Deep-sequencing of human Argonaute-associated small RNAs provides insight into miRNA sorting and reveals Argonaute association with RNA fragments of diverse origin

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SUPPLEMENTARY MATERIAL

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I. SUPPLEMENTARY DISCUSSION/METHODS

Handling tags that fail to match exactly to the genome
The most compelling reasons to include tags that do not match exactly to the genome in analyses like the ones presented in this study are 1) the demonstrated effects of nucleotidyltransferase enzymes in altering the 3' ends of classes of small RNA (1), (2), (3), (4), (5), (6) and 2) the observation that classes of non-coding RNA are subjected to chemical modification events or RNA editing events (7), (8), (9). Having said this, in the interest of avoiding reporting false positives, we decided against including potential RNA precursors wherein the most frequently-mapping tag was not exactly matching unless there was compelling evidence otherwise. For example, tags mapping to the *CYP46A1* mRNA gene contain two mismatches (Table 2), but we feel these mismatches represent *bona fide* THP-1 specific SNPs because 1) the tags map to no other location in the genome exactly, with one mismatch or with two mismatches 2) all tags mapping to this portion of the genome contain the mismatches, and 3) the resulting change to the CYP46A1 exon results in a conservative amino acid substitution from a leucine to an isoleucine residue, a substitution shared in CYP46A1 gene homologues from closely-related organisms (see Fig. 3B).

quantitative RT-PCR (qRT-PCR)
qRT-PCR was performed in 20-μl reaction mixture with 2μl of the RT reaction (Materials and Methods) and 2x QuantiTect SYBR Green RT-PCR Master Mix (Qiagen) using the specific primer and miScript Universal primer on an ABI 7500 Fast real time PCR system (Applied Biosystems). PCR parameters consisted of heating at 95°C for 15 min, followed by 40 cycles of 94°C for 15 s, 60°C for 30 s and 70°C for 20 s. The following primers were used as the specific primer in addition to primers listed in the Materials and Methods of the main text: CYP46A1-F (5'-AGATGTACCGTGCGATTCAGAC-3'), tRNA-His-GTG-F (5'-CGTATAGTGGTTAGTACTCTGCG-3'). RNU1A miScript primer (Hs_RNU1A_1, Qiagen) was used as an internal expression control.

II. SUPPLEMENTARY FIGURE LEGENDS

Supplementary Figure S1. Pairing probability profile comparison for miRNA loci enriched in their association across all AGO proteins and miRNA loci depleted in their association across all AGO proteins. (A) Boxplots depict pairing probabilities, representing the double-stranded character, along the miRNA strand from positions 1-19. Boxplots in the left-hand column correspond to double-stranded character of the set of miRNA enriched across all Ago proteins while boxplots to the right correspond to double-stranded character of the set of miRNA depleted across all Ago proteins. Profiles were constructed in each AGO-library, to account for potential differences in primary mature isomir and primary star isomir (Materials and Methods). (B) P-values of Wilcoxon rank sum test generated from comparing the pairing probabilities at nucleotide positions 1-19 are plotted. Red line plotted at the designated level of significance, *p*=0.01.

Supplementary Figure S2. qRT-PCR validation of selected findings. (A) Ct values from qRT-PCR experiments for miR-338-3p, as-miR-338-5p, miR-155, CYP146A1, tRNA[His-GTG], and RNU1A (primers designed for as-miR-155 failed to amplify) in THP-1 complete cell RNA extract (n=3). (B) Ct values from qRT-PCR for miR-338-3p, as-miR-338-5p, and miR-155 (as-miR-155 failed to amplify) in HeLa

complete cell RNA extract (n=2). (C) Ct values from qRT-PCR for CYP46A1, tRNA$^{His-GTG}$, miR-338-3p, as-miR-338-5p, and miR-155 (primers designed for as-miR-155 failed to amplify) in RNA extracted from AGO1-, AGO2-, and AGO3-IP experiments (n=3, except for miR-338-3p and as-miR-338-5p where n=2). (D) Gel electrophoresis of qRT-PCR amplified products. Primers designed for tRNA$^{His-GTG}$ are detecting the fragment identified in deep sequenced libraries, not the full-length tRNA.

Supplementary Figure S3. **Alignments of putative seed regions from sequences identified in Table 2**. Alignments of all putative seed regions wherein sufficient homology to construct an alignment between regions exists. Regions of homology are identified by axtChain program (10), which is based on BLASTZ (11) whole genome alignments. Alignments constructed for all species for which axtChain (10) identifies a homologous region.

Supplementary Figure S4. **Comparison of distances of 21-base pair mature miRNA and 29-base pair tRNA fragment identified as associating with the AGO1 protein**. Rendering of ribbon backbone of tRNA$^{GLU-CTC}$ (12) and 21 bases of a single strand of synthetic 24-basepair miRNA duplex (13). The tRNA fragment identified in Ago1 library is colored green on the structure of the tRNA. Dashed yellow lines trace distance between the terminal atoms of the tRNA fragment and miRNA strand, with distance in Angstroms labeled to the right. Despite difference in absolute nucleotide length, distance between ends of the tRNA fragment is consistent with established length of DICER1-mediated cleavage (14), (15). RNA rendered in SWISS-PDB Viewer (16).

Supplementary Figure S5. Superimposition of tRNA$^{GLU-CTC}$ on active site of DICER1 enzyme (14). DICER1 is rendered as a ribbon drawing with helices in purple and strands in orange and manganese ions as grey spheres. The tRNA structure is also rendered as a ribbon drawing and colored in grey, with the portion of the tRNA corresponding to the sequence enriched in the Ago1 library colored in green. A view of the DICER1 active site is given on the left, with known active site residues rendered as ball and stick drawings. Yellow circles highlight the location of the primary active site residues. A side view, relative to the active site, is given on the right. The location of the PAZ domain is marked by a red circle. Drawings rendered in SWISS-PDB Viewer (16).

Supplementary Figure S6. Distribution of tag counts over randomized genome regions. *x*-axis of all plots measures tag counts recovered in randomized genome regions over 1000 trials, *y*-axis measures the number of trials which recovered a given tag count. Red line at the right of each plot is located at the number of actual tags in the AGO-IP libraries recovered from promoter regions.

Supplementary Figure S7. Distance from TSS and length distribution of promoter-derived, AGO-associating short RNA tags. (A) Histogram reporting total counts of 5' start sites for unique, promoter-derived, AGO-associating tags in 10-bp windows around the Refseq-defined TSS (tags from all AGO-IP libraries are pooled). Relative increased concentration between 0 and -100 nucleotides from the transcription start site roughly agrees with similar distributions for tiRNA and TSSa-RNAs (17),(18). (B) Length distributions for complete cell and pooled AGO-IP promoter-derived tags. The AGO-IP libraries are noticeably shifted to the right, largely lacking the 18-19 basepair tag lengths seen in the complete cell RNA.

Supplementary Figure S8. Distribution of miRNA loci with recovered anti-sense tags across genome features. An observation that anti-sense miRNA tags are disproportionately recovered from intronic regions prompted an investigation into the genome location of asmiRNA loci across different species. The proportion of miRNA loci with anti-sense tags are plotted against the background of all sense miRNA loci across different species. Genome locations are color-coded according to the legend on the right. Abbreviations used: as, anti-sense; hsa, *Homo sapiens*; mmu, *Mus musculus*; gga, *Gallus gallus*; dme, *Drosophila melanogaster*; cel, *Caenorhabditis elegans*; ath, *Arabidopsis thaliana*.

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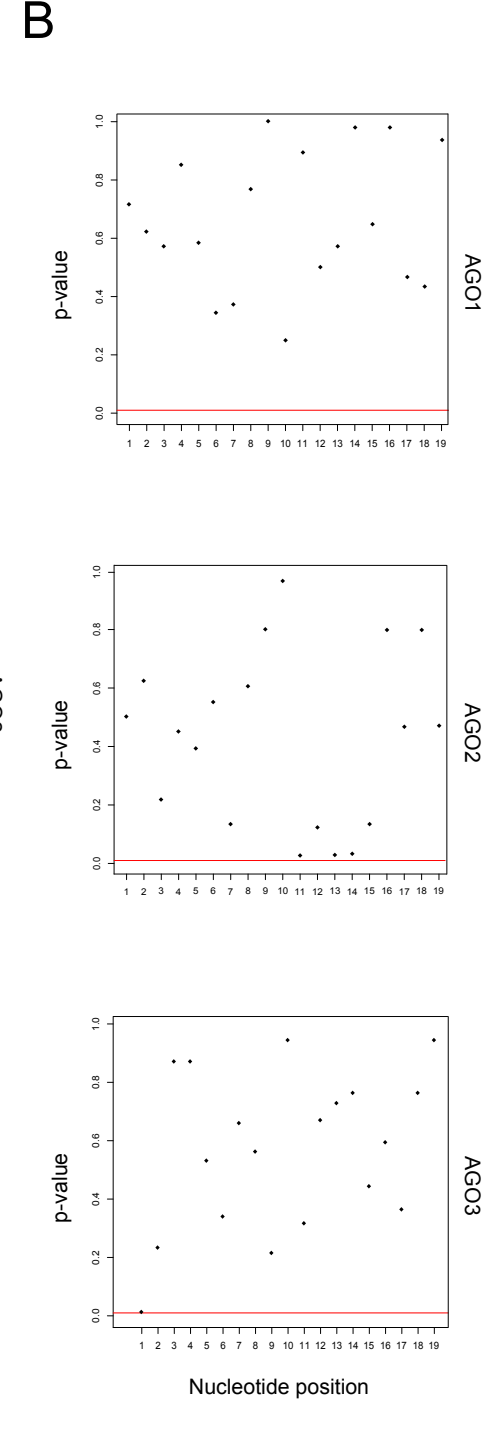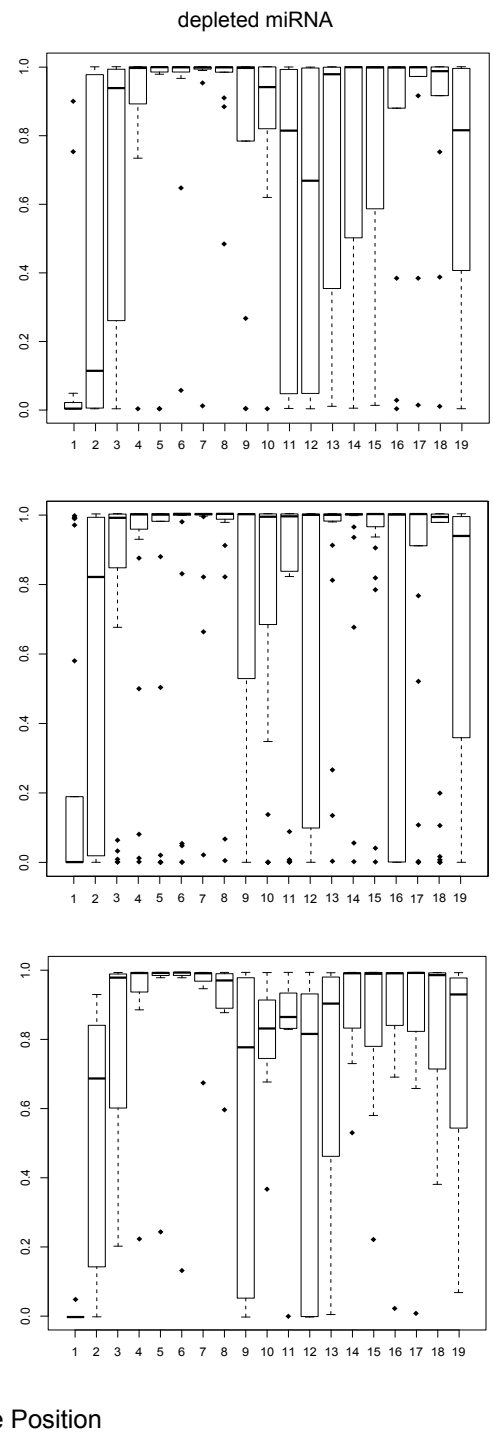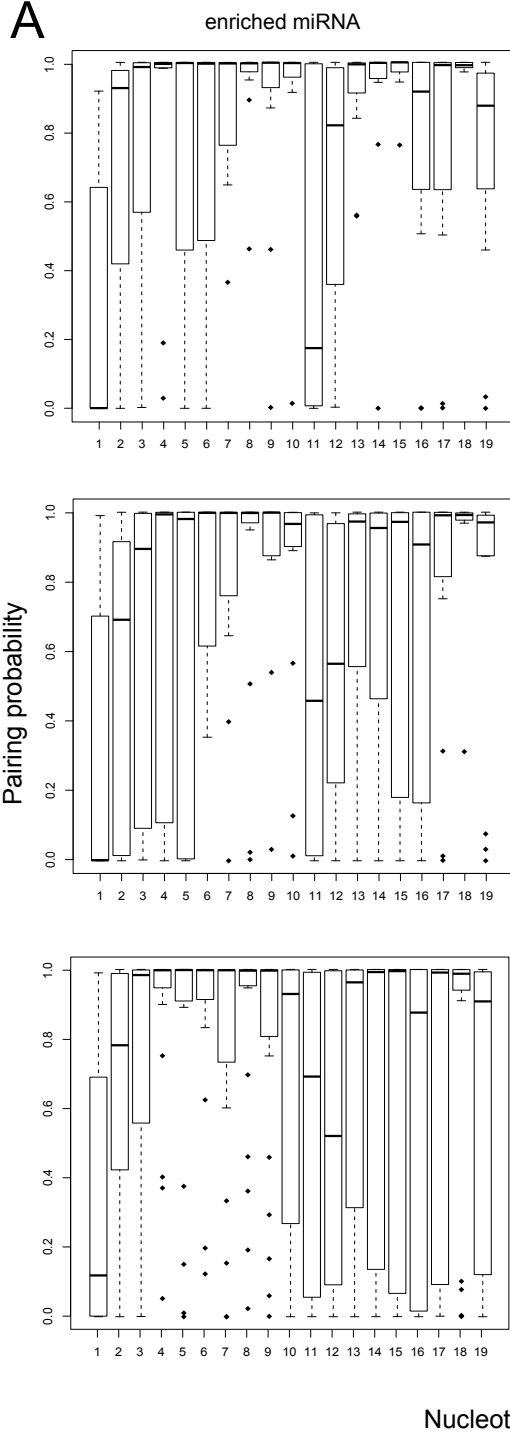
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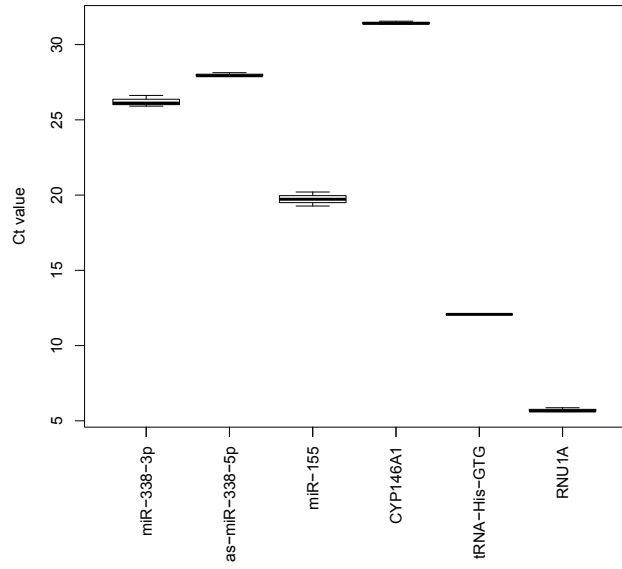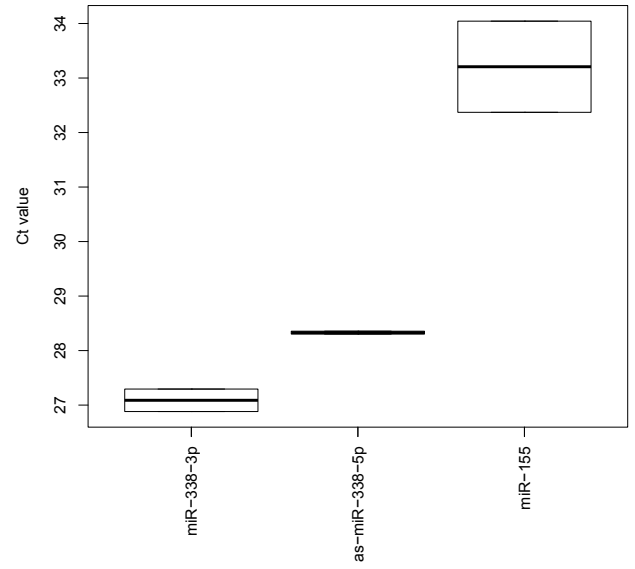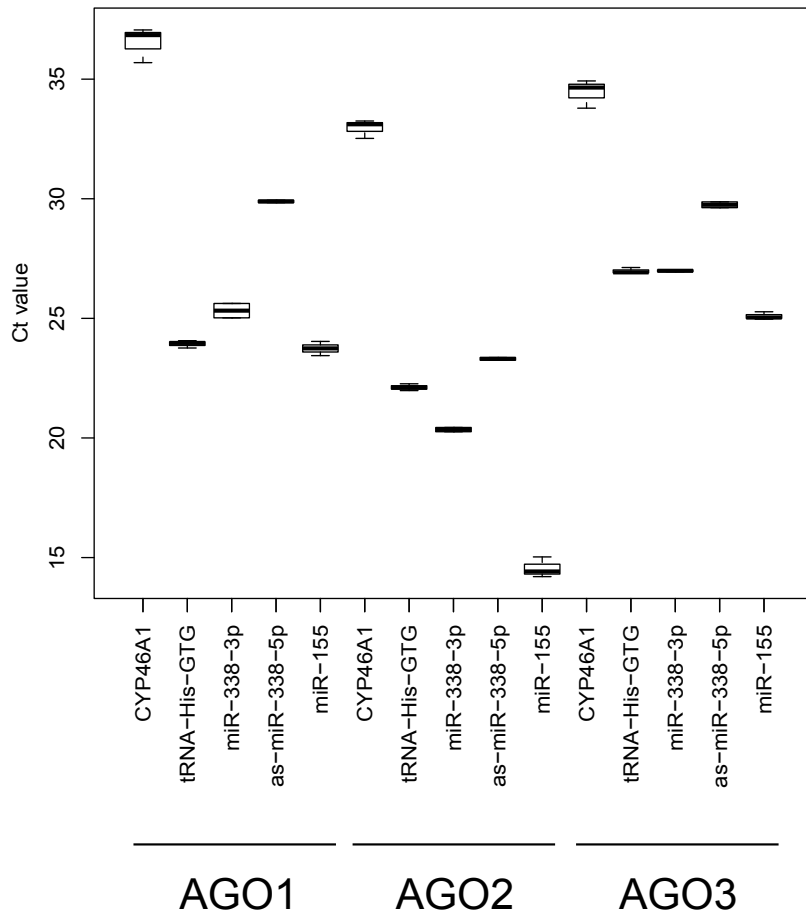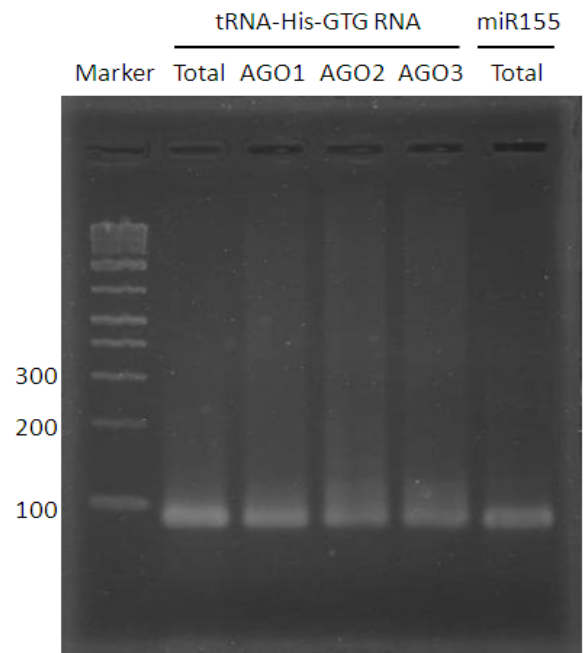
Supplementary Figure S2.

