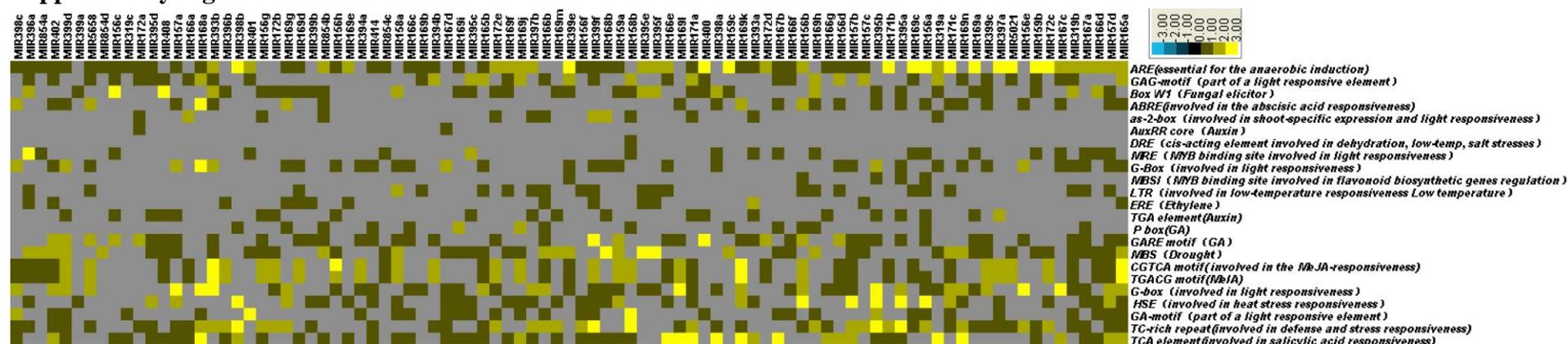


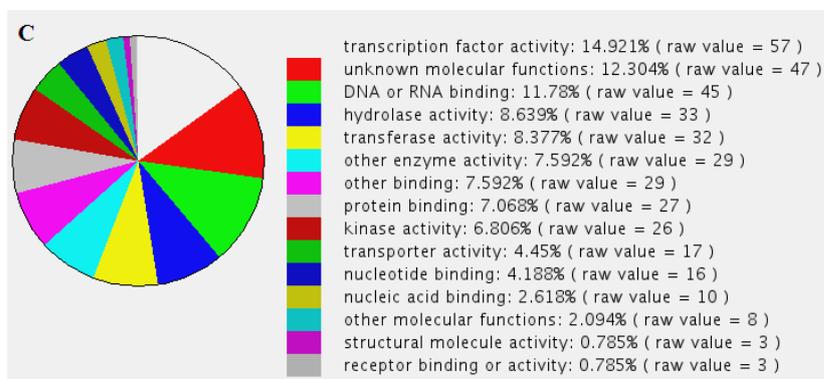
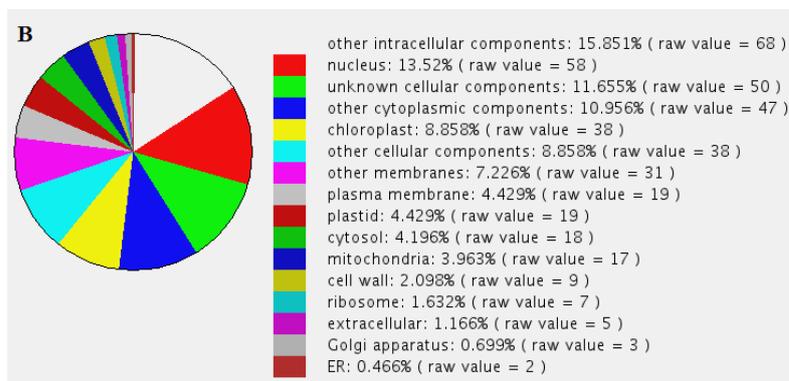
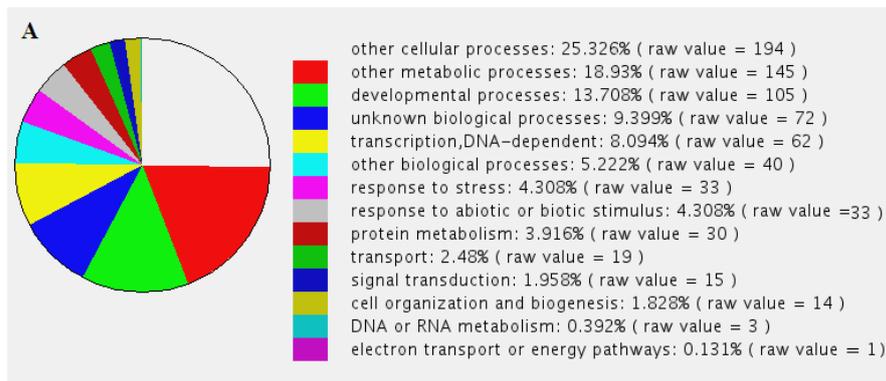
Genome-wide analyses of abiotic stress-related microRNAs and their targets in *Arabidopsis thaliana*

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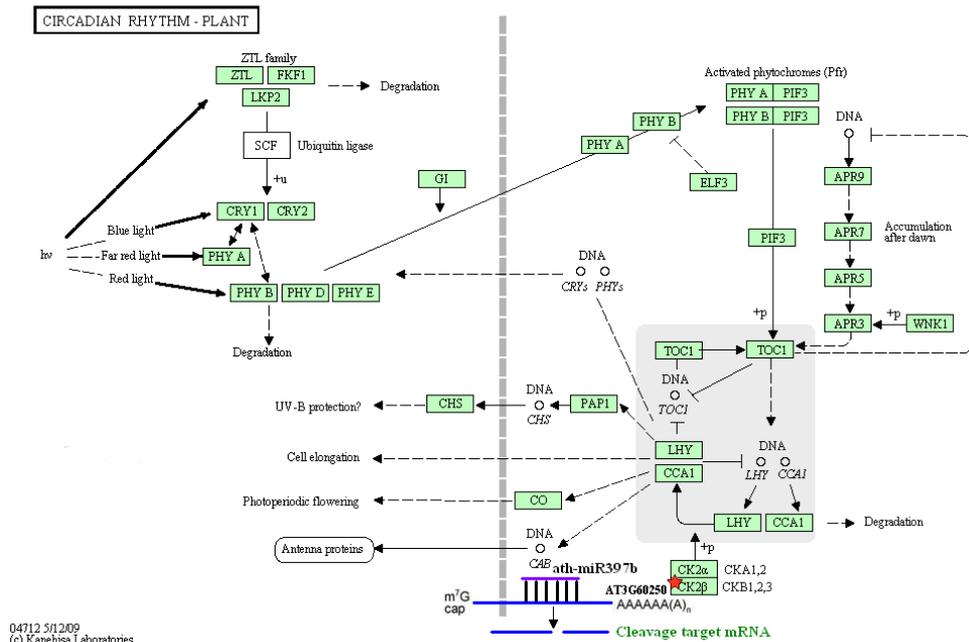
Supplementary Figures



Supplementary Figure 1 The predicted stress-response cis-regulatory elements in the upstream regions of miRNA genes. The matched cis-regulatory element numbers of each miRNA were used for hierarchical cluster analysis. Different values of color key show the different matched numbers. Bright yellow indicates that the miRNA genes contain more than two stress-responsive cis-regulatory elements in the upstream promoters regions, whereas gray indicates that a gene does not contain predicted elements in its promoter. The miRNAs are marked on the top of the picture.



