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(54) **TISSUE-SPECIFIC MICRORNAS AND COMPOSITIONS AND USES THEREOF**

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(21) Appl. No.: **14/079,864**

(22) Filed: **Nov. 14, 2013**

Related U.S. Application Data

(60) Division of application No. 12/688,680, filed on Jan. 15, 2010, now Pat. No. 8,586,726, which is a continuation-in-part of application No. PCT/US08/70082, filed on Jul. 15, 2008.

(60) Provisional application No. 60/950,474, filed on Jul. 18, 2007, provisional application No. 61/020,625, filed on Jan. 11, 2008.

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(52) **U.S. Cl.**
CPC ***C12N 15/113*** (2013.01)
USPC ..... **514/44 A**; 536/24.5; 435/375

(57) **ABSTRACT**

The invention provides for isolated nucleic acid sequences of newly discovered micro RNAs that have been identified to exist in normal Human B cells and/or in tumor-related Human B cells, using an integrated bioinformatics method and pipeline described herein.

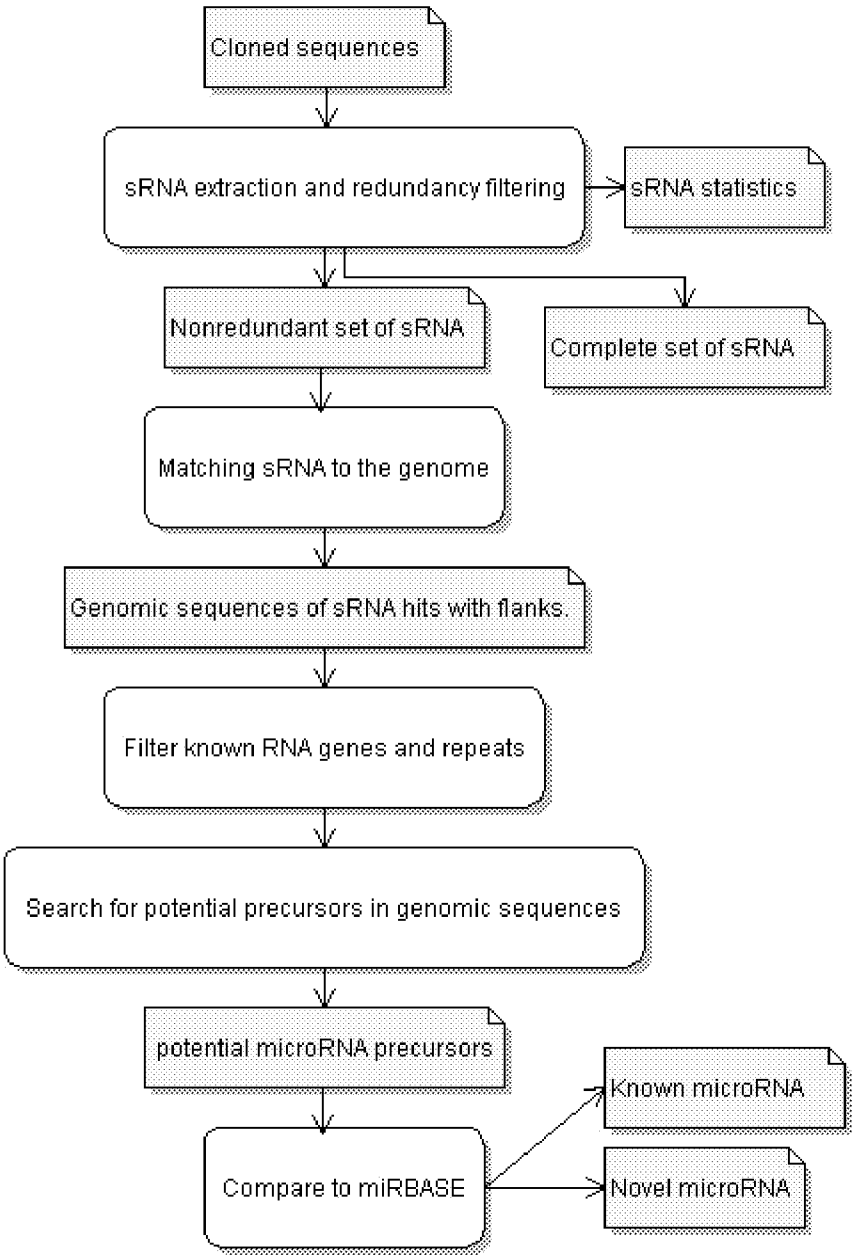

Cloned sequences
sRNA extraction and redundancy filtering
sRNA statistics
Nonredundant set of sRNA
Complete set of sRNA
Matching sRNA to the genome
Genomic sequences of sRNA hits with flanks.
Filter known RNA genes and repeats
Search for potential precursors in genomic sequences
potential microRNA precursors
Known microRNA
Compare to miRBASE
Novel microRNA

FIG. 1

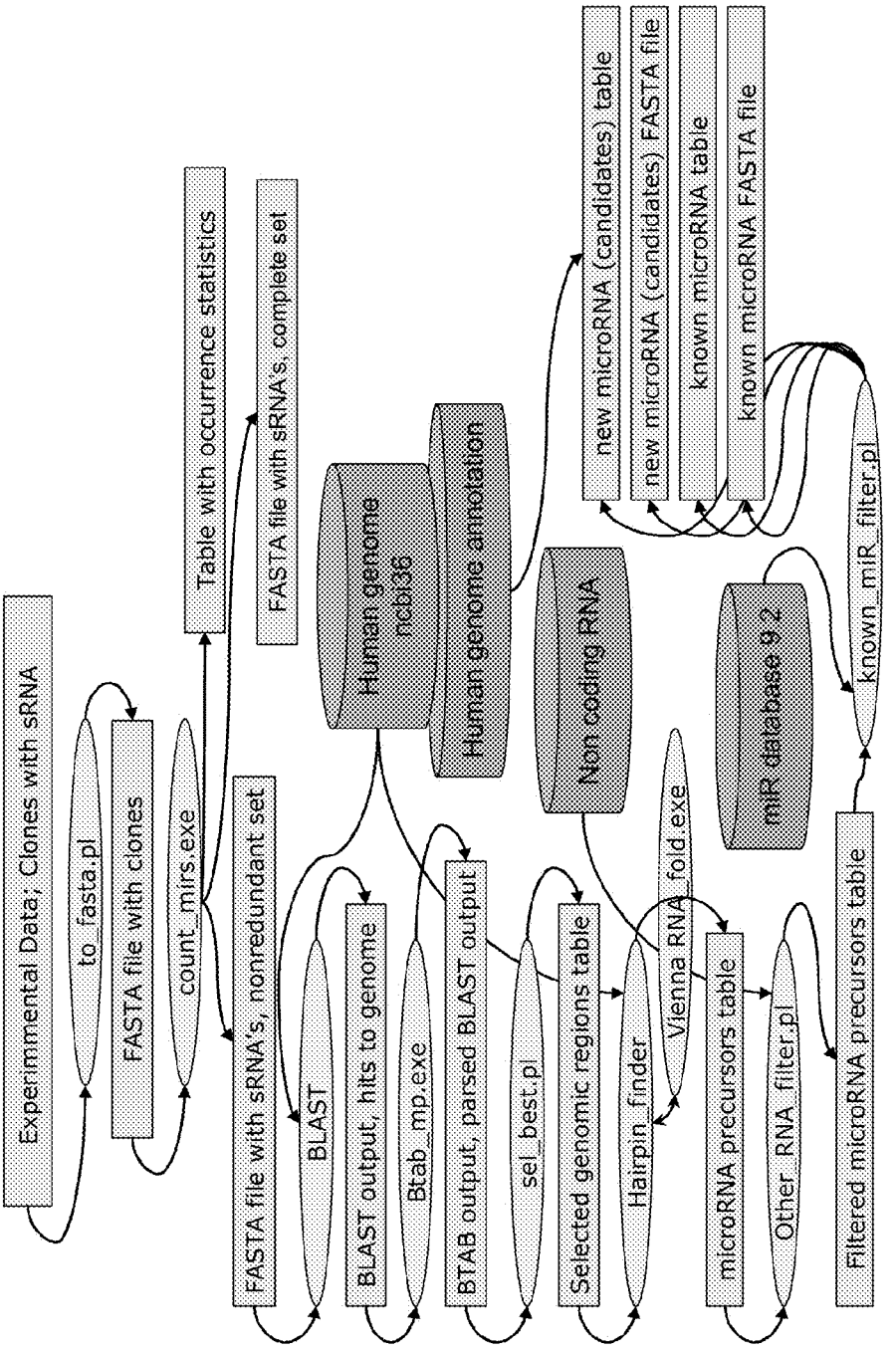

Experimmental Data; Clones with sRNA
to_fasta.pl
FASTA file with clones
count_mirs.exe
Table with occurrence statistics
FASTA file with sRNA's, nonredundant set
FASTA file with sRNA's, complete set
BLAST
Human genome ncbi36
BLAST output, hits to genome
Btab_mp.exe
Human genome annotation
BTAB output, parsed BLAST output
sel_best.pl
Non coding RNA
Selected genomic regions table
Hairpin_finder
Vienna RNA_fold.exe
new microRNA (candidates) table
new microRNA (candidates) FASTA file
known microRNA table
known microRNA FASTA file
miR database 9.2
known_miR_filter.pl
microRNA precursors table
Other_RNA_filter.pl
Filtered microRNA precursors table

FIG. 2

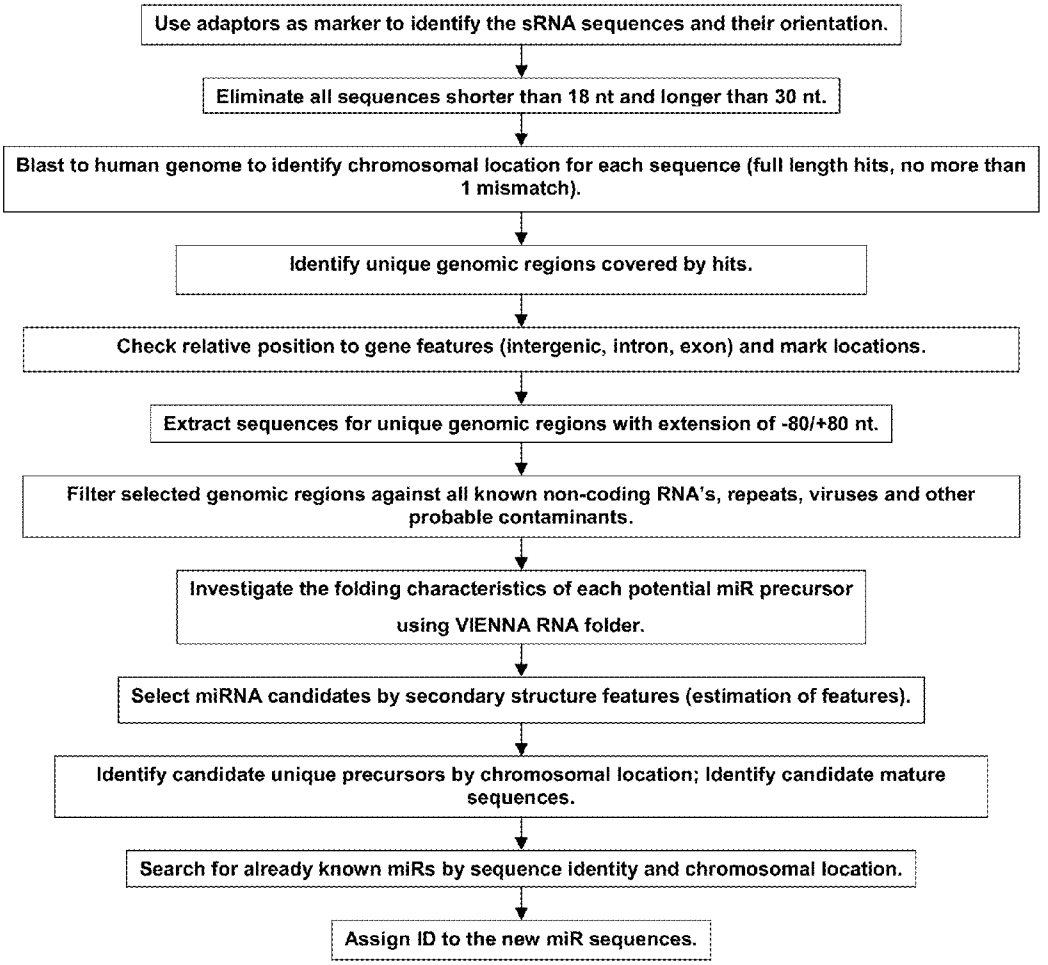

Use adaptors as marker to identify the sRNA sequences and their orientation.
Eliminate all sequences shorter than 18 nt and longer than 30 nt.
Blast to human genome to identify chromosomal location for each sequence (full length hits, no more than 1 mismatch).
Identify unique genomic regions covered by hits.
Check relative position to gene features (intergenic, intron, exon) and mark locations.
Extract sequences for unique genomic regions with extension of -80/+80 nt.
Filter selected genomic regions against all known non-coding RNA's, repeats, viruses and other probable contaminants.
Investigate the folding characteristics of each potential miR precursor using VIENNA RNA folder.
Select miRNA candidates by secondary structure features (estimation of features).
Identify candidate unique precursors by chromosomal location; Identify candidate mature sequences.
Search for already known miRs by sequence identity and chromosomal location.
Assign ID to the new miR sequences.

FIG. 3

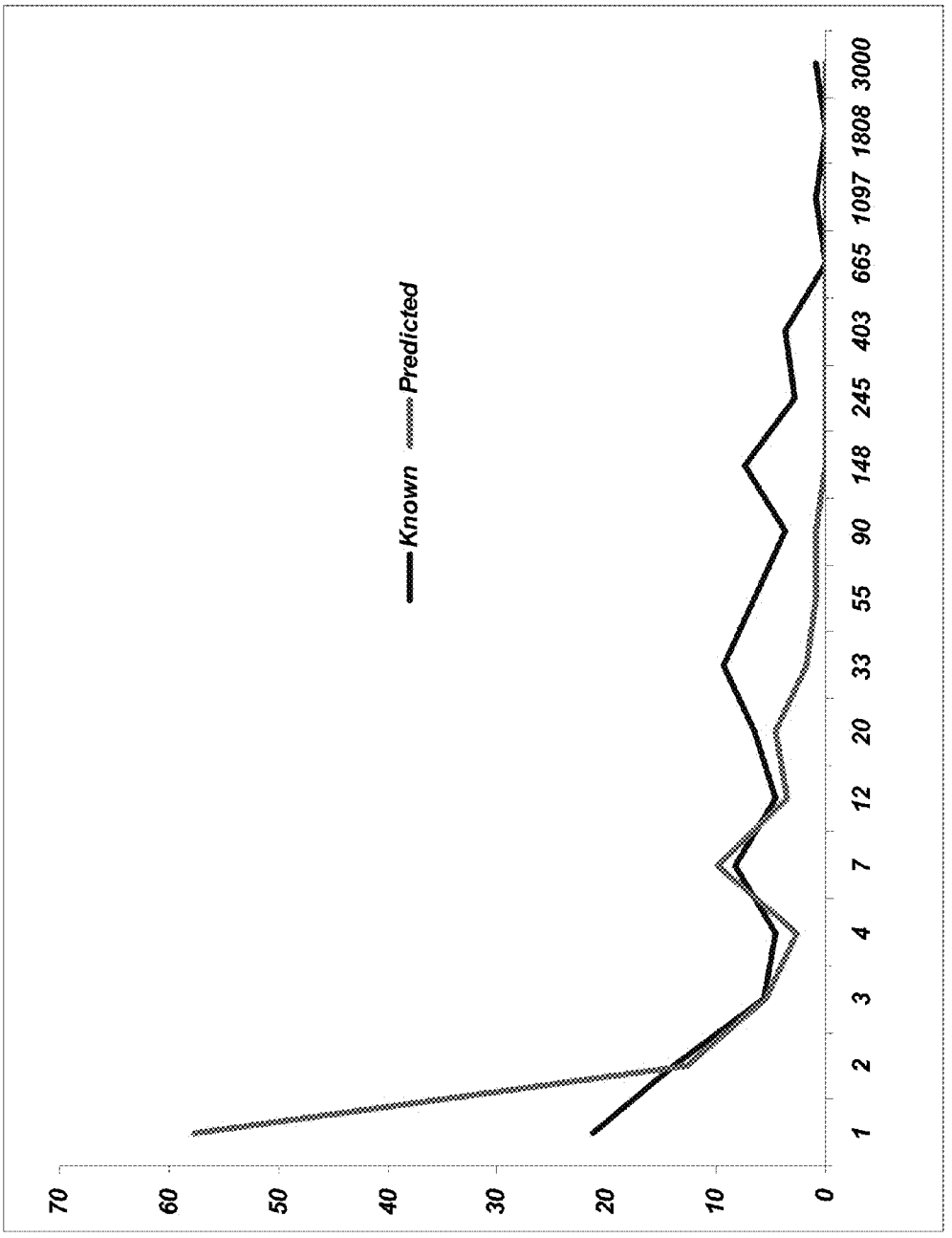

Known
Predicted
70
60
50
40
30
20
10
0
1
2
3
4
7
12
20
33
55
90
148
245
403
665
1097
1808
3000

FIG. 4

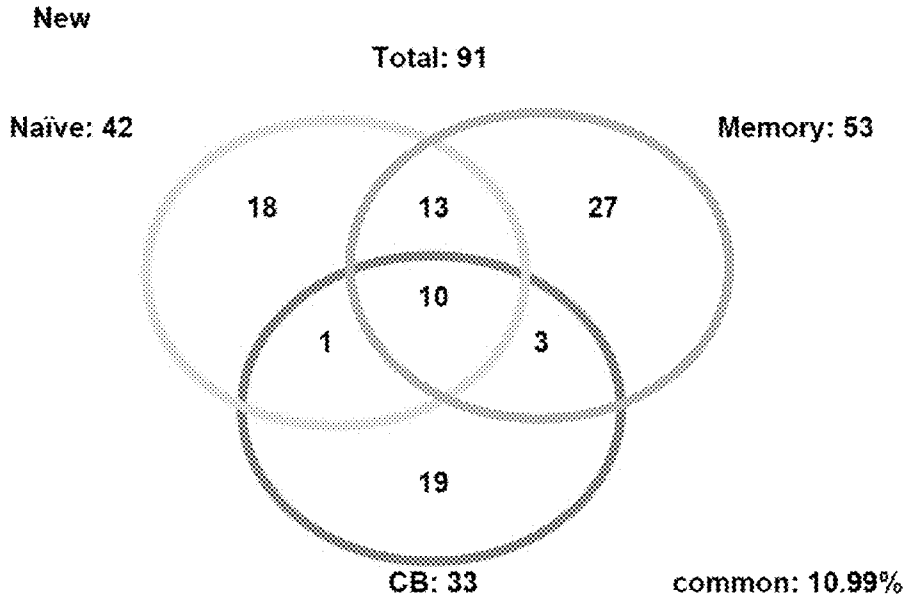

New
Total: 91
Naïve: 42
Memory: 53
18
13
27
10
1
3
19
CB: 33
common: 10.99%

FIG. 5

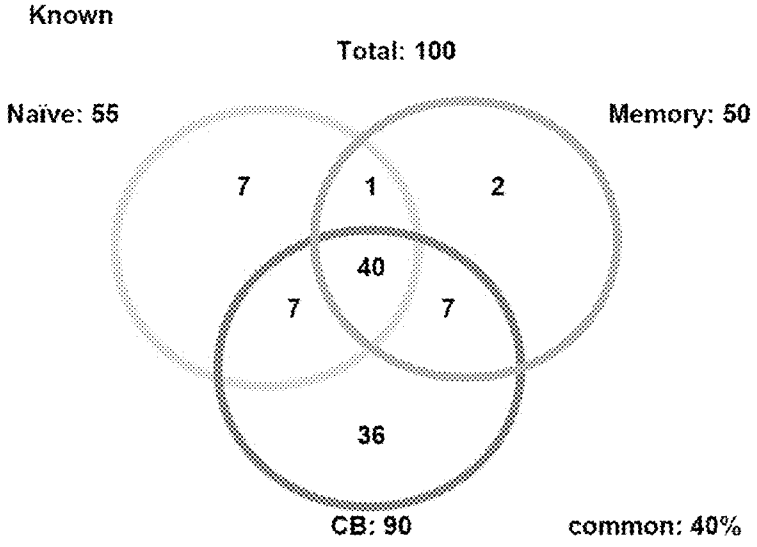

Known
Total: 100
Naïve: 55
Memory: 50
7
1
2
40
7
7
36
CB: 90
common: 40%

FIG. 6

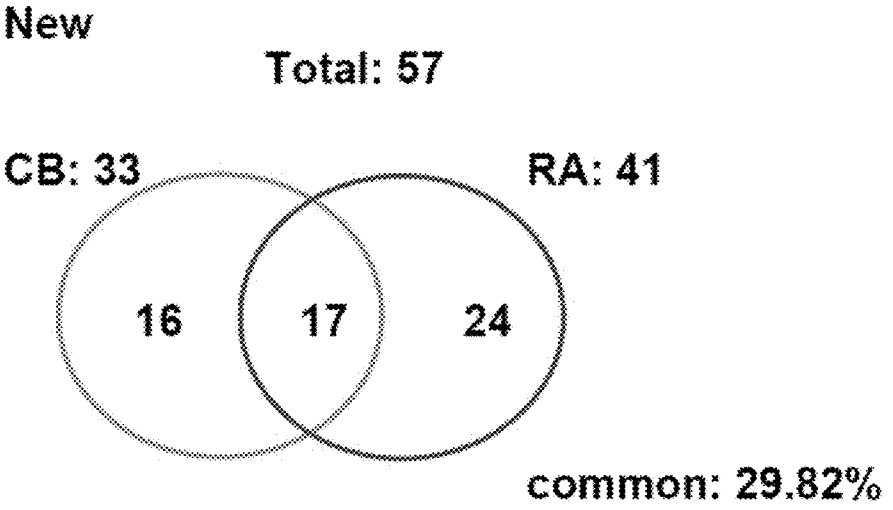

New
Total: 57
CB: 33
RA: 41
16
17
24
common: 29.82%

FIG. 7

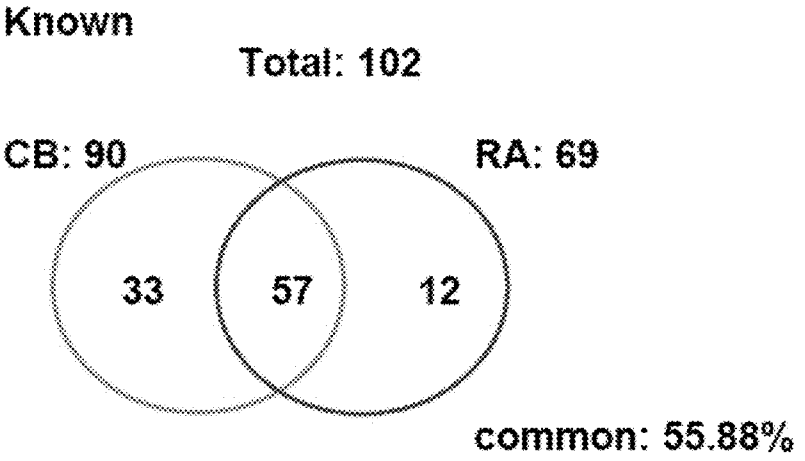
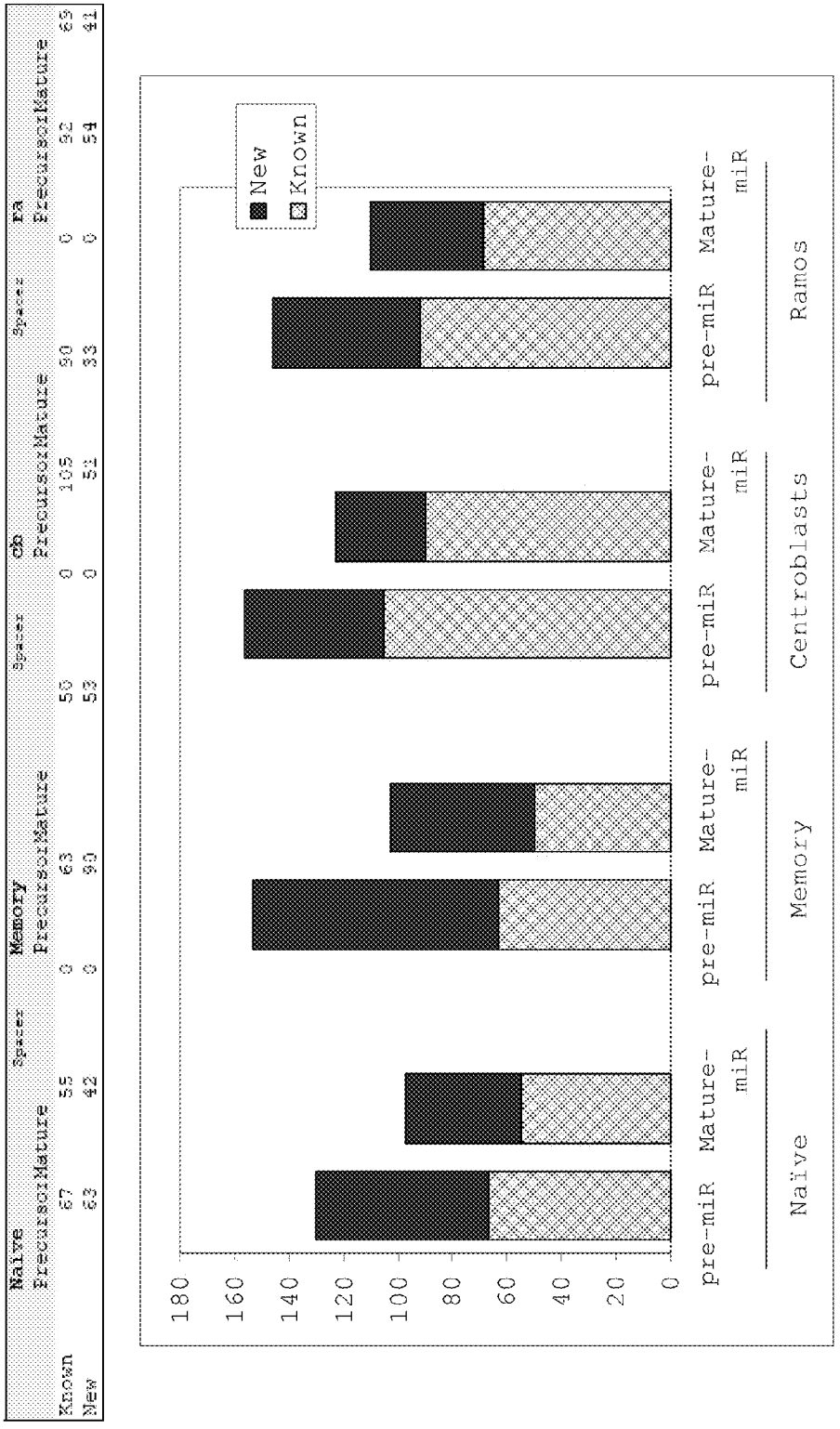

Known
Total: 102
CB: 90
RA: 69
33
57
12
common: 55.88%

FIG. 8



	Naïve		Spacer	Memory		Spacer	Cb		Spacer	Ra	
	Precursor	Mature		Precursor	Mature		Precursor	Mature		Precursor	Mature
Known	67	55	0	63	53	0	105	53	0	92	69
New	63	42	0	90	53	0	51	33	0	54	41

FIG. 9

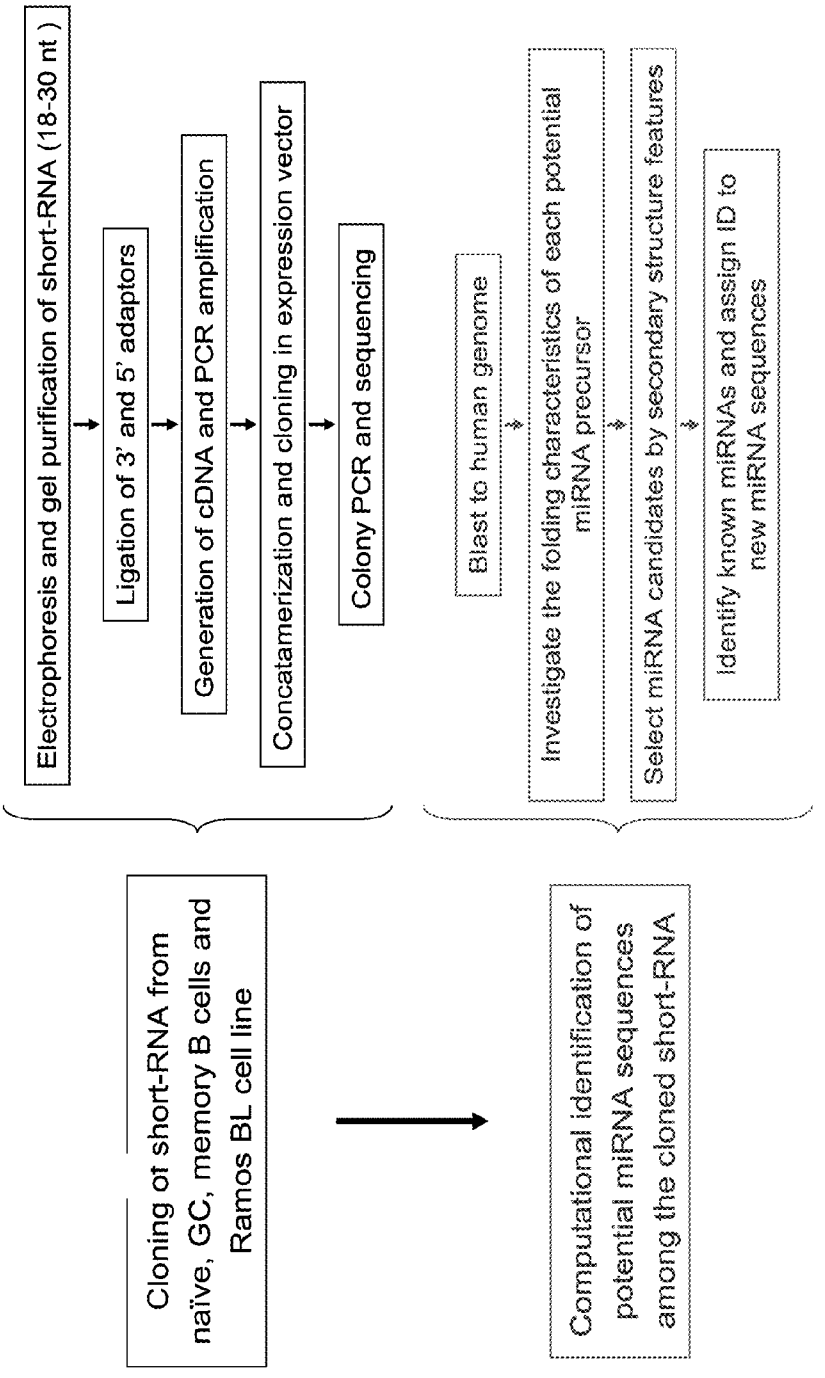

Cloning of short-RNA from naïve, GC, memory B cells and Ramos BL cell line
Electrophoresis and gel purification of short-RNA (18-30 nt)
Ligation of 3' and 5' adaptors
Generation of cDNA and PCR amplification
Concatamerization and cloning in expression vector
Colony PCR and sequencing
Computational identification of potential miRNA sequences among the cloned short-RNA
Blast to human genome
Investigate the folding characteristics of each potential miRNA precursor
Select miRNA candidates by secondary structure features
Identify known miRNAs and assign ID to new miRNA sequences

FIG. 10

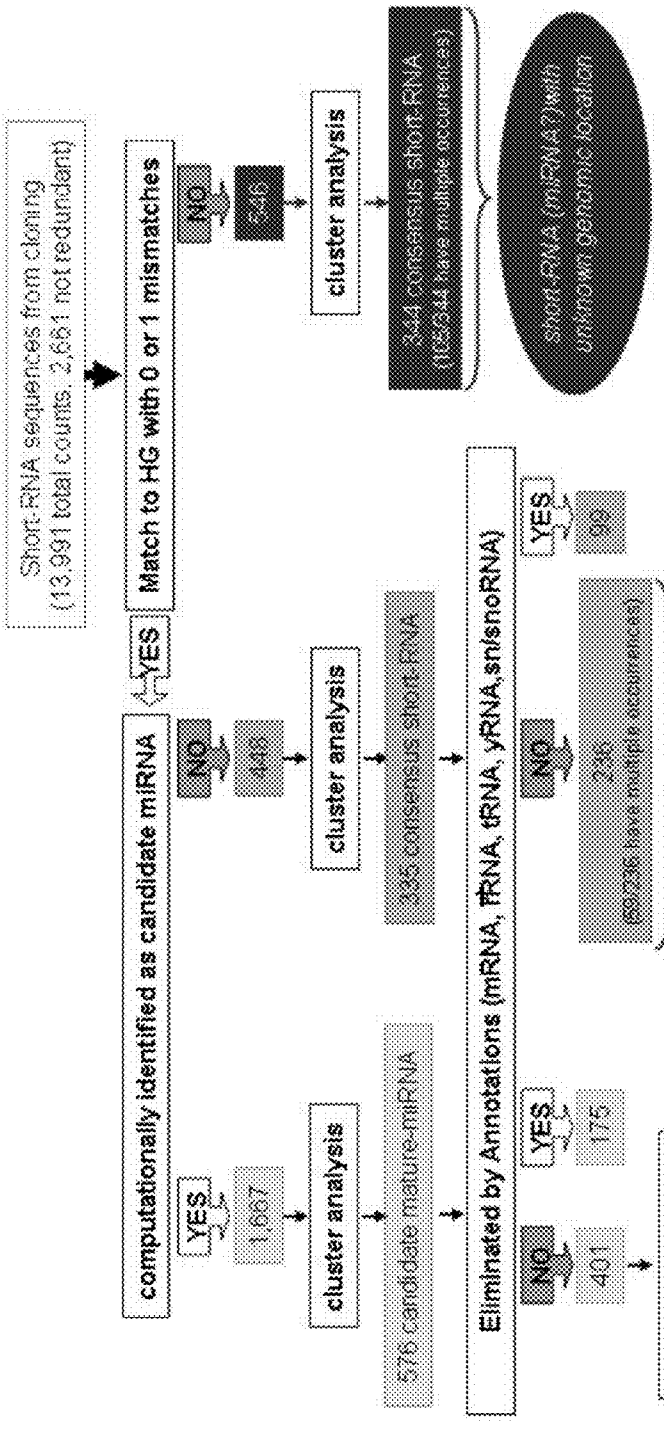

Short-RNA sequences from cloning
(13,991 total counts, 2,661 not redundant)
Match to HG with 0 or 1 mismatches
YES
NO
646
cluster analysis
344 consensus short-RNA
(163244 have multiple occurrences)
Short-RNA (miRNA?) with unknown genomic location
computationally identified as candidate miRNA
YES
1,667
cluster analysis
376 candidate mature-miRNA
NO
449
cluster analysis
335 consensus short-RNA
Eliminated by Annotations (mRNA, tRNA, rRNA, snRNA,snoRNA)
NO
401
miRBase (v.11.0)
YES
129
known miR
NO
272
new miR
miRNA
YES
175
NO
238
(69736 have multiple occurrences)
short-RNA of unknown location
YES
89

FIG. 11

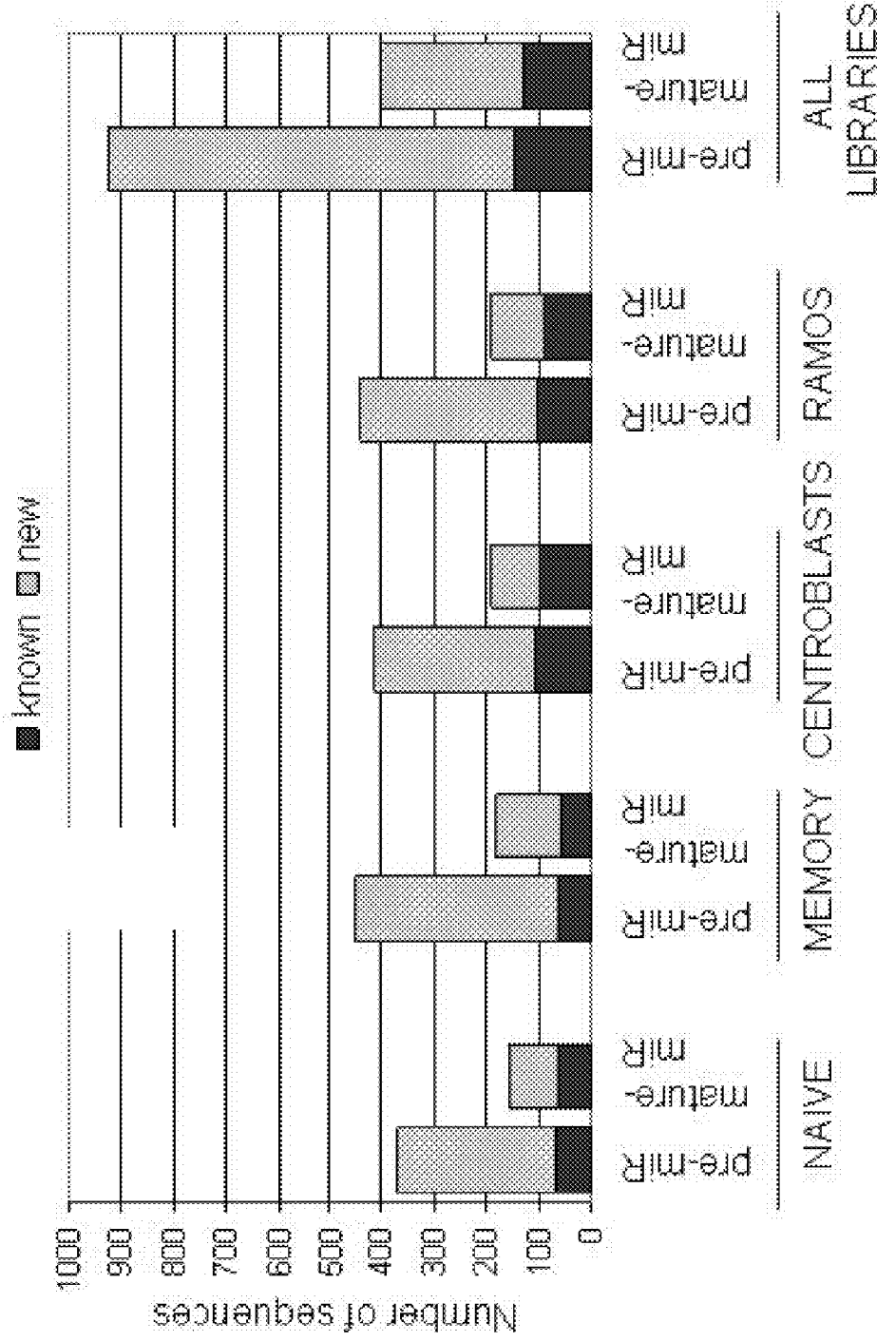
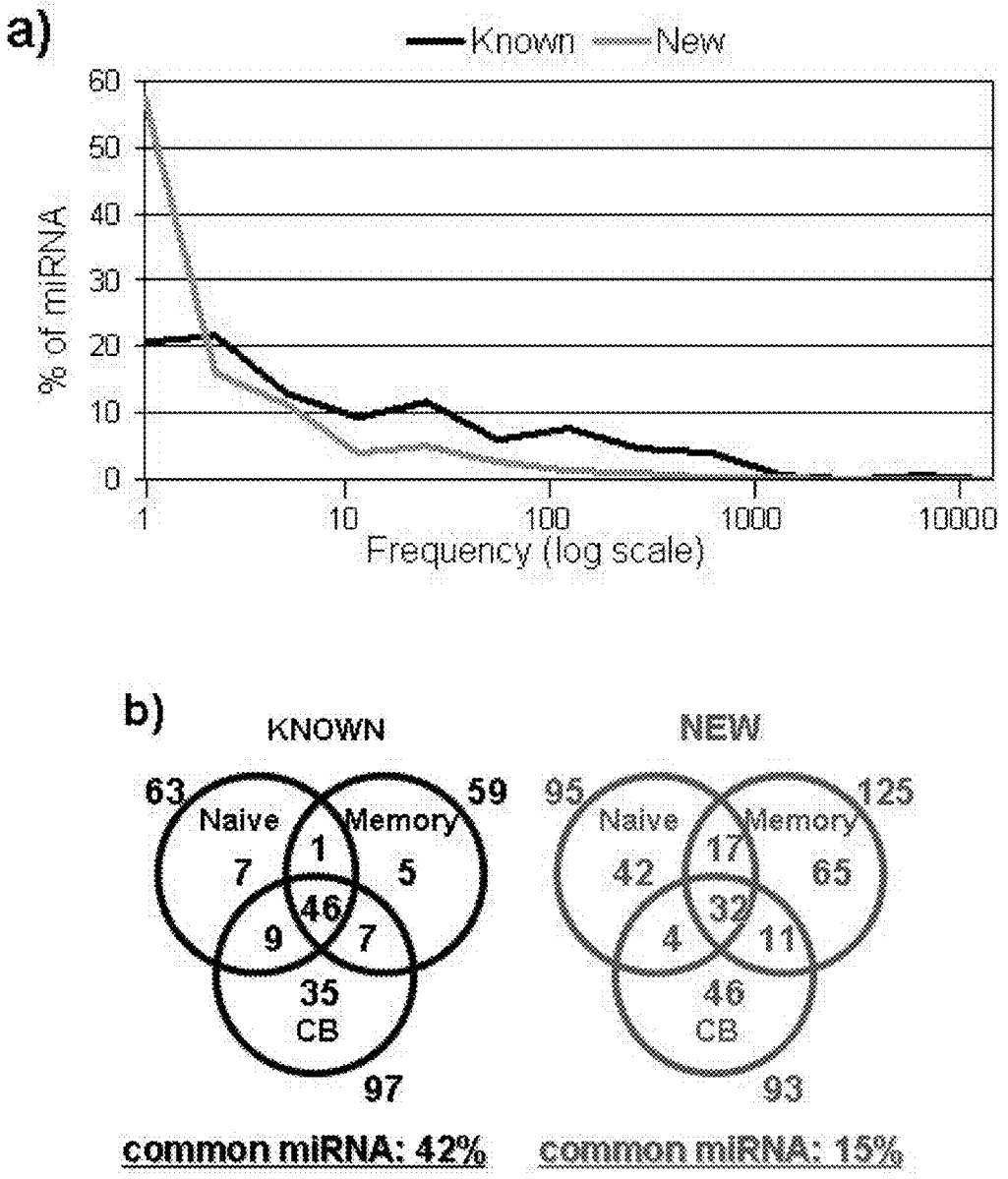

known
new
Number of sequences
1000
900
800
700
600
500
400
300
200
100
0
pre-miR
mature-miR
NAIVE
MEMORY
CENTROBLASTS
RAMOS
ALL LIBRARIES

FIG. 12


a)
Known
New
% of miRNA
60
50
40
30
20
10
0
1
10
100
1000
10000
Frequency (log scale)
b)
KNOWN
63
Naive
59
Memory
7
1
5
46
9
7
35
CB
97
common miRNA: 42%
NEW
95
Naive
125
Memory
42
17
65
32
4
11
46
CB
93
common miRNA: 15%

FIGS. 13A-B

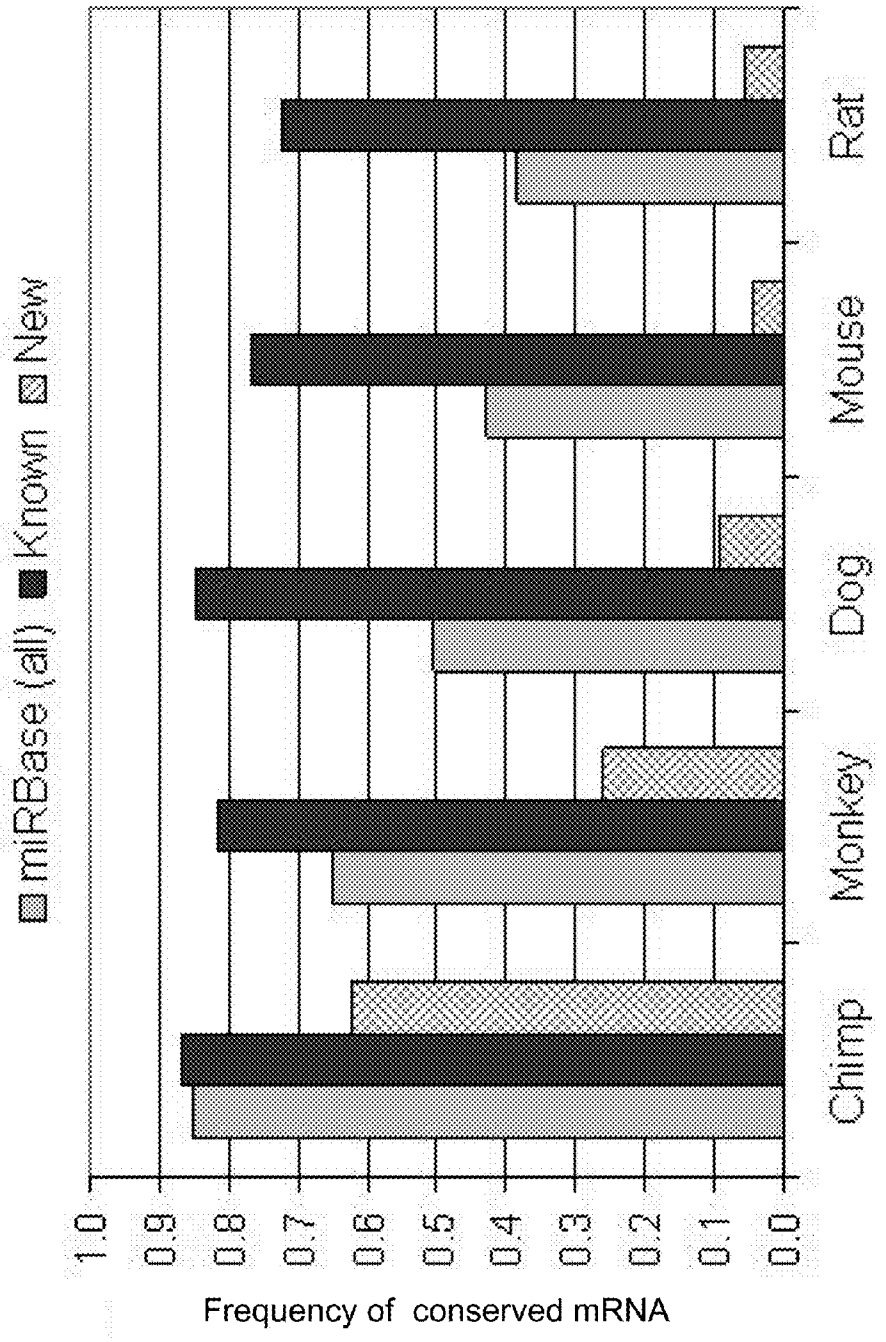

miRBase (all)
Known
New
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Frequency of conserved mRNA
Chimp
Monkey
Dog
Mouse
Rat

FIG. 13C

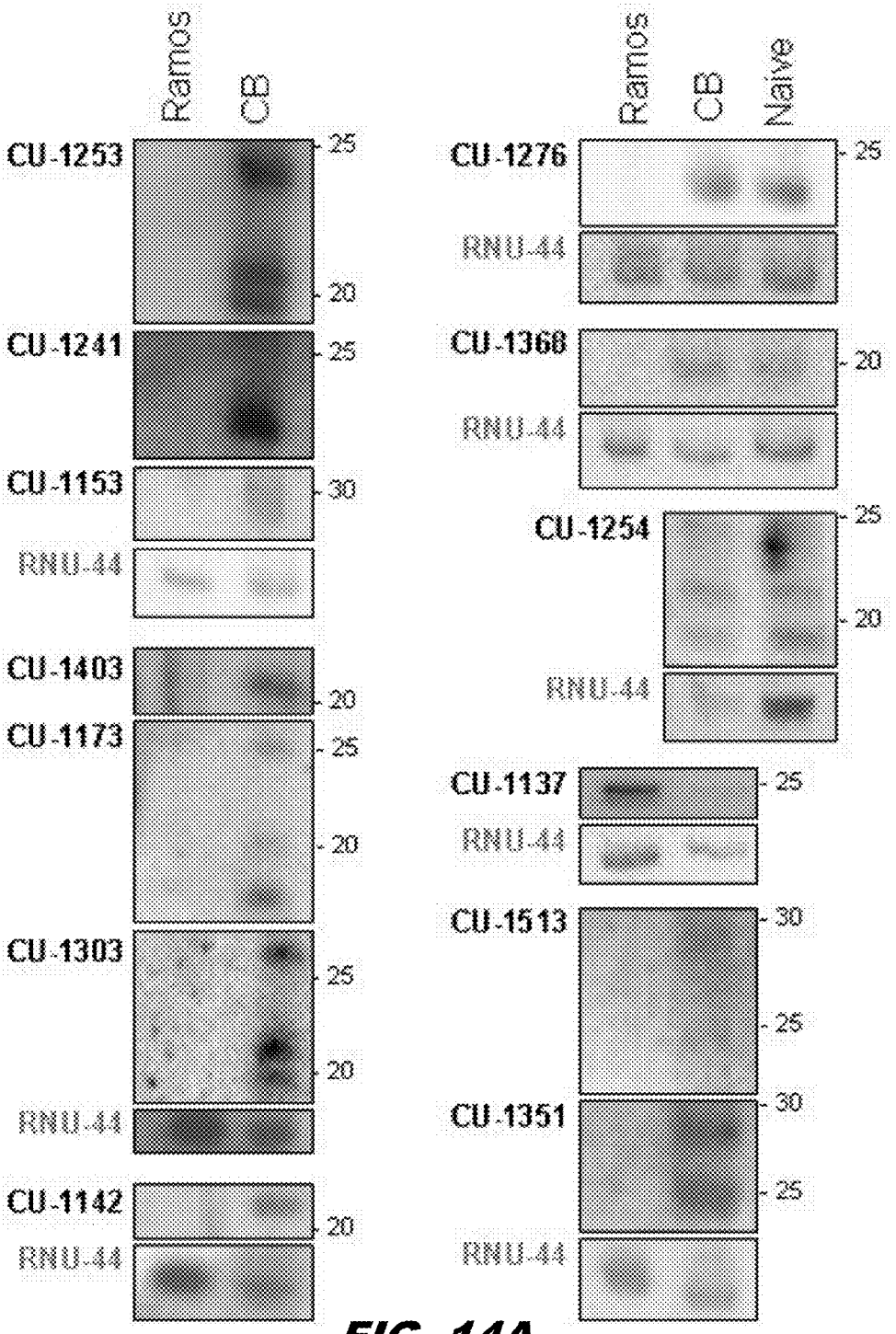

Ramos
CB
CU-1253
25
20
CU-1241
25
CU-1153
30
RNU-44
CU-1403
20
CU-1173
25
20
CU-1303
25
20
RNU-44
CU-1142
20
RNU-44
Ramos
CB
Naive
CU-1276
25
RNU-44
CU-1368
20
RNU-44
CU-1254
25
20
RNU-44
CU-1137
25
RNU-44
CU-1513
30
25
CU-1351
30
25
RNU-44

FIG. 14A

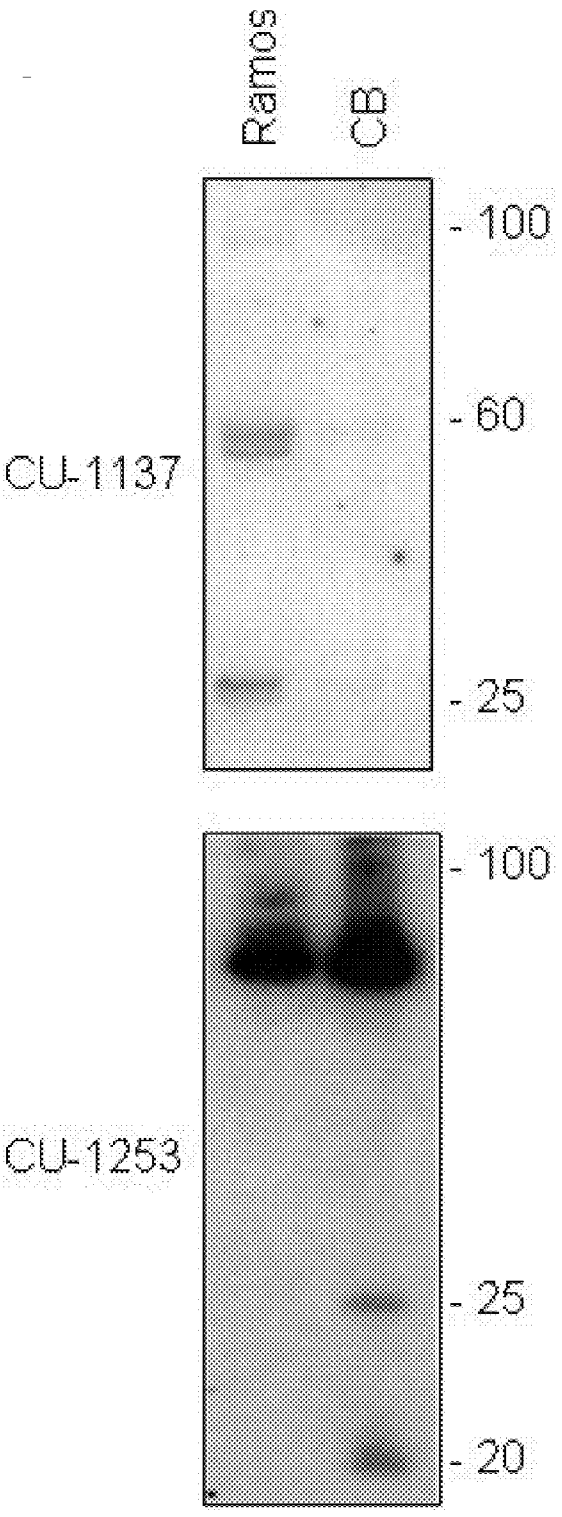


FIG. 14B

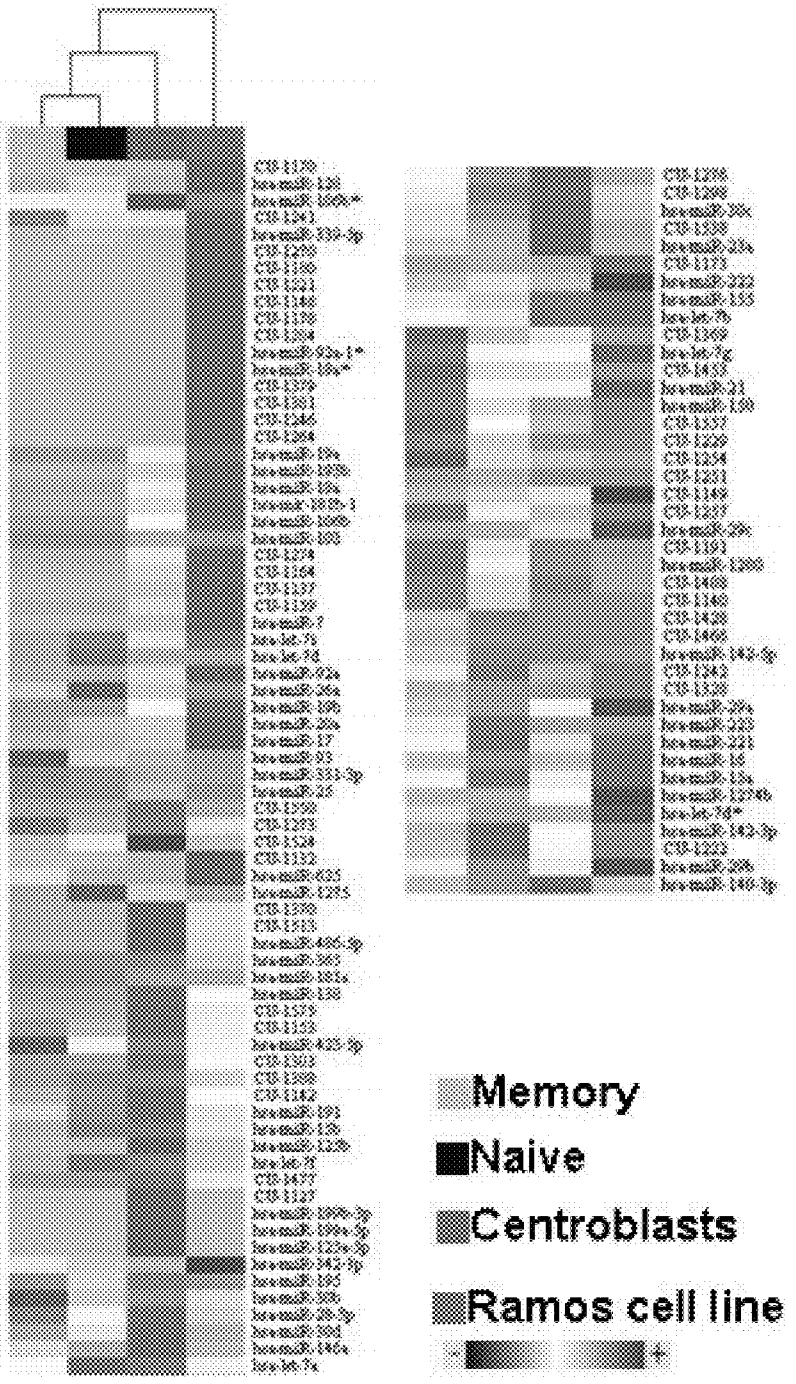


FIG. 15A

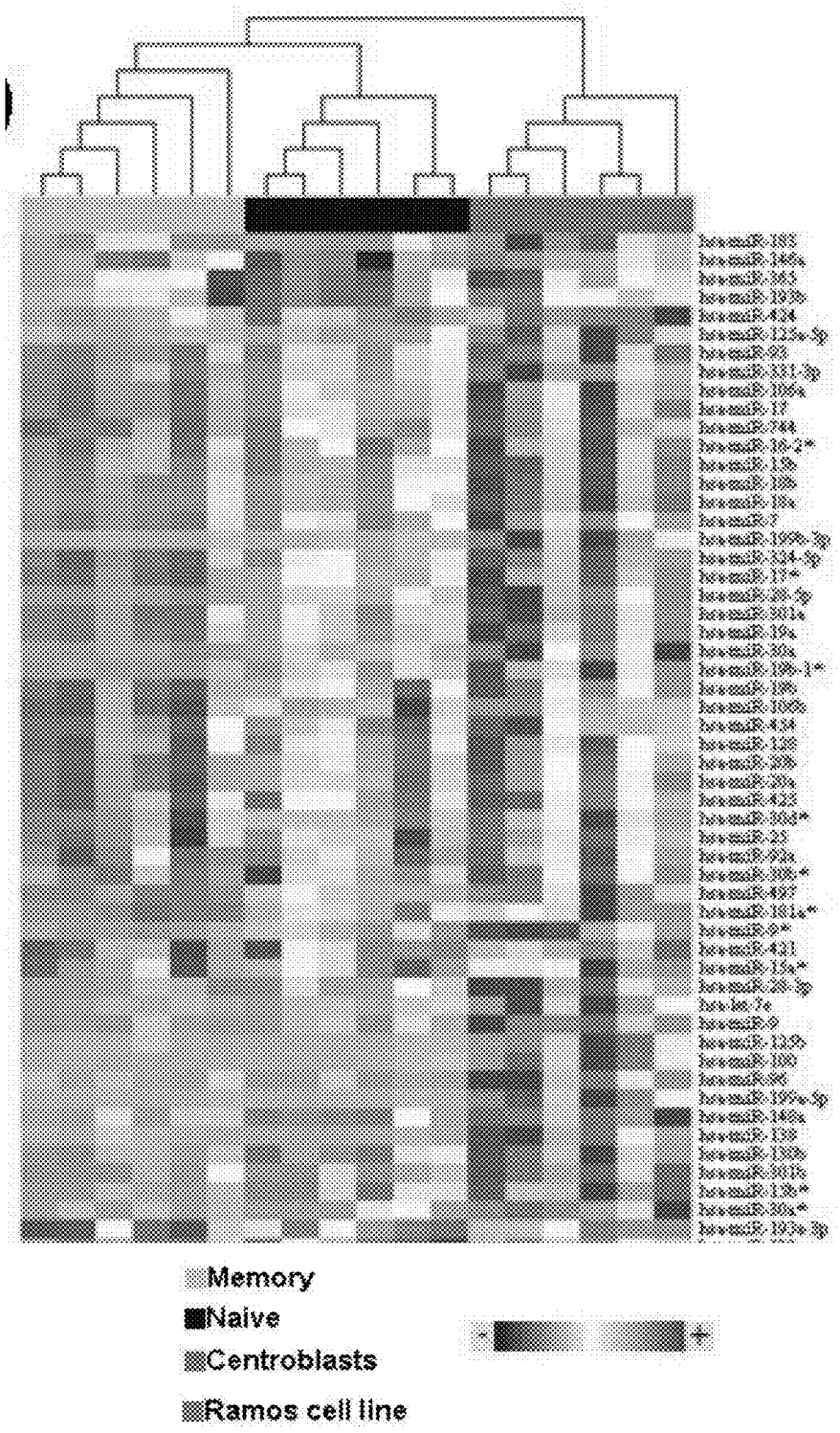


FIG. 15B-cont

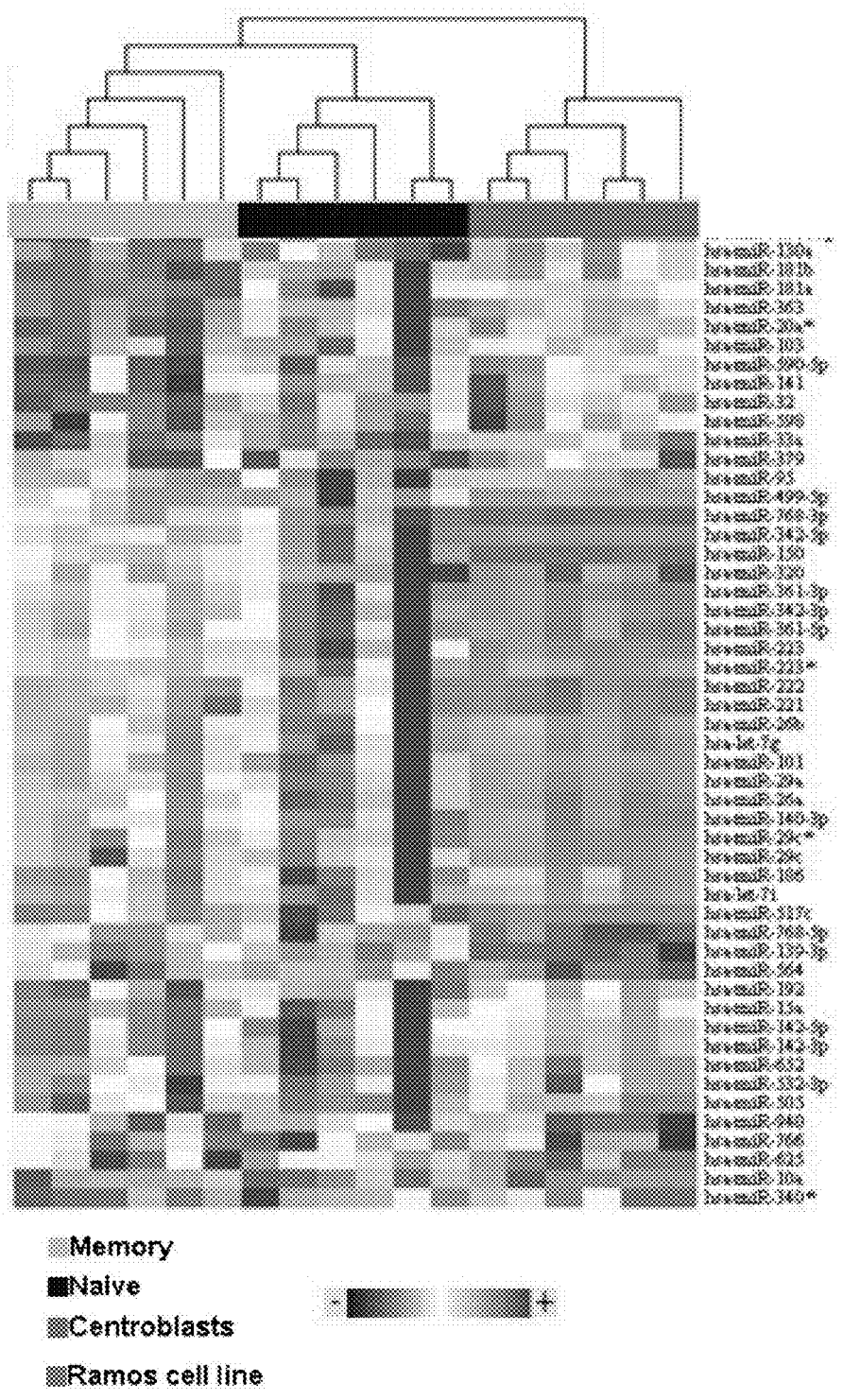


FIG. 15B - cont.

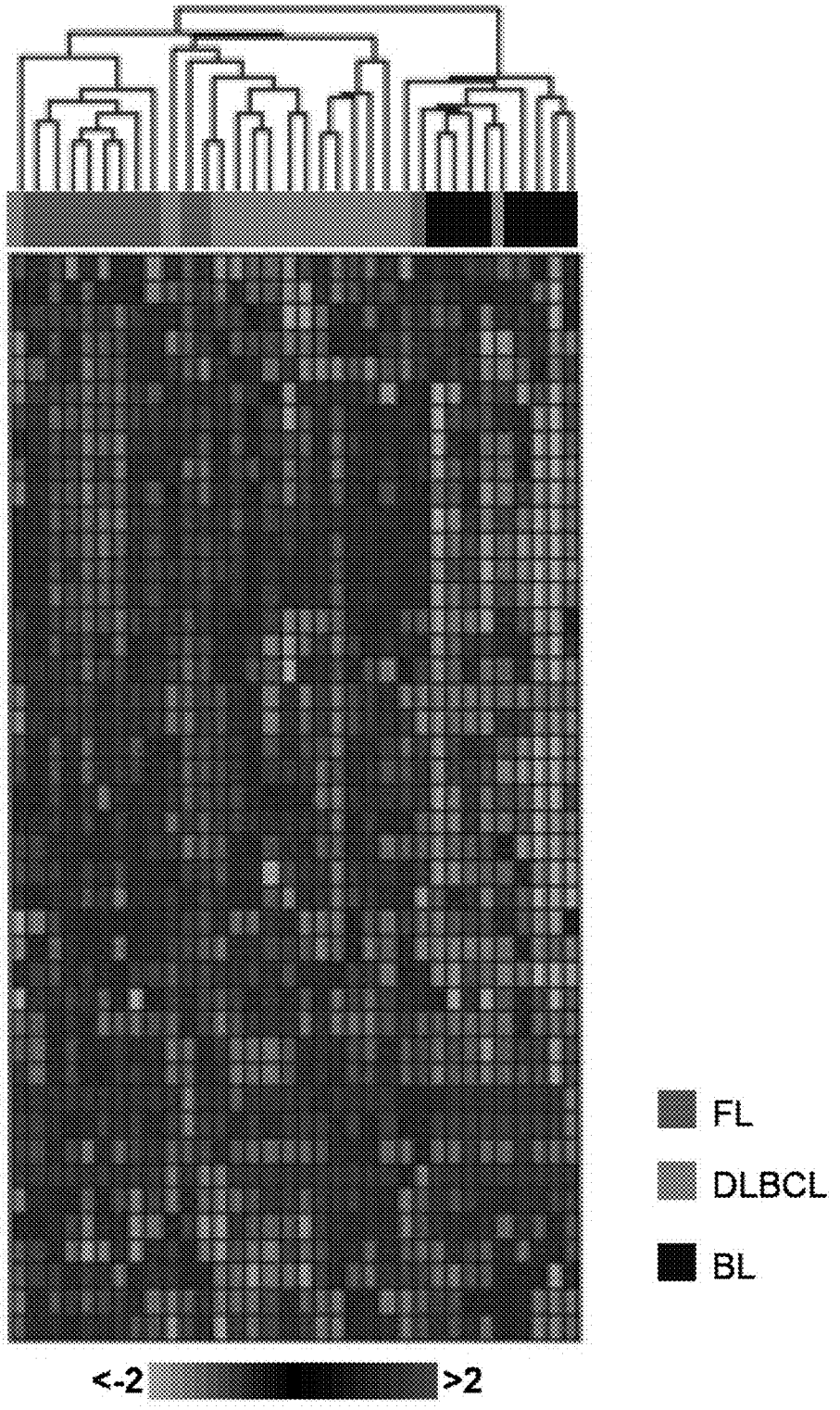
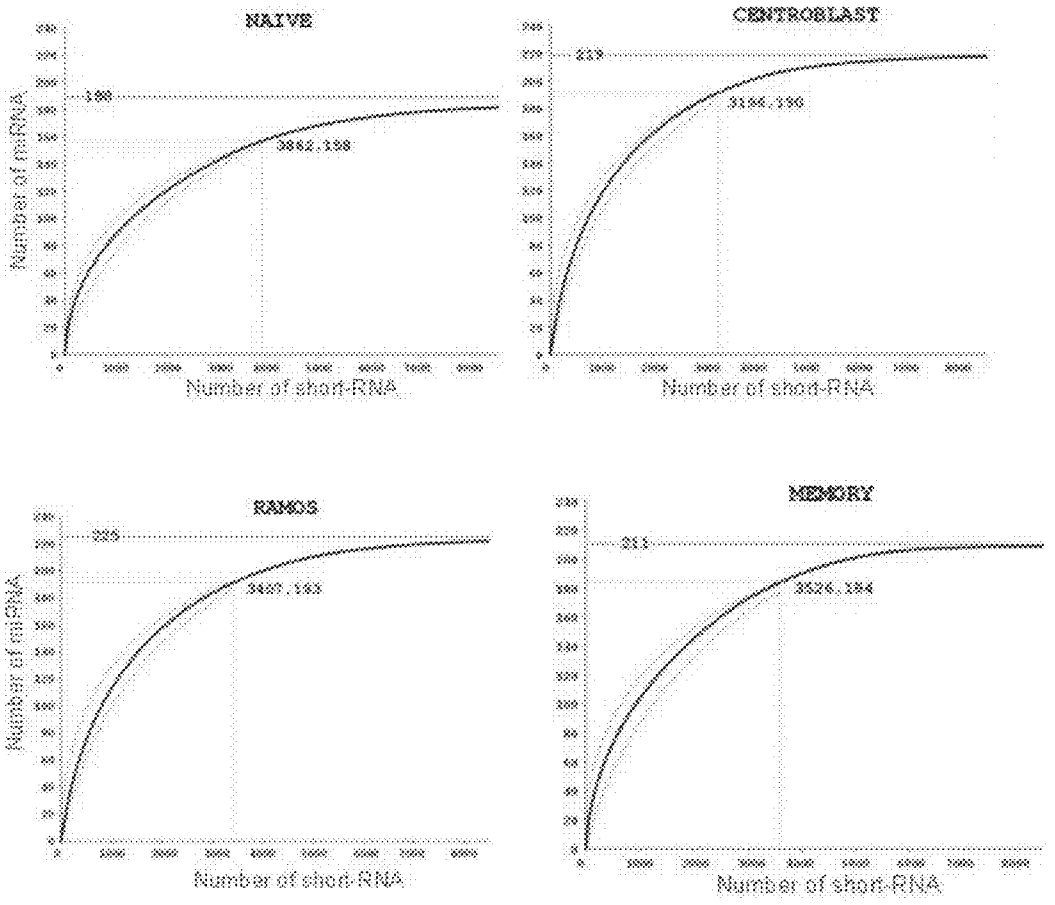


FIG. 16



	Naive	Memory	Centroblasts	Ramos
Completeness	84.0%	87.2%	86.8%	85.8%
Estimated total mature miRNA	188	211	219	225

FIG. 17

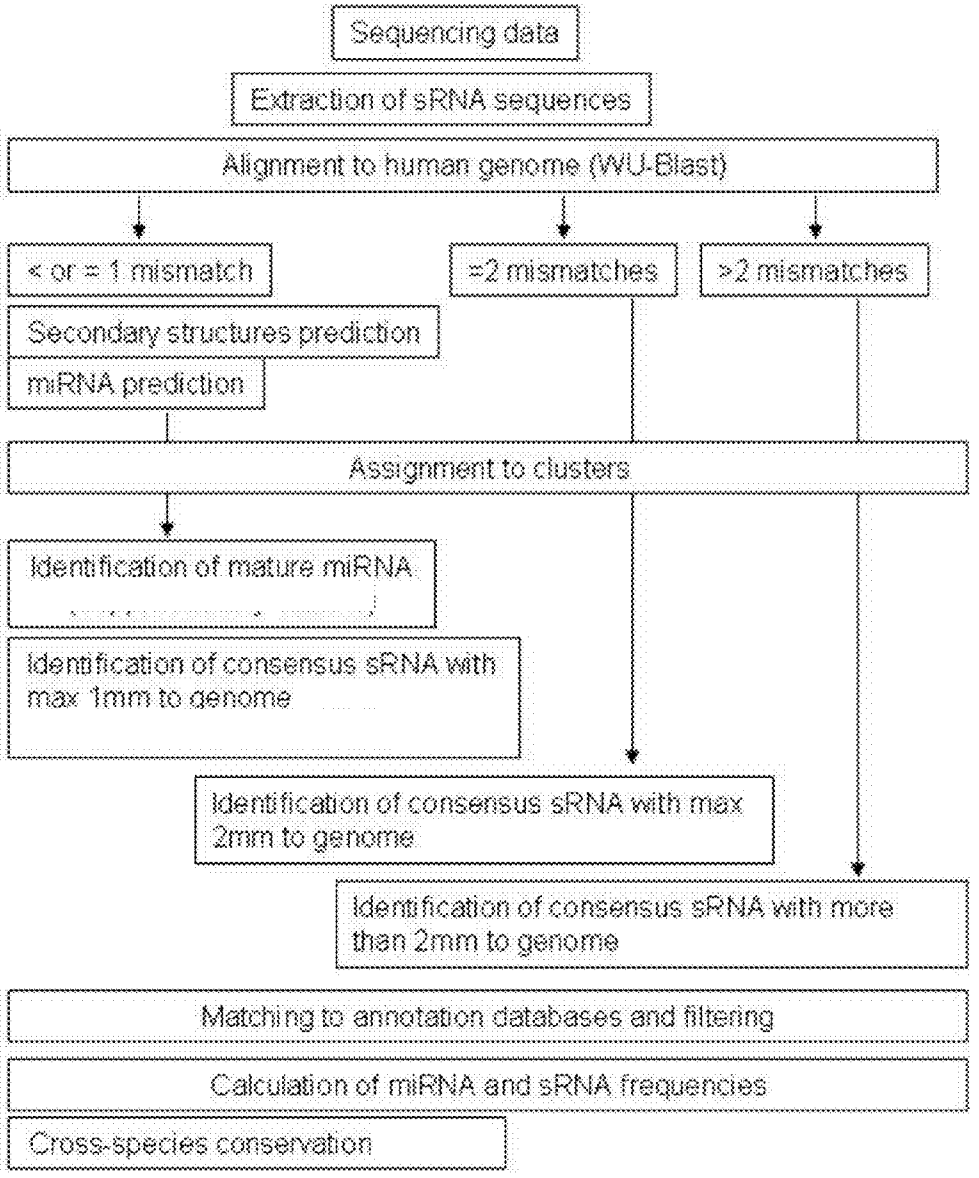

Sequencing data
Extraction of sRNA sequences
Alignment to human genome (WU-Blast)
< or = 1 mismatch
=2 mismatches
>2 mismatches
Secondary structures prediction
miRNA prediction
Assignment to clusters
Identification of mature miRNA
Identification of consensus sRNA with max 1mm to genome
Identification of consensus sRNA with max 2mm to genome
Identification of consensus sRNA with more than 2mm to genome
Matching to annotation databases and filtering
Calculation of miRNA and sRNA frequencies
Cross-species conservation

FIG. 18

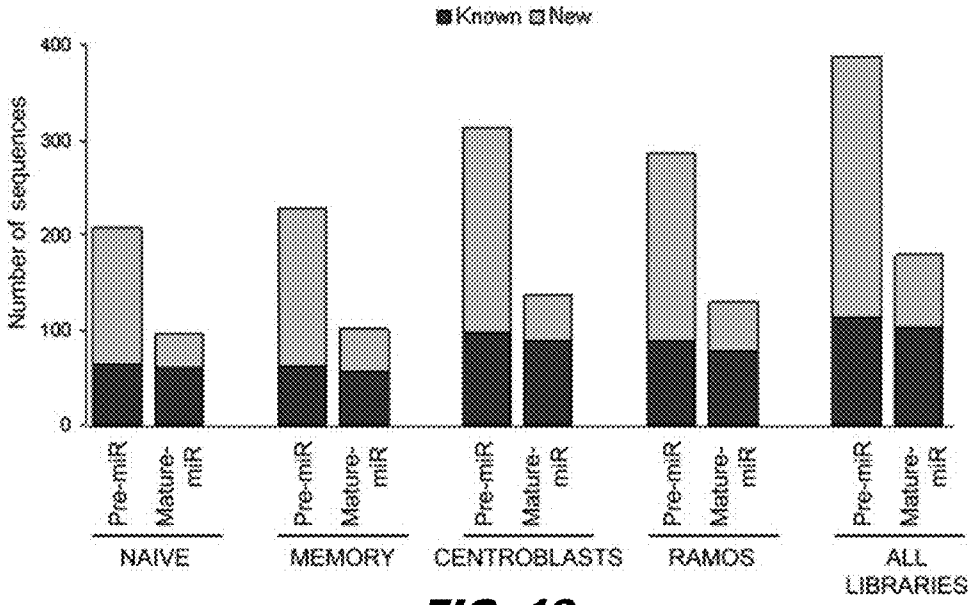


FIG. 19

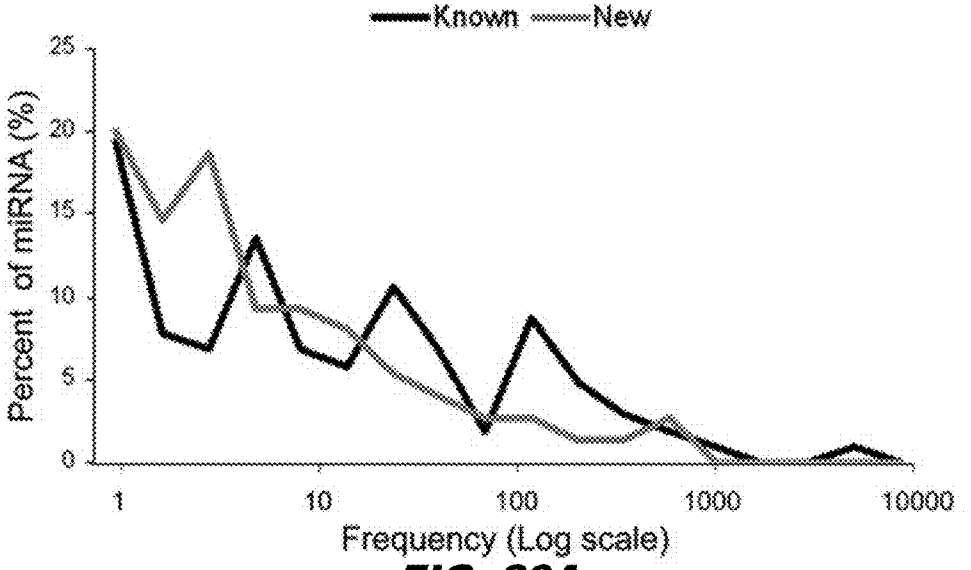


FIG. 20A

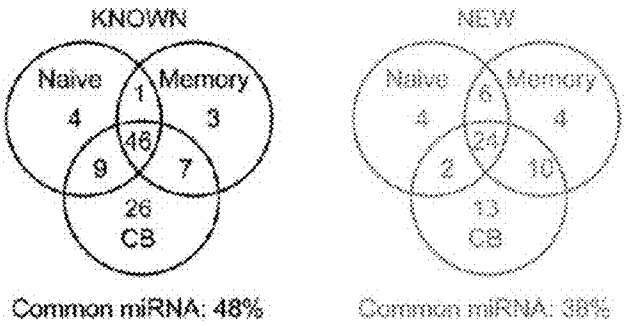


FIG. 20B

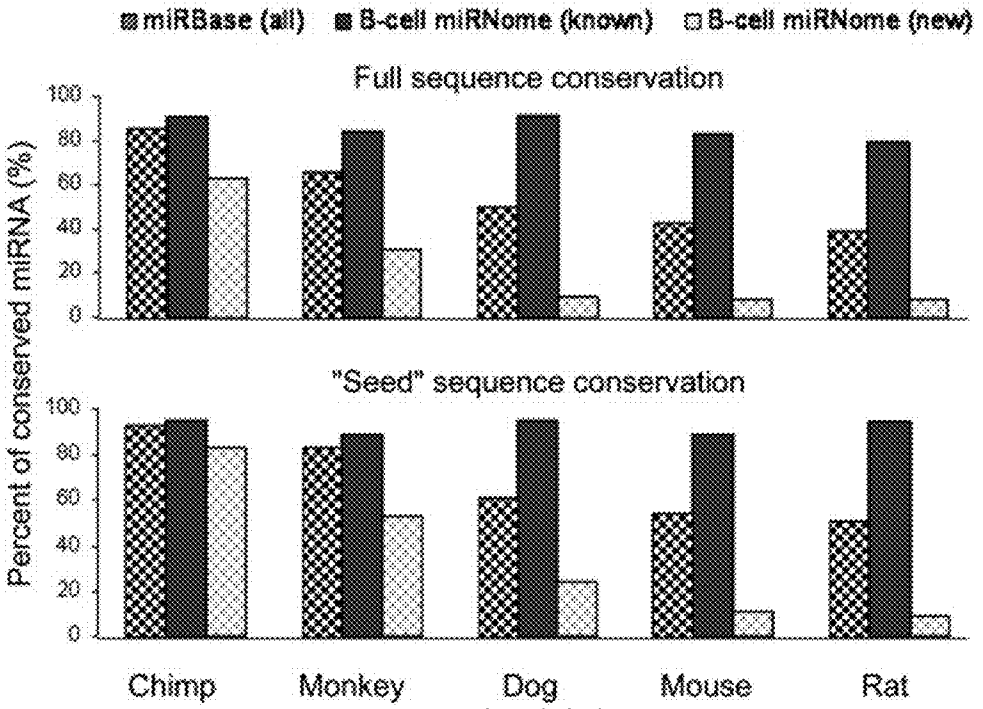


FIG. 20C

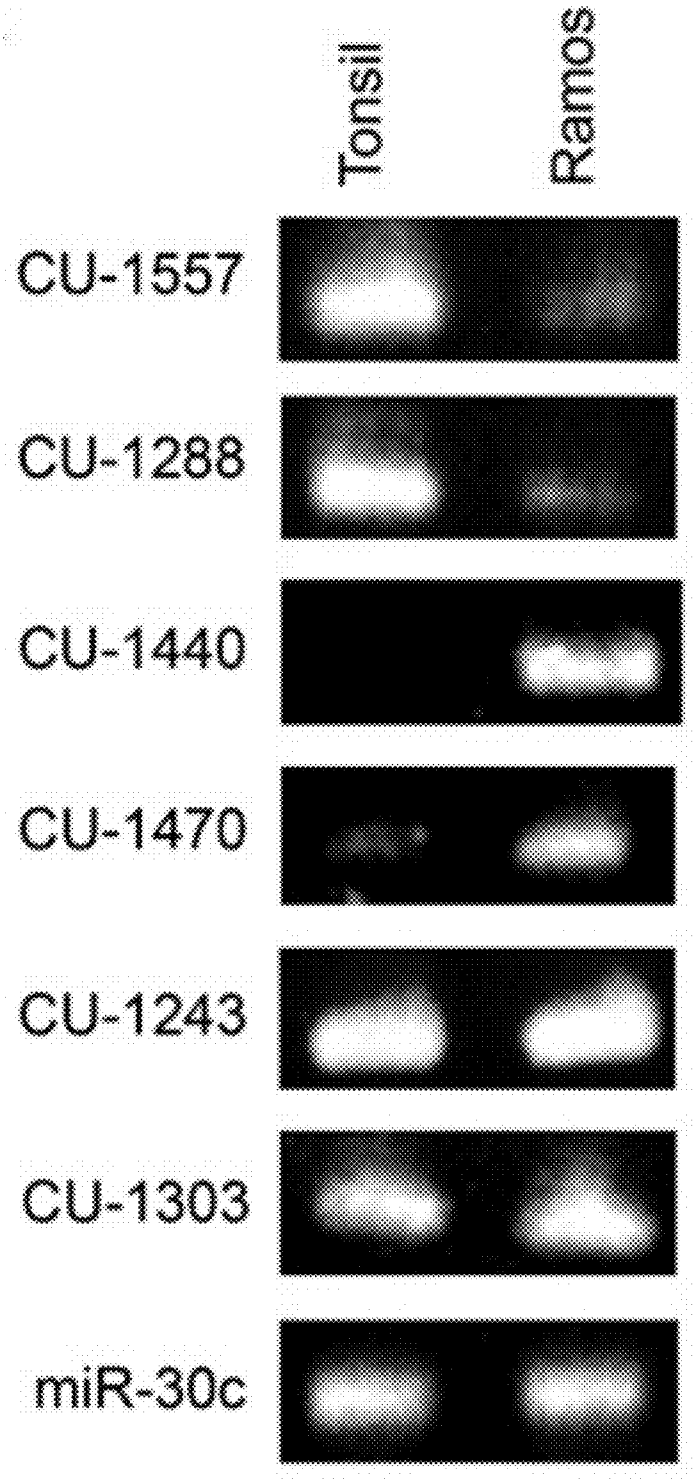

Tonsil
Ramos
CU-1557
CU-1288
CU-1440
CU-1470
CU-1243
CU-1303
miR-30c

FIG. 21A

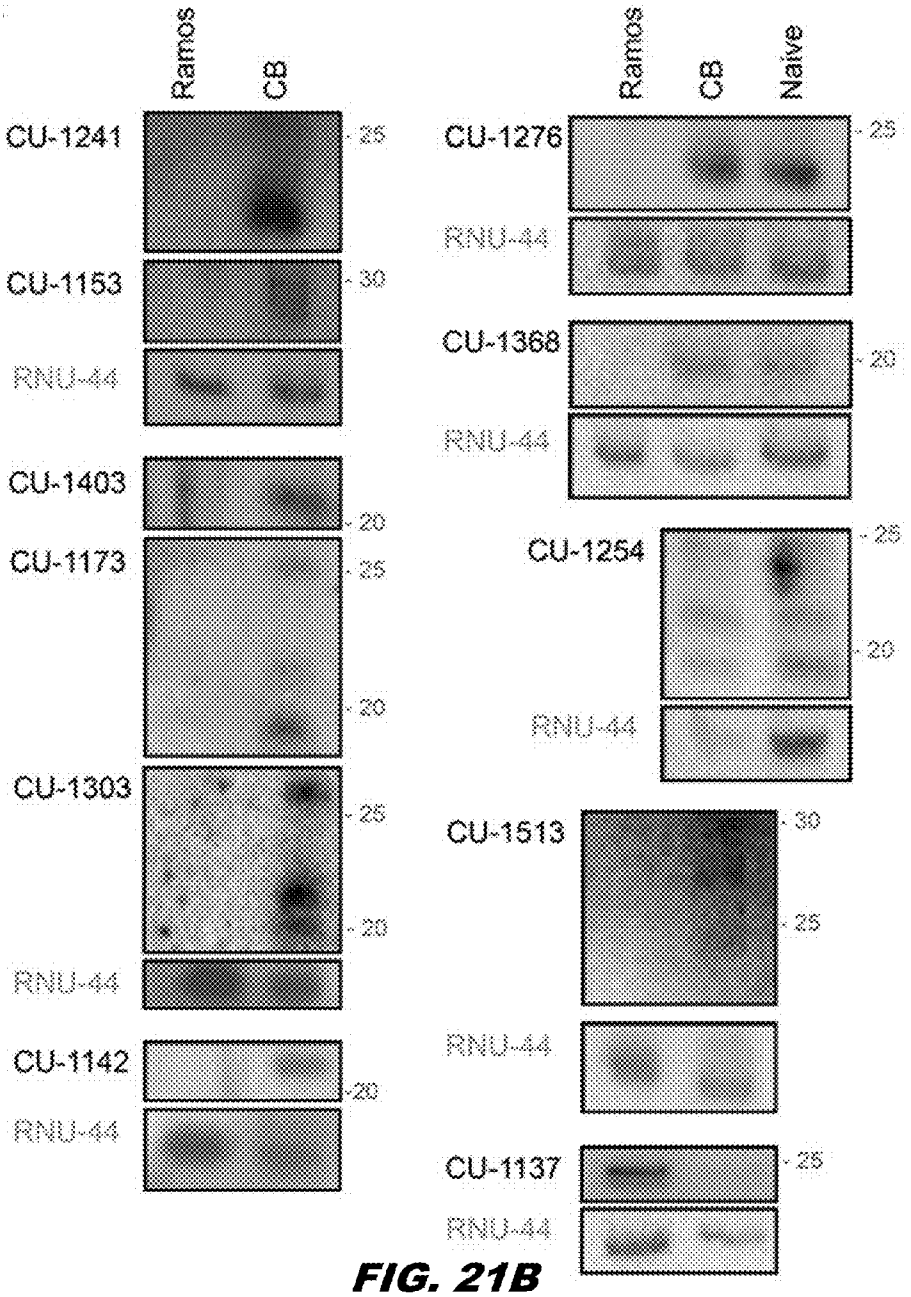

Ramos
CB
CU-1241
35
CU-1153
30
RNU-44
CU-1403
20
CU-1173
35
20
CU-1303
25
20
RNU-44
CU-1142
20
RNU-44
Ramos
CB
Naive
CU-1276
25
RNU-44
CU-1368
20
RNU-44
CU-1254
25
20
RNU-44
CU-1513
30
25
RNU-44
CU-1137
25
RNU-44

FIG. 21B

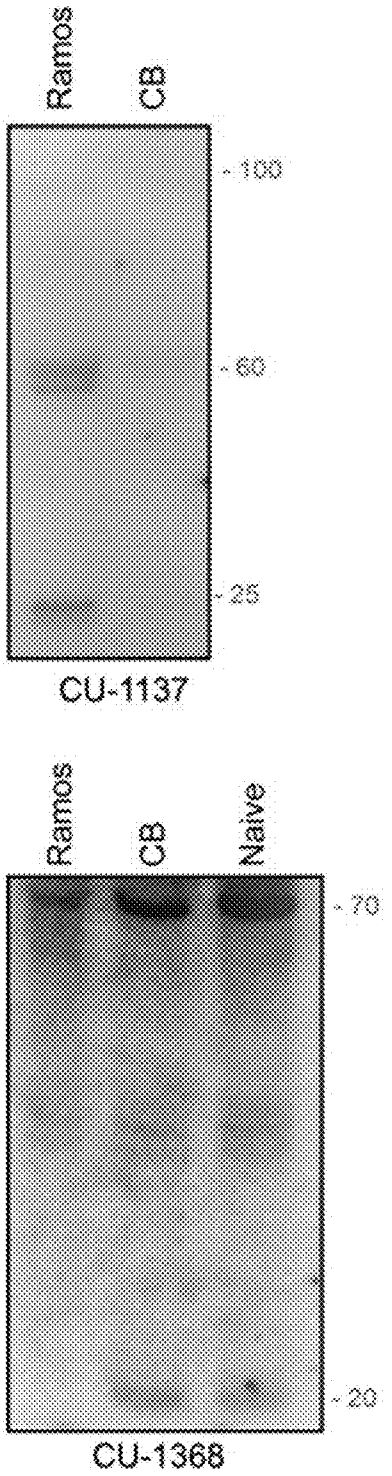


FIG. 21C

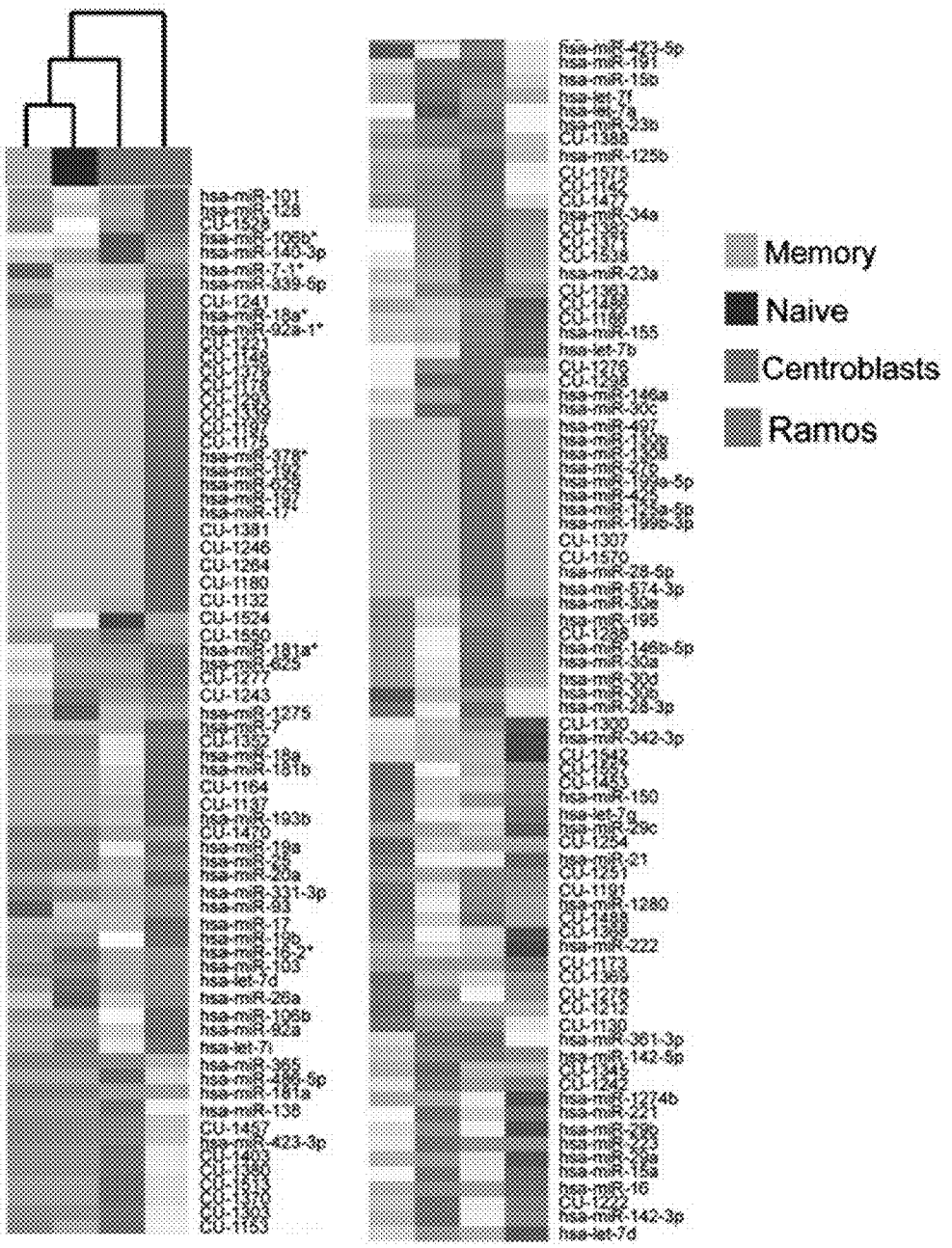


FIG. 22A

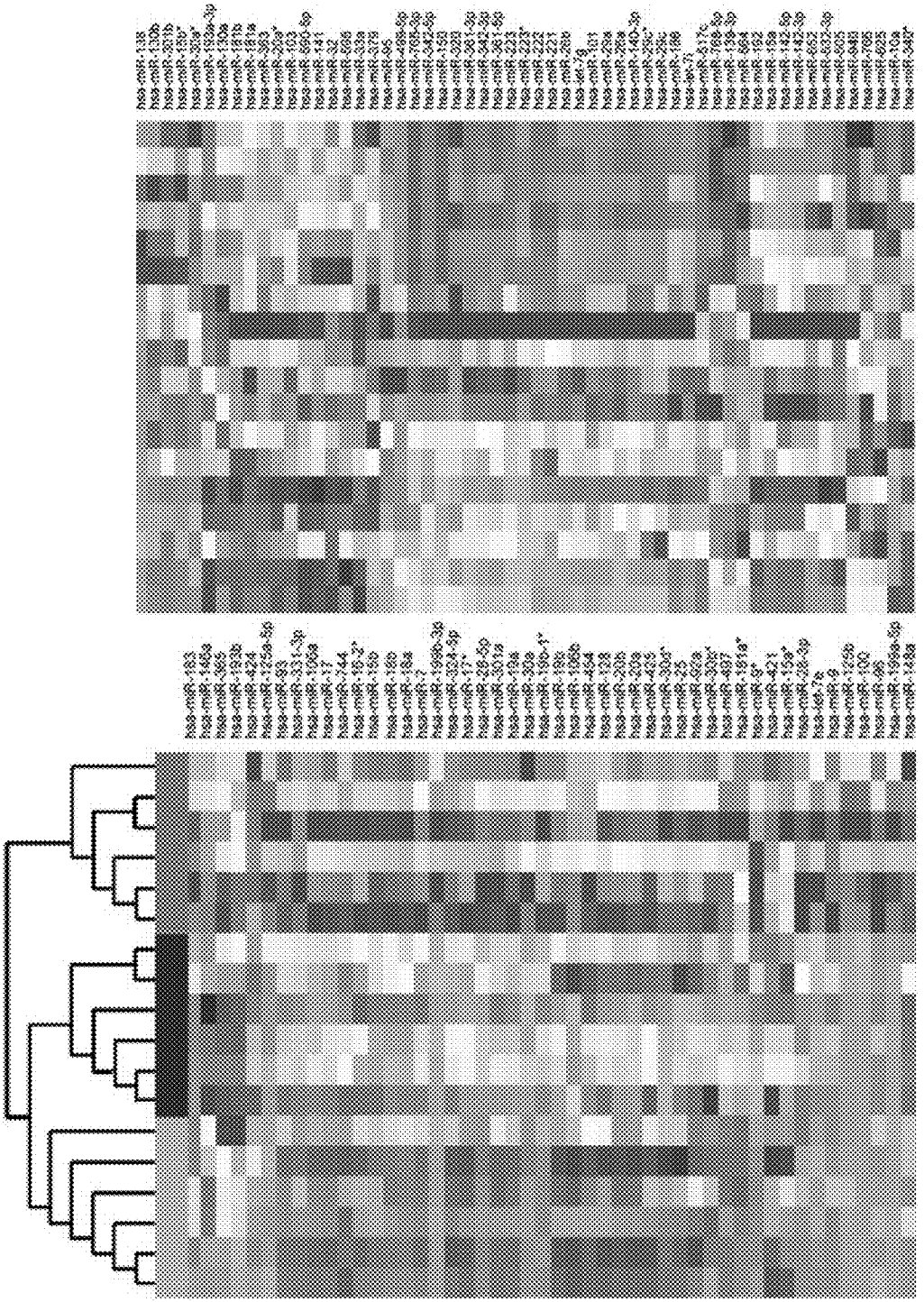
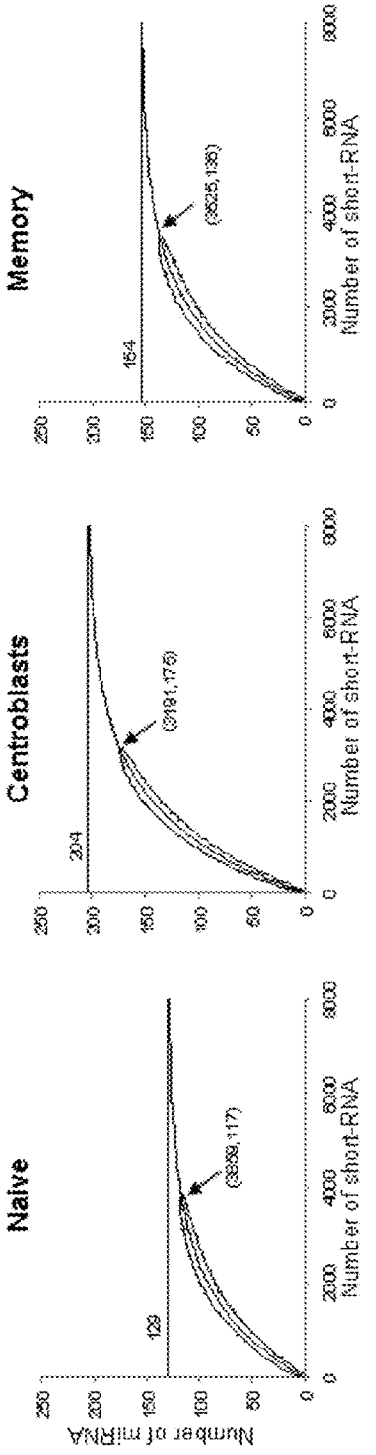


FIG. 22B



	Naive	Centroblasts	Memory	Ramos
Completeness	90.7%	85.8%	88.3%	91%
Estimated total mature miRNA	129	204	154	189

FIG. 23

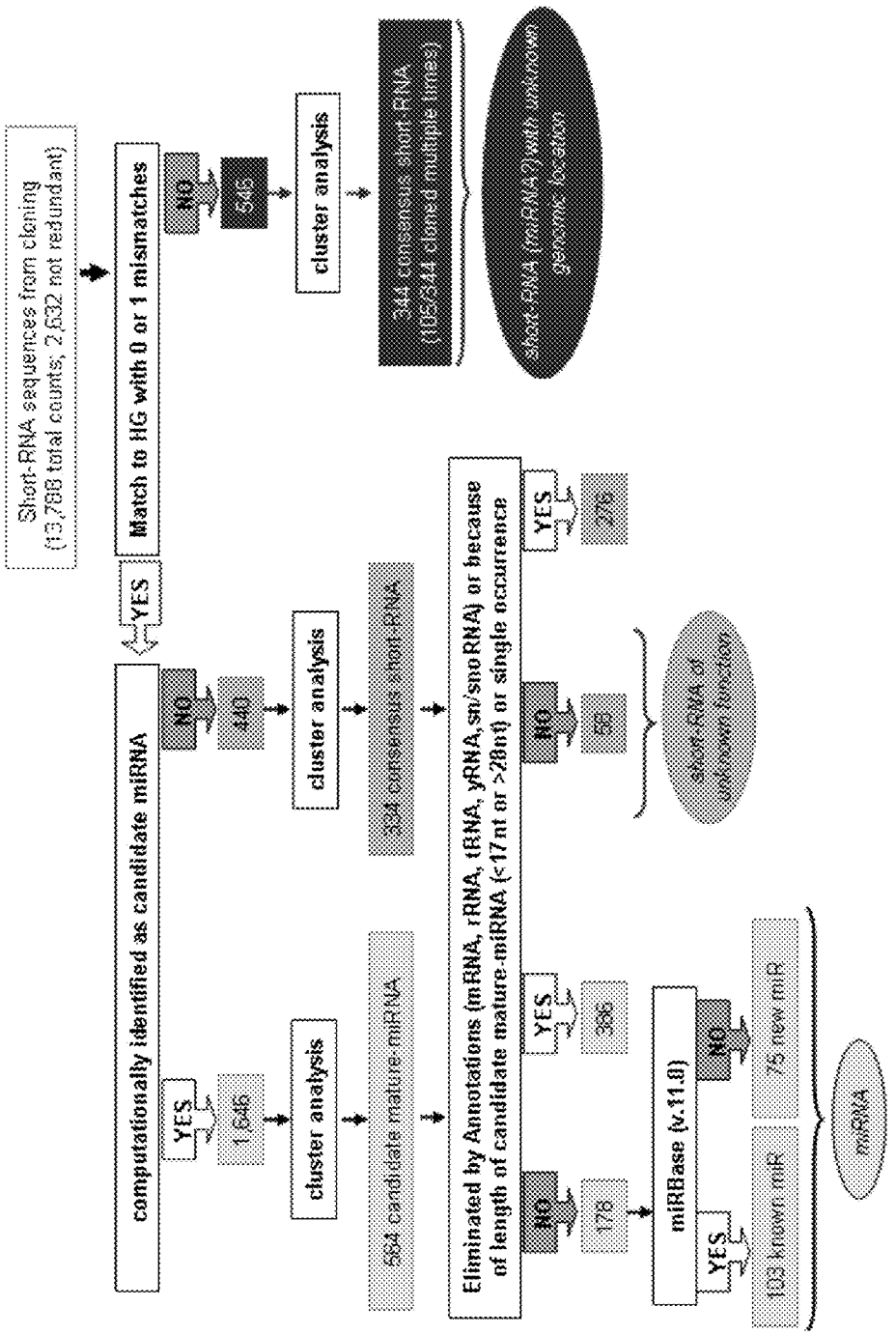

Short-RNA sequences from cloning
(13,788 total counts; 2,632 not redundant)
Match to HG with 0 or 1 mismatches
YES
NO
545
cluster analysis
344 consensus short-RNA
(105/344 cloned multiple times)
short-RNA (miRNA?) with unknown genomic location
computationally identified as candidate miRNA
YES
1,646
NO
440
cluster analysis
564 candidate mature-miRNA
cluster analysis
334 consensus short-RNA
Eliminated by Annotations (mRNA, rRNA, tRNA, yRNA, sn/snoRNA) or because of length of candidate mature-miRNA (<17nt or >28nt) or single occurrence
NO
178
YES
366
NO
58
YES
276
short-RNA of unknown function
miRBase (v.11.0)
YES
103 known miR
NO
75 new miR
miRNA

FIG. 24

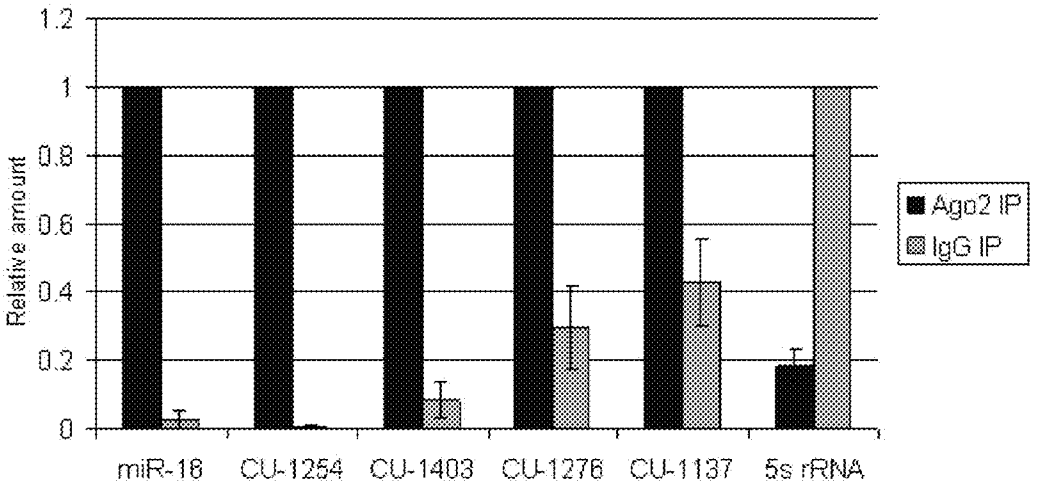

1.2
1
0.8
0.6
0.4
0.2
0
Relative amount
Ago2 IP
IgG IP
miR-18
CU-1254
CU-1403
CU-1276
CU-1137
5s rRNA

FIG. 25

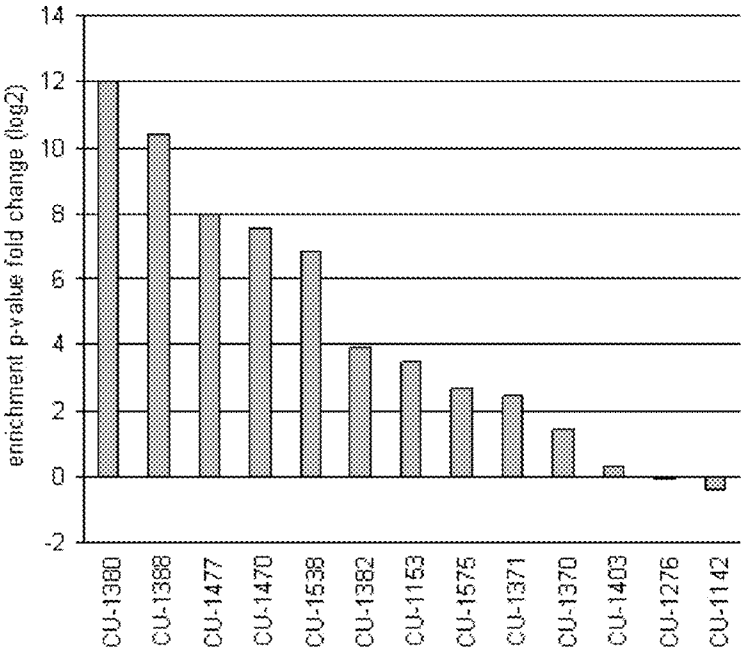

14
12
10
8
6
4
2
0
-2
enrichment p-value fold change (log2)
CU-1380
CU-1388
CU-1477
CU-1470
CU-1538
CU-1382
CU-1153
CU-1575
CU-1371
CU-1370
CU-1403
CU-1276
CU-1142

FIG. 26

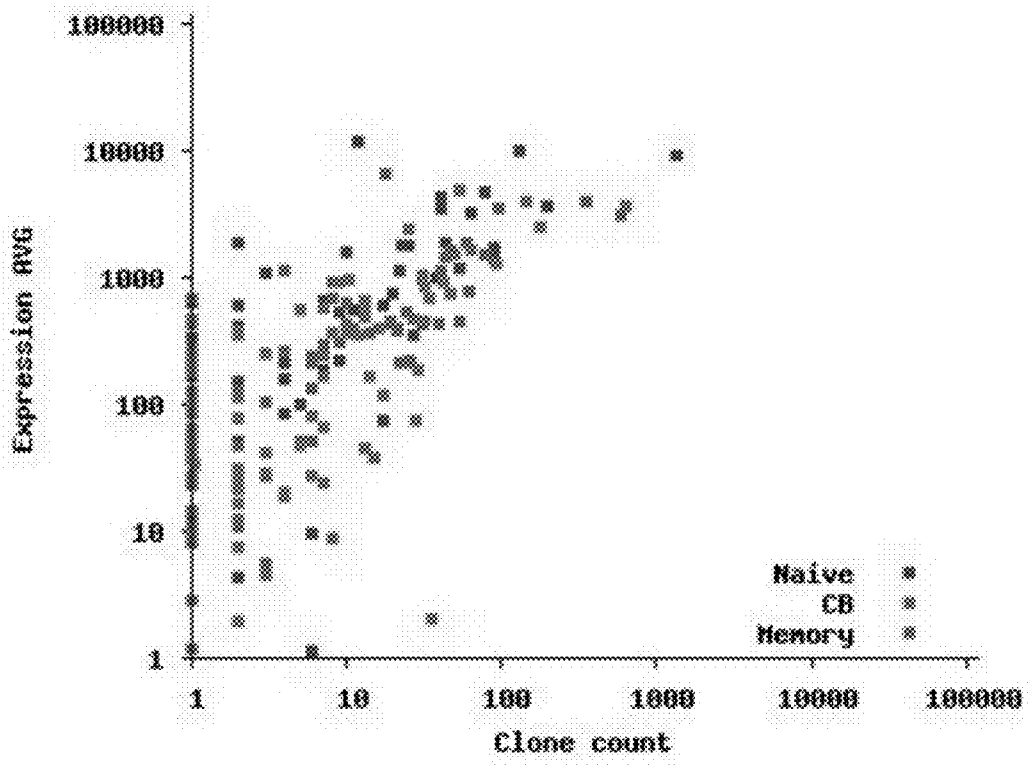

100000
10000
1000
100
10
1
Expression AVG
1
10
100
1000
10000
100000
Clone count
Naive
CB
Memory

FIG. 27

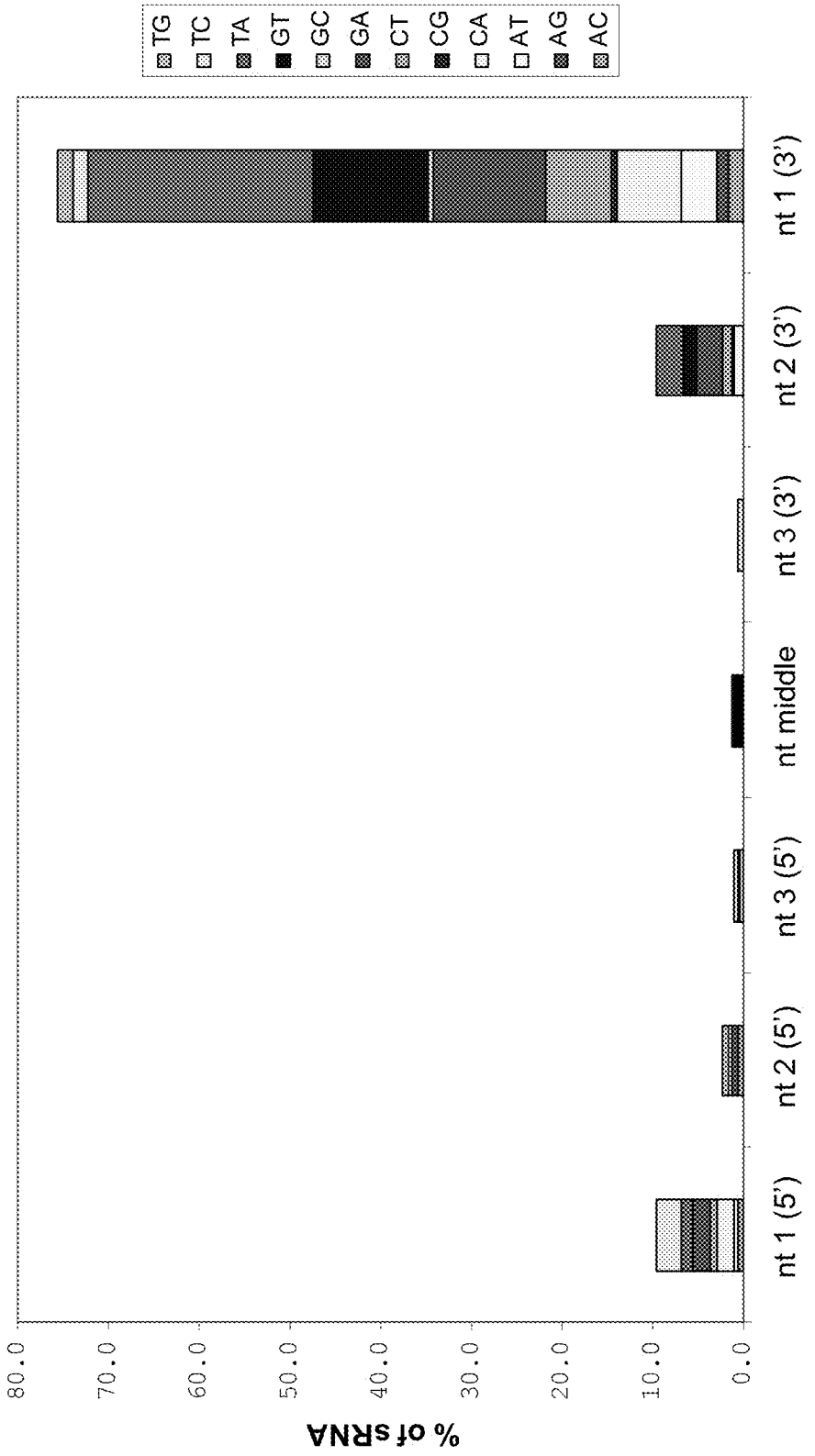

TG
TC
TA
GT
GC
GA
CT
CG
CA
AT
AG
AC
80.0
70.0
60.0
50.0
40.0
30.0
20.0
10.0
0.0
% of sRNA
nt 1 (5')
nt 2 (5')
nt 3 (5')
nt middle
nt 3 (3')
nt 2 (3')
nt 1 (3')
Position

FIG. 28

TISSUE-SPECIFIC MICRORNAS AND COMPOSITIONS AND USES THEREOF

[0001] This application is a Divisional of U.S. patent application Ser. No. 12/688,680, filed Jan. 15, 2010, which is a Continuation-In-Part of International Patent Application No. PCT/US2008/070082, filed Jul. 15, 2008, which claims priority of U.S. Provisional Patent Application No. 60/950,474, filed Jul. 18, 2007, and of U.S. Provisional Patent Application No. 61/020,625, filed Jan. 11, 2008 each of which is incorporated herewith in its entirety.

