

Supplementary Data 1. *Nematostella* miRNAs. miRNA (red), miRNA* (blue) and variant miRNA-miRNA* pairs (green) are highlighted. All sequences mapping to locus are included, together with predicted fold. Scaffold and coordinate values reference the *Nematostella* genome¹³. The location of each miRNA with respect to predicted genes (intergenic or overlapping) is indicated, together with the gene identifier for any overlapping genes. Pairs of miRNAs located close (<50 kb) to each other and deriving from the same strand are noted as potential miRNA clusters. 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.

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miR-100
AUCGACCCGUAGAUCCGAACUUGUGGAGUUUACCCACAGGCUCGUUUUACGGAUCAAAAC
...(((.....(((.....(((.....))))))))).....
Total cloned: 4973 shared 5' end with miRNA: 428 shared 3' end with miRNA: 25
Scaffold: scaffold_82 Coordinates: 122023-122084 Strand: Plus Location: Intergenic
miRNA
...ACCCGUAGAUCCGAACUUGUGG..... 22 3583 1
Shared 5' Terminus
...ACCCGUAGAUCCGAA..... 15 5 4
...ACCCGUAGAUCCGAAC..... 16 11 4
...ACCCGUAGAUCCGAACU..... 17 6 1
...ACCCGUAGAUCCGAACUU..... 18 6 1
...ACCCGUAGAUCCGAACUUG..... 19 20 1
...ACCCGUAGAUCCGAACUUGU..... 20 64 1
...ACCCGUAGAUCCGAACUUGUG..... 21 82 1
...ACCCGUAGAUCCGAACUUGUGGA..... 23 234 1
Shared 3' Terminus
.....GUAGAUCCGAACUUGUGG..... 18 1 1
.....CGUAGAUCCGAACUUGUGG..... 19 1 1
.....CCGUAGAUCCGAACUUGUGG..... 20 6 1
.....CCCGUAGAUCCGAACUUGUGG..... 21 17 1
Subsequence
.....CCCGUAGAUCCGAACUUGU..... 19 3 1
Others
.....CCCGUAGAUCCGAACUUGUGGA..... 22 1 1
.....ACAGGCUCGUUUUACG..... 17 3 1
.....ACAGGCUCGUUUUACGG..... 18 11 1
.....ACAGGCUCGUUUUACGGA..... 19 93 1
.....ACAGGCUCGUUUUACGGAU..... 20 243 1
.....ACAGGCUCGUUUUACGGAUC..... 21 70 1
.....ACAGGCUCGUUUUACGGAUCA..... 22 483 1
.....ACAGGCUCGUUUUACGGAUCAA..... 23 1 1
.....ACAGGCUCGUUUUACGGAUCAAA..... 24 1 1
.....CAGGCUCGUUUUACGG..... 17 2 1
.....CAGGCUCGUUUUACGGA..... 18 3 1
.....CAGGCUCGUUUUACGGAU..... 19 5 1
.....CAGGCUCGUUUUACGGAUCA..... 21 5 1
.....AGGCUCGUUUUACGGAUCA..... 20 12 1
.....GCUUGUUUUACGGAUCA..... 18 1 1

miR-2022
GAUAAGAUCGCCUGAAAGUCGGGAUAAAUCAACUGUCAAGUGGUUGUCAUUUUGCUAGUUGCUUUUGUCCCGCCUUUUUCGCGAAUUGAUCAC
(((.....(((.....(((.....(((.....))))))))).....))).....
Total cloned: 192 shared 5' end with miRNA: 7 shared 3' end with miRNA: 4
Scaffold: scaffold_148 Coordinates: 501354-501446 Strand: Plus Location: Intergenic
miRNA
.....UUUGCUAGUUGCUUUUGUCCCGC..... 23 162 1
Shared 5' Terminus
.....UUUGCUAGUUGCUUUUGUCC..... 20 2 1
.....UUUGCUAGUUGCUUUUGUCCG..... 22 5 1
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Shared 3' Terminus
.....GCUAGUUGCUUUUGUCCCGC..... 20 1 1
.....UGCUAGUUGCUUUUGUCCCGC..... 21 1 1
.....UUGCUAGUUGCUUUUGUCCCGC..... 22 2 1
Subsequence
Others
.....GGGAUAAUCAACUGU..... 16 3 1
.....GGGAUAAUCAACUGUCAAGU..... 21 1 1
.....GGGAUAAUCAACUGUCAAGU..... 22 15 1

