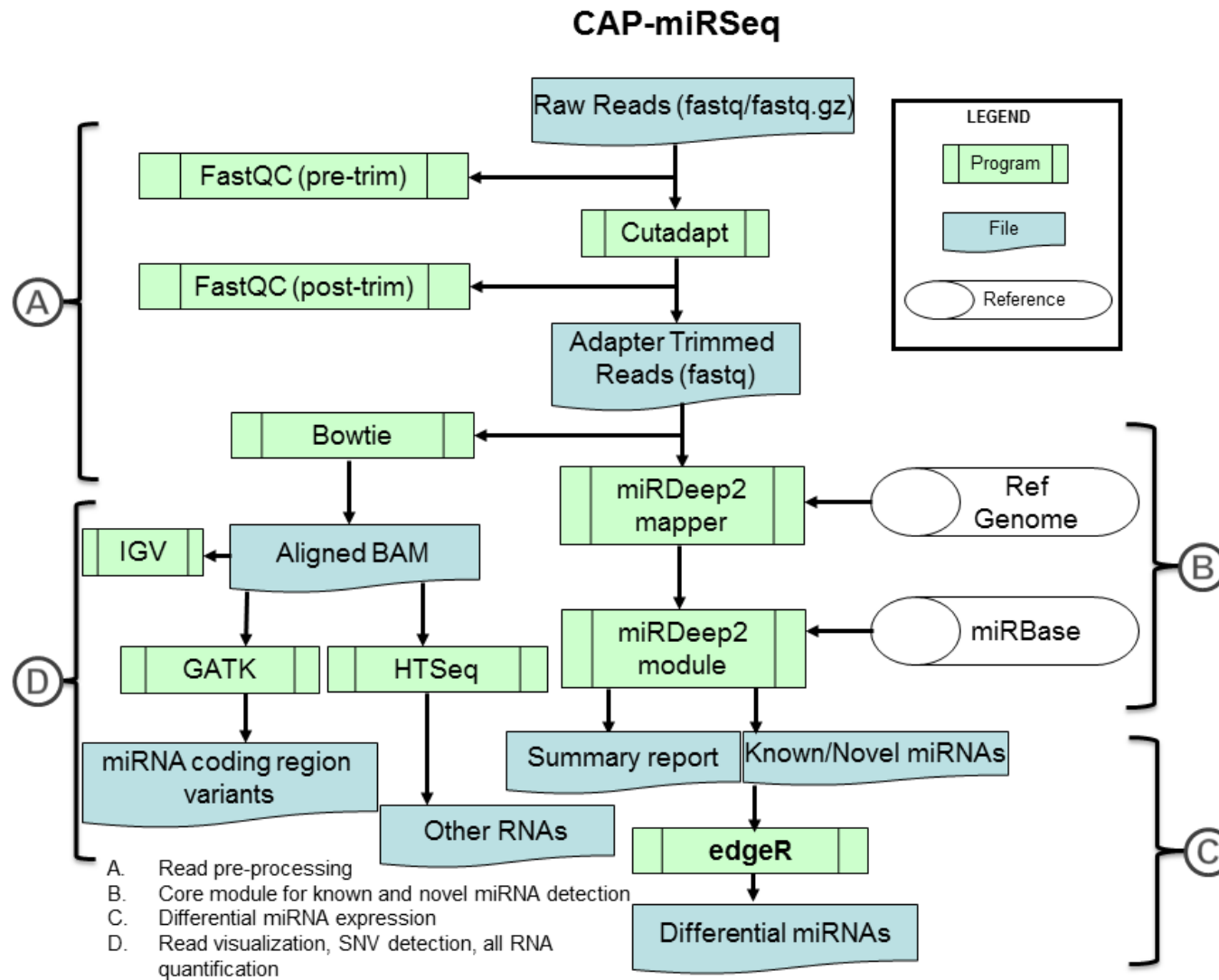


## SUPPLEMENTARY MATERIAL

Supplementary Figure S1. Microtranscriptome analysis pipeline.



Supplementary Table S1. Significantly changed micro-RNAs.