Supplementary Figure 2 The profile of the expression proportion of biological_process (A), cellular_component (B) and molecular function (C) in the GO functional classes.



Supplementary Figure 3 The example of circadian rhythm (ath04712) pathway involved to the predicted miRNA target gene AT3G60250. The targeted miRNA ath-miR397b is also shown in the picture.

Supplementary Tables

Supplementary Table 1. The information of *Arabidopsis thaliana* 92 stress-related genes.

Number	Acc. number of Nucleotide	Acc. number of Protein	Species	Gene description	Resistance type	Pubmed id
1	NM_001036984 .1	NP_001032061. 1	<i>Arabidopsi s thaliana</i>	CAP160 protein	drought;cold	8448363
2	NM_001084854 .1	NP_001078323. 1	<i>Arabidopsi s thaliana</i>	aquaporin PIP1-1	salt	18234665
3	NM_001125801 .1	NP_001119273. 1	<i>Arabidopsi s thaliana</i>	vegetative storage protein 1	drought;cold	17003050
4	NM_001161154 .1	NP_001154626. 1	<i>Arabidopsi s thaliana</i>	abscisic acid-insensitive 5-like protein 7	drought	11884679
5	NM_001198228 .1	NP_001185157. 1	<i>Arabidopsi s thaliana</i>	abscisic acid-insensitive 5-like protein 5	drought	16284313
6	NM_001202786 .1	NP_001189715. 1	<i>Arabidopsi s thaliana</i>	Gamma-glutamyl phosphate reductase	submergence	10441499
7	NM_001204009 .1	NP_001190938. 1	<i>Arabidopsi s thaliana</i>	Floral homeotic protein APETALA 2	cold	21958703
8	NM_001247571 .1	NP_001234500. 1	<i>Arabidopsi s thaliana</i>	protein phosphatase 2C	drought	16963523

9	NM_100042.3	NP_171666.1	<i>Arabidopsis thaliana</i>	cytochrome P450, family 86, subfamily A, polypeptide 4	drought;cold	15709153
10	NM_100153.3	NP_171773.1	<i>Arabidopsis thaliana</i>	1,4-beta-D-xylan synthase	drought;salt	20409003
11	NM_101083.3	NP_563899.1	<i>Arabidopsis thaliana</i>	nitrate transporter 1.1	drought	12509525
12	NM_101378.2	NP_172962.1	<i>Arabidopsis thaliana</i>	E3 ubiquitin-protein ligase RHA2A	drought	21478368
13	NM_101405.3	NP_172988.1	<i>Arabidopsis thaliana</i>	ethylene-responsive transcription factor WIN1	drought	15319479
14	NM_101437.4	NP_173021.1	<i>Arabidopsis thaliana</i>	Pyrophosphate-energized vacuolar membrane proton pump 1	drought;salt	20492547
15	NM_101519	NP_564001	<i>Arabidopsis thaliana</i>	Molybdenum cofactor sulfurase	drought	21889046
16	NM_101894.3	NP_173468.1	<i>Arabidopsis thaliana</i>	dehydrin COR47	cold	16653076
17	NM_102538.2	NP_174094.1	<i>Arabidopsis thaliana</i>	zinc finger protein STZ/ZAT10	drought;salt;cold	15333755
18	NM_102998.3	NP_174541.1	<i>Arabidopsis thaliana</i>	transcription factor MYC2	drought;cold	15173567
19	NM_103516.3	NP_175056.1	<i>Arabidopsis thaliana</i>	Ras-related protein Rab-18	drought;cold	12232173
20	NM_104113	NP_175644	<i>Arabidopsis thaliana</i>	Xanthoxin dehydrogenase	drought;salt	11842158
21	NM_104167.5	NP_175697.1	<i>Arabidopsis thaliana</i>	NAC domain-containing protein 19	drought	15319476
22	NM_105048.2	NP_176558.1	<i>Arabidopsis thaliana</i>	cytochrome P450, family 86, subfamily A, polypeptide 7	drought;cold	15709153
23	NM_105331.3	NP_176833.1	<i>Arabidopsis thaliana</i>	putative WRKY transcription factor 63	drought	20487379
24	NM_105471.3	NP_176968.1	<i>Arabidopsis thaliana</i>	hydroxypyruvate reductase	drought	19529821
25	NM_105996.3	NP_177479.1	<i>Arabidopsis thaliana</i>	homeobox-leucine zipper protein HDG11	drought	18451323
26	NM_106362.2	NP_177837.1	<i>Arabidopsis thaliana</i>	alcohol dehydrogenase class-P	cold	12231733
27	NM_106708.3	NP_178175.1	<i>Arabidopsis thaliana</i>	acetylornithine aminotransferase	drought	17449808
28	NM_111527.2	NP_566285.1	<i>Arabidopsis thaliana</i>	beta-glucosidase-like SFR2	cold	11130713

29	NM_111953.2	NP_187727.1	<i>Arabidopsis thaliana</i>	omega-3 fatty acid desaturase	cold	16292565
30	NM_112418.3	NP_188169.1	<i>Arabidopsis thaliana</i>	NAC domain-containing protein 55	drought	15319476
31	NM_112681.3	NP_188427.2	<i>Arabidopsis thaliana</i>	phosphoethanolamine N-methyltransferase 1	temperature-sensitive	12215503
32	NM_112848.1	NP_188592.1	<i>Arabidopsis thaliana</i>	zinc-finger protein 2	drought;salt;cold	15333755
33	NM_113358.2	NP_189093.1	<i>Arabidopsis thaliana</i>	multiprotein-bridging factor 1c	drought;salt;heat	16244138
34	NM_113514.3	NP_189238.2	<i>Arabidopsis thaliana</i>	regulator of G-protein signaling 1	drought	21325279
35	NM_113586.3	NP_189309.2	<i>Arabidopsis thaliana</i>	transcription factor ICE1	cold	17416732
36	NM_114433.2	NP_190150.1	<i>Arabidopsis thaliana</i>	extracellular signal-regulated kinase 1/2	salt;cold	10717008
37	NM_115202.2	NP_190910.1	<i>Arabidopsis thaliana</i>	aquaporin PIP2-1	salt	18234664
38	NM_115410.3	NP_191112.1	<i>Arabidopsis thaliana</i>	E3 ubiquitin-protein ligase SDIR1	drought;salt	17573536
39	NM_115457.2	NP_191158.1	<i>Arabidopsis thaliana</i>	hypothetical protein	salt;cold	19061521
40	NM_115498.3	NP_191199.1	<i>Arabidopsis thaliana</i>	putative WRKY transcription factor 70	disease	14742872
41	NM_116260.3	NP_191946.1	<i>Arabidopsis thaliana</i>	cytochrome P450 86A2	drought;cold	15709153
42	NM_116730.5	NP_192401.5	<i>Arabidopsis thaliana</i>	SENSITIVE TO FREEZING 6; SFR6; TIJ1.2; TIJ1_2	drought;cold	19067974
43	NM_117099.5	NP_567354.1	<i>Arabidopsis thaliana</i>	sodium transporter HKT1	salt	19783197
44	NM_117896.2	NP_193521.1	<i>Arabidopsis thaliana</i>	abscisic acid receptor PYR1	drought	20713515
45	NM_118679.1	NP_567719.1	<i>Arabidopsis thaliana</i>	dehydration-responsive element-binding protein 1C	drought;cold	15173567
46	NM_118680.1	NP_567720.1	<i>Arabidopsis thaliana</i>	dehydration-responsive element-binding protein 1A	drought;salt	15834008
47	NM_118681.3	NP_567721.1	<i>Arabidopsis thaliana</i>	dehydration-responsive element-binding protein 1B	drought;cold	15173567
48	NM_118875.3	NP_567773.1	<i>Arabidopsis thaliana</i>	NAC domain-containing	drought	15319476

