Figure S6

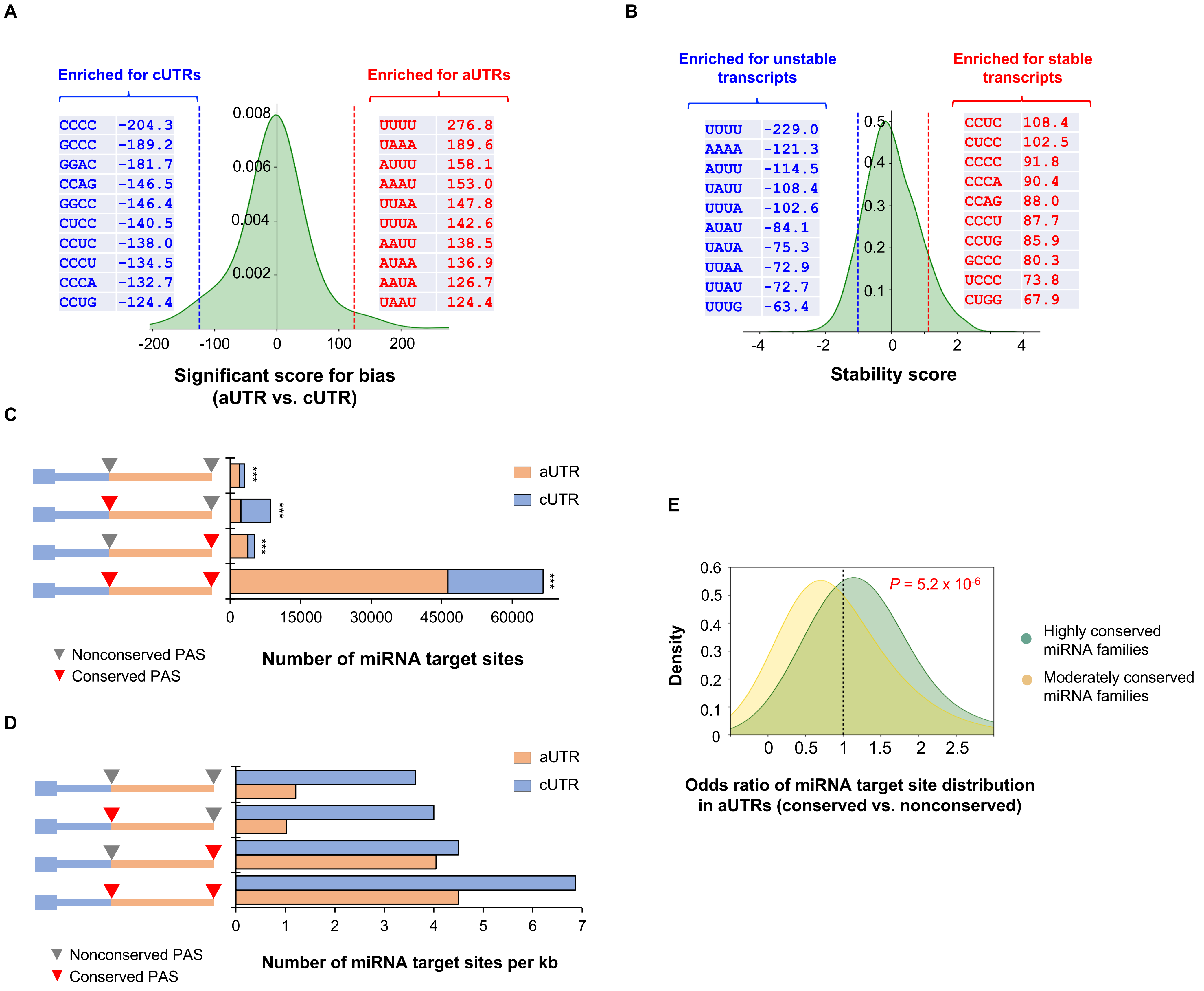

Figure S6. **(A)** Tetramers enriched for cUTRs or aUTRs. **(B)** Tetramers enriched for 3'UTRs of stable or unstable transcripts. **(C)** Number of predicted miRNA target sites in aUTRs and cUTRs of four groups of genes. miRNA target site prediction is based on TargetScan. The gene grouping is based on the conservation pattern of 3'UTR PASs, as illustrated on the left. **(D)** miRNA target site density in cUTRs and aUTRs. miRNA target site density is defined as number of target site per kb. The gene grouping is based on the conservation pattern of 3'UTR PASs, as illustrated on the left. **(E)** Odds ratio of miRNA target site distribution between conserved and nonconserved aUTRs for highly conserved miRNA families and moderately conserved miRNA families. miRNA conservation is defined by TargetScan ("Family Conservation" score = 1 for moderately conserved miRNAs, and = 2 for highly conserved ones).