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Supplementary Methods

Annotation of small RNAs

To know the exact positions of the small RNAs in the genome, we aligned the small RNA sequences with the genome using blastn (<ftp://ftp.ncbi.nlm.nih.gov/genbank/>) with a perfect match criterion. To identify small RNAs corresponding to various repeats (rRNA, tRNA, retrotransposon, DNA transposon etc.), the genomic positions of repeats were retrieved from the University of California, Santa Cruz (UCSC) web site (<http://hgdownload.cse.ucsc.edu/downloads.html>) and compared with the genomic positions of small RNAs. If the genomic position of a certain small RNA overlapped with any repeats by 15 nt, this small RNA was considered to be repeat-derived. Repeat names were retrieved from all positions where the small RNA was mapped, and if multiple repeat names were retrieved, the class (such as LTR/MaLR or rRNA) and subclass (such as IAP), where applicable, were determined according to the majority of positions (Supplementary Table 2). If the top two repeats had the same number of positions, we did not determine the class or subclass. To identify small RNAs corresponding to tRNAs, rRNAs, snRNAs, snoRNAs, scRNAs, miRNAs, piRNAs (known ones from adult testis) and mRNAs based on sequence similarity, we extracted the sequences of these RNAs from the flat files of GenBank and downloaded the

sequences from the following databases: tRNAs, Genomic tRNA Database (<http://lowelab.ucsc.edu/GtRNAdb/Mmuscl/>); rRNAs, European ribosomal RNA database (<http://www.psb.ugent.be/rRNA/index.html>); snoRNAs, snoRNA database (<http://www-snorna.biotoul.fr>) and RNA database (<http://jsm-research.imb.uq.edu.au/rnadbl/>); piRNAs, RNA database (<http://jsm-research.imb.uq.edu.au/rnadbl/>); miRNAs, miRBase (<http://microrna.sanger.ac.uk/sequences/index.shtml>); mRNAs, Refseq Genes (<ftp://ftp.ncbi.nih.gov/refseq/>) and Ensemble Genes (<http://www.ensembl.org/index.html>). Then blastn search (<ftp://ftp.ncbi.nih.gov/blast/>) was performed using our small RNA sequences as queries and the sequences downloaded as above as a database. Since the sequences downloaded in our database could not cover all RNA species present in cells, we aligned the small RNA sequences with the RNA sequences in the database using a 90% match criterion including indels. Namely, we allowed a single base mismatch for 17-19 nt small RNAs, 2 mismatches for 20-29 nt small RNAs, 3 mismatches for 30-39 nt small RNAs and 4 base mismatches for 40 nt small RNAs. We first used blastn program with an option not masking repeat sequences (-F, F) and extracted the best hit regions on the RNAs deposited in the database with extra 5 bases at both ends. Since blastn is a local alignment program, we re-aligned the small RNAs with the extracted RNA fragments

using an in-house global alignment program¹. This program uses Needleman/Wunsch's global alignment algorithm² with Gotoh's affine gap penalty³, to find the optimal alignment (including indels) of two sequences considering their entire length. It uses dynamic programming methods to ensure the optimal global alignment by exploring all possible alignments and choosing the best. Except that our global alignment program can also take account of out gap penalty, it is almost the same as the "needle" program included in the EMBOSS package⁴. Finally, the repeat annotations based on genomic position and the annotations based on sequence similarity were combined. If a small RNA had more than one annotation, we used the following order of priority: rRNA, tRNA, snoRNA, sc/srpRNA, miRNA, rasiRNA, piRNA and mRNA. The non-annotated sequences were classified as unknown.

Identification of siRNA clusters

For identification of candidates for siRNA clusters, we considered only small RNAs from growing oocytes that (1) constituted clusters, (2) hit the genome 1-10 times and (3) were annotated as repeat, mRNA, piRNA or unknown. A total of 444 small RNA clusters were subjected to the selection. We used the series of criteria described below to select siRNA clusters of the respective classes. The small RNA clusters selected at each filtering step in the three procedures are schematically shown in Supplementary Fig. 9.

Selection procedure for hp-siRNA cluster

1. Select clusters in which more than three small RNA sequences hit two times within a certain 5 kbp region. These two hits should lie in opposite orientations. (4/444)
2. In the clusters, the small RNAs of all pairs should be arranged in a symmetrical manner to form an inverted repeat. (4/4) The boundaries of the cluster are re-determined by the positions of the outermost pairs.
3. More than three unique hit small RNA sequences should be mapped within the cluster. (4/4)
4. More than 90% of the unique small RNA sequences should lie in the same orientation. (4/4)
5. More than 80% of small RNA sequences that constitute the cluster should be 19-23 nt in length. (4/4)

If only step 5 is applied to the 444 small RNA clusters, 106 meet its criterion. Thus, it is highly significant that all 4 clusters selected by steps 1-4 meet the criterion of step 5 ($P = 0.034$; χ^2 test). The low p-value at step 5 and absence of clusters that dropped off at steps 2-4 suggest that inverted-repeat structures are found only among the 19-23 nt small RNA clusters.

Selection procedure for trans-nat-siRNA cluster

1. Select pairs of clusters, in which the partner clusters share more than two small

RNAs unique to the pair. (43/444; 23 pairs) (Three of the 43 clusters paired with two clusters.)

2. In each cluster of a pair, more than 90 % of unique small RNAs should be derived from the same strand. (17/43; 9 pairs)

3. In each pair, the shared unique small RNAs identified in step 1 should lie in the same orientation as the other unique small RNAs in one cluster but should lie in the opposite orientation in the other cluster. (16/17; 8 pairs)

4. More than 80% of small RNA sequences that constitute the cluster should be 19-23 nt in length. (14/16; 7 pairs) ($P = 1.2 \times 10^{-8}$; χ^2 test)

The low p-value at step 4 and the fact that only one pair dropped off at step 3 suggest that the sense/antisense relationship is highly unique to the 19-23 nt small RNA clusters.

Selection procedure for cis-nat-siRNA cluster

1. Select clusters in which some unique small RNAs hit the sense strand while other unique small RNAs hit the antisense strand. [Number of sense (or antisense) unique small RNA sequences] / [Number of total unique small RNA sequences] should be between 0.25 and 0.75. (70/444)

2. The cluster should contain more than 10 small RNA sequences. (35/70)

3. More than 80% of small RNA sequences that constitute the cluster should be 19-23

nt in length. (17/35) ($P = 0.0013$; χ^2 test)

Some piRNA clusters contain both sense and antisense piRNAs, and therefore step 1 would select both piRNA and siRNA clusters. Step 3 was therefore designed to exclude piRNA clusters; however, some piRNA clusters were not filtered out due to the presence of only a small number of small RNA sequences. We therefore added step 2 to decrease the false positive rate. The low p-value at step 3 suggests that 19-23 nt small RNA clusters were enriched by steps 1 and 2.

Of the top 30 clusters in terms of the number of mapped small RNA species, 25 clusters were either piRNA clusters or one of three classes of siRNA cluster (hp-siRNA, trans-nat-siRNA or cis-nat-siRNA) (Supplementary Fig. 10).

Prediction of miRNA-type hairpin structure

To find miRNA-type hairpin structures, RNAsnp⁵ and randfold⁶ programs were used. The criteria used for selection were described previously⁷. After excluding the sequences that (1) completely match known miRNAs and (2) are annotated as r/t/sn/sno/sc/srpRNA, only 19-23 nt sequences that (1) were cloned more than three times and (2) hit the genome uniquely were used for this analysis. As a positive control, known miRNA loci registered in miRBase (Ref. 8) were used. As a negative control, randomly selected loci from the mouse genome were analyzed.

Oligo Sequences

Primer name	Sequence
<i>Primers used for expression analysis of small RNA pathway components</i>	
Dicer F	TGGCACCAGCAAGAGACTCA
Dicer R	CTGGGAGATGCGATTTTGGGA
Ago1 F	GGCATCTCAAGAATACCTACTCAG
Ago1 R	CTACCACTGCTGTGATAGATGGT
Ago2 F	TCAAGCTGGAGAAGGACTATCAGC
Ago2 R	TGATCTTCGTGTCCACGGTTGTG
Ago3 F	TCCCTGCACCAGCATATTACG
Ago3 R	TGTGGATCTCGCCCATTGC
Ago4 F	AGATAAAATGGAAAGGGTGGGG
Ago4 R	AATGTGAAGGACGGCTGGTTC
Actin F	CCACCACAGCTGAGAGGGAA
Actin R	AGCCACCGATCCACACAGAG
<i>Primers used for quantitative PCR of individual small RNAs</i>	
Universal primer F (5' linker sequence)	AAAGATCCTGCAGGTGCGTCA
Plant MIR164	TGCACGTGCCCTGCTTCT
let7f F	ACTATAACAATCTACTACCTCA
miR-16 F	GCCAATATTTACGTGCTGCTA

miR-103 F	CATAGCCCTGTACAATGCTGCT
miR-183 F	GTGAATTCTACCAGTGCCATA
25-26 nt small RNA1 F	GACTCTAGATACCGGGGTTCA
25-26 nt small RNA2 F	TGTCCTGCTACTCCGTGCCTA
25-26 nt small RNA3 F	AAGCCAGTCTAATAGCCACAA
25-26 nt small RNA4 F	TACCAATCCCAGCAATGCC
hp-siRNA1 F (21 nt small RNA1 F)	GCTCTAAGGGCACCGTT
hp-siRNA2 F (21 nt small RNA2 F)	ACAGCATCTGCGAAGGC
cis-nat-siRNA1 F (21 nt small RNA3 F)	ACCGCCTAAAGGTTTGTC

Primers used for 5'RACE analysis of cis-nat-siRNA clusters

Kif4 exon3 R	CTGCCCATAGGCCAGGACAGTTGCA
Kif4 exon2 R (for 2 nd PCR)	CCTGTTTCAGTAGAGGGGTCAAACACA
Pdzd11 exon3 R	CTGCCCATAGGCCAGGACAGTTGCA
Pdzd11 exon2 R (for 2 nd PCR)	GTCATCATAGGGAATCCGGTTGTCCA

Primers used for quantitative PCR of mRNAs and retrotransposons

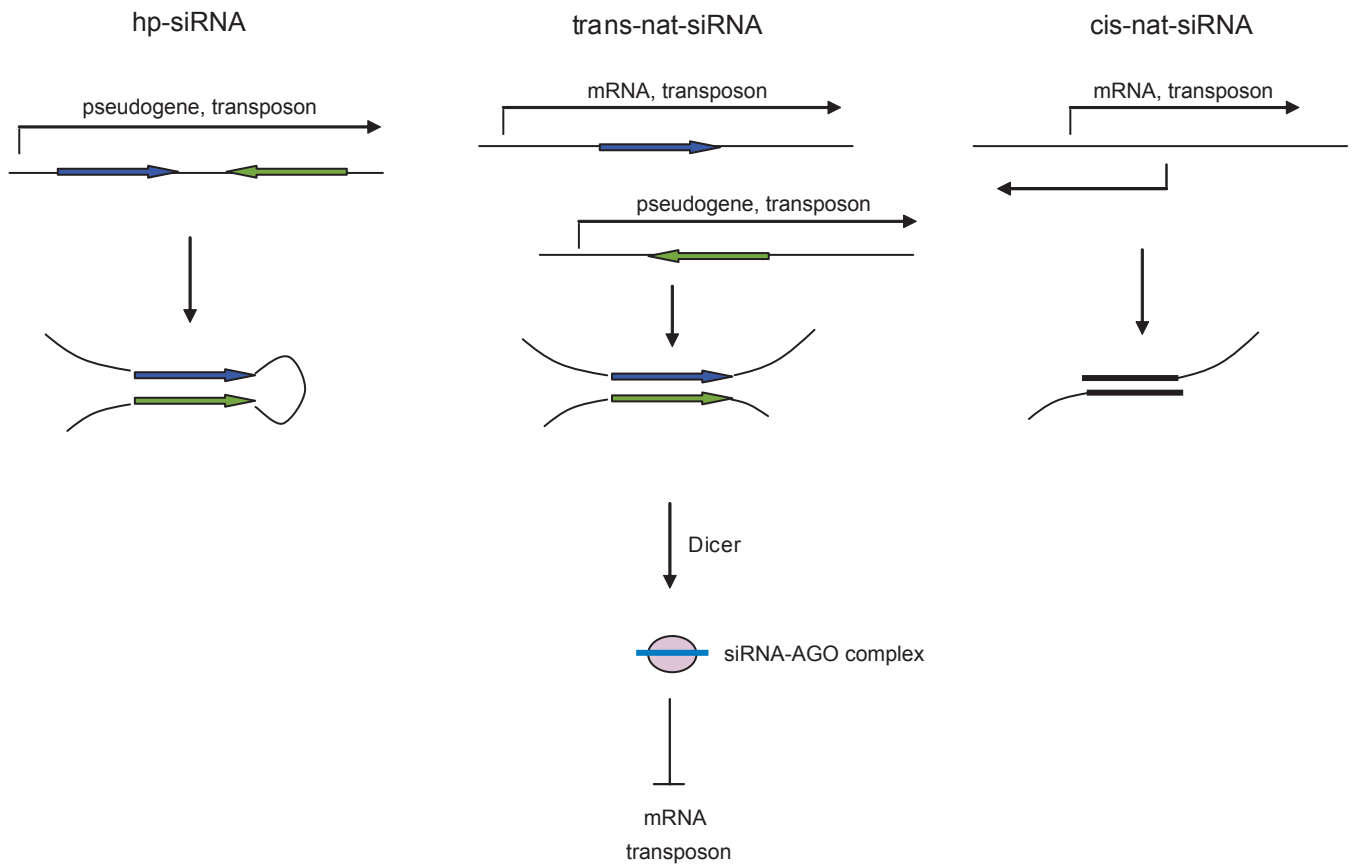
Rangap1 F	ATGGCTGAGACTCTGAAGACTCTG
Rangap1 R	ACGGACAGCATCTGCGATGGCAAC
Ppp4r F	CCTGCTCCAGTGGACAGCTCCT
Ppp4r R	GCAGACTTGCTGTTGGTGTCAG

Kif4 F	GTAAGAGTGGCACTGCGTTGTCG
Kif4 R	TAAAGACCTCTTCCTGTTTCAGTAGAG
Pdzd F	AAGCTGGCTAGACCTCTGAGA
Pdzd R	GAACTCCTAGTACAGTACAGT
Beta-actin F	ACAGCTTCTTTGCAGCTCCT
Beta-actin R	ATTCCCACCATCACACCCTG
GAPD F	ATGACATCAAGAAGGTGGTG
GAPD R	CATACCAGGAAATGAGCTTG
EGFP F	GAACCGCATCGAGCTGAAGG
EGFP R	CGGATCTTGAAGTTCACCTTGATGC
IAP1 F	ACAAGAAAAGAAGCCCGTGA
IAP1 R	GCCAGAACATGTGTCAATGG
L1Md F	GAGACATAACAACAGATCCTGA
L1Md R	GAACTTTGGTACCTGGTATCTG
RLTR10 F	GTGAAGGTAGAGGTCTGATC
RLTR10 R	GAAGGTATGTCTGATTGCATG
MTA F	ATGTCTTGGGGAGGACTGTG
MTA R	AGCCCCAGCTAACCAGAACT

Supplementary References

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7. Berezikov, E. et al. Diversity of microRNAs in human and chimpanzee brain. *Nat Genet* **38**, 1375-1377 (2006).
8. Griffiths-Jones, S., Grocock, R. J., van Dongen, S., Bateman, A. & Enright, A. J. miRBase: microRNA sequences, targets and gene nomenclature. *Nucleic Acids Res* **34**, D140-144 (2006).
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Supplementary Figure 1

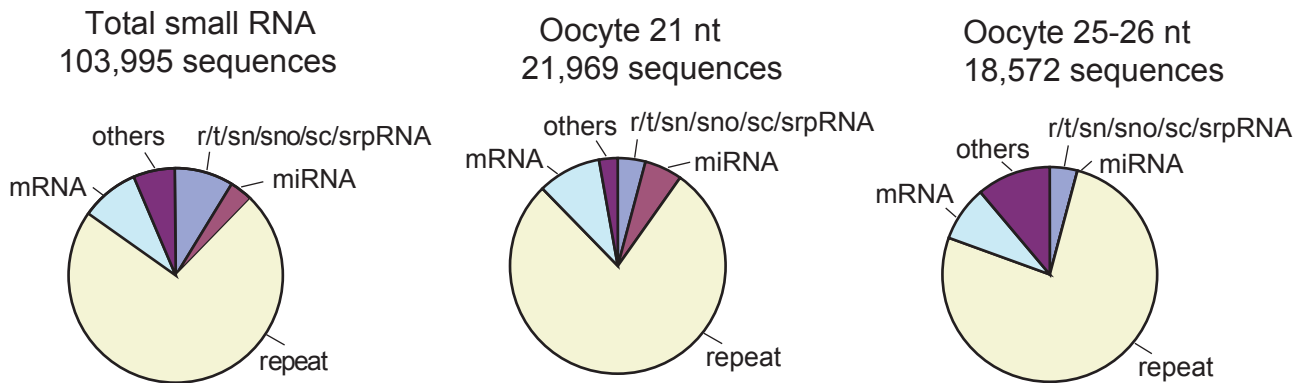


Supplementary Figure 1. siRNA pathways in mouse oocytes.

