

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
hupA	+	4198304	4198576

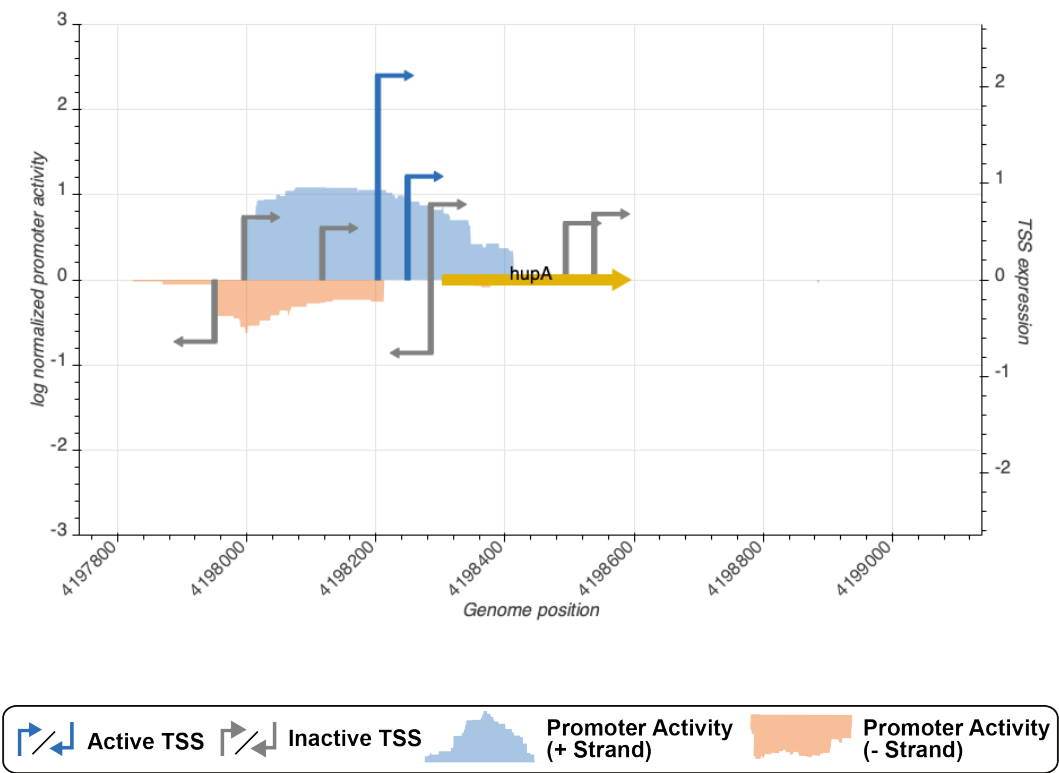


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_16463_storz	4197946	-	0.6419117	inactive
TSS_16467_regulondb	4198245	+	1.0737537	active
TSS_16469_regulondb	4198281	+	0.7827547	inactive
TSS_16464_storz	4197992	+	0.6490985	inactive
TSS_16466_storz_regulondb	4198199	+	2.1206535	active
TSS_16468_storz	4198281	-	0.7589229	inactive
TSS_16465_storz	4198113	+	0.5368769	inactive

TSS Scanning Mutagenesis

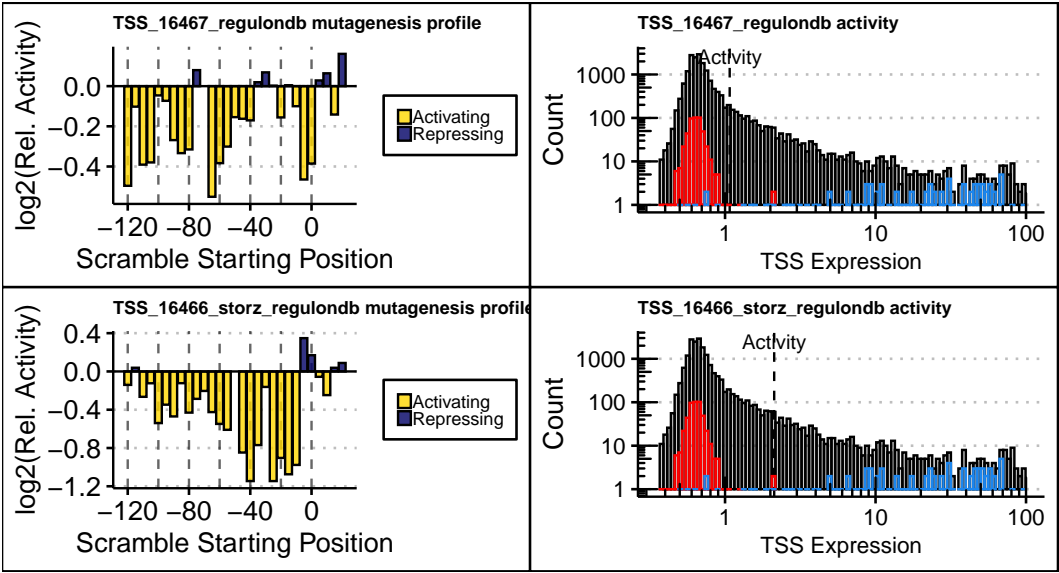


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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