Supplementary Figure S3. Alignments of putative seed regions from sequences
identified in Table 2.


```
##U12 alignment

seed        GAUGCCU
human       GGAUGCCUGGGGAGUUGCGAUCUGCCCG
mouse       GGAUGCCUGGGGUGACGCGAUCUGCCCG
rat         GGAUGCCUAGGUAACGCGAUCUGCCCG
dog         GGAUGCCUGGGGAGCCGCGAUCUGCCCG
chicken     GGAUGCCCAGGUGCAAUGAUCUGCCCG

##U1--little to no conservation

##U2--little to no conservation

##U2-like--little to no conservation

##VTRNA1-1--little to no conservation

##ACA45

seed        AGGUAGA
human       AAGGUAGAUAGAACAGGUCUUG
rat         AAGGUAGAUAGAACAGGUCUUG
mouse       AAGGUAGAUAGAACAGGUCUUG
dog         AAGGUAGAUAGAACAGGUCUUG
chicken     AUGGUGGA-AGAACAAGGCCUG

##ACA25

seed        UUCUCUA
human   GUUCUCUAUAGGAAGCCAUAG-CA
dog     GUUCUCCAUUGGAUGCCACGGUCA
rat     GUUCUUCACAGGGCAAAUCGGGCA
mouse   GUUCUUCACAGAGAAAAUCCUGCA

##U17a--little to no conservation

##U17b--little to no conservation

##HBI-100

seed        CUGAUCG
human       UCUGAUCGUUCCCCUCCGUACAG
mouse       UCCGAUCGUUCCCCUCCAUACAA
rat         UCUGAUCGUUCACCUCCAUACAA
dog         UCUGAUCGUUCCCCUCCAUACAA
chicken     CUGGAUCGUUCCCCUCCAUACAU

##ACA47

seed        CGGUCUG
human   ACGGUCUGGGGAAAGGCUCCUGUGUU
mouse   ACGGUCUGGGGAAAAGGCUCCUGUGUG
rat     ACGGUCUGGGGAAAGGCUCCUGUGUG
dog     AUGGUCUGCGGAAAGGCUCCUGUGUG

##ACA17

seed        CUGUGUC
human       UCUGUGUCAUUAGGUGGCAGAGAU
mouse       UGUGCGUCAGUAGGUGGCAGAGAG
rat         UUUGUGUCAGUAGGUGGCGGAGAG
dog         UUUGUGUCAUUGGGUGGCAGAAAG
chicken     NUUGUGUCAUUAGGUGGCAGAGAU

##mitochondrial tRNA-Ser

seed        AGAAAGC
human   GAGAAAGC-UCACAAGAACUGCUAACU
mouse   AAGAAAGA-UUGCAAGAACUGCUAAUU
```

```
rat      AAGAAAGU-AUGCAAGAACUGCUAAUU
dog      GAAAAAGUACUGCAAGAACUGCUAAUU
```

##mitochondrial tRNA-Cys

```
seed       GCUCCGA
human    AGCUCCGAGGUG-AUUUUCAUAUUGAAUUGCA
mouse    GGUCUUAAGGUG-AUAUUCAUGUCGAAUUGCA
rat      AGCCUUAAGGUG-AUUAUCAUGUCGAAUUGCA
dog      AGCUCCGUGGUGAAUUUUCAUAUUGAAUUGCA
chicken  GACUCUGUAGUG-AAGUUCAUAAUGAGUUGCA
```

##tRNA-His-GTG--little to no conservation

##mitochondrial tRNA-Met

```
seed       GUAAGGU
human    AGUAAGGUCAGCU-AAAUAAGCUAUCGGGCCC
mouse    AGUAAGGUCAGCU-AAUUAAGCUAUCGGGCCC
rat      AGUAAGGUCAGCU-AACUAAGCUAUCGGGCCC
dog      AGUAAGGUCAGCUAAAAUUAAGCUAUCGGGCCC
chicken  AGUAAGGUCAGCU-AACUAAGCUAUCGGGCCC
```

##tRNA-Glu-CTC--little to no conservation

##tRNA-Leu-CAA--little to no conservation

##28S-like--little to no conservation

##CLTC

```
seed       AGUUGUU
human    CAGUUGUUCAUGAUAUUUAGAAGCCACC
mouse    CAGCUGUUCGUGAUAUUUAGAAGCCACC
rat      CAGCUGUUCAUGAUAUUUAGAAGCGACC
dog      CAGCUGUUCGUGAUAUUUAGAAGCCACC
chicken  UAGCUGUUCGUGGUAUUUUGAAGCUACC
```

##WEE1

```
seed       CAAUUCU
human    UCAAUUCUAUUCGUAAUUGUUCUGCACU
rat      UCAAUUCUAUUCGUAACUGCUCUGCGCU
mouse    UCAAUUCUAUUCGUAACUGCUCUGCGCU
dog      UCAAUUCUAUUCGUAAUUGUUCUGCACU
chicken  UCAGCUCUAUCCGCAGCUGCUCUGCGCU
```

