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miRanda v1.0b microRNA Target Scanning Algorithm
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(2003) Genome Biology; 5(1):R1.

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Current Settings:

=====
Query Filename: rubber\_tree\_miRNA.txt
Reference Filename: MN047299.txt
Gap Open Penalty:-8.000000
Gap Extend: -2.000000
Score Threshold 50.000000
Energy Threshold -20.000000 kcal/mol
Scaling Parameter: 2.000000
=====

Read Sequence:hbr-miR156
(19 nt)
Read Sequence:MN047299.1 Rubber tree capillovirus 1
(6811 nt)

=====
Performing Scan: hbr-miR159a vs MN047299.1
=====

Forward: Score: 113.000000 Q:2 to 22 R:2178 to 2201 Align Len (23)
(73.91%) (82.61%)

Query: 3' AUCUCG-AGGGAAGUUAG--GUUU 5'
||:|| | :||||||| |||
Ref: 5' CAGGGCATATCTTCAATCTGCAA 3'

Energy: -20.200001 kCal/Mol

Scores for this hit:

>hbr-miR159a MN047299.1 113.00 -20.20 0.00 2 22 2178 2201
23 73.91% 82.61%

=====
Performing Scan: hbr-miR319 vs MN047299.1
=====

Forward: Score: 72.000000 Q:2 to 22 R:2992 to 3018 Align Len (26)
(65.38%) (69.23%)

Query: 3' UCCCUCGA-G-GGAAGUC----AGGUU 5'
|||||:| | ||||| |||||
Ref: 5' TGGGAGTTACAGATTCGGTGCTTTCAA 3'

Energy: -20.240000 kCal/Mol

Scores for this hit:

>hbr-miR319 MN047299.1 72.00 -20.24 0.00 2 22 2992 3018 26
65.38% 69.23%

=====
Performing Scan: hbr-miR396a vs MN047299.1
=====

Forward: Score: 126.000000 Q:3 to 22 R:6676 to 6694 Align Len (19)
(84.21%) (89.47%)

Query: 3' UCUUUCAGUUCUUUCGACAC 5'
: ||| || ||||| |||||
Ref: 5' CTGAAGGTC-AGAAAGCTGTG 3'

Energy: -24.700001 kCal/Mol

Scores for this hit:

>hbr-miR396a MN047299.1 126.00 -24.70 0.00 3 22 6676 6694
19 84.21% 89.47%

=====
Performing Scan: hbr-miR396b vs MN047299.1
=====

Forward: Score: 110.000000 Q:2 to 22 R:6678 to 6700 Align Len (23)
(78.26%) (78.26%)

Query: 3' GUCAAGUUCUUUCGACAC---CUU 5'
|| || ||||| ||||| |||
Ref: 5' AAGGTC-AGAAAGCTGTGTTTGAA 3'

Energy: -20.280001 kCal/Mol

Scores for this hit:

>hbr-miR396b MN047299.1 110.00 -20.28 0.00 2 22 6678 6700
23 78.26% 78.26%

=====
Performing Scan: hbr-miR398 vs MN047299.1
=====

Forward: Score: 104.000000 Q:2 to 22 R:1839 to 1858 Align Len (20)
(80.00%) (80.00%)

Query: 3' GUACACUAGAGUCCAGCGAGG 5'  
| | | | | | | | | | | |  
Ref: 5' AAGGTGAGC-CATGTTGCTCC 3'

Energy: -21.370001 kCal/Mol

Scores for this hit:

>hbr-miR398 MN047299.1 104.00 -21.37 0.00 2 22 1839 1858 20  
80.00% 80.00%

=====

Performing Scan: hbr-miR408b vs MN047299.1

=====

Forward: Score: 90.000000 Q:1 to 22 R:6498 to 6521 Align Len (24)  
(70.83%) (75.00%)

Query: 3' AGUACGAGACG---GACAAGGGUCA 5'  
| | | | : | | | | | | | | | |  
Ref: 5' TCATTTTCTGCAGGCTG-ACCCAGC 3'