| Id             | C_root1 | C_root2 | OH_Root1 | OH_Root2 | norm.C_ro<br>ot1 | norm.C_ro<br>ot2 | norm.OH_<br>Root1 | norm.OH_<br>Root2 | baseMean | C     | OH    | FC    | log2FoldC<br>hange | pvalue   | padj     | tagwise.di<br>spersion | trended.di<br>spersion |
|----------------|---------|---------|----------|----------|------------------|------------------|-------------------|-------------------|----------|-------|-------|-------|--------------------|----------|----------|------------------------|------------------------|
| ath-miR156g    | 37      | 21      | 5        | 3        | 38               | 22               | 6                 | 2                 | 17,17    | 30    | 4     | 0,132 | -2,923             | 2,15E-07 | 8,77E-06 | 0,0514                 | 0,0916                 |
| ath-miR159c    | 1926    | 1416    | 973      | 1051     | 1988             | 1500             | 1124              | 861               | 1368,06  | 1744  | 992   | 0,568 | -0,815             | 0,000499 | 0,011615 | 0,0252                 | 0,0229                 |
| ath-miR169f-3p | 443     | 460     | 253      | 352      | 457              | 487              | 292               | 288               | 381,24   | 472   | 290   | 0,614 | -0,703             | 0,001487 | 0,027815 | 0,0206                 | 0,0273                 |
| ath-miR160c-3p | 129     | 86      | 51       | 65       | 133              | 91               | 59                | 53                | 84,09    | 112   | 56    | 0,499 | -1,003             | 0,003513 | 0,044049 | 0,0431                 | 0,0424                 |
|                |         |         |          |          |                  |                  |                   |                   |          |       |       |       |                    |          |          |                        |                        |
| Id             | C_root1 | C_root2 | OH_Root1 | OH_Root2 | norm.C_ro<br>ot1 | norm.C_ro<br>ot2 | norm.OH_<br>Root1 | norm.OH_<br>Root2 | baseMean | C     | OH    | FC    | log2FoldC<br>hange | pvalue   | padj     | tagwise.di<br>spersion | trended.di<br>spersion |
| ath-miR319b    | 193     | 104     | 487      | 583      | 199              | 110              | 562               | 477               | 337,28   | 154   | 520   | 3,354 | 1,746              | 8,48E-10 | 1,38E-07 | 0,0331                 | 0,0279                 |
| ath-miR394b-5p | 8       | 6       | 52       | 51       | 8                | 6                | 60                | 42                | 29,1     | 7     | 51    | 6,799 | 2,765              | 1,27E-08 | 1,03E-06 | 0,0502                 | 0,0687                 |
| ath-miR394a    | 8       | 7       | 51       | 51       | 8                | 7                | 59                | 42                | 29,08    | 8     | 50    | 6,28  | 2,651              | 2,66E-08 | 1,45E-06 | 0,0485                 | 0,0687                 |
| ath-miR158a-3p | 17087   | 7852    | 25441    | 29845    | 17636            | 8319             | 29377             | 24438             | 19942,39 | 12978 | 26908 | 2,073 | 1,052              | 0,000246 | 0,006692 | 0,0387                 | 0,0206                 |
| ath-miR319a    | 467     | 370     | 696      | 896      | 482              | 392              | 804               | 734               | 602,84   | 437   | 769   | 1,758 | 0,814              | 0,000246 | 0,006692 | 0,0216                 | 0,0252                 |
| ath-miR161.2   | 111     | 97      | 215      | 214      | 115              | 103              | 248               | 175               | 160,21   | 109   | 212   | 1,941 | 0,957              | 0,001536 | 0,027815 | 0,0363                 | 0,0338                 |
| ath-miR165a-3p | 3169    | 1832    | 3904     | 4883     | 3271             | 1941             | 4508              | 3998              | 3429,52  | 2606  | 4253  | 1,632 | 0,707              | 0,002504 | 0,040807 | 0,0257                 | 0,0216                 |
| ath-miR160b    | 32      | 12      | 62       | 62       | 33               | 13               | 72                | 51                | 42,03    | 23    | 62    | 2,647 | 1,404              | 0,003335 | 0,044049 | 0,0793                 | 0,0574                 |
