Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
yqfA	-	3041170	3040511

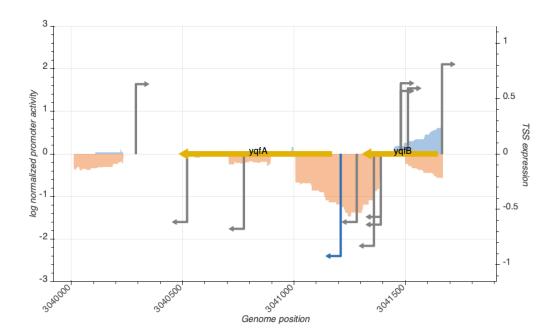


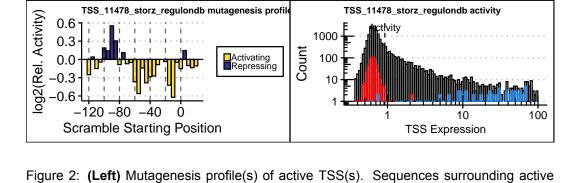


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_11484_regulondb	3041661	+	0.8082665	inactive
TSS_11478_storz_regulondb	3041206	-	0.9208536	active
TSS_11481_regulondb	3041386	-	0.5677658	inactive
TSS_11482_storz	3041476	+	0.5677658	inactive
TSS_11483_storz	3041508	+	0.5914950	inactive
TSS_11481_regulondb	3041386	-	0.6374255	inactive
TSS_11482_storz	3041476	+	0.6374255	inactive
TSS_11479_regulondb	3041278	-	0.6139024	inactive
TSS_11480_storz	3041355	-	0.8291135	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).