

Operon Promoter Landscape

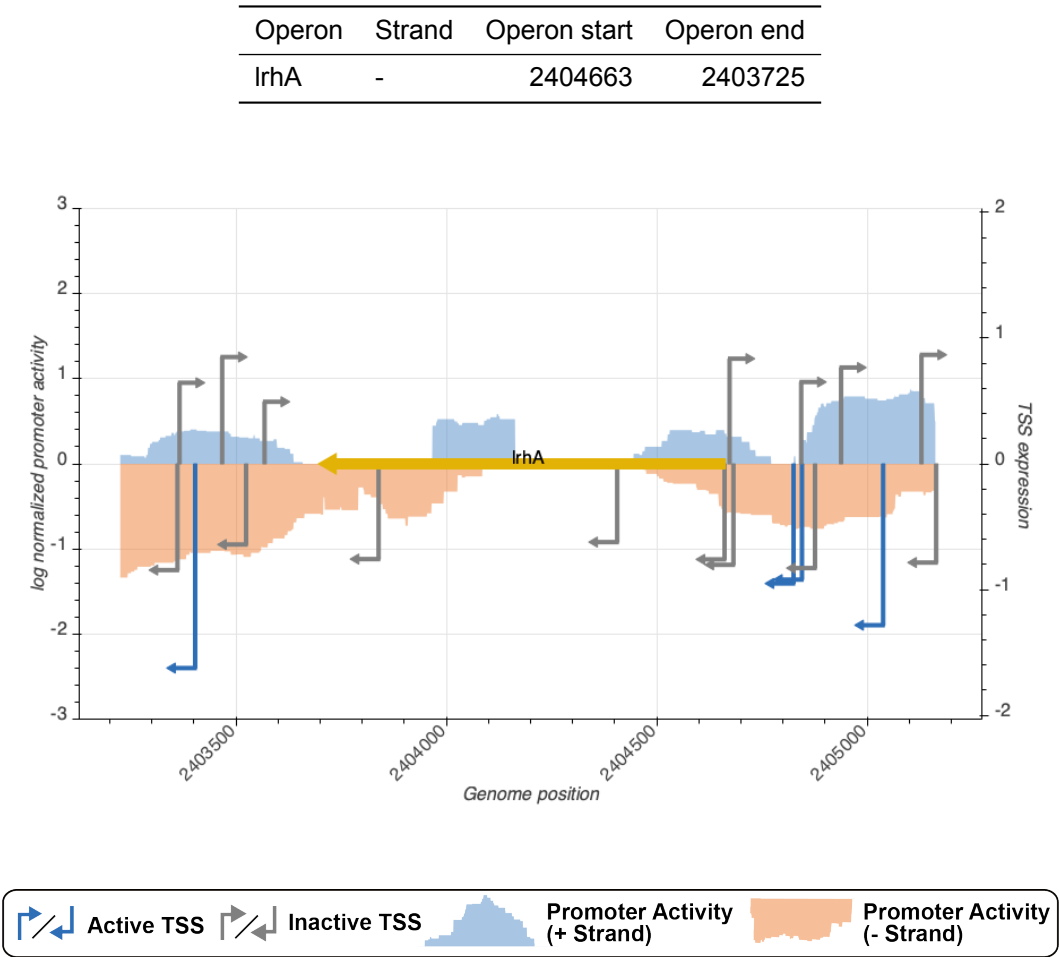


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_9059_storz	2404821	-	0.9514336	active
TSS_9057_storz	2404669	+	0.8362715	inactive
TSS_9058_regulondb	2404678	-	0.8032381	inactive
TSS_9061_wanner	2404841	-	0.9208536	active
TSS_9067_storz	2405160	-	0.7849424	inactive
TSS_9064_storz	2404934	+	0.7656573	inactive
TSS_9065_storz_regulondb	2405034	-	1.2830901	active
TSS_9066_storz	2405125	+	0.8669911	inactive
TSS_9062_storz	2404872	-	0.8291135	inactive
TSS_9060_storz	2404839	+	0.6505984	inactive

TSS Scanning Mutagenesis

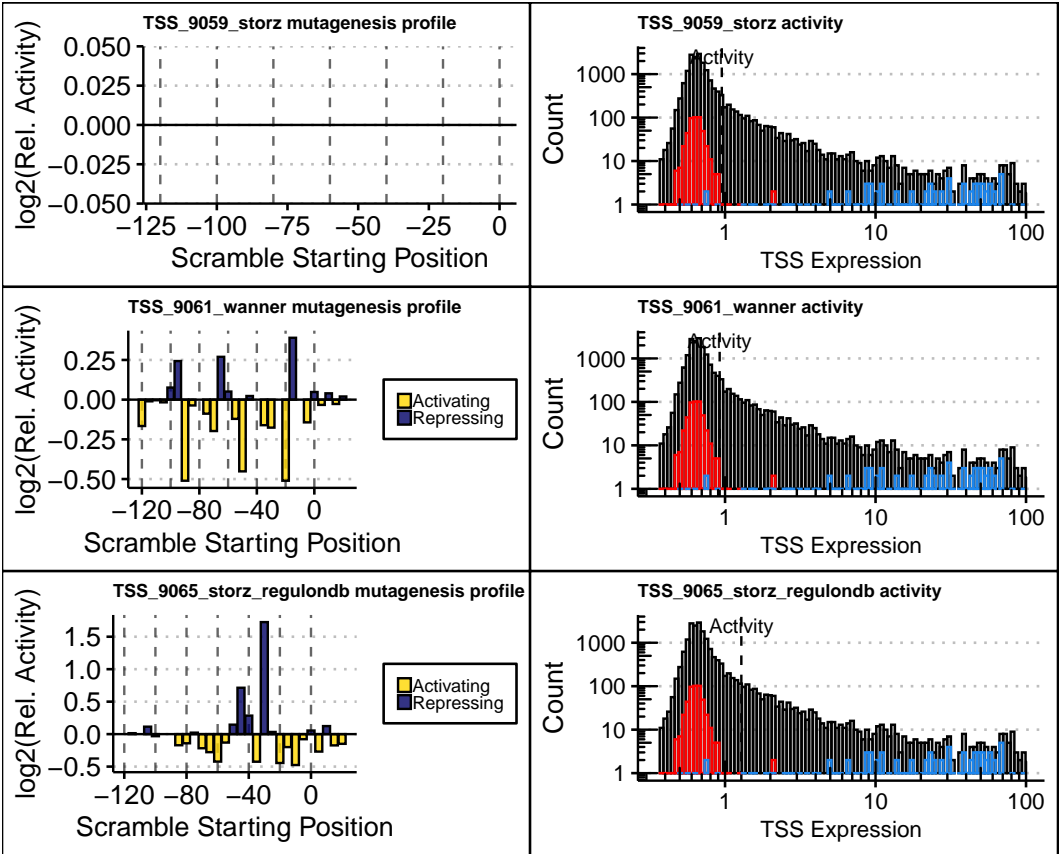


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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