Operon Promoter Landscape
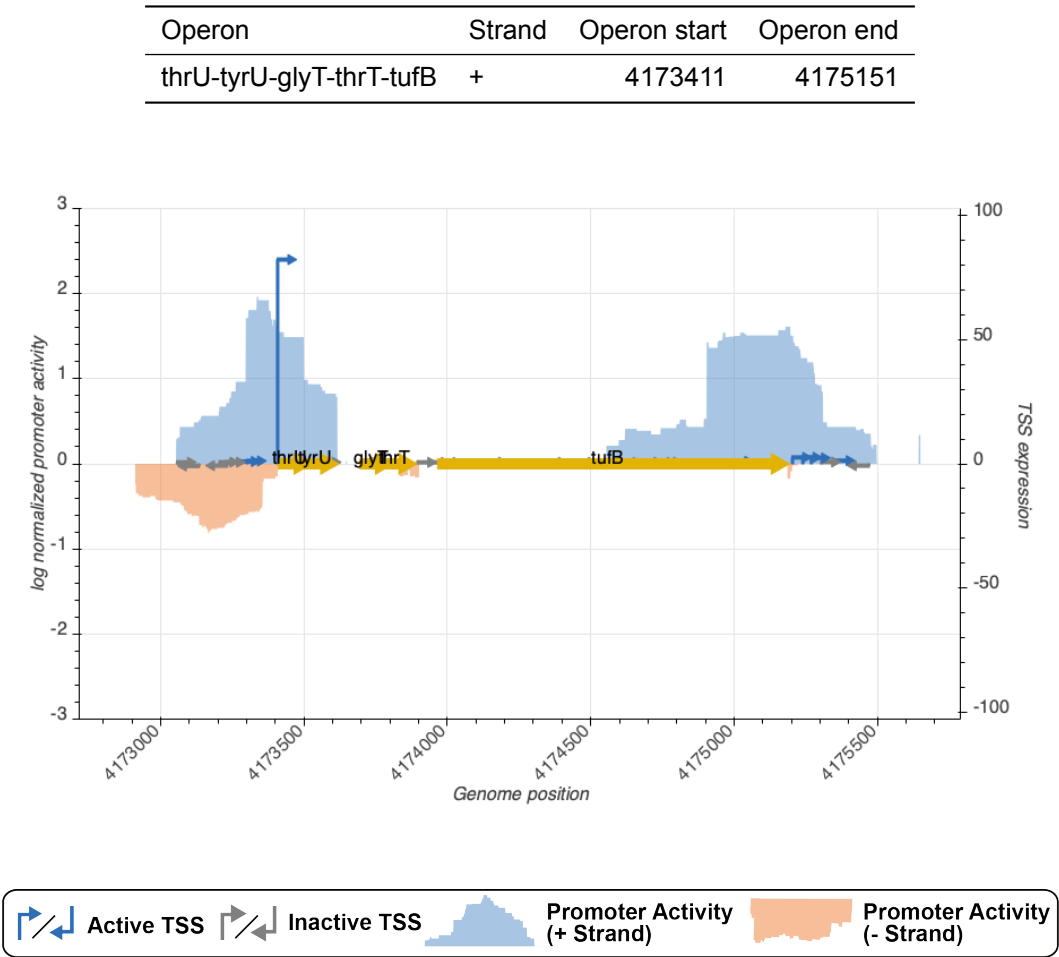
Operon	Strand	Operon start	Operon end
thrU-tyrU-glyT-thrT-tufB	+	4173411	4175151

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_16315_storz	4173227	-	0.7210096	inactive
TSS_16316_regulondb	4173277	+	0.9582154	active
TSS_16312_wanner	4173129	-	0.8591571	inactive
TSS_16317_storz	4173298	+	1.1752201	active
TSS_16311_storz	4173054	+	0.6211834	inactive
TSS_16314_storz	4173225	+	0.6359097	inactive
TSS_16313_storz	4173202	+	0.6777446	inactive
TSS_16318_storz_regulondb	4173404	+	82.3555104	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).