

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.

miR-100

AUCCGAACCCGUAGAUCCGAACUUGUGGAGUUUCACCACAGGCUCGUUUUCUAACGGAUCAAAAC

.....((.((((((.(((((.((((((.....))))))))))))....))).....)).....)).....

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.....

Shared 5' Terminus

| | 22 | 3583 | 1 |
|---------------------------------|----|------|---|
|ACCCGUAGAUCCGA..... | 15 | 5 | 4 |
|ACCCGUAGAUCCGAAC..... | 16 | 11 | 4 |
|ACCCGUAGAUCCGAACU..... | 17 | 6 | 1 |
|ACCCGUAGAUCCGAACU..... | 18 | 6 | 1 |
|ACCCGUAGAUCCGAACUUG..... | 19 | 20 | 1 |
|ACCCGUAGAUCCGAACUUGU..... | 20 | 64 | 1 |
|ACCCGUAGAUCCGAACUUGU..... | 21 | 82 | 1 |
|ACCCGUAGAUCCGAACUUGGA..... | 23 | 234 | 1 |

Shared 3' Terminus

| | 18 | 1 | 1 |
|-------------------------------|----|----|---|
|GUAGAUCCGAACUUGUGG..... | 19 | 1 | 1 |
|CGUAGAUCCGAACUUGUGG..... | 20 | 6 | 1 |
|CGUAGAUCCGAACUUGUGG..... | 21 | 17 | 1 |

Subsequence

| | 19 | 3 | 1 |
|--------------------------------|----|---|---|
|CCCCGUAGAUCCGAACUUGU..... | | | |

Others

| | 22 | 1 | 1 |
|-------------------------------------|----|-----|---|
|ACAGGCUCGUUUUCUAACGG..... | 17 | 3 | 1 |
|ACAGGCUCGUUUUCUAACGG..... | 18 | 11 | 1 |
|ACAGGCUCGUUUUCUAACCGGA..... | 19 | 93 | 1 |
|ACAGGCUCGUUUUCUAACCGGA..... | 20 | 243 | 1 |
|ACAGGCUCGUUUUCUAACCGGAUC..... | 21 | 70 | 1 |
|ACAGGCUCGUUUUCUAACCGGAUC..... | 22 | 483 | 1 |
|ACAGGCUCGUUUUCUAACCGAUCAA..... | 23 | 1 | 1 |
|ACAGGCUCGUUUUCUAACCGAUCAA..... | 24 | 1 | 1 |
|CAGGCUCGUUUUCUAACCGA..... | 17 | 2 | 1 |
|CAGGCUCGUUUUCUAACCGA..... | 18 | 3 | 1 |
|CAGGCUCGUUUUCUAACCGA..... | 19 | 5 | 1 |
|CAGGCUCGUUUUCUAACCGAUC..... | 21 | 5 | 1 |
|AGGCUCGUUUUCUAACCGAUC..... | 20 | 12 | 1 |
|GCUCGUUUUCUAACCGAUC..... | 18 | 1 | 1 |

miR-2022

GAUAAGAUCGGCCUGAAAGUCGGAUAAAUCAACUGUCAAGUGGUUGUCAUUUGCUUAGUUCGUUUJUGUCCCGCUUUUCUGCGAAUUGAUCA

((((.....(((((((.(((((.((((((.(((((.....)))))))).....)))))))).....)).....)).....)).....)).....)).....

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

.....UUUGCUAGUUGCUUUUGUCCCG.....

Shared 5' Terminus

| | 23 | 162 | 1 |
|------------|----|-----|---|
|UUUGC | 20 | 2 | 1 |
|UUUGC | 22 | 5 | 1 |

| Shared 3' Terminus | | | |
|------------------------------------|--|-------------------------------|---|
| | .GCUAGUUGCUUUUGUCCCGC..... | 20 | 1 |
| | .UGCUAGUUGCUUUUGUCCCGC..... | 21 | 1 |
| | .UUGCUAGUUGCUUUUGUCCCGC..... | 22 | 1 |
| Subsequence | | | |
| Others | | | |
| | .GGGAUAUAUCAACUGU..... | 16 | 3 |
| | .GGGAUAUAUCAACUGUCAAGU..... | 21 | 1 |
| | .GGGAUAUAUCAACUGUCAAGUG..... | 22 | 15 |
| miR-2023 | | | |
| GAGUUUCGUGACAUACCUGUGU | CUGCACCUUGUAAUUCUAUC | CGUCAGAGAA | AAGAAGUACAAAGUGGUAGGG |
| | | | AAGGGUGUGUJCAGAUUGACAA |
| | | | |
| 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 | | | |
| | .AAAGAAGUACAAAGUGGUAGGG..... | 21 | 20458 |
| Shared 5' Terminus | | | |
| | .AAAGAAGUACAAAGUG..... | 15 | 2 |
| | .AAAGAAGUACAAAGUGG..... | 16 | 15 |
| | .AAAGAAGUACAAAGUGU..... | 17 | 74 |
| | .AAAGAAGUACAAAGUGUA..... | 18 | 250 |
| | .AAAGAAGUACAAAGUGGUAG..... | 19 | 2838 |
| | .AAAGAAGUACAAAGUGGUAGG..... | 20 | 4242 |
| | .AAAGAAGUACAAAGUGGUAGGG..... | 22 | 286 |
| | .AAAGAAGUACAAAGUGGUAGGGAA..... | 23 | 9 |
| Shared 3' Terminus | | | |
| | .GUACAAGUGGUAGGG..... | 15 | 15 |
| | .AGUACAAGUGGUAGGG..... | 16 | 18 |
| | .AAGUACAAGUGGUAGGG..... | 17 | 105 |
| | .GAAGUACAAGUGGUAGGG..... | 18 | 8 |
| | .AGAAGUACAAGUGGUAGGG..... | 19 | 39 |
| | .AAGAAGUACAAAGUGGUAGGG..... | 20 | 248 |
| | .CGUCAGAUGAAAAGAAGUACAAAGUGGUAGGG..... | 30 | 1 |
| Subsequence | | | |
| | .AAGAAGUACAAAGUGG..... | 15 | 2 |
| | .AAGAAGUACAAAGUGU..... | 16 | 1 |
| | .AAGAAGUACAAAGUGUA..... | 17 | 3 |
| | .AAGAAGUACAAAGUGUAG..... | 18 | 66 |
| | .AAGAAGUACAAAGUGGUAG..... | 19 | 52 |
| | .AGAAGUACAAAGUGGUAGU..... | 15 | 8 |
| | .AGAAGUACAAAGUGUAGUA..... | 16 | 6 |
| | .AGAAGUACAAAGUGGUAG..... | 17 | 45 |
| | .AGAAGUACAAAGUGGUAG..... | 18 | 26 |
| | .GAAGUACAAGUGGUAG..... | 16 | 4 |
| | .GAAGUACAAGUGGUAGG..... | 17 | 2 |
| | .AAGUACAAGUGGUAG..... | 15 | 7 |
| | .AAGUACAAGUGGUAGG..... | 16 | 20 |
| | .AGUACAAGUGGUAGG..... | 15 | 7 |
| Others | | | |
| | .UCUGCCACCUGUAAUUCUAUC..... | 21 | 1 |
| | .UCUGCCACCUGUAAUUCUA..... | 22 | 1 |
| | .CUGGCCACCUGUAAUUCUA..... | 18 | 1 |
| | .CUGGCCACCUGUAAUUCUAJ..... | 19 | 1 |
| | .CUGGCCACCUGUAAUUCUAUC..... | 20 | 32 |
| | .CUGGCCACCUGUAAUUCUA..... | 21 | 80 |
| | .UGCACACCUGUAAUUCUAUC..... | 19 | 1 |
| | .GAAAGAAGUACAAAGUGGUAG..... | 20 | 1 |
| | .AAGAAGUACAAAGUGGUAGGG..... | 21 | 9 |
| | .AAGAAGUACAAAGUGGUAGGG..... | 20 | 8 |
| | .GAAGUACAAGUGGUAGGGAA..... | 20 | 1 |
| miR-2024a | | | |
| UUCAGAAUAUUGGUGCUGGGCAAAAGGUCACAUU | UUGCACAAACACCAAUAUUCUGAGG | | |
| | | | |
| | | | |
| 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 | | | |
| | .UUGCACAAACACCAAUAUUCUGA..... | 22 | 4808 |
| Shared 5' Terminus | | | |
| | .UUGCACAAACACCAAU..... | 15 | 1 |
| | .UUGCACAAACACCAAUA..... | 16 | 7 |

| | | | | |
|---|---------------------------------|------------------------------|---|-----------------|
| | .UUGCACAAACACCAAAU..... | 17 | 5 | 7 |
| | .UUGCACAAACACCAAAU..... | 18 | 14 | 7 |
| | .UUGCACAAACACCAAAU..... | 19 | 15 | 7 |
| | .UUGCACAAACACCAAAU..... | 20 | 215 | 7 |
| | .UUGCACAAACACCAAAU..... | 21 | 379 | 1 |
| | .UUGCACAAACACCAAAU..... | 23 | 11 | 1 |
| Shared 3' Terminus | | | | |
| | .CAACACCAAUAUUCUGA..... | 17 | 1 | 1 |
| | .CACAAACACCAAUAUUCUGA..... | 19 | 13 | 1 |
| | .GCACAAACACCAAUAUUCUGA..... | 20 | 3 | 1 |
| | .UGCACAAACACCAAUAUUCUGA..... | 21 | 29 | 1 |
| | .UUUUGCACAAACACCAAUAUUCUGA..... | 24 | 1 | 1 |
| Subsequence | | | | |
| | .UGCACAAACACCAAUAUUCU..... | 19 | 4 | 7 |
| | .UGCACAAACACCAAUAUUCUG..... | 20 | 2 | 1 |
| Others | | | | |
| | .AGAAAUUJUGGUGUGGG..... | 17 | 3 | 2 |
| | .AGAAAUUJUGGUGUGGGCAA..... | 20 | 1 | 2 |
| | .AGAAAUUJUGGUGUGGGCAA..... | 21 | 5 | 2 |
| | .AGAAAUUJUGGUGUGGGCAA..... | 22 | 63 | 2 |
| | .GAUAUUJUGGUGUGGGCAA..... | 21 | 1 | 2 |
| | .AAAGGUACACAUUUUGCACAA..... | 20 | 1 | 2 |
| miR-2024b | | | | |
| CAUCAGGUAGACUUGCUU | CAGAAUAIJUGGUGCUGGGCAA | AGGUACACAUUJUGGACAAU | UCCAAUUCUGA | GSCACUUCUGCUGAA |
| | | | | |
| Total cloned: 360 | shared 5' end with miRNA: 26 | shared 3' end with miRNA: 1 | | |
| Scaffold: scaffold_126 | Coordinates: 87406-87493 | Strand: Minus | Location: Intergenic; likely part of a miRNA cluster with miR-2024a,c,d,e | |
| miRNA | | | | |
| | .UUGGCACAAUUCCAAUAUUCUGA..... | 22 | 179 | 1 |
| Shared 5' Terminus | | | | |
| | .UUGGCACAAUUCCAAUAU..... | 18 | 2 | 1 |
| | .UUGGCACAAUUCCAAUAUUCU..... | 20 | 6 | 1 |
| | .UUGGCACAAUUCCAAUAUUCUG..... | 21 | 18 | 1 |
| Shared 3' Terminus | | | | |
| | .UGCACAAUUCCAAUAUUCUGA..... | 21 | 1 | 1 |
| Others | | | | |
| CAUCAGGUAGACUUGCU..... | | 17 | 1 | 6 |
| CAUCAGGUAGACUUGCUUC..... | | 19 | 63 | 6 |
| .AUCAAGGUAGACUUGCUUC..... | | 18 | 2 | 7 |
| ...CAGGUAGACUUGCUUC..... | | 16 | 13 | 8 |
|AGGUAGACUUGCUUC..... | | 15 | 1 | 8 |
|AGAAAUUJUGGUGUGGG..... | | 17 | 3 | 2 |
|AGAAAUUJUGGUGUGGGCAA..... | | 20 | 1 | 2 |
|AGAAAUUJUGGUGUGGGCAA..... | | 21 | 5 | 2 |
|AGAAAUUJUGGUGUGGGCAA..... | | 22 | 63 | 2 |
|GAUAUUJUGGUGUGGGCAA..... | | 21 | 1 | 2 |
|AAAGGUACACAUUUUGCACAA..... | | 20 | 1 | 2 |
| miR-2024c | | | | |
| UGCUCUCAAAUAUCGGUGUUGGUAAAAGGUACACAGUACCGUAUUGUGA | AGCA | | | |
| | | | | |
| Total cloned: 7053 | shared 5' end with miRNA: 2480 | shared 3' end with miRNA: 35 | | |
| Scaffold: scaffold_126 | Coordinates: 87171-87234 | Strand: Minus | Location: Intergenic; likely part of a miRNA cluster with miR-2024a,b,d,e | |
| miRNA | | | | |
| | .UUAACACAGUACCGUAUUGUGA..... | 22 | 4252 | 3 |
| Shared 5' Terminus | | | | |
| | .UUAACACAGUACCGGAU..... | 15 | 2 | 3 |
| | .UUAACACAGUACCGGA..... | 16 | 1 | 3 |
| | .UUAACACAGUACCGGAU..... | 17 | 6 | 3 |
| | .UUAACACAGUACCGGAU..... | 18 | 45 | 3 |
| | .UUAACACAGUACCGGAU..... | 19 | 46 | 3 |
| | .UUAACACAGUACCGGAU..... | 20 | 284 | 3 |
| | .UUAACACAGUACCGGAU..... | 21 | 1378 | 3 |
| | .UUAACACAGUACCGGAU..... | 23 | 715 | 3 |
| | .UUAACACAGUACCGGAU..... | 24 | 3 | 3 |
| Shared 3' Terminus | | | | |
| | .GUACCGGAUAIJUGUGA..... | 15 | 2 | 9 |
| | .AGUACCGGAUAIJUGUGA..... | 16 | 1 | 9 |
| | .CAGUACCGGAUAIJUGUGA..... | 17 | 1 | 9 |
| | .ACAGUACCGGAUAIJUGUGA..... | 18 | 4 | 8 |
| | .ACACAGUACCGGAUAIJUGUGA..... | 20 | 6 | 7 |

