Supplementary Data 2. *Amphimedon* miRNAs. miRNA (red) and miRNA* (blue) are highlighted. All sequences mapping to locus are included, together with predicted fold. Scaffold and coordinate values reference the *Amphimedon* assembly[16]. The location of each miRNA with respect to predicted genes (intergenic or overlapping) is indicated, together with the gene identifier for any overlapping genes. The three columns to the right of each sequence are: (i) length of sequence, (ii) number of reads for that sequence, and (iii) number of matches to the genome.

```
miR-2014
UGCUGUGGUAUUGUAGGUCGGGCCUGGGGGGCAGGUGGAAGGAAUGGCGGCCAAAAGCGGCAAGGGAGAGCGAUGGUUGCACUGCACUAGUUCUCUUUGCUGCUGCGGGCUGCUAACCUCCUGCCAAACAAGUCCGAUCUACAAGACCACGGCU
.(((((((.((((((((((((.((...(((((.((......(((((((((...((((((((((.(((((..((((.((...)))))))))))))))))))))))))))...)))))))).)).))))))...)).)))))))))))).))))))))).
Total cloned: 17843        shared 5' end with miRNA: 9332       shared 3' end with miRNA: 159
Scaffold: Contig13491      Coordinates: 457366-457520    Strand: Minus        Location: Intronic; overlapping gene (g29485) is encoded on Plus strand
miRNA
..............................................................................................UGCCAAACAAGUCCGAUCUACA............         22      7711      1
Shared 5' Terminus
.....................................................................................UGCCAAACAAGUCCGA...............         16        74      1
.....................................................................................UGCCAAACAAGUCCGAU..............         17        65      1
.....................................................................................UGCCAAACAAGUCCGAUC.............         18       124      1
.....................................................................................UGCCAAACAAGUCCGAUCU............         19        98      1
.....................................................................................UGCCAAACAAGUCCGAUCUA...........         20      4697      1
.....................................................................................UGCCAAACAAGUCCGAUCUAC..........         21      4268      1
.....................................................................................UGCCAAACAAGUCCGAUCUACAA........         23         6      1
Shared 3' Terminus
....................................................................................CAAGUCCGAUCUACA............         15         2      1
..................................................................................AACAAGUCCGAUCUACA............         17         6      1
.................................................................................AAACAAGUCCGAUCUACA............         18        20      1
................................................................................CAAACAAGUCCGAUCUACA............         19        10      1
...............................................................................CCAAACAAGUCCGAUCUACA............         20        14      1
..............................................................................GCCAAACAAGUCCGAUCUACA............         21       101      1
.............................................................................CUGCCAAACAAGUCCGAUCUACA............         23         6      1
Subsequence
...............................................................................GCCAAACAAGUCCGA................         15         1      1
...............................................................................GCCAAACAAGUCCGAU...............         16         1      1
...............................................................................GCCAAACAAGUCCGAUC..............         17         6      1
...............................................................................GCCAAACAAGUCCGAUCU.............         18         1      1
...............................................................................GCCAAACAAGUCCGAUCUA............         19        45      1
...............................................................................GCCAAACAAGUCCGAUCUAC...........         20        67      1
................................................................................CCAAACAAGUCCGAUC..............         16         1      1
................................................................................CCAAACAAGUCCGAUCU.............         17         1      1
................................................................................CCAAACAAGUCCGAUCUA............         18         8      1
................................................................................CCAAACAAGUCCGAUCUAC...........         19         6      1
.................................................................................CAAACAAGUCCGAUCUA............         17         8      1
