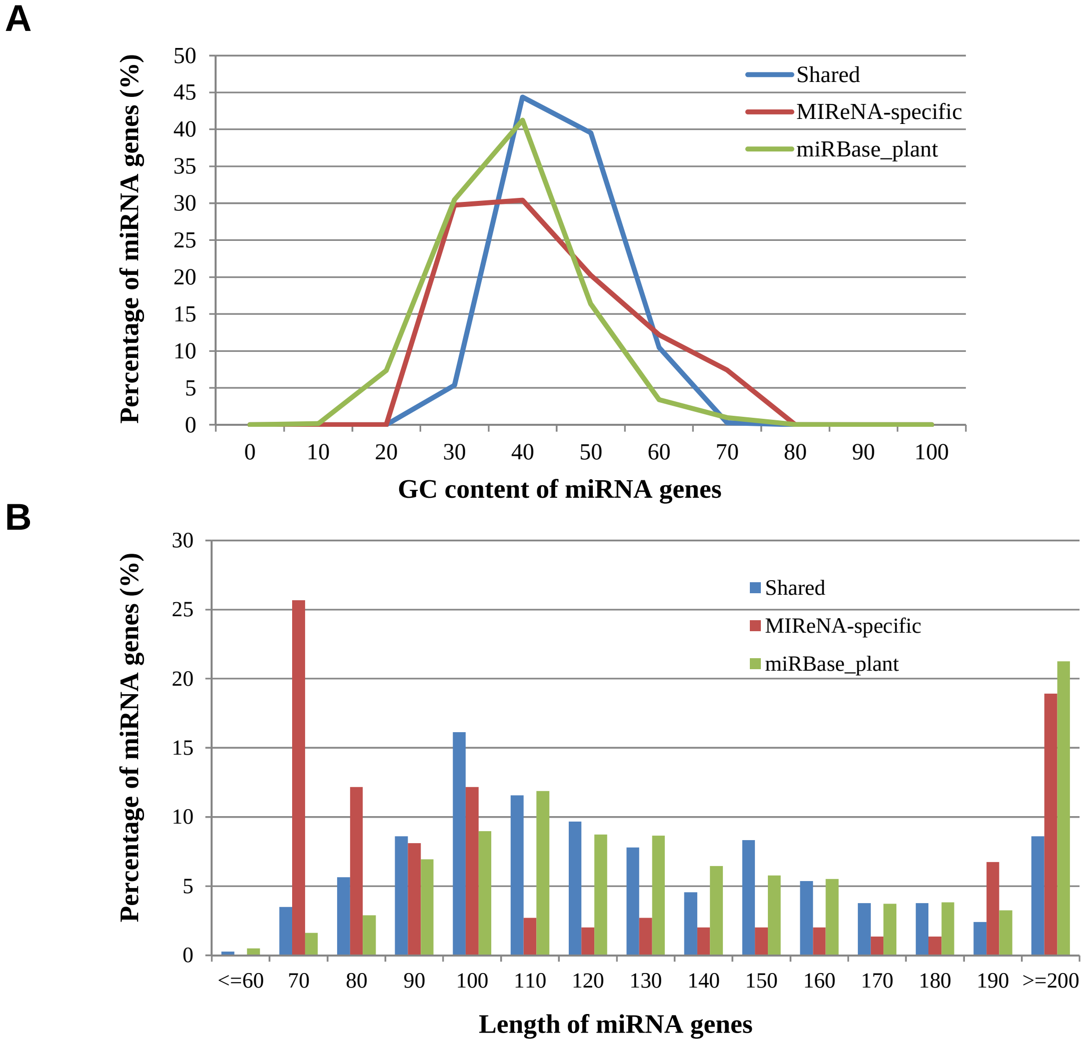
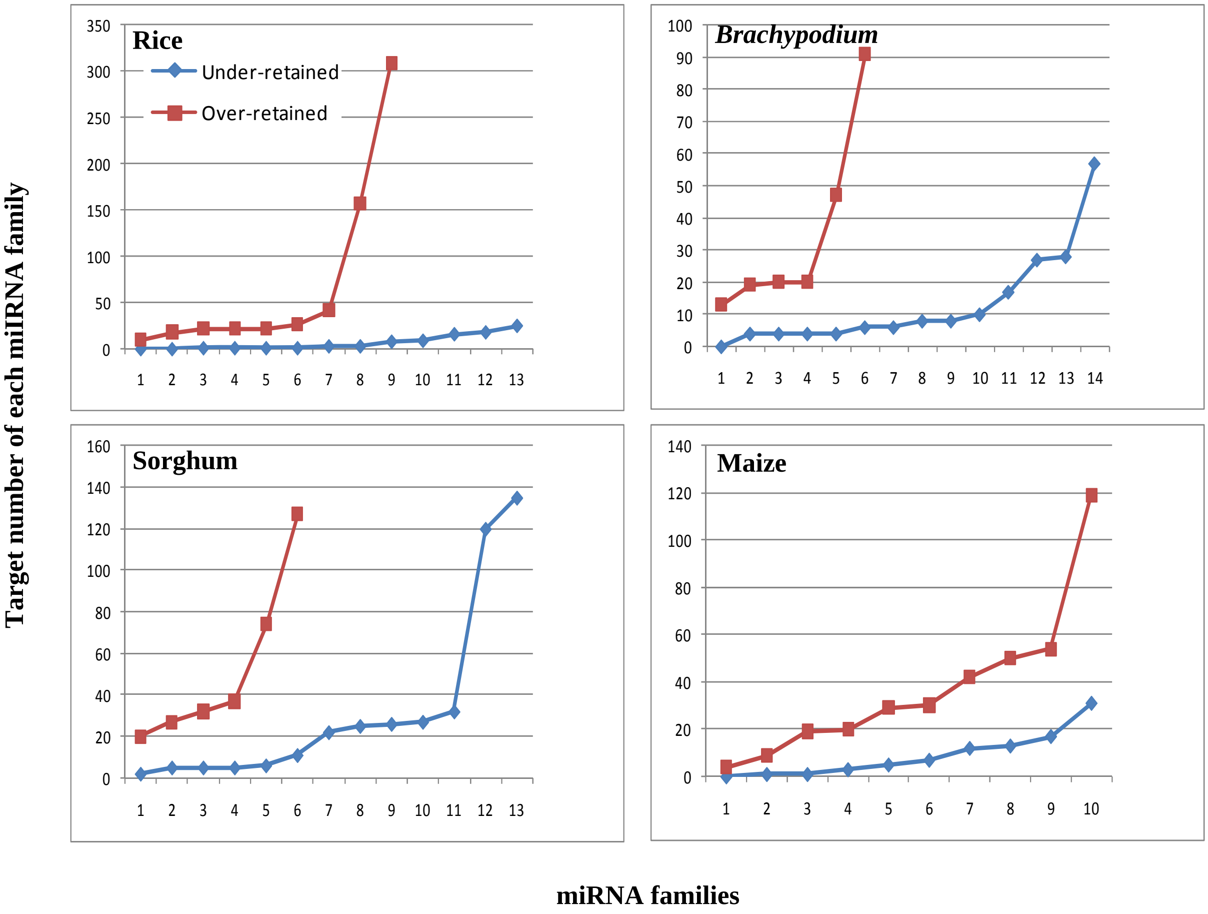


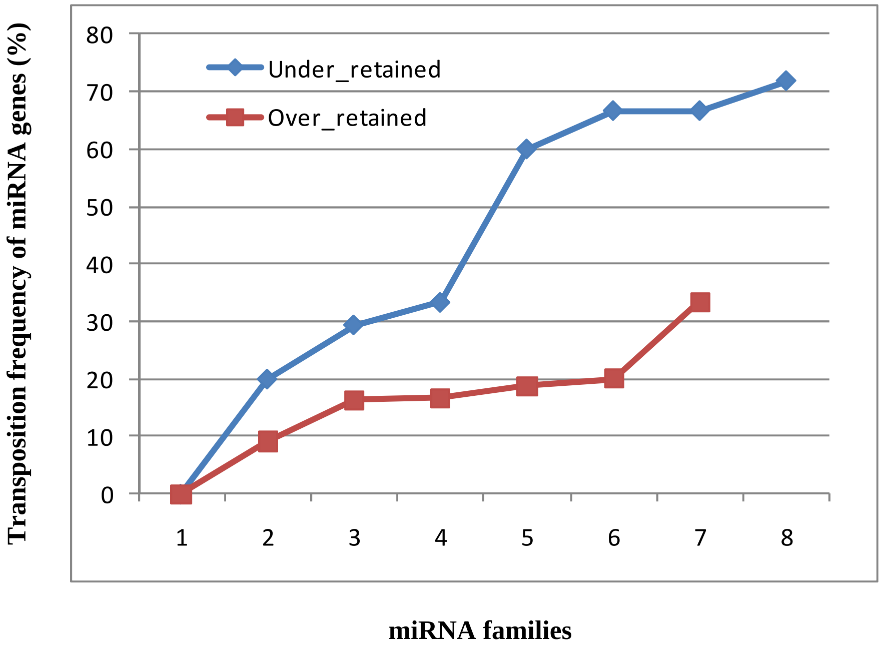
C

Species	Chromosome_region	MIReNA-specific	Shared	Fisher's Exact Test
Brachypodium	Sub-telomeric	23	55	*p-value* = 0,011
	Peri-centromeric	18	16	
Rice	Sub-telomeric	22	86	*p-value* = 0,015
	Peri-centromeric	16	24	
Sorghum	Sub-telomeric	34	74	*p-value* = 0
	Peri-centromeric	65	19	
Maize	Sub-telomeric	33	91	*p-value* = 0,023
	Peri-centromeric	23	30	
Total	Sub-telomeric	112	306	*p-value* = 0
	Peri-centromeric	122	89	

Supplemental Figure 1: Comparison between miRBase and MIReNA datasets.
A- GC content among shared, MIReNA-specific miRNA genes in four grass species, and total plant miRNA genes in miRBase database. **B-** Length distribution among shared, MIReNA-specific miRNA genes in four grass species, and total plant miRNA genes in miRBase database. **C-** The different distribution in the different chromosome region between shared and MIReNA-specific miRNA genes.



<u>Supplemental Figure 2</u>: Positive correlation between over-retained miRNA families and the number of target genes in monocots.
The figures illustrates the number of targets gene (y-axis) as a function of the number miRNA families (x-axis) for the under- (blue curve) and over- (red curve) retained miRNAs observed in rice, *Brachypodium*, sorghum, and maize genomes.



Supplemental Figure 3: Transposition frequency of grass miRNA families.
The figures illustrates the transposition frequency of miRNAs (y-axis) as a function of the number miRNA families (x-axis) for the under- (blue curve) and over- (red curve) retained miRNA observed in rice, *Brachypodium*, sorghum and maize genomes.

Supplemental Table 1. Conserved and duplicated miRNA genes identified in monocots.
The table provides the number of miRNAs from the 22 considered families (first column) in rice, sorghum, maize and *Brachypodium*. For each species are mentioned the number of detected miRNAs ('MIReNA' column), the number and percentage of orthologs ('Ortholog' column), and the number of paralogs ('Paralogs' column).