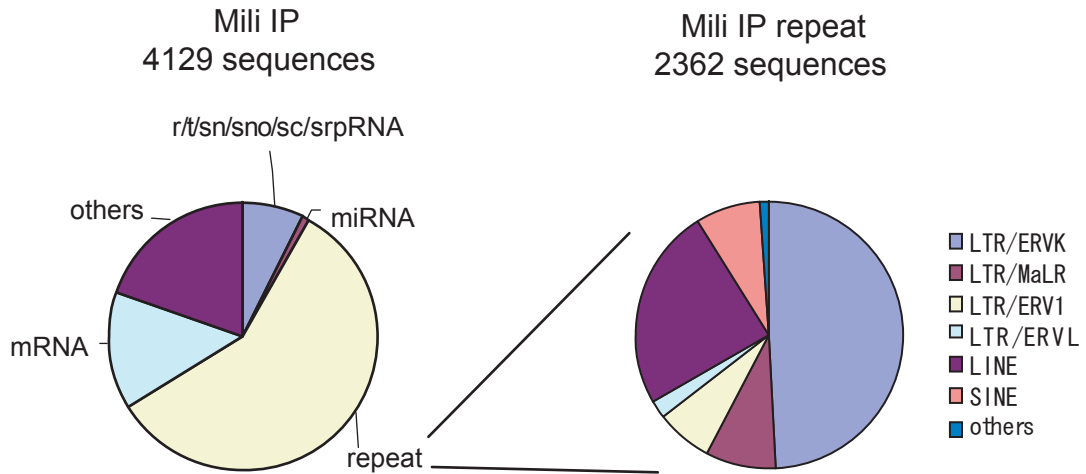
Double-stranded RNAs, which are the precursors of siRNAs, are produced in three different ways. Blue and green arrows indicate homologous sequences oriented in opposite directions.

Supplementary Figure 2

a



b

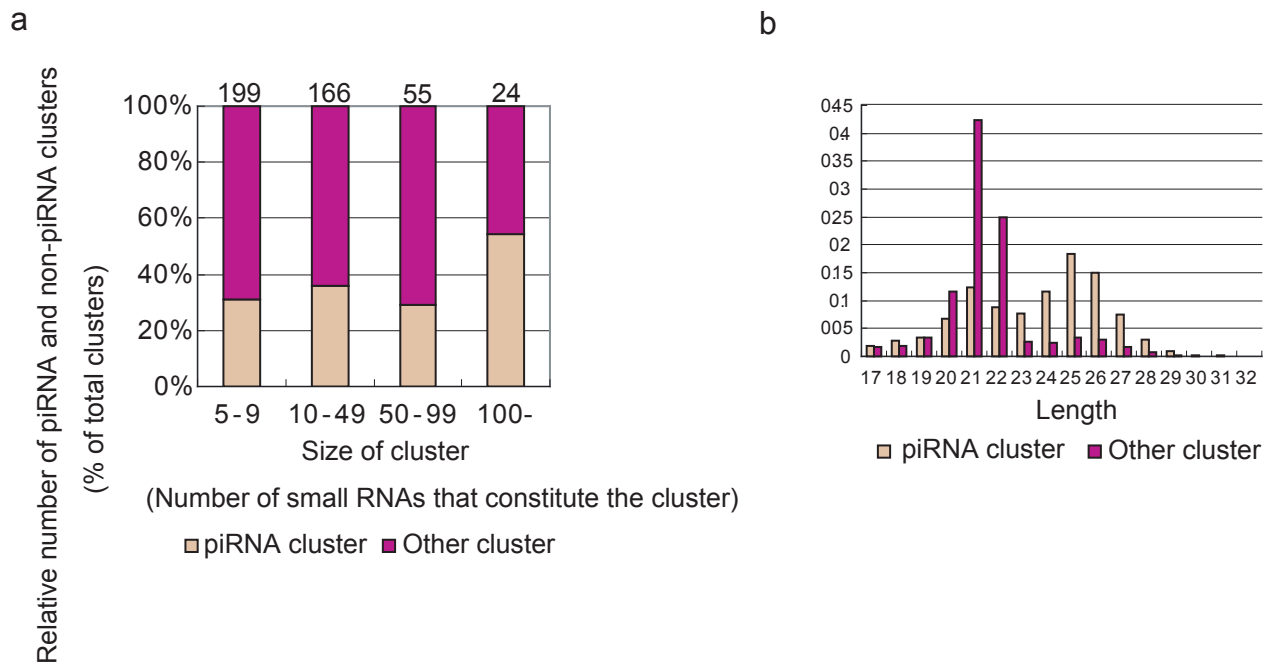


Supplementary Figure 2. Annotation of small RNAs.

(a) Annotation of total (left), 21 nt (middle) and 25-26 nt (right) small RNAs from growing oocytes.

(b) Annotation of Mili-IP small RNAs from P8 ovaries.

Supplementary Figure 3

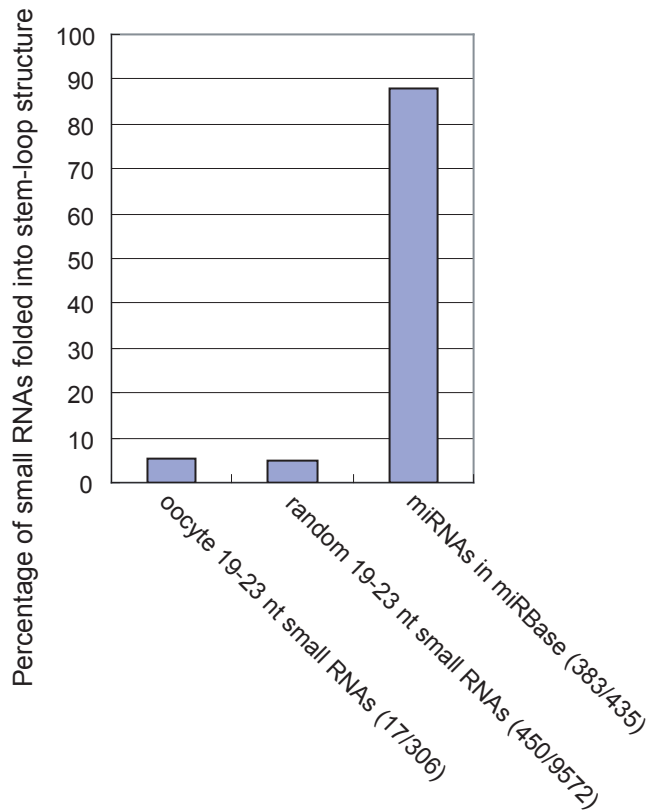


Supplementary Figure 3. piRNA clusters and 21 nt small RNA clusters.

(a) The ratio of the number of piRNA clusters to that of the other small RNA clusters in oocytes. About half of the clusters with more than 100 mapped small RNAs were non-piRNA clusters. The numbers above the bars denote the total number of clusters of the indicated size.

(b) The length distribution of small RNAs that constitute piRNA and other clusters. The small RNAs from the piRNA clusters showed two peaks: the one at 21 nt is due to the fact that some piRNA clusters contain siRNAs (for example, see Supplementary Figure 7).

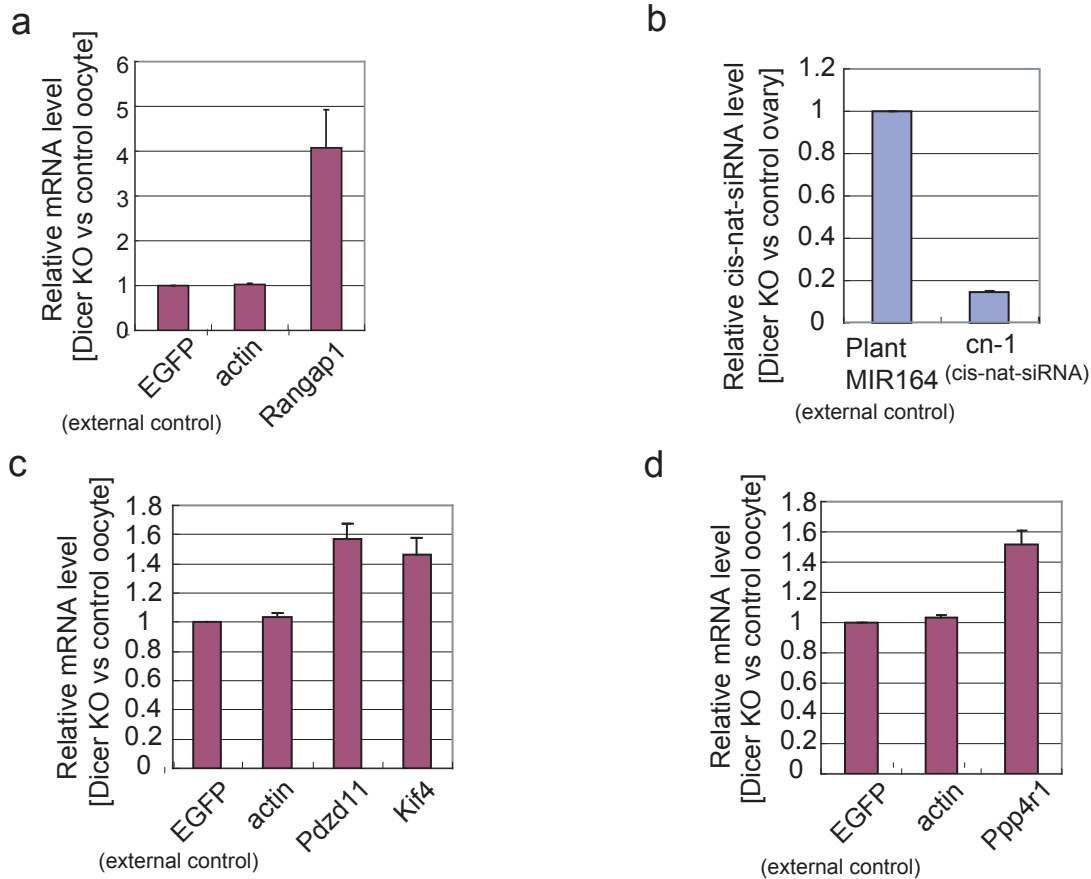
Supplementary Figure 4



Supplementary Figure 4. Most of the genomic sequences encompassing 19-23 nt small RNAs from growing oocytes do not form an miRNA-type hairpin structure.

The RNAshapes program and randfold program were used to predict whether sequences form an miRNA-type hairpin structure. miRNA sequences registered in miRBase and 19-23 nt sequences randomly retrieved from the mouse genome were also analyzed as positive and negative controls respectively. The number of sequences with a hairpin structure and the total number of analyzed sequences are shown in parentheses.

Supplementary Figure 5



Supplementary Figure 5. Dicer-dependent regulation of target mRNAs and Dicer-dependent accumulation of cis-nat-siRNAs.

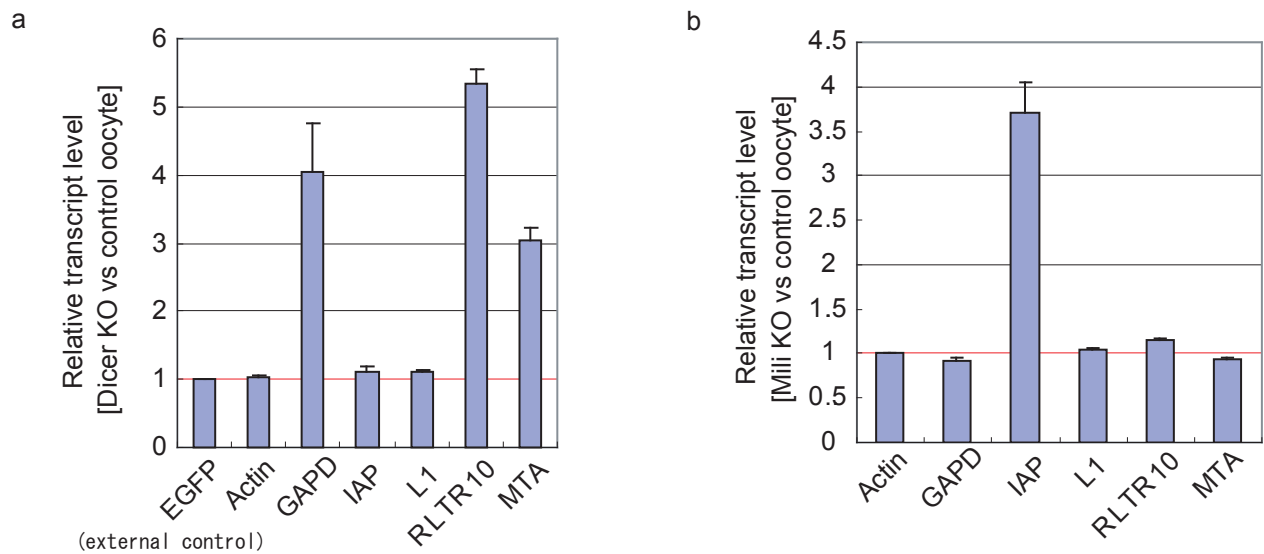
(a) Quantitative RT-PCR analysis of Rangap1, the founding source gene of Au76, in conditional Dicer KO oocytes. Error bars represent S.E. (n=3). The amounts of the EGFP (external control), actin (internal control) and Rangap1 mRNAs in conditional Dicer KO oocytes were divided by those in oocytes that do not express Cre recombinase.

(b) Quantitative RT-PCR analysis of a cis-nat-siRNA derived from Pdzd11/Kif4 locus in conditional Dicer KO ovaries. The amounts of this RNA in conditional Dicer KO ovaries relative to those in ovaries that do not express Cre recombinase are shown. MIR164 served as an external control. Error bars represent S.D. (n=3). Amplified products were sequenced and confirmed.

(c) Quantitative RT-PCR analysis of Pdzd11 and Kif4. Error bars represent S.E. (n=3). The amounts of EGFP (external control), actin (internal control), Pdzd11 and Kif4 mRNAs in conditional Dicer KO oocytes were divided by those in oocytes that do not express Cre recombinase.

(d) Quantitative RT-PCR analysis of Ppp4r1 mRNA. Error bars represent S.E. (n=3). The amounts of EGFP (external control), actin (internal control) and Ppp4r1 mRNAs in conditional Dicer KO oocytes were divided by those in oocytes that do not express Cre recombinase.

Supplementary Figure 6

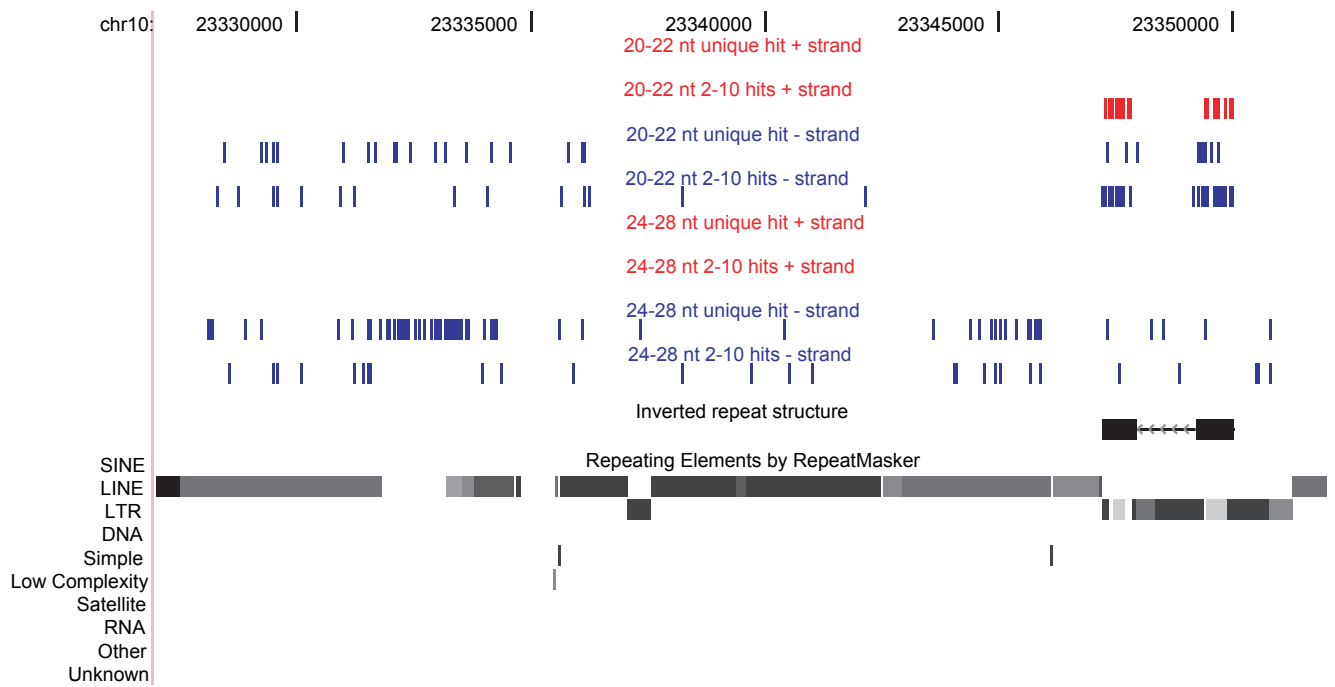


Supplementary Figure 6. Both piRNA and siRNA pathways repress retrotransposons. Recently, Murchison et al. reported that some retrotransposons were activated in conditional Dicer KO oocytes⁹, while Tang et al. reported that retrotransposons were unchanged in the same mutants¹⁰. They examined fully grown oocytes and MII oocytes, respectively, and used beta-actin and Gapdh as an internal control, respectively. We used an external control to exclude the possible misinterpretation of the results due to a change in expression of the internal control transcripts by Dicer KO. In addition, we examined earlier stage (growing stage) oocytes to minimize the secondary effects caused by the mutation.

