Operon Promoter Landscape

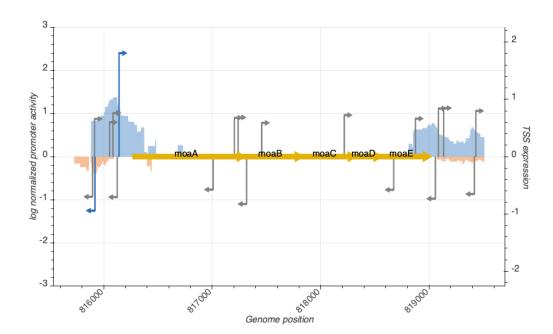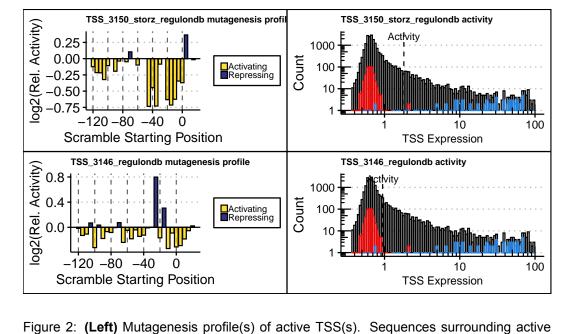| Operon	Strand	Operon start	Operon end
moaABCDE	+	816267	818970

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_3144_wanner	815893	-	0.7008546	inactive
TSS_3147_regulondb	816050	+	0.5998978	inactive
TSS_3148_regulondb	816081	+	0.7626515	inactive
TSS_3150_storz_regulondb	816137	+	1.8077294	active
TSS_3149_storz	816120	-	0.7073438	inactive
TSS_3146_regulondb	815915	-	0.9437842	active
TSS_3145_storz	815911	+	0.6588340	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).