Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yrbG-kdsDC-lptCAB-rpoN-hpf-ptsN-rapZ-npr	+	3338297	3346260

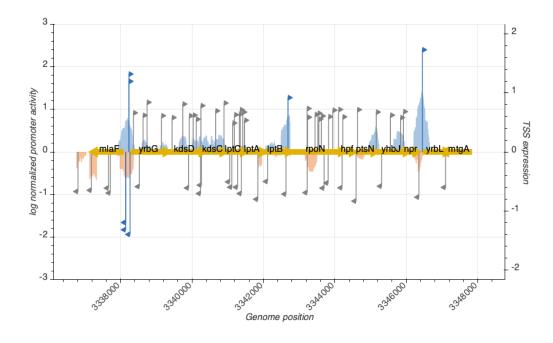




Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_12716_storz	3338143	-	1.197019	active
TSS_12717_storz_regulondb	3338233	+	1.197019	active
TSS_12716_storz	3338143	-	1.321336	active
TSS_12717_storz_regulondb	3338233	+	1.321336	active
TSS_12718_storz_wanner	3338265	-	1.399591	active

TSS Scanning Mutagenesis

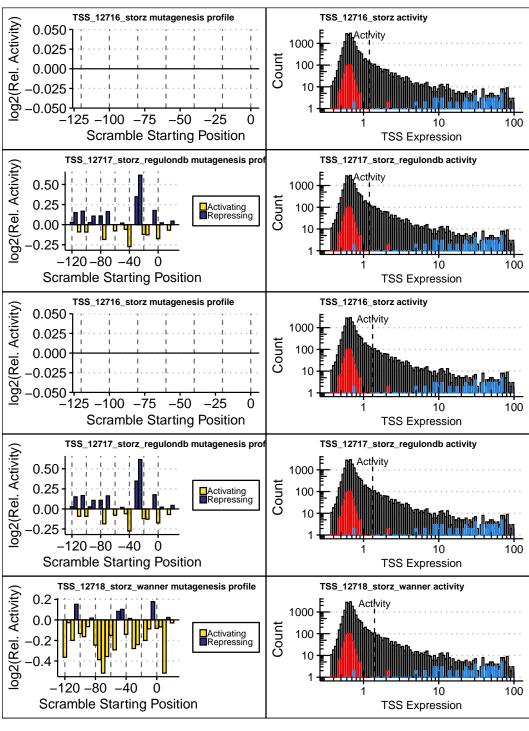


Figure 2: (Left) Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals spanning the promoter. Bar color identifies the region as a putative activator (yellow) or repressor (purple). (Right) Dashed line indicates the ex-

pression 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

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constitutive promoters from the BioBrick registry (blue).