

=====

```
miranda v3.3a      microRNA Target Scanning Algorithm
```

=====

(c) 2003 Memorial Sloan-Kettering Cancer Center, New York

Authors: Anton Enright, Bino John, Chris Sander and Debora Marks  
(mirnatargets (at) cbio.mskcc.org - reaches all authors)

Software written by: Anton Enright  
Distributed for anyone to use under the GNU Public License (GPL),  
See the files 'COPYING' and 'LICENSE' for details

If you use this software please cite:  
Enright AJ, John B, Gaul U, Tuschl T, Sander C and Marks DS;  
(2003) Genome Biology; 5(1):R1.

miranda comes with ABSOLUTELY NO WARRANTY;  
This is free software, and you are welcome to redistribute it  
under certain conditions; type `miranda --license' for details.

Current Settings:

=====

```
Query Filename:  apple_mirna.fa
Reference Filename:  apple.fa
Gap Open Penalty:-9.000000
Gap Extend Penalty:  -4.000000
Score Threshold: 140.000000
Energy Threshold:-20.000000 kcal/mol
Scaling Parameter:   4.000000
```

=====

```
Read Sequence:mdm-miR156a (20 nt)
Read Sequence:KU870525.1 (7545 nt)
```

=====

```
Performing Scan: mdm-miR156a vs KU870525.1
```

=====

```
Score for this Scan:
No Hits Found above Threshold
Complete
```

```
Read Sequence:mdm-miR156b (20 nt)
Read Sequence:KU870525.1 (7545 nt)
```

=====

```
Performing Scan: mdm-miR156b vs KU870525.1
```

=====

```
Score for this Scan:
No Hits Found above Threshold
Complete
```

```
Read Sequence:mdm-miR156c (20 nt)
Read Sequence:KU870525.1 (7545 nt)
```

=====

```
Performing Scan: mdm-miR156c vs KU870525.1
```

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156d (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156d vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156e (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156e vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156f (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156f vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156g (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156g vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156h (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156h vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156i (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156i vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156j (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156j vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156k (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156k vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156l (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156l vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156m (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156m vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156n (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156n vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156o (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156o vs KU870525.1

=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR156p vs KU870525.1  
=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156q (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR156q vs KU870525.1  
=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156r (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR156r vs KU870525.1  
=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156s (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR156s vs KU870525.1  
=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156t (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR156t vs KU870525.1  
=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156u (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR156u vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156v (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156v vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156w (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156w vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156x (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156x vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156y (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156y vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156z (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156z vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR156aa (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR156aa vs KU870525.1

```
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR156ab (21 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
Performing Scan: mdm-miR156ab vs KU870525.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR156ac (21 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
Performing Scan: mdm-miR156ac vs KU870525.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR156ad (20 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
Performing Scan: mdm-miR156ad vs KU870525.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR156ae (20 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
Performing Scan: mdm-miR156ae vs KU870525.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR159a (20 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
Performing Scan: mdm-miR159a vs KU870525.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR159b (20 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
Performing Scan: mdm-miR159b vs KU870525.1
```

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR159c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR159c vs KU870525.1

=====

Forward: Score: 151.000000 Q:2 to 20 R:4379 to 4399 Align Len (18)  
(72.22%) (83.33%)

Query: 3' uuUCCUCUCCUCUCCUUAAG 5'  
| |:| | | |:| | | | |  
Ref: 5' gcAAGGGAGTATAGGAATTc 3'

Energy: -20.240000 kCal/Mol

Scores for this hit:

>mdm-miR159c	KU870525.1	151.00	-20.24	2	20	4379	4399	18
	72.22%	83.33%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR159c	KU870525.1	151.00	-20.24	151.00	-20.24
34	21	7545	4379		

Complete

Read Sequence:mdm-miR159d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR159d vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR159e (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR159e vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR159f (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR159f vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR160a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR160a vs KU870525.1

=====

Forward: Score: 142.000000 Q:2 to 16 R:4197 to 4218 Align Len (15)  
(80.00%) (86.67%)

Query: 3' accguaUGUCCCU-CGGUCCGu 5'

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

Ref: 5' aaatggACAGAGAGGCCAGGTt 3'

Energy: -22.490000 kCal/Mol

Scores for this hit:

>mdm-miR160a	KU870525.1	142.00	-22.49	2	16	4197	4218	15
80.00%	86.67%							

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR160a	KU870525.1	142.00	-22.49	142.00	-22.49
38	21	7545	4197		

Complete

Read Sequence:mdm-miR160b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR160b vs KU870525.1

=====

Forward: Score: 142.000000 Q:2 to 16 R:4197 to 4218 Align Len (15)  
(80.00%) (86.67%)

Query: 3' accguaUGUCCCU-CGGUCCGu 5'

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

Ref: 5' aaatggACAGAGAGGCCAGGTt 3'

Energy: -22.490000 kCal/Mol

Scores for this hit:

>mdm-miR160b	KU870525.1	142.00	-22.49	2	16	4197	4218	15
80.00%	86.67%							

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR160b	KU870525.1	142.00	-22.49	142.00	-22.49
39	21	7545	4197		



Complete

Read Sequence:mdm-miR160c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR160c vs KU870525.1

=====

Forward: Score: 142.000000 Q:2 to 16 R:4197 to 4218 Align Len (15)  
(80.00%) (86.67%)

Query: 3' accguaUGUCCCU-CGGUCCGu 5'

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

Ref: 5' aaatggACAGAGAGGCCAGGTt 3'

Energy: -22.490000 kCal/Mol

Scores for this hit:

>mdm-miR160c	KU870525.1	142.00	-22.49	2	16	4197	4218	15
	80.00%	86.67%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR160c	KU870525.1	142.00	-22.49	142.00	-22.49
40	21	7545	4197		

Complete

Read Sequence:mdm-miR160d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR160d vs KU870525.1

=====

Forward: Score: 142.000000 Q:2 to 16 R:4197 to 4218 Align Len (15)  
(80.00%) (86.67%)

Query: 3' accguaUGUCCCU-CGGUCCGu 5'

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

Ref: 5' aaatggACAGAGAGGCCAGGTt 3'

Energy: -22.490000 kCal/Mol

Scores for this hit:

>mdm-miR160d	KU870525.1	142.00	-22.49	2	16	4197	4218	15
	80.00%	86.67%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR160d	KU870525.1	142.00	-22.49	142.00	-22.49
41	21	7545	4197		

Complete

Read Sequence:mdm-miR160e (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR160e vs KU870525.1

=====

Forward: Score: 142.000000 Q:2 to 16 R:4197 to 4218 Align Len (15)  
(80.00%) (86.67%)

Query: 3' accguaUGUCCCU-CGGUCCGu 5'

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

Ref: 5' aaatggACAGAGAGGCCAGGTt 3'

Energy: -22.490000 kCal/Mol

Scores for this hit:

>mdm-miR160e	KU870525.1	142.00	-22.49	2	16	4197	4218	15
	80.00%	86.67%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>mdm-miR160e	KU870525.1	142.00	-22.49	142.00	-22.49
42	21	7545	4197		

Complete

Read Sequence:mdm-miR162a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR162a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR162b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR162b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR164a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR164a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR164b (21 nt)

Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR164b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR164c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR164c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR164d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR164d vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR164e (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR164e vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR164f (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR164f vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR166a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR166a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR166b (21 nt)

Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR166b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR166c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR166c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR166d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR166d vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR166e (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR166e vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR166f (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR166f vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR166g (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR166g vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR166h (21 nt)

Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR166h vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR166i (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR166i vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR166j (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR166j vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR167a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR167a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR167b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR167b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR167c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR167c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR167d (21 nt)

Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR167d vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR167e (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR167e vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR167f (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR167f vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR167g (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR167g vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR167h (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR167h vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR167i (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR167i vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR167j (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR167j vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR168a (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR168a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR168b (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR168b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR169a (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR169a vs KU870525.1

=====

Forward: Score: 143.000000 Q:2 to 20 R:4217 to 4237 Align Len (18)  
(66.67%) (77.78%)

Query: 3' ggCCGUUCAGUAGGAACCGAc 5'

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

Ref: 5' ttGGAAGGGGATGTTTGGCTg 3'

Energy: -22.690001 kCal/Mol

Scores for this hit:

>mdm-miR169a	KU870525.1	143.00	-22.69	2	20	4217	4237	18
		66.67%	77.78%					

Forward: Score: 140.000000 Q:2 to 19 R:3355 to 3374 Align Len (17)  
(70.59%) (82.35%)

Query: 3' ggcCGUUCAGUAGGAACCGAc 5'

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

Ref: 5' ttcGCAAGGGGT-CTTGGTTg 3'

Energy: -23.129999 kCal/Mol

Scores for this hit:

>mdm-miR169a	KU870525.1	140.00	-23.13	2 19	3355 3374	17
70.59%	82.35%					

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR169a	KU870525.1	283.00	-45.82	143.00	-23.13
73	21	7545	4217 3355		

Complete

Read Sequence:mdm-miR169b (22 nt)

Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR169b vs KU870525.1

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR169c (21 nt)

Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR169c vs KU870525.1

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR169d (21 nt)

Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR169d vs KU870525.1

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR169e (22 nt)

Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR169e vs KU870525.1

Forward: Score: 146.000000 Q:2 to 21 R:1571 to 1588 Align Len (19)  
(68.42%) (78.95%)

Query: 3' ggUUUGUUGCGAGAAGAGAAGu 5'

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

Ref: 5' tcAGAC-ATGC---TCTCTTca 3'

Energy: -21.170000 kCal/Mol



Scores for this hit:

```
>mdm-miR169e      KU870525.1 146.00      -21.17      2 21 1571 1588 19
      68.42%      78.95%
```

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

```
>>mdm-miR169e      KU870525.1 146.00      -21.17      146.00      -21.17
      77      22      7545      1571
```

Complete

Read Sequence:mdm-miR169f (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR169f vs KU870525.1

=====

Forward: Score: 146.000000 Q:2 to 21 R:1571 to 1588 Align Len (19)  
(68.42%) (78.95%)

Query: 3' ggUUUGUUGCGAGAAGAGAAGu 5'

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

Ref: 5' tcAGAC-ATGC---TCTCTTCa 3'

Energy: -21.170000 kCal/Mol

Scores for this hit:

```
>mdm-miR169f      KU870525.1 146.00      -21.17      2 21 1571 1588 19
      68.42%      78.95%
```

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

```
>>mdm-miR169f      KU870525.1 146.00      -21.17      146.00      -21.17
      78      22      7545      1571
```

Complete

Read Sequence:mdm-miR169g (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR169g vs KU870525.1

=====

Forward: Score: 143.000000 Q:2 to 20 R:4217 to 4237 Align Len (18)  
(66.67%) (77.78%)

Query: 3' ggCCGUUCAGUAGGAACCGAc 5'

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

Ref: 5' ttGGAAGGGGATGTTTGGCTg 3'

Energy: -22.690001 kCal/Mol

Scores for this hit:

>mdm-miR169g      KU870525.1 143.00      -22.69      2 20 4217 4237 18  
66.67%      77.78%

Forward: Score: 140.000000 Q:2 to 19 R:3355 to 3374 Align Len (17)  
(70.59%) (82.35%)

Query: 3' ggcCGUUCAGUAGGAACCGAc 5'  
          ||||| :| |||||:|  
Ref: 5' ttcGCAAGGGGT-CTTGGTTg 3'

Energy: -23.129999 kCal/Mol

Scores for this hit:

>mdm-miR169g      KU870525.1 140.00      -23.13      2 19 3355 3374 17  
70.59%      82.35%

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR169g      KU870525.1 283.00      -45.82      143.00      -23.13  
79 21 7545 4217 3355

Complete

Read Sequence:mdm-miR169h (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR169h vs KU870525.1

=====

Forward: Score: 143.000000 Q:2 to 20 R:4217 to 4237 Align Len (18)  
(66.67%) (77.78%)

Query: 3' ggCCGUUCAGUAGGAACCGAc 5'  
          || | |:| || :|||||  
Ref: 5' ttGGAAGGGGATGTTTGGCTg 3'

Energy: -22.690001 kCal/Mol

Scores for this hit:

>mdm-miR169h      KU870525.1 143.00      -22.69      2 20 4217 4237 18  
66.67%      77.78%

Forward: Score: 140.000000 Q:2 to 19 R:3355 to 3374 Align Len (17)  
(70.59%) (82.35%)

Query: 3' ggcCGUUCAGUAGGAACCGAc 5'  
          ||||| :| |||||:|  
Ref: 5' ttcGCAAGGGGT-CTTGGTTg 3'

Energy: -23.129999 kCal/Mol

Scores for this hit:

>mdm-miR169h      KU870525.1 140.00      -23.13      2 19 3355 3374 17  
70.59%      82.35%

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR169h      KU870525.1 283.00      -45.82      143.00      -23.13  
80 21 7545 4217 3355

Complete

Read Sequence:mdm-miR169i (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR169i vs KU870525.1

=====

Forward: Score: 143.000000 Q:2 to 20 R:4217 to 4237 Align Len (18)  
(66.67%) (77.78%)

Query: 3' ggCCGUUCAGUAGGAACCGAc 5'

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

Ref: 5' ttGGAAGGGGATGTTTGGCTg 3'

Energy: -22.690001 kCal/Mol

Scores for this hit:

>mdm-miR169i      KU870525.1 143.00      -22.69      2 20 4217 4237 18  
66.67%      77.78%

Forward: Score: 140.000000 Q:2 to 19 R:3355 to 3374 Align Len (17)  
(70.59%) (82.35%)

Query: 3' ggcCGUUCAGUAGGAACCGAc 5'

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

Ref: 5' ttcGCAAGGGGT-CTTGGTTg 3'

Energy: -23.129999 kCal/Mol

Scores for this hit:

>mdm-miR169i      KU870525.1 140.00      -23.13      2 19 3355 3374 17  
70.59%      82.35%

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR169i      KU870525.1 283.00      -45.82      143.00      -23.13  
81 21 7545 4217 3355

Complete

Read Sequence:mdm-miR169j (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR169j vs KU870525.1

=====

Forward: Score: 143.000000 Q:2 to 20 R:4217 to 4237 Align Len (18)  
(66.67%) (77.78%)

Query: 3' ggCCGUUCAGUAGGAACCGAc 5'

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

Ref: 5' ttGGAAGGGGATGTTTGGCTg 3'

Energy: -22.690001 kCal/Mol

Scores for this hit:

>mdm-miR169j	KU870525.1	143.00	-22.69	2 20	4217 4237	18
	66.67%	77.78%				

Forward: Score: 140.000000 Q:2 to 19 R:3355 to 3374 Align Len (17)  
(70.59%) (82.35%)

Query: 3' ggcCGUUCAGUAGGAACCGAc 5'

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

Ref: 5' ttcGCAAGGGGT-CTTGGTTg 3'

Energy: -23.129999 kCal/Mol

Scores for this hit:

>mdm-miR169j	KU870525.1	140.00	-23.13	2 19	3355 3374	17
	70.59%	82.35%				

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR169j	KU870525.1	283.00	-45.82	143.00	-23.13
82 21	7545 4217 3355				

Complete

Read Sequence:mdm-miR169k (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR169k vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR169l (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR169l vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR169m (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR169m vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR169n (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR169n vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR169o (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR169o vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171d vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171e (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171e vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171f-3p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171f-3p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171f-5p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171f-5p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171g (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171g vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171h (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171h vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171i (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171i vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171j (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171j vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171k (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171k vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171l (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171l vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171m (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171m vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171n (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171n vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171o (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171o vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR171q (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR171q vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172a (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172b (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172c (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete



Read Sequence:mdm-miR172d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172d vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172e (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172e vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172f (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172f vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172g (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172g vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172h (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172h vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172i (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172i vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172j (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172j vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172k (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172k vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172l (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172l vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172m (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172m vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172n (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172n vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172o (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172o vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR172p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR172p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR319a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR319a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR319b-3p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR319b-3p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR319b-5p (20 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR319b-5p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR319b-5p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR319b-5p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR319c-5p (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR319c-5p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR319d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR319d vs KU870525.1

=====

Forward: Score: 152.000000 Q:2 to 20 R:6744 to 6762 Align Len (18)  
(66.67%) (83.33%)

Query: 3' acUCACUUACUCAGCCGUCAa 5'  
          :| |:| |: | ||| |  
Ref: 5' aaGGAGGATGG--CGGCAGTt 3'

Energy: -20.860001 kCal/Mol

Scores for this hit:

>mdm-miR319d	KU870525.1	152.00	-20.86	2	20	6744	6762	18
		66.67%	83.33%					

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR319d	KU870525.1	152.00	-20.86	152.00	-20.86			
	127 21 7545 6744							

Complete

Read Sequence:mdm-miR319e (20 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR319e vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR319f (20 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR319f vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR319g (20 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR319g vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR319h (22 nt)

Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR319h vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR390a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR390a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR390b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR390b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR390c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR390c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR390d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR390d vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR390e (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR390e vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR390f (21 nt)

Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR390f vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR391 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR391 vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR393a (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR393a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR393b (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR393b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR393c (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR393c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR393d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR393d vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR393e (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR393e vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR393f (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR393f vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR393g (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR393g vs KU870525.1

=====

Forward: Score: 150.000000 Q:2 to 19 R:3091 to 3111 Align Len (17)  
(70.59%) (88.24%)

Query: 3' uuaGGUUUCCCUAUCGUACUa 5'  
          :| :| ||||:|||||  
Ref: 5' gagTCTGATGGATGGCATGAc 3'

Energy: -21.170000 kCal/Mol

Scores for this hit:

>mdm-miR393g	KU870525.1	150.00	-21.17	2	19	3091	3111	17
	70.59%	88.24%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR393g	KU870525.1	150.00	-21.17	150.00	-21.17
	145 21 7545 3091				

Complete

Read Sequence:mdm-miR393h (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR393h vs KU870525.1

=====

Forward: Score: 150.000000 Q:2 to 19 R:3091 to 3111 Align Len (17)  
(70.59%) (88.24%)

Query: 3' uuaGGUUUCCCUAUCGUACUa 5'  
          :| :| ||||:|||||

Ref: 5' gagTCTGATGGATGGCATGAc 3'

Energy: -21.170000 kCal/Mol

Scores for this hit:

>mdm-miR393h	KU870525.1	150.00	-21.17	2	19	3091	3111	17
	70.59%	88.24%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR393h	KU870525.1	150.00	-21.17	150.00	-21.17
	146	21	7545	3091	

Complete

Read Sequence:mdm-miR394a (20 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR394a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR394b (20 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR394b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR395a (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR395a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR395b (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR395b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR395c (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====



```
Performing Scan: mdm-miR395c vs KU870525.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR395d-3p (21 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
Performing Scan: mdm-miR395d-3p vs KU870525.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR395d-5p (21 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
Performing Scan: mdm-miR395d-5p vs KU870525.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR395e (21 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
Performing Scan: mdm-miR395e vs KU870525.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR395f (21 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
Performing Scan: mdm-miR395f vs KU870525.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR395g-3p (21 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
Performing Scan: mdm-miR395g-3p vs KU870525.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:mdm-miR395g-5p (21 nt)
Read Sequence:KU870525.1 (7545 nt)
=====
```

Performing Scan: mdm-miR395g-5p vs KU870525.1

=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR395h (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====  
Performing Scan: mdm-miR395h vs KU870525.1

=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR395i-3p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====  
Performing Scan: mdm-miR395i-3p vs KU870525.1

=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR395i-5p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====  
Performing Scan: mdm-miR395i-5p vs KU870525.1

=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR395j (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====  
Performing Scan: mdm-miR395j vs KU870525.1

=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR395k (20 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====  
Performing Scan: mdm-miR395k vs KU870525.1

=====

Forward: Score: 168.000000 Q:2 to 17 R:4691 to 4710 Align Len (15)  
(86.67%) (93.33%)

Query: 3' uuacUUCACAAACUCCUUUg 5'  
          |:| |||||  
Ref: 5' aggcAGGAGTTTGAGGAAAc 3'

Energy: -20.850000 kCal/Mol

Scores for this hit:

>mdm-miR395k	KU870525.1	168.00	-20.85	2	17	4691	4710	15
	86.67%	93.33%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR395k	KU870525.1	168.00	-20.85	168.00	-20.85
	162	20	7545	4691	

Complete

Read Sequence:mdm-miR395l (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR395l vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR396a (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR396a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR396b (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR396b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR396c (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR396c vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR396d (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR396d vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR396e (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR396e vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR396f (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR396f vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR396g (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR396g vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR397a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR397a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR397b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR397b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR398a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR398a vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR398b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR398b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR398c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR398c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR399a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR399a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR399b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR399b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR399c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR399c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR399d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR399d vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR399e (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR399e vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR399f (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR399f vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR399g (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR399g vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR399h (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR399h vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR399i (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR399i vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR399j (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR399j vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR399k (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR399k vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR403a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR403a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR403b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR403b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR408a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR408a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR408b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR408b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR408c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR408c vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR408d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR408d vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR477a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR477a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR477b (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR477b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR482a-3p (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR482a-3p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR482a-5p (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR482a-5p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR482b (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR482b vs KU870525.1



=====  
Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR482c (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR482c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR482d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR482d vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR530a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR530a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR530b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR530b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR530c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR530c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR535a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====  
Performing Scan: mdm-miR535a vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR535b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR535b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR535c (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR535c vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR535d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR535d vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR827 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR827 vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR828a (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR828a vs KU870525.1  
=====

