

Operon Promoter Landscape

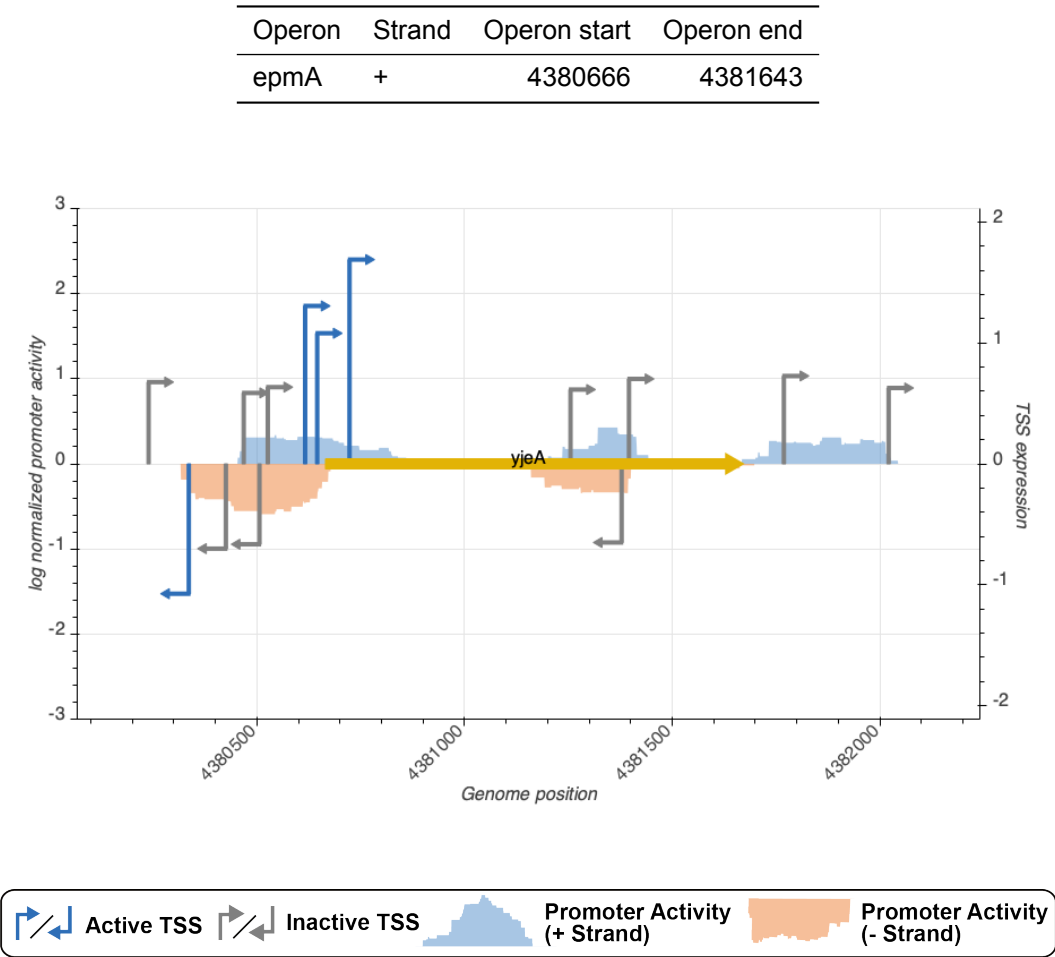


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_17118_storz	4380464	+	0.5861024	inactive
TSS_17119_wanner	4380502	-	0.6648691	inactive
TSS_17115_storz	4380235	+	0.6755228	inactive
TSS_17121_storz	4380612	+	1.3048303	active
TSS_17122_storz_wanner_regulondb	4380641	+	1.0791152	active
TSS_17120_storz	4380522	+	0.6338880	inactive
TSS_17117_regulondb	4380421	-	0.7010062	inactive
TSS_17116_regulondb	4380332	-	1.0737537	active

TSS Scanning Mutagenesis

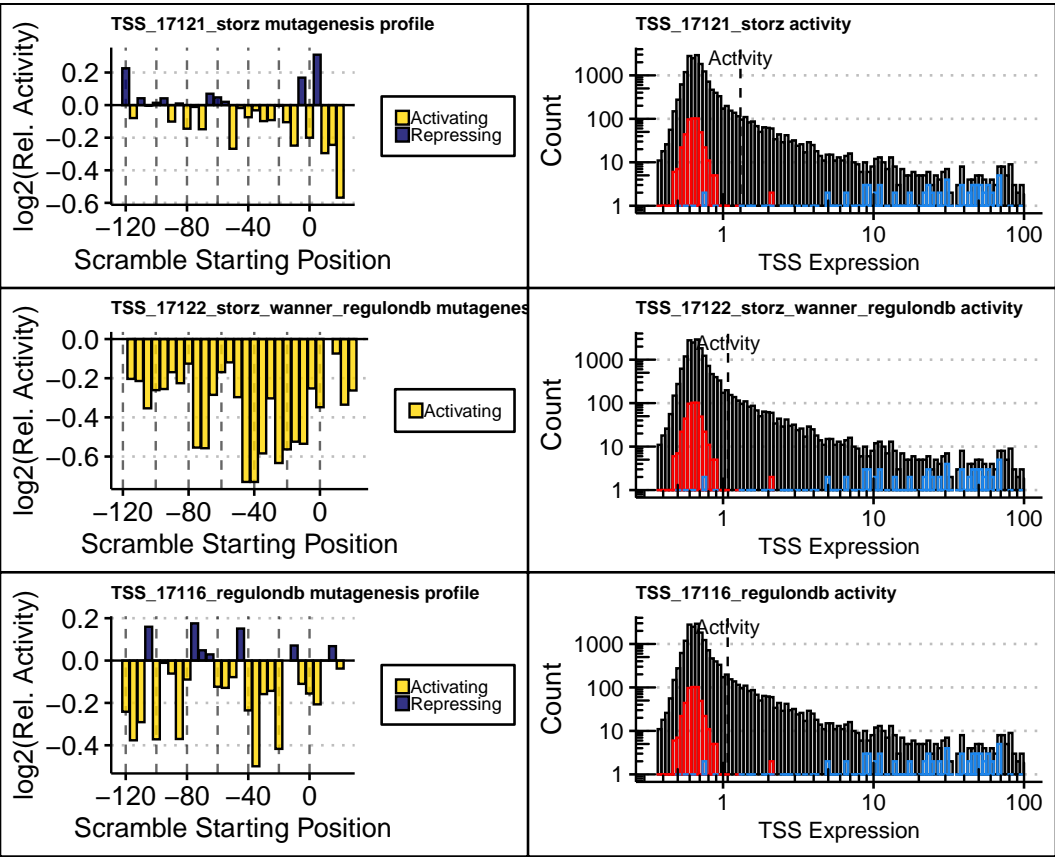


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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