| ath-miR165b    | 3581    | 2106    | 4348     | 5452     | 3696             | 2231             | 5021              | 4464              | 3853,05  | 2964  | 4742  | 1,6   | 0,678              | 0,00344  | 0,044049 | 0,0253                 | 0,0215                 |
| ath-miR167b    | 104     | 115     | 143      | 322      | 107              | 122              | 165               | 264               | 164,49   | 114   | 214   | 1,878 | 0,909              | 0,003964 | 0,046149 | 0,0407                 | 0,0335                 |
| ath-miR167a-5p | 104     | 115     | 142      | 318      | 107              | 122              | 164               | 260               | 163,38   | 114   | 212   | 1,858 | 0,894              | 0,004582 | 0,04668  | 0,0406                 | 0,0336                 |
| ath-miR396a-5p | 676     | 493     | 856      | 1116     | 698              | 522              | 988               | 914               | 780,57   | 610   | 951   | 1,558 | 0,64               | 0,004514 | 0,04668  | 0,0229                 | 0,0243                 |
|                |         |         |          |          |                  |                  |                   |                   |          |       |       |       |                    |          |          |                        |                        |
| Id             | C_root1 | C_root2 | 4H_Root1 | 4H_Root2 | norm.C_ro<br>ot1 | norm.C_ro<br>ot2 | norm.4H_<br>Root1 | norm.4H_<br>Root2 | baseMean | C     | 4H    | FC    | log2FoldC<br>hange | pvalue   | padj     | tagwise.di<br>spersion | trended.di<br>spersion |
| ath-miR156g    | 37      | 21      | 7        | 6        | 34               | 20               | 8                 | 7                 | 16,91    | 27    | 8     | 0,267 | -1,905             | 8E-05    | 0,001681 | 0,035                  | 0,0256                 |

|                 |         |         |          |          |              |              |               |               |          |       |       |        |                |          |          |                    |                    |
|-----------------|---------|---------|----------|----------|--------------|--------------|---------------|---------------|----------|-------|-------|--------|----------------|----------|----------|--------------------|--------------------|
| ath-miR169f-3p  | 443     | 460     | 179      | 228      | 405          | 431          | 194           | 249           | 319,73   | 418   | 222   | 0,529  | -0,918         | 9,28E-05 | 0,001732 | 0,0227             | 0,0256             |
| ath-miR160c-3p  | 129     | 86      | 39       | 52       | 118          | 81           | 42            | 57            | 74,39    | 100   | 50    | 0,499  | -1,004         | 0,002003 | 0,030597 | 0,0353             | 0,0256             |
| ath-miR159c     | 1926    | 1416    | 893      | 944      | 1762         | 1327         | 968           | 1029          | 1271,48  | 1544  | 998   | 0,647  | -0,629         | 0,00311  | 0,043541 | 0,0208             | 0,0256             |
| ath-miR399c-3p  | 44      | 38      | 19       | 14       | 40           | 36           | 21            | 15            | 27,93    | 38    | 18    | 0,474  | -1,076         | 0,003387 | 0,04377  | 0,0252             | 0,0256             |
|                 |         |         |          |          |              |              |               |               |          |       |       |        |                |          |          |                    |                    |
| Id              | C_root1 | C_root2 | 4H_Root1 | 4H_Root2 | norm.C_root1 | norm.C_root2 | norm.4H_Root1 | norm.4H_Root2 | baseMean | C     | 4H    | FC     | log2FoldChange | pvalue   | padj     | tagwise.dispersion | trended.dispersion |
| ath-miR319b     | 193     | 104     | 373      | 413      | 177          | 97           | 404           | 450           | 282,15   | 137   | 427   | 3,115  | 1,639          | 2,21E-08 | 3,71E-06 | 0,0353             | 0,0256             |
| ath-miR8175     | 1       | 1       | 10       | 16       | 1            | 1            | 11            | 17            | 7,53     | 1     | 14    | 13,569 | 3,762          | 2,02E-07 | 1,7E-05  | 0,0088             | 0,0256             |