(a) Quantitative RT-PCR analysis of some retrotransposons in Dicer KO oocytes. Error bars represent S.E. (n=4). Oocytes that did not express Cre recombinase were used as controls. As an external control, a certain amount of EGFP mRNA was added per oocyte before isolation of total RNAs. The values were normalized by the relative level of EGFP mRNA. Note that small RNAs corresponding to GAPD were found in the oocyte small RNA library (data not shown).

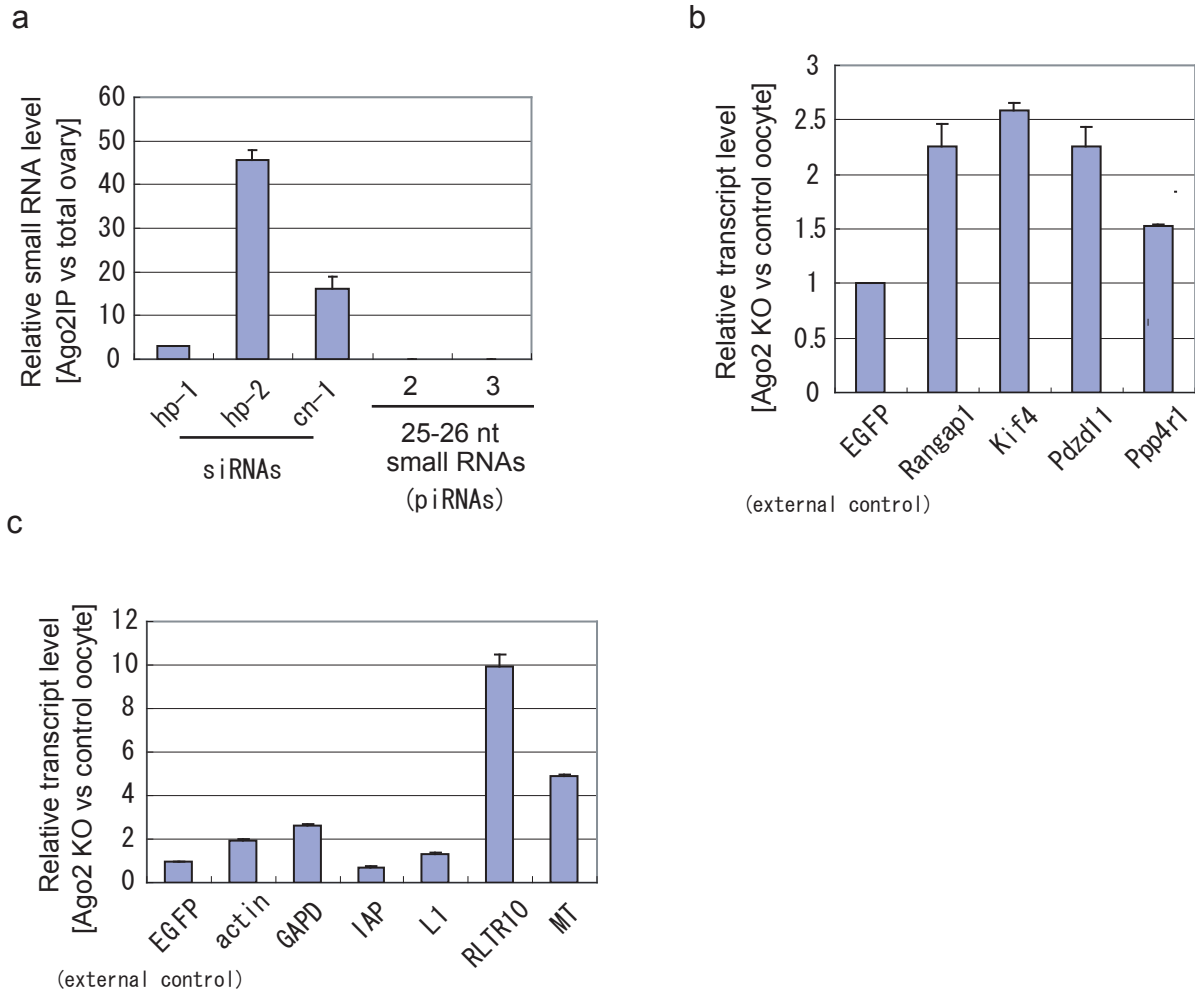
(b) Quantitative RT-PCR analysis of some retrotransposons in Mili KO oocytes. Error bars represent S.E. (n=4). Mili +/- oocytes were used for controls. The values were normalized by the relative level of beta-actin mRNA.

Supplementary Figure 7



Supplementary Figure 7. A peculiar cluster in which both siRNAs and piRNAs are mapped. The small RNAs mapped in this region are represented by red (plus-strand) or blue (minus-strand) bars. Small RNAs that hit the genome only once and those that hit the genome 2-10 times are indicated in different rows. The thick black bars represent the inverted repeat structure that constitutes the stem of a hairpin predicted by Mfold. Repeat elements identified by RepeatMasker are also shown.

Supplementary Figure 8



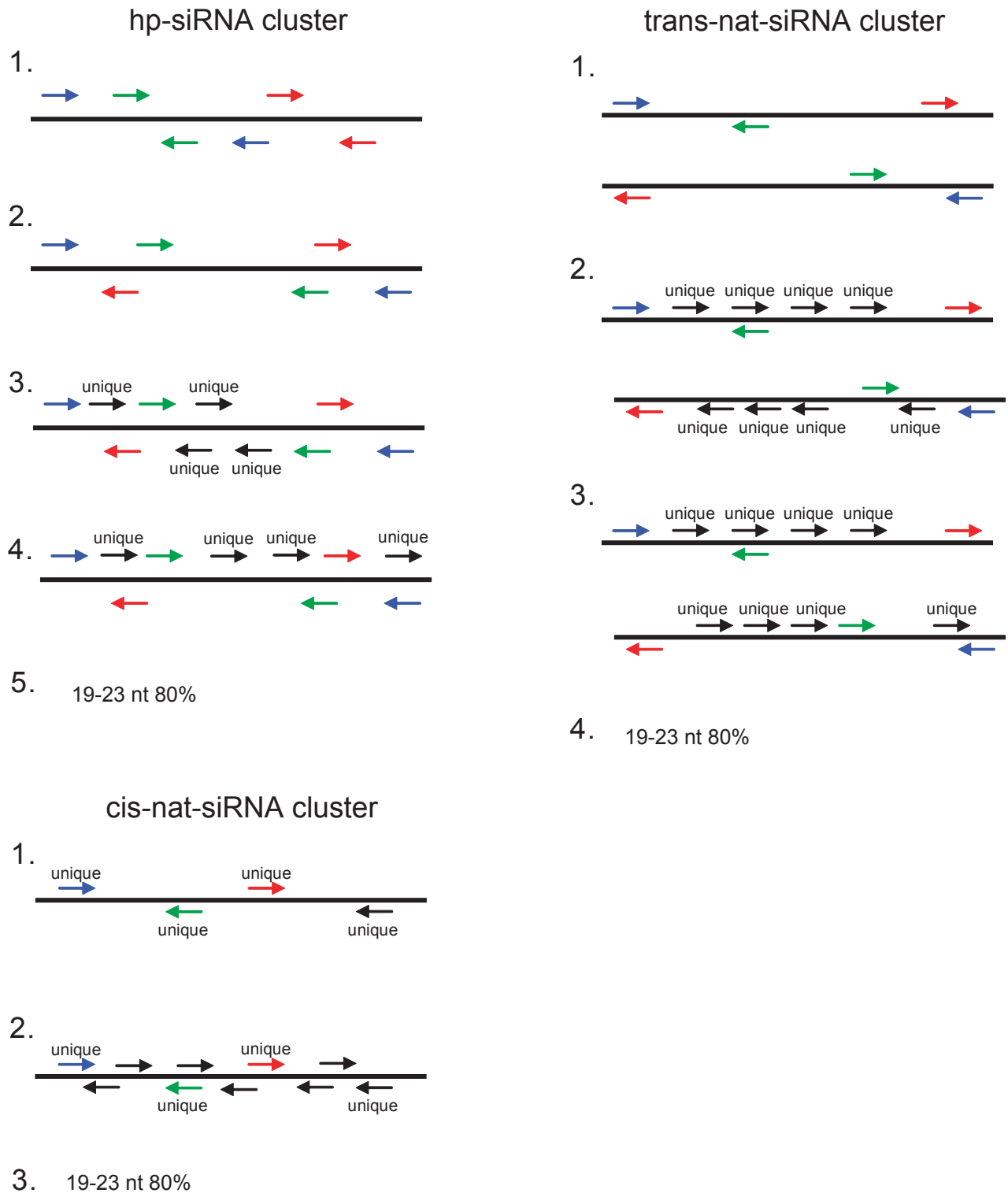
Supplementary Figure 8. Ago2-dependent regulation of mRNAs and retrotransposons by endogenous siRNAs.

(a) Quantitative RT-PCR analysis of selected endogenous siRNAs and piRNAs in total and Ago2-IP small RNAs from P8 ovaries. The amount of each RNA species in the Ago2-IP library was divided by that in the total small RNA library. Experiments were repeated three times. Some piRNAs were also tested but were undetectable in the Ago2-IP library. Amplified products were sequenced and confirmed to have the correct sequences. Error bars represent S.D. (n=3)

(b) Quantitative RT-PCR analysis of target mRNAs in Ago2 KO oocytes. Error bars represent S.E. (n=3). The amounts of EGFP (external control), Rangap1, Kif4, Pdzd11 and PPP4r1 mRNAs in conditional Ago2 KO oocytes were divided by those in oocytes that did not express Cre recombinase.

(c) Quantitative RT-PCR analysis of some retrotransposons in Ago2 KO oocytes. Error bars represent S.E. (n=3). The amounts of EGFP (external control), beta-actin and retrotransposons in conditional Ago2 KO oocytes were divided by those in oocytes that did not express Cre recombinase.

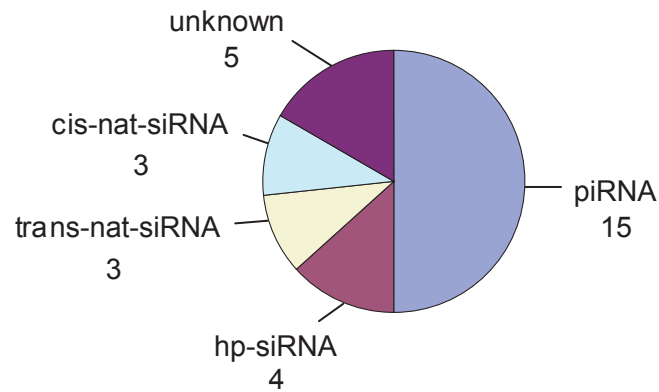
Supplementary Figure 9



Supplementary Figure 9. Diagrams showing the type of clusters selected at each filtering step of the bioinformatics siRNA cluster selection.

Arrows indicate small RNAs mapped to the region. The homologous small RNAs in a cluster are indicated in the same color (blue, green and red arrows in hp-siRNA and trans-nat-siRNA clusters). The small RNAs that uniquely hit the genome are indicated as “unique” above the arrows.

Supplementary Figure 10



Supplementary Figure 10. Classification of top 30 clusters.

The top 30 largest clusters, in terms of the number of small RNA species mapped within the respective cluster, are classified according to the class of small RNAs and the origin of siRNA precursors. When a cluster was annotated as both piRNA and siRNA clusters, we designated this cluster as an siRNA cluster. We analyzed only the top 30 largest clusters, because most of the smaller clusters did not meet the criteria due to the small number of unique small RNAs that constituted the clusters.

Supplementary Table 1. Annotation of small RNAs

RNA class	No. of reads (%)					
	oocyte total	oocyte 20- 22 nt	oocyte 25- 27 nt	Mili IP	Mili IP 20- 22 nt	Mili IP 25-27 nt
rRNA	5047 (5)	1593 (3)	558 (2)	143 (3)	34 (7)	15 (0.8)
tRNA	3767 (4)	978 (2)	440 (2)	154 (4)	17 (3)	39 (2)
sn_snoRNA	395 (0.4)	128 (0.3)	59 (0.3)	21 (0.5)	3 (0.6)	2 (0.1)
sc_srpRNA	119 (0.1)	43 (0.1)	26 (0.1)	13 (0.3)	2 (0.4)	3 (0.2)
miRNA	3587 (3)	2815 (6)	1 (0)	34 (0.8)	25 (5)	0 (0)
pachytene piRNA ¹	104 (0.1)	50 (0.1)	20 (0.1)	8 (0.2)	0 (0)	6 (0.3)
mRNA	9420 (9)	4445 (11)	1872 (8)	609 (15)	80 (16)	284 (15)
repeat	74989 (72)	35488 (96)	18035 (77)	2362 (57)	272 (56)	1128 (80)
unknown ²	6567 (6)	1419 (3)	2482 (11)	785 (19)	55 (11)	403 (21)
total	103995 (100)	46959 (100)	23493 (100)	4129 (100)	488 (100)	1880 (100)

1 This class represents small RNAs that are annotated as piRNA in mouse adult testis.

2 This class represents small RNAs that are not classified in any other classes.

Supplementary Table 2. Annotation of repeat small RNAs

class	subclass	Number of clones (growing oocytes)				Number of clones (Milli IP)					
		Total	20-22 nt +	20-22 nt -	25-27 nt +	25-27 nt -	Total	20-22 nt +	20-22 nt -	25-27 nt +	25-27 nt -
DNA/MER1_type	MER5A	6				1				1	
DNA/MER1_type	URR1A	6				3				1	
DNA/MER1_type	RCHARR1	4				3				1	
DNA/MER1_type	URR1B	4			1	2				1	
DNA/MER1_type	Charlie5	3	1								
DNA/MER1_type	RMER30	2	1		1						
DNA/MER1_type	Charlie8	1									
DNA/MER1_type	MER112	1									
DNA/MER1_type	MER20	1	1								
DNA/MER1_type	MER58B	1			1						
DNA/MER1_type	MER5A1	1	1								
DNA/MER1_type	MER5B	1								1	
DNA/MER1_type	Charlie1									1	
DNA/MER1_type	MER2									1	
DNA/MER1_type total		31	4	0	3	9	7	0	0	1	2
DNA/MER2_type	MER44A	2									
DNA/MER2_type	MER82	2									
DNA/MER2_type	Tigger7	2									
DNA/MER2_type	MER2	1			1						
DNA/MER2_type	Tigger5	1			1						
DNA/MER2_type total		8	0	0	2	0	0	0	0	0	0
DNA/Tip100	Arthur1	1									
DNA/Tip100	MER115	1									
DNA/Tip100	FordPrefect						1				
DNA/Tip100 total		2	0	0	0	0	1	0	0	0	0
LINE/CR1	L3	4			1						
LINE/CR1	L3_Mars	3			2						
LINE/CR1	L3b	1									
LINE/CR1 total		8	0	0	3	0	0	0	0	0	0
LINE/L1	L1Md_F2	7100	1123	1445	718	1431	161	10	22	19	44
LINE/L1	L1Md_A	2640	539	487	427	352	111	10	2	23	33
LINE/L1	L1Md_T	2408	381	618	393	315	79	6	8	15	21
LINE/L1	L1Md_Gf	949	254	261	123	37	38	1	3	9	3
LINE/L1	L1_Mus1	783	110	73	136	206	33			3	10
LINE/L1	L1Md_F	751	82	147	78	207	31	1	2	2	13
LINE/L1	L1_Mus2	496	31	53	62	194	30			1	17
LINE/L1	L1Md_F3	393	35	61	43	110	9	1		3	2
LINE/L1	L1_Mus3	353	37	48	54	83	10		2	3	1
LINE/L1	Lx	183	14	16	31	64	5				2
LINE/L1	L1_Mm	125	8	20	13	51	5				4
LINE/L1	Lx8	79	2	5	4	8	11			2	2
LINE/L1	L1_Mur1	41	1		1	25	1	1			
LINE/L1	MusHAL1	38	2	4	3	8	5			1	2
LINE/L1	Lx5	36	3	3	12	3	5	1		1	
LINE/L1	L1_Mus4	35	4	5	10	6	2			1	
LINE/L1	L1VL1	32	10	2	9	6	1			1	
LINE/L1	L1VL2	32	10		7	4	5			1	2
LINE/L1	L1_Mur3	30	1	2		6	3				1
LINE/L1	L1VL4	29	6	2	3	5	2			1	
LINE/L1	L1_Mur2	28	1		9	5	1				
LINE/L1	Lx3_Mus	22	7	1	3	5	3		2		
LINE/L1	Lx2	21	1	2	4	3	2			1	
LINE/L1	Lx9	20	2	1	2	4					
LINE/L1	L1_Rod	18					1				1
LINE/L1	Lx2B	17	1	2	2	1					
LINE/L1	Lx4B	14									
LINE/L1	Lx7	14	2	1	2	1	1				
LINE/L1	Lx4A	11			2						
LINE/L1	L1M5	10		3							
LINE/L1	Lx6	10	1	1	2	2					
LINE/L1	L1M2	9		1	1	3					
LINE/L1	Lx2A1	8				2					
LINE/L1	Lx3B	8	1	1	1						
LINE/L1	Lx3A	7	1		2						
LINE/L1	Lx3C	7		1		1	1				
LINE/L1	L1MA8	4			1	2					
LINE/L1	L1MCA	4				2					
LINE/L1	L1MA6	3			1	1	1				