Energy: -23.270000 kCal/Mol

Scores for this hit:

>hbr-miR408b MN047299.1 90.00 -23.27 0.00 1 22 6498 6521 24  
70.83% 75.00%

=====

Performing Scan: hbr-miR482a vs MN047299.1

=====

Forward: Score: 117.000000 Q:2 to 23 R:5332 to 5354 Align Len (22)  
(86.36%) (90.91%)

Query: 3' GAAGA-ACGGGUCGUGGGUAGA 5'  
| | | | | | : | | | | | | | | | |  
Ref: 5' ATTCTCTTCTCAGTCACTTGTCT 3'

Energy: -26.120001 kCal/Mol

Scores for this hit:

>hbr-miR482a MN047299.1 117.00 -26.12 0.00 2 23 5332 5354  
22 86.36% 90.91%

=====

Performing Scan: hbr-miR2118 vs MN047299.1

=====

Forward: Score: 97.000000 Q:2 to 22 R:5480 to 5501 Align Len (21)  
(71.43%) (80.95%)

Query: 3' AGUGAGGGUAGGU-GGGUAAAG 5'  
| : | | | : | | | | | | | | | |  
Ref: 5' ACTTTCCGGATTATCCCATTTC 3'

Energy: -20.020000 kCal/Mol

Scores for this hit:

```
>hbr-miR2118      MN047299.1  97.00 -20.02      0.00  2 22  5480 5501   21
      71.43%      80.95%
```

Performing Scan: hbr-miR6167 vs MN047299.1

Forward: Score: 105.000000 Q:3 to 21 R:5985 to 6004 Align Len (19)  
(84.21%) (84.21%)

Query: 3' AGUUUCGA-AGGUGGACCCAU 5'

||||| | || |||||

Ref: 5' AAAAAGCTATACAGCTGGGTA 3'

Energy: -23.070000 kCal/Mol

Scores for this hit:

```
>hbr-miR6167      MN047299.1 105.00      -23.07      0.00  3 21  5985 6004
      19  84.21%      84.21%
```

Performing Scan: hbr-miR6168 vs MN047299.1

Forward: Score: 91.000000 Q:1 to 22 R:5056 to 5077 Align Len (22)  
(77.27%) (86.36%)

Query: 3' GUCGUCAGGUGGCGU-GGUUCU 5'

: ||||| |||| | |||||

Ref: 5' TGGCAGT-CATTCCAGTCAAGA 3'

Energy: -21.170000 kCal/Mol

Scores for this hit:

```
>hbr-miR6168      MN047299.1  91.00 -21.17      0.00  1 22  5056 5077   22
      77.27%      86.36%
```

Performing Scan: hbr-miR6171 vs MN047299.1

Forward: Score: 114.000000 Q:1 to 22 R:1633 to 1654 Align Len (21)  
(80.95%) (80.95%)

Query: 3' UUUCGGAAGUCGUUAGGUGUA 5'

|||| || ||||| |||||

Ref: 5' AAAGAATTGAGCAGTGCACAT 3'

Energy: -20.430000 kCal/Mol

Scores for this hit:

```
>hbr-miR6171      MN047299.1 114.00      -20.43      0.00  1 22  1633 1654
      21  80.95%      80.95%
```

Performing Scan: hbr-miR6484 vs MN047299.1

Forward: Score: 117.000000 Q:2 to 22 R:5994 to 6016 Align Len (22)  
(72.73%) (81.82%)

Query: 3' GGUAGAUACG--UCUCGGGUAAU 5'  
          || ||: |: |||||  
Ref: 5' ACAGCTGGGTAAAGAGCTCATTA 3'

Energy: -20.730000 kCal/Mol

Scores for this hit:

>hbr-miR6484	MN047299.1	117.00	-20.73	0.00	2	22	5994	6016
	22	72.73%	81.82%					

Resulted have computed and are shown below. If there are no results shown, it means your chosen parameters yielded no results.  
Note: The p-value represents the likelihood that the target site loci is random. That is, a lower p-value represents a greater chance that the loci contains a valid MRE

hbr_miR6168	MN047299.1 Rubber tree capillovirus 1 target	from/to=[145,164]
-19.80	TCTGAGTCACTGCTCCAGGA TCTTGGTGCGGTGGACTGCTG	
....(((((((((((((((((((( )))))))).))))).))....	15	20 0.218000
hbr_miR319	MN047299.1 Rubber tree capillovirus 1 target	from/to=[569,587]
-18.90	ACTTAGCTCTGCAGTCCAC TTGGACTGAAGGGAGCTCCCT	
....(((((((((((((((((((( )))))))).))))).))....	13	19 0.172000
hbr_miR6168	MN047299.1 Rubber tree capillovirus 1 target	from/to=[647,664]
-18.10	CAGCAACACAACCCAAGA TCTTGGTGCGGTGGACTGCTG	
(((((.(((.(((((((( )))))))).)))))....	15	18 0.021000
hbr_miR6167	MN047299.1 Rubber tree capillovirus 1 target	
from/to=[1058,1077]	-16.90 GCCGGGTGAGGACCTGGGTG TACCCAGGTGGAAGCTTTGA	
...((((....(((((((( ))))))))....	13	20 0.254000
hbr_miR398	MN047299.1 Rubber tree capillovirus 1 target	
from/to=[1838,1857]	-18.10 AAGGTGAGCCATGTTGCTCC GGAGCGACCTGAGATCACATG	
...(((((((((((((((((((( )))))))).))))....	15	20 0.239000
hbr_miR319	MN047299.1 Rubber tree capillovirus 1 target	
from/to=[3204,3224]	-16.70 AGGAGAGAGTCAAGGGTCCAG TTGGACTGAAGGGAGCTCCCT	
(((((.(((.(((.(((((((( )))))))).))))....	15	21 0.104000
hbr_miR482a	MN047299.1 Rubber tree capillovirus 1 target	
from/to=[3951,3973]	-17.10 CAACTTGTATGAGCAATCCATCA	
AGATGGGTGGCTGGGCAAGAAG ...(((((((((((((((((((( )))))))).))))....	15	23 0.265000
hbr_miR396a	MN047299.1 Rubber tree capillovirus 1 target	
from/to=[6675,6693]	-21.30 TGAAGGTCAGAAAGCTGTG CACAGCTTTCTTGAAGCTTTCT	
.(((((((((((((((((((( ))))))))))....	18	19 0.380000

RNAhybrid  
Individual hits

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR156  
length: 19

mfe: -20.6 kcal/mol  
p-value: undefined

position 6492  
target 5' U C G 3'  
GCUUUU AUUUUCUG CAG  
CGAGAG UAGAAGAC GUU  
miRNA 3' A A 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR159a  
length: 21

mfe: -24.8 kcal/mol  
p-value: undefined

position 2177  
target 5' C AUA G 3'  
AGGGC UCUUCAUCU  
UCUCG GGAAGUUAGG  
miRNA 3' A AG UUU 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR166a  
length: 19

mfe: -25.0 kcal/mol  
p-value: undefined

position 1060  
target 5' C GG A G U 3'  
G UGAGG CCUGG UGA  
C ACUUC GGACC GCU  
miRNA 3' C UU AG 5'

---

dataset: 1  
target: MN047299.1

length: 6811  
miRNA : hbr-miR166b  
length: 22

mfe: -28.5 kcal/mol  
p-value: undefined

position 6125  
target 5' A UAGA A A 3'  
GGGGA GGAGCU GUCUGG  
CCCUU CUUCGG CAGGCU  
miRNA 3' C UA AC 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR319  
length: 21

mfe: -29.8 kcal/mol  
p-value: undefined

position 5323  
target 5' U AAU UC A 3'  
GGGGGC UCUCU UCAGUC  
CCCUCG AGGGA AGUCAG  
miRNA 3' U GUU 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR396a  
length: 21

