

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
aroKB-damX-dam-rpe-gph-trpS	-	3517086	3510656

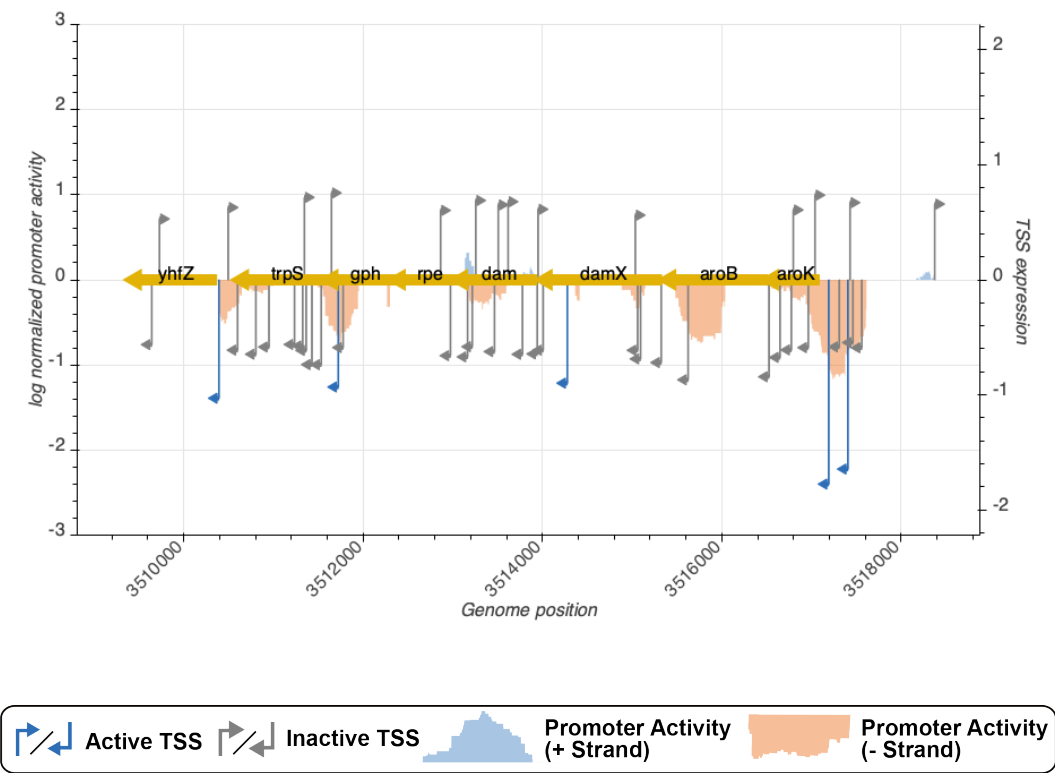


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_13612_storz	3517306	-	0.5830922	inactive
TSS_13611_storz_wanner_regulondb	3517188	-	1.7771494	active
TSS_13613_storz_wanner_regulondb	3517402	-	1.6464779	active
TSS_13615_storz	3517458	-	0.5457644	inactive
TSS_13614_storz	3517426	+	0.6716716	inactive
TSS_13616_storz	3517557	-	0.5910825	inactive

TSS Scanning Mutagenesis

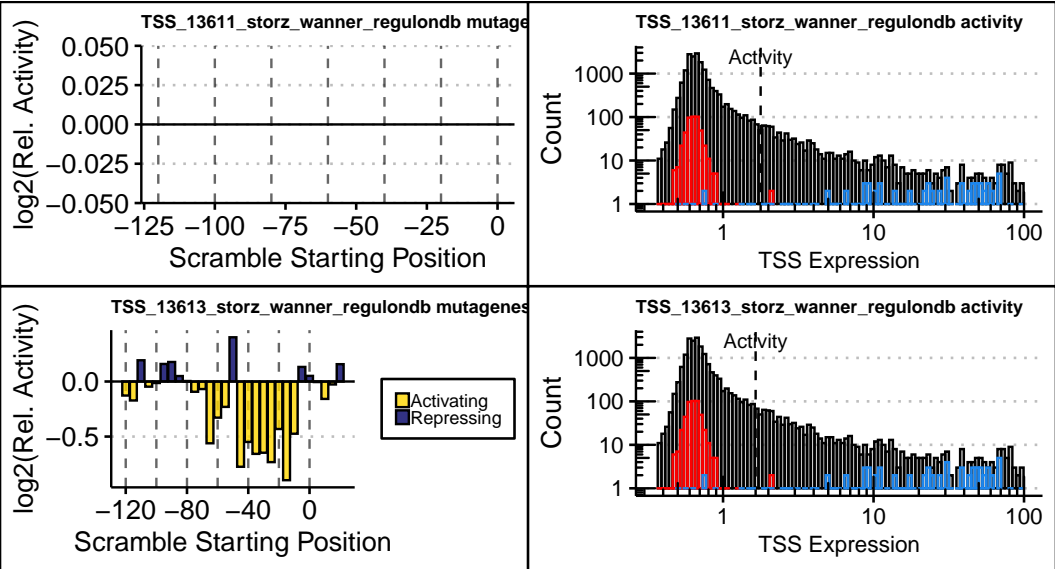


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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