Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
slp-dctR	+	3651984	3653236

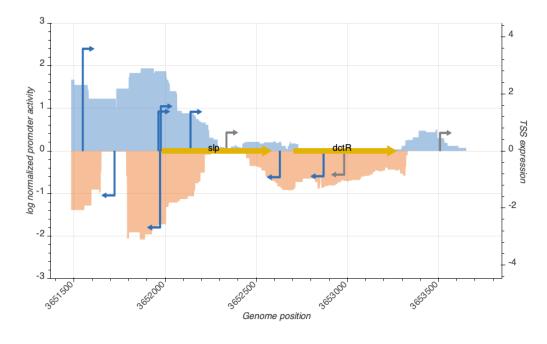


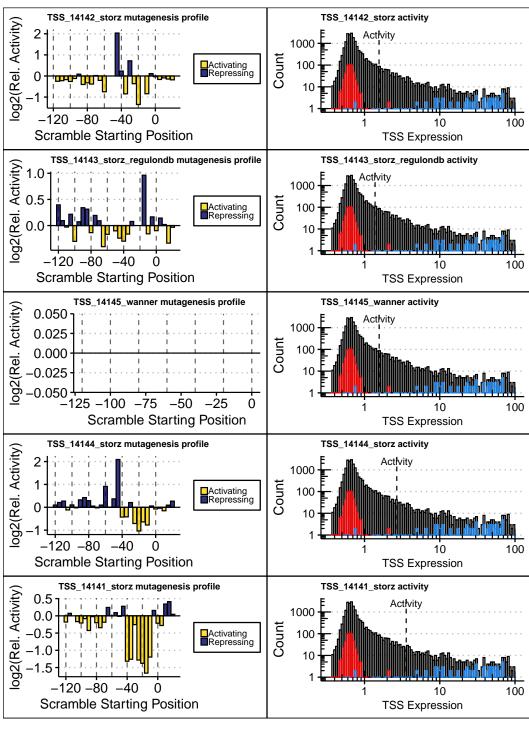


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_14142_storz	3651718	-	1.558705	active
TSS_14143_storz_regulondb	3651959	+	1.380705	active
TSS_14145_wanner	3651972	+	1.565124	active
TSS_14144_storz	3651968	-	2.684057	active
TSS_14141_storz	3651544	+	3.582068	active

TSS Scanning Mutagenesis



Scramble Starting Position

TSS Expression

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 ex-

pression 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

1

constitutive promoters from the BioBrick registry (blue).