## **Operon Promoter Landscape**

Operon	Strand	Operon start	Operon end
kgtP	-	2723768	2722470

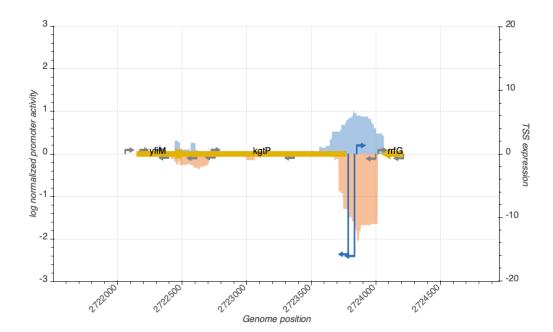


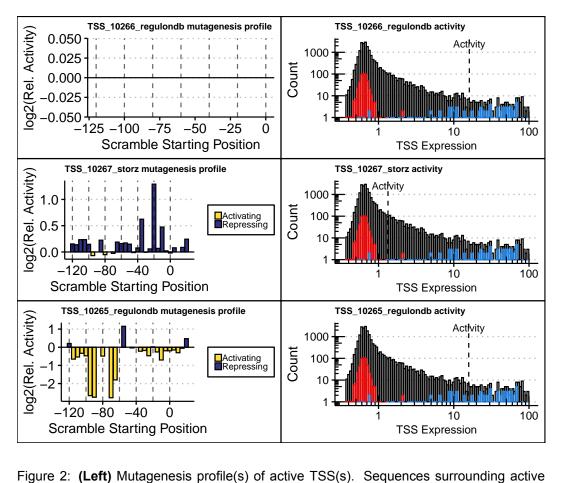


Figure 1: **Promoter activity in rich media (LB) surrounding query operon**. 17,767 previously reported TSSs were evaluated by measuring the promoter activity (right Y-axis) of the 150 bp surrounding the TSS (-120 to +30) to determine which were active or inactive. The genome-wide promoter activity (left 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**

TCC name	TCC position	Ctrond	TCC activity	Catagoni
TSS name	TSS position	Strand	TSS activity	Category
TSS_10266_regulondb	2723831	-	16.0919506	active
TSS_10270_storz	2724210	-	0.6755228	inactive
TSS_10268_storz	2723995	-	0.7560992	inactive
TSS_10267_storz	2723848	+	1.3363408	active
TSS_10269_storz	2724015	+	0.6139024	inactive
TSS_10265_regulondb	2723782	-	15.8058065	active

## TSS Scanning Mutagenesis



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).