

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
topA	+	1329072	1331669

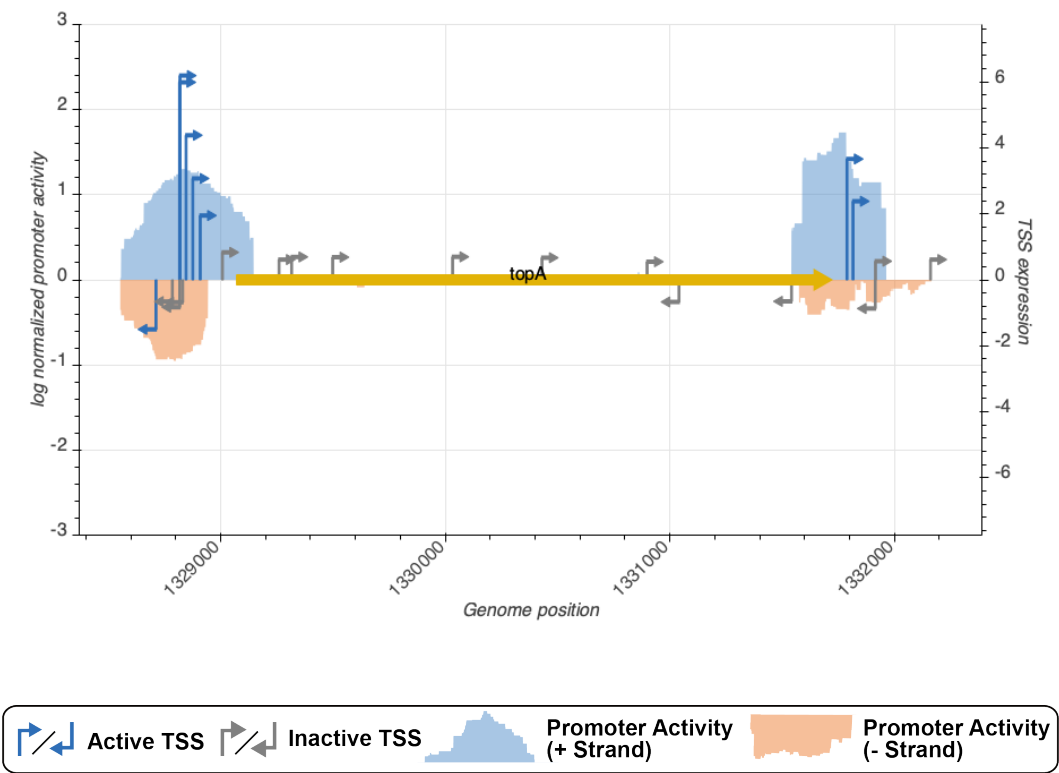


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_5249_regulondb	1328842	+	4.3807986	active
TSS_5250_regulondb	1328872	+	3.0720985	active
TSS_5252_storz_regulondb	1329004	+	0.8329888	inactive
TSS_5246_regulondb	1328814	-	0.8291135	inactive
TSS_5247_regulondb	1328815	+	6.1893072	active
TSS_5244_regulondb	1328781	-	0.6596471	inactive
TSS_5251_wanner	1328905	+	1.9483580	active
TSS_5248_regulondb	1328827	-	0.6784602	inactive
TSS_5245_storz_regulondb	1328813	+	5.9862678	active
TSS_5243_regulondb	1328708	-	1.5004366	active

TSS Scanning Mutagenesis

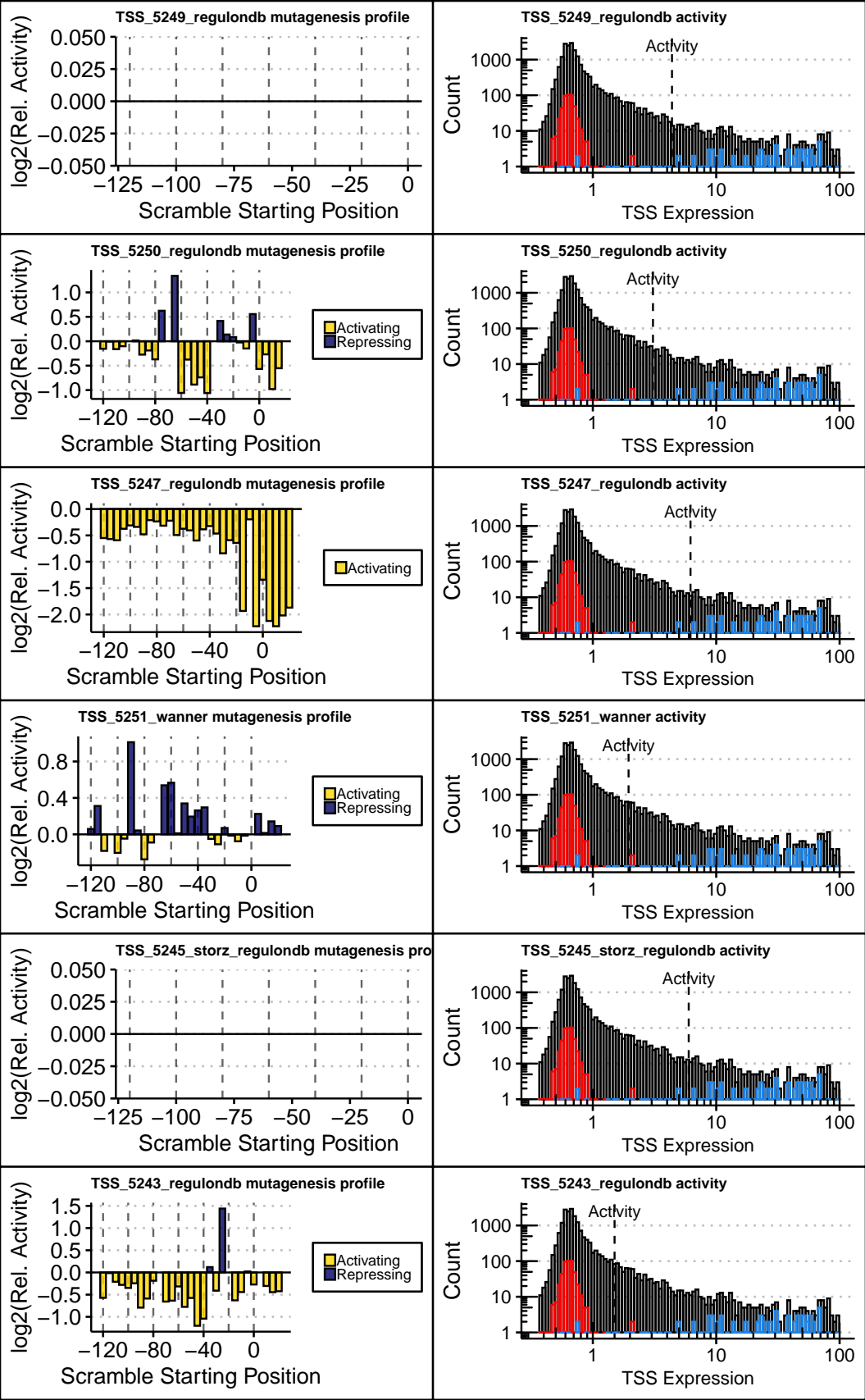


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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