| | | | | |
|---|---|-----------------------------|--|---|
| Subsequence |UACACAGUACCGAUUAUUGUGA..... | 21 | 21 | 3 |
| |UACACAGUACCGAUUAUUGU..... | 19 | 5 | 3 |
| |UACACAGUACCGAUUAUUGUG..... | 20 | 5 | 3 |
| |ACACAGUACCGAUUAUUGU..... | 18 | 1 | 7 |
| |CAGUACCGAUUAUUGU..... | 15 | 1 | 9 |
| Others |AAAAUAUCGGUGUUGGG..... | 17 | 1 | 9 |
| |AAAAUAUCGGUGUUGGGUAA..... | 20 | 20 | 8 |
| |AAAAUAUCGGUGUUGGGUAAA..... | 21 | 55 | 7 |
| |AAAAUAUCGGUGUUGGGUAAAA..... | 22 | 165 | 7 |
| |AAAAUAUCGGUGUUGGGUAAA..... | 19 | 1 | 8 |
| |AAAAUAUCGGUGUUGGGUAAA..... | 21 | 3 | 7 |
| |AAUAUCGGUGUUGGGUAAA..... | 19 | 1 | 7 |
| |AAUAUCGGUGUUGGGUAAA..... | 20 | 1 | 7 |
| |AAUAUCGGUGUUGGGUAAA..... | 19 | 1 | 7 |
| |AAUAUCGGUGUUGGGUAAA..... | 18 | 3 | 7 |
| |AUCGGUGUUGGGUAAA..... | 16 | 1 | 7 |
| |AUCGGUGUUGGGUAAA..... | 17 | 1 | 7 |
| |UUUACACAGUACCGAUUAUUG..... | 21 | 1 | 3 |
| |UUUACACAGUACCGAUUAUUG..... | 22 | 1 | 3 |
| |UACACAGUACCGAUUAUUGAA..... | 22 | 19 | 3 |
| miR-2024d |UUGGCACAUCACCAAUGUUCUGA..... | 22 | 2865 | 2 |
| AAAGAGCAGGAGACUUGCUUCAGAAUAUJGGUACUGGCCAAA..... |GGUCACGUUJGGCACACCAAUUGUCUGAAGCACUUCUGCUGAAGGAACUAGGAAUUAACAAGA..... | | | |
|(((((.....(((((((((((((.....((.....))))))))))))))))))))..... | | | | |
| Total cloned: 4294 | shared 5' end with miRNA: 1266 | shared 3' end with miRNA: 4 | | |
| Scaffold: scaffold_126 | Coordinates: 84451-84561 | Strand: Minus | Location: Intergenic; likely part of a mirRNA cluster with miR-2024a,b,c,e | |
| miRNA | | | | |
| Shared 5' Terminus |UUGGCACAUCACCAAUGUUCUGA..... | 22 | 2865 | 2 |
| |UUGGCACAUCACCAAU..... | 15 | 4 | 2 |
| |UUGGCACAUCACCAUAG..... | 16 | 1 | 2 |
| |UUGGCACAUCACCAUAGU..... | 17 | 11 | 2 |
| |UUGGCACAUCACCAUAGUU..... | 18 | 104 | 2 |
| |UUGGCACAUCACCAUAGUUC..... | 19 | 100 | 2 |
| |UUGGCACAUCACCAUAGUUCU..... | 20 | 690 | 2 |
| |UUGGCACAUCACCAUAGUUCUG..... | 21 | 347 | 2 |
| |UUGGCACAUCACCAUAGUUCUGAG..... | 23 | 9 | 2 |
| Shared 3' Terminus |UGCACAUCAACCAAUGUUCUGA..... | 21 | 3 | 2 |
| |GCACAUCAACCAAUGUUCUGA..... | 20 | 1 | 2 |
| Subsequence |UGCACAUCAACCAAUGU..... | 17 | 3 | 2 |
| |UGCACAUCAACCAAUGUUCU..... | 19 | 6 | 2 |
| |UGCACAUCAACCAAUGUUCUG..... | 20 | 2 | 2 |
| Others |GACCAAGUAGACUUGCUC..... | 19 | 1 | 1 |
| |AGCAGGUAGACUUGCUC..... | 18 | 1 | 1 |
| |GCAGGUAGACUUGCUC..... | 17 | 1 | 1 |
| |CAGGUAGACUUGCUC..... | 16 | 13 | 8 |
| |AGGUAGACUUGCUC..... | 15 | 1 | 8 |
| |AGAAUAUJGGUACUGG..... | 16 | 1 | 2 |
| |AGAAUAUJGGUACUGG..... | 17 | 1 | 2 |
| |AGAAUAUJGGUACUGGCCAA..... | 20 | 1 | 2 |
| |AGAAUAUJGGUACUGGCCAAA..... | 21 | 6 | 2 |
| |AAUAUJGGUACUGGCCAA..... | 22 | 115 | 2 |
| |AAUAUJGGUACUGGCCAA..... | 18 | 1 | 2 |
| |AAUAUJGGUACUGGCCAA..... | 19 | 1 | 2 |
| |AAUAUJGGUACUGGCCAA..... | 21 | 1 | 2 |
| |AAUAUJGGUACUGGCCAA..... | 21 | 1 | 2 |
| |ACUGGCCAAAAGGUACGUU..... | 22 | 1 | 2 |
| |UUUUGCACAUCAACCAAUGUUC..... | 22 | 1 | 2 |
| |CUGCUGAAGGAACUAG..... | 16 | 1 | 8 |
| |UGAAGGAACUAGGAAUUA..... | 20 | 1 | 5 |

miR-2024e
 AGUCGUACUGCUUCAAAUAUCGGUGUUGGGUAAA.....GGUCACAUUJGUACAGUACCGAUUAUUGUGAAGCACGUUJGGCAAUUA
 ..((.(((((.....((.....)))))))).....)).....
 Total cloned: 6248 shared 5' end with miRNA: 1224 shared 3' end with miRNA: 37
 Scaffold: scaffold_126 Coordinates: 84222-84307 Strand: Minus Location: Intergenic; likely part of a mirRNA cluster with miR-2024a,b,c,d
 miRNA

.....UUCAACAGUACCGAUUAUUGUGA.....

| Shared 5' Terminus | | | |
|---------------------------|------------------------------------|---------------------------------|---|
| | .UUCAACAGUACCGAU..... | 15 | 1 |
| | .UUCAACAGUACCGAUA..... | 16 | 1 |
| | .UUCAACAGUACCGAUAU..... | 17 | 2 |
| | .UUCAACAGUACCGAUAUU..... | 18 | 43 |
| | .UUCAACAGUACCGAUAUUG..... | 19 | 58 |
| | .UUCAACAGUACCGAUAUUGU..... | 20 | 205 |
| | .UUCAACAGUACCGAUAUUGUG..... | 21 | 418 |
| | .UUCAACAGUACCGAUAUUGUGAA..... | 23 | 494 |
| Shared 3' Terminus | | | |
| | .GUACCGAUUAUUGUGA..... | 15 | 2 |
| | .AGUACCGAUUAUUGUGA..... | 16 | 1 |
| | .CAGUACCGAUUAUUGUGA..... | 17 | 1 |
| | .ACAGUACCGAUUAUUGUGA..... | 18 | 4 |
| | .AACAGUACCGAUUAUUGUGA..... | 19 | 12 |
| | .CAACAGUACCGAUUAUUGUGA..... | 20 | 6 |
| | .UCAACAGUACCGAUUAUUGUGA..... | 21 | 11 |
| Subsequence | | | |
| | .UCAACAGUACCGAUUAUUG..... | 18 | 1 |
| | .UCAACAGUACCGAUUAUUGU..... | 19 | 3 |
| | .UCAACAGUACCGAUUAUUGUG..... | 20 | 6 |
| | .AACAGUACCGAUUAUUGUG..... | 17 | 1 |
| | .AACAGUACCGAUUAUUGUG..... | 18 | 3 |
| | .CAGUACCGAUUAUUGUG..... | 15 | 1 |
| Others | | | |
| | .AAAAUAUCGGUGUUGGG..... | 17 | 1 |
| | .AAAAUAUCGGUGUUGGGUAAA..... | 20 | 20 |
| | .AAAAUAUCGGUGUUGGGUAAA..... | 21 | 55 |
| | .AAAAUAUCGGUGUUGGGUAAA..... | 22 | 165 |
| | .AAAAUAUCGGUGUUGGGUAAA..... | 19 | 1 |
| | .AAAAUAUCGGUGUUGGGUAAA..... | 21 | 3 |
| | .AAAAUAUCGGUGUUGGGUAAA..... | 19 | 1 |
| | .AAAAUAUCGGUGUUGGGUAAA..... | 20 | 1 |
| | .AAAAUAUCGGUGUUGGGUAAA..... | 19 | 1 |
| | .UAUCGGUGUUGGGUAAA..... | 18 | 3 |
| | .AUCGGUGUUGGGUAAA..... | 16 | 1 |
| | .AUCGGUGUUGGGUAAA..... | 17 | 1 |
| | .UCAACAGUACCGAUUAUUGUGA..... | 22 | 6 |
| | .AACAGUACCGAUUAUUGUGAA..... | 20 | 2 |
| miR-2024f | | | |
| ACAUCAGGUAGACUUCGUUC | CAGAGUAUUGGCCUUGGCAAAA | GGUCACAUUUJUGCACAUACCAAUAUUCUGA | GGCACUUCUCUGCUAGGGAACU |
| | | | |
| Total cloned: 4331 | shared 5' end with miRNA: 343 | shared 3' end with miRNA: 14 | |
| Scaffold: scaffold_282 | Coordinates: 93286-93380 | Strand: Minus | Location: Intergenic; likely part of a miRNA cluster with miR-2024g |
| miRNA | | | |
| | .UUGCACAUUACCAAAUUCUGA..... | 22 | 3839 |
| Shared 5' Terminus | | | |
| | .UUGCACAUUACCAAAU..... | 17 | 1 |
| | .UUGCACAUUACCAAAU..... | 18 | 6 |
| | .UUGCACAUUACCAAAUUC..... | 19 | 4 |
| | .UUGCACAUUACCAAAUUCU..... | 20 | 135 |
| | .UUGCACAUUACCAAAUUCUG..... | 21 | 187 |
| | .UUGCACAUUACCAAAUUCUGAG..... | 23 | 10 |
| Shared 3' Terminus | | | |
| | .AUUACCAAAUUCUGA..... | 16 | 4 |
| | .ACAAUACCAAAUUCUGA..... | 18 | 1 |
| | .CACAAUACCAAAUUCUGA..... | 19 | 2 |
| | .UGCACAUUACCAAAUUCUGA..... | 21 | 7 |
| Subsequence | | | |
| | .UGCACAUUACCAAAUUCUG..... | 20 | 6 |
| Others | | | |
| ACAUCAGGUAGACUUCGUUC..... | | 20 | 3 |
| .CAUCAGGUAGACUUCGU..... | | 17 | 1 |
| .CAUCAGGUAGACUUCGUUC..... | | 19 | 63 |
| .AUCAAGGUAGACUUCGUUC..... | | 18 | 2 |
| .CAGGUAGACUUCGUUC..... | | 16 | 13 |
| .AGGUAGACUUCGUUC..... | | 15 | 1 |
| | .AGAGUAUUGGCCUUGGCAAAA..... | 21 | 3 |
| | .AGAGUAUUGGCCUUGGCAAAA..... | 22 | 44 |
| | UUUUGCACAUUACCAAAUUCU..... | 22 | 1 |

