Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
fepDGC	-	621412	618607

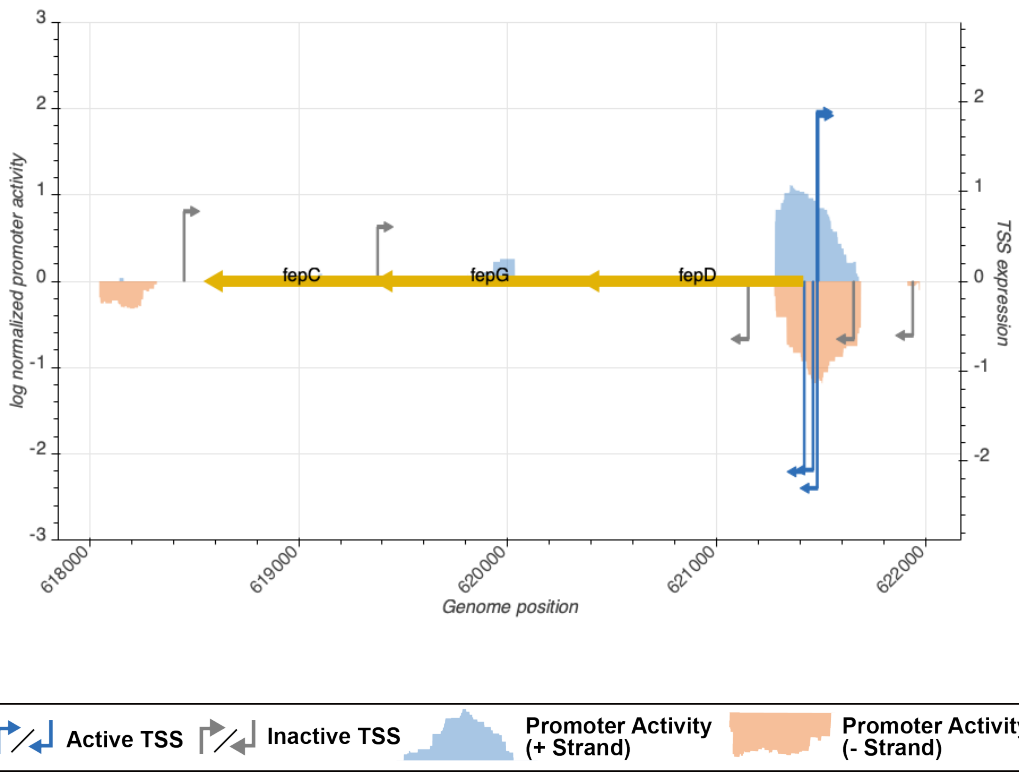

Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_2378_storz_regulondb	621481	+	1.8417072	active
TSS_2377_storz	621477	-	2.3015585	active
TSS_2375_storz_regulondb	621457	-	2.0984590	active
TSS_2379_storz	621651	-	0.6435875	inactive
TSS_2376_storz_regulondb	621476	+	1.8802200	active
TSS_2374_regulondb	621415	-	2.1189111	active

TSS Scanning Mutagenesis

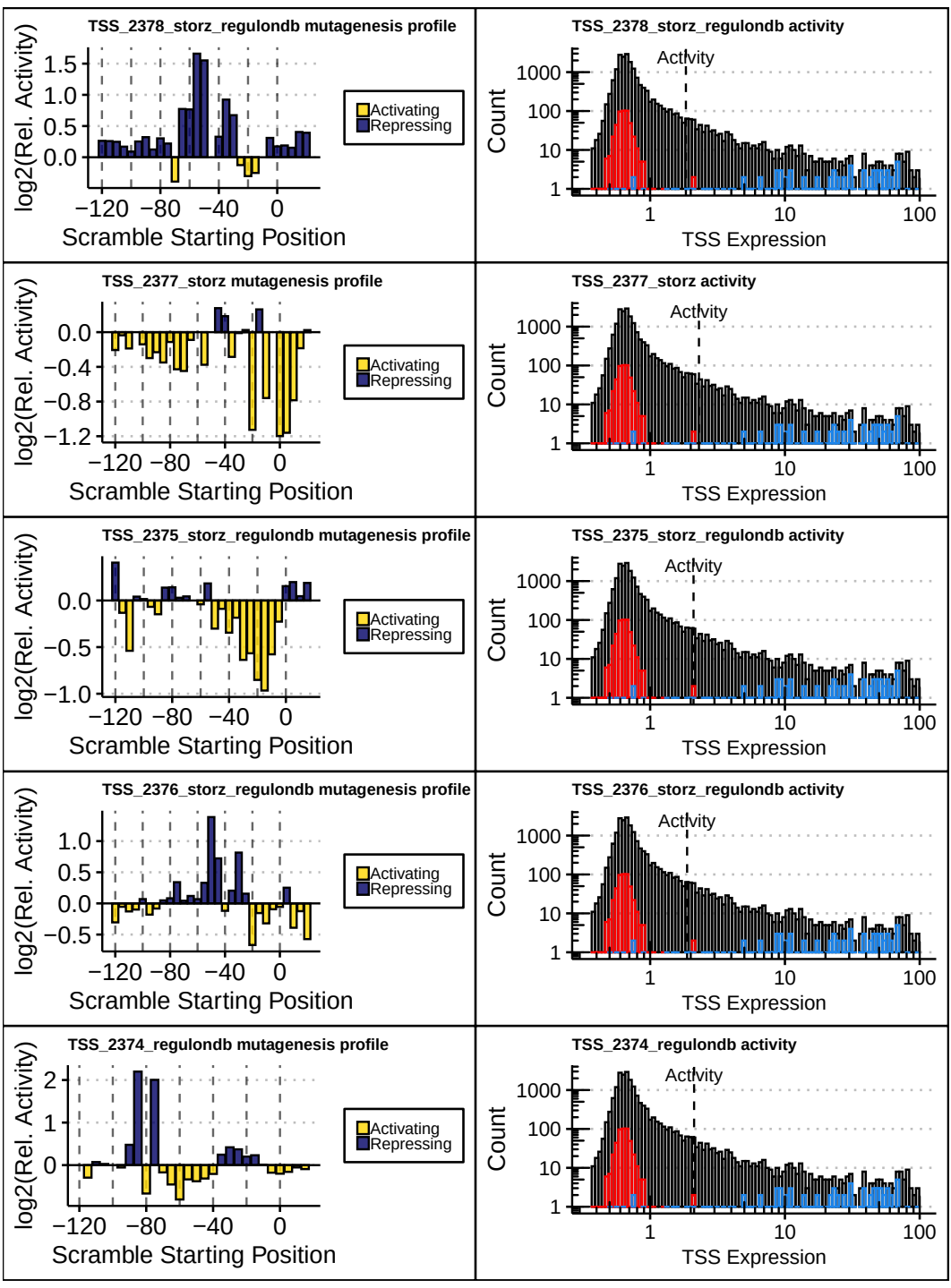

Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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