Operon Promoter Landscape
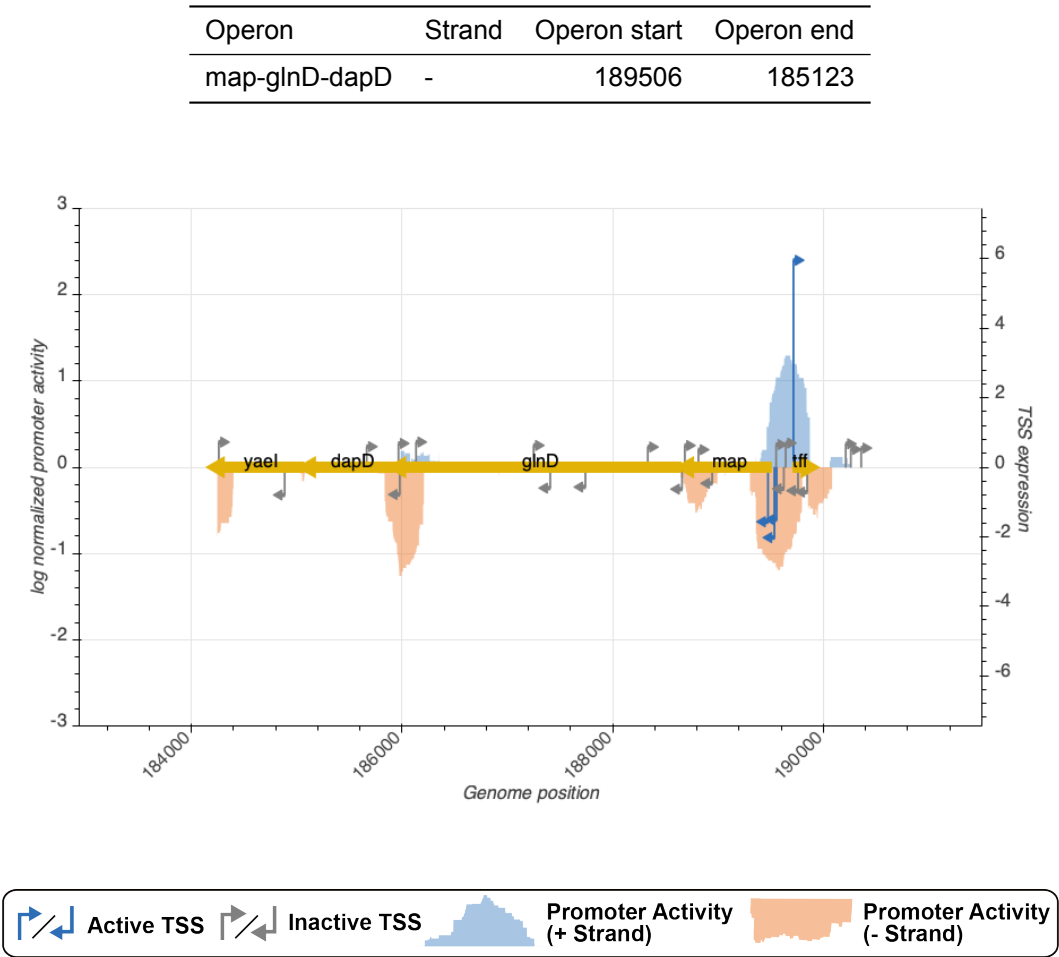
Operon	Strand	Operon start	Operon end
map-glnD-dapD	-	189506	185123

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_781_storz	189548	+	0.6527342	inactive
TSS_785_regulondb	189712	+	5.9601721	active
TSS_780_regulondb	189532	-	2.0267091	active
TSS_787_storz	189843	-	0.7169868	inactive
TSS_786_storz	189756	-	0.6759832	inactive
TSS_782_storz_regulondb	189553	-	1.5086972	active
TSS_784_regulondb	189639	+	0.6952805	inactive
TSS_783_storz_regulondb	189621	-	0.6206003	inactive

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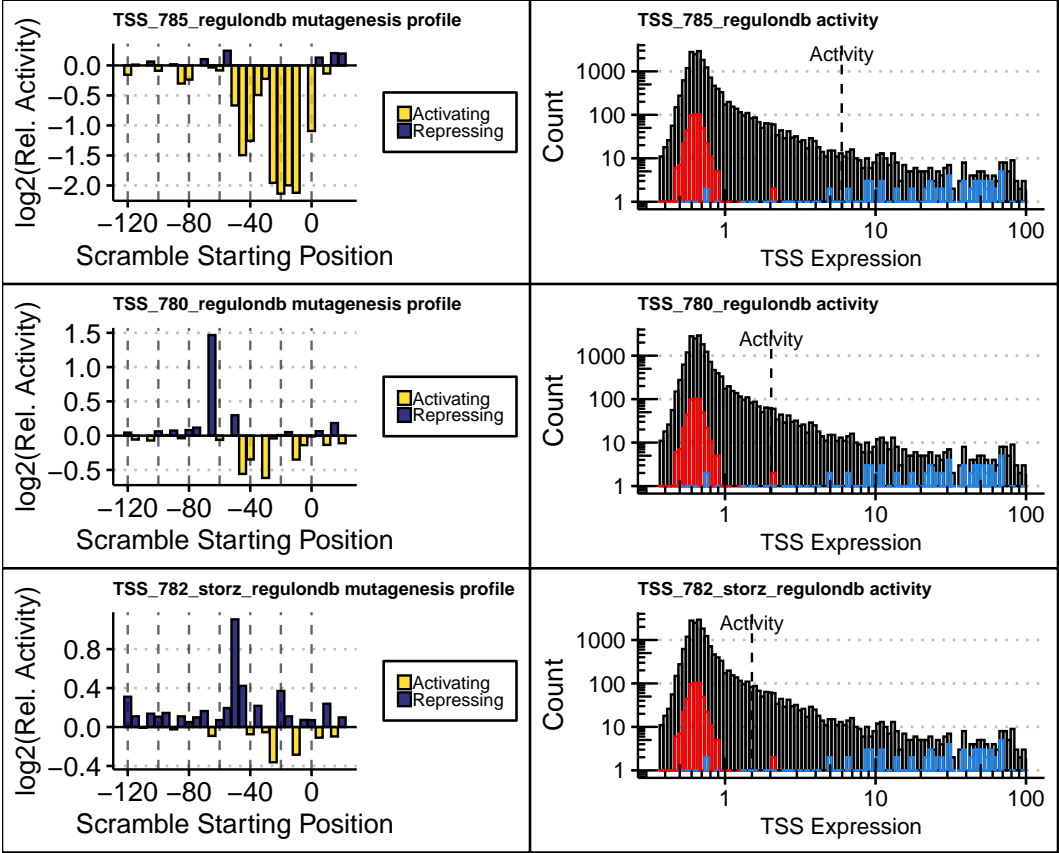
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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