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miR-2023
GAGUUGCGUGACAUAACCGUGUCUGCCACCUGUAUUUCUAUCACGUCAGAUGAAGAAAGUACAAGUGGUAGGGAAAGGGUGUGUCAUGACAA
..((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
Total cloned: 28994 shared 5' end with miRNA: 7716 shared 3' end with miRNA: 434
Scaffold: scaffold_294 Coordinates: 142037-142130 Strand: Plus Location: Intergenic
miRNA
.....AAGAAGUACAAGUGGUAGGG..... 21 20458 1

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Shared 5' Terminus
.....AAAGAAGUACAAGUG..... 15 2 2
.....AAAGAAGUACAAGUGG..... 16 15 1
.....AAAGAAGUACAAGUGGU..... 17 74 1
.....AAAGAAGUACAAGUGGUA..... 18 250 1
.....AAAGAAGUACAAGUGGUAG..... 19 2838 1
.....AAAGAAGUACAAGUGGUAGG..... 20 4242 1
.....AAAGAAGUACAAGUGGUAGGA..... 22 286 1
.....AAAGAAGUACAAGUGGUAGGAA..... 23 9 1

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Shared 3' Terminus
.....GUACAAGUGGUAGGG..... 15 15 1
.....AGUACAAGUGGUAGGG..... 16 18 1
.....AAGUACAAGUGGUAGGG..... 17 105 1
.....GAAGUACAAGUGGUAGGG..... 18 8 1
.....AGAAGUACAAGUGGUAGGG..... 19 39 1
.....AAGAAGUACAAGUGGUAGGG..... 20 248 1
.....CGUCAGAUGAAAGAAGUACAAGUGGUAGGG..... 30 1 1
Subsequence
.....AAGAAGUACAAGUGG..... 15 2 3
.....AAGAAGUACAAGUGGU..... 16 1 3
.....AAGAAGUACAAGUGGUA..... 17 3 3
.....AAGAAGUACAAGUGGUAG..... 18 66 3
.....AAGAAGUACAAGUGGUAGG..... 19 52 1
.....AGAAGUACAAGUGGU..... 15 8 3
.....AGAAGUACAAGUGGUA..... 16 6 3
.....AGAAGUACAAGUGGUAG..... 17 45 3
.....AGAAGUACAAGUGGUAGG..... 18 26 1
.....GAAGUACAAGUGGUAG..... 16 4 3
.....GAAGUACAAGUGGUAGG..... 17 2 1
.....AAGUACAAGUGGUAG..... 15 7 3
.....AAGUACAAGUGGUAGG..... 16 20 1
.....AGUACAAGUGGUAGG..... 15 7 1

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Others
.....UCUGCCACCUGUAUUUCUAUC..... 21 1 1
.....UCUGCCACCUGUAUUUCUAUCA..... 22 1 1
.....CUGCCACCUGUAUUUCUA..... 18 1 1
.....CUGCCACCUGUAUUUCUAU..... 19 1 1
.....CUGCCACCUGUAUUUCUAUC..... 20 32 1
.....CUGCCACCUGUAUUUCUAUCA..... 21 80 1
.....UGCCACCUGUAUUUCUAUC..... 19 1 1
.....GAAAGAAGUACAAGUGGUAG..... 20 1 1
.....AAGAAGUACAAGUGGUAGGA..... 21 9 1
.....AGAAGUACAAGUGGUAGGGA..... 20 8 1
.....GAAGUACAAGUGGUAGGAA..... 20 1 1

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miR-2024a
UUCAGAAUAUUGGUGCUGGGCAAAGGUCACAUUUGGCACAACACCAAUUAUUCUGAGG
..((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
Total cloned: 5576 shared 5' end with miRNA: 641 shared 3' end with miRNA: 47
Scaffold: scaffold_126 Coordinates: 91276-91334 Strand: Minus Location: Intergenic; likely part of a miRNA cluster with miR-2024b,c,d,e
miRNA
.....UUGCACAACACCAAUUAUCUGA..... 22 4808 1
Shared 5' Terminus
.....UUGCACAACACCAAU..... 15 1 10
.....UUGCACAACACCAAUA..... 16 1 7

