Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
bamD	+	2734168	2734905

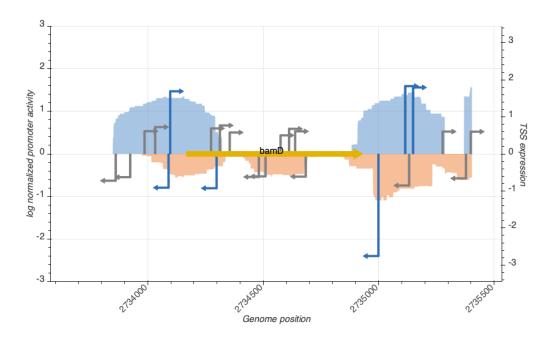


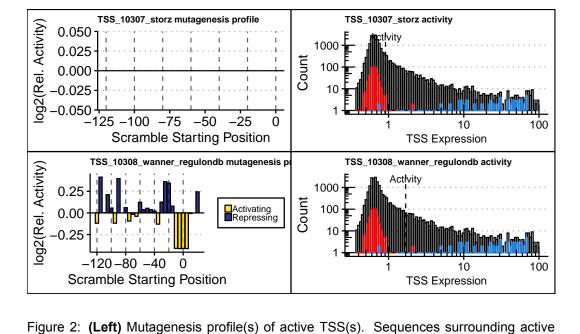


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_10305_storz_regulondb	2733982	+	0.6139024	inactive
TSS_10307_storz	2734086	-	0.9116586	active
TSS_10303_regulondb	2733857	-	0.7230918	inactive
TSS_10308_wanner_regulondb	2734093	+	1.6908237	active
TSS_10304_regulondb	2733920	-	0.6279070	inactive
TSS_10306_regulondb	2734028	+	0.7254547	inactive

TSS Scanning Mutagenesis



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).