Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
rrsD-ileU-alaU-rrlD-rrfD-thrV-rrfF	-	3426784	3421445

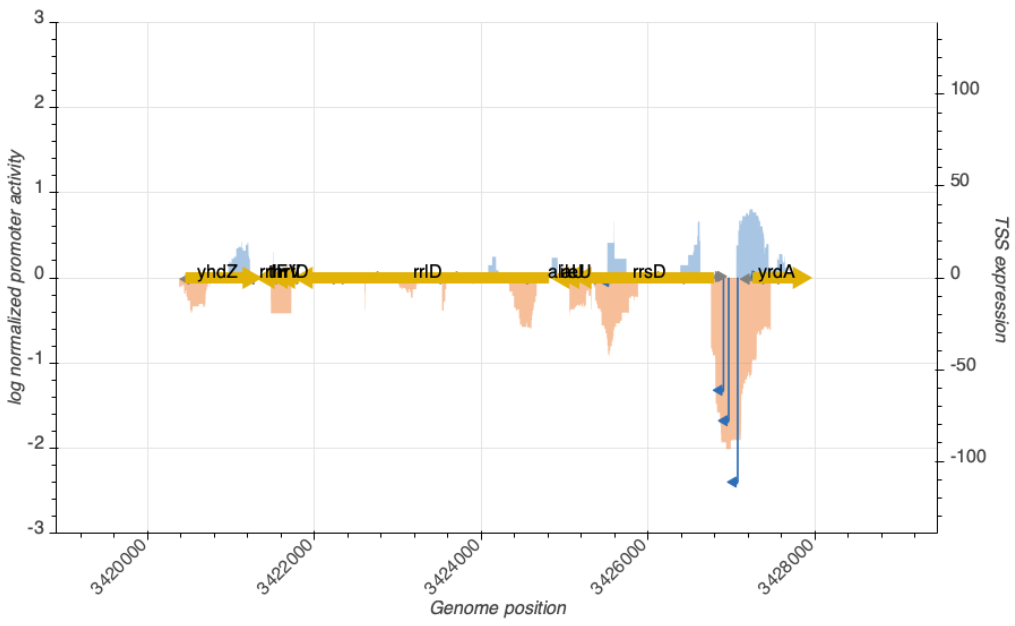

Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_13131_storz	3427225	-	0.6952777	inactive
TSS_13127_storz	3426820	+	0.7455889	inactive
TSS_13128_regulondb	3426899	-	61.2677284	active
TSS_13126_storz	3426793	+	0.6425506	inactive
TSS_13130_storz_regulondb	3427069	-	111.3248058	active
TSS_13129_storz_wanner	3426961	-	77.8862528	active
TSS_13132_regulondb	3427233	+	1.0257813	active

TSS Scanning Mutagenesis

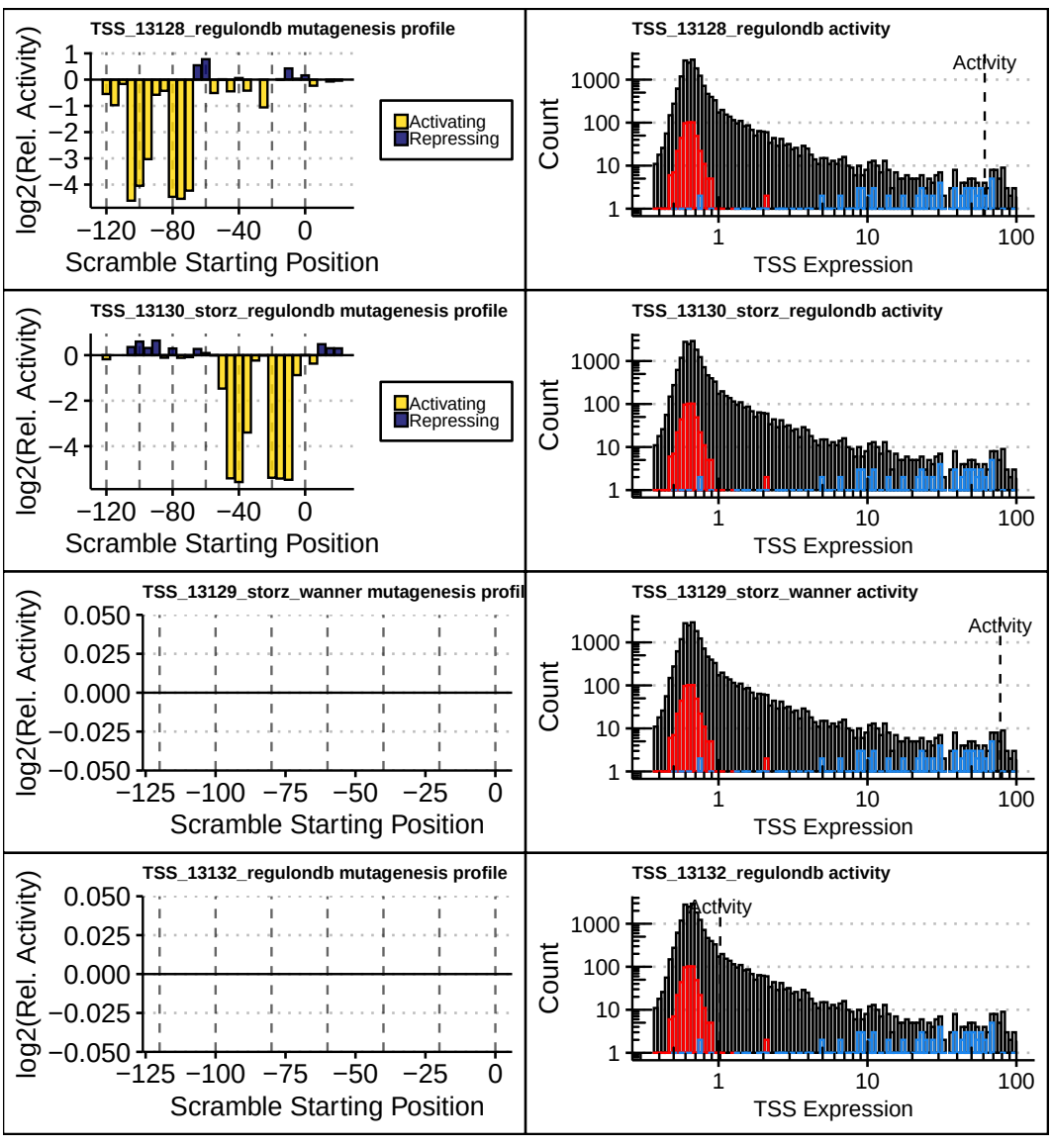

Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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