

Supplemental Table 3A. Newly-identified miRNAs, miRNA-like long hairpins and their target genes

miRNA family	miRNA sequence	Len	No. of Loci	No. of reads		Location	Predicted target(s) ^b
				miRNA	miRNA* ^a		
miR1846a-c_5p	AGUGAGGAGGCCGGGCCGCU	21	3	6	2	Chr10, 11, 12, intergenic	Os02g43950 (0.5) Os10g12320 (0.5)
miR1846d.2_3p	UAUCCGGCGCCGCAGGGAGG	20	1	5	2	Chr1, intergenic	XM_463600 (0.0) Os02g47810 (3.5) Os09g28400 (3.5) Os09g38390 (2.5)
miR1847_5p ^c	UGCAGUUUGCAGUUGUGGCAC	21	1	6	0	Chr1, intergenic	Os11g27240 (3.5)
miR1847_3p ^c	UGGCCACAUUUAGUGCCACAAC	24	1	5	1	Chr1, intergenic	Os04g40590 (1.0)
miR1848	CCUCGCCGCGCGCGUGCA	21	1	8	1	Chr4, intergenic/gene	Os02g36110 (2.5) Os08g10649 (2.5) Os12g18374 (2.5) Os06g45330 (3.0) Os11g14400 (3.0) Os01g42540 (3.5) Os02g36070 (3.5) Os06g13160 (3.5) Os06g20120 (3.5) Os07g39530 (3.5) Os10g41270 (3.5)
miR1849	UAUCGUAUCCUAGGUUGGUUU	21	1	18	1	Chr4, intron	-
miR1850	UGGAAAGUUGGGAGAUUGGGG	21	1	2234	13	Chr5, intergenic	AK068321 (1.5) AK106712 (2.0) Os04g33510 (2.5) Os09g29200 (3.5) Os01g61520 (1.0)
miR1851 ^d	CGUCUGGGAUGGCAUUUUGGC	21	1	10	0	Chr5, gene/intergenic	-
miR1852	AUAUGGAUUCAGAAUGCAGGU	21	1	10	1	Chr5, intron	-
miR1853	UAAUUGGGGAUGUUCGGUUGC	21	1	6	2	Chr8, intergenic	Os02g38340 (3.5) Os09g26340 (3.5) Os12g38770 (3.0)
miR1854	UGGUGAAAUUUGUAGAUUGGA	21	1	6	2	Chr8, intergenic	AK109729 (3.0)
miR1855	AGCACUGGAGUAGCCAAGAGA	21	1	8	1	Chr11, intergenic	Os05g08370 (3.0) Os01g46610 (3.5)
miR1856	UAUGCGUAAGACGGAUUCGUA	21	1	28	3	Chr11, intron	-
miR1857	UCAUGCUCCAAGAAAACCAGG	21	1	7	2	Chr11, intron	-
miR1858a-b ^d	GAGAGGAGGACGGAGUGGGGC	21	2	25	0	Chr9, intergenic	Os01g53800 (0.5) Os01g54010 (1.5) Os04g34230 (1.5) Os07g26000 (1.5) Os04g35880 (2.0) Os01g21650 (3.0) Os01g21850 (3.0) Os03g19410 (3.0) Os06g36330 (3.0) Os02g20560 (3.5) Os02g53530 (3.5) Os06g13810 (3.5) Os08g23730 (3.5) AA754051 (EST, 3.0)