mfe: -27.2 kcal/mol  
p-value: undefined

position 6675  
target 5' U U 3'  
GAAGG UC AGAAAGCUGUG  
CUUUC AG UCUUUCGACAC  
miRNA 3' U A U 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR396b  
length: 21

mfe: -25.1 kcal/mol  
p-value: undefined



position 823  
target 5' U U U CG U 3'  
GGUUCA GAG GC GUGGA  
UCAAGU CUU CG CACCU  
miRNA 3' G U U A U 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR398  
length: 21

mfe: -25.1 kcal/mol  
p-value: undefined

position 1840  
target 5' G G U U 3'  
GUGA C CA GUUGCUC  
CACU G GU CAGCGAGG  
miRNA 3' GUA A A C 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR408a  
length: 22

mfe: -25.8 kcal/mol  
p-value: undefined

position 573  
target 5' A AG A UU C 3'  
GCUCUGC UCC C UCUU  
CGAGACG AGG G AGAA  
miRNA 3' A GACA UC 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR408b  
length: 22

mfe: -25.3 kcal/mol  
p-value: undefined

position 6497  
target 5' U UU AGG A C 3'  
UCAU UCUGC CUG CCCAG  
AGUA AGACG GAC GGGUC  
miRNA 3' CG AA A 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR476  
length: 20

mfe: -21.3 kcal/mol  
p-value: undefined

position 6176  
target 5' U GG C C 3'  
GAU UGCAAA GGAGGG  
CUG ACGUUU CUUCCU  
miRNA 3' AA AAU 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR482a  
length: 22

mfe: -29.3 kcal/mol  
p-value: undefined

position 5334  
target 5' C U 3'  
UCUU CUCAGUCACUUGUCU  
AGAA GGGUCGGUGGGUAGA  
miRNA 3' GA C 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR482b  
length: 21

mfe: -24.3 kcal/mol  
p-value: undefined

position 6500  
target 5' A G A G 3'  
UUUUCU CAGGCUG CCCA  
GAAAGG GUUUGGC GGGU  
miRNA 3' A AAG 5'

---

dataset: 1  
target: MN047299.1  
length: 6811

miRNA : hbr-miR2118  
length: 21

mfe: -27.8 kcal/mol  
p-value: undefined

position 6592  
target 5' U            GUUUA            G            3'  
          UCGCUUCUG            CCACCCA  
          AGUGAGGGU            GGUGGGU  
miRNA 3'                    A                    AAAG 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR6166  
length: 23

mfe: -21.7 kcal/mol  
p-value: undefined

position 1515  
target 5' A                    AG                    C 3'  
          ACCA            GUCCC            AUCUAAU  
          UGGU            UAGGG            UAGGUUA  
miRNA 3'                    ACAU                    CAA                    5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR6167  
length: 20

mfe: -26.9 kcal/mol  
p-value: undefined

position 5984  
target 5' A            AUA G            A 3'  
          AAAGCU            CA CUGGGUA  
          UUUCGA            GU GACCCAU  
miRNA 3' AG            AG G            5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR6168  
length: 21

mfe: -28.6 kcal/mol  
p-value: undefined

position 1641  
target 5' G G AUAAAU A 3'  
AGCAGU CAC CCAAGA  
UCGUCA GUG GGUUCU  
miRNA 3' G G GCGU 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR6169  
length: 21

mfe: -23.3 kcal/mol  
p-value: undefined

position 3882  
target 5' A UU UAA U 3'  
AGAGGG AGG GGAAUAGCU  
UCUCUC UUC UCUUUAUGA  
miRNA 3' UU U 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR6170  
length: 21

mfe: -20.2 kcal/mol  
p-value: undefined

position 6660  
target 5' U CAGGA AAGG A 3'  
UCCCUCUU CUG UC  
AGGGAGAG GAC AG  
miRNA 3' U AA AA AAC 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR6171  
length: 21

mfe: -25.8 kcal/mol  
p-value: undefined

position 2043  
target 5' U AUUACUAGAG A G 3'  
AAGCC UCAG AAUCCACA  
UUCGG AGUC UUAGGUGU  
miRNA 3' U A G A 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR6172  
length: 21