[0002] All patents, patent applications and publications cited herein are hereby incorporated by reference in their entirety. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art as known to those skilled therein as of the date of the invention described and claimed herein.

[0003] This patent disclosure contains material that is subject to copyright protection. The copyright owner has no objection to the facsimile reproduction by anyone of the patent document or the patent disclosure as it appears in the U.S. Patent and Trademark Office patent file or records, but otherwise reserves any and all copyright rights.

GOVERNMENT INTERESTS

[0004] The work described herein was supported in whole, or in part, by National Cancer Institute Grant No. R01-CA109755 "Genetic Network Interference with Combinatorial Phenotypes", and National Institute of Allergy and Infectious Diseases Grant No. R01 AI066116 "Regulatory Modules in Normal and Transformed b-Cell". The Government has certain rights to the invention.

SEQUENCE LISTING

[0005] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Jan. 27, 2014, is named 19240.740US5_SL.txt and is 1,135,002 bytes in size.

Lengthy Table

[0006] A lengthy table (for example, Table 11) is referenced in this application and has been filed as an Appendix to this invention. The specification of the application contains reference to the single table, Table 11, which consists of more than 51 pages, and is hereby incorporated by reference in its entirety. Table 11 contains information encompassing gene sequences pertaining to the analysis of cross-species conservation for miRNAs. The Table displays results for conservation of full-length mature miRNA sequences, and seed of the mature sequence.

BACKGROUND OF THE INVENTION

[0007] Various nucleic acid species are capable of modifying gene expression. These species include antisense RNA, siRNA, microRNA, RNA and DNA aptamers, antagomirs, and decoy RNAs. Each of these nucleic acid species can inhibit target nucleic acid activity, including gene expression.

[0008] MicroRNAs (miRNAs, miRs) are 20-23 nucleotides (nt) RNA molecules that are produced by the processing of a larger enclosing stem-loop structure (>50 bp), called precursors, by cellular enzymes. miRNAs are processed from hairpin precursors of 70 nt (pre-miRNA) which are derived from primary transcripts (pri-miRNA) through sequential cleavage by the RNAse III enzymes drosha and dicer. miRNAs target the messenger RNA of other genes by binding to their 3' UTR and interfering with their translation or causing degradation by enzyme targeting double-stranded RNA. miRNAs are non-coding RNAs (ncRNAs) that exist in a variety of organisms, including mammals, and are conserved in evolution. Many miRNAs tend to be clustered and transcribed as polycistrons and often have similar spatial temporal expression patterns. miRNAs have been implicated in various biological processes including developmental timing, differentiation, apoptosis, cell proliferation, organ development, and metabolism

SUMMARY OF THE INVENTION

[0009] The invention is based, at least in part, on the discovery of newly-identified microRNAs from normal and tumor-related Human B cells. Accordingly, in one aspect, the invention features an isolated nucleic acid, wherein the nucleic acid: (a) consists of from about 14 to about 31 nucleotides in length; (b) exhibits expression in a human tissue; (c) has a nucleotide sequence not present in an exon; and (d) consists essentially of a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1-130 and 1094, and a nucleotide sequence which is about 97%, about 98%, or about 99% identical to a nucleic acid sequence comprising any one of SEQ ID NOS: 1-130 and 1094. In one embodiment, the nucleic acid is single stranded. In another embodiment, the nucleic acid is double-stranded. In a further embodiment, the human tissue comprises a lymphocyte. In some embodiments, the human tissue is a B cell. In other embodiments, the B cell comprises a Naïve B cell, a centroblast, a memory B cell, or a Ramos Burkitt Lymphoma cell.

[0010] An aspect of the invention provides for an isolated nucleic acid, wherein the nucleic acid: (a) consists of from about 14 to about 31 nucleotides in length; (b) exhibits expression in a human tissue; (c) has a nucleotide sequence not present in an exon; and (d) consists essentially of a nucleotide sequence selected from the group consisting of SEQ ID NOS: 131-401, and a nucleotide sequence which is about 97%, about 98%, or about 99% identical to a nucleic acid sequence having a SEQ ID NO: 131-401. In one embodiment, the nucleic acid is single stranded. In another embodiment, the nucleic acid is double-stranded. In a further embodiment, the human tissue comprises a lymphocyte. In some embodiments, the human tissue is a B cell. In other embodiments, the B cell comprises a Naïve B cell, a centroblast, a memory B cell, or a Ramos Burkitt Lymphoma cell.

[0011] The invention provides for an isolated nucleic acid that is complementary to a nucleic acid described in the aspects herein. In one embodiment, the nucleic acid is single stranded. In another embodiment, the nucleic acid is double-stranded.

[0012] The invention provides for an isolated nucleic acid that is complementary to all but 1, 2, 3, 4, or 5 nucleotides of the nucleic acids described in the aspects herein. In one embodiment, the nucleic acid is complementary to at least 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or 31 contiguous nucleotides of a nucleic acid described in the aspects herein consisting from about 14 to about 31 nucleotides in length. In one embodiment, the nucleic acid is single stranded. In another embodiment, the nucleic acid is double-stranded.

[0013] The invention provides for a composition comprising one or more nucleic acids of described in the aspects herein, in any combination or permutation thereof. In one embodiment, the composition further comprises one or more carriers, excipients, solvents, bases, or a combination thereof.

[0014] The invention provides for a composition comprising one or more nucleic acids, wherein the one or more nucleic acids consist essentially of a nucleotide sequence of any one of SEQ ID NOS: 1-401 and 1094. In one embodiment, the composition further comprises one or more carriers, excipients, solvents, bases, or a combination thereof.

[0015] The invention provides for a method for modulating the activity of a target nucleic acid in a cell, wherein the method comprises contacting a cell with a nucleic acid described in the aspects herein. In one embodiment, the target nucleic acid is a mRNA, a mature miRNA, or a precursor to a mature miRNA. In another embodiment, the cell is a hematopoetic cell. In a further embodiment, the cell is a B cell. In some embodiments, the cell is in vitro or in vivo.

BRIEF DESCRIPTION OF THE FIGURES

[0016] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

[0017] FIG. **1** is a flow diagram of a computational pipeline.

[0018] FIG. **2** is a flow diagram of a computational pipeline.

[0019] FIG. **3** is a flow diagram of a computational pipeline.

[0020] FIG. **4** is a graph depicting frequency distributions.

[0021] FIG. **5** is a diagram for new miRNAs identified in CB, Memory, and Naïve cells.

[0022] FIG. **6** is a diagram for known miRNAs identified in CB, Memory, and Naïve cells.

[0023] FIG. **7** is a diagram for new miRNAs identified in CB and RA cells.

[0024] FIG. **8** is a diagram for known miRNAs identified in CB and RA cells

[0025] FIG. **9** is a bar graph depicting computational predictions of precursors from cloned mature miRNA.

[0026] FIG. **10** is a schematic depicting the experimental procedure. The experimental approach includes two main steps: cloning and sequencing of short-RNA and computational analysis of sequences in order to identify potential miRNAs.

[0027] FIG. **11** is a diagram representing the Computational analysis of short-RNA libraries. Short-RNA sequences were grouped in three main categories: miRNAs, short-RNAs of unknown function and short-RNAs not matching the human genome. Short-RNA sequences were aligned to the human genome (hg18 assembly) and if a favorable match was identified the sequences were subject to computational identification of candidate miRNAs. Short-RNAs which aligned in the same genomic location were clustered and considered as supporting sequences for the same miRNA. Annotations were used to eliminate RNA aligning with mRNA, tRNA, rRNA and other non-coding RNA species. Overall, 401 unique candidate mature miRNA were identified and compared to the miRBase database to detect previously reported miRNA. Among the short-RNAs lacking miRNA features 30% were annotated and the remaining might represent a part of the transcriptome whose functions are still unknown. Short-RNAs which could be matched to the human genome only with 2 or more mismatches were considered as potential short-RNA or miRNA with unknown genomic locations.

[0028] FIG. **12** is a bar graph depicting a computational prediction of precursors and mature miRNA. The number of predicted precursor miRNAs (pre-miR) and mature miRNAs (mature-miR) are plotted independently for each library and overall. The sequences matching miRNAs deposited in the miRBase database (v.11.0) are defined as "known" and conversely the sequences not previously reported are named "new".

[0029] FIG. **13**A is a line graph depicting the analysis of miRNA identified in B cells short-RNA libraries. It shows the previously reported (known) miRNA and newly identified (new) miRNAs as occurring in naïve, centroblasts, memory and Ramos cells.

[0030] FIG. **13**B are schematics depicting number of miRNAs specifically or commonly identified in naïve, centroblasts and memory B cell short-RNA libraries. A larger overlap is observed for known compared to new miRNA (42% versus 15%).

[0031] FIG. **13**C is a bar graph depicting the conservation analysis for orthologous miRNAs was performed in 5 mammal species for all miRNA reported in the miRBase database (miRBase-all) and for known and new mature miRNA identified in B cell libraries. Frequency of conserved miRNAs in each species is displayed.

[0032] FIG. **14** are photographs depicting the detection of miRNA by Northern Blot. FIG. **14**A shows the detection of newly identified mature-miRNA species by Northern Blot in Ramos cell line, centroblasts (CB), and naïve B cells isolated from human tonsils. The naming of miRNA is provisional. FIG. **14**B shows images displaying both the mature (20-25 nt) and the precursor (60-80 nt) miRNA species. miRNA expression can be regulated at transcriptional level (top panel) or at the processing level (bottom panel) when intermediate forms (pre-miRNA) are generated but are not fully processed to mature miRNA.

[0033] FIG. **15** is an image of a microarray-based miRNA expression profiling that distinguishes developmental stages of normal as well as malignant B cells. FIG. **15**A represents unsupervised clustering performed using miRNA frequencies values (>=0.16) calculated as the fraction of the total pool of cloned miRNAs represented by a given miRNA in a library FIG. **15**B Unsupervised clustering of microarray-based miRNA expression profiles distinguishes centroblasts, naïve and memory B cells purified from tonsil tissue of six patients/each.

[0034] FIG. **16** is an image of a microarray-based miRNA expression profiling of GC-derived lymphomas. Unsupervised clustering of miRNA expression profiles of Burkitt lymphomas (BL), follicular lymphomas (FL) and diffuse large B cell lymphomas (DLBCL).

[0035] FIG. **17** are graphs demonstrating the complexity of libraries. The curves represent the estimation of the numbers of mature miRNA expressed in each library. Discarding outliers (extreme 5%), the lowest and highest miRNA counts observed per library sample are plotted. The current set of predicted mature miRNAs represents more than 80% of the estimated miRNA set expressed in the libraries.

[0036] FIG. **18** is flow chart depicting an overview of computational analysis for the short RNA libraries.

[0037] FIG. **19** is a graph of the predicted precursor and mature miRNAs. The number of predicted precursor miRNAs (pre-miR) and mature miRNAs (mature-miR) are plot-

ted independently for each library and overall. Throughout the figures, the sequences matching miRNAs deposited in the miRBase database (v.11.0) are defined as "known," and the sequences that to our knowledge have not been previously reported are named "new."

[0038] FIGS. **20**A-**20**C show graphs and charts pertaining to the abundance and evolutionary conservation of the B-cell miRNome. FIG. **20**A is a graph of the frequencies of previously reported (known) and to our knowledge newly identified (new) miRNAs as occurring in naïve, centroblasts, memory and Ramos cells. Single occurrences miRNAs are not included. FIG. **20**B are Venn diagrams showing the number of miRNAs cloned multiple times and identified in naïve, centroblasts and memory B cells. A larger overlap is observed for known compared to new miRNA (48% versus 38%). FIG. **20**C are bar graphs that show the conservation analysis for orthologous miRNAs that was performed in 5 mammal species for all miRNA reported in the miRBase database (miRBase-all) and for known and new mature miRNA expressed in the B-cell libraries. The percentages of miRNAs having either perfect conservation for the entire mature miRNA (top panel) or for its seeds (bottom panel) are displayed.

[0039] FIGS. **21**A-**21**C are photographs showing the detection of previously unreported miRNAs by RT-PCR and RNA blot. FIG. **21**A shows representative results of RT-PCR detection of miRNA in Ramos cell line and tonsil cells. miR-30c was used as loading control. FIG. **21**B shows the detection of mature-miRNA species by RNA blot in Ramos cell line, centroblasts (CB) and naïve B cells isolated from human tonsils. RNU44 was used as loading control. FIG. **21**C are RNA blot images displaying both the mature (20-25 nt) and the precursor (60-80 nt) miRNA species. miRNA expression can be regulated at transcriptional level (top panel) or at the processing level (bottom panel) when intermediate forms (pre-miRNA) are generated but are not fully processed to mature miRNA. The naming of miRNAs is provisional.

[0040] FIGS. **22**A-B are a schematic that shows miRNA expression profiling distinguishes developmental stages of normal as well as malignant B cells. FIG. **22**A depicts unsupervised clustering performed using miRNA frequencies values (A.08) calculated as the fraction of the total pool of cloned miRNAs represented by a given miRNA in a library. FIG. **22**B shows unsupervised clustering of microarray-based miRNA expression profiles distinguishes centroblasts, naïve and memory B cells purified from tonsil tissue of six patients/each.

[0041] FIG. **23** are graphs that show the complexity of the libraries. The curves represent the estimation of the numbers of mature miRNA (including single occurrence candidate miRNA) expressed in each library. Discarding outliers (extreme 5%), the lowest and highest miRNA counts observed per library sample are plotted. The current set of predicted mature miRNAs represents more than 85% of the estimated miRNA set expressed in the libraries.

[0042] FIG. **24** is a schematic that shows the computational analysis of short-RNA libraries. Short-RNA sequences were grouped in three main categories: miRNAs, short-RNAs of unknown function and short-RNAs not matching the human genome.

[0043] FIG. **25** is a bar graph that shows new miRNAs are found in association with Ago2 protein complex. New miRNAs as well as known (miR-16) are enriched in Ago2 compared to control IgG immunoprecipitates (IP). The binding is specific since other RNA species (5s rRNA) are not enriched in the Ago2 immunoprecipitates. Bars represent the internally normalized average of two independent qPCR assays, each from two sets of three pooled immunoprecipitations. Error bars are the standard deviation of the measurements. The 4 new miRNAs found to be associated with the Ago2 complex are representative of miRNA cloned at higher level in non-GC B cells (CU-1254), in GC B cells (CU-1403; CU-1276) or aberrantly over-expressed in Ramos Burkitt lymphoma cells (CU-1137).

[0044] FIG. **26** is a bar graph that shows enrichment for predicted miRNA targets in genes down-regulated in GC compared to Naïve B cells. Target prediction was performed for 15 new miRNAs expressed at higher level in GC compared to naïve B cells (>3 fold) by miRanda v1.0 and RNA22. Targets predicted by both algorithms were tested for enrichment in the down-regulated genes of the GC transcriptome. Eleven out of 15 GC-over-expressed miRNAs showed an increase in their candidate target enrichment p-value in GC vs. naïve down-regulated genes compared to control populations (memory vs. naïve), two showed a decrease and two showed no differences. Enrichment p-values are reported in Table 13.

[0045] FIG. **27** is a plot showing the correlation measurement between cloning and miRNA expression array data. miRNA normalized clone counts and average expressions measured by miRNA expression arrays are represented in a scatter plot format. The plot includes data for miRNAs which have been cloned more than once and were represented on the Agilent Human miRNA Microarray. Overall, this analysis include 89 miRNA sequences distributed as following in the three libraries: 54 in naïve, 80 in centroblasts (CB) and 48 in memory. The Spearman correlation is 0.7 corresponding to a p-value <3.9e-28.

[0046] FIG. **28** is a bar graph showing the analysis of single nucleotide mismatches identified in cloned known miRNA. The plot represents the percentage of short-RNA corresponding to known miRNA and displaying mismatches to the human genome. Nucleotide in position 1 to 3 starting from both 5'- and 3'-end as well as all remaining middle nucleotides (nt middle) of each sRNA were analyzed for single substitutions.

DETAILED DESCRIPTION OF THE INVENTION

[0047] This invention provides for the discovery of a large number of new micro RNAs that have been identified to exist in normal Human B cells and/or in tumor-related Human B cells, using an integrated bioinformatics method and pipeline described herein.

[0048] Micro RNAs (miRNAs) are naturally-occurring 19 to 25 nucleotide transcripts found in over one hundred distinct organisms (such as nematodes, fruit flies, and humans). miRNAs can be processed from 60- to 70-nucleotide foldback RNA precursor structures, which are transcribed from the miRNA gene. The miRNA precursor processing reaction requires Dicer RNase III and Argonaute family members (Sasaki et al., 2003 Genomics 82, 323-330). The miRNA precursor or processed miRNA products are easily detected, and an alteration in the levels of these molecules within a cell can indicate a perturbation in the chromosomal region containing the miRNA gene.

[0049] At least 222 separate miRNA genes have been identified in the human genome. For example, 2 miRNA genes (miR15a and miR16a) have been localized to a homozygously deleted region on chromosome 13 that is correlated

with chronic lymphocytic leukemia (Calin et al. (2002), Proc. Natl. Acad. Sci. USA 99:15524-29). However, the distribution of miRNA genes throughout the genome, and the relationship of the miRNA genes to diverse chromosomal features, has not been systematically studied. A further review of miRNAs is provided in U.S. Pat. No. 7,232,806, U.S. Patent Application Publication No. 2006/0105360, and in the references: Landgraf et al., 2007, *Cell* 129: 1401-1414; Mendell, J T, 2005 *Cell Cycle* 4(9):1179-84; Shivdasani R A, 2006 *Blood* 108(12):3646-53; Hwang and Mendell, 2006 *Br J Cancer* 94(6):776-80; Hammond S M, 2006; *Curr Opin Genet Dev.* 16(1):4-9; Osada and Takahashi, 2007 *Carcinogenesis* 28(1): 2-12; and Zhang et al., 2007 *Dev Biol.* 302(1):1-12, all of which are hereby incorporated by reference in their entirety.

[0050] All nucleic acid sequences herein are given in the 5' to 3' direction, for example the mature miRNA sequences listed in Table 1 (SEQ ID NOS: 1-401).

[0051] The unprocessed miRNA gene transcript is called a miRNA precursor (pre-miRNA) and comprises an RNA transcript of about 70 nucleotides in length. The pre-miRNA can be processed by digestion with an RNAse (such as, Dicer, Argonaut, or RNAse III, e.g., *E. coli* RNAse III)) into an active 19-25 nucleotide RNA molecule. This active 19-25 nucleotide RNA molecule is also called the processed miRNA gene transcript.

[0052] The active 19-25 nucleotide RNA molecule can be obtained from the miRNA precursor through natural processing routes (for example, using intact cells or cell lysates) or by synthetic processing routes (for example, using isolated processing enzymes, such as isolated Dicer, Argonaut, or RNAase III). The active 19-25 nucleotide RNA molecule can also be produced directly by biological or chemical syntheses, without having been processed from the miRNA precursor.

[0053] The invention provides for an isolated nucleic acid that: (a) consists of from about 14 to about 31 nucleotides in length; (b) exhibits expression in a human tissue; and (c) has a nucleotide sequence not present in an exon. In one embodiment, the isolated nucleic acid consists essentially of a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1-401 and 1094, and a nucleotide sequence which is about 97%, about 98%, or about 99% identical to a nucleic acid sequence comprising any one of SEQ ID NOS: 1-401 and 1094. In some embodiments, the human tissue comprises a lymphocyte (for example, a human B cell). In other embodiments, the B cell comprises a Naïve B cell, a centroblast, or a memory B cell.

[0054] For example, an isolated nucleic acid, such as a miRNA of the invention, can be synthesized, or altered, or removed from the natural state through human intervention. A synthetic miRNA, or a miRNA partially or completely separated from the coexisting materials of its natural state, is considered isolated. An isolated miRNA can exist in substantially purified form, or can exist in a cell into which the miRNA has been delivered.

[0055] An isolated nucleic acid, such as a miRNA of the invention, can be obtained using a number of standard techniques utilized in the art. For example, the miRNA gene products can be chemically synthesized or recombinantly produced using methods known in the art. For example, a miRNA can be chemically synthesized using appropriately protected ribonucleoside phosphoramidites and a conventional DNA/RNA synthesizer. Commercial suppliers of synthetic RNA molecules or synthesis reagents include, e.g., Proligo (Hamburg, Germany), Dharmacon Research (Lafayette, Colo., USA), Rosetta Genomics (North Brunswick, N.J.), Pierce Chemical (part of Perbio Science, Rockford, Ill., USA), Glen Research (Sterling, Va., USA), ChemGenes (Ashland, Mass., USA), Ambion (Foster City, Calif., USA), and Cruachem (Glasgow, UK).

[0056] miRNA can also be expressed from recombinant circular or linear DNA plasmids using any suitable promoter. Suitable promoters for expressing RNA from a plasmid include, e.g., the U6 or H1 RNA pol III promoter sequences, or the cytomegalovirus promoters. Selection of other suitable promoters is within the skill in the art. Recombinant plasmids can comprise inducible or regulatable promoters for expression of the miRNA in cancer cells (such as hematopoietic cells, i.e., B cells). For example, a miRNA or a precursor miRNA of the invention (such as a miRNA molecule comprising any one of SEQ ID NOS: 1-401 and 1094) can be placed under the control of the CMV intermediate-early promoter, whereby the nucleic acid sequences encoding the miRNA molecule are located 3' of the promoter, so that the promoter can initiate transcription of the miRNA gene product coding sequences.

[0057] miRNAs expressed from recombinant plasmids can be isolated from cultured cell expression systems by standard techniques. miRNAs which are expressed from recombinant plasmids can also be delivered to, and expressed directly in, the cancer cells. A miRNA can be expressed as an RNA precursor molecule from a single plasmid, and the precursor molecules are subsequently processed into functional miRNAs by a suitable processing system, including the processing systems naturally existing within a cell. Other suitable processing systems include, e.g., the in vitro *Drosophila* cell lysate system as described in U.S. Application Publication No. 2002/0086356 to Tuschl et al. and the *E. coli* RNAse III system described in U.S. Application Publication No. 2004/0014113 to Yang et al., which are herein incorporated by reference in their entireties.

[0058] Plasmids suitable for expressing a miRNA of the invention, methods for inserting nucleic acid sequences into the plasmid to express the miRNA of interest, and methods of delivering the recombinant plasmid to cells of interest are well-established and practiced in the art. See, for example, Zeng et al. (2002), *Molecular Cell* 9:1327-1333; Tuschl (2002), *Nat. Biotechnol,* 20:446-448; Brummelkamp et al. (2002), *Science* 296:550-553; Miyagishi et al. (2002), *Nat. Biotechnol.* 20:497-500; Paddison et al. (2002), *Genes Dev.* 16:948-958; Lee et al. (2002), *Nat. Biotechnol.* 20:500-505; and Paul et al. (2002), *Nat. Biotechnol.* 20:505-508, the entire disclosures of which are herein incorporated by reference.

[0059] miRNA molecules of the invention can also be expressed from recombinant viral vectors. The RNA expressed from the recombinant viral vectors can either be isolated from cultured cell expression systems by standard techniques, or can be expressed directly in cancer cells (such as hematopoietic cells, i.e., B cells). For example, the recombinant viral vectors can comprise sequences that encode the miRNA molecule of interest and any suitable promoter for expressing the RNA sequences. Vectors can also comprise inducible or regulatable promoters for expression of the miRNA molecule in cells, such as cancer cell. As discussed previously, non-limiting examples of suitable promoters include the U6 or H1 RNA pol III promoter sequences, or the cytomegalovirus promoters. Selection of other suitable promoters is practiced by those of ordinary skill in the art.

[0060] Any viral vector that can harbor the nucleotide sequences for the miRNA molecules of the invention can be used. Non-limiting examples of such vectors include: vectors derived from adenovirus (AV); adeno-associated virus (AAV); retroviruses (e.g., lentiviruses (LV), Rhabdoviruses, murine leukemia virus); herpes virus, and the like. The tropism of the viral vectors can be modified by pseudotyping the vectors with envelope proteins or other surface antigens from other viruses, or by substituting different viral capsid proteins, as appropriate. For example, lentiviral vectors can be pseudotyped with surface proteins from vesicular stomatitis virus (VSV), rabies, Ebola, Mokola, and the like. For example, AAV vectors can be made to target different cells by engineering the vectors to express different capsid protein serotypes. An AAV vector expressing a serotype 2 capsid on a serotype 2 genome is called AAV 2/2. This serotype 2 capsid gene in the AAV 2/2 vector can be replaced by a serotype 5 capsid gene to produce an AAV 2/5 vector. Techniques for constructing AAV vectors which express different capsid protein serotypes are within the skill in the art; see, e.g., Rabinowitz J. E. et al. (2002), *J Virol* 76:791-801, the entire disclosure of which is herein incorporated by reference.

[0061] Recombinant viral vectors suitable for expressing miRNA molecules of the invention, methods for inserting nucleic acid sequences for expressing RNA in the vector, methods of delivering the viral vector to cells of interest, and recovery of the expressed RNA molecules are within the skill in the art. See, for example, Dornburg (1995), *Gene Therap.* 2:301-310; Eglitis (1988), *Biotechniques* 6:608-614; Miller (1990), *Hum. Gene Therap.* 1:5-14; and Anderson (1998), *Nature* 392:25-30, the entire disclosures of which are herein incorporated by reference. Useful viral vectors can be those derived from AV and AAV. A suitable AV vector for expressing an mRNA molecule of the invention, a method for constructing the recombinant AV vector, and a method for delivering the vector into target cells, are described in Xia et al. (2002), *Nat. Biotech.* 20:1006-1010, the entire disclosure of which is herein incorporated by reference. Suitable AAV vectors for expressing a miRNA molecule having a sequence shown in Table 1 (i.e., any one of SEQ ID NOS: 1-401), methods for constructing the recombinant AAV vector, and methods for delivering the vectors into target cells are described in Samulski et al. (1987), *J. Virol.* 61:3096-3101; Fisher et al. (1996), *J Virol.,* 70:520-532; Samulski et al. (1989), *J. Virol.* 63:3822-3826; U.S. Pat. No. 5,252,479; U.S. Pat. No. 5,139,941; International Patent Application No. WO 94/13788; and International Patent Application No. WO 93/24641, the entire disclosures of which are herein incorporated by reference.

[0062] Inhibition of RNA can effectively inhibit expression of a gene from which the RNA is transcribed. Inhibitors are selected from the group comprising: siRNA; interfering RNA or RNAi; dsRNA; RNA Polymerase III transcribed DNAs; ribozymes; and antisense nucleic acid, which can be RNA, DNA, or artificial nucleic acid. Also within the scope of the present invention are oligonucleotide sequences that include antisense oligonucleotides, antagomirs (also referred to as miRNA inhibitory nucleic acids), aptamers, and ribozymes that function to inhibit miRNA expression via purportedly binding to or degrading a miRNA molecule comprising any one of SEQ ID NOS: 1-401 and 1094.

[0063] The invention provides for a nucleic acid molecule that is substantially complementary to an isolated nucleic acid of the invenion described above. "Substantially complementary" means that two sequences are substantially complementary that a duplex can be formed between them. The duplex can have one or more mismatches but the region of duplex formation is sufficient to down-regulate expression of the target nucleic acid. The region of substantial complementarity can be perfectly paired. In one embodiment, there can be nucleotide mismatches in the region of substantial complementarity. In one embodiment, the region of substantial complementarity will have no more than 1, 2, 3, 4, or 5 mismatches.

[0064] For example, an antagomir, an antisense RNA, a small interfering RNA (siRNA), a short hairpin RNA (snRNA), and the like) can be complementary to the guide strand of a miRNA having a nucleotide sequence shown in Table 1, positioned in the RNA silencing complex. This nucleic acid molecule can be single stranded or can be double stranded, and can inhibit the expression or activity of a miRNA molecule of the invention. In one embodiment, the nucleic acid molecule that inhibits a miRNA molecule of the invention (such as those described above) can complement at least 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or 31 contiguous nucleotides of a miRNA having a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-401 and 1094, and a nucleotide sequence which is about 97%, about 98%, or about 99% identical to a nucleic acid sequence comprising any one of SEQ ID NOS: 1-401 and 1094.

[0065] The invention also provides a method for modulating a target nucleic acid in a cell (for example, a miRNA molecule having a nucleotide sequence comprising any one of SEQ ID NOS: 1-401 and 1094) via contacting the cell with a nucleic acid of the invention (for example, those described above). For example, the nucleic acid can be substantially complementary to at least 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or 31 contiguous nucleotides of a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-401 and 1094, and a nucleotide sequence which is about 97%, about 98%, or about 99% identical to a nucleic acid sequence comprising any one of SEQ ID NOS: 1-401 and 1094.

[0066] Expression of a miRNA molecule of the invention can be inhibited by an antisense oligonucleotide. Antisense oligonucleotides can comprise antisense DNA, RNA, and DNA/RNA molecule and act via altering the activity of the target RNA by binding to a target nucleic acid (such as a miRNA of interest) by means of RNA-RNA, RNA-DNA or RNA-PNA (protein nucleic acid) interactions (for a review, see Stein and Cheng, 1993 *Science* 261, 1004 and Woolf et al., U.S. Pat. No. 5,849,902). Antisense oligonucleotides suitable for use in the present methods are single-stranded nucleic acids (e.g., RNA, DNA, RNA-DNA chimeras, PNA) that generally comprise a nucleic acid sequence complementary to a contiguous nucleic acid sequence in a miRNA molecule. For example, the antisense oligonucleotide comprises a nucleic acid sequence that is 50-100% complementary, 75-100% complementary, or 95-100% complementary to a contiguous nucleic acid sequence in a miRNA molecule of the invention having a nucleic acid sequence of SEQ ID NO: 1-401, shown in Table 1. However, in some instances, an antisense molecule can form a loop and binds to a substrate nucleic acid which forms a loop. Thus, an antisense molecule can be complementary to two (or more) non-contiguous substrate sequences, or two (or more) non-contiguous sequence portions of an antisense molecule can be complementary to a

target sequence, or both. For a review of current antisense strategies, see Schmajuk et al., 1999, *J. Biol. Chem.,* 274, 21783-21789; Delihas et al., 1997, *Nature,* 15, 751-753; Stein et al., 1997, *Antisense N A. Drug Dev.,* 7, 151; Crooke, 2000, *Methods Enzymol.,* 313, 3-45; Crooke, 1998, *Biotech. Genet. Eng. Rev.,* 15, 121-157; Crooke, 1997, *Ad. Pharmacol.,* 40, 1-49.

[0067] Antisense DNA can also be used to target nucleic acid by means of DNA-RNA interactions, thereby activating RNase H, which digests the target nucleic acid in the duplex. The antisense oligonucleotides can comprise one or more RNAse H activating region, which is capable of activating RNAse H to cleave a target nucleic acid. Antisense DNA can be synthesized chemically or expressed via the use of a single stranded DNA expression vector or equivalent thereof. An RNase H activating region refers to a region (generally greater than or equal to 4-25 nucleotides in length, for example, from 5-11 nucleotides in length) of a nucleic acid compound capable of binding to a target nucleic acid to form a non-covalent complex that is recognized by cellular RNase H enzyme (see for example Arrow et al., U.S. Pat. No. 5,849, 902; Arrow et al., U.S. Pat. No. 5,989,912). The RNase H enzyme binds to a nucleic acid compound-target nucleic acid complex and cleaves the target nucleic acid sequence.

[0068] Antisense nucleic acids can be produced chemically or biologically, or can be expressed from a recombinant plasmid or viral vector, as described above for the isolated miRNA molecules. For example, antisense oligonucleotides of at least about 15 bases and complementary to unique regions of the miRNA molecules of the invention can be synthesized, e.g., by conventional phosphodiester techniques (Dallas et al., (2006) *Med. Sci. Monit.* 12(4):RA67-74; Kalota et al., (2006) *Handb. Exp. Pharmacol.* 173:173-96; Lutzelburger et al., (2006) *Handb. Exp. Pharmacol.* 173:243-59). Exemplary methods for producing and testing are within the skill in the art; see, e.g., Stein and Cheng (1993), *Science* 261:1004 and U.S. Pat. No. 5,849,902 to Woolf et al., the entire disclosures of which are herein incorporated by reference.

[0069] Antisense polynucleotides include, but are not limited to: morpholinos, 2'-O-methyl polynucleotides, DNA, RNA and the like. RNA polymerase III transcribed DNAs contain promoters, such as the U6 promoter. These DNAs can be transcribed to produce small hairpin RNAs in the cell that can function as siRNA or linear RNAs that can function as antisense RNA. The inhibitor can be polymerized in vitro, recombinant RNA, contain chimeric sequences, or derivatives of these groups. The inhibitor can contain ribonucleotides, deoxyribonucleotides, synthetic nucleotides, or any suitable combination such that the target RNA and/or gene is inhibited. In addition, these forms of nucleic acid can be single, double, triple, or quadruple stranded. (see for example Bass (2001) *Nature,* 411, 428 429; Elbashir et al., (2001) *Nature,* 411, 494 498; and PCT Publication Nos. WO 00/44895, WO 01/36646, WO 99/32619, WO 00/01846, WO 01/29058, WO 99/07409, WO 00/44914).

[0070] siRNA comprises a double stranded structure that can contain 15 to 50 base pairs, or 21 to 25 base pairs, and having a nucleotide sequence identical or nearly identical to an expressed target gene or RNA within the cell. The siRNA comprise a sense RNA strand and a complementary antisense RNA strand annealed together by standard Watson-Crick base-pairing interactions. The sense strand comprises a nucleic acid sequence which is substantially identical to a nucleic acid sequence contained within the target miRNA molecule. "Substantially identical" to a target sequence contained within the target mRNA refers to a nucleic acid sequence that is identical to the target sequence, or that differs from the target sequence by one or two nucleotides. The sense and antisense strands of the siRNA can comprise two complementary, single-stranded RNA molecules, or can comprise a single molecule in which two complementary portions are base-paired and are covalently linked by a single-stranded "hairpin" area.

[0071] The siRNA can also be altered RNA that differs from naturally-occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siRNA or to one or more internal nucleotides of the siRNA, or modifications that make the siRNA resistant to nuclease digestion, or the substitution of one or more nucleotides in the siRNA with deoxyribonucleotides. One or both strands of the siRNA can also comprise a 3' overhang. As used herein, a 3' overhang refers to at least one unpaired nucleotide extending from the 3'-end of a duplexed RNA strand. For example, the siRNA can comprise at least one 3' overhang of from 1 to about 6 nucleotides (which includes ribonucleotides or deoxyribonucleotides) in length, or from 1 to about 5 nucleotides in length, or from 1 to about 4 nucleotides in length, or from about 2 to about 4 nucleotides in length. For example, each strand of the siRNA can comprise 3' overhangs of dithymidylic acid ("TT") or diuridylic acid ("uu").

[0072] siRNA can be produced chemically or biologically, or can be expressed from a recombinant plasmid or viral vector, as described above for the miRNA molecules of the invention having a sequence shown in Table 1. Exemplary methods for producing and testing dsRNA or siRNA molecules are described in U.S. Patent Application Publication No. 2002/0173478 to Gewirtz, U.S. Patent Application Publication No. 2007/0072204 to Hannon et al., and in U.S. Patent Application Publication No. 2004/0018176 to Reich et al., the entire disclosures of which are herein incorporated by reference.

[0073] Expression of a miRNA molecule of the invention can also be inhibited by a short hairpin RNA (shRNA). The hairpin RNAs can be synthesized exogenously or can be formed by transcribing from RNA polymerase III promoters in vivo. Examples of making and using such hairpin RNAs for gene silencing in mammalian cells are described in, for example, Paddison et al., 2002, *Genes Dev,* 16:948-58; McCaffrey et al., 2002, *Nature,* 418:38-9; McManus et al., 2002, *RNA,* 8:842-50; Yu et al., 2002, *Proc Natl Acad Sci USA,* 99:6047-52). Such hairpin RNAs are engineered in cells or in an animal to ensure continuous and stable suppression of a desired gene. It is known in the art that siRNAs can be produced by processing a hairpin RNA in the cell.

[0074] Expression of a miRNA molecule of the invention can also be inhibited by a ribozyme. Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA sequences (for example those shown in Table 1), followed by endonucleolytic cleavage. Engineered hammerhead motif ribozyme molecules that specifically and efficiently catalyze endonucleolytic cleavage of a miRNA sequence shown in Table 1, are also within the scope of the present invention. Scanning

the target molecule for ribozyme cleavage sites that include the following sequences, GUA, GUU, and GUC initially identifies specific ribozyme cleavage sites within any potential RNA target. Once identified, short RNA sequences of between about 15 and 20 ribonucleotides corresponding to the region of the target gene containing the cleavage site can be evaluated for predicted structural features such as secondary structure that can render the oligonucleotide sequence unsuitable.

[0075] The suitability of candidate targets can also be evaluated by testing their accessibility to hybridization with complementary oligonucleotides using, e.g., ribonuclease protection assays (see Romkes et al., 2005, *Methods Mol Biol.;* 291:387-98; Dvorak et al., 2003, *Biomed Pap Med Fac Univ Palacky Olomouc Czech Repub* 147(2):131-5). The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, 1988, *Nature,* 334:585-591. Ribozymes can also include RNA endoribonucleases such as the one which occurs naturally in *Tetrahymena thermophila* (known as the IVS or L-19 IVS RNA) and which has been described (see, e.g., Zaug, et al., 1984, *Science,* 224:574-578; Zaug and Cech, 1986, *Science,* 231:470-475; Zaug, et al., 1986, *Nature,* 324: 429-433; published International patent application No. WO88/04300 by University Patents Inc.; Been and Cech, 1986, *Cell,* 47:207-216).

[0076] Both the antisense oligonucleotides and ribozymes of the present invention can be prepared by known methods. These include techniques for chemical synthesis such as, e.g., by solid phase phosphoamite chemical synthesis. Alternatively, antisense RNA molecules can be generated by in vitro or in vivo transcription of DNA sequences encoding the RNA molecule. Such DNA sequences can be incorporated into a wide variety of vectors that incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters.

[0077] Alternatively, expression of a miRNA molecule of the invention can be inhibited by an antagomir. An antagomir is a single-stranded, double stranded, partially double stranded or hairpin structured chemically modified oligonucleotide agent that comprises at least 12 or more contiguous nucleotides substantially complementary to an endogenous miRNA or agents that include 12 or more contiguous nucleotides substantially complementary to a target sequence of an miRNA or pre-miRNA nucleotide sequence. The antagomir can be RNA, DNA, or a combination of RNA and DNA, and is antisense with respect to its target nucleotide sequence. An antagomir can target RNA, e.g., an endogenous pre-miRNA or miRNA of the subject. For example, the antagomir can target a miRNA having a nucleic acid sequence shown in Table 1. Exemplary methods for producing and testing antagomirs are discussed in U.S. Patent Application Publication No. 2007/0123482 and U.S. Patent Application Publication No. 005/0182005, in addition to Mattes et al., 2007 *Am J Resp Cell Mol Biol* 36: 8-12; Krützfeldt et al., 2007 *Nuc Acid Res* 35(9): 2885-2892, which are all incorporated by reference in their entireties.

[0078] Various modifications to the nucleic acid molecules of the present invention can be introduced as a means of increasing intracellular stability and half-life. Some modifications include but are not limited to the addition of flanking sequences of ribonucleotides or deoxyribonucleotides to the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2'-O-methyl rather than phosphodiesterase linkages within the oligonucleotide backbone.

[0079] Expression of a miRNA molecule of the invention can be inhibited by an aptamer. Aptamer nucleic acid sequences are readily made that bind to a wide variety of target molecules. The aptamer nucleic acid sequences of the invention can be comprised entirely of RNA or partially of RNA, or entirely or partially of DNA and/or other nucleotide analogs. A nucleic acid aptamer is a nucleic acid or a nucleic acid-like molecule that is capable of binding to a specific molecule of interest with high affinity and specificity. A nucleic acid aptamer also can be a nucleic acid molecule that mimics the three dimensional structure of active portions of miRNAs. A nucleic acid-aptamer can be between about 9 and about 300 nucleotides or the like in length. More commonly, an aptamer is between about 30 and about 100 nucleotides or the like in length.

[0080] Aptamers are developed to bind specific ligands by employing known in vivo or in vitro selection techniques known as SELEX (Systematic Evolution of Ligands by Exponential Enrichment). Nucleic acid-aptamers can be prepared by any known method, including synthetic, recombinant, and purification methods. Such methods are described in, for example, Ellington and Szostak (1990) *Nature* 346:818, Tuerk and Gold (1990) *Science* 249:505, James W., (2001) *Current Opinion in Pharmacology,* 1:540-546, Colas et al., (1996) *Nature* 380:548-550, U.S. Pat. No. 5,582,981; PCT Publication No. WO 00/20040; U.S. Pat. No. 5,270,163; Lorsch and Szostak (1994) *Biochem.* 33:973; Mannironi et al., (1997) *Biochem.* 36:9726; Blind (1999) *Proc. Nat'l. Acad. Sci. USA* 96:3606-3610; Huizenga and Szostak (1995) *Biochem.* 34:656-665; PCT Publication Nos. WO 99/54506, WO 99/27133, and WO 97/42317; and U.S. Pat. No. 5,756,291, all of which are incorporated by reference in their entireties.

[0081] Expression of a given miRNA molecule can be inhibited or decreased by inducing RNA interference of the miRNA molecule with an isolated double-stranded or single-stranded RNA molecule. For example, the miRNA inhibitor molecule can be those molecules discussed above, such as an antagomir, an antisense RNA, a small interfering RNA (siRNA), a short hairpin RNA (snRNA), and the like) which has at least about 75%, 80%, 90%, 95%, 98%, 99% or 100%, sequence homology to a portion of a miRNA molecule having a sequence shown in Table 1. For further discussion of modulation of miRNA expression, see: Lu et al., (2005) *Adv Genet.* 54:117-42; Leung and Whittaker (2005) *Pharmacol Ther.* 107(2):222-39; Takeshita and Ochiva (2006) *Cancer Sci.* 97(8):689-96; and Alexander et al., (2007) Arch Immunol Ther Exp (Warsz). 2007 May-June; 55(3):139-49.

[0082] A subject in need thereof, according to the invention, can refer to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals. In some embodiments, the subject can be a mouse, a rat, a bird, a dog, a cat, a cow, a horse, a sheep, or a pig. In exemplary embodiments, a mammal is a human.

[0083] Methods for determining RNA expression levels in cells from a biological sample are within the level of skill in the art. For example, tissue sample can be removed from a subject suspected of having cancer associated with a cancer-associated chromosomal feature by conventional biopsy techniques. In another example, a blood sample can be removed from the subject, and white blood cells isolated for DNA extraction by standard techniques. The blood or tissue sample should be obtained from the subject prior to initiation

of radiotherapy, chemotherapy or other therapeutic treatment. A corresponding control tissue or blood sample can be obtained from unaffected tissues of the subject, from a normal human individual or population of normal individuals, or from cultured cells corresponding to the majority of cells in the subject's sample. The control tissue or blood sample is then processed along with the sample from the subject, so that the levels of miRNA molecules in cells from the subject's sample can be compared to the corresponding miRNA molecule levels from cells of the control sample. For example, the relative miRNA expression in the control and normal samples can be conveniently determined with respect to one or more RNA expression standards. The standards can comprise, for example, a zero miRNA expression level, the miRNA expression level in a standard cell line, or the average level of miRNA expression previously obtained for a population of normal human controls.

[0084] Suitable techniques for determining the level of RNA transcripts of a gene of interest in cells are within the skill in the art. According to one such method, total cellular RNA can be purified from cells by homogenization in the presence of nucleic acid extraction buffer, followed by centrifugation. Nucleic acids are precipitated, and DNA is removed by treatment with DNase and precipitation. The RNA molecules are then separated by gel electrophoresis on agarose gels according to standard techniques, and transferred to nitrocellulose filters by, e.g., the so-called "Northern" blotting technique. The RNA is then immobilized on the filters by heating. Detection and quantification of specific RNA is accomplished using appropriately labeled DNA or RNA probes complementary to the RNA in question. See, for example, *Molecular Cloning: A Laboratory Manual*, J. Sambrook et al., eds., 2nd edition, Cold Spring Harbor Laboratory Press, 1989, Chapter 7, the entire disclosure of which is incorporated by reference.

[0085] Suitable probes for Northern blot hybridization of a given miRNA molecule can be produced from the nucleic acid sequences provided in Table 1. Methods for preparation of labeled DNA and RNA probes, and the conditions for hybridization thereof to target nucleotide sequences, are described in *Molecular Cloning: A Laboratory Manual*, J. Sambrook et al., eds., 2nd edition, Cold Spring Harbor Laboratory Press, 1989, Chapters 10 and 11, the disclosures of which are herein incorporated by reference. For example, the nucleic acid probe can be labeled with, e.g., a radionuclide such as ^{3}H, ^{32}P, ^{33}P, ^{14}C, or ^{35}S; a heavy metal; or a ligand capable of functioning as a specific binding pair member for a labeled ligand (e.g., biotin, avidin or an antibody), a fluorescent molecule, a chemiluminescent molecule, an enzyme or the like.

[0086] Probes can be labeled to high specific activity by either the nick translation method of Rigby et al. (1977), *J. Mol. Biol.* 113:237-251 or by the random priming method of Fienberg et al. (1983), *Anal. Biochem.* 132:6-13, the entire disclosures of which are herein incorporated by reference. Fienberg et al. provides a useful method for synthesizing ^{32}P-labeled probes of high specific activity from single-stranded DNA or from RNA templates. For example, by replacing preexisting nucleotides with highly radioactive nucleotides according to the nick translation method, ^{32}P-labeled nucleic acid probes can be prepared with a specific activity well in excess of 10^{8} cpm/microgram. Autoradiographic detection of hybridization can then be performed by exposing hybridized filters to photographic film. Densitometric scanning of the photographic films exposed by the hybridized filters provides an accurate measurement of miRNA molecule levels. Using another approach, miRNA molecule levels can be quantified by computerized imaging systems, such the Molecular Dynamics 400-B 2D Phosphorimager available from Amersham Biosciences, Piscataway, N.J.

[0087] Where radionuclide labeling of DNA or RNA probes is not practical, the random-primer method can be used to incorporate an analogue, for example, the dTTP analogue 5-(N—(N-biotinyl-epsilon-aminocaproyl)-3-aminoallyl)deoxyuridine triphosphate, into the probe molecule. The biotinylated probe oligonucleotide can be detected by reaction with biotin-binding proteins, such as avidin, streptavidin, and antibodies (e.g., anti-biotin antibodies) coupled to fluorescent dyes or enzymes that produce color reactions.

[0088] In addition to Northern and other RNA blotting hybridization techniques, determining the levels of RNA transcripts can be accomplished using the technique of in situ hybridization. This technique requires fewer cells than the Northern blotting technique, and involves depositing whole cells onto a microscope cover slip and probing the nucleic acid content of the cell with a solution containing radioactive or otherwise labeled nucleic acid (e.g., cDNA or RNA) probes. This technique is well-suited for analyzing tissue biopsy samples from subjects. The practice of the in situ hybridization technique is described in more detail in U.S. Pat. No. 5,427,916, the entire disclosure of which is incorporated herein by reference. Suitable probes for in situ hybridization of a given miRNA molecule can be produced from the nucleic acid sequences provided in Table 1, as described above.

[0089] The relative number of miRNA transcripts in cells can also be determined by reverse transcription of miRNA transcripts, followed by amplification of the reverse-transcribed transcripts by polymerase chain reaction (RT-PCR). The levels of miRNA gene transcripts can be quantified in comparison with an internal standard, for example, the level of mRNA from a housekeeping gene present in the same sample, such as myosin or glyceraldehyde-3-phosphate dehydrogenase (G3PDH). The methods for quantitative RT-PCR and variations thereof are within the skill in the art.

[0090] It is desirable to simultaneously determine the expression level of a plurality of different of miRNA molecules in a sample, for example determine the expression level of the transcripts of known miRNAs correlated with cancer or other cell division disorders (for example, a hematopoietic cell division disorder, such as a B cell lymphoma). Since examining cancer-specific expression levels for hundreds of miRNA molecules is time consuming, requires a large amount of total RNA (at least 20 μg for each Northern blot) and utilizes autoradiographic techniques that require radioactive isotopes, an oligolibrary in microchip format can be constructed containing a set of probe oligonucleotides specific for a set of miRNA molecules (for example, miRNA molecules having any one nucleic acid sequence of SEQ ID NOS: 1-401, shown in Table 1, or any one miRNA molecule of Table 7, Table 9, or Table 10).

[0091] A nucleic acid microchip array is a plurality of probe elements, each probe element comprising one or more nucleic acid molecules immobilized on one or more solid surfaces to which sample nucleic acids can be hybridized. Microarrays are known in the art and comprise a surface to which probes that correspond in sequence to gene products (e.g., cDNAs, mRNAs, cRNAs, polypeptides, and fragments

thereof), can be specifically hybridized or bound at a known position. The microarray can be an array (i.e., a matrix) in which each position represents a discrete binding site for an RNA, and in which binding sites are present for products of most of the genes in the organism's genome, or a specific tissue or cellular subset of the organism. Here, the binding site can be a nucleic acid or nucleic acid analogue to which a cognate cDNA or RNA, such as miRNA molecule of the invention, can specifically hybridize. The nucleic acid or analogue of the binding site can be, e.g., a synthetic miRNA oligomer.

[0092] The nucleic acid or analogue is attached to a solid support, which can be made from glass, plastic (e.g., polypropylene, nylon), polyacrylamide, nitrocellulose, or other materials. A useful method for attaching the nucleic acids to a surface is by printing on glass plates, as is described generally by Schena et al., 1995. See also DeRisi et al., 1996; Shalon et al., 1996; Schena et al., 1996. Each of these articles is incorporated by reference in its entirety.

[0093] The microchip is prepared from gene-specific oligonucleotide probes generated from known miRNAs. A nucleic acid array can contain two different oligonucleotide probes for each miRNA, one containing the active sequence and the other being specific for the precursor of the miRNA (for example, see Table 1). The array can also contain controls such as one or more mouse sequences differing from human orthologs by only a few bases, which can serve as controls for hybridization stringency conditions. tRNAs from both species can also be printed on the microchip, providing an internal, relatively stable positive control for specific hybridization. One or more appropriate controls for non-specific hybridization can also be included on the microchip. For this purpose, sequences are selected based upon the absence of any homology with any known miRNAs. For example, the array can also contain miRNA sequences found to be specific for human B cells. Non-limiting examples of such miRNA's include: mir-15, mir-17, mir-14, mir-124a-3, mir-99b, mir-167a, mir-167b, mir-129-1, mir-30c-2, mir-143, mir-27b, mir-125b-1, mir-128a, mir-140, mir-142, mir-191, mir-125b-2, mir-127, mir-129-2, mir-146a, mir-154, mir-185, mir-186, mir-322, mir-124a-1, mir-124a-2, mir-30c-1, mir-302a, and mir-99b.

[0094] The microchip can be fabricated by techniques known in the art. For example, probe oligonucleotides of an appropriate length, e.g., 40 nucleotides, are 5'-amine modified at position C6 and printed using commercially available microarray systems, e.g., the GeneMachine OmniGrid™ 100 Microarrayer and Amersham CodeLink™ activated slides. Labeled cDNA oligomer corresponding to the target RNAs is prepared by reverse transcribing the target RNA with labeled primer. Following first strand synthesis, the RNA/DNA hybrids are denatured to degrade the RNA templates. The labeled target cDNAs thus prepared are then hybridized to the microarray chip under hybridizing conditions, e.g. 6.times. SSPE/30% formamide at 25° C. for 18 hours, followed by washing in 0.75.times.TNT at 37° C. for 40 minutes. At positions on the array where the immobilized probe DNA recognizes a complementary target cDNA in the sample, hybridization occurs. The labeled target cDNA marks the exact position on the array where binding occurs, allowing automatic detection and quantification. The output consists of a list of hybridization events, indicating the relative abundance of specific cDNA sequences, and therefore the relative abundance of the corresponding complementary miRs, in the patient sample. According to one embodiment, the labeled cDNA oligomer is a biotin-labeled cDNA, prepared from a biotin-labeled primer. The microarray is then processed by direct detection of the biotin-containing transcripts using, e.g., Streptavidin-Alexa647 conjugate, and scanned utilizing conventional scanning methods. Images intensities of each spot on the array are proportional to the abundance of the corresponding miR in the patient sample.

[0095] Other methods for making microarrays (see U.S. Patent Application Publication No. 2006/0051771, which is incorporate by reference in its entirety), e.g., by masking (Fodor et al., 1991; Maskos and Southern, 1992), can also be used. In principal, any type of array, for example, dot blots on a nylon hybridization membrane (see Sambrook et al., 1989, which is incorporated in its entirety for all purposes), can be used, although, as will be recognized by those of skill in the art, very small arrays are useful because hybridization volumes will be smaller.

[0096] Labeled cDNA can be prepared from mRNA by oligo dT-primed or random-primed reverse transcription, both of which are well known in the art. Reverse transcription can be carried out in the presence of a dNTP conjugated to a detectable label, for example, a fluorescently labeled dNTP. Alternatively, isolated mRNA can be converted to labeled antisense RNA synthesized by in vitro transcription of double-stranded cDNA in the presence of labeled dNTPs (Lockhart et al., 1996, which is incorporated by reference in its entirety for all purposes). In alternative embodiments, the cDNA or aRNA probe can be synthesized in the absence of detectable label and can be labeled subsequently, e.g., by incorporating biotinylated dNTPs or rNTP, or some similar means (e.g., photo-cross-linking a psoralen derivative of biotin to RNAs), followed by addition of labeled streptavidin (e.g., phycoerythrin-conjugated streptavidin) or the equivalent. Alternatively, cDNA or aRNA can be labeled indirectly by incorporation of 5-(3-aminoallyl) dNTPs or rNTPs to provide a amine reactive group for subsequent addition of label with any moiety bearing an N-Hydroxysuccinimide (NHS) ester.

[0097] Fluorescently labeled probes can be used, including suitable fluorophores such as fluorescein, lissamine, phycoerythrin, rhodamine (Perkin Elmer Cetus), Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7, FluorX (Amersham) and others (see, e.g., Kricka, 1992, *Nonisotopic DNA Probe Techniques*, Academic Press San Diego, Calif.). It will be appreciated that pairs of fluorophores are chosen that have distinct emission spectra so that they can be easily distinguished. In another embodiment, a label other than a fluorescent label is used. For example, a radioactive label, or a pair of radioactive labels with distinct emission spectra, can be used (see Zhao et al., 1995; Pietu et al., 1996).

[0098] The analysis of microarray data can be accomplished using methods of statistical analysis known to those skilled in the art. For example, clustering analysis is commonly used for interpretation of microarray data. It provides both a visual representation of complex data and a method for measuring similarity between experiments. Some widely used methods for clustering microarray data include: hierarchical, K-means, and self-organizing map.

[0099] Southern blot hybridization techniques are also within the skill in the art. For example, genomic DNA isolated from a subject's sample can be digested with restriction endonucleases. This digestion generates restriction fragments of the genomic DNA that can be separated by electrophoresis,

for example, on an agarose gel. The restriction fragments are then blotted onto a hybridization membrane (e.g., nitrocellulose or nylon), and hybridized with labeled probes specific for a given miRNA molecule(s). A deletion or mutation of these genes is indicated by an alteration of the restriction fragment patterns on the hybridization membrane, as compared to DNA from a control sample that has been treated identically to the DNA from the subject's sample. Probe labeling and hybridization conditions suitable for detecting alterations in gene structure or sequence can be readily determined by one of ordinary skill in the art. The miRNA nucleic acid probes for Southern blot hybridization can be designed based upon the nucleic acid sequences having SEQ ID NOS: 1-401, provided in Table 1, or any one miRNA molecule of Table 7, Table 9, or Table 10. Nucleic acid probe hybridization can then be detected by exposing hybridized filters to photographic film, or by employing computerized imaging systems, such the Molecular Dynamics 400-B 2D Phosphorimager available from Amersham Biosciences, Piscataway, N.J.

[0100] Human miRNAs are associated with different classes of chromosomal features that are subsequently associated with cancer (Xu and Li (2007) *Chin Med J* (Engl). 120(11):996-9; Bandres et al., (2007) *DNA Cell Biol.* 26(5): 273-82). These cancers are purportedly partly caused by perturbing the chromosome or genomic DNA caused by the cancer-associated chromosomal feature, which can affect expression of oncogenes or tumor-suppressor genes located near the site of perturbation. A given cancer can be treated by restoring the level of miRNA expression associated with that cancer to normal. For example, if the level of miRNA expression is down-regulated in cancer cells of a subject, then the cancer can be treated by increasing the miRNA expression level. Alternatively, if the miRNA expression level is up-regulated in cancer cells of a subject, then the cancer can be treated by decreasing the miRNA expression level.

[0101] For example, the level of a miRNA in a cancerous or neoplastic cell of a subject (for example a hematopoietic malignancy or a hematopoietic neoplasm) is first determined relative to control cells. Techniques suitable for determining the relative level of a miRNA molecule in cells have been described above. If miRNA expression is down-regulated in the cancer or neoplastic cell relative to control cells, then the cancer or neoplastic cells are treated with an effective amount of a composition comprising an isolated miRNA molecule which is down-regulated (for example, a miRNA of the invention comprising any one of SEQ ID NOS: 1-401, as shown in Table 1, or any one miRNA molecule of Table 7, Table 9, or Table 10). If miRNA expression is up-regulated in cancer or neoplastic cells relative to control cells, then the cancer or neoplastic cells are treated with an effective amount of a composition that inhibits miRNA expression (for example, a miRNA of the invention comprising any one of SEQ ID NOS: 1-401, as shown in Table 1, or any one miRNA molecule of Table 7, Table 9, or Table 10).

[0102] One skilled in the art can also readily determine an appropriate dosage for the administration of an isolated miRNA molecule to a given subject. For example, a miRNA molecule can be administered to the subject once (e.g., as a single injection or deposition). Alternatively, a miRNA molecule of the invention can be administered once or twice daily to a subject for a period of from about two to about twenty-eight days, for example, from about seven to about ten days. Furthermore, the miRNA molecule of the invention can be co-administrated with another therapeutic, such as a chemotherapy drug. Where a dosage regimen comprises multiple administrations, the effective amount of the miRNA molecule administered to the subject can comprise the total amount of gene product administered over the entire dosage regimen.

[0103] The miRNA molecules of the invention comprising any one of SEQ ID NOS: 1-401, as shown in Table 1, or any one miRNA molecule of Table 7, Table 9, or Table 10, can be administered to a subject by any means suitable for delivering the miRNA molecules to cells of the subject, such as hematopoietic cells (either cancerous or neoplastic). For example, miRNA molecules can be administered by methods suitable to transfect cells (such as of the subject with the miRNA molecules of the invention. Transfection methods for eukaryotic cells (such as hematopoietic malignant cells or a hematopoietic neoplastic cells) are well known in the art, and include direct injection of the nucleic acid into the nucleus or pronucleus of a cell; electroporation; liposome transfer or transfer mediated by lipophilic materials; receptor mediated nucleic acid delivery, bioballistic or particle acceleration; calcium phosphate precipitation, and transfection mediated by viral vectors.

[0104] The compositions of this invention can be formulated and administered to inhibit a variety of disease states by any means that produces contact of the active ingredient with the agent's site of action in the body of a mammal They can be administered by any conventional means available for use in conjunction with pharmaceuticals, either as individual therapeutic active ingredients or in a combination of therapeutic active ingredients. They can be administered alone, but are generally administered with a pharmaceutical carrier selected on the basis of the chosen route of administration and standard pharmaceutical practice.

[0105] Pharmaceutical compositions for use in accordance with the invention can be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. The therapeutic compositions of the invention can be formulated for a variety of routes of administration, including systemic and topical or localized administration. Techniques and formulations generally can be found in *Remmington's Pharmaceutical Sciences*, Meade Publishing Co., Easton, Pa. (1985), the entire disclosure of which is herein incorporated by reference. For systemic administration, injection is useful, including intramuscular, intravenous, intraperitoneal, and subcutaneous. For injection, the therapeutic compositions of the invention can be formulated in liquid solutions, for example, in physiologically compatible buffers such as Hank's solution or Ringer's solution. In addition, the therapeutic compositions can be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms are also included. Pharmaceutical compositions of the present invention are characterized as being at least sterile and pyrogen-free. These pharmaceutical formulations include formulations for human and veterinary use.

[0106] The present pharmaceutical formulations comprise the miRNA molecules of the invention comprising any one of SEQ ID NOS: 1-401, as shown in Table 1, or any one miRNA molecule of Table 7, Table 9, or Table 10 (e.g., 0.1 to 90% by weight), or a physiologically acceptable salt thereof, mixed with a pharmaceutically-acceptable carrier. The pharmaceutical formulations of the invention can also comprise the miRNA molecules of the invention comprising any one of SEQ ID NOS: 1-401, as shown in Table 1, or any one miRNA molecule of Table 7, Table 9, or Table 10, which are encapsulated by liposomes and a pharmaceutically-acceptable car-

rier. Useful pharmaceutically-acceptable carriers are water, buffered water, normal saline, 0.4% saline, 0.3% glycine, hyaluronic acid, and the like.

[0107] Pharmaceutical compositions of the invention can also comprise conventional pharmaceutical excipients and/or additives. Suitable pharmaceutical excipients include stabilizers, antioxidants, osmolality adjusting agents, buffers, and pH adjusting agents. Suitable additives include physiologically biocompatible buffers (e.g., tromethamine hydrochloride), additions of chelants (such as, for example, DTPA or DTPA-bisamide) or calcium chelate complexes (as for example calcium DTPA, CaNaDTPA-bisamide), or, optionally, additions of calcium or sodium salts (for example, calcium chloride, calcium ascorbate, calcium gluconate or calcium lactate). Pharmaceutical compositions of the invention can be packaged for use in liquid form, or can be lyophilized.

[0108] For solid pharmaceutical compositions of the invention, conventional nontoxic solid pharmaceutically-acceptable carriers can be used; for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like.

[0109] For oral administration, the therapeutic compositions can take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g., magnesium stearate, talc or silica); disintegrants (e.g., potato starch or sodium starch glycolate); or wetting agents (e.g., sodium lauryl sulphate). The tablets can be coated by methods well known in the art. Liquid preparations for oral administration can take the form of, for example, solutions, syrups or suspensions, or they can be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations can be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (e.g., lecithin or acacia); non-aqueous vehicles (e.g., ationd oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (e.g., methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations can also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

[0110] Preparations for oral administration can be suitably formulated to give controlled release of the active agent. For buccal administration the therapeutic compositions can take the form of tablets or lozenges formulated in a conventional manner. For administration by inhalation, the compositions for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit can be determined by providing a valve to deliver a metered amount. Capsules and cartridges of e.g., gelatin for use in an inhaler or insufflate or can be formulated containing a powder mix of the therapeutic agents and a suitable powder base such as lactose or starch.

[0111] The therapeutic compositions can be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection can be presented in unit dosage form, e.g., in ampoules or in multidose containers, with an added preservative. The compositions can take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and can contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient can be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

[0112] Suitable enteral administration routes for the present methods include oral, rectal, or intranasal delivery. Suitable parenteral administration routes include intravascular administration (e.g. intravenous bolus injection, intravenous infusion, intra-arterial bolus injection, intra-arterial infusion and catheter instillation into the vasculature); peri- and intra-tissue injection (e.g., peri-tumoral and intra-tumoral injection, intra-retinal injection, or subretinal injection); subcutaneous injection or deposition including subcutaneous infusion (such as by osmotic pumps); direct application to the tissue of interest, for example by a catheter or other placement device (e.g., a retinal pellet or a suppository or an implant comprising a porous, non-porous, or gelatinous material); and inhalation. The miRNA molecules of the invention are administered by injection or infusion.

[0113] In addition to the formulations described previously, the therapeutic compositions can also be formulated as a depot preparation. Such long acting formulations can be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the therapeutic compositions can be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

[0114] Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration bile salts and fusidic acid derivatives. In addition, detergents can be used to facilitate permeation. Transmucosal administration can be through nasal sprays or using suppositories. For topical administration, the compositions of the invention are formulated into ointments, salves, gels, or creams as generally known in the art. A wash solution can be used locally to treat an injury or inflammation to accelerate healing. For oral administration, the therapeutic compositions are formulated into conventional oral administration forms such as capsules, tablets, and tonics.

[0115] A composition of the present invention can also be formulated as a sustained and/or timed release formulation. Such sustained and/or timed release formulations can be made by sustained release means or delivery devices that are well known to those of ordinary skill in the art, such as those described in U.S. Pat. Nos. 3,845,770; 3,916,899; 3,536,809; 3,598,123; 4,008,719; 4,710,384; 5,674,533; 5,059,595; 5,591,767; 5,120,548; 5,073,543; 5,639,476; 5,354,556; and 5,733,566, the disclosures of which are each incorporated herein by reference. The pharmaceutical compositions of the present invention can be used to provide slow or sustained release of one or more of the active ingredients using, for example, hydropropylmethyl cellulose, other polymer matrices, gels, permeable membranes, osmotic systems, multilayer coatings, microparticles, liposomes, microspheres, or the like, or a combination thereof to provide the desired release

profile in varying proportions. Suitable sustained release formulations known to those of ordinary skill in the art, including those described herein, can be readily selected for use with the pharmaceutical compositions of the invention. Thus, single unit dosage forms suitable for oral administration, such as, but not limited to, tablets, capsules, gel caps, caplets, powders, and the like, that are adapted for sustained release are encompassed by the present invention.

[0116] In the present methods, the miRNA molecules of the current invention comprising any one of SEQ ID NOS: 1-401, as shown in Table 1, or any one miRNA molecule of Table 7, Table 9, or Table 10, can be administered to the subject either as naked RNA, in conjunction with a delivery reagent, or as a nucleic acid (e.g., a recombinant plasmid or viral vector) comprising sequences which expresses the gene product. Suitable delivery reagents for administration of the miRNA molecules include the Mirus Transit TKO lipophilic reagent; lipofectin; lipofectamine; cellfectin; or polycations (e.g., polylysine), or liposomes.

[0117] The dosage administered will be a therapeutically effective amount of the composition sufficient to result in amelioration of symptoms of B cell lymphoma disease and can vary depending upon known factors such as the pharmacodynamic characteristics of the particular active ingredient and its mode and route of administration; age, sex, health and weight of the recipient; nature and extent of symptoms; kind of concurrent treatment, frequency of treatment and the effect desired.

[0118] Toxicity and therapeutic efficacy of therapeutic compositions of the present invention can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (The Dose Lethal To 50% Of The Population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD50/ED50. Therapeutic agents which exhibit large therapeutic indices are useful. Therapeutic compositions that exhibit some toxic side effects can be used.

[0119] Appropriate doses of small molecule agents depends upon a number of factors known to those or ordinary skill in the art, e.g., a physician. The dose(s) of the small molecule will vary, for example, depending upon the identity, size, and condition of the subject or sample being treated, further depending upon the route by which the composition is to be administered, if applicable, and the effect which the practitioner desires the small molecule to have upon the nucleic acid or polypeptide of the invention. Exemplary doses include milligram or microgram amounts of the small molecule per kilogram of subject or sample weight (e.g., about 1 microgram per kilogram to about 500 milligrams per kilogram, about TOO micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram.

[0120] These methods described herein are by no means all-inclusive, and further methods to suit the specific application will be apparent to the ordinary skilled artisan. Moreover, the effective amount of the compositions can be further approximated through analogy to compounds known to exert the desired effect.

[0121] The practice of aspects of the present invention can employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, Molecular Cloning A Laboratory Manual, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989); DNA Cloning, Volumes I and II (D. N. Glover ed., 1985); Oligonucleotide Synthesis (M. J. Gait ed., 1984); Mullis et al. U.S. Pat. No. 4,683,195; Nucleic Acid Hybridization (B. D. Hames & S. J. Higgins eds. 1984); Transcription And Translation (B. D. Hames & S. J. Higgins eds. 1984); Culture Of Animal Cells (R. I. Freshney, Alan R. Liss, Inc., 1987); Immobilized Cells And Enzymes (IRL Press, 1986); B. Perbal, A Practical Guide To Molecular Cloning (1984); the treatise, Methods In Enzymology (Academic Press, Inc., N.Y.); Gene Transfer Vectors For Mammalian Cells (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); Methods In Enzymology, Vols. 154 and 155 (Wu et al. eds), Immunochemical Methods In Cell And Molecular Biology (Mayer and Walker, eds., Academic Press, London, 1987); Handbook Of Experimental Immunology, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); Manipulating the Mouse Embryo, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). All patents, patent applications and references cited herein are incorporated in their entirety by reference.

EXAMPLES

[0122] A number of Examples are provided below to facilitate a more complete understanding of the present invention. The following examples illustrate the exemplary modes of making and practicing the present invention. However, the scope of the invention is not limited to specific embodiments disclosed in these Examples, which are for purposes of illustration only, since alternative methods can be utilized to obtain similar results.

Example 1

Experimental Analysis

[0123] We have used an established process for the identification of miRNAs candidates by sequencing size-fractionated cDNA libraries from three normal B cell populations, including Naïve B cells, Centroblasts and Memory B cells and from a Burkitt Lymphoma cell line (Ramos). Briefly, short RNAs (sRNA) extracted from the cells were linked to adaptor oligonucleotides, reverse transcribed, PCR amplified, cloned into an expression vector, and sequenced. Individual sequences, corresponding to short RNAs, were then analyzed bioinformatically to determine whether they would constitute appropriate miRNA candidates.

[0124] Bioinformatics Analysis:

[0125] The computational analysis starts with the identification of short RNA (sRNA) sequences from cloned cDNA sequences using the adaptor oligonucleotides as oriented markers. Then, each sRNA was matched to the human genome (ncbi36, October 2006) by using Megablast (NCBI).

[0126] A Bayesian evidence integration scheme was used to identify candidate sRNAs from partial matches to the human genome. Single and multiple base mismatches can occur for several reasons, including polymorphisms, sequencing errors, PCR errors that are more frequent in the 3' and 5' region of the miRNA cDNA, and RNA editing enzymes.

[0127] To identify sequences that correspond to real sRNAs, we used the following Bayesian approach to compute the posterior probability that a sequence is a candidate miRNA genomic match given specific base pair substitutions under the assumption that individual mutations are uncorrelated (Naïve Bayes). The individual $p(m_i|\text{match})$ and $p(m_i)$ can be measured using matches to the miRNAs deposited in the miRNABase database. Sequences with $p(\text{match}|m_1, m_2, \ldots, m_n)>0.5$ were considered bona-fide matches to the human genome sequences and further processed together with the exact matching ones. $m_1, m_2, \ldots, m_n$:

$$p(\text{match}\mid m_1, m_2, \ldots, m_n) = p(m_1, m_2, \ldots, m_n \mid \text{match})\frac{p(\text{match})}{p(m_1, m_2, \ldots, m_n)} = p(\text{match})\prod\frac{p(m_i \mid \text{match})}{p(m_i)}$$

[0128] Resulting sRNA genome locations, both for exact and partial matches, were analyzed and merged, if necessary, to remove overlapping sequences. For each sRNA hit a sequence from −80 bp upstream to +80 b.p. downstream of the sRNA match was selected leading to a set of candidate microRNA genes, including the full length precursors.

[0129] These longer sequences were then analyzed to determine if they can lead to the formation of precursor miRNA structures, including favorable energetics to for the established stem-loop secondary RNA structure required for further miRNA processing. Using a set of established mammalian miRNA's and data from the scientific literature the following criteria were established:

[0130] 1. Mature sequence, which is defined by matching sRNA's, should occupy only one arm of hairpin (not the loop).

[0131] 2. Loop structure cannot be shorter that 3 b.p. or longer than 20 b.p.

[0132] 3. Hairpin stem should not host additional secondary RNA structures with more than 10 b.p.

[0133] 4. The ratio between the number of complementary base pairs and the total number of base pairs comprising hairpin arms should be bigger than 0.55.

[0134] 5. Free energy should not be bigger than −20 kcal/mole.

[0135] We do not apply highly popular conservation criteria because of:

[0136] significant incompleteness of many genome assemblies especially in intergenic regions

[0137] Risk to lose unique or diverged miRNA's (this invention is directed to obtaining an exhaustive search and outcome)

[0138] Possibility of further experimental verification of candidates.

[0139] Since the exact sites of transcription initiation and termination for miRNA genes is not known and since concentration and temperature can vary, it is important to consider not just the optimal folding variant but an entire distribution of variants near the optimal one. We used the Vienna RNA package to perform this type of analysis, with appropriate modifications to allow the analysis of suboptimal folding variants.

[0140] Candidate miRNA genes were filtered against non-coding RNA database and repeats database (repbase). Database of human non-coding RNA's is manually compiled and contains genes like ribosomal RNA's, snRNA, tRNA's, Y-RNA and others. Comparison performed using MEGA-BLAST program (NCBI).

[0141] Finally, candidate miRNAs emerging from this analysis were compared to miRNABase database to identify previously known miRNAs. Candidate miRNAs that were not identified in the miRNABase were considered. Diagrams illustrating these steps are included as FIGS. **1-3**.

[0142] Validation:

[0143] Some of the newly identified miRNAs were tested by Northern in the corresponding population in which the sRNA was isolated.

[0144] Newly Identified miRNAs

[0145] The following have been identified as newly identified miRNAs (miRNAs) in one or more of the four B cell populations from which the size-fractionated cDNA libraries were isolated.

Example 2

Protocol for microRNA Cloning

[0146] Preparation and Labeling of Decade Marker (Ambion #7778)

[0147] Decade marker is radio labeled using [γ-^{32}P]ATP according to the manufacturer instructions.

[0148] Labeling of the RNA Carrier

[0149] 20 pmol of #909 carrier RNA oligo is radio labeled using [γ-^{32}P]ATP and T4 Polynucleotide kinase (NEB).

[0150] Purification of 18-26Mers from Total RNA

[0151] A 15% denaturing polyacrylamide gel was prepared using the Sequagel System (National Diagnostics) following the manufacturer instructions. A metal plate was placed on the front of the gel and was pre-run at 50 W for 30 minutes using a running buffer of 0.5×TBE. Each RNA sample [10 μg of total RNA] was subsequently spiked 1 pmol (2.5 μl) of [γ-^{32}P] labeled-#909 carrier and an equal volume of 2×RNA loading buffer (Ambion) was added. For total RNA, extraction procedures like Trizol Reagent (Invitrogen) that purify all sizes RNA are recommended. Samples were then boiled for 5 minutes and were loaded with decade marker. After samples were loaded onto the gel, it was run for 3-4 hours at 50 W. After the gel was run, the apparatus was disassemble and one of the glass pieces was removed. The hot area of the gel was cut out and placed on the side of the lane for alignment with the markers. The gel was subsequently covered with a plastic wrap and was exposed to a phosphoimage screen for about 30 minutes to an 1 hour. The gel image was printed at 100% magnification and placed under the glass. It was then aligned with the hot spot that had been previously cut. The RNA band was cut approximately from 18mers up to 26mers using the marker and the 1 nt ladder below the carrier as reference. RNA was eluted from the gel using 2 ml of 0.3M NaCl in DEPC H_2O, and the eluted sample was subsequently rotated overnight at 4° C. The supernatant was then recovered and 450 μl (max) was distributed into separate tubes. A 2× volume of 100% EtOH and 10 μg glycogen were added to each tube, which were then incubated at −20° C. for at least 2 hours. Samples were then spun for 30 minutes at 14,000 rpm, and were subsequently washed with 75% EtOH. The pellets were then air dried and dissolved in 10 μl DEPC H_2O.

[0152] 3'-Adaptor Ligation and Purification

[0153] The following were first mixed in a tube and were then incubated at 25° C. for 6 hours:

1.5 µl	10X 3'Ligation Buffer*
7.5 µl	purified small RNA
2 µl	App.17.91 [100 pmol/µl] (adenylated)
1.5 µl	T4 RNA Ligase [30 U/µl] (Amersham)
2.5 µl	H_2O

*500 mM Tris-HCl (pH 7.5), 100 mM $MgCl_2$, 100 mM DTT, 600 µg/ml BSA. Store at −20° C.

[0154] 15 µl of 2× Loading Buffer (Ambion) was added to the samples and boiled for 5 minutes, which were then loaded onto a 12% denaturing polyacrylamide gel that was prepared using the Sequagel System (National Diagnostics) following the manufacturer instructions. A metal plate was placed on the front of the gel and was pre-run at 50 W for 30 minutes using a running buffer of 0.5×TBE. The decade RNA marker and 1 µl of [γ-^{32}P] labeled-#909 carrier was then loaded into separated lanes and run for 3-4 hours at 50 W. After the gel was run, the apparatus was disassemble and the gel was exposed to a phosphoimage screen for 2-4 hours. The gel image was printed at 100% magnification and placed under the glass. The ligation product ranging approximately from 35 up to 42-45 nt was cut and RNA was eluted from the gel using 2 ml of 0.3M NaCl in DEPC H_2O. The eluted sample was subsequently rotated overnight at 4° C. The supernatant was then recovered and 450_111 (max) was distributed into separate tubes. A 2× volume of 100% EtOH and 10 mg glycogen were added to each tube, which were then incubated at −20° C. for at least 2 hours. Samples were then spun for 30 minutes at 14,000 rpm, and were subsequently washed with 75% EtOH. The pellets were then air dried and dissolved in 12 µl DEPC H_2O.

[0155] 5'-Adaptor Ligation and Purification

[0156] The following were first mixed in a tube and were then incubated at 25° C. for 6 hours:

1 µl	10X Ligation Buffer (Amersham)
6 µl	purified small RNA
2 µl	17.93 oligo [100 pmol/µl]
1 µl	T4 RNA Ligase [30 U/µl] (Amersham)

[0157] Samples can be stored at 4° C. after the 6 hour incubation until further processed. 10 µl of 2× Loading Buffer (Ambion) was added to the samples and boiled for 5 minutes, which were then loaded onto a 10% denaturing polyacrylamide gel that was prepared using the Sequagel System (National Diagnostics) following the manufacturer instructions. A metal plate was placed on the front of the gel and was pre-run at 50 W for 30 minutes using a running buffer of 0.5×TBE. The decade RNA marker and 1 µl of [γ-^{32}P] labeled-#909 carrier was then loaded into separated lanes and run for 3 hours at 50 W. After the gel was run, the apparatus was disassemble and the gel was exposed to a phosphoimage screen for 12-18 hours. The gel image was printed at 100% magnification and placed under the glass. The ligation product ranging approximately from 35 up to 48-62 nt was cut and RNA was eluted from the gel using 2 ml of 0.3M NaCl in DEPC H_2O. The eluted sample was subsequently rotated overnight at 4° C. The supernatant was then recovered and 450 µl (max) was distributed into separate tubes. A 2× volume of 100% EtOH and 10 ng glycogen were added to each tube, which were then incubated at −20° C. for at least 2 hours. Samples were then spun for 30 minutes at 14,000 rpm, and were subsequently washed with 75% EtOH. The pellets were then air dried and dissolved in 20 µl DEPC H_2O.

[0158] Reverse Transcription

[0159] The following were first mixed in a PCR tube and were then incubated at 80° C. for 2 minutes:

10 µl	ligated RNA
3 µl	#918 primer [100 µM]

[0160] The sample was subsequently spun down to cool. Using the First Strand Synthesis System kit (Invitrogen), the following was added to the sample which was then incubated at 48° C. for 2 minutes:

5 µl	5X First Strand Buffer
7 µl	dNTPs
3 µl	0.1M DTT

[0161] 3 µl of SuperScriptII (Invitrogen) was then added to the sample, which was further incubated at 48° C. for 1 hour. Samples can then be stored at −20° C. until further processing.

[0162] PCR Amplification

[0163] The PCR reaction was prepared as follows:

[0164] 5% Reverse Transcription product

[0165] 1×PCR buffer

[0166] 1.5 mM $MgCl_2$

[0167] 0.8 mM dNTP

[0168] 2 µM #913 primer

[0169] 2 µM #914 primer

[0170] 2 U Taq polymerase

[0171] The sample was then amplified according to the following protocol:

2' 94° C. 30" 94° C. 30" 52° C. 30" 72° C. 10' 72° C.	}	X30 cycles

[0172] The sample was then extracted using Phenol/CIA and was precipitated with sodium acetate. The sample was then spun for 30 minutes at 14,000 rpm, and was subsequently washed with 75% EtOH. The pellet was then air dried and dissolved in 45 µl DEPC H_2O.

[0173] PACI Digestion

[0174] The digestion was prepared as follows and was subsequently incubate at 37° C. for 90 minutes:

[0175] 1×NEB Buffer 1

[0176] 1×BSA

[0177] 1,000 U/µl PACI

[0178] 42.5 µl DNA

[0179] The sample was then extracted using Phenol/CIA and was precipitated with sodium acetate. The sample was then spun for 30 minutes at 14,000 rpm, and was subsequently washed with 75% EtOH. The pellet was then air dried and

dissolved in 15 μl DEPC H_2O. Non-denaturing Loading Buffer was added to the sample and the sample was subsequently loaded onto a 12% non-denaturing acrylimide gel using pUC19/Sau3AI as a marker (Ambion #7760), which was run at 13 W for approximately 1 hr. The gel was then stained with 1:10,000 SybrGold (Molecular Probes #S-11494) in 0.5×TBE for 30 to 60 minutes. The smear of digested samples was then cut between 46 and 75 nt according to the marker size. Cut out samples were then eluted with 500 μl of 0.3M NaCl in 1.5 ml screw top tubes, rotating overnight at 4° C. Samples were spun briefly, and about 450 μl of eluted volume was recovered for each sample. The samples were then extracted using Phenol/CIA and were precipitated with sodium acetate. The samples were then spun for 30 minutes at 14,000 rpm, and were subsequently washed with 75% EtOH. The pellet was then air dried and dissolved in 10 μl DEPC H_2O. If the amount of digested product on the gel appeared to be low, a second PCR amplification was required.

[0180] Second PCR Amplification

[0181] The PCR reaction was prepared as follows:

[0182] 2% Reverse Transcription product

[0183] 1×PCR buffer

[0184] 1.5 mM $MgCl_2$

[0185] 0.8 mM dNTP

[0186] 2 μM #913 primer

[0187] 2 μM #914 primer

[0188] 2 U Taq polymerase

[0189] The sample was then amplified according to the following protocol:

2' 94° C. 30" 94° C. 30" 52° C. 30" 72° C. 10' 72° C.	}	X20 cycles

[0190] The amount of product generated was examined via adding non-denaturing Loading Buffer to 5 μl of sample, which was then loaded onto a 12% non-denaturing acrylimide gel, and was subsequently run at 13 W for approximately 1 hr. Samples were cut out and eluted with 500 μl of 0.3M NaCl in 1.5 ml screw top tubes, rotating overnight at 4° C. Samples were spun briefly, and about 450 μl of eluted volume was recovered for each sample. The samples were then extracted using Phenol/CIA and were precipitated with sodium acetate. The samples were then spun for 30 minutes at 14,000 rpm, and were subsequently washed with 75% EtOH. The pellet was then air dried and dissolved in 45 DEPC H_2O. Samples were further quantified, wherein amount of sampled needed to be within the range of 200-500 ng/μl.

[0191] BanI Digestion

[0192] The following digestion was prepared for each sample as follows, and were subsequently incubated at 37° C. for 2.5 hours:

[0193] 1×NEB Buffer 4

[0194] 1×BSA

[0195] 1000 U/μl BanI

[0196] Samples were then extracted using Phenol/CIA and were precipitated with sodium acetate. The samples were spun for 30 minutes at 14,000 rpm, and were subsequently washed with 75% EtOH. The pellet was then air dried and dissolved in 26 μl DEPC H_2O.

[0197] Concatemerization

[0198] The following sample was mixed in a 0.5 or 0.2 ml tube as follows, and was incubated at 25° C. for 2 hours:

26 μl	Digested DNA
3 μl	10X Ligation Buffer (Roche)
1 μl	T4 DNA Ligase [5 U/μl] (Roche)
1 μl	of dNTP as well as 1 μl of DNA Polymerase I was subsequently added,

and the sample was then incubated at 16° C. for 1 hour. The sample was run on a 2% LM agarose-EtBr gel in 0.5×TBE with 100 bp Ladder loaded in the first lane. The concatamers were then cut starting from about 500 bp and above. Samples were then gel purified with QlAquick gel extraction kit (Qiagen cat.#28706), using the manufacturer's instructions.

[0199] Vector Digestion

[0200] The pCR2.1-TOPO (Invitrogen, 3.9 Kb) vector was digested according to the manufacturer's instructions for the EcoRV enzyme (NEB). The samples was then subjected to gel electrophoresis using a 1% agarose gel. The sample was then gel purified with QlAquick gel extraction kit (Qiagen cat.#28706), using the manufacturer's instructions.

[0201] Ligation

[0202] The ligation reaction was set up using the Rapid Ligation Kit (Roche cat.#11635379001) according to the procedure recommended by the manufacturer. 10 μl of the ligation product was used for transformation in high efficiency bacteria (One Shot OminMAX—Invitrogen cat.# C8540-03). X-gal/IPTG Ampicillin agarose plates were prepared fresh and a specified volume of the transformation reaction was spread onto the plates. Plated samples were then incubated overnight at 37° C. Colonies were then obtained the next day and grown in 30 μl of LB medium at 37° C. for 1 hour. Once DNA was obtained from the amplified bacteria, 2.5 μl was used as template for the colony PCR reaction.

[0203] Colony PCR

[0204] The PCR reaction was prepared as follows:

[0205] 2.5 μl template

[0206] 1×PCR buffer

[0207] 1.5 mM $MgCl_2$

[0208] 0.8 mM dNTP

[0209] 0.2 μM #913 primer

[0210] 0.2 μM #914 primer

[0211] 1 U Taq polymerase

[0212] The sample was then amplified according to the following protocol:

5' 94° C. 30" 94° C. 30" 52° C. 30" 72° C. 10' 72° C.	}	X30 cycles

[0213] 1 μl of PCR product was examined on a 1.5% agarose gel and clones were selected carrying an insert longer than 350 bp. Samples were then confirmed by sequencing.

[0214] Oligonucleotides

909 carrier RNA oligo:
[SEQ ID NO: 517]
5'-(P)-UGUCAGUUUGUUAAUUAACCCAA-3'

5' phosphate; 3' none; includes PACI restriction site

App. 17.91 (3' end Donor oligo):
[SEQ ID NO: 518]
5'-rAppCTGTAGGCACCATCAAT/3ddC-3'

5' adenylated containing a pyrophosphate; 3' modified terminal dideoxy-C(ddC) (available from IDT Inc. as the "miRNA cloning linker"); includes BanI restriction site.

17.93 (5' end Acceptor oligo):
[SEQ ID NO: 519]
5'-ATCGTAGGCACCTGAAA-3'

It includes BanI restriction site.

#918 RT primer oligo:
[SEQ ID NO: 520]
5'-ATTGATGGTGCCTAC-3'

It includes BanI restriction site.

#913 (5' PCR primer oligo):
[SEQ ID NO: 521]
5'-ATCGTAGGCACCTGAAA-3'

It includes BanI restriction site.

#914 (3' PCR primer oligo):
[SEQ ID NO: 522]
5'-ATTGATGGTGCCTACAG-3'

It includes BanI restriction site.

[0215] Screening/Sequencing Primers:

M13F
[SEQ ID NO: 523]
5'-GTAAAACGACGGCCAG-3'

M13R
[SEQ ID NO: 524]
5'-CAGGAAACAGCTATGAC-3'

REFERENCES

[0216] Lau et al., Science (2001) 294:858-62; Chen et al., Science (2004) 303: 83-6

Example 3

Identification of the Human Mature B Cells miRNome

[0217] The discovery of microRNAs (miRNAs) has added a new dimension to the mechanisms that regulate gene expression in normal cell development. Initial evidence also shows that structural or functional alterations of miRNAs are associated with tumorigenesis. The full set of microRNAs (miRNAs) in the human genome is not known. Since presently known miRNAs have been identified by virtue of their abundant expression in a few cell types, tissue-specific miRNAs may remain unrevealed. To understand the role of miRNAs in B-cell function and lymphomagenesis, short-RNA libraries were generated from normal human B cells at different stages of development (naïve, germinal-center, memory) and from a Burkitt lymphoma cell-line. The combination of cloning and computational analysis identified 401 miRNA (miRNome) expressed during normal B-cell development and/or in transformed B-cells. Most notably, this analysis identified 272 new miRNAs that were not previously reported. Numerous miRNAs are expressed in a stage-specific as well as transformation-specific fashion, suggesting specific functional roles. These results significantly increase the number of presently known miRNAs and provide a resource for the study of their role in B-cell development, immune function, and lymphomagenesis.

[0218] A new level of post-transcriptional regulation has been revealed with the discovery of microRNAs (miRNAs) a class of short-RNAs that impair translation or induce mRNA degradation by binding to the 3' untranslated region of target mRNA[1,2]. The most recent release of the miRBase database (v.11.0)[3,4] reports 839 human miRNAs, but the discovery of miRNAs is still an on-going process with variable predictions about the total number of miRNAs expressed in mammalian cells ranging from one thousand to several thousands[5,6]. The reported miRNAs have been identified from a limited number of cell types or from tissues whose cellular heterogeneity may favor the identification of ubiquitous and abundant miRNA. In fact, a recent report aiming to the identification of the miRNA expression profiles from 26 different mammalian tissues and cell types led to the discovery of only 12 new human miRNA[7]. These findings led to the conclusion that most miRNAs are known and that most of them are ubiquitously expressed[7]. Nonetheless, additional analyses of purified cell populations may lead to the identification of tissue- and stage of differentiation-specific miRNAs, as has been the case for messenger RNAs.

[0219] The role of specific miRNAs in B-cell immunity and malignancy has only just begun to be elucidated. Using mouse models, miR-155 has been demonstrated to affect regulation of germinal center response through modulation of cytokine production[8,9]. Recently, miR-150 has been shown to target c-Myb, a critical transcription factor involved in the control of B cell differentiation[10]. In B cell lymphomas, 13q31 amplification has been associated with the over-expression of the miR-17-92 cluster and its enforced expression in a murine B cell lymphoma model showed a role in accelerating tumor development[11]. Furthermore, miR-15a and miR-16 have been implicated in the pathogenesis of B cell chronic lymphocytic leukemia (CLL)[12,13].

[0220] To further explore the role of miRNAs in B cell function and lymphomagenesis, this study was aimed at identifying the miRNAs expressed (miRNome) in the human mature B-cell compartment, including naïve, germinal centers (GCs), and memory B cells. These B cell subpopulations are relevant for the development of antibody-mediated immunity as well as for tumorigenesis, since common human B-cell malignancies originate from the malignant transformation of GC B cells (most B-cell non-Hodgkin lymphomas, B-NHL), or naïve and memory B cells (mantle cell lym-

phoma and chronic lymphocytic leukemia)[14,15]. Using a combination of cloning and computational analysis, we report the identification of 401 miRNA representing the mature B cell miRNome, including 272 new miRNAs, and illustrate their pattern of expression during B cell differentiation and transformation.

[0221] Construction of Short-RNA Libraries from Human B Cell Sub-Populations

[0222] Short-RNA libraries were generated by cloning RNA fractions of 18-30 nt from human centroblasts, naïve and memory B cells purified from tonsils as well as from the Burkitt lymphoma cell line Ramos, which is representative of malignant transformation of GC B cells (FIG. **10**). Approximately 3,500 sequences were analyzed from each library, corresponding to 13,991 total short-RNAs (2,661 non-redundant sequences). Using a bootstrap approach[16,17], we estimated the expected number of miRNAs that could be predicted using our computational pipeline from various size of short-RNA libraries. The results suggested that at the current sequencing depth, 80% of the possible predictions have been identified FIG. **17**).

[0223] The cloned sequences were matched to the human genome assembly from March 2006 (hgl 8) to retrieve the genomic regions from which the short-RNAs originated. One or more genomic locations were identified for approximately 80% of the cloned sequences considering both perfect matches and single mismatches. Consistent with previous observations, 3'-end mismatches were the most common and showed a clear preference for A in the last position ([18]. Approximately 546 short-RNA sequences did not align to the human genome according to the above criteria and are likely due to PCR errors introduced during the cloning procedure (FIG. **11**). Nevertheless, a small subset of these short-RNAs lacking a corresponding genomic region in *Homo sapiens* have been cloned with high frequencies in multiple libraries and showed differential expression during B cell differentiation, suggesting they may represent bona fide short-RNA species. However, given the difficulty of assigning genomic coordinates to these sequences they were omitted from further analyses.

[0224] Computational Prediction of miRNA Precursors

[0225] In order to identify candidate miRNAs among the cloned sequences, we developed a computational pipeline aiming at the identification of potential miRNA precursors based on the investigation of their genomic location and folding characteristics (FIG. **18** and Supplementary Methods). Briefly, short RNA sequences were mapped to the human genome and candidate genomic precursors (+/−90 nt) were then retrieved and analyzed for secondary structure, size and energy of the loop, and number of complimentary base pairs in the stem of the loop (Supplementary Methods). The prediction was performed on the full set of non-redundant short-RNAs (2,115 sequences) for which one or more genomic locations could be identified (FIG. **11**). The analysis led to the identification of candidate precursors for 1,667 short-RNA sequences, which were then clustered to account for the variability observed at the miRNA 3'-ends (and less dramatically at the 5'-ends) including nucleotide substitutions and deletions. Moreover, editing of miRNA has been previously reported[19,20] and a few cases compatible with an editing process have been observed in the libraries described here. Since most clusters of short-RNA are affected by these modifications, we applied the following criteria in order to define mature miRNA sequences: i) each nucleotide must occur in more than 50% of the cloned sequences; sequences supported by a short-RNA set that is fully contained in a larger set were eliminated while matching clusters with partial containment were merged (Supplementary Methods). After annotating each candidate mature miRNA, those which had evidences of originating from mRNA, rRNA, tRNA and other ncRNA (yRNA, sn/snoRNA) and occurred once were eliminated. Overall, the computational analysis identified 401 mature miRNA (Table 1).

[0226] The human miRNAs deposited in the miRBase database (v.11.0) were identified only at the end of the analysis and any lack of prediction was checked by matching the starting set with the final predictions. Overall, previously reported miRNA represented 32% of cloned and computationally validated mature miRNA. In addition, our analysis identified 146 previously reported precursors as well as 761 genomic locations containing precursors potentially coding for 272 new mature miRNA and 19 new precursors for 8 mature miRNAs deposited in the miRBase database (FIG. **12** and Table 1).