| ath-miR157a-3p  | 65      | 44      | 126      | 119      | 59           | 41           | 137           | 130           | 91,75    | 50    | 134   | 2,638  | 1,4            | 5,24E-07 | 2,2E-05  | 0,0243             | 0,0256             |
| ath-miR157b-3p  | 65      | 44      | 126      | 119      | 59           | 41           | 137           | 130           | 91,75    | 50    | 134   | 2,638  | 1,4            | 4,68E-07 | 2,2E-05  | 0,024              | 0,0256             |
| ath-miR394a     | 8       | 7       | 22       | 42       | 7            | 7            | 24            | 46            | 20,88    | 7     | 35    | 4,943  | 2,305          | 6,56E-06 | 0,000197 | 0,0567             | 0,0256             |
| ath-miR394b-5p  | 8       | 6       | 21       | 42       | 7            | 6            | 23            | 46            | 20,37    | 6     | 34    | 5,209  | 2,381          | 7,03E-06 | 0,000197 | 0,0622             | 0,0256             |
| ath-miR161.2    | 111     | 97      | 157      | 181      | 102          | 91           | 170           | 197           | 139,99   | 96    | 184   | 1,908  | 0,932          | 6,57E-05 | 0,001576 | 0,0184             | 0,0256             |
| ath-miR158a-3p  | 17087   | 7852    | 20193    | 23756    | 15628        | 7359         | 21896         | 25892         | 17693,98 | 11494 | 23894 | 2,079  | 1,056          | 0,000347 | 0,00583  | 0,0409             | 0,0256             |
| ath-miR160b     | 32      | 12      | 49       | 37       | 29           | 11           | 53            | 40            | 33,49    | 20    | 46    | 2,293  | 1,197          | 0,004398 | 0,047429 | 0,0518             | 0,0256             |
| ath-miR1888a    | 5       | 6       | 15       | 10       | 5            | 6            | 16            | 11            | 9,34     | 6     | 14    | 2,629  | 1,394          | 0,004568 | 0,047429 | 0,0004             | 0,0256             |
| ath-miR319a     | 467     | 370     | 498      | 578      | 427          | 347          | 540           | 630           | 485,97   | 387   | 585   | 1,511  | 0,596          | 0,004799 | 0,047429 | 0,0192             | 0,0256             |
| ath-miR3932b-5p | 0       | 17      | 29       | 30       | 0            | 16           | 31            | 33            | 20,02    | 8     | 32    | 3,999  | 2              | 0,004149 | 0,047429 | 0,1607             | 0,0256             |

Supplementary Table S2 . Primer sequences used in the experiments.

| Primer name         | Accession | Primer sequence 5'-3'                                | Application               |
|---------------------|-----------|------------------------------------------------------|---------------------------|
| PP2AA3_F            | AT1G13320 | TAACGTGGCCAAAAATGATGC                                | RT-qPCR - reference       |
| PP2AA3_R            |           | GTTCTCCACAACCGCTTGGT                                 | RT-qPCR - reference       |
| UPL7_F              | AT3G53090 | TTCAAATACTTGCAGCCAACCTT                              | RT-qPCR - reference       |
| UPL7_R              |           | CCCAAAGAGAGGTATCACAAGAGACT                           | RT-qPCR - reference       |
| APX2_F              | AT3G09640 | TCATCTCTGGTAGACTGGACAAA                              | RT-qPCR                   |
| APX2_R              |           | CACATCTCTTAGATGATCCACACC                             | RT-qPCR                   |
| CAT2_F              | AT4G35090 | TCTGGTGCTCCTGTATGGAA                                 | RT-qPCR                   |
| CAT2_R              |           | TGGTAATCCTCAAGAAGGATAGGA                             | RT-qPCR                   |
| RRTF1_F             | AT4G34410 | TCGGGTATGCATTATCCTAACA                               | RT-qPCR                   |
| RRTF1_R             |           | AAGCTCTTGCTCCGGTGA                                   | RT-qPCR                   |
| ELIP1_F             | AT3G22840 | GCACAAAGTTTAGCGACTTGC                                | RT-qPCR                   |
| ELIP1_R             |           | CGCAACGAATCCAACCAT                                   | RT-qPCR                   |
| ath-sno85_R1        | AJ505658  | GGTCCAGTTTTTTTTTTTTTTTACATGTA                        | RT-qPCR - reference       |
| ath-sno85_F1        |           | GGTGCAATTCAAAAGCCCTT                                 | RT-qPCR - reference       |