Forward: Score: 149.000000 Q:2 to 21 R:6033 to 6052 Align Len (19)  
(73.68%) (84.21%)

Query: 3' acCUUAUGAGUAAACUCGUUCu 5'  
          |:| ||| |||||:|  
Ref: 5' tgGGAAACT--TTTGAGCAGGc 3'

Energy: -20.719999 kCal/Mol

Scores for this hit:

>mdm-miR828a	KU870525.1	149.00	-20.72	2 21	6033 6052	19
	73.68%	84.21%				

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR828a	KU870525.1	149.00	-20.72	149.00	-20.72
	208 22	7545 6033			

Complete

Read Sequence:mdm-miR828b (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR828b vs KU870525.1

=====

Forward: Score: 149.000000 Q:2 to 21 R:6033 to 6052 Align Len (19)  
(73.68%) (84.21%)

Query: 3' acCUUAUGAGUAAACUCGUUCu 5'

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

Ref: 5' tgGGAAACT--TTTGAGCAGGc 3'

Energy: -20.719999 kCal/Mol

Scores for this hit:

>mdm-miR828b	KU870525.1	149.00	-20.72	2 21	6033 6052	19
	73.68%	84.21%				

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR828b	KU870525.1	149.00	-20.72	149.00	-20.72
	209 22	7545 6033			

Complete

Read Sequence:mdm-miR858 (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR858 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR1511 (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR1511 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR2111a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR2111a vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR2111b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR2111b vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR2118a (22 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR2118a vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR2118b (22 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR2118b vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR2118c (22 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR2118c vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR3627a (20 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR3627a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR3627b (20 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR3627b vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR3627c (20 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR3627c vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR3627d (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR3627d vs KU870525.1

=====

Forward: Score: 161.000000 Q:2 to 20 R:2376 to 2395 Align Len (18)  
(77.78%) (83.33%)

Query: 3' aaGUACAGUGUCCUCCUACCu 5'  
          || || |:| |||||  
Ref: 5' ttCAGGT-ATATGAGGATGGg 3'

Energy: -22.400000 kCal/Mol

Scores for this hit:

>mdm-miR3627d	KU870525.1	161.00	-22.40	2	20	2376	2395	18
		77.78%	83.33%					

Forward: Score: 161.000000 Q:2 to 20 R:6736 to 6755 Align Len (18)  
(77.78%) (83.33%)

Query: 3' aaGUACAGUGUCCUCCUACCu 5'  
          || | |:| |||||  
Ref: 5' atCA-GACGAAGGAGGATGGc 3'

Energy: -24.370001 kCal/Mol

Scores for this hit:

>mdm-miR3627d	KU870525.1	161.00	-24.37	2	20	6736	6755	18
		77.78%	83.33%					

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR3627d KU870525.1 322.00 -46.77 161.00 -24.37  
220 21 7545 2376 6736

Complete

Read Sequence:mdm-miR5225a (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR5225a vs KU870525.1

=====

Forward: Score: 156.000000 Q:2 to 21 R:182 to 203 Align Len (19)  
(63.16%) (78.95%)

Query: 3' cgUGGUAGAGUGGAAGCUGUCu 5'

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

Ref: 5' agATTACCACAATCTCGACAGg 3'

Energy: -21.700001 kCal/Mol

Scores for this hit:

>mdm-miR5225a KU870525.1 156.00 -21.70 2 21 182 203 19  
63.16% 78.95%

Forward: Score: 146.000000 Q:2 to 21 R:6226 to 6251 Align Len (23)  
(69.57%) (78.26%)

Query: 3' cgUGGUAGA-GU---GGAAGCUGUCu 5'

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

Ref: 5' gaACCATGTGCAGGTTCTTTGACAGc 3'

Energy: -21.670000 kCal/Mol

Scores for this hit:

>mdm-miR5225a KU870525.1 146.00 -21.67 2 21 6226 6251 23  
69.57% 78.26%

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR5225a KU870525.1 302.00 -43.37 156.00 -21.70  
221 22 7545 182 6226

Complete

Read Sequence:mdm-miR5225b (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR5225b vs KU870525.1

=====

Forward: Score: 156.000000 Q:2 to 21 R:182 to 203 Align Len (19)  
(63.16%) (78.95%)

Query: 3' cgUGGUAGAGUGGAAGCUGUCu 5'

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

Ref: 5' agATTACCACAATCTCGACAGg 3'

Energy: -21.700001 kCal/Mol

Scores for this hit:

>mdm-miR5225b	KU870525.1	156.00	-21.70	2	21	182	203	19
	63.16%	78.95%						

Forward: Score: 146.000000 Q:2 to 21 R:6226 to 6251 Align Len (23)  
(69.57%) (78.26%)

Query: 3' cgUGGUAGA-GU---GGAAGCUGUCu 5'

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

Ref: 5' gaACCATGTGCAGGTTCTTTGACAGc 3'

Energy: -21.670000 kCal/Mol

Scores for this hit:

>mdm-miR5225b	KU870525.1	146.00	-21.67	2	21	6226	6251	23
	69.57%	78.26%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR5225b	KU870525.1	302.00	-43.37	156.00	-21.70
	222 22 7545 182 6226				

Complete

Read Sequence:mdm-miR5225c (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR5225c vs KU870525.1

=====

Forward: Score: 155.000000 Q:2 to 21 R:7297 to 7319 Align Len (20)  
(65.00%) (80.00%)

Query: 3' cgUGGUAG-AGUGGGUGCUGUCu 5'

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

Ref: 5' aaACTTTCGTCTGTTACGACAGa 3'

Energy: -23.110001 kCal/Mol

Scores for this hit:

>mdm-miR5225c	KU870525.1	155.00	-23.11	2	21	7297	7319	20
	65.00%	80.00%						

Forward: Score: 141.000000 Q:2 to 14 R:4719 to 4740 Align Len (12)  
(83.33%) (91.67%)

Query: 3' cgugguagaGUGGGUGCUGUCu 5'

|| |||||:||

Ref: 5' caaagagtgcAGCCACGATAGg 3'

Energy: -21.950001 kCal/Mol

Scores for this hit:

>mdm-miR5225c	KU870525.1	141.00	-21.95	2	14	4719	4740	12
	83.33%	91.67%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>mdm-miR5225c	KU870525.1	296.00	-45.06	155.00	-23.11
	223	22	7545	7297	4719

Complete

Read Sequence:mdm-miR7120a-3p (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7120a-3p vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR7120a-5p (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7120a-5p vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR7120b-3p (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7120b-3p vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR7120b-5p (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7120b-5p vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold



Complete

Read Sequence:mdm-miR7121a (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7121a vs KU870525.1

=====

Forward: Score: 145.000000 Q:2 to 15 R:149 to 171 Align Len (15)  
(73.33%) (80.00%)

Query: 3' ugucccgCUAGUG--GUUCUCCu 5'

|| |:| |||||

Ref: 5' tcctacaGAACGCCACAAGAGGa 3'

Energy: -20.639999 kCal/Mol

Scores for this hit:

>mdm-miR7121a	KU870525.1	145.00	-20.64	2	15	149	171	15
73.33%	80.00%							

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR7121a	KU870525.1	145.00	-20.64	145.00	-20.64
228	21	7545	149		

Complete

Read Sequence:mdm-miR7121b (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7121b vs KU870525.1

=====

Forward: Score: 145.000000 Q:2 to 15 R:149 to 171 Align Len (15)  
(73.33%) (80.00%)

Query: 3' ugucccgCUAGUG--GUUCUCCu 5'

|| |:| |||||

Ref: 5' tcctacaGAACGCCACAAGAGGa 3'

Energy: -20.639999 kCal/Mol

Scores for this hit:

>mdm-miR7121b	KU870525.1	145.00	-20.64	2	15	149	171	15
73.33%	80.00%							

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR7121b	KU870525.1	145.00	-20.64	145.00	-20.64
229	21	7545	149		

Complete

Read Sequence:mdm-miR7121c (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7121c vs KU870525.1

=====

Forward: Score: 145.000000 Q:2 to 15 R:149 to 171 Align Len (15)  
(73.33%) (80.00%)

Query: 3' ugucccgCUAGUG--GUUCUCCu 5'

|| |:| |||||

Ref: 5' tcctacaGAACGCCACAAGAGGa 3'

Energy: -20.639999 kCal/Mol

Scores for this hit:

>mdm-miR7121c	KU870525.1	145.00	-20.64	2	15	149	171	15
73.33%	80.00%							

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>mdm-miR7121c	KU870525.1	145.00	-20.64	145.00	-20.64
230	21	7545	149		

Complete

Read Sequence:mdm-miR7121d (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7121d vs KU870525.1

=====

Forward: Score: 145.000000 Q:2 to 15 R:149 to 171 Align Len (15)  
(73.33%) (80.00%)

Query: 3' cgucccgCUAGUG--GUUCUCCu 5'

|| |:| |||||

Ref: 5' tcctacaGAACGCCACAAGAGGa 3'

Energy: -20.360001 kCal/Mol

Scores for this hit:

>mdm-miR7121d	KU870525.1	145.00	-20.36	2	15	149	171	15
73.33%	80.00%							

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>mdm-miR7121d	KU870525.1	145.00	-20.36	145.00	-20.36
231	21	7545	149		

Complete

Read Sequence:mdm-miR7121e (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====
Performing Scan: mdm-miR7121e vs KU870525.1
=====

Forward: Score: 145.000000 Q:2 to 15 R:149 to 171 Align Len (15)
(73.33%) (80.00%)

Query: 3' cgucccgCUAGUG--GUUCUCCu 5'

|| |:| |||

Ref: 5' tcctacaGAACGCCACAAGAGGa 3'

Energy: -20.360001 kCal/Mol

Scores for this hit:

>mdm-miR7121e KU870525.1 145.00 -20.36 2 15 149 171 15
73.33% 80.00%

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>mdm-miR7121e KU870525.1 145.00 -20.36 145.00 -20.36
232 21 7545 149

Complete

Read Sequence:mdm-miR7121f (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====
Performing Scan: mdm-miR7121f vs KU870525.1
=====

Forward: Score: 145.000000 Q:2 to 15 R:149 to 171 Align Len (15)
(73.33%) (80.00%)

Query: 3' cgucccgCUAGUG--GUUCUCCu 5'

|| |:| |||

Ref: 5' tcctacaGAACGCCACAAGAGGa 3'

Energy: -20.360001 kCal/Mol

Scores for this hit:

>mdm-miR7121f KU870525.1 145.00 -20.36 2 15 149 171 15
73.33% 80.00%

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>mdm-miR7121f KU870525.1 145.00 -20.36 145.00 -20.36
233 21 7545 149

Complete

Read Sequence:mdm-miR7121g (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====
Performing Scan: mdm-miR7121g vs KU870525.1

=====

Forward: Score: 145.000000 Q:2 to 15 R:149 to 171 Align Len (15)  
(73.33%) (80.00%)

Query: 3' cgucccgCUAGUG--GUUCUCCu 5'

|| |:| |||||

Ref: 5' tcctacaGAACGCCACAAGAGGa 3'

Energy: -20.360001 kCal/Mol

Scores for this hit:

>mdm-miR7121g	KU870525.1	145.00	-20.36	2	15	149	171	15
73.33%	80.00%							

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR7121g	KU870525.1	145.00	-20.36	145.00	-20.36
234	21	7545	149		

Complete

Read Sequence:mdm-miR7121h (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7121h vs KU870525.1

=====

Forward: Score: 145.000000 Q:2 to 15 R:149 to 171 Align Len (15)  
(73.33%) (80.00%)

Query: 3' cgucccgCUAGUG--GUUCUCCu 5'

|| |:| |||||

Ref: 5' tcctacaGAACGCCACAAGAGGa 3'

Energy: -20.360001 kCal/Mol

Scores for this hit:

>mdm-miR7121h	KU870525.1	145.00	-20.36	2	15	149	171	15
73.33%	80.00%							

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR7121h	KU870525.1	145.00	-20.36	145.00	-20.36
235	21	7545	149		

Complete

Read Sequence:mdm-miR7122a (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7122a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR7122b (22 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7122b vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR7123a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7123a vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR7123b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7123b vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR7124a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7124a vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR7124b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7124b vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR7125 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR7125 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR7126-3p (22 nt)  
Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR7126-3p vs KU870525.1

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR7126-5p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR7126-5p vs KU870525.1

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR7127a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR7127a vs KU870525.1

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR7127b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR7127b vs KU870525.1

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR7128 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR7128 vs KU870525.1

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR10978a (22 nt)  
Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR10978a vs KU870525.1

Score for this Scan:

No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR10978b (22 nt)  
Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR10978b vs KU870525.1

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR10979 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR10979 vs KU870525.1

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR10980a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR10980a vs KU870525.1

Forward: Score: 155.000000 Q:3 to 20 R:6561 to 6581 Align Len (17)  
(82.35%) (88.24%)

Query: 3' guACCGACGUUCAGGGUCCac 5'  
          ||| | :|||||||  
Ref: 5' ccTGGATTTAAGTCCCAGGat 3'

Energy: -25.040001 kCal/Mol

Scores for this hit:

>mdm-miR10980a	KU870525.1	155.00	-25.04	3	20	6561	6581	17
	82.35%	88.24%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR10980a	KU870525.1	155.00	-25.04	155.00	-25.04
	251	21	7545	6561	

Complete

Read Sequence:mdm-miR10980b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR10980b vs KU870525.1

Forward: Score: 155.000000 Q:3 to 20 R:6561 to 6581 Align Len (17)  
(82.35%) (88.24%)

Query: 3' guACCGACGUUCAGGGUCCac 5'  
||| | : |||||  
Ref: 5' ccTGGATTTAAGTCCCAGGat 3'

Energy: -25.040001 kCal/Mol

Scores for this hit:

>mdm-miR10980b	KU870525.1	155.00	-25.04	3	20	6561	6581	17
	82.35%	88.24%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR10980b	KU870525.1	155.00	-25.04	155.00	-25.04
	252	21	7545	6561	

Complete

Read Sequence:mdm-miR10981a (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10981a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10981b (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10981b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10981c (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10981c vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10981d (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10981d vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold



Complete

Read Sequence:mdm-miR10982a (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10982a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10982b (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10982b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10982c (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10982c vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10982d (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10982d vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10983 (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10983 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10984a-3p (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10984a-3p vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10984a-5p (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10984a-5p vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10984b-3p (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10984b-3p vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10984b-5p (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10984b-5p vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10985 (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10985 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10986 (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10986 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10987 (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10987 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10988 (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10988 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10989a (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10989a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10989b (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10989b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10989c (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10989c vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10989d (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10989d vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10989e (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10989e vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10990 (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10990 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10991a (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10991a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10991b (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10991b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10991c (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10991c vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10991d (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10991d vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10991e (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10991e vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10992 (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10992 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10993a (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10993a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10993b (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10993b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10993c (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10993c vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10993d (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10993d vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10993e (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10993e vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10993f (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10993f vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10994-3p (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10994-3p vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10994-5p (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10994-5p vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10995 (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10995 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10996a (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10996a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10996b (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR10996b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10997 (21 nt)

Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR10997 vs KU870525.1

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10998 (22 nt)

Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR10998 vs KU870525.1

Forward: Score: 140.000000 Q:2 to 21 R:3899 to 3920 Align Len (19)  
(63.16%) (73.68%)

Query: 3' uuCAGGAUCUGACUUAGGGUUC 5'

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

Ref: 5' atGACCTTCGGAGAGTCCCAAg 3'

Energy: -23.510000 kCal/Mol

Scores for this hit:

>mdm-miR10998	KU870525.1	140.00	-23.51	2	21	3899	3920	19
	63.16%	73.68%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>mdm-miR10998	KU870525.1	140.00	-23.51	140.00	-23.51
	294	22	7545	3899	

Complete

Read Sequence:mdm-miR10999a (21 nt)

Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR10999a vs KU870525.1

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR10999b (21 nt)

Read Sequence:KU870525.1 (7545 nt)

Performing Scan: mdm-miR10999b vs KU870525.1

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR11000 (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11000 vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11001 (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11001 vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11002a (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11002a vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11002b (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11002b vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11002c-3p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11002c-3p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11002c-5p (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11002c-5p vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete



Read Sequence:mdm-miR11003 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11003 vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11004 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11004 vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11005 (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11005 vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11006 (22 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11006 vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11007 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11007 vs KU870525.1  
=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11008 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)  
=====

Performing Scan: mdm-miR11008 vs KU870525.1  
=====

Forward: Score: 169.000000 Q:2 to 20 R:6150 to 6172 Align Len (20)  
(85.00%) (85.00%)

Query: 3' agAAGAUAAA-AC-ACGCCAGUg 5'

Ref: 5' aaTTCTATTGCGTTGCGGTCA 3'

Energy: -23.270000 kCal/Mol

Scores for this hit:

>mdm-miR11008	KU870525.1	169.00	-23.27	2	20	6150	6172	20
	85.00%	85.00%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>mdm-miR11008	KU870525.1	169.00	-23.27	169.00	-23.27
	308	21	7545	6150	

Complete

Read Sequence:mdm-miR11009 (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11009 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR11010 (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11010 vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR11011a (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11011a vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR11011b (21 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11011b vs KU870525.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:mdm-miR11012a (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11012a vs KU870525.1

=====

Forward: Score: 148.000000 Q:2 to 17 R:4585 to 4604 Align Len (15)  
(80.00%) (86.67%)

Query: 3' cccacgUAACGUAUCCGUCGCc 5'

||| :| |||||

Ref: 5' cgcaaaATT-TA-AGGCAGCGg 3'

Energy: -21.110001 kCal/Mol

Scores for this hit:

>mdm-miR11012a	KU870525.1	148.00	-21.11	2	17	4585	4604	15
		80.00%	86.67%					

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>mdm-miR11012a	KU870525.1	148.00	-21.11	148.00	-21.11
	313	22	7545	4585	

Complete

Read Sequence:mdm-miR11012b (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11012b vs KU870525.1

=====

Forward: Score: 148.000000 Q:2 to 17 R:4585 to 4604 Align Len (15)  
(80.00%) (86.67%)

Query: 3' cccacgUAACGUAUCCGUCGCc 5'

||| :| |||||

Ref: 5' cgcaaaATT-TA-AGGCAGCGg 3'

Energy: -21.110001 kCal/Mol

Scores for this hit:

>mdm-miR11012b	KU870525.1	148.00	-21.11	2	17	4585	4604	15
		80.00%	86.67%					

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>mdm-miR11012b	KU870525.1	148.00	-21.11	148.00	-21.11
	314	22	7545	4585	

Complete

Read Sequence:mdm-miR11013 (22 nt)

Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11013 vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11014 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11014 vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11015 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11015 vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11016 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11016 vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11017 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11017 vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11018 (22 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11018 vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11019 (22 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11019 vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:mdm-miR11020 (21 nt)  
Read Sequence:KU870525.1 (7545 nt)

=====

Performing Scan: mdm-miR11020 vs KU870525.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Scan Complete

