Operon Promoter Landscape

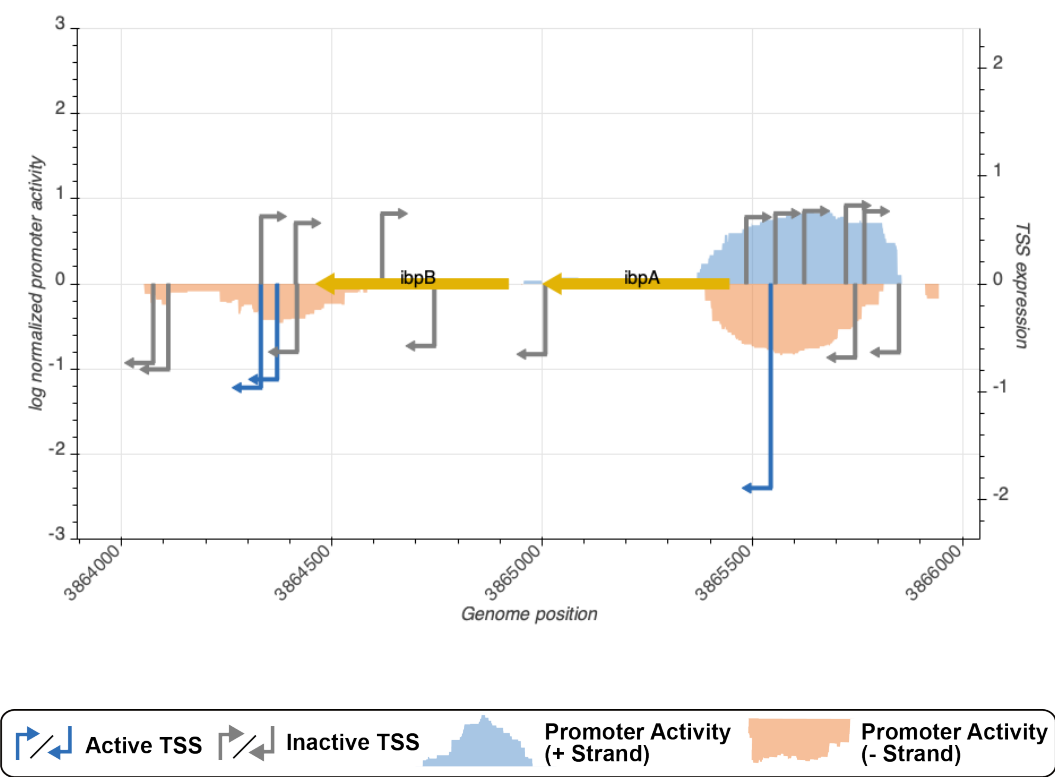| Operon	Strand	Operon start	Operon end
ibpAB	-	3865445	3864492

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_14983_wanner	3865540	-	1.8933389	active
TSS_14989_storz	3865845	-	0.6344425	inactive
TSS_14985_storz	3865620	+	0.6750625	inactive
TSS_14984_storz	3865551	+	0.6524152	inactive
TSS_14987_storz	3865741	-	0.6832254	inactive
TSS_14986_storz	3865719	+	0.7261218	inactive
TSS_14988_storz	3865763	+	0.6722323	inactive
TSS_14982_storz	3865482	+	0.6175633	inactive

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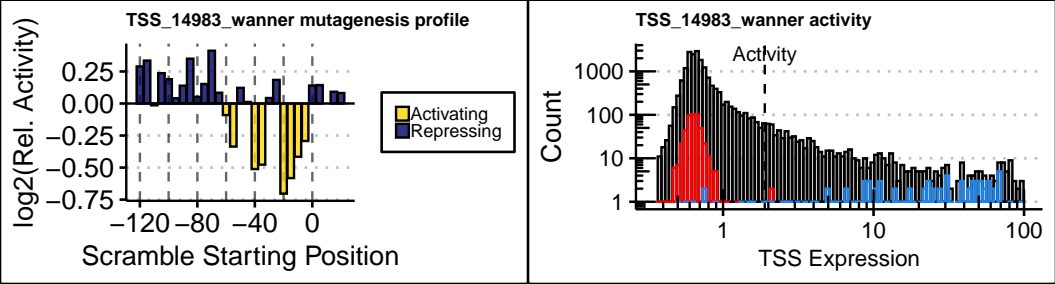
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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