Operon Promoter Landscape
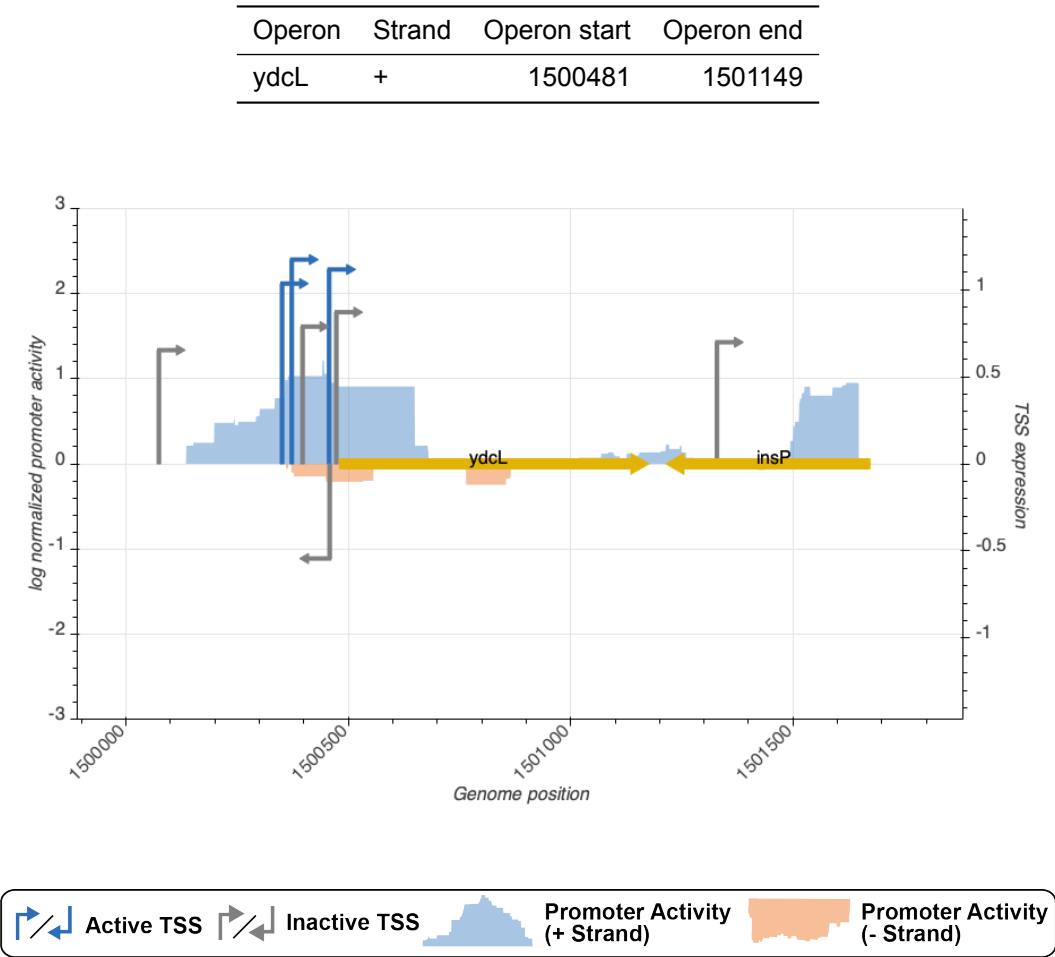
Operon	Strand	Operon start	Operon end
ydcL	+	1500481	1501149

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_5846_storz_wanner	1500453	+	1.1152177	active
TSS_5848_regulondb	1500469	+	0.8698869	inactive
TSS_5847_storz	1500454	-	0.5432514	inactive
TSS_5844_regulondb	1500369	+	1.1719059	active
TSS_5841_storz	1500070	+	0.6524152	inactive
TSS_5843_regulondb	1500347	+	1.0340717	active
TSS_5845_regulondb	1500393	+	0.7874976	inactive

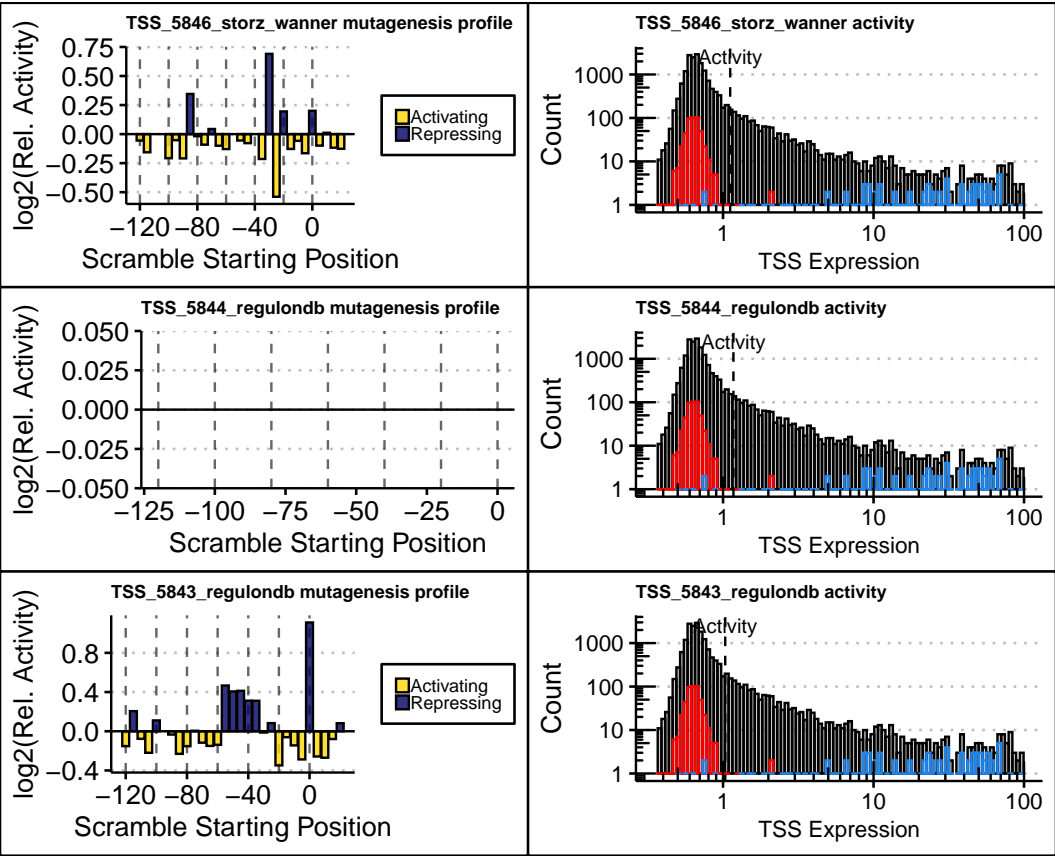## TSS Scanning Mutagenesis

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).