			<i>s thaliana</i>	protein 72		
49	NM_119329.3	NP_567882.1	<i>Arabidopsi s thaliana</i>	WRKY transcription factor 18	disease	16603654
50	NM_119562.4	NP_567949.1	<i>Arabidopsi s thaliana</i>	abscisic acid-insensitive 5-like protein 6	drought;cold	15834008
51	NM_120328.4	NP_195870.1	<i>Arabidopsi s thaliana</i>	heat shock 70kDa protein 1/8	drought;salt;cold	19443614
52	NM_120575.2	NP_568146.1	<i>Arabidopsi s thaliana</i>	phospholipid-transportin g ATPase 1	cold	11148289
53	NM_120623.2	NP_196160.1	<i>Arabidopsi s thaliana</i>	dehydration-responsive element-binding protein 2A	cold	19502356
54	NM_120894.4	NP_196429.1	<i>Arabidopsi s thaliana</i>	movement protein binding protein 2C	drought	19074626
55	NM_120946.4	NP_196476.1	<i>Arabidopsi s thaliana</i>	serine/threonine-protein kinase SRK2G	osmotic	21220313
56	NM_121157.1	NP_196680.1	<i>Arabidopsi s thaliana</i>	ethylene-responsive transcription factor SHINE 2	drought	15319481
57	NM_121371	NP_196872	<i>Arabidopsi s thaliana</i>	elongator complex protein 1	drought	16943431
58	NM_121601.2	NP_197100.1	<i>Arabidopsi s thaliana</i>	stress-induced protein KIN1	cold	17965713
59	NM_122448.3	NP_197921.1	<i>Arabidopsi s thaliana</i>	ethylene-responsive transcription factor SHINE 3	drought	15319480
60	NM_123392.1	NP_198844.1	<i>Arabidopsi s thaliana</i>	protein farnesyltransferase subunit beta	drought	16045476
61	NM_123683.2	NP_199131.1	<i>Arabidopsi s thaliana</i>	zinc-finger protein 3	drought;salt;cold	15333755
62	NM_124322.3	NP_199756.1	<i>Arabidopsi s thaliana</i>	basic leucine-zipper 1	drought;salt	21938515
63	NM_124486.2	NP_568750.1	<i>Arabidopsi s thaliana</i>	ERD1 protein	drought	17233795
64	NM_124578.1	NP_200012.1	<i>Arabidopsi s thaliana</i>	dehydration-responsive element-binding protein 1D	drought	12018849
65	NM_124610.2	NP_200044.1 ?	<i>Arabidopsi s thaliana</i>	low-temperature-respons ive protein 78/desiccation-responsiv e protein 29A	cold	12481097
66	NM_125276.2	NP_200694.1	<i>Arabidopsi s thaliana</i>	cytochrome P450 86A1	drought;cold	15709153

67	NM_125434.3	NP_200849.2	<i>Arabidopsis thaliana</i>	E3 SUMO-protein ligase SIZ1	drought	17905899
68	NM_125871	NP_201280	<i>Arabidopsis thaliana</i>	ethylene-responsive transcription factor ABR1	drought;salt	16227468
69	NM_126130.2	NP_201531.1	<i>Arabidopsis thaliana</i>	transcription factor MYB44	drought;salt	18162593
70	NM_126145.2	NP_201546.1	<i>Arabidopsis thaliana</i>	zinc-finger protein 1	drought;salt;cold	15333755
71	NM_126177.2	NP_565253.1	<i>Arabidopsis thaliana</i>	putative E3 ubiquitin-protein ligase RHA2B	drought	21478367
72	NM_126259.3	NP_178307.2	<i>Arabidopsis thaliana</i>	sodium/hydrogen exchanger 7		10823923
73	NM_127335.1	NP_565424.1	<i>Arabidopsis thaliana</i>	histidine kinase 1	submergence	18441212
74	NM_127721.3	NP_179744.1	<i>Arabidopsis thaliana</i>	dehydrin LEA	drought	21115661
75	NM_128597.2	NP_180603.2	<i>Arabidopsis thaliana</i>	thylakoidal processing peptidase 1	oxidative	19641031
76	NM_128704.1	NP_180705.1	<i>Arabidopsis thaliana</i>	F-box protein DOR	drought	18835996
77	NM_128898.3	NP_180896.1	<i>Arabidopsis thaliana</i>	caleosin-related protein	drought	20952421
78	NM_129637.2	NP_181607.1	<i>Arabidopsis thaliana</i>	WRKY DNA-binding protein 54	disease	22268143
79	NM_129815.4	NP_181782.1	<i>Arabidopsis thaliana</i>	cold-regulated protein 15a	cold	17293435
80	NM_129941.3	NP_181907.1	<i>Arabidopsis thaliana</i>	mitogen-activated protein kinase 6	salt;cold	10717008
81	NM_130160.2	NP_182121.1	<i>Arabidopsis thaliana</i>	cytochrome P450, family 86, subfamily A, polypeptide 8	drought;cold	15709153
82	NM_130287.2	NP_182241.1	<i>Arabidopsis thaliana</i>	myb domain protein 2	drought;cold	15173567
83	NM_179163.3	NP_849494.2	<i>Arabidopsis thaliana</i>	guanine nucleotide-binding protein subunit beta	drought	18541915
84	NM_179415.1	NP_849746.1	<i>Arabidopsis thaliana</i>	protein SENSITIVE TO PROTON RHIZOTOXICITY 1	acid	19704731
85	NM_179763.3	NP_850094.1	<i>Arabidopsis thaliana</i>	CBL-interacting serine/threonine-protein kinase 3	cold	12566581