	Rice			Sorghum			Maize			Brachypodium		
	MIReNA	**orthologs**	**paralogs**	**MIReNA**	**orthologs**	**paralogs**	**MIReNA**	**orthologs**	**paralogs**	**MIReNA**	**orthologs**	**paralogs**
miR156/157	22	10 (45%)	5	32	10 (31%)	4	25	8 (32%)	3	13	10 (77%)	2
miR159	6	2 (33%)	0	2	1 (50%)	0	12	1 (8%)	1	7	2 (29%)	1
miR160	13	3 (23%)	1	5	2 (40%)	0	5	0 (0%)	0	4	2 (50%)	0
miR164	5	4 (80%)	1	6	2 (33%)	0	5	4 (80%)	1	4	2 (50%)	0
miR166	8	5 (63%)	2	5	4 (80%)	0	9	5 (56%)	0	6	5 (83%)	0
miR167	10	10 (100%)	2	12	10 (83%)	2	12	9 (75%)	2	7	6 (86%)	1
miR168	1	0 (0%)	0	2	0 (0%)	0	0	0 (0%)	0	0	0 (0%)	0
miR169	14	13 (93%)	2	25	15 (60%)	4	20	9 (45%)	1	12	8 (67%)	2
miR170/171	7	6 (86%)	0	12	7 (58%)	1	8	6 (75%)	2	3	2 (67%)	0
miR172	4	4 (100%)	0	32	4 (13%)	0	10	2 (20%)	0	6	2 (33%)	0
miR319	3	1 (33%)	0	3	2 (67%)	0	2	2 (100%)	0	4	0 (0%)	0
miR390	1	1 (100%)	0	2	1 (50%)	0	2	1 (50%)	0	1	1 (100%)	0
miR393	4	4 (100%)	0	1	1 (100%)	0	6	3 (50%)	0	4	4 (100%)	0
miR394	1	1 (100%)	0	2	1 (50%)	0	2	1 (50%)	1	1	0 (0%)	0
miR395	17	13 (76%)	0	17	11 (65%)	0	18	10 (56%)	5	19	8 (42%)	0
miR396	3	3 (100%)	1	4	3 (75%)	1	7	4 (57%)	3	6	4 (67%)	1
miR397	1	0 (0 %)	0	1	0 (0%)	0	2	0 (0%)	0	0	0 (0%)	0
miR398	1	1 (100%)	0	0	0 (0%)	0	3	1 (33%)	1	1	0 (0%)	0
miR399	9	9 (100%)	2	11	10 (91%)	2	18	4 (22%)	0	9	5 (56%)	1
miR528	4	1 (25%)	0	3	1 (33%)	0	5	1 (20%)	1	1	0 (0%)	0
miR529	13	2 (15%)	1	15	2 (13%)	0	5	2 (40%)	0	3	2 (67%)	0
miR535	3	0 (0%)	0	0	0 (0%)	0	1	0 (0%)	0	1	0 (0%)	0
total	150	93 (62%)	17	192	87 (45%)	14	177	73 (41%)	21	112	63 (56%)	8

<u>Supplemental Table 2.</u> Conserved and duplicated miRNA genes identified in eudicots.

The table provides the number of miRNAs from the 22 considered families (first column) in grape, Arabidopsis, soybean, poplar and cacao. For each species are mentioned the number of detected miRNAs (‘MIReNA’ column), the number and percentage of ortholog (‘Ortholog’ column), and the number of paralogs (‘Paralogs’ column).

	Grape			Arabidopsis			Soybean			Poplar			Cacao		
	MIReNA	orthologs	paralogs	MIReNA	orthologs	paralogs	MIReNA	orthologs	paralogs	MIReNA	orthologs	paralogs	MIReNA	orthologs	paralogs
miR156/157	17	7 (41%)	2	20	4 (20%)	2	57	5 (8%)	12	16	4 (25%)	5	13	2 (15%)	0
miR159	5	1 (20%)	0	3	0	0	8	1 (13%)	1	5	0	0	3	0	0
miR160	4	1 (25%)	0	1	0	0	3	1 (33%)	1	3	0	0	0	0	0
miR164	4	1 (25%)	0	3	0	0	12	0	5	8	1 (13%)	3	5	0	0
miR166	5	1 (20%)	0	4	1 (25%)	1	9	0	1	6	0	2	3	0	0
miR167	5	3 (60%)	1	3	1 (33%)	0	9	3 (33%)	3	4	2 (50%)	1	1	0	0
miR168	0	0	0	2	0	0	0	0	0	2	0	0	2	0	0
miR169	26	2 (7%)	0	10	1 (10%)	1	28	0	8	22	0	3	13	2 (15%)	1
miR170/171	7	2 (28%)	0	3	0	1	14	1 (7%)	3	8	2 (25%)	2	5	3 (60%)	1
miR172	6	2 (33%)	2	7	2 (29%)	1	19	2 (10%)	5	7	0	1	6	2 (33%)	1
miR319	2	0	0	2	0	0	11	0	2	5	0	0	1	0	0
miR390	2	1 (50%)	0	2	1 (50%)	0	7	1 (14%)	3	4	0	2	1	0	0
miR393	4	0	0	2	0	1	19	0	4	7	0	1	2	0	0
miR394	3	0	0	2	0	1	4	0	1	2	0	1	2	0	0
miR395	15	0	1	5	0	2	14	0	2	7	0	2	4	0	0
miR396	6	2 (33%)	1	2	0	0	10	0	4	8	2 (25%)	1	5	1 (20%)	0
miR397	0	0	0	1	0	0	3	0	1	2	0	0	0	0	0
miR398	3	1 (33%)	0	3	1 (33%)	0	3	0	1	2	0	0	2	0	0
miR399	7	4 (57%)	0	6	0	1	18	0	7	6	4 (33%)	1	8	0	1
miR528	13	0	1	0	0	0	0	0	0	0	0	0	0	0	0
miR529	13	0	0	9	0	2	25	0	3	8	0	0	7	0	0
miR535	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
total	147	28 (19%)	8	90	11 (12%)	13	274	14 (5%)	67	132	15 (11%)	25	84	10 (12%)	4

Supplemental Table 3. Over-retention frequency of miRNA families in rice, *Brachypodium*, sorghum and maize.
Note: Osa: rice; Bdi: *Brachypodium*; Sbi: sorghum; Zma: maize; ORM_fam: Over-retained miRNA families; TM_fam: total miRNA families with at least members; ORMF_FR: frequency of over-retained miRNA families.

Species	#ORM_fam	#TM_fam	ORMF_FR(%)
Osa	9	17	52.94
Bdi	6	15	40.00
Sbi	6	18	33.33
Zma	11	20	55.00
Average	8	17.5	45.32

Supplemental Table 4. Over-retained miRNA families in rice, *Brachypodium*, sorghum and maize.

The table delivers the miRNA families with members retained (between rice [Osa], *Brachypodium* [Bdi], sorghum [Sbi], and maize [Zma]) at the intra-specific syntenic regions after WGD, i.e., defined as over-retained miRNAs.

Osa	Bdi	Sbi	Zma
miR156	miR156	miR156	miR156
--	miR159	--	miR159
miR160	--	--	--
miR164	--	--	miR164
miR166	--	--	--
miR167	miR167	miR167	miR167
miR169	miR169	miR169	miR169
--	--	miR171	miR171
--	--	--	miR394
--	--	--	miR395
miR396	miR396	miR396	miR396
miR399	miR399	miR399	--
miR529	--	--	--
--	--	--	miR398
--	--	--	miR528

<u>Supplemental Table 5.</u> Under-retained miRNA families in rice, *Brachypodium*, sorghum and maize.

The table delivers the miRNA family with no members conserved ((between rice [Osa], *Brachypodium* [Bdi], sorghum [Sbi], and maize [Zma]) at the intra-specific syntenic regions after WGD, i.e., defined as under-retained miRNAs.

Osa	Bdi	Sbi	Zma
miR159	--	miR159	--
--	miR160	miR160	miR160
--	miR164	miR164	miR166
--	miR166	miR166	miR166
miR168	--	miR168	--
miR171	miR171	--	--
miR172	miR172	miR172	miR172
miR319	miR319	miR319	miR319
miR390	miR390	miR390	miR390
miR393	miR393	miR393	miR393
miR394	miR394	miR394	--
miR395	miR395	miR395	--
miR397		miR397	miR397
miR398	miR398	--	--
--	--	--	miR399
miR528	miR528	miR528	
--	miR529	miR529	miR529
miR535	miR535	--	miR535

<u>Supplemental Table 6.</u> Number of miRNA targets in rice, *Brachypodium*, sorghum and maize. MiRNA families in the gray shadow regions are over-retained after WGD.

OSA		SBI		BDI		ZMA	
Family	#Target	Family	#Target	Family	#Target	Family	#Target
miR390	0	miR390	2	miR398	0	miR390	0
miR398	0	miR319	5	miR171	4	miR397	1
miR168	1	miR394	5	miR390	4	miR398	1
miR319	1	miR397	5	miR393	4	miR319	3
miR394	1	miR159	6	miR535	4	miR393	5
miR528	1	miR168	11	miR319	6	miR160	7
miR393	3	miR528	22	miR394	6	miR166	12
miR535	3	miR160	25	miR166	8	miR399	13
miR171	8	miR166	26	miR528	8	miR529	17
miR397	9	miR395	27	miR160	10	miR172	31
miR172	16	miR164	32	miR395	17	miR394	4
miR159	18	miR529	120	miR172	27	miR171	9
miR395	25	miR172	135	miR529	28	miR167	19
miR160	10	miR399	20	miR164	57	miR159	20
miR167	18	miR171	27	miR159	13	miR395	29
miR166	22	miR396	32	miR396	19	miR528	30
miR169	22	miR167	37	miR167	20	miR164	42
miR396	22	miR169	74	miR169	20	miR169	50
miR399	27	miR156	127	miR399	47	miR396	54
miR164	42			miR156	91	miR156	119
miR156	157						
miR529	309						

Supplemental Table 7. MiRNA target gene enrichment analysis in GO biological process categories.