| ath-sno101_R1       | AJ505631  | GACCAGTAGTTATCAACAAGCGA                              | RT-qPCR - reference       |
| ath-sno101_F1       |           | ACACTTGATCTCTGAACTTCACA                              | RT-qPCR - reference       |
| ath-sno85_RV1       | AJ505658  | GTGCATTCAAAGCCCTTACA                                 | TT-RTqPCR - reference     |
| ath-sno85_FW1       |           | GCTTTGAAAGAGAGAGAGAGAG                               | TT-RTqPCR - reference     |
| ath-sno101_RV1      | AJ505631  | GTTGATAACTACTGGTCTGCTGAT                             | TT-RTqPCR - reference     |
| ath-sno101_FW1      |           | TGTGAAGAGAGAGAGAGAGAG                                | TT-RTqPCR - reference     |
| ath-miR157a_RV1     | AT1G66783 | CGCTCTCTAGCCTTCTGTC                                  | TT-RTqPCR                 |
| ath-miR157a_FW1     |           | GCGCTAGATTTCTCCTTGAG                                 | TT-RTqPCR                 |
| ath-miR158a-3p_Rv1  | AT3G10745 | GCGTCCCAAATGTAGACAAA                                 | TT-RTqPCR                 |
| ath-miR158a-3p_FW1  |           | TTTGGGAGGAGAGAGAGAGAG                                | TT-RTqPCR                 |
| ath-miR158b_RV1     | AT1G55591 | CGCCCCAAATGTAGACAAA                                  | TT-RTqPCR                 |
| ath-miR158b_FW1     |           | TTTGGGGATTTCGTGGCTGAG                                | TT-RTqPCR                 |
| ath-miR160b-5p_RV1  | AT4G17788 | TGCCTGGCTCCCTGTATG                                   | TT-RTqPCR                 |
| ath-miR160b-5p_FW1  |           | CCAGGCACACACACAGAC                                   | TT-RTqPCR                 |
| ath-miR167b-5p_F1   | AT3G63375 | GAAGCTGCCAGCATGA                                     | RT-qPCR                   |
| ath-miR167b-5p_R2   |           | CAGGTCCAGTTTTTTTTTTTTTTTAGA                          | RT-qPCR                   |
| ath-miR169f-3p_F1   | AT3G14385 | GCAAGTTGACCTTGGCT                                    | RT-qPCR                   |
| ath-miR169f-3p_R1   |           | TCCAGTTTTTTTTTTTTTTTGCAGA                            | RT-qPCR                   |
| ath-miR319b_RV1     | AT5G41663 | TTGGACTGAAGGGAGCTC                                   | TT-RTqPCR                 |
| ath-miR319b_FW1     |           | GTCAGTCAAGCAGAGAAGAG                                 | TT-RTqPCR                 |
| ath-miR394a_RV1     | AT1G20375 | GTTGGCATTCTGTCCACC                                   | TT-RTqPCR                 |
| ath-miR394a_FW1     |           | ATGCCAAAGAGAGAGAGAGAG                                | TT-RTqPCR                 |
| ath-miR8175_1_RV1   | AT2G05455 | GATCCCGGCAACGGC                                      | TT-RTqPCR                 |
| ath-miR8175_1_FW1   |           | GGGGATCAGAGATAGAAAGAG                                | TT-RTqPCR                 |
| RT-ath-snoR85_1     | AJ505658  | TTTGAAAGAGAGAGAGAGCTAGAGAACCTAGCTCAATAGGAAGACATGT    | RT reaction TT- reference |
| RT-ath-snoR101_1    | AJ505631  | TGTGAAGAGAGAGAGAGAGCTAGAGAACCTAGCTCATTAGGAAGAGCATC   | RT reaction TT- reference |
| RT-ath-miR157a_1    | AT1G66783 | GCTAGATTTCTCCTTGAGCTAGGTTGACTAGCTCTTCTATATTGATGAC    | RT reaction TT            |
| RT-ath-miR158a-3p_1 | AT3G10745 | TTTGGGAGGAGAGAGAGAGCTAGAGAACCTAGCTCAGTTGGAGGTGCTTT   | RT reaction TT            |
| RT-ath-miR158b_1    | AT1G55591 | TTTGGGGATTTCGTGGCTGAGCTAGGTTGACTAGCTCTTCTATTGCTTT    | RT reaction TT            |
| RT-ath-miR160b-5p_1 | AT4G17788 | CCAGGCACACACACAGACGTAGAGAACCTACGTCCACCATACATGGCAT    | RT reaction TT            |
| RT-ath-miR319b_1    | AT5G41663 | TCAGTCAAGCAGAGAAGAGCTAGAGAACCTAGCTCAAGACCAATAGGGAG   | RT reaction TT            |
| RT-ath-miR394a_1    | AT1G20375 | ATGCCAAAGAGAGAGAGAGCTAGAGAACCTAGCTCAATAAGAAGGGAGGT   | RT reaction TT            |
| RT-ath-miR8175_1    | AT2G05455 | GGGGATCAGAGATAGAAAGAGCTAGAGAACCTAGCTCAATAGGAAGTGGCGC | RT reaction TT            |

**Supplementary Table S3.** he Hits from the prediction of mRNA targets for confirmed miRNAs, obtained using the psRNATarget software. A higher expectation value (Exp.) indicates less similarity between small RNA and the target candidate (lower probability of true interaction). The target gene regulation can be realized by its cleavage or translation inhibition.