86	NM_179974.3	NP_850305.2	<i>Arabidopsi s thaliana</i>	nuclear transcription factor Y subunit B-1	drought	17923671
87	NM_201737.2	NP_973466.1	<i>Arabidopsi s thaliana</i>	non-specific lipid-transfer protein 7	drought	16361524
88	NM_201929.2	NP_973657.1	<i>Arabidopsi s thaliana</i>	dehydration-induced protein ERD15	drought;cold	17056758
89	NM_202441.2	NP_974170.1	<i>Arabidopsi s thaliana</i>	serine/threonine-protein kinase SRK2C	drought	15561775
90	NM_001035635 .2	NP_001030712. 1	<i>Arabidopsi s thaliana</i>	myrosinase-binding-like protein	drought	17003050
91	NM_202837.1	NP_974566.1	<i>Arabidopsi s thaliana</i>	calcineurin B-like protein 1	drought;salt;cold	20113489
92	XM_002318580 .1	XP_002318616. 1	<i>Arabidopsi s thaliana</i>	calcium dependent protein kinase 10	drought	20805328

Supplementary Table 2. 94 stress-related miRNAs in *Arabidopsis thaliana*.

miRNAs_type	Mature_ miRNAs	miRNA_family	Sequence	Environmental stress factors	Reference
ath-miR156	ath-miR 156a	MIR156	UGACAGAAGAGAGUGA GCAC	High-salinity expressed;Putative UV-B responsive miRNA genes	Liu et al.,2008;Zhou et al. 2007
	ath-miR 156b	MIR156	UGACAGAAGAGAGUGA GCAC		
	ath-miR 156c	MIR156	UGACAGAAGAGAGUGA GCAC		
	ath-miR 156d	MIR156	UGACAGAAGAGAGUGA GCAC		
	ath-miR 156e	MIR156	UGACAGAAGAGAGUGA GCAC		
	ath-miR 156f	MIR156	UGACAGAAGAGAGUGA GCAC		
	ath-miR 156g	MIR156	CGACAGAAGAGAGUGA GCAC		
	ath-miR 156h	MIR156	UGACAGAAGAAAGAGA GCAC		
	ath-miR 156i	No annotation in Rfam	UGACAGAAGAGAGAGA GCAG		
	ath-miR 156j	No annotation in Rfam	UGACAGAAGAGAGAGA GCAC		
ath-miR157	ath-miR 157a	MIR156	UUGACAGAAGAUAGAG AGCAC	Drought-regulated;Putative UV-B responsive miRNA genes	Liu et al.,2008;Zhou et al.,2007
	ath-miR 157b	MIR156	UUGACAGAAGAUAGAG AGCAC		
	ath-miR 157c	MIR156	UUGACAGAAGAUAGAG AGCAC		

	ath-miR 157d	MIR156	UGACAGAAGAUAGAGA GCAC		
ath-miR158	ath-miR 158a	MIR158	UCCCAAAUGUAGACAA AGCA	High-salinity expressed	Liu et al.,2008
	ath-miR 158b	MIR158	CCCCAAAUGUAGACAA AGCA		
ath-miR159	ath-miR 159a	MIR159	UUUGGAUUGAAGGGAG CUCUA		
	ath-miR 159b	MIR159	UUUGGAUUGAAGGGAG CUCUU	Putative UV-B responsive miRNA genes;high-salinity regulated	Zhou et al. 2007;Liu et al.,2008
	ath-miR 159c	MIR159	UUUGGAUUGAAGGGAG CUCCU		
ath-miR165	ath-miR 165a	MIR166	UCGGACCAGGCUUCAU CCCC	Putative UV-B responsive miRNA genes;up-regulated by both high salinity and cold	Zhou et al.,2007;Liu et al.,2008
	ath-miR 165b	MIR166	UCGGACCAGGCUUCAU CCCC		
ath-miR166	ath-miR 166a	MIR166	UCGGACCAGGCUUCAU UCCCC		
	ath-miR 166b	MIR166	UCGGACCAGGCUUCAU UCCCC		
	ath-miR 166c	MIR166	UCGGACCAGGCUUCAU UCCCC		
	ath-miR 166d	MIR166	UCGGACCAGGCUUCAU UCCCC	Putative UV-B responsive miRNA genes	Zhou et al.,2007
	ath-miR 166e	MIR166	UCGGACCAGGCUUCAU UCCCC		
	ath-miR 166f	MIR166	UCGGACCAGGCUUCAU UCCCC		
ath-miR167	ath-miR 167a	MIR167_1	UGAAGCUGCCAGCAUG AUCUA		
	ath-miR 167b	MIR167_1	UGAAGCUGCCAGCAUG AUCUA	Putative UV-B responsive miRNA genes;high-salinity,drought regulated	Zhou et al.,2007;Liu et al.,2008
	ath-miR 167c	MIR167_2	UAAGCUGCCAGCAUGA UCUUG		
	ath-miR 167d	MIR167_1	UGAAGCUGCCAGCAUG AUCUGG		
ath-miR168	ath-miR 168a	MIR168	UCGCUUGGUGCAGGUC GGGAA	Putative UV-B responsive miRNA genes;response to high-salinity,drought-,cold-stress	Zhou et al. 2007;Liu et al.,2008
	ath-miR 168b	MIR168	UCGCUUGGUGCAGGUC GGGAA		
ath-miR169	ath-miR 169a	MIR169_2	CAGCCAAGGAUGACUU GCCGA	High-salinity,cold-regulated;Temperature-r esponsive miRNAs;Putative UV-B	Liu et al.,2008;Lee et

	ath-miR 169b	MIR169_2	CAGCCAAGGAUGACUU GCCGG	responsive miRNA genes	al.,2010;Zhou et al. 2007
	ath-miR 169c	MIR169_2	CAGCCAAGGAUGACUU GCCGG		
	ath-miR 169d	MIR169_2	UGAGCCAAGGAUGACU UGCCG		
	ath-miR 169e	MIR169_2	UGAGCCAAGGAUGACU UGCCG		
	ath-miR 169f	MIR169_2	UGAGCCAAGGAUGACU UGCCG		
	ath-miR 169g	MIR169_2	UGAGCCAAGGAUGACU UGCCG		
	ath-miR 169h	MIR169_1	UAGCCAAGGAUGACUU GCCUG		
	ath-miR 169i	MIR169_1	UAGCCAAGGAUGACUU GCCUG		
	ath-miR 169j	MIR169_1	UAGCCAAGGAUGACUU GCCUG		
	ath-miR 169k	MIR169_1	UAGCCAAGGAUGACUU GCCUG		
	ath-miR 169l	MIR169_1	UAGCCAAGGAUGACUU GCCUG		
	ath-miR 169m	MIR169_1	UAGCCAAGGAUGACUU GCCUG		
	ath-miR 169n	MIR169_1	UAGCCAAGGAUGACUU GCCUG		
	ath-miR 171a	MIR171_1	UGAUUGAGCCGCGCCA AUAUC		
ath-miR171	ath-miR 171b	MIR171_1	UUGAGCCGUGCCAAUA UCACG	Putative UV-B responsive miRNA genes;response to high-salinity,drought-,cold-stress	Zhou et al. 2007;Liu et al.,2008
	ath-miR 171c	MIR171_1	UUGAGCCGUGCCAAUA UCACG		
	ath-miR 172a	MIR172	AGAAUCUUGAUGAUGC UGCAU		
	ath-miR 172b	MIR172	AGAAUCUUGAUGAUGC UGCAU		
ath-miR172	ath-miR 172c	MIR172	AGAAUCUUGAUGAUGC UGCAG	Cold-regulated;Putative UV-B responsive miRNA genes	Liu et al.,2008;Zhou et al. 2007
	ath-miR 172d	MIR172	AGAAUCUUGAUGAUGC UGCAG		
	ath-miR 172e	MIR172	GGAUCUUGAUGAUGC UGCAU		
ath-miR319	ath-miR 319a	MIR159	UUGGACUGAAGGGAGC UCCCU	up-regulated by both high salinity and cold	Liu et al.2008