Over-Retained miRNA (OR-miRNA) and Under-retained miRNAs (UR-miRNA) (as defined in the legends of Table S3 and S4) with the list of their target genes in statistically enriched GO terms are listed. Adjusted *p-value*, based on Benjamini and Hochberg correction applied on hypergeometric test, is given. Cluster frequency represents total number of genes annotated to that GO term divided by total number of genes in the test set. Total frequency represents total number of genes annotated to that GO term divided by the total number of genes in the reference set. Since one gene can be related to multiple GO terms, the sum of the percentages in each column is not a relevant parameter.

species	GO	Description	P-value	FDR	cluster freq	total freq	genes	miRNA
RESPONSE TO STIMULUS								
Bdi_OR	9719	response to endogenous stimulus	1.01E-04	8.05E-03	4/92 4.3%	24/8800 0.2%	BRADI3G04920 BRADI5G25770 BRADI4G01730 BRADI1G32550	miR167
	9725	response to hormone stimulus	1.01E-04	8.05E-03	4/92 4.3%	24/8800 0.2%	BRADI3G04920 BRADI5G25770 BRADI4G01730 BRADI1G32550	miR167
	10033	response to organic substance	1.20E-04	8.05E-03	4/92 4.3%	25/8800 0.2%	BRADI3G04920 BRADI5G25770 BRADI4G01730 BRADI1G32550	miR167
Osa_OR	10033	response to organic substance	3.17E-10	3.13E-08	8/511 1.5%	26/45432 0.0%	LOC_OS06G46410 LOC_OS02G06910 LOC_OS10G33940 LOC_OS04G59430 LOC_OS02G41800 LOC_OS04G57610 LOC_OS12G41950 LOC_OS06G47150	miR160 miR167
	9719	response to endogenous stimulus	3.17E-10	3.13E-08	8/511 1.5%	26/45432 0.0%	LOC_OS06G46410 LOC_OS02G06910 LOC_OS10G33940 LOC_OS04G59430 LOC_OS02G41800 LOC_OS04G57610 LOC_OS12G41950 LOC_OS06G47150	miR160 miR167
	9725	response to hormone stimulus	3.17E-10	3.13E-08	8/511 1.5%	26/45432 0.0%	LOC_OS06G46410 LOC_OS02G06910 LOC_OS10G33940 LOC_OS04G59430 LOC_OS02G41800 LOC_OS04G57610 LOC_OS12G41950 LOC_OS06G47150	miR160 miR167
Zm_OR	9719	response to endogenous stimulus	1.06E-07	6.28E-06	7/174 4.0%	38/16863 0.2%	GRMZM2G028980 GRMZM2G089640 GRMZM2G475882 GRMZM2G078274 GRMZM2G035405 GRMZM2G378580 GRMZM2G073750	miR159 miR167
	50896	response to stimulus	7.33E-04	7.86E-03	35/174 20.1%	1950/16863 11.5%	AC210013.4 GRMZM2G111082 GRMZM2G154987 GRMZM2G450128 GRMZM2G060721 GRMZM2G114850 GRMZM2G009892 GRMZM2G378580 AC212570.3 GRMZM2G073750 GRMZM2G089640 GRMZM2G146380 GRMZM2G377589 GRMZM2G035405 AY530952.1 GRMZM2G023840 GRMZM2G178261 GRMZM2G028980 AC189750.4 GRMZM2G103812 GRMZM2G104262 GRMZM2G078274	miR156 miR159 miR164 miR167 miR169 miR395 miR396 miR528

							GRMZM2G107562 GRMZM2G018484 GRMZM2G040785 GRMZM2G059887 AC204352.3 GRMZM2G152808 GRMZM2G047456 GRMZM2G475882 GRMZM2G164909 GRMZM2G405581 AC233899.1 GRMZM2G136525 GRMZM2G166940		
Bdi_UR	9719	response to endogenous stimulus	2.30E-06	2.07E-04	5/82 6.0%	24/8800 0.2%	BRADI3G28950 BRADI3G49320 BRADI5G15900 BRADI5G27400 BRADI1G33160	miR160	
	9725	response to hormone stimulus	2.30E-06	2.07E-04	5/82 6.0%	24/8800 0.2%	BRADI3G28950 BRADI3G49320 BRADI5G15900 BRADI5G27400 BRADI1G33160	miR160	
	42221	response to chemical stimulus	2.04E-03	2.23E-02	8/82 9.7%	247/8800 2.8%	BRADI3G28950 BRADI3G49320 BRADI5G15900 BRADI5G18830 BRADI5G27400 BRADI5G27210 BRADI1G33160 BRADI3G51590	miR160 miR166	miR164
BIOLOGY REGULATION									
Bdi_UR	45449	regulation of transcription	1.36E-05	3.58E-04	23/82 28.0%	960/8800 10.9%	BRADI5G15900 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR166 miR393 miR529	miR164 miR172 miR398
	6355	regulation of transcription, DNA-dependent	8.90E-05	1.21E-03	16/82 19.5%	590/8800 6.7%	BRADI5G15900 BRADI2G29960 BRADI1G03880 BRADI2G37800 BRADI5G00700 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI1G47670 BRADI3G28970 BRADI5G27400 BRADI1G13910 BRADI1G53650 BRADI4G01890 BRADI2G06210 BRADI1G33160	miR160 miR172 miR529	miR166 miR398
	10468	regulation of gene expression	1.85E-05	3.66E-04	23/82 28.0%	978/8800 11.1%	BRADI5G15900 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR166 miR393 miR529	miR164 miR172 miR398
	9889	regulation of biosynthetic process	1.64E-05	3.58E-04	23/82 28.0%	971/8800 11.0%	BRADI5G15900 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR166 miR393 miR529	miR164 miR172 miR398

31326	regulation of cellular biosynthetic process	1.64E-05	3.58E-04	23/82 28.0%	971/8800 11.0%	BRADI5G15900 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR164 miR166 miR172 miR393 miR398 miR529
10556	regulation of macromolecule biosynthetic process	1.64E-05	3.58E-04	23/82 28.0%	971/8800 11.0%	BRADI5G15900 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR164 miR166 miR172 miR393 miR398 miR529
50794	regulation of cellular process	2.07E-04	2.66E-03	24/82 29.2%	1219/8800 13.8%	BRADI5G15900 BRADI2G54230 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR164 miR166 miR172 miR393 miR398 miR528 miR529
50789	regulation of biological process	5.69E-04	6.90E-03	24/82 29.2%	1303/8800 14.8%	BRADI5G15900 BRADI2G54230 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR164 miR166 miR172 miR393 miR398 miR528 miR529
65007	biological regulation	1.42E-03	1.63E-02	24/82 29.2%	1388/8800 15.7%	BRADI5G15900 BRADI2G54230 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR164 miR166 miR172 miR393 miR398 miR528 miR529
51171	regulation of nitrogen compound metabolic process	8.75E-06	3.58E-04	24/82 29.2%	1005/8800 11.4%	BRADI5G15900 BRADI2G54230 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR164 miR166 miR172 miR393 miR398 miR528 miR529

	19219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	8.75E-06	3.58E-04	24/82 29.2%	1005/8800 11.4%	BRADI5G15900 BRADI2G54230 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR164 miR166 miR172 miR393 miR398 miR528 miR529
	31323	regulation of cellular metabolic process	1.27E-05	3.58E-04	24/82 29.2%	1027/8800 11.6%	BRADI5G15900 BRADI2G54230 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR164 miR166 miR172 miR393 miR398 miR528 miR529
	80090	regulation of primary metabolic process	2.38E-05	4.33E-04	24/82 29.2%	1066/8800 12.1%	BRADI5G15900 BRADI2G54230 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR164 miR166 miR172 miR393 miR398 miR528 miR529
	19222	regulation of metabolic process	3.78E-05	6.33E-04	24/82 29.2%	1096/8800 12.4%	BRADI5G15900 BRADI2G54230 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR164 miR166 miR172 miR393 miR398 miR528 miR529
	60255	regulation of macromolecule metabolic process	5.12E-05	7.97E-04	23/82 28.0%	1042/8800 11.8%	BRADI5G15900 BRADI1G03880 BRADI2G29960 BRADI1G17660 BRADI2G53260 BRADI2G37800 BRADI5G00700 BRADI3G47630 BRADI2G57100 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI3G46900 BRADI1G47670 BRADI3G28970 BRADI4G02060 BRADI5G27400 BRADI1G13910 BRADI1G32660 BRADI1G53650 BRADI2G06210 BRADI4G01890 BRADI1G33160	miR160 miR164 miR166 miR172 miR393 miR398 miR529
	51252	regulation of RNA metabolic process	8.90E-05	1.21E-03	16/82 19.5%	590/8800 6.7%	BRADI5G15900 BRADI2G29960 BRADI1G03880 BRADI2G37800 BRADI5G00700 BRADI3G52840 BRADI3G28950 BRADI3G49320 BRADI1G47670 BRADI3G28970 BRADI5G27400 BRADI1G13910 BRADI1G53650 BRADI4G01890 BRADI2G06210 BRADI1G33160	miR160 miR166 miR172 miR398 miR529
Osa_UR	31326	regulation of cellular biosynthetic process	1.43E-03	1.84E-02	10/95 10.5%	1538/45432 3.3%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430	miR159 miR172 miR395

						LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	
9889	regulation of biosynthetic process	1.43E-03	1.84E-02	10/95 10.5%	1538/45432 3.3%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395
10556	regulation of macromolecule biosynthetic process	1.43E-03	1.84E-02	10/95 10.5%	1538/45432 3.3%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395
51171	regulation of nitrogen compound metabolic process	1.46E-03	1.84E-02	10/95 10.5%	1543/45432 3.3%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395
50794	regulation of cellular process	5.82E-03	3.62E-02	10/95 10.5%	1873/45432 4.1%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395
65007	biological regulation	3.98E-03	2.83E-02	11/95 11.5%	2070/45432 4.5%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS06G40700 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395 miR398
31323	regulation of cellular metabolic process	1.93E-03	1.84E-02	10/95 10.5%	1602/45432 3.5%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395
60255	regulation of macromolecule metabolic process	2.02E-03	1.84E-02	10/95 10.5%	1612/45432 3.5%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395
80090	regulation of primary metabolic process	2.20E-03	1.84E-02	10/95 10.5%	1631/45432 3.5%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395
19222	regulation of metabolic process	2.63E-03	2.00E-02	10/95 10.5%	1672/45432 3.6%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040	miR159 miR172 miR395

							LOC_OS04G46384 LOC_OS05G41166	
	50789	regulation of biological process	7.99E-03	4.73E-02	10/95 10.5%	1963/45432 4.3%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395
	51252	regulation of RNA metabolic process	5.86E-03	3.62E-02	6/95 6.3%	776/45432 1.7%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS07G13170 LOC_OS05G03040	miR172 miR395
	45449	regulation of transcription	1.16E-03	1.84E-02	10/95 10.5%	1495/45432 3.2%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395
	10468	regulation of gene expression	1.58E-03	1.84E-02	10/95 10.5%	1559/45432 3.4%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395
	6355	regulation of transcription, DNA-dependent	5.75E-03	3.62E-02	6/95 6.3%	773/45432 1.7%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS07G13170 LOC_OS05G03040	miR172 miR395
	19219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.46E-03	1.84E-02	10/95 10.5%	1543/45432 3.3%	LOC_OS11G06020 LOC_OS06G43220 LOC_OS03G52239 LOC_OS03G60430 LOC_OS02G15760 LOC_OS07G13170 LOC_OS01G12700 LOC_OS05G03040 LOC_OS04G46384 LOC_OS05G41166	miR159 miR172 miR395
Sbi_UR	10556	regulation of macromolecule biosynthetic process,	1.15E-06	7.65E-05	56/212 26.4%	2689/19262 13.9%	SB04G026610 SB10G025390 SB03G000840 SB08G021460 SB01G006380 SB01G003400 SB08G021350 SB06G024630 SB01G021280 SB01G010930 SB03G029330 SB08G016670 SB10G027913 SB10G027790 SB06G024360 SB03G000530 SB03G002660 SB10G006690 SB10G004590 SB08G006330 SB06G019010 SB04G009390 SB03G037560 SB10G020490 SB07G027160 SB02G020900 SB03G000560 SB10G010430 SB01G029650 SB02G007000 SB09G020160 SB01G019130 SB08G006300 SB07G000645 SB10G024180 SB06G024510 SB10G025053 SB01G037670 SB10G027220 SB10G022530 SB04G022260 SB07G019850 SB06G033970 SB06G022810 SB04G023990 SB04G032570 SB04G032590 SB02G030600 SB06G025190 SB02G000900 SB01G013710 SB01G019120 SB01G050000 SB10G000520 SB09G029840 SB06G024820	miR160 miR164 miR166 miR172 miR319 miR390 miR394 miR395 miR397 miR528 miR529

