

>miR1508-3P

Score: 2.5 Deg: 16:2290:44:6096 T_00052443

Query: 1 CTAGAAAGAGAGAGAGCCGT-T

22

[illegible]

Sbjct: 2299 AATCTTTCTCTCTTTCGGTGCAC 2277

Value	Count
1	16
2	4
3	3
4	4
5	1
6	2
7	2
8	1
9	1
10	2
11	1
12	2
13	1
14	1
15	1
16	1

>miR1508-3P

Score: 2.5 Deg: 7:788:7:222 T_00040034

Query: 1 CTAGAAAGAGAGAGACCGTT

22

```
*| | | | | | | | | | | | | | *|***
```

Sbjct: 797 CATCTTTCTCTCTCTCGACTTT 776

Line	Tick Mark Position (approx. %)	Value
1	25	2
2	25	1
3	25	2
4	25	1
5	10	1
6	10	1
7	10	7
8	10	5
9	10	3
10	10	1
11	10	1
12	10	1
13	10	2
14	10	2
15	10	1

||-----2
|-----3

>miR156a

Score: 1.5 Deg: 10:1311:27:223T_00091783

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1319 ACTGTCTTCTCTCTCGTGT 1299
|||||*|||||*
||||-----1
||||-----2
|||-----6
||-----6
||-----10
|-----1

>miR156a

Score: 1.5 Deg: 10:1668:27:226T_00091779

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1676 ACTGTCTTCTCTCTCGTGT 1656
|||||*|||||*
||||-----1
||||-----2
|||-----6
||-----6
||-----10
|-----1

>miR156a

Score: 1.5 Deg: 10:2823:27:234T_00091781

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 2831 ACTGTCTTCTCTCTCGTGT 2811
|||||*|||||*
||||-----1
||||-----2
|||-----6
||-----6
||-----10

|-----1

>miR156a

Score: 1.5 Deg: 10:1470:27:223T_00091782

Query: 1 TGACAGAAGAGAGTGAGCAC
21

|||||*|||||*
Sbjct: 1478 ACTGTCTTCTCTCTCGTGT 1458
||||-----1
||||-----2
|||-----6
||-----6
||-----10
|-----1

>miR156a

Score: 1.5 Deg: 10:1199:27:223T_00091784

Query: 1 TGACAGAAGAGAGTGAGCAC
21

|||||*|||||*
Sbjct: 1207 ACTGTCTTCTCTCTCGTGT 1187
||||-----1
||||-----2
|||-----6
||-----6
||-----10
|-----1

>miR156a

Score: 1.5 Deg: 10:1496:27:226T_00091780

Query: 1 TGACAGAAGAGAGTGAGCAC
21

|||||*|||||*
Sbjct: 1504 ACTGTCTTCTCTCTCGTGT 1484
||||-----1
||||-----2
|||-----6
||-----6
||-----10
|-----1

>miR156a

Score: 2.5 Deg: 22:1017:24:363T_00090332

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1025 ACTGTCTTCTATCTCTCGTGC 1005

|||||||*|*|*|*|*|*|*|

| | | | | | | | |-----2
| | | | | | |-----1
| | | | | |-----1
| | | | |-----1
| | | |-----2
| | |-----3
| |-----22
|-----1
|-----2

>miR156a

Score: 2.5 Deg: 22:1088:24:371T_00090336

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1096 ACTGTCTTCTATCTCTCGTGC 1076

|||||||*|*|*|*|*|*|*|

| | | | | | | | |-----2
| | | | | | |-----1
| | | | | |-----1
| | | | |-----1
| | | |-----2
| | |-----3
| |-----22
|-----1
|-----2

>miR156a

Score: 2.5 Deg: 22:1171:24:378T_00090333

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1179 ACTGTCTTCTATCTCTCGTGC 1159

|||||||*|*|*|*|*|*|*|

| | | | | | | | |-----2
| | | | | | |-----1
| | | | | |-----1
| | | | |-----1
| | |-----2

```

| | | |-----3
| | |-----22
| |-----1
|-----2

```

>miR156a

Score: 2.5 Deg: 22:1129:24:363T_00090331

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

          |||||*||*||*
Sbjct: 1137 ACTGTCTTCTATCTCTCGTGC 1117
          | | | | | |-----2
          | | | | | |-----1
          | | | | |-----1
          | | | |-----1
          | | | |-----2
          | | |-----3
          | |-----22
          |-----1
          |-----2

```

>miR156a

Score: 2.5 Deg: 22:958:24:363 T_00090335

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

          |||||*||*||*
Sbjct: 966 ACTGTCTTCTATCTCTCGTGC 946
          | | | | | |-----2
          | | | | | |-----1
          | | | | |-----1
          | | | |-----1
          | | | |-----2
          | | |-----3
          | |-----22
          |-----1
          |-----2

```

>miR156a

Score: 2.5 Deg: 22:941:24:361 T_00090334

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

          |||||*||*||*

```

Sbjct: 949 ACTGTCTTCTATCTCTCGTGC 929

```

      | | | | | | | | |-----2
      | | | | | | |-----1
      | | | | | |-----1
      | | | | |-----1
      | | | |-----2
      | | |-----3
      | |-----22
      |-----1
      |-----2

```

>miR156a
 Score: 2.0 Deg: 79:1218:79:519T_00059648

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

Sbjct: 1226 ACTGTCTTCTCTCTCTCGTAC 1206

```

      | | | | | | | | | * | | | | **
      | | | | | | |-----1
      | | | | | | |-----3
      | | | | | | |-----2
      | | | | | |-----2
      | | | | |-----50
      | | | |-----79
      | | |-----3
      | |-----3
      | |-----1
      |-----1
      |-----1

```

>miR156a
 Score: 1.5 Deg: 9:1100:9:46 T_00080616

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

Sbjct: 1109 ACTGTCTTCTCTCTCTCGTGT 1089

```

      | | | | | | | | * | | | | *
      | | | | |-----1
      | | | |-----1
      | |-----6
      |-----9
      |-----4

```

>miR156a
 Score: 1.5 Deg: 9:1250:9:33 T_00080613

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1259 ACTGTCTTCTCTCTCTCGTGT 1239
|||||*|||||*
|| | |-----1
|| | |-----1
|| |-----6
||-----9
|-----4

>miR156a
Score: 1.5 Deg: 9:1195:9:64 T_00080614

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1204 ACTGTCTTCTCTCTCTCGTGT 1184
|||||*|||||*
|| | |-----1
|| | |-----1
|| |-----6
||-----9
|-----4

>miR156a
Score: 1.5 Deg: 9:1124:9:46 T_00080615

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1133 ACTGTCTTCTCTCTCTCGTGT 1113
|||||*|||||*
|| | |-----1
|| | |-----1
|| |-----6
||-----9
|-----4

>miR156a
Score: 1.5 Deg: 9:1250:9:64 T_00080612

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1259 ACTGTCTTCTCTCTCTCGTGT 1239
|||||*|||||*
|| | |-----1

```

      ||      |      |-----1
      ||      |-----6
      ||-----9
      |-----4

```

>miR156a

Score: 1.5 Deg: 12:1418:12:64 T_00046313

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

      |||||*|||*
Sbjct: 1427 ACTGTCTTCTCTCTCGTGT 1407
      |   |||  |   |-----1
      |   |||  |   |-----1
      |   |||  |-----4
      |   |||-----1
      |   ||-----12
      |   |-----10
      |-----2

```

>miR156a

Score: 1.5 Deg: 77:2106:83:749T_00052738

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

      |||||*|||*
Sbjct: 2114 ACTGTCTTCTCTCTCGTGC 2094
      |   |||||  |||-----1
      |   |||||  |||-----1
      |   |||||  |-----1
      |   |||||-----1
      |   |||||-----1
      |   |||||-----1
      |   |||||-----1
      |   ||||-----1
      |   |||-----9
      |   ||-----56
      |   |-----77
      |-----1

```

>miR156a

Score: 1.5 Deg: 77:443:77:327 T_00052739

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

      |||||*|||*

```

Sbjct: 451 ACTGTCTTCTCTCTCGTGC 431

```
| ||||| | || |-----1
| ||||| | || |-----1
| ||||| | |-----1
| ||||| |-----1
| ||||| |-----1
| ||||| |-----1
| |||| |-----1
| ||| |-----1
| || |-----9
| |-----56
|-----77
|-----1
```

>miR156a

Score: 1.5 Deg: 77:2114:83:749T_00052737

Query: 1 TGACAGAAGAGAGTGAGCAC

21

|||||||*|||*|

Sbjct: 2122 ACTGTCTTCTCTCTCGTGC 2102

```
| ||||| | || |-----1
| ||||| | || |-----1
| ||||| | |-----1
| ||||| |-----1
| ||||| |-----1
| ||||| |-----1
| |||| |-----1
| ||| |-----1
| || |-----9
| |-----56
|-----77
|-----1
```

>miR156a

Score: 1.5 Deg: 5:2012:5:54 T_00071663

Query: 1 TGACAGAAGAGAGTGAGCAC

21

|||||||*|||*|

Sbjct: 2021 ACTGTCTTCTCTCTCGTGT 2001

```
| | | |-----1
| | |-----1
| | |-----1
| |-----5
|-----4
|-----1
```

>miR156a
Score: 1.5 Deg: 5:1901:5:45 T_00071657

```

Query:          1 TGACAGAAGAGAGTGAGCAC
                21
                |||||
Sbjct:       1910 ACTGTCTTCTCTCTCTCGTGT 1890

```

Sbjct: 1910 ACTGTCTTCTCTCTCGTGT 1890

 | || | |-----1
 | || | |-----1
 | || |-----1
 | ||-----5
 | |-----4
 |-----1

```
>miR156a
Score: 1.5 Deg: 5:1222:5:44 T 00071664
```

```

Query:          1 TGACAGAAGAGAGTGAGCAC
                21
                |||||*|||*
Sbjct:       1231 ACTGTCTTCTCTCTCGTGT 1211

```

|||||*|||*
 Sbjct: 1231 ACTGTCTTCTCTCTCGT 1211
 | | | | |-----1
 | | | | |-----1
 | | | | |-----1
 | | |-----5
 | |-----4
 |-----1

>miR156a
Score: 1.5 Deg: 5:2528:631:10547 T 00071658

```

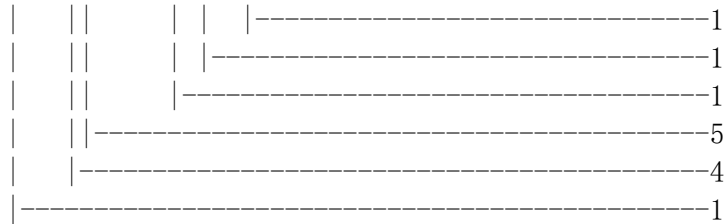
Query:          1 TGACAGAAGAGAGTGAGCAC
                21
                |||||*|||*
Sbjct:       2537 ACTGTCTTCTCTCTCGTGT 2517

```

|||||*|||*
 Sbjct: 2537 ACTGTCTTCTCTCTCGTG 2517
 | | | | |-----1
 | | | | |-----1
 | | | | |-----1
 | | |-----5
 | |-----4
 |-----1

```
>miR156a
Score: 1.5 Deg: 5:1457:5:53 T 00071665
```

Sbjct: 1466 ACTGTCTTCTCTCTCTCGTGT 1446



```
>miR156a
```

Score: 1.5 Deg: 5:2084:631:10538 T_00071656

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 2093 ACTGTCTTCTCTCTCGTGT 2073

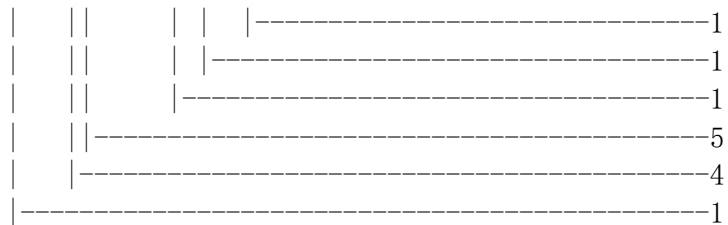


```
>miR156a
```

Score: 1.5 Deg: 5:1826:5:53 T_00071661

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1835 ACTGTCTTCTCTCTCTCGTGT 1815



```
>miR156a
```

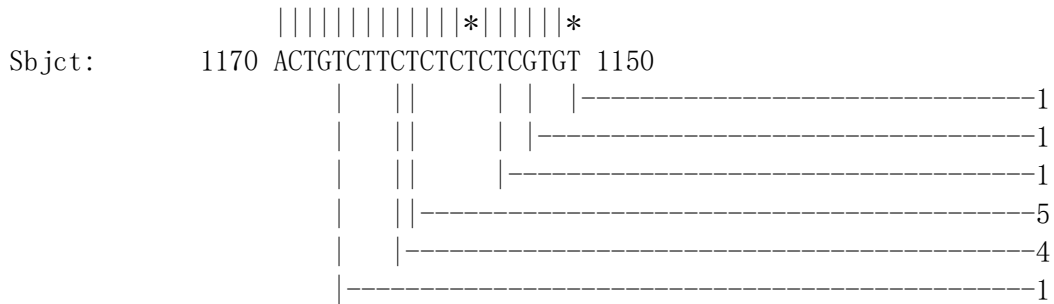
Score: 1.5 Deg: 5:1160:5:44 T_00071667

Query: 1 TGACAGAAGAGAGTGAGCAC
21



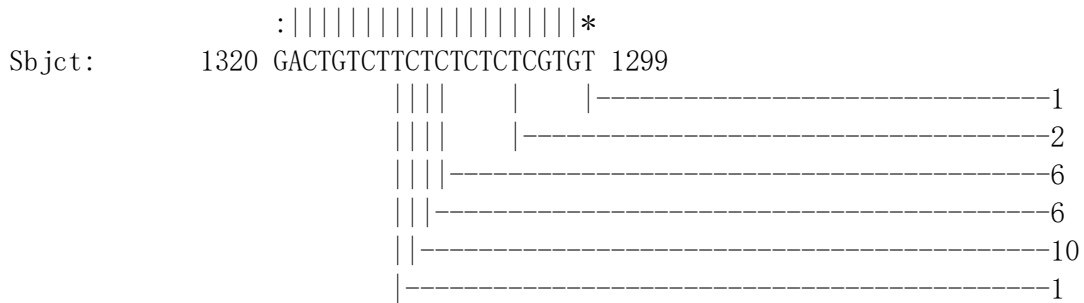
>miR156a
Score: 1.5 Deg: 5:1161:5:44 T_00071666

Query: 1 TGACAGAAGAGAGTGAGCAC
21



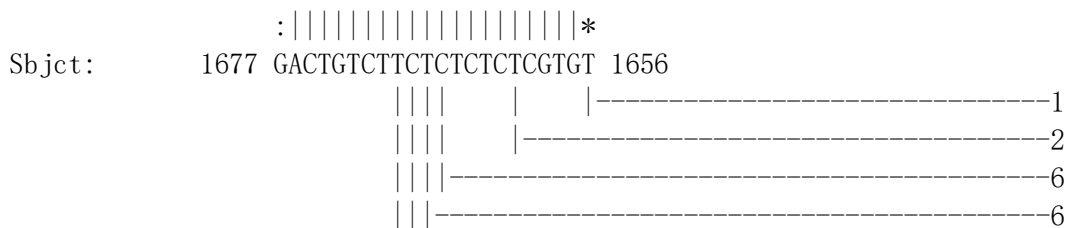
>miR156b-5p
Score: 0.8 Deg: 10:1311:27:223T_00091783

Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156b-5p
Score: 0.8 Deg: 10:1668:27:226T_00091779

Query: 1 TTGACAGAAGAGAGAGAGCAC
22



||-----10
|-----1

>miR156b-5p

Score: 0.8 Deg: 10:2823:27:234T_00091781

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

:|||||||||||||||||*
Sbjct: 2832 GACTGTCTTCTCTCTCTCGTGT 2811
|||| |-----1
|||| |-----2
|||-----6
||-----6
||-----10
|-----1

>miR156b-5p

Score: 0.8 Deg: 10:1470:27:223T_00091782

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

:|||||||||||||||||*
Sbjct: 1479 GACTGTCTTCTCTCTCTCGTGT 1458
|||| |-----1
|||| |-----2
|||-----6
||-----6
||-----10
|-----1

>miR156b-5p

Score: 0.8 Deg: 10:1199:27:223T_00091784

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

:|||||||||||||||||*
Sbjct: 1208 GACTGTCTTCTCTCTCTCGTGT 1187
|||| |-----1
|||| |-----2
|||-----6
||-----6
||-----10
|-----1

>miR156b-5p
Score: 0.8 Deg: 10:1496:27:226T_00091780

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156b-5p
Score: 1.5  Deg: 22:1017:24:363T_00090332
```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156b-5p
Score: 1.5  Deg: 22:1088:24:371T_00090336
```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```

      | |-----1
      |-----2

```

>miR156b-5p
 Score: 1.5 Deg: 22:1171:24:378T_00090333

```

Query:          1 TTGACAGAAGAGAGAGAGCAC
                22
                |||||*|||*
Sbjct:    1180 AACTGTCTTCTATCTCTCGTGC 1159
              | | | | | | |-----2
              | | | | | |-----1
              | | | | |-----1
              | | | |-----1
              | | |-----2
              | |-----3
              | |-----22
              |-----1
              |-----2

```

>miR156b-5p
 Score: 1.5 Deg: 22:1129:24:363T_00090331

```

Query:          1 TTGACAGAAGAGAGAGAGCAC
                22
                |||||*|||*
Sbjct:    1138 AACTGTCTTCTATCTCTCGTGC 1117
              | | | | | | |-----2
              | | | | |-----1
              | | | |-----1
              | | |-----1
              | |-----2
              | |-----3
              | |-----22
              |-----1
              |-----2

```

>miR156b-5p
 Score: 1.5 Deg: 22:958:24:363 T_00090335

```

Query:          1 TTGACAGAAGAGAGAGAGCAC
                22
                |||||*|||*
Sbjct:    967 AACTGTCTTCTATCTCTCGTGC 946
              | | | | | |-----2

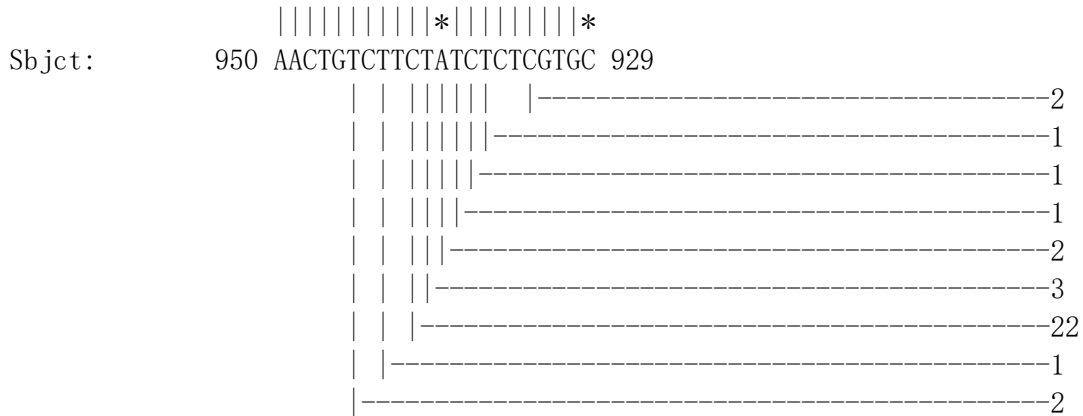
```



>miR156b-5p

Score: 1.5 Deg: 22:941:24:361 T_00090334

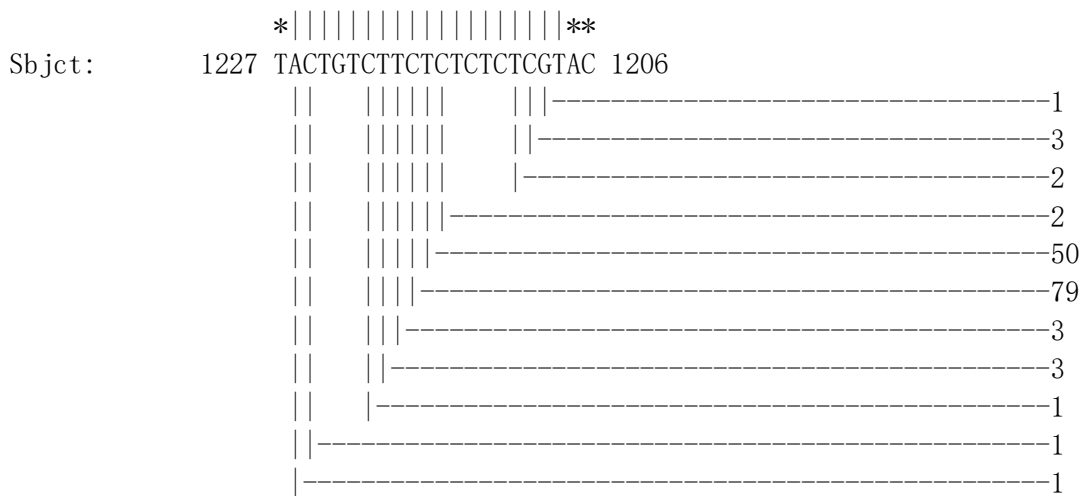
Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156b-5p

Score: 1.5 Deg: 79:1218:79:519T_00059648

Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156b-5p

Score: 0.5 Deg: 9:1100:9:46 T_00080616

Query: 1 TTGACAGAAGAGAGAGAGCAC

22

Sbjct: 1110 AACTGTCTTCTCTCTCTCGTGT 1089

|||||*
|| | | |-----1
|| | |-----1
|| |-----6
||-----9
|-----4

>miR156b-5p

Score: 0.5 Deg: 9:1250:9:33 T_00080613

Query: 1 TTGACAGAAGAGAGAGAGCAC

22

Sbjct: 1260 AACTGTCTTCTCTCTCTCGTGT 1239

|||||*
|| | | |-----1
|| | |-----1
|| |-----6
||-----9
|-----4

>miR156b-5p

Score: 0.5 Deg: 9:1195:9:64 T_00080614

Query: 1 TTGACAGAAGAGAGAGAGCAC

22

Sbjct: 1205 AACTGTCTTCTCTCTCTCGTGT 1184

|||||*
|| | | |-----1
|| | |-----1
|| |-----6
||-----9
|-----4

>miR156b-5p

Score: 0.5 Deg: 9:1124:9:46 T_00080615

Query: 1 TTGACAGAAGAGAGAGAGCAC

22

|||||*

Sbjct: 1134 AACTGTCTTCTCTCTCTCGTGT 1113

```

      ||      |      |  -----1
      ||      |      |  -----1
      ||      |  -----6
      ||  -----9
      |-----4

```

>miR156b-5p
 Score: 0.5 Deg: 9:1250:9:64 T_00080612

Query: 1 TTGACAGAAGAGAGAGAGCAC
 22

Sbjct: 1260 AACTGTCTTCTCTCTCTCGTGT 1239

```

      |||||*
      ||      |      |  -----1
      ||      |      |  -----1
      ||      |  -----6
      ||  -----9
      |-----4

```

>miR156b-5p
 Score: 1.0 Deg: 12:1418:12:64 T_00046313

Query: 1 TTGACAGAAGAGAGAGAGCAC
 22

Sbjct: 1428 TACTGTCTTCTCTCTCTCGTGT 1407

```

      *|||*
      | ||| |      |  -----1
      | ||| |      |  -----1
      | ||| |  -----4
      | |||  -----1
      | ||  -----12
      | |  -----10
      |-----2

```

>miR156b-5p
 Score: 0.5 Deg: 77:2106:83:749T_00052738

Query: 1 TTGACAGAAGAGAGAGAGCAC
 22

Sbjct: 2115 AACTGTCTTCTCTCTCTCGTGC 2094

```

      |||||*
      | ||||| ||  -----1
      | ||||| ||  -----1

```

```
>miR156b-5p
Score: 0.5 Deg: 77:443:77:327 T_00052739
```

[illegible]

```
>miR156b-5p
Score: 0.5 Deg: 77:2114:83:749T 00052737
```

[illegible]

>miR156b-5p
Score: 1.0 Deg: 5:2528:631:10547 T_00071658

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156b-5p
Score: 1.0 Deg: 5:1457:5:53 T_00071665
```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156b-5p
Score: 1.0 Deg: 5:2084:631:10538 T_00071656
```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156b-5p
Score: 1.0 Deg: 5:1826:5:53 T_00071661
```

```
>miR156b-5p
Score: 1.0 Deg: 5:1826:5:53 T_00071661
```


Diagram illustrating a sequence of 10 horizontal lines, each with a vertical tick mark at a specific position and a corresponding number to its right:

- Line 1: Tick mark at position 1, number 1.
- Line 2: Tick mark at position 2, number 1.
- Line 3: Tick mark at position 3, number 1.
- Line 4: Tick mark at position 4, number 1.
- Line 5: Tick mark at position 5, number 5.
- Line 6: Tick mark at position 6, number 4.
- Line 7: Tick mark at position 7, number 1.

Score: 1.0 Deg: 5:2217:631:10547 T_00071662

* | | | | | | | | | | | *

Diagram illustrating a sequence of steps or components, numbered 1 through 10, connected by horizontal lines. The diagram shows a series of vertical lines on the left, with horizontal lines extending to the right, labeled 1 through 10. The connections are as follows:

- Step 1: A vertical line on the left, with a horizontal line extending to the right, labeled 1.
- Step 2: A vertical line on the left, with a horizontal line extending to the right, labeled 2.
- Step 3: A vertical line on the left, with a horizontal line extending to the right, labeled 3.
- Step 4: A vertical line on the left, with a horizontal line extending to the right, labeled 4.
- Step 5: A vertical line on the left, with a horizontal line extending to the right, labeled 5.
- Step 6: A vertical line on the left, with a horizontal line extending to the right, labeled 6.
- Step 7: A vertical line on the left, with a horizontal line extending to the right, labeled 7.
- Step 8: A vertical line on the left, with a horizontal line extending to the right, labeled 8.
- Step 9: A vertical line on the left, with a horizontal line extending to the right, labeled 9.
- Step 10: A vertical line on the left, with a horizontal line extending to the right, labeled 10.

Score: 1.0 Deg: 5:1161:5:44 T_00071666

* | | | | | | | | | | | | | | | *

Diagram illustrating a sequence of steps or a process flow, numbered 1 through 10. The steps are represented by vertical lines connected by horizontal lines, indicating a sequential process.

Score: 0.8 Deg: 10:1311:27:223T_00091783

: | | | | | | | | | | | | | | *

```
|||-----6
||-----6
||-----10
|-----1
```

>miR156c-5p

Score: 0.8 Deg: 10:1668:27:226T_00091779

Query: 1 TTGACAGAAGAGAGAGGCAC

22

:|||||||||||||||*|

Sbjct: 1677 GACTGTCTTCTCTCTCGTGT 1656

```
|||-----1
|||-----2
|||-----6
||-----6
||-----10
|-----1
```

>miR156c-5p

Score: 0.8 Deg: 10:2823:27:234T_00091781

Query: 1 TTGACAGAAGAGAGAGGCAC

22

:|||||||||||||||*|

Sbjct: 2832 GACTGTCTTCTCTCTCGTGT 2811

```
|||-----1
|||-----2
|||-----6
||-----6
||-----10
|-----1
```

>miR156c-5p

Score: 0.8 Deg: 10:1470:27:223T_00091782

Query: 1 TTGACAGAAGAGAGAGGCAC

22

:|||||||||||||||*|

Sbjct: 1479 GACTGTCTTCTCTCTCGTGT 1458

```
|||-----1
|||-----2
|||-----6
||-----6
||-----10
```

|-----1

>miR156c-5p

Score: 0.8 Deg: 10:1199:27:223T_00091784

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

:|||||||||||||||*
Sbjct: 1208 GACTGTCTTCTCTCTCTCGTGT 1187
||| |-----1
||| |-----2
|||-----6
||-----6
|-----10
|-----1

>miR156c-5p

Score: 0.8 Deg: 10:1496:27:226T_00091780

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

:|||||||||||||||*
Sbjct: 1505 GACTGTCTTCTCTCTCTCGTGT 1484
||| |-----1
||| |-----2
|||-----6
||-----6
|-----10
|-----1

>miR156c-5p

Score: 1.5 Deg: 22:1017:24:363T_00090332

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||||||*|||||||*
Sbjct: 1026 AACTGTCTTCTATCTCTCGTGC 1005
| | ||||| |-----2
| | |||||-----1
| | |||||-----1
| | ||||-----1
| | |||-----2
| | ||-----3
| |-----22
|-----1

|-----2

>miR156c-5p

Score: 1.5 Deg: 22:1088:24:371T_00090336

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Sbjet: 1097 AACTGTCTTCTATCTCTCGTGC 1076
| | | | | | | | * | | | | | | *
| | | | | | |-----2
| | | | | |-----1
| | | | |-----1
| | | |-----1
| | |-----2
| |-----3
|-----22
|-----1
|-----2

>miR156c-5p

Score: 1.5 Deg: 22:1171:24:378T_00090333

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Sbjet: 1180 AACTGTCTTCTATCTCTCGTGC 1159
| | | | | | | | * | | | | | | *
| | | | | | |-----2
| | | | | |-----1
| | | | |-----1
| | | |-----1
| | |-----2
| |-----3
|-----22
|-----1
|-----2

>miR156c-5p

Score: 1.5 Deg: 22:1129:24:363T_00090331

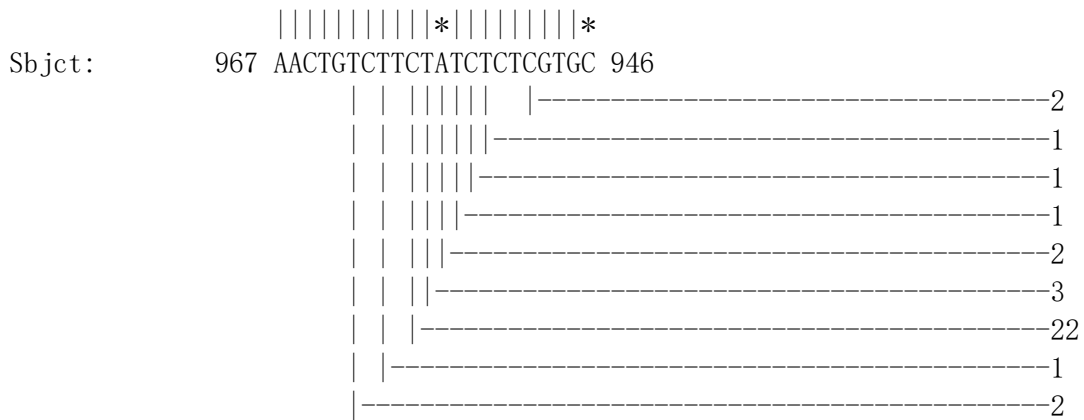
Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Sbjet: 1138 AACTGTCTTCTATCTCTCGTGC 1117
| | | | | | |-----2
| | | | |-----1



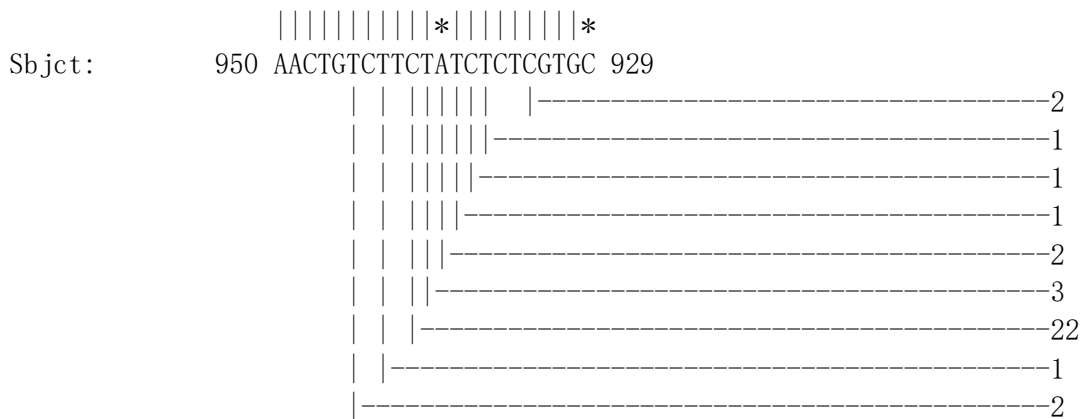
>miR156c-5p
Score: 1.5 Deg: 22:958:24:363 T_00090335

Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156c-5p
Score: 1.5 Deg: 22:941:24:361 T_00090334

Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156c-5p
Score: 1.5 Deg: 79:1218:79:519T_00059648

```

Query:          1 TTGACAGAAGAGAGAGAGCAC
                22
                *|||
Sbjct:    1227 TACTGTCTTCTCTCTCTCGTAC 1206
                |||
                |||-----1
                |||-----3
                |||-----2
                |||-----2
                |||-----50
                |||-----79
                |||-----3
                |||-----3
                |||-----1
                |||-----1
                |||-----1

```

```

>miR156c-5p
  Score: 0.5  Deg: 9:1100:9:46   T_00080616

```

```

Query:          1 TTGACAGAAGAGAGAGAGCAC
                22
                |||
Sbjct:    1110 AACTGTCTTCTCTCTCTCGTGT 1089
                |||
                |||-----1
                |||-----1
                |||-----6
                |||-----9
                |||-----4

```

```

>miR156c-5p
  Score: 0.5  Deg: 9:1250:9:33   T_00080613

```

```

Query:          1 TTGACAGAAGAGAGAGAGCAC
                22
                |||
Sbjct:    1260 AACTGTCTTCTCTCTCTCGTGT 1239
                |||
                |||-----1
                |||-----1
                |||-----6
                |||-----9
                |||-----4

```

```

>miR156c-5p
  Score: 0.5  Deg: 9:1195:9:64   T_00080614

```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Sbjct: 1205 AACTGTCTTCTCTCTCTCGTGT 1184
|||||*
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156c-5p
Score: 0.5 Deg: 9:1124:9:46 T_00080615

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Sbjct: 1134 AACTGTCTTCTCTCTCTCGTGT 1113
|||||*
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156c-5p
Score: 0.5 Deg: 9:1250:9:64 T_00080612

