Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
fkpA	-	3475441	3474629

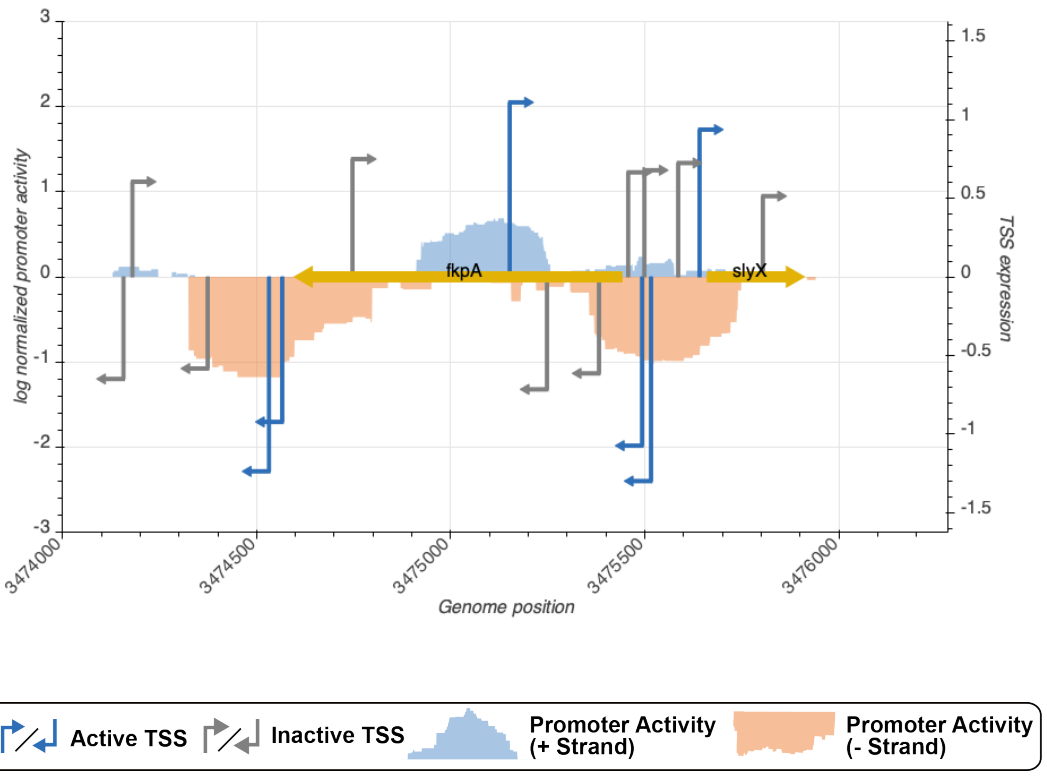

Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_13460_storz	3475582	+	0.7238071	inactive
TSS_13456_regulondb	3475453	+	0.6641523	inactive
TSS_13458_storz_wanner	3475495	+	0.6778959	inactive
TSS_13459_regulondb	3475512	-	1.2987494	active
TSS_13461_regulondb	3475637	+	0.9361436	active
TSS_13462_storz	3475800	+	0.5131178	inactive
TSS_13457_wanner	3475489	-	1.0737537	active

TSS Scanning Mutagenesis

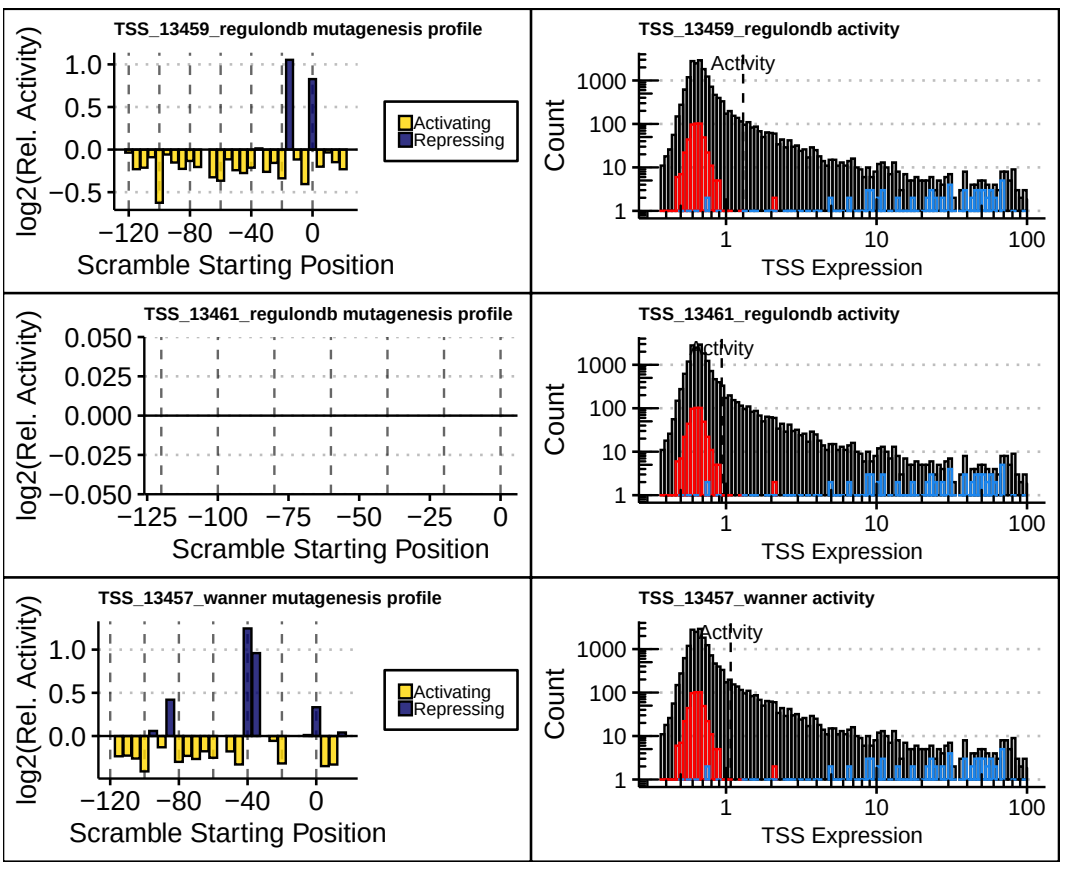

Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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