Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
fxsA	+	4366687	4367163

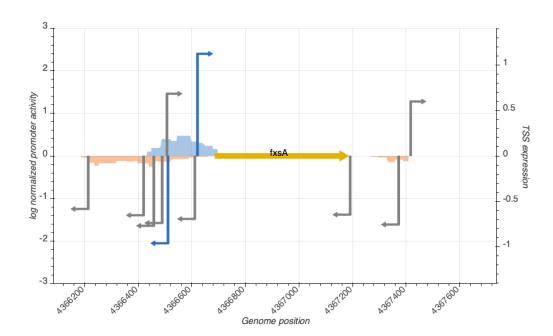




Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_17040_storz	4366503	+	0.6839256	inactive
TSS_17037_regulondb	4366416	-	0.6521274	inactive
TSS_17039_storz	4366485	-	0.7371433	inactive
TSS_17038_storz_wanner_regulondb	4366454	-	0.7679535	inactive
TSS_17036_storz	4366209	-	0.5830922	inactive
TSS_17043_storz	4366617	+	1.1227424	active
TSS_17042_storz	4366607	-	0.6927642	inactive
TSS_17041_storz	4366507	-	0.9604739	active

TSS Scanning Mutagenesis

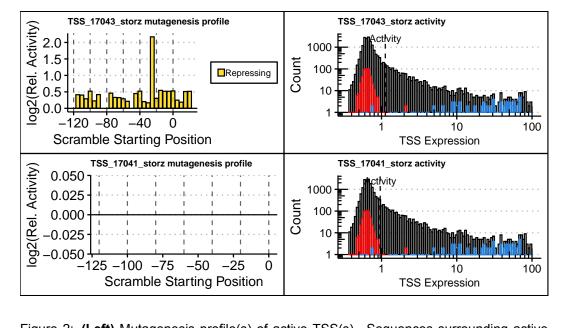


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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