## **Operon Promoter Landscape**

Oper	on Stra	nd Operon	start Operon end	
pgsA	-	199	00841 1990293	,

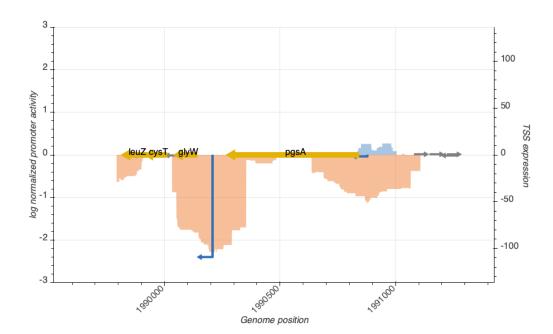




Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_7646_storz	1991080	+	0.6875790	inactive
TSS_7647_storz	1991147	+	0.6809580	inactive
TSS_7645_storz_regulondb	1990874	-	1.5857227	active
TSS_7649_storz	1991260	-	0.6084309	inactive
TSS_7648_storz	1991222	+	0.6139024	inactive

## TSS Scanning Mutagenesis

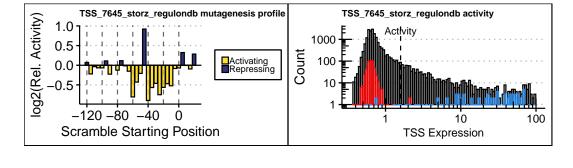


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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