

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yhaJ	-	3252236	3251340

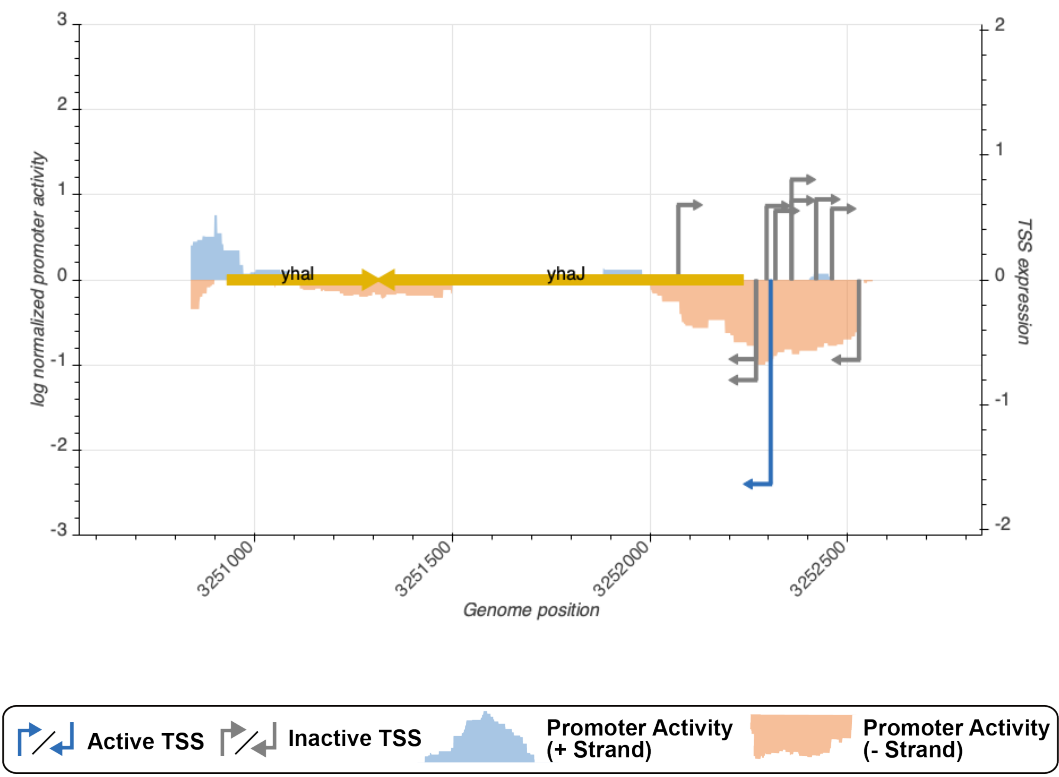


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_12344_regulondb	3252291	+	0.5914281	inactive
TSS_12345_storz_wanner	3252301	-	1.6365337	active
TSS_12349_storz	3252456	+	0.5697468	inactive
TSS_12348_storz	3252416	+	0.6447913	inactive
TSS_12343_storz_regulondb	3252264	-	0.6354802	inactive
TSS_12347_storz	3252354	+	0.6354802	inactive
TSS_12343_storz_regulondb	3252264	-	0.8031401	inactive
TSS_12347_storz	3252354	+	0.8031401	inactive
TSS_12350_storz	3252524	-	0.6409540	inactive
TSS_12346_regulondb	3252313	+	0.5527424	inactive

TSS Scanning Mutagenesis

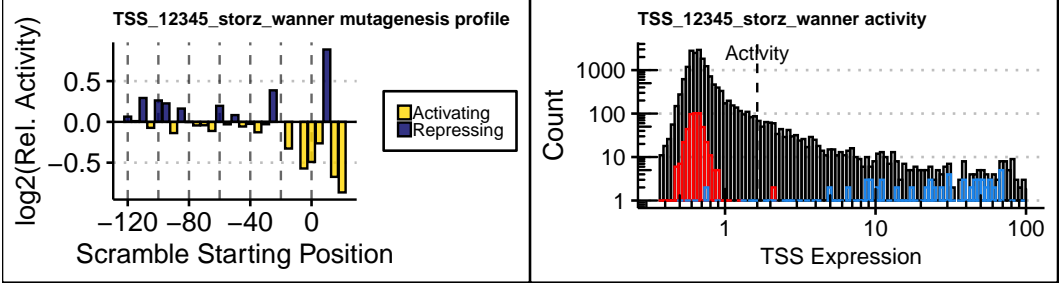


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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