

```
=====
miranda v3.3a      microRNA Target Scanning Algorithm
=====
(c) 2003 Memorial Sloan-Kettering Cancer Center, New York
```

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Enright AJ, John B, Gaul U, Tuschl T, Sander C and Marks DS;
(2003) Genome Biology; 5(1):R1.

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Current Settings:

```
=====
Query Filename:    ./seq/mirna/sof_mirna.fasta
Reference Filename: ./seq/gene/sof/KY548506.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:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)
=====
Performing Scan: sof-miR156 vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====
Score for this Scan:
No Hits Found above Threshold
Complete
```

```
Read Sequence:sof-miR159a (21 nt)
Read
Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)
=====
Performing Scan: sof-miR159a vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====
Score for this Scan:
No Hits Found above Threshold
```

Complete

Read Sequence:sof-miR159b (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: sof-miR159b vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:sof-miR159c (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: sof-miR159c vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:sof-miR159d (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: sof-miR159d vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:sof-miR159e (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: sof-miR159e vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:sof-miR167a (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

```
=====
Performing Scan: sof-miR167a vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====
```

Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:sof-miR167b (21 nt)
Read
Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

```
=====
Performing Scan: sof-miR167b vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====
```

Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:sof-miR168a (21 nt)
Read
Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

```
=====
Performing Scan: sof-miR168a vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====
```

Forward: Score: 146.000000 Q:2 to 20 R:547 to 568 Align Len (19)
(68.42%) (84.21%)

Query: 3' caGGGCUAG-ACGUGGUUCGCU 5'
 |:| | |: | |:| | | | |
Ref: 5' aaCTCGCTTGTCATCAAGCGa 3'

Energy: -23.510000 kCal/Mol

Scores for this hit:

>sof-miR168a
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
146.00 -23.51 2 20 547 568 19 68.42% 84.21%

Forward: Score: 140.000000 Q:2 to 19 R:2562 to 2581 Align Len (17)
(64.71%) (88.24%)

Query: 3' cagGGCUAGACGUGGUUCGCU 5'
 ::| | | | | |:| | | | |
Ref: 5' atgTTGATCCG-GCTAAGCGt 3'

Energy: -19.139999 kCal/Mol

Scores for this hit:

```

>sof-miR168a
  KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
  140.00      -19.14      2 19  2562 2581   17   64.71%      88.24%

  Forward: Score: 132.000000  Q:3 to 17  R:1827 to 1845 Align Len (14)
(85.71%) (85.71%)

  Query:      3' cagggCUAGACGUGGUUCGcu 5'
              ||||| | |||||
  Ref:        5' tagtgGATCT-C-CCAAGCac 3'

  Energy:     -15.610000 kCal/Mol

Scores for this hit:
>sof-miR168a
  KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
  132.00      -15.61      3 17  1827 1845   14   85.71%      85.71%

Score for this Scan:
Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max
Energy,Strand,Len1,Len2,Positions
>>sof-miR168a
  KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
  418.00      -58.26      146.00      -23.51      9      21   9575   547
2562 1827
Complete

Read Sequence:sof-miR168b (20 nt)
Read
Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)
=====
Performing Scan: sof-miR168b vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====

  Forward: Score: 145.000000  Q:2 to 18  R:2562 to 2581 Align Len (16)
(68.75%) (87.50%)

  Query:      3' cagGGCUAGACGGGUUCGcu 5'
              ::||| | |:|||
  Ref:        5' atgTTGATCCGGCTAAGCGt 3'

  Energy:     -20.400000 kCal/Mol

Scores for this hit:
>sof-miR168b
  KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
  145.00      -20.40      2 18  2562 2581   16   68.75%      87.50%

  Forward: Score: 141.000000  Q:3 to 16  R:1827 to 1845 Align Len (13)
(92.31%) (92.31%)

```

Query: 3' cagggCUAGACGGGUUCGcu 5'
 ||||| |||||
 Ref: 5' tagtgGATCT-CCCAAGCac 3'
 Energy: -19.320000 kCal/Mol

Scores for this hit:

>sof-miR168b
 KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
 141.00 -19.32 3 16 1827 1845 13 92.31% 92.31%

Forward: Score: 132.000000 Q:2 to 19 R:547 to 568 Align Len (19)
 (63.16%) (78.95%)

Query: 3' caGGGCUAG-ACG-GGUUCGcu 5'
 |:|| |:| :|||
 Ref: 5' aaCTCGCTTGTCCATCAAGCGa 3'
 Energy: -22.570000 kCal/Mol

Scores for this hit:

>sof-miR168b
 KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
 132.00 -22.57 2 19 547 568 19 63.16% 78.95%

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max
 Energy,Strand,Len1,Len2,Positions
 >>sof-miR168b

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
 418.00 -62.29 145.00 -22.57 10 20 9575
 2562 1827 547
 Complete

Read Sequence:sof-miR396 (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
 (9575 nt)

=====

Performing Scan: sof-miR396 vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Forward: Score: 142.000000 Q:2 to 16 R:3634 to 3655 Align Len (15)
 (73.33%) (93.33%)

Query: 3' gucaagUUCUUUC-GACACCUu 5'
 ::||| :|||
 Ref: 5' gctcggGGGAAAGTTTGTGGa 3'
 Energy: -20.270000 kCal/Mol