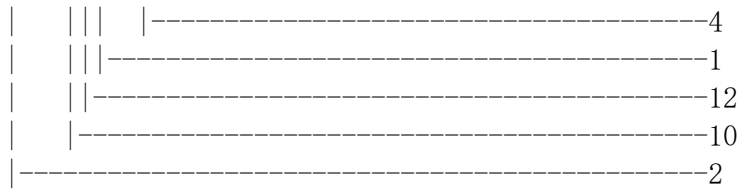
Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Sbjct: 1260 AACTGTCTTCTCTCTCTCGTGT 1239
|||||*
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156c-5p
Score: 1.0 Deg: 12:1418:12:64 T_00046313

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

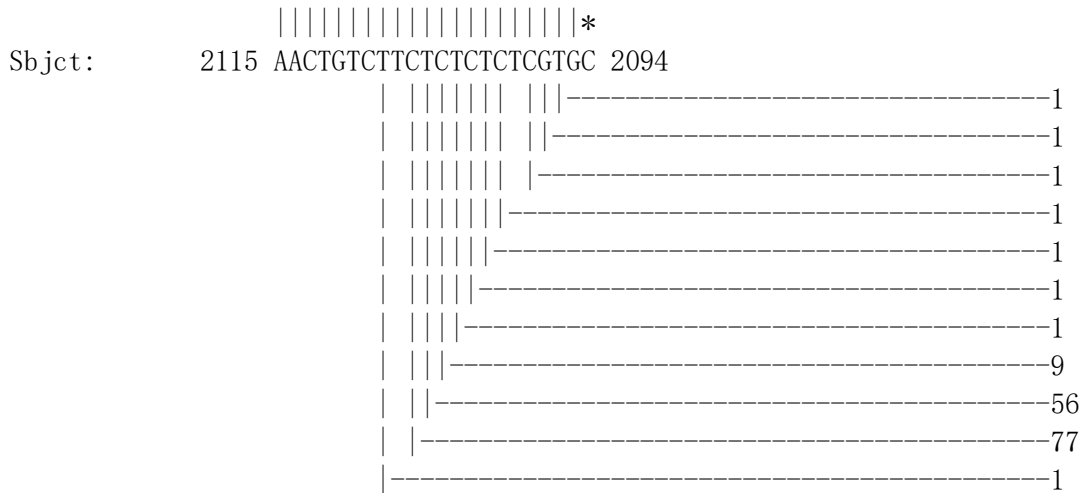
Sbjct: 1428 TACTGTCTTCTCTCTCTCGTGT 1407
|||||
| || | |-----1
| || | |-----1



>miR156c-5p

Score: 0.5 Deg: 77:2106:83:749T_00052738

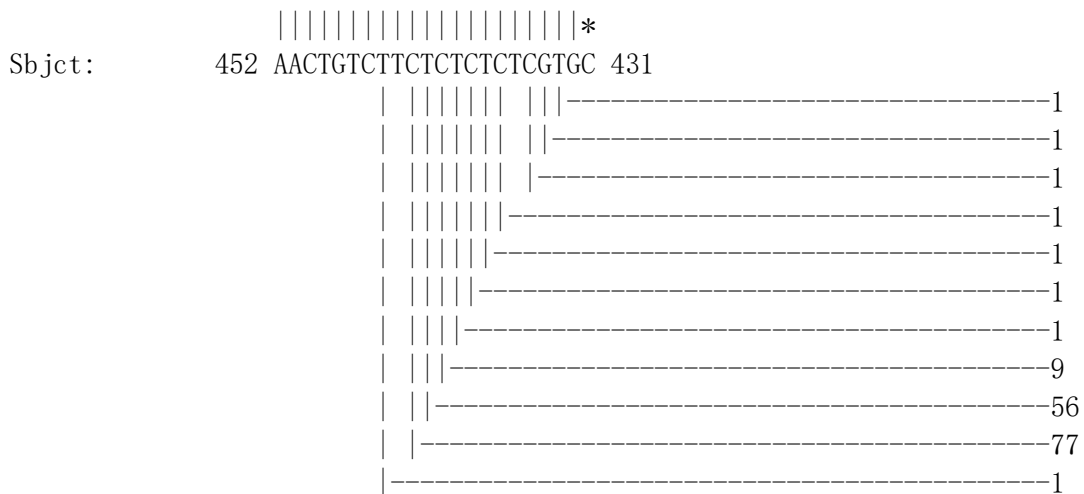
Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156c-5p

Score: 0.5 Deg: 77:443:77:327 T_00052739

Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156c-5p
Score: 0.5 Deg: 77:2114:83:749T_00052737

```
Query:          1 TTGACAGAAGAGAGAGAGCAC
                22
                |||||
Sbjct:    2123 AACTGTCTTCTCTCTCTCGTGC 2102
                |||||
                |-----1
                |-----1
                |-----1
                |-----1
                |-----1
                |-----1
                |-----1
                |-----9
                |-----56
                |-----77
                |-----1
```

>miR156c-5p
Score: 1.0 Deg: 5:2012:5:54 T_00071663

```
Query:          1 TTGACAGAAGAGAGAGAGCAC
                22
                *|||
Sbjct:    2022 TACTGTCTTCTCTCTCTCGTGT 2001
                |||
                |-----1
                |-----1
                |-----1
                |-----5
                |-----4
                |-----1
```

>miR156c-5p
Score: 1.0 Deg: 5:1901:5:45 T_00071657

```
Query:          1 TTGACAGAAGAGAGAGAGCAC
                22
                *|||
Sbjct:    1911 TACTGTCTTCTCTCTCTCGTGT 1890
                |||
                |-----1
                |-----1
                |-----1
                |-----5
                |-----4
```

|-----1

>miR156c-5p

Score: 1.0 Deg: 5:1222:5:44 T_00071664

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||
Sbjct: 1232 TACTGTCTTCTCTCTCGTGT 1211
| | |-----1
| | |-----1
| | |-----1
| |-----5
| |-----4
|-----1

>miR156c-5p

Score: 1.0 Deg: 5:2528:631:10547 T_00071658

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||
Sbjct: 2538 TACTGTCTTCTCTCTCGTGT 2517
| | |-----1
| | |-----1
| | |-----1
| |-----5
| |-----4
|-----1

>miR156c-5p

Score: 1.0 Deg: 5:1457:5:53 T_00071665

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||
Sbjct: 1467 TACTGTCTTCTCTCTCGTGT 1446
| | |-----1
| | |-----1
| | |-----1
| |-----5
| |-----4
|-----1

>miR156c-5p

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156c-5p
Score: 1.0 Deg: 5:1826:5:53 T_00071661
```

Sbjct: 1836 TACTGTCTTCTCTCTCGTGT 1815

| | |-----1
| | |-----1
| | |-----1
| |-----5
| |-----4
|-----1

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

>miR156c-5p
Score: 1.0 Deg: 5:2345:5:54 T_00071659

Query: 1 TTGACAGAAGAGAGAGAGCAC

[illegible]

Score: 1.0 Deg: 5:1931:631:10538 T_00071660

Sbjct: 1941 TACTGTCTTCTCTCTCGTGT 1920

 | | | |-----1
 | | | |-----1
 | | |-----1
 | |-----5
 | |-----4
 |-----1

Score: 1.0 Deg: 5:2217:631:10547 T 00071662

Sbjct: 2227 TACTGTCTTCTCTCTCGTGT 2206

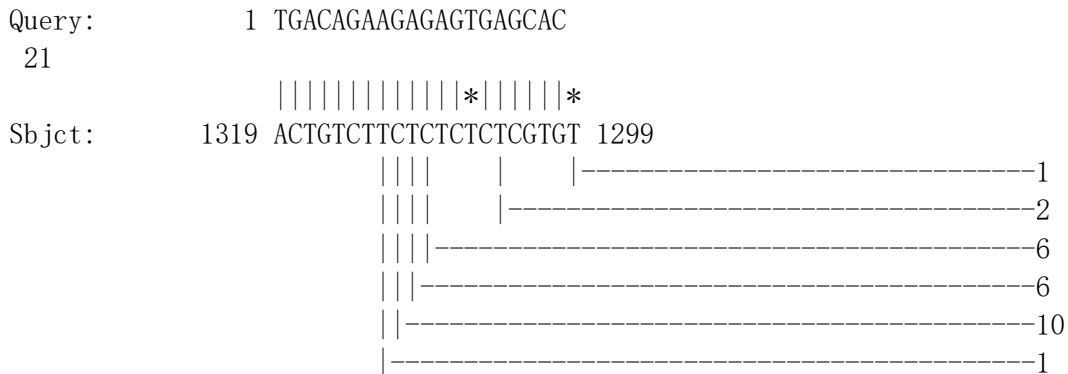
 | | |-----1
 | | |-----1
 | | |-----1
 | |-----5
 | |-----4
 |-----1

Score: 1.0 Deg: 5:1161:5:44 T_00071666

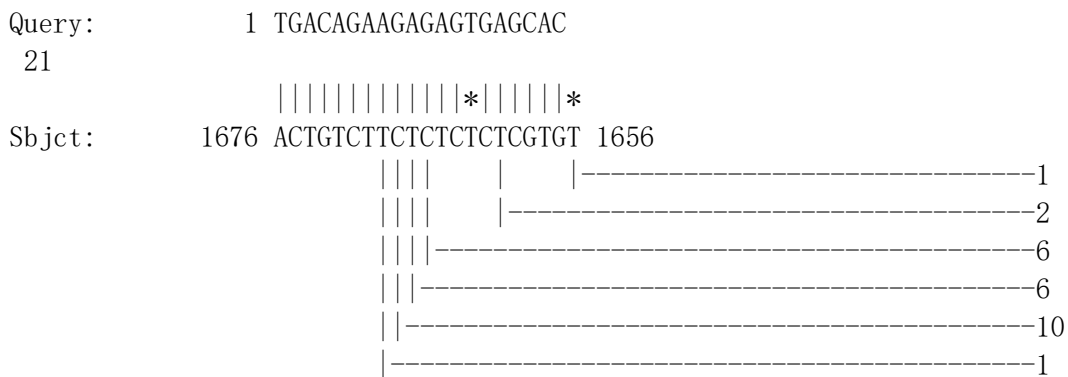
Sbjct: 1171 TACTGTCTTCTCTCTCTCGTGT 1150



>miR156d-5p
 Score: 1.5 Deg: 10:1311:27:223T_00091783



>miR156d-5p
 Score: 1.5 Deg: 10:1668:27:226T_00091779



>miR156d-5p
 Score: 1.5 Deg: 10:2823:27:234T_00091781



```

      |||-----6
      ||-----10
      |-----1

```

>miR156d-5p
 Score: 1.5 Deg: 10:1470:27:223T_00091782

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

```

      |||||*|||*
Sbjct: 1478 ACTGTCTTCTCTCTCGTGT 1458
      ||| |-----1
      ||| |-----2
      |||-----6
      ||-----6
      ||-----10
      |-----1

```

>miR156d-5p
 Score: 1.5 Deg: 10:1199:27:223T_00091784

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

```

      |||||*|||*
Sbjct: 1207 ACTGTCTTCTCTCTCGTGT 1187
      ||| |-----1
      ||| |-----2
      |||-----6
      ||-----6
      ||-----10
      |-----1

```

>miR156d-5p
 Score: 1.5 Deg: 10:1496:27:226T_00091780

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

```

      |||||*|||*
Sbjct: 1504 ACTGTCTTCTCTCTCGTGT 1484
      ||| |-----1
      ||| |-----2
      |||-----6
      ||-----6
      ||-----10
      |-----1

```

>miR156d-5p
Score: 2.5 Deg: 22:1017:24:363T_00090332

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1025 ACTGTCTTCTATCTCTCGTGC 1005
| | | | | | | * | * | | | | *
| | | | | | |-----2
| | | | | |-----1
| | | | |-----1
| | | |-----1
| | |-----2
| |-----3
|-----22
|-----1
|-----2

>miR156d-5p
Score: 2.5 Deg: 22:1088:24:371T_00090336

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1096 ACTGTCTTCTATCTCTCGTGC 1076
| | | | | | | * | * | | | | *
| | | | | | |-----2
| | | | | |-----1
| | | | |-----1
| | | |-----1
| | |-----2
| |-----3
|-----22
|-----1
|-----2

>miR156d-5p
Score: 2.5 Deg: 22:1171:24:378T_00090333

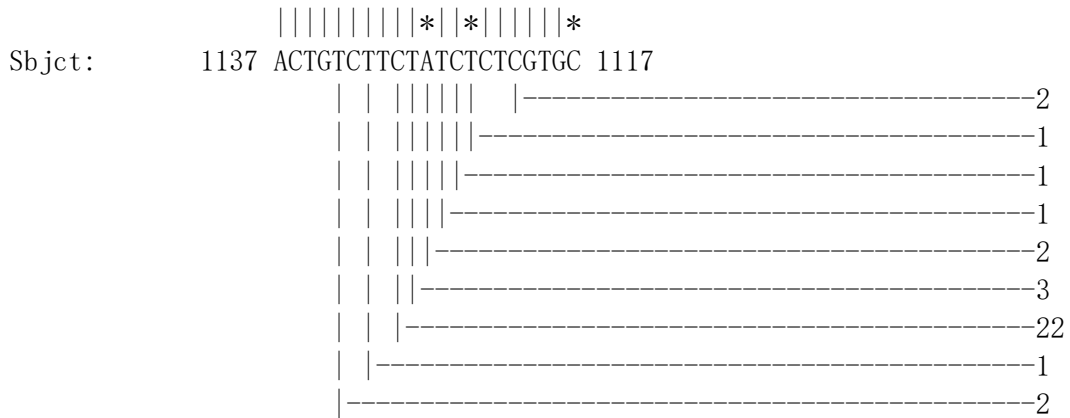
Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1179 ACTGTCTTCTATCTCTCGTGC 1159
| | | | | | | * | * | | | | *
| | | | | | |-----2
| | | | | |-----1
| | | |-----1



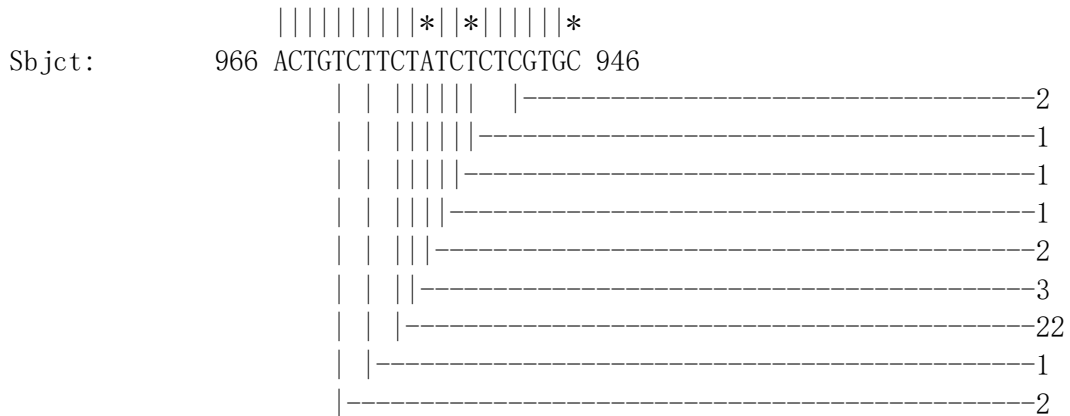
>miR156d-5p
Score: 2.5 Deg: 22:1129:24:363T_00090331

Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156d-5p
Score: 2.5 Deg: 22:958:24:363 T_00090335

Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156d-5p
Score: 2.5 Deg: 22:941:24:361 T_00090334

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

          |||||*||*|||*
Sbjct:    949 ACTGTCTTCTATCTCTCGTGC 929
          |||||-----2
          |||||-----1
          |||||-----1
          |||||-----1
          |||-----2
          |||-----3
          |||-----22
          ||-----1
          |-----2

```

>miR156d-5p

Score: 2.0 Deg: 79:1218:79:519T_00059648

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

          |||||*|||**
Sbjct:    1226 ACTGTCTTCTCTCTCGTAC 1206
          |||||-----1
          |||||-----3
          |||||-----2
          |||||-----2
          |||||-----50
          |||||-----79
          |||||-----3
          |||||-----3
          |||-----1
          ||-----1
          |-----1

```

>miR156d-5p

Score: 1.5 Deg: 9:1100:9:46 T_00080616

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

          |||||*|||*
Sbjct:    1109 ACTGTCTTCTCTCTCGTGT 1089
          |||-----1
          |||-----1
          |||-----6
          ||-----9
          |-----4

```

>miR156d-5p

Score: 1.5 Deg: 9:1250:9:33 T_00080613

Query: 1 TGACAGAAGAGAGTGAGCAC

21

Sbjct: 1259 ACTGTCTTCTCTCTCTCGTGT 1239

|||||*|||||*
||| | |-----1
||| | |-----1
||| |-----6
||-----9
|-----4

>miR156d-5p

Score: 1.5 Deg: 9:1195:9:64 T_00080614

Query: 1 TGACAGAAGAGAGTGAGCAC

21

Sbjct: 1204 ACTGTCTTCTCTCTCTCGTGT 1184

|||||*|||||*
||| | |-----1
||| | |-----1
||| |-----6
||-----9
|-----4

>miR156d-5p

Score: 1.5 Deg: 9:1124:9:46 T_00080615

Query: 1 TGACAGAAGAGAGTGAGCAC

21

Sbjct: 1133 ACTGTCTTCTCTCTCTCGTGT 1113

|||||*|||||*
||| | |-----1
||| | |-----1
||| |-----6
||-----9
|-----4

>miR156d-5p

Score: 1.5 Deg: 9:1250:9:64 T_00080612

Query: 1 TGACAGAAGAGAGTGAGCAC

21

|||||*|||||*

Sbjct: 1259 ACTGTCTTCTCTCTCTCGTGT 1239

```

      ||  |  |  |  |-----1
      ||  |  |  |-----1
      ||  |-----6
      ||-----9
      |-----4

```

>miR156d-5p
 Score: 1.5 Deg: 12:1418:12:64 T_00046313

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

|||||||*|||*
 Sbjct: 1427 ACTGTCTTCTCTCTCTCGTGT 1407

```

      |  |||  |  |-----1
      |  |||  |-----1
      |  |||  |-----4
      |  ||-----1
      |  |-----12
      |-----10
      |-----2

```

>miR156d-5p
 Score: 1.5 Deg: 77:2106:83:749T_00052738

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

|||||||*|||*
 Sbjct: 2114 ACTGTCTTCTCTCTCTCGTGC 2094

```

      |  |||||  ||-----1
      |  |||||  ||-----1
      |  |||||  |-----1
      |  |||||-----1
      |  ||||-----1
      |  ||||-----1
      |  |||-----1
      |  ||-----9
      |  |-----56
      |-----77
      |-----1

```

>miR156d-5p
 Score: 1.5 Deg: 77:443:77:327 T_00052739

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

      |||||*|||*
Sbjct: 451 ACTGTCTTCTCTCTCGTGC 431
      | ||||| ||-----1
      | ||||| ||-----1
      | ||||| |-----1
      | ||||| |-----1
      | ||||| |-----1
      | ||||| |-----1
      | |||| |-----1
      | ||| |-----9
      | || |-----56
      | |-----77
      |-----1
```

>miR156d-5p

Score: 1.5 Deg: 77:2114:83:749T_00052737

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```

      |||||*|||*
Sbjct: 2122 ACTGTCTTCTCTCTCGTGC 2102
      | ||||| ||-----1
      | ||||| ||-----1
      | ||||| |-----1
      | ||||| |-----1
      | ||||| |-----1
      | ||||| |-----1
      | |||| |-----1
      | ||| |-----1
      | || |-----9
      | || |-----56
      | |-----77
      |-----1
```

>miR156d-5p

Score: 1.5 Deg: 5:2012:5:54 T_00071663

Query: 1 TGACAGAAGAGAGTGAGCAC
21

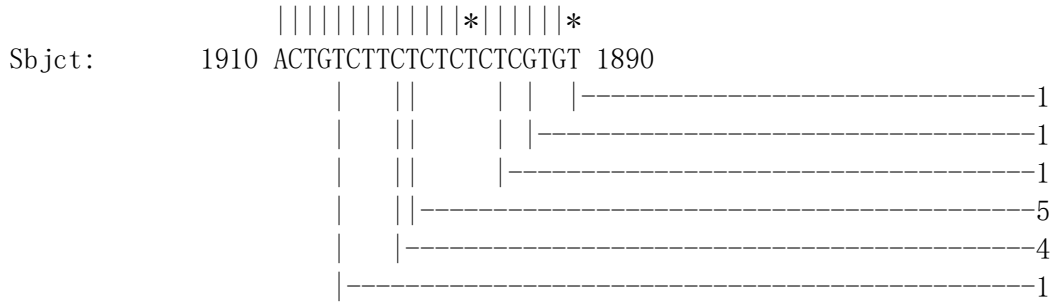
```

      |||||*|||*
Sbjct: 2021 ACTGTCTTCTCTCTCGTGT 2001
      | || |-----1
      | || |-----1
      | || |-----1
      | ||-----5
```



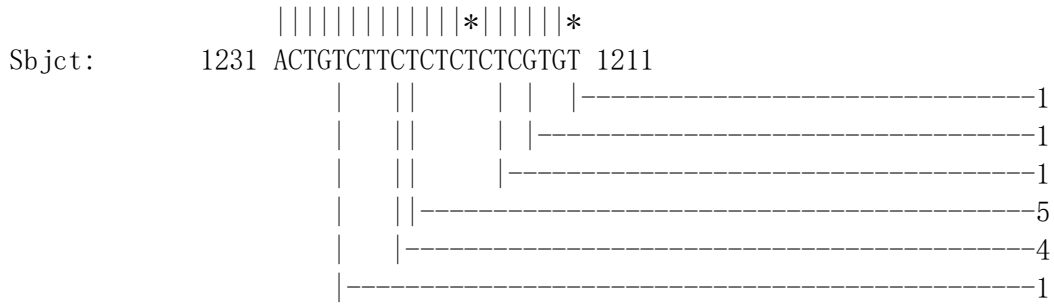
>miR156d-5p
Score: 1.5 Deg: 5:1901:5:45 T_00071657

Query: 1 TGACAGAAGAGAGTGAGCAC
21



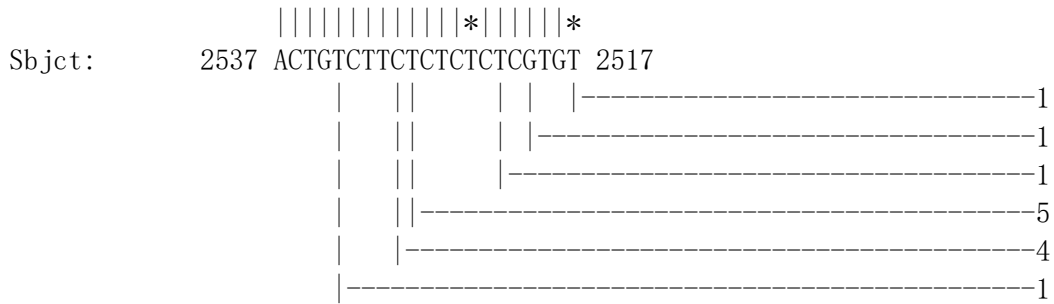
>miR156d-5p
Score: 1.5 Deg: 5:1222:5:44 T_00071664

Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156d-5p
Score: 1.5 Deg: 5:2528:631:10547 T_00071658

Query: 1 TGACAGAAGAGAGTGAGCAC
21



```
>miR156d-5p
Score: 1.5 Deg: 5:1457:5:53 T_00071665
```

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```

Query:          1 TGACAGAAGAGAGTGAGCAC
21
                |||||*|||*
Sbjct: 1466 ACTGTCTTCTCTCTCGTGT 1446
           |   |   |   |-----1
           |   |   |   |-----1
           |   |   |   |-----1
           |   |-----5
           |   |-----4
           |-----1

```

```
>miR156d-5p
Score: 1.5 Deg: 5:2084:631:10538 T_00071656
```

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```

Query:      1 TGACAGAAGAGAGTGAGCAC
21
          |||||*|||*
Sbjct: 2093 ACTGTCTTCTCTCTCGTGT 2073
          |  |  |  |  |-----1
          |  |  |  |  |-----1
          |  |  |  |  |-----1
          |  |  |-----5
          |  |-----4
          |-----1

```

```
>miR156d-5p
Score: 1.5  Deg: 5:1826:5:53    T_00071661
```

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```

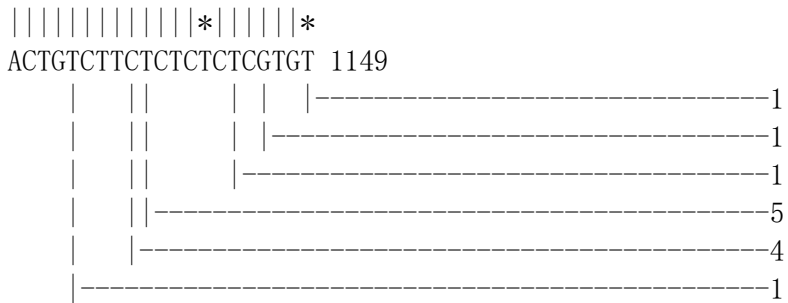
Query:      1 TGACAGAAGAGAGTGAGCAC
            21
            |||||*|||*
Sbjct: 1835 ACTGTCTTCTCTCTCGTGT 1815
            |  |  |  |  |-----1
            |  |  |  |  |-----1
            |  |  |  |  |-----1
            |  |  |-----5
            |  |-----4
            |-----1

```

```
>miR156d-5p
Score: 1.5 Deg: 5:1160:5:44 T_00071667
```

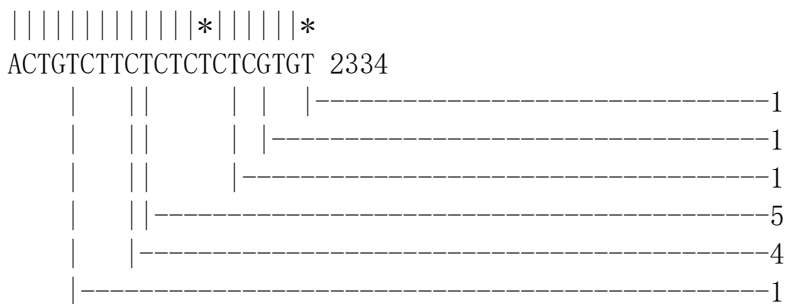
```
>miR156d-5p
Score: 1.5 Deg: 5:1160:5:44 T_00071667
```

Sbjct: 1169 ACTGTCTTCTCTCTCTCGTGT 1149



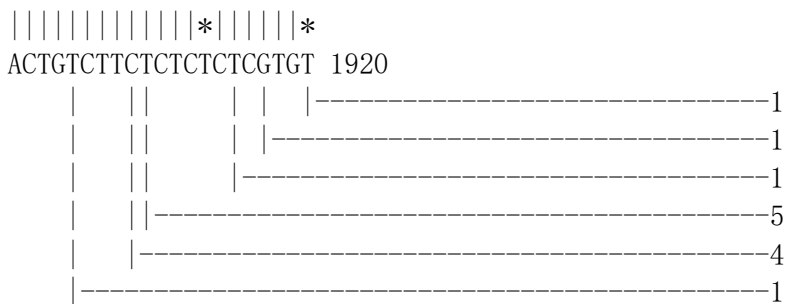
Score: 1.5 Deg: 5:2345:5:54 T_00071659

Sbjct: 2354 ACTGTCTTCTCTCTCGTGT 2334



Score: 1.5 Deg: 5:1931:631:10538 T_00071660

Sbjct: 1940 ACTGTCTTCTCTCTCGTGT 1920



Score: 1.5 Deg: 5:2217:631:10547 T_00071662

| | | | | | | | | | *

Sbjct: 2226 ACTGTCTTCTCTCTCTCGTGT 2206

```

      |  |  |  |  |  |  |-----1
      |  |  |  |  |  |-----1
      |  |  |  |  |  |-----1
      |  |  |  |  |  |-----5
      |  |  |  |  |  |-----4
      |  |  |  |  |  |-----1

```

>miR156d-5p
 Score: 1.5 Deg: 5:1161:5:44 T_00071666

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

|||||||*|||*
 Sbjct: 1170 ACTGTCTTCTCTCTCTCGTGT 1150

```

      |  |  |  |  |  |-----1
      |  |  |  |  |  |-----1
      |  |  |  |  |  |-----1
      |  |  |  |  |  |-----5
      |  |  |  |  |  |-----4
      |  |  |  |  |  |-----1

```

>miR156e-5p
 Score: 0.8 Deg: 10:1311:27:223T_00091783

Query: 1 TTGACAGAAGAGAGAGAGCAC
 22

:|||||||*
 Sbjct: 1320 GACTGTCTTCTCTCTCTCGTGT 1299

```

      |||  |  |-----1
      |||  |  |-----2
      |||-----6
      ||-----6
      ||-----10
      |-----1

```

>miR156e-5p
 Score: 0.8 Deg: 10:1668:27:226T_00091779

Query: 1 TTGACAGAAGAGAGAGAGCAC
 22

:|||||||*
 Sbjct: 1677 GACTGTCTTCTCTCTCTCGTGT 1656

```

      |||  |  |-----1

```



||-----10
|-----1

>miR156e-5p

Score: 0.8 Deg: 10:1496:27:226T_00091780

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

:|||||||||||||||*
Sbjct: 1505 GACTGTCTTCTCTCTCTCGTGT 1484
|||||-----1
|||||-----2
||||-----6
||-----6
||-----10
|-----1

>miR156e-5p

Score: 1.5 Deg: 22:1017:24:363T_00090332

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

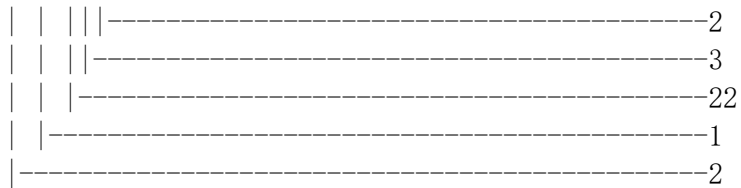
||||||||||*|||||||*
Sbjct: 1026 AACTGTCTTCTATCTCTCGTGC 1005
|||-----2
|||-----1
|||-----1
|||-----1
|||-----2
|||-----3
||-----22
||-----1
|-----2

>miR156e-5p

Score: 1.5 Deg: 22:1088:24:371T_00090336

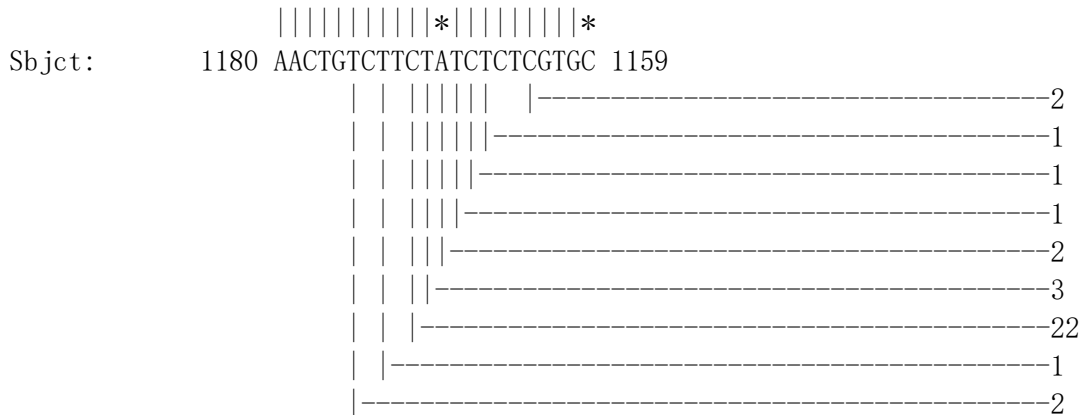
Query: 1 TTGACAGAAGAGAGAGAGCAC
22

||||||||||*|||||||*
Sbjct: 1097 AACTGTCTTCTATCTCTCGTGC 1076
|||-----2
|||-----1
|||-----1
|||-----1



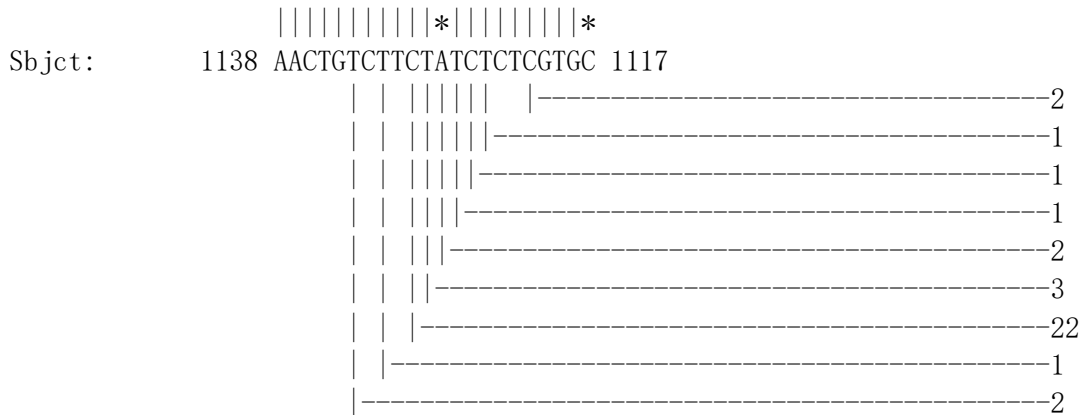
>miR156e-5p
 Score: 1.5 Deg: 22:1171:24:378T_00090333

Query: 1 TTGACAGAAGAGAGAGAGCAC
 22



>miR156e-5p
 Score: 1.5 Deg: 22:1129:24:363T_00090331

Query: 1 TTGACAGAAGAGAGAGAGCAC
 22



>miR156e-5p
 Score: 1.5 Deg: 22:958:24:363 T_00090335

Query: 1 TTGACAGAAGAGAGAGAGCAC
 22

Sbjct:

	*									**	
127	TACTGTCTTCTCTCTCGTAC	1206									
				-----	1						
				-----	3						
				-----	2						
				-----	2						
				-----	50						
				-----	79						
				-----	3						
				-----	3						
				-----	1						

| |-----1
|-----1

>miR156e-5p

Score: 0.5 Deg: 9:1100:9:46 T_00080616

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||||*
Sbjct: 1110 AACTGTCTTCTCTCTCTCGTGT 1089
| | |-----1
| | |-----1
| |-----6
|-----9
|-----4

>miR156e-5p

Score: 0.5 Deg: 9:1250:9:33 T_00080613

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||||*
Sbjct: 1260 AACTGTCTTCTCTCTCTCGTGT 1239
| | |-----1
| | |-----1
| |-----6
|-----9
|-----4

>miR156e-5p

Score: 0.5 Deg: 9:1195:9:64 T_00080614

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||||*
Sbjct: 1205 AACTGTCTTCTCTCTCTCGTGT 1184
| | |-----1
| | |-----1
| |-----6
|-----9
|-----4

>miR156e-5p

Score: 0.5 Deg: 9:1124:9:46 T_00080615

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Sbjct: 1134 AACTGTCTTCTCTCTCTCGTGT 1113
|||||*
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156e-5p
Score: 0.5 Deg: 9:1250:9:64 T_00080612

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Sbjct: 1260 AACTGTCTTCTCTCTCTCGTGT 1239
|||||*
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156e-5p
Score: 1.0 Deg: 12:1418:12:64 T_00046313

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Sbjct: 1428 TACTGTCTTCTCTCTCTCGTGT 1407
|||||
| || | |-----1
| || | |-----1
| || |-----4
| ||-----1
| |-----12
|-----10
|-----2

>miR156e-5p
Score: 0.5 Deg: 77:2106:83:749T_00052738

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||||*

Sbjct: 2115 AACTGTCTTCTCTCTCTCGTGC 2094

