

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
nadB	+	2708442	2710064

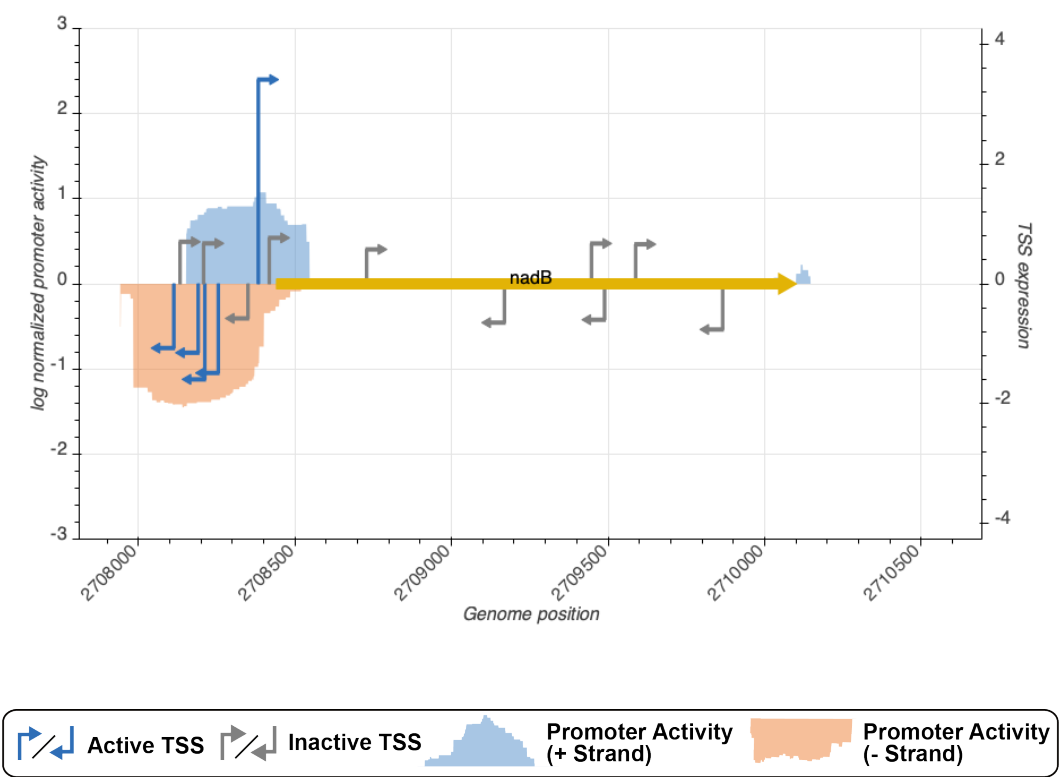


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_10195_wanner	2708251	-	1.4891162	active
TSS_10193_storz	2708204	+	0.6755228	inactive
TSS_10197_regulondb	2708379	+	3.4128680	active
TSS_10190_regulondb	2708109	-	1.0737537	active
TSS_10194_regulondb	2708208	-	1.5962131	active
TSS_10198_regulondb	2708414	+	0.7679535	inactive
TSS_10191_storz	2708129	+	0.7019316	inactive
TSS_10192_storz	2708187	-	1.1513547	active
TSS_10196_storz	2708346	-	0.5776030	inactive

TSS Scanning Mutagenesis

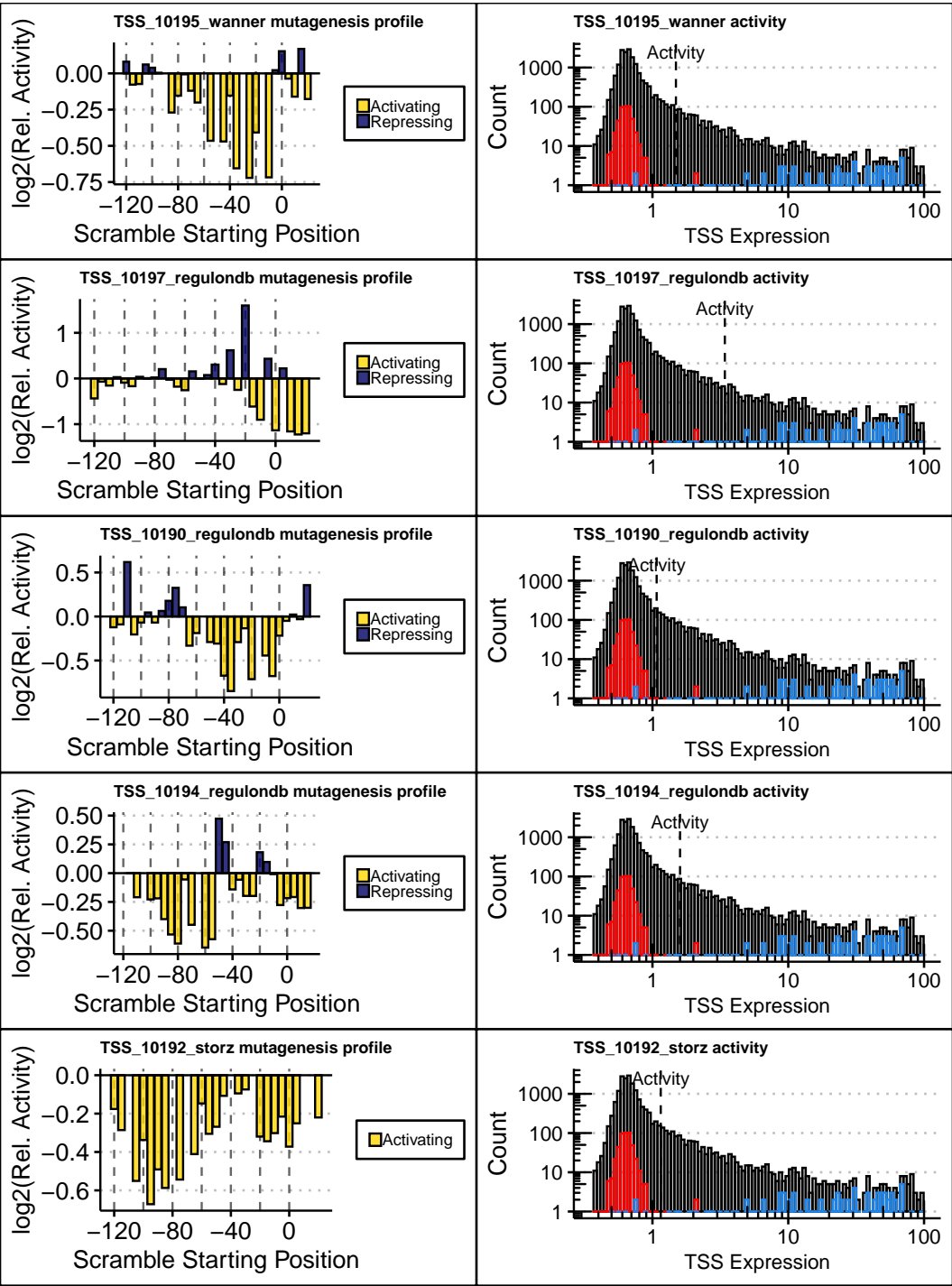


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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