51171	regulation of nitrogen compound metabolic process,	1.63E-06	9.27E-05	57/212 26.8%	2789/19262 14.4%	SB04G026610 SB10G025390 SB03G000840 SB08G021460 SB01G006380 SB01G003400 SB08G021350 SB06G024630 SB01G021280 SB01G010930 SB03G029330 SB08G016670 SB10G027913 SB10G027790 SB06G024360 SB03G000530 SB03G002660 SB10G006690 SB10G004590 SB08G006330 SB06G019010 SB04G009390 SB03G037560 SB10G020490 SB07G027160 SB02G020900 SB03G000560 SB10G010430 SB01G029650 SB02G007000 SB02G039740 SB09G020160 SB01G019130 SB08G006300 SB07G000645 SB10G024180 SB06G024510 SB10G025053 SB01G037670 SB10G027220 SB04G022260 SB10G022530 SB07G019850 SB06G033970 SB06G022810 SB04G023990 SB04G032570 SB04G032590 SB02G030600 SB06G025190 SB02G000900 SB01G013710 SB01G019120 SB01G050000 SB10G000520 SB09G029840 SB06G024820	miR160 miR164 miR166 miR172 miR319 miR390 miR394 miR395 miR397 miR528 miR529
45449	regulation of transcription,	2.30E-07	2.37E-05	56/212 26.4%	2560/19262 13.2%	SB04G026610 SB10G025390 SB03G000840 SB08G021460 SB01G006380 SB01G003400 SB08G021350 SB06G024630 SB01G021280 SB01G010930 SB03G029330 SB08G016670 SB10G027913 SB10G027790 SB06G024360 SB03G000530 SB03G002660 SB10G006690 SB10G004590 SB08G006330 SB06G019010 SB04G009390 SB03G037560 SB10G020490 SB07G027160 SB02G020900 SB03G000560 SB10G010430 SB01G029650 SB02G007000 SB09G020160 SB01G019130 SB08G006300 SB07G000645 SB10G024180 SB06G024510 SB10G025053 SB01G037670 SB10G027220 SB10G022530 SB04G022260 SB07G019850 SB06G033970 SB06G022810 SB04G023990 SB04G032570 SB04G032590 SB02G030600 SB06G025190 SB02G000900 SB01G013710 SB01G019120 SB01G050000 SB10G000520 SB09G029840 SB06G024820	miR160 miR164 miR166 miR172 miR319 miR390 miR394 miR395 miR397 miR528 miR529
10468	regulation of gene expression,	5.44E-07	4.40E-05	60/212 28.3%	2906/19262 15.0%	SB04G026610 SB10G025390 SB03G000840 SB08G021460 SB01G006380 SB01G003400 SB08G021350 SB06G024630 SB01G021280 SB01G010930 SB03G029330 SB08G016670 SB10G027913 SB10G027790 SB06G024360 SB03G000530 SB03G002660 SB10G006690 SB10G004590 SB08G006330 SB06G019010 SB04G009390 SB03G037560 SB10G020490 SB07G027160 SB06G025560 SB02G020900 SB03G000560 SB10G010430 SB01G029650 SB04G038420 SB02G007000 SB02G039740	miR160 miR164 miR166 miR168 miR172 miR319 miR390 miR394 miR395 miR397 miR528 miR529

							SB09G020160 SB01G019130 SB08G006300 SB07G000645 SB10G024180 SB06G024510 SB01G037670 SB10G025053 SB10G027220 SB04G022260 SB10G022530 SB07G019850 SB06G033970 SB06G022810 SB04G023990 SB04G032570 SB04G032590 SB02G030600 SB06G025190 SB02G000900 SB01G013710 SB01G019120 SB01G050000 SB10G000520 SB09G029840 SB10G031030 SB06G024820	
	19219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,	1.32E-06	8.34E-05	57/212 26.8%	2771/19262 14.3%	SB04G026610 SB10G025390 SB03G000840 SB08G021460 SB01G006380 SB01G003400 SB08G021350 SB06G024630 SB01G021280 SB01G010930 SB03G029330 SB08G016670 SB10G027913 SB10G027790 SB06G024360 SB03G000530 SB03G002660 SB10G006690 SB10G004590 SB08G006330 SB06G019010 SB04G009390 SB03G037560 SB10G020490 SB07G027160 SB02G020900 SB03G000560 SB10G010430 SB01G029650 SB02G007000 SB02G039740 SB09G020160 SB01G019130 SB08G006300 SB07G000645 SB10G024180 SB06G024510 SB10G025053 SB01G037670 SB10G027220 SB04G022260 SB10G022530 SB07G019850 SB06G033970 SB06G022810 SB04G023990 SB04G032570 SB04G032590 SB02G030600 SB06G025190 SB02G000900 SB01G013710 SB01G019120 SB01G050000 SB10G000520 SB09G029840 SB06G024820	miR160 miR164 miR166 miR172 miR319 miR390 miR394 miR395 miR397 miR528 miR529
Zm_UR	6350	transcription	9.23E-04	1.75E-02	16/50 32.0%	2364/16863 14.0%	AC207656.3 GRMZM2G178102 GRMZM2G085751 GRMZM2G409974 GRMZM2G010357 AC225147.4 GRMZM2G081406 GRMZM2G369356 GRMZM2G390641 GRMZM2G005284 GRMZM2G109987 AC187157.4 GRMZM2G126239 GRMZM2G017414 GRMZM2G176175 GRMZM2G076602	miR160 miR166 miR172 miR399 miR529
Sbi_OR	45449	regulation of transcription,	4.59E-05	5.42E-03	40/160 25.0%	2560/19262 13.2%	SB01G019050 SB01G009330 SB09G002225 SB02G003070 SB01G029650 SB08G021460 SB04G034800 SB10G027100 SB08G021080 SB07G000645 SB01G006020 SB04G004430 SB05G021480 SB08G021350 SB10G025053 SB06G015640 SB06G027465 SB01G040270 SB04G030770 SB06G032500 SB10G027220 SB06G024630 SB01G021280 SB01G050333 SB08G019930 SB01G010930 SB02G002720 SB01G012170 SB04G032590 SB04G032570 SB06G025710 SB04G004940 SB10G029190	miR160 miR166 miR172 miR390 miR395 miR397 miR528 miR529

						SB10G006690 SB10G027280 SB10G000520 SB10G001350 SB04G031890 SB08G021690 SB06G024820	
31326	regulation of cellular biosynthetic process,	5.06E-05	5.42E-03	42/160 26.2%	2757/19262 14.3%	SB01G019050 SB01G009330 SB09G002225 SB01G029650 SB02G003070 SB08G021460 SB04G034800 SB10G027100 SB08G021080 SB07G000645 SB01G006020 SB05G007370 SB04G004430 SB05G021480 SB08G021350 SB10G025053 SB06G015640 SB06G027465 SB01G040270 SB04G030770 SB06G032500 SB10G027220 SB06G024630 SB01G021280 SB01G050333 SB08G019930 SB01G010930 SB02G002720 SB01G012170 SB04G032590 SB04G032570 SB06G025710 SB04G004940 SB10G029190 SB10G006690 SB10G027280 SB10G000520 SB10G001350 SB09G028700 SB04G031890 SB08G021690 SB06G024820	miR160 miR166 miR172 miR390 miR395 miR397 miR528 miR529
9889	regulation of biosynthetic process,	5.14E-05	5.42E-03	42/160 26.2%	2759/19262 14.3%	SB01G019050 SB01G009330 SB09G002225 SB01G029650 SB02G003070 SB08G021460 SB04G034800 SB10G027100 SB08G021080 SB07G000645 SB01G006020 SB05G007370 SB04G004430 SB05G021480 SB08G021350 SB10G025053 SB06G015640 SB06G027465 SB01G040270 SB04G030770 SB06G032500 SB10G027220 SB06G024630 SB01G021280 SB01G050333 SB08G019930 SB01G010930 SB02G002720 SB01G012170 SB04G032590 SB04G032570 SB06G025710 SB04G004940 SB10G029190 SB10G006690 SB10G027280 SB10G000520 SB10G001350 SB09G028700 SB04G031890 SB08G021690 SB06G024820	miR160 miR166 miR172 miR390 miR395 miR397 miR528 miR529
10556	regulation of macromolecule biosynthetic process,	6.29E-05	5.71E-03	41/160 25.6%	2689/19262 13.9%	SB01G019050 SB01G009330 SB09G002225 SB02G003070 SB01G029650 SB08G021460 SB04G034800 SB10G027100 SB08G021080 SB07G000645 SB01G006020 SB04G004430 SB05G021480 SB08G021350 SB10G025053 SB06G015640 SB06G027465 SB01G040270 SB04G030770 SB06G032500 SB10G027220 SB06G024630 SB01G021280 SB01G050333 SB08G019930 SB01G010930 SB02G002720 SB01G012170 SB04G032590 SB04G032570 SB06G025710 SB04G004940 SB10G029190 SB10G006690 SB10G027280 SB10G000520 SB10G001350 SB09G028700 SB04G031890	miR160 miR166 miR172 miR390 miR395 miR397 miR528 miR529

						SB08G021690 SB06G024820	
51171	regulation of nitrogen compound metabolic process,	6.62E-05	5.71E-03	42/160 26.2%	2789/19262 14.4%	SB01G019050 SB01G009330 SB09G002225 SB01G029650 SB02G003070 SB08G021460 SB04G034800 SB10G027100 SB01G016830 SB08G021080 SB07G000645 SB01G006020 SB05G007370 SB04G004430 SB05G021480 SB08G021350 SB10G025053 SB06G015640 SB06G027465 SB01G040270 SB04G030770 SB06G032500 SB10G027220 SB06G024630 SB01G021280 SB01G050333 SB08G019930 SB01G010930 SB02G002720 SB01G012170 SB04G032590 SB04G032570 SB06G025710 SB04G004940 SB10G029190 SB10G006690 SB10G027280 SB10G000520 SB10G001350 SB04G031890 SB08G021690 SB06G024820	miR160 miR166 miR172 miR390 miR395 miR397 miR528 miR529
60255	regulation of macromolecule metabolic process,	1.15E-04	8.16E-03	45/160 28.1%	3146/19262 16.3%	SB01G019050 SB01G009330 SB09G002225 SB01G029650 SB02G003070 SB08G021460 SB04G034800 SB10G027100 SB01G016830 SB08G021080 SB07G000645 SB01G006020 SB04G004430 SB05G021480 SB08G021350 SB10G025053 SB06G015640 SB06G027465 SB01G040270 SB04G030770 SB06G032500 SB10G027220 SB06G024630 SB01G021280 SB01G050333 SB08G019930 SB01G010930 SB02G002720 SB01G012170 SB04G032590 SB04G032570 SB06G025710 SB09G019410 SB04G004940 SB10G029190 SB10G006690 SB10G027280 SB04G011020 SB10G000520 SB10G001350 SB01G000490 SB09G028700 SB04G031890 SB08G021690 SB06G024820	miR160 miR166 miR172 miR390 miR395 miR397 miR528 miR529
10468	regulation of gene expression,	1.69E-04	8.42E-03	42/160 26.2%	2906/19262 15.0%	SB01G019050 SB01G009330 SB09G002225 SB01G029650 SB02G003070 SB08G021460 SB04G034800 SB10G027100 SB08G021080 SB07G000645 SB01G006020 SB04G004430 SB05G021480 SB08G021350 SB10G025053 SB06G015640 SB06G027465 SB01G040270 SB04G030770 SB06G032500 SB10G027220 SB06G024630 SB01G021280 SB01G050333 SB08G019930 SB01G010930 SB02G002720 SB01G012170 SB04G032590 SB04G032570 SB06G025710 SB09G019410 SB04G004940	miR160 miR166 miR172 miR390 miR395 miR397 miR528 miR529