.................................................................................CAAACAAGUCCGAUCUAC...........         18         4      1
..................................................................................AAACAAGUCCGAUCUA............         16        10      1
..................................................................................AAACAAGUCCGAUCUAC...........         17         6      1
...................................................................................AACAAGUCCGAUCUAC...........         16         3      1
Others
.............UAGGUCGGGCCUGGGG...............................................................         16         2      1
.............UAGGUCGGGCCUGGGGG..............................................................         17         1      1
.............UAGGUCGGGCCUGGGGGG.............................................................         18         2      1
.............UAGGUCGGGCCUGGGGGGC............................................................         19         3      1
.............UAGGUCGGGCCUGGGGGGCA...........................................................         20        10      1
.............UAGGUCGGGCCUGGGGGGCAG..........................................................         21        46      1
.............UAGGUCGGGCCUGGGGGGCAGG.........................................................         22       178      1
.............UAGGUCGGGCCUGGGGGGCAGGU........................................................         23        22      1
..............AGGUCGGGCCUGGGGGGC............................................................         18         1      1
..............AGGUCGGGCCUGGGGGGCAG..........................................................         20         5      1
..............AGGUCGGGCCUGGGGGGCAGG.........................................................         21        25      1
..............AGGUCGGGCCUGGGGGGCAGGU........................................................         22         2      1
...............GGUCGGGCCUGGGGGG.............................................................         16         9      1
...............GGUCGGGCCUGGGGGGC............................................................         17         4      1
...............GGUCGGGCCUGGGGGGCA...........................................................         18         1      1
...............GGUCGGGCCUGGGGGGCAG..........................................................         19         6      1
...............GGUCGGGCCUGGGGGGCAGG.........................................................         20        57      1
...............GGUCGGGCCUGGGGGGCAGGU........................................................         21         4      1
................GUCGGGCCUGGGGGGCAGG.........................................................         19         6      1
................GUCGGGCCUGGGGGGCAGGU........................................................         20         2      1
.................UCGGGCCUGGGGGGCAGG.........................................................         18        59      1
.................UCGGGCCUGGGGGGCAGGU........................................................         19         3      1
..................CGGGCCUGGGGGGCAGG.........................................................         17         9      1
..................CGGGCCUGGGGGGCAGGU........................................................         18         2      1
...................GGGCCUGGGGGGCAGG.........................................................         16         2      3
...................GGGCCUGGGGGGCAGGUG.......................................................         18         1      1
........................................AGCGGCAAGGGAGAGC...................................         16         1      1
.................................CGGCAAGGGAGAGCGAUGG........................................         19         2      1
.....................................................AGUUCUCUUUGCUGCUGCGGGCUGCUAA..........         28         1      1
...............................................................................UCCUGCCAAACAAGUCCGA.............         19         1      1
...............................................................................CUGCCAAACAAGUCCGA..............         17         1      1
...............................................................................CUGCCAAACAAGUCCGAUCUA..........         21         1      1
...............................................................................CUGCCAAACAAGUCCGAUCUAC.........         22         4      1

miR-2015
UCUCAUGAUGAUUGUCAUGUAUUGUGGAGGGGAGAGACUUUAAGGAGUAGCUUUACUGUCUCCAUGAGCUCACCUCUCCAUCAUGCAUGACAAAACUAGUGAGA
(((((...((.(((((((.(((((((((.(((.(((...(((((((.....))))..)))))))...))))))))).)).))))))))).)).)))))))