Scores for this hit:

```
>sof-miR396 KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
      142.00      -20.27      2 16 3634 3655 15 73.33% 93.33%
```

Score for this Scan:

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

>>sof-miR396

```
      KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
      142.00      -20.27      142.00      -20.27      11 21 9575
```

3634

Complete

Read Sequence:sof-miR408a (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: sof-miR408a vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Forward: Score: 130.000000 Q:2 to 20 R:139 to 161 Align Len (20)
(75.00%) (80.00%)

Query: 3' cgGUCCCUUCU-CCGU-CACGUc 5'

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

Ref: 5' ttCCGGCGAGATGGCAGGTGCA 3'

Energy: -23.270000 kCal/Mol

Scores for this hit:

>sof-miR408a

```
      KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
      130.00      -23.27      2 20 139 161 20 75.00% 80.00%
```

Score for this Scan:

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

>>sof-miR408a

```
      KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
      130.00      -23.27      130.00      -23.27      12 21 9575 139
```

Complete

Read Sequence:sof-miR408b (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: sof-miR408b vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Forward: Score: 130.000000 Q:2 to 20 R:139 to 161 Align Len (20)
(75.00%) (80.00%)

Query: 3' cgGUCCCUUCU-CCGU-CACGUc 5'
| || :||| |||| |||||

Ref: 5' ttCCGGCGAGATGGCAGGTGCAt 3'

Energy: -23.270000 kCal/Mol

Scores for this hit:

>sof-miR408b

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
130.00 -23.27 2 20 139 161 20 75.00% 80.00%

Score for this Scan:

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

>>sof-miR408b

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
130.00 -23.27 130.00 -23.27 13 21 9575 139

Complete

Read Sequence:sof-miR408c (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: sof-miR408c vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Forward: Score: 130.000000 Q:2 to 20 R:139 to 161 Align Len (20)
(75.00%) (80.00%)

Query: 3' cgGUCCCUUCU-CCGU-CACGUc 5'
| || :||| |||| |||||

Ref: 5' ttCCGGCGAGATGGCAGGTGCAt 3'

Energy: -23.270000 kCal/Mol

Scores for this hit:

>sof-miR408c

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
130.00 -23.27 2 20 139 161 20 75.00% 80.00%

Score for this Scan:

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

>>sof-miR408c

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
130.00 -23.27 130.00 -23.27 14 21 9575 139

Complete

Read Sequence:sof-miR408d (21 nt)

Read
Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: sof-miR408d vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Forward: Score: 130.000000 Q:2 to 20 R:139 to 161 Align Len (20)
(75.00%) (80.00%)

Query: 3' cgGUCCCUUCU-CCGU-CACGUc 5'

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

Ref: 5' ttCCGGCGAGATGGCAGGTGCA 3'

Energy: -23.270000 kCal/Mol

Scores for this hit:

>sof-miR408d

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
130.00 -23.27 2 20 139 161 20 75.00% 80.00%

Score for this Scan:

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

>>sof-miR408d

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
130.00 -23.27 130.00 -23.27 15 21 9575 139

Complete

Read Sequence:sof-miR408e (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: sof-miR408e vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:ssp-miR166 (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: ssp-miR166 vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Forward: Score: 146.000000 Q:2 to 20 R:4178 to 4199 Align Len (19)
(68.42%) (84.21%)

Query: 3' ccCCUU-ACUUCGGACCAGGCu 5'
 |||| |::| |||||:|
Ref: 5' atGGAACCTGGGACTGGTTCGa 3'

Energy: -22.320000 kCal/Mol

Scores for this hit:

>ssp-miR166 KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
146.00 -22.32 2 20 4178 4199 19 68.42% 84.21%

Score for this Scan:

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

>>ssp-miR166
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
146.00 -22.32 146.00 -22.32 17 21 9575

4178

Complete

Read Sequence:ssp-miR169 (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: ssp-miR169 vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Forward:Score: 133.000000 Q:2 to 16 R:7798 to 7817 Align Len (14)
(71.43%) (85.71%)

Query: 3' ggccguUCAGUAGGAACCGAu 5'
 :|| || :|||||
Ref: 5' actaatGGTAAT-TTTGGCTt 3'

Energy: -15.520000 kCal/Mol

Scores for this hit:

>ssp-miR169 KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
133.00 -15.52 2 16 7798 7817 14 71.43% 85.71%

Score for this Scan:

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

>>ssp-miR169
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
133.00 -15.52 133.00 -15.52 18 21 9575

7798

Complete

Read Sequence:ssp-miR437a (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

```
=====
Performing Scan: ssp-miR437a vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====
Score for this Scan:
No Hits Found above Threshold
Complete
```

```
Read Sequence:ssp-miR437b (21 nt)
Read
Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)
```

```
=====
Performing Scan: ssp-miR437b vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====
Score for this Scan:
No Hits Found above Threshold
Complete
```

```
Read Sequence:ssp-miR437c (21 nt)
Read
Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)
```

```
=====
Performing Scan: ssp-miR437c vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====
Score for this Scan:
No Hits Found above Threshold
Complete
```

```
Read Sequence:ssp-miR528 (21 nt)
Read
Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)
```

```
=====
Performing Scan: ssp-miR528 vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====
```

```
Forward: Score: 146.000000 Q:2 to 19 R:6376 to 6393 Align Len (17)
(70.59%) (76.47%)
```

```
Query:      3' gagGAGACGUACGGGAAGGu 5'
           ||:| ||  |||||
Ref:        5' ggaCTTTCCA--CCCTTCCc 3'
```

```
Energy: -15.820000 kCal/Mol
```

```
Scores for this hit:
>ssp-miR528 KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
146.00      -15.82      2 19 6376 6393 17 70.59% 76.47%
```

