

Supplemental Figure 6

A. Predicted target genes of the newly identified miRNAs

miR1846a-c_5p

5' GGC GGCCCCCGGCCUCCUCACU 3' LOC_Os02g43950 (Expressed protein)
:|||||
3' UCGCCGGGGCCGGAGGAGUGA 5' miR1846a-c_5p, 0.5

5' GGC GGCCCCCGGCCUCCUCACU 3' LOC_Os10g12320 (Expressed protein)
:|||||
3' UCGCCGGGGCCGGAGGAGUGA 5' miR1846a-c_5p, 0.5

5' AGCCGCGCGGCCUCCUCUCU 3' LOC_Os01g74520 (Ubiquinone biosynthesis methyltransferase coq5, putative)
||| ||| ||| ||| ||| |||
3' UCGCCGGGGCCGGAGGAGUGA 5' miR1846a-c_5p, 4.0

5' ACCGCGCGGCCUCCUCUCU 3' LOC_Os05g08930 (Chloroplast lumen common family protein, putative)
| || | ||| ||| ||| |||
3' UCGCCGGGGCCGGAGGAGUGA 5' miR1846a-c_5p, 4.0

5' CGCGCGCGGCCUCCUCCU 3' LOC_Os12g09630 (Hypothetical protein)
||| ||| ||| ||| ||| |||
3' UCGCCGGGGCCGGAGGAGUGA 5' miR1846a-c_5p, 4.0

miR1846d.2_3p

5' CCUCCUGCGGCGCCGAUA 3' XM_463600 (Predicted mRNA, no annotated function)
|||||
3' GGAGGGACGCCGCGGCCUAU 5' miR1846d.2_3p, 0

5' CCGCACGGCGGCGCCGAGA 3' LOC_02g47810 (Dof domain, zinc finger family protein)
|| | | ||| ||| ||| :|
3' GGAGGGACGCCGCGGCCUAU 5' miR1846d.2_3p, 3.5

5' CUUCGCCGCGGCGCCGAUA 3' LOC_09g28400 (Alpha-amylase isozyme 3A precursor)
|: || | ||| ||| ||| |||
3' GGAGGGACGCCGCGGCCUAU 5' miR1846d.2_3p, 3.5

5' UCUUCCUACGGCGCCGAUC 3' LOC_01g68720 (Expressed protein)
: ||: ||| ||| ||| ||| |||
3' GGAGGGACGCCGCGGCCUAU 5' miR1846d.2_3p, 4.0

5' CAUCGUGGGCGCCGGAUG 3' LOC_08g39220 (Wall-associated kinase-like 1, putative)
| || ||| ||| ||| ||| :
3' GGAGGGACGCCGCGGCCUAU 5' miR1846d.2_3p, 4.0

5' GCCCGCGGCGGCGCCGAUC 3' LOC_02g49800 (Eukaryotic aspartyl protease family protein)
| ||| ||| ||| ||| ||| |||
3' GGAGGGACGCCGCGGCCUAU 5' miR1846d.2_3p, 5.0

miR1847_5p

5' GUUCCACAAUUGCAUACUGCA 3' LOC_Os09g38390 (PB1 domain containing protein)
|| ||| ||| : ||| ||| |||
3' CACGGUGUUGACGUUUGACGU 5' miR1847_5p, 2.5

5' AUGGCACAUUGGAAACUGCA 3' LOC_Os03g12450 (Nup133 nucleoporin family protein)
|| ||| ||| ||| ||| ||| |||
3' CACGGUGUUGACGUUUGACGU 5' miR1847_5p, 4.0

5' AUGACUACUGCAAACUCCA 3' LOC_Os05g25890 (Expressed protein)
|| | ||| ||| ||| ||| ||| |||
3' CACGGUGUUGACGUUUGACGU 5' miR1847_5p, 4.0

5' GAGUCACAGCUGCAAACUGCC 3' LOC_Os06g05640 (Hypothetical protein)
| |: ||| : ||| ||| ||| ||| |||
3' CACGGUGUUGACGUUUGACGU 5' miR1847_5p, 4.0

miR1847_3p

5' GUUGUGACCCUGACAAGUGGCCA 3' LOC_Os11g27240 (Pentatricopeptide, putative)
||||| | ||: ||| ||| ||| |||
3' CAACACCGUGAUUGUACACCCGGU 5' miR1847_3p, 3.5

miR1848

5' UGCGCGCGCGGCGGCGAGG 3' LOC_Os04g40590 (Membrane bound O-acyl transferase)
|||: ||| ||| ||| ||| ||| |||
3' ACGUGCGCGCGGCGGCCGUCC 5' miR1848, 1.0

5' UCCGCGCGCGCGGCGGAGG 3' LOC_Os08g10649 (GTP-binding protein ERG, putative)
| |: ||| ||| ||| ||| ||| |||
3' ACGUGCGCGCGGCGGCCGUCC 5' miR1848, 2.5

miR1848

5' GGUACGCGCGCGGCGCGAGG 3' LOC_Os12g18374 (NB-ARC domain containing protein)
|:||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 2.5

5' UCCGCGCGCACGCCGGCGAGG 3' LOC_Os02g36110 (Cytochrome P450 76C2)
|:||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 2.5

5' UGCAGGCGAGCGCCGGCGUGG 3' LOC_Os11g14400 (Polygalacturonase family protein)
|||| | ||||| ||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 3.0

5' AGCAGGCGGGCGCCGGCGAGG 3' LOC_Os06g45330 (Endonuclease V, putative, expressed)
||| ||| ||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 3.0