##CYP46A1

```
seed       GAUGUAC
human    AGAUGUACCGUGCGCUCCAGACUGU
mouse    AGAUGUACCGCGCGCUUCAGACUGU
rat      AGAUGUACCGUGCGAUUCAGACUGU
dog      AGAUGUACCACGCAAUCCAGACUGU
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Supplementary Figure S4.
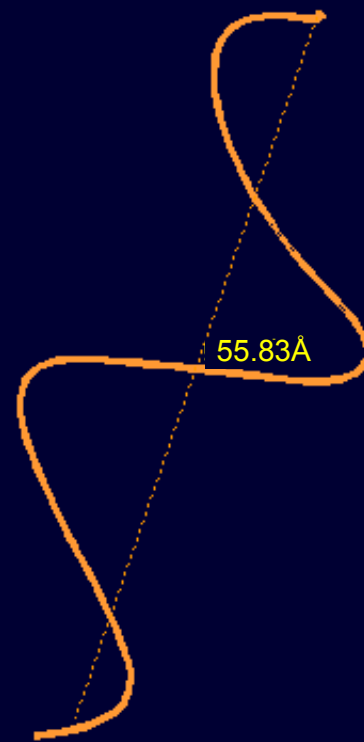
tRNA^GLU (pdb: 2DER)   miRNA (pdb: 3A6P)

Supplementary Figure S5.

Active site view

Side view

PDB: 2FFL

AGO1-IP
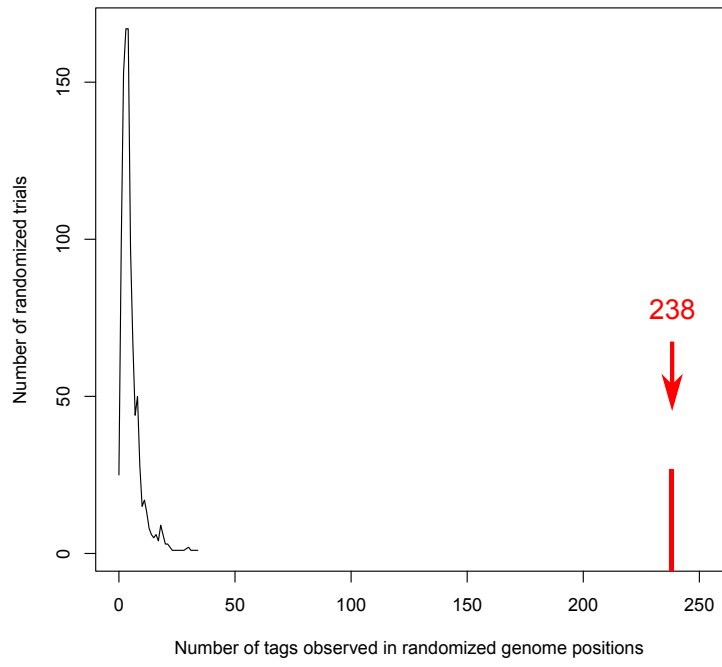
AGO2-IP

AGO3-IP
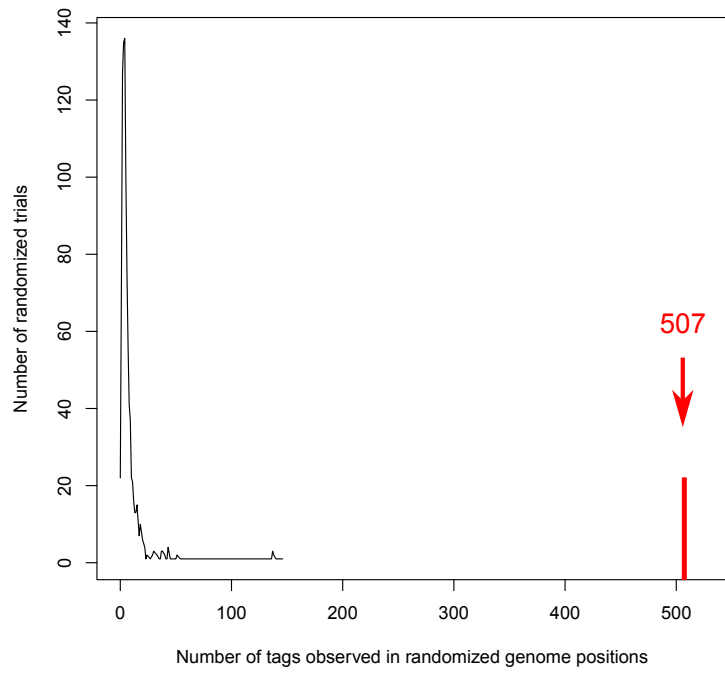
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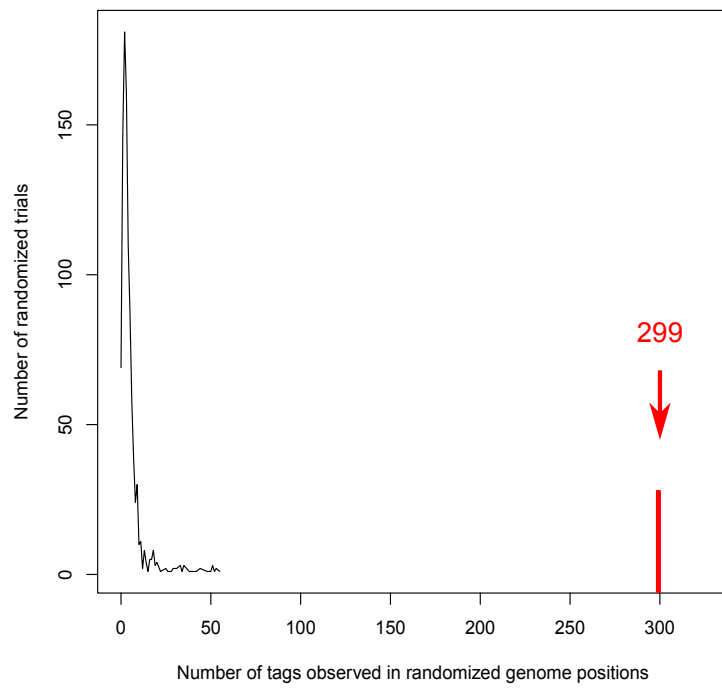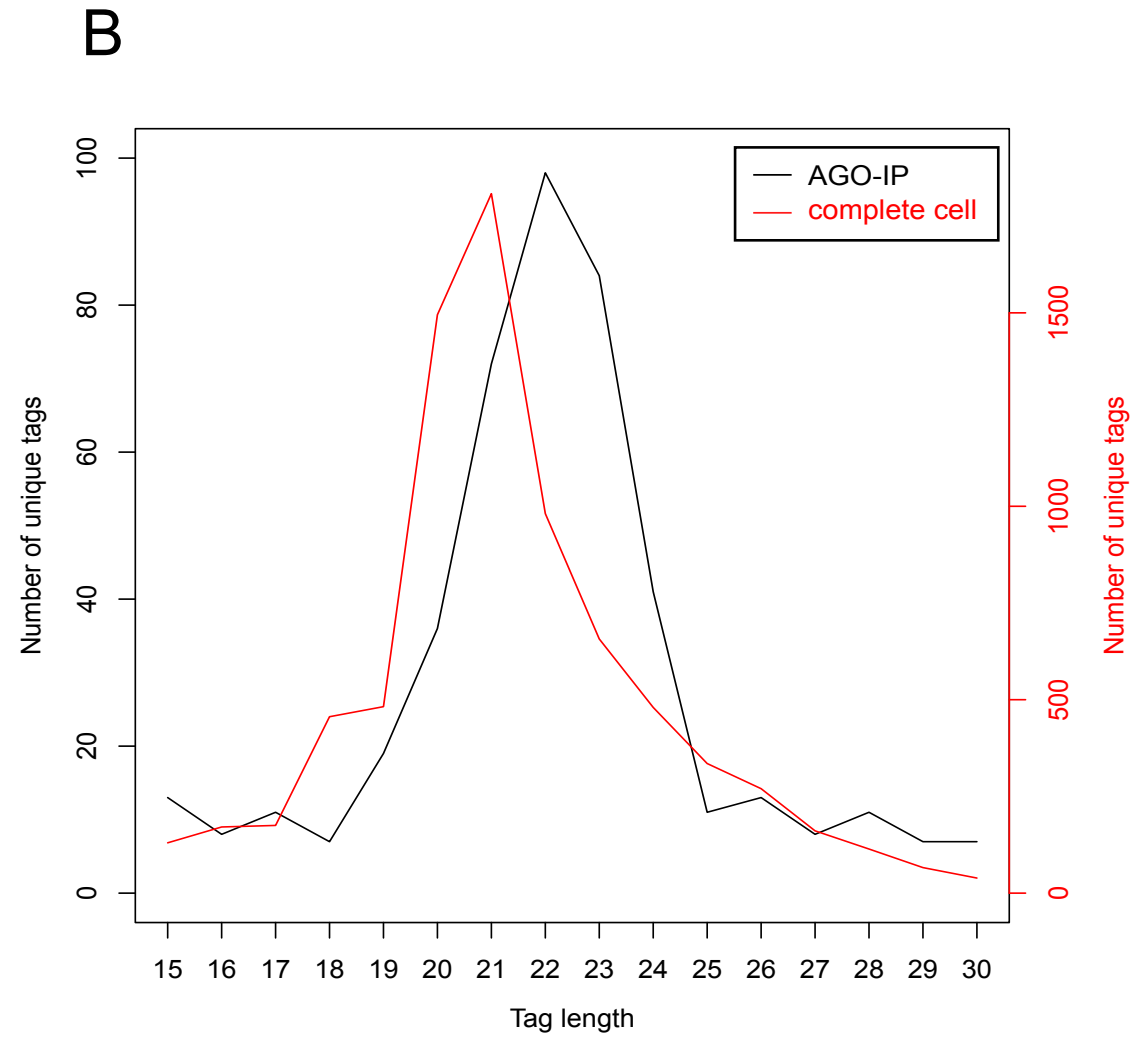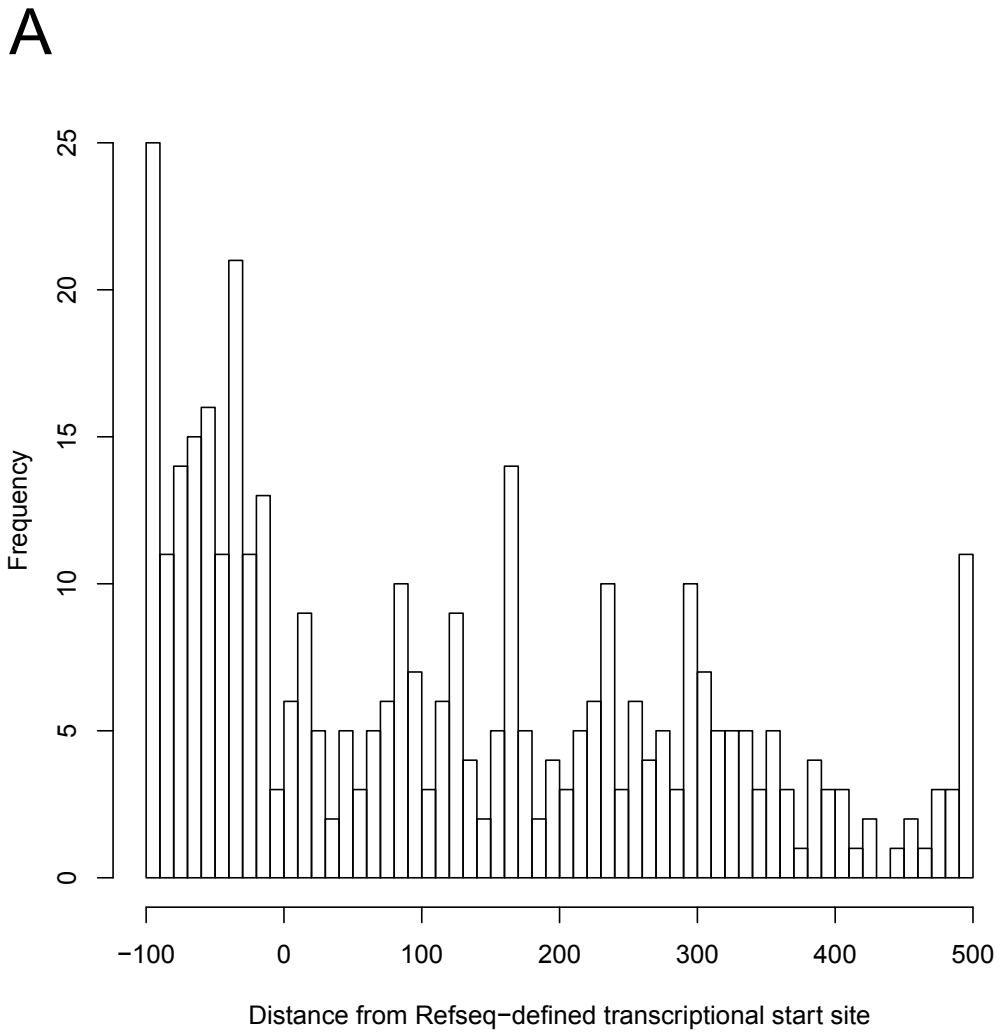
Supplementary Figure S7.

Supplementary Figure S8.

Supplementary Table S1. Raw tags counts mapping to different classes of RNA.

	miRNA	snoRNA	piRNA	tRNA	snRNA	as mRNA	sense mRNA	vRNA	other	total
total cell	2998143	57516.6	17937.8	5326.1	1986.2	14414.1	20563.0	377.9	270612.9	3386878
AGO1-IP	1132269	2104.5	188.7	137.1	1232.0	1707.4	6187.0	19.7	20906.1	1164751
AGO2-IP	5230907	4784.0	94.1	50.6	67.9	2108.5	5241.0	12.0	108476.5	5351742
AGO3-IP	1459554	2403.0	80.3	46.2	202.8	1497.5	4210.0	115.9	23021.6	1491131

Supplementary Table S2. Normalized counts of sequences mapping to miRNA loci in the AGO1-, AGO2-, and AGO3-associating small RNA libraries.

**minimum 100tpm in at least one condition

miRNA loci	AGO1-associating	AGO2-associating	AGO3-associating
hsa-let-7a	96507.1	98652.0	102478.8
hsa-let-7b	23367.7	38847.3	36273.1
hsa-let-7d	1437.8	1249.3	1633.7
hsa-let-7d*	87.8	41.6	114.8
hsa-let-7e	234.7	290.6	424.8
hsa-let-7f	57184.6	60343.4	56246.6
hsa-let-7g	11953.6	12076.7	18551.3
hsa-let-7i	4889.1	2854.9	3587.1
hsa-miR-101	3207.2	3457.6	3577.4
hsa-miR-103	13160.6	10479.8	9829.1
hsa-miR-106b	2509.4	1581.0	2545.1
hsa-miR-10a	111.4	251.6	136.5
hsa-miR-125a-5p	1712.2	2664.0	2108.7
hsa-miR-126	2572.7	2398.2	2770.7
hsa-miR-126*	814.3	490.4	1295.4
hsa-miR-128	99.6	38.1	63.3
hsa-miR-1307	172.5	417.4	760.9
hsa-miR-1307*	1378.0	519.1	934.1
hsa-miR-130b	185.3	507.4	185.6
hsa-miR-140-3p	2534.1	6987.5	3879.7
hsa-miR-140-5p	985.8	656.4	1785.8
hsa-miR-142-3p	129620.5	128978.3	113941.4
hsa-miR-142-5p	1797.9	651.8	2388.5
hsa-miR-143	311.7	496.1	372.1
hsa-miR-146a	139.3	226.4	191.4
hsa-miR-146b-5p	5699.3	14394.2	7035.8
hsa-miR-148a	9058.4	8522.1	5780.3
hsa-miR-148b	2087.3	1596.7	1407.8
hsa-miR-148b*	60.0	140.3	132.4
hsa-miR-151-3p	457.2	584.2	506.2
hsa-miR-152	1531.2	1586.3	1103.9
hsa-miR-155	9027.4	8018.6	10096.3
hsa-miR-15a	2315.1	1230.3	1053.6
hsa-miR-15b	512.7	296.4	298.3
hsa-miR-15b*	32.1	16.3	39.1
hsa-miR-16	6481.4	6424.4	5195.8
hsa-miR-17	9273.1	12802.2	9423.0
hsa-miR-17*	493.9	751.9	1326.2
hsa-miR-181a*	168.2	121.7	253.1

hsa-miR-181b	442.4	624.9	217.2
hsa-miR-182	48.2	981.5	100.7
hsa-miR-183	1762.3	2592.5	1539.9
hsa-miR-185	1799.0	1565.9	2324.3
hsa-miR-186	6700.1	7817.0	17184.6
hsa-miR-18a	2308.0	2299.2	2185.4
hsa-miR-191	17961.6	9304.6	18964.5
hsa-miR-192	125.3	144.4	202.2
hsa-miR-193a-5p	163.9	146.7	452.1
hsa-miR-196b	3385.3	3812.1	3056.7
hsa-miR-197	706.1	351.3	585.3
hsa-miR-199a-3p	152.2	125.8	202.6
hsa-miR-19a	1446.2	800.6	1727.6
hsa-miR-19b	2821.5	1861.4	3416.2
hsa-miR-20a	36472.8	32233.8	31279.5
hsa-miR-20b	133.9	172.1	133.2
hsa-miR-21	166040.9	144170.0	156325.4
hsa-miR-210	1592.3	1537.2	2448.5
hsa-miR-22	256.1	188.7	308.0
hsa-miR-221	1869.8	1626.7	2862.3
hsa-miR-221*	121.5	121.6	202.9
hsa-miR-222	5157.1	849.3	3608.2
hsa-miR-223	3610.9	4018.9	4473.1
hsa-miR-223*	215.4	16.3	266.4
hsa-miR-23a	3110.6	2841.7	2408.5
hsa-miR-23b	195.1	165.2	169.4
hsa-miR-24	20689.6	19378.0	31405.0
hsa-miR-24-2*	136.1	118.7	601.1
hsa-miR-25	379.3	450.9	379.6
hsa-miR-26a	1418.7	888.6	1276.2
hsa-miR-26b	1519.4	1100.2	1412.8
hsa-miR-27a	16881.9	8505.5	14212.2
hsa-miR-27a*	36.4	93.0	89.1
hsa-miR-27b	1945.6	1665.7	1227.6
hsa-miR-28-5p	303.0	289.4	377.7
hsa-miR-28-3p	546.3	603.3	671.8
hsa-miR-29a	1476.3	1006.3	2505.8
hsa-miR-29b	651.3	248.2	738.5
hsa-miR-301a	77.1	180.9	99.9
hsa-miR-30a	170.0	170.8	139.9
hsa-miR-30b	559.3	454.6	380.5
hsa-miR-30c	49856.6	33876.5	33601.2
hsa-miR-30d	16286.2	23503.8	15734.7
hsa-miR-30e	152182.4	162668.6	144536.8
hsa-miR-32	540.0	591.5	434.6
hsa-miR-320a	943.8	1967.0	1110.5
hsa-miR-338-3p	173.8	115.5	138.3

hsa-miR-339-3p	452.2	1075.0	708.5
hsa-miR-339-5p	311.8	164.6	359.5
hsa-miR-33a	424.0	622.9	813.0
hsa-miR-340	212.1	172.0	143.1
hsa-miR-342-3p	4222.8	4698.6	10903.8
hsa-miR-342-5p	235.7	171.5	216.5
hsa-miR-345	255.0	216.7	339.7
hsa-miR-34c-5p	963.3	929.2	1017.4
hsa-miR-361-5p	384.4	364.3	468.5
hsa-miR-363	153.2	155.4	162.3
hsa-miR-374a*	337.5	410.1	571.1
hsa-miR-374a	222.7	172.1	215.3
hsa-miR-374b	255.0	138.2	146.5
hsa-miR-378	2869.3	2602.7	3555.2
hsa-miR-423-5p	1530.1	974.0	1335.4
hsa-miR-423-3p	5185.0	4491.5	3996.2
hsa-miR-424	88.8	78.0	94.3
hsa-miR-425	15347.1	18135.8	17868.1
hsa-miR-425*	381.5	307.9	702.7
hsa-miR-484	113.6	67.7	134.0
hsa-miR-532-5p	240.0	309.3	421.2
hsa-miR-532-3p	32.1	35.8	25.0
hsa-miR-589	53.6	60.6	51.6
hsa-miR-590-5p	150.0	116.6	144.9
hsa-miR-590-3p	132.9	110.7	154.0
hsa-miR-598	229.3	486.7	233.8
hsa-miR-628-5p	99.6	43.2	114.9
hsa-miR-652	363.2	289.8	235.6
hsa-miR-671-5p	43.9	29.8	54.9
hsa-miR-744	437.1	212.2	253.9
hsa-miR-769-5p	166.0	226.2	213.1
hsa-miR-886-5p	90.3	118.5	130.5
hsa-miR-9	3302.0	4411.0	3492.5
hsa-miR-9-3*	96.0	78.6	89.4
hsa-miR-92a	17580.1	25516.4	18717.3
hsa-miR-92b	188.6	159.3	251.4
hsa-miR-93	4780.0	13381.2	4753.0
hsa-miR-96	827.2	677.3	672.7
hsa-miR-98	1023.0	926.3	837.2
hsa-miR-99b	2045.5	2800.7	1667.6

Supplementary Table S3. Fold change in abundance for tags mapping to miRNA loci associating with AGO proteins relative to sequenced tags in the complete cell.

**minimum 100tpm in at least one condition

(A) complete cell vs. AGO1

miRNA loci	direction of fold change	complete cell normalized counts	AGO1-associating normalized counts	fold change
hsa-let-7a	-	161941.2	96507.1	1.7
hsa-let-7b	-	97778.7	23367.7	4.2
hsa-let-7d	-	2839.8	1437.8	2.0
hsa-let-7d*	-	103.1	87.8	1.2
hsa-let-7e	-	719.5	234.7	3.1
hsa-let-7f	-	62332.0	57184.6	1.1
hsa-let-7g	-	20324.3	11953.6	1.7
hsa-let-7i	-	5394.1	4889.1	1.1
hsa-miR-101	-	3556.2	3207.2	1.1
hsa-miR-103	+	10468.1	13160.6	1.3
hsa-miR-106b	+	2116.0	2509.4	1.2
hsa-miR-10a	+	42.0	111.4	2.7
hsa-miR-125a-5p	+	499.4	1712.2	3.4
hsa-miR-126	+	1710.3	2572.7	1.5
hsa-miR-126*	+	589.8	814.3	1.4
hsa-miR-1274b	-	246.9	26.5	9.3
hsa-miR-128	-	146.6	99.6	1.5
hsa-miR-1307	-	446.0	172.5	2.6
hsa-miR-1307*	+	152.3	1378.0	9.0
hsa-miR-130b	-	1231.7	185.3	6.6
hsa-miR-130b*	+	40.9	109.8	2.7
hsa-miR-140-3p	-	2903.0	2534.1	1.1
hsa-miR-140-5p	-	1093.7	985.8	1.1
hsa-miR-142-3p	+	85046.9	129620.5	1.5
hsa-miR-142-5p	-	5309.0	1797.9	3.0
hsa-miR-143	-	335.5	311.7	1.1
hsa-miR-146a	-	140.9	139.3	1.0
hsa-miR-146b-5p	-	12774.7	5699.3	2.2
hsa-miR-148a	+	6650.3	9058.4	1.4
hsa-miR-148b	+	1711.6	2087.3	1.2
hsa-miR-148b*	-	143.0	60.0	2.4
hsa-miR-151-3p	+	417.0	457.2	1.1
hsa-miR-152	-	1644.7	1531.2	1.1
hsa-miR-155	-	10185.0	9027.4	1.1
hsa-miR-15a	+	1683.3	2315.1	1.4
hsa-miR-15b	-	820.9	512.7	1.6
hsa-miR-15b*	-	105.9	32.1	3.3
hsa-miR-16	-	10592.6	6481.4	1.6
hsa-miR-17	-	12523.8	9273.1	1.4
hsa-miR-17*	-	502.6	493.9	1.0
hsa-miR-181a*	-	185.7	168.2	1.1
hsa-miR-181b	+	366.5	442.4	1.2

hsa-miR-182	-	209.8	48.2	4.4
hsa-miR-183	+	1461.7	1762.3	1.2
hsa-miR-185	-	2044.3	1799.0	1.1
hsa-miR-186	+	3096.4	6700.1	2.2
hsa-miR-18a	+	1835.8	2308.0	1.3
hsa-miR-191	+	8949.6	17961.6	2.0
hsa-miR-192	-	156.0	125.3	1.2
hsa-miR-193a-5p	+	68.8	163.9	2.4
hsa-miR-196b	-	3638.2	3385.3	1.1
hsa-miR-197	+	470.0	706.1	1.5
hsa-miR-199a-3p	-	198.3	152.2	1.3
hsa-miR-199b-5p	+	74.1	106.1	1.4
hsa-miR-19a	-	1676.8	1446.2	1.2
hsa-miR-19b	-	3501.1	2821.5	1.2
hsa-miR-200c	+	47.2	113.6	2.4
hsa-miR-20a	+	28358.3	36472.8	1.3
hsa-miR-20b	+	112.8	133.9	1.2
hsa-miR-21	+	78358.7	166040.9	2.1
hsa-miR-210	-	3315.2	1592.3	2.1
hsa-miR-22	+	169.4	256.1	1.5
hsa-miR-221	-	1931.9	1869.8	1.0
hsa-miR-221*	-	201.3	121.5	1.7
hsa-miR-222	+	1751.9	5157.1	2.9
hsa-miR-223	+	3254.0	3610.9	1.1
hsa-miR-223*	+	169.4	215.4	1.3
hsa-miR-23a	+	2638.5	3110.6	1.2
hsa-miR-23b	+	180.0	195.1	1.1
hsa-miR-24	-	32400.6	20689.6	1.6
hsa-miR-24-2*	+	120.6	136.1	1.1
hsa-miR-25	-	754.8	379.3	2.0
hsa-miR-26a	-	2681.0	1418.7	1.9
hsa-miR-26b	-	2462.6	1519.4	1.6
hsa-miR-27a	+	5800.7	16881.9	2.9
hsa-miR-27a*	-	174.7	36.4	4.8
hsa-miR-27b	+	923.3	1945.6	2.1
hsa-miR-28-5p	-	442.2	303.0	1.5
hsa-miR-28-3p	+	464.7	546.3	1.2
hsa-miR-29a	+	1212.0	1476.3	1.2
hsa-miR-29b	+	545.4	651.3	1.2
hsa-miR-301a	-	205.7	77.1	2.7
hsa-miR-30a	+	102.6	170.0	1.7
hsa-miR-30b	-	1818.3	559.3	3.3
hsa-miR-30c	+	39624.4	49856.6	1.3
hsa-miR-30d	+	11636.3	16286.2	1.4
hsa-miR-30e	-	159026.9	152182.4	1.0
hsa-miR-32	-	710.7	540.0	1.3
hsa-miR-320a	-	1959.1	943.8	2.1
hsa-miR-338-3p	+	112.2	173.8	1.5
hsa-miR-339-3p	-	578.4	452.2	1.3
hsa-miR-339-5p	+	284.0	311.8	1.1

hsa-miR-33a	-	608.4	424.0	1.4
hsa-miR-340	-	261.9	212.1	1.2
hsa-miR-342-3p	+	2541.3	4222.8	1.7
hsa-miR-342-5p	-	359.2	235.7	1.5
hsa-miR-345	-	313.6	255.0	1.2
hsa-miR-34c-5p	-	2014.6	963.3	2.1
hsa-miR-361-5p	+	374.3	384.4	1.0
hsa-miR-363	+	78.6	153.2	1.9
hsa-miR-374a*	-	406.1	337.5	1.2
hsa-miR-374a	+	161.7	222.7	1.4
hsa-miR-374b	-	318.9	255.0	1.3
hsa-miR-378	-	3793.1	2869.3	1.3
hsa-miR-423-5p	-	3967.7	1530.1	2.6
hsa-miR-423-3p	+	3133.5	5185.0	1.7
hsa-miR-424	-	343.6	88.8	3.9
hsa-miR-425	+	7601.8	15347.1	2.0
hsa-miR-425*	+	286.8	381.5	1.3
hsa-miR-454	+	86.4	175.7	2.0
hsa-miR-484	-	244.4	113.6	2.2
hsa-miR-532-5p	-	347.4	240.0	1.4
hsa-miR-532-3p	-	127.9	32.1	4.0
hsa-miR-589	-	136.0	53.6	2.5
hsa-miR-590-5p	+	144.2	150.0	1.0
hsa-miR-590-3p	+	86.4	132.9	1.5
hsa-miR-598	+	130.3	229.3	1.8
hsa-miR-627	+	97.3	109.3	1.1
hsa-miR-628-5p	-	124.6	99.6	1.3
hsa-miR-652	-	411.4	363.2	1.1
hsa-miR-660	+	36.3	130.7	3.6
hsa-miR-671-5p	-	127.9	43.9	2.9
hsa-miR-744	+	426.5	437.1	1.0
hsa-miR-769-5p	-	244.0	166.0	1.5
hsa-miR-886-5p	-	128.7	90.3	1.4
hsa-miR-9	-	4193.8	3302.0	1.3
hsa-miR-92a	+	14252.1	17580.1	1.2
hsa-miR-92b	-	207.7	188.6	1.1
hsa-miR-93	-	5091.1	4780.0	1.1
hsa-miR-9-3*	-	113.5	96.0	1.2
hsa-miR-95	+	91.6	117.9	1.3
hsa-miR-96	+	685.9	827.2	1.2
hsa-miR-98	+	845.4	1023.0	1.2
hsa-miR-99b	+	564.5	2045.5	3.6

(B) complete cell vs. AGO2

miRNA loci	direction of fold change	complete cell normalized counts	AGO2-associating normalized counts	fold change
hsa-let-7a	-	161941.2	98652.0	1.6
hsa-let-7b	-	97778.7	38847.3	2.5
hsa-let-7d	-	2839.8	1249.3	2.3

hsa-let-7d*	-	103.1	41.6	2.5
hsa-let-7e	-	719.5	290.6	2.5
hsa-let-7f	-	62332.0	60343.4	1.0
hsa-let-7g	-	20324.3	12076.7	1.7
hsa-let-7i	-	5394.1	2854.9	1.9
hsa-miR-101	-	3556.2	3457.6	1.0
hsa-miR-103	+	10468.1	10479.8	1.0
hsa-miR-106b	-	2116.0	1581.0	1.3
hsa-miR-106b*	+	97.3	134.5	1.4
hsa-miR-10a	+	42.0	251.6	6.0
hsa-miR-125a-5p	+	499.4	2664.0	5.3
hsa-miR-126	+	1710.3	2398.2	1.4
hsa-miR-126*	-	589.8	490.4	1.2
hsa-miR-1274b	-	246.9	3.6	68.8
hsa-miR-128	-	146.6	38.1	3.9
hsa-miR-1307	-	446.0	417.4	1.1
hsa-miR-1307*	+	152.3	519.1	3.4
hsa-miR-130b	-	1231.7	507.4	2.4
hsa-miR-140-3p	+	2903.0	6987.5	2.4
hsa-miR-140-5p	-	1093.7	656.4	1.7
hsa-miR-142-3p	+	85046.9	128978.3	1.5
hsa-miR-142-5p	-	5309.0	651.8	8.1
