

Operon Promoter Landscape

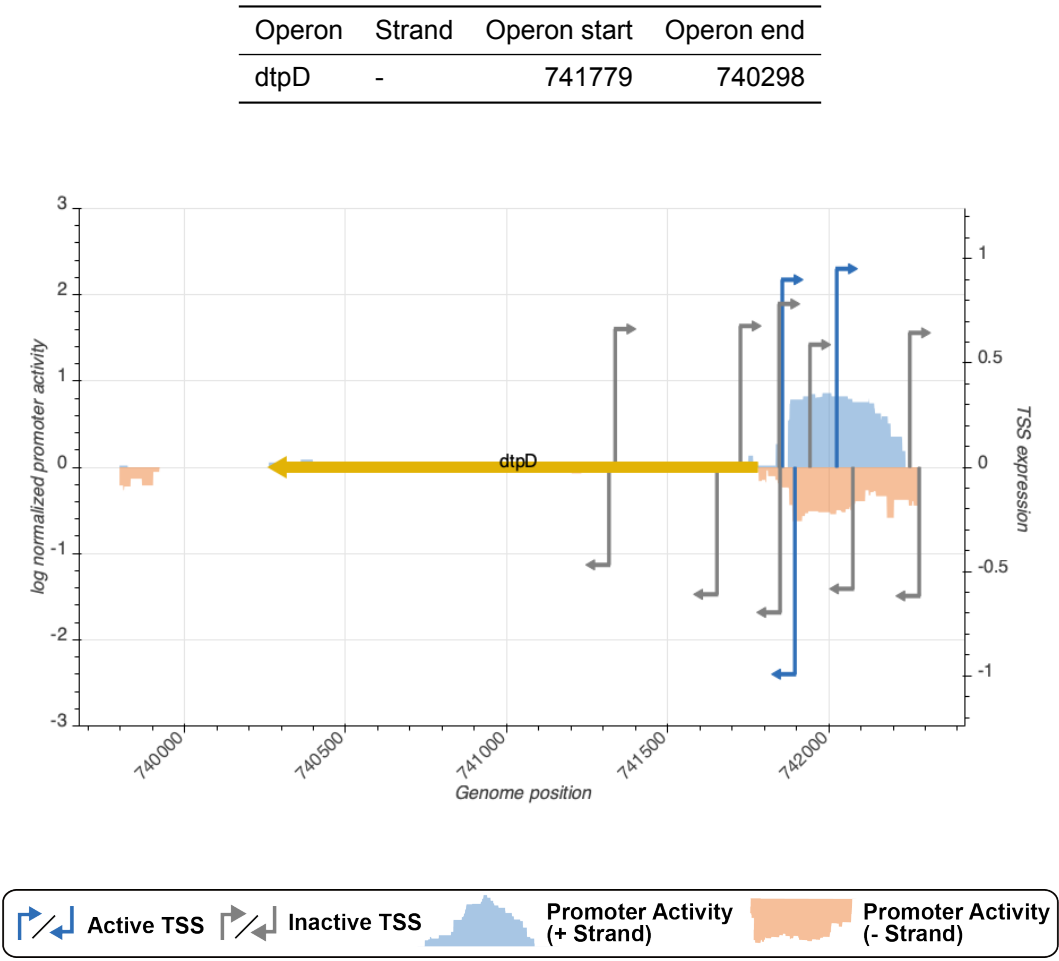


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_2838_regulondb	741842	+	0.7828982	inactive
TSS_2844_storz	742071	-	0.5830922	inactive
TSS_2839_regulondb	741845	-	0.6961009	inactive
TSS_2842_wanner	741938	+	0.5874936	inactive
TSS_2840_storz	741852	+	0.8990107	active
TSS_2846_storz	742277	-	0.6170700	inactive
TSS_2845_storz	742248	+	0.6442553	inactive
TSS_2841_wanner	741891	-	0.9922070	active
TSS_2843_storz_regulondb	742021	+	0.9514336	active

TSS Scanning Mutagenesis

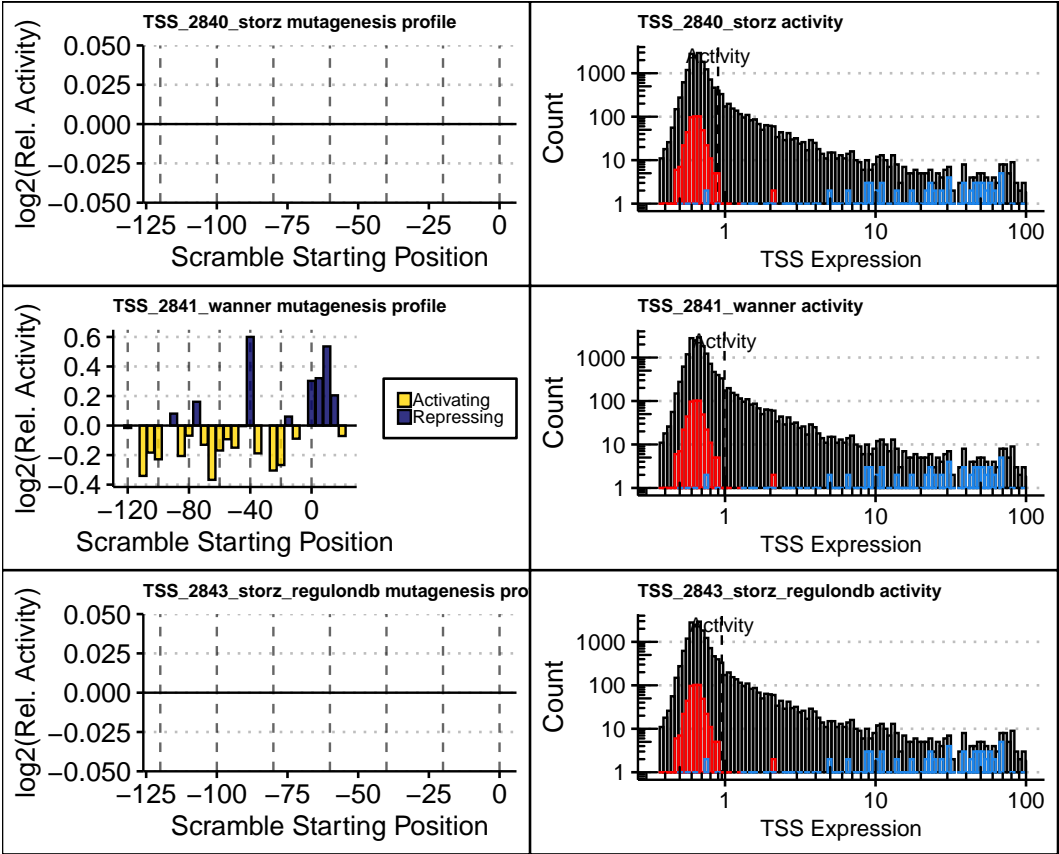


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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