TABLE 1A

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1026	1	TGTAGTGTTTCCTACTTTATGGA	Mature:hsa-miR-142-3p:MIMAT0000434
CU-1064	2	TAGCTTATCAGACTGATGTTGA	Mature:hsa-miR-21:MIMAT0000076
CU-1061	3	TAAAGTGCTTATAGTGCAGGTAG	Mature:hsa-miR-20a:MIMAT0000075
CU-1035	4	TAGCAGCACATCATGGTTTACA	Mature:hsa-miR-15b:MIMAT0000417
CU-1037	5	TAGCAGCACGTAAATATTGGCG	Mature:hsa-miR-16:MIMAT0000069
CU-1001	6	TGAGGTAGTAGGTTGTATAGTT	Mature:hsa-let-7a:MIMAT0000062
CU-1116	7	TATTGCACTTGTCCCGGCCTGT	Mature:hsa-miR-92a:MIMAT0000092
CU-1018	8	TCCCACCGCTGCCACCA	Mature:hsa-miR-1280:MIMAT0005946
CU-1006	9	TGAGGTAGTAGATTGTATAGTT	Mature:hsa-let-7f:MIMAT0000067
CU-1079	10	TAGCACCATCTGAAATCGGTTA	Mature:hsa-miR-29a:MIMAT0000086

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1033	11	TAGCAGCACATAATGGTTTGT	Mature:hsa-miR-15a:MIMAT0000068
CU-1124	12	CCCATAAAGTAGAAAGCACTA	Mature:hsa-miR-142-5p:MIMAT0000433
CU-1007	13	TGAGGTAGTAGTTTGTACAGTT	Mature:hsa-let-7g:MIMAT0000414
CU-1008	14	TGAGGTAGTAGTTTGTGCTGTT	Mature:hsa-let-7i:MIMAT0000415
CU-1082	15	TAGCACCATTTGAAATCGGTTA	Mature:hsa-miR-29c:MIMAT0000681
CU-1085	16	TGTAAACATCCTACACTCTCAGC	Mature:hsa-miR-30c:MIMAT0000244
CU-1039	17	CAAAGTGCTTACAGTGCAGGTAG	Mature:hsa-miR-17:MIMAT0000070
CU-1071	18	CATTGCACTTGTCTCGGTCTGA	Mature:hsa-miR-25:MIMAT0000081
CU-1046	19	CAACGGAATCCCAAAAGCAGCTG	Mature:hsa-miR-191:MIMAT0000440
CU-1057	20	TGTGCAAATCCATGCAAAACTGA	Mature:hsa-miR-19b:MIMAT0000074
CU-1024	21	TACCACAGGGTAGAACCACGGA	Mature:hsa-miR-140-3p:MIMAT0004597
CU-1084	22	TGTAAACATCCTACACTCAGCT	Mature:hsa-miR-30b:MIMAT0000420
CU-1003	23	TGAGGTAGTAGGTTGTGTGGTT	Mature:hsa-let-7b:MIMAT0000063
CU-1080	24	TAGCACCATTTGAAATCAGTGTT	Mature:hsa-miR-29b:MIMAT0000100
CU-1012	25	TAAAGTGCTGACAGTGCAGAT	Mature:hsa-miR-106b:MIMAT0000680
CU-1092	26	TCCCTGTCCTCCAGGAGCTC	Mature:hsa-miR-339-5p:MIMAT0000764
CU-1072	27	TTCAAGTAATCCAGGATAGGCT	Mature:hsa-miR-26a:MIMAT0000082
CU-1118	28	CAAAGTGCTGTTCGTGCAGGTAG	Mature:hsa-miR-93:MIMAT0000093
CU-1067	29	TGTCAGTTTGTCAAATACCCCA	Mature:hsa-miR-223:MIMAT0000280
CU-1027	30	TGAGAACTGAATTCCATGGGTT	Mature:hsa-miR-146a:MIMAT0000449
CU-1029	31	TCTCCCAACCCTTGTACCAGT	Mature:hsa-miR-150:MIMAT0000451
CU-1015	32	TCCCTGAGACCCTAACTTGTGA	Mature:hsa-miR-125b:MIMAT0000423
CU-1093	33	TCTCACACAGAAATCGCACCCGTC	Mature:hsa-miR-342-3p:MIMAT0000753
CU-1016	34	GTCCCTGTTCGGGCGCCA	Mature:hsa-miR-1274b:MIMAT0005938
CU-1056	35	TGTGCAAATCTATGCAAAACTGA	Mature:hsa-miR-19a:MIMAT0000073
CU-1086	36	TGTAAACATCCCCGACTGGAAG	Mature:hsa-miR-30d:MIMAT0000245
CU-1065	37	AGCTACATTGTCTGCTGGGTT	Mature:hsa-miR-221:MIMAT0000278
CU-1004	38	AGAGGTAGTAGGTTGCATAGTT	Mature:hsa-let-7d:MIMAT0000065
CU-1011	39	CCGCACTGTGGGTACTTGCT	Star:hsa-miR-106b*:MIMAT0004672
CU-1010	40	AGCAGCATTGTACAGGGCTATGA	Mature:hsa-miR-103:MIMAT0000101
CU-1050	41	AACTGGCCCTCAAAGTCCCGCT	Mature:hsa-miR-193b:MIMAT0002819
CU-1091	42	GCCCCTGGGCCTATCCTAGAA	Mature:hsa-miR-331-3p:MIMAT0000760
CU-1023	43	AGCTGGTGTTGTGAATCAGGCCGT	Mature:hsa-miR-138:MIMAT0000430
CU-1101	44	TGAGGGGCAGAGAGCGAGACTT	Mature:hsa-miR-423-5p:MIMAT0004748
CU-1066	45	AGCTACATCTGGCTACTGGGTCT	Mature:hsa-miR-222:MIMAT0000279
CU-1017	46	GTGGGGGAGAGGCTGTA	Mature:hsa-miR-1275:MIMAT0005929
CU-5001	47	CTATACGACCTGCTGCCTTTC	Star:hsa-let-7d*:MIMAT0004484

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1032	48	TTAATGCTAATCGTGATAGGGGT	Mature:hsa-miR-155:MIMAT0000646
CU-1108	49	AGGGGGAAAGTTCTATAGTC	Mature:hsa-miR-625:MIMAT0003294
CU-1055	50	ACAGTAGTCTGCACATTGGTT	Mature:hsa-miR-199b-3p:MIMAT0004563
CU-1042	51	AACATTCAACGCTGTCGGTGAGTT	Mature:hsa-miR-181a:MIMAT0000256
CU-1113	52	TGGAAGACTAGTGATTTTGTTGT	Mature:hsa-miR-7:MIMAT0000252
CU-1098	53	TAATGCCCCTAAAAATCCTTAT	Mature:hsa-miR-365:MIMAT0000710
CU-1052	54	TAGCAGCACAGAAATATTGGCA	Mature:hsa-miR-195:MIMAT0000461
CU-1568	55	TGAGGTAGTAGGTTGTAT	Mature:hsa-let-7c:MIMAT0000064
CU-1103	56	TCCTGTACTGAGCTGCCCCGAG	Mature:hsa-miR-486-5p:MIMAT0002177
CU-1014	57	TCCCTGAGACCCTTTAACCTGTGA	Mature:hsa-miR-125a-5p:MIMAT0000443
CU-1068	58	ATCACATTGCCAGGGATTTCCA	Mature:hsa-miR-23a:MIMAT0000078
CU-1019	59	TCACAGTGAACCGGTCTCTTT	Mature:hsa-miR-128:MIMAT0000424
CU-1076	60	CACTAGATTGTGAGCTCCTGGA	Mature:hsa-miR-28-3p:MIMAT0004502
CU-1111	61	CAACAAATCACAGTCTGCCAT	Star:hsa-miR-7-1*:MIMAT0004553
CU-1062	62	CAAAGTGCTTATAGTGCAGGTAG	Mature:hsa-miR-20b-mm:MIMAT0001413
CU-1115	63	AGGTTGGGATCGGTTGCAATGCT	Star:hsa-miR-92a-1*:MIMAT0004507
CU-1126	64	ACATTCATTGCTGTCGGTGGGTT	Mature:hsa-mir-181b-1:MI0000270
CU-1096	65	TCCCCCAGGTGTGATTCTGATT	Mature:hsa-miR-361-3p:MIMAT0004682
CU-1054	66	CCCAGTGTTCAGACTACCTGTTC	Mature:hsa-miR-199a-5p:MIMAT0000231
CU-1125	67	ACCAATATTACTGTGCTGCTT	Star:hsa-miR-16-2*:MIMAT0004518
CU-1087	68	TGTAAACATCCTTGACTGGAAGCT	Mature:hsa-miR-30e:MIMAT0000692
CU-1045	69	TAAGGTGCATCTAGTGCAGATA	Mature:hsa-miR-18a:MIMAT0000072
CU-1069	70	ATCACATTGCCAGGGATTACCA	Mature:hsa-miR-23b:MIMAT0000418
CU-1044	71	ACTGCCCTAAGTGCTCCTTCTG	Star:hsa-miR-18a*:MIMAT0002891
CU-1083	72	TGTAAACATCCTCGACTGGA	Mature:hsa-miR-30a:MIMAT0000087
CU-1009	73	TACAGTACTGTGATAACTGAAG	Mature:hsa-miR-101:MIMAT0000099
CU-1030	74	CTAGACTGAAGCTCCTTGAGG	Mature:hsa-miR-151-3p:MIMAT0000757
CU-1095	75	TGGCAGTGTCTTAGCTGGTTGTT	Mature:hsa-miR-34a:MIMAT0000255
CU-1119	76	TGAGGTAGTAAGTTGTATTGTT	Mature:hsa-miR-98:MIMAT0000096
CU-1028	77	TGAGAACTGAATTCCATAGGCTGT	Mature:hsa-miR-146b-5p:MIMAT0002809
CU-1031	78	TCGAGGAGCTCACAGTCTAGTA	Mature:hsa-miR-151-5p:MIMAT0004697
CU-1100	79	AGCTCGGTCTGAGGCCCCTCAG	Mature:hsa-miR-423-3p:MIMAT0001340
CU-1038	80	ACTGCAGTGAAGGCACTTGTAG	Star:hsa-miR-17*:MIMAT0000071
CU-1040	81	ACCATCGACCGTTGATTGTA	Star:hsa-miR-181a*:MIMAT0000270
CU-1053	82	TTCACCACCTTCTCCACCCAG	Mature:hsa-miR-197:MIMAT0000227
CU-1075	83	TTCACAGTGGCTAAGTTCTG	Mature:hsa-miR-27b:MIMAT0000419

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1073	84	TTCAAGTAATTCAGGATAGGTT	Mature:hsa-miR-26b:MIMAT0000083
CU-1110	85	TGGGTTTACGTTGGGAGAACT	Mature:hsa-miR-629:MIMAT0004810
CU-1088	86	TGGGTTGAGAGGGCGA	Mature:hsa-miR-320a:MIMAT0000510
CU-1005	87	TGAGGTAGGAGGTTGTATAGTT	Mature:hsa-let-7e:MIMAT0000066
CU-1081	88	TGACCGATTTCTCCTGGTGTT	Star:hsa-miR-29c*:MIMAT0004673
CU-1117	89	TATTGCACTCGTCCCGGCC	Mature:hsa-miR-92b:MIMAT0003218
CU-1094	90	GGGGTGCTATCTGTGATTGA	Mature:hsa-miR-342-5p:MIMAT0004694
CU-1021	91	GCATGGGTGGTTCAGTGGTAGAA	Mature:hsa-miR-1308:MIMAT0005947
CU-1089	92	CTGGCCCTCTCTGCCCTT	Mature:hsa-miR-328:MIMAT0000752
CU-1047	93	CTGACCTATGAATTGACAGC	Mature:hsa-miR-192:MIMAT0000222
CU-1099	94	CTCCTGACTCCAGGTCCTGTG	Star:hsa-miR-378*:MIMAT0000731
CU-1105	95	CGTCAACACTTGCTGGTT	Mature:hsa-miR-505:MIMAT0002876
CU-1034	96	CGAATCATTATTTGCTGCTCT	Star:hsa-miR-15b*:MIMAT0004586
CU-5002	97	CATCGGGAATGTCGTGTCCGCC	Star:hsa-miR-425*:MI0001448
CU-1025	98	CAGTGGTTTTACCCTATGGTA	Mature:hsa-miR-140-5p:MIMAT0000431
CU-1022	99	CAGTGCAATGATGAAAGGGCAT	Mature:hsa-miR-130b:MIMAT0000691
CU-1104	100	CAGCAGCACACTGTGGTTTGT	Mature:hsa-miR-497:MIMAT0002820
CU-1106	101	CACGCTCATGCACACACCCAC	Mature:hsa-miR-574-3p:MIMAT0003239
CU-1077	102	AAGGAGCTCACAGTCTATTGAG	Mature:hsa-miR-28-5p:MIMAT0000085
CU-1123	103	TTGGTCCCCTTCAACCAGCTGT	Mature:hsa-miR-133a:MIMAT0000427
CU-1074	104	TTCACAGTGGCTAAGTTCCGA	Mature:hsa-miR-27a:MIMAT0000084
CU-1097	105	TTATCAGAATCTCCAGGGGTAA	Mature:hsa-miR-361-5p:MIMAT0000703
CU-1043	106	TGGAGAGAAAGGCAGTTCCTGAT	Mature:hsa-miR-185:MIMAT0000455
CU-1112	107	TGAGACCTCTGGGTTCTGAGCT	Mature:hsa-miR-769-5p:MIMAT0003886
CU-1122	108	TCTTTGGTTATCTAGCTGTATGA	Mature:hsa-miR-9:MIMAT0000441
CU-1109	109	TCTAGTAAGAGTGGCAGTCGA	Mature:hsa-miR-628-3p:MIMAT0003297
CU-1090	110	TATTGCACATTACTAAGTTGA	Mature:hsa-miR-32:MIMAT0000090
CU-1013	111	TAAGGCACGCGGTGAATGCCA	Mature:hsa-miR-124:MIMAT0000422
CU-1058	112	TAACACTGTCTGGTAACGATGTT	Mature:hsa-miR-200a:MIMAT0000682
CU-1059	113	GTGAAATGTTTAGGACCACTAG	Mature:hsa-miR-203:MIMAT0000264
CU-1102	114	GCAGTCCATGGGCATATACACA	Mature:hsa-miR-455-3p:MIMAT0004784
CU-1107	115	GAGCTTATTCATAAAAGTGCAG	Mature:hsa-miR-590-5p:MIMAT0003258
CU-1114	116	CTGCCCTGGCCCGAGGGACCGA	Mature:hsa-miR-874:MIMAT0004911
CU-1002	117	CTATACAACCTACTGCCTTC	Star:hsa-let-7b*:MIMAT0004482
CU-1049	118	CGGGGTTTTGAGGGCGAGATGA	Star:hsa-miR-193b*:MIMAT0004767
CU-1051	119	CCAGTGGGGCTGCTGTTATCTG	Star:hsa-miR-194*:MIMAT0004671
CU-1036	120	CCAGTATTAACTGTGCTGCTGA	Star:hsa-miR-16-1*:MIMAT0004489

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1121	121	CACCCGTAGAACCGACCTTGCG	Mature:hsa-miR-99b:MIMAT0000689
CU-1120	122	CAAGCTCGTGTCTGTGGGTCCG	Star:hsa-miR-99b*:MIMAT0004678
CU-1063	123	CAACACCAGTCGATGGGCTGTA	Star:hsa-miR-21*:MIMAT0004494
CU-1070	124	AGGCGGAGACTTGGGCAATT	Star:hsa-miR-25*:MIMAT0004498
CU-1060	125	ACTGCATTATGAGCACTTAAAGT	Star:hsa-miR-20a*:MIMAT0004493
CU-1078	126	ACTGATTTCTTTTGGTGTTCA	Star:hsa-miR-29a*:MIMAT0004503
CU-1020	127	ACTCGGCGTGGCGTCGGTCGTGG	Mature:hsa-miR-1307:MIMAT0005951
CU-1041	128	ACCACTGACCGTTGACTGTAC	Star:hsa-miR-181a-2*:MIMAT0004558
CU-1048	129	AACTGGCCTACAAAGTCCCAGT	Mature:hsa-miR-193a-3p:MIMAT0000459
CU-1127	130	TGTCTGAGCGTCGCT	preCursor:hsa-mir-1826:MI0008194
CU-1132	131	GCCGGGTACTTTCGTATTTT	NEW
CU-1137	132	GCTAAGGAAGTCCTGTGCTCAGTTTT	NEW
CU-1130	133	CCCGGGTTTCGGCACCA	NEW
CU-1136	134	TCGGGCGGGAGTGGTGGCTTT	NEW
CU-1383	135	TAGAGGCACCGCCTGCCCA	NEW
CU-1131	136	CGGGGCGCGGCCTCGCTG	NEW
CU-1135	137	CCCACGGGGGTCTCCGGGCGAG	NEW
CU-1392	138	CCCACGGGAAACAGCA	NEW
CU-1133	139	CAGCCCGGCCTGGCTCCTCCAT	NEW
CU-1134	140	CACGGAAGGTGGCCCGG	NEW
CU-1170	141	CTGTAGGCACCTGAAA	NEW
CU-1153	142	CCCCCCACTGCTAAATTTGACTGGCTT	NEW
CU-1191	143	GCCCGCATCCTCCACCA	NEW
CU-1140	144	CCCGGCCAACGCACCA	NEW
CU-1173	145	ATCCCACTCCTGACACCA	NEW
CU-1149	146	CCGGGCGGAAACACCA	NEW
CU-1159	147	TGTCAGTTTGTTAATTA	NEW
CU-1178	148	AGGGTGTGCGTGTTTTT	NEW
CU-1142	149	TCGATTCCCGGCCCATGCACCA	NEW
CU-1164	150	GAGAGCGCTCGGTTTTT	NEW
CU-1148	151	TGGTGTGGTCTGTTGTTTT	NEW
CU-1221	152	TGTGCTCCGGAGTTACCTCGTTT	NEW
CU-1186	153	TCCCCGACACCTCCACCA	NEW
CU-1224	154	CTGTAGGCATCATCAAT	NEW
CU-1180	155	AACCGAGCGTCCAAGCTCTTTCCATTTT	NEW
CU-1155	156	TCCCCGCACCTCCACCA	NEW

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1212	157	TCCCCGGCACTTCCACCA	NEW
CU-1213	158	TCACCCCATAAACACCA	NEW
CU-1193	159	CTGTAGGCACCATCATAA	NEW
CU-1202	160	CCCACCAGAGTCGCCA	NEW
CU-1220	161	TTCCCCGACGGGGAGCCA	NEW
CU-1175	162	GGCGTGATTCATACCTTTT	NEW
CU-1194	163	GCGGGCGGACCTTTT	NEW
CU-1205	164	CGGCTCGAAGGACCA	NEW
CU-1187	165	CCCCGGCCCCGCGTA	NEW
CU-1206	166	CCCACCTCTGACACCA	NEW
CU-1210	167	CCACGAGGTCGGCCGG	NEW
CU-1156	168	CAGGATCGGCCCACT	NEW
CU-1197	169	ATGTGGTGGCTTACTTTT	NEW
CU-1183	170	ATCCCGGACGAGCCCA	NEW
CU-1570	171	ATCCCCAGCATCTCCACCA	NEW
CU-1146	172	AGAAAGGCCGAATTTTA	NEW
CU-1165	173	TGTCAGTTTTTACCCAA	NEW
CU-1160	174	TGTCAGTTTGAACCCAA	NEW
CU-1189	175	TGTAGTGTTTCTTACTTTA	NEW
CU-1219	176	TGGCGAAGGTCGGCCGCG	NEW
CU-1203	177	TGCAGGGCCGGCGGGGAGG	NEW
CU-1211	178	TCGGGCGGCGGGCGT	NEW
CU-1190	179	TCGGCTTTCCCTGCTAACTGGGCTTTTT	NEW
CU-1144	180	TCAGAGCGCGGGCCGACCCC	NEW
CU-1376	181	TCAACACCCACTCCCTC	NEW
CU-1138	182	TATCAATGATGCTTCTGAGA	NEW
CU-1384	183	TAACCCCAGGGTTGGTCA	NEW
CU-1154	184	GGGGTCCCCGGTAGA	NEW
CU-1171	185	GGGCGTGGGTGTGATGATTC	NEW
CU-1199	186	GGGAGGTGAGTAGGTCTG	NEW
CU-1226	187	GGAGACGTGGCCGAGAG	NEW
CU-1572	188	GCGGAATACCACGGGGA	NEW
CU-1151	189	GCAGGCGGGGGATTAGCTA	NEW
CU-1227	190	GCAGCGGAACGTCGGCGCGC	NEW
CU-1200	191	GACGTCACCCTCCTCA	NEW
CU-1152	192	CTTGGACTAACCTGGTGTA	NEW
CU-1158	193	CTGTAGGCCACCATCCA	NEW

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1216	194	CTGTAGGCACCACCA	NEW
CU-1188	195	CTGGTAGGCACCTGAAA	NEW
CU-1157	196	CTGATGTTGATGCATATGATGACA	NEW
CU-1207	197	CGGTGGAACCTGCATTGGTTT	NEW
CU-1181	198	CGGGGCCGGGGCTAGGGT	NEW
CU-1185	199	CGGGCCGCCCCCGCCCACCG	NEW
CU-1163	200	CGGGCCCCGGGGCTCG	NEW
CU-1366	201	CGGCCTATCCGGAATGCCCC	NEW
CU-1225	202	CGGACCTCCCTGGCCC	NEW
CU-1145	203	CGCGGCCAGTGTCCCCTTGTA	NEW
CU-1201	204	CGACACACGGCCCGTGGCGC	NEW
CU-1141	205	CCTCATAAATACCGG	NEW
CU-1172	206	CCTCACTGGGGGCTCCA	NEW
CU-1209	207	CCTCACCTGGAGCACCA	NEW
CU-1147	208	CCGTACTGGCCACCA	NEW
CU-1223	209	CCGCCGCCCCCCCCT	NEW
CU-1217	210	CCGCCCCGACCTTAGCTA	NEW
CU-1176	211	CCCGTCCGCTGCGCCA	NEW
CU-1139	212	CCCGTCCACTCCGCCA	NEW
CU-1166	213	CCCCGGCCCATGCACCA	NEW
CU-1177	214	CCCCGGCATCTCCATCA	NEW
CU-1214	215	CCCCAGTACCTCCACCA	NEW
CU-1184	216	CCCAGCGGTGCCTCCA	NEW
CU-1574	217	CCACGCTCTGCTACCA	NEW
CU-1360	218	CCACCCTGGAGCCTCCGT	NEW
CU-1150	219	ATGGTAGGCACCTGAAA	NEW
CU-1162	220	ATGGGCGGTCCTCGTT	NEW
CU-1179	221	ATGGCCTGGACCCCACTCCT	NEW
CU-1161	222	ATGGCCGCATATATTTT	NEW
CU-1218	223	ATCCTGTTCGTGACGCCA	NEW
CU-1204	224	ATCCTGCTCACAGCCCCA	NEW
CU-1168	225	AGCGAGGGTTCCGCCGGCC	NEW
CU-1195	226	ACTGGGGAGGGGGAGGAGCCTCGAGG	NEW
CU-1215	227	ACCCCGAGGGGACGGGCG	NEW
CU-1208	228	ACAGCGCTGTGTTCCCGT	NEW
CU-1192	229	ACAAAAAAAAAAGCCCAACCCT	NEW

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1373	230	AACTAAAACCCCTACGCA	NEW
CU-1196	231	AAAGGAGCCGAATCTTT	NEW
CU-1251	232	CCCACCCAGGGACGCCA	refseqGeneIntron-annotate
CU-1254	233	TCCCCGGCACCTCCACCA	refseqGeneIntron-annotate
CU-1298	234	ATCCCGGACGAGCCCCCA	refseqGeneIntron-annotate
CU-1229	235	CCCACGTTGGGCGCCA	refseqGeneIntron-annotate
CU-1276	236	TCGATTCCCGGCCAATGCACCA	refseqGeneIntron-annotate
CU-1303	237	ATCCCACTTCTGACACCA	refseqGeneIntron-annotate
CU-1270	238	TCGTAGGCACCTGAAA	refseqGeneIntron-annotate
CU-1242	239	TCCCCGTACGGGCCACCA	refseqGeneIntron-annotate
CU-1273	240	TTGACCGCTCTGACCA	refseqGeneIntron-annotate
CU-1328	241	CCCAGCGGGGCCTCCA	refseqGeneIntron-annotate
CU-1257	242	CAGGAACGGTGCACCA	mRNAall-annotate; refseqGeneIntron-annotate
CU-1241	243	AGTCCCATCTGGGTCGCCA	refseqGeneIntron-annotate
CU-1575	244	CCCCCCACTGCTAAATTTGACTGGA	refseqGeneIntron-annotate; rnaGene-annotate
CU-1274	245	GTTTGTTAATTAACCCAA	refseqGeneIntron-annotate
CU-1243	246	GTCCCTTCGTGGTCGCCA	refseqGeneIntron-annotate
CU-1284	247	CTGTAGCACCTGAAA	mRNAall-annotate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1300	248	TCCTCACACGGGGCACCA	refseqGeneIntron-annotate
CU-1278	249	TAACGGCCGCGGTACCC	refseqGeneIntron-annotate
CU-1264	250	GAGGGGGACCAAAAAAAA	refseqGeneIntron-annotate
CU-1275	251	CCCGCATTCTCCACCA	refseqGeneIntron-annotate
CU-1246	252	AGGGGGGTAAAAAAAAA	refseqGeneIntron-annotate
CU-1315	253	TCCACCGCTGCCACCA	refseqGeneIntron-annotate
CU-1277	254	GAGCCATGATGATACCACTGAGC	refseqGeneIntron-annotate
CU-1288	255	CGTCCATGATGTTCCGCAA	mRNAall-annotate; snoRNA-annotate; piRNA-annotate; wgRNA-annotate; refseqGeneIntron-annotate
CU-1234	256	CATCCTCTGCTACCA	mRNAall-annotate; refseqGeneIntron-annotate; exEID-annotate
CU-1345	257	AGAACACTACGAGCCACA	mRNA-annotate; refseqGeneIntron-annotate
CU-1352	258	ACCCCACTTCTGGTACCA	refseqGeneIntron-annotate
CU-1323	259	TGTATTGTGAGACATTC	mRNAall-annotate; refseqGeneIntron-annotate; wgRNA-annotate; rnaGene-annotate
CU-1324	260	TCTCGGTGGAACCTCCA	refseqGeneIntron-annotate
CU-1302	261	TCCCCGGCACCTCCAA	refseqGeneIntron-annotate
CU-1269	262	TACCGAGCCTGGTGATAGC	refseqGeneIntron-annotate
CU-1281	263	GCAGCGCCAGCCTCCCGCCCTAC	refseqGeneIntron-annotate
CU-1292	264	CCGCCTGGGGAGTAC	refseqGeneIntron-annotate

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1339	265	ATCCCCAGCACCTCCACCA	refseqGeneIntron-annotate
CU-1293	266	AGCAGTGATGTCCTGAAAATTCTGAAG	refseqGeneIntron-annotate
CU-1307	267	ACCCCACTATGCTTAGCCCT	mRNA-annotate; refseqGeneIntron-annotate
CU-1294	268	AAAGGACCTGGCGGTGCTTC	mRNA-annotate; refseqGeneIntron-annotate
CU-1325	269	TTTGCCACACTGCAACACCTT	refseqGeneIntron-annotate
CU-1333	270	TTCCTTGGATGTCTGAGTGAC	refseqGeneIntron-annotate
CU-1310	271	TTAAACCACCAAGATCGCTGATGCAC	refseqGeneIntron-annotate
CU-1299	272	TGTTCGCCGACCGTTGA	refseqGeneIntron-annotate
CU-1265	273	TGGGGTCTGGGAGGGA	refseqGeneIntron-annotate
CU-1322	274	TGGGAGAGCAGGGTATTGT	refseqGeneIntron-annotate
CU-1279	275	TGCAGATGATGTAAAAGA	snoRNA-annotate; refseqGeneIntron-annotate; wgRNA-annotate; rnaGene-annotate
CU-1267	276	TCGCTATGATGATGGATTCCAAAA	mRNAall-annotate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1308	277	TCCGAAAGGCCTCCCGCACCG	refseqGeneIntron-annotate
CU-1331	278	TCCCGCACCTCCACCA	refseqGeneIntron-annotate
CU-1297	279	TAGATGAATAGGTAAAGAG	refseqGeneIntron-annotate
CU-1235	280	GTGTATGATGACCTCATGTAGCCTGAAC	refseqGeneIntron-annotate
CU-1253	281	GTGAAGCGTTCCATATTTTT	mRNAall-annotate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1348	282	GGGGGGGGGTTTGGAA	refseqGeneIntron-annotate
CU-1337	283	GGGGGGAGGGAAGGCAA	refseqGeneIntron-annotate
CU-1316	284	GGGGGCTGGGCTGGGTA	refseqGeneIntron-annotate
CU-1343	285	GGGGCCGCCGCCTGTGT	refseqGeneIntron-annotate
CU-1326	286	GGGAGTCCGCGGCGAGC	refseqGeneIntron-annotate
CU-1329	287	GGGACCTGGGGACCA	refseqGeneIntron-annotate
CU-1286	288	GGCTTGGTCTAGGGGTA	refseqGeneIntron-annotate
CU-1332	289	GGCTGGGACCCTGGACAC	refseqGeneIntron-annotate
CU-1262	290	GGCGACCTGCGACTCCTT	refseqGeneIntron-annotate
CU-1236	291	GGAGGGGGGAAACAAA	refseqGeneIntron-annotate
CU-1317	292	GGAGGGGGGAAAAAAAAAA	computGene-annotate; refseqGeneIntron-annotate
CU-1327	293	GGAAGACCTGCACCACTGTC	mRNAall-annotate; computGene-annotate; refseqGeneIntron-annotate; exEID-annotate
CU-1239	294	GCGGGTGTCAGGCCT	refseqGeneIntron-annotate
CU-1266	295	GCCGGGCGTGGTGGTCTG	refseqGeneIntron-annotate
CU-1261	296	GCCGCCGAGACCCCAGGACCC	refseqGeneIntron-annotate
CU-1260	297	GCAGCCGTGCTTTTA	refseqGeneIntron-annotate
CU-1259	298	GCAAATGATGCCCTCTGATC	refseqGeneIntron-annotate

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1349	299	GAGGGGGGTCAAAAAAA	refseqGeneIntron-annotate
CU-1272	300	CTTGATGATGAGCAGGATCTGAGT	refseqGeneIntron-annotate
CU-1341	301	CTGTAGGCACTGAAA	refseqGeneIntron-annotate
CU-1231	302	CTGTAGGCACCATTAA	refseqGeneIntron-annotate
CU-1313	303	CTGCTTAAGTCCTGACCAG	refseqGeneIntron-annotate
CU-1296	304	CTGAGCACCTTTCCCTTCC	refseqGeneIntron-annotate
CU-1291	305	CTAGCCCCAAACCCA	piRNA-annotate; refseqGeneIntron-annotate
CU-1245	306	CGGTCACACGATTAACCCA	mRNA-annotate; refseqGeneIntron-annotate
CU-1338	307	CGGGGGGAGGAAAAAA	refseqGeneIntron-annotate
CU-1268	308	CGGGGGGAAAAAAAAA	refseqGeneIntron-annotate
CU-1290	309	CGGGGCCGCACGCGC	refseqGeneIntron-annotate
CU-1319	310	CGGGAGTGGGGTGGCGCCCAG	refseqGeneIntron-annotate
CU-1318	311	CGGGAGCCCCGGGTT	refseqGeneIntron-annotate
CU-1569	312	CGGACCTGATAAATTCCCAC	refseqGeneIntron-annotate
CU-1320	313	CGCGGCTCTTGCGGT	refseqGeneIntron-annotate
CU-1249	314	CGCCTGAGTCAGAAC	refseqGeneIntron-annotate
CU-1240	315	CGCCGCCGCCCCCCCC	mRNAall-annotate; refseqGeneIntron-annotate; exEID-annotate
CU-1351	316	CCTTCCTTGGATGTCTGAGTGAG	mRNAall-annotate; refseqGeneIntron-annotate; wgRNA-annotate; rnaGene-annotate
CU-1354	317	CCTCGCTGGGGCCTCCA	refseqGeneIntron-annotate
CU-1233	318	CCTCACAGGGACGCCA	refseqGeneIntron-annotate
CU-1289	319	CCTAGGAGTGCGACAATT	mRNAall-annotate; refseqGeneIntron-annotate; wgRNA-annotate; rnaGene-annotate
CU-1283	320	CCGCTCTGAGACCTA	refseqGeneIntron-annotate
CU-1228	321	CCGCCCGTCACCCTCCTCAAGTA	mRNA-annotate; refseqGeneIntron-annotate
CU-1344	322	CCCGGGCGGCACACCA	refseqGeneIntron-annotate
CU-1271	323	CCCGCGGGCTTGCTGGGCGTCCC	refseqGeneIntron-annotate
CU-1321	324	CCCCTGCGATTTCCCCA	refseqGeneIntron-annotate; rnaGene-annotate
CU-1285	325	CCCCGGCATCTCCACTA	refseqGeneIntron-annotate
CU-1571	326	CCCCAGTGAGTGCCCTCTTCC	refseqGeneIntron-annotate
CU-1353	327	CCCAGAGACGCCGTCCTCGA	refseqGeneIntron-annotate
CU-1355	328	CCCACCGAGGATGCCA	refseqGeneIntron-annotate
CU-1238	329	CCATCACTACCCACCA	refseqGeneIntron-annotate
CU-1347	330	CCACTCCAGCCTAGCCCC	refseqGeneIntron-annotate
CU-1295	331	CAGTACAGGCACACCTC	refseqGeneIntron-annotate
CU-1256	332	CACGTCGGGGTCCCCA	refseqGeneIntron-annotate
CU-1250	333	CACGATTAACCCAAGTC	mRNA-annotate; refseqGeneIntron-annotate

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1305	334	CACCACACCCGGGCCA	refseqGeneIntron-annotate
CU-1287	335	CAACACAGGCATGCT	refseqGeneIntron-annotate
CU-1314	336	ATAGGGTTTACGACCTCGATGTTGGATCA	refseqGeneIntron-annotate
CU-1311	337	ATACCATGATGAACAATAGCTGAGA	refseqGeneIntron-annotate
CU-1282	338	AGGGTTCAGCTGTCTC	refseqGeneIntron-annotate
CU-1350	339	AGGCTGTGATGGACCTGGCTGAGCCTG	refseqGeneIntron-annotate
CU-1252	340	AGAGAGTAGGGGGAGGT	refseqGeneIntron-annotate
CU-1334	341	ACTGTCCCTGTCTACTA	refseqGeneIntron-annotate
CU-1340	342	ACCGCATCTGGCCTATTTTT	refseqGeneIntron-annotate
CU-1342	343	ACCAGACCTCCTGTGCGAAG	refseqGeneIntron-annotate
CU-1304	344	ACAGCCCGGATCCCAGCCCACTTA	refseqGeneIntron-annotate
CU-1230	345	ACACTGAGCCACAACCCA	refseqGeneIntron-annotate
CU-1312	346	AAGGGCTTGGCTTAATTA	refseqGeneIntron-annotate
CU-1255	347	AACCCGGAAGGCGGAGGTTGCGG	computGene-annotate; refseqGeneIntron-annotate
CU-1336	348	AACCCCACACCAACC	refseqGeneIntron-annotate
CU-1346	349	AACAAGCTTCTTTGACGTCCCATCCAC	refseqGeneIntron-annotate
CU-1369	350	TCCCCGGCATCTCCACCA	computGene-annotate
CU-1370	351	CTGATTGCTCCTGTCTGATT	mRNAall-annotate; exEID-annotate; rnaGene-annotate
CU-1371	352	TCTAGAGGAGCCTGTTCTGTA	mRNA-annotate
CU-1381	353	TCGATTCCCGGTCAGGGAACCA	repeats-annotate
CU-1380	354	ATAGGTTTGGTCCTAGCCTTTCT	piRNA-annotate
CU-1363	355	CGTTCGCGCTTTCCCCTG	rnaGene-annotate
CU-1396	356	TAAGTGTTTGTGGGTTA	rnaGene-annotate
CU-1361	357	GGCGGCGGGAGACCCA	computGene-annotate
CU-1359	358	CCCCGGCAGGTTTGA	rnaGene-annotate
CU-1573	359	TGCCGTGATCGTATAGTGGTTA	piRNA-annotate
CU-1169	360	TCAGACTACTCTCCTCCGCCCATT	mRNAall-annotate
CU-1167	361	GGACACAGAGGCTTCG	mRNAall-annotate
CU-1395	362	CTGACAGCCGGGGTTTTGGA	computGene-annotate
CU-1365	363	CGGCGGGGCCTGGAGTCTG	mRNAall-annotate; computGene-annotate; exEID-annotate
CU-1375	364	CCTGGCTCGCTGCGCCA	computGene-annotate
CU-1182	365	CCGCCCCACCCCGCGCGC	mRNAall-annotate; exEID-annotate
CU-1174	366	CCCGAACGCTGCCAACCC	exEID-annotate
CU-1385	367	AGACCCGCGGGCGCTCTCCAGTC	rnaGene-annotate
CU-1524	368	CCCCCACAACCGCGCTTGACTAGC	mRNAall-annotate; yRNA-eliminate; rnaGene-annotate
CU-1453	369	CCCTGCTCGCTGCGCCA	refseqGeneExon-eliminate

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1477	370	CTCCCACTGCTTCACTTGACTAGC	yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1466	371	CCCATCCTCGTCGCCA	refseqGeneExon-eliminate
CU-1222	372	TCACGTCGGGGTCACCA	Morozov-eliminate
CU-1388	373	TCCCTGGTGGTCTAGTGGTTAGGATTCG	tRNAcomputational-annotate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1428	374	GGTAGCGTGGCCGAG	tRNAcomputational-annotate; tRNA-eliminate; HStRNA-eliminate; rnaGene-annotate
CU-1488	375	TCCTGCCGCGGTCGCCA	refseqGeneExon-eliminate
CU-1557	376	GGAGAGAACGCGGTCTGAGTGGT	snoRNA-eliminate; wgRNA-annotate; rnaGene-annotate
CU-1379	377	TCGGGTGCGAGAGGTCCCGGGT	tRNAcomputational-annotate; HStRNA-eliminate; rnaGene-annotate
CU-1542	378	GGCTGGTCCGATGGTAGTGGGTT	mRNAall-annotate; yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1550	379	CGGAAGCGTGCTGGGCCC	tRNAcomputational-annotate; tRNA-eliminate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1232	380	CCCGGGCGGCGCACCA	Morozov-eliminate; refseqGeneIntron-annotate
CU-1513	381	GCGGGTGATGCGAACTGGAGTCTGAGC	computGene-annotate; snoRNA-annotate; snoRNA-eliminate; wgRNA-annotate; rnaGene-annotate
CU-1368	382	GACGAGGTGGCCGAGTGG	tRNAcomputational-annotate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1474	383	GGGGGTGTAGCTCAG	tRNAcomputational-annotate; tRNA-eliminate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1470	384	CTCCTGGCTGGCTCGCCA	mRNAall-annotate; computGene-annotate; refseqGeneExon-eliminate; exEID-annotate
CU-1471	385	CGGGAGGCCCGGGTT	rnaGene-annotate; tRNAcomputational-annotate; piRNA-annotate; tRNA-eliminate; refseqGeneIntron-annotate; mRNA-annotate; HStRNA-eliminate
CU-1538	386	GGCTGGTCCGAGTGCAGTGGTGTTTA	yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1486	387	CTGCTGTGATGACATTC	computGene-annotate; snoRNA-annotate; snoRNA-eliminate; wgRNA-annotate; rnaGene-annotate
CU-1386	388	TGTCACGCGGGAGACC	tRNAcomputational-annotate; mRNAall-annotate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1382	389	TCCTCGTTAGTATAGTGGTGAGTATCCC	tRNAcomputational-annotate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1433	390	GGCCGGTTAGCTCAG	mRNAall-annotate; exEID-annotate; rnaGene-annotate; tRNAcomputational-annotate; piRNA-annotate; refseqGeneIntron-annotate; refseqGeneExon-eliminate; HStRNA-eliminate
CU-1403	391	GCATTGGTGGTTCAGTGGTAGA	rnaGene-annotate; tRNAcomputational-annotate; piRNA-annotate; tRNA-eliminate; refseqGeneIntron-annotate; HStRNA-eliminate

TABLE 1A-continued

List of known and newly identified mature miRNAs.

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1362	392	CTGTCACGCGGGAGA	tRNAcomputational-annotate; mRNAall-annotate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1490	393	CTACGGGGATGATTTT	mRNAall-annotate; snoRNA-annotate; snoRNA-eliminate; wgRNA-annotate; rnaGene-annotate
CU-1469	394	CCAGGGGCTGAGGGCA	snoRNA-eliminate; refseqGeneIntron-annotate; wgRNA-annotate
CU-1457	395	TTCTCACTACTGCACTTGACTA	mRNAall-annotate; yRNA-eliminate; refseqGeneIntron-annotate; exEID-annotate; rnaGene-annotate
CU-1440	396	TGGTTATCACGTTCGCC	tRNAcomputational-annotate; tRNA-eliminate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1528	397	TAGGGGTATGATTCTCGCT	tRNAcomputational-annotate; tRNA-eliminate; HStRNA-eliminate; rnaGene-annotate
CU-1545	398	CCACGAGGAAGAGAGGTAGC	snoRNA-eliminate; wgRNA-annotate; snoRNA-annotate
CU-1244	399	GTCAGGATGGCCGAGCGGTCT	tRNAcomputational-annotate; rnaGene-annotate; HStRNA-eliminate; refseqGeneIntron-annotate
CU-1390	400	GGGGATGTAGCTCAG	tRNAcomputational-annotate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1377	401	GCAGCGATGGCCGAG	tRNAcomputational-annotate; HStRNA-eliminate; rnaGene-annotate

TABLE 1B

List of known and newly identified mature miRNAs including information on frequencies.

		Corrected Counts				Frequencies			
Mature miRNA sequence	SEQ ID NO.	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
TGTAGTGTTTCCTACTTTATGGA	1	1329	592	635	391	38.5	19.83	24.93	16.02
TAGCTTATCAGACTGATGTTGA	2	196	353	144	13	5.68	11.83	5.65	0.53
TAAAGTGCTTATAGTGCAGGTAG	3	54	19	49.82	257.89	1.56	0.64	1.96	10.57
TAGCAGCACATCATGGTTTACA	4	38	61	176.84	105	1.1	2.04	6.94	4.3
TAGCAGCACGTAAATATTGGCG	5	131	97	53	35	3.79	3.25	2.08	1.43
TGAGGTAGTAGGTTGTATAGTT	6	62.84	78.99	92.19	63.25	1.82	2.65	3.62	2.59
TATTGCACTTGTCCCGGCCTGT	7	17	21	46	207	0.49	0.7	1.81	8.48
TCCCACCGCTGCCACCA	8	68	97	25	28	1.97	3.25	0.98	1.15
TGAGGTAGTAGATTGTATAGTT	9	41.28	44	64	51.38	1.2	1.47	2.51	2.11
TAGCACCATCTGAAATCGGTTA	10	78	60	42	22	2.26	2.01	1.65	0.9
TAGCAGCACATAATGGTTTGT	11	90	39	32.16	8	2.61	1.31	1.26	0.33
CCCATAAAGTAGAAAGCACTA	12	88	53	7	10	2.55	1.78	0.27	0.41
TGAGGTAGTAGTTTGTACAGTT	13	41.28	47	30.77	21.16	1.2	1.57	1.21	0.87
TGAGGTAGTAGTTTGTGCTGTT	14	23	24	32	42	0.67	0.8	1.26	1.72

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

Mature miRNA sequence	SEQ ID NO.	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
TAGCACCATTTGAAATCGGTTA	15	44	41	16	1	1.27	1.37	0.63	0.04
TGTAAACATCCTACACTCTCAGC	16	27	25	26	20	0.78	0.84	1.02	0.82
CAAAGTGCTTACAGTGCAGGTAG	17	9	6	10.18	65.04	0.26	0.2	0.4	2.67
CATTGCACTTGTCTCGGTCTGA	18	11	9	34	39	0.32	0.3	1.33	1.6
CAACGGAATCCCAAAAGCAGCTG	19	17	21	36	18	0.49	0.7	1.41	0.74
TGTGCAAATCCATGCAAAACTGA	20	0	1	25	65	0	0.03	0.98	2.66
TACCACAGGGTAGAACCACGGA	21	31	22	17	21	0.9	0.74	0.67	0.86
TGTAAACATCCTACACTCAGCT	22	31	11	27	16	0.9	0.37	1.06	0.66
TGAGGTAGTAGGTTGTGTGGTT	23	19.48	19	29	5.08	0.56	0.64	1.14	0.21
TAGCACCATTTGAAATCAGTGTT	24	22	14	12	4	0.64	0.47	0.47	0.16
TAAAGTGCTGACAGTGCAGAT	25	7	6	13	26	0.2	0.2	0.51	1.07
TCCCTGTCCTCCAGGAGCTC	26	6	3	3	32	0.17	0.1	0.12	1.31
TTCAAGTAATCCAGGATAGGCT	27	2	8	13	16	0.06	0.27	0.51	0.66
CAAAGTGCTGTTCGTGCAGGTAG	28	9	2	13	14	0.26	0.07	0.51	0.57
TGTCAGTTTGTCAAATACCCCA	29	25	10	1	0	0.72	0.34	0.04	0
TGAGAACTGAATTCCATGGGTT	30	4	7	21	4	0.12	0.23	0.82	0.16
TCTCCCAACCCTTGTACCAGT	31	12	18	2	0	0.35	0.6	0.08	0
TCCCTGAGACCCTAACTTGTGA	32	0	1	28	2	0	0.03	1.1	0.08
TCTCACACAGAAATCGCACCCGTC	33	10	8	8	3	0.29	0.27	0.31	0.12
GTCCCTGTTCGGGCGCCA	34	12	10	6	1	0.35	0.34	0.24	0.04
TGTGCAAATCTATGCAAAACTGA	35	0	0	9	19	0	0	0.35	0.78
TGTAAACATCCCCGACTGGAAG	36	7	3	14	3	0.2	0.1	0.55	0.12
AGCTACATTGTCTGCTGGGTT	37	17	6	4	0	0.49	0.2	0.16	0
AGAGGTAGTAGGTTGCATAGTT	38	2	4	10	10	0.06	0.13	0.39	0.41
CCGCACTGTGGGTACTTGCT	39	8	6	2	8	0.23	0.2	0.08	0.33
AGCAGCATTGTACAGGGCTATGA	40	1	1	10	11	0.03	0.03	0.39	0.45
AACTGGCCCTCAAAGTCCCGCT	41	0	0	2	21	0	0	0.08	0.86
GCCCCTGGGCCTATCCTAGAA	42	1	0	10	10	0.03	0	0.39	0.41
AGCTGGTGTTGTGAATCAGGCCGT	43	0	0	15	5	0	0	0.59	0.2
TGAGGGGCAGAGAGCGAGACTT	44	5	1	7	4	0.14	0.03	0.27	0.16
AGCTACATCTGGCTACTGGGTCT	45	6	6	5	0	0.17	0.2	0.2	0
GTGGGGGAGAGGCTGTA	46	2	6	3	5	0.06	0.2	0.12	0.2
CTATACGACCTGCTGCCTTTC	47	6	3	4	1	0.17	0.1	0.16	0.04
TTAATGCTAATCGTGATAGGGGT	48	3	4	5	1	0.09	0.13	0.2	0.04

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

Mature miRNA sequence	SEQ ID NO.	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
AGGGGGAAAGTTCTATAGTC	49	0	2	0	11	0	0.07	0	0.45
ACAGTAGTCTGCACATTGGTT	50	0	0	13	0	0	0	0.51	0
AACATTCAACGCTGTCGGTGAG TT	51	0	0	7	6	0	0	0.27	0.25
TGGAAGACTAGTGATTTTGTTGT	52	1	1	1	8	0.03	0.03	0.04	0.33
TAATGCCCCTAAAAATCCTTAT	53	0	0	6	4	0	0	0.24	0.16
TAGCAGCACAGAAATATTGGCA	54	4	0	5	0	0.12	0	0.2	0
TGAGGTAGTAGGTTGTAT	55	0.11	0.01	0.01	0.13	0	0	0	0.01
TCCTGTACTGAGCTGCCCCGAG	56	0	0	7	1	0	0	0.27	0.04
TCCCTGAGACCCTTTAACCTGTGA	57	0	0	8	0	0	0	0.31	0
ATCACATTGCCAGGGATTTCCA	58	0	0.5	7	0	0	0.02	0.27	0
TCACAGTGAACCGGTCTCTTT	59	1	0	0	6	0.03	0	0	0.25
CACTAGATTGTGAGCTCCTGGA	60	2	0	4	1	0.06	0	0.16	0.04
CAACAAATCACAGTCTGCCAT	61	3	0	1	3	0.09	0	0.04	0.12
CAAAGTGCTTATAGTGCAGGTAG	62	0	1	1	0.08	0	0.03	0.04	0
AGGTTGGGATCGGTTGCAATGCT	63	0	0	0	7	0	0	0	0.29
ACATTCATTGCTGTCGGTGGGTT	64	0	0	1	6	0	0	0.04	0.25
TCCCCCAGGTGTGATTCTGATT	65	4	1	0	1	0.12	0.03	0	0.04
CCCAGTGTTCAGACTACCTGTTC	66	0	0	6	0	0	0	0.24	0
ACCAATATTACTGTGCTGCTT	67	1	1	2	2	0.03	0.03	0.08	0.08
TGTAAACATCCTTGACTGGAAGCT	68	2	0	3	0	0.06	0	0.12	0
TAAGGTGCATCTAGTGCAGATA	69	0	0	1	4	0	0	0.04	0.16
ATCACATTGCCAGGGATTACCA	70	0	0.5	3	1	0	0.02	0.12	0.04
ACTGCCCTAAGTGCTCCTTCTG	71	0	0	0	5	0	0	0	0.2
TGTAAACATCCTCGACTGGA	72	1	0	3	0	0.03	0	0.12	0
TACAGTACTGTGATAACTGAAG	73	1	0	0	3	0.03	0	0	0.12
CTAGACTGAAGCTCCTTGAGG	74	2	1	1	0	0.06	0.03	0.04	0
TGGCAGTGTCTTAGCTGGTTGTT	75	0	1	2	0	0	0.03	0.08	0
TGAGGTAGTAAGTTGTATTGTT	76	0	1	1	1	0	0.03	0.04	0.04
TGAGAACTGAATTCCATAGGCT GT	77	1	0	2	0	0.03	0	0.08	0
TCGAGGAGCTCACAGTCTAGTA	78	1	0	1	1	0.03	0	0.04	0.04
AGCTCGGTCTGAGGCCCCTCAG	79	0	0	2	1	0	0	0.08	0.04
ACTGCAGTGAAGGCACTTGTAG	80	0	0	0	3	0	0	0	0.12
ACCATCGACCGTTGATTGTA	81	0	1	0	2	0	0.03	0	0.08
TTCACCACCTTCTCCACCCAG	82	0	0	0	2	0	0	0	0.08

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

Mature miRNA sequence	SEQ ID NO.	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
TTCACAGTGGCTAAGTTCTG	83	0	0	2	0	0	0	0.08	0
TTCAAGTAATTCAGGATAGGTT	84	0	0	1	1	0	0	0.04	0.04
TGGGTTTACGTTGGGAGAACT	85	0	0	0	2	0	0	0	0.08
TGGGTTGAGAGGGCGA	86	1	0	1	0	0.03	0	0.04	0
TGAGGTAGGAGGTTGTATAGTT	87	0	0	1.02	0	0	0	0.04	0
TGACCGATTTCTCCTGGTGTT	88	2	0	0	0	0.06	0	0	0
TATTGCACTCGTCCCGGCC	89	0	0	1	1	0	0	0.04	0.04
GGGGTGCTATCTGTGATTGA	90	2	0	0	0	0.06	0	0	0
GCATGGGTGGTTCAGTGGTAGAA	91	0	0	2	0	0	0	0.08	0
CTGGCCCTCTCTGCCCTT	92	0	0	1	1	0	0	0.04	0.04
CTGACCTATGAATTGACAGC	93	0	0	0	2	0	0	0	0.08
CTCCTGACTCCAGGTCCTGTG	94	0	0	0	2	0	0	0	0.08
CGTCAACACTTGCTGGTT	95	0	0	1	1	0	0	0.04	0.04
CGAATCATTATTTGCTGCTCT	96	0	0	1	1	0	0	0.04	0.04
CATCGGGAATGTCGTGTCCGCC	97	0	2	0	0	0	0.07	0	0
CAGTGGTTTTACCCTATGGTA	98	0	0	1	1	0	0	0.04	0.04
CAGTGCAATGATGAAAGGGCAT	99	0	0	2	0	0	0	0.08	0
CAGCAGCACACTGTGGTTTGT	100	0	0	2	0	0	0	0.08	0
CACGCTCATGCACACACCCAC	101	0	0	2	0	0	0	0.08	0
AAGGAGCTCACAGTCTATTGAG	102	0	0	2	0	0	0	0.08	0
TTGGTCCCCTTCAACCAGCTGT	103	0	0	1	0	0	0	0.04	0
TTCACAGTGGCTAAGTTCCGA	104	0	1	0	0	0	0.03	0	0
TTATCAGAATCTCCAGGGGTAA	105	1	0	0	0	0.03	0	0	0
TGGAGAGAAAGGCAGTTCCTGAT	106	0	0	1	0	0	0	0.04	0
TGAGACCTCTGGGTTCTGAGCT	107	0	0	0	1	0	0	0	0.04
TCTTTGGTTATCTAGCTGTATGA	108	0	0	0	1	0	0	0	0.04
TCTAGTAAGAGTGGCAGTCGA	109	0	0	0	1	0	0	0	0.04
TATTGCACATTACTAAGTTGA	110	1	0	0	0	0.03	0	0	0
TAAGGCACGCGGTGAATGCCA	111	1	0	0	0	0.03	0	0	0
TAACACTGTCTGGTAACGATGTT	112	0	0	0	1	0	0	0	0.04
GTGAAATGTTTAGGACCACTAG	113	0	0	1	0	0	0	0.04	0
GCAGTCCATGGGCATATACACA	114	0	0	1	0	0	0	0.04	0
GAGCTTATTCATAAAAGTGCAG	115	0	0	1	0	0	0	0.04	0
CTGCCCTGGCCCGAGGGACCGA	116	0	0	0	1	0	0	0	0.04
CTATACAACCTACTGCCTTC	117	0	0	1	0	0	0	0.04	0

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

Mature miRNA sequence	SEQ ID NO.	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
CGGGGTTTTGAGGGCGAGATGA	118	0	0	0	1	0	0	0	0.04
CCAGTGGGGCTGCTGTTATCTG	119	0	0	1	0	0	0	0.04	0
CCAGTATTAACTGTGCTGCTGA	120	0	0	0	1	0	0	0	0.04
CACCCGTAGAACCGACCTTGCG	121	0	0	1	0	0	0	0.04	0
CAAGCTCGTGTCTGTGGGTCCG	122	0	0	1	0	0	0	0.04	0
CAACACCAGTCGATGGGCTGTA	123	0	0	0	1	0	0	0	0.04
AGGCGGAGACTTGGGCAATT	124	0	0	0	1	0	0	0	0.04
ACTGCATTATGAGCACTTAAAGT	125	0	0	0	1	0	0	0	0.04
ACTGATTTCTTTTGGTGTTCA	126	0	0	0	1	0	0	0	0.04
ACTCGGCGTGGCGTCGGTCGTGG	127	0	0	0	1	0	0	0	0.04
ACCACTGACCGTTGACTGTAC	128	0	1	0	0	0	0.03	0	0
AACTGGCCTACAAAGTCCCAGT	129	0	0	1	0	0	0	0.04	0
TGTCTGAGCGTCGCT	130	0	0	4	0	0	0	0.16	0
GCCGGGTACTTTCGTATTTT	131	3	3	0	34	0.09	0.1	0	1.39
GCTAAGGAAGTCCTGTGCTCAG TTTT	132	0	0	1	19	0	0	0.04	0.78
CCCGGGTTTCGGCACCA	133	0	3	0	1	0	0.1	0	0.04
TCGGGCGGGAGTGGTGGCTTT	134	0	0	0	1	0	0	0	0.04
TAGAGGCACCGCCTGCCCA	135	0	1	0	0	0	0.03	0	0
CGGGGCGCGGCCTCGCTG	136	1	0	0	0	0.03	0	0	0
CCCACGGGGGTCTCCGGGCGAG	137	1	0	0	0	0.03	0	0	0
CCCACGGGAAACAGCA	138	0	1	0	0	0	0.03	0	0
CAGCCCGGCCTGGCTCCTCCAT	139	0	1	0	0	0	0.03	0	0
CACGGAAGGTGGCCCGG	140	0	1	0	0	0	0.03	0	0
CTGTAGGCACCTGAAA	141	1	0	0	148.06	0.03	0	0	6.07
CCCCCCACTGCTAAATTTGACTG GCTT	142	18	8	61	22	0.52	0.27	2.39	0.9
GCCCGCATCCTCCACCA	143	38	61	2	4	1.1	2.04	0.08	0.16
CCCGGCCAACGCACCA	144	28.76	36.71	4.12	4	0.83	1.23	0.16	0.16
ATCCCACTCCTGACACCA	145	7	13	11.31	3	0.2	0.44	0.44	0.12
CCGGGCGGAAACACCA	146	9	9	6	0	0.26	0.3	0.24	0
TGTCAGTTTGTTAATTA	147	1	1	3	16	0.03	0.03	0.12	0.66
AGGGTGTGCGTGTTTTT	148	0	0	0	20	0	0	0	0.82
TCGATTCCCGGCCCATGCACCA	149	1	2	10	4	0.03	0.07	0.39	0.16
GAGAGCGCTCGGTTTTT	150	0	0	1	9	0	0	0.04	0.37
TGGTGTGGTCTGTTGTTTT	151	0	0	0	9	0	0	0	0.37

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

Mature miRNA sequence	SEQ ID NO.	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
TGTGCTCCGGAGTTACCTCGTTT	152	0	0	0	8	0	0	0	0.33
TCCCCGACACCTCCACCA	153	2	2	2	1	0.06	0.07	0.08	0.04
CTGTAGGCATCATCAAT	154	0	0	1	3.57	0	0	0.04	0.15
AACCGAGCGTCCAAGCTCTTTC CATTTT	155	0	0	0	5	0	0	0	0.2
TCCCCGCACCTCCACCA	156	0	2	1	1	0	0.07	0.04	0.04
TCCCCGGCACTTCCACCA	157	0	3	0	0	0	0.1	0	0
TCACCCCATAAACACCA	158	2	1	0	0	0.06	0.03	0	0
CTGTAGGCACCATCATAA	159	0	0	0	2.43	0	0	0	0.1
CCCACCAGAGTCGCCA	160	1	2	0	0	0.03	0.07	0	0
TTCCCCGACGGGGAGCCA	161	1	0	0	1	0.03	0	0	0.04
GGCGTGATTCATACCTTTT	162	0	0	0	2	0	0	0	0.08
GCGGGCGGACCTTTT	163	1	1	0	0	0.03	0.03	0	0
CGGCTCGAAGGACCA	164	0	2	0	0	0	0.07	0	0
CCCCGGCCCCGCGTA	165	0	2	0	0	0	0.07	0	0
CCCACCTCTGACACCA	166	0	1	1	0	0	0.03	0.04	0
CCACGAGGTCGGCCGG	167	0	2	0	0	0	0.07	0	0
CAGGATCGGCCCACT	168	2	0	0	0	0.06	0	0	0
ATGTGGTGGCTTACTTTT	169	0	0	0	2	0	0	0	0.08
ATCCCGGACGAGCCCA	170	0	2	0	0	0	0.07	0	0
ATCCCCAGCATCTCCACCA	171	0	0	2	0	0	0	0.08	0
AGAAAGGCCGAATTTTA	172	0	0	1	1	0	0	0.04	0.04
TGTCAGTTTTTACCCAA	173	0	0	0	1	0	0	0	0.04
TGTCAGTTTGAACCCAA	174	0	0	0	1	0	0	0	0.04
TGTAGTGTTTCTTACTTTA	175	1	0	0	0	0.03	0	0	0
TGGCGAAGGTCGGCCGCG	176	0	1	0	0	0	0.03	0	0
TGCAGGGCCGGCGGGGAGG	177	0	1	0	0	0	0.03	0	0
TCGGGCGGCGGGCGT	178	1	0	0	0	0.03	0	0	0
TCGGCTTTCCCTGCTAACTGGG CTTTTT	179	0	0	0	1	0	0	0	0.04
TCAGAGCGCGGGCCGACCCC	180	1	0	0	0	0.03	0	0	0
TCAACACCCACTCCCTC	181	0	1	0	0	0	0.03	0	0
TATCAATGATGCTTCTGAGA	182	0	0	0	1	0	0	0	0.04
TAACCCCAGGGTTGGTCA	183	0	1	0	0	0	0.03	0	0
GGGGTCCCCGGTAGA	184	0	1	0	0	0	0.03	0	0
GGGCGTGGGTGTGATGATTC	185	0	0	0	1	0	0	0	0.04

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

Mature miRNA sequence	SEQ ID NO.	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
GGGAGGTGAGTAGGTCTG	186	0	1	0	0	0	0.03	0	0
GGAGACGTGGCCGAGAG	187	0	1	0	0	0	0.03	0	0
GCGGAATACCACGGGGA	188	0	1	0	0	0	0.03	0	0
GCAGGCGGGGGATTAGCTA	189	1	0	0	0	0.03	0	0	0
GCAGCGGAACGTCGGCGCGC	190	0	1	0	0	0	0.03	0	0
GACGTCACCCTCCTCA	191	0	1	0	0	0	0.03	0	0
CTTGGACTAACCTGGTGTA	192	0	0	1	0	0	0	0.04	0
CTGTAGGCCACCATCCA	193	0	0	0	1	0	0	0	0.04
CTGTAGGCACCACCA	194	1	0	0	0	0.03	0	0	0
CTGGTAGGCACCTGAAA	195	0	0	0	1	0	0	0	0.04
CTGATGTTGATGCATATGATGACA	196	0	0	0	1	0	0	0	0.04
CGGTGGAACCTGCATTGGTTT	197	0	0	1	0	0	0	0.04	0
CGGGGCCGGGGCTAGGGT	198	0	1	0	0	0	0.03	0	0
CGGGCCGCCCCCGCCCACCG	199	0	1	0	0	0	0.03	0	0
CGGGCCCCGGGGCTCG	200	0	1	0	0	0	0.03	0	0
CGGCCTATCCGGAATGCCCC	201	0	1	0	0	0	0.03	0	0
CGGACCTCCCTGGCCC	202	1	0	0	0	0.03	0	0	0
CGCGGCCAGTGTCCCCTTGTA	203	1	0	0	0	0.03	0	0	0
CGACACACGGCCCGTGGCGC	204	1	0	0	0	0.03	0	0	0
CCTCATAAATACCGG	205	0	1	0	0	0	0.03	0	0
CCTCACTGGGGGCTCCA	206	1	0	0	0	0.03	0	0	0
CCTCACCTGGAGCACCA	207	0	0	1	0	0	0	0.04	0
CCGTACTGGCCACCA	208	0	1	0	0	0	0.03	0	0
CCGCCGCCCCCCCCT	209	0	1	0	0	0	0.03	0	0
CCGCCCCGACCTTAGCTA	210	0	1	0	0	0	0.03	0	0
CCCGTCCGCTGCGCCA	211	0	1	0	0	0	0.03	0	0
CCCGTCCACTCCGCCA	212	0	1	0	0	0	0.03	0	0
CCCCGGCCCATGCACCA	213	0	1	0	0	0	0.03	0	0
CCCCGGCATCTCCATCA	214	1	0	0	0	0.03	0	0	0
CCCCAGTACCTCCACCA	215	0	1	0	0	0	0.03	0	0
CCCAGCGGTGCCTCCA	216	0	1	0	0	0	0.03	0	0
CCACGCTCTGCTACCA	217	1	0	0	0	0.03	0	0	0
CCACCCTGGAGCCTCCGT	218	0	1	0	0	0	0.03	0	0
ATGGTAGGCACCTGAAA	219	0	0	0	1	0	0	0	0.04
ATGGGCGGTCCTCGTT	220	0	1	0	0	0	0.03	0	0

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

Mature miRNA sequence	SEQ ID NO.	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
ATGGCCTGGACCCCACTCCT	221	0	0	0	1	0	0	0	0.04
ATGGCCGCATATATTTT	222	0	0	0	1	0	0	0	0.04
ATCCTGTTCGTGACGCCA	223	0	0	1	0	0	0	0.04	0
ATCCTGCTCACAGCCCCA	224	0	1	0	0	0	0.03	0	0
AGCGAGGGTTCCGCCGGCC	225	0	0	0	1	0	0	0	0.04
ACTGGGGAGGGGGAGGAGCCT CGAGG	226	0	0	0	1	0	0	0	0.04
ACCCCGAGGGGACGGGCG	227	0	1	0	0	0	0.03	0	0
ACAGCGCTGTGTTCCCGT	228	0	0	1	0	0	0	0.04	0
ACAAAAAAAAAAGCCCAACCCT	229	0	0	0	1	0	0	0	0.04
AACTAAAACCCCTACGCA	230	0	0	1	0	0	0	0.04	0
AAAGGAGCCGAATCTTT	231	0	0	1	0	0	0	0.04	0
CCCACCCAGGGACGCCA	232	223	218	6	2	6.46	7.3	0.24	0.08
TCCCCGGCACCTCCACCA	233	60.47	101.82	40.28	34	1.75	3.41	1.58	1.39
ATCCCGGACGAGCCCCCA	234	48	60	80	45	1.39	2.01	3.14	1.84
CCCACGTTGGGCGCCA	235	37	50	1	0	1.07	1.68	0.04	0
TCGATTCCCGGCCAATGCACCA	236	2.24	15.29	35.88	4	0.06	0.51	1.41	0.16
ATCCCACTTCTGACACCA	237	11	9	26.69	14	0.32	0.3	1.05	0.57
TCGTAGGCACCTGAAA	238	0	0	0	7.94	0	0	0	0.33
TCCCCGTACGGGCCACCA	239	11	6	3	2	0.32	0.2	0.12	0.08
TTGACCGCTCTGACCA	240	4	9	2	5	0.12	0.3	0.08	0.2
CCCAGCGGGGCCTCCA	241	11	8	1	0	0.32	0.27	0.04	0
CAGGAACGGTGCACCA	242	6	10	2	0	0.17	0.34	0.08	0
AGTCCCATCTGGGTCGCCA	243	4	2	3	6	0.12	0.07	0.12	0.25
CCCCCCACTGCTAAATTTGACTG GA	244	1	1	6	2	0.03	0.03	0.24	0.08
GTTTGTTAATTAACCCAA	245	0	0	1	5	0	0	0.04	0.2
GTCCCTTCGTGGTCGCCA	246	1	2	1	2	0.03	0.07	0.04	0.08
CTGTAGCACCTGAAA	247	0	0	0	6	0	0	0	0.25
TCCTCACACGGGGCACCA	248	2	1	2	0	0.06	0.03	0.08	0
TAACGGCCGCGGTACCC	249	0	3	1	0	0	0.1	0.04	0
GAGGGGGACCAAAAAAAA	250	0	0	0	4	0	0	0	0.16
CCCGCATTCTCCACCA	251	3	0	1	0	0.09	0	0.04	0
AGGGGGGTAAAAAAAAA	252	0	0	0	4	0	0	0	0.16
TCCACCGCTGCCACCA	253	0	3	0	0	0	0.1	0	0
GAGCCATGATGATACCACTGAGC	254	0	1	0	2	0	0.03	0	0.08

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

Mature miRNA sequence	SEQ ID NO.	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
CGTCCATGATGTTCCGCAA	255	1	0	2	0	0.03	0	0.08	0
CATCCTCTGCTACCA	256	3	0	0	0	0.09	0	0	0
AGAACACTACGAGCCACA	257	3	0	0	0	0.09	0	0	0
ACCCCACTTCTGGTACCA	258	0	0	1	2	0	0	0.04	0.08
TGTATTGTGAGACATTC	259	0	1	1	0	0	0.03	0.04	0
TCTCGGTGGAACCTCCA	260	0	0	1	1	0	0	0.04	0.04
TCCCCGGCACCTCCAA	261	0	1.01	0	0	0	0.03	0	0
TACCGAGCCTGGTGATAGC	262	0	1	1	0	0	0.03	0.04	0
GCAGCGCCAGCCTCCCGCCCTAC	263	2	0	0	0	0.06	0	0	0
CCGCCTGGGGAGTAC	264	0	2	0	0	0	0.07	0	0
ATCCCCAGCACCTCCACCA	265	0	0	0	2	0	0	0	0.08
AGCAGTGATGTCCTGAAAATTCT GAAG	266	0	0	0	2	0	0	0	0.08
ACCCCACTATGCTTAGCCCT	267	0	0	2	0	0	0	0.08	0
AAAGGACCTGGCGGTGCTTC	268	1	0	1	0	0.03	0	0.04	0
TTTGCCACACTGCAACACCTT	269	0	0	1	0	0	0	0.04	0
TTCCTTGGATGTCTGAGTGAC	270	0	0	1	0	0	0	0.04	0
TTAAACCACCAAGATCGCTGATG CAC	271	0	0	1	0	0	0	0.04	0
TGTTCGCCGACCGTTGA	272	0	0	1	0	0	0	0.04	0
TGGGGTCTGGGAGGGA	273	0	1	0	0	0	0.03	0	0
TGGGAGAGCAGGGTATTGT	274	1	0	0	0	0.03	0	0	0
TGCAGATGATGTAAAAGA	275	0	0	1	0	0	0	0.04	0
TCGCTATGATGATGGATTCCAAAA	276	0	0	1	0	0	0	0.04	0
TCCGAAAGGCCTCCCGCACCG	277	0	0	1	0	0	0	0.04	0
TCCCGCACCTCCACCA	278	0	0	1	0	0	0	0.04	0
TAGATGAATAGGTAAAGAG	279	0	0	1	0	0	0	0.04	0
GTGTATGATGACCTCATGTAGC CTGAAC	280	0	0	0	1	0	0	0	0.04
GTGAAGCGTTCCATATTTTT	281	0	0	1	0	0	0	0.04	0
GGGGGGGGGTTTGGAA	282	0	0	0	1	0	0	0	0.04
GGGGGGAGGGAAGGCAA	283	0	0	1	0	0	0	0.04	0
GGGGGCTGGGCTGGGTA	284	0	1	0	0	0	0.03	0	0
GGGGCCGCCGCCTGTGT	285	1	0	0	0	0.03	0	0	0
GGGAGTCCGCGGCGAGC	286	0	0	0	1	0	0	0	0.04
GGGACCTGGGGACCA	287	1	0	0	0	0.03	0	0	0

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

		Corrected Counts				Frequencies			
Mature miRNA sequence	SEQ ID NO.	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
GGCTTGGTCTAGGGGTA	288	0	0	0	1	0	0	0	0.04
GGCTGGGACCCTGGACAC	289	0	0	0	1	0	0	0	0.04
GGCGACCTGCGACTCCTT	290	0	1	0	0	0	0.03	0	0
GGAGGGGGGAAACAAA	291	0	0	0	1	0	0	0	0.04
GGAGGGGGGAAAAAAAAAA	292	0	0	0	1	0	0	0	0.04
GGAAGACCTGCACCACTGTC	293	0	1	0	0	0	0.03	0	0
GCGGGTGTCAGGCCT	294	1	0	0	0	0.03	0	0	0
GCCGGGCGTGGTGGTCTG	295	0	1	0	0	0	0.03	0	0
GCCGCCGAGACCCCAGGACCC	296	1	0	0	0	0.03	0	0	0
GCAGCCGTGCTTTTA	297	0	1	0	0	0	0.03	0	0
GCAAATGATGCCCTCTGATC	298	0	0	0	1	0	0	0	0.04
GAGGGGGGTCAAAAAAA	299	0	0	0	1	0	0	0	0.04
CTTGATGATGAGCAGGATCTGAGT	300	0	0	0	1	0	0	0	0.04
CTGTAGGCACTGAAA	301	0	0	0	1	0	0	0	0.04
CTGTAGGCACCATTAA	302	0	0	0	1	0	0	0	0.04
CTGCTTAAGTCCTGACCAG	303	0	0	1	0	0	0	0.04	0
CTGAGCACCTTTCCCTTCC	304	0	1	0	0	0	0.03	0	0
CTAGCCCCAAACCCA	305	1	0	0	0	0.03	0	0	0
CGGTCACACGATTAACCCA	306	0	0	1	0	0	0	0.04	0
CGGGGGGAGGAAAAAA	307	0	0	0	1	0	0	0	0.04
CGGGGGGAAAAAAAAA	308	0	0	0	1	0	0	0	0.04
CGGGGCCGCACGCGC	309	1	0	0	0	0.03	0	0	0
CGGGAGTGGGGTGGCGCCCAG	310	1	0	0	0	0.03	0	0	0
CGGGAGCCCCGGGTT	311	1	0	0	0	0.03	0	0	0
CGGACCTGATAAATTCCCAC	312	0	0	1	0	0	0	0.04	0
CGCGGCTCTTGCGGT	313	1	0	0	0	0.03	0	0	0
CGCCTGAGTCAGAAC	314	1	0	0	0	0.03	0	0	0
CGCCGCCGCCCCCCCC	315	0	1	0	0	0	0.03	0	0
CCTTCCTTGGATGTCTGAGTGAG	316	0	0	1	0	0	0	0.04	0
CCTCGCTGGGGCCTCCA	317	1	0	0	0	0.03	0	0	0
CCTCACAGGGACGCCA	318	1	0	0	0	0.03	0	0	0
CCTAGGAGTGCGACAATT	319	0	0	0	1	0	0	0	0.04
CCGCTCTGAGACCTA	320	0	1	0	0	0	0.03	0	0
CCGCCCGTCACCCTCCTCAAGTA	321	0	0	1	0	0	0	0.04	0
CCCGGGCGGCACACCA	322	0	1	0	0	0	0.03	0	0

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

Mature miRNA sequence	SEQ ID NO.	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
CCCGCGGGCTTGCTGGGCGTCCC	323	0	1	0	0	0	0.03	0	0
CCCCTGCGATTTCCCCA	324	0	1	0	0	0	0.03	0	0
CCCCGGCATCTCCACTA	325	1	0	0	0	0.03	0	0	0
CCCCAGTGAGTGCCCTCTTCC	326	0	1	0	0	0	0.03	0	0
CCCAGAGACGCCGTCCTCGA	327	1	0	0	0	0.03	0	0	0
CCCACCGAGGATGCCA	328	1	0	0	0	0.03	0	0	0
CCATCACTACCCACCA	329	0	1	0	0	0	0.03	0	0
CCACTCCAGCCTAGCCCC	330	0	1	0	0	0	0.03	0	0
CAGTACAGGCACACCTC	331	0	1	0	0	0	0.03	0	0
CACGTCGGGGTCCCCA	332	1	0	0	0	0.03	0	0	0
CACGATTAACCCAAGTC	333	0	0	1	0	0	0	0.04	0
CACCACACCCGGGCCA	334	1	0	0	0	0.03	0	0	0
CAACACAGGCATGCT	335	0	1	0	0	0	0.03	0	0
ATAGGGTTTACGACCTCGATGTTGGATCA	336	0	0	1	0	0	0	0.04	0
ATACCATGATGAACAATAGCTGAGA	337	0	0	0	1	0	0	0	0.04
AGGGTTCAGCTGTCTC	338	1	0	0	0	0.03	0	0	0
AGGCTGTGATGGACCTGGCTGAGCCTG	339	0	0	0	1	0	0	0	0.04
AGAGAGTAGGGGGAGGT	340	0	1	0	0	0	0.03	0	0
ACTGTCCCTGTCTACTA	341	0	0	0	1	0	0	0	0.04
ACCGCATCTGGCCTATTTTT	342	0	0	0	1	0	0	0	0.04
ACCAGACCTCCTGTGCGAAG	343	0	0	0	1	0	0	0	0.04
ACAGCCCGGATCCCAGCCCACTTA	344	0	0	0	1	0	0	0	0.04
ACACTGAGCCACAACCCA	345	0	0	1	0	0	0	0.04	0
AAGGGCTTGGCTTAATTA	346	0	0	1	0	0	0	0.04	0
AACCCGGAAGGCGGAGGTTGCGG	347	0	0	0	1	0	0	0	0.04
AACCCCACACCAACC	348	0	0	0	1	0	0	0	0.04
AACAAGCTTCTTTGACGTCCCATCCAC	349	0	0	0	1	0	0	0	0.04
TCCCCGGCATCTCCACCA	350	116.53	275.18	104.72	59	3.38	9.22	4.11	2.42
CTGATTGCTCCTGTCTGATT	351	0	0	6	1	0	0	0.24	0.04
TCTAGAGGAGCCTGTTCTGTA	352	0	1	3	0	0	0.03	0.12	0
TCGATTCCCGGTCAGGGAACCA	353	0	0	0	4	0	0	0	0.16

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

Mature miRNA sequence	SEQ ID NO.	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
ATAGGTTTGGTCCTAGCCTTTCT	354	0	0	3	1	0	0	0.12	0.04
CGTTCGCGCTTTCCCCTG	355	0	1	2	0	0	0.03	0.08	0
TAAGTGTTTGTGGGTTA	356	1	1	0	0	0.03	0.03	0	0
GGCGGCGGGAGACCCA	357	1	1	0	0	0.03	0.03	0	0
CCCCGGCAGGTTTGA	358	0	2	0	0	0	0.07	0	0
TGCCGTGATCGTATAGTGGTTA	359	0	0	1	0	0	0	0.04	0
TCAGACTACTCTCCTCCGCCCATT	360	0	0	1	0	0	0	0.04	0
GGACACAGAGGCTTCG	361	0	1	0	0	0	0.03	0	0
CTGACAGCCGGGGTTTTGGA	362	0	0	0	1	0	0	0	0.04
CGGCGGGGCCTGGAGTCTG	363	1	0	0	0	0.03	0	0	0
CCTGGCTCGCTGCGCCA	364	1	0	0	0	0.03	0	0	0
CCGCCCCACCCCGCGCGC	365	0	1	0	0	0	0.03	0	0
CCCGAACGCTGCCAACCC	366	0	1	0	0	0	0.03	0	0
AGACCCGCGGGCGCTCTCCAGTC	367	0	0	1	0	0	0	0.04	0
CCCCCACAACCGCGCTTGACTAGC	368	12	11	7	9	0.35	0.37	0.27	0.37
CCCTGCTCGCTGCGCCA	369	7	20	5	1	0.2	0.67	0.2	0.04
CTCCCACTGCTTCACTTGACTAGC	370	2	2	18	9	0.06	0.07	0.71	0.37
CCCATCCTCGTCGCCA	371	16	11	1	1	0.46	0.37	0.04	0.04
TCACGTCGGGGTCACCA	372	16	4	5	1	0.46	0.13	0.2	0.04
TCCCTGGTGGTCTAGTGGTTAGGATTCG	373	0	1	10	6	0	0.03	0.39	0.25
GGTAGCGTGGCCGAG	374	10	6	0	0	0.29	0.2	0	0
TCCTGCCGCGGTCGCCA	375	6	8	0	1	0.17	0.27	0	0.04
GGAGAGAACGCGGTCTGAGTGGT	376	3	7	1	0	0.09	0.23	0.04	0
TCGGGTGCGAGAGGTCCCGGGT	377	0	0	0	10	0	0	0	0.41
GGCTGGTCCGATGGTAGTGGGTT	378	4	3	3	0	0.12	0.1	0.12	0
CGGAAGCGTGCTGGGCCC	379	1	5	0	4	0.03	0.17	0	0.16
CCCGGGCGGCGCACCA	380	5	4	0	0	0.14	0.13	0	0
GCGGGTGATGCGAACTGGAGTCTGAGC	381	0	0	6	1	0	0	0.24	0.04
GACGAGGTGGCCGAGTGG	382	2	3	2	0	0.06	0.1	0.08	0
GGGGGTGTAGCTCAG	383	4	2	0	0	0.12	0.07	0	0
CTCCTGGCTGGCTCGCCA	384	0	0	3	3	0	0	0.12	0.12
CGGGAGGCCCGGGTT	385	3	3	0	0	0.09	0.1	0	0
GGCTGGTCCGAGTGCAGTGGTGTTTA	386	0	1	4	0	0	0.03	0.16	0

TABLE 1B-continued

List of known and newly identified mature miRNAs including information on frequencies.

Mature miRNA sequence	SEQ ID NO.	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Frequencies Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
CTGCTGTGATGACATTC	387	1	2	2	0	0.03	0.07	0.08	0
TGTCACGCGGGAGACC	388	0.5	0	1	1.4	0.01	0	0.04	0.06
TCCTCGTTAGTATAGTGGTGAGT ATCCC	389	0	1	3	0	0	0.03	0.12	0
GGCCGGTTAGCTCAG	390	2	2	0	0	0.06	0.07	0	0
GCATTGGTGGTTCAGTGGTAGA	391	0	0	3	1	0	0	0.12	0.04
CTGTCACGCGGGAGA	392	0.5	0	0	2.6	0.01	0	0	0.11
CTACGGGGATGATTTT	393	3	1	0	0	0.09	0.03	0	0
CCAGGGGCTGAGGGCA	394	1	3	0	0	0.03	0.1	0	0
TTCTCACTACTGCACTTGACTA	395	0	0	2	1	0	0	0.08	0.04
TGGTTATCACGTTCGCC	396	0	2	0	1	0	0.07	0	0.04
TAGGGGTATGATTCTCGCT	397	1	0	0	2	0.03	0	0	0.08
CCACGAGGAAGAGAGGTAGC	398	2	1	0	0	0.06	0.03	0	0
GTCAGGATGGCCGAGCGGTCT	399	0	1	1	0	0	0.03	0.04	0
GGGGATGTAGCTCAG	400	1	1	0	0	0.03	0.03	0	0
GCAGCGATGGCCGAG	401	0	2	0	0	0	0.07	0	0

[0227] Three hundred and thirty five sequences aligned to genomic regions which did not fulfill the criteria for miRNA precursors (FIG. **11**). About 30% of these non-miRNA sequences were annotated and may represent degradation products originating from other RNA species (FIG. **11** and Table 2).

TABLE 2

Characterization of short-RNA libraries. Number of non-redundant short-RNAs cloned in each library (naive, memory, and centroblast B cells, and Ramos cell line) and overall (Total).

RNA species	Naïve	Memory	Centroblasts	Ramos	Total
Total (non redundant)	683	710	744	765	2115
miRNA	498	485	564	590	1453
miRNA other*	5	3	7	4	19
tRNA	27	33	32	29	108
tRNA	61	99	34	16	174
mRNA	76	72	25	34	176
yRNA	11	11	31	21	53
piRNA	46	54	70	62	148
Repeats	1	1	0	1	2
Mitochondrial genome	12	36	54	11	101

TABLE 2-continued

Characterization of short-RNA libraries. Number of non-redundant short-RNAs cloned in each library (naive, memory, and centroblast B cells, and Ramos cell line) and overall (Total).

RNA species	Naïve	Memory	Centroblasts	Ramos	Total
Human viruses	1	4	0	0	5
E. Coli	5	4	0	0	7
Not Annotated	66	64	74	113	262

*miRNA other includes fragments of miRNA precursors, not mature

[0228] Each short-RNA is annotated according to the listed RNA species. Results shown in Table 2 refer only to short-RNAs with good-qulaity matches to the human genome. The same short-RNA may match to multiple databases and therefore the overall sum does not correspond to the total number of short-RNAs. The databeses used in the analysis depicted in Table 2 is detailed in the Supplementary Methods section.

[0229] The remaining (236 sequences), however, mapped to genomic regions that lack annotations and may therefore represent a part of the transcriptome whose functions are unknown (Table 3A-3B and Table 4A-4B).

TABLE 3A

List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-5016	402	AATGACACGATCACTCCCGTTGAG	Mature:hsa-miR-425:MIMAT0003393
CU-5019	403	GGAGGGGGGGTAAAAAAAA	NEW
CU-5020	404	CCCCGGCATCTCCACC	NEW
CU-5004	405	GAAGCGGGTGCTCTTATTTT	NEW
CU-5021	406	ACCGGGCGGAAACACCA	NEW
CU-5022	407	TCCCGGGTTCAAATCCCGGACGAGCCCCCA	NEW
CU-5008	408	GTGTAAGCAGGGTCGTTTT	NEW
CU-6003	409	ATCCCACCGCTGCTACCA	NEW
CU-5023	410	GGGAAGGTGACCTGAC	NEW
CU-5007	411	CTCCCGCCTTTTTTCCC	NEW
CU-5024	412	CGGAGCAAGAGCGT	NEW
CU-5025	413	CCCCGTACTGGCCACCA	NEW
CU-5026	414	CCCCCGGCACCATCAATA	NEW
CU-5027	415	CAGCCTAGCCCCTACCC	NEW
CU-5005	416	CAGAAGGTCTCACTTTT	NEW
CU-5006	417	AGTATTCTCTGTGGCTTT	NEW
CU-5028	418	TGGAGTGACTATATGGATGCCCCC	NEW
CU-5029	419	TCTGATAGCTTACTTT	NEW
CU-5030	420	TCGAGCCCCAGTGGAACCAC	NEW
CU-5031	421	TCGAATCCTGTTCGTGACGCCA	NEW
CU-5032	422	TCCTCCCCACACTCATCGCCCTTACCA	NEW
CU-5033	423	TATACTACAAGGACACCA	NEW
CU-5034	424	TAGTGGGTGAAAAAAAAAAA	NEW
CU-5035	425	TACCACACATTCGAAGAACCCGTA	NEW
CU-5036	426	TACAAAACCCACCCCATTCCTCCCCA	NEW
CU-5037	427	GCCCTCCTAATGACCTCC	NEW
CU-5038	428	CTTCCCTCTACACTTATCATC	NEW
CU-5039	429	CGGGCGGCCTGCGCTCTCA	NEW
CU-5040	430	CCCGAGGCCGTGTGCAAATGCAT	NEW
CU-5041	431	CCCCCAGTACCTCCACCA	NEW
CU-5042	432	CCCCCACTGCTAAACTTGACTGGCTTT	NEW
CU-5043	433	CCCACTCCACCTTACTACCA	NEW
CU-5044	434	CCCAAGAACAGGGTGACCA	NEW
CU-5045	435	CCAGTCGCGGCCAAATCA	NEW
CU-5046	436	CCAGCTTCACCAAGGTATTGGTTA	NEW

TABLE 3A-continued

List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-5047	437	CCAGAAAAAACAGGCCTC	NEW
CU-5048	438	CATCATAATCGGAGGCTTTGGCAAC	NEW
CU-5049	439	CAGCAGGGGTAATAAGTGAAATCAAA	NEW
CU-5050	440	CAATGGTGCAGCCGCTATTAAAGGTTCA	NEW
CU-5051	441	CAACTCCTACATACTTCCCCC	NEW
CU-5052	442	ATTCAAAAAAGAGTACCA	NEW
CU-5053	443	ATGCATCTCATATGCGAATAGGAATGC	NEW
CU-5054	444	ATCCCACTTCTGTACCA	NEW
CU-5055	445	ATAACACTAGAAAGTTGGGGCAGATTGC	NEW
CU-5056	446	ACGTGGGCACATTACCCGTCTGACCTGA	NEW
CU-5057	447	ACCCCTTATTAACCCA	NEW
CU-5058	448	ACAAGGCACACCTACACCCCTTATCCC	NEW
CU-5059	449	AAAAGACACCCCCCCACCA	NEW
CU-5060	450	AAAACCCCTACGCATTTATAT	NEW
CU-5061	451	AAAAAGACACCCCCCACCA	NEW
CU-5003	452	ACCCCACTCCTGGTACCA	refseqGeneIntron-annotate
CU-5009	453	TGCCCCCATGTCTAACAACATGGCTA	refseqGeneIntron-annotate; rnaGene-annotate
CU-5013	454	GGCCGGTGATGAGAACT	mRNAall-annotate; refseqGeneIntron-annotate; wgRNA-annotate; snoRNA-annotate
CU-5062	455	CCCCGCCTGTTTACC	refseqGeneIntron-annotate
CU-5063	456	CCCACTTCTGACACCA	computGene-annotate; refseqGeneIntron-annotate; exEID-annotate
CU-5064	457	CACCACCTCTTGCTCAGCC	mRNA-annotate; refseqGeneIntron-annotate
CU-5014	458	CTGGAAAGTGCACTTGGACGAACA	refseqGeneIntron-annotate
CU-5065	459	TGACCGCTCTGACCAC	refseqGeneIntron-annotate
CU-5066	460	TGAAGTCCCTTTGCTTTGTT	refseqGeneIntron-annotate
CU-5067	461	TGAACACACAATAGCTAAGACCC	mRNA-annotate; refseqGeneIntron-annotate
CU-5068	462	TCGCCTTACCCCCCACTA	refseqGeneIntron-annotate
CU-5069	463	TCGATAAACCCCGATCAACCT	mRNA-annotate; refseqGeneIntron-annotate
CU-5070	464	TCCCCGTCACCTCCACCA	refseqGeneIntron-annotate
CU-5071	465	TCCCCGGCACTCCACCA	refseqGeneIntron-annotate
CU-5072	466	TCCCCCCGCTGCCACCA	refseqGeneIntron-annotate
CU-5073	467	TCCCCCCCATCTCCACCA	refseqGeneIntron-annotate
CU-5074	468	TACACACCGCCCGTCACCC	mRNA-annotate; refseqGeneIntron-annotate
CU-5075	469	GGCCGGTGATGAGAACTTCTCCC	mRNAall-annotate; refseqGeneIntron-annotate; wgRNA-annotate; snoRNA-annotate
CU-5076	470	GCTTAGCCTAGCCACACCCCCACG	mRNA-annotate; refseqGeneIntron-annotate

TABLE 3A-continued

List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-5077	471	GCTCGCCAGAACACTACGA	mRNA-annotate; refseqGeneIntron-annotate
CU-5078	472	GCCGGGGGGCGGGCGCA	refseqGeneIntron-annotate
CU-5079	473	GAACCGGGCGGGAACACCA	refseqGeneIntron-annotate
CU-5080	474	CGCCGCAGTACTGATCATTC	refseqGeneIntron-annotate
CU-5081	475	CCGCACCAATAGGATCCTCC	refseqGeneIntron-annotate
CU-5082	476	CCCGGCCGACGCACCA	refseqGeneIntron-annotate
CU-5083	477	CCACCCCATCATACTCTTTC	refseqGeneIntron-annotate
CU-5084	478	CACCCCCCAGCTCCTCCTTT	refseqGeneIntron-annotate
CU-5085	479	ATAAGTAACATGAAAACATTCTCCTC	refseqGeneIntron-annotate
CU-5086	480	ACTGCTCGCCAGAACAC	mRNA-annotate; refseqGeneIntron-annotate
CU-5087	481	ACCCTGGTGTGGGATCTGCCCGATC	refseqGeneIntron-annotate
CU-5088	482	AACCTCACCACCTCTTTCT	refseqGeneIntron-annotate
CU-5089	483	AAAAGACACCCCCCACACCA	refseqGeneIntron-annotate
CU-5011	484	GCTAAACCTAGCCCCAAACCC	piRNA-annotate
CU-5010	485	GGCCGTGATCGTATA	piRNA-annotate
CU-5090	486	TGGGATGCGAGAGGTCCCGGGT	rnaGene-annotate
CU-5091	487	CTGAACTCCTCACACCC	piRNA-annotate
CU-5092	488	ATTAATCCCCTGGCCCAACCCG	computGene-annotate
CU-5093	489	AGCCCCAAACCCACTCCAC	piRNA-annotate
CU-5094	490	CGCGACCTCAGATCAGAC	rRNA-eliminate; piRNA-annotate; refseqGeneIntron-annotate
CU-5015	491	TCAAGTGATGTCATCTTACTACTGAGA	mRNAall-annotate; snoRNA-annotate; snoRNA-eliminate; wgRNA-annotate; rnaGene-annotate
CU-5095	492	TTGGGTGCGAGAGGTCCCGGGT	tRNAcomputational-annotate; tRNA-eliminate; HStRNA-eliminate; rnaGene-annotate
CU-5096	493	TCTCGGTGGGACCTCCA	refseqGeneExon-eliminate
CU-5097	494	CCGCCCCCCGTTCCCCC	rRNA-eliminate
CU-5098	495	CCCACTGCTAAATTTGACTGGCTT	mRNAall-annotate; yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-5099	496	ACAGACCAAGAGCCTTC	tRNA-eliminate; rnaGene-annotate
CU-5100	497	TGTAGTAGTCAATTAATGGATATTA	refseqGeneExon-eliminate
CU-5101	498	TGGTTATCACGTTCGCCTCACACGCGA	tRNAcomputational-annotate; tRNA-eliminate; HStRNA-eliminate; rnaGene-annotate
CU-5102	499	TGGGAATACCGGGTG	rRNA-eliminate; rnaGene-annotate; piRNA-annotate; refseqGeneIntron-annotate
CU-5103	500	TGGCGGCCAAGCGTTCATAGCGACGTC	rRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-5104	501	TCGTCATCCAGCTAAGGGCTCAGA	mRNAall-annotate; refseqGeneExon-eliminate; exEID-annotate

TABLE 3A-continued

List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-5105	502	TCGCCTGCCACGCGGGAGGCCCGGGT	rnaGene-annotate; tRNAcomputational-annotate; tRNA-eliminate; refseqGeneIntron-annotate; mRNA-annotate; HStRNA-eliminate
CU-5106	503	TCCCACTGCTTCACTTGA	yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-5107	504	GTTTAGACGGGCTCACATCACCCCA	tRNA-eliminate; piRNA-annotate; refseqGeneIntron-annotate
CU-5108	505	GCTAACTCATGCCCCCATGTC	tRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-5109	506	GACTGTGGTGGTTGAATATA	mRNAall-annotate; computGene-annotate; refseqGeneExon-eliminate; exEID-annotate
CU-5110	507	CGCGACCTCAGATCAGACGTGGCGACC	rRNA-eliminate; piRNA-annotate; refseqGeneIntron-annotate
CU-5111	508	CGCCGCCGCCCCCCC	mRNAall-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; exEID-annotate
CU-5112	509	CGCCCGACTACCACCACATCCA	mRNAall-annotate; computGene-annotate; refseqGeneExon-eliminate; exEID-annotate
CU-5113	510	CCCCCCTCCACGCGCCC	rRNA-eliminate; refseqGeneIntron-annotate
CU-5114	511	CCCCACCCCGCGCCCTC	rRNA-eliminate; refseqGeneIntron-annotate
CU-5115	512	CAGAGTGTAGCTTAACACAAAGCACCCAA	tRNA-eliminate; piRNA-annotate; rnaGene-annotate
CU-5116	513	CAATCTTGGCATGTTGGTCTGGTCACCCA	mRNAall-annotate; refseqGeneExon-eliminate; exEID-annotate
CU-5117	514	CAAAGCATCGCGAAGGCCC	mRNAall-annotate; rRNA-eliminate; piRNA-annotate; rnaGene-annotate
CU-5118	515	AACACCCTGATTGCTCCTGTCTGAT	mRNAall-annotate; exEID-annotate; snoRNA-annotate; refseqGeneExon-eliminate; rnaGene-annotate; snoRNA-eliminate; wgRNA-annotate
CU-5119	516	AAAAAGGGCCTAAAGAAGATGCA	mRNAall-annotate; computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; exEID-annotate

TABLE 3B

List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs including information on frequencies.

		Corrected Counts				Frequencies			
SEQ ID NO:	Short-RNA sequence	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
525	AATGACACGATCACTCCCG TTGAG	0	0	7	0	0	0	3.98	0
526	GGAGGGGGGGTAAAAAAAA	0	0	1	0	0	0	0.57	0
527	CCCCGGCATCTCCACC	1	0	0	0	1.72	0	0	0
528	GAAGCGGGTGCTCTTATTTT	5	23	25	224	8.62	20.35	14.2	65.31
529	ACCGGGCGGAAACACCA	9	14	60	20	15.52	12.39	34.09	5.83
530	TCCCGGGTTCAAATCCCGG ACGAGCCCCCA	0	0	4	37	0	0	2.27	10.79
531	GTGTAAGCAGGGTCGTTTT	0	0	0	7	0	0	0	2.04
532	ATCCCACCGCTGCTACCA	0	1	0	2	0	0.88	0	0.58

TABLE 3B-continued

List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs including information on frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
533	GGGAAGGTGACCTGAC	2	0	0	0	3.45	0	0	0
534	CTCCCGCCTTTTTTCCC	0	2	0	0	0	1.77	0	0
535	CGGAGCAAGAGCGT	2	0	0	0	3.45	0	0	0
536	CCCCGTACTGGCCACCA	2	0	0	0	3.45	0	0	0
537	CCCCCGGCACCATCAATA	0	0	1	1	0	0	0.57	0.29
538	CAGCCTAGCCCCTACCC	0	2	0	0	0	1.77	0	0
539	CAGAAGGTCTCACTTTT	0	1	0	1	0	0.88	0	0.29
540	AGTATTCTCTGTGGCTTT	0	0	0	2	0	0	0	0.58
541	TGGAGTGACTATATGGATG CCCCC	0	0	1	0	0	0	0.57	0
542	TCTGATAGCTTACTTT	0	1	0	0	0	0.88	0	0
543	TCGAGCCCCAGTGGAACCAC	0	0	1	0	0	0	0.57	0
544	TCGAATCCTGTTCGTGACG CCA	0	0	0	1	0	0	0	0.29
545	TCCTCCCCACACTCATCGC CCTTACCA	0	0	1	0	0	0	0.57	0
546	TATACTACAAGGACACCA	0	0	0	1	0	0	0	0.29
547	TAGTGGGTGAAAAAAAAAA AA	0	0	0	1	0	0	0	0.29
548	TACCACACATTCGAAGAAC CCGTA	0	0	1	0	0	0	0.57	0
549	TACAAAACCCACCCCATTC CTCCCCA	0	1	0	0	0	0.88	0	0
550	GCCCTCCTAATGACCTCC	0	0	1	0	0	0	0.57	0
551	CTTCCCTCTACACTTATCATC	0	0	1	0	0	0	0.57	0
552	CGGGCGGCCTGCGCTCTCA	1	0	0	0	1.72	0	0	0
553	CCCGAGGCCGTGTGCAAAT GCAT	0	0	1	0	0	0	0.57	0
554	CCCCCAGTACCTCCACCA	0	1	0	0	0	0.88	0	0
555	CCCCCACTGCTAAACTTGA CTGGCTTT	0	0	1	0	0	0	0.57	0
556	CCCACTCCACCTTACTACCA	0	0	0	1	0	0	0	0.29
557	CCCAAGAACAGGGTGACCA	0	0	0	1	0	0	0	0.29
558	CCAGTCGCGGCCAAATCA	0	1	0	0	0	0.88	0	0
559	CCAGCTTCACCAAGGTATT GGTTA	0	0	1	0	0	0	0.57	0
560	CCAGAAAAAACAGGCCTC	0	0	0	1	0	0	0	0.29
561	CATCATAATCGGAGGCTTT GGCAAC	0	0	1	0	0	0	0.57	0

TABLE 3B-continued

List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs including information on frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
562	CAGCAGGGGTAATAAGTGAAATCAAA	0	0	1	0	0	0	0.57	0
563	CAATGGTGCAGCCGCTATTAAAGGTTCA	0	0	0	1	0	0	0	0.29
564	CAACTCCTACATACTTCCCCC	1	0	0	0	1.72	0	0	0
565	ATTCAAAAAAGAGTACCA	0	0	1	0	0	0	0.57	0
566	ATGCATCTCATATGCGAATAGGAATGC	0	0	1	0	0	0	0.57	0
567	ATCCCACTTCTGTACCA	0	1	0	0	0	0.88	0	0
568	ATAACACTAGAAAGTTGGGGCAGATTGC	0	0	1	0	0	0	0.57	0
569	ACGTGGGCACATTACCCGTCTGACCTGA	0	0	0	1	0	0	0	0.29
570	ACCCCTTATTAACCCA	0	1	0	0	0	0.88	0	0
571	ACAAGGCACACCTACACCCCTTATCCC	0	0	1	0	0	0	0.57	0
572	AAAAGACACCCCCCCACCA	0	0	0	1	0	0	0	0.29
573	AAAACCCCTACGCATTTATAT	0	0	1	0	0	0	0.57	0
574	AAAAAGACACCCCCCACCA	0	0	0	1	0	0	0	0.29
575	ACCCCACTCCTGGTACCA	1	11	5	6	1.72	9.73	2.84	1.75
576	TGCCCCCATGTCTAACAACATGGCTA	7	4	1	1	12.07	3.54	0.57	0.29
577	GGCCGGTGATGAGAACT	4	3	0	0	6.9	2.65	0	0
578	CCCCGCCTGTTTACC	0	5	2	0	0	4.42	1.14	0
579	CCCACTTCTGACACCA	3	4	0	0	5.17	3.54	0	0
580	CACCACCTCTTGCTCAGCC	1	3	0	0	1.72	2.65	0	0
581	CTGGAAAGTGCACTTGGACGAACA	0	2	0	0	0	1.77	0	0
582	TGACCGCTCTGACCAC	0	1	0	0	0	0.88	0	0
583	TGAAGTCCCTTTGCTTTGTT	1	0	0	0	1.72	0	0	0
584	TGAACACACAATAGCTAAGACCC	0	0	1	0	0	0	0.57	0
585	TCGCCTTACCCCCCACTA	0	1	0	0	0	0.88	0	0
586	TCGATAAACCCCGATCAACCT	0	0	1	0	0	0	0.57	0
587	TCCCCGTCACCTCCACCA	0	0	1	0	0	0	0.57	0
588	TCCCCGGCACTCCACCA	0	0	1	0	0	0	0.57	0
589	TCCCCCCGCTGCCACCA	1	0	0	0	1.72	0	0	0
590	TCCCCCCCATCTCCACCA	0	0	1	0	0	0	0.57	0

TABLE 3B-continued

List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs including information on frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
591	TACACACCGCCCGTCACCC	0	0	1	0	0	0	0.57	0
592	GGCCGGTGATGAGAACTTC TCCC	1	0	0	0	1.72	0	0	0
593	GCTTAGCCTAGCCACACCC CCACG	0	0	1	0	0	0	0.57	0
594	GCTCGCCAGAACACTACGA	0	0	1	0	0	0	0.57	0
595	GCCGGGGGGCGGGCGCA	0	1	0	0	0	0.88	0	0
596	GAACCGGGCGGGAACACCA	0	0	0	1	0	0	0	0.29
597	CGCCGCAGTACTGATCATTC	0	0	1	0	0	0	0.57	0
598	CCGCACCAATAGGATCCTCC	0	1	0	0	0	0.88	0	0
599	CCCGGCCGACGCACCA	1	0	0	0	1.72	0	0	0
600	CCACCCCATCATACTCTTTC	0	0	1	0	0	0	0.57	0
601	CACCCCCCAGCTCCTCCTTT	1	0	0	0	1.72	0	0	0
602	ATAAGTAACATGAAAACATT CTCCTC	0	0	1	0	0	0	0.57	0
603	ACTGCTCGCCAGAACAC	0	0	1	0	0	0	0.57	0
604	ACCCTGGTGTGGGATCTGC CCGATC	0	0	1	0	0	0	0.57	0
605	AACCTCACCACCTCTTTCT	0	0	1	0	0	0	0.57	0
606	AAAAGACACCCCCCACACCA	0	0	0	1	0	0	0	0.29
607	GCTAAACCTAGCCCCAAAC CC	9	16	13	18	15.52	14.16	7.39	5.25
608	GGCCGTGATCGTATA	2	0	0	0	3.45	0	0	0
609	TGGGATGCGAGAGGTCCC GGGT	0	0	0	1	0	0	0	0.29
610	CTGAACTCCTCACACCC	0	1	0	0	0	0.88	0	0
611	ATTAATCCCCTGGCCCAAC CCG	0	0	0	1	0	0	0	0.29
612	AGCCCCAAACCCACTCCAC	0	0	1	0	0	0	0.57	0
613	CGCGACCTCAGATCAGAC	1	5	8	1	1.72	4.42	4.55	0.29
614	TCAAGTGATGTCATCTTACT ACTGAGA	0	0	3	1	0	0	1.7	0.29
615	TTGGGTGCGAGAGGTCCC GGGT	0	0	0	3	0	0	0	0.87
616	TCTCGGTGGGACCTCCA	0	2	0	0	0	1.77	0	0
617	CCGCCCCCCGTTCCCCC	1	1	0	0	1.72	0.88	0	0
618	CCCACTGCTAAATTTGACT GGCTT	0	0	1	1	0	0	0.57	0.29
619	ACAGACCAAGAGCCTTC	0	0	2	0	0	0	1.14	0

TABLE 3B-continued

List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs including information on frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
620	TGTAGTAGTCAATTAATGGATATTA	0	0	1	0	0	0	0.57	0
621	TGGTTATCACGTTCGCCTCACACGCGA	0	0	0	1	0	0	0	0.29
622	TGGGAATACCGGGTG	0	0	1	0	0	0	0.57	0
623	TGGCGGCCAAGCGTTCATAGCGACGTC	0	0	0	1	0	0	0	0.29
624	TCGTCATCCAGCTAAGGGCTCAGA	0	0	1	0	0	0	0.57	0
625	TCGCCTGCCACGCGGGAGGCCCGGGT	0	0	1	0	0	0	0.57	0
626	TCCCACTGCTTCACTTGA	0	0	0	1	0	0	0	0.29
627	GTTTAGACGGGCTCACATCACCCCA	0	0	1	0	0	0	0.57	0
628	GCTAACTCATGCCCCCATGTC	0	0	1	0	0	0	0.57	0
629	GACTGTGGTGGTTGAATATA	0	0	0	1	0	0	0	0.29
630	CGCGACCTCAGATCAGACGTGGCGACC	0	0	1	0	0	0	0.57	0
631	CGCCGCCGCCCCCCC	0	1	0	0	0	0.88	0	0
632	CGCCCGACTACCACCACATCCA	1	0	0	0	1.72	0	0	0
633	CCCCCCTCCACGCGCCC	0	1	0	0	0	0.88	0	0
634	CCCCACCCCGCGCCCTC	0	1	0	0	0	0.88	0	0
635	CAGAGTGTAGCTTAACACAAAGCACCCAA	0	0	1	0	0	0	0.57	0
636	CAATCTTGGCATGTTGGTCTGGTCACCCA	0	0	1	0	0	0	0.57	0
637	CAAAGCATCGCGAAGGCCC	0	0	1	0	0	0	0.57	0
638	AACACCCTGATTGCTCCTGTCTGAT	0	0	1	0	0	0	0.57	0
639	AAAAAGGGCCTAAAGAAGATGCA	0	0	1	0	0	0	0.57	0

TABLE 4A

List of short-RNA consensus with maximum 1 mismatch to the human genome.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6232	640	TGGCTCAGTTCAGCAGGAACAGT	Mature:hsa-miR-24:MIMAT0000080
CU-6180	641	GTGGGGGAGAGGCTGTCGA	Mature:hsa-miR-1275:MIMAT0005929
CU-6130	642	CGGGGCAGCTCAGTACAGGATT	Mature:hsa-miR-486-3p:MIMAT0004762

TABLE 4A-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6044	643	AATTGCACGGTATCCATCTGTAT	Mature:hsa-miR-363:MIMAT0000707
CU-6133	644	CGGGGGAGCGCCGCGTA	NEW
CU-6215	645	TCGATCCCGGGTTTCGGCACCA	NEW
CU-6072	646	ATCGTATCCCACTTCTGACACCA	NEW
CU-6030	647	ATCCTGCCGACTACGCCA	NEW
CU-6210	648	TCGAATCCCACTCCTGACACCA	NEW
CU-6069	649	ATCCCATCCTCGTCGCCA	NEW
CU-6216	650	TCGATTCCCCGACGGGGAGCCA	NEW
CU-6071	651	ATCCGGGTGCCCCCTCCA	NEW
CU-6202	652	TCCCGGGCGGCGCACCA	NEW
CU-6066	653	ATCCCACCAGAGTCGCCA	NEW
CU-6192	654	TCAAATCACGTCGGGGTCACCA	NEW
CU-6239	655	TGTCAGTTTGTTAATTGACCCAA	NEW
CU-6214	656	TCGATCCCCGTACGGGCCACCA	NEW
CU-6213	657	TCGAGCCTCACCTGGAGCACCA	NEW
CU-6206	658	TCCGGCTCGAAGGACCA	NEW
CU-6006	659	GGCAATACGAGCACCCTG	NEW
CU-6004	660	CCGGGGCGTCTCGTAC	NEW
CU-6056	661	AGCGGCTGTGCACAAA	NEW
CU-6242	662	TGTCAGTTTGTTTAATCCAA	NEW
CU-6241	663	TGTCAGTTTGTTATTACCAA	NEW
CU-6237	664	TGTCAGGCACCATCAATAA	NEW
CU-6225	665	TGATCTTGACACTTAAAGCC	NEW
CU-6219	666	TCGTAGGCACCATCAAT	NEW
CU-6211	667	TCGACTCCCGGTATGGGAACCA	NEW
CU-6187	668	TAGGGAGGTTATGATTAACTTTT	NEW
CU-6183	669	TAAAGTGCTTAGTGCAGGTA	NEW
CU-6181	670	GTTTATGTTGCTTACCTCC	NEW
CU-6176	671	GTAGATAAAATATTGGCG	NEW
CU-6163	672	GGCGGGGACGACGTCAG	NEW
CU-6162	673	GGCGGCGTCGCGGCGGGTC	NEW
CU-6161	674	GGAGGGGGTGAACAAAAAGAAAAA	NEW
CU-6159	675	GCTAAACCTAGCCCCAAACCCACTCCACA	NEW
CU-6142	676	CTGGATAGCGCACTTCGTT	NEW
CU-6129	677	CGGGCGAGGGGCGGACGTTCG	NEW
CU-6123	678	CGGACCTATACCGGA	NEW

TABLE 4A-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6096	679	CCCCGGGTTCAATCCCCGGCACCTCCACCA	NEW
CU-6088	680	CCCCCCACAACCGCGAA	NEW
CU-6087	681	CCCAGCATCTCCTGTGTTTA	NEW
CU-6086	682	CCCACGTTGGGACGCCA	NEW
CU-6064	683	ATCACGTCCGTGCCTCCA	NEW
CU-6063	684	ATAGCAATGTCAGCAGTACCT	NEW
CU-6051	685	ACCCTGCTCGCTGCGCCA	refseqGeneIntron-annotate
CU-6198	686	TCCCACCCAGGGACGCCA	refseqGeneIntron-annotate
CU-6218	687	TCGTAGGCACATCAATA	refseqGeneIntron-annotate
CU-6007	688	CCCCCACAACCGCGTA	refseqGeneIntron-annotate
CU-6001	689	ACCCCGTCCGTGCCTCCA	refseqGeneIntron-annotate
CU-6039	690	AAAAAAGACACCCCCCACA	refseqGeneIntron-annotate
CU-6005	691	TGTCAGTTTGTTAACCCAA	refseqGeneIntron-annotate
CU-6204	692	TCCCTGTGGTCTAGTGGTTAGG	refseqGeneIntron-annotate
CU-6172	693	GGGGGGGTAAAAAAA	refseqGeneIntron-annotate
CU-6171	694	GGGGGGGGAAAAAAAA	refseqGeneIntron-annotate
CU-6128	695	CGGGCCCGGGTCTTCCC	refseqGeneIntron-annotate
CU-6002	696	CCGCCCCCCGTTCCCCCCA	refseqGeneIntron-annotate
CU-6050	697	ACCCCCGGCTCCTCCACCA	refseqGeneIntron-annotate
CU-6244	698	TTTGGTGGAAATTTTTTGA	refseqGeneIntron-annotate
CU-6240	699	TGTCAGTTTGTTATACCAA	refseqGeneIntron-annotate
CU-6238	700	TGTCAGTTTGTAATTATCCCAA	refseqGeneIntron-annotate
CU-6236	701	TGTCAATTTTTAACCCAA	refseqGeneIntron-annotate
CU-6227	702	TGCTAGGGTAAAAAAAAAA	refseqGeneIntron-annotate
CU-6226	703	TGCAACTCCAAATAAAAGTACCA	refseqGeneIntron-annotate
CU-6224	704	TGAGGTAACGGGGAATTA	refseqGeneIntron-annotate
CU-6209	705	TCCTCGGCATCTCCACCA	refseqGeneIntron-annotate
CU-6197	706	TCATATGAAGTCACCCTAGCCATC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6196	707	TCAGTTTGTTTATTAACCCAA	refseqGeneIntron-annotate
CU-6195	708	TCAGCGTGTCTTTGCCCT	refseqGeneIntron-annotate
CU-6194	709	TCACTGGTGGTCTAGTGGT	refseqGeneIntron-annotate; rnaGene-annotate
CU-6193	710	TCACAATGCTGCCACCA	refseqGeneIntron-annotate
CU-6189	711	TAGTTGTTAATTAACCCAA	refseqGeneIntron-annotate
CU-6188	712	TAGTCCTCATCGCCCTCC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6184	713	TAAAGTGCTTATAGTGCGGGTAA	refseqGeneIntron-annotate

TABLE 4A-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6179	714	GTCCCACCAGAGTCGCCA	refseqGeneIntron-annotate
CU-6170	715	GGGGGAGGGGCCAAAAAAA	refseqGeneIntron-annotate
CU-6167	716	GGGACGCCGCGGTGTCG	refseqGeneIntron-annotate
CU-6166	717	GGGAATACCGGGTGCTTTAGGCTT	refseqGeneIntron-annotate; rnaGene-annotate
CU-6160	718	GGAAGAAGGTGGTGGTATA	refseqGeneIntron-annotate
CU-6156	719	GCGGTGAAATGCGTA	computGene-annotate; Ecoli-annotate; refseqGeneIntron-annotate
CU-6154	720	GCGGGGAAGGTGGCAAA	refseqGeneIntron-annotate
CU-6152	721	GCGACGACCTCGCGCCCACCTGGTCA	refseqGeneIntron-annotate
CU-6151	722	GCCACCCGATACTGCTGT	refseqGeneIntron-annotate
CU-6150	723	GATGTATGCTTTGTTTCTGTT	refseqGeneIntron-annotate
CU-6148	724	GAGGGGGATTTAGAAAAAAA	refseqGeneIntron-annotate
CU-6147	725	GAAGGAAAGTTCTATAGT	refseqGeneIntron-annotate
CU-6146	726	GAAGCGGCTCTCTTATTT	refseqGeneIntron-annotate
CU-6145	727	GAACGAGACTCTGGCATGCTGA	refseqGeneIntron-annotate; rnaGene-annotate
CU-6143	728	CTGGTAGGCCCATCAAT	refseqGeneIntron-annotate
CU-6132	729	CGGGGCCGATCGCGCGC	computGene-annotate; refseqGeneIntron-annotate
CU-6125	730	CGGCCCCGGGTTCCTCCC	computGene-annotate; refseqGeneIntron-annotate
CU-6118	731	CGAGCCCGGTTAGTA	refseqGeneIntron-annotate; rnaGene-annotate
CU-6117	732	CGACTCTTAGCGGTGGA	piRNA-annotate; refseqGeneIntron-annotate
CU-6116	733	CGAATCCCACTTCTGACACCA	refseqGeneIntron-annotate
CU-6113	734	CGAAAGGGAATCGGGTC	refseqGeneIntron-annotate
CU-6112	735	CCTTAGGTCGCTGGTAAA	refseqGeneIntron-annotate
CU-6108	736	CCGTGCGAGAATACCA	refseqGeneIntron-annotate
CU-6107	737	CCGGTCTCTCAAGCGGCC	refseqGeneIntron-annotate
CU-6099	738	CCCGGCCCTCGCGCGTCC	computGene-annotate; refseqGeneIntron-annotate
CU-6094	739	CCCCGGCATTTCCACCA	computGene-annotate; refseqGeneIntron-annotate
CU-6090	740	CCCCCCCGGCTCCTCCACCA	refseqGeneIntron-annotate
CU-6089	741	CCCCCCACAACCGCTA	refseqGeneIntron-annotate
CU-6085	742	CCCAAGTATTGACTCACCC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6084	743	CCAGTAAGCGCGAGTC	refseqGeneIntron-annotate
CU-6082	744	CCAAAGAAAGCACGTAGAG	refseqGeneIntron-annotate
CU-6081	745	CATGTTTAACGGCCGCGGT	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6080	746	CAGTTTGTAATTAACCCAA	refseqGeneIntron-annotate
CU-6079	747	CAGGAACGGCGCACCA	computGene-annotate; refseqGeneIntron-annotate
CU-6078	748	CAGAACCCTCTAAATCCCC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6076	749	CACCCGGCTGTGTGCACATGTGT	miRBASE-annotate; computGene-annotate; refseqGeneIntron-annotate; wgRNA-annotate

TABLE 4A-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6075	750	CAATTGGACCAATCTATC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6074	751	ATTCCTGTACTGCGATA	refseqGeneIntron-annotate
CU-6070	752	ATCCCTGCGGCGTCTCCA	refseqGeneIntron-annotate
CU-6067	753	ATCCCACCGCTGCCATCA	refseqGeneIntron-annotate
CU-6062	754	AGTCAATAGAAGCCGGCGTA	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6061	755	AGGTTCGTTTGTAAAAA	refseqGeneIntron-annotate
CU-6060	756	AGGTCCTGGGTTTAAGTGT	computGene-annotate; refseqGeneIntron-annotate
CU-6058	757	AGGGGGAAGTTCTATAGTC	refseqGeneIntron-annotate
CU-6057	758	AGGCTGTGATGCTCTCNTGAGCCCT	refseqGeneIntron-annotate
CU-6055	759	AGCCCCTCTCCGGCCCTTA	refseqGeneIntron-annotate
CU-6054	760	ACTACCACCTACCTCCC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6052	761	ACGCCCTTCCCCCCCTTCTTT	miRBASE-annotate; refseqGeneIntron-annotate
CU-6049	762	ACCCCACTCCTGGTGCAC	refseqGeneIntron-annotate
CU-6048	763	ACCACCTGATCCCTTCCC	refseqGeneIntron-annotate
CU-6047	764	ACAGCTAAGCACCCACCA	refseqGeneIntron-annotate
CU-6045	765	ACACATGTTTAACGGCC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6043	766	AATTAGGGACCTGTATG	refseqGeneIntron-annotate
CU-6042	767	AATGGCCCATTTGGGCAAACA	computGene-annotate; refseqGeneIntron-annotate
CU-6041	768	AAAGCGGCTGTGCAAACA	refseqGeneIntron-annotate
CU-6212	769	TCGACTCCTGGCTGGCTCGCCA	wgRNA-annotate
CU-6200	770	TCCCCGGCATCTCCACCAA	computGene-annotate
CU-6157	771	GCGGTGGATCACTCGGCTCGTGCGT	rnaGene-annotate
CU-6105	772	CCGGGTGTTGTAGA	mRNAall-annotate; exEID-annotate
CU-6235	773	TGTAGCGTGGCCGAGCGGT	rnaGene-annotate
CU-6234	774	TGGGGCGACCTCGGAGCAG	mitochondrion-annotate
CU-6230	775	TGGCGTCCTAAGCCAGGGATTGTGGGT	rnaGene-annotate
CU-6229	776	TGGCAGGGGAGATACCATGATTT	rnaGene-annotate
CU-6222	777	TCTGATCAGGGTGAGCATC	mitochondrion-annotate
CU-6220	778	TCGTAGGCACCATCCAT	computGene-annotate
CU-6165	779	GGGAAACGGGGCGCGGCTG	rnaGene-annotate
CU-6137	780	CTACTCCTGCTCGCATCTGCTATA	mitochondrion-annotate
CU-6135	781	CGGGTGGGTTTTTACCGG	computGene-annotate
CU-6120	782	CGAGGAATTCCCAGTAAG	rnaGene-annotate
CU-6115	783	CGAACGCACTTGCGGCCCC	rnaGene-annotate
CU-6093	784	CCCCGCGCGGGTTCGAATC	rnaGene-annotate
CU-6059	785	AGGGGTATGATTCCCGCTT	rnaGene-annotate

TABLE 4A-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6131	786	CGGGGCCACGCGCGCGTC	mRNA-annotate; rRNA-eliminate
CU-6032	787	TGGCGCTGCGGGATGAAC	rRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1153	788	CCCCCCACTGCTAAATTTGACTGGCTT	yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6182	789	TAAAGGTTCGTTTGTAAAA	computGene-annotate; refseqGeneExon-eliminate
CU-6033	790	CGGGGCCGAGGGAGCGA	rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6174	791	GGGTTAGGCCTCTTTT	tRNA-eliminate; rnaGene-annotate
CU-6141	792	CTGCGGAAGGATCATTA	rRNA-eliminate; rnaGene-annotate
CU-6101	793	CCCTACCCCCCCGG	rRNA-eliminate; refseqGeneIntron-annotate
CU-6034	794	CCCGCCGGGTCCGCCC	computGene-annotate; rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6035	795	CCCCGCGCCCTCTCTCTCTC	rRNA-eliminate; refseqGeneIntron-annotate
CU-6028	796	CAGGCCTCCCTGGAATC	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6029	797	AGTCCCACCCGGGGTACCA	computGene-annotate; refseqGeneExon-eliminate
CU-6243	798	TTGACACGCCCCAGTGCCCTGT	refseqGeneExon-eliminate
CU-6233	799	TGGGAGCGGGCGGGCGGTC	rRNA-eliminate; rnaGene-annotate
CU-6231	800	TGGCGTGGAGCCGGGCGT	rRNA-eliminate; refseqGeneIntron-annotate
CU-6228	801	TGGAGGTCCGTAGCGGT	rRNA-eliminate; mRNA-annotate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6223	802	TGAAGAAGGTCTCGAACA	computGene-annotate; refseqGeneExon-eliminate
CU-6221	803	TCTCGCCGGGGCTTCCA	computGene-annotate; refseqGeneExon-eliminate; rnaGene-annotate
CU-6217	804	TCGTAGCACCATCAATAA	computGene-annotate; refseqGeneExon-eliminate
CU-6208	805	TCCGGGTCCCCCCTCCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6207	806	TCCGGGGCTGCACGCGCGCT	rRNA-eliminate; rnaGene-annotate
CU-6205	807	TCCGGCCGTGTCGGT	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6203	808	TCCCTGTCCTCCAGGAGT	miRBASE-annotate; computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; wgRNA-annotate
CU-6201	809	TCCCCTCCTCGTCGCCA	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6199	810	TCCCAGGTAGTCTAGTGGT	refseqGeneExon-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6191	811	TATTCATTTATCCCCAGCCTAT	miRBASE-annotate; snoRNA-eliminate; refseqGeneIntron-annotate; wgRNA-annotate; rnaGene-annotate
CU-6190	812	TAGTTGTTATAACCCAA	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6186	813	TAGATCACCCCCTCCCC	mitochondrion-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6185	814	TACCGGCACCTGGCGCC	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6178	815	GTATAGGGGCGAAAGAC	rRNA-eliminate; mRNA-annotate; refseqGeneIntron-annotate; rnaGene-annotate

TABLE 4A-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6177	816	GTAGCTGGTTCCCTCCGAA	rRNA-eliminate; mRNA-annotate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6175	817	GGTAAGAAGCCCGGCTC	computGene-annotate; rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6173	818	GGGGGGGTTTAAAAAAAAA	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6169	819	GGGGCGCACTACCGGCC	refseqGeneExon-eliminate
CU-6168	820	GGGAGAGGCTGTCGCTGCG	computGene-annotate; refseqGeneExon-eliminate
CU-6164	821	GGCGGGTGAAGCGGCG	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6158	822	GCGGTTCCGGCGGCGTC	rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6155	823	GCGGGGCGCCTAGGCCTGGTTTGT	refseqGeneExon-eliminate
CU-6153	824	GCGGCGGTCGGCGGGCGGCGGG	rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6149	825	GAGGGGGGGGGTGGGGGGGGA	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6144	826	CTGTCGGCCACCATCAT	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6140	827	CTGCAACTCGACCCCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6139	828	CTCCTCTCCCCGCCCGCCG	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6138	829	CTCAAAGATTAAGCCATGCATGTCTA	rRNA-eliminate; rnaGene-annotate
CU-6136	830	CTACGCCGCGACGAG	computGene-annotate; rRNA-eliminate
CU-6134	831	CGGGTGACGGGGAATCAGGGTT	rRNA-eliminate; rnaGene-annotate
CU-6127	832	CGGGCAGCTTCCGGGA	computGene-annotate; rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6126	833	CGGGAGGCCCGGGTCCTG	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6124	834	CGGCCCCGCATCCTCCC	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6122	835	CGCGGGTAAACGGCGGGAGTAACTAT	mRNAall-annotate; rRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6121	836	CGCCCCCCGTTCCCCCCTCC	rRNA-eliminate
CU-6119	837	CGAGCGGAAACACCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6114	838	CGAACCCGGCACCGC	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6111	839	CCTCGGGCCGATCGCAC	rRNA-eliminate; rnaGene-annotate
CU-6110	840	CCTATATATCTTACCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6109	841	CCGTGGCGGCGACGACC	computGene-annotate; rRNA-eliminate; refseqGeneExon-eliminate
CU-6106	842	CCGGGTTCCGGCACCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6104	843	CCGCGAGGGGGGCCCG	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate

TABLE 4A-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6103	844	CCGCCTCACGGGACCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6102	845	CCGCCCGTCCCCGCCCCTTG	rRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6100	846	CCCGGGGCCGCGGTTCCG	computGene-annotate; rRNA-eliminate; refseqGeneIntron-annotate
CU-6098	847	CCCGAGCCGCCTGGAT	computGene-annotate; rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6097	848	CCCGACGGCCGAACT	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6095	849	CCCCGGGGAGCCCGGCGGG	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6092	850	CCCCCTCGCGGCCCTCCCC	rRNA-eliminate; refseqGeneIntron-annotate
CU-6091	851	CCCCCCGTGGCGGCGAC	rRNA-eliminate; refseqGeneIntron-annotate
CU-6083	852	CCACCCAGGGCACGCCA	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6077	853	CACGGGTGACGGGGAA	computGene-annotate; rnaGene-annotate; refseqGeneIntron-annotate; rRNA-eliminate; refseqGeneExon-eliminate; piRNA-annotate
CU-6073	854	ATGGGGAGGAAAAAAAAAAAAA	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6068	855	ATCCCACCGCTGCCCCCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6065	856	ATCACGTCGGTCACCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6053	857	ACGGGAAACCTCACCCGGCCCGG	rRNA-eliminate; piRNA-annotate; rnaGene-annotate
CU-6046	858	ACAGAGGCTTACGACCCCTTATTT	mitochondrion-annotate; tRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6040	859	AAAAAGGCATAATTAAACTT	mitochondrion-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate

TABLE 4B

List of short-RNA consensus with maximum 1 mismatch to the human genome.
Table includes information on genomic frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
860	TGGCTCAGTTCAGCAGGAACAGT	0	0	1	0	0	0	1.05	0
861	GTGGGGGAGAGGCTGTCGA	0	0	0	1	0	0	0	0.81
862	CGGGGCAGCTCAGTACAGGATT	0	0	1	0	0	0	1.05	0
863	AATTGCACGGTATCCATCTGTAT	0	0	1	0	0	0	1.05	0
864	CGGGGGAGCGCCGCGTA	2	0	0	0	2.04	0	0	0
865	TCGATCCCGGGTTTCGGCACCA	0	0	1	0	0	0	1.05	0

TABLE 4B-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
866	ATCGTATCCCACTTCTGACACCA	0	0	0	1	0	0	0	0.81
867	ATCCTGCCGACTACGCCA	13	15	13	6	13.27	13.76	13.68	4.88
868	TCGAATCCCACTCCTGACACCA	1	2	7	7	1.02	1.83	7.37	5.69
869	ATCCCATCCTCGTCGCCA	0	0	10	3	0	0	10.53	2.44
870	TCGATTCCCCGACGGGGAGCCA	1	1	1	9	1.02	0.92	1.05	7.32
871	ATCCGGGTGCCCCCTCCA	2	4	0	1	2.04	3.67	0	0.81
872	TCCCGGGCGGCGCACCA	2	2	1	0	2.04	1.83	1.05	0
873	ATCCCACCAGAGTCGCCA	0	0	2	3	0	0	2.11	2.44
874	TCAAATCACGTCGGGGTCACCA	0	1	2	0	0	0.92	2.11	0
875	TGTCAGTTTGTTAATTGACCCAA	0	0	1	1	0	0	1.05	0.81
876	TCGATCCCCGTACGGGCCACCA	0	0	1	1	0	0	1.05	0.81
877	TCGAGCCTCACCTGGAGCACCA	0	0	2	0	0	0	2.11	0
878	TCCGGCTCGAAGGACCA	0	0	2	0	0	0	2.11	0
879	GGCAATACGAGCACCCTG	2	0	0	0	2.04	0	0	0
880	CCGGGGCGTCTCGTAC	2	0	0	0	2.04	0	0	0
881	AGCGGCTGTGCACAAA	0	0	0	2	0	0	0	1.63
882	TGTCAGTTTGTTTAATCCAA	0	0	0	1	0	0	0	0.81
883	TGTCAGTTTGTTATTACCAA	0	0	0	1	0	0	0	0.81
884	TGTCAGGCACCATCAATAA	0	0	0	1	0	0	0	0.81
885	TGATCTTGACACTTAAAGCC	0	0	0	1	0	0	0	0.81
886	TCGTAGGCACCATCAAT	0	0	0	1	0	0	0	0.81
887	TCGACTCCCGGTATGGGAACCA	0	0	0	1	0	0	0	0.81
888	TAGGGAGGTTATGATTAACTTTT	0	0	0	1	0	0	0	0.81
889	TAAAGTGCTTAGTGCAGGTA	0	0	0	1	0	0	0	0.81
890	GTTTATGTTGCTTACCTCC	0	0	1	0	0	0	1.05	0
891	GTAGATAAAATATTGGCG	1	0	0	0	1.02	0	0	0
892	GGCGGGGACGACGTCAG	0	0	0	1	0	0	0	0.81
893	GGCGGCGTCGCGGCGGGTC	0	1	0	0	0	0.92	0	0
894	GGAGGGGGTGAACAAAAAGAAAAA	0	0	0	1	0	0	0	0.81

