Operon Promoter Landscape
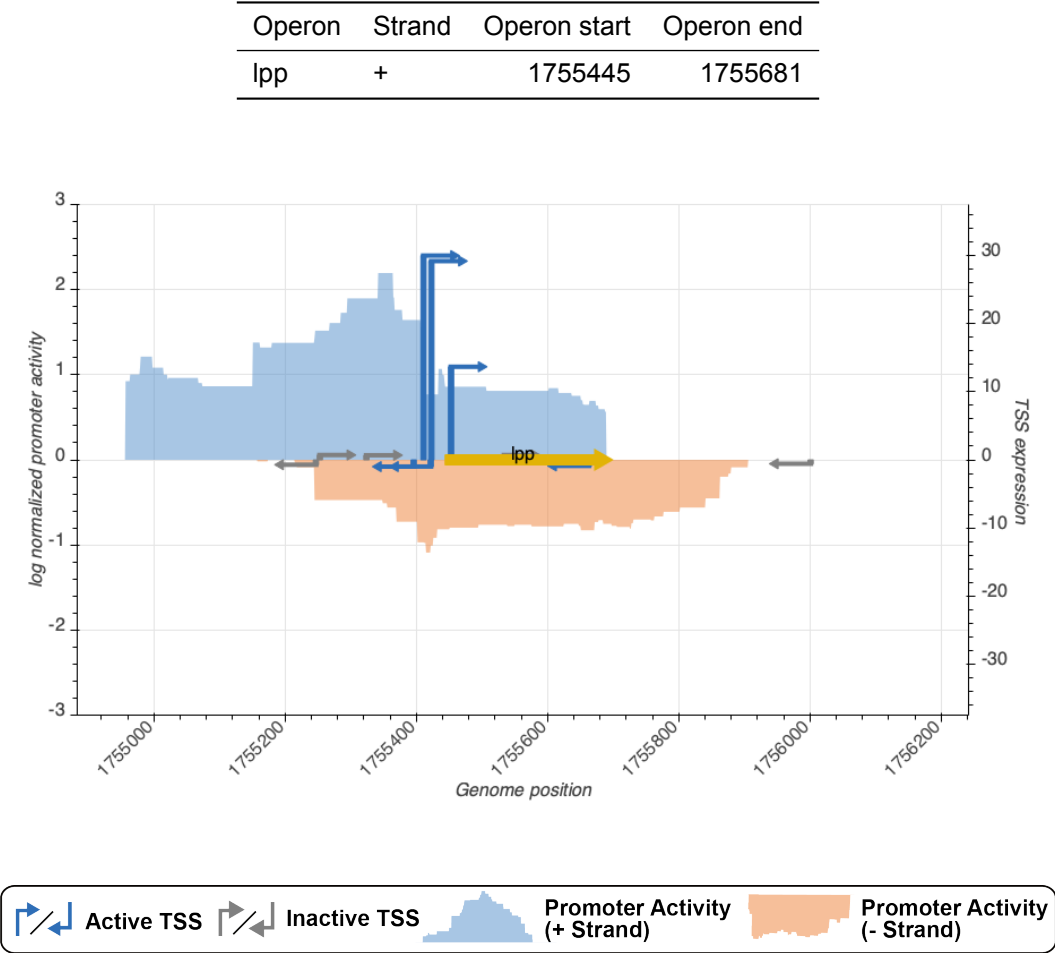
Operon	Strand	Operon start	Operon end
lpp	+	1755445	1755681

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_6746_storz	1755243	-	0.7175593	inactive
TSS_6752_regulondb	1755419	+	29.1629045	active
TSS_6751_wanner	1755418	-	0.9891953	active
TSS_6748_regulondb	1755320	+	0.6750625	inactive
