Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ydcY	+	1515672	1515905

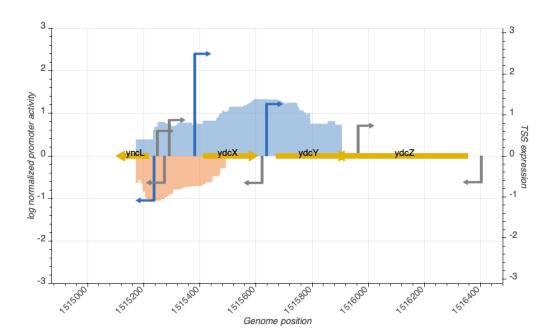


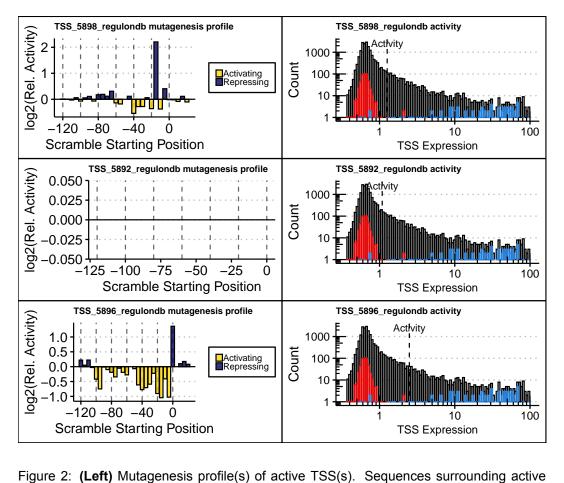


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_5898_regulondb	1515634	+	1.2642862	active
TSS_5897_storz	1515618	-	0.6575882	inactive
TSS_5894_regulondb	1515270	-	0.6524152	inactive
TSS_5895_storz	1515287	+	0.8744081	inactive
TSS_5893_regulondb	1515245	+	0.6093812	inactive
TSS_5892_regulondb	1515233	-	1.0859913	active
TSS_5896_regulondb	1515378	+	2.4900203	active

TSS Scanning Mutagenesis



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).