| | | | | |
|---|---|------------------------------|---|---|
| miR-2024g | | | | |
| ACCAAUAAUGGUCAUCGUUUC | AAAAUAUCGGUGUUGGGUAAAAGGUACC UUUUAACACAGUACCGAUAUUGUGA | AGCACGUUUGCAAA | | |
|(((((.....(((((.....((.....)))))))))))).....)).))).))).).. | | | | |
| 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 | | | | |
| Shared 5' Terminus |UAACACAGUACCGAUAUUGUGA. | 22 | 1570 | 4 |
|UAACACAGUACCGAUAU..... | 17 | 1 | 4 | |
|UAACACAGUACCGAUAUJU..... | 18 | 7 | 4 | |
|UAACACAGUACCGAUAUUG..... | 19 | 24 | 4 | |
|UAACACAGUACCGAUAUJUGU..... | 20 | 80 | 4 | |
|UAACACAGUACCGAUAUJUGUG..... | 21 | 248 | 4 | |
|UAACACAGUACCGAUAUJUGUGA..... | 23 | 141 | 4 | |
| Shared 3' Terminus |GUACCGGAAUUAUUGUGA..... | 15 | 2 | 9 |
|AGUACCGGAAUUAUUGUGA..... | 16 | 1 | 9 | |
|CAGUACCGGAAUUAUUGUGA..... | 17 | 1 | 9 | |
|ACAGUACCGGAAUUAUUGUGA..... | 18 | 4 | 8 | |
|ACACAGUACCGGAAUUAUUGUGA..... | 20 | 6 | 7 | |
|AACACAGUACCGGAAUUAUUGUGA..... | 21 | 27 | 4 | |
|UUACACAGUACCGGAAUUAUUGUGA..... | 23 | 4 | 4 | |
| Subsequence |AACACAGUACCGGAAUUAUUG..... | 18 | 1 | 4 |
|AACACAGUACCGGAAUUAUUGUG..... | 20 | 1 | 4 | |
|ACACAGUACCGGAAUUAUUGUG..... | 18 | 1 | 7 | |
|CAGUACCGGAAUUAUUGUG..... | 15 | 1 | 9 | |
| Others |CCAUAAGUGCUCACUGCUUC..... | 20 | 1 | 5 |
|CAAUAAGUGCUCACUGCUUC..... | 19 | 2 | 5 | |
|UAAGUGCUCACUGCUUC..... | 16 | 1 | 5 | |
|AAGUGCUCACUGCUUC..... | 15 | 1 | 8 | |
|AAAAUAUCGGUGUUGGG..... | 17 | 1 | 9 | |
|AAAAUAUCGGUGUUGGGUAAA..... | 20 | 20 | 8 | |
|AAAAUAUCGGUGUUGGGUAAA..... | 21 | 55 | 7 | |
|AAAUAUCGGUGUUGGGUAAA..... | 22 | 165 | 7 | |
|AAAUAUCGGUGUUGGGUAAA..... | 19 | 1 | 8 | |
|AAAUAUCGGUGUUGGGUAAA..... | 21 | 3 | 7 | |
|AAUAUCGGUGUUGGGUAAA..... | 19 | 1 | 7 | |
|AAUAUCGGUGUUGGGUAAA..... | 20 | 1 | 7 | |
|AAUAUCGGUGUUGGGUAAA..... | 19 | 1 | 7 | |
|AAUAUCGGUGUUGGGUAAA..... | 18 | 3 | 7 | |
|AAUCGGUGUUGGGUAAA..... | 16 | 1 | 7 | |
|AAUCGGUGUUGGGUAAA..... | 17 | 1 | 7 | |
|UUUAACACAGUACCGGAAUUAUUGUG..... | 23 | 1 | 4 | |
|UUUAACACAGUACCGGAAUUAUJU..... | 19 | 2 | 4 | |
|UUACACAGUACCGGAAUUAUJU..... | 21 | 4 | 4 | |
|UUACACAGUACCGGAAUUAUJUG..... | 22 | 3 | 4 | |
|AACACAGUACCGGAAUUAUUGUGA..... | 22 | 8 | 4 | |
| miR-2025 | | | | |
| AACAAUUAGGCCACAUACAA | AGCUUUCGAUGGUAAGAAAUCUUAGUGA UUUUUAGCCGCGGAAGUUGU | GUUGCCUGGCCAAUUAUACAUU | | |
|(((((.....(((((.....((.....)))))))))))).....)).))).).. | | | | |
| 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 | | | | |
| Shared 5' Terminus |UUUUUAGCCGCGGAAGUUGU. | 22 | 6210 | 1 |
|UUUUUAGCCGCGGA..... | 16 | 2 | 1 | |
|UUUUUAGCCGCGGA..... | 17 | 5 | 1 | |
|UUUUUAGCCGCGGAAG..... | 18 | 9 | 1 | |
|UUUUUAGCCGCGGAAGU..... | 19 | 22 | 1 | |
|UUUUUAGCCGCGGAAGU..... | 20 | 65 | 1 | |
|UUUUUAGCCGCGGAAGUUG..... | 21 | 225 | 1 | |
|UUUUUAGCCGCGGAAGUUGUG..... | 23 | 1 | 1 | |
| Shared 3' Terminus |UAGCCGCGGAAGUUGU..... | 17 | 1 | 1 |
|UAAGCCGCGGAAGUUGU..... | 18 | 1 | 1 | |
|UUUAGCCGCGGAAGUUGU..... | 19 | 3 | 1 | |
|UUUAGCCGCGGAAGUUGU..... | 20 | 13 | 1 | |
|UUUUUAGCCGCGGAAGUUGU..... | 21 | 80 | 1 | |
| Subsequence | | | | |

| | | | | |
|--|---------------------------------|-------------------------------|----------------------|---|
| Others |UUUUUAGCCCGCGGAAGUU..... | 19 | 2 | 1 |
| |UUUUUAGCCCGCGGAAGUUG..... | 20 | 1 | 1 |
| |ACGUUUUCGAUGGUAGA..... | 17 | 1 | 1 |
| |ACGUUUUCGAUGGUAGAAAAA..... | 20 | 1 | 1 |
| |ACGUUUUCGAUGGUAGAAAAU..... | 21 | 6 | 1 |
| |ACGUUUUCGAUGGUAGAAAUC..... | 22 | 31 | 1 |
| |GCUUUUCGAUGGUAGAAAUC..... | 21 | 2 | 1 |
| miR-2026 | | | | |
| ACUUGUGCCCCGGUUUCAAAUGCUACUGAUGGAAGUUGGUUCCAUCAGUGGUAUUUGAAGUUAGAGACGCCAGAA | | | | |
| ..(((((((.(((.(((((((((.)))))))((.)))))).)))))).(....))). | | | | |
| 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 | | | | |
|UUUCAAAUGUCUACUGAUGGA..... | 21 | 1680 | 1 | |
| Shared 5' Terminus | | | | |
|UUUCAAAUGUCUACUGAU..... | 18 | 1 | 2 | |
|UUUCAAAUGUCUACUGAUG..... | 19 | 3 | 2 | |
|UUUCAAAUGUCUACUGAUGG..... | 20 | 20 | 1 | |
|UUUCAAAUGUCUACUGAUGGA..... | 22 | 1436 | 1 | |
| Shared 3' Terminus | | | | |
|AUGUCUACUGAUGGA..... | 15 | 6 | 1 | |
|AAAUUGUCUACUGAUGGA..... | 17 | 1 | 1 | |
|CAAUUGUCUACUGAUGGA..... | 18 | 2 | 1 | |
|UCAAUUGUCUACUGAUGGA..... | 19 | 3 | 1 | |
|UCAAUUGUCUACUGAUGGA..... | 20 | 29 | 1 | |
| Subsequence | | | | |
|UUCAA AUGUCUACUGAUG..... | 18 | 2 | 2 | |
| Others | | | | |
|UUCAA AUGUCUACUGAUGGA..... | 21 | 13 | 1 | |
|UCAA AUGUCUACUGAUGGA..... | 20 | 1 | 1 | |
|CAAUUGUCUACUGAUGGA..... | 19 | 4 | 1 | |
|AAAUGUCUACUGAUGGA..... | 18 | 1 | 1 | |
|AUGUCUACUGAUGGA..... | 16 | 1 | 1 | |
|UGUCUACUGAUGGA..... | 15 | 3 | 2 | |
|CCAUCAGUGGGUAUJU..... | 16 | 1 | 1 | |
|CCAUCAGUGGGUAUJUGA..... | 19 | 1 | 1 | |
|CCAUCAGUGGGUAUJUGAAG..... | 20 | 10 | 1 | |
|CCAUCAGUGGGUAUJUGAAGU..... | 21 | 38 | 1 | |
|CCAUCAGUGGGUAUJUGAAGU..... | 22 | 59 | 1 | |
|CAUCAGUGGGUAUJUGAAGU..... | 21 | 2 | 1 | |
|CAGUGGGUAUJUGAAG..... | 16 | 1 | 2 | |
|AGUGGGUAUJUGAAG..... | 16 | 1 | 1 | |
| miR-2027 | | | | |
| AAUCGGAGACCUUAAGGCUU <u>GC</u> UUUGGUAAUUUGCA <u>UC</u> GUUGCACAU <u>GC</u> AUUUU <u>AC</u> CAAA <u>AG</u> <u>CA</u> UU <u>U</u> <u>A</u> <u>U</u> <u>G</u> GU <u>C</u> <u>A</u> <u>G</u> <u>A</u> <u>G</u> AA | | | | |
| ..((..(((.(((.(((.(((.(((.(((.((.(((...)))))))))))))))).....)).))))...(....))). | | | | |
| 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 | | | | |
|AUGCGAUUUUACCAAA <u>AG</u> <u>CA</u> | 22 | 639 | 1 | |
| Shared 5' Terminus | | | | |
|AUGCGAUUUUACCAAA..... | 17 | 1 | 1 | |
|AUGCGAUUUUACCAAAAU..... | 18 | 17 | 1 | |
|AUGCGAUUUUACCAAA <u>A</u> U..... | 19 | 30 | 1 | |
|AUGCGAUUUUACCAAA <u>A</u> U..... | 20 | 32 | 1 | |
|AUGCGAUUUUACCAAA <u>A</u> U..... | 21 | 366 | 1 | |
|AUGCGAUUUUACCAAA <u>A</u> U..... | 23 | 559 | 1 | |
|AUGCGAUUUUACCAAA <u>A</u> U..... | 24 | 41 | 1 | |
|AUGCGAUUUUACCAAA <u>A</u> U..... | 25 | 1 | 1 | |
| Shared 3' Terminus | | | | |
|AUUUUACCAAA <u>A</u> U..... | 17 | 2 | 3 | |
|GGCAUUUUACCAAA <u>A</u> U..... | 20 | 4 | 1 | |
|GGCAUUUUACCAAA <u>A</u> U..... | 21 | 107 | 1 | |
| Subsequence | | | | |
|UGCGAUUUUACCAAA <u>A</u> U..... | 20 | 44 | 1 | |
|GGCAUUUUACCAAA <u>A</u> U..... | 19 | 3 | 1 | |
|GAUUUUACCAAA <u>A</u> U..... | 17 | 1 | 1 | |
|GAUUUUACCAAA <u>A</u> U..... | 15 | 1 | 4 | |
| Others | | | | |
|UGCUUGUUGGUAAU..... | 17 | 2 | 1 | |

