

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

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(2003) Genome Biology; 5(1):R1.

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Current Settings:

=====
Query Filename: ./seq/mirna/sof_mirna.fasta
Reference Filename: ./seq/gene/sof/NC_038382.fasta
Gap Open Penalty: -9.000000
Gap Extend Penalty: -4.000000
Score Threshold: 130.000000
Energy Threshold: -15.000000 kcal/mol
Scaling Parameter: 4.000000
=====
Read Sequence:sof-miR156 (20 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR156 vs NC_038382.1
=====

Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:sof-miR159a (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR159a vs NC_038382.1
=====

Forward: Score: 138.000000 Q:2 to 19 R:5282 to 5302 Align Len
(17) (64.71%) (76.47%)

Query: 3' gucUCGAGGGAAGUUAGGUUu 5'
 || ||: |||||:||
Ref: 5' attAGACCCTCACAATCTAAa 3'

Energy: -17.180000 kCal/Mol

Scores for this hit:

>sof-miR159a	NC_038382.1	138.00	-17.18	2	19	5282	5302
17	64.71%	76.47%					

Forward: Score: 131.000000 Q:2 to 20 R:6739 to 6759 Align Len
(18) (55.56%) (72.22%)

Query: 3' guCUCGAGGGAAGUUAGGUUu 5'
 |: | :|| |||||:|
Ref: 5' caGGACATCCAGAAATCCGaa 3'

Energy: -18.110001 kCal/Mol

Scores for this hit:

>sof-miR159a	NC_038382.1	131.00	-18.11	2	20	6739	6759
18	55.56%	72.22%					

Score for this Scan:

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

>>sof-miR159a	NC_038382.1	269.00	-35.29	138.00	-
18.11	21	7444	5282	6739	

Complete

Read Sequence:sof-miR159b (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR159b vs NC_038382.1
=====

Forward: Score: 138.000000 Q:2 to 19 R:5282 to 5302 Align Len
(17) (64.71%) (76.47%)

Query: 3' gucUCGAGGGAAGUUAGGUUu 5'
 || ||: |||||:||
Ref: 5' attAGACCCTCACAATCTAAa 3'

Energy: -17.180000 kCal/Mol

Scores for this hit:

>sof-miR159b	NC_038382.1	138.00	-17.18	2	19	5282	5302
17	64.71%	76.47%					

Forward: Score: 131.000000 Q:2 to 20 R:6739 to 6759 Align Len
(18) (55.56%) (72.22%)

Query: 3' guCUCGAGGGAAGUUAGGUUu 5'
|: |:| | ||| |:|
Ref: 5' caGGACATCCAGAAATCCGaa 3'

Energy: -18.110001 kCal/Mol

Scores for this hit:

>sof-miR159b	NC_038382.1	131.00	-18.11	2	20	6739	6759
18	55.56%	72.22%					

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max
Energy,Strand,Len1,Len2,Positions
>>sof-miR159b NC_038382.1 269.00 -35.29 138.00 -
18.11 3 21 7444 5282 6739
Complete

Read Sequence:sof-miR159c (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR159c vs NC_038382.1
=====

Forward: Score: 131.000000 Q:2 to 20 R:6739 to 6759 Align Len
(18) (55.56%) (72.22%)

Query: 3' ucCUCGAGGGAAGUUAGGUUc 5'
|: |:| | ||| |:|
Ref: 5' caGGACATCCAGAAATCCGaa 3'

Energy: -16.700001 kCal/Mol

Scores for this hit:

>sof-miR159c	NC_038382.1	131.00	-16.70	2	20	6739	6759
18	55.56%	72.22%					

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max
Energy,Strand,Len1,Len2,Positions
>>sof-miR159c NC_038382.1 131.00 -16.70 131.00 -
16.70 4 21 7444 6739
Complete

Read Sequence:sof-miR159d (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome

(7444 nt)

=====
Performing Scan: sof-miR159d vs NC_038382.1
=====

Forward: Score: 138.000000 Q:2 to 19 R:5282 to 5302 Align Len
(17) (64.71%) (76.47%)

Query: 3' guCUCGAGGGAAGUUAGGUUu 5'
|| ||: ||||:|
Ref: 5' attAGACCCCTACAATCTAAa 3'

Energy: -17.180000 kCal/Mol

Scores for this hit:

>sof-miR159d NC_038382.1 138.00 -17.18 2 19 5282 5302
17 64.71% 76.47%

Forward: Score: 131.000000 Q:2 to 20 R:6739 to 6759 Align Len
(18) (55.56%) (72.22%)

Query: 3' guCUCGAGGGAAGUUAGGUUu 5'
|: |:| | ||||:|
Ref: 5' caGGACATCCAGAAATCCGAa 3'

Energy: -18.110001 kCal/Mol

Scores for this hit:

>sof-miR159d NC_038382.1 131.00 -18.11 2 20 6739 6759
18 55.56% 72.22%

Score for this Scan:

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

>>sof-miR159d NC_038382.1 269.00 -35.29 138.00 -
18.11 5 21 7444 5282 6739

Complete

Read Sequence:sof-miR159e (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR159e vs NC_038382.1
=====

