

## Results for 1: 645,466,4-6,454,931 (-)

Chromosome: 1

Position: 645,466,4-6,454,931 (268 nt)

Strand: -

G+C: 30.60 %

miRNA sequence: UUAGAGAUUUUAGUUGGUU-  
UAAUU

miRNA depth: 44 (weight: 44)

Candidates with the same miRNA: none

miRNA precursor:

```
= GUUAAACUAAAAUUGGCAUUGGUUUAGAGAUUUUAGUUGGUU-
UAAUUCAAUUUACAAAA (((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
CUUGAUGGGUAAUUGGGUAAACCAUUGAAACCAUUAACCAUACAACCUAACUUAUUUU
.....
AUUCAUCAAACCAAUUGACUCAUCAAUUAUUGACUCAUACAACUCAUUUGAGUCAAAAU
.....
UUUCAACUCAUACGGUUUAUGGGUUGAGUUGAAUUGAGUUGACCAAUGAAUUUUGACCC
.....))))).....))))).....))))).....))))).....))))).....))))).....))))).....))
AUUUUGAUACCCCUAAUUGUAGUAUAGC )...)).....))))).....))))).....))))) =
```

Stability of the secondary structure of the precursor: *MFE* -23.95 kcal/mol | *AMFE* -25.11 | *MFEI* -0.82

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 204

### Distribution of reads: one island

miRBase alignment: presence of alignments that cover the miRNA locus

Results for 1: 651,467,7-6,514,930 (+)

Chromosome: 1

**Position: 651,467,7-6,514,930 (254 nt)**

Strand: +

G+C: 16.14 %

miRNA sequence: CUUAUUUACAAUGUCAUGCUACU

miRNA depth: 27 (weight: 27)

Candidates with the same miRNA: none

miRNA precursor:

= GUAUUUUUGUUAAACAAUAUUUUAAAAUAAAGUUUUUGUU-  
UAAAUAUUUGUUCUACU (((.....(((.(((((((.(((((((.(((((((((((.....  
AAACGUUUUUUGUUUAAAUAACAAUCAUGUAUUUGAACUUAUUUACAAUGUCAUGCUA  
.....  
CUGACAUUAAUUAUUUAGGCAUGAAAAUAUUUAAUUAAGAUUUAAAUCUUCUAAAUUCU  
.....  
UGCUUUUAGAGUUAUUUAUACAUUAUUUAAAGAGGCAAAAAAUAUUAUUUUUUUAAAUAU  
.....))))))))))..)))..)))))))))  
UAUUUAUAUAUAUAU ).))).....))) =

Stability of the secondary structure of the precursor: *MFE* -7.12 kcal/mol | *AMFE* -14.80 | *MFEI* -0.92

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 35

Distribution of reads: one island

miRBase alignment: presence of alignments, which do not overlap the miRNA locus

Results for 1: 653,840,0-6,538,487 (-)

Chromosome: 1

Position: 653,840,0-6,538,487 (88 nt)

Strand: -

G+C: 38.64 %

miRNA sequence: AGAUGAUGGGGCUUAGAUGAUGGGC

miRNA depth: 760 (weight: 380)

Candidates with the same miRNA: 1\_\_6543374-6543768-6

miRNA precursor:

= CCCUAGAAACAUCUAGAUGAUGGGGCUUAGAUGAUGGGCCU-  
 UAUA AUGGGCAUCCAUCUUU ((((((.((((... ((((((((((..(((.(((((((((((.....))))..)))))))))  
 AUUCAUAACA UUUUUUUUGUUGUUGGGG )))))).))))).))))).)))))) =  
 This stem-loop structure is the MFE structure.

Stability of the secondary structure of the precursor: *MFE* -25.80 kcal/mol | *AMFE* -29.32 | *MFEI* -0.76

Stability of the miRNA duplex (mirdup): yes

Total number of reads mapped to the precursor: 1210

## Distribution of reads: two islands

miRBase alignment: none

Results for 1: 653,870,3-6,538,797 (+)

Chromosome: 1

Position: 653,870,3-6,538,797 (95 nt)

Strand: +

**G+C: 27.37 %**

miRNA sequence: AUAGAUCGGUAAAAGCAUGUU-  
UUC

miRNA depth: 4 (weight: 4)

Candidates with the same miRNA: none

miRNA precursor:

= GAUCGAUGAUUUAUAGUAUAGAUCGGUAAAAGCAUGUUUUCAAU-  
GAUUCAAUAAAGAAGAG (((.((((((((.((((.((((((((((((((....((.....))))))  
AAUCAUGC UUAUCAUUGUUCUAUAAUACUAUC)).))))))))))))))..)))))))).)))  
= This stem-loop structure is the MFE structure.