| | | | | |
|-------|--------------------------------|----|-----|---|
| | UGCUGUUGUGGUAAAUIUUG. | 18 | 5 | 1 |
| | UGCUGUUGGUAAAUIUUGC. | 19 | 11 | 1 |
| | UGCUGUUGGUAAAUIUJGCA. | 20 | 87 | 1 |
| | UGCUGUUGGUAAAUIUJGCAU. | 21 | 214 | 1 |
| | UGCUGUUGGUAAAUIUJGCAUC. | 22 | 11 | 1 |
| | UGCUGUUGGUAAAUIUJGCAUCU. | 23 | 192 | 1 |
| | GCUGUUGGUAAAUIUJGCAU. | 20 | 1 | 1 |
| | GCUGUUGGUAAAUIUJGCAUCU. | 22 | 1 | 1 |
| | CUUGUGGUAAAUIUJGCAUCU. | 21 | 1 | 1 |
| | UCUGUUGCACAUJGUUUACAAAA. | 27 | 1 | 1 |
| | CAUGCGAUIUACAAAAAU. | 19 | 1 | 1 |
| | UGGCAUIUACAAAAAUGCAAU. | 22 | 164 | 1 |
| | UGGCAUIUACCAAUAUGCAAU. | 23 | 3 | 1 |
| | GCGAUIUACCAAUAUGCAAU. | 21 | 1 | 1 |

miR-2028
AGGACGAGGGAGUCUAAAGUUCGCCUGGUUCUUAUUAUAGAACUAGCAGGAGCAUUAAGAUACAGUCGUCAAAAC
..((((((...(((((((((((((.(((((((((....))))))))))))))))))))....))))....)))
Total cloned: 1643 shared 5' end with miRNA: 835 shared 3' end with miRNA: 4
Scaffold: scaffold_6 Coordinates: 334196-334279 Strand: Minus Location: Intergenic
miRNA

| | | | | |
|--------------------|---------------------------------------|----|-----|---|
| | .UAAUGUUCUCUGCUUGUUCUA. | 21 | 496 | 1 |
| Shared 5' Terminus | UAAUGUUCUCUGCUUUC. | 15 | 2 | 1 |
| | UAAUGUUCUCUGCUUGU. | 16 | 5 | 1 |
| | UAAUGUUCUCUGCUUGUU. | 17 | 21 | 1 |
| | UAAUGUUCUCUGCUUGUUU. | 18 | 131 | 1 |
| | UAAUGUUCUCUGCUUGUUC. | 19 | 85 | 1 |
| | UAAUGUUCUCUGCUUGUCCU. | 20 | 260 | 1 |
| | UAAUGUUCUCUGCUUGUCCU. | 22 | 288 | 1 |
| | UAAUGUUCUCUGCUUGUCCUUA. | 23 | 32 | 1 |
| | UAAUGUUCUCUGCUUGUCCUUAU. | 24 | 10 | 1 |
| | UAAUGUUCUCUGCUUGUCCUUAUA. | 25 | 1 | 1 |
| Shared 3' Terminus | AUGUUCUCUGCUUGUUCUA. | 19 | 1 | 1 |
| | AAUGUUCUCUGCUUGUUCUA. | 20 | 3 | 1 |
| Subsequence | AAUGUUCUCUGCUUGUUCU. | 17 | 2 | 1 |
| | AAUGUUCUCUGCUUGUUCU. | 19 | 2 | 1 |
| | GUUCUCUGCUUGUUCU. | 16 | 1 | 1 |
| Others | AAUGUUCUCUGCUUGUUCUA. | 21 | 1 | 1 |
| | UAAUAAUJAGGAACUAGCAGGAGCAUUAAG. | 30 | 1 | 1 |
| | UAAUAAUJAGGAACUAGCAGGAGCAUUAAG. | 28 | 4 | 1 |
| | AUAAUJAGGAACUAGCAGGAGCAUUAAG. | 27 | 1 | 1 |
| | UAAUJAGGAACUAGCAGGAGCAUUAAG. | 22 | 2 | 1 |
| | UAAUJAGGAACUAGCAGGAGCAUUA. | 25 | 2 | 1 |
| | UAAUJAGGAACUAGCAGGAGCAUUAAG. | 26 | 10 | 1 |
| | AUUAGGAACUACAGGAGCAUUA. | 23 | 1 | 1 |
| | AUUAGGAACUACAGGAGCAUUA. | 24 | 1 | 1 |
| | AUUAGGAACUACAGGAGCAUUAAG. | 25 | 6 | 1 |
| | UUAGGAACUACAGGAGCAUUA. | 22 | 3 | 1 |
| | UUAGGAACUACAGGAGCAUUA. | 23 | 2 | 1 |
| | UUAGGAACUACAGGAGCAUUAAG. | 24 | 5 | 1 |
| | UAGGAACUACAGGAGCA. | 18 | 1 | 1 |
| | UAGGAACUACAGGAGCAUUA. | 20 | 4 | 1 |
| | UAGGAACUACAGGAGCAUUA. | 21 | 16 | 1 |
| | UAGGAACUACAGGAGCAUUA. | 22 | 66 | 1 |
| | UAGGAACUACAGGAGCAUUAAG. | 23 | 130 | 1 |
| | UAGGAACUACAGGAGCAUUAAG. | 24 | 3 | 1 |
| | UAGGAACUACAGGAGCAUUAAG. | 25 | 1 | 1 |
| | UAGGAACUACAGGAGCAUUAAG. | 27 | 1 | 1 |
| | AGGAACUACAGGAGCAUUA. | 20 | 1 | 1 |
| | AGGAACUACAGGAGCAUUA. | 21 | 5 | 1 |
| | AGGAACUACAGGAGCAUUAAG. | 22 | 25 | 1 |
| | GGAACUACAGGAGCAUUA. | 17 | 1 | 1 |
| | GGAACUACAGGAGCAUUA. | 19 | 1 | 1 |
| | GGAACUACAGGAGCAUUAAG. | 21 | 9 | 1 |

miR-2029
 CAUGUGGGCAUUUAGGUGAUACGCAAUCCUAGGUUACCAUGUCAGAUGGUAAACUAUGGAUUGC_{GC}CUUCUCCUAACUUGCCUACUGCAAUGCU
 ..(((..(((.((..((((((.((.(((((.....))))))).))).))).))).))).)))....
 Total cloned: 1607 shared 5' end with miRNA: 377 shared 3' end with miRNA: 6
 Scaffold: scaffold_83 Coordinates: 157639-157736 Strand: Plus Location: Intronic; overlapping gene (186367) is encoded on same (plus) strand
 miRNA
UACGCAAUCCUAGGUUACCAU..... 22 720 1
 Shared 5' Terminus
UACGCAAUCCUAGGUUACCAU..... 15 1 1
UACGCAAUCCUAGGUU..... 16 2 1
UACGCAAUCCUAGGUU..... 17 4 1
UACGCAAUCCUAGGUU..... 18 13 1
UACGCAAUCCUAGGUU..... 19 39 1
UACGCAAUCCUAGGUU..... 20 69 1
UACGCAAUCCUAGGUUACCA..... 21 247 1
UACGCAAUCCUAGGUUACCAU..... 24 1 1
UACGCAAUCCUAGGUUACCAU..... 28 1 1
 Shared 3' Terminus
ACGCAAUCCUAGGUUACCAU..... 21 6 1
 Subsequence
ACGCAAUCCUAGGUUAC..... 18 1 1
ACGCAAUCCUAGGUUACCA..... 20 3 1
 Others
AUACGCAAUCCUAGGUUACCA..... 22 2 1
CAUGCAGAUGGUAAACUAUGGAUJG..... 26 1 1
UGGUAAACUAUGGUU..... 16 1 1
UGGUAAACUAUGGUU..... 17 6 1
UGGUAAACUAUGGUU..... 18 2 1
UGGUAAACUAUGGUUJGG..... 19 34 1
UGGUAAACUAUGGUUJGG..... 20 16 1
UGGUAAACUAUGGUUJGGCGU..... 21 31 1
UGGUAAACUAUGGUUJGGCGU..... 22 27 1
UGGUAAACUAUGGUUJGGCGU..... 23 11 1
UGGUAAACUAUGGUUJGGCGU..... 24 11 1
GGUAACUAUGGUU..... 15 1 1
GGUAACUAUGGUU..... 16 1 1
GGUAACUAUGGUUJGG..... 17 1 1
GGUAACUAUGGUUJGG..... 18 1 1
GGUAACUAUGGUUJGGCG..... 19 3 1
GGUAACUAUGGUUJGGCGU..... 20 7 1
GGUAACUAUGGUUJGGCGU..... 21 5 1
GGUAACUAUGGUUJGGCGU..... 22 21 1
GGUAACUAUGGUUJGGCGU..... 23 7 1
GUAACUAUGGUUJGGCGU..... 16 2 1
GUAACUAUGGUUJGGCG..... 17 1 1
GUAACUAUGGUUJGGCG..... 18 7 1
GUAACUAUGGUUJGGCGU..... 19 39 1
GUAACUAUGGUUJGGCGU..... 20 38 1
GUAACUAUGGUUJGGCGU..... 21 29 1
GUAACUAUGGUUJGGCGU..... 22 84 1
UAAACUAUGGUUJGGCGU..... 19 4 1
UAAACUAUGGUUJGGCGU..... 20 7 1
UAAACUAUGGUUJGGCGU..... 21 83 1
AAACUAUGGUUJGGCGU..... 18 2 1
AAACUAUGGUUJGGCGU..... 19 1 1
AAACUAUGGUUJGGCGU..... 20 12 1
CUAUGGUUJGGCGU..... 15 1 2
UAUGGUUJGGCGU..... 16 1 1

miR-2030
 ACACCCACAGUAUGGCCGUAAGCAUAACAUUGUAAGAGAUUGUAGGAACCUCUUUACAUUGUUGUGC_{GU}U_{GA}CGGAUAUGCUGAAUAGU
 ..(((..(((.((..(((.....)).))).))).))).))....
 Total cloned: 1349 shared 5' end with miRNA: 317 shared 3' end with miRNA: 22
 Scaffold: scaffold_507 Coordinates: 85571-85660 Strand: Minus Location: Intergenic
 miRNA
AAGCAUAACAUUGUAAGAGAUU..... 22 999 1
 Shared 5' Terminus
UAGCAUAACAUGGUUAG..... 17 3 1
UAGCAUAACAUGGUUAGA..... 18 2 1
UAGCAUAACAUGGUUAGAG..... 19 7 1
UAGCAUAACAUGGUUAGAGA..... 20 124 1
UAGCAUAACAUGGUUAGAGAU..... 21 177 1