	ath-miR 319b	MIR159	UUGGACUGAAGGGAGC UCCCU		
	ath-miR 319c	MIR159	UUGGACUGAAGGGAGC UCCCU		
ath-miR393	ath-miR 393a	MIR393	UCCAAAGGGAUCGCAU UGAUCC	up-regulated by both high salinity and cold;Putative UV-B responsive	Sunkar and Zhu, 2004;Liu et al.2008
	ath-miR 393b	MIR393	UCCAAAGGGAUCGCAU UGAUCC		
ath-miR394	ath-miR 394a	MIR394	UUGGCAUUCUGUCCAC CUCC	High-salinity regulated	Liu et al.,2008
	ath-miR 394b	MIR394	UUGGCAUUCUGUCCAC CUCC		
	ath-miR 395a	MIR395	CUGAAGUGUUUGGGGG AACUC		
	ath-miR 395b	MIR395	CUGAAGUGUUUGGGGG GACUC	involved in sulfate and inorganic phosphate starvation	Jones-Rhoades and Bartel
ath-miR395	ath-miR 395c	MIR395	CUGAAGUGUUUGGGGG GACUC	responses;Regulation seed germination of Arabidopsis under salt or dehydration	2004; Fujii et al. 2005;Zhou
	ath-miR 395d	MIR395	CUGAAGUGUUUGGGGG AACUC	stress	et al. 2007;Kim
	ath-miR 395e	MIR395	CUGAAGUGUUUGGGGG AACUC	conditions;Putative UV-B responsive miRNA genes	et al.,2010
	ath-miR 395f	MIR395	CUGAAGUGUUUGGGGG GACUC		
ath-miR396	ath-miR 396a	MIR396	UUCCACAGCUUCUUG AACUG	response to	Liu et al.,2008
	ath-miR 396b	MIR396	UUCCACAGCUUCUUG AACUU	high-salinity,drought-,cold-stress	
	ath-miR 397a	MIR397	UCAUUGAGUGCAGCGU UGAUG	Regulated by different abiotic stress treatments;Cold-regulated	Liu et al.,2008;Sunkar and zhu,2004
	ath-miR 397b	MIR397	UCAUUGAGUGCAGCGU UGAUG		
	ath-miR 398a	MIR398	UGUGUUCUCAGGUCAC CCCUU	Expressed under	Sunkar et al.
ath-miR398	ath-miR 398b	MIR398	UGUGUUCUCAGGUCAC CCCUG	oxidative stress conditions;Putative UV-B responsive miRNA genes;Highly expressed	2006;zhou et al.,2011
	ath-miR 398c	MIR398	UGUGUUCUCAGGUCAC CCCUG	under phosphate starvation	
	ath-miR 399a	MIR399	UGCCAAAGGAGAUUUG CCCUG		Jones-Rhoades and Bartel
ath-miR399	ath-miR 399b	MIR399	UGCCAAAGGAGAGUUG CCCUG	Expressed under stress conditions	2004; Fujii et al. 2005;Bari
	ath-miR 399c	MIR399	UGCCAAAGGAGAGUUG CCCUG		et al , 2006; Chiou et al ,

	ath-miR 399d	MIR399	UGCCAAAGGAGAUUUG CCCCG		2006
	ath-miR 399e	MIR399	UGCCAAAGGAGAUUUG CCUCG		
	ath-miR 399f	MIR399	UGCCAAAGGAGAUUUG CCCCG		
ath-miR400	ath-miR 400	MIR400	UAUGAGAGUAUUUAAA GUCAC	Cold-regulated	Liu et al.,2008
ath-miR401	ath-miR 401	No annotation in Rfam	CGAAACUGGUGUCGAC CGACA	Putative UV-B responsive miRNA genes	Zhou et al. 2007
ath-miR402	ath-miR 402	MIR402	UUCGAGGCCUAUUAAA CCUCUG	Regulated by different abiotic stress treatments	Sunkar and zhu,2004
ath-miR408	ath-miR 408	MIR408	AUGCACUGCCUCUCCCC UGGC	Drought-,cold-regulated	Liu et al.,2008
ath-miR414	ath-miR 414	MIR414	UCAUCUUCAUCAUCAU CGUCA	Abscisic acid mediated signaling pathway, leaf senescence, response to abscisic acid stimulus, response to cold, response to salt stress, response to water deprivation	
ath-miR5021	ath-miR 5021	No annotation in Rfam	UGAGAAGAAGAAGAAG AAAA	High-affinity potassium ion import, proton transport, regulation of reactive oxygen species metabolic process, response to hydrogen peroxide, response to oxidative stress, response to reactive oxygen species, response to salt stress, sodium ion export, sodium ion transport	
ath-miR5658	ath-miR 5658	No annotation in Rfam	AUGAUGAUGAUGAUGA UGAAA		Newly identified
	ath-miR 854a	MIR854	GAUGAGGAUAGGGAGG AGGAG		
	ath-miR 854b	MIR854	GAUGAGGAUAGGGAGG AGGAG	Potassium ion transport, response to osmotic stress, response to salt stress, sodium ion export, sodium ion transport	
ath-miR854	ath-miR 854c	MIR854	GAUGAGGAUAGGGAGG AGGAG		
	ath-miR 854d	MIR854	GAUGAGGAUAGGGAGG AGGAG		
	ath-miR 854e	MIR854	GAUGAGGAUAGGGAGG AGGAG		

Note: The eight miRNAs found to be newly related with abiotic stress response were shown in gray mark.

Supplementary Table 3. The distribution of miRNA families in *Arabidopsis thaliana*.

