Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
trmA	-	4161293	4160193

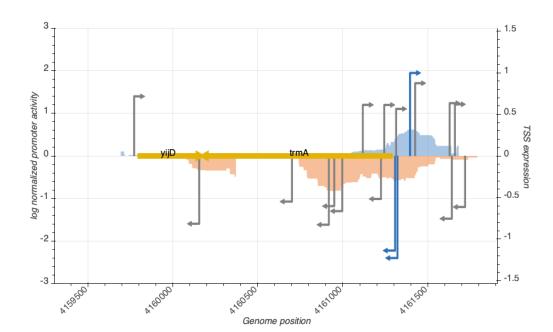




Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_16252_storz	4161625	+	0.6342447	inactive
TSS_16251_storz_regulondb	4161422	+	0.8744081	inactive
TSS_16250_storz	4161392	+	0.9973037	active
TSS_16247_wanner	4161304	-	1.1377442	active
TSS_16255_storz	4161716	-	0.6139024	inactive
TSS_16253_storz	4161638	-	0.7543486	inactive
TSS_16254_storz	4161656	+	0.6206908	inactive
TSS_16248_storz	4161310	+	0.5654182	inactive
TSS_16249_storz_regulondb	4161318	-	1.2278048	active

TSS Scanning Mutagenesis

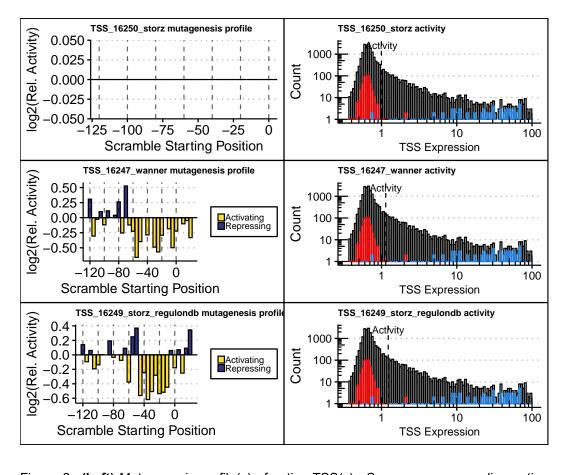


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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