hsa-miR-143	+	335.5	496.1	1.5
hsa-miR-146a	+	140.9	226.4	1.6
hsa-miR-146b-5p	+	12774.7	14394.2	1.1
hsa-miR-148a	+	6650.3	8522.1	1.3
hsa-miR-148b	-	1711.6	1596.7	1.1
hsa-miR-148b*	-	143.0	140.3	1.0
hsa-miR-151-3p	+	417.0	584.2	1.4
hsa-miR-152	-	1644.7	1586.3	1.0
hsa-miR-155	-	10185.0	8018.6	1.3
hsa-miR-15a	-	1683.3	1230.3	1.4
hsa-miR-15b	-	820.9	296.4	2.8
hsa-miR-15b*	-	105.9	16.3	6.5
hsa-miR-16	-	10592.6	6424.4	1.6
hsa-miR-17	+	12523.8	12802.2	1.0
hsa-miR-17*	+	502.6	751.9	1.5
hsa-miR-181a*	-	185.7	121.7	1.5
hsa-miR-181b	+	366.5	624.9	1.7
hsa-miR-182	+	209.8	981.5	4.7
hsa-miR-183	+	1461.7	2592.5	1.8
hsa-miR-185	-	2044.3	1565.9	1.3
hsa-miR-186	+	3096.4	7817.0	2.5
hsa-miR-18a	+	1835.8	2299.2	1.3
hsa-miR-191	+	8949.6	9304.6	1.0
hsa-miR-192	-	156.0	144.4	1.1
hsa-miR-193a-5p	+	68.8	146.7	2.1
hsa-miR-194	+	70.9	102.9	1.5
hsa-miR-196b	+	3638.2	3812.1	1.0
hsa-miR-197	-	470.0	351.3	1.3

hsa-miR-199a-3p	-	198.3	125.8	1.6
hsa-miR-19a	-	1676.8	800.6	2.1
hsa-miR-19b	-	3501.1	1861.4	1.9
hsa-miR-20a	+	28358.3	32233.8	1.1
hsa-miR-20b	+	112.8	172.1	1.5
hsa-miR-21	+	78358.7	144170.0	1.8
hsa-miR-210	-	3315.2	1537.2	2.2
hsa-miR-22	+	169.4	188.7	1.1
hsa-miR-221	-	1931.9	1626.7	1.2
hsa-miR-221*	-	201.3	121.6	1.7
hsa-miR-222	-	1751.9	849.3	2.1
hsa-miR-223	+	3254.0	4018.9	1.2
hsa-miR-223*	-	169.4	16.3	10.4
hsa-miR-23a	+	2638.5	2841.7	1.1
hsa-miR-23b	-	180.0	165.2	1.1
hsa-miR-24	-	32400.6	19378.0	1.7
hsa-miR-24*	-	120.6	118.7	1.0
hsa-miR-25	-	754.8	450.9	1.7
hsa-miR-26a	-	2681.0	888.6	3.0
hsa-miR-26b	-	2462.6	1100.2	2.2
hsa-miR-27a	+	5800.7	8505.5	1.5
hsa-miR-27a*	-	174.7	93.0	1.9
hsa-miR-27b	+	923.3	1665.7	1.8
hsa-miR-28-5p	-	442.2	289.4	1.5
hsa-miR-28-3p	+	464.7	603.3	1.3
hsa-miR-29a	-	1212.0	1006.3	1.2
hsa-miR-29b	-	545.4	248.2	2.2
hsa-miR-301a	-	205.7	180.9	1.1
hsa-miR-30a	+	102.6	170.8	1.7
hsa-miR-30b	-	1818.3	454.6	4.0
hsa-miR-30c	-	39624.4	33876.5	1.2
hsa-miR-30d	+	11636.3	23503.8	2.0
hsa-miR-30e	+	159026.9	162668.6	1.0
hsa-miR-32	-	710.7	591.5	1.2
hsa-miR-320a	+	1959.1	1967.0	1.0
hsa-miR-338-3p	+	112.2	115.5	1.0
hsa-miR-339-3p	+	578.4	1075.0	1.9
hsa-miR-339-5p	-	284.0	164.6	1.7
hsa-miR-33a	+	608.4	622.9	1.0
hsa-miR-340	-	261.9	172.0	1.5
hsa-miR-342-3p	+	2541.3	4698.6	1.8
hsa-miR-342-5p	-	359.2	171.5	2.1
hsa-miR-345	-	313.6	216.7	1.4
hsa-miR-34c-5p	-	2014.6	929.2	2.2
hsa-miR-361-5p	-	374.3	364.3	1.0
hsa-miR-362-5p	+	26.9	103.8	3.9
hsa-miR-363	+	78.6	155.4	2.0
hsa-miR-374a*	+	406.1	410.1	1.0
hsa-miR-374a	+	161.7	172.1	1.1
hsa-miR-374b	-	318.9	138.2	2.3

hsa-miR-378	-	3793.1	2602.7	1.5
hsa-miR-423-5p	-	3967.7	974.0	4.1
hsa-miR-423-3p	+	3133.5	4491.5	1.4
hsa-miR-424	-	343.6	78.0	4.4
hsa-miR-425	+	7601.8	18135.8	2.4
hsa-miR-425*	+	286.8	307.9	1.1
hsa-miR-454	+	86.4	121.2	1.4
hsa-miR-484	-	244.4	67.7	3.6
hsa-miR-532-5p	-	347.4	309.3	1.1
hsa-miR-532-3p	-	127.9	35.8	3.6
hsa-miR-577	+	67.2	149.9	2.2
hsa-miR-589	-	136.0	60.6	2.2
hsa-miR-590-5p	-	144.2	116.6	1.2
hsa-miR-590-3p	+	86.4	110.7	1.3
hsa-miR-598	+	130.3	486.7	3.7
hsa-miR-628-5p	-	124.6	43.2	2.9
hsa-miR-652	-	411.4	289.8	1.4
hsa-miR-671-5p	-	127.9	29.8	4.3
hsa-miR-744	-	426.5	212.2	2.0
hsa-miR-769-5p	-	244.0	226.2	1.1
hsa-miR-886-5p	-	128.7	118.5	1.1
hsa-miR-9	+	4193.8	4411.0	1.1
hsa-miR-92a	+	14252.1	25516.4	1.8
hsa-miR-92b	-	207.7	159.3	1.3
hsa-miR-93	+	5091.1	13381.2	2.6
hsa-miR-9-3*	-	113.5	78.6	1.4
hsa-miR-95	+	91.6	125.4	1.4
hsa-miR-96	-	685.9	677.3	1.0
hsa-miR-98	+	845.4	926.3	1.1
hsa-miR-99b	+	564.5	2800.7	5.0

(C) complete cell vs. AGO3

miRNA loci	direction of fold change	complete cell normalized counts	AGO3-associating normalized counts	fold change
hsa-let-7a	-	161941.2	102478.8	1.6
hsa-let-7b	-	97778.7	36273.1	2.7
hsa-let-7d	-	2839.8	1633.7	1.7
hsa-let-7d*	+	103.1	114.8	1.1
hsa-let-7e	-	719.5	424.8	1.7
hsa-let-7f	-	62332.0	56246.6	1.1
hsa-let-7g	-	20324.3	18551.3	1.1
hsa-let-7i	-	5394.1	3587.1	1.5
hsa-miR-101	+	3556.2	3577.4	1.0
hsa-miR-103	-	10468.1	9829.1	1.1
hsa-miR-106b	+	2116.0	2545.1	1.2
hsa-miR-106b*	+	97.3	128.2	1.3
hsa-miR-10a	+	42.0	136.5	3.3
hsa-miR-125a-5p	+	499.4	2108.7	4.2
hsa-miR-126	+	1710.3	2770.7	1.6

hsa-miR-126*	+	589.8	1295.4	2.2
hsa-miR-1274b	-	246.9	82.9	3.0
hsa-miR-128	-	146.6	63.3	2.3
hsa-miR-1307	+	446.0	760.9	1.7
hsa-miR-1307*	+	152.3	934.1	6.1
hsa-miR-130b	-	1231.7	185.6	6.6
hsa-miR-140-3p	+	2903.0	3879.7	1.3
hsa-miR-140-5p	+	1093.7	1785.8	1.6
hsa-miR-142-3p	+	85046.9	113941.4	1.3
hsa-miR-142-5p	-	5309.0	2388.5	2.2
hsa-miR-143	+	335.5	372.1	1.1
hsa-miR-146a	+	140.9	191.4	1.4
hsa-miR-146b-5p	-	12774.7	7035.8	1.8
hsa-miR-148a	-	6650.3	5780.3	1.2
hsa-miR-148b	-	1711.6	1407.8	1.2
hsa-miR-148b*	-	143.0	132.4	1.1
hsa-miR-151-3p	+	417.0	506.2	1.2
hsa-miR-152	-	1644.7	1103.9	1.5
hsa-miR-155	-	10185.0	10096.3	1.0
hsa-miR-15a	-	1683.3	1053.6	1.6
hsa-miR-15b	-	820.9	298.3	2.8
hsa-miR-15b*	-	105.9	39.1	2.7
hsa-miR-16	-	10592.6	5195.8	2.0
hsa-miR-17	-	12523.8	9423.0	1.3
hsa-miR-17*	+	502.6	1326.2	2.6
hsa-miR-181a*	+	185.7	253.1	1.4
hsa-miR-181b	-	366.5	217.2	1.7
hsa-miR-182	-	209.8	100.7	2.1
hsa-miR-183	+	1461.7	1539.9	1.1
hsa-miR-185	+	2044.3	2324.3	1.1
hsa-miR-186	+	3096.4	17184.6	5.5
hsa-miR-18a	+	1835.8	2185.4	1.2
hsa-miR-191	+	8949.6	18964.5	2.1
hsa-miR-192	+	156.0	202.2	1.3
hsa-miR-193a-5p	+	68.8	452.1	6.6
hsa-miR-194	+	70.9	104.9	1.5
hsa-miR-196b	-	3638.2	3056.7	1.2
hsa-miR-197	+	470.0	585.3	1.2
hsa-miR-199a-3p	+	198.3	202.6	1.0
hsa-miR-199b-5p	+	74.1	193.1	2.6
hsa-miR-199b-3p	+	69.3	101.3	1.5
hsa-miR-19a	+	1676.8	1727.6	1.0
hsa-miR-19b	-	3501.1	3416.2	1.0
hsa-miR-200c	+	47.2	141.5	3.0
hsa-miR-20a	+	28358.3	31279.5	1.1
hsa-miR-20b	+	112.8	133.2	1.2
hsa-miR-21	+	78358.7	156325.4	2.0
hsa-miR-21*	+	38.3	134.9	3.5
hsa-miR-210	-	3315.2	2448.5	1.4
hsa-miR-22	+	169.4	308.0	1.8

hsa-miR-221	+	1931.9	2862.3	1.5
hsa-miR-221*	+	201.3	202.9	1.0
hsa-miR-222	+	1751.9	3608.2	2.1
hsa-miR-222*	+	90.8	186.5	2.1
hsa-miR-223	+	3254.0	4473.1	1.4
hsa-miR-223*	+	169.4	266.4	1.6
hsa-miR-23a	-	2638.5	2408.5	1.1
hsa-miR-23b	-	180.0	169.4	1.1
hsa-miR-24	-	32400.6	31405.0	1.0
hsa-miR-24-2*	+	120.6	601.1	5.0
hsa-miR-25	-	754.8	379.6	2.0
hsa-miR-26a	-	2681.0	1276.2	2.1
hsa-miR-26b	-	2462.6	1412.8	1.7
hsa-miR-27a	+	5800.7	14212.2	2.5
hsa-miR-27a*	-	174.7	89.1	2.0
hsa-miR-27b	+	923.3	1227.6	1.3
hsa-miR-28-5p	-	442.2	377.7	1.2
hsa-miR-28-3p	+	464.7	671.8	1.4
hsa-miR-29a	+	1212.0	2505.8	2.1
hsa-miR-29a*	+	39.9	161.5	4.0
hsa-miR-29b	+	545.4	738.5	1.4
hsa-miR-301a	-	205.7	99.9	2.1
hsa-miR-30a	+	102.6	139.9	1.4
hsa-miR-30b	-	1818.3	380.5	4.8
hsa-miR-30c	-	39624.4	33601.2	1.2
hsa-miR-30d	+	11636.3	15734.7	1.4
hsa-miR-30e	-	159026.9	144536.8	1.1
hsa-miR-30e*	+	41.1	168.2	4.1
hsa-miR-32	-	710.7	434.6	1.6
hsa-miR-320a	-	1959.1	1110.5	1.8
hsa-miR-338-3p	+	112.2	138.3	1.2
hsa-miR-339-3p	+	578.4	708.5	1.2
hsa-miR-339-5p	+	284.0	359.5	1.3
hsa-miR-33a	+	608.4	813.0	1.3
hsa-miR-340	-	261.9	143.1	1.8
hsa-miR-342-3p	+	2541.3	10903.8	4.3
hsa-miR-342-5p	-	359.2	216.5	1.7
hsa-miR-345	+	313.6	339.7	1.1
hsa-miR-34c-5p	-	2014.6	1017.4	2.0
hsa-miR-361-5p	+	374.3	468.5	1.3
hsa-miR-363	+	78.6	162.3	2.1
hsa-miR-374a*	+	406.1	571.1	1.4
hsa-miR-374a	+	161.7	215.3	1.3
hsa-miR-374b	-	318.9	146.5	2.2
hsa-miR-378	-	3793.1	3555.2	1.1
hsa-miR-423-5p	-	3967.7	1335.4	3.0
hsa-miR-423-3p	+	3133.5	3996.2	1.3
hsa-miR-424	-	343.6	94.3	3.6
hsa-miR-425	+	7601.8	17868.1	2.4
hsa-miR-425*	+	286.8	702.7	2.5

hsa-miR-455-3p	+	69.2	114.8	1.7
hsa-miR-484	-	244.4	134.0	1.8
hsa-miR-532-5p	+	347.4	421.2	1.2
hsa-miR-532-3p	-	127.9	25.0	5.1
hsa-miR-577	+	67.2	149.0	2.2
hsa-miR-589	-	136.0	51.6	2.6
hsa-miR-590-5p	+	144.2	144.9	1.0
hsa-miR-590-3p	+	86.4	154.0	1.8
hsa-miR-598	+	130.3	233.8	1.8
hsa-miR-627	+	97.3	187.3	1.9
hsa-miR-628-5p	-	124.6	114.9	1.1
hsa-miR-652	-	411.4	235.6	1.7
hsa-miR-671-5p	-	127.9	54.9	2.3
hsa-miR-744	-	426.5	253.9	1.7
hsa-miR-769-5p	-	244.0	213.1	1.1
hsa-miR-886-5p	+	128.7	130.5	1.0
hsa-miR-9	-	4193.8	3492.5	1.2
hsa-miR-92a	+	14252.1	18717.3	1.3
hsa-miR-92b	+	207.7	251.4	1.2
hsa-miR-93	-	5091.1	4753.0	1.1
hsa-miR-9-3*	-	113.5	89.4	1.3
hsa-miR-96	-	685.9	672.7	1.0
hsa-miR-98	-	845.4	837.2	1.0
hsa-miR-99b	+	564.5	1667.6	3.0

Supplementary Table S4. Candidate novel miRNAs from AGO-IP library enrichment relative total cell RNA library.

annotation	name	chromosome	strand	AGO1 sequence	length	counts, complete cell	counts	fold change	start position	stop position	genome matching	number of mapping sites	AGO2 sequence	length	counts, complete cell	counts	fold change	start position	stop position	genome matching	number of mapping sites	AGO3 sequence	length	counts, complete cell	counts	fold change	start position	stop position	genome matching	number of mapping sites	comments
no annotation		chr18	+	ATCCCACTCCTGACACCATT	20	1.2	10.3	8.7	1681856	1681876	E	1																			
		chr1	+	AGTTGCCTTTTTGTTCCCATGC	22	3.2	11.2	3.4	85372076	85372098	E	1	AGTTGCCTTTTTGTTCCCATGC	22	3.2	18.3	5.6	85372076	85372098	E	1	AGTTGCCTTTTTGTTCCCATGC	22	3.2	11.4	3.5	85372076	85372098	E	1	
		chr2	-	TCCGAGTCACGGCACCAGA	19	5.6	11.2	2.0	216495725	216495744	E	1										TCCGAGTCACGGCACCAGA	19	5.6	16.8	3.0	216495725	216495744	E	1	
		chr10	-																			ATCCCACTCCTGACACCAT	19	1.0	10.6	10.1	96926499	96926518	E	2	
		chr22	-																			GGAGGAACCTTGGAGCTTCGGC	22	5.9	18.8	3.2	29886047	29886069	E	1	
mRNA, sense	ZC3HAV1	chr7	-	AATTACAGATTGTCTCAGAGA	21	9.7	13.7	1.4	138379422	138379443	E	1	AATTACAGATTGTCTCAGAGA	21	9.7	12.1	1.2	138379422	138379443	E	1	AATTACAGATTGTCTCAGAGA	21	9.7	23.5	2.4	138379422	138379443	E	1	exonic
	MBNL1	chr3	+	ATTGCCATTTCTGAGACACAGT	22	10.9	28.3	2.6	153663827	153663849	E	1	ATTGCCATTTCTGAGACACAGT	22	10.9	12.3	1.1	153663827	153663849	E	1	ATTGCCATTTCTGAGACACAGT	22	10.9	14.8	1.4	153663827	153663849	E	1	exonic
	SMARCC1	chr3	-	TCCCCGGCACCTCCACCAAA	20	7.1	11.2	1.6	47697816	47697836	M5GA	1										TCCCCGGCACCTCCACCAAA	20	7.1	15.4	2.2	47697816	47697836	M5GA	1	intronic
	TOMM40L	chr1	+	ACTGAATCCTCTTTTCCTCAGT	22	8.0	18.0	2.3	159463650	159463672	M21TG	2										ACTGAATCCTCTTTTCCTCAGT	22	8.0	18.1	2.3	159463650	159463672	M21TG	2	identified in sense-antisense screen (Chen J NAR 2004)
	PTK2B	chr8	+	TTGGCTGGTCTCTGCTCCGCAGA	23	2.1	10.3	5.0	27346846	27346869	M22AG	1																			intronic, located at edge of splice junction
	SLC9A3R1	chr17	+	TCTCTCGGCTCCTCGCGGCTCG	22	4.4	40.4	9.1	70256396	70256418	E	1																			exonic
	FAM107B	chr10	-										CTGGACTGAGCCATGCTACTG	21	13.9	20.4	1.5	14799413	14799434	E	2	CTGGACTGAGCCATGCTACTG	21	13.9	18.7	1.3	14799413	14799434	E	2	intronic
	LOC400931	chr22	+																			GGGACCCATCCTGCCTGCTGTGG	22	4.4	13.4	3.0	44865633	44865655	E	1	identified in sense-antisense screen (Chen J NAR 2004)
mRNA, antisense	TBC1D22A	chr22	-	TCCCCGGCATCTCCACCAT	19	6.2	18.9	3.0	45942779	45942798	M5GA	1										TCCCCGGCATCTCCACCAT	19	6.2	57.0	9.2	45942779	45942798	M5GA	1	intronic
	SAMD4A	chr14	-	ACTGGACTTGGAGTCAGAAGA	21	15.8	14.2	-1.1	54178149	54178170	E	2	ACTGGACTTGGAGTCAGAAGA	21	15.8	24.2	1.5	54178149	54178170	E	2										intronic
	RICH2	chr17	-										CTGGACTGAGCCATGCTACTG	21	9.1	12.1	1.3	12761355	12761376	E	2	CTGGACTGAGCCATGCTACTG	21	9.1	13.5	1.5	12761355	12761376	E	2	intronic
	PLD5	chr1	+																			TGAGGTAGTAGATTGTATTT	20	1.5	12.7	8.6	240567185	240567205	M5TC	1	intronic

