Operon Promoter Landscape

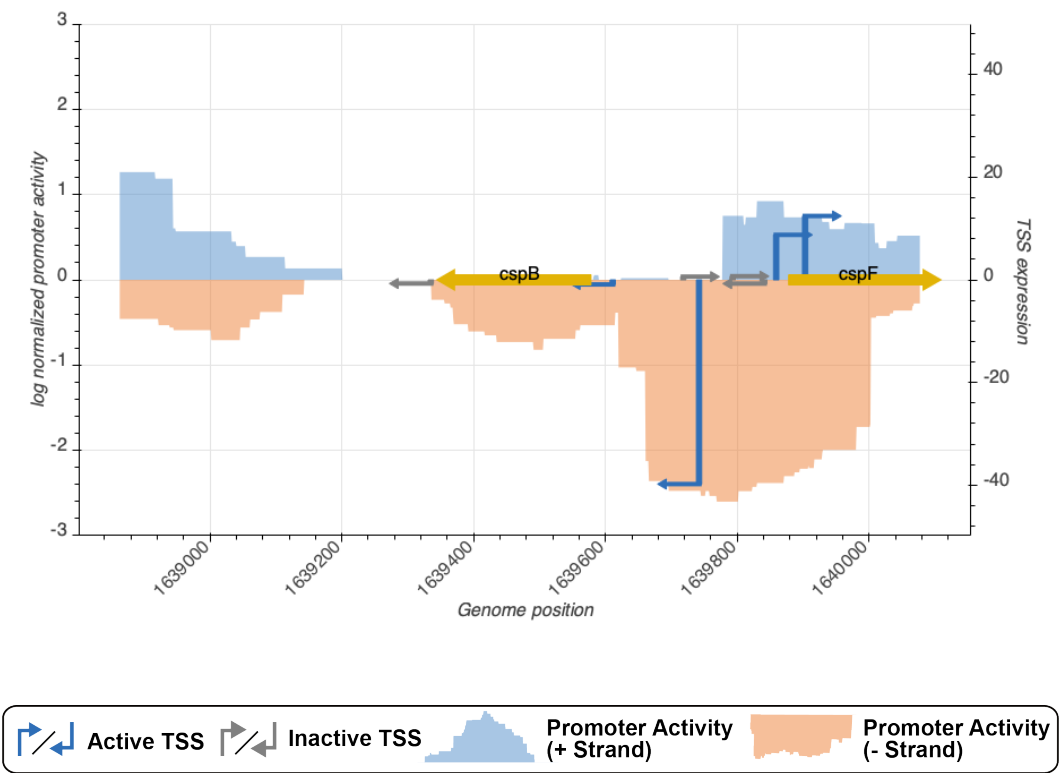| Operon	Strand	Operon start	Operon end
cspB	-	1639578	1639363

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_6276_regulondb	1639714	+	0.6139024	inactive
TSS_6279_storz	1639837	-	0.7407878	inactive
TSS_6278_regulondb	1639789	+	0.7019139	inactive
TSS_6280_regulondb	1639855	+	8.7545388	active
TSS_6275_storz	1639607	-	0.9008573	active
TSS_6277_wanner	1639738	-	39.7758515	active
TSS_6281_storz	1639899	+	12.4297973	active

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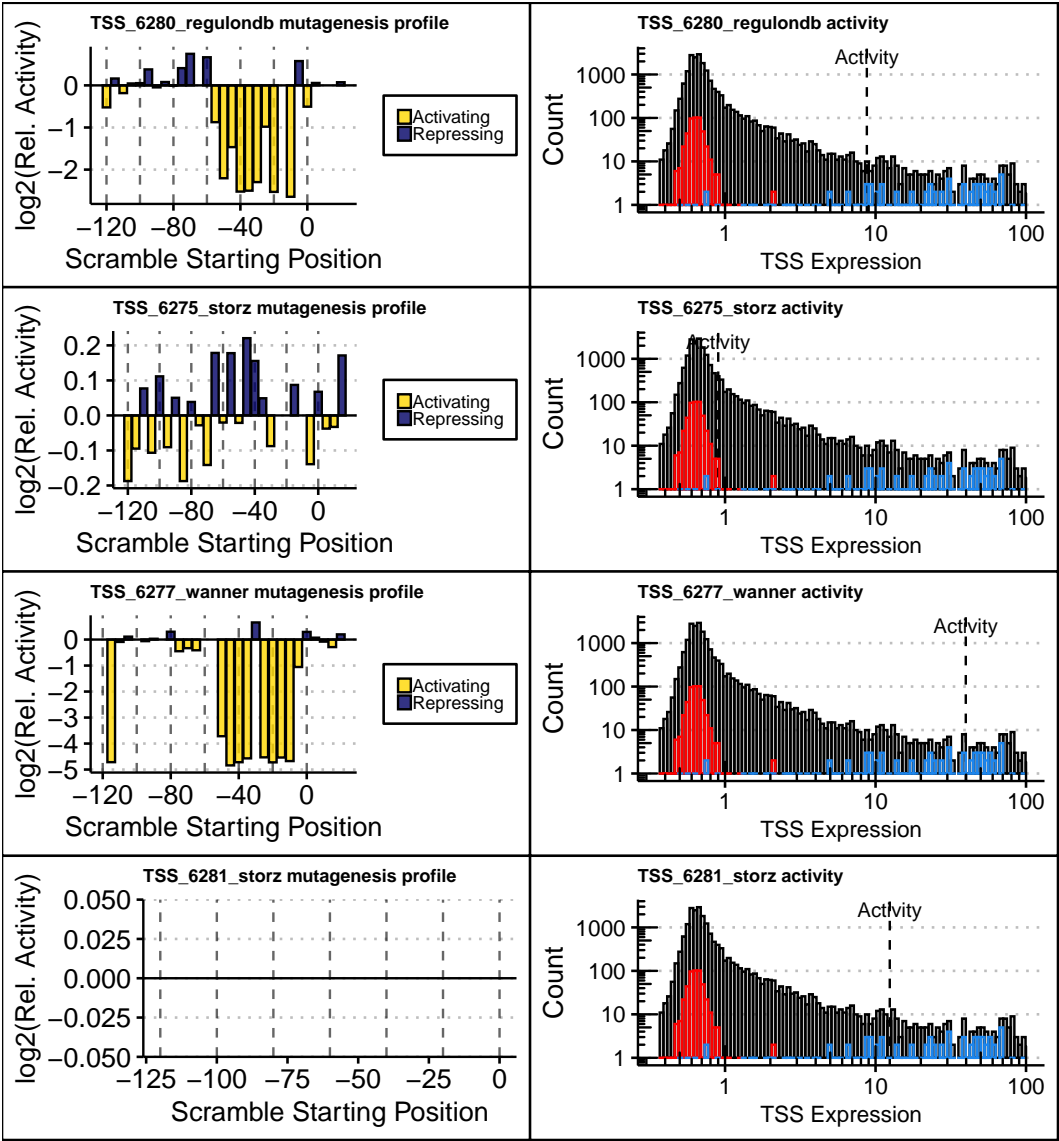
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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