Operon Promoter Landscape

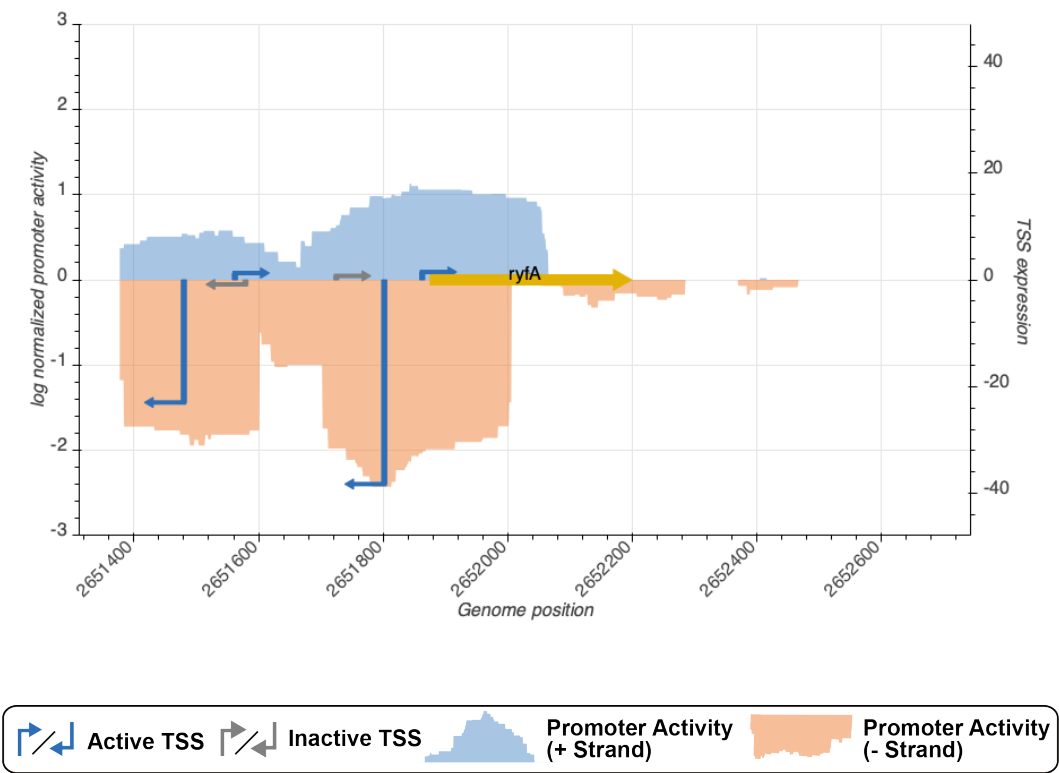| Operon	Strand	Operon start	Operon end
ryfA	+	2651877	2652180

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

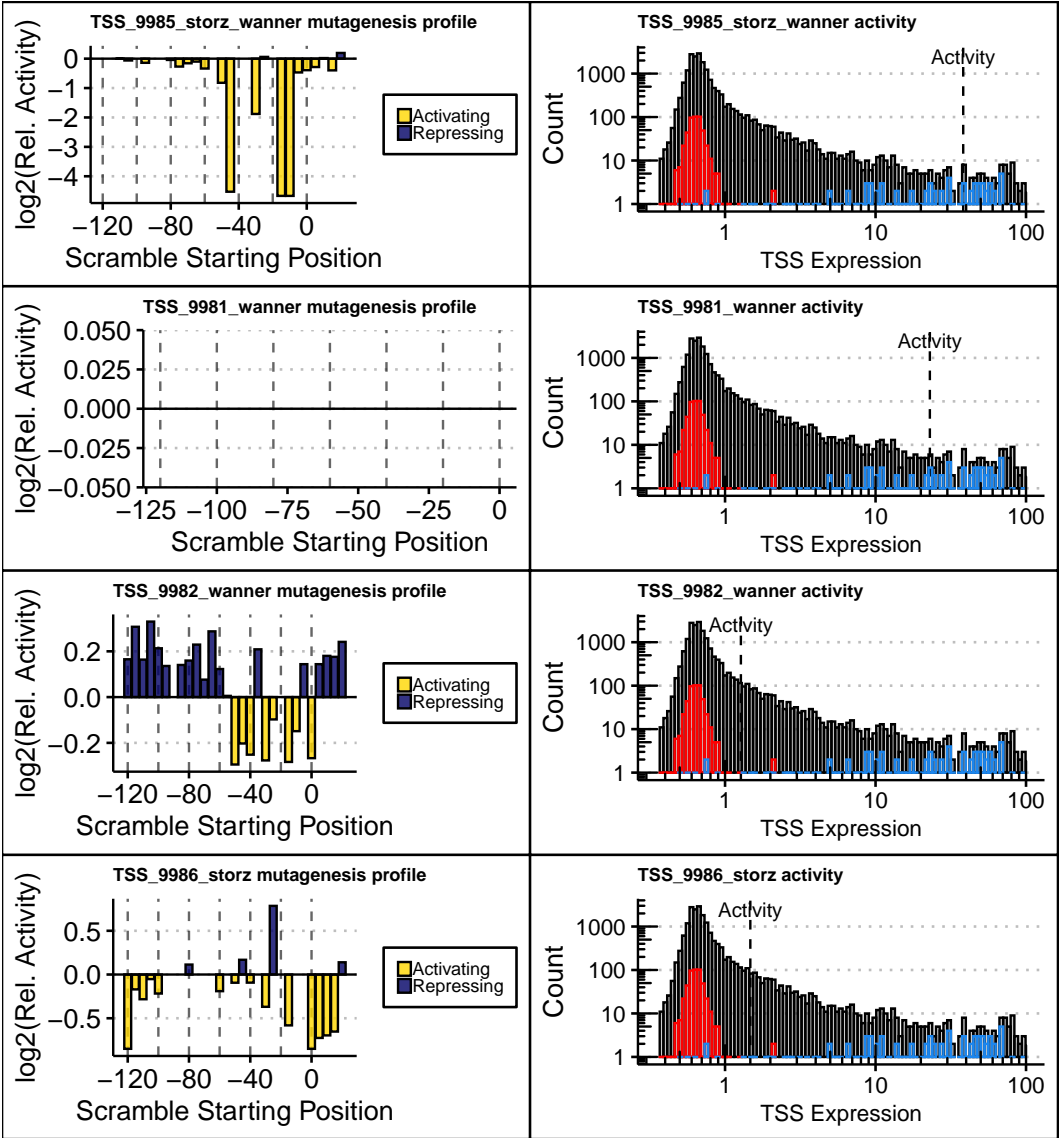| TSS name	TSS position	Strand	TSS activity	Category
TSS_9983_storz	2651575	-	0.8500550	inactive
TSS_9985_storz_wanner	2651798	-	38.2401323	active
TSS_9981_wanner	2651476	-	22.9582660	active
TSS_9982_wanner	2651558	+	1.2740358	active
TSS_9984_regulondb	2651721	+	0.7294454	inactive
TSS_9986_storz	2651859	+	1.4722400	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).