Stability of the secondary structure of the precursor: *MFE* -22.00 kcal/mol | *AMFE* -23.16 | *MFEI* -0.85

Stability of the miRNA duplex (mirdup): yes

Total number of reads mapped to the precursor: 11

## Distribution of reads: random

miRBase alignment: none

Results for 1: 654,324,2-6,543,337 (+)

Chromosome: 1

Position: 654,324,2-6,543,337 (96 nt)

Strand: +

G+C: 36.46 %

miRNA sequence:

miRNA depth: (weight: )

Candidates with the same miRNA: none

miRNA precursor:

= GAGUAAUUGUAUGUUGCACUCUUUUUCCCUAAACCAUGGUUUUUC-  
CCAUUGGGUUUUCU (((((( (((((( (((((( (((((( (((((( (((((( (((((( ((((((  
GGUAAGGUUUUAAUGAGGCAGCAUUUCAAAUACU))))))))))))))))))))))))))))))  
= This stem-loop structure is the MFE structure.

Stability of the secondary structure of the precursor: *MFE*  
-30.00 kcal/mol | *AMFE* -31.25 | *MFEI* -0.86

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 24

Distribution of reads: random

miRBase alignment: none

Results for 1: 654,329,1-6,543,423 (+)

Chromosome: 1

Position: 654,329,1-6,543,423 (133 nt)

Strand: +

G+C: 39.10 %

miRNA sequence:

miRNA depth: (weigh: )

Candidates with the same miRNA: none

miRNA precursor:

= UGGGUUUUCCUGGUAAGGUUUUAAUGAGGCAGCAUUU-  
CAAAUACUUUACGAGUUAUGAU ((((((..(((..(((((((((((.(((..((((((((((((((..((..(((((  
ACUAUAAUGGUCAUCAGGGGGAGUGUUAUGAAUAAAGAUGGAUGCCCAUUAUAAGGCCCA  
.(.....))))))..)))))..))))....))..)))))..)))))..)))))..)))))..)))))..)))))  
UCAUCUAAGCCCA )))...)))))) = This stem-loop structure is the MFE  
structure.

Stability of the secondary structure of the precursor: *MFE*  
-36.40 kcal/mol | *AMFE* -27.37 | *MFEI* -0.7

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 261

Distribution of reads: random

miRBase alignment: none

Results for 1: 654,337,4-6,543,768 (-)

Chromosome: 1

Position: 654,337,4-6,543,768 (395 nt)

Strand: -

G+C: 37.97 %

miRNA sequence: AGAUGAUGGGCUUAGAUGAUGGGC

miRNA depth: 760 (weight: 380)

Candidates with the same miRNA: 1\_\_6538400-6538487-1

miRNA precursor:

```
= UGUUUGAACAAAUGUGGAUCCAUAUUGGGCUCAUUGAUGACUAU-
UGGAUUAGGGCCCAU ((((((((((.(((.(((((((((((((((.(((((((((((.
UUGGUUCGCCGUUUGGCACGCUACAGCCACAAAUGACACGUGUAGGAGAGGAAGACGGAG
.....
UUAACGGGGAUGGUCACGGGAUCAUCCAAUGAACGUCAGUUAUUUUAUGACUCAUUUGU
.....
AUUUGGCCACGUCAAAAUAUUUAGCAAAAUCAAAUAUUUUAACUUCUUUUUUGUUAUAA
.....
ACAGAGAAAGAGAUAGAAGAAAUGAGUGUGUUAUCCAUUGAGAUAAAGGGUUCUUUAUA
.....
```

UAGGAGUACAAGGAAAAGGGUAAAACCCUAGAAACAUCUAGAUGAUGGGCUUAGAUGAUG  
 .....)))))  
 GGCCUUAUAAUGGGCAUCCAUCUUUAUUCUAACA )))).)))).).)))).).)))).)))).)))).)))).  
 =

Stability of the secondary structure of the precursor: *MFE*  
 -26.26 kcal/mol | *AMFE* -27.29 | *MFEI* -0.72

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 1376

Distribution of reads: random

miRBase alignment: none

Results for 1: 659,298,4-6,593,131 (+)