| | | | | |
|--------------------|---|-------------------------------|------------------------------|--|
| | UAGCAUAAACAUUGUAAGAGAUG..... | 23 | 1 | 1 |
| | UAGCAUAAACAUUGUAAGAGAUGU..... | 24 | 1 | 1 |
| | UAGCAUAAACAUUGUAAGAGAUGUAG..... | 27 | 1 | 1 |
| | UAGCAUAAACAUUGUAAGAGAUGUAGAA..... | 29 | 1 | 1 |
| Shared 3' Terminus |ACAUUGUAAGAGAU..... | 15 | 2 | 1 |
| | AUACAUUGUAAGAGAU..... | 18 | 1 | 1 |
| | CAUACAUUGUAAGAGAU..... | 19 | 1 | 1 |
| | GCAUACAUUGUAAGAGAU..... | 20 | 2 | 1 |
| | AGCAUACAUUGUAAGAGAU..... | 21 | 16 | 1 |
| Subsequence |AGCAUAAACAUUGUAAGAGAU..... | 20 | 5 | 1 |
| Others |CCUCUUUACAUUGUUGUCU..... | 20 | 1 | 1 |
| | CCUCUUUACAUUGUUGUCUGUA..... | 23 | 5 | 1 |
| miR-2031 | AGACCACCUAAA <u>UACGGCACUCUAAUUUUGGUACU</u> UUUAAG <u>UACCAUAAAAGAGUGCCGUAU</u> UUAGGGGUUAA(((((((((.....))))))))))))))))))))))))))))..... | | | |
| Total cloned: | 785 | shared 5' end with miRNA: 253 | shared 3' end with miRNA: 30 | |
| Scaffold: | scaffold_48 | Coordinates: 869416-869493 | Strand: Plus | Location: Intronic; overlapping gene (18) is encoded on same (plus) strand |
| miRNA | <u>UACGGCACUCUAAUUUUGGUACU</u> | 23 | 232 | 2 |
| Shared 5' Terminus |UACGGCACUCUAAUUUAGG..... | 19 | 2 | 2 |
| | UACGGCACUCUAAUUUAGGU..... | 20 | 42 | 2 |
| | UACGGCACUCUAAUUUAGGUA..... | 21 | 106 | 2 |
| | UACGGCACUCUAAUUUAGGUAC..... | 22 | 102 | 2 |
| | UACGGCACUCUAAUUUAGGUACUU..... | 25 | 1 | 1 |
| Shared 3' Terminus |CGGCACUCUAAUUUAGGUACU..... | 21 | 3 | 2 |
| | ACGGCACUCUAAUUUAGGUACU..... | 22 | 27 | 2 |
| Subsequence |ACGGCACUCUAAUUUAGGU..... | 19 | 2 | 2 |
| | ACGGCACUCUAAUUUAGGU..... | 20 | 24 | 2 |
| | ACGGCACUCUAAUUUAGGUAC..... | 21 | 14 | 2 |
| Others |AUACGGCACUCUAAUUUAGGU..... | 21 | 1 | 2 |
| | UACCAUAAAAGAGUGCCG..... | 19 | 37 | 2 |
| | UACCAUAAAAGAGUGCCGU..... | 20 | 11 | 2 |
| | UACCAUAAAAGAGUGCCGU..... | 21 | 12 | 2 |
| | UACCAUAAAAGAGUGCCGU..... | 22 | 110 | 2 |
| | <u>UACCAUAAAAGAGUGCCGUAU</u> | 23 | 9 | 2 |
| | UACCAUAAAAGAGUGCCGUAUU..... | 24 | 1 | 2 |
| | UACCAUAAAAGAGUGCCGUAUU..... | 25 | 1 | 2 |
| | ACCAUAAAAGAGUGCCGU..... | 19 | 4 | 2 |
| | ACCAUAAAAGAGUGCCGU..... | 20 | 2 | 2 |
| | ACCAUAAAAGAGUGCCGU..... | 21 | 29 | 2 |
| | CCAUAAAAGAGUGCCGU..... | 20 | 4 | 2 |
| | CAUAAAAGAGUGCCGU..... | 19 | 3 | 2 |
| | CAUAAAAGAGUGCCGUAU..... | 20 | 3 | 2 |
| | CAUAAAAGAGUGCCGUAU..... | 21 | 1 | 2 |
| | AUAUAUAGAGUGCCG..... | 15 | 1 | 2 |
| | AAUAGAGUGCCGUAU..... | 15 | 1 | 2 |
| miR-2032a | UCGGCAGACUCGGUUGCUG <u>UCGCUGCGACAGUUAGCUAG</u> CAUUUUUGCGAGGUACUGUUGCAGCAUC <u>AUGACUGUGAGGUCAUU</u>((((((.....(((((.....((.....)))))))))))).....(.....)).))..... | | | |
| Total cloned: | 184 | shared 5' end with miRNA: 71 | shared 3' end with miRNA: 0 | |
| Scaffold: | scaffold_161 | Coordinates: 473284-473375 | Strand: Minus | Location: Intergenic; likely part of a miRNA cluster with miR-2032b |
| miRNA | <u>UCGCUGCGACAGUUAGCUAG</u> | 20 | 45 | 1 |
| Shared 5' Terminus |UCGCUGCGACAGUUAGCU..... | 18 | 1 | 1 |
| | UCGCUGCGACAGUUAGCUA..... | 19 | 14 | 1 |
| | UCGCUGCGACAGUUAGCUAGC..... | 21 | 16 | 1 |
| | UCGCUGCGACAGUUAGCUAGCA..... | 22 | 36 | 1 |
| | UCGCUGCGACAGUUAGCUAGCAU..... | 23 | 3 | 1 |
| | UCGCUGCGACAGUUAGCUAGCAUU..... | 24 | 1 | 1 |
| Others |CGAGGUACUGUUGCA..... | 16 | 1 | 3 |
| | CGAGGUACUGUUGCAGC..... | 18 | 2 | 3 |

| | | | |
|------------------------|----|----|---|
| CGAGGUACUGUUJGCAGCA. | 19 | 3 | 3 |
| CGAGGUACUGUJGCAGCAU. | 20 | 7 | 3 |
| CGAGGUACUGUJGCAGCAUC. | 22 | 13 | 3 |
| .GAGGUACUGUJGCAG. | 16 | 1 | 4 |
| .GAGGUACUGUJGCAGCAU. | 19 | 15 | 3 |
| .GAGGUACUGUJGCAGCAUC. | 20 | 1 | 3 |
| .GAGGUACUGUJGCAGCAUCC. | 21 | 16 | 3 |
| .GAGGUACUGUJGCAGCAUCC. | 22 | 1 | 3 |
| .AGGUACUGUJGCAGCAU. | 18 | 4 | 3 |
| .AGGUACUGUJGCAGCAUC. | 19 | 1 | 3 |
| .AGGUACUGUJGCAGCAUCC. | 20 | 2 | 3 |
| .AGGUACUGUJGCAGCAUCCA. | 21 | 1 | 3 |

miR-2032b

GCGAGCUCACCGUUGCG **UCGCUGCAACAGUUAGCUAG** CAUUUAUUGC **G** AGGUACUGUUGCAGCAUCC **A** UGACUGUGAGG
..(((((.(((..(((((.(((((..(((((..((.((.((..)))))).)).))).)))).)).))).))).)))

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 (119389) is encoded on same (minus) strand
miRNA

| | | | |
|----------------------------|----|----|---|
| UCGCUGCAACAGUUAGCUAG. | 20 | 27 | 2 |
| Shared 5' Terminus | | | |
| ..UCGCUGCAACAGUUAGCUA. | 19 | 4 | 2 |
| ..UCGCUGCAACAGUUAGCUAGC. | 21 | 3 | 2 |
| ..UCGCUGCAACAGUUAGCUAGCA. | 22 | 15 | 2 |
| ..UCGCUGCAACAGUUAGCUAGCAU. | 23 | 1 | 2 |
| Shared 3' Terminus | | | |
| ..CGCUGAACAGUUAGCUAG. | 19 | 1 | 2 |
| Subsequence | | | |
| Others | | | |
| ..CGAGGUACUGUJGCAGCA. | 16 | 1 | 3 |
| ..CGAGGUACUGUJGCAGC. | 18 | 2 | 3 |
| ..CGAGGUACUGUJGCAGCA. | 19 | 3 | 3 |
| ..CGAGGUACUGUJGCAGCAU. | 20 | 7 | 3 |
| ..CGAGGUACUGUJGCAGCAUCC. | 22 | 13 | 3 |
| ..GAGGUACUGUJGCAG. | 16 | 1 | 4 |
| ..GAGGUACUGUJGCAGCAU. | 19 | 15 | 3 |
| ..GAGGUACUGUJGCAGCAUC. | 20 | 1 | 3 |
| ..GAGGUACUGUJGCAGCAUCC. | 21 | 16 | 3 |
| ..GAGGUACUGUJGCAGCAUCA. | 22 | 1 | 3 |
| ..AGGUACUGUJGCAGCAU. | 18 | 4 | 3 |
| ..AGGUACUGUJGCAGCAUC. | 19 | 1 | 3 |
| ..AGGUACUGUJGCAGCAUCC. | 20 | 2 | 3 |
| ..AGGUACUGUJGCAGCAUCCA. | 21 | 1 | 3 |

miR-2033

CGACAUAUCUUUCUGACUCUG **AGCUAAUGAUGAGAGAAU** AAACAUUGC **C** UGAUAGACAACUUGAAU **U** CCCUCGUUA **C** UGAAGU **J** CUA **U** GAGCCUCGUCCCCUUCUGCCUU
..((((.(((.(((.(((.(((.(((.((.((.((..((.((..)))))..))).)).))).))).))).))).)))

