## **Operon Promoter Landscape**

Operon	Strand	Operon start	Operon end
putA	-	1078105	1074143

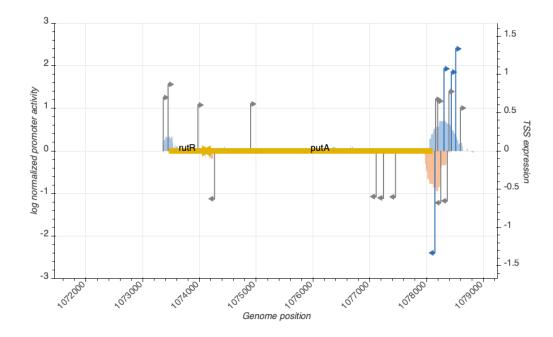




Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_4157_storz	1078363	-	0.6524152	inactive
TSS_4158_regulondb	1078391	+	0.7766077	inactive
TSS_4154_storz	1078193	+	0.6501477	inactive
TSS_4153_storz	1078157	+	0.6745168	inactive
TSS_4161_storz	1078594	+	0.5606682	inactive
TSS_4155_storz	1078248	-	0.6771430	inactive
TSS_4160_regulondb	1078511	+	1.3347198	active
TSS_4159_regulondb	1078433	+	1.0303146	active
TSS_4152_wanner	1078144	-	1.3325640	active
TSS_4156_storz	1078304	+	1.0737537	active

## TSS Scanning Mutagenesis

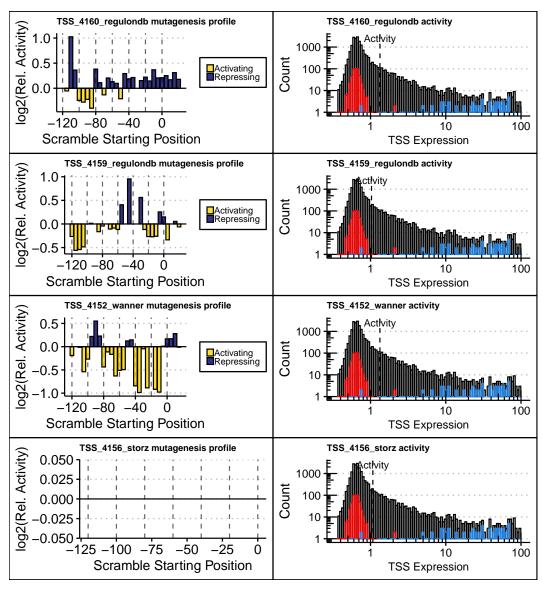


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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

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