Table S5. List of best potential mRNA targets for non-miRNA fragments found in association with AGO proteins.

precursor type	name	sequence	potential seed sequence	match type(s)	number of 3' UTR match(es)	number of predicted targeted genes
anti-sense mRNA	*CLTC*	CAGUUGUUCAUGAUAUUUAGAAGCCAC	AGUUGUU	8mer, 7mer-m8	1, 1	1
				8mer	1	35
	WEE1	UCAAUUCUAUUCGUAAUUGUUCUGCAC	CAAUUCU	8mer	2	2
				7mer-m8	2	3
				8mer	1	89
sense mRNA	*CYP46A1*	AGAUGUACCGUGCGAUUCAGACUGU	GAUGUAC	8mer, 7mer-m8	1,1	2
				8mer	1	37
snRNA	U12	GGAUGCCUGGGAGUUGCGAUCUGCCCG	GAUGCCU	8mer	1	35
	U1	GGGGGACUGCGUUCGCGCUUUCCCCUG	GGGGACU	8mer	1	38
	U2	GUACCUCCAGGAACGGUGCACCA	UACCUCC	8mer	1	22
	U2-like	AAAUGGAUUUUUGGAGCAGGGAGAUGGAAU	AAUGGAU	8mer, 7mer-1A	1,1	1
				7mer-m8	2	2
				8mer	1	29
vault RNA	VTRNA1-1	GACCCGCGGGCGCUCUCCAGUCCUUU	ACCCGCG	7mer-m8	1	1
				7mer-1A	1	5
	ACA45	AAGGUAGAUAGAACAGGUCUUG	AGGUAGA	8mer	2	1
				7mer-1A	5	1
				8mer, 7mer-m8	1,1	1
				8mer, 7mer-1A	1,1	1
				7mer-m8	2	4
				8mer	1	30
	ACA25	GUUCUCUAUAGGAAGCCAUAGC	UUCUCUA	8mer	2	3
				8mer, 7mer-m8	1,1	2
				8mer,7mer-1A	1,1	5

RNA	Name	Sequence	Seed	Site type	Count	Number
snoRNA				7mer-m8	2	2
				8mer	1	158
	U17a/U17b	UCCAACGUGGAUACACCCGGGAGGUC	CCAACGU	8mer	1	3
	HBI-100	UCUGAUCGUUCCCUCCAUACA	CUGAUCG	8mer	1	1
	ACA47	ACGGUCUGGGGAAAGGCUCCUGUGUU	CGGUCUG	8mer	1	2
	ACA17	UCUGUGUCAUUAGGUGGCAGAGA	CUGUGUC	8mer	2	1
				8mer, 7mer-m8	1,1	2
				8mer, 7mer-1A	1,1	2
				7mer-m8	2	1
				8mer	1	66
tRNA	mitochondrial tRNA-Ser	GAGAAAGCUCACAAGAACUGCUAACU	AGAAAGC	8mer, 7mer-m8	2,1	1
				8mer, 7mer-m8	1,1	5
				8mer,7mer-1A	1,1	7
				7mer-m8,7mer-1A	1,2	1
				7mer-m8	2	12
				8mer	1	104
	mitochondrial tRNA-Cys	AGCUCCGAGGUGAUUUUCAUAUUGAAUUGC	GCUCCGA	8mer	1	4
	tRNA-His-GTG	CGUAUAGUGGUUAGUACUCUGCGUUG	GUAUAGU	8mer	1	19
	mitochondrial tRNA-Met	AGUAAGGUCAGCUAAAUAAGCUAUCGGGCC	GUAAGGU	8mer	4	1
				8mer	3	2
				8mer	1	25
	tRNA-Glu-CTC	UCCCUGGUGGUCUAGUGGUUAGGAUUCGG	CCCUGGU	8mer, 7mer-m8	1,1	1
				8mer, 7mer-1A	1,1	1
				7mer-m8	2	1
				8mer	1	74
	tRNA-Leu-CAA	GUAAGCACCUUGCCUGCGGGCU	UAAGCAC	8mer	2	1
				8mer, 7mer-m8	1,1	1
				8mer, 7mer-1A	1,1	8
				7mer-m8	2	2
				8mer	1	103
rRNA	28S-like pseudogene	ACCAAGCGUUGGAUUGUUC	CCAAGCG	8mer	1	4

Supplementary Table S6. Raw count for sequences mapping to promoter regions of coding genes.

	unique promoter tags	total promoter tags	percent of total library tags	fold change relative to AGO2
total cell	7820	8497	0.251%	n/a
AGO1-IP	130	238	0.020%	2.16
AGO2-IP	185	507	0.009%	1.00
AGO3-IP	131	299	0.020%	2.12

Supplementary Table S7. List of genome locations for promoter-associated AGO-interacting tags

AGO1-IP library

chromosome	genome start	genome stop	tag	count	strand	refseq transcripts(s)	refseq strand	partial tiRNA overlap	tiRNA match
chr1	174443150	174443172	AAAGCGGCTTGGGACAGACAGA	1	-	NM_001001740;NM_022457	-		
chr15	63948442	63948470	AAATCTCGGTGGAACCTGCATTGGTTTT	1	-	NM_004663	+		
chr22	35639638	35639664	AAGACTGGTCTCTCCCACCACACAGA	1	+	NM_000395	+		
chrX	103288748	103288771	AAGAGCACAGACTTTGAAACCTG	1	+	NM_001012755	-		
chr20	62071592	62071608	AAGCGCCCGGCCGCGC	3	-	NM_020713	-		
chr14	93665664	93665679	AAGTTGGGACCCGGA	1	-	NM_032036	-		
chr1	226712119	226712142	AATGTCCGGTCGTGGTAAGCAGG	1	-	NM_033445;NM_175055	-		
chr18	72858119	72858144	ACAGCGGACCCGAAGAATGCCTGGC	1	-	NM_001025081;NM_001025090;NM_001025092;NM_002385	-		
chr19	55918448	55918476	ACAGGAAGAGAGAAGCTGGGAGAATCGG	1	+	NM_002975	+		
chr20	61622561	61622583	ACCCCGCGCGCGCCTCTCTGTC	1	+	NM_024299	+	x	
chr19	803306	803325	ACCCCGGAGCCCCAGCCCC	1	+	NM_001972	+		
chr4	77081160	77081183	ACCCGGGCTCCGACAGCGGCTGC	1	-	NM_001042402;NM_014435	-		
chr1	33055515	33055536	ACCTGGCTGGACTCGCGTGAC	1	-	NM_001017406;NM_022753	+		
chr17	77109708	77109729	ACGGGGTTGGAGGAGGGGGGC	1	+	NM_001077182;NM_012418	+		
chr15	48766186	48766199	ACTCGGCTTCTGCTGC	1	-	NM_017672	-		
chr12	48002980	48003001	ACTGAGGGTACAGTTGATCGT	1	-	NM_001100620;NM_005480	+		
chr19	40925690	40925691	ACTGGCCACTGAGTTCC	1	-	NM_024660	-		
chr8	110415350	110415379	AGACCTCTGTTGGATCCCCGCTTCGAGGG	1	-	NM_020189;NM_032869	+		
chr1	148868535	148868550	AGAGAACCCTGCGGA	1	-	NM_004436;NM_207042;NM_207043;NM_207044;NM_207045;NM_207046;NM_207047;NM_207168	-		
chr14	19881247	19881266	AGAGAACGGGGCTCCGCGC	1	-	NM_001042618;NM_005484	+		
chr18	18767363	18767385	AGCGCGGGCTGTCCGGAGGGGT	1	+	NM_002894;NM_203291;NM_203292	+		
chr14	19881350	19881376	AGCTGAGTGCGTCCTGTCACTCCACT	1	-	NM_001042618;NM_005484	+		
chr6	26151768	26151791	AGGATGGTAAGAAGCGTAAGCGC	1	-	NM_021062	-		
chr19	44518466	44518477	AGGCCTGTGGACAGAAC	1	-	NM_004877	-		
chr1	41100837	41100853	AGGGATTCGGTCTGGC	1	+	NM_133467	-		
chr15	46890503	46890527	AGGGTAAGGGGATCTGCTAGAAGT	1	-	NM_014985	-		
chr2	47986300	47986325	AGTGTCGCGGCCGCGCCCGGTGCAG	1	-	NM_012167;NM_018693;NM_025133	-		
chr8	62789920	62789943	AGTTTGTCTCGGTCCTTTGGAAC	1	+	NM_001164754;NM_001164755;NM_001164756;NM_004318;NM_032466	-		
chr14	19881381	19881410	ATAGGGCGGAGGGAAGCTCATCAGTGGGG	1	-	NM_001042618;NM_005484	+		
chr19	41672411	41672433	ATTCCTGTCCGCGCCTTGCGTC	1	+	NM_001145343;NM_001145344;NM_001145345;NM_032838	-		
chr6	31728214	31728235	ATTTGGGGATCTCGAAGCGAT	1	+	NM_001098534;NM_004639;NM_080702;NM_080703	-		
chr6	26381140	26381164	ATTTTCCTGTGGTCATTTGACGGT	1	+	NM_003525	+		
chr1	152458981	152459004	CAAATCATGCGCTTTGCAATGAA	1	-	NM_001127320	+		
chr14	19881114	19881138	CAATGGCTGAGGTGAGGTACCCCG	1	-	NM_001042618;NM_005484	+		
chr22	41877338	41877358	CACCTCTCCCGCGGGACGCG	1	-	NM_000714;NM_007311	+		
chr3	197714930	197714945	CACCTTTCGGGCGCC	1	+	NM_152617	-		
chr14	50367707	50367729	CAGCGGAGGGAGGAGCGGGCGG	1	+	NM_016350;NM_020921;NM_182944;NM_182946	-		
chr6	32034929	32034959	CAGCTGCTGTGGCTCCAGGATGATGGAGAC	1	+	NM_002904	-		
chr6	37062280	37062304	CCCTGGCTTCGGGAGTTTTCTCTG	1	+	NM_014341	-		
chr19	4675141	4675167	CCGGCCAACGCATGCGGTACCACTTT	1	+	NM_139159	-		
chr2	88136334	88136355	CCTCTCCGCCACCTCCACCGC	1	-	NM_016618	-	x	
chr7	27206742	27206750	CCTCTGGGACTGTTTTCTTTCCAG	1	+	NM_000522	-		
chr6	31731249	31731266	CCTGATCTTGAAGAAGT	1	-	NM_019101	+		
chr12	8126155	8126173	CGACCGAGTTGGAGTACGAGTCTGTGCTGT	2	+	NM_015509	+		
chr9	114288568	114288594	CGCGGGCCCAGGACGTGTAGTAGGGAGC	1	+	NM_133465	+		

chr	start	end	sequence			ID				
chr11	46595692	46595713	CGGATGAAAACAAACACTAAC	1	+	NM_001142673;NM_014741;NM_173811	+			
chr1	178867833	178867853	CGGCGGAGGAGGAGAGAAGC	1	+	NM_001135669;NM_004736	+			
chr1	212521080	212521102	CGGCGGCTCCCCGCTCCCCGGA	1	-	NM_020197	+			
chr15	61268615	61268638	CGGGCGTGCCCCGCGAGGACTGT	1	-	NM_016530	+			
chr14	19881241	19881260	CGGGGGCTCCGCGCGAGGTC	1	-	NM_001042618;NM_005484	+			
chr10	70517887	70517910	CGTGCAGCTGGGAGAGCTAGACT	1	+	NM_002727	+	x		
chr9	35647986	35648011	CGTGCTGAAGGCCTGTATCCTAGGC	1	-	NM_174923	+			
chr3	39399914	39399918	CTACGGTGCTGAAGC	1	+	NM_017875	+	x		
chr16	45212753	45212768	CTGACGGGTCGCTGA	1	-	NM_024745	-			
chr2	85515223	85515248	CTTCTCACTACTGCACTTGACTAGA	1	+	NM_198482	+			
chr8	104496802	104496817	GAACTCCTAGCGGAC	1	+	NM_030780	-			
chr17	7963192	7963216	GAAGAGCCCGGATAGCTCAGTCGG	1	+	NM_001165960;NM_021628	-			
chr16	88422388	88422409	GACCCTGCGCGGCGGAAGGCG	1	+	NM_032451	+			
chr21	44544268	44544290	GACGGACCCTGGACGGAGCAGG	1	-	NM_002626	+			
chr14	19881241	19881265	GAGAACGGGGCTCCGCGCGAGGTC	1	-	NM_001042618;NM_005484	+			
chr14	19881145	19881174	GAGCTTGGAACAGACTCACGGCCAGCGAA	1	-	NM_001042618;NM_005484	+			
chr22	29886048	29886068	GAGGAACCTTGGAGCTTCGG	1	-	NM_001135824;NM_001135825;NM_152267	-			
chr6	32034145	32034169	GAGGAGGCTCTGCAGAAGAAATTC	1	-	NM_006929	+			
chr1	40715676	40715706	GAGGCCAGGCGAGACACCCGGCTGCGGCCT	1	+	NM_198494	+			
chr11	33235754	33235771	GATGAGGGAGACGGGCC	1	-	NM_001048200;NM_005734	+			
chr9	35647974	35648001	GCCTGTATCCTAGGCTACACACTGAGG	1	-	NM_174923	+			
chr17	45401060	45401076	GCGGCACCCTCCCAGCCCCGGC	1	+	NM_138281	+			
chr1	213322965	213322987	GCGTGGCGGCGGCGGCGGCGGC	1	+	NM_001017425;NM_014217	+			
chr8	6553009	6553028	GCTCCCTCGGGCCGGACGT	1	-	NM_018361	+			
chr3	45705482	45705499	GCTCGCGATGTCTGTTT	1	-	NM_014016	+			
chr12	60940430	60940451	GCTGCCACCTCCCCTACCGCT	1	+	NM_006313	+			
chr3	159306546	159306567	GGAAAAAAAGAGCGGGGCTCTGCTGGC	1	-	NM_001163678;NM_003030;NM_006884	-			
chr15	91244068	91244086	GGAAAAACTTGAATTTAT	1	+	NM_001042572;NM_001271	+			
chr14	19881158	19881175	GGAGCTTGGAACAGACT	1	-	NM_001042618;NM_005484	+			
chr22	29886048	29886069	GGAGGAACCTTGGAGCTTCGG	1	-	NM_001135824;NM_001135825;NM_152267	-			
chr22	29886047	29886069	GGAGGAACCTTGGAGCTTCGGC	1	-	NM_001135824;NM_001135825;NM_152267	-			
chr22	29886046	29886069	GGAGGAACCTTGGAGCTTCGGCA	1	-	NM_001135824;NM_001135825;NM_152267	-			
chr12	119609348	119609365	GGAGGCCTGAGAGCGAC	1	+	NM_014730	+	x		
chr3	142253112	142253129	GGCCCCCGGCGCGCCGG	1	-	NM_080862	+			
chr14	19881113	19881134	GGCTGAGGTGAGGTACCCCGC	1	-	NM_001042618;NM_005484	+			
chr10	129595088	129595103	GGGTCCCGGCGGAGT	1	+	NM_006504	+			
chr9	35647985	35648015	GGTTCGTGCTGAAGGCCTGTATCCTAGGCT	1	-	NM_174923	+			
chr22	30476039	30476057	GTAGACCTGGCGACGACG	1	-	NM_173566	-			
chr2	17798354	17798373	GTAGGGTGAAGGCGCGCGC	1	-	NM_001130009;NM_001142286;NM_024624;NM_182625	+			
chr4	140436307	140436318	GTCGAGTCGGCCTGC	2	+	NM_002494	-			
chr1	39729925	39729946	GTCGCCCCTGCGCTGCGCGGA	1	+	NM_181809	+			
chr22	36575404	36575415	GTCTTATCCCGCTGATGATT	1	+	NM_016091	+			
chr15	63948442	63948462	GTGGAACCTGCATTGGTTTT	1	-	NM_004663	+			
chr14	19881363	19881387	GTGGGGCCACGAGCTGAGTGCGTC	1	-	NM_001042618;NM_005484	+			
chr9	35647995	35648017	GTGGTTCGTGCTGAAGGCCTGT	1	-	NM_174923	+			
chr14	19881113	19881141	GTTCAATGGCTGAGGTGAGGTACCCCGC	2	-	NM_001042618;NM_005484	+			
chr10	70517882	70517910	GTTGGCGTGCAGCTGGGAGAGCTAGACT	1	+	NM_002727	+	x		
chr1	205992069	205992091	GTTGGGGATTGTTGCGTCCCAT	1	+	NM_002389;NM_153826;NM_172350;NM_172351;NM_172352;NM_172353;NM_172354;NM_172355;NM_172356;NM_172357;NM_172358;NM_172359;NM_172360;NM_172361	+			
chr7	6596498	6596526	GTTGTACCACCTGGACATCTACTTCAGC	1	+	NM_024067	+			
chr12	52180694	52180724	GTTTCCGCAGGGCTCTGGAGCTGGTGCAGG	1	-	NM_004178;NM_134323	+			
chr8	49036068	49036091	TACTCGCCAGGTGGACTCGGAGT	1	+	NM_001081640;NM_005914;NM_006904;NM_182746	-			
chr12	6923270	6923293	TAGGCTTTCTGGCTTTTTACCGG	1	+	NM_138425	+			

chromosome	genome start	genome stop	tag	count	strand	refseq transcript(s)	refseq strand	partial tiRNA overlap	tiRNA match
chr17	15788922	15788945	TCACGCTCGAGCTCGGAGGCTGT	1	-	NM_000676	+		
chr1	201162904	201162927	TCCCGAGCCGCCTGCTAGCCCCG	1	-	NM_021633	-		
chr1	243094354	243094375	TCCGCTCTGCAGCACGAACCC	1	-	NM_004501;NM_031844	-		
chr19	44618693	44618716	TCGACTACCGCAGCTCTTCTTTG	1	+	NM_001020	-		
chr14	22468832	22468850	TCGCAGCTTCGCTGCGTG	1	+	NM_001039619;NM_006109	-		
chr6	122834624	122834647	TCGGAAAGGCGAGAAAGAAGCTG	1	-	NM_020755;NM_181794	-		
chr14	68934720	68934737	TCGGCAGCTGCTGTAGC	1	-	NM_004450;NM_018375	-		
chr12	6923265	6923288	TCTAGTAGGCTTTCTGGCTTTTT	1	+	NM_138425	+		
chr17	70256396	70256416	TCTCTCGGCTCCTCGCGGCT	6	+	NM_004252	+	x	x
chr17	70256396	70256417	TCTCTCGGCTCCTCGCGGCTC	1	+	NM_004252	+	x	x
chr17	70256396	70256418	TCTCTCGGCTCCTCGCGGCTCG	47	+	NM_004252	+	x	x
chr17	70256396	70256419	TCTCTCGGCTCCTCGCGGCTCGC	45	+	NM_004252	+	x	x
