

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
gcvA	-	2940589	2939672

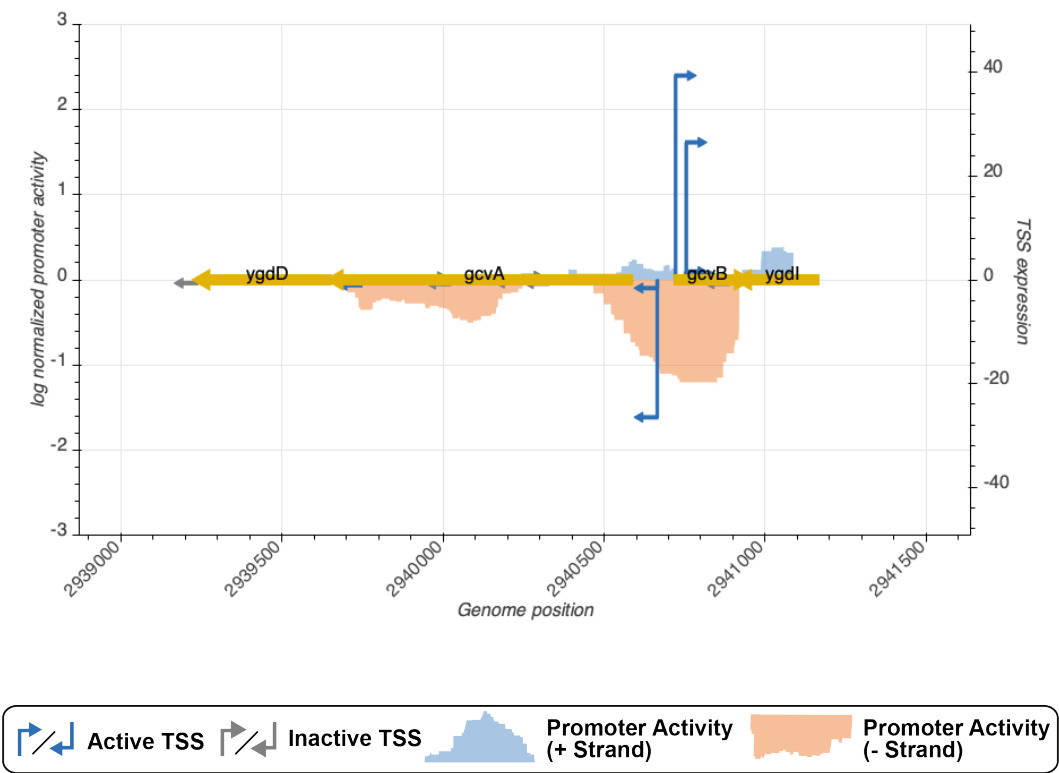


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_11099_regulondb	2940751	+	1.5970379	active
TSS_11097_storz_regulondb	2940661	-	1.5970379	active
TSS_11100_regulondb	2940782	+	0.8975689	active
TSS_11102_storz	2941030	+	0.5767730	inactive
TSS_11099_regulondb	2940751	+	26.4859254	active
TSS_11097_storz_regulondb	2940661	-	26.4859254	active
TSS_11101_storz	2940882	-	0.7700102	inactive
TSS_11098_storz_regulondb	2940718	+	39.3619003	active

TSS Scanning Mutagenesis

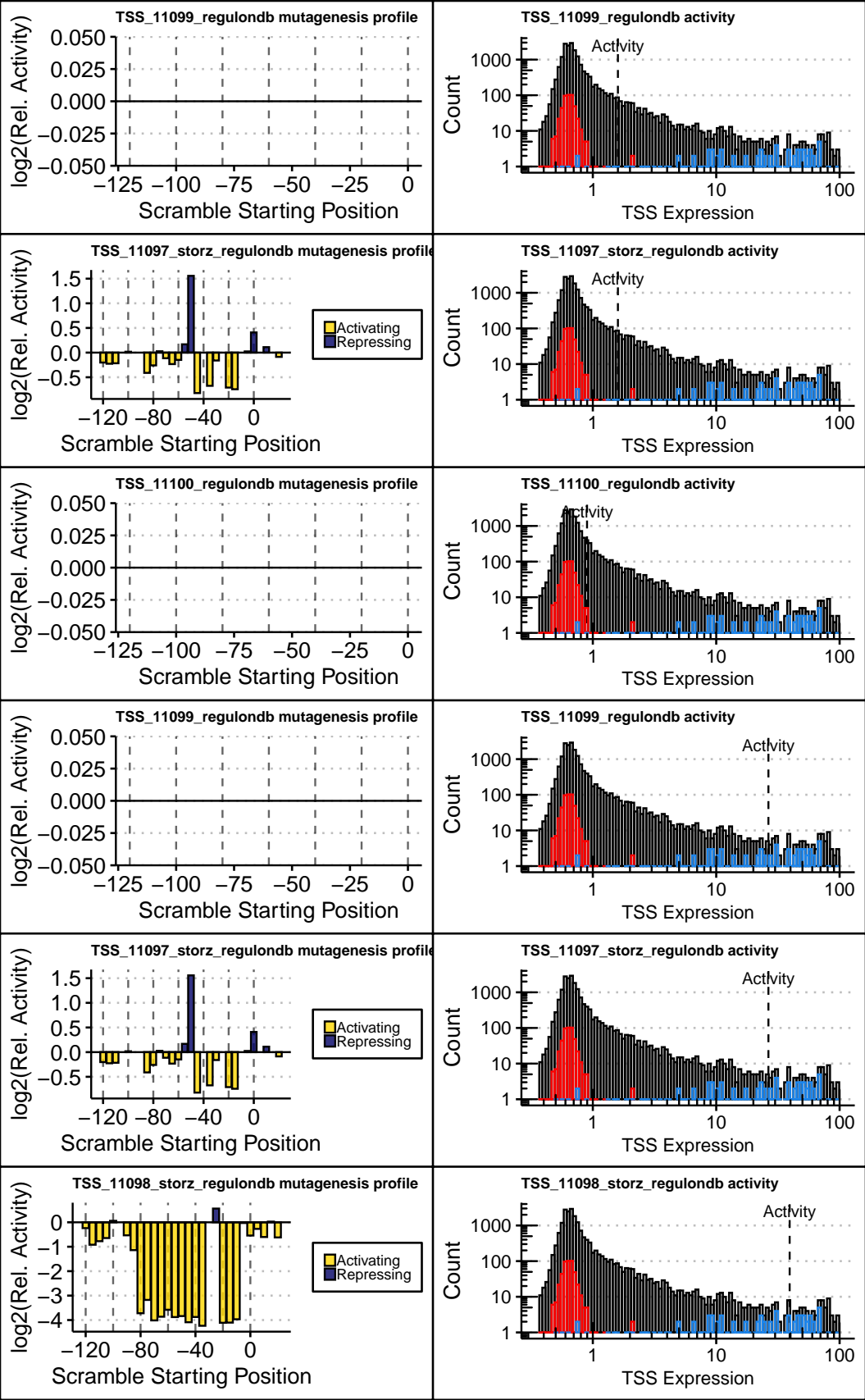


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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