Score for this Scan:

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

>>ssp-miR528

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

146.00 -15.82 146.00 -15.82 22 21 9575

6376

Complete

Read Sequence:ssp-miR827 (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: ssp-miR827 vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:ssp-miR444a (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: ssp-miR444a vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Forward: Score: 132.000000 Q:2 to 13 R:8501 to 8521 Align Len (11)
(72.73%) (90.91%)

Query: 3' uucgaacucCGUUGUUGACGu 5'

| | : | | : | | | |

Ref: 5' ccggcaaccGGAGCAGCTGCa 3'

Energy: -18.420000 kCal/Mol

Scores for this hit:

>ssp-miR444a

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

132.00 -18.42 2 13 8501 8521 11 72.73% 90.91%

Score for this Scan:

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

>>ssp-miR444a

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

132.00 -18.42 132.00 -18.42 24 21 9575

8501

Complete

Read Sequence:ssp-miR444b (21 nt)

Read
Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: ssp-miR444b vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====

Forward: Score: 132.000000 Q:2 to 13 R:8501 to 8521 Align Len (11)
(72.73%) (90.91%)

Query: 3' uucgaacucCGUUGUUGACGu 5'
 | |:|:|:|

Ref: 5' ccggcaaccGGAGCAGCTGCa 3'

Energy: -18.420000 kCal/Mol

Scores for this hit:

>ssp-miR444b
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
132.00 -18.42 2 13 8501 8521 11 72.73% 90.91%

Score for this Scan:

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

>>ssp-miR444b
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
132.00 -18.42 132.00 -18.42 25 21 9575
8501
Complete

Read Sequence:ssp-miR444c-3p (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: ssp-miR444c-3p vs
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
=====

Forward: Score: 130.000000 Q:2 to 11 R:8501 to 8521 Align Len (9)
(77.78%) (100.00%)

Query: 3' uucgaacucugUUGUUGACGu 5'
 | |:|:|:|

Ref: 5' ccggcaaccggAGCAGCTGCa 3'

Energy: -18.420000 kCal/Mol

Scores for this hit:

>ssp-miR444c-3p
KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
130.00 -18.42 2 11 8501 8521 9 77.78% 100.00%

Forward: Score: 130.000000 Q:3 to 16 R:9268 to 9289 Align Len (14)
(85.71%) (92.86%)

Query: 3' uucgaaCUCUGU-UGUUGACgu 5'

||||| |||:|

Ref: 5' tacagaGAGACACACAGCTGgc 3'

Energy: -19.360001 kCal/Mol

Scores for this hit:

>ssp-miR444c-3p

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
130.00 -19.36 3 16 9268 9289 14 85.71% 92.86%

Score for this Scan:

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

>>ssp-miR444c-3p

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
260.00 -37.78 130.00 -19.36 26 21 9575

8501 9268

Complete

Read Sequence:ssp-miR1128 (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: ssp-miR1128 vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:ssp-miR1432 (21 nt)

Read

Sequence:KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward
(9575 nt)

=====

Performing Scan: ssp-miR1432 vs

KY548506.2.1|KY548506.2.1assembly=CEL116|chr=X|strand=forward

=====

Forward: Score: 133.000000 Q:2 to 20 R:7523 to 7546 Align Len (21)
(66.67%) (71.43%)

Query: 3' caGCC-ACAGUAG--AAAGGACUc 5'

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

Ref: 5' ggCGGTTGGAATCGACTTCTTGAg 3'

Energy: -22.320000 kCal/Mol

Scores for this hit:

>ssp-miR1432

KY548506.2.1 KY548506.2.1assembly=CEL116 chr=X strand=forward							
133.00	-22.32	2	20	7523	7546	21	66.67% 71.43%

Score for this Scan:

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

Energy,Strand,Len1,Len2,Positions

>>ssp-miR1432

KY548506.2.1 KY548506.2.1assembly=CEL116 chr=X strand=forward							
133.00	-22.32	133.00	-22.32	28	21	9575	