TABLE 4B-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
895	GCTAAACCTAGCCCCAAACC CACTCCACA	0	0	0	1	0	0	0	0.81
896	CTGGATAGCGCACTTCGTT	0	0	0	1	0	0	0	0.81
897	CGGGCGAGGGGCGGACGTT CG	0	0	1	0	0	0	1.05	0
898	CGGACCTATACCGGA	1	0	0	0	1.02	0	0	0
899	CCCCGGGTTCAATCCCCGG CACCTCCACCA	0	0	1	0	0	0	1.05	0
900	CCCCCCACAACCGCGAA	0	1	0	0	0	0.92	0	0
901	CCCAGCATCTCCTGTGTTTA	0	1	0	0	0	0.92	0	0
902	CCCACGTTGGGACGCCA	1	0	0	0	1.02	0	0	0
903	ATCACGTCCGTGCCTCCA	0	1	0	0	0	0.92	0	0
904	ATAGCAATGTCAGCAGTACCT	0	0	1	0	0	0	1.05	0
905	ACCCTGCTCGCTGCGCCA	9	17	4	7	9.18	15.6	4.21	5.69
906	TCCCACCCAGGGACGCCA	8	2	1	0	8.16	1.83	1.05	0
907	TCGTAGGCACATCAATA	0	0	0	4	0	0	0	3.25
908	CCCCCACAACCGCGTA	0	4	0	0	0	3.67	0	0
909	ACCCCGTCCGTGCCTCCA	2	1	1	0	2.04	0.92	1.05	0
910	AAAAAAGACACCCCCCACA	0	0	0	3	0	0	0	2.44
911	TGTCAGTTTGTTAACCCAA	0	0	0	2	0	0	0	1.63
912	TCCCTGTGGTCTAGTGGTTA GG	0	0	1	1	0	0	1.05	0.81
913	GGGGGGGTAAAAAAA	0	0	0	1	0	0	0	0.81
914	GGGGGGGGAAAAAAAA	0	0	0	1	0	0	0	0.81
915	CGGGCCCGGGTCTTCCC	1	1	0	0	1.02	0.92	0	0
916	CCGCCCCCCGTTCCCCCCA	0	2	0	0	0	1.83	0	0
917	ACCCCCGGCTCCTCCACCA	0	1	0	1	0	0.92	0	0.81
918	TTTGGTGGAAATTTTTTGA	0	0	0	1	0	0	0	0.81
919	TGTCAGTTTGTTATACCAA	0	0	0	1	0	0	0	0.81
920	TGTCAGTTTGTAATTATCCC AA	0	0	0	1	0	0	0	0.81
921	TGTCAATTTTTAACCCAA	0	0	0	1	0	0	0	0.81
922	TGCTAGGGTAAAAAAAAAA	0	0	0	1	0	0	0	0.81
923	TGCAACTCCAAATAAAAGTA CCA	0	0	0	1	0	0	0	0.81
924	TGAGGTAACGGGGAATTA	0	0	0	1	0	0	0	0.81
925	TCCTCGGCATCTCCACCA	0	0	1	0	0	0	1.05	0

TABLE 4B-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
926	TCATATGAAGTCACCCTAGC CATC	0	0	1	0	0	0	1.05	0
927	TCAGTTTGTTTATTAACCCAA	0	0	0	1	0	0	0	0.81
928	TCAGCGTGTCTTTGCCCT	1	0	0	0	1.02	0	0	0
929	TCACTGGTGGTCTAGTGGT	0	1	0	0	0	0.92	0	0
930	TCACAATGCTGCCACCA	1	0	0	0	1.02	0	0	0
931	TAGTTGTTAATTAACCCAA	0	0	0	1	0	0	0	0.81
932	TAGTCCTCATCGCCCTCC	0	1	0	0	0	0.92	0	0
933	TAAAGTGCTTATAGTGCGGG TAA	0	0	0	1	0	0	0	0.81
934	GTCCCACCAGAGTCGCCA	0	0	1	0	0	0	1.05	0
935	GGGGGAGGGGCCAAAAAAA	0	0	0	1	0	0	0	0.81
936	GGGACGCCGCGGTGTCG	1	0	0	0	1.02	0	0	0
937	GGGAATACCGGGTGCTTTA GGCTT	0	1	0	0	0	0.92	0	0
938	GGAAGAAGGTGGTGGTATA	0	0	0	1	0	0	0	0.81
939	GCGGTGAAATGCGTA	1	0	0	0	1.02	0	0	0
940	GCGGGGAAGGTGGCAAA	0	0	0	1	0	0	0	0.81
941	GCGACGACCTCGCGCCCAC CTGGTCA	0	1	0	0	0	0.92	0	0
942	GCCACCCGATACTGCTGT	0	1	0	0	0	0.92	0	0
943	GATGTATGCTTTGTTTCTGTT	0	0	1	0	0	0	1.05	0
944	GAGGGGGATTTAGAAAAAAA	0	0	0	1	0	0	0	0.81
945	GAAGGAAAGTTCTATAGT	0	0	0	1	0	0	0	0.81
946	GAAGCGGCTCTCTTATTT	0	0	0	1	0	0	0	0.81
947	GAACGAGACTCTGGCATGC TGA	0	0	1	0	0	0	1.05	0
948	CTGGTAGGCCCATCAAT	0	0	0	1	0	0	0	0.81
949	CGGGGCCGATCGCGCGC	0	1	0	0	0	0.92	0	0
950	CGGCCCCGGGTTCCTCCC	1	0	0	0	1.02	0	0	0
951	CGAGCCCGGTTAGTA	1	0	0	0	1.02	0	0	0
952	CGACTCTTAGCGGTGGA	0	0	1	0	0	0	1.05	0
953	CGAATCCCACTTCTGACACCA	0	0	0	1	0	0	0	0.81
954	CGAAAGGGAATCGGGTC	1	0	0	0	1.02	0	0	0
955	CCTTAGGTCGCTGGTAAA	0	0	1	0	0	0	1.05	0
956	CCGTGCGAGAATACCA	0	1	0	0	0	0.92	0	0
957	CCGGTCTCTCAAGCGGCC	1	0	0	0	1.02	0	0	0

TABLE 4B-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
958	CCCGGCCCTCGCGCGTCC	0	1	0	0	0	0.92	0	0
959	CCCCGGCATTTCCACCA	0	0	1	0	0	0	1.05	0
960	CCCCCCCGGCTCCTCCACCA	0	0	0	1	0	0	0	0.81
961	CCCCCCACAACCGCTA	0	1	0	0	0	0.92	0	0
962	CCCAAGTATTGACTCACCC	0	1	0	0	0	0.92	0	0
963	CCAGTAAGCGCGAGTC	1	0	0	0	1.02	0	0	0
964	CCAAAGAAAGCACGTAGAG	0	0	0	1	0	0	0	0.81
965	CATGTTTAACGGCCGCGGT	0	0	1	0	0	0	1.05	0
966	CAGTTTGTAATTAACCCAA	0	0	0	1	0	0	0	0.81
967	CAGGAACGGCGCACCA	0	0	1	0	0	0	1.05	0
968	CAGAACCCTCTAAATCCCC	0	0	1	0	0	0	1.05	0
969	CACCCGGCTGTGTGCACATGTGT	1	0	0	0	1.02	0	0	0
970	CAATTGGACCAATCTATC	0	0	1	0	0	0	1.05	0
971	ATTCCTGTACTGCGATA	0	0	0	1	0	0	0	0.81
972	ATCCCTGCGGCGTCTCCA	0	0	0	1	0	0	0	0.81
973	ATCCCACCGCTGCCATCA	0	1	0	0	0	0.92	0	0
974	AGTCAATAGAAGCCGGCGTA	0	0	1	0	0	0	1.05	0
975	AGGTTCGTTTGTAAAAA	0	0	0	1	0	0	0	0.81
976	AGGTCCTGGGTTTAAGTGT	0	0	0	1	0	0	0	0.81
977	AGGGGGAAGTTCTATAGTC	0	0	0	1	0	0	0	0.81
978	AGGCTGTGATGCTCTCNTGAGCCCT	0	0	1	0	0	0	1.05	0
979	AGCCCCTCTCCGGCCCTTA	0	1	0	0	0	0.92	0	0
980	ACTACCACCTACCTCCC	1	0	0	0	1.02	0	0	0
981	ACGCCCTTCCCCCCCTTCTTT	0	0	0	1	0	0	0	0.81
982	ACCCCACTCCTGGTGCAC	1	0	0	0	1.02	0	0	0
983	ACCACCTGATCCCTTCCC	1	0	0	0	1.02	0	0	0
984	ACAGCTAAGCACCCACCA	0	0	1	0	0	0	1.05	0
985	ACACATGTTTAACGGCC	1	0	0	0	1.02	0	0	0
986	AATTAGGGACCTGTATG	0	0	1	0	0	0	1.05	0
987	AATGGCCCATTTGGGCAAACA	0	0	0	1	0	0	0	0.81
988	AAAGCGGCTGTGCAAACA	0	0	0	1	0	0	0	0.81
989	TCGACTCCTGGCTGGCTCGCCA	0	2	2	1	0	1.83	2.11	0.81
990	TCCCCGGCATCTCCACCAA	0	1	2	0	0	0.92	2.11	0

TABLE 4B-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
991	GCGGTGGATCACTCGGCTC GTGCGT	0	0	0	3	0	0	0	2.44
992	CCGGGTGTTGTAGA	2	0	0	0	2.04	0	0	0
993	TGTAGCGTGGCCGAGCGGT	0	1	0	0	0	0.92	0	0
994	TGGGGCGACCTCGGAGCAG	0	0	1	0	0	0	1.05	0
995	TGGCGTCCTAAGCCAGGGA TTGTGGGT	0	0	0	1	0	0	0	0.81
996	TGGCAGGGGAGATACCATG ATTT	0	0	1	0	0	0	1.05	0
997	TCTGATCAGGGTGAGCATC	0	1	0	0	0	0.92	0	0
998	TCGTAGGCACCATCCAT	0	0	0	1	0	0	0	0.81
999	GGGAAACGGGGCGCGGCTG	0	1	0	0	0	0.92	0	0
1000	CTACTCCTGCTCGCATCTGC TATA	0	0	1	0	0	0	1.05	0
1001	CGGGTGGGTTTTTACCGG	1	0	0	0	1.02	0	0	0
1002	CGAGGAATTCCCAGTAAG	0	0	1	0	0	0	1.05	0
1003	CGAACGCACTTGCGGCCCC	1	0	0	0	1.02	0	0	0
1004	CCCCGCGCGGGTTCGAATC	1	0	0	0	1.02	0	0	0
1005	AGGGGTATGATTCCCGCTT	0	0	0	1	0	0	0	0.81
1006	CGGGGCCACGCGCGCGTC	3	6	0	0	3.06	5.5	0	0
1007	TGGCGCTGCGGGATGAAC	0	3	1	0	0	2.75	1.05	0
1008	CCCCCCACTGCTAAATTTGA CTGGCTT	0	0	2	2	0	0	2.11	1.63
1009	TAAAGGTTCGTTTGTAAAA	0	0	0	3	0	0	0	2.44
1010	CGGGGCCGAGGGAGCGA	1	2	0	0	1.02	1.83	0	0
1011	GGGTTAGGCCTCTTTT	0	1	1	0	0	0.92	1.05	0
1012	CTGCGGAAGGATCATTA	1	0	1	0	1.02	0	1.05	0
1013	CCCTACCCCCCCGG	0	2	0	0	0	1.83	0	0
1014	CCCGCCGGGTCCGCCC	2	0	0	0	2.04	0	0	0
1015	CCCCGCGCCCTCTCTCTCTC	0	2	0	0	0	1.83	0	0
1016	CAGGCCTCCCTGGAATC	2	0	0	0	2.04	0	0	0
1017	AGTCCCACCCGGGGTACCA	0	0	0	2	0	0	0	1.63
1018	TTGACACGCCCCAGTGCCC TGT	1	0	0	0	1.02	0	0	0
1019	TGGGAGCGGGCGGGCGGTC	0	1	0	0	0	0.92	0	0
1020	TGGCGTGGAGCCGGGCGT	0	1	0	0	0	0.92	0	0
1021	TGGAGGTCCGTAGCGGT	1	0	0	0	1.02	0	0	0

TABLE 4B-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts				Frequencies			
		Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1022	TGAAGAAGGTCTCGAACA	0	0	0	1	0	0	0	0.81
1023	TCTCGCCGGGGCTTCCA	0	1	0	0	0	0.92	0	0
1024	TCGTAGCACCATCAATAA	0	0	0	1	0	0	0	0.81
1025	TCCGGGTCCCCCCTCCA	0	1	0	0	0	0.92	0	0
1026	TCCGGGGCTGCACGCGCGCT	0	1	0	0	0	0.92	0	0
1027	TCCGGCCGTGTCGGT	1	0	0	0	1.02	0	0	0
1028	TCCCTGTCCTCCAGGAGT	0	0	0	1	0	0	0	0.81
1029	TCCCCTCCTCGTCGCCA	1	0	0	0	1.02	0	0	0
1030	TCCCAGGTAGTCTAGTGGT	1	0	0	0	1.02	0	0	0
1031	TATTCATTTATCCCCAGCCTAT	0	1	0	0	0	0.92	0	0
1032	TAGTTGTTATAACCCAA	0	0	0	1	0	0	0	0.81
1033	TAGATCACCCCCTCCCC	0	1	0	0	0	0.92	0	0
1034	TACCGGCACCTGGCGCC	1	0	0	0	1.02	0	0	0
1035	GTATAGGGGCGAAAGAC	0	0	1	0	0	0	1.05	0
1036	GTAGCTGGTTCCCTCCGAA	0	0	0	1	0	0	0	0.81
1037	GGTAAGAAGCCCGGCTC	0	0	1	0	0	0	1.05	0
1038	GGGGGGGTTTAAAAAAAAA	0	0	0	1	0	0	0	0.81
1039	GGGGCGCACTACCGGCC	1	0	0	0	1.02	0	0	0
1040	GGGAGAGGCTGTCGCTGCG	0	0	0	1	0	0	0	0.81
1041	GGCGGGTGAAGCGGCG	0	1	0	0	0	0.92	0	0
1042	GCGGTTCCGGCGGCGTC	0	1	0	0	0	0.92	0	0
1043	GCGGGGCGCCTAGGCCTGGTTTGT	1	0	0	0	1.02	0	0	0
1044	GCGGCGGTCGGCGGGCGGCGGG	1	0	0	0	1.02	0	0	0
1045	GAGGGGGGGGGTGGGGGGGA	0	0	0	1	0	0	0	0.81
1046	CTGTCGGCCACCATCAT	0	0	0	1	0	0	0	0.81
1047	CTGCAACTCGACCCCA	0	1	0	0	0	0.92	0	0
1048	CTCCTCTCCCCGCCCGCCG	0	0	1	0	0	0	1.05	0
1049	CTCAAAGATTAAGCCATGCATGTCTA	0	0	1	0	0	0	1.05	0
1050	CTACGCCGCGACGAG	1	0	0	0	1.02	0	0	0
1051	CGGGTGACGGGGAATCAGGGTT	1	0	0	0	1.02	0	0	0
1052	CGGGCAGCTTCCGGGA	0	0	0	1	0	0	0	0.81
1053	CGGGAGGCCCGGGTCCTG	1	0	0	0	1.02	0	0	0

TABLE 4B-continued

List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic frequencies.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Frequencies Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1054	CGGCCCCGCATCCTCCC	1	0	0	0	1.02	0	0	0
1055	CGCGGGTAAACGGCGGGAG TAACTAT	0	0	1	0	0	0	1.05	0
1056	CGCCCCCCGTTCCCCCCTCC	0	1	0	0	0	0.92	0	0
1057	CGAGCGGAAACACCA	1	0	0	0	1.02	0	0	0
1058	CGAACCCGGCACCGC	1	0	0	01.02	0	0	0	
1059	CCTCGGGCCGATCGCAC	0	0	1	0	0	0	1.05	0
1060	CCTATATATCTTACCA	0	1	0	0	0	0.92	0	0
1061	CCGTGGCGGCGACGACC	0	1	0	0	0	0.92	0	0
1062	CCGGGTTCCGGCACCA	1	0	0	01.02	0	0	0	
1063	CCGCGAGGGGGGCCCG	1	0	0	01.02	0	0	0	
1064	CCGCCTCACGGGACCA	1	0	0	01.02	0	0	0	
1065	CCGCCCGTCCCCGCCCCTTG	0	1	0	0	0	0.92	0	0
1066	CCCGGGGCCGCGGTTCCG	1	0	0	01.02	0	0	0	
1067	CCCGAGCCGCCTGGAT	0	1	0	0	0	0.92	0	0
1068	CCCGACGGCCGAACT	0	1	0	0	0	0.92	0	0
1069	CCCCGGGGAGCCCGGCGGG	1	0	0	01.02	0	0	0	
1070	CCCCCTCGCGGCCCTCCCC	0	1	0	0	0	0.92	0	0
1071	CCCCCCGTGGCGGCGAC	0	1	0	0	0	0.92	0	0
1072	CCACCCAGGGCACGCCA	1	0	0	01.02	0	0	0	
1073	CACGGGTGACGGGGAA	1	0	0	01.02	0	0	0	
1074	ATGGGGAGGAAAAAAAAAAA AAA	0	0	0	1	0	0	0	0.81
1075	ATCCCACCGCTGCCCCCA	0	0	0	1	0	0	0	0.81
1076	ATCACGTCGGTCACCA	0	0	0	1	0	0	0	0.81
1077	ACGGGAAACCTCACCCGGC CCGG	0	0	1	0	0	0	1.05	0
1078	ACAGAGGCTTACGACCCCTT ATTT	0	0	1	0	0	0	1.05	0
1079	AAAAAGGCATAATTAAACTT	0	0	1	0	0	0	1.05	0

[0230] Interestingly, several of these non-annotated sequences (i.e. CU-5004, CU-5021, CU-6030, CU-6069) were cloned multiple times and showed differential expression across libraries, suggesting they may represent short-RNAs with characteristics distinct from those currently recognized in "classic" miRNAs.

[0231] In conclusion, the generation of short-RNA libraries from normal and neoplastic B cells led to the identification of 401 bona fide miRNAs as well as other short-RNA species of unknown function.

[0232] Abundance and Evolutionary Conservation

[0233] Previously reported miRNAs appeared to be more abundant than newly discovered miRNAs (FIG. **13**A). Approximately 21% of previously reported miRNAs appeared in the libraries as single occurrences compared to 57% of the newly discovered miRNAs. Approximately 42% of known miRNAs were expressed at all stages of mature B cell development, while newly identified miRNAs showed a more distinct stage-specificity (FIG. **13**B), consistent with the notion that presently known miRNAs are mostly representative of ubiquitously expressed miRNAs.

[0234] Regardless of their novelty, stage-specific miRNAs were observed with frequencies (defined as the fraction of the total pool of cloned miRNAs represented by a given miRNA) ranging between 0.03 and 0.6% of their respective libraries. The most abundant GC-associated miRNAs showed restricted expression in GC B cells and, if unaffected by transformation, in Ramos cells. However, in naïve and memory B cell libraries only the rarest miRNAs were truly exclusive in their expression and most of the non-GC-specific miRNAs were expressed in both naïve and memory cells albeit at different levels.

[0235] In order to investigate the presence of orthologous miRNA in other mammalian species, we relied on UCSC-provided Blastz pairwise alignments between human and target species and investigated conservation using two complementary methods, detailed in Supplementary Methods. The analysis was performed on the complete set of miRNAs deposited in the miRBase database and on the miRNAs (known and new) represented in the B cell libraries. Alignments of the human mature miRNA to its target species were required to have either perfect conservation of the entire mature miRNA sequence (FIG. **13**C) or conservation of seeds composed of seven bases starting from the second position of the human mature sequence followed by conservation of 3 bases starting from the 12th, 13th or 14th position as suggested by[21]. The majority of miRBase miRNAs showed conservation across mammalian genomes, from primates to rodents. Conservation frequency mimicked known phylogenetic distances to human, with the highest conservation in chimp and lowest in rat. The conservation frequencies of known and new miRNAs in B cells were similar in chimp (*Pan troglodytes*) and monkey (*Macacus rhesus*), especially when conservation requirements were restricted to the seed region of miRNAs. However, conservation frequencies in dog, mouse and rat were significantly divergent, with known miRNAs more likely to exhibit conservation than new candidate miRNAs (FIG. **13**C). In summary, new miRNAs expressed at specific stages of B cell differentiation were less abundant and showed a lower level of conservation across species.

[0236] Validation of Newly Discovered miRNA

[0237] The newly identified miRNAs were investigated by Northern Blot analysis in order to validate their existence in vivo. Northern Blot analyses were performed using B cell lines and cells isolated from tonsil tissue obtained from multiple donors. Among 23 candidate miRNAs that have been cloned in any of the four libraries with 1-100 occurrences, 13 were detectable by Northern Blot (FIG. **14**A). Detection of several miRNAs represented by low number of occurrences in the libraries was successful only upon enrichment for the short-RNA fraction, suggesting that low-abundance miRNA could be below the level of detection by Northern blotting. Overall, approximately 55% of the newly cloned and computationally validated miRNAs were detectable by Northern Blot.

[0238] Transcriptional and Post-Transcriptional Regulation

[0239] Most newly identified miRNAs showed a long abundant transcript (>150 nt) that might correspond to the primary miRNA transcript and a second transcript (~60-80 nt) consistent with the precursor miRNA. As shown in FIG. **14**B (top panel), the precursor miRNA and the correspondent mature miRNA may be produced in some cell type but not in others, suggesting transcriptional regulation. Conversely in some cases the miRNA precursor species may be present in cell types that lack expression of the mature form (FIG. **14**B, bottom panel) suggesting the existence of a second level of regulation targeting the Dicer-dependent pre-miRNA processing[22-24].

[0240] Distinct miRNA Signatures in Normal B Cells

[0241] miRNA representation in the four constructed libraries suggested differential expression of miRNAs during B cell differentiation and GC transit (FIG. **13**B). The correlation among miRNA profiles from normal B cells and Ramos cell line was further investigated by hierarchical clustering using miRNA frequencies (defined as the fraction of the total pool of cloned miRNAs represented by a given miRNA in a library) obtained from the cloning data (FIG. **15**A). Naïve and memory B cells appeared similar, sharing a large fraction of the most abundant miRNA. Conversely, centroblasts and Ramos cells showed more distinct miRNA profiles with a sizeable fraction of abundant miRNA being specifically expressed in each library.

[0242] We also performed miRNA expression profiling of centroblasts, naïve and memory B cells (six donors/each) using a microarray representative of 723 known human miRNAs (miRBase v.10.1). Each B cell population showed a distinct miRNA expression profile. Consistent with the cloning data (FIGS. **13**B and **15**A) GC B cells appeared to be quite distinct from naïve and memory B cells which instead shared expression of a large fraction of miRNAs (FIG. **15**A). The main differences between naïve and memory B cells resided in the level of miRNA expression. The expression of several miRNAs was tested by qRT-PCR analysis which confirmed that the microarray data were accurate for the relative quantification.

[0243] miRNA Signatures can Identify Subtypes of B Cell Malignancies

[0244] The miRNA library generated from Ramos BL cell line demonstrated that tumors can display specific miRNA expression signatures. To investigate whether these signatures can identify subtypes of B cell malignancies, miRNA expression profiling was performed using the same microarray platform on a panel of GC-derived malignancies including BL (8), DLBCL (16) and FL (10). Unsupervised clustering analysis of the tumor miRNA profiles was able to identify three major clusters enriched for samples belonging to each

malignant phenotype (FIG. **16**). These tumors can be discriminated as well by gene expression profiling however it requires the use of a higher number of features. These results show that tumors deriving from the same stage of B cell differentiation acquire distinct miRNA expression profiles as consequence of malignant transformation.

DISCUSSION

[0245] The combination of cloning procedures and computational tools led us to the identification of a large fraction of known as well as newly discovered miRNA expressed during B cell differentiation. These findings have general implications for the understanding of the total miRNA content of the human genome as well as for future studies on the role of miRNAs in B cell differentiation, function and lymphomagenesis.

[0246] The discovery of >250 new miRNAs and of their tissue-specific pattern of expression are in sharp contrast with previous reports that suggested, based on the discovery of only 12 new human miRNA[7] from an analysis of 26 different organ systems and cell types, that most miRNAs are ubiquitously expressed and that most miRNAs have already been identified[7]. These discordant results and conclusions may be partially due to the significantly higher number of clones per library sequenced in this study (3500 versus 1300 on average in[7]) which allowed the detection of low abundant miRNA species and to the criteria applied in the miRNA prediction (see Supplementary Methods).

[0247] The relatively lower degree of evolutionary conservation of tissue-specifc miRNAs (FIG. **13**C) may have prevented the cross-species identification of miRNAs using murine libraries[18,25]. Consistent with these observations, a recent report on short-RNAs in mouse embryonic stem cells discovered new Dicer-dependent miRNAs characterized by both low abundance and low level of conservation[26]. Thus, a large number of low-abundance, recently evolved, tissue-specific miRNAs remain to be discovered.

[0248] Two categories of short-RNAs were identified that could not be annotated as bona fide miRNAs. The first category is represented by those short-RNAs that could not be accurately mapped to the genome. Considering that a fraction of these RNAs were cloned multiple times and showed a stage-specific behavior, such short-RNAs do actually exist and that the lack of a match to the human genome may be due to polymorphisms, editing and other post-transcriptional modifications or to an incomplete/inaccurate sequencing of the corresponding genomic regions. The second category is represented by short-RNAs for which classic pre-miRNA structures could not be identified in the genome and no similarity to other non-coding RNA was found in the available databases. These short-RNAs may either be miRNA for which RNA secondary structure prediction algorithms failed to predict the correct hairpin structure or may represent new miRNA species of presently unknown mechanism of generation or other not yet described types of short-RNAs.

[0249] The stage specific expression of various miRNAs, especially in GC B cells, suggests highly specialized regulatory functions in B cell biology. The role of miRNAs that show cell type-specific functions in lymphocytes has just begun to be elucidated[8-10,27]. The miRNAs specifically associated to GC or non-GC B cells by either cloning or miRNA expression profiling (FIG. **15**) have not been previously reported in B cell differentiation with the exception of miR-150[10]. The miR-17-92 cluster, previously reported as a potential oncogene[11], was found over-expressed in Ramos cell line compared to GC B cells possibly as a consequence of the transformation process.

[0250] Specificity in mature miRNA expression may be regulated at the transcriptional as well as at the post-transcriptional, i.e. pre-miRNA processing, level. Pre-miRNA accumulation in absence of a mature miRNA can occur in a cell type-restricted manner, suggesting the presence of a regulation mechanism at the pre-miRNA processing step. Both regulatory mechanisms may act during normal differentiation and may also be dysregulated during transformation as a consequence of genetic or epigenetic alterations[22-24]. The expanded B cell miRNome described here can be used to identify specific differences in miRNA expression in normal versus lymphoma cells that can guide searches for these tumor alterations.

[0251] miRNA expression profile differences between GC and non-GC B cells resembled those observed by expression profiling of coding genes[28], consistent with the previous observation that miRNA profiling may be equally or more informative in discriminating cell phenotypes[29]. miRNA expression profiling, especially if including new B-cell specific miRNAs, may be useful in the differential diagnosis of lymphoid malignancies.

[0252] Materials and Methods

[0253] Generation of Short-RNA Libraries

[0254] Purification of naïve, memory and GC B cells was performed as previously reported[28] using magnetic cell sorting of mononucleated cells obtained from human tonsils. Total RNA was purified using the Trizol Reagent (Invitrogen) following the manufacturer's indications. The short-RNA libraries were generated using an established protocol described in detail in[30]. Briefly, total RNA was separated on 15% polyacrylamide gel and the fragment corresponding to 18-28 nucleotides length was excised. The purified small RNAs were linked to adaptor oligonucleotides and gel purified. Upon adaptor ligation, RNA was reverse transcribed and cDNA was PCR amplified and cloned into pCR2.1-TOPO vector (Invitrogen). Sequencing was performed on colony PCR amplicons.

[0255] Computational Identification of Mature and Precursor miRNAs

[0256] The bioinformatics miRNA analysis pipeline (FIG. **18**) includes: (a) identification of short-RNAs from each library, (b) identification of exact and partial matches of the short-RNA sequences to the human genome, (c) testing each short-RNA genomic region for compatibility with hairpin secondary structures, (d) clustering genomic regions to predict mature miRNAs, (e) annotating and filtering short-RNAs and miRNAs candidates, (f) estimation of predicted miRNA frequencies in the libraries and (g) clustering short-RNAs that do not support miRNA candidates. The details are reported in the Supplementary Methods.

[0257] Orthology Analysis

[0258] The identification of putative orthologous sequences of known and predicted precursor and mature human miRNAs in chimp (panTro2), monkey (rheMac2), dog (canFam2) mouse (mm8) and rat (m4) was performed using UCSC-provided Blastz[31] pairwise alignments between human and target species. The details are reported in the Supplementary Methods.

[0259] miRNA Expression Profiling

[0260] The miRNA expression profiles were generated using the Human miRNA Microarray kit (Agilent Technolo-

gies) that allows detection of 723 known human (miRBase v.10.1) and 76 human viral miRNAs following the manufacturer's indications. Analysis of raw data was performed using the Feature Extraction Software 9.5.3.1 (Agilent Technologies). The dendrograms (FIG. **15**) were generated using a hierarchical clustering algorithm based on the average-linkage method[32,33] and Spearman's correlation as provided by the geWorkbench platform (http://www.geworkbench.org).

[0261] Northern Blot

[0262] Total RNA and small RNA fractions were purified using the Trizol Reagent (Invitrogen) and the PureLink miRNA Isolation Kit (Invitrogen), respectively, following the manufacturer's indications. Electrophoresis was performed on 15% denaturing polyacrylamide gel and then RNA was transferred on Duralon UV membrane (Stratagene) using a semidry transfer apparatus. Pre-hybridization and hybridization were performed in 5×SSC, 20 mM Na_2HPO_4 pH 7.2, 7% SDS, 3×Denhardt's Solution. Oligonucleotide probes were [γ-^{32}P]-ATP labeled by polynucleotide kinase (Fermentas). The list of oligonucleotides is reported in Table 5.

[0263] After over-night hybridization, membranes were washed at the same temperature in 3×SSC, 25 mM NaH_2PO_4 pH 7.5, 5% SDS, 10×Denhardt's Solution for 15-20' and in 1×SSC, 1% SDS for 5'. Images were obtained by exposure to phosphoimager cassette and acquisition by Storm 840 Phosphoimager (Molecular Dynamics) and by film exposure for approximately 2 weeks.

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TABLE 5

Listing of Oligonucleotide Probe Sequences

ID	mature miRNA sequence (5'-3')	SEQ ID NO:	Probe sequence (5'-3')	SEQ ID NO:
CU-1303	ATCCCACTTCTGAC ACCA	237	TGGTGTCAGAAGTGGGAT	1080
CU-1403	GCATTGGTGGTTCA GTGGTAGA	391	TCTACCACTGAACCACCAATGC	1081
CU-1253	GTGAAGCGTTCCAT ATTTTT	281	AAAAATATGGAACGCTTCAC	1082
CU-1513	GCGGGTGATGCGA ACTGGAGTCTGAGC	381	GCTCAGACTCCAGTTCGCATCAC CCGC	1083
CU-1173	ATCCCACTCCTGAC ACCA	145	TGGTGTCAGGAGTGGGAT	1084
CU-1276	TCGATTCCCGGCCA ATGCACCA	236	TGGTGCATTGGCCGGGAATCGA	1085
CU-1368	GACGAGGTGGCCG AGTGG	382	AACCACTCGGCCACCTCGTC	1086
CU-1254	TCCCCGGCACCTC CACCA	233	TGGTGGAGGTGCCGGGGA	1087
CU-1137	GCTAAGGAAGTCCT GTGCTCAGTTTT	132	AAAACTGAGCACAGGACTTCCTT AGC	1088
CU-1153	CCCCCCACTGCTAA ATTTGACTGGCTT	142	AAGCCAGTCAAATTTAGCAGTGG GGGG	1089
CU-1241	AGTCCCATCTGGGT CGCCA	243	TGGCGACCCAGATGGGACT	1090
CU-1351	CCTTCCTTGGATGT CTGAGTGAG	316	CTCACTCAGACATCCAAGGAAGG	1091
CU-1142	TCGATTCCCGGCCC ATGCACCA	149	TGGTGCATGGGCCGGGAATCGA	1092

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[0300] Supplementary Methods

[0301] Bioinformatics Analysis of Short-RNA Libraries

[0302] The bioinformatics microRNA (miRNA) analysis pipeline includes (a) identification of short-RNAs from each library, (b) identification of exact and partial matches of the short-RNA sequences to the human genome, (c) testing each short-RNA genomic region for compatibility with hairpin secondary structures, (d) clustering genomic regions to predict mature miRNAs, (e) annotating and filtering short-RNAs and miRNAs candidates, (f) estimation of predicted miRNA frequencies in the libraries, (g) clustering short-RNAs that do not support miRNAs candidates.

[0303] a. Identification of Short-RNAs from Cloned cDNA Sequences:

[0304] Short-RNA sequences of length 15-30 bp were recovered from within cloned cDNA sequences using 8 bp adaptor oligonucleotides as oriented markers. An exact ≥6 bp match to the suffix of the 5' daptor oligonucleotide and the prefix of the 3' adaptor oligonucleotide were required. All short-RNAs of length 17 to 27 nt (length range of miRNAs deposited in the miRBase database v11.0) that are bounded by adaptors were reported, and short-RNAs containing adaptor fragments were tagged as lower confidence observations. miRNA candidates supported by low confidence short-RNAs were later evaluated individually and discarded by expert decision. The remaining ones are listed here: CU-1153 is supported by 29 short-RNAs including 1 low confidence; CU-1293 and CU-1079 are supported by low confidence short-RNAs including sequence fragments that could not originate from linkers.

[0305] b. Mapping to the Human Genome:

[0306] Each short-RNA was aligned to the human genome assembly from March 2006 (hg18) using WU-Blast. WU-Blast was ran locally optimal, with default word length 6, maximum allowed separation 2, no gaps, and no high scoring pair consistency. All WU-Blast reported matches were retrieved and mismatches marked. Only the genomic matches

with the smallest number of mismatches were recorded, and we refer to them as short-RNA genomic locations.

[0307] c. Testing Short-RNA Genomic Locations for Hairpin Secondary Structures:

[0308] Short-RNA genomic locations were tested for compatibility with hairpin secondary structures. The criteria were established upon investigation of the characteristics of mammalian miRNA precursors deposited in the miRBase database (v.11.0)[s1,s2]. Only short-RNAs that have genomic locations compatible with a hairpin structure were used to define putative miRNAs and their precursors. A short-RNA genomic location was considered if the following criteria were satisfied: i) one or more hairpin structures were predicted in the genomic region starting at most 90 bases upstream and ending at most 90 bases downstream of the short-RNA genomic location; ii) the lowest free-energy predicted secondary structure for the containing region was a hairpin with maximum fold free energy of −8 joules, which is the maximum fold free energy observed for miRBase miRNAs; iii) the short-RNA genomic location could not overlap the predicted hairpin loop, which was required to be 3-20 bp long (the range of hairpin-loop lengths observed in the miRBase database); iv) the ratio between the number of complementary base pairs and the total number of base pairs in the stem was larger than 0.645, which is the minimum ratio observed in miRBase database. We used RNAfold 1.6, a part of the ViennaRNA package (http://www.tbi.univie.ac.at/~ivo/RNA/), with temperature set to 37° C. to predict the lowest energy secondary RNA structure for each candidate genomic sequence.

[0309] d. Prediction of Mature miRNA:

[0310] Short-RNA genomic locations consistent with hairpin secondary structures (smirREGs) were clustered based on genomic region overlap, and smirREG clusters were pruned, split, merged, accepted, or eliminated iteratively. Clusters were first constructed from smirREGs corresponding to: (1) regions perfectly aligned to short-RNAs; (2) regions aligned to short-RNAs with 1-mismatch, represented by an 'A' in the last position; and (3) regions aligned to short-RNAs with 1-mismatch, where the associated short-RNAs had no perfect matches, were not used in (1) or (2) and were 1-mismatch away from short RNAs associated with smirREGs defined in (1) or (2). These smirREGs are major contributors to each region cluster. Regions associated with perfectly matching short-RNAs and 1-mismatch short-RNAs that were not used to define smirREG clusters, but overlapped 5 or fewer such clusters were tagged as minor contributors and added to the overlapping smirREG clusters. Each cluster was pruned or divided by identifying regions corresponding to short-RNAs where more than 25% of the region is supported by no more than 50% of the observations. For each cluster, all such regions were identified and first minor then major contributors with the largest ratio of unsupported portions to total length were iteratively removed until at least 75% of every contributing region was supported by more than 50% of the observations.

[0311] One exception is represented by CU-1088 cluster where a short-RNA was included despite the fact that only 70% of its sequence contributed to the majority observation. This exception was made because this short-RNA was the only one matching a known mature miRNA (miR-320a) and it was left out by the 75% rule.

[0312] Pruned smirREGs were merged and used to construct new and possibly overlapping clusters, but minor contributors were discarded. Finally, smirREG clusters were used to define putative mature miRNAs. The mature sequence was defined as the majority nucleotide in each position supported by more than 50% of the observations, with the genomic sequence allowed to break ties. SmirREG clusters were matched based on mature sequence containment. Clusters corresponding to a short-RNA set that is fully contained in a set corresponding to a matched cluster were eliminated, and matching clusters with partial containment were merged. The process was repeated until no elimination or merging was needed. Finally, a putative precursor was identified for each smirREG cluster following the procedure described in (c) with the added restriction that no more than 5 positions in the mature sequence were allowed to dangle off of the precursor region encapsulated by complimentary base pairs. When the mature region dangled off of the precursor region (but no more than 5 bases), the precursor was extended with non complimentary bases to include the mature region.

[0313] The mature miRNA prediction was followed by the elimination of incompatible predictions. Putative miRNAs whose predicted locations overlapped loops of known miRNAs or precursors of other higher-confidence predictions that could not form mature-star pairs were eliminated. Predicted miRNAs that were entirely composed of low confidence single-observation short-RNAs that contained linker fragments were also eliminated, with the exception of CU-1293 as described in (a). Mature miRNA predictions of length shorter than 17 nt or longer than 28 nt were discarded. Candidate miRNAs that were supported by a single observation were tagged as lower confidence predictions; some of these are likely to be miRNA, but others may be degradation products of previously unannotated RNA.

[0314] e. Annotation and Filtering of Candidate miRNA and sRNA:

[0315] Putative miRNAs and short RNAs were matched to several RNA databases (see below) via regular expression scans (for sequence databases) or genomic region containment (for databases that specify genomic regions). Databases identifying validated human mRNA, tRNA, snoRNA and yRNA were used to eliminate putative miRNA candidates with one observation and to annotate putative miRNAs with multiple observations. All putative miRNAs matching rRNAs were eliminated regardless of the number of observations because of the extreme abundance of rRNAs. Other RNA databases were used for annotation purposes only.

[0316] Precursor and mature miRNA as well as sRNA sequences were aligned to several sequence databases (see below) using the BLAST and MEGABLAST programs from NCBI. Candidate miRNA precursors showing a full match to non-coding RNAs (tRNA, rRNA, snoRNA, other nc-RNA) or to mRNA were disregarded. Predicted precursor and mature miRNAs were further classified as either "known" or "new" based on whether exact matches can be found in miRBAse database. Short-RNA sequences included in miRNA precursor, but not overlapping the mature miRNA, were considered as degradation products of miRNA precursor processing and marked as "miRNA other" (Table 6). All cloned short-RNA were annotated using the databases reported below and results are showed in Table 2.

TABLE 6

Databases used for annotation of short-RNA and miRNA.

Name/Description	Source	Version/Date
miRBASE	Sanger Institute, http://microrna.sanger.ac.uk/sequences	version 11.0
Human fraction of REPBASE	GIRI, http://www.girinst.org/Repbase_Update.html	version 12.02
Human tRNA	EMBL, http://www.trna.uni-bayreuth.de, Bayreuth Univ., Germany	September 2007 edition
Human snoRNA	The University of Queensland, Australia, IMB, http://imb.uq.edu.au	September 2006 edition
Human rRNA	NCBI, ftp://ftp.ncbi.nlm/nih.gov, compiled manually	Downloaded January 2007
Human yRNA	NCBI, ftp://ftp.ncbi.nlm/nih.gov, compiled manually	Downloaded January 2007
Non coding RNA	Compiled manually combining resources from NCBI, ftp://ftp.ncbi.nlm/nih.gov and IMB http://imb.uq.edu.au	Compiled in October 2006 using current ENTREZ and September 2006 edition of Univ. of Queensland database
VECTOR databases	NCBI, ftp://ftp.ncbi.nlm/nih.gov	Downloaded January 2007
Human protein coding genes and mRNA	NCBI annotation for human genome, ftp://ftp.ncbi.nlm/nih.gov	Downloaded January 2007
mRNA dataset	NCBI, ftp://ftp.ncbi.nlm/nih.gov compiled manually using ENTRES NR database	Downloaded January 2007
exEID (exon subset of EID database)	University of Toledo, Ohio, http://hsc.utoledo.edu/bioinfo/eid/	September 2005 (hs35p1)
Human mitochondrial genome	NCBI, ftp://ftp.ncbi.nlm/nih.gov	Downloaded January 2007
Human EST database	NCBI, ftp://ftp.ncbi.nlm/nih.gov	
Human viral genomes	NCBI, http://www.ncbi.nlm.nih.gov, viral genomes section	Compiled in March 2007
E. coli genomes	NCBI, ftp://ftp.ncbi.nlm/nih.gov	Downloaded August 2007
RefGene Intron	UCSC, http://genome.ucsc.edu, annotation track for hg18	annotation track for hg18
RefGene Exon	UCSC, http://genome.ucsc.edu, annotation track for hg18	annotation track for hg18
rnaGenes	UCSC, http://genome.ucsc.edu, annotation track for hg18	annotation track for hg18
wgRNA	UCSC, http://genome.ucsc.edu, annotation track for hg18	annotation track for hg18
snoRNA database	EMBL, http://www-snorna.biotoul.fr/	Version 3
Genscan	MIT, http://genes.mit.edu/GENSCAN.html	Version 1.0
Computational tRNA prdiction	UCSC, http://genome.ucsc.edu, annotation track for hg18	annotation track for hg18
piRNA	The University of Queensland, Australia, IMB, http://imb.uq.edu.au	September 2006 edition
Morozov database	Manually curated	Version 1.0

[0317] f. Estimation of Mature miRNA Frequencies:

[0318] Short-RNAs may contribute to more than one miRNA. In order to compare observation frequencies of predicted miRNAs we normalized the contribution of each supporting short-RNA to its associated predicted miRNA in each library. Short-RNAs supporting a single miRNA prediction were not affected, but the level of support of short-RNAs associated with several miRNAs was prorated. The normalization procedure was performed iteratively. First, for each library, we assigned an observation frequency to each miRNA, taken to be the sum of the library-specific observations across all of its supporting short-RNAs. Second, for each short-RNA observed in this library, we computed sum, the sum of the observation frequencies of the predicted miRNAs it supports. Then, short-RNA support for each miRNA was adjusted to be the number of its observations multiplied by the ratio between the observation frequency of this miRNA and sum. Finally, the frequency of each predicted miRNA was recalculated to be the sum of the adjusted frequencies of the short-RNAs supporting it. To compare the abundance of predicted miRNAs across libraries we normalized the frequencies of observations in each library to sum to 100%, comparing frequencies of observations in each library rather than raw observations. This normalization step was necessary due to the variability between the total number of observations across libraries.

[0319] g. Clustering Short-RNAs.

[0320] Short-RNAs that did not support predicted miRNAs were categorized according to the quality of their best alignments to hg18. These short-RNA were clustered following the procedure described in (c) but with no secondary structure requirements (Table 2 and Tables 9-10). Table 3 and Tables 9-10 were constructed from perfect matches and single mismatches, respectively, as described in (c). Tables 4 and 5 smirREGs were constructed from single-mismatches, double mismatches and three or more mismatches, respectively.

[0321] Estimation of Libraries Complexity

[0322] A bootstrap technique was used to estimate the total number of miRNAs expressed in each library and the number of short-RNAs must be sequenced to achieve a complete coverage. Bootstrapping is a statistical technique for estimating properties of an "estimator" by measuring those properties in multiple subsets of the samples[s3,s4]. Specifically, we estimated the distribution of mature miRNAs obtained by random sub-sampling different size short-RNA libraries from each complete library. For each size N=10, 20, . . . N_t, where N_t is the total number of short-RNAs in the library, we randomly sampled 1000 libraries of size N and computed the number r(N) of inferred miRNAs, resulting in a distribution p(r(N)) for which we could compute standard statistical parameters such as average, variance, mode and median. Based on this sampling, we can extrapolate p(r(N)) for increasing values of N to determine at which point it is no longer efficient to use larger values of N to increase miRNA coverage. To achieve this, we fitted the data to the parametric function $f(x)=K*(1-e^{-mx})$. Since we include both experimentally confirmed and putative mature miRNAs and since bootstrapping can produce optimistic results we expect that the estimated values constitute an upper boundary on the real library complexity.

[0323] Based on this analysis, we estimated that the total numbers of mature miRNAs are: 188 (naïve), 211 (memory), 219 (centroblasts) and 225 (Ramos). Thus, the libraries sequenced in this study cover respectively 84.0% (naïve), 87.2% (memory), 86.8% (centroblasts), and 85.8% (Ramos) of the expressed miRNAs in these cellular phenotypes. FIG. **17** gives the 95% confidence intervals for p(r(N)) at each sampling point, in addition to the curve of the associated extrapolated function for each library. Clearly, the bootstrap analysis estimate of the total number of miRNA is correct only if the abundance of the miRNAs expressed in the sampled populations closely matches that of known miRNA in miRBase. This is not unreasonable if, as was done here, only miRNAs that are specific to a B cell differentiation stage or transformation are considered. Thus, this does not estimate the total number of miRNA expressed across all human cell types, stages of differentiation and neoplastic transformations, which could be several fold larger than what was estimated from the B cell clone libraries.

[0324] Orthology and Conservation Analysis

[0325] We investigated conservation of known and predicted precursor and mature human miRNA in chimp (panTro2), monkey (rheMac2), dog (canFam2) mouse (mm8) and rat (rn4). We obtained 678 miRNA precursor sequences from miRBase (v.11.0); 677 (672 unique) mature miRNAs; and 170 (167 unique) star sequences. In total, we obtained 947 locations for mature and star mirBase sequences. We predicted 926 precursors of which 146 match miRBase precursors and 780 are newly predicted. Categorizing these by their corresponding mature sequences, 762 precursors correspond to mature miRNAs that are not included in the miRBase and 164 precursors are associated with 129 predicted miRNAs that match miRBase miRNAs. Of the 762 newly predicted precursors, one overlaps with a miRBase precursor and its corresponding predicted miRNA is a candidate star sequence; 19 precursors associated with 8 mature sequences listed in miRBase database.

[0326] Here, we predicted 762 miRNA genomic locations associated with unique mature miRNA sequences not included in miRBase. Of these 762 predicted miRNA genomic locations, one overlaps with a miRBase precursor and is a candidate star sequence. We identified 164 precursors associated with 129 predicted miRNAs matching the sequence of known miRNAs; 19 of the 164 precursors, associated with 9 known miRNAs, do not match known precursors. miRNA conservation has been repeatedly used to help identify putative miRNA mappings to genomes. To identify putative ortholog miRNAs we relied on UCSC-provided Blastz pairwise alignments between human and target species[s5]. We used two related but complementary methods: (1) map the mature human miRNA to its ortholog location as specified by pairwise alignment; and (2) map the precursor of the human miRNA to its ortholog location as specified by pairwise alignment, expanding the human region to include at least 80 bases from both sides of the mature region, and identifying regions in the target that match the sequence of the mature human miRNA.

[0327] Method 1 is the simplest but fails to account for alignment inaccuracies and local mutations that may shift the position of the mature sequence in the target species. Method 2 accounts for locally imperfect Blastz mapping, but relies on conservation of larger regions that may not be subject to the same selective pressure as the mature miRNA. Alignment-based mapping of the human mature miRNA to its target were required to have either perfect conservation of the entire mature miRNA sequence or conservation of seeds composed of seven bases starting from the second position of the human mature sequence followed by conservation of 3 bases starting from the 12th, 13th, or 14th position as suggested by[s6]. We scanned the entire mapped ortholog region for a match to the human mature sequence or to its seed.

[0328] Comparison with Previously Reported miRNA Prediction from Short-RNA Libraries

[0329] Landgraf et al.[s7] used more restrictive miRNA charachterizations for mature miRNA prediction, annotation and conservation. They required that at least 60% of the observations associated with a predicted miRNA align at the 5' end. We made no such restriction, and some of the miRNAs with the highest number of observations in our libraries, such as CU-1026 and CU-1018, are supported by a high proportion of 5'-misaligned cloned sequences. Landgraf et al. eliminated predictions that can be derived from repeat sequences by excluding precursors that contain more than 30% repetitive elements and that match hg18 more than 10 times with at least 75% identity. We annotated mature sequences that match known repeats but did not eliminate them. Finally, Landgraf et al. formulated extensive criteria for sequence orthology, requiring sequence conservation greater than 75% in multiple alignments across vertebrates and either restricting the 20 5'-most misaligned nucleotides to be transitions or requiring 100% conservation in positions 2 through 8 and 90% conservation overall. We, as described above, simply considered full conservation and seed-based conservation, mapping human to primates, dog and rodents.

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Example 4

miRNome of Human Mature B Cells

[0337] Summary:

[0338] The full set of microRNAs (miRNAs) in the human genome is not known. Because presently known miRNAs have been identified by virtue of their abundant expression in a few cell types, many tissue-specific miRNAs remain unrevealed. To understand the role of miRNAs in B cell function and lymphomagenesis, we generated short-RNA libraries from normal human B cells at different stages of development (naive, germinal center, memory) and from a Burkitt lymphoma cell line. A combination of cloning and computational analysis identified 178 miRNAs (miRNome) expressed in normal and/or transformed B cell libraries. Most notably, the B cell miRNome included 75 miRNAs which to our knowledge have not been previously reported and of which 66 have been validated by RNA blot and/or RT-PCR analyses. Numerous miRNAs were expressed in a stage- or transformation-specific fashion in B cells, suggesting specific functional or pathologic roles. These results provide a resource for studying the role of miRNAs in B cell development, immune function, and lymphomagenesis.

[0339] A new mechanism of post-transcriptional regulation has been revealed with the discovery of microRNAs (miRNAs), a class of short RNAs that impair translation or induce mRNA degradation by binding to the 3' untranslated region of target mRNA ([Bartel, 2004] and [Kim, 2005]). A recent release of the miRBase database (v.11.0) ([Griffiths-Jones, 2006] and [Griffiths-Jones et al., 2006]) reports 847 human miRNAs. However, the discovery of miRNAs is still an ongoing process with variable predictions about the total number of miRNAs expressed in mammalian cells ranging from one thousand to several thousands ([Bentwich et al., 2005] and [Miranda et al., 2006]). The reported miRNAs have been identified from a limited number of cell types or from tissues whose cellular heterogeneity may favor the identification of ubiquitous and abundant miRNA. In fact, a recent report aiming for the identification of miRNA expression profiles from a large panel of different mammalian tissues and cell types led to the discovery of only 12 previously unreported human miRNA (Landgraf et al., 2007). These findings led to the conclusion that most miRNAs are known and that most of them are ubiquitously expressed (Landgraf et al., 2007). Nonetheless, additional analyses of purified cell populations have led to the identification of tissue- and stage of differentiation-specific miRNAs in a few tissues, suggesting the existence of tissue-specific miRNA expression ([Calabrese et al., 2007] and [Cummins et al., 2006]).

[0340] The role of miRNAs in B lymphocyte development and B cell lymphomagenesis is largely unknown. A critical stage of the differentiation process leading to effector B cells is represented by the germinal centers (GC), the structures that develop when mature naive B cells encounter the antigen in the secondary lymphoid organs and are stimulated to proliferate and differentiate into GC centroblasts (CB). During the GC reaction, B cells undergo somatic hypermutation of their immunoglobulin-variable regions and class switch recombination. B cells that have acquired the ability to express high-affinity immunoglobulins are then positively selected and further differentiate into the final effectors of the humoral immune response, i.e., memory B cells and plasma cells (Klein and Dalla-Favera, 2008). Naive, GC, and memory B cells are also relevant targets of disease because each of these B cell subpopulations can be affected by malignant transformation leading to different types of lymphomas and leukemias ([Klein and Dalla-Favera, 2008] and [Kuppers and Dalla-Favera, 2001]).

[0341] Several initial observations suggest an important role of specific miRNAs in B cell function and malignancy. Via mouse models, miR-155 has been demonstrated to affect regulation of the GC response through modulation of cytokine production ([Rodriguez et al., 2007] and [Thai et al., 2007]) and by direct post-transcriptional regulation of the activation-induced cytidine deaminase (AID) ([Dorsett et al., 2008] and [Teng et al., 2008]). Recently, miR-150 has been shown to target MYB, a critical transcription factor involved in the control of B cell differentiation (Xiao et al., 2007). In B cell lymphomas, 13q31 amplification has been associated with the overexpression of the miR-17-92 cluster and its enforced expression in a murine B cell lymphoma model showed a role in accelerating tumor development (He et al., 2005). Furthermore, miR-15a and miR-16 have been implicated in the pathogenesis of B cell chronic lymphocytic leukemia (CLL) ([Calin et al., 2002] and [Calin et al., 2005]).

[0342] As a basis for a comprehensive analysis of the role of miRNAs in B cell function and lymphomagenesis, this study was aimed at identifying the miRNAs expressed (miRNome) in the human mature B cell compartment, including naive, GC, and memory B cells. By using a combination of cloning and computational analysis, we report the identification of 178 miRNAs representing the mature B cell miRNome, including 75 previously unreported miRNAs. The results show that normal B cell subpopulations are characterized by specific miRNA "signatures," suggesting functional roles of miRNAs in B cell differentiation and transformation.

[0343] Results

[0344] Construction of Short-RNA Libraries from Human B Cell Subpopulations.

[0345] Short-RNA libraries were generated by cloning RNA fractions of 15-30 nt from human centroblasts, naive, and memory B cells purified from tonsils, as well as from the Burkitt lymphoma cell line Ramos, which is representative of malignant transformation of GC B cells. Approximately 3,500 sequences were analyzed from each library, corresponding to 13,788 total short-RNAs (2,632 nonredundant sequences). By using a bootstrap approach ([Harrell, 2001] and [Davison and Hinkley, 1997]), we estimated that more than 85% of the complexity of the libraries has been examined (FIG. **23**).

[0346] Mapping of Short-RNA Sequences to the Human Genome.

[0347] The cloned sequences were subjected to a computational analysis (see Supplemental Experimental Procedures described in Example 3) summarized in the flowchart illustrated in FIG. **24**. Each cloned sequence was first matched to the human genome assembly (March 2006, hg18) to retrieve the genomic regions from which the short RNAs originated. One or more genomic locations were identified for 2086 (80%) of the cloned sequences considering both perfect matches and single mismatches (FIG. **24**). Consistent with previous observations, 3'-end mismatches were the most common and showed a clear preference for A in the last position (Neilson et al., 2007). The failure of 546 short-RNA sequences to align with the human genome is likely due, at least in part, to errors introduced by PCR during the cloning procedure (FIG. **24**). However, a small subset of these short RNAs lacking a corresponding genomic region in *Homo sapiens* have been cloned with high frequencies in multiple libraries and showed differential expression during B cell differentiation, suggesting that they may represent bona fide short-RNA species, which cannot be mapped on the current reference genome probably because of polymorphisms and/or post-transcriptional modifications. However, given the difficulty of assigning genomic coordinates to these sequences, they were omitted from further analyses.

[0348] Computational Prediction of Precursor and Mature miRNAs.

[0349] In order to identify candidate miRNAs among the cloned short-RNA sequences, we developed a computational pipeline aiming at the identification of potential miRNA precursors based on the investigation of their genomic location and folding characteristics (FIG. **18** and Supplemental Experimental Procedures in Example 3). In brief, short RNA sequences were mapped to the human genome and their respective candidate genomic precursors (±90 nt) were retrieved and analyzed for secondary structure, size and energy of the loop, and number of complimentary base pairs in the stem of the loop. The prediction was performed on the full set of nonredundant short RNAs (2632 sequences) for which one or more genomic locations could be identified (FIG. **24**). The analysis led to the identification of candidate miRNA precursors for 1646 short-RNA sequences, which were then clustered allowing for (1) the variability observed at the mature miRNA 3' ends (and less dramatically at the 5' ends) including nucleotide substitutions and deletions, and (2) the possibility of miRNA editing as previously reported ([Kawahara et al., 2007] and [Luciano et al., 2004]) (Supplemental Experimental Procedures in Example 3). After annotating each candidate mature miRNA, those which matched mRNA, rRNA, tRNA, post-transcriptionally modified t-RNA, and other ncRNA (yRNA, sn/snoRNA) sequences, and were present only once in the libraries were not considered further. The remaining sequences were still considered miRNAs based on criteria (identification of genomic loci consistent with a pre-miRNA, length, recurrence, differential expression, detection in the Ago complex) that suggest their existence as bona fide miRNA. Moreover, consistent with the miRNA length of the *Homo sapiens* miRBase database (v11.0), only mature candidate miRNAs of length 17-28 nt were considered.

[0350] Overall, the analysis identified 178 mature miRNAs, of which 103 were known and 75 were not previously reported, to our knowledge (Table 7 and FIG. **24**). Computational prediction of precursor miRNAs (pre-miRNA) identified 114 precursors already reported to potentially code for the 103 known mature miRNA, and 274 genomic locations containing new candidate pre-miRNA associated with the 75 previously unreported and 8 known mature miRNAs (FIG. **19** and Table 7).

TABLE 7

(PART A) List of known and newly identified bona fide and candidate mature miRNAs and their predicted precursors. Genomic locations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1026	1	TGTAGTGTTTCCTACTTTATGGA	Mature:hsa-miR-142-3p:MIMAT0000434
CU-1064	2	TAGCTTATCAGACTGATGTTGA	Mature:hsa-miR-21:MIMAT0000076
CU-1061	3	TAAAGTGCTTATAGTGCAGGTAG	Mature:hsa-miR-20a:MIMAT0000075
CU-1035	4	TAGCAGCACATCATGGTTTACA	Mature:hsa-miR-15b:MIMAT0000417
CU-1037	5	TAGCAGCACGTAAATATTGGCG	Mature:hsa-miR-16:MIMAT0000069
CU-1001	6	TGAGGTAGTAGGTTGTATAGTT	Mature:hsa-let-7a:MIMAT0000062
CU-1116	7	TATTGCACTTGTCCCGGCCTGT	Mature:hsa-miR-92a:MIMAT0000092
CU-1018	8	TCCCACCGCTGCCACCA	Mature:hsa-miR-1280:MIMAT0005946
CU-1006	9	TGAGGTAGTAGATTGTATAGTT	Mature:hsa-let-7f:MIMAT0000067
CU-1079	10	TAGCACCATCTGAAATCGGTTA	Mature:hsa-miR-29a:MIMAT0000086
CU-1033	11	TAGCAGCACATAATGGTTTGT	Mature:hsa-miR-15a:MIMAT0000068
CU-1124	12	CCCATAAAGTAGAAAGCACTA	Mature:hsa-miR-142-5p:MIMAT0000433

TABLE 7-continued

(PART A) List of known and newly identified bona fide and candidate mature miRNAs and their predicted precursors. Genomic locations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1007	13	TGAGGTAGTAGTTTGTACAGTT	Mature:hsa-let-7g:MIMAT0000414
CU-1008	14	TGAGGTAGTAGTTTGTGCTGTT	Mature:hsa-let-7i:MIMAT0000415
CU-1082	15	TAGCACCATTTGAAATCGGTTA	Mature:hsa-miR-29c:MIMAT0000681
CU-1085	16	TGTAAACATCCTACACTCTCAGC	Mature:hsa-miR-30c:MIMAT0000244
CU-1039	17	CAAAGTGCTTACAGTGCAGGTAG	Mature:hsa-miR-17:MIMAT0000070
CU-1071	18	CATTGCACTTGTCTCGGTCTGA	Mature:hsa-miR-25:MIMAT0000081
CU-1046	19	CAACGGAATCCCAAAAGCAGCTG	Mature:hsa-miR-191:MIMAT0000440
CU-1057	20	TGTGCAAATCCATGCAAAACTGA	Mature:hsa-miR-19b:MIMAT0000074
CU-1024	21	TACCACAGGGTAGAACCACGGA	Mature:hsa-miR-140-3p:MIMAT0004597
CU-1084	22	TGTAAACATCCTACACTCAGCT	Mature:hsa-miR-30b:MIMAT0000420
CU-1003	23	TGAGGTAGTAGGTTGTGTGGTT	Mature:hsa-let-7b:MIMAT0000063
CU-1080	24	TAGCACCATTTGAAATCAGTGTT	Mature:hsa-miR-29b:MIMAT0000100
CU-1012	25	TAAAGTGCTGACAGTGCAGAT	Mature:hsa-miR-106b:MIMAT0000680
CU-1092	26	TCCCTGTCCTCCAGGAGCTC	Mature:hsa-miR-339-5p:MIMAT0000764
CU-1072	27	TTCAAGTAATCCAGGATAGGCT	Mature:hsa-miR-26a:MIMAT0000082
CU-1118	28	CAAAGTGCTGTTCGTGCAGGTAG	Mature:hsa-miR-93:MIMAT0000093
CU-1067	29	TGTCAGTTTGTCAAATACCCCA	Mature:hsa-miR-223:MIMAT0000280
CU-1027	30	TGAGAACTGAATTCCATGGGTT	Mature:hsa-miR-146a:MIMAT0000449
CU-1029	31	TCTCCCAACCCTTGTACCAGT	Mature:hsa-miR-150:MIMAT0000451
CU-1015	32	TCCCTGAGACCCTAACTTGTGA	Mature:hsa-miR-125b:MIMAT0000423
CU-1093	33	TCTCACACAGAAATCGCACCCGTC	Mature:hsa-miR-342-3p:MIMAT0000753
CU-1016	34	GTCCCTGTTCGGGCGCCA	Mature:hsa-miR-1274b:MIMAT0005938
CU-1056	35	TGTGCAAATCTATGCAAAACTGA	Mature:hsa-miR-19a:MIMAT0000073
CU-1086	36	TGTAAACATCCCCGACTGGAAG	Mature:hsa-miR-30d:MIMAT0000245
CU-1065	37	AGCTACATTGTCTGCTGGGTT	Mature:hsa-miR-221:MIMAT0000278
CU-1004	38	AGAGGTAGTAGGTTGCATAGTT	Mature:hsa-let-7d:MIMAT0000065
CU-1011	39	CCGCACTGTGGGTACTTGCT	Star:hsa-miR-106b*:MIMAT0004672
CU-1010	40	AGCAGCATTGTACAGGGCTATGA	Mature:hsa-miR-103:MIMAT0000101
CU-1050	41	AACTGGCCCTCAAAGTCCCGCT	Mature:hsa-miR-193b:MIMAT0002819
CU-1091	42	GCCCCTGGGCCTATCCTAGAA	Mature:hsa-miR-331-3p:MIMAT0000760
CU-1023	43	AGCTGGTGTTGTGAATCAGGCCGT	Mature:hsa-miR-138:MIMAT0000430
CU-1101	44	TGAGGGGCAGAGAGCGAGACTT	Mature:hsa-miR-423-5p:MIMAT0004748
CU-1066	45	AGCTACATCTGGCTACTGGGTCT	Mature:hsa-miR-222:MIMAT0000279
CU-1017	46	GTGGGGGAGAGGCTGTA	Mature:hsa-miR-1275:MIMAT0005929

TABLE 7-continued

(PART A) List of known and newly identified bona fide and candidate mature miRNAs and their predicted precursors. Genomic locations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-5001	47	CTATACGACCTGCTGCCTTTC	Star:hsa-let-7d*:MIMAT0004484
CU-1032	48	TTAATGCTAATCGTGATAGGGGT	Mature:hsa-miR-155:MIMAT0000646
CU-1108	49	AGGGGGAAAGTTCTATAGTC	Mature:hsa-miR-625:MIMAT0003294
CU-1055	50	ACAGTAGTCTGCACATTGGTT	Mature:hsa-miR-199b-3p:MIMAT0004563
CU-1042	51	AACATTCAACGCTGTCGGTGAGTT	Mature:hsa-miR-181a:MIMAT0000256
CU-1113	52	TGGAAGACTAGTGATTTTGTTGT	Mature:hsa-miR-7:MIMAT0000252
CU-1098	53	TAATGCCCCTAAAAATCCTTAT	Mature:hsa-miR-365:MIMAT0000710
CU-1052	54	TAGCAGCACAGAAATATTGGCA	Mature:hsa-miR-195:MIMAT0000461
CU-1568	55	TGAGGTAGTAGGTTGTAT	Mature:hsa-let-7c:MIMAT0000064
CU-1103	56	TCCTGTACTGAGCTGCCCCGAG	Mature:hsa-miR-486-5p:MIMAT0002177
CU-1014	57	TCCCTGAGACCCTTTAACCTGTGA	Mature:hsa-miR-125a-5p:MIMAT0000443
CU-1068	58	ATCACATTGCCAGGGATTTCCA	Mature:hsa-miR-23a:MIMAT0000078
CU-1019	59	TCACAGTGAACCGGTCTCTTT	Mature:hsa-miR-128:MIMAT0000424
CU-1076	60	CACTAGATTGTGAGCTCCTGGA	Mature:hsa-miR-28-3p:MIMAT0004502
CU-1111	61	CAACAAATCACAGTCTGCCAT	Star:hsa-miR-7-1*:MIMAT0004553
CU-1062	62	CAAAGTGCTTATAGTGCAGGTAG	Mature:hsa-miR-20b-mm:MIMAT0001413
CU-1115	63	AGGTTGGGATCGGTTGCAATGCT	Star:hsa-miR-92a-1*:MIMAT0004507
CU-1126	64	ACATTCATTGCTGTCGGTGGGTT	Mature:hsa-miR-181b:MI0000270
CU-5016	1093	AATGACACGATCACTCCCGTTGAG	Mature:hsa-miR-425:MIMAT0003393
CU-1096	65	TCCCCCAGGTGTGATTCTGATT	Mature:hsa-miR-361-3p:MIMAT0004682
CU-1054	66	CCCAGTGTTCAGACTACCTGTTC	Mature:hsa-miR-199a-5p:MIMAT0000231
CU-1125	67	ACCAATATTACTGTGCTGCTT	Star:hsa-miR-16-2*:MIMAT0004518
CU-1087	68	TGTAAACATCCTTGACTGGAAGCT	Mature:hsa-miR-30e:MIMAT0000692
CU-1045	69	TAAGGTGCATCTAGTGCAGATA	Mature:hsa-miR-18a:MIMAT0000072
CU-1069	70	ATCACATTGCCAGGGATTACCA	Mature:hsa-miR-23b:MIMAT0000418
CU-1044	71	ACTGCCCTAAGTGCTCCTTCTG	Star:hsa-miR-18a*:MIMAT0002891
CU-1083	72	TGTAAACATCCTCGACTGGA	Mature:hsa-miR-30a:MIMAT0000087
CU-1009	73	TACAGTACTGTGATAACTGAAG	Mature:hsa-miR-101:MIMAT0000099
CU-1030	74	CTAGACTGAAGCTCCTTGAGG	Mature:hsa-miR-151-3p:MIMAT0000757
CU-1088	1094	TGGGTTGAGAGGGCGAA	Mature:hsa-miR-320a:MIMAT0000510
CU-1095	75	TGGCAGTGTCTTAGCTGGTTGTT	Mature:hsa-miR-34a:MIMAT0000255
CU-1119	76	TGAGGTAGTAAGTTGTATTGTT	Mature:hsa-miR-98:MIMAT0000096
CU-1028	77	TGAGAACTGAATTCCATAGGCTGT	Mature:hsa-miR-146b-5p:MIMAT0002809
CU-1031	78	TCGAGGAGCTCACAGTCTAGTA	Mature:hsa-miR-151-5p:MIMAT0004697

TABLE 7-continued

(PART A) List of known and newly identified bona fide and candidate mature miRNAs and their predicted precursors. Genomic locations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1100	79	AGCTCGGTCTGAGGCCCCTCAG	Mature:hsa-miR-423-3p:MIMAT0001340
CU-1038	80	ACTGCAGTGAAGGCACTTGTAG	Star:hsa-miR-17*:MIMAT0000071
CU-1040	81	ACCATCGACCGTTGATTGTA	Star:hsa-miR-181a*:MIMAT0000270
CU-1053	82	TTCACCACCTTCTCCACCCAG	Mature:hsa-miR-197:MIMAT0000227
CU-1075	83	TTCACAGTGGCTAAGTTCTG	Mature:hsa-miR-27b:MIMAT0000419
CU-1073	84	TTCAAGTAATTCAGGATAGGTT	Mature:hsa-miR-26b:MIMAT0000083
CU-1110	85	TGGGTTTACGTTGGGAGAACT	Mature:hsa-miR-629:MIMAT0004810
CU-1005	87	TGAGGTAGGAGGTTGTATAGTT	Mature:hsa-let-7e:MIMAT0000066
CU-1081	88	TGACCGATTTCTCCTGGTGTT	Star:hsa-miR-29c*:MIMAT0004673
CU-1117	89	TATTGCACTCGTCCCGGCC	Mature:hsa-miR-92b:MIMAT0003218
CU-1094	90	GGGGTGCTATCTGTGATTGA	Mature:hsa-miR-342-5p:MIMAT0004694
CU-1021	91	GCATGGGTGGTTCAGTGGTAGAA	Mature:hsa-miR-1308:MIMAT0005947
CU-1089	92	CTGGCCCTCTCTGCCCTT	Mature:hsa-miR-328:MIMAT0000752
CU-1047	93	CTGACCTATGAATTGACAGC	Mature:hsa-miR-192:MIMAT0000222
CU-1099	94	CTCCTGACTCCAGGTCCTGTG	Star:hsa-miR-378*:MIMAT0000731
CU-1105	95	CGTCAACACTTGCTGGTT	Mature:hsa-miR-505:MIMAT0002876
CU-1034	96	CGAATCATTATTTGCTGCTCT	Star:hsa-miR-15b*:MIMAT0004586
CU-5002	97	CATCGGGAATGTCGTGTCCGCC	Star:hsa-miR-425*:MI0001448
CU-1025	98	CAGTGGTTTTACCCTATGGTA	Mature:hsa-miR-140-5p:MIMAT0000431
CU-1022	99	CAGTGCAATGATGAAAGGGCAT	Mature:hsa-miR-130b:MIMAT0000691
CU-1104	100	CAGCAGCACACTGTGGTTTGT	Mature:hsa-miR-497:MIMAT0002820
CU-1106	101	CACGCTCATGCACACACCCAC	Mature:hsa-miR-574-3p:MIMAT0003239
CU-1077	102	AAGGAGCTCACAGTCTATTGAG	Mature:hsa-miR-28-5p:MIMAT0000085
CU-1132	131	GCCGGGTACTTTCGTATTTT	NEW
CU-1137	132	GCTAAGGAAGTCCTGTGCTCAGTTTT	NEW
CU-1178	148	AGGGTGTGCGTGTTTTT	NEW
CU-1164	150	GAGAGCGCTCGGTTTTT	NEW
CU-1148	151	TGGTGTGGTCTGTTGTTTT	NEW
CU-1221	152	TGTGCTCCGGAGTTACCTCGTTT	NEW
CU-1180	155	AACCGAGCGTCCAAGCTCTTTCCATTTT	NEW
CU-1155	156	TCCCCGCACCTCCACCA	NEW
CU-1175	162	GGCGTGATTCATACCTTTT	NEW
CU-1197	169	ATGTGGTGGCTTACTTTT	NEW
CU-1146	172	AGAAAGGCCGAATTTTA	NEW
CU-1212	157	TCCCCGGCACTTCCACCA	NEW

TABLE 7-continued

(PART A) List of known and newly identified bona fide and candidate mature miRNAs and their predicted precursors. Genomic locations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1251	232	CCCACCCAGGGACGCCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1254	233	TCCCCGGCACCTCCACCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1298	234	ATCCCGGACGAGCCCCCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1153	142	CCCCCCACTGCTAAATTTGACTGGCTT	refseqGeneIntron-annotate; rnaGene-annotate
CU-1276	236	TCGATTCCCGGCCAATGCACCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1303	237	ATCCCACTTCTGACACCA	computGene-annotate; refseqGeneIntron-annotate; tRNAprefix-annotate
CU-1242	239	TCCCCGTACGGGCCACCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1241	243	AGTCCCATCTGGGTCGCCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1575	244	CCCCCCACTGCTAAATTTGACTGGA	refseqGeneIntron-annotate; rnaGene-annotate
CU-1243	246	GTCCCTTCGTGGTCGCCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1300	248	TCCTCACACGGGGCACCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1278	249	TAACGGCCGCGGTACCC	refseqGeneIntron-annotate
CU-1264	250	GAGGGGGACCAAAAAAAA	refseqGeneIntron-annotate
CU-1130	133	CCCGGGTTTCGGCACCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1380	354	ATAGGTTTGGTCCTAGCCTTTCT	piRNA-annotate; refseqGeneIntron-annotate
CU-1246	252	AGGGGGGTAAAAAAAAA	refseqGeneIntron-annotate
CU-1277	254	GAGCCATGATGATACCACTGAGC	refseqGeneIntron-annotate
CU-1345	257	AGAACACTACGAGCCACA	mRNA-annotate; refseqGeneIntron-annotate
CU-1352	258	ACCCCACTTCTGGTACCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1324	260	TCTCGGTGGAACCTCCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1269	262	TACCGAGCCTGGTGATAGC	refseqGeneIntron-annotate
CU-1281	263	GCAGCGCCAGCCTCCCGCCCTAC	refseqGeneIntron-annotate
CU-1339	265	ATCCCCAGCACCTCCACCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1293	266	AGCAGTGATGTCCTGAAAATTCTGAAG	refseqGeneIntron-annotate
CU-1307	267	ACCCCACTATGCTTAGCCCT	mRNA-annotate; refseqGeneIntron-annotate
CU-1294	268	AAAGGACCTGGCGGTGCTTC	mRNA-annotate; refseqGeneIntron-annotate
CU-1369	350	TCCCCGGCATCTCCACCA	computGene-annotate; tRNAprefix-annotate
CU-1191	143	GCCCGCATCCTCCACCA	tRNAprefix-annotate;
CU-1173	145	ATCCCACTCCTGACACCA	tRNAprefix-annotate;
CU-1142	149	TCGATTCCCGGCCCATGCACCA	tRNAprefix-annotate;
CU-1186	153	TCCCCGACACCTCCACCA	tRNAprefix-annotate;
CU-1371	352	TCTAGAGGAGCCTGTTCTGTA	mRNA-annotate
CU-1381	353	TCGATTCCCGGTCAGGGAACCA	repeats-annotate; tRNAprefix-annotate

TABLE 7-continued

(PART A) List of known and newly identified bona fide and candidate mature miRNAs and their predicted precursors. Genomic locations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1213	158	TCACCCCATAAACACCA	tRNAprefix-annotate;
CU-1363	355	CGTTCGCGCTTTCCCCTG	rnaGene-annotate
CU-1220	161	TTCCCCGACGGGGAGCCA	tRNAprefix-annotate;
CU-1396	356	TAAGTGTTTGTGGGTTA	rnaGene-annotate
CU-1570	171	ATCCCCAGCATCTCCACCA	tRNAprefix-annotate;
CU-1524	368	CCCCCACAACCGCGCTTGACTAGC	mRNAall-annotate; yRNA-eliminate; rnaGene-annotate
CU-1453	369	CCCTGCTCGCTGCGCCA	tRNAprefix-annotate; refseqGeneExon-eliminate;
CU-1477	370	CTCCCACTGCTTCACTTGACTAGC	yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1222	372	TCACGTCGGGGTCACCA	refseqGeneExon-eliminate; tRNAprefix-annotate
CU-1388	373	TCCCTGGTGGTCTAGTGGTTAGGATTCG	tRNAcomputational-annotate; refseqGeneIntron-annotate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1488	375	TCCTGCCGCGGTCGCCA	tRNAprefix-annotate; refseqGeneExon-eliminate;
CU-1557	376	GGAGAGAACGCGGTCTGAGTGGT	snoRNA-eliminate; wgRNA-annotate; rnaGene-annotate
CU-1379	377	TCGGGTGCGAGAGGTCCCGGGT	tRNAcomputational-annotate; HStRNA-eliminate; rnaGene-annotate
CU-1542	378	GGCTGGTCCGATGGTAGTGGGTT	mRNAall-annotate; yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1550	379	CGGAAGCGTGCTGGGCCC	tRNAcomputational-annotate; tRNA-eliminate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1513	381	GCGGGTGATGCGAACTGGAGTCTGAGC	computGene-annotate; snoRNA-annotate; refseqGeneExon-eliminate; rnaGene-annotate; snoRNA-eliminate; wgRNA-annotate
CU-1368	382	GACGAGGTGGCCGAGTGG	tRNAcomputational-annotate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1370	351	CTGATTGCTCCTGTCTGATT	mRNAall-annotate; refseqGeneExon-eliminate; wgRNA-annotate; exEID-annotate; rnaGene-annotate
CU-1470	384	CTCCTGGCTGGCTCGCCA	mRNAall-annotate; computGene-annotate; exEID-annotate; tRNAprefix-annotate; refseqGeneIntron-annotate; refseqGeneExon-eliminate;
CU-1538	386	GGCTGGTCCGAGTGCAGTGGTGTTTA	yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1486	387	CTGCTGTGATGACATTC	computGene-annotate; snoRNA-annotate; refseqGeneExon-eliminate; rnaGene-annotate; snoRNA-eliminate; wgRNA-annotate
CU-1382	389	TCCTCGTTAGTATAGTGGTGAGTATCCC	tRNAcomputational-annotate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1403	391	GCATTGGTGGTTCAGTGGTAGA	rnaGene-annotate; tRNAcomputational-annotate; piRNA-annotate; tRNA-eliminate; refseqGeneIntron-annotate; HStRNA-eliminate
CU-1457	395	TTCTCACTACTGCACTTGACTA	mRNAall-annotate; exEID-annotate; yRNA-eliminate; rnaGene-annotate; refseqGeneIntron-annotate; refseqGeneExon-eliminate

TABLE 7-continued

(PART A) List of known and newly identified bona fide and candidate mature miRNAs and their predicted precursors. Genomic locations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1440	396	TGGTTATCACGTTCGCC	tRNAcomputational-annotate; tRNA-eliminate; rnaGene-annotate; HStRNA-eliminate; piRNA-annotate
CU-1528	397	TAGGGGTATGATTCTCGCT	tRNAcomputational-annotate; tRNA-eliminate; HStRNA-eliminate; rnaGene-annotate
CU-1288	255	CGTCCATGATGTTCCGCAA	mRNAall-annotate; snoRNA-annotate; refseqGeneIntron-annotate; refseqGeneExon-eliminate; piRNA-annotate; wgRNA-annotate
CU-1545	398	CCACGAGGAAGAGAGGTAGC	snoRNA-annotate; snoRNA-eliminate; wgRNA-annotate; rnaGene-annotate
CU-1323	259	TGTATTGTGAGACATTC	mRNAall-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; wgRNA-annotate; rnaGene-annotate
CU-1244	399	GTCAGGATGGCCGAGCGGTCT	tRNAcomputational-annotate; rnaGene-annotate; HStRNA-eliminate; refseqGeneIntron-annotate
		Candidate miRNAs observed only once in any of the four libraries	
CU-1123	103	TTGGTCCCCTTCAACCAGCTGT	Mature:hsa-miR-133a:MIMAT0000427
CU-1074	104	TTCACAGTGGCTAAGTTCCGA	Mature:hsa-miR-27a:MIMAT0000084
CU-1097	105	TTATCAGAATCTCCAGGGGTAA	Mature:hsa-miR-361-5p:MIMAT0000703
CU-1043	106	TGGAGAGAAAGGCAGTTCCTGAT	Mature:hsa-miR-185:MIMAT0000455
CU-1112	107	TGAGACCTCTGGGTTCTGAGCT	Mature:hsa-miR-769-5p:MIMAT0003886
CU-1122	108	TCTTTGGTTATCTAGCTGTATGA	Mature:hsa-miR-9:MIMAT0000441
CU-1109	109	TCTAGTAAGAGTGGCAGTCGA	Mature:hsa-miR-628-3p:MIMAT0003297
CU-1090	110	TATTGCACATTACTAAGTTGA	Mature:hsa-miR-32:MIMAT0000090
CU-1013	111	TAAGGCACGCGGTGAATGCCA	Mature:hsa-miR-124:MIMAT0000422
CU-1058	112	TAACACTGTCTGGTAACGATGTT	Mature:hsa-miR-200a:MIMAT0000682
CU-1059	113	GTGAAATGTTTAGGACCACTAG	Mature:hsa-miR-203:MIMAT0000264
CU-1102	114	GCAGTCCATGGGCATATACACA	Mature:hsa-miR-455-3p:MIMAT0004784
CU-1107	115	GAGCTTATTCATAAAAGTGCAG	Mature:hsa-miR-590-5p:MIMAT0003258
CU-1114	116	CTGCCCTGGCCCGAGGGACCGA	Mature:hsa-miR-874:MIMAT0004911
CU-1002	117	CTATACAACCTACTGCCTTC	Star:hsa-let-7b*:MIMAT0004482
CU-1049	118	CGGGGTTTTGAGGGCGAGATGA	Star:hsa-miR-193b*:MIMAT0004767
CU-1051	119	CCAGTGGGGCTGCTGTTATCTG	Star:hsa-miR-194*:MIMAT0004671
CU-1036	120	CCAGTATTAACTGTGCTGCTGA	Star:hsa-miR-16-1*:MIMAT0004489
CU-1121	121	CACCCGTAGAACCGACCTTGCG	Mature:hsa-miR-99b:MIMAT0000689
CU-1120	122	CAAGCTCGTGTCTGTGGGTCCG	Star:hsa-miR-99b*:MIMAT0004678
CU-1063	123	CAACACCAGTCGATGGGCTGTA	Star:hsa-miR-21*:MIMAT0004494
CU-1070	124	AGGCGGAGACTTGGGCAATT	Star:hsa-miR-25*:MIMAT0004498
CU-1060	125	ACTGCATTATGAGCACTTAAAGT	Star:hsa-miR-20a*:MIMAT0004493

TABLE 7-continued

(PART A) List of known and newly identified bona fide and candidate mature miRNAs and their predicted precursors. Genomic locations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1078	126	ACTGATTTCTTTTGGTGTTCA	Star:hsa-miR-29a*:MIMAT0004503
CU-1020	127	ACTCGGCGTGGCGTCGGTCGTGG	Mature:hsa-miR-1307:MIMAT0005951
CU-1041	128	ACCACTGACCGTTGACTGTAC	Star:hsa-miR-181a-2*:MIMAT0004558
CU-1048	129	AACTGGCCTACAAAGTCCCAGT	Mature:hsa-miR-193a-3p:MIMAT0000459
CU-1136	134	TCGGGCGGGAGTGGTGGCTTT	NEW
CU-1383	135	TAGAGGCACCGCCTGCCCA	NEW
CU-1131	136	CGGGGCGCGGCCTCGCTG	NEW
CU-1135	137	CCCACGGGGGTCTCCGGGCGAG	NEW
CU-1133	139	CAGCCCGGCCTGGCTCCTCCAT	NEW
CU-1134	140	CACGGAAGGTGGCCCGG	NEW
CU-1160	174	TGTCAGTTTGAACCCAA	NEW
CU-1189	175	TGTAGTGTTTCTTACTTTA	NEW
CU-1219	176	TGGCGAAGGTCGGCCGCG	NEW
CU-1190	179	TCGGCTTTCCCTGCTAACTGGGCTTTTT	NEW
CU-1144	180	TCAGAGCGCGGGCCGACCCC	NEW
CU-1384	183	TAACCCCAGGGTTGGTCA	NEW
CU-1171	185	GGGCGTGGGTGTGATGATTC	NEW
CU-1199	186	GGGAGGTGAGTAGGTCTG	NEW
CU-1226	187	GGAGACGTGGCCGAGAG	NEW
CU-1572	188	GCGGAATACCACGGGGA	NEW
CU-1151	189	GCAGGCGGGGGATTAGCTA	NEW
CU-1227	190	GCAGCGGAACGTCGGCGCGC	NEW
CU-1152	192	CTTGGACTAACCTGGTGTA	NEW
CU-1207	197	CGGTGGAACCTGCATTGGTTT	NEW
CU-1181	198	CGGGGCCGGGGCTAGGGT	NEW
CU-1185	199	CGGGCCGCCCCCGCCCACCG	NEW
CU-1366	201	CGGCCTATCCGGAATGCCCC	NEW
CU-1145	203	CGCGGCCAGTGTCCCCTTGTA	NEW
CU-1201	204	CGACACACGGCCCGTGGCGC	NEW
CU-1172	206	CCTCACTGGGGGCTCCA	NEW
CU-1217	210	CCGCCCCGACCTTAGCTA	NEW
CU-1177	214	CCCCGGCATCTCCATCA	NEW
CU-1360	218	CCACCCTGGAGCCTCCGT	NEW
CU-1179	221	ATGGCCTGGACCCCACTCCT	NEW

TABLE 7-continued

(PART A) List of known and newly identified bona fide and candidate mature miRNAs and their predicted precursors. Genomic locations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1161	222	ATGGCCGCATATATTTT	NEW
CU-1168	225	AGCGAGGGTTCCGCCGGCC	NEW
CU-1195	226	ACTGGGGAGGGGGAGGAGCCTCGAGG	NEW
CU-1215	227	ACCCCGAGGGGACGGGCG	NEW
CU-1208	228	ACAGCGCTGTGTTCCCGT	NEW
CU-1373	230	AACTAAAACCCCTACGCA	NEW
CU-1196	231	AAAGGAGCCGAATCTTT	NEW
CU-1204	224	ATCCTGCTCACAGCCCCA	NEW
CU-1325	269	TTTGCCACACTGCAACACCTT	refseqGeneIntron-annotate
CU-1310	271	TTAAACCACCAAGATCGCTGATGCAC	refseqGeneIntron-annotate
CU-1299	272	TGTTCGCCGACCGTTGA	refseqGeneIntron-annotate
CU-1165	173	TGTCAGTTTTTACCCAA	refseqGeneIntron-annotate
CU-1322	274	TGGGAGAGCAGGGTATTGT	refseqGeneIntron-annotate
CU-1203	177	TGCAGGGCCGGCGGGGAGG	refseqGeneIntron-annotate
CU-1308	277	TCCGAAAGGCCTCCCGCACCG	refseqGeneIntron-annotate
CU-1376	181	TCAACACCCACTCCCTC	refseqGeneIntron-annotate
CU-1138	182	TATCAATGATGCTTCTGAGA	refseqGeneIntron-annotate
CU-1297	279	TAGATGAATAGGTAAAGAG	refseqGeneIntron-annotate
CU-1235	280	GTGTATGATGACCTCATGTAGCCTGAAC	refseqGeneIntron-annotate
CU-1253	281	GTGAAGCGTTCCATATTTTT	mRNAall-annotate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1337	283	GGGGGGAGGGAAGGCAA	refseqGeneIntron-annotate
CU-1316	284	GGGGGCTGGGCTGGGTA	refseqGeneIntron-annotate
CU-1343	285	GGGGCCGCCGCCTGTGT	refseqGeneIntron-annotate
CU-1326	286	GGGAGTCCGCGGCGAGC	refseqGeneIntron-annotate
CU-1286	288	GGCTTGGTCTAGGGGTA	refseqGeneIntron-annotate
CU-1332	289	GGCTGGGACCCTGGACAC	refseqGeneIntron-annotate
CU-1262	290	GGCGACCTGCGACTCCTT	refseqGeneIntron-annotate
CU-1317	292	GGAGGGGGGAAAAAAAAAA	computGene-annotate; refseqGeneIntron-annotate
CU-1266	295	GCCGGGCGTGGTGGTCTG	refseqGeneIntron-annotate
CU-1261	296	GCCGCCGAGACCCCAGGACCC	refseqGeneIntron-annotate
CU-1259	298	GCAAATGATGCCCTCTGATC	refseqGeneIntron-annotate
CU-1349	299	GAGGGGGGTCAAAAAAA	refseqGeneIntron-annotate
CU-1272	300	CTTGATGATGAGCAGGATCTGAGT	refseqGeneIntron-annotate

TABLE 7-continued

(PART A) List of known and newly identified bona fide and candidate mature miRNAs and their predicted precursors. Genomic locations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1313	303	CTGCTTAAGTCCTGACCAG	refseqGeneIntron-annotate
CU-1157	196	CTGATGTTGATGCATATGATGACA	refseqGeneIntron-annotate
CU-1296	304	CTGAGCACCTTTCCCTTCC	refseqGeneIntron-annotate
CU-1245	306	CGGTCACACGATTAACCCA	mRNA-annotate; refseqGeneIntron-annotate
CU-1319	310	CGGGAGTGGGGTGGCGCCCAG	refseqGeneIntron-annotate
CU-1569	312	CGGACCTGATAAATTCCCAC	refseqGeneIntron-annotate
CU-1351	316	CCTTCCTTGGATGTCTGAGTGAG	mRNAall-annotate; refseqGeneIntron-annotate; wgRNA-annotate; rnaGene-annotate
CU-1354	317	CCTCGCTGGGGCCTCCA	tRNAprefix-annotate; refseqGeneIntron-annotate;
CU-1228	321	CCGCCCGTCACCCTCCTCAAGTA	mRNA-annotate; refseqGeneIntron-annotate
CU-1271	323	CCCGCGGGCTTGCTGGGCGTCCC	refseqGeneIntron-annotate
CU-1166	213	CCCCGGCCCATGCACCA	refseqGeneIntron-annotate;
CU-1285	325	CCCCGGCATCTCCACTA	refseqGeneIntron-annotate
CU-1571	326	CCCCAGTGAGTGCCCTCTTCC	refseqGeneIntron-annotate
CU-1353	327	CCCAGAGACGCCGTCCTCGA	refseqGeneIntron-annotate
CU-1347	330	CCACTCCAGCCTAGCCCC	refseqGeneIntron-annotate
CU-1295	331	CAGTACAGGCACACCTC	refseqGeneIntron-annotate
CU-1250	333	CACGATTAACCCAAGTC	mRNA-annotate; refseqGeneIntron-annotate
CU-1311	337	ATACCATGATGAACAATAGCTGAGA	refseqGeneIntron-annotate
CU-1350	339	AGGCTGTGATGGACCTGGCTGAGCCTG	refseqGeneIntron-annotate
CU-1252	340	AGAGAGTAGGGGGAGGT	refseqGeneIntron-annotate
CU-1334	341	ACTGTCCCTGTCTACTA	refseqGeneIntron-annotate
CU-1340	342	ACCGCATCTGGCCTATTTTT	refseqGeneIntron-annotate
CU-1342	343	ACCAGACCTCCTGTGCGAAG	refseqGeneIntron-annotate
CU-1304	344	ACAGCCCGGATCCCAGCCCACTTA	refseqGeneIntron-annotate
CU-1230	345	ACACTGAGCCACAACCCA	refseqGeneIntron-annotate
CU-1192	229	ACAAAAAAAAAAGCCCAACCCT	refseqGeneIntron-annotate
CU-1312	346	AAGGGCTTGGCTTAATTA	refseqGeneIntron-annotate
CU-1255	347	AACCCGGAAGGCGGAGGTTGCGG	computGene-annotate; refseqGeneIntron-annotate
CU-1346	349	AACAAGCTTCTTTGACGTCCCATCCAC	refseqGeneIntron-annotate
CU-1573	359	TGCCGTGATCGTATAGTGGTTA	piRNA-annotate
CU-1395	362	CTGACAGCCGGGGTTTTGGA	computGene-annotate
CU-1365	363	CGGCGGGGCCTGGAGTCTG	mRNAall-annotate; computGene-annotate; exEID-annotate
CU-1375	364	CCTGGCTCGCTGCGCCA	computGene-annotate
CU-1209	207	CCTCACCTGGAGCACCA	tRNAprefix-annotate;

TABLE 7-continued

(PART A) List of known and newly identified bona fide and candidate mature miRNAs and their predicted precursors. Genomic locations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

ID	SEQ ID NO.	Mature miRNA sequence	Annotations
CU-1174	366	CCCGAACGCTGCCAACCC	exEID-annotate
CU-1214	215	CCCCAGTACCTCCACCA	tRNAprefix-annotate;
CU-1218	223	ATCCTGTTCGTGACGCCA	tRNAprefix-annotate;
CU-1385	367	AGACCCGCGGGCGCTCTCCAGTC	rnaGene-annotate

TABLE 7

(PART B) List of known and newly identified bona fide and candidate mature miRNAs. Counts and annotations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

	SEQ	Corrected Counts				Frequencies			
Mature miRNA sequence	ID NO.	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
TGTAGTGTTTCCTACTTTATGGA	1	1329	592	635	391	40.74	21.5	25.55	17.89
TAGCTTATCAGACTGATGTTGA	2	196	353	144	13	6.01	12.82	5.79	0.59
TAAAGTGCTTATAGTGCAGGTAG	3	54	19	49.82	257.89	1.66	0.69	2	11.8
TAGCAGCACATCATGGTTTACA	4	38	61	176.84	105	1.16	2.21	7.12	4.8
TAGCAGCACGTAAATATTGGCG	5	131	97	53	35	4.02	3.52	2.13	1.6
TGAGGTAGTAGGTTGTATAGTT	6	62.84	78.99	92.19	63.25	1.93	2.87	3.71	2.89
TATTGCACTTGTCCCGGCCTGT	7	17	21	46	207	0.52	0.76	1.85	9.47
TCCCACCGCTGCCACCA	8	68	97	25	28	2.08	3.52	1.01	1.28
TGAGGTAGTAGATTGTATAGTT	9	41.28	44	64	51.38	1.27	1.6	2.58	2.35
TAGCACCATCTGAAATCGGTTA	10	78	60	42	22	2.39	2.18	1.69	1.01
TAGCAGCACATAATGGTTTGT	11	90	39	32.16	8	2.76	1.42	1.29	0.37
CCCATAAAGTAGAAAGCACTA	12	88	53	7	10	2.7	1.92	0.28	0.46
TGAGGTAGTAGTTTGTACAGTT	13	41.28	47	30.77	21.16	1.27	1.71	1.24	0.97
TGAGGTAGTAGTTTGTGCTGTT	14	23	24	32	42	0.71	0.87	1.29	1.92
TAGCACCATTTGAAATCGGTTA	15	44	41	16	1	1.35	1.49	0.64	0.05
TGTAAACATCCTACACTCTCAGC	16	27	25	26	20	0.83	0.91	1.05	0.91
CAAAGTGCTTACAGTGCAGGTAG	17	9	6	10.18	65.04	0.28	0.22	0.41	2.98
CATTGCACTTGTCTCGGTCTGA	18	11	9	34	39	0.34	0.33	1.37	1.78
CAACGGAATCCCAAAAGCAGCTG	19	17	21	36	18	0.52	0.76	1.45	0.82
TGTGCAAATCCATGCAAAACTGA	20	0	1	25	65	0	0.04	1.01	2.97
TACCACAGGGTAGAACCACGGA	21	31	22	17	21	0.95	0.8	0.68	0.96
TGTAAACATCCTACACTCAGCT	22	31	11	27	16	0.95	0.4	1.09	0.73
TGAGGTAGTAGGTTGTGTGGTT	23	19.48	19	29	5.08	0.6	0.69	1.17	0.23

TABLE 7-continued

(PART B) List of known and newly identified bona fide and candidate mature miRNAs. Counts and annotations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

	SEQ	Corrected Counts				Frequencies			
Mature miRNA sequence	ID NO.	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
TAGCACCATTTGAAATCAGTGTT	24	22	14	12	4	0.67	0.51	0.48	0.18
TAAAGTGCTGACAGTGCAGAT	25	7	6	13	26	0.21	0.22	0.52	1.19
TCCCTGTCCTCCAGGAGCTC	26	6	3	3	32	0.18	0.11	0.12	1.46
TTCAAGTAATCCAGGATAGGCT	27	2	8	13	16	0.06	0.29	0.52	0.73
CAAAGTGCTGTTCGTGCAGGTAG	28	9	2	13	14	0.28	0.07	0.52	0.64
TGTCAGTTTGTCAAATACCCCA	29	25	10	1	0	0.77	0.36	0.04	0
TGAGAACTGAATTCCATGGGTT	30	4	7	21	4	0.12	0.25	0.85	0.18
TCTCCCAACCCTTGTACCAGT	31	12	18	2	0	0.37	0.65	0.08	0
TCCCTGAGACCCTAACTTGTGA	32	0	1	28	2	0	0.04	1.13	0.09
TCTCACACAGAAATCGCACCCGTC	33	10	8	8	3	0.31	0.29	0.32	0.14
GTCCCTGTTCGGGCGCCA	34	12	10	6	1	0.37	0.36	0.24	0.05
TGTGCAAATCTATGCAAAACTGA	35	0	0	9	19	0	0	0.36	0.87
TGTAAACATCCCCGACTGGAAG	36	7	3	14	3	0.21	0.11	0.56	0.14
AGCTACATTGTCTGCTGGGTT	37	17	6	4	0	0.52	0.22	0.16	0
AGAGGTAGTAGGTTGCATAGTT	38	2	4	10	10	0.06	0.15	0.4	0.46
CCGCACTGTGGGTACTTGCT	39	8	6	2	8	0.25	0.22	0.08	0.37
AGCAGCATTGTACAGGGCTATGA	40	1	1	10	11	0.03	0.04	0.4	0.5
AACTGGCCCTCAAAGTCCCGCT	41	0	0	2	21	0	0	0.08	0.96
GCCCCTGGGCCTATCCTAGAA	42	1	0	10	10	0.03	0	0.4	0.46
AGCTGGTGTTGTGAATCAGGCCGT	43	0	0	15	5	0	0	0.6	0.23
TGAGGGGCAGAGAGCGAGACTT	44	5	1	7	4	0.15	0.04	0.28	0.18
AGCTACATCTGGCTACTGGGTCT	45	6	6	5	0	0.18	0.22	0.2	0
GTGGGGGAGAGGCTGTA	46	2	6	3	5	0.06	0.22	0.12	0.23
CTATACGACCTGCTGCCTTTC	47	6	3	4	1	0.18	0.11	0.16	0.05
TTAATGCTAATCGTGATAGGGGT	48	3	4	5	1	0.09	0.15	0.2	0.05
AGGGGGAAAGTTCTATAGTC	49	0	2	0	11	0	0.07	0	0.5
ACAGTAGTCTGCACATTGGTT	50	0	0	13	0	0	0	0.52	0
AACATTCAACGCTGTCGGTGAGTT	51	0	0	7	6	0	0	0.28	0.27
TGGAAGACTAGTGATTTTGTTGT	52	1	1	1	8	0.03	0.04	0.04	0.37
TAATGCCCCTAAAAATCCTTAT	53	0	0	6	4	0	0	0.24	0.18
TAGCAGCACAGAAATATTGGCA	54	4	0	5	0	0.12	0	0.2	0
TGAGGTAGTAGGTTGTAT	55	0.11	0.01	0.01	0.13	0	0	0	0.01

TABLE 7-continued

(PART B) List of known and newly identified bona fide and candidate mature miRNAs. Counts and annotations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

	SEQ	Corrected Counts				Frequencies			
Mature miRNA sequence	ID NO.	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
TCCTGTACTGAGCTGCCCCGAG	56	0	0	7	1	0	0	0.28	0.05
TCCCTGAGACCCTTTAACCTGTGA	57	0	0	8	0	0	0	0.32	0
ATCACATTGCCAGGGATTTCCA	58	0	0.5	7	0	0	0.02	0.28	0
TCACAGTGAACCGGTCTCTTT	59	1	0	0	6	0.03	0	0	0.27
CACTAGATTGTGAGCTCCTGGA	60	2	0	4	1	0.06	0	0.16	0.05
CAACAAATCACAGTCTGCCAT	61	3	0	1	3	0.09	0	0.04	0.14
CAAAGTGCTTATAGTGCAGGTAG	62	0	1	1	0.08	0	0.04	0.04	0
AGGTTGGGATCGGTTGCAATGCT	63	0	0	0	7	0	0	0	0.32
ACATTCATTGCTGTCGGTGGGTT	64	0	0	1	6	0	0	0.04	0.27
AATGACACGATCACTCCCGTTGAG	1095	0	0	7	0	0	0	0.28	0
TCCCCCAGGTGTGATTCTGATT	65	4	1	0	1	0.12	0.04	0	0.05
CCCAGTGTTCAGACTACCTGTTC	66	0	0	6	0	0	0	0.24	0
ACCAATATTACTGTGCTGCTT	67	1	1	2	2	0.03	0.04	0.08	0.09
TGTAAACATCCTTGACTGGAAGCT	68	2	0	3	0	0.06	0	0.12	0
TAAGGTGCATCTAGTGCAGATA	69	0	0	1	4	0	0	0.04	0.18
ATCACATTGCCAGGGATTACCA	70	0	0.5	3	1	0	0.02	0.12	0.05
ACTGCCCTAAGTGCTCCTTCTG	71	0	0	0	5	0	0	0	0.23
TGTAAACATCCTCGACTGGA	72	1	0	3	0	0.03	0	0.12	0
TACAGTACTGTGATAACTGAAG	73	1	0	0	3	0.03	0	0	0.14
CTAGACTGAAGCTCCTTGAGG	74	2	1	1	0	0.06	0.04	0.04	0
TGGGTTGAGAGGGCGAA	1094	1	0	1	1	0.03	0	0.04	0.05
TGGCAGTGTCTTAGCTGGTTGTT	75	0	1	2	0	0	0.04	0.08	0
TGAGGTAGTAAGTTGTATTGTT	76	0	1	1	1	0	0.04	0.04	0.05
TGAGAACTGAATTCCATAGGCTGT	77	1	0	2	0	0.03	0	0.08	0
TCGAGGAGCTCACAGTCTAGTA	78	1	0	1	1	0.03	0	0.04	0.05
AGCTCGGTCTGAGGCCCCTCAG	79	0	0	2	1	0	0	0.08	0.05
ACTGCAGTGAAGGCACTTGTAG	80	0	0	0	3	0	0	0	0.14
ACCATCGACCGTTGATTGTA	81	0	1	0	2	0	0.04	0	0.09
TTCACCACCTTCTCCACCCAG	82	0	0	0	2	0	0	0	0.09
TTCACAGTGGCTAAGTTCTG	83	0	0	2	0	0	0	0.08	0
TTCAAGTAATTCAGGATAGGTT	84	0	0	1	1	0	0	0.04	0.05
TGGGTTTACGTTGGGAGAACT	85	0	0	0	2	0	0	0	0.09
TGAGGTAGGAGGTTGTATAGTT	87	0	0	1.02	0	0	0	0.04	0

TABLE 7-continued

(PART B) List of known and newly identified bona fide and candidate mature miRNAs. Counts and annotations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

	SEQ	Corrected Counts				Frequencies			
Mature miRNA sequence	ID NO.	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
TGACCGATTTCTCCTGGTGTT	88	2	0	0	0	0.06	0	0	0
TATTGCACTCGTCCCGGCC	89	0	0	1	1	0	0	0.04	0.05
GGGGTGCTATCTGTGATTGA	90	2	0	0	0	0.06	0	0	0
GCATGGGTGGTTCAGTGGTAGAA	91	0	0	2	0	0	0	0.08	0
CTGGCCCTCTCTGCCCTT	92	0	0	1	1	0	0	0.04	0.05
CTGACCTATGAATTGACAGC	93	0	0	0	2	0	0	0	0.09
CTCCTGACTCCAGGTCCTGTG	94	0	0	0	2	0	0	0	0.09
CGTCAACACTTGCTGGTT	95	0	0	1	1	0	0	0.04	0.05
CGAATCATTATTTGCTGCTCT	96	0	0	1	1	0	0	0.04	0.05
CATCGGGAATGTCGTGTCCGCC	97	0	2	0	0	0	0.07	0	0
CAGTGGTTTTACCCTATGGTA	98	0	0	1	1	0	0	0.04	0.05
CAGTGCAATGATGAAAGGGCAT	99	0	0	2	0	0	0	0.08	0
CAGCAGCACACTGTGGTTTGT	100	0	0	2	0	0	0	0.08	0
CACGCTCATGCACACACCCAC	101	0	0	2	0	0	0	0.08	0
AAGGAGCTCACAGTCTATTGAG	102	0	0	2	0	0	0	0.08	0
GCCGGGTACTTTCGTATTTT	131	3	3	0	34	0.09	0.11	0	1.56
GCTAAGGAAGTCCTGTGCTCAG TTTT	132	0	0	1	19	0	0	0.04	0.87
AGGGTGTGCGTGTTTTT	148	0	0	0	20	0	0	0	0.91
GAGAGCGCTCGGTTTTT	150	0	0	1	9	0	0	0.04	0.41
TGGTGTGGTCTGTTGTTTT	151	0	0	0	9	0	0	0	0.41
TGTGCTCCGGAGTTACCTCGTTT	152	0	0	0	8	0	0	0	0.37
AACCGAGCGTCCAAGCTCTTTC CATTTT	155	0	0	0	5	0	0	0	0.23
TCCCCGCACCTCCACCA	156	0	2	1	1	0	0.07	0.04	0.05
GGCGTGATTCATACCTTTT	162	0	0	0	2	0	0	0	0.09
ATGTGGTGGCTTACTTTT	169	0	0	0	2	0	0	0	0.09
AGAAAGGCCGAATTTTA	172	0	0	1	1	0	0	0.04	0.05
TCCCCGGCACTTCCACCA	157	0	3	0	0	0	0.11	0	0
CCCACCCAGGGACGCCA	232	223	218	6	2	6.84	7.92	0.24	0.09
TCCCCGGCACCTCCACCA	233	60.47	101.82	40.28	34	1.85	3.7	1.62	1.56
ATCCCGGACGAGCCCCCA	234	48	60	80	45	1.47	2.18	3.22	2.06
CCCCCCACTGCTAAATTTGACTG GCTT	142	18	8	61	22	0.55	0.29	2.45	1.01
TCGATTCCCGGCCAATGCACCA	236	4	18	36	4	0.12	0.65	1.45	0.18
ATCCCACTTCTGACACCA	237	11	9	26.69	14	0.34	0.33	1.07	0.64

TABLE 7-continued

(PART B) List of known and newly identified bona fide and candidate mature miRNAs. Counts and annotations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

	SEQ	Corrected Counts				Frequencies			
Mature miRNA sequence	ID NO.	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
TCCCCGTACGGGCCACCA	239	11	6	3	2	0.34	0.22	0.12	0.09
AGTCCCATCTGGGTCGCCA	243	4	2	3	6	0.12	0.07	0.12	0.27
CCCCCCACTGCTAAATTTGACTGGA	244	1	1	6	2	0.03	0.04	0.24	0.09
GTCCCTTCGTGGTCGCCA	246	1	2	1	2	0.03	0.07	0.04	0.09
TCCTCACACGGGGCACCA	248	2	1	2	0	0.06	0.04	0.08	0
TAACGGCCGCGGTACCC	249	0	3	1	0	0	0.11	0.04	0
GAGGGGGACCAAAAAAAA	250	0	0	0	4	0	0	0	0.18
CCCGGGTTTCGGCACCA	133	0	3	0	1	0	0.11	0	0.05
ATAGGTTTGGTCCTAGCCTTTCT	354	0	0	3	1	0	0	0.12	0.05
AGGGGGGTAAAAAAAAA	252	0	0	0	4	0	0	0	0.18
GAGCCATGATGATACCACTGAGC	254	0	1	0	2	0	0.04	0	0.09
AGAACACTACGAGCCACA	257	3	0	0	0	0.09	0	0	0
ACCCCACTTCTGGTACCA	258	0	0	1	2	0	0	0.04	0.09
TCTCGGTGGAACCTCCA	260	0	0	1	1	0	0	0.04	0.05
TACCGAGCCTGGTGATAGC	262	0	1	1	0	0	0.04	0.04	0
GCAGCGCCAGCCTCCCGCCCTAC	263	2	0	0	0	0.06	0	0	0
ATCCCCAGCACCTCCACCA	265	0	0	0	2	0	0	0	0.09
AGCAGTGATGTCCTGAAAATTCTGAAG	266	0	0	0	2	0	0	0	0.09
ACCCCACTATGCTTAGCCCT	267	0	0	2	0	0	0	0.08	0
AAAGGACCTGGCGGTGCTTC	268	1	0	1	0	0.03	0	0.04	0
TCCCCGGCATCTCCACCA	350	116.53	275.18	104.72	59	3.57	9.99	4.21	2.7
GCCCGCATCCTCCACCA	143	38	61	2	4	1.16	2.21	0.08	0.18
ATCCCACTCCTGACACCA	145	7	13	11.31	3	0.21	0.47	0.46	0.14
TCGATTCCCGGCCCATGCACCA	149	1	2	10	4	0.03	0.07	0.4	0.18
TCCCCGACACCTCCACCA	153	2	2	2	1	0.06	0.07	0.08	0.05
TCTAGAGGAGCCTGTTCTGTA	352	0	1	3	0	0	0.04	0.12	0
TCGATTCCCGGTCAGGGAACCA	353	0	0	0	4	0	0	0	0.18
TCACCCCATAAACACCA	158	2	1	0	0	0.06	0.04	0	0
CGTTCGCGCTTTCCCCTG	355	0	1	2	0	0	0.04	0.08	0
TTCCCCGACGGGGAGCCA	161	1	0	0	1	0.03	0	0	0.05
TAAGTGTTTGTGGGTTA	356	1	1	0	0	0.03	0.04	0	0
ATCCCCAGCATCTCCACCA	171	0	0	2	0	0	0	0.08	0
CCCCCACAACCGCGCTTGACTA	368	12	11	7	9	0.37	0.4	0.28	0.41

TABLE 7-continued

(PART B) List of known and newly identified bona fide and candidate mature miRNAs. Counts and annotations are provided for all candidate miRNA. Frequencies have been calculated only for bona fide miRNA (cloned at least 2 times in the B cell libraries).

	SEQ	Corrected Counts				Frequencies			
Mature miRNA sequence	ID NO.	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)	Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
GC									
CCCTGCTCGCTGCGCCA	369	7	20	5	1	0.21	0.73	0.2	0.05
CTCCCACTGCTTCACTTGACTAGC	370	2	2	18	9	0.06	0.07	0.72	0.41
TCACGTCGGGGTCACCA	372	16	4	5	1	0.49	0.15	0.2	0.05
TCCCTGGTGGTCTAGTGGTTAG GATTCG	373	0	1	10	6	0	0.04	0.4	0.27
TCCTGCCGCGGTCGCCA	375	6	8	0	1	0.18	0.29	0	0.05
GGAGAGAACGCGGTCTGAGTG GT	376	3	7	1	0	0.09	0.25	0.04	0
TCGGGTGCGAGAGGTCCCGGGT	377	0	0	0	10	0	0	0	0.46
GGCTGGTCCGATGGTAGTGGGTT	378	4	3	3	0	0.12	0.11	0.12	0
CGGAAGCGTGCTGGGCCC	379	1	5	0	4	0.03	0.18	0	0.18
GCGGGTGATGCGAACTGGAGTC TGAGC	381	0	0	6	1	0	0	0.24	0.05
GACGAGGTGGCCGAGTGG	382	2	3	2	0	0.06	0.11	0.08	0
CTGATTGCTCCTGTCTGATT	351	0	0	6	1	0	0	0.24	0.05
CTCCTGGCTGGCTCGCCA	384	0	0	3	3	0	0	0.12	0.14
GGCTGGTCCGAGTGCAGTGGTG TTTA	386	0	1	4	0	0	0.04	0.16	0
CTGCTGTGATGACATTC	387	1	2	2	0	0.03	0.07	0.08	0
TCCTCGTTAGTATAGTGGTGAGT ATCCC	389	0	1	3	0	0	0.04	0.12	0
GCATTGGTGGTTCAGTGGTAGA	391	0	0	3	1	0	0	0.12	0.05
TTCTCACTACTGCACTTGACTA	395	0	0	2	1	0	0	0.08	0.05
TGGTTATCACGTTCGCC	396	0	2	0	1	0	0.07	0	0.05
TAGGGGTATGATTCTCGCT	397	1	0	0	2	0.03	0	0	0.09
CGTCCATGATGTTCCGCAA	255	1	0	2	0	0.03	0	0.08	0
CCACGAGGAAGAGAGGTAGC	398	2	1	0	0	0.06	0.04	0	0
TGTATTGTGAGACATTC	259	0	1	1	0	0	0.04	0.04	0
GTCAGGATGGCCGAGCGGTCT	399	0	1	1	0	0	0.04	0.04	0

[0351] A sizeable number of sequences (334) aligned to genomic regions that did not fulfill the criteria for miRNA precursors (FIG. **24**). About 80% of these sequences were annotated or cloned only once and may represent degradation products originating from other RNA species (FIG. **24** and Table 8). The remaining (58 sequences), however, mapped to genomic regions that lack annotations and may therefore represent a part of the transcriptome whose functions are unknown (Table 9 and Table 10). Interestingly, several of these nonannotated sequences (i.e., CU-5004, CU-5021, CU-6030, CU-6069) were cloned multiple times and showed differential expression across libraries (Table 9 and Table 10), suggesting that they may represent short RNAs with characteristics distinct from those currently recognized in "classic" miRNAs.

[0352] In conclusion, the generation of short-RNA libraries from normal and neoplastic B cells led to the identification of 178 mature miRNAs cloned multiple times as well as other short-RNA species of unknown function.

TABLE 8

Characterization of short-RNA libraries. Number of not redundant short-RNAs cloned in each library (naïve B cells, memory B cells, centroblasts and Ramos cell line) and overall (total). Each short-RNA is annotated according to the listed RNA species. Results shown here refer only to short-RNA with matches to the human genome. The same short-RNA might match to multiple databases and therefore the overall sum does not correspond to the total number of short-RNAs.

