

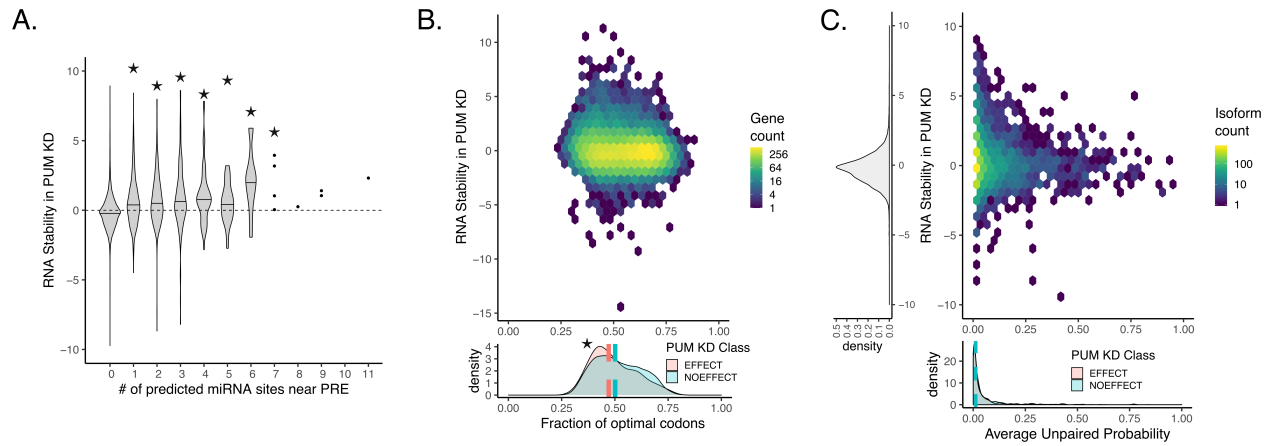


Figure S3: Additional features considered in determining PUM-mediated decay. **A)** Count of predicted conserved miRNA sites from conserved families that overlapped within 100 bp of a PRE for each gene. Stars indicate statistical significance from a Wilcoxon rank sum test compared to the 0 overlapping miRNA case. Stability in PUM knockdown is represented by a normalized interaction term between time and condition, where positive values indicate stabilization upon PUM knockdown and negative values indicate destabilization upon PUM knockdown (see Methods for details). **B)** (Above) Relationship between the fraction of optimal codons as determined by the Codon Stability Coefficient determined in HEK293 cells [105] and PUM-mediated effect as measured in our Bru-seq data. (Below) Marginal density plots of the fraction optimal codons for genes in the EFFECT and NOEFFECT classes. Median fraction optimal codons for each class are plotted with dotted lines. A significant ($p < 0.05$, two-sided permutation test, $n = 1000$) difference in medians between the classes is indicated by a star. **C)** (Above) Relationship between the probability of a given PRE being unpaired in predicted RNA secondary structure. Only genes with a PRE with > 0 probability of being unpaired where shown in the heatmap. All other genes are shown in the marginal y-axis density plot. (Below) Marginal density plot for genes in the EFFECT and NOEFFECT classes with median probabilities for each class shown as dotted lines. See Methods for details of secondary structure prediction.