## RNA22 v2 results

Results have been 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

```
mdm_miR160a      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[2133,2151]      -19.80 AGGTTTGCGCGGCCGGGCT
      TGCCTGGCTCCCTGTATGCCA .(((.(((.(((((((. .)))))))))...))))).
      15      19      0.006200
mdm_miR160b      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[2133,2151]      -19.80 AGGTTTGCGCGGCCGGGCT
      TGCCTGGCTCCCTGTATGCCA .(((.(((.(((((((. .)))))))))...))))).
      15      19      0.006200
mdm_miR160c      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[2133,2151]      -19.80 AGGTTTGCGCGGCCGGGCT
      TGCCTGGCTCCCTGTATGCCA .(((.(((.(((((((. .)))))))))...))))).
      15      19      0.006200
mdm_miR160d      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[2133,2151]      -19.80 AGGTTTGCGCGGCCGGGCT
      TGCCTGGCTCCCTGTATGCCA .(((.(((.(((((((. .)))))))))...))))).
      15      19      0.006200
mdm_miR160e      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[2133,2151]      -19.80 AGGTTTGCGCGGCCGGGCT
      TGCCTGGCTCCCTGTATGCCA .(((.(((.(((((((. .)))))))))...))))).
      15      19      0.006200
mdm_miR160a      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[4424,4445]      -18.20 CAATTCAGAGAGGAGGCAGGCC
      TGCCTGGCTCCCTGTATGCCA .....(((((.(((((((. .)))))))))...))))).
      12      22      0.145000
mdm_miR160b      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[4424,4445]      -18.20 CAATTCAGAGAGGAGGCAGGCC
      TGCCTGGCTCCCTGTATGCCA .....(((((.(((((((. .)))))))))...))))).
      12      22      0.145000
mdm_miR160c      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[4424,4445]      -18.20 CAATTCAGAGAGGAGGCAGGCC
      TGCCTGGCTCCCTGTATGCCA .....(((((.(((((((. .)))))))))...))))).
      12      22      0.145000
mdm_miR160d      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[4424,4445]      -18.20 CAATTCAGAGAGGAGGCAGGCC
      TGCCTGGCTCCCTGTATGCCA .....(((((.(((((((. .)))))))))...))))).
      12      22      0.145000
mdm_miR160e      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[4424,4445]      -18.20 CAATTCAGAGAGGAGGCAGGCC
      TGCCTGGCTCCCTGTATGCCA .....(((((.(((((((. .)))))))))...))))).
      12      22      0.145000
mdm_miR164a      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[6096,6113]      -21.10 ACTTTGGTCACTTCTCCA
      TGGAGAAGCAGGGCACATGCC ....(((((((.(((((((. .)))))))))...))))).
      13      18      0.107000
mdm_miR169o      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometarget from/to=[345,363]      -16.00 ATCACTCTCACCTGGTTG
```

```

TAGCCAGGGATGACTTGCCT .....((((((((((( ))) )))))))..)).....
12      19      0.123000
mdm_miR166f      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[963,985]      -19.70 AGGAGGAGGTCAGGAGGTTTGGG
ACCAGGCTTCATTCCCCTCGG ..((((((.....(((((((((.
.))))) ))))...))))).. 15      23      0.094700
mdm_miR167a      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[975,996]      -16.30 GGAGGTTTGGGCCATATGATCT
AGATCATCTGGCAGTTTCACC ((.((.((.(((((.((((((( ))) )))))))..)))).))..))..))
16      22      0.094700
mdm_miR168a      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[2504,2525]      -20.70 ATCATCGACCTGAAGCAAGGGA
TCGCTTGGTGCAGGTCGGGAA ..(((((((((((.(((((.(( ))) )))))))..)))))..))..))..
17      22      0.136000
mdm_miR168b      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[2504,2525]      -20.70 ATCATCGACCTGAAGCAAGGGA
TCGCTTGGTGCAGGTCGGGAA ..(((((((((((.(((((.(( ))) )))))))..)))))..))..))..
17      22      0.136000
mdm_miR168a      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[3030,3051]      -15.90 AACCTGATTGAATTCAGTCGA
TCGCTTGGTGCAGGTCGGGAA ..(((((((((((...((((((( ))) )))))))..)))))..))..
16      22      0.053500
mdm_miR168b      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[3030,3051]      -15.90 AACCTGATTGAATTCAGTCGA
TCGCTTGGTGCAGGTCGGGAA ..(((((((((((...((((((( ))) )))))))..)))))..))..
16      22      0.053500
mdm_miR167b      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[3231,3252]      -16.70 GTGAAATGCTGGAAAAGGTTCA
TGAAGCTGCCAGCATGATCTA ..(((((((((((...((((((( ))) )))))))..)))))..))..
15      22      0.091800
mdm_miR167c      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[3231,3252]      -16.70 GTGAAATGCTGGAAAAGGTTCA
TGAAGCTGCCAGCATGATCTA ..(((((((((((...((((((( ))) )))))))..)))))..))..
15      22      0.091800
mdm_miR167d      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[3231,3252]      -16.70 GTGAAATGCTGGAAAAGGTTCA
TGAAGCTGCCAGCATGATCTA ..(((((((((((...((((((( ))) )))))))..)))))..))..
15      22      0.091800
mdm_miR167e      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[3231,3252]      -16.70 GTGAAATGCTGGAAAAGGTTCA
TGAAGCTGCCAGCATGATCTA ..(((((((((((...((((((( ))) )))))))..)))))..))..
15      22      0.091800
mdm_miR167f      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[3231,3252]      -16.70 GTGAAATGCTGGAAAAGGTTCA
TGAAGCTGCCAGCATGATCTA ..(((((((((((...((((((( ))) )))))))..)))))..))..
15      22      0.091800
mdm_miR167g      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[3231,3252]      -16.70 GTGAAATGCTGGAAAAGGTTCA
TGAAGCTGCCAGCATGATCTA ..(((((((((((...((((((( ))) )))))))..)))))..))..
15      22      0.091800
mdm_miR167h      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[3230,3252]      -16.70 TGTGAAATGCTGGAAAAGGTTCA
TGAAGCTGCCAGCATGATCTTA ...(((((((((((...((((((( ))) )))))))..)))))..
15      23      0.091800
mdm_miR167i      KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa      from/to=[3230,3252]      -16.70 TGTGAAATGCTGGAAAAGGTTCA

```

TGAAGCTGCCAGCATGATCTTA ...((((((...(((  
 )))))).)))))... 15 23 0.091800  
 mdm\_miR167j KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[3230,3252] -16.70 TGTGAAATGCTGAAAAGGTTCA  
 TGAAGCTGCCAGCATGATCTTA ...((((((...(((  
 )))))).)))))... 15 23 0.091800  
 mdm\_miR166f KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[4194,4217] -15.40 ACGAAATGGACAGAGAGGCCAGGT  
 ACCAGGCTTCATTCCCCTCGG .(((...(((...(((  
 )))))).)))))... 15 24 0.239000  
 mdm\_miR164b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[6093,6113] -15.50 GCCACTTTGGTCACTTCTCCA  
 TGGAGAAGCAGGGCACGTGCA ..(((....(((.(((  
 )))))))... 14 21 0.107000  
 mdm\_miR164c KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[6093,6113] -15.50 GCCACTTTGGTCACTTCTCCA  
 TGGAGAAGCAGGGCACGTGCA ..(((....(((.(((  
 )))))))... 14 21 0.107000  
 mdm\_miR164d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[6093,6113] -15.50 GCCACTTTGGTCACTTCTCCA  
 TGGAGAAGCAGGGCACGTGCA ..(((....(((.(((  
 )))))))... 14 21 0.107000  
 mdm\_miR164e KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[6093,6113] -15.50 GCCACTTTGGTCACTTCTCCA  
 TGGAGAAGCAGGGCACGTGCA ..(((....(((.(((  
 )))))))... 14 21 0.107000  
 mdm\_miR164f KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[6093,6113] -15.50 GCCACTTTGGTCACTTCTCCA  
 TGGAGAAGCAGGGCACGTGCA ..(((....(((.(((  
 )))))))... 14 21 0.107000  
 mdm\_miR171a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[6071,6093] -16.90 GTTCAATTTGGATAGTGGCTCAG  
 TTGAGCCGCGTCAATATCTCC .....(((...(((  
 )))))))... 12 23 0.107000  
 mdm\_miR171b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[6071,6093] -16.90 GTTCAATTTGGATAGTGGCTCAG  
 TTGAGCCGCGTCAATATCTCC .....(((...(((  
 )))))))... 12 23 0.107000  
 mdm\_miR169e KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[6750,6773] -15.80 GATGGCGGCAGTTCTAAATCTTCA  
 TGAAGAGAAGAGCGTTGTTTGG ...((((((...(((  
 )))))).)))))... 17 24 0.028700  
 mdm\_miR169f KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[6750,6773] -15.80 GATGGCGGCAGTTCTAAATCTTCA  
 TGAAGAGAAGAGCGTTGTTTGG ...((((((...(((  
 )))))).)))))... 17 24 0.028700  
 mdm\_miR168a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[7265,7286] -16.40 AAAGTGAATTTGCAAAAAGTGA  
 TCGCTTGGTGCAGGTTCGGGAA ...(((....(((  
 )))))))... 16 22 0.086300  
 mdm\_miR168b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[7265,7286] -16.40 AAAGTGAATTTGCAAAAAGTGA  
 TCGCTTGGTGCAGGTTCGGGAA ...(((....(((  
 )))))))... 16 22 0.086300  
 mdm\_miR171o KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[836,856] -16.40 CTGAGCTCCAGCAGCATCTG



TGGGATGTTGGTATGGTTCAA .((((((...(((.....)))))))).)))).  
 16 21 0.049700  
 mdm\_miR319c\_5p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[952,973] -15.60 GGATCTACTCAAGGAGGAGGTC  
 GAGCTCTTCTTCAGTCCAGTCC (((...(((.....)))))))).)))).  
 17 22 0.094700  
 mdm\_miR319h KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[952,973] -15.60 GGATCTACTCAAGGAGGAGGTC  
 GAGCTCTTCTTCAGTCCAGTCC (((...(((.....)))))))).)))).  
 17 22 0.094700  
 mdm\_miR319c\_5p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[1743,1765] -20.70 AGACTGAATTTGAAAGGGAGGTC  
 GAGCTCTTCTTCAGTCCAGTCC .((((...(((.....)))))))). 17 23 0.045700  
 mdm\_miR319h KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[1743,1765] -20.70 AGACTGAATTTGAAAGGGAGGTC  
 GAGCTCTTCTTCAGTCCAGTCC .((((...(((.....)))))))). 17 23 0.045700  
 mdm\_miR171f\_3p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[3230,3253] -15.00 TGTGAAATGCTGGAAAAGGTTTCAG  
 TTGAGCCGTGCCAATATCACG (((...(((.....)))))))). 17 24 0.091800  
 mdm\_miR171m KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[3230,3253] -15.70 TGTGAAATGCTGGAAAAGGTTTCAG  
 TTGAGCCGTGCCAATATCACG (((...(((.....)))))))). 17 24 0.091800  
 mdm\_miR171n KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[3230,3253] -15.70 TGTGAAATGCTGGAAAAGGTTTCAG  
 TTGAGCCGTGCCAATATCACG (((...(((.....)))))))). 17 24 0.091800  
 mdm\_miR319c\_5p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[3236,3259] -15.70 ATGCTGGAAAAGGTTTCAGGGGCTG  
 GAGCTCTTCTTCAGTCCAGTCC ..((((...(((.....)))))))). 15 24 0.091800  
 mdm\_miR319h KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[3236,3259] -15.70 ATGCTGGAAAAGGTTTCAGGGGCTG  
 GAGCTCTTCTTCAGTCCAGTCC ..((((...(((.....)))))))). 15 24 0.091800  
 mdm\_miR171f\_5p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[5101,5123] -15.60 CTTTGGGTGGGATGACAGTATTC  
 GGATATTGGTCCGGTTCAATA ..((((...(((.....)))))))). 16 23 0.235000  
 mdm\_miR171q KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[5101,5123] -15.60 CTTTGGGTGGGATGACAGTATTC  
 GGATATTGGTCCGGTTCAATA ..((((...(((.....)))))))). 16 23 0.235000  
 mdm\_miR319a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[5195,5220] -15.20  
 GGGGAATTTTCCACATTTTGTTCAG TTGGACTGAAGGGAGCTCCCT  
 (((...(((.....)))))))). 18 26  
 0.357000  
 mdm\_miR319b\_3p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
 complete genometaget from/to=[5195,5220] -15.20  
 GGGGAATTTTCCACATTTTGTTCAG TTGGACTGAAGGGAGCTCCCT  
 (((...(((.....)))))))). 18 26  
 0.357000

mdm\_miR171j KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6071,6093] -19.40 GTTCAATTTGGATAGTGGCTCAG  
TTGAGCCGCGCCAATATCACT .....((((...(((((((.  
)))))))).)))).)..... 12 23 0.107000

mdm\_miR171k KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6071,6093] -19.40 GTTCAATTTGGATAGTGGCTCAG  
TTGAGCCGCGCCAATATCACT .....((((...(((((((.  
)))))))).)))).)..... 12 23 0.107000

mdm\_miR171l KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6071,6093] -19.40 GTTCAATTTGGATAGTGGCTCAG  
TTGAGCCGCGCCAATATCACT .....((((...(((((((.  
)))))))).)))).)..... 12 23 0.107000

mdm\_miR171p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6071,6093] -16.90 GTTCAATTTGGATAGTGGCTCAG  
TTGAGCCGCGTCAATATCTCC .....((((...(((((((.  
)))))))).)))).)..... 12 23 0.107000

mdm\_miR171f\_5p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6651,6671] -18.70 GGGAAAGCTGGACCGAAGTCC  
GGATATTGGTCCGGTTCAATA .....(((((((.(.((( )))..)))))))).).....  
13 21 0.371000

mdm\_miR171q KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6651,6671] -18.70 GGGAAAGCTGGACCGAAGTCC  
GGATATTGGTCCGGTTCAATA .....(((((((.(.((( )))..)))))))).).....  
13 21 0.371000

mdm\_miR319d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6744,6762] -18.10 AAGGAGGATGGCGGCAGTT  
AACTGCCGACTCATTCCTCA ..((.((((((((((((((( )))..)))))))).).....  
16 19 0.028700

mdm\_miR394a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[2587,2609] -17.90 GGAGGGGAGGACAAGCGTGACGA

mdm\_miR394b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[2587,2609] -17.90 GGAGGGGAGGACAAGCGTGACGA

mdm\_miR393d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[3092,3111] -22.70 AGTCTGATGGATGGCATGAC  
ATCATGCGATCCCTTCGGACG .(((((((.(.(((((((. )))))).)))).).....  
16 20 0.239000

mdm\_miR393e KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[3092,3111] -22.70 AGTCTGATGGATGGCATGAC  
ATCATGCGATCCCTTCGGACG .(((((((.(.(((((((. )))))).)))).).....  
16 20 0.239000

mdm\_miR393f KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[3092,3111] -22.70 AGTCTGATGGATGGCATGAC  
ATCATGCGATCCCTTCGGACG .(((((((.(.(((((((. )))))).)))).).....  
16 20 0.239000

mdm\_miR393g KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[3092,3111] -21.10 AGTCTGATGGATGGCATGAC  
ATCATGCTATCCCTTTGGATT .(((..((.(((((((((((((((. )))))).)))).).....  
15 20 0.239000

mdm\_miR393h KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[3092,3111] -21.10 AGTCTGATGGATGGCATGAC  
ATCATGCTATCCCTTTGGATT .(((..((.(((((((((((((((. )))))).)))).).....  
15 20 0.239000

mdm\_miR395k KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[4691,4710] -18.00 AGGCAGGAGTTTGAGGAAAC  
GTTTCCTCAAACACTTCATT ....((((((((((((((((((( )))..)))))))).).....  
15 20 0.070900

mdm\_miR395d\_5p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[5181,5201] -15.90 TAATGAGATTACAGGGGAAT  
GTTCCCTTGACCACTTCATTG (((((((.....(((((((( )))))))).....))))))  
16 21 0.357000

mdm\_miR395g\_5p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[5181,5201] -15.90 TAATGAGATTACAGGGGAAT  
GTTCCCTTGACCACTTCATTG (((((((.....(((((((( )))))))).....))))))  
16 21 0.357000

mdm\_miR395i\_5p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[5181,5201] -15.90 TAATGAGATTACAGGGGAAT  
GTTCCCTTGACCACTTCATTG (((((((.....(((((((( )))))))).....))))))  
16 21 0.357000

mdm\_miR395j KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[5181,5201] -15.90 TAATGAGATTACAGGGGAAT  
GTTCCCTTGACCACTTCATTG (((((((.....(((((((( )))))))).....))))))  
16 21 0.357000

mdm\_miR395l KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[5592,5613] -15.00 AGGTTTTGACCAGATTTTTCAT  
CTGAAGTGTGGGGGAACCC .((((((..((((((.(((((. ))))))..)))))).))))).  
17 22 0.080000

mdm\_miR399a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[6083,6104] -16.20 TAGTGGCTCAGCCACTTTGGTC  
TGCCAAAGGAGAATTGCCCTG (((.((((.....((.((((((. ))))))..))....))))))  
14 22 0.107000

mdm\_miR399b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[6083,6104] -16.20 TAGTGGCTCAGCCACTTTGGTC  
TGCCAAAGGAGAATTGCCCTG (((.((((.....((.((((((. ))))))..))....))))))  
14 22 0.107000

mdm\_miR399c KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[6083,6104] -16.20 TAGTGGCTCAGCCACTTTGGTC  
TGCCAAAGGAGAATTGCCCTG (((.((((.....((.((((((. ))))))..))....))))))  
14 22 0.107000

mdm\_miR399d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[6083,6104] -16.50 TAGTGGCTCAGCCACTTTGGTC  
TGCCAAAGGAGAGTTGCCCTA (((.((((.....((.((((((. ))))))..))....))))))  
14 22 0.107000

mdm\_miR393d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[6423,6443] -19.30 ATCCCGAGGGGAATGTTTGA  
ATCATGCGATCCCTTCGGACG ...((((((((((.((((((. )))).)))).))))))...  
15 21 0.385000

mdm\_miR393e KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[6423,6443] -19.30 ATCCCGAGGGGAATGTTTGA  
ATCATGCGATCCCTTCGGACG ...((((((((((.((((((. )))).)))).))))))...  
15 21 0.385000

mdm\_miR393f KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[6423,6443] -19.30 ATCCCGAGGGGAATGTTTGA  
ATCATGCGATCCCTTCGGACG ...((((((((((.((((((. )))).)))).))))))...  
15 21 0.385000

mdm\_miR394a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[6746,6766] -16.90 GGAGGATGGCGGCAGTTCTAA  
TTGGCATTCTGTCCACCTCC (((((((.....(((((((( ))))))..))))))...  
18 21 0.028700

mdm\_miR394b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaarget from/to=[6746,6766] -16.90 GGAGGATGGCGGCAGTTCTAA  
TTGGCATTCTGTCCACCTCC (((((((.....(((((((( ))))))..))))))...  
18 21 0.028700

mdm\_miR7121a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[153,171] -16.40 ACAGAACGCCACAAGAGGA  
TCCTCTTGGTGATCGCCCTGT ((((((((.(((((((( ( )))))))).)))...))))  
16 19 0.277000

mdm\_miR7121b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[153,171] -16.40 ACAGAACGCCACAAGAGGA  
TCCTCTTGGTGATCGCCCTGT ((((((((.(((((((( ( )))))))).)))...))))  
16 19 0.277000

mdm\_miR7121a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[961,980] -15.40 CAAGGAGGAGGTCAGGAGGT  
TCCTCTTGGTGATCGCCCTGT ..(((.(((.(((((((( ( )))))))).)))...))..  
13 20 0.094700

mdm\_miR7121b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[961,980] -15.40 CAAGGAGGAGGTCAGGAGGT  
TCCTCTTGGTGATCGCCCTGT ..(((.(((.(((((((( ( )))))))).)))...))..  
13 20 0.094700

mdm\_miR5225a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[1364,1386] -15.70 ACATCAGACAGACCATTGACAGT

mdm\_miR5225b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[1364,1386] -15.70 ACATCAGACAGACCATTGACAGT

mdm\_miR535a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[1652,1671] -18.60 ATGCGCTCTTCTCGATGTTA  
TGACAACGAGAGAGAGCACGC .(((.(((((((( ( )))))))).)))...  
17 20 0.011800

mdm\_miR535d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[1652,1671] -17.90 ATGCGCTCTTCTCGATGTTA  
TGACGACGAGAGAGAGCACGC .(((.(((((((( ( )))))))).)))...  
17 20 0.011800

mdm\_miR5225c KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[1718,1740] -16.50 GCAACTGACACAAACAGGGCAGA

mdm\_miR482a\_3p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[2135,2157] -18.30 GTTTCGCGCGCCGGGCTTGTGAG

mdm\_miR408a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[2376,2400] -18.70  
TTCAGGTATATGAGGATGGGTGCAG ATGCACTGCCTCTTCCCTGGC  
..(((.(((.(((((((( ( )))))))).)))...)).. 15 25  
0.159000

mdm\_miR3627d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[2376,2395] -19.30 TTCAGGTATATGAGGATGGG  
TCCATCCTCCTGTGACATGAA ((((((((.(((((((( ( )))))))).)))...))))  
17 20 0.159000

mdm\_miR7121a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[2574,2594] -15.00 TTCAGGTGATGTCGGAGGGGA  
TCCTCTTGGTGATCGCCCTGT .....(((.(((.(((((((( ( )))))))).)))...)).....  
13 21 0.281000

mdm\_miR7121b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[2574,2594] -15.00 TTCAGGTGATGTCGGAGGGGA  
TCCTCTTGGTGATCGCCCTGT .....(((.(((.(((((((( ( )))))))).)))...)).....  
13 21 0.281000

mdm\_miR3627d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[3541,3559] -15.60 TAAGCTTCACATGGATGGA  
TCCATCCTCCTGTGACATGAA .....(((.(((.(((((((( ( )))))))).)))...)).....  
12 19 0.329000

mdm\_miR477a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa from/to=[3659,3680] -15.60 ATGAGGCTTTTCAAGGAAGGGA  
ACTCTCCCTCAAGAGCTTCTC ..(((.(((.(((((((( ( )))))))).)))...)).....

```

16      22      0.136000
mdm_miR477b    KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[3658,3680]      -15.70  AATGAGGCTTTTCAAGGAAGGGA
mdm_miR530a    KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[4683,4701]      -15.20  ACCAGTGCAGGCAGGAGTT
                TGCATTTGCACCTGCACTTGT  ((.(((((((((((.(.  .)).))))))..))))))..))
16      19      0.070900
mdm_miR530b    KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[4683,4701]      -15.20  ACCAGTGCAGGCAGGAGTT
                TGCATTTGCACCTGCACTTGT  ((.(((((((((((.(.  .)).))))))..))))))..))
16      19      0.070900
mdm_miR530c    KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[4683,4701]      -15.20  ACCAGTGCAGGCAGGAGTT
                TGCATTTGCACCTGCACTTGT  ((.(((((((((((.(.  .)).))))))..))))))..))
16      19      0.070900
mdm_miR399i    KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[6083,6104]      -16.20  TAGTGGCTCAGCCACTTTGGTC
                TGCCAAAGGAGAGTTGCCCTG  (((.(((.....(..(((((((.  .)))))))))..))....))))))
14      22      0.107000
mdm_miR399j    KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[6083,6104]      -16.20  TAGTGGCTCAGCCACTTTGGTC
                TGCCAAAGGAGAGTTGCCCTG  (((.(((.....(..(((((((.  .)))))))))..))....))))))
14      22      0.107000
mdm_miR530a    KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[6312,6332]      -15.40  GACCCATTAGGTGCAAGCGCT
                TGCATTTGCACCTGCACTTGT  .....(((((((((((.(.  .)).))))))))).....
12      21      0.221000
mdm_miR530b    KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[6312,6332]      -15.40  GACCCATTAGGTGCAAGCGCT
                TGCATTTGCACCTGCACTTGT  .....(((((((((((.(.  .)).))))))))).....
12      21      0.221000
mdm_miR530c    KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[6312,6332]      -15.40  GACCCATTAGGTGCAAGCGCT
                TGCATTTGCACCTGCACTTGT  .....(((((((((((.(.  .)).))))))))).....
12      21      0.221000
mdm_miR7121a   KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[6415,6434]      -18.30  AGCATGAGATCCCGAGGGGA
                TCCTCTTGGTGATCGCCCTGT  .....(.(((((((((((  )))))))))).))....
14      20      0.385000
mdm_miR7121b   KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[6415,6434]      -18.30  AGCATGAGATCCCGAGGGGA
                TCCTCTTGGTGATCGCCCTGT  .....(.(((((((((((  )))))))))).))....
14      20      0.385000
mdm_miR482a_5p KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[6657,6677]      -15.50  GCTGGACCGAAGTCCATTGCT
                AGGAATGGGCTGTTTGGGAAGA  .((...(((((((((((.  .))..))))))..))))..)).
16      21      0.371000
mdm_miR3627d   KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genometa  target from/to=[6736,6755]      -19.80  ATCAGACGAAGGAGGATGGC
                TCCATCTCCTGTGACATGAA  .(((..((.(((((((((((.  .)))))))))..))....)).
15      20      0.028700
mdm_miR7121c   KU870525.1 Apple chlorotic leaf spot virus isolate
SY03, complete genome  target from/to=[153,171]      -16.40
                ACAGAACGCCACAAGAGGA  TCCTCTTGGTGATCGCCCTGT  ((((..((.(((((((((((
)))))))).))..))....))  16      19      0.277000
mdm_miR7121c   KU870525.1 Apple chlorotic leaf spot virus isolate SY03,

