Operon Promoter Landscape

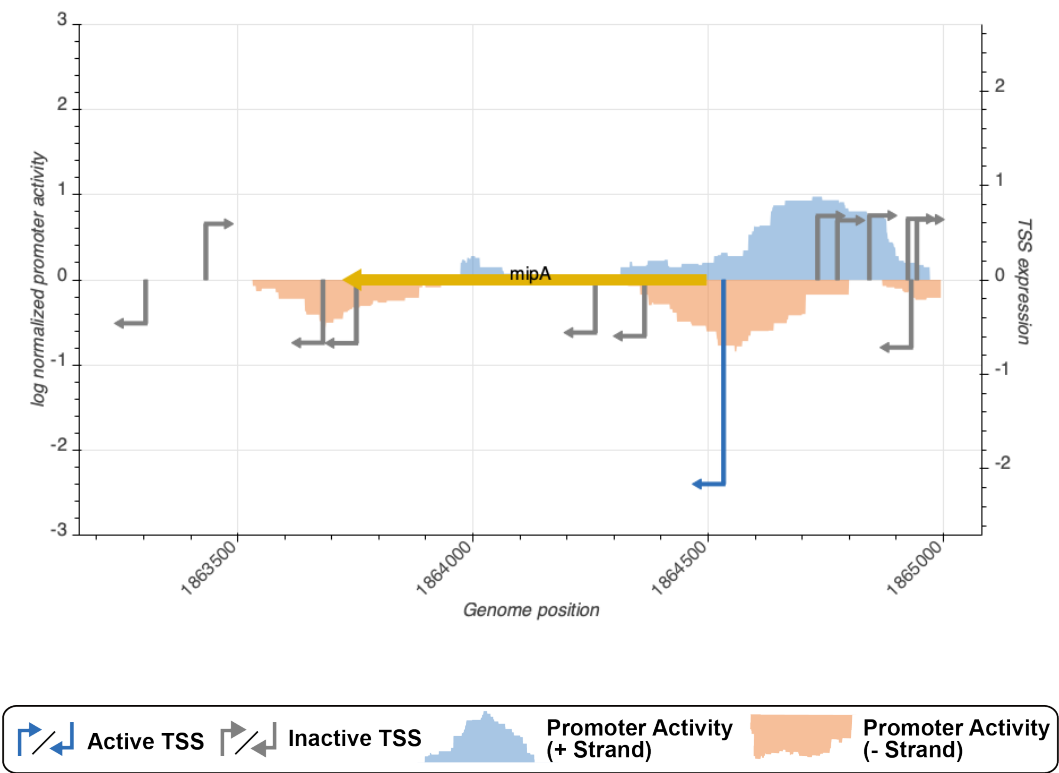| Operon	Strand	Operon start	Operon end
mipA	-	1864496	1863750

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_7125_wanner	1864529	-	2.1614418	active
TSS_7130_storz	1864928	-	0.7158358	inactive
TSS_7129_storz	1864921	+	0.6455196	inactive
TSS_7127_storz	1864771	+	0.6293075	inactive
TSS_7131_storz	1864940	+	0.6383318	inactive
TSS_7126_wanner	1864729	+	0.6765543	inactive
TSS_7128_regulondb	1864839	+	0.6802152	inactive

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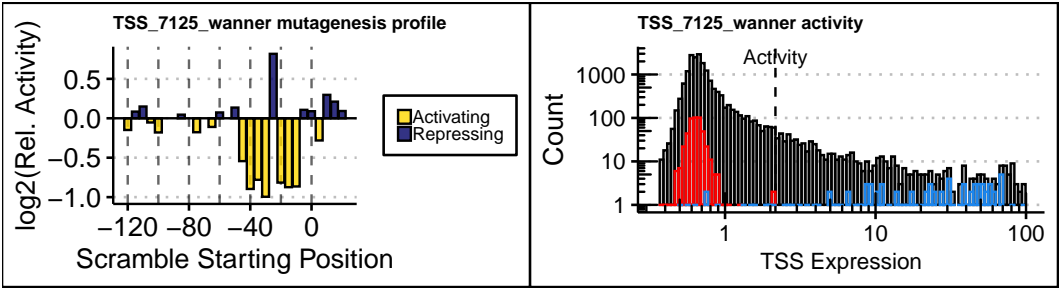
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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