Total cloned: 5501  shared 5' end with miRNA: 640        shared 3' end with miRNA: 52
Scaffold: Contig13453      Coordinates: 293384-293489    Strand: Minus        Location: Intergenic
miRNA
..........................................................ACCUCUCCAUCAUGCAUGACA............         21      2063      1
Shared 5' Terminus
.........................................................ACCUCUCCAUCAUGCAU................         17        19      1
```

```
                                                                      .ACCUCUCCAUCAUGCAUG..............        18    8      1
                                                                      .ACCUCUCCAUCAUGCAUGA.............        19    26     1
                                                                      .ACCUCUCCAUCAUGCAUGAC............        20    587    1
Shared 3' Terminus
                                                                      ...UCCAUCAUGCAUGACA............          16    1      2
                                                                      ..CUCCAUCAUGCAUGACA............          17    2      2
                                                                      .UCUCCAUCAUGCAUGACA............          18    3      1
                                                                      ..CUCCAUCAUGCAUGACA............          19    6      1
                                                                      .CCUCCAUCAUGCAUGACA............          20    23     1
                                                                      CACCUCCAUCAUGCAUGACA............         22    15     1
                                                                      UCACCUCCAUCAUGCAUGACA............        23    2      1
Subsequence
                                                                      .CCUCCAUCAUGCAUGAC.............          19    11     1
                                                                      CUCCAUCAUGCAUGAC.............            18    2      1
                                                                      UCUCCAUCAUGCAUGAC.............           17    1      1
                                                                      CUCCAUCAUGCAUGAC.............            16    1      2
                                                                      UCCAUCAUGCAUGAC.............             15    1      4
Others
         .UCAUGUAUUGUGGAGGG.............                                                                       17    4      1
         .UCAUGUAUUGUGGAGGGG............                                                                       18    26     1
         .UCAUGUAUUGUGGAGGGGA...........                                                                       19    509    1
         .UCAUGUAUUGUGGAGGGGAG..........                                                                       20    1031   1
         .UCAUGUAUUGUGGAGGGGAGA.........                                                                       21    1086   1
         .UCAUGUAUUGUGGAGGGGAGAGA.......                                                                       23    1      1
         .CAUGUAUUGUGGAGGGGA...........                                                                        18    4      1
         .CAUGUAUUGUGGAGGGGAG..........                                                                        19    13     1
         .CAUGUAUUGUGGAGGGGAGA.........                                                                        20    11     1
         .AUGUAUUGUGGAGGGGA...........                                                                         17    4      1
         .AUGUAUUGUGGAGGGGAG..........                                                                         18    9      1
         .AUGUAUUGUGGAGGGGAGA.........                                                                         19    6      1
         .UGUAUUGUGGAGGGGA...........                                                                          16    1      1
         .UGUAUUGUGGAGGGGAGA.........                                                                          18    1      1
         .GUAUUGUGGAGGGGA...........                                                                           15    1      1
         .GUAUUGUGGAGGGGAG..........                                                                           16    1      1
         .GUAUUGUGGAGGGGAGA.........                                                                           17    4      1
         .AUUGUGGAGGGGAGA.........                                                                             15    2      2
                             .GACUUUAAGGAGUAGC.............                                                    16    1      1
                                                                      .CACCUCUCCAUCAUGCAUGAC............        21    15     1

miR-2016
AGGUGAUUCAAGAGGCACUGUAGAUUGGGCUUGGUCGGCAGAUGAAUAAAAGAGAUUAAGUUUUUGUCCUUUUUCAAAAGAAGACACUAGCUUGAUGCAACUCUUAAAUCUGCUGUCCAGUCUUAAUCUACAGGGCAGACAGUCCUCAGCAGU
.(.(((........((.(((((((((((.((((.(((((((((......((((((((((((..((((.((((.....)))).)))))..)))))))))....)))))..))))))))).)))).)))))))))).)).........)))).)...