mfe: -22.3 kcal/mol  
p-value: undefined

position 4500  
target 5' C CUA U 3'  
ACU UGAACAUGGUCU  
UGA AUUUGUGCCAGG  
miRNA 3' AAGAA U 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR6173  
length: 20

mfe: -24.3 kcal/mol  
p-value: undefined

position 3749  
target 5' A AG G G 3'  
AGU GUCCAU G GCGGCU  
UCA UAGGUA C UGCCGA  
miRNA 3' G AAA 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR6174  
length: 21

mfe: -24.0 kcal/mol  
p-value: undefined

position 4303  
target 5' A UAUGA U 3'  
CAGAGUCUGAU AGCUU  
GUUUCAGACUG UCGAA  
miRNA 3' UCGUA 5'

---

dataset: 1  
target: MN047299.1  
length: 6811  
miRNA : hbr-miR6175

length: 21

mfe: -25.5 kcal/mol

p-value: undefined

position 5118

```
target 5' A      U      C      CUU      U 3'
          UUGA GCCUUA AAAGCU  ACC
          AACU CGGGAU UUUCGG  UGG
miRNA  3' G                                  U 5'
```

dataset: 1

target: MN047299.1

length: 6811

miRNA : hbr-miR6482

length: 22

mfe: -24.9 kcal/mol

p-value: undefined

position 2163

```
target 5' U      AG      GG A      3'
          CUGGGU GGU  ACCAG  C
          GACCCA CUA  UGGUC  G
miRNA  3' C      A      AA GAC 5'
```

dataset: 1

target: MN047299.1

length: 6811

miRNA : hbr-miR6483

length: 22

mfe: -20.1 kcal/mol

p-value: undefined

position 1267

```
target 5'      C      A      A 3'
          CCUGGAG  UUC GCAGUG
          GGACUUU  AAG UGUUAU
miRNA  3' CUA      UA  A      5'
```

dataset: 1

target: MN047299.1

length: 6811

miRNA : hbr-miR6484

length: 21

mfe: -24.7 kcal/mol

p-value: undefined

position 5993

```
target 5' A G GG AA G 3'
        CA CU GU AGAGCUCAUUA
        GU GA CG UCUCGGGUAU
miRNA 3' G A UA 5'
```

---

```
dataset: 1
target: MN047299.1
length: 6811
miRNA : hbr-miR6485
length: 20
```

```
mfe: -22.4 kcal/mol
p-value: undefined
```

```
position 3042
target 5' C AAG G 3'
        UAUGCUC GCAUCU
        AUACGAG UGUAGG
miRNA 3' A AAGA AU 5'
```

---

```
dataset: 1
target: MN047299.1
length: 6811
miRNA : hbr-miR9386
length: 22
```

```
mfe: -24.0 kcal/mol
p-value: undefined
```

```
position 370
target 5' C AA A A 3'
        CUUUCAU UUUU AGCUGCAAA
        GAAGGUG AAAG UUGACGUUU
miRNA 3' C C 5'
```