5' AGCUCGUGCGCGCCGGCGACG 3' LOC_Os01g42540 (ENT domain containing protein)
|| ||:||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 3.5

5' UCCGCGCGCACGCCGGGGAGG 3' LOC_Os02g36070 (Cytochrome P450 family protein)
|:||||| ||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 3.5

5' UGCUCGUGCUCGCCGGCGCGG 3' LOC_Os06g13160 (Plant viral-response family protein)
||| ||:| ||||| ||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 3.5

5' UACCCGCGUGCGCCGGCGAUG 3' LOC_Os06g20120 (Hypothetical protein)
| | |||:||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 3.5

5' UCCGCGCCCGCGCCGGCGACG 3' LOC_Os07g39530 (NPH3 family protein)
|:|||| ||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 3.5

5' GGCACGUGCACGCCGGCGCGG 3' LOC_Os10g41270 (Lipase family protein)
|||||:| ||||| ||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 3.5

5' CGCAGGCCCGCGCCGGCGUGG 3' LOC_Os01g16770 (Alpha-expansin 15 precursor, putative)
||| || ||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' UGCUCGAGCUCGCCGGCGCGG 3' LOC_Os02g02040 (Protein kinase domain containing protein)
||| || || ||||| ||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' GGGACGCGCACGCCUGCGAGG 3' LOC_Os03g05070 (Xyloglucan galactosyltransferase KATAMARI 1, putative)
| ||||| ||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' AGAACGCCCGCGCCGGCGACG 3' LOC_Os03g30250 (Phytochelatin synthetase-like conserved region family protein)
| |||| ||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' CGCACCCGUCGCCGGCGCGG 3' LOC_Os03g08720 (Transferase family protein)
|||| ||| ||||| ||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' CGCACGCCCGCGCCGGCGAGA 3' LOC_Os04g54970 (Hypothetical protein)
|||| || ||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' UGCUCGAGCUCGCCGGCGACG 3' LOC_Os04g52800 (Hypothetical protein)
||| || || ||||| ||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' UGCCCUCCCGCGCCGACGAGG 3' LOC_Os04g40400 (Eukaryotic translation initiation factor 4B, putative)
||| | | ||||| |||||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' AGAACGCGCUCGCCGGCGCGG 3' LOC_Os06g08710 (Leucine Rich Repeat family protein)
| ||||| ||||| ||
3' ACGUGCGCGCGGCCGCUCC 5' miR1848, 4.0

miR1848

5' AGCUCGCCCCGCGCCGUCGAGG 3' LOC_Os06g44430 (Protein kinase domain containing protein)
|| ||| ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' UCCAGGCGCUCGACGGCGAGG 3' LOC_Os07g38030 (GRAS family transcription factor containing protein)
|| ||| ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' GGGACGCGCUCGCCGGCGUGG 3' LOC_Os08g04710 (Hypothetical protein)
|| ||||| ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' CGCUCGCCCCGCGCCGGCGACG 3' LOC_Os08g37520 (Pentatricopeptide, putative)
|| ||| ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' UGCUCGAGCUCGCCGGCGACG 3' LOC_Os08g39320 (Hypothetical protein)
||| || || ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' UGGAGGAGCGCGCCGCGAGG 3' LOC_Os09g14510 (Peroxin-3 family protein)
|| || ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' CGCCCGCCGCGCCGCGAGG 3' LOC_Os09g36070 (Cytochrome P450 family protein)
|| ||| ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' AGCACGGGCACGGCGGCGAGG 3' LOC_Os09g37200 (Transferase family protein)
||||| || || ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' AGCACGCCUCGCCGGAGAGG 3' LOC_Os10g32509 (Hypothetical protein)
||||| || ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' UGGAGGCACGCGCCAGCGAGG 3' LOC_Os10g40300 (Hypothetical protein)
|| || ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' UGAAGGCGAGCGGCGGCGAGG 3' LOC_Os11g42340 (Hypothetical protein)
|| || ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' UCCUCGAGCGCGCCGCGAGG 3' LOC_Os12g42370 (Expressed protein)
|| || ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 4.0

5' UGGACGAGCUCGCCGGCGAGU 3' LOC_Os04g32980 (Expressed protein)
|| ||| || ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 5.0

5' CGCACCCGCUCCCGGCGAGA 3' LOC_Os11g42290, LOC_11g42370 (Transferase family protein, expressed)
||||| || ||||| |||||
3' ACGUGCGCGCGCGGCCGCUCC 5' miR1848, 5.0

miR1850

5' CCCCAAACUCCAAACUUUCCA 3' AK068321 (No annotation available for this full length cDNA)
||||| ||:|||||||
3' GGGGUUAGAGGGUUGAAAGGU 5' miR1850, 1.5

5' CCCCCAACUCCAAACUUUCCA 3' AK106712 (No annotation available for this full length cDNA)
|||| ||||| |||||
3' GGGGUUAGAGGGUUGAAAGGU 5' miR1850, 2.0

5' CCCCCAACUCCAAACUUUCCA 3' LOC_Os04g33510 (Expressed protein)
|||| || ||:|||||||
3' GGGGUUAGAGGGUUGAAAGGU 5' miR1850, 2.5