Total cloned: 37606          shared 5' end with miRNA: 12659          shared 3' end with miRNA: 519
Scaffold: Contig13514     Coordinates: 90512-90665     Strand: Minus     Location: Intergenic
miRNA
                   .UAGAUUGGGCUUGGUCGGCAGA....................................                                 22    24016  2
Shared 5' Terminus
                   .UAGAUUGGGCUUGGU.                                                                           15    4      2
                   .UAGAUUGGGCUUGGUC.                                                                          16    47     2
                   .UAGAUUGGGCUUGGUCG.                                                                         17    33     2
                   .UAGAUUGGGCUUGGUCGG.                                                                        18    1090   2
                   .UAGAUUGGGCUUGGUCGGC.                                                                       19    558    2
                   .UAGAUUGGGCUUGGUCGGCA.                                                                      20    1807   2
                   .UAGAUUGGGCUUGGUCGGCAG.                                                                     21    8946   2
                   .UAGAUUGGGCUUGGUCGGCAGAU.                                                                   23    173    2
                   .UAGAUUGGGCUUGGUCGGCAGAUG.                                                                  24    1      2
Shared 3' Terminus
                         .GGCUUGGUCGGCAGA.                                                                     15    9      2
                        .GGGCUUGGUCGGCAGA.                                                                     16    45     2
                       .UGGGCUUGGUCGGCAGA.                                                                     17    69     2
                      .UUGGGCUUGGUCGGCAGA.                                                                     18    74     2
                     .AUUGGGCUUGGUCGGCAGA.                                                                     19    13     2
                    .GAUUGGGCUUGGUCGGCAGA.                                                                     20    49     2
                   .AGAUUGGGCUUGGUCGGCAGA.                                                                     21    260    2
Subsequence
                   .AGAUUGGGCUUGGUC.                                                                           15    1      2
                   .AGAUUGGGCUUGGUCG.                                                                          16    2      2
                   .AGAUUGGGCUUGGUCGG.                                                                         17    14     2
                   .AGAUUGGGCUUGGUCGGC.                                                                        18    10     2
                   .AGAUUGGGCUUGGUCGGCA.                                                                       19    27     2
                   .AGAUUGGGCUUGGUCGGCAG.                                                                      20    107    2
                    .GAUUGGGCUUGGUCGG.                                                                         16    2      2
                    .GAUUGGGCUUGGUCGGCA.                                                                       18    5      2
                    .GAUUGGGCUUGGUCGGCAG.                                                                      19    38     2
                     .AUUGGGCUUGGUCGGC.                                                                        16    1      2
                     .AUUGGGCUUGGUCGGCA.                                                                       17    4      2
                     .AUUGGGCUUGGUCGGCAG.                                                                      18    18     2
                      .UUGGGCUUGGUCGGC.                                                                        15    4      2
                      .UUGGGCUUGGUCGGCA.                                                                       16    9      2
                      .UUGGGCUUGGUCGGCAG.                                                                      17    53     2
                       .UGGGCUUGGUCGGCA.                                                                       15    3      2
                       .UGGGCUUGGUCGGCAG.                                                                      16    83     2
                        .GGGCUUGGUCGGCAG.                                                                      15    2      2
Others
                   .AGAUUGGGCUUGGUCGGCAGAU.                                                                    22    1      2
                    .GAUUGGGCUUGGUCGGCAGAU.                                                                    21    1      2
                         .GGCUUGGUCGGCAGAU.                                                                    16    1      2
                               .GAGAUUAAGUUUUUGUCCU.                                                           19    1      1
                                                                      .UGCUGUCCAGUCUUAAUC.                      18    1      1
                                                                      .UGCUGUCCAGUCUUAAUCUA.                    20    2      1
                                                                      .UGCUGUCCAGUCUUAAUCUAC.                   21    9      1
                                                                      .UGCUGUCCAGUCUUAAUCUACA.                  22    7      1
                                                                      .GCUGUCCAGUCUUAAUCUA.                     19    2      1
                                                                      .GCUGUCCAGUCUUAAUCUAC.                    20    2      1
                                                                      .GCUGUCCAGUCUUAAUCUACA.                   21    1      1
                                                                      .UGUCCAGUCUUAAUCUAC.                      18    1      1
```

```
miR-2017
AAUGGAUGAGGGAUUGAGUACACGGGGUAUGGGUAGUGCUUCCAGCAAGGAUUAUAAUUAUAAAGUCCAUUUAAGCACUACCUGUGCACCUGUGUGCCCAAACCUAUCCAUAUC
.(((((((.(((..(((.(((((((((((((((((((((.......(((((.((....)).)))))....)))))))))))))))).))))))))).))).))))))))))...
