

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
pgi	+	4231781	4233430

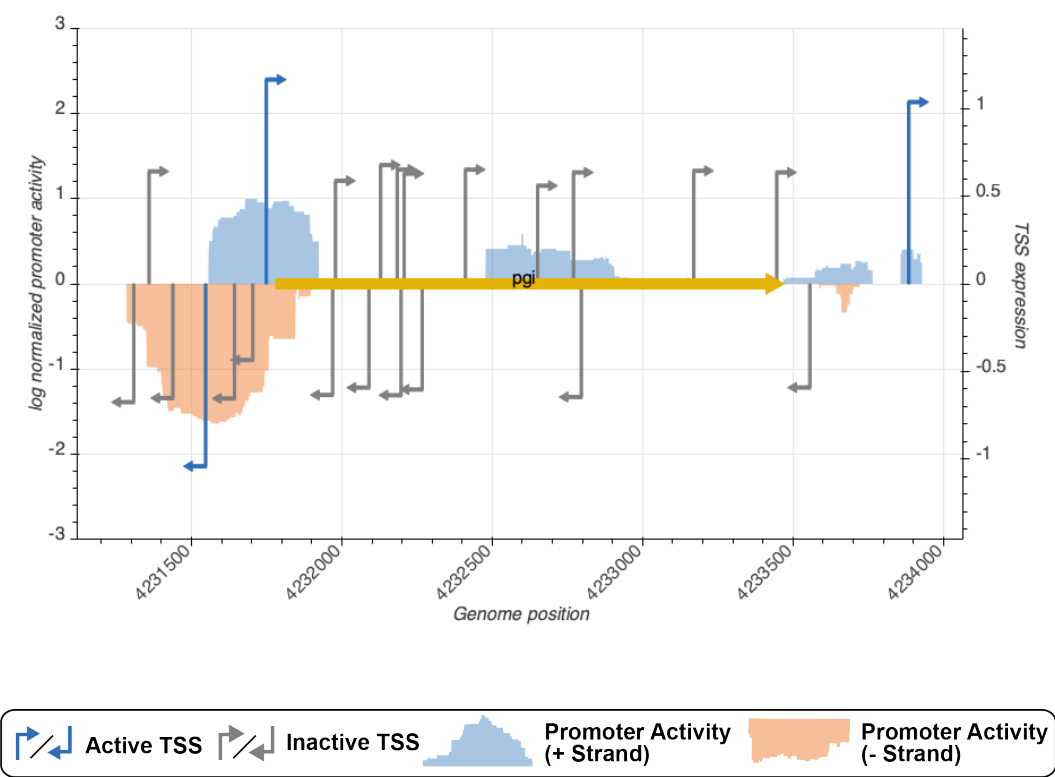


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_16574_regulondb	4231304	-	0.6755228	inactive
TSS_16576_storz	4231434	-	0.6524152	inactive
TSS_16579_storz	4231700	-	0.4349434	inactive
TSS_16578_regulondb	4231639	-	0.6544967	inactive
TSS_16580_regulondb	4231745	+	1.1661844	active
TSS_16575_wanner	4231355	+	0.6419117	inactive
TSS_16577_wanner	4231543	-	1.0417293	active

TSS Scanning Mutagenesis

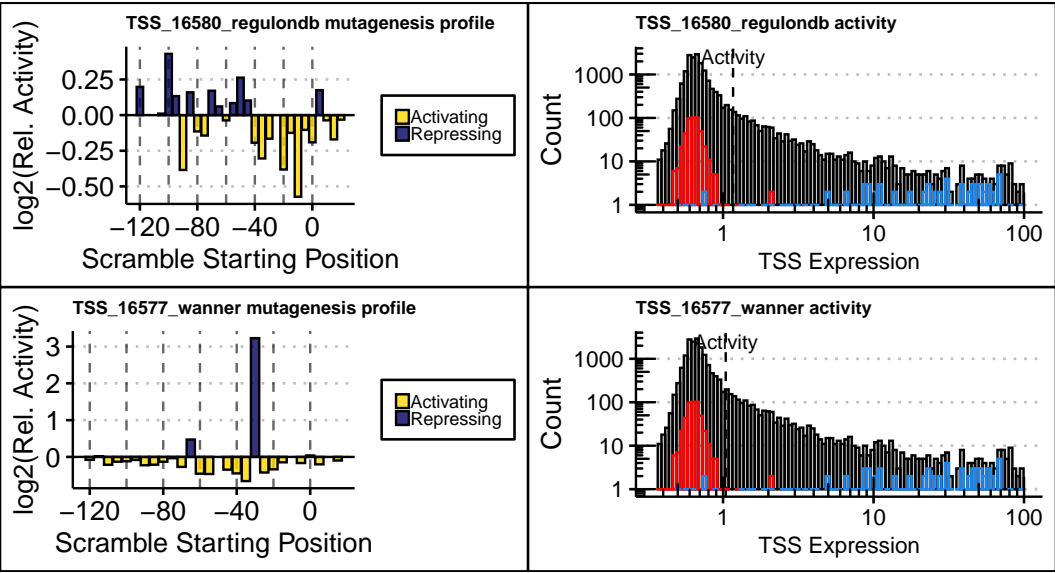


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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