

Operon Promoter Landscape

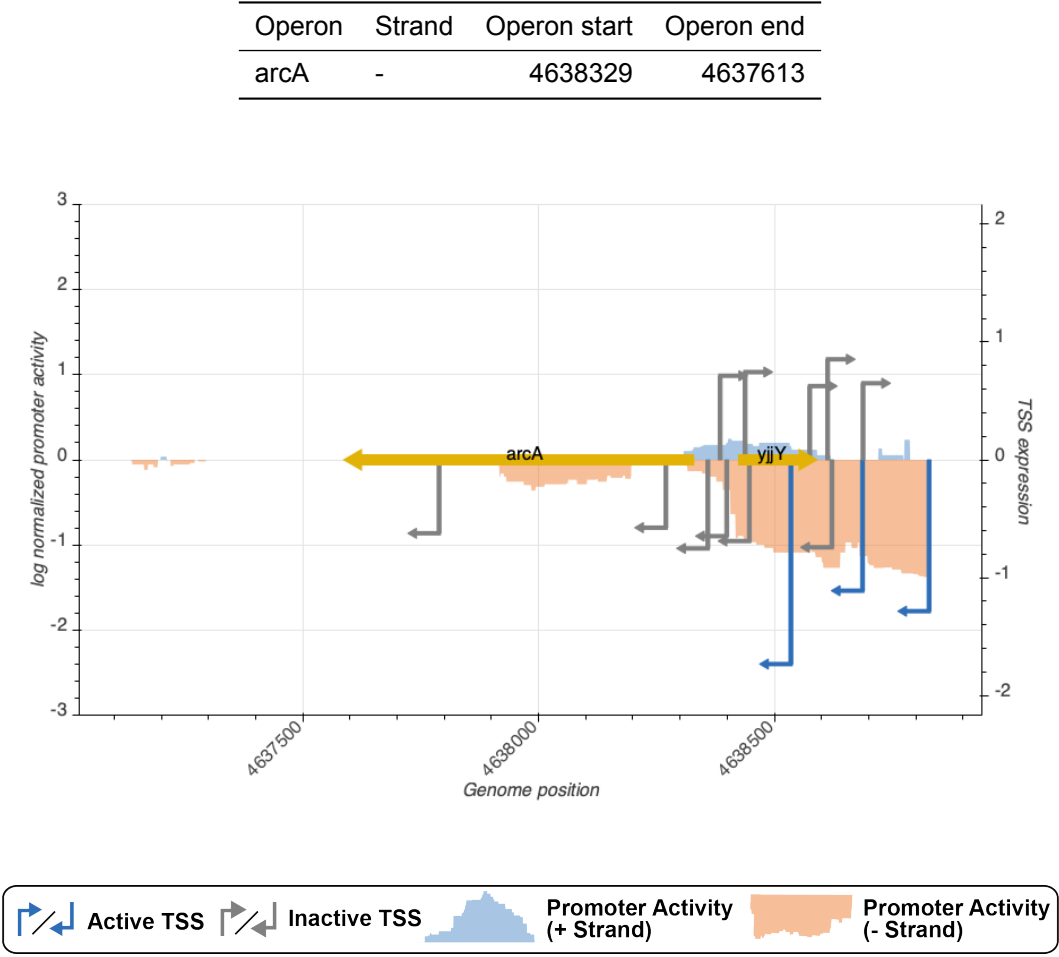


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_18119_storz	4638434	+	0.7445031	inactive
TSS_18116_regulondb	4638355	-	0.7512440	inactive
TSS_18128_regulondb	4638824	-	1.2838234	active
TSS_18122_storz	4638571	+	0.6252349	inactive
TSS_18123_wanner	4638609	+	0.8527954	inactive
TSS_18117_regulondb	4638381	+	0.7129477	inactive
TSS_18118_storz	4638395	-	0.6469581	inactive
TSS_18124_storz_wanner	4638618	-	0.7418947	inactive
TSS_18126_storz	4638684	+	0.6495780	inactive
TSS_18120_regulondb	4638443	-	0.6887733	inactive
TSS_18121_regulondb	4638531	-	1.7322758	active
TSS_18125_regulondb	4638683	-	1.1101585	active

TSS Scanning Mutagenesis

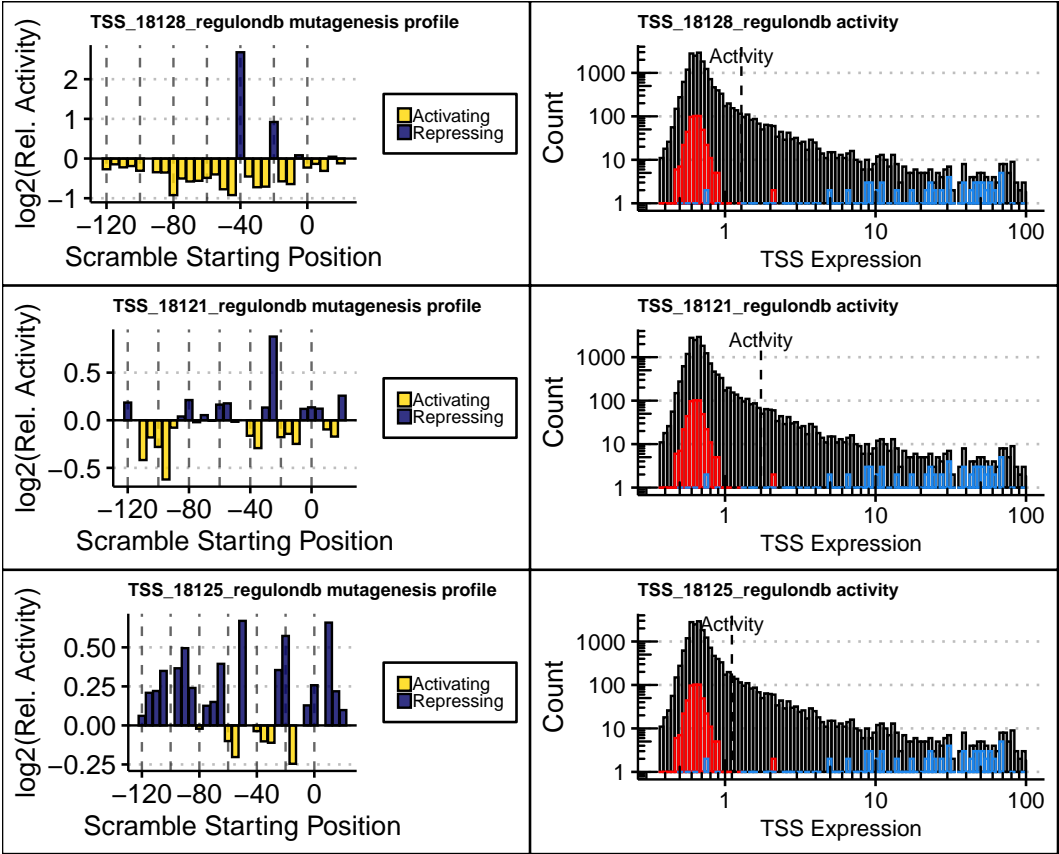


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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