RNA species	Naive	Memory	Centroblasts	Ramos	Total
Total (non redundant)	680	709	740	740	2086
miRNA	424	408	528	538	1259
miRNA other*	1	0	3	0	4
tRNA	27	33	32	29	108
rRNA	61	99	34	16	174
mRNA	76	72	25	34	176
snoRNA	8	13	15	6	40
yRNA	11	11	31	21	53
piRNA	46	54	70	62	148

TABLE 8-continued

Characterization of short-RNA libraries. Number of not redundant short-RNAs cloned in each library (naïve B cells, memory B cells, centroblasts and Ramos cell line) and overall (total). Each short-RNA is annotated according to the listed RNA species. Results shown here refer only to short-RNA with matches to the human genome. The same short-RNA might match to multiple databases and therefore the overall sum does not correspond to the total number of short-RNAs.

RNA species	Naive	Memory	Centroblasts	Ramos	Total
Repeats	1	1	0	1	2
Mitochondrial genome	12	36	54	11	101
Human viruses	1	4	0	0	5
E. Coli	5	4	0	0	7
Not Annotated	111	119	97	134	375

*miRNA other: includes fragments of miRNA precursors, not mature.

The databases used in this analysis are detailed in Supplementary Methods.

TABLE 9

(PART A) List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs. Table includes information on genomic locations and annotations.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-5004	1096	GAAGCGGGTGCTCTTATTTT	NEW
CU-5008	1097	GTGTAAGCAGGGTCGTTTT	NEW
CU-6003	1098	ATCCCACCGCTGCTACCA	NEW
CU-5023	1099	GGGAAGGTGACCTGAC	NEW
CU-5007	1100	CTCCCGCCTTTTTTCCC	NEW
CU-5024	1101	CGGAGCAAGAGCGT	NEW
CU-5026	1102	CCCCCGGCACCATCAATA	NEW
CU-5027	1103	CAGCCTAGCCCCTACCC	NEW
CU-5005	1104	CAGAAGGTCTCACTTTT	NEW
CU-5006	1105	AGTATTCTCTGTGGCTTT	NEW
CU-5028	1106	TGGAGTGACTATATGGATGCCCCC	NEW
CU-5029	1107	TCTGATAGCTTACTTT	NEW
CU-5030	1108	TCGAGCCCCAGTGGAACCAC	NEW
CU-5032	1109	TCCTCCCCACACTCATCGCCCTTACCA	NEW
CU-5033	1110	TATACTACAAGGACACCA	NEW
CU-5034	1111	TAGTGGGTGAAAAAAAAAAAA	NEW
CU-5035	1112	TACCACACATTCGAAGAACCCGTA	NEW
CU-5036	1113	TACAAAAoGGGGTAAAAAAAA	NEW
CU-5037	1115	GCCCTCCTAATGACCTCC	NEW
CU-5038	1116	CTTCCCTCTACACTTATCATC	NEW
CU-5039	1117	CGGGCGGCCTGCGCTCTCA	NEW
CU-5040	1118	CCCGAGGCCGTGTGCAAATGCAT	NEW
CU-5020	1119	CCCCGGCATCTCCACC	NEW

TABLE 9-continued

(PART A) List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs. Table includes information on genomic locations and annotations.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-5041	1120	CCCCCAGTACCTCCACCA	NEW
CU-5042	1121	CCCCCACTGCTAAACTTGACTGGCTTT	NEW
CU-5043	1122	CCCACTCCACCTTACTACCA	NEW
CU-5044	1123	CCCAAGAACAGGGTGACCA	NEW
CU-5045	1124	CCAGTCGCGGCCAAATCA	NEW
CU-5046	1125	CCAGCTTCACCAAGGTATTGGTTA	NEW
CU-5047	1126	CCAGAAAAAACAGGCCTC	NEW
CU-5048	1127	CATCATAATCGGAGGCTTTGGCAAC	NEW
CU-5049	1128	CAGCAGGGGTAATAAGTGAAATCAAA	NEW
CU-5050	1129	CAATGGTGCAGCCGCTATTAAAGGTTCA	NEW
CU-5051	1130	CAACTCCTACATACTTCCCCC	NEW
CU-5053	1131	ATGCATCTCATATGCGAATAGGAATGC	NEW
CU-5054	1132	ATCCCACTTCTGTACCA	NEW
CU-5055	1133	ATAACACTAGAAAGTTGGGGCAGATTGC	NEW
CU-5056	1134	ACGTGGGCACATTACCCGTCTGACCTGA	NEW
CU-5057	1135	ACCCCTTATTAACCCA	NEW
CU-5058	1136	ACAAGGCACACCTACACCCCTTATCCC	NEW
CU-5059	1137	AAAAGACACCCCCCCACCA	NEW
CU-5060	1138	AAAACCCCTACGCATTTATAT	NEW
CU-5061	1139	AAAAAGACACCCCCCACCA	NEW
CU-5011	1140	GCTAAACCTAGCCCCAAACCC	piRNA-annotate; refseqGeneIntron-annotate
CU-5003	1141	ACCCCACTCCTGGTACCA	refseqGeneIntron-annotate
CU-5009	1142	TGCCCCCATGTCTAACAACATGGCTA	refseqGeneIntron-annotate; rnaGene-annotate
CU-5062	1143	CCCCGCCTGTTTACC	refseqGeneIntron-annotate
CU-5063	1144	CCCACTTCTGACACCA	computGene-annotate; refseqGeneIntron-annotate; exEID-annotate
CU-5064	1145	CACCACCTCTTGCTCAGCC	mRNA-annotate; refseqGeneIntron-annotate
CU-5014	1146	CTGGAAAGTGCACTTGGACGAACA	refseqGeneIntron-annotate
CU-5065	1147	TGACCGCTCTGACCAC	refseqGeneIntron-annotate
CU-5066	1148	TGAAGTCCCTTTGCTTTGTT	refseqGeneIntron-annotate
CU-5067	1149	TGAACACACAATAGCTAAGACCC	mRNA-annotate; refseqGeneIntron-annotate
CU-5068	1150	TCGCCTTACCCCCCACTA	refseqGeneIntron-annotate
CU-5069	1151	TCGATAAACCCCGATCAACCT	mRNA-annotate; refseqGeneIntron-annotate
CU-5070	1152	TCCCCGTCACCTCCACCA	refseqGeneIntron-annotate
CU-5071	1153	TCCCCGGCACTCCACCA	refseqGeneIntron-annotate

TABLE 9-continued

(PART A) List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs. Table includes information on genomic locations and annotations.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-5072	1154	TCCCCCCGCTGCCACCA	refseqGeneIntron-annotate
CU-5073	1155	TCCCCCCCATCTCCACCA	refseqGeneIntron-annotate
CU-5074	1156	TACACACCGCCCGTCACCC	mRNA-annotate; refseqGeneIntron-annotate
CU-5076	1157	GCTTAGCCTAGCCACACCCCCACG	mRNA-annotate; refseqGeneIntron-annotate
CU-5077	1158	GCTCGCCAGAACACTACGA	mRNA-annotate; refseqGeneIntron-annotate
CU-5078	1159	GCCGGGGGGCGGGCGCA	refseqGeneIntron-annotate
CU-5079	1160	GAACCGGGCGGGAACACCA	refseqGeneIntron-annotate
CU-5080	1161	CGCCGCAGTACTGATCATTC	refseqGeneIntron-annotate
CU-5081	1162	CCGCACCAATAGGATCCTCC	refseqGeneIntron-annotate
CU-5082	1163	CCCGGCCGACGCACCA	refseqGeneIntron-annotate
CU-5083	1164	CCACCCCATCATACTCTTTC	refseqGeneIntron-annotate
CU-5084	1165	CACCCCCCAGCTCCTCCTTT	refseqGeneIntron-annotate
CU-5085	1166	ATAAGTAACATGAAAACATTCTCCTC	refseqGeneIntron-annotate
CU-5086	1167	ACTGCTCGCCAGAACAC	mRNA-annotate; refseqGeneIntron-annotate
CU-5087	1168	ACCCTGGTGTGGGATCTGCCCGATC	refseqGeneIntron-annotate
CU-5088	1169	AACCTCACCACCTCTTTCT	refseqGeneIntron-annotate
CU-5089	1170	AAAAGACACCCCCCACACCA	refseqGeneIntron-annotate
CU-5021	1171	ACCGGGGCGGAAACACCA	tRNAprefix-annotate
CU-5022	1172	TCCCGGGTTCAAATCCCGGACGAGCCCCCA	tRNAprefix-annotate
CU-5010	1173	GGCCGTGATCGTATA	piRNA-annotate
CU-5025	1174	CCCCGTACTGGCCACCA	tRNAprefix-annotate
CU-5090	1175	TGGGATGCGAGAGGTCCCGGGT	rnaGene-annotate
CU-5031	1176	TCGAATCCTGTTCGTGACGCCA	tRNAprefix-annotate
CU-5091	1177	CTGAACTCCTCACACCC	piRNA-annotate
CU-5052	1178	ATTCAAAAAAGAGTACCA	tRNAprefix-annotate
CU-5092	1179	ATTAATCCCCTGGCCCAACCCG	computGene-annotate
CU-5093	1180	AGCCCCAAACCCACTCCAC	piRNA-annotate
CU-5094	1181	CGCGACCTCAGATCAGAC	rRNA-eliminate; piRNA-annotate; refseqGeneIntron-annotate
CU-5013	1182	GGCCGGTGATGAGAACT	mRNAall-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; wgRNA-annotate; snoRNA-annotate
CU-5015	1183	TCAAGTGATGTCATCTTACTACTGAGA	mRNAall-annotate; snoRNA-annotate; refseqGeneExon-eliminate; rnaGene-annotate; refseqGeneIntron-annotate; snoRNA-eliminate; wgRNA-annotate
CU-5095	1184	TTGGGTGCGAGAGGTCCCGGGT	tRNAcomputational-annotate; tRNA-eliminate; HStRNA-eliminate; rnaGene-annotate

TABLE 9-continued

(PART A) List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs. Table includes information on genomic locations and annotations.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-5096	1185	TCTCGGTGGGACCTCCA	tRNAprefix-annotate; refseqGeneExon-eliminate
CU-5097	1186	CCGCCCCCCGTTCCCCC	rRNA-eliminate
CU-5098	1187	CCCACTGCTAAATTTGACTGGCTT	mRNAall-annotate; yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-5099	1188	ACAGACCAAGAGCCTTC	tRNA-eliminate; rnaGene-annotate
CU-5100	1189	TGTAGTAGTCAATTAATGGATATTA	refseqGeneExon-eliminate
CU-5101	1190	TGGTTATCACGTTCGCCTCACACGCGA	tRNAcomputational-annotate; tRNA-eliminate; HStRNA-eliminate; rnaGene-annotate
CU-5102	1191	TGGGAATACCGGGTG	rRNA-eliminate; rnaGene-annotate; piRNA-annotate; refseqGeneIntron-annotate
CU-5103	1192	TGGCGGCCAAGCGTTCATAGCGACGTC	rRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-5104	1193	TCGTCATCCAGCTAAGGGCTCAGA	mRNAall-annotate; refseqGeneExon-eliminate; exEID-annotate
CU-5105	1194	TCGCCTGCCACGCGGGAGGCCCGGGT	rnaGene-annotate; tRNAcomputational-annotate; tRNA-eliminate; refseqGeneIntron-annotate; mRNA-annotate; HStRNA-eliminate
CU-5106	1195	TCCCACTGCTTCACTTGA	yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-5107	1196	GTTTAGACGGGCTCACATCACCCCA	tRNA-eliminate; piRNA-annotate; refseqGeneIntron-annotate
CU-5075	1197	GGCCGGTGATGAGAACTTCTCCC	mRNAall-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; wgRNA-annotate; snoRNA-annotate
CU-5108	1198	GCTAACTCATGCCCCCATGTC	tRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-5109	1199	GACTGTGGTGGTTGAATATA	mRNAall-annotate; computGene-annotate; refseqGeneExon-eliminate; exEID-annotate
CU-5110	1200	CGCGACCTCAGATCAGACGTGGCGACC	rRNA-eliminate; piRNA-annotate; refseqGeneIntron-annotate
CU-5111	1201	CGCCGCCGCCCCCCC	mRNAall-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; exEID-annotate
CU-5112	1202	CGCCCGACTACCACCACATCCA	mRNAall-annotate; computGene-annotate; refseqGeneExon-eliminate; exEID-annotate
CU-5113	1203	CCCCCCTCCACGCGCCC	rRNA-eliminate; refseqGeneIntron-annotate
CU-5114	1204	CCCCACCCCGCGCCCTC	rRNA-eliminate; refseqGeneIntron-annotate
CU-5115	1205	CAGAGTGTAGCTTAACACAAAGCACCCAA	tRNA-eliminate; piRNA-annotate; rnaGene-annotate
CU-5116	1206	CAATCTTGGCATGTTGGTCTGGTCACCCA	mRNAall-annotate; refseqGeneExon-eliminate; exEID-annotate
CU-5117	1207	CAAAGCATCGCGAAGGCCC	mRNAall-annotate; rRNA-eliminate; piRNA-annotate; rnaGene-annotate
CU-5118	1208	AACACCCTGATTGCTCCTGTCTGAT	mRNAall-annotate; exEID-annotate; snoRNA-annotate; refseqGeneExon-eliminate; rnaGene-annotate; snoRNA-eliminate; wgRNA-annotate
CU-5119	1209	AAAAAGGGCCTAAAGAAGATGCA	mRNAall-annotate; computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; exEID-annotate

TABLE 9

(PART B) List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs. Table includes information on counts.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1210	GAAGCGGGTGCTCTTATTTT	5	23	25	224
1211	GTGTAAGCAGGGTCGTTTT	0	0	0	7
1212	ATCCCACCGCTGCTACCA	0	1	0	2
1213	GGGAAGGTGACCTGAC	2	0	0	0
1214	CTCCCGCCTTTTTTCCC	0	2	0	0
1215	CGGAGCAAGAGCGT	2	0	0	0
1216	CCCCCGGCACCATCAATA	0	0	1	1
1217	CAGCCTAGCCCCTACCC	0	2	0	0
1218	CAGAAGGTCTCACTTTT	0	1	0	1
1219	AGTATTCTCTGTGGCTTT	0	0	0	2
1220	TGGAGTGACTATATGGATGCCCCC	0	0	1	0
1221	TCTGATAGCTTACTTT	0	1	0	0
1222	TCGAGCCCCAGTGGAACCAC	0	0	1	0
1223	TCCTCCCCACACTCATCGCCCTTACCA	0	0	1	0
1224	TATACTACAAGGACACCA	0	0	0	1
1225	TAGTGGGTGAAAAAAAAAAAA	0	0	0	1
1226	TACCACACATTCGAAGAACCCGTA	0	0	1	0
1227	TACAAAACCCACCCCATTCCTCCCCA	0	1	0	0
1228	GGAGGGGGGGTAAAAAAAA	0	0	1	0
1229	GCCCTCCTAATGACCTCC	0	0	1	0
1230	CTTCCCTCTACACTTATCATC	0	0	1	0
1231	CGGGCGGCCTGCGCTCTCA	1	0	0	0
1232	CCCGAGGCCGTGTGCAAATGCAT	0	0	1	0
1233	CCCCGGCATCTCCACC	1	0	0	0
1234	CCCCCAGTACCTCCACCA	0	1	0	0
1235	CCCCCACTGCTAAACTTGACTGGCTTT	0	0	1	0
1236	CCCACTCCACCTTACTACCA	0	0	0	1
1237	CCCAAGAACAGGGTGACCA	0	0	0	1
1238	CCAGTCGCGGCCAAATCA	0	1	0	0
1239	CCAGCTTCACCAAGGTATTGGTTA	0	0	1	0
1240	CCAGAAAAAACAGGCCTC	0	0	0	1

TABLE 9-continued

(PART B) List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs. Table includes information on counts.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1241	CATCATAATCGGAGGCTTTGGC AAC	0	0	1	0
1242	CAGCAGGGGTAATAAGTGAAAT CAAA	0	0	1	0
1243	CAATGGTGCAGCCGCTATTAAA GGTTCA	0	0	0	1
1244	CAACTCCTACATACTTCCCCC	1	0	0	0
1245	ATGCATCTCATATGCGAATAGGA ATGC	0	0	1	0
1246	ATCCCACTTCTGTACCA	0	1	0	0
1247	ATAACACTAGAAAGTTGGGGCA GATTGC	0	0	1	0
1248	ACGTGGGCACATTACCCGTCTG ACCTGA	0	0	0	1
1249	ACCCCTTATTAACCCA	0	1	0	0
1250	ACAAGGCACACCTACACCCCTT ATCCC	0	0	1	0
1251	AAAAGACACCCCCCCACCA	0	0	0	1
1252	AAAACCCCTACGCATTTATAT	0	0	1	0
1253	AAAAAGACACCCCCCACCA	0	0	0	1
1254	GCTAAACCTAGCCCCAAACCC	9	16	13	18
1255	ACCCCACTCCTGGTACCA	1	11	5	6
1256	TGCCCCCATGTCTAACAACATG GCTA	7	4	1	1
1257	CCCCGCCTGTTTACC	0	5	2	0
1258	CCCACTTCTGACACCA	3	4	0	0
1259	CACCACCTCTTGCTCAGCC	1	3	0	0
1260	CTGGAAAGTGCACTTGGACGAA CA	0	2	0	0
1261	TGACCGCTCTGACCAC	0	1	0	0
1262	TGAAGTCCCTTTGCTTTGTT	1	0	0	0
1263	TGAACACACAATAGCTAAGACCC	0	0	1	0
1264	TCGCCTTACCCCCCACTA	0	1	0	0
1265	TCGATAAACCCCGATCAACCT	0	0	1	0
1266	TCCCCGTCACCTCCACCA	0	0	1	0
1267	TCCCCGGCACTCCACCA	0	0	1	0
1268	TCCCCCCGCTGCCACCA	1	0	0	0
1269	TCCCCCCCATCTCCACCA	0	0	1	0

TABLE 9-continued

(PART B) List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs. Table includes information on counts.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1270	TACACACCGCCCGTCACCC	0	0	1	0
1271	GCTTAGCCTAGCCACACCCCCACG	0	0	1	0
1272	GCTCGCCAGAACACTACGA	0	0	1	0
1273	GCCGGGGGGCGGGCGCA	0	1	0	0
1274	GAACCGGGCGGGAACACCA	0	0	0	1
1275	CGCCGCAGTACTGATCATTC	0	0	1	0
1276	CCGCACCAATAGGATCCTCC	0	1	0	0
1277	CCCGGCCGACGCACCA	1	0	0	0
1278	CCACCCCATCATACTCTTTC	0	0	1	0
1279	CACCCCCCAGCTCCTCCTTT	1	0	0	0
1280	ATAAGTAACATGAAAACATTCTCCTC	0	0	1	0
1281	ACTGCTCGCCAGAACAC	0	0	1	0
1282	ACCCTGGTGTGGGATCTGCCCGATC	0	0	1	0
1283	AACCTCACCACCTCTTTCT	0	0	1	0
1284	AAAAGACACCCCCCACACCA	0	0	0	1
1285	ACCGGGCGGAAACACCA	9	14	60	20
1286	TCCCGGGTTCAAATCCCGGACGAGCCCCCA	0	0	4	37
1287	GGCCGTGATCGTATA	2	0	0	0
1288	CCCCGTACTGGCCACCA	2	0	0	0
1289	TGGGATGCGAGAGGTCCCGGGT	0	0	0	1
1290	TCGAATCCTGTTCGTGACGCCA	0	0	0	1
1291	CTGAACTCCTCACACCC	0	1	0	0
1292	ATTCAAAAAAGAGTACCA	0	0	1	0
1293	ATTAATCCCCTGGCCCAACCCG	0	0	0	1
1294	AGCCCCAAACCCACTCCAC	0	0	1	0
1295	CGCGACCTCAGATCAGAC	1	5	8	1
1296	GGCCGGTGATGAGAACT	4	3	0	0
1297	TCAAGTGATGTCATCTTACTACTGAGA	0	0	3	1
1298	TTGGGTGCGAGAGGTCCCGGGT	0	0	0	3
1299	TCTCGGTGGGACCTCCA	0	2	0	0
1300	CCGCCCCCCGTTCCCCC	1	1	0	0
1301	CCCACTGCTAAATTTGACTGGCTT	0	0	1	1

TABLE 9-continued

(PART B) List of short-RNA lacking genomic locations with appropriate RNA secondary structures to be defined miRNAs. Table includes information on counts.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1302	ACAGACCAAGAGCCTTC	0	0	2	0
1303	TGTAGTAGTCAATTAATGGATATTA	0	0	1	0
1304	TGGTTATCACGTTCGCCTCACACGCGA	0	0	0	1
1305	TGGGAATACCGGGTG	0	0	1	0
1306	TGGCGGCCAAGCGTTCATAGCGACGTC	0	0	0	1
1307	TCGTCATCCAGCTAAGGGCTCAGA	0	0	1	0
1308	TCGCCTGCCACGCGGGAGGCCCGGGT	0	0	1	0
1309	TCCCACTGCTTCACTTGA	0	0	0	1
1310	GTTTAGACGGGCTCACATCACCCCA	0	0	1	0
1311	GGCCGGTGATGAGAACTTCTCCC	1	0	0	0
1312	GCTAACTCATGCCCCCATGTC	0	0	1	0
1313	GACTGTGGTGGTTGAATATA	0	0	0	1
1314	CGCGACCTCAGATCAGACGTGGCGACC	0	0	1	0
1315	CGCCGCCGCCCCCCC	0	1	0	0
1316	CGCCCGACTACCACCACATCCA	1	0	0	0
1317	CCCCCCTCCACGCGCCC	0	1	0	0
1318	CCCCACCCCGCGCCCTC	0	1	0	0
1319	CAGAGTGTAGCTTAACACAAAGCACCCAA	0	0	1	0
1320	CAATCTTGGCATGTTGGTCTGGTCACCCA	0	0	1	0
1321	CAAAGCATCGCGAAGGCCC	0	0	1	0
1322	AACACCCTGATTGCTCCTGTCTGAT	0	0	1	0
1323	AAAAAGGGCCTAAAGAAGATGCA	0	0	1	0

TABLE 10

(PART A) List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic locations and annotations.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6232	1324	TGGCTCAGTTCAGCAGGAACAGT	Mature:hsa-miR-24:MIMAT0000080
CU-6180	1325	GTGGGGGAGAGGCTGTCGA	Mature:hsa-miR-1275:MIMAT0005929
CU-6130	1326	CGGGGCAGCTCAGTACAGGATT	Mature:hsa-miR-486-3p:MIMAT0004762
CU-6044	1327	AATTGCACGGTATCCATCTGTAT	Mature:hsa-miR-363:MIMAT0000707
CU-6239	1328	TGTCAGTTTGTTAATTGACCCAA	NEW
CU-6006	1329	GGCAATACGAGCACCCTG	NEW
CU-6133	1330	CGGGGGAGCGCCGCGTA	NEW
CU-6004	1331	CCGGGGCGTCTCGTAC	NEW
CU-6056	1332	AGCGGCTGTGCACAAA	NEW
CU-6242	1333	TGTCAGTTTGTTTAATCCAA	NEW
CU-6241	1334	TGTCAGTTTGTTATTACCAA	NEW
CU-6237	1335	TGTCAGGCACCATCAATAA	NEW
CU-6225	1336	TGATCTTGACACTTAAAGCC	NEW
CU-6219	1337	TCGTAGGCACCATCAAT	NEW
CU-6215	1338	TCGATCCCGGGTTTCGGCACCA	NEW
CU-6211	1339	TCGACTCCCGGTATGGGAACCA	NEW
CU-6187	1340	TAGGGAGGTTATGATTAACTTTT	NEW
CU-6183	1341	TAAAGTGCTTAGTGCAGGTA	NEW
CU-6181	1342	GTTTATGTTGCTTACCTCC	NEW
CU-6176	1343	GTAGATAAAATATTGGCG	NEW
CU-6163	1344	GGCGGGGACGACGTCAG	NEW
CU-6162	1345	GGCGGCGTCGCGGCGGGTC	NEW
CU-6161	1346	GGAGGGGGTGAACAAAAAGAAAAA	NEW
CU-6159	1347	GCTAAACCTAGCCCCAAACCCACTCCACA	NEW
CU-6142	1348	CTGGATAGCGCACTTCGTT	NEW
CU-6129	1349	CGGGCGAGGGGCGGACGTTCG	NEW
CU-6123	1350	CGGACCTATACCGGA	NEW
CU-6096	1351	CCCCGGGTTCAATCCCCGGCACCTCCACCA	NEW
CU-6088	1352	CCCCCCACAACCGCGAA	NEW
CU-6087	1353	CCCAGCATCTCCTGTGTTTA	NEW
CU-6086	1354	CCCACGTTGGGACGCCA	NEW
CU-6072	1355	ATCGTATCCCACTTCTGACACCA	NEW
CU-6064	1356	ATCACGTCCGTGCCTCCA	NEW
CU-6063	1357	ATAGCAATGTCAGCAGTACCT	NEW
CU-6051	1358	ACCCTGCTCGCTGCGCCA	tRNAprefix-annotate; refseqGeneIntron-annotate

TABLE 10-continued

(PART A) List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic locations and annotations.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6198	1359	TCCCACCCAGGGACGCCA	tRNAprefix-annotate; refseqGeneIntron-annotate
CU-6218	1360	TCGTAGGCACATCAATA	refseqGeneIntron-annotate
CU-6007	1361	CCCCCACAACCGCGTA	refseqGeneIntron-annotate
CU-6001	1362	ACCCCGTCCGTGCCTCCA	tRNAprefix-annotate; refseqGeneIntron-annotate
CU-6039	1363	AAAAAAGACACCCCCCACA	refseqGeneIntron-annotate
CU-6005	1364	TGTCAGTTTGTTAACCCAA	refseqGeneIntron-annotate
CU-6204	1365	TCCCTGTGGTCTAGTGGTTAGG	refseqGeneIntron-annotate
CU-6172	1366	GGGGGGGTAAAAAAA	refseqGeneIntron-annotate
CU-6171	1367	GGGGGGGGAAAAAAAA	refseqGeneIntron-annotate
CU-6128	1368	CGGGCCCGGGTCTTCCC	refseqGeneIntron-annotate
CU-6002	1369	CCGCCCCCCGTTCCCCCCA	refseqGeneIntron-annotate
CU-6050	1370	ACCCCCGGCTCCTCCACCA	tRNAprefix-annotate; refseqGeneIntron-annotate
CU-6244	1371	TTTGGTGGAAATTTTTTGA	refseqGeneIntron-annotate
CU-6240	1372	TGTCAGTTTGTTATACCAA	refseqGeneIntron-annotate
CU-6238	1373	TGTCAGTTTGTAATTATCCCAA	refseqGeneIntron-annotate
CU-6236	1374	TGTCAATTTTTAACCCAA	refseqGeneIntron-annotate
CU-6227	1375	TGCTAGGGTAAAAAAAAAA	refseqGeneIntron-annotate
CU-6226	1376	TGCAACTCCAAATAAAAGTACCA	tRNAprefix-annotate; refseqGeneIntron-annotate
CU-6224	1377	TGAGGTAACGGGGAATTA	refseqGeneIntron-annotate
CU-6209	1378	TCCTCGGCATCTCCACCA	refseqGeneIntron-annotate
CU-6197	1379	TCATATGAAGTCACCCTAGCCATC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6196	1380	TCAGTTTGTTTATTAACCCAA	refseqGeneIntron-annotate
CU-6195	1381	TCAGCGTGTCTTTGCCCT	refseqGeneIntron-annotate
CU-6194	1382	TCACTGGTGGTCTAGTGGT	refseqGeneIntron-annotate; rnaGene-annotate
CU-6193	1383	TCACAATGCTGCCACCA	refseqGeneIntron-annotate
CU-6189	1384	TAGTTGTTAATTAACCCAA	refseqGeneIntron-annotate
CU-6188	1385	TAGTCCTCATCGCCCTCC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6184	1386	TAAAGTGCTTATAGTGCGGGTAA	refseqGeneIntron-annotate
CU-6179	1387	GTCCCACCAGAGTCGCCA	tRNAprefix-annotate; refseqGeneIntron-annotate
CU-6170	1388	GGGGGAGGGGCCAAAAAAA	refseqGeneIntron-annotate
CU-6167	1389	GGGACGCCGCGGTGTCG	refseqGeneIntron-annotate
CU-6166	1390	GGGAATACCGGGTGCTTTAGGCTT	refseqGeneIntron-annotate; rnaGene-annotate
CU-6160	1391	GGAAGAAGGTGGTGGTATA	refseqGeneIntron-annotate
CU-6156	1392	GCGGTGAAATGCGTA	computGene-annotate; Ecoli-annotate; refseqGeneIntron-annotate

TABLE 10-continued

(PART A) List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic locations and annotations.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6154	1393	GCGGGGAAGGTGGCAAA	refseqGeneIntron-annotate
CU-6152	1394	GCGACGACCTCGCGCCCACCTGGTCA	refseqGeneIntron-annotate
CU-6151	1395	GCCACCCGATACTGCTGT	refseqGeneIntron-annotate
CU-6150	1396	GATGTATGCTTTGTTTCTGTT	refseqGeneIntron-annotate
CU-6148	1397	GAGGGGGATTTAGAAAAAAA	refseqGeneIntron-annotate
CU-6147	1398	GAAGGAAAGTTCTATAGT	refseqGeneIntron-annotate
CU-6146	1399	GAAGCGGCTCTCTTATTT	refseqGeneIntron-annotate
CU-6145	1400	GAACGAGACTCTGGCATGCTGA	refseqGeneIntron-annotate; rnaGene-annotate
CU-6143	1401	CTGGTAGGCCCATCAAT	refseqGeneIntron-annotate
CU-6132	1402	CGGGGCCGATCGCGCGC	computGene-annotate; refseqGeneIntron-annotate
CU-6125	1403	CGGCCCCGGGTTCCTCCC	computGene-annotate; refseqGeneIntron-annotate
CU-6118	1404	CGAGCCCGGTTAGTA	refseqGeneIntron-annotate; rnaGene-annotate
CU-6117	1405	CGACTCTTAGCGGTGGA	piRNA-annotate; refseqGeneIntron-annotate
CU-6116	1406	CGAATCCCACTTCTGACACCA	tRNAprefix-annotate; refseqGeneIntron-annotate
CU-6113	1407	CGAAAGGGAATCGGGTC	refseqGeneIntron-annotate
CU-6112	1408	CCTTAGGTCGCTGGTAAA	refseqGeneIntron-annotate
CU-6108	1409	CCGTGCGAGAATACCA	tRNAprefix-annotate; refseqGeneIntron-annotate
CU-6107	1410	CCGGTCTCTCAAGCGGCC	refseqGeneIntron-annotate
CU-6099	1411	CCCGGCCCTCGCGCGTCC	computGene-annotate; refseqGeneIntron-annotate
CU-6094	1412	CCCCGGCATTTCCACCA	computGene-annotate; refseqGeneIntron-annotate
CU-6090	1413	CCCCCCCGGCTCCTCCACCA	refseqGeneIntron-annotate
CU-6089	1414	CCCCCCACAACCGCTA	refseqGeneIntron-annotate
CU-6085	1415	CCCAAGTATTGACTCACCC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6084	1416	CCAGTAAGCGCGAGTC	refseqGeneIntron-annotate
CU-6082	1417	CCAAAGAAAGCACGTAGAG	refseqGeneIntron-annotate
CU-6081	1418	CATGTTTAACGGCCGCGGT	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6080	1419	CAGTTTGTAATTAACCCAA	refseqGeneIntron-annotate
CU-6079	1420	CAGGAACGGCGCACCA	computGene-annotate; refseqGeneIntron-annotate
CU-6078	1421	CAGAACCCTCTAAATCCCC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6076	1422	CACCCGGCTGTGTGCACATGTGT	miRBASE-annotate; computGene-annotate; refseqGeneIntron-annotate; wgRNA-annotate
CU-6075	1423	CAATTGGACCAATCTATC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6074	1424	ATTCCTGTACTGCGATA	refseqGeneIntron-annotate
CU-6070	1425	ATCCCTGCGGCGTCTCCA	refseqGeneIntron-annotate
CU-6067	1426	ATCCCACCGCTGCCATCA	refseqGeneIntron-annotate
CU-6062	1427	AGTCAATAGAAGCCGGCGTA	mitochondrion-annotate; refseqGeneIntron-annotate

TABLE 10-continued

(PART A) List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic locations and annotations.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6061	1428	AGGTTCGTTTGTAAAAA	refseqGeneIntron-annotate
CU-6060	1429	AGGTCCTGGGTTTAAGTGT	computGene-annotate; refseqGeneIntron-annotate
CU-6058	1430	AGGGGGAAGTTCTATAGTC	refseqGeneIntron-annotate
CU-6057	1431	AGGCTGTGATGCTCTCNTGAGCCCT	refseqGeneIntron-annotate
CU-6055	1432	AGCCCCTCTCCGGCCCTTA	refseqGeneIntron-annotate
CU-6054	1433	ACTACCACCTACCTCCC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6052	1434	ACGCCCTTCCCCCCCTTCTTT	miRBASE-annotate; refseqGeneIntron-annotate
CU-6049	1435	ACCCCACTCCTGGTGCAC	refseqGeneIntron-annotate
CU-6048	1436	ACCACCTGATCCCTTCCC	refseqGeneIntron-annotate
CU-6047	1437	ACAGCTAAGCACCCACCA	refseqGeneIntron-annotate
CU-6045	1438	ACACATGTTTAACGGCC	mitochondrion-annotate; refseqGeneIntron-annotate
CU-6043	1439	AATTAGGGACCTGTATG	refseqGeneIntron-annotate
CU-6042	1440	AATGGCCCATTTGGGCAAACA	computGene-annotate; refseqGeneIntron-annotate
CU-6041	1441	AAAGCGGCTGTGCAAACA	refseqGeneIntron-annotate
CU-6030	1442	ATCCTGCCGACTACGCCA	tRNAprefix-annotate
CU-6210	1443	TCGAATCCCACTCCTGACACCA	tRNAprefix-annotate
CU-6069	1444	ATCCCATCCTCGTCGCCA	tRNAprefix-annotate
CU-6216	1445	TCGATTCCCCGACGGGGAGCCA	tRNAprefix-annotate
CU-6071	1446	ATCCGGGTGCCCCCTCCA	tRNAprefix-annotate
CU-6212	1447	TCGACTCCTGGCTGGCTCGCCA	tRNAprefix-annotate; wgRNA-annotate
CU-6202	1448	TCCCGGGCGGCGCACCA	tRNAprefix-annotate
CU-6066	1449	ATCCCACCAGAGTCGCCA	tRNAprefix-annotate
CU-6200	1450	TCCCCGGCATCTCCACCAA	computGene-annotate
CU-6192	1451	TCAAATCACGTCGGGGTCACCA	tRNAprefix-annotate
CU-6157	1452	GCGGTGGATCACTCGGCTCGTGCGT	rnaGene-annotate
CU-6214	1453	TCGATCCCCGTACGGGCCACCA	tRNAprefix-annotate
CU-6213	1454	TCGAGCCTCACCTGGAGCACCA	tRNAprefix-annotate
CU-6206	1455	TCCGGCTCGAAGGACCA	tRNAprefix-annotate
CU-6105	1456	CCGGGTGTTGTAGA	mRNAall-annotate; exEID-annotate
CU-6235	1457	TGTAGCGTGGCCGAGCGGT	rnaGene-annotate
CU-6234	1458	TGGGGCGACCTCGGAGCAG	mitochondrion-annotate
CU-6230	1459	TGGCGTCCTAAGCCAGGGATTGTGGGT	rnaGene-annotate
CU-6229	1460	TGGCAGGGGAGATACCATGATTT	rnaGene-annotate
CU-6222	1461	TCTGATCAGGGTGAGCATC	mitochondrion-annotate
CU-6220	1462	TCGTAGGCACCATCCAT	computGene-annotate

TABLE 10-continued

(PART A) List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic locations and annotations.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6165	1463	GGGAAACGGGGCGCGGCTG	rnaGene-annotate
CU-6137	1464	CTACTCCTGCTCGCATCTGCTATA	mitochondrion-annotate
CU-6135	1465	CGGGTGGGTTTTTACCGG	computGene-annotate
CU-6120	1466	CGAGGAATTCCCAGTAAG	rnaGene-annotate
CU-6115	1467	CGAACGCACTTGCGGCCCC	rnaGene-annotate
CU-6093	1468	CCCCGCGCGGGTTCGAATC	rnaGene-annotate
CU-6059	1469	AGGGGTATGATTCCCGCTT	rnaGene-annotate
CU-6131	1470	CGGGGCCACGCGCGCGTC	mRNA-annotate; rRNA-eliminate
CU-6032	1471	TGGCGCTGCGGGATGAAC	rRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-1153	1472	CCCCCCACTGCTAAATTTGACTGGCTT	yRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6182	1473	TAAAGGTTCGTTTGTAAAA	computGene-annotate; refseqGeneExon-eliminate
CU-6033	1474	CGGGGCCGAGGGAGCGA	rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6174	1475	GGGTTAGGCCTCTTTT	tRNA-eliminate; rnaGene-annotate
CU-6141	1476	CTGCGGAAGGATCATTA	rRNA-eliminate; rnaGene-annotate
CU-6101	1477	CCCTACCCCCCCGG	rRNA-eliminate; refseqGeneIntron-annotate
CU-6034	1478	CCCGCCGGGTCCGCCC	computGene-annotate; rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6035	1479	CCCCGCGCCCTCTCTCTCTC	rRNA-eliminate; refseqGeneIntron-annotate
CU-6028	1480	CAGGCCTCCCTGGAATC	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6029	1481	AGTCCCACCCGGGGTACCA	computGene-annotate; refseqGeneExon-eliminate; tRNAprefix-annotate
CU-6243	1482	TTGACACGCCCCAGTGCCCTGT	refseqGeneExon-eliminate
CU-6233	1483	TGGGAGCGGGCGGGCGGTC	rRNA-eliminate; rnaGene-annotate
CU-6231	1484	TGGCGTGGAGCCGGGCGT	rRNA-eliminate; refseqGeneIntron-annotate
CU-6228	1485	TGGAGGTCCGTAGCGGT	rRNA-eliminate; mRNA-annotate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6223	1486	TGAAGAAGGTCTCGAACA	computGene-annotate; refseqGeneExon-eliminate
CU-6221	1487	TCTCGCCGGGGCTTCCA	computGene-annotate; refseqGeneExon-eliminate; rnaGene-annotate
CU-6217	1488	TCGTAGCACCATCAATAA	computGene-annotate; refseqGeneExon-eliminate
CU-6208	1489	TCCGGGTCCCCCCTCCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6207	1490	TCCGGGGCTGCACGCGCGCT	rRNA-eliminate; rnaGene-annotate
CU-6205	1491	TCCGGCCGTGTCGGT	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6203	1492	TCCCTGTCCTCCAGGAGT	miRBASE-annotate; computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; wgRNA-annotate
CU-6201	1493	TCCCCTCCTCGTCGCCA	refseqGeneExon-eliminate; refseqGeneIntron-annotate

TABLE 10-continued

(PART A) List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic locations and annotations.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6199	1494	TCCCAGGTAGTCTAGTGGT	refseqGeneExon-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6191	1495	TATTCATTTATCCCCAGCCTAT	miRBASE-annotate; snoRNA-eliminate; refseqGeneIntron-annotate; wgRNA-annotate; rnaGene-annotate
CU-6190	1496	TAGTTGTTATAACCCAA	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6186	1497	TAGATCACCCCCTCCCC	mitochondrion-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6185	1498	TACCGGCACCTGGCGCC	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6178	1499	GTATAGGGGCGAAAGAC	rRNA-eliminate; mRNA-annotate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6177	1500	GTAGCTGGTTCCCTCCGAA	rRNA-eliminate; mRNA-annotate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6175	1501	GGTAAGAAGCCCGGCTC	computGene-annotate; rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6173	1502	GGGGGGGTTTAAAAAAAAA	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6169	1503	GGGGCGCACTACCGGCC	refseqGeneExon-eliminate
CU-6168	1504	GGGAGAGGCTGTCGCTGCG	computGene-annotate; refseqGeneExon-eliminate
CU-6164	1505	GGCGGGTGAAGCGGCG	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6158	1506	GCGGTTCCGGCGGCGTC	rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6155	1507	GCGGGGCGCCTAGGCCTGGTTTGT	refseqGeneExon-eliminate
CU-6153	1508	GCGGCGGTCGGCGGGCGGCGGG	rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6149	1509	GAGGGGGGGGGTGGGGGGGGA	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6144	1510	CTGTCGGCCACCATCAT	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6140	1511	CTGCAACTCGACCCCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6139	1512	CTCCTCTCCCCGCCCGCCG	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6138	1513	CTCAAAGATTAAGCCATGCATGTCTA	rRNA-eliminate; rnaGene-annotate
CU-6136	1514	CTACGCCGCGACGAG	computGene-annotate; rRNA-eliminate
CU-6134	1515	CGGGTGACGGGGAATCAGGGTT	rRNA-eliminate; rnaGene-annotate
CU-6127	1516	CGGGCAGCTTCCGGGA	computGene-annotate; rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6126	1517	CGGGAGGCCCGGGTCCTG	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6124	1518	CGGCCCCGCATCCTCCC	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6122	1519	CGCGGGTAAACGGCGGGAGTAACTAT	mRNAall-annotate; rRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6121	1520	CGCCCCCCGTTCCCCCCTCC	rRNA-eliminate

TABLE 10-continued

(PART A) List of short-RNA consensus with maximum 1 mismatch to the human genome. Table includes information on genomic locations and annotations.

ID	SEQ ID NO:	Short-RNA sequence	Annotations
CU-6119	1521	CGAGCGGAAACACCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; tRNAprefix-annotate
CU-6114	1522	CGAACCCGGCACCGC	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6111	1523	CCTCGGGCCGATCGCAC	rRNA-eliminate; rnaGene-annotate
CU-6110	1524	CCTATATATCTTACCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; tRNAprefix-annotate
CU-6109	1525	CCGTGGCGGCGACGACC	computGene-annotate; rRNA-eliminate; refseqGeneExon-eliminate
CU-6106	1526	CCGGGTTCCGGCACCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6104	1527	CCGCGAGGGGGGCCCG	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6103	1528	CCGCCTCACGGGACCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6102	1529	CCGCCCGTCCCCGCCCCTTG	rRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6100	1530	CCCGGGGCCGCGGTTCCG	computGene-annotate; rRNA-eliminate; refseqGeneIntron-annotate
CU-6098	1531	CCCGAGCCGCCTGGAT	computGene-annotate; rRNA-eliminate; refseqGeneExon-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6097	1532	CCCGACGGCCGAACT	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6095	1533	CCCCGGGGAGCCCGGCGGG	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6092	1534	CCCCCTCGCGGCCCTCCCC	rRNA-eliminate; refseqGeneIntron-annotate
CU-6091	1535	CCCCCCGTGGCGGCGAC	rRNA-eliminate; refseqGeneIntron-annotate
CU-6083	1536	CCACCCAGGGCACGCCA	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6077	1537	CACGGGTGACGGGGAA	computGene-annotate; rnaGene-annotate; refseqGeneIntron-annotate; rRNA-eliminate; refseqGeneExon-eliminate; piRNA-annotate
CU-6073	1538	ATGGGGAGGAAAAAAAAAAAAA	refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6068	1539	ATCCCACCGCTGCCCCCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6065	1540	ATCACGTCGGTCACCA	computGene-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate
CU-6053	1541	ACGGGAAACCTCACCCGGCCCGG	rRNA-eliminate; piRNA-annotate; rnaGene-annotate
CU-6046	1542	ACAGAGGCTTACGACCCCTTATTT	mitochondrion-annotate; tRNA-eliminate; refseqGeneIntron-annotate; rnaGene-annotate
CU-6040	1543	AAAAAGGCATAATTAAACTT	mitochondrion-annotate; refseqGeneExon-eliminate; refseqGeneIntron-annotate

TABLE 10

(PART B) List of short-RNA consensus with maximum 1 mismatch to the human genome, including count information.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1544	TGGCTCAGTTCAGCAGGAACAGT	0	0	1	0
1545	GTGGGGGAGAGGCTGTCGA	0	0	0	1
1546	CGGGGCAGCTCAGTACAGGATT	0	0	1	0
1547	AATTGCACGGTATCCATCTGTAT	0	0	1	0
1548	TGTCAGTTTGTTAATTGACCCAA	0	0	1	1
1549	GGCAATACGAGCACCCTG	2	0	0	0
1550	CGGGGGAGCGCCGCGTA	2	0	0	0
1551	CCGGGGCGTCTCGTAC	2	0	0	0
1552	AGCGGCTGTGCACAAA	0	0	0	2
1553	TGTCAGTTTGTTTAATCCAA	0	0	0	1
1554	TGTCAGTTTGTTATTACCAA	0	0	0	1
1555	TGTCAGGCACCATCAATAA	0	0	0	1
1556	TGATCTTGACACTTAAAGCC	0	0	0	1
1557	TCGTAGGCACCATCAAT	0	0	0	1
1558	TCGATCCCGGGTTTCGGCACCA	0	0	1	0
1559	TCGACTCCCGGTATGGGAACCA	0	0	0	1
1560	TAGGGAGGTTATGATTAACTTTT	0	0	0	1
1561	TAAAGTGCTTAGTGCAGGTA	0	0	0	1
1562	GTTTATGTTGCTTACCTCC	0	0	1	0
1563	GTAGATAAAATATTGGCG	1	0	0	0
1564	GGCGGGGACGACGTCAG	0	0	0	1
1565	GGCGGCGTCGCGGCGGGTC	0	1	0	0
1566	GGAGGGGGTGAACAAAAAGAAAAA	0	0	0	1
1567	GCTAAACCTAGCCCCAAACCCAC TCCACA	0	0	0	1
1568	CTGGATAGCGCACTTCGTT	0	0	0	1
1569	CGGGCGAGGGGCGGACGTTCG	0	0	1	0
1570	CGGACCTATACCGGA	1	0	0	0
1571	CCCCGGGTTCAATCCCCGGCACC TCCACCA	0	0	1	0
1572	CCCCCCACAACCGCGAA	0	1	0	0
1573	CCCAGCATCTCCTGTGTTTA	0	1	0	0
1574	CCCACGTTGGGACGCCA	1	0	0	0
1575	ATCGTATCCCACTTCTGACACCA	0	0	0	1
1576	ATCACGTCCGTGCCTCCA	0	1	0	0
1577	ATAGCAATGTCAGCAGTACCT	0	0	1	0

TABLE 10-continued

(PART B) List of short-RNA consensus with maximum 1 mismatch to the human genome, including count information.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1578	ACCCTGCTCGCTGCGCCA	9	17	4	7
1579	TCCCACCCAGGGACGCCA	8	2	1	0
1580	TCGTAGGCACATCAATA	0	0	0	4
1581	CCCCCACAACCGCGTA	0	4	0	0
1582	ACCCCGTCCGTGCCTCCA	2	1	1	0
1583	AAAAAAGACACCCCCCACA	0	0	0	3
1584	TGTCAGTTTGTTAACCCAA	0	0	0	2
1585	TCCCTGTGGTCTAGTGGTTAGG	0	0	1	1
1586	GGGGGGGTAAAAAAA	0	0	0	1
1587	GGGGGGGGAAAAAAAA	0	0	0	1
1588	CGGGCCCGGGTCTTCCC	1	1	0	0
1589	CCGCCCCCCGTTCCCCCCA	0	2	0	0
1590	ACCCCCGGCTCCTCCACCA	0	1	0	1
1591	TTTGGTGGAAATTTTTTGA	0	0	0	1
1592	TGTCAGTTTGTTATACCAA	0	0	0	1
1593	TGTCAGTTTGTAATTATCCCAA	0	0	0	1
1594	TGTCAATTTTTAACCCAA	0	0	0	1
1595	TGCTAGGGTAAAAAAAAAA	0	0	0	1
1596	TGCAACTCCAAATAAAAGTACCA	0	0	0	1
1597	TGAGGTAACGGGGAATTA	0	0	0	1
1598	TCCTCGGCATCTCCACCA	0	0	1	0
1599	TCATATGAAGTCACCCTAGCCATC	0	0	1	0
1600	TCAGTTTGTTTATTAACCCAA	0	0	0	1
1601	TCAGCGTGTCTTTGCCCT	1	0	0	0
1602	TCACTGGTGGTCTAGTGGT	0	1	0	0
1603	TCACAATGCTGCCACCA	1	0	0	0
1604	TAGTTGTTAATTAACCCAA	0	0	0	1
1605	TAGTCCTCATCGCCCTCC	0	1	0	0
1606	TAAAGTGCTTATAGTGCGGGTAA	0	0	0	1
1607	GTCCCACCAGAGTCGCCA	0	0	1	0
1608	GGGGGAGGGGCCAAAAAAA	0	0	0	1
1609	GGGACGCCGCGGTGTCG	1	0	0	0
1610	GGGAATACCGGGTGCTTTAGGCTT	0	1	0	0
1611	GGAAGAAGGTGGTGGTATA	0	0	0	1

TABLE 10-continued

(PART B) List of short-RNA consensus with maximum 1 mismatch to the human genome, including count information.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1612	GCGGTGAAATGCGTA	1	0	0	0
1613	GCGGGGAAGGTGGCAAA	0	0	0	1
1614	GCGACGACCTCGCGCCCACCTGGTCA	0	1	0	0
1615	GCCACCCGATACTGCTGT	0	1	0	0
1616	GATGTATGCTTTGTTTCTGTT	0	0	1	0
1617	GAGGGGGATTTAGAAAAAAA	0	0	0	1
1618	GAAGGAAAGTTCTATAGT	0	0	0	1
1619	GAAGCGGCTCTCTTATTT	0	0	0	1
1620	GAACGAGACTCTGGCATGCTGA	0	0	1	0
1621	CTGGTAGGCCCATCAAT	0	0	0	1
1622	CGGGGCCGATCGCGCGC	0	1	0	0
1623	CGGCCCCGGGTTCCTCCC	1	0	0	0
1624	CGAGCCCGGTTAGTA	1	0	0	0
1625	CGACTCTTAGCGGTGGA	0	0	1	0
1626	CGAATCCCACTTCTGACACCA	0	0	0	1
1627	CGAAAGGGAATCGGGTC	1	0	0	0
1628	CCTTAGGTCGCTGGTAAA	0	0	1	0
1629	CCGTGCGAGAATACCA	0	1	0	0
1630	CCGGTCTCTCAAGCGGCC	1	0	0	0
1631	CCCGGCCCTCGCGCGTCC	0	1	0	0
1632	CCCCGGCATTTCCACCA	0	0	1	0
1633	CCCCCCCGGCTCCTCCACCA	0	0	0	1
1634	CCCCCCACAACCGCTA	0	1	0	0
1635	CCCAAGTATTGACTCACCC	0	1	0	0
1636	CCAGTAAGCGCGAGTC	1	0	0	0
1637	CCAAAGAAAGCACGTAGAG	0	0	0	1
1638	CATGTTTAACGGCCGCGGT	0	0	1	0
1639	CAGTTTGTAATTAACCCAA	0	0	0	1
1640	CAGGAACGGCGCACCA	0	0	1	0
1641	CAGAACCCTCTAAATCCCC	0	0	1	0
1642	CACCCGGCTGTGTGCACATGTGT	1	0	0	0
1643	CAATTGGACCAATCTATC	0	0	1	0
1644	ATTCCTGTACTGCGATA	0	0	0	1
1645	ATCCCTGCGGCGTCTCCA	0	0	0	1

TABLE 10-continued

(PART B) List of short-RNA consensus with maximum 1 mismatch to the human genome, including count information.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1646	ATCCCACCGCTGCCATCA	0	1	0	0
1647	AGTCAATAGAAGCCGGCGTA	0	0	1	0
1648	AGGTTCGTTTGTAAAAA	0	0	0	1
1649	AGGTCCTGGGTTTAAGTGT	0	0	0	1
1650	AGGGGGAAGTTCTATAGTC	0	0	0	1
1651	AGGCTGTGATGCTCTCNTGAGCCCT	0	0	1	0
1652	AGCCCCTCTCCGGCCCTTA	0	1	0	0
1653	ACTACCACCTACCTCCC	1	0	0	0
1654	ACGCCCTTCCCCCCCTTCTTT	0	0	0	1
1655	ACCCCACTCCTGGTGCAC	1	0	0	0
1656	ACCACCTGATCCCTTCCC	1	0	0	0
1657	ACAGCTAAGCACCCACCA	0	0	1	0
1658	ACACATGTTTAACGGCC	1	0	0	0
1659	AATTAGGGACCTGTATG	0	0	1	0
1660	AATGGCCCATTTGGGCAAACA	0	0	0	1
1661	AAAGCGGCTGTGCAAACA	0	0	0	1
1662	ATCCTGCCGACTACGCCA	13	15	13	6
1663	TCGAATCCCACTCCTGACACCA	1	2	7	7
1664	ATCCCATCCTCGTCGCCA	0	0	10	3
1665	TCGATTCCCCGACGGGGAGCCA	1	1	1	9
1666	ATCCGGGTGCCCCCTCCA	2	4	0	1
1667	TCGACTCCTGGCTGGCTCGCCA	0	2	2	1
1668	TCCCGGGCGGCGCACCA	2	2	1	0
1669	ATCCCACCAGAGTCGCCA	0	0	2	3
1670	TCCCCGGCATCTCCACCAA	0	1	2	0
1671	TCAAATCACGTCGGGGTCACCA	0	1	2	0
1672	GCGGTGGATCACTCGGCTCGTGCGT	0	0	0	3
1673	TCGATCCCCGTACGGGCCACCA	0	0	1	1
1674	TCGAGCCTCACCTGGAGCACCA	0	0	2	0
1675	TCCGGCTCGAAGGACCA	0	0	2	0
1676	CCGGGTGTTGTAGA	2	0	0	0
1677	TGTAGCGTGGCCGAGCGGT	0	1	0	0
1678	TGGGGCGACCTCGGAGCAG	0	0	1	0

TABLE 10-continued

(PART B) List of short-RNA consensus with maximum 1 mismatch to the human genome, including count information.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1679	TGGCGTCCTAAGCCAGGGATTGTGGGT	0	0	0	1
1680	TGGCAGGGGAGATACCATGATTT	0	0	1	0
1681	TCTGATCAGGGTGAGCATC	0	1	0	0
1682	TCGTAGGCACCATCCAT	0	0	0	1
1683	GGGAAACGGGGCGCGGCTG	0	1	0	0
1684	CTACTCCTGCTCGCATCTGCTATA	0	0	1	0
1685	CGGGTGGGTTTTTACCGG	1	0	0	0
1686	CGAGGAATTCCCAGTAAG	0	0	1	0
1687	CGAACGCACTTGCGGCCCC	1	0	0	0
1688	CCCCGCGCGGGTTCGAATC	1	0	0	0
1689	AGGGGTATGATTCCCGCTT	0	0	0	1
1690	CGGGGCCACGCGCGCGTC	3	6	0	0
1691	TGGCGCTGCGGGATGAAC	0	3	1	0
1692	CCCCCCACTGCTAAATTTGACTGGCTT	0	0	2	2
1693	TAAAGGTTCGTTTGTAAAA	0	0	0	3
1694	CGGGGCCGAGGGAGCGA	1	2	0	0
1695	GGGTTAGGCCTCTTTT	0	1	1	0
1696	CTGCGGAAGGATCATTA	1	0	1	0
1697	CCCTACCCCCCCGG	0	2	0	0
1698	CCCGCCGGGTCCGCCC	2	0	0	0
1699	CCCCGCGCCCTCTCTCTCTC	0	2	0	0
1700	CAGGCCTCCCTGGAATC	2	0	0	0
1701	AGTCCCACCCGGGGTACCA	0	0	0	2
1702	TTGACACGCCCCAGTGCCCTGT	1	0	0	0
1703	TGGGAGCGGGCGGGCGGTC	0	1	0	0
1704	TGGCGTGGAGCCGGGCGT	0	1	0	0
1705	TGGAGGTCCGTAGCGGT	1	0	0	0
1706	TGAAGAAGGTCTCGAACA	0	0	0	1
1707	TCTCGCCGGGGCTTCCA	0	1	0	0
1708	TCGTAGCACCATCAATAA	0	0	0	1
1709	TCCGGGTCCCCCCTCCA	0	1	0	0
1710	TCCGGGGCTGCACGCGCGCT	0	1	0	0
1711	TCCGGCCGTGTCGGT	1	0	0	0

TABLE 10-continued

(PART B) List of short-RNA consensus with maximum 1 mismatch to the human genome, including count information.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1712	TCCCTGTCCTCCAGGAGT	0	0	0	1
1713	TCCCCTCCTCGTCGCCA	1	0	0	0
1714	TCCCAGGTAGTCTAGTGGT	1	0	0	0
1715	TATTCATTTATCCCCAGCCTAT	0	1	0	0
1716	TAGTTGTTATAACCCAA	0	0	0	1
1717	TAGATCACCCCCTCCCC	0	1	0	0
1718	TACCGGCACCTGGCGCC	1	0	0	0
1719	GTATAGGGGCGAAAGAC	0	0	1	0
1720	GTAGCTGGTTCCCTCCGAA	0	0	0	1
1721	GGTAAGAAGCCCGGCTC	0	0	1	0
1722	GGGGGGGTTTAAAAAAAAA	0	0	0	1
1723	GGGGCGCACTACCGGCC	1	0	0	0
1724	GGGAGAGGCTGTCGCTGCG	0	0	0	1
1725	GGCGGGTGAAGCGGCG	0	1	0	0
1726	GCGGTTCCGGCGGCGTC	0	1	0	0
1727	GCGGGGCGCCTAGGCCTGGTTTGT	1	0	0	0
1728	GCGGCGGTCGGCGGGCGGCGGG	1	0	0	0
1729	GAGGGGGGGGGTGGGGGGGGA	0	0	0	1
1730	CTGTCGGCCACCATCAT	0	0	0	1
1731	CTGCAACTCGACCCCA	0	1	0	0
1732	CTCCTCTCCCCGCCCGCCG	0	0	1	0
1733	CTCAAAGATTAAGCCATGCATGTCTA	0	0	1	0
1734	CTACGCCGCGACGAG	1	0	0	0
1735	CGGGTGACGGGGAATCAGGGTT	1	0	0	0
1736	CGGGCAGCTTCCGGGA	0	0	0	1
1737	CGGGAGGCCCGGGTCCTG	1	0	0	0
1738	CGGCCCCGCATCCTCCC	1	0	0	0
1739	CGCGGGTAAACGGCGGGAGTAACTAT	0	0	1	0
1740	CGCCCCCCGTTCCCCCCTCC	0	1	0	0
1741	CGAGCGGAAACACCA	1	0	0	0
1742	CGAACCCGGCACCGC	1	0	0	0
1743	CCTCGGGCCGATCGCAC	0	0	1	0
1744	CCTATATATCTTACCA	0	1	0	0

TABLE 10-continued

(PART B) List of short-RNA consensus with maximum 1 mismatch to the human genome, including count information.

SEQ ID NO:	Short-RNA sequence	Corrected Counts Naïve (N)	Memory (M)	Centroblasts (CB)	Ramos (RA)
1745	CCGTGGCGGCGACGACC	0	1	0	0
1746	CCGGGTTCCGGCACCA	1	0	0	0
1747	CCGCGAGGGGGGCCCG	1	0	0	0
1748	CCGCCTCACGGGACCA	1	0	0	0
1749	CCGCCCGTCCCCGCCCCTTG	0	1	0	0
1750	CCCGGGGCCGCGGTTCCG	1	0	0	0
1751	CCCGAGCCGCCTGGAT	0	1	0	0
1752	CCCGACGGCCGAACT	0	1	0	0
1753	CCCCGGGGAGCCCGGCGGG	1	0	0	0
1754	CCCCCTCGCGGCCCTCCCC	0	1	0	0
1755	CCCCCCGTGGCGGCGAC	0	1	0	0
1756	CCACCCAGGGCACGCCA	1	0	0	0
1757	CACGGGTGACGGGGAA	1	0	0	0
1758	ATGGGGAGGAAAAAAAAAAAAA	0	0	0	1
1759	ATCCCACCGCTGCCCCCA	0	0	0	1
1760	ATCACGTCGGTCACCA	0	0	0	1
1761	ACGGGAAACCTCACCCGGCCCGG	0	0	1	0
1762	ACAGAGGCTTACGACCCCTTATTT	0	0	1	0
1763	AAAAAGGCATAATTAAACTT	0	0	1	0

[0353] Abundance and Evolutionary Conservation.

[0354] Previously reported miRNAs appeared to be generally more abundant than newly discovered miRNAs. Approximately 50% of previously reported miRNAs appeared in the libraries with more than 10 occurrences compared to 29% of the newly discovered miRNAs (FIG. **20**A). Moreover, 48% of known miRNAs were expressed at all stages of mature B-cell development, while newly identified miRNAs showed a more distinct stage-specificity (FIG. **20**B), consistent with the notion that presently known miRNAs are mostly representative of ubiquitously expressed miRNAs.

[0355] In order to investigate the presence of orthologous miRNA in other mammalian species, we relied on UCSC-provided Blastz pairwise alignments between human and target species and investigated conservation using two complementary methods, detailed in Supplemental Experimental Procedures. The analysis was performed on the complete set of miRNAs deposited in the miRBase database and on the miRNAs (known and new) represented in the B-cell libraries. Alignments of the human mature miRNA to its target species were required to have either perfect conservation of the entire mature miRNA sequence or conservation of seeds composed of seven bases starting from the second position of the human mature sequence followed by conservation of 3 bases starting from the 12th, 13th or 14th position as suggested by (Grimson et al., 2007) (FIG. **20**C and Appendix Table 11).

[0356] The majority of miRBase-miRNAs showed conservation across mammalian genomes, from primates to rodents. Conservation frequency mimicked known phylogenetic distances to human, with the highest conservation in chimp and lowest in rat. The conservation frequencies of known and newly identified miRNAs in B cells were similar in chimp (*Pan troglodytes*) and monkey (*Macacus rhesus*), especially when conservation requirements were restricted to the seed region of miRNAs. However, conservation frequencies in dog, mouse and rat were significantly divergent, with known miRNAs more likely to exhibit conservation than new candidate miRNAs (FIG. **20**C and Appendix Table 11). In summary, previously unreported miRNAs expressed at specific stages of B-cell differentiation were generally less abundant and showed a lower degree of conservation across species, as shown for other tissue-specific miRNAs.

[0357] Validation of Previously Unreported miRNAs.

[0358] All 75 newly identified miRNAs were investigated by RT-PCR analysis in order to independently validate their existence in vivo in B-cell lines and cells isolated from ton-

sils. Positive results were obtained in 66 of the cases (see FIG. **21**A for representative results and Table 12). Eighteen previously unreported miRNAs were also tested by RNA blot analysis and 11 were detectable (FIG. **21**B and Table 12), either using total cellular RNA or upon enrichment for the short-RNA fraction. Overall, 88% of the newly cloned and computationally validated miRNAs were detectable by RNA blot and/or RT-PCR. The validation process also led to the identification of numerous miRNA which are differentially regulated either in normal versus transformed cells (see examples CU-1440, CU-1241, CU-1276 and CU-1137 in FIG. **21**) as well as during the GC reaction (FIG. **22**).

TABLE 12

Summary of results obtained from the Northern Blot and/or RT-PCR analyses performed on newly identified mature miRNAs cloned multiple times in the B-cell libraries.

ID	Seq ID No.	Mature miRNA sequence	Northern Blot	RT-PCR
CU-1369	1764	TCCCCGGCATCTCCACCA	negative	positive
CU-1254	1765	TCCCCGGCACCTCCACCA	positive	positive
CU-1298	1766	ATCCCGGACGAGCCCCCA	not tested	positive
CU-1303	1767	ATCCCACTTCTGACACCA	positive	positive
CU-1173	1768	ATCCCACTCCTGACACCA	positive	positive
CU-1242	1769	TCCCCGTACGGGCCACCA	not tested	positive
CU-1550	1770	CGGAAGCGTGCTGGGCCC	not tested	positive
CU-1186	1771	TCCCCGACACCTCCACCA	not tested	positive
CU-1368	1772	GACGAGGTGGCCGAGTGG	positive	positive
CU-1243	1773	GTCCCTTCGTGGTCGCCA	not tested	positive
CU-1470	1774	CTCCTGGCTGGCTCGCCA	not tested	positive
CU-1300	1775	TCCTCACACGGGGCACCA	not tested	positive
CU-1264	1776	GAGGGGGACCAAAAAAAA	not tested	negative
CU-1212	1777	TCCCCGGCACTTCCACCA	not tested	positive
CU-1345	1778	AGAACACTACGAGCCACA	not tested	positive
CU-1352	1779	ACCCCACTTCTGGTACCA	negative	positive
CU-1363	1780	CGTTCGCGCTTTCCCCTG	not tested	negative
CU-1220	1781	TTCCCCGACGGGGAGCCA	not tested	positive
CU-1197	1782	ATGTGGTGGCTTACTTTT	not tested	positive
CU-1241	1783	AGTCCCATCTGGGTCGCCA	positive	positive
CU-1148	1784	TGGTGTGGTCTGTTGTTTT	not tested	positive
CU-1288	1785	CGTCCATGATGTTCCGCAA	not tested	positive
CU-1528	1786	TAGGGGTATGATTCTCGCT	not tested	negative
CU-1175	1787	GGCGTGATTCATACCTTTT	not tested	positive
CU-1570	1788	ATCCCCAGCATCTCCACCA	not tested	positive
CU-1269	1789	TACCGAGCCTGGTGATAGC	not tested	positive
CU-1339	1790	ATCCCCAGCACCTCCACCA	not tested	positive
CU-1132	1791	GCCGGGTACTTTCGTATTTT	not tested	negative
CU-1370	1792	CTGATTGCTCCTGTCTGATT	not tested	positive
CU-1545	1793	CCACGAGGAAGAGAGGTAGC	not tested	negative
CU-1307	1794	ACCCCACTATGCTTAGCCCT	not tested	positive
CU-1294	1795	AAAGGACCTGGCGGTGCTTC	not tested	positive

TABLE 12-continued

Summary of results obtained from the Northern Blot and/or RT-PCR analyses performed on newly identified mature miRNAs cloned multiple times in the B-cell libraries.

ID	Seq ID No.	Mature miRNA sequence	Northern Blot	RT-PCR
CU-1371	1796	TCTAGAGGAGCCTGTTCTGTA	not tested	positive
CU-1244	1797	GTCAGGATGGCCGAGCGGTCT	not tested	positive
CU-1276	1798	TCGATTCCCGGCCAATGCAC CA	positive	positive
CU-1142	1799	TCGATTCCCGGCCCATGCAC CA	positive	positive
CU-1379	1800	TCGGGTGCGAGAGGTCCCG GGT	negative	positive
CU-1381	1801	TCGATTCCCGGTCAGGGAAC CA	not tested	positive
CU-1403	1802	GCATTGGTGGTTCAGTGGTA GA	positive	positive
CU-1457	1803	TTCTCACTACTGCACTTGACTA	not tested	positive
CU-1557	1804	GGAGAGAACGCGGTCTGAGT GGT	not tested	positive
CU-1542	1805	GGCTGGTCCGATGGTAGTGG GTT	not tested	positive
CU-1221	1806	TGTGCTCCGGAGTTACCTCG TTT	not tested	negative
CU-1380	1807	ATAGGTTTGGTCCTAGCCTTT CT	not tested	positive
CU-1277	1808	GAGCCATGATGATACCACTG AGC	not tested	positive
CU-1281	1809	GCAGCGCCAGCCTCCCGCCC TAC	not tested	positive
CU-1524	1810	CCCCCACAACCGCGCTTGAC TAGC	not tested	positive
CU-1477	1811	CTCCCACTGCTTCACTTGACT AGC	not tested	positive
CU-1575	1812	CCCCCCACTGCTAAATTTGAC TGGA	not tested	positive
CU-1137	1813	GCTAAGGAAGTCCTGTGCTC AGTTTT	positive	positive
CU-1538	1814	GGCTGGTCCGAGTGCAGTGG TGTTTA	not tested	positive
CU-1153	1815	CCCCCCACTGCTAAATTTGAC TGGCTT	positive	positive
CU-1513	1816	GCGGGTGATGCGAACTGGAG TCTGAGC	positive	positive
CU-1293	1817	AGCAGTGATGTCCTGAAAATT CTGAAG	not tested	negative
CU-1388	1818	TCCCTGGTGGTCTAGTGGTT AGGATTCG	negative	positive
CU-1180	1819	AACCGAGCGTCCAAGCTCTT TCCATTTT	not tested	positive

TABLE 12-continued

Summary of results obtained from the Northern Blot and/or RT-PCR analyses performed on newly identified mature miRNAs cloned multiple times in the B-cell libraries.

ID	Seq ID No.	Mature miRNA sequence	Northern Blot	RT-PCR
CU-1382	1820	TCCTCGTTAGTATAGTGGTGA GTATCCC	negative	positive
CU-1251	1821	CCCACCCAGGGACGCCA	negative	positive
CU-1191	1822	GCCCGCATCCTCCACCA	negative	positive
CU-1453	1823	CCCTGCTCGCTGCGCCA	not tested	positive
CU-1222	1824	TCACGTCGGGGTCACCA	not tested	positive
CU-1178	1825	AGGGTGTGCGTGTTTTT	not tested	positive
CU-1488	1826	TCCTGCCGCGGTCGCCA	not tested	positive
CU-1164	1827	GAGAGCGCTCGGTTTTT	not tested	negative
CU-1486	1828	CTGCTGTGATGACATTC	not tested	positive
CU-1130	1829	CCCGGGTTTCGGCACCA	not tested	positive
CU-1155	1830	TCCCCGCACCTCCACCA	not tested	positive
CU-1278	1831	TAACGGCCGCGGTACCC	not tested	positive
CU-1246	1832	AGGGGGGTAAAAAAAAA	not tested	positive
CU-1440	1833	TGGTTATCACGTTCGCC	not tested	positive
CU-1213	1834	TCACCCCATAAACACCA	not tested	positive
CU-1146	1835	AGAAAGGCCGAATTTTA	not tested	positive
CU-1323	1836	TGTATTGTGAGACATTC	not tested	positive
CU-1324	1837	TCTCGGTGGAACCTCCA	not tested	positive
CU-1396	1838	TAAGTGTTTGTGGGTTA	not tested	negative

[0359] In order to gain preliminary evidence of the functionality of the previously unreported miRNAs, a small subset of these miRNAs which were fully validated at the expression level was tested for incorporation in the functional miRNA-mRNA complex by co-immunoprecipitation with Ago2 proteins (Mourelatos et al., 2002). The results showed that the RNA fraction associated with the Ago complex was indeed enriched for each of the four tested previously unreported miRNAs (FIG. **25**), confirming that the identified sequences enter the expected miRNA functional pathway.

[0360] Indirect clues on the functionality of miRNAs may also be obtained analyzing the effect of stage-specific miRNAs on the corresponding transcriptome since most miRNAs have been showed to affect the expression of their targets albeit to a modest degree (Filipowicz et al., 2008). Toward this end, the targets of 15 previously unreported GC-over-expressed miRNAs were predicted by two algorithms (miRanda and RNA22) (John et al., 2004; Miranda et al., 2006) and were tested for enrichment in genes down-regulated in GC versus naïve B cells. Eleven out of 15 miRNA showed an increase (and only two a decrease) in their candidate target enrichment p-value for GC down-regulated genes compared to control populations (FIG. **26** and Table 13). These results suggest that indeed miRNAs associated with GC B cells specifically affect the GC transcriptome.

TABLE 13

Enrichment for predicted miRNA targets in genes down regulated in CB and in memory compared to naïve B cells.

CB over-expressed miRNA	Targets enrichment in genes downregulated in CB vs N (p-value)	Targets enrichment in genes downregulated in M vs N (p-value)
CU-1380	0.0001	0.4079
CU-1388	0.0002	0.2699
CU-1477	0.0002	0.0514
CU-1538	0.0014	0.1609
CU-1142	0.0016	0.0012
CU-1382	0.0016	0.0242
CU-1403	0.0026	0.0032
CU-1470	0.0029	0.5392
CU-1276	0.0193	0.0187
CU-1371	0.0413	0.2252
CU-1153	0.091	1
CU-1575	0.1598	1
CU-1370	0.1708	0.4595
CU-1303	1	1
CU-1513	1	1

[0361] In summary, previously unreported miRNAs identified by cloning and computational analysis were validated at the expression level by multiple detection methods. For a small subset tested, their incorporation in the Ago complex and their activity on the GC transcriptome suggests biological functionality.

[0362] Transcriptional and Post-Transcriptional Regulation.

[0363] Most newly identified miRNAs tested by RNA blot showed a long abundant transcript (>150 nt) likely corresponding to the primary miRNA transcript and a second transcript (~60-80 nt) consistent with the precursor miRNA. As shown in FIG. **21**C (top panel), the precursor miRNA and the correspondent mature miRNA may be produced in some cell type but not in others, suggesting transcriptional regulation. Conversely, the relative abundance of precursor and mature miRNA was different is some cell types (FIG. **21**C, bottom panel) suggesting the existence of post-transcriptional regulation most likely targeting the Dicer-dependent pre-miRNA processing (Lee et al., 2007; Michael et al., 2003; Thomson et al., 2006).

[0364] Taken together, these observations suggest that the expression of mature miRNAs may be affected by both transcriptional and post-transcriptional regulatory mechanisms.

[0365] Distinct miRNA Signatures in Normal B-Cell Subpopulations.

[0366] In order to further investigate whether specific miRNA regulation occurred in normal B-cell development or in transformed cells, miRNA representation was examined in libraries constructed from naïve, GC and memory B cells, as well as from the Ramos BL cell line. Differential expression of numerous known and newly identified miRNAs was evident during B-cell differentiation and GC transit as shown by hierarchical clustering using miRNA frequencies (defined as the fraction of the total pool of cloned miRNAs represented by a given miRNA in a library) obtained from the cloning data (FIG. **22**A). Naïve and memory B cells appeared similar, sharing a large fraction of the most abundant miRNAs. Conversely, centroblasts showed a more distinct miRNA profile with a sizeable fraction of abundant miRNAs being specifically expressed in the CB library, suggesting specific functions. Some miRNAs were expressed in the GC-derived Ramos cells, but not in normal GC B cells, or vice versa in the normal but not in the tumor cells, suggesting that malignant transformation affects miRNA expression.

[0367] To independently validate results of the cloning experiment, miRNA expression profiling was performed of centroblasts, naïve and memory B cells (six donors/each) using a commercial microarray representative of 723 known human miRNAs (miRBase v.10.1). The Spearman correlation between cloning and microarray data is 0.7 corresponding to a p-value<3.9e-28 (FIG. **27**). Each B-cell population showed a distinct miRNA expression profile. Consistent with the cloning data (FIG. **22**A), GC B cells appeared to be quite distinct from naïve and memory B cells, which instead shared expression of a large fraction of miRNAs (FIG. **22**B). The expression of several miRNAs was tested by qRT-PCR analysis, which confirmed that the microarray data were quantitatively accurate. Overall, these results show that the GC reaction is characterized by the specific expression of multiple miRNAs.

[0368] Discussion

[0369] The combination of cloning procedures and computational tools used in this study led to the identification of a large fraction of miRNA expressed during B-cell differentiation. These included 75 previously unreported miRNAs, as well as a potentially distinct class of short-RNAs not fulfilling current criteria for miRNAs. These findings have general implications for the understanding of the total miRNA content of the human genome as well as for future studies on the role of miRNAs in B-cell differentiation, function and lymphomagenesis.

[0370] The discovery of 75 previously unreported miRNAs expressed in normal and/or malignant B cells is in contrast with a previous study that reported the discovery of only 12 new human miRNA (Landgraf et al., 2007) from an analysis of a large panel of different organ systems and cell types and suggested that most miRNAs have already been identified and are ubiquitously expressed (Landgraf et al., 2007). These discordant results and conclusions may be due i) to the higher number of clones per library sequenced in this study (3500 versus 1300 on average in (Landgraf et al., 2007)), which allowed the detection of low-abundance miRNA species and ii) to the criteria applied in the miRNA identification which do not include conservation and allow consideration of repetitive elements (see Supplemental Experimental Procedures in Example 3). Moreover, the relatively lower degree of evolutionary conservation of previously unreported miRNAs may have prevented the cross-species identification of miRNAs using murine libraries (Chen et al., 2004; Neilson et al., 2007). Consistent with these observations, a recent report on short-RNAs in mouse embryonic stem cells discovered Dicer-dependent miRNAs characterized by both low abundance and low degree of conservation (Calabrese et al., 2007). Since 88% of the previously unreported miRNAs have been independently detected by RT-PCR and/or RNA blot analyses, our cloning and computational approach is largely validated.

[0371] We note that a fraction of the validated miRNAs display similarity to the 3'-end of post-transcriptionally modified tRNAs, raising the possibility that they may derive from loci with t-RNA homology or by direct processing of t-RNAs. We also identified a large set of candidate miRNAs (101 unreported, to our knowledge, and 27 known) that have been cloned as single occurrences in the B-cell libraries (Table 7). This group of candidate miRNAs has not yet been fully investigated, but nevertheless they may include bona fide miRNAs because 3 out of 3 tested were detectable by RNA blot or RT-PCR analyses. Thus, our data in B cells suggest that a large number of low-abundance, recently evolved, tissue-specific miRNAs remain to be discovered.

[0372] Two categories of short-RNAs were identified that could not be annotated as bona fide miRNAs. The first category is represented by short-RNAs which display all features required by the computational pipeline to be defined as candidate miRNAs, but nevertheless have an atypical length (<17 nt or >28 nt; 75 candidate miRNAs). Sequences belonging to this first category may include bona fide miRNAs since 2 out of 2 tested were detectable by RT-PCR. The second category is represented by those short-RNAs for which classic pre-miRNA structures could not be identified in the genome and no similarity to other non-coding RNA was found in the available databases. These short-RNAs may either be miRNA for which RNA secondary structure prediction algorithms failed to predict the correct hairpin structure or may represent new miRNA species of presently unknown mechanism of generation or other not yet described types of short-RNAs.

[0373] Finally, this analysis led to the discovery of short-RNAs that could not be accurately mapped to the genome. Considering that a fraction of these RNAs were cloned multiple times and showed a stage-specific behavior, we suggest that such short-RNAs do actually exist and that the lack of a match to the human genome may be due to polymorphisms, editing and other post-transcriptional modifications or to an incomplete or inaccurate sequencing of the corresponding genomic regions.

[0374] The specificity in mature miRNA expression appears to be regulated at the transcriptional as well as at the post-transcriptional, i.e. pre-miRNA processing, level. Indeed, the accumulation of pre-miRNA in absence of a mature miRNA can occur in a cell type-restricted manner, suggesting the presence of a mechanism of regulation at the pre-miRNA processing step. Both regulatory mechanisms may act during normal differentiation and may also be dys-regulated during transformation as a consequence of genetic or epigenetic alterations (Lee et al., 2007; Michael et al., 2003; Thomson et al., 2006). Indeed, miRNAs CU-1137 and CU-1368 represent examples of transcriptional activation and post-transcriptional silencing associated with malignant transformation, respectively.

[0375] The stage-specific expression of various miRNAs strongly suggests highly specialized regulatory functions in B-cell biology. The role of miRNAs that show cell type-specific functions in lymphocytes has just begun to be elucidated (Dorsett et al., 2008; Li et al., 2007; Rodriguez et al., 2007; Teng et al., 2008; Thai et al., 2007; Xiao et al., 2007). The miRNAs specifically associated with GC or non-GC B cells by either cloning or miRNA expression profiling have not been previously reported in B-cell differentiation with the exception of miR-150 (Xiao et al., 2007). For example the miR-199 and miR-125 families as well as miR-138 show a distinct expression in GC B cells although none of these miRNAs has been investigated for a role in this cell compartment. The extent of post-transcriptional regulation added by miRNAs will be fully uncovered only in the context of the complex network of cellular interactions (Basso et al., 2005), which will require the integration of large scale gene and miRNA expression data.

[0376] miRNA expression can be affected by malignant transformation. For instance, the miR-17-92 cluster, previously reported as a potential oncogene (He et al., 2005), was found over-expressed in Ramos cell line compared to GC B cells. Moreover, several miRNAs (i.e. CU-1137, CU-1148) show expression in Ramos cells and in several additional BL cell lines, but not in their normal GC counterpart. Vice versa, as observed for the miR-199 family, the expression of some miRNAs is lost in the tumor cells. The data herein represents a useful basis to investigate whether lymphoma-associated chromosomal lesions affect genomic regions associated with miRNA expression.

[0377] Finally, the differences in miRNA expression profile between GC and non-GC B cells resembled those observed by expression profiling of coding genes (Klein et al., 2003), consistent with the previous observation that miRNA profiling may be equally or more informative in discriminating tumor phenotypes (Calin et al., 2005; Lu et al., 2005). This suggests that miRNA expression profiling, especially if including new B-cell specific miRNAs, may be useful in the differential diagnosis of lymphoid malignancies.

[0378] The expanded B-cell miRNome described here represents a resource which can be used to identify miRNAs expressed during the GC transit as well as specific differences in miRNA expression in normal versus lymphoma cells, and which can guide studies to unveil the function of miRNAs in normal B cell development and lymphomagenesis.

[0379] Experimental Procedures

[0380] Generation of Short-RNA Libraries.

[0381] Purification of naïve, memory and GC B cells was performed as previously reported (Klein et al., 2003) using magnetic cell sorting of mononucleated cells obtained from human tonsils. Total RNA was purified using the Trizol Reagent (Invitrogen) following the manufacturer's indications. The short-RNA libraries were generated using an established protocol described in detail in (Lau et al., 2001). Briefly, total RNA was separated on 15% polyacrylamide gel and the fragment corresponding to 15-30 nucleotides length was excised. The purified small RNAs were linked to adaptor oligonucleotides and gel purified. Upon adaptor ligation, RNA was reverse transcribed and cDNA was PCR amplified and cloned into pCR2.1-TOPO vector (Invitrogen). Sequencing was performed on colony PCR amplicons.

[0382] Computational Identification of Precursor and Mature miRNAs.

[0383] The bioinformatics miRNA analysis pipeline (FIG. **18**) includes: (a) identification of short-RNAs from each library, (b) identification of exact and partial matches of the short-RNA sequences to the human genome, (c) testing each short-RNA genomic region for compatibility with hairpin secondary structures, (d) clustering genomic regions to predict mature miRNAs, (e) annotating and filtering short-RNAs and miRNAs candidates, (f) estimation of predicted miRNA frequencies in the libraries and (g) clustering short-RNAs that do not support miRNA candidates. The details are reported in the Supplemental Experimental Procedures in Example.

[0384] Orthology Analysis.

[0385] The identification of putative orthologous sequences of known and predicted precursor and mature human miRNAs in chimp (panTro2), monkey (rheMac2), dog (canFam2), mouse (mm8) and rat (rn4) was performed using UCSC-provided Blastz (Schwartz et al., 2003) pairwise alignments between human and target species. The details are reported below.

[0386] miRNA Expression Profiling.

[0387] The miRNA expression profiles were generated using the Human miRNA Microarray kit (Agilent Technologies) that allows detection of 723 known human (miRBase v.10.1) and 76 human viral miRNAs, following the manufacturer's indications. Analysis of raw data was performed using the Feature Extraction Software 9.5.3.1 (Agilent Technologies). The dendrograms (FIG. **22**) were generated using a hierarchical clustering algorithm based on the average-linkage method (Eisen et al., 1998; Hartigan, 1975) and Spearman's correlation as provided by the geWorkbench platform (http://www.geworkbench.org).

[0388] RT-PCR Analysis.

[0389] Small RNA fractions were purified using the Trizol Reagent (Invitrogen) and the PureLink miRNA Isolation Kit (Invitrogen), following the manufacturer's indications. RT-PCR was performed as previously described (Sharbati-Tehrani et al., 2008). Briefly, miRNA sequences were reverse-transcribed from 50 ng short-RNA using Superscript III First Strand Synthesis Kit (Invitrogen), in the presence of 0.2 μM RTFS primer (miRNA-specific primers, see Table 14). $1/10^{th}$ of the cDNA volume was then used as template for 34 cycles of PCR amplification in the presence of 4 nM SS primer

(miRNA-specific primers, see Table 14) and 0.4 μM each of MPF and MPR universal primers (Table 14). PCR products were separated on 12% non-denaturing polyacrylamide gel, detected by SybrGold (1:10,000 dilution; Invitrogen) and visualized under UV light.

TABLE 14

List of probes and primers used for Northern Blot and RT-PCR analyses, respectively.

ID	Seq ID No.	mature miRNA sequence (5'-3')	Seq ID No.	Probe sequence (5'-3')	Hybridization Temperature [° C.]
CU-1137	1839	GCTAAGGAA GTCCTGTGCT CAGTTTT	1926	AAAACTGAGCACAG GACTTCCTTAGC	60
CU-1142	1840	TCGATTCCCG GCCCATGCA CCA	1927	TGGTGCATGGGCCG GGAATCGA	55
CU-1153	1841	CCCCCCACT GCTAAATTTG ACTGGCTT	1928	AAGCCAGTCAAATTT AGCAGTGGGGGG	50
CU-1173	1842	ATCCCACTCC TGACACCA	1929	TGGTGTCAGGAGTG GGAT	50
CU-1241	1843	AGTCCCATCT GGGTCGCCA	1930	TGGCGACCCAGATG GGACT	55
CU-1254	1844	TCCCCGGCA CCTCCACCA	1931	TGGTGGAGGTGCCG GGGA	55
CU-1276	1845	TCGATTCCCG GCCAATGCA CCA	1932	TGGTGCATTGGCCG GGAATCGA	60
CU-1303	1846	ATCCCACTTC TGACACCA	1933	TGGTGTCAGAAGTG GGAT	50
CU-1368	1847	GACGAGGTG GCCGAGTGG	1934	AACCACTCGGCCAC CTCGTC	60
CU-1403	1848	GCATTGGTG GTTCAGTGGT AGA	1935	TCTACCACTGAACCA CCAATGC	60
CU-1513	1849	GCGGGTGAT GCGAACTGG AGTCTGAGC	1936	GCTCAGACTCCAGT TCGCATCACCCGC	50

ID	Seq ID No.	mature miRNA sequence (5'-3')	Seq ID No.	RTFS primer sequence (5'-3')	SS primer sequence (5'-3')
CU-1130	1850	CCCGGGTTT CGGCACCA	1937	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGC**	SEQ ID NO: 2013 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CCCGGGTTT CG**
CU-1132	1851	GCCGGGTAC TTTCGTATTTT	1938	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AAAATACG**	SEQ ID NO: 2014 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GCCGGGTAC TTT**
CU-1137	1852	GCTAAGGAA GTCCTGTGCT CAGTTTT	1939	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AAAACTGAGC**	SEQ ID NO: 2015 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GCTAAGGAA GTCCTGT**

TABLE 14-continued

List of probes and primers used for Northern Blot and RT-PCR analyses, respectively.

CU-1138	1853	TATCAATGAT GCTTCTGAGA	1940	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TCTCAG**	SEQ ID NO: 2016 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TATCAATGAT GCTT**
CU-1142	1854	TCGATTCCCG GCCCATGCA CCA	1941	TGTCAGGCAACCGT ATCACCGTGAGTGG TT**TGGTGC**	SEQ ID NO: 2017 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCGATTCCCG GCCCAT**
CU-1146	1855	AGAAAGGCC GAATTTTA	1942	TGTCAGGCAACCGT ATTCACCGTGAGTG[GT**TAAAATTCGG**	SEQ ID NO: 2018 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**AGAAAGGCCG**
CU-1148	1856	TGGTGTGGT CTGTTGTTTT	1943	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AAAACAACAG**	SEQ ID NO: 2019 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TGGTGTGGT CTG**
CU-1153	1857	CCCCCCACT GCTAAATTTG ACTGGCTT	1944	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AAGCCA**	SEQ ID NO: 2020 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CCCCCCACT GCTAAATTTG**
CU-1155	1858	TCCCCGCAC CTCCACCA	1945	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGG**	SEQ ID NO: 2021 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCCCCGCAC CT**
CU-1164	1859	GAGAGCGCT CGGTTTTT	1946	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AAAAACCG**	SEQ ID NO: 2022 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GAGAGCGCT**
CU-1173	1860	ATCCCACTCC TGACACCA	1947	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGT**	SEQ ID NO: 2023 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**ATCCCACTCC TG**
CU-1175	1861	GGCGTGATT CATACCTTTT	1948	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AAAAGGTATG**	SEQ ID NO: 2024 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GGCGTGATT CAT**
CU-1178	1862	AGGGTGTGC GTGTTTTT	1949	TGTCAGGCAACCGT ATTCACCGTGAGTG[GT**AAAAACACGC**	SEQ ID NO: 2025 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**AGGGTGTGC GT**
CU-1180	1863	AACCGAGCG TCCAAGCTCT TTCCATTTT	1950	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AAAATG**	SEQ ID NO: 2026 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**AACCGAGCG TCCAAGCTCT**
CU-1186	1864	TCCCCGACA CCTCCACCA	1951	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGG**	SEQ ID NO: 2027 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCCCCGACA CCT**
CU-1191	1865	GCCCGCATC CTCCACCA	1952	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGG**	SEQ ID NO: 2028 CGTCAGATGTCCGA GTAGAGGGGGAAC

TABLE 14-continued

List of probes and primers used for Northern Blot and RT-PCR analyses, respectively.

					GGCG**GCCCGCATC CT**
CU-1197	1866	ATGTGGTGG CTTACTTTT	1953	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AAAAGTAAGC**	SEQ ID NO: 2029 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**ATGTGGTGG CTT**
CU-1212	1867	TCCCCGGCA CTTCCACCA	1954	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGG**	SEQ ID NO: 2030 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCCCCGGCA CTT**
CU-1213	1868	TCACCCCATA AACACCA	1955	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGT**	SEQ ID NO: 2031 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCACCCCATAA**
CU-1220	1869	TTCCCCGAC GGGGAGCCA	1956	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGCTC**	SEQ ID NO: 2032 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TTCCCCGAC GGG**
CU-1221	1870	TGTGCTCCG GAGTTACCTC GTTT	1957	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AAACGAGG**	SEQ ID NO: 2033 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TGTGCTCCG GAGTTA**
CU-1222	1871	TCACGTCGG GGTCACCA	1958	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGA**	SEQ ID NO: 2034 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCACGTCGG GG**
CU-1241	1872	AGTCCCATCT GGGTCGCCA	1959	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGCGA**	SEQ ID NO: 2035 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**AGTCCCATCT GGG**
CU-1242	1873	TCCCCGTAC GGGCCACCA	1960	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGG**	SEQ ID NO: 2036 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCCCCGTAC GGG**
CU-1243	1874	GTCCCTTCGT GGTCGCCA	1961	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGCGA**	SEQ ID NO: 2037 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GTCCCTTCGT GG**
CU-1244	1875	GTCAGGATG GCCGAGCGG TCT	1962	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AGACCG**	SEQ ID NO: 2038 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GTCAGGATG GCCGAG**
CU-1246	1876	AGGGGGGTA AAAAAAAA	1963	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TTTTTTT**	SEQ ID NO: 2039 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**AGGGGGGTA AA**
CU-1251	1877	CCCACCCAG GGACGCCA	1964	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGCGT**	SEQ ID NO: 2040 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CCCACCCAG GG**

TABLE 14-continued

List of probes and primers used for Northern Blot and RT-PCR analyses, respectively.

CU-1254	1878	TCCCCGGCA CCTCCACCA	1965	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGG**	SEQ ID NO: 2041 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCCCCGGCA CCT**
CU-1264	1879	GAGGGGGAC CAAAAAAAA	1966	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TTTTTTTTGG**	SEQ ID NO: 2042 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GAGGGGGA**
CU-1269	1880	TACCGAGCC TGGTGATAGC	1967	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**GCTATC**	SEQ ID NO: 2043 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TACCGAGCC TGGT**
CU-1276	1881	TCGATTCCCG GCCAATGCA CCA	1968	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGCATTG**	SEQ ID NO: 2044 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCGATTCCCG GC**
CU-1277	1882	GAGCCATGA TGATACCACT GAGC	1969	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**GCTCAG**	SEQ ID NO: 2045 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GAGCCATGA TGATACCA**
CU-1278	1883	TAACGGCCG CGGTACCC	1970	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**GGGTAC**	SEQ ID NO: 2046 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TAACGGCCG CG**
CU-1281	1884	GCAGCGCCA GCCTCCCGC CCTAC	1971	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**GTAGGG**	SEQ ID NO: 2047 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GCAGCGCCA GCCTCCCG**
CU-1288	1885	CGTCCATGAT GTTCCGCAA	1972	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TTGCGG**	SEQ ID NO: 2048 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CGTCCATGAT GTT**
CU-1293	1886	AGCAGTGAT GTCCTGAAA ATTCTGAAG	1973	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**CTTCAGAATTT**	SEQ ID NO: 2049 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**AGCAGTGAT GTCCTGA**
CU-1294	1887	AAAGGACCT GGCGGTGCT TC	1974	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**GAAGCA**	SEQ ID NO: 2050 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**AAAGGACCT** GGCG**G**
CU-1298	1888	ATCCCGGAC GAGCCCCCA	1975	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGGGG**	SEQ ID NO: 2051 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**ATCCCGGAC GAG**
CU-1300	1889	TCCTCACAC GGGGCACCA	1976	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGC**	SEQ ID NO: 2052 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCCTCACAC GGG**
CU-1303	1890	ATCCCACTTC TGACACCA	1977	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGT**	SEQ ID NO: 2053 CGTCAGATGTCCGA GTAGAGGGGGAAC

TABLE 14-continued

List of probes and primers used for Northern Blot and RT-PCR analyses, respectively.

					GGCG**ATCCCACTTC TG**
CU-1307	1891	ACCCCACTAT GCTTAGCCCT	1978	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AGGGCT**	SEQ ID NO: 2054 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**ACCCCACTAT GCTT**
CU-1323	1892	TGTATTGTGA GACATTC	1979	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**GAATGT**	SEQ ID NO: 2055 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TGTATTGTGAG**
CU-1324	1893	TCTCGGTGG AACCTCCA	1980	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGAGG**	SEQ ID NO: 2056 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCTCGGTGG AA**
CU-1339	1894	ATCCCCAGC ACCTCCACCA	1981	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGG**	SEQ ID NO: 2057 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**ATCCCCAGC ACCT**
CU-1345	1895	AGAACACTA CGAGCCACA	1982	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGTGGC**	SEQ ID NO: 2058 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**AGAACACTA CGA**
CU-1352	1896	ACCCCACTTC TGGTACCA	1983	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTACCA**	SEQ ID NO: 2059 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**ACCCCACTTC**
CU-1363	1897	CGTTCGCGC TTTCCCCTG	1984	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**CAGGGGAAAG**	SEQ ID NO: 2060 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CGTTCGCG**
CU-1368	1898	GACGAGGTG GCCGAGTGG	1985	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**CCACTC**	SEQ ID NO: 2061 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GACGAGGTG GCC**
CU-1369	1899	TCCCCGGCA TCTCCACCA	1986	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGG**	SEQ ID NO: 2062 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCCCCGGCA TCT**
CU-1370_MOD	1900	CTGATTGCTC CTATCTGATT	1987	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AATCAG**	SEQ ID NO: 2063 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CTGATTGCTC CTAT**
CU-1371	1901	TCTAGAGGA GCCTGTTCTG TA	1988	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TACAGA**	SEQ ID NO: 2064 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCTAGAGGA GCCTGT**
CU-1379	1902	TCGGGTGCG AGAGGTCCC GGGT	1989	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**ACCCGGGACC**	SEQ ID NO: 2065 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCGGGTGCG AGA**

TABLE 14-continued

List of probes and primers used for Northern Blot and RT-PCR analyses, respectively.

CU-1380	1903	ATAGGTTTGG TCCTAGCCTT TCT	1990	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTAGAAAG**	SEQ ID NO: 2066 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**ATAGGTTTGG TCCTAGC**
CU-1381	1904	TCGATTCCCG GTCAGGGAA CCA	1991	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTTGGTTC**	SEQ ID NO: 2067 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCGATTCCCG GTCAGG**
CU-1382	1905	TCCTCGTTAG TATAGTGGTG AGTATCCC	1992	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTGGGATA**	SEQ ID NO: 2068 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCCTCGTTAG TATAGTGGT**
CU-1388	1906	TCCCTGGTG GTCTAGTGGT TAGGATTCG	1993	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTCGAATC**	SEQ ID NO: 2069 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCCCTGGTG GTCTAGTGGT**
CU-1396	1907	TAAGTGTTTG TGGGTTA	1994	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTTAACCCACA**	SEQ ID NO: 2070 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TAAGTGTT**
CU-1403	1908	GCATTGGTG GTTCAGTGGT AGA	1995	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTTCTACC**	SEQ ID NO: 2071 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GCATTGGTG GTTCAGT**
CU-1440	1909	TGGTTATCAC GTTCGCC	1996	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTGGCGAACGT**	SEQ ID NO: 2072 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TGGTTATC**
CU-1453	1910	CCGTGCTCG CTGCGCCA	1997	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTTGGCGC**	SEQ ID NO: 2073 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CCCTGCTCG CT**
CU-1457	1911	TTCTCACTAC TGCACTTGAC TA	1998	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTTAGTCA**	SEQ ID NO: 2074 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TTCTCACTAC TGCACT**
CU-1470	1912	CTGCTGGCT GGGTCGCCA	1999	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTTGGCGA**	SEQ ID NO: 2075 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CTCCTGGCT GGC**
CU-1477	1913	CTGCCACTG CTTCACTTGA CTAGC	2000	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTGCTAGT**	SEQ ID NO: 2076 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CTCCCACTG CTTCACTTG**
CU-1486	1914	CTGCTGTGAT GACATTC	2001	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTGAATGT**	SEQ ID NO: 2077 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CTGCTGTGATG**
CU-1488	1915	TCCTGCCGC GGTCGCCA	2002	TGTCAGGCAACCGT ATTCACCGTGAGTG **GTTGGCGA**	SEQ ID NO: 2078 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TCCTGCCGC**

TABLE 14-continued

List of probes and primers used for Northern Blot and RT-PCR analyses, respectively.

					GG
CU-1513	1916	GCGGGTGAT GGGAACTGG AGTCTGAGC	2003	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**GCTCAG**	SEQ ID NO: 2079 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GCGGGTGAT GCGAACTGGA**
CU-1524	1917	CCCCCACAA CCGCGCTTG ACTAGC	2004	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**GCTAGT**	SEQ ID NO: 2080 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CCCCCACAA CCGCGCTTG**
CU-1528	1918	TAGGGGTAT GATTCTCGCT	2005	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AGCGAG**	SEQ ID NO: 2081 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**TAGGGGTAT GATT**
CU-1538	1919	GGCTGGTCC GAGTGCAGT GGTGTTTA	2006	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TAAACACCAC**	SEQ ID NO: 2082 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GGCTGGTCC GAGTGCAGTG**
CU-1542	1920	GGCTGGTCC GATGGTAGT GGGTT	2007	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**AACCCA**	SEQ ID NO: 2083 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GGCTGGTCC GATGGTAG**
CU-1545	1921	CCACGAGGA AGAGAGGTA GC	2008	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**GCTACCTCT**	SEQ ID NO: 2084 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CCACGAGGA AG**
CU-1550	1922	CGGAAGGGT GCTGGGCCC	2009	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**GGGCCC**	SEQ ID NO: 2085 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CGGAAGCGT GCT**
CU-1557	1923	GGAGAGAAC GCGGTCTGA GTGGT	2010	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**ACCACT**	SEQ ID NO: 2086 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**GGAGAGAAC GCGGTCTG**
CU-1570	1924	ATCCCCAGC ATCTCCACCA	2011	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TGGTGG**	SEQ ID NO: 2087 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**ATCCCCAGC ATCT**
CU-1575	1925	CCCCCCACT GGTAAATTTG ACTGGA	2012	TGTCAGGCAACCGT ATTCACCGTGAGTG GT**TCCAGT**	SEQ ID NO: 2088 CGTCAGATGTCCGA GTAGAGGGGGAAC GGCG**CCCCCCACT GCTAAATTTG**

Universal primer ID	Universal primer sequences (5'-3')
MPF	SEQ ID NO: 2089 TGTCAGGCAACCGTATTC ACC

TABLE 14-continued

List of probes and primers used for Northern Blot and RT-PCR analyses, respectively.

MPR	SEQ ID NO: 2090 CGTCAGATGTCCGAGTAG AGG

Control Primer ID	Control primer sequences (5'-3')
5s_rRNA_FWD	SEQ ID NO: 2091 GCCCGATCTCGTCTGATCT
5s_rRNA_REV	SEQ ID NO: 2092 AGCCTACAGCACCCGGTA TT

[0390] RNA Blot.

[0391] Total RNA and small RNA fractions were purified using the Trizol Reagent (Invitrogen) and the PureLink miRNA Isolation Kit (Invitrogen), respectively, following the manufacturer's indications. Electrophoresis was performed on 15% denaturing polyacrylamide gel and then RNA was transferred on Duralon UV membrane (Stratagene) using a semidry transfer apparatus. Pre-hybridization and hybridization were performed in 5×SSC, 20 mM Na_2HPO_4 pH7.2, 7% SDS, 3×Denhardt's Solution. Oligonucleotide probes were [γ-^{32}P]-ATP labeled by polynucleotide kinase (Fermentas). The list of oligonucleotides and their hybridization temperature is reported in Table S8. After over-night hybridization, membranes were washed at the same temperature in 3×SSC, 25 mM NaH_2PO_4 pH 7.5, 5% SDS, 10×Denhardt's Solution for 15-20' and in 1×SSC, 1% SDS for 5'. Images were obtained by exposure to phosphoimager cassette and acquisition by Storm 840 Phosphoimager (Molecular Dynamics) and by film exposure for approximately 2 weeks.

[0392] Estimation of Library Complexity.

[0393] A bootstrap technique was used to estimate the total number of miRNAs expressed in each library and the number of short-RNAs must be sequenced to achieve a complete coverage. Bootstrapping is a statistical technique for estimating properties of an "estimator" by measuring those properties in multiple subsets of the samples (Harrell, 2001; Hinkley, 1997). Specifically, we estimated the distribution of mature miRNAs obtained by random sub-sampling different size short-RNA libraries from each complete library. For each size N=10, 20, . . . N_t, where N_t is the total number of short-RNAs in the library, we randomly sampled 1000 libraries of size N and computed the number r(N) of inferred miRNAs, resulting in a distribution p(r(N)) for which we could compute standard statistical parameters such as average, variance, mode and median. Based on this sampling, we can extrapolate p(r(1V)) for increasing values of N to determine at which point it is no longer efficient to use larger values of N to increase miRNA coverage. To achieve this, we fitted the data to the parametric function $f(x)=K*(1-e^{-mx})$.

[0394] Since we include both experimentally confirmed and putative mature miRNAs and since bootstrapping can produce optimistic results we expect that the estimated values constitute an upper boundary on the real library complexity. Based on this analysis, we estimated that the total numbers of mature miRNAs are: 129 (naïve), 154 (memory), 204 (centroblasts) and 189 (Ramos). Thus, the libraries sequenced in this study cover respectively 90.7% (naïve), 88.3% (memory), 85.8% (centroblasts), and 91% (Ramos) of the expressed miRNAs in these cellular phenotypes. FIG. **23** gives the 95% confidence intervals for p(r(N)) at each sampling point, in addition to the curve of the associated extrapolated function for each library. Clearly, the bootstrap analysis estimate of the total number of miRNA is correct only if the abundance of the miRNAs expressed in the sampled populations closely matches that of known miRNA in miRBase. This is not unreasonable if, as done here, only miRNAs that are specific to a B cell differentiation stage or transformation are considered. Thus, this does not estimate the total number of miRNA expressed across all human cell types, stages of differentiation and neoplastic transformations, which could be several fold larger than what was estimated from the B cell libraries.

[0395] Orthology and Conservation Analysis.

[0396] We investigated conservation of known and predicted precursor and mature human miRNA in chimp (panTro2), monkey (rheMac2), dog (canFam2) mouse (mm8) and rat (rn4). We obtained 678 miRNA precursor sequences from miRBase (v.11.0), 666 mature miRNAs and 167 star sequences. In total, we obtained 947 locations for mature and star mirBase sequences. We predicted 388 precursors of which 114 match miRBase precursors and 274 are newly predicted. Categorizing these by their corresponding mature sequences, 255 precursors correspond to mature miRNAs that are not included in the miRBase and 133 precursors are associated with 103 predicted miRNAs that match miRBase miRNAs. Of the 274 newly predicted precursors, 19 associated with 8 mature sequences listed in miRBase database.

[0397] miRNA conservation has been repeatedly used to help identify putative miRNA mappings to genomes. To identify putative ortholog miRNAs we relied on UCSC-provided Blastz pairwise alignments between human and target species (Schwartz et al., 2003). We used two related but complementary methods: (1) map the mature human miRNA to its ortholog location as specified by pairwise alignment; and (2) map the precursor of the human miRNA to its ortholog location as specified by pairwise alignment, expanding the human region to include at least 80 bases from both sides of the mature region, and identifying regions in the target that match the sequence of the mature human miRNA.

[0398] Method 1 is the simplest but fails to account for alignment inaccuracies and local mutations that may shift the position of the mature sequence in the target species. Method

2 accounts for locally imperfect Blastz mapping, but relies on conservation of larger regions that may not be subject to the same selective pressure as the mature miRNA. Alignment-based mapping of the human mature miRNA to its target were required to have either perfect conservation of the entire mature miRNA sequence or conservation of seeds composed of seven bases starting from the second position of the human mature sequence followed by conservation of 3 bases starting from the 12th, 13th or 14th position as suggested by (Grimson et al., 2007) (Appendix Table 11). We scanned the entire mapped ortholog region for a match to the human mature sequence or to its seed.

[0399] miRNA Target Prediction and Analysis.

[0400] Target predictions for not previously reported miRNAs were performed by miRanda v1.0 (John et al., 2004) and RNA22 (Miranda et al., 2006) using recommended parameters with the exception of RNA22 energy threshold that was changed from default −25.0 kcal/mol to −20.0 kcal/mol.

[0401] In order to investigate the potential effect of miRNAs on the transcriptome, predicted targets were tested for enrichment in genes down-regulated in the same population over-expressing the tested miRNA. Over-expressed miRNA were selected based on a minimum frequency value>0.08 and a three-fold increase in their cloning frequency comparing CB vs. naïve or memory B cell libraries. Genes differentially expressed across normal B cell populations were identified based on intensity fold change greater than 1.5, and p-value under 0.01 according to a non-parametric U test applied to six biological replicates per cell type (gene expression data are available from GEO database; GSE2350).

[0402] For each miRNA, using a Fisher exact test, we compared the numbers of down- and up-regulated predicted targets to down- and up-regulated genes that are not predicted targets. Setting a p-value threshold of 0.01, targets of most GC-specific miRNAs were significantly down regulated in CB. Conversely, targets of naïve- and memory-specific miRNAs were not significantly differentially regulated. Therefore the analysis was focused on targets of the 15 GC-specific miRNAs. Predicted targets of 8 out of 15 miRNAs showed significant enrichment (p-value<0.001) in genes down-regulated in GC compared to naïve B cells and 2 of them showed enrichment for genes down-regulated in a control population (memory compared to naive) (Table 13). We can conclude that targets of GC-specific miRNAs are significantly more likely to be down regulated in CB than in naive B cells with p<0.05 according to a Fisher exact test. Moreover, down-regulation p-values in CB were systematically lower than in memory (FIG. **26** and Table 13). Of the target sets for the 15 GC-specific miRNAs, 11 were more significantly down regulated in CB, 2 were more significantly down regulated in the control population (memory), and 2 were not down regulated in either (FIG. **26**). Using down-regulation in memory as control, we therefore conclude that down-regulation p-values are lower for CB with p<0.05 according to a binomial test with an $^{11}/_{15}$ rate under a null hypothesis of equally likely odds for greater down regulation. In summary, while targets of naive and memory specific miRNAs were not found differentially expressed in our data, we were able to demonstrate that predicted targets of GC-specific miRNAs are enriched in genes that are down regulated in GC.

[0403] Correlation Between Cloning and Microarray miRNA Profiling.

[0404] In order to compare cloning and microarray data, we focused on the 89 miRNAs for which both types of data were available. A significant correlation (p-value≤3.9e-28) was shown between cloning and miRNA microarray data as measured by Spearman correlation. The corresponding scatter plot is shown in FIG. **27**. Furthermore, to investigate if miRNA cloning counts were predictive of differential expression as measured by miRNA microarray, we identified 39 miRNAs whose cloning frequency was at least 2 fold greater in one normal B cell subset relative to each of the remaining two subsets. Of these, 25 (64.1%) miRNAs were found to be over-expressed in the same B cell subset according to miRNA microarray profiling. Over-expression was measured using a one sided U test, with threshold corresponding to p<0.01. We used permutation testing to estimate the significance of the success rate, randomly shuffling expression labels while keeping clone frequencies unchanged. The distribution of confirmed clone predictions using the shuffled expression data had mean of 1.2% and standard deviation of 5.1%, corresponding to 12.2 standard deviations away from our prediction success rate and a p-value near zero. We conclude that miRNA cloning counts are predictive of miRNAs concentration levels and differential expression.

[0405] Immunoprecipitation.

[0406] Immunoprecipitations were performed from Ramos cells grown in IMDM, 10% fetal bovine serum, 1% Penicillin/Streptomycin. 1-2×10^8 cells were collected and resuspended in 1 ml lysis buffer (10 mM Tris pH 7.5, 2 mM MgCl2, 10 mM KCl, 2.5 mM DTT, 1× protease inhibitors, 40 U/ul Ambion Superase-IN). Lysate supernatant was mixed with 500 ul ATP depletion mix (450 mM KCl, 100 mM glucose, 0.5 U/ul Sigma-Aldrich hexokinase). Cleared supernatant was divided equally between paramagnetic protein G beads (New England Biolabs) bound to either a monoclonal rat antibody raised against human Ago2 protein (Rudel et al., 2008) or total purified rat IgG (Sigma-Aldrich). Beads were incubated with lysate under rotation for 2 hours at 4° C., then washed three times with ice-cold lysis buffer and collected in Trizol (Invitrogen) for RNA extraction. RNA from three sequential immunoprecipitations was pooled and $^1/_{10}{}^{th}$ of yield was used for reverse transcription of each miRNA species using Superscript III First Strand Synthesis Kit (Invitrogen), in the presence of 0.2 μM RTFS primer (miRNA-specific primers, see Table S8). cDNA was also generated from reverse transcription in the presence of random hexamers to test expression of 5s rRNA. $^1/_{10}{}^{th}$ of the cDNA volume was used as template for SYBR (Applied Biosystems) qPCR amplification in the presence of 4 nM SS primer (miRNA-specific primers, see Table 14) and 0.4 μM each of MPF and MPR universal or 0.4 μM each of 5sRNA primers (Table 14). Each qPCR reaction was performed in triplicate. The tested miRNA were selected based on the availability of optimized qRT-PCR conditions among the ones detectable both by RNA blot and RT-PCR.

[0407] Accession numbers. The miRNA array profiles data are available from the GEO repository (GSE15144).

