Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ydgH	+	1676451	1677395

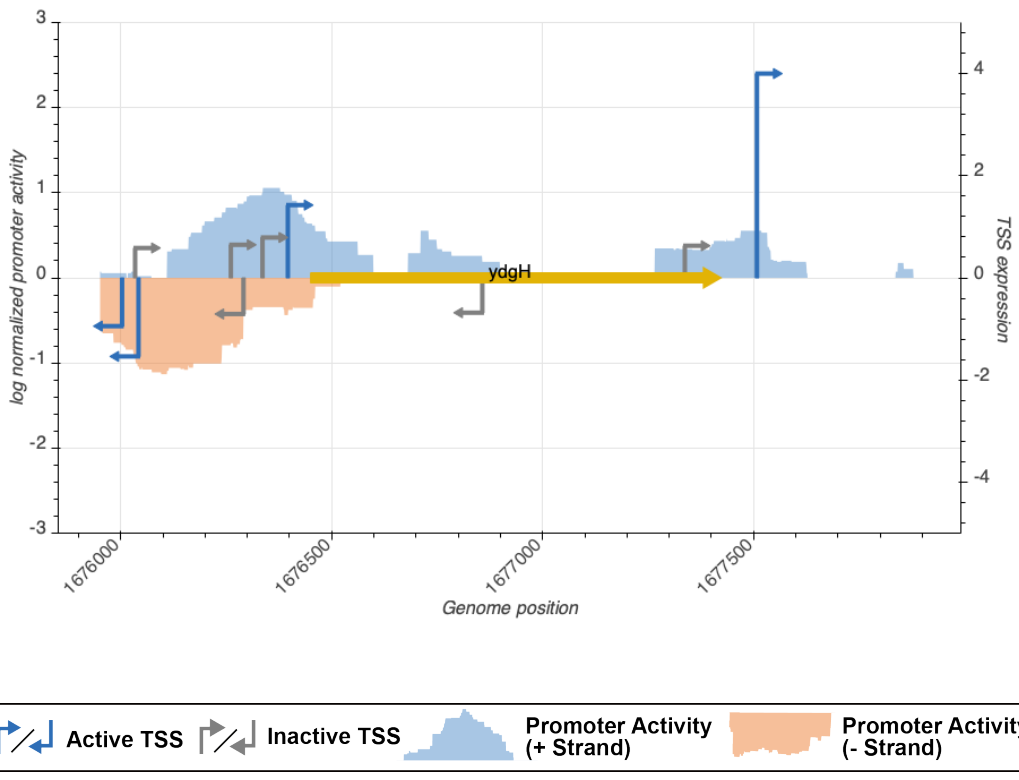

Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_6452_storz	1676287	-	0.7095006	inactive
TSS_6449_storz	1676030	+	0.5856597	inactive
TSS_6448_regulondb	1675999	-	0.9474268	active
TSS_6450_storz_regulondb	1676038	-	1.5423921	active
TSS_6453_regulondb	1676332	+	0.7914766	inactive
TSS_6454_regulondb	1676392	+	1.4271380	active
TSS_6451_storz	1676257	+	0.6480727	inactive

TSS Scanning Mutagenesis

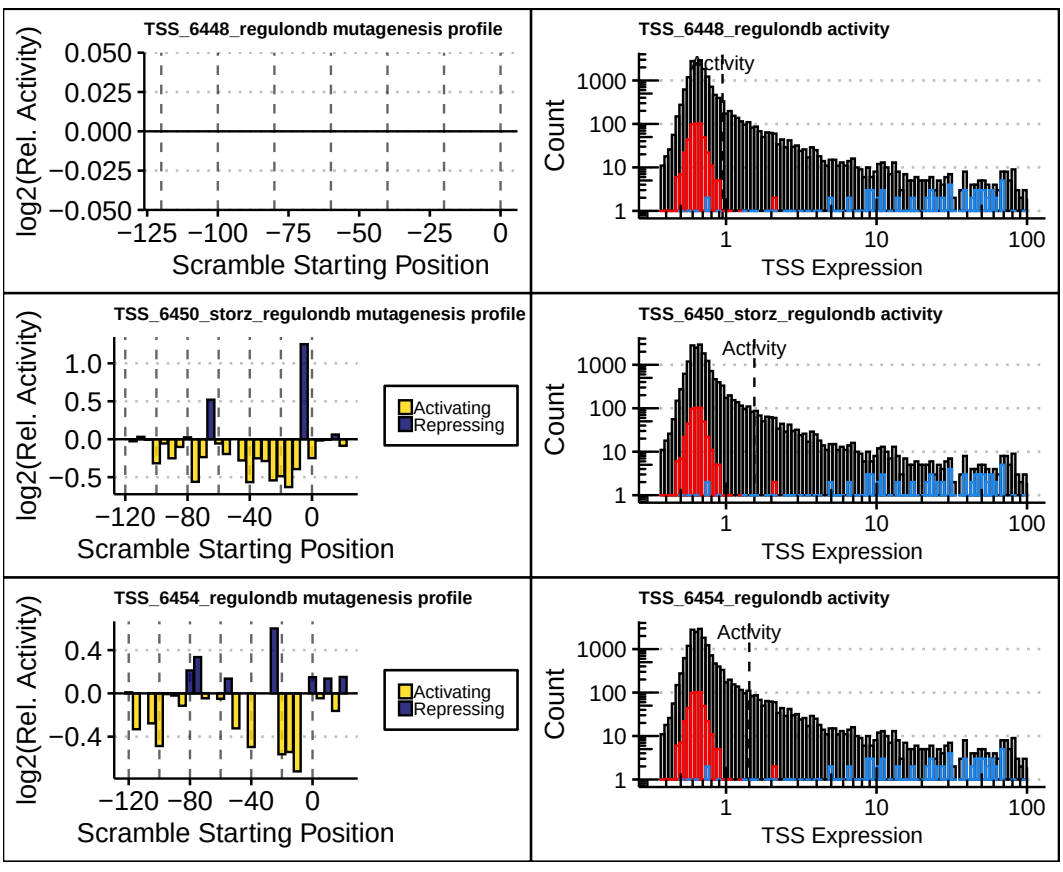

Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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