```

complete genometa target from/to=[961,980] -15.40 CAAGGAGGAGGTCAGGAGGT  
TCCTCTTGGTGATCGCCCTGT ..(((..(((.....))))))....  
13 20 0.094700

mdm\_miR10978a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[1644,1667] -17.70 TTGTGATGATGCGCTCTTCTCGAT  
mdm\_miR10978b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[1644,1667] -17.70 TTGTGATGATGCGCTCTTCTCGAT  
mdm\_miR10979 KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[2150,2170] -15.30 CTTGTGAGAACTGTTGGTAAT  
CTTGCCGATAGATTTGGGGAG (((..(((.....))))))....  
17 21 0.006200

mdm\_miR7121c KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[2574,2594] -15.00 TTCAGGTGATGTCGGAGGGGA  
TCCTCTTGGTGATCGCCCTGT .....(((.....))))....  
13 21 0.281000

mdm\_miR7121d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[2574,2594] -15.00 TTCAGGTGATGTCGGAGGGGA  
TCCTCTTGGTGATCGCCCTGC .....(((.....))))....  
13 21 0.281000

mdm\_miR7121e KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[2574,2594] -15.00 TTCAGGTGATGTCGGAGGGGA  
TCCTCTTGGTGATCGCCCTGC .....(((.....))))....  
13 21 0.281000

mdm\_miR7121f KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[2574,2594] -15.00 TTCAGGTGATGTCGGAGGGGA  
TCCTCTTGGTGATCGCCCTGC .....(((.....))))....  
13 21 0.281000

mdm\_miR7121g KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[2574,2594] -15.00 TTCAGGTGATGTCGGAGGGGA  
TCCTCTTGGTGATCGCCCTGC .....(((.....))))....  
13 21 0.281000

mdm\_miR7121h KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[2574,2594] -15.00 TTCAGGTGATGTCGGAGGGGA  
TCCTCTTGGTGATCGCCCTGC .....(((.....))))....  
13 21 0.281000

mdm\_miR10984b\_3p KU870525.1 Apple chlorotic leaf spot virus isolate  
SY03, complete genome target from/to=[2584,2607] -15.10  
GTCGGAGGGGAGGACAAGCGTGAC CTCACGTACGCTGTCCGAGAA  
..(((.....)))).... 13 24  
0.281000

mdm\_miR10980a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[2630,2650] -16.70 TTCAGCTTTGAGTCCAAGGTC  
CACCTGGGACTTGCAGCCATG ....(((.....))))....  
14 21 0.257000

mdm\_miR10980b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[2630,2650] -16.70 TTCAGCTTTGAGTCCAAGGTC  
CACCTGGGACTTGCAGCCATG ....(((.....))))....  
14 21 0.257000

mdm\_miR10980a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[4198,4218] -15.60 AATGGACAGAGAGGCCAGGTT  
CACCTGGGACTTGCAGCCATG .(((.....))))....  
13 21 0.239000

mdm\_miR10980b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometa target from/to=[4198,4218] -15.60 AATGGACAGAGAGGCCAGGTT  
CACCTGGGACTTGCAGCCATG .(((.....))))....  
13 21 0.239000

mdm\_miR7121d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[4538,4556] -15.90 GCAGCTATCAAGAAGAGGT  
TCCTCTTGGTGATCGCCCTGC ((((((.(((..(((((. .))))))..))))..))))  
15 19 0.201000

mdm\_miR7121e KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[4538,4556] -15.90 GCAGCTATCAAGAAGAGGT  
TCCTCTTGGTGATCGCCCTGC ((((((.(((..(((((. .))))))..))))..))))  
15 19 0.201000

mdm\_miR7121f KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[4538,4556] -15.90 GCAGCTATCAAGAAGAGGT  
TCCTCTTGGTGATCGCCCTGC ((((((.(((..(((((. .))))))..))))..))))  
15 19 0.201000

mdm\_miR7121g KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[4538,4556] -15.90 GCAGCTATCAAGAAGAGGT  
TCCTCTTGGTGATCGCCCTGC ((((((.(((..(((((. .))))))..))))..))))  
15 19 0.201000

mdm\_miR7121h KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[4538,4556] -15.90 GCAGCTATCAAGAAGAGGT  
TCCTCTTGGTGATCGCCCTGC ((((((.(((..(((((. .))))))..))))..))))  
15 19 0.201000

mdm\_miR10983 KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[5399,5418] -16.90 TTTTGCGGGTGGAGGCTTTG  
CAGAGCAAAACAGTCGTGGAA (((..(((..(((..(((( )))))..))))..))))  
14 20 0.329000

mdm\_miR10981a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6085,6105] -18.70 GTGGCTCAGCCACTTTGGTCA  
TGACCAACATATATGGGCCGT .(((((((.....((((((( )))))))..))))..))))..  
14 21 0.107000

mdm\_miR10981b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6085,6105] -18.70 GTGGCTCAGCCACTTTGGTCA  
TGACCAACATATATGGGCCGT .(((((((.....((((((( )))))))..))))..))))..  
14 21 0.107000

mdm\_miR7121c KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6415,6434] -18.30 AGCATGAGATCCCGAGGGGA  
TCCTCTTGGTGATCGCCCTGT .....(.((((((((((((((( ))))))))))..))))..  
14 20 0.385000

mdm\_miR7121d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6415,6434] -18.30 AGCATGAGATCCCGAGGGGA  
TCCTCTTGGTGATCGCCCTGC .....(.((((((((((((((( ))))))))))..))))..  
14 20 0.385000

mdm\_miR7121e KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6415,6434] -18.30 AGCATGAGATCCCGAGGGGA  
TCCTCTTGGTGATCGCCCTGC .....(.((((((((((((((( ))))))))))..))))..  
14 20 0.385000

mdm\_miR7121f KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6415,6434] -18.30 AGCATGAGATCCCGAGGGGA  
TCCTCTTGGTGATCGCCCTGC .....(.((((((((((((((( ))))))))))..))))..  
14 20 0.385000

mdm\_miR7121g KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6415,6434] -18.30 AGCATGAGATCCCGAGGGGA  
TCCTCTTGGTGATCGCCCTGC .....(.((((((((((((((( ))))))))))..))))..  
14 20 0.385000

mdm\_miR7121h KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genometaget from/to=[6415,6434] -18.30 AGCATGAGATCCCGAGGGGA  
TCCTCTTGGTGATCGCCCTGC .....(.((((((((((((((( ))))))))))..))))..  
14 20 0.385000

```
mmdm_miR11002a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[558,579] -15.60 CCACTCCTGAGAGGTACCCCTG  
GAGGATGAGCTTCGGCGGTGA .(((((((((((((.(((.)))..)))))))).))).  
16 22 0.060100  
mmdm_miR11002b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[558,579] -15.60 CCACTCCTGAGAGGTACCCCTG  
GAGGATGAGCTTCGGCGGTGA .(((((((((((((.(((.)))..)))))))).))).  
16 22 0.060100  
mmdm_miR11002c_3p KU870525.1 Apple chlorotic leaf spot virus isolate  
SY03, complete genome target from/to=[558,579] -15.60  
CCACTCCTGAGAGGTACCCCTG GAGGATGAGCTTCGGCGGTGA .(((((((((((((.(((.)))..)))))))).))).  
.))))).))))).))))).))))). 16 22 0.060100  
mmdm_miR10993c KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[972,993] -19.70 TCAGGAGGTTTGGGCCATATGA  
ACATGTGGTGTAACCATCCTGT .(((((((((((((.(((.)))..)))))))).))).  
17 22 0.094700  
mmdm_miR10993d KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[972,993] -19.70 TCAGGAGGTTTGGGCCATATGA  
ACATGTGGTGTAACCATCCTGT .(((((((((((((.(((.)))..)))))))).))).  
17 22 0.094700  
mmdm_miR10993e KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[972,993] -19.70 TCAGGAGGTTTGGGCCATATGA  
ACATGTGGTGTAACCATCCTGT .(((((((((((((.(((.)))..)))))))).))).  
17 22 0.094700  
mmdm_miR10993f KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[972,993] -19.70 TCAGGAGGTTTGGGCCATATGA  
ACATGTGGTGTAACCATCCTGT .(((((((((((((.(((.)))..)))))))).))).  
17 22 0.094700  
mmdm_miR10995 KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[960,983] -16.10 TCAAGGAGGAGGTCAGGAGGTTTG  
mmdm_miR11019 KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[964,984] -15.40 GGAGGAGGTCAGGAGGTTTGG  
CCAGATGATCATAATCTCCTGA ..(((((((((((((.(((.)))..)))))))).))).  
15 21 0.094700  
mmdm_miR10994_3p KU870525.1 Apple chlorotic leaf spot virus isolate  
SY03, complete genome target from/to=[2217,2236] -15.60  
GCATAGGAAAGAGGAGAGCA TGCTTTTTTCTTGACCATAGC ((...(((.(((((((((((((  
)))))))))))).)))))) 16 20 0.286000  
mmdm_miR10996a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[3100,3122] -15.10 GGATGGCATGACAGGGATAGTGT  
mmdm_miR11002a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[4139,4159] -16.20 TCATCTGTTAAACTCATTCTA  
GAGGATGAGCTTCGGCGGTGA ((((((((((((((((.(((.)))..)))))))).))).  
17 21 0.380000  
mmdm_miR11002b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[4139,4159] -16.20 TCATCTGTTAAACTCATTCTA  
GAGGATGAGCTTCGGCGGTGA ((((((((((((((((.(((.)))..)))))))).))).  
17 21 0.380000  
mmdm_miR11002c_3p KU870525.1 Apple chlorotic leaf spot virus isolate  
SY03, complete genome target from/to=[4139,4159] -16.20  
TCATCTGTTAAACTCATTCTA GAGGATGAGCTTCGGCGGTGA ((((((((((((((((.(((.)))..)))))))).))).  
17 21 0.380000  
mmdm_miR11012a KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[4582,4604] -18.82 CTACGCAAATTTAAGGCAGCGG  
mmdm_miR11012b KU870525.1 Apple chlorotic leaf spot virus isolate SY03,  
complete genomestarget from/to=[4582,4604] -18.82 CTACGCAAATTTAAGGCAGCGG
```



```

mdm_miR10995    KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genom  target from/to=[4695,4718]    -15.70 AGGAGTTTGAGGAAACCAAGCTTT
mdm_miR11002a   KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genom  target from/to=[5331,5350]    -15.30 ACACCCATGAGTTCATTTTG
      GAGGATGAGCTTCGGCGGTGA  .((((((.(((((((((((.  .)))))))))))).)).)).).
      16      20      0.311000
mdm_miR11002b   KU870525.1 Apple chlorotic leaf spot virus isolate SY03,
complete genom  target from/to=[5331,5350]    -15.30 ACACCCATGAGTTCATTTTG
      GAGGATGAGCTTCGGCGGTGA  .((((((.(((((((((((.  .)))))))))))).)).)).).
      16      20      0.311000
mdm_miR11002c_3p    KU870525.1 Apple chlorotic leaf spot virus isolate
SY03, complete genome  target from/to=[5331,5350]    -15.30
      ACACCCATGAGTTCATTTTG  GAGGATGAGCTTCGGCGGTGA  .((((((.(((((((((((.
      .)))))))))))).)).)).).  16      20      0.311000

```

TAPIR

```
#-----  
# Search parameters  
# score <= 9  
# mfe_ratio >= 0.2  
#-----
```

```
target      KU870525.1  
miRNA       mdm-miR156p  
score       8.5  
mfe_ratio   0.44  
start       6758  
seed_gap    0  
seed_mismatch 1  
seed_gu     1  
gap         0  
mismatch    5  
gu          1  
miRNA_3'    CACGAGAGAUAGAAGACAGUC  
aln         ..|o|||..|||||||..||o|.   
target_5'   CAGUUCUAAAUCUUCAGUUAA  
//  
target      KU870525.1  
miRNA       mdm-miR156q  
score       8.5  
mfe_ratio   0.44  
start       6758  
seed_gap    0  
seed_mismatch 1  
seed_gu     1  
gap         0  
mismatch    5  
gu          1  
miRNA_3'    CACGAGAGAUAGAAGACAGUC  
aln         ..|o|||..|||||||..||o|.   
target_5'   CAGUUCUAAAUCUUCAGUUAA  
//  
target      KU870525.1  
miRNA       mdm-miR156r  
score       8.5  
mfe_ratio   0.44  
start       6758  
seed_gap    0  
seed_mismatch 1  
seed_gu     1  
gap         0  
mismatch    5  
gu          1  
miRNA_3'    CACGAGAGAUAGAAGACAGUC  
aln         ..|o|||..|||||||..||o|.   
target_5'   CAGUUCUAAAUCUUCAGUUAA  
//  
target      KU870525.1  
miRNA       mdm-miR156s  
score       8.5  
mfe_ratio   0.44  
start       6758
```

```

seed_gap      0
seed_mismatch 1
seed_gu       1
gap           0
mismatch      5
gu            1
miRNA_3'      CACGAGAGAUAGAAGACAGUC
aln           ..|o|||..|o|||..|o|.
target_5'     CAGUUCUAAAUCUUCAGUUA
//
target        KU870525.1
miRNA         mdm-miR156x
score         8.5
mfe_ratio     0.45
start         6758
seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      3
gu            1
miRNA_3'      CACGAGAGAUAGAAGACAGU
aln           ..|o|||..|o|||..|o|.
target_5'     CAGUUCUAAAUCUUCAGUUA
//
target        KU870525.1
miRNA         mdm-miR156y
score         8.5
mfe_ratio     0.45
start         6758
seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      3
gu            1
miRNA_3'      CACGAGAGAUAGAAGACAGU
aln           ..|o|||..|o|||..|o|.
target_5'     CAGUUCUAAAUCUUCAGUUA
//
target        KU870525.1
miRNA         mdm-miR156z
score         8.5
mfe_ratio     0.45
start         6758
seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      3
gu            1
miRNA_3'      CACGAGAGAUAGAAGACAGU
aln           ..|o|||..|o|||..|o|.
target_5'     CAGUUCUAAAUCUUCAGUUA
//
target        KU870525.1
miRNA         mdm-miR156aa

```

```

score            8.5
mfe_ratio        0.45
start            6758
seed_gap         0
seed_mismatch    2
seed_gu         1
gap              0
mismatch         3
gu              1
miRNA_3'         CACGAGAGAUAGAAGACAGU
aln              ..|o|||..||||||..||o|
target_5'        CAGUUCUAAAUCUUCAGUUA
//
target           KU870525.1
miRNA            mdm-miR156ab
score            7.5
mfe_ratio        0.46
start            6758
seed_gap         0
seed_mismatch    1
seed_gu         1
gap              0
mismatch         4
gu              1
miRNA_3'         CACGAGAGAUAGAAGACAGUU
aln              ..|o|||..||||||..||o||
target_5'        CAGUUCUAAAUCUUCAGUUAA
//
target           KU870525.1
miRNA            mdm-miR156ac
score            7.5
mfe_ratio        0.46
start            6758
seed_gap         0
seed_mismatch    1
seed_gu         1
gap              0
mismatch         4
gu              1
miRNA_3'         CACGAGAGAUAGAAGACAGUU
aln              ..|o|||..||||||..||o||
target_5'        CAGUUCUAAAUCUUCAGUUAA
//
target           KU870525.1
miRNA            mdm-miR156ad
score            8
mfe_ratio        0.60
start            7293
seed_gap         0
seed_mismatch    1
seed_gu         1
gap              0
mismatch         5
gu              0
miRNA_3'         CACGAGUGAAAGAAGACAGU
aln              |.....||||||..||||o|
target_5'        GGCGAAACUUUCGUCUGUUA

```

```

//
target      KU870525.1
miRNA       mdm-miR156ae
score       8
mfe_ratio   0.60
start       7293
seed_gap    0
seed_mismatch 1
seed_gu     1
gap         0
mismatch    5
gu          0
miRNA_3'    CACGAGUGAAAGAAGACAGU
aln         |.....|.|.|.|.|.|.|.|.|.|.|
target_5'   GGCGAAACUUUCGUCUGUUA
//
target      KU870525.1
miRNA       mdm-miR167a
score       9
mfe_ratio   0.52
start       976
seed_gap    0
seed_mismatch 1
seed_gu     0
gap         0
mismatch    7
gu          0
miRNA_3'    CCACUUUGACGGUCUACUAGA
aln         |..|.....|.|.|.|.|.|.|.|
target_5'   GAGGUUUGGGCCAUAUGAUCU
//
target      KU870525.1
miRNA       mdm-miR168a
score       8.5
mfe_ratio   0.56
start       2505
seed_gap    0
seed_mismatch 3
seed_gu     0
gap         0
mismatch    2
gu          1
miRNA_3'    AAGGGCUGGACGUGGUUCGCU
aln         |..o|||.|.|.|.|.|.|.|
target_5'   UCAUCGACCUGAAGCAAGGGA
//
target      KU870525.1
miRNA       mdm-miR168b
score       8.5
mfe_ratio   0.56
start       2505
seed_gap    0
seed_mismatch 3
seed_gu     0
gap         0
mismatch    2
gu          1

```

```

miRNA_3'      AAGGGCUGGACGUGGUUCGCU
aln           |..o|||||||.|.||||.||
target_5'     UCAUCGACCUGAAGCAAGGGA
//
target        KU870525.1
miRNA         mdm-miR169b
score         8.5
mfe_ratio     0.53
start         6678
seed_gap      0
seed_mismatch 2
seed_gu       0
gap           0
mismatch      3
gu            3
miRNA_3'      CGUCCGUUUAGUAGGAACCGAU
aln           .|||..ooo|||||.|||.||
target_5'     UCAGAAGGGUCAUCCGUGGAUA
//
target        KU870525.1
miRNA         mdm-miR169k
score         7
mfe_ratio     0.69
start         200
seed_gap      0
seed_mismatch 3
seed_gu       0
gap           1
mismatch      0
gu            0
miRNA_3'      GUCCGUUCAGUAGGAACCGAU
aln           ||||.|||||||.|||.|||
target_5'     CAGG-AAGUCAUCAGCGGCUA
//
target        KU870525.1
miRNA         mdm-miR169l
score         7
mfe_ratio     0.69
start         200
seed_gap      0
seed_mismatch 3
seed_gu       0
gap           1
mismatch      0
gu            0
miRNA_3'      GUCCGUUCAGUAGGAACCGAU
aln           ||||.|||||||.|||.|||
target_5'     CAGG-AAGUCAUCAGCGGCUA
//
target        KU870525.1
miRNA         mdm-miR169m
score         7
mfe_ratio     0.69
start         200
seed_gap      0
seed_mismatch 3
seed_gu       0

```

```

gap                1
mismatch          0
gu                0
miRNA_3'          GUCCGUUCAGUAGGAACCGAU
aln               ||||.|||||||...|||||
target_5'         CAGG-AAGUCAUCAGCGGCUA
//
target            KU870525.1
miRNA             mdm-miR169n
score             7
mfe_ratio         0.69
start            200
seed_gap          0
seed_mismatch     3
seed_gu           0
gap              1
mismatch          0
gu                0
miRNA_3'          GUCCGUUCAGUAGGAACCGAU
aln               ||||.|||||||...|||||
target_5'         CAGG-AAGUCAUCAGCGGCUA
//
target            KU870525.1
miRNA             mdm-miR169o
score             9
mfe_ratio         0.57
start            200
seed_gap          0
seed_mismatch     3
seed_gu           0
gap              0
mismatch          3
gu                0
miRNA_3'          UCCGUUCAGUAGGGACCGAU
aln               ..|.|||||||...|||||
target_5'         CAGGAAGUCAUCAGCGGCUA
//
target            KU870525.1
miRNA             mdm-miR171m
score             9
mfe_ratio         0.58
start            700
seed_gap          0
seed_mismatch     3
seed_gu           1
gap              0
mismatch          2
gu                0
miRNA_3'          ACACUUAUAACCGUGCCGAGUU
aln               ||.||||.|||||.|.o.||||
target_5'         UGAGAUUUUGGCAGGUUACAA
//
target            KU870525.1
miRNA             mdm-miR171n
score             9
mfe_ratio         0.58
start            700