LINE/L1	L1MCb	3									
LINE/L1	L1MD	3				1		1		1	
LINE/L1	L1M3	2						1			
LINE/L1	L1M4	2			1						
LINE/L1	L1MA4	2									
LINE/L1	L1MB4	2			1						
LINE/L1	L1MDa	2									
LINE/L1	L1ME1	2			2						
LINE/L1	L1MEe	2	1								
LINE/L1	L1M	1				1					
LINE/L1	L1M4c	1									
LINE/L1	L1MA5	1				1					
LINE/L1	L1MA5A	1									
LINE/L1	L1MA7	1									
LINE/L1	L1MB5	1									
LINE/L1	L1MB7	1									
LINE/L1	L1MC	1									
LINE/L1	L1MC4	1			1						
LINE/L1	L1MD2	1									
LINE/L1	L1ME3	1									
LINE/L1	L1ME3B	1									
LINE/L1	Lx2A	1	1								
LINE/L1	L1MB3							2			
LINE/L1 total		16801	2672	3266	2164	3156	561	32	41	87	158
LINE/L2	L2	39	16	1	6	4	2	1	1		
LINE/L2 total		39	16	1	6	4	2	1	1	0	0
LINE/RTE	L4						1				1
LINE/RTE total		0	0	0	0	0	1	0	0	0	1
Low_complexity	CT-rich	15	1			2					
Low_complexity	G-rich	12	3	4							
Low_complexity	GA-rich	10		1			1			1	
Low_complexity	GC-rich	9	1	5		1					
Low_complexity	C-rich	7	2	1							
Low_complexity	AT-rich	3				1					
Low_complexity total		56	7	11	0	4	1	0	0	1	0
LTR/ERV1	LTRIS_Mm	2590	883	969	32	88	11		1		3
LTR/ERV1	LTRIS_Mm-int	1806	358	390	152	367	47		2		22
LTR/ERV1	LTRIS_Mus	1001	389	298	41	35	5	1	1		1
LTR/ERV1	LTRIS_Mus-int	623	63	121	25	273	5	1			3
LTR/ERV1	RLTR6_Mm	271		2							
LTR/ERV1	RLTR6_Mm-int	217	1	15	4	104	13	1	2		4
LTR/ERV1	RLTR5_Mm-int	173	1	11		100	10				5
LTR/ERV1	MuRRS-int	88	16	14	4	24					
LTR/ERV1	MURVY-LTR	78		11		35	12		1		8
LTR/ERV1	MuRRS4-int	69	12	11	9	17	2				
LTR/ERV1	MURVY-int	58		8	11	27	11		2	3	3
LTR/ERV1	RLTR5_Mm	52		10		21	8				2
LTR/ERV1	LTRIS2	43		23		14	1				1
LTR/ERV1	RLTR4_Mm-int	38	7	1	17	1	3			3	
LTR/ERV1	RodERV21	37		5		15	3			1	
LTR/ERV1	RLTR1B	26	2	2		16	7				4
LTR/ERV1	RLTR14-int	24	1		12	9	1			1	
LTR/ERV1	RLTR6-int	22		2		16	2				
LTR/ERV1	MMERGLN-int	16		4		5	5				4
LTR/ERV1	RLTR1B-int	14	1	2	4	1					
LTR/ERV1	LTRIS2-int	7									
LTR/ERV1	RLTR4_Mm	7	5	1							
LTR/ERV1	RMER2	6	1		1	2					
LTR/ERV1	MMVL30-int	5			1	2	4				2
LTR/ERV1	LTRIS4-int	4		3		1					
LTR/ERV1	MER52-int	4		1		2					
LTR/ERV1	MuLV-int	4			2						
LTR/ERV1	MER21B	3					2				2
LTR/ERV1	RLTR23	3		1		1					
LTR/ERV1	LTR37B-int	2	2								
LTR/ERV1	LTRIS3	2			1						
LTR/ERV1	RLTR1	2									
LTR/ERV1	RMER5	2			1		1				
LTR/ERV1	LTRIS4	1		1							
LTR/ERV1	MER31-int	1			1						
LTR/ERV1	RLTR14	1				1					

LTR/ERV1	RLTR1C	1				1						
LTR/ERV1	RLTR1D-int	1										
LTR/ERV1	RMER21B	1					1			1		
LTR/ERV1	RMER5-int	1	1									
LTR/ERV1	MER67B						1			1		
LTR/ERV1	RLTR24						1			1		
LTR/ERV1 total		7304	1742	1907	318	1178	156	3	9	11	64	
LTR/ERVK	RLTR10-int	4557	1238	551	1192	138	256	23	7	118	12	
LTR/ERVK	IAPLTR1a_Mm-int	4021	914	598	1228	123	123	9	8	44	10	
LTR/ERVK	IAPLTR1_Mm-int	2910	698	287	975	66	200	22	5	102	2	
LTR/ERVK	RLTR10	1679	446	309	351	71	63	5	5	31	2	
LTR/ERVK	MMERVK10C	1140	333	199	170	151	73	2	2	12	23	
LTR/ERVK	IAP-d	606	113	176	55	92	35	1	3	1	14	
LTR/ERVK	IAPLTR2_Mm-int	603	62	156	105	99	24		2	7	7	
LTR/ERVK	IAPLTR2_Mm	462	53	115	39	118	16			3	4	
LTR/ERVK	RLTR10A	390	37	136	25	36	9	1	1		2	
LTR/ERVK	RLTRETN_Mm-int	367	40	54	45	102	34	1	3	6	15	
LTR/ERVK	IAPEz-int	342	72	70	71	24	14			5	7	
LTR/ERVK	IAPLTR1_Mm	334	79	76	54	15	15	1		8	1	
LTR/ERVK	RMER17A2	314	27	26	70	59	20	2	1	4	6	
LTR/ERVK	RLTR10B2	283	4	58	1	143	14		3		6	
LTR/ERVK	RLTR10A-int	222	47	47	43	24	10	3	1	2		
LTR/ERVK	IAPLTR1a_Mm	221	50	27	44	14	5		1	2	2	
LTR/ERVK	RLTRETN_Mm	207	22	41	4	57	14		2	1	5	
LTR/ERVK	ETnERV	204	15	35	11	63	30				19	
LTR/ERVK	IAPEY3-int	190	15	23	25	68	13		2		5	
LTR/ERVK	IAPLTR2b-int	172	19	57	18	28	6	1	1		4	
LTR/ERVK	RLTR27	132	1	13		78	7		1		5	
LTR/ERVK	RLTR22_Mus	118	18	12	49	8	19		1	6	4	
LTR/ERVK	MERVK26	112		17		45	10				6	
LTR/ERVK	RLTR10C	111	16	28	5	22	3			1		
LTR/ERVK	RMER19A	110	12		52	1	5			4		
LTR/ERVK	RLTR9E	76	1	10	1	36	9		2		5	
LTR/ERVK	RLTR13B1	65	2	10		25	9				6	
LTR/ERVK	MurERV4	61		16		30	10		1		4	
LTR/ERVK	RLTR13D5	54		5	1	34	9				7	
LTR/ERVK	ETnERV2	51	1	6	7	18	7	1			3	
LTR/ERVK	RMER17B	50		9	4	22	6				4	
LTR/ERVK	RLTR10D	48	1	6		28	6				2	
LTR/ERVK	IAPEY_LTR-int	44	1	7	3	21	10	1			5	
LTR/ERVK	RMER4B	44	28	6		4						
LTR/ERVK	MurERV4_19	39	4		17							
LTR/ERVK	RLTR9A	38		3		20	10		1		7	
LTR/ERVK	IAPLTR2b	34	3	7	4	5	3	1				
LTR/ERVK	RLTR19-int	33	4		16		4			2		
LTR/ERVK	IAPLTR2a-int	29	6	7	5	1	1			1		
LTR/ERVK	RMER4A	29	22	1	2							
LTR/ERVK	RLTR22_Mur	28	1	3	15	2						
LTR/ERVK	RLTR44E	26		3		18	4				4	
LTR/ERVK	IAPLTR4_I	25		11		6	1		1			
LTR/ERVK	IAPLTR3-int	24	2	3		6	6		1		1	
LTR/ERVK	RMER16	24		7		10	3				2	
LTR/ERVK	RMER19B	22	6		6	3	3			1		
LTR/ERVK	RLTR45	20		1		11						
LTR/ERVK	RLTR9D	19	1	3		7	1					
LTR/ERVK	RLTR21	18		1		10	2					
LTR/ERVK	RMER16-int	17	1	2	2	5	3				1	
LTR/ERVK	IAPEY3_LTR	15	2	6		3	1				1	
LTR/ERVK	IAPEY2_LTR-int	14		3		9	4				3	
LTR/ERVK	RLTR13A3	14	1	1		8						
LTR/ERVK	RLTR45-int	13	1		4	3						
LTR/ERVK	MMETn-int	11	1	3	1	5						
LTR/ERVK	BGLII_B	10	1			5	3				2	
LTR/ERVK	IAPEY2_LTR	10				4	1					
LTR/ERVK	IAPEY3_LTR-int	10	2	1	1	2	4		1		2	
LTR/ERVK	IAPLTR2a	10	1	3	1	3						
LTR/ERVK	RLTR10E	10	1			6	1				1	
LTR/ERVK	RMER17A	10		2		4						
LTR/ERVK	RLTR16	9			1							
LTR/ERVK	RMER17D	9	1		2	3						
LTR/ERVK	RMER19C	9	1		3	1	2	1		1		

LTR/ERVK	MYSERV	8	2	4					
LTR/ERVK	IAPLTR3	7	3	2	1				
LTR/ERVK	MYSERV16_I	7	1	3					
LTR/ERVK	RLTR8	7	4			2			
LTR/ERVK	RMER13B	7		2	1				
LTR/ERVK	ETnERV3	6		1	1				
LTR/ERVK	IAPLTR4-int	6	4	1					
LTR/ERVK	MYSERV6	6	1	1			1		
LTR/ERVK	RLTR17	6		1	1				
LTR/ERVK	RMER17C	6	2	1		1			
LTR/ERVK	BGLII	5	3	1					
LTR/ERVK	RLTR13B4	5		1	3				
LTR/ERVK	RLTR13D6	5	1	1	1		2		2
LTR/ERVK	RLTR44-int	5			1				
LTR/ERVK	RMER20B	5		1	1				
LTR/ERVK	IAPLTR4	4		1	1	1			
LTR/ERVK	RLTR13C2	4	1	2		1	1		1
LTR/ERVK	RLTR15	4			1				
LTR/ERVK	RLTR25A	4			2				
LTR/ERVK	RLTR27-int	4		1	1				
LTR/ERVK	RLTR42-int	4	1		2	1	1		
LTR/ERVK	RLTR44A-int	4	1			2			
LTR/ERVK	RLTR44C	4		1					
LTR/ERVK	RLTR46-int	4	3	1			1		
LTR/ERVK	RMER12	4	1		2				
LTR/ERVK	RMER13A	4	1				1		1
LTR/ERVK	RMER17D2	4		1		3	1		1
LTR/ERVK	RMER6D	4	4						
LTR/ERVK	RLTR12B	3			1				
LTR/ERVK	RLTR13A2	3				1			
LTR/ERVK	RLTR20A2	3							
LTR/ERVK	RLTR25B	3		1					
LTR/ERVK	RLTR31B_Mm	3	1		1				
LTR/ERVK	BGLII-int	2							
LTR/ERVK	RLTR12A	2							
LTR/ERVK	RLTR13D1	2					2		
LTR/ERVK	RLTR19	2							
LTR/ERVK	RLTR20A	2			1				
LTR/ERVK	RLTR20B3	2	1						
LTR/ERVK	RLTR31A_Mm	2	1						
LTR/ERVK	RLTR3_Mm-int	2		1					
LTR/ERVK	RLTR44B	2				1			
LTR/ERVK	RLTR44E-int	2					1		1
LTR/ERVK	RLTR9C	2			1				
LTR/ERVK	RNERVK23	2			1				
LTR/ERVK	BGLII_A	1							
LTR/ERVK	BGLII_B-int	1							
LTR/ERVK	BGLII_Mus	1			1				
LTR/ERVK	RLTR10B	1							
LTR/ERVK	RLTR11A	1	1						
LTR/ERVK	RLTR11B	1					1		1
LTR/ERVK	RLTR13A	1				1			
LTR/ERVK	RLTR13B2	1							
LTR/ERVK	RLTR13D3	1							
LTR/ERVK	RLTR13D4	1							
LTR/ERVK	RLTR19B	1							
LTR/ERVK	RLTR20A1	1			1				
LTR/ERVK	RLTR20D	1					1		1
LTR/ERVK	RLTR26	1				1			
LTR/ERVK	RLTR31_Mur	1							
LTR/ERVK	RLTR42	1							
LTR/ERVK	RLTR44A	1					1		1
LTR/ERVK	RLTR44B-int	1	1						
LTR/ERVK	RLTR44D	1			1				
LTR/ERVK	RLTR9A2	1					1		
LTR/ERVK	RLTR9B	1					1		
LTR/ERVK	RLTR9F	1	1						
LTR/ERVK	RMER12B	1							
LTR/ERVK	RMER17B-int	1							
LTR/ERVK	RMER6B	1							
LTR/ERVK	SRV_MM-int	1							

LTR/ERVK	RMER17C-int					2		1			
LTR/ERVK	IAPEYLTR					1		1			
LTR/ERVK	RLTR20C					1					
LTR/ERVK	RLTR13C1					1		1			
LTR/ERVK total		21087	4466	3272	4759	2052	1158	75	59	366	226
LTR/ERVL	MT2_Mm	535	116	85	99	62	32	2		13	3
LTR/ERVL	MERVL-_Mm	347	54	61	87	42	12	2		2	
LTR/ERVL	MT2C_Mm	258	12	67	8	103	7		2	1	1
LTR/ERVL	RMER15-int	15				8	1				
LTR/ERVL	MT2A	12	2		1	2	1				1
LTR/ERVL	RMER15	9	2	1		2					
LTR/ERVL	MERVL	8	2	1	1	2					
LTR/ERVL	MERVL-C_Mm	6		1	1						
LTR/ERVL	MT2B2	6	2	1	1	1					
LTR/ERVL	MERVL-A	5	2	1							
LTR/ERVL	MT2B	4	1	2							
LTR/ERVL	MERVL-B	3			3						
LTR/ERVL	MERVL_2A	3		1			1				
LTR/ERVL	RLTR28	3									
LTR/ERVL	RMER10B	3	3								
LTR/ERVL	MER54A	2									
LTR/ERVL	MER70B	2									
LTR/ERVL	MER74A	2				1					
LTR/ERVL	MLT2B4	2		1	1						
LTR/ERVL	ERVL	1									
LTR/ERVL	ERVL-B4	1									
LTR/ERVL	HERV16	1			1						
LTR/ERVL	HERV40	1									
LTR/ERVL	LTR16A1	1									
LTR/ERVL	LTR16C	1									
LTR/ERVL	LTR16D	1				1					
LTR/ERVL	LTR40a	1				1					
LTR/ERVL	MER68	1									
LTR/ERVL	MERVL-B4	1				1					
LTR/ERVL	RMER10A	1									
LTR/ERVL total		1236	196	222	203	226	54	4	2	16	5
LTR/MaLR	MTA_Mm-int	7813	3021	1409	1213	124	87	10	12	21	7
LTR/MaLR	MTC	7620	142	6949	13	8	2				
LTR/MaLR	MTA_Mm	7418	2252	1748	949	377	58	1	2	27	
LTR/MaLR	MTB_Mm	400	263	22	4	6	2				1
LTR/MaLR	MTB	344	46	107	17	52	5	1		1	2
LTR/MaLR	MTC-int	164	21	5	78		2			2	
LTR/MaLR	MTD	118	9	41	7	7	5		2	2	
LTR/MaLR	MTB-int	65	18	21	3	1					
LTR/MaLR	ORR1E	64		1	2	1	1				
LTR/MaLR	ORR1A2-int	54	15	10	8		1			1	
LTR/MaLR	ORR1A2	48	13	6	6	4	2			1	
LTR/MaLR	ORR1A0-int	33	4	2	11	2	5			2	
LTR/MaLR	ORR1A1-int	25	5	7	3		3				
LTR/MaLR	ORR1A3-int	22		6		9	3				2
LTR/MaLR	ORR1D1	20		2	1	10	1				
LTR/MaLR	MTB_Mm-int	16	9	4	2						
LTR/MaLR	ORR1A0	13	7			1					
LTR/MaLR	MLT1G3	12									
LTR/MaLR	ORR1A4-int	12	5	1	3		1		1		
LTR/MaLR	ORR1A4	11	1	1		6	3				3
LTR/MaLR	ORR1B1	10			2	1	2			1	1
LTR/MaLR	MTE2a	9			2	3					
LTR/MaLR	MT-int	8	2	1	1						
LTR/MaLR	MTEb	8		1	1	2	1				1
LTR/MaLR	ORR1D2	8				3					
LTR/MaLR	MTE2b	7			1	3					
LTR/MaLR	MTEa	7	1	1	1	2	2				1
LTR/MaLR	ORR1B1-int	7	2		1						
LTR/MaLR	MTD-int	6	2		3		1			1	
LTR/MaLR	MLT1D	5			2						
LTR/MaLR	ORR1B2	5	1								
LTR/MaLR	ORR1D1-int	5	1		1						
LTR/MaLR	MLT1C	4	1				1				1
LTR/MaLR	ORR1C1	4	2		2						
LTR/MaLR	ORR1C2	4			1		1				

