

Operon Promoter Landscape

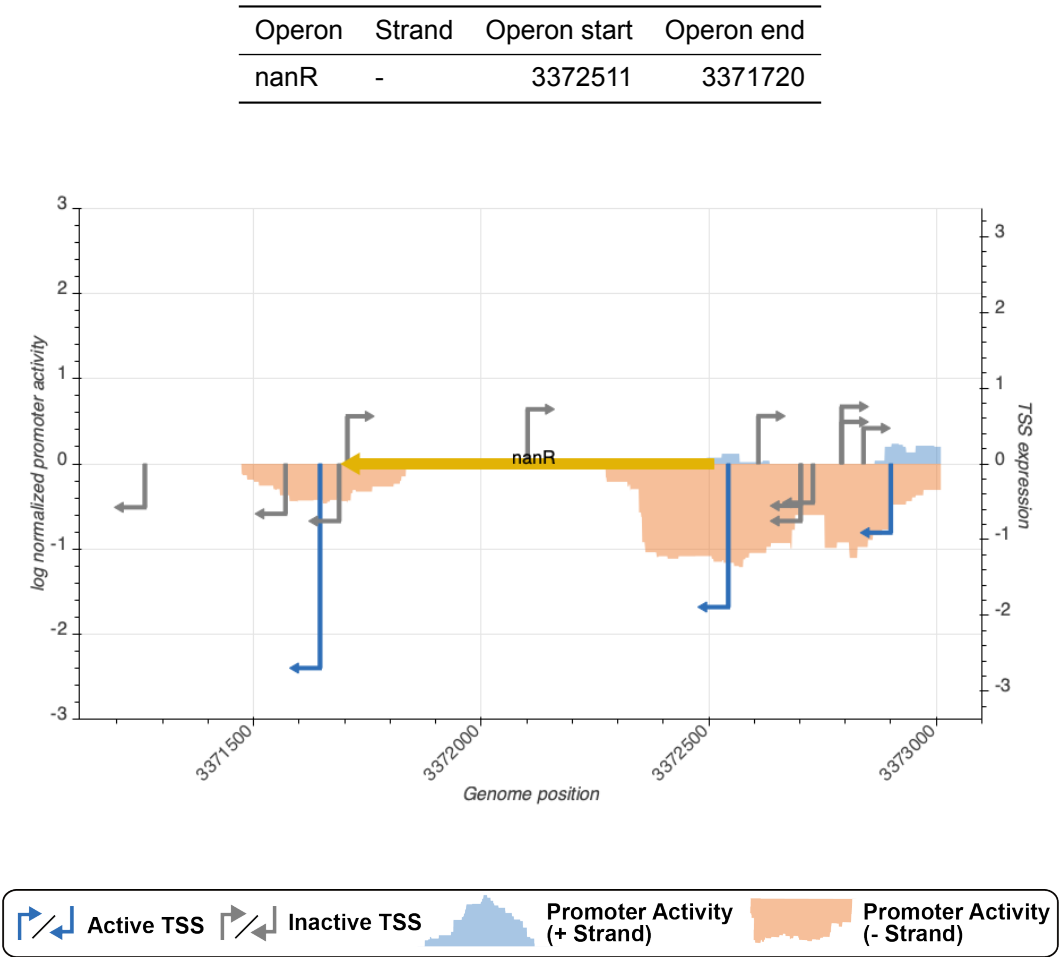


Figure 1: **Promoter activity in rich media (LB) surrounding query operon.** 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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_12884_regulondb	3372605	+	0.6301634	inactive
TSS_12886_regulondb	3372725	-	0.5134151	inactive
TSS_12889_storz	3372896	-	0.9086917	active
TSS_12887_regulondb	3372788	+	0.7543486	inactive
TSS_12885_regulondb	3372698	-	0.7543486	inactive
TSS_12883_wanner	3372539	-	1.8901900	active
TSS_12887_regulondb	3372788	+	0.5533697	inactive
TSS_12885_regulondb	3372698	-	0.5533697	inactive
TSS_12888_storz	3372836	+	0.4702749	inactive

TSS Scanning Mutagenesis

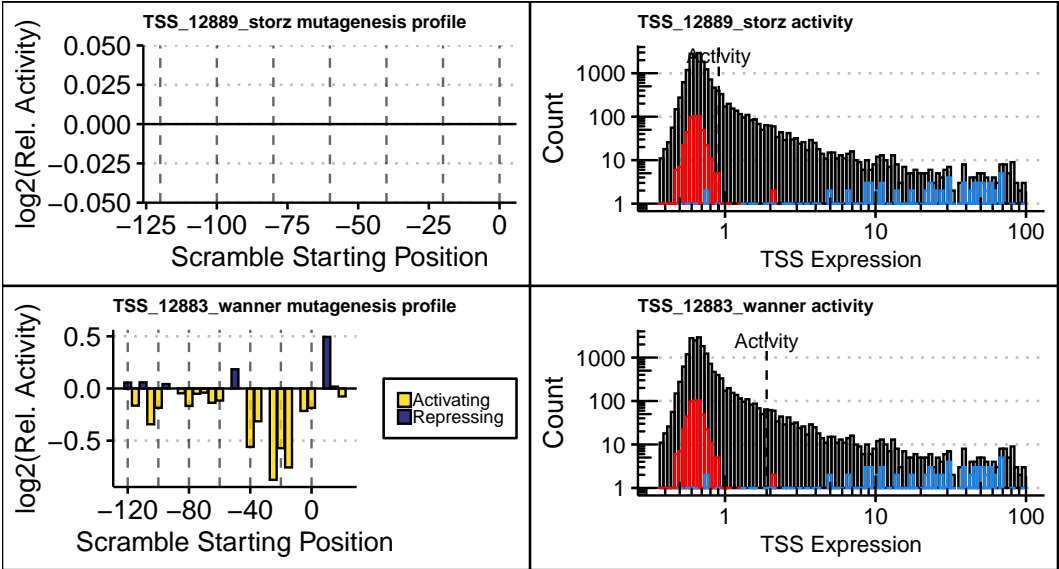


Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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