

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ompR-envZ	-	3534606	3532538

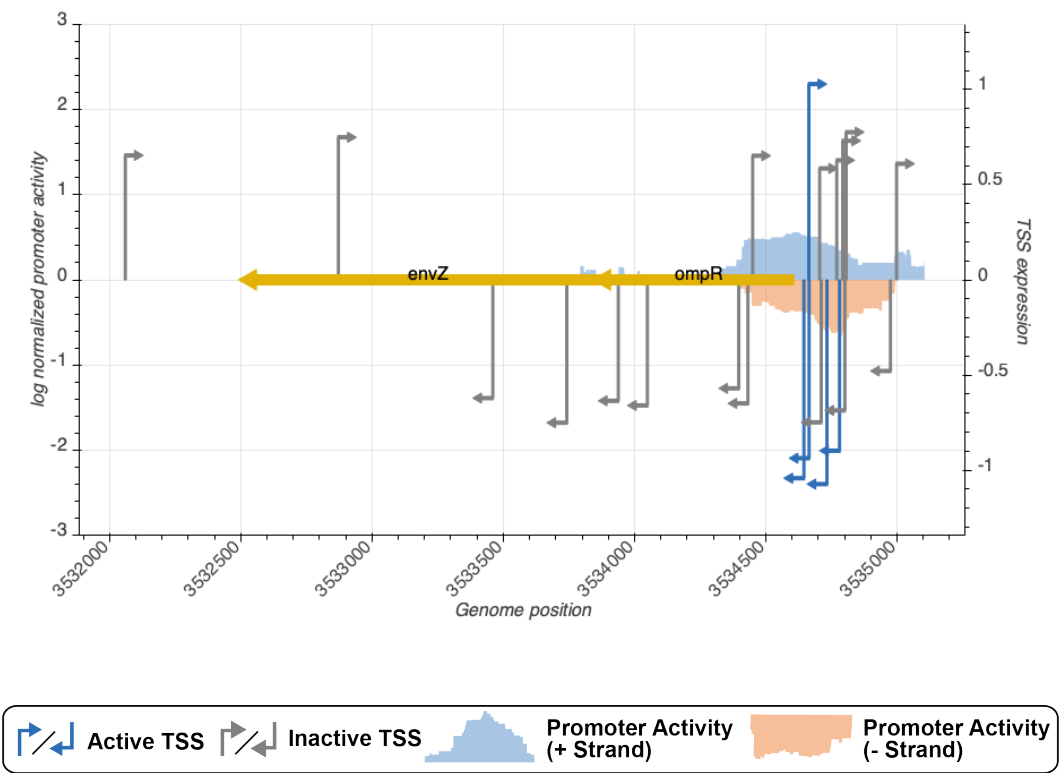


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_13686_regulondb	3534661	-	0.9378425	active
TSS_13693_storz	3534797	-	0.6864418	inactive
TSS_13696_storz	3534994	+	0.6101950	inactive
TSS_13695_storz_wanner	3534971	-	0.4794439	inactive
TSS_13689_regulondb	3534729	-	1.0737537	active
TSS_13685_wanner	3534660	+	1.0291579	active
TSS_13690_regulondb	3534766	+	0.6284063	inactive
TSS_13684_storz	3534641	-	1.0429435	active
TSS_13692_storz	3534789	+	0.7308868	inactive
TSS_13694_regulondb	3534802	+	0.7763383	inactive
TSS_13688_storz_regulondb	3534707	-	0.7490217	inactive
TSS_13691_storz_regulondb	3534777	-	0.8983683	active
TSS_13687_storz	3534701	+	0.5857851	inactive

TSS Scanning Mutagenesis

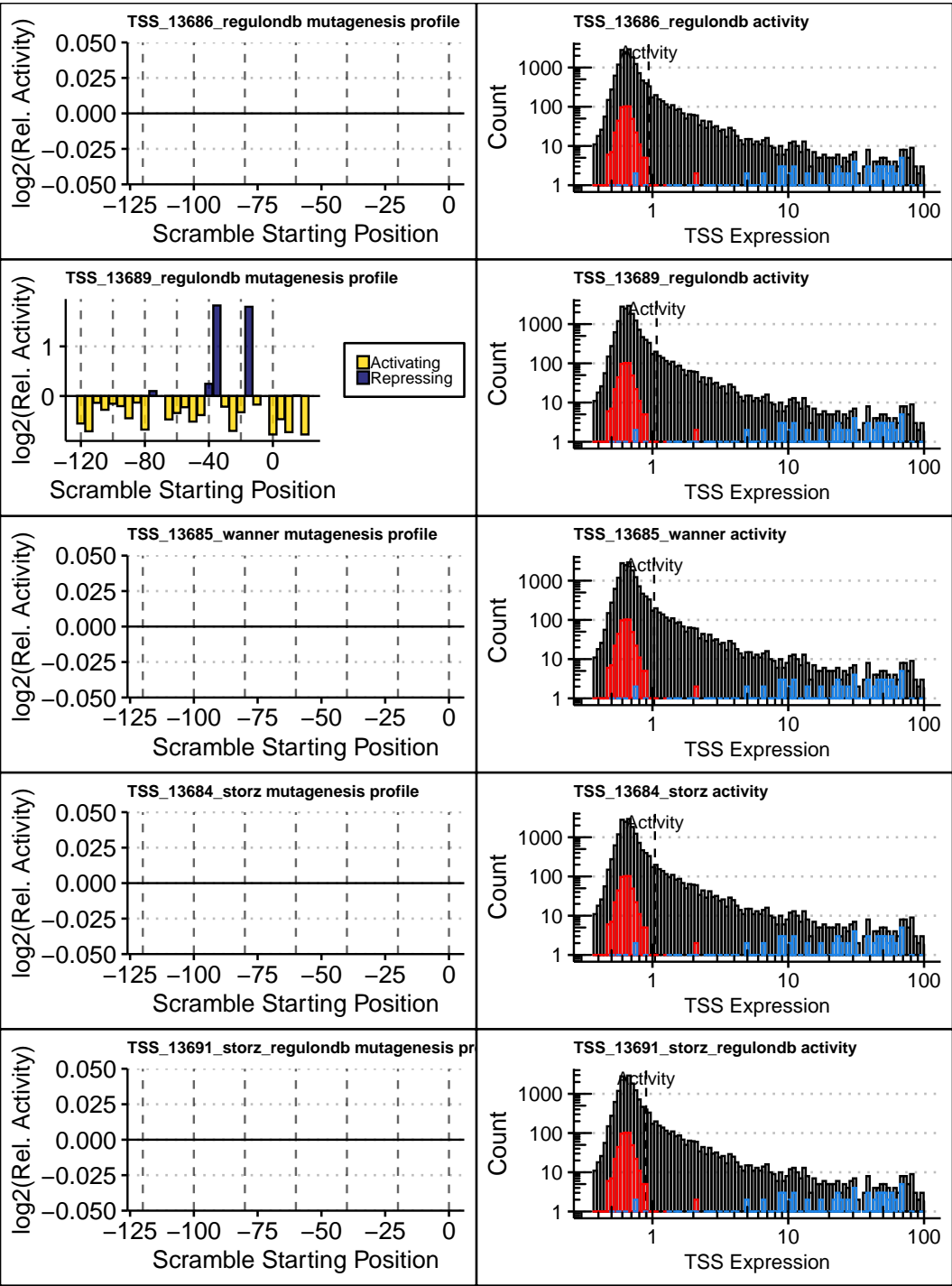


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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