

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
hemL	-	174882	173602

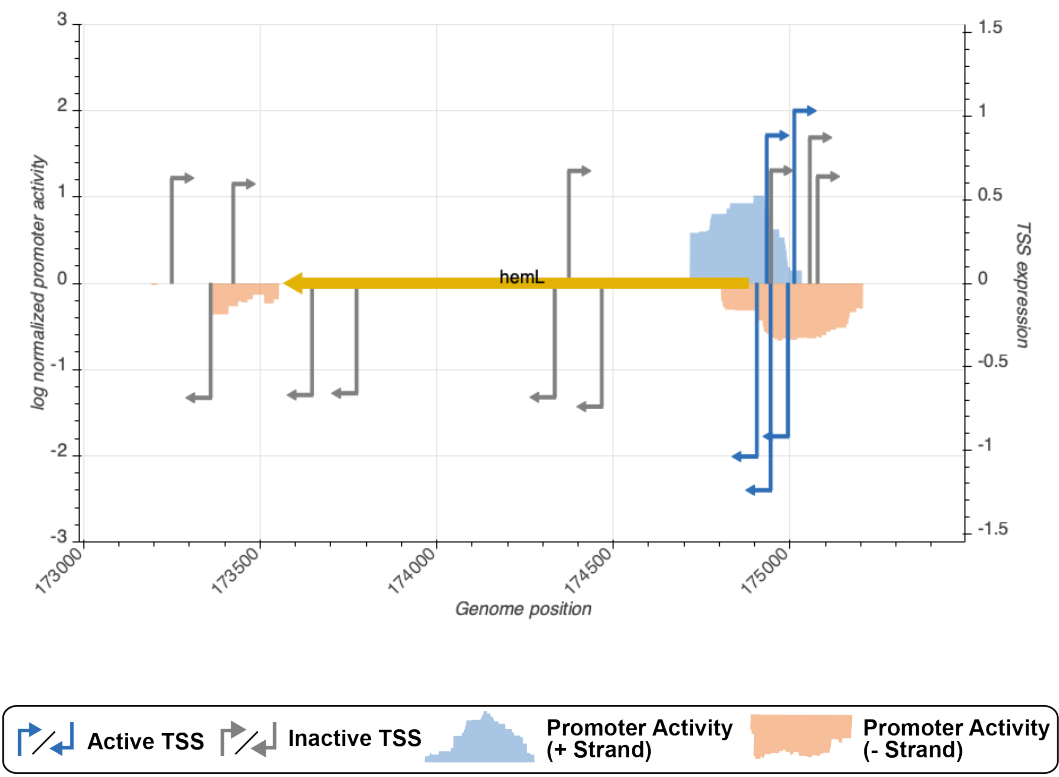


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_715_regulondb	174930	+	0.8854117	active
TSS_720_regulondb	175052	+	0.8726980	inactive
TSS_721_regulondb	175074	+	0.6395776	inactive
TSS_719_regulondb	175008	+	1.0333115	active
TSS_717_regulondb	174942	+	0.6750625	inactive
TSS_718_storz_wanner	174990	-	0.9176266	active
TSS_714_regulondb	174902	-	1.0384223	active
TSS_716_regulondb	174941	-	1.2400034	active

TSS Scanning Mutagenesis

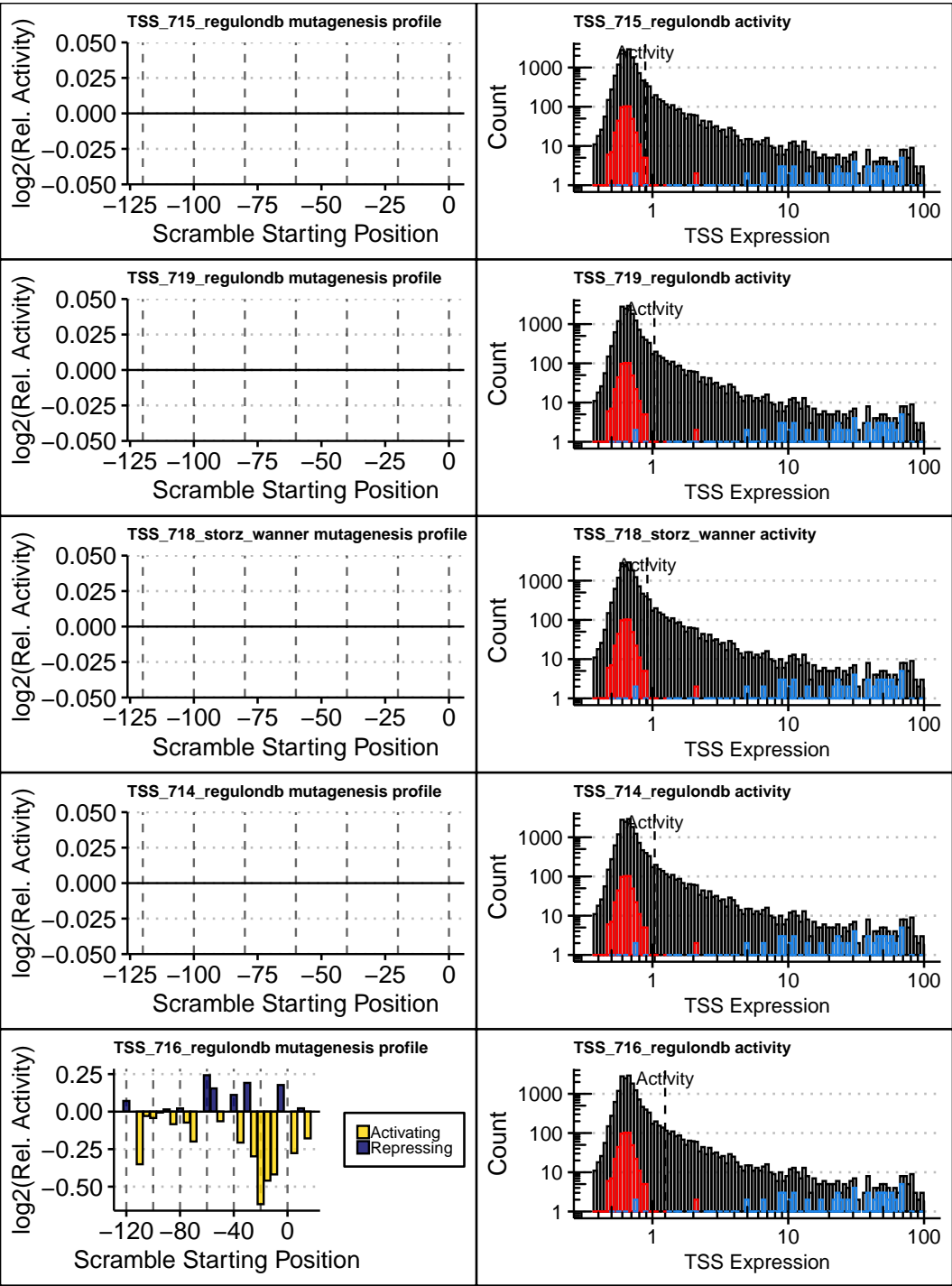


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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