

miR-15a	3' – guguuugguaauacacgacgau – 5'
miR-15a perfect match UTR	5' ...cacaacc <u>au</u> gugcugcua... 3'
miR-15a	3' – guguuugguaauacacgacgau – 5'
miR-15a bulge match UTR	5' ...cacaacc <u>au</u> -- c agugcugcua... 3'

Figure S1 - Schematic of reporter UTRs. Related to Figure 1.

Schematic of reporter UTR sequences illustrating miR-15a binding to the perfect and bulged sequences in the 3' UTR of Renilla luciferase.

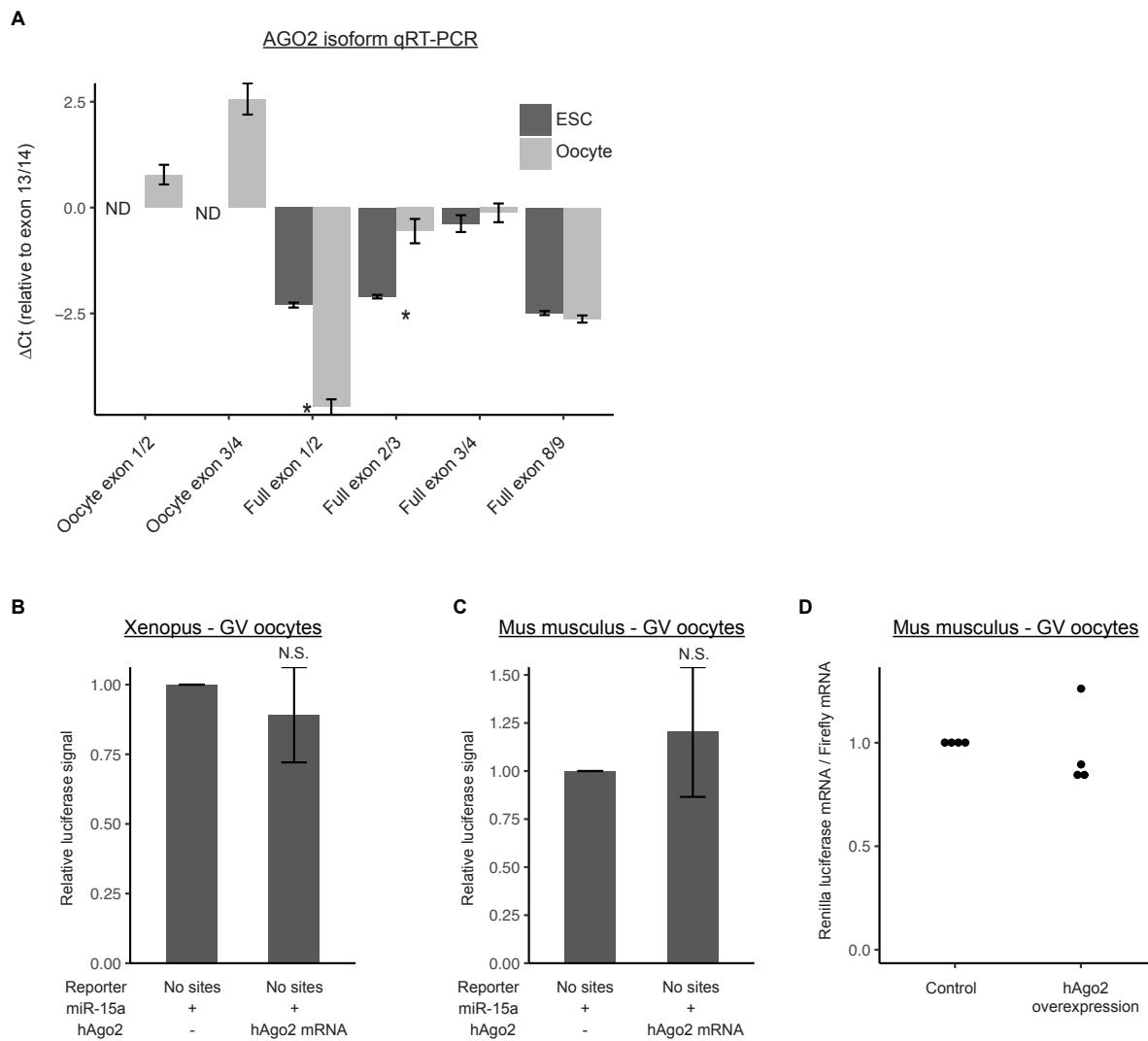


Figure S2 – Characterization of Oocyte-specific Ago2 isoform. Related to Figure 2.