7523

Complete

Scan Complete

RNA22 v2 results

Maximum folding energy was set -14Kcal/mol

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

miR Name	transcript name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
sof_miR168a	KY548506.1 Sugarcane mosaic virus	846	-14.20	ATTCAGATC--CAC-AAGCGA : CAGGGCTAGACGTGGTTCGCT	3.2E-1
sof_miR168b	KY548506.1 Sugarcane mosaic virus	846	-14.60	ATTCAGATC--CACAAGCGA : CAGGGCTAGACGGGTTCGCT	3.2E-1
sof_miR168a	KY548506.1 Sugarcane mosaic virus	1296	-18.70	CTCCTGAGGACGCAATGAAAGCGA : CAGGGCT-AGACGT--GGTTCGCT	1.24E-1
ssp_miR1432	KY548506.1 Sugarcane mosaic virus	1315	-15.40	AGCGAGTGTC-TCTTTGTTGGA : CAGC-CACAGTAGAAAGGACTC	1.24E-1
sof_miR159c	KY548506.1 Sugarcane mosaic virus	3730	-17.80	AGGAGC-C--GTTGGTTCAGG : : TCCTCGAGGGAAGTTAGGTTC	7.65E-2
sof_miR159c	KY548506.1 Sugarcane mosaic virus	3847	-18.00	AGGTCCACCTTTCAATGTAAG : : : : TCCTCGAGGGAAGTTAGGTTC	5.35E-2
ssp_miR444a	KY548506.1 Sugarcane mosaic virus	5311	-14.20	AGGC-ACAGGCATGCAATTCCA : : : TTCGAACTCCGT-TGTTGACGT	8.17E-3
ssp_miR444b	KY548506.1 Sugarcane mosaic virus	5311	-14.20	AGGC-ACAGGCATGCAATTCCA : : : TTCGAACTCCGT-TGTTGACGT	8.17E-3
sof_miR408a	KY548506.1 Sugarcane mosaic virus	5538	-15.30	ACCAAGGAAAGAACAAGCGCAG CGGTCCCTT-CTCCGTCACGTC	1.57E-1
sof_miR408b	KY548506.1 Sugarcane mosaic virus	5538	-15.30	ACCAAGGAAAGAACAAGCGCAG CGGTCCCTT-CTCCGTCACGTC	1.57E-1
sof_miR408c	KY548506.1 Sugarcane mosaic virus	5538	-15.30	ACCAAGGAAAGAACAAGCGCAG CGGTCCCTT-CTCCGTCACGTC	1.57E-1

miR Name	transcript name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
sof_miR408d	KY548506.1 Sugarcane mosaic virus	5538	-15.30	ACCAAGGAAAGAACAAGCGCAG CGGTCCCTT-CTCCGTCACGTC	1.57E-1
sof_miR408e	KY548506.1 Sugarcane mosaic virus	5538	-15.30	ACCAAGGAAAGAACAAGCGCAG CGGTCCCTT-CTCAGTCACGTC	1.57E-1
ssp_miR444c_3p	KY548506.1 Sugarcane mosaic virus	5552	-18.50	AAGCGCAGTAGACAGAAGCTGCG : : : TTCG-AAC-TCTGTTGTTGACGT	1.57E-1
sof_miR396	KY548506.1 Sugarcane mosaic virus	6821	-14.20	AGTGTCTGA-AGAGCAATGTGGAA : : GTCAAGTTCTTTTCG--ACACCTT	2.21E-1
ssp_miR444a	KY548506.1 Sugarcane mosaic virus	8502	-18.00	CGGCAACCGG-AGCAGCTGCA : : : TTCGAACTCCGTTGTTGACGT	9.19E-2
ssp_miR444b	KY548506.1 Sugarcane mosaic virus	8502	-18.00	CGGCAACCGG-AGCAGCTGCA : : : TTCGAACTCCGTTGTTGACGT	9.19E-2
ssp_miR444c_3p	KY548506.1 Sugarcane mosaic virus	9181	-14.30	CCACATGCAGATGAAGGCTGCA : TTCGAAC-TCTGTTGTTGACGT	3.07E-1
sof_miR167a	KY548506.1 Sugarcane mosaic virus	9520	-14.10	CGGA- CAGCGCTGAGGATGGCTTTG : : : : : GTCTAGT-ACGA--CC- GTCGAAGT	2.11E-1
sof_miR167b	KY548506.1 Sugarcane mosaic virus	9520	-14.10	CGGA- CAGCGCTGAGGATGGCTTTG : : : : : GTCTAGT-ACGA--CC- GTCGAAGT	2.11E-1

Tapirhybrid

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

```
target      KY548506.1  
miRNA       sof-miR159c  
score       7  
mfe_ratio   0.58  
start       3847  
seed_gap    0  
seed_mismatch 1  
seed_gu     2  
gap         0  
mismatch    3  
gu          0  
miRNA_3'    UCCUCGAGGGAAGUUAGGUUC  
aln         |||.|.|||o|||||.o|||  
target_5'   AGGUCCACCUUUCAAUGUAAG  
//
```

```
target      KY548506.1  
miRNA       sof-miR159e  
score       8  
mfe_ratio   0.46  
start       1159  
seed_gap    0  
seed_mismatch 2  
seed_gu     0  
gap         0  
mismatch    4  
gu          0  
miRNA_3'    UUCUCGAGGAAAGUUAGGUUU  
aln         ||.|||.|.|||.|||||.||  
target_5'   AAAAGACCGUUGCAAUCCUAA  
//
```

```
target      KY548506.1  
miRNA       sof-miR168b  
score       9  
mfe_ratio   0.46  
start       406  
seed_gap    0  
seed_mismatch 2  
seed_gu     1  
gap         0  
mismatch    4  
gu          0  
miRNA_3'    CAGGGCUAGACGGGUUCGCU  
aln         ..|.|||.|||.|||.|||o||  
target_5'   UCCACGACCUACCAAAGUGA  
//
```

```
target      KY548506.1  
miRNA       ssp-miR437a  
score       8  
mfe_ratio   0.69  
start       4869
```

```

seed_gap      0
seed_mismatch 3
seed_gu       0
gap           1
mismatch      1
gu            0
miRNA_3'      UUCAGUUUGAAGAGAUUGAAA
aln           |||||.|||||..|||||..
target_5'     AAGUC-AACUUCAAUAACUGG
//
target        KY548506.1
miRNA         ssp-miR528
score         8.5
mfe_ratio     0.60
start         122
seed_gap      0
seed_mismatch 3
seed_gu       0
gap           1
mismatch      1
gu            1
miRNA_3'      GAGG-AGACGUACGGGGAAGGU
aln           ||||.||.||||.||..|||||o
target_5'     CUCCUUCGGCAUUCGACUCCG
//
target        KY548506.1
miRNA         ssp-miR444c-3p
score         7.5
mfe_ratio     0.59
start         5583
seed_gap      0
seed_mismatch 2
seed_gu       1
gap           0
mismatch      2
gu            1
miRNA_3'      UUCGAACUCUGUUGUUGACGU
aln           ||||..|||||o|||||.|.lo
target_5'     AAGCACGAGAUAAACAAUACG
//
target        KY548506.1
miRNA         ssp-miR1128
score         8
mfe_ratio     0.66
start         4534
seed_gap      0
seed_mismatch 3
seed_gu       1
gap           1
mismatch      0
gu            0
miRNA_3'      AAACCCUGCCUCCCUCAUCAU
aln           |||||..|||..o|||.l
target_5'     UUUGGGAC-GAGUUGGUAGGA
//