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miR-2024g
ACCAAUAGGUCUACUGCUUCAAUUUACGGUUGGUAAGGUCACCUUUUAAACACAGUACCGAUUUUGAGGACGCUUUUGCAA
.....(((((((.(((((((((((((((((((.(((((((.)))))....)))))....)))))....)))))....)))))....)))))....
Total cloned: 2396 shared 5' end with miRNA: 501 shared 3' end with miRNA: 45
Scaffold: scaffold_282 Coordinates: 93046-93135 Strand: Minus Location: Intergenic; likely part of a miRNA cluster with miR-2024f
miRNA

.....UAAACACAGUACCGAUUUUGAGG.....	22	1570	4
Shared 5' Terminus			
.....UAAACACAGUACCGAUUU.....	17	1	4
.....UAAACACAGUACCGAUUU.....	18	7	4
.....UAAACACAGUACCGAUUUUG.....	19	24	4
.....UAAACACAGUACCGAUUUUGU.....	20	80	4
.....UAAACACAGUACCGAUUUUGUG.....	21	248	4
.....UAAACACAGUACCGAUUUUGUGAA.....	23	141	4
Shared 3' Terminus			
.....GUACCGAUUUUGAGG.....	15	2	9
.....AGUACCGAUUUUGAGG.....	16	1	9
.....CAGUACCGAUUUUGAGG.....	17	1	9
.....ACAGUACCGAUUUUGAGG.....	18	4	8
.....ACACAGUACCGAUUUUGAGG.....	20	6	7
.....AACACAGUACCGAUUUUGAGG.....	21	27	4
.....UUAAACACAGUACCGAUUUUGAGG.....	23	4	4
Subsequence			
.....AACACAGUACCGAUUUUG.....	18	1	4
.....AACACAGUACCGAUUUUGUG.....	20	1	4
.....ACACAGUACCGAUUUUGUG.....	18	1	7
.....CAGUACCGAUUUUGUG.....	15	1	9
Others			
.....CCAAUAGGUCUACUGCUUC.....	20	1	5
.....CAAUAGGUCUACUGCUUC.....	19	2	5
.....UAAGUCUACUGCUUC.....	16	1	5
.....AAGUCUACUGCUUC.....	15	1	8
.....AAAAUACGGUUGG.....	17	1	9
.....AAAAUACGGUUGGUA.....	20	20	8
.....AAAAUACGGUUGGUA.....	21	55	7
.....AAAAUACGGUUGGUA.....	22	165	7
.....AAAAUACGGUUGGUA.....	19	1	8
.....AAAAUACGGUUGGUA.....	21	3	7
.....AAUACGGUUGGUA.....	19	1	7
.....AAUACGGUUGGUA.....	20	1	7
.....AAUACGGUUGGUA.....	19	1	7
.....AUAACGGUUGGUA.....	18	3	7
.....AUCGGUUGGUA.....	16	1	7
.....AUCGGUUGGUA.....	17	1	7
.....UUUAAACACAGUACCGAUUUUGUG.....	23	1	4
.....UUAAACACAGUACCGAUUU.....	19	2	4
.....UUAAACACAGUACCGAUUUUG.....	21	4	4
.....UUAAACACAGUACCGAUUUUGUG.....	22	3	4
.....AACACAGUACCGAUUUUGUGAA.....	22	8	4

miR-2025
AACAAUAGGCCCAUACAAGCUUUGGUCUAGAAAUUCUUUAGUAGUUUUUUAGCCCGGAAGUUGUGUUGCCUGGCCAAUUAUACCAUU
.....(((((((.(((((((((((((((((((.(((((((.)))))....)))))....)))))....)))))....)))))....)))))....
Total cloned: 6681 shared 5' end with miRNA: 329 shared 3' end with miRNA: 98
Scaffold: scaffold_51 Coordinates: 151655-151750 Strand: Minus Location: Intergenic
miRNA

