

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
rrsG-gltW-rrlG-rrfG	-	2729179	2724091

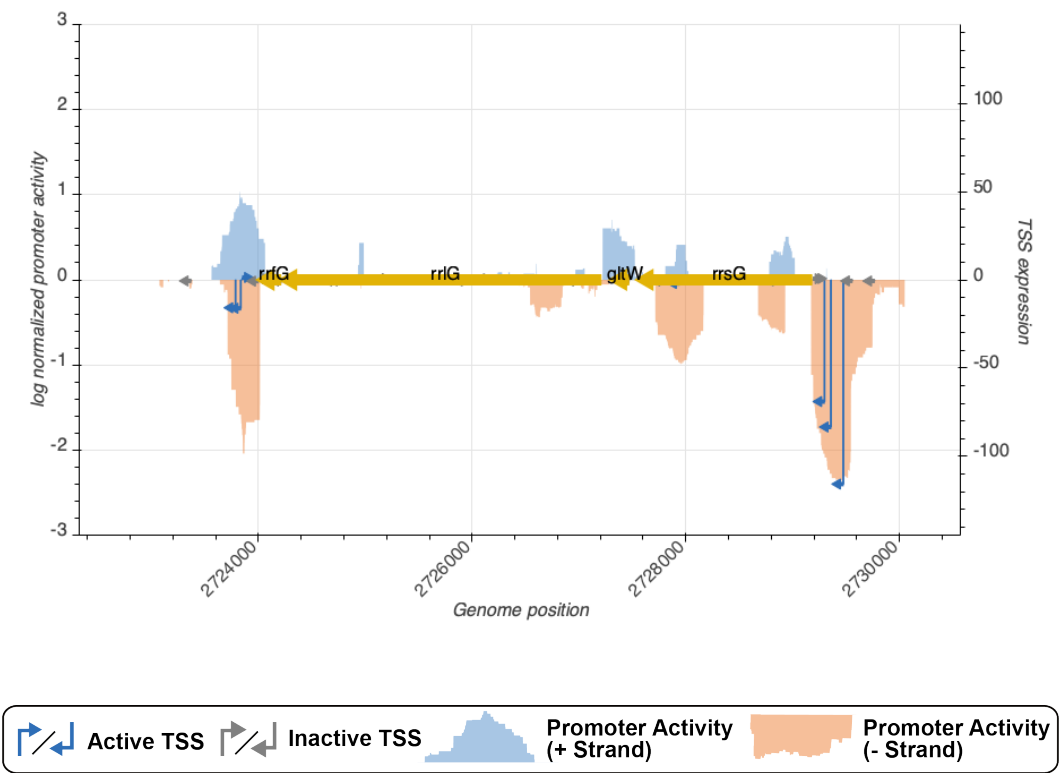


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_10285_storz	2729215	+	0.7402951	inactive
TSS_10286_regulondb	2729294	-	68.9169741	active
TSS_10291_storz	2729553	-	0.5972719	inactive
TSS_10284_storz	2729188	+	0.6139024	inactive
TSS_10288_storz_regulondb	2729354	-	83.3295198	active
TSS_10290_storz_wanner_regulondb	2729470	-	115.6534937	active

TSS Scanning Mutagenesis

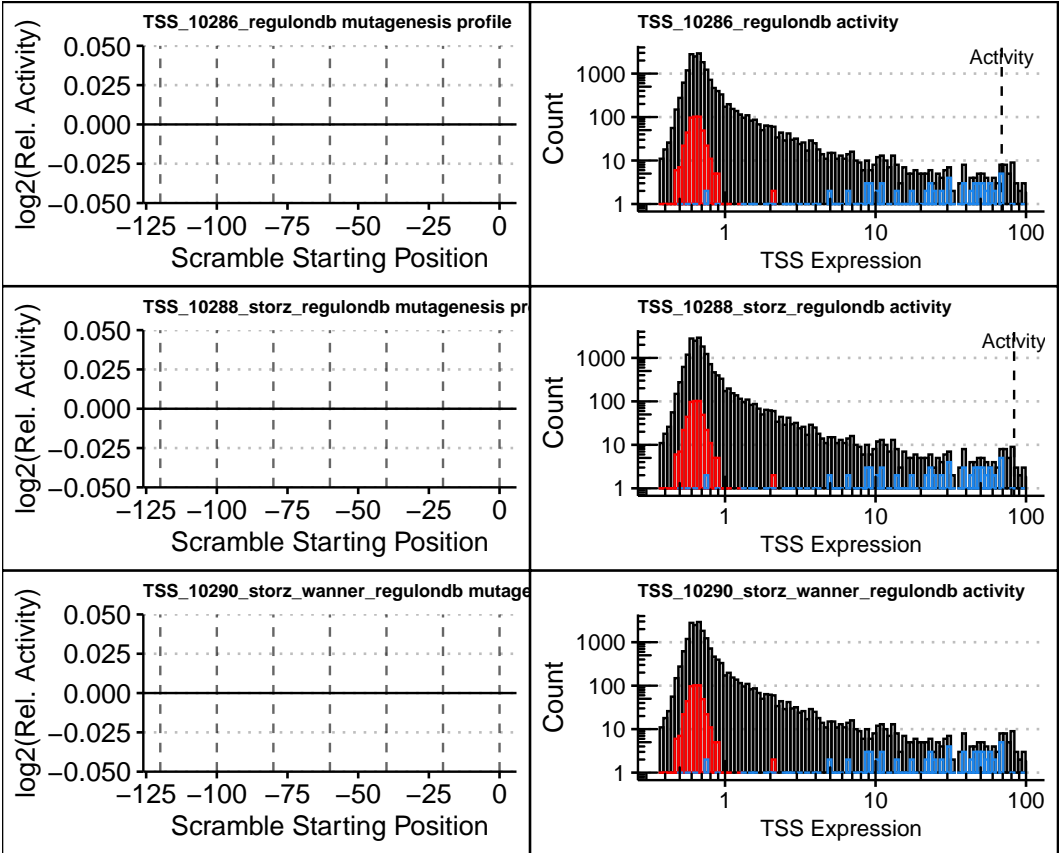


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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