Number	Family	miRNA	Copy Numbers	Family Members
1	MIPF0000008	MIR156	12	ath-miR156a, ath-MIR156b, ath-MIR156c, ath-MIR156d, ath-MIR156e, ath-MIR156f, ath-MIR156g, ath-miR156h, ath-MIR157a, ath-MIR157b, ath-miR157c, ath-MIR157d
2	MIPF0000035	MIR172	5	ath-MIR172a, ath-MIR172b, ath-miR172c, ath-MIR172d, ath-miR172e
3	MIPF0000294	MIR158	2	ath-miR158a, ath-miR158b
4	MIPF0000010	MIR159	6	ath-miR159a, ath-miR159b, ath-miR159c, ath-miR319a, ath-miR319b, ath-miR319c
5	MIPF0000004	MIR166	9	ath-miR165a, ath-MIR165b, ath-MIR166a, ath-MIR166b, ath-miR166c, ath-MIR166d, ath-MIR166e, ath-miR166f, ath-MIR166g
6	MIPF0000023	MIR167_1	3	ath-miR167a, ath-miR167b, ath-miR167d
7	MIPF0000125	MIR167_2	1	ath-miR167c
8	MIPF0000081	MIR168	2	ath-miR168a, ath-MIR168b
9	MIPF0000012	MIR169_1	7	ath-MIR169h, ath-MIR169i, ath-MIR169j, ath-MIR169k, ath-MIR169l, ath-MIR169m, ath-MIR169n
10	MIPF0000037	MIR169_2	7	ath-MIR169a, ath-MIR169b, ath-MIR169c, ath-miR169d, ath-MIR169e, ath-MIR169f, ath-miR169g
11	MIPF0000030	MIR171_1	3	ath-miR171a, ath-miR171b, ath-miR171c
12	MIPF0000083	MIR393	2	ath-miR393a, ath-miR393b
13	MIPF0000100	MIR394	2	ath-miR394a, ath-MIR394b
14	MIPF0000016	MIR395	6	ath-MIR395a, ath-MIR395b, ath-miR395c, ath-MIR395d, ath-miR395e, ath-MIR395f
15	MIPF0000047	MIR396	2	ath-miR396a, ath-miR396b
16	MIPF0000120	MIR397	2	ath-miR397a, ath-miR397b
17	MIPF0000107	MIR398	3	ath-miR398a, ath-miR398b, ath-miR398c
18	MIPF0000015	MIR399	6	ath-miR399a, ath-MIR399b, ath-MIR399c, ath-MIR399d, ath-MIR399e, ath-MIR399f
19	MIPF0001157	MIR400	1	ath-miR400
20	MIPF0001123	MIR402	1	ath-miR402
21	MIPF0000102	MIR408	1	ath-miR408
22	MIPF0000375	MIR414	1	ath-miR414
23	MIPF0000361	MIR854	5	ath-miR854a, ath-miR854b, ath-miR854c, ath-miR854d, ath-miR854e

Supplementary Table 4. The repeat sequences prediction in the pre-miRNA sequences.

MiRNA_Name	Matching_Position	Matching_Repeat	Repeat Class/Family
ath-miR156b	151-173	+ (TC) _n	Simple_repeat
ath-miR157c	121-147	+ (GA) _n	Simple_repeat
ath-miR167c	52-81; 60-82	+ AT_rich	Low_complexity

ath-miR169a	87-106	+ (T)n	Simple_repeat
ath-miR401	1-250	C Athila4B_LTR	LTR/Gypsy
ath-miR414	1-62	+ (CAT)n	Simple_repeat
ath-miR5658	2-21	+ (ATG)n	Simple_repeat
ath-miR854a	1-221	+ Athila6A_I-int	LTR/Gypsy
ath-miR854b	1-221	+ Athila6A_I-int	LTR/Gypsy
ath-miR854c	1-221	+ Athila6A_I-int	LTR/Gypsy
ath-miR854d	1-221	+ Athila6A_I-int	LTR/Gypsy
ath-miR854e	1-221	+ Athila6A_I-int	LTR/Gypsy

Supplementary Table 5. The CpG islands predicted in the upstream of miRNA genes.

MicroRNA	Islands_Numbers	Position	Obs/Exp ratio
ath-miR156a	1	1226..1441	1.19
ath-miR166b	1	1490..1921	1.08
ath-miR167b	1	1458..1817	0.83
ath-miR172e	1	475..871	1.35
ath-miR395d	1	92..291	0.87
ath-miR395e	1	1013..1270	0.91
ath-miR395f	1	1735..1941	1.00
ath-miR398a	1	691..984	1.12
ath-miR399a	1	50..267	1.30
ath-miR399c	1	1665..1942	1.44
ath-miR400	1	167..486	1.16
ath-miR408	1	448..805	0.82
ath-miR854b	1	887..1168	1.15
ath-miR854e	2	50..593	1.82
ath-miR854e		1590..1886	0.81
ath-miR5658	1	993..1294	0.98
ath-miR5021	1	1637..1918	0.80

Supplementary Table 6. The cis-acting regulatory element in the upstream of the stress-related miRNAs.

Cis-acting regulatory element	microRNAs
ABRE(involved in the abscisic acid responsiveness)	miR854b(1);miR5658(2);miR402(1);miR399d(1);miR399c(1);miR398a(1);miR395b(1);miR395a(1);miR393b(1);miR171c(1);miR169n(1);miR169l(1);miR169h(1);miR167c(1);miR167b(1);miR165a(1);miR156a(1);miR156d(1);miR156e(1);miR157a(1);miR157d(1);miR398c(2);miR169k(2);miR169g(2);miR156b(2);miR168a(3)
ARE(essential for the anaerobic induction)	miR5658(1);miR854d(1);miR854c(1);miR854a(1);miR414(1);miR402(1);miR399f(1);miR399d(1);miR398c(1);miR396a(1);miR395d(1);miR394b(1);miR393a(1);miR319c(1);miR172a(1);miR1

