## **Operon Promoter Landscape**

Operon	Strand	Operon start	Operon end
ompA	-	1019276	1018236

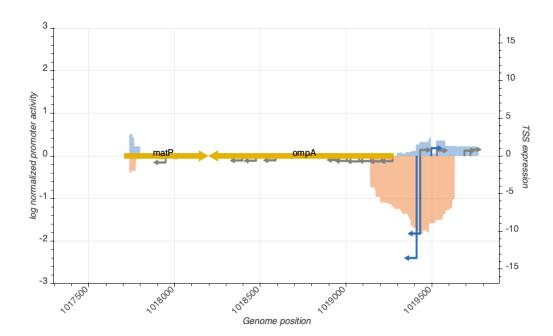


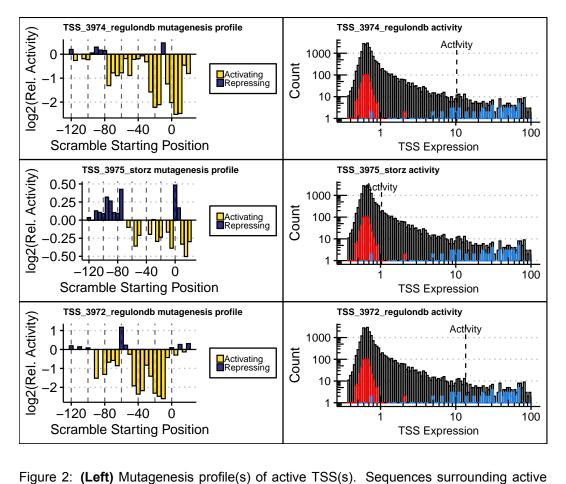


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_3973_storz	1019427	+	0.7936150	inactive
TSS_3978_storz	1019721	+	0.8427014	inactive
TSS_3974_regulondb	1019428	-	10.3004094	active
TSS_3975_storz	1019493	+	1.0312620	active
TSS_3972_regulondb	1019407	-	13.5484678	active
TSS_3976_wanner	1019525	+	0.7256533	inactive
TSS_3977_storz	1019686	+	0.6973025	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).