Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ymgF	+	1218206	1218424

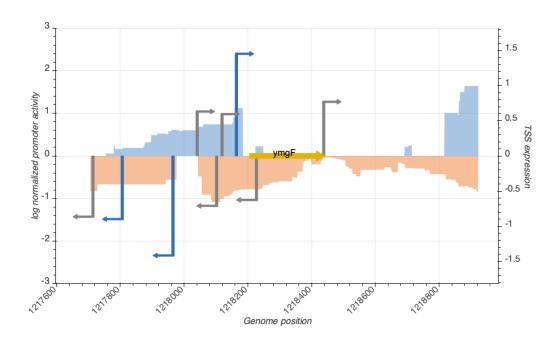


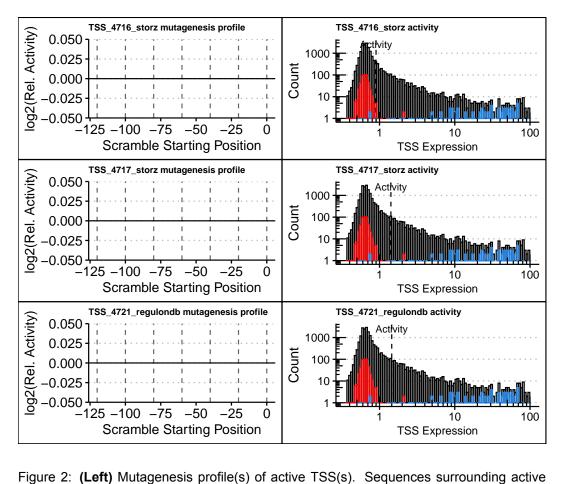


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_4716_storz	1217802	-	0.8990107	active
TSS_4717_storz	1217961	-	1.4165174	active
TSS_4718_regulondb	1218037	+	0.6318371	inactive
TSS_4721_regulondb	1218160	+	1.4527874	active
TSS_4719_wanner	1218098	-	0.7104607	inactive
TSS_4715_storz	1217710	-	0.8645984	inactive
TSS_4720_storz	1218115	+	0.5944963	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).