Forward: Score: 142.000000 Q:2 to 19 R:5282 to 5302 Align Len
(17) (70.59%) (76.47%)

Query: 3' uucUCGAGGAAAGUUAGGUUu 5'
|| ||| ||||:|

Ref: 5' attAGACCCTCACAATCTAAa 3'

Energy: -15.810000 kCal/Mol

Scores for this hit:

>sof-miR159e	NC_038382.1	142.00	-15.81	2	19	5282	5302
17	70.59%	76.47%					

Score for this Scan:

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

>>sof-miR159e	NC_038382.1	142.00	-15.81	142.00	-
15.81	6	21	7444	5282	

Complete

Read Sequence:sof-miR167a (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus clone 1, complete genome (7444 nt)

Performing Scan: sof-miR167a vs NC_038382.1

Forward: Score: 132.000000 Q:2 to 19 R:5846 to 5865 Align Len (17) (76.47%) (82.35%)

Query: 3' gucUAGUACGACCGUCGAAGu 5'

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

Ref: 5' aaaATCAAGTT-GCAGCCTCa 3'

Energy: -16.080000 kCal/Mol

Scores for this hit:

>sof-miR167a	NC_038382.1	132.00	-16.08	2	19	5846	5865
17	76.47%	82.35%					

Score for this Scan:

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

>>sof-miR167a	NC_038382.1	132.00	-16.08	132.00	-
16.08	7	21	7444	5846	

Complete

Read Sequence:sof-miR167b (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus clone 1, complete genome (7444 nt)

Performing Scan: sof-miR167b vs NC_038382.1

Forward: Score: 132.000000 Q:2 to 19 R:5846 to 5865 Align Len
(17) (76.47%) (82.35%)

Query: 3' gucUAGUACGACCGUCGAAGu 5'
 |||| |:| ||||| ||
Ref: 5' aaaATCAAGTT-GCAGCCTCa 3'

Energy: -16.080000 kCal/Mol

Scores for this hit:

>sof-miR167b	NC_038382.1	132.00	-16.08	2 19	5846	5865
17	76.47%	82.35%				

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max
Energy,Strand,Len1,Len2,Positions
>>sof-miR167b NC_038382.1 132.00 -16.08 132.00 -
16.08 8 21 7444 5846
Complete

Read Sequence:sof-miR168a (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR168a vs NC_038382.1
=====

Forward: Score: 130.000000 Q:2 to 17 R:5506 to 5525 Align Len
(15) (73.33%) (93.33%)

Query: 3' cagggCUAGACGUGGUUCGcu 5'
 |||:| ||||:|:|
Ref: 5' gagtgGATTT-CACCAGGTGg 3'

Energy: -21.240000 kCal/Mol

Scores for this hit:

>sof-miR168a	NC_038382.1	130.00	-21.24	2 17	5506	5525
15	73.33%	93.33%				

Forward: Score: 130.000000 Q:2 to 18 R:7050 to 7068 Align Len
(16) (68.75%) (75.00%)

Query: 3' caggGCUAGACGUGGUUCGcu 5'
 ||| || ||||:|
Ref: 5' gttacGAGATG--CCAAGTga 3'

Energy: -18.459999 kCal/Mol

Scores for this hit:

>sof-miR168a NC_038382.1 130.00 -18.46 2 18 7050 7068
16 68.75% 75.00%

Score for this Scan:

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

>>sof-miR168a NC_038382.1 260.00 -39.70 130.00 -
21.24 9 21 7444 5506 7050

Complete

Read Sequence:sof-miR168b (20 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR168b vs NC_038382.1
=====

Forward: Score: 134.000000 Q:2 to 17 R:7050 to 7068 Align Len
(15) (73.33%) (80.00%)

Query: 3' caggGCUAGACGGGUUCGCU 5'

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

Ref: 5' gttacGAGATG-CCAAGTGA 3'

Energy: -20.059999 kCal/Mol

Scores for this hit:

>sof-miR168b NC_038382.1 134.00 -20.06 2 17 7050 7068
15 73.33% 80.00%

Score for this Scan:

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

>>sof-miR168b NC_038382.1 134.00 -20.06 134.00 -
20.06 10 20 7444 7050

Complete

Read Sequence:sof-miR396 (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR396 vs NC_038382.1
=====

Forward: Score: 158.000000 Q:2 to 20 R:3394 to 3415 Align Len
(19) (68.42%) (84.21%)

Query: 3' guCAAGUUC-UUUCGACACCUu 5'

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

Ref: 5' agGATTAGGTGATGCTGTGGA 3'

Energy: -19.990000 kCal/Mol

Scores for this hit:

>sof-miR396	NC_038382.1	158.00	-19.99	2	20	3394	3415
19	68.42%	84.21%					

Score for this Scan:

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

>>sof-miR396	NC_038382.1	158.00	-19.99	158.00	-
19.99	11	21	7444	3394	

Complete

Read Sequence:sof-miR408a (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR408a vs NC_038382.1
=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:sof-miR408b (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR408b vs NC_038382.1
=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:sof-miR408c (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR408c vs NC_038382.1
=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:sof-miR408d (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====