5' CUCCCAACUCCAAACUUCCA 3' LOC_Os09g29200 (Glutathione S-transferase, N-terminal domain containing protein)
|:|| || ||||| |||||
3' GGGGUUAGAGGGUUGAAAGGU 5' miR1850, 3.5

miR1851

5' GCCAAAUGCCAUCCCGGACG 3' LOC_Os01g61520 (Hypothetical protein)
|||||:|||||
3' CGGUUUUACGGUAGGGUCUGC 5' miR1851, 0.5

miR1852

5' ACCCGAACUCUGAUUCCAUAU 3' LOC_Os03g62690 (Pentatricopeptide, putative)
||| ||| ||||| |||||
3' UGGACGUAAGACUUAGGUUAUA 5' miR1852, 4.0

5' ACCUCCUUAACUGAAUGCAUAU 3' LOC_Os07g11280 (Pentatricopeptide, putative)
|||| | | ||||| |||||
3' UGGACGUAAGACUUAGGUUAUA 5' miR1852, 4.0

miR1853

5' GCAUCCAUAUCCCAAUUG 3' LOC_02g38340 (Actin-like protein 3)
||| || | ||||| |||||
3' CGUUGGCUUGUAGGGGUAAU 5' miR1853, 3.5

5' GCCACCAAAAUCCCAAUUC 3' LOC_09g26340 (Histone H4, putative)
|| ||| || ||||| |||||
3' CGUUGGCUUGUAGGGGUAAU 5' miR1853, 3.5

miR1854

5' UCCAGUAUGCAAUUUCAACA 3' LOC_12g38770 (Diphosphonucleotide phosphatase 1)
||||:| | :||||||| ||
3' AGGUUAGAUGUUAAAGUGGU 5' miR1854, 3.0

miR1855

5' GCUGUUGGCUACUCCAAUGCU 3' AK109729 (No annotated function)
|| ||||| ||||| |||||
3' AGAGAACCGAUGAGGUCACGA 5' miR1855, 3.0

5' UUUUUAUAGCUACUUCAGUGCU 3' LOC_Os05g08370 (Cellulose synthase A catalytic subunit 1)
|:| || |||||:|||||||
3' AGAGAACCGAUGAGGUCACGA 5' miR1855, 3.0

5' ACUCUUGCCAACUUCAGUGCU 3' LOC_Os01g46610 (Isocitrate dehydrogenase, chloroplast precursor)
||||| | |||:|||||||
3' AGAGAACCGAUGAGGUCACGA 5' miR1855, 3.5

miR1857

5' CGUGGUCUCCUUGGAGCAAGA 3' LOC_Os03g30750 (Hypothetical protein)
| |||| | ||||| || ||
3' GGACCAAAAGAACCUCGUACU 5' miR1857, 4.0

miR1858

5' GCCCUACUCCGUCCUCUCUC 3' LOC_Os01g53800 (Transferrin receptor-like dimerisation domain containing protein)
||||:||||||| |||||
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 0.5

5' GCCCUACUCCGUCCUCUCGC 3' LOC_Os01g54010 (Transferrin receptor-like dimerisation domain containing protein)
||||:||||||| |||||
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 1.5

5' GCCCAACUCCGUCCUCUCGC 3' LOC_Os04g34230 (Zinc finger, C3HC4 type family protein)
||||:||||||| |||||
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 1.5

5' GCUCCACCCGUCCUCUCUC 3' LOC_Os07g26000 (F-box domain containing protein)
||:|||| ||||| |||||
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 1.5

5' UCCCCCUCCGUCCUCUCUC 3' LOC_Os04g35880 (DDT domain containing protein)
|||| ||||| |||||
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 2.0

5' CCCCUACUUCGUCCUCUCGC 3' LOC_Os01g21650 (Expressed protein)
|||:|||:||||||| ||
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 3.0

5' GUCCCCUACGUCCUCUCUC 3' LOC_Os01g21850 (Protein transport protein, putative)
|:|||| || |||||:||||
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 3.0

5' GCUCCUCUUCGUCCUCUCGC 3' LOC_Os03g19410 (Prolyl oligopeptidase family protein)
||:|| |||:||||||| ||
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 3.0

miR1858

5' GUCCAACUUCGUCCUCCUCGC 3' LOC_Os06g36330 (MATE efflux family protein)
|:| | | | | | | | | | | | | | |
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 3.0

5' GCUCGACGCCGUCCUCCUCCC 3' LOC_Os02g20560 (Fasciclin domain containing protein)
|:| | | | | | | | | | | | | | |
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 3.5

5' CCCCUCUUCGUCCCCUCUC 3' LOC_Os02g53530 (Zinc finger protein)
| | | | | | | | | | | | | | |
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 3.5

5' CCUCCCCUCCGUCCUCCGCUC 3' LOC_Os06g13810 (Pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta subunit)
|:| | | | | | | | | | | | | | |
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 3.5

5' CCCC CGCGCCGUCCUCCUCUC 3' LOC_Os08g23730 (GMP synthase)
| | | | | | | | | | | | | | |
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 3.5

5' CCGCGACUCCGUCCUCCUCGC 3' LOC_Os01g73200 (Peroxidase 12 precursor, putative)
| | | | | | | | | | | | | | |
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 4.0

5' GCCGCUCGCCGUCCUCCUCCC 3' LOC_Os02g04800 (Avirulence-responsive protein, putative)
| | | | | | | | | | | | | | |
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 4.0

