## **Operon Promoter Landscape**

Operon	Strand	Operon start	Operon end
rluF	+	4228377	4229249

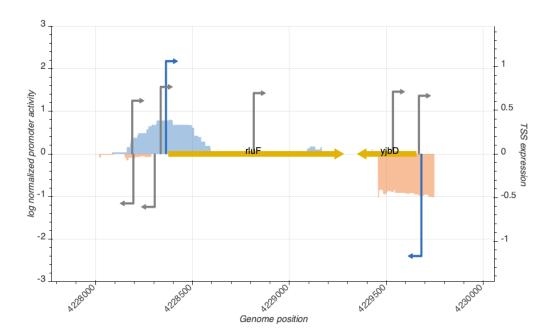




Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_16557_regulondb	4228185	+	0.6095025	inactive
TSS_16560_regulondb	4228332	+	0.7671862	inactive
TSS_16558_storz_regulondb	4228191	-	0.5667578	inactive
TSS_16559_wanner	4228301	-	0.6066153	inactive
TSS_16561_storz_wanner	4228359	+	1.0616646	active

## TSS Scanning Mutagenesis

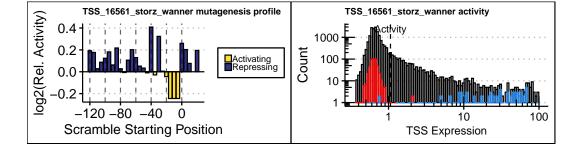


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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