## **Operon Promoter Landscape**

Operon	Strand	Operon start	Operon end
yfhH	+	2696781	2697629

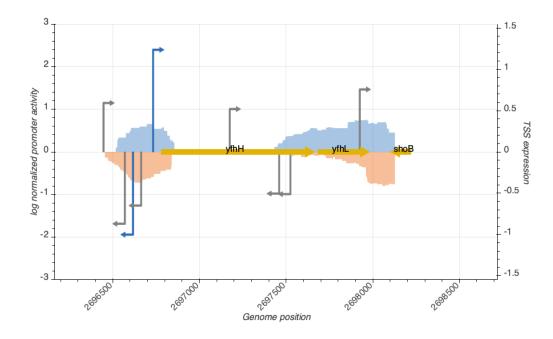


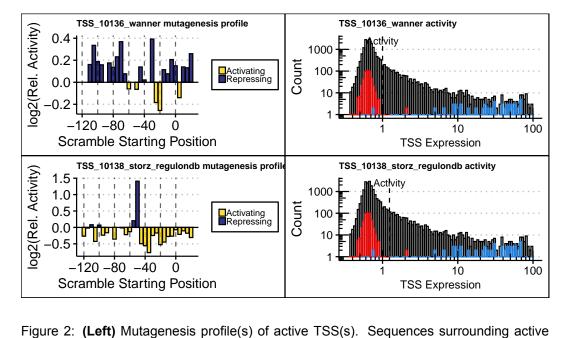


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_10135_storz	2696566	-	0.8698869	inactive
TSS_10134_wanner	2696443	+	0.5926540	inactive
TSS_10136_wanner	2696613	-	1.0015509	active
TSS_10137_regulondb	2696660	-	0.6496003	inactive
TSS_10138_storz_regulondb	2696729	+	1.2368747	active

## 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).