5' CCCC GACGCCGUCCUUAUCUC 3' LOC_Os09g24970 (Expressed protein)
| | | | | | | | | | | | | | |
3' CGGGGUGAGGCAGGAGGAGAG 5' miR1858, 4.0

miR1859

5' CUGGAUUGGAUGUCAUGGAAA 3' AA754051 (EST) (Similar to Rice mRNA for nucleoside diphosphate kinase)
| | | | | | | | | | | | | | |
3' AACCUUACCUGCAGUAUCCUUU 5' miR1859, 3.0

miR1860

5' AGCGAGAGCCUAGCUUCUAGAU 3' LOC_11g38120 (F-box domain containing protein)
| | | | | | | | | | | | | | |
3' UCUCUUUUGGAUCGAAGGUCUA 5' miR1860, 2.5

5' CGAGGAAAGCUAGCUUUCAGAU 3' LOC_09g36100 (Expressed protein)
| | | | | | | | | | | | | | |
3' UCUCUUUUGGAUCGAAGGUCUA 5' miR1860, 3.0

miR1861h, j

5' CCCAGUUUCUCCUCAAGACCG 3' LOC_Os05g51790 (Structural maintenance of chromosomes family protein)
| | | | | | | | | | | | | | |
3' GAGUCAAGGACGGAGUUCUGGC 5' miR1861h, j, 2.5

miR1861b, f, i, l

5' CCCAGUUUCUCCUCAAGACCG 3' LOC_Os05g51790 (Structural maintenance of chromosomes family protein)
| | | | | | | | | | | | | | |
3' GAGUCAAGGACGGAGUUCUAGC 5' miR1861b, f, i, l, 3.5

miR1861n

5' UUGAGCUCUUGCCACAAGAUCA 3' LOC_Os03g03710 (RNB-like protein)
: | | | | | | | | | | | | | | |
3' GAGUCGAGGACGGUGUUCUAGC 5' miR1861n, 3.0

miR1862a-c

5' UGUCCCACAAAAACCAACCUAGU 3' LOC_Os01g58240 (Subtilisin N-terminal Region family protein)
: | | | | | | | | | | | | | | |
3' GCAGGGUUUUUUUGGUUGGAGCA 5' miR1862a-c, 3.5

5' CAUCCCAUAAAAACCAACCUAGU 3' LOC_Os06g37610 (Cyclopropane-fatty-acyl-phospholipid synthase family protein)
| | | | | | | | | | | | | | |
3' GCAGGGUUUUUUUGGUUGGAGCA 5' miR1862a-c, 4.0

miR1862d

5' UGUCCCACAAAAACCAACCUAGU 3' LOC_Os02g30730 (SART-1 family protein)
: | | | | | | | | | | | | | | |
3' GCAGGGUUUUUUUGGUUGGAGCA 5' miR1862d, 3.0

5' UGUCCCACAAAAACCAACCUAGU 3' LOC_Os01g58240 (Subtilisin N-terminal Region family protein)
: | | | | | | | | | | | | | | |
3' GCAGGGUUUUUUUGGUUGGAGCA 5' miR1862d, 3.5

miR1862e

5' CCGUCCCAUAAAAACAAUCUAG 3' LOC_04g31120 (Beta scruin)

||||||| || |||||
3' GGCAGGGUUUUUUUUGUUUAGAUC 5' miR1862e, 2.0

5' CUGUCCCAUAAAAACAAUCUAG 3' LOC_02g30730 (SART-1 family protein)

||:||||| || |||||
3' GGCAGGGUUUUUUUUGUUUAGAUC 5' miR1862e, 2.5

miR1867

5' ACUCCUCUGCCCUAAAAA 3' AU058111 (EST, no annotated function)

||||||| || |||||
3' UGAGGGAGACAGGAUCUUUUUUU 5' PI_miR28, 2.0

miR1872

5' UUACCCGUCACAAACUCACAGUUC 3' LOC_0s12g14230 (Hypothetical protein)

||||||| || |||||
3' AAUGGGCAGUGUCUGAAUGUCAAG 5' miR1872, 2.0

5' UUAGCAGUUACAGACUUACAGUUA 3' LOC_0s06g46910 (Zinc finger family protein)

||| | ||:|||||
3' AAUGGGCAGUGUCUGAAUGUCAAG 5' miR1872, 3.5

miR1876

5' GGGCCAACUCGCAACCUACUUUAU 3' AK066235 (No annotated function)

||||| |:|:|||||:|||||
3' CCCGGUCGGGUGUUUGGGUGAAUA 5' miR1876, 2.5

miR1883a-b

5' UUCAUUCUAGACCCGUCACAGGU 3' LOC_12g15260 (Hypothetical protein)

||||||| | |||||
3' AAGGUAAGAGCCGGGCAGUGUCCA 5' miR1883a-b, 2.0

miR529b

5' GAGCUGUGCUCUCUCUUCU 3' LOC_0s08g39890 and LOC_0s09g31438 (SBP-domain protein 5, putative)

:|||||:|||||
3' UUCGACAUGAGAGAGAGAAGA 5' miR529b, 1.0

5' CAACUGUGCUCUCUCUUCU 3' LOC_0s01g69830 (SBP-domain protein 5, putative)

| ||||:|||||
3' UUCGACAUGAGAGAGAGAAGA 5' miR529b, 2.5

5' CAGCUGUCCUCUCUCUCCU 3' LOC_0s05g14010 (Expressed protein)

||||| |||||
3' UUCGACAUGAGAGAGAGAAGA 5' miR529b, 3.0

5' AUGUUUACUCUCUCUUUCU 3' LOC_0s01g65780 (Secondary cell wall-related glycosyltransferase family 8, putative)

| |:| |||||:|||||
3' UUCGACAUGAGAGAGAGAAGA 5' miR529b, 3.0

5' GAUCUUUACUCUCCUCUUCU 3' LOC_0s06g28840 (Expressed protein)

