

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
metZWV	+	2945409	2945705

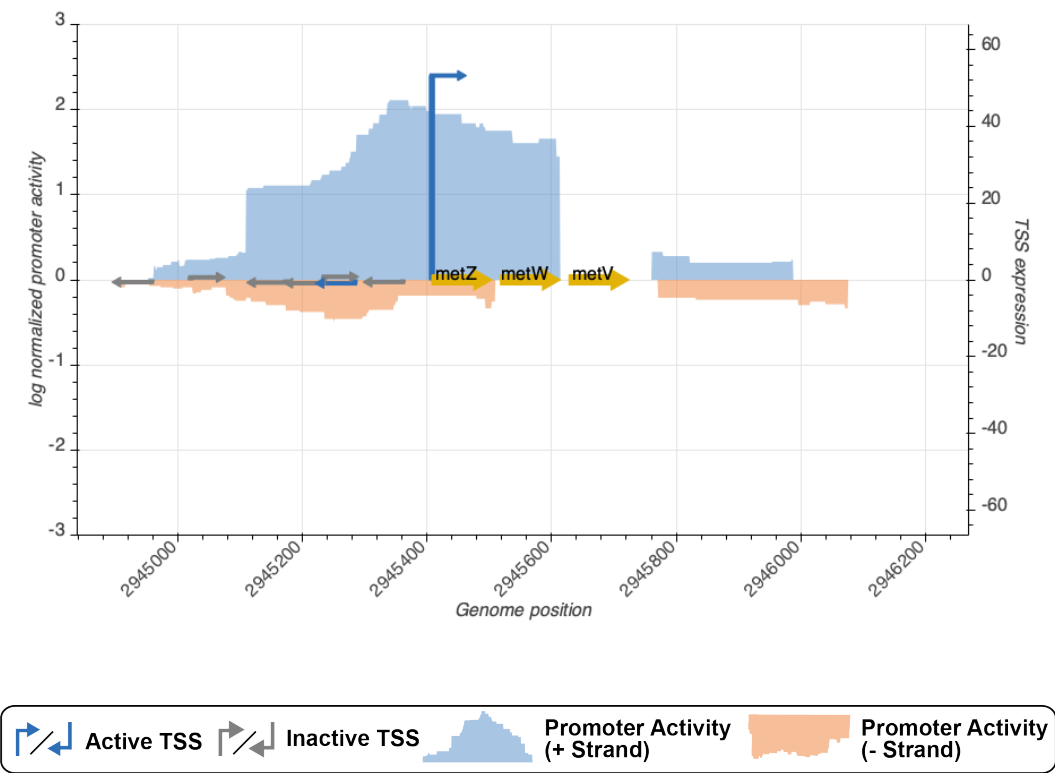


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_11125_storz_regulondb	2945404	+	53.2138716	active
TSS_11122_storz	2945231	+	0.8045739	inactive
TSS_11119_storz	2945017	+	0.6427197	inactive
TSS_11118_storz	2944954	-	0.5942172	inactive
TSS_11124_storz	2945357	-	0.5713306	inactive
TSS_11121_storz	2945230	-	0.8624047	inactive
TSS_11120_storz	2945170	-	0.7118763	inactive
TSS_11123_wanner	2945280	-	0.8953703	active

TSS Scanning Mutagenesis

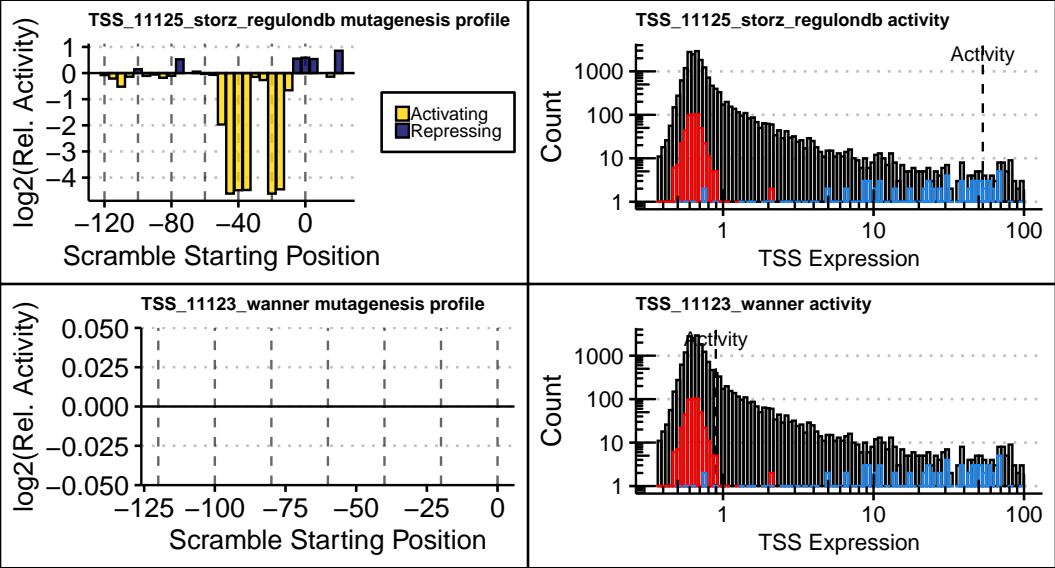


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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