TSS_6749_storz	1755392	-	0.9967282	active
TSS_6750_storz_regulondb	1755407	+	29.9700768	active
TSS_6747_storz	1755249	+	0.7072268	inactive

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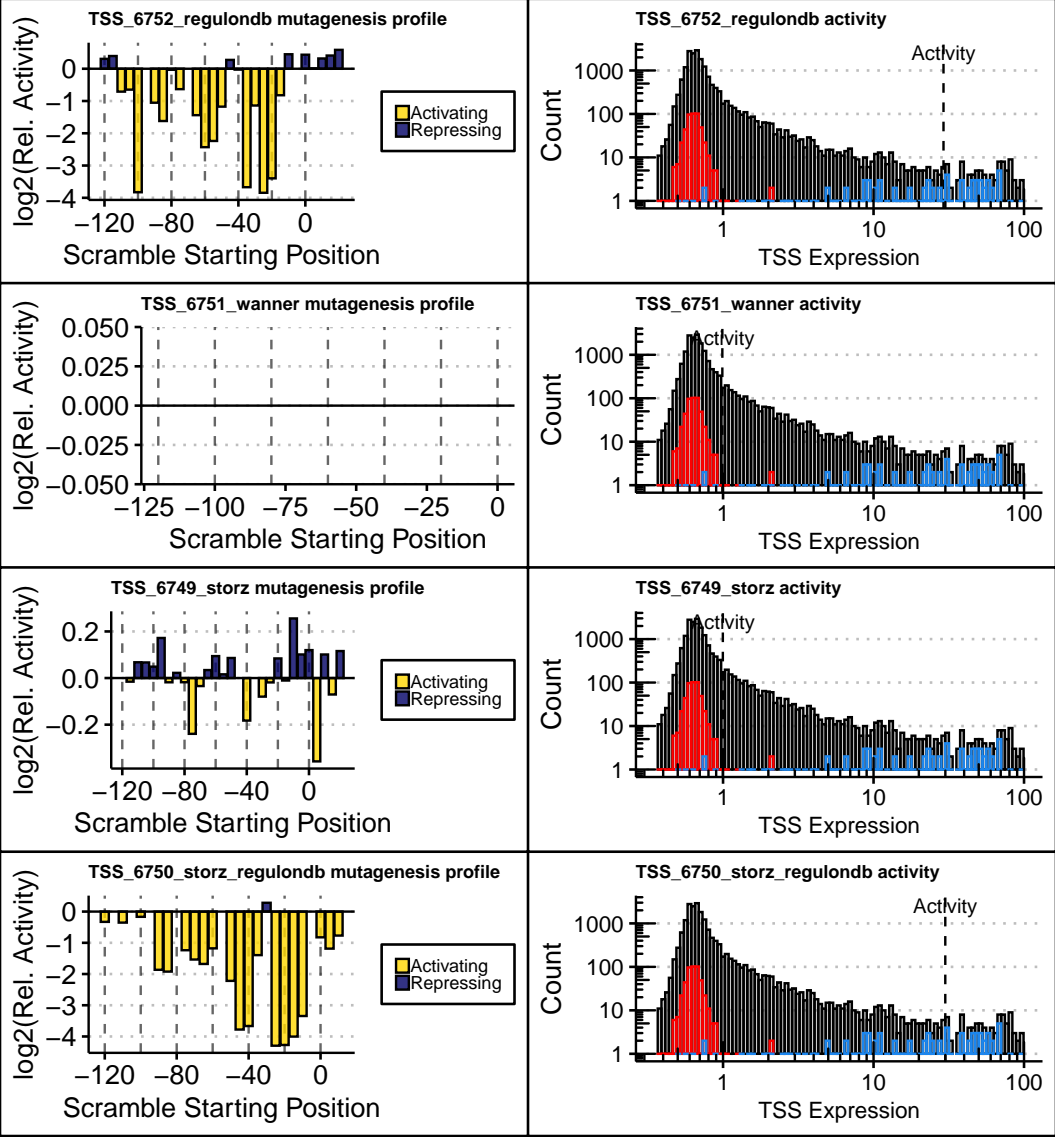
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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