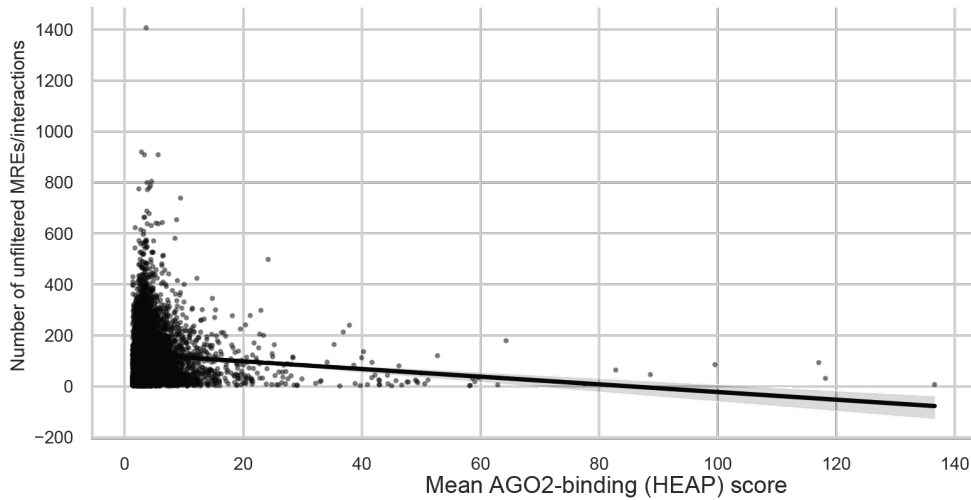


Table of Contents

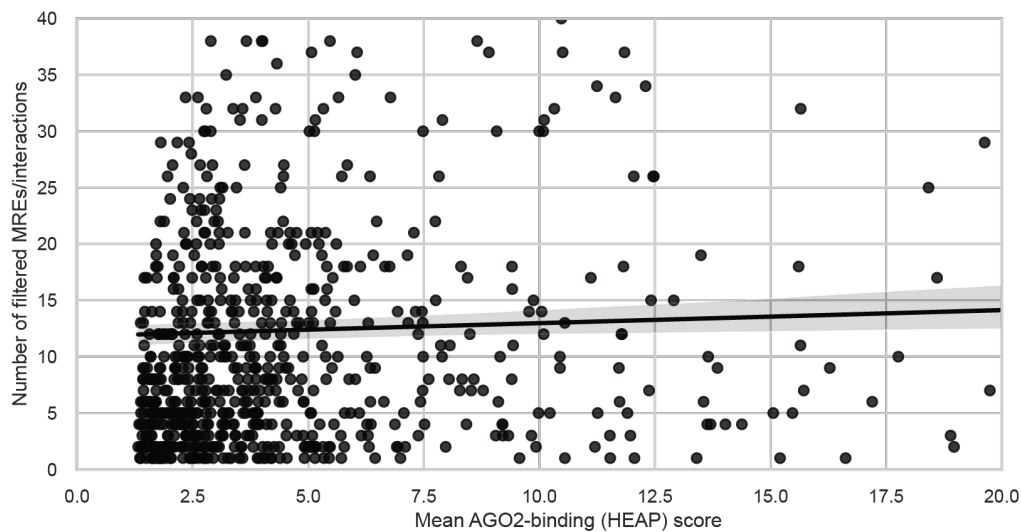
Appendix Fig S1. Correlation between AGO2 binding and number of predicted miRNA interactions	p2
Appendix Fig S2. Number of miRNA copies per cell, highlighting miR-290-295 cluster	p3
Fig S3. Luciferase reporter assay with Tfap4 3'UTR in HEK293T cells	p4
References	p5

Appendix Fig S1

A



B

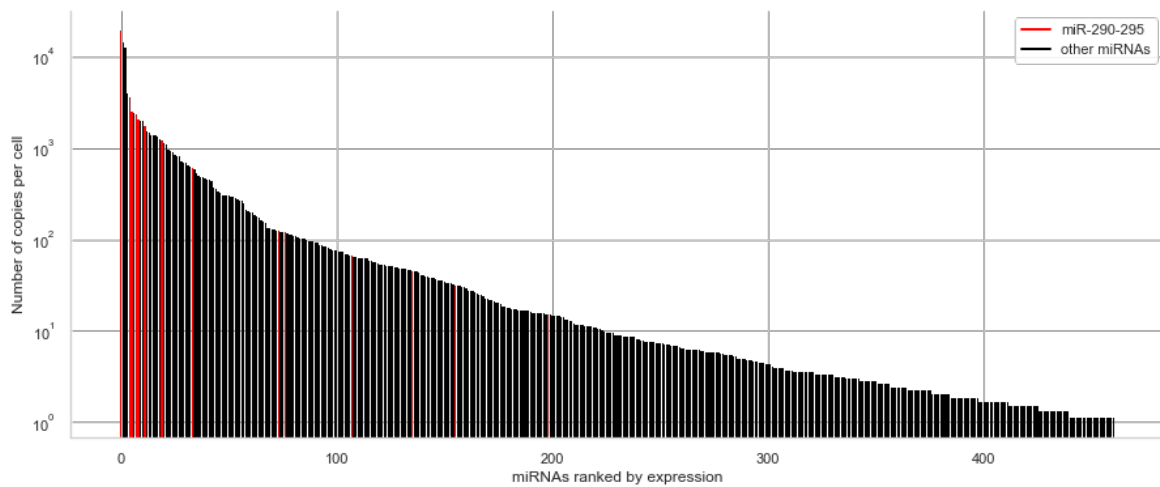


(No) correlation between the mean AGO2-binding peak intensities (HEAP) and the number of unfiltered MREs/interactions. Data are represented on a per-gene basis (one dot per gene) for unfiltered targets/interactions (A) and filtered (as described in the paper) targets/interactions (B).