chr17	70256396	70256420	TCTCTCGGCTCCTCGCGGCTCGCG	2	+	NM_004252	+	x	
chr1	202033243	202033263	TCTGGTACGAATTGTGGAGA	1	+	NM_001174108	+		
chr15	83724873	83724896	TGAAGCGCCTGTGCTCTGCCGAG	2	+	NM_006738;NM_007200	+	x	x
chr15	83724873	83724897	TGAAGCGCCTGTGCTCTGCCGAGA	2	+	NM_006738;NM_007200	+	x	
chr22	20326041	20326045	TGACCCAGTATCAGAGAGGGCCTAGG	1	+	NM_022044	+		
chr19	10352582	10352604	TGACCCTAGGACACAGCTGCAT	1	+	NM_003331	-		
chr10	88403986	88404011	TGAGTGTGTGTGTGTGAGTGTGTGA	5	-	NM_001030015;NM_033282	+		
chr15	65204813	65204829	TGCATGGACCTCTGTC	1	+	NM_001145102	+		
chr2	27127643	27127659	TGCCCGCATCCTCCAC	1	+	NM_001035507;NM_021831	+		
chr18	41932207	41932234	TGCGGCTGCAGAAGTACCGCCTGCGGA	1	-	NM_004046	-		
chr1	46855112	46855136	TGGCGGGGCCGGGGCGGAGCTGGC	1	-	NM_201403	-		
chr8	145553091	145553113	TGGCTGCTGCCGGGTCCTGCGC	1	+	NM_012162;NM_024531;NM_024555	-		
chr1	40496145	40496165	TGGGCTAGTGAACGCGGCGA	1	-	NM_005857	+		
chr1	40496142	40496165	TGGGCTAGTGAACGCGGCGAAGT	1	-	NM_005857	+		
chr18	17538706	17538729	TGGTCGGGAGTAGGCAGCGGCGC	1	-	NM_138340	-		
chr15	43280713	43280735	TGTGGAAACAATGGTACGGCAA	1	+	NM_138356	-		
chr2	85515224	85515248	TTCTCACTACTGCACTTGACTAGA	2	+	NM_198482	+		
chr20	18436483	18436505	TTGATTGGCCAGTGGACAGCGC	1	+	NM_001172745;NM_001172746;NM_006363;NM_032985;NM_032986	+		
chrY	15243288	15243308	TTGGAGTTTTCGAAAGACTT	1	+	NM_001164238	+		
chr15	43280712	43280735	TTGTGGAAACAATGGTACGGCAA	1	+	NM_138356	-		
chr11	767649	767670	TTTGGCCCCGGCGGGTTCGGC	1	+	NM_182612	-		

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chromosome	genome start	genome stop	tag	count	strand	refseq transcript(s)	refseq strand	partial tiRNA overlap	tiRNA match
chr20	43767202	43767224	AAAGACATAGTTGCAAGATGGG	1	-	NM_172006;NM_172131	-		
chr18	3441686	3441690	AACGCGCGGAGCTTCCCTCTGC	1	+	NM_170695;NM_173210	+		
chr10	105117798	105117813	AACGCTGCTACCTCCGCAGGC	1	+	NM_006951	+		
chr4	140442112	140442134	AACTGAACAGACCGACAGAGGC	1	-	NM_057175	+		
chrX	103288748	103288771	AAGAGCACAGACTTTGAAACCTG	4	+	NM_001012755	-		
chr2	160181472	160181495	AATACTGTAGCTTTGAGTTTGCA	1	+	NM_013450	-		
chr1	219119312	219119334	AATGAGCGCTCGGATCGAGGTC	1	+	NM_021958	+		
chr3	135686764	135686777	ACAAGATAATCAGTGTGCCCTGG	1	-	NM_001042383;NM_001042384;NM_001042400;NM_015391;NM_025180	+		
chr8	95801110	95801131	ACAGCTGTAGCTCCTGGCCGC	1	-	NM_181787	+		
chr17	40750530	40750551	ACATGCGCCCTCGGCTTCTGG	1	+	NM_003954	-		
chr2	113310804	113310827	ACCAAACCTCTTCGAGGCACAAG	1	-	NM_000576	-		
chr21	35343417	35343439	ACCACAAGTTGGGTAGCCTGGC	1	-	NM_001754	-		
chr7	100302542	100302566	ACCATGAATAAAAGACCAAAACAC	1	+	NM_003302	+		
chr4	77081159	77081183	ACCCGGGCTCCGACAGCGGCTGCA	1	-	NM_001042402;NM_014435			
chrX	71442451	71442469	ACCGGACTTGGAGTCAGA	1	-	NM_001144885;NM_001144887	-		
chr14	94693807	94693828	ACCTTGGCGTTGGGCCGCAGT	2	+	NM_177438	-		
chr22	41877376	41877398	ACTCGCGTCCCCGCGGGACCGG	1	-	NM_000714;NM_007311	+		
chr11	77383495	77383515	ACTGCCTCGCCACTGTACGG	1	+	NM_033547	-		
chr13	31787664	31787685	ACTGCTGCGCCTCTGCTGCGC	3	+	NM_000059	+		
chr16	84204441	84204460	ACTGGGCGACGGTGGCTCC	1	+	NM_014615	+		
chr5	130627153	130627176	AGAGCCCATCCTCTGACCACTGC	1	-	NM_001038702;NM_020240	+		
chr1	180627525	180627548	AGAGTCGAGAGTGGGAGAAGAGC	1	-	NM_001033056	-		
chr14	23675234	23675254	AGCGCCCTACCGCTTTCGCT	1	+	NM_006263;NM_176783	+	x	x
chr1	100276278	100276299	AGCGGCTCGGCCCGGCAGTAG	1	+	NM_033055	+	x	
chr22	29886044	29886067	AGGAACCTTGGAGCTTCGGCAGC	1	-	NM_001135824;NM_001135825;NM_152267	-		

chr	start	end	sequence	n	strand	NM			
chr7	142788539	142788559	AGGCTGCTCCGGACCGGGAC	1	+	NM_001010972;NM_003461	+		
chr7	142788539	142788561	AGGCTGCTCCGGACCGGGACGC	1	+	NM_001010972;NM_003461	+		
chr15	87588038	87588059	AGGGACCGCCGATGAGCACGC	1	+	NM_001113378;NM_018193	+		
chr3	109790867	109790890	AGTCCTTGCTCCTGACTGTCAGT	1	-	NM_014648;NM_020890	+		
chr2	27504996	27505017	AGTTCGGTTGCGCTGCGGAGC	1	+	NM_013392	+		
chr21	44485219	44485241	ATCTCCCGCGCCCCGAGGTTGC	1	-	NM_015259	-		
chr12	54497725	54497752	ATGGCGACCGAGACGGTGGAGCTCCAT	1	-	NM_014182;NM_033082	+		
chr17	57360256	57360280	ATTCTGGTAGGCTCTGATTTCCAG	1	+	NM_020748	-		
chr7	99451161	99451184	ATTGTGTCTGTGTCGAGGCGTCG	1	+	NM_003439	+	x	
chr5	134815992	134816015	CAAACTCTCAGCAGTGGAATTGC	1	-	NM_001099221	-		
chr6	53038007	53038033	CACGCGGGTTGGGCTTGAGGTTCGGC	1	+	NM_033480;NM_033481	+		
chr17	15788922	15788944	CACGCTCGAGCTCGGAGGCTGT	1	-	NM_000676	+		
chr9	4974858	4974880	CAGCCGGGCACCAGCGTTTCGC	1	+	NM_004972	+		
chr16	73292456	73292478	CAGTCCTTCTCATACTGTGTCC	1	+	NM_001142497;NM_152649	-		
chr16	83618902	83618923	CAGTCGCCGCAGCAGCCGAGT	1	+	NM_014732	+		
chr9	94936299	94936321	CATGGACTCGGGAACCGAGGAG	1	-	NM_004148	-		
chr11	59334821	59334826	CCCCACTGAGCGGTGTCCTGAGC	1	-	NM_017840	-		
chr11	123117539	123117559	CCCGCGCGGCTCGGATCCGG	1	-	NM_003455	-		
chr10	135042786	135042807	CCCTCGGACTGCCCGGACCGC	1	+	NM_152911;NM_207127;NM_207128	+		
chr2	10359990	10360003	CCCTTCCCACGCCTGTTCGGGG	1	-	NM_002149	+		
chr4	689592	689613	CCGACGCGGCGCTCGGCTCGG	1	+	NM_006315	+		
chr6	71434291	71434299	CCGCCGCCGCCCCTCCTCCCGT	1	+	NM_001044305;NM_021940	+		
chr1	44213285	44213288	CCGCCGTCGCCGCCATGACGGGG	1	+	NM_001039457;NM_004047	+		
chr15	77024399	77024419	CCGCGGACCCTGAGCGCAAG	1	-	NM_004390;NM_148979	-	x	
chr15	77024396	77024419	CCGCGGACCCTGAGCGCAAGAGC	1	-	NM_004390;NM_148979	-	x	
chr1	1500261	1500284	CCGCGGCCCGGCGTTTCGTCTCT	1	+	NM_014188	-		
chr6	10831060	10831083	CCGGAGTTGGACCTGGGACTTGC	1	+	NM_001165258;NM_016462	+		
chr2	85051572	85051595	CCGGCGGTCGCGACGGGGGCGAC	1	-	NM_020122	+		
chr1	1465627	1465650	CCGGGGCCGGGGGGGCGCCGGGG	1	-	NM_001114748	-		
chr2	65069634	65069656	CCTCGGGGCCAGAGGGCCCGGG	1	-	NM_003038	+		
chr1	151910403	151910426	CGAAACCATCCTCTGCTATCGGA	1	+	NM_004515	-		
chr3	33113609	33113630	CGAAGCGGCCGGCCTGGGCGC	1	-	NM_000404;NM_001039770;NM_001079811;NM_001135602;NM_0011362 38	-		
chr7	4781598	4781621	CGCGACCCCGGAACCTCGGCACT	1	-	NM_014855	+		
chr4	53938499	53938522	CGCGGCGGCCACCTGGGCCTGGT	1	-	NM_001134937;NM_001134938;NM_030917	+		
chr22	49311120	49311141	CGCTCGTACTCTCCGACCGCG	1	-	NM_001169109;NM_001169110;NM_001169111;NM_005138	-		
chr9	74169914	74169938	CGGCCGGGACGCGGAGCTGTGTGC	1	-	NM_001102420;NM_001102421;NM_006007	-		
chr6	149680522	149680544	CGGCGACGCCGCCCAGCCGTCG	2	+	NM_015093	+		
chr8	144750386	144750409	CGGCGCATCCCGGTCGTGGAAGC	1	-	NM_001130053;NM_001130054;NM_001130055;NM_001130056;NM_001130057;NM_001960;NM_032378;NM_032862	-		
chr2	241944405	241944425	CGGCTGCTGCTTGCGACTGC	1	+	NM_014808	+		
chr11	1367306	1367327	CGGGACCTGGGAGCCTCCAGC	1	-	NM_003957	+		
chr1	153379597	153379625	CGGGCCGCGCGGGGAAGGGGAGACGTGG	1	-	NM_018973;NM_153741	-		
chr17	32790479	32790500	CGGGCCGCGGGCGGGCCCTGG	1	+	NM_198836	+		
chr16	66614408	66614427	CGGTCCGGGTCGAACCAGC	1	+	NM_017803	+		
chr11	57236670	57236686	CGGTCTTGGCACCTCT	1	+	NM_001144012;NM_015959;NM_153450	+		
chr1	43005228	43005254	CGGTTCCGTTAGGTCTGAGGGAGCGA	1	-	NM_001146289;NM_022356;NM_024097	-	x	
chr5	133368434	133368454	CGTCCAGGCCGGGCCAGGGT	1	+	NM_003374	-		
chr3	48569711	48569731	CGTGCGGGTCACGTAGGCCTCG	1	-	NM_004567	-		
chr1	158190967	158190993	CTATGTTGCTGTGATCATTTGATCTT	1	+	NM_001146172;NM_001146173;NM_033438	-		
chr16	65196151	65196167	CTCCGGGCGCGAGAAGAGGGGAGCCAG	1	+	NM_001048251;NM_144601;NM_181553;NM_181554	+		
chr22	31200795	31200817	CTCGGTCTCTGGAATAGAGCGC	1	-	NM_001033024;NM_012179	+	x	

chr	start	end	sequence	count	strand	NM			
chr2	10870610	10870630	CTCTCGGGGTGCTGCTCGGA	1	+	NM_005742	-		
chr1	115061153	115061176	CTCTGGGTAAAGAGGCCGTTTAT	1	-	NM_002524	-		
chr2	112729100	112729122	CTCTGGGTCCGTCTCGTCGCGT	1	-	NM_032494	-		
chr6	36272360	36272382	CTGAACAGGAGCGAGAGCGCGA	1	-	NM_015695	+		
chr2	85692614	85692636	CTGCGTCCCCGGCTCCTGATGG	1	-	NM_001013649	-		
chr12	54838422	54838445	GAAAAGGTCCCGGAGAGCTGAGC	1	+	NM_021019;NM_079423	+	x	
chrX	118776605	118776628	GAAGGGCAGCTAACGCTGGACAC	1	+	NM_001105576	+		
chr2	159533211	159533233	GACCGGCTGGAGCGCGGAGCGC	1	+	NM_001145909;NM_033394	+		
chr14	94693806	94693827	GACCTTGGCGTTGGGCCGCAG	1	+	NM_177438	-		
chr17	77129793	77129816	GACGGGCCCGCGCGCACGATGGC	1	-	NM_025161	-		
chr5	175017719	175017738	GAGGCGAACCGGGTGCGGA	1	+	NM_001131055	+		
chr17	24741817	24741841	GAGGGCCTCGGCTGTGTGAGGACT	1	+	NM_020791	+		
chr4	8322424	8322446	GATGCCCCTGCCGCCCTGACGC	1	+	NM_053044	+	x	x
chr1	159451698	159451722	GCACAGTGCTGTCAGAACGGCCGA	1	+	NM_004106	+	x	
chr5	65476265	65476288	GCACCCGGGTTCCGCCGTCCTGC	1	+	NM_001077199;NM_139168	+		
chr10	44775255	44775279	GCAGCTCCGGTGCAAGCGAGGACA	1	+	NM_032023	+		
chr11	525536	525558	GCCGCCCGTGCCCTGCGCCCGC	1	-	NM_001130442;NM_005343;NM_176795	-		
chr11	118393950	118393971	GCCTAAGGACGACAAGAAGAAG	1	-	NM_001028;NM_016146	-		
chr9	92603674	92603695	GCCTCTCTCCTCCCGCCGGAC	1	-	NM_001135052;NM_001174168;NM_003177	+		
chr1	115102134	115102149	GCGAGAGAAGCGAGA	1	-	NM_001007553;NM_001130523;NM_007158	-		
chr13	100125047	100125069	GCGGGTGCCTGGAGCCGCCAGA	1	-	NM_001079669;NM_032813	-		
chr5	130998738	130998757	GCTAGAGTTCGGACCTTGT	1	-	NM_001164386;NM_001164387;NM_001164388;NM_001164389;NM_001164390;NM_016340	-		
chr19	54188902	54188924	GCTAGCCTAGAGGAGCCAGAAC	1	+	NM_001161587;NM_002103;NM_006666	-		
chr3	142688558	142688580	GCTCCGCCTCGCCCGGCTACGC	1	+	NM_006506	+		
chr2	27518600	27518623	GCTGTAATAAAAGTCTACTTTTT	1	+	NM_001168364;NM_173853	+		
chr22	29886048	29886069	GGAGGAACCTTGGAGCTTCGG	11	-	NM_001135824;NM_001135825;NM_152267	-		
chr22	29886047	29886069	GGAGGAACCTTGGAGCTTCGGC	29	-	NM_001135824;NM_001135825;NM_152267	-		
chr22	29886046	29886069	GGAGGAACCTTGGAGCTTCGGCA	2	-	NM_001135824;NM_001135825;NM_152267	-		
chr22	29886045	29886069	GGAGGAACCTTGGAGCTTCGGCAG	2	-	NM_001135824;NM_001135825;NM_152267	-		
chr6	26312869	26312899	GGCGGAAAGGGACTGGGTAAAGGAGGCGCT	1	+	NM_003545	+		
chr6	74420358	74420385	GGGCCGGCGCTCCCTTCTCTGCCAGGTGGC	1	-	NM_012434	-	x	
chr2	27200091	27200113	GGTCGCCTAGTGCCTCGCGCGG	1	-	NM_032604	+		
chr1	37930515	37930533	GTAGTAGTTTGTATAGTT	1	+	NM_018101	+		
chr2	48521241	48521263	GTCCAAGATGGCGACCTGGAAC	1	-	NM_001135629;NM_001135630;NM_152994	+		
chr1	114216294	114216317	GTCCGGGTAGAAGACATGTCACT	1	-	NM_012411;NM_015967	-		
chr1	39729925	39729945	GTCGCCCCTGCGCTGCGCGG	1	+	NM_181809	+		
chr4	76817495	76817517	GTCGGAGGAAGGGGGCGGCGAG	1	-	NM_012297;NM_203504;NM_203505	-		
chr10	134201297	134201318	GTCGGCGGCGGCTGCGGGAAC	1	+	NM_005539	+		
chr17	35532187	35532207	GTGGAGGCCGCGGCTGAGGC	1	-	NM_001012241	+		
chr9	99858813	99858834	GTGGGTCTCGCAGCGTTGCTC	1	+	NM_018946	+		
chr1	180628154	180628175	GTTCCCAAGGCCTGGAAGAGC	1	+	NM_001033044;NM_002065	-		
chr22	18222343	18222363	GTTCCCGACTCCGGCAAGAG	1	-	NM_024627;NM_053004	-		
chr21	33774396	33774415	TATCTACGGTTCCGGGCAG	1	+	NM_006134	-		
chr11	67032694	67032715	TCAAAGCCCTGCGTCCTTCGG	1	-	NM_005851	-		
chr1	112740356	112740378	TCAGCCGCTGTGGATGGGGAGT	2	+	NM_018704	+		
chr11	113149599	113149622	TCAGCGTTGGTTCCCGTCTTGGC	3	-	NM_004724	-		
chr2	200483900	200483922	TCAGGGCTTAAAAGGGAGACAT	1	-	NM_153689	+		
chr6	43135118	43135146	TCATCTAGGAGCACCGAGCAGCTTGGCT	1	-	NM_015950;NM_138343;NM_201521;NM_201522;NM_201523	-		
chr16	48744361	48744382	TCCATGCGGCCTCGTCCACGC	1	+	NM_001040284;NM_001040285	+		
chr10	73646195	73646200	TCCCCTCTCTGGCCACTTTTTCT	1	+	NM_015947;NM_173473	-		