LTR/MaLR	MLT1F	3			1						
LTR/MaLR	MTEa-int	3									
LTR/MaLR	ORR1A1	3	1				2			1	
LTR/MaLR	ORR1A3	3		1		1					
LTR/MaLR	ORR1C1-int	3			1						
LTR/MaLR	MLT1A	2		1	1			1			
LTR/MaLR	MLT1A0	2				1		2		1	1
LTR/MaLR	MLT1A1	2	1								
LTR/MaLR	MLT1E-int	2									
LTR/MaLR	MLT1E1	2	1					1		1	
LTR/MaLR	MLT1E3	2									
LTR/MaLR	MLT1I	2			2						
LTR/MaLR	ORR1C2-int	2									
LTR/MaLR	ORR1E-int	2	1		1						
LTR/MaLR	MLT1B	1			1						
LTR/MaLR	MLT1E	1				1		1		1	
LTR/MaLR	MLT1E2	1									
LTR/MaLR	MLT1F1	1									
LTR/MaLR	MLT1H	1			1						
LTR/MaLR	MTE2a-int	1				1					
LTR/MaLR total		24408	5847	10347	2346	626	196	12	17	63	20
Other	RMER1B	15			1	2					
Other	RMER1A	4			1	1					
Other	RMER1C	4		1		1	1				
Other total		23	0	1	2	4	1	0	0	0	0
Satellite	MMSAT4	10	2		4		3			2	
Satellite	ZP3AR	2		1							
Satellite total		12	2	1	4	0	3	0	0	2	0
Simple_repeat	(CCA)n	18	3		1						
Simple_repeat	(TG)n	13	3	1		6					
Simple_repeat	(CA)n	8	4		2	1	1			1	
Simple_repeat	(CGG)n	8	3	3	1						
Simple_repeat	(CAG)n	7	2			2	1				1
Simple_repeat	(CTG)n	6	3	1	1	1					
Simple_repeat	(CAA)n	5				3					
Simple_repeat	(GA)n	4									
Simple_repeat	(TGG)n	4									
Simple_repeat	(ATG)n	3	1		1						
Simple_repeat	(CACCT)n	3			2						
Simple_repeat	(CAT)n	3	1								
Simple_repeat	(CCG)n	3	1		1						
Simple_repeat	(TCC)n	3		1							
Simple_repeat	(TTT)n	3									
Simple_repeat	(CATATA)n	2									
Simple_repeat	(CCCCAG)n	2			1						
Simple_repeat	(TA)n	2		1		1					
Simple_repeat	(TC)n	2				1					
Simple_repeat	(TTTC)n	2									
Simple_repeat	(ACTG)n	1									
Simple_repeat	(ATGGTG)n	1									
Simple_repeat	(ATTG)n	1				1					
Simple_repeat	(CAAAA)n	1									
Simple_repeat	(CACAG)n	1				1					
Simple_repeat	(CACG)n	1									
Simple_repeat	(CAGA)n	1									
Simple_repeat	(CAGAG)n	1			1						
Simple_repeat	(CAGAGA)n	1									
Simple_repeat	(CAGG)n	1				1					
Simple_repeat	(CATA)n	1									
Simple_repeat	(CCCCA)n	1	1								
Simple_repeat	(CCCG)n	1									
Simple_repeat	(CCCGG)n	1		1							
Simple_repeat	(CCGCG)n	1									
Simple_repeat	(CCTG)n	1			1						
Simple_repeat	(CGGAG)n	1	1								
Simple_repeat	(CGGG)n	1	1								
Simple_repeat	(CGGGG)n	1									
Simple_repeat	(CTA)n	1									
Simple_repeat	(CTGTG)n	1									
Simple_repeat	(G)n	1									
Simple_repeat	(GGA)n	1	1								

Simple_repeat	(GGAA)n	1									
Simple_repeat	(TCG)n	1									
Simple_repeat	(TCTCTG)n	1									
Simple_repeat	(TCTG)n	1	1								
Simple_repeat	(TGAG)n	1				1					
Simple_repeat	(A)n								1		
Simple_repeat	(CAA)n								1		
Simple_repeat	(TTG)n								1		
Simple_repeat total		129	25	9	12	19	5	0	1	1	1
SINE/Alu	B1_Mus1	445	123	79	48	43	26	2	6	3	3
SINE/Alu	B1_Mus2	192	28	23	37	16	10	1	2	1	1
SINE/Alu	B1_Mm	139	30	32	24	6	13	1	1	4	
SINE/Alu	B1_Mur3	53	7	4	15	5	2			1	1
SINE/Alu	B1_Mur4	36	6	9	4	5	3		1		1
SINE/Alu	PB1D10	33	1	2	10	5	2				
SINE/Alu	B1_Mur2	22		4	3	5	8		1		3
SINE/Alu	B1F	22	3		2	6	4				3
SINE/Alu	B1_Mur1	19		2	5	1	10			2	1
SINE/Alu	PB1D7	17	2	3	1	6	3				1
SINE/Alu	B1F2	13	1	1	5	1	4				
SINE/Alu	PB1	11	3		2		2				1
SINE/Alu	B1F1	9		2	1	3	1				
SINE/Alu	PB1D9	8		1	1	2					
SINE/Alu total		1019	204	162	158	104	88	4	11	11	15
SINE/B2	B3	220	136	2	15	13	17			6	4
SINE/B2	B2_Mm2	79	25	19	7	3	13	1		3	1
SINE/B2	B3A	49	7	2	6	7	4				
SINE/B2	B2_Mm1a	20	4	3	4	1	6	1	1		2
SINE/B2	B2_Mm1t	19	7	6		1	5				3
SINE/B2 total		387	179	32	32	25	45	2	1	9	10
SINE/B4	B4A	71	5	28	5	4	21	1			5
SINE/B4	ID_B1	69	6	10	8	15	9				4
SINE/B4	RSINE1	37	5	3	2	7	5	1	1		
SINE/B4	B4	26	1	2	5	9	7			1	4
SINE/B4 total		203	17	43	20	35	42	2	1	1	13
SINE/ID	ID4_	11	1		2	5					
SINE/ID	ID4	7		2		2	1				
SINE/ID	ID	4			1						
SINE/ID	ID2						1				1
SINE/ID total		22	1	2	3	7	2	0	0	0	1
SINE/MIR	MIRb	16	1	1	4	2	5				2
SINE/MIR	MIR	15	2	1	5		1				1
SINE/MIR	MIR3	5		1							
SINE/MIR	MIRm	4				1					
SINE/MIR	MIR_Mars	3		1							
SINE/MIR	THER1_MD	1									
SINE/MIR total		44	3	4	9	3	6	0	0	0	3
Unknown	MurSatRep1	9	1		4						
Unknown total		9	1	0	4	0	0	0	0	0	0
Total		72828	15382	19280	10048	7452	2331	135	143	568	519

Supplementary Table 2. Annotation of repeat small RNAs

class	subclass	Number of clones (growing oocytes)				Number of clones (Mili IP)					
		Total	20-22 nt +	20-22 nt -	25-27 nt +	25-27 nt -	Total	20-22 nt +	20-22 nt -	25-27 nt +	25-27 nt -
DNA/MER1_type	MER5A	6				1	1				
DNA/MER1_type	URR1A	6				3	1				
DNA/MER1_type	RCHARR1	4				3	1				
DNA/MER1_type	URR1B	4			1	2	1				
DNA/MER1_type	Charlie5	3	1								
DNA/MER1_type	RMER30	2	1		1						
DNA/MER1_type	Charlie8	1									
DNA/MER1_type	MER112	1									
DNA/MER1_type	MER20	1	1								
DNA/MER1_type	MER58B	1			1						
DNA/MER1_type	MER5A1	1	1								
DNA/MER1_type	MER5B	1					1				1
DNA/MER1_type	Charlie1						1				1
DNA/MER1_type	MER2						1			1	
DNA/MER1_type total		31	4	0	3	9	7	0	0	1	2
DNA/MER2_type	MER44A	2									
DNA/MER2_type	MER82	2									
DNA/MER2_type	Tigger7	2									
DNA/MER2_type	MER2	1			1						
DNA/MER2_type	Tigger5	1			1						
DNA/MER2_type total		8	0	0	2	0	0	0	0	0	0
DNA/Tip100	Arthur1	1									
DNA/Tip100	MER115	1									
DNA/Tip100	FordPrefect						1				
DNA/Tip100 total		2	0	0	0	0	1	0	0	0	0
LINE/CR1	L3	4			1						
LINE/CR1	L3_Mars	3			2						
LINE/CR1	L3b	1									
LINE/CR1 total		8	0	0	3	0	0	0	0	0	0
LINE/L1	L1Md_F2	7100	1123	1445	718	1431	161	10	22	19	44
LINE/L1	L1Md_A	2640	539	487	427	352	111	10	2	23	33
LINE/L1	L1Md_T	2408	381	618	393	315	79	6	8	15	21
LINE/L1	L1Md_Gf	949	254	261	123	37	38	1	3	9	3
LINE/L1	L1_Mus1	783	110	73	136	206	33			3	10
LINE/L1	L1Md_F	751	82	147	78	207	31	1	2	2	13
LINE/L1	L1_Mus2	496	31	53	62	194	30			1	17
LINE/L1	L1Md_F3	393	35	61	43	110	9	1		3	2
LINE/L1	L1_Mus3	353	37	48	54	83	10		2	3	1
LINE/L1	Lx	183	14	16	31	64	5				2
LINE/L1	L1_Mm	125	8	20	13	51	5				4
LINE/L1	Lx8	79	2	5	4	8	11			2	2
LINE/L1	L1_Mur1	41	1		1	25	1	1			
LINE/L1	MusHAL1	38	2	4	3	8	5			1	2
LINE/L1	Lx5	36	3	3	12	3	5	1		1	
LINE/L1	L1_Mus4	35	4	5	10	6	2			1	
LINE/L1	L1VL1	32	10	2	9	6	1			1	
LINE/L1	L1VL2	32	10		7	4	5			1	2
LINE/L1	L1_Mur3	30	1	2		6	3				1
LINE/L1	L1VL4	29	6	2	3	5	2			1	
LINE/L1	L1_Mur2	28	1		9	5	1				
LINE/L1	Lx3_Mus	22	7	1	3	5	3		2		
LINE/L1	Lx2	21	1	2	4	3	2			1	
LINE/L1	Lx9	20	2	1	2	4					
LINE/L1	L1_Rod	18					1				1
LINE/L1	Lx2B	17	1	2	2	1					
LINE/L1	Lx4B	14									
LINE/L1	Lx7	14	2	1	2	1	1				
LINE/L1	Lx4A	11			2						
LINE/L1	L1M5	10		3							
LINE/L1	Lx6	10	1	1	2	2					
LINE/L1	L1M2	9		1	1	3					
LINE/L1	Lx2A1	8				2					
LINE/L1	Lx3B	8	1	1	1						
LINE/L1	Lx3A	7	1		2						
LINE/L1	Lx3C	7		1		1	1				
LINE/L1	L1MA8	4			1	2					
LINE/L1	L1MCA	4				2					
LINE/L1	L1MA6	3			1	1	1				

LINE/L1	L1MCb	3									
LINE/L1	L1MD	3				1		1		1	
LINE/L1	L1M3	2						1			
LINE/L1	L1M4	2			1						
LINE/L1	L1MA4	2									
LINE/L1	L1MB4	2			1						
LINE/L1	L1MDa	2									
LINE/L1	L1ME1	2			2						
LINE/L1	L1MEe	2	1								
LINE/L1	L1M	1				1					
LINE/L1	L1M4c	1									
LINE/L1	L1MA5	1				1					
LINE/L1	L1MA5A	1									
LINE/L1	L1MA7	1									
LINE/L1	L1MB5	1									
LINE/L1	L1MB7	1									
LINE/L1	L1MC	1									
LINE/L1	L1MC4	1			1						
LINE/L1	L1MD2	1									
LINE/L1	L1ME3	1									
LINE/L1	L1ME3B	1									
LINE/L1	Lx2A	1	1								
LINE/L1	L1MB3							2			
LINE/L1 total		16801	2672	3266	2164	3156	561	32	41	87	158
LINE/L2	L2	39	16	1	6	4	2	1	1		
LINE/L2 total		39	16	1	6	4	2	1	1	0	0
LINE/RTE	L4						1				1
LINE/RTE total		0	0	0	0	0	1	0	0	0	1
Low_complexity	CT-rich	15	1			2					
Low_complexity	G-rich	12	3	4							
Low_complexity	GA-rich	10		1			1			1	
Low_complexity	GC-rich	9	1	5		1					
Low_complexity	C-rich	7	2	1							
Low_complexity	AT-rich	3				1					
Low_complexity total		56	7	11	0	4	1	0	0	1	0
LTR/ERV1	LTRIS_Mm	2590	883	969	32	88	11		1		3
LTR/ERV1	LTRIS_Mm-int	1806	358	390	152	367	47		2		22
LTR/ERV1	LTRIS_Mus	1001	389	298	41	35	5	1	1		1
LTR/ERV1	LTRIS_Mus-int	623	63	121	25	273	5	1			3
LTR/ERV1	RLTR6_Mm	271		2							
LTR/ERV1	RLTR6_Mm-int	217	1	15	4	104	13	1	2		4
LTR/ERV1	RLTR5_Mm-int	173	1	11		100	10				5
LTR/ERV1	MuRRS-int	88	16	14	4	24					
LTR/ERV1	MURVY-LTR	78		11		35	12		1		8
LTR/ERV1	MuRRS4-int	69	12	11	9	17	2				
LTR/ERV1	MURVY-int	58		8	11	27	11		2	3	3
LTR/ERV1	RLTR5_Mm	52		10		21	8				2
LTR/ERV1	LTRIS2	43		23		14	1				1
LTR/ERV1	RLTR4_Mm-int	38	7	1	17	1	3			3	
LTR/ERV1	RodERV21	37		5		15	3			1	
LTR/ERV1	RLTR1B	26	2	2		16	7				4
LTR/ERV1	RLTR14-int	24	1		12	9	1			1	
LTR/ERV1	RLTR6-int	22		2		16	2				
LTR/ERV1	MMERGLN-int	16		4		5	5				4
LTR/ERV1	RLTR1B-int	14	1	2	4	1					
LTR/ERV1	LTRIS2-int	7									
LTR/ERV1	RLTR4_Mm	7	5	1							
LTR/ERV1	RMER2	6	1		1	2					
LTR/ERV1	MMVL30-int	5			1	2	4				2
LTR/ERV1	LTRIS4-int	4		3		1					
LTR/ERV1	MER52-int	4		1		2					
LTR/ERV1	MuLV-int	4			2						
LTR/ERV1	MER21B	3					2				2
LTR/ERV1	RLTR23	3		1		1					
LTR/ERV1	LTR37B-int	2	2								
LTR/ERV1	LTRIS3	2			1						
LTR/ERV1	RLTR1	2									
LTR/ERV1	RMER5	2			1		1				
LTR/ERV1	LTRIS4	1		1							
LTR/ERV1	MER31-int	1			1						
LTR/ERV1	RLTR14	1				1					