						SB10G029190 SB10G006690 SB10G027280 SB10G000520 SB10G001350 SB09G028700 SB04G031890 SB08G021690 SB06G024820	
31323	regulation of cellular metabolic process,	1.87E-04	8.86E-03	45/160 28.1%	3211/19262 16.6%	SB01G019050 SB01G009330 SB09G002225 SB01G029650 SB02G003070 SB08G021460 SB04G034800 SB10G027100 SB01G016830 SB08G021080 SB07G000645 SB01G006020 SB05G007370 SB04G004430 SB05G021480 SB08G021350 SB10G025053 SB06G015640 SB06G027465 SB01G040270 SB04G030770 SB06G032500 SB10G027220 SB06G024630 SB01G021280 SB07G002195 SB01G050333 SB08G019930 SB01G010930 SB02G002720 SB01G012170 SB04G032590 SB04G032570 SB06G025710 SB04G004940 SB10G029190 SB10G006690 SB10G027280 SB04G011020 SB10G000520 SB10G001350 SB09G028700 SB04G031890 SB08G021690 SB06G024820	miR160 miR166 miR172 miR390 miR395 miR397 miR528 miR529
65007	biological regulation,	1.37E-04	8.16E-03	76/160 47.5%	6424/19262 33.3%	SB01G019050 SB03G025480 SB01G009330 SB09G002225 SB10G022170 SB04G003135 SB02G003070 SB08G021460 SB03G025340 SB04G025540 SB10G027100 SB08G001450 SB01G035230 SB02G031370 SB08G021080 SB05G007370 SB04G004430 SB08G021350 SB01G040270 SB04G030770 SB06G024630 SB01G021280 SB01G010930 SB08G019930 SB02G002720 SB01G012170 SB03G002580 SB04G010990 SB06G025710 SB04G004940 SB01G049280 SB07G022880 SB03G028400 SB10G006690 SB10G027280 SB04G011020 SB10G001310 SB02G013180 SB10G001350 SB01G000490 SB09G028700 SB04G031890 SB08G021690 SB06G022560 SB07G018020 SB03G039890 SB08G000480 SB09G022130 SB01G029650 SB04G034800 SB02G005920 SB03G040700 SB01G016830 SB07G000645 SB01G006020 SB05G021480 SB10G025053 SB06G015640 SB06G027465 SB06G032500 SB10G027220 SB07G002195 SB01G050333 SB03G034440 SB03G047160 SB03G025700 SB04G032590 SB04G032570 SB09G019410 SB08G000660 SB10G029190 SB02G008860 SB01G018450 SB10G000520 SB05G000450 SB06G024820	miR160 miR164 miR166 miR172 miR319 miR390 miR395 miR397 miR528 miR529

	80090	regulation of primary metabolic process,	1.64E-04	8.42E-03	44/160 27.5%	3096/19262 16.0%	SB01G019050 SB01G009330 SB09G002225 SB01G029650 SB02G003070 SB08G021460 SB04G034800 SB10G027100 SB01G016830 SB08G021080 SB07G000645 SB01G006020 SB04G004430 SB05G021480 SB08G021350 SB10G025053 SB06G015640 SB06G027465 SB01G040270 SB04G030770 SB06G032500 SB10G027220 SB06G024630 SB01G021280 SB01G050333 SB08G019930 SB01G010930 SB02G002720 SB01G012170 SB04G032590 SB04G032570 SB06G025710 SB04G004940 SB10G029190 SB10G006690 SB10G027280 SB04G011020 SB10G000520 SB10G001350 SB01G000490 SB09G028700 SB04G031890 SB08G021690 SB06G024820	miR160 miR166 miR172 miR390 miR395 miR397 miR528 miR529
	19219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,	1.24E-04	8.16E-03	41/160 25.6%	2771/19262 14.3%	SB01G019050 SB01G009330 SB09G002225 SB02G003070 SB01G029650 SB08G021460 SB04G034800 SB10G027100 SB01G016830 SB08G021080 SB07G000645 SB01G006020 SB04G004430 SB05G021480 SB08G021350 SB10G025053 SB06G015640 SB06G027465 SB01G040270 SB04G030770 SB06G032500 SB10G027220 SB06G024630 SB01G021280 SB01G050333 SB08G019930 SB01G010930 SB02G002720 SB01G012170 SB04G032590 SB04G032570 SB06G025710 SB04G004940 SB10G029190 SB10G006690 SB10G027280 SB10G000520 SB10G001350 SB04G031890 SB08G021690 SB06G024820	miR160 miR166 miR172 miR390 miR395 miR397 miR528 miR529
Zma_OR	10467	gene expression	5.99E-03	3.21E-02	49/174 28.1%	3376/16863 20.0%	GRMZM2G063522 GRMZM2G435219 GRMZM2G125777 GRMZM2G009892 GRMZM2G114850 AC197246.3 GRMZM2G073750 GRMZM2G048993 GRMZM2G067743 GRMZM2G099862 GRMZM2G018414 GRMZM2G034876 GRMZM2G028980 GRMZM2G139700 GRMZM2G088842 GRMZM2G390470 GRMZM2G334165 GRMZM2G393433 GRMZM2G087095 GRMZM2G385641 GRMZM2G125243 GRMZM2G475882 GRMZM2G124566 GRMZM2G014193 GRMZM2G164909 GRMZM2G146688 GRMZM2G017414 AC233899.1 GRMZM2G435255 GRMZM2G098594 AC210013.4 AC233853.1 GRMZM2G098696 GRMZM2G378580 GRMZM2G089640 GRMZM2G129147 GRMZM2G146380 GRMZM2G004619 GRMZM2G035405 AY530952.1 GRMZM2G041223	miR156 miR159 miR164 miR167 miR169 miR395 miR396 miR528

							GRMZM2G031001 GRMZM2G178261 GRMZM2G079727 GRMZM2G078274 GRMZM2G001139 GRMZM2G164020 AC210792.5 GRMZM2G105335	
	6350	transcription	2.43E-05	7.16E-04	45/174 25.8%	2364/16863 14.0%	GRMZM2G098594 AC233853.1 GRMZM2G098696 GRMZM2G435219 GRMZM2G063522 GRMZM2G125777 GRMZM2G114850 GRMZM2G009892 GRMZM2G378580 AC197246.3 GRMZM2G073750 GRMZM2G048993 GRMZM2G099862 GRMZM2G067743 GRMZM2G018414 GRMZM2G089640 GRMZM2G146380 GRMZM2G129147 GRMZM2G004619 GRMZM2G035405 AY530952.1 GRMZM2G031001 GRMZM2G041223 GRMZM2G178261 GRMZM2G079727 GRMZM2G034876 GRMZM2G028980 GRMZM2G139700 GRMZM2G088842 GRMZM2G078274 GRMZM2G334165 GRMZM2G001139 GRMZM2G087095 GRMZM2G393433 GRMZM2G385641 GRMZM2G125243 GRMZM2G475882 GRMZM2G124566 AC210792.5 GRMZM2G146688 GRMZM2G164909 GRMZM2G017414 AC233899.1 GRMZM2G435255 GRMZM2G105335	miR156 miR159 miR164 miR167 miR169 miR395 miR396 miR528
METABOLIC PROCESS								
Osa_UR	44237	cellular metabolic process	1.72E-03	1.84E-02	25/95 26.3%	6557/45432 14.4%	LOC_OS03G60430 LOC_OS05G41166 LOC_OS11G06020 LOC_OS11G40400 LOC_OS02G58640 LOC_OS04G46384 LOC_OS10G05069 LOC_OS06G43220 LOC_OS03G53230 LOC_OS02G15760 LOC_OS01G12700 LOC_OS05G05810 LOC_OS03G03610 LOC_OS06G08810 LOC_OS07G01460 LOC_OS10G06810 LOC_OS03G52239 LOC_OS07G13170 LOC_OS01G46570 LOC_OS05G03040 LOC_OS03G15120 LOC_OS10G40600	miR159 miR171 miR172 miR393 miR395

							LOC_OS01G53280 LOC_OS12G19180 LOC_OS01G52500	
	8152	metabolic process	2.68E-03	2.00E-02	32/95 33.6%	9518/45432 20.9%	LOC_OS03G22634 LOC_OS03G60430 LOC_OS05G41166 LOC_OS11G06020 LOC_OS11G40400 LOC_OS02G58640 LOC_OS04G46384 LOC_OS10G05069 LOC_OS11G10750 LOC_OS06G43220 LOC_OS03G53230 LOC_OS02G15760 LOC_OS01G12700 LOC_OS05G05810 LOC_OS03G03610 LOC_OS06G08810 LOC_OS06G40700 LOC_OS07G01460 LOC_OS10G06810 LOC_OS03G52239 LOC_OS07G13170 LOC_OS05G23924 LOC_OS01G46570 LOC_OS03G07140 LOC_OS05G03040 LOC_OS03G15120 LOC_OS10G40600 LOC_OS01G53280 LOC_OS12G19180 LOC_OS04G04950 LOC_OS12G25700 LOC_OS01G52500	miR159 miR168 miR171 miR172 miR393 miR395 miR397 miR398
	9058	biosynthetic process	1.20E-03	1.84E-02	16/95 16.8%	3274/45432 7.2%	LOC_OS06G43220 LOC_OS03G60430 LOC_OS02G15760 LOC_OS01G12700 LOC_OS03G03610 LOC_OS05G41166 LOC_OS11G06020 LOC_OS03G52239 LOC_OS07G13170 LOC_OS01G46570 LOC_OS05G03040 LOC_OS03G15120 LOC_OS10G40600 LOC_OS01G53280 LOC_OS04G46384 LOC_OS12G19180	miR159 miR171 miR172 miR393 miR395
	44249	cellular biosynthetic process	5.73E-04	1.84E-02	16/95 16.8%	3054/45432 6.7%	LOC_OS06G43220 LOC_OS03G60430 LOC_OS02G15760 LOC_OS01G12700 LOC_OS03G03610 LOC_OS05G41166 LOC_OS11G06020 LOC_OS03G52239 LOC_OS07G13170 LOC_OS01G46570 LOC_OS05G03040 LOC_OS03G15120 LOC_OS10G40600 LOC_OS01G53280 LOC_OS04G46384 LOC_OS12G19180	miR159 miR171 miR172 miR393 miR395
	6310	DNA recombination	6.48E-04	1.84E-02	3/95 3.1%	80/45432 0.1%	LOC_OS05G05810 LOC_OS07G01460 LOC_OS10G06810	miR395
	34645	cellular macromolecule biosynthetic process	8.24E-04	1.84E-02	14/95 14.7%	2546/45432 5.6%	LOC_OS06G43220 LOC_OS02G15760 LOC_OS03G60430 LOC_OS01G12700 LOC_OS03G03610 LOC_OS05G41166 LOC_OS11G06020 LOC_OS03G52239 LOC_OS07G13170 LOC_OS05G03040 LOC_OS10G40600 LOC_OS01G53280 LOC_OS04G46384 LOC_OS12G19180	miR159 miR171 miR172 miR393 miR395