---

```
#-----  
# Search parameters  
# score <= 9  
# mfe ratio >= 0.2  
#-----
```

```
target      MN047299.1  
miRNA       hbr-miR396a  
score       5.5  
mfe_ratio   0.66  
start       6674  
seed_gap    1  
seed_mismatch 0  
seed_gu     0  
gap         0  
mismatch    3  
gu          1  
miRNA_3'    UCUUUCAAGUUCUUUCGACAC  
aln         ..o|||.||.|||||||  
target_5'    CUGAAGGUC-AGAAAGCUGUG  
//
```

```
target      MN047299.1  
miRNA       hbr-miR6167  
score       8.5  
mfe_ratio   0.50  
start       2716  
seed_gap    0  
seed_mismatch 3  
seed_gu     0  
gap         0  
mismatch    2  
gu          1  
miRNA_3'    AGUUUCGAAGGUGGACCCAU  
aln         |||.|.o|.||.||||.||  
target_5'    UCACAAUUGCCCCUGGAUA  
//
```

```
target      MN047299.1  
miRNA       hbr-miR6169  
score       7.5  
mfe_ratio   0.55  
start       5291  
seed_gap    0  
seed_mismatch 1  
seed_gu     1  
gap         0  
mismatch    4  
gu          1  
miRNA_3'    UCUCUCUUUUCUCUUUAUGAU  
aln         o...|||||||o|||.||.  
target_5'    GUCAAGAAAAGAGGAAUUCUC  
//
```

```
target      MN047299.1  
miRNA       hbr-miR6171  
score       6  
mfe_ratio   0.64  
start       1633  
seed_gap    0
```



```
seed_mismatch 1
seed_gu       1
gap           0
mismatch      3
gu            0
miRNA_3'      UUUCGGAAGUCGUUAGGUGUA
aln           ||||..||.||||o|.|||||
target_5'     AAAGAAUUGAGCAGUGCACAU
//
target        MN047299.1
miRNA         hbr-miR6483
score         8
mfe_ratio     0.41
start         106
seed_gap      0
seed_mismatch 2
seed_gu       0
gap           0
mismatch      4
gu            0
miRNA_3'      CUAGGACUUUUAAAGAUGUUAU
aln           |.|...|||||||.||.|||||
target_5'     GCUGAAGAAAAUUACUUCAAUA
//
```

#Please import the downloaded file into Microsoft Excel or other  
spreadsheets software

hbr-miR482a	MN047299.1	6.5	-1.0	1	22	627	648	
	AGAUGGGUGGCUGGGCAAGAAG		:::	.....	.....			
	GAUUUCGCUAGCUUCCUAUCA	Cleavage			Rubber tree	capillovirus 1	2	
hbr-miR6167	MN047299.1	6.5	-1.0	1	20	1459	1478	
	UACCCAGGUGGAAGCUUUGA	:::::	.....	.....	:	UCAAGCAUUUCAGUUGGGAA		
	Cleavage				Rubber tree	capillovirus 1	3	
hbr-miR6167	MN047299.1	6.5	-1.0	1	20	4806	4825	
	UACCCAGGUGGAAGCUUUGA	::	.....	:	.....	AUACAGUUUUGAAUUGGGUG		
	Translation				Rubber tree	capillovirus 1	3	
hbr-miR6169	MN047299.1	6.5	-1.0	1	21	5357	5376	
	UAGUAUUUCUCUUUUCUCUCU	:::	.....	.....	.....	CAAGAUUAAAG-GAAAUGUUG		
	Translation				Rubber tree	capillovirus 1	4	
hbr-miR6483	MN047299.1	6.5	-1.0	1	22	3183	3204	
	UAUUGUAGAAAUUUUCAGGAUC	::	:	:	:	.....		
	CUCACUCACAACUCUUACAAUA	Translation			Rubber tree	capillovirus 1	3	
hbr-miR9386	MN047299.1	6.5	-1.0	1	22	4422	4443	
	UUUGCAGUUCGAAAGUGGAAGC	:::	.....	.....	.....			
	CAAAACACAUUUGGAUAGCAAG	Cleavage			Rubber tree	capillovirus 1	3	
hbr-miR159a	MN047299.1	7.0	-1.0	1	21	4786	4806	
	UUUGGAUUGAAGGGAGCUCUA	.....	:::	.....	.....	UCGUACUCCUUGAGUACAAA		
	Cleavage				Rubber tree	capillovirus 1	6	
hbr-miR159a	MN047299.1	7.0	-1.0	1	21	263	283	
	UUUGGAUUGAAGGGAGCUCUA	::	:::	.....	.....	UAACUCUAUCUCCAGUUCAAA		
	Translation				Rubber tree	capillovirus 1	6	
hbr-miR2118	MN047299.1	7.0	-1.0	1	21	2092	2112	
	GAAUUGGGUGGAUGGGAGUGA	:	.....	:::	.....	UGGUUCAUAUGCCUCCAUUUA		
	Translation				Rubber tree	capillovirus 1	1	
hbr-miR319	MN047299.1	7.0	-1.0	1	21	2548	2568	
	UUGGACUGAAGGGAGCUCUCCU	:::	.....	.....	.....	CAGGACUUUCUUUUGAUCUCA		
	Cleavage				Rubber tree	capillovirus 1	1	
hbr-miR396b	MN047299.1	7.0	-1.0	1	21	5836	5856	
	UUCCACAGCUUUCUUGAACUG	:::	:	.....	:	CAGGUUCAGAAAAUUUUGGAU		
	Cleavage				Rubber tree	capillovirus 1	2	
hbr-miR396b	MN047299.1	7.0	-1.0	1	21	6677	6696	
	UUCCACAGCUUUCUUGAACUG	::	:::	.....	.....	AAGGUCA-GAAAGCUGUGUUU		
	Cleavage				Rubber tree	capillovirus 1	2	
hbr-miR398	MN047299.1	7.0	-1.0	1	21	1838	1857	
	GGAGCGACCUGAGAUCACAUG	:	.....	:	.....	AAGGUGAGC-CAUGUUGCUC		
	Cleavage				Rubber tree	capillovirus 1	1	
hbr-miR6166	MN047299.1	7.0	-1.0	1	23	786	808	
	AUUGGAUAACGGGAUUACAUGGU		:	:::	.....			
	GGGUUCUGAACCCUAUAUUCAG	Translation			Rubber tree	capillovirus 1	1	
hbr-miR6167	MN047299.1	7.0	-1.0	1	20	980	999	
	UACCCAGGUGGAAGCUUUGA	.....	.....	:	.....	UUAAGGAUUUCAAUUUGGUU		
	Cleavage				Rubber tree	capillovirus 1	3	
hbr-miR6171	MN047299.1	7.0	-1.0	1	21	4284	4304	
	AUGUGGAUUGCUGAAGGCUUU	::	:	.....	.....	AGAUUUCUCAUCAAUUCUGUAC		
	Translation				Rubber tree	capillovirus 1	5	
hbr-miR6171	MN047299.1	7.0	-1.0	1	21	3673	3693	
	AUGUGGAUUGCUGAAGGCUUU	:::	.....	.....	.....	AGGGAAUUCAUCGGUUUAUGU		
	Translation				Rubber tree	capillovirus 1	5	