LTR/ERV1	RLTR1C	1				1						
LTR/ERV1	RLTR1D-int	1										
LTR/ERV1	RMER21B	1					1			1		
LTR/ERV1	RMER5-int	1	1									
LTR/ERV1	MER67B						1			1		
LTR/ERV1	RLTR24						1			1		
LTR/ERV1 total		7304	1742	1907	318	1178	156	3	9	11	64	
LTR/ERVK	RLTR10-int	4557	1238	551	1192	138	256	23	7	118	12	
LTR/ERVK	IAPLTR1a_Mm-int	4021	914	598	1228	123	123	9	8	44	10	
LTR/ERVK	IAPLTR1_Mm-int	2910	698	287	975	66	200	22	5	102	2	
LTR/ERVK	RLTR10	1679	446	309	351	71	63	5	5	31	2	
LTR/ERVK	MMERVK10C	1140	333	199	170	151	73	2	2	12	23	
LTR/ERVK	IAP-d	606	113	176	55	92	35	1	3	1	14	
LTR/ERVK	IAPLTR2_Mm-int	603	62	156	105	99	24		2	7	7	
LTR/ERVK	IAPLTR2_Mm	462	53	115	39	118	16			3	4	
LTR/ERVK	RLTR10A	390	37	136	25	36	9	1	1		2	
LTR/ERVK	RLTRETN_Mm-int	367	40	54	45	102	34	1	3	6	15	
LTR/ERVK	IAPEZ-int	342	72	70	71	24	14			5	7	
LTR/ERVK	IAPLTR1_Mm	334	79	76	54	15	15	1		8	1	
LTR/ERVK	RMER17A2	314	27	26	70	59	20	2	1	4	6	
LTR/ERVK	RLTR10B2	283	4	58	1	143	14		3		6	
LTR/ERVK	RLTR10A-int	222	47	47	43	24	10	3	1	2		
LTR/ERVK	IAPLTR1a_Mm	221	50	27	44	14	5		1	2	2	
LTR/ERVK	RLTRETN_Mm	207	22	41	4	57	14		2	1	5	
LTR/ERVK	ETnERV	204	15	35	11	63	30				19	
LTR/ERVK	IAPEY3-int	190	15	23	25	68	13		2		5	
LTR/ERVK	IAPLTR2b-int	172	19	57	18	28	6	1	1		4	
LTR/ERVK	RLTR27	132	1	13		78	7		1		5	
LTR/ERVK	RLTR22_Mus	118	18	12	49	8	19		1	6	4	
LTR/ERVK	MERVK26	112		17		45	10				6	
LTR/ERVK	RLTR10C	111	16	28	5	22	3			1		
LTR/ERVK	RMER19A	110	12		52	1	5			4		
LTR/ERVK	RLTR9E	76	1	10	1	36	9		2		5	
LTR/ERVK	RLTR13B1	65	2	10		25	9				6	
LTR/ERVK	MurERV4	61		16		30	10		1		4	
LTR/ERVK	RLTR13D5	54		5	1	34	9				7	
LTR/ERVK	ETnERV2	51	1	6	7	18	7	1			3	
LTR/ERVK	RMER17B	50		9	4	22	6				4	
LTR/ERVK	RLTR10D	48	1	6		28	6				2	
LTR/ERVK	IAPEY_LTR-int	44	1	7	3	21	10	1			5	
LTR/ERVK	RMER4B	44	28	6		4						
LTR/ERVK	MurERV4_19	39	4		17							
LTR/ERVK	RLTR9A	38		3		20	10		1		7	
LTR/ERVK	IAPLTR2b	34	3	7	4	5	3	1				
LTR/ERVK	RLTR19-int	33	4		16		4			2		
LTR/ERVK	IAPLTR2a-int	29	6	7	5	1	1			1		
LTR/ERVK	RMER4A	29	22	1	2							
LTR/ERVK	RLTR22_Mur	28	1	3	15	2						
LTR/ERVK	RLTR44E	26		3		18	4				4	
LTR/ERVK	IAPLTR4_I	25		11		6	1		1			
LTR/ERVK	IAPLTR3-int	24	2	3		6	6		1		1	
LTR/ERVK	RMER16	24		7		10	3				2	
LTR/ERVK	RMER19B	22	6		6	3	3			1		
LTR/ERVK	RLTR45	20		1		11						
LTR/ERVK	RLTR9D	19	1	3		7	1					
LTR/ERVK	RLTR21	18		1		10	2					
LTR/ERVK	RMER16-int	17	1	2	2	5	3				1	
LTR/ERVK	IAPEY3_LTR	15	2	6		3	1				1	
LTR/ERVK	IAPEY2_LTR-int	14		3		9	4				3	
LTR/ERVK	RLTR13A3	14	1	1		8						
LTR/ERVK	RLTR45-int	13	1		4	3						
LTR/ERVK	MMETn-int	11	1	3	1	5						
LTR/ERVK	BGLII_B	10	1			5	3				2	
LTR/ERVK	IAPEY2_LTR	10				4	1					
LTR/ERVK	IAPEY3_LTR-int	10	2	1	1	2	4		1		2	
LTR/ERVK	IAPLTR2a	10	1	3	1	3						
LTR/ERVK	RLTR10E	10	1			6	1				1	
LTR/ERVK	RMER17A	10		2		4						
LTR/ERVK	RLTR16	9			1							
LTR/ERVK	RMER17D	9	1		2	3						
LTR/ERVK	RMER19C	9	1		3	1	2	1		1		

LTR/ERVK	MYSERV	8	2	4					
LTR/ERVK	IAPLTR3	7	3	2	1				
LTR/ERVK	MYSERV16_I	7	1	3					
LTR/ERVK	RLTR8	7	4			2			
LTR/ERVK	RMER13B	7		2	1				
LTR/ERVK	ETnERV3	6		1	1				
LTR/ERVK	IAPLTR4-int	6	4	1					
LTR/ERVK	MYSERV6	6	1	1			1		
LTR/ERVK	RLTR17	6		1	1				
LTR/ERVK	RMER17C	6	2	1		1			
LTR/ERVK	BGLII	5	3	1					
LTR/ERVK	RLTR13B4	5		1	3				
LTR/ERVK	RLTR13D6	5	1	1	1		2		2
LTR/ERVK	RLTR44-int	5			1				
LTR/ERVK	RMER20B	5		1	1				
LTR/ERVK	IAPLTR4	4		1	1	1			
LTR/ERVK	RLTR13C2	4	1	2		1	1		1
LTR/ERVK	RLTR15	4			1				
LTR/ERVK	RLTR25A	4			2				
LTR/ERVK	RLTR27-int	4		1	1				
LTR/ERVK	RLTR42-int	4	1		2	1	1		
LTR/ERVK	RLTR44A-int	4	1			2			
LTR/ERVK	RLTR44C	4		1					
LTR/ERVK	RLTR46-int	4	3	1			1		
LTR/ERVK	RMER12	4	1		2				
LTR/ERVK	RMER13A	4	1				1		1
LTR/ERVK	RMER17D2	4		1		3	1		1
LTR/ERVK	RMER6D	4	4						
LTR/ERVK	RLTR12B	3			1				
LTR/ERVK	RLTR13A2	3				1			
LTR/ERVK	RLTR20A2	3							
LTR/ERVK	RLTR25B	3		1					
LTR/ERVK	RLTR31B_Mm	3	1		1				
LTR/ERVK	BGLII-int	2							
LTR/ERVK	RLTR12A	2							
LTR/ERVK	RLTR13D1	2					2		
LTR/ERVK	RLTR19	2							
LTR/ERVK	RLTR20A	2			1				
LTR/ERVK	RLTR20B3	2	1						
LTR/ERVK	RLTR31A_Mm	2	1						
LTR/ERVK	RLTR3_Mm-int	2		1					
LTR/ERVK	RLTR44B	2				1			
LTR/ERVK	RLTR44E-int	2					1		1
LTR/ERVK	RLTR9C	2			1				
LTR/ERVK	RNERVK23	2			1				
LTR/ERVK	BGLII_A	1							
LTR/ERVK	BGLII_B-int	1							
LTR/ERVK	BGLII_Mus	1			1				
LTR/ERVK	RLTR10B	1							
LTR/ERVK	RLTR11A	1	1						
LTR/ERVK	RLTR11B	1					1		1
LTR/ERVK	RLTR13A	1				1			
LTR/ERVK	RLTR13B2	1							
LTR/ERVK	RLTR13D3	1							
LTR/ERVK	RLTR13D4	1							
LTR/ERVK	RLTR19B	1							
LTR/ERVK	RLTR20A1	1			1				
LTR/ERVK	RLTR20D	1					1		1
LTR/ERVK	RLTR26	1				1			
LTR/ERVK	RLTR31_Mur	1							
LTR/ERVK	RLTR42	1							
LTR/ERVK	RLTR44A	1					1		1
LTR/ERVK	RLTR44B-int	1	1						
LTR/ERVK	RLTR44D	1			1				
LTR/ERVK	RLTR9A2	1						1	
LTR/ERVK	RLTR9B	1					1		
LTR/ERVK	RLTR9F	1	1						
LTR/ERVK	RMER12B	1							
LTR/ERVK	RMER17B-int	1							
LTR/ERVK	RMER6B	1							
LTR/ERVK	SRV_MM-int	1							

LTR/ERVK	RMER17C-int					2		1			
LTR/ERVK	IAPEYLTR					1		1			
LTR/ERVK	RLTR20C					1					
LTR/ERVK	RLTR13C1					1		1			
LTR/ERVK total		21087	4466	3272	4759	2052	1158	75	59	366	226
LTR/ERVL	MT2_Mm	535	116	85	99	62	32	2		13	3
LTR/ERVL	MERVL-_Mm	347	54	61	87	42	12	2		2	
LTR/ERVL	MT2C_Mm	258	12	67	8	103	7		2	1	1
LTR/ERVL	RMER15-int	15				8	1				
LTR/ERVL	MT2A	12	2		1	2	1				1
LTR/ERVL	RMER15	9	2	1		2					
LTR/ERVL	MERVL	8	2	1	1	2					
LTR/ERVL	MERVL-C_Mm	6		1	1						
LTR/ERVL	MT2B2	6	2	1	1	1					
LTR/ERVL	MERVL-A	5	2	1							
LTR/ERVL	MT2B	4	1	2							
LTR/ERVL	MERVL-B	3			3						
LTR/ERVL	MERVL_2A	3		1			1				
LTR/ERVL	RLTR28	3									
LTR/ERVL	RMER10B	3	3								
LTR/ERVL	MER54A	2									
LTR/ERVL	MER70B	2									
LTR/ERVL	MER74A	2				1					
LTR/ERVL	MLT2B4	2		1	1						
LTR/ERVL	ERVL	1									
LTR/ERVL	ERVL-B4	1									
LTR/ERVL	HERV16	1			1						
LTR/ERVL	HERV40	1									
LTR/ERVL	LTR16A1	1									
LTR/ERVL	LTR16C	1									
LTR/ERVL	LTR16D	1				1					
LTR/ERVL	LTR40a	1				1					
LTR/ERVL	MER68	1									
LTR/ERVL	MERVL-B4	1				1					
LTR/ERVL	RMER10A	1									
LTR/ERVL total		1236	196	222	203	226	54	4	2	16	5
LTR/MaLR	MTA_Mm-int	7813	3021	1409	1213	124	87	10	12	21	7
LTR/MaLR	MTC	7620	142	6949	13	8	2				
LTR/MaLR	MTA_Mm	7418	2252	1748	949	377	58	1	2	27	
LTR/MaLR	MTB_Mm	400	263	22	4	6	2				1
LTR/MaLR	MTB	344	46	107	17	52	5	1		1	2
LTR/MaLR	MTC-int	164	21	5	78		2			2	
LTR/MaLR	MTD	118	9	41	7	7	5		2	2	
LTR/MaLR	MTB-int	65	18	21	3	1					
LTR/MaLR	ORR1E	64		1	2	1	1				
LTR/MaLR	ORR1A2-int	54	15	10	8		1			1	
LTR/MaLR	ORR1A2	48	13	6	6	4	2			1	
LTR/MaLR	ORR1A0-int	33	4	2	11	2	5			2	
LTR/MaLR	ORR1A1-int	25	5	7	3		3				
LTR/MaLR	ORR1A3-int	22		6		9	3				2
LTR/MaLR	ORR1D1	20		2	1	10	1				
LTR/MaLR	MTB_Mm-int	16	9	4	2						
LTR/MaLR	ORR1A0	13	7			1					
LTR/MaLR	MLT1G3	12									
LTR/MaLR	ORR1A4-int	12	5	1	3		1		1		
LTR/MaLR	ORR1A4	11	1	1		6	3				3
LTR/MaLR	ORR1B1	10			2	1	2			1	1
LTR/MaLR	MTE2a	9			2	3					
LTR/MaLR	MT-int	8	2	1	1						
LTR/MaLR	MTEb	8		1	1	2	1				1
LTR/MaLR	ORR1D2	8				3					
LTR/MaLR	MTE2b	7			1	3					
LTR/MaLR	MTEa	7	1	1	1	2	2				1
LTR/MaLR	ORR1B1-int	7	2		1						
LTR/MaLR	MTD-int	6	2		3		1			1	
LTR/MaLR	MLT1D	5			2						
LTR/MaLR	ORR1B2	5	1								
LTR/MaLR	ORR1D1-int	5	1		1						
LTR/MaLR	MLT1C	4	1				1				1
LTR/MaLR	ORR1C1	4	2		2						
LTR/MaLR	ORR1C2	4			1		1				

LTR/MaLR	MLT1F	3			1						
LTR/MaLR	MTEa-int	3									
LTR/MaLR	ORR1A1	3	1				2			1	
LTR/MaLR	ORR1A3	3		1		1					
LTR/MaLR	ORR1C1-int	3			1						
LTR/MaLR	MLT1A	2		1	1			1			
LTR/MaLR	MLT1A0	2				1		2		1	1
LTR/MaLR	MLT1A1	2	1								
LTR/MaLR	MLT1E-int	2									
LTR/MaLR	MLT1E1	2	1					1		1	
LTR/MaLR	MLT1E3	2									
LTR/MaLR	MLT1I	2			2						
LTR/MaLR	ORR1C2-int	2									
LTR/MaLR	ORR1E-int	2	1		1						
LTR/MaLR	MLT1B	1			1						
LTR/MaLR	MLT1E	1				1		1		1	
LTR/MaLR	MLT1E2	1									
LTR/MaLR	MLT1F1	1									
LTR/MaLR	MLT1H	1			1						
LTR/MaLR	MTE2a-int	1				1					
LTR/MaLR total		24408	5847	10347	2346	626	196	12	17	63	20
Other	RMER1B	15			1	2					
Other	RMER1A	4			1	1					
Other	RMER1C	4		1		1	1				
Other total		23	0	1	2	4	1	0	0	0	0
Satellite	MMSAT4	10	2		4		3			2	
Satellite	ZP3AR	2		1							
Satellite total		12	2	1	4	0	3	0	0	2	0
Simple_repeat	(CCA)n	18	3		1						
Simple_repeat	(TG)n	13	3	1		6					
Simple_repeat	(CA)n	8	4		2	1	1			1	
Simple_repeat	(CGG)n	8	3	3	1						
Simple_repeat	(CAG)n	7	2			2	1				1
Simple_repeat	(CTG)n	6	3	1	1	1					
Simple_repeat	(CAA)n	5				3					
Simple_repeat	(GA)n	4									
Simple_repeat	(TGG)n	4									
Simple_repeat	(ATG)n	3	1		1						
Simple_repeat	(CACCT)n	3			2						
Simple_repeat	(CAT)n	3	1								
Simple_repeat	(CCG)n	3	1		1						
Simple_repeat	(TCC)n	3		1							
Simple_repeat	(TTT)n	3									
Simple_repeat	(CATATA)n	2									
Simple_repeat	(CCCCAG)n	2			1						
Simple_repeat	(TA)n	2		1		1					
Simple_repeat	(TC)n	2				1					
Simple_repeat	(TTTC)n	2									
Simple_repeat	(ACTG)n	1									
Simple_repeat	(ATGGTG)n	1									
Simple_repeat	(ATTG)n	1				1					
Simple_repeat	(CAAAA)n	1									
Simple_repeat	(CACAG)n	1				1					
Simple_repeat	(CACG)n	1									
Simple_repeat	(CAGA)n	1									
Simple_repeat	(CAGAG)n	1			1						
Simple_repeat	(CAGAGA)n	1									
Simple_repeat	(CAGG)n	1				1					
Simple_repeat	(CATA)n	1									
Simple_repeat	(CCCCA)n	1	1								
Simple_repeat	(CCCG)n	1									
Simple_repeat	(CCCGG)n	1		1							
Simple_repeat	(CCGCG)n	1									
Simple_repeat	(CCTG)n	1			1						
Simple_repeat	(CGGAG)n	1	1								
Simple_repeat	(CGGG)n	1	1								
Simple_repeat	(CGGGG)n	1									
Simple_repeat	(CTA)n	1									
Simple_repeat	(CTGTG)n	1									
Simple_repeat	(G)n	1									
Simple_repeat	(GGA)n	1	1								