Total cloned: 1725   shared 5' end with miRNA: 891        shared 3' end with miRNA: 31
Scaffold: Contig13219        Coordinates: 71849-71963        Strand: Minus        Location: Intergenic
miRNA
.......................................................UACCUGUGCACCUGUGUGCCCA..............                  22       640       1
Shared 5' Terminus
.......................................................UACCUGUGCACCUGUG...................                  16       16        1
.......................................................UACCUGUGCACCUGUGU..................                  17       38        1
.......................................................UACCUGUGCACCUGUGUG.................                  18       71        1
.......................................................UACCUGUGCACCUGUGUGC................                  19       176       1
.......................................................UACCUGUGCACCUGUGUGCC...............                  20       66        1
.......................................................UACCUGUGCACCUGUGUGCCC..............                  21       518       1
.......................................................UACCUGUGCACCUGUGUGCCCAA............                  23       6         1
Shared 3' Terminus
.........................................................UGUGCACCUGUGUGCCCA..............                  18       1         1
.........................................................CCUGUGCACCUGUGUGCCCA..............                20       9         1
.........................................................ACCUGUGCACCUGUGUGCCCA..............                21       18        1
.........................................................CUACCUGUGCACCUGUGUGCCCA..............              23       3         1
Subsequence
.........................................................ACCUGUGCACCUGUG....................                15       3         1
.........................................................ACCUGUGCACCUGUGUGC................                18       2         1
.........................................................ACCUGUGCACCUGUGUGCCC..............                20       11        1
.........................................................CCUGUGCACCUGUGUGCCC..............                 19       3         1
.........................................................CUGUGCACCUGUGUGCCC..............                  18       1         1
Others
...........AGUACACGGGGUAUGG................                                                                 16       4         1
...........AGUACACGGGGUAUGGG...............                                                                 17       1         1
...........AGUACACGGGGUAUGGGU..............                                                                 18       2         1
...........AGUACACGGGGUAUGGGUA.............                                                                 19       2         1
...........AGUACACGGGGUAUGGGUAG............                                                                 20       11        1
...........AGUACACGGGGUAUGGGUAGU...........                                                                 21       93        1
............GUACACGGGGUAUGGGG..............                                                                 16       1         1
............GUACACGGGGUAUGGGUAG............                                                                 19       2         1
............GUACACGGGGUAUGGGUAGU...........                                                                 20       2         1
..............UACACGGGGUAUGGGU.............                                                                 16       1         1
..............UACACGGGGUAUGGGUAG...........                                                                 18       1         1
..............UACACGGGGUAUGGGUAGU..........                                                                 19       4         1
..............UACACGGGGUAUGGGUAGUG.........                                                                 20       1         1
...............ACACGGGGUAUGGGUAG...........                                                                 17       3         1
...............ACACGGGGUAUGGGUAGU..........                                                                 18       4         1
................CACGGGGUAUGGGUAGU..........                                                                 17       1         1
.................ACGGGGUAUGGGUAG...........                                                                 15       4         2
.................ACGGGGUAUGGGUAGU..........                                                                 16       3         1
..................CGGGGUAUGGGUAGU..........                                                                 15       1         1
.............................GCUUCCAGCAAGGAUUAUAA.........                                                   20       1         1
.........................................................CUACCUGUGCACCUGUGUGCCC..............               22       1         1

miR-2018
CUGCAUGAGUUACAGUGUGUCGGAGCCGGAGGUUCCGGAGAAAGAUAAAAGCCCAUGCAGGCAUUGGAAUGACAUAAACCGGUUGUACUGGUUUGUUCCAUUGUUUGGUGCAAUGGCUUAGCCUCCGGGACCUUGGACCUCGACACACAGUGCCAUGCA
..(((((.((.((.((((((((((..(.(.(((((((((((...(.....((((..((((((((.(((((.....((((((((((.....)))))))))))).))))...))))...))))).)))))..))))))))))).).).))))))))).))))))))).