:| || ||||| |||||
3' UUCGACAUGAGAGAGAGAAGA 5' miR529b, 3.5

5' AUGCUGCAUUCUCUAUCUUCU 3' LOC_0s08g35939 (Expressed protein)

| |||| |:||||| |||||
3' UUCGACAUGAGAGAGAGAAGA 5' miR529b, 3.5

5' UAGCUCUCCUUAUCUCUUCU 3' LOC_0s07g25484 (Hypothetical protein)

|||| | || |||||
3' UUCGACAUGAGAGAGAGAAGA 5' miR529b, 4.0

5' GAGCUCUCCUCUCUCUCC 3' LOC_0s03g57900 (AN1-like Zinc finger family protein)

:|||| | |||||
3' UUCGACAUGAGAGAGAGAAGA 5' miR529b, 4.5

5' CAGUUAUACUCUCUCUCC 3' LOC_0s08g34820 (F-box domain containing protein)

||:| |||||
3' UUCGACAUGAGAGAGAGAAGA 5' miR529b, 4.5

miR531b

5' CGGCGCGCGGCGGCGGCGAG 3' LOC_0s01g59819 (Glycosyl hydrolase family 1 protein)

||||:|||:||| |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 2.0

5' CGGCGCGCGGCGCGGCGAG 3' LOC_0s04g55240 (VQ motif family protein)

||||:|||:||| |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 2.0

miR531b

5' AGGCGCGCGGCCCCGGCGAG 3' LOC_Os09g36600 (Nodulin-like family protein)
|||:||||:|||||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 2.0

5' UGGCCCCGCCCGCCCGGCGAG 3' LOC_Os10g34420 (LysM domain containing protein)
:|||| ||| |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 2.5

5' CGGCGCCCGGCCCCGGCGGG 3' LOC_Os12g35610 (Respiratory burst oxidase homolog, putative)
||||:| |:|||||||:|
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 2.5

5' CCGCACGCCGCGCGGCGAG 3' LOC_Os03g58010 (Acetyltransferase, GNAT family protein)
| ||||| ||| |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 3.0

5' UGGCGCGCCGCCCGGCGAG 3' LOC_Os02g45700 (Fringe protein, putative)
:||||:|||| ||||| |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 3.0

5' CGGUACACCGCCCCGGCGCG 3' LOC_Os02g55040 (Vacuolar ATP synthase subunit D 1, putative)
|||:|| | |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 3.0

5' CUGCGCGCGCGCGGCGAG 3' LOC_Os04g47520 (Axi 1, putative)
| ||:|||| || |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 3.5

5' CGCCAGGCGUCUCCGGCGAG 3' LOC_Os09g33970 (Expressed protein)
|| || || |:|||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 3.5

5' CGCCGCGCGUGCGCGGCGAG 3' LOC_Os10g39820 (Zinc knuckle family protein)
|| |:|||| || |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 3.5

5' CGCCGCGCGCGCGGCGAG 3' LOC_Os11g04830 (Expressed protein)
|| |:|||| || |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 3.5

5' GGGCAUGAAGCACCGGCGAG 3' LOC_Os11g31140 (Hypothetical protein)
||||:| ||| |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 3.5

5' GGCCACUCAGCCCCGACGAG 3' LOC_Os01g39970 (Protein kinase domain containing protein)
| ||| ||||| |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 4.0

5' CGCCCCGCGCACCGGCGAG 3' LOC_Os07g44560 (AMP-binding enzyme family protein)
|| | ||| || |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 4.0

5' CCGCCGCGUGCCCGGCGAG 3' LOC_Os09g02380 (Hypothetical protein)
| || ||| |||| |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 4.0

5' AGGCUCGCCGCGCGGCGAG 3' LOC_Os09g31462 (Hypothetical protein)
||| ||| || |||||
3' GCCGUGCGUCGGGGCCGCUC 5' miR531b, 4.0

miR806i_as

5' UUA AAAAGUCAACGGCGUCAUA 3' LOC_Os03g19380 (CP12, putative)
| |||||
3' UACUUUUCAGUUGCCGAGUGU 5' miR806i_as, 2.5

5' UUA AAAAGUCAACGGCGUCAUA 3' LOC_Os09g33710 (Glycosyl hydrolase family 1 protein)
| |||||
3' UACUUUUCAGUUGCCGAGUGU 5' miR806i_as, 2.5

5' UUA AAAAGUCAACGGCGUCAA 3' LOC_Os10g33510 (Hypothetical protein)
| |||||
3' UACUUUUCAGUUGCCGAGUGU 5' miR806i_as, 3.0

miR806j_as

5' AAAAAGUCAACGGCGUCAUACAUU 3' LOC_Os03g19380 (CP12, putative)
|||||||:|||||||
3' AUUUUCAGUUGUCGCAGUAUGUAA 5' miR806j_as, 1.5

5' AAAAAGUCAACGGCGUCAUACAUU 3' LOC_Os09g33710 (Glycosyl hydrolase family 1 protein)
|||||||:|||||||
3' AUUUUCAGUUGUCGCAGUAUGUAA 5' miR806j_as, 1.5

5' AAAAAGUCAACAGCGUCAAACAUU 3' LOC_Os03g62330 (Expressed protein)
|||||||:|||||||
3' AUUUUCAGUUGUCGCAGUAUGUAA 5' miR806j_as, 2.0