chr3	41215646	41215667	TCCCCTGTCCCAAGCCCGACG	1	-	NM_001098209;NM_001098210;NM_001904	+		
chr1	201162907	201162927	TCCCGAGCCGCCTGCTAGCC	1	-	NM_021633	-		

chr	start	end	sequence	count	strand	gene	c1	c2	c3
chr20	44426375	44426394	TCCCGGCGCACTCCCAGAG	1	-	NM_015945;NM_173073;NM_173179	-		
chr3	37259630	37259652	TCCGAACTCGCTGCACTGGAGG	1	-	NM_001172713;NM_002078	+		
chr9	99858650	99858675	TCCGCGGCCCTCTCCTGTGCGAGGC	1	-	NM_018946	+		
chr1	40399711	40399727	TCCGGCGGTAGCGGGAGCCGGA	1	+	NM_012421	+		
chr2	73193696	73193717	TCCGGGCTGGTCTGCGGCTGC	1	-	NM_015470	-		
chr7	26207635	26207657	TCCGGTCACTGTCCTCGCCCCG	1	+	NM_002137;NM_007276;NM_016587;NM_031243	-		
chr1	111308025	111308046	TCCGGTTTCTGCGCGGTGCGC	1	-	NM_001006945;NM_018372	-		
chr17	23950471	23950493	TCCGTGGATGGAGAAGAGGAAT	1	+	NM_006461	-		
chr21	44544276	44544299	TCCTCGCAGGACGGACCCTGGAC	1	-	NM_002626	+		
chr1	232812194	232812216	TCGCCCCGGTCTGGAGGCCCGC	1	-	NM_001077397;NM_182972	-		
chr16	3010411	3010413	TCGCTGCGCCGGTTGCTGCGGC	1	+	NM_016639	+	x	
chr17	40654729	40654748	TCGGCCTCGCCTCGGTGGC	1	+	NM_005892	+		
chr10	13430186	13430202	TCGGCGCGGCCCTGCGGGAGC	1	+	NM_012247	-		
chr2	242322725	242322746	TCGGCGGCTCTGGGCCTGCGG	1	+	NM_152783	+		
chr19	38485170	38485172	TCTAACTCCCCCATGGAGTCGGC	1	-	NM_004364	-		
chr3	17759434	17759456	TCTCCCTGCTTCCAACCGGCGC	1	+	NM_001134380	-		
chr3	17759434	17759458	TCTCCCTGCTTCCAACCGGCGCGC	1	+	NM_001134380	-		
chr17	70256398	70256419	TCTCGGCTCCTCGCGGCTCGC	1	+	NM_004252	+	x	
chr17	70256396	70256416	TCTCTCGGCTCCTCGCGGCT	8	+	NM_004252	+	x	x
chr17	70256396	70256417	TCTCTCGGCTCCTCGCGGCTC	4	+	NM_004252	+	x	x
chr17	70256396	70256418	TCTCTCGGCTCCTCGCGGCTCG	91	+	NM_004252	+	x	x
chr17	70256396	70256419	TCTCTCGGCTCCTCGCGGCTCGC	143	+	NM_004252	+	x	x
chr17	70256396	70256420	TCTCTCGGCTCCTCGCGGCTCGCG	1	+	NM_004252	+	x	
chr17	77129799	77129819	TCTGACGGGCCCGCGCGCAC	1	-	NM_025161	-		
chr20	61639505	61639532	TCTGAGGGGTTGGGAAGGCAGCGCCTGC	1	-	NM_005975	-		
chr9	6403210	6403231	TCTGCGCGGCGCAGACATGGC	1	+	NM_152896	+		
chr9	6403210	6403232	TCTGCGCGGCGCAGACATGGCC	1	+	NM_152896	+		
chr17	57360258	57360280	TCTGGTAGGCTCTGATTTCCAG	1	+	NM_020748	-		
chr17	71292205	71292227	TGAAACTGGAGCGCCTGGAGGA	1	-	NM_001080419	+		
chr16	29738904	29738927	TGAAATAAAAGATGCAGAGCTAT	1	+	NM_005115;NM_017458	+		
chr15	83724873	83724896	TGAAGCGCCTGTGCTCTGCCGAG	12	+	NM_006738;NM_007200	+	x	x
chr15	83724873	83724897	TGAAGCGCCTGTGCTCTGCCGAGA	8	+	NM_006738;NM_007200	+	x	
chr19	10352582	10352604	TGACCCTAGGACACAGCTGCAT	1	+	NM_003331	-		
chr19	50618574	50618595	TGACGCTATGGAGCTCTCGGA	1	-	NM_001166049;NM_001983;NM_202001	-		
chr17	78009558	78009580	TGAGCGCGCGGACTGTCCCGAG	1	-	NM_001038618;NM_001083608;NM_012336;NM_031968	+		
chr1	148473739	148473760	TGAGGCCGAGAAGGCAACCGC	6	+	NM_001136479	-		
chr14	19881113	19881131	TGAGGTGAGGTACCCCGC	1	-	NM_001042618;NM_005484	+		
chr10	88403986	88404011	TGAGTGTGTGTGTGTGAGTGTGTGA	2	-	NM_001030015;NM_033282	+		
chr1	227506483	227506502	TGATATGATAGAATGTGGC	1	+	NM_006542	+		
chr19	59061456	59061476	TGCAGTCGTCCCGGGCGCGG	1	-	NM_001020820	+		
chr10	71833933	71833957	TGCCGCTGCTGTTGCTCCTGAGGC	2	+	NM_004096	+		
chr10	75211855	75211876	TGCGGGGTCGTCTGGCGCGGT	1	+	NM_203298	+		
chr3	47798639	47798668	TGCGGTCAACAACCGCAGGTGGGTTATGT	1	+	NM_003074	-		
chr4	106614583	106614604	TGCGGTTGGGGACCAGTGCAG	1	-	NM_001034191;NM_006903;NM_176866;NM_176867;NM_176869	-		
chr10	5766815	5766834	TGCTAGCGCCGGTCAGAGA	1	+	NM_017782	+		
chr19	2895884	2895904	TGCTCACCTGCGCCGGTCGC	1	-	NM_021217	-		
chr22	42651046	42651051	TGCTGCGGATCAGGACCCGA	1	+	NM_025225	+		
chr3	191714388	191714409	TGGACGGTCCCGCCCGCCGCC	1	-	NM_001167928;NM_001167929;NM_001167930;NM_001167931;NM_001182;NM_134470	+		
chr15	76210898	76210920	TGGCCCCGGGAGACGCTGCCCG	1	+	NM_006383	-		
chr4	38722911	38722930	TGGCGCCGCCTGACGGAGC	1	+	NM_001007075;NM_001171654	+		
chr11	74137301	74137322	TGGGAACTGAGGGGCTTTACT	1	-	NM_001098638	+		
chr1	40496142	40496165	TGGGCTAGTGAACGCGGCGAAGT	4	-	NM_005857	+		
chr1	247099165	247099187	TGTCCCTCTCGCCCGCGTCGGC	1	-	NM_024836	+		
chr14	90650804	90650826	TGTGCCTGCGGCAGCCCAGAAC	2	-	NM_001102367	+		
chr1	111308025	111308047	TTTCCGGTTTCTGCGCGGTGCGC	1	-	NM_001006945;NM_018372			
chr10	52054087	52054111	TTCGCAAACTCGTGCCTGGCTTCC	1	-	NM_147156	-		
chr8	62789909	62789931	TTCGGCTTTCCAGTTTGTCTCG	1	+	NM_001164754;NM_001164755;NM_001164756;NM_004318;NM_032466	-		
chr2	85515224	85515248	TTCTCACTACTGCACTTGACTAGA	2	+	NM_198482	+		

AGO3-IP library

chromosome	genome start	genome stop	tag	count	strand	refseq transcript(s)	refseq strand	partial tiRNA overlap	tiRNA match
chr1	27089792	27089809	AAAAGCTGGGTTGAGTG	1	-	NM_018066	-		
chr3	47530298	47530321	AAACGATGGGCTTCTCTGTGCGA	1	+	NM_001031703	-		
chr1	15351381	15351407	AACAGCTCGACAGAACCTTGGCGTCC	1	-	NM_001136216;NM_001136217	+		
chr4	76817530	76817553	AACTCGCGGCTCTCCGGCTTCCG	1	-	NM_012297;NM_203504;NM_203505			
chrX	103288748	103288771	AAGAGCACAGACTTTGAAACCTG	1	+	NM_001012755	-		
chr19	1799667	1799683	AAGGTCGGGCGGCGGC	1	-	NM_020695	-		
chr1	84745130	84745154	AATCGGTTTTTCTGAAGGAGATTG	1	+	NM_005274	-		
chr22	29317806	29317830	ACGTGGAGCGATGGGAGGCCTTGA	1	-	NM_014303	-		
chr17	6880093	6880114	ACTCAGTTCCACCCTCTGGCT	1	-	NM_201566	+		
chr7	91602144	91602167	ACTGGGGCACCTCGAACTGTGGC	1	+	NM_000786;NM_001146152	-		
chr4	104009346	104009371	ACTGTGTGCGATGAGATAAGCATGT	1	-	NM_001008388;NM_181890;NM_181893	+		
chr17	53784509	53784531	AGAACAACAGGGAGATAGACGA	1	+	NM_003168	-		
chr1	44229542	44229565	AGCGCTTGGAGAACCAGGATGGC	1	-	NM_152499	+		
chr1	159550660	159550684	AGCTCTGCCTAGCTGGTTTGCTGG	1	-	NM_001035511;NM_001035512;NM_001035513;NM_003001	+		
chr6	44295156	44295182	AGGCTCCGGAAAGGGACGGGGTTAGG	1	-	NM_001078174;NM_004955	+		
chr7	142788539	142788559	AGGCTGCTCCGGACCGGGAC	1	+	NM_001010972;NM_003461	+		
chr7	142788539	142788562	AGGCTGCTCCGGACCGGGACGCA	1	+	NM_001010972;NM_003461	+		
chr16	2873272	2873293	AGGTAACAGCGCGAGCTGAGG	1	+	NM_001142499;NM_001142500;NM_138439	+		
chr9	139220354	139220377	AGGTTGGAACCTGAAAGAGAAGA	1	+	NM_001144026;NM_001144027;NM_001144028;NM_014434;NM_053045	+		
chr19	4675075	4675104	ATCAGGGCGTTGGTGGTATAGTGGTTAGC	1	+	NM_139159	-		
chr19	8361277	8361298	ATCCCGCCGGAAGCGCCAGGA	1	+	NM_004218	+		
chr15	63948446	63948468	ATCTCGGTGGAACCTGCATTGG	1	-	NM_004663	+		
chr1	40399658	40399682	ATGGCGGACGGAAAGGGAGACGCC	1	+	NM_012421	+	x	
chr15	78003542	78003569	ATTCGGGGGAGACGTAGTTTACTTTGTT	1	+	NM_001100880	-		
chr22	41877336	41877358	CACCTCTCCCGCGGGACGCGCT	1	-	NM_000714;NM_007311	+		
chr8	38082602	38082605	CACGGGCGGTGGGAGCTGAGG	1	+	NM_001105214;NM_004674	+		
chr17	31231431	31231460	CAGCACGTGGACCTCGCACAGCCTCTCCC	1	-	NM_002985	-		
chr11	63809932	63809954	CCACGACCTGAGCCGGCTCTCC	1	+	NM_001170880;NM_020155	+		
chr9	102155160	102155182	CCCCCTGCTCTGTGGGAACCGG	1	+	NM_001161584;NM_017746	-		
chr11	66162779	66162800	CCCTGCTGGTTTCTGTGCGGG	1	+	NM_002896	+		
chr19	3013611	3013634	CCGCCTCCCCGTGGCCCGCCCGC	1	+	NM_001130;NM_198969;NM_198970	-		
chr1	1500261	1500282	CCGCGGCCCGGCGTTTCGTCT	1	+	NM_014188	-		
chr15	72694300	72694321	CCGGCCTCGCGAGCGTCGCGC	1	-	NM_001130028	+		
chr17	57909620	57909646	CCGGCTGACGGGCCGCAACGCGAGGG	1	-	NM_001112707;NM_006852	+		
chr7	27206742	27206750	CCTCTGGGACTGTTTTCTTTCCAG	1	+	NM_000522	-		
chr6	31902990	31902997	CCTGAGAAACGGACCGGCTCTC	1	-	NM_005346	+		
chr5	151118532	151118554	CCTGGACGGAGAGAGGAGGTGA	1	+	NM_004045	-		
chr8	57149594	57149605	CGCGGTCGTAAGGGCTGAGGATTT	1	-	NM_001023;NM_001146227	-	x	
chr9	139619975	139619990	CGGTGAGGCCGCGGC	1	+	NM_152285	+	x	x
chr18	802823	802827	CGTAGCGCTGAGAAG	1	-	NM_005433	-		
chr10	70517908	70517933	CTAAGTTGGTCATGATGCAGAAGCTACTC	1	+	NM_002727	+		
chr8	42870808	42870828	CTCTGTCGCCGGGAACTGGC	1	-	NM_001160223;NM_001160224;NM_001160225;NM_030954;NM_032410	-		
chr13	31787665	31787685	CTGCTGCGCCTCTGCTGCGC	1	+	NM_000059	+		
chr22	35255536	35255557	CTGCTTAATGTGAAACTCAGC	1	+	NM_003753	-		
chr19	12638446	12638470	CTGGACTCAGCAGGCCCCTGGACC	1	-	NM_000528;NM_001099737;NM_001173498	-		
chr20	30409527	30409548	CTGGGTGGAGTCTCGCGAGGT	1	-	NM_001164603;NM_015338	+		
chr13	99539405	99539425	CTGGTCGCTGCCGGACGGCG	1	+	NM_000282;NM_001127692	+	x	
chr4	6693093	6693116	CTTTCCCGTTACCTCTGTGCGTC	2	-	NM_033296	+		
chr19	54160428	54160452	GAACAGATCCGGGGACTCTCTTCC	1	+	NM_000146	+	x	
chr21	44544268	44544290	GACGGACCCTGGACGGAGCAGG	1	-	NM_002626	+		
chr1	226202219	226202244	GAGCGCGATGGTCGGCCGCCGAGGC	1	-	NM_003395	-		
chr6	26264536	26264563	GAGTCCCGGCCAGTGCCTCTGCTTCCG	1	+	NM_005321	+	x	
chr5	87600363	87600386	GAGTCTCTCGGCTCAAGGACCGG	1	-	NM_153354	-		
chr4	8322424	8322446	GATGCCCCTGCCGCCCTGACGC	1	+	NM_053044	+	x	x

chr	start	end	sequence	count	strand	NM			
chr3	50687564	50687588	GATGCGCCGCCCACTGCCCCGCGC	1	+	NM_004947	+		
chr5	141318752	141318776	GATTCCAGAAGCTGCAAGAACCTG	1	+	NM_016580	-		
chr2	85051353	85051376	GCCCCGCCTGGGGCGGGCCTAGG	1	-	NM_020122	+		
chr18	18969711	18969732	GCCGCCATTGTGTCCGTCTGC	1	-	NM_001100619	+		
chr1	22136374	22136395	GCCGCGCTGTCCCGAGCTGGC	1	-	NM_005529	-		
chr10	82158144	82158166	GCCGCGGTCTCCTAGCTCCGGT	1	-	NM_032333	+		
chr1	94117463	94117485	GCCTTCTACAGCTCTGAAATGC	1	-	NM_014597	-		
chr8	103737094	103737122	GCGCTGAGCGCGGCGGCGGCGGGAGCGG	1	-	NM_005655	-	x	
chr6	36103313	36103339	GCGGACCGGGGAAGGAAGAGAGAAGC	1	-	NM_001315;NM_139012;NM_139013;NM_139014	+		
chr1	153222457	153222477	GGAACAAGGGAAAGAGCCGG	1	+	NM_025207;NM_201398	+		
chr15	70863117	70863143	GGAAGAGGCGCGGGCTAGGAAAGGAG	1	-	NM_031284	-		
chr22	29886049	29886069	GGAGGAACCTTGGAGCTTCG	1	-	NM_001135824;NM_001135825;NM_152267	-		
chr22	29886048	29886069	GGAGGAACCTTGGAGCTTCGG	9	-	NM_001135824;NM_001135825;NM_152267	-		
chr22	29886047	29886069	GGAGGAACCTTGGAGCTTCGGC	28	-	NM_001135824;NM_001135825;NM_152267	-		
chr22	29886046	29886069	GGAGGAACCTTGGAGCTTCGGCA	4	-	NM_001135824;NM_001135825;NM_152267	-		
chr12	119609348	119609365	GGAGGCCTGAGAGCGAC	1	+	NM_014730	+	x	
chr1	44213225	44213246	GGGACGGACGGTGGACGCTGG	1	+	NM_001039457;NM_004047	+		
chr22	40414935	40414958	GTCGAAGAAGGAACGTACTTTGG	1	+	NM_001003796			
chr1	74436344	74436364	GTCTCAGGAGCAGATGGCCG	1	-	NM_001105659;NM_001112808;NM_003838	-		
chr12	94953922	94953945	GTGCGGTTCCTCGTTAGTATAGT	1	+	NM_000895	-		
chr9	35647998	35648017	GTGGTTCGTGCTGAAGGCC	1	-	NM_174923	+		
chr9	35647995	35648017	GTGGTTCGTGCTGAAGGCCTGT	1	-	NM_174923	+		
chr3	168854292	168854315	GTTAGTTAAAGAGATTTTTGGGA	1	-	NM_178824	-		
chr17	59923568	59923589	GTTGAGTGATGGGAGAGTGTG	1	-	NM_007215	-		
chr10	70517882	70517910	GTTGGCGTGCAGCTGGGAGAGCTAGACT	2	-	NM_002727	+	x	
chr1	166516914	166516929	GTTGGGTAACGGCTC	1	+	NM_005149	+		
chr11	70841925	70841950	TACCTCGCTGGGACCCTGGTCTTGC	1	+	NM_018161	+		
chr6	49538912	49538934	TACGCCCCCAGAGTCGTCCGGC	1	-	NM_000255;NM_018132			
chr7	155129946	155129968	TCAAACATTTGGGTTTCAGGAG	1	+	NM_053043	+		
chr1	111545113	111545136	TCACTTCTCAACTTGGTCAACGG	1	+	NM_024901	-		
chr10	1085229	1085253	TCAGACGTCTCGAGGCTCGCGTTC	1	+	NM_004508	-		
chr11	113149599	113149622	TCAGCGTTGGTTCCCGTCTTGGC	1	-	NM_004724	-		
chr1	233358821	233358842	TCAGGCTCTGCCGCGGACGAC	1	-	NM_014765	-		
chr4	658407	658426	TCCACACCCCAGACTGCGG	1	+	NM_007100			
chr3	41215645	41215667	TCCCCTGTCCCAAGCCCGACGC	1	-	NM_001098209;NM_001098210;NM_001904	+		
chrX	68301963	68301985	TCCGAGAGCTCTGCTTCTCTGA	1	-	NM_001032396;NM_022368;NM_145119	-		