| miRNA          | miRNA sequence        | Exp. | Inhibition  | Target Acc. | Target name    | Target function                                                          |
|----------------|-----------------------|------|-------------|-------------|----------------|--------------------------------------------------------------------------|
| ath-miR160b    | UGCCUGGCUCCUGUAUGCCA  | 0.5  | Cleavage    | AT1G77850.1 | ARF17          | auxin response factor 17                                                 |
| ath-miR160b    | UGCCUGGCUCCUGUAUGCCA  | 1    | Cleavage    | AT2G28350.1 | ARF10          | auxin response factor 10                                                 |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 1    | Cleavage    | AT1G27340.1 |                | Galactose oxidase/kelch repeat superfamily protein                       |
| ath-miR160b    | UGCCUGGCUCCUGUAUGCCA  | 1.5  | Cleavage    | AT4G30080.1 | ARF16          | auxin response factor 16                                                 |
| ath-miR169f-3p | GCAAGUUGACCUUGGCUCUGC | 2.5  | Cleavage    | AT1G13470.1 |                | Protein of unknown function (DUF1262)                                    |
| ath-miR169f-3p | GCAAGUUGACCUUGGCUCUGC | 2.5  | Cleavage    | AT5G51220.1 |                | ubiquinol-cytochrome C chaperone family protein                          |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 2.5  | Cleavage    | AT4G24860.1 |                | P-loop containing nucleoside triphosphate hydrolases superfamily protein |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 2.5  | Cleavage    | AT3G58570.1 |                | P-loop containing nucleoside triphosphate hydrolases superfamily protein |
| ath-miR169f-3p | GCAAGUUGACCUUGGCUCUGC | 3    | Cleavage    | AT3G59770.1 | SAC9           | sacI homology domain-containing protein / WW domain-containing protein   |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 3    | Cleavage    | AT4G20430.2 |                | Subtilase family protein                                                 |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 3    | Cleavage    | AT5G36170.2 | HCF109, ATPRFB | high chlorophyll fluorescent 109                                         |
| ath-miR169f-3p | GCAAGUUGACCUUGGCUCUGC | 3.5  | Cleavage    | AT4G34580.1 | COW1, SRH1     | Sec14p-like phosphatidylinositol transfer family protein                 |
| ath-miR169f-3p | GCAAGUUGACCUUGGCUCUGC | 3.5  | Cleavage    | AT1G67580.2 |                | Protein kinase superfamily protein                                       |
| ath-miR169f-3p | GCAAGUUGACCUUGGCUCUGC | 3.5  | Cleavage    | AT1G79075.2 |                | other RNA                                                                |
| ath-miR169f-3p | GCAAGUUGACCUUGGCUCUGC | 3.5  | Cleavage    | AT1G42070.1 |                | transposable element gene                                                |
| ath-miR169f-3p | GCAAGUUGACCUUGGCUCUGC | 3.5  | Cleavage    | AT3G16760.1 |                | Tetratricopeptide repeat (TPR)-like superfamily protein                  |
| ath-miR169f-3p | GCAAGUUGACCUUGGCUCUGC | 3.5  | Translation | AT5G55780.1 |                | Cysteine/Histidine-rich C1 domain family protein                         |
| ath-miR169f-3p | GCAAGUUGACCUUGGCUCUGC | 3.5  | Cleavage    | AT5G18830.3 | SPL7           | squamosa promoter binding protein-like 7                                 |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 3.5  | Translation | AT5G20580.1 |                | BEST Arabidopsis thaliana protein match is                               |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 3.5  | Translation | AT1G01320.2 |                | Tetratricopeptide repeat (TPR)-like superfamily protein                  |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 3.5  | Cleavage    | AT3G48460.1 |                | GDSL-like Lipase/Acylhydrolase superfamily protein                       |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 3.5  | Cleavage    | AT2G33585.1 |                | unknown protein; has 31 Blast hits to 31 proteins in 12 species          |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 3.5  | Cleavage    | AT5G56630.1 | PFK7           | phosphofructokinase 7                                                    |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 3.5  | Cleavage    | AT1G40104.1 |                | unknown protein; FUNCTIONS IN                                            |
| ath-miR394a    | UUGGCAUUCUGUCCACCUCC  | 3.5  | Translation | AT5G26749.2 |                | C2H2 and C2HC zinc fingers superfamily protein                           |

|             |                      |     |             |             |                       |                                                                           |
