Operon Promoter Landscape
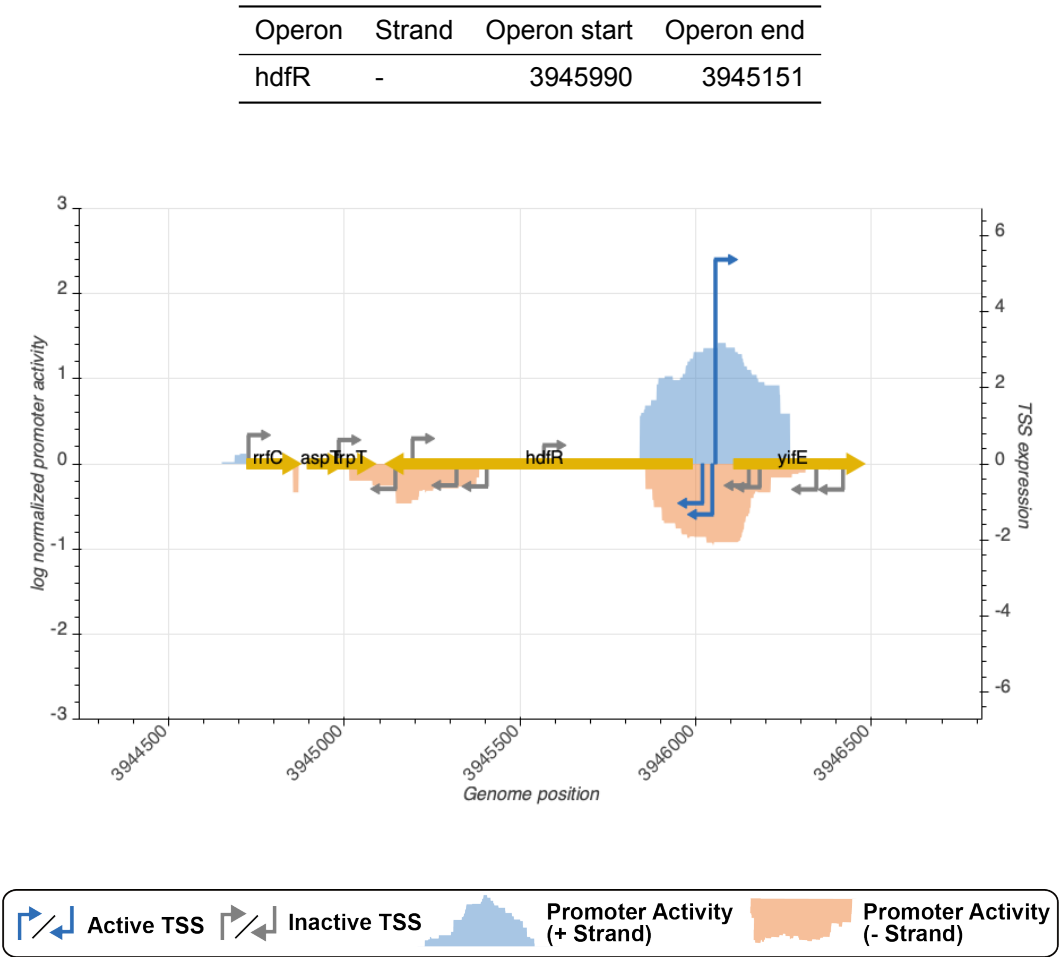
Operon	Strand	Operon start	Operon end
hdfR	-	3945990	3945151

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_15324_wanner	3946339	-	0.6727101	inactive
TSS_15320_storz	3946043	-	1.3308727	active
TSS_15322_storz	3946147	-	0.5698878	inactive
TSS_15325_storz	3946415	-	0.6750625	inactive
TSS_15321_storz	3946052	+	5.3727344	active
TSS_15319_storz	3946015	-	1.0354054	active
TSS_15323_storz	3946178	-	0.6136722	inactive

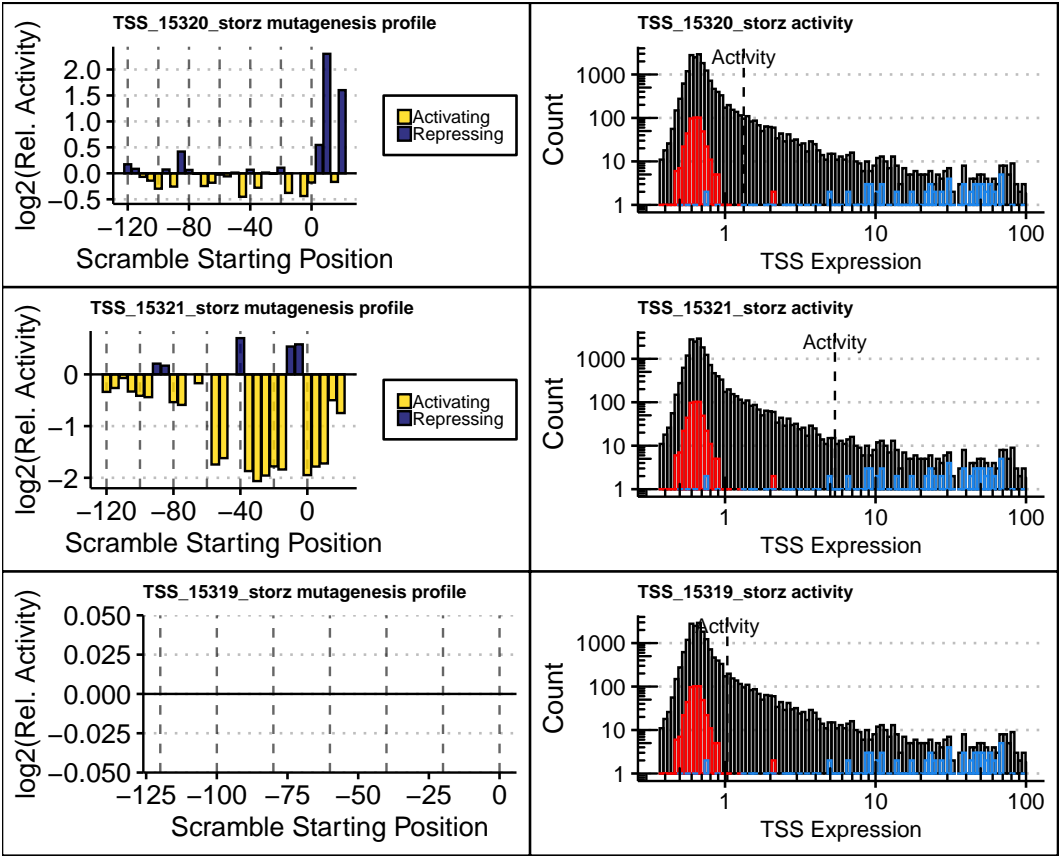## TSS Scanning Mutagenesis

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).

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