Operon Promoter Landscape

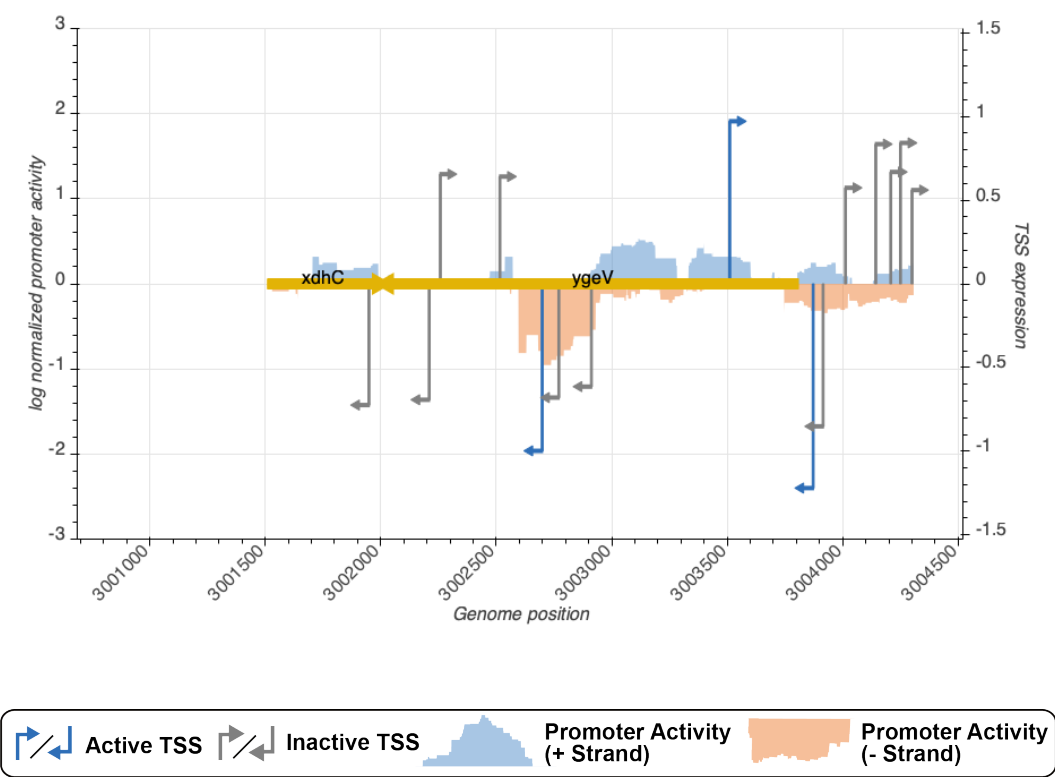| Operon	Strand	Operon start	Operon end
ygeV	-	3003808	3002030

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_11342_regulondb	3004139	+	0.8344498	inactive
TSS_11343_storz	3004204	+	0.6682124	inactive
TSS_11344_regulondb	3004246	+	0.8418552	inactive
TSS_11345_storz	3004296	+	0.5600436	inactive
TSS_11339_wanner	3003868	-	1.2201023	active
TSS_11340_storz	3003911	-	0.8513535	inactive
TSS_11341_storz	3004008	+	0.5735894	inactive

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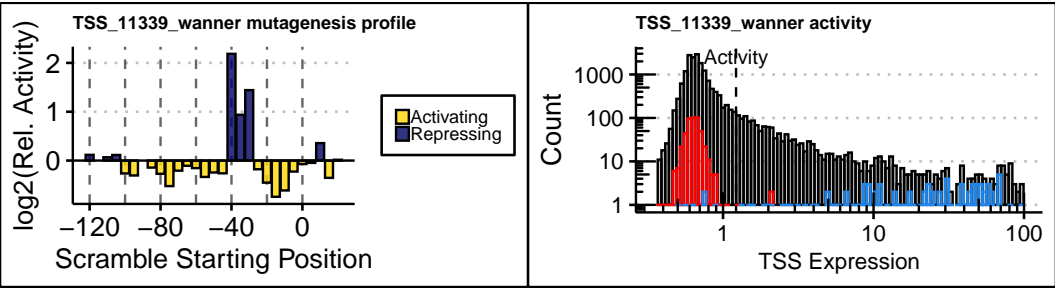
Figure 2: **(Left)** Mutagenesis profile(s) of active TSS(s). Sequences surrounding active TSSs were systematically mutated to identify regions controlling expression. Bar height indicates the relative change in promoter activity as a result of scrambling nucleotides within 10 bp regions at 5 bp intervals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