miR1859	UUUCCUAUGACGUCCAUUCCAA	22	1	216	46	Chr1, intergenic	Os11g38120 (2.5)
miR1860	AUCUGGAAGCUAGGUUUUCUCU	22	1	31	14	Chr1, 5' UTR	Os09g36100 (3.0)
miR1861a	UGAUCUUGAGGCAGAAACUGAG	22	2	11	1	Chr1, intergenic	-
miR1861b, f, i, l ^f	CGAUCUUGAGGCAGGAACUGAG	22	4	280	0-1	Chr2, 5, 6, 9, intergenic	Os05g51790 (3.5)
miR1861c ^f	CGAUCUUGUAGCAAGAACUGAG	22	1	2	0	Chr2, intergenic	-
miR1861d ^f	UGGUCUUGAGGCAGGAACUGAG	22	1	3	1	Chr4, intergenic	-
miR1861e, k, m ^f	CGGUCUUGUGGCAAGAACUGAG	22	3	3	0	Chr4, 8, 9, intergenic	-
miR1861g ^f	CAGUCUUGUGGCAAGAACUGAG	22	1	0	0	Chr5, intergenic	-
miR1861h, j ^f	CGGUCUUGAGGCAGGAACUGAG	22	2	91	0-8	Chr6, 8, intergenic	Os05g51790 (2.5)
miR1861n ^f	CGAUCUUGUGGCAGGAGCUGAG	22	1	3	1	Chr12, intergenic	Os03g03710 (3.0)
miR1862a-c	ACGAGGUUGGUUUUUUUUGGGACG	24	3	121	0-1	Chr1, 8, 10, intron or intergenic	Os01g58240 (3.5)
miR1862d ^h	ACUAGGUUUUGUUUUUUUUGGGACG	24	1	259	5	Chr10, intron	Os02g30730 (3.0) Os01g58240 (3.5)
miR1862e	CUAGAUUUUUUUUUUUGGGACGG	24	1	116	4	Chr11, intron	Os04g31120 (2.0) Os02g30730 (2.5)
miR1863	AGCUCUGAUACCAUGUUAUAG	24	1	29	1	Chr2, intergenic	-
miR1864	UUGUAGUAAACGUGAUGGUCAAUGU	24	1	44	2	Chr2, intron	-
miR1865	UGCUGUGAUGGUGAUUCUUCGAC	24	1	9	3	Chr3, intergenic	-
miR1866	GAGGGAUUUUGCGGGAUUUUCACG	24	1	77	3	Chr3, intergenic	-
miR1867	UUUUUUUUUCUAGGACAGAGGGAGU	24	1	127	2	Chr3, intron	AU058111 (EST, 2.0)
miR1868 ^g	UCACGGAAAACGAGGGAGCAGCCA	24	1	137	1	Chr4, intron	-
miR1869	UGAGAACAUAUGGCAUGGGAGGUUA	24	1	10	1	Chr4, intergenic	-
miR1870 ^d	UGCUGAAUUAGACCUAGUGGGCAU	24	1	594	0	Chr6, intron	-
miR1871	AUGGCUCUGAUCAUGUUGGUUU	24	1	17	2	Chr6, intron	-