	9059	macromolecule biosynthetic process	8.37E-04	1.84E-02	14/95 14.7%	2550/45432 5.6%	LOC_OS06G43220 LOC_OS02G15760 LOC_OS03G60430 LOC_OS01G12700 LOC_OS03G03610 LOC_OS05G41166 LOC_OS11G06020 LOC_OS03G52239 LOC_OS07G13170 LOC_OS05G03040 LOC_OS10G40600 LOC_OS01G53280 LOC_OS04G46384 LOC_OS12G19180	miR159 miR171 miR172 miR393 miR395
zma_OR	90304	nucleic acid metabolic process	6.88E-05	1.35E-03	52/174 29.8%	3013/16863 17.8%	GRMZM2G097640 GRMZM2G063522 GRMZM2G435219 GRMZM2G125777 GRMZM2G009892 GRMZM2G114850 AC212570.3 AC197246.3 GRMZM2G073750 GRMZM2G048993 GRMZM2G099862 GRMZM2G067743 GRMZM2G018414 GRMZM2G377589 GRMZM2G043453 GRMZM2G034876 GRMZM2G028980 GRMZM2G139700 GRMZM2G088842 GRMZM2G104262 GRMZM2G334165 GRMZM2G393433 GRMZM2G087095 GRMZM2G385641 GRMZM2G125243 GRMZM2G475882 GRMZM2G124566 GRMZM2G146688 GRMZM2G164909 GRMZM2G017414 AC233899.1 GRMZM2G435255 GRMZM2G098594 AC233853.1 GRMZM2G098696 GRMZM2G378580 GRMZM2G089640 GRMZM2G129147 GRMZM2G146380 GRMZM2G004619 GRMZM2G035405 AY530952.1 GRMZM2G041223 GRMZM2G112598 GRMZM2G031001 GRMZM2G178261 GRMZM2G079727 GRMZM2G078274 GRMZM2G041352 GRMZM2G001139 AC210792.5 GRMZM2G105335	miR156 miR159 miR164 miR167 miR169 miR395 miR396 miR528
	6807	nitrogen compound metabolic process	9.33E-04	7.86E-03	59/174 33.9%	3932/16863 23.3%	GRMZM2G097640 GRMZM2G063522 GRMZM2G435219 GRMZM2G125777 GRMZM2G114850 GRMZM2G009892 AC212570.3 AC197246.3 GRMZM2G073750 GRMZM2G048993 GRMZM2G174807 GRMZM2G099862 GRMZM2G067743 GRMZM2G018414 GRMZM2G377589 GRMZM2G043453 GRMZM2G034876 AC233751.1 GRMZM2G028980 GRMZM2G139700 GRMZM2G088842 GRMZM2G104262 GRMZM2G334165 GRMZM2G393433 GRMZM2G087095 GRMZM2G385641 GRMZM2G125243 GRMZM2G475882 GRMZM2G124566 GRMZM2G146688 GRMZM2G164909 GRMZM2G017414 AC233899.1	miR156 miR159 miR164 miR167 miR169 miR395 miR396 miR528

							GRMZM2G435255 GRMZM2G098594 AC210013.4 GRMZM2G097258 AC233853.1 GRMZM2G098696 GRMZM2G378580 GRMZM2G086869 GRMZM2G089640 GRMZM2G146380 GRMZM2G129147 GRMZM2G004619 GRMZM2G071589 GRMZM2G035405 AY530952.1 GRMZM2G031001 GRMZM2G041223 GRMZM2G112598 GRMZM2G178261 GRMZM2G079727 GRMZM2G078274 GRMZM2G041352 GRMZM2G001139 GRMZM2G478709 AC210792.5 GRMZM2G105335	
	34641	cellular nitrogen compound metabolic process	9.33E-04	7.86E-03	59/174 33.9%	3932/16863 23.3%	GRMZM2G097640 GRMZM2G063522 GRMZM2G435219 GRMZM2G125777 GRMZM2G114850 GRMZM2G009892 AC212570.3 AC197246.3 GRMZM2G073750 GRMZM2G048993 GRMZM2G174807 GRMZM2G099862 GRMZM2G067743 GRMZM2G018414 GRMZM2G377589 GRMZM2G043453 GRMZM2G034876 AC233751.1 GRMZM2G028980 GRMZM2G139700 GRMZM2G088842 GRMZM2G104262 GRMZM2G334165 GRMZM2G393433 GRMZM2G087095 GRMZM2G385641 GRMZM2G125243 GRMZM2G475882 GRMZM2G124566 GRMZM2G146688 GRMZM2G164909 GRMZM2G017414 AC233899.1 GRMZM2G435255 GRMZM2G098594 AC210013.4 GRMZM2G097258 AC233853.1 GRMZM2G098696 GRMZM2G378580 GRMZM2G086869 GRMZM2G089640 GRMZM2G146380 GRMZM2G129147 GRMZM2G004619 GRMZM2G071589 GRMZM2G035405 AY530952.1 GRMZM2G031001 GRMZM2G041223 GRMZM2G112598 GRMZM2G178261 GRMZM2G079727 GRMZM2G078274 GRMZM2G041352 GRMZM2G001139 GRMZM2G478709 AC210792.5 GRMZM2G105335	miR156 miR159 miR164 miR167 miR169 miR395 miR396 miR528

	6139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	9.33E-04	7.86E-03	59/174 33.9%	3932/16863 23.3%	GRMZM2G097640 GRMZM2G063522 GRMZM2G435219 GRMZM2G125777 GRMZM2G114850 GRMZM2G009892 AC212570.3 AC197246.3 GRMZM2G073750 GRMZM2G048993 GRMZM2G174807 GRMZM2G099862 GRMZM2G067743 GRMZM2G018414 GRMZM2G377589 GRMZM2G043453 GRMZM2G034876 AC233751.1 GRMZM2G028980 GRMZM2G139700 GRMZM2G088842 GRMZM2G104262 GRMZM2G334165 GRMZM2G393433 GRMZM2G087095 GRMZM2G385641 GRMZM2G125243 GRMZM2G475882 GRMZM2G124566 GRMZM2G146688 GRMZM2G164909 GRMZM2G017414 AC233899.1 GRMZM2G435255 GRMZM2G098594 AC210013.4 GRMZM2G097258 AC233853.1 GRMZM2G098696 GRMZM2G378580 GRMZM2G086869 GRMZM2G089640 GRMZM2G146380 GRMZM2G129147 GRMZM2G004619 GRMZM2G071589 GRMZM2G035405 AY530952.1 GRMZM2G031001 GRMZM2G041223 GRMZM2G112598 GRMZM2G178261 GRMZM2G079727 GRMZM2G078274 GRMZM2G041352 GRMZM2G001139 GRMZM2G478709 AC210792.5 GRMZM2G105335	miR156 miR159 miR164 miR167 miR169 miR395 miR396 miR528
	9059	macromolecule biosynthetic process	5.99E-03	3.21E-02	49/174 28.1%	3376/16863 20.0%	GRMZM2G063522 GRMZM2G435219 GRMZM2G125777 GRMZM2G009892 GRMZM2G114850 AC197246.3 GRMZM2G073750 GRMZM2G048993 GRMZM2G067743 GRMZM2G099862 GRMZM2G018414 GRMZM2G034876 GRMZM2G028980 GRMZM2G139700 GRMZM2G088842 GRMZM2G390470 GRMZM2G334165 GRMZM2G393433 GRMZM2G087095 GRMZM2G385641 GRMZM2G125243 GRMZM2G475882 GRMZM2G124566 GRMZM2G014193 GRMZM2G164909 GRMZM2G146688 GRMZM2G017414 AC233899.1 GRMZM2G435255 GRMZM2G098594 AC210013.4 AC233853.1 GRMZM2G098696 GRMZM2G378580 GRMZM2G089640 GRMZM2G129147 GRMZM2G146380 GRMZM2G004619 GRMZM2G035405 AY530952.1 GRMZM2G041223	miR156 miR159 miR164 miR167 miR169 miR395 miR396 miR528

						GRMZM2G031001 GRMZM2G178261 GRMZM2G079727 GRMZM2G078274 GRMZM2G001139 GRMZM2G164020 AC210792.5 GRMZM2G105335	
34645	cellular macromolecule biosynthetic process	5.99E-03	3.21E-02	49/174 28.1%	3376/16863 20.0%	GRMZM2G063522 GRMZM2G435219 GRMZM2G125777 GRMZM2G009892 GRMZM2G114850 AC197246.3 GRMZM2G073750 GRMZM2G048993 GRMZM2G067743 GRMZM2G099862 GRMZM2G018414 GRMZM2G034876 GRMZM2G028980 GRMZM2G139700 GRMZM2G088842 GRMZM2G390470 GRMZM2G334165 GRMZM2G393433 GRMZM2G087095 GRMZM2G385641 GRMZM2G125243 GRMZM2G475882 GRMZM2G124566 GRMZM2G014193 GRMZM2G164909 GRMZM2G146688 GRMZM2G017414 AC233899.1 GRMZM2G435255 GRMZM2G098594 AC210013.4 AC233853.1 GRMZM2G098696 GRMZM2G378580 GRMZM2G089640 GRMZM2G129147 GRMZM2G146380 GRMZM2G004619 GRMZM2G035405 AY530952.1 GRMZM2G041223 GRMZM2G031001 GRMZM2G178261 GRMZM2G079727 GRMZM2G078274 GRMZM2G001139 GRMZM2G164020 AC210792.5 GRMZM2G105335	miR156 miR159 miR164 miR167 miR169 miR395 miR396 miR528
44249	cellular biosynthetic process	5.99E-03	3.21E-02	49/174 28.1%	3376/16863 20.0%	GRMZM2G063522 GRMZM2G435219 GRMZM2G125777 GRMZM2G009892 GRMZM2G114850 AC197246.3 GRMZM2G073750 GRMZM2G048993 GRMZM2G067743 GRMZM2G099862 GRMZM2G018414 GRMZM2G034876 GRMZM2G028980 GRMZM2G139700 GRMZM2G088842 GRMZM2G390470 GRMZM2G334165 GRMZM2G393433 GRMZM2G087095 GRMZM2G385641 GRMZM2G125243 GRMZM2G475882 GRMZM2G124566 GRMZM2G014193 GRMZM2G164909 GRMZM2G146688	miR156 miR159 miR164 miR167 miR169 miR395 miR396 miR528