```

#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
sof-miR159a	KY548506.1	5.5	-1.0	1	21	5911	5931	UUUGGAUUGAAGGGAGCUCUG	::: :::	GCAAGCUUUCUUUAUUCAAAA		Cleavage Sugarcane mosaic virus 3	
sof-miR159b	KY548506.1	5.5	-1.0	1	21	5911	5931	UUUGGAUUGAAGGGAGCUCUG	::: :::	GCAAGCUUUCUUUAUUCAAAA		Cleavage Sugarcane mosaic virus 3	
sof-miR159c	KY548506.1	5.5	-1.0	1	21	3847	3867	CUUGGAUUGAAGGGAGCUCCU	::: : ::: :::	AGGUCCACCUUUCAAUGUAAG		Cleavage Sugarcane mosaic virus 2	
sof-miR159d	KY548506.1	5.5	-1.0	1	21	5911	5931	UUUGGAUUGAAGGGAGCUCUG	::: :::	GCAAGCUUUCUUUAUUCAAAA		Cleavage Sugarcane mosaic virus 3	
sof-miR159e	KY548506.1	5.5	-1.0	1	21	3847	3867	UUUGGAUUGAAGGGAGCUCUU	::: : ::: :::	AGGUCCACCUUUCAAUGUAAG		Cleavage Sugarcane mosaic virus 2	
sof-miR168a	KY548506.1	5.5	-1.0	1	21	9129	9149	UCGCUUGGUGCAGAUCCGGGAC	::: ::: :::	CUUUCGAUUUUUACGAAGUGA		Translation Sugarcane mosaic virus 3	
sof-miR156	KY548506.1	6.5	-1.0	1	20	5909	5928	UGACAGAAGAGAGUGAGCAC	::: ::: :::	UUGCAAGCUUUCUUUAUUCA		Cleavage Sugarcane mosaic virus 1	
sof-miR159a	KY548506.1	6.5	-1.0	1	21	1804	1824	UUUGGAUUGAAGGGAGCUCUG	::: ::: ::: :::	AGGAAAUUCCAUGACCCAAA		Translation Sugarcane mosaic virus 3	
sof-miR159b	KY548506.1	6.5	-1.0	1	21	1804	1824	UUUGGAUUGAAGGGAGCUCUG	::: ::: ::: :::	AGGAAAUUCCAUGACCCAAA		Translation Sugarcane mosaic virus 3	
sof-miR159c	KY548506.1	6.5	-1.0	1	21	5911	5931	CUUGGAUUGAAGGGAGCUCCU	::: ::: ::: :::	GCAAGCUUUCUUUAUUCAAAA		Cleavage Sugarcane mosaic virus 2	
sof-miR159d	KY548506.1	6.5	-1.0	1	21	1804	1824	UUUGGAUUGAAGGGAGCUCUG	::: ::: ::: :::	AGGAAAUUCCAUGACCCAAA		Translation Sugarcane mosaic virus 3	
sof-miR168a	KY548506.1	6.5	-1.0	1	21	2971	2991	UCGCUUGGUGCAGAUCCGGGAC	: .. ::: ::: :::	AUAUUGGUUUGUACCAGACGU		Cleavage Sugarcane mosaic virus 3	
sof-miR168b	KY548506.1	6.5	-1.0	1	20	2562	2581	UCGCUUGGUGCAGAUCCGGGAC	: .. ::: : ::: :::	AUGUUGAUCCGGCUAAGCGU		Translation Sugarcane mosaic virus 1	
sof-miR396	KY548506.1	6.5	-1.0	1	21	7116	7135	UCCACAGCUUUCUUGAACUG	::: ::: ::: :::	CAGUU-GAGAGAGUCGUGAAA		Cleavage Sugarcane mosaic virus 1	
sof-miR159a	KY548506.1	7.0	-1.0	1	21	3847	3867	UUUGGAUUGAAGGGAGCUCUG	: ::: ::: :::	AGGUCCACCUUUCAAUGUAAG		Cleavage Sugarcane mosaic virus 3	
sof-miR159b	KY548506.1	7.0	-1.0	1	21	3847	3867	UUUGGAUUGAAGGGAGCUCUG	: ::: ::: :::	AGGUCCACCUUUCAAUGUAAG		Cleavage Sugarcane mosaic virus 3	

```

sof-miR159d KY548506.1 7.0 -1.0 1 21 3847 3867
    UUUGGAUUGAAGGGAGCUCUG : ::::::::::: .... AGGUCCACCUUCAAUGUAAG
    Cleavage Sugarcane mosaic virus 3
sof-miR159e KY548506.1 7.0 -1.0 1 21 6712 6732
    UUUGGAUUGAAAGGAGCUCUU :::: : :: ::::::::::: AGGAUGGCAUUAAAUCCGAA
    Translation Sugarcane mosaic virus 2
sof-miR167a KY548506.1 7.0 -1.0 1 21 2427 2447
    UGAAGCUGCCAGCAUGAUCUG ::::: :::: :. ::::: AAGGUCUAGCUGCUAUUUUCG
    Cleavage Sugarcane mosaic virus 1
sof-miR167b KY548506.1 7.0 -1.0 1 21 2427 2447
    UGAAGCUGCCAGCAUGAUCUG ::::: :::: :. ::::: AAGGUCUAGCUGCUAUUUUCG
    Cleavage Sugarcane mosaic virus 1
sof-miR168a KY548506.1 7.0 -1.0 1 21 547 568 UCGCUUGGUGCA-
GAUCGGGAC :::: :. : ::::::::::: AACUCGCUUGUCCAUCAAGCGA Translation
    Sugarcane mosaic virus 3
sof-miR408e KY548506.1 7.0 -1.0 1 21 6544 6564
    CUGCACUGACUCUUCCCUGGC :: :. :. ::::: ::::: AACAACGGACGGUCA AUGUGG
    Cleavage Sugarcane mosaic virus 1

