Operon Promoter Landscape

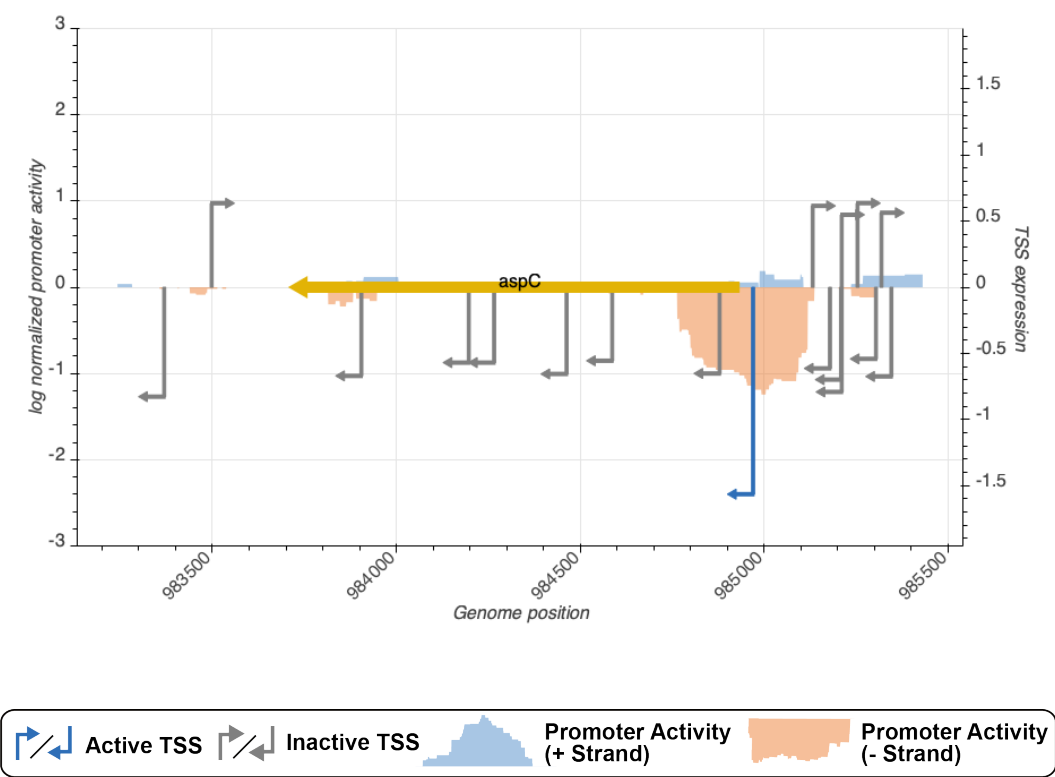| Operon	Strand	Operon start	Operon end
aspC	-	984932	983742

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_3824_storz	985128	+	0.6155258	inactive
TSS_3832_regulondb	985342	-	0.6750625	inactive
TSS_3828_regulondb	985207	-	0.7920590	inactive
TSS_3827_storz	985207	+	0.5483142	inactive
TSS_3830_regulondb	985300	-	0.5420878	inactive
TSS_3826_regulondb	985205	-	0.6990459	inactive
TSS_3829_storz	985250	+	0.6359097	inactive
TSS_3823_wanner_regulondb	984966	-	1.5657365	active
TSS_3825_storz	985175	-	0.6139024	inactive
TSS_3831_storz	985315	+	0.5633858	inactive

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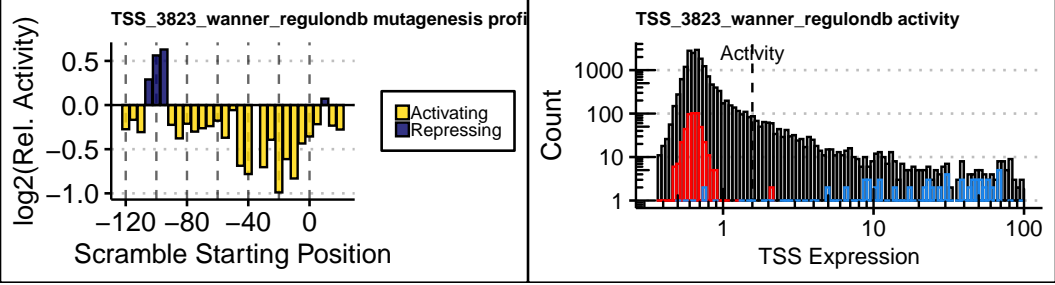
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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