							GRMZM2G017414 AC233899.1 GRMZM2G435255 GRMZM2G098594 AC210013.4 AC233853.1 GRMZM2G098696 GRMZM2G378580 GRMZM2G089640 GRMZM2G129147 GRMZM2G146380 GRMZM2G004619 GRMZM2G035405 AY530952.1 GRMZM2G041223 GRMZM2G031001 GRMZM2G178261 GRMZM2G079727 GRMZM2G078274 GRMZM2G001139 GRMZM2G164020 AC210792.5 GRMZM2G105335	
zm_UR	6807	nitrogen compound metabolic process	2.57E-03	1.95E-02	21/50 42.0%	3932/16863 23.3%	AC207656.3 GRMZM2G178102 GRMZM2G409974 GRMZM2G085751 GRMZM2G035520 GRMZM2G010357 AC225147.4 GRMZM2G081406 GRMZM2G369356 GRMZM2G390641 AC215260.3 GRMZM2G005284 GRMZM2G104325 GRMZM2G109987 AC187157.4 GRMZM2G126239 GRMZM2G017414 AC203369.3 GRMZM2G144821 GRMZM2G176175 GRMZM2G076602	miR160 miR166 miR172 miR399 miR529
	34641	cellular nitrogen compound metabolic process	2.57E-03	1.95E-02	21/50 42.0%	3932/16863 23.3%	AC207656.3 GRMZM2G178102 GRMZM2G409974 GRMZM2G085751 GRMZM2G035520 GRMZM2G010357 AC225147.4 GRMZM2G081406 GRMZM2G369356 GRMZM2G390641 AC215260.3 GRMZM2G005284 GRMZM2G104325 GRMZM2G109987 AC187157.4 GRMZM2G126239 GRMZM2G017414 AC203369.3 GRMZM2G144821 GRMZM2G176175 GRMZM2G076602	miR160 miR166 miR172 miR399 miR529
	6139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.57E-03	1.95E-02	21/50 42.0%	3932/16863 23.3%	AC207656.3 GRMZM2G178102 GRMZM2G409974 GRMZM2G085751 GRMZM2G035520 GRMZM2G010357 AC225147.4 GRMZM2G081406 GRMZM2G369356 GRMZM2G390641 AC215260.3 GRMZM2G005284 GRMZM2G104325 GRMZM2G109987 AC187157.4 GRMZM2G126239 GRMZM2G017414 AC203369.3 GRMZM2G144821 GRMZM2G176175 GRMZM2G076602	miR160 miR166 miR172 miR399 miR529
	90304	nucleic acid metabolic process	4.57E-03	2.90E-02	17/50 34.0%	3013/16863 17.8%	AC207656.3 GRMZM2G178102 GRMZM2G409974 GRMZM2G085751 GRMZM2G010357 AC225147.4 GRMZM2G081406 GRMZM2G369356	miR160 miR166 miR172 miR399 miR529

							GRMZM2G390641 GRMZM2G005284 GRMZM2G109987 AC187157.4 GRMZM2G126239 AC203369.3 GRMZM2G017414 GRMZM2G176175 GRMZM2G076602	
DEVELOPMENT								
sbi_UR	48830	adventitious root development,	1.65E-11	9.66E-09	9/212 4.2%	29/19262 0.1%	SB01G019130 SB02G003530 SB04G026610 SB04G038420 SB10G027790 SB02G003520 SB10G031030 SB06G033970 SB06G025560	miR160 miR166 miR168 miR172 miR395
	48507	meristem development,	1.70E-11	9.66E-09	17/212 8.0%	181/19262 0.9%	SB04G023990 SB08G021460 SB01G047250 SB01G019000 SB03G002660 SB01G003400 SB02G007000 SB01G013710 SB08G006330 SB01G019120 SB04G001190 SB01G050000 SB08G021350 SB06G019010 SB10G025053 SB10G027220 SB06G022930	miR160 miR164 miR166 miR172 miR394 miR395 miR529
	10154	fruit development,	5.04E-11	1.90E-08	33/212 15.5%	797/19262 4.1%	SB03G029790 SB08G005050 SB02G025575 SB04G026610 SB04G038420 SB08G021460 SB08G023040 SB08G002250 SB01G003400 SB02G007000 SB01G011010 SB01G019130 SB02G043080 SB08G021350 SB10G025053 SB10G027220 SB01G021280 SB06G022810 SB04G023990 SB10G027790 SB01G001240 SB02G025680 SB01G017690 SB03G002660 SB08G007250 SB02G000900 SB01G013710 SB08G006330 SB01G019120 SB06G019010 SB10G031030 SB01G043290 SB06G025560	miR159 miR160 miR164 miR166 miR168 miR172 miR390 miR395 miR397 miR528 miR529
	10014	meristem initiation,	1.58E-09	4.48E-07	8/212 3.7%	32/19262 0.1%	SB04G023990 SB01G013710 SB08G006330 SB01G019120 SB01G050000 SB06G019010 SB08G021350 SB03G002660	miR164 miR166 miR172
	48316	seed development,	6.43E-09	1.46E-06	29/212 13.6%	766/19262 3.9%	SB03G029790 SB08G005050 SB02G025575 SB04G038420 SB08G021460 SB08G023040 SB08G002250 SB01G003400 SB02G007000 SB01G011010 SB02G043080 SB08G021350 SB10G025053 SB10G027220 SB01G021280 SB04G023990 SB01G001240 SB02G025680 SB01G017690 SB03G002660 SB08G007250 SB02G000900 SB01G013710 SB08G006330 SB01G019120 SB06G019010 SB10G031030 SB01G043290 SB06G025560	miR159 miR160 miR164 miR166 miR168 miR172 miR390 miR395 miR397 miR528 miR529
	10072	primary shoot apical meristem specification,	9.76E-09	1.84E-06	7/212 3.3%	26/19262 0.1%	SB04G023990 SB01G013710 SB08G006330 SB01G019120 SB06G019010 SB08G021350 SB03G002660	miR164 miR166 miR172
	9855	determination of bilateral symmetry,	3.71E-08	6.01E-06	5/212 2.3%	10/19262 0.0%	SB01G013710 SB01G019120 SB01G050000 SB08G021350 SB03G002660	miR166 miR172

48508	embryonic meristem development,	5.94E-08	8.41E-06	7/212 3.3%	33/19262 0.1%	SB04G023990 SB01G013710 SB08G006330 SB01G019120 SB06G019010 SB08G021350 SB03G002660	miR164 miR166 miR172
9793	embryonic development ending in seed dormancy,	1.36E-07	1.72E-05	25/212 11.7%	680/19262 3.5%	SB03G029790 SB08G005050 SB02G025575 SB04G038420 SB08G021460 SB08G023040 SB08G002250 SB01G011010 SB02G043080 SB08G021350 SB10G027220 SB01G021280 SB04G023990 SB02G025680 SB01G017690 SB03G002660 SB08G007250 SB02G000900 SB01G013710 SB08G006330 SB01G019120 SB06G019010 SB10G031030 SB01G043290 SB06G025560	miR159 miR160 miR164 miR166 miR168 miR172 miR390 miR395 miR397 miR528 miR529
7389	pattern specification process,	1.58E-07	1.78E-05	18/212 8.4%	370/19262 1.9%	SB10G027913 SB06G022810 SB04G023990 SB04G026610 SB10G027790 SB08G021460 SB03G002660 SB01G003400 SB02G007000 SB01G013710 SB01G019130 SB08G006330 SB01G019120 SB01G050000 SB08G021350 SB06G019010 SB10G025053 SB10G027220	miR160 miR164 miR166 miR172 miR395 miR529
48442	sepal development,	1.72E-06	9.27E-05	4/212 1.8%	9/19262 0.0%	SB06G022810 SB01G019130 SB04G026610 SB10G027790	miR160 miR166 miR172
48464	flower calyx development,	1.72E-06	9.27E-05	4/212 1.8%	9/19262 0.0%	SB06G022810 SB01G019130 SB04G026610 SB10G027790	miR160 miR166 miR172
9933	meristem structural organization,	1.87E-06	9.27E-05	8/212 3.7%	76/19262 0.3%	SB04G023990 SB01G013710 SB08G006330 SB01G019120 SB01G050000 SB06G019010 SB08G021350 SB03G002660	miR164 miR166 miR172
3002	regionalization,	1.88E-06	9.27E-05	15/212 7.0%	310/19262 1.6%	SB10G027913 SB06G022810 SB04G023990 SB08G021460 SB03G002660 SB01G003400 SB02G007000 SB01G013710 SB08G006330 SB01G019120 SB01G050000 SB08G021350 SB06G019010 SB10G025053 SB10G027220	miR160 miR164 miR166 miR172 miR395 miR529
10073	meristem maintenance,	2.07E-06	9.77E-05	8/212 3.7%	77/19262 0.3%	SB02G007000 SB01G013710 SB04G001190 SB10G025053 SB08G021350 SB01G047250 SB03G002660 SB01G003400	miR164 miR166 miR172 miR394 miR395 miR529
48608	reproductive structure development,	3.25E-07	3.07E-05	36/212 16.9%	1312/19262 6.8%	SB03G029790 SB08G005050 SB02G025575 SB04G026610 SB04G038420 SB08G021460 SB08G023040 SB08G002250 SB01G003400 SB02G007000 SB01G011010 SB01G019130 SB02G043080 SB08G021350 SB10G025053 SB10G027220 SB01G021280 SB06G033970 SB06G022810 SB04G023990 SB10G027790 SB01G001240 SB01G047250 SB02G025680 SB03G000530 SB01G017690 SB03G002660 SB08G007250 SB02G000900 SB01G013710	miR159 miR160 miR164 miR166 miR168 miR172 miR390 miR394 miR395 miR397 miR528 miR529

							SB08G006330 SB01G019120 SB06G019010 SB10G031030 SB01G043290 SB06G025560	
	48829	root cap development,	4.87E-07	4.24E-05	4/212 1.8%	7/19262 0.0%	SB06G022810 SB01G019130 SB04G026610 SB10G027790	miR160 miR166 miR172
	48367	shoot development,	6.18E-07	4.67E-05	20/212 9.4%	495/19262 2.5%	SB06G022810 SB04G023990 SB04G026610 SB10G027790 SB04G038420 SB08G021460 SB01G019000 SB03G002660 SB01G013710 SB01G019130 SB08G006330 SB01G019120 SB08G021350 SB06G019010 SB10G027220 SB10G031030 SB06G022930 SB06G025560 SB10G000980 SB02G020900	miR160 miR164 miR166 miR168 miR172 miR394 miR529
	22621	shoot system development,	7.23E-07	5.12E-05	20/212 9.4%	500/19262 2.5%	SB06G022810 SB04G023990 SB04G026610 SB10G027790 SB04G038420 SB08G021460 SB01G019000 SB03G002660 SB01G013710 SB01G019130 SB08G006330 SB01G019120 SB08G021350 SB06G019010 SB10G027220 SB10G031030 SB06G022930 SB06G025560 SB10G000980 SB02G020900	miR160 miR164 miR166 miR168 miR172 miR394 miR529
sbi_OR	48367	shoot development,	8.26E-07	3.00E-04	17/160 10.6%	495/19262 2.5%	SB01G009330 SB04G028510 SB08G021460 SB02G022011 SB04G034800 SB01G049280 SB02G008860 SB02G031370 SB10G001350 SB04G004430 SB05G021480 SB08G021350 SB06G027465 SB04G030770 SB10G027220 SB04G031890 SB01G012170	miR156 miR167 miR169 miR171 miR396
	48366	leaf development,	8.88E-07	3.00E-04	14/160 8.7%	337/19262 1.7%	SB01G009330 SB04G028510 SB08G021460 SB04G034800 SB02G008860 SB10G001350 SB04G004430 SB05G021480 SB08G021350 SB06G027465 SB10G027220 SB04G030770 SB04G031890 SB01G012170	miR156 miR167 miR169 miR171 miR396
	22621	shoot system development,	9.48E-07	3.00E-04	17/160 10.6%	500/19262 2.5%	SB01G009330 SB04G028510 SB08G021460 SB02G022011 SB04G034800 SB01G049280 SB02G008860 SB02G031370 SB10G001350 SB04G004430 SB05G021480 SB08G021350 SB06G027465 SB04G030770 SB10G027220 SB04G031890 SB01G012170	miR156 miR167 miR169 miR171 miR396

48827	phyllome development,	3.21E-06	7.61E-04	14/160 8.7%	376/19262 1.9%	SB01G009330 SB04G028510 SB08G021460 SB04G034800 SB02G008860 SB10G001350 SB04G004430 SB05G021480 SB08G021350 SB06G027465 SB10G027220 SB04G030770 SB04G031890 SB01G012170	miR156 miR167 miR169 miR171 miR396
9942	longitudinal axis specification,	2.00E-05	3.80E-03	4/160 2.5%	20/19262 0.1%	SB04G004430 SB08G021460 SB06G032500 SB10G027220	miR167 miR169
7291	sperm individualization,	3.06E-05	4.83E-03	3/160 1.8%	8/19262 0.0%	SB08G000480 SB05G007370 SB05G000450	miR156
10386	lateral root primordium development,	1.17E-04	8.16E-03	3/160 1.8%	12/19262 0.0%	SB04G004430 SB08G021460 SB10G027220	miR167 miR169
10305	leaf vascular tissue pattern formation,	1.38E-04	8.16E-03	4/160 2.5%	32/19262 0.1%	SB04G004430 SB08G021460 SB06G032500 SB10G027220	miR167 miR169
10051	xylem and phloem pattern formation,	1.68E-04	8.42E-03	6/160 3.7%	98/19262 0.5%	SB04G028510 SB04G004430 SB08G021350 SB08G021460 SB06G032500 SB10G027220	miR156 miR167 miR169 miR171

Supplemental Table 8. Sorghum miRNAs co-localizing with CACTA TEs.
Sorghum repeat sequences were downloaded from MIPs (http://mips.helmholtz-muenchen.de/plant/sorghum/), and were mapped to sorghum pseudomolecules. The locations of miRNA genes and the repeats were compared. miRNA genes located inside repeat regions were listed here.