Performing Scan: sof-miR408d vs NC_038382.1

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

Read Sequence:sof-miR408e (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: sof-miR408e vs NC_038382.1

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

Read Sequence:ssp-miR166 (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR166 vs NC_038382.1

=====
Forward: Score: 144.000000 Q:2 to 18 R:3249 to 3271 Align Len
(18) (72.22%) (83.33%)

Query: 3' ccccUUACU--UCGGACCAGGCu 5'
| ||| ||:|||||:|
Ref: 5' agacACTGAAGAGTCTGGTCTGt 3'

Energy: -21.450001 kCal/Mol

Scores for this hit:
>ssp-miR166 NC_038382.1 144.00 -21.45 2 18 3249 3271
18 72.22% 83.33%

Forward: Score: 139.000000 Q:2 to 20 R:5589 to 5609 Align Len
(18) (61.11%) (77.78%)

Query: 3' ccCCUUACUUCGGACCAGGCu 5'
| |||| :|||||:|
Ref: 5' taGTAATGCCATTTGGTCTGa 3'

Energy: -17.549999 kCal/Mol

Scores for this hit:
>ssp-miR166 NC_038382.1 139.00 -17.55 2 20 5589 5609
18 61.11% 77.78%

Forward: Score: 132.000000 Q:2 to 14 R:94 to 116 Align Len
(14) (71.43%) (85.71%)

Query: 3' ccccuuacUUCGG--ACCAGGCu 5'

|||:| ||||:|

Ref: 5' agctgtacAAGTCTATGGTTCGa 3'

Energy: -16.670000 kCal/Mol

Scores for this hit:

>ssp-miR166	NC_038382.1	132.00	-16.67	2	14	94	116
14	71.43%	85.71%					

Forward: Score: 132.000000 Q:3 to 20 R:5761 to 5779 Align Len
(17) (76.47%) (88.24%)

Query: 3' ccCCUUACUUCGGACCAGGcu 5'

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

Ref: 5' aaGGAATG--GTCTGGTCTta 3'

Energy: -21.740000 kCal/Mol

Scores for this hit:

>ssp-miR166	NC_038382.1	132.00	-21.74	3	20	5761	5779
17	76.47%	88.24%					

Score for this Scan:

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

>>ssp-miR166	NC_038382.1	547.00	-77.41	144.00	-		
21.74	17	21	7444	3249	5589	94	5761

Complete

Read Sequence:ssp-miR169 (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR169 vs NC_038382.1
=====

Score for this Scan:

No Hits Found above Threshold
Complete

Read Sequence:ssp-miR437a (21 nt)

Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR437a vs NC_038382.1

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

Read Sequence:ssp-miR437b (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR437b vs NC_038382.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:ssp-miR437c (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR437c vs NC_038382.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:ssp-miR528 (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR528 vs NC_038382.1
=====

Forward: Score: 147.000000 Q:2 to 18 R:7426 to 7444 Align Len
(16) (75.00%) (75.00%)

Query: 3' gaggAGACGUACGGGGAAGGu 5'
 || || | |||||
Ref: 5' gcgaTCCGC-CCCCCTTCC- 3'

Energy: -18.370001 kCal/Mol

Scores for this hit:
>ssp-miR528 NC_038382.1 147.00 -18.37 2 18 7426 7444
16 75.00% 75.00%

Forward: Score: 133.000000 Q:2 to 15 R:7395 to 7417 Align Len
(15) (73.33%) (80.00%)

Query: 3' gaggagaCGUAC--GGGGAAGGu 5'
 ||| | ||:|||||
Ref: 5' gtagagcGCAAGATCCTCTTCCg 3'

Energy: -18.059999 kCal/Mol

Scores for this hit:

>ssp-miR528	NC_038382.1	133.00	-18.06	2 15 7395 7417
15	73.33%	80.00%		

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max
Energy,Strand,Len1,Len2,Positions
>>ssp-miR528 NC_038382.1 280.00 -36.43 147.00 -
18.37 22 21 7444 7426 7395
Complete

Read Sequence:ssp-miR827 (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR827 vs NC_038382.1
=====

Forward: Score: 136.000000 Q:2 to 17 R:5378 to 5398 Align Len
(15) (80.00%) (86.67%)

Query: 3' acaaaCGACUACCAGUAGAUu 5'
 ||||:|| ||| |||
Ref: 5' gaaagGCTGGTGTTCAACTat 3'

Energy: -16.400000 kCal/Mol

Scores for this hit:

>ssp-miR827	NC_038382.1	136.00	-16.40	2 17 5378 5398
15	80.00%	86.67%		

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max
Energy,Strand,Len1,Len2,Positions
>>ssp-miR827 NC_038382.1 136.00 -16.40 136.00 -
16.40 23 21 7444 5378
Complete

Read Sequence:ssp-miR444a (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR444a vs NC_038382.1
=====

Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:ssp-miR444b (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR444b vs NC_038382.1
=====

Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:ssp-miR444c-3p (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR444c-3p vs NC_038382.1
=====

Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:ssp-miR1128 (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR1128 vs NC_038382.1
=====

Forward: Score: 136.000000 Q:2 to 18 R:6141 to 6163 Align Len
(18) (77.78%) (83.33%)

Query: 3' aaacCCUGCCU--CCCUCAUCAu 5'
 | | | : | | | | | | | | | | | |
Ref: 5' gtatGGATGGATGGGGAGGAGTc 3'

Energy: -22.969999 kCal/Mol

Scores for this hit:
>ssp-miR1128 NC_038382.1 136.00 -22.97 2 18 6141 6163
 18 77.78% 83.33%

Score for this Scan:
Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max
Energy,Strand,Len1,Len2,Positions
>>ssp-miR1128 NC_038382.1 136.00 -22.97 136.00 -
22.97 27 21 7444 6141

Complete

Read Sequence:ssp-miR1432 (21 nt)
Read Sequence:NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone 1, complete genome
(7444 nt)

=====
Performing Scan: ssp-miR1432 vs NC_038382.1
=====

Forward: Score: 152.000000 Q:2 to 18 R:6070 to 6091 Align Len
(17) (76.47%) (76.47%)

Query: 3' cagcCACAGUAGA-AAGGACUc 5'

||| || | |||||

Ref: 5' aattGTGGCAAATCTTCCTGAt 3'

Energy: -15.480000 kCal/Mol

Scores for this hit:

>ssp-miR1432	NC_038382.1	152.00	-15.48	2	18	6070	6091
17	76.47%	76.47%					

Score for this Scan:

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

>>ssp-miR1432	NC_038382.1	152.00	-15.48	152.00	-
15.48	28	21	7444	6070	

Complete

Scan Complete

RNA22 algorithm results of SCBGAV-

sof-miR167a NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[1310,1329] -15.80 AACCTCGACTGGTAGTTTCC
TGAAGCTGCCAGCATGATCTG(((.(((((((((((. .))))))))))....
14 20 0.162000

sof-miR167b NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[1310, 1329]-15.80 AACCTCGACTGGTAGTTTCC
TGAAGCTGCCAGCATGATCTG(((.(((((((((((. .))))))))))....
14 20 0.162000

ssp-miR528 NC_038382.1 Sugarcane bacilliform Guadeloupe A virus clone
target from/to=[1310,1330] -13.70 AACCTCGACTGGTAGTTTCCA
TGAAGGGGGCATGCAGAGGAG ..(((.....(((.((((((()))....
12 21 0.162000

sof-miR168a NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[1723,1743] -12.60 AGCAAGAACAGTACCAGGAGA
TCGCTTGGTGCAGATCGGGAC ..((.(((.(((((((((((. ()))....
14 21 0.037600

sof-miR408a NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[1735,1753] -13.70 ACCAGGAGAAGTACTGTAT

