Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yceD-rpmF-plsX-fabHDG-acpP-fabF	+	1146017	1152403

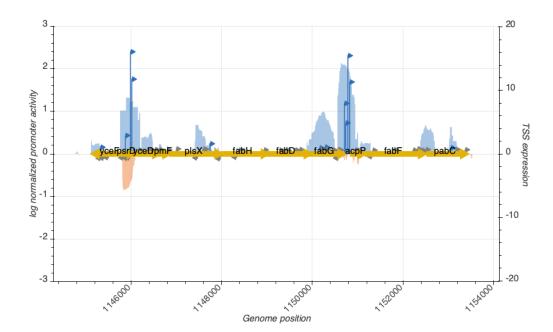


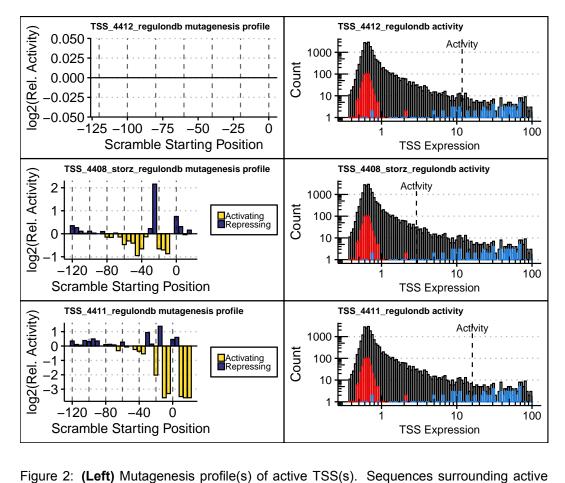


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_4412_regulondb	1146014	+	11.7870958	active
TSS_4408_storz_regulondb	1145872	+	2.9108493	active
TSS_4407_regulondb	1145830	-	0.6177537	inactive
TSS_4410_regulondb	1145972	-	0.6225765	inactive
TSS_4411_regulondb	1145984	+	16.1042592	active
TSS_4409_storz_wanner	1145923	-	0.6909279	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).