```

```

seed_gap      0
seed_mismatch 3
seed_gu       1
gap           0
mismatch      2
gu            0
miRNA_3'      ACACUAUAACCGUGCCGAGUU
aln           ||.||||.|||||.|.o.||||
target_5'     UGAGAUUUUGGCAGGUUACAA
//
target        KU870525.1
miRNA         mdm-miR319b-5p
score         8.5
mfe_ratio     0.38
start         5373
seed_gap      0
seed_mismatch 3
seed_gu       0
gap           0
mismatch      2
gu            1
miRNA_3'      CUCACCUGACUUCUUUCGAG
aln           .||||.||.||||.||||.|o
target_5'     AAGUGAACAGAACAAAGGUU
//
target        KU870525.1
miRNA         mdm-miR319d
score         9
mfe_ratio     0.55
start         7387
seed_gap      0
seed_mismatch 3
seed_gu       1
gap           0
mismatch      2
gu            0
miRNA_3'      ACUCACUUACUCAGCCGUCAA
aln           ||.||||.||.|||o.|||||
target_5'     UGUGUGAUUAUGUUCGCAGUU
//
target        KU870525.1
miRNA         mdm-miR319e
score         8.5
mfe_ratio     0.38
start         5373
seed_gap      0
seed_mismatch 3
seed_gu       0
gap           0
mismatch      2
gu            1
miRNA_3'      CUCACCUGACUUCUUUCGAG
aln           .||||.||.||||.||||.|o
target_5'     AAGUGAACAGAACAAAGGUU
//
target        KU870525.1
miRNA         mdm-miR319f

```



```

score            8.5
mfe_ratio        0.38
start            5373
seed_gap         0
seed_mismatch    3
seed_gu         0
gap              0
mismatch         2
gu              1
miRNA_3'         CUCACCUGACUUCUUUCGAG
aln              .||||.||.||||.||||.|o
target_5'        AAGUGAACAGAACAAAGGUU
//
target           KU870525.1
miRNA            mdm-miR319g
score            8.5
mfe_ratio        0.38
start            5373
seed_gap         0
seed_mismatch    3
seed_gu         0
gap              0
mismatch         2
gu              1
miRNA_3'         CUCACCUGACUUCUUUCGAG
aln              .||||.||.||||.||||.|o
target_5'        AAGUGAACAGAACAAAGGUU
//
target           KU870525.1
miRNA            mdm-miR390a
score            9
mfe_ratio        0.47
start            687
seed_gap         1
seed_mismatch    1
seed_gu         0
gap              0
mismatch         5
gu              0
miRNA_3'         CCGCGAUAGGGAGGACUCGAA
aln              ....||.||||.||||||.||
target_5'        UAGUCUUUCCC-CCUGAGAUU
//
target           KU870525.1
miRNA            mdm-miR390b
score            9
mfe_ratio        0.47
start            687
seed_gap         1
seed_mismatch    1
seed_gu         0
gap              0
mismatch         5
gu              0
miRNA_3'         CCGCGAUAGGGAGGACUCGAA
aln              ....||.||||.||||||.||
target_5'        UAGUCUUUCCC-CCUGAGAUU

```

```

//
target      KU870525.1
miRNA       mdm-miR390c
score       9
mfe_ratio   0.47
start       687
seed_gap    1
seed_mismatch 1
seed_gu     0
gap         0
mismatch    5
gu          0
miRNA_3'    CCGCGAUAGGGAGGACUCGAA
aln         ....||.||||.||||||.||
target_5'   UAGUCUUUCCC-CCUGAGAUU
//
target      KU870525.1
miRNA       mdm-miR390d
score       9
mfe_ratio   0.47
start       687
seed_gap    1
seed_mismatch 1
seed_gu     0
gap         0
mismatch    5
gu          0
miRNA_3'    CCGCGAUAGGGAGGACUCGAA
aln         ....||.||||.||||||.||
target_5'   UAGUCUUUCCC-CCUGAGAUU
//
target      KU870525.1
miRNA       mdm-miR390e
score       9
mfe_ratio   0.47
start       687
seed_gap    1
seed_mismatch 1
seed_gu     0
gap         0
mismatch    5
gu          0
miRNA_3'    CCGCGAUAGGGAGGACUCGAA
aln         ....||.||||.||||||.||
target_5'   UAGUCUUUCCC-CCUGAGAUU
//
target      KU870525.1
miRNA       mdm-miR390f
score       9
mfe_ratio   0.47
start       687
seed_gap    1
seed_mismatch 1
seed_gu     0
gap         0
mismatch    5
gu          0

```

```

miRNA_3'      CCGCGAUAGGGAGGACUCGAA
aln           ....|||.||||.|||||||.||
target_5'     UAGUCUUUCCC-CCUGAGAUU
//
target        KU870525.1
miRNA         mdm-miR393d
score         9
mfe_ratio     0.60
start         3091
seed_gap      0
seed_mismatch 1
seed_gu       0
gap           0
mismatch      6
gu            2
miRNA_3'      GCAGGCUUCCCUAGCGUACUA
aln           ...o|.o|.||||.|||||.
target_5'     GAGUCUGAUGGAUGGCAUGAC
//
target        KU870525.1
miRNA         mdm-miR393e
score         9
mfe_ratio     0.60
start         3091
seed_gap      0
seed_mismatch 1
seed_gu       0
gap           0
mismatch      6
gu            2
miRNA_3'      GCAGGCUUCCCUAGCGUACUA
aln           ...o|.o|.||||.|||||.
target_5'     GAGUCUGAUGGAUGGCAUGAC
//
target        KU870525.1
miRNA         mdm-miR393f
score         9
mfe_ratio     0.60
start         3091
seed_gap      0
seed_mismatch 1
seed_gu       0
gap           0
mismatch      6
gu            2
miRNA_3'      GCAGGCUUCCCUAGCGUACUA
aln           ...o|.o|.||||.|||||.
target_5'     GAGUCUGAUGGAUGGCAUGAC
//
target        KU870525.1
miRNA         mdm-miR394a
score         7
mfe_ratio     0.49
start         1426
seed_gap      0
seed_mismatch 2
seed_gu       0

```

```

gap                0
mismatch          3
gu                0
miRNA_3'          CCUCCACCUGUCUUACGGUU
aln               .|.|||.|||||.|||.||||
target_5'         UGUGGAGGACAGUAUCCCAA
//
target            KU870525.1
miRNA             mdm-miR394b
score             7
mfe_ratio         0.49
start            1426
seed_gap          0
seed_mismatch     2
seed_gu           0
gap              0
mismatch         3
gu              0
miRNA_3'          CCUCCACCUGUCUUACGGUU
aln               .|.|||.|||||.|||.||||
target_5'         UGUGGAGGACAGUAUCCCAA
//
target            KU870525.1
miRNA             mdm-miR395a
score             9
mfe_ratio         0.47
start            1970
seed_gap          0
seed_mismatch     2
seed_gu           1
gap              0
mismatch         4
gu              0
miRNA_3'          CUCAAGGGGGUUUGUGAAGUC
aln               .|||.|||.|||||o|.|||.
target_5'         AAGGUCGCCCCAAUAGUGCAC
//
target            KU870525.1
miRNA             mdm-miR395b
score             9
mfe_ratio         0.47
start            1970
seed_gap          0
seed_mismatch     2
seed_gu           1
gap              0
mismatch         4
gu              0
miRNA_3'          CUCAAGGGGGUUUGUGAAGUC
aln               .|||.|||.|||||o|.|||.
target_5'         AAGGUCGCCCCAAUAGUGCAC
//
target            KU870525.1
miRNA             mdm-miR395c
score             9
mfe_ratio         0.47
start            1970

```

```

seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      4
gu            0
miRNA_3'      CUCAAGGGGGUUUGUGAAGUC
aln           .||.||.|||||o|.|.||.
target_5'     AAGGUCGCCCCAAUAGUGCAC
//
target        KU870525.1
miRNA         mdm-miR395d-3p
score         9
mfe_ratio     0.47
start         1970
seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      4
gu            0
miRNA_3'      CUCAAGGGGGUUUGUGAAGUC
aln           .||.||.|||||o|.|.||.
target_5'     AAGGUCGCCCCAAUAGUGCAC
//
target        KU870525.1
miRNA         mdm-miR395e
score         9
mfe_ratio     0.47
start         1970
seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      4
gu            0
miRNA_3'      CUCAAGGGGGUUUGUGAAGUC
aln           .||.||.|||||o|.|.||.
target_5'     AAGGUCGCCCCAAUAGUGCAC
//
target        KU870525.1
miRNA         mdm-miR395f
score         9
mfe_ratio     0.47
start         1970
seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      4
gu            0
miRNA_3'      CUCAAGGGGGUUUGUGAAGUC
aln           .||.||.|||||o|.|.||.
target_5'     AAGGUCGCCCCAAUAGUGCAC
//
target        KU870525.1
miRNA         mdm-miR395g-3p

```

```

score          9
mfe_ratio      0.47
start          1970
seed_gap       0
seed_mismatch  2
seed_gu        1
gap            0
mismatch       4
gu             0
miRNA_3'       CUCAAGGGGGUUUGUGAAGUC
aln            .||.||.|||||||o|.|.||.
target_5'      AAGGUCGCCCCAAAUAGUGCAC
//
target         KU870525.1
miRNA          mdm-miR395h
score          9
mfe_ratio      0.47
start          1970
seed_gap       0
seed_mismatch  2
seed_gu        1
gap            0
mismatch       4
gu             0
miRNA_3'       CUCAAGGGGGUUUGUGAAGUC
aln            .||.||.|||||||o|.|.||.
target_5'      AAGGUCGCCCCAAAUAGUGCAC
//
target         KU870525.1
miRNA          mdm-miR395i-3p
score          9
mfe_ratio      0.47
start          1970
seed_gap       0
seed_mismatch  2
seed_gu        1
gap            0
mismatch       4
gu             0
miRNA_3'       CUCAAGGGGGUUUGUGAAGUC
aln            .||.||.|||||||o|.|.||.
target_5'      AAGGUCGCCCCAAAUAGUGCAC
//
target         KU870525.1
miRNA          mdm-miR395k
score          4
mfe_ratio      0.68
start          4691
seed_gap       0
seed_mismatch  0
seed_gu        0
gap            0
mismatch       3
gu             2
miRNA_3'       UUACUUCACAAACUCCUUUG
aln            |o..|o|.|||||||
target_5'      AGGCAGGAGUUUGAGGAAAC

```

```
//
target            KU870525.1
miRNA             mdm-miR396a
score             8.5
mfe_ratio         0.47
start             2702
seed_gap          0
seed_mismatch     2
seed_gu           0
gap               0
mismatch          4
gu                1
miRNA_3'          GACAAGUUCUUUCGACACCUU
aln               .|...|||...|||.|||o
target_5'         AUUCACAAGAAACCUGAGGAG
//
target            KU870525.1
miRNA             mdm-miR396c
score             8.5
mfe_ratio         0.52
start             2702
seed_gap          0
seed_mismatch     2
seed_gu           0
gap               0
mismatch          4
gu                1
miRNA_3'          UUCAAGUUCUUUCGACACCUU
aln               |....|||...|||.|||o
target_5'         AUUCACAAGAAACCUGAGGAG
//
target            KU870525.1
miRNA             mdm-miR396d
score             8.5
mfe_ratio         0.52
start             2702
seed_gap          0
seed_mismatch     2
seed_gu           0
gap               0
mismatch          4
gu                1
miRNA_3'          UUCAAGUUCUUUCGACACCUU
aln               |....|||...|||.|||o
target_5'         AUUCACAAGAAACCUGAGGAG
//
target            KU870525.1
miRNA             mdm-miR396e
score             8.5
mfe_ratio         0.52
start             2702
seed_gap          0
seed_mismatch     2
seed_gu           0
gap               0
mismatch          4
gu                1
```

miRNA_3'	UUCAAGUUCUUUCGACACCUU
aln	.... ..... ... ...
target_5'	AUUCACAAGAAACCUGAGGAG
//	
target	KU870525.1
miRNA	mdm-miR396f
score	9
mfe_ratio	0.43
start	6447
seed_gap	0
seed_mismatch	2
seed_gu	0
gap	0
mismatch	5
gu	0
miRNA_3'	GUCAAGUUCUUUCGGCACCUCU
aln	.. ... ..... .....
target_5'	AUGGGGAAGAAAACCGUGAAA
//	
target	KU870525.1
miRNA	mdm-miR396g
score	9
mfe_ratio	0.43
start	6447
seed_gap	0
seed_mismatch	2
seed_gu	0
gap	0
mismatch	5
gu	0
miRNA_3'	GUCAAGUUCUUUCGGCACCUCU
aln	.. ... ..... .....
target_5'	AUGGGGAAGAAAACCGUGAAA
//	
target	KU870525.1
miRNA	mdm-miR397a
score	7.5
mfe_ratio	0.48
start	3331
seed_gap	0
seed_mismatch	2
seed_gu	1
gap	0
mismatch	2
gu	1
miRNA_3'	AAAGUAGUUGCGACGUGAGUU
aln	.  o.   .   .o
target_5'	UUUGAUUUACUCUGAAUCAA
//	
target	KU870525.1
miRNA	mdm-miR397b
score	7.5
mfe_ratio	0.48
start	3331
seed_gap	0
seed_mismatch	2
seed_gu	1



```

gap                0
mismatch           2
gu                 1
miRNA_3'           AAAGUAGUUGCGACGUGAGUU
aln                |||.||o.|||.|||.||o|||
target_5'          UUUGAUUUACUCUGAAUUCAA
//
target             KU870525.1
miRNA              mdm-miR398b
score              9
mfe_ratio          0.70
start              6839
seed_gap           0
seed_mismatch      3
seed_gu            2
gap                0
mismatch           1
gu                 0
miRNA_3'           GUCCCCGCUGGACUCUUGUGU
aln                |||||.||o|..o|||||.|
target_5'          CAGGGGCAAUCCUGGAACAGA
//
target             KU870525.1
miRNA              mdm-miR398c
score              9
mfe_ratio          0.70
start              6839
seed_gap           0
seed_mismatch      3
seed_gu            2
gap                0
mismatch           1
gu                 0
miRNA_3'           GUCCCCGCUGGACUCUUGUGU
aln                |||||.||o|..o|||||.|
target_5'          CAGGGGCAAUCCUGGAACAGA
//
target             KU870525.1
miRNA              mdm-miR399e
score              9
mfe_ratio          0.52
start              1443
seed_gap           0
seed_mismatch      2
seed_gu            1
gap                0
mismatch           4
gu                 0
miRNA_3'           GGCUCGUUUAGAGGAAACCGU
aln                |...|.....|o||.||||..
target_5'          CAAAUCAAUUCUUCUAUGGGC
//
target             KU870525.1
miRNA              mdm-miR399f
score              9
mfe_ratio          0.52
start              1443

```

```

seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      4
gu            0
miRNA_3'      GGCUCGUUUAGAGGAAACCGU
aln           |..|.|||||||o||.||||..
target_5'     CAAAUCAAUCUUCUAUGGGC
//
target        KU870525.1
miRNA         mdm-miR399g
score         9
mfe_ratio     0.52
start         1443
seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      4
gu            0
miRNA_3'      GGCUCGUUUAGAGGAAACCGU
aln           |..|.|||||||o||.||||..
target_5'     CAAAUCAAUCUUCUAUGGGC
//
target        KU870525.1
miRNA         mdm-miR399h
score         9
mfe_ratio     0.52
start         1443
seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      4
gu            0
miRNA_3'      GGCUCGUUUAGAGGAAACCGU
aln           |..|.|||||||o||.||||..
target_5'     CAAAUCAAUCUUCUAUGGGC
//
target        KU870525.1
miRNA         mdm-miR403a
score         8.5
mfe_ratio     0.54
start         2053
seed_gap      0
seed_mismatch 3
seed_gu       0
gap           0
mismatch      2
gu            1
miRNA_3'      GCUCAAACACGCACUUAGAUAU
aln           ||||.||||..||.||||o
target_5'     CGAGGUUGAACGGGACUCUAG
//
target        KU870525.1
miRNA         mdm-miR403b

```

```

score            8.5
mfe_ratio        0.54
start            2053
seed_gap         0
seed_mismatch    3
seed_gu          0
gap              0
mismatch         2
gu               1
miRNA_3'         GCUCAAACACGCACUUAGAUU
aln              ||||.||||..||.||.||||o
target_5'        CGAGGUUGAACGGGACUCUAG
//
target           KU870525.1
miRNA            mdm-miR477a
score            9
mfe_ratio        0.50
start            2028
seed_gap         0
seed_mismatch    2
seed_gu          0
gap              0
mismatch         4
gu               2
miRNA_3'         CUCUUCGAGAACUCCCUCUCA
aln              .o|..|o|||||||.|.||.
target_5'        AGGUCGUUCUUGAGGAAAAGG
//
target           KU870525.1
miRNA            mdm-miR482a-3p
score            8
mfe_ratio        0.48
start            2136
seed_gap         0
seed_mismatch    1
seed_gu          0
gap              0
mismatch         5
gu               2
miRNA_3'         AUCCUUACCCGCCCGAACCCUU
aln              |..|.o.|.|.|||||||.||o
target_5'        UUGCGCGGCCGCGGCUUGUGAG
//
target           KU870525.1
miRNA            mdm-miR482b
score            8.5
mfe_ratio        0.34
start            2207
seed_gap         0
seed_mismatch    1
seed_gu          0
gap              0
mismatch         6
gu               1
miRNA_3'         CCUUACCCUCCCUAUCCUUUCU
aln              ..o.|.|.|.|.|||||||
target_5'        CCGCUUGCACGCAUAGGAAAGA

```

```

//
target      KU870525.1
miRNA       mdm-miR530a
score       8
mfe_ratio   0.57
start       4730
seed_gap    0
seed_mismatch 1
seed_gu     0
gap         0
mismatch    5
gu          2
miRNA_3'    UGUUCACGUCCACGUUUACGU
aln         o|.|.|.|.o|.|.|.|.|.|.|.|.|.|.
target_5'   GCCACGAUAGGUGCACAUGCU
//
target      KU870525.1
miRNA       mdm-miR530b
score       8
mfe_ratio   0.57
start       4730
seed_gap    0
seed_mismatch 1
seed_gu     0
gap         0
mismatch    5
gu          2
miRNA_3'    UGUUCACGUCCACGUUUACGU
aln         o|.|.|.|.o|.|.|.|.|.|.|.|.|.|.
target_5'   GCCACGAUAGGUGCACAUGCU
//
target      KU870525.1
miRNA       mdm-miR530c
score       8
mfe_ratio   0.57
start       4730
seed_gap    0
seed_mismatch 1
seed_gu     0
gap         0
mismatch    5
gu          2
miRNA_3'    UGUUCACGUCCACGUUUACGU
aln         o|.|.|.|.o|.|.|.|.|.|.|.|.|.|.
target_5'   GCCACGAUAGGUGCACAUGCU
//
target      KU870525.1
miRNA       mdm-miR3627d
score       8.5
mfe_ratio   0.51
start       6567
seed_gap    0
seed_mismatch 3
seed_gu     0
gap         0
mismatch    2
gu          1

```

```

miRNA_3'      AAGUACAGUGUCCUCCUACCU
aln           ||o|.|||.|||||.||..||
target_5'     UUUAAAGUCCCAGGAUGAGAGA
//
target        KU870525.1
miRNA         mdm-miR5225c
score         9
mfe_ratio     0.46
start         4490
seed_gap      0
seed_mismatch 2
seed_gu       0
gap           0
mismatch      4
gu            2
miRNA_3'      CGUGGUAGAGUGGGUGCUGUCU
aln           |.|.|||.o.o|||||.||||.|
target_5'     GAAGCAGUGUACCCAAGACAU
//
target        KU870525.1
miRNA         mdm-miR7120a-3p
score         9
mfe_ratio     0.52
start         2867
seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      4
gu            0
miRNA_3'      CGUGCAAUAUAACAGUCUGAC
aln           |.|.|||.o|||||.|||||.
target_5'     GGACUUUCUGUUGGAAGACUU
//
target        KU870525.1
miRNA         mdm-miR7120b-3p
score         9
mfe_ratio     0.52
start         2867
seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      4
gu            0
miRNA_3'      CGUGCAAUAUAACAGUCUGAC
aln           |.|.|||.o|||||.|||||.
target_5'     GGACUUUCUGUUGGAAGACUU
//
target        KU870525.1
miRNA         mdm-miR7121a
score         7
mfe_ratio     0.58
start         1755
seed_gap      0
seed_mismatch 1
seed_gu       2