```

      | ||||| | || -----1
      | ||||| | || -----1
      | ||||| | | -----1
      | ||||| | -----1
      | ||||| | -----1
      | ||||| | -----1
      | ||||| | -----1
      | ||| | -----9
      | || | -----56
      | | -----77
      | -----1

```

>miR156e-5p
 Score: 0.5 Deg: 77:443:77:327 T_00052739

Query: 1 TTGACAGAAGAGAGAGAGCAC
 22

|||||||*
 Sbjct: 452 AACTGTCTTCTCTCTCTCGTGC 431

```

      | ||||| | || -----1
      | ||||| | || -----1
      | ||||| | | -----1
      | ||||| | -----1
      | ||||| | -----1
      | ||||| | -----1
      | ||||| | -----1
      | ||||| | -----1
      | ||| | -----9
      | || | -----56
      | | -----77
      | -----1

```

>miR156e-5p
 Score: 0.5 Deg: 77:2114:83:749T_00052737

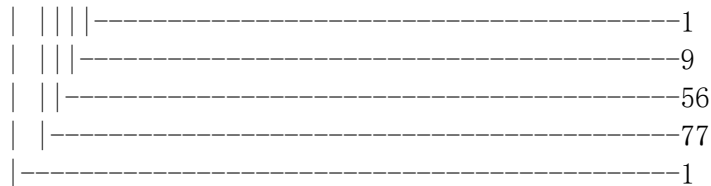
Query: 1 TTGACAGAAGAGAGAGAGCAC
 22

|||||||*
 Sbjct: 2123 AACTGTCTTCTCTCTCTCGTGC 2102

```

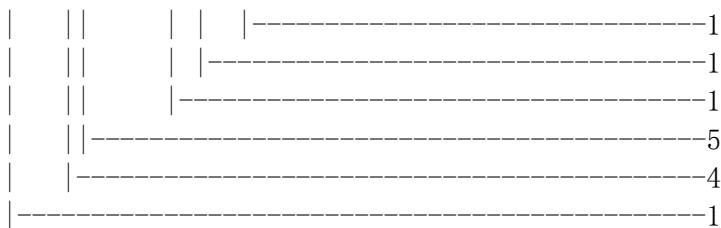
      | ||||| | || -----1
      | ||||| | || -----1
      | ||||| | | -----1
      | ||||| | -----1
      | ||||| | -----1
      | ||||| | -----1

```



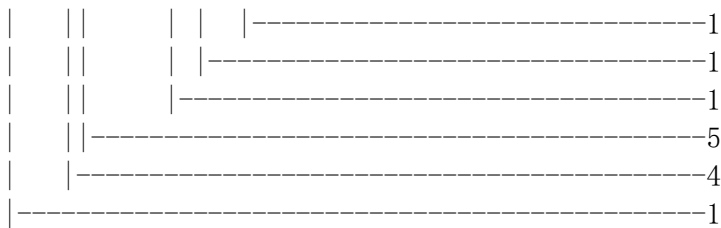
>miR156e-5p
Score: 1.0 Deg: 5:2012:5:54 T_00071663

Query: 1 TTGACAGAAGAGAGAGAGCAC
22
Sbjct: 2022 TACTGTCTTCTCTCTCTCGTGT 2001



>miR156e-5p
Score: 1.0 Deg: 5:1901:5:45 T_00071657

Query: 1 TTGACAGAAGAGAGAGAGCAC
22
Sbjct: 1911 TACTGTCTTCTCTCTCTCGTGT 1890



>miR156e-5p
Score: 1.0 Deg: 5:1222:5:44 T_00071664

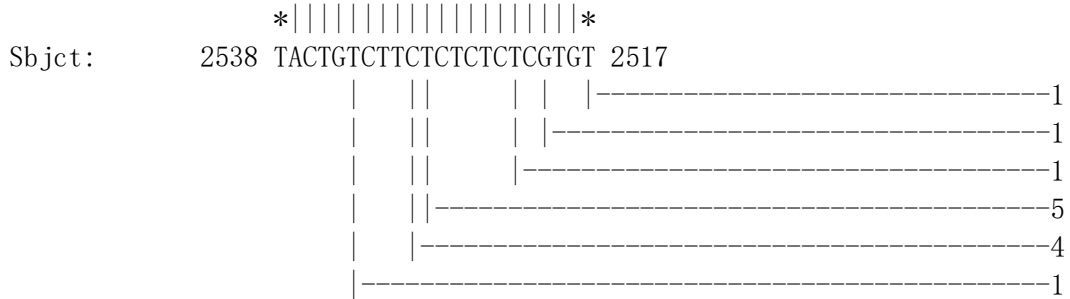
Query: 1 TTGACAGAAGAGAGAGAGCAC
22
Sbjct: 1232 TACTGTCTTCTCTCTCTCGTGT 1211





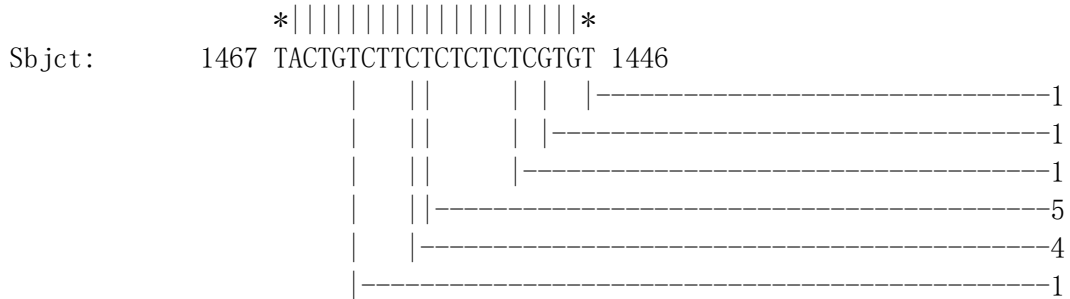
>miR156e-5p
Score: 1.0 Deg: 5:2528:631:10547 T_00071658

Query: 1 TTGACAGAAGAGAGAGAGCAC
22



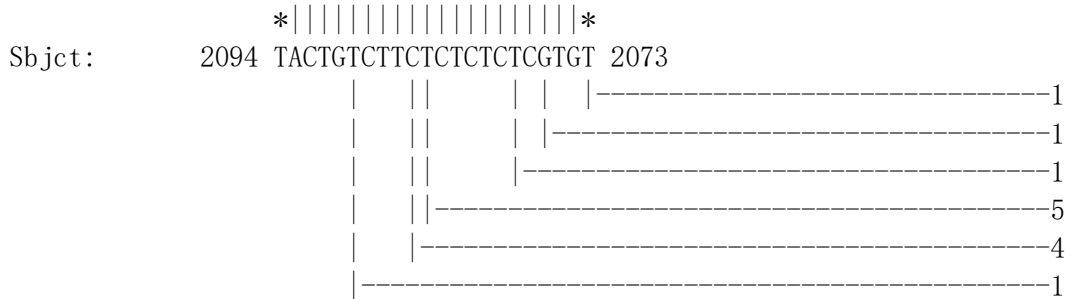
>miR156e-5p
Score: 1.0 Deg: 5:1457:5:53 T_00071665

Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156e-5p
Score: 1.0 Deg: 5:2084:631:10538 T_00071656

Query: 1 TTGACAGAAGAGAGAGAGCAC
22



```
>miR156e-5p
Score: 1.0 Deg: 5:1826:5:53 T_00071661
```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156e-5p
Score: 1.0 Deg: 5:1160:5:44 T_00071667
```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156e-5p
      Score: 1.0  Deg: 5:2345:5:54    T_00071659
```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156e-5p
Score: 1.0 Deg: 5:1931:631:10538 T_00071660
```

```
>miR156e-5p
Score: 1.0 Deg: 5:1931:631:10538 T_00071660
```


Sbjct: 1319 ACTGTCTTCTCTCTCTCGTGT 1299

```
|||||-----1
|||||-----2
||||-----6
|||-----6
||-----10
|-----1
```

>miR156f-5p

Score: 1.5 Deg: 10:1668:27:226T_00091779

Query: 1 TGACAGAAGAGAGTGAGCAC

21

|||||||*|||*|

Sbjct: 1676 ACTGTCTTCTCTCTCTCGTGT 1656

```
|||||-----1
|||||-----2
||||-----6
|||-----6
||-----10
|-----1
```

>miR156f-5p

Score: 1.5 Deg: 10:2823:27:234T_00091781

Query: 1 TGACAGAAGAGAGTGAGCAC

21

|||||||*|||*|

Sbjct: 2831 ACTGTCTTCTCTCTCTCGTGT 2811

```
|||||-----1
|||||-----2
||||-----6
|||-----6
||-----10
|-----1
```

>miR156f-5p

Score: 1.5 Deg: 10:1470:27:223T_00091782

Query: 1 TGACAGAAGAGAGTGAGCAC

21

|||||||*|||*|

Sbjct: 1478 ACTGTCTTCTCTCTCTCGTGT 1458

```
|||||-----1
|||||-----2
```

```

|||-----6
||-----6
||-----10
|-----1

```

>miR156f-5p
 Score: 1.5 Deg: 10:1199:27:223T_00091784

```

Query:      1 TGACAGAAGAGAGTGAGCAC
21
          |||||*|||*
Sbjct:    1207 ACTGTCTTCTCTCTCGTGT 1187
          |||-----1
          |||-----2
          |||-----6
          ||-----6
          ||-----10
          |-----1

```

>miR156f-5p
 Score: 1.5 Deg: 10:1496:27:226T_00091780

```

Query:      1 TGACAGAAGAGAGTGAGCAC
21
          |||||*|||*
Sbjct:    1504 ACTGTCTTCTCTCTCGTGT 1484
          |||-----1
          |||-----2
          |||-----6
          ||-----6
          ||-----10
          |-----1

```

>miR156f-5p
 Score: 2.5 Deg: 22:1017:24:363T_00090332

```

Query:      1 TGACAGAAGAGAGTGAGCAC
21
          |||||*|*|||*
Sbjct:    1025 ACTGTCTTCTATCTCTCGTGC 1005
          |||||-----2
          |||||-----1
          |||||-----1
          |||||-----1
          ||||-----2

```

```

| | | |-----3
| | |-----22
| |-----1
|-----2

```

>miR156f-5p

Score: 2.5 Deg: 22:1088:24:371T_00090336

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```

          |||||*||*|||*
Sbjct: 1096 ACTGTCTTCTATCTCTCGTGC 1076
          | | | | | |-----2
          | | | | | |-----1
          | | | | |-----1
          | | | |-----1
          | | | |-----2
          | | |-----3
          | |-----22
          |-----1
          |-----2

```

>miR156f-5p

Score: 2.5 Deg: 22:1171:24:378T_00090333

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```

          |||||*||*|||*
Sbjct: 1179 ACTGTCTTCTATCTCTCGTGC 1159
          | | | | | |-----2
          | | | | | |-----1
          | | | | |-----1
          | | | |-----1
          | | | |-----2
          | | |-----3
          | |-----22
          |-----1
          |-----2

```

>miR156f-5p

Score: 2.5 Deg: 22:1129:24:363T_00090331

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```

          |||||*||*|||*

```

Sbjct: 1137 ACTGTCTTCTATCTCTCGTGC 1117

```

      | | | | | | | |-----2
      | | | | | | |-----1
      | | | | | | |-----1
      | | | | | | |-----1
      | | | | | | |-----2
      | | | | | | |-----3
      | | | | | | |-----22
      | | | | | | |-----1
      | | | | | | |-----2

```

>miR156f-5p
 Score: 2.5 Deg: 22:958:24:363 T_00090335

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

|||||||*|*|*|*|*|*|*|

Sbjct: 966 ACTGTCTTCTATCTCTCGTGC 946

```

      | | | | | | | |-----2
      | | | | | | |-----1
      | | | | | | |-----1
      | | | | | | |-----1
      | | | | | | |-----1
      | | | | | | |-----2
      | | | | | | |-----3
      | | | | | | |-----22
      | | | | | | |-----1
      | | | | | | |-----2

```

>miR156f-5p
 Score: 2.5 Deg: 22:941:24:361 T_00090334

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

|||||||*|*|*|*|*|*|*|

Sbjct: 949 ACTGTCTTCTATCTCTCGTGC 929

```

      | | | | | | | |-----2
      | | | | | | |-----1
      | | | | | | |-----1
      | | | | | | |-----1
      | | | | | | |-----1
      | | | | | | |-----2
      | | | | | | |-----3
      | | | | | | |-----22
      | | | | | | |-----1
      | | | | | | |-----2

```

>miR156f-5p
Score: 2.0 Deg: 79:1218:79:519T_00059648

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1226 ACTGTCTTCTCTCTCTCGTAC 1206

|||||*|||**

|| ||||| ||-----1
|| ||||| ||-----3
|| ||||| |-----2
|| |||||-----2
|| ||||-----50
|| |||-----79
|| ||-----3
|| |-----3
||-----1
|-----1
|-----1

>miR156f-5p
Score: 1.5 Deg: 9:1100:9:46 T_00080616

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1109 ACTGTCTTCTCTCTCTCGTGT 1089

|||||*|||*

|| | |-----1
|| | |-----1
|| |-----6
||-----9
|-----4

>miR156f-5p
Score: 1.5 Deg: 9:1250:9:33 T_00080613

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1259 ACTGTCTTCTCTCTCTCGTGT 1239

|||||*|||*

|| | |-----1
|| | |-----1
|| |-----6
||-----9
|-----4

>miR156f-5p

Score: 1.5 Deg: 9:1195:9:64 T_00080614

Query: 1 TGACAGAAGAGAGTGAGCAC

21

Sbjct: 1204 ACTGTCTTCTCTCTCTCGTGT 1184

|||||*|||||*
||| | |-----1
||| | |-----1
||| |-----6
||-----9
|-----4

>miR156f-5p

Score: 1.5 Deg: 9:1124:9:46 T_00080615

Query: 1 TGACAGAAGAGAGTGAGCAC

21

Sbjct: 1133 ACTGTCTTCTCTCTCTCGTGT 1113

|||||*|||||*
||| | |-----1
||| | |-----1
||| |-----6
||-----9
|-----4

>miR156f-5p

Score: 1.5 Deg: 9:1250:9:64 T_00080612

Query: 1 TGACAGAAGAGAGTGAGCAC

21

Sbjct: 1259 ACTGTCTTCTCTCTCTCGTGT 1239

|||||*|||||*
||| | |-----1
||| | |-----1
||| |-----6
||-----9
|-----4

>miR156f-5p

Score: 1.5 Deg: 12:1418:12:64 T_00046313

Query: 1 TGACAGAAGAGAGTGAGCAC

21

|||||*|||||*

Diagram illustrating a sequence of horizontal bars (rows) with varying lengths, labeled with numbers on the right:

- Row 1: Length 1
- Row 2: Length 1
- Row 3: Length 4
- Row 4: Length 1
- Row 5: Length 12
- Row 6: Length 10
- Row 7: Length 2

|||||*|||*

[illegible]

| | | | | | | | | | * | | | | | *

Diagram illustrating a sequence of steps or stages, numbered 1 through 10. Each step is represented by a vertical bar and a horizontal dashed line extending to the right. The steps are arranged vertically, with the first three steps having a vertical bar with three segments, the next four having a vertical bar with four segments, and the last three having a vertical bar with five segments. The horizontal dashed lines are of varying lengths, with the last three being significantly longer than the first seven.

|-----1

>miR156f-5p

Score: 1.5 Deg: 77:2114:83:749T_00052737

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjet: 2122 ACTGTCTTCTCTCTCGTGC 2102
| | | | | | | | | * | | | | *
| | | | | | | | |-----1
| | | | | | | | |-----1
| | | | | | | | |-----1
| | | | | | | | |-----1
| | | | | | | | |-----1
| | | | | | | | |-----1
| | | | | | | | |-----1
| | | | | | | | |-----1
| | | | | | | | |-----9
| | | | | | | | |-----56
| | | | | | | | |-----77
|-----1

>miR156f-5p

Score: 1.5 Deg: 5:2012:5:54 T_00071663

Query: 1 TGACAGAAGAGAGTGAGCAC
21

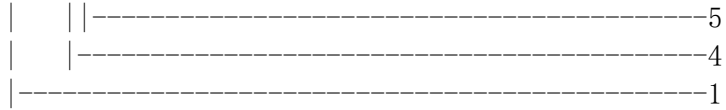
Sbjet: 2021 ACTGTCTTCTCTCTCGTGT 2001
| | | | | | | | | * | | | | *
| | | | | | | | |-----1
| | | | | | | | |-----1
| | | | | | | | |-----1
| | | | | | | | |-----5
| | | | | | | | |-----4
|-----1

>miR156f-5p

Score: 1.5 Deg: 5:1901:5:45 T_00071657

Query: 1 TGACAGAAGAGAGTGAGCAC
21

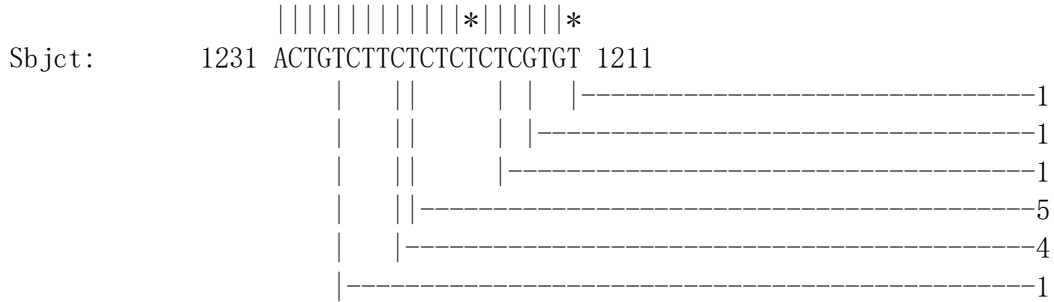
Sbjet: 1910 ACTGTCTTCTCTCTCGTGT 1890
| | | | | | | | | * | | | | *
| | | | | | | | |-----1
| | | | | | | | |-----1
| | | | | | | | |-----1



>miR156f-5p

Score: 1.5 Deg: 5:1222:5:44 T_00071664

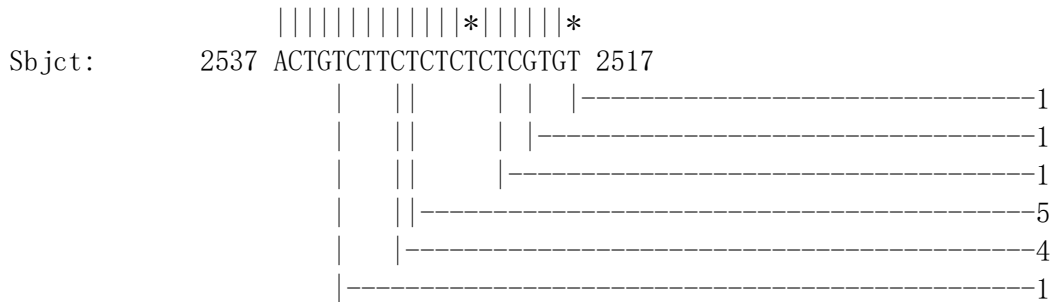
Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156f-5p

Score: 1.5 Deg: 5:2528:631:10547 T_00071658

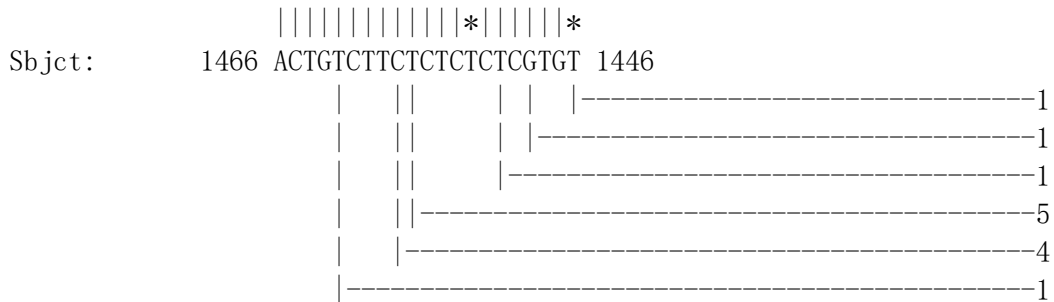
Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156f-5p

Score: 1.5 Deg: 5:1457:5:53 T_00071665

Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156f-5p
Score: 1.5 Deg: 5:2084:631:10538 T_00071656

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 2093 ACTGTCTTCTCTCTCTCGTGT 2073
|||||*|||||*
| | | | |
| | | | |-----1
| | | | |-----1
| | | | |-----1
| | | | |-----5
| | | | |-----4
| | | | |-----1

>miR156f-5p
Score: 1.5 Deg: 5:1826:5:53 T_00071661

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1835 ACTGTCTTCTCTCTCTCGTGT 1815
|||||*|||||*
| | | | |
| | | | |-----1
| | | | |-----1
| | | | |-----1
| | | | |-----5
| | | | |-----4
| | | | |-----1

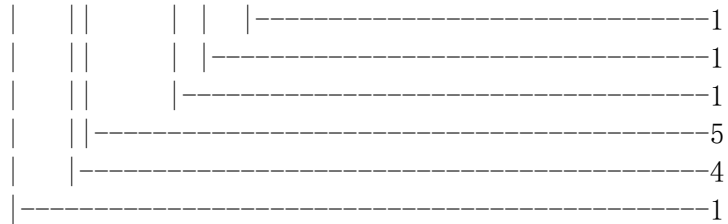
>miR156f-5p
Score: 1.5 Deg: 5:1160:5:44 T_00071667

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1169 ACTGTCTTCTCTCTCTCGTGT 1149
|||||*|||||*
| | | | |
| | | | |-----1
| | | | |-----1
| | | | |-----1
| | | | |-----5
| | | | |-----4
| | | | |-----1

>miR156f-5p
Score: 1.5 Deg: 5:2345:5:54 T_00071659

Sbjct: 2354 ACTGTCTTCTCTCTCTCGTGT 2334



```
>miR156f-5p
Score: 1.5 Deg: 5:1931:631:10538 T_00071660
```

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1940 ACTGTCTTCTCTCTCTCGTGT 1920



```
>miR156f-5p
Score: 1.5  Deg: 5:2217:631:10547  T_00071662
```

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 2226 ACTGTCTTCTCTCTCTCGTGT 2206



```
>miR156f-5p
Score: 1.5 Deg: 5:1161:5:44 T_00071666
```

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```

          |||||*|||*
Sbjct:    1170 ACTGTCTTCTCTCTCGTGT 1150
          |  |  |  |  |-----1
          |  |  |  |  |-----1
          |  |  |  |  |-----1
          |  |  |-----5
          |  |-----4
          |-----1

```

>miR156g
 Score: 0.8 Deg: 10:1311:27:223T_00091783

```

Query:      1 TTGACAGAAGAGAGAGAGCAC
           22
          :|||*
Sbjct:    1320 GACTGTCTTCTCTCTCGTGT 1299
          |||  |-----1
          |||  |-----2
          |||-----6
          ||-----6
          ||-----10
          |-----1

```

>miR156g
 Score: 0.8 Deg: 10:1668:27:226T_00091779

```

Query:      1 TTGACAGAAGAGAGAGAGCAC
           22
          :|||*
Sbjct:    1677 GACTGTCTTCTCTCTCGTGT 1656
          |||  |-----1
          |||  |-----2
          |||-----6
          ||-----6
          ||-----10
          |-----1

```

>miR156g
 Score: 0.8 Deg: 10:2823:27:234T_00091781

```

Query:      1 TTGACAGAAGAGAGAGAGCAC
           22
          :|||*
Sbjct:    2832 GACTGTCTTCTCTCTCGTGT 2811
          |||  |-----1

```


||-----10
|-----1

>miR156g

Score: 1.5 Deg: 22:1017:24:363T_00090332

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||||||*|||||||*
Sbjct: 1026 AACTGTCTTCTATCTCTCGTGC 1005
| | | | | | |-----2
| | | | | |-----1
| | | | |-----1
| | | |-----1
| | |-----2
| |-----3
|-----22
|-----1
|-----2

>miR156g

Score: 1.5 Deg: 22:1088:24:371T_00090336

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||||||*|||||||*
Sbjct: 1097 AACTGTCTTCTATCTCTCGTGC 1076
| | | | | | |-----2
| | | | | |-----1
| | | | |-----1
| | | |-----1
| | |-----2
| |-----3
|-----22
|-----1
|-----2

>miR156g

Score: 1.5 Deg: 22:1171:24:378T_00090333

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||||||*|||||||*
Sbjct: 1180 AACTGTCTTCTATCTCTCGTGC 1159
| | | | | |-----2

```
>miR156g
Score: 1.5 Deg: 22:941:24:361 T_00090334
```

Sbjct: 950 AACTGTCTTCTATCTCTCGTGC 929

| | | | | | | | | *

[illegible]

```
>miR156g
Score: 1.5  Deg: 79:1218:79:519T_00059648
```

Sbjct: 1227 TACTGTCTTCTCTCTCTCGTAC 1206

[illegible][illegible]

```
>miR156g
Score: 0.5 Deg: 9:1100:9:46 T_00080616
```

Sbjct: 1110 AACTGTCTTCTCTCTCTCGTGT 1089

|||||

|-----4

>miR156g

Score: 0.5 Deg: 9:1250:9:33 T_00080613

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||||*
Sbjct: 1260 AACTGTCTTCTCTCTCTCGTGT 1239
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156g

Score: 0.5 Deg: 9:1195:9:64 T_00080614

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||||*
Sbjct: 1205 AACTGTCTTCTCTCTCTCGTGT 1184
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156g

Score: 0.5 Deg: 9:1124:9:46 T_00080615

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

|||||*
Sbjct: 1134 AACTGTCTTCTCTCTCTCGTGT 1113
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156g

Score: 0.5 Deg: 9:1250:9:64 T_00080612

Query: 1 TTGACAGAAGAGAGAGAGCAC

22

```

      |||||
Sbjct: 1260 AACTGTCTTCTCTCTCTCGTGT 1239
      ||  |  |  |-----1
      ||  |  |  |-----1
      ||  |  |-----6
      ||-----9
      |-----4
```

>miR156g

Score: 1.0 Deg: 12:1418:12:64 T_00046313

Query: 1 TTGACAGAAGAGAGAGAGCAC

22

```

      *|||
Sbjct: 1428 TACTGTCTTCTCTCTCTCGTGT 1407
      |  |||  |  |-----1
      |  |||  |  |-----1
      |  |||  |-----4
      |  |||-----1
      |  ||-----12
      |  |-----10
      |-----2
```

>miR156g

Score: 0.5 Deg: 77:2106:83:749T_00052738

Query: 1 TTGACAGAAGAGAGAGAGCAC

22

```

      |||||
Sbjct: 2115 AACTGTCTTCTCTCTCTCGTGC 2094
      |  |||||  |||-----1
      |  |||||  |||-----1
      |  |||||  |-----1
      |  |||||-----1
      |  |||||-----1
      |  |||||-----1
      |  |||||-----1
      |  |||||-----1
      |  |||-----9
      |  ||-----56
      |  |-----77
      |-----1
```

>miR156g

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156g
```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

>miR156g

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

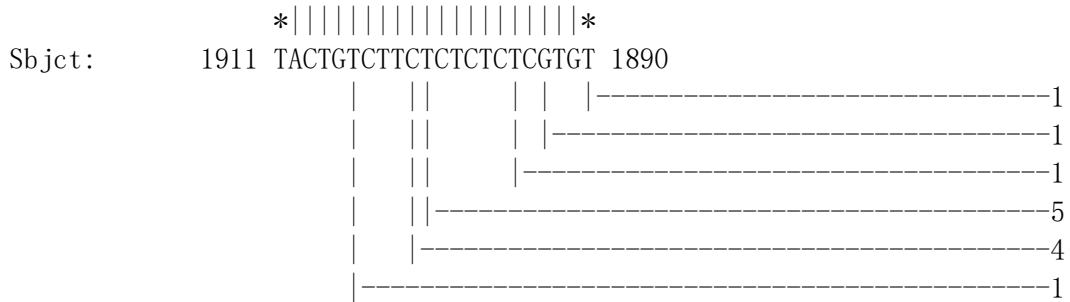
Sbjet: 2022 TACTGTCTTCTCTCTCTCGTGT 2001



>miR156g

Score: 1.0 Deg: 5:1901:5:45 T_00071657

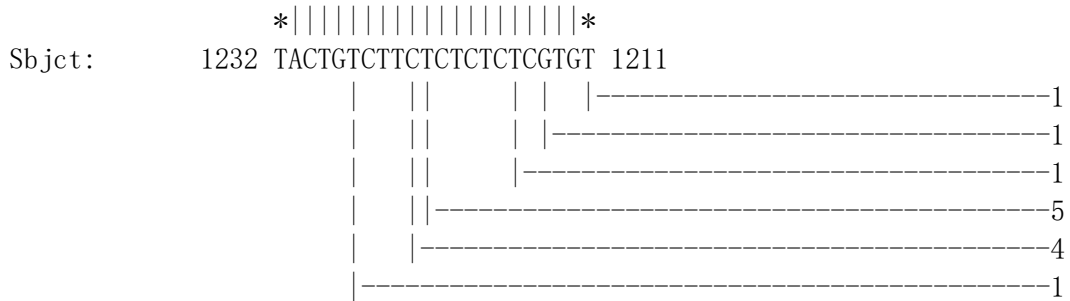
Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156g

Score: 1.0 Deg: 5:1222:5:44 T_00071664

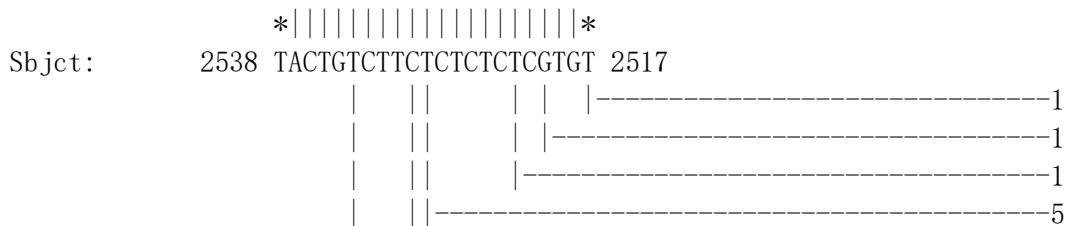
Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156g

Score: 1.0 Deg: 5:2528:631:10547 T_00071658

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

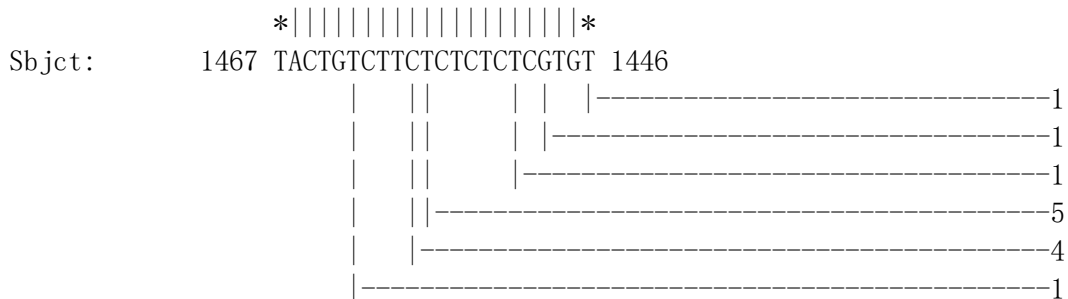




>miR156g

Score: 1.0 Deg: 5:1457:5:53 T_00071665

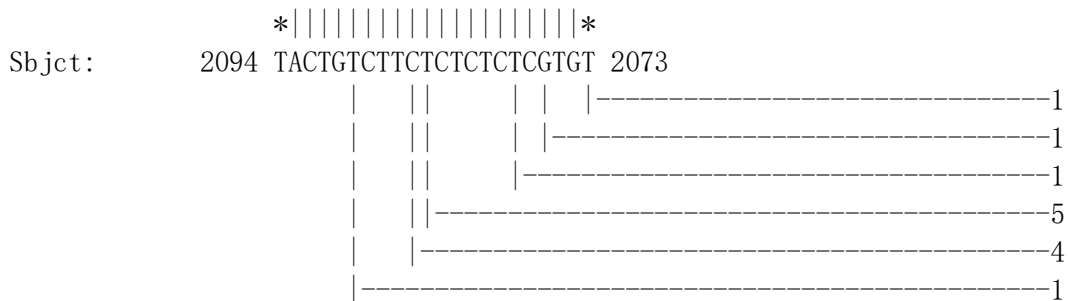
Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156g

Score: 1.0 Deg: 5:2084:631:10538 T_00071656

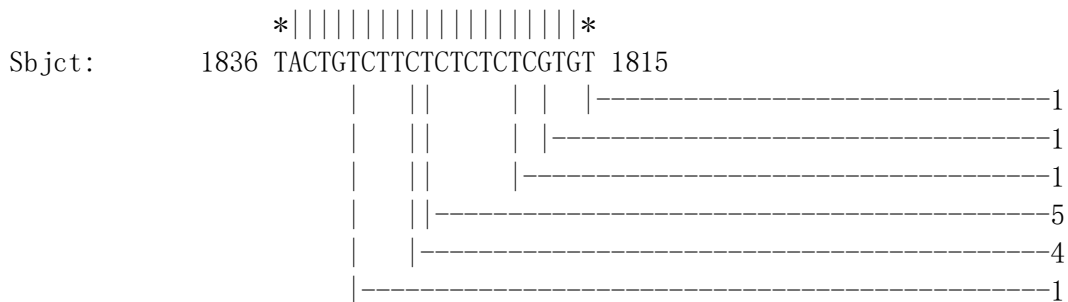
Query: 1 TTGACAGAAGAGAGAGAGCAC
22



>miR156g

Score: 1.0 Deg: 5:1826:5:53 T_00071661

Query: 1 TTGACAGAAGAGAGAGAGCAC
22