5' AAAAAGUCAACGGCGUCAAACAUU 3' LOC_Os01g73250 (ABA/WDS induced protein)
|||||||:|||||||
3' AUUUUCAGUUGUCGCAGUAUGUAA 5' miR806j_as, 2.5

5' GAAAAGUUAACGGCGUCGUACAUU 3' LOC_Os04g09900 (Terpene synthase, N-terminal domain containing protein)
|||||||:|||||||
3' AUUUUCAGUUGUCGCAGUAUGUAA 5' miR806j_as, 2.5

5' AAAAAGUCAACGGCGUCAAACAUU 3' LOC_Os09g30454 (Wall-associated kinase-like 1)
|||||||:|||||||
3' AUUUUCAGUUGUCGCAGUAUGUAA 5' miR806j_as, 2.5

5' AAAAAGUCAACGGCGUCAAACAUU 3' LOC_Os11g34460 (Adagio 3, putative)
|||||||:|||||||
3' AUUUUCAGUUGUCGCAGUAUGUAA 5' miR806j_as, 2.5

miR812f (two target sites in the same gene)

5' CCGUGCCCAACUUUAUUCGUCCGU 3' LOC_Os02g07960 (Leucine Rich Repeat family protein)
|||||:|||||||
3' GGCACAGGUUGAAAUAGUAGGCA 5' miR812f, 1.5

5' UCGUGCCCAACUUUGAUCAUCCGU 3' LOC_Os02g07960 (Leucine Rich Repeat family protein)
:|||||:|||||||
3' GGCACAGGUUGAAAUAGUAGGCA 5' miR812f, 2.0

miR812g-j

5' UGCCCAACUUUAUUCGUCCGUCUU 3' LOC_Os02g07960 (Leucine Rich Repeat family protein)
||:|||||||
3' ACAGGUUGAAAUAGUAGGCAGAA 5' miR812g-j, 1.5

5' CGUCCAACUUUGAUCGUCCGUCUU 3' LOC_Os02g53180 (1-aminocyclopropane-1-carboxylate oxidase 1)
|||||||:|||||||
3' ACAGGUUGAAAUAGUAGGCAGAA 5' miR812g-j, 2.0

5' CGCCCAACUUUGAUCAUCCGUCUU 3' LOC_Os04g47140 (Expressed protein)
|:|||||||
3' ACAGGUUGAAAUAGUAGGCAGAA 5' miR812g-j, 2.5

miR1428b_3p

5' AAUAUUCACAGCUUUUUCUUA 3' LOC_Os09g16449 (ABC transporter family protein)
|:|||||||
3' GUUUAAGUGCCGAAAUAGAAU 5' miR1428b_3p, 4.0

miR1428e_3p

5' CAAAUACAAGGCAUUAUCUUC 3' LOC_Os03g17980 (Carbon catabolite derepressing protein kinase)
|||||:|||||||
3' GUUUAAGUACCGAAUAGAAU 5' miR1428e_3p, 3.0

5' CGAAUUCUUUGCAUUAUCUUA 3' AK109886 (No annotation available for this full length cDNA)
|:|||||||
3' GUUUAAGUACCGAAUAGAAU 5' miR1428e_3p, 3.5

5' CAAAUACAAGGCAUUAUCUUC 3' LOC_Os08g37800 (Carbon catabolite derepressing protein kinase)
|||||:|||||||
3' GUUUAAGUACCGAAUAGAAU 5' miR1428e_3p, 4.0

B. Predicted target genes of the candidate miRNAs

PI_miR56_5'

5' AAAAAUCUAUGUCAUCGUCCA 3' LOC_Os01g64290 (Expressed protein)
|||||||:|||||||:||||
3' UUUUUAGGUACAGUAGUAGGU 5' PI_miR56_5', 1.0

5' AAGAAUCCUGUCUUAUCCA 3' LOC_Os01g34350 (RNA dependent RNA polymerase family protein)
||:||||| |||| |||||||
3' UUUUUAGGUACAGUAGUAGGU 5' PI_miR56_5', 2.5

5' AUAAGCCAUGCCAUAUCCA 3' LOC_Os11g35580 (NB-ARC domain containing protein)
| ||| |||| |||||||
3' UUUUUAGGUACAGUAGUAGGU 5' PI_miR56_5', 3.0

PI_miR56_3'

5' UGUGGACGAUGACAUGGAUUU 3' LOC_Os01g31870 (Natural resistance-associated macrophage protein)
|||:|||||||:|||||
3' UCACUUGCUACUGUAUCUAAA 5' PI_miR56_3', 2.0

5' AGUCAUGAUGACAAGAUUU 3' LOC_Os12g31880 (Eukaryotic translation initiation factor 5B, putative)
||| ||:||||||| |||||||
3' UCACUUGCUACUGUAUCUAAA 5' PI_miR56_3', 2.5

PI_miR58_5'

5' AUAGACCAUGCCUAUACCUAC 3' UniGene, Os#S16415035
| ||| ||||||||| |||||
3' UCUCUAGUACGGAUAGGAUG 5' PI_miR58_5', 3.0

PI_miR58_3'

5' AGGUAGGGAUAGGCAUGAUCU 3' UniGene, Os#S16415035
||||||| ||||||||| |||
3' ACCAUCCAUAUCCGUACCAGA 5' PI_miR58_3', 2.0

PI_miR59_5'