Chromosome: 1

Position: 659,298,4-6,593,131 (148 nt)

Strand: +

G+C: 36.49 %

miRNA sequence: AAAGAUAAAGCGGAUUAAACUGUU

miRNA depth: 12 (weight: 12)

Candidates with the same miRNA: none

miRNA precursor:

= GACGGACAAAUCUGUUUAUGUUUGUAGUGUUGAGGACUCAAAAAAAAAAAAACU-  
 CAUUGCU ((((((... (((((((((( (((((((((( (((((((((( (((((((((( ((((((((((  
 GACCAACUACAAACCGCUUUUACAUAACAAUAGAGUUGCUCCGCAAUGGUUUGUUGUCUA  
 ((((((((( .....)))))).)))))))))))))).))  
 CCCUAAAGAUAAAGCGGAUUAAACUGUU ).))) .))))))))))))))...))))) =  
 This stem-loop structure is the MFE structure.



Stability of the secondary structure of the precursor: *MFE*  
-34.20 kcal/mol | *AMFE* -23.11 | *MFEI* -0.63

Stability of the miRNA duplex (mirdup): yes

Total number of reads mapped to the precursor: 22

Distribution of reads: one island

miRBase alignment: none

Results for 4: 50,512,-50,681 (+)

Chromosome: 4

Position: 50,512,-50,681 (170 nt)

Strand: +

G+C: 51.18 %

miRNA sequence:

miRNA depth: (weigh: )

Candidates with the same miRNA: none

miRNA precursor:

```
= GGUGAGCUGGACAAGCUAGGAUGAACUAGCUAGCUAAGUUAGGU-  
GAGCUAAACCAGCUGG ((((((.(((.(((((((((.(((.(((((.(((.(.....  
AAGACUAGCUAGCUCAGCUAGGUGAGCUGACCGACAGCUCGACUGAGCUCGGUGAGCUGA  
.....  
UCGUGUACUGACCCAGCUGGGUGGUCAUUCUAAGUAAGAUCUUGCUUACU  
.....)))))..)))))..)))))..))..))..))))) =
```

Stability of the secondary structure of the precursor: *MFE* -36.38 kcal/mol | *AMFE* -45.29 | *MFEI* -0.89

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 21

## Distribution of reads: random

miRBase alignment: none

Results for 4: 77,043,-77,331 (-)

Chromosome: 4

Position: 77,043,-77,331 (289 nt)

**Strand: -**

G+C: 46.37 %

miRNA sequence:

miRNA depth: (weight: )

Candidates with the same miRNA: none

miRNA precursor:

[illegible]

Stability of the secondary structure of the precursor: *MFE* -59.19 kcal/mol | *AMFE* -35.54 | *MFEI* -0.77

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 213

### Distribution of reads: random

miRBase alignment: none

Results for 4: 77,276,-77,585 (+)

Chromosome: 4

Position: 77,276,-77,585 (310 nt)

Strand: +

G+C: 45.16 %

miRNA sequence:

miRNA depth: (weight: )

Candidates with the same miRNA: none

miRNA precursor:

= AUAAUAGAGUGUGGGUUAUCCAACCUAAAACCAAUUGGCAAUAGGU-  
GAAGAGGCCCAUAUC (((((( ((((((((((((((((((((((... ((((((((((... (((((... ((((((((((...  
UUAUAUAUACCACUUAAGAUCUUAUUC AACUCCGAUGUGGGGAUAUUAUCCCUAAUACGC  
.....  
CCCCUCGAGAUGAUGGUUCUUCUAGCCAUUGAUCUCGAUAUGUUUGGGCAUGGAUCGGCG  
.....  
GGCCAAGUAUUGGGCCGGACCGAUGUGGAUCGGGUUGAGUAUGUGCGGAUCGGGGUCUGA  
.....  
UACCAUAUCAGACUGUGGGCUUCCAACGUAAAACUAAUUGGCAAUAGGUGGAGAGGCUCA  
.....)))))))))..)).)..))))))..))))..).))))))  
UAUCUUAUAU )))))).))) =

Stability of the secondary structure of the precursor: *MFE*  
-43.29 kcal/mol | *AMFE* -36.81 | *MFEI* -0.82

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 103

Distribution of reads: random

miRBase alignment: presence of alignments, which do not  
overlap the miRNA locus

Results for 4: 2,979,01-,298,116 (-)