```
>miR156g
Score: 1.0 Deg: 5:1160:5:44 T_00071667
```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156g
Score: 1.0 Deg: 5:2345:5:54 T_00071659
```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156g
Score: 1.0 Deg: 5:1931:631:10538 T_00071660
```

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Query: 1 TTGACAGAAGAGAGAGAGCAC
22

```
>miR156g
Score: 1.0 Deg: 5:2217:631:10547 T_00071662
```

Score: 1.0 Deg: 5:2217:631:10547 T_00071662

Sbjct: 2227 TACTGTCTTCTCTCTCTCGTGT 2206



Query: 1 TTGACAGAAGAGAGAGAGCAC
22

Diagram illustrating a sequence of steps or tasks, numbered 1 through 10, connected by horizontal dashed lines, suggesting a flow or timeline.

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Query: 1 TGACAGAAGAGAGTGAGCAC
21

| | | | | | | | | | *

Sbjct: 1676 ACTGTCTTCTCTCTCTCGTGT 1656

```

      ||||      |      |-----1
      ||||      |-----2
      ||||-----6
      |||-----6
      ||-----10
      |-----1

```

>miR156h-5p
 Score: 1.5 Deg: 10:2823:27:234T_00091781

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

Sbjct: 2831 ACTGTCTTCTCTCTCTCGTGT 2811

```

      |||||-----1
      ||||      |-----2
      ||||-----6
      |||-----6
      ||-----10
      |-----1

```

>miR156h-5p
 Score: 1.5 Deg: 10:1470:27:223T_00091782

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

Sbjct: 1478 ACTGTCTTCTCTCTCTCGTGT 1458

```

      |||||-----1
      ||||      |-----2
      ||||-----6
      |||-----6
      ||-----10
      |-----1

```

>miR156h-5p
 Score: 1.5 Deg: 10:1199:27:223T_00091784

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

Sbjct: 1207 ACTGTCTTCTCTCTCTCGTGT 1187

```

      |||||-----1
      ||||      |-----2

```

```

      |||-----6
      ||-----6
      ||-----10
      |-----1

```

>miR156h-5p

Score: 1.5 Deg: 10:1496:27:226T_00091780

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

      |||||*|||*
Sbjct: 1504 ACTGTCTTCTCTCTCGTGT 1484
      ||| |-----1
      ||| |-----2
      |||-----6
      ||-----6
      ||-----10
      |-----1

```

>miR156h-5p

Score: 2.5 Deg: 22:1017:24:363T_00090332

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

      |||||*|*|||*
Sbjct: 1025 ACTGTCTTCTATCTCTCGTGC 1005
      |||||-----2
      |||||-----1
      |||||-----1
      |||||-----1
      ||||-----2
      |||-----3
      ||-----22
      |-----1
      |-----2

```

>miR156h-5p

Score: 2.5 Deg: 22:1088:24:371T_00090336

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

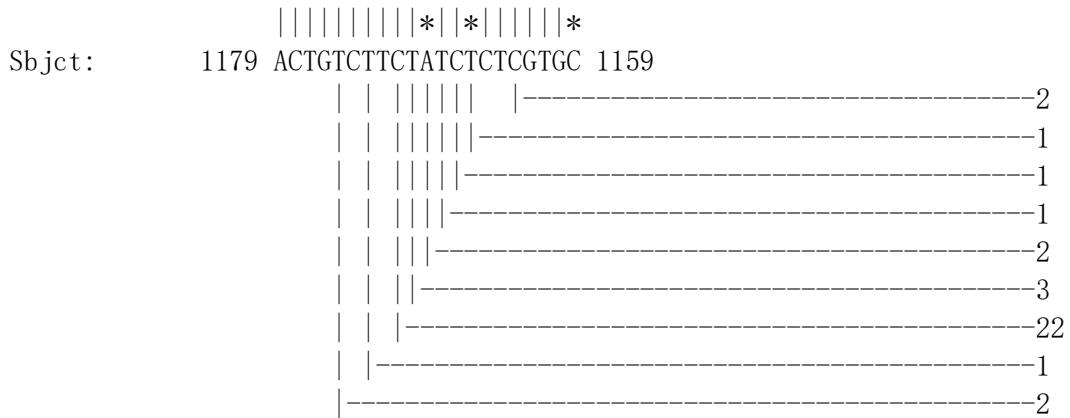
      |||||*|*|||*
Sbjct: 1096 ACTGTCTTCTATCTCTCGTGC 1076
      |||||-----2
      |||||-----1

```



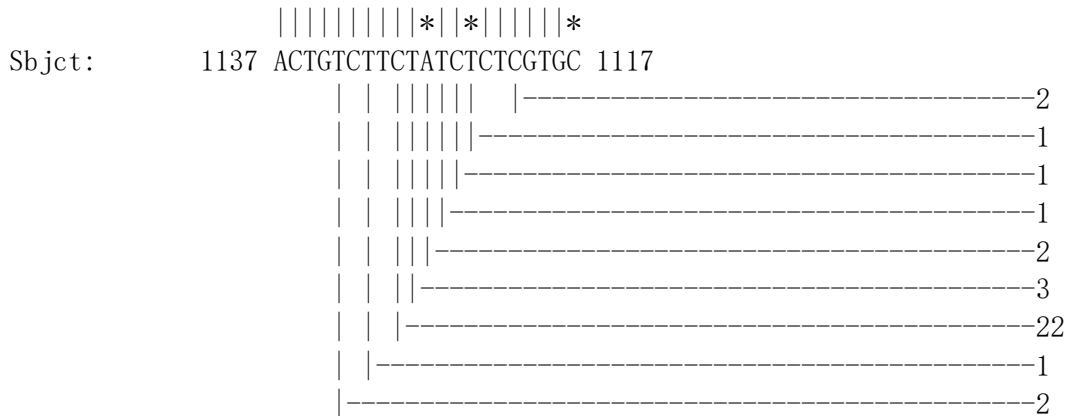
>miR156h-5p
 Score: 2.5 Deg: 22:1171:24:378T_00090333

Query: 1 TGACAGAAGAGAGTGAGCAC
 21



>miR156h-5p
 Score: 2.5 Deg: 22:1129:24:363T_00090331

Query: 1 TGACAGAAGAGAGTGAGCAC
 21



>miR156h-5p
 Score: 2.5 Deg: 22:958:24:363 T_00090335

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 966 ACTGTCTTCTATCTCTCGTGC 946
|||||||*|*|*|*|*
| | | | | | |-----2
| | | | | |-----1
| | | | |-----1
| | | |-----1
| | |-----2
| |-----3
|-----22
|-----1
|-----2

>miR156h-5p
Score: 2.5 Deg: 22:941:24:361 T_00090334

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 949 ACTGTCTTCTATCTCTCGTGC 929
|||||||*|*|*|*|*
| | | | | | |-----2
| | | | | |-----1
| | | | |-----1
| | | |-----1
| | |-----2
| |-----3
|-----22
|-----1
|-----2

>miR156h-5p
Score: 2.0 Deg: 79:1218:79:519T_00059648

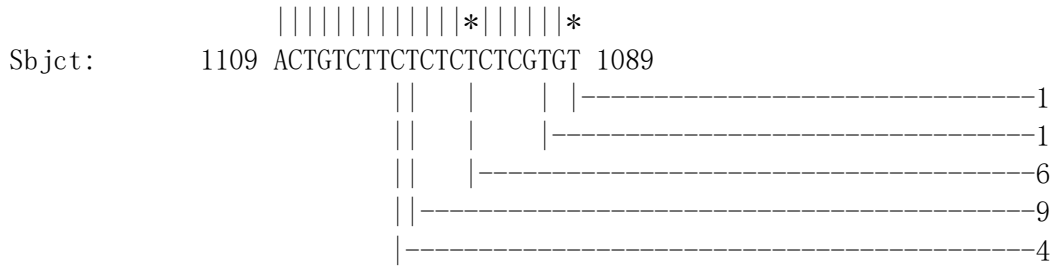
Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1226 ACTGTCTTCTCTCTCGTAC 1206
|||||||*|*|*|*|*
| | | | | |-----1
| | | | |-----3
| | | |-----2
| | |-----2
| |-----50
|-----79
|-----3



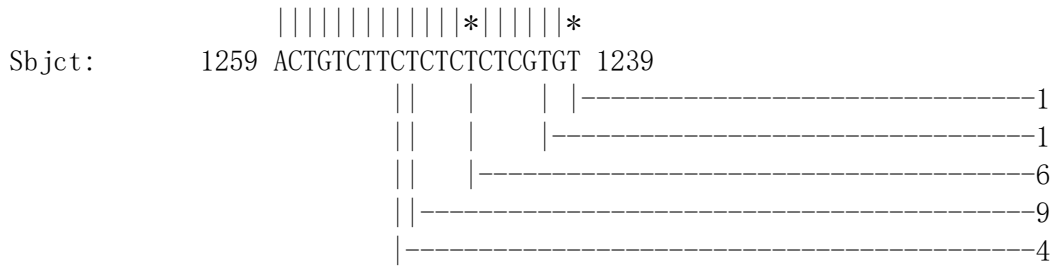
>miR156h-5p
Score: 1.5 Deg: 9:1100:9:46 T_00080616

Query: 1 TGACAGAAGAGAGTGAGCAC
21



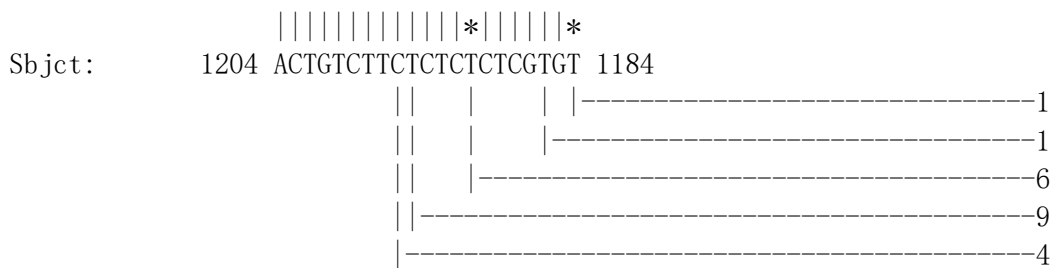
>miR156h-5p
Score: 1.5 Deg: 9:1250:9:33 T_00080613

Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156h-5p
Score: 1.5 Deg: 9:1195:9:64 T_00080614

Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156h-5p

Score: 1.5 Deg: 9:1124:9:46 T_00080615

Query: 1 TGACAGAAGAGAGTGAGCAC

21

|||||||*|||*
Sbjct: 1133 ACTGTCTTCTCTCTCGTGT 1113
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156h-5p

Score: 1.5 Deg: 9:1250:9:64 T_00080612

Query: 1 TGACAGAAGAGAGTGAGCAC

21

|||||||*|||*
Sbjct: 1259 ACTGTCTTCTCTCTCGTGT 1239
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156h-5p

Score: 1.5 Deg: 12:1418:12:64 T_00046313

Query: 1 TGACAGAAGAGAGTGAGCAC

21

|||||||*|||*
Sbjct: 1427 ACTGTCTTCTCTCTCGTGT 1407
| || | |-----1
| || | |-----1
| || |-----4
| ||-----1
| |-----12
| |-----10
|-----2

>miR156h-5p

Score: 1.5 Deg: 77:2106:83:749T_00052738

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

          |||||*|||*
Sbjct:    2114 ACTGTCTTCTCTCTCGTGC 2094
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----9
          | ||||| |||-----56
          | ||||| |||-----77
          |-----1

```

>miR156h-5p
 Score: 1.5 Deg: 77:443:77:327 T_00052739

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

```

          |||||*|||*
Sbjct:    451 ACTGTCTTCTCTCTCGTGC 431
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----9
          | ||||| |||-----56
          | ||||| |||-----77
          |-----1

```

>miR156h-5p
 Score: 1.5 Deg: 77:2114:83:749T_00052737

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

```

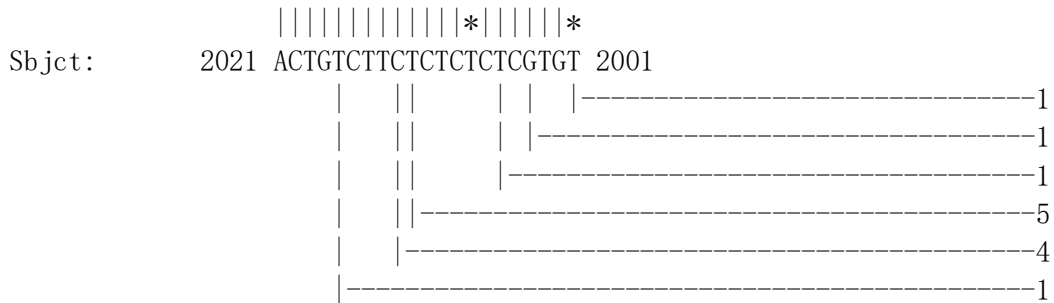
          |||||*|||*
Sbjct:    2122 ACTGTCTTCTCTCTCGTGC 2102
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1
          | ||||| |||-----1

```



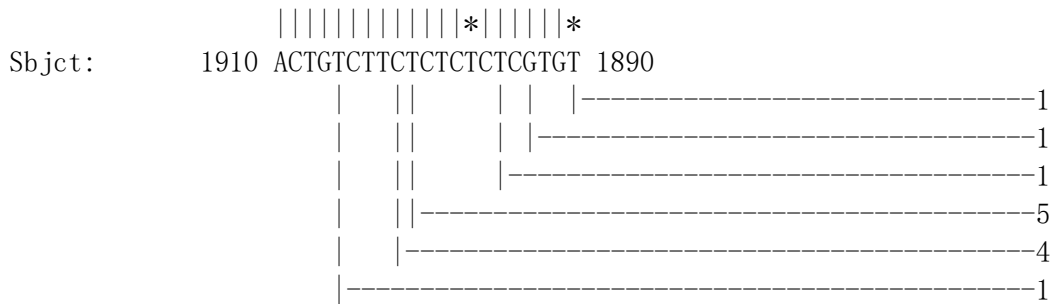
>miR156h-5p
 Score: 1.5 Deg: 5:2012:5:54 T_00071663

Query: 1 TGACAGAAGAGAGTGAGCAC
 21



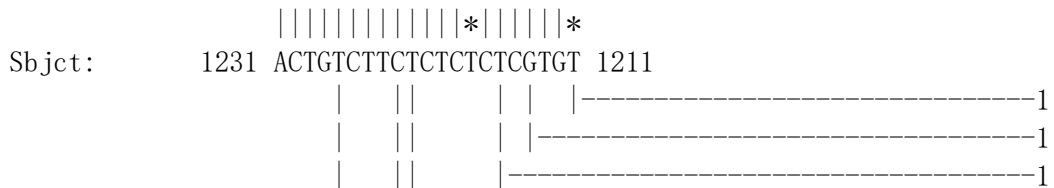
>miR156h-5p
 Score: 1.5 Deg: 5:1901:5:45 T_00071657

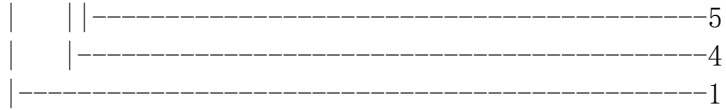
Query: 1 TGACAGAAGAGAGTGAGCAC
 21



>miR156h-5p
 Score: 1.5 Deg: 5:1222:5:44 T_00071664

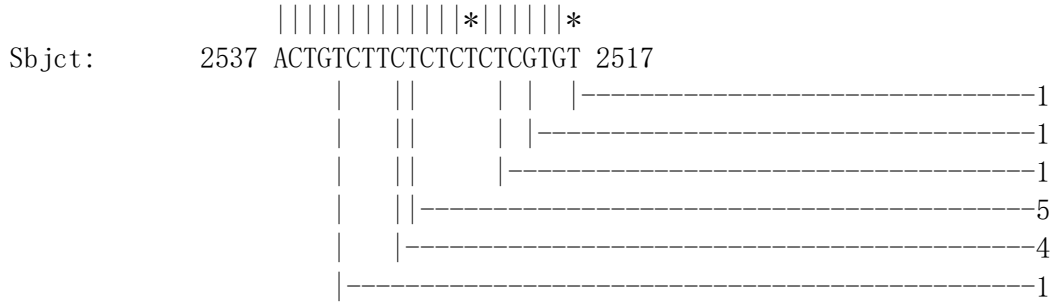
Query: 1 TGACAGAAGAGAGTGAGCAC
 21





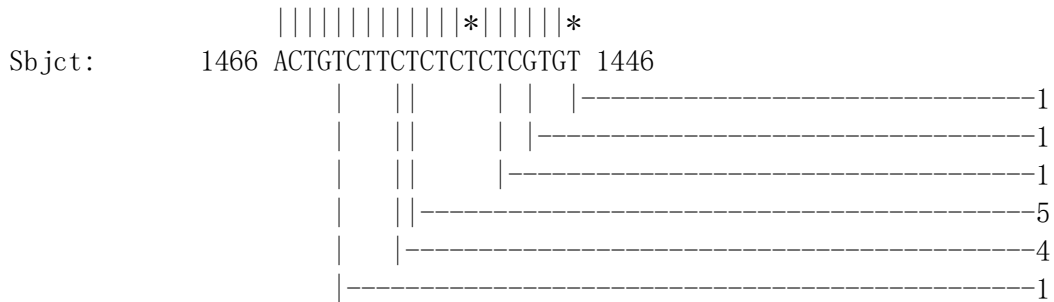
>miR156h-5p
Score: 1.5 Deg: 5:2528:631:10547 T_00071658

Query: 1 TGACAGAAGAGAGTGAGCAC
21



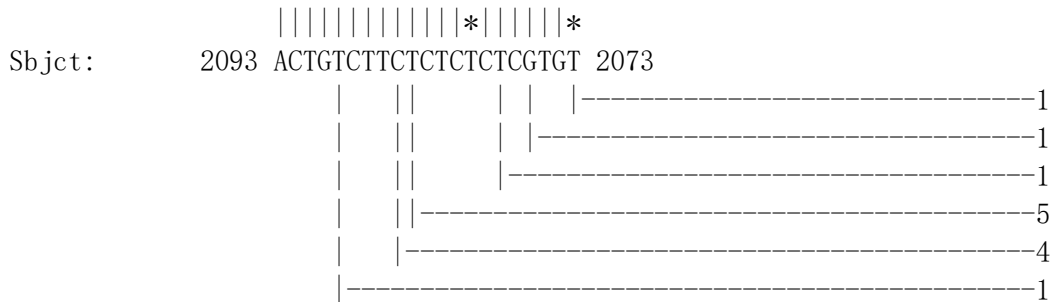
>miR156h-5p
Score: 1.5 Deg: 5:1457:5:53 T_00071665

Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156h-5p
Score: 1.5 Deg: 5:2084:631:10538 T_00071656

Query: 1 TGACAGAAGAGAGTGAGCAC
21



Score: 1.5 Deg: 5:1826:5:53 T_00071661

Sbjct: 1835 ACTGTCTTCTCTCTCGTGT 1815

| | | | | | | | * | | | *

| | |-----1

| | |-----1

| | |-----1

| |-----5

| |-----4

|-----1

Score: 1.5 Deg: 5:1160:5:44 T_00071667

Sbjct: 1169 ACTGTCTTCTCTCTCGTGT 1149

| | | | | | | | * | | | | *

| | |-----1

| | |-----1

| | |-----1

| |-----5

| |-----4

|-----1

Score: 1.5 Deg: 5:2345:5:54 T_00071659

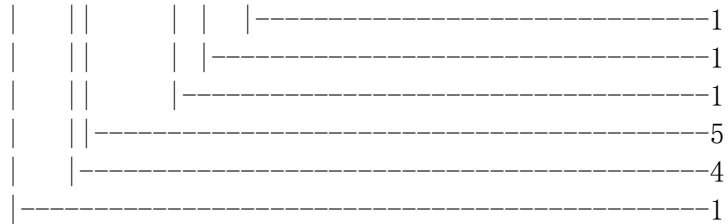
Sbjct: 2354 ACTGTCTTCTCTCTCGTGT 2334

|||||*|||*

-----1
-----1
-----1
-----5
-----4
-----1

Score: 1.5 Deg: 5:1931:631:10538 T_00071660

Sbjct: 1940 ACTGTCTTCTCTCTCTCGTGT 1920



```
>miR156h-5p
Score: 1.5  Deg: 5:2217:631:10547  T_00071662
```

Query: 1 TGACAGAAGAGAGTGAGCAC
21

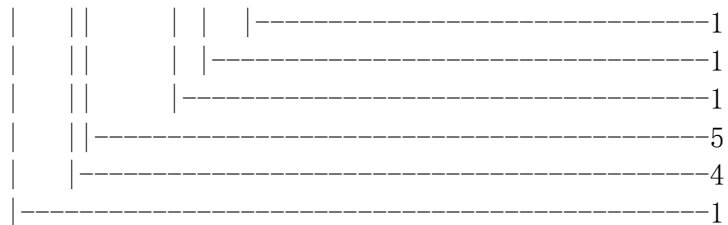
Sbjct: 2226 ACTGTCTTCTCTCTCTCGTGT 2206



```
>miR156h-5p
Score: 1.5  Deg: 5:1161:5:44    T_00071666
```

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1170 ACTGTCTTCTCTCTCTCGTGT 1150



```
>miR156i-5p
Score: 1.5 Deg: 10:1311:27:223T_00091783
```

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```

          |||||*|||*
Sbjct:    1319 ACTGTCTTCTCTCTCGTGT 1299
          |||||-----1
          |||||-----2
          ||||-----6
          ||||-----6
          ||-----10
          |-----1

```

>miR156i-5p
 Score: 1.5 Deg: 10:1668:27:226T_00091779

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

```

          |||||*|||*
Sbjct:    1676 ACTGTCTTCTCTCTCGTGT 1656
          |||||-----1
          |||||-----2
          ||||-----6
          ||||-----6
          ||-----10
          |-----1

```

>miR156i-5p
 Score: 1.5 Deg: 10:2823:27:234T_00091781

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

```

          |||||*|||*
Sbjct:    2831 ACTGTCTTCTCTCTCGTGT 2811
          |||||-----1
          |||||-----2
          ||||-----6
          ||||-----6
          ||-----10
          |-----1

```

>miR156i-5p
 Score: 1.5 Deg: 10:1470:27:223T_00091782

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

```

          |||||*|||*
Sbjct:    1478 ACTGTCTTCTCTCTCGTGT 1458
          |||||-----1

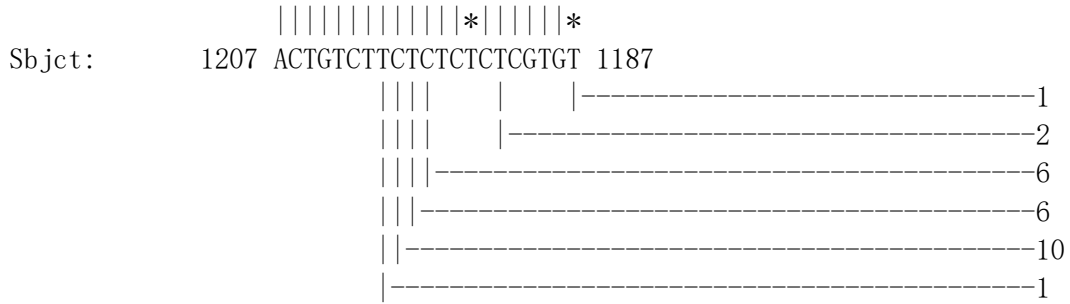
```



>miR156i-5p

Score: 1.5 Deg: 10:1199:27:223T_00091784

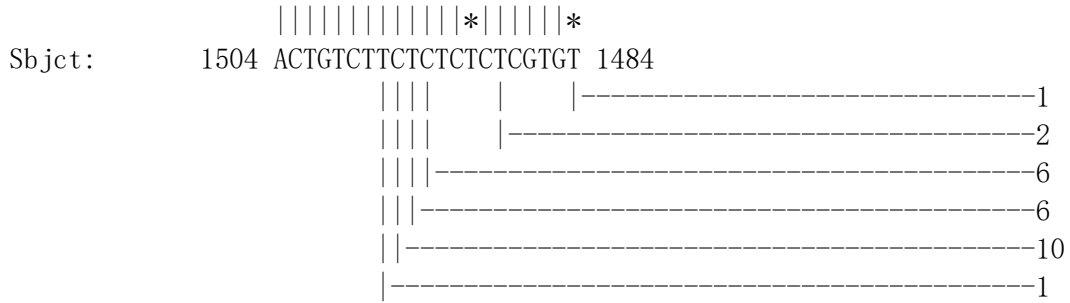
Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156i-5p

Score: 1.5 Deg: 10:1496:27:226T_00091780

Query: 1 TGACAGAAGAGAGTGAGCAC
21

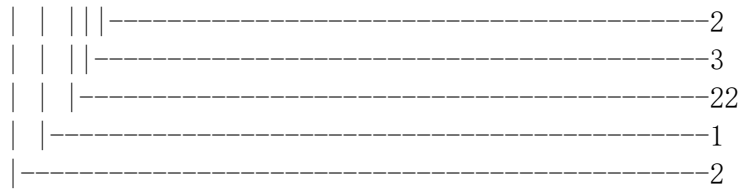


>miR156i-5p

Score: 2.5 Deg: 22:1017:24:363T_00090332

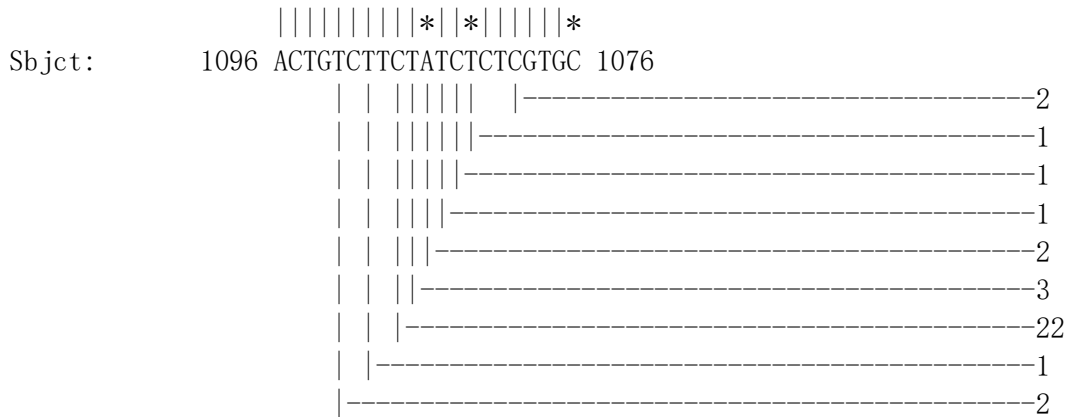
Query: 1 TGACAGAAGAGAGTGAGCAC
21





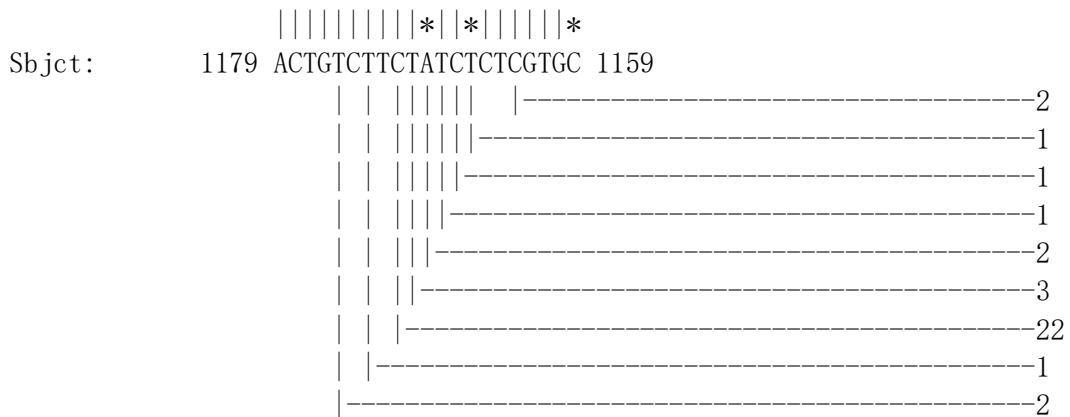
>miR156i-5p
Score: 2.5 Deg: 22:1088:24:371T_00090336

Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156i-5p
Score: 2.5 Deg: 22:1171:24:378T_00090333

Query: 1 TGACAGAAGAGAGTGAGCAC
21



>miR156i-5p
Score: 2.5 Deg: 22:1129:24:363T_00090331

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```

          |||||*||*|||*
Sbjct:    1137 ACTGTCTTCTATCTCTCGTGC 1117
          | | | | | | |-----2
          | | | | | |-----1
          | | | | |-----1
          | | | |-----1
          | | |-----2
          | |-----3
          |-----22
          |-----1
          |-----2

```

>miR156i-5p
 Score: 2.5 Deg: 22:958:24:363 T_00090335

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

```

          |||||*||*|||*
Sbjct:    966 ACTGTCTTCTATCTCTCGTGC 946
          | | | | | | |-----2
          | | | | | |-----1
          | | | | |-----1
          | | | |-----1
          | | |-----2
          | |-----3
          |-----22
          |-----1
          |-----2

```

>miR156i-5p
 Score: 2.5 Deg: 22:941:24:361 T_00090334

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

```

          |||||*||*|||*
Sbjct:    949 ACTGTCTTCTATCTCTCGTGC 929
          | | | | | | |-----2
          | | | | | |-----1
          | | | | |-----1
          | | | |-----1
          | | |-----2
          | |-----3
          |-----22
          |-----1
          |-----2

```

>miR156i-5p
Score: 2.0 Deg: 79:1218:79:519T_00059648

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1226 ACTGTCTTCTCTCTCTCGTAC 1206
|||||*|||**
|| ||||| ||-----1
|| ||||| ||-----3
|| ||||| |-----2
|| |||||-----2
|| |||||-----50
|| ||||-----79
|| ||-----3
|| ||-----3
|| |-----1
||-----1
|-----1

>miR156i-5p
Score: 1.5 Deg: 9:1100:9:46 T_00080616

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1109 ACTGTCTTCTCTCTCGTGT 1089
|||||*|||*
|| | |-----1
|| | |-----1
|| |-----6
||-----9
|-----4

>miR156i-5p
Score: 1.5 Deg: 9:1250:9:33 T_00080613

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1259 ACTGTCTTCTCTCTCGTGT 1239
|||||*|||*
|| | |-----1
|| | |-----1
|| |-----6
||-----9
|-----4

>miR156i-5p
Score: 1.5 Deg: 9:1195:9:64 T_00080614

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1204 ACTGTCTTCTCTCTCTCGTGT 1184
|||||*|||||*
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156i-5p
Score: 1.5 Deg: 9:1124:9:46 T_00080615

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1133 ACTGTCTTCTCTCTCTCGTGT 1113
|||||*|||||*
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156i-5p
Score: 1.5 Deg: 9:1250:9:64 T_00080612

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1259 ACTGTCTTCTCTCTCTCGTGT 1239
|||||*|||||*
|| | |-----1
|| | |-----1
|| |-----6
|-----9
|-----4

>miR156i-5p
Score: 1.5 Deg: 12:1418:12:64 T_00046313

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```

          |||||*|||*
Sbjct: 1427 ACTGTCTTCTCTCTCGTGT 1407
          |  |||  |  |-----1
          |  |||  |  |-----1
          |  |||  |  |-----4
          |  |||  |  |-----1
          |  ||  |-----12
          |  |-----10
          |-----2

```

>miR156i-5p
 Score: 1.5 Deg: 77:2106:83:749T_00052738

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

```

          |||||*|||*
Sbjct: 2114 ACTGTCTTCTCTCTCGTGC 2094
          |  |||||  |||-----1
          |  |||||  |||-----1
          |  |||||  |-----1
          |  |||||  |-----1
          |  |||||  |-----1
          |  |||||  |-----1
          |  ||||  |-----1
          |  |||  |-----1
          |  ||  |-----9
          |  |-----56
          |-----77
          |-----1