5' CAGCGGUGAUCUACACAAGAA 3' LOC_Os07g26650 (Hypothetical protein)
|| ||:||||||||||| |||
3' GUAGCUACUAGAUGUGUCCU 5' PI_miR59_5', 2.5

5' CCUUGCUGAUCUACAAAAGGA 3' LOC_Os02g20160 (Pentatricopeptide, putative)
| |:| ||||||||| |||||
3' GUAGCUACUAGAUGUGUCCU 5' PI_miR59_5', 3.5

5' CCUCUAUGAACUACAUAGGA 3' LOC_Os08g07290 (HEAT repeat family protein)
| || |||| |||||:|||||
3' GUAGCUACUAGAUGUGUCCU 5' PI_miR59_5', 3.5

PI_miR60_3'a-b

5' CCAACGUUUGACCACUUGUCUUAU 3' LOC_Os04g5200 (Methionine aminopeptidase, putative)
|||||||:|||||||
3' CGUUGCAAACUGGUGAGCAGAAUA 5' PI_miR60_3'a-b, 1.5

5' ACAACGUUUGAUCACUCGUCUUAU 3' LOC_Os07g40450 (Expressed protein)
|||||||:|||||||
3' CGUUGCAAACUGGUGAGCAGAAUA 5' PI_miR60_3'a-b, 1.5

5' CCAACGUUUGACCAUUCGUCUUAU 3' LOC_Os11g34910 (Expressed protein)
|||||||:|||||||
3' CGUUGCAAACUGGUGAGCAGAAUA 5' PI_miR60_3'a-b, 1.5

PI_miR63_3'

5' GCGAGGAGACCGGGGUCACC 3' LOC_Os02g43950 (Expressed protein)
||||||| ||||:|||||
3' CCGCUCCUCCGGCCUCAGUGG 5' PI_miR63_3', 1.5

5' GCCGAGGAGCCGGAGUCAGC 3' LOC_Os12g27340 (Hypothetical protein)
| ||||||||| |||||
3' CCGCUCCUCCGGCCUCAGUGG 5' PI_miR63_3', 2.0

5' GGCGACGACCGCGGAGUCACC 3' LOC_Os12g27810 (F-box domain containing protein)
||||| || |||||||||
3' CCGCUCCUCCGGCCUCAGUGG 5' PI_miR63_3', 2.0

5' GGUGAGGAGACCGGGGUCACC 3' LOC_Os12g33290 (Hypothetical protein)
||:||||| ||||:|||||
3' CCGCUCCUCCGGCCUCAGUGG 5' PI_miR63_3', 2.0

5' AGCGAGGAGACCGGGGUCACC 3' LOC_Os10g12320 (Hypothetical protein)
 ||||| ||||:|||||
 3' CCGCUCCUCCGGCCUCAGUGG 5' PI_miR63_3', 2.5

5' GGGUGGACGCCGGAGUCGCC 3' LOC_Os12g10320 (Uncharacterized plant-specific domain TIGR01627 family protein)
 || ||| |||||:||
 3' CCGCUCCUCCGGCCUCAGUGG 5' PI_miR63_3', 3.5

5' GUCGGGACGCCGGAGCCACC 3' LOC_Os05g16230 (Expressed protein)
 | |:|||| ||||| ||||
 3' CCGCUCCUCCGGCCUCAGUGG 5' PI_miR63_3', 3.5

PI_miR66_3'a-b

5' GUAAAGUUUGACCACUCGUCUUUAU 3' LOC_Os01g12820 (Harpin-induced protein 1 containing protein)
 |:||||| ||||| |||||
 3' CGUUGCAAACUGGUGAGCAGAAUA 5' PI_miR66_3'a-b, 0.5

5' GUAAAGUUUGACCACUCGUCUUUAU 3' LOC_Os01g15970 (Expressed protein)
 |:||||| ||||| |||||
 3' CGUUGCAAACUGGUGAGCAGAAUA 5' PI_miR66_3'a-b, 0.5

5' GUAAAGUUUGACUACUCGUCUUUAU 3' LOC_Os12g16350 (3-hydroxyisobutyryl-coenzyme A hydrolase)
 |:||||| |:||||| |||||
 3' CGUUGCAAACUGGUGAGCAGAAUA 5' PI_miR66_3'a-b, 1.0

5' GCAACGUUUGACAACUUGUCUUUAU 3' LOC_Os03g50390 (Protein kinase, putative)
 ||||| ||||| |:|||||
 3' CGUUGCAAACUGGUGAGCAGAAUA 5' PI_miR66_3'a-b, 1.5

C. Predicted target genes of the phased small RNAs from the newly-identified MIRNA-like long hairpin

06g21900_P2_5'

5' CCUGAUGUUGUCCUCAGACA 3' LOC_Os08g22750 (Hypothetical protein)
 |||| || ||||| ||||
 3' GGACCACCACAAGGAGUCCGU 5' 06g21900_P2(+), 3.0

5' CUUGCUGCUGUCCUAAGGCA 3' LOC_Os05g06530 (Expressed protein)
 |:|| || ||||| |||||
 3' GGACCACCACAAGGAGUCCGU 5' 06g21900_P2(+), 3.5

06g21900_P3_5'

5' GGUGCUCCACCAGGACAACGC 3' LOC_Os02g48570 (POU family protein)
 ||||| ||||| |||||
 3' CCACGAGGUGGUCCUCUUGCG 5' 06g21900_P3(+), 1.0

