Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
ychE	+	1297821	1298468

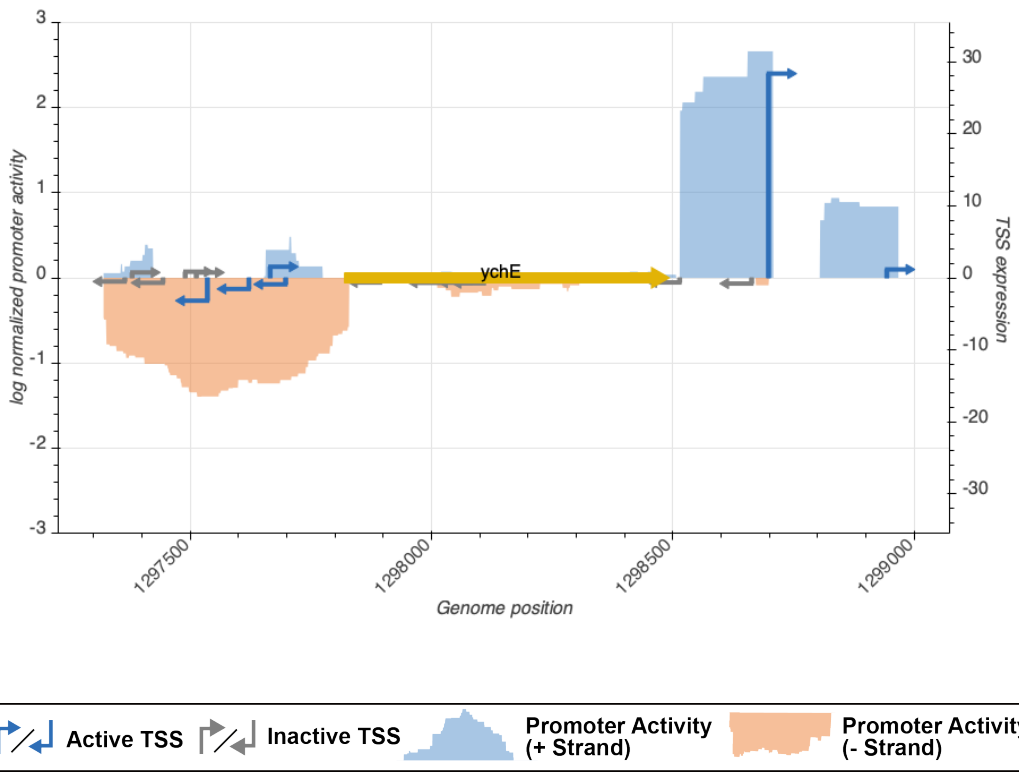

Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_5083_storz	1297662	+	1.5425942	active
TSS_5084_storz	1297694	-	0.8990107	active
TSS_5077_storz	1297376	+	0.7435025	inactive
TSS_5080_storz	1297509	+	0.7362225	inactive
TSS_5076_regulondb	1297361	-	0.5124043	inactive
TSS_5078_regulondb	1297440	-	0.6909279	inactive
TSS_5079_storz	1297486	+	0.8449790	inactive
TSS_5082_storz	1297618	-	1.5475093	active
TSS_5081_storz_regulondb	1297532	-	3.1725826	active

TSS Scanning Mutagenesis

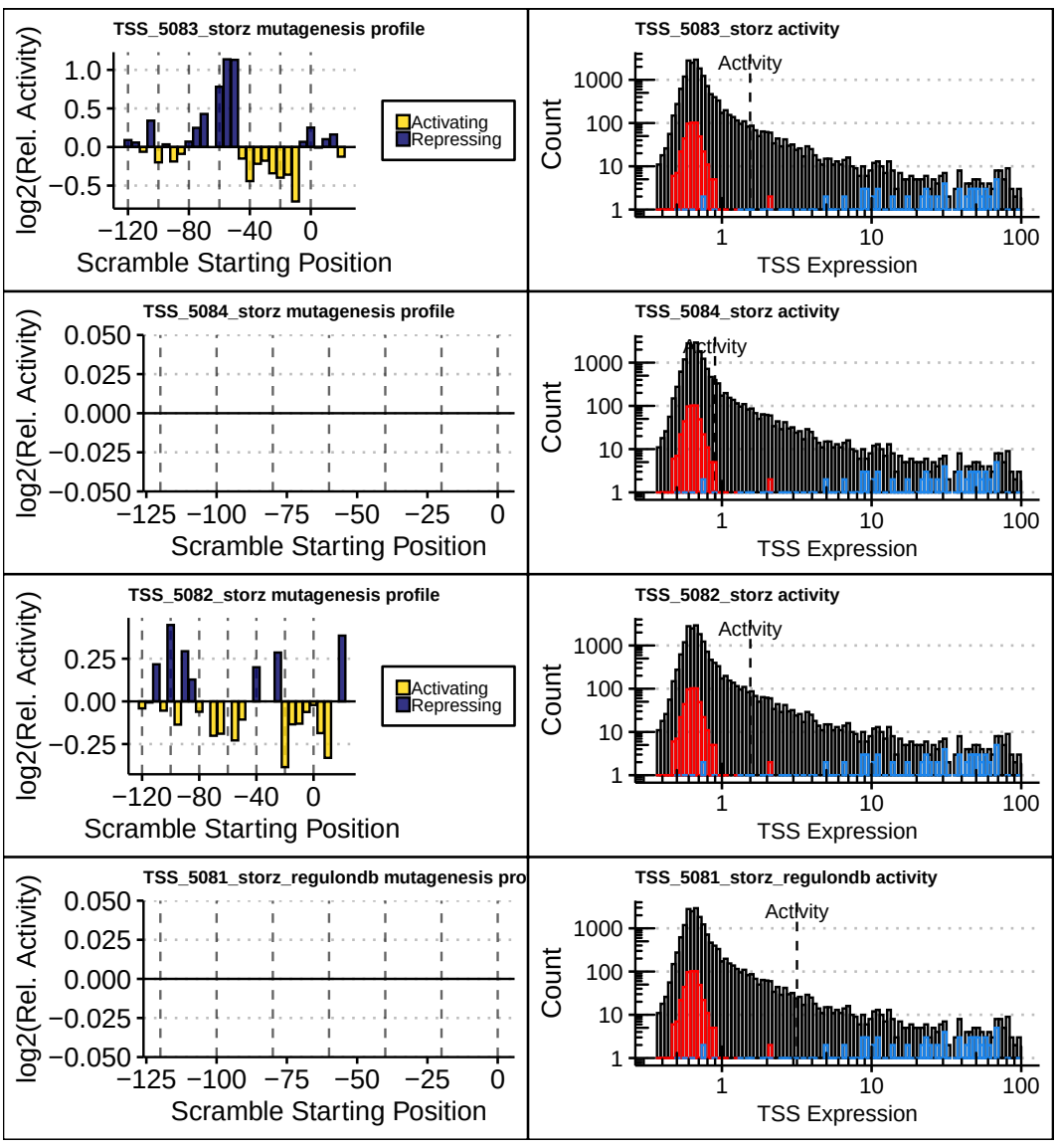

Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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