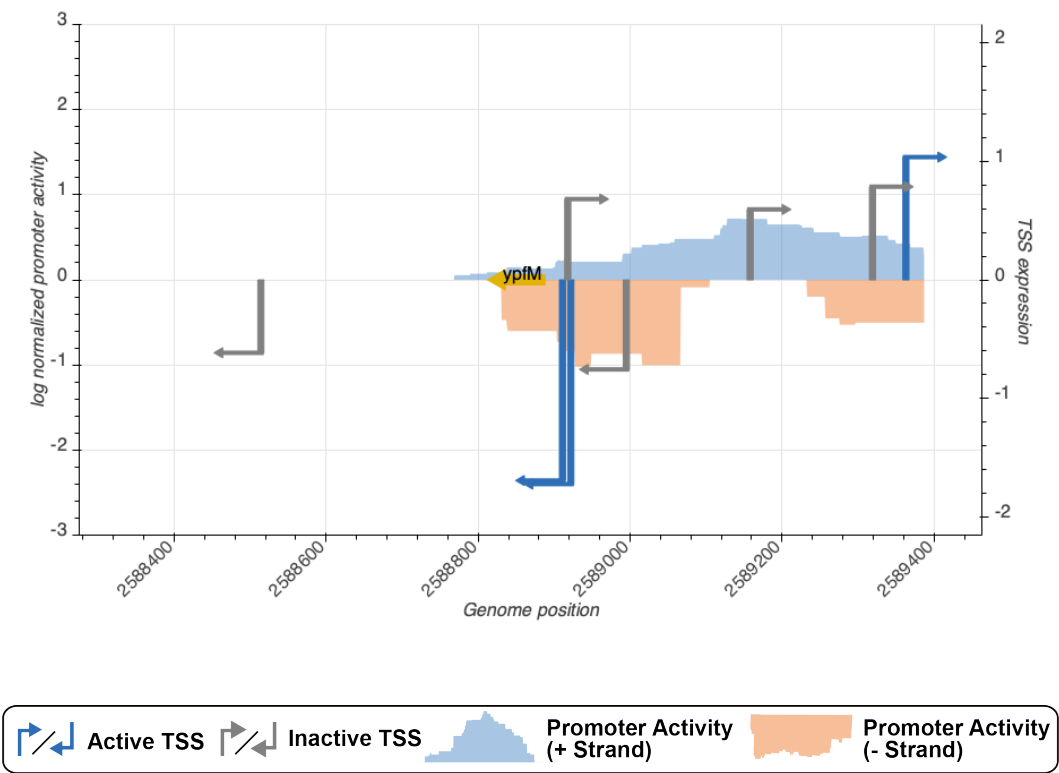| Operon	Strand	Operon start	Operon end
ypfM	-	2588888	2588829

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_9739_storz	2588914	+	0.6797692	inactive
TSS_9738_regulondb	2588907	-	1.6888071	active
TSS_9740_regulondb	2588918	-	1.7187668	active
TSS_9745_regulondb	2589359	+	1.0326578	active
TSS_9741_wanner	2588991	-	0.7541378	inactive
TSS_9744_regulondb	2589315	+	0.7834724	inactive
TSS_9743_storz	2589154	+	0.5922956	inactive

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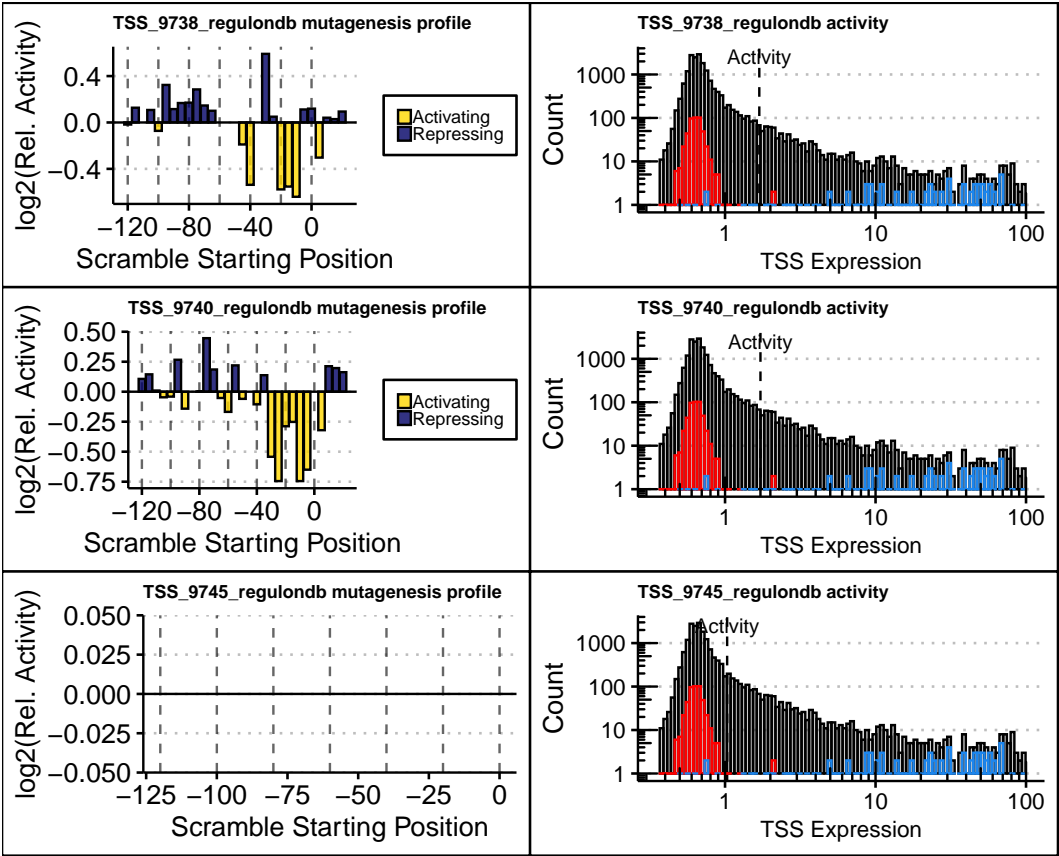
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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