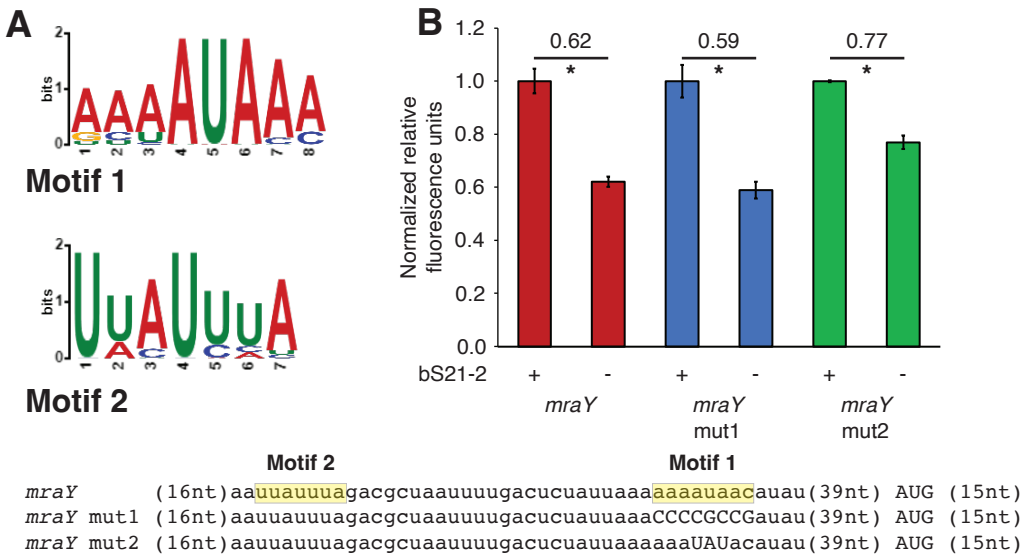

Figure 4. STREME-detected motifs are not necessary for bS21-2-responsive translation in the mraY 5′ UTR. (A) Logos of two sequence motifs generated by STREME, found to be enriched in the 5′ UTRs of the 20 most bS21-2-responsive genes compared to shuffled sequences. Motif 1 was detected in 19/20 input sequences; Motif 2 was detected in 18/20 input sequences. **(B)** Top: Relative fluorescence is reported for indicated translational fusion reporters in cells with (+; WT) or without (-; Δ*rpsU2*) bS21-2, in biological triplicate. Error bars represent 1 SD. *p<0.05 by t-test. Experiments were repeated twice and data from a representative experiment are shown. Bottom: Alignment of modifications to *mraY* 5′ UTR. Nucleotides altered from WT are capitalized. Motifs are highlighted in yellow. Values in parenthesis indicates the number of identical nts omitted from the ends of the UTRs.