Operon Promoter Landscape

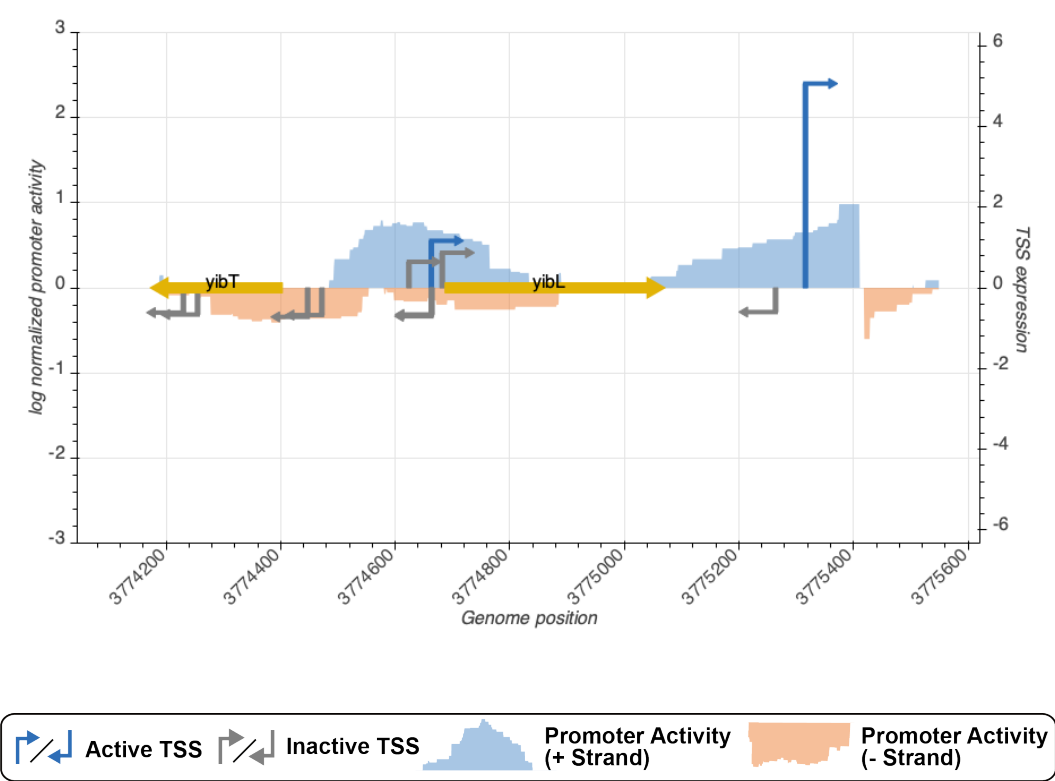| Operon	Strand	Operon start	Operon end
yibL	+	3774688	3775050

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_14623_regulondb	3774443	-	0.7202744	inactive
TSS_14626_wanner	3774659	-	0.7052534	inactive
TSS_14622_storz	3774251	-	0.6622272	inactive
TSS_14628_storz	3774660	-	0.6604324	inactive
TSS_14629_wanner	3774678	+	0.8695032	inactive
TSS_14621_storz	3774226	-	0.6139024	inactive
TSS_14627_regulondb	3774659	+	1.1666448	active
TSS_14625_regulondb	3774620	+	0.6456617	inactive
TSS_14624_wanner	3774468	-	0.6755228	inactive

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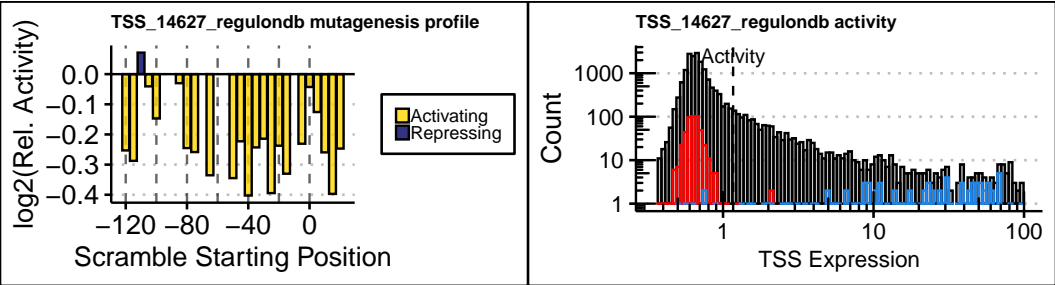
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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