

Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
glpD	+	3560036	3561541

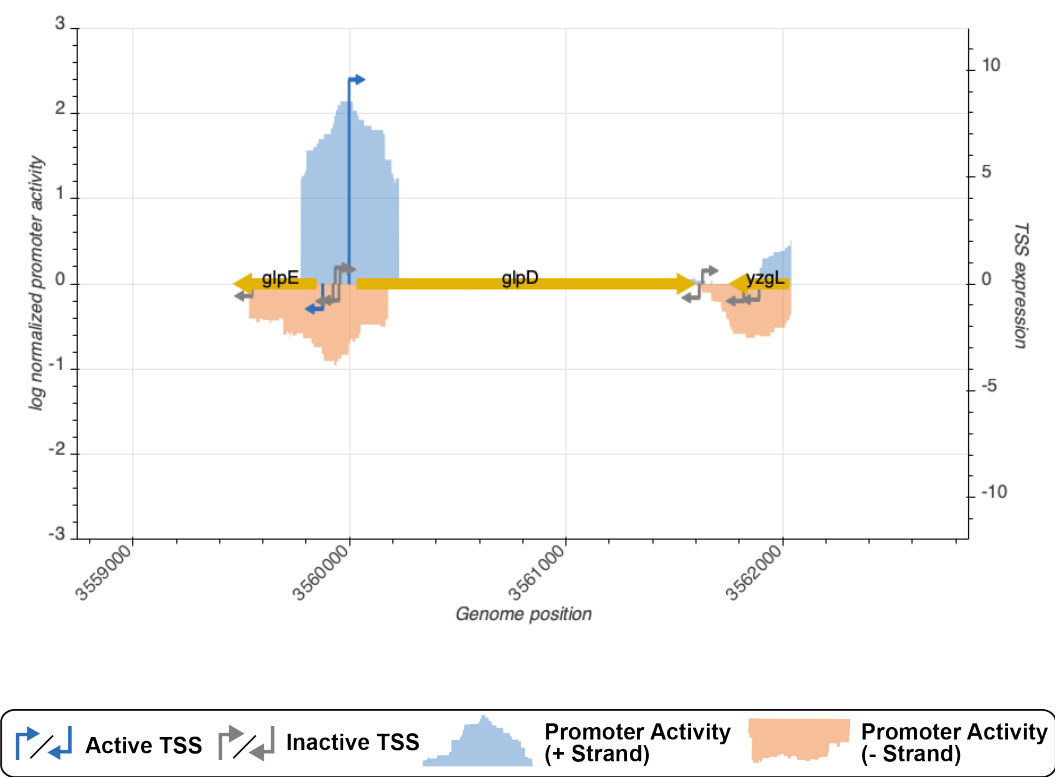


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_13802_storz	3559947	-	0.7679535	inactive
TSS_13798_storz	3559546	-	0.5688721	inactive
TSS_13801_wanner	3559930	+	0.7602889	inactive
TSS_13803_storz	3559952	+	0.6716716	inactive
TSS_13804_regulondb	3559994	+	9.5550271	active
TSS_13799_regulondb	3559872	-	1.1709358	active
TSS_13800_storz	3559920	-	0.8155224	inactive

TSS Scanning Mutagenesis

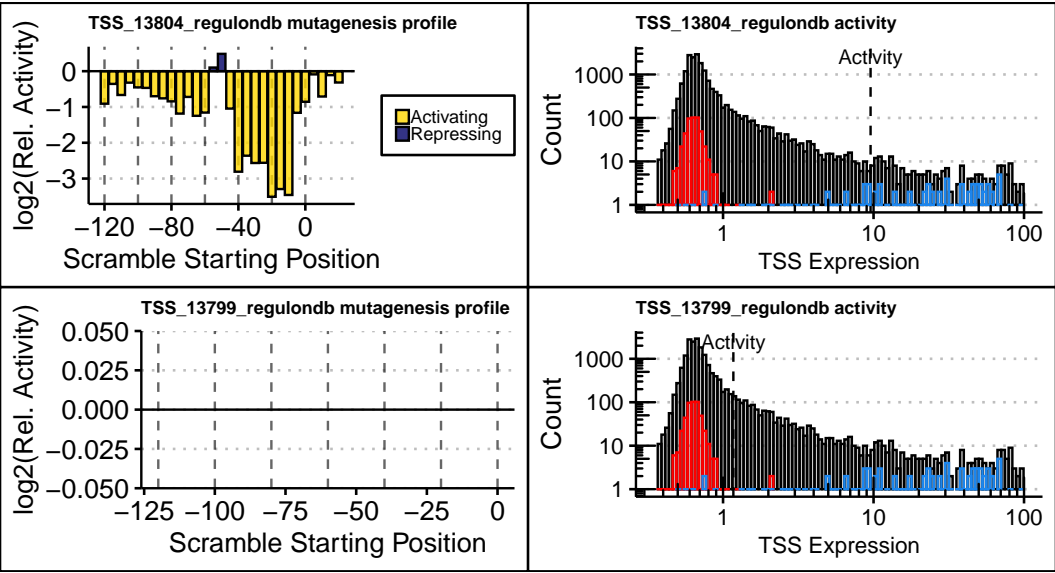


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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