```

>miR156i-5p
 Score: 1.5 Deg: 77:443:77:327 T_00052739

Query: 1 TGACAGAAGAGAGTGAGCAC
 21

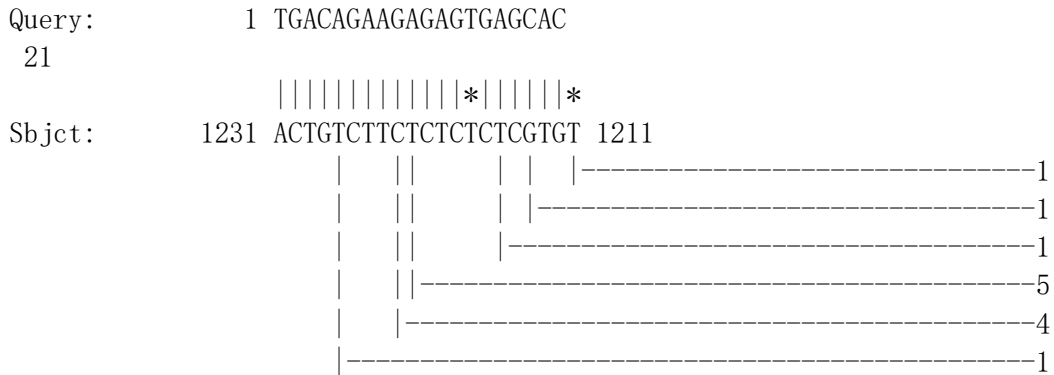
```

          |||||*|||*
Sbjct: 451 ACTGTCTTCTCTCTCGTGC 431
          |  |||||  |||-----1
          |  |||||  |||-----1
          |  |||||  |-----1
          |  |||||  |-----1
          |  |||||  |-----1
          |  |||||  |-----1
          |  ||||  |-----1
          |  |||  |-----1
          |  ||  |-----9
          |  |-----56

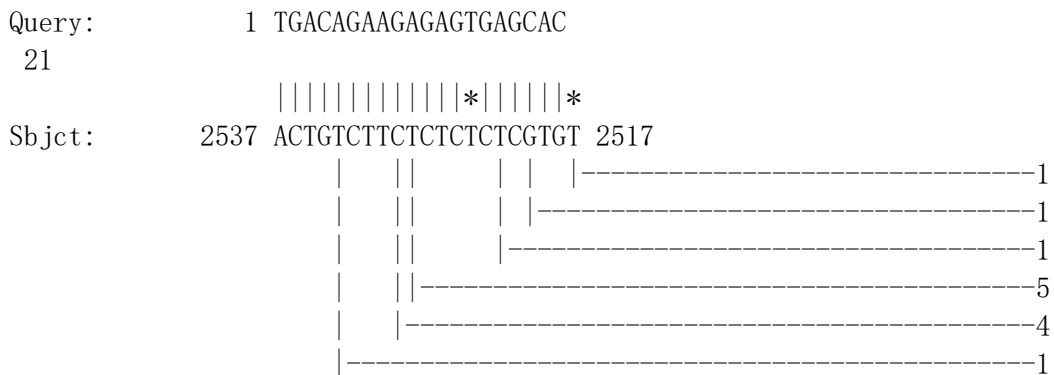
```



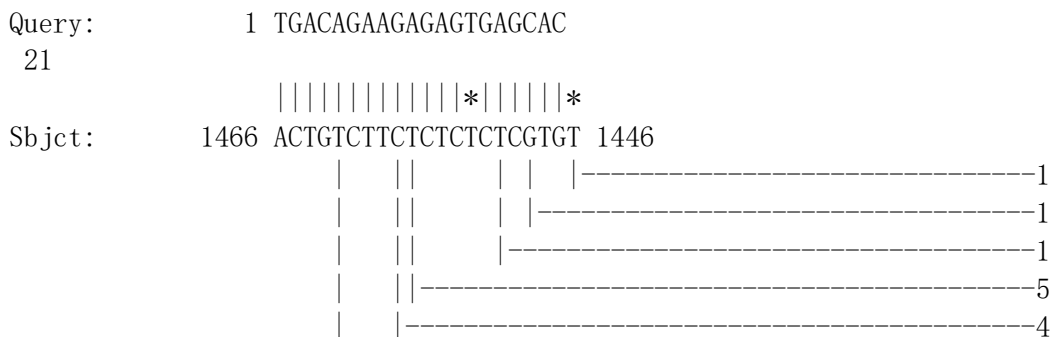

>miR156i-5p
Score: 1.5 Deg: 5:1222:5:44 T_00071664



>miR156i-5p
Score: 1.5 Deg: 5:2528:631:10547 T_00071658



>miR156i-5p
Score: 1.5 Deg: 5:1457:5:53 T_00071665



|-----1

>miR156i-5p

Score: 1.5 Deg: 5:2084:631:10538 T_00071656

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 2093 ACTGTCTTCTCTCTCTCGTGT 2073
|||||*|||||*
| | |-----1
| | |-----1
| | |-----1
| |-----5
| |-----4
|-----1

>miR156i-5p

Score: 1.5 Deg: 5:1826:5:53 T_00071661

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1835 ACTGTCTTCTCTCTCTCGTGT 1815
|||||*|||||*
| | |-----1
| | |-----1
| | |-----1
| |-----5
| |-----4
|-----1

>miR156i-5p

Score: 1.5 Deg: 5:1160:5:44 T_00071667

Query: 1 TGACAGAAGAGAGTGAGCAC
21

Sbjct: 1169 ACTGTCTTCTCTCTCTCGTGT 1149
|||||*|||||*
| | |-----1
| | |-----1
| | |-----1
| |-----5
| |-----4
|-----1

>miR156i-5p

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```
>miR156i-5p
```

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```
>miR156i-5p
```

Query: 1 TGACAGAAGAGAGTGAGCAC
21

```
>miR156i-5p
```

Query: 1 TGACAGAAGAGAGTGAGCAC

21

```

      |||||*|||*
Sbjct: 1170 ACTGTCTTCTCTCTCGTGT 1150
      |  |  |  |  |-----1
      |  |  |  |  |-----1
      |  |  |  |  |-----1
      |  |  |  |  |-----5
      |  |  |  |  |-----4
      |-----1

```

>miR160a-5P

Score: 1.0 Deg: 7:1830:8:191 T_00057636

Query: 1 TGCCTGGCTCCCTGTATGCCA
22

```

      |||||*
Sbjct: 1839 ACGGACCGAGGGACATACGGAC 1818
      |  |  |  |-----1
      |  |  |  |-----1
      |  |  |  |-----1
      |  |  |  |-----3
      |  |  |  |-----1
      |-----7

```

>miR160a-5P

Score: 1.0 Deg: 7:1576:8:186 T_00057635

Query: 1 TGCCTGGCTCCCTGTATGCCA
22

```

      |||||*
Sbjct: 1585 ACGGACCGAGGGACATACGGAC 1564
      |  |  |  |-----1
      |  |  |  |-----1
      |  |  |  |-----1
      |  |  |  |-----3
      |  |  |  |-----1
      |-----7

```

>miR160a-5P

Score: 1.0 Deg: 7:1535:8:185 T_00057634

Query: 1 TGCCTGGCTCCCTGTATGCCA
22

```

      |||||*

```

Sbjct: 1544 ACGGACCGAGGGACATACGGAC 1523

```

      |||-----1
      |||-----1
      |||-----1
      ||-----3
      |-----1
      |-----7

```

>miR160b-5P
 Score: 1.0 Deg: 7:1830:8:191 T_00057636

Query: 1 TGCCTGGCTCCCTGTATGCCA
 22

|||||||**

Sbjct: 1839 ACGGACCGAGGGACATACGGAC 1818

```

      |||-----1
      |||-----1
      |||-----1
      ||-----3
      |-----1
      |-----7

```

>miR160b-5P
 Score: 1.0 Deg: 7:1576:8:186 T_00057635

Query: 1 TGCCTGGCTCCCTGTATGCCA
 22

|||||||**

Sbjct: 1585 ACGGACCGAGGGACATACGGAC 1564

```

      |||-----1
      |||-----1
      |||-----1
      ||-----3
      |-----1
      |-----7

```

>miR160b-5P
 Score: 1.0 Deg: 7:1535:8:185 T_00057634

Query: 1 TGCCTGGCTCCCTGTATGCCA
 22

|||||||**

Sbjct: 1544 ACGGACCGAGGGACATACGGAC 1523

```

      |||-----1

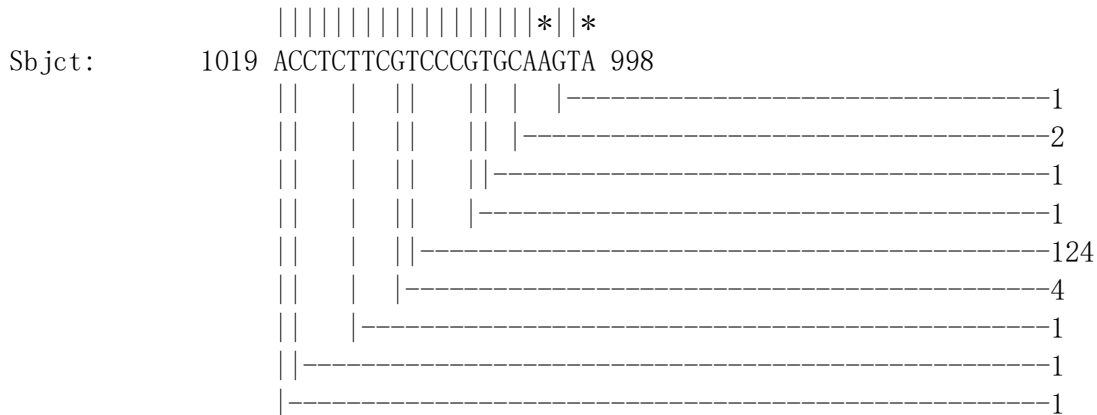
```



>miR164a-5p

Score: 1.0 Deg: 124:1010:124:445 T_00052644

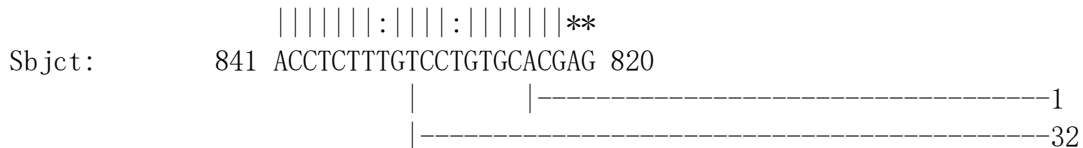
Query: 1 TGGAGAAGCAGGGCACGTGCA
22



>miR164a-5p

Score: 2.0 Deg: 32:832:32:113 T_00059787

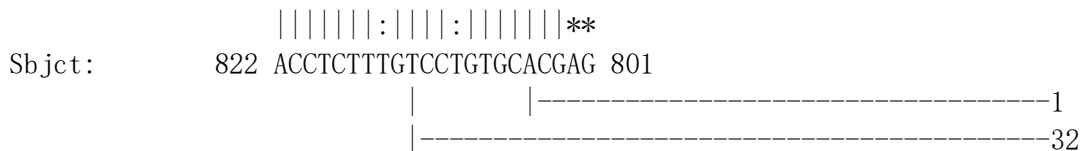
Query: 1 TGGAGAAGCAGGGCACGTGCA
22



>miR164a-5p

Score: 2.0 Deg: 32:813:32:113 T_00059786

Query: 1 TGGAGAAGCAGGGCACGTGCA
22



>miR164a-5p

Score: 2.2 Deg: 7:928:7:192 T_00079376

Query: 1 TGGAGAAGCAGGGCACGTGCA
22

: ||||| |||||*|||*|*
Sbjct: 937 GCCTCTTCGTCCAGTGCAC-TC 917
|-----1
|-----7

>miR164a-5p
Score: 2.0 Deg: 7:955:205:1253T_00073807

Query: 1 TGGAGAAGCAGGGCACGTGCA
22

||||| |||||*||**
Sbjct: 964 ACCTCTTCGTCCCGTGAACGAG 943
||-----1
|-----7

>miR164a-5p
Score: 2.0 Deg: 7:984:205:1254T_00073806

Query: 1 TGGAGAAGCAGGGCACGTGCA
22

||||| |||||*||**
Sbjct: 993 ACCTCTTCGTCCCGTGAACGAG 972
||-----1
|-----7

>miR164b-5p
Score: 1.0 Deg: 124:1010:124:445 T_00052644

Query: 1 TGGAGAAGCAGGGCACGTGCA
22

||||| |||||*||*
Sbjct: 1019 ACCTCTTCGTCCCGTGCAAGTA 998
|| | | | |-----1
|| | | | |-----2
|| | | | |-----1
|| | | | |-----1
|| | |-----124
|| |-----4
||-----1
|-----1
|-----1

>miR164b-5p
Score: 2.0 Deg: 32:832:32:113 T_00059787

```
Query:          1 TGGAGAAGCAGGGCACGTGCA
                22
                |||||:||||:|||||**
Sbjct:          841 ACCTCTTTGTCCTGTGCACGAG 820
                  |         |-----1
                  |-----32
```

>miR164b-5p
Score: 2.0 Deg: 32:813:32:113 T_00059786

```
Query:          1 TGGAGAAGCAGGGCACGTGCA
                22
                |||||:||||:|||||**
Sbjct:          822 ACCTCTTTGTCCTGTGCACGAG 801
                  |         |-----1
                  |-----32
```

>miR164b-5p
Score: 2.2 Deg: 7:928:7:192 T_00079376

```
Query:          1 TGGAGAAGCAGGGCACGTGCA
                22
                :|||||||*|||||*|*
Sbjct:          937 GCCTCTTCGTCCAGTGCAC-TC 917
                  |         |-----1
                  |-----7
```

>miR164b-5p
Score: 2.0 Deg: 7:955:205:1253T_00073807

```
Query:          1 TGGAGAAGCAGGGCACGTGCA
                22
                |||||*|||**
Sbjct:          964 ACCTCTTCGTCCCGTGAACGAG 943
                  ||-----1
                  |-----7
```

>miR164b-5p
Score: 2.0 Deg: 7:984:205:1254T_00073806

```
Query:          1 TGGAGAAGCAGGGCACGTGCA
                22
```

```

          |||||*||**
Sbjct:    993 ACCTCTTCGTCCCGTGAACGAG 972
          ||-----1
          |-----7

```

>miR164c-5p
 Score: 1.0 Deg: 124:1010:124:445 T_00052644

```

Query:      1 TGGAGAAGCAGGGCACGTGCA
22
          |||||*||*
Sbjct:    1019 ACCTCTTCGTCCCGTGCAAGTA 998
          || | | | |-----1
          || | | | |-----2
          || | | | |-----1
          || | | | |-----1
          || | | |-----124
          || | |-----4
          || |-----1
          ||-----1
          |-----1

```

>miR164c-5p
 Score: 2.0 Deg: 32:832:32:113 T_00059787

```

Query:      1 TGGAGAAGCAGGGCACGTGCA
22
          |||||:||||:||||**
Sbjct:    841 ACCTCTTTGTCCTGTGCACGAG 820
          | |-----1
          |-----32

```

>miR164c-5p
 Score: 2.0 Deg: 32:813:32:113 T_00059786

```

Query:      1 TGGAGAAGCAGGGCACGTGCA
22
          |||||:||||:||||**
Sbjct:    822 ACCTCTTTGTCCTGTGCACGAG 801
          | |-----1
          |-----32

```

>miR164c-5p
 Score: 2.2 Deg: 7:928:7:192 T_00079376

Query: 1 TGGAGAAGCAGGGCACGTGCA
22

:|||||||*|||*|*

Sbjct: 937 GCCTCTTCGTCCAGTGAC-TC 917

|-----1
|-----7

>miR164c-5p

Score: 2.0 Deg: 7:955:205:1253T_00073807

Query: 1 TGGAGAAGCAGGGCACGTGCA
22

|||||||*||**

Sbjct: 964 ACCTCTTCGTCCCGTGAACGAG 943

||-----1
|-----7

>miR164c-5p

Score: 2.0 Deg: 7:984:205:1254T_00073806

Query: 1 TGGAGAAGCAGGGCACGTGCA
22

|||||||*||**

Sbjct: 993 ACCTCTTCGTCCCGTGAACGAG 972

||-----1
|-----7

>miR164d-5p

Score: 1.0 Deg: 124:1010:124:445 T_00052644

Query: 1 TGGAGAAGCAGGGCACGTGCA
22

|||||||*||*

Sbjct: 1019 ACCTCTTCGTCCCGTGCAAGTA 998

|| | | | |-----1
|| | | | |-----2
|| | | | |-----1
|| | | | |-----1
|| | | |-----124
|| | |-----4
|| |-----1
||-----1
|-----1

>miR164d-5p

Score: 2.0 Deg: 32:832:32:113 T_00059787

```
Query:      1 TGGAGAAGCAGGGCACGTGCA
            22
            |||||:||||:|||||**
Sbjct:      841 ACCTCTTTGTCCTGTGCACGAG 820
              |         |-----1
              |-----32
```

>miR164d-5p
Score: 2.0 Deg: 32:813:32:113 T_00059786

```
Query:      1 TGGAGAAGCAGGGCACGTGCA
            22
            |||||:||||:|||||**
Sbjct:      822 ACCTCTTTGTCCTGTGCACGAG 801
              |         |-----1
              |-----32
```

>miR164d-5p
Score: 2.2 Deg: 7:928:7:192 T_00079376

```
Query:      1 TGGAGAAGCAGGGCACGTGCA
            22
            :|||||||*|||||*|*
Sbjct:      937 GCCTCTTCGTCCAGTGCAC-TC 917
              |         |-----1
              |-----7
```

>miR164d-5p
Score: 2.0 Deg: 7:955:205:1253T_00073807

```
Query:      1 TGGAGAAGCAGGGCACGTGCA
            22
            |||||*|||**
Sbjct:      964 ACCTCTTCGTCCCGTGAACGAG 943
              ||-----1
              |-----7
```

>miR164d-5p
Score: 2.0 Deg: 7:984:205:1254T_00073806

```
Query:      1 TGGAGAAGCAGGGCACGTGCA
            22
            |||||*|||**
```

Sbjct: 993 ACCTCTTCGTCCCGTGAACGAG 972

```

      ||-----1
      |-----7

```

>miR164e-5p

Score: 1.0 Deg: 124:1010:124:445 T_00052644

Query: 1 TGGAGAAGCAGGGCACGTGCA

22

|||||||*|*|

Sbjct: 1019 ACCTCTTCGTCCCGTGCAAGTA 998

```

      ||-----1
      ||-----2
      ||-----1
      ||-----1
      ||-----124
      ||-----4
      ||-----1
      ||-----1
      |-----1

```

>miR164e-5p

Score: 2.0 Deg: 32:832:32:113 T_00059787

Query: 1 TGGAGAAGCAGGGCACGTGCA

22

|||||:|||||**

Sbjct: 841 ACCTCTTTGTCCTGTGCACGAG 820

```

      |-----1
      |-----32

```

>miR164e-5p

Score: 2.0 Deg: 32:813:32:113 T_00059786

Query: 1 TGGAGAAGCAGGGCACGTGCA

22

|||||:|||||**

Sbjct: 822 ACCTCTTTGTCCTGTGCACGAG 801

```

      |-----1
      |-----32

```

>miR164e-5p

Score: 2.2 Deg: 7:928:7:192 T_00079376

Query: 1 TGGAGAAGCAGGGCACGTGCA

22

```
          :|||||||*|||*|*
Sbjct:    937 GCCTCTTCGTCCAGTGCAC-TC 917
          |         |-----1
          |-----7
```

>miR164e-5p

Score: 2.0 Deg: 7:955:205:1253T_00073807

```
Query:      1 TGGAGAAGCAGGGCACGTGCA
22
```

```
          |||||||*||**
Sbjct:     964 ACCTCTTCGTCCCGTGAACGAG 943
          ||-----1
          |-----7
```

>miR164e-5p

Score: 2.0 Deg: 7:984:205:1254T_00073806

```
Query:      1 TGGAGAAGCAGGGCACGTGCA
22
```

```
          |||||||*||**
Sbjct:     993 ACCTCTTCGTCCCGTGAACGAG 972
          ||-----1
          |-----7
```

>miR166a-3p

Score: 2.2 Deg: 168:1340:168:232 T_00088111

```
Query:      1 TCGGACCAGGCTTCATTCCCC
22
```

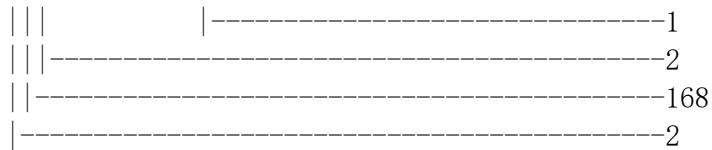
```
          :|||||||:|***
Sbjct:    1349 GGCCTGGTCCGAAGTAGGGTCC 1328
          ||         |-----1
          ||-----2
          |-----168
          |-----2
```

>miR166a-3p

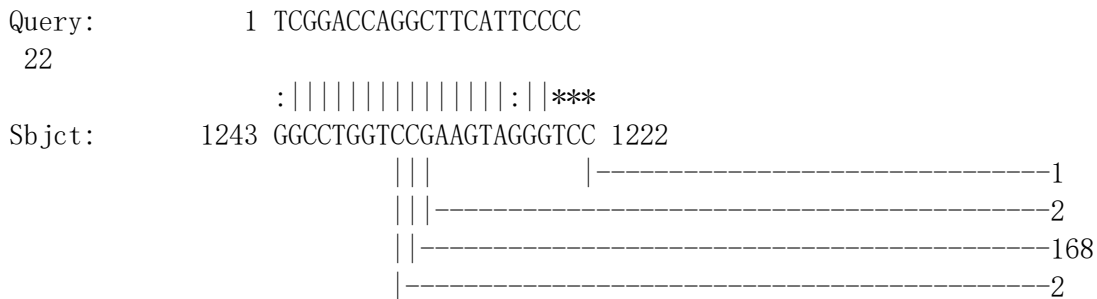
Score: 2.2 Deg: 168:1211:168:231 T_00088109

```
Query:      1 TCGGACCAGGCTTCATTCCCC
22
```

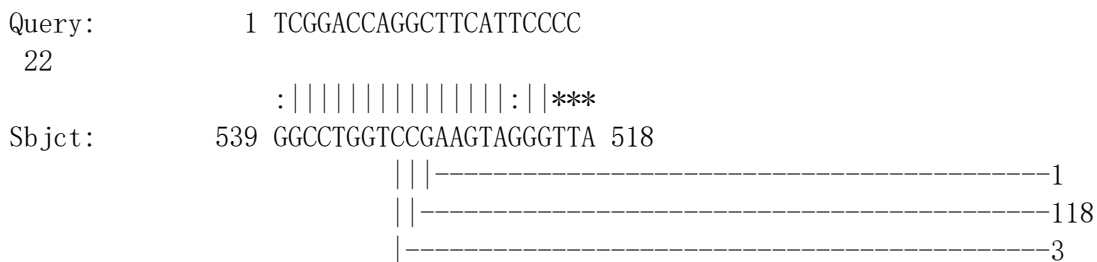
```
          :|||||||:|***
Sbjct:    1220 GGCCTGGTCCGAAGTAGGGTCC 1199
```



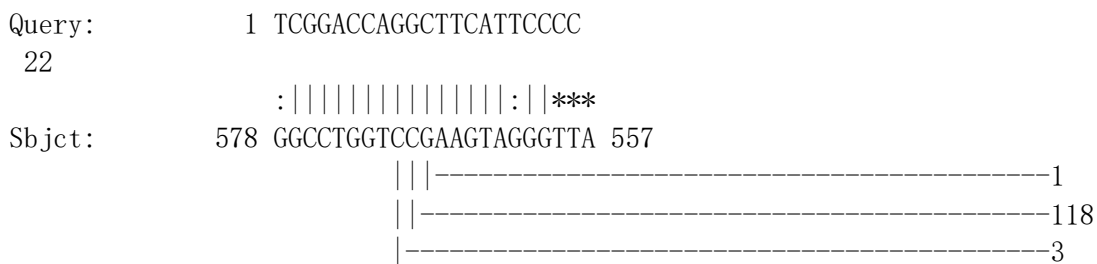
>miR166a-3p
Score: 2.2 Deg: 168:1234:168:232 T_00088110



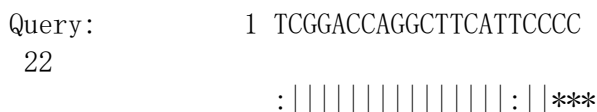
>miR166a-3p
Score: 2.2 Deg: 118:530:118:378 T_00058154



>miR166a-3p
Score: 2.2 Deg: 118:569:118:461 T_00058151



>miR166a-3p
Score: 2.2 Deg: 118:404:118:379 T_00058150



Sbjct: 413 GGCCTGGTCCGAAGTAGGGTTA 392
||-----1
||-----118
|-----3

>miR166a-3p
Score: 2.2 Deg: 118:569:118:379 T_00058152

Query: 1 TCGGACCAGGCTTCATTCCCC
22
:|||||||||||||:|***
Sbjct: 578 GGCCTGGTCCGAAGTAGGGTTA 557
||-----1
||-----118
|-----3

>miR166a-3p
Score: 2.2 Deg: 118:530:118:461 T_00058153

Query: 1 TCGGACCAGGCTTCATTCCCC
22
:|||||||||||||:|***
Sbjct: 539 GGCCTGGTCCGAAGTAGGGTTA 518
||-----1
||-----118
|-----3

>miR166a-3p
Score: 2.2 Deg: 118:404:118:461 T_00058149

Query: 1 TCGGACCAGGCTTCATTCCCC
22
:|||||||||||||:|***
Sbjct: 413 GGCCTGGTCCGAAGTAGGGTTA 392
||-----1
||-----118
|-----3

>miR166a-3p
Score: 2.2 Deg: 367:1463:631:8376 T_00069032

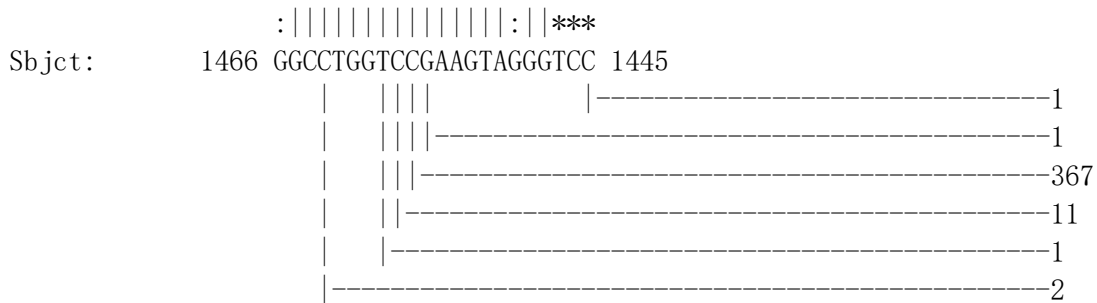
Query: 1 TCGGACCAGGCTTCATTCCCC
22
:|||||||||||||:|***
Sbjct: 1472 GGCCTGGTCCGAAGTAGGGTCC 1451



>miR166a-3p

Score: 2.2 Deg: 367:1457:631:8125 T_00069033

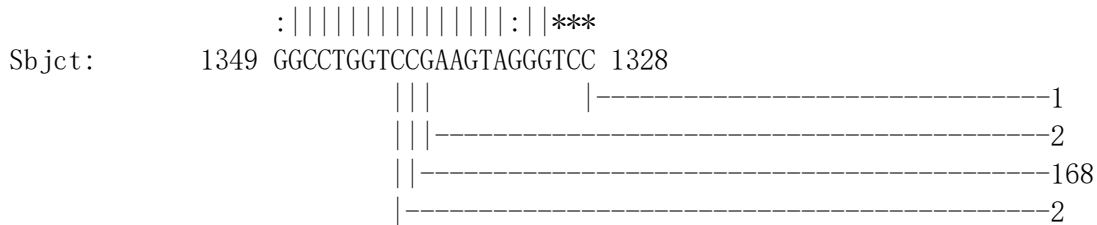
Query: 1 TCGGACCAGGCTTCATTCCCC
22



>miR166b-3p

Score: 2.2 Deg: 168:1340:168:232 T_00088111

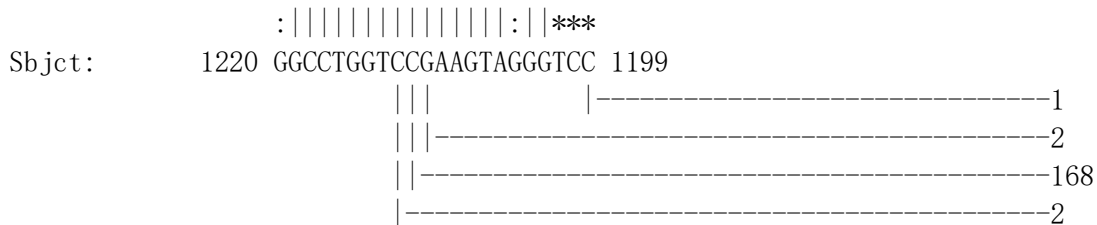
Query: 1 TCGGACCAGGCTTCATTCCCC
22



>miR166b-3p

Score: 2.2 Deg: 168:1211:168:231 T_00088109

Query: 1 TCGGACCAGGCTTCATTCCCC
22



>miR166b-3p
Score: 2.2 Deg: 168:1234:168:232 T_00088110

```
Query:          1 TCGGACCAGGCTTCATTCCCC
22
               :|||||:|||||:|***
Sbjct:        1243 GGCCTGGTCCGAAGTAGGGTCC 1222
                  |||-----1
                  |||-----2
                  ||-----168
                  |-----2
```

>miR166b-3p
Score: 2.2 Deg: 118:530:118:378 T_00058154

```
Query:          1 TCGGACCAGGCTTCATTCCCC
22
               :|||||:|||||:|***
Sbjct:        539 GGCCTGGTCCGAAGTAGGGTTA 518
                  |||-----1
                  ||-----118
                  |-----3
```

>miR166b-3p
Score: 2.2 Deg: 118:569:118:461 T_00058151

```
Query:          1 TCGGACCAGGCTTCATTCCCC
22
               :|||||:|||||:|***
Sbjct:        578 GGCCTGGTCCGAAGTAGGGTTA 557
                  |||-----1
                  ||-----118
                  |-----3
```

>miR166b-3p
Score: 2.2 Deg: 118:404:118:379 T_00058150

```
Query:          1 TCGGACCAGGCTTCATTCCCC
22
               :|||||:|||||:|***
Sbjct:        413 GGCCTGGTCCGAAGTAGGGTTA 392
                  |||-----1
                  ||-----118
                  |-----3
```

>miR166b-3p
Score: 2.2 Deg: 118:569:118:379 T_00058152

Query: 1 TCGGACCAGGCTTCATTCCCC
22
:|||||||||||||||:|***
Sbjct: 578 GGCCTGGTCCGAAGTAGGGTTA 557
||-----1
||-----118
|-----3

>miR166b-3p
Score: 2.2 Deg: 118:530:118:461 T_00058153

Query: 1 TCGGACCAGGCTTCATTCCCC
22
:|||||||||||||||:|***
Sbjct: 539 GGCCTGGTCCGAAGTAGGGTTA 518
||-----1
||-----118
|-----3

>miR166b-3p
Score: 2.2 Deg: 118:404:118:461 T_00058149

Query: 1 TCGGACCAGGCTTCATTCCCC
22
:|||||||||||||||:|***
Sbjct: 413 GGCCTGGTCCGAAGTAGGGTTA 392
||-----1
||-----118
|-----3

>miR166b-3p
Score: 2.2 Deg: 367:1463:631:8376 T_00069032

Query: 1 TCGGACCAGGCTTCATTCCCC
22
:|||||||||||||||:|***
Sbjct: 1472 GGCCTGGTCCGAAGTAGGGTCC 1451
| | | |-----1
| | | |-----1
| | |-----367
| |-----11
|-----1

|-----2

>miR166b-3p

Score: 2.2 Deg: 367:1457:631:8125 T_00069033

Query: 1 TCGGACCAGGCTTCATTCCCC
22

:|||||||||||||:|***
Sbjct: 1466 GGCCTGGTCCGAAGTAGGGTCC 1445
| ||| |-----1
| ||| |-----1
| || |-----367
| || |-----11
| |-----1
|-----2

>miR166c-3p

Score: 2.2 Deg: 168:1340:168:232 T_00088111

Query: 1 TCGGACCAGGCTTCATTCCCC
22

:|||||||||||||:|***
Sbjct: 1349 GGCCTGGTCCGAAGTAGGGTCC 1328
|| |-----1
|| |-----2
|-----168
|-----2

>miR166c-3p

Score: 2.2 Deg: 168:1211:168:231 T_00088109

Query: 1 TCGGACCAGGCTTCATTCCCC
22

:|||||||||||||:|***
Sbjct: 1220 GGCCTGGTCCGAAGTAGGGTCC 1199
|| |-----1
|| |-----2
|-----168
|-----2

>miR166c-3p

Score: 2.2 Deg: 168:1234:168:232 T_00088110

Query: 1 TCGGACCAGGCTTCATTCCCC
22

```
          :|||||:|***
Sbjct:    1243 GGCCTGGTCCGAAGTAGGGTCC 1222
          |||-----1
          ||-----2
          ||-----168
          |-----2
```

>miR166c-3p
Score: 2.2 Deg: 118:530:118:378 T_00058154

```
Query:      1 TCGGACCAGGCTTCATTCCCC
           22
          :|||||:|***
Sbjct:      539 GGCCTGGTCCGAAGTAGGGTTA 518
          ||-----1
          ||-----118
          |-----3
```

>miR166c-3p
Score: 2.2 Deg: 118:569:118:461 T_00058151

```
Query:      1 TCGGACCAGGCTTCATTCCCC
           22
          :|||||:|***
Sbjct:      578 GGCCTGGTCCGAAGTAGGGTTA 557
          ||-----1
          ||-----118
          |-----3
```

>miR166c-3p
Score: 2.2 Deg: 118:404:118:379 T_00058150

```
Query:      1 TCGGACCAGGCTTCATTCCCC
           22
          :|||||:|***
Sbjct:      413 GGCCTGGTCCGAAGTAGGGTTA 392
          ||-----1
          ||-----118
          |-----3
```

>miR166c-3p
Score: 2.2 Deg: 118:569:118:379 T_00058152

```
Query:      1 TCGGACCAGGCTTCATTCCCC
           22
```

```

      :|||||:|***
Sbjct: 578 GGCCTGGTCCGAAGTAGGGTTA 557
      ||-----1
      ||-----118
      |-----3

```

>miR166c-3p
 Score: 2.2 Deg: 118:530:118:461 T_00058153

```

Query: 1 TCGGACCAGGCTTCATTCCCC
22
      :|||||:|***
Sbjct: 539 GGCCTGGTCCGAAGTAGGGTTA 518
      ||-----1
      ||-----118
      |-----3

```

>miR166c-3p
 Score: 2.2 Deg: 118:404:118:461 T_00058149

```

Query: 1 TCGGACCAGGCTTCATTCCCC
22
      :|||||:|***
Sbjct: 413 GGCCTGGTCCGAAGTAGGGTTA 392
      ||-----1
      ||-----118
      |-----3

```

>miR166c-3p
 Score: 2.2 Deg: 367:1463:631:8376 T_00069032

```

Query: 1 TCGGACCAGGCTTCATTCCCC
22
      :|||||:|***
Sbjct: 1472 GGCCTGGTCCGAAGTAGGGTCC 1451
      | |||-----1
      | |||-----1
      | |||-----367
      | ||-----11
      | -----1
      |-----2