.....UUUUUUAGCCCGGAAGUUGU.....	22	6210	1
Shared 5' Terminus			
.....UUUUUUAGCCCGGA.....	16	2	1
.....UUUUUUAGCCCGGA.....	17	5	1
.....UUUUUUAGCCCGGAAG.....	18	9	1
.....UUUUUUAGCCCGGAAGU.....	19	22	1
.....UUUUUUAGCCCGGAAGUU.....	20	65	1
.....UUUUUUAGCCCGGAAGUUG.....	21	225	1
.....UUUUUUAGCCCGGAAGUUGU.....	23	1	1
Shared 3' Terminus			
.....UAGCCCGGAAGUUGU.....	17	1	1
.....UUAGCCCGGAAGUUGU.....	18	1	1
.....UUUAGCCCGGAAGUUGU.....	19	3	1
.....UUUUAGCCCGGAAGUUGU.....	20	13	1
Subsequence			
.....UUUUUUAGCCCGGAAGUUGU.....	21	80	1

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.....UUUUUAGCCCGCGGAAGUU.....19      2      1
.....UUUUUAGCCCGCGGAAGUUG.....20      1      1
Others
.....AGCUUUCGAUGGCUAGA.....17      1      1
.....AGCUUUCGAUGGCUAGAAAA.....20      1      1
.....AGCUUUCGAUGGCUAGAAAAU.....21      6      1
.....AGCUUUCGAUGGCUAGAAAAUC.....22      31     1
.....GCUUUCGAUGGCUAGAAAAUC.....21      2      1

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miR-2026

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ACUUGUGUCCCCCGUUUCAAAUGUCUACUGAUGGAAGUUGGUUCCAUCAGUGGGUUAUUUGAAGUUAGAGACGCAGAA
..(((((((.(.((((((((((((((((((.....))))))))))))))))))))))..)))))..))..)))))..
Total cloned: 3319 shared 5' end with miRNA: 1460 shared 3' end with miRNA: 41
Scaffold: scaffold_61 Coordinates: 667308-667387 Strand: Minus Location: Intergenic
miRNA

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.....UUUCAAAUGUCUACUGAUGGA.....21      1680    1
Shared 5' Terminus
.....UUUCAAAUGUCUACUGAU.....18      1      2
.....UUUCAAAUGUCUACUGAUG.....19      3      2
.....UUUCAAAUGUCUACUGAUGG.....20      20     1
.....UUUCAAAUGUCUACUGAUGGAA.....22      1436    1
Shared 3' Terminus
.....AUGUCUACUGAUGGA.....15      6      1
.....AAAUGUCUACUGAUGGA.....17      1      1
.....CAAUGUCUACUGAUGGA.....18      2      1
.....UCAAAUGUCUACUGAUGGA.....19      3      1
.....UUCAAAUGUCUACUGAUGGA.....20      29     1
Subsequence
.....UUCAAAUGUCUACUGAUG.....18      2      2
Others
.....UUCAAAUGUCUACUGAUGGAA.....21      13     1
.....UCAAAUGUCUACUGAUGGAA.....20      1      1
.....CAAUGUCUACUGAUGGAA.....19      4      1
.....AAAUGUCUACUGAUGGAA.....18      1      1
.....AUGUCUACUGAUGGAA.....16      1      1
.....UGUCUACUGAUGGAA.....15      3      2
.....CCAUCAGUGGGUUAUU.....16      1      1
.....CCAUCAGUGGGUUAUUUGAA.....19      1      1
.....CCAUCAGUGGGUUAUUUGAAG.....20      10     1
.....CCAUCAGUGGGUUAUUUGAAGU.....21      38     1
.....CCAUCAGUGGGUUAUUUGAAGUU.....22      59     1
.....CAUCAGUGGGUUAUUUGAAGUU.....21      2      1
.....CAGUGGGUUAUUUGAAG.....16      1      2
.....AGUGGGUUAUUUGAAGU.....16      1      1

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miR-2027

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AAUCCGAGAGCCUUAAGGCUUGCUUGUUGGUAAUUUUGCAUCUGUUGCAUUGCGAUUUUACCAAAAUGCAAUUCUUUAUGGUUCAGUGAUCAGGAA
..(((..(((((((.(((((((((((((((.....))))))))))))))))))))..)))))..))..)))))..((...)))).
Total cloned: 2543 shared 5' end with miRNA: 1047 shared 3' end with miRNA: 113
Scaffold: scaffold_241 Coordinates: 295171-295267 Strand: Plus Location: Intergenic
miRNA