Chromosome: 4

Position: 2,979,01-,298,116 (216 nt)

Strand: -

G+C: 31.02 %

miRNA sequence:

miRNA depth: (weight: )

Candidates with the same miRNA: none

miRNA precursor:

```
= CAUGUUUUAAAUGGUAGUUAACUCUUAGUUCAUGUUUUAAAUGGC-
CACAUUAAAGUCGA ((((((((.(((((((.(((((((.(((((((.
UGUUUUAAAUGACCACAAUUUAAAACUUGACUAAUAAAGUCGUUAAACGGAUGAUACAGA
.....
AGUUAGAAGUCCGUUAAUGACUGAUAAACGGCAUGUCUAUUUUGGCCUGGUUAAACGAAUA
.....
AUCAUGUUUUAAAAGUUAGUUAACGUUUAGUUCAUG ..))))).))))).)))))))).))))))..))))
=
```

Stability of the secondary structure of the precursor: *MFE*  
-13.88 kcal/mol | *AMFE* -24.54 | *MFEI* -0.79

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 301

Distribution of reads: random

miRBase alignment: none

Results for 4: 2,981,93-,298,561 (-)

Chromosome: 4

Position: 2,981,93-,298,561 (369 nt)

Strand: -

G+C: 30.89 %

miRNA sequence: AAGCAGAACCCAAGAACAUGUUU

miRNA depth: 176 (weight: 176)

Candidates with the same miRNA: none

miRNA precursor:

```
=          GUUAAUGACUGCUAAUCUAUCCAAAACAACGUCGUUUGA-
GAAUAAUCGAAAGAACAUAAA ((((((((((... ((((((((((... ((((((((((((((...
GAUUUUUUCCAUAUGAAAUUCCAUAUCAAAGUUUUUAGCAGAACCCAAGAACAUGU
(((((((((((... ((((((((((...
UGAUUAUAGAGUAACCGCAGUGCCAGUAAUUGGAAGCAAUAAAGGUGUUUUCGUUUAU
.....
AUUUUUUUUUUUUUUUUUUUUUAGGAUUAUGGAAGCAAUUGAAGACUCAUUUAAGAUAU
.....
GUUCGUCUUGUUUGAGCGGUUGUAGAAUAGAUUUGGGGAACUGGAGUUUCAUUUAGAAA
.....))))))))))...))))
```



Stability of the secondary structure of the precursor: *MFE* -23.80 kcal/mol | *AMFE* -20.88 | *MFEI* -0.7

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 36

### Distribution of reads: random

miRBase alignment: none

Results for 4: 4,343,04-,434,483 (+)

Chromosome: 4

Position: 4,343,04-,434,483 (180 nt)

Strand: +

**G+C: 31.11 %**

miRNA sequence: AGUGACCAUUGGAGCAUCGUGCCU

miRNA depth: 72 (weight: 72)

Candidates with the same miRNA: none

miRNA precursor:

$$\begin{aligned}
&= \text{UGACUCUAUUUUAGAGGCUGCUCCAAUGGUCACAUGUAAAAUA-} \\
&\text{GAAUUUUCUUUAAAAUA } ((((((((((((((.((((((((((((((((((((...(((((((((((.(((((((.((((((( \\
&\text{GAGGAGAUAUCAUCUCUAUAAUAAAGAUCUCUACAUUUAGUCUCUAUUUUUUUCCUAUU} \\
&(\text{.....}))))))))) \\
&\text{UUUGAGGAAACUCUAUUUUAAAAGUGACCAUUGGAGCAUCGUGCCUAUAAAAUAGGGUCA} \\
&)).)))))).)))))))).\dots)))))))).\dots)))))).))))))))) \\
&=
\end{aligned}$$

Stability of the secondary structure of the precursor: *MFE*  
-66.37 kcal/mol | *AMFE* -40.94 | *MFEI* -1.32

Stability of the miRNA duplex (mirdup): yes

Total number of reads mapped to the precursor: 152

Distribution of reads: two islands

miRBase alignment: presence of alignments, which do not  
overlap the miRNA locus

Results for 4: 6,182,59-,618,526 (-)

Chromosome: 4

Position: 6,182,59-,618,526 (268 nt)

Strand: -

G+C: 15.67 %

miRNA sequence:

miRNA depth: (weigh: )

