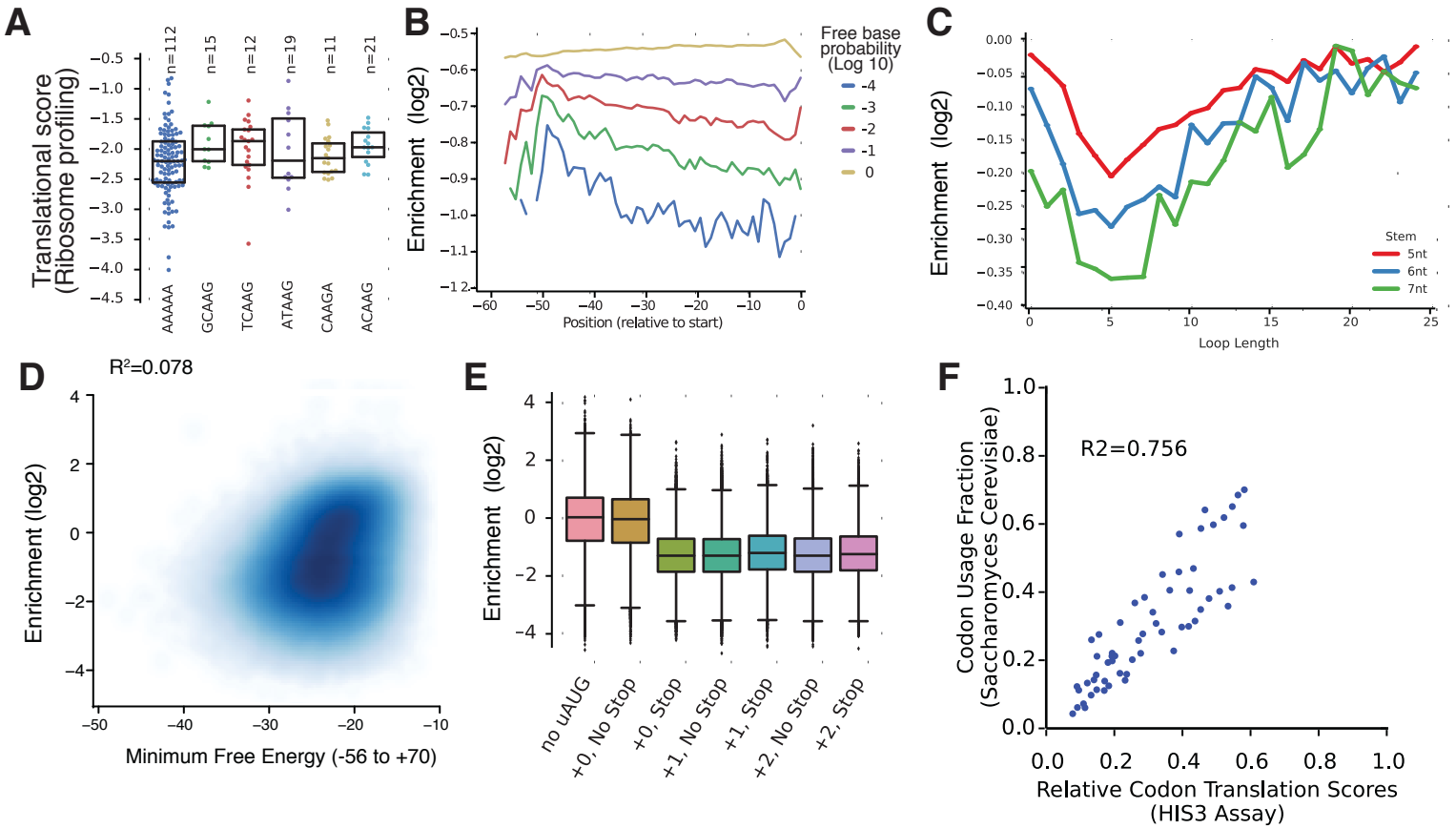

Supplemental Figure 2. (A) Translational scores from the ribosome profiling dataset of UTRs (Pop et al. 2014) containing the -5 to -1 sequences highlighted in Fig. 1c. Numbers above represent the number of yeast genes with these sequences at -5 to -1. (B) Free base probability was calculated across the 50 nucleotide region of the 5' UTR. Free base probabilities were grouped and each group's average enrichment of protein expression was calculated. (C) The mean enrichment of hairpins with stem lengths of 5-7 nucleotides and loop lengths of 0-25 nucleotides. (D) Correlation of MFE and enrichment was measured, with R2 of 0.078. (E) Enrichment scores of 5' UTRs were categorized based on the occurrence and relative frame shift of uAUGs and in-frame stop codons. Stop codons in-frame with a uAUG have a significant effect on enrichment in any frame. (F) Comparison of yeast codon usage frequency and per-codon enrichment from codons added by 5' UTRs with in-frame uAUGs.