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 (114611) is encoded on same (plus) strand
miRNA

| | | | |
|------------------------------|----|----|---|
| AGCUAAUGAUGAGAGAAU. | 18 | 15 | 2 |
| Shared 5' Terminus | | | |
| ..AGCUAAUGAUGAGAG. | 15 | 1 | 3 |
| ..AGCUAAUGAUGAGAGA. | 16 | 10 | 2 |
| ..AGCUAAUGAUGAGAGAA. | 17 | 12 | 2 |
| ..AGCUAAUGAUGAGAGAAC. | 19 | 4 | 2 |
| ..AGCUAAUGAUGAGAGAUCA. | 20 | 5 | 2 |
| ..AGCUAAUGAUGAGAGAAUCA. | 21 | 7 | 2 |
| ..AGCUAAUGAUGAGAGAAUCAA. | 22 | 12 | 2 |
| ..AGCUAAUGAUGAGAGAAUCAAC. | 23 | 3 | 2 |
| ..AGCUAAUGAUGAGAGAAUCAACCA. | 24 | 1 | 2 |
| ..AGCUAAUGAUGAGAGAAUCAAACAU. | 26 | 4 | 2 |
| Shared 3' Terminus | | | |
| ..GCUAAUGAUGAGAGAAU. | 17 | 4 | 2 |
| ..GAGCUAAUGAUGAGAGAAU. | 19 | 1 | 2 |
| Subsequence | | | |
| ..GCUAAUGAUGAGAGA. | 15 | 4 | 2 |
| ..GCUAAUGAUGAGAGAA. | 16 | 4 | 2 |
| Others | | | |
| ..GAGCUAAUGAUGAGAG. | 16 | 1 | 2 |
| ..GAGCUAAUGAUGAGAGA. | 17 | 2 | 2 |

| | | | |
|-------------------------------------|----|---|---|
| GAGCUUAUGAUGAGAGAA.. | 18 | 1 | 2 |
| GAGCUUAUGAUGAGAACU.. | 20 | 2 | 2 |
| ..GCUAAUGAUGAGAACU.. | 18 | 6 | 2 |
| ..GCUAAUGAUGAGAGAAU.. | 19 | 1 | 2 |
| ..GCUAAUGAUGAGAGAAC.. | 21 | 2 | 2 |
| ..GCUAAUGAUGAGAACAA.. | 22 | 2 | 2 |
| ..GCUAAUGAUGAGAACAAAC.. | 23 | 1 | 2 |
| ..GCUAAUGAUGAGAACAAAC.. | 24 | 1 | 2 |
| ..GCUAAUGAUGAGAACAAAC.. | 25 | 3 | 2 |
| ..GCUAAUGAUGAGAACAAACU.. | 27 | 1 | 2 |
|UUGCCUGAU AUGCUAAAUGUAGACAUC.. | 28 | 1 | 1 |
|GCCUGAU AUGCUAAAUGUAGACAACU.. | 25 | 1 | 1 |
|CUAAAUGAGACAAUCU.. | 17 | 1 | 1 |
|AAUGUAGACAAUCUUGAAUUC.. | 22 | 1 | 1 |
|AAUCUUGAAUUCUCGUUUACUGAAGUUC.. | 28 | 1 | 1 |
|AUCUUAUUCUCUCGUUUACUGAAGUJU.. | 26 | 2 | 1 |
|CUUGAAUUCUCGUUUACUGAAGUJU.. | 24 | 3 | 1 |
|CUUGAAUUCUCGUUUACUGAAGUUC.. | 25 | 1 | 1 |
|UGAAAUUCCUCGUUUACUGAAGU.. | 23 | 1 | 1 |
|UGAAAUUCCUCGUUUACUGAAGUUC.. | 24 | 1 | 1 |
|UGAAAUUCCUCGUUUACUGAAGUCA.. | 25 | 1 | 1 |
|UGAAAUUCCUCGUUUACUGAAGU.. | 19 | 1 | 2 |
|UGAAAUUCCUCGUUUACUGAAGUUC.. | 23 | 2 | 1 |
|UGAAAUUCCUCGUUUACUGAAGUJCA.. | 24 | 3 | 1 |
|GAAUUCCUCGUUUACUGAAGU.. | 21 | 1 | 1 |
|GAAUUCCUCGUUUACUGAAGUUC.. | 22 | 2 | 1 |
|AAUUCUCGUUUACUGAAGU.. | 19 | 1 | 1 |
|AAUCCUCGUUUACUGAAGU.. | 19 | 5 | 1 |
|AAUCCUCGUUUACUGAAGUCA.. | 21 | 2 | 1 |
|UUCCUCGUUUACUGAAGU.. | 18 | 4 | 1 |
|UUCCUCGUUUACUGAAGUJC.. | 19 | 1 | 1 |
|UCCUCGUUUACUGAAGUCA.. | 19 | 1 | 1 |
|CCUCGUUACUGAAGUUC.. | 17 | 2 | 1 |
|CUCGUUACUGAAGU.. | 15 | 2 | 2 |
|CUCGUUACUGAAGUCA.. | 16 | 2 | 2 |
|CUCGUUACUGAAGUCA.. | 17 | 1 | 1 |

miR-2034
 GUGAAAAGAGUGUAGUUUUACUGAUGUUUUUAGAAUUAAGCCCCCUAAAUGAAGGGCUAAUGCAAAAAAUGUCAGUGCAA AUGCAUGAA CUUACAA
 (((.....(((((((.....(((((.....)))))))))))..))))....))..

Total cloned: 138 shared 5' end with miRNA: 69 shared 3' end with miRNA: 1
 Scaffold: scaffold_4 Coordinates: 1299750-1299846 Strand: Minus Location: Intergenic
 miRNA

| | | | |
|---|----|----|---|
| <u>GCUAUAGCAAAAAAUGUCAGU</u> | 21 | 59 | 1 |
| Shared 5' Terminus | | | |
| <u>GCUAUAGCAAAAAAUGUCA</u> | 19 | 4 | 1 |
| <u>GCUAUAGCAAAAAAUGUCAG</u> | 20 | 34 | 1 |
| <u>GCUAUAGCAAAAAAUGUCAGUG</u> | 22 | 31 | 1 |
| Shared 3' Terminus | | | |
|CUAAUGCAAAAAAUGUCAGU..... | 20 | 1 | 1 |
| Subsequence | | | |
| Others | | | |
|CUGAUGUUUUUAGAAUUAAG.. | 19 | 2 | 1 |
|CUGAUGUUUUUAGAAUUAAGCC.. | 21 | 1 | 1 |
| <u>CUGAUGUUUUUAGAAUAGCCC</u> | 22 | 2 | 1 |
|UGAUGUUUUUAGAAUUAAG.. | 18 | 3 | 1 |
|UAAUGCAAAAAAUGUCAGUG..... | 20 | 1 | 1 |

miR-2035
 GUGGGUUAUUACAUGGUCUGUUACAAGGGAUGAAGUGCUCGAGUUUCGAGUUCCCUUUGUGACAGCCCAUGGGAGAAU
((.....(((((.....(((((.....)))))))))))..))..

Total cloned: 132 shared 5' end with miRNA: 44 shared 3' end with miRNA: 3
 Scaffold: scaffold_153 Coordinates: 549189-549267 Strand: Plus Location: Intergenic
 miRNA

| | | | |
|---|----|----|---|
| <u>ACAUGGUCUGUUACAAGGGA</u> | 20 | 37 | 2 |
| Shared 5' Terminus | | | |
|ACAUGGUCUGUUACAAG.. | 17 | 1 | 2 |
|ACAUGGUCUGUUACAAGG.. | 18 | 6 | 2 |
|ACAUGGUCUGUUACAAGGG.. | 19 | 6 | 2 |
|ACAUGGUCUGUUACAAGGGAU.. | 21 | 29 | 2 |
|ACAUGGUCUGUUACAAGGGGAUG.. | 22 | 1 | 2 |
|ACAUGGUCUGUUACAAGGGGAAG.. | 25 | 1 | 2 |

| | | | | |
|--|---|------------------------------|-----------------------------|--|
| Shared 3' Terminus |UGGUCUGUUACAAGGGAA..... | 17 | 2 | 2 |
| |CAUGGUCUGUUACAAGGGAA..... | 19 | 1 | 2 |
| Subsequence | | | | |
| Others |CAUGGUCUGUUACAAGGGAA..... | 20 | 1 | 2 |
| |UCGUUACAAAGGAUAGA..... | 17 | 1 | 2 |
| |UCGUUACAAAGGAUAGUGC..... | 23 | 1 | 2 |
| |UCCCCUUGUACAGCCCAUUGGG..... | 23 | 1 | 2 |
| |UCCCCUUGUACAGCCCAU..... | 18 | 4 | 2 |
| |UCCCCUUGUACAGCCCAU..... | 19 | 1 | 2 |
| |UCCCCUUGUACAGCCCAU..... | 20 | 1 | 2 |
| |UCCCCUUGUACAGCCCAU..... | 22 | 5 | 2 |
| |CCUUGUACAGCCCAU..... | 17 | 3 | 2 |
| |CCUUGUACAGCCCAU..... | 18 | 9 | 2 |
| |CCUUGUACAGCCCAU..... | 19 | 5 | 2 |
| |CCUUGUACAGCCCAU..... | 20 | 12 | 2 |
| |CCUUGUACAGCCCAU..... | 21 | 1 | 2 |
| |CCUUGUACAGCCCAU..... | 19 | 3 | 2 |
| mir-2036 | | | | |
| UAAGAGAGUCGUGCCAGGACC <ins>CGGUGAGAACGUACGUACGUAGCA</ins> CUUGACGAUG <ins>UAUAUJUGUACGACUCUCAUCGU</ins> AUCCUGCACGGCAAUGAACA |(((((((.....((((((.....((.....)))).....)))).....)))).....))))..... | | | |
| Total cloned: | 117 | shared 5' end with miRNA: 47 | shared 3' end with miRNA: 3 | |
| Scaffold: | scaffold_24 | Coordinates: 1097560-1097654 | Strand: Minus | Location: Intergenic |
| miRNA |UUAUJUGUACGACUCUCAUCGU..... | 23 | 51 | 1 |
| Shared 5' Terminus | | | | |
| |UUAUJUGUACGACUCUCA..... | 18 | 10 | 1 |
| |UUAUJUGUACGACUCUCAU..... | 19 | 9 | 1 |
| |UUAUJUGUACGACUCUCAU..... | 20 | 8 | 1 |
| |UUAUJUGUACGACUCUCAUCG..... | 21 | 3 | 1 |
| |UUAUJUGUACGACUCUCAUCG..... | 22 | 11 | 1 |
| |UUAUJUGUACGACUCUCAUCGU..... | 24 | 6 | 1 |
| Shared 3' Terminus | | | | |
| |UAUJUGUACGACUCUCAUCGU..... | 21 | 1 | 1 |
| |UAUJUGUACGACUCUCAUCGU..... | 22 | 2 | 1 |
| Subsequence | | | | |
| |UAUJUGUACGACUCUCAU..... | 17 | 1 | 1 |
| |UAUJUGUACGACUCUCAUCGU..... | 20 | 1 | 1 |
| Others | | | | |
| |CGGUGAGAACGUACGUAGC..... | 21 | 3 | 1 |
| | <ins>CGGUGAGAACGUACGUAGCA</ins> | 22 | 11 | 1 |
| mir-2037 | | | | |
| AGCUAGGUUCUUGGUACCGUG <ins>GUAAAAGCGUCCAAGCACCCUUCUUGGCAGUGUGAUJUGGAGACUUUUACGU</ins> GGUCUGAGAACGUACAUAC |(((((((.....((((((.....((.....)))).....)))).....)))).....))))..... | | | |
| Total cloned: | 116 | shared 5' end with miRNA: 21 | shared 3' end with miRNA: 4 | |
| Scaffold: | scaffold_433 | Coordinates: 29618-29710 | Strand: Plus | Location: Intergenic |
| miRNA |UGUGAUJUGGAGACUUUUACGU..... | 22 | 86 | 1 |
| Shared 5' Terminus | | | | |
| |UGUGAUJUGGAGACUUU..... | 16 | 1 | 1 |
| |UGUGAUJUGGAGACUUU..... | 17 | 1 | 1 |
| |UGUGAUJUGGAGACUUU..... | 18 | 3 | 1 |
| |UGUGAUJUGGAGACUUUAC..... | 19 | 4 | 1 |
| |UGUGAUJUGGAGACUUUAC..... | 20 | 2 | 1 |
| |UGUGAUJUGGAGACUUUACCG..... | 21 | 10 | 1 |
| Shared 3' Terminus | | | | |
| |GUGAUJUGGAGACUUUUACGU..... | 21 | 4 | 1 |
| Others | | | | |
| |GGUAAAAGCCGUCCAAGCA..... | 19 | 1 | 1 |
| |GGUAAAAGCCGUCCAAGCCU..... | 23 | 2 | 1 |
| | <ins>UAAAAGCCGUCCAAGCAC</ins> | 19 | 2 | 1 |
| mir-2038 | | | | |
| AACCUUGAGGCCUUAGUGUC <ins>ACCCUGAUGACCUUAGUGUACCCUGAUGACCUUAAUGUCACCAUGAUGA</ins> CCUUAGUGUCACCCUGAUGA |((((.....((((.....((.....)))).....)))).....))))..... | | | |
| Total cloned: | 116 | shared 5' end with miRNA: 52 | shared 3' end with miRNA: 1 | |
| Scaffold: | scaffold_3 | Coordinates: 358418-358509 | Strand: Plus | Location: Intronic; overlapping gene (238021) is encoded on same (plus) strand |
| miRNA | <ins>ACCUUAUGUCACCAUGAUGA</ins> | 21 | 36 | 2 |