|-------------|----------------------|-----|-------------|-------------|-----------------------|---------------------------------------------------------------------------|
| ath-miR394a | UUGGCAUUCUGUCCACCUCC | 3.5 | Cleavage    | AT5G19097.1 |                       | transposable element gene                                                 |
| ath-miR394a | UUGGCAUUCUGUCCACCUCC | 3.5 | Cleavage    | AT5G63120.2 |                       | P-loop containing nucleoside triphosphate hydrolases superfamily protein  |
| ath-miR394a | UUGGCAUUCUGUCCACCUCC | 3.5 | Cleavage    | AT3G23300.1 |                       | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein  |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 3.5 | Cleavage    | AT5G28641.1 |                       | transposable element gene                                                 |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 3.5 | Cleavage    | AT1G22040.1 |                       | Galactose oxidase/kelch repeat superfamily protein                        |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 3.5 | Cleavage    | AT5G47500.1 |                       | Pectin lyase-like superfamily protein                                     |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 3.5 | Cleavage    | AT3G05520.2 |                       | Subunits of heterodimeric actin filament capping protein Capz superfamily |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 3.5 | Cleavage    | AT5G36890.2 | BGLU42                | beta glucosidase 42                                                       |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 3.5 | Translation | AT5G55340.1 |                       | MBOAT (membrane bound O-acyl transferase) family protein                  |
| ath-miR160b | UGCCUGGCUCCUGUAUGCCA | 4   | Cleavage    | AT1G07970.1 |                       | CONTAINS InterPro DOMAIN/s                                                |
| ath-miR160b | UGCCUGGCUCCUGUAUGCCA | 5   | Cleavage    | ATMG00880.1 | ORF187                | hypothetical protein                                                      |
| ath-miR160b | UGCCUGGCUCCUGUAUGCCA | 5   | Translation | AT4G19640.1 | ARA7, ARA-7, ATRABF2B | Ras-related small GTP-binding family protein                              |
| ath-miR160b | UGCCUGGCUCCUGUAUGCCA | 5   | Translation | AT1G32270.1 | ATSYP24, SYP24        | syntaxin, putative                                                        |
| ath-miR160b | UGCCUGGCUCCUGUAUGCCA | 5   | Cleavage    | AT1G64190.1 |                       | 6-phosphogluconate dehydrogenase family protein                           |
| ath-miR160b | UGCCUGGCUCCUGUAUGCCA | 5   | Cleavage    | AT3G09450.1 |                       | CONTAINS InterPro DOMAIN/s                                                |
| ath-miR160b | UGCCUGGCUCCUGUAUGCCA | 5   | Cleavage    | AT1G79830.1 | GC5                   | golgin candidate 5                                                        |
| ath-miR160b | UGCCUGGCUCCUGUAUGCCA | 5   | Cleavage    | AT2G07682.1 |                       | transposable element gene                                                 |
| ath-miR160b | UGCCUGGCUCCUGUAUGCCA | 5   | Cleavage    | AT4G15100.1 | scpl30                | serine carboxypeptidase-like 30                                           |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 5   | Cleavage    | AT3G22850.1 |                       | Aluminium induced protein with YGL and LRDR motifs                        |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 5   | Cleavage    | AT5G53440.1 |                       | unknown protein; FUNCTIONS IN                                             |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 5   | Cleavage    | AT4G23440.1 |                       | Disease resistance protein (TIR-NBS class)                                |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 5   | Translation | AT4G33430.1 | BAK1,RKS10, SERK3     | BRI1-associated receptor kinase                                           |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 5   | Cleavage    | AT3G25560.3 | NIK2                  | NSP-interacting kinase 2                                                  |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 5   | Cleavage    | AT2G36250.2 | FTSZ2-1, ATFTSZ2-1    | Tubulin/FtsZ family protein                                               |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 5   | Cleavage    | AT3G25560.2 | NIK2                  | NSP-interacting kinase 2                                                  |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 5   | Cleavage    | AT3G47990.1 | SIS3                  | SUGAR-INSENSITIVE 3                                                       |
| ath-miR8175 | GAUCCCCGGCAACGGCGCCA | 5   | Cleavage    | AT1G67320.1 |                       | DNA primase, large subunit family                                         |