A) qRT-PCR with primers spanning exons in full length or oocyte specific AGO2. Data is ΔCt in embryonic stem cells and GV oocytes relative to primers spanning exon 13/14. Embryonic stem cell N=2, oocyte N=3. ND = Not detected. Asterisks (*) represent significantly different data from the corresponding 'ESC' control data (Student's T-test, $p<0.05$). Luciferase assays in (B) Xenopus GV oocytes or (C) mouse GV oocytes following injection of miR-15a mimic, reporter lacking target sites, plus and minus wild-type AGO2 mRNA. N=10 for B, N=2 for C. D) RT-qPCR for Renilla 4x Bulge and Firefly in either control (WT or LSL-GFP-myc-hAgo2/+; Zp3-Cre-) or AGO2 overexpressing (injected with AGO2 mRNA or LSL-GFP-myc-hAGO2/++; Zp3-Cre+) mouse GV oocytes along with miR-15a mimic. Dots represent biological replicates. N=4. All error bars represent standard deviation. N.S. = not significant.

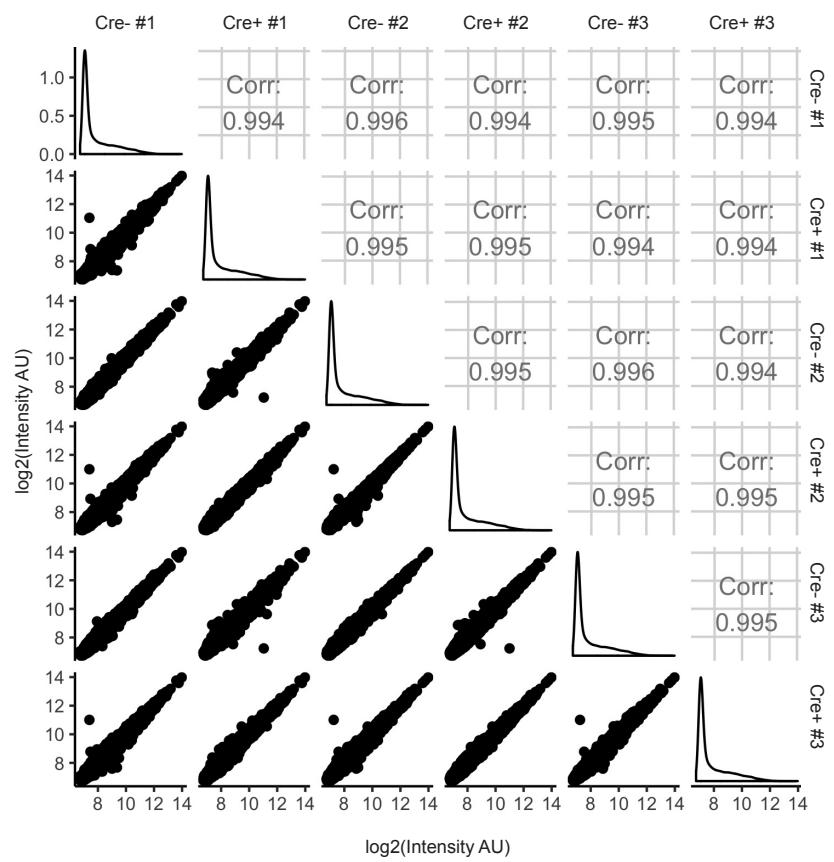


Figure S3 – Correlations between arrays. Related to Figure 3.

