

Operon Promoter Landscape

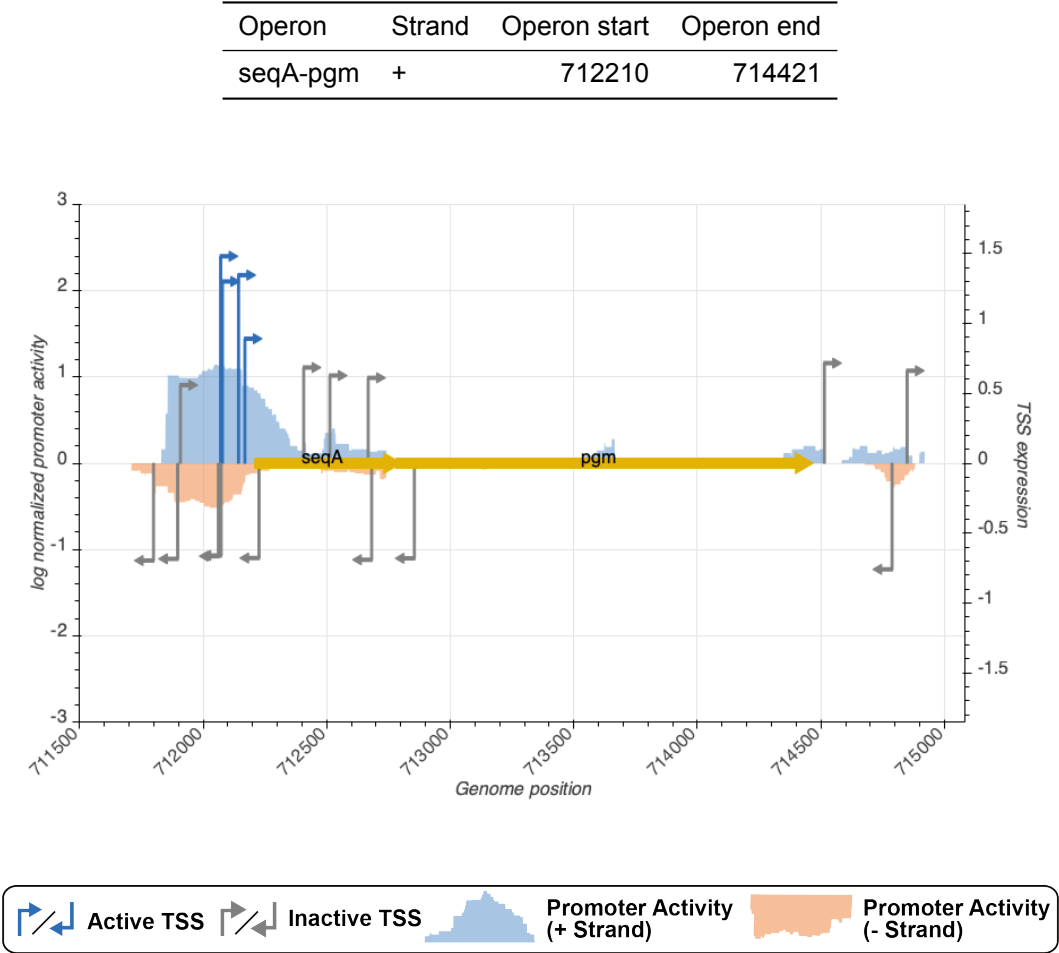


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_2761_regulondb	712069	-	0.6600572	inactive
TSS_2763_regulondb	712139	+	1.3456037	active
TSS_2756_storz	711795	-	0.6961009	inactive
TSS_2760_storz	712067	+	1.4803132	active
TSS_2757_storz	711893	-	0.6839256	inactive
TSS_2764_regulondb	712165	+	0.8902736	active
TSS_2759_storz	712058	-	0.6649449	inactive
TSS_2758_storz	711904	+	0.5586037	inactive
TSS_2762_storz_regulondb	712074	+	1.3000571	active

