

mRNA half-life analysis (Extended Data Fig. 10f)

Half-lives of transcripts with FH-AGO2^{5XA} CLIP clusters in their 3' UTRs were obtained from a previously published study³⁸. Genes that had half-lives assigned to more than one RefSeq mRNA isoform were removed to avoid ambiguity. Genes in the top quartile of half-lives were defined as having a long half-life ($N = 273$) and genes in the bottom quartile of half-lives were defined as having a short half-life ($N = 274$). The total number of CLIP reads in clusters in a given 3' UTR were obtained for each replicate and edgeR (v 3.8.6)⁴⁶ was used to calculate the normalized fold change of CLIP coverage comparing FH-AGO2^{5XA} to FH-AGO2^{WT}.

Data Availability

All high-throughput sequencing data generated in the course of this study (CRISPR-Cas9 screens, RNA-seq, eCLIP) have been deposited in GEO under accession code GSE89946.

Supplementary References

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