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TABLE 11

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

(1) Conservation of full-length mature miRNA sequence

miRNA identified in B cell libraries and deposited in miRBase database				Conservation				
		Seq ID						
ID	Genomic Coordinates	No.	Sequence	Chimp	Monkey	Dog	Mouse	Rat
CU-1001	chr11: 121522485-121522507	2093	TGAGGTAGTAGGTTGTATAGTT	Yes	Yes	Yes	Yes	Yes
CU-1001	chr9: 95978064-95978086	2094	TGAGGTAGTAGGTTGTATAGTT	Yes	Yes	Yes	Yes	Yes
CU-1003	chr22: 44888234-44888256	2095	TGAGGTAGTAGGTTGTGTGGTT	Yes	Yes	Yes	Yes	Yes
CU-1004	chr9: 95980943-95980965	2096	AGAGGTAGTAGGTTGCATAGTT	Yes	Yes	Yes	Yes	Yes
CU-1005	chr19: 56887857-56887879	2097	TGAGGTAGGAGGTTGTATAGTT	Yes	Yes	Yes	Yes	Yes
CU-1006	chrX: 53600931-53600953	2098	TGAGGTAGTAGATTGTATAGTT	Yes	Yes	Yes	Yes	Yes
CU-1007	chr3: 52277391-52277413	2099	TGAGGTAGTAGTTTGTACAGTT	Yes	Yes	Yes	Yes	No
CU-1008	chr12: 61283737-61283759	2100	TGAGGTAGTAGTTTGTGCTGTT	Yes	Yes	Yes	Yes	Yes
CU-1009	chr1: 65296711-65296733	2101	TACAGTACTGTGATAACTGAAG	Yes	Yes	Yes	Yes	Yes
CU-1009	chr9: 4840344-4840366	2102	TACAGTACTGTGATAACTGAAG	Yes	Yes	Yes	No	No
CU-1010	chr20: 3846187-3846210	2103	AGCAGCATTGTACAGGGCTATGA	Yes	Yes	Yes	Yes	Yes
CU-1011	chr7: 99529562-99529582	2104	CCGCACTGTGGGTACTTGCT	Yes	Yes	Yes	Yes	Yes
CU-1012	chr7: 99529601-99529622	2105	TAAAGTGCTGACAGTGCAGAT	Yes	Yes	Yes	Yes	Yes
CU-1014	chr19: 56888332-56888356	2106	TCCCTGAGACCCTTTAACCTGTGA	Yes	Yes	Yes	Yes	Yes
CU-1015	chr21: 16884443-16884465	2107	TCCCTGAGACCCTAACTTGTGA	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1016	chr6: 131417431-131417449	2108	GTCCCTGTTCGGGCGCCA	No	Yes	No	No	No
CU-1016	chr19: 62716222-62716240	2109	GTCCCTGTTCGGGCGCCA	Yes	No	No	No	No
CU-1017	chr1: 150066843-150066860	2110	GTGGGGGAGAGGCTGTA	No	No	No	No	No
CU-1018	chr7: 35602718-35602735	2111	TCCCACCGCTGCCACCA	No	No	No	No	No
CU-1018	chr2: 72555764-72555781	2112	TCCCACCGCTGCCACCA	No	No	No	No	No
CU-1018	chrX: 55565708-55565725	2113	TCCCACCGCTGCCACCA	No	No	No	No	No
CU-1018	chr1: 225154598-225154615	2114	TCCCACCGCTGCCACCA	No	No	No	No	No
CU-1018	chr11: 95714259-95714276	2115	TCCCACCGCTGCCACCA	No	No	No	No	No
CU-1018	chr7: 5368308-5368325	2116	TCCCACCGCTGCCACCA	No	No	No	No	No
CU-1018	chr6: 140362954-140362971	2117	TCCCACCGCTGCCACCA	No	No	No	No	No
CU-1019	chr2: 136139485-136139506	2118	TCACAGTGAACCGGTCTCTTT	Yes	Yes	Yes	Yes	Yes
CU-1021	chr1: 159701881-159701904	2119	GCATGGGTGGTTCAGTGGTAGAA	Yes	Yes	No	No	No
CU-1021	chr1: 159694521-159694544	2120	GCATGGGTGGTTCAGTGGTAGAA	Yes	Yes	No	No	No
CU-1021	chr1: 159687090-159687113	2121	GCATGGGTGGTTCAGTGGTAGAA	Yes	Yes	No	No	No
CU-1021	chr21: 17749025-17749048	2122	GCATGGGTGGTTCAGTGGTAGAA	Yes	Yes	No	No	No
CU-1021	chr1: 159679717-159679740	2123	GCATGGGTGGTTCAGTGGTAGAA	No	Yes	Yes	No	No
CU-1022	chr22: 20337642-20337664	2124	CAGTGCAATGATGAAAGGGCAT	Yes	Yes	Yes	Yes	Yes
CU-1023	chr3: 44130729-44130753	2125	AGCTGGTGTTGTGAATCAGGCCGT	No	No	Yes	Yes	Yes
CU-1024	chr16: 68524545-68524567	2126	TACCACAGGGTAGAACCACGGA	Yes	Yes	Yes	Yes	Yes
CU-1025	chr16: 68524506-68524527	2127	CAGTGGTTTTACCCTATGGTA	Yes	Yes	Yes	Yes	Yes
CU-1026	chr17: 53763604-53763627	2128	TGTAGTGTTTCCTACTTTATGGA	Yes	Yes	Yes	Yes	Yes
CU-1027	chr5: 159844956-159844978	2129	TGAGAACTGAATTCCATGGGTT	Yes	Yes	Yes	Yes	Yes
CU-1028	chr10: 104186266-104186290	2130	TGAGAACTGAATTCCATAGGCTGT	Yes	No	Yes	Yes	Yes
CU-1029	chr19: 54695901-54695922	2131	TCTCCCAACCCTTGTACCAGT	Yes	Yes	Yes	Yes	Yes
CU-1030	chr17: 17715007-17715028	2132	CTAGACTGAAGCTCCTTGAGG	Yes	Yes	No	No	No
CU-1030	chr7: 150838585-150838606	2133	CTAGACTGAAGCTCCTTGAGG	Yes	No	No	No	No
CU-1031	chrX: 53425327-53425349	2134	TCGAGGAGCTCACAGTCTAGTA	Yes	No	No	No	No
CU-1031	chr8: 141811902-141811924	2135	TCGAGGAGCTCACAGTCTAGTA	Yes	Yes	Yes	No	No
CU-1032	chr21: 25868165-25868188	2136	TTAATGCTAATCGTGATAGGGGT	Yes	Yes	Yes	No	No
CU-1033	chr13: 49521304-49521325	2137	TAGCAGCACATAATGGTTTGT	Yes	Yes	Yes	Yes	No
CU-1033	chr7: 3516339-3516360	2138	TAGCAGCACATAATGGTTTGT	No	No	No	No	No
CU-1034	chr3: 161605126-161605147	2139	CGAATCATTATTTGCTGCTCT	Yes	Yes	Yes	Yes	Yes
CU-1035	chr3: 161605088-161605110	2140	TAGCAGCACATCATGGTTTACA	Yes	Yes	Yes	Yes	Yes
CU-1037	chr3: 161605235-161605257	2141	TAGCAGCACGTAAATATTGGCG	Yes	Yes	Yes	Yes	Yes
CU-1037	chr13: 49521163-49521185	2142	TAGCAGCACGTAAATATTGGCG	Yes	Yes	Yes	Yes	No
CU-1038	chr13: 90800909-90800931	2143	ACTGCAGTGAAGGCACTTGTAG	Yes	No	Yes	No	No
CU-1039	chr13: 90800872-90800895	2144	CAAAGTGCTTACAGTGCAGGTAG	Yes	No	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1040	chr1: 197094822-197094842	2145	ACCATCGACCGTTGATTGTA	Yes	Yes	Yes	Yes	Yes
CU-1042	chr9: 126494579-126494603	2146	AACATTCAACGCTGTCGGTGAGTT	Yes	Yes	Yes	Yes	Yes
CU-1042	chr1: 197094858-197094882	2147	AACATTCAACGCTGTCGGTGAGTT	Yes	Yes	Yes	Yes	Yes
CU-1044	chr13: 90801051-90801073	2148	ACTGCCCTAAGTGCTCCTTCTG	Yes	No	Yes	Yes	Yes
CU-1045	chr13: 90801010-90801032	2149	TAAGGTGCATCTAGTGCAGATA	Yes	No	Yes	Yes	Yes
CU-1046	chr3: 49033108-49033131	2150	CAACGGAATCCCAAAAGCAGCTG	Yes	Yes	Yes	Yes	Yes
CU-1047	chr11: 64415251-64415271	2151	CTGACCTATGAATTGACAGC	Yes	Yes	Yes	Yes	Yes
CU-1050	chr16: 14305374-14305396	2152	AACTGGCCCTCAAAGTCCCGCT	Yes	Yes	No	No	No
CU-1052	chr17: 6861708-6861730	2153	TAGCAGCACAGAAATATTGGCA	Yes	Yes	Yes	Yes	Yes
CU-1053	chr1: 109943084-109943105	2154	TTCACCACCTTCTCCACCCAG	Yes	Yes	Yes	No	No
CU-1054	chr1: 170380354-170380377	2155	CCCAGTGTTCAGACTACCTGTTC	Yes	Yes	Yes	Yes	Yes
CU-1054	chr19: 10789144-10789167	2156	CCCAGTGTTCAGACTACCTGTTC	Yes	Yes	Yes	Yes	No
CU-1055	chr19: 10789105-10789126	2157	ACAGTAGTCTGCACATTGGTT	Yes	Yes	Yes	Yes	No
CU-1055	chr1: 170380317-170380338	2158	ACAGTAGTCTGCACATTGGTT	Yes	Yes	Yes	Yes	Yes
CU-1055	chr9: 130046845-130046866	2159	ACAGTAGTCTGCACATTGGTT	Yes	Yes	Yes	Yes	No
CU-1056	chr13: 90801193-90801216	2160	TGTGCAAATCTATGCAAAACTGA	Yes	No	Yes	Yes	Yes
CU-1057	chrX: 133131378-133131401	2161	TGTGCAAATCCATGCAAAACTGA	Yes	Yes	Yes	Yes	Yes
CU-1057	chr13: 90801499-90801522	2162	TGTGCAAATCCATGCAAAACTGA	Yes	Yes	Yes	Yes	Yes
CU-1061	chr13: 90801326-90801349	2163	TAAAGTGCTTATAGTGCAGGTAG	Yes	No	Yes	Yes	Yes
CU-1062	chrX: 133131545-133131568	2164	CAAAGTGCTTATAGTGCAGGTAG	No	No	No	No	No
CU-1064	chr17: 55273415-55273437	2165	TAGCTTATCAGACTGATGTTGA	Yes	Yes	Yes	Yes	Yes
CU-1065	chrX: 45490553-45490574	2166	AGCTACATTGTCTGCTGGGTT	Yes	Yes	Yes	Yes	Yes
CU-1066	chrX: 45491383-45491406	2167	AGCTACATCTGGCTACTGGGTCT	No	Yes	Yes	Yes	Yes
CU-1067	chrX: 65155503-65155525	2168	TGTCAGTTTGTCAAATACCCCA	Yes	Yes	Yes	Yes	Yes
CU-1068	chr19: 13808407-13808429	2169	ATCACATTGCCAGGGATTTCCA	Yes	Yes	Yes	Yes	Yes
CU-1069	chr9: 96887367-96887389	2170	ATCACATTGCCAGGGATTACCA	Yes	Yes	Yes	Yes	Yes
CU-1071	chr7: 99529129-99529151	2171	CATTGCACTTGTCTCGGTCTGA	No	Yes	Yes	Yes	Yes
CU-1072	chr12: 56504707-56504729	2172	TTCAAGTAATCCAGGATAGGCT	Yes	Yes	Yes	Yes	No
CU-1072	chr3: 37985907-37985929	2173	TTCAAGTAATCCAGGATAGGCT	Yes	Yes	Yes	Yes	Yes
CU-1073	chr2: 218975623-218975645	2174	TTCAAGTAATTCAGGATAGGTT	Yes	Yes	Yes	Yes	Yes
CU-1075	chr9: 96887607-96887627	2175	TTCACAGTGGCTAAGTTCTG	Yes	Yes	Yes	Yes	Yes
CU-1076	chr3: 189889315-189889337	2176	CACTAGATTGTGAGCTCCTGGA	Yes	Yes	Yes	No	Yes
CU-1077	chr3: 189889275-189889297	2177	AAGGAGCTCACAGTCTATTGAG	Yes	Yes	Yes	Yes	Yes
CU-1079	chr7: 130212046-130212068	2178	TAGCACCATCTGAAATCGGTTA	No	Yes	Yes	Yes	Yes
CU-1080	chr1: 206042417-206042440	2179	TAGCACCATTTGAAATCAGTGTT	Yes	Yes	Yes	Yes	Yes
CU-1081	chr1: 206041871-206041892	2180	TGACCGATTTCTCCTGGTGTT	Yes	Yes	Yes	Yes	Yes
CU-1082	chr1: 206041832-206041854	2181	TAGCACCATTTGAAATCGGTTA	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1083	chr6: 72170020-72170040	2182	TGTAAACATCCTCGACTGGA	Yes	Yes	Yes	Yes	Yes
CU-1084	chr8: 135881994-135882016	2183	TGTAAACATCCTACACTCAGCT	Yes	Yes	Yes	Yes	Yes
CU-1085	chr1: 40995558-40995581	2184	TGTAAACATCCTACACTCTCAGC	Yes	Yes	Yes	Yes	Yes
CU-1086	chr8: 135886343-135886365	2185	TGTAAACATCCCCGACTGGAAG	Yes	Yes	Yes	Yes	Yes
CU-1087	chr1: 40992629-40992653	2186	TGTAAACATCCTTGACTGGAAGCT	Yes	Yes	Yes	Yes	Yes
CU-1088	chr8: 22158432-22158448	2187	TGGGTTGAGAGGGCGA	Yes	Yes	Yes	Yes	Yes
CU-1089	chr16: 65793734-65793752	2188	CTGGCCCTCTCTGCCCTT	Yes	No	Yes	Yes	Yes
CU-1091	chr12: 94226386-94226407	2189	GCCCCTGGGCCTATCCTAGAA	Yes	Yes	Yes	Yes	Yes
CU-1092	chr7: 1029154-1029174	2190	TCCCTGTCCTCCAGGAGCTC	Yes	Yes	Yes	Yes	No
CU-1092	chr10: 22978473-22978493	2191	TCCCTGTCCTCCAGGAGCTC	No	No	No	No	No
CU-1093	chr14: 99645804-99645828	2192	TCTCACACAGAAATCGCACCCGTC	Yes	Yes	Yes	Yes	Yes
CU-1094	chr14: 99645763-99645783	2193	GGGGTGCTATCTGTGATTGA	Yes	Yes	Yes	Yes	Yes
CU-1095	chr1: 9134379-9134402	2194	TGGCAGTGTCTTAGCTGGTTGTT	Yes	Yes	Yes	Yes	Yes
CU-1096	chrX: 85045302-85045324	2195	TCCCCCAGGTGTGATTCTGATT	Yes	Yes	Yes	Yes	Yes
CU-1098	chr17: 26926609-26926631	2196	TAATGCCCCTAAAAATCCTTAT	Yes	Yes	Yes	Yes	Yes
CU-1098	chr16: 14310697-14310719	2197	TAATGCCCCTAAAAATCCTTAT	Yes	Yes	Yes	Yes	Yes
CU-1099	chr5: 149092584-149092605	2198	CTCCTGACTCCAGGTCCTGTG	Yes	Yes	Yes	No	Yes
CU-1100	chr17: 25468274-25468296	2199	AGCTCGGTCTGAGGCCCCTCAG	Yes	Yes	Yes	Yes	Yes
CU-1101	chr17: 25468238-25468260	2200	TGAGGGGCAGAGAGCGAGACTT	Yes	Yes	Yes	Yes	Yes
CU-1103	chr8: 41637118-41637140	2201	TCCTGTACTGAGCTGCCCCGAG	Yes	Yes	Yes	Yes	No
CU-1104	chr17: 6862021-6862042	2202	CAGCAGCACACTGTGGTTTGT	Yes	Yes	Yes	Yes	Yes
CU-1105	chrX: 138833988-138834006	2203	CGTCAACACTTGCTGGTT	Yes	Yes	Yes	Yes	Yes
CU-1106	chr4: 38546107-38546128	2204	CACGCTCATGCACACACCCAC	No	No	Yes	Yes	No
CU-1108	chr14: 65007623-65007643	2205	AGGGGGAAAGTTCTATAGTC	Yes	No	No	No	No
CU-1108	chr14: 65007586-65007606	2206	AGGGGGAAAGTTCTATAGTC	Yes	No	No	No	No
CU-1110	chr15: 68158819-68158840	2207	TGGGTTTACGTTGGGAGAACT	No	No	No	No	No
CU-1111	chr9: 85774506-85774527	2208	CAACAAATCACAGTCTGCCAT	Yes	Yes	Yes	Yes	Yes
CU-1113	chr9: 85774546-85774569	2209	TGGAAGACTAGTGATTTTGTTGT	Yes	Yes	Yes	Yes	Yes
CU-1113	chr15: 86956090-86956113	2210	TGGAAGACTAGTGATTTTGTTGT	Yes	Yes	Yes	Yes	Yes
CU-1113	chr19: 4721711-4721734	2211	TGGAAGACTAGTGATTTTGTTGT	Yes	Yes	Yes	No	No
CU-1115	chr13: 90801578-90801601	2212	AGGTTGGGATCGGTTGCAATGCT	Yes	No	Yes	No	No
CU-1116	chrX: 133131239-133131261	2213	TATTGCACTTGTCCCGGCCTGT	Yes	Yes	Yes	No	No
CU-1116	chr13: 90801615-90801637	2214	TATTGCACTTGTCCCGGCCTGT	Yes	Yes	Yes	Yes	Yes
CU-1117	chr1: 153431651-153431670	2215	TATTGCACTCGTCCCGGCC	No	Yes	Yes	Yes	Yes
CU-1118	chr7: 99529373-99529396	2216	CAAAGTGCTGTTCGTGCAGGTAG	Yes	Yes	Yes	Yes	Yes
CU-1119	chrX: 53599984-53600006	2217	TGAGGTAGTAAGTTGTATTGTT	Yes	Yes	Yes	Yes	Yes
CU-1124	chr17: 53763644-53763665	2218	CCCATAAAGTAGAAAGCACTA	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1125	chr3: 161605277-161605298	2219	ACCAATATTACTGTGCTGCTT	Yes	Yes	No	No	No
CU-1126	chr9: 126495825-126495848	2220	ACATTCATTGCTGTCGGTGGGTT	Yes	Yes	Yes	Yes	Yes
CU-1126	chr1: 197094675-197094698	2221	ACATTCATTGCTGTCGGTGGGTT	Yes	Yes	Yes	Yes	Yes
CU-1568	chr21: 16834028-16834046	2222	TGAGGTAGTAGGTTGTAT	Yes	Yes	Yes	Yes	Yes
CU-5001	chr9: 95980997-95981018	2223	CTATACGACCTGCTGCCTTTC	Yes	Yes	Yes	Yes	Yes
CU-5002	chr3: 49032596-49032618	2224	CATCGGGAATGTCGTGTCCGCC	Yes	Yes	Yes	Yes	No
CU-5016	chr3: 49032634-49032658	2225	AATGACACGATCACTCCCGTTGAG	Yes	Yes	Yes	Yes	Yes

new miRNA identified in B cell libraries

		Seq. ID		Conservation				
ID	Genomic Coordinates	NO.	Sequence	Chimp	Monkey	Dog	Mouse	Rat
CU-1130	chr4: 84650562-84650579	2226	CCCGGGTTTCGGCACCA	Yes	No	No	No	No
CU-1130	chr7: 152741807-152741824	2227	CCCGGGTTTCGGCACCA	No	No	No	No	No
CU-1132	chr12: 123990125-123990145	2228	GCCGGGTACTTTCGTATTTT	No	No	No	No	No
CU-1137	chr17: 8030990-8031016	2229	GCTAAGGAAGTCCTGTGCTCAGTTTT	Yes	No	No	No	No
CU-1142	chr5: 180625271-180625293	2230	TCGATTCCCGGCCCATGCACCA	No	No	No	No	No
CU-1142	chr21: 17748974-17748996	2231	TCGATTCCCGGCCCATGCACCA	No	No	No	No	No
CU-1142	chr1: 159687142-159687164	2232	TCGATTCCCGGCCCATGCACCA	No	No	No	No	No
CU-1142	chr1: 159701933-159701955	2233	TCGATTCCCGGCCCATGCACCA	No	No	No	No	No
CU-1142	chr1: 159679769-159679791	2234	TCGATTCCCGGCCCATGCACCA	No	No	No	No	No
CU-1142	chr1: 159694573-159694595	2235	TCGATTCCCGGCCCATGCACCA	No	No	No	No	No
CU-1146	chr16: 3142975-3142992	2236	AGAAAGGCCGAATTTTA	No	No	No	No	No
CU-1148	chr10: 5935660-5935679	2237	TGGTGTGGTCTGTTGTTTT	Yes	No	No	No	No
CU-1153	chr14: 22388241-22388268	2238	CCCCCCACTGCTAAATTTGACTGGCTT	No	No	No	No	No
CU-1153	chr17: 35653067-35653094	2239	CCCCCCACTGCTAAATTTGACTGGCTT	Yes	No	No	No	No
CU-1155	chr20: 58490320-58490337	2240	TCCCCGCACCTCCACCA	Yes	Yes	No	No	No
CU-1164	chr6: 29057409-29057426	2241	GAGAGCGCTCGGTTTTT	No	No	No	No	No
CU-1173	chr18: 1681856-1681874	2242	ATCCCACTCCTGACACCA	Yes	No	No	No	No
CU-1175	chr11: 59075015-59075034	2243	GGCGTGATTCATACCTTTT	No	No	No	No	No
CU-1178	chr6: 28723944-28723961	2244	AGGGTGTGCGTGTTTTT	Yes	No	No	No	No
CU-1180	chr19: 38359877-38359905	2245	AACCGAGCGTCCAAGCTCTTTCCATTTT	No	No	No	No	No
CU-1186	chr18: 73990174-73990192	2246	TCCCCGACACCTCCACCA	No	No	No	No	No
CU-1191	chr12: 46439968-46439985	2247	GCCCGCATCCTCCACCA	Yes	No	No	No	No
CU-1197	chr15: 38673296-38673314	2248	ATGTGGTGGCTTACTTTT	No	No	No	No	No
CU-1212	chr20: 60596937-60596955	2249	TCCCCGGCACTTCCACCA	No	No	No	No	No
CU-1213	chr3: 73875819-73875836	2250	TCACCCCATAAACACCA	Yes	Yes	No	No	No
CU-1220	chr1: 159706825-159706843	2251	TTCCCCGACGGGGAGCCA	No	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1220	chr1: 159692034-159692052	2252	TTCCCCGACGGGGAGCCA	No	No	No	No	No
CU-1220	chr1: 159677235-159677253	2253	TTCCCCGACGGGGAGCCA	No	No	No	No	No
CU-1220	chr1: 159699444-159699462	2254	TTCCCCGACGGGGAGCCA	No	No	No	No	No
CU-1220	chr1: 159684653-159684671	2255	TTCCCCGACGGGGAGCCA	No	No	No	No	No
CU-1221	chr17: 34564245-34564268	2256	TGTGCTCCGGAGTTACCTCGTTT	No	No	No	No	No
CU-1222	chrX: 70920902-70920919	2257	TCACGTCGGGGTCACCA	Yes	No	No	No	No
CU-1241	chr2: 167308360-167308379	2258	AGTCCCATCTGGGTCGCCA	No	No	No	No	No
CU-1241	chr1: 29814092-29814111	2259	AGTCCCATCTGGGTCGCCA	No	No	No	No	No
CU-1241	chrX: 51239676-51239695	2260	AGTCCCATCTGGGTCGCCA	Yes	Yes	No	No	No
CU-1241	chr13: 22997399-22997418	2261	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr6: 70235237-70235256	2262	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr6: 141377023-141377042	2263	AGTCCCATCTGGGTCGCCA	No	No	No	No	No
CU-1241	chr16: 21555749-21555768	2264	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr3: 97152533-97152552	2265	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chrX: 70638471-70638490	2266	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr2: 47181625-47181644	2267	AGTCCCATCTGGGTCGCCA	No	No	No	No	No
CU-1241	chr3: 114548556-114548575	2268	AGTCCCATCTGGGTCGCCA	No	No	No	No	No
CU-1241	chr8: 107870541-107870560	2269	AGTCCCATCTGGGTCGCCA	No	No	No	No	No
CU-1241	chr10: 118251348-118251367	2270	AGTCCCATCTGGGTCGCCA	No	No	No	No	No
CU-1241	chr13: 110648656-110648675	2271	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr1: 74982888-74982907	2272	AGTCCCATCTGGGTCGCCA	No	No	No	No	No
CU-1241	chr1: 74982864-74982883	2273	AGTCCCATCTGGGTCGCCA	No	No	No	No	No
CU-1241	chrX: 120113204-120113223	2274	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1242	chr7: 148897373-148897391	2275	TCCCCGTACGGGCCACCA	Yes	No	No	No	No
CU-1242	chr6: 159071498-159071516	2276	TCCCCGTACGGGCCACCA	Yes	No	No	No	No
CU-1243	chr1: 173342843-173342861	2277	GTCCCTTCGTGGTCGCCA	No	No	No	No	No
CU-1243	chr19: 55148120-55148138	2278	GTCCCTTCGTGGTCGCCA	No	No	No	No	No
CU-1243	chrX: 117299486-117299504	2279	GTCCCTTCGTGGTCGCCA	No	No	No	No	No
CU-1243	chr8: 4429174-4429192	2280	GTCCCTTCGTGGTCGCCA	Yes	No	No	No	No
CU-1243	chr11: 84485385-84485403	2281	GTCCCTTCGTGGTCGCCA	Yes	No	No	No	No
CU-1243	chr21: 26073725-26073743	2282	GTCCCTTCGTGGTCGCCA	Yes	No	No	No	No
CU-1243	chr5: 77142069-77142087	2283	GTCCCTTCGTGGTCGCCA	Yes	No	No	No	No
CU-1243	chr19: 8350798-8350816	2284	GTCCCTTCGTGGTCGCCA	No	No	No	No	No
CU-1243	chr12: 20827096-20827114	2285	GTCCCTTCGTGGTCGCCA	No	No	No	No	No
CU-1244	chr1: 159766817-159766838	2286	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr1: 159700155-159700176	2287	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr1: 159677946-159677967	2288	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	Yes	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1244	chr1: 159685364-159685385	2289	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr16: 55891954-55891975	2290	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr1: 159692745-159692766	2291	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr1: 159707536-159707557	2292	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr1: 240532967-240532988	2293	GTCAGGATGGCCGAGCGGTCT	Yes	No	No	No	No
CU-1246	chr14: 65014334-65014351	2294	AGGGGGGTAAAAAAAAA	Yes	No	No	No	No
CU-1246	chr14: 93614119-93614136	2295	AGGGGGGTAAAAAAAAA	No	No	No	No	No
CU-1251	chr12: 31408926-31408943	2296	CCCACCCAGGGACGCCA	No	No	No	No	No
CU-1251	chr17: 34161556-34161573	2297	CCCACCCAGGGACGCCA	No	No	No	No	No
CU-1251	chr1: 146614798-146614815	2298	CCCACCCAGGGACGCCA	No	No	No	No	No
CU-1251	chr19: 33728787-33728804	2299	CCCACCCAGGGACGCCA	No	No	No	No	No
CU-1251	chr9: 136463072-136463089	2300	CCCACCCAGGGACGCCA	No	No	No	No	No
CU-1254	chr4: 2032401-2032419	2301	TCCCCGGCACCTCCACCA	No	No	No	No	No
CU-1264	chr3: 37897506-37897524	2302	GAGGGGGACCAAAAAAAA	Yes	No	No	No	No
CU-1269	chr17: 21946878-21946897	2303	TACCGAGCCTGGTGATAGC	No	No	No	No	No
CU-1269	chr11: 102785624-102785643	2304	TACCGAGCCTGGTGATAGC	Yes	No	No	No	No
CU-1276	chr17: 7969840-7969862	2305	TCGATTCCCGGCCAATGCACCA	No	No	No	No	No
CU-1276	chr19: 39807750-39807772	2306	TCGATTCCCGGCCAATGCACCA	No	No	No	No	No
CU-1277	chr1: 153990335-153990358	2307	GAGCCATGATGATACCACTGAGC	Yes	No	No	No	No
CU-1278	chr5: 79981714-79981731	2308	TAACGGCCGCGGTACCC	Yes	Yes	No	No	No
CU-1278	chr3: 97818860-97818877	2309	TAACGGCCGCGGTACCC	Yes	Yes	No	No	No
CU-1281	chr1: 173235999-173236022	2310	GCAGCGCCAGCCTCCCGCCCTAC	Yes	No	No	No	No
CU-1288	chr19: 54685975-54685994	2311	CGTCCATGATGTTCCGCAA	No	No	No	No	No
CU-1293	chr2: 38390703-38390730	2312	AGCAGTGATGTCCTGAAAATTCTGAAG	No	No	No	No	No
CU-1294	chr5: 79983107-79983127	2313	AAAGGACCTGGCGGTGCTTC	Yes	No	No	No	No
CU-1294	chr11: 10487796-10487816	2314	AAAGGACCTGGCGGTGCTTC	Yes	No	No	No	No
CU-1294	chr13: 108874524-108874544	2315	AAAGGACCTGGCGGTGCTTC	Yes	No	No	No	No
CU-1298	chr16: 3178151-3178169	2316	ATCCCGGACGAGCCCCCA	No	No	No	No	No
CU-1298	chr22: 44955360-44955378	2317	ATCCCGGACGAGCCCCCA	Yes	No	No	No	No
CU-1298	chr11: 49720969-49720987	2318	ATCCCGGACGAGCCCCCA	Yes	No	No	No	No
CU-1298	chr16: 3174130-3174148	2319	ATCCCGGACGAGCCCCCA	No	No	No	No	No
CU-1298	chr11: 75624513-75624531	2320	ATCCCGGACGAGCCCCCA	No	No	No	No	No
CU-1300	chr6: 101499628-101499646	2321	TCCTCACACGGGGCACCA	Yes	No	No	No	No
CU-1300	chr7: 106814117-106814135	2322	TCCTCACACGGGGCACCA	Yes	No	No	No	No
CU-1303	chr4: 151694303-151694321	2323	ATCCCACTTCTGACACCA	Yes	Yes	No	No	No
CU-1303	chr1: 212585032-212585050	2324	ATCCCACTTCTGACACCA	Yes	No	No	No	No
CU-1303	chr3: 194813519-194813537	2325	ATCCCACTTCTGACACCA	Yes	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1303	chr2: 55018611-55018629	2326	ATCCCACTTCTGACACCA	Yes	Yes	No	No	No
CU-1303	chr5: 143373194-143373212	2327	ATCCCACTTCTGACACCA	No	Yes	No	No	No
CU-1303	chr1: 36261536-36261554	2328	ATCCCACTTCTGACACCA	Yes	No	No	No	No
CU-1303	chr12: 67663402-67663420	2329	ATCCCACTTCTGACACCA	Yes	Yes	No	No	No
CU-1303	chr4: 119344866-119344884	2330	ATCCCACTTCTGACACCA	No	Yes	No	No	No
CU-1303	chr12: 70175143-70175161	2331	ATCCCACTTCTGACACCA	Yes	Yes	No	No	No
CU-1307	chr1: 9557438-9557458	2332	ACCCCACTATGCTTAGCCCT	Yes	Yes	No	No	Yes
CU-1323	chr2: 232028754-232028771	2333	TGTATTGTGAGACATTC	Yes	No	No	No	No
CU-1324	chr4: 3167100-3167117	2334	TCTCGGTGGAACCTCCA	No	No	No	No	No
CU-1324	chr15: 63948450-63948467	2335	TCTCGGTGGAACCTCCA	No	No	No	No	No
CU-1339	chr8: 141129909-141129928	2336	ATCCCCAGCACCTCCACCA	No	No	No	No	No
CU-1345	chr11: 10487827-10487845	2337	AGAACACTACGAGCCACA	Yes	No	No	No	No
CU-1345	chr5: 79983138-79983156	2338	AGAACACTACGAGCCACA	Yes	No	No	No	No
CU-1345	chr13: 108874555-108874573	2339	AGAACACTACGAGCCACA	Yes	No	No	No	No
CU-1352	chr12: 12693348-12693366	2340	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr5: 119090314-119090332	2341	ACCCCACTTCTGGTACCA	No	No	No	No	No
CU-1352	chr14: 56457992-56458010	2342	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr7: 7637279-7637297	2343	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr1: 34288353-34288371	2344	ACCCCACTTCTGGTACCA	No	No	No	No	No
CU-1352	chr1: 107581087-107581105	2345	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr7: 66011743-66011761	2346	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr7: 119683539-119683557	2347	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr18: 16775205-16775223	2348	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr2: 6916389-6916407	2349	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr6: 98788231-98788249	2350	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr1: 201394394-201394412	2351	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chrX: 85448496-85448514	2352	ACCCCACTTCTGGTACCA	No	Yes	No	No	No
CU-1352	chr8: 140073141-140073159	2353	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr12: 8391052-8391070	2354	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chrX: 77289492-77289510	2355	ACCCCACTTCTGGTACCA	No	No	No	No	No
CU-1352	chr2: 116637798-116637816	2356	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr4: 72493755-72493773	2357	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr15: 94045767-94045785	2358	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chrX: 85947724-85947742	2359	ACCCCACTTCTGGTACCA	No	Yes	No	No	No
CU-1352	chr20: 60081974-60081992	2360	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr18: 31113119-31113137	2361	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr11: 8446114-8446132	2362	ACCCCACTTCTGGTACCA	No	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1352	chr6: 140796063-140796081	2363	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr22: 19662967-19662985	2364	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chrX: 116622706-116622724	2365	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr22: 43646515-43646533	2366	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr11: 3516223-3516241	2367	ACCCCACTTCTGGTACCA	No	No	No	No	No
CU-1352	chr10: 123734159-123734177	2368	ACCCCACTTCTGGTACCA	No	No	No	No	No
CU-1352	chr18: 120806-120824	2369	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr1: 174219317-174219335	2370	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr7: 156114211-156114229	2371	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr3: 107173811-107173829	2372	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1363	chr1: 17095207-17095225	2373	CGTTCGCGCTTTCCCCTG	Yes	Yes	No	No	No
CU-1363	chr1: 147460729-147460747	2374	CGTTCGCGCTTTCCCCTG	No	Yes	No	No	No
CU-1363	chr14: 34085816-34085834	2375	CGTTCGCGCTTTCCCCTG	Yes	Yes	No	No	No
CU-1363	chr14: 34095182-34095200	2376	CGTTCGCGCTTTCCCCTG	Yes	Yes	No	No	No
CU-1368	chr6: 27173063-27173081	2377	GACGAGGTGGCCGAGTGG	Yes	Yes	Yes	No	No
CU-1368	chr6: 28288793-28288811	2378	GACGAGGTGGCCGAGTGG	Yes	Yes	No	No	No
CU-1368	chr11: 65872166-65872184	2379	GACGAGGTGGCCGAGTGG	Yes	Yes	Yes	Yes	Yes
CU-1368	chr15: 38673378-38673396	2380	GACGAGGTGGCCGAGTGG	Yes	Yes	Yes	No	Yes
CU-1368	chr6: 27373753-27373771	2381	GACGAGGTGGCCGAGTGG	Yes	Yes	No	No	No
CU-1368	chr2: 228333400-228333418	2382	GACGAGGTGGCCGAGTGG	Yes	No	No	No	No
CU-1368	chr6: 28673159-28673177	2383	GACGAGGTGGCCGAGTGG	Yes	Yes	No	No	No
CU-1368	chr17: 8030908-8030926	2384	GACGAGGTGGCCGAGTGG	Yes	Yes	No	No	Yes
CU-1369	chr15: 94627153-94627171	2385	TCCCCGGCATCTCCACCA	No	No	No	No	No
CU-1370	chr1: 232795752-232795772	2386	CTGATTGCTCCTGTCTGATT	No	No	No	No	No
CU-1371	chr13: 108874496-108874517	2387	TCTAGAGGAGCCTGTTCTGTA	Yes	No	No	No	No
CU-1379	chr1: 165950616-165950638	2388	TCGGGTGCGAGAGGTCCCGGGT	Yes	Yes	Yes	Yes	Yes
CU-1380	chr11: 10488308-10488331	2389	ATAGGTTTGGTCCTAGCCTTTCT	No	No	No	No	No
CU-1381	chr1: 169836691-169836713	2390	TCGATTCCCGGTCAGGGAACCA	No	No	No	No	No
CU-1382	chr6: 27555431-27555459	2391	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr1: 159677282-159677310	2392	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	Yes	No	No
CU-1382	chr17: 8066324-8066352	2393	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	No	No	No	No
CU-1382	chr1: 159699491-159699519	2394	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr1: 159692081-159692109	2395	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr6: 27579501-27579529	2396	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr1: 159684700-159684728	2397	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr12: 123990189-123990217	2398	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr12: 94953929-94953957	2399	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	Yes	Yes	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1382	chr12: 123977887-123977915	2400	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	No	No	No	No
CU-1382	chr1: 159706872-159706900	2401	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1388	chr1: 144110633-144110661	2402	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr1: 159698476-159698504	2403	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr1: 159705856-159705884	2404	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr1: 159683685-159683713	2405	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr1: 247135069-247135097	2406	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr1: 159691065-159691093	2407	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr6: 126143129-126143157	2408	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	No	No	Yes	Yes
CU-1396	chr1: 556086-556103	2409	TAAGTGTTTGTGGGTTA	No	No	No	No	No
CU-1403	chr17: 7969788-7969810	2410	GCATTGGTGGTTCAGTGGTAGA	No	Yes	Yes	No	Yes
CU-1403	chr16: 69370491-69370513	2411	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	Yes	No	No
CU-1403	chr1: 17061002-17061024	2412	GCATTGGTGGTTCAGTGGTAGA	No	No	Yes	No	No
CU-1403	chr3: 15524502-15524524	2413	GCATTGGTGGTTCAGTGGTAGA	Yes	No	No	No	No
CU-1403	chr16: 69380097-69380119	2414	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	Yes	Yes	Yes
CU-1403	chr1: 227740226-227740248	2415	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	No	No	No
CU-1403	chr1: 16745069-16745091	2416	GCATTGGTGGTTCAGTGGTAGA	Yes	No	Yes	No	No
CU-1403	chr1: 159760309-159760331	2417	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	No	No	No
CU-1403	chr2: 156965953-156965975	2418	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	No	No	No
CU-1403	chrX: 64154569-64154591	2419	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	No	No	No
CU-1403	chr6: 27978713-27978735	2420	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	No	No	No
CU-1440	chr5: 180533270-180533287	2421	TGGTTATCACGTTCGCC	Yes	Yes	No	No	No
CU-1440	chr5: 180456690-180456707	2422	TGGTTATCACGTTCGCC	Yes	Yes	No	No	No
CU-1440	chr6: 27281886-27281903	2423	TGGTTATCACGTTCGCC	Yes	Yes	No	No	No
CU-1440	chr1: 147565219-147565236	2424	TGGTTATCACGTTCGCC	Yes	Yes	No	No	No
CU-1440	chr5: 180461899-180461916	2425	TGGTTATCACGTTCGCC	Yes	Yes	No	No	No
CU-1453	chr3: 191522810-191522827	2426	CCCTGCTCGCTGCGCCA	No	No	No	No	No
CU-1457	chr7: 43102939-43102961	2427	TTCTCACTACTGCACTTGACTA	Yes	No	No	No	No
CU-1457	chr14: 67153778-67153800	2428	TTCTCACTACTGCACTTGACTA	Yes	No	No	No	No
CU-1457	chr1: 238571371-238571393	2429	TTCTCACTACTGCACTTGACTA	No	Yes	No	No	No
CU-1457	chr2: 147946177-147946199	2430	TTCTCACTACTGCACTTGACTA	Yes	Yes	No	No	No
CU-1470	chr16: 30675216-30675234	2431	CTCCTGGCTGGCTCGCCA	Yes	Yes	No	No	No
CU-1470	chr14: 43074235-43074253	2432	CTCCTGGCTGGCTCGCCA	Yes	No	No	No	No
CU-1477	chr17: 26124435-26124459	2433	CTCCCACTGCTTCACTTGACTAGC	No	No	No	No	No
CU-1477	chr17: 27331095-27331119	2434	CTCCCACTGCTTCACTTGACTAGC	No	No	No	No	No
CU-1477	chr10: 21810723-21810747	2435	CTCCCACTGCTTCACTTGACTAGC	Yes	No	No	No	No
CU-1477	chr14: 99119179-99119203	2436	CTCCCACTGCTTCACTTGACTAGC	No	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1477	chr11: 107460922-107460946	2437	CTCCCACTGCTTCACTTGACTAGC	Yes	No	No	No	No
CU-1477	chr4: 154407515-154407539	2438	CTCCCACTGCTTCACTTGACTAGC	No	Yes	No	No	No
CU-1486	chr17: 59577172-59577189	2439	CTGCTGTGATGACATTC	No	Yes	No	No	No
CU-1488	chr1: 4671944-4671961	2440	TCCTGCCGCGGTCGCCA	No	No	No	No	No
CU-1513	chr17: 59577217-59577244	2441	GCGGGTGATGCGAACTGGAGTCTGAGC	Yes	No	No	No	No
CU-1524	chr7: 148269562-148269586	2442	CCCCCACAACCGCGCTTGACTAGC	Yes	Yes	No	No	No
CU-1528	chr17: 8066916-8066935	2443	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr6: 27167511-27167530	2444	TAGGGGTATGATTCTCGCT	Yes	Yes	Yes	No	No
CU-1528	chr14: 20222026-20222045	2445	TAGGGGTATGATTCTCGCT	Yes	Yes	No	Yes	Yes
CU-1528	chr14: 20151440-20151459	2446	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr6: 26663488-26663507	2447	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr16: 3172676-3172695	2448	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr14: 20147375-20147394	2449	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr5: 180548500-180548519	2450	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr16: 3148935-3148954	2451	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr16: 3179646-3179665	2452	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr4: 18668214-18668233	2453	TAGGGGTATGATTCTCGCT	Yes	No	No	No	No
CU-1528	chr1: 165950597-165950616	2454	TAGGGGTATGATTCTCGCT	Yes	Yes	Yes	No	Yes
CU-1528	chr16: 3182001-3182020	2455	TAGGGGTATGATTCTCGCT	Yes	No	No	No	No
CU-1528	chr11: 75624216-75624235	2456	TAGGGGTATGATTCTCGCT	Yes	Yes	Yes	No	No
CU-1528	chr16: 3162061-3162080	2457	TAGGGGTATGATTCTCGCT	No	Yes	No	No	No
CU-1528	chr7: 128210751-128210770	2458	TAGGGGTATGATTCTCGCT	Yes	Yes	Yes	Yes	Yes
CU-1538	chrX: 16840335-16840361	2459	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	No	No	No	No
CU-1538	chr13: 98986625-98986651	2460	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	No	No	No	No
CU-1538	chr10: 128599365-128599391	2461	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	No	No	No	No
CU-1538	chr7: 148311779-148311805	2462	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	No	No	No	No
CU-1538	chr15: 73062744-73062770	2463	GGCTGGTCCGAGTGCAGTGGTGTTTA	No	No	No	No	No
CU-1538	chrX: 116932310-116932336	2464	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	No	No	No	No
CU-1538	chr11: 47705094-47705120	2465	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	No	No	No	No
CU-1542	chr7: 148291339-148291362	2466	GGCTGGTCCGATGGTAGTGGGTT	Yes	Yes	Yes	No	No
CU-1542	chr6: 33275355-33275378	2467	GGCTGGTCCGATGGTAGTGGGTT	Yes	Yes	No	No	No
CU-1545	chr17: 19031996-19032016	2468	CCACGAGGAAGAGAGGTAGC	No	No	No	No	No
CU-1550	chr6: 26438546-26438564	2469	CGGAAGCGTGCTGGGCCC	Yes	Yes	No	No	No
CU-1550	chr6: 27853657-27853675	2470	CGGAAGCGTGCTGGGCCC	Yes	Yes	No	No	No
CU-1550	chr6: 26421369-26421387	2471	CGGAAGCGTGCTGGGCCC	Yes	Yes	No	No	No
CU-1550	chr6: 27408781-27408799	2472	CGGAAGCGTGCTGGGCCC	Yes	Yes	No	No	No
CU-1550	chr6: 27668617-27668635	2473	CGGAAGCGTGCTGGGCCC	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1557	chr17: 19033934-19033957	2474	GGAGAGAACGCGGTCTGAGTGGT	Yes	No	No	No	No
CU-1557	chr17: 18907957-18907980	2475	GGAGAGAACGCGGTCTGAGTGGT	Yes	No	No	No	No
CU-1557	chr17: 19032115-19032138	2476	GGAGAGAACGCGGTCTGAGTGGT	Yes	No	No	No	No
CU-1557	chr17: 18956457-18956480	2477	GGAGAGAACGCGGTCTGAGTGGT	Yes	No	No	No	No
CU-1557	chr17: 18906143-18906166	2478	GGAGAGAACGCGGTCTGAGTGGT	Yes	No	No	No	No
CU-1570	chr17: 36922634-36922653	2479	ATCCCCAGCATCTCCACCA	Yes	No	No	No	No
CU-1575	chr7: 148291405-148291430	2480	CCCCCCACTGCTAAATTTGACTGGA	No	No	No	No	No

All human miRNA deposited in miRBase database

		Seq. ID		Conservation				
ID	Genomic Coordinates	No.	Sequence	Chimp	Monkey	Dog	Mouse	Rat
hsa-mir-1322	chr8: 10720294-10720313	2481	CAGCATCAGCAGCATCATC	Yes	No	No	No	No
hsa-mir-1323	chr19: 58867043-58867065	2482	TCAAAACTGAGGGGCATTTTCT	Yes	Yes	No	No	No
hsa-mir-1321	chrX: 84977492-84977510	2483	CAGGGAGGTGAATGTGAT	No	No	No	No	No
hsa-mir-29c*	chr1: 206041870-206041892	2484	GAACACCAGGAGAAATCGGTCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1324	chr3: 75762663-75762687	2485	CCAGACAGAATTCTATGCACTTTC	No	No	No	No	No
hsa-mir-675	chr11: 1974605-1974628	2486	CACTGTGGGCCCTCTCCGCACCA	No	Yes	No	No	No
hsa-mir-183*	chr7: 129202003-129202025	2487	TTATGGCCCTTCGGTAATTCAC	Yes	Yes	Yes	Yes	Yes
hsa-mir-335*	chr7: 129923238-129923260	2488	TTTTTCATTATTGCTCCTGACC	Yes	Yes	Yes	Yes	No
hsa-mir-19a*	chr13: 90801158-90801180	2489	AGTTTTGCATAGTTGCACTACA	Yes	No	Yes	Yes	No
hsa-mir-132*	chr17: 1900008-1900030	2490	AGTAACAATCGAAAGCCACGGT	No	Yes	Yes	Yes	Yes
hsa-mir-182	chr7: 129197522-129197546	2491	AGTGTGAGTTCTACCATTGCCAAA	Yes	Yes	Yes	No	No
hsa-mir-122	chr18: 54269299-54269321	2492	TGGAGTGTGACAATGGTGTTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-16-2*	chr3: 161605278-161605300	2493	CCAATATTACTGTGCTGCTTTA	Yes	No	No	No	No
hsa-mir-124	chr8: 65454320-65454340	2494	TAAGGCACGCGGTGAATGCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-124	chr8: 9798320-9798340	2495	GGCATTCACCGCGTGCCTTA	No	Yes	Yes	Yes	Yes
hsa-mir-124	chr20: 61280348-61280368	2496	TAAGGCACGCGGTGAATGCC	No	Yes	Yes	Yes	Yes
hsa-mir-126	chr9: 138684925-138684947	2497	TCGTACCGTGAGTAATAATGCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-31*	chr9: 21502119-21502141	2498	ATGGCAATATGTTGGCATAGCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-128	chr2: 136139485-136139506	2499	TCACAGTGAACCGGTCTCTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-128	chr3: 35761022-35761043	2500	TCACAGTGAACCGGTCTCTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-19a	chr13: 90801193-90801216	2501	TGTGCAAATCTATGCAAAACTGA	Yes	No	Yes	Yes	Yes
hsa-mir-524-5p	chr19: 58906082-58906104	2502	CTACAAAGGGAAGCACTTTCTC	Yes	No	No	No	No
hsa-mir-19b	chrX: 133131378-133131401	2503	TCAGTTTTGCATGGATTTGCACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-19b	chr13: 90801499-90801522	2504	TGTGCAAATCCATGCAAAACTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-148b*	chr12: 53017290-53017312	2505	AAGTTCTGTTATACACTCAGGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-1257	chr20: 59962071-59962092	2506	GGTCAGAACCCATCATTCACT	No	No	No	No	No
hsa-mir-1254	chr10: 70189097-70189121	2507	AGCCTGGAAGCTGGAGCCTGCAGT	Yes	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-455-3p	chr9: 116011587-116011608	2508	GCAGTCCATGGGCATATACAC	Yes	Yes	Yes	No	No
hsa-mir-1253	chr17: 2598182-2598203	2509	TGCAGGCTGATCTTCTTCTCT	Yes	No	No	No	No
hsa-mir-1250	chr17: 76721659-76721680	2510	AAAGGCCACATCCAGCACCGT	Yes	No	No	No	No
hsa-mir-1251	chr12: 96409821-96409842	2511	ACTCTAGCTGCCAAAGGCGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1258	chr2: 180433852-180433873	2512	AGTTAGGATTAGGTCGTGGAA	Yes	Yes	No	No	No
hsa-mir-1258	chr2: 180433816-180433837	2513	TTCCACGACCTAATCCTAACT	Yes	Yes	No	No	No
hsa-mir-1259	chr20: 47330268-47330289	2514	ATATATGATGACTTAGCTTTT	Yes	Yes	No	No	No
hsa-mir-1207-3p	chr8: 129130630-129130648	2515	TCAGCTGGCCCTCATTTC	Yes	No	No	No	No
hsa-mir-34c-3p	chr11: 110889418-110889440	2516	AATCACTAACCACACGGCCAGG	Yes	Yes	Yes	No	No
hsa-mir-489	chr7: 92951194-92951216	2517	GCTGCCGTATATGTGATGTCAC	Yes	Yes	No	No	No
hsa-mir-488	chr1: 175265132-175265153	2518	GACCAAGAAATAGCCTTTCAA	Yes	Yes	Yes	No	No
hsa-mir-556-5p	chr1: 160578974-160578996	2519	GATGAGCTCATTGTAATATGAG	Yes	No	No	No	No
hsa-mir-484	chr16: 15644658-15644680	2520	TCAGGCTCAGTCCCCTCCCGAT	Yes	Yes	No	Yes	Yes
hsa-mir-523*	chr19: 58893465-58893487	2521	CTCTAGAGGGAAGCGCTTTCTG	Yes	No	No	No	No
hsa-mir-125b-1*	chr11: 121475686-121475708	2522	AGCTCCCAAGAGCCTAACCCGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-7-2*	chr15: 86956130-86956152	2523	CAACAAATCCCAGTCTACCTAA	Yes	No	No	No	No
hsa-mir-569	chr3: 172307161-172307182	2524	ACTTTCCAGGATTCATTAACT	Yes	Yes	No	No	No
hsa-mir-574-5p	chr4: 38546071-38546094	2525	TGAGTGTGTGTGTGTGAGTGTGT	No	No	Yes	Yes	No
hsa-mir-342-5p	chr14: 99645762-99645783	2526	AGGGGTGCTATCTGTGATTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-379	chr14: 100558160-100558181	2527	TGGTAGACTATGGAACGTAGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-520b	chr19: 58896332-58896353	2528	AAAGTGCTTCCTTTTAGAGGG	Yes	Yes	No	No	No
hsa-mir-520e	chr19: 58870829-58870850	2529	AAAGTGCTTCCTTTTTGAGGG	Yes	No	No	No	No
hsa-mir-371-5p	chr19: 58982745-58982765	2530	ACTCAAACTGTGGGGGCACT	Yes	Yes	Yes	No	No
hsa-mir-520g	chr19: 58917285-58917309	2531	ACAAAGTGCTTCCCTTTAGAGTGT	Yes	No	No	No	No
hsa-mir-520f	chr19: 58877278-58877300	2532	AAGTGCTTCCTTTTAGAGGGTT	Yes	No	No	No	No
hsa-mir-520h	chr19: 58937631-58937653	2533	ACAAAGTGCTTCCCTTTAGAGT	Yes	No	No	No	No
hsa-mir-219-5p	chr9: 130194775-130194796	2534	AGAATTGCGTTTGGACAATCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-219-5p	chr6: 33283609-33283630	2535	TGATTGTCCAAACGCAATTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-140-5p	chr16: 68524506-68524528	2536	CAGTGGTTTTACCCTATGGTAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-423-5p	chr17: 25468238-25468261	2537	TGAGGGGCAGAGAGCGAGACTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-30b*	chr8: 135881956-135881978	2538	GAAGTAAACATCCACCTCCCAG	Yes	Yes	Yes	No	No
hsa-mir-195	chr17: 6861709-6861730	2539	GCCAATATTTCTGTGCTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-194	chr11: 64415451-64415473	2540	TCCACATGGAGTTGCTGTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-194	chr1: 218358170-218358192	2541	TCCACATGGAGTTGCTGTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-197	chr1: 109943084-109943106	2542	TTCACCACCTTCTCCACCCAGC	Yes	Yes	Yes	No	No
hsa-mir-191	chr3: 49033108-49033131	2543	CAGCTGCTTTTGGGATTCCGTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-190	chr15: 60903222-60903244	2544	TGATATGTTTGATATATTAGGT	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-192	chr11: 64415250-64415271	2545	GGCTGTCAATTCATAGGTCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-449a	chr5: 54502170-54502192	2546	ACCAGCTAACAATACACTGCCA	No	Yes	Yes	Yes	Yes
hsa-mir-339-3p	chr7: 1029116-1029139	2547	CGGCTCTGTCGTCGAGGCGCTCA	No	Yes	No	No	No
hsa-mir-508-5p	chrX: 146126189-146126212	2548	CATGAGTGACGCCCTCTGGAGTA	No	No	No	No	No
hsa-mir-1284	chr3: 71673879-71673901	2549	GAAAAGCCAGGGTCTGTATAGA	Yes	No	No	No	No
hsa-mir-362-5p	chrX: 49660315-49660339	2550	AATCCTTGGAACCTAGGTGTGAGT	Yes	Yes	Yes	No	No
hsa-mir-125a-3p	chr19: 56888370-56888392	2551	ACAGGTGAGGTTCTTGGGAGCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-34a*	chr1: 9134338-9134360	2552	AGGGCAGTATACTTGCTGATTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-373	chr19: 58983813-58983836	2553	GAAGTGCTTCGATTTTGGGGTGT	No	Yes	No	No	No
hsa-mir-502-3p	chrX: 49665996-49666018	2554	AATGCACCTGGGCAAGGATTCA	Yes	Yes	Yes	No	No
hsa-mir-200b	chr1: 1092402-1092424	2555	TAATACTGCCTGGTAATGATGA	No	No	Yes	Yes	Yes
hsa-mir-200c	chr12: 6943165-6943188	2556	TAATACTGCCGGGTAATGATGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-200a	chr1: 1093158-1093180	2557	TAACACTGTCTGGTAACGATGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-410	chr14: 100602050-100602071	2558	AATATAACACAGATGGCCTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-411	chr14: 100559429-100559450	2559	TAGTAGACCGTATAGCGTACG	Yes	Yes	Yes	Yes	Yes
hsa-mir-412	chr14: 100601589-100601612	2560	ACTTCACCTGGTCCACTAGCCGT	Yes	Yes	No	Yes	Yes
hsa-mir-555	chr1: 153582779-153582800	2561	ATCAGAGGTTCAGCTTACCCT	Yes	No	No	No	No
hsa-mir-554	chr1: 149784910-149784931	2562	GCTAGTCCTGACTCAGCCAGT	Yes	Yes	No	No	No
hsa-mir-493*	chr14: 100405164-100405186	2563	TTGTACATGGTAGGCTTTCATT	No	Yes	Yes	Yes	Yes
hsa-mir-550	chr7: 30295955-30295978	2564	AGTGCCTGAGGGAGTAAGAGCCC	Yes	Yes	No	No	No
hsa-mir-550	chr7: 32739138-32739161	2565	AGTGCCTGAGGGAGTAAGAGCCC	Yes	Yes	No	No	No
hsa-mir-553	chr1: 100519399-100519420	2566	AAAACGGTGAGATTTTGTTTT	Yes	No	No	No	No
hsa-mir-193a-5p	chr17: 26911147-26911169	2567	TGGGTCTTTGCGGGCGAGATGA	Yes	Yes	Yes	No	No
hsa-mir-876-3p	chr9: 28853633-28853655	2568	TGAATTACTTTGTAAACCACCA	Yes	Yes	Yes	No	No
hsa-mir-139-3p	chr11: 72003757-72003779	2569	ACTCCAACAGGGCCGCGTCTCC	Yes	Yes	No	Yes	Yes
hsa-mir-30a	chr6: 72170018-72170040	2570	CTTCCAGTCGAGGATGTTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-30b	chr8: 135881994-135882016	2571	AGCTGAGTGTAGGATGTTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-30c	chr1: 40995558-40995581	2572	TGTAAACATCCTACACTCTCAGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-30c	chr6: 72143426-72143449	2573	GCTGAGAGTGTAGGATGTTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-30d	chr8: 135886343-135886365	2574	CTTCCAGTCGGGGATGTTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-30e	chr1: 40992629-40992651	2575	TGTAAACATCCTTGACTGGAAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-374b*	chrX: 73355116-73355138	2576	AATGATAATACAACCTGCTAAG	Yes	Yes	No	Yes	No
hsa-mir-548b-3p	chr6: 119431925-119431947	2577	ACAAAAGCAACTGAGGTTCTTG	Yes	No	No	No	No
hsa-mir-515-5p	chr19: 58874081-58874105	2578	TTCTCCAAAAGAAAGCACTTTCTG	Yes	No	No	No	No
hsa-mir-515-5p	chr19: 58880087-58880111	2579	TTCTCCAAAAGAAAGCACTTTCTG	Yes	No	No	No	No
hsa-mir-429	chr1: 1094297-1094319	2580	TAATACTGTCTGGTAAAACCGT	No	Yes	No	No	No
hsa-mir-486-5p	chr8: 41637118-41637140	2581	TCCTGTACTGAGCTGCCCCGAG	Yes	Yes	Yes	Yes	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-486-5p	chr8: 41637158-41637180	2582	CTCGGGGCAGCTCAGTACAGGA	Yes	Yes	Yes	Yes	No
hsa-mir-1206	chr8: 129090328-129090349	2583	TGTTCATGTAGATGTTTAAGC	Yes	No	No	No	No
hsa-mir-99a	chr21: 16833291-16833313	2584	AACCCGTAGATCCGATCTTGTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-188-3p	chrX: 49654901-49654922	2585	CTCCCACATGCAGGGTTTGCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-99b	chr19: 56887682-56887704	2586	CACCCGTAGAACCGACCTTGCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-300	chr14: 100577503-100577525	2587	TATACAAGGGCAGACTCTCTCT	Yes	No	No	No	No
hsa-mir-193b	chr16: 14305374-14305396	2588	AACTGGCCCTCAAAGTCCCGCT	Yes	Yes	No	No	No
hsa-mir-1203	chr17: 43588846-43588867	2589	GAGCTGCATCCTGGCTCCGGG	Yes	No	No	No	No
hsa-mir-30c-1*	chr1: 40995597-40995619	2590	CTGGGAGAGGGTTGTTTACTCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-19b-2*	chrX: 133131422-133131444	2591	TGAAATGCAAACCTGCAAAACT	Yes	Yes	Yes	No	No
hsa-mir-1286	chr22: 18616667-18616688	2592	AGGGCTCATCTTGGTCCTGCA	Yes	No	No	No	No
hsa-let-7g*	chr3: 52277335-52277356	2593	GCAAGGCAGTGGCCTGTACAG	Yes	Yes	Yes	Yes	No
hsa-mir-361-3p	chrX: 85045301-85045324	2594	AAATCAGAATCACACCTGGGGGA	Yes	Yes	Yes	Yes	No
hsa-mir-518a-5p	chr19: 58926084-58926104	2595	CTGCAAAGGGAAGCCCTTTC	Yes	No	No	No	No
hsa-mir-518a-5p	chr19: 58934413-58934433	2596	CTGCAAAGGGAAGCCCTTTC	Yes	No	No	No	No
hsa-mir-604	chr10: 29873953-29873972	2597	GTCCTGAATTCCGCAGCCT	No	No	No	No	No
hsa-mir-485-5p	chr14: 100591516-100591538	2598	AGAGGCTGGCCGTGATGAATTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-452*	chrX: 150878761-150878783	2599	CACTTACTTCTTTGCAGATGAG	Yes	Yes	Yes	No	No
hsa-mir-450b-5p	chrX: 133501926-133501948	2600	TATTCAGGAACATATTGCAAAA	Yes	Yes	Yes	No	No
hsa-mir-505	chrX: 138833984-138834006	2601	AGGAAACCAGCAAGTGTTGACG	Yes	Yes	Yes	No	Yes
hsa-mir-299-5p	chr14: 100559889-100559911	2602	TGGTTTACCGTCCCACATACAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-181a-2*	chr9: 126494617-126494639	2603	ACCACTGACCGTTGACTGTACC	Yes	Yes	No	No	No
hsa-mir-29b-2*	chr1: 206042459-206042481	2604	CTAAGCCACCATGTGAAACCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-323-3p	chr14: 100561871-100561892	2605	CACATTACACGGTCGACCTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1256	chr1: 21187456-21187478	2606	AGCTAGTGAGAAGTCAATGCCT	Yes	Yes	No	No	No
hsa-mir-144*	chr17: 24212726-24212748	2607	CTTACAGTATATGATGATATCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-1280	chr3: 129563701-129563718	2608	TCCCACCGCTGCCACCC	Yes	No	No	No	No
hsa-mir-379*	chr14: 100558198-100558220	2609	TATGTAACATGGTCCACTAACT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1252	chr12: 78337171-78337193	2610	AGAAGGAAATTGAATTCATTTA	No	No	No	No	No
hsa-mir-324-5p	chr17: 7067384-7067407	2611	ACACCAATGCCCTAGGGGATGCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-516b*	chr19: 58920562-58920580	2612	TGCTTCCTTTCAGAGGGT	Yes	No	No	No	No
hsa-mir-516b*	chr19: 58931970-58931988	2613	TGCTTCCTTTCAGAGGGT	Yes	Yes	No	No	No
hsa-mir-18b	chrX: 133131779-133131802	2614	CTAACTGCACTAGATGCACCTTA	Yes	Yes	Yes	No	No
hsa-mir-17	chr13: 90800872-90800895	2615	CAAAGTGCTTACAGTGCAGGTAG	Yes	No	Yes	Yes	Yes
hsa-mir-16	chr3: 161605235-161605257	2616	TAGCAGCACGTAAATATTGGCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-16	chr13: 49521163-49521185	2617	CGCCAATATTTACGTGCTGCTA	Yes	Yes	Yes	Yes	No
hsa-mir-26b*	chr2: 218975658-218975680	2618	CCTGTTCTCCATTACTTGGCTC	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-618	chr12: 79853705-79853728	2619	ACTCAGAAGGACAAGTAGAGTTT	Yes	Yes	No	No	No
hsa-mir-331-3p	chr12: 94226386-94226407	2620	GCCCCTGGGCCTATCCTAGAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-605	chr10: 52729353-52729376	2621	TAAATCCCATGGTGCCTTCTCCT	Yes	No	No	No	No
hsa-mir-376a	chr14: 100576914-100576935	2622	ATCATAGAGGAAAATCCACGT	Yes	Yes	Yes	No	No
hsa-mir-376a	chr14: 100576207-100576228	2623	ATCATAGAGGAAAATCCACGT	Yes	Yes	Yes	No	No
hsa-mir-376b	chr14: 100576586-100576608	2624	ATCATAGAGGAAAATCCATGTT	Yes	Yes	Yes	No	No
hsa-mir-376c	chr14: 100575821-100575842	2625	AACATAGAGGAAATTCCACGT	Yes	Yes	Yes	No	No
hsa-mir-601	chr9: 125204666-125204688	2626	CTCCTCCAACAATCCTAGACCA	Yes	Yes	No	No	No
hsa-mir-600	chr9: 124913660-124913683	2627	GAGCAAGGCTCTTGTCTGTAAGT	Yes	No	No	No	No
hsa-mir-603	chr10: 24604679-24604701	2628	CACACACTGCAATTACTTTTGC	No	No	No	No	No
hsa-mir-602	chr9: 139852706-139852729	2629	GACACGGGCGACAGCTGCGGCCC	No	No	No	No	No
hsa-mir-609	chr10: 105968596-105968616	2630	AGAGATGAGAGAAACACCCT	Yes	No	No	No	No
hsa-mir-608	chr10: 102724746-102724771	2631	AGGGGTGGTGTTGGGACAGCTCCGT	No	No	No	No	No
hsa-mir-551b*	chr3: 169752356-169752378	2632	GAAATCAAGCGTGGGTGAGACC	Yes	Yes	No	No	No
hsa-mir-544	chr14: 100584801-100584823	2633	ATTCTGCATTTTTAGCAAGTTC	Yes	Yes	Yes	No	No
hsa-mir-664*	chr1: 218440550-218440574	2634	ATCCAATCATTTTCCCTAGCCAGT	Yes	Yes	No	No	No
hsa-mir-409-5p	chr14: 100601403-100601426	2635	AGGTTACCCGAGCAACTTTGCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-136*	chr14: 100420839-100420861	2636	CATCATCGTCTCAAATGAGTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1282	chr15: 41873221-41873241	2637	AAGCAGAAAAAGGCAAACGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-519c-5p	chr19: 58881549-58881571	2638	CTCTAGAGGGAAGCGCTTTCTG	Yes	No	No	No	No
hsa-mir-1208	chr8: 129231554-129231574	2639	TCACTGTTCAGACAGGCGGA	Yes	Yes	No	No	No
hsa-mir-1205	chr8: 129042067-129042087	2640	TCTGCAGGGTTTGCTTTGAG	Yes	No	No	No	No
hsa-mir-663b	chr2: 132731012-132731034	2641	CCTCAGGCACGGCCGGGCCACC	Yes	No	No	No	No
hsa-mir-1201	chr14: 19864455-19864479	2642	TCAGAGCATGTGTTTAATCAGGCT	Yes	Yes	No	No	No
hsa-mir-1200	chr7: 36925532-36925554	2643	GAGGCTCAGAATGGCTCAGGAG	No	No	No	No	No
hsa-mir-338-5p	chr17: 76714317-76714339	2644	CACTCAGCACCAGGATATTGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1202	chr6: 156309634-156309655	2645	GTGCCAGCTGCAGTGGGGGAG	Yes	Yes	No	No	No
hsa-mir-501-5p	chrX: 49661082-49661104	2646	AATCCTTTGTCCCTGGGTGAGA	Yes	Yes	No	No	No
hsa-mir-519b-5p	chr19: 58890290-58890312	2647	CTCTAGAGGGAAGCGCTTTCTG	Yes	Yes	No	No	No
hsa-mir-101*	chr1: 65296747-65296769	2648	AGCATCAGCACTGTGATAACTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-511	chr10: 17927127-17927148	2649	GTGTCTTTTGCTCTGCAGTCA	Yes	No	No	No	No
hsa-mir-511	chr10: 18174056-18174077	2650	GTGTCTTTTGCTCTGCAGTCA	Yes	No	No	No	No
hsa-mir-510	chrX: 146161587-146161609	2651	GTGATTGCCACTCTCCTGAGTA	No	No	No	No	No
hsa-let-7a*	chr9: 95978115-95978136	2652	CTATACAATCTACTGTCTTTC	Yes	Yes	Yes	Yes	Yes
hsa-let-7a*	chr22: 44887343-44887364	2653	CTATACAATCTACTGTCTTTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-514	chrX: 146173864-146173885	2654	TCTACTCACAGAAGTGTCAAT	Yes	Yes	No	No	No
hsa-mir-514	chrX: 146171166-146171187	2655	TCTACTCACAGAAGTGTCAAT	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-514	chrX: 146168475-146168496	2656	TCTACTCACAGAAGTGTCAAT	Yes	No	No	No	No
hsa-mir-524-3p	chr19: 58906119-58906140	2657	GAAGGCGCTTCCCTTTGGAGT	Yes	No	No	No	No
hsa-mir-491-5p	chr9: 20706118-20706140	2658	AGTGGGGAACCCTTCCATGAGG	Yes	Yes	Yes	Yes	No
hsa-mir-18b*	chrX: 133131737-133131759	2659	GCCAGAAGGGGCATTTAGGGCA	No	Yes	No	No	No
hsa-mir-411*	chr14: 100559464-100559486	2660	TATGTAACACGGTCCACTAACC	Yes	Yes	Yes	Yes	Yes
hsa-mir-548d-3p	chr8: 124429469-124429491	2661	GCAAAAGAAACTGTGGTTTTTG	No	No	No	No	No
hsa-mir-548d-3p	chr17: 62898081-62898103	2662	GCAAAAGAAACTGTGGTTTTTG	No	No	No	No	No
hsa-mir-490-3p	chr7: 136238528-136238550	2663	CAACCTGGAGGACTCCATGCTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-576-3p	chr4: 110629356-110629378	2664	AAGATGTGGAAAAATTGGAATC	Yes	Yes	No	No	No
hsa-mir-34a	chr1: 9134380-9134402	2665	ACAACCAGCTAAGACACTGCCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-34b	chr11: 110888921-110888943	2666	CAATCACTAACTCCACTGCCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-654-5p	chr14: 100576323-100576345	2667	TGGTGGGCCGCAGAACATGTGC	Yes	Yes	No	No	No
hsa-mir-216a	chr2: 56069658-56069680	2668	TCACAGTTGCCAGCTGAGATTA	No	Yes	Yes	Yes	Yes
hsa-mir-216b	chr2: 56081402-56081424	2669	TCACATTTGCCTGCAGAGATTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-590-3p	chr7: 73243518-73243539	2670	TAATTTTATGTATAAGCTAGT	Yes	No	Yes	No	No
hsa-mir-939	chr8: 145590215-145590239	2671	CACCCCCAGAGCCTCAGCTCCCCA	Yes	Yes	No	No	No
hsa-mir-938	chr10: 29931245-29931267	2672	ACTGGGTTCACCTTTAAGGGCA	Yes	No	No	No	No
hsa-mir-34c-5p	chr11: 110889385-110889408	2673	AGGCAGTGTAGTTAGCTGATTGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-15a*	chr13: 49521266-49521288	2674	TGAGGCAGCACAATATGGCCTG	Yes	Yes	Yes	No	No
hsa-mir-933	chr2: 175740615-175740637	2675	GGGAGAGGTCTCCCTGCGCACA	Yes	Yes	No	No	No
hsa-mir-499-3p	chr20: 33041908-33041930	2676	AACATCACAGCAAGTCTGTGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-937	chr8: 144967128-144967150	2677	GGCAGAGAGTCAGAGCGCGGAT	Yes	No	No	No	No
hsa-mir-936	chr10: 105797898-105797920	2678	CTGCGATTCCTCCCTCTACTGT	Yes	No	No	No	No
hsa-mir-935	chr19: 59177427-59177450	2679	CCAGTTACCGCTTCCGCTACCGC	Yes	No	No	No	Yes
hsa-mir-654-3p	chr14: 100576358-100576380	2680	TATGTCTGCTGACCATCACCTT	Yes	Yes	No	Yes	No
hsa-mir-93*	chr7: 99529335-99529357	2681	CGGGAAGTGCTAGCTCAGCAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-516b	chr19: 58920522-58920544	2682	ATCTGGAGGTAAGAAGCACTTT	Yes	No	No	No	No
hsa-mir-516b	chr19: 58931925-58931947	2683	ATCTGGAGGTAAGAAGCACTTT	Yes	Yes	No	No	No
hsa-mir-551a	chr1: 3467133-3467154	2684	TGGAAACCAAGAGTGGGTCGC	Yes	Yes	Yes	No	No
hsa-mir-551b	chr3: 169752395-169752416	2685	GCGACCCATACTTGGTTTCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-345	chr14: 99843965-99843987	2686	GCTGACTCCTAGTCCAGGGCTC	Yes	No	No	No	No
hsa-mir-346	chr10: 88014483-88014506	2687	AGAGGCAGGCATGCGGGCAGACA	Yes	Yes	Yes	No	No
hsa-mir-340	chr5: 179374966-179374988	2688	AATCAGTCTCATTGCTTTATAA	Yes	Yes	Yes	Yes	No
hsa-mir-106a	chrX: 133131939-133131962	2689	CTACCTGCACTGTAAGCACTTTT	Yes	Yes	Yes	No	No
hsa-mir-23b*	chr9: 96887329-96887351	2690	TGGGTTCCTGGCATGCTGATTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-106b	chr7: 99529601-99529622	2691	ATCTGCACTGTCAGCACTTTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-194*	chr11: 64415415-64415437	2692	CAGATAACAGCAGCCCCACTGG	Yes	Yes	No	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-519a*	chr19: 58947476-58947498	2693	CTCTAGAGGGAAGCGCTTTCTG	Yes	No	No	No	No
hsa-mir-519e	chr19: 58875056-58875078	2694	AAGTGCCTCCTTTTAGAGTGTT	Yes	No	No	No	No
hsa-mir-519d	chr19: 58908465-58908487	2695	CAAAGTGCCTCCCTTTAGAGTG	Yes	No	No	No	No
hsa-mir-769-3p	chr19: 51214097-51214120	2696	CTGGGATCTCCGGGGTCTTGGTT	No	No	No	No	No
hsa-mir-519a	chr19: 58947514-58947536	2697	AAAGTGCATCCTTTTAGAGTGT	Yes	No	No	No	No
hsa-mir-519a	chr19: 58957462-58957484	2698	AAAGTGCATCCTTTTAGAGTGT	Yes	Yes	No	No	No
hsa-mir-943	chr4: 1957927-1957948	2699	CTGGAGGACGGCAACAGTCAG	Yes	No	No	No	No
hsa-mir-940	chr16: 2261807-2261828	2700	AAGGCAGGGCCCCCGCTCCCC	Yes	Yes	Yes	No	No
hsa-mir-941	chr20: 62021710-62021733	2701	CACCCGGCTGTGTGCACATGTGC	No	No	No	No	No
hsa-mir-941	chr20: 62021598-62021621	2702	CACCCGGCTGTGTGCACATGTGC	No	No	No	No	No
hsa-mir-941	chr20: 62021291-62021314	2703	CACCCGGCTGTGTGCACATGTGC	Yes	No	No	No	No
hsa-mir-423-3p	chr17: 25468274-25468297	2704	AGCTCGGTCTGAGGCCCCTCAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-203	chr14: 103653558-103653580	2705	GTGAAATGTTTAGGACCACTAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-202	chr10: 134911032-134911052	2706	TTCCCATGCCCTATACCTCT	Yes	No	No	No	No
hsa-mir-205	chr1: 207672133-207672155	2707	TCCTTCATTCCACCGGAGTCTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-204	chr9: 72614766-72614788	2708	AGGCATAGGATGACAAAGGGAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-526a	chr19: 58921993-58922015	2709	CTCTAGAGGGAAGCACTTTCTG	Yes	No	No	No	No
hsa-mir-526a	chr19: 58901331-58901353	2710	CTCTAGAGGGAAGCACTTTCTG	Yes	No	No	No	No
hsa-mir-28-3p	chr3: 189889315-189889337	2711	CACTAGATTGTGAGCTCCTGGA	Yes	Yes	Yes	No	Yes
hsa-mir-302a*	chr4: 113788828-113788851	2712	AGCAAGTACATCCACGTTTAAGT	Yes	Yes	Yes	No	No
hsa-mir-548c-3p	chr12: 63302615-63302637	2713	CAAAAATCTCAATTACTTTTGC	Yes	No	No	No	No
hsa-mir-424*	chrX: 133508339-133508360	2714	ATAGCAGCGCCTCACGTTTTG	Yes	Yes	Yes	No	No
hsa-mir-886-5p	chr5: 135444163-135444186	2715	CCGCTTGAGCTAACTCCGACCCG	Yes	Yes	No	No	No
hsa-mir-877*	chr6: 30660152-30660173	2716	TCCTCTTCTCCCTCCTCCCAG	Yes	Yes	No	Yes	Yes
hsa-mir-29b	chr7: 130212765-130212788	2717	AACACTGATTTCAAATGGTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-29b	chr1: 206042417-206042440	2718	AACACTGATTTCAAATGGTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-29c	chr1: 206041832-206041854	2719	TAACCGATTTCAAATGGTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-29a	chr7: 130212046-130212068	2720	TAACCGATTTCAGATGGTGCTA	No	Yes	Yes	Yes	Yes
hsa-mir-20a	chr13: 90801326-90801349	2721	TAAAGTGCTTATAGTGCAGGTAG	Yes	No	Yes	Yes	Yes
hsa-mir-640	chr19: 19406931-19406952	2722	ATGATCCAGGAACCTGCCTCT	Yes	Yes	No	No	No
hsa-mir-129-5p	chr11: 43559533-43559554	2723	CTTTTTGCGGTCTGGGCTTGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-129-5p	chr7: 127635164-127635185	2724	CTTTTTGCGGTCTGGGCTTGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-20b	chrX: 133131545-133131568	2725	CTACCTGCACTATGAGCACTTTG	Yes	Yes	No	Yes	Yes
hsa-mir-645	chr20: 48635789-48635808	2726	TCTAGGCTGGTACTGCTGA	Yes	No	No	No	No
hsa-mir-644	chr20: 32517850-32517869	2727	AGTGTGGCTTTCTTAGAGC	Yes	No	No	No	No
hsa-mir-647	chr20: 62044487-62044508	2728	GAAGGAAGTGAGTGCAGCCAC	No	No	No	No	No
hsa-mir-646	chr20: 58316986-58317005	2729	AAGCAGCTGCCTCTGAGGC	Yes	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-649	chr22: 19718479-19718501	2730	GACTCTTGAACAACACAGGTTT	Yes	Yes	No	No	No
hsa-mir-648	chr22: 16843693-16843712	2731	ACCAGTGCCCTGCACACTT	No	No	No	No	No
hsa-mir-760	chr1: 94085023-94085043	2732	CGGCTCTGGGTCTGTGGGGA	Yes	Yes	No	Yes	Yes
hsa-mir-766	chrX: 118664753-118664775	2733	GCTGAGGCTGTGGGGCTGGAGT	Yes	No	No	No	No
hsa-mir-765	chr1: 155172571-155172592	2734	CATCACCTTCCTTCTCCTCCA	Yes	No	No	No	No
hsa-mir-628-3p	chr15: 53452443-53452464	2735	TCGACTGCCACTCTTACTAGA	Yes	Yes	Yes	No	No
hsa-mir-337-5p	chr14: 100410604-100410625	2736	GAACGGCTTCATACAGGAGTT	Yes	Yes	No	No	No
hsa-mir-373*	chr19: 58983775-58983797	2737	ACTCAAAATGGGGGCGCTTTCC	Yes	No	No	No	No
hsa-mir-369-5p	chr14: 100601695-100601717	2738	AGATCGACCGTGTTATATTCGC	Yes	Yes	No	Yes	Yes
hsa-mir-1285	chr7: 91671276-91671298	2739	AGGTCTCACTTTGTTGCCCAGA	Yes	No	No	No	No
hsa-mir-1285	chr2: 70333568-70333590	2740	AGGTCTCACTTTGTTGCCCAGA	No	No	No	No	No
hsa-mir-222*	chrX: 45491422-45491444	2741	AGGATCTACACTGGCTACTGAG	No	Yes	Yes	Yes	Yes
hsa-mir-298	chr20: 56826729-56826753	2742	TGGGAGAACCTCCCTGCTTCTGCT	Yes	No	No	No	No
hsa-mir-206	chr6: 52117157-52117179	2743	TGGAATGTAAGGAAGTGTGTGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-297	chr4: 112001228-112001249	2744	CATGCACATGCACACATACAT	Yes	No	No	No	No
hsa-mir-589*	chr7: 5501990-5502014	2745	TCTGGGAACCGGCATTTGTTCTGA	No	No	No	No	No
hsa-mir-124*	chr20: 61280310-61280332	2746	CGTGTTCACAGCGGACCTTGAT	No	Yes	Yes	Yes	Yes
hsa-mir-124*	chr8: 9798357-9798379	2747	ATCAAGGTCCGCTGTGAACACG	No	Yes	Yes	Yes	Yes
hsa-mir-124*	chr8: 65454283-65454305	2748	CGTGTTCACAGCGGACCTTGAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-185*	chr22: 18400710-18400732	2749	AGGGGCTGGCTTTCCTCTGGTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-486-3p	chr8: 41637160-41637181	2750	CGGGGCAGCTCAGTACAGGAT	Yes	Yes	Yes	Yes	No
hsa-mir-486-3p	chr8: 41637117-41637138	2751	ATCCTGTACTGAGCTGCCCCG	Yes	Yes	Yes	Yes	No
hsa-mir-1243	chr4: 114247471-114247493	2752	AACTGGATCAATTATAGGAGTG	Yes	Yes	No	No	No
hsa-mir-616*	chr12: 56199272-56199294	2753	AAGTCACTGAAGGGTTTTGAGT	No	No	No	No	No
hsa-mir-1245	chr2: 189551106-189551127	2754	AAGTGATCTAAAGGCCTACAT	Yes	No	No	No	No
hsa-mir-1244	chr12: 12156206-12156232	2755	AAGTAGTTGGTTTGTATGAGATGGTT	Yes	Yes	Yes	Yes	No
hsa-mir-1244	chr12: 9283334-9283360	2756	AACCATCTCATACAAACCAACTACTT	Yes	Yes	Yes	Yes	No
hsa-mir-1244	chr2: 232286321-232286347	2757	AAGTAGTTGGTTTGTATGAGATGGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1244	chr5: 118338233-118338259	2758	AAGTAGTTGGTTTGTATGAGATGGTT	Yes	Yes	Yes	Yes	No
hsa-mir-1247	chr14: 101096451-101096473	2759	TCCGGGGACGAACGGGACGGGT	Yes	Yes	No	Yes	Yes
hsa-mir-1246	chr2: 177173997-177174016	2760	CCTGCTCCAAAAATCCATT	Yes	Yes	No	No	No
hsa-mir-1249	chr22: 43975502-43975524	2761	TGAAGAAGGGGGGGAAGGGCGT	Yes	Yes	Yes	Yes	No
hsa-mir-491-3p	chr9: 20706152-20706174	2762	CTTATGCAAGATTCCCTTCTAC	Yes	Yes	Yes	Yes	No
hsa-mir-148a*	chr7: 25956104-25956126	2763	AGTCGGAGTGTCTCAGAACTTT	Yes	Yes	Yes	Yes	No
hsa-mir-92b*	chr1: 153431610-153431632	2764	AGGGACGGGACGCGGTGCAGTG	No	Yes	Yes	No	Yes
hsa-mir-548o	chr7: 101833199-101833221	2765	GCAAAAGTAACTGCAGTTTTGG	Yes	Yes	No	No	No
hsa-mir-891b	chrX: 144890309-144860331	2766	TCAATGACTCAGGTAAGTTGCA	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-548m	chrX: 94204846-94204867	2767	CAAAAACCACAAATACCTTTG	No	No	No	No	No
hsa-mir-548l	chr11: 93839358-93839380	2768	GACAAAACCCGCAAATACTTTT	Yes	Yes	No	No	No
hsa-mir-548k	chr11: 69807739-69807761	2769	AAAAGTACTTGCGGATTTTGCT	Yes	No	No	No	No
hsa-mir-1283	chr19: 58883559-58883581	2770	TCTACAAAGGAAAGCGCTTTCT	Yes	No	No	No	No
hsa-mir-1283	chr19: 58953310-58953332	2771	TCTACAAAGGAAAGCGCTTTCT	No	No	No	No	No
hsa-mir-548i	chrX: 83367460-83367482	2772	GGCAAAATCCGCAATTACTTTT	No	No	No	No	No
hsa-mir-548i	chr3: 126992025-126992047	2773	GGCAAAATCCGCAATTACTTTT	Yes	No	No	No	No
hsa-mir-548i	chr8: 7983961-7983983	2774	GGCAAAATCCGCAATTACTTTT	Yes	No	No	No	No
hsa-mir-548i	chr4: 9166975-9166997	2775	GGCAAAATCCGCAATTACTTTT	Yes	No	No	No	No
hsa-mir-548h	chr17: 13387638-13387660	2776	GACAAAAACCGCGATTACTTTT	No	No	No	No	No
hsa-mir-548h	chr8: 26962359-26962381	2777	GACAAAAACCGCGATTACTTTT	No	No	No	No	No
hsa-mir-548h	chr14: 63631554-63631576	2778	GACAAAAACCGCGATTACTTTT	Yes	No	No	No	No
hsa-mir-548h	chr16: 11307848-11307870	2779	GACAAAAACCGCGATTACTTTT	No	No	No	No	No
hsa-mir-548g	chr4: 148485244-148485266	2780	GTACAAAAGTAATTACAGTTTT	No	No	No	No	No
hsa-mir-548f	chr5: 109877443-109877462	2781	AAAAGTAATTACAGTTTTT	Yes	No	No	No	No
hsa-mir-548f	chr7: 146706065-146706084	2782	AAAAGTAATTACAGTTTTT	No	No	No	No	No
hsa-mir-548f	chrX: 32569527-32569546	2783	AAAAGTAATTACAGTTTTT	Yes	No	No	No	No
hsa-mir-548f	chr2: 212999252-212999271	2784	AAAAGTAATTACAGTTTTT	No	No	No	No	No
hsa-mir-548f	chr10: 56037654-56037673	2785	AAAAGTAATTACAGTTTTT	No	No	No	No	No
hsa-mir-496	chr14: 100596717-100596739	2786	TGAGTATTACATGGCCAATCTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-497	chr17: 6862021-6862042	2787	ACAAACCACAGTGTGCTGCTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-190b	chr1: 152432812-152432833	2788	AACCCAATATCAAACATATCA	Yes	Yes	Yes	Yes	No
hsa-mir-492	chr12: 93752333-93752356	2789	AGGACCTGCGGGACAAGATTCTT	No	No	No	No	No
hsa-mir-493	chr14: 100405205-100405227	2790	TGAAGGTCTACTGTGTGCCAGG	No	Yes	Yes	No	Yes
hsa-mir-199b-5p	chr9: 130046882-130046905	2791	GAACAGATAGTCTAAACACTGGG	Yes	No	Yes	No	No
hsa-mir-891a	chrX: 144917050-144917072	2792	TCAGTGGCTCAGGTTCGTTGCA	No	No	No	No	No
hsa-mir-500*	chrX: 49659829-49659851	2793	ATGCACCTGGGCAAGGATTCTG	Yes	Yes	Yes	No	No
hsa-mir-105*	chrX: 151311355-151311377	2794	TAGCACATGCTCAAACATCCGT	Yes	Yes	Yes	No	Yes
hsa-mir-105*	chrX: 151313548-151313570	2795	TAGCACATGCTCAAACATCCGT	Yes	Yes	No	No	Yes
hsa-mir-513c	chrX: 146078962-146078984	2796	ATAAACGACACCTCCTTGAGAA	No	No	No	No	No
hsa-mir-513b	chrX: 146088302-146088324	2797	ATAAATGACACCTCCTTGTGAA	No	Yes	No	No	No
hsa-mir-18a*	chr13: 90801051-90801074	2798	ACTGCCCTAAGTGCTCCTTCTGG	Yes	No	Yes	Yes	Yes
hsa-mir-548p	chr5: 100180100-100180122	2799	AAAGTAACTGCAGTTTTTGCTA	Yes	No	No	No	No
hsa-mir-24-1*	chr9: 96888129-96888151	2800	TGCCTACTGAGCTGATATCAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-582-5p	chr5: 59035248-59035271	2801	AGTAACTGGTTGAACAACTGTAA	Yes	Yes	Yes	No	No
hsa-mir-668	chr14: 100591389-100591412	2802	TGTCACTCGGCTCGGCCCACTAC	Yes	Yes	No	Yes	Yes
hsa-mir-516a-5p	chr19: 58951821-58951844	2803	TTCTCGAGGAAAGAAGCACTTTC	Yes	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-516a-5p	chr19: 58956213-58956236	2804	TTCTCGAGGAAAGAAGCACTTTC	Yes	No	No	No	No
hsa-mir-30a*	chr6: 72169977-72169999	2805	GCTGCAAACATCCGACTGAAAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-183	chr7: 129202042-129202064	2806	AGTGAATTCTACCAGTGCCATA	Yes	Yes	Yes	Yes	Yes
hsa-mir-186	chr1: 71305951-71305973	2807	AGCCCAAAAGGAGAATTCTTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-187	chr18: 31738795-31738817	2808	CCGGCTGCAACACAAGACACGA	No	Yes	Yes	Yes	Yes
hsa-mir-184	chr15: 77289236-77289258	2809	TGGACGGAGAACTGATAAGGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-185	chr22: 18400675-18400697	2810	TGGAGAGAAAGGCAGTTCCTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-198	chr3: 121597239-121597261	2811	GAACCTATCTCCCCTCTGGACC	Yes	No	No	No	No
hsa-let-7b	chr22: 44888234-44888256	2812	TGAGGTAGTAGGTTGTGTGGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-455-5p	chr9: 116011549-116011571	2813	TATGTGCCTTTGGACTACATCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-518c	chr19: 58903861-58903884	2814	CAAAGCGCTTCTCTTTAGAGTGT	Yes	No	No	No	No
hsa-mir-770-5p	chr14: 100388498-100388521	2815	TCCAGTACCACGTGTCAGGGCCA	Yes	Yes	No	No	No
hsa-mir-380	chr14: 100561145-100561167	2816	TATGTAATATGGTCCACATCTT	Yes	No	No	No	No
hsa-mir-381	chr14: 100582057-100582079	2817	TATACAAGGGCAAGCTCTCTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-382	chr14: 100590405-100590427	2818	GAAGTTGTTCGTGGTGGATTCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-383	chr8: 14755362-14755384	2819	AGCCACAATCACCTTCTGATCT	Yes	Yes	Yes	No	No
hsa-mir-384	chrX: 76056103-76056123	2820	TATGAACAATTTCTAGGAAT	No	Yes	No	No	No
hsa-mir-661	chr8: 145091361-145091385	2821	ACGCGCAGGCCAGAGACCCAGGCA	No	No	No	No	No
hsa-mir-421	chrX: 73354951-73354974	2822	GCGCCCAATTAATGTCTGTTGAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-518f	chr19: 58895132-58895153	2823	GAAAGCGCTTCTCTTTAGAGG	Yes	No	No	No	No
hsa-mir-660	chrX: 49664603-49664625	2824	TACCCATTGCATATCGGAGTTG	Yes	Yes	Yes	No	No
hsa-mir-425	chr3: 49032635-49032658	2825	TCAACGGGAGTGATCGTGTCATT	Yes	Yes	Yes	Yes	Yes
hsa-mir-424	chrX: 133508376-133508397	2826	TTCAAAACATGAATTGCTGCTG	Yes	Yes	Yes	No	No
hsa-mir-518c*	chr19: 58903823-58903646	2827	TCTCTGGAGGGAAGCACTTTCTG	Yes	No	No	No	No
hsa-mir-543	chr14: 100568122-100568144	2828	AAACATTCGCGGTGCACTTCTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-18a	chr13: 90801010-90801033	2829	TAAGGTGCATCTAGTGCAGATAG	Yes	No	Yes	Yes	Yes
hsa-mir-138-1*	chr3: 44130769-44130791	2830	GCTACTTCACAACACCAGGGCC	No	No	No	Yes	No
hsa-let-7e*	chr19: 56887902-56887924	2831	CTATACGGCCTCCTAGCTTTCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-545	chrX: 73423685-73423707	2832	GCACACAATAAATGTTTGCTGA	Yes	Yes	No	No	No
hsa-mir-549	chr15: 78921388-78921409	2833	AGAGCTCATCCATAGTTGTCA	Yes	Yes	No	No	No
hsa-mir-549	chr15: 78921423-78921444	2834	TGACAACTATGGATGAGCTCT	Yes	Yes	No	No	No
hsa-mir-133a	chr20: 60572621-60572643	2835	TTTGGTCCCCTTCAACCAGCTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-133a	chr18: 17659670-17659692	2836	CAGCTGGTTGAAGGGGACCAAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-574-3p	chr4: 38546107-38546129	2837	CACGCTCATGCACACACCCACA	No	No	Yes	Yes	No
hsa-mir-133b	chr6: 52121744-52121766	2838	TTTGGTCCCCTTCAACCAGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1237	chr11: 63892730-63892751	2839	TCCTTCTGCTCCGTCCCCCAG	Yes	No	No	No	No
hsa-mir-220c	chr19: 53755391-53755413	2840	AGTCTTCACAACAGCCCTGTGT	No	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-369-3p	chr14: 100601730-100601751	2841	AATAATACATGGTTGATCTTT	Yes	Yes	No	Yes	Yes
hsa-mir-518e	chr19: 58924956-58924977	2842	AAAGCGCTTCCCTTCAGAGTG	Yes	No	No	No	No
hsa-mir-519e*	chr19: 58875018-58875040	2843	TTCTCCAAAAGGGAGCACTTTC	Yes	No	No	No	No
hsa-mir-15a	chr13: 49521303-49521325	2844	CACAAACCATTATGTGCTGCTA	Yes	Yes	Yes	Yes	No
hsa-mir-769-5p	chr19: 51214058-51214080	2845	TGAGACCTCTGGGTTCTGAGCT	No	No	No	No	No
hsa-mir-15b	chr3: 161605088-161605110	2846	TAGCAGCACATCATGGTTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-453	chr14: 100592322-100592345	2847	AGGTTGTCCGTGGTGAGTTCGCA	Yes	Yes	Yes	No	No
hsa-mir-876-5p	chr9: 28853672-28853694	2848	TGGTGATTCACAAAGAAATCCA	Yes	Yes	Yes	No	No
hsa-mir-1226	chr3: 47866101-47866123	2849	TCACCAGCCCTGTGTTCCCTAG	Yes	Yes	No	No	No
hsa-mir-802	chr21: 36014899-36014922	2850	CAGTAACAAAGATTCATCCTTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-520a-5p	chr19: 58885960-58885981	2851	CTCCAGAGGGAAGTACTTTCT	Yes	No	No	No	No
hsa-mir-552	chr1: 34907801-34907822	2852	TTGTCTAACCAGTCACCTGTT	Yes	No	No	No	No
hsa-mir-147b	chr15: 43512587-43512609	2853	GTGTGCGGAAATGCTTCTGCTA	Yes	No	Yes	Yes	Yes
hsa-mir-432*	chr14: 100420633-100420654	2854	CTGGATGGCTCCTCCATGTCT	Yes	Yes	Yes	No	No
hsa-mir-650	chr22: 21495284-21495305	2855	AGGAGGCAGCGCTCTCAGGAC	Yes	Yes	No	No	No
hsa-mir-146a*	chr5: 159844992-159845014	2856	CCTCTGAAATTCAGTTCTTCAG	No	No	No	No	No
hsa-mir-335	chr7: 129923202-129923225	2857	TCAAGAGCAATAACGAAAAATGT	Yes	Yes	Yes	Yes	No
hsa-mir-520d-3p	chr19: 58915214-58915236	2858	AAAGTGCTTCTCTTTGGTGGGT	Yes	No	No	No	No
hsa-mir-19b-1*	chr13: 90801461-90801484	2859	AGTTTTGCAGGTTTGCATCCAGC	Yes	No	Yes	Yes	Yes
hsa-mir-1231	chr1: 200044365-200044386	2860	GTGTCTGGGCGGACAGCTGC	No	No	No	No	No
hsa-mir-146b-3p	chr10: 104186302-104186324	2861	TGCCCTGTGGACTCAGTTCTGG	Yes	No	No	No	No
hsa-mir-875-5p	chr8: 100618233-100618255	2862	CACCTGATAAAACTGAGGTATA	Yes	Yes	Yes	Yes	Yes
hsa-mir-874	chr5: 137011169-137011191	2863	TCGGTCCCTCGGGCCAGGGCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-873	chr9: 28878922-28878943	2864	AGGAGACTCACAAGTTCCTGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-15b*	chr3: 161605126-161605148	2865	CGAATCATTATTTGCTGCTCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-25*	chr7: 99529168-99529189	2866	CAATTGCCCAAGTCTCCGCCT	Yes	Yes	Yes	Yes	No
hsa-mir-1185	chr14: 100579080-100579101	2867	AGAGGATACCCTTTGTATGTT	Yes	Yes	Yes	No	No
hsa-mir-1185	chr14: 100580301-100580322	2868	AGAGGATACCCTTTGTATGTT	Yes	Yes	Yes	No	No
hsa-mir-720	chr3: 165541848-165541865	2869	TCTCGCTGGGGCCTCCA	Yes	No	No	No	No
hsa-mir-409-3p	chr14: 100601435-100601457	2870	GAATGTTGCTCGGTGAACCCCT	Yes	Yes	No	Yes	Yes
hsa-mir-1182	chr1: 229222209-229222232	2871	GTCACATCCCTCCCAAGACCCTC	Yes	Yes	No	No	No
hsa-mir-1179	chr15: 86952355-86952376	2872	AAGCATTCTTTCATTGGTTGG	Yes	Yes	No	No	No
hsa-mir-1178	chr12: 118635836-118635857	2873	CTAGGGAAGAACAGTGAGCAA	Yes	Yes	No	No	No
hsa-mir-367*	chr4: 113788519-113788541	2874	AGAGTTGCATATTAGCAACAGT	Yes	Yes	Yes	No	No
hsa-mir-150	chr19: 54695900-54695922	2875	CACTGGTACAAGGGTTGGGAGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-153	chr7: 157059801-157059823	2876	GATCACTTTTGTGACTATGCAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-153	chr2: 219867091-219867113	2877	GATCACTTTTGTGACTATGCAA	No	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-152	chr17: 43469538-43469559	2878	CCAAGTTCTGTCATGCACTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-155	chr21: 25868165-25868188	2879	TTAATGCTAATCGTGATAGGGGT	Yes	Yes	Yes	No	No
hsa-mir-154	chr14: 100595858-100595880	2880	TAGGTTATCCGTGTTGCCTTCG	Yes	Yes	No	Yes	Yes
hsa-mir-634	chr17: 62213711-62213733	2881	AACCAGCACCCCAACTTTGGAC	Yes	No	No	No	No
hsa-mir-377*	chr14: 100598145-100598167	2882	AGAGGTTGCCCTTGGTGAATTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-1228	chr12: 55874604-55874624	2883	TCACACCTGCCTCGCCCCCC	No	Yes	No	No	No
hsa-mir-199a-5p	chr1: 170380354-170380377	2884	GAACAGGTAGTCTGAACACTGGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-199a-5p	chr19: 10789144-10789167	2885	GAACAGGTAGTCTGAACACTGGG	Yes	Yes	Yes	Yes	No
hsa-mir-767-5p	chrX: 151312608-151312631	2886	CATGCTCAGACAACCATGGTGCA	No	Yes	No	No	No
hsa-mir-151-3p	chr8: 141811867-141811888	2887	CCTCAAGGAGCTTCAGTCTAG	Yes	Yes	No	No	No
hsa-mir-154*	chr14: 100595894-100595916	2888	AATCATACACGGTTGACCTATT	Yes	Yes	No	Yes	Yes
hsa-mir-483-5p	chr11: 2111986-2112008	2889	CTCCCTTCTTTCCTCCCGTCTT	No	No	No	No	No
hsa-mir-33a	chr22: 40626898-40626919	2890	GTGCATTGTAGTTGCATTGCA	Yes	No	Yes	Yes	Yes
hsa-mir-33b	chr17: 17657935-17657955	2891	GCAATGCAACAGCAATGCAC	Yes	Yes	Yes	No	No
hsa-mir-1304	chr11: 93106537-93106559	2892	CACATCTCACTGTAGCCTCAAA	No	Yes	No	No	No
hsa-mir-25	chr7: 99529129-99529151	2893	TCAGACCGAGACAAGTGCAATG	No	Yes	Yes	Yes	Yes
hsa-mir-1306	chr22: 18453634-18453652	2894	ACGTTGGCTCTGGTGGTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-1307	chr10: 105144047-105144069	2895	CACGACCGACGCCACGCCGAGT	Yes	Yes	Yes	No	No
hsa-mir-1300	chr15: 51017866-51017884	2896	CAGCAGCCTCCTTCTCAA	Yes	No	Yes	Yes	No
hsa-mir-21	chr17: 55273415-55273437	2897	TAGCTTATCAGACTGATGTTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-22	chr17: 1563957-1563979	2898	ACAGTTCTTCAACTGGCAGCTT	Yes	No	Yes	Yes	Yes
hsa-mir-596	chr8: 1752818-1752839	2899	AAGCCTGCCCGGCTCCTCGGG	No	No	No	No	No
hsa-mir-599	chr8: 100618054-100618074	2900	GTTTGATAAACTGACACAAC	Yes	Yes	Yes	No	No
hsa-mir-598	chr8: 10930140-10930162	2901	TGACGATGACAACGATGACGTA	Yes	No	No	No	No
hsa-mir-610	chr11: 28034990-28035011	2902	TCCCAGCACACATTTAGCTCA	Yes	No	No	No	No
hsa-mir-610	chr11: 28034952-28034973	2903	TGAGCTAAATGTGTGCTGGGA	Yes	No	No	No	No
hsa-mir-611	chr11: 61316547-61316570	2904	GTCAGACCCCGAGGGGTCCTCGC	No	Yes	No	No	No
hsa-mir-616	chr12: 56199232-56199254	2905	CTGCTCAAACCCTCCAATGACT	Yes	No	No	No	No
hsa-mir-617	chr12: 79750502-79750524	2906	GCCACCTTCAAATGGGAAGTCT	Yes	No	No	No	No
hsa-mir-614	chr12: 12960082-12960105	2907	GAACGCCTGTTCTTGCCAGGTGG	Yes	No	No	No	No
hsa-mir-517c	chr19: 58936434-58936456	2908	ATCGTGCATCCTTTTAGAGTGT	No	No	No	No	No
hsa-mir-517b	chr19: 58916184-58916206	2909	TCGTGCATCCCTTTAGAGTGTT	Yes	No	No	No	No
hsa-mir-517a	chr19: 58907386-58907408	2910	ATCGTGCATCCCTTTAGAGTGT	Yes	No	No	No	No
hsa-mir-495	chr14: 100569893-100569915	2911	AAACAAACATGGTGCACTTCTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-671-3p	chr7: 150566506-150566527	2912	TCCGGTTCTCAGGGCTCCACC	Yes	Yes	Yes	Yes	Yes
hsa-mir-135a*	chr3: 52303287-52303309	2913	CGCCACGGCTCCAATCCCTATA	Yes	Yes	Yes	Yes	No
hsa-mir-513a-3p	chrX: 146102707-146102730	2914	CCTTCTCAGAAAGGTGAAATTTA	No	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-513a-3p	chrX: 146115069-146115092	2915	CCTTCTCAGAAAGGTGAAATTTA	Yes	No	No	No	No
hsa-mir-525-5p	chr19: 58892612-58892633	2916	CTCCAGAGGGATGCACTTTCT	Yes	Yes	No	No	No
hsa-mir-758	chr14: 100562160-100562182	2917	TTTGTGACCTGGTCCACTAACC	Yes	No	Yes	Yes	Yes
hsa-mir-187*	chr18: 31738831-31738853	2918	GCCCGGGTCCTGTGTTGTAGCC	No	No	No	Yes	Yes
hsa-mir-520d-5p	chr19: 58915176-58915196	2919	CTACAAAGGGAAGCCCTTTC	Yes	Yes	No	No	No
hsa-mir-522*	chr19: 58946291-58946313	2920	CTCTAGAGGGAAGCGCTTTCTG	Yes	No	No	No	No
hsa-mir-101	chr9: 4840344-4840365	2921	TACAGTACTGTGATAACTGAA	Yes	Yes	Yes	No	No
hsa-mir-101	chr1: 65296712-65296733	2922	TTCAGTTATCACAGTACTGTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-299-3p	chr14: 100559921-100559943	2923	TATGTGGGATGGTAAACCGCTT	No	No	No	No	No
hsa-mir-107	chr10: 91342492-91342515	2924	TGATAGCCCTGTACAATGCTGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1278	chr1: 191372304-191372326	2925	TAGTACTGTGCATATCATCTAT	No	No	No	No	No
hsa-mir-1279	chr12: 67953234-67953251	2926	AGAAAGAAGCAATATGA	No	No	Yes	Yes	No
hsa-mir-219-1-3p	chr6: 33283650-33283672	2927	AGAGTTGAGTCTGGACGTCCCG	Yes	Yes	Yes	No	No
hsa-mir-541	chr14: 100600637-100600659	2928	TGGTGGGCACAGAATCTGGACT	No	No	No	No	No
hsa-mir-1270	chr19: 20371127-20371150	2929	ACACAGCTCTTCCATATCTCCAG	No	No	No	No	No
hsa-mir-1271	chr5: 175727568-175727590	2930	CTTGGCACCTAGCAAGCACTCA	Yes	Yes	No	No	No
hsa-mir-1272	chr15: 62841722-62841748	2931	TTTCAGAATTTGCTGCCATCATCATC	Yes	No	No	No	No
hsa-mir-1273	chr8: 101105388-101105413	2932	AAGAAAGAGTCTTGCTTTGTCGCCC	Yes	No	No	No	No
hsa-mir-1275	chr6: 34075772-34075789	2933	GACAGCCTCTCCCCCAC	Yes	No	No	No	No
hsa-mir-1276	chr15: 84114782-84114802	2934	TGTCTCCACAGGGCTCTTTA	Yes	No	No	No	No
hsa-mir-1277	chrX: 117404430-117404452	2935	TACGTAGATATATATGTATTTT	No	Yes	Yes	No	No
hsa-mir-488*	chr1: 175265170-175265191	2936	TTGAGAGTGCCATTATCTGGG	Yes	Yes	Yes	No	Yes
hsa-mir-219-2-3p	chr9: 130194731-130194753	2937	ACAGATGTCCAGCCACAATTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-142-5p	chr17: 53763642-53763663	2938	AGTAGTGCTTTCTACTTTATG	Yes	Yes	Yes	Yes	Yes
hsa-mir-615-3p	chr12: 52714060-52714082	2939	TCCGAGCCTGGGTCTCCCTCTT	Yes	Yes	No	Yes	Yes
hsa-mir-130b	chr22: 20337642-20337664	2940	CAGTGCAATGATGAAAGGGCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-506	chrX: 146119962-146119983	2941	TCTACTCAGAAGGGTGCCTTA	Yes	Yes	No	No	No
hsa-mir-507	chrX: 146120211-146120232	2942	TTCACTCCAAAAGGTGCAAAA	Yes	Yes	No	No	No
hsa-mir-504	chrX: 137577586-137577608	2943	GATAGAGTGCAGACCAGGGTCT	Yes	Yes	Yes	Yes	No
hsa-mir-885-5p	chr3: 10411214-10411236	2944	AGAGGCAGGGTAGTGTAATGGA	Yes	Yes	Yes	No	No
hsa-mir-944	chr3: 191030457-191030479	2945	AAATTATTGTACATCGGATGAG	Yes	No	No	No	No
hsa-mir-500	chrX: 49659790-49659813	2946	TAATCCTTGCTACCTGGGTGAGA	Yes	Yes	Yes	No	No
hsa-let-7d*	chr9: 95980997-95981019	2947	CTATACGACCTGCTGCCTTTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-545*	chrX: 73423723-73423745	2948	TCATCTAATAAACATTTACTGA	Yes	Yes	No	No	No
hsa-mir-942	chr1: 117438799-117438821	2949	TCTTCTCTGTTTTGGCCATGTG	Yes	No	No	No	No
hsa-mir-200a*	chr1: 1093120-1093142	2950	CATCTTACCGGACAGTGCTGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-130a*	chr11: 57165266-57165288	2951	TTCACATTGTGCTACTGTCTGC	Yes	Yes	Yes	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-1266	chr15: 50356654-50356677	2952	AGCCCTGTTCTACAGCCCTGAGG	Yes	No	No	No	No
hsa-mir-548a-3p	chr6: 18680053-18680075	2953	CAAAACTGGCAATTACTTTTGC	Yes	No	No	No	No
hsa-mir-548a-3p	chr6: 135602050-135602072	2954	CAAAACTGGCAATTACTTTTGC	Yes	No	No	No	No
hsa-mir-548a-3p	chr8: 105565787-105565809	2955	GCAAAAGTAATTGCCAGTTTTG	No	No	No	No	No
hsa-mir-557	chr1: 166611445-166611468	2956	GTTTGCACGGGTGGGCCTTGTCT	Yes	No	No	No	No
hsa-mir-1238	chr19: 10523858-10523878	2957	CTTCCTCGTCTGTCTGCCCC	No	No	No	No	No
hsa-mir-920	chr12: 24256671-24256691	2958	GGGGAGCTGTGGAAGCAGTA	Yes	No	No	No	No
hsa-mir-921	chr1: 164390633-164390658	2959	GAATCCTGGTTCTGTCCCTCACTAG	No	No	No	No	No
hsa-mir-922	chr3: 198885765-198885788	2960	GACGTAGTCCTATTCTCTGCTGC	No	No	No	No	No
hsa-mir-923	chr17: 30502320-30502341	2961	AGTTTCTTTTCCTCCGCTGAC	Yes	No	No	No	No
hsa-mir-924	chr18: 35456114-35456134	2962	GCAAGACATCACAAGACTCT	Yes	No	No	No	No
hsa-mir-193b*	chr16: 14305337-14305359	2963	CGGGGTTTTGAGGGCGAGATGA	Yes	Yes	Yes	Yes	No
hsa-mir-378	chr5: 149092622-149092643	2964	ACTGGACTTGGAGTCAGAAGG	Yes	Yes	Yes	No	No
hsa-mir-320c	chr18: 20155677-20155697	2965	AAAAGCTGGGTTGAGAGGGT	Yes	No	No	No	No
hsa-mir-320c	chr18: 17517517-17517537	2966	AAAAGCTGGGTTGAGAGGGT	Yes	Yes	No	No	No
hsa-mir-320b	chr1: 222511373-222511395	2967	TTGCCCTCTCAACCCAGCTTTT	Yes	Yes	No	No	No
hsa-mir-320b	chr1: 117015931-117015953	2968	AAAAGCTGGGTTGAGAGGGCAA	Yes	Yes	No	No	No
hsa-mir-320a	chr8: 22158432-22158454	2969	TCGCCCTCTCAACCCAGCTTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-324-3p	chr17: 7067350-7067370	2970	CCAGCAGCACCTGGGGCAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-370	chr14: 100447275-100447297	2971	GCCTGCTGGGGTGGAACCTGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-431*	chr14: 100417158-100417180	2972	CAGGTCGTCTTGCAGGGCTTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-372	chr19: 58982996-58983019	2973	AAAGTGCTGCGACATTTGAGCGT	Yes	Yes	No	No	No
hsa-mir-375	chr2: 219574613-219574635	2974	TCACGCGAGCCGAACGAACAAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-422a	chr15: 61950240-61950262	2975	GCCTTCTGACCCTAAGTCCAGT	Yes	No	No	No	No
hsa-mir-377	chr14: 100598183-100598205	2976	ATCACACAAAGGCAACTTTTGT	Yes	Yes	Yes	Yes	No
hsa-mir-362-3p	chrX: 49660352-49660374	2977	AACACACCTATTCAAGGATTCA	Yes	Yes	Yes	No	No
hsa-mir-579	chr5: 32430254-32430277	2978	AATCGCGGTTTATACCAAATGAA	Yes	No	No	No	No
hsa-mir-578	chr4: 166526903-166526924	2979	CTTCTTGTGCTCTAGGATTGT	Yes	No	No	No	No
hsa-mir-24-2*	chr19: 13808139-13808161	2980	CTGTGTTTCAGCTCAGTAGGCA	Yes	Yes	Yes	No	No
hsa-mir-573	chr4: 24130972-24130996	2981	CTGATCAGTTACACATCACTTCAG	No	No	No	No	No
hsa-mir-572	chr4: 10979608-10979628	2982	GTCCGCTCGGCGGTGGCCCA	Yes	Yes	No	No	No
hsa-mir-571	chr4: 334005-334026	2983	TGAGTTGGCCATCTGAGTGAG	No	No	No	No	No
hsa-mir-570	chr3: 196911510-196911532	2984	CGAAAACAGCAATTACCTTTGC	No	No	No	No	No
hsa-mir-577	chr4: 115797378-115797399	2985	TAGATAAAATATTGGTACCTG	Yes	Yes	No	No	No
hsa-mir-520c-3p	chr19: 58902571-58902593	2986	AAAGTGCTTCCTTTTAGAGGGT	Yes	No	No	No	No
hsa-mir-509-3-5p	chrX: 146148905-146148927	2987	CATGATTGCCACGTCTGCAGTA	Yes	No	No	No	No
hsa-mir-23a*	chr19: 13808443-13808465	2988	AAATCCCATCCCCAGGAACCCC	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-518f*	chr19: 58895095-58895117	2989	CTCTAGAGGGAAGCACTTTCTC	Yes	No	No	No	No
hsa-mir-195*	chr17: 6861670-6861692	2990	GGAGCAGCACAGCCAATATTGG	Yes	Yes	No	Yes	Yes
hsa-mir-576-5p	chr4: 110629317-110629339	2991	ATTCTAATTTCTCCACGTCTTT	No	No	No	No	No
hsa-mir-575	chr4: 83893528-83893547	2992	GCTCCTGTCCAACTGGCTC	Yes	No	No	No	No
hsa-mir-21*	chr17: 55273453-55273474	2993	CAACACCAGTCGATGGGCTGT	Yes	Yes	No	No	No
hsa-mir-27b*	chr9: 96887565-96887587	2994	AGAGCTTAGCTGATTGGTGAAC	Yes	Yes	Yes	Yes	Yes
hsa-mir-217	chr2: 56063658-56063681	2995	TCCAATCAGTTCCTGATGCAGTA	Yes	Yes	Yes	No	No
hsa-mir-214	chr1: 170374578-170374600	2996	ACTGCCTGTCTGTGCCTGCTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-215	chr1: 218357880-218357901	2997	GTCTGTCAATTCATAGGTCAT	Yes	Yes	No	No	No
hsa-mir-212	chr17: 1900333-1900354	2998	GGCCGTGACTGGAGACTGTTA	No	No	Yes	Yes	Yes
hsa-mir-210	chr11: 558111-558133	2999	TCAGCCGCTGTCACACGCACAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-211	chr15: 29144589-29144611	3000	AGGCGAAGGATGACAAAGGGAA	Yes	No	No	No	No
hsa-mir-92a	chrX: 133131239-133131261	3001	ACAGGCCGGGACAAGTGCAATA	Yes	Yes	Yes	No	No
hsa-mir-92a	chr13: 90801615-90801637	3002	TATTGCACTTGTCCCGGCCTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-92b	chr1: 153431651-153431673	3003	TATTGCACTCGTCCCGGCCTCC	No	Yes	Yes	Yes	Yes
hsa-mir-218	chr4: 20139019-20139040	3004	TTGTGCTTGATCTAACCATGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-218	chr5: 168127793-168127814	3005	ACATGGTTAGATCAAGCACAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-515-3p	chr19: 58874118-58874140	3006	GAGTGCCTTCTTTTGGAGCGTT	Yes	No	No	No	No
hsa-mir-515-3p	chr19: 58880124-58880146	3007	GAGTGCCTTCTTTTGGAGCGTT	Yes	No	No	No	No
hsa-mir-1	chr18: 17662973-17662995	3008	ATACATACTTCTTTACATTCCA	Yes	Yes	Yes	Yes	No
hsa-mir-1	chr20: 60562002-60562024	3009	TGGAATGTAAAGAAGTATGTAT	Yes	Yes	Yes	Yes	No
hsa-mir-425*	chr3: 49032595-49032617	3010	GGGCGGACACGACATTCCCGAT	Yes	Yes	Yes	Yes	No
hsa-mir-522	chr19: 58946329-58946351	3011	AAAATGGTTCCCTTTAGAGTGT	Yes	Yes	No	No	No
hsa-mir-7	chr9: 85774546-85774569	3012	ACAACAAAATCACTAGTCTTCCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-7	chr15: 86956090-86956113	3013	TGGAAGACTAGTGATTTTGTTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-7	chr19: 4721711-4721734	3014	TGGAAGACTAGTGATTTTGTTGT	Yes	Yes	Yes	No	No
hsa-mir-9	chr15: 87712266-87712289	3015	TCTTTGGTTATCTAGCTGTATGA	No	Yes	Yes	Yes	Yes
hsa-mir-9	chr1: 154656807-154656830	3016	TCATACAGCTAGATAACCAAAGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-9	chr5: 87998475-87998498	3017	TCATACAGCTAGATAACCAAAGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-615-5p	chr12: 52714017-52714039	3018	GGGGGTCCCCGGTGCTCGGATC	Yes	Yes	No	Yes	Yes
hsa-mir-512-3p	chr19: 58861794-58861816	3019	AAGTGCTGTCATAGCTGAGGTC	Yes	No	No	No	No
hsa-mir-512-3p	chr19: 58864278-58864300	3020	AAGTGCTGTCATAGCTGAGGTC	No	No	No	No	No
hsa-mir-202*	chr10: 134911066-134911088	3021	CAAAGAAGTATATGCATAGGAA	Yes	No	Yes	Yes	Yes
hsa-mir-888*	chrX: 144884003-144884025	3022	TTCACCCAAAGAGGTGTCAGTC	No	No	No	No	No
hsa-mir-143*	chr5: 148788699-148788721	3023	GGTGCAGTGCTGCATCTCTGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-526b	chr19: 58889471-58889494	3024	CTCTTGAGGGAAGCACTTTCTGT	Yes	Yes	No	No	No
hsa-mir-656	chr14: 100602855-100602876	3025	AATATTATACAGTCAACCTCT	Yes	Yes	Yes	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-657	chr17: 76713685-76713708	3026	CCTAGAGAGGGTGAGAACCTGCC	Yes	No	No	No	No
hsa-mir-655	chr14: 100585699-100585721	3027	ATAATACATGGTTAACCTCTTT	Yes	No	Yes	No	No
hsa-mir-652	chrX: 109185272-109185293	3028	AATGGCGCCACTAGGGTTGTG	Yes	Yes	No	No	No
hsa-mir-653	chr7: 92950070-92950091	3029	CAGTAGAGATTGTTTCAACAC	Yes	Yes	No	Yes	No
hsa-mir-518a-3p	chr19: 58926121-58926143	3030	GAAAGCGCTTCCCTTTGCTGGA	No	No	No	No	No
hsa-mir-518a-3p	chr19: 58934450-58934472	3031	GAAAGCGCTTCCCTTTGCTGGA	Yes	No	No	No	No
hsa-mir-651	chrX: 8055020-8055042	3032	TTTAGGATAAGCTTGACTTTTG	No	No	No	No	No
hsa-mir-302f	chr18: 26132899-26132916	3033	TAATTGCTTCCATGTTT	Yes	Yes	No	No	No
hsa-mir-1184	chrX: 154265958-154265981	3034	GGAAGCCATCAAGTCGCTGCAGG	Yes	Yes	No	No	No
hsa-mir-1184	chrX: 154340431-154340454	3035	CCTGCAGCGACTTGATGGCTTCC	Yes	Yes	No	No	No
hsa-mir-1184	chrX: 153768844-153768867	3036	GGAAGCCATCAAGTCGCTGCAGG	Yes	Yes	No	No	No
hsa-mir-302d	chr4: 113788610-113788633	3037	ACACTCAAACATGGAAGCACTTA	Yes	Yes	No	Yes	No
hsa-mir-302c	chr4: 113788970-113788993	3038	CCACTGAAACATGGAAGCACTTA	Yes	Yes	Yes	No	No
hsa-mir-302b	chr4: 113789093-113789116	3039	CTACTAAAACATGGAAGCACTTA	Yes	Yes	Yes	Yes	No
hsa-mir-1180	chr17: 19188418-19188440	3040	ACACACCCACGCGAGCCGGAAA	Yes	Yes	No	No	No
hsa-mir-1181	chr19: 10375180-10375201	3041	CGGCTCGGGTGGCGGCGACGG	Yes	No	No	No	No
hsa-mir-629*	chr15: 68158779-68158801	3042	GCTGGGCTTACGTTGGGAGAAC	No	No	No	No	No
hsa-mir-302e	chr11: 7212577-7212594	3043	TAAGTGCTTCCATGCTT	Yes	Yes	No	No	No
hsa-mir-103	chr5: 167920486-167920509	3044	TCATAGCCCTGTACAATGCTGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-103	chr20: 3846187-3846210	3045	AGCAGCATTGTACAGGGCTATGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-100	chr11: 121528192-121528214	3046	CACAAGTTCGGATCTACGGGTT	Yes	Yes	No	Yes	Yes
hsa-mir-138-2*	chr16: 55449986-55450008	3047	GCTATTTCACGACACCAGGGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-122*	chr18: 54269335-54269357	3048	AACGCCATTATCACACTAAATA	Yes	Yes	Yes	Yes	No
hsa-mir-105	chrX: 151311392-151311415	3049	ACCACAGGAGTCTGAGCATTTGA	Yes	Yes	Yes	No	No
hsa-mir-105	chrX: 151313585-151313608	3050	ACCACAGGAGTCTGAGCATTTGA	Yes	Yes	No	No	No
hsa-mir-223*	chrX: 65155461-65155483	3051	CGTGTATTTGACAAGCTGAGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-363*	chrX: 133131120-133131142	3052	AAATTGCATCGTGATCCACCCG	No	Yes	Yes	No	Yes
hsa-mir-28-5p	chr3: 189889275-189889297	3053	AAGGAGCTCACAGTCTATTGAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-150*	chr19: 54695865-54695887	3054	CTGTCCCCCAGGCCTGTACCAG	Yes	Yes	No	No	Yes
hsa-mir-99a*	chr21: 16833328-16833350	3055	CAAGCTCGCTTCTATGGGTCTG	Yes	Yes	Yes	No	No
hsa-mir-1825	chr20: 30289293-30289311	3056	TCCAGTGCCCTCCTCTCC	Yes	Yes	No	No	No
hsa-mir-129*	chr7: 127635208-127635230	3057	AAGCCCTTACCCCAAAAAGTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-556-3p	chr1: 160579013-160579035	3058	ATATTACCATTAGCTCATCTTT	Yes	No	No	No	No
hsa-mir-10b	chr2: 176723302-176723325	3059	TACCCTGTAGAACCGAATTTGTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-1827	chr12: 99107840-99107858	3060	TGAGGCAGTAGATTGAAT	Yes	Yes	No	No	No
hsa-mir-10a	chr17: 44012264-44012287	3061	CACAAATTCGGATCTACAGGGTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-623	chr13: 98806400-98806423	3062	ATCCCTTGCAGGGGCTGTTGGGT	No	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-622	chr13: 89681496-89681517	3063	ACAGTCTGCTGAGGTTGGAGC	Yes	No	No	No	No
hsa-mir-621	chr13: 40282961-40282982	3064	GGCTAGCAACAGCGCTTACCT	Yes	No	No	No	No
hsa-mir-620	chr12: 115070762-115070782	3065	ATTTCTATATCTATCTCCAT	No	No	No	No	No
hsa-mir-127-5p	chr14: 100419090-100419112	3066	CTGAAGCTCAGAGGGCTCTGAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-626	chr15: 39771134-39771153	3067	AGCTGTCTGAAAATGTCTT	Yes	No	No	No	No
hsa-mir-625	chr14: 65007622-65007643	3068	GGACTATAGAACTTTCCCCCT	Yes	No	No	No	No
hsa-mir-625	chr14: 65007586-65007607	3069	AGGGGGAAAGTTCTATAGTCC	Yes	No	No	No	No
hsa-mir-182*	chr7: 129197481-129197502	3070	TAGTTGGCAAGTCTAGAACCA	Yes	Yes	Yes	Yes	No
hsa-mir-1292	chr20: 2581424-2581449	3071	TGGGAACGGGTTCCGGCAGACGCTG	Yes	No	No	No	No
hsa-mir-342-3p	chr14: 99645804-99645827	3072	TCTCACACAGAAATCGCACCCGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1290	chr1: 19096158-19096177	3073	TCCCTGATCCAAAAATCCA	Yes	No	No	No	No
hsa-mir-1291	chr12: 47334543-47334567	3074	ACTGCTGGTCTTCAGTCAGGGCCA	Yes	No	No	No	No
hsa-mir-1296	chr10: 64802777-64802799	3075	GGAGATGGAGCCAGGGCCCTAA	Yes	Yes	Yes	No	No
hsa-mir-1297	chr13: 53784116-53784133	3076	CACCTGAATTACTTGAA	Yes	Yes	Yes	No	No
hsa-mir-1294	chr5: 153706905-153706927	3077	TGTGAGGTTGGCATTGTTGTCT	Yes	No	No	No	No
hsa-mir-1225-5p	chr16: 2080264-2080286	3078	CCCCCCACTGGGCCGTACCCAC	Yes	Yes	Yes	Yes	Yes
hsa-mir-509-5p	chrX: 146148020-146148041	3079	TGATTGCCACTGTCTGCAGTA	Yes	No	No	No	No
hsa-mir-509-5p	chrX: 146149795-146149816	3080	TGATTGCCACTGTCTGCAGTA	Yes	No	No	No	No
hsa-mir-1224-3p	chr3: 185441950-185441971	3081	CCCCACCTCCTCTCTCCTCAG	Yes	Yes	Yes	No	No
hsa-mir-140-3p	chr16: 68524545-68524566	3082	TACCACAGGGTAGAACCACGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-532-3p	chrX: 49654549-49654571	3083	CCTCCCACACCCAAGGCTTGCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1298	chrX: 113855922-113855944	3084	TTCATTCGGCTGTCCAGATGTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-26b	chr2: 218975623-218975644	3085	TTCAAGTAATTCAGGATAGGT	Yes	Yes	Yes	Yes	Yes
hsa-let-7f-2*	chrX: 53600881-53600903	3086	GGAAAGACAGTAGACTGTATAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-585	chr5: 168623197-168623216	3087	TAGCATACAGATACGCCCA	No	No	No	No	No
hsa-mir-490-5p	chr7: 136238491-136238511	3088	CCATGGATCTCCAGGTGGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-519c-3p	chr19: 58881587-58881609	3089	AAAGTGCATCTTTTTAGAGGAT	Yes	No	No	No	No
hsa-mir-513a-5p	chrX: 146115109-146115127	3090	ATGACACCTCCCTGTGAA	Yes	Yes	No	No	No
hsa-mir-513a-5p	chrX: 146102747-146102765	3091	ATGACACCTCCCTGTGAA	Yes	Yes	No	No	No
hsa-mir-591	chr7: 95686969-95686989	3092	ACAATGAGAACCCATGGTCT	Yes	No	No	No	No
hsa-mir-191*	chr3: 49033067-49033089	3093	GGGGACGAAATCCAAGCGCAGC	Yes	Yes	No	No	No
hsa-mir-1305	chr4: 183327489-183327511	3094	TTTTCAACTCTAATGGGAGAGA	No	No	No	No	No
hsa-mir-624	chr14: 30553625-30553646	3095	AGGTAATACCAATACCTTGTG	Yes	No	No	No	No
hsa-mir-593	chr7: 127509226-127509245	3096	TGTCTCTGCTGGGGTTTCT	Yes	Yes	No	No	No
hsa-mir-302a	chr4: 113788790-113788813	3097	TCACCAAAACATGGAAGCACTTA	Yes	Yes	No	Yes	No
hsa-mir-592	chr7: 126485437-126485459	3098	ACATCATCGCATATTGACACAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1293	chr12: 48914231-48914253	3099	GCACAAATCTCCAGACCACCCA	Yes	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-30e*	chr1: 40992671-40992693	3100	CTTTCAGTCGGATGTTTACAGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-432	chr14: 100420585-100420608	3101	TCTTGGAGTAGGTCATTGGGTGG	Yes	Yes	Yes	No	No
hsa-mir-629	chr15: 68158819-68158840	3102	AGTTCTCCCAACGTAAACCCA	No	No	No	No	No
hsa-mir-96*	chr7: 129201772-129201794	3103	CATATTGGCACTGCACATGATT	Yes	Yes	Yes	No	Yes
hsa-mir-1301	chr2: 25405023-25405047	3104	GAAGTCACTCCCAGGCAGCTGCAA	No	No	Yes	No	No
hsa-mir-200b*	chr1: 1092366-1092388	3105	CATCTTACTGGGCAGCATTGGA	No	No	Yes	Yes	Yes
hsa-mir-181c*	chr19: 13846576-13846598	3106	AACCATCGACCGTTGAGTGGAC	Yes	Yes	Yes	Yes	Yes
hsa-mir-508-3p	chrX: 146126154-146126177	3107	TCTACTCCAAAAGGCTACAATCA	No	No	No	No	No
hsa-mir-1303	chr5: 154045579-154045601	3108	TTTAGAGACGGGGTCTTGCTCT	Yes	No	No	No	No
hsa-mir-539	chr14: 100583418-100583440	3109	GGAGAAATTATCCTTGGTGTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-10b*	chr2: 176723341-176723363	3110	ACAGATTCGATTCTAGGGGAAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-612	chr11: 64968519-64968544	3111	GCTGGGCAGGGCTTCTGAGCTCCTT	Yes	No	No	No	No
hsa-mir-613	chr12: 12808909-12808929	3112	AGGAATGTTCCTTCTTTGCC	Yes	No	No	No	No
hsa-mir-1295	chr1: 169337502-169337523	3113	TCACCCAGATCTGCGGCCTAA	Yes	No	No	No	No
hsa-mir-196a	chr17: 44064892-44064914	3114	CCCAACAACATGAAACTACCTA	Yes	Yes	Yes	Yes	No
hsa-mir-196a	chr12: 52671812-52671834	3115	TAGGTAGTTTCATGTTGTTGGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-196b	chr7: 27175671-27175693	3116	CCCAACAACAGGAAACTACCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-296-3p	chr20: 56826075-56826097	3117	GGAGAGCCTCCACCCAACCCTC	Yes	Yes	No	Yes	Yes
hsa-mir-518d-3p	chr19: 58929994-58930015	3118	CAAAGCGCTTCCCTTTGGAGC	Yes	No	No	No	No
hsa-mir-1308	chrX: 21990211-21990229	3119	CCACTGAACCACCCATGC	No	No	No	No	No
hsa-mir-92a-2*	chrX: 133131278-133131300	3120	GTAATGCAACAAATCCCCACCC	Yes	Yes	No	No	No
hsa-mir-658	chr22: 36570239-36570264	3121	ACCAACGGACCTACTTCCCTCCGCC	No	No	No	No	No
hsa-mir-106b*	chr7: 99529560-99529582	3122	GCAGCAAGTACCCACAGTGCGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-374a*	chrX: 73423854-73423876	3123	AATTACAATACAATCTGATAAG	Yes	Yes	No	No	No
hsa-mir-595	chr7: 158018185-158018206	3124	AGACACACCACGGCACACTTC	Yes	No	No	No	No
hsa-mir-518d-5p	chr19: 58929957-58929979	3125	CTCTAGAGGGAAGCACTTTCTG	Yes	No	No	No	No
hsa-mir-590-5p	chr7: 73243478-73243500	3126	GAGCTTATTCATAAAAGTGCAG	Yes	Yes	No	No	No
hsa-mir-448	chrX: 113964342-113964364	3127	TTGCATATGTAGGATGTCCCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-326	chr11: 74723799-74723819	3128	CTGGAGGAAGGGCCCAGAGG	Yes	No	Yes	Yes	Yes
hsa-mir-325	chrX: 76142279-76142302	3129	ACACTTACTGGACACCTACTAGG	No	Yes	No	No	No
hsa-mir-632	chr17: 27701300-27701319	3130	GTGTCTGCTTCCTGTGGGA	Yes	Yes	No	No	No
hsa-mir-328	chr16: 65793730-65793752	3131	ACGGAAGGGCAGAGAGGGCCAG	Yes	No	Yes	Yes	Yes
hsa-mir-329	chr14: 100563240-100563262	3132	AACACACCTGGTTAACCTCTTT	Yes	Yes	No	No	No
hsa-mir-329	chr14: 100562923-100562945	3133	AACACACCTGGTTAACCTCTTT	Yes	Yes	Yes	No	No
hsa-mir-659	chr22: 36573645-36573667	3134	TGGGGACCCTCCCTGAACCAAG	No	No	No	No	No
hsa-mir-214*	chr1: 170374619-170374641	3135	GCACAGCAAGTGTAGACAGGCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-483-3p	chr11: 2111947-2111968	3136	AAGACGGGAGGAGAGGAGTGA	No	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-376a*	chr14: 100576877-100576899	3137	GTAGATTCTCCTTCTATGAGTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-218-1*	chr4: 20139062-20139084	3138	ATGGTTCCGTCAAGCACCATGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-302d*	chr4: 113788649-113788671	3139	GCAAGTGCCTCCATGTTAAAGT	Yes	Yes	Yes	Yes	No
hsa-mir-887	chr5: 15988337-15988359	3140	GTGAACGGGCGCCATCCCGAGG	No	Yes	No	No	No
hsa-mir-380*	chr14: 100561110-100561132	3141	TGGTTGACCATAGAACATGCGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-32*	chr9: 110848331-110848353	3142	AAATATCACACACACTAAATTG	Yes	Yes	Yes	Yes	No
hsa-mir-889	chr14: 100584038-100584059	3143	TTAATATCGGACAACCATTGT	Yes	Yes	Yes	No	No
hsa-mir-768-5p	chr16: 70349860-70349886	3144	ATCACTCCGTACTTTCATCCTCCAAC	Yes	Yes	No	No	No
hsa-mir-501-3p	chrX: 49661119-49661141	3145	AATGCACCCGGGCAAGGATTCT	Yes	No	No	No	No
hsa-mir-485-3p	chr14: 100591553-100591575	3146	GTCATACACGGCTCTCCTCTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1234	chr8: 145596285-145596307	3147	GTGGGGTGGGTGGTCAGGCCGA	Yes	Yes	No	No	No
hsa-mir-22*	chr17: 1563995-1564017	3148	TAAAGCTTGCCACTGAAGAACT	Yes	No	Yes	Yes	Yes
hsa-mir-125a-5p	chr19: 56888332-56888356	3149	TCCCTGAGACCCTTTAACCTGTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-643	chr19: 57476921-57476943	3150	ACTTGTATGCTAGCTCAGGTAG	Yes	No	No	No	No
hsa-mir-147	chr9: 122047083-122047103	3151	GCAGAAGCATTTCCACACAC	Yes	Yes	No	No	No
hsa-mir-144	chr17: 24212691-24212711	3152	AGTACATCATCTATACTGTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-145	chr5: 148790416-148790439	3153	GTCCAGTTTTCCCAGGAATCCCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-143	chr5: 148788733-148788754	3154	TGAGATGAAGCACTGTAGCTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-597	chr8: 9636606-9636628	3155	TGTGTCACTCGATGACCACTGT	Yes	No	No	No	No
hsa-mir-141	chr12: 6943578-6943600	3156	TAACACTGTCTGGTAAAGATGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-512-5p	chr19: 58864241-58864264	3157	CACTCAGCCTTGAGGGCACTTTC	Yes	No	No	No	No
hsa-mir-512-5p	chr19: 58861757-58861780	3158	CACTCAGCCTTGAGGGCACTTTC	Yes	No	No	No	No
hsa-mir-323-5p	chr14: 100561836-100561858	3159	AGGTGGTCCGTGGCGCGTTCGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-224	chrX: 150877758-150877779	3160	AACGGAACCACTAGTGACTTG	Yes	Yes	Yes	No	Yes
hsa-mir-223	chrX: 65155503-65155525	3161	TGTCAGTTTGTCAAATACCCCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-222	chrX: 45491385-45491406	3162	ACCCAGTAGCCAGATGTAGCT	No	Yes	Yes	Yes	Yes
hsa-mir-221	chrX: 45490551-45490574	3163	GAAACCCAGCAGACAATGTAGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-149	chr2: 241044104-241044127	3164	TCTGGCTCCGTGTCTTCACTCCC	Yes	Yes	Yes	Yes	No
hsa-mir-520a-3p	chr19: 58885998-58886020	3165	AAAGTGCTTCCCTTTGGACTGT	Yes	Yes	No	No	No
hsa-mir-548c-5p	chr12: 63302579-63302601	3166	AAAAGTAATTGCGGTTTTTGCC	Yes	No	No	No	No
hsa-mir-374b	chrX: 73355146-73355168	3167	CACTTAGCAGGTTGTATTATAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-26a	chr12: 56504707-56504729	3168	AGCCTATCCTGGATTACTTGAA	Yes	Yes	Yes	Yes	No
hsa-mir-26a	chr3: 37985907-37985929	3169	TTCAAGTAATCCAGGATAGGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-374a	chrX: 73423884-73423906	3170	CACTTATCAGGTTGTATTATAA	Yes	Yes	Yes	No	No
hsa-mir-1302	chr9: 99165698-99165719	3171	TTTAGCATAAGTATGTCCCAA	Yes	Yes	No	No	No
hsa-mir-1302	chr15: 100318229-100318250	3172	TTTAGCATAAGTATGTCCCAA	Yes	Yes	No	No	No
hsa-mir-1302	chr12: 111617269-111617290	3173	TTTAGCATAAGTATGTCCCAA	Yes	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-1302	chr8: 142665522-142865543	3174	TTTAGCATAAGTATGTCCCAA	Yes	Yes	No	No	No
hsa-mir-1302	chr2: 114057050-114057071	3175	TTTAGCATAAGTATGTCCCAA	Yes	Yes	No	No	No
hsa-mir-1302	chr1: 20300-20321	3176	TTGGGACATACTTATGCTAAA	Yes	Yes	No	No	No
hsa-mir-1302	chr7: 18133381-18133402	3177	TTTAGCATAAGTATGTCCCAA	Yes	No	No	No	No
hsa-mir-1302	chr19: 23044-23065	3178	TTGGGACATACTTATGCTAAA	Yes	Yes	No	No	No
hsa-mir-1302	chr2: 207842296-207842317	3179	TTTAGCATAAGTATGTCCCAA	No	Yes	No	No	No
hsa-mir-1302	chr9: 20215-20236	3180	TTGGGACATACTTATGCTAAA	Yes	Yes	No	No	No
hsa-mir-1302	chr20: 48664632-48664653	3181	TTTAGCATAAGTATGTCCCAA	No	No	No	No	No
hsa-mir-624*	chr14: 30553662-30553684	3182	TGAACACAAGGTACTGGTACTA	Yes	No	No	No	No
hsa-mir-619	chr12: 107754827-107754851	3183	ACTGGGCACAAACATGTCCAGGTC	Yes	No	No	No	No
hsa-mir-586	chr6: 45273448-45273470	3184	GGACCTAAAAATACAATGCATA	Yes	No	No	No	No
hsa-mir-587	chr6: 107338707-107338728	3185	TTTCCATAGGTGATGAGTCAC	Yes	No	No	No	No
hsa-mir-584	chr5: 148422128-148422150	3186	CTCAGTCCCAGGCAAACCATAA	Yes	Yes	No	No	No
hsa-mir-30d*	chr8: 135886303-135886325	3187	GCAGCAAACATCTGACTGAAAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-450a	chrX: 133502088-133502110	3188	ATATTAGGAACACATCGCAAAA	Yes	Yes	Yes	Yes	No
hsa-mir-450a	chrX: 133502259-133502281	3189	ATATTAGGAACACATCGCAAAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-583	chr5: 95440612-95440633	3190	CAAAGAGGAAGGTCCCATTAC	Yes	No	No	No	No
hsa-mir-580	chr5: 36183765-36183787	3191	CCTAATGATTCATCATTCTCAA	Yes	No	No	No	No
hsa-mir-581	chr5: 53283150-53283171	3192	ACTGATCTAGAGAACACAAGA	Yes	No	No	No	No
hsa-mir-129-3p	chr11: 43559575-43559597	3193	AAGCCCTTACCCCAAAAAGCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-331-5p	chr12: 94226351-94226373	3194	CTAGGTATGGTCCCAGGGATCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-665	chr14: 100411164-100411184	3195	ACCAGGAGGCTGAGGCCCCT	Yes	Yes	No	No	No
hsa-mir-664	chr1: 218440513-218440536	3196	TGTAGGCTGGGGATAAATGAATA	Yes	Yes	No	No	No
hsa-mir-663	chr20: 26136878-26136900	3197	GCGGTCCCGCGGCGCCCCGCCT	Yes	No	No	No	No
hsa-mir-662	chr16: 760243-760264	3198	TCCCACGTTGTGGCCCAGCAG	No	Yes	No	No	No
hsa-mir-588	chr6: 126847484-126847505	3199	TTGGCCACAATGGGTTAGAAC	Yes	No	No	No	No
hsa-mir-589	chr7: 5502029-5502051	3200	CTCAGAGCAGACGTGGTTCTCA	No	Yes	No	No	No
hsa-mir-220a	chrX: 122523693-122523714	3201	AAAGTGTCAGATACGGTGTGG	Yes	No	No	No	No
hsa-mir-220b	chr19: 6446968-6446989	3202	CCACCACCGTGTCTGACACTT	Yes	No	No	No	No
hsa-mir-371-3p	chr19: 58982781-58982804	3203	AAGTGCCGCCATCTTTTGAGTGT	Yes	No	No	No	No
hsa-mir-744	chr17: 11925950-11925972	3204	TGCGGGGCTAGGGCTAACAGCA	Yes	Yes	Yes	Yes	No
hsa-mir-934	chrX: 135460716-135460738	3205	TGTCTACTACTGGAGACACTGG	Yes	No	No	No	No
hsa-mir-628-5p	chr15: 53452480-53452502	3206	CCTCTAGTAAATATGTCAGCAT	Yes	Yes	Yes	No	No
hsa-mir-888	chrX: 144884039-144884060	3207	TGACTGACAGCTTTTTGAGTA	No	Yes	No	No	No
hsa-mir-126*	chr9: 138684888-138684909	3208	CATTATTACTTTTGGTACGCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-99b*	chr19: 56887720-56887742	3209	CAAGCTCGTGTCTGTGGGTCCG	Yes	Yes	No	Yes	Yes
hsa-mir-137	chr1: 98284234-98284257	3210	CTACGCGTATTCTTAAGCAATAA	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-138	chr14: 100420805-100420828	3211	ACTCCATTTGTTTTGATGATGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-149*	chr2: 241044145-241044166	3212	AGGGAGGGACGGGGGCTGTGC	Yes	Yes	Yes	No	No
hsa-mir-134	chr14: 100590783-100590805	3213	TGTGACTGGTTGACCAGAGGGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-138	chr16: 55449939-55449962	3214	AGCTGGTGTTGTGAATCAGGCCG	Yes	Yes	No	Yes	Yes
hsa-mir-138	chr3: 44130729-44130752	3215	AGCTGGTGTTGTGAATCAGGCCG	No	No	Yes	Yes	Yes
hsa-mir-1269	chr4: 66825202-66825224	3216	CTGGACTGAGCCGTGCTACTGG	No	No	No	No	No
hsa-mir-1268	chr15: 20014622-20014640	3217	CCCCCACCACCACGCCCG	No	No	No	No	No
hsa-mir-196a*	chr12: 52671849-52671871	3218	CGGCAACAAGAAACTGCCTGAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-20b*	chrX: 133131508-133131530	3219	CTGGAAGTGCCCATACTACAGT	Yes	No	No	No	No
hsa-mir-199a-3p	chr19: 10789104-10789126	3220	TAACCAATGTGCAGACTACTGT	Yes	Yes	Yes	Yes	No
hsa-mir-199a-3p	chr1: 170380316-170380338	3221	TAACCAATGTGCAGACTACTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1263	chr3: 165372004-165372026	3222	ACTCAGTATGCCAGGGTACCAT	Yes	No	No	No	No
hsa-mir-1262	chr1: 68421846-68421868	3223	ATCCTTCTACAAATTCACCCAT	Yes	Yes	No	No	No
hsa-mir-1261	chr11: 90241995-90242014	3224	AAGCCAAAGCCTTATCCAT	Yes	No	No	No	No
hsa-mir-1260	chr14: 76802326-76802344	3225	ATCCCACCTCTGCCACCA	No	Yes	No	No	No
hsa-mir-1267	chr13: 106981565-106981586	3226	TGGGGATTACACTTCAACAGG	Yes	No	No	No	No
hsa-mir-151-5p	chr8: 141811903-141811924	3227	ACTAGACTGTGAGCTCCTCGA	Yes	Yes	Yes	No	No
hsa-mir-1265	chr10: 14518593-14518615	3228	CAGGATGTGGTCAAGTGTTGTT	Yes	No	No	No	No
hsa-mir-1264	chrX: 113793426-113793449	3229	CAAGTCTTATTTGAGCACCTGTT	Yes	Yes	Yes	No	No
hsa-mir-125b-2*	chr21: 16884480-16884502	3230	TCACAAGTCAGGCTCTTGGGAC	Yes	Yes	Yes	No	Yes
hsa-mir-33a*	chr22: 40626938-40626960	3231	CAATGTTTCCACAGTGCATCAC	Yes	No	No	Yes	Yes
hsa-mir-339-5p	chr7: 1029151-1029174	3232	CGTGAGCTCCTGGAGGACAGGGA	Yes	Yes	No	Yes	No
hsa-mir-708*	chr11: 78790723-78790745	3233	CTAGAAGCTCACAGTCTAGTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-1255a	chr4: 102470544-102470567	3234	AATCTACTTTCTTTGCTCATCCT	No	No	No	No	No
hsa-mir-1255b	chr4: 36104421-36104443	3235	AACCACTTTCTTTGCTCATCCG	No	No	No	No	No
hsa-mir-1255b	chr1: 166234526-166234548	3236	CGGATGAGCAAAGAAAGTGGTT	Yes	No	No	No	No
hsa-mir-7-1*	chr9: 85774505-85774527	3237	TATGGCAGACTGTGATTTGTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-199b-3p	chr9: 130046844-130046866	3238	TAACCAATGTGCAGACTACTGT	Yes	Yes	Yes	Yes	No
hsa-mir-641	chr19: 45480349-45480373	3239	GAGGTGACTCTATCCTATGTCTTT	No	No	No	No	No
hsa-mir-193a-3p	chr17: 26911181-26911203	3240	AACTGGCCTACAAAGTCCCAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-186*	chr1: 71305912-71305934	3241	CCCAAAAAATTCACCTTTGGGC	Yes	No	Yes	No	Yes
hsa-mir-139-5p	chr11: 72003794-72003816	3242	CTGGAGACACGTGCACTGTAGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-671-5p	chr7: 150566467-150566490	3243	AGGAAGCCCTGGAGGGGCTGGAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-582-3p	chr5: 59035212-59035234	3244	GGTTCAGTTGTTCAACCAGTTA	Yes	Yes	No	No	No
hsa-mir-548d-5p	chr17: 62898117-62898139	3245	GGCAAAAACCACAATTACTTTT	Yes	No	No	No	No
hsa-mir-548d-5p	chr8: 124429505-124429527	3246	GGCAAAAACCACAATTACTTTT	No	No	No	No	No
hsa-mir-130b*	chr22: 20337604-20337625	3247	ACTCTTTCCCTGTTGCACTAC	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-let-7f-1*	chr9: 95978511-95978533	3248	CTATACAATCTATTGCCTTCCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-767-3p	chrX: 151312574-151312597	3249	AGAAACCATGGGGTATGAGCAGA	No	Yes	No	No	No
hsa-mir-363	chrX: 133131077-133131099	3250	TACAGATGGATACCGTGCAATT	No	Yes	Yes	Yes	Yes
hsa-mir-32	chr9: 110848372-110848394	3251	TGCAACTTAGTAATGTGCAATA	Yes	Yes	Yes	Yes	Yes
hsa-mir-31	chr9: 21502156-21502177	3252	AGCTATGCCAGCATCTTGCCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-525-3p	chr19: 58892649-58892671	3253	GAAGGCGCTTCCCTTTAGAGCG	Yes	No	No	No	No
hsa-mir-181d	chr19: 13846723-13846746	3254	AACATTCATTGTTGTCGGTGGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-568	chr3: 115518071-115518091	3255	GTGTGTATACATTTATACAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-548b-5p	chr6: 119431961-119431983	3256	GGCCAAAACCACAATTACTTTT	No	No	No	No	No
hsa-mir-559	chr2: 47458332-47458353	3257	TAAAGTAAATATGCACCAAAA	Yes	No	No	No	No
hsa-mir-559	chr2: 47458372-47458393	3258	TTTTGGTGCATATTTACTTTA	Yes	No	No	No	No
hsa-mir-181a	chr9: 126494579-126494602	3259	AACATTCAACGCTGTCGGTGAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-181a	chr1: 197094859-197094882	3260	ACTCACCGACAGCGTTGAATGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-181b	chr9: 126495824-126495847	3261	AACATTCATTGCTGTCGGTGGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-181b	chr1: 197094676-197094699	3262	ACCCACCGACAGCAATGAATGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-181c	chr19: 13846538-13846560	3263	AACATTCAACCTGTCGGTGAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-34b*	chr11: 110888884-110888907	3264	TAGGCAGTGTCATTAGCTGATTG	Yes	Yes	No	No	No
hsa-mir-188-5p	chrX: 49654862-49654883	3265	CATCCCTTGCATGGTGGAGGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-367	chr4: 113788481-113788503	3266	TCACCATTGCTAAAGTGCAATT	Yes	Yes	Yes	Yes	No
hsa-mir-365	chr17: 26926609-26926631	3267	TAATGCCCCTAAAAATCCTTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-365	chr16: 14310697-14310719	3268	TAATGCCCCTAAAAATCCTTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-449b	chr5: 54502290-54502312	3269	GCCAGCTAACAATACACTGCCT	Yes	Yes	Yes	No	No
hsa-mir-29a*	chr7: 130212084-130212106	3270	CTGAACACCAAAAGAAATCAGT	No	Yes	Yes	Yes	Yes
hsa-let-7c*	chr21: 16834050-16834072	3271	TAGAGTTACACCCTGGGAGTTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-558	chr2: 32610783-32610802	3272	TGAGCTGCTGTACCAAAAT	Yes	Yes	No	No	No
hsa-mir-10a*	chr17: 44012224-44012246	3273	TATTCCCCTAGATACGAATTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-518e*	chr19: 58924918-58924940	3274	CTCTAGAGGGAAGCGCTTTCTG	Yes	No	No	No	No
hsa-mir-561	chr2: 188870523-188870545	3275	CAAAGTTTAAGATCCTTGAAGT	Yes	No	No	No	No
hsa-mir-562	chr2: 232745666-232745686	3276	AAAGTAGCTGTACCATTTGC	Yes	Yes	No	No	No
hsa-mir-563	chr3: 15890332-15890351	3277	AGGTTGACATACGTTTCCC	No	No	No	No	No
hsa-mir-361-5p	chrX: 85045341-85045363	3278	GTACCCCTGGAGATTCTGATAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-566	chr3: 50185777-50185796	3279	GGGCGCCTGTGATCCCAAC	Yes	No	No	No	No
hsa-mir-567	chr3: 113314352-113314375	3280	AGTATGTTCTTCCAGGACAGAAC	Yes	No	No	No	No
hsa-mir-642	chr19: 50870040-50870062	3281	GTCCCTCTCCAAATGTGTCTTG	Yes	Yes	No	No	No
hsa-mir-192*	chr11: 64415206-64415228	3282	CTGTGACCTATGGAATTGGCAG	Yes	Yes	Yes	Yes	No
hsa-mir-92a-1*	chr13: 90801578-90801601	3283	AGGTTGGGATCGGTTGCAATGCT	Yes	No	Yes	No	No
hsa-mir-27a*	chr19: 13808300-13808322	3284	TGCTCACAAGCAGCTAAGCCCT	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-564	chr3: 44878398-44878417	3285	AGGCACGGTGTCAGCAGGC	Yes	No	No	No	No
hsa-mir-106a*	chrX: 133131903-133131925	3286	GTAAGAAGTGCTTACATTGCAG	No	No	No	No	No
hsa-mir-26a-1*	chr3: 37985946-37985968	3287	CCTATTCTTGGTTACTTGCACG	Yes	Yes	Yes	Yes	Yes
hsa-mir-498	chr19: 58869295-58869318	3288	TTTCAAGCCAGGGGGCGTTTTTC	Yes	Yes	No	No	No
hsa-mir-454*	chr17: 54569970-54569992	3289	GCAGAGACAATATTGATAGGGT	Yes	Yes	No	No	No
hsa-mir-502-5p	chrX: 49665960-49665981	3290	ATCCTTGCTATCTGGGTGCTA	Yes	Yes	Yes	No	No
hsa-mir-218-2*	chr5: 168127750-168127772	3291	CGCGGTGCTTGACAGAACCATG	Yes	Yes	Yes	Yes	Yes
hsa-mir-30c-2*	chr6: 72143387-72143409	3292	AGAGTAAACAGCCTTCTCCCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-526b*	chr19: 58889508-58889530	3293	GAAAGTGCTTCCTTTTAGAGGC	Yes	Yes	No	No	No
hsa-mir-542-5p	chrX: 133503095-133503118	3294	TCTCGTGACATGATGATCCCCGA	No	Yes	Yes	Yes	Yes
hsa-mir-433	chr14: 100418038-100418060	3295	ATCATGATGGGCTCCTCGGTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-27a	chr19: 13808260-13808281	3296	GCGGAACTTAGCCACTGTGAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-27b	chr9: 96887607-96887628	3297	TTCACAGTGGCTAAGTTCTGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-330-3p	chr19: 50834106-50834129	3298	TCTCTGCAGGCCGTGTGCTTTGC	Yes	Yes	Yes	No	No
hsa-mir-431	chr14: 100417115-100417136	3299	TGTCTTGCAGGCCGTCATGCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-520c-5p	chr19: 58902533-58902555	3300	CTCTAGAGGGAAGCACTTTCTG	Yes	No	No	No	No
hsa-mir-708	chr11: 78790768-78790791	3301	CCCAGCTAGATTGTAAGCTCCTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-17*	chr13: 90800909-90800931	3302	ACTGCAGTGAAGGCACTTGTAG	Yes	No	Yes	No	No
hsa-mir-1197	chr14: 100561709-100561730	3303	TAGGACACATGGTCTACTTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-548a-5p	chr8: 105565823-105565845	3304	GGTAAAACTCGCAATTACTTTT	No	Yes	No	No	No
hsa-mir-1248	chr3: 187987157-187987184	3305	ACCTTCTTGTATAAGCACTGTGCTAAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-208b	chr14: 22957045-22957067	3306	ACAAACCTTTTGTTCGTCTTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-208a	chr14: 22927650-22927672	3307	ACAAGCTTTTTGCTCGTCTTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-499-5p	chr20: 33041871-33041892	3308	TTAAGACTTGCAGTGATGTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-29b-1*	chr7: 130212805-130212829	3309	TCTAAACCACCATATGAAACCAGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-378*	chr5: 149092584-149092606	3310	CTCCTGACTCCAGGTCCTGTGT	Yes	Yes	Yes	No	Yes
hsa-mir-16-1*	chr13: 49521121-49521143	3311	TCAGCAGCACAGTTAATACTGG	Yes	Yes	Yes	No	No
hsa-mir-338-3p	chr17: 76714281-76714303	3312	CAACAAAATCACTGATGCTGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-145*	chr5: 148790454-148790476	3313	GGATTCCTGGAAATACTGTTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-337-3p	chr14: 100410642-100410664	3314	CTCCTATATGATGCCTTTCTTC	Yes	Yes	No	Yes	Yes
hsa-mir-593*	chr7: 127509163-127509188	3315	AGGCACCAGCCAGGCATTGCTCAGC	Yes	No	No	No	No
hsa-mir-130a	chr11: 57165300-57165322	3316	CAGTGCAATGTTAAAAGGGCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-627	chr15: 40279119-40279141	3317	TCCTCTTTTCTTAGAGACTCAC	Yes	Yes	No	No	No
hsa-mir-892b	chrX: 144886417-144886439	3318	TCTACCCAGAAAGGAGCCAGTG	Yes	Yes	No	No	No
hsa-mir-892a	chrX: 144885888-144885909	3319	CTACGCAGAAAGGACACAGTG	Yes	Yes	No	No	No
hsa-mir-548n	chr7: 34946940-34946962	3320	ACAAAATCCACAATTACTTTTG	Yes	No	No	No	No
hsa-mir-768-3p	chr16: 70349813-70349841	3321	GTCAGCAGTTTGAGTGTCAGCATTGTGA	No	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-630	chr15: 70666671-70666693	3322	AGTATTCTGTACCAGGGAAGGT	Yes	No	No	No	No
hsa-mir-631	chr15: 73433043-73433064	3323	GCTGAGGTCTGGGCCAGGTCT	No	Yes	No	No	No
hsa-mir-1287	chr10: 100145017-100145039	3324	GACTCGAACCACTGATCCAGCA	No	No	No	No	No
hsa-mir-633	chr17: 58375367-58375390	3325	CTAATAGTATCTACCACAATAAA	Yes	Yes	No	No	No
hsa-mir-1281	chr22: 39818494-39818511	3326	TCGCCTCCTCCTCTCCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-635	chr17: 63932246-63932269	3327	GGACATTGTTTCAGTGCCCAAGT	Yes	No	No	No	No
hsa-mir-636	chr17: 72244142-72244165	3328	TGCGGGCGGGACGAGCAAGCACA	No	No	No	No	No
hsa-mir-637	chr19: 3912426-3912450	3329	ACGCAGAGCCCGAAAGCCCCCAGT	Yes	No	No	No	No
hsa-mir-638	chr19: 10690094-10690119	3330	AGGGATCGCGGGCGGGTGGCGGCCT	No	No	No	No	No
hsa-mir-639	chr19: 14501414-14501437	3331	ATCGCTGCGGTTGCGAGCGCTGT	No	No	No	No	No
hsa-mir-1289	chr5: 132791205-132791228	3332	AAAATGCAGATTCCTGGACTCCA	Yes	Yes	No	No	No
hsa-mir-1289	chr20: 33505225-33505248	3333	AAAATGCAGATTCCTGGACTCCA	Yes	Yes	No	No	No
hsa-mir-1288	chr17: 16126096-16126117	3334	TGGACTGCCCTGATCTGGAGA	Yes	Yes	No	No	No
hsa-mir-548j	chr22: 25281239-25281261	3335	ACCAAAGACCGCAATTACTTTT	No	No	No	No	No
hsa-mir-518b	chr19: 58897852-58897874	3336	CAAAGCGCTCCCCTTTAGAGGT	Yes	No	No	No	No
hsa-let-7c	chr21: 16834028-16834050	3337	TGAGGTAGTAGGTTGTATGGTT	Yes	Yes	Yes	Yes	Yes
hsa-let-7a	chr22: 44887295-44887317	3338	TGAGGTAGTAGGTTGTATAGTT	Yes	Yes	Yes	No	No
hsa-let-7a	chr11: 121522485-121522507	3339	AACTATACAACCTACTACCTCA	Yes	Yes	Yes	Yes	Yes
hsa-let-7a	chr9: 95978064-95978086	3340	TGAGGTAGTAGGTTGTATAGTT	Yes	Yes	Yes	Yes	Yes
hsa-let-7f	chrX: 53600931-53600953	3341	AACTATACAATCTACTACCTCA	Yes	Yes	Yes	Yes	Yes
hsa-let-7f	chr9: 95978455-95978477	3342	TGAGGTAGTAGATTGTATAGTT	Yes	Yes	Yes	Yes	Yes
hsa-let-7g	chr3: 52277391-52277413	3343	AACTGTACAAACTACTACCTCA	Yes	Yes	Yes	Yes	No
hsa-let-7d	chr9: 95980943-95980965	3344	AGAGGTAGTAGGTTGCATAGTT	Yes	Yes	Yes	Yes	Yes
hsa-let-7e	chr19: 56887857-56887879	3345	TGAGGTAGGAGGTTGTATAGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-516a-3p	chr19: 58956258-58956276	3346	TGCTTCCTTTCAGAGGGT	Yes	No	No	No	No
hsa-mir-516a-3p	chr19: 58951866-58951884	3347	TGCTTCCTTTCAGAGGGT	Yes	No	No	No	No
hsa-let-7i	chr12: 61283737-61283759	3348	TGAGGTAGTAGTTTGTGCTGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-503	chrX: 133508066-133508089	3349	CTGCAGAACTGTTCCCGCTGCTA	Yes	Yes	No	No	No
hsa-mir-494	chr14: 100565770-100565792	3350	TGAAACATACACGGGAAACCTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-519b-3p	chr19: 58890328-58890350	3351	AAAGTGCATCCTTTTAGAGGTT	Yes	No	No	No	No
hsa-mir-1207-5p	chr8: 129130586-129130607	3352	TGGCAGGGAGGCTGGGAGGGG	Yes	No	No	No	No
hsa-let-7b*	chr22: 44888288-44888310	3353	CTATACAACCTACTGCCTTCCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-181a*	chr1: 197094820-197094842	3354	GGTACAATCAACGGTCGATGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-548e	chr10: 112738725-112738747	3355	AAAAACTGAGACTACTTTTGCA	No	No	No	No	No
hsa-mir-125b	chr21: 16884443-16884465	3356	TCCCTGAGACCCTAACTTGTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-125b	chr11: 121475726-121475748	3357	TCACAAGTTAGGGTCTCAGGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-9*	chr1: 154656769-154656791	3358	ACTTTCGGTTATCTAGCTTTAT	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-9*	chr5: 87998439-87998461	3359	ACTTTCGGTTATCTAGCTTTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-9*	chr15: 87712305-87712327	3360	ATAAAGCTAGATAACCGAAAGT	Yes	No	Yes	Yes	Yes
hsa-mir-301b	chr22: 20337313-20337336	3361	CAGTGCAATGATATTGTCAAAGC	Yes	Yes	Yes	No	No
hsa-mir-301a	chr17: 54583291-54583314	3362	GCTTTGACAATACTATTGCACTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-98	chrX: 53599984-53600006	3363	AACAATACAACTTACTACCTCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-550*	chr7: 30295994-30296016	3364	TGTCTTACTCCCTCAGGCACAT	Yes	No	No	No	No
hsa-mir-550*	chr7: 32739177-32739199	3365	TGTCTTACTCCCTCAGGCACAT	Yes	No	No	No	No
hsa-mir-505*	chrX: 138834020-138834042	3366	ACATCAATACTTCCTGGCTCCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-142-3p	chr17: 53763604-53763627	3367	TCCATAAAGTAGGAAACACTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-487a	chr14: 100588583-100588605	3368	AATCATACAGGGACATCCAGTT	Yes	Yes	Yes	No	No
hsa-mir-93	chr7: 99529373-99529396	3369	CTACCTGCACGAACAGCACTTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-95	chr4: 8057938-8057960	3370	TGCTCAATAAATACCCGTTGAA	Yes	Yes	Yes	No	No
hsa-mir-96	chr7: 129201814-129201837	3371	AGCAAAAATGTGCTAGTGCCAAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-200c*	chr12: 6943126-6943148	3372	CGTCTTACCCAGCAGTGTTTGG	No	Yes	Yes	Yes	Yes
hsa-mir-527	chr19: 58949096-58949116	3373	CTGCAAAGGGAAGCCCTTTC	Yes	No	No	No	No
hsa-mir-521	chr19: 58943754-58943776	3374	AACGCACTTCCCTTTAGAGTGT	Yes	No	No	No	No
hsa-mir-521	chr19: 58911712-58911734	3375	AACGCACTTCCCTTTAGAGTGT	Yes	No	No	No	No
hsa-mir-127-3p	chr14: 100419124-100419146	3376	TCGGATCCGTCTGAGCTTGGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-523	chr19: 58893502-58893525	3377	GAACGCGCTTCCCTATAGAGGGT	Yes	No	No	No	No
hsa-mir-135b	chr1: 203684111-203684134	3378	TCACATAGGAATGAAAAGCCATA	Yes	Yes	Yes	Yes	Yes
hsa-mir-135a	chr3: 52303325-52303348	3379	TCACATAGGAATAAAAAGCCATA	Yes	Yes	Yes	Yes	Yes
hsa-mir-135a	chr12: 96481742-96481765	3380	TATGGCTTTTTATTCCTATGTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-146b-5p	chr10: 104186266-104186288	3381	TGAGAACTGAATTCCATAGGCT	Yes	No	Yes	Yes	Yes
hsa-mir-509-3p	chrX: 146148871-146148893	3382	CTACCCACAGACGTACCAATCA	No	No	No	No	No
hsa-mir-509-3p	chrX: 146147984-146148006	3383	CTACCCACAGACGTACCAATCA	No	No	No	No	No
hsa-mir-509-3p	chrX: 146149759-146149781	3384	CTACCCACAGACGTACCAATCA	No	No	No	No	No
hsa-mir-33b*	chr17: 17657895-17657917	3385	GGGCTGCACTGCCGAGGCACTG	Yes	Yes	Yes	No	No
hsa-mir-744*	chr17: 11926007-11926029	3386	CTGTTGCCACTAACCTCAACCT	Yes	Yes	Yes	Yes	No
hsa-mir-1274a	chr5: 41511503-41511521	3387	GTCCCTGTTCAGGCGCCA	Yes	No	No	No	No
hsa-mir-532-5p	chrX: 49654512-49654534	3388	CATGCCTTGAGTGTAGGACCGT	Yes	Yes	Yes	Yes	No
hsa-mir-1274b	chr19: 62716222-62716239	3389	TGGCGCCCGAACAGGGA	Yes	No	No	No	No
hsa-let-7i*	chr12: 61283793-61283815	3390	CTGCGCAAGCTACTGCCTTGCT	Yes	Yes	No	Yes	Yes
hsa-mir-132	chr17: 1899972-1899994	3391	CGACCATGGCTGTAGACTGTTA	No	Yes	Yes	Yes	Yes
hsa-mir-20a*	chr13: 90801362-90801384	3392	ACTGCATTATGAGCACTTAAAG	Yes	No	Yes	No	No
hsa-mir-23a	chr19: 13808408-13808429	3393	GGAAATCCCTGGCAATGTGAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-23b	chr9: 96887367-96887388	3394	ATCACATTGCCAGGGATTACC	Yes	Yes	Yes	Yes	Yes
hsa-mir-542-3p	chrX: 133503059-133503081	3395	TTTCAGTTATCAATCTGTCACA	No	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-148b	chr12: 53017328-53017350	3396	TCAGTGCATCACAGAACTTTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-148a	chr7: 25956066-25956088	3397	ACAAAGTTCTGTAGTGCACTGA	Yes	Yes	Yes	Yes	No
hsa-mir-886-3p	chr5: 135444086-135444107	3398	AAGGGTCAGTAAGCACCCGCG	Yes	Yes	No	No	No
hsa-mir-24	chr19: 13808102-13808124	3399	CTGTTCCTGCTGAACTGAGCCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-24	chr9: 96888166-96888188	3400	TGGCTCAGTTCAGCAGGAACAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-330-5p	chr19: 50834146-50834168	3401	GCCTAAGACACAGGCCCAGAGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-497*	chr17: 6861980-6862002	3402	TCTAACACCACAGTGTGGTTTG	Yes	Yes	No	Yes	Yes
hsa-mir-451	chr17: 24212546-24212568	3403	AACTCAGTAATGGTAACGGTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-452	chrX: 150878805-150878827	3404	TCAGTTTCCTCTGCAAACAGTT	Yes	Yes	Yes	Yes	No
hsa-mir-340*	chr5: 179374924-179374946	3405	GCTATAAAGTAACTGAGACGGA	Yes	Yes	Yes	Yes	No
hsa-mir-454	chr17: 54569929-54569952	3406	ACCCTATAAGCAATATTGCACTA	Yes	Yes	Yes	No	No
hsa-mir-890	chrX: 144883530-144883551	3407	CAACTGATGCCTTTCCAAGTA	Yes	No	No	No	No
hsa-mir-135b*	chr1: 203684073-203684095	3408	CCCATGGCTTTTAGCCCTACAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-875-3p	chr8: 100618200-100618221	3409	CACAACCTCAGTGTTTCCAGG	No	No	No	No	No
hsa-mir-541*	chr14: 100600593-100600618	3410	AAAGGATTCTGCTGTCGGTCCCACT	No	Yes	No	No	No
hsa-mir-26a-2*	chr12: 56504669-56504691	3411	GAAACAAGTAATCAAGAATAGG	Yes	Yes	Yes	No	No
hsa-mir-302c*	chr4: 113789006-113789028	3412	CAGCAGGTACCCCCATGTTAAA	Yes	Yes	Yes	No	No
hsa-mir-885-3p	chr3: 10411182-10411204	3413	TATCCACTACACCCCGCTGCCT	Yes	Yes	Yes	No	No
hsa-mir-450b-3p	chrX: 133501889-133501911	3414	TATGGATGCAAAATGATCCCAA	Yes	Yes	No	No	No
hsa-mir-296-5p	chr20: 56826110-56826131	3415	ACAGGATTGAGGGGGGGCCCT	Yes	Yes	No	Yes	Yes
hsa-mir-221*	chrX: 45490592-45490614	3416	AAATCTACATTGTATGCCAGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-100*	chr11: 121528157-121528179	3417	CATACCTATAGATACAAGCTTG	Yes	No	No	No	No
hsa-mir-302b*	chr4: 113789130-113789152	3418	GAAAGCACTTCCATGTTAAAGT	Yes	Yes	No	No	No
hsa-mir-487b	chr14: 100582594-100582616	3419	AATCGTACAGGGTCATCCACTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-607	chr10: 98578430-98578451	3420	GTTATAGATCTGGATTTGAAC	No	No	No	No	No
hsa-mir-625*	chr14: 65007623-65007645	3421	GACTATAGAACTTTCCCCCTCA	Yes	No	No	No	No
hsa-mir-625*	chr14: 65007584-65007606	3422	TGAGGGGGAAAGTTCTATAGTC	Yes	No	No	No	No
hsa-mir-141*	chr12: 6943536-6943558	3423	CATCTTCCAGTACAGTGTTGGA	Yes	Yes	Yes	No	No
hsa-mir-606	chr10: 76982281-76982302	3424	AAACTACTGAAAATCAAAGAT	No	No	No	No	No
hsa-mir-155*	chr21: 25868204-25868226	3425	CTCCTACATATTAGCATTAACA	Yes	No	No	No	No
hsa-mir-146a	chr5: 159844956-159844978	3426	TGAGAACTGAATTCCATGGGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1183	chr7: 21477247-21477274	3427	CACTGTAGGTGATGGTGAGAGTGGGCA	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