Total cloned: 1529   shared 5' end with miRNA: 149        shared 3' end with miRNA: 4
Scaffold: Contig13491        Coordinates: 58767-58926        Strand: Minus        Location: Intergenic
miRNA
................UGUCGGAGCCGGAGGUUCCGGA........................                                               22       1160      1
Shared 5' Terminus
................UGUCGGAGCCGGAGG...............                                                               15       1         1
................UGUCGGAGCCGGAGGUU.............                                                               17       6         1
................UGUCGGAGCCGGAGGUUC............                                                               18       6         1
................UGUCGGAGCCGGAGGUUCC...........                                                               19       9         1
................UGUCGGAGCCGGAGGUUCCG..........                                                               20       3         1
................UGUCGGAGCCGGAGGUUCCGG.........                                                               21       122       1
................UGUCGGAGCCGGAGGUUCCGGAG.......                                                               23       2         1
Shared 3' Terminus
.................GUCGGAGCCGGAGGUUCCGGA........................                                               21       4         1
Subsequence
.................UCGGAGCCGGAGGUUCCGG..........                                                               19       1         1
Others
.................UCGGAGCCGGAGGUUCCGGAG.......                                                                21       1         1
............................................UGGAAUGACAUAAACCGGUUGU........................                   22       5         1
...............................................................CGGGACCUUGGACCUCGAC.............             19       1         1
...............................................................CGGGACCUUGGACCUCGACA............            20       8         1
...............................................................CGGGACCUUGGACCUCGACAC...........            21       25        1
...............................................................CGGGACCUUGGACCUCGACACA..........            22       107       1
................................................................GGGACCUUGGACCUCGA.............              17       1         1
................................................................GGGACCUUGGACCUCGACA............            19       10        1
................................................................GGGACCUUGGACCUCGACAC...........            20       10        1
................................................................GGGACCUUGGACCUCGACACA..........            21       45        1
.................................................................GGACCUUGGACCUCGACAC...........            19       1         1
..................................................................GACCUUGGACCUCGACACA...........           18       1         1

miR-2019
GAGACUGCGCCCGCUACCGAUUCAAAGUGAUCGGGUUGCCGUCUGAGCUCUAGCUAGCCAUACCCAGGCCUUGUUAACUUAACCAGUCCUAGAGAAGGCUCUGGCUCACACGGUAGCUUGCUCACUUAGAAACGGCCGAGGCGCUACU
......(((((((((...(((.(((.(((((((((.(((((((((((((.((..(((((.(.(.(((.((.((((...)))).))).)))).).)).)))))))))))))).))).))))))))))))))))))))).)))).))).).))))))....
Total cloned: 11574   shared 5' end with miRNA: 5999        shared 3' end with miRNA: 56
Scaffold: Contig13362        Coordinates: 48947-49095        Strand: Plus        Location: Intergenic
miRNA
.......................AAAGUGAUCGGGUUGCCGUCUG.........                                                       22       4484      1
Shared 5' Terminus
.......................AAAGUGAUCGGGUUG.........                                                              15       38        1
.......................AAAGUGAUCGGGUUGC........                                                              16       51        1
.......................AAAGUGAUCGGGUUGCC.......                                                              17       61        1
.......................AAAGUGAUCGGGUUGCCG......                                                              18       264       1
.......................AAAGUGAUCGGGUUGCCGU.....                                                              19       125       1
.......................AAAGUGAUCGGGUUGCCGUC....                                                              20       164       1
.......................AAAGUGAUCGGGUUGCCGUCU...                                                              21       4121      1
```

```
.....................AAAGUGAUCGGGUUGCCGUCUGA...........................................................................    23    1171    1
.....................AAAGUGAUCGGGUUGCCGUCUGAG..........................................................................    24    4    1
Shared 3' Terminus
...............................GAUCGGGUUGCCGUCUG.......................................................................    17    11    1
..............................UGAUCGGGUUGCCGUCUG.......................................................................    18    6    1
