

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yhdU	+	3410643	3410822

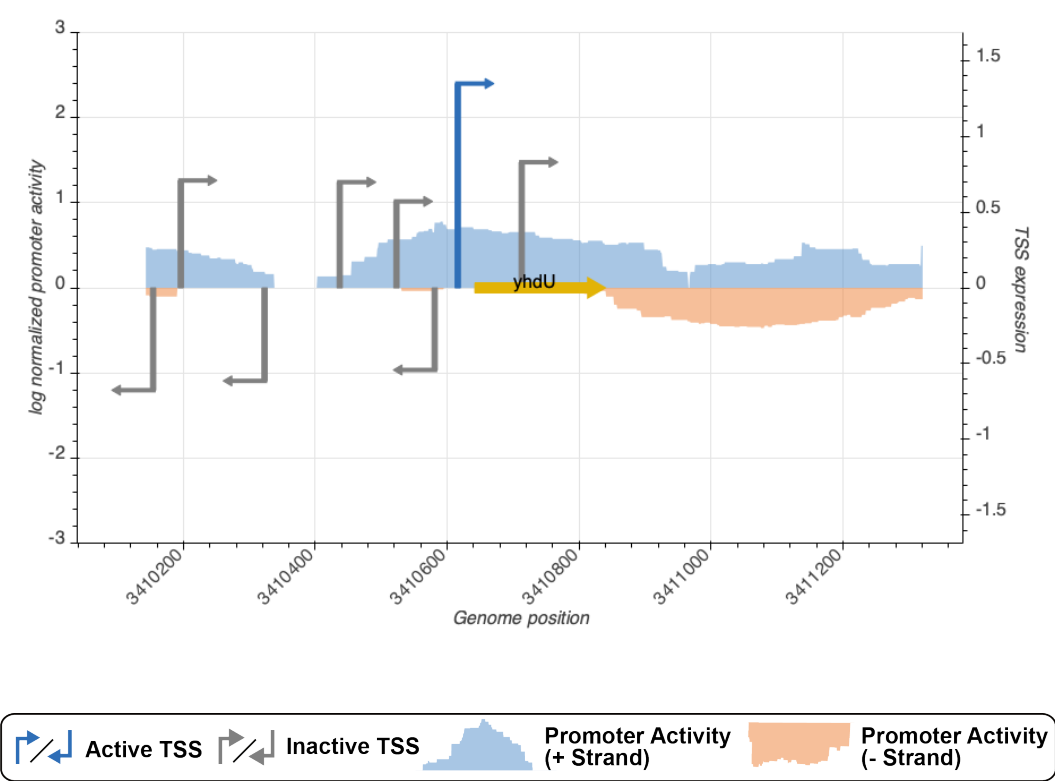


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_13063_storz	3410319	-	0.6139024	inactive
TSS_13061_storz	3410150	-	0.6750625	inactive
TSS_13066_storz	3410577	-	0.5417711	inactive
TSS_13062_storz	3410192	+	0.7080152	inactive
TSS_13064_storz	3410433	+	0.6970698	inactive
TSS_13067_storz_wanner	3410612	+	1.3471108	active
TSS_13065_regulondb	3410519	+	0.5698878	inactive

TSS Scanning Mutagenesis

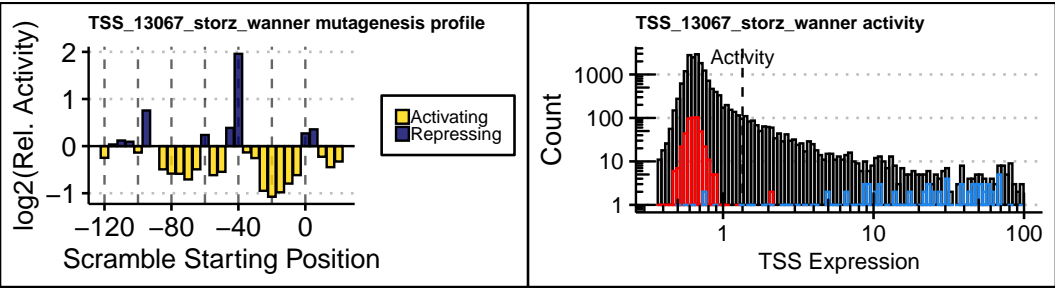


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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