

Operon Promoter Landscape

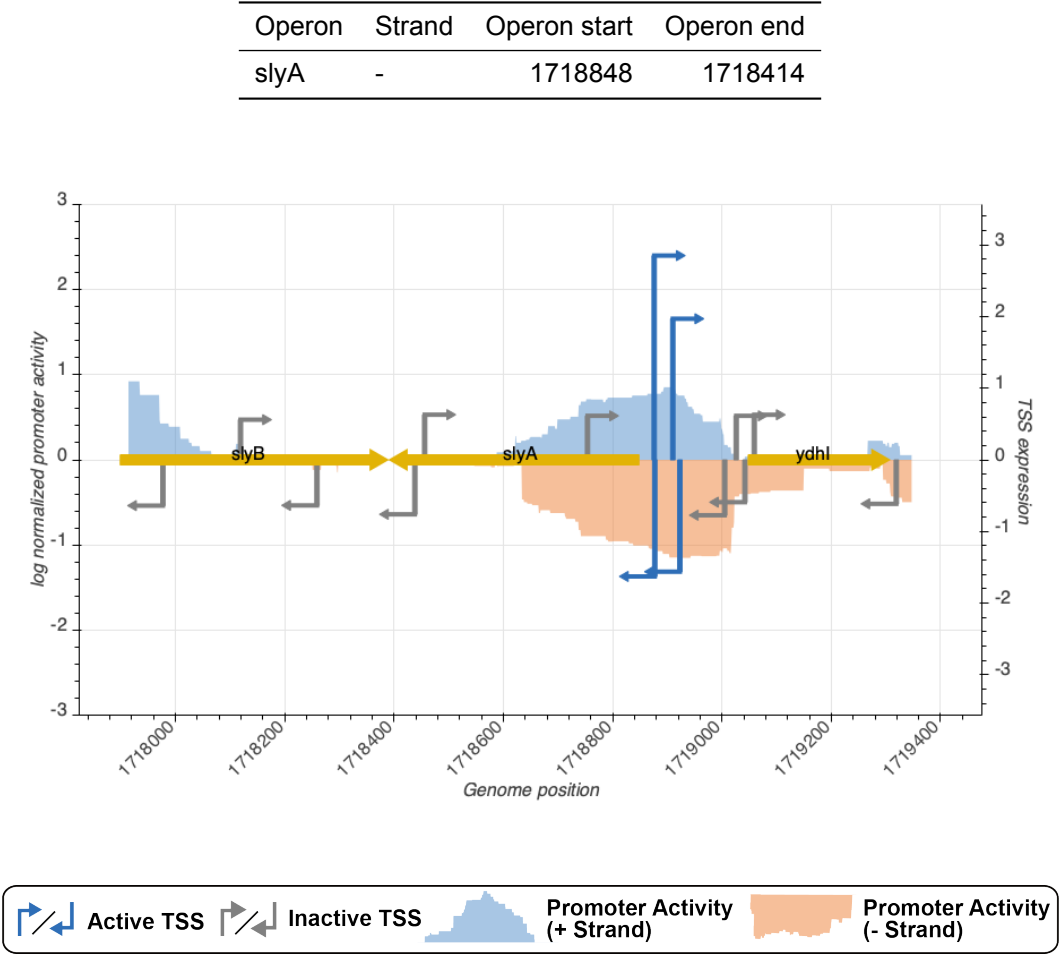


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_6599_storz	1719001	-	0.7733030	inactive
TSS_6601_regulondb	1719038	-	0.5912551	inactive
TSS_6595_storz	1718872	+	2.8510833	active
TSS_6602_storz	1719055	+	0.6293075	inactive
TSS_6596_regulondb	1718873	-	1.6276470	active
TSS_6597_storz	1718906	+	1.9691240	active
TSS_6603_wanner	1719315	-	0.6139024	inactive
TSS_6600_regulondb	1719022	+	0.6139024	inactive
TSS_6598_wanner	1718919	-	1.5612844	active

