Operon Promoter Landscape

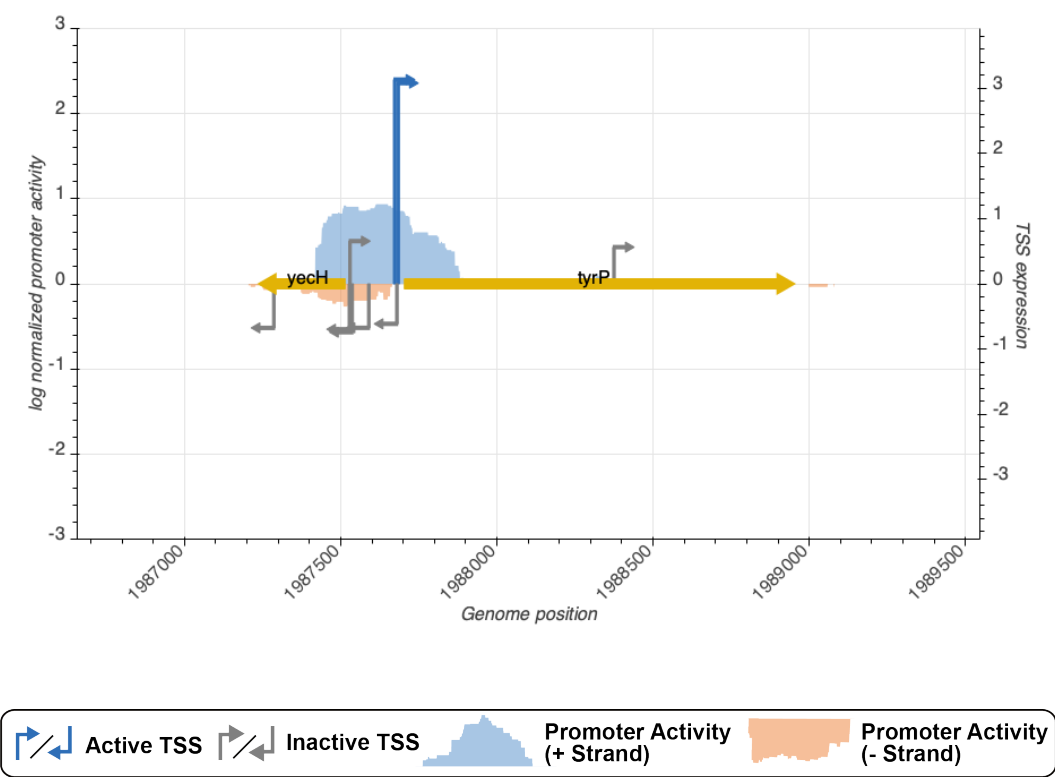| Operon	Strand	Operon start	Operon end
tyrP	+	1987705	1988916

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_7632_storz	1987282	-	0.6758895	inactive
TSS_7636_storz_regulondb	1987586	-	0.6746828	inactive
TSS_7638_regulondb	1987676	-	0.6139024	inactive
TSS_7635_storz	1987533	-	0.7421594	inactive
TSS_7633_wanner	1987524	-	0.6968530	inactive
TSS_7639_wanner	1987680	+	3.0795048	active
TSS_7634_regulondb	1987526	+	0.6551851	inactive
TSS_7637_regulondb	1987669	+	3.1338897	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).