A) Log2 quantile normalized intensity values between replicates of LSL-GFP-myc-hAGO2/LSL-GFP-myc-hAGO2; Zp3-Cre+ and Zp3-Cre- mouse GV oocytes injected with miR-15a mimic.

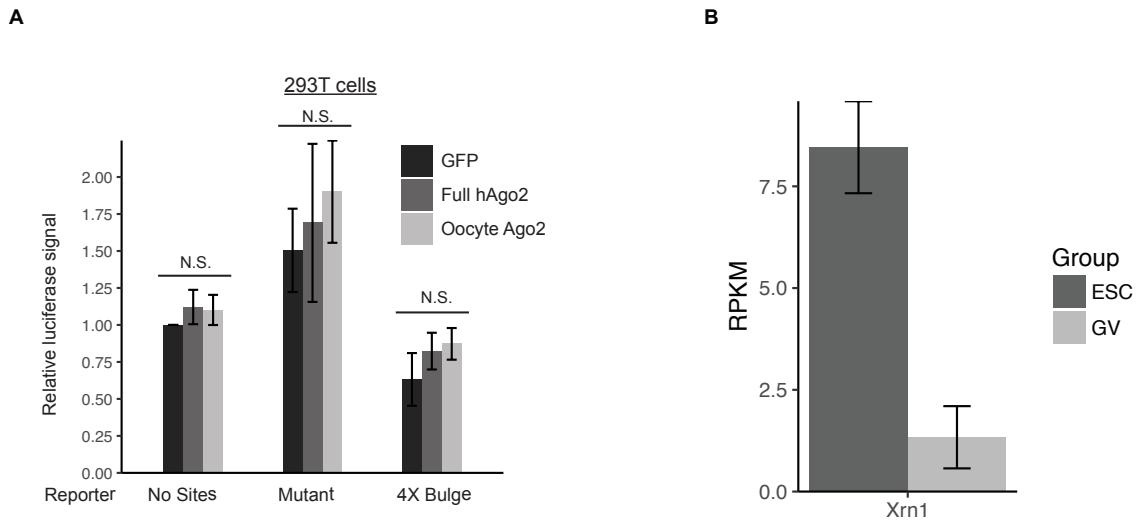


Figure S4 – Evaluation of additional potential mechanisms that impact miRNA activity. Related to Figure 4.
 A) Luciferase assay in HEK-293T cells transfected with psiCHECK2, a vector containing Firefly luciferase and Renilla luciferase with either no let-7 sites, mutated sites, or 4X Bulge sites in the 3' UTR for Renilla luciferase. psiCHECK2 was co-transfected with either GFP, full length hAGO2, or truncated oocyte AGO2. Luciferase data is a ratio of Renilla signal over Firefly signal. Full and truncated AGO2 is not significantly different from GFP control in all cases. All error bars represent standard deviation. N.S. = not significant. B) RNA-Seq expression of Xrn1 in mouse embryonic stem cells and mouse GV oocytes.

