

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
rsgA	-	4389532	4388480

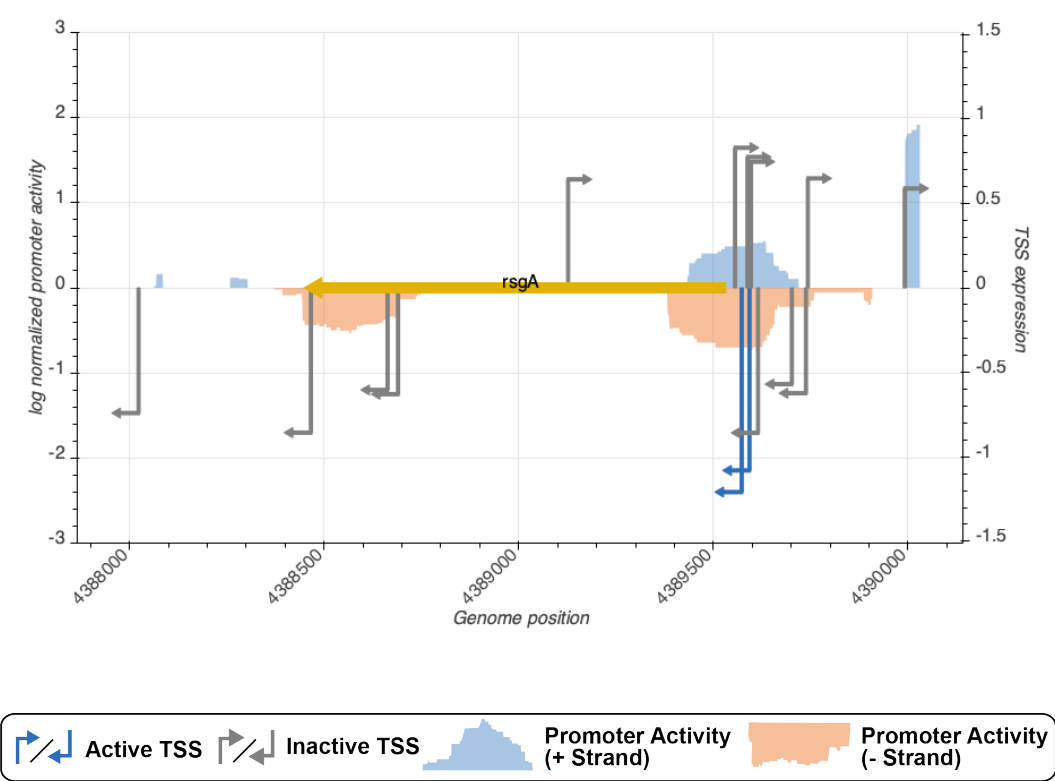


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_17153_wanner	4389611	-	0.8578947	inactive
TSS_17150_regulondb	4389584	+	0.7742690	inactive
TSS_17155_storz	4389734	-	0.6235306	inactive
TSS_17156_regulondb	4389739	+	0.6475954	inactive
TSS_17154_storz	4389698	-	0.5698878	inactive
TSS_17149_storz	4389569	-	1.2086923	active
TSS_17152_regulondb	4389593	+	0.7460921	inactive
TSS_17151_regulondb	4389589	-	1.0805623	active
TSS_17157_storz	4389988	+	0.5877704	inactive
TSS_17148_wanner	4389552	+	0.8291135	inactive

TSS Scanning Mutagenesis

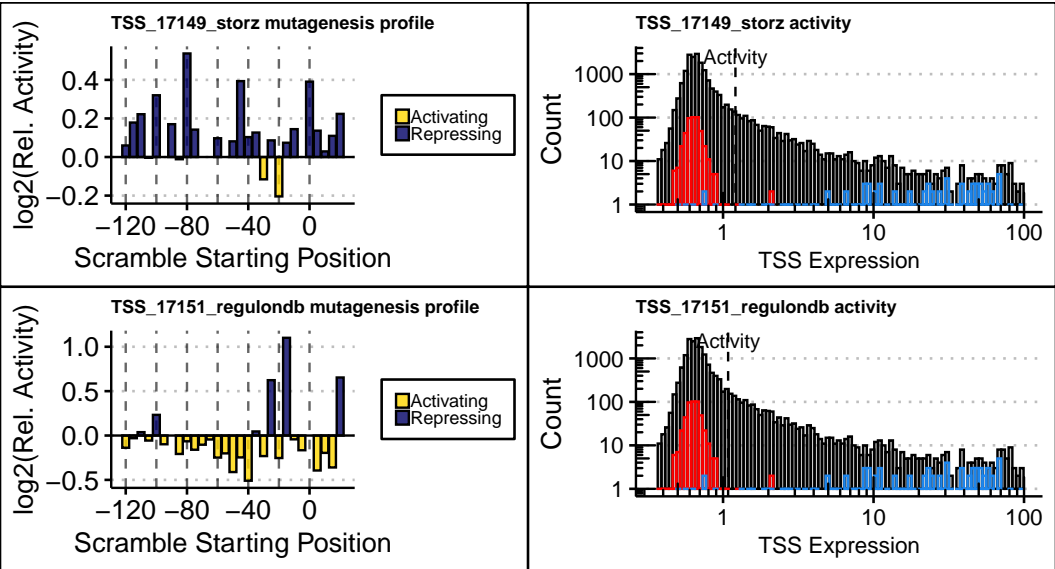


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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