5' GGCUCUCCAGCAGGAGAUCCG 3' LOC_Os04g59160 (Peroxidase family protein)
 || ||||| ||||| ||||
 3' CCACGAGGUGGUCCUCUUGCG 5' 06g21900_P3(+), 3.0

5' GGCUCUAACCAGGAGAAGGC 3' LOC_Os08g07810 (Strictosidine synthase family protein)
 || |||| ||||| ||||
 3' CCACGAGGUGGUCCUCUUGCG 5' 06g21900_P3(+), 3.0

5' GCUCGUGGCCAGGUGAACGC 3' LOC_Os03g54770 (Cleavage stimulation factor, 50 kDa subunit, putative)
 | |||| |:|||| |||||
 3' CCACGAGGUGGUCCUCUUGCG 5' 06g21900_P3(+), 3.5

5' GGUGGUACAUCAGGAGAUCCG 3' LOC_Os07g04530 (GYF domain containing protein)
 |||| | ||:||||| ||||
 3' CCACGAGGUGGUCCUCUUGCG 5' 06g21900_P3(+), 3.5

06g21900_P4_5'

5' GGAGGCAGUCAAUAGAGUCAG 3' LOC_Os03g18454 (Gamma interferon inducible lysosomal thiol reductase family protein)
 |||| |:|||| |||||
 3' GCUCGCGCGGUUAUCGAGUC 5' 06g21900_P4(+), 3.5

06g21900_P6_5'

5' CUUCUUCUCUCUCUCUGC 3' LOC_Os02g39630 (Iron-stress related protein, putative)
 | |||||:||||| ||||
 3' GUAGAAGAGGGAGAAGACAG 5' 06g21900_P6(+), 2.5

5' CACCUUCUCCUCUUCUGCG 3' LOC_Os04g43210 (Sugar transporter family protein)
 || ||||:||||| ||||
 3' GUAGAAGAGGGAGAAGACAG 5' 06g21900_P6(+), 2.5

5' CAUCCUCUCCUCUCUGC 3' LOC_Os08g41690 (Expressed protein)
 |||| ||:|||| |||||
 3' GUAGAAGAGGGAGAAGACAG 5' 06g21900_P6(+), 2.5

5' CAUCAUCACCCUCUUCUGUUC 3' LOC_Os09g25784 (Integral membrane protein DUF6 containing protein)
|||| || ||||| ||||| ||
3' GUAGAAGAGGGAGAAGACACG 5' 06g21900_P6(+), 3.0

5' GAUCCUCUCACUUUUCUGUGC 3' LOC_Os09g19560 (Protein arginine N-methyltransferase 1, putative)
||| |||| ||: ||||| |||||
3' GUAGAAGAGGGAGAAGACACG 5' 06g21900_P6(+), 3.5

06g21900_P1_3'

5' UGACCAUGGCAAGGCUGAAGA 3' LOC_Os03g18490 (Expressed protein)
| ||||| ||||| ||||| |||||
3' CCAGGUACCGUUGCGACUUCU 5' 06g21900_P1(-), 3.0

5' GCUUCAUGCCAAGGCUGAAGA 3' LOC_Os03g13590 (Tropomyosin, putative)
| |: |||| || ||||| |||||
3' CCAGGUACCGUUGCGACUUCU 5' 06g21900_P1(-), 3.5

06g21900_P2_3'

5' ACCGCCGAAGAUCAUCACCA 3' LOC_Os09g37100 (Phospholipase D delta, putative)
||||| ||||| ||||| |||||
3' GGGCGGCCUUCUUGUAGUGGU 5' 06g21900_P2(-), 2.0

5' UCCGCCGAAGAACUUCACCA 3' LOC_Os05g04380 (Peroxidase family protein)
: ||||| ||||| ||||| |||||
3' GGGCGGCCUUCUUGUAGUGGU 5' 06g21900_P2(-), 2.5

5' CCGCGGGGAGAACAUACAGCA 3' LOC_Os01g24030 (Adenosine monophosphate binding protein 2 AMPBP2, putative)
|| || || ||: ||||| ||||| ||
3' GGGCGGCCUUCUUGUAGUGGU 5' 06g21900_P2(-), 3.5

5' CCGCGGGGAGAACAUACAGCA 3' LOC_Os03g19240 (AMP-binding enzyme family protein)
|| || ||: ||||| ||||| ||
3' GGGCGGCCUUCUUGUAGUGGU 5' 06g21900_P2(-), 3.5

06g21900_P4_3'

5' UGCUGAAGUUGUUGCUGGCCA 3' LOC_Os02g57780 (Expressed protein)
||||| ||||| ||||| |||||
3' ACGACUACAACAACCACCGGU 5' 06g21900_P4(-), 2.0

5' UGUUGGUGUUGGUGGUGGCCA 3' LOC_Os03g60720 (Alpha-expansin 4 precursor, putative)
||: ||: ||||| ||||| |||||
3' ACGACUACAACAACCACCGGU 5' 06g21900_P4(-), 2.0

5' CGCUGCUGUUGUUGGUAGCCA 3' LOC_Os01g70940 (Potassium transporter 7, putative)
|||| ||||| ||||| |||||
3' ACGACUACAACAACCACCGGU 5' 06g21900_P4(-), 3.0

06g21900_P6_3'

5' AAGCACUAAAGAGGGCAGAGA 3' LOC_Os12g17310 (Myosin heavy chain, putative)
||||| ||||| ||||| |||||: |||||
3' UUCGUGAUUUCUCCCGUUUCU 5' 06g21900_P6(-), 0.5