```

>miR166c-3p
 Score: 2.2 Deg: 367:1457:631:8125 T_00069033

```

Query:          1 TCGGACCAGGCTTCATTCCCC
                22
                :|||||:|||||:|***
Sbjct:         1466 GGCCTGGTCCGAAGTAGGGTCC 1445
                  |   |||   |-----1
                  |   |||   |-----1
                  |   ||   |-----367
                  |   ||   |-----11
                  |   |   |-----1
                  |-----2

```

>miR169c
 Score: 2.5 Deg: 19:1476:19:150T_00065068

```

Query:          1 TAGCCAAGGATGACTTGCCTG
                22
                *|||||:||||*|||||*
Sbjct:         1485 TTCGGTTCTTACTTAACGGACT 1464
                  |   |-----19
                  |-----2

```

>miR169c
 Score: 2.5 Deg: 19:1902:19:159T_00065067

```

Query:          1 TAGCCAAGGATGACTTGCCTG
                22
                *|||||:||||*|||||*
Sbjct:         1911 TTCGGTTCTTACTTAACGGACT 1890
                  |   |-----19
                  |-----2

```

>miR169c
 Score: 2.5 Deg: 14:1593:33:498T_00083345

```

Query:          1 TAGCCAAGGATGACTTGCCTG
                22
                *|||||:||||*|::*
Sbjct:         1602 CTCGGTTCCTACTGAA-GGGTA 1582
                  |   |||   ||-----2
                  |   |||   |-----2
                  |   |||   |-----14
                  |   ||   |-----3
                  |   |   |-----2
                  |-----1

```

|-----1

>miR169c

Score: 2.5 Deg: 14:1577:33:498T_00083347

Query: 1 TAGCCAAGGATGACTTGCCTG
22

*| | | | | | | | | | | | | | *| | : : *
Sbjct: 1586 CTCGGTTCCTACTGAA-GGGTA 1566
| | | | |-----2
| | | | |-----2
| | | |-----14
| | |-----3
| |-----2
|-----1
|-----1

>miR169c

Score: 2.5 Deg: 14:1544:33:498T_00083343

Query: 1 TAGCCAAGGATGACTTGCCTG
22

*| | | | | | | | | | | | | | *| | : : *
Sbjct: 1553 CTCGGTTCCTACTGAA-GGGTA 1533
| | | | |-----2
| | | | |-----2
| | | |-----14
| | |-----3
| |-----2
|-----1
|-----1

>miR169c

Score: 2.5 Deg: 14:1523:33:497T_00083346

Query: 1 TAGCCAAGGATGACTTGCCTG
22

*| | | | | | | | | | | | | | *| | : : *
Sbjct: 1532 CTCGGTTCCTACTGAA-GGGTA 1512
| | | | |-----2
| | | | |-----2
| | | |-----14
| | |-----3
| |-----2
|-----1

|-----1

>miR169c

Score: 2.5 Deg: 14:1538:33:497T_00083344

Query: 1 TAGCCAAGGATGACTTGCCTG
22

*| | | | | | | | | | | | | | *| | : : *
Sbjct: 1547 CTCGGTTCCTACTGAA-GGGTA 1527
| | | | |-----2
| | | | |-----2
| | | |-----14
| | |-----3
| |-----2
|-----1
|-----1

>miR169c

Score: 2.5 Deg: 14:1161:14:305T_00083342

Query: 1 TAGCCAAGGATGACTTGCCTG
22

*| | | | | | | | | | | | | | *| | : : *
Sbjct: 1170 CTCGGTTCCTACTGAA-GGGTA 1150
| | | | |-----2
| | | | |-----2
| | | |-----14
| | |-----3
| |-----2
|-----1
|-----1

>miR169d

Score: 2.5 Deg: 19:1476:19:150T_00065068

Query: 1 TAGCCAAGGATGACTTGCCTG
22

*| | | | | : | | | *| | | | | *
Sbjct: 1485 TTCGGTTCCTACTTAACGGACT 1464
|-----19
|-----2

>miR169d

Score: 2.5 Deg: 19:1902:19:159T_00065067

```

Query:          1 TAGCCAAGGATGACTTGCCTG
22
               *|||:||||*|||*
Sbjct:         1911 TTCGGTTCTTACTTAACGGACT 1890
                  |-----19
                  |-----2

```

>miR169d
 Score: 2.5 Deg: 14:1593:33:498T_00083345

```

Query:          1 TAGCCAAGGATGACTTGCCTG
22
               *|||:||||*|||:~*
Sbjct:         1602 CTCGGTTCCTACTGAA-GGGTA 1582
                  |   ||-----2
                  |   ||-----2
                  |   ||-----14
                  |   ||-----3
                  |   ||-----2
                  |   ||-----1
                  |-----1

```

>miR169d
 Score: 2.5 Deg: 14:1577:33:498T_00083347

```

Query:          1 TAGCCAAGGATGACTTGCCTG
22
               *|||:||||*|||:~*
Sbjct:         1586 CTCGGTTCCTACTGAA-GGGTA 1566
                  |   ||-----2
                  |   ||-----2
                  |   ||-----14
                  |   ||-----3
                  |   ||-----2
                  |   ||-----1
                  |-----1

```

>miR169d
 Score: 2.5 Deg: 14:1544:33:498T_00083343

```

Query:          1 TAGCCAAGGATGACTTGCCTG
22
               *|||:||||*|||:~*
Sbjct:         1553 CTCGGTTCCTACTGAA-GGGTA 1533
                  |   ||-----2

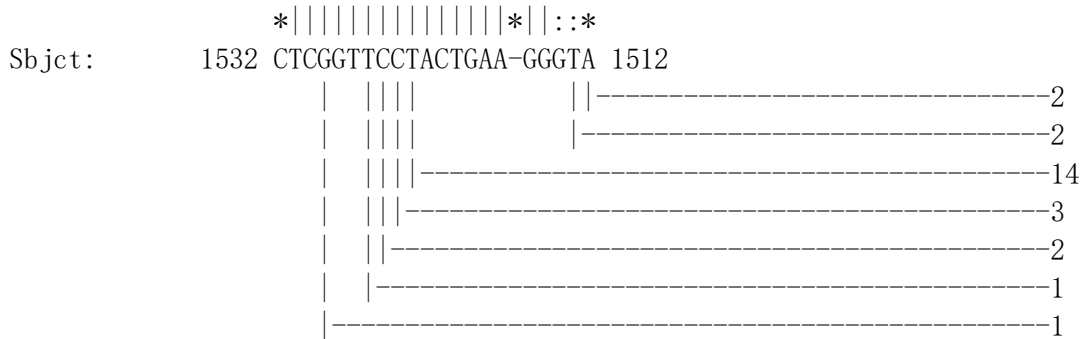
```



>miR169d

Score: 2.5 Deg: 14:1523:33:497T_00083346

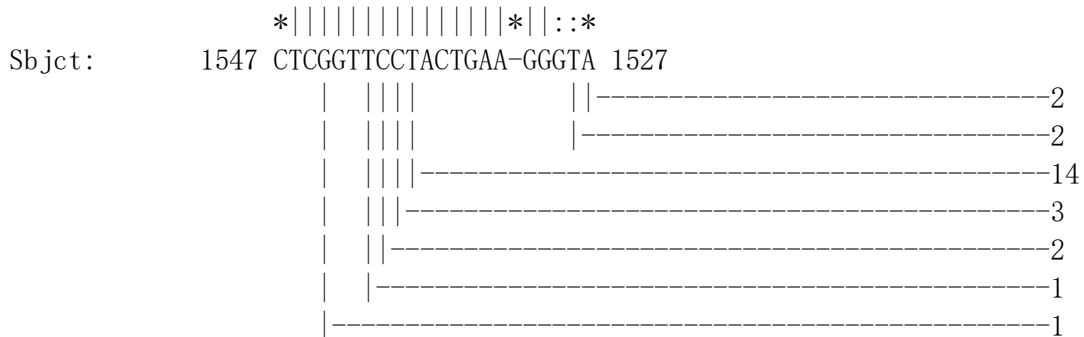
Query: 1 TAGCCAAGGATGACTTGCCTG
22



>miR169d

Score: 2.5 Deg: 14:1538:33:497T_00083344

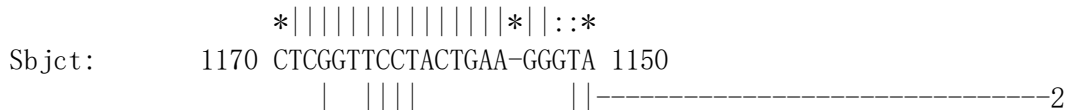
Query: 1 TAGCCAAGGATGACTTGCCTG
22



>miR169d

Score: 2.5 Deg: 14:1161:14:305T_00083342

Query: 1 TAGCCAAGGATGACTTGCCTG
22




```

Query:      1 AGAATCTTGATGATGCTGCA-T
            22

            |||||:|||||||*|*
Sbjct:     1860 TCTTAGGACTACTACGACGTCAT 1838
            |||  |||  |-----1
            |||  |||  |-----1
            |||  |||  |-----1
            |||  |||  |-----621
            |||  |-----2
            |||  |-----1
            ||  |-----2
            |-----1

```

```

Query:      1 AGAATCTTGATGATGCTGCA-T
22

          |||||:|||||||*|*
Sbjct:    743 TCTTAGGACTACTACGACGTCAT 721
          |||  |||  |-----1
          |||  |||  |-----1
          |||  |||  |-----1
          |||  |||  |-----621
          |||  |-----2
          |||  |-----1
          ||  |-----2
          |-----1

```

```

Query:      1 AGAATCTTGATGATGCTGCA-T
22

          |||||:|||||||*|*
Sbjct: 2178 TCTTAGGACTACTACGACGTCAT 2156
          |||  |||  ||-----1
          |||  |||  ||-----1
          |||  |||  |-----1
          |||  |||  |-----621
          |||  |||  |-----2
          |||  |-----1
          |||  |-----2

```

|-----1

>miR172a-3p

Score: 1.5 Deg: 621:1808:621:1455 T_00087825

Query: 1 AGAATCTTGATGATGCTGCA-T
22

Sbjct: 1817 TCTTAGGACTACTACGACGTCAT 1795
|||:|||||||*|*
| | | | | |-----1
| | | | | |-----1
| | | | |-----1
| | | |-----621
| | |-----2
| |-----1
|-----2
|-----1

>miR172a-3p

Score: 1.5 Deg: 621:2219:621:1466 T_00087827

Query: 1 AGAATCTTGATGATGCTGCA-T
22

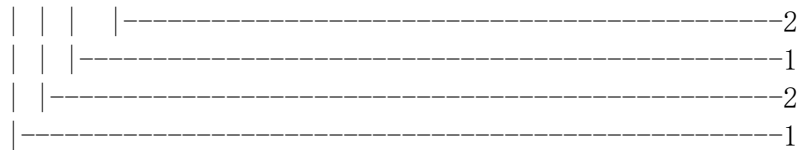
Sbjct: 2228 TCTTAGGACTACTACGACGTCAT 2206
|||:|||||||*|*
| | | | | |-----1
| | | | | |-----1
| | | | |-----1
| | | |-----621
| | |-----2
| |-----1
|-----2
|-----1

>miR172a-3p

Score: 1.5 Deg: 621:2130:621:1456 T_00087828

Query: 1 AGAATCTTGATGATGCTGCA-T
22

Sbjct: 2139 TCTTAGGACTACTACGACGTCAT 2117
|||:|||||||*|*
| | | | | |-----1
| | | | | |-----1
| | | | |-----1
| | | |-----621



>miR172a-3p

Score: 1.5 Deg: 9:561:17:50 T_00081649

Query: 1 AGAATCTTGATGATGCTGC-AT

22

|||||:|||||||*|*|

Sbjct: 570 TCTTAGGACTACTACGACGTTAC 548



>miR172a-3p

Score: 2.0 Deg: 7:2392:205:1270 T_00014183

Query: 1 AGAATCTTGATGATGCTGCAT

22

*||||:|||||||**

Sbjct: 2401 CCTTAGGACTACTACGACGTCG 2380



>miR172a-3p

Score: 2.0 Deg: 7:2240:205:1269 T_00014181

Query: 1 AGAATCTTGATGATGCTGCAT

22

*||||:|||||||**

Sbjct: 2249 CCTTAGGACTACTACGACGTCG 2228



>miR172a-3p

Score: 2.0 Deg: 7:2189:205:1265 T_00014179

Query: 1 AGAATCTTGATGATGCTGCAT

22

*||||:|||||||**

Sbjct: 2198 CCTTAGGACTACTACGACGTCG 2177



```
      |  |-----1
      |-----7
```

>miR172a-3p

Score: 2.0 Deg: 7:1352:28:148 T_00014174

Query: 1 AGAATCTTGATGATGCTGCAT
22

```
      *||| |:|||||||**
Sbjct: 1361 CCTTAGGACTACTACGACGTCG 1340
      |  |-----1
      |-----1
      |-----7
```

>miR172a-3p

Score: 2.0 Deg: 7:2105:205:1265 T_00014178

Query: 1 AGAATCTTGATGATGCTGCAT
22

```
      *||| |:|||||||**
Sbjct: 2114 CCTTAGGACTACTACGACGTCG 2093
      |  |-----1
      |-----1
      |-----7
```

>miR172a-3p

Score: 2.0 Deg: 7:1349:28:146 T_00014175

Query: 1 AGAATCTTGATGATGCTGCAT
22

```
      *||| |:|||||||**
Sbjct: 1358 CCTTAGGACTACTACGACGTCG 1337
      |  |-----1
      |-----1
      |-----7
```

>miR172a-3p

Score: 2.0 Deg: 7:2420:205:1272 T_00014182

Query: 1 AGAATCTTGATGATGCTGCAT
22

```
      *||| |:|||||||**
Sbjct: 2429 CCTTAGGACTACTACGACGTCG 2408
      |  |-----1
      |-----1
```

|-----7

>miR172a-3p

Score: 2.0 Deg: 7:2159:205:1265 T_00014177

Query: 1 AGAATCTTGATGATGCTGCAT
22

*|||:|||||||**
Sbjct: 2168 CCTTAGGACTACTACGACGTCG 2147
| |-----1
| |-----1
|-----7

>miR172a-3p

Score: 2.0 Deg: 7:1349:28:146 T_00014176

Query: 1 AGAATCTTGATGATGCTGCAT
22

*|||:|||||||**
Sbjct: 1358 CCTTAGGACTACTACGACGTCG 1337
| |-----1
| |-----1
|-----7

>miR172a-3p

Score: 2.0 Deg: 7:2235:205:1267 T_00014180

Query: 1 AGAATCTTGATGATGCTGCAT
22

*|||:|||||||**
Sbjct: 2244 CCTTAGGACTACTACGACGTCG 2223
| |-----1
| |-----1
|-----7

>miR172a-3p

Score: 2.0 Deg: 7:2485:205:1273 T_00014186

Query: 1 AGAATCTTGATGATGCTGCAT
22

*|||:|||||||**
Sbjct: 2494 CCTTAGGACTACTACGACGTCG 2473
| |-----1
| |-----1
|-----7

>miR172a-3p
Score: 2.0 Deg: 7:2415:205:1270 T_00014185

Query: 1 AGAATCTTGATGATGCTGCAT
22
*|||||:|||||||**
Sbjct: 2424 CCTTAGGACTACTACGACGTCG 2403
| |-----1
| |-----1
|-----7

>miR172a-3p
Score: 2.0 Deg: 7:2418:205:1272 T_00014184

Query: 1 AGAATCTTGATGATGCTGCAT
22
*|||||:|||||||**
Sbjct: 2427 CCTTAGGACTACTACGACGTCG 2406
| |-----1
| |-----1
|-----7

>miR172b-3p
Score: 1.5 Deg: 9:748:12:67 T_00059075

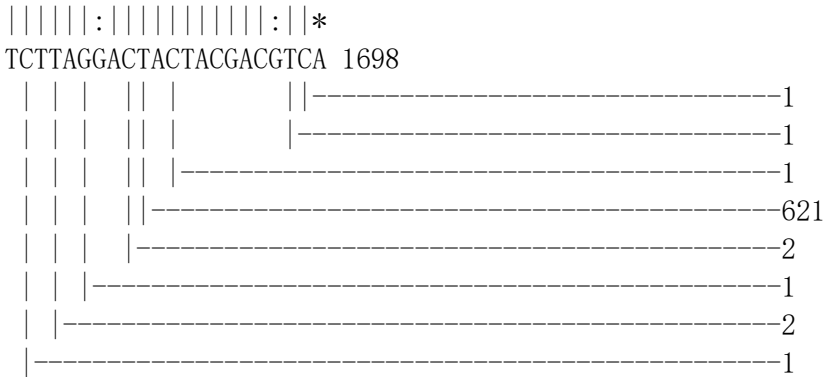
Query: 1 AGAATCTTGATGATGCTGTAG
22
|||||:|||||||:|*
Sbjct: 757 TCTTAGGACTACTACGACGTTA 736
| |-----1
|-----9

>miR172b-3p
Score: 1.5 Deg: 9:792:12:67 T_00059076

Query: 1 AGAATCTTGATGATGCTGTAG
22
|||||:|||||||:|*
Sbjct: 801 TCTTAGGACTACTACGACGTTA 780
| |-----1
|-----9

>miR172b-3p
Score: 1.2 Deg: 621:1710:621:1460 T_00087826

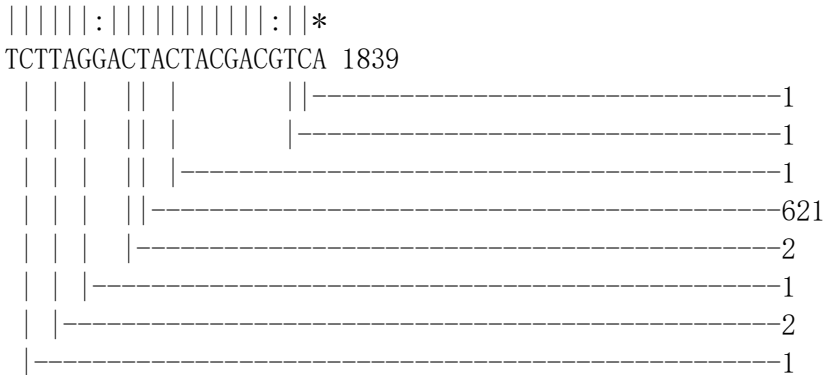
Sbjct: 1719 TCTTAGGACTACTACGACGTCA 1698



>miR172b-3p
Score: 1.2 Deg: 621:1851:621:1456 T_00087824

Query: 1 AGAATCTTGATGATGCTGTAG
22

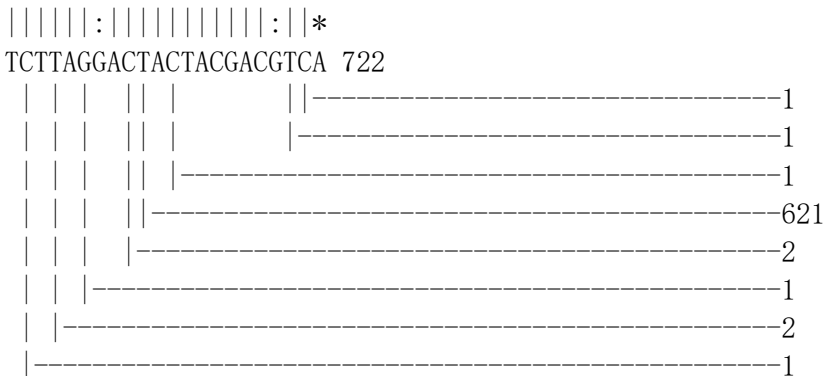
Sbjct: 1860 TCTTAGGACTACTACGACGTCA 1839



>miR172b-3p
Score: 1.2 Deg: 621:734:621:1156 T_00087822

Query: 1 AGAATCTTGATGATGCTGTAG
22

Sbjct: 743 TCTTAGGACTACTACGACGTCA 722



>miR172b-3p
Score: 1.2 Deg: 621:2169:621:1460 T_00087823

```
Query:          1 AGAATCTTGATGATGCTGTAG
                22
                |||||:|||||||:|*
Sbjct:    2178 TCTTAGGACTACTACGACGTCA 2157
                |||  |||  |-----1
                |||  |||  |-----1
                |||  |||  |-----1
                |||  |||  |-----621
                |||  |||  |-----2
                |||  |||  |-----1
                |||  |||  |-----2
                |||  |||  |-----1
```

>miR172b-3p
Score: 1.2 Deg: 621:1808:621:1455 T_00087825

```
Query:          1 AGAATCTTGATGATGCTGTAG
                22
                |||||:|||||||:|*
Sbjct:    1817 TCTTAGGACTACTACGACGTCA 1796
                |||  |||  |-----1
                |||  |||  |-----1
                |||  |||  |-----1
                |||  |||  |-----621
                |||  |||  |-----2
                |||  |||  |-----1
                |||  |||  |-----2
                |||  |||  |-----1
```

>miR172b-3p
Score: 1.2 Deg: 621:2219:621:1466 T_00087827

```
Query:          1 AGAATCTTGATGATGCTGTAG
                22
                |||||:|||||||:|*
Sbjct:    2228 TCTTAGGACTACTACGACGTCA 2207
                |||  |||  |-----1
                |||  |||  |-----1
                |||  |||  |-----1
                |||  |||  |-----621
                |||  |||  |-----2
```

```

      | | |-----1
      | |-----2
      |-----1

```

>miR172b-3p
 Score: 1.2 Deg: 621:2130:621:1456 T_00087828

```

Query:      1 AGAATCTTGATGATGCTGTAG
            22
           |||||:|||||||:|*
Sbjct:    2139 TCTTAGGACTACTACGACGTCA 2118
           | | | | | | |-----1
           | | | | | | |-----1
           | | | | | |-----1
           | | | | |-----621
           | | | |-----2
           | | |-----1
           |-----2
           |-----1

```

>miR172b-3p
 Score: 1.5 Deg: 9:561:17:50 T_00081649

```

Query:      1 AGAATCTTGATGATGCTGTAG
            22
           |||||:|||||||:|*
Sbjct:    570 TCTTAGGACTACTACGACGTTA 549
           |-----1
           |-----9

```

>miR172b-3p
 Score: 1.8 Deg: 7:2392:205:1270 T_00014183

```

Query:      1 AGAATCTTGATGATGCTGTAG
            22
           *|||:|||||||:|*
Sbjct:    2401 CCTTAGGACTACTACGACGTCG 2380
           | |-----1
           |-----1
           |-----7

```

>miR172b-3p
 Score: 1.8 Deg: 7:2240:205:1269 T_00014181

Query: 1 AGAATCTTGATGATGCTGTAG

22

```
          *|||:|||||||:|*
Sbjct:    2249 CCTTAGGACTACTACGACGTCG 2228
           |   |   |-----1
           |   |-----1
           |-----7
```

>miR172b-3p

Score: 1.8 Deg: 7:2189:205:1265 T_00014179

Query: 1 AGAATCTTGATGATGCTGTAG

22

```
          *|||:|||||||:|*
Sbjct:    2198 CCTTAGGACTACTACGACGTCG 2177
           |   |   |-----1
           |   |-----1
           |-----7
```

>miR172b-3p

Score: 1.8 Deg: 7:1352:28:148 T_00014174

Query: 1 AGAATCTTGATGATGCTGTAG

22

```
          *|||:|||||||:|*
Sbjct:    1361 CCTTAGGACTACTACGACGTCG 1340
           |   |   |-----1
           |   |-----1
           |-----7
```

>miR172b-3p

Score: 1.8 Deg: 7:2105:205:1265 T_00014178

Query: 1 AGAATCTTGATGATGCTGTAG

22

```
          *|||:|||||||:|*
Sbjct:    2114 CCTTAGGACTACTACGACGTCG 2093
           |   |   |-----1
           |   |-----1
           |-----7
```

>miR172b-3p

Score: 1.8 Deg: 7:1349:28:146 T_00014175

Query: 1 AGAATCTTGATGATGCTGTAG

22

```

          *|||:|||||||:|*
Sbjct:    1358 CCTTAGGACTACTACGACGTCG 1337
          |   |   |-----1
          |   |-----1
          |-----7

```

>miR172b-3p
Score: 1.8 Deg: 7:2420:205:1272 T_00014182

```

Query:      1 AGAATCTTGATGATGCTGTAG
           22
          *|||:|||||||:|*
Sbjct:    2429 CCTTAGGACTACTACGACGTCG 2408
          |   |   |-----1
          |   |-----1
          |-----7

```

>miR172b-3p
Score: 1.8 Deg: 7:2159:205:1265 T_00014177

```

Query:      1 AGAATCTTGATGATGCTGTAG
           22
          *|||:|||||||:|*
Sbjct:    2168 CCTTAGGACTACTACGACGTCG 2147
          |   |   |-----1
          |   |-----1
          |-----7

```

>miR172b-3p
Score: 1.8 Deg: 7:1349:28:146 T_00014176

```

Query:      1 AGAATCTTGATGATGCTGTAG
           22
          *|||:|||||||:|*
Sbjct:    1358 CCTTAGGACTACTACGACGTCG 1337
          |   |   |-----1
          |   |-----1
          |-----7

```

>miR172b-3p
Score: 1.8 Deg: 7:2235:205:1267 T_00014180

```

Query:      1 AGAATCTTGATGATGCTGTAG
           22
          *|||:|||||||:|*

```

Sbjct: 2244 CCTTAGGACTACTACGACGTCG 2223

```

      | | |-----1
      | |-----1
      |-----7

```

>miR172b-3p
 Score: 1.8 Deg: 7:2485:205:1273 T_00014186

Query: 1 AGAATCTTGATGATGCTGTAG
 22

|||:|||||||:|
 Sbjct: 2494 CCTTAGGACTACTACGACGTCG 2473

```

      | | |-----1
      | |-----1
      |-----7

```

>miR172b-3p
 Score: 1.8 Deg: 7:2415:205:1270 T_00014185

Query: 1 AGAATCTTGATGATGCTGTAG
 22

|||:|||||||:|
 Sbjct: 2424 CCTTAGGACTACTACGACGTCG 2403

```

      | | |-----1
      | |-----1
      |-----7

```

>miR172b-3p
 Score: 1.8 Deg: 7:2418:205:1272 T_00014184

Query: 1 AGAATCTTGATGATGCTGTAG
 22

|||:|||||||:|
 Sbjct: 2427 CCTTAGGACTACTACGACGTCG 2406

```

      | | |-----1
      | |-----1
      |-----7

```

>miR393a-5p
 Score: 1.5 Deg: 109:1993:631:3423 T_00032843

Query: 1 TCCAAAGGGATCGCATTG-ATCC
 23

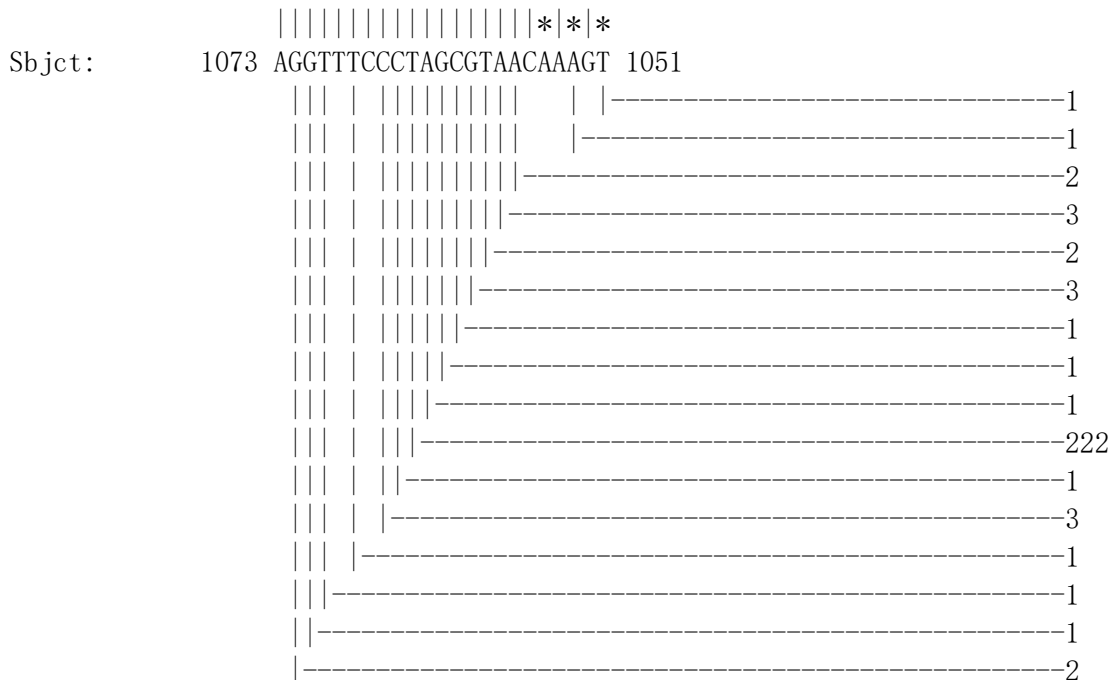
|||||||**||*
 Sbjct: 2002 AGGTTTCCCTAGCGTAACAGAGGT 1979



>miR393a-5p

Score: 1.5 Deg: 222:1064:222:1728 T_00015134

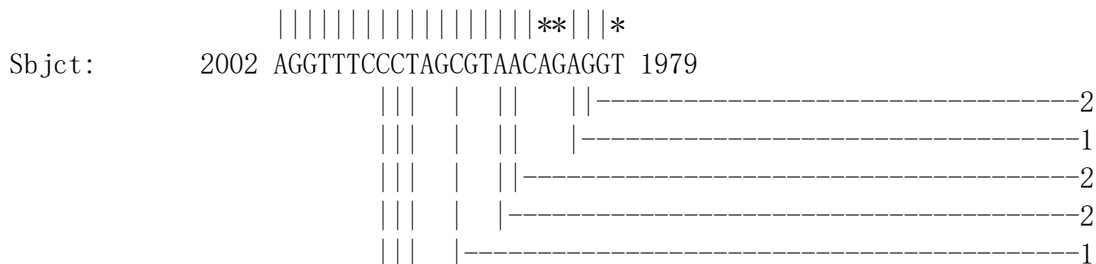
Query: 1 TCCAAAGGGATCGCATTGATCC
23



>miR393b-5p

Score: 1.5 Deg: 109:1993:631:3423 T_00032843

Query: 1 TCCAAAGGGATCGCATTG-ATCC
23



```

| | |-----109
| |-----5
|-----1

```

>miR393b-5p

Score: 1.5 Deg: 222:1064:222:1728 T_00015134

Query: 1 TCCAAAGGGATCGCATTGATCC
23

```

| | | | | | | | | | | | | | | | * | * | *
Sbjct: 1073 AGGTTTCCCTAGCGTAACAAAGT 1051
| | | | | | | | | | | | | | |-----1
| | | | | | | | | | | | | | |-----1
| | | | | | | | | | | | | | |-----2
| | | | | | | | | | | | | | |-----3
| | | | | | | | | | | | | | |-----2
| | | | | | | | | | | | | | |-----3
| | | | | | | | | | | | | | |-----1
| | | | | | | | | | | | | | |-----1
| | | | | | | | | | | | | | |-----1
| | | | | | | | | | | | | | |-----222
| | | | | | | | | | | | | | |-----1
| | | | | | | | | | | | | | |-----3
| | | | | | | | | | | | | | |-----1
| | | | | | | | | | | | | | |-----1
| | | | | | | | | | | | | | |-----1
| | | | | | | | | | | | | | |-----2

```

>miR397-5p

Score: 2.5 Deg: 16:256:36:4541T_00008962

Query: 1 TCATTGAGTGCAGCGTTGATG
22

```

| * | | | | | | | | | * | | | | | *
Sbjct: 265 ACTAACTCACGTCTCAACTACT 244
| | | | | | | | | | | | | | |-----9
| | | | | | | | | | | | | | |-----8
| | | | | | | | | | | | | | |-----4
| | | | | | | | | | | | | | |-----4
| | | | | | | | | | | | | | |-----5
| | | | | | | | | | | | | | |-----1
| | | | | | | | | | | | | | |-----2
| | | | | | | | | | | | | | |-----4
| | | | | | | | | | | | | | |-----1
| | | | | | | | | | | | | | |-----2
| | | | | | | | | | | | | | |-----1

```

```

|||||  ||-----16
|||||  |-----5
|||||-----15
|||-----10
||-----6
||-----8
|-----9

```

>miR397-5p

Score: 1.2 Deg: 33:571:33:785 T_00059025

Query: 1 TCATTGAGTGCAGCGTTGATG
22

```

|||||||:|||||||:~*
Sbjct: 580 AGTAACTCGCGTCGCAACTATT 559
      |||||-----2
      |||||-----1
      |||||-----3
      |||||-----3
      |||||-----2
      |||||-----3
      |||||-----1
      |||||-----5
      |||||-----1
      |||||-----2
      |||||-----3
      |||||-----2
      |||||-----33
      |||||-----3
      |||-----3
      ||-----4
      |-----2
      |-----1

```

>miR399a-3p

Score: 1.5 Deg: 5:369:6:352 T_00083396

Query: 1 TGCCAAAGGAGATTTGTCCTA
22

```

|||||||:|*~*
Sbjct: 378 ACGGTTTCCTCTAAACGGGTG 357
      |-----1
      |-----5

```

>miR399a-3p

Score: 1.5 Deg: 5:933:6:374 T_00083395

Query: 1 TGCCAAAGGAGATTGTCCTA

22

|||||:|*|*

Sbjct: 942 ACGGTTTCCTCTAAACGGGTG 921

|-----1
|-----5

>miR399a-3p

Score: 1.5 Deg: 5:1027:433:7904 T_00083397

Query: 1 TGCCAAAGGAGATTGTCCTA

22

|||||:|*|*

Sbjct: 1036 ACGGTTTCCTCTAAACGGGTG 1015

|-----1
|-----5

>miR399a-3p

Score: 1.5 Deg: 5:451:433:5148T_00083398

Query: 1 TGCCAAAGGAGATTGTCCTA

22

|||||:|*|*

Sbjct: 460 ACGGTTTCCTCTAAACGGGTG 439

|-----1
|-----5

>miR399b-3p

Score: 1.5 Deg: 5:369:6:352 T_00083396

Query: 1 TGCCAAAGGAGATTGTCCTA

22

|||||:|*|*

Sbjct: 378 ACGGTTTCCTCTAAACGGGTG 357

|-----1
|-----5

>miR399b-3p

Score: 1.5 Deg: 5:933:6:374 T_00083395

Query: 1 TGCCAAAGGAGATTGTCCTA

22

|||||:|*|*

Sbjct: 942 ACGGTTTCCTCTAAACGGGTTG 921

```

      |           |-----1
      |-----5

```

>miR399b-3p
 Score: 1.5 Deg: 5:1027:433:7904 T_00083397

Query: 1 TGCCAAAGGAGATTGTCCTA
 22

```

      |||||:|*|*
Sbjct: 1036 ACGGTTTCCTCTAAACGGGTTG 1015
      |           |-----1
      |-----5