(2) Conservation of seed sequence

miRNA identified in B cell libraries and deposited in miRBase database				Conservation				
ID	Genomic Coordinates	Seq ID No.	Sequence	Chimp	Monkey	Dog	Mouse	Rat
CU-1001	chr11: 121522485-121522507	3428	TGAGGTAGTAGGTTGTATAGTT	Yes	Yes	Yes	Yes	Yes
CU-1001	chr9: 95978064-95978086	3429	TGAGGTAGTAGGTTGTATAGTT	Yes	Yes	Yes	Yes	Yes
CU-1003	chr22: 44888234-44888256	3430	TGAGGTAGTAGGTTGTGTGGTT	Yes	Yes	Yes	Yes	Yes
CU-1004	chr9: 95980943-95980965	3431	AGAGGTAGTAGGTTGCATAGTT	Yes	Yes	Yes	Yes	Yes
CU-1005	chr19: 56887857-56887879	3432	TGAGGTAGGAGGTTGTATAGTT	Yes	Yes	Yes	Yes	Yes
CU-1006	chrX: 53600931-53600953	3433	TGAGGTAGTAGATTGTATAGTT	Yes	Yes	Yes	Yes	Yes
CU-1007	chr3: 52277391-52277413	3434	TGAGGTAGTAGTTTGTACAGTT	Yes	Yes	Yes	Yes	No
CU-1008	chr12: 61283737-61283759	3435	TGAGGTAGTAGTTTGTGCTGTT	Yes	Yes	Yes	Yes	Yes
CU-1009	chr1: 65296711-65296733	3436	TACAGTACTGTGATAACTGAAG	Yes	Yes	Yes	Yes	Yes
CU-1009	chr9: 4840344-4840366	3437	TACAGTACTGTGATAACTGAAG	Yes	Yes	Yes	Yes	Yes
CU-1010	chr20: 3846187-3846210	3438	AGCAGCATTGTACAGGGCTATGA	Yes	Yes	Yes	Yes	Yes
CU-1011	chr7: 99529562-99529582	3439	CCGCACTGTGGGTACTTGCT	Yes	Yes	Yes	Yes	Yes
CU-1012	chr7: 99529601-99529622	3440	TAAAGTGCTGACAGTGCAGAT	Yes	Yes	Yes	Yes	Yes
CU-1014	chr19: 56888332-56888356	3441	TCCCTGAGACCCTTTAACCTGTGA	Yes	Yes	Yes	Yes	Yes
CU-1015	chr21: 16884443-16884465	3442	TCCCTGAGACCCTAACTTGTGA	Yes	Yes	Yes	Yes	Yes
CU-1016	chr6: 131417431-131417449	3443	GTCCCTGTTCGGGCGCCA	Yes	Yes	No	No	No
CU-1016	chr19: 62716222-62716240	3444	GTCCCTGTTCGGGCGCCA	Yes	No	No	No	No
CU-1017	chr1: 150066843-150066860	3445	GTGGGGGAGAGGCTGTA	Yes	No	No	No	No
CU-1018	chr7: 35602718-35602735	3446	TCCCACCGCTGCCACCA	No	No	No	No	No
CU-1018	chr2: 72555764-72555781	3447	TCCCACCGCTGCCACCA	No	No	No	No	No
CU-1018	chrX: 55565708-55565725	3448	TCCCACCGCTGCCACCA	No	No	No	No	No
CU-1018	chr1: 225154598-225154615	3449	TCCCACCGCTGCCACCA	Yes	No	No	No	No
CU-1018	chr11: 95714259-95714276	3450	TCCCACCGCTGCCACCA	Yes	Yes	Yes	No	No
CU-1018	chr7: 5368308-5368325	3451	TCCCACCGCTGCCACCA	Yes	Yes	No	No	No
CU-1018	chr6: 140362954-140362971	3452	TCCCACCGCTGCCACCA	Yes	No	No	No	No
CU-1019	chr2: 136139485-136139506	3453	TCACAGTGAACCGGTCTCTTT	Yes	Yes	Yes	Yes	Yes
CU-1021	chr1: 159701881-159701904	3454	GCATGGGTGGTTCAGTGGTAGAA	Yes	Yes	No	No	No
CU-1021	chr1: 159694521-159694544	3455	GCATGGGTGGTTCAGTGGTAGAA	Yes	Yes	No	No	No
CU-1021	chr1: 159687090-159687113	3456	GCATGGGTGGTTCAGTGGTAGAA	Yes	Yes	No	No	No
CU-1021	chr21: 17749025-17749048	3457	GCATGGGTGGTTCAGTGGTAGAA	Yes	Yes	No	No	No
CU-1021	chr1: 159679717-159679740	3458	GCATGGGTGGTTCAGTGGTAGAA	No	Yes	Yes	No	No
CU-1022	chr22: 20337642-20337664	3459	CAGTGCAATGATGAAAGGGCAT	Yes	Yes	Yes	Yes	Yes
CU-1023	chr3: 44130729-44130753	3460	AGCTGGTGTTGTGAATCAGGCCGT	No	No	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1024	chr16: 68524545-68524567	3461	TACCACAGGGTAGAACCACGGA	Yes	Yes	Yes	Yes	Yes
CU-1025	chr16: 68524506-68524527	3462	CAGTGGTTTTACCCTATGGTA	Yes	Yes	Yes	Yes	Yes
CU-1026	chr17: 53763604-53763627	3463	TGTAGTGTTTCCTACTTTATGGA	Yes	Yes	Yes	Yes	Yes
CU-1027	chr5: 159844956-159844978	3464	TGAGAACTGAATTCCATGGGTT	Yes	Yes	Yes	Yes	Yes
CU-1028	chr10: 104186266-104186290	3465	TGAGAACTGAATTCCATAGGCTGT	Yes	No	Yes	Yes	Yes
CU-1029	chr19: 54695901-54695922	3466	TCTCCCAACCCTTGTACCAGT	Yes	Yes	Yes	Yes	Yes
CU-1030	chr17: 17715007-17715028	3467	CTAGACTGAAGCTCCTTGAGG	Yes	Yes	No	No	No
CU-1030	chr7: 150838585-150838606	3468	CTAGACTGAAGCTCCTTGAGG	Yes	No	No	No	No
CU-1031	chrX: 53425327-53425349	3469	TCGAGGAGCTCACAGTCTAGTA	Yes	Yes	No	No	No
CU-1031	chr8: 141811902-141811924	3470	TCGAGGAGCTCACAGTCTAGTA	Yes	Yes	Yes	No	No
CU-1032	chr21: 25868165-25868188	3471	TTAATGCTAATCGTGATAGGGGT	Yes	Yes	Yes	Yes	No
CU-1033	chr13: 49521304-49521325	3472	TAGCAGCACATAATGGTTTGT	Yes	Yes	Yes	Yes	No
CU-1033	chr7: 3516339-3516360	3473	TAGCAGCACATAATGGTTTGT	Yes	Yes	No	No	No
CU-1034	chr3: 161605126-161605147	3474	CGAATCATTATTTGCTGCTCT	Yes	Yes	Yes	Yes	Yes
CU-1035	chr3: 161605088-161605110	3475	TAGCAGCACATCATGGTTTACA	Yes	Yes	Yes	Yes	Yes
CU-1037	chr3: 161605235-161605257	3476	TAGCAGCACGTAAATATTGGCG	Yes	Yes	Yes	Yes	Yes
CU-1037	chr13: 49521163-49521185	3477	TAGCAGCACGTAAATATTGGCG	Yes	Yes	Yes	Yes	No
CU-1038	chr13: 90800909-90800931	3478	ACTGCAGTGAAGGCACTTGTAG	Yes	No	Yes	Yes	Yes
CU-1039	chr13: 90800872-90800895	3479	CAAAGTGCTTACAGTGCAGGTAG	Yes	Yes	Yes	Yes	Yes
CU-1040	chr1: 197094822-197094842	3480	ACCATCGACCGTTGATTGTA	Yes	Yes	Yes	Yes	Yes
CU-1042	chr9: 126494579-126494603	3481	AACATTCAACGCTGTCGGTGAGTT	Yes	Yes	Yes	Yes	Yes
CU-1042	chr1: 197094858-197094882	3482	AACATTCAACGCTGTCGGTGAGTT	Yes	Yes	Yes	Yes	Yes
CU-1044	chr13: 90801051-90801073	3483	ACTGCCCTAAGTGCTCCTTCTG	Yes	No	Yes	Yes	Yes
CU-1045	chr13: 90801010-90801032	3484	TAAGGTGCATCTAGTGCAGATA	Yes	Yes	Yes	Yes	Yes
CU-1046	chr3: 49033108-49033131	3485	CAACGGAATCCCAAAAGCAGCTG	Yes	Yes	Yes	Yes	Yes
CU-1047	chr11: 64415251-64415271	3486	CTGACCTATGAATTGACAGC	Yes	Yes	Yes	Yes	Yes
CU-1050	chr16: 14305374-14305396	3487	AACTGGCCCTCAAAGTCCCGCT	Yes	Yes	Yes	Yes	No
CU-1052	chr17: 6861708-6861730	3488	TAGCAGCACAGAAATATTGGCA	Yes	Yes	Yes	Yes	Yes
CU-1053	chr1: 109943084-109943105	3489	TTCACCACCTTCTCCACCCAG	Yes	Yes	Yes	No	No
CU-1054	chr1: 170380354-170380377	3490	CCCAGTGTTCAGACTACCTGTTC	Yes	Yes	Yes	Yes	Yes
CU-1054	chr19: 10789144-10789167	3491	CCCAGTGTTCAGACTACCTGTTC	Yes	Yes	Yes	Yes	No
CU-1055	chr19: 10789105-10789126	3492	ACAGTAGTCTGCACATTGGTT	Yes	Yes	Yes	Yes	Yes
CU-1055	chr1: 170380317-170380338	3493	ACAGTAGTCTGCACATTGGTT	Yes	Yes	Yes	Yes	Yes
CU-1055	chr9: 130046845-130046866	3494	ACAGTAGTCTGCACATTGGTT	Yes	Yes	Yes	Yes	No
CU-1056	chr13: 90801193-90801216	3495	TGTGCAAATCTATGCAAAACTGA	Yes	No	Yes	Yes	Yes
CU-1057	chrX: 133131378-133131401	3496	TGTGCAAATCCATGCAAAACTGA	Yes	Yes	Yes	Yes	Yes
CU-1057	chr13: 90801499-90801522	3497	TGTGCAAATCCATGCAAAACTGA	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1061	chr13: 90801326-90801349	3498	TAAAGTGCTTATAGTGCAGGTAG	Yes	Yes	Yes	Yes	Yes
CU-1062	chrX: 133131545-133131568	3499	CAAAGTGCTTATAGTGCAGGTAG	Yes	Yes	Yes	Yes	Yes
CU-1064	chr17: 55273415-55273437	3500	TAGCTTATCAGACTGATGTTGA	Yes	Yes	Yes	Yes	Yes
CU-5016	chr3: 49032634-49032658	3501	AATGACACGATCACTCCCGTTGAG	Yes	Yes	Yes	Yes	Yes
CU-1065	chrX: 45490553-45490574	3502	AGCTACATTGTCTGCTGGGTT	Yes	Yes	Yes	Yes	Yes
CU-1066	chrX: 45491383-45491406	3503	AGCTACATCTGGCTACTGGGTCT	No	Yes	Yes	Yes	Yes
CU-1067	chrX: 65155503-65155525	3504	TGTCAGTTTGTCAAATACCCCA	Yes	Yes	Yes	Yes	Yes
CU-1068	chr19: 13808407-13808429	3505	ATCACATTGCCAGGGATTTCCA	Yes	Yes	Yes	Yes	Yes
CU-1069	chr9: 96887367-96887389	3506	ATCACATTGCCAGGGATTACCA	Yes	Yes	Yes	Yes	Yes
CU-1071	chr7: 99529129-99529151	3507	CATTGCACTTGTCTCGGTCTGA	Yes	Yes	Yes	Yes	Yes
CU-1072	chr12: 56504707-56504729	3508	TTCAAGTAATCCAGGATAGGCT	Yes	Yes	Yes	Yes	Yes
CU-1072	chr3: 37985907-37985929	3509	TTCAAGTAATCCAGGATAGGCT	Yes	Yes	Yes	Yes	Yes
CU-1073	chr2: 218975623-218975645	3510	TTCAAGTAATTCAGGATAGGTT	Yes	Yes	Yes	Yes	Yes
CU-1075	chr9: 96887607-96887627	3511	TTCACAGTGGCTAAGTTCTG	Yes	Yes	Yes	Yes	Yes
CU-1076	chr3: 189889315-189889337	3512	CACTAGATTGTGAGCTCCTGGA	Yes	Yes	Yes	Yes	Yes
CU-1077	chr3: 189889275-189889297	3513	AAGGAGCTCACAGTCTATTGAG	Yes	Yes	Yes	Yes	Yes
CU-1079	chr7: 130212046-130212068	3514	TAGCACCATCTGAAATCGGTTA	Yes	Yes	Yes	Yes	Yes
CU-1080	chr1: 206042417-206042440	3515	TAGCACCATTTGAAATCAGTGTT	Yes	Yes	Yes	Yes	Yes
CU-1081	chr1: 206041871-206041892	3516	TGACCGATTTCTCCTGGTGTT	Yes	Yes	Yes	Yes	Yes
CU-1082	chr1: 206041832-206041854	3517	TAGCACCATTTGAAATCGGTTA	Yes	Yes	Yes	Yes	Yes
CU-1083	chr6: 72170020-72170040	3518	TGTAAACATCCTCGACTGGA	Yes	Yes	Yes	Yes	Yes
CU-1084	chr8: 135881994-135882016	3519	TGTAAACATCCTACACTCAGCT	Yes	Yes	Yes	Yes	Yes
CU-1085	chr1: 40995558-40995581	3520	TGTAAACATCCTACACTCTCAGC	Yes	Yes	Yes	Yes	Yes
CU-1086	chr8: 135886343-135886365	3521	TGTAAACATCCCCGACTGGAAG	Yes	Yes	Yes	Yes	Yes
CU-1087	chr1: 40992629-40992653	3522	TGTAAACATCCTTGACTGGAAGCT	Yes	Yes	Yes	Yes	Yes
CU-1088	chr8: 22158432-22158448	3523	TGGGTTGAGAGGGCGA	Yes	Yes	Yes	Yes	Yes
CU-1089	chr16: 65793734-65793752	3524	CTGGCCCTCTCTGCCCTT	Yes	No	Yes	Yes	Yes
CU-1091	chr12: 94226386-94226407	3525	GCCCCTGGGCCTATCCTAGAA	Yes	Yes	Yes	Yes	Yes
CU-1092	chr7: 1029154-1029174	3526	TCCCTGTCCTCCAGGAGCTC	Yes	Yes	Yes	Yes	No
CU-1092	chr10: 22978473-22978493	3527	TCCCTGTCCTCCAGGAGCTC	Yes	Yes	No	No	No
CU-1093	chr14: 99645804-99645828	3528	TCTCACACAGAAATCGCACCCGTC	Yes	Yes	Yes	Yes	Yes
CU-1094	chr14: 99645763-99645783	3529	GGGGTGCTATCTGTGATTGA	Yes	Yes	Yes	Yes	Yes
CU-1095	chr1: 9134379-9134402	3530	TGGCAGTGTCTTAGCTGGTTGTT	Yes	Yes	Yes	Yes	Yes
CU-1096	chrX: 85045302-85045324	3531	TCCCCCAGGTGTGATTCTGATT	Yes	Yes	Yes	Yes	Yes
CU-1098	chr17: 26926609-26926631	3532	TAATGCCCCTAAAAATCCTTAT	Yes	Yes	Yes	Yes	Yes
CU-1098	chr16: 14310697-14310719	3533	TAATGCCCCTAAAAATCCTTAT	Yes	Yes	Yes	Yes	Yes
CU-1099	chr5: 149092584-149092605	3534	CTCCTGACTCCAGGTCCTGTG	Yes	Yes	Yes	No	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1100	chr17: 25468274-25468296	3535	AGCTCGGTCTGAGGCCCCTCAG	Yes	Yes	Yes	Yes	Yes
CU-1101	chr17: 25468238-25468260	3536	TGAGGGGCAGAGAGCGAGACTT	Yes	Yes	Yes	Yes	Yes
CU-1103	chr8: 41637118-41637140	3537	TCCTGTACTGAGCTGCCCCGAG	Yes	Yes	Yes	Yes	Yes
CU-1104	chr17: 6862021-6862042	3538	CAGCAGCACACTGTGGTTTGT	Yes	Yes	Yes	Yes	Yes
CU-1105	chrX: 138833988-138834006	3539	CGTCAACACTTGCTGGTT	Yes	Yes	Yes	Yes	Yes
CU-1106	chr4: 38546107-38546128	3540	CACGCTCATGCACACACCCAC	No	No	Yes	Yes	No
CU-1108	chr14: 65007623-65007643	3541	AGGGGGAAAGTTCTATAGTC	Yes	No	No	No	No
CU-1108	chr14: 65007586-65007606	3542	AGGGGGAAAGTTCTATAGTC	Yes	No	No	No	No
CU-1110	chr15: 68158819-68158840	3543	TGGGTTTACGTTGGGAGAACT	No	No	No	No	No
CU-1111	chr9: 85774506-85774527	3544	CAACAAATCACAGTCTGCCAT	Yes	Yes	Yes	Yes	Yes
CU-1113	chr9: 85774546-85774569	3545	TGGAAGACTAGTGATTTTGTTGT	Yes	Yes	Yes	Yes	Yes
CU-1113	chr15: 86956090-86956113	3546	TGGAAGACTAGTGATTTTGTTGT	Yes	Yes	Yes	Yes	Yes
CU-1113	chr19: 4721711-4721734	3547	TGGAAGACTAGTGATTTTGTTGT	Yes	Yes	Yes	Yes	Yes
CU-1115	chr13: 90801578-90801601	3548	AGGTTGGGATCGGTTGCAATGCT	Yes	No	Yes	No	No
CU-1116	chrX: 133131239-133131261	3549	TATTGCACTTGTCCCGGCCTGT	Yes	Yes	Yes	Yes	Yes
CU-1116	chr13: 90801615-90801637	3550	TATTGCACTTGTCCCGGCCTGT	Yes	Yes	Yes	Yes	Yes
CU-1117	chr1: 153431651-153431670	3551	TATTGCACTCGTCCCGGCC	No	Yes	Yes	Yes	Yes
CU-1118	chr7: 99529373-99529396	3552	CAAAGTGCTGTTCGTGCAGGTAG	Yes	Yes	Yes	Yes	Yes
CU-1119	chrX: 53599984-53600006	3553	TGAGGTAGTAAGTTGTATTGTT	Yes	Yes	Yes	Yes	Yes
CU-1124	chr17: 53763644-53763665	3554	CCCATAAAGTAGAAAGCACTA	Yes	Yes	Yes	Yes	Yes
CU-1125	chr3: 161605277-161605298	3555	ACCAATATTACTGTGCTGCTT	Yes	Yes	Yes	Yes	Yes
CU-1126	chr9: 126495825-126495848	3556	ACATTCATTGCTGTCGGTGGGTT	Yes	Yes	Yes	Yes	Yes
CU-1126	chr1: 197094675-197094698	3557	ACATTCATTGCTGTCGGTGGGTT	Yes	Yes	Yes	Yes	Yes
CU-1568	chr21: 16834028-16834046	3558	TGAGGTAGTAGGTTGTAT	Yes	Yes	Yes	Yes	Yes
CU-5001	chr9: 95980997-95981018	3559	CTATACGACCTGCTGCCTTTC	Yes	Yes	Yes	Yes	Yes
CU-5002	chr3: 49032596-49032618	3560	CATCGGGAATGTCGTGTCCGCC	Yes	Yes	Yes	Yes	Yes

new miRNA identified in B cell libraries

		Seq ID		Conservation				
ID	Genomic Coordinates	No.	Sequence	Chimp	Monkey	Dog	Mouse	Rat
CU-1130	chr4: 84650562-84650579	3561	CCCGGGTTTCGGCACCA	Yes	No	No	No	No
CU-1130	chr7: 152741807-152741824	3562	CCCGGGTTTCGGCACCA	No	No	No	No	No
CU-1132	chr12: 123990125-123990145	3563	GCCGGGTACTTTCGTATTTT	No	No	No	No	No
CU-1137	chr17: 8030990-8031016	3564	GCTAAGGAAGTCCTGTGCTCAGTTTT	Yes	No	No	No	No
CU-1142	chr5: 180625271-180625293	3565	TCGATTCCCGGCCCATGCACCA	No	No	No	No	No
CU-1142	chr21: 17748974-17748996	3566	TCGATTCCCGGCCCATGCACCA	Yes	No	No	No	No
CU-1142	chr1: 159687142-159687164	3567	TCGATTCCCGGCCCATGCACCA	Yes	Yes	No	No	No
CU-1142	chr1: 159701933-159701955	3568	TCGATTCCCGGCCCATGCACCA	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1142	chr1: 159679769-159679791	3569	TCGATTCCCGGCCCATGCACCA	No	Yes	Yes	No	No
CU-1142	chr1: 159694573-159694595	3570	TCGATTCCCGGCCCATGCACCA	Yes	Yes	No	No	No
CU-1146	chr16: 3142975-3142992	3571	AGAAAGGCCGAATTTTA	Yes	No	No	No	No
CU-1148	chr10: 5935660-5935679	3572	TGGTGTGGTCTGTTGTTTT	Yes	No	No	No	No
CU-1153	chr14: 22388241-22388268	3573	CCCCCCACTGCTAAATTTGACTGGCTT	Yes	Yes	No	No	No
CU-1153	chr17: 35653067-35653094	3574	CCCCCCACTGCTAAATTTGACTGGCTT	Yes	No	No	No	No
CU-1155	chr20: 58490320-58490337	3575	TCCCCGCACCTCCACCA	Yes	Yes	No	No	No
CU-1164	chr6: 29057409-29057426	3576	GAGAGCGCTCGGTTTTT	Yes	No	No	No	No
CU-1173	chr18: 1681856-1681874	3577	ATCCCACTCCTGACACCA	Yes	No	No	No	No
CU-1175	chr11: 59075015-59075034	3578	GGCGTGATTCATACCTTTT	Yes	No	No	No	No
CU-1178	chr6: 28723944-28723961	3579	AGGGTGTGCGTGTTTTT	Yes	No	No	No	No
CU-1180	chr19: 38359877-38359905	3580	AACCGAGCGTCCAAGCTCTTTCCATTTT	Yes	Yes	No	No	No
CU-1186	chr18: 73990174-73990192	3581	TCCCCGACACCTCCACCA	No	No	No	No	No
CU-1191	chr12: 46439968-46439985	3582	GCCCGCATCCTCCACCA	Yes	No	No	No	No
CU-1197	chr15: 38673296-38673314	3583	ATGTGGTGGCTTACTTTT	Yes	No	No	No	No
CU-1212	chr20: 60596937-60596955	3584	TCCCCGGCACTTCCACCA	No	No	No	No	No
CU-1213	chr3: 73875819-73875836	3585	TCACCCCATAAACACCA	Yes	Yes	Yes	No	No
CU-1220	chr1: 159706825-159706843	3586	TTCCCCGACGGGGAGCCA	Yes	Yes	No	No	No
CU-1220	chr1: 159692034-159692052	3587	TTCCCCGACGGGGAGCCA	Yes	Yes	No	No	No
CU-1220	chr1: 159677235-159677253	3588	TTCCCCGACGGGGAGCCA	Yes	Yes	Yes	No	No
CU-1220	chr1: 159699444-159699462	3589	TTCCCCGACGGGGAGCCA	Yes	Yes	No	No	No
CU-1220	chr1: 159684653-159684671	3590	TTCCCCGACGGGGAGCCA	Yes	Yes	No	No	No
CU-1221	chr17: 34564245-34564268	3591	TGTGCTCCGGAGTTACCTCGTTT	No	No	No	No	No
CU-1222	chrX: 70920902-70920919	3592	TCACGTCGGGGTCACCA	Yes	No	No	No	No
CU-1241	chr2: 167308360-167308379	3593	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr1: 29814092-29814111	3594	AGTCCCATCTGGGTCGCCA	Yes	Yes	No	No	No
CU-1241	chrX: 51239676-51239695	3595	AGTCCCATCTGGGTCGCCA	Yes	Yes	No	No	No
CU-1241	chr13: 22997399-22997418	3596	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr6: 70235237-70235256	3597	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr6: 141377023-141377042	3598	AGTCCCATCTGGGTCGCCA	Yes	Yes	No	No	No
CU-1241	chr16: 21555749-21555768	3599	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr3: 97152533-97152552	3600	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chrX: 70638471-70638490	3601	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr2: 47181625-47181644	3602	AGTCCCATCTGGGTCGCCA	No	No	No	No	No
CU-1241	chr3: 114548556-114548575	3603	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr8: 107870541-107870560	3604	AGTCCCATCTGGGTCGCCA	No	Yes	No	No	No
CU-1241	chr10: 118251348-118251367	3605	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1241	chr13: 110648656-110648675	3606	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1241	chr1: 74982888-74982907	3607	AGTCCCATCTGGGTCGCCA	No	Yes	No	No	No
CU-1241	chr1: 74982864-74982883	3608	AGTCCCATCTGGGTCGCCA	No	Yes	No	No	No
CU-1241	chrX: 120113204-120113223	3609	AGTCCCATCTGGGTCGCCA	Yes	No	No	No	No
CU-1242	chr7: 148897373-148897391	3610	TCCCCGTACGGGCCACCA	Yes	No	No	No	No
CU-1242	chr6: 159071498-159071516	3611	TCCCCGTACGGGCCACCA	Yes	No	No	No	No
CU-1243	chr1: 173342843-173342861	3612	GTCCCTTCGTGGTCGCCA	No	No	No	No	No
CU-1243	chr19: 55148120-55148138	3613	GTCCCTTCGTGGTCGCCA	Yes	No	No	No	No
CU-1243	chrX: 117299486-117299504	3614	GTCCCTTCGTGGTCGCCA	No	No	No	No	No
CU-1243	chr8: 4429174-4429192	3615	GTCCCTTCGTGGTCGCCA	Yes	No	No	No	No
CU-1243	chr11: 84485385-84485403	3616	GTCCCTTCGTGGTCGCCA	Yes	Yes	No	No	No
CU-1243	chr21: 26073725-26073743	3617	GTCCCTTCGTGGTCGCCA	Yes	No	No	No	No
CU-1243	chr5: 77142069-77142087	3618	GTCCCTTCGTGGTCGCCA	Yes	No	No	No	No
CU-1243	chr19: 8350798-8350816	3619	GTCCCTTCGTGGTCGCCA	Yes	No	No	No	No
CU-1243	chr12: 20827096-20827114	3620	GTCCCTTCGTGGTCGCCA	No	No	No	No	No
CU-1244	chr1: 159766817-159766838	3621	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr1: 159700155-159700176	3622	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr1: 159677946-159677967	3623	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	Yes	No	No
CU-1244	chr1: 159685364-159685385	3624	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr16: 55891954-55891975	3625	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr1: 159692745-159692766	3626	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr1: 159707536-159707557	3627	GTCAGGATGGCCGAGCGGTCT	Yes	Yes	No	No	No
CU-1244	chr1: 240532967-240532988	3628	GTCAGGATGGCCGAGCGGTCT	Yes	No	No	No	No
CU-1246	chr14: 65014334-65014351	3629	AGGGGGGTAAAAAAAAA	Yes	No	No	No	No
CU-1246	chr14: 93614119-93614136	3630	AGGGGGGTAAAAAAAAA	Yes	No	No	No	No
CU-1251	chr12: 31408926-31408943	3631	CCCACCCAGGGACGCCA	No	No	No	No	No
CU-1251	chr17: 34161556-34161573	3632	CCCACCCAGGGACGCCA	Yes	Yes	Yes	No	No
CU-1251	chr1: 146614798-146614815	3633	CCCACCCAGGGACGCCA	Yes	No	No	No	No
CU-1251	chr19: 33728787-33728804	3634	CCCACCCAGGGACGCCA	Yes	No	No	No	No
CU-1251	chr9: 136463072-136463089	3635	CCCACCCAGGGACGCCA	Yes	No	No	No	No
CU-1254	chr4: 2032401-2032419	3636	TCCCCGGCACCTCCACCA	No	Yes	No	No	No
CU-1264	chr3: 37897506-37897524	3637	GAGGGGGACCAAAAAAAA	Yes	Yes	No	No	No
CU-1269	chr17: 21946878-21946897	3638	TACCGAGCCTGGTGATAGC	No	No	No	No	No
CU-1269	chr11: 102785624-102785643	3639	TACCGAGCCTGGTGATAGC	Yes	No	No	No	No
CU-1276	chr17: 7969840-7969862	3640	TCGATTCCCGGCCAATGCACCA	No	Yes	Yes	No	Yes
CU-1276	chr19: 39807750-39807772	3641	TCGATTCCCGGCCAATGCACCA	No	No	No	No	No
CU-1277	chr1: 153990335-153990358	3642	GAGCCATGATGATACCACTGAGC	Yes	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1278	chr5: 79981714-79981731	3643	TAACGGCCGCGGTACCC	Yes	Yes	No	No	No
CU-1278	chr3: 97818860-97818877	3644	TAACGGCCGCGGTACCC	Yes	Yes	No	No	No
CU-1281	chr1: 173235999-173236022	3645	GCAGCGCCAGCCTCCCGCCCTAC	Yes	No	No	No	No
CU-1288	chr19: 54685975-54685994	3646	CGTCCATGATGTTCCGCAA	No	No	No	No	No
CU-1293	chr2: 38390703-38390730	3647	AGCAGTGATGTCCTGAAAATTCTGAAG	No	No	No	No	No
CU-1294	chr5: 79983107-79983127	3648	AAAGGACCTGGCGGTGCTTC	Yes	No	No	No	No
CU-1294	chr11: 10487796-10487816	3649	AAAGGACCTGGCGGTGCTTC	Yes	No	No	No	No
CU-1294	chr13: 108874524-108874544	3650	AAAGGACCTGGCGGTGCTTC	Yes	No	No	No	No
CU-1298	chr16: 3178151-3178169	3651	ATCCCGGACGAGCCCCCA	Yes	No	No	No	No
CU-1298	chr22: 44955360-44955378	3652	ATCCCGGACGAGCCCCCA	Yes	No	No	No	No
CU-1298	chr11: 49720969-49720987	3653	ATCCCGGACGAGCCCCCA	Yes	Yes	No	No	No
CU-1298	chr16: 3174130-3174148	3654	ATCCCGGACGAGCCCCCA	Yes	No	No	No	No
CU-1298	chr11: 75624513-75624531	3655	ATCCCGGACGAGCCCCCA	Yes	No	Yes	No	No
CU-1300	chr6: 101499628-101499646	3656	TCCTCACACGGGGCACCA	Yes	Yes	No	No	No
CU-1300	chr7: 106814117-106814135	3657	TCCTCACACGGGGCACCA	Yes	Yes	No	No	No
CU-1303	chr4: 151694303-151694321	3658	ATCCCACTTCTGACACCA	Yes	Yes	No	No	No
CU-1303	chr1: 212585032-212585050	3659	ATCCCACTTCTGACACCA	Yes	No	No	No	No
CU-1303	chr3: 194813519-194813537	3660	ATCCCACTTCTGACACCA	Yes	No	No	No	No
CU-1303	chr2: 55018611-55018629	3661	ATCCCACTTCTGACACCA	Yes	Yes	No	No	No
CU-1303	chr5: 143373194-143373212	3662	ATCCCACTTCTGACACCA	No	Yes	No	No	No
CU-1303	chr1: 36261536-36261554	3663	ATCCCACTTCTGACACCA	Yes	No	No	No	No
CU-1303	chr12: 67663402-67663420	3664	ATCCCACTTCTGACACCA	Yes	Yes	No	No	No
CU-1303	chr4: 119344866-119344884	3665	ATCCCACTTCTGACACCA	No	Yes	No	No	No
CU-1303	chr12: 70175143-70175161	3666	ATCCCACTTCTGACACCA	Yes	Yes	No	No	No
CU-1307	chr1: 9557438-9557458	3667	ACCCCACTATGCTTAGCCCT	Yes	Yes	No	Yes	Yes
CU-1323	chr2: 232028754-232028771	3668	TGTATTGTGAGACATTC	Yes	No	No	No	No
CU-1324	chr4: 3167100-3167117	3669	TCTCGGTGGAACCTCCA	Yes	No	No	No	No
CU-1324	chr15: 63948450-63948467	3670	TCTCGGTGGAACCTCCA	No	No	No	No	No
CU-1339	chr8: 141129909-141129928	3671	ATCCCCAGCACCTCCACCA	Yes	Yes	No	No	No
CU-1345	chr11: 10487827-10487845	3672	AGAACACTACGAGCCACA	Yes	No	No	No	No
CU-1345	chr5: 79983138-79983156	3673	AGAACACTACGAGCCACA	Yes	No	No	No	No
CU-1345	chr13: 108874555-108874573	3674	AGAACACTACGAGCCACA	Yes	No	No	No	No
CU-1352	chr12: 12693348-12693366	3675	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr5: 119090314-119090332	3676	ACCCCACTTCTGGTACCA	No	No	No	No	No
CU-1352	chr14: 56457992-56458010	3677	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr7: 7637279-7637297	3678	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr1: 34288353-34288371	3679	ACCCCACTTCTGGTACCA	No	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1352	chr1: 107581087-107581105	3680	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr7: 66011743-66011761	3681	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr7: 119683539-119683557	3682	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr18: 16775205-16775223	3683	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr2: 6916389-6916407	3684	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr6: 98788231-98788249	3685	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr1: 201394394-201394412	3686	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chrX: 85448496-85448514	3687	ACCCCACTTCTGGTACCA	No	Yes	No	No	No
CU-1352	chr8: 140073141-140073159	3688	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr12: 8391052-8391070	3689	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chrX: 77289492-77289510	3690	ACCCCACTTCTGGTACCA	No	No	No	No	No
CU-1352	chr2: 116637798-116637816	3691	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr4: 72493755-72493773	3692	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr15: 94045767-94045785	3693	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chrX: 85947724-85947742	3694	ACCCCACTTCTGGTACCA	No	Yes	No	No	No
CU-1352	chr20: 60081974-60081992	3695	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr18: 31113119-31113137	3696	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr11: 8446114-8446132	3697	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr6: 140796063-140796081	3698	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr22: 19662967-19662985	3699	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chrX: 116622706-116622724	3700	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr22: 43646515-43646533	3701	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr11: 3516223-3516241	3702	ACCCCACTTCTGGTACCA	No	No	No	No	No
CU-1352	chr10: 123734159-123734177	3703	ACCCCACTTCTGGTACCA	No	No	No	No	No
CU-1352	chr18: 120806-120824	3704	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr1: 174219317-174219335	3705	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1352	chr7: 156114211-156114229	3706	ACCCCACTTCTGGTACCA	Yes	No	No	No	No
CU-1352	chr3: 107173811-107173829	3707	ACCCCACTTCTGGTACCA	Yes	Yes	No	No	No
CU-1363	chr1: 17095207-17095225	3708	CGTTCGCGCTTTCCCCTG	Yes	Yes	No	No	No
CU-1363	chr1: 147460729-147460747	3709	CGTTCGCGCTTTCCCCTG	No	Yes	No	No	No
CU-1363	chr14: 34085816-34085834	3710	CGTTCGCGCTTTCCCCTG	Yes	Yes	No	No	No
CU-1363	chr14: 34095182-34095200	3711	CGTTCGCGCTTTCCCCTG	Yes	Yes	No	No	No
CU-1368	chr6: 27173063-27173081	3712	GACGAGGTGGCCGAGTGG	Yes	Yes	Yes	No	No
CU-1368	chr6: 28288793-28288811	3713	GACGAGGTGGCCGAGTGG	Yes	Yes	No	No	No
CU-1368	chr11: 65872166-65872184	3714	GACGAGGTGGCCGAGTGG	Yes	Yes	Yes	Yes	Yes
CU-1368	chr15: 38673378-38673396	3715	GACGAGGTGGCCGAGTGG	Yes	Yes	Yes	No	Yes
CU-1368	chr6: 27373753-27373771	3716	GACGAGGTGGCCGAGTGG	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1368	chr2: 228333400-228333418	3717	GACGAGGTGGCCGAGTGG	Yes	No	No	No	No
CU-1368	chr6: 28673159-28673177	3718	GACGAGGTGGCCGAGTGG	Yes	Yes	No	No	No
CU-1368	chr17: 8030908-8030926	3719	GACGAGGTGGCCGAGTGG	Yes	Yes	No	No	Yes
CU-1369	chr15: 94627153-94627171	3720	TCCCCGGCATCTCCACCA	No	No	No	No	No
CU-1370	chr1: 232795752-232795772	3721	CTGATTGCTCCTGTCTGATT	No	Yes	No	No	No
CU-1371	chr13: 108874496-108874517	3722	TCTAGAGGAGCCTGTTCTGTA	Yes	No	Yes	Yes	No
CU-1379	chr1: 165950616-165950638	3723	TCGGGTGCGAGAGGTCCCGGGT	Yes	Yes	Yes	Yes	Yes
CU-1380	chr11: 10488308-10488331	3724	ATAGGTTTGGTCCTAGCCTTTCT	Yes	No	No	No	No
CU-1381	chr1: 169836691-169836713	3725	TCGATTCCCGGTCAGGGAACCA	No	No	No	No	No
CU-1382	chr6: 27555431-27555459	3726	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr1: 159677282-159677310	3727	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	Yes	No	No
CU-1382	chr17: 8066324-8066352	3728	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr1: 159699491-159699519	3729	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr1: 159692081-159692109	3730	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr6: 27579501-27579529	3731	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr1: 159684700-159684728	3732	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr12: 123990189-123990217	3733	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1382	chr12: 94953929-94953957	3734	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	Yes	Yes	No
CU-1382	chr12: 123977887-123977915	3735	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	No	No	No	No
CU-1382	chr1: 159706872-159706900	3736	TCCTCGTTAGTATAGTGGTGAGTATCCC	Yes	Yes	No	No	No
CU-1388	chr1: 144110633-144110661	3737	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr1: 159698476-159698504	3738	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr1: 159705856-159705884	3739	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr1: 159683685-159683713	3740	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr1: 247135069-247135097	3741	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr1: 159691065-159691093	3742	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	No	No
CU-1388	chr6: 126143129-126143157	3743	TCCCTGGTGGTCTAGTGGTTAGGATTCG	Yes	Yes	No	Yes	Yes
CU-1396	chr1: 556086-556103	3744	TAAGTGTTTGTGGGTTA	No	No	No	No	No
CU-1403	chr17: 7969788-7969810	3745	GCATTGGTGGTTCAGTGGTAGA	No	Yes	Yes	No	Yes
CU-1403	chr16: 69370491-69370513	3746	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	Yes	No	No
CU-1403	chr1: 17061002-17061024	3747	GCATTGGTGGTTCAGTGGTAGA	No	No	Yes	No	No
CU-1403	chr3: 15524502-15524524	3748	GCATTGGTGGTTCAGTGGTAGA	Yes	No	No	No	No
CU-1403	chr16: 69380097-69380119	3749	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	Yes	Yes	Yes
CU-1403	chr1: 227740226-227740248	3750	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	No	No	No
CU-1403	chr1: 16745069-16745091	3751	GCATTGGTGGTTCAGTGGTAGA	Yes	No	Yes	No	No
CU-1403	chr1: 159760309-159760331	3752	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	No	No	No
CU-1403	chr2: 156965953-156965975	3753	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1403	chrX: 64154569-64154591	3754	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	No	No	No
CU-1403	chr6: 27978713-27978735	3755	GCATTGGTGGTTCAGTGGTAGA	Yes	Yes	No	No	No
CU-1440	chr5: 180533270-180533287	3756	TGGTTATCACGTTCGCC	Yes	Yes	No	No	No
CU-1440	chr5: 180456690-180456707	3757	TGGTTATCACGTTCGCC	Yes	Yes	No	No	No
CU-1440	chr6: 27281886-27281903	3758	TGGTTATCACGTTCGCC	Yes	Yes	No	No	No
CU-1440	chr1: 147565219-147565236	3759	TGGTTATCACGTTCGCC	Yes	Yes	No	No	No
CU-1440	chr5: 180461899-180461916	3760	TGGTTATCACGTTCGCC	Yes	Yes	No	No	No
CU-1453	chr3: 191522810-191522827	3761	CCCTGCTCGCTGCGCCA	Yes	Yes	No	No	No
CU-1457	chr7: 43102939-43102961	3762	TTCTCACTACTGCACTTGACTA	Yes	No	No	No	No
CU-1457	chr14: 67153778-67153800	3763	TTCTCACTACTGCACTTGACTA	Yes	No	No	No	No
CU-1457	chr1: 238571371-238571393	3764	TTCTCACTACTGCACTTGACTA	Yes	Yes	No	No	No
CU-1457	chr2: 147946177-147946199	3765	TTCTCACTACTGCACTTGACTA	Yes	Yes	No	No	No
CU-1470	chr16: 30675216-30675234	3766	CTCCTGGCTGGCTCGCCA	Yes	Yes	No	No	No
CU-1470	chr14: 43074235-43074253	3767	CTCCTGGCTGGCTCGCCA	Yes	No	No	No	No
CU-1477	chr17: 26124435-26124459	3768	CTCCCACTGCTTCACTTGACTAGC	No	Yes	No	No	No
CU-1477	chr17: 27331095-27331119	3769	CTCCCACTGCTTCACTTGACTAGC	Yes	Yes	No	No	No
CU-1477	chr10: 21810723-21810747	3770	CTCCCACTGCTTCACTTGACTAGC	Yes	No	No	No	No
CU-1477	chr14: 99119179-99119203	3771	CTCCCACTGCTTCACTTGACTAGC	Yes	Yes	No	No	No
CU-1477	chr11: 107460922-107460946	3772	CTCCCACTGCTTCACTTGACTAGC	Yes	Yes	No	No	No
CU-1477	chr4: 154407515-154407539	3773	CTCCCACTGCTTCACTTGACTAGC	Yes	Yes	No	No	No
CU-1486	chr17: 59577172-59577189	3774	CTGCTGTGATGACATTC	Yes	Yes	No	No	No
CU-1488	chr1: 4671944-4671961	3775	TCCTGCCGCGGTCGCCA	Yes	Yes	No	No	No
CU-1513	chr17: 59577217-59577244	3776	GCGGGTGATGCGAACTGGAGTCTGAGC	Yes	No	Yes	No	No
CU-1524	chr7: 148269562-148269586	3777	CCCCCACAACCGCGCTTGACTAGC	Yes	Yes	Yes	No	No
CU-1528	chr17: 8066916-8066935	3778	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr6: 27167511-27167530	3779	TAGGGGTATGATTCTCGCT	Yes	Yes	Yes	No	No
CU-1528	chr14: 20222026-20222045	3780	TAGGGGTATGATTCTCGCT	Yes	Yes	No	Yes	Yes
CU-1528	chr14: 20151440-20151459	3781	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr6: 26663488-26663507	3782	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr16: 3172676-3172695	3783	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr14: 20147375-20147394	3784	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr5: 180548500-180548519	3785	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr16: 3148935-3148954	3786	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr16: 3179646-3179665	3787	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr4: 18668214-18668233	3788	TAGGGGTATGATTCTCGCT	Yes	No	No	No	No
CU-1528	chr1: 165950597-165950616	3789	TAGGGGTATGATTCTCGCT	Yes	Yes	Yes	No	Yes
CU-1528	chr16: 3182001-3182020	3790	TAGGGGTATGATTCTCGCT	Yes	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

