Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ppiD	+	461139	463010

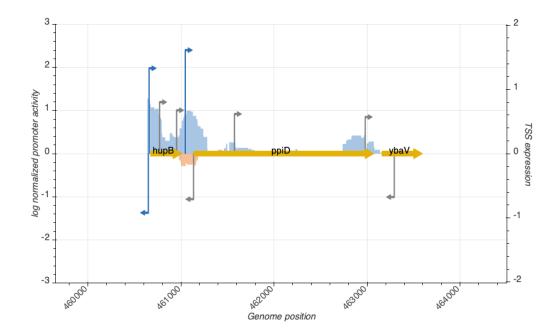


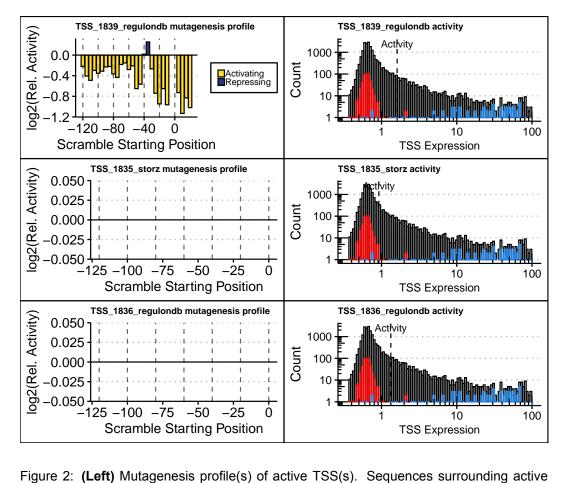


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_1837_regulondb	460767	+	0.8019313	inactive
TSS_1840_storz	461132	-	0.7095977	inactive
TSS_1839_regulondb	461043	+	1.6117815	active
TSS_1835_storz	460646	-	0.9208536	active
TSS_1836_regulondb	460654	+	1.3290924	active
TSS_1838_storz	460950	+	0.6755228	inactive

TSS Scanning Mutagenesis



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).