.............................GUGAUCGGGUUGCCGUCUG.......................................................................    19    3    1
............................AGUGAUCGGGUUGCCGUCUG.......................................................................    20    11    1
.........................AAAGUGAUCGGGUUGCCGUCUG.......................................................................    21    25    1
Subsequence
............................AAGUGAUCGGGUUGC............................................................................    15    1    1
............................AAGUGAUCGGGUUGCC...........................................................................    16    3    1
..........................AAGUGAUCGGGUUGCCGU..........................................................................    18    2    1
..........................AAGUGAUCGGGUUGCCGUC.........................................................................    19    4    1
..........................AAGUGAUCGGGUUGCCGUCU........................................................................    20    29    1
...........................AGUGAUCGGGUUGCCGU..........................................................................    17    3    2
...........................AGUGAUCGGGUUGCCGUC.........................................................................    18    1    1
...........................AGUGAUCGGGUUGCCGUCU........................................................................    19    5    1
............................AGUGAUCGGGUUGCCGUCU.......................................................................    18    3    1
.............................GAUCGGGUUGCCGUCU.........................................................................    16    1    1
Others
..........................AAGUGAUCGGGUUGCCGUCUGA.......................................................................    22    8    1
...........................AGUGAUCGGGUUGCCGUCUGA......................................................................    21    3    1
............................GUGAUCGGGUUGCCGUCUGA......................................................................    20    1    1
.............................UGAUCGGGUUGCCGUCUGA......................................................................    19    1    1
..............................GAUCGGGUUGCCGUCUGA......................................................................    18    1    1
                                                    UAGAGAAGGCUCUGGCUCA..............................................    19    1    1
                                                      CACGGUAGCUUGCUCA..............................................    16    4    1
                                                      CACGGUAGCUUGCUCAC.............................................    17    39    1
                                                      CACGGUAGCUUGCUCACU............................................    18    23    1
                                                      CACGGUAGCUUGCUCACUU...........................................    19    29    1
                                                      CACGGUAGCUUGCUCACUUA..........................................    20    30    1
                                                      CACGGUAGCUUGCUCACUUAG.........................................    21    393    1
                                                      CACGGUAGCUUGCUCACUUAGA........................................    22    416    1
                                                      CACGGUAGCUUGCUCACUUAGAA.......................................    23    1    1
                                                       ACGGUAGCUUGCUCA..............................................    15    2    1
                                                       ACGGUAGCUUGCUCACUU...........................................    18    1    1
                                                       ACGGUAGCUUGCUCACUUA..........................................    19    1    1
                                                       ACGGUAGCUUGCUCACUUAG.........................................    20    11    1
                                                       ACGGUAGCUUGCUCACUUAGA........................................    21    12    1
                                                        CGGUAGCUUGCUCACUU...........................................    17    2    1
                                                        CGGUAGCUUGCUCACUUA..........................................    18    2    1
                                                        GGUAGCUUGCUCACUUAG..........................................    18    1    1
                                                          AGCUUGCUCACUUAGA..........................................    16    1    1

miR-2020
AGGGAUUUCCAGUGCUGGGUAGUGUGUCUUUUCGGAAUACAGUCACAAACCAGACUGACCGGUUUCUCAUUAUAACCGGACUGACAGGUUUCUCAUUCCGGAAGGGCAUACUAACCAGCACUGGGUCCCA
.(((((..((((((((((.((((((((((((((((((.(((((........))))).(((((((.........))))))).............))))))))))))))))).)))))))))))))).
