Operon Promoter Landscape

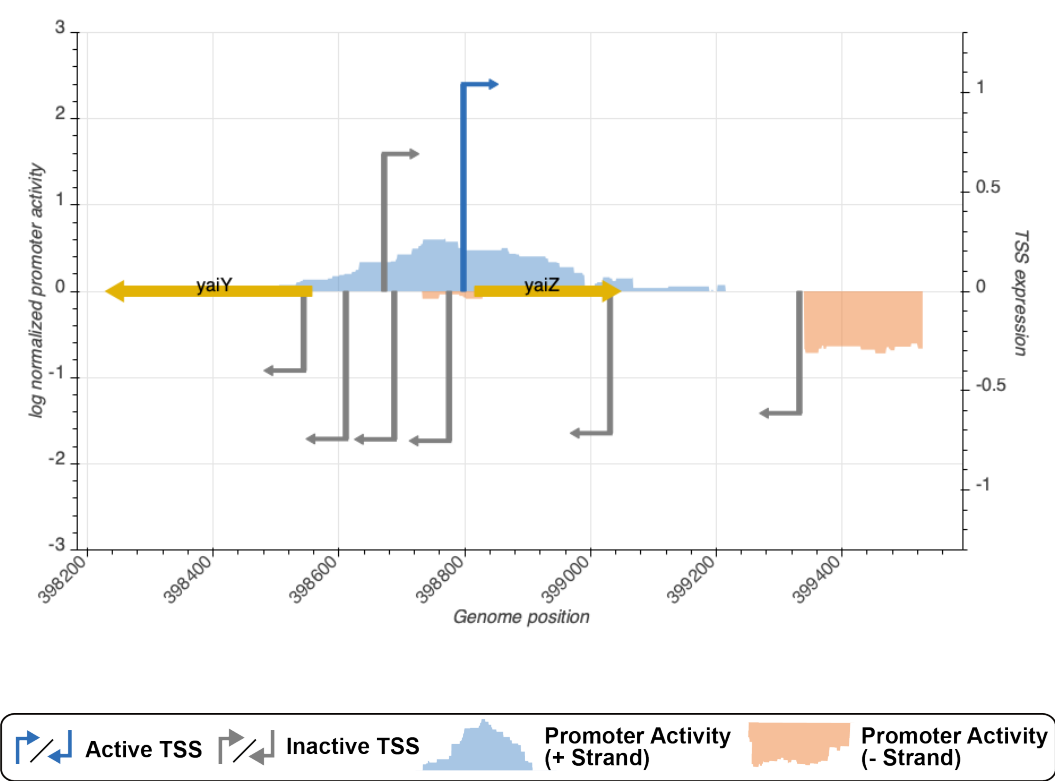| Operon	Strand	Operon start	Operon end
yaiZ	+	398817	399029

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

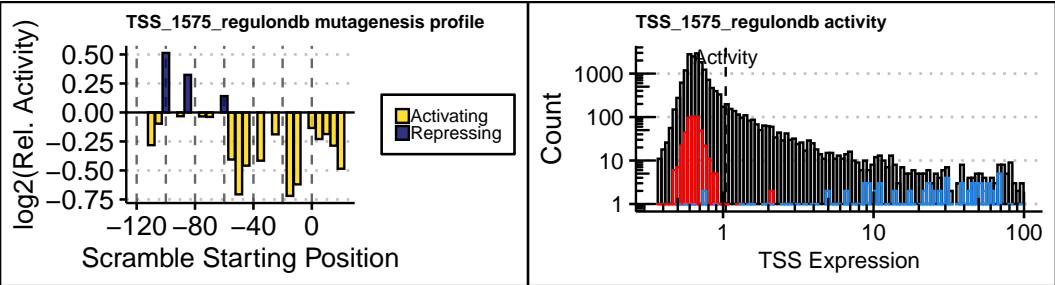| TSS name	TSS position	Strand	TSS activity	Category
TSS_1572_storz_regulondb	398668	+	0.6909279	inactive
TSS_1574_regulondb	398771	-	0.7529025	inactive
TSS_1573_regulondb	398684	-	0.7452456	inactive
TSS_1575_regulondb	398794	+	1.0413885	active
TSS_1571_wanner	398607	-	0.7431024	inactive
TSS_1570_storz	398540	-	0.3993270	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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