Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ydcI	-	1493095	1492172

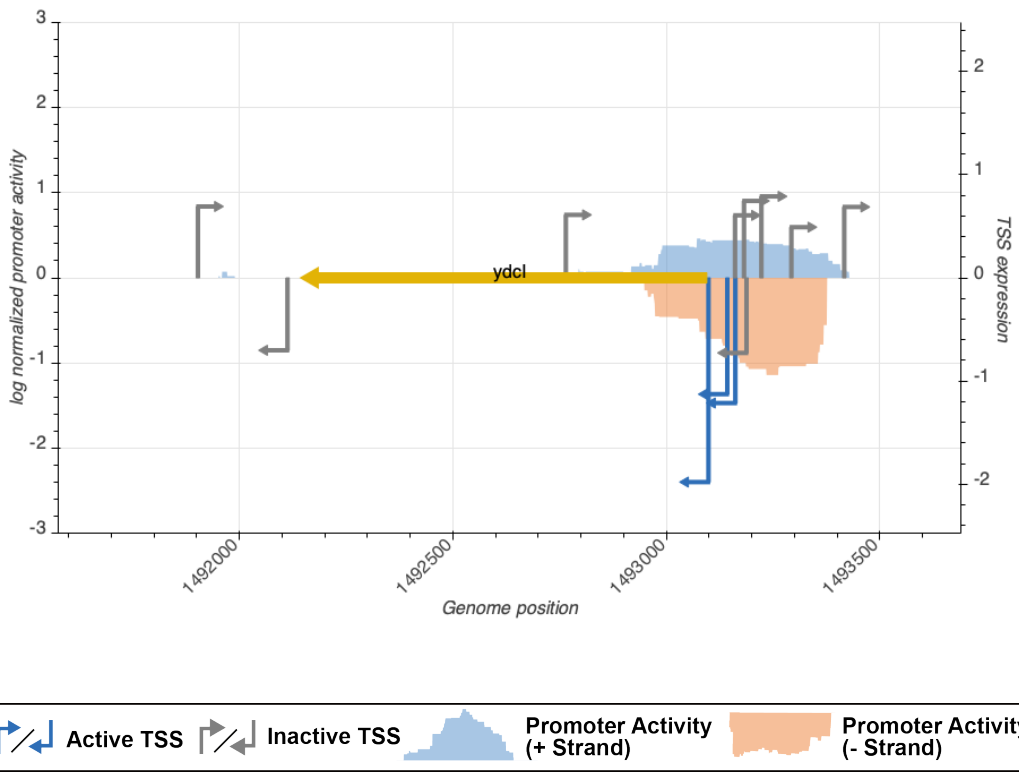

Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_5806_storz	1493413	+	0.6863930	inactive
TSS_5800_regulondb	1493157	+	0.6048406	inactive
TSS_5801_regulondb	1493158	-	1.2123997	active
TSS_5799_wanner	1493139	-	1.1266376	active
TSS_5805_storz	1493289	+	0.4906615	inactive
TSS_5804_storz	1493219	+	0.7889263	inactive
TSS_5803_storz	1493184	-	0.7269824	inactive
TSS_5802_regulondb	1493178	+	0.7449597	inactive

TSS Scanning Mutagenesis

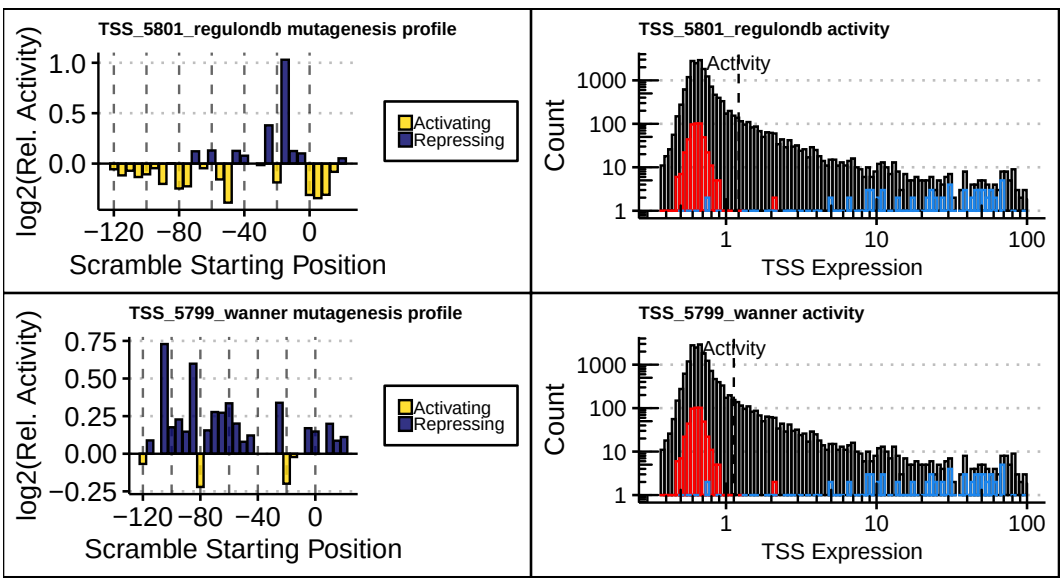

Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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