

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ppiB-lpxH	-	553660	552441

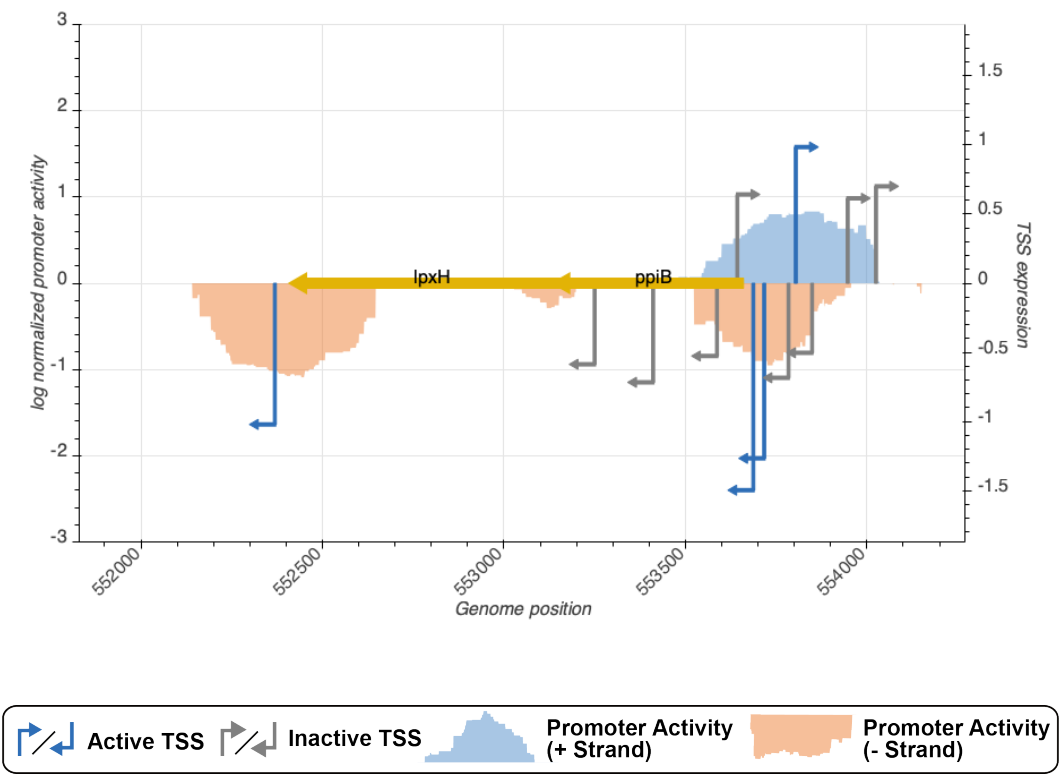


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_2127_storz	554021	+	0.7007376	inactive
TSS_2122_storz_regulondb	553713	-	1.2657421	active
TSS_2123_wanner	553780	-	0.6834017	inactive
TSS_2121_regulondb	553683	-	1.4960465	active
TSS_2124_storz_regulondb	553800	+	0.9844446	active
TSS_2125_storz	553845	-	0.5028991	inactive
TSS_2126_storz	553943	+	0.6139024	inactive

TSS Scanning Mutagenesis

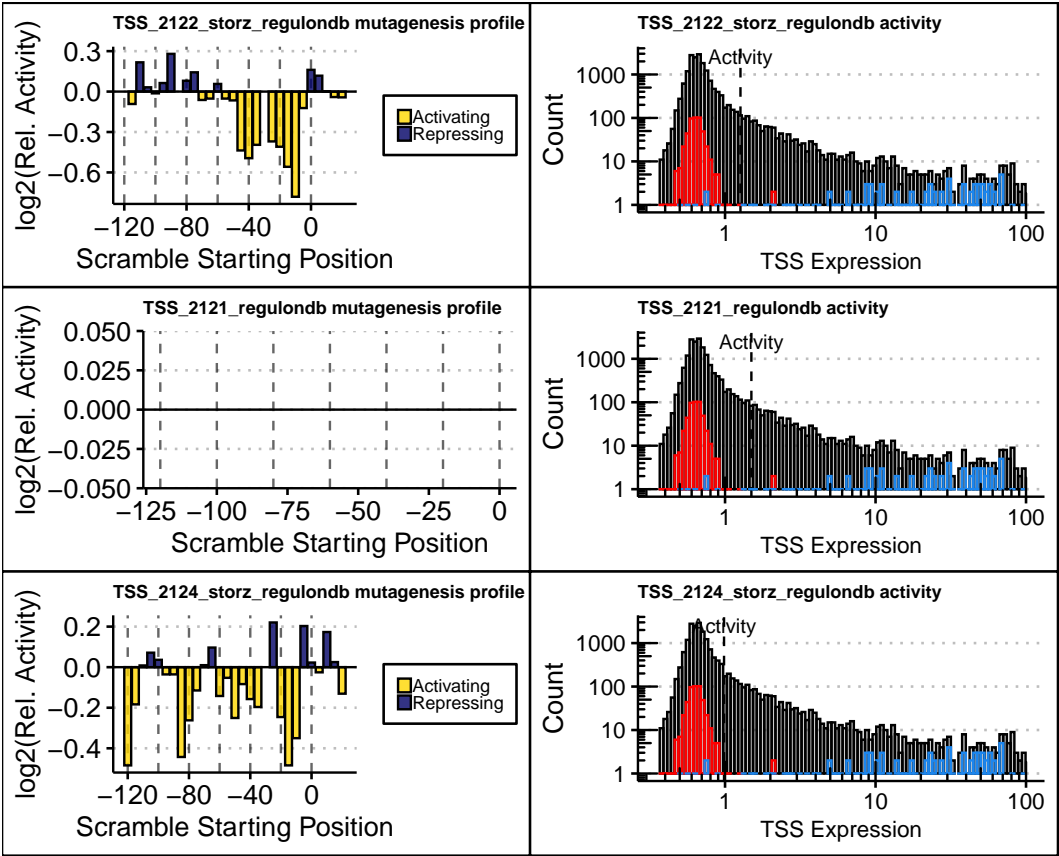


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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