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.....AUGCGAUUUUACCAAAAUGCAA.....22      639    1
Shared 5' Terminus
.....AUGCGAUUUUACCAAAA.....17      1      1
.....AUGCGAUUUUACCAAAAU.....18      17     1
.....AUGCGAUUUUACCAAAAUG.....19      30     1
.....AUGCGAUUUUACCAAAAUGC.....20      32     1
.....AUGCGAUUUUACCAAAAUGCA.....21      366    1
.....AUGCGAUUUUACCAAAAUGCAA.....23      559    1
.....AUGCGAUUUUACCAAAAUGCAAU.....24      41     1
.....AUGCGAUUUUACCAAAAUGCAAUC.....25      1      1
Shared 3' Terminus
.....AUUUUACCAAAAUGCAA.....17      2      3
.....GCGAUUUUACCAAAAUGCAA.....20      4      1
.....UGCGAUUUUACCAAAAUGCAA.....21      107    1
Subsequence
.....UGCGAUUUUACCAAAAUGCA.....20      44     1
.....GCGAUUUUACCAAAAUGCA.....19      3      1
.....GAUUUUUACCAAAAUGCA.....17      1      1
.....UUUUACCAAAAUGCA.....15      1      4
Others
.....UGCUGUUGGUAAUUUU.....17      2      1

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.....CGAGGUAACUGUUGCAGCA.....	19	3	3
.....CGAGGUAACUGUUGCAGCAU.....	20	7	3
.....CGAGGUAACUGUUGCAGCAUCC.....	22	13	3
.....GAGGUAACUGUUGCAG.....	16	1	4
.....GAGGUAACUGUUGCAGCAU.....	19	15	3
.....GAGGUAACUGUUGCAGCAUC.....	20	1	3
.....GAGGUAACUGUUGCAGCAUCC.....	21	16	3
.....GAGGUAACUGUUGCAGCAUCA.....	22	1	3
.....AGGUAACUGUUGCAGCAU.....	18	4	3
.....AGGUAACUGUUGCAGCAUC.....	19	1	3
.....AGGUAACUGUUGCAGCAUCC.....	20	2	3
.....AGGUAACUGUUGCAGCAUCCA.....	21	1	3

miR-2032b

GCGAGCUCACCGUUGCUGUCGCGCAACAGUUAGCUAGCAUUUAUUGCGAGGUAACUGUUGCAGCAUCCAUGACUGUGAGG
..(((((((.....(((.....(((.....(((.....(((.....(((.....(((.....(((.....))).....))).....))).....))).....))).....))).....)))))).....

Total cloned: 119 shared 5' end with miRNA: 23 shared 3' end with miRNA: 1
Scaffold: scaffold_161 Coordinates: 427058-427139 Strand: Minus Location: Intronic; likely part of a miRNA cluster with miR-2032a;
overlapping gene (l19389) is encoded on same (minus) strand

miRNA.....UCGCGCAACAGUUAGCUAG.....	20	27	2
Shared 5' Terminus			
.....UCGCGCAACAGUUAGCUA.....	19	4	2
.....UCGCGCAACAGUUAGCUAGC.....	21	3	2
.....UCGCGCAACAGUUAGCUAGCA.....	22	15	2
.....UCGCGCAACAGUUAGCUAGCAU.....	23	1	2
Shared 3' Terminus			
.....CGCGCAACAGUUAGCUAG.....	19	1	2
Subsequence			
Others			
.....CGAGGUAACUGUUGCA.....	16	1	3
.....CGAGGUAACUGUUGCAGC.....	18	2	3
.....CGAGGUAACUGUUGCAGCA.....	19	3	3
.....CGAGGUAACUGUUGCAGCAU.....	20	7	3
.....CGAGGUAACUGUUGCAGCAUCC.....	22	13	3
.....GAGGUAACUGUUGCAG.....	16	1	4
.....GAGGUAACUGUUGCAGCAU.....	19	15	3
.....GAGGUAACUGUUGCAGCAUC.....	20	1	3
.....GAGGUAACUGUUGCAGCAUCC.....	21	16	3
.....GAGGUAACUGUUGCAGCAUCCA.....	22	1	3
.....AGGUAACUGUUGCAGCAU.....	18	4	3
.....AGGUAACUGUUGCAGCAUC.....	19	1	3
.....AGGUAACUGUUGCAGCAUCC.....	20	2	3
.....AGGUAACUGUUGCAGCAUCCA.....	21	1	3

