Operon Promoter Landscape
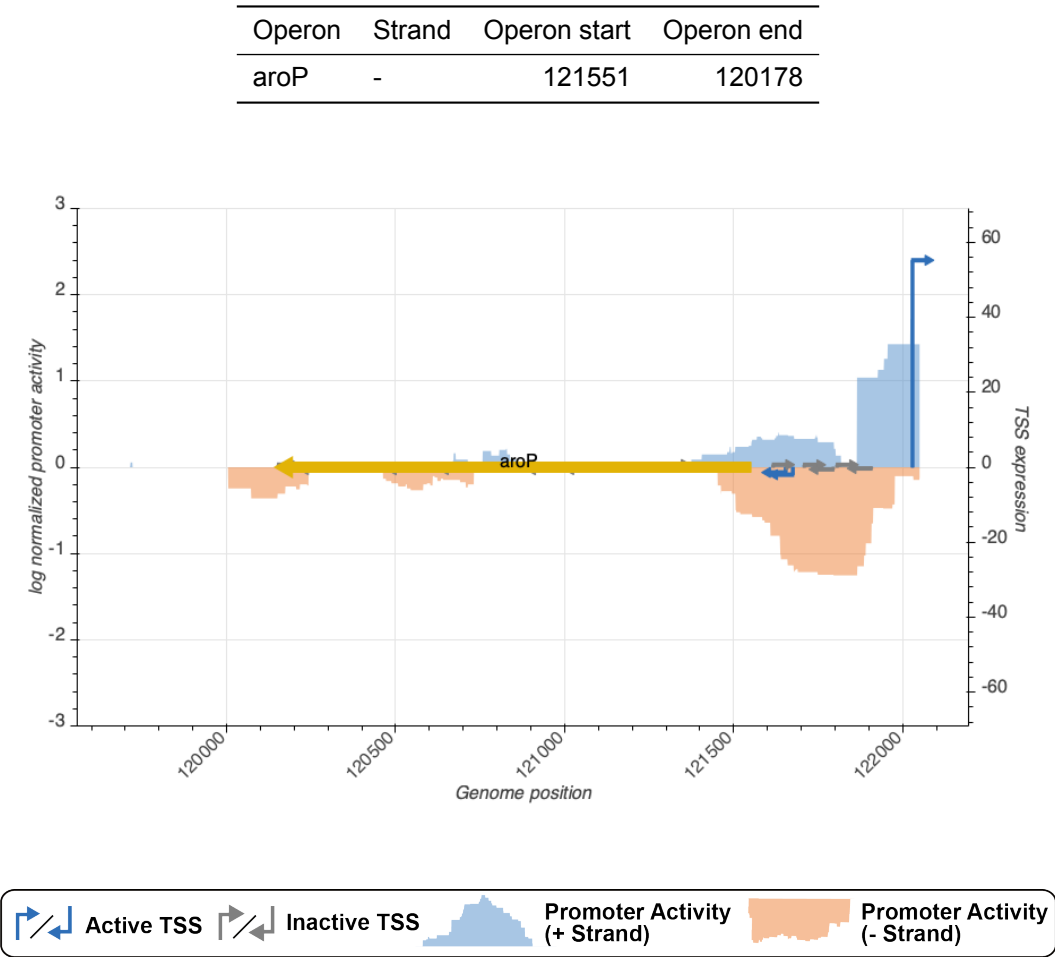
Operon	Strand	Operon start	Operon end
aroP	-	121551	120178

Active TSS   **Inactive TSS**   **Promoter Activity (+ Strand)**   **Promoter Activity (- Strand)**

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_515_storz	121705	+	0.6402208	inactive
TSS_514_regulondb	121671	-	1.9946073	active
TSS_519_storz	122025	+	55.2247499	active
TSS_513_regulondb	121650	-	1.3904379	active
TSS_517_storz	121802	+	0.6536615	inactive
TSS_512_storz	121613	+	0.6734608	inactive
TSS_516_storz	121790	-	0.5720355	inactive
TSS_518_storz	121903	-	0.3287941	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).