Operon Promoter Landscape
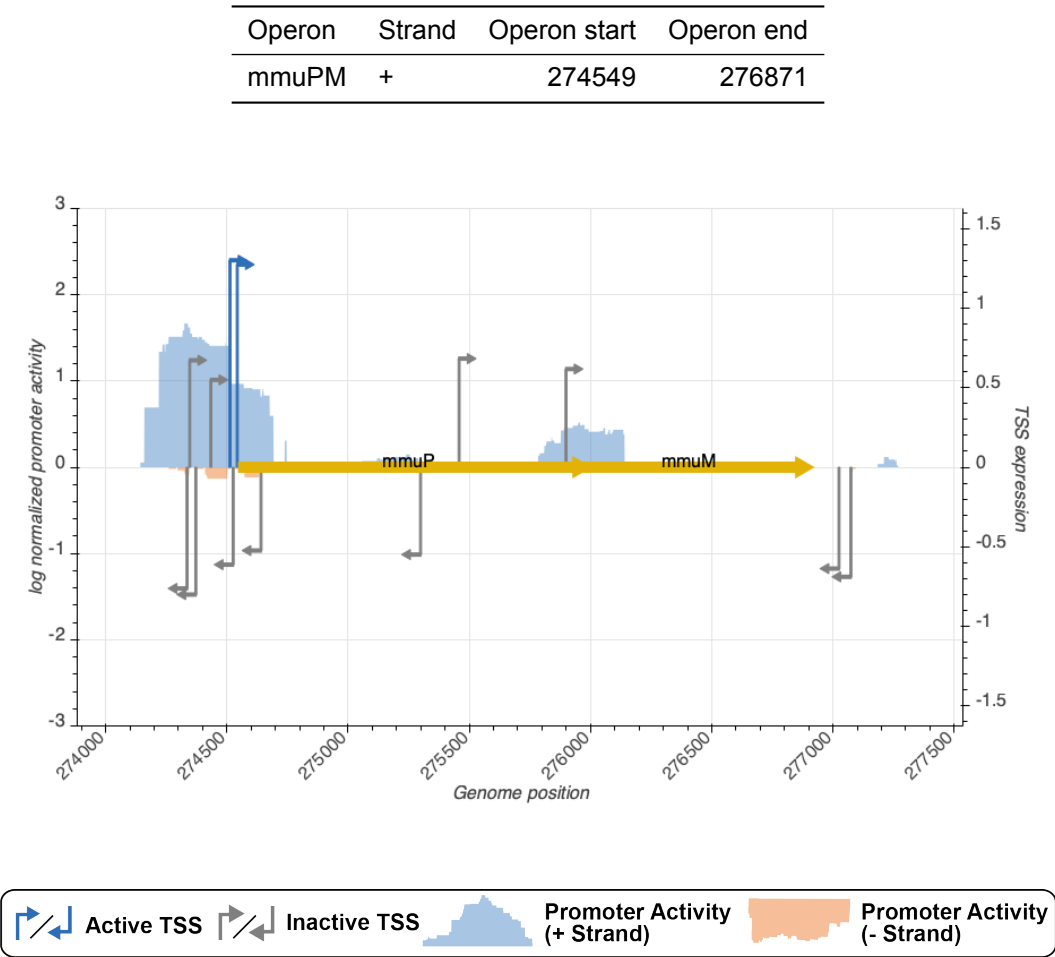
Operon	Strand	Operon start	Operon end
mmuPM	+	274549	276871

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_1173_storz	274368	-	0.8024896	inactive
TSS_1172_regulondb	274343	+	0.6742580	inactive
TSS_1177_regulondb	274539	+	1.2773845	active
TSS_1176_regulondb	274522	-	0.6139024	inactive
TSS_1175_regulondb	274509	+	1.3043211	active
TSS_1171_storz_regulondb	274332	-	0.7638980	inactive
TSS_1174_regulondb	274430	+	0.5504818	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).