Operon Promoter Landscape

Operon	Strand	Operon start	Operon end
dnaK-tpke11-dnaJ	+	12163	15298

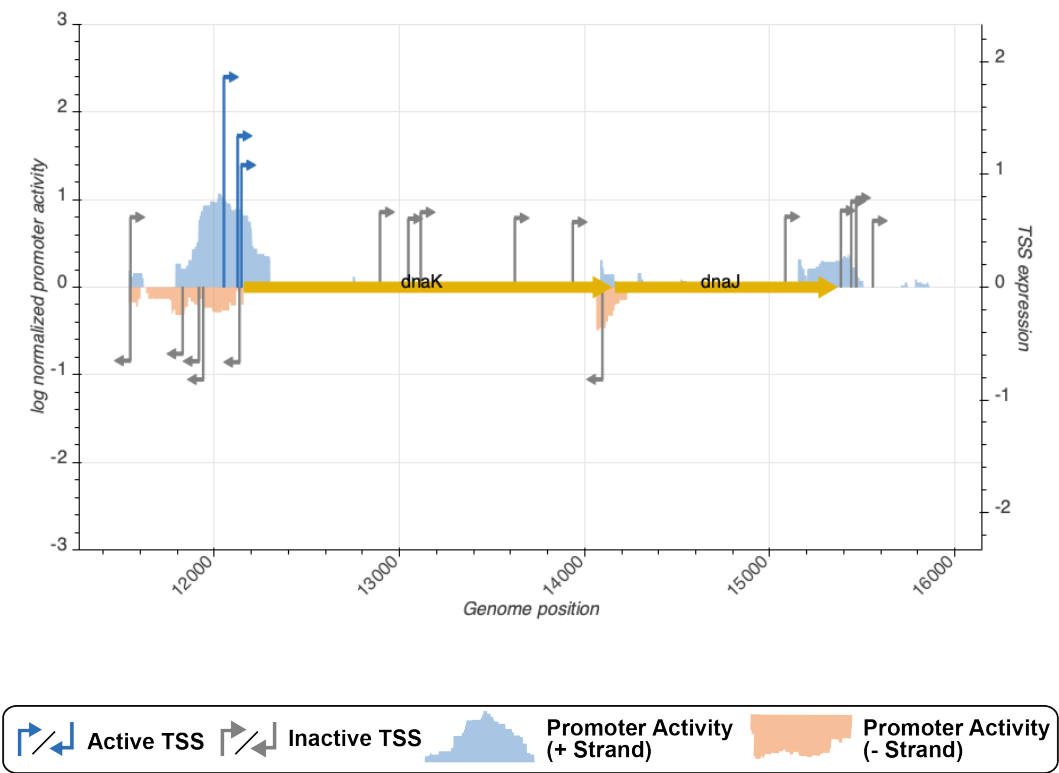| Active TSS | Inactive TSS | Promoter Activity (+ Strand) | Promoter Activity (- Strand) |

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_68_storz	12132	-	0.6652528	inactive
TSS_64_regulondb	11913	-	0.6568896	inactive
TSS_65_storz	11936	-	0.8189202	inactive
TSS_63_regulondb	11825	-	0.5912551	inactive
TSS_66_storz_regulondb	12048	+	1.8649654	active
TSS_69_regulondb	12142	+	1.0834774	active
TSS_67_wanner	12122	+	1.3428827	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).