miR1872	GAACUGUAAGUCUGUGACGGGUAA	24	1	5	1	Chr6, intergenic	Os12g14230 (2.0) Os06g46910 (2.5)
miR1873	UCAACAUGGUAUCAGAGCUGGAAG	24	1	41	3	Chr7, intron	-
miR1874	UAUGGAUGGAGGUUAACCCGAUG	24	1	350	113	Chr8, intergenic	-
miR1875	ACAAUGGAGUGAAGUGCAACAGAA	24	1	30	1	Chr9, 3' UTR	-
miR1876 ^h	AUAAGUGGGUUUGUGGGCUGGCC	24	1	13	0	Chr10, intron	AK066235 (2.5)
miR1877	AGAUGACAUGUGAAUGAUGAGGGG	24	1	246	6	Chr9, intergenic	-
miR1878	ACUUAUCUGGACACUAUAAAAGA	24	1	11	2	Chr9, intergenic	-
miR1879 ^d	GUGUUUGGUUAGGGAUGAGGUGG	24	1	40	0	Chr10, intron	-
miR1880	UUCCAAGCGGGCCACUUAAGCAUU	24	1	18	1	Chr11, intron	-
miR1881 ^d	AAUGUUAUUGUAGCGUGGUGGUGU	24	1	75	0	Chr12, intergenic	-
miR1882a-h	AGAUUGCUUUAAGGUCAUUUCUU	24	8	17	0-4	Chr3, 4, 7, 8, 10, 11, 12, intragenic or 5' UTR	-
miR1883a-b	ACCUGUGACGGGCCGAGAAUGGAA	24	2	24	0-4	Chr11, intron or intergenic	Os12g15260 (2.0)
miR529b	AGAAGAGAGAGAGUACAGCUU	21	1	24	1	Chr4, intergenic	Os08g39890 (1.0) Os09g21438 (1.0) Os01g69830 (2.5) Os01g65780 (3.0) Os05g14010 (3.0) Os06g28840 (3.5) Os08g35939 (3.5) Os01g59819 (2.0) Os04g55240 (2.0) Os09g36600 (2.0) Os10g34420 (2.5) Os12g35610 (2.5) Os02g45700 (3.0) Os02g55040 (3.0) Os03g58010 (3.0) Os04g47520 (3.5) Os09g33970 (3.5) Os10g39820 (3.5) Os11g04830 (3.5) Os11g31140 (3.5) Os03g19380 (2.5) Os09g33710 (2.5) Os10g33510 (3.0) Os03g19380 (1.5) Os09g33710 (1.5) Os03g62330 (2.0) Os01g73250 (2.5) Os04g09900 (2.5) Os09g30454 (2.5) Os11g34460 (2.5) Os02g07960 (1.5, 2.0)
miR531b	CUCGCCGGGGCUGCGUGCCG	20	1	5	1	Chr1, intergenic	Os02g07960 (1.5) Os02g53180 (2.0) Os04g47140 (2.5)
miR806i_as	UGUGACGCCGUUGACUUUUCAU	22	1	11	2	Chr2, intron	Os03g17980 (3.0) AK109886 (3.5) Os08g37800 (4.0)
miR806j_as ^h	AAUGUAGACGCUGUUGACUUUUA	24	1	25	1	Chr10, intron	-
miR812f	ACGGAUGAUUAAAGUUGGACACGG	24	1	145	1	Chr4, intergenic	-
miR812g-j	AAGACGGAUGAUUAAAGUUGGACA	24	4	327	0-2	Chr3, 7, 8, intergenic, or intron	-
miR1423b_5p ^g	CAACUACACGUUGGGCGCUCGA	22	1	389	28	Chr4, intron	-
miR1428b, c, d_3p ^e	UAAGAUAAUGCCAUGAAUUCG	21	3	1	0	Chr1, 2, 3, intergenic	-
miR1428e_3p ^e	UAAGAUAAUGCCAUGAAUUUG	21	1	27	13	Chr3, intergenic	-
miR1429.2 ⁱ	GUUGCACGGGUUUGUAUGUUGCAG	24	1	192	13	Chr8, intron	-