Simple_repeat	(GGAA)n	1									
Simple_repeat	(TCG)n	1									
Simple_repeat	(TCTCTG)n	1									
Simple_repeat	(TCTG)n	1	1								
Simple_repeat	(TGAG)n	1				1					
Simple_repeat	(A)n								1		
Simple_repeat	(CAA)n								1		
Simple_repeat	(TTG)n								1		
Simple_repeat total		129	25	9	12	19	5	0	1	1	1
SINE/Alu	B1_Mus1	445	123	79	48	43	26	2	6	3	3
SINE/Alu	B1_Mus2	192	28	23	37	16	10	1	2	1	1
SINE/Alu	B1_Mm	139	30	32	24	6	13	1	1	4	
SINE/Alu	B1_Mur3	53	7	4	15	5	2			1	1
SINE/Alu	B1_Mur4	36	6	9	4	5	3		1		1
SINE/Alu	PB1D10	33	1	2	10	5	2				
SINE/Alu	B1_Mur2	22		4	3	5	8		1		3
SINE/Alu	B1F	22	3		2	6	4				3
SINE/Alu	B1_Mur1	19		2	5	1	10			2	1
SINE/Alu	PB1D7	17	2	3	1	6	3				1
SINE/Alu	B1F2	13	1	1	5	1	4				
SINE/Alu	PB1	11	3		2		2				1
SINE/Alu	B1F1	9		2	1	3	1				
SINE/Alu	PB1D9	8		1	1	2					
SINE/Alu total		1019	204	162	158	104	88	4	11	11	15
SINE/B2	B3	220	136	2	15	13	17			6	4
SINE/B2	B2_Mm2	79	25	19	7	3	13	1		3	1
SINE/B2	B3A	49	7	2	6	7	4				
SINE/B2	B2_Mm1a	20	4	3	4	1	6	1	1		2
SINE/B2	B2_Mm1t	19	7	6		1	5				3
SINE/B2 total		387	179	32	32	25	45	2	1	9	10
SINE/B4	B4A	71	5	28	5	4	21	1			5
SINE/B4	ID_B1	69	6	10	8	15	9				4
SINE/B4	RSINE1	37	5	3	2	7	5	1	1		
SINE/B4	B4	26	1	2	5	9	7			1	4
SINE/B4 total		203	17	43	20	35	42	2	1	1	13
SINE/ID	ID4_	11	1		2	5					
SINE/ID	ID4	7		2		2	1				
SINE/ID	ID	4			1						
SINE/ID	ID2						1				1
SINE/ID total		22	1	2	3	7	2	0	0	0	1
SINE/MIR	MIRb	16	1	1	4	2	5				2
SINE/MIR	MIR	15	2	1	5		1				1
SINE/MIR	MIR3	5		1							
SINE/MIR	MIRm	4				1					
SINE/MIR	MIR_Mars	3		1							
SINE/MIR	THER1_MD	1									
SINE/MIR total		44	3	4	9	3	6	0	0	0	3
Unknown	MurSatRep1	9	1		4						
Unknown total		9	1	0	4	0	0	0	0	0	0
Total		72828	15382	19280	10048	7452	2331	135	143	568	519

Supplementary Table 3. Small RNA clusters in mouse oocytes

#	Chr	Genomic position (UCSC mm8)	strand	No. of small RNAs				Class of cluster
				kind	clone			
					total	19-23 nt	24-28 nt	
1	chr10	82789601-82918207	+	3654	4816	1548	2993	piRNA
2	chr10	117640185-117677987	+/-	1970	2630	1101	1376	piRNA
3	chr12	68565038-68604191	+	1327	2220	698	1387	piRNA
4	chr10	23296600-23350790	+/-	637	983	715	211	hp-siRNA piRNA
5	chr17	12661727-12663173	+/-	485	979	928	4	hp-siRNA
6	chr10	43898893-43918070	+	201	289	84	194	piRNA
7	chr4	56961570-56982731	-	196	225	93	113	piRNA
8	chr9	120636483-120636924	-	167	7306	7215	7	(hp-siRNA) ¹
9	chr17	5728780-5735259	+	151	194	76	103	piRNA
10	chr11	91737385-91742415	+/-	144	194	82	95	
11	chr7	75642809-75654236	-	143	167	36	120	piRNA
12	chr9	72892591-72910671	+	137	165	49	100	piRNA
13	chr5	137948929-137951678	+/-	126	136	122	4	
14	chrX	96828731-96829310	+/-	117	135	126	0	cis-nat-siRNA
15	chr10	26385021-26438068	+	112	146	43	91	piRNA
16	chr2	4936975-4938574	+/-	109	152	145	0	hp-siRNA
17	chr7	6177907-6256415	-	94	108	29	72	piRNA
19	chr9	51583810-51592553	+/-	86	239	227	5	piRNA
18	chr17	26648484-26664411	+/-	86	148	142	2	
20	chr8	72590252-72654897	-	85	98	28	66	piRNA
21	chr13	50650072-50654460	+/-	74	103	54	42	piRNA
22	chr12	17091603-17238365	+/-	70	87	28	53	piRNA
23	chr8	102034513-102037171	+/-	69	77	73	1	trans-nat-siRNA (27) ²
24	chr3	96347880-96358820	+/-	68	81	65	15	
25	chr9	114357265-114364731	+/-	68	76	66	4	cis-nat-siRNA piRNA
26	chr9	69155319-69165534	-	67	82	44	35	piRNA
27	chr17	65702757-65789029	+/-	63	72	65	4	trans-nat-siRNA (23) piRNA
28	chr14	104076918-104093492	+/-	61	69	58	5	trans-nat-siRNA (36) piRNA
29	chr10	11373862-11392299	+/-	59	73	36	34	
30	chr5	114103753-114204341	+/-	58	60	54	4	cis-nat-siRNA
31	chr9	71397396-71412177	+	56	61	37	22	
32	chr12	81255978-81259024	+/-	55	73	37	30	
33	chrX	63037425-63071159	-	54	169	161	1	
34	chr3	51314104-51329858	+	51	60	11	46	piRNA
35	chr1	133805031-133859700	+	51	55	15	39	piRNA
36	chr14	73933479-73963644	+/-	47	51	46	1	trans-nat-siRNA (28)
37	chr8	120091309-120100997	+	46	52	11	39	piRNA
38	chr2	152105312-152106270	+/-	45	53	52	0	cis-nat-siRNA
39	chr6	94383256-94384938	+/-	45	46	42	1	
40	chr18	6545990-6551168	+/-	43	59	32	25	
41	chr5	134841245-134845867	+	43	49	7	39	piRNA
42	chr8	26918337-26920176	+/-	42	51	46	1	
43	chr6	12062918-12066410	+	41	59	24	35	
44	chr16	55973878-55985107	+/-	41	43	21	21	
45	chr9	107809098-107905674	+/-	38	49	38	9	trans-nat-siRNA (70) piRNA
46	chr1	21336888-21371325	+/-	38	44	39	3	
47	chr7	142706327-142740466	-	38	43	11	30	piRNA
48	chr18	34545947-34546947	+/-	36	45	45	0	
49	chr11	40538801-40551528	-	36	45	27	18	
50	chr12	81366581-81378202	-	36	40	19	20	piRNA
51	chr7	46835269-46843697	-	35	40	37	2	

52	chr1	158478810-158485558	+	35	38	10	26	piRNA
53	chr5	30418401-30436754	+/-	35	37	34	0	trans-nat-siRNA (98)
54	chr8	13100313-13119892	+	35	36	10	22	
55	chr13	7235082-7235113	+/-	33	53	22	25	
56	chr1	87414685-87432169	+/-	33	36	32	2	
57	chr1	134811729-134819209	-	33	36	11	25	piRNA
58	chr2	4750393-4755465	+/-	33	33	32	1	trans-nat-siRNA (113)
59	chr6	92115112-92137605	+	32	34	10	18	piRNA
60	chr7	4721830-4731169	+/-	32	32	26	4	
61	chr18	13101545-13114997	+	29	35	8	22	
62	chr6	5190821-5209596	-	29	33	12	21	
63	chr11	20724935-20730342	+/-	29	31	28	1	trans-nat-siRNA (76)
64	chr7	142390136-142391477	+/-	28	54	23	20	
65	chr16	15365996-15374973	+/-	28	33	23	9	
66	chr12	98618839-98620440	+/-	28	30	21	8	
67	chr11	3807801-3903952	+/-	28	30	24	4	
68	chrX	119194985-119199429	+/-	27	42	26	13	
69	chr12	88704274-88709701	+/-	27	40	11	28	
70	chr2	6050173-6051282	+/-	27	32	28	0	trans-nat-siRNA (45)
71	chr12	100365867-100381179	+/-	27	27	21	5	
72	chr16	94460947-94468144	+/-	27	27	24	3	
73	chr6	120852611-120941581	+	26	32	8	21	
74	chr13	47019741-47021917	+/-	26	30	29	1	
75	chr10	127092173-127103365	+	26	29	6	22	
76	chr7	67463293-67469209	+/-	26	29	25	2	trans-nat-siRNA (63)
77	chr6	83328817-83341495	-	26	29	7	20	
78	chr14	23274157-23289711	-	26	28	7	19	piRNA
79	chr14	48088967-48178294	+/-	26	28	24	2	cis-nat-siRNA
80	chr14	99971053-99979397	+/-	25	44	40	2	
81	chr17	4355914-4359443	+/-	25	29	13	15	
82	chr6	95209508-95276509	+/-	25	27	23	3	cis-nat-siRNA piRNA
83	chr2	61664560-61669772	+/-	24	33	9	23	
84	chr8	126304234-126307701	+/-	24	28	28	0	cis-nat-siRNA
85	chr6	136363113-136365436	+/-	24	27	24	2	
86	chr17	20683993-20699062	+/-	24	26	10	14	
87	chr15	64993143-65005963	+/-	24	26	5	19	
88	chr3	95268019-95291969	-	24	24	9	14	piRNA
89	chr1	178671614-178672755	+/-	23	24	23	0	cis-nat-siRNA
90	chr13	10738676-10740678	-	23	24	8	11	
91	chr15	95901456-95903957	-	22	24	16	7	
92	chr6	113675860-113694543	+	22	23	5	18	piRNA
93	chr2	167165313-167176760	+/-	22	23	2	19	piRNA
94	chr2	5464350-5465948	-	21	25	22	2	
95	chr5	129335255-129342749	+/-	21	23	21	1	
96	chr15	72923976-72933199	-	21	22	10	10	piRNA
97	chr12	31659934-31661154	+/-	21	21	21	0	cis-nat-siRNA piRNA
98	chr4	116658019-116664346	+/-	21	21	21	0	trans-nat-siRNA (53)
99	chr7	89817431-89817586	+	20	164	148	2	
100	chr19	44616735-44632652	+	20	23	7	12	piRNA
101	chr3	100597893-100601590	-	20	21	7	12	piRNA
102	chr18	61318900-61324893	-	20	21	5	16	piRNA
103	chr9	67451766-67454167	+	19	156	139	3	
104	chr1	120505455-120512436	+	19	22	5	17	piRNA
105	chr4	135812545-135820680	+	19	21	9	12	piRNA
106	chr16	11574160-11597424	+	19	21	10	8	piRNA
107	chr1	34758131-34764196	-	19	21	8	12	piRNA

108	chr5	45509068-45539400	+/-	19	20	9	11	
109	chr13	51156805-51163152	+	19	20	5	14	
110	chr17	63160920-63172370	-	19	20	7	11	
111	chr17	13278068-13292672	-	19	20	7	13	piRNA
112	chr6	40331826-40339075	-	19	19	4	14	piRNA
113	chr7	80168083-80185766	+/-	19	19	18	0	trans-nat-siRNA (58)
114	chr10	57540697-57545694	+/-	18	25	18	6	
115	chr12	99700460-99731966	-	18	22	8	14	piRNA
116	chr3	9413355-9420647	-	18	20	7	12	piRNA
117	chr7	4962602-4964465	+/-	18	19	16	0	
118	chr4	142703898-142704269	+/-	18	19	18	0	
119	chr16	78133719-78138023	-	18	19	17	1	
120	chr3	103149689-103158115	+/-	18	19	17	0	cis-nat-siRNA
121	chr9	114933907-114946738	+	18	18	6	11	
122	chr4	131168448-131195984	+/-	18	18	17	0	cis-nat-siRNA
123	chr4	149061674-149061849	+	17	159	156	2	
124	chr18	74783814-74783981	+/-	17	21	19	0	
125	chr3	50464302-50466857	+/-	17	20	18	1	
126	chr9	3261498-3277798	-	17	20	6	13	piRNA
127	chr1	44994426-44999804	-	17	20	10	10	
128	chr10	116997414-116999574	+/-	17	20	19	0	cis-nat-siRNA
129	chr11	22468219-22495726	-	17	19	7	11	
130	chr6	8545951-8547015	+	17	18	15	1	trans-nat-siRNA (210)
131	chr3	138868338-138876679	+	17	18	4	14	
132	chr9	14287825-14300982	-	17	17	7	9	
133	chr10	119869799-119882982	+/-	17	17	15	0	
134	chr2	121235120-121235783	+	16	54	52	0	
135	chr6	38619537-38628567	-	16	20	8	10	piRNA
136	chr11	94555502-94566332	+/-	16	18	10	6	
137	chr6	81297736-81305583	+	16	18	9	7	
138	chr16	16824580-16840264	+	16	17	3	14	piRNA
139	chr8	54248043-54253836	-	16	17	6	9	
140	chr14	73259745-73270682	-	16	17	3	12	
141	chr9	20658329-20677052	-	16	16	7	3	
142	chr11	45495223-45511026	-	16	16	5	9	piRNA
143	chr4	152484173-152486536	+/-	16	16	15	0	hp-siRNA
144	chr18	67526739-67577405	+	15	23	12	11	
145	chr7	81780492-81780533	+/-	15	19	9	4	
146	chr5	115559558-115561624	-	15	17	16	1	
147	chr8	13461792-13477199	+	15	16	4	12	piRNA
148	chr1	95406795-95423206	+	15	16	5	9	piRNA
149	chr11	103695150-103746901	-	15	16	1	13	
150	chr5	148619879-148633587	+/-	15	15	9	3	piRNA
151	chr8	26616361-26631112	+/-	14	20	4	11	
152	chr1	13159784-13175383	+/-	14	17	15	2	
153	chr3	96577455-96646117	+/-	14	16	7	2	
154	chr19	42703016-42704723	+	14	16	5	10	
155	chr1	185510729-185517260	+	14	16	6	10	
156	chr10	60823950-60829144	-	14	15	3	10	
157	chr8	129295474-129304740	+	14	14	5	8	
158	chrX	88694245-88694342	+/-	13	23	23	0	
159	chr18	68375963-68389552	+/-	13	18	8	10	piRNA
160	chr11	105870896-105882464	+	13	18	5	12	piRNA
161	chr3	6245265-6248969	-	13	16	1	15	
162	chr13	43206331-43212159	-	13	16	10	6	piRNA
163	chr3	132775264-132780217	+/-	13	15	12	3	