A: Correlation between the number of predicted MREs (seed matching binding sites, excluding 6mers) and the mean intensity of gene-associated HEAP peaks (i.e., peak size). Pearson correlation coefficient: -0.08.

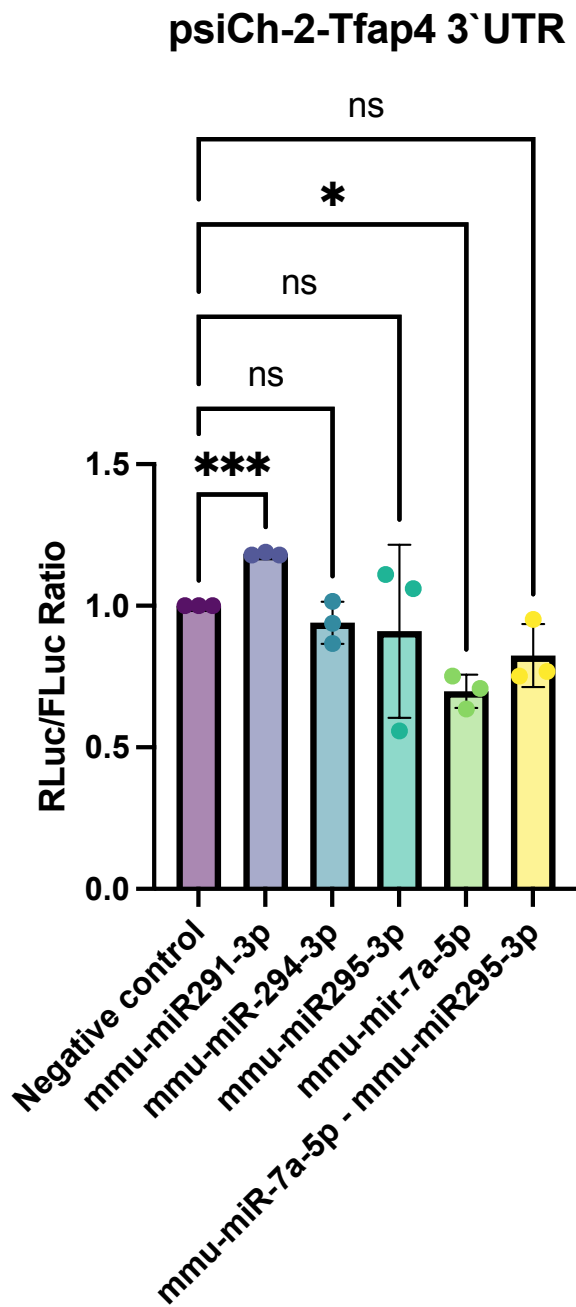
B: Correlation between the number of filtered interactions (as described in the paper) and the mean intensity of gene-associated HEAP peaks (i.e., peak size). Pearson correlation coefficient: 0.9, $p < 0.02$.

Appendix Fig S2



miRNA	Number of copies per cell
mmu-miR-295-3p	19440
mmu-miR-292a-5p	3556
mmu-miR-292a-3p	2466
mmu-miR-293-5p	2324
mmu-miR-291a-5p	2059
mmu-miR-293-3p	1723
mmu-miR-294-3p	1208
mmu-miR-291a-3p	602
mmu-miR-290a-5p	124
mmu-miR-295-5p	118
mmu-miR-291b-5p	66
mmu-miR-294-5p	45
mmu-miR-291b-3p	31
mmu-miR-290a-3p	15

The total number of miRNAs in mESCs has previously been estimated by (Calabrese *et al.*, 2007) at 110,000 copies per cell. Harnessing their finding, we used our sequencing data to derive the number of copies per cell for each miRNA sequence, as previously performed by (Gu *et al.*, 2016). Only miRNAs with at least 1 copy per cell are shown.



Luciferase reporter assay performed in HEK293T cells using the *Tfap4* 3'UTR, which was cloned into the psiCheck2 dual luciferase vector. Cells were transfected with the miRNA mimics listed above to a final concentration of 20 nM. Luciferase signal was measured 48 hours after transfection.

References:

Calabrese, J. M. *et al.* (2007) 'RNA sequence analysis defines Dicer's role in mouse embryonic stem cells', *PNAS*, 104(46), pp. 18097–18102. doi: 0709193104 [pii] 10.1073/pnas.0709193104.

Gu, K. L. *et al.* (2016) 'Pluripotency-associated miR-290/302 family of microRNAs promote the dismantling of naive pluripotency', *Cell Research*, 26(3), pp. 350–366. doi: 10.1038/cr.2016.2.