| | | | | |
|---|---|--|----|---|
| Shared 5' Terminus |ACCUUAUGUCACCAUGAU..... | 19 | 8 | 2 |
| |ACCUUAUGUCACCAUGAUG..... | 20 | 8 | 2 |
| |ACCUUAUGUCACCAUGAUGAC..... | 22 | 35 | 2 |
| |ACCUUAUGUCACCAUGAUGACC..... | 23 | 1 | 2 |
| Shared 3' Terminus |CCUUAUGUCACCAUGAUGA..... | 20 | 1 | 2 |
| Subsequence | | | | |
| Others |CACCCUGAUGACCACUAGUG..... | 19 | 2 | 6 |
| |CACCCUGAUGACCACUAGUG..... | 19 | 2 | 6 |
| |CACCCUGAUGACCACUAGUG..... | 20 | 3 | 6 |
| |CACCCUGAUGACCACUAGUG..... | 20 | 3 | 6 |
| |CACCCUGAUGACCACUAGUG..... | 22 | 2 | 6 |
| |CACCCUGAUGACCACUAGUGA..... | 22 | 2 | 6 |
| |ACCCUGAUGACCACUAGUGU..... | 19 | 5 | 6 |
| |ACCCUGAUGACCACUAGUGU..... | 19 | 5 | 6 |
| |ACCCUGAUGACCACUAGUGUCA..... | 21 | 1 | 6 |
| |ACCCUGAUGACCACUAGUGUCA..... | 21 | 1 | 6 |
| |CCUUAUGUCACCAUGAUGAC..... | 21 | 1 | 2 |
| miR-2039 | | | | |
| UUGUAUA <ins>AGCCUACCUUUUUUUUUUUUUAAUUGUAA</ins> AUAAAUAAGGUAGGCUCUAA |((((((((.....))))))))..... | | | |
| 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 |AUAAAUAAGGUAGGCUCU..... | 20 | 43 | 1 |
| Shared 5' Terminus |AUAAAUAAGGUAGGCUCU..... | 18 | 9 | 2 |
| |AUAAAUAAGGUAGGCUCU..... | 19 | 4 | 1 |
| |AUAAAUAAGGUAGGCUCU..... | 21 | 7 | 1 |
| |AUAAAUAAGGUAGGCUCU..... | 22 | 13 | 1 |
| Shared 3' Terminus |AAAUAUAAGGUAGGCUCU..... | 22 | 1 | 1 |
| Subsequence | | | | |
| Others |UAAGCCUACCUUUUUUUUUU..... | 21 | 1 | 1 |
| |UAAGCCUACCUUUUUUUUUU..... | 22 | 1 | 1 |
| |UAAGCCUACCUUUUUUUUUU..... | 23 | 1 | 1 |
| |AAGCCUACCUUUUUUUUUU..... | 21 | 2 | 1 |
| |AAGCCUACCUUUUUUUUUU..... | 22 | 1 | 1 |
| |AGCCUACCUUUUUUUUUU..... | 20 | 1 | 2 |
| |AAAUAUAAGGUAGGCUC..... | 21 | 1 | 1 |
| miR-2040a | | | | |
| GAUCGUGAUGCCUACACCUUCGGGUACGUACUGAGCGCUCCUCGUUJUGUCGUACUGCCCCUGAAGGUAGGUCCUGCGCUCUUAC |((((((.....((((((.....((.....))))....))))....))))....))))..... | | | |
| 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 |UUUGUCUCGUAAACUGCCCCUGAAG..... | 23 | 39 | 2 |
| Shared 5' Terminus |UUUGUCUCGUAAACUGCCCCUGA..... | 21 | 1 | 2 |
| |UUUGUCUCGUAAACUGCCCCUGA..... | 22 | 4 | 2 |
| Shared 3' Terminus |UGUCUCGUAAACUGCCCCUGAAG..... | 21 | 3 | 2 |
| |UGUCUCGUAAACUGCCCCUGAAG..... | 22 | 1 | 2 |
| |CUCCUCGUUJUGUCGUAAACUGCCCCUGAAG..... | 30 | 1 | 2 |
| Subsequence | | | | |
| Others |UGUCUCGUAAACUGCCCC..... | 17 | 1 | 2 |
| |UGUCUCGUAAACUGCCCC..... | 19 | 3 | 2 |
| |UGUCUCGUAAACUGCCCC..... | 20 | 8 | 2 |
| |UCGGGUACGUACGACAU..... | 18 | 1 | 2 |
| |UCGGGUACGUACGACAU..... | 20 | 3 | 2 |
| |UCGGGUACGUACGACAU..... | 21 | 8 | 2 |
| |UCGGGUACGUACGACAU..... | 22 | 1 | 2 |
| |UCGGGUACGUACGACAU..... | 23 | 1 | 2 |

miR-2040b
 AGAUCAUAGAUACCACCUUCAGGUACGUACGACGAGCGCUCCUCGUUCGUACUACUGCCCCUGAAGGGGUCCUGGCUCUUUA
((.....(((((((((.....((.....))))....))))....)))).....)).....
 Total cloned: 71 shared 5' end with miRNA: 14 shared 3' end with miRNA: 2
 Scaffold: scaffold_82 Coordinates: 49686-49778 Strand: Plus Location: Intergenic
 miRNA
UUCGUCUCGUACUGCCCCUGAAG..... 23 27 2
 Shared 5' TerminusUUCGUCUCGUACUGCCCC........ 19 3 2
UUCGUCUCGUACUGCCCC........ 22 11 2
 Shared 3' TerminusUCGUCUCGUACUGCCCCUGAAG..... 22 2 2
 Subsequence
 OthersUUCAGGUACGUACGACACGA..... 21 2 2
UUCAGGUACGUACGACACGAC..... 23 10 2
UCAGGUACGUACGACACGA..... 20 1 2
UCAGGUACGUACGACACGAG..... 21 3 2
UCAGGUACGUACGACACGGAC..... 22 4 2
UCAGGUACGUACGACACGGCG..... 23 1 2
CAGGUACGUACGACACGGAG..... 20 1 2
CAGGUACGUACGACACGGAC..... 21 2 2
CAGGUACGUACGACACGGCG..... 22 1 2
AGGUACGUACGACACGAGC..... 20 1 2
UCGUCUCGUACUGCCCCUGAAGG..... 23 2 2

miR-2041
 AUUCUCGAAACCCAGGGUAUUUUCUUCUACGUUUCACGUCCAGAGUAAAAGUAGAGCAAAACUCCUGGGUUUCGAGGAUAG
 ((((((.....((((((.....((.....))))....))))....))))....)))).....
 Total cloned: 72 shared 5' end with miRNA: 0 shared 3' end with miRNA: 7
 Scaffold: scaffold_19 Coordinates: 418368-418456 Strand: Minus Location: Intergenic
 miRNA
UGAACGUUAGAGCAAAUACU..... 22 57 2
 Shared 3' TerminusGAAACGUUAGAGCAAAUACU..... 21 7 2
 OthersAUUUUGCUCUUACGUUUCA..... 19 4 1
AUUUUGCUCUUACGUUUACACU..... 21 4 1

miR-2042
 UUUACAAUGACGACACCCCUUAUAAAUCAUCCUUGCACUACUUAGUCGUACAUUUGAAGUAGUAAAUGAAGGUUGUUCCUGACUCGC
((.....((.....((.....((.....))))....)))).....)).....
 Total cloned: 72 shared 5' end with miRNA: 4 shared 3' end with miRNA: 0
 Scaffold: scaffold_231 Coordinates: 5525-5613 Strand: Minus Location: Intergenic; likely part of a miRNA cluster with miR-2043
 miRNA
UUAUAAAUCAUCCUUGCACAC..... 22 24 1
 Shared 5' TerminusUUAUAAAUCAUCCUUGCACACU..... 23 4 1
 Shared 3' TerminusCGUACAUUGAUGAUUUUAUGA..... 20 5 1
 Subsequence
 OthersCGUACAUUGAUGAUUUUAUGAA..... 21 20 1
CGUACAUUGAUGAUUUUAUGAAG..... 22 19 1

miR-2043
 AUGUACGGCCGCCUAGAAAAUAGAAAAGCUUCCGGUUUUUUGACAUCCAAUACCGGAGGUUUUUUGUGUCCAUUUCGUGACCAGAAUC
((..(.....((((((.....((.....))))....))))....)))).....)
 Total cloned: 10 shared 5' end with miRNA: 5 shared 3' end with miRNA: 0
 Scaffold: scaffold_231 Coordinates: 5179-5273 Strand: Minus Location: Intergenic; likely part of a miRNA cluster with miR-2042
 miRNA
UACCGGAGGUUUUUCUGUG..... 19 3 1
 Shared 5' TerminusUACCGGAGGUUUUUCUGUG..... 20 3 1
UACCGGAGGUUUUUCUGUG..... 22 2 1
 OthersAAAAGAAAAGCUUCCGGUUUU..... 22 1 1
AAUAGAAAAGCUUCCGGUUUU..... 20 1 1

miR-2044a
GUACUGAUUCGAAUCUCUUAUAUCGCCUUUJAGGUUAUUUCUUA**UGCCCUAAAAGACGGUAUAG**AGAUUACACAGCUGGACA
((...(((.....((((((.((((((.((((((.((.((....))))))))))))))))))))....)).
Total cloned: 13 shared 5' end with miRNA: 4 shared 3' end with miRNA: 0
Scaffold: scaffold_14 Coordinates: 1321782-1321871 Strand: Plus Location: Intergenic; likely part of a miRNA cluster with miR-2044b;
miRNA
Shared 5' Terminus **UGCCCUAAAAGACGGUAUAG** 22 6 1
..... UGCCCUAAAAGACGGUAU 19 1 1
..... UGCCCUAAAAGACGGUAU 20 1 1
..... UGCCCUAAAAGACGGUAU 21 2 1
Others **UAUAUCGCCUUUJAGGUUA** 20 2 3
..... **UAUAUCGCCUUUJAGGUUAU** 22 1 3

miR-2044b
GUACUGAUUCGAAUCUCUUAUAUCGCCUUUJAGGUUAUUUCUUA**ACCCUAAAAGACGGUAUAG**AGAUUACACAGCUGGACA
((...(((.....((((((.((((((.((((((.((.((....))))))))))))))))))))....)).
Total cloned: 69 shared 5' end with miRNA: 16 shared 3' end with miRNA: 0
Scaffold: scaffold_14 Coordinates: 1324935-1325024 Strand: Plus Location: Exonic; likely part of a miRNA cluster with miR-2044a;
overlapping gene (199356) is encoded on same (plus) strand
miRNA
Shared 5' Terminus **ACCCUAAAAGACGGUAUAG** 22 50 2
..... UACCCUAAAAGACCGUA 18 1 2
..... UACCCUAAAAGACGGUAU 19 4 2
..... UACCCUAAAAGACCGGUU 20 4 2
..... UACCCUAAAAGACGGUUA 21 7 2
Others **UAUAUCGCCUUUJAGGUUA** 20 2 3
..... **UAUAUCGCCUUUJAGGUUAU** 22 1 3