CTGCACTGCCTCTTCCTGGC .(((((((.((((.((((.))))).)))..))))).
15 19 0.037600
sof-miR408b NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[1735,1753] -13.70 ACCAGGAGAAGTACTGTAT
CTGCACTGCCTCTTCCTGGC .(((((((.((((.((((.))))).)))..))))).
15 19 0.037600
sof-miR408c NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[1735,1753] -13.70 ACCAGGAGAAGTACTGTAT
CTGCACTGCCTCTTCCTGGC .(((((((.((((.((((.))))).)))..))))).
15 19 0.037600
sof-miR408d NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[1735,1753] -13.70 ACCAGGAGAAGTACTGTAT
CTGCACTGCCTCTTCCTGGC .(((((((.((((.((((.))))).)))..))))).
15 19 0.037600
ssp-miR528 NC_038382.1 Sugarcane bacilliform Guadeloupe A virus clone
target from/to=[2839,2858] -12.10 AACCACTGAATTCCCATTCA
TGGAAGGGGCATGCAGAGGAG ..((.(...(((.(((()))).)))....))..
13 20 0.061000
sof-miR396 NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[2867,2886] -12.70 AGAAGACCGAGAGTGTGGGA
TTCCACAGCTTTCTTGAAGTGTG(((((((((())))))).))).....
12 20 0.102000
sof-miR396 NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[3394,3415] -17.80 AGGATTAGGTGATGCTGTGGAG
TTCCACAGCTTTCTTGAAGTGTG .(((.(...(((....(((((((
))))))))).)).. 16 22 0.030200
sof-miR396 NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[4115,4133] -13.90 GACTGCAAGAAATGTGGAA
TTCCACAGCTTTCTTGAAGTGTG(((((((((())))))).))).....
14 19 0.077600
ssp-miR444a NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[4103,4121] -16.30 AAGCACAGGGTTGACTGCA
TGCAGTTGTTGCTCAAGCTT (((...(((.((((((())))))).)))....))
15 19 0.077600
ssp-miR444b NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[4103,4121] -16.30 AAGCACAGGGTTGACTGCA
TGCAGTTGTTGCTCAAGCTT (((...(((.((((((())))))).)))....))
15 19 0.077600
ssp-miR444c-3p NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[4656,4675] -12.80 CAATCCTAGACACAGGTGCA
TGCAGTTGTTGCTCAAGCTT(((((((.(((()))).)))..)))).....
12 20 0.261000
sof-miR159a NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[5067,5085] -12.30 AAGAGTTTATATCTCCAAA
TTTGATTGAAGGGAGCTCTG .(((((((...(((((())))))).)))..))))).
15 19 0.277000
sof-miR159b NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[5067,5085] -12.30 AAGAGTTTATATCTCCAAA
TTTGATTGAAGGGAGCTCTG .(((((((...(((((())))))).)))..))))).
15 19 0.277000
sof-miR159d NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[5067,5085] -12.30 AAGAGTTTATATCTCCAAA

```

TTTGATTGAAGGGAGCTCTG .(((((((...(((((((
15 19 0.277000
sof-miR159e NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[5067,5085] -13.20 AAGAGTTTATATCTCCAAA
TTTGATTGAAAGGAGCTCTT ((((((((((...(((((((
16 19 0.277000
sof-miR168a NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[5137,5159] -14.30 GCACTGGGAGAAAAACCAAGTGG
TCGCTTGGTGCAGATCGGGAC (..(((((((...(((((((
)))))))))...)))))..) 14 23 0.129000
sof-miR159e NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[5284,5302] -12.40 TAGACCCTCACAATCTAAA
TTTGATTGAAAGGAGCTCTT .(((((((...(((((((
16 19 0.007820
sof-miR168a NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[5506,5525] -17.70 GAGTGGATTTCACCAGGTGG
TCGCTTGGTGCAGATCGGGAC ...(((((((...(((((((
)))))))))...)))))..) 16 20 0.311000
sof-miR168b NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[5506,5525] -13.70 GAGTGGATTTCACCAGGTGG
TCGCTTGGGAGATCGGGAC ...(((((((...(((((((
)))))))))...)))))..) 14 20 0.311000
ssp-miR169 NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[6389,6409] -13.30 CCTTCAAGGGTTAGATGGCTA
TAGCCAAGGATGACTTGCCGG (..(((((((...(((((((
)))))))))...)))))..) 15 21 0.149000
sof-miR408e NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[6985,7003] -12.60 AGCAGTGACGTCAATGCGG
CTGCACTGACTCTCCCTGGC ..(((((((...(((((((
)))))))))...)))))..) 14 19 0.056700
sof-miR168a NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[7012,7030] -12.30 GACCCGAACCACTAGATGG
TCGCTTGGTGCAGATCGGGAC ..(((((((...(((((((
)))))))))...)))))..) 14 19 0.186000
sof-miR168a NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[7050,7068] -17.10 GTTACGAGATGCCAAGTGA
TCGCTTGGTGCAGATCGGGAC (..(((((((...(((((((
)))))))))...)))))..) 15 19 0.347000
sof-miR168b NC_038382.1 Sugarcane bacilliform Guadeloupe A virus
clone target from/to=[7050,7068] -19.40 GTTACGAGATGCCAAGTGA
TCGCTTGGGAGATCGGGAC (..(((((((...(((((((
)))))))))...)))))..) 15 19 0.347000

```

Sugarcane bacilliform Guadeloupe A virus
NCBI Reference Sequence: NC_038382.1

```

dataset: 1
target: NC_038382.1
length: 7444
miRNA : sof-miR156
length: 20
mfe: -23.2 kcal/mol

```


p-value: undefined
position 7104
target 5' C GUG UG UAGCUUUUAUCC U 3'
UGC C UCUCU UUUGUC
ACG G AGAGA AGACAG
miRNA 3' C A UG U 5'

dataset: 1
target: NC_038382.1
length: 7444
miRNA : sof-miR159a
length: 21
mfe: -25.4 kcal/mol
p-value: undefined
position 1659
target 5' G ACA A AUGGUUGUAG C 3'
GGAGC CCCU UCA AUCCAAA
UCUCG GGA AGU UAGGUUU
miRNA 3' G A 5'

dataset: 1
target: NC_038382.1
length: 7444
miRNA : sof-miR159b
length: 21
mfe: -25.4 kcal/mol
p-value: undefined
position 1659
target 5' G ACA A AUGGUUGUAG C 3'
GGAGC CCCU UCA AUCCAAA
UCUCG GGA AGU UAGGUUU
miRNA 3' G A 5'

dataset: 1
target: NC_038382.1
length: 7444
miRNA : sof-miR159c
length: 21
mfe: -28.0 kcal/mol
p-value: undefined

position 6896
target 5' C CGG AUA C 3'
AGGAGC CC GAUCCAGG
UCCUCG GG UUAGGUUC
miRNA 3' A GAAG 5'

dataset: 1
target: NC_038382.1
length: 7444
miRNA : sof-miR159d

length: 21
mfe: -25.4 kcal/mol
p-value: undefined
position 1659
target 5' G ACA A AUGGUUGUAG C 3'
GGAGC CCCU UCA AUCCAAA
UCUCG GGG A AGU UAGGUUU
miRNA 3' G A 5'