```

ssp-miR444c-3p	KY548506.1	5.5	-1.0	1	21	2367	2387
UGCAGUUGUUGUCUCAAGCUU	::::: : ::::::::::					UAGCUUUUAUAAUAAUUGUU	
Cleavage	Sugarcane mosaic virus 6						
ssp-miR166	KY548506.1	6.0	-1.0	1	21	4179	4199
UCGGACCAGGCUUCAUCCCC	:: : : ... ::::::::::					UGGAACUUGGGACUGGUUCGA	
Translation	Sugarcane mosaic virus 1						
ssp-miR444c-3p	KY548506.1	6.0	-1.0	1	21	5583	5603
UGCAGUUGUUGUCUCAAGCUU	:::: : :::::::::: : ::					AAGCACGAGAUAAACAAAUACG	
Cleavage	Sugarcane mosaic virus 6						
ssp-miR444b.1	KY548506.1	6.5	-1.0	1	21	7142	7162
UUGUGGCUUUCUUGCAAGUUG	... :::::::::: : : ::::					CGGGAUGCAGGAAUGCAGCAA	
Cleavage	Sugarcane mosaic virus 4						
ssp-miR444b.1	KY548506.1	6.5	-1.0	1	21	3992	4011
UUGUGGCUUUCUUGCAAGUUG	::::: : : :: :::::					AUAUUUG-ACGAAUGCCACAU	
Cleavage	Sugarcane mosaic virus 4						
ssp-miR444c-3p	KY548506.1	6.5	-1.0	1	21	3441	3460
UGCAGUUGUUGUCUCAAGCUU	::::: : :::::::::: : ::::					GAGUUUU-GACAACACCUGUU	
Cleavage	Sugarcane mosaic virus 6						
ssp-miR1432	KY548506.1	7.0	-1.0	1	21	3980	4000
CUCAGGAAAGAUGACACCGAC	:: : ::::: : : :::::					UACGAUUUCAUCAUAUUUGAC	
Cleavage	Sugarcane mosaic virus 1						
ssp-miR437b	KY548506.1	7.0	-1.0	1	21	727	747
AAAGUUAGACAAGUUUGACAU	: : . : : ::::::::::					AGGCUGUAGUGGUUUGACUUU	
Translation	Sugarcane mosaic virus 1						
ssp-miR437c	KY548506.1	7.0	-1.0	1	21	2981	3001
AAAGUUAGAGAAGUCUGACUU	::::: : ::::: : ::					GUACCAGACGUCUUUAGAUUA	
Cleavage	Sugarcane mosaic virus 1						
ssp-miR444a	KY548506.1	7.0	-1.0	1	21	1058	1077
UGCAGUUGUUGCCUCAAGCUU	::::: : ::::: : ::					GAGUUUGGGGCGA-AGCUAUA	
Cleavage	Sugarcane mosaic virus 3						
ssp-miR444a	KY548506.1	7.0	-1.0	1	21	2367	2387
UGCAGUUGUUGCCUCAAGCUU	::::: : : ::::::::::					UAGCUUUUAUAAUAAUUGUU	
Cleavage	Sugarcane mosaic virus 3						
ssp-miR444a	KY548506.1	7.0	-1.0	1	21	6641	6661
UGCAGUUGUUGCCUCAAGCUU	:::: : ::::: : :: : :					UUCUUUGUGGCGAUGCCUGAA	
Cleavage	Sugarcane mosaic virus 3						
ssp-miR444b.1	KY548506.1	7.0	-1.0	1	21	1058	1078
UUGUGGCUUUCUUGCAAGUUG	::::: . . ::::::::::					GAGUUUGGGGCGAAGCUAUAC	
Translation	Sugarcane mosaic virus 4						
ssp-miR444b.1	KY548506.1	7.0	-1.0	1	21	715	735
UUGUGGCUUUCUUGCAAGUUG	::::: : : ::::::::::					AGGUUUCAAACAAGGCUGUAG	
Translation	Sugarcane mosaic virus 4						
ssp-miR444b.2	KY548506.1	7.0	-1.0	1	21	1058	1077
UGCAGUUGUUGCCUCAAGCUU	::::: : ::::: : ::					GAGUUUGGGGCGA-AGCUAUA	
Cleavage	Sugarcane mosaic virus 3						
ssp-miR444b.2	KY548506.1	7.0	-1.0	1	21	2367	2387
UGCAGUUGUUGCCUCAAGCUU	::::: : : ::::::::::					UAGCUUUUAUAAUAAUUGUU	
Cleavage	Sugarcane mosaic virus 3						
ssp-miR444b.2	KY548506.1	7.0	-1.0	1	21	6641	6661
UGCAGUUGUUGCCUCAAGCUU	:::: : ::::: : :: : :					UUCUUUGUGGCGAUGCCUGAA	
Cleavage	Sugarcane mosaic virus 3						
ssp-miR444c-3p	KY548506.1	7.0	-1.0	1	21	1763	1783
UGCAGUUGUUGUCUCAAGCUU	::::: : : :: ::					UACUCUGAGAUAAUACCUCCA	
Cleavage	Sugarcane mosaic virus 6						