miR-2045
AGGUUGAUGAGCUUAUAAGAUAAAUGCCAUAAUGUUUUUAUGGCAUUUAUCUUGAUAA**AG**CUCAUUGGUACCA
((...((((((.((((((.((((((.((.((....))))))))))))))))....)).
Total cloned: 46 shared 5' end with miRNA: 5 shared 3' end with miRNA: 1
Scaffold: scaffold_23 Coordinates: 707879-707957 Strand: Minus Location: Intronic; overlapping gene (200699) is encoded on same (minus) strand
miRNA
Shared 5' Terminus **UAUGGCAUUUAUCUUGAUAA** 22 14 3
..... UAUGGCAUUUAUCUUGUA 20 2 3
..... UAUGGCAUUUAUCUUGAUAA 21 2 3
..... UAUGGCAUUUAUCUUGAUAAAGC 24 1 3
Shared 3' Terminus **UAUGGCAUUUAUCUUGAUAA** 23 1 3
Others **UUUAUCAAGAUAAAUGCCAUA** 21 3 3
..... **UUUAUCAAGAUAAAUGCCAUA** 22 10 3
..... **UUUAUCAAGAUAAAUGCCAUA** 20 1 3
..... **UUUAUCAAGAUAAAUGCCAUA** 21 3 3
..... **UUUAUCAAGAUAAAUGCCAUA** 22 8 3
..... **UUUAUCAAGAUAAAUGCCAUA** 23 1 3

miR-2046
UCUUAUAAAUGACAAUAGUUUCCCAGAGUGUUGAGUCAUACAAGAUUUCUUGGUUU**GUAGGUAAAUCUCUGGUAC**UAGAUUCCAAAUA
((...(((.....((((((.((((((.((.((....))))))))))))....)).
Total cloned: 41 shared 5' end with miRNA: 11 shared 3' end with miRNA: 2
Scaffold: scaffold_43 Coordinates: 185998-186099 Strand: Plus Location: Intronic; overlapping gene (163685) is encoded on same (plus) strand
miRNA
Shared 5' Terminus **UCCCAGAGUGUUGAGUCAUACAA** 24 21 1
..... UCCCAGAGUGUUGAGUCAU 20 2 1
..... UCCCAGAGUGUUGAGUCAU 21 1 1
..... UCCCAGAGUGUUGAGUCAUAC 22 3 1
..... UCCCAGAGUGUUGAGUCAUACAA 23 3 1
..... UCCCAGAGUGUUGAGUCAUACAG 25 2 1
Shared 3' Terminus **GGUUGAGUCAUACAA** 17 1 2
..... **UUCCCAGAGUGUUGAGUCAUACAA** 25 1 1
Subsequence **CCCAGAGUGUUGAGUCAUACAA** 22 1 1
Others

| | | | | |
|---|---|----|----|---|
| | .GUAGGUUAUUAAUCUCUGGUA..... | 22 | 1 | 1 |
| | .GUAU <u>GGUAAUUAAUCUCUGGUA</u> CA..... | 24 | 1 | 1 |
| |UAUGGUAUUJAACUUCUGG..... | 19 | 1 | 1 |
| |UAUGGUAAUUAAUCUCUGGUA..... | 21 | 2 | 1 |
| |AUGGUAAUUAAUCUCUGGUA..... | 20 | 1 | 1 |
| mir-2047 | | | | |
| AGAGUAAA UUUUU AUGGCAUUA CAUCACUUCAUAGCUA JUUUACU <u>C</u> UUAAG <u>G</u> UAUUU <u>A</u> GCUA <u>U</u> GA <u>A</u> U <u>C</u> ACAUAAA UUU U <u>G</u> AC | | | | |
|(((((.....(((((((.....))))))))))((.....))))))..... | | | | |
| Total cloned: 36 shared 5' end with miRNA: 10 shared 3' end with miRNA: 1 | | | | |
| Scaffold: scaffold_261 Coordinates: 230224-230315 Strand: Plus Location: Intergenic | | | | |
| miRNA | | | | |
| CAUCACUUCAUAGCUA UUUUACUCU..... | | 24 | 11 | 1 |
| Shared 5' Terminus |CAUCACUUCAUAGCUA <u>U</u> UAC..... | 21 | 1 | 1 |
| | CAUCACUUCAUAGCUA UUUUACU..... | 22 | 4 | 1 |
| |CAUCACUUCAUAGCUA <u>U</u> UAC..... | 23 | 5 | 1 |
| Shared 3' Terminus |ACUUCAUAGCUA <u>U</u> UACU..... | 20 | 1 | 2 |
| Others |ACA <u>CACUUCAUAGCUA</u> UUAC..... | 22 | 2 | 1 |
| |ACA <u>CACUUCAUAGCUA</u> UUUAC..... | 23 | 1 | 1 |
| |UAAA <u>UAGCUA</u> UAG <u>GU</u> A <u>U</u> CA..... | 22 | 6 | 1 |
| |UAAA <u>UAGCUA</u> UAG <u>GU</u> G <u>U</u> A <u>U</u> CAA..... | 23 | 2 | 1 |
| |UAAA <u>UAGCUA</u> UAG <u>GU</u> G <u>U</u> A <u>U</u> CAA..... | 24 | 3 | 1 |
| mir-2048 | | | | |
| AUCCGGAGUAAUUCGUACUCU <u>A</u> UUCGCGAGCAG <u>GU</u> AC <u>U</u> C <u>U</u> CG <u>G</u> GA <u>A</u> U <u>G</u> ACAGGUUUU <u>G</u> ACCAAGA | | | | |
|((.((.....(((((.....((((((.....((.((.....))))))))))))))).....((.....))))....)) | | | | |
| Total cloned: 29 shared 5' end with miRNA: 11 shared 3' end with miRNA: 0 | | | | |
| Scaffold: scaffold_3670 Coordinates: 1175-1277 Strand: Plus Location: Intergenic | | | | |
| miRNA | | | | |
|UUCGCCGAGCAG <u>AUGU</u> CGGAGA..... | | 22 | 5 | 2 |
| Shared 5' Terminus |UUCGCCGAGCAG <u>A</u> GU..... | 16 | 1 | 4 |
| |UUCGCCGAGCAG <u>A</u> GU <u>G</u> C..... | 18 | 3 | 3 |
| |UUCGCCGAGCAG <u>A</u> GU <u>G</u> C <u>G</u> | 19 | 4 | 3 |
| |UUCGCCGAGCAG <u>A</u> GU <u>G</u> C <u>G</u> G..... | 21 | 3 | 2 |
| Others |UCGCCGAGCAG <u>A</u> GU <u>G</u> CGAG..... | 22 | 1 | 2 |
| |GUCAGACAU <u>C</u> UGC <u>C</u> UC <u>G</u> CGAA..... | 21 | 1 | 1 |
| |GUCAGACAU <u>C</u> UGC <u>C</u> UC <u>G</u> CG <u>A</u> U..... | 22 | 2 | 1 |
| |UCA <u>GACAU</u> C <u>C</u> UC <u>G</u> CGCA..... | 19 | 2 | 1 |
| |UCA <u>GACAU</u> C <u>C</u> UC <u>G</u> CG <u>CA</u> | 20 | 3 | 1 |
| |UCA <u>GACAU</u> C <u>C</u> UC <u>G</u> CG <u>CA</u> U..... | 21 | 1 | 1 |
| |UCA <u>GACAU</u> C <u>C</u> UC <u>G</u> CG <u>CA</u> U..... | 22 | 2 | 1 |
| mir-2049 | | | | |
| GUAAAAG GG GUUUU GUUUU AGAGCUU <u>G</u> AGGGAGAACAGUG <u>G</u> AGAAAG <u>G</u> U <u>C</u> CCU <u>A</u> AG <u>A</u> C <u>AC</u> CU <u>G</u> AA <u>A</u> AC <u>AA</u> AC <u>G</u> CA <u>U</u> A | | | | |
|((.((.....(((((.....((.((.....)))))))).....((.....)))).....)).....)) | | | | |
| Total cloned: 25 shared 5' end with miRNA: 1 shared 3' end with miRNA: 0 | | | | |
| Scaffold: scaffold_26 Coordinates: 921450-921535 Strand: Plus Location: Intergenic | | | | |
| miRNA | | | | |
|ACACCU <u>G</u> AA <u>A</u> AC <u>AA</u> AC <u>G</u> C <u>AA</u> | | 20 | 19 | 1 |
| Shared 5' Terminus |ACACCU <u>G</u> AA <u>A</u> AC <u>AA</u> AC <u>G</u> C <u>AA</u> | 21 | 1 | 1 |
| Others |GGGUUUU GUUUU AGAGCUU..... | 19 | 1 | 1 |
| |GGGUUUU GUUUU AGAGCUU..... | 21 | 1 | 1 |
| |UCUCCC <u>C</u> UAGAC <u>AC</u> CU <u>G</u> AA..... | 21 | 2 | 1 |
| |CACC <u>U</u> GA <u>A</u> AC <u>AA</u> AC <u>G</u> C <u>AA</u> | 20 | 1 | 1 |
| mir-2050 | | | | |
| AUCAUCCAU <u>G</u> AG <u>C</u> GU <u>U</u> U <u>C</u> AA <u>G</u> CAAA <u>G</u> CA <u>C</u> AA <u>U</u> GA <u>A</u> GA <u>U</u> GA <u>A</u> AC <u>G</u> CU <u>U</u> CG <u>U</u> GU <u>A</u> | | | | |
|((.((.((.((.((.((.((.((.....((.((.....)))))))))))).....)).....)))).....)).....))..... | | | | |
| Total cloned: 22 shared 5' end with miRNA: 6 shared 3' end with miRNA: 3 | | | | |
| Scaffold: scaffold_7 Coordinates: 126992-127092 Strand: Minus Location: Intergenic | | | | |
| miRNA | | | | |
|C AA U <u>G</u> C <u>A</u> C <u>G</u> CAA <u>A</u> U <u>G</u> GA <u>A</u> GA..... | | 23 | 8 | 3 |
| Shared 5' Terminus |C AA U <u>G</u> C <u>A</u> C <u>G</u> CAA <u>A</u> U <u>G</u> GA..... | 20 | 3 | 5 |
| |C AA U <u>G</u> C <u>A</u> C <u>G</u> CAA <u>A</u> U <u>G</u> GA <u>A</u> | 21 | 2 | 3 |

| | | | | | |
|--------------------|--|---------------------------|--|---------------------------|------------|
| | CAAAUGCACGCAAAGAAGAUG..... | 22 | 1 | 3 | |
| Shared 3' Terminus |UGCACGCAAAGAAGAUGA..... | 19 | 3 | 3 | |
| Subsequence |AAAUGCACGCAAAGAAGA..... | 19 | 1 | 6 | |
| Others |GAUCUCAUGUGCAUGCAUUUACA..... | 22 | 2 | 1 | |
| |CAUGUGCAUGCAUUUACA..... | 18 | 1 | 2 | |
| |UGAAAUACGUCUCAUGGAU | 19 | 1 | 4 | |
| miR-2051 | GUCAUUUCAUGGCGCGAGAA | CCGGGUCCCCAGUCAUAAACGU | CAUUGCACAUUUGAUUGCUGUGAUCUGGUUUCCGUGUCGAUGUAAC | | |
| |(((((.....((.((((((.((((((.((.....)).))))))).))))).)))))).))))..... | | | | |
| Total cloned: | 21 | shared 5' end with miRNA: | 7 | shared 3' end with miRNA: | 1 |
| Scaffold: | scaffold_13 | Coordinates: | 1048108-1048200 | Strand: | Plus |
| mirNA | | | | Location: | Intergenic |
| | AUUUGAUUGCUGUGAUCUGGUU..... | 23 | 8 | 1 | |
| Shared 5' Terminus |AUUUGAUUGCUGUGAUCUG..... | 19 | 6 | 1 | |
| |AUUUGAUUGCUGUGAUCUGG..... | 20 | 1 | 1 | |
| Shared 3' Terminus |UUUGAUUGCUGUGAUCUGGUU..... | 22 | 1 | 1 | |
| Subsequence |UUUGAUUGCUGUGAUCUGG..... | 19 | 1 | 1 | |
| |UUUGAUUGCUGUGAUCUGGUU..... | 21 | 1 | 1 | |
| Others |CCGGGUCCCCAGUCAUAAAC..... | 21 | 1 | 1 | |
| |CCGGGUCCCCAGUCAUAAACGU..... | 23 | 2 | 1 | |