```

```

gap                0
mismatch          3
gu                0
miRNA_3'          UGUCCCCGCUAGUGGUUCUCCU
aln               |.|||||.|.|||o|o|||||.|
target_5'         AAAGGGAGUUCAUCGAGAGAA
//
target            KU870525.1
miRNA             mdm-miR7121b
score             7
mfe_ratio         0.58
start            1755
seed_gap          0
seed_mismatch     1
seed_gu           2
gap               0
mismatch          3
gu                0
miRNA_3'          UGUCCCCGCUAGUGGUUCUCCU
aln               |.|||||.|.|||o|o|||||.|
target_5'         AAAGGGAGUUCAUCGAGAGAA
//
target            KU870525.1
miRNA             mdm-miR7121c
score             7
mfe_ratio         0.58
start            1755
seed_gap          0
seed_mismatch     1
seed_gu           2
gap               0
mismatch          3
gu                0
miRNA_3'          UGUCCCCGCUAGUGGUUCUCCU
aln               |.|||||.|.|||o|o|||||.|
target_5'         AAAGGGAGUUCAUCGAGAGAA
//
target            KU870525.1
miRNA             mdm-miR7121d
score             8
mfe_ratio         0.54
start            1755
seed_gap          0
seed_mismatch     1
seed_gu           2
gap               0
mismatch          4
gu                0
miRNA_3'          CGUCCCCGCUAGUGGUUCUCCU
aln               ..|||||.|.|||o|o|||||.|
target_5'         AAAGGGAGUUCAUCGAGAGAA
//
target            KU870525.1
miRNA             mdm-miR7121e
score             8
mfe_ratio         0.54
start            1755

```

```

seed_gap      0
seed_mismatch 1
seed_gu       2
gap           0
mismatch      4
gu            0
miRNA_3'      CGUCCCGCUAGUGGUUCUCCU
aln           ..|||||.|.|||o|o|||||.|
target_5'     AAAGGGAGUUCAUCGAGAGAA
//
target        KU870525.1
miRNA         mdm-miR7121f
score         8
mfe_ratio     0.54
start         1755
seed_gap      0
seed_mismatch 1
seed_gu       2
gap           0
mismatch      4
gu            0
miRNA_3'      CGUCCCGCUAGUGGUUCUCCU
aln           ..|||||.|.|||o|o|||||.|
target_5'     AAAGGGAGUUCAUCGAGAGAA
//
target        KU870525.1
miRNA         mdm-miR7121g
score         8
mfe_ratio     0.54
start         1755
seed_gap      0
seed_mismatch 1
seed_gu       2
gap           0
mismatch      4
gu            0
miRNA_3'      CGUCCCGCUAGUGGUUCUCCU
aln           ..|||||.|.|||o|o|||||.|
target_5'     AAAGGGAGUUCAUCGAGAGAA
//
target        KU870525.1
miRNA         mdm-miR7121h
score         8
mfe_ratio     0.54
start         1755
seed_gap      0
seed_mismatch 1
seed_gu       2
gap           0
mismatch      4
gu            0
miRNA_3'      CGUCCCGCUAGUGGUUCUCCU
aln           ..|||||.|.|||o|o|||||.|
target_5'     AAAGGGAGUUCAUCGAGAGAA
//

```

```

target      KU870525.1
miRNA       mdm-miR7125
score       9
mfe_ratio   0.47
start       5806
seed_gap    0
seed_mismatch 1
seed_gu     1
gap         0
mismatch    5
gu          2
miRNA_3'    UUCGAUCAACGUUAUUCAAGC
aln         .o.o...|||.|||o|||||
target_5'   UGAUCCAUUGGAAUGAGUUCG
//
target      KU870525.1
miRNA       mdm-miR10980a
score       6.5
mfe_ratio   0.63
start       6561
seed_gap    0
seed_mismatch 1
seed_gu     0
gap         0
mismatch    4
gu          1
miRNA_3'    GUACCGACGUUCAGGGUCCAC
aln         |.|||.|.o|||||||...
target_5'   CCUGGAUUUAAGUCCCAGGAU
//
target      KU870525.1
miRNA       mdm-miR10980b
score       6.5
mfe_ratio   0.63
start       6561
seed_gap    0
seed_mismatch 1
seed_gu     0
gap         0
mismatch    4
gu          1
miRNA_3'    GUACCGACGUUCAGGGUCCAC
aln         |.|||.|.o|||||||...
target_5'   CCUGGAUUUAAGUCCCAGGAU
//
target      KU870525.1
miRNA       mdm-miR10981c
score       8
mfe_ratio   0.39
start       5024
seed_gap    0
seed_mismatch 2
seed_gu     0
gap         0
mismatch    4
gu          0
miRNA_3'    AACCUAAAACUAAUUGCCGA

```



```

aln          .|.|||.|||.|.|.|
target_5'    GUUGAAUCUGAUUACACAGCU
//
target       KU870525.1
miRNA        mdm-miR10981d
score        8
mfe_ratio    0.39
start        5024
seed_gap     0
seed_mismatch 2
seed_gu      0
gap          0
mismatch     4
gu           0
miRNA_3'     AACCUAAAACUAAUUUGCCGA
aln          .|.|||.|||.|.|.|
target_5'    GUUGAAUCUGAUUACACAGCU
//
target       KU870525.1
miRNA        mdm-miR10983
score        9
mfe_ratio    0.42
start        3324
seed_gap     0
seed_mismatch 2
seed_gu      0
gap          0
mismatch     4
gu           2
miRNA_3'     AAGGUGCUGACAAAACGAGAC
aln          |||.o...o|||.||||
target_5'    UUCAGAAUUUGAUUUACUCUG
//
target       KU870525.1
miRNA        mdm-miR10986
score        9
mfe_ratio    0.65
start        5404
seed_gap     0
seed_mismatch 3
seed_gu      2
gap          0
mismatch     1
gu           0
miRNA_3'     GCCCACCACUGAAACCACGGU
aln          |||||.|o|||||.|.o.|
target_5'    CGGGUGGAGGCUUUGCUAUGA
//
target       KU870525.1
miRNA        mdm-miR10989a
score        8
mfe_ratio    0.53
start        3173
seed_gap     0
seed_mismatch 1
seed_gu      1
gap          0

```

mismatch	5
gu	0
miRNA_3'	AGCUGACUAUAAUUUUCGAAAC
aln	. . . . . . . . .o . . . .
target_5'	ACCUCUGAGAUGAGAAGCUUUA
//	
target	KU870525.1
miRNA	mdm-mir10989b
score	8
mfe_ratio	0.53
start	3173
seed_gap	0
seed_mismatch	1
seed_gu	1
gap	0
mismatch	5
gu	0
miRNA_3'	AGCUGACUAUAAUUUUCGAAAC
aln	. . . . . . . . .o . . . .
target_5'	ACCUCUGAGAUGAGAAGCUUUA
//	
target	KU870525.1
miRNA	mdm-mir10989c
score	8
mfe_ratio	0.53
start	3173
seed_gap	0
seed_mismatch	1
seed_gu	1
gap	0
mismatch	5
gu	0
miRNA_3'	AGCUGACUAUAAUUUUCGAAAC
aln	. . . . . . . . .o . . . .
target_5'	ACCUCUGAGAUGAGAAGCUUUA
//	
target	KU870525.1
miRNA	mdm-mir10989d
score	8
mfe_ratio	0.53
start	3173
seed_gap	0
seed_mismatch	1
seed_gu	1
gap	0
mismatch	5
gu	0
miRNA_3'	AGCUGACUAUAAUUUUCGAAAC
aln	. . . . . . . . .o . . . .
target_5'	ACCUCUGAGAUGAGAAGCUUUA
//	
target	KU870525.1
miRNA	mdm-mir10989e
score	8
mfe_ratio	0.53
start	3173
seed gap	0

```
seed_mismatch 1
seed_gu      1
gap          0
mismatch     5
gu           0
miRNA_3'    AGCUGACUAUAAUUUUCGAAAC
aln          .|.|||.|.|.|o|||||.
target_5'   ACCUCUGAGAUGAGAAGCUUUA
//
target       KU870525.1
miRNA        mdm-mir10991a
score        9
mfe_ratio    0.47
start        4997
seed_gap     0
seed_mismatch 1
seed_gu      0
gap          0
mismatch     7
gu           0
miRNA_3'    CCUAGCUUAAAGUUACCGAGC
aln          ..|..|..|.|.|.|.|.|.
target_5'   AAAAGGUUUUCCAAUGGCUC
//
target       KU870525.1
miRNA        mdm-mir10991b
score        9
mfe_ratio    0.47
start        4997
seed_gap     0
seed_mismatch 1
seed_gu      0
gap          0
mismatch     7
gu           0
miRNA_3'    CCUAGCUUAAAGUUACCGAGC
aln          ..|..|..|.|.|.|.|.|.
target_5'   AAAAGGUUUUCCAAUGGCUC
//
target       KU870525.1
miRNA        mdm-mir10991c
score        9
mfe_ratio    0.47
start        4997
seed_gap     0
seed_mismatch 1
seed_gu      0
gap          0
mismatch     7
gu           0
miRNA_3'    CCUAGCUUAAAGUUACCGAGC
aln          ..|..|..|.|.|.|.|.|.
target_5'   AAAAGGUUUUCCAAUGGCUC
//
target       KU870525.1
miRNA        mdm-mir10991d
score        9
```

```
mfe_ratio      0.47
start          4997
seed_gap       0
seed_mismatch  1
seed_gu        0
gap            0
mismatch       7
gu             0
miRNA_3'       CCUAGCUUAAAGUUACCGAGC
aln            ..|..|..||.|
target_5'      AAAAGGUUUUCCAUGGCUC
//
target         KU870525.1
miRNA          mdm-mir10991e
score          9
mfe_ratio      0.47
start          4997
seed_gap       0
seed_mismatch  1
seed_gu        0
gap            0
mismatch       7
gu             0
miRNA_3'       CCUAGCUUAAAGUUACCGAGC
aln            ..|..|..||.|
target_5'      AAAAGGUUUUCCAUGGCUC
//
target         KU870525.1
miRNA          mdm-mir10994-3p
score          6
mfe_ratio      0.61
start          5976
seed_gap       0
seed_mismatch  1
seed_gu        0
gap            0
mismatch       4
gu             0
miRNA_3'       CGAUACCAGUUCUUUUUUCGU
aln            ||..||.|
target_5'      GCGUUGUUCAAGAAAAAUGC
//
target         KU870525.1
miRNA          mdm-mir11001
score          8.5
mfe_ratio      0.57
start          6858
seed_gap       0
seed_mismatch  2
seed_gu        0
gap            0
mismatch       4
gu             1
miRNA_3'       AUCCACCUCAGGUAAGAACAU
aln            .|...|
target_5'      GACACUGGAGUCCAUCUUCGCG
//
```

target	KU870525.1
miRNA	mdm-miR11016
score	8
mfe_ratio	0.52
start	5979
seed_gap	0
seed_mismatch	2
seed_gu	0
gap	0
mismatch	4
gu	0
miRNA_3'	AACUAGACCUUUUUAAUACCU
aln	.   .       .   .
target_5'	UUGUUCAAGAAAAUGCUGGU
//	

# psRNATarget

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

miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end	Target_start	Target_end	miRNA_aligned_fragment	alignment	Target_aligned_fragment	Inhibition	Target_Desc.	Multiplicity
mdm-miR156ab	KU870525.1	5.0	-1.0	1	21	6758	6778	UUGACAGAAGAUAGAGAGCAC	:::: ::::: ::::: CAGUUCUAAAUCUUCAGUUAA	Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete genome	1
mdm-miR156ac	KU870525.1	5.0	-1.0	1	21	6758	6778	UUGACAGAAGAUAGAGAGCAC	:::: ::::: ::::: CAGUUCUAAAUCUUCAGUUAA	Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete genome	1
mdm-miR159c	KU870525.1	5.0	-1.0	1	21	4379	4399	GAAUUCUUCUCCUCUCCUUU	: :::: : ::::: GCAAGGGAGUAUAGGGAAUUC	Translation		Apple chlorotic leaf spot virus isolate SY03, complete genome	2
mdm-miR394a	KU870525.1	5.0	-1.0	1	20	1426	1445	UUGGCAUUCUGUCCACCUC	: :: ::::: :: ::::: UGUGGAGGACAGUAUCCCAA	Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete genome	3
mdm-miR394b	KU870525.1	5.0	-1.0	1	20	1426	1445	UUGGCAUUCUGUCCACCUC	: :: ::::: :: ::::: UGUGGAGGACAGUAUCCCAA	Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete genome	3
mdm-miR7121a	KU870525.1	5.0	-1.0	1	21	1755	1775	UCCUCUUGGUGAUCGCCCUGU	: :::: : ::::: AAAGGGAGUUAUCGAGAGAA	Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete genome	1
mdm-miR7121b	KU870525.1	5.0	-1.0	1	21	1755	1775	UCCUCUUGGUGAUCGCCCUGU	: :::: : ::::: AAAGGGAGUUAUCGAGAGAA	Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete genome	1
mdm-miR7121c	KU870525.1	5.0	-1.0	1	21	1755	1775	UCCUCUUGGUGAUCGCCCUGU	: :::: : ::::: AAAGGGAGUUAUCGAGAGAA	Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete genome	1
mdm-miR7121d	KU870525.1	5.0	-1.0	1	21	1755	1775	UCCUCUUGGUGAUCGCCCUGC	: :::: : ::::: AAAGGGAGUUAUCGAGAGAA	Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete genome	2
mdm-miR7121e	KU870525.1	5.0	-1.0	1	21	1755	1775	UCCUCUUGGUGAUCGCCCUGC	: :::: : ::::: AAAGGGAGUUAUCGAGAGAA	Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete genome	2
mdm-miR7121f	KU870525.1	5.0	-1.0	1	21	1755	1775	UCCUCUUGGUGAUCGCCCUGC	: :::: : ::::: AAAGGGAGUUAUCGAGAGAA	Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete genome	2
mdm-miR7121g	KU870525.1	5.0	-1.0	1	21	1755	1775	UCCUCUUGGUGAUCGCCCUGC	: :::: : ::::: AAAGGGAGUUAUCGAGAGAA				

Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2							
mdm-miR7121h	KU870525.1	5.0	-1.0	1	21	1755	1775		
	UCCUCUUGGUGAUCGCCUGC	:	:	:	:	:	:	AAAGGGAGUUCAUCGAGAGAA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2							
mdm-miR156p	KU870525.1	6.0	-1.0	1	21	6758	6778		
	CUGACAGAAGAUAGAGAGCAC	:	:	:	:	:	:	CAGUUCUAAAUCUUCAGUUAA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	1							
mdm-miR156q	KU870525.1	6.0	-1.0	1	21	6758	6778		
	CUGACAGAAGAUAGAGAGCAC	:	:	:	:	:	:	CAGUUCUAAAUCUUCAGUUAA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	1							
mdm-miR156r	KU870525.1	6.0	-1.0	1	21	6758	6778		
	CUGACAGAAGAUAGAGAGCAC	:	:	:	:	:	:	CAGUUCUAAAUCUUCAGUUAA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	1							
mdm-miR156s	KU870525.1	6.0	-1.0	1	21	6758	6778		
	CUGACAGAAGAUAGAGAGCAC	:	:	:	:	:	:	CAGUUCUAAAUCUUCAGUUAA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	1							
mdm-miR166a	KU870525.1	6.0	-1.0	1	21	781	801		
	UCGGACCAGGCUUCAUCCCC	:	:	:	:	:	:	GCCCGAUGGAGUUCGGUCUGA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2							
mdm-miR166b	KU870525.1	6.0	-1.0	1	21	781	801		
	UCGGACCAGGCUUCAUCCCC	:	:	:	:	:	:	GCCCGAUGGAGUUCGGUCUGA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2							
mdm-miR166c	KU870525.1	6.0	-1.0	1	21	781	801		
	UCGGACCAGGCUUCAUCCCC	:	:	:	:	:	:	GCCCGAUGGAGUUCGGUCUGA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2							
mdm-miR166d	KU870525.1	6.0	-1.0	1	21	781	801		
	UCGGACCAGGCUUCAUCCCC	:	:	:	:	:	:	GCCCGAUGGAGUUCGGUCUGA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2							
mdm-miR166e	KU870525.1	6.0	-1.0	1	21	781	801		
	UCGGACCAGGCUUCAUCCCC	:	:	:	:	:	:	GCCCGAUGGAGUUCGGUCUGA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2							
mdm-miR166f	KU870525.1	6.0	-1.0	1	21	781	801		
	UCGGACCAGGCUUCAUCCCC	:	:	:	:	:	:	GCCCGAUGGAGUUCGGUCUGA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2							
mdm-miR166g	KU870525.1	6.0	-1.0	1	21	781	801		
	UCGGACCAGGCUUCAUCCCC	:	:	:	:	:	:	GCCCGAUGGAGUUCGGUCUGA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2							
mdm-miR166h	KU870525.1	6.0	-1.0	1	21	781	801		
	UCGGACCAGGCUUCAUCCCC	:	:	:	:	:	:	GCCCGAUGGAGUUCGGUCUGA	
Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2							

mdm-miR166i KU870525.1 6.0 -1.0 1 21 781 801  
 UCGGACCAGGCUUCAUCCCC .....: GCCCGAUGGAGUUCGGUCUGA  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 2

mdm-miR2111a KU870525.1 6.0 -1.0 1 21 5147 5167  
 UAAUCUGCAUCCUGAGGUUUA ..:: ....: UGUACACUGGGUUGCAGAUUG  
 Translation Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 3

mdm-miR2111b KU870525.1 6.0 -1.0 1 21 5147 5167  
 UAAUCUGCAUCCUGAGGUUUA ..:: ....: UGUACACUGGGUUGCAGAUUG  
 Translation Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 3

mdm-miR390a KU870525.1 6.0 -1.0 1 21 6321 6341  
 AAGCUCAGGAGGGGAUAGCGCC ::::: : : .....: GGUGCAAGCGCUUUUGGGUUU  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 1

mdm-miR390b KU870525.1 6.0 -1.0 1 21 6321 6341  
 AAGCUCAGGAGGGGAUAGCGCC ::::: : : .....: GGUGCAAGCGCUUUUGGGUUU  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 1

mdm-miR390c KU870525.1 6.0 -1.0 1 21 6321 6341  
 AAGCUCAGGAGGGGAUAGCGCC ::::: : : .....: GGUGCAAGCGCUUUUGGGUUU  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 1

mdm-miR390d KU870525.1 6.0 -1.0 1 21 6321 6341  
 AAGCUCAGGAGGGGAUAGCGCC ::::: : : .....: GGUGCAAGCGCUUUUGGGUUU  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 1

mdm-miR390e KU870525.1 6.0 -1.0 1 21 6321 6341  
 AAGCUCAGGAGGGGAUAGCGCC ::::: : : .....: GGUGCAAGCGCUUUUGGGUUU  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 1

mdm-miR390f KU870525.1 6.0 -1.0 1 21 6321 6341  
 AAGCUCAGGAGGGGAUAGCGCC ::::: : : .....: GGUGCAAGCGCUUUUGGGUUU  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 1

mdm-miR395a KU870525.1 6.0 -1.0 1 21 6286 6306  
 CUGAAGUGUUUGGGGGAACUC .....: .....: AUUUUCUUCUAGAAGCUUCA  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395a KU870525.1 6.0 -1.0 1 21 690 710  
 CUGAAGUGUUUGGGGGAACUC .....: ..: .....: UCUUUCCCCCUGAGAUUUUGG  
 Translation Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395b KU870525.1 6.0 -1.0 1 21 6286 6306  
 CUGAAGUGUUUGGGGGAACUC .....: .....: AUUUUCUUCUAGAAGCUUCA  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395b KU870525.1 6.0 -1.0 1 21 690 710  
 CUGAAGUGUUUGGGGGAACUC .....: ..: .....: UCUUUCCCCCUGAGAUUUUGG  
 Translation Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395c KU870525.1 6.0 -1.0 1 21 6286 6306  
 CUGAAGUGUUUGGGGGAACUC .....: .....: AUUUUCUUCUAGAAGCUUCA



```

    Cleavage    Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395c KU870525.1 6.0 -1.0 1 21 690 710
    CUGAAGUGUUUGGGGGAACUC      :::::::::: : : ::::: UCUUUCCCCCUGAGAUUUUUGG
    Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395d KU870525.1 6.0 -1.0 1 21 6286 6306
    CUGAAGUGUUUGGGGGAACUC      ::::::::::: : ::::: AUUUUCUUCUAGAAGCUUCA
    Cleavage    Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395d KU870525.1 6.0 -1.0 1 21 690 710
    CUGAAGUGUUUGGGGGAACUC      :::::::::: : : ::::: UCUUUCCCCCUGAGAUUUUUGG
    Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395e KU870525.1 6.0 -1.0 1 21 6286 6306
    CUGAAGUGUUUGGGGGAACUC      ::::::::::: : ::::: AUUUUCUUCUAGAAGCUUCA
    Cleavage    Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395e KU870525.1 6.0 -1.0 1 21 690 710
    CUGAAGUGUUUGGGGGAACUC      :::::::::: : : ::::: UCUUUCCCCCUGAGAUUUUUGG
    Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395f KU870525.1 6.0 -1.0 1 21 6286 6306
    CUGAAGUGUUUGGGGGAACUC      ::::::::::: : ::::: AUUUUCUUCUAGAAGCUUCA
    Cleavage    Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395f KU870525.1 6.0 -1.0 1 21 690 710
    CUGAAGUGUUUGGGGGAACUC      :::::::::: : : ::::: UCUUUCCCCCUGAGAUUUUUGG
    Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395g KU870525.1 6.0 -1.0 1 21 6286 6306
    CUGAAGUGUUUGGGGGAACUC      ::::::::::: : ::::: AUUUUCUUCUAGAAGCUUCA
    Cleavage    Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395g KU870525.1 6.0 -1.0 1 21 690 710
    CUGAAGUGUUUGGGGGAACUC      :::::::::: : : ::::: UCUUUCCCCCUGAGAUUUUUGG
    Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395h KU870525.1 6.0 -1.0 1 21 6286 6306
    CUGAAGUGUUUGGGGGAACUC      ::::::::::: : ::::: AUUUUCUUCUAGAAGCUUCA
    Cleavage    Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395h KU870525.1 6.0 -1.0 1 21 690 710
    CUGAAGUGUUUGGGGGAACUC      :::::::::: : : ::::: UCUUUCCCCCUGAGAUUUUUGG
    Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395i KU870525.1 6.0 -1.0 1 21 6286 6306
    CUGAAGUGUUUGGGGGAACUC      ::::::::::: : ::::: AUUUUCUUCUAGAAGCUUCA
    Cleavage    Apple chlorotic leaf spot virus isolate SY03, complete
genome        5
mdm-miR395i KU870525.1 6.0 -1.0 1 21 690 710
    CUGAAGUGUUUGGGGGAACUC      :::::::::: : : ::::: UCUUUCCCCCUGAGAUUUUUGG
    Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome        5