TSS Scanning Mutagenesis

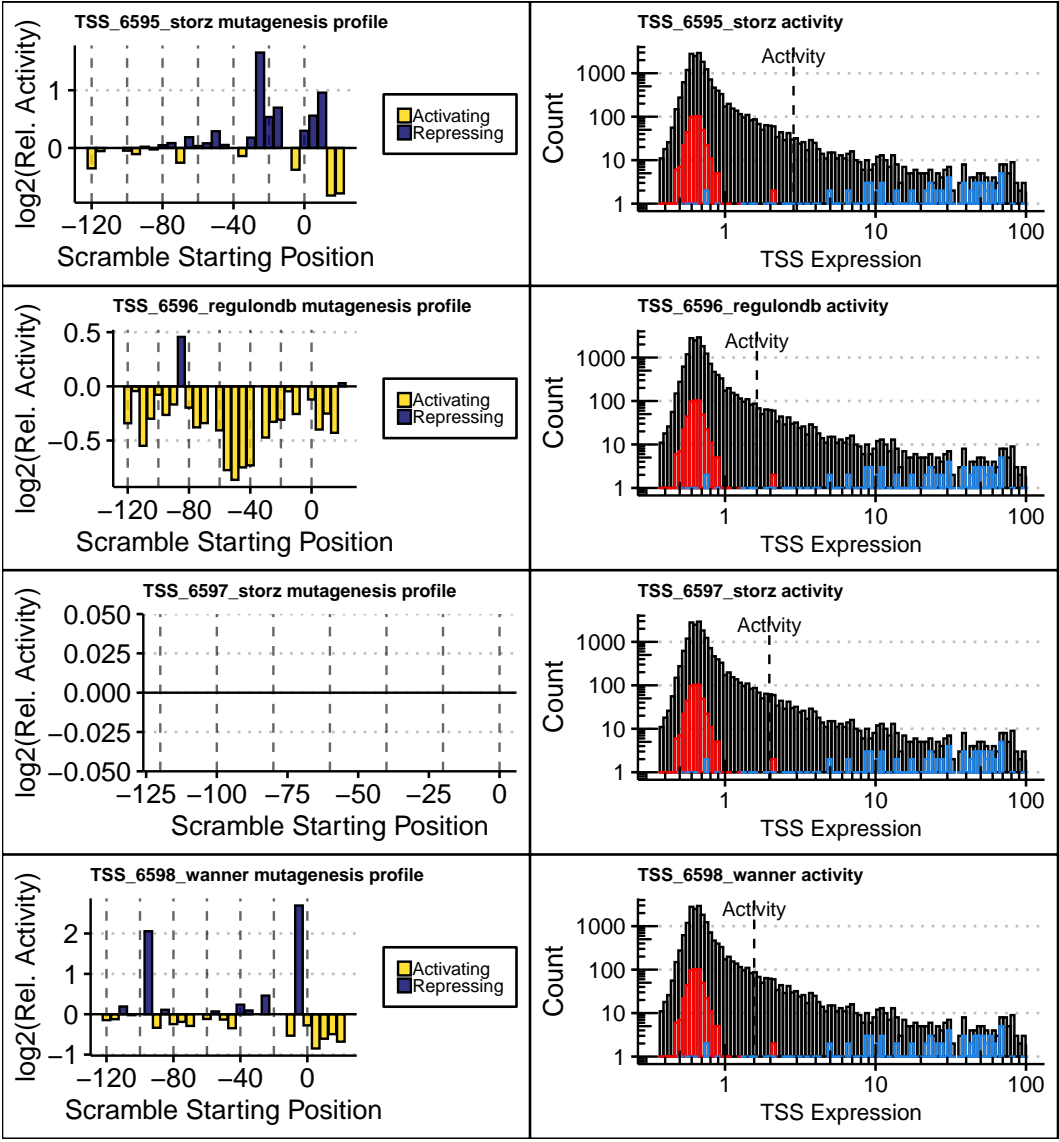


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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