Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
trxA	+	3963784	3964113

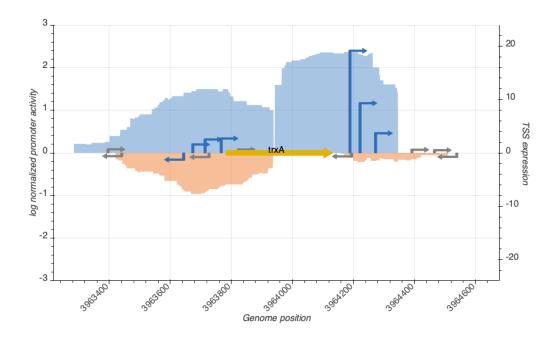




Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_15408_storz	3963392	+	0.6750625	inactive
TSS_15411_regulondb	3963670	+	1.5815468	active
TSS_15413_storz	3963723	-	0.7774563	inactive
TSS_15410_regulondb	3963640	-	1.2632897	active
TSS_15414_regulondb	3963763	+	2.7008898	active
TSS_15412_regulondb	3963710	+	2.5167743	active
TSS_15409_storz	3963437	-	0.5976847	inactive

TSS Scanning Mutagenesis

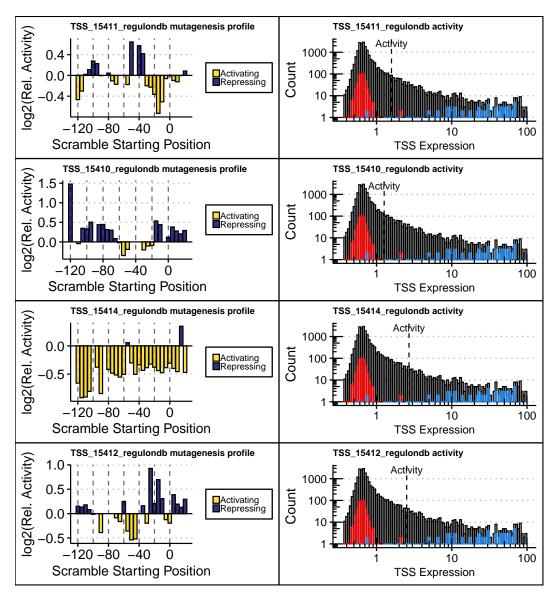


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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