	71a(1);miR169k(1);miR169i(1);miR169g(1);miR169d(1);miR169b(1);miR168b(1);miR168a(1); miR167b(1);miR166g(1);miR166f(1);miR166c(1);miR165b(1);miR159a(1);miR156c(1);miR156 d(1);miR156f(1);miR156h(1);miR157a(1);miR157b(1);miR157c(1);miR854b(2);miR401(2);miR 397b(2);miR395f(2);miR395e(2);miR393b(2);miR319b(2);miR319a(2);miR172e(2);miR172d(2); miR169j(2);miR169f(2);miR169e(2);miR167c(2);miR167a(2);miR166e(2);miR166d(2);miR165a (2);miR156b(2);miR157d(2);miR5021(3);miR399e(3);miR398b(3);miR169c(3);miR169a(3);miR 159b(3);miR156a(3);miR400(4);miR397a(4);miR172c(4);miR171c(4);miR159c(4);miR171b(7) miR854b(1);miR397b(1);miR393a(1);miR319a(1);miR172e(1);miR172a(1);miR171a(1);miR166 b(1);miR158b(1);miR156g(1);miR399f(2);miR168b(2);miR166a(2)
as-2-box (involved in shoot-specific expression and light responsiveness)	
AuxRR core (Auxin)	miR172a(1);miR167d(1)
Box W1 (Fungal elicitor)	miR854b(1);miR400(1);miR399e(1);miR399c(1);miR399b(1);miR399a(1);miR396b(1);miR395c (1);miR395b(1);miR395a(1);miR319a(1);miR172e(1);miR172b(1);miR171a(1);miR169m(1);mi R169i(1);miR169g(1);miR169f(1);miR169d(1);miR169a(1);miR159c(1);miR159b(1);miR159a(1);miR158b(1);miR156g(1);miR157d(1);miR398a(2);miR396a(2);miR395f(2);miR395e(2);miR39 3b(2);miR319b(2);miR169h(2);miR166d(2);miR158a(2);miR156c(3);miR408(4) miR854c(1);miR854a(1);miR408(1);miR402(1);miR399e(1);miR398c(1);miR396a(1);miR319b(1);miR172d(1);miR171c(1);miR171b(1);miR171a(1);miR169c(1);miR166e(1);miR166d(1);miR1 66b(1);miR166a(1);miR165b(1);miR156d(1);miR157b(1);miR157d(1);miR5658(2);miR5021(2); miR399f(2);miR399d(2);miR399c(2);miR397a(2);miR396b(2);miR394b(2);miR394a(2);miR172 e(2);miR172c(2);miR172b(2);miR169l(2);miR169j(2);miR169d(2);miR159a(2);miR158b(2);miR 156b(2);miR156g(2);miR158a(2);miR393b(3);miR169k(3);miR156h(3);miR165a(5)
CGTCA motif (involved in the MeJA-responsiveness)	
DRE (cis-acting element involved in dehydration, low-temp, salt stresses)	miR158b(1)
ERE (Ethylene)	miR402(1);miR399f(1);miR399b(1);miR396b(1);miR396a(1);miR395f(1);miR395e(1);miR169g(1);miR169e(1);miR169d(1);miR166b(1);miR165a(1);miR157c(1);miR393a(2)
GAG-motif (part of a light responsive element)	miR5658(1);miR5021(1);miR408(1);miR402(1);miR401(1);miR400(1);miR399f(1);miR399c(1); miR396a(1);miR395d(1);miR393b(1);miR319b(1);miR172a(1);miR169n(1);miR169f(1);miR169 c(1);miR169b(1);miR167c(1);miR167b(1);miR166f(1);miR166e(1);miR166b(1);miR166a(1);mi R159b(1);miR156c(1);miR399e(2);miR395c(2);miR394b(2);miR319a(2);miR171a(2);miR169j(2);miR169h(2);miR168a(2);miR165b(2);miR165a(2);miR158b(2);miR156d(2);miR157c(2)
GA-motif (part of a light responsive element)	miR402(1);miR400(1);miR399f(1);miR399d(1);miR397a(1);miR395c(1);miR394a(1);miR319c(1);miR319b(1);miR172e(1);miR171c(1);miR169j(1);miR169i(1);miR169h(1);miR169c(1);miR16 8a(1);miR167d(1);miR167b(1);miR166f(1);miR166d(1);miR166c(1);miR166b(1);miR165a(1);mi R156a(1);miR156f(1);miR157d(1);miR158a(1);miR398c(2);miR395b(2);miR401(3);miR158b(3) miR854b(1);miR414(1);miR408(1);miR399c(1);miR399b(1);miR395d(1);miR395b(1);miR395a(1);miR394b(1);miR394a(1);miR393b(1);miR393a(1);miR319b(1);miR172e(1);miR169l(1);miR1 69k(1);miR169d(1);miR169a(1);miR167a(1);miR166f(1);miR166e(1);miR166c(1);miR166b(1); miR165a(1);miR156a(1);miR156e(1);miR156g(1);miR157a(1);miR157b(1);miR157c(1);miR157 d(1);miR158a(1);miR5658(2);miR402(2);miR399d(2);miR172d(2);miR172a(2);miR159a(2);miR 156b(2);miR156c(2);miR156d(2);miR399f(3);miR400(5)
GARE motif (GA)	

G-Box (involved in light responsiveness)	miR5658(1);miR414(1);miR402(1);miR399f(1);miR399e(1);miR399c(1);miR398a(1);miR395a(1);miR394a(1);miR319b(1);miR319a(1);miR169n(1);miR169g(1);miR169d(1);miR168b(1);miR167c(1);miR167a(1);miR166e(1);miR166c(1);miR165b(1);miR165a(1);miR159a(1);miR156d(1);miR156h(1);miR157b(1);miR157d(1);miR158a(1);miR399d(2);miR398c(2);miR395b(2);miR393b(2);miR167d(2);miR156e(2);miR157a(2);miR168a(4)
G-box (involved in light responsiveness)	miR414(1);miR399f(1);miR399e(1);miR398a(1);miR395f(1);miR395e(1);miR394a(1);miR319b(1);miR319a(1);miR172e(1);miR172b(1);miR171a(1);miR169i(1);miR169b(1);miR169a(1);miR168b(1);miR167d(1);miR167a(1);miR166g(1);miR166f(1);miR166c(1);miR159a(1);miR156a(1);miR156d(1);miR156h(1);miR157b(1);miR5658(2);miR402(2);miR399d(2);miR399c(2);miR398c(2);miR397b(2);miR395a(2);miR171c(2);miR169n(2);miR169k(2);miR169g(2);miR166b(2);miR165b(2);miR165a(2);miR156b(2);miR157d(2);miR395b(3);miR393b(3);miR169l(3);miR167c(3);miR156e(3);miR157a(6);miR168a(7)
HSE (involved in heat stress responsiveness)	miR854b(1);miR414(1);miR399f(1);miR399b(1);miR399a(1);miR397b(1);miR397a(1);miR396a(1);miR395c(1);miR393a(1);miR172c(1);miR171a(1);miR169n(1);miR169m(1);miR169j(1);miR169i(1);miR169f(1);miR169e(1);miR168b(1);miR167d(1);miR167a(1);miR166e(1);miR166d(1);miR165a(1);miR156f(1);miR158a(1);miR395d(2);miR171c(2);miR169k(2);miR169g(2);miR159a(2);miR157a(2);miR157d(2);miR398b(3);miR395b(3);miR395a(3);miR156b(3);miR157b(3);miR156a(4)
LTR (involved in low-temperature responsiveness Low temperature)	miR5658(1);miR399f(1);miR397b(1);miR396a(1);miR395f(1);miR395e(1);miR319b(1);miR171c(1);miR169h(1);miR169f(1);miR169d(1);miR169c(1);miR169b(1);miR167a(1);miR166e(1);miR166b(1);miR165b(1);miR156a(1);miR156b(1);miR156d(1);miR156f(1);miR157d(1);miR158a(2)
MBSI (MYB binding site involved in flavonoid biosynthetic genes regulation)	miR399e(1);miR395b(1);miR395a(1);miR156a(1);miR156b(1)
MBS (Drought)	miR5021(1);miR854c(1);miR408(1);miR401(1);miR399c(1);miR395d(1);miR395c(1);miR393b(1);miR319b(1);miR319a(1);miR172c(1);miR172b(1);miR169j(1);miR169i(1);miR169f(1);miR169a(1);miR167d(1);miR167b(1);miR167a(1);miR166f(1);miR166d(1);miR165b(1);miR159b(1);miR156g(1);miR156h(1);miR157a(1);miR157b(1);miR157c(1);miR157d(1);miR854d(2);miR854b(2);miR854a(2);miR402(2);miR399e(2);miR399d(2);miR396a(2);miR171c(2);miR169n(2);miR169m(2);miR169h(2);miR166b(2);miR165a(2);miR159c(2);miR159a(2);miR158a(2);miR168b(3);miR395f(4);miR395e(4)
MRE (MYB binding site involved in light responsiveness)	miR854c(1);miR854a(1);miR401(1);miR398a(1);miR393a(1);miR169h(1);miR169c(1);miR169a(1);miR167c(1);miR167b(1);miR167a(1);miR166d(1);miR159b(1);miR158b(1);miR156a(1);miR156c(1);miR157d(1);miR395c(2);miR396a(3)
P box(GA)	miR854b(1);miR414(1);miR398b(1);miR169h(1);miR169g(1);miR167b(1);miR167a(1);miR166c(1);miR166b(1);miR159c(1);miR158b(1);miR156a(1);miR156b(1);miR169j(2);miR169i(2)
TCA element(involved in salicylic acid responsiveness)	miR854b(1);miR414(1);miR408(1);miR399f(1);miR399d(1);miR398c(1);miR397b(1);miR396b(1);miR395d(1);miR395c(1);miR395b(1);miR395a(1);miR319c(1);miR171b(1);miR169m(1);miR169i(1);miR169f(1);miR169e(1);miR169d(1);miR168b(1);miR167d(1);miR167a(1);miR166d(1);miR166c(1);miR166a(1);miR165b(1);miR159b(1);miR159a(1);miR158b(1);miR156c(1);miR156f(1);miR156g(1);miR157a(1);miR158a(1);miR402(2);miR398b(2);miR393a(2);miR169j(2);miR167c(2);miR166g(2);miR165a(2);miR156d(2);miR157b(2);miR157d(2);miR319a(3);miR169k(3);miR168a(3);miR167b(3);miR166e(3);miR398a(4);miR171a(4);miR169n(4);miR169l(4)