dataset: 1
target: NC_038382.1
length: 7444
miRNA : sof-miR159e
length: 21
mfe: -25.5 kcal/mol
p-value: undefined
position 733
target 5' C U GCA C 3'
GAGA CUCCUUUU GAUCCGG
UUCU GAGGAAAG UUAGGUU
miRNA 3' C U 5'

dataset: 1
target: NC_038382.1
length: 7444
miRNA : sof-miR167a
length: 21
mfe: -26.6 kcal/mol
p-value: undefined
position 1304
target 5' G ACCUC A C 3'
GGGUCA G CUGGUAGUUUC
UCUAGU C GACCGUCGAAG
miRNA 3' G A U 5'

dataset: 1
target: NC_038382.1
length: 7444
miRNA : sof-miR167b
length: 21

mfe: -26.6 kcal/mol
p-value: undefined
position 1304
target 5' G ACCUC A C 3'
GGGUCA G CUGGUAGUUUC
UCUAGU C GACCGUCGAAG
miRNA 3' G A U 5'

dataset: 1
target: NC_038382.1
length: 7444

miRNA : sof-miR168a
length: 21
mfe: -25.6 kcal/mol
p-value: undefined

position 6084
target 5' U AGA U UCCUGAGA A 3'
 UCCUGAUCU GC ACC AAGC
 AGGGCUAGA CG UGG UUCG
miRNA 3' C CU 5'

dataset: 1
target: NC_038382.1
length: 7444
miRNA : sof-miR168b
length: 20
mfe: -25.6 kcal/mol
p-value: undefined
position 6937

target 5' A UU UGACG A 3'
 U GAUCUGCU UAAGC
 G CUAGACGG GUUCG
miRNA 3' CA GG CU 5'

dataset: 1
target: NC_038382.1
length: 7444
miRNA : sof-miR396
length: 21
mfe: -24.9 kcal/mol
p-value: undefined

position 3394
target 5' A A UGAU A 3'
 GG UUAGG GCUGUGGAG
 UC AGUUC CGACACCUU
miRNA 3' G A UUU 5'

psRNATargt-SCBGAV-

miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end	Target_start	Target_end	miRNA_aligned_fragment	Target_Desc.
sof-miR396	NC_038382.1	5.5	-1.0	1	21	5732	5752	UUCCACAGCUUUCUUGAACUG CAUUUGAAGAAUUUAUGGAA	Cleavage Sugarcane
sof-miR159a	NC_038382.1	6.0	-1.0	1	21	3779	3799	UUUGGAUUGAAGGGAGCUCUG CUGGACUCUCUUGAAUUGAA	Cleavage Sugarcane

