Operon Promoter Landscape

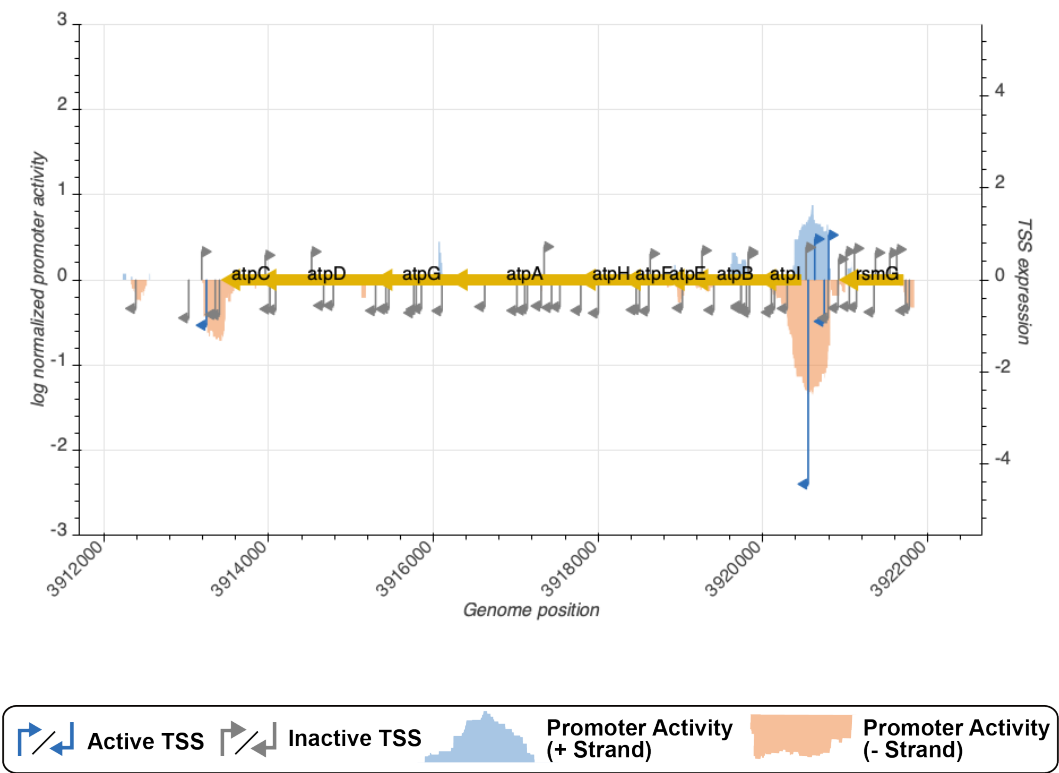| Operon	Strand	Operon start	Operon end
atpIBEFHAGDC	-	3920463	3913576

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_15202_storz	3920789	-	0.8322686	inactive
TSS_15204_storz	3920910	-	0.6146697	inactive
TSS_15201_storz	3920743	-	0.9048316	active
TSS_15199_wanner	3920547	-	4.4513679	active
TSS_15200_storz	3920627	+	0.8892138	active
TSS_15198_storz	3920522	+	0.7084786	inactive
TSS_15203_storz	3920796	+	0.9766954	active
TSS_15205_storz	3920918	+	0.4521286	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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