ssp-miR444c-3p	KY548506.1	7.0	-1.0	1	21	7663	7683
	UGCAGUUGUUGUCUCAAGCUU		GGAUUUGGGAGAACGAAUGUU	
	Translation Sugarcane mosaic virus 6						
ssp-miR444c-3p	KY548506.1	7.0	-1.0	1	21	9282	9302
	UGCAGUUGUUGUCUCAAGCUU		:	CAGCUGGCGACGUUAGUCGCA
	Cleavage Sugarcane mosaic virus 6						

Individual hits

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR156
length: 20

mfe: -23.9 kcal/mol
p-value: undefined

position 9402
target 5' G UG GU C 3'
GCUU UCUC UUCUG
CGAG AGAG AAGAC
miRNA 3' CA UG AGU 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR159a
length: 21

mfe: -23.2 kcal/mol
p-value: undefined

position 8953
target 5' A AU AA U 3'
AGAGU UCCUUUAA CCAG
UCUCG AGGGAAGUU GGUU
miRNA 3' G A U 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR159b
length: 21

mfe: -23.2 kcal/mol
p-value: undefined

position 8953
target 5' A AU AA U 3'
AGAGU UCCUUUAA CCAG
UCUCG AGGGAAGUU GGUU
miRNA 3' G A U 5'

dataset: 1
target: KY548506.1
length: 9575

miRNA : sof-miR159c
length: 21

mfe: -25.4 kcal/mol
p-value: undefined

position 1830
target 5' U U AAGCACG CC U 3'
GGA CUCCC UCA UCCAAG
CCU GAGGG AGU AGGUUC
miRNA 3' U C A U 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR159d
length: 21

mfe: -23.2 kcal/mol
p-value: undefined

position 8953
target 5' A AU AA U 3'
AGAGU UUCCUUUAA CCAG
UCUCG AGGGAAGUU GGUU
miRNA 3' G A U 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR159e
length: 21

mfe: -21.6 kcal/mol
p-value: undefined

position 8952
target 5' A AUU AAAA U 3'
AAGAGU UCCUUU CCAG
UUCUCG AGGAAA GGUU
miRNA 3' GUUA U 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR167a
length: 21

mfe: -24.4 kcal/mol
p-value: undefined

position 2699
target 5' G AUUAAACCA AUG A U 3'
UAGAUCA UGC GGCAG UUA
GUCUAGU ACG CCGUC AAGU
miRNA 3' A G 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR167b
length: 21

mfe: -24.4 kcal/mol
p-value: undefined

position 2699
target 5' G AUUAAACCA AUG A U 3'
UAGAUCA UGC GGCAG UUA
GUCUAGU ACG CCGUC AAGU
miRNA 3' A G 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR168a
length: 21

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

position 1296
target 5' C GGAC AUGA G 3'
UCCUGA GCA AAGCGA
AGGGCU CGU UUCGCU
miRNA 3' C AGA GG 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR168b
length: 20

mfe: -27.0 kcal/mol
p-value: undefined

position 1818
target 5' A AAAAAUAGUG A 3'
CCC GAUCU CCCAAGC
GGG CUAGA GGGUUCG
miRNA 3' CA C CU 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR396
length: 21

mfe: -27.6 kcal/mol
p-value: undefined

position 5016
target 5' A U UAC G 3'
UAGUUCAAG AGCUGU GGGA
GUCAAGUUC UCGACA CCUU
miRNA 3' UU 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR408a
length: 21

mfe: -27.3 kcal/mol
p-value: undefined

position 8355
target 5' U UACUU AUUACAAUGA AUGUUGUCCAUCAG G 3'
GCCAGGG GGAGG AG GCAG
CGGUCCC UCUC C UC CGUC
miRNA 3' U G A 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR408b
length: 21