sof-miR159b	NC_038382.1	6.0	-1.0	1	21	3779	3799	
	UUUGGAUUGAAGGGAGCUCUG	CUGGACUCUCUUGAAUUAGAA	Cleavage	Sugarcane				
bacilliform Guadeloupe A virus		2						
sof-miR159d	NC_038382.1	6.0	-1.0	1	21	3779	3799	
	UUUGGAUUGAAGGGAGCUCUG	CUGGACUCUCUUGAAUUAGAA	Cleavage	Sugarcane				
bacilliform Guadeloupe A virus		2						
sof-miR156	NC_038382.1	6.5	-1.0	1	20	3309	3328	
	UGACAGAAGAGAGUGAGCAC	AUGAUUACUCCAUUUGUCC	Translation					
Sugarcane bacilliform Guadeloupe A virus		1						
sof-miR159e	NC_038382.1	6.5	-1.0	1	21	5282	5302	
	UUUGGAUUGAAGGGAGCUCUU	AUUAGACCCUCACAAUCUAAA	Translation					
Sugarcane bacilliform Guadeloupe A virus		3						
sof-miR159a	NC_038382.1	7.0	-1.0	1	21	5282	5302	
	UUUGGAUUGAAGGGAGCUCUG	AUUAGACCCUCACAAUCUAAA	Translation					
Sugarcane bacilliform Guadeloupe A virus		2						
sof-miR159b	NC_038382.1	7.0	-1.0	1	21	5282	5302	
	UUUGGAUUGAAGGGAGCUCUG	AUUAGACCCUCACAAUCUAAA	Translation					
Sugarcane bacilliform Guadeloupe A virus		2						
sof-miR159c	NC_038382.1	7.0	-1.0	1	21	3779	3799	
	CUUGGAUUGAAGGGAGCUCU	CUGGACUCUCUUGAAUUAGAA	Cleavage	Sugarcane				
bacilliform Guadeloupe A virus		1						
sof-miR159d	NC_038382.1	7.0	-1.0	1	21	5282	5302	
	UUUGGAUUGAAGGGAGCUCUG	AUUAGACCCUCACAAUCUAAA	Translation					
Sugarcane bacilliform Guadeloupe A virus		2						
sof-miR159e	NC_038382.1	7.0	-1.0	1	21	6318	6338	
	UUUGGAUUGAAGGGAGCUCUU	AGAAGGAACUUGUGAUCCGAA	Translation					
Sugarcane bacilliform Guadeloupe A virus		3						
sof-miR167a	NC_038382.1	7.0	-1.0	1	21	5846	5865	
	UGAAGCUGCCAGCAUGAUCUG	AAAAUCAAGUUG-CAGCCUCA	Cleavage	Sugarcane				
bacilliform Guadeloupe A virus		1						
sof-miR167b	NC_038382.1	7.0	-1.0	1	21	5846	5865	
	UGAAGCUGCCAGCAUGAUCUG	AAAAUCAAGUUG-CAGCCUCA	Cleavage	Sugarcane				
bacilliform Guadeloupe A virus		1						
sof-miR159e	NC_038382.1	7.5	-1.0	1	21	5590	5610	
	UUUGGAUUGAAGGGAGCUCUU	AGUAAUGCCAUUUGGUCUGAA	Cleavage	Sugarcane				
bacilliform Guadeloupe A virus		3						
sof-miR396	NC_038382.1	7.5	-1.0	1	21	3394	3415	UUCCACAGC-
	UUUCUUGAACUG	AGGAUUAGGUGAUGCUGUGGAG	Cleavage	Sugarcane				
bacilliform Guadeloupe A virus		2						
ssp-miR396	NC_038382.1	5.5	-1.0	1	21	5732	5752	
	UUCCACAGCUUUCUUGAACUG	CAUUUGAAGAAUUUAUGGAA	Cleavage	Sugarcane				
bacilliform Guadeloupe A virus		2						
ssp-miR444a	NC_038382.1	5.5	-1.0	1	21	80	100	
	UGCAGUUGUUGCCUCAAGCUU	UGAUUUGGGUUAUAGCUGUA	Cleavage	Sugarcane				
bacilliform Guadeloupe A virus		3						
ssp-miR444b.2	NC_038382.1	5.5	-1.0	1	21	80	100	
	UGCAGUUGUUGCCUCAAGCUU	UGAUUUGGGUUAUAGCUGUA	Cleavage	Sugarcane				
bacilliform Guadeloupe A virus		3						
ssp-miR444c-3p	NC_038382.1	5.5	-1.0	1	21	80	100	
	UGCAGUUGUUGUCUCAAGCUU	UGAUUUGGGUUAUAGCUGUA	Cleavage	Sugarcane				
bacilliform Guadeloupe A virus		3						

ssp-miR159a	NC_038382.1	6.0	-1.0	1	21	3779	3799
	UUUGGAUUGAAGGGAGCUCUG						
	CUGGACUCUCUUGAAUUAGAA					Cleavage	Sugarcane
bacilliform Guadeloupe A virus		2					
ssp-miR444b.1	NC_038382.1	6.0	-1.0	1	21	756	776
	UUGUGGCUUUCUUGCAAGUUG						
	GCAAGAGCAAGAAAGUCAGAA					Cleavage	Sugarcane
bacilliform Guadeloupe A virus		13					
ssp-miR156	NC_038382.1	6.5	-1.0	1	21	3308	3328
	UGACAGAAGAGAGUGAGCACA						
	AAUGAUUACUCCAUIUGUCC					Translation	
	Sugarcane bacilliform Guadeloupe A virus	1					
ssp-miR166	NC_038382.1	6.5	-1.0	1	21	981	1001
	UCGGACCAGGCUUCAUCCCC						
	GCAGACUGAGGCUUUGACUGA					Cleavage	Sugarcane
bacilliform Guadeloupe A virus		1					
ssp-miR444b.1	NC_038382.1	6.5	-1.0	1	21	2615	2634
	UUGUGGCUUUCUUGCAAGUUG						
	CAAUUU-UUGGAAAGCCUCA					Cleavage	Sugarcane
bacilliform Guadeloupe A virus		13					
ssp-miR444b.1	NC_038382.1	6.5	-1.0	1	21	5009	5028
	UUGUGGCUUUCUUGCAAGUUG						
	GAACU-GCAAGAGUACUAUAA					Cleavage	Sugarcane
bacilliform Guadeloupe A virus		13					
ssp-miR444b.1	NC_038382.1	6.5	-1.0	1	21	5731	5750
	UUGUGGCUUUCUUGCAAGUUG						
	GCAUUUG-AAGAAUUUAUGG					Cleavage	Sugarcane
bacilliform Guadeloupe A virus		13					
ssp-miR444b.1	NC_038382.1	6.5	-1.0	1	21	4471	4490
	UUGUGGCUUUCUUGCAAGUUG						
	GUAUUUG-AACAAAUCACAG					Translation	
	Sugarcane bacilliform Guadeloupe A virus	13					
ssp-miR444c-3p	NC_038382.1	6.5	-1.0	1	21	4940	4959
	UGCAGUUGUUGUCUCAAGCUU						
	AAGAUUAUGACAACAG-UGCA					Cleavage	Sugarcane
bacilliform Guadeloupe A virus		3					
ssp-miR528	NC_038382.1	6.5	-1.0	1	21	2897	2917
	UGGAAGGGGCAUGCAGAGGAG						
	GAGUUCUACAUGUUACCUCCA					Cleavage	Sugarcane
bacilliform Guadeloupe A virus		1					
ssp-miR444a	NC_038382.1	6.75	-1.0	1	21	775	797
	UGCAGUUGUUGC--CUCAAGCUU						
	AAGCGUGAGCUGCAAGAAUUGCA					Cleavage	
	Sugarcane bacilliform Guadeloupe A virus	3					
ssp-miR444b.2	NC_038382.1	6.75	-1.0	1	21	775	797
	UGCAGUUGUUGC--CUCAAGCUU						
	AAGCGUGAGCUGCAAGAAUUGCA					Cleavage	
	Sugarcane bacilliform Guadeloupe A virus	3					
ssp-miR159a	NC_038382.1	7.0	-1.0	1	21	5282	5302
	UUUGGAUUGAAGGGAGCUCUG						
	AUUAGACCCUCACAAUCUAAA					Translation	
	Sugarcane bacilliform Guadeloupe A virus	2					
ssp-miR167b	NC_038382.1	7.0	-1.0	1	21	5846	5865
	UGAAGCUGCCAGCAUGAUCUG						
	AAAAUCAAGUUG-CAGCCUCA					Cleavage	Sugarcane
bacilliform Guadeloupe A virus		1					
ssp-miR444b.1	NC_038382.1	7.0	-1.0	1	21	5249	5269
	UUGUGGCUUUCUUGCAAGUUG						
	AAACAUGUGAAGAAGCUGUUA					Translation	
	Sugarcane bacilliform Guadeloupe A virus	13					
ssp-miR444c-3p	NC_038382.1	7.25	-1.0	1	21	775	797
	UGCAGUUGUUGU--CUCAAGCUU						
	AAGCGUGAGCUGCAAGAAUUGCA					Cleavage	
	Sugarcane bacilliform Guadeloupe A virus	3					
ssp-miR396	NC_038382.1	7.5	-1.0	1	21	3394	3415
	UUUCUUGAACUG						
	AGGAUUAGGUGAUGCUGUGGAG					Cleavage	Sugarcane
bacilliform Guadeloupe A virus		2					