```

mdm-miR397a	KU870525.1	6.0	-1.0	1	21	3331	3351
UUGAGUGCAGCGUUGAUGAAA :: :: :: :: :::: UUUGAUUUACUCUGAAUUCAA							
Translation Apple chlorotic leaf spot virus isolate SY03, complete genome 3							
mdm-miR397b	KU870525.1	6.0	-1.0	1	21	3331	3351
UUGAGUGCAGCGUUGAUGAAA :: :: :: :: :::: UUUGAUUUACUCUGAAUUCAA							
Translation Apple chlorotic leaf spot virus isolate SY03, complete genome 3							
mdm-miR398b	KU870525.1	6.0	-1.0	1	21	2601	2621
UGUGUUCUCAGGUCGCCCCUG : : :::: :: :::: GCGUGACGAUCAGGGGUACACA							
Translation Apple chlorotic leaf spot virus isolate SY03, complete genome 1							
mdm-miR398c	KU870525.1	6.0	-1.0	1	21	2601	2621
UGUGUUCUCAGGUCGCCCCUG : : :::: :: :::: GCGUGACGAUCAGGGGUACACA							
Translation Apple chlorotic leaf spot virus isolate SY03, complete genome 1							
mdm-miR482a-5p	KU870525.1	6.0	-1.0	1	22	4111	4132
AGGAAUGGGCUGUUUGGGAAGA :: :: :::::							
GGCUUCAAGAGAGUUAUUCUA Cleavage Apple chlorotic leaf spot virus isolate SY03, complete genome 2							
mdm-miR482b	KU870525.1	6.0	-1.0	1	22	2207	2228
UCUUUCCUAUCCCUCCAUUC : : : : :::::							
CCGCUUGCACGCAUAGGAAAGA Translation Apple chlorotic leaf spot virus isolate SY03, complete genome 2							
mdm-miR535a	KU870525.1	6.0	-1.0	1	21	1652	1671
UGACAACGAGAGAGAGCACGC .: :::: :::: :::: AUGCGCUCU-UCUCGAUGUUA							
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete genome 1							
mdm-miR7120a	KU870525.1	6.0	-1.0	1	21	4556	4576
UGUUAUAUUGUCAGAUUGUCA : ::::::::::::::: : UUGC GG UUGAUAAUGUCGCC							
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete genome 3							
mdm-miR7120b	KU870525.1	6.0	-1.0	1	21	4556	4576
UGUUAUAUUGUCAGAUUGUCA : ::::::::::::::: : UUGC GG UUGAUAAUGUCGCC							
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete genome 3							
mdm-miR159a	KU870525.1	6.5	-1.0	1	20	3333	3352
CUUGGAUUGAAGGGGAGCUCC :: .: .: : ::::: UGAUUUACUCUGAAUUCAAG							
Translation Apple chlorotic leaf spot virus isolate SY03, complete genome 2							
mdm-miR159b	KU870525.1	6.5	-1.0	1	20	3333	3352
CUUGGAUUGAAGGGGAGCUCC :: .: .: : ::::: UGAUUUACUCUGAAUUCAAG							
Translation Apple chlorotic leaf spot virus isolate SY03, complete genome 2							
mdm-miR164b	KU870525.1	6.5	-1.0	1	21	2670	2689
UGGAGAAGCAGGGCACGUGCA :: :: ::::: ::::: UGGAC-UGCCUUUUUUCUUCG							
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete genome 1							
mdm-miR164c	KU870525.1	6.5	-1.0	1	21	2670	2689
UGGAGAAGCAGGGCACGUGCA :: :: ::::: ::::: UGGAC-UGCCUUUUUUCUUCG							
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete genome 1							
mdm-miR164d	KU870525.1	6.5	-1.0	1	21	2670	2689
UGGAGAAGCAGGGCACGUGCA :: :: ::::: ::::: UGGAC-UGCCUUUUUUCUUCG							

```

Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 1
mdm-miR164e KU870525.1 6.5 -1.0 1 21 2670 2689
UGGAGAAGCAGGGCACGUGCA :: :: ::::: ::::: UGGAC-UGCCUUUUUUCUUCG
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 1
mdm-miR164f KU870525.1 6.5 -1.0 1 21 2670 2689
UGGAGAAGCAGGGCACGUGCA :: :: ::::: ::::: UGGAC-UGCCUUUUUUCUUCG
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 1
mdm-miR169b KU870525.1 6.5 -1.0 1 22 6678 6699
UAGCCAAGGAUGAUUUGCCUGC ::: ..... :: ::
UCAGAAGGGUCAUCCGUGGAUA Cleavage Apple chlorotic leaf spot virus
isolate SY03, complete genome 1
mdm-miR169e KU870525.1 6.5 -1.0 1 22 2669 2689
UGAAGAGAAGAGCGUUGUUUGG ::::: :: ::::: CUGGACUGC-
CUUUUUUCUUCG Cleavage Apple chlorotic leaf spot virus isolate
SY03, complete genome 1
mdm-miR169f KU870525.1 6.5 -1.0 1 22 2669 2689
UGAAGAGAAGAGCGUUGUUUGG ::::: :: ::::: CUGGACUGC-
CUUUUUUCUUCG Cleavage Apple chlorotic leaf spot virus isolate
SY03, complete genome 1
mdm-miR395a KU870525.1 6.5 -1.0 1 21 1970 1990
CUGAAGUGUUUGGGGGAACUC :: :: ::::: : :: AAGGUCGCCCAAUAGUGCAC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 5
mdm-miR395a KU870525.1 6.5 -1.0 1 21 5208 5228
CUGAAGUGUUUGGGGGAACUC : :... .. ::::: CAUUUUUGUUCAACACUUUGG
Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome 5
mdm-miR395b KU870525.1 6.5 -1.0 1 21 1970 1990
CUGAAGUGUUUGGGGGAACUC :: :: ::::: : :: AAGGUCGCCCAAUAGUGCAC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 5
mdm-miR395b KU870525.1 6.5 -1.0 1 21 5208 5228
CUGAAGUGUUUGGGGGAACUC : :... .. ::::: CAUUUUUGUUCAACACUUUGG
Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome 5
mdm-miR395c KU870525.1 6.5 -1.0 1 21 1970 1990
CUGAAGUGUUUGGGGGAACUC :: :: ::::: : :: AAGGUCGCCCAAUAGUGCAC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 5
mdm-miR395c KU870525.1 6.5 -1.0 1 21 5208 5228
CUGAAGUGUUUGGGGGAACUC : :... .. ::::: CAUUUUUGUUCAACACUUUGG
Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome 5
mdm-miR395d KU870525.1 6.5 -1.0 1 21 1970 1990
CUGAAGUGUUUGGGGGAACUC :: :: ::::: : :: AAGGUCGCCCAAUAGUGCAC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 5
mdm-miR395d KU870525.1 6.5 -1.0 1 21 5208 5228
CUGAAGUGUUUGGGGGAACUC : :... .. ::::: CAUUUUUGUUCAACACUUUGG
Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome 5

```

mdm-miR395e KU870525.1 6.5 -1.0 1 21 1970 1990  
 CUGAAGUGUUUGGGGAACUC :: :: ::::: : : AAGGUCGCCCCAAAUAGUGCAC  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395e KU870525.1 6.5 -1.0 1 21 5208 5228  
 CUGAAGUGUUUGGGGAACUC : :... .. ::::: CAUUUUUGUUCAACACUUUGG  
 Translation Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395f KU870525.1 6.5 -1.0 1 21 1970 1990  
 CUGAAGUGUUUGGGGAACUC :: :: ::::: : : AAGGUCGCCCCAAAUAGUGCAC  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395f KU870525.1 6.5 -1.0 1 21 5208 5228  
 CUGAAGUGUUUGGGGAACUC : :... .. ::::: CAUUUUUGUUCAACACUUUGG  
 Translation Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395g KU870525.1 6.5 -1.0 1 21 1970 1990  
 CUGAAGUGUUUGGGGAACUC :: :: ::::: : : AAGGUCGCCCCAAAUAGUGCAC  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395g KU870525.1 6.5 -1.0 1 21 5208 5228  
 CUGAAGUGUUUGGGGAACUC : :... .. ::::: CAUUUUUGUUCAACACUUUGG  
 Translation Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395h KU870525.1 6.5 -1.0 1 21 1970 1990  
 CUGAAGUGUUUGGGGAACUC :: :: ::::: : : AAGGUCGCCCCAAAUAGUGCAC  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395h KU870525.1 6.5 -1.0 1 21 5208 5228  
 CUGAAGUGUUUGGGGAACUC : :... .. ::::: CAUUUUUGUUCAACACUUUGG  
 Translation Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395i KU870525.1 6.5 -1.0 1 21 1970 1990  
 CUGAAGUGUUUGGGGAACUC :: :: ::::: : : AAGGUCGCCCCAAAUAGUGCAC  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR395i KU870525.1 6.5 -1.0 1 21 5208 5228  
 CUGAAGUGUUUGGGGAACUC : :... .. ::::: CAUUUUUGUUCAACACUUUGG  
 Translation Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 5

mdm-miR396a KU870525.1 6.5 -1.0 1 21 2702 2722  
 UUCCACAGCUUUCUUGAACAG ::::: : : AUUCACAAGAAACCUGAGGAG  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 2

mdm-miR396a KU870525.1 6.5 -1.0 1 21 3376 3396  
 UUCCACAGCUUUCUUGAACAG :: ::::: : : GUGUCCGAGAAAGUUUUUGGC  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 2

mdm-miR396b KU870525.1 6.5 -1.0 1 21 2702 2722  
 UUCCACAGCUUUCUUGAACUG ::::: : : AUUCACAAGAAACCUGAGGAG  
 Cleavage Apple chlorotic leaf spot virus isolate SY03, complete  
 genome 2

mdm-miR396b KU870525.1 6.5 -1.0 1 21 3376 3396  
 UUCCACAGCUUUCUUGAACUG :: ::::: : : GUGUCCGAGAAAGUUUUUGGC

```

Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 2
mdm-miR396c KU870525.1 6.5 -1.0 1 21 2702 2722
UCCACAGCUUUCUUGAACUU ::::: :::: AUUCACAAGAAACCUGAGGAG
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 2
mdm-miR396c KU870525.1 6.5 -1.0 1 21 3376 3396
UCCACAGCUUUCUUGAACUU :: ::::: : : GUGUCCGAGAAAGUUUUUGGC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 2
mdm-miR396d KU870525.1 6.5 -1.0 1 21 2702 2722
UCCACAGCUUUCUUGAACUU ::::: :::: AUUCACAAGAAACCUGAGGAG
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 2
mdm-miR396d KU870525.1 6.5 -1.0 1 21 3376 3396
UCCACAGCUUUCUUGAACUU :: ::::: : : GUGUCCGAGAAAGUUUUUGGC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 2
mdm-miR396e KU870525.1 6.5 -1.0 1 21 2702 2722
UCCACAGCUUUCUUGAACUU ::::: :::: AUUCACAAGAAACCUGAGGAG
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 2
mdm-miR396e KU870525.1 6.5 -1.0 1 21 3376 3396
UCCACAGCUUUCUUGAACUU :: ::::: : : GUGUCCGAGAAAGUUUUUGGC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 2
mdm-miR398a KU870525.1 6.5 -1.0 1 21 6890 6910
UGUGUUCUCAGGUCACCCCUU :: ::::: : : UCCAGGGGACCUCGGAACAGA
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 2
mdm-miR399e KU870525.1 6.5 -1.0 1 21 1443 1463
UGCCAAAGGAGAUUUGCUCGG : ::::: : : CAAAUCAAUCUUCUAUGGGC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 1
mdm-miR399f KU870525.1 6.5 -1.0 1 21 1443 1463
UGCCAAAGGAGAUUUGCUCGG : ::::: : : CAAAUCAAUCUUCUAUGGGC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 1
mdm-miR399g KU870525.1 6.5 -1.0 1 21 1443 1463
UGCCAAAGGAGAUUUGCUCGG : ::::: : : CAAAUCAAUCUUCUAUGGGC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 1
mdm-miR399h KU870525.1 6.5 -1.0 1 21 1443 1463
UGCCAAAGGAGAUUUGCUCGG : ::::: : : CAAAUCAAUCUUCUAUGGGC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 1
mdm-miR408b KU870525.1 6.5 -1.0 1 21 2668 2688
ACAGGGAAGAGGUAGAGCAUG :: ::::: : : ACUGGACUGCCUUUUUCUUC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 1
mdm-miR408c KU870525.1 6.5 -1.0 1 21 2668 2688
ACAGGGAAGAGGUAGAGCAUG :: ::::: : : ACUGGACUGCCUUUUUCUUC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 1

```

mdm-miR408d	KU870525.1	6.5	-1.0	1	21	2668	2688		
	ACAGGGAAGAGGUAGAGCAUG			::	::::::::::::		ACUGGACUGCCUUUUUUCUUC		
	Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	1						
mdm-miR5225c	KU870525.1	6.5	-1.0	1	22	266	287		
	UCUGUCGUGGGUGAGAUGGUGC			::	::::::::::::		..:::		
	UUCUCUUUUUACCUACCGGAGA			Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	5			
mdm-miR535d	KU870525.1	6.5	-1.0	1	21	1652	1671		
	UGACGACGAGAGAGAGCACGC			::	:::::	:::::	:::::	AUGCGCUCU-UCUCGAUGUUA	
	Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	1						
mdm-miR7125	KU870525.1	6.5	-1.0	1	21	5489	5509		
	CGAACUUAUUGCAACUAGCUU			:	::	:::::	:::	UUGAUGGAUGUGAUAGAUUCC	
	Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2						
mdm-miR7126	KU870525.1	6.5	-1.0	1	21	1910	1930		
	AAAGUAUCAAGGAGCGCAAAG			:	::	:::::	:	:::::	CGUUUAGUCCUAGCUACUUG
	Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	1						
mdm-miR858	KU870525.1	6.5	-1.0	1	21	6846	6866		
	UUCGUUGUCUGUUCGACCUGA			:	:::::	:::::	:::::	AAUCCUGGAACAGACACUGGA	
	Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	3						
mdm-miR156ad	KU870525.1	7.0	-1.0	1	20	7293	7312		
	UGACAGAAGAAAGUGAGCAC			:::::	:::::			GGCGAAACUUUCGUCUGUUA	
	Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2						
mdm-miR156ad	KU870525.1	7.0	-1.0	1	20	2674	2693		
	UGACAGAAGAAAGUGAGCAC			:::	.	:::::	:::	CUGCCUUUUUUCUUCGGUGG	
	Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2						
mdm-miR156ae	KU870525.1	7.0	-1.0	1	20	7293	7312		
	UGACAGAAGAAAGUGAGCAC			:::::	:::::			GGCGAAACUUUCGUCUGUUA	
	Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2						
mdm-miR156ae	KU870525.1	7.0	-1.0	1	20	2674	2693		
	UGACAGAAGAAAGUGAGCAC			:::	.	:::::	:::	CUGCCUUUUUUCUUCGGUGG	
	Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2						
mdm-miR159a	KU870525.1	7.0	-1.0	1	20	375	394		
	CUUGGAUUGAAGGGAGCUCC			::	:	:::::	:::::	AGAACCACCUUUUAUUUAAU	
	Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2						
mdm-miR159b	KU870525.1	7.0	-1.0	1	20	375	394		
	CUUGGAUUGAAGGGAGCUCC			::	:	:::::	:::::	AGAACCACCUUUUAUUUAAU	
	Cleavage	Apple chlorotic leaf spot virus isolate SY03, complete genome	2						
mdm-miR159c	KU870525.1	7.0	-1.0	1	21	2033	2053		
	GAAUUCUUCUCCUCUCCUUU			:::::	:::::	:::		GUUCUUGAGGAAAAGGAACUC	
	Translation	Apple chlorotic leaf spot virus isolate SY03, complete genome	2						
mdm-miR166a	KU870525.1	7.0	-1.0	1	21	7335	7355		
	UCGGACCAGGCUUCAUCCCC			::	:::::	:::::	:	UGCUAAAAGAGGUUUGGUUUA	

```

      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         2
mdm-miR166b KU870525.1 7.0 -1.0 1 21 7335 7355
      UCGGACCAGGCUUCAUUC CCC      :: :::::::::::::: : UGCUAAAGAGGUUUGGUUUAA
      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         2
mdm-miR166c KU870525.1 7.0 -1.0 1 21 7335 7355
      UCGGACCAGGCUUCAUUC CCC      :: :::::::::::::: : UGCUAAAGAGGUUUGGUUUAA
      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         2
mdm-miR166d KU870525.1 7.0 -1.0 1 21 7335 7355
      UCGGACCAGGCUUCAUUC CCC      :: :::::::::::::: : UGCUAAAGAGGUUUGGUUUAA
      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         2
mdm-miR166e KU870525.1 7.0 -1.0 1 21 7335 7355
      UCGGACCAGGCUUCAUUC CCC      :: :::::::::::::: : UGCUAAAGAGGUUUGGUUUAA
      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         2
mdm-miR166f KU870525.1 7.0 -1.0 1 21 7335 7355
      UCGGACCAGGCUUCAUUC CCC      :: :::::::::::::: : UGCUAAAGAGGUUUGGUUUAA
      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         2
mdm-miR166g KU870525.1 7.0 -1.0 1 21 7335 7355
      UCGGACCAGGCUUCAUUC CCC      :: :::::::::::::: : UGCUAAAGAGGUUUGGUUUAA
      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         2
mdm-miR166h KU870525.1 7.0 -1.0 1 21 7335 7355
      UCGGACCAGGCUUCAUUC CCC      :: :::::::::::::: : UGCUAAAGAGGUUUGGUUUAA
      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         2
mdm-miR166i KU870525.1 7.0 -1.0 1 21 7335 7355
      UCGGACCAGGCUUCAUUC CCC      :: :::::::::::::: : UGCUAAAGAGGUUUGGUUUAA
      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         2
mdm-miR167a KU870525.1 7.0 -1.0 1 21 1297 1317
      AGAUCAUCUGGCAGUUUCACC      : .. :: :::::::::::::: AAUUGGUCUAGCGGAUGAUUU
      Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome         1
mdm-miR169c KU870525.1 7.0 -1.0 1 21 6679 6699
      UAGCCAAGGAUGACUUGCCCG      ..:::::::::::: :: :: CAGAAGGGUCAUCCGUGGAUA
      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         1
mdm-miR169d KU870525.1 7.0 -1.0 1 21 6679 6699
      UAGCCAAGGAUGACUUGCCCG      ..:::::::::::: :: :: CAGAAGGGUCAUCCGUGGAUA
      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         1
mdm-miR171o KU870525.1 7.0 -1.0 1 21 836 856
      UGGGAUGUUGGUUAUGGUUCAAA      ::::: : :::::::::::::: CUGAGCUCCAGCAGCAUUCUG
      Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome         3
mdm-miR171o KU870525.1 7.0 -1.0 1 21 581 601
      UGGGAUGUUGGUUAUGGUUCAAA      :: : :::::::::::::: CCAAAGAAAACCAACAUUUUC
      Cleavage   Apple chlorotic leaf spot virus isolate SY03, complete
genome         3