MiRNA_name	Fam	MiRNA_chr	MiRNA_loci	CACTA_name	CACTA_chr	CACTA_start	CACTA_end
S125	168	chromosome_6	14647882	CACTA_9307	chromosome_6	14647453	14653423
S167	169	chromosome_7	40450314	CACTA_10954	chromosome_7	40450210	40452050
S13	172	chromosome_1	45078364	CACTA_0956	chromosome_1	45073289	45079344
S15	172	chromosome_1	46214211	CACTA_0987	chromosome_1	46209351	46215759
S16	172	chromosome_1	46215203	CACTA_0987	chromosome_1	46209351	46215759
S38	172	chromosome_2	56429006	CACTA_3908	chromosome_2	56418355	56429472
S63	172	chromosome_3	52113844	CACTA_5479	chromosome_3	52112159	52114312
S107	172	chromosome_5	6929611	CACTA_7559	chromosome_5	6928165	6930077
S110	172	chromosome_5	9797325	CACTA_7670	chromosome_5	9792584	9798600
S116	172	chromosome_5	46749674	CACTA_8392	chromosome_5	46745458	46750140
S121	172	chromosome_5	60798258	CACTA_8883	chromosome_5	60792361	60798714
S123	172	chromosome_6	1477179	CACTA_8989	chromosome_6	1471096	1477644
S156	172	chromosome_7	3408080	CACTA_10376	chromosome_7	3403514	3408546
S163	172	chromosome_7	15073370	CACTA_10673	chromosome_7	15068307	15073836
S170	172	chromosome_7	53585560	CACTA_11194	chromosome_7	53581009	53586016
S186	172	chromosome_8	18212165	CACTA_11907	chromosome_8	18207150	18212631
S195	172	chromosome_8	44197738	CACTA_12293	chromosome_8	44192672	44198204
S196	172	chromosome_8	45986917	CACTA_12333	chromosome_8	45982009	45987383
S210	172	chromosome_9	16896660	CACTA_13049	chromosome_9	16891281	16899546
S231	172	chromosome_10	20795501	CACTA_2111	chromosome_10	20791855	20796292
S234	172	chromosome_10	25878314	CACTA_2191	chromosome_10	25869096	25878780
S119	172	chromosome_5	53444396	CACTA_8666	chromosome_5	53439630	53444862
S191	172	chromosome_8	38488898	CACTA_12167	chromosome_8	38483981	38489364

Supplemental Table 9. Sorghum miRNAs co-localizing with retrotransposons.

Sorghum repeat sequences were downloaded from MIPs (http://mips.helmholtz-muenchen.de/plant/sorghum/), and were mapped to sorghum pseudomolecules. The locations of miRNA genes and the repeats were compared. miRNA genes located inside repeat regions were listed here.

MiRNA	Fam	MiRNA_chr	MiRNA_loci	Repeat_name	TE_class	Repeat_chr	Repeat_start	Repeat_end
S182	156	chromosome_8	3685194	Zm1S_101L	RLC	chromosome_8	3678570	3722990
S128	160	chromosome_6	34672498	LTR_Sb_chr_09_740	RLG	chromosome_6	34665696	34716252
S128	160	chromosome_6	34672498	LTR_Sb_chr_04_8	RLG	chromosome_6	34670994	34674987
S190	160	chromosome_8	35825207	LTR_Sb_chr_10_185	RLG	chromosome_8	35821807	35831038
S193	164	chromosome_8	43308656	LTR_Sb_chr_05_919	RLX	chromosome_8	43308568	43312716
S211	164	chromosome_9	22254387	LTR_Sb_chr_08_237	RLX	chromosome_9	22246193	22255377
S12[a]	166	chromosome_1	27013469	TSB1	DXX	chromosome_1	26713547	27108523
S177[a]	169	chromosome_7	61071183	LTR_Sb_chr_07_952	RLX	chromosome_7	61031190	61082951
S175[a,b]	169	chromosome_7	61062642	LTR_Sb_chr_07_952	RLX	chromosome_7	61031190	61082951
S174[a,b]	169	chromosome_7	61058645	LTR_Sb_chr_07_952	RLX	chromosome_7	61031190	61082951
S176[a,b]	169	chromosome_7	61068030	LTR_Sb_chr_07_952	RLX	chromosome_7	61031190	61082951
S35	171	chromosome_2	47093982	167252	RLG	chromosome_2	47090884	47101721
S162[a,c]	171	chromosome_7	7609192	TSB1	DXX	chromosome_7	7607068	7621136
S189	171	chromosome_8	28393889	LTR_Sb_chr_05_355	RLX	chromosome_8	28315431	28439686
S189	171	chromosome_8	28393889	LTR_Sb_chr_08_166	RLG	chromosome_8	28390716	28404257
S67	390	chromosome_3	59556688	LTR_Sb_chr_01_468	RLG	chromosome_3	59554775	59558261
S56[a,c]	393	chromosome_3	6521860	LTR_Sb_chr_04_821	RLX	chromosome_3	6454045	6524936
S93	395	chromosome_4	55506096	LTR_Sb1_00012_513_2frag	RLG	chromosome_4	55503929	55506357
S127	395	chromosome_6	29530218	sb_mite_stow1_6	DXX	chromosome_6	29521794	29544199
S127	395	chromosome_6	29530218	LTR_Sb_chr_06_589	RLX	chromosome_6	29522161	29534206
S34	395	chromosome_2	41031623	LTR_Sb_chr_10_471	RLX	chromosome_2	41023490	41033785
S34	395	chromosome_2	41031623	121128	RLX	chromosome_2	41027231	41033785
S14	528	chromosome_1	45464230	LTR_Sb_chr_06_12	RLX	chromosome_1	45460744	45464814

S25[a]	528	chromosome_1	71476713	LTR_Sb_chr_01_31_2frag	RLX	chromosome_1	71465645	71518660
S45	529	chromosome_2	62916250	LTR_Sb_chr_01_85	RLX	chromosome_2	62908764	62928982
S84	529	chromosome_4	26708986	LTR_Sb_chr_07_793	RLG	chromosome_4	26695016	26709484
S124	529	chromosome_6	12301200	LTR_Sb_chr_05_493	RLX	chromosome_6	12289973	12324395
S124	529	chromosome_6	12301200	LTR_Sb_chr_01_113	RLX	chromosome_6	12296375	12303476
S126	529	chromosome_6	25434422	LTR_Sb_chr_07_80	RLG	chromosome_6	25423769	25457149
S126	529	chromosome_6	25434422	LTR_Sb_chr_07_537	RLX	chromosome_6	25429593	25438852
S136	529	chromosome_6	52010926	LTR_Sb_chr_02_1099	RLX	chromosome_6	51985994	52073162
S188	529	chromosome_8	22744157	LTR_Sb_chr_08_329	RLG	chromosome_8	22735570	22747691
S212	529	chromosome_9	24058551	LTR_Sb_chr_09_376	RLX	chromosome_9	24048852	24063021
S213	529	chromosome_9	30854735	LTR_Sb1_00023_988	RLG	chromosome_9	30847233	30858284
S37	156	chromosome_2	54338257	LTR_Sb_chr_05_838	RLG	chromosome_2	54290809	54377919
S85	156	chromosome_4	34641453	LTR_Sb_chr_03_716	RLX	chromosome_4	34640647	34644014
S233	156	chromosome_10	23656923	LTR_Sb_chr_10_348	RLX	chromosome_10	23649530	23657456
S32	156	chromosome_2	20337063	LTR_Sb_chr_02_222	RLX	chromosome_2	20336259	20344091
S169	156	chromosome_7	50900223	LTR_Sb_chr_07_399	RLX	chromosome_7	50859526	50907384
S69[a,c]	167	chromosome_3	64088383	LTR_Sb_chr_08_848	RLX	chromosome_3	64079722	64162578
S31	167	chromosome_2	20219834	LTR_Sb_chr_05_371	RLX	chromosome_2	20218303	20220033
S20	172	chromosome_1	57701721	TSB1	DXX	chromosome_1	57681712	57783446
S237	172	chromosome_10	46113277	LTR_Sb1_00010_169	RLX	chromosome_10	46109238	46113347
S225[a]	399	chromosome_10	1544258	LTR_Sb_chr_10_17	RLX	chromosome_10	1538717	1603205

[a] miRNAs located in the grass syntenic region; [b] miRNAs are retained after WGDs;
[c] miRNAs have an ortholog associated with repeat elements

Supplemental Table 10. Over-retained miRNA families with lower transposition frequency. Transposed miRNAs (each family with minimum two members) are listed according to the family (first column), number of transposition events identified (second column), expresses in total (third column), and percentage (fourth column).

Family	#Transposition	#Total	%
Over-retained			
156	6	32	18.75
167	2	12	16.67
169	5	25	20
171	4	12	33.33
399	1	11	9.09
396	0	4	0
Average	3	16	16.31
Under-retained			
160	3	5	60
164	2	6	33.33
166	1	5	20
172	23	32	71.88
319	0	3	0
395	5	17	29.41
528	2	3	66.67
529	10	15	66.67
Average	5.75	10.75	43.495

Supplemental Table 11. Preferential distribution of transposed miRNAs between duplicated ancient chromosome pairs.
Transposed miRNAs are listed according to their location on the ancestral chromosome (first column), on the modern sorghum chromosomes (second column), and number of transposed miRNAs identified (third column).

Ancestor chr	Sorghum_chr	#miRNA_transposed
A1	chromosome_3	2
A5	chromosome_9	4
A8	chromosome_7	5
A9	chromosome_2	8
A11	chromosome_8	10
A12	chromosome_5	5
A2	chromosome_4	3
A4	chromosome_6	11
A6	chromosome_10	5
A3	chromosome_1	1
A7	chromosome_2	0
A10	chromosome_1	4