ssp-miR444a	NC_038382.1	7.5	-1.0	1	21	1463	1482
	UGCAGUUGUUGCCUCAAGCUU	GAACUUGAAGUAAUGGC-GCA	Cleavage				Sugarcane
bacilliform	Guadeloupe A virus	3					
ssp-miR444b.1	NC_038382.1	7.5	-1.0	1	21	7034	7056
	UUGUGGCUUUCUUGCA--AGUUG	UAACUAGUGUGACAGGGUUACGA					
	Translation	Sugarcane bacilliform	Guadeloupe A virus	13			
ssp-miR444b.1	NC_038382.1	7.5	-1.0	1	21	3494	3515
	UUGUGGCUUUCUUGCA-AGUUG	GAAUUAUGUGAGAAGGUAGCAU	Cleavage				
	Sugarcane bacilliform	Guadeloupe A virus	13				
ssp-miR444b.1	NC_038382.1	7.5	-1.0	1	21	3968	3988
	UUGUGGCUUUCUUGCAAGUUG	UAUUUGGUAGGAGAACCAUCA	Cleavage				Sugarcane
bacilliform	Guadeloupe A virus	13					
ssp-miR444b.1	NC_038382.1	7.5	-1.0	1	21	7278	7298
	UUGUGGCUUUCUUGCAAGUUG	CUCUAUAUAAGGAGGCCAUGU	Cleavage				Sugarcane
bacilliform	Guadeloupe A virus	13					
ssp-miR444b.1	NC_038382.1	7.5	-1.0	1	21	4045	4065
	UUGUGGCUUUCUUGCAAGUUG	GAGUUUUGAAGAAGCUCUAUGU	Cleavage				Sugarcane
bacilliform	Guadeloupe A virus	13					
ssp-miR444b.1	NC_038382.1	7.5	-1.0	1	21	6099	6119
	UUGUGGCUUUCUUGCAAGUUG	UACCUCUGAGAAAGCAAUCA	Cleavage				Sugarcane
bacilliform	Guadeloupe A virus	13					
ssp-miR444b.1	NC_038382.1	7.5	-1.0	1	21	1193	1212
	UUGUGGCUUUCUUGCAAGUUG	GCAAUUG-AAUACAGCCAUAU	Translation				
	Sugarcane bacilliform	Guadeloupe A virus	13				
ssp-miR444b.2	NC_038382.1	7.5	-1.0	1	21	1463	1482
	UGCAGUUGUUGCCUCAAGCUU	GAACUUGAAGUAAUGGC-GCA	Cleavage				Sugarcane
bacilliform	Guadeloupe A virus	3					
ssp-miR827	NC_038382.1	7.5	-1.0	1	21	5378	5398
	UUAGAUGACCAUCAGCAAACA	GAAAGGCUGGUGUUCAACUAU	Cleavage				Sugarcane
bacilliform	Guadeloupe A virus	1					