TC-rich repeat(involved in defense and stress responsiveness)	miR5658(1);miR5021(1);miR414(1);miR402(1);miR399d(1);miR399c(1);miR399b(1);miR398c(1);miR398a(1);miR397a(1);miR396a(1);miR395d(1);miR394b(1);miR319b(1);miR172a(1);miR171c(1);miR169l(1);miR169k(1);miR169c(1);miR169a(1);miR167d(1);miR167a(1);miR166g(1);miR166a(1);miR165b(1);miR165a(1);miR159b(1);miR156b(1);miR157a(1);miR157d(1);miR397b(2);miR396b(2);miR393b(2);miR172e(2);miR172c(2);miR172b(2);miR171b(2);miR171a(2);miR169n(2);miR169m(2);miR169h(2);miR169g(2);miR168a(2);miR166b(2);miR156a(2);miR156e(2);miR156f(2);miR156g(2);miR157b(2);miR157c(2);miR399f(3);miR395b(3);miR395a(3);miR398b(4);miR158b(4)
TGA element(Auxin)	miR408(1);miR400(1);miR399d(1);miR397b(1);miR395d(1);miR395c(1);miR395b(1);miR395a(1);miR393a(1);miR172b(1);miR171a(1);miR169m(1);miR169a(1);miR168b(1);miR166g(1);miR156a(1);miR156c(1);miR156g(1);miR156h(1);miR157a(1);miR397a(2)
TGACG motif(MelA)	miR854c(1);miR854a(1);miR408(1);miR402(1);miR399e(1);miR398c(1);miR396a(1);miR319b(1);miR172d(1);miR171c(1);miR171b(1);miR171a(1);miR169c(1);miR166e(1);miR166d(1);miR166b(1);miR166a(1);miR165b(1);miR156a(1);miR156d(1);miR157b(1);miR157d(1);miR5658(2);miR5021(2);miR399f(2);miR399d(2);miR399c(2);miR397a(2);miR396b(2);miR394b(2);miR394a(2);miR172e(2);miR172c(2);miR172b(2);miR169l(2);miR169j(2);miR169d(2);miR159a(2);miR158b(2);miR156b(2);miR156g(2);miR156h(2);miR158a(2);miR393b(3);miR169k(3);miR165a(5)

Note: The numbers in the bracket represent the number of the predicted cis-acting regulatory element upstream the stress-related miRNAs.

Supplemenatry Table 7. 14 *Arabidopsis thaliana* miRNA targets involved in 26 pathways.

miRNA ID	Gene ID	Gene Name	KEGG_PATHWAY
ath-miR159a/b/c	AT4G37770	1-aminocyclopropane-1-carboxylate synthase 8	ath00270:Cysteine and methionine metabolism; ath01070:Biosynthesis of plant hormones;
ath-miR414	AT5G39740	60S ribosomal protein L5-2	ath03010:Ribosome
ath-miR854a/b/c/d/e	AT1G08065	alpha carbonic anhydrase	ath00910:Nitrogen metabolism
ath-miR171a	AT3G05530	regulatory particle triple-A ATPase RNA binding	ath03050:Proteasome
ath-miR395a/d/e	AT3G45630	(RRM/RBD/RNP motifs) family protein Pseudouridine synthase/archaeosine	ath03018:RNA degradation ath00230:Purine metabolism;
ath-miR395a/d/e	AT4G14680	transglycosylase-like family protein	ath00450:Selenoamino acid metabolism; ath00920:Sulfur metabolism
ath-miR395a/b/c/d/e/f	AT5G13630	magnesium-chelatase subunit chlH, chloroplast	ath00860:Porphyrin and chlorophyll metabolism

ath-miR395a/b/c/ d/e/f	AT5G43780	APS4	ath00230:Purine metabolism; ath00450:Selenoamino acid metabolism; ath00920:Sulfur metabolism;
ath-miR414	AT5G57580	Calmodulin-binding protein	ath04070:Phosphatidylinositol signaling system
ath-miR396a/b	AT5G57590	adenosylmethionine-8-amino -7-oxononanoate transaminases	ath00780:Biotin metabolism
ath-miR397a/b	AT3G60250	Casein kinase II subunit beta-3	ath04712:Circadian rhythm
ath-miR5658	AT2G36460	Fructose-bisphosphate aldolase	ath00010:Glycolysis / Gluconeogenesis; ath00030:Pentose phosphate pathway; ath00051:Fructose and mannose metabolism; ath00710:Carbon fixation in photosynthetic organisms; ath01061:Biosynthesis of phenylpropanoids; ath01062:Biosynthesis of terpenoids and steroids; ath01063:Biosynthesis of alkaloids derived from shikimate pathway; ath01064:Biosynthesis of alkaloids derived from ornithine, lysine and nicotinic acid; ath01065:Biosynthesis of alkaloids derived from histidine and purine; ath01066:Biosynthesis of alkaloids derived from terpenoid and polyketide; ath01070:Biosynthesis of plant hormones;
ath-miR159b	AT4G15530	Pyruvate, phosphate dikinase 1, chloroplastic	ath00620:Pyruvate metabolism; ath00710:Carbon fixation in photosynthetic organisms ath00020:Citrate cycle (TCA cycle); ath00640:Propanoate metabolism; ath01061:Biosynthesis of phenylpropanoids; ath01062:Biosynthesis of terpenoids and steroids; ath01063:Biosynthesis of alkaloids derived from shikimate pathway;
ath-miR171b/c	AT5G23250	Succinyl-CoA ligase [GDP-forming] subunit alpha-2, mitochondrial	ath01064:Biosynthesis of alkaloids derived from ornithine, lysine and nicotinic acid; ath01065:Biosynthesis of alkaloids derived from histidine and purine; ath01066:Biosynthesis of alkaloids derived from terpenoid and polyketide; ath01070:Biosynthesis of plant hormones;