TSS Scanning Mutagenesis

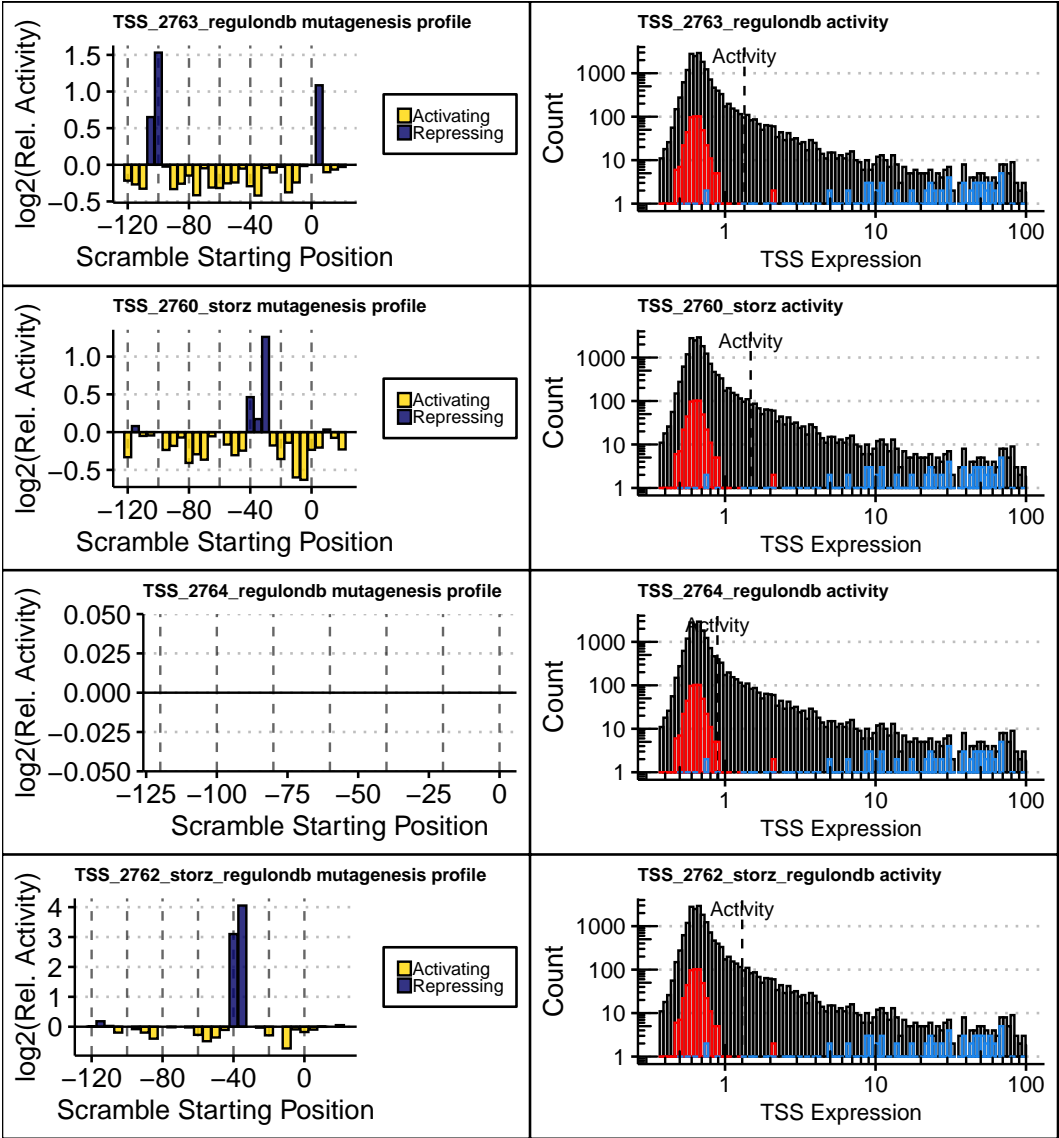


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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