164	chr5	114624821-114635985	+-	13	15	3	10	
165	chr8	107238704-107244407	-	13	15	4	9	piRNA
166	chr8	112618024-112624628	-	13	15	7	8	piRNA
167	chr2	161038825-161061882	+	13	15	3	10	piRNA
168	chr18	42771363-42775698	+-	13	14	12	1	cis-nat-siRNA
169	chr2	129491799-129522359	+-	13	14	6	5	
170	chr17	45032004-45035472	-	13	14	12	1	
171	chr3	26802295-26807902	-	13	14	6	7	
172	chr6	39801276-39803027	+-	13	13	9	4	
173	chr1	191154111-191172227	-	13	13	2	11	
174	chr17	28315845-28321841	-	13	13	4	8	
175	chrX	4293190-4303399	-	13	13	2	9	
176	chr5	104082608-104095309	+	13	13	1	12	piRNA
177	chr18	16208720-16215946	-	13	13	6	6	piRNA
178	chr3	97186697-97195680	+	12	16	3	9	
179	chr10	48222016-48224017	+-	12	15	10	4	piRNA
180	chr17	9158916-9161441	+	12	14	12	0	
181	chr7	23903778-23927741	+-	12	13	9	3	
182	chr11	5428058-5434381	-	12	13	3	7	piRNA
183	chr10	41870533-41874493	-	12	13	3	9	piRNA
184	chr11	6049181-6050516	-	12	13	5	7	
185	chr11	95582191-95588104	+	12	12	3	8	piRNA
186	chr5	115404297-115411357	-	12	12	2	10	piRNA
187	chrX	17234869-17242153	-	12	12	5	5	
188	chr1	167702458-167706714	-	12	12	5	7	piRNA
189	chr18	65748663-65761591	+	12	12	4	5	piRNA
190	chr2	100920049-100927042	+-	12	12	4	7	
191	chr5	21320263-21320558	-	11	13	7	5	
192	chr2	28644737-28662243	-	11	13	3	9	piRNA
193	chrX	63882324-63887081	+	11	13	4	7	
194	chr1	37384478-37387632	-	11	13	4	9	piRNA
195	chr9	43894126-43903893	-	11	13	1	10	piRNA
196	chr4	139999570-140014688	-	11	12	3	8	piRNA
197	chr9	63445448-63450576	-	11	12	1	11	
198	chr16	96097712-96109333	-	11	12	3	9	
199	chr11	53260720-53281062	+	11	12	7	2	
200	chr14	75149422-75152155	+-	11	12	11	1	cis-nat-siRNA
201	chr2	24771332-24783870	+-	11	11	5	4	piRNA
202	chr5	135230763-135231375	+-	11	11	11	0	cis-nat-siRNA
203	chr15	83182267-83192941	-	11	11	3	7	
204	chr14	28860563-28869129	+	11	11	3	8	piRNA
205	chr15	93068290-93072348	-	11	11	3	8	piRNA
206	chr4	151146856-151150721	+	11	11	6	5	
207	chr13	64202446-64205517	-	11	11	7	4	piRNA
208	chr13	38352627-38353981	+-	10	13	13	0	cis-nat-siRNA
209	chr1	74913195-74918326	+	10	12	12	0	cis-nat-siRNA
210	chr10	4540955-4546987	+-	10	11	10	0	trans-nat-siRNA (130)
211	chr2	112370289-112374057	+	10	11	1	7	
212	chr5	78340488-78343421	+-	10	11	7	1	
213	chr10	126400198-126402431	+	10	11	9	2	piRNA
214	chr5	136194266-136273055	+-	10	10	5	5	piRNA
215	chr5	90691748-90711649	+	10	10	4	4	piRNA
216	chr7	5678553-5678593	+-	10	10	5	4	
217	chr5	72859514-72862801	+-	10	10	9	1	
218	chr16	24897620-24906135	+	10	10	1	8	piRNA
219	chr11	115401202-115420852	-	10	10	3	7	

220	chr4	120389015-120393077	+	10	10	3	7	piRNA
221	chr2	160450912-160462914	-	10	10	2	8	piRNA
222	chr13	51987033-51999657	+	9	12	3	9	
223	chr11	88781089-88788871	-	9	11	10	0	
224	chr15	34562755-34571836	-	9	11	0	10	
225	chr12	87403420-87410427	+	9	11	2	9	
226	chr4	138165033-138169671	-	9	11	4	7	piRNA
227	chr3	9233185-9234811	+/-	9	10	9	0	
228	chr15	34220753-34228625	+	9	10	1	9	
229	chr9	27097633-27106063	+	9	10	5	4	piRNA
230	chr14	45001894-45007212	+	9	10	3	5	
231	chr15	80759962-80766473	+	9	10	2	7	piRNA
232	chr11	79501642-79513861	+	9	9	3	5	piRNA
233	chr3	33615089-33619227	+/-	9	9	7	2	
234	chr5	108731683-108733445	-	9	9	7	2	
235	chr7	121863096-121872704	+	9	9	4	5	piRNA
236	chr1	49238587-49241102	+/-	9	9	5	4	piRNA
237	chr15	98690860-98700158	+/-	9	9	8	0	
238	chr1	91411467-91412653	+/-	9	9	7	1	
239	chr4	127374823-127379960	+/-	9	9	3	6	
240	chr19	5388341-5388997	+/-	9	9	7	1	
241	chr16	10614394-10622645	+/-	9	9	4	5	piRNA
242	chr4	47122099-47127933	+	8	10	2	8	
243	chr6	83771865-83774455	-	8	10	1	9	
244	chr18	44543508-44555328	+/-	8	10	3	6	piRNA
245	chr9	76900901-76903575	+	8	9	1	7	
246	chr8	126133046-126141010	+/-	8	9	7	1	
247	chr13	96436922-96438213	+	8	9	5	1	piRNA
248	chr11	120441863-120445572	-	8	9	5	4	
249	chr11	61499101-61501230	+/-	8	9	8	1	
250	chr5	143804666-143818933	+/-	8	8	3	4	
251	chr6	89517913-89527260	-	8	8	4	4	
252	chr15	98361734-98370374	+/-	8	8	7	0	piRNA
253	chr8	119843540-119853024	+/-	8	8	3	4	
254	chr2	151999779-152005308	+	8	8	1	6	piRNA
255	chr7	52448319-52452629	+/-	8	8	3	5	
256	chr9	110102368-110108278	-	8	8	0	8	
257	chr11	97211493-97214410	+	8	8	2	6	
258	chr8	128934772-128950365	+	8	8	3	4	piRNA
259	chr9	8004651-8004985	+/-	8	8	8	0	
260	chrX	6311562-6322912	-	8	8	0	7	piRNA
261	chr16	93562473-93562692	+	8	8	4	4	
262	chr5	111509922-111515929	-	8	8	4	4	
263	chr8	119356863-119366277	-	8	8	1	7	
264	chr18	33326187-33328502	-	8	8	2	6	piRNA
265	chr19	41637815-41653825	+/-	8	8	1	6	piRNA
266	chr1	174213609-174219938	+	8	8	0	8	piRNA
267	chr7	139986307-139988398	+	8	8	2	6	
268	chr19	46932520-46939165	+/-	8	8	2	5	piRNA
269	chr4	117254902-117258913	-	8	8	2	5	
270	chr5	36808213-36816089	-	8	8	1	7	
271	chr5	110721206-110727475	+/-	8	8	6	1	
272	chr13	24995115-25000178	-	8	8	4	4	
273	chr2	33272500-33276347	-	8	8	1	7	piRNA
274	chr3	134792701-134794491	+/-	8	8	4	3	
275	chr1	183038958-183038981	-	7	16	15	0	

276	chr15	42185408-42185433	+	7	11	8	2	
277	chr2	152952822-152961368	+	7	10	3	7	
278	chr5	141012034-141013417	+/-	7	10	5	4	
279	chr17	5120193-5134102	+	7	10	3	7	piRNA
280	chr4	62619564-62623539	+	7	9	3	6	
281	chr19	15709187-15721356	-	7	9	1	8	piRNA
282	chr1	74631966-74634487	+	7	9	1	8	piRNA
283	chr18	87604937-87613299	+/-	7	9	5	0	
284	chr10	14336030-14345739	+/-	7	9	6	3	
285	chr3	8557865-8568358	+/-	7	8	0	7	
286	chr2	28507994-28512110	+	7	8	0	7	piRNA
287	chr15	76159740-76166157	+/-	7	8	7	1	
288	chr5	113729437-113734901	+	7	8	1	7	piRNA
289	chr1	172033076-172035869	-	7	8	5	3	piRNA
290	chr6	54570452-54574287	+	7	8	3	5	piRNA
291	chr4	45417642-45421236	-	7	8	2	6	piRNA
292	chr17	38152580-38164996	-	7	8	1	7	
293	chr1	90095231-90097373	-	7	8	3	5	piRNA
294	chr9	7184560-7184854	+/-	7	7	6	0	
295	chr17	27617719-27629066	+/-	7	7	0	6	piRNA
296	chr4	146309698-146315785	+/-	7	7	3	2	
297	chr12	18317514-18321029	+	7	7	2	5	
298	chr11	60712602-60723112	-	7	7	3	4	
299	chr6	134822441-134824157	+	7	7	3	3	piRNA
300	chr4	126814167-126816934	+/-	7	7	5	1	
301	chr2	3775123-3781227	+/-	7	7	3	3	
302	chr6	128147654-128152146	-	7	7	2	5	piRNA
303	chr18	35392471-35402296	-	7	7	0	6	
304	chr1	105032976-105041994	+/-	7	7	3	3	
305	chr18	80467071-80471925	+/-	7	7	6	1	
306	chr16	8574827-8579722	-	7	7	1	5	
307	chr11	59271657-59278844	+	7	7	1	6	piRNA
308	chr4	140950037-140956836	-	7	7	0	6	piRNA
309	chr12	88049245-88060501	+/-	7	7	3	3	piRNA
310	chr9	59284219-59284554	+/-	7	7	6	0	
311	chr11	77331551-77338484	+	6	9	1	8	
312	chr8	113884363-113892285	-	6	8	6	2	piRNA
313	chr10	80993410-80999321	+/-	6	8	4	4	
314	chr14	25927114-25932205	+	6	8	1	6	piRNA
315	chr15	62920430-62925880	-	6	7	3	2	
316	chr14	63769408-63772627	-	6	7	0	7	piRNA
317	chr14	83953963-83954918	+/-	6	7	3	3	
318	chr4	3793047-3798960	+/-	6	7	3	4	
319	chr16	18414509-18422102	+	6	7	0	7	piRNA
320	chr7	99795112-99800393	-	6	7	2	5	piRNA
321	chr12	82635238-82643169	-	6	7	5	2	piRNA
322	chr3	76055232-76060954	+/-	6	7	4	3	
323	chr11	4765167-4772453	+	6	7	7	0	
324	chr2	164511521-164517325	+/-	6	7	4	3	
325	chr16	32197122-32197924	+/-	6	7	6	0	
326	chr12	105433762-105434028	+/-	6	7	6	1	
327	chr2	153088831-153096012	+	6	7	0	5	
328	chr15	62198518-62207195	+/-	6	7	4	3	
329	chr4	44132697-44137830	+	6	7	0	7	
330	chr6	26704111-26704153	+/-	6	7	4	1	
331	chr12	8936286-8939367	+	6	7	2	2	piRNA

332	chr2	143631434-143634165	+ -	6	6	2	3	
333	chr6	142968662-142972444	-	6	6	2	2	
334	chr5	147045545-147047971	-	6	6	0	4	piRNA
335	chr5	110872541-110883104	+	6	6	3	3	piRNA
336	chr7	81476972-81483420	-	6	6	1	5	
337	chr13	111459564-111461024	+ -	6	6	5	1	
338	chr8	43042317-43048284	+	6	6	1	4	
339	chr8	124482114-124491255	+ -	6	6	5	1	
340	chr9	35106703-35108480	+ -	6	6	6	0	
341	chr4	59864700-59866047	-	6	6	1	5	piRNA
342	chrX	14035030-14039295	+	6	6	2	3	
343	chr4	100596727-100605257	+	6	6	0	6	
344	chr9	119284785-119288559	+	6	6	1	5	piRNA
345	chr7	121428230-121437711	-	6	6	2	4	piRNA
346	chr5	33980708-33988920	+	6	6	6	0	
347	chr1	35832995-35842811	+ -	6	6	3	3	
348	chr10	36287103-36291897	+	6	6	1	5	
349	chr10	87500596-87509391	-	6	6	2	3	
350	chr1	180173816-180174451	+ -	6	6	5	0	
351	chr16	98214356-98218563	-	6	6	1	5	
352	chr12	105166117-105171063	-	6	6	3	3	piRNA
353	chr13	56480018-56491622	+	6	6	2	4	
354	chr16	14908733-14911890	-	6	6	4	2	
355	chr12	3901604-3911961	+	6	6	1	5	piRNA
356	chr4	150779848-150787415	+ -	6	6	2	1	
357	chr10	5988630-5991767	-	6	6	4	1	
358	chr4	125836721-125844131	-	6	6	2	3	piRNA
359	chr4	78320998-78322438	+	6	6	4	1	
360	chr11	97605437-97613251	+	5	35	2	0	
361	chr13	115316811-115316831	-	5	28	26	0	
362	chr9	69999182-69999201	-	5	24	2	0	
363	chr7	139809052-139809072	-	5	18	15	0	piRNA
364	chr8	98213653-98221198	-	5	12	6	6	
365	chr5	82107595-82107614	+	5	12	11	1	
366	chr5	136552505-136556146	-	5	8	1	7	
367	chr1	186523196-186523276	-	5	8	8	0	
368	chr4	118903961-118904197	-	5	7	7	0	
369	chr13	29347957-29355599	+ -	5	7	0	7	piRNA
370	chr5	147264217-147269361	+ -	5	7	4	3	
371	chr11	118844500-118847128	+	5	6	0	3	
372	chr15	31920753-31927669	+	5	6	0	6	
373	chr15	81512032-81515042	+	5	6	2	4	
374	chr5	143132237-143136224	-	5	6	2	3	piRNA
375	chr10	75483331-75487605	+ -	5	6	2	4	
376	chr13	43313523-43315005	+ -	5	6	4	2	
377	chr1	173177956-173178961	+ -	5	6	6	0	
378	chr3	36756981-36760554	+ -	5	6	5	1	
379	chr11	3093081-3093843	+ -	5	6	5	1	
380	chr6	85389576-85397467	+	5	6	4	2	
381	chr5	34492245-34494538	-	5	6	4	2	
382	chr18	34896583-34899483	+	5	6	3	3	
383	chr3	11164754-11169061	-	5	6	2	4	
384	chr1	60421864-60425159	+	5	6	1	4	
385	chr1	162841119-162849022	-	5	6	3	3	piRNA
386	chr18	44787043-44787518	+ -	5	6	2	3	piRNA
387	chr13	56745618-56751271	+	5	6	0	5	piRNA

388	chr19	35550807-35554633	+	5	5	1	4	
389	chr8	73281801-73286707	+/-	5	5	5	0	
390	chr6	36578038-36579473	+	5	5	1	4	
391	chr5	136387678-136395935	+/-	5	5	3	2	
392	chr1	152898423-152904530	+	5	5	2	3	
393	chr18	75293767-75302159	+	5	5	1	4	
394	chr10	69585523-69588019	+/-	5	5	1	1	piRNA
395	chr5	135601446-135610329	-	5	5	2	3	piRNA
396	chr4	37556395-37556418	+/-	5	5	3	2	
397	chr19	47314742-47316298	-	5	5	1	3	piRNA
398	chr4	134684500-134686381	-	5	5	1	3	piRNA
399	chr4	132469647-132470934	+	5	5	1	4	piRNA
400	chr9	21658122-21660328	-	5	5	1	4	
401	chr1	136571507-136574950	-	5	5	0	5	piRNA
402	chr4	115586752-115594523	+/-	5	5	4	1	
403	chr6	118538604-118538644	+	5	5	3	2	
404	chrX	16663535-16669345	-	5	5	2	3	piRNA
405	chr9	70871324-70880973	+	5	5	0	4	
406	chr3	138046044-138046063	-	5	5	1	0	
407	chr9	63554665-63556113	+/-	5	5	4	1	
408	chr6	116658718-116660694	-	5	5	1	3	
409	chr6	116367342-116373718	+	5	5	3	2	piRNA
410	chr6	147031958-147037907	+/-	5	5	1	4	
411	chr1	46207886-46210345	+	5	5	2	3	
412	chr7	130413235-130414520	+	5	5	1	4	
413	chr7	67600806-67610020	+	5	5	2	3	
414	chr11	60353966-60355183	+/-	5	5	3	1	
415	chr2	38546330-38549443	-	5	5	1	4	piRNA
416	chr2	25757145-25761954	-	5	5	3	0	
417	chr12	92038250-92044184	+/-	5	5	2	3	
418	chr13	58137185-58137856	+/-	5	5	5	0	
419	chr16	94918792-94919700	+	5	5	1	4	
420	chr9	65863575-65864527	+/-	5	5	4	1	
421	chr11	97899431-97901848	-	5	5	3	2	piRNA
422	chr11	117824890-117831372	+	5	5	3	2	
423	chr12	85531341-85540000	+	5	5	1	3	
424	chr13	11550798-11555216	-	5	5	5	0	
425	chr13	23941242-23942569	+/-	5	5	3	2	
426	chr15	27541614-27550415	-	5	5	1	4	
427	chr2	76541713-76550299	-	5	5	2	3	piRNA
428	chr12	111711571-111714318	+	5	5	2	3	
429	chr13	73976093-73982302	+/-	5	5	3	1	
430	chr13	12668452-12676580	-	5	5	0	5	piRNA
431	chr2	163308159-163309840	+	5	5	2	2	
432	chr2	131996629-132001619	+	5	5	2	2	piRNA
433	chr2	21280255-21286211	+/-	5	5	0	5	
434	chr4	25598518-25603682	+/-	5	5	1	4	
435	chr11	57201351-57202592	-	5	5	2	3	
436	chr3	62691658-62692423	+/-	5	5	4	1	
437	chr3	19341644-19349828	-	5	5	0	4	
438	chr10	33971755-33972395	+/-	5	5	4	0	
439	chr5	66190136-66191498	+	5	5	2	2	piRNA
440	chr19	3171146-3172891	+	5	5	1	4	
441	chr14	25746223-25752890	-	5	5	1	3	
442	chr17	9027586-9032570	+	5	5	1	4	
443	chr2	26727417-26730230	-	5	5	0	4	

444 chr15 81650780-81656011 +- 5 5 2 3

¹ This hp-siRNA cluster was found by observation, not by the computational search.

² The number in the parenthesis after "trans-nat-siRNA" represents the partner cluster.