miR-2033

CGACAUAUCUUUCUGACUCUGAGCUAUAUGAGAGAAUCAAACAUGCCGUAUUGCUAAAUGAGACAACUCUGAAAUUCCCGUUUCAGAAUUCAUGAGCUCGUGUCCUUCUGCCU
(((((((.....(((.....(((.....(((.....(((.....(((.....(((.....(((.....))).....))).....))).....))).....))).....))).....)))))).....

Total cloned: 154 shared 5' end with miRNA: 59 shared 3' end with miRNA: 5
Scaffold: scaffold_127 Coordinates: 217396-217517 Strand: Plus Location: Intronic; overlapping gene (l14611) is encoded on same (plus) strand

miRNA.....AGCUAUAUGAGAGAAU.....	18	15	2
Shared 5' Terminus			
.....AGCUAUAUGAGAGAG.....	15	1	3
.....AGCUAUAUGAGAGAGAG.....	16	10	2
.....AGCUAUAUGAGAGAGAGAA.....	17	12	2
.....AGCUAUAUGAGAGAGAGAAUC.....	19	4	2
.....AGCUAUAUGAGAGAGAGAAUCA.....	20	5	2
.....AGCUAUAUGAGAGAGAGAAUCA.....	21	7	2
.....AGCUAUAUGAGAGAGAGAAUCA.....	22	12	2
.....AGCUAUAUGAGAGAGAGAAUCA.....	23	3	2
.....AGCUAUAUGAGAGAGAGAAUCA.....	24	1	2
.....AGCUAUAUGAGAGAGAGAAUCA.....	26	4	2
Shared 3' Terminus			
.....GCUAUAUGAGAGAGAAU.....	17	4	2
.....GAGCUAUAUGAGAGAGAAU.....	19	1	2
Subsequence			
.....GCUAUAUGAGAGAGAG.....	15	4	2
.....GCUAUAUGAGAGAGAGAA.....	16	4	2
Others			
.....GAGCUAUAUGAGAGAGAG.....	16	1	2
.....GAGCUAUAUGAGAGAGAGAA.....	17	2	2


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Shared 5' Terminus
.....ACCUAAUGUCACCAUGAU.....19      8      2
.....ACCUAAUGUCACCAUGAU.....20      8      2
.....ACCUAAUGUCACCAUGAUGAC.....22     35     2
.....ACCUAAUGUCACCAUGAUGACC.....23      1      2
Shared 3' Terminus
.....CCUAAUGUCACCAUGAUGA.....20      1      2
Subsequence
Others
.....CACCCUGAUGACCUUAGUG.....19      2      6
.....CACCCUGAUGACCUUAGUG.....19      2      6
.....CACCCUGAUGACCUUAGUGU.....20      3      6
.....CACCCUGAUGACCUUAGUGU.....20      3      6
.....CACCCUGAUGACCUUAGUGUCA.....22      2      6
.....CACCCUGAUGACCUUAGUGUCA.....22      2      6
.....ACCCUGAUGACCUUAGUGU.....19      5      6
.....ACCCUGAUGACCUUAGUGU.....19      5      6
.....ACCCUGAUGACCUUAGUGUCA.....21      1      6
.....ACCCUGAUGACCUUAGUGUCA.....21      1      6
.....CCUAAUGUCACCAUGAUGAC.....21      1      2

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miR-2039
UUGUAUAAGCCUACCUUUUUUUUUUAUUAUGUAAUAAAAUAAAGGUAGGCUCUCUAA
.....((((((((((((((((((.....)))))))))))))).....
Total cloned: 85 shared 5' end with miRNA: 33 shared 3' end with miRNA: 1
Scaffold: scaffold_264 Coordinates: 119656-119716 Strand: Minus Location: Intronic; overlapping gene (40331) is encoded on same (minus) strand
miRNA

