Operon Promoter Landscape

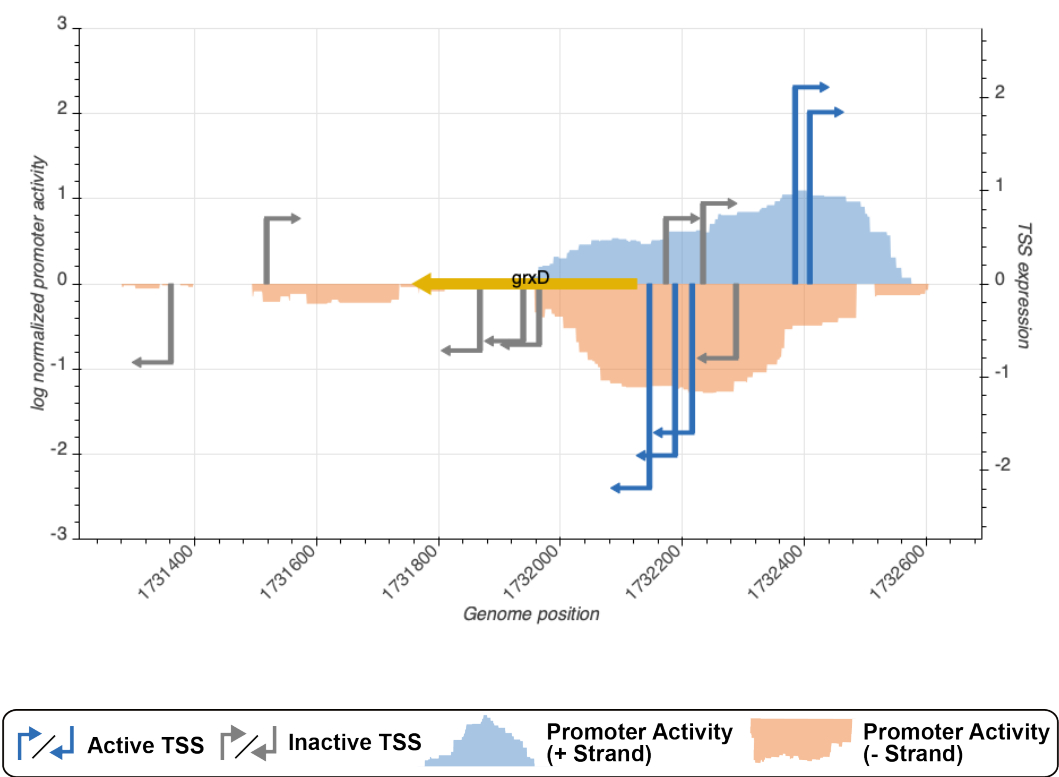| Operon	Strand	Operon start	Operon end
grxD	-	1732125	1731778

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_6639_storz	1732169	+	0.7020172	inactive
TSS_6642_storz	1732230	+	0.8620459	inactive
TSS_6645_storz	1732405	+	1.8417072	active
TSS_6640_regulondb	1732184	-	1.8417072	active
TSS_6641_wanner	1732212	-	1.5966008	active
TSS_6638_regulondb	1732142	-	2.1910928	active
TSS_6644_regulondb	1732381	+	2.1091719	active
TSS_6643_storz	1732284	-	0.7973826	inactive

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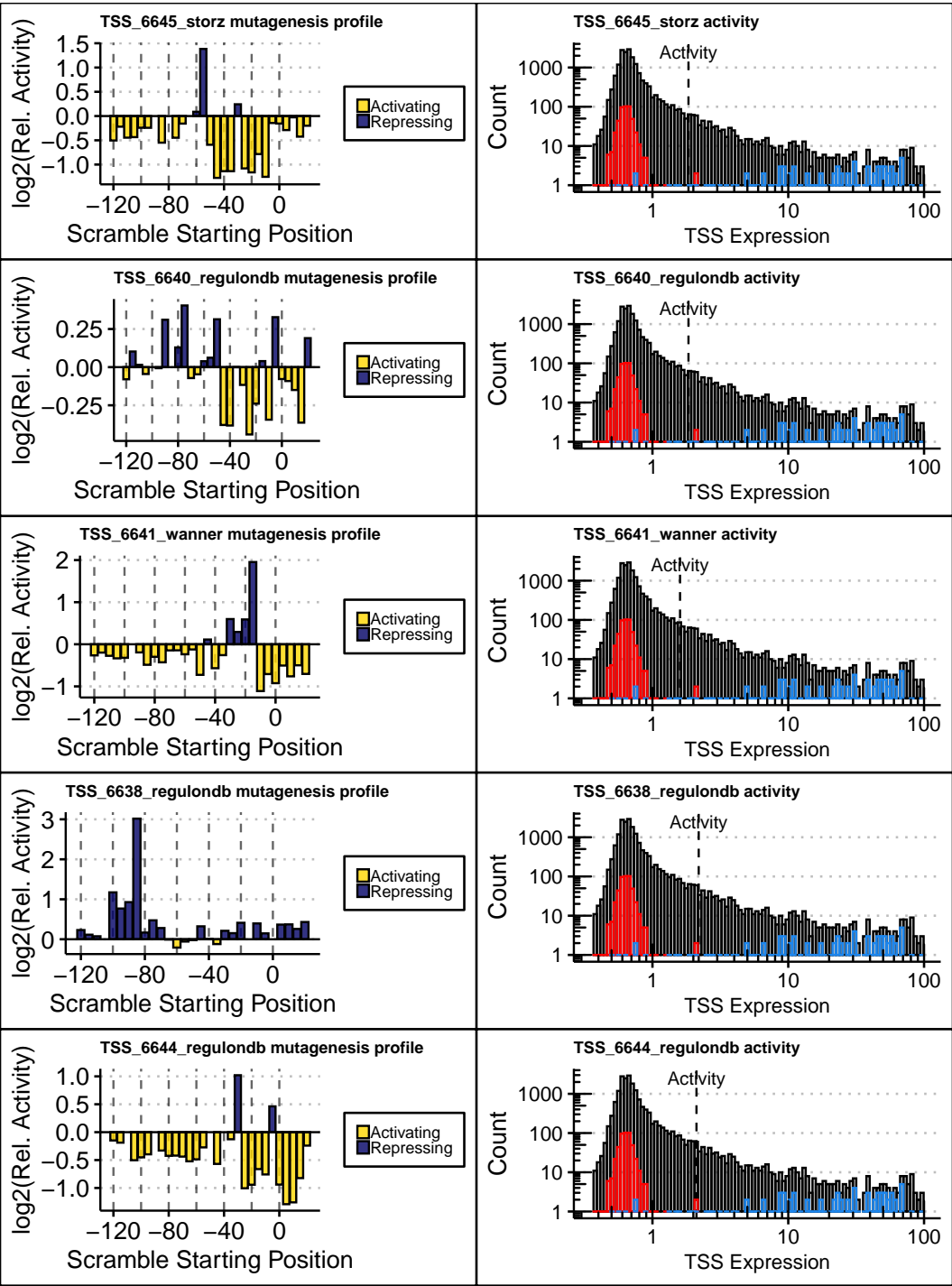
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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