Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
sdaCB	+	2926251	2928965

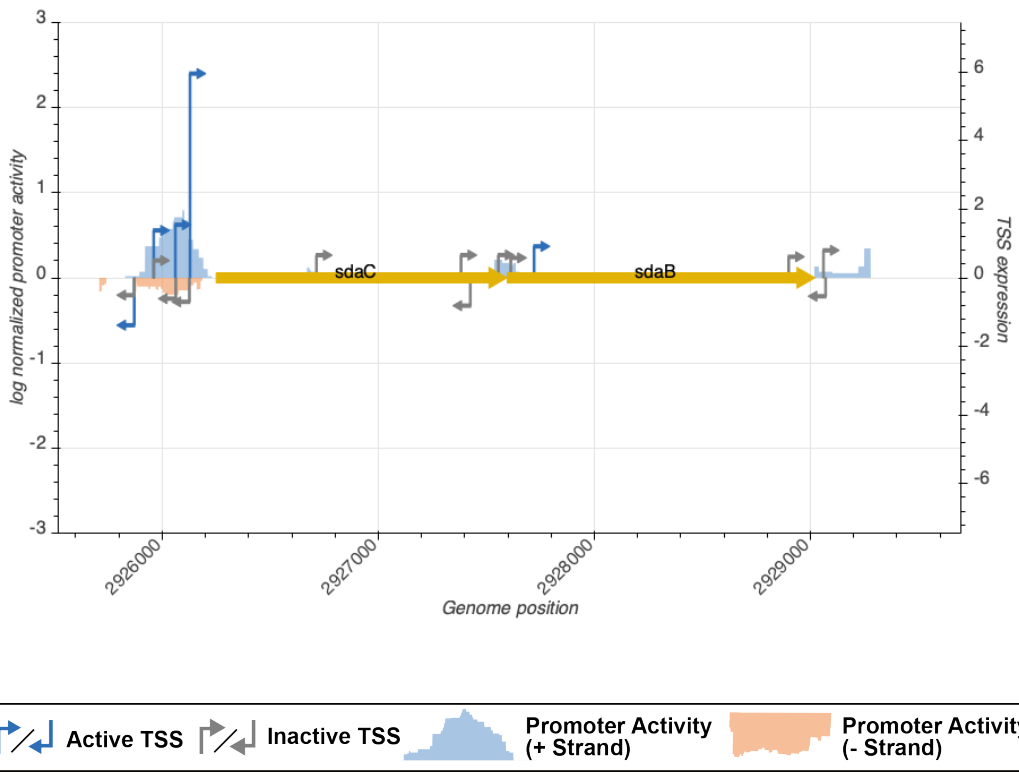

Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_11039_storz	2925957	+	0.5051275	inactive
TSS_11038_storz	2925867	-	0.5051275	inactive
TSS_11038_storz	2925867	-	1.3809351	active
TSS_11039_storz	2925957	+	1.3809351	active
TSS_11043_storz_wanner	2926125	+	5.9532420	active
TSS_11042_storz	2926122	-	0.7006385	inactive
TSS_11041_storz	2926059	-	0.6068933	inactive
TSS_11040_regulondb	2926057	+	1.5471140	active

TSS Scanning Mutagenesis

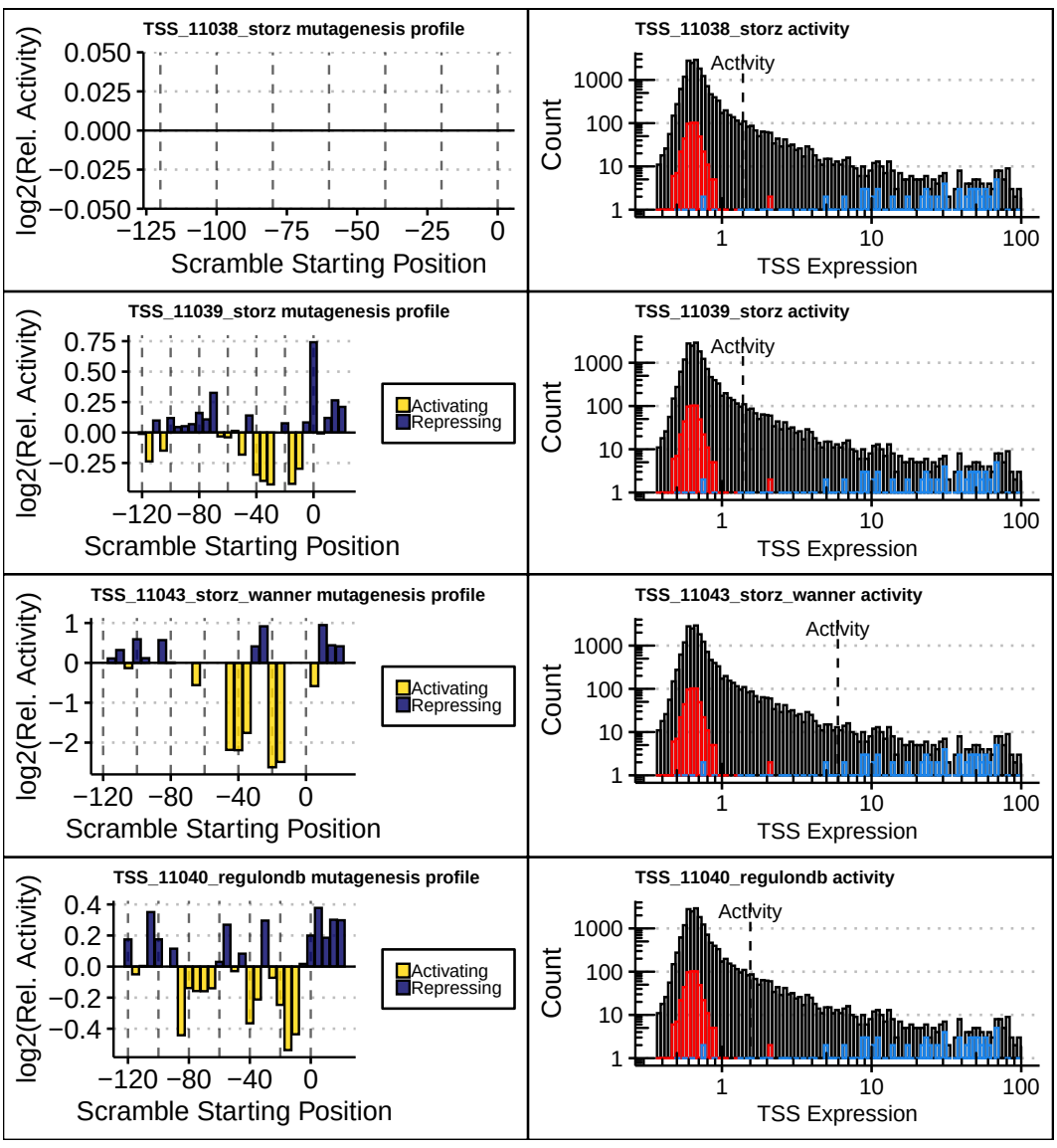

Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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