```

>miR399b-3p
 Score: 1.5 Deg: 5:451:433:5148T_00083398

Query: 1 TGCCAAAGGAGATTGTCCTA
 22

```

      |||||:|*|*
Sbjct: 460 ACGGTTTCCTCTAAACGGGTTG 439
      |           |-----1
      |-----5

```

>miR399c-3P
 Score: 2.0 Deg: 63:403:63:419 T_00093857

Query: 1 TGCCAAAGGAGAGTTGCCCTG
 22

```

      *|||*|||*
Sbjct: 412 TCGGTTTCCTCCCAACGGGACT 391
      |||||  ||  ||  ||-----2
      |||||  ||  ||  ||-----2
      |||||  ||  ||  ||-----2
      |||||  ||  ||-----1
      |||||  ||  ||-----1
      |||||  ||  ||-----63
      |||||  ||  ||-----5
      |||||  ||  ||-----1
      |||||  ||  ||-----3
      |||||  ||  ||-----2
      |||||  ||  ||-----1
      |||||  ||  ||-----3
      |||||  ||  ||-----1
      |||||  ||  ||-----2

```

```
>miR399c-3P
Score: 2.0 Deg: 63:403:63:492 T_00093858
```

Query: 1 TGCCAAAGGAGAGTTGCCCTG
22

```

Query:      1  TGCCAAAGGAGAGTTGCCCTG
22

          *|||*|||*
Sbjct:    412 TCGGTTTCCTCCCAACGGGACT 391
          ||| || | | |-----2
          ||| || | | |-----2
          ||| || | | |-----2
          ||| || | | |-----1
          ||| || | | |-----1
          ||| || | | |-----63
          ||| || | | |-----5
          ||| || | | |-----1
          ||| || | | |-----3
          ||| || | | |-----2
          ||| || | | |-----1
          ||| || | | |-----3
          || |-----1
          |-----2

```

```
>miR399c-3P
Score: 2.0 Deg: 63:367:63:262 T_00089452
```

Query: 1 TGCCAAAGGAGAGTTGCCCTG
22

```

Query:      1 TGCCAAAGGAGAGTTGCCCTG
22
           *|||*|||*
Sbjct:    376 TCGGTTTCCTCCCAACGGGACT 355
           ||| || | |-----2
           ||| || |-----2
           ||| || |-----2
           ||| || |-----1
           ||| || |-----1
           ||| || |-----63
           ||| || |-----5
           ||| || |-----1
           ||| || |-----3
           ||| || |-----2
           ||| || |-----1
           ||| || |-----3
           || |-----1
           ||-----2

```

>miR399c-3P

Score: 2.2 Deg: 5:369:6:352 T_00083396

Query: 1 TGCCAAAGGAGAGTTGCCCTG
22

Sbjct: 378 ACGGTTTCCTCTAAACGGGTG 357
|||||*|||*:*
|-----1
|-----5

>miR399c-3P

Score: 2.2 Deg: 5:933:6:374 T_00083395

Query: 1 TGCCAAAGGAGAGTTGCCCTG
22

Sbjct: 942 ACGGTTTCCTCTAAACGGGTG 921
|||||*|||*:*
|-----1
|-----5

>miR399c-3P

Score: 2.2 Deg: 5:1027:433:7904 T_00083397

Query: 1 TGCCAAAGGAGAGTTGCCCTG
22

Sbjct: 1036 ACGGTTTCCTCTAAACGGGTG 1015
|||||*|||*:*
|-----1
|-----5

>miR399c-3P

Score: 2.2 Deg: 5:451:433:5148T_00083398

Query: 1 TGCCAAAGGAGAGTTGCCCTG
22

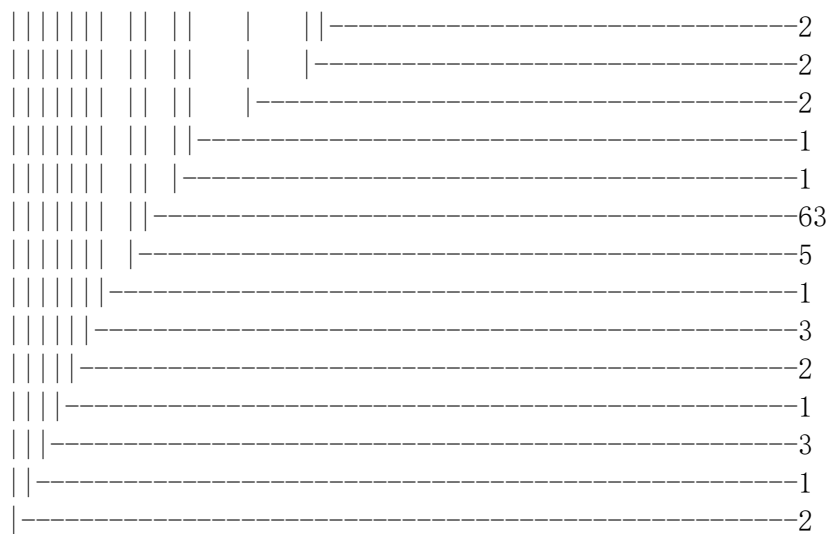
Sbjct: 460 ACGGTTTCCTCTAAACGGGTG 439
|||||*|||*:*
|-----1
|-----5

>miR399d-3p

Score: 2.5 Deg: 63:403:63:419 T_00093857

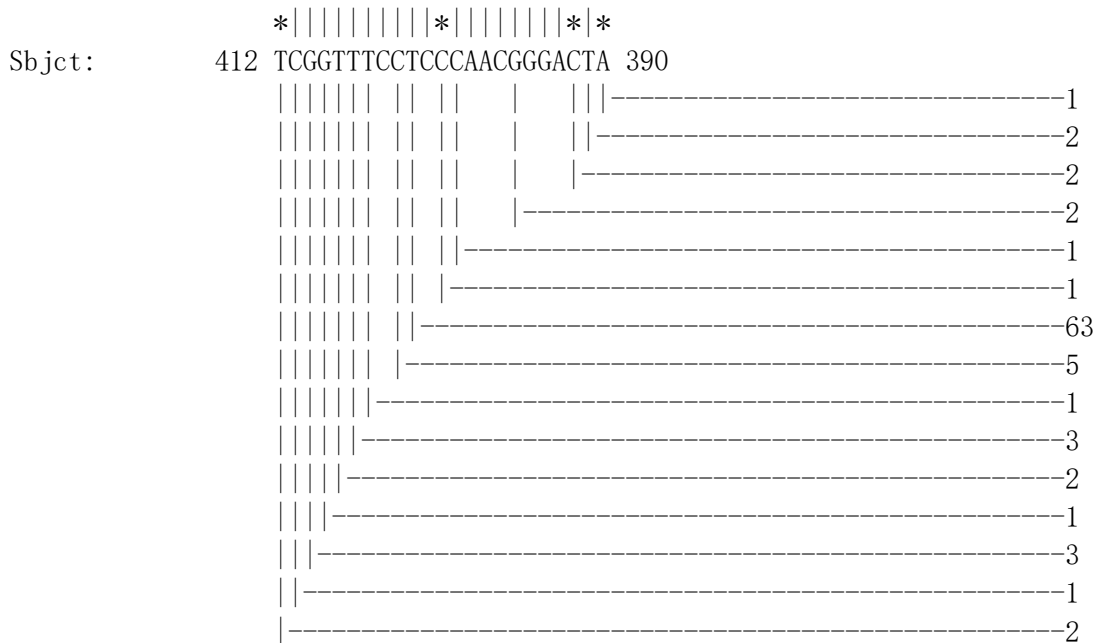
Query: 1 TGCCAAAGGAGAGTTGCCCT-A
22

Sbjct: 412 TCGGTTTCCTCCCAACGGGACTA 390
||||||*|||*|||*
|-----1
|-----5



>miR399d-3p
 Score: 2.5 Deg: 63:403:63:492 T_00093858

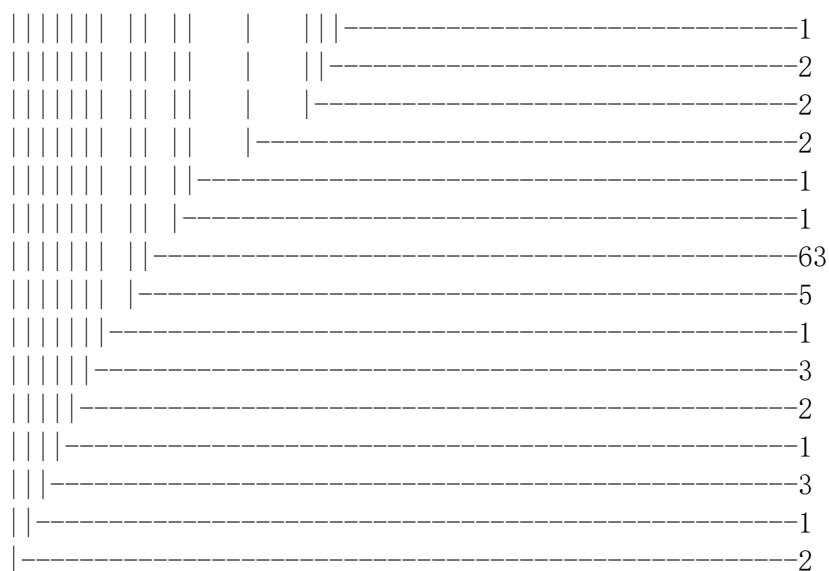
Query: 1 TGCCAAAGGAGAGTTGCCCT-A
 22



>miR399d-3p
 Score: 2.5 Deg: 63:367:63:262 T_00089452

Query: 1 TGCCAAAGGAGAGTTGCCCT-A
 22

Sbjet: 376 TCGGTTTCCTCCCAACGGGACTA 354



>miR399d-3p
 Score: 2.0 Deg: 5:369:6:352 T_00083396

Query: 1 TGCCAAAGGAGAGTTGCCCTA
 22
 |||||*|||*|*
 Sbjet: 378 ACGGTTTCCTCTAAACGGGTG 357
 |-----1
 |-----5

>miR399d-3p
 Score: 2.0 Deg: 5:933:6:374 T_00083395

Query: 1 TGCCAAAGGAGAGTTGCCCTA
 22
 |||||*|||*|*
 Sbjet: 942 ACGGTTTCCTCTAAACGGGTG 921
 |-----1
 |-----5

>miR399d-3p
 Score: 2.0 Deg: 5:1027:433:7904 T_00083397

Query: 1 TGCCAAAGGAGAGTTGCCCTA
 22
 |||||*|||*|*
 Sbjet: 1036 ACGGTTTCCTCTAAACGGGTG 1015
 |-----1
 |-----5

>miR399d-3p

Score: 2.0 Deg: 5:451:433:5148T_00083398

Query: 1 TGCCAAAGGAGAGTTGCCCTA

22

Sbjct: 460 ACGGTTTCCTCTAAACGGGTG 439

|-----1
|-----5

>miR403-3P

Score: 0.8 Deg: 48:3295:48:229T_00080897

Query: 1 TTAGATTACGCACAAACTCG

22

Sbjct: 3304 AATCTAAGTGC GTTTGGGCT 3283

|-----1
|-----48

>CsmiRNA-n5a-5p

Score: 1.5 Deg: 18:1869:26:3282 T_00019479

Query: 1 CACATCAAAAAATGCTCGCACC

23

Sbjct: 1878 GTGTAGTTTCTTACGAGCGTGA 1856

|-----1
|-----1
|-----1
|-----1
|-----18
|-----1
|-----1
|-----1
|-----1
|-----2
|-----2
|-----2
|-----2
|-----2
|-----3

>CsmiRNA-n5b-5p

Score: 1.5 Deg: 18:1869:26:3282 T_00019479

```

Query:          1 CACATCAAAAAATGCTCGCACC
                23
                |||||*|||||||*
Sbjct:      1878 GTGTAGTTTCTTACGAGCGTGA 1856
                ||||| | | |-----1
                ||||| | | |-----1
                ||||| | | |-----1
                ||||| | | |-----1
                ||||| | | |-----18
                ||||| | | |-----1
                ||||| | | |-----1
                ||||| | | |-----1
                ||||| | | |-----2
                ||||| | | |-----2
                ||||| | | |-----2
                ||||| | | |-----2
                ||||| | | |-----2
                ||||| | | |-----2
                ||||| | | |-----3

```

>CsmiRNA-n10a-3p
 Score: 2.0 Deg: 20:1660:21:1136 T_00069888

```

Query:          1 TAATGCAGTGCGAACTCTCTA
                22
                |*|||:|||||||*
Sbjct:      1669 AATACGTTACGCTTGAGAGATA 1648
                | ||| | | |-----1
                | ||| | | |-----1
                | ||| | | |-----1
                | ||| | | |-----1
                | ||| | | |-----1
                | ||| | | |-----20
                | ||| | | |-----1
                | ||| | | |-----2
                | ||| | | |-----1
                | ||| | | |-----2

```

>CsmiRNA-n10b-3p
 Score: 2.0 Deg: 20:1660:21:1136 T_00069888

```

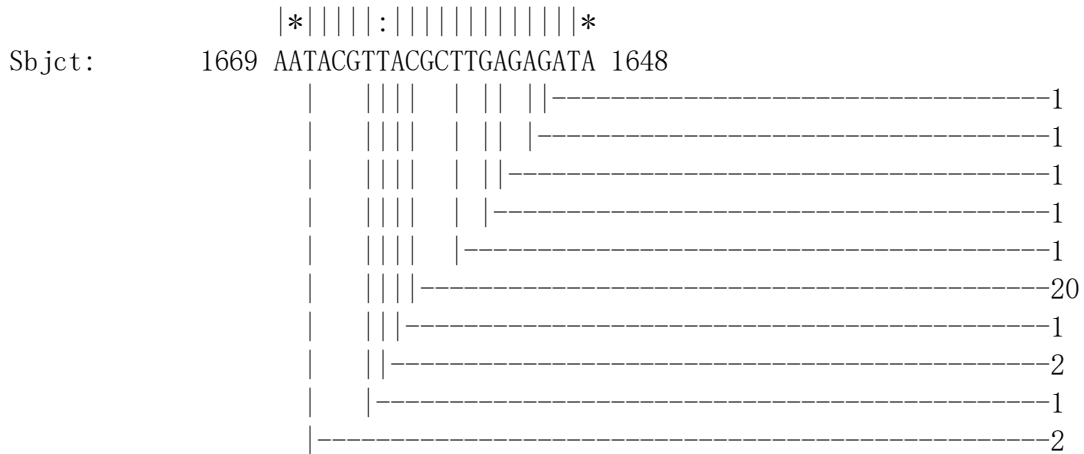
Query:          1 TAATGCAGTGCGAACTCTCTA
                22
                |*|||:|||||||*
Sbjct:      1669 AATACGTTACGCTTGAGAGATA 1648
                | ||| | | |-----1

```



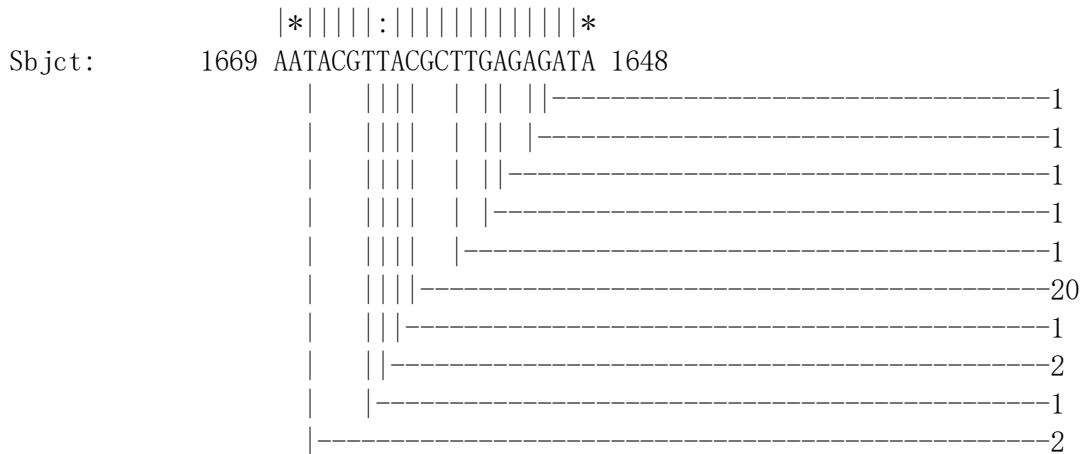
>CsmiRNA-n10c-3p
Score: 2.0 Deg: 20:1660:21:1136 T_00069888

Query: 1 TAATGCAGTGCGAACTCTCTA
22



>CsmiRNA-n10d-3p
Score: 2.0 Deg: 20:1660:21:1136 T_00069888

Query: 1 TAATGCAGTGCGAACTCTCTA
22



>CsmiRNA-n27a.2

Score: 2.5 Deg: 9:762:9:254 T_00013618

Query: 1 AATACAATACGACATAATACGGCG

25

Sbjct:

771 TTATGTTATGCTGGTTTATGCCGCA 747

```

|||||**|||||*
|||-----1
|||-----2
|||-----1
|||-----6
|||-----1
|||-----2
|||-----9
|||-----3
|||-----2
|||-----1
|||-----7
|||-----4
|||-----2
|||-----2
|||-----2
```

>CsmiRNA-n27a.2

Score: 2.5 Deg: 9:1946:433:1737 T_00013615

Query: 1 AATACAATACGACATAATACGGCG

25

Sbjct:

1955 TTATGTTATGCTGGTTTATGCCGCA 1931

```

|||||**|||||*
|||-----1
|||-----2
|||-----1
|||-----6
|||-----1
|||-----2
|||-----9
|||-----3
|||-----2
|||-----1
|||-----7
|||-----4
|||-----2
|||-----2
```

|-----2

>CsmiRNA-n27a.2

Score: 2.5 Deg: 9:2739:433:1746 T_00013616

Query: 1 AATACAATACGACATAATACGGCG
25

Sbjct: 2748 TTATGTTATGCTGGTTTATGCCGCA 2724
||| |-----1
||| |-----2
||| |-----1
||| |-----6
||| |-----1
||| |-----2
||| |-----9
||| |-----3
||| |-----2
||| |-----1
||| |-----7
||| |-----4
||| |-----2
||| |-----2
||| |-----2

>CsmiRNA-n27a.2

Score: 2.5 Deg: 9:1977:433:1744 T_00013614

Query: 1 AATACAATACGACATAATACGGCG
25

Sbjct: 1986 TTATGTTATGCTGGTTTATGCCGCA 1962
||| |-----1
||| |-----2
||| |-----1
||| |-----6
||| |-----1
||| |-----2
||| |-----9
||| |-----3
||| |-----2
||| |-----1
||| |-----7
||| |-----4
||| |-----2

```
||-----2
|-----2
```

>CsmiRNA-n27a.2

Score: 2.5 Deg: 9:2108:433:1742 T_00013617

Query: 1 AATACAATACGACATAATACGGCG
25

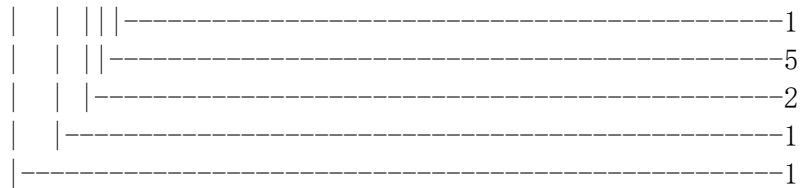
```
|||||||**|||||*
Sbjct: 2117 TTATGTTATGCTGGTTTATGCCGCA 2093
||-----1
||-----2
||-----1
||-----6
||-----1
||-----2
||-----9
||-----3
||-----2
||-----1
||-----7
||-----4
||-----2
||-----2
||-----2
```

>CsmiRNA-n27g-3p

Score: 2.0 Deg: 5:2286:631:2756 T_00015473

Query: 1 ATCTAATACGGCGTTCCAAACGAA
25

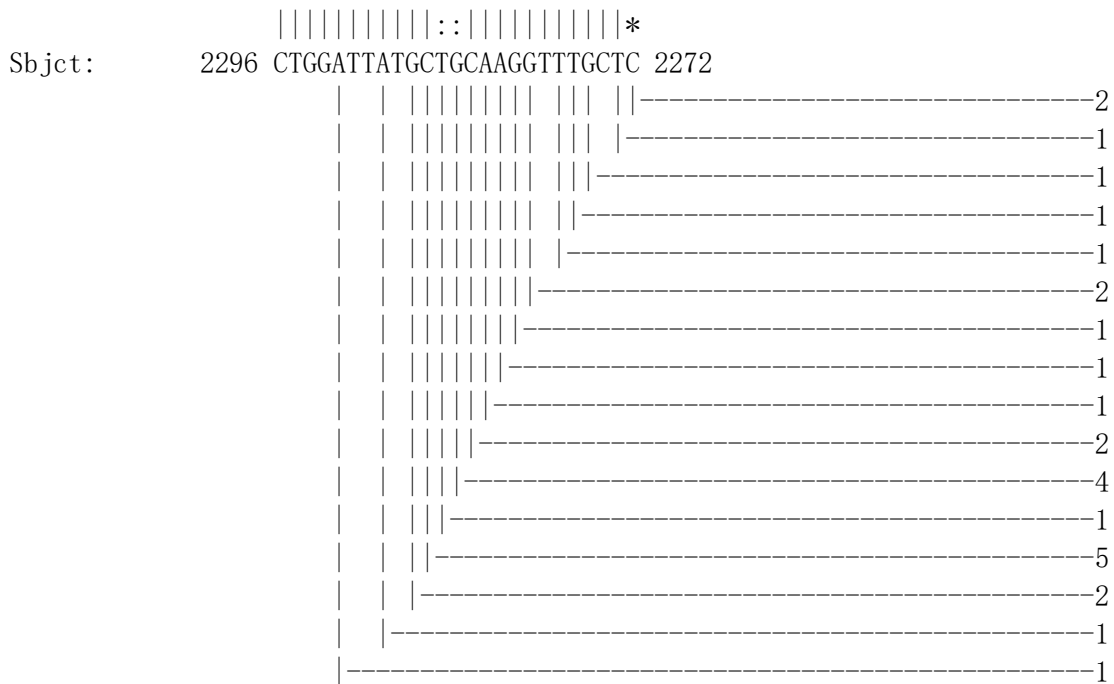
```
|:|||||:||||||**
Sbjct: 2295 TGGATTATGCTGCAAGGTTTGCTCG 2271
|-----1
|-----2
|-----1
|-----1
|-----1
|-----1
|-----1
|-----2
|-----1
|-----1
|-----1
|-----2
|-----4
```



>CsmiRNA-n271

Score: 1.5 Deg: 5:2286:631:2756 T_00015473

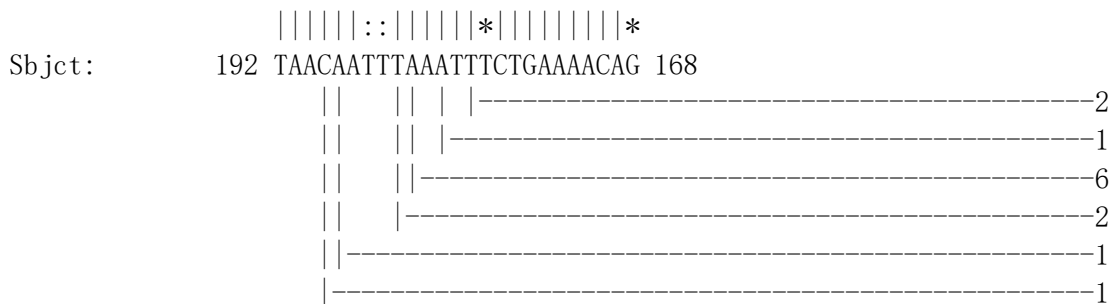
Query: 1 GACCTAATACGGTGTTCACAAACGA
25



>CsmiRNA-n30n.2

Score: 2.5 Deg: 6:183:6:60 T_00085947

Query: 1 ATTGTTGGATTAAATGACTTTTGT
25



>CsmiRNA-n30n.2

Score: 2.5 Deg: 6:3060:6:267 T_00058209

Query: 1 ATTGTTGGATTTAATGACTTTTGT
25

Sbjct: 3069 TAACAATTTAAATTTCTGAAAACAG 3045
|||||:|||||*|||||||*
|| |-----2
|| |-----1
||-----6
|-----2

>CsmiRNA-n30n.2

Score: 2.5 Deg: 6:1259:6:104 T_00058207

Query: 1 ATTGTTGGATTTAATGACTTTTGT
25

Sbjct: 1268 TAACAATTTAAATTTCTGAAAACAG 1244
|||||:|||||*|||||||*
|| |-----2
|| |-----1
||-----6
|-----2

>CsmiRNA-n30n.2

Score: 2.5 Deg: 6:3031:6:305 T_00058208

Query: 1 ATTGTTGGATTTAATGACTTTTGT
25

Sbjct: 3040 TAACAATTTAAATTTCTGAAAACAG 3016
|||||:|||||*|||||||*
|| |-----2
|| |-----1
||-----6
|-----2

>miR171a-3p

Score: 1.0 Deg: 71:417:71:404 T_00060987

Query: 1 TGATTGAGCCGTGCCAATATC
22

Sbjct: 429 ACTAACTCGGCGGTTATAGG 408
|||||||:|||||||*
|-----71
|-----4

>miR171a-3p

Score: 1.0 Deg: 101:481:101:342 T_00010373

```
Query:      1 TGATTGAGCCGTGCCAATATC
            22
            |||||:|||||*
Sbjct:      493 ACTAACTCGGCGCGTTATAGG 472
              ||-----101
              ||-----1
              |-----18
```

>miR171b-3p
Score: 1.0 Deg: 71:417:71:404 T_00060987

```
Query:      1 TGATTGAGCCGTGCCAATATC
            22
            |||||:|||||*
Sbjct:      429 ACTAACTCGGCGCGTTATAGG 408
              |-----71
              |-----4
```

>miR171b-3p
Score: 1.0 Deg: 101:481:101:342 T_00010373

```
Query:      1 TGATTGAGCCGTGCCAATATC
            22
            |||||:|||||*
Sbjct:      493 ACTAACTCGGCGCGTTATAGG 472
              ||-----101
              ||-----1
              |-----18
```

>miR171c-3p
Score: 1.0 Deg: 71:417:71:404 T_00060987

```
Query:      1 TGATTGAGCCGTGCCAATATC
            22
            |||||:|||||*
Sbjct:      429 ACTAACTCGGCGCGTTATAGG 408
              |-----71
              |-----4
```

>miR171c-3p
Score: 1.0 Deg: 101:481:101:342 T_00010373

Query: 1 TGATTGAGCCGTGCCAATATC

22

```

      |||||:|||||*
Sbjct: 493 ACTAACTCGGCGGTTATAGG 472
      ||-----101
      ||-----1
      |-----18

```

>miR171d-3P

Score: 1.0 Deg: 71:417:71:404 T_00060987

Query: 1 TGATTGAGCCGTGCCAATATC

22

```

      |||||:|||||*
Sbjct: 429 ACTAACTCGGCGGTTATAGG 408
      ||-----71
      |-----4

```

>miR171d-3P

Score: 1.0 Deg: 101:481:101:342 T_00010373

Query: 1 TGATTGAGCCGTGCCAATATC

22

```

      |||||:|||||*
Sbjct: 493 ACTAACTCGGCGGTTATAGG 472
      ||-----101
      ||-----1
      |-----18

```

>miR171e-3p

Score: 1.0 Deg: 71:417:71:404 T_00060987

Query: 1 TGATTGAGCCGTGCCAATATC

22

```

      |||||:|||||*
Sbjct: 429 ACTAACTCGGCGGTTATAGG 408
      ||-----71
      |-----4

```

>miR171e-3p

Score: 1.0 Deg: 101:481:101:342 T_00010373

Query: 1 TGATTGAGCCGTGCCAATATC

22

```

      |||||:|||||*
Sbjct: 493 ACTAACTCGGCGGTTATAGG 472
      ||-----101

```

```

| |-----1
|-----18

```

>miR171f-3p

Score: 1.0 Deg: 71:417:71:404 T_00060987

Query: 1 TGATTGAGCCGTGCCAATATC
22

```

|||||||:|||||||*
Sbjct: 429 ACTAACTCGGCGCGTTATAGG 408
| |-----71
|-----4

```

>miR171f-3p

Score: 1.0 Deg: 101:481:101:342 T_00010373

Query: 1 TGATTGAGCCGTGCCAATATC
22

```

|||||||:|||||||*
Sbjct: 493 ACTAACTCGGCGCGTTATAGG 472
| |-----101
| |-----1
|-----18

```

>miR530-5P

Score: 0.8 Deg: 24:1277:26:827T_00079842

Query: 1 TCTGCATTTGCACCTGCACCT
22

```

:|||||||*
Sbjct: 1288 GGACGTAAACGTGGACGTGGAC 1267
| |-----1
| |-----24
|-----1

```

>miR530-5P

Score: 0.8 Deg: 24:1277:26:815T_00079843

Query: 1 TCTGCATTTGCACCTGCACCT
22

```

:|||||||*
Sbjct: 1288 GGACGTAAACGTGGACGTGGAC 1267
| |-----1
| |-----24
|-----1

```

>miR5658

Score: 2.2 Deg: 6:1386:630:2486 T_00032450

Query: 1 ATGATGATCATCATGATGAT-A

22

Sbjct: 1398 TACTACTACTAGTACTACTGCTC 1376

|||||||*|||||||:|*|*
|| | |-----6
|| |-----2
||-----1
|-----2

>miR5658

Score: 2.2 Deg: 6:1386:630:2485 T_00032452

Query: 1 ATGATGATCATCATGATGAT-A

22

Sbjct: 1398 TACTACTACTAGTACTACTGCTC 1376

|||||||*|||||||:|*|*
|| | |-----6
|| |-----2
||-----1
|-----2

>CsmiRNA-n27g-3p

Score: 2.5 Deg: 6:759:9:254 T_00013618

Query: 1 ATCTAATACGGCGTTCCAAACGAA

25

Sbjct: 760 TGGTTTATGCCGCAAGGTTTGCTCG 736

|:|*|||||||*|*|*
|| | |-----1
|| | |-----1
|| | |-----1
|| | |-----2
||-----1
||-----6
|-----1

>CsmiRNA-n27g-3p

Score: 2.5 Deg: 6:1943:433:1737 T_00013615

Query: 1 ATCTAATACGGCGTTCCAAACGAA

25

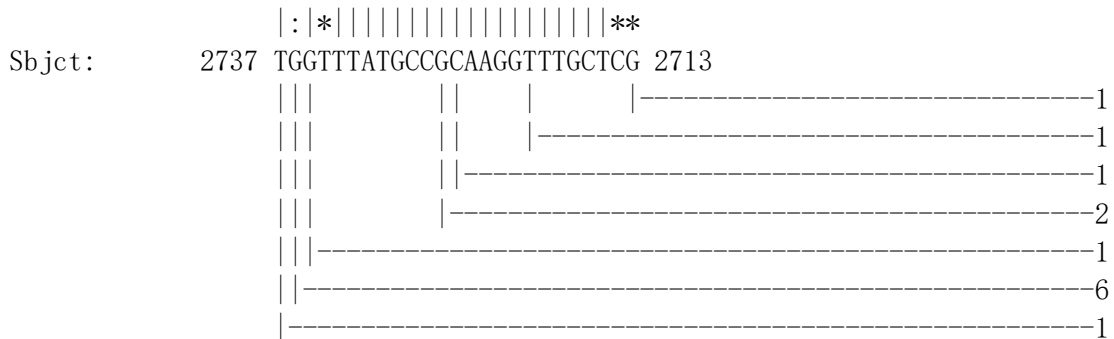
Sbjct: 1944 TGGTTTATGCCGCAAGGTTTGCTCG 1920

|:|*|||||||*|*|*
|| | |-----1
|| | |-----1



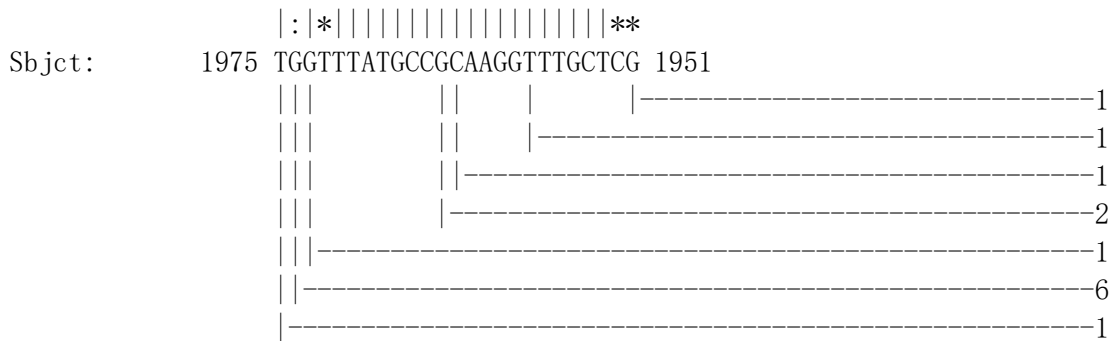
>CsmiRNA-n27g-3p
Score: 2.5 Deg: 6:2736:433:1746 T_00013616