Candidates with the same miRNA: none

miRNA precursor:

```
= AAAAAAUUGCAAGAUUAUCAUAUAAGUCACUCAACCAUAUACAGUA-  
GAAACUCUAUAAAU ((((((((((.(((((((.(((((((.((.((((.....(((((((.....  
UAAUAAUGUUGGGACCAUGAAAUUUUAUUAUUUUAUAGUGAUUAUUAAUUUAUCCUAUAAA  
.....  
UUAAUAUUUUAUUAUUUUAUCGUUAUAAGUUAUAAUAAUUAUUAAUUUAUAAAAUAAUUUAUGU  
.....  
AAAAUACAAUACUAUAUUCUUUUUAAAAUGUUUUUAAUUAUUUUUCUAUAUGCUUUGUUG  
.....))))))......)))))  
UUUGUAUAUAUAAUUAUGUUAGUUUUUU ..)))))))))))).)))))))) =
```



Stability of the secondary structure of the precursor: *MFE*  
-12.02 kcal/mol | *AMFE* -19.74 | *MFEI* -1.26

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 119

Distribution of reads: random

miRBase alignment: none

Results for 4: 7,432,81-,743,392 (-)

Chromosome: 4

Position: 7,432,81-,743,392 (112 nt)

Strand: -

G+C: 22.32 %

miRNA sequence: AUUUAGGGAAUCUAGUUUU-  
UACUC

miRNA depth: 19 (weight: 19)

Candidates with the same miRNA: none

miRNA precursor:

= GAUUUUAAAAUUUUGGUUUCCCUACAAUUUGAAAAACUAUUUUGU-  
UGUAAUUUCCAUUC ((... (((((..(((.(((((((.((((((((((((((((.....(((.((((.....  
AUGAUUUUAGUUUUUUAGUUUUUCUAAAAUUUAGGGAAUCUAGUUUUUACUC  
..))))..)).....))))))))..))))))))..))))..))))..)) = This stem-loop structure is the  
MFE structure.

Stability of the secondary structure of the precursor: *MFE* -19.50 kcal/mol | *AMFE* -17.41 | *MFEI* -0.78

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 25

Distribution of reads: one island

miRBase alignment: none

Results for 4: 7,433,86-,743,470 (-)

Chromosome: 4

Position: 7,433,86-,743,470 (85 nt)

Strand: -

G+C: 22.35 %

miRNA sequence: AAGGUCUUGAAUGUUUUGUA-GAUU

miRNA depth: 31 (weight: 31)

Candidates with the same miRNA: none

miRNA precursor:

= UAAGGUCUUGAAUGUUUUGUAGAUUUUGUAAGAGUUUUUGGAUUU-  
UGUUUUUCAAAAACU ((((((((((.((((.((((.....(((((((((((.....))))))))))  
UAUUUUCAUAACAAUCAAGAUUUUA )))))).)).)))))) = This stem-  
loop structure is the MFE structure.

Stability of the secondary structure of the precursor: *MFE*  
-24.00 kcal/mol | *AMFE* -28.24 | *MFEI* -1.26

Stability of the miRNA duplex (mirdup): yes

Total number of reads mapped to the precursor: 44

Distribution of reads: one island

miRBase alignment: none

Results for 4: 9,831,83-,983,345 (-)

Chromosome: 4

Position: 9,831,83-,983,345 (163 nt)

Strand: -

G+C: 23.31 %

miRNA sequence:

miRNA depth: (weigh: )

Candidates with the same miRNA: none

miRNA precursor:

```
= UCAAGUGAGAAACUAUGAGAUACUCUCUACAAGCCAUCAUUACAU-  
UUCUCUUCUUUAAU ((((((.(((((((.(((((.(((.(((((. .....  
UGAUUCAAUUUUUACACUAAAAUAAAAAUUAAUCAUAUAUAAAAUUAUAUAAAAUAC  
.....  
UAAUAUUUUUCUUGUUCGAGAAACUUUUUGGGUUUCUCCUUGA  
......)))))..))))....)))).))))) =
```

Stability of the secondary structure of the precursor: *MFE* -20.14 kcal/mol | *AMFE* -18.77 | *MFEI* -0.81

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 247

Distribution of reads: random

miRBase alignment: presence of alignments, which do not overlap the miRNA locus

Results for 4: 9,832,92-,983,369 (+)

Chromosome: 4

Position: 9,832,92-,983,369 (78 nt)

Strand: +

G+C: 35.90 %

miRNA sequence: AUGUAAUGAUGGCUUGUAGA-GAGU

miRNA depth: 279 (weight: 279)

Candidates with the same miRNA: none

miRNA precursor:

= AGAAGAGAAAUGUAAUGAUGGCUUGUAGAGAGUAUCUCAUAGUUU-CUCACUUGAGAAACU (((((((((.....(..(((((((((((.....))))))))))))))))) = This stem-loop structure is the MFE structure.