Total cloned: 13936      shared 5' end with miRNA: 3856      shared 3' end with miRNA:: 141
Scaffold: Contig13308      Coordinates: 86340-86470      Strand: Minus      Location: Intergenic
miRNA
..............UGGGUAGUGUGUCUUUUCGGA....................................................................................    21    9844    1
Shared 5' Terminus
..............UGGGUAGUGUGUCUUU.........................................................................................    16    173    1
..............UGGGUAGUGUGUCUUUU........................................................................................    17    7    1
..............UGGGUAGUGUGUCUUUUC.......................................................................................    18    34    1
..............UGGGUAGUGUGUCUUUUCG......................................................................................    19    109    1
..............UGGGUAGUGUGUCUUUUCGG.....................................................................................    20    3468    1
..............UGGGUAGUGUGUCUUUUCGGAA...................................................................................    22    65    1
Shared 3' Terminus
....................GUGUGUCUUUUCGGA....................................................................................    15    1    1
...................AGUGUGUCUUUUCGGA....................................................................................    16    4    1
..................UAGUGUGUCUUUUCGGA....................................................................................    17    1    1
.................GUAGUGUGUCUUUUCGGA....................................................................................    18    2    1
................GGUAGUGUGUCUUUUCGGA....................................................................................    19    3    1
...............GGGUAGUGUGUCUUUUCGGA....................................................................................    20    125    1
.............CUGGGUAGUGUGUCUUUUCGGA....................................................................................    22    5    1
Subsequence
...............GGGUAGUGUGUCUUU.........................................................................................    15    1    1
..............GGGUAGUGUGUCUUUUCG.......................................................................................    18    3    1
..............GGGUAGUGUGUCUUUUCGG......................................................................................    19    70    1
...............GUAGUGUGUCUUUUCG........................................................................................    17    1    1
...............GGUAGUGUGUCUUUUCGG......................................................................................    18    1    1
................GUAGUGUGUCUUUUCGG......................................................................................    17    1    1
.................UAGUGUGUCUUUUCGG......................................................................................    16    2    1
Others
.............CUGGGUAGUGUGUCUUUUCGG.....................................................................................    21    5    1
...............GGGUAGUGUGUCUUUUCGGAA...................................................................................    21    5    1
                                                                   CGGAAGGGCAUACUAACCAGC..........................    21    5    1
                                                                      AAGGGCAUACUAACCAGC..........................    18    1    1

miR-2021
AGUGUUGUUGAUGUCCAUGGAAUAUCGGCACCCAUCCAGUUAAAACCUUCAACGAUCCACUCGUGCAGCUAUGGGUCCCUAGACUAGCACCAGUGGGUGAUUGUGUCAGGAGGUGUGUGAUGGUGGUCGGUGUUUCGUGGACACCAACAAUGCAA
.(((((((((.((((((((((((((..(((((((......(((((.(((((((((.(((((((((.(....).))).).).)))))).)))))..))))))).).).)))))).))).)))))))))..)))))))))..
Total cloned:  7642      shared 5' end with miRNA: 2156      shared 3' end with miRNA: 50
Scaffold: Contig13311      Coordinates: 134175-134330      Strand: Plus      Location: Intronic; overlapping gene (g20806) is encoded on Minus strand
miRNA
.....................................................................................UGGUGGUCGGUGUUUCGUGGA..............    21    5381    1
Shared 5' Terminus
.....................................................................................UGGUGGUCGGUGUUU.................    15    5    1
.....................................................................................UGGUGGUCGGUGUUUC................    16    15    1
.....................................................................................UGGUGGUCGGUGUUUCG...............    17    17    1
.....................................................................................UGGUGGUCGGUGUUUCGU..............    18    52    1
.....................................................................................UGGUGGUCGGUGUUUCGUG.............    19    81    1
.....................................................................................UGGUGGUCGGUGUUUCGUGG............    20    1985    1
.....................................................................................UGGUGGUCGGUGUUUCGUGGAC..........    22    1    1
Shared 3' Terminus
..................................................................................................GGUCGGUGUUUCGUGGA..............    17    6    1
```

```
.......................................................................................................UGGUCGGUGUUUCGUGGA..............       18       17       1
......................................................................................................GUGGUCGGUGUUUCGUGGA..............       19        2       1
.....................................................................................................GGUGGUCGGUGUUUCGUGGA..............       20       25       1
Subsequence
......................................................................................................GGUGGUCGGUGUUUCGUGG...............       19       12       1
.......................................................................................................GUGGUCGGUGUUUCGUGG...............       18        1       1
.........................................................................................................UGGUCGGUGUUUCGUG................       16        1       1
.........................................................................................................UGGUCGGUGUUUCGUGG...............       17        4       1
........................................................................................................GGUCGGUGUUUCGUGG...............       16        2       1
Others
...............CAUGGAAUAUCGGCACCCA.......................................................................................................       19        1       1
..............CAUGGAAUAUCGGCACCCAU.......................................................................................................       20        8       1
..............CAUGGAAUAUCGGCACCCAUC......................................................................................................       21       25       1
...............UGGAAUAUCGGCACCCA.........................................................................................................       17        1       1
```