## **Operon Promoter Landscape**

Operon	Strand	Operon start	Operon end	
yabl	+	71351	72115	

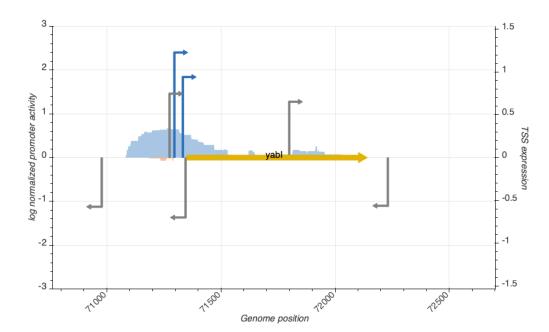


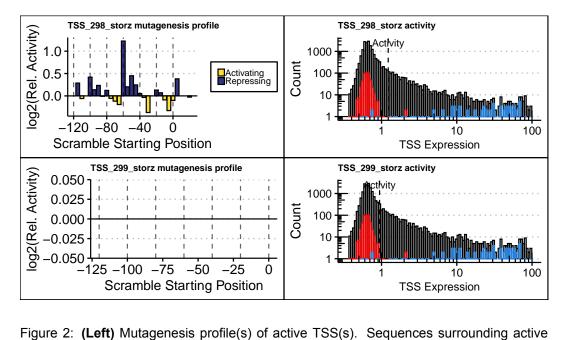


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_296_storz	70974	-	0.5744037	inactive
TSS_298_storz	71292	+	1.2278048	active
TSS_299_storz	71329	+	0.9418054	active
TSS_300_storz	71341	-	0.6998884	inactive
TSS_297_regulondb	71271	+	0.7469870	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).