Stability of the secondary structure of the precursor: *MFE* -25.80 kcal/mol | *AMFE* -33.08 | *MFEI* -0.92

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 567

### Distribution of reads: one island

miRBase alignment: none

### Results for 4: 9,855,65-,985,737 (+)

Chromosome: 4

Position: 9,855,65-,985,737 (173 nt)

Strand: +

**G+C: 36.42 %**

miRNA sequence: GAGAGAGAGAGAGAGAGA-  
GAG

miRNA depth: 4 (weight: 0.12)

Candidates with the same miRNA: none

miRNA precursor:

[illegible]

Stability of the secondary structure of the precursor: *MFE* -24.93 kcal/mol | *AMFE* -27.63 | *MFEI* -0.76

Stability of the miRNA duplex (mirdup): yes

Total number of reads mapped to the precursor: 10

### Distribution of reads: one island

miRBase alignment: none

### Results for 4: 100,111,5-1,001,209 (+)

Chromosome: 4

Position: 100,111,5-1,001,209 (95 nt)

Strand: +

G+C: 15.79 %

miRNA sequence:

miRNA depth: (weight: )

Candidates with the same miRNA: none

miRNA precursor:

= GUAAAGAUGAUUUAAAAUAUAUGAUUUAUUUUAUUUGAUUU-  
UAAAGUAUAGUAAACU (((((((((((((((((((((...((((((((((..(.....)..))))))..  
GUGAGUUGUAUAUGUUUUUAUGAUUUAUCUAUUAU )))...)))))))))..))))..))))))..)))  
= This stem-loop structure is the MFE structure.

Stability of the secondary structure of the precursor: *MFE*  
-12.50 kcal/mol | *AMFE* -13.16 | *MFEI* -0.83

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 164

Distribution of reads: random

miRBase alignment: none

Results for 4: 102,384,7-1,024,244 (-)

Chromosome: 4

Position: 102,384,7-1,024,244 (398 nt)

Strand: -

G+C: 34.17 %

miRNA sequence:

miRNA depth: (weigh: )

Candidates with the same miRNA: none

miRNA precursor:

```
= AACUUUCAAAAAAUGGCCAAAUUAACCGUGAACUUUUGAAAUG-
GUCGUUUUAUACCUCAA ((((((.((((((((((((((((((((((((((((((((
AAAAAAGUUGAUUUCUAAUUUAACCUAUAAUUUAUUGUUGACUUCUAAUUUAACAUUAA
.((((((((((((((((((((((((((((((((((((((((((((((((((((((((
UUUAUCGUUGACCCAGCCAAAUAGACUCACCGUUAACACUCCUUAACAGCGCUCCUAACA
.....
GCCGUUACAAAACAUGGCCUAAACAGCCGUUAUCGUUGGUUUAAGGACAAAACAGUUGUU
.....
AGUUAACGCUGUUAGGAGAGCUGUUAAGAAGUGUUA AUGGUGAGUCGAUUUGGCCGUGUCA
.....
```

ACGAUAACUUAUAGGUUAAAUAAGAAGUCAACUUUUUGUUGAGGUAAUAAAACGGCCAUUU  
 .....))  
 CAAAAAUUCAUGGUUAAUUUGGCCACUUUUUAAAAGUU )))))).))  
 =

Stability of the secondary structure of the precursor: *MFE*  
 -110.57 kcal/mol | *AMFE* -54.27 | *MFEI* -1.59

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 364

Distribution of reads: random

miRBase alignment: presence of alignments, which do not  
 overlap the miRNA locus

Results for 4: 111,657,0-1,116,885 (-)

Chromosome: 4

Position: 111,657,0-1,116,885 (316 nt)

Strand: -

G+C: 28.48 %

miRNA sequence: ACGAAUCAAAACAGUGAAAAGU-  
 GAC

miRNA depth: 604 (weight: 302)

Candidates with the same miRNA: none

miRNA precursor:

= UUUAAGGGUUAAGUUGUAUACUAGUCACUUUUUAAAAUUUAAUU-  
 GAAAAAUAGUCACUU (((((((.....((((.....((((((((((((.....((((((((((((.....((((((((((((.....  
 UACUAUUUAUAAUUUGCAAAUAGUCACUUUUCACUGUUUGAUUCGUACACUUAGUUUGU  
 (((((((((((((((.....((((((((((((((((((((((((((((.....((((



[illegible]

Stability of the secondary structure of the precursor: *MFE*  
-152.00 kcal/mol | *AMFE* -48.10 | *MFEI* -1.69

Stability of the miRNA duplex (mirdup): yes

Total number of reads mapped to the precursor: 1438

Distribution of reads: one island

miRBase alignment: presence of alignments that cover the  
miRNA locus

Results for 4: 119,006,1-1,190,301 (-)

Chromosome: 4

Position: 119,006,1-1,190,301 (241 nt)

Strand: -

G+C: 24.07 %

miRNA sequence:

miRNA depth: (weight: )

Candidates with the same miRNA: none

miRNA precursor:

```
= UAUUCCCUCCGUCCACUAAGAUGAAUUUUUAAAAUUUCACAU-
UGUUUAAGAAUAUU (((((((((.((((((.((((((((((((((((.....
GUAUAAAGACAAUUUUUAACCUCUUAUAUACUUUAAAAUAAUAAUAAUAAUUAUCUAA
.....
UUUUUUAGUAAGGAUAAAACGGGAAAACAGUUUUUAAAAUUUGCAUUGGAAAUAUAAAACU
.....
UCUAUCUUUGUGGGACAAAUUUUUUCCUAGAAAAUUUAUCUUUAUGGGACAGAGGGAGU
.....))))))))))))..))))).))))))
A ) =
```

Stability of the secondary structure of the precursor: *MFE*  
-35.00 kcal/mol | *AMFE* -23.69 | *MFEI* -0.98

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 101

Distribution of reads: random

miRBase alignment: presence of alignments, which do not  
overlap the miRNA locus

Results for 4: 121,201,8-1,212,144 (+)

Chromosome: 4

Position: 121,201,8-1,212,144 (127 nt)

Strand: +

G+C: 33.07 %

miRNA sequence:

miRNA depth: (weigh: )

Candidates with the same miRNA: none

miRNA precursor:

= UAUUGAACAUUGAGUAGGAUCUUAAGUGGUAUAUAGAAUAUGAGC-  
CUCUCCACUCAUUGC ((((((..((((((((((((..((((((((((((..((((((((((((((((((((..  
CAAUUGAUUUUGAGUGGAGAUAGCUUAUAUCUUAUAUAUAUCACUAGAUCUACUCAAGU  
.....))))))))).))))))....))))))))))))))))))))))..  
UUCAAUG ))))))) = This stem-loop structure is the MFE structure.

Stability of the secondary structure of the precursor: *MFE*  
-66.10 kcal/mol | *AMFE* -52.05 | *MFEI* -1.57

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 94

Distribution of reads: random

miRBase alignment: none

Results for 4: 123,091,5-1,231,313 (-)

Chromosome: 4

Position: 123,091,5-1,231,313 (399 nt)

Strand: -

G+C: 33.58 %

miRNA sequence: AUCACAAUCGCGGUACAGUAAACG

miRNA depth: 7 (weigh: 7)

Candidates with the same miRNA: none

miRNA precursor:

```
= AUCCGCGUUUAUUUAUACCGCUAUUGUGAUUUACCCGACUAAUCC-
CACUCACACAAAAAAG ((((((((((((((.((((((.(((((((((((((((((((((((((((.((((((((
CAAUCUAUGUGAUCAAUGAGAGUAGUUCUAGUUCUUUAUUGAUUUAGAUUGUCAUUGGAA
.....
CAAUCUUCAACCUUUUUUGUCUAUCUUGGAUGAUGUAUUUUUCGGAAAAUGAUUCUCUUUA
.....
AGAUGAUUUUUUAGGUUGACUGAUUGAUUUUGGAGUCUUAUCUAUCCUUAUGAUUAGGA
.....
GUUUUAUCUAGUUCGAUUUGUCAUUUUCCUUAACCAAUUAACACAACACAUAACAUAUAUA
.....
```

.....).))))))

