Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
gltA	-	753691	752408

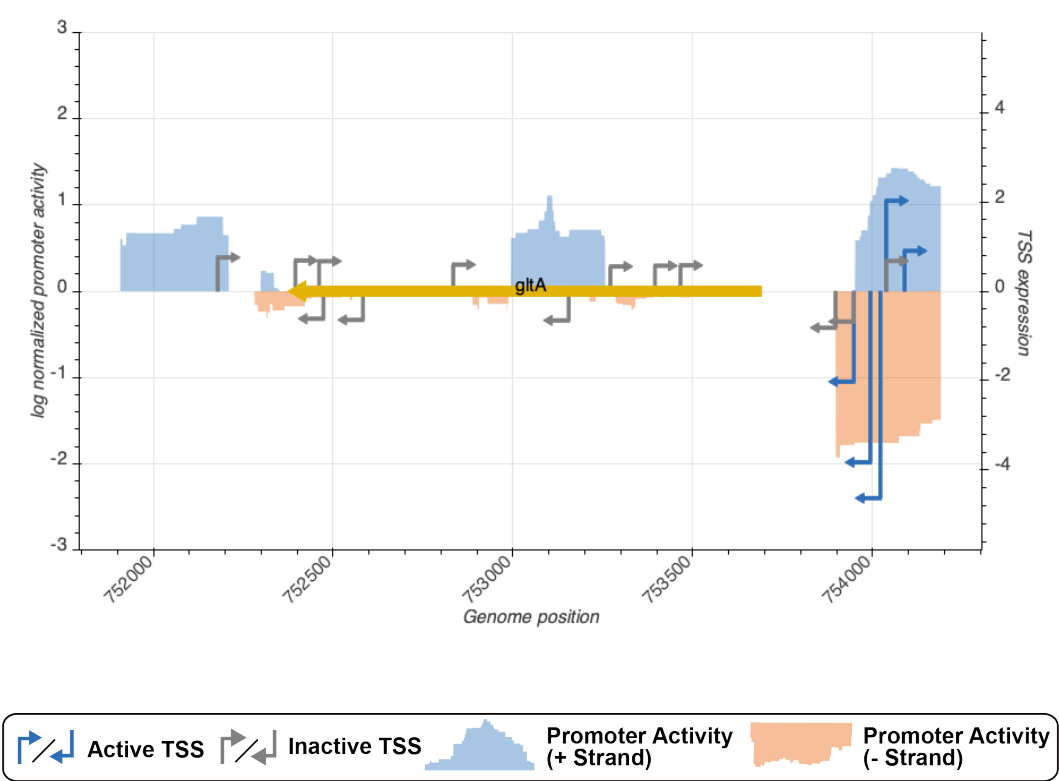|	Active TSS		Inactive TSS		Promoter Activity (+ Strand)		Promoter Activity (- Strand)

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_2891_storz	753944	-	0.6762023	inactive
TSS_2894_storz	754034	+	0.6762023	inactive
TSS_2895_storz	754085	+	0.9031555	active
TSS_2890_regulondb	753893	-	0.8163719	inactive
TSS_2891_storz	753944	-	2.0225818	active
TSS_2894_storz	754034	+	2.0225818	active
TSS_2892_regulondb	753990	-	3.8256361	active
TSS_2893_wanner	754018	-	4.6280663	active

TSS Scanning Mutagenesis

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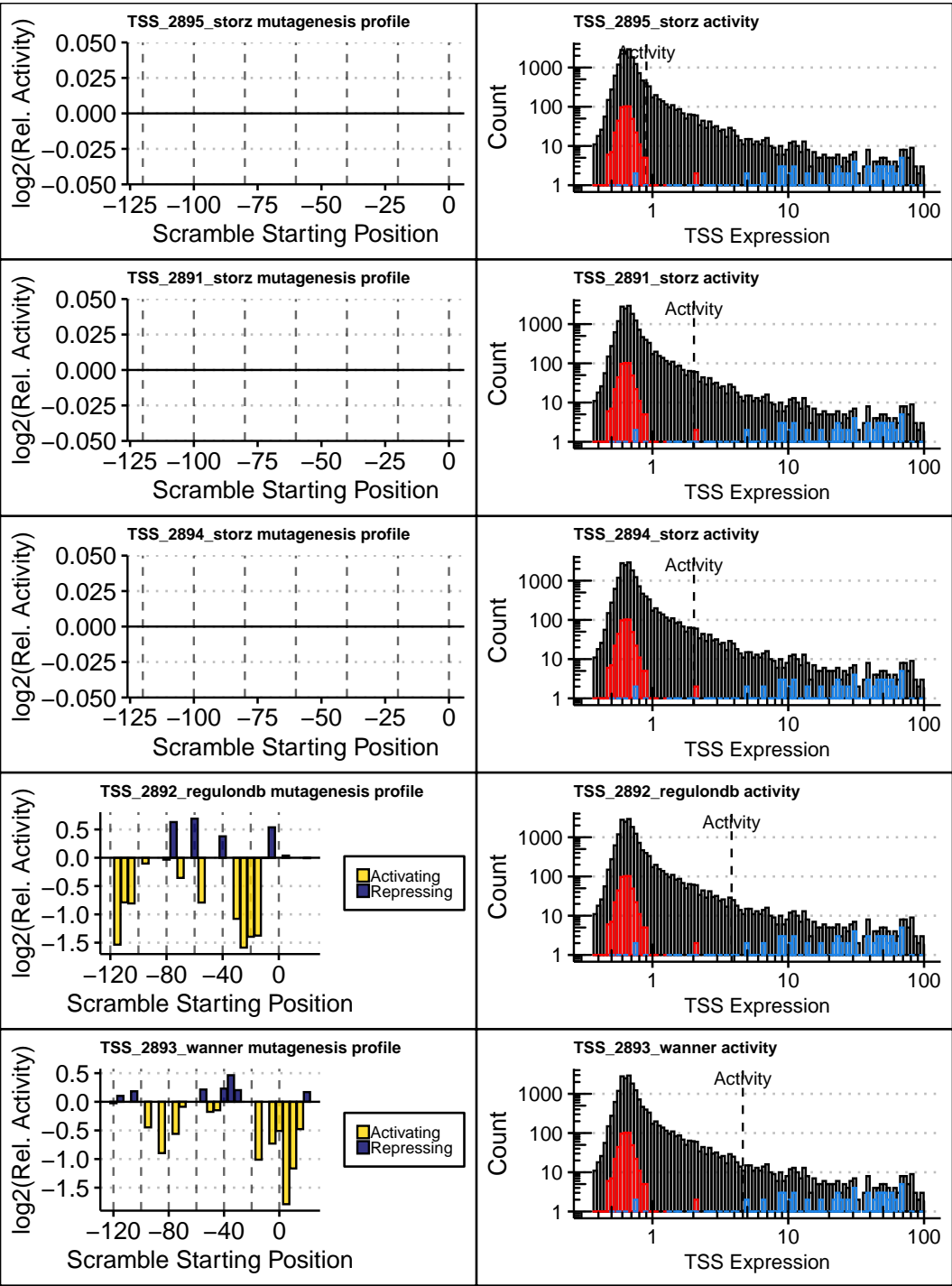
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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