chr4	141897180	141897203	TCGAGCTCCCGAAGTCGCCGCGC	1	+	NM_015130	-		
chr10	104604021	104604040	TCGCTAACTGAAATGATGG	1	+	NM_001136200;NM_144591	+		
chr16	3010411	3010413	TCGCTGCGCCGGTTGCTGCGGC	1	+	NM_016639	+	x	
chr9	135192878	135192899	TCGGCGTTCGTTTGGCCGCGC	1	-	NM_006753	-		
chr3	40541265	40541287	TCTAAGCCCGGCTTTCTCCGGC	1	-	NM_001098414;NM_198484	+	x	
chr2	88136331	88136353	TCTCCGCCACCTCCACCGCGGAC	1	-	NM_016618	-		
chr2	10870577	10870599	TCTCGGCTCGCACCGCCTCAGC	1	+	NM_005742	-		
chr17	70256396	70256417	TCTCTCGGCTCCTCGCGGCTC	1	+	NM_004252	+	x	x
chr17	70256396	70256418	TCTCTCGGCTCCTCGCGGCTCG	35	+	NM_004252	+	x	x
chr17	70256396	70256419	TCTCTCGGCTCCTCGCGGCTCGC	77	+	NM_004252	+	x	x
chr17	70256396	70256420	TCTCTCGGCTCCTCGCGGCTCGCG	3	+	NM_004252	+	x	
chr3	185562060	185562083	TCTGCTCTCGGCCTCCCGGGCTG	1	-	NM_001171087;NM_001171088;NM_001171089;NM_004366	-		
chr9	35647951	35647972	TCTGTTCCTCCCCTTTCCGCC	1	-	NM_174923	+		
chr8	48813216	48813231	TGAAGAGCGCGGCGC	1	+	NM_005195	-	x	
chr15	83724873	83724896	TGAAGCGCCTGTGCTCTGCCGAG	9	+	NM_006738;NM_007200	+	x	x
chr15	83724873	83724897	TGAAGCGCCTGTGCTCTGCCGAGA	4	+	NM_006738;NM_007200	+		
chr19	10352582	10352604	TGACCCTAGGACACAGCTGCAT	3	+	NM_003331	-		
chr1	89763051	89763072	TGAGCCCGCAGCCTCCGGCAG	1	+	NM_001134476	+		
chr1	148473739	148473760	TGAGGCCGAGAAGGCAACCGC	1	+	NM_001136479	-		
chr10	88403985	88404011	TGAGTGTGTGTGTGTGAGTGTGTGAA	1	-	NM_001030015;NM_033282	+		
chr2	27127643	27127659	TGCCCGCATCCTCCAC	1	+	NM_001035507;NM_021831	+		
chr19	62703102	62703124	TGCCGGAAGCTGGTTGTTCGCT	1	+	NM_198542	+		
chr7	6065463	6065491	TGCGCTCTGGTGGGCTCGTCTACCGGCG	1	+	NM_001134335;NM_014413	+		
chr9	35647986	35648009	TGCTGAAGGCCTGTATCCTAGGC	1	-	NM_174923	+		
chr9	109292102	109292120	TGGAGCCGAGCTGACGCC	1	+	NM_004235	-		
chr6	27966525	27966548	TGGCCCGGACGAAGCAGACAGCT	1	-	NM_003535	-		
chr5	133775608	133775629	TGGCTCCTCAGACCGCCGCAG	1	+	NM_080656	-		

chr14	19881113	19881135	TGGCTGAGGTGAGGTACCCCGC	1	-	NM_001042618;NM_005484	+	
chr17	31974698	31974720	TGGGCCCGGCGCCCTTCTCGGA	1	-	NM_024835	+	
chr1	40496143	40496165	TGGGCTAGTGAACGCGGCGAAG	1	-	NM_005857	+	
chr1	40496142	40496165	TGGGCTAGTGAACGCGGCGAAGT	1	-	NM_005857	+	
chr1	204875270	204875293	TGGGTCCCTGGCGCGAGCTGTAG	1	-	NM_001004023;NM_003582	+	
chr2	48521240	48521265	TGGTCCAAGATGGCGACCTGGAACG	1	-	NM_001135629;NM_001135630;NM_152994	+	
chr14	90650804	90650826	TGTGCCTGCGGCAGCCCAGAAC	1	-	NM_001102367	+	
chr1	28842119	28842139	TTCACTGGGGCAGTCTCTGC	1	-	NM_001135218;NM_005644	-	
chr2	20714507	20714529	TTCCGGAGCACCCAGGCTGAGC	1	+	NM_022460	-	
chr2	85515224	85515248	TTCTCACTACTGCACTTGACTAGA	3	+	NM_198482	+	
chr7	148523568	148523588	TTCTTCTTCTCCCTGGCCGA	1	+	NM_003575	+	
chr1	41100505	41100518	TTGCTCCGCCCGGCCGAGC	1	-	NM_133467	-	x
chr15	43280712	43280732	TTGTGGAAACAATGGTACGG	1	+	NM_138356	-	
chr15	43280712	43280735	TTGTGGAAACAATGGTACGGCAA	2	+	NM_138356	-	

Supplementary Table S8. List of asmiRNA tags recovered across phylogenetically-diverse animals and *Arabidopsis.*

Mouse

miRNA loci	Sequences	ES cells-Whitehead	ES cells-UCSF	oocytes
miR-126-3p	primary sense isomir	179		
	AUUAUUACUCACGGUACGAGUU	1		
miR-126-5p	CAUUAUUACUUUUGGUACGCG		105	
	CGCGUACCAAAAGUAAUAAUGU		1	
miR-150*	primary sense isomir	4		
	UCCCCCAGGCCUGUACCAGGGU	1		
miR-24-1*	primary sense isomir	9		
	UGAUAUCAGCUCAGUAGGCAC	1		
	UGAUAUCAGCUCAGUAGGCA	1		
miR-24	primary sense isomir	3272		3684
	UGUUCCUGCUGAACUGAGCCAG	1		1
	GUUCCUGCUGAACUGAGCCAGU	1		3
	UUCCUGCUGAACUGAGCCAGU			2
	UGUUCCUGCUGAACUGAGCCAGU			1
miR-291a-5p	primary sense isomir	9685	32437	
	GGGCCUCCACUUUGAUGGCCG	1	0	
	AGAGGGCCUCCACUUUGAUGGCC	1	1	
miR-1-1-3p	UGGAAUGUAAAGAAGUAUGUAU		77	
	ACAUACUUCUUUACAUUCCAUA		2	
	UACAUACUUCUUUACAUUCCA		1	
miR-124-1*	CGUGUUCACAGCGGACCUUGAU		55	
	UCAAGGUCCGCUGUGAACACGG		1	
miR-141*	CAUCUUCCAGUGCAGUGUUGGA		37	
	CAACACUGCACUGGAAGAUG		1	
miR-218-2-5p	UUGUGCUUGAUCUAACCAUGUG		42	
	AUGGUUAGAUCAAGCACAAA		1	
miR-219-1-3p	AGAGUUGCGUCUGGACGUCCCG		4	
	GGACGUCCAGACGCAACUCUCG		1	
miR-335-5p	UCAAGAGCAAUAACGAAAAAUG		491	
	CAUUUUUCGUUAUUGCUCUUGA		1	
miR-337-5p	CGGCGUCAUGCAGGAGUUGAUU		788	
	ACUCCUGCAUGACGCCGUUCCC		1	
miR-337-3p	primary sense isomir			4
	AGAAAGGCAUCAUAUAGGAGCUG			1
miR-338-3p	UCCAGCAUCAGUGAUUUUGUUGA		26	16
	UCAACAAAAUCACUGAUGCUG		1	
	UCAACAAAAUCACUGAUGCUGGA			1
miR-34b-3p	primary sense isomir			8
	UGGCAGUGGAGUUAGUGAUUGU			2

References: 19, 20, 21

Chicken

miRNA loci	Sequences	embryo
miR-10a	primary sense isomir	38445
	CAAAUUCGGAUCUACAGGGUAC	1
miR-10a*	primary sense isomir	219
	UCCCCUAGAUACGAAUUUGUG	1
miR-124a-5p	primary sense isomir	648
	UCAAGGUCCGCUGUGAACACGG	78
	CAAGGUCCGCUGUGAACACGG	6
	UCAAGGUCCGCUGUGAACACGGA	1
miR-126	primary sense isomir	908
	GCAUUAUUACUCACGGUACGAG	1
miR-1559-3p	primary sense isomir	15
	CUCGAUGCAUACAUGUAACUCC	4
	GCUCGAUGCAUACAUGUAACUCC	1
miR-1751	primary sense isomir	2
	GAUGCAGGAACAGAGCAGCUCA	2
miR-184-5p	primary sense isomir	2
	UGGGCUGGAAAAGUGAUAAGGG	3
	UGGGCUGGAAAAGUGAUAAGGGG	1
	UGGGCUGGAAAAGUGAUAAGG	1
miR-187-5p	primary sense isomir	186
	CAUGUCCUGUGUUGUAGCCGG	1
miR-193a-5p	primary sense isomir	625
	AUCUCGCCCGCAAAGACCCAG	1
miR-193a-3p	primary sense isomir	469
	UGGGACUUUGUAGGCCAGUUGA	2

miR-199-2-5p	primary sense isomir	4044
	AGGUAGUCUGAACACUGGGGCG	1
miR-205a	primary sense isomir	605
	GACUCCGGUGGAAUGAAGGACA	1
	CAGACUCCGGUGGAAUGAAGGA	1
miR-205b	primary sense isomir	209
	GAUUCCGGUGGAAUGAAGGGCA	1
miR-21-3p	primary sense isomir	292
	CAGCCUACCGACUGUUGUUGCC	1
miR-216b-5p	primary sense isomir	1576
	UCACAUUUGCCUGCAGAGAUUU	5
	UCACAUUUGCCUGCAGAGAUU	1
	CACAUUUGCCUGCAGAGAUUU	1
miR-217-3p	primary sense isomir	18
	AAUGCAUUAGGAACUGAUGGUG	1
miR-219-5p	primary sense isomir	1651
	CACAAGAAUUGCGUUUGGACAA	2043
	CACAAGAAUUGCGUUUGGACA	1829
	CACAAGAAUUGCGUUUGGACAAU	1456
	ACAAGAAUUGCGUUUGGACAAU	149
	AGAAUUGCGUUUGGACAAUCA	107
	CACAAGAAUUGCGUUUGGAC	94
	ACAAGAAUUGCGUUUGGACAA	89
	ACAAGAAUUGCGUUUGGACA	57
	AGAAUUGCGUUUGGACAAUCAG	52
	GCACAAGAAUUGCGUUUGGACA	12
	AGAAUUGCGUUUGGACAAUC	10
	AAGAAUUGCGUUUGGACAAUCA	7
	GCACAAGAAUUGCGUUUGGACAA	3
	CAAGAAUUGCGUUUGGACAAUCA	2
	CAAGAAUUGCGUUUGGACAAU	2
	AGAAUUGCGUUUGGACAAU	2
	AAGAAUUGCGUUUGGACAAU	2
	GCACAAGAAUUGCGUUUGGACAAU	1
	CACAAGAAUUGCGUUUGGACAAUC	1
	ACAAGAAUUGCGUUUGGACAAUC	1
	AAGAAUUGCGUUUGGACAAUCAG	1
miR-219-3p	primary sense isomir	7222
	GAUGUCCAGACACAAUUCUUG	19
	AGAUGUCCAGACACAAUUCUUG	8
	GAUGUCCAGACACAAUUCUU	4
	AGAUGUCCAGACACAAUUCUU	1
miR-24-5p	primary sense isomir	4
	AUAUCAGCUCAGUAGGCACCGG	2
miR-365-1	primary sense isomir	340
	AGGAUUUUUAGGGGCAUUAUGA	3
	AGGAUUUUUAGGGGCAUUAU	1
	AAGGAUUUUUAGGGGCAUUAU	1
miR-449c*	primary sense isomir	3
	UGGAGUGCCGUGAGCAGCUGU	1
miR-7	primary sense isomir	2477
	AACAAAAUCACUAGUCUUCCAGA	1
miR-7-2-3p	primary sense isomir	18
	AGGCAGACUGUGACUUGUUGU	105
	AGGCAGACUGUGACUUGUUG	15
	AGGCAGACUGUGACUUGUUGUG	4

Reference: 22

Drosophila melanogaster

miRNA loci	Sequences	embryo	head tissue	body tissue
miR-276a	primary sense isomir	26407		
	AGCACGGUAUGAAGUUCCUAC	3		
miR-305	primary sense isomir	21848		832
	CAGAGCACCUGAUGAAGUACAAU	14		1
	CAGAGCACCUGAUGAAGUACAA	1		
miR-307*	primary sense isomir		1403	
	UCACACCCAGGUUGAGUGAGUC		1	
miR-92a	primary sense isomir	41615		
	GCCGGGACAAGUGCAAUGUUUA	3		
miR-978*	primary sense isomir	14		
	UAAGCCAGUGGCGUAGAUUGCA	1		
miR-984	primary sense isomir		4	
	AUUCCAACCGUAUUUACCUCA		2	
	primary sense isomir	7307	16	11

miRNA loci	Sequences			
miR-iab-4-5p	GGAUACAUUCAGUAUACGUUUA	101		1
	AGGAUACAUUCAGUAUACGUUUA	12	1	
	GGAUACAUUCAGUAUACGUUU	6		
	AGGAUACAUUCAGUAUACGUUU	6		1
miR-iab-4-3p	primary sense isomir	509		3
	UUACGUAUACUGAAGGUAUACCG	10		1
	UUACGUAUACUGAAGGUAUACCGG	5		
	UUACGUAUACUGAAGGUAUACC	5		
	UUACGUAUACUGAAGGUAUACCGGA	1		
	UUACGUAUACUGAAGGUAUA			1

References: 23, 24

C. elegans

miRNA loci	Sequences	Bristol strain	hermaphroditic embyro	young adult	miRBase star sequence?
miR-232-5p	primary sense isomir	45		19	yes
	AAAAUCAUCGAAACUGCAGGGAU	5			
	AAAUCAUCGAAACUGCAGGGAU	4			
	GAUAAAAUCAUCGAAACUGCA	3			
	UAAAAUCAUCGAAACUGCAGGGAU			1	
miR-239a-3p	primary sense isomir	888			yes
	UUUGCACUAGACUAGACACUGGA	1			
miR-250-5p	primary sense isomir	150			yes
	GAUCACGAGGCAACUGAAGG	4			
miR-260-5p	primary sense isomir	250			yes
	UCUAUCGACCUGGUAAAGCA	2			
miR-38	primary sense isomir	12073			
	CUCCAGUUUUUCUCCCGGUGAUA	2			
miR-52-3p	primary sense isomir	536	129		yes
	GCUACCCUUUCAUUGUAACGUGA	1			
	GCUACCCUUUCAUUGUAACG	1	1		
miR-55-5p	primary sense isomir	113			yes
	UAACCGAUAGGUUUCUGCCGA	12			
	UAACCGAUAGGUUUCUGCCGAG	3			
miR-58-5p	primary sense isomir		28	70	yes
	GAUGAGAUGCGAAGAGUAGGGCA		20	2	
	GAUGAGAUGCGAAGAGUAGGGC		2		
	GAUGAGAUGCGAAGAGUAGGGCAA		1		
	GAUGAGAUGCGAAGAGUAGG		1		
miR-60-5p	primary sense isomir	317			yes
	GAUUUUAUGGCACUCUUCCAG	2			
miR-67-5p	primary sense isomir	45			yes
	UAACAACCGGCAGAAUGAGCGGA	3			
miR-67	primary sense isomir	31029			
	UACUCUUUCUAGGAGGUUGUGAU	4			
miR-71-3p	primary sense isomir	729	6		yes
	GGCGAAAAACAGAAUAGUGAUAC	1			
	GGCGAAAAACAGAAUAGUGA	1	1		
miR-72-3p	primary sense isomir		2		yes
	GUGGCAGAAUGUGGCGAAGCUGA		1		
miR-74-5p	primary sense isomir	82	4		yes
	GCUGGGAAAGAGAUGGAAGC	6			
	GCUGGGAAAGAGAUGGAAGCCCGA		1		
miR-786-5p	primary sense isomir	18			yes
	AAAUACCCCAACUGAUAUUCGAU	14			
	AAAUACCCCAACUGAUAUUCGA	1			
miR-786-3p	primary sense isomir		1		
	UGAACAUCAUUCAGGGCAUUAC		1		
miR-80-5p	primary sense isomir	2923			
	GUUCAGAAUCAUGUCGAAAGCU	2			
miR-85-5p	primary sense isomir	6			yes
	UCAAACUAUUGAAAAAUCGGGCU	1			
miR-90-5p	primary sense isomir	718		36	yes
	UGAUAUCGUCGUUGAAAGCCGCUC	2		1	
	GUUGAUAUCGUCGUUGAAAG	1			
	UGAUAUCGUCGUUGAAAGCCGCU			1	
	GUUGAUAUCGUCGUUGAAAGCCG			1	

References: 25, 26

Arabidopsis thaliana

miRNA loci	Sequences	inflorescence tissue	TAIR star sequence?
MIR-156a-3p	primary sense isomir	5	yes

MIR-156a-3p	UCUGACAGAAAGAGCAGUGAGCA	1	
MIR-157a/157b	UUGACAGAAGAUAGAGAGCAC	27123	
	AUCUGUGCUCUCUAUCUUCUGUCAA	1	
MIR-157a/157b-3p	primary sense isomir	80	yes
	GGUGAUGACAGAAGGCUAGAGA	1	
	GAUGACAGAAGGCUAGAGAGCA	1	
	ACAGAAGGCUAGAGAGCACAA	1	
MIR-157c-3p	primary sense isomir	2	yes
	GGUGACAGAAGUAUAGAGAGCAC	1	
MIR-161-5p	primary sense isomir	13347	
	CCCCGAUGUAGUCACUUUCAA	1	
MIR-163	primary sense isomir	82	
	UCGAAGUUCCAAGUCCUCUUCAA	1	
MIR-169b-3p	primary sense isomir	3	yes
	AGCCGAAGGACAACUUGCCAGAAAU	1	
	AGCCGAAGGACAACUUGCCAGAA	1	
	AGCCGAAGGACAACUUGCCA	1	
MIR-171b/171c	primary sense isomir	56	
	UGAUAUUGGCACGGCUCAAUC	1	
MIR-172e-5p	primary sense isomir	231	yes
	UGAAUCUUAAUGGUGCUGCAU	1	
	UGAAUCUUAAUGGUGCUGCA	1	
	GUGAAUCUUAAUGGUGCUGCA	1	
MIR-172e	primary sense isomir	148	
	UGCAGCAUCAUCAAGAUUCCC	1	
MIR-391-3p	primary sense isomir	106	yes
	AUUGCUACGUAGGAGAGAUA	1	
MIR-833-5p	primary sense isomir	5	
	UUGAACUAGACCGAGUACAACAA	1	
	UAGACCGAGUACAACAAACAA	1	
	AGACCGAGUACAACAAACAAAC	1	
	AGACCGAGUACAACAAACAAA	1	
	AGACCGAGUACAACAAACAA	1	
	ACUAGACCGAGUACAACAAACA	1	
MIR-833-3p	primary sense isomir	3	
	UAGACCGAUGUCAACAAACAAG	1	
	CCGAUGUCAACAAACAAGCUG	1	
	AGCUAGACCGAUGUCAACAAA	1	
	AGACCGAUGUCAACAAACAAGC	1	
MIR-843-3p	primary sense isomir	1	yes
	UUUAGAUCGAGCUUCACAGGA	1	
MIR-851-5p	primary sense isomir	23	yes
	UGGAUCGCGAACCGAGACGAC	1	
MIR-866-3p	primary sense isomir	1	
	UUCAAAGACGGAUUUUGUUA	1	
	UCAAAGACGGAUUUUGUUAA	1	
	CUUCAAAGACGGAUUUUGUU	1	

Reference: 27