**-70.02 kcal/mol** | *AMFE* **-33.20** | *MFEI* **-0.99**

Stability of the miRNA duplex (mirdup): yes

Total number of reads mapped to the precursor: 36

### Distribution of reads: one island

miRBase alignment: none

### Results for 4: 123,126,4-1,231,345 (+)

Chromosome: 4

**Position:** 123,126,4-1,231,345 (82 nt)

Strand: +

G+C: 40.24 %

miRNA sequence: AAACGCGGAUUUGUGGUUAAU-CUC

miRNA depth: 48 (weight: 24)

Candidates with the same miRNA: none

miRNA precursor:

= UGAGUGGGAUUAGUCGGGUAAAUCACAAUAGCGGUAAAUAAACGCG-  
GAUUUGUGGUUAA ((((((.(((((((((((((((..((((((((((..(((.....))))....)))))))).)..

UCUCGAUUAAUGACCGGUUCA .)()))).)))).).))))) = This stem-loop structure is the MFE structure.

Stability of the secondary structure of the precursor: *MFE*  
-22.20 kcal/mol | *AMFE* -27.07 | *MFEI* -0.67

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 69

Distribution of reads: one island

miRBase alignment: none

Results for 4: 127,078,3-1,270,953 (-)

Chromosome: 4

Position: 127,078,3-1,270,953 (171 nt)

Strand: -

G+C: 47.95 %

miRNA sequence: CGGAGAAGCUGUAGGCGCUU-  
UAUC

miRNA depth: 13 (weight: 13)

Candidates with the same miRNA: none

miRNA precursor:

```
= GCGGAGAAGCUGUAGGCGCUUUAUCGAGAGGUUUUGUGUACGGGCU-
UCUGCUAAGGUUUG (((((((((..(((((((...((((((((((.....
CUCGUGGCAACUAGGAUGGGACUCCAACUCUUUGGUAUCUUCGAGUUGUGGAAAUCACGC
.....
AAAUUCCGAGUUUAGCUUCUCGGAUUCGGUGUUUCUUCUCUUAUUUCCGC
.....)))))))))....))))))..).)...)))))) =
```

Stability of the secondary structure of the precursor: *MFE*  
-23.20 kcal/mol | *AMFE* -29.53 | *MFEI* -0.62

Stability of the miRNA duplex (mirdup): yes

Total number of reads mapped to the precursor: 66

Distribution of reads: one island

miRBase alignment: none

Results for 4: 143,878,0-1,438,882 (+)

Chromosome: 4

Position: 143,878,0-1,438,882 (103 nt)

Strand: +

G+C: 35.92 %

miRNA sequence: UGUCCGUUGGAGAUUCUAU-  
UGCCU

miRNA depth: 7 (weigh: 7)

Candidates with the same miRNA: none

miRNA precursor:

= CAUUUUCUGGGCAAAUCAAGAAAUGGAAUCUUUAAUA-  
GACUAAACAUUGAUGUCAAGG ((((((.(((((((.....(((((((((((((((.(((.(((((((.(((((((...)  
AUAUGAGUGAUUGUCCGUUGGAGAUUCUAUUGCCUUGGUGAUG  
))))).))))).))))))))))))))))).)).))) = This stem-loop structure is the MFE  
structure.

Stability of the secondary structure of the precursor: *MFE* -32.90 kcal/mol | *AMFE* -31.94 | *MFEI* -0.89

Stability of the miRNA duplex (mirdup): yes

Total number of reads mapped to the precursor: 17

## Distribution of reads: random

miRBase alignment: none

Results for 4: 143,920,3-1,439,307 (-)

Chromosome: 4

Position: 143,920,3-1,439,307 (105 nt)

**Strand: -**

**G+C: 28.57 %**

miRNA sequence:

miRNA depth: (weight: )

Candidates with the same miRNA: none

miRNA precursor:

= CCAAUAGUGAGAAGAGAAAUGUCAUGAUGGGUUGUAAAGAGUAU-  
CUCAGAAUUAACUUUC ((((((.( ((((((((((.( (((((((.( ((((((.( ..... (((( ..... )))  
UACACUUUAUUUCCGUCAUUUUCAUUAUUUUUUUUUUUUUAUUGUG  
))) .)))))).)))))) . . )))).)))))))).)))))) .) = This stem-loop structure is the MFE  
structure.



Stability of the secondary structure of the precursor: *MFE*  
-24.30 kcal/mol | *AMFE* -23.14 | *MFEI* -0.81

Stability of the miRNA duplex (mirdup): no

Total number of reads mapped to the precursor: 98

Distribution of reads: random

miRBase alignment: none