

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
dapA-bamC	-	2597782	2595853

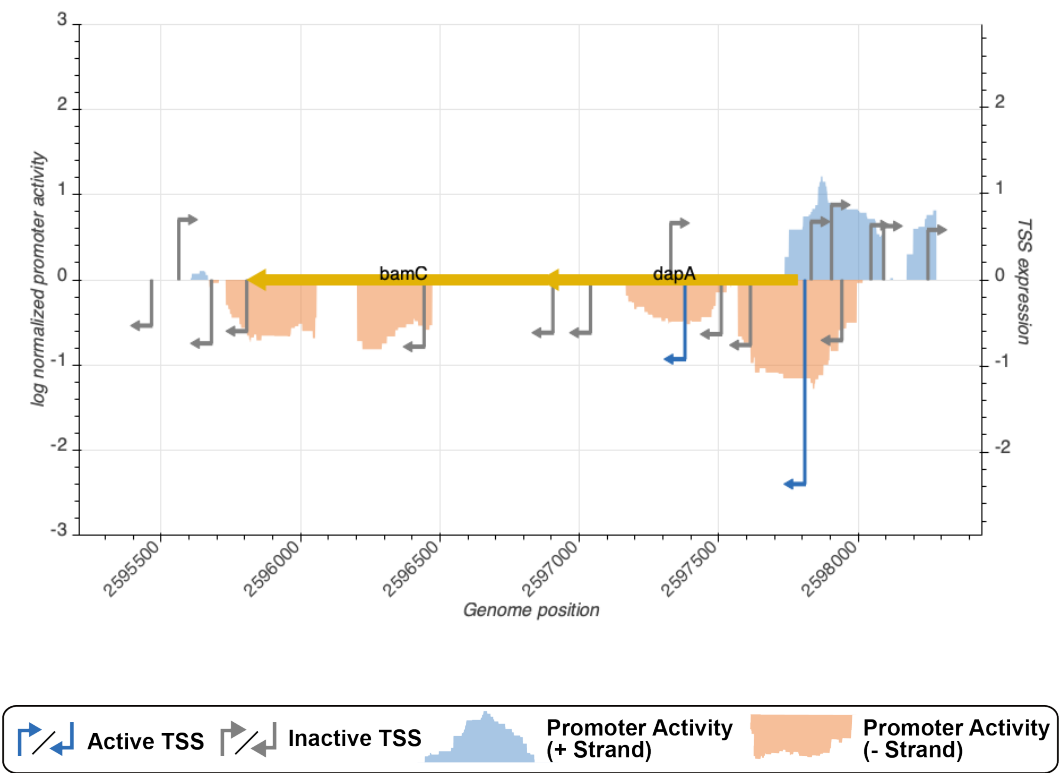


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_9779_storz	2597938	-	0.7015562	inactive
TSS_9781_storz	2598088	+	0.6243559	inactive
TSS_9778_storz_regulondb	2597901	+	0.8698869	inactive
TSS_9780_storz	2598042	+	0.6342891	inactive
TSS_9777_regulondb	2597828	+	0.6750625	inactive
TSS_9776_wanner	2597805	-	2.3712155	active
TSS_9783_regulondb	2598247	+	0.5802980	inactive

TSS Scanning Mutagenesis

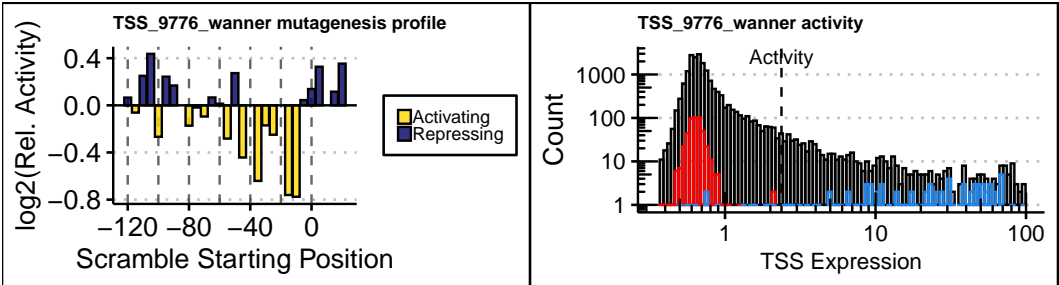


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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