Query: 1 ATCTAATACGGCGTTCCAAACGAA
25



>CsmiRNA-n27g-3p
Score: 2.5 Deg: 6:1974:433:1744 T_00013614

Query: 1 ATCTAATACGGCGTTCCAAACGAA
25



>CsmiRNA-n27g-3p
Score: 2.5 Deg: 6:2105:433:1742 T_00013617

Query: 1 ATCTAATACGGCGTTCCAAACGAA
25

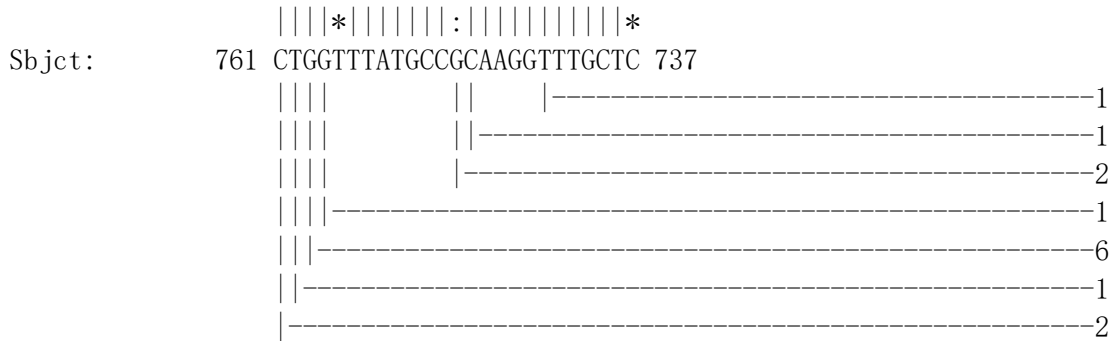




>CsmiRNA-n271

Score: 2.0 Deg: 6:759:9:254 T_00013618

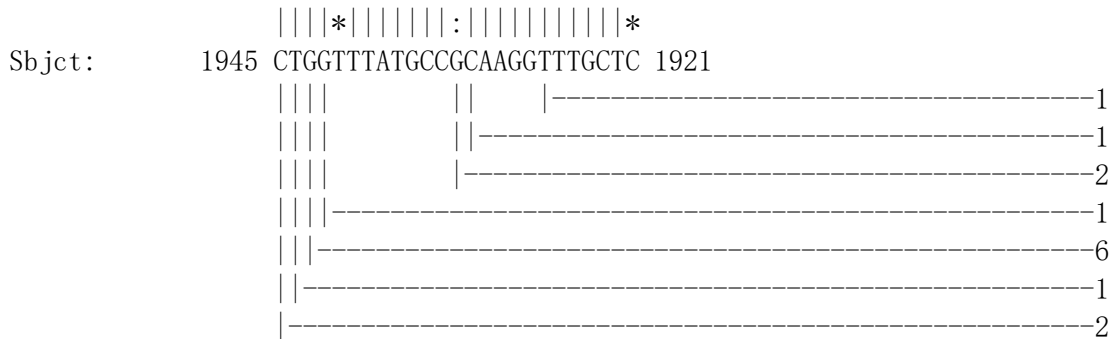
Query: 1 GACCTAATACGGTGTTCACAAACGA
25



>CsmiRNA-n271

Score: 2.0 Deg: 6:1943:433:1737 T_00013615

Query: 1 GACCTAATACGGTGTTCACAAACGA
25



>CsmiRNA-n271

Score: 2.0 Deg: 6:2736:433:1746 T_00013616

Query: 1 GACCTAATACGGTGTTCACAAACGA
25



```

|||-----1
||-----6
|-----1
|-----2

```

>CsmiRNA-n271

Score: 2.0 Deg: 6:1974:433:1744 T_00013614

Query: 1 GACCTAATACGGTGTTCACAAACGA
25

```

||||*|||||:|||||||*
Sbjct: 1976 CTGGTTTATGCCGCAAGGTTTGCTC 1952
||||-----1
||||-----1
||||-----2
||||-----1
||-----6
|-----1
|-----2

```

>CsmiRNA-n271

Score: 2.0 Deg: 6:2105:433:1742 T_00013617

Query: 1 GACCTAATACGGTGTTCACAAACGA
25

```

||||*|||||:|||||||*
Sbjct: 2107 CTGGTTTATGCCGCAAGGTTTGCTC 2083
||||-----1
||||-----1
||||-----2
||||-----1
||-----6
|-----1
|-----2

```

>CsmiRNA-n30a

Score: 2.0 Deg: 6:183:6:60T_00085947

Query: 1 AAGATTGTTGGATTAAAGACTTT
25

```

*|||||||:|||||||*
Sbjct: 195 CTCTAACAATTTAAATTTCTGAAAA 171
||  ||  |-----2
||  ||  |-----1
||  ||  |-----6
||  ||  |-----2

```

```

||-----1
|-----1

```

>CsmiRNA-n30a

Score: 2.0 Deg: 6:3060:6:267 T_00058209

Query: 1 AAGATTGTTGGATTAAAGACTTT
25

```

*|||||||:::|||||||*
Sbjct: 3072 CTCTAACAATTTAAATTTCTGAAAA 3048
|| | |-----2
|| | |-----1
|| | |-----6
| |-----2

```

>CsmiRNA-n30a

Score: 2.0 Deg: 6:1259:6:104 T_00058207

Query: 1 AAGATTGTTGGATTAAAGACTTT
25

```

*|||||||:::|||||||*
Sbjct: 1271 CTCTAACAATTTAAATTTCTGAAAA 1247
|| | |-----2
|| | |-----1
|| | |-----6
| |-----2

```

>CsmiRNA-n30a

Score: 2.0 Deg: 6:3031:6:305 T_00058208

Query: 1 AAGATTGTTGGATTAAAGACTTT
25

```

*|||||||:::|||||||*
Sbjct: 3043 CTCTAACAATTTAAATTTCTGAAAA 3019
|| | |-----2
|| | |-----1
|| | |-----6
| |-----2

```

>CsmiRNA-n30c.1-3p

Score: 2.5 Deg: 5:725:631:5310T_00078015

Query: 1 AGTTCAGGGGGTAGGATTGGTAC
25

```

|||||||:::*||||:|*
Sbjct: 736 TCAAGTCCCCGTAATAATTATGT 712
|| |-----1

```

||-----5
|-----2

>CsmiRNA-n30c.1-3p

Score: 2.5 Deg: 5:1381:631:5317 T_00078013

Query: 1 AGTTCAGGGGGTAGGATTGGTAC
25

|||||||:|*|||:|*
Sbjct: 1392 TCAAGTCCCCGTACTAAATTATGT 1368
||-----1
||-----5
|-----2

>CsmiRNA-n30c.1-3p

Score: 2.5 Deg: 5:1165:631:5317 T_00078014

Query: 1 AGTTCAGGGGGTAGGATTGGTAC
25

|||||||:|*|||:|*
Sbjct: 1176 TCAAGTCCCCGTACTAAATTATGT 1152
||-----1
||-----5
|-----2

>CsmiRNA-n30d

Score: 2.0 Deg: 5:727:5:201 T_00053092

Query: 1 AACATCTTAATAGTTCAGGAAGA
25

||||||:|||||||**|*
Sbjct: 746 TTGTTAGAGTTATCAAGTCCTCATA 722
||-----1
||-----5
|-----2

>CsmiRNA-n30e.2-5p

Score: 1.5 Deg: 6:183:6:60 T_00085947

Query: 1 TTGAGATGGTTAAATTTAAAGACT
25

|||||*|||||||*
Sbjct: 197 AACTCTAACAATTTAAATTTCTGAA 173
|-----2
|-----1
|-----6
|-----2

```

      |      | |-----1
      |      |-----1
      |-----1

```

>CsmiRNA-n30e.2-5p
 Score: 2.5 Deg: 6:2168:6:31 T_00095104

Query: 1 TTGAGATGGTTAAATTTAAAGACT
 25

```

      |||||*|||||||*|||*|*
Sbjct: 2182 AACTCTAACAATTTAAA-TTCTTAA 2159
      |      | | |-----2
      |      | | |-----1
      |      | |-----6
      |      | |-----2
      |-----1

```

>CsmiRNA-n30e.2-5p
 Score: 1.5 Deg: 6:3060:6:267 T_00058209

Query: 1 TTGAGATGGTTAAATTTAAAGACT
 25

```

      |||||*|||||||*
Sbjct: 3074 AACTCTAACAATTTAAATTTCTGAA 3050
      |      | | |-----2
      |      | | |-----1
      |      | |-----6
      |      | |-----2
      |-----1

```

>CsmiRNA-n30e.2-5p
 Score: 1.5 Deg: 6:1259:6:104 T_00058207

Query: 1 TTGAGATGGTTAAATTTAAAGACT
 25

```

      |||||*|||||||*
Sbjct: 1273 AACTCTAACAATTTAAATTTCTGAA 1249
      |      | | |-----2
      |      | | |-----1
      |      | |-----6
      |      | |-----2
      |-----1

```

>CsmiRNA-n30e.2-5p
 Score: 1.5 Deg: 6:3031:6:305 T_00058208

```

Query:          1 TTGAGATGGTTAAATTTAAAGACT
                25
                |||||*|||||||*
Sbjct:         3045 AACTCTAACAATTTAAATTCTGAA 3021
                |         || |-----2
                |         || |-----1
                |         ||-----6
                |         |-----2
                |-----1

```

>CsmiRNA-n30e.2-5p
 Score: 2.5 Deg: 6:1025:6:56 T_00060631

```

Query:          1 TTGAGATGGTTAAATTTAAAGACT
                25
                |||||*|||||||*|||*|*
Sbjct:         1039 AACTCTAACAATTTAAA-TTCTTAA 1016
                |         || |-----2
                |         || |-----1
                |         ||-----6
                |         |-----2
                |-----1

```

>CsmiRNA-n30g.1
 Score: 1.5 Deg: 6:1741:7:490 T_00037223

```

Query:          1 ATTGAGATTGTTACATTTAA
                21
                |||||*|||||*
Sbjct:         1756 TAACTCTAACAATTTAAATTC 1736
                |         || || |-----2
                |         || || |-----1
                |         || ||-----6
                |         ||-----1
                |         |-----1
                |         |-----1
                |-----1

```

>CsmiRNA-n30g.1
 Score: 1.5 Deg: 6:995:6:138 T_00078037

```

Query:          1 ATTGAGATTGTTACATTTAA
                21
                |||||*|||||*
Sbjct:         1010 TAACTCTAACAATTTAAATTC 990
                | || |-----2

```

Score: 1.5 Deg: 6:12:10:680 T_00050514

Query: 1 ATTGAGATTGTTACATTTAA
21

Sbjct: 27 TAACTCTAACAATTTAAATTC 7

|||||*|||*
| | | |-----2
| | |-----1
| |-----6
|-----1
-----1

>CsmiRNA-n30g.1

Score: 1.5 Deg: 6:12:10:681 T_00050513

Query: 1 ATTGAGATTGTTACATTAA
21

Sbjct: 27 TAACTCTAACAATTTAAATTC 7
 | | | | |-----2
 | | |-----1
 | |-----6
 |-----1
 |-----1

>CsmiRNA-n30g.1

Score: 1.5 Deg: 6:12:10:678 T_00050515

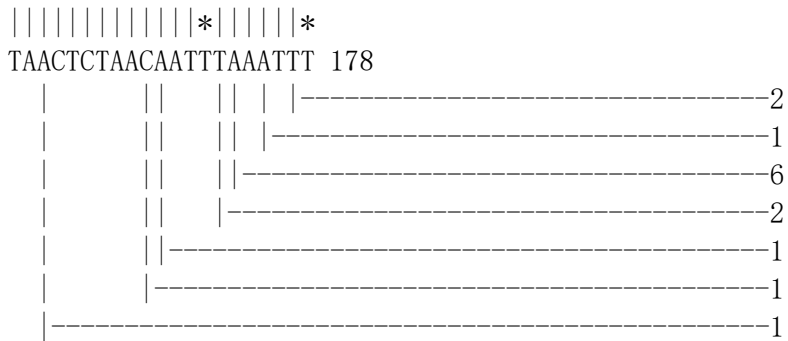
Query: 1 ATTGAGATTGTTACATTAA
21

Sbjct: 27 TAACTCTAACAATTTAAATTC 7
 | | | | |-----2
 | | |-----1
 | |-----6
 |-----1
 -----1

>CsmiRNA-n30g.1

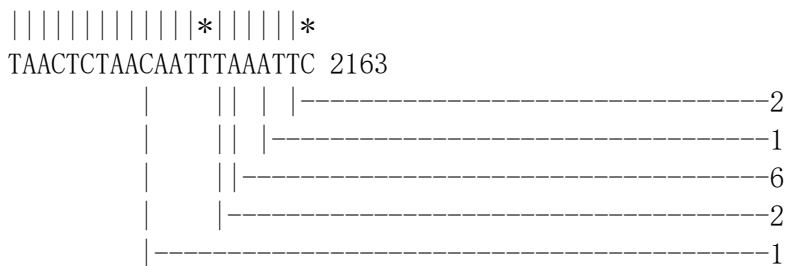
Score: 1.5 Deg: 6:183:6:60T_00085947

Sbjct: 198 TAACTCTAACAATTTAAATTT 178



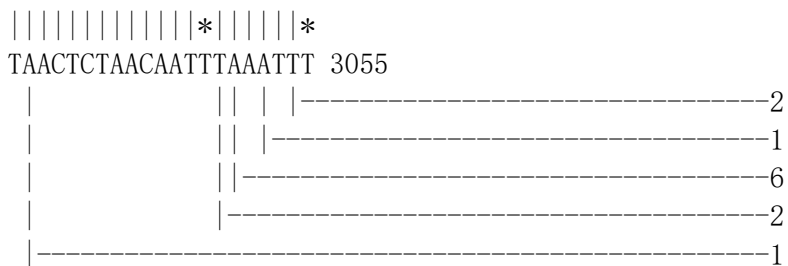
Score: 1.5 Deg: 6:2168:6:31 T_00095104

Sbjct: 2183 TAACTCTAACAATTTAAATTC 2163



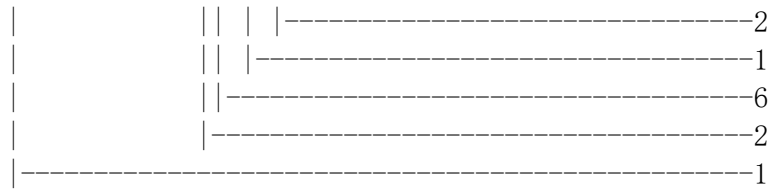
Score: 1.5 Deg: 6:3060:6:267 T_00058209

Sbjct: 3075 TAACTCTAACAATTTAAATTT 3055



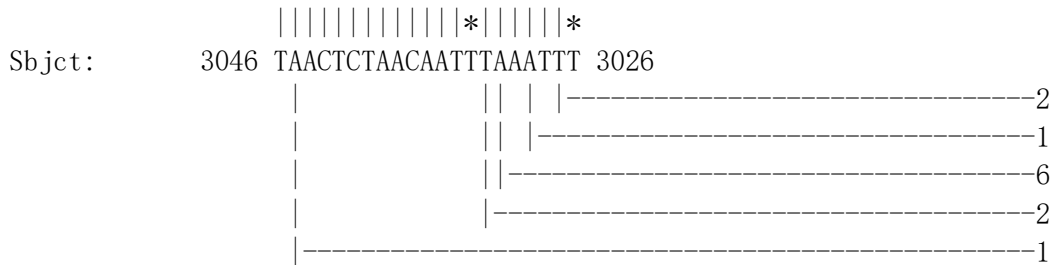
Score: 1.5 Deg: 6:1259:6:104 T_00058207

Sbjct: 1274 TAACTCTAACAATTTAAATTT 1254



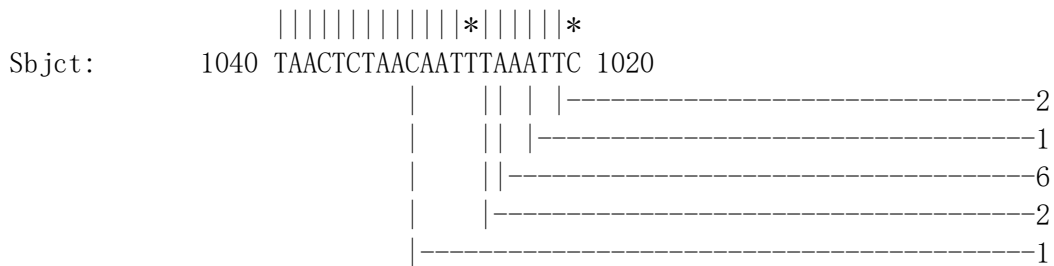
>CsmiRNA-n30g.1
Score: 1.5 Deg: 6:3031:6:305 T_00058208

Query: 1 ATTGAGATTGTTACATTTAA
21



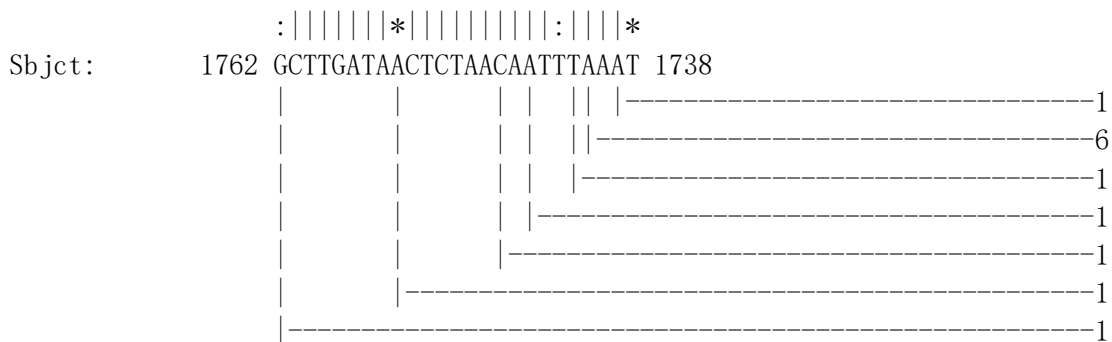
>CsmiRNA-n30g.1
Score: 1.5 Deg: 6:1025:6:56 T_00060631

Query: 1 ATTGAGATTGTTACATTTAA
21



>CsmiRNA-n30h.1
Score: 2.0 Deg: 6:1741:7:490 T_00037223

Query: 1 TGAACATATCGAGATTGTTAGATT
25



>CsmiRNA-n30h.1

Score: 2.0 Deg: 6:995:6:138 T_00078037

Query: 1 TGAACATCGAGATTGTTAGATT

25

:|||||*|||||||:||||*

Sbjct: 1016 GCTTGATAACTCTAACAATTTAAAT 992

| | |-----1
| |-----6
| |-----1
|-----1

>CsmiRNA-n30h.1

Score: 2.0 Deg: 6:12:10:680 T_00050514

Query: 1 TGAACATCGAGATTGTTAGATT

25

:|||||*|||||||:||||*

Sbjct: 33 GCTTGATAACTCTAACAATTTAAAT 9

| | |-----1
| |-----6
| |-----1
|-----1

>CsmiRNA-n30h.1

Score: 2.0 Deg: 6:12:10:681 T_00050513

Query: 1 TGAACATCGAGATTGTTAGATT

25

:|||||*|||||||:||||*

Sbjct: 33 GCTTGATAACTCTAACAATTTAAAT 9

| | |-----1
| |-----6
| |-----1
|-----1

>CsmiRNA-n30h.1

Score: 2.0 Deg: 6:12:10:678 T_00050515

Query: 1 TGAACATCGAGATTGTTAGATT

25

:|||||*|||||||:||||*

Sbjct: 33 GCTTGATAACTCTAACAATTTAAAT 9

| | |-----1
| |-----6
| |-----1
|-----1

>CsmiRNA-n30h.1

Score: 1.8 Deg: 6:183:6:60T_00085947

Query: 1 TGAACATCGAGATTGTTAGATT
25

Sbjct: 204 ACTTGATAACTCTAACAATTTAAAT 180
|||||||*|||||||:||||*
| | |-----1
| | |-----6
| | |-----2
| |-----1
|-----1
|-----1

>CsmiRNA-n30h.1

Score: 1.8 Deg: 6:2168:6:31 T_00095104

Query: 1 TGAACATCGAGATTGTTAGATT
25

Sbjct: 2189 ACTTGATAACTCTAACAATTTAAAT 2165
|||||||*|||||||:||||*
| | |-----1
| | |-----6
| |-----2
|-----1

>CsmiRNA-n30h.1

Score: 1.8 Deg: 6:3060:6:267 T_00058209

Query: 1 TGAACATCGAGATTGTTAGATT
25

Sbjct: 3081 ACTTGATAACTCTAACAATTTAAAT 3057
|||||||*|||||||:||||*
| | |-----1
| | |-----6
| |-----2
|-----1

>CsmiRNA-n30h.1

Score: 1.8 Deg: 6:1259:6:104 T_00058207

Query: 1 TGAACATCGAGATTGTTAGATT
25

Sbjct: 1280 ACTTGATAACTCTAACAATTTAAAT 1256
|||||||*|||||||:||||*
| | |-----1
| | |-----6
| |-----2
|-----1



>CsmiRNA-n30h.1

Score: 1.8 Deg: 6:3031:6:305 T_00058208

Query: 1 TGAAGTATCGAGATTGTTAGATT
25

Sbjct: 3052 ACTTGATAACTCTAACAATTTAAAT 3028
|||||*|||||:||||*
| | |-----1
| | |-----6
| | |-----2
|-----1

>CsmiRNA-n30h.1

Score: 1.8 Deg: 6:1025:6:56 T_00060631

Query: 1 TGAAGTATCGAGATTGTTAGATT
25

Sbjct: 1046 ACTTGATAACTCTAACAATTTAAAT 1022
|||||*|||||:||||*
| | |-----1
| | |-----6
| | |-----2
|-----1

>CsmiRNA-n30m

Score: 2.5 Deg: 6:183:6:60 T_00085947

Query: 1 ATTGAGATTATTAGATTTAAGGAT
25

Sbjct: 198 TAACTCTAACAATTTAAATTTCTGA 174
|||||*|||:|||||:|*
| | |-----2
| | |-----1
| | |-----6
| | |-----2
| |-----1
|-----1
|-----1

>CsmiRNA-n30m

Score: 2.2 Deg: 6:2168:6:31 T_00095104

Query: 1 ATTGAGATTATTAGATTTAAGGAT

25

```

          |||||*|||:|||||:|||*
Sbjct:    2183 TAACTCTAACAATTAAATTCTTAA 2159
              |   || |-----2
              |   || |-----1
              |   || |-----6
              |   |-----2
              |-----1

```

>CsmiRNA-n30m

Score: 2.5 Deg: 6:3060:6:267 T_00058209

Query: 1 ATTGAGATTATTAGATTTAAGGAT

25

```

          |||||*|||:|||||:|||*
Sbjct:    3075 TAACTCTAACAATTAAATTTCTGA 3051
              |           || |-----2
              |           || |-----1
              |           || |-----6
              |           |-----2
              |-----1

```

>CsmiRNA-n30m

Score: 2.5 Deg: 6:1259:6:104 T_00058207

Query: 1 ATTGAGATTATTAGATTTAAGGAT

25

```

          |||||*|||:|||||:|||*
Sbjct:    1274 TAACTCTAACAATTAAATTTCTGA 1250
              |           || |-----2
              |           || |-----1
              |           || |-----6
              |           |-----2
              |-----1

```

>CsmiRNA-n30m

Score: 2.5 Deg: 6:3031:6:305 T_00058208

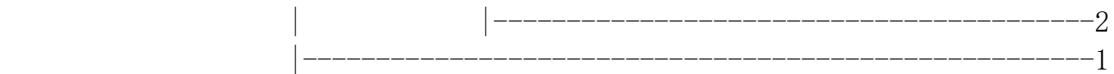
Query: 1 ATTGAGATTATTAGATTTAAGGAT

25

```

          |||||*|||:|||||:|||*
Sbjct:    3046 TAACTCTAACAATTAAATTTCTGA 3022
              |           || |-----2
              |           || |-----1
              |           || |-----6

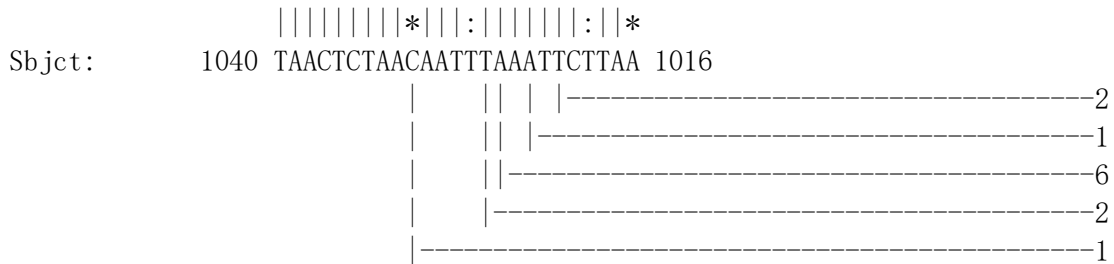
```



>CsmiRNA-n30m

Score: 2.2 Deg: 6:1025:6:56 T_00060631

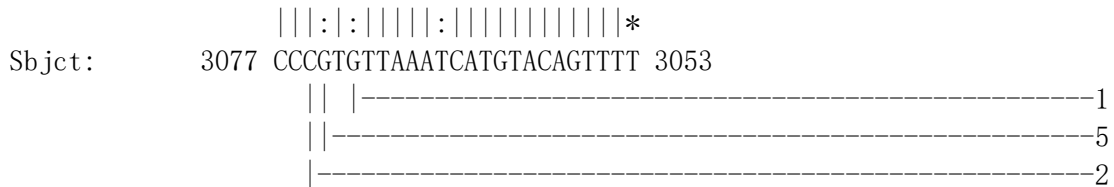
Query: 1 ATTGAGATTATTAGATTTAAGGAT
25



>CsmiRNA-n30n.1

Score: 2.0 Deg: 5:3074:5:57 T_00058193

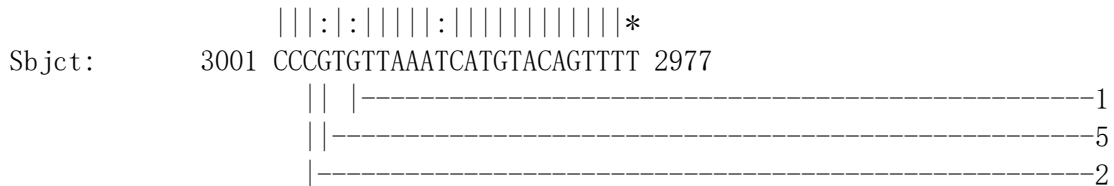
Query: 1 GGGTATAATTTGGTACATGTCAAA
25



>CsmiRNA-n30n.1

Score: 2.0 Deg: 5:2998:5:57 T_00058194

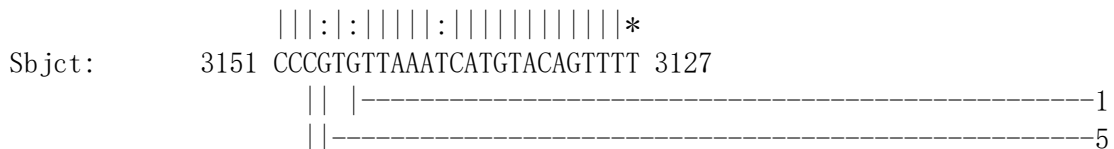
Query: 1 GGGTATAATTTGGTACATGTCAAA
25



>CsmiRNA-n30n.1

Score: 2.0 Deg: 5:3148:5:62 T_00058192

Query: 1 GGGTATAATTTGGTACATGTCAAA
25



|-----2

>CsmiRNA-n30n.1

Score: 2.0 Deg: 5:3023:5:57 T_00058196

Query: 1 GGGTATAATTTGGTACATGTCAAA
25

||||:|||||:|||||||*
Sbjct: 3026 CCCGTGTTAAATCATGTACAGTTT 3002
|| |-----1
|| |-----5
|-----2

>CsmiRNA-n30n.1

Score: 2.0 Deg: 5:2944:5:57 T_00058195

Query: 1 GGGTATAATTTGGTACATGTCAAA
25

||||:|||||:|||||||*
Sbjct: 2947 CCCGTGTTAAATCATGTACAGTTT 2923
|| |-----1
|| |-----5
|-----2

>CsmiRNA-n30n.1

Score: 2.0 Deg: 5:1086:26:635 T_00050741

Query: 1 GGGTATAATTTGGTACATGTCAAA
25

||||:|||||:|||||||*
Sbjct: 1089 CCCGTGTTAAATCATGTACAGTTT 1065
|| |-----1
|| |-----5
|-----2

>CsmiRNA-n30o-5p

Score: 1.0 Deg: 5:140:5:56 T_00091038

Query: 1 CTTTGACATGTACTAAATTATGGT
25

|||||||*|*
Sbjct: 156 GAAACTGTACATGATTTAATACAAA 132
| |-----1
| |-----5
|-----1

>CsmiRNA-n30o-5p

Score: 1.0 Deg: 5:140:5:56T_00091039

Query: 1 CTTTGACATGTACTAAATTATGGT
25

Sbjct: 156 GAAACTGTACATGATTTAATACAAA 132
|||||*|*
| | |-----1
| |-----5
|-----1

>CsmiRNA-n30o-5p

Score: 1.0 Deg: 5:359:5:55T_00091040

Query: 1 CTTTGACATGTACTAAATTATGGT
25

Sbjct: 375 GAAACTGTACATGATTTAATACAAA 351
|||||*|*
| | |-----1
| |-----5
|-----1

>CsmiRNA-n30o-5p

Score: 1.0 Deg: 5:140:5:56T_00091037

Query: 1 CTTTGACATGTACTAAATTATGGT
25

Sbjct: 156 GAAACTGTACATGATTTAATACAAA 132
|||||*|*
| | |-----1
| |-----5
|-----1

>CsmiRNA-n30o-5p

Score: 1.0 Deg: 5:140:5:58T_00091036

Query: 1 CTTTGACATGTACTAAATTATGGT
25

Sbjct: 156 GAAACTGTACATGATTTAATACAAA 132
|||||*|*
| | |-----1
| |-----5
|-----1

>CsmiRNA-n31p

Score: 2.2 Deg: 6:183:6:60T_00085947

Query: 1 GAGATGGTTAGATTTAAGGACTTT
25

||||*|||:|||||:|||||*
Sbjct: 195 CTCTAACAATTTAAATTTCTGAAAA 171

```

      ||  ||  |-----2
      ||  ||  |-----1
      ||  ||  |-----6
      ||  ||  |-----2
      ||  |-----1
      |-----1
      |-----1

```

>CsmiRNA-n31p
Score: 2.2 Deg: 6:3060:6:267 T_00058209

Query: 1 GAGATGGTTAGATTTAAGGACTTT
25

||||*|||:|||||:|||||*
Sbjct: 3072 CTCTAACAATTTAAATTTCTGAAAA 3048

```

      ||  |-----2
      ||  |-----1
      ||  |-----6
      |-----2

```

>CsmiRNA-n31p
Score: 2.2 Deg: 6:1259:6:104 T_00058207

Query: 1 GAGATGGTTAGATTTAAGGACTTT
25

||||*|||:|||||:|||||*
Sbjct: 1271 CTCTAACAATTTAAATTTCTGAAAA 1247

```

      ||  |-----2
      ||  |-----1
      ||  |-----6
      |-----2

```

>CsmiRNA-n31p
Score: 2.2 Deg: 6:3031:6:305 T_00058208

Query: 1 GAGATGGTTAGATTTAAGGACTTT
25

||||*|||:|||||:|||||*
Sbjct: 3043 CTCTAACAATTTAAATTTCTGAAAA 3019

```

      ||  |-----2
      ||  |-----1
      ||  |-----6
      |-----2

```

>CsmiRNA-n54a.2

Score: 1.8 Deg: 5:2430:33:75 T_00094820

Query: 1 ACTGCAACCACTTTAGAACTCAA

25

Sbjct: 2432 TGACGTTGGTGAAATTTTAGGTTT 2408

|||||:|*:*

|| |-----1

|| |-----1

||-----1

|-----5

>CsmiRNA-n54a.2

Score: 1.8 Deg: 5:2413:33:76 T_00094821

Query: 1 ACTGCAACCACTTTAGAACTCAA

25

Sbjct: 2415 TGACGTTGGTGAAATTTTAGGTTT 2391

|||||:|*:*

|| |-----1

|| |-----1

||-----1

|-----5

>CsmiRNA-n54a.2

Score: 1.8 Deg: 5:2498:33:76 T_00094823

Query: 1 ACTGCAACCACTTTAGAACTCAA

25

Sbjct: 2500 TGACGTTGGTGAAATTTTAGGTTT 2476

|||||:|*:*

|| |-----1

|| |-----1

||-----1

|-----5

>CsmiRNA-n54a.2

Score: 1.8 Deg: 5:2515:33:75 T_00094822

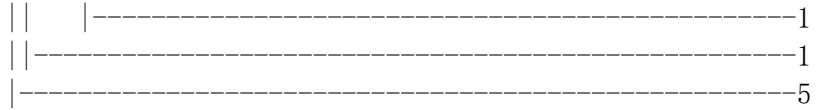
Query: 1 ACTGCAACCACTTTAGAACTCAA

25

Sbjct: 2517 TGACGTTGGTGAAATTTTAGGTTT 2493

|||||:|*:*

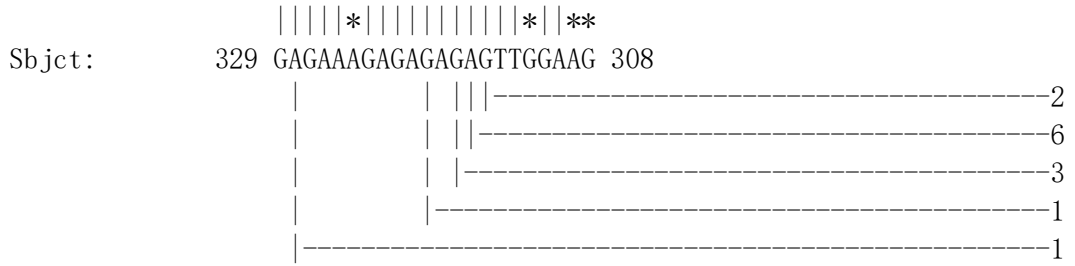
|| |-----1



>CsmiRNA-n56b.1

Score: 2.5 Deg: 6:316:6:162 T_00067103

Query: 1 CTCTTCCTCTCTCTCAAAGT
22



>CsmiRNA-n56b.1

Score: 2.5 Deg: 6:605:6:166 T_00067102

Query: 1 CTCTTCCTCTCTCTCAAAGT
22