^aSome miRNAs were annotated without the corresponding miRNA*s because they belong to multiple member miRNA families, a long hairpin (see note d), are the most abundant small RNA from a hairpin with other miRNA/miRNA* pair(s) (miR1858, miR1870, miR1879 and miR1881), or are in tandem configuration with other miRNAs (miR1876).

^bPredicted target(s) with a score of 3.5 or less (except Os08g37800, which has a score of 4 and is a confirmed target of miR1428e_3p). The score is shown in parenthesis. See Supplemental Figure 6 for predicted targets with a score between 4 and 5.

^cThese two miRNAs are from the 5' and 3' arms of the same hairpin. miR1847_5p does not have the corresponding miRNA* but has more reads than miR1847_3p, therefore it was annotated as a putative miRNA.

^dmiR1851 is a long hairpin from which three phased small RNAs were generated. The putative miRNA/miRNA* pair was detected in two phases, and the most abundant phased small RNA is annotated as miRNA even though it does not have exact miRNA*.

^emiR1428d_3p and e_3p are tandem miRNAs.

^fmiR1861b and c, d and e, f and g, j and k, and l and m are tandem miRNAs, respectively; no exact miRNA but a variant was sequenced for miR1861g.

^gmiR1423b_5p and miR1868 are tandem miRNAs.

^hmiR1862d, miR1876 and miR806j_as are tandem miRNAs; as: antisense strand.

ⁱPutative mirtron.

Supplemental Table 3B. Candidate miRNAs and their target genes

miRNA family	miRNA sequence	Len	No. of Loci	No. of reads	Location	No. of predicted target(s) ^a
PI_miR52_5'	UUCUAGUUGACCAACAUACCACC	24	1	2	Chr1, intron	-
PI_miR52_3'	UGGUUUGUUGGCAUUGUAGGAA	22	1	2		-
PI_miR53_5'	ACUCUGAUUCUAGAAUUUUUGCGU	24	1	3	Chr1, intergenic	-
PI_miR53_3'	GCAAAAAUCCAGAAUCGGAUCC	23	1	1		-
PI_miR54_5'	UGUCUCACAUGGUUUCUGAGCUUA	24	1	1	Chr2, intergenic	-
PI_miR54_3'	GGCUCUGAUACCAUGUGAGGUUUG	24	1	4		-
PI_miR55_5'	CGGUUCCUGUCCCAAGAUCCGAG	22	1	1	Chr2, intergenic	-
PI_miR55_3'	CGAUCUUGUAGCAAGAACUGAG	22	1	2		-
PI_miR56_5'	UGGAUGAUAGCAUGGAUUUUU	21	1	2	Chr4, intron	3
PI_miR56_3'	AAAUCUAUGUCAUCGUUCACU	21	1	1		3
PI_miR57_5'	UUAUUUUUGUAGACGGUCCCCU	23	1	1	Chr4, intron	-
PI_miR57_3'	AGGGGUGUCUACAAAAUUGUCAU	24	1	4		-
PI_miR58_5'	GUAGGGAUAGCAUGAUCUCU	21	1	4	Chr5, intron	1
PI_miR58_3'	AGACCAUGCCUUAUACCUACCA	21	1	2		1
PI_miR59_5'	UCCUUGUGUAGAUCAUCGAUG	21	1	3	Chr6, CDS	3
PI_miR59_3'	UUGUGUAGAUCAUCGAUCUU	21	1	1		-
PI_miR60_5'	AAUGGCUUGUCUUGUUUUGUGUGC	24	1	4	Chr6, intron	-
PI_miR60_3'	ACGCAAAACGAGCCAAGUCAUUU	24	1	3		-
PI_miR61_5'	UACAUGUAUAAAAUUCUGAGGAUG	24	1	4	Chr8, intron	-
PI_miR61_3'	UCCUCAGGAUUUUUAUACAUGUAAA	24	1	1		-
PI_miR62_5'	GUGGGUUUCUGUGCCAACGUUGA	24	1	1	Chr8, intergenic	-
PI_miR62_3'	AAACGUUGGCACGGAACACACGG	24	1	2		-
PI_miR63_5'	AACGAGGAGGCCGGGACCACCGG	23	1	3	Chr9, 5' UTR	-
PI_miR63_3'	GGUGACUCCGGCCUCCUCGCC	21	1	1		7
PI_miR64_5'	CGCUCCACGUAGGCAACAAUU	21	1	2	Chr11, intron	-
PI_miR64_3'	UAGUUGCCUACAUGGAGCGCC	21	1	1		-
PI_miR65_5'	CGCTGTTGTGACTTTAGGGTAT	22	1	2	Chr11, intergenic	-
PI_miR65_3'	ACTCTAGAGTAACACGCGAGCAGT	24	1	1		-
PI_miR66_5'a-b	AACGUUUGACCACUUGUCUUUU	23	2	1	Chr11, intergenic	-
PI_miR66_3'a-b	AUAAGACGAGUGGUCAAACGUUGC	24	2	4		7

^aPredicted target(s) with a score of 3.5 or less. Number of target genes is shown in the parentheses. See Supplemental Figure 6B for alignments and target gene identifiers.