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hbr-miR6171 MN047299.1 7.0 -1.0 1 21 4540 4561 AUGUGGAU-
UGCUGAAGGCUUU : :: . :::: :::::: AUAGAUGACAGCAUAUCCAUAU Cleavage
Rubber tree capillovirus 1 5
hbr-miR6174 MN047299.1 7.0 -1.0 1 21 5542 5563 AUGCUAAG-
CUGUCAGACUUUG ::: ::::: :: :::::: UUGAGUAUGGCGGACUCAGCAU Cleavage
Rubber tree capillovirus 1 1
hbr-miR6175 MN047299.1 7.0 -1.0 1 21 569 589
UGGUGGCUUUUAGGGCUCAAG : :::::. .. :::: ACUUAGCUCUGCAGUCCACUU
Translation Rubber tree capillovirus 1 1
hbr-miR6482 MN047299.1 7.0 -1.0 1 22 399 420
CAGGAACUGGUAUCAACCCAGC :: : :::: ::::: :
GAAGGCUAAAUACUUGUUUCAG Cleavage Rubber tree capillovirus 1 1
hbr-miR6483 MN047299.1 7.0 -1.0 1 22 5666 5687
UAUUGUAGAAAUUUUCAGGAUC :: ::::::. . ::
AUCCCAGGAAAUUUUGGGAGUU Cleavage Rubber tree capillovirus 1 3
hbr-miR9386 MN047299.1 7.0 -1.0 1 22 2179 2200
UUUGCAGUUCGAAAGUGGAAGC .. :: : ::::::
GGGCAUAUCUCAAUCUGCAAA Translation Rubber tree capillovirus 1 3

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