Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
rpoZ-spoT-trmH-recG	+	3820129	3825314

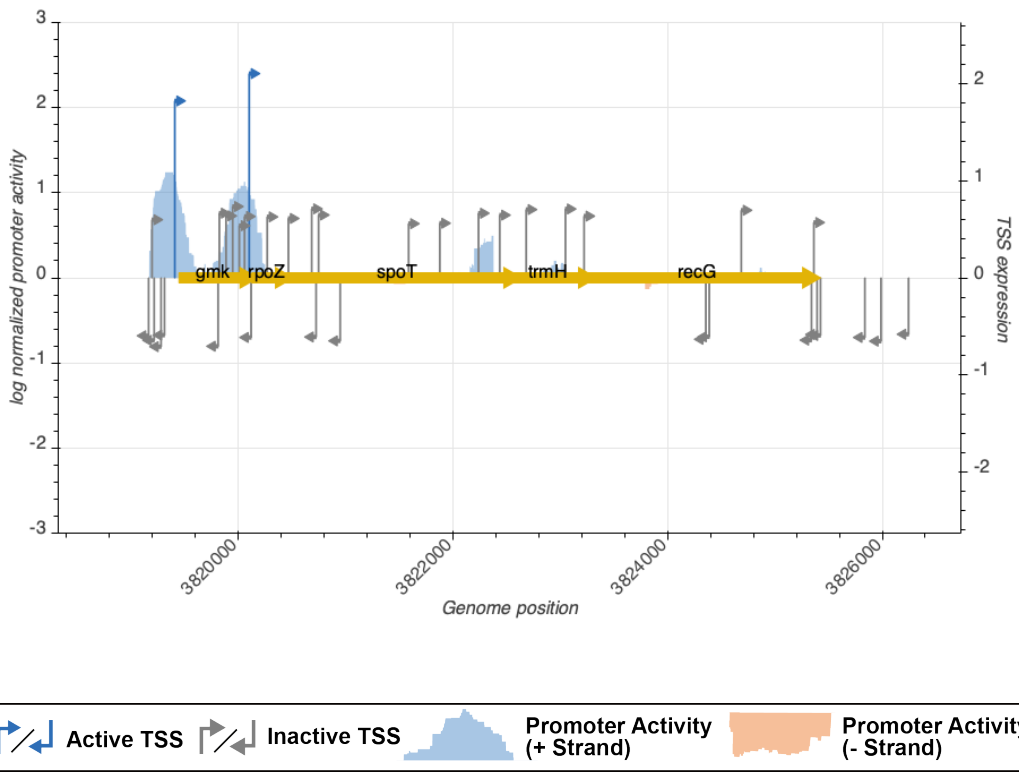

Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_14811_storz	3819810	-	0.7048114	inactive
TSS_14818_wanner	3820118	-	0.6139024	inactive
TSS_14812_storz	3819822	+	0.6662798	inactive
TSS_14813_regulondb	3819884	+	0.6383318	inactive
TSS_14817_regulondb	3820100	+	2.1037588	active
TSS_14815_regulondb	3820008	+	0.5368769	inactive
TSS_14816_regulondb	3820057	+	0.6321431	inactive
TSS_14814_storz_regulondb	3819946	+	0.7346137	inactive

TSS Scanning Mutagenesis

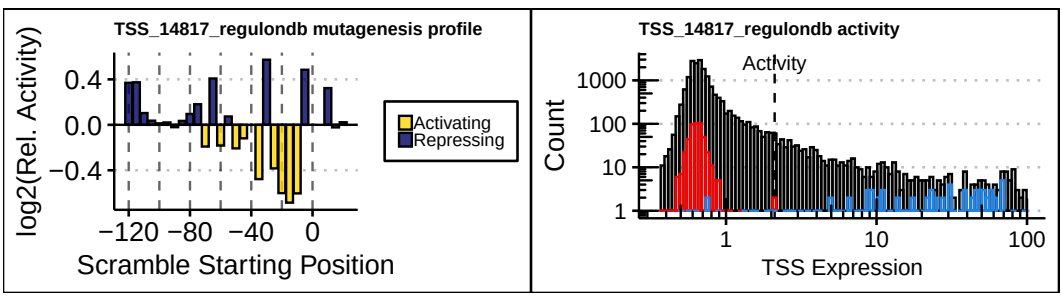

Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals 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).