Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
cydAB	+	770681	773404

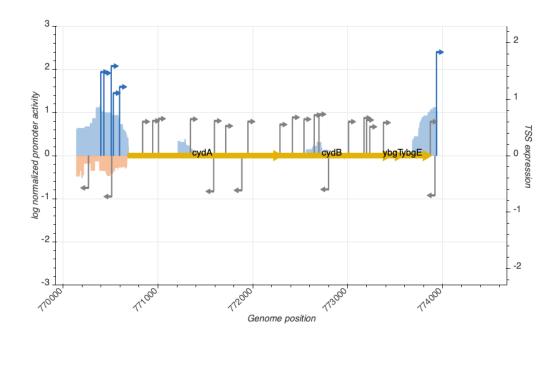


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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.

Promoter Activity

(+ Strand)

Promoter Activity

(- Strand)

TSS Summary

TSS name	TSS position	Strand	TSS activity	Category
TSS_2949_storz_regulondb	770393	+	1.4781378	active
TSS_2951_regulondb	770503	+	1.5826560	active
TSS_2952_storz	770508	-	0.7229845	inactive
TSS_2953_regulondb	770525	+	1.1058094	active
TSS_2948_storz	770263	-	0.5703145	inactive
TSS_2950_regulondb	770425	+	1.4595720	active
TSS_2954_regulondb	770591	+	1.2153371	active

TSS Scanning Mutagenesis

Active TSS | Inactive TSS

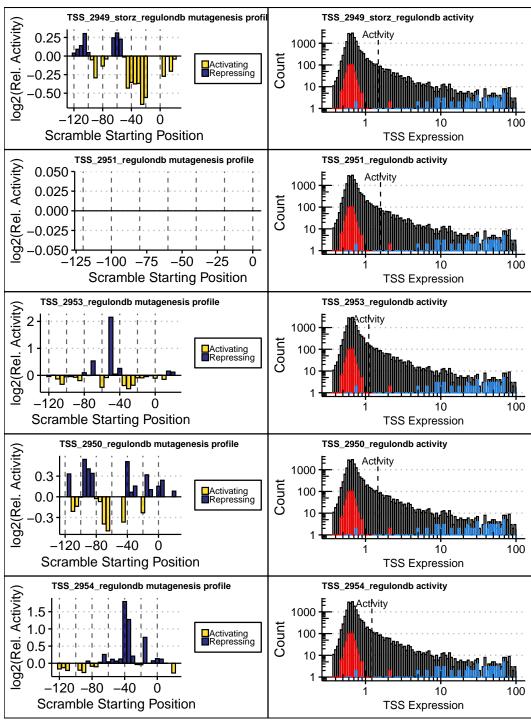


Figure 2: (Left) Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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

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a putative activator (yellow) or repressor (purple). (Right) Dashed line indicates the ex-