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.....AUAAAAUAAAGGUAGGCUCU...20      43      1
Shared 5' Terminus
.....AUAAAAUAAAGGUAGGCUCU.....18      9      2
.....AUAAAAUAAAGGUAGGCUC.....19      4      1
.....AUAAAAUAAAGGUAGGCUCUC...21      7      1
.....AUAAAAUAAAGGUAGGCUCUCU..22     13     1
Shared 3' Terminus
.....AAAUAAAAUAAAGGUAGGCUCU...22      1      1
Subsequence
Others
.....UAAGCCUACCUUUUUUUUUUU.....21      1      1
.....UAAGCCUACCUUUUUUUUUUU.....22      1      1
.....UAAGCCUACCUUUUUUUUUUU.....23      1      1
.....AAGCCUACCUUUUUUUUUUU.....21      2      1
.....AAGCCUACCUUUUUUUUUUU.....22      1      1
.....AGCCUACCUUUUUUUUUUU.....20      1      2
.....AAAUAAAAUAAAGGUAGGCUC...21      1      1

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miR-2040a
GAUCGUGAUGCCUACAACCUUCGGGUCAGCUACGACAUAGCGCUCUCGUAUCUGCCCGAAGGUAGUCUGGCGUCUUUC
.....(((((((((((((((((((.....)))))))))))))).....
Total cloned: 75 shared 5' end with miRNA: 5 shared 3' end with miRNA: 5
Scaffold: scaffold_108 Coordinates: 81029-81121 Strand: Minus Location: Intergenic
miRNA

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.....UUUGUCUGUAACUGCCCGAAG.....23     39     2
Shared 5' Terminus
.....UUUGUCUGUAACUGCCCGA.....21      1      2
.....UUUGUCUGUAACUGCCCGA.....22      4      2
Shared 3' Terminus
.....UGUCUGUAACUGCCCGAAG.....21      3      2
.....UGUCUGUAACUGCCCGAAG.....22      1      2
.....CUCCUGUUUGUCUGUAACUGCCCGAAG.....30      1      2
Subsequence
.....UGUCUGUAACUGCCCU.....17      1      2
.....UGUCUGUAACUGCCCGA.....19      3      2
.....UGUCUGUAACUGCCCGA.....20      8      2
Others
.....UCGGGUCAGCUACGACAU.....18      1      2
.....UCGGGUCAGCUACGACAUGA.....20      3      2
.....UCGGGUCAGCUACGACAUGAG.....21      8      2
.....UCGGGUCAGCUACGACAUGAGC.....22      1      2
.....UCGGGUCAGCUACGACAUGAGCG.....23      1      2

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.....CAAUGCACGCAAUGAAGAUG.....                22      1      3
Shared 3' Terminus
.....UGCACGCAAUGAAGAUGA.....                19      3      3
Subsequence
.....AAUGCACGCAAUGAAGA.....                19      1      6
Others
.....GAUUCAUGUGCAUGCAUUUACA.....                22      2      1
.....CAUGUGCAUGCAUUUACA.....                18      1      2
.....UUGAAUACGUCUCAUGGAU.....                19      1      4

miR-2051
GUCAUUUCAUGGCGGAGAACCCGGGUCCAGUCAUCAAAACGUCAUUGCACAUUUGAUUGCUGUGAUCUGGUUUUCCGUGUCGAUGUAUAAAC
.....(((((((((((((.....)))))))))))))))))))))).....
Total cloned: 21 shared 5' end with miRNA: 7 shared 3' end with miRNA: 1
Scaffold: scaffold_13 Coordinates: 1048108-1048200 Strand: Plus Location: Intergenic
miRNA
.....AUUUGAUUGCUGUGAUCUGGUUU.....                23      8      1
Shared 5' Terminus
.....AUUUGAUUGCUGUGAUCUG.....                19      6      1
.....AUUUGAUUGCUGUGAUCUGG.....                20      1      1
Shared 3' Terminus
.....UUUGAUUGCUGUGAUCUGGUUU.....                22      1      1
Subsequence
.....UUUGAUUGCUGUGAUCUGG.....                19      1      1
.....UUUGAUUGCUGUGAUCUGGUU.....                21      1      1
Others
.....CCGGGUCCAGUCAUCAAAAC.....                21      1      1
.....CCGGGUCCAGUCAUCAAAACGU.....                23      2      1

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