```

mdm-miR171o	KU870525.1	7.0	-1.0	1	21	5985	6005
	UGGGAUGUUGGUUAUGGUUCAAA	:	:	:	:	:	AAGAAAAAUGCUGGUGUUUCU
Cleavage	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	3						
mdm-miR172a	KU870525.1	7.0	-1.0	1	20	5580	5599
	AGAAUCUUGAUGAUGCUGCA	:	:	:	:	:	UAAAUAUCAUCAGGUUUUG
Cleavage	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172a	KU870525.1	7.0	-1.0	1	20	7180	7199
	AGAAUCUUGAUGAUGCUGCA	:	:	:	:	:	UUCGACUUCAACAAGGGUCU
Translation	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172b	KU870525.1	7.0	-1.0	1	20	5580	5599
	AGAAUCUUGAUGAUGCUGCA	:	:	:	:	:	UAAAUAUCAUCAGGUUUUG
Cleavage	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172b	KU870525.1	7.0	-1.0	1	20	7180	7199
	AGAAUCUUGAUGAUGCUGCA	:	:	:	:	:	UUCGACUUCAACAAGGGUCU
Translation	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172c	KU870525.1	7.0	-1.0	1	20	5580	5599
	AGAAUCUUGAUGAUGCUGCA	:	:	:	:	:	UAAAUAUCAUCAGGUUUUG
Cleavage	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172c	KU870525.1	7.0	-1.0	1	20	7180	7199
	AGAAUCUUGAUGAUGCUGCA	:	:	:	:	:	UUCGACUUCAACAAGGGUCU
Translation	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172d	KU870525.1	7.0	-1.0	1	21	5579	5599
	AGAAUCUUGAUGAUGCUGCAU	:	:	:	:	:	UAAAUAUCAUCAGGUUUUG
Cleavage	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172d	KU870525.1	7.0	-1.0	1	21	7179	7199
	AGAAUCUUGAUGAUGCUGCAU	:	:	:	:	:	GUUCGACUUCAACAAGGGUCU
Translation	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172e	KU870525.1	7.0	-1.0	1	21	5579	5599
	AGAAUCUUGAUGAUGCUGCAU	:	:	:	:	:	UAAAUAUCAUCAGGUUUUG
Cleavage	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172e	KU870525.1	7.0	-1.0	1	21	7179	7199
	AGAAUCUUGAUGAUGCUGCAU	:	:	:	:	:	GUUCGACUUCAACAAGGGUCU
Translation	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172f	KU870525.1	7.0	-1.0	1	21	5579	5599
	AGAAUCUUGAUGAUGCUGCAU	:	:	:	:	:	UAAAUAUCAUCAGGUUUUG
Cleavage	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172f	KU870525.1	7.0	-1.0	1	21	7179	7199
	AGAAUCUUGAUGAUGCUGCAU	:	:	:	:	:	GUUCGACUUCAACAAGGGUCU
Translation	Apple chlorotic leaf spot virus isolate SY03,	complete					
genome	2						
mdm-miR172g	KU870525.1	7.0	-1.0	1	21	5579	5599
	AGAAUCUUGAUGAUGCUGCAU	:	:	:	:	:	UAAAUAUCAUCAGGUUUUG



[illegible]

mdm-miR2111a	KU870525.1	7.0	-1.0	1	21	1021	1043
UAAUCUGCAUCCUG--AGGUUUA			.....	.....	...		
AAAACCUGUCAGGGUGCCUAUUC			Cleavage		Apple chlorotic leaf spot		
virus isolate SY03, complete genome		3					
mdm-miR2111a	KU870525.1	7.0	-1.0	1	21	4893	4912
UAAUCUGCAUCCUGAGGUUUA		: : : : :	.....			UCAGCC-CAUGGUGCAGAUAC	
Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete					
genome		3					
mdm-miR2111b	KU870525.1	7.0	-1.0	1	21	1021	1043
UAAUCUGCAUCCUG--AGGUUUA			.....	.....	...		
AAAACCUGUCAGGGUGCCUAUUC			Cleavage		Apple chlorotic leaf spot		
virus isolate SY03, complete genome		3					
mdm-miR2111b	KU870525.1	7.0	-1.0	1	21	4893	4912
UAAUCUGCAUCCUGAGGUUUA		: : : : :	.....			UCAGCC-CAUGGUGCAGAUAC	
Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete					
genome		3					
mdm-miR319a	KU870525.1	7.0	-1.0	1	21	2232	2252
UUGGACUGAAGGGAGCUCCCU		: : : .	.....			GAGCAGCCUACUUCUGUCUGG	
Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete					
genome		1					
mdm-miR319b	KU870525.1	7.0	-1.0	1	21	2232	2252
UUGGACUGAAGGGAGCUCCCU		: : : .	.....			GAGCAGCCUACUUCUGUCUGG	
Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete					
genome		1					
mdm-miR393a	KU870525.1	7.0	-1.0	1	22	1578	1599
UCCAAAGGGAUCGCAUUGAUCU		: : : : :	.....				
UGCUCUCUUCAACUCCUUUGG		Translation	Apple chlorotic leaf spot virus				
isolate SY03, complete genome		1					
mdm-miR393b	KU870525.1	7.0	-1.0	1	22	1578	1599
UCCAAAGGGAUCGCAUUGAUCU		: : : : :	.....				
UGCUCUCUUCAACUCCUUUGG		Translation	Apple chlorotic leaf spot virus				
isolate SY03, complete genome		1					
mdm-miR393c	KU870525.1	7.0	-1.0	1	22	1578	1599
UCCAAAGGGAUCGCAUUGAUCU		: : : : :	.....				
UGCUCUCUUCAACUCCUUUGG		Translation	Apple chlorotic leaf spot virus				
isolate SY03, complete genome		1					
mdm-miR393d	KU870525.1	7.0	-1.0	1	21	3092	3111
AUC AUGCGAUCCCUUCGGACG		.....	: : : : :			AGUCUGAUGG-AUGGCAUGAC	
Translation		Apple chlorotic leaf spot virus isolate SY03, complete					
genome		2					
mdm-miR393d	KU870525.1	7.0	-1.0	1	21	6423	6443
AUC AUGCGAUCCCUUCGGACG		.....	: : : : :			AUCCCGAGGGGAAUGUUUGGA	
Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete					
genome		2					
mdm-miR393e	KU870525.1	7.0	-1.0	1	21	3092	3111
AUC AUGCGAUCCCUUCGGACG		.....	: : : : :			AGUCUGAUGG-AUGGCAUGAC	
Translation		Apple chlorotic leaf spot virus isolate SY03, complete					
genome		2					
mdm-miR393e	KU870525.1	7.0	-1.0	1	21	6423	6443
AUC AUGCGAUCCCUUCGGACG		.....	: : : : :			AUCCCGAGGGGAAUGUUUGGA	
Cleavage		Apple chlorotic leaf spot virus isolate SY03, complete					
genome		2					
mdm-miR393f	KU870525.1	7.0	-1.0	1	21	3092	3111
AUC AUGCGAUCCCUUCGGACG		.....	: : : : :			AGUCUGAUGG-AUGGCAUGAC	

Translation Apple chlorotic leaf spot virus isolate SY03, complete genome 2

mdm-miR393f KU870525.1 7.0 -1.0 1 21 6423 6443  
AUCAUGCGAUCCCUUCGGACG :::::::::: ... .. AUCCCGAGGGGAAUGUUUGGA  
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete genome 2

mdm-miR394a KU870525.1 7.0 -1.0 1 20 4195 4215 UUGGCAU-  
UCUGUCCACCUC :: :::::::::: : :::: CGAAAUGGACAGAGAGGCCAG Cleavage  
Apple chlorotic leaf spot virus isolate SY03, complete genome 3

mdm-miR394a KU870525.1 7.0 -1.0 1 20 4360 4378  
UUGGCAUUCUGUCCACCUC :: :::: ::::: :::: AGAACUGGAAAGAAU-CCAG  
Translation Apple chlorotic leaf spot virus isolate SY03, complete genome 3

mdm-miR394b KU870525.1 7.0 -1.0 1 20 4195 4215 UUGGCAU-  
UCUGUCCACCUC :: :::::::::: : :::: CGAAAUGGACAGAGAGGCCAG Cleavage  
Apple chlorotic leaf spot virus isolate SY03, complete genome 3

mdm-miR394b KU870525.1 7.0 -1.0 1 20 4360 4378  
UUGGCAUUCUGUCCACCUC :: :::: ::::: :::: AGAACUGGAAAGAAU-CCAG  
Translation Apple chlorotic leaf spot virus isolate SY03, complete genome 3

mdm-miR395a KU870525.1 7.0 -1.0 1 21 4121 4142 CUGAAGUGUUUGGGG-  
GAACUC ::::: ..... :::: GAGUUCAUUCUAAGUUCUUCAU Cleavage  
Apple chlorotic leaf spot virus isolate SY03, complete genome 5

mdm-miR395b KU870525.1 7.0 -1.0 1 21 4121 4142 CUGAAGUGUUUGGGG-  
GAACUC ::::: ..... :::: GAGUUCAUUCUAAGUUCUUCAU Cleavage  
Apple chlorotic leaf spot virus isolate SY03, complete genome 5

mdm-miR395c KU870525.1 7.0 -1.0 1 21 4121 4142 CUGAAGUGUUUGGGG-  
GAACUC ::::: ..... :::: GAGUUCAUUCUAAGUUCUUCAU Cleavage  
Apple chlorotic leaf spot virus isolate SY03, complete genome 5

mdm-miR395d KU870525.1 7.0 -1.0 1 21 4121 4142 CUGAAGUGUUUGGGG-  
GAACUC ::::: ..... :::: GAGUUCAUUCUAAGUUCUUCAU Cleavage  
Apple chlorotic leaf spot virus isolate SY03, complete genome 5

mdm-miR395e KU870525.1 7.0 -1.0 1 21 4121 4142 CUGAAGUGUUUGGGG-  
GAACUC ::::: ..... :::: GAGUUCAUUCUAAGUUCUUCAU Cleavage  
Apple chlorotic leaf spot virus isolate SY03, complete genome 5

mdm-miR395f KU870525.1 7.0 -1.0 1 21 4121 4142 CUGAAGUGUUUGGGG-  
GAACUC ::::: ..... :::: GAGUUCAUUCUAAGUUCUUCAU Cleavage  
Apple chlorotic leaf spot virus isolate SY03, complete genome 5

mdm-miR395g KU870525.1 7.0 -1.0 1 21 4121 4142 CUGAAGUGUUUGGGG-  
GAACUC ::::: ..... :::: GAGUUCAUUCUAAGUUCUUCAU Cleavage  
Apple chlorotic leaf spot virus isolate SY03, complete genome 5

mdm-miR395h KU870525.1 7.0 -1.0 1 21 4121 4142 CUGAAGUGUUUGGGG-  
GAACUC ::::: ..... :::: GAGUUCAUUCUAAGUUCUUCAU Cleavage  
Apple chlorotic leaf spot virus isolate SY03, complete genome 5

mdm-miR395i KU870525.1 7.0 -1.0 1 21 4121 4142 CUGAAGUGUUUGGGG-  
GAACUC ::::: ..... :::: GAGUUCAUUCUAAGUUCUUCAU Cleavage  
Apple chlorotic leaf spot virus isolate SY03, complete genome 5

mdm-miR396f KU870525.1 7.0 -1.0 1 21 6447 6467  
UCCACGGCUUUCUUGAACUG ::::: ::::: :: AUGGGGAAGAAAACCGUGAAA  
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete genome 4

mdm-miR396f KU870525.1 7.0 -1.0 1 21 2702 2722  
UCCACGGCUUUCUUGAACUG ::::: ::::: AUUCACAAGAAACCUGAGGAG

```

Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 4
mdm-miR396f KU870525.1 7.0 -1.0 1 21 3376 3396
UCCACGGCUUUCUUGAACUG :: : : : : : : : : GUGUCCGAGAAAGUUUUUGGC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 4
mdm-miR396f KU870525.1 7.0 -1.0 1 21 2655 2674
UCCACGGCUUUCUUGAACUG ::: : : : : : : : : : UCGUAAAAGGAAGAC-UGGAC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 4
mdm-miR396g KU870525.1 7.0 -1.0 1 21 6447 6467
UCCACGGCUUUCUUGAACUG : : : : : : : : : : AUGGGGAAGAAAACCGUGAAA
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 4
mdm-miR396g KU870525.1 7.0 -1.0 1 21 2702 2722
UCCACGGCUUUCUUGAACUG : : : : : : : : : : AUUCACAAGAAACCUGAGGAG
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 4
mdm-miR396g KU870525.1 7.0 -1.0 1 21 3376 3396
UCCACGGCUUUCUUGAACUG :: : : : : : : : : GUGUCCGAGAAAGUUUUUGGC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 4
mdm-miR396g KU870525.1 7.0 -1.0 1 21 2655 2674
UCCACGGCUUUCUUGAACUG ::: : : : : : : : : : UCGUAAAAGGAAGAC-UGGAC
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 4
mdm-miR397a KU870525.1 7.0 -1.0 1 21 6152 6172
UGAGUGCAGCGUUGAUGAAA :: : : : : : : : : UUCUAUUUGCGUUGCGGUCAU
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 3
mdm-miR397a KU870525.1 7.0 -1.0 1 21 88 108
UGAGUGCAGCGUUGAUGAAA : : : : : : : : : : AUACAAUAACAUUGUAUUGCA
Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome 3
mdm-miR397b KU870525.1 7.0 -1.0 1 21 6152 6172
UGAGUGCAGCGUUGAUGAAA :: : : : : : : : : UUCUAUUUGCGUUGCGGUCAU
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 3
mdm-miR397b KU870525.1 7.0 -1.0 1 21 88 108
UGAGUGCAGCGUUGAUGAAA : : : : : : : : : : AUACAAUAACAUUGUAUUGCA
Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome 3
mdm-miR398a KU870525.1 7.0 -1.0 1 21 5832 5852
UGUGUUCUCAGGUCACCCCUU ::: : : : : : : : : : AAGGUCAUGCCGAGGACAUA
Translation Apple chlorotic leaf spot virus isolate SY03, complete
genome 2
mdm-miR408a KU870525.1 7.0 -1.0 1 21 1410 1430
AUGCACUGCCUCUUCCUGGC :: : : : : : : : : : GGGAGGAAAGAGUCUGUGUGG
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 2
mdm-miR408a KU870525.1 7.0 -1.0 1 21 2218 2237
AUGCACUGCCUCUUCCUGGC : : : : : : : : : : CAUAGGAAAGAGG-AGAGCAG
Cleavage Apple chlorotic leaf spot virus isolate SY03, complete
genome 2

```

```

mdm-miR482a-5p    KU870525.1  7.0   -1.0  1      22     131    152
      AGGAAUGGGCUGUUUGGAAGA      ..... :
      AGAGAUCAA AUGGCCUUCUCCU Cleavage Apple chlorotic leaf spot virus
isolate SY03, complete genome      2
mdm-miR482b KU870525.1  7.0   -1.0  1      22     6432   6456
      UCUUUCUAUCCCUCC---CAUUC      ..... :
      GGAAUGUUUGGAAUGAUGGGAAGA      Cleavage Apple chlorotic leaf spot
virus isolate SY03, complete genome      2
mdm-miR5225a     KU870525.1  7.0   -1.0  1      22     5233   5254
      UCUGUCGAAGGUGAGAUGGUGC      ..... :
      UAUGGUGUUCACCUUCUGCAGG Cleavage Apple chlorotic leaf spot virus
isolate SY03, complete genome      4
mdm-miR5225a     KU870525.1  7.0   -1.0  1      22     182    203
      UCUGUCGAAGGUGAGAUGGUGC      ... : : : :
      AGAUUACCACAAUCUCGACAGG Translation Apple chlorotic leaf spot virus
isolate SY03, complete genome      4
mdm-miR5225a     KU870525.1  7.0   -1.0  1      22     1340   1360
      UCUGUCGAAGGUGAGAUGGUGC      .... : : : : : : : AAACCA-
CUAGCUUUUGAUUAU Cleavage Apple chlorotic leaf spot virus isolate
SY03, complete genome      4
mdm-miR5225a     KU870525.1  7.0   -1.0  1      22     6065   6086
      UCUGUCGAAGGUGAGAUGGUGC      ... : : : :
      AUUCCGGUUCAAUUUGGAUAGU Translation Apple chlorotic leaf spot virus
isolate SY03, complete genome      4
mdm-miR5225b     KU870525.1  7.0   -1.0  1      22     5233   5254
      UCUGUCGAAGGUGAGAUGGUGC      ..... :
      UAUGGUGUUCACCUUCUGCAGG Cleavage Apple chlorotic leaf spot virus
isolate SY03, complete genome      4
mdm-miR5225b     KU870525.1  7.0   -1.0  1      22     182    203
      UCUGUCGAAGGUGAGAUGGUGC      ... : : : :
      AGAUUACCACAAUCUCGACAGG Translation Apple chlorotic leaf spot virus
isolate SY03, complete genome      4
mdm-miR5225b     KU870525.1  7.0   -1.0  1      22     1340   1360
      UCUGUCGAAGGUGAGAUGGUGC      .... : : : : : : : AAACCA-
CUAGCUUUUGAUUAU Cleavage Apple chlorotic leaf spot virus isolate
SY03, complete genome      4
mdm-miR5225b     KU870525.1  7.0   -1.0  1      22     6065   6086
      UCUGUCGAAGGUGAGAUGGUGC      ... : : : :
      AUUCCGGUUCAAUUUGGAUAGU Translation Apple chlorotic leaf spot virus
isolate SY03, complete genome      4
mdm-miR5225c     KU870525.1  7.0   -1.0  1      22     182    203
      UCUGUCGUGGGUGAGAUGGUGC      ... : : : :
      AGAUUACCACAAUCUCGACAGG Translation Apple chlorotic leaf spot virus
isolate SY03, complete genome      5
mdm-miR5225c     KU870525.1  7.0   -1.0  1      22     592    613
      UCUGUCGUGGGUGAGAUGGUGC      :: : : : : : :
      CAACAUUUUCAUACAUGACGAA Translation Apple chlorotic leaf spot virus
isolate SY03, complete genome      5
mdm-miR5225c     KU870525.1  7.0   -1.0  1      22     6200   6221
      UCUGUCGUGGGUGAGAUGGUGC      ..... : : : :
      CAGCUAUCCAUUAGUGUCAGG Cleavage Apple chlorotic leaf spot virus
isolate SY03, complete genome      5
mdm-miR5225c     KU870525.1  7.0   -1.0  1      22     4490   4511
      UCUGUCGUGGGUGAGAUGGUGC      : : : : : : : :

```

	GAAGCAGUGUACCCAAGACAUA	Cleavage							Apple chlorotic leaf spot virus isolate SY03, complete genome	5	
mdm-mir7120a	KU870525.1	7.0	-1.0	1	21	5218	5239	UGUUUAU-UUGUCAGAUUGUCA	::: ::::: : : : : CAACACUUUGGCAAAUAUGGUG	Cleavage	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	3
mdm-mir7120a	KU870525.1	7.0	-1.0	1	21	3088	3107	UGUUUAU-AUUGUCAGAUUGUCA	: : : : : : : : : : : CAAGAGUCUGAUGG-AUGGCA	Cleavage	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	3
mdm-mir7120b	KU870525.1	7.0	-1.0	1	21	5218	5239	UGUUUAU-UUGUCAGAUUGUCA	::: ::::: : : : : CAACACUUUGGCAAAUAUGGUG	Cleavage	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	3
mdm-mir7120b	KU870525.1	7.0	-1.0	1	21	3088	3107	UGUUUAU-AUUGUCAGAUUGUCA	: : : : ~~~~~~ : : : : : CAAGAGUCUGAUGG-AUGGCA	Cleavage	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	3
mdm-mir7121d	KU870525.1	7.0	-1.0	1	21	1488	1508	UCCUCUUGGUGAUCGCCCGUC	:: : : : : : : : : : UCAUGCCCCAUGAUGAAGAGGG	Translation	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	2
mdm-mir7121e	KU870525.1	7.0	-1.0	1	21	1488	1508	UCCUCUUGGUGAUCGCCCGUC	:: : : : : : : : : : UCAUGCCCCAUGAUGAAGAGGG	Translation	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	2
mdm-mir7121f	KU870525.1	7.0	-1.0	1	21	1488	1508	UCCUCUUGGUGAUCGCCCGUC	:: : : : ~::~ : : : : : UCAUGCCCCAUGAUGAAGAGGG	Translation	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	2
mdm-mir7121g	KU870525.1	7.0	-1.0	1	21	1488	1508	UCCUCUUGGUGAUCGCCCGUC	:: : : : ~::~ : : : : : UCAUGCCCCAUGAUGAAGAGGG	Translation	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	2
mdm-mir7121h	KU870525.1	7.0	-1.0	1	21	1488	1508	UCCUCUUGGUGAUCGCCCGUC	:: : : : ~::~ : : : : : UCAUGCCCCAUGAUGAAGAGGG	Translation	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	2
mdm-mir7123a	KU870525.1	7.0	-1.0	1	21	1567	1586	AAGAGCGGAUGUGUAAAAGG	..... : : : : : : : : : : UUUUUCAGACAUGCUCU-CUCUU	Cleavage	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	1
mdm-mir7123b	KU870525.1	7.0	-1.0	1	21	1567	1586	AAGAGCGGAUGUGUAAAAGG	..... : : : : : : : : : : UUUUUCAGACAUGCUCU-CUCUU	Cleavage	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	1
mdm-mir7125	KU870525.1	7.0	-1.0	1	21	5806	5826	CGAACUUAAUUGCAACUAGCUU	::: ::::: : : : : : : : : UGAUCCAUUGGAAUGAGAUUCG	Translation	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	2
mdm-mir858	KU870525.1	7.0	-1.0	1	21	4296	4315	UUCGUUGUCUGUUCGACCUGA	::: : : : : : : : : : : : : UCAAG-CUGACAGACAGUGCA	Cleavage	
										Apple chlorotic leaf spot virus isolate SY03, complete genome	3
mdm-mir858	KU870525.1	7.0	-1.0	1	21	4465	4485	UUCGUUGUCUGUUCGACCUGA	: : : : : : : : : : : CAAAGUUAACCAAGCAAUGAG		

Cleavage genome	3	Apple chlorotic leaf spot virus isolate SY03, complete
--------------------	---	--