Let7Perfect Sense	TCGAATAAACTATACAACCTACTACCTCC
Let7Perfect Anti	GGCCGGAGGTAGTAGGTTGTATAGTTAT
Let7Bulge Sense1	TCGAATAAACTATACACATACTACCTCCGATACTATACACATACTA CCTCACCGCGT
Let7Bulge Sense2	ACTATACACATACTACCTCTCACACTATACACATACTACCTCC
Let7Bulge Anti1	GGCCGGAGGTAGTATGTGTAGTGAGAGGTAGTATGTGTATA GTACCGCGT
Let7Bulge Anti2	GAGGTAGTATGTGTAGTATCGGAGGTAGTATGTGTAGTTAT
Let7Mutant Sense1	TCGAATAAACTATACACATAATCCATCCGATACTATACACATAATC CATCACCGCGT
Let7Mutant Sense2	ACTATACACATAATCCATCTCACACTATACACATAATCCATCC
Let7Mutant Anti1	GGCCGGATGGATTATGTGTAGTGTGAGATGGATTATGTGTATA TACCGCGT
Let7Mutant Anti2	GATGGATTATGTGTAGTATCGGATGGATTATGTGTAGTTAT
miR15Perfect Sense	TCGAATAACACAAACCATTATGTGCTGCTAC
miR15Perfect Anti	GGCCGTAGCAGCACATAATGGTTGTGTTAT
miR15Bulge Sense1	TCGAATAAcacaaaccatCAgtgtgctaCGATcacaaaccatCAgtgtgctaACGCGT
miR15Bulge Sense2	cacaaaccatCAgtgtgctaTCACcacaaaccatCAgtgtgctaC
miR15Bulge Anti1	GGCCGTAGCAGCACTGATGGTTGTGGTGTAGCAGCACTGATGGT TTGTGACCGCGT
miR15Bulge Anti2	TAGCAGCACTGATGGTTGTGATCGTAGCAGCACTGATGGTTGTG TTAT
miR15Mutant Sense1	TCGAATAACACAAACCATTAGTCGGATACGATCACAAACCATTCA GTTCGGATAACGCGT
miR15Mutant Sense2	CACAAACCATTAGTCGGATATCACCACAAACCATTAGTCGGATA C
miR15Mutant Anti1	GGCCGTATCCGAAC TGATGGTTGTGGTGTAGTCCGAAC TGATGGT TTGTGACCGCGT
miR15Mutant Anti2	TATCCGAAC TGATGGTTGTGATCGTATCCGAAC TGATGGTTGTG TTAT

Rosa26 Ago2 common genotyping	CCAAAGTCGCTCTGAGTTGTTATC
Rosa26 Ago2 WT RVS genotyping	GAGCGGGAGAAATGGATATG
Rosa26 Ago2 MUT RVS genotyping	CGGGCCATTACCGTAAG
Cre genotyping FWD genotyping	tggcgccatggtgcaggtt
Cre genotyping RVS genotyping	cggtgctaaccagcggtttc
Il2 genotyping FWD genotyping	ctaggccacagaattgaaagatct
Il2 genotyping RVS genotyping	gttagtgaaattctagcatcatcc
RPL7 qPCR FWD	gattgtggagccatacattgca
RPL7 qPCR RVS	tgcgcgtgcctcggttgt
mouse human Ago2 qPCR FWD	ctcacctggcgccttc
mouse human Ago2 qPCR RVS	agaggatggcttcctcage
Oocyte Exon 1 - Exon 2	AGAACCTTCCTGCCTTCCTTC
Oocyte Exon 1 - Exon 2	TTGAAGGCATATCCTGGGATGG
WT Exon 2 - Exon 3	GGACATCAAACCTGAGAAATGCC
WT Exon 2 - Exon 3	TCCATCAAACACTGGCTTCC
Oocyte Exon 3 - Exon 4	TACACAGCAATGCCCTTCC
Oocyte Exon 3 - Exon 4	CAGTTCATGCTTCTGCTCTTGC
WT Exon 1 - Exon 2	GCAACGCCACCATGTACTC
WT Exon 1 - Exon 2	TTGAAGGCATATCCTGGGATGG
WT Exon 3 - Exon 4	AGCCAGTGTGATGGAAGG
WT Exon 3 - Exon 4	ATGCGATCTTGCTTCTCC
WT Exon 8 - Exon 9	cagacaatcagacacctcaaccatg
WT Exon 8 - Exon 9	cacttgcgttcgtttgt

WT Exon 13 - Exon 14	acagaccctatccaaatctctgc
WT Exon 13 - Exon 14	atgacagggtgctggaacac
Renilla qPCR FWD	ACGCAAACGCATGATCACTG
Renilla qPCR RVS	GCAGAAAAATCACGGCGTTC
Firefly qPCR FWD	CGTGCCAGAGTCTTCGACA
Firefly qPCR RVS	ACAGGCGGTGCGATGAG

Table S1: Oligonucleotides used in this study. Related to STAR Methods.