mfe: -27.3 kcal/mol
p-value: undefined

position 8355
target 5' U UACUU AUUACAAUGA AUGUUGUCCAUCAG G 3'
GCCAGGG GGAGG AG GCAG
CGGUCCC UCUC C UC CGUC
miRNA 3' U G A 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : sof-miR408c

length: 21

mfe: -27.3 kcal/mol

p-value: undefined

position 8355

```
target 5' U      UACUU      AUUACAAUGA  AUGUUGUCCAUCAG  G 3'
          GCCAGGG      GGAGG      AG      GCAG
          CGGUCCC      UCUC      UC      CGUC
miRNA  3'      U      G      A      5'
```

dataset: 1

target: KY548506.1

length: 9575

miRNA : sof-miR408d

length: 21

mfe: -27.3 kcal/mol

p-value: undefined

position 8355

```
target 5' U      UACUU      AUUACAAUGA  AUGUUGUCCAUCAG  G 3'
          GCCAGGG      GGAGG      AG      GCAG
          CGGUCCC      UCUC      UC      CGUC
miRNA  3'      U      G      A      5'
```

dataset: 1

target: KY548506.1

length: 9575

miRNA : sof-miR408e

length: 21

mfe: -24.8 kcal/mol

p-value: undefined

position 3633

```
target 5' G  U      A      U      G A 3'
          GC CGGGGGA AGUU GUG A
          CG GUCCCUU UCAG CAC U
miRNA  3'      C      U      G C 5'
```

dataset: 1

target: KY548506.1

length: 9575

miRNA : ssp-miR166

length: 21

mfe: -24.9 kcal/mol

p-value: undefined

position 3714

```
target 5' A      UUUUACUCCGA      GU      A 3'
          GGAGU      GGAGCC  UGGUUC
          CCUUA      CUUCGG  ACCAGG
miRNA  3' CC                                  CU 5'
```

```
dataset: 1
target: KY548506.1
length: 9575
miRNA : ssp-miR169
length: 21
```

```
mfe: -28.0 kcal/mol
p-value: undefined
```

```
position 8458
target 5' U      AA      AC      A 3'
          CCGGCAAGU  CGUU      GGC
          GGCCGUUCA  GUAG      CCG
miRNA  3'                                  GAA  AU 5'
```

```
dataset: 1
target: KY548506.1
length: 9575
miRNA : ssp-miR437a
length: 21
```

```
mfe: -21.2 kcal/mol
p-value: undefined
```

```
position 4868
target 5' A      AA      G 3'
          AAGUC AACUUC  UAACU
          UUCAG UUGAAG  AUUGA
miRNA  3'      U      AG      AA 5'
```

```
dataset: 1
target: KY548506.1
length: 9575
miRNA : ssp-miR437b
length: 21
```

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

```
position 2416
target 5' A      AAUCAAG      G 3'
          GUUAAA      GUCUAGCU
          CAGUUU      CAGAUUGA
miRNA  3' UA      GAA      AA 5'
```

dataset: 1
target: KY548506.1
length: 9575
miRNA : ssp-miR437c
length: 21

mfe: -21.9 kcal/mol
p-value: undefined

position 9395
target 5' A G UUG GUUUCU U 3'
AAGU AGGCU UCUC GCUUU
UUCA UCUGA AGAG UGAAA
miRNA 3' G AU 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : ssp-miR528
length: 21

mfe: -26.5 kcal/mol
p-value: undefined

position 121
target 5' C CG U GA G 3'
CUCCUU GCAU C CUUCCG
GAGGAG CGUA G GAAGGU
miRNA 3' A C GG 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : ssp-miR827
length: 21

mfe: -23.2 kcal/mol
p-value: undefined

position 6338
target 5' A C AGAGAU A 3'
UUGCU GA UGGUCAUC
AACGA CU ACCAGUAG
miRNA 3' ACA AUU 5'

dataset: 1
target: KY548506.1
length: 9575
miRNA : ssp-miR444a
length: 21

```

position 1057
target 5' C          AAGCUAU          GAAU          A 3'
          GAGUUUGGGGGCG          ACAA          CUGCA
          UUCGAACUCCGU          UGUU          GACGU
miRNA 3'

```

```

position 1057
target 5' C          AAGCUAU          GAAU          A 3'
          GAGUUUUGGGGCG          ACAA          CUGCA
          UUCGAACUCCGU          UGUU          GACGU
miRNA 3'

```

```

position 1057
target 5' C          AAGCUAU      GAAU      A 3'
          GAGUUUGGGGCG      ACAA      CUGCA
          UUCGAACUCUGU      UGUU      GACGU

miRNA 3'                                     5'

```

```

position  4533
target 5' G          UU          G  3'

```

```

      UUUGGGAC GAG  GGUAG
      AAACCCUG CUC  UCAUC
miRNA  3'          C   CC      AU 5'
```

```
dataset: 1
target: KY548506.1
length: 9575
miRNA : ssp-miR1432
length: 21
```

```
mfe: -22.2 kcal/mol
p-value: undefined
```

```
position 1316
target 5'  G  A              G  A 3'
          CG GUGUC UCUUU UUGG
          GC CACAG AGAAA GACU
miRNA  3' CA              U    G    C 5'
```
