Operon Promoter Landscape

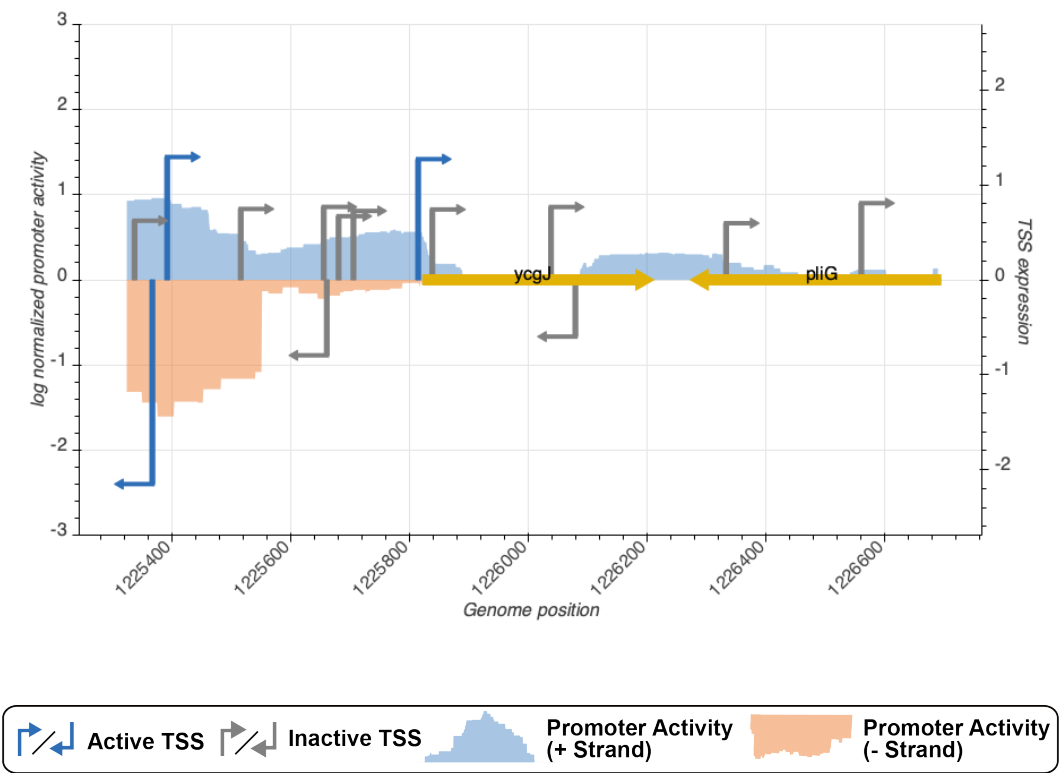| Operon	Strand	Operon start	Operon end
ycgJ	+	1225823	1226191

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_4753_storz_regulondb	1225387	+	1.2943269	active
TSS_4754_storz	1225511	+	0.7465280	inactive
TSS_4751_storz	1225332	+	0.6229642	inactive
TSS_4752_wanner_regulondb	1225362	-	2.1520654	active
TSS_4756_storz	1225651	+	0.7679535	inactive
TSS_4760_storz	1225810	+	1.2718194	active
TSS_4759_regulondb	1225701	+	0.7262586	inactive
TSS_4758_storz	1225676	+	0.6705321	inactive
TSS_4757_storz	1225656	-	0.7954302	inactive

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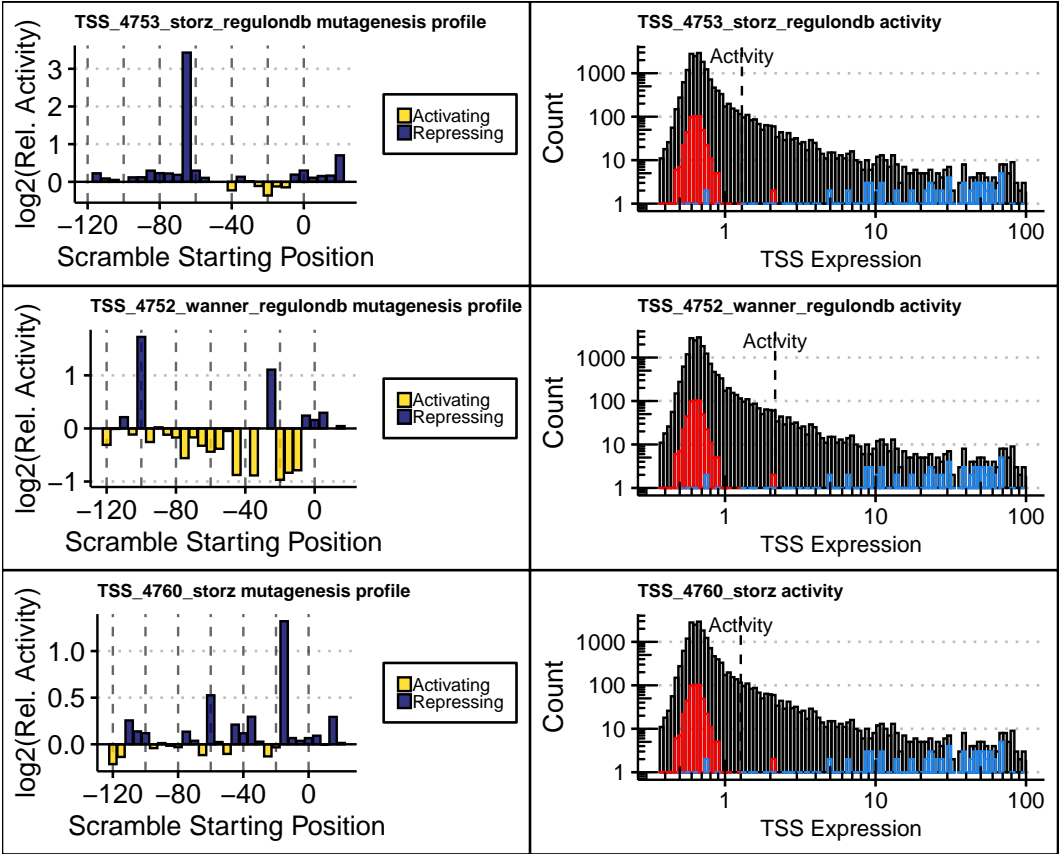
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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