CU-1528	chr11: 75624216-75624235	3791	TAGGGGTATGATTCTCGCT	Yes	Yes	Yes	No	No
CU-1528	chr16: 3162061-3162080	3792	TAGGGGTATGATTCTCGCT	Yes	Yes	No	No	No
CU-1528	chr7: 128210751-128210770	3793	TAGGGGTATGATTCTCGCT	Yes	Yes	Yes	Yes	Yes
CU-1538	chrX: 16840335-16840361	3794	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	No	No	No	No
CU-1538	chr13: 98986625-98986651	3795	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	Yes	No	No	No
CU-1538	chr10: 128599365-128599391	3796	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	Yes	No	No	No
CU-1538	chr7: 148311779-148311805	3797	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	No	Yes	No	No
CU-1538	chr15: 73062744-73062770	3798	GGCTGGTCCGAGTGCAGTGGTGTTTA	No	No	No	No	No
CU-1538	chrX: 116932310-116932336	3799	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	Yes	No	No	No
CU-1538	chr11: 47705094-47705120	3800	GGCTGGTCCGAGTGCAGTGGTGTTTA	Yes	No	No	No	No
CU-1542	chr7: 148291339-148291362	3801	GGCTGGTCCGATGGTAGTGGGTT	Yes	Yes	Yes	No	No
CU-1542	chr6: 33275355-33275378	3802	GGCTGGTCCGATGGTAGTGGGTT	Yes	Yes	No	No	No
CU-1545	chr17: 19031996-19032016	3803	CCACGAGGAAGAGAGGTAGC	No	No	No	No	No
CU-1550	chr6: 26438546-26438564	3804	CGGAAGCGTGCTGGGCCC	Yes	Yes	No	No	No
CU-1550	chr6: 27853657-27853675	3805	CGGAAGCGTGCTGGGCCC	Yes	Yes	No	No	No
CU-1550	chr6: 26421369-26421387	3806	CGGAAGCGTGCTGGGCCC	Yes	Yes	No	No	No
CU-1550	chr6: 27408781-27408799	3807	CGGAAGCGTGCTGGGCCC	Yes	Yes	No	No	No
CU-1550	chr6: 27668617-27668635	3808	CGGAAGCGTGCTGGGCCC	Yes	Yes	No	No	No
CU-1557	chr17: 19033934-19033957	3809	GGAGAGAACGCGGTCTGAGTGGT	Yes	No	No	No	No
CU-1557	chr17: 18907957-18907980	3810	GGAGAGAACGCGGTCTGAGTGGT	Yes	No	No	No	No
CU-1557	chr17: 19032115-19032138	3811	GGAGAGAACGCGGTCTGAGTGGT	Yes	No	No	No	No
CU-1557	chr17: 18956457-18956480	3812	GGAGAGAACGCGGTCTGAGTGGT	Yes	No	No	No	No
CU-1557	chr17: 18906143-18906166	3813	GGAGAGAACGCGGTCTGAGTGGT	Yes	No	No	No	No
CU-1570	chr17: 36922634-36922653	3814	ATCCCCAGCATCTCCACCA	Yes	No	No	No	No
CU-1575	chr7: 148291405-148291430	3815	CCCCCCACTGCTAAATTTGACTGGA	Yes	Yes	Yes	No	No

miRNA deposited in miRBase database

		Seq ID		Conservation				
ID	Genomic Coordinates	No.	Sequence	Chimp	Monkey	Dog	Mouse	Rat
hsa-mir-1322	chr8: 10720294-10720313	3816	CAGCATCAGCAGCATCATC	Yes	No	No	No	No
hsa-mir-1323	chr19: 58867043-58867065	3817	TCAAAACTGAGGGGCATTTTCT	Yes	Yes	No	No	No
hsa-mir-1321	chrX: 84977492-84977510	3818	CAGGGAGGTGAATGTGAT	Yes	No	No	No	No
hsa-mir-29c*	chr1: 206041870-206041892	3819	GAACACCAGGAGAAATCGGTCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1324	chr3: 75762663-75762687	3820	CCAGACAGAATTCTATGCACTTTC	No	No	No	No	No
hsa-mir-675	chr11: 1974605-1974628	3821	CACTGTGGGCCCTCTCCGCACCA	No	Yes	Yes	Yes	Yes
hsa-mir-183*	chr7: 129202003-129202025	3822	TTATGGCCCTTCGGTAATTCAC	Yes	Yes	Yes	Yes	Yes
hsa-mir-335*	chr7: 129923238-129923260	3823	TTTTTCATTATTGCTCCTGACC	Yes	Yes	Yes	Yes	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-19a*	chr13: 90801158-90801180	3824	AGTTTTGCATAGTTGCACTACA	Yes	No	Yes	Yes	Yes
hsa-mir-132*	chr17: 1900008-1900030	3825	AGTAACAATCGAAAGCCACGGT	No	Yes	Yes	Yes	Yes
hsa-mir-182	chr7: 129197522-129197546	3826	AGTGTGAGTTCTACCATTGCCAAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-122	chr18: 54269299-54269321	3827	TGGAGTGTGACAATGGTGTTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-16-2*	chr3: 161605278-161605300	3828	CCAATATTACTGTGCTGCTTTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-124	chr8: 65454320-65454340	3829	TAAGGCACGCGGTGAATGCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-124	chr8: 9798320-9798340	3830	GGCATTCACCGCGTGCCTTA	No	Yes	Yes	Yes	Yes
hsa-mir-124	chr20: 61280348-61280368	3831	TAAGGCACGCGGTGAATGCC	No	Yes	Yes	Yes	Yes
hsa-mir-126	chr9: 138684925-138684947	3832	TCGTACCGTGAGTAATAATGCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-31*	chr9: 21502119-21502141	3833	ATGGCAATATGTTGGCATAGCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-128	chr2: 136139485-136139506	3834	TCACAGTGAACCGGTCTCTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-128	chr3: 35761022-35761043	3835	TCACAGTGAACCGGTCTCTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-19a	chr13: 90801193-90801216	3836	TGTGCAAATCTATGCAAAACTGA	Yes	No	Yes	Yes	Yes
hsa-mir-524-5p	chr19: 58906082-58906104	3837	CTACAAAGGGAAGCACTTTCTC	Yes	Yes	No	No	No
hsa-mir-19b	chrX: 133131378-133131401	3838	TCAGTTTTGCATGGATTTGCACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-19b	chr13: 90801499-90801522	3839	TGTGCAAATCCATGCAAAACTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-148b*	chr12: 53017290-53017312	3840	AAGTTCTGTTATACACTCAGGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-1257	chr20: 59962071-59962092	3841	GGTCAGAACCCATCATTCACT	No	No	No	No	No
hsa-mir-1254	chr10: 70189097-70189121	3842	AGCCTGGAAGCTGGAGCCTGCAGT	Yes	Yes	No	No	No
hsa-mir-455-3p	chr9: 116011587-116011608	3843	GCAGTCCATGGGCATATACAC	Yes	Yes	Yes	Yes	Yes
hsa-mir-1253	chr17: 2598182-2598203	3844	TGCAGGCTGATCTTCTTCTCT	Yes	No	No	No	No
hsa-mir-1250	chr17: 76721659-76721680	3845	AAAGGCCACATCCAGCACCGT	Yes	Yes	No	No	No
hsa-mir-1251	chr12: 96409821-96409842	3846	ACTCTAGCTGCCAAAGGCGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1258	chr2: 180433852-180433873	3847	AGTTAGGATTAGGTCGTGGAA	Yes	Yes	No	No	No
hsa-mir-1258	chr2: 180433816-180433837	3848	TTCCACGACCTAATCCTAACT	Yes	Yes	No	No	No
hsa-mir-1259	chr20: 47330268-47330289	3849	ATATATGATGACTTAGCTTTT	Yes	Yes	No	No	No
hsa-mir-1207-3p	chr8: 129130630-129130648	3850	TCAGCTGGCCCTCATTTC	Yes	Yes	No	Yes	No
hsa-mir-34c-3p	chr11: 110889418-110889440	3851	AATCACTAACCACACGGCCAGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-489	chr7: 92951194-92951216	3852	GCTGCCGTATATGTGATGTCAC	Yes	Yes	Yes	No	Yes
hsa-mir-488	chr1: 175265132-175265153	3853	GACCAAGAAATAGCCTTTCAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-556-5p	chr1: 160578974-160578996	3854	GATGAGCTCATTGTAATATGAG	Yes	No	No	No	No
hsa-mir-484	chr16: 15644658-15644680	3855	TCAGGCTCAGTCCCCTCCCGAT	Yes	Yes	No	Yes	Yes
hsa-mir-523*	chr19: 58893465-58893487	3856	CTCTAGAGGGAAGCGCTTTCTG	Yes	No	No	No	No
hsa-mir-125b-1*	chr11: 121475686-121475708	3857	AGCTCCCAAGAGCCTAACCCGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-7-2*	chr15: 86956130-86956152	3858	CAACAAATCCCAGTCTACCTAA	Yes	Yes	No	No	No
hsa-mir-569	chr3: 172307161-172307182	3859	ACTTTCCAGGATTCATTAACT	Yes	Yes	Yes	No	No
hsa-mir-574-5p	chr4: 38546071-38546094	3860	TGAGTGTGTGTGTGTGAGTGTGT	No	No	Yes	Yes	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-342-5p	chr14: 99645762-99645783	3861	AGGGGTGCTATCTGTGATTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-379	chr14: 100558160-100558181	3862	TGGTAGACTATGGAACGTAGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-520b	chr19: 58896332-58896353	3863	AAAGTGCTTCCTTTTAGAGGG	Yes	Yes	No	No	No
hsa-mir-520e	chr19: 58870829-58870850	3864	AAAGTGCTTCCTTTTTGAGGG	Yes	No	No	No	No
hsa-mir-371-5p	chr19: 58985745-58982765	3865	ACTCAAACTGTGGGGGCACT	Yes	Yes	Yes	No	Yes
hsa-mir-520g	chr19: 58917285-58917309	3866	ACAAAGTGCTTCCCTTTAGAGTGT	Yes	Yes	No	No	No
hsa-mir-520f	chr19: 58877278-58877300	3867	AAGTGCTTCCTTTTAGAGGGTT	Yes	No	No	No	No
hsa-mir-520h	chr19: 58937631-58937653	3868	ACAAAGTGCTTCCCTTTAGAGT	Yes	No	No	No	No
hsa-mir-219-5p	chr9: 130194775-130194796	3869	AGAATTGCGTTTGGACAATCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-219-5p	chr6: 33283609-33283630	3870	TGATTGTCCAAACGCAATTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-140-5p	chr16: 68524506-68524528	3871	CAGTGGTTTTACCCTATGGTAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-423-5p	chr17: 25468238-25468261	3872	TGAGGGGCAGAGAGCGAGACTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-30b*	chr8: 135881956-135881978	3873	GAAGTAAACATCCACCTCCCAG	Yes	Yes	Yes	No	No
hsa-mir-195	chr17: 6861709-6861730	3874	GCCAATATTTCTGTGCTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-194	chr11: 64415451-64415473	3875	TCCACATGGAGTTGCTGTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-194	chr1: 218358170-218358192	3876	TCCACATGGAGTTGCTGTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-197	chr1: 109943084-109943106	3877	TTCACCACCTTCTCCACCCAGC	Yes	Yes	Yes	No	No
hsa-mir-191	chr3: 49033108-49033131	3878	CAGCTGCTTTTGGGATTCCGTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-190	chr15: 60903222-60903244	3879	TGATATGTTTGATATATTAGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-192	chr11: 64415250-64415271	3880	GGCTGTCAATTCATAGGTCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-449a	chr5: 54502170-54502192	3881	ACCAGCTAACAATACACTGCCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-339-3p	chr7: 1029116-1029139	3882	CGGCTCTGTCGTCGAGGCGCTCA	Yes	Yes	No	Yes	Yes
hsa-mir-508-5p	chrX: 146126189-146126212	3883	CATGAGTGACGCCCTCTGGAGTA	Yes	Yes	No	No	No
hsa-mir-1284	chr3: 71673879-71673901	3884	GAAAAGCCAGGGTCTGTATAGA	Yes	No	No	Yes	Yes
hsa-mir-362-5p	chrX: 49660315-49660339	3885	AATCCTTGGAACCTAGGTGTGAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-125a-3p	chr19: 56888370-56888392	3886	ACAGGTGAGGTTCTTGGGAGCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-34a*	chr1: 9134338-9134360	3887	AGGGCAGTATACTTGCTGATTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-373	chr19: 58983813-58983836	3888	GAAGTGCTTCGATTTTGGGGTGT	Yes	Yes	Yes	No	No
hsa-mir-502-3p	chrX: 49665996-49666018	3889	AATGCACCTGGGCAAGGATTCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-200b	chr1: 1092402-1092424	3890	TAATACTGCCTGGTAATGATGA	No	No	Yes	Yes	Yes
hsa-mir-200c	chr12: 6943165-6943188	3891	TAATACTGCCGGGTAATGATGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-200a	chr1: 1093158-1093180	3892	TAACACTGTCTGGTAACGATGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-410	chr14: 100602050-100602071	3893	AATATAACACAGATGGCCTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-411	chr14: 100559429-100559450	3894	TAGTAGACCGTATAGCGTACG	Yes	Yes	Yes	Yes	Yes
hsa-mir-412	chr14: 100601589-100601612	3895	ACTTCACCTGGTCCACTAGCCGT	Yes	Yes	No	Yes	Yes
hsa-mir-555	chr1: 153582779-153582800	3896	ATCAGAGGTTCAGCTTACCCT	Yes	Yes	No	Yes	No
hsa-mir-554	chr1: 149784910-149784931	3897	GCTAGTCCTGACTCAGCCAGT	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-493*	chr14: 100405164-100405186	3898	TTGTACATGGTAGGCTTTCATT	No	Yes	Yes	Yes	Yes
hsa-mir-550	chr7: 30295955-30295978	3899	AGTGCCTGAGGGAGTAAGAGCCC	Yes	Yes	No	No	No
hsa-mir-550	chr7: 32739138-32739161	3900	AGTGCCTGAGGGAGTAAGAGCCC	Yes	Yes	No	No	No
hsa-mir-553	chr1: 100519399-100519420	3901	AAAACGGTGAGATTTTGTTTT	Yes	No	No	No	No
hsa-mir-193a-5p	chr17: 26911147-26911169	3902	TGGGTCTTTGCGGGCGAGATGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-876-3p	chr9: 28853633-28853655	3903	TGAATTACTTTGTAAACCACCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-139-3p	chr11: 72003757-72003779	3904	ACTCCAACAGGGCCGCGTCTCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-30a	chr6: 72170018-72170040	3905	CTTCCAGTCGAGGATGTTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-30b	chr8: 135881994-135882016	3906	AGCTGAGTGTAGGATGTTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-30c	chr1: 40995558-40995581	3907	TGTAAACATCCTACACTCTCAGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-30c	chr6: 72143426-72143449	3908	GCTGAGAGTGTAGGATGTTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-30d	chr8: 135886343-135886365	3909	CTTCCAGTCGGGGATGTTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-30e	chr1: 40992629-40992651	3910	TGTAAACATCCTTGACTGGAAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-374b*	chrX: 73355116-73355138	3911	AATGATAATACAACCTGCTAAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-548b-3p	chr6: 119431925-119431947	3912	ACAAAAGCAACTGAGGTTCTTG	Yes	No	No	No	No
hsa-mir-515-5p	chr19: 58874081-58874105	3913	TTCTCCAAAAGAAAGCACTTTCTG	Yes	Yes	No	No	No
hsa-mir-515-5p	chr19: 58880087-58880111	3914	TTCTCCAAAAGAAAGCACTTTCTG	Yes	Yes	No	No	No
hsa-mir-429	chr1: 1094297-1094319	3915	TAATACTGTCTGGTAAAACCGT	No	Yes	Yes	Yes	Yes
hsa-mir-486-5p	chr8: 41637118-41637140	3916	TCCTGTACTGAGCTGCCCCGAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-486-5p	chr8: 41637158-41637180	3917	CTCGGGGCAGCTCAGTACAGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1206	chr8: 129090328-129090349	3918	TGTTCATGTAGATGTTTAAGC	Yes	Yes	No	No	No
hsa-mir-99a	chr21: 16833291-16833313	3919	AACCCGTAGATCCGATCTTGTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-188-3p	chrX: 49654901-49654922	3920	CTCCCACATGCAGGGTTTGCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-99b	chr19: 56887682-56887704	3921	CACCCGTAGAACCGACCTTGCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-300	chr14: 100577503-100577525	3922	TATACAAGGGCAGACTCTCTCT	Yes	No	No	No	No
hsa-mir-193b	chr16: 14305374-14305396	3923	AACTGGCCCTCAAAGTCCCGCT	Yes	Yes	Yes	Yes	No
hsa-mir-1203	chr17: 43588846-43588867	3924	GAGCTGCATCCTGGCTCCGGG	Yes	Yes	No	No	No
hsa-mir-30c-1*	chr1: 40995597-40995619	3925	CTGGGAGAGGGTTGTTTACTCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-19b-2*	chrX: 133131422-133131444	3926	TGAAATGCAAACCTGCAAAACT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1286	chr22: 18616667-18616688	3927	AGGGCTCATCTTGGTCCTGCA	Yes	No	No	No	No
hsa-let-7g*	chr3: 52277335-52277356	3928	GCAAGGCAGTGGCCTGTACAG	Yes	Yes	Yes	Yes	No
hsa-mir-361-3p	chrX: 85045301-85045324	3929	AAATCAGAATCACACCTGGGGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-518a-5p	chr19: 58926084-58926104	3930	CTGCAAAGGGAAGCCCTTTC	Yes	No	No	No	No
hsa-mir-518a-5p	chr19: 58934413-58934433	3931	CTGCAAAGGGAAGCCCTTTC	Yes	No	No	No	No
hsa-mir-604	chr10: 29873953-29873972	3932	GTCCTGAATTCCGCAGCCT	Yes	Yes	No	No	No
hsa-mir-485-5p	chr14: 100591516-100591538	3933	AGAGGCTGGCCGTGATGAATTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-452*	chrX: 150878761-150878783	3934	CACTTACTTCTTTGCAGATGAG	Yes	Yes	Yes	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-450b-5p	chrX: 133501926-133501948	3935	TATTCAGGAACATATTGCAAAA	Yes	Yes	Yes	No	No
hsa-mir-505	chrX: 138833984-138834006	3936	AGGAAACCAGCAAGTGTTGACG	Yes	Yes	Yes	Yes	Yes
hsa-mir-299-5p	chr14: 100559889-100559911	3937	TGGTTTACCGTCCCACATACAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-181a-2*	chr9: 126494617-126494639	3938	ACCACTGACCGTTGACTGTACC	Yes	Yes	Yes	No	No
hsa-mir-29b-2*	chr1: 206042459-206042481	3939	CTAAGCCACCATGTGAAACCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-323-3p	chr14: 100561871-100561892	3940	CACATTACACGGTCGACCTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1256	chr1: 21187456-21187478	3941	AGCTAGTGAGAAGTCAATGCCT	Yes	Yes	No	No	No
hsa-mir-144*	chr17: 24212726-24212748	3942	CTTACAGTATATGATGATATCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-1280	chr3: 129563701-129563718	3943	TCCCACCGCTGCCACCC	Yes	Yes	No	No	No
hsa-mir-379*	chr14: 100558198-100558220	3944	TATGTAACATGGTCCACTAACT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1252	chr12: 78337171-78337193	3945	AGAAGGAAATTGAATTCATTTA	Yes	Yes	No	No	No
hsa-mir-324-5p	chr17: 7067384-7067407	3946	ACACCAATGCCCTAGGGGATGCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-516b*	chr19: 58920562-58920580	3947	TGCTTCCTTTCAGAGGGT	Yes	No	No	No	No
hsa-mir-516b*	chr19: 58931970-58931988	3948	TGCTTCCTTTCAGAGGGT	Yes	Yes	No	No	No
hsa-mir-18b	chrX: 133131779-133131802	3949	CTAACTGCACTAGATGCACCTTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-17	chr13: 90800872-90800895	3950	CAAAGTGCTTACAGTGCAGGTAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-16	chr3: 161605235-161605257	3951	TAGCAGCACGTAAATATTGGCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-16	chr13: 49521163-49521185	3952	CGCCAATATTTACGTGCTGCTA	Yes	Yes	Yes	Yes	No
hsa-mir-26b*	chr2: 218975658-218975680	3953	CCTGTTCTCCATTACTTGGCTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-618	chr12: 79853705-79853728	3954	ACTCAGAAGGACAAGTAGAGTTT	Yes	Yes	No	No	No
hsa-mir-331-3p	chr12: 94226386-94226407	3955	GCCCCTGGGCCTATCCTAGAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-605	chr10: 52729353-52729376	3956	TAAATCCCATGGTGCCTTCTCCT	Yes	No	No	No	No
hsa-mir-376a	chr14: 100576914-100576935	3957	ATCATAGAGGAAAATCCACGT	Yes	Yes	Yes	No	No
hsa-mir-376a	chr14: 100576207-100576228	3858	ATCATAGAGGAAAATCCACGT	Yes	Yes	Yes	No	Yes
hsa-mir-376b	chr14: 100576586-100576608	3959	ATCATAGAGGAAAATCCATGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-376c	chr14: 100575821-100575842	3960	ATCATAGAGGAAATTCCACGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-601	chr9: 125204666-125204688	3961	CTCCTCCAACAATCCTAGACCA	Yes	Yes	No	No	No
hsa-mir-600	chr9: 124913660-124913683	3962	GAGCAAGGCTCTTGTCTGTAAGT	Yes	Yes	No	No	No
hsa-mir-603	chr10: 24604679-24604701	3963	CACACACTGCAATTACTTTTGC	No	Yes	No	No	No
hsa-mir-602	chr9: 139852706-139852729	3964	GACACGGGCGACAGCTGCGGCCC	Yes	No	No	No	No
hsa-mir-609	chr10: 105968596-105968616	3965	AGAGATGAGAGAAACACCCT	Yes	Yes	No	No	No
hsa-mir-608	chr10: 102724746-102724771	3966	AGGGGTGGTGTTGGGACAGCTCCGT	Yes	No	No	No	No
hsa-mir-551b*	chr3: 169752356-169752378	3967	GAAATCAAGCGTGGGTGAGACC	Yes	Yes	Yes	Yes	Yes
hsa-mir-544	chr14: 100584801-100584823	3968	ATTCTGCATTTTTAGCAAGTTC	Yes	Yes	Yes	Yes	No
hsa-mir-664*	chr1: 218440550-218440574	3969	ATCCAATCATTTTCCCTAGCCAGT	Yes	Yes	Yes	No	No
hsa-mir-409-5p	chr14: 100601403-100601426	3970	AGGTTACCCGAGCAACTTTGCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-136*	chr14: 100420839-100420861	3971	CATCATCGTCTCAAATGAGTCT	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-1282	chr15: 41873221-41873241	3972	AAGCAGAAAAAGGCAAACGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-519c-5p	chr19: 58881549-58881571	3973	CTCTAGAGGGAAGCGCTTTCTG	Yes	No	No	No	No
hsa-mir-1208	chr8: 129231554-129231574	3974	TCACTGTTCAGACAGGCGGA	Yes	Yes	No	Yes	Yes
hsa-mir-1205	chr8: 129042067-129042087	3975	TCTGCAGGGTTTGCTTTGAG	Yes	No	No	Yes	Yes
hsa-mir-663b	chr2: 132731012-132731034	3976	CCTCAGGCACGGCCGGGCCACC	Yes	No	No	No	No
hsa-mir-1201	chr14: 19864455-19864479	3977	TCAGAGCATGTGTTTAATCAGGCT	Yes	Yes	Yes	No	No
hsa-mir-1200	chr7: 36925532-36925554	3978	GAGGCTCAGAATGGCTCAGGAG	Yes	No	No	No	No
hsa-mir-338-5p	chr17: 76714317-76714339	3979	CACTCAGCACCAGGATATTGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1202	chr6: 156309634-156309655	3980	GTGCCAGCTGCAGTGGGGGAG	Yes	Yes	No	No	No
hsa-mir-501-5p	chrX: 49661082-49661104	3981	AATCCTTTGTCCCTGGGTGAGA	Yes	Yes	No	Yes	Yes
hsa-mir-519b-5p	chr19: 58890290-58890312	3982	CTCTAGAGGGAAGCGCTTTCTG	Yes	Yes	No	No	No
hsa-mir-101*	chr1: 65296747-65296769	3983	AGCATCAGCACTGTGATAACTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-511	chr10: 17927127-17927148	3984	GTGTCTTTTGCTCTGCAGTCA	Yes	Yes	Yes	No	No
hsa-mir-511	chr10: 18174056-18174077	3985	GTGTCTTTTGCTCTGCAGTCA	Yes	Yes	Yes	No	No
hsa-mir-510	chrX: 146161587-146161609	3986	GTGATTGCCACTCTCCTGAGTA	Yes	Yes	Yes	No	No
hsa-let-7a*	chr9: 95978115-95978136	3987	CTATACAATCTACTGTCTTTC	Yes	Yes	Yes	Yes	Yes
hsa-let-7a*	chr22: 44887343-44887364	3988	CTATACAATCTACTGTCTTTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-514	chrX: 146173864-146173885	3989	TCTACTCACAGAAGTGTCAAT	Yes	Yes	No	No	No
hsa-mir-514	chrX: 146171166-146171187	3990	TCTACTCACAGAAGTGTCAAT	Yes	Yes	Yes	No	No
hsa-mir-514	chrX: 146168475-146168496	3991	TCTACTCACAGAAGTGTCAAT	Yes	No	Yes	No	No
hsa-mir-524-3p	chr19: 58906119-58906140	3992	GAAGGCGCTTCCCTTTGGAGT	Yes	No	No	No	No
hsa-mir-491-5p	chr9: 20706118-20706140	3993	AGTGGGGAACCCTTCCATGAGG	Yes	Yes	Yes	Yes	No
hsa-mir-18b*	chrX: 133131737-133131759	3994	GCCAGAAGGGGCATTTAGGGCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-411*	chr14: 100559464-100559486	3995	TATGTAACACGGTCCACTAACC	Yes	Yes	Yes	Yes	Yes
hsa-mir-548d-3p	chr8: 124429469-124429491	3996	GCAAAAGAAACTGTGGTTTTTG	No	Yes	No	No	No
hsa-mir-548d-3p	chr17: 62898081-62898103	3997	GCAAAAGAAACTGTGGTTTTTG	No	No	No	No	No
hsa-mir-490-3p	chr7: 136238528-136238550	3998	CAACCTGGAGGACTCCATGGCTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-576-3p	chr4: 110629356-110629378	3999	AAGATGTGGAAAAATTGGAATC	Yes	Yes	No	No	No
hsa-mir-34a	chr1: 9134380-9134402	4000	ACAACCAGCTAAGACACTGCCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-34b	chr11: 110888921-110888943	4001	CAATCACTAACTCCACTGCCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-654-5p	chr14: 100576323-100576345	4002	TGGTGGGCCGCAGAACATGTGC	Yes	Yes	No	No	No
hsa-mir-216a	chr2: 56069658-56069680	4003	TCACAGTTGCCAGCTGAGATTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-216b	chr2: 56081402-56081424	4004	TCACATTTGCCTGCAGAGATTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-590-3p	chr7: 73243518-73243539	4005	TAATTTTATGTATAAGCTAGT	Yes	Yes	Yes	No	Yes
hsa-mir-939	chr8: 145590215-145590239	4006	CACCCCCAGAGCCTCAGCTCCCCA	Yes	Yes	No	No	No
hsa-mir-938	chr10: 29931245-29931267	4007	ACTGGGTTCACCTTTAAGGGCA	Yes	No	No	No	No
hsa-mir-34c-5p	chr11: 110889385-110889408	4008	AGGCAGTGTAGTTAGCTGATTGC	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-15a*	chr13: 49521266-49521288	4009	TGAGGCAGCCACAATATGGCCTG	Yes	Yes	Yes	Yes	No
hsa-mir-933	chr2: 175740615-175740637	4010	GGGAGAGGTCTCCCTGCGCACA	Yes	Yes	No	No	No
hsa-mir-499-3p	chr20: 33041908-33041930	4011	AACATCACAGCAAGTCTGTGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-937	chr8: 144967128-144967150	4012	GGCAGAGAGTCAGAGCGCGGAT	Yes	No	No	No	No
hsa-mir-936	chr10: 105797898-105797920	4013	CTGCGATTCCTCCCTCTACTGT	Yes	Yes	No	No	No
hsa-mir-935	chr19: 59177427-59177450	4014	CCAGTTACCGCTTCCGCTACCGC	Yes	No	No	No	Yes
hsa-mir-654-3p	chr14: 100576358-100576380	4015	TATGTCTGCTGACCATCACCTT	Yes	Yes	Yes	Yes	No
hsa-mir-93*	chr7: 99529335-99529357	4016	CGGGAAGTGCTAGCTCAGCAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-516b	chr19: 58920522-58920544	4017	ATCTGGAGGTAAGAAGCACTTT	Yes	No	No	No	No
hsa-mir-516b	chr19: 58931925-58931947	4018	ATCTGGAGGTAAGAAGCACTTT	Yes	Yes	No	No	No
hsa-mir-551a	chr1: 3467133-3467154	4019	TGGAAACCAAGAGTGGGTCGC	Yes	Yes	Yes	No	No
hsa-mir-551b	chr3: 169752395-169752416	4020	GCGACCCATACTTGGTTTCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-345	chr14: 99843965-99843987	4021	GCTGACTCCTAGTCCAGGGCTC	Yes	No	Yes	No	No
hsa-mir-346	chr10: 88014483-88014506	4022	AGAGGCAGGCATGCGGGCAGACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-340	chr5: 179374966-179374988	4023	AATCAGTCTCATTGCTTTATAA	Yes	Yes	Yes	Yes	No
hsa-mir-106a	chrX: 133131939-133131962	4024	CTACCTGCACTGTAAGCACTTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-23b*	chr9: 96887329-96887351	4025	TGGGTTCCTGGCATGCTGATTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-106b	chr7: 99529601-99529622	4026	ATCTGCACTGTCAGCACTTTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-194*	chr11: 64415415-64415437	4027	CAGATAACAGCAGCCCCACTGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-519a*	chr19: 58947476-58947498	4028	CTCTAGAGGGAAGCGCTTTCTG	Yes	No	No	No	No
hsa-mir-519e	chr19: 58875056-58875078	4029	AAGTGCCTCCTTTTAGAGTGTT	Yes	No	No	No	No
hsa-mir-519d	chr19: 58908465-58908487	4030	CAAAGTGCCTCCCTTTAGAGTG	Yes	Yes	No	No	No
hsa-mir-769-3p	chr19: 51214097-51214120	4031	CTGGGATCTCCGGGGTCTTGGTT	No	No	Yes	No	No
hsa-mir-519a	chr19: 58947514-58947536	4032	AAAGTGCATCCTTTTAGAGTGT	Yes	Yes	No	No	No
hsa-mir-519a	chr19: 58957465-58957484	4033	AAAGTGCATCCTTTTAGAGTGT	Yes	Yes	No	No	No
hsa-mir-943	chr4: 1957927-1957948	4034	CTGGAGGACGGCAACAGTCAG	Yes	No	No	No	No
hsa-mir-940	chr16: 2261807-2261828	4035	AAGGCAGGGCCCCCGCTCCCC	Yes	Yes	Yes	No	No
hsa-mir-941	chr20: 62021710-62021733	4036	CACCCGGCTGTGTGCACATGTGC	Yes	No	No	No	No
hsa-mir-941	chr20: 62021598-62021621	4037	CACCCGGCTGTGTGCACATGTGC	Yes	No	No	No	No
hsa-mir-941	chr20: 62021291-62021314	4038	CACCCGGCTGTGTGCACATGTGC	Yes	No	No	No	No
hsa-mir-423-3p	chr17: 25468274-25468297	4039	AGCTCGGTCTGAGGCCCCTCAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-203	chr14: 103653558-103653580	4040	GTGAAATGTTTAGGACCACTAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-202	chr10: 134911032-134911052	4041	TTCCCATGCCCTATACCTCT	Yes	No	Yes	Yes	Yes
hsa-mir-205	chr1: 207672133-207672155	4042	TCCTTCATTCCACCGGAGTCTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-204	chr9: 72614766-72614788	4043	AGGCATAGGATGACAAAGGGAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-526a	chr19: 58921993-58922015	4044	CTCTAGAGGGAAGCACTTTCTG	Yes	No	No	No	No
hsa-mir-526a	chr19: 58901331-58901353	4045	CTCTAGAGGGAAGCACTTTCTG	Yes	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-28-3p	chr3: 189889315-189889337	4046	CACTAGATTGTGAGCTCCTGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-302a*	chr4: 113788828-113788851	4047	AGCAAGTACATCCACGTTTAAGT	Yes	Yes	Yes	Yes	No
hsa-mir-548c-3p	chr12: 63302615-63302637	4048	CAAAAATCTCAATTACTTTTGC	Yes	Yes	No	No	No
hsa-mir-424*	chrX: 133508339-133508360	4049	ATAGCAGCGCCTCACGTTTTG	Yes	Yes	Yes	No	No
hsa-mir-886-5p	chr5: 135444163-135444186	4050	CCGCTTGAGCTAACTCCGACCCG	Yes	Yes	No	No	No
hsa-mir-877*	chr6: 30660152-30660173	4051	TCCTCTTCTCCCTCCTCCCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-29b	chr7: 130212765-130212788	4052	AACACTGATTTCAAATGGTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-29b	chr1: 206042417-206042440	4053	AACACTGATTTCAAATGGTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-29c	chr1: 206041832-206041854	4054	TAACCGATTTCAAATGGTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-29a	chr7: 130212046-130212068	4055	TAACCGATTTCAGATGGTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-20a	chr13: 90801326-90801349	4056	TAAAGTGCTTATAGTGCAGGTAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-640	chr19: 19406931-19406952	4057	ATGATCCAGGAACCTGCCTCT	Yes	Yes	No	No	No
hsa-mir-129-5p	chr11: 43559533-43559554	4058	CTTTTTGCGGTCTGGGCTTGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-129-5p	chr7: 127635164-127635185	4059	CTTTTTGCGGTCTGGGCTTGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-20b	chrX: 133131545-133131568	4060	CTACCTGCACTATGAGCACTTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-645	chr20: 48635789-48635808	4061	TCTAGGCTGGTACTGCTGA	Yes	No	No	No	No
hsa-mir-644	chr20: 32517850-32517869	4062	AGTGTGGCTTTCTTAGAGC	Yes	Yes	No	No	No
hsa-mir-647	chr20: 62044487-62044508	4063	GAAGGAAGTGAGTGCAGCCAC	No	No	No	No	No
hsa-mir-646	chr20: 58316986-58317005	4064	AAGCAGCTGCCTCTGAGGC	Yes	No	No	No	No
hsa-mir-649	chr22: 19718479-19718501	4065	GACTCTTGAACAACACAGGTTT	Yes	Yes	No	No	No
hsa-mir-648	chr22: 16843693-16843712	4066	ACCAGTGCCCTGCACACTT	Yes	Yes	No	No	No
hsa-mir-760	chr1: 94085023-94085043	4067	CGGCTCTGGGTCTGTGGGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-766	chrX: 118664753-118664775	4068	GCTGAGGCTGTGGGGCTGGAGT	Yes	Yes	No	No	No
hsa-mir-765	chr1: 155172571-155172592	4069	CATCACCTTCCTTCTCCTCCA	Yes	Yes	No	No	No
hsa-mir-628-3p	chr15: 53452443-53452464	4070	TCGACTGCCACTCTTACTAGA	Yes	Yes	Yes	No	No
hsa-mir-337-5p	chr14: 100410604-100410625	4071	GAACGGCTTCATACAGGAGTT	Yes	Yes	No	No	No
hsa-mir-373*	chr19: 58983775-58983797	4072	ACTCAAAATGGGGGCGCTTTCC	Yes	No	No	No	No
hsa-mir-369-5p	chr14: 100601695-100601717	4073	AGATCGACCGTGTTATATTCGC	Yes	Yes	No	Yes	Yes
hsa-mir-1285	chr7: 91671276-91671298	4074	AGGTCTCACTTTGTTGCCCAGA	Yes	No	No	No	No
hsa-mir-1285	chr2: 70333568-70333590	4075	AGGTCTCACTTTGTTGCCCAGA	Yes	No	No	No	No
hsa-mir-222*	chrX: 45491422-45491444	4076	AGGATCTACACTGGCTACTGAG	No	Yes	Yes	Yes	Yes
hsa-mir-298	chr20: 56826729-56826753	4077	TGGGAGAACCTCCCTGCTTCTGCT	Yes	Yes	No	No	No
hsa-mir-206	chr6: 52117157-52117179	4078	TGGAATGTAAGGAAGTGTGTGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-297	chr4: 112001228-112001249	4079	CATGCACATGCACACATACAT	Yes	Yes	Yes	No	No
hsa-mir-589*	chr7: 5501990-5502014	4080	TCTGGGAACCGGCATTTGTTCTGA	Yes	No	Yes	No	No
hsa-mir-124*	chr20: 61280310-61280332	4081	CGTGTTCACAGCGGACCTTGAT	No	Yes	Yes	Yes	Yes
hsa-mir-124*	chr8: 9798357-9798379	4082	ATCAAGGTCCGCTGTGAACACG	No	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-124*	chr8: 65454283-65454305	4083	CGTGTTCACAGCGGACCTTGAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-185*	chr22: 18400710-18400732	4084	AGGGGCTGGCTTTCCTCTGGTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-486-3p	chr8: 41637160-41637181	4085	CGGGGCAGCTCAGTACAGGAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-486-3p	chr8: 41637117-41637138	4086	ATCCTGTACTGAGCTGCCCCG	Yes	Yes	Yes	Yes	No
hsa-mir-1243	chr4: 114247471-114247493	4087	AACTGGATCAATTATAGGAGTG	Yes	Yes	No	No	No
hsa-mir-616*	chr12: 56199272-56199294	4088	AAGTCACTGAAGGGTTTTGAGT	Yes	Yes	No	No	No
hsa-mir-1245	chr2: 189551106-189551127	4089	AAGTGATCTAAAGGCCTACAT	Yes	No	No	No	No
hsa-mir-1244	chr12: 12156206-12156232	4090	AAGTAGTTGGTTTGTATGAGATGGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1244	chr12: 9283334-9283360	4091	AACCATCTCATACAAACCAACTACTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1244	chr2: 232286321-232286347	4092	AAGTAGTTGGTTTGTATGAGATGGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1244	chr5: 118338233-118338259	4093	AAGTAGTTGGTTTGTATGAGATGGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1247	chr14: 101096451-101096473	4094	TCCGGGGACGAACGGGACGGGT	Yes	Yes	No	Yes	Yes
hsa-mir-1246	chr2: 177173997-177174016	4095	CCTGCTCCAAAAATCCATT	Yes	Yes	Yes	No	No
hsa-mir-1249	chr22: 43975502-43975524	4096	TGAAGAAGGGGGGGAAGGGCGT	Yes	Yes	Yes	Yes	No
hsa-mir-491-3p	chr9: 20706152-20706174	4097	CTTATGCAAGATTCCCTTCTAC	Yes	Yes	Yes	Yes	No
hsa-mir-148a*	chr7: 25956104-25956126	4098	AGTCGGAGTGTCTCAGAACTTT	Yes	Yes	Yes	Yes	No
hsa-mir-92b*	chr1: 153431610-153431632	4099	AGGGACGGGACGCGGTGCAGTG	No	Yes	Yes	Yes	Yes
hsa-mir-548o	chr7: 101833199-101833221	4100	GCAAAAGTAACTGCAGTTTTGG	Yes	Yes	No	No	No
hsa-mir-891b	chrX: 144890309-144890331	4101	TCAATGACTCAGGTAAGTTGCA	Yes	Yes	No	No	No
hsa-mir-548m	chrX: 94204846-94204867	4102	CAAAAACCACAAATACCTTTG	No	No	No	No	No
hsa-mir-548l	chr11: 93839358-93839380	4103	GACAAAACCCGCAAATACTTTT	Yes	Yes	No	No	No
hsa-mir-548k	chr11: 69807739-69807761	4104	AAAAGTACTTGCGGATTTTGCT	Yes	No	No	No	No
hsa-mir-1283	chr19: 58883559-58883581	4105	TCTACAAAGGAAAGCGCTTTCT	Yes	Yes	No	No	No
hsa-mir-1283	chr19: 58953310-58953332	4106	TCTACAAAGGAAAGCGCTTTCT	No	No	No	No	No
hsa-mir-548i	chrX: 83367460-83367482	4107	GGCAAAATCCGCAATTACTTTT	No	No	No	No	No
hsa-mir-548i	chr3: 126992025-126992047	4108	GGCAAAATCCGCAATTACTTTT	Yes	No	No	No	No
hsa-mir-548i	chr8: 7983961-7983983	4109	GGCAAAATCCGCAATTACTTTT	Yes	No	No	No	No
hsa-mir-548i	chr4: 9166975-9166997	4110	GGCAAAATCCGCAATTACTTTT	Yes	No	No	No	No
hsa-mir-548h	chr17: 13387638-13387660	4111	GACAAAAACCGCGATTACTTTT	No	Yes	No	No	No
hsa-mir-548h	chr8: 26962359-26962381	4112	GACAAAAACCGCGATTACTTTT	No	No	No	No	No
hsa-mir-548h	chr14: 63631554-63631576	4113	GACAAAAACCGCGATTACTTTT	Yes	Yes	No	No	No
hsa-mir-548h	chr16: 11307848-11307870	4114	GACAAAAACCGCGATTACTTTT	Yes	Yes	No	No	No
hsa-mir-548g	chr4: 148485244-148485266	4115	GTACAAAAGTAATTACAGTTTT	Yes	No	No	No	No
hsa-mir-548f	chr5: 109877443-109877462	4116	AAAAGTAATTACAGTTTTT	Yes	Yes	No	No	No
hsa-mir-548f	chr7: 146706065-146706084	4117	AAAAGTAATTACAGTTTTT	Yes	Yes	No	No	No
hsa-mir-548f	chrX: 32569527-32569546	4118	AAAAGTAATTACAGTTTTT	Yes	Yes	No	No	No
hsa-mir-548f	chr2: 212999252-212999271	4119	AAAAGTAATTACAGTTTTT	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-548f	chr10: 56037654-56037673	4120	AAAAGTAATTACAGTTTTT	No	No	No	No	No
hsa-mir-496	chr14: 100596717-100596739	4121	TGAGTATTACATGGCCAATCTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-497	chr17: 6862021-6862042	4122	ACAAACCACAGTGTGCTGCTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-190b	chr1: 152432812-152432833	4123	AACCCAATATCAAACATATCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-492	chr12: 93752333-93752356	4124	AGGACCTGCGGGACAAGATTCTT	Yes	Yes	Yes	No	No
hsa-mir-493	chr14: 100405205-100405227	4125	TGAAGGTCTACTGTGTGCCAGG	No	Yes	Yes	No	Yes
hsa-mir-199b-5p	chr9: 130046882-130046905	4126	GAACAGATAGTCTAAACACTGGG	Yes	No	Yes	Yes	No
hsa-mir-891a	chrX: 144917050-144917072	4127	TCAGTGGCTCAGGTTCGTTGCA	Yes	Yes	No	No	No
hsa-mir-500*	chrX: 49659829-49659851	4128	ATGCACCTGGGCAAGGATTCTG	Yes	Yes	Yes	No	No
hsa-mir-105*	chrX: 151311355-151311377	4129	TAGCACATGCTCAAACATCCGT	Yes	Yes	Yes	No	Yes
hsa-mir-105*	chrX: 151313548-151313570	4130	TAGCACATGCTCAAACATCCGT	Yes	Yes	Yes	No	Yes
hsa-mir-513c	chrX: 146078962-146078984	4131	ATAAACGACACCTCCTTGAGAA	No	No	No	No	No
hsa-mir-513b	chrX: 146088302-146088324	4132	ATAAATGACACCTCCTTGTGAA	Yes	Yes	No	No	No
hsa-mir-18a*	chr13: 90801051-90801074	4133	ACTGCCCTAAGTGCTCCTTCTGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-548p	chr5: 100180100-100180122	4134	AAAGTAACTGCAGTTTTTGCTA	Yes	No	No	No	No
hsa-mir-24-1*	chr9: 96888129-96888151	4135	TGCCTACTGAGCTGATATCAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-582-5p	chr5: 59035248-59035271	4136	AGTAACTGGTTGAACAACTGTAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-668	chr14: 100591389-100591412	4137	TGTCACTCGGCTCGGCCCACTAC	Yes	Yes	No	Yes	Yes
hsa-mir-516a-5p	chr19: 58951821-58951844	4138	TTCTCGAGGAAAGAAGCACTTTC	Yes	Yes	No	No	No
hsa-mir-516a-5p	chr19: 58956213-58956236	4139	TTCTCGAGGAAAGAAGCACTTTC	Yes	Yes	No	No	No
hsa-mir-30a*	chr6: 72169977-72169999	4140	GCTGCAAACATCCGACTGAAAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-183	chr7: 129202042-129202064	4141	AGTGAATTCTACCAGTGCCATA	Yes	Yes	Yes	Yes	Yes
hsa-mir-186	chr1: 71305951-71305973	4142	AGCCCAAAAGGAGAATTCTTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-187	chr18: 31738795-31738817	4143	CCGGCTGCAACACAAGACACGA	No	Yes	Yes	Yes	Yes
hsa-mir-184	chr15: 77289236-77289258	4144	TGGACGGAGAACTGATAAGGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-185	chr22: 18400675-18400697	4145	TGGAGAGAAAGGCAGTTCCTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-198	chr3: 121597239-121597261	4146	GAACCTATCTCCCCTCTGGACC	Yes	Yes	No	No	No
hsa-let-7b	chr22: 44888234-44888256	4147	TGAGGTAGTAGGTTGTGTGGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-455-5p	chr9: 116011549-116011571	4148	TATGTGCCTTTGGACTACATCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-518c	chr19: 58903861-58903884	4149	CAAAGCGCTTCTCTTTAGAGTGT	Yes	Yes	No	No	No
hsa-mir-770-5p	chr14: 100388498-100388521	4150	TCCAGTACCACGTGTCAGGGCCA	Yes	Yes	No	No	No
hsa-mir-380	chr14: 100561145-100561167	4151	TATGTAATATGGTCCACATCTT	Yes	Yes	Yes	No	No
hsa-mir-381	chr14: 100582057-100582079	4152	TATACAAGGGCAAGCTCTCTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-382	chr14: 100590405-100590427	4153	GAAGTTGTTCGTGGTGGATTCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-383	chr8: 14755362-14755384	4154	AGCCACAATCACCTTCTGATCT	Yes	Yes	Yes	No	No
hsa-mir-384	chrX: 76056103-76056123	4155	TATGAACAATTTCTAGGAAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-661	chr8: 145091361-145091385	4156	ACGCGCAGGCCAGAGACCCAGGCA	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-421	chrX: 73354951-73354974	4157	GCGCCCAATTAATGTCTGTTGAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-518f	chr19: 58895132-58895153	4158	GAAAGCGCTTCTCTTTAGAGG	Yes	Yes	No	No	No
hsa-mir-660	chrX: 49664603-49664625	4159	TACCCATTGCATATCGGAGTTG	Yes	Yes	Yes	No	No
hsa-mir-425	chr3: 49032635-49032658	4160	TCAACGGGAGTGATCGTGTCATT	Yes	Yes	Yes	Yes	Yes
hsa-mir-424	chrX: 133508375-133508397	4161	TTCAAAACATGAATTGCTGCTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-518c*	chr19: 58903823-58903846	4162	TCTCTGGAGGGAAGCACTTTCTG	Yes	Yes	No	No	No
hsa-mir-543	chr14: 100568122-100568144	4163	AAACATTCGCGGTGCACTTCTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-18a	chr13: 90801010-90801033	4164	TAAGGTGCATCTAGTGCAGATAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-138-1*	chr3: 44130769-44130791	4165	GCTACTTCACAACACCAGGGCC	No	No	Yes	Yes	Yes
hsa-let-7e*	chr19: 56887902-56887924	4166	CTATACGGCCTCCTAGCTTTCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-545	chrX: 73423685-73423707	4167	GCACACAATAAATGTTTGCTGA	Yes	Yes	No	No	No
hsa-mir-549	chr15: 78921388-78921409	4168	AGAGCTCATCCATAGTTGTCA	Yes	Yes	No	No	No
hsa-mir-549	chr15: 78921423-78921444	4169	TGACAACTATGGATGAGCTCT	Yes	Yes	No	No	No
hsa-mir-133a	chr20: 60572621-60572643	4170	TTTGGTCCCCTTCAACCAGCTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-133a	chr18: 17659670-17659692	4171	CAGCTGGTTGAAGGGGACCAAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-574-3p	chr4: 38546107-38546129	4172	CACGCTCATGCACACACCCACA	No	No	Yes	Yes	No
hsa-mir-133b	chr6: 52121744-52121766	4173	TTTGGTCCCCTTCAACCAGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1237	chr11: 63892730-63892751	4174	TCCTTCTGCTCCGTCCCCCAG	Yes	Yes	No	No	No
hsa-mir-220c	chr19: 53755391-53755413	4175	AGTCTTCACAACAGCCCTGTGT	Yes	No	No	No	No
hsa-mir-369-3p	chr14: 100601730-100601751	4176	AATAATACATGGTTGATCTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-518e	chr19: 58924956-58924977	4177	AAAGCGCTTCCCTTCAGAGTG	Yes	No	No	No	No
hsa-mir-519e*	chr19: 58875018-58875040	4178	TTCTCCAAAAGGGAGCACTTTC	Yes	Yes	No	No	No
hsa-mir-15a	chr13: 49521303-49521325	4179	CACAAACCATTATGTGCTGCTA	Yes	Yes	Yes	Yes	No
hsa-mir-769-5p	chr19: 51214058-51214080	4180	TGAGACCTCTGGGTTCTGAGCT	No	No	No	No	No
hsa-mir-15b	chr3: 161605088-161605110	4181	TAGCAGCACATCATGGTTTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-453	chr14: 100592322-100592345	4182	AGGTTGTCCGTGGTGAGTTCGCA	Yes	Yes	Yes	No	Yes
hsa-mir-876-5p	chr9: 28853672-28853694	4183	TGGTGATTCACAAAGAAATCCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1226	chr3: 47866101-47866123	4184	TCACCAGCCCTGTGTTCCCTAG	Yes	Yes	No	No	Yes
hsa-mir-802	chr21: 36014899-36014922	4185	CAGTAACAAAGATTCATCCTTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-520a-5p	chr19: 58885960-58885981	4186	CTCCAGAGGGAAGTACTTTCT	Yes	Yes	No	No	No
hsa-mir-552	chr1: 34907801-34907822	4187	TTGTCTAACCAGTCACCTGTT	Yes	Yes	No	No	No
hsa-mir-147b	chr15: 43512587-43512609	4188	GTGTGCGGAAATGCTTCTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-432*	chr14: 100420633-100420654	4189	CTGGATGGCTCCTCCATGTCT	Yes	Yes	Yes	Yes	No
hsa-mir-650	chr22: 21495284-21495305	4190	AGGAGGCAGCGCTCTCAGGAC	Yes	Yes	No	No	No
hsa-mir-146a*	chr5: 159844992-159845014	4191	CCTCTGAAATTCAGTTCTTCAG	No	No	Yes	Yes	No
hsa-mir-335	chr7: 129923202-129923225	4192	TCAAGAGCAATAACGAAAAATGT	Yes	Yes	Yes	Yes	No
hsa-mir-520d-3p	chr19: 58915214-58915236	4193	AAAGTGCTTCTCTTTGGTGGGT	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-19b-1*	chr13: 90801461-90801484	4194	AGTTTTGCAGGTTTGCATCCAGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-1231	chr1: 200044365-200044385	4195	GTGTCTGGGCGGACAGCTGC	No	Yes	No	No	No
hsa-mir-146b-3p	chr10: 104186302-104186324	4169	TGCCCTGTGGACTCAGTTCTGG	Yes	No	No	No	No
hsa-mir-875-5p	chr8: 100618233-100618255	4197	CACCTGATAAAACTGAGGTATA	Yes	Yes	Yes	Yes	Yes
hsa-mir-874	chr5: 137011169-137011191	4198	TCGGTCCCTCGGGCCAGGGCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-873	chr9: 28878922-28878943	4199	AGGAGACTCACAAGTTCCTGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-15b*	chr3: 161605126-161605148	4200	CGAATCATTATTTGCTGCTCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-25*	chr7: 99529168-99529189	4201	CAATTGCCCAAGTCTCCGCCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1185	chr14: 100579080-100579101	4202	AGAGGATACCCTTTGTATGTT	Yes	Yes	Yes	No	No
hsa-mir-1185	chr14: 100580301-100580322	4203	AGAGGATACCCTTTGTATGTT	Yes	Yes	Yes	No	No
hsa-mir-720	chr3: 165541848-165541865	4204	TCTCGCTGGGGCCTCCA	Yes	No	No	No	No
hsa-mir-409-3p	chr14: 100601435-100601457	4205	GAATGTTGCTCGGTGAACCCCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1182	chr1: 229222209-229222232	4206	GTCACATCCCTCCCAAGACCCTC	Yes	Yes	No	No	No
hsa-mir-1179	chr15: 86952355-86952376	4207	AAGCATTCTTTCATTGGTTGG	Yes	Yes	No	No	No
hsa-mir-1178	chr12: 118635836-118635857	4208	CTAGGGAAGAACAGTGAGCAA	Yes	Yes	No	No	No
hsa-mir-367*	chr4: 113788519-113788541	4209	AGAGTTGCATATTAGCAACAGT	Yes	Yes	Yes	Yes	No
hsa-mir-150	chr19: 54695900-54695922	4210	CACTGGTACAAGGGTTGGGAGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-153	chr7: 157059801-157059823	4211	GATCACTTTTGTGACTATGCAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-153	chr2: 219867091-219867113	4212	GATCACTTTTGTGACTATGCAA	No	Yes	Yes	No	No
hsa-mir-152	chr17: 43469538-43469559	4213	CCAAGTTCTGTCATGCACTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-155	chr21: 25868165-25868188	4214	TTAATGCTAATCGTGATAGGGGT	Yes	Yes	Yes	Yes	No
hsa-mir-154	chr14: 100595858-100595880	4215	TAGGTTATCCGTGTTGCCTTCG	Yes	Yes	No	Yes	Yes
hsa-mir-634	chr17: 62213711-62213733	4216	AACCAGCACCCCAACTTTGGAC	Yes	No	No	No	No
hsa-mir-377*	chr14: 100598145-100598167	4217	AGAGGTTGCCCTTGGTGAATTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-1228	chr12: 55874604-55874624	4218	TCACACCTGCCTCGCCCCCC	No	Yes	No	No	No
hsa-mir-199a-5p	chr1: 170380354-170380377	4219	GAACAGGTAGTCTGAACACTGGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-199a-5p	chr19: 10789144-10789167	4220	GAACAGGTAGTCTGAACACTGGG	Yes	Yes	Yes	Yes	No
hsa-mir-767-5p	chrX: 151312608-151312631	4221	CATGCTCAGACAACCATGGTGCA	No	Yes	No	Yes	Yes
hsa-mir-151-3p	chr8: 141811867-141811888	4222	CCTCAAGGAGCTTCAGTCTAG	Yes	Yes	Yes	No	No
hsa-mir-154*	chr14: 100595894-100595916	4223	AATCATACACGGTTGACCTATT	Yes	Yes	No	Yes	Yes
hsa-mir-483-5p	chr11: 2111986-2112008	4224	CTCCCTTCTTTCCTCCCGTCTT	No	No	No	Yes	Yes
hsa-mir-33a	chr22: 40626898-40626919	4225	GTGCATTGTAGTTGCATTGCA	Yes	No	Yes	Yes	Yes
hsa-mir-33b	chr17: 17657935-17657955	4226	GCAATGCAACAGCAATGCAC	Yes	Yes	Yes	No	No
hsa-mir-1304	chr11: 93106537-93106559	4227	CACATCTCACTGTAGCCTCAAA	Yes	Yes	No	No	No
hsa-mir-25	chr7: 99529129-99529151	4228	TCAGACCGAGACAAGTGCAATG	Yes	Yes	Yes	Yes	Yes
hsa-mir-1306	chr22: 18453634-18453652	4229	ACGTTGGCTCTGGTGGTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-1307	chr10: 105144047-105144069	4230	CACGACCGACGCCACGCCGAGT	Yes	Yes	Yes	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-1300	chr15: 51017866-51017884	4231	CAGCAGCCTCCTTCTCAA	Yes	No	Yes	Yes	Yes
hsa-mir-21	chr17: 55273415-55273437	4232	TAGCTTATCAGACTGATGTTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-22	chr17: 1563957-1563979	4233	ACAGTTCTTCAACTGGCAGCTT	Yes	No	Yes	Yes	Yes
hsa-mir-596	chr8: 1752818-1752839	4234	AAGCCTGCCCGGCTCCTCGGG	Yes	Yes	No	No	No
hsa-mir-599	chr8: 100618054-100618074	4235	GTTTGATAAACTGACACAAC	Yes	Yes	Yes	Yes	No
hsa-mir-598	chr8: 10930140-10930162	4236	TGACGATGACAACGATGACGTA	Yes	No	No	Yes	Yes
hsa-mir-610	chr11: 28034990-28035011	4237	TCCCAGCACACATTTAGCTCA	Yes	No	No	No	No
hsa-mir-610	chr11: 28034952-28034973	4238	TGAGCTAAATGTGTGCTGGGA	Yes	No	No	No	No
hsa-mir-611	chr11: 61316547-61316570	4239	GTCAGACCCCGAGGGGTCCTCGC	Yes	Yes	No	No	No
hsa-mir-616	chr12: 56199232-56199254	4240	CTGCTCAAACCCTCCAATGACT	Yes	Yes	No	No	No
hsa-mir-617	chr12: 79750502-79750524	4241	GCCACCTTCAAATGGGAAGTCT	Yes	Yes	No	No	No
hsa-mir-614	chr12: 12960082-12960105	4242	GAACGCCTGTTCTTGCCAGGTGG	Yes	No	No	No	No
hsa-mir-517c	chr19: 58936434-58936456	4243	ATCGTGCATCCTTTTAGAGTGT	Yes	Yes	No	No	No
hsa-mir-517b	chr19: 58916184-58916206	4244	TCGTGCATCCCTTTAGAGTGTT	Yes	No	No	No	No
hsa-mir-517a	chr19: 58907386-58907408	4245	ATCGTGCATCCCTTTAGAGTGT	Yes	Yes	No	No	No
hsa-mir-495	chr14: 100569893-100569915	4246	AAACAAACATGGTGCACTTCTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-671-3p	chr7: 150566506-150566527	4247	TCCGGTTCTCAGGGCTCCACC	Yes	Yes	Yes	Yes	Yes
hsa-mir-135a*	chr3: 52303287-52303309	4248	CGCCACGGCTCCAATCCCTATA	Yes	Yes	Yes	Yes	No
hsa-mir-513a-3p	chrX: 146102707-146102730	4249	CCTTCTCAGAAAGGTGAAATTTA	Yes	No	No	No	No
hsa-mir-513a-3p	chrX: 146115069-146115092	4250	CCTTCTCAGAAAGGTGAAATTTA	Yes	Yes	No	No	No
hsa-mir-525-5p	chr19: 58892612-58892633	4251	CTCCAGAGGGATGCACTTTCT	Yes	Yes	No	No	No
hsa-mir-758	chr14: 100562160-100562182	4252	TTTGTGACCTGGTCCACTAACC	Yes	Yes	Yes	Yes	Yes
hsa-mir-187*	chr18: 31738831-31738853	4253	GCCCGGGTCCTGTGTTGTAGCC	No	Yes	Yes	Yes	Yes
hsa-mir-520d-5p	chr19: 58915176-58915196	4254	CTACAAAGGGAAGCCCTTTC	Yes	Yes	No	No	No
hsa-mir-522*	chr19: 58946291-58946313	4255	CTCTAGAGGGAAGCGCTTTCTG	Yes	Yes	No	No	No
hsa-mir-101	chr9: 4840344-4840365	4256	TACAGTACTGTGATAACTGAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-101	chr1: 65296712-65296733	4257	TTCAGTTATCACAGTACTGTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-299-3p	chr14: 100559921-100559943	4258	TATGTGGGATGGTAAACCGCTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-107	chr10: 91342492-91342515	4259	TGATAGCCCTGTACAATGCTGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1278	chr1: 191372304-191372326	4260	TAGTACTGTGCATATCATCTAT	Yes	Yes	Yes	No	No
hsa-mir-1279	chr12: 67953234-67953251	4261	AGAAAGAAGCAATATGA	Yes	No	Yes	Yes	Yes
hsa-mir-219-1-3p	chr6: 33283650-33283672	4262	AGAGTTGAGTCTGGACGTCCCG	Yes	Yes	Yes	No	No
hsa-mir-541	chr14: 100600637-100600659	4263	TGGTGGGCACAGAATCTGGACT	Yes	Yes	Yes	No	No
hsa-mir-1270	chr19: 20371127-20371150	4264	ACACAGCTCTTCCATATCTCCAG	No	No	No	No	No
hsa-mir-1271	chr5: 175727568-175727590	4265	CTTGGCACCTAGCAAGCACTCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1272	chr15: 62841722-62841748	4266	TTTCAGAATTTGCTGCCATCATCATC	Yes	No	No	No	No
hsa-mir-1273	chr8: 101105388-101105413	4267	AAGAAAGAGTCTTGCTTTGTCGCCC	Yes	No	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-1275	chr6: 34075772-34075789	4268	GACAGCCTCTCCCCCAC	Yes	Yes	No	No	No
hsa-mir-1276	chr15: 84114782-84114802	4269	TGTCTCCACAGGGCTCTTTA	Yes	No	No	No	No
hsa-mir-1277	chrX: 117404430-117404452	4270	TACGTAGATATATATGTATTTT	No	Yes	Yes	No	No
hsa-mir-488*	chr1: 175265170-175265191	4271	TTGAGAGTGCCATTATCTGGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-219-2-3p	chr9: 130194731-130194753	4272	ACAGATGTCCAGCCACAATTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-142-5p	chr17: 53763642-53763663	4273	AGTAGTGCTTTCTACTTTATG	Yes	Yes	Yes	Yes	Yes
hsa-mir-615-3p	chr12: 52714060-52714082	4274	TCCGAGCCTGGGTCTCCCTCTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-130b	chr22: 20337642-20337664	4275	CAGTGCAATGATGAAAGGGCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-506	chrX: 146119962-146119983	4276	TCTACTCAGAAGGGTGCCTTA	Yes	Yes	Yes	No	No
hsa-mir-507	chrX: 146120211-146120232	4277	TTCACTCCAAAAGGTGCAAAA	Yes	Yes	No	No	No
hsa-mir-504	chrX: 137577586-137577608	4278	GATAGAGTGCAGACCAGGGTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-885-5p	chr3: 10411214-10411236	4279	AGAGGCAGGGTAGTGTAATGGA	Yes	Yes	Yes	No	No
hsa-mir-944	chr3: 191030457-191030479	4280	AAATTATTGTACATCGGATGAG	Yes	Yes	No	No	No
hsa-mir-500	chrX: 49659790-49659813	4281	TAATCCTTGCTACCTGGGTGAGA	Yes	Yes	Yes	Yes	No
hsa-let-7d*	chr9: 95980997-95981019	4282	CTATACGACCTGCTGCCTTTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-545*	chrX: 73423723-73423745	4283	TCATCTAATAAACATTTACTGA	Yes	Yes	No	No	Yes
hsa-mir-942	chr1: 117438799-117438821	4284	TCTTCTCTGTTTTGGCCATGTG	Yes	Yes	No	No	No
hsa-mir-200a*	chr1: 1093120-1093142	4285	CATCTTACCGGACAGTGCTGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-130a*	chr11: 57165266-57165288	4286	TTCACATTGTGCTACTGTCTGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-1266	chr15: 50356654-50356677	4287	AGCCCTGTTCTACAGCCCTGAGG	Yes	Yes	No	No	No
hsa-mir-548a-3p	chr6: 18680053-18680075	4288	CAAAACTGGCAATTACTTTTGC	Yes	No	No	No	No
hsa-mir-548a-3p	chr6: 135602050-135602072	4289	CAAAACTGGCAATTACTTTTGC	Yes	No	No	No	No
hsa-mir-548a-3p	chr8: 105565787-105565809	4290	GCAAAAGTAATTGCCAGTTTTG	No	Yes	No	No	No
hsa-mir-557	chr1: 166611445-166611468	4291	GTTTGCACGGGTGGGCCTTGTCT	Yes	No	No	No	No
hsa-mir-1238	chr19: 10523858-10523878	4292	CTTCCTCGTCTGTCTGCCCC	No	No	No	No	No
hsa-mir-920	chr12: 24256671-24256691	4293	GGGGAGCTGTGGAAGCAGTA	Yes	Yes	No	No	No
hsa-mir-921	chr1: 164390633-164390658	4294	GAATCCTGGTTCTGTCCCTCACTAG	Yes	Yes	No	No	No
hsa-mir-922	chr3: 198885765-198885788	4295	GACGTAGTCCTATTCTCTGCTGC	Yes	Yes	No	No	No
hsa-mir-923	chr17: 30502320-30502341	4296	AGTTTCTTTTCCTCCGCTGAC	Yes	No	No	No	No
hsa-mir-924	chr18: 35456114-35456134	4297	GCAAGACATCACAAGACTCT	Yes	Yes	No	No	No
hsa-mir-193b*	chr16: 14305337-14305359	4298	CGGGGTTTTGAGGGCGAGATGA	Yes	Yes	Yes	Yes	No
hsa-mir-378	chr5: 149092622-149092643	4299	ACTGGACTTGGAGTCAGAAGG	Yes	Yes	Yes	No	No
hsa-mir-320c	chr18: 20155677-20155697	4300	AAAAGCTGGGTTGAGAGGGT	Yes	No	Yes	Yes	Yes
hsa-mir-320c	chr18: 17517517-17517537	4301	AAAAGCTGGGTTGAGAGGGT	Yes	Yes	Yes	Yes	No
hsa-mir-320b	chr1: 222511373-222511395	4302	TTGCCCTCTCAACCCAGCTTTT	Yes	Yes	No	No	No
hsa-mir-320b	chr1: 117015931-117015953	4303	AAAAGCTGGGTTGAGAGGGCAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-320a	chr8: 22158432-22158454	4304	TCGCCCTCTCAACCCAGCTTTT	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-324-3p	chr17: 7067350-7067370	4305	CCAGCAGCACCTGGGGCAGT	Yes	Yes	Yes Yes	Yes
hsa-mir-370	chr14: 100447275-100447297	4306	GCCTGCTGGGGTGGAACCTGGT	Yes	Yes	Yes Yes	Yes
hsa-mir-431*	chr14: 100417158-100417180	4307	CAGGTCGTCTTGCAGGGCTTCT	Yes	Yes	Yes Yes	Yes
hsa-mir-372	chr19: 58982996-58983019	4308	AAAGTGCTGCGACATTTGAGCGT	Yes	Yes	Yes No	Yes
hsa-mir-375	chr2: 219574613-219574635	4309	TCACGCGAGCCGAACGAACAAA	Yes	Yes	Yes Yes	Yes
hsa-mir-422a	chr15: 61950240-61950262	4310	GCCTTCTGACCCTAAGTCCAGT	Yes	Yes	No No	No
hsa-mir-377	chr14: 100598183-100598205	4311	ATCACACAAAGGCAACTTTTGT	Yes	Yes	Yes Yes	Yes
hsa-mir-362-3p	chrX: 49660352-49660374	4312	AACACACCTATTCAAGGATTCA	Yes	Yes	Yes Yes	Yes
hsa-mir-579	chr5: 32430254-32430277	4313	AATCGCGGTTTATACCAAATGAA	Yes	Yes	No No	No
hsa-mir-578	chr4: 166526903-166526924	4314	CTTCTTGTGCTCTAGGATTGT	Yes	Yes	No No	No
hsa-mir-24-2*	chr19: 13808139-13808161	4315	CTGTGTTTCAGCTCAGTAGGCA	Yes	Yes	Yes Yes	Yes
hsa-mir-573	chr4: 24130972-24130996	4316	CTGATCAGTTACACATCACTTCAG	Yes	Yes	No No	No
hsa-mir-572	chr4: 10979608-10979628	4317	GTCCGCTCGGCGGTGGCCCA	Yes	Yes	No No	No
hsa-mir-571	chr4: 334005-334026	4318	TGAGTTGGCCATCTGAGTGAG	Yes	Yes	No No	No
hsa-mir-570	chr3: 196911510-196911532	4319	CGAAAACAGCAATTACCTTTGC	No	No	No No	No
hsa-mir-577	chr4: 115797378-115797399	4320	TAGATAAAATATTGGTACCTG	Yes	Yes	No No	No
hsa-mir-520c-3p	chr19: 58902571-58902593	4321	AAAGTGCTTCCTTTTAGAGGGT	Yes	Yes	No No	No
hsa-mir-509-3-5p	chrX: 146148905-146148927	4322	CATGATTGCCACGTCTGCAGTA	Yes	No	No No	Yes
hsa-mir-23a*	chr19: 13808443-13808465	4323	AAATCCCATCCCCAGGAACCCC	Yes	Yes	Yes Yes	Yes
hsa-mir-518f*	chr19: 58895095-58895117	4324	CTCTAGAGGGAAGCACTTTCTC	Yes	Yes	No No	No
hsa-mir-195*	chr17: 6861670-6861692	4325	GGAGCAGCACAGCCAATATTGG	Yes	Yes	Yes Yes	Yes
hsa-mir-576-5p	chr4: 110629317-110629339	4326	ATTCTAATTTCTCCACGTCTTT	Yes	Yes	No No	No
hsa-mir-575	chr4: 83893528-83893547	4327	GCTCCTGTCCAACTGGCTC	Yes	No	No No	No
hsa-mir-21*	chr17: 55273453-55273474	4328	CAACACCAGTCGATGGGCTGT	Yes	Yes	No Yes	Yes
hsa-mir-27b*	chr9: 96887565-96887587	4329	AGAGCTTAGCTGATTGGTGAAC	Yes	Yes	Yes Yes	Yes
hsa-mir-217	chr2: 56063658-56063681	4330	TCCAATCAGTTCCTGATGCAGTA	Yes	Yes	Yes Yes	Yes
hsa-mir-214	chr1: 170374578-170374600	4331	ACTGCCTGTCTGTGCCTGCTGT	Yes	Yes	Yes Yes	Yes
hsa-mir-215	chr1: 218357880-218357901	4332	GTCTGTCAATTCATAGGTCAT	Yes	Yes	Yes Yes	Yes
hsa-mir-212	chr17: 1900333-1900354	4333	GGCCGTGACTGGAGACTGTTA	No	Yes	Yes Yes	Yes
hsa-mir-210	chr11: 558111-558133	4334	TCAGCCGCTGTCACACGCACAG	Yes	Yes	Yes Yes	Yes
hsa-mir-211	chr15: 29144589-29144611	4335	AGGCGAAGGATGACAAAGGGAA	Yes	Yes	Yes Yes	Yes
hsa-mir-92a	chrX: 133131239-133131261	4336	ACAGGCCGGGACAAGTGCAATA	Yes	Yes	Yes Yes	Yes
hsa-mir-92a	chr13: 90801615-90801637	4337	TATTGCACTTGTCCCGGCCTGT	Yes	Yes	Yes Yes	Yes
hsa-mir-92b	chr1: 153431651-153431673	4338	TATTGCACTCGTCCCGGCCTCC	No	Yes	Yes Yes	Yes
hsa-mir-218	chr4: 20139019-20139040	4339	TTGTGCTTGATCTAACCATGT	Yes	Yes	Yes Yes	Yes
hsa-mir-218	chr5: 168127793-168127814	4340	ACATGGTTAGATCAAGCACAA	Yes	Yes	Yes Yes	Yes
hsa-mir-515-3p	chr19: 58874118-58874140	4341	GAGTGCCTTCTTTTGGAGCGTT	Yes	No	No No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-515-3p	chr19: 58880124-58880146	4342	GAGTGCCTTCTTTTGGAGCGTT	Yes	No	No	No	No
hsa-mir-1	chr18: 17662973-17662995	4343	ATACATACTTCTTTACATTCCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1	chr20: 60562002-60562024	4344	TGGAATGTAAAGAAGTATGTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-425*	chr3: 49032595-49032617	4345	GGGCGGACACGACATTCCCGAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-522	chr19: 58946329-58946351	4346	AAAATGGTTCCCTTTAGAGTGT	Yes	Yes	No	No	No
hsa-mir-7	chr9: 85774546-85774569	4347	ACAACAAAATCACTAGTCTTCCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-7	chr15: 86956090-86956113	4348	TGGAAGACTAGTGATTTTGTTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-7	chr19: 4721711-4721734	4349	TGGAAGACTAGTGATTTTGTTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-9	chr15: 87712266-87712289	4350	TCTTTGGTTATCTAGCTGTATGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-9	chr1: 154656807-154656830	4351	TCATACAGCTAGATAACCAAAGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-9	chr5: 87998475-87998498	4352	TCATACAGCTAGATAACCAAAGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-615-5p	chr12: 52714017-52714039	4353	GGGGGTCCCCGGTGCTCGGATC	Yes	Yes	Yes	Yes	Yes
hsa-mir-512-3p	chr19: 58861794-58861816	4354	AAGTGCTGTCATAGCTGAGGTC	Yes	No	No	No	No
hsa-mir-512-3p	chr19: 58864278-58864300	4355	AAGTGCTGTCATAGCTGAGGTC	No	Yes	No	No	No
hsa-mir-202*	chr10: 134911066-134911088	4356	CAAAGAAGTATATGCATAGGAA	Yes	No	Yes	Yes	Yes
hsa-mir-888*	chrX: 144884003-144884025	4357	TTCACCCAAAGAGGTGTCAGTC	No	Yes	No	No	No
hsa-mir-143*	chr5: 148788699-148788721	4358	GGTGCAGTGCTGCATCTCTGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-526b	chr19: 58889471-58889494	4359	CTCTTGAGGGAAGCACTTTCTGT	Yes	Yes	No	No	No
hsa-mir-656	chr14: 100602855-100602876	4360	AATATTATACAGTCAACCTCT	Yes	Yes	Yes	No	No
hsa-mir-657	chr17: 76713685-76713708	4361	CCTAGAGAGGGTGAGAACCTGCC	Yes	Yes	No	No	No
hsa-mir-655	chr14: 100585699-100585721	4362	ATAATACATGGTTAACCTCTTT	Yes	No	Yes	No	No
hsa-mir-652	chrX: 109185272-109185293	4363	AATGGCGCCACTAGGGTTGTG	Yes	Yes	No	No	No
hsa-mir-653	chr7: 92950070-92950091	4364	CAGTAGAGATTGTTTCAACAC	Yes	Yes	Yes	Yes	Yes
hsa-mir-518a-3p	chr19: 58926121-58926143	4365	GAAAGCGCTTCCCTTTGCTGGA	Yes	No	No	No	No
hsa-mir-518a-3p	chr19: 58934450-58934472	4366	GAAAGCGCTTCCCTTTGCTGGA	Yes	No	No	No	No
hsa-mir-651	chrX: 8055020-8055042	4367	TTTAGGATAAGCTTGACTTTTG	Yes	No	No	No	No
hsa-mir-302f	chr18: 26132899-26132916	4368	TAATTGCTTCCATGTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1184	chrX: 154265958-154265981	4369	GGAAGCCATCAAGTCGCTGCAGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-1184	chrX: 154340431-154340454	4370	CCTGCAGCGACTTGATGGCTTCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-1184	chrX: 153768844-153768867	4371	GGAAGCCATCAAGTCGCTGCAGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-302d	chr4: 113788610-113788633	4372	ACACTCAAACATGGAAGCACTTA	Yes	Yes	Yes	Yes	No
hsa-mir-302c	chr4: 113788970-113788993	4373	CCACTGAAACATGGAAGCACTTA	Yes	Yes	Yes	Yes	No
hsa-mir-302b	chr4: 113789093-113789116	4374	CTACTAAAACATGGAAGCACTTA	Yes	Yes	Yes	Yes	No
hsa-mir-1180	chr17: 19188418-19188440	4375	ACACACCCACGCGAGCCGGAAA	Yes	Yes	Yes	No	No
hsa-mir-1181	chr19: 10375180-10375201	4376	CGGCTCGGGTGGCGGCGACGG	Yes	Yes	No	No	No
hsa-mir-629*	chr15: 68158779-68158801	4377	GCTGGGCTTACGTTGGGAGAAC	No	No	No	No	No
hsa-mir-302e	chr11: 7212577-7212594	4378	TAAGTGCTTCCATGCTT	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-103	chr5: 167920486-167920509	4379	TCATAGCCCTGTACAATGCTGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-103	chr20: 3846187-3846210	4380	AGCAGCATTGTACAGGGCTATGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-100	chr11: 121528192-121528214	4381	CACAAGTTCGGATCTACGGGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-138-2*	chr16: 55449986-55450008	4382	GCTATTTCACGACACCAGGGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-122*	chr18: 54269335-54269357	4383	AACGCCATTATCACACTAAATA	Yes	Yes	Yes	Yes	Yes
hsa-mir-105	chrX: 151311392-151311415	4384	ACCACAGGAGTCTGAGCATTTGA	Yes	Yes	Yes	No	No
hsa-mir-105	chrX: 151313585-151313608	4385	ACCACAGGAGTCTGAGCATTTGA	Yes	Yes	Yes	No	No
hsa-mir-223*	chrX: 65155461-65155483	4386	CGTGTATTTGACAAGCTGAGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-363*	chrX: 133131120-133131142	4387	AAATTGCATCGTGATCCACCCG	No	Yes	Yes	Yes	Yes
hsa-mir-28-5p	chr3: 189889275-189889297	4388	AAGGAGCTCACAGTCTATTGAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-150*	chr19: 54695865-54695887	4389	CTGTCCCCCAGGCCTGTACCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-99a*	chr21: 16833328-16833350	4390	CAAGCTCGCTTCTATGGGTCTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-1825	chr20: 30289293-30289311	4391	TCCAGTGCCCTCCTCTCC	Yes	Yes	No	No	No
hsa-mir-129*	chr7: 127635208-127635230	4392	AAGCCCTTACCCCAAAAAGTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-556-3p	chr1: 160579013-160579035	4393	ATATTACCATTAGCTCATCTTT	Yes	No	No	No	No
hsa-mir-10b	chr2: 176723302-176723325	4394	TACCCTGTAGAACCGAATTTGTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-1827	chr12: 99107840-99107858	4395	TGAGGCAGTAGATTGAAT	Yes	Yes	No	No	No
hsa-mir-10a	chr17: 44012264-44012287	4396	CACAAATTCGGATCTACAGGGTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-623	chr13: 98806400-98806423	4397	ATCCCTTGCAGGGGCTGTTGGGT	Yes	Yes	No	No	No
hsa-mir-622	chr13: 89681496-89681517	4398	ACAGTCTGCTGAGGTTGGAGC	Yes	No	No	No	No
hsa-mir-621	chr13: 40282961-40282982	4399	GGCTAGCAACAGCGCTTACCT	Yes	No	No	No	No
hsa-mir-620	chr12: 115070762-115070782	4400	ATTTCTATATCTATCTCCAT	Yes	No	No	No	No
hsa-mir-127-5p	chr14: 100419090-100419112	4401	CTGAAGCTCAGAGGGCTCTGAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-626	chr15: 39771134-39771153	4402	AGCTGTCTGAAAATGTCTT	Yes	No	No	No	No
hsa-mir-625	chr14: 65007622-65007643	4403	GGACTATAGAACTTTCCCCCT	Yes	No	No	No	No
hsa-mir-625	chr14: 65007586-65007607	4404	AGGGGGAAAGTTCTATAGTCC	Yes	No	No	No	No
hsa-mir-182*	chr7: 129197481-129197502	4405	TAGTTGGCAAGTCTAGAACCA	Yes	Yes	Yes	Yes	No
hsa-mir-1292	chr20: 2581424-2581449	4406	TGGGAACGGGTTCCGGCAGACGCTG	Yes	No	No	No	No
hsa-mir-342-3p	chr14: 99645804-99645827	4407	TCTCACACAGAAATCGCACCCGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1290	chr1: 19096158-19096177	4408	TCCCTGATCCAAAAATCCA	Yes	Yes	No	No	No
hsa-mir-1291	chr12: 47334543-47334567	4409	ACTGCTGGTCTTCAGTCAGGGCCA	Yes	Yes	Yes	No	No
hsa-mir-1296	chr10: 64802777-64802799	4410	GGAGATGGAGCCAGGGCCCTAA	Yes	Yes	Yes	No	No
hsa-mir-1297	chr13: 53784116-53784133	4411	CACCTGAATTACTTGAA	Yes	Yes	Yes	No	No
hsa-mir-1294	chr5: 153706905-153706927	4412	TGTGAGGTTGGCATTGTTGTCT	Yes	No	No	No	No
hsa-mir-1225-5p	chr16: 2080264-2080286	4413	CCCCCCACTGGGCCGTACCCAC	Yes	Yes	Yes	Yes	Yes
hsa-mir-509-5p	chrX: 146148020-146148041	4414	TGATTGCCACTGTCTGCAGTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-509-5p	chrX: 146149795-146149816	4415	TGATTGCCACTGTCTGCAGTA	Yes	Yes	No	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-1224-3p	chr3: 185441950-185441971	4416	CCCCACCTCCTCTCTCCTCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-140-3p	chr16: 68524545-68524566	4417	TACCACAGGGTAGAACCACGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-532-3p	chrX: 49654549-49654571	4418	CCTCCCACACCCAAGGCTTGCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1298	chrX: 113855922-113855944	4419	TTCATTCGGCTGTCCAGATGTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-26b	chr2: 218975623-218975644	4420	TTCAAGTAATTCAGGATAGGT	Yes	Yes	Yes	Yes	Yes
hsa-let-7f-2*	chrX: 53600881-53600903	4421	GGAAAGACAGTAGACTGTATAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-585	chr5: 168623197-168623216	4422	TAGCATACAGATACGCCCA	Yes	No	No	No	No
hsa-mir-490-5p	chr7: 136238491-136238511	4423	CCATGGATCTCCAGGTGGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-519c-3p	chr19: 58881587-58881609	4424	AAAGTGCATCTTTTTAGAGGAT	Yes	Yes	No	No	No
hsa-mir-513a-5p	chrX: 146115109-146115127	4425	ATGACACCTCCCTGTGAA	Yes	Yes	Yes	No	No
hsa-mir-513a-5p	chrX: 146102747-146102765	4426	ATGACACCTCCCTGTGAA	Yes	Yes	Yes	No	No
hsa-mir-591	chr7: 95686969-95686989	4427	ACAATGAGAACCCATGGTCT	Yes	No	No	No	No
hsa-mir-191*	chr3: 49033067-49033089	4428	GGGGACGAAATCCAAGCGCAGC	Yes	Yes	Yes	No	No
hsa-mir-1305	chr4: 183327489-183327511	4429	TTTTCAACTCTAATGGGAGAGA	No	No	No	Yes	No
hsa-mir-624	chr14: 30553625-30553646	4430	AGGTAATACCAATACCTTGTG	Yes	No	No	No	No
hsa-mir-593	chr7: 127509226-127509245	4431	TGTCTCTGCTGGGGTTTCT	Yes	Yes	No	No	No
hsa-mir-302a	chr4: 113788790-113788813	4432	TCACCAAAACATGGAAGCACTTA	Yes	Yes	Yes	Yes	No
hsa-mir-592	chr7: 126485437-126485459	4433	ACATCATCGCATATTGACACAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-1293	chr12: 48914231-48914253	4434	GCACAAATCTCCAGACCACCCA	Yes	Yes	No	No	No
hsa-mir-30e*	chr1: 40992671-40992693	4435	CTTTCAGTCGGATGTTTACAGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-432	chr14: 100420585-100420608	4436	TCTTGGAGTAGGTCATTGGGTGG	Yes	Yes	Yes	Yes	No
hsa-mir-629	chr15: 68158819-68158840	4437	AGTTCTCCCAACGTAAACCCA	No	No	No	No	No
hsa-mir-96*	chr7: 129201772-129201794	4438	CATATTGGCACTGCACATGATT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1301	chr2: 25405023-25405047	4439	GAAGTCACTCCCAGGCAGCTGCAA	No	No	Yes	Yes	Yes
hsa-mir-200b*	chr1: 1092366-1092388	4440	CATCTTACTGGGCAGCATTGGA	No	No	Yes	Yes	Yes
hsa-mir-181c*	chr19: 13846576-13846598	4441	AACCATCGACCGTTGAGTGGAC	Yes	Yes	Yes	Yes	Yes
hsa-mir-508-3p	chrX: 146126154-146126177	4442	TCTACTCCAAAAGGCTACAATCA	Yes	No	No	No	No
hsa-mir-1303	chr5: 154045579-154045601	4443	TTTAGAGACGGGGTCTTGCTCT	Yes	Yes	No	No	No
hsa-mir-539	chr14: 100583418-100583440	4444	GGAGAAATTATCCTTGGTGTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-10b*	chr2: 176723341-176723363	4445	ACAGATTCGATTCTAGGGGAAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-612	chr11: 64968519-64968544	4446	GCTGGGCAGGGCTTCTGAGCTCCTT	Yes	Yes	No	No	No
hsa-mir-613	chr12: 12808909-12808929	4447	AGGAATGTTCCTTCTTTGCC	Yes	No	No	No	No
hsa-mir-1295	chr1: 169337502-169337523	4448	TCACCCAGATCTGCGGCCTAA	Yes	Yes	No	No	No
hsa-mir-196a	chr17: 44064892-44064914	4449	CCCAACAACATGAAACTACCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-196a	chr12: 52671812-52671834	4450	TAGGTAGTTTCATGTTGTTGGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-196b	chr7: 27175671-27175693	4451	CCCAACAACAGGAAACTACCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-296-3p	chr20: 56826075-56826097	4452	GGAGAGCCTCCACCCAACCCTC	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-518d-3p	chr19: 58929994-58930015	4453	CAAAGCGCTTCCCTTTGGAGC	Yes	Yes	No	No	No
hsa-mir-1308	chrX: 21990211-21990229	4454	CCACTGAACCACCCATGC	No	No	No	No	No
hsa-mir-92a-2*	chrX: 133131278-133131300	4455	GTAATGCAACAAATCCCCACCC	Yes	Yes	No	No	No
hsa-mir-658	chr22: 36570239-36570264	4456	ACCAACGGACCTACTTCCCTCCGCC	Yes	No	No	Yes	Yes
hsa-mir-106b*	chr7: 99529560-99529582	4457	GCAGCAAGTACCCACAGTGCGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-374a*	chrX: 73423854-73423876	4458	AATTACAATACAATCTGATAAG	Yes	Yes	Yes	No	No
hsa-mir-595	chr7: 158018185-158018206	4459	AGACACACCACGGCACACTTC	Yes	Yes	No	No	No
hsa-mir-518d-5p	chr19: 58929957-58929979	4460	CTCTAGAGGGAAGCACTTTCTG	Yes	No	No	No	No
hsa-mir-590-5p	chr7: 73243478-73243500	4461	GAGCTTATTCATAAAAGTGCAG	Yes	Yes	Yes	No	No
hsa-mir-448	chrX: 113964342-113964364	4462	TTGCATATGTAGGATGTCCCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-326	chr11: 74723799-74723819	4463	CTGGAGGAAGGGCCCAGAGG	Yes	No	Yes	Yes	Yes
hsa-mir-325	chrX: 76142279-76142302	4464	ACACTTACTGGACACCTACTAGG	No	Yes	Yes	Yes	Yes
hsa-mir-632	chr17: 27701300-27701319	4465	GTGTCTGCTTCCTGTGGGA	Yes	Yes	Yes	No	No
hsa-mir-328	chr16: 65793730-65793752	4466	ACGGAAGGGCAGAGAGGGCCAG	Yes	No	Yes	Yes	Yes
hsa-mir-329	chr14: 100563240-100563262	4467	AACACACCTGGTTAACCTCTTT	Yes	Yes	Yes	No	Yes
hsa-mir-329	chr14: 100562923-100562945	4468	AACACACCTGGTTAACCTCTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-659	chr22: 36573645-36573667	4469	TGGGGACCCTCCCTGAACCAAG	Yes	Yes	No	No	No
hsa-mir-214*	chr1: 170374619-170374641	4470	GCACAGCAAGTGTAGACAGGCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-483-3p	chr11: 2111947-2111968	4471	AAGACGGGAGGAGAGGAGTGA	No	No	Yes	Yes	Yes
hsa-mir-376a*	chr14: 100576877-100576899	4472	GTAGATTCTCCTTCTATGAGTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-218-1*	chr4: 20139062-20139084	4473	ATGGTTCCGTCAAGCACCATGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-302d*	chr4: 113788649-113788671	4474	GCAAGTGCCTCCATGTTAAAGT	Yes	Yes	Yes	Yes	No
hsa-mir-887	chr5: 15988337-15988359	4475	GTGAACGGGCGCCATCCCGAGG	No	Yes	No	No	No
hsa-mir-380*	chr14: 100561110-100561132	4476	TGGTTGACCATAGAACATGCGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-32*	chr9: 110848331-110848353	4477	AAATATCACACACACTAAATTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-889	chr14: 100584038-100584059	4478	TTAATATCGGACAACCATTGT	Yes	Yes	Yes	No	No
hsa-mir-768-5p	chr16: 70349860-70349886	4479	ATCACTCCGTACTTTCATCCTCCAAC	Yes	Yes	Yes	No	No
hsa-mir-501-3p	chrX: 49661119-49661141	4480	AATGCACCCGGGCAAGGATTCT	Yes	No	Yes	Yes	Yes
hsa-mir-485-3p	chr14: 100591553-100591575	4481	GTCATACACGGCTCTCCTCTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1234	chr8: 145596285-145596307	4482	GTGGGGTGGGTGGTCAGGCCGA	Yes	Yes	No	No	No
hsa-mir-22*	chr17: 1563995-1564017	4483	TAAAGCTTGCCACTGAAGAACT	Yes	No	Yes	Yes	Yes
hsa-mir-125a-5p	chr19: 56888332-56888356	4484	TCCCTGAGACCCTTTAACCTGTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-643	chr19: 57476921-57476943	4485	ACTTGTATGCTAGCTCAGGTAG	Yes	Yes	No	No	No
hsa-mir-147	chr9: 122047083-122047103	4486	GCAGAAGCATTTCCACACAC	Yes	Yes	No	Yes	No
hsa-mir-144	chr17: 24212691-24212711	4487	AGTACATCATCTATACTGTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-145	chr5: 148790416-148790439	4488	GTCCAGTTTTCCCAGGAATCCCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-143	chr5: 148788733-148788754	4489	TGAGATGAAGCACTGTAGCTC	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-597	chr8: 9636606-9636628	4490	TGTGTCACTCGATGACCACTGT	Yes	Yes	No	No	No
hsa-mir-141	chr12: 6943578-6943600	4491	TAACACTGTCTGGTAAAGATGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-512-5p	chr19: 58864241-58864264	4492	CACTCAGCCTTGAGGGCACTTTC	Yes	Yes	No	No	No
hsa-mir-512-5p	chr19: 58861757-58861780	4493	CACTCAGCCTTGAGGGCACTTTC	Yes	Yes	No	No	No
hsa-mir-323-5p	chr14: 100561836-100561858	4494	AGGTGGTCCGTGGCGCGTTCGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-224	chrX: 150877758-150877779	4495	AACGGAACCACTAGTGACTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-223	chrX: 65155503-65155525	4496	TGTCAGTTTGTCAAATACCCCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-222	chrX: 45491385-45491406	4497	ACCCAGTAGCCAGATGTAGCT	No	Yes	Yes	Yes	Yes
hsa-mir-221	chrX: 45490551-45490574	4498	GAAACCCAGCAGACAATGTAGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-149	chr2: 241044104-241044127	4499	TCTGGCTCCGTGTCTTCACTCCC	Yes	Yes	Yes	Yes	No
hsa-mir-520a-3p	chr19: 58885998-58886020	4500	AAAGTGCTTCCCTTTGGACTGT	Yes	Yes	No	No	No
hsa-mir-548c-5p	chr12: 63302579-63302601	4501	AAAAGTAATTGCGGTTTTTGCC	Yes	Yes	No	No	No
hsa-mir-374b	chrX: 73355146-73355168	4502	CACTTAGCAGGTTGTATTATAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-26a	chr12: 56504707-56504729	4503	AGCCTATCCTGGATTACTTGAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-26a	chr3: 37985907-37985929	4504	TTCAAGTAATCCAGGATAGGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-374a	chrX: 73423884-73423906	4505	CACTTATCAGGTTGTATTATAA	Yes	Yes	Yes	Yes	No
hsa-mir-1302	chr9: 99165698-99165719	4506	TTTAGCATAAGTATGTCCCAA	Yes	Yes	No	No	No
hsa-mir-1302	chr15: 100318229-100318250	4507	TTTAGCATAAGTATGTCCCAA	Yes	Yes	No	No	No
hsa-mir-1302	chr12: 111617269-111617290	4508	TTTAGCATAAGTATGTCCCAA	Yes	No	No	No	No
hsa-mir-1302	chr8: 142865522-142865543	4509	TTTAGCATAAGTATGTCCCAA	Yes	Yes	No	No	No
hsa-mir-1302	chr2: 114057050-114057071	4510	TTTAGCATAAGTATGTCCCAA	Yes	Yes	No	No	No
hsa-mir-1302	chr1: 20300-20321	4511	TTGGGACATACTTATGCTAAA	Yes	Yes	No	No	No
hsa-mir-1302	chr7: 18133381-18133402	4512	TTTAGCATAAGTATGTCCCAA	Yes	Yes	No	No	No
hsa-mir-1302	chr19: 23044-23065	4513	TTGGGACATACTTATGCTAAA	Yes	Yes	No	No	No
hsa-mir-1302	chr2: 207842296-207842317	4514	TTTAGCATAAGTATGTCCCAA	Yes	Yes	No	No	No
hsa-mir-1302	chr9: 20215-20236	4515	TTGGGACATACTTATGCTAAA	Yes	Yes	No	No	No
hsa-mir-1302	chr20: 48664632-48664653	4516	TTTAGCATAAGTATGTCCCAA	No	No	No	No	No
hsa-mir-624*	chr14: 30553662-30553684	4517	TGAACACAAGGTACTGGTACTA	Yes	Yes	No	No	No
hsa-mir-619	chr12: 107754827-107754851	4518	ACTGGGCACAAACATGTCCAGGTC	Yes	No	No	No	No
hsa-mir-586	chr6: 45273448-45273470	4519	GGACCTAAAAATACAATGCATA	Yes	Yes	No	No	No
hsa-mir-587	chr6: 107338707-107338728	4520	TTTCCATAGGTGATGAGTCAC	Yes	No	No	No	No
hsa-mir-584	chr5: 148422128-148422150	4521	CTCAGTCCCAGGCAAACCATAA	Yes	Yes	No	No	No
hsa-mir-30d*	chr8: 135886303-135886325	4522	GCAGCAAACATCTGACTGAAAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-450a	chrX: 133502088-133502110	4523	ATATTAGGAACACATCGCAAAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-450a	chrX: 133502259-133502281	4524	ATATTAGGAACACATCGCAAAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-583	chr5: 95440612-95440633	4525	CAAAGAGGAAGGTCCCATTAC	Yes	Yes	No	No	No
hsa-mir-580	chr5: 36183765-36183787	4526	CCTAATGATTCATCATTCTCAA	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-581	chr5: 53283150-53283171	4527	ACTGATCTAGAGAACACAAGA	Yes	Yes	No	No	No
hsa-mir-129-3p	chr11: 43559575-43559597	4528	AAGCCCTTACCCCAAAAAGCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-331-5p	chr12: 94226351-94226373	4529	CTAGGTATGGTCCCAGGGATCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-665	chr14: 100411164-100411184	4530	ACCAGGAGGCTGAGGCCCCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-664	chr1: 218440513-218440536	4531	TGTAGGCTGGGGATAAATGAATA	Yes	Yes	No	Yes	Yes
hsa-mir-663	chr20: 26136878-26136900	4532	GCGGTCCCGCGGCGCCCCGCCT	Yes	No	No	No	No
hsa-mir-662	chr16: 760243-760264	4533	TCCCACGTTGTGGCCCAGCAG	No	Yes	Yes	Yes	Yes
hsa-mir-588	chr6: 126847484-126847505	4534	TTGGCCACAATGGGTTAGAAC	Yes	No	No	No	No
hsa-mir-589	chr7: 5502029-5502051	4535	CTCAGAGCAGACGTGGTTCTCA	Yes	Yes	Yes	No	No
hsa-mir-220a	chrX: 122523693-122523714	4536	AAAGTGTCAGATACGGTGTGG	Yes	Yes	No	No	No
hsa-mir-220b	chr19: 6446968-6446989	4537	CCACCACCGTGTCTGACACTT	Yes	Yes	Yes	Yes	No
hsa-mir-371-3p	chr19: 58982781-58982804	4538	AAGTGCCGCCATCTTTTGAGTGT	Yes	Yes	Yes	No	Yes
hsa-mir-744	chr17: 11925950-11925972	4539	TGCGGGGCTAGGGCTAACAGCA	Yes	Yes	Yes	Yes	No
hsa-mir-934	chrX: 135460716-135460738	4540	TGTCTACTACTGGAGACACTGG	Yes	Yes	No	No	No
hsa-mir-628-5p	chr15: 53452480-53452502	4541	CCTCTAGTAAATATGTCAGCAT	Yes	Yes	Yes	No	Yes
hsa-mir-888	chrX: 144884039-144884060	4542	TGACTGACAGCTTTTTGAGTA	Yes	Yes	No	No	No
hsa-mir-126*	chr9: 138684888-138684909	4543	CATTATTACTTTTGGTACGCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-99b*	chr19: 56887720-56887742	4544	CAAGCTCGTGTCTGTGGGTCCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-137	chr1: 98284234-98284257	4545	CTACGCGTATTCTTAAGCAATAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-136	chr14: 100420805-100420828	4546	ACTCCATTTGTTTTGATGATGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-149*	chr2: 241044145-241044166	4547	AGGGAGGGACGGGGGCTGTGC	Yes	Yes	Yes	Yes	No
hsa-mir-134	chr14: 100590783-100590805	4548	TGTGACTGGTTGACCAGAGGGG	Yes	Yes	Yes	Yes	Yes
hsa-mir-138	chr16: 55449939-55449962	4549	AGCTGGTGTTGTGAATCAGGCCG	Yes	Yes	Yes	Yes	Yes
hsa-mir-138	chr3: 44130729-44130752	4550	AGCTGGTGTTGTGAATCAGGCCG	No	No	Yes	Yes	Yes
hsa-mir-1269	chr4: 66825202-66825224	4551	CTGGACTGAGCCGTGCTACTGG	Yes	Yes	No	No	No
hsa-mir-1268	chr15: 20014622-20014640	4552	CCCCCACCACCACGCCCG	No	No	No	No	No
hsa-mir-196a*	chr12: 52671849-52671871	4553	CGGCAACAAGAAACTGCCTGAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-20b*	chrX: 133131508-133131530	4554	CTGGAAGTGCCCATACTACAGT	Yes	Yes	Yes	No	No
hsa-mir-199a-3p	chr19: 10789104-10789126	4555	TAACCAATGTGCAGACTACTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-199a-3p	chr1: 170380316-170380338	4556	TAACCAATGTGCAGACTACTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1263	chr3: 165372004-165372026	4557	ACTCAGTATGCCAGGGTACCAT	Yes	No	No	No	No
hsa-mir-1262	chr1: 68421846-68421868	4558	ATCCTTCTACAAATTCACCCAT	Yes	Yes	No	No	No
hsa-mir-1261	chr11: 90241995-90242014	4559	AAGCCAAAGCCTTATCCAT	Yes	Yes	No	No	No
hsa-mir-1260	chr14: 76802326-76802344	4560	ATCCCACCTCTGCCACCA	Yes	Yes	No	No	No
hsa-mir-1267	chr13: 106981565-106981586	4561	TGGGGATTACACTTCAACAGG	Yes	Yes	No	No	No
hsa-mir-151-5p	chr8: 141811903-141811924	4562	ACTAGACTGTGAGCTCCTCGA	Yes	Yes	Yes	No	No
hsa-mir-1265	chr10: 14518593-14518615	4563	CAGGATGTGGTCAAGTGTTGTT	Yes	Yes	No	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-1264	chrX: 113793426-113793449	4564	CAAGTCTTATTTGAGCACCTGTT	Yes	Yes	Yes	No	Yes
hsa-mir-125b-2*	chr21: 16884480-16884502	4565	TCACAAGTCAGGCTCTTGGGAC	Yes	Yes	Yes	Yes	Yes
hsa-mir-33a*	chr22: 40626938-40626960	4566	CAATGTTTCCACAGTGCATCAC	Yes	No	Yes	Yes	Yes
hsa-mir-339-5p	chr7: 1029151-1029174	4567	CGTGAGCTCCTGGAGGACAGGGA	Yes	Yes	Yes	Yes	No
hsa-mir-708*	chr11: 78790723-78790745	4568	CTAGAAGCTCACAGTCTAGTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-1255a	chr4: 102470544-102470567	4569	AATCTACTTTCTTTGCTCATCCT	Yes	Yes	No	No	No
hsa-mir-1255b	chr4: 36104421-36104443	4570	AACCACTTTCTTTGCTCATCCG	Yes	No	No	No	No
hsa-mir-1255b	chr1: 166234526-166234548	4571	CGGATGAGCAAAGAAAGTGGTT	Yes	No	No	No	No
hsa-mir-7-1*	chr9: 85774505-85774527	4572	TATGGCAGACTGTGATTTGTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-199b-3p	chr9: 130046844-130046866	4573	TAACCAATGTGCAGACTACTGT	Yes	Yes	Yes	Yes	No
hsa-mir-641	chr19: 45480349-45480373	4574	GAGGTGACTCTATCCTATGTCTTT	Yes	No	No	No	No
hsa-mir-193a-3p	chr17: 26911181-26911203	4575	AACTGGCCTACAAAGTCCCAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-186*	chr1: 71305912-71305934	4576	CCCAAAAAATTCACCTTTGGGC	Yes	Yes	Yes	No	Yes
hsa-mir-139-5p	chr11: 72003794-72003816	4577	CTGGAGACACGTGCACTGTAGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-671-5p	chr7: 150566467-150566490	4578	AGGAAGCCCTGGAGGGGCTGGAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-582-3p	chr5: 59035212-59035234	4579	GGTTCAGTTGTTCAACCAGTTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-548d-5p	chr17: 62898117-62898139	4580	GGCAAAAACCACAATTACTTTT	Yes	No	No	No	No
hsa-mir-548d-5p	chr8: 124429505-124429527	4581	GGCAAAAACCACAATTACTTTT	No	Yes	No	No	No
hsa-mir-130b*	chr22: 20337604-20337625	4582	ACTCTTTCCCTGTTGCACTAC	Yes	Yes	Yes	Yes	Yes
hsa-let-7f-1*	chr9: 95978511-95978533	4583	CTATACAATCTATTGCCTTCCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-767-3p	chrX: 151312574-151312597	4584	AGAAACCATGGGGTATGAGCAGA	No	Yes	Yes	Yes	Yes
hsa-mir-363	chrX: 133131077-133131099	4585	TACAGATGGATACCGTGCAATT	No	Yes	Yes	Yes	Yes
hsa-mir-32	chr9: 110848372-110848394	4586	TGCAACTTAGTAATGTGCAATA	Yes	Yes	Yes	Yes	Yes
hsa-mir-31	chr9: 21502156-21502177	4587	AGCTATGCCAGCATCTTGCCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-525-3p	chr19: 58892649-58892671	4588	GAAGGCGCTTCCCTTTAGAGCG	Yes	Yes	No	No	No
hsa-mir-181d	chr19: 13646723-13846746	4589	AACATTCATTGTTGTCGGTGGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-568	chr3: 115518071-115518091	4590	GTGTGTATACATTTATACAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-548b-5p	chr6: 119431961-119431983	4591	GGCCAAAACCACAATTACTTTT	Yes	No	No	No	No
hsa-mir-559	chr2: 47458332-47458353	4592	TAAAGTAAATATGCACCAAAA	Yes	No	No	No	No
hsa-mir-559	chr2: 47458372-47458393	4593	TTTTGGTGCATATTTACTTTA	Yes	No	No	No	No
hsa-mir-181a	chr9: 126494579-126494602	4594	AACATTCAACGCTGTCGGTGAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-181a	chr1: 197094859-197094882	4595	ACTCACCGACAGCGTTGAATGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-181b	chr9: 126495824-126495847	4596	AACATTCATTGCTGTCGGTGGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-181b	chr1: 197094676-197094699	4597	ACCCACCGACAGCAATGAATGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-181c	chr19: 13646538-13846560	4598	AACATTCAACCTGTCGGTGAGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-34b*	chr11: 110888884-110888907	4599	TAGGCAGTGTCATTAGCTGATTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-188-5p	chrX: 49654862-49654883	4600	CATCCCTTGCATGGTGGAGGG	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-367	chr4: 113788481-113788503	4601	TCACCATTGCTAAAGTGCAATT	Yes	Yes	Yes	Yes	No
hsa-mir-365	chr17: 26926609-26926631	4602	TAATGCCCCTAAAAATCCTTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-365	chr16: 14310697-14310719	4603	TAATGCCCCTAAAAATCCTTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-449b	chr5: 54502290-54502312	4604	GCCAGCTAACAATACACTGCCT	Yes	Yes	Yes	No	Yes
hsa-mir-29a*	chr7: 130212084-130212106	4605	CTGAACACCAAAAGAAATCAGT	Yes	Yes	Yes	Yes	Yes
hsa-let-7c*	chr21: 16834050-16834072	4606	TAGAGTTACACCCTGGGAGTTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-558	chr2: 32610783-32610802	4607	TGAGCTGCTGTACCAAAAT	Yes	Yes	No	No	No
hsa-mir-10a*	chr17: 44012224-44012246	4608	TATTCCCCTAGATACGAATTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-518e*	chr19: 58924918-58924940	4609	CTCTAGAGGGAAGCGCTTTCTG	Yes	Yes	No	No	No
hsa-mir-561	chr2: 188870523-188870545	4610	CAAAGTTTAAGATCCTTGAAGT	Yes	Yes	No	No	No
hsa-mir-562	chr2: 232745666-232745686	4611	AAAGTAGCTGTACCATTTGC	Yes	Yes	No	No	No
hsa-mir-563	chr3: 15890332-15890351	4612	AGGTTGACATACGTTTCCC	Yes	No	No	No	No
hsa-mir-361-5p	chrX: 85045341-85045363	4613	GTACCCCTGGAGATTCTGATAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-566	chr3: 50185777-50185796	4614	GGGCGCCTGTGATCCCAAC	Yes	Yes	No	No	No
hsa-mir-567	chr3: 113314352-113314375	4615	AGTATGTTCTTCCAGGACAGAAC	Yes	No	No	No	No
hsa-mir-642	chr19: 50870040-50870062	4616	GTCCCTCTCCAAATGTGTCTTG	Yes	Yes	No	No	No
hsa-mir-192*	chr11: 64415206-64415226	4617	CTGTGACCTATGGAATTGGCAG	Yes	Yes	Yes	Yes	No
hsa-mir-92a-1*	chr13: 90801578-90801601	4618	AGGTTGGGATCGGTTGCAATGCT	Yes	No	Yes	No	No
hsa-mir-27a*	chr19: 13808300-13808322	4619	TGCTCACAAGCAGCTAAGCCCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-564	chr3: 44878398-44878417	4620	AGGCACGGTGTCAGCAGGC	Yes	Yes	No	No	No
hsa-mir-106a*	chrX: 133131903-133131925	4621	GTAAGAAGTGCTTACATTGCAG	Yes	Yes	Yes	No	No
hsa-mir-26a-1*	chr3: 37985946-37985968	4622	CCTATTCTTGGTTACTTGCACG	Yes	Yes	Yes	Yes	Yes
hsa-mir-498	chr19: 58869295-58869318	4623	TTTCAAGCCAGGGGGCGTTTTTC	Yes	Yes	No	No	No
hsa-mir-454*	chr17: 54569970-54569992	4624	GCAGAGACAATATTGATAGGGT	Yes	Yes	Yes	No	No
hsa-mir-502-5p	chrX: 49665960-49665981	4625	ATCCTTGCTATCTGGGTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-218-2*	chr5: 168127750-168127772	4626	CGCGGTGCTTGACAGAACCATG	Yes	Yes	Yes	Yes	Yes
hsa-mir-30c-2*	chr6: 72143387-72143409	4627	AGAGTAAACAGCCTTCTCCCAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-526b*	chr19: 58889508-58889530	4628	GAAAGTGCTTCCTTTTAGAGGC	Yes	Yes	No	No	No
hsa-mir-542-5p	chrX: 133503095-133503118	4629	TCTCGTGACATGATGATCCCCGA	No	Yes	Yes	Yes	Yes
hsa-mir-433	chr14: 100418038-100418060	4630	ATCATGATGGGCTCCTCGGTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-27a	chr19: 13808260-13808281	4631	GCGGAACTTAGCCACTGTGAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-27b	chr9: 96887607-96887628	4632	TTCACAGTGGCTAAGTTCTGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-330-3p	chr19: 50834106-50834129	4633	TCTCTGCAGGCCGTGTGCTTTGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-431	chr14: 100417115-100417136	4634	TGTCTTGCAGGCCGTCATGCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-520c-5p	chr19: 58902533-58902555	4635	CTCTAGAGGGAAGCACTTTCTG	Yes	No	No	No	No
hsa-mir-708	chr11: 78790768-78790791	4636	CCCAGCTAGATTGTAAGCTCCTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-17*	chr13: 90800909-90800931	4637	ACTGCAGTGAAGGCACTTGTAG	Yes	No	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-1197	chr14: 100561709-100561730	4638	TAGGACACATGGTCTACTTGCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-548a-5p	chr8: 105565823-105565845	4639	GGTAAAACTCGCAATTACTTTT	No	Yes	No	No	No
hsa-mir-1248	chr3: 187987157-187987184	4640	ACCTTCTTGTATAAGCACTGTGCTAAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-208b	chr14: 22957045-22957067	4641	ACAAACCTTTTGTTCGTCTTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-208a	chr14: 22927650-22927672	4642	ACAAGCTTTTTGCTCGTCTTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-499-5p	chr20: 33041871-33041892	4643	TTAAGACTTGCAGTGATGTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-29b-1*	chr7: 130212805-130212829	4644	TCTAAACCACCATATGAAACCAGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-378*	chr5: 149092584-149092606	4645	CTCCTGACTCCAGGTCCTGTGT	Yes	Yes	Yes	No	Yes
hsa-mir-16-1*	chr13: 49521121-49521143	4646	TCAGCAGCACAGTTAATACTGG	Yes	Yes	Yes	Yes	No
hsa-mir-338-3p	chr17: 76714281-76714303	4647	CAACAAAATCACTGATGCTGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-145*	chr5: 148790454-148790476	4648	GGATTCCTGGAAATACTGTTCT	Yes	Yes	Yes	Yes	Yes
hsa-mir-3373p	chr14: 100410642-100410664	4649	CTCCTATATGATGCCTTTCTTC	Yes	Yes	No	Yes	Yes
hsa-mir-593*	chr7: 127509163-127509188	4650	AGGCACCAGCCAGGCATTGCTCAGC	Yes	No	No	No	No
hsa-mir-130a	chr11: 57165300-57165322	4651	CAGTGCAATGTTAAAAGGGCAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-627	chr15: 40279119-40279141	4652	TCCTCTTTTCTTAGAGACTCAC	Yes	Yes	No	No	No
hsa-mir-892b	chrX: 144886417-144886439	4653	TCTACCCAGAAAGGAGCCAGTG	Yes	Yes	No	No	No
hsa-mir-892a	chrX: 144885888-144885909	4654	CTACGCAGAAAGGACACAGTG	Yes	Yes	No	No	No
hsa-mir-548n	chr7: 34946940-34946962	4655	ACAAAATCCACAATTACTTTTG	Yes	No	No	No	No
hsa-mir-768-3p	chr16: 70349813-70349841	4656	GTCAGCAGTTTGAGTGTCAGCATTGTGA	Yes	Yes	Yes	No	No
hsa-mir-630	chr15: 70666671-70666693	4657	AGTATTCTGTACCAGGGAAGGT	Yes	Yes	No	No	No
hsa-mir-631	chr15: 73433043-73433064	4658	GCTGAGGTCTGGGCCAGGTCT	Yes	Yes	Yes	No	No
hsa-mir-1287	chr10: 100145017-100145039	4659	GACTCGAACCACTGATCCAGCA	Yes	Yes	Yes	No	No
hsa-mir-633	chr17: 58375367-58375390	4660	CTAATAGTATCTACCACAATAAA	Yes	Yes	No	No	No
hsa-mir-1281	chr22: 39818494-39818511	4661	TCGCCTCCTCCTCTCCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-635	chr17: 63932246-63932269	4662	GGACATTGTTTCAGTGCCCAAGT	Yes	No	No	No	No
hsa-mir-636	chr17: 72244142-72244165	4663	TGCGGGCGGGACGAGCAAGCACA	Yes	Yes	No	No	No
hsa-mir-637	chr19: 3912426-3912450	4664	ACGCAGAGCCCGAAAGCCCCCAGT	Yes	No	No	No	No
hsa-mir-638	chr19: 10690094-10690119	4665	AGGGATCGCGGGCGGGTGGCGGCCT	No	Yes	Yes	No	No
hsa-mir-639	chr19: 14501414-14501437	4666	ATCGCTGCGGTTGCGAGCGCTGT	No	No	No	No	No
hsa-mir-1289	chr5: 132791205-132791228	4667	AAAATGCAGATTCCTGGACTCCA	Yes	Yes	No	No	No
hsa-mir-1289	chr20: 33505225-33505248	4668	AAAATGCAGATTCCTGGACTCCA	Yes	Yes	No	No	No
hsa-mir-1288	chr17: 16126096-16126117	4669	TGGACTGCCCTGATCTGGAGA	Yes	Yes	No	No	No
hsa-mir-548j	chr22: 25281239-25281261	4670	ACCAAAGACCGCAATTACTTTT	Yes	No	No	No	No
hsa-mir-518b	chr19: 58897852-58897874	4671	CAAAGCGCTCCCCTTTAGAGGT	Yes	Yes	No	No	No
hsa-let-7c	chr21: 16834028-16834050	4672	TGAGGTAGTAGGTTGTATGGTT	Yes	Yes	Yes	Yes	Yes
hsa-let-7a	chr22: 44887295-44887317	4673	TGAGGTAGTAGGTTGTATAGTT	Yes	Yes	Yes	Yes	Yes
hsa-let-7a	chr11: 121522485-121522507	4674	AACTATACAACCTACTACCTCA	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-let-7a	chr9: 95978064-95978086	4675	TGAGGTAGTAGGTTGTATAGTT	Yes	Yes	Yes	Yes	Yes
hsa-let-7f	chrX: 53600931-53600953	4676	AACTATACAATCTACTACCTCA	Yes	Yes	Yes	Yes	Yes
hsa-let-7f	chr9: 95978455-95978477	4677	TGAGGTAGTAGATTGTATAGTT	Yes	Yes	Yes	Yes	Yes
hsa-let-7g	chr3: 52277391-52277413	4678	AACTGTACAAACTACTACCTCA	Yes	Yes	Yes	Yes	No
hsa-let-7d	chr9: 95980943-95980965	4679	AGAGGTAGTAGGTTGCATAGTT	Yes	Yes	Yes	Yes	Yes
hsa-let-7e	chr19: 56887857-56887879	4680	TGAGGTAGGAGGTTGTATAGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-516a-3p	chr19: 58956258-58956276	4681	TGCTTCCTTTCAGAGGGT	Yes	No	No	No	No
hsa-mir-516a-3p	chr19: 58951866-58951884	4682	TGCTTCCTTTCAGAGGGT	Yes	No	No	No	No
hsa-let-7i	chr12: 61283737-61283759	4683	TGAGGTAGTAGTTTGTGCTGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-503	chrX: 133508066-133508089	4684	CTGCAGAACTGTTCCCGCTGCTA	Yes	Yes	Yes	Yes	Yes
hsa-mir-494	chr14: 100565770-100565792	4685	TGAAACATACACGGGAAACCTC	Yes	Yes	Yes	Yes	Yes
hsa-mir-519b-3p	chr19: 58890328-58890350	4686	AAAGTGCATCCTTTTAGAGGTT	Yes	Yes	No	No	No
hsa-mir-1207-5p	chr8: 129130586-129130607	4687	TGGCAGGGAGGCTGGGAGGGG	Yes	No	No	No	No
hsa-let-7b*	chr22: 44888288-44888310	4688	CTATACAACCTACTGCCTTCCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-181a*	chr1: 197094820-197094842	4689	GGTACAATCAACGGTCGATGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-548e	chr10: 112738725-112738747	4690	AAAAACTGAGACTACTTTTGCA	Yes	No	No	No	No
hsa-mir-125b	chr21: 16884443-16884465	4691	TCCCTGAGACCCTAACTTGTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-125b	chr11: 121475726-121475748	4692	TCACAAGTTAGGGTCTCAGGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-9*	chr1: 154656769-154656791	4693	ACTTTCGGTTATCTAGCTTTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-9*	chr5: 87998439-87998461	4694	ACTTTCGGTTATCTAGCTTTAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-9*	chr15: 87712305-87712327	4695	ATAAAGCTAGATAACCGAAAGT	Yes	No	Yes	Yes	Yes
hsa-mir-301b	chr22: 20337313-20337336	4696	CAGTGCAATGATATTGTCAAAGC	Yes	Yes	Yes	Yes	Yes
hsa-mir-301a	chr17: 54583291-54583314	4697	GCTTTGACAATACTATTGCACTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-98	chrX: 53599984-53600006	4698	AACAATACAACTTACTACCTCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-550*	chr7: 30295994-30296016	4699	TGTCTTACTCCCTCAGGCACAT	Yes	Yes	No	No	No
hsa-mir-550*	chr7: 32739177-32739199	4700	TGTCTTACTCCCTCAGGCACAT	Yes	Yes	No	No	No
hsa-mir-505*	chrX: 138834020-138834042	4701	ACATCAATACTTCCTGGCTCCC	Yes	Yes	Yes	Yes	Yes
hsa-mir-142-3p	chr17: 53763604-53763627	4702	TCCATAAAGTAGGAAACACTACA	Yes	Yes	Yes	Yes	Yes
hsa-mir-487a	chr14: 100588583-100588605	4703	AATCATACAGGGACATCCAGTT	Yes	Yes	Yes	No	No
hsa-mir-93	chr7: 99529373-99529396	4704	CTACCTGCACGAACAGCACTTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-95	chr4: 8057938-8057960	4705	TGCTCAATAAATACCCGTTGAA	Yes	Yes	Yes	No	No
hsa-mir-96	chr7: 129201814-129201837	4706	AGCAAAAATGTGCTAGTGCCAAA	Yes	Yes	Yes	Yes	Yes
hsa-mir-200c*	chr12: 6943126-6943148	4707	CGTCTTACCCAGCAGTGTTTGG	No	Yes	Yes	Yes	Yes
hsa-mir-527	chr19: 58949096-58949116	4708	CTGCAAAGGGAAGCCCTTTC	Yes	No	No	No	No
hsa-mir-521	chr19: 58943754-58943776	4709	AACGCACTTCCCTTTAGAGTGT	Yes	No	No	No	No
hsa-mir-521	chr19: 58911712-58911734	4710	AACGCACTTCCCTTTAGAGTGT	Yes	No	No	No	No
hsa-mir-127-3p	chr14: 100419124-100419146	4711	TCGGATCCGTCTGAGCTTGGCT	Yes	Yes	Yes	Yes	Yes

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-523	chr19: 58893502-58893525	4712	GAACGCGCTTCCCTATAGAGGGT	Yes	No	No	No	No
hsa-mir-135b	chr1: 203684111-203684134	4713	TCACATAGGAATGAAAAGCCATA	Yes	Yes	Yes	Yes	Yes
hsa-mir-135a	chr3: 52303325-52303348	4714	TCACATAGGAATAAAAAGCCATA	Yes	Yes	Yes	Yes	Yes
hsa-mir-135a	chr12: 96481742-96481765	4715	TATGGCTTTTTATTCCTATGTGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-146b-5p	chr10: 104186266-104186288	4716	TGAGAACTGAATTCCATAGGCT	Yes	No	Yes	Yes	Yes
hsa-mir-509-3p	chrX: 146148871-146148893	4717	CTACCCACAGACGTACCAATCA	Yes	Yes	No	No	No
hsa-mir-509-3p	chrX: 146147984-146148006	4718	CTACCCACAGACGTACCAATCA	Yes	Yes	No	No	No
hsa-mir-509-3p	chrX: 146149759-146149781	4719	CTACCCACAGACGTACCAATCA	Yes	Yes	No	No	No
hsa-mir-33b*	chr17: 17657895-17657917	4720	GGGCTGCACTGCCGAGGCACTG	Yes	Yes	Yes	No	No
hsa-mir-744*	chr17: 11926007-11926029	4721	CTGTTGCCACTAACCTCAACCT	Yes	Yes	Yes	Yes	No
hsa-mir-1274a	chr5: 41511503-41511521	4722	GTCCCTGTTCAGGCGCCA	Yes	Yes	No	No	No
hsa-mir-532-5p	chrX: 49654512-49654534	4723	CATGCCTTGAGTGTAGGACCGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1274b	chr19: 62716222-62716239	4724	TGGCGCCCGAACAGGGA	Yes	No	No	No	No
hsa-let-71*	chr12: 61283793-61283815	4725	CTGCGCAAGCTACTGCCTTGCT	Yes	Yes	No	Yes	Yes
hsa-mir-132	chr17: 1899972-1899994	4726	CGACCATGGCTGTAGACTGTTA	No	Yes	Yes	Yes	Yes
hsa-mir-20a*	chr13: 90801362-90801384	4727	ACTGCATTATGAGCACTTAAAG	Yes	No	Yes	Yes	Yes
hsa-mir-23a	chr19: 13808408-13808429	4728	GGAAATCCCTGGCAATGTGAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-23b	chr9: 96887367-96887388	4729	ATCACATTGCCAGGGATTACC	Yes	Yes	Yes	Yes	Yes
hsa-mir-542-3p	chrX: 133503059-133503081	4730	TTTCAGTTATCAATCTGTCACA	No	Yes	Yes	Yes	Yes
hsa-mir-148b	chr12: 53017328-53017350	4731	TCAGTGCATCACAGAACTTTGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-148a	chr7: 25956066-52956088	4732	ACAAAGTTCTGTAGTGCACTGA	Yes	Yes	Yes	Yes	No
hsa-mir-886-3p	chr5: 135444086-135444107	4733	AAGGGTCAGTAAGCACCCGCG	Yes	Yes	No	No	No
hsa-mir-24	chr19: 13808102-13808124	4734	CTGTTCCTGCTGAACTGAGCCA	Yes	Yes	Yes	Yes	Yes
hsa-mir-24	chr9: 96888166-96888188	4735	TGGCTCAGTTCAGCAGGAACAG	Yes	Yes	Yes	Yes	Yes
hsa-mir-330-5p	chr19: 50834146-50834168	4736	GCCTAAGACACAGGCCCAGAGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-497*	chr17: 6861980-6862002	4737	TCTAACACCACAGTGTGGTTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-451	chr17: 24212546-24212568	4738	AACTCAGTAATGGTAACGGTTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-452	chrX: 150878805-150878827	4739	TCAGTTTCCTCTGCAAACAGTT	Yes	Yes	Yes	Yes	No
hsa-mir-340*	chr5: 179374924-179374946	4740	GCTATAAAGTAACTGAGACGGA	Yes	Yes	Yes	Yes	No
hsa-mir-454	chr17: 54569929-54569952	4741	ACCCTATAAGCAATATTGCACTA	Yes	Yes	Yes	No	No
hsa-mir-890	chrX: 144883530-144883551	4742	CAACTGATGCCTTTCCAAGTA	Yes	No	No	No	No
hsa-mir-135b*	chr1: 203684073-203684095	4743	CCCATGGCTTTTAGCCCTACAT	Yes	Yes	Yes	Yes	Yes
hsa-mir-875-3p	chr8: 100618200-100618221	4744	CACAACCTCAGTGTTTCCAGG	Yes	Yes	Yes	No	No
hsa-mir-541*	chr14: 100600593-100600618	4745	AAAGGATTCTGCTGTCGGTCCCACT	No	Yes	No	No	No
hsa-mir-26a-2*	chr12: 56504669-56504691	4746	GAAACAAGTAATCAAGAATAGG	Yes	Yes	Yes	No	No
hsa-mir-302c*	chr4: 113789006-113789028	4747	CAGCAGGTACCCCCATGTTAAA	Yes	Yes	Yes	Yes	No
hsa-mir-885-3p	chr3: 10411182-10411204	4748	TATCCACTACACCCCGCTGCCT	Yes	Yes	Yes	No	No

TABLE 11-continued

Analysis of cross-species conservation for miRNAs. Table displays results for conservation of (1) full-lenght mature miRNA sequences, (2) seed of the mature sequence.

hsa-mir-450b-3p	chrX: 133501889-133501911	4749	TATGGATGCAAAATGATCCCAA	Yes	Yes	Yes	No	No
hsa-mir-296-5p	chr20: 56826110-56826131	4750	ACAGGATTGAGGGGGGGCCCT	Yes	Yes	No	Yes	Yes
hsa-mir-221*	chrX: 45490592-45490614	4751	AAATCTACATTGTATGCCAGGT	Yes	Yes	Yes	Yes	Yes
hsa-mir-100*	chr11: 121528157-121528179	4752	CATACCTATAGATACAAGCTTG	Yes	Yes	Yes	Yes	Yes
hsa-mir-302b*	chr4: 113789130-113789152	4753	GAAAGCACTTCCATGTTAAAGT	Yes	Yes	Yes	No	No
hsa-mir-487b	chr14: 100582594-100582616	4754	AATCGTACAGGGTCATCCACTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-607	chr10: 98578430-98578451	4755	GTTATAGATCTGGATTTGAAC	Yes	No	No	No	No
hsa-mir-625*	chr14: 65007623-65007645	4756	GACTATAGAACTTTCCCCCTCA	Yes	No	No	No	No
hsa-mir-625*	chr14: 65007684-65007606	4757	TGAGGGGGAAAGTTCTATAGTC	Yes	No	No	No	No
hsa-mir-141*	chr12: 6943536-6943558	4758	CATCTTCCAGTACAGTGTTGGA	Yes	Yes	Yes	Yes	Yes
hsa-mir-606	chr10: 76982281-76982302	4759	AAACTACTGAAAATCAAAGAT	Yes	Yes	No	No	No
hsa-mir-155*	chr21: 25868204-25868226	4760	CTCCTACATATTAGCATTAACA	Yes	Yes	Yes	No	No
hsa-mir-146a	chr5: 159844956-159844978	4761	TGAGAACTGAATTCCATGGGTT	Yes	Yes	Yes	Yes	Yes
hsa-mir-1183	chr7: 21477247-21477244	4762	CACTGTAGGTGATGGTGAGAGTGGGCA	Yes	Yes	No	No	No

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20140171484A1). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

1. An isolated nucleotide sequence

consisting of from about 14 to about 31 nucleotides in length;

and

consisting essentially of a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1-130 and 1094, wherein the nucleotide sequence is about 97%, about 98%, or about 99% identical to a nucleic acid sequence comprising any one of SEQ ID NOS: 1-130 and 1094.

2. An isolated nucleotide sequence

consisting of from about 14 to about 31 nucleotides in length;

and

consisting essentially of a nucleotide sequence selected from the group consisting of SEQ ID NOS: 131-401, wherein the nucleotide sequence is about 97%, about 98%, or about 99% identical to a nucleic acid sequence having a SEQ ID NO: 131-401, and wherein the nucleotide sequence is not SEQ ID NO: 236.

3. An isolated nucleotide sequence that is complementary to a nucleotide sequence of claim **1** or **2**.

4. An isolated nucleotide sequence that is complementary to all but 1, 2, 3, 4, or 5 nucleotides of the nucleotide sequence of claim **1** or **2**.

5. The nucleotide sequence of claim **3**, wherein the nucleotide sequence is complementary to at least 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or 31 contiguous nucleotides of the nucleotide sequence of claim **1**.

6. The nucleotide sequence of claim **3**, wherein the nucleotide sequence is complementary to at least 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or 31 contiguous nucleotides of the nucleotide sequence of claim **2**.

7. The nucleotide sequence of claim **1** or **2**, wherein the nucleotide sequence is single stranded.

8. The nucleotide sequence of claim **3**, wherein the nucleotide sequence is single stranded.

9. The nucleotide sequence of claim **4**, wherein the nucleotide sequence is single stranded.

10. The nucleotide sequence of claim **1** or **2**, wherein the nucleotide sequence is double stranded.

11. The nucleotide sequence of claim **3**, wherein the nucleotide sequence is double stranded.

12. The nucleotide sequence of claim **4**, wherein the nucleotide sequence is double stranded.

13. The acid nucleotide sequence of claim **1** or **2**, wherein the nucleotide sequence is expressed in a lymphocyte.

14. The nucleotide sequence of claim **1** or **2**, wherein the nucleotide sequence is expressed in a B cell.

15. The nucleotide sequence of claim **14**, wherein the B cell comprises a Naïve B cell, a centroblast, a memory B cell, or a Ramos Burkitt Lymphoma cell.

16. A composition comprising one or more nucleotide sequences of claim **1**, **2**, **3**, or **4**, in any combination or permutation thereof.

17. A composition comprising one or more nucleotide sequences, wherein the one or more nucleotide sequences consist essentially of a nucleotide sequence of any one of SEQ ID NOS: 1-401 and 1094, and wherein the nucleotide sequence is not SEQ ID NO: 236.

18. The composition of claim **16**, further comprising one or more carriers, excipients, solvents, bases, or a combination thereof.

19. The composition of claim **17**, further comprising one or more carriers, excipients, solvents, bases, or a combination thereof.

20. A method for modulating the activity of a target nucleic acid in a cell, the method comprising contacting a cell with a nucleotide sequence of claim **1**, **2**, **3**, or **4**.

21. The method of claim **20**, wherein the target nucleic acid is a mRNA, a mature miRNA, or a precursor to a mature miRNA.

22. The method of claim **20**, wherein the cell is a hematopoetic cell.

23